

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0001	contig31566	GTT	3	12	TGTTGGAATAGTGGTTGATTCGG	62.932	AGCGATCTAACTTGGACTCAATGC	63.051	100
HM_0002	contig16009	TGT	3	21	CGAGATCTAGGAAgCACCATCtG	63.128	TCaACCTCATGCTCACCTACTCta	63.265	89
HM_0003	contig01096	AAG	3	12	AGTTGGAACTGGGACTACTGATGC	62.925	CAAGAACCTACCTCTCTCATTGAA	62.782	157
HM_0004	contig46492	TCA	3	12	ATTTTAGTCTCTCCAGAAAAATCg	62.888	TCGATCAGAAAGCAAGGAAAGaG	63.214	160
HM_0005	contig10748	TGT	3	15	TTCACCCGTGGTACAATTTCTCT	63.019	CGAGAAATTTTCAAAITTCAGCTC	62.533	141
HM_0006	contig19898	TGA	3	12	GGATGGTGTGCGAGAAAGGCTACTA	62.923	TCTGGACTTCTTACTCTTCCGCTC	62.497	130
HM_0007	contig02757	CTA	3	12	GTTCTCCCGCACTTGTtTctATG	63.239	ACGCAAGAAACAGAACTCTTCAAG	63.245	126
HM_0008	contig37674	CTG	3	12	ATAACACCTTCCCGATTTCCATTC	63.376	GGCAGAGCGTTAGCAGTAGCAGTA	64.211	160
HM_0009	contig34175	TCG	3	12	CTCTCTCCtGGTCTTgCTCTCaTc	62.898	TTCTCGAGATGAGTTCGGAGATTt	62.686	154
HM_0010	contig23826	CCT	3	12	AaAGCTGGAGTtCGcCAAGAG	62.923	GGCTAGGATAGGGAGATGCAGATA	62.83	145
HM_0011	contig18883	GGT	3	15	TCATTGATGATTTCTcCGGCTAGT	63.223	TGAAGTGTATGCGACCATCAITCT	62.951	153
HM_0012	contig51104	CGT	3	15	AATGGGGACTTCCATCATCAATTC	64.303	GGTGTCaAAATACGcCGCAATTAC	64.59	125
HM_0013	contig47077	AGG	3	18	TCTGGCATTGGTCTTTACATAGA	63.038	TAAGCGTTGGTGACCTTCTTCTTC	63.031	159
HM_0014	contig10977	TCA	3	12	TTAcCTGGATACCATTCGATCTCC	62.482	TTGACAATCCCaAAGGTTTTAAGC	62.532	154
HM_0015	contig44435	GAG	3	18	CTTCAAGCATTCaCAGCTCACAC	63.173	CcAACAACCACTCTCTCTCTGA	62.906	109
HM_0016	contig29161	TTG	3	12	cAaCCCCtTCTCTTtCAACT	62.968	TTTGTGCTTTAATCTgtTTGGGT	62.932	124
HM_0017	contig11328	GAA	3	12	GGAAAAGAGACTTACCCTGAATGG	62.299	GTTGCTCGTGTGCAATaGAAAGAA	62.772	154
HM_0018	contig02208	CGA	3	12	CAATCCTTGGTGGTtTAAGTCATC	63.009	ATATTGGCTGTATGCTGTATTCGC	63.373	155
HM_0019	contig14520	ATC	3	12	CTTTTtCATTCTCTGCGAAATtGG	63.216	AGCCAGCATCTGTTAAAGCGAAC	63.171	83
HM_0020	contig50106	TGA	3	12	AaCACTCCAATTTGGcAGTCCtTa	63.121	TGCAAAcCTCCCTTTtATTCTTGA	63.109	101
HM_0021	contig48344	TCC	3	12	CAGCCGTCCAATTTGATCTCTTCT	62.923	CCATAAAGGTGACCCGAAGTACAC	62.921	143
HM_0022	contig36424	CCA	3	15	AACCACTCcAAACCtAATcACAA	62.907	CtTTAGTGGTTTGGGGAGCTAGG	63.379	153
HM_0023	contig22620	AGA	3	12	ATAGACCGCTGATGATAGAGCTTGG	63.048	GTTCAAACTCGATCCCAACAACCTTC	63.013	141
HM_0024	contig21081	GCT	3	12	AACCAATTtGAGGTGAAAGGAACAA	63.006	ATTGCACCATGtGtGtGATATGTA	63.275	159
HM_0025	contig28509	CCA	3	18	CATGAGACCAAGAAcATCGAagAT	63	GTGAGATTtTtGAGGTATGCAGGCT	62.94	160
HM_0026	contig04543	GAT	3	15	GAAAGCGATGGGGTtGTGAATaA	63.233	TTAAGAAAGGCCATACAGCAGAA	63.228	105
HM_0027	contig18836	CAC	3	18	ATCCCCAAaTagAATCAACCACT	62.974	ATGAGAAAACagGTGCAAAATGGT	63.035	155
HM_0028	contig12441	CAC	3	12	ATTTCTCCCTTAAATCTCTCTCTC	63.029	TGATTGGAGGATTtTtTGAGAGCG	63.743	153
HM_0029	contig38911	GAT	3	12	CGAGCTCGAACAAGATTAACACAA	62.969	TGCCTTGAATAGGAATGACACtCA	63.038	156
HM_0030	contig21467	GGT	3	12	CTTACTTGGGgAGGGTACAGCAAT	63.791	AACCTTCTCCAGCAACAACAACCT	62.922	106
HM_0031	contig01551	CAC	3	24	TGGGTGTTTGTGGGAGTAGTtGTA	62.723	TGAAGTTTCTtGAGTgAGTCTGTG	62.93	134
HM_0032	contig01642	ACT	3	12	ATTGATTTTTCTGGGATCGACTGA	63.099	tATTGaAAAGCTgATCCCATCGAG	63.62	159
HM_0033	contig09809	TCT	3	15	ACTCGGAAGTATTCTGTATCTGG	63	AGACAcCAACAACTGATGCTTGA	63.173	94
HM_0034	contig28998	AGC	3	12	TTGGTAGGTTcAGCTTCTCTGTCT	62.835	AAGAAATcCTCCCAAGAGTGAC	63.071	134
HM_0035	contig38948	GGT	3	18	GTGCTTcGAGATGTAGAATTtGGC	63.248	CCAAACACAATGAAGAAGAAAGCaG	62.31	159
HM_0036	contig35244	CTT	3	12	GTGcATCAGATTtGcGaGTAGTAT	62.759	GTAAGCCGATCGAAGTACTGATT	62.94	140
HM_0037	contig06669	TCT	3	12	GTGATGAGATTAGCAAAAGCTGCG	63.576	TTCTAcCCAAGATCAAGTTGAGGG	62.782	131
HM_0038	contig16648	GGT	3	12	GCTTGAATTCTACTCCACGGTGT	62.838	CACAACATCTCAATCTCTCCAAT	63.419	100
HM_0039	contig02468	CCA	3	12	TGAACAGCAAGCAATTCAAGGATA	63.059	GTGGAGCTGAAACTGTTGTtGTTG	63.181	145
HM_0040	contig38744	CAT	3	12	ATGATGTTCAACAAGATCGCAAA	62.848	TGGCTTAGGATTCTCAATGGATAAG	62.506	129
HM_0041	contig49457	GCC	3	15	CGTGATCTCCaAcTCTTCTTGAT	63	AGCTGCCCGGATTtAcCTATTTT	63.2	154
HM_0042	contig02334	TCT	3	12	TTGAATCCGATATCGATCTCTCTG	61.735	TcTGTGTCAAGAGACTGAAACTTGC	62.201	135
HM_0043	contig02493	AGA	3	24	GCTGACCAAACTCTAGTGTAGTTG	62.562	GCGGTACGGTCTCGTCTCTATC	63.459	160
HM_0044	contig44645	TTT	3	12	AGGCCTCTGTCTCACTCCTCTGA	63.015	CCTGCCACTACTGCAATATAAGGG	63.039	137
HM_0045	contig18955	GTG	3	12	GGAGGGGAAACACCTATGACAGATT	62.794	CAATCCACCACTTCCACAATC	62.092	105
HM_0046	contig23746	TCC	3	15	TCGACATCGACTtGTTGTtAATG	63.265	GAAGGGAAgGaAGGAATATCATCG	63.259	120
HM_0047	contig19987	TCA	3	12	AGTTTTCTCTGAGAGGCTCGGAAT	62.986	GCTGCTgGaCTTGAAGATTCTGAT	63.247	145
HM_0048	contig11596	CGA	3	12	GATCATCAAACTGATCCCTCGTCT	62.89	TTTACGACGACGACATTGACATTt	62.758	150
HM_0049	contig07826	CCT	3	15	CCACTGTGCAAACTCCGTAGTAAT	63.348	GAAGAGTCTTTTGGGGAAAGAA	63.062	145
HM_0050	contig41069	ATG	3	12	TCAAGGGAGTGAACATTATCACCA	62.803	GCCATCATGAAATtAGTTTCCACC	62.817	151
HM_0051	contig02188	TAC	3	12	AaAGTGCCTAaCCaAcACTCCaA	63.129	GTAATAATCTCGCGCTTCTCTGAA	63.043	135
HM_0052	contig16057	TCT	3	12	CATACCTTGGCTAAATCTCTGCG	62.945	TTGAGGAAGAAATCGAAGTgGAAG	62.993	158
HM_0053	contig13763	GAA	3	15	CTTTGcCCCGGATTcATGTTTTAC	62.813	CAAGAAAGCAATTCTCGAGTCCCT	63.215	88
HM_0054	contig37551	GGC	3	12	ATGCAAAATTCACATCACTCTGAC	62.504	GGTTATCAGACCAAGTGGGTATGGA	63.318	141
HM_0055	contig46159	GAG	3	15	GAACCAATGGCACACTTCCATATC	63.762	TCATAGAACTTCTCTTTCagTGCC	63.222	151
HM_0056	contig19224	ATC	3	12	CCGAGGATGCAACAGGTACTCTACT	63.036	GACGACCTAGTtACGATTGTGACAG	62.236	121
HM_0057	contig39910	AGT	3	15	TTTGTGAACAGGGAATCATGGgA	63.206	CTTGACTTGGGtGTGCTAGTtTG	62.955	140
HM_0058	contig06141	AGG	3	12	CCAGGAGGATTtTGGGAACTAGC	63.278	TCACATCTTCTCTCTCCGCTCT	62.782	135
HM_0059	contig01526	TCA	3	12	AAAGGGAGCAGAAAGTGGgTAAC	63.005	AATTATCAGCCGACTTCTAGCTGC	62.744	98
HM_0060	contig29391	GAA	3	12	GgcTtAATTTTACgAGGGAGATGG	63.187	AAGTACTGACTGAAACACTGGGG	62.805	144
HM_0061	contig12294	TGA	3	15	TGACATTGCAATTCaAGTACCTCT	63.009	TCATTCACTaCAAGGCTcACGCT	62.741	143
HM_0062	contig36796	GGA	3	12	TGAGGAAGAGTACAGCTTGAAGA	62.997	AGAATTGATCAAGTTGAAACCCC	63.578	137
HM_0063	contig24706	TAC	3	15	CTGAAGCAATTtGAAGAAcAAGGGT	62.921	GTGGTGGTGGAGGAACATAGACAT	63.449	124
HM_0064	contig23579	ATC	3	12	AGACCCAATGATCTCGAATCTCTC	63.007	AAGCAGTAGTtTCGGCAAAATGAAG	62.957	158
HM_0065	contig39568	GTG	3	15	gCCTCTTGAGCTTGGAAATCTCTGA	63.125	GTAACAACAGAGTCAACCGCTACC	63.263	96
HM_0066	contig34923	CAT	3	12	AGGGTTTTGGTGTGATTGTtGTT	62.822	AGTGGTAGCAATGGGCTTATGTGT	63.06	126
HM_0067	contig39980	CAT	3	18	TTCCAACATCCCTATCTCCACATT	62.887	AAGGCGAGAAGGAGAGTGAAGATT	63.096	87
HM_0068	contig28329	TTC	3	30	CcATTTCATCTATCTTCACTGCC	63.112	GaAAAGAAAGAAATTTtGGGGAA	62.863	160
HM_0069	contig15666	TGG	3	21	GGTGGCTGAGTGGAGACTGACTA	64.118	CaAAAcCCCTAGTGTCTCATCCAC	64.09	142
HM_0070	contig49352	TCT	3	18	AAGGAAAAaGCATCCAGTACCTTC	62.995	GCTTCAACCGATCTTAATCCTCTT	63.093	124
HM_0071	contig13444	TGC	3	12	GAAACCGtGACCTCAACTTTTTGG	63.125	CTTGGCCTAtGGTTTGTCTCTTA	62.932	125
HM_0072	contig27013	TCT	3	24	TGTGAGTGAGTGGCATAACGATT	63.078	TCAATATTCATGTCTCTGaTGC	62.501	155
HM_0073	contig38335	CCA	3	18	GGCATGTAGGCCACTATCAAC	63.723	GATTTCATAGGGCTTtGtCTGGGT	62.995	143
HM_0074	contig21039	AGA	3	15	AGCTGCAGCAATTtCCCAaA	63.045	GAAGTGAACCACTCTTCTTCCAA	62.997	94
HM_0075	contig36561	TGG	3	18	TGATCGATATTGTAGGgTTTTGCT	62.925	CAGTCATCGGAACCTCATCG	62.891	160
HM_0076	contig12565	TAT	3	12	CAAGaGATGATCAGGGTTCaAAT	62.672	gaCAGaGcGtTtTtTtTtTtTtTtTt	62.712	158
HM_0077	contig10671	CAT	3	12	ATGAGTGAGTGCATCCtGTAAACC	62.68	TGCTACTAGTTTTGCTCTGTCCTC	62.933	152
HM_0078	contig03695	TCT	3	24	TAATTCAGACCACTCTTCACTCT	62.368	aAGTTGAAGAGAGAAAGGGAACCG	63.28	160
HM_0079	contig13240	GTG	3	12	TCCAGCATCTCTTTATCTTCTGTTT	62.063	AGTGTAAACAACCTTCTGCAACCCC	62.737	151
HM_0080	contig15629	CAG	3	15	GCAAAATGCATCTCACAGATTcAGA	63.723	AGAAATGCCCTTTTCACTCGAGATT	64.426	91
HM_0081	contig00416	GTG	3	18	CGATTCCATTACCATTTTCTTCCG	63.014	CAACTCAATCTCAGTtCTCTTg	63.527	154
HM_0082	contig19688	GGC	3	12	GTGGCGTGGGATAGTTTTATACG	62.759	CCAGCGCGGTACTACTACTCT	63.055	108
HM_0083	contig23789	CCA	3	15	TGAGCAACAAATCCGTAACCTCT	63.239	GATTGGAAGGTTTCAAACTCAA	62.619	142
HM_0084	contig10506	CTT	3	12	GGAACAACCTGAAATCTTGTCTCT	62.809	CAAAACAGAGTCTCTGATGGAGAA	62.919	158
HM_0085	contig22363	TCG	3	12	CTGTTTCAACATCTCACACAATCC	62.922	GTTCTCCGATGTATTCAAACTGC	63.137	157
HM_0086	contig51205	ACG	3	15	ACAACACCCCTACCTCCATAATC	63.386	ACCTCTGCTTCTcGTGATAGT	62.837	116
HM_0087	contig23212	ATC	3	15	ACGTTCTGTGACGTcAGAAATAGAT	63.255	ATGGAACCTTTCaCTTCCCAATC	63.578	148
HM_0088	contig40626	AAT	3	18	GCACCTATGtGGcAaTGTTATTA	62.062	CAAAATGAGGTCTATCAACCGAGA	61.656	160
HM_0089	contig30383	TCA	3	12	GGTCATCTTCCACTTGGTGAGGT	62.925	TCAAGCATACCAATCAAAACCTCT	62.922	102
HM_0090	contig26832	CAC	3	18	GGTGCTCTCTTCCACTTCACT	62.179	GGACGATaATAACAACACCGTCT	62.95	122
HM_0091	contig21420	ACA	3	12	GAGTTGTGGCATAACAATAAaGG	62.935	TGGATTCAATaATAACCGAATGGC	63.02	97
HM_0092	contig09296	TCT	3	21	TcTACAGTGAAGCaTAATATGTGgA	62.289	CTTATCGCGCTTAATCAAGCTGTG	63.134	143
HM_0093	contig43289	ATC	3	12	TTCTACAgTGGGCACTATTCCACC	63.329	aAGTAATTTTTCCCGCTCTTGTG	63.476	132
HM_0094	contig14768	CTC	3	15	GCCaCAAACTCTCAAAACATA	62.426	TGAACAGGTTGGTGCAGACTGAA	62.916	160
HM_0095	contig06643	TGA	3	15	TACtCTCTTTCTGGTTCTGGTGG	62.993	CAAGGGCTCAATGAACCATCAA	62.552	156

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SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0096	contig39949	TAA	3	12	CAAAAAATCAACCAAGCTCTGAATAA	62.639	AGGGAAAAATATCCAATTGAGG	62.489	115
HM_0097	contig33941	CTG	3	12	GTGGGTGGGTAGGATATTGTGAT	62.425	CTTTGTGTTCCAAATCTGAATGG	62.814	160
HM_0098	contig04793	TCA	3	12	ATACCTATTTTACGGCGCCATT	62.86	TGAAGAACAGAACGAGGAGTGA	62.351	135
HM_0099	contig10275	AAC	3	18	GGCAAAAAATGATTCAAGACACACA	63.27	GTACATACgGACGATTTTGGAGC	62.95	159
HM_0100	contig02549	TTC	3	15	CCCAAAATCCAAAAACCTTAATC	62.785	GCTGTGAAGAATAAAGACGAAGAG	62.659	106
HM_0101	contig41242	GTA	3	30	AAATTGATGTGCAACTCTGTGACCT	63.242	GCAGAGCATTTGATTGGTTGATTG	62.861	154
HM_0102	contig07831	CTT	3	15	GTGTTGCCATGAAACAATCACTA	63.168	ACCACAGCCCTTTGTCAITTAGTC	62.725	142
HM_0103	contig09783	TCC	3	15	TGAgCACAAAGAGCTTCTACGTTTT	62.778	CCCATTTTCCGGAATAAAAAATCAT	63.07	159
HM_0104	contig45804	AGC	3	12	CCTCtCACTGCCATCCATTTTTTA	63.209	GAAATCAACAACAATCCGAGITCC	63.013	114
HM_0105	contig04059	ACC	3	21	GTTGAGCAACCAAGCTCTCTTT	63.036	GACCAAAATGCCTCAAGAAgATG	63.219	138
HM_0106	contig06330	CAT	3	12	CATACACGTGTCTTGTGACATA	63.216	ATGGCAGTTCTGTAAATATGGGGA	62.815	120
HM_0107	contig23369	CTG	3	12	TGGACTTCTAGACCCCTGAGTTG	62.993	CAAGCAGGGGAAAGAAAGTTTGCTA	63.036	129
HM_0108	contig19358	CGA	3	12	AATCTGAAAAAGATTTCCGGCTC	63.896	CATCGACCAATCAACAACCTAACCA	63.15	160
HM_0109	contig09714	GTG	3	12	AATGAAGATGGGTAAAGGAAGGAG	62.863	CtTCTCCTCAATTCATCACAGGT	62.884	81
HM_0110	contig13416	AAC	3	18	CCCAACTGtCTGGTTTTGCTT	63.212	AGTCTTGAATCCAGCTACTGCTT	62.864	112
HM_0111	contig12399	CAT	3	24	CcACTTGTCTCCACGTGAC	61.9	GACatTGACATTGACATTGACGAC	61.587	133
HM_0112	contig43245	CAA	3	18	CCCAACCAACGATTAATCTATCT	62.174	CTAGGGTTTTTATGTGCGGGTATG	62.744	93
HM_0113	contig38154	CTT	3	12	AATTTTAAAGCTCTCATTGTCCCC	62.797	ATGGGATTTGCAATCTGTCTTTGT	63.026	116
HM_0114	contig04453	TTC	3	15	AACAGGTCCAGAGAAAGGGTGATG	62.895	TTTTAAATCGGCTTTGGTTGAAGA	63.022	140
HM_0115	contig42349	ATT	3	12	TGtCTTGAGATCTAATGTTGGCA	63.038	CCTGTCCAAACCTAAAGGCTAGT	63.001	160
HM_0116	contig16388	CCG	3	12	GACAATACGGAGAACGGAGAGAAA	62.91	CGTTCTTCAAAATGGAGAATACGG	63.014	154
HM_0117	contig17535	TTA	3	12	GCCTAATTACACTTTACaCGTTGG	62.227	TTGTAAAAACGACAGCGGTTATGC	62.841	147
HM_0118	contig03728	TGG	3	15	AAGAAACCCAAAGACCCAAAGAAAG	62.977	GGAAACACGGAAGAAAGAAAGGGT	62.992	132
HM_0119	contig10898	TCC	3	15	AaCCAAAGGCCCAATTCTCTG	63.31	AGTTTTCAATCCCAATCTcCAAT	63.069	131
HM_0120	contig49936	GAT	3	15	TGAGTGCCAAAGCTTGTGCAATG	63.087	TCTCACCTTCaTTGGCTCTCTCTC	63.217	114
HM_0121	contig17543	TCT	3	24	TCGGATTtGgTGAGAATTCACTTT	63.108	GAAGAAGAAGCAGACGAAGACGAC	63.04	140
HM_0122	contig44651	TAG	3	12	CATCCAATATCaCCTCCTCTCTG	62.983	CTACCTTCAATCCCAACCATTCa	63.3	150
HM_0123	contig35718	TCA	3	12	GATTTTGCAATCCAAGAGCTGACT	63.039	GTAATGCGTGTGCCAGACTATGAG	63.091	157
HM_0124	contig38707	CGG	3	12	CGTACATCGAGTAGAACACACGCA	63.506	GATCGAGAACACCACTCTCTCT	63.886	122
HM_0125	contig46034	TCT	3	24	TACAGAAATGTTTGGCCGCTCTGA	62.845	AGAAAACAGGTGGTGAGCTACTG	63.033	160
HM_0126	contig28152	TCT	3	18	GCaaAaCgCaGaTTAtAaTGCCCTC	63.028	TTCAAGCAAGGTGAAGACCAATCG	62.71	157
HM_0127	contig02993	TGA	3	15	TTTGGGTTAGAATTGACCAATTG	63.097	TACACaCaACCGaAAAGTCTCTc	62.753	121
HM_0128	contig13233	GGT	3	21	AGCAACAACGACaCTGAGATCTTG	62.961	TCTCaAAACCACAGCAGTCATCTC	62.937	137
HM_0129	contig28543	TCT	3	12	AAGGTTTGGaAGATCAACCACTTCa	63.212	TCGATTGGGGTTGTAAGAAATTTG	63.204	143
HM_0130	contig28223	ACG	3	12	TTTCTCTCTCTGCTGCACTTTC	63.009	GTTGAATGACTGAGaAGGGGCTAT	63.763	126
HM_0131	contig02548	GAA	3	12	TGTTCACTCTCTGGCTGTGAGAG	63.04	CTGACTACCAcCAATtCTTTTT	62.696	150
HM_0132	contig43495	CAT	3	12	CCATHGCGCTGactAATTTCTCTG	63.014	AtTCaTTTTTagCTTCGCAACAC	62.667	80
HM_0133	contig12520	AGA	3	18	GGTTCTGATTGGGTGATTATCAGG	63	ATCaGAATCAGATGCAACCTCTCC	63.007	106
HM_0134	contig17172	GAA	3	12	CAGATAAAGGTGGTGTCTCTTTG	63.003	TGTTGGGAGAGTTTTGTGTGTGTG	63.371	153
HM_0135	contig41901	TGG	3	15	CTAcAAaCTGAACCTGGTCTGGTG	63.177	TTCAAGATTGGCACTAGAGTTGTG	62.741	155
HM_0136	contig30302	TGG	3	18	CGCTGAGTCTTGCTTAATGGGTAG	63.45	TCTTCAGATTCAATTTCCGATAGC	62.804	147
HM_0137	contig05360	TCT	3	12	ATCAaTATTTCTGGCTTGTCTTG	62.641	GAAGTCTTGATTGGCAAGGTTGT	62.824	159
HM_0138	contig03852	TCC	3	12	TGAACACCTCAAGTACCTTGCTA	63.07	AATGTGGATTTCTCTCGGaACAG	62.798	160
HM_0139	contig12096	TCT	3	18	ATCTCCTTCTCTCTGCTATCCT	62.865	CAATTATTTTGAAGTTTGCATCG	62.683	160
HM_0140	contig26031	GCA	3	12	ATACAATACCTgCGgTCAACATCT	62.94	AAATTGCAaGGAAAgTGGGTTCA	63.006	159
HM_0141	contig25991	TCC	3	12	AAGGTGGCGATTAGAGGGAAGAG	63.392	CtGATCGGAGTACAGGAGAGGTa	62.997	157
HM_0142	contig27558	TCT	3	12	CAGAAGCTCTCAACCGACACATT	62.935	TCCTTACCAACATCATGAATCC	63.188	128
HM_0143	contig14204	GAA	3	15	GGAAATGATTGAAAGGGTGAAGTTG	62.996	GAGTCTCTGTGGGTAAAAATCCAA	62.684	156
HM_0144	contig28284	GAA	3	12	CAAGTATGTCTCCATAAAAGGAGG	62.371	GGAGCCTTTAGTgCCATCTCAGT	63.131	158
HM_0145	contig08009	CCA	3	12	CCGAATATGACCTCAATCTTCTG	63.005	GAAAGTGGAGATGGAAGGAGGTTT	63.071	152
HM_0146	contig01026	AAT	3	12	TCACTTAAATGATTCAAAaCTATCCG	60.862	ACACAAATGCAACAAATTAAGTCA	60.703	111
HM_0147	contig32065	ACC	3	12	TCCAAGCGCTCTTGAATATAGAC	63.022	AGACAACCATAGGTGGTGAATGCT	63.141	120
HM_0148	contig46301	CAG	3	12	AAGTAAGTCATCTGTGGTGAAGCG	62.933	TCTCCCTAGCTGGATTTCATACCA	63.206	148
HM_0149	contig18778	ACC	3	12	GAGTACAAACCCATCAAGTCCCAAC	63.014	GAATGAATaCTCTGGTGGGTTG	63.009	84
HM_0150	contig01526	GCT	3	12	TCTCTCtCAGGGTCAATCTTTG	63.085	GGAGTGGCTCATGAAAAAGAGAAA	63.009	140
HM_0151	contig02277	GGT	3	12	CTGCTCATTTTGGTTTGTGCTG	63.357	CAACCCCATGATCTCAACTCTAA	63.513	146
HM_0152	contig29750	ACC	3	12	AATCTACATGATCGAGTACCTGGa	62.425	TGTTTGCACTGAAGGCTTGTGAT	63.087	102
HM_0153	contig49995	TTC	3	18	CAAAAGgCCCTAAACCTCTCAGA	63.176	AATCATGCCCTGCTAATTGAAGAA	63.13	122
HM_0154	contig45884	GAG	3	12	ACGAAGGAGATATGAGACGGACT	63.611	GCTTCTCTGCaACTCTCTTCCAC	63.04	157
HM_0155	contig07377	CTT	3	12	GATGtGCCACATGAAGAAAAGTA	62.645	GAATAAGCGCAACCAgAAACC	63.067	154
HM_0156	contig07993	GGT	3	12	CGTACGAGTACTGTGGATAGTGGC	63.096	AATACCTTACTACCAACaCCCC	62.41	156
HM_0157	contig41426	TCA	3	30	CCATAATAAAATCCGCTGgTGTA	63.026	GGAAAACTCAgAAAGaAGGGaAA	62.863	159
HM_0158	contig01201	GTG	3	12	GTGGTGGAAAATaTATGGGGCAAC	63.553	ACCACACCAcCactTCTTaTc	63.455	87
HM_0159	contig44856	TCC	3	21	TTCATTTTTACCcACTACTACGgA	62.93	TGTTGGTTTTGTGAGTGTGTTTTg	62.093	108
HM_0160	contig33912	CTC	3	21	ATTTCTCCTTGGGCTGAAGTTTTT	63.09	TTCTTCTCGTGTCTCATCATCA	63.257	152
HM_0161	contig37740	GGT	3	21	AATTTCTCAACGCGTTCCTCTTAC	62.972	CATCACCCACAACCTACGAAAAACA	63.159	140
HM_0162	contig36350	TCA	3	18	CGTTTTATGTCATGCTCTCAACC	63.026	GAGGATGATGGAATTGAGCTGTTT	62.802	140
HM_0163	contig03315	TGA	3	12	ATACCGAaTGGAATACGGAaTGCTA	62.737	GGTGTGGTGTTCATaCaAAAG	62.592	105
HM_0164	contig39893	ATC	3	12	CCCCACAAGTCAAGAGAGAAGAGA	63.085	GACTCGATGTCAATTGAAGAAGAG	62.503	137
HM_0165	contig30155	GAG	3	12	TACTCATTCGGTGTGGTGTGTTCT	63.278	ACGATCTGATCAAGACTCCCTGTG	62.576	155
HM_0166	contig35788	GGC	3	12	GGGATCGTGAAGTAAAGTCTGTGC	63.577	TCTTCTCACTTGTCTACAAAAGCC	63.142	142
HM_0167	contig07016	TTC	3	12	TCTCCTTGAACCAAGTCTCCAC	62.997	GGAGGCAAAAAGAAAGAGAGGAAG	62.98	84
HM_0168	contig30900	TTC	3	18	GAACCCCTTTGAAGATGaCTCAGA	62.987	CGCAGAGGAACAGATCACTATCA	62.831	144
HM_0169	contig11838	TCT	3	12	ATTCTCGTCAATAGTTGTCTCGc	62.94	AGAGGGCTTTTACCTCTGAGAGC	62.543	112
HM_0170	contig24548	GGA	3	12	GAAAAGGAGTGTAAAGTGGAGCA	63.031	CGCAGACAAGTGAACATCAAGAT	62.741	151
HM_0171	contig08936	CCA	3	18	TAGCCAAAGCAAGATTACCCAATA	63.034	GGGTAAACAGAGGAGGGAaataGGA	62.863	144
HM_0172	contig22320	GTA	3	12	TTCTGTCTAGAAGTtGGGGGG	62.793	AACCAAGCTAGGCTCTTGTGATG	63.044	141
HM_0173	contig32009	GGT	3	12	AAGAAGCTGGCGGATAAGGAGATt	63.02	ACAACtGCTATCCAATAGCAAAACA	62.885	130
HM_0174	contig07900	TAC	3	12	GGATAATTTCCAAGTGTtTtGcT	62.718	GGTGAITTTaCAATAcGCCAAGG	62.746	155
HM_0175	contig43979	GGT	3	12	TGTGCTCAAAATGGAGGTACGAGC	63.758	CCAGACGTCAAGACTCaAAAGAGA	63.23	118
HM_0176	contig00898	GGT	3	24	AGGTGTGTTTTCGGTTTAGGGTTT	63.106	TCTCCCTCTCTCATCTGTaAAA	63.083	136
HM_0177	contig45862	CTA	3	18	GACAATTGGAAGAATCAACCGAaC	63.013	ACACCATCTACTTTCGCCATTGTT	63.048	113
HM_0178	contig07216	TTG	3	18	CTTTGTTGAGCTACGTTGGGAG	63.337	cCaACCAATCAATATGGGTGATA	63.706	159
HM_0179	contig01325	AGA	3	12	GCATATTCAATCAGCCAGCAAAA	62.369	TTTTCCCGCTTTTTCTTTCTTCT	62.977	120
HM_0180	contig05392	ACT	3	12	ATGTGGTtGAGACCTGTTTCTTCA	62.933	CTCAATTTTTCTTGGATCATGGG	63.083	127
HM_0181	contig33906	ATT	3	12	TGTGGAGTAGGAGGAGGATATGGA	63.191	AAAACAGGGGCTTCATATTCACAA	62.922	110
HM_0182	contig41076	TGA	3	12	TTGGGTTCTGGTCTTCTGATGAT	63.204	ATGtGTgGGAaAAATGAACACC	63.121	136
HM_0183	contig09926	CGG	3	12	GGGAAGGTTGGGTTCTTtagTAG	62.397	ACCCCAACTCAaCTCTCTCTGA	62.677	152
HM_0184	contig32260	GGT	3	24	AaCTCATCAACcTGGTGAGGTC	63.792	tCTTCAAACTTCTCAgTgGCTcT	63.225	159
HM_0185	contig49304	TCC	3	15	CAAAATGAAAGGAATCACTCGAA	60.016	GGATCGTTAGCGAGCAAAAA	60.343	121
HM_0186	contig09059	TTC	3	15	CTGCATCaGGCTGTTTACTTCAA	62.958	GTGCGGTGTGATTaAAAAACCTTT	63.595	146
HM_0187	contig27512	AAT	3	12	GACCTGATCACTTCACAGGCAATA	62.609	TGCAATCTCTTGATTCCAATATC	63.314	143
HM_0188	contig31738	AGA	3	12	GTGGGGTTCGGAAGAGTAAAAAG	63.375	GCTTCTGAATATGACGAGGAGGA	63.013	117
HM_0189	contig33759	TTC	3	18	CCCAATAATTCACTACTATTGGGC	62.823	ATTTGGAGATTGTGATCCGAAGAA	63.099	129
HM_0190	contig30630	TCG	3	21	TTGACCCCTCTTTTATCTCTCC	62.875	gATTGATTTCCTCTGAGATCAAC	63.329	133

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0191	contig24885	TGT	3	12	AAAACCTTGATCCATCCAACTCTCG	62.813	GTTTTGTACACTGGTCAGGGGAAG	63.12	149
HM_0192	contig17739	CTT	3	12	TGTGCTTGCTGTAAAACTGAGAG	62.969	ATGCTCCCATATAGACAGCTGTTTC	63.468	138
HM_0193	contig27776	GAA	3	12	TCGGAATGCAACGAATTAGATGA	62.935	GAACCTGGGGAAGGAGAAAAAGATG	63.465	96
HM_0194	contig25333	CTT	3	30	TTGGACGAAATGCCTCACTTGAT	63.965	AGTAACTCAAAATCGCGAAATGCC	64.591	134
HM_0195	contig43085	CAC	3	12	GATTCCTGAGTGGTTAGCGAAGGA	63.022	AGACACCACCATCTCTCTCTTGG	62.895	152
HM_0196	contig49824	GGA	3	12	AGTGTGATGAGGGTAATTGGGAA	62.897	aAAACATGCACCTCCAAAAACCT	63.02	101
HM_0197	contig25167	TCA	3	12	TTTtAGAAATTGATCGCAGAAGG	62.948	CAATATTTGGAGCtCtCAAGAA	63.517	156
HM_0198	contig24358	GAG	3	12	TATCCCTCtCAATAATACACCC	63.353	TGGATTGGTGGTTTtCtCAAGTTA	62.935	147
HM_0199	contig43233	ACC	3	15	GCAAAACCCTCAATCAGTACCTC	63.026	AGACCATCGAAATGCTTGCTTC	62.822	160
HM_0200	contig34751	GAG	3	12	ACTCATCAAGAAGATGGGACAAG	62.884	GGTAGACACTGATTGGCTGAAAC	63.242	102
HM_0201	contig42742	CCT	3	12	TTTGGGTGGGAGTTGATTTTCTT	63.006	TTATAGCTCGCTCTCAACATGC	62.888	140
HM_0202	contig23153	CTT	3	15	TCAATCCTTGCTGATTTCCtTtC	63	GTGATCATTaCaaagAAAGCGCT	62.854	95
HM_0203	contig21090	TCA	3	15	GAGAGGGAGAGGCTGCAGTACTTT	62.791	GATTGACAACAGCATGATGATTC	62.944	97
HM_0204	contig03487	GTT	3	12	ATCTCGAAACCATAGCAATCCATC	62.609	GTGAAAGCATAGGGGTGTTGTA	63.444	83
HM_0205	contig27009	TCA	3	12	AGTCAAGCTCTGCAACTCAACT	62.949	ACTTTGAAGAAGCGACATTGTTG	63.762	156
HM_0206	contig06630	CAC	3	21	AACAAGCAGACAACATCAACCCTT	63.25	AGAGTTGGAGTGGTGGTGGAAAT	63.212	102
HM_0207	contig02125	CCG	3	12	CTCGAACCAACACTCCTTATTTCA	63.629	CTATGCGAGAAGCGTGGCAG	64.36	142
HM_0208	contig39673	CCA	3	12	CCACCAGCTTAAATCCCAATTA	63.034	GGTGGTCAGACAAGAAATGGTAGC	63.242	155
HM_0209	contig29927	AGA	3	12	AAGTAACAACCTCCAAAGCCACAA	63.138	GAAAAGGATTAAGTGGGTGTCCT	62.78	152
HM_0210	contig07639	ATC	3	15	CTtGTTTTGTTTTGCTCTGAACtAa	62.089	AATCCCACTcCAAAAAGAAAG	62.968	107
HM_0211	contig21273	GTC	3	18	AaGgaTGTGtTcTtCtTtaGggTC	62.995	GCAtgAGCAGCAGAGcTAGAAAt	62.338	89
HM_0212	contig48213	GAT	3	12	CAAAAGaTGGGATTtGAGGAACAC	62.996	CCAATTTCTGGCGATATTTGACTC	63.021	99
HM_0213	contig40231	GGT	3	18	CCTAACGGAACAGGAGCAGAAAGTA	63.028	ACtGTTAAAGTCACCAcAcCCTAT	62.922	153
HM_0214	contig42728	GAC	3	12	GCAGGTGAGACtTGATAAAGAGTGA	62.045	TAGGGTTTTCTCGACATCTTGG	62.701	111
HM_0215	contig23253	TCT	3	21	GTCTTACCCTCGGATCAATCTCAA	62.786	GTTGTTCTTGTCAGTATGGAGC	62.91	159
HM_0216	contig47498	AAC	3	30	TCtTCTGCTTCTTGCTAAATCGG	63.134	AGTAAATTTTGGGTTGGGTCCTG	62.808	156
HM_0217	contig14167	AAT	3	12	CGTtATGATGtTGtGGAGCTCTG	63.061	AGTCGGTTCTTCTcTCTCCTCTG	63.488	135
HM_0218	contig48604	GGT	3	24	GGGACTGTTTTGGCTGTGGTTATAG	63.031	GTTCTCTCTCAGAAAGTcCCCAAT	63.071	85
HM_0219	contig18376	CAT	3	12	GCAGAATAGAAAAGGAGAAAGGGGA	63.172	ACTGCTCTCGAAGTGTtAGgaAG	62.909	146
HM_0220	contig37222	TGG	3	12	ACCTTGAAACAACAAAGCTGGTGA	62.724	ATGGATTGATCAGAAAGGTCCAA	62.987	157
HM_0221	contig17084	GAA	3	12	GCTCTGTTTgTtCtAggTTGAA	62.726	TCTATAATGGGcTTGGCTGCTA	61.912	95
HM_0222	contig24442	TTC	3	12	GCTGCCAAATGCTGATCTCTAAT	62.953	AAGGAGTCTGATCGTCTAAcCC	63.075	149
HM_0223	contig38543	AGG	3	12	CTCATGAGAATCGCTCTGCTCTG	63.714	GATCTACTCATCAAGCTCGTCGAA	63.148	159
HM_0224	contig26887	CAA	3	12	TATCTCCATCTCAATCTCgCATTT	63.012	CGGTGAGATTtGATCGGAAATAG	63.005	127
HM_0225	contig21998	GGT	3	12	AGAATAGCTGACACGGAGCACAGC	63.04	gCGTACTCTTtCTCTCTCACTTA	62.151	131
HM_0226	contig21917	AAC	3	12	CAGGTGGAGGAGCACAATCTACTAC	62.511	CTTTTATTGGCCCACTCTCTAT	62.795	142
HM_0227	contig33066	GGC	3	12	ACGGCAACCCGGAGTtATTTAGTA	62.957	GGAGTCTCCACTACGTTCTCGAA	63.01	122
HM_0228	contig07792	AGT	3	12	CCTAGAAAAGCAGACAGTGTCTGC	63.566	GAATAGGAGACGTtGAAACCAcCA	63.537	110
HM_0229	contig16155	CTT	3	12	TGTACTCTTtAATAAATCGCGCG	62.771	CTCCGTGATGTCAAAAGAGAAAGT	63.01	137
HM_0230	contig27156	TGG	3	12	TGCAGAAATTGAAGTAGCCATTGA	63.059	AGAGCAAGAAAAcAGaAgAGGCAAA	62.933	132
HM_0231	contig20782	GAA	3	12	AGGTAAACAGCTGAAGTCGTTCTCG	63.146	CTGGCAGAGTCTGGTCTATGTCT	63.236	111
HM_0232	contig14816	GTG	3	12	ATTCCCCCAAATTAGAAATACCCCT	63.225	AAAAATCCTCCACCAcACATCTG	62.691	105
HM_0233	contig36634	AAT	3	30	AAACAAGGaCtAcTcACCTCTcaca	62.397	TCAAGATTTTGAACCAAGGcCtaA	63.109	142
HM_0234	contig17567	CAT	3	12	CTCTACACTTtCtCCCCGAGAAT	63.177	CGGAGAGTCTTGAAGGAACAGA	63.098	156
HM_0235	contig29178	GGA	3	21	ATCGCATCTCGAATCATCAAGAC	62.704	TTTTCTCTCTCCaAAAAATaGGA	62.301	126
HM_0236	contig02011	GGT	3	12	CAGATtGTGAAGcCTcAAAGTGAGG	62.502	CGGAATCGATtAGGCATTGTGtT	63.237	120
HM_0237	contig52391	CGA	3	12	AAGTTTCAATGTCCAACTCTtGGC	62.824	cTCTCtCaAATCGCTTtTTTAgc	62.558	114
HM_0238	contig45335	TCC	3	21	TTGTTCGAGCAAGTCCCTTAGAC	63.031	AACGTCCGATGATCACAATCCAT	63.709	110
HM_0239	contig12378	TGT	3	12	AGATAGGTACAGCTTACATGGCGG	62.755	TCTAGTTGTCGCCGAGACTGAATA	62.426	149
HM_0240	contig08248	GTG	3	15	GGGGAGGTTCTAGGCCTGATTAT	62.867	CATTATCATTGGCtAAAGGGTTTA	63.013	153
HM_0241	contig28145	TCC	3	18	AATTGGATCAAAACCGGAAATTT	63.137	GAAAGTGGAGTGTAACAGGAGGCC	62.512	157
HM_0242	contig46607	ATC	3	12	GTTCGAATCTCTCATtACACACCC	62.913	AGGCCAGAATAGTTAGCGGATCT	62.73	131
HM_0243	contig17567	TTG	3	15	ACACTGGGTCTAGCTGTCTTTTT	62.539	CAGCAATAGTACCACCTCTGACTG	62.222	97
HM_0244	contig05205	TTC	3	12	AGACATAAAGGAGCTGAGGTGGTG	63.023	ATTCCAAAAGATGGTATGAAGCCA	62.912	105
HM_0245	contig15519	TAT	3	12	TCATAAACGCTTAAACCACTCCA	61.953	TCCTATTGGTAACAATTTTGGATCA	62.746	160
HM_0246	contig02775	CCA	3	18	AGCCCCCTAAACTACTGCTACCAA	63.406	GGTTATGGTgGCTATGGTAGTGTCT	62.55	88
HM_0247	contig26230	AAG	3	18	GATcGTTCTCGATCTCATGTCTCA	62.914	CGCGTTAGCTAGACCGTTTACTCT	62.596	160
HM_0248	contig10424	TCT	3	15	ATTGTCACTCGGAGTGTCTTCTCC	63.005	CtCAAGGGAAACCCtAGCTCTCA	63.176	104
HM_0249	contig45962	TCA	3	12	ACGGAAACCTGATTCTCTCTCTT	63.604	CAATTGTCTGACAGAGACGAAGA	62.919	152
HM_0250	contig20563	TGA	3	12	AGACCCtACCcAATtACCcAAAA	62.885	ATGTCATCTcGTCGCTTAGGAG	63.035	107
HM_0251	contig00970	AAG	3	15	ATGCGAAGACACAGCCTGCTA	63.317	GAGGTGGTCCCTAAAAATTCATCT	62.769	129
HM_0252	contig47537	GAA	3	21	CGATGACGAGAAGGAGCAGAGGTAG	62.933	TCAGATTcAaACCCTTTCCAACCT	62.784	138
HM_0253	contig25977	CTT	3	18	AATCAACACATCTGGGTCACTGA	62.086	TGAGGAAGAAGTAGAATCTGAACACG	62.23	149
HM_0254	contig41975	TGA	3	12	GGTCGAGGGGAGGAGAAGAAGAAG	63.161	TTGTTTATTGCTTTGGATTGGT	63.115	157
HM_0255	contig09361	CCT	3	18	GTAACCTACTACTCAGcCGCCCA	64.71	TTCGATTCCAATGTGTCGTAAT	63.954	88
HM_0256	contig39024	AAT	3	12	ATGAACCTTGGTCTTGACTGGAG	62.895	TTGCTAAACAGGGGATCACAATCT	63.121	151
HM_0257	contig04588	AGA	3	12	CATTGACGCGTtTTAGTtCTCAT	62.839	TAATCCGGGAAGTTGAGTTTTCa	63.002	106
HM_0258	contig20561	TAC	3	15	TTGGTtAAATtTGtGGGTTGGACTT	62.714	CcAaACATTTCCCAATtTCCATTC	62.493	146
HM_0259	contig32007	CGC	3	12	AAAATGgTTTTCTcGGGTTCTCT	63.4	AGCAAGAGATTGAATGGGtTTTG	62.716	158
HM_0260	contig00376	TCA	3	12	ATCTCATCTGCACCACTAAGCTC	63.031	TGAGGATGAATTTGATGAGAGAAG	63.132	100
HM_0261	contig36981	CGC	3	12	CCATTCTGCTTAAATCCCAATTC	62.912	TTTCTATTcCagAcACCCTCTCAG	62.015	144
HM_0262	contig07274	CTG	3	15	AGCTTCTCAGCTCTTCTATCGC	62.504	TCAATTGTAGCCTCACCACTCTC	62.58	160
HM_0263	contig41621	CCT	3	24	CCAGTATCTCAGCTTCTCTTCTT	63.285	CCTCTCATCTCTCTTTTATTGCT	63.078	123
HM_0264	contig07931	CTT	3	12	TTAGATGTCAAACTGTGTGATGGA	62.803	gtgtgagaagagaactaggtctgc	63.053	138
HM_0265	contig13683	TGA	3	12	TGGGACGATTAAAGTCTCAACAA	63.009	CTCTGCCATCAcAAGTACAGAGGA	62.933	157
HM_0266	contig13227	ATC	3	15	GCCTTAGGACCAAGGAAGCAGAG	61.85	GGTGATGTTTTAGGTCTGTGGAT	62.599	160
HM_0267	contig12203	CAG	3	12	CTAGCATCGGAGTACCGtccTcTA	63.031	CCGAATCTAATAGCGATaCAACGG	62.945	135
HM_0268	contig36835	TAG	3	12	CCAGTtCTCTGGGAGTTGGAGTC	62.677	TGTAACAACCAcCACCcAATcAGTT	62.621	141
HM_0269	contig31837	GTG	3	12	lCTtGAGCGAAATtGATACGGATt	63.13	ACCAAGaAAAAATGcAtCGATCAAC	63.444	111
HM_0270	contig01453	CGT	3	12	AATGGGATATAATTGTCATGACGGA	63.421	TTGAAAGGAGGAAGATTTTGGTG	62.688	146
HM_0271	contig09301	TTT	3	12	CATCTTCGATTTCTTGCTGAGGTT	63.022	GCGATCGATGAGTACAGACCAAA	62.728	86
HM_0272	contig49031	TAC	3	21	ATAAATCTATGGGCTTTCGGATCG	63.481	TTTCCACAGTAAGCTCACCCCTAC	62.822	123
HM_0273	contig13917	ATC	3	12	ACTGATGATGCATCTGTGTTCTG	62.968	TGCCTTAAACCTGGATCAATCTT	63.121	115
HM_0274	contig46784	CCA	3	24	ACGCCCTGAGATATTtGATCTGTC	62.816	ACAGCTTCGACTTCAACATCTCTC	63.073	125
HM_0275	contig52477	TTC	3	36	GGAGTATCCATGGAAAGCAATGA	63.42	GAAGaGAAGAGTGACTCGAAGGG	62.909	129
HM_0276	contig46010	TGG	3	18	CCTAAGAAATTGAACCAAGGCTCT	63.682	ACTAACTTGATCAGAATGGGTGgG	62.811	116
HM_0277	contig29345	AAG	3	18	CgAAaAGAAaACGAaATCGAAATG	63.022	AGTTGGATTACCGGATCTCTTATT	63.007	91
HM_0278	contig05515	GTC	3	12	GACAAGGTGCTTTGGGAGATT	61.703	TcIATTGATGAACAGTGGATGCC	62.397	117
HM_0279	contig25565	AGA	3	12	TTTTATCTCACTCAAAAGGCGATC	62.705	GtCAAGTTGGAGTATCCTCAGCA	62.829	135
HM_0280	contig34695	CAT	3	12	TCATTTTCAAAAGCATATcAGAGTC	60.034	ATTTAGCGGGTTGAGTGGTATGT	60.976	160
HM_0281	contig07611	CTC	3	15	GAGTGATCTTGAATCTCCAGAAC	62.548	GTGTCAGTGAGCTTCTACAATGGG	62.291	160
HM_0282	contig27356	AAT	3	12	AAGATTGAAGTGGGAGGAGAT	62.753	ACACACAACaGACAGATGCATGA	62.866	137
HM_0283	contig01824	CAT	3	12	GAGgCGAAGAATTTGAAGTAACCA	62.826	GGGAAATTTGAAGAATGATAATGGG	62.798	152
HM_0284	contig00479	TTA	3	12	CAAAAGAGAGACAGATGTGTGGA	62.798	CACGAcCTTAAAAACACATcTTCG	62.123	95
HM_0285	contig23480	CCA	3	18	AATTCTTGACCAACGACTCTCCGA	63.129	AAGaGAACCCATTtTGATGGTGG	63.425	150

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0286	contig28555	ACC	3	15	AAATGGCCCAAGACtCAAGAAATC	63.79	GTTTGGAGGTCatCAAtttcATC	62.889	157
HM_0287	contig08081	AAG	3	24	GCGAGAACGATAAACACAgCAAT	63.677	TCTTCTATCACAGTACCACAGGC	62.829	124
HM_0288	contig07085	TCA	3	18	TCTACTTCCAGCTGTAATCCTCTC	63	TATGGACGCAAGGATGAAGAAAT	63.021	91
HM_0289	contig30195	TCT	3	12	TCCGATATCAGGATGAACCTTGCT	63.223	AGAGAAGAAGCTGtGAAGGACG	63.669	124
HM_0290	contig35693	CGC	3	12	CTGCTTCGTGGTGCAGCAATC	63.049	tTaCCACTACCGTTACAAGGACCG	63.337	126
HM_0291	contig09334	CGG	3	12	CTGCCGATTTCATATTCACTTCA	63.15	ATCCCCGGTAACtCAACAAAGTT	63.999	130
HM_0292	contig35006	CTT	3	15	ACTGGTGAAGGTTCAACAAAGGAAG	62.906	TCACCACCTCAACCTCATCAATTA	62.803	126
HM_0293	contig34919	ACC	3	15	CTCAGTACTCGCTCCTCTCGAAG	62.704	GGCGATTtATtGCTCGAAGGT	63.139	119
HM_0294	contig02256	ACC	3	12	CACAGACCAGATCAACTTCTCTCT	63.106	GTGAATGTTGTGAACCTGAGGGGt	62.933	112
HM_0295	contig24825	CTT	3	15	GAACAGGTtGTGGAAAGCTGAAGG	63.437	AAATGCAACGAAGAGTtTCTGGAC	62.936	160
HM_0296	contig06305	GAT	3	12	CCCAGCTTGTAAATTTCTCACTC	63.239	GTCGTGCCATCTCATAGAAACT	62.827	106
HM_0297	contig34882	GAA	3	12	AGAGATCTTGAAGCTTGGCAGTA	62.936	CATAAGTACCCTATCTCTCTGCT	61.985	158
HM_0298	contig23688	GGC	3	12	GCTGCGTAGCCAATGAAGAAGA	63.934	GTCGGCTACTACAGCGACCG	63.188	110
HM_0299	contig28497	AAG	3	12	aGAGTGAAGAAAGCAATGATGGAAG	63.115	ATaAGTTAGGGTGAAGGCCGAGAC	63.008	127
HM_0300	contig13585	CTG	3	12	ACTGACCCCACTCAAAAGACAAAT	63.014	TCGACAGAGCCATAGTTTGGTACA	63.061	81
HM_0301	contig21047	CCA	3	12	CAGGCCCTAAAGTACCACAAATG	62.929	GGTTTCaAGAAAGGTTTGGTAGT	62.791	94
HM_0302	contig01701	TAC	3	12	ACAACCTCCGAGGATAACAAAGAG	62.631	CGTTGATAAACTTTGAGAGAGGGG	62.397	81
HM_0303	contig20779	AGA	3	12	GTGAAAAAGCCTTCTCGTCAATGG	63.03	tttgacagaaagccctagctg	62.918	144
HM_0304	contig21404	GTG	3	21	GAGTGTGAAGCAGGAGGATTTACG	62.549	CTTGCTCTCTCTCATCTCAGC	62.898	140
HM_0305	contig35383	CGC	3	15	CGAACCTCTACAGCTTCTCTCA	63.325	CTTGAATGTGCATTCTGGACTTTG	63.048	159
HM_0306	contig20346	CCT	3	12	AACCATATAAGTCAcACCCCTT	62.888	CTGTCTAGTTGTGGAGCAAGAT	63.023	136
HM_0307	contig38360	GCA	3	15	CATCATCTCagTTTGGTCAAGCAc	63.164	AcTGAATCTCTCTTgGagGCACc	63.217	156
HM_0308	contig24597	ATC	3	12	TcATGAGATTGACGTAGAGtCAGC	62.914	AAACCGTCAATCAgACATTTCA	62.913	107
HM_0309	contig28827	AGA	3	12	TTGCAGTTGGAAGTATGACAGAG	63.04	CAGGTgATGGAGATGGGATATAG	62.873	160
HM_0310	contig26378	TCA	3	21	GGGAGGGTACGATTGTCTTCTGTA	62.698	CTGAACATTCAACAAATCCACACG	62.814	137
HM_0311	contig22710	GAA	3	12	ATTCTGAAATGCTGCTGGAAAGAT	62.523	ACCCGACTTGACCGCTTTATTTA	63.028	114
HM_0312	contig41541	CAT	3	15	aCCAAACAGtTCTCTATTgtCcA	63.111	CGATGATCTGGGATTGAGATTAGG	63.086	148
HM_0313	contig34379	GAG	3	15	ACATCATCTCGAGTGAACATCTCG	62.57	GCTTTGCTGAAATGTGGAAAGATT	62.841	140
HM_0314	contig51115	AAG	3	12	GCCATGACAACTCATCTAGCTCAA	62.847	CaAAGCCCaTCTCATCTCAATTCT	62.9	108
HM_0315	contig00229	CGC	3	12	CCTTGTCTGCTCTCTCTCGTATT	62.933	GTCGTCGAGTGTCTTGAAGTGTG	63.185	127
HM_0316	contig05726	CCG	3	12	AGACGATAACAAAGTTTGACCTCG	62.822	ACAAtgtcgatTCAATGTCTCTGT	62.832	150
HM_0317	contig17511	TGA	3	12	AGGTGCAaCTAACTGTGACTTGG	62.822	GGTCaAgcaaaTCAaAcCaTCTCT	63.026	156
HM_0318	contig50879	GGT	3	21	GAGAGTGAAGTGAAGCGAGATGAT	63.351	AAACTCTCTACACTCCACCACC	63.93	159
HM_0319	contig31936	CAG	3	12	CTTCTCAGCTCATGGCTACTCTC	63.027	GCCaAACTTATgGACATtTCAAC	63.026	134
HM_0320	contig03965	GGT	3	12	TTTGAAGaGGGTGACGAAAGAAAG	63.003	CCATaCACATTCAaGAAGCGCCA	63.059	110
HM_0321	contig32975	AGA	3	12	GAGAAGGACGAGAATAGGAACAA	63.102	GTGGTCAGAGAGCTTcaAAACAA	62.947	144
HM_0322	contig34454	CGC	3	12	TTTCTAGGTGCTCTTCACTCTCC	62.91	CACCGACTCAATAGAGAACGGCT	62.946	130
HM_0323	contig21140	GAT	3	15	TGAGGAaGAGGACAGTGATGATGA	63.352	TACCGGatTTaAAAGGCaAAATG	62.737	130
HM_0324	contig35697	GGT	3	12	GTTTGAGGGCGCTTTTATTGTG	63.597	TACAGCCACAAGAGACCAAAAGT	62.737	116
HM_0325	contig06064	TTC	3	12	TCTATATTGATCTTCCGGCTGTG	63.249	GcAGTCCAACCAAGGACTAACCA	63.065	123
HM_0326	contig01474	TGA	3	12	ATaGAGaAGTtGgAAATcGgCAATc	63.798	CGGATCAAAATGACCTTCTTCA	63.009	85
HM_0327	contig16530	TCC	3	24	gTAAATCCATCCCTATTACCCCAT	62.974	AGCAAAAGGAaAATGAACCTGACCA	63.227	113
HM_0328	contig05274	GAA	3	12	CCGGAAGACCGAGATAGAAATCTT	63.078	GGGAATTTTATCAGCATCAACCAA	63.213	121
HM_0329	contig27587	ACC	3	12	TGATTCTGTGGAGGTAGAAATCACA	62.921	gaGGATCTTGCTATGGGTGTTTGG	63.022	113
HM_0330	contig04286	GAG	3	12	GGTTTTGAGGTACCGGAGATTTTC	63.184	AACCATTTCTCTATTCTCTCCaT	63.277	135
HM_0331	contig13026	TCA	3	15	CTTCAACCTCAaCACCATTCAAA	63.357	GGGAAGGGGTAGCATTaAGaAGa	62.888	83
HM_0332	contig24884	TGA	3	15	CTTGACCTGCTGGCTGCTCT	63.784	TTTCTACAAAGAGGAGGAGCTGTAA	63.905	154
HM_0333	contig00983	GCA	3	12	CAAAAGTTTGGGATGATCAATGGAT	63.198	ATCCCAAGCCCTTAATAGCTCCTG	63.004	113
HM_0334	contig12499	CCA	3	12	TGTGAAGGGGCTCTTGACTTTAG	62.993	GTGGAGATGTGTGGATCAATGAGA	63.482	156
HM_0335	contig19123	TTG	3	12	TGGTTGATTTTCAATTCTTCGAT	63.009	GCCGGAAGAAGAACTGTAGTCA	63.031	130
HM_0336	contig15756	TGA	3	15	aaaGgTAAgTGCTAATGCCACCTCA	63.043	CCTACTACTACACACACCAACCC	62.919	140
HM_0337	contig08406	TCA	3	12	CTAGAGCATCTTGGCAAGATCA	62.922	TTATTGGGAAAGGAGGAGCTGTAA	62.315	156
HM_0338	contig01757	TTC	3	21	GCTGTTCTTTGGTCTTCTTGCTC	62.838	GGGAGGACATTTTGTTCAGAGA	62.784	122
HM_0339	contig38799	GGT	3	15	TAATGAGGGAGGAGGAATGCTG	62.996	ACAGAGAAGCAACGAATAATCC	63.048	148
HM_0340	contig20738	GAA	3	15	GAACTCGTGAGGACAGACAGACT	63.355	GTTCCGTGACAATACATTGGGATT	63.125	155
HM_0341	contig17067	CCG	3	12	ATTGCTCTCCAGATCTGCTTCTC	62.382	CGGAGATTAGGGTTCTCGAAGTT	63.086	90
HM_0342	contig04023	CGA	3	12	ACTCCAACCAACCCCTCATCATAC	63.449	GCTCATcGtCTGtCTACATCT	63.146	153
HM_0343	contig07568	CCA	3	24	TTTGAAACTCTCATAGCTCCACCTC	62.91	CTCGTTTGGCTTTGaAAATATG	63.05	136
HM_0344	contig30018	GAA	3	18	AGAAAAAGGGAAGGCCCAAAAAAC	63.098	GCCTGATTTTTCgCATCTTTGTTA	63.538	160
HM_0345	contig21191	GAG	3	18	CACACAGCAGCTTATCATCATC	63.069	ATCATTAAAGGCTCCAATCTCTC	62.977	102
HM_0346	contig07242	TCT	3	12	CGGTGTAAGAAGTCATCTTCATCA	62.712	AGACCTGAAATGAAGCATACGAG	62.923	127
HM_0347	contig21399	GAT	3	12	CCATAAACACCAAGATTCTGGAG	63.104	TCATAGTCTtGGGTTTTTCGaAATTA	63.009	116
HM_0348	contig31707	TTC	3	12	AATtCCAATCTCATCGAAGAACTG	62.786	AGGCAGAATGAGAAGATGGAATG	62.9	129
HM_0349	contig21996	CTA	3	18	GGaAGCCAATCAAGAAGAAACAAAT	62.995	CATAACTGATTTCAAATGGCCCA	62.132	139
HM_0350	contig04833	AAC	3	24	TAGAATCACCACCAAGCAAAACAT	62.726	AAGCTCTGTAATCGTCTGGTGGT	63.163	129
HM_0351	contig05840	TTC	3	15	GATACCTCTTCTCGGCATCTCC	62.572	ACTCCACTTTTCTCAAAACCCAG	62.906	141
HM_0352	contig33275	CCA	3	15	TGGAACCTCTACCAAGTTTCTCCAC	62.895	CCTCTTCTCCCTCATGCTTATGAA	62.996	133
HM_0353	contig17909	AGA	3	15	CGTCCAATGgAGGAAaAGTAAAG	62.22	GCAGAGCAAGATGATGACAAATTTTC	61.827	157
HM_0354	contig20941	TCA	3	12	AAaAaCTtGATACcCAGAGACGA	63.231	GCAGTTGaATaAATCGCTTTAcG	63.062	108
HM_0355	contig23970	TTC	3	15	AAGGAAGGAGATcGAGtAGagCA	62.922	ACATAGCAAGGAGAAGAAATGACG	63.162	94
HM_0356	contig26435	TTC	3	12	GAATTCTATGGTCTCCGAGAAAG	62.509	GcATCTCTACCTATGtctCctA	62.789	157
HM_0357	contig27464	CCA	3	12	AGAGTAgCaCAGCATGTGACTTGG	62.975	AATGACACTGTTGATTTCGAGCCT	63.356	149
HM_0358	contig10431	GAA	3	12	CATTGAGGAAGTCTCCAAAGCTA	63.006	ATCAAGATTGGTTGCACCTGACTG	62.622	85
HM_0359	contig28952	GTG	3	15	TGAGAACCACCTATCTCTCAAG	62.984	TATGGGTCTGCAACTCCACCTAAT	63.022	115
HM_0360	contig20682	TGA	3	12	TGGATTGTATTGGAATGTTGGTG	62.818	TGCTTGGTCTTctCTCagAACT	62.909	119
HM_0361	contig04127	CGG	3	15	GAGATCcACGgtGgTTgAAAA	63.336	CGCTCATGAGACCTTAAACAAT	63.769	98
HM_0362	contig36846	CGG	3	12	TTGCTTTTCAAAGCCTTGATCTC	63.009	TGATCGTGAATGGGCTCTGTaTa	62.834	128
HM_0363	contig35724	CGG	3	12	GTCACGGGTGTTCTAAATGGTTA	63.227	GGCTCAGTGATGGTTGTAAAGTT	62.972	137
HM_0364	contig13570	TTC	3	12	ATTTCCCTCTTATCTCGTGGTG	62.397	AGGAGGATGAAGAACTGGTCTG	63.106	103
HM_0365	contig11964	AAT	3	15	GCCACCTGAAAAACCaGTACAAAC	63.044	GAGAGGATGTTGAATGGAAATGG	62.987	124
HM_0366	contig30120	TCT	3	21	AACATCGAAGCTTTCTCTCTGTA	62.698	TACGGAACATAAGATGAGGATAAAATGC	63.021	101
HM_0367	contig51422	GAA	3	15	GTTCCCTTTTGTCTCTCATCTC	62.876	GTTTGTCTCTCTCTCTCTCTC	62.863	119
HM_0368	contig11816	CTC	3	12	TTCTCTTTTCCCTCTGCTGTG	63.003	GagTGAGGAGGATaATAGGAgGcg	63.589	158
HM_0369	contig07699	AGA	3	21	TATCGTTAATCTGCTGGCTCACT	63.251	TCTTCGCTCGCTCTATAATCAAC	62.828	139
HM_0370	contig33916	GAG	3	15	ATGTTGAGGGTGATGAATTTTGTG	63.026	TaAGGAACTCATCTCTCTCTCC	63.156	110
HM_0371	contig22713	TTC	3	12	TCCAATGTTTTCGACATGATATA	63.462	CTCTGATTAAGCAGCGGTCACTC	63.671	136
HM_0372	contig34373	TGA	3	12	AGTAAATCGTGTGACTCGTGGT	63.263	CCATGGTTCAACAACATCTCAGT	62.382	147
HM_0373	contig34122	AAG	3	15	AAAAAGAGTTGAGGGGAAGGTG	62.977	AGATGGGAAGGTTCAACACAGG	62.895	154
HM_0374	contig34789	CCG	3	12	AGCAACACATCTCTTTGCAAGTC	62.2	GTGTGTAAGAAAAAGGGTCCgTGT	62.624	147
HM_0375	contig11255	AAT	3	12	TGTTGACCAAAaCTCTCCCAATAA	62.918	GAGATTGATGTGGTTCAACGTTT	63.444	118
HM_0376	contig01666	TAG	3	15	GAGAGATCTCGTACtGgaTGGGA	62.99	CgGGGcATCTGAAGAAGTTAGATA	62.813	125
HM_0377	contig01797	CAC	3	12	GTCTATGACTACTGACCTGACAGC	63.199	TTCTCTTAAAGTCCGTGATGTGT	63.225	105
HM_0378	contig01598	TCT	3	12	TCACGCTTCTTCTCTCTCTGCT	62.71	CAACAGTGACATACCAAAAGGAA	62.295	123
HM_0379	contig15377	TCG	3	12	ATATAAGTGACAGCAGACAGGCA	62.95	GGGCTTGATATGATGTGTGGTT	63.236	152
HM_0380	contig03647	CAC	3	15	CTGATCTCTCAGAAGCCCCATA	63.616	GATCATCATATGTTGGaGGAAAA	63.19	157

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0381	contig26753	TGA	3	15	GAGaGAaATGGgTATgGgATATGG	61.895	TTGGGAATGTAGGGAaGATTTGA	62.884	140
HM_0382	contig38122	AGA	3	12	GGGgTTCACAAAATTCATGTAGTG	62.298	cattctcttccattctgccact	62.811	153
HM_0383	contig19569	GAG	3	12	AATAAAGAGGAATCGGTGGAGAG	62.971	ATATACAGcCTTgCaCcatgaAT	62.843	80
HM_0384	contig33948	TCG	3	12	CATTATCGAGTGtGCAgTCCAATC	62.951	GCAGTGAGCTGGATGATGATATTG	63.059	159
HM_0385	contig17800	CCA	3	12	ACACCGACAACCACTAACAACT	63.181	GTTCCGGTTTCCATATCAGGAgtTTG	63.009	129
HM_0386	contig07558	TTG	3	15	TCTCTAACTTCACACCTTTTCGC	63.031	CTCCCTCAAAAATAGCCCAACAC	63.129	141
HM_0387	contig32955	GGA	3	15	GTTGGAGGAATAGGTAAATTGGAGGG	63.065	CGATCACTGCTCAATCAAACTAATA	63.372	157
HM_0388	contig13632	GAT	3	15	TAGTGTGTGAGCTGAcTGTGGTG	62.637	AcCTCCACCTCTCACTTTTCATA	62.368	119
HM_0389	contig37069	GAA	3	12	CTTCGTATGaaacaATCAcCAcCA	63.15	TCCgggaATTTCctcttCTCAAT	63.259	101
HM_0390	contig47251	GTG	3	15	TAATTGGTGTGGTGTGCAAAAT	63.529	GGTCATGGTGTAAACCAATACAGC	62.756	136
HM_0391	contig51908	TGT	3	30	TGCTGTAATTGTGTGGGTTTT	63.641	CTCTCACTCCACATCAATCGACAT	62.694	159
HM_0392	contig16272	GTG	3	24	GAGGAGGCCCTAATCATCTCTTT	62.977	aAAAAACAACCAACCAACCAAT	63.554	152
HM_0393	contig24287	AAT	3	12	GAATTTTCAATTCATGGTGCAGAAA	62.41	GGTCGGACATGATAAGCATAAATA	62.263	157
HM_0394	contig17947	AAC	3	12	CATATGGTTCACTCTAgACGCA	62.528	ATTTCtGTGAGACgTTTGgGATT	63.386	105
HM_0395	contig10376	CTT	3	12	TTTGATGCGAGTCTTTTCACTATT	62.972	TATATCTTTTCTCAAGGCAACGC	62.748	142
HM_0396	contig06953	TGG	3	12	AACCTCCGGTGGATACATCTCTTT	63.09	TCATGGCTTAGTGAATcACCTTCA	63.038	159
HM_0397	contig43179	TGG	3	12	AAaaGgTGGTGGcACTGTATTGT	62.946	GTCGTACTCTCCAAGcGCTTCTC	62.823	95
HM_0398	contig04798	GAG	3	12	CTAGTATTGGGTTTGGGTGATGGA	63.202	CTTCTACCTAATTCAGACGCCCTG	62.521	144
HM_0399	contig27680	GCG	3	12	ATTCACTGATCGGCTCTCTCAGG	63.035	AGGGGAGGAGCaGAATGTAaAAC	62.995	94
HM_0400	contig06816	AAG	3	12	tCCCATCTACCTTCAAAATtCTCA	63.378	TTTGCTTCAATCAATtGCTCTT	62.935	157
HM_0401	contig26753	AAC	3	12	GGTTGAAAATGAGGGTTTGACAG	63.006	CAGAGATGAAGCCTTTGTAAGGGA	63.006	133
HM_0402	contig28667	TGA	3	12	CATTAGCAATCTGTTCGGGTGT	63.444	CTGTGTCTAAcAAAGAATGGCTCAA	62.859	156
HM_0403	contig29762	CAG	3	12	CCCAATTGTGAAGTCTGGAAACCC	62.907	GACACGGCTCTTATGTCAAAAC	63.146	87
HM_0404	contig33988	TGT	3	24	CTTCAAAAGCTGCTGCTGATACAT	62.054	TTCTCAGAGACAAATGCATGGAAG	62.817	145
HM_0405	contig37888	TGA	3	15	TTACCACTCTGCTGTCTCTGTTG	62.824	gTTTGTGTAATGAATGATGCG	62.629	130
HM_0406	contig13877	CAC	3	12	CTTCACCGACGAATCCTCAAAAG	62.351	TGTTGGTGGGGAACAGGATAGTA	62.894	110
HM_0407	contig04351	GGT	3	21	GCAACCACTGCAAAATCTCTCTT	63.048	GGAAGACAACAAGGACACCAAGT	63.34	139
HM_0408	contig35800	TCT	3	12	AGGGTCTAGCTTCACTCTCTCTC	62.667	TGGACAACCAcAATTAATGAGGA	62.499	110
HM_0409	contig18556	ACC	3	12	AGAGCCATCAGATTCTCGAGCATT	63.444	TGAAGTGTGAAGATGGTTGTGTT	62.933	154
HM_0410	contig20689	TCG	3	12	AGCTTCACTTTTCTCTTCTCGT	62.911	TAACAATTTCTAATGCGCGATCCAC	63.332	123
HM_0411	contig11149	GAT	3	15	TTACAATAGTCCCTCAAAAGTTG	62.557	TTTGACAGATGAAGTACCATTTGA	61.762	160
HM_0412	contig17818	TCA	3	12	GAGCAAGAGGAGAAAGTATGAGC	63.031	AATCATCATGACATCCAAGTCCA	62.867	156
HM_0413	contig49610	TGG	3	15	AGATGGTGTGTATCAGCTGGC	63.726	TCGGGTTCaATACCAATGGATAC	63.009	160
HM_0414	contig16706	CCG	3	12	GCTTTTAAAGTATTCTGGTCTGG	63.348	TTGGAAGGGCAAAAACCTGTGATA	63.109	141
HM_0415	contig39658	CCT	3	12	CGACTCTTCTCCGACTTTCTTCAc	62.909	CTAAGCTTTTCTCTGCTTTCTGCTG	62.954	152
HM_0416	contig08886	TTC	3	12	CCaAGTCTCAAGCTCTCTCATA	62.984	AGACCCAAATCAGATCAGTCTCTC	63.017	129
HM_0417	contig29078	CGG	3	12	TGCGGTGGAGAGGATATAGTTG	63.529	GCCCTGGAACCCCTAGATAGAGAG	62.78	152
HM_0418	contig35683	GAT	3	12	GTCGGAATCTCTGCTGAGTTTGT	63.249	gagccagcagtgaaaAGAGaGTGT	63.48	155
HM_0419	contig34855	CAT	3	12	GATGAAGTCTCCATACCCCTCTCT	62.964	TTGAGATTTGACTCTGAGGACGA	62.473	128
HM_0420	contig13982	CAC	3	15	GAGCAAAAATGGAGGAAGATGATG	63.211	GTTATCACAAAGGCTgAGGGGAC	63.219	157
HM_0421	contig20226	TCT	3	12	AGGCAAGACCATCATAAAGGATC	62.929	TATGAACCCGTTGAAACCCCACT	62.823	114
HM_0422	contig16518	GAC	3	18	GACGAAACCATCTGAACTTTTTC	63.444	GAGGCACGTCACTGAGATCAACTA	62.951	156
HM_0423	contig18164	GGT	3	12	CTAGCCGATGCATTGTGTCATTa	63.283	ATTACATGGCCGCTAGGTTTATT	62.937	157
HM_0424	contig15223	AAG	3	12	AGAAAGCTCCCGCAGAGAAGAAG	64.639	gGACCTGTTTCAGCACCTTGAATA	63.648	147
HM_0425	contig16701	TGG	3	12	TTTGCTTTTCCACTGAAAGATTga	62.212	GACCATAAACAAAGAGcGTTCACTC	62.913	149
HM_0426	contig33805	GTG	3	18	GtgaCACTGaaGAAGAGGTGGTGA	62.921	CATCTATTCCcggcCTATATCCAT	63.275	158
HM_0427	contig05381	TGA	3	12	GATTTTGCAGAGGTGTGATTTTC	63.236	CCAACAaaaAGCACTTTTGGAAATC	63.027	141
HM_0428	contig18920	AGC	3	12	TGAATTGGGATACCTTCTGTGCT	63.009	aCTCCAGTCTGGACATTCTCTGT	62.672	143
HM_0429	contig29398	GTG	3	12	AGTGATATCTCTTGCATTGAGC	62.929	CGAAACCTTAATATTGCCAATCAA	63.118	138
HM_0430	contig03446	ATG	3	15	GAACCTAGGAGGTGCCAAAGCTAC	63.616	TCTTCATCTCTCTGCTCACTCTCA	62.677	135
HM_0431	contig35696	GCG	3	12	CtCTTAAATTGATCATCATCGGC	63.012	GAGcGTGTCCtTCTTTCaACTGT	62.922	157
HM_0432	contig19051	CAC	3	12	GGTACAACCTGACCCCACTCAATC	63.014	AGGATTGTGGCCAAGGATGTT	62.884	143
HM_0433	contig33426	CCT	3	12	GcTtCATTGTGTCCTCTCTCAGAT	63.017	CTGGTAAAGGAGTTGGAAGAGCAG	62.708	140
HM_0434	contig13040	CCA	3	15	AGCATCAGTtCtCACTCTTCA	63.03	GCACAATCCCAAAAGAGACAAGAT	62.813	153
HM_0435	contig05414	GCC	3	12	TCCTTGAGAGTGTCTGAAACCA	63.343	CaGTTGAATCGGAGAGATGTTGA	62.698	148
HM_0436	contig46159	TTC	3	15	TAAATTTGTACCAAGTTGAGCCA	62.256	AAATTCGTTTGGCAACTCTTATCA	62.935	92
HM_0437	contig09899	GAG	3	12	AGGGAGCCTATTCTCAAAAACAA	62.411	GTGATACCTTCACTGGGCTGTTCT	62.925	115
HM_0438	contig00140	TCT	3	18	CTTTAGCCACTCTGATTCCTCCA	63.212	CTTTTCTCTGCTCAAAAACGCTG	63.218	160
HM_0439	contig41660	AAT	3	12	AAaATTAACCCtaacGATGTGGC	61.515	TTCTcTgtTGTCTATAAGCATGtC	61.958	80
HM_0440	contig18738	TGG	3	15	TAGTCTCTGTTGCTCTGAATGGG	63.519	AGATCTCACATGTTCCCTCTCACTC	62.994	106
HM_0441	contig07761	TTT	3	15	GTGTATCCGGACTTTGTTGTTC	62.923	TTCTCAGGCAAAAAGAGAAAAGAA	62.701	135
HM_0442	contig02163	CCT	3	18	ctACATCGGTAGtCgTcaCAcAA	63.389	GAATGATTGGGATGTTGATGATGA	63.008	140
HM_0443	contig31912	TCA	3	12	GAACATTGCAAGCTGAGATCAGTG	63.401	TGCTGTTCTGGCTAGAGAAGGG	63.22	148
HM_0444	contig37827	CGG	3	12	CTGTGCaGATGATGAATTTGAAGG	63.038	ATACTGCTAATAGGCGTGAAGATGC	62.681	159
HM_0445	contig38172	GAT	3	12	TATGGACTGAAGACGACCTGTCTG	62.812	ATGAAGCTCAAGTTCAACCTCTG	63.124	124
HM_0446	contig42401	TGA	3	12	ACCAaATGCATTGTGCTGATG	63.074	cCtccTTTTctcTTCTCTTCTCT	62.762	149
HM_0447	contig07631	TCA	3	12	CCATGGCTTCTGTAATCTAGCCTT	63.789	CCCTGATGATGATTCAAGAGGCA	64.619	121
HM_0448	contig18684	GAA	3	12	GCCACAGTATACCAATCGAGTTC	63.039	gTTCTGCTTCAAAcAAGGAATTGG	63.227	156
HM_0449	contig18604	CGT	3	21	GTATGCTCCATAGCTCATCTGCT	62.956	CAATCCACTGCACTCAAGATCT	63.28	135
HM_0450	contig00018	CAC	3	12	cATAGCTGaCACCTTCCCTGATCT	63.014	AAAACCCATATCTGAGCTTTGtGTC	62.634	124
HM_0451	contig34655	TGA	3	12	TctAcCAcACCCCACTACTCATT	63.01	CATCTCTCTCTGTTCAAGCCAAAT	63.022	150
HM_0452	contig23754	GTG	3	15	TACCAAGGGAGACCAAGAAACAA	63.1	TGCTACTGAAGCTATGCAATCCAA	63.184	116
HM_0453	contig25097	TGG	3	12	CGGACTTctGTGGTGGAGTT	63.82	GTTTGGTCTCCTCTGATTTCTCC	63.588	124
HM_0454	contig12396	ATC	3	12	CTAGATCCATGGGATTGCTATTCTG	62.974	AGATGCTATGTTGCACAAAGAGGG	62.923	119
HM_0455	contig13107	ACC	3	12	CtCtTtTtGtCcagacTtactca	62.993	GCTCAGAGACGGGAACAGAAATAA	63.022	134
HM_0456	contig32464	CGA	3	15	GCCAGTCGAAGACTCTTCTATCCA	63.022	cGTCTTgaTCTTTATAGTCGCGGT	62.851	121
HM_0457	contig03504	CCT	3	12	CCTTATGGATATGGCGCAAGTAGT	62.559	AGGATGATAATACCTCCTATTGGC	63.382	147
HM_0458	contig28498	CAC	3	12	ACaAGACCACTGCGCAATGAAAGC	63.163	CTCaGAAGCCCTAcCAATGTTCT	63.023	85
HM_0459	contig10536	CTT	3	15	GGCAAAAGGCTAGAGGAGCTGAT	63.537	AAGAAACTGGTGGagGTTTGAAGT	62.906	129
HM_0460	contig20552	CCT	3	15	CTCACTCTCTCTATCTCTTCACTA	62.974	TGGAAGAAGAATTTGAAGATCGAA	62.41	152
HM_0461	contig19725	ATC	3	12	TCTATAGCGCAACACATCAATCCC	63.432	AGATAAACCTTGGCGGTTTCTAA	63.194	154
HM_0462	contig51144	TCA	3	12	CATCGAATACGTGTTTCTCCACAA	63.265	CAGGCACTGGAAGAAGAATAAAA	62.811	154
HM_0463	contig10126	GGT	3	12	CGTAAGTCGATCCCTGTGTTTTC	63.031	ACTCCACACATTTTCTTCTTCTCT	63.285	158
HM_0464	contig10960	ATC	3	12	GAATACCAATTATCAACTCCCACTCA	62.462	TCAATTCAAGATGGTTGATGGTGAC	63.248	99
HM_0465	contig14837	TAA	3	12	AGCTCAAAATCAACCCAAACAGAA	63.227	GCCCGTTTAAcAAAAAGAGTCAAA	62.558	95
HM_0466	contig33067	CAT	3	12	TTCCCTTTATCAAGCCATAAGCAAA	63.026	AGCATGGAAATTTTACGTCTCAAA	63.03	104
HM_0467	contig01214	GAG	3	12	CATCGTCAATTTGAGACTTTTCT	62.935	CAAGaGCaGGTCTCattTCTCTTC	62.698	123
HM_0468	contig10744	GTT	3	12	CATTGGTGTGAGGAGATCGAAG	63.111	AAACACAACAATGGACTCAGCAA	62.958	135
HM_0469	contig03555	GCG	3	12	ATGGACCGGAGGAGGATTGAAGG	63.967	GAGaGAGGCGCGTCAATTGG	64.389	95
HM_0470	contig51421	GAA	3	15	GTTCCCTTTTGTCTCTCATCTCT	62.876	GTTTGTCTCTCTCTCTCTCTCTCT	62.863	119
HM_0471	contig29456	ATC	3	15	CTTCTCGATCTTGAACGCTGAC	63.66	gATCAACGATCAACTTTCACTCTCT	62.901	101
HM_0472	contig05898	TGG	3	15	CACCTGATTAAATGCTTTTGGGAG	63.014	AAACGAGAAGCCTCTTGAATCTcT	63.096	159
HM_0473	contig27832	TTC	3	12	AACTTGAAGGAGCTCAAGCTCTTT	62.996	AACGACGCAaAGATCTACCTCAAG	63.044	158
HM_0474	contig07376	AGG	3	12	GATAAGCGGGAGCTTCGTATGTT	62.842	CTAAAGGATATGCACACCTCCAC	63.022	159
HM_0475	contig31109	GAG	3	12	TGATCACTTTGGGACGTGATGTT	63.251	CTAACTTCTCGTAATCGACAGCa	62.883	120

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0476	contig33866	GGT	3	15	ACTTATTTTCGAGATGCTTGGGTG	62.729	CTCTACATCGCTCAACCACAGc	63.573	160
HM_0477	contig32752	ACC	3	18	AAATAACCTACCACTGTTGTCGCC	63.184	TTTGGGGGTGAGTATGTTGATT	63.636	119
HM_0478	contig00101	GGC	3	12	AGACATGTTCCGATGAATGAGGAT	63.111	ATTCTCACAAACAATAGCCGAACC	62.634	81
HM_0479	contig07368	ACT	3	18	cTCGTTCaCTCTTTCgATTCTCTC	62.698	TTCaATAAGATACTCTCCGTGGC	62.718	145
HM_0480	contig02878	GGA	3	18	ACGCAGCTTTGAGAAATTCATTAT	63.245	TGGTAACcATgGAGTGACITtGaA	62.814	117
HM_0481	contig33485	TCA	3	12	GTGAGCCAACACTCTCTCAGGCATT	63.154	TCAAATACAGAAAGCTCgaAAAGGC	63.043	137
HM_0482	contig02041	GGC	3	15	TCACTCTCCAGAAATACCGGCTTAT	63.113	CTACCCGGATGCAGAAAATGG	63.767	156
HM_0483	contig45108	TTC	3	15	ATAGCCCTTCAAAATCCAATGTTCAC	62.713	CCACTACTCTCTCGagAATTTCA	62.088	138
HM_0484	contig07995	GTT	3	15	CCAATAGATCCAACAAATTTGGGG	63.709	AACAATATGCGTATTATCAGGGCG	63.158	145
HM_0485	contig12330	GGT	3	30	ACCACAGTGACAAACAGAGTGAT	63.074	CGACGAATACTACTCTCCACAACA	62.411	136
HM_0486	contig20674	CAT	3	15	CAAGcCACCATCACAAcATAA	63.273	ACACTACAACCGTTTTGATTGGGT	62.835	91
HM_0487	contig31092	TTG	3	24	TGAAGAAACACTTGCTTGATCACC	62.726	TCCAGAAAGaGAGATGtAAAGGC	63	129
HM_0488	contig45798	GAG	3	12	ACCAAAGAGcGAGAGTGAAGATG	63.238	TGGTTACCTATGGCCATGTCTcIT	63.022	81
HM_0489	contig13936	TGG	3	18	TATGATATCCCAATGTTCCGGTGC	63.121	CACCATCCCTTATTACAATTCCTC	63.558	148
HM_0490	contig36051	CAC	3	12	ACGAACGTAGTCCCTCTCTCTCT	63.416	ACCTTcATTTCaTAcccAGTGTGC	63.456	153
HM_0491	contig11934	GCA	3	15	ATCCACAACCAAGCTGAATCAAT	63.026	GTGGTGAGAAATTTGGTGAGGACT	62.795	156
HM_0492	contig13011	TCA	3	12	TTTCTCCCATTTCTcACAcAc	63.232	ATGCAcAGTgGaAAACGATGaGTA	62.962	99
HM_0493	contig41206	GTA	3	12	AaCCcAGATCAATTCCAATTCCT	63.069	GGAGaGCAAAATcTCAgTCCAATTC	62.586	103
HM_0494	contig31516	GAA	3	21	GAAGGGCTCCAAGATATTCGATT	62.903	TcAAAAATCCCTTATTTCGCTTCA	62.908	153
HM_0495	contig27368	CCT	3	12	CATCTCTCAGCAGCCTTAAAAAG	62.728	TTCATGATTGAACGTGAGAAAT	62.108	107
HM_0496	contig44380	ATC	3	15	tcTGATAcTcAaTaaCTCCAAGGAAGG	62.163	TGATGATCAAgagGTTCAACCAA	62.907	124
HM_0497	contig33973	TCT	3	12	AGCTTCAACTcAACCCCTATTCTC	62.995	AGATAATTcGATGGTgGGAGTGAA	63	123
HM_0498	contig26074	ACT	3	15	TGAATCAATGTCTACCACTGTGTG	63.062	TCAGGAAGGAAGAAGATTAGAAATTGA	62.815	107
HM_0499	contig28976	CCG	3	15	GTAGGCCACGAACATAAATCGAT	62.647	GTGGTAGAGGGGCAATCATCTCAA	63.643	150
HM_0500	contig05169	ACT	3	12	CCCCTAATTATCTTCTCATTTCTCGT	62.076	CATTTCCTGGGTTCTTTCTAGGTC	62.873	156
HM_0501	contig48543	GAA	3	15	GTTCCCTTTTTGTTCTCATCTCT	62.876	GTTTGTTCTCTCTCTCTCTCTCT	62.863	119
HM_0502	contig34462	AGT	3	18	GCATATCCAGCATTACCAACATT	63.146	GtTTTTGTGGTGGCAGTATGATT	63.462	137
HM_0503	contig01302	ACT	3	12	AATTATATCGAATCGGGGGTCTCTC	63.492	ATGGCCGTGTTGAAATCAAGATA	63.743	116
HM_0504	contig36958	TAT	3	15	AGCTTCGATTACCACAAAAAGCAT	62.37	ATATGCCTAACGTTCTCTGTGTGT	63.171	153
HM_0505	contig50616	GAT	3	21	AGAGGAAAAAGAACCGTACATCTG	63.01	TCCTTGTCTTGAAGGTCAACATA	63.048	121
HM_0506	contig10782	AGC	3	18	TAGTtGGTTtTcCTTGcGAGAGAG	63.015	CCGATCTATAtTtGGCAGAACCA	63.316	153
HM_0507	contig34460	GTG	3	12	CTCTGAGTAGCTGAAGGAGGTGGT	62.485	CCAATTcGAGTTTTCCACAACATT	63.324	142
HM_0508	contig35925	AGG	3	12	AGGAGATGTTTGTCTTGGAAATC	62.813	AGAGGTGTTTCTGTTCAACCCAAG	62.906	98
HM_0509	contig05865	CCG	3	12	TAAGCCCTCTGTTGTGCAATTTTA	63.122	ATGAGAACTCCATTGGCATTGTTT	63.026	133
HM_0510	contig30622	TCG	3	12	GAGAAGTCTAGTGGTCTGCAAGGC	62.823	CTTCTCATCACCGACCATACAT	63.431	148
HM_0511	contig04524	GAT	3	12	GCATTGTCCTTCTGGTCTGTGA	63.648	TAAACTGTGAGAAGCTAATGCCCC	62.839	132
HM_0512	contig25167	ATT	3	18	TGATGAACCAATTTGGGTTCTCTT	62.8	GGTAGTACCAGCAATGGAAGCAGT	62.851	144
HM_0513	contig23711	ACC	3	15	ACAACCTCTCTTCAACAGCAGCTT	62.949	TCTTCTTATGGGCAGGATGTTAA	63.005	158
HM_0514	contig08770	GGA	3	15	ATCTGCATCAGAGTCCTCTCTCTC	62.457	GATCTGATaAGTTcAGACCCCTCG	62.469	155
HM_0515	contig02923	ATC	3	18	GAGCTGCTAATTGCAAAAGTGAAA	61.981	GCTCaAAtATgGAAGCTTTTAGCA	62.035	158
HM_0516	contig43669	TCG	3	12	GTTtAGTAGGGCGATGTTGAATGG	62.935	CtGgAGATCtTGAGATGaTgGaGg	63.515	158
HM_0517	contig37406	GAA	3	12	TTGAAATTGGGGGTGAGAGATAA	63.091	CTTCTTCAATCTCCGATCAACT	62.786	137
HM_0518	contig27840	ACT	3	12	AACAACCTGGTCCATAATGGGAGA	62.897	AACAACCTCTTGTTGTGTCATGTT	63.023	108
HM_0519	contig07404	CCA	3	15	TACATCAGGGTCTGGAATTCCTCT	62.672	CTTCAAAATGCACAATGGAAGCAAC	62.972	112
HM_0520	contig47299	GAA	3	12	TATCACTCAGAAACCCCAACTCCA	63.026	AACCTGAGAAATCAATGGTCCAAC	62.996	151
HM_0521	contig00169	CAT	3	18	CCCAAACTCACTCTCAATGAGAC	62.368	TGTGGGTTGTTGTCATTGTAATTg	61.766	160
HM_0522	contig22964	TTG	3	18	AGGGTTGGGAGGAGAAGAAATG	62.843	TTGAGAAGCATTTCCACaAAAGAA	62.212	159
HM_0523	contig24994	TCT	3	12	TTTTtGTTtCCGTTGTTtGAAAGAT	62.919	GAAATTGACATTTCAAGTCAAGGG	63.108	159
HM_0524	contig11111	GAA	3	15	GCTCGTCTTCTCAATTTCTCGTT	63.208	TGGTCGAGTCTTCTTAAATTgCtTc	63.132	148
HM_0525	contig03604	GGT	3	15	ATTAACTCAAAACACTCGGTGGTG	63.227	TTCAAAATTCAGCTACCCCTCAAC	62.716	142
HM_0526	contig26254	CTC	3	15	AATGATGACAGGAATGATTGGG	63.327	ATATCGCAATCAGACCTTTGGAG	63.635	155
HM_0527	contig24524	AGT	3	24	CTCACAGCGTCAATCAATACAT	63.401	ACGATTGTCTCAGAAGAATCACT	62.613	141
HM_0528	contig17625	TCG	3	18	GCTGAGtGTTtGATTtGTTGTGc	63.091	ACTAGCTCTGAGagGACGGGAAT	62.999	122
HM_0529	contig14536	TCA	3	21	CCATTTCCACAATAGGTTTGTCA	63.097	CTCCTACTATGATGGCCGGAACAT	62.716	111
HM_0530	contig52530	TGA	3	15	TCGTAGTGCTCTATCAGCTCTTGC	62.353	AATTCAATCCCACATGGAACCAAC	63.112	135
HM_0531	contig39682	GGT	3	15	CGTTCTCGATCTACATTTCCGTT	62.923	CCGTTTGTACAATCTGTTCTGTA	63.273	108
HM_0532	contig19848	CTC	3	12	GTATGCTGGTGGGACGACAGT	63.623	GCTGAGAAGTTGGGTAATGCTCTC	62.727	135
HM_0533	contig20693	GAT	3	15	AATCGGAAATTAATGTCTGGGGAT	62.881	CCAATCGAAATAGACACTTTGGCT	62.729	144
HM_0534	contig34811	ATT	3	12	ATTGTTGGATTGGGAAATCACT	62.937	GAGATCACCTTGGAGAGTTCTTG	62.664	117
HM_0535	contig52062	TGA	3	24	ACGTCTACATCTTCTGCTCTCTCG	63.137	CTCATCTCAAAACCAACCAATA	63.3	159
HM_0536	contig39032	CAG	3	18	GTTTCTCATGTCAAGACAATCCCC	63.106	GCTGCTGAGAAATAGCCTTCAAAA	63.15	128
HM_0537	contig02871	CGG	3	12	CTATTATCCACAATCGCGGAAG	63.027	ATCGGGTTAATGGGTTGAGAGATT	63.081	152
HM_0538	contig51280	CCA	3	12	CACCGCAAGTTTCAAGATCAAAATC	62.968	TACTTGTAGGtTtCtTGGGtGGT	62.103	97
HM_0539	contig41416	GAG	3	12	TtGTTAGCTAGGagGAGTGGGAAG	62.201	GgTTGGTTGCTTtGtttGTTATTTC	62.839	160
HM_0540	contig18476	ATC	3	12	TACTCCAAGGGCTTCAGAAAGTTG	63.015	AAAATTTACAAAAGTTCCTCCGCA	62.897	96
HM_0541	contig19526	AGT	3	12	CTAGAAGTCAACTGCTTGCTCCTC	63.036	TCCACTGCTGTCAAAATAGCTGAC	62.858	125
HM_0542	contig00169	ATC	3	15	cTCCCTTGAGGACTACAACTCGTG	63.545	ATCAGGATATAGGCCACTCCACAC	63.45	142
HM_0543	contig10593	GAA	3	12	GAGACGAGTTCGCTTGGTGA	63.936	GGGTTTGGGTTTGTATGGAAACT	63.285	114
HM_0544	contig33468	CCA	3	12	CAATGTCGGGAAAAAGTGAAGG	62.906	CTTTAGAGGGCGAGGACGCTG	62.204	92
HM_0545	contig21455	ATG	3	12	CTCTCCCTTGGCTTTCAGATATT	63.086	CAGTAGCAACTgAaAgCCTTCTcC	62.835	149
HM_0546	contig52141	CTT	3	12	ACTTTCTGGCTTTTGTTTTCTCC	62.91	AAATCCAAGGATGAGACACTGAG	62.884	156
HM_0547	contig39263	CCT	3	12	TCAGACCATCTATTCTCACCCCTC	62.874	ACACTCTGTTTGGAAAGGAAAAACG	62.82	136
HM_0548	contig15788	CAC	3	15	AAAAGAGCTGCTAATGTGACACC	62.949	ATGACTGCAATGGAATGGTATGTG	63.055	156
HM_0549	contig16240	CCA	3	18	ATATCCCTCACCTAAGATCGTC	62.772	AACAAGAAAGTCAGGGGAGTGTG	62.906	159
HM_0550	contig03270	TCT	3	12	CTGAtCtaCATGGCTCTCCGTTTC	63.444	CAACAACGAGAAGGAGATTGAACc	63.325	160
HM_0551	contig10387	CAA	3	12	CTCTCGCTTCAATTCGGATACCT	62.899	GACTgGGAGcAgGAGAAGTAACAA	63.124	160
HM_0552	contig11114	GGT	3	12	CACCATAAGAGTTGgAAAAGGTGC	63.129	CaTgGCTaAGATTGtAgGCTCTT	63.035	140
HM_0553	contig20652	TTT	3	18	TTGATGATCCGATTGATACGATTCT	62.177	GTGACATTACGAATCAACAGAGCG	63.078	160
HM_0554	contig18933	TCT	3	15	TGCTTCTTCTACCTCTCTTCGAGT	62.835	CCAGTCCAAGTGTGTTCAATAG	61.971	143
HM_0555	contig04714	AAG	3	12	AGCCAAAAATCCCAAAATGCAATC	63.486	CAGTGTCTTgGAAATTTGGAGcgaG	63.331	156
HM_0556	contig27918	GTA	3	12	CCTCATtTCCCTtACCCAAATAC	62.875	TGAAACTGAAACCTAGaaCTcCaa	62.411	91
HM_0557	contig38240	CCA	3	12	AAAACCCAACCTCAAGTCCACAA	63.015	GTGGATCGTCTCTGGATTACCTGT	62.798	129
HM_0558	contig21909	GGC	3	12	ACAGAGCATCATGCCATCGAAAT	63.253	GATTcAGTTTTCTGATCACTCGCC	63.45	148
HM_0559	contig12957	CTA	3	12	GGTGGTTcAgCTTGAATACTTGTG	62.103	TTCTCCATCAACACGATGACAGT	63.044	111
HM_0560	contig06134	TCT	3	12	GCATTCACTCTTTGAAAAGCAC	62.308	GCAGTAGATAACTTGAATGGGCTG	62.975	156
HM_0561	contig13797	CTT	3	18	ATACCAAGTTCGGGATGAACATTG	63.027	ATCCGGTAAGCTGTTAAAGAGGC	63.028	144
HM_0562	contig41644	GAT	3	15	TCTCGCTatAGGGACACCTTCATC	62.913	GTCGCTGGAACtCaTATCATCTCT	63.133	116
HM_0563	contig47132	GGA	3	15	CTACTAGGCCGTATAGCGACGATG	63.264	CAGAGAGCGaCAAAAATCAGAGAA	62.945	112
HM_0564	contig39243	CTT	3	36	AGAACCAAGTTGGCCAGATGTTA	62.072	TCAAGAAGCTCCTAACGAATCTGA	61.692	157
HM_0565	contig03739	GAT	3	12	gATAGGACATGAAATGgGcATAAG	62.832	tCCcATTCTcTcCTCTCTATGCT	61.933	131
HM_0566	contig22384	GTG	3	15	TGCAATGAATTTCTTCTCTGCG	63.142	TAATTCCATcAcCGTGTAAAGGACC	63.219	121
HM_0567	contig30235	AGT	3	12	ATGAGAACCTTcAGGCAATGtGTAAG	62.94	ATAAAACCTTcAGTtGACGGACCA	63.019	116
HM_0568	contig00699	GAG	3	12	CGGCTGTGGGAGAAGATACAGAC	63.672	TGTCAACCCACCTCCATaGAATG	63.227	127
HM_0569	contig17187	GAC	3	12	AAATGGTCCGAAGTGTCTGTGAAA	63.019	AGCCAGGCAAAATACAAGAAAGTG	62.849	143
HM_0570	contig10834	AAG	3	12	TTCCAGAGGTTCTCGTAAATACCAC	62.698	GCTACCTCGGGTCACAGTATGATT	62.727	142

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0571	contig00729	GCT	3	18	GATCTTGTCTCTGCTGAGAAGCAC	63.794	CAACAACCCCAAGTTTCTCAAATC	63.006	157
HM_0572	contig41308	CAC	3	15	GaCCaAGAAATCCcATGTCaAaC	63.278	TTAATGGTGGGTTGATGGAGTCT	62.691	126
HM_0573	contig06592	GTT	3	12	ATTGAGCCACTCTCTCTTCTTC	62.986	ACAATgGGcTGCTAAGAAAAACAA	63.146	96
HM_0574	contig48683	AGA	3	12	IGCCCTGTGTACATAAGCTCTGTT	62.236	AACTCGAGGTctTCAGTGTTTTGG	63.02	122
HM_0575	contig00585	TCT	3	24	TAATTCAGACCCACTCTTCACCT	62.368	aAGTTGAAGAGAGAAAGGGAACCG	63.28	160
HM_0576	contig00216	CAG	3	12	ATAAGAAGAAGCTGTGTTCTCCG	62.215	CGGAGCTAGGTTAAACCCcttCTC	62.714	128
HM_0577	contig24199	CGA	3	12	CGATCATCACACTAAACATGcGAA	63.141	TTGTAACGTTcCtTTTCTCTCCG	62.821	131
HM_0578	contig11684	ACC	3	12	cTCTTTTGACTAACcGCTCTCT	63.199	CGTGCTCTTGGTGCTAGTAATCT	63.057	133
HM_0579	contig21545	CTT	3	12	ATTTCTTTTGAGGCCTTTGAGTCC	63.09	AacTCATCCCTTAGGctTCGAT	63.5	153
HM_0580	contig04783	TGA	3	15	AGTTTGACGCTGAACAGATTGAT	63.468	TTGAACCATGAACCATACATCACC	62.924	137
HM_0581	contig05499	CCA	3	15	TAATGCTCACTAGACCGTCCAACA	63.061	CACAAAGAACAAACAGCCTCCTT	62.931	150
HM_0582	contig27925	CGA	3	18	GATAAGATAATGAACGTCAACGGC	62.94	TCTTCATCGATATGAACCTCGTGC	62.617	101
HM_0583	contig47583	CTT	3	15	CTTGCCAATGTGCAATCTGTAAGTT	63.659	TCGGAGTCCAATCGAATTTAAATG	63.304	144
HM_0584	contig31717	TTC	3	15	TGGGTATGATCTCAGTTTCTCCA	63.154	GTGTCCTATTGGGTGTCTCTCT	63.005	111
HM_0585	contig02141	CCA	3	12	TGCTCTCTTATGCTACGTTCA	63.061	AGCGGAGGACAGAGATTGATT	62.68	83
HM_0586	contig08791	GCC	3	12	CGTCTCTTATACGGAAGAGCTGA	63.129	GGTTgAgCTGCTACtatTTTCGG	62.464	144
HM_0587	contig30815	CTA	3	15	CTATTACCACGAATCCACCTTCT	62.633	gGGGAATTGGCATCATCATTATC	63.51	100
HM_0588	contig08907	CTT	3	12	aTGCTGGTTAGCTCACTCTGGTAGC	63.064	TTATCCCTAgATCCCATCCAATG	63.057	133
HM_0589	contig10916	CCG	3	15	GGTAGTACTGCTCGCATCGCT	62.979	TGATGATGGGAAGAAGAAGAGAGG	63.076	140
HM_0590	contig27032	CTT	3	12	TTCCAGAAATCATCCACTTGTAG	63.513	GCCAAAGAAGAGGAAGAAGAAGACC	63.084	110
HM_0591	contig12341	TCA	3	12	GGGTGCTAGGAGTTTCAAGATAC	62.55	GTGGTGGTaAAGTTGACAgAATG	62.739	123
HM_0592	contig19707	GAA	3	18	ATTTTGGTGCTTGGTTTGTATAGG	62.437	TCCAAGTTAGAGGCTTTTCTCCC	63.18	132
HM_0593	contig26865	GAT	3	15	CACATGTCTGTTTTCACCTTCAC	62.972	CAGCTGCTGACAATGAAGAAGAG	62.739	150
HM_0594	contig15067	TTG	3	12	GGTGGTCAATCGGTTTATTTTCAG	62.813	TAACAGGCGTGCTATCTAAGACCA	62.255	123
HM_0595	contig35335	CCG	3	12	CTGACTTCGATTCCCGCTTG	63.131	CTCAGGTGCTGTTTCTGTGTCT	62.927	154
HM_0596	contig21606	AAT	3	12	GCCTCTTTAAATTTATTTTCAGGA	61.276	CGTACACAACATATATGAATATTGCACC	61.024	135
HM_0597	contig15710	ATG	3	15	AAATGCACTGTAGTGGTGGTGATG	63.065	GCAACTGCAAGATGAATTCtCA	62.746	146
HM_0598	contig38913	GGC	3	15	TTACAAACCTTTCCACCCCAAAAA	62.717	GAAGACGGGTGATCTTTTACAC	63.23	115
HM_0599	contig03121	TTC	3	12	TTTCTTATTGGCTTGCTCTTCA	63.322	CTTATCTCGCCTGGATCATCTG	63.317	159
HM_0600	contig15155	GTT	3	24	ATTGAAGCcGAGTTTGAGAAGATG	63.022	GCCAATCTGCTCCTTTTGATAGC	63.226	152
HM_0601	contig06490	CAA	3	12	AGGTTTAgTGCAACCGcAGTAG	62.872	CtGGtTAAGcCTGGAaATaAcGg	63.013	107
HM_0602	contig50268	TCT	3	12	TTGAACAAGTCATCTCCAGTAA	63.048	CATCGGAAGAGCAAAAcGAT	63.758	113
HM_0603	contig25274	CAT	3	15	AACTCAGCAATTGAAGTATGGGA	63.121	CTCtTgTTTTCCCATCTCTcCTT	63.164	149
HM_0604	contig24707	ACA	3	12	AAGCTAACTGGAAGCCTCTGGGT	62.899	TGCACATGTTCAAGTTTGGTCTTT	62.958	122
HM_0605	contig05181	TCT	3	12	AACCTTCCACTGCAGATCAAAAAC	62.824	ATGCCATATGATCCTCTGAAGAA	63.103	129
HM_0606	contig03104	GGT	3	12	TGCTAGGATACCGATGACTCCAAT	63.125	ATTTATTGCCCAATGTGGTCTAC	63.154	123
HM_0607	contig33249	CTT	3	15	CAGGGGTGACAGAATAATGATGAGAG	62.327	TtGCTTTTGTGATCAAGTCCGTA	62.956	151
HM_0608	contig30003	CGG	3	15	CTTCTATCCAGATGGAATCGGT	62.659	GCGAAAACCTCCCAACAGAAATG	63.025	123
HM_0609	contig29565	CAA	3	15	CAAGACAATAATGATCCACAGATGC	62.938	ATCGGTCTTCTCATGCTCATAGTC	62.816	136
HM_0610	contig19942	GGT	3	12	TCTCTTTCTGTTGGTCTAATG	62.919	CCTAAAAACCCACTTCAAAAACCC	62.986	114
HM_0611	contig42716	CCA	3	12	GGTCAGGAGAGCATATCAGGGT	63.088	TCCACCTGTAGATTTGGGAAGTTT	62.186	152
HM_0612	contig04021	TGT	3	21	GGGGGCTCTGTTGATGTTGAT	63.458	GAGCAACAGATCGAAGAAACATT	62.926	160
HM_0613	contig24328	TCA	3	12	TAGGCTCTGAGAGATCTTCTCTGA	62.987	AAATGGTTCTGGTCTATGCAAT	63.15	132
HM_0614	contig21041	CAC	3	12	TtCCCCcAtTATCAGaATCAaTG	63.08	AGTTGGGTGTCGACTAAGAGCTTC	62.311	146
HM_0615	contig36104	CAA	3	24	AATCGAACCCACCTGAAATGGTACA	63.747	TGGTaATGTTGGTgGTTGTTGT	63.389	160
HM_0616	contig24557	GGT	3	12	TCCCATTAATCTGGAATAGATCGC	62.507	ATCTCCCAACCTTTCAGTTTCTCC	63.071	150
HM_0617	contig09424	ATC	3	15	TAATTTCAAAGGGTGATTTGGGTG	63.097	GTTTGTTCGACAGCATGTCAAcT	62.769	160
HM_0618	contig02465	TGA	3	15	AAAAGAAGTCAATTGCAAAAGGGTG	62.728	GAAITtgGGGAActaCAATaGcCC	62.995	116
HM_0619	contig44273	CGA	3	15	GATCCGAAAAATCTGGCCTTTAC	63.191	GAGAAGATcgCCGATAAGTTTTCAC	62.523	117
HM_0620	contig10334	CTT	3	18	TACTTTTCTCCCAATTTCCGGTAT	62.98	ATCGATTATTCACTCTCGGGCATA	62.821	118
HM_0621	contig15923	GAT	3	12	GAATTGGAGGGATGAAGAATGAaG	62.254	AACCTCTCaAcAGaCAATTCcCA	62.795	80
HM_0622	contig30029	GCA	3	12	CAATTATGAGGGCTTTGTTTTTCG	62.93	GCATACAAGCGTCTTTTCTTGGC	63.28	160
HM_0623	contig25541	TGG	3	21	TTTCTTGAATCTCGGATGTGGC	63.743	ACCACCTCTCCGACACCTT	63.212	157
HM_0624	contig09510	GGC	3	15	gTTTGGGAgTGGGAgTGG	63.898	TTCTtTtTCTCAACTTCGCCCTC	63.121	130
HM_0625	contig29387	AAG	3	18	ACTCAAAACGACGCTGTTGTATG	62.569	GAGTGTAGAGGTGGTGACTCTGG	63.561	159
HM_0626	contig26167	TAT	3	12	TACTGGAATGAAAGCGTTGTGTA	62.956	GCCCAAAACAAACaATGATGAGAT	63.334	124
HM_0627	contig13234	CCG	3	12	CTGCGCTTCTCTTCTTCTTCC	63.989	TTGATTCAAAATGAGTGGCAGTG	63.367	113
HM_0628	contig02554	GTT	3	12	ACAAACAATaGTCGCGGCAAT	63.067	GTTGGGCAGAGAAGGGATAGAGAT	63.185	115
HM_0629	contig31093	TGC	3	15	GTGATGGCGATGATGTACAAGC	62.734	CTAGCATGGGACCCCAATTCTAC	63.022	141
HM_0630	contig47500	GGT	3	12	CCATGATCAACAACACCCACTAC	62.607	GCATCTTtaAcGgAGTCTCTCCT	63.302	145
HM_0631	contig06225	AGC	3	12	GACACATCACTGGAGTCAcCAaC	63.049	TGCTGCAATTAAAGTCGACGAGAG	64.045	121
HM_0632	contig42470	AGA	3	12	TCTCTTCAACCAACCACTAACGAG	62.905	CTTGAAACTACACAACCCACTCTC	62.906	141
HM_0633	contig00223	AGA	3	15	IGATGAaTATgTtGAGCTGTGAGA	63.053	tTcCaTgGATcCaATtTtctCTTC	62.607	106
HM_0634	contig45979	GCT	3	24	AAAAGCAGTGTGTTTGGTGTG	62.426	CCTCAGCTACTcCaTGTATTCCGG	63.227	109
HM_0635	contig25073	TGG	3	12	ACAAGCTGAACAATCAATTTTGT	63.035	CCCAATTGGCCAATGtagTAGTGT	63.239	127
HM_0636	contig37699	CCA	3	15	GTCCcATaTGAaACcCAATATCA	62.889	TCCAAGTCCAAGTCTCTCTAGC	63.124	149
HM_0637	contig26270	CGT	3	15	GATACCCAATTCTGTTTGAAGTC	63.026	AATTCAAGACTTGAATCTCAACCG	62.798	146
HM_0638	contig34906	TCT	3	12	CAGATCCTGAAGATCCAGTGCCA	62.786	TTTGTGTCGAAGTCTGTAAGCA	63.057	137
HM_0639	contig49182	GTG	3	15	tGAAGGGcATGAGGtTTGTACT	63.031	GAITtCCCCAATAAAAcGCAAAAC	63.671	125
HM_0640	contig34766	GGA	3	30	TGCTGCAGCTGAACCTGACTCT	63.105	CTACACAACCTCATGTTcCACCAC	62.827	160
HM_0641	contig39096	TCA	3	21	TGCTCTCTCAAGCTCAaTcTCA	62.831	TTTATCAGGTGAGGCAAACTACAT	62.821	138
HM_0642	contig01439	CCG	3	12	TCCACTGATAGCTAGCTAGTAACCCC	63.215	GTTTGCTGCTGctAaTTGCTACTCT	62.949	93
HM_0643	contig01265	CTT	3	21	GGGTCAATAATCACTgggAaGACCC	62.974	CTGTCACTGTACTGTTCTCGACCG	63.4	144
HM_0644	contig33059	GAG	3	12	GCATAAAAGGATTTTGGGAAAG	62.989	TCTGCAACATTGCTAGTCAAGTTC	62.858	141
HM_0645	contig16701	GGA	3	12	TTGAAAGTTGAGGAGTCCGAGAT	62.598	ATCGCCACCCTCGTATTTACTCT	63.148	102
HM_0646	contig10998	TGC	3	12	ATGAGTTGCTGCTGTTGGAAAGT	63.849	AAACATGCCCTTCAGCTTAATTC	63.694	87
HM_0647	contig02014	GAA	3	15	GGTAATGATTGGTGGGATGTTGT	63.013	GCTGGCAACACTGCTGACTCTCt	63.176	149
HM_0648	contig15814	TCA	3	12	ACCTATCAACGCACTCAATTTAT	62.935	ACCAAGAAGAACCCTCAAAATCA	62.284	155
HM_0649	contig05937	CTC	3	21	CAACAAGTTTCTCTGACtGACTCG	62.596	ACCCTCAATAACTAAGACGGAGGA	63.488	158
HM_0650	contig27586	GTT	3	21	GCCAAAATCTCCACCAAGTGTAGT	62.725	AGCAACAGTTTCAAGACTCATCAGC	62.2	151
HM_0651	contig19293	TTC	3	15	CaACcTtTATTtCAGCAaTTTGAA	63.311	TGAAGGACGAGGACCAaATTATC	62.481	235
HM_0652	contig39043	CTA	3	15	ACTTCATGAAGGtCTCTCATGCTC	63.017	TTCTcATCATTTCAAAcCTCAATT	62.987	93
HM_0653	contig21493	TGC	3	12	AAAGCATGATTCTTCATTGTGCC	62.608	ACGAGGAGCCAAAAAGAGTTTAC	63.11	158
HM_0654	contig07801	ATC	3	12	GGAGGAACAAGCTGTGAGAAAGTA	62.91	ACTTGATGATGAATCATGGACCTC	62.994	133
HM_0655	contig14452	TCT	3	12	caCAACAGAGCAAGATATCCCAT	63.549	CCATCAAAATCCAATaATAAGCCG	62.634	160
HM_0656	contig09331	AAG	3	12	AAACATGTGGTAGGACGAGAAAGCC	62.838	AAAAACTGCCCAAGTAAAAAGAC	63.024	99
HM_0657	contig25184	CAC	3	12	CATCTACTGCTCCCTCTCACCAG	63.557	AGCCAATTGGATCATTCTTTTGAA	63.009	148
HM_0658	contig21848	AGA	3	15	CATCTACTGCTCTCGCACATTTA	62.643	CCTCTCCGATTCTCTCTCAGATT	63.266	87
HM_0659	contig02249	CTT	3	12	TGTAGTCTGCTGTTTGCCTCAATT	63.129	TGATAAATCAAAACAGGCAGACAGA	63.059	135
HM_0660	contig05495	GGT	3	15	AATTGCAGAGAAGAAGTGAACGC	63.15	CTTCTCGGTTACTTCGAGAAGATG	63.36	155
HM_0661	contig25694	TTG	3	18	CAGGAATCTTTGACAGCTGTTT	62.921	TAAGCaAtAACTTGAAGGCCCAA	63.034	97
HM_0662	contig17096	CTT	3	12	CCACCAAATATTCACATCTTTTC	62.691	AATGGTGTGGTGTGcTGATCTT	63.014	122
HM_0663	contig10104	GGT	3	12	GAATCATCAAGCTTCTGCTCTT	64	GACCTTTTGTCTCTCTCAAACTC	63.374	154
HM_0664	contig36582	CGA	3	12	GATGGGTCTTGCTAAGCTCGTA	61.906	TGATGGATATGATTACATACGCCG	62.851	97
HM_0665	contig50271	CCA	3	12	CACCAACCAAGTATAAgTCCGC	62.817	GGTGGGGGGAaGacGATTGTAGACT	62.91	152

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0666	contig12814	AGA	3	12	CTTTGTTGGTTTCTGCTGTTGG	62.864	CATAC TAGAAAGCCAGTTGGTGG	63.125	121
HM_0667	contig50824	TTG	3	15	TGGTAACCTTTGGAGCTCATGAACA	62.814	CGACCCTGTACTCTTGTCTCTCC	62.691	109
HM_0668	contig23479	GCC	3	12	GGAAATAAATCAAGGAATCCCA	63.248	ATGATGGTTGAGACTGGTTGGTT	63.014	130
HM_0669	contig37123	TCA	3	12	TATTTCCATCATCTGCTGCTCAT	62.605	ACATGAAGGAGACAATCAGGAGG	62.884	110
HM_0670	contig22920	GGT	3	18	CAGAAATGGAGGCGAGAAATAgA	62.996	TTAAACAATGtCAGAAATGATGGC	62.325	113
HM_0671	contig24108	TGA	3	18	GATACGGATTAGTGGGAAACCCAT	63.282	ATTCAACTGCAAAACCCAGAATTA	62.922	141
HM_0672	contig40270	GAT	3	12	TGATGACAAAGATGAGGATGAGGA	63.113	cCaTTTTAGTTCGTCTACTGtGtC	63.129	131
HM_0673	contig31689	CAT	3	12	ATAGACTAAACCCCTCACCAGACC	63.008	GGCCAGATGATACAAAAGAACCA	63.121	104
HM_0674	contig30611	ACT	3	12	cAGTAGGCTGCTGATTGTCTCAT	62.936	TCTTACTATCTCCGACGACCTGC	63.035	101
HM_0675	contig31858	TTG	3	12	GTTCTTGGTTGCTAGTGTCTgCT	63.163	CACtCTCCGCaCAAgAGGACT	63.141	121
HM_0676	contig08355	ATC	3	15	CATCAaCATTATTGACAGAAGCCG	62.845	TTGAAACAACCTCAAAACCGAATTT	63.027	111
HM_0677	contig05140	GTT	3	12	CACGGTCTCTCATAGCAACTTTT	62.933	GAACCAGAGTTTTCTTCCAGTCCA	62.997	104
HM_0678	contig01982	CTT	3	12	GCATAGAGAATCGCCAGTAAAC	63.166	CTGAGAATCTGAGAGGTTTGGGC	63.64	123
HM_0679	contig15510	TCT	3	24	AAACCGAGATTAAATGGTGGgAG	63.47	CgGTTGGAATTaCGGAATAGaAA	63.013	137
HM_0680	contig40457	AAG	3	12	TGCACAAATCTGAAATCTCCTTAC	62.126	gCCGACACGACACTAGGATAGAC	62.512	150
HM_0681	contig31499	TGA	3	15	TCATCATCGACAAAATGTACCG	63.046	GTAGATACAAAGAGCACACGC	62.25	146
HM_0682	contig05109	TTG	3	12	ACTCTCCAACCGCAATATTCACAT	63.039	TCCTCCTCTCTCTCTTCTCAT	63.152	159
HM_0683	contig07247	TGA	3	15	TGGAATTAGAGACTTCATCCCCag	62.771	CATCTCTTTCCGAAGATTGAGAGC	62.8	153
HM_0684	contig50392	TTG	3	12	CGGAGATTGTGATGAGATTGACG	62.919	TACCTTCTCTGTCTCACCACACT	62.574	143
HM_0685	contig37575	TCA	3	18	AGGGACTTTGAGTGCATGGTTATC	62.713	GTTCAAGAACTCACAGGCCAGAC	63.57	156
HM_0686	contig05338	TGT	3	24	CACCACCAACGTGTTTGTGTTTAT	62.969	CACCTCAAAcTGAGATGTCCAAG	63.026	109
HM_0687	contig16760	GGT	3	15	ATACACCGGAATACCCCTTATCGG	63.187	GAGTTCAGAAAGCCATCACAAA	62.726	119
HM_0688	contig02498	GAA	3	12	CATTTTAGCCAGATAGGAACCC	63.084	GAAGAACTTGGCTCTGAGATTGAT	62.926	152
HM_0689	contig05517	GGT	3	15	AACGAAAGCATaAGTATGGGGCTT	63.221	GTGTACGGAAGGATGAAGAATTG	63.009	159
HM_0690	contig29976	ATT	3	15	ACAGATcaTCATCGATGGATGGG	63.372	TGTGTgaGTTGACATTGACCTTCA	62.833	145
HM_0691	contig03195	GTA	3	12	TAGAGCAAGATTTATGCGGGAAC	62.748	TGAGGCATATCAATGCTCACATTT	62.85	147
HM_0692	contig14346	AGA	3	15	CTTGACGTCCTCTCTCTCACCT	63.208	AAACCTTAGCCGCGACACAT	64.052	138
HM_0693	contig50951	TAA	3	12	CGGGAATAGGTAACTCGGTGATT	63.602	GATGACATGcCTATcCTTCATTCT	63.007	148
HM_0694	contig29591	CGT	3	12	ACACGATCTCCCTATTATGCTCG	63.014	ATcTCTTGGACGAGGAATCTCT	62.876	102
HM_0695	contig15219	CTG	3	12	GCACTCTTATCTCTCTGCTGGGA	63.23	GAAGAAAGAAATAGGAGGGAGGCA	62.98	140
HM_0696	contig39490	ATG	3	12	TGCATGGGTTAGTAGGCTaGATG	63.54	GagCTgactGACACGATGAATGAC	63.412	107
HM_0697	contig24222	TCC	3	12	TCTACCGACTCTTTTACGCTCT	63.022	GACAGGCTAGGTAGAGAGGGAGC	63.109	131
HM_0698	contig24682	ATT	3	12	CTGAACCTGCGTCAGTGATTGAAA	63.711	GGGCTATTCACTTGAGTGCTCTTG	63.561	137
HM_0699	contig41103	TAG	3	12	CCGCTAGAGTCCTCTTATGTAT	62.62	AAGGTTTGGTTGATGGATGAGCT	62.795	117
HM_0700	contig03805	CAC	3	12	TCCTCTGTCAACAAATTC3A00	62.918	TGCAGAAAGTCCAAAACACTTCAA	63.159	84
HM_0701	contig12506	TCA	3	12	AAaCCGTGCAAGaCTaCaGCAAC	62.768	cagagatggctgattggatga	62.7	147
HM_0702	contig10918	GAA	3	12	TTACTAGCGAATCTCTGAGCTGTT	62.755	TTGATCAATATGAGaAgAgGGG	62.566	148
HM_0703	contig06522	GCA	3	12	gCCTAATGAAAGGATTGACATGC	63.037	TGTCACTGTATCTATGAGTCCGC	62.623	156
HM_0704	contig08955	GGT	3	12	ATTTTCAGTTGGTTGATGGCACT	63.035	ACCACCTCGAATCTCCAACTTC	62.901	87
HM_0705	contig08430	TCC	3	18	CTCAATATTAAAGAGAGGCCCA	63.655	AGAATCAGGGGCGACATGTTGAAT	62.926	128
HM_0706	contig05056	CAC	3	15	GGAGCTACGAGAGGACAGATGIA	63.128	CacCaATTTTCTgTGTCTCaATg	63.607	100
HM_0707	contig01906	TCT	3	12	ATAGCTGATCTTTTCCGGATTTC	62.893	TAGGGTCTGGTGCTcTGCTAATTC	63.035	129
HM_0708	contig37481	TCA	3	12	CTGATGATATGGACAAACCAAAA	63.025	ACGtCTGCCCTCAATCTTACCTT	63.511	125
HM_0709	contig33900	GTG	3	15	AAAAATGAGACAAaCAGGTGGTGG	63.432	CTTCCAAGCAACATCAAGATTC	63.219	86
HM_0710	contig02291	GTG	3	18	GACTTCGAGTTTTTTCGAGATCGG	63.528	CTCCCTTACCTGAAATCTCAGAAC	62.684	141
HM_0711	contig11579	CCG	3	12	TCAAGTCTTCAAACTCTCCGGTC	63.111	ATGTTTTCCCTCGAGACGTCAGTC	63.027	115
HM_0712	contig35284	GTA	3	12	GTAATGGTTTGAATTTTGAAGGA	63.305	ATGCTCTGATTGGATGAGAAATGG	63.413	146
HM_0713	contig10101	TTC	3	12	TTGCAGTGAAATCTTTTATAATGGA	62.945	TTACTCGGACATCTTACCTCTGG	62.605	156
HM_0714	contig01530	AGT	3	15	GAAGGTGGTGGTCACTTGGATT	62.807	CTTCTTTGCTCTTAAACCCAC	63.384	140
HM_0715	contig04499	TAG	3	30	tttttGGGGTTTTTGTGAATTGAT	62.8	CTCATTGCTCAATTGTTTCACAC	62.948	99
HM_0716	contig11598	GGA	3	12	CCAAAGTCATGGAGAGCAAGGTT	62.895	CAGaAACTCAACGCCTgATACTT	62.933	159
HM_0717	contig18450	TCA	3	12	CATCTGTAATTGACCAAGAgGtT	62.684	GTGAATTCAACACATGCTTTCTGG	62.948	101
HM_0718	contig46297	ACC	3	12	GGCGTTGAGAAGGTGACAGCTAGA	63.238	TGACGTACACACGAGAACGACTT	63.194	154
HM_0719	contig13440	TCT	3	18	TctTCCCTCAATAATGAAACCA	62.803	TCACCAAAATCaAAAGGGAACAT	62.8	137
HM_0720	contig11761	AGC	3	12	TTCCACTAAATCTCTCTTCTGC	62.011	AGGTGGCAAGGTTGTTAAATCA	62.932	105
HM_0721	contig13418	AGG	3	12	GATAGGAAACGAGGTAAAGCGGat	62.915	ATCTTTCGAAATCAAGCTTGGAGC	62.935	124
HM_0722	contig13581	TGA	3	18	GTGGCTCTGTTGGCTTGACAGTTA	62.635	CAACAAGATCGGTCTGCTCTGATA	62.831	143
HM_0723	contig35766	TTC	3	12	ACTCATCATCTTCTCCGCTCCTc	62.89	GATTTCGTgTGGTGTGTAATTG	62.629	84
HM_0724	contig27071	GAA	3	12	GACGACTGTAGATCAAGAAATGGTGA	62.838	GGAAAGCTTAAAGGCTGTTCAAAT	63.016	97
HM_0725	contig27970	AGA	3	15	CCATACAAATCCCAATCTTCTGCT	63.211	GGGGTAAAGAGATTGAGGGAAGA	62.958	147
HM_0726	contig47258	CTA	3	15	CGCGACTACTACTGCTACTGCTGA	62.201	AGTTTCATTGGTGGGCTGCAAT	63.033	149
HM_0727	contig37860	TCT	3	18	ACATCACAGCAAACTCGAGACTCA	63.164	CTAAGcCTGTAAGCCGCTCTCTCT	63.808	157
HM_0728	contig31904	ACA	3	12	CCAAATCTGTCGACCAAGAAAAA	63.511	TGCTATTTTGTCTCTCTTTTCGG	62.919	131
HM_0729	contig06790	ACC	3	15	CCATGAAGCAAGAGTGGTAATCC	63.112	TTACGAGTTGAACCTTGACATGGT	62.972	150
HM_0730	contig29804	CCG	3	12	AAGCTTTTCAAGCTGTGATGAAA	64.382	GTGGTGGTGTGGAAGGGAAGT	63.433	148
HM_0731	contig32581	TGG	3	15	TGGCCGTACAAATAGGGTCAATTA	63.521	ACCATAACCCACCAGATCCATA	63.532	160
HM_0732	contig10851	GGA	3	15	AATGGCTTGGGATTTAAGTGATACA	62.826	ATTTTgGAAGCGCACACAT	62.701	93
HM_0733	contig09401	GGT	3	12	TGCTGAGAGGATGAATTTGGTGA	63.038	CTATTGCTCACTCTACTCGCCG	63.557	135
HM_0734	contig32933	TCT	3	15	CTTGATCaTAAaTGAGACATCC	62.902	AGTTTTTGACGACGCAATTAAGT	62.383	96
HM_0735	contig04444	AAG	3	12	AAaAGAGAGTGACCAACCTAGGCC	63.201	TAAAAATGTTAGGTGGTAGGGCG	62.371	144
HM_0736	contig00917	TAG	3	15	TGTTGTTGaCTACACtCGGTTgT	62.958	TGATCAATCGCACaAAAATcTGT	62.848	122
HM_0737	contig00060	CAC	3	21	CTCTCTCAAAATGGACATCCC	63.181	CTTGAGTGTGAGGCGGTGTAGT	63.886	87
HM_0738	contig44817	GAT	3	15	ACCTGAACCTCAAGCTGACGACT	63.269	CaATTGTGCCCCCTCTTCTCTCT	62.968	116
HM_0739	contig31347	CTC	3	12	CCAGAGTCTTGTCTCTCTCTCTG	62.984	AGCAACATTGGACACAATAAGGGT	62.936	150
HM_0740	contig17066	CCA	3	15	TCCAACCTCCTCTTATCAGATCA	62.245	GGGTGTTGCATATTTGAAAGAGg	62.922	158
HM_0741	contig17107	TGG	3	15	ACTTGTGGCGAACATCTGAGAC	63.731	CGGAACCGATACCTACTCTCGT	63.703	143
HM_0742	contig17258	AGA	3	12	CCATCCAAATTATCATCAAGAGC	63.95	CTCTACACAGGGTCAAGCTGAT	63.023	85
HM_0743	contig17444	CGG	3	15	ACTTCTCGATCACTGCTGCTCTCT	63.15	GCTCTGTCCATTGTAGAGCTCCTT	62.411	157
HM_0744	contig24570	TCA	3	12	CACACTTGGCACTTCAGTATCTT	62.822	CATCAAGTCAAGGGGAACCTAACT	62.822	122
HM_0745	contig25991	TAT	3	15	GTTTTACAATTTGGGGCAGAGTTC	62.828	TCTGTTCTTATCTCATGGATGCG	62.594	140
HM_0746	contig17067	TCC	3	12	CGGAGTCAAAATCTTCACTCTCT	62.985	GGGTGGTGAATGATAAGTCTTG	62.936	90
HM_0747	contig03237	TGG	3	12	TTTTGATACATCGACGGGATGAG	62.211	GGCGTAAATCTGGGCTTTTATC	63.099	159
HM_0748	contig05800	AGG	3	15	GGAGaGAAcTAGAGaAGCGGAAGA	62.795	AACCTTTTCGAGTGAAGATGTC	63.027	145
HM_0749	contig28446	CCA	3	12	GCAACCTGGTGGGTTGTATCTCACT	62.626	TCTGTAGGAAGGACAAGGCTAA	62.728	107
HM_0750	contig04849	TAC	3	15	ACCCCAATTGAAAAaCaCCTCTCT	63.285	cAAAGTTGTGATTGTTAAAGCTGGG	63.046	113
HM_0751	contig19995	TCA	3	12	TCAACTGCTCGTAATAAAATCCA	62.946	GAAGCAAAATGTAAGTCCCAATCC	63.046	140
HM_0752	contig29355	AGA	3	15	GCTCCTTCAACAGGACTTGTCTCT	62.809	GTTCAAGTTGtGCTCTCTGTTCT	63.226	151
HM_0753	contig16744	GCT	3	12	ATCTgATTgTTGAACCCATTGaa	63.732	TgGaCAACaAGGCTATGAAGTGA	63.038	153
HM_0754	contig17411	CTT	3	12	GGCCCACTCTCTTCTTCAACTAT	63.193	GTTTTTGAAGAAATGAAATCGAAGG	63.038	120
HM_0755	contig25268	GCT	3	21	TGATTATATCCCTGGTGTGCTCG	63.237	GGTGGAATGTTCAAGCGGTATGTTT	62.549	138
HM_0756	contig05302	GAG	3	12	AATACTTCTCTTGGCATATTcG	63.38	GGGTTTCCAATCATCAAGAAACG	62.813	146
HM_0757	contig44300	CCA	3	12	ACCCAAATCAACCAATTTCTCTCT	63.078	GTCGAAGCGCTGAATATGCTCTT	62.963	119
HM_0758	contig33725	GAT	3	15	AGCTCTCATAACTGATTCCAACCG	62.923	TCTGCTGtCTTGAAGTTCAGAGaa	62.724	82
HM_0759	contig22245	GGA	3	12	AACTCGGAGGATGATACAGAGACG	63.014	CTGTCCATTTCACTGTAACCTCTT	62.933	94
HM_0760	contig41290	GGA	3	12	GTATGAGGgATGGAAaAGTGGACA	63.419	TATTTCAACCAACAAAGGAGGGA	62.894	98

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0761	contig13581	ATC	3	15	TACTTGATGACCTGATGAGCa	64.399	TGAATTGCTGATTGCTGCTCTGT	63.401	125
HM_0762	contig14100	GGA	3	12	GCTGTAGCTGACTAGCAGGTAGG	63.698	CACCACTCACTcCCCCAgTc	62.981	131
HM_0763	contig18236	GGT	3	12	CCAGTATGTTGTCTCTTTCCACG	63.136	GTCATCAACACCAACCAACG	63.45	80
HM_0764	contig13930	AGA	3	12	ACCAaCGGTACCAATGCTTATACA	63.552	ATTAGAGTGTGATGTTGGGTGGG	63.325	160
HM_0765	contig16894	GGT	3	18	CATGGTTTgAGGTGGCTCAT	64.394	CTCAAGGGTACCCACCACCTAT	64.417	119
HM_0766	contig16196	TGC	3	18	AGCTGCAAGCATAAAGAGGTgATCT	62.853	AATATcCAAGGACTCTTGCCAG	63.783	157
HM_0767	contig09794	CTT	3	12	GAACAGGACTCAATTTGCTCCAT	63.782	CCAAGGTGCTACTGCTGATGAAGA	62.948	82
HM_0768	contig20675	CTC	3	12	CCCCAGACGATGCTGATCTACTCT	63.23	CCGTGTGAAGCAAAAGaAGGTAAg	63.337	105
HM_0769	contig00176	TCT	3	12	TGCATCTCAATCAAGTTCACCCCT	62.425	GATGTTGGTCAGTAAACGATTGCG	62.861	92
HM_0770	contig40282	GAA	3	24	TATCTCCAGAGACCACTTCGAG	63.325	CAGGGTCAGAGCAATAAAGAGAA	63.006	134
HM_0771	contig32123	CTT	3	15	CTCACTCCCCAATATGGGAAAAA	63.278	ATGATGATGCTGTTTCGGAGTACC	63.45	136
HM_0772	contig04061	TCT	3	15	AGCCAAATCACAAAATCCCAAACT	63.991	gAAGAAGGCAGAAAACCTAGGAGA	63.381	109
HM_0773	contig08989	GCC	3	12	TCATCAAGAAGCAACTCGATCA	63.481	CTCGTACTCTCATCTTCGTCAT	63.026	158
HM_0774	contig48614	TGG	3	12	GTTGTGATTGTTTGIGGTgGAT	63.057	TCACGTgTGGTTCGAATACATAC	62.948	128
HM_0775	contig17435	CCA	3	21	TCCTTTATCTCCCATGGTGTCTTA	62.983	AGAGGATAGTGGAGGACCTTTTG	63.068	124
HM_0776	contig26283	CAG	3	12	GATTTTATCAGCAATCGACGCTCT	63.062	CTCCAAAGGAAACATTTTGGATG	62.894	143
HM_0777	contig08426	CTC	3	18	ATCCAAATCCCAATGTCACAAc	63.308	TCCTTCGTTGGCTTTATGGTTTA	62.93	154
HM_0778	contig09801	TTG	3	12	ATcTGTGAGTCAATGCTGTTCTGT	63.173	CTAATCTCCCAAGAAAACCAAAc	63.168	132
HM_0779	contig33631	TGA	3	18	CCATTGTAGACATCGTAGGGTTT	62.633	AagAAAAAGAAAGGGAACGGAAg	62.689	151
HM_0780	contig36118	CTT	3	12	TCAACACTCTTCCCTTATCCGTC	62.798	GATGATGATGAATGGGTGAAGAAG	62.876	128
HM_0781	contig17413	GAA	3	15	tcTCTGTcTAGTGACCTCCGACcT	62.896	AGATTGGGCGAAGACAGGGTAG	63.853	158
HM_0782	contig19309	TCT	3	18	CTTTATGCCAATTTGTCACCTC	62.922	GCTTTGGCATATCATTTGAAAGGAA	63.533	160
HM_0783	contig25066	CTC	3	12	ATcTcTTAGCCCACTTCGgTCTg	63.154	TATTGCTCAACTCGTGAGAAACA	63.163	158
HM_0784	contig39598	GCA	3	12	AGGTTGATGGAGACTTGAGAGTGG	63.106	ATATCGACATCAGATGGGAAATGG	63.203	149
HM_0785	contig17327	AAG	3	18	aTAATCTCTCTCGCTTCGgATT	62.706	TCCTTCACGGATGTTGATTATTCG	62.325	148
HM_0786	contig12448	CAT	3	15	TACAAAAACCAACAAAGCCAGTG	63.28	GTCCTCAAGTTTCGAGGACTGGTTC	62.693	98
HM_0787	contig37334	CGA	3	15	CTGAGACGAGTATCGGAGgAgA	62.895	GCCGATATGCTTCAGGATTACATT	62.548	102
HM_0788	contig48172	TTC	3	12	GCCTCTCCTAGCTCTCAACGAAT	62.397	AAAGGATCCCAAGAAAGTGAAGG	61.941	154
HM_0789	contig49695	GGC	3	18	GTACTGGAGATCCCCAATCCAAAG	64.09	CAACCACAACAGCAGCATCTCA	64.011	102
HM_0790	contig37277	CTG	3	24	TGAGGACTTATCATGTTTGGGACA	62.803	CCAGTTGGACAAGTATACCTCTCG	63.765	137
HM_0791	contig21653	GTG	3	15	AaTAATGGGTAATGCAAGGGTGAG	64.178	TCACACCATCAGATGCCAAACCTC	63.465	144
HM_0792	contig24850	CTT	3	30	GTCACaCctTGTCTCACTCTCT	63.015	GAGGTAAGGTTGCaAAATGTGCG	63.039	137
HM_0793	contig45237	GAA	3	15	GTTCTCATCTCTCTCCCCATCA	62.977	TGCAAAAACGAAATCTTCATTCAA	62.846	152
HM_0794	contig22621	CTT	3	15	CAGCTGCTGCTTCTCTCTTTTT	62.658	GAAGAGAAAGTTCAGAGTCAGCCC	62.061	154
HM_0795	contig50371	ATC	3	12	TCTAGCACCAACACATCATCA	62.964	ATTCTGCTCTTACCACAATGACG	63.678	129
HM_0796	contig14885	CTT	3	12	TGGCCACTCTCATCAATCTATCA	63.028	tTTTGGGCTCTGtATGCaATTAT	63.632	96
HM_0797	contig19833	AAG	3	30	TCAGGGGGTTTAACTATGGGAG	63.453	ACATAGATTGaCAgcccCCAATTC	64.418	111
HM_0798	contig19366	GAG	3	15	AATCATTTCTCGTACAACGACGGT	63.048	ACCAAGTCATGCTCTTCTCTCTG	62.895	140
HM_0799	contig34654	TCA	3	21	GTACAATGGCAATGTGTTCTTTGG	62.643	TTCAAGAAAGTGGAGAGGAAAGC	63.225	134
HM_0800	contig07997	ATT	3	12	ATACTACATGAGAGCAACCAAGCA	63.091	CCCATCTCTCTTAAACGTTTCCC	62.989	113
HM_0801	contig21440	TAG	3	12	CCACCAATATCCAATCACCACTT	63.108	GGGGTCATATGCTTTGAAACTCTG	63.121	122
HM_0802	contig41993	GGT	3	18	CGCGTTATACGCAACTGAATTGGT	62.786	GCTGCTAGTGGGTGATGAAATTG	62.323	104
HM_0803	contig10390	CAA	3	18	CCCCGTAAGTGATATCCAAGTGA	63.312	CGGGCTCCTTGTATTATGTGTTT	62.451	111
HM_0804	contig19847	CCT	3	12	TCCGAGTAACATACCACTCTCTCT	63.401	CACGTCTcCGAGGATGACaAc	64.18	157
HM_0805	contig29527	TCT	3	12	AATTCAAGAGCATCAACCAAGCA	63.138	AAACAGCAATTTCCTCAACCAAAA	63.027	145
HM_0806	contig12517	TCC	3	15	CTTCGTCGTCTCCTCGTAGTTTC	62.723	GCATACTAGGTGGTGGATTGGAG	63.022	145
HM_0807	contig37019	CAA	3	18	CAAAACCAACATATTCAATCAAAc	61.893	CTCAACCAACACACCACTAAGGA	62.501	152
HM_0808	contig27062	AAC	3	15	TCaAaCAACaGTAAcCCATCACAGA	62.841	GAGCTTCTGTTTCAATTCAGGCG	62.827	132
HM_0809	contig27302	GGA	3	12	CTCCTCTCTCTCTCACCATCG	63.64	CCACTCTGTTACTCTCCACCACCT	63.011	135
HM_0810	contig08868	GAA	3	12	GAAGATTCTAGGGTTACGGCTGGT	63.008	CTTCTCTCTGCTGCTATCGTCTT	63.238	110
HM_0811	contig24799	TTC	3	12	GATTTCAATGGCTATGGGCTTAGG	63.839	GCAATCGAAAGCTGAAATAGCAG	63.456	84
HM_0812	contig23083	TGG	3	24	CATGATCAGACCAAACTCTTCCA	62.578	gaAGGAGCATGATTGCaAAAGAA	62.912	124
HM_0813	contig31034	TCA	3	12	TGTGCAATGCTCTCTCTCTCC	63.009	AAGGCAGCAGCTTACTACAATGa	62.171	126
HM_0814	contig29072	CCA	3	18	ACACTGATCAACCCAACTCAATT	63.014	GTTGCTCGAACAAGAAATCAACT	62.936	102
HM_0815	contig25006	CTT	3	12	GTCAAAACAGCTTTGATCAGTCGA	62.844	TCACATTATTATTCAGATGGGC	63.117	128
HM_0816	contig16661	TCT	3	15	GTTGCTGATCAAAATCACTTGCTG	63.065	GATGCaAAATTTCTCAGTTCAACCC	63.125	129
HM_0817	contig40651	TCA	3	12	GATGCTCTGCTGCTGATCTCTG	63.171	CtGTAACCGTGCTTGCTCAAT	62.657	149
HM_0818	contig13954	CCT	3	18	AGCACAATGTTGAATTAGGCCTCT	62.744	ATTGTAATTGCTGCGCTTACTCT	62.757	156
HM_0819	contig36012	TGC	3	18	AATGTTCTGCGAAATaCAAACTCG	63.444	AGATCTCAAAATCTCGTCACTCG	62.9	133
HM_0820	contig18069	GAA	3	21	CACGCAAGaGACCACACAGTTTAT	62.649	tcTTTTGATTTCaACTCCACTCC	62.784	106
HM_0821	contig20749	CTT	3	12	GATTCATTGGGATTGGACAGTTGG	62.7	TTCCGAATTTCTCTcATTTGTT	63.126	137
HM_0822	contig43372	CAT	3	18	TGCTGCAgAgCATAGTCATAATC	62.762	AATACGGTCAAAAAGCATGCAGAT	63.058	129
HM_0823	contig33888	GCT	3	12	AAGAGCTATTATCCAGCACTTG	62.851	gGAGGTGCATTGGACTGATTAGAG	63.331	145
HM_0824	contig21074	TTC	3	12	ACTCTTCACTCTTCCACTGGG	62.906	CTGTTTGAGAACTCCACCGATCG	63.01	146
HM_0825	contig14186	GTG	3	12	ATCATCTCCCTCCACTTCTCTCT	63.27	AGCCTGTGCTAGTGATTCAAGGG	62.946	160
HM_0826	contig06460	TGA	3	12	TTGAGATTCTGAGGATGGGAAG	62.871	GGGTGATCATTAGGCACCTCTTCA	63.643	130
HM_0827	contig09602	ATT	3	18	ACAAGAAGcGgATTgTTGTAGGA	63.239	ATGCTTGATGAAGAGGAGGATTG	62.9	152
HM_0828	contig46023	ACC	3	15	CTCTCTCTCAAAAGCAAGAGTGA	63.32	taGATGATGTGACGAGGACGGTG	63.383	159
HM_0829	contig04204	ATG	3	30	CCAACAACCTAGCAGCACTTATCA	62.426	GGACTTAGTTGCACTGGGATGTC	62.242	210
HM_0830	contig39786	GCA	3	12	CGGGTTCTCTCCGACTGAATAAT	63.783	TGTACCAAGGTGACCAAGCaGTA	62.955	153
HM_0831	contig12278	ATT	3	21	CACCATAGGACTGATCGGGATT	62.571	TCAGTCAACCAAGGAGGTCTTCTC	63.21	122
HM_0832	contig34392	AAC	3	15	CACCTTTGGAGCTAAGCTGCTCT	62.75	CTGTGGCTGTGAAACCAATTTTC	62.933	128
HM_0833	contig26434	GAA	3	15	TGAGCAGATTTTgATcTCTGTGC	62.951	GAGGTGAGCTCTAGATTATGTCTCA	62.45	119
HM_0834	contig02662	GTG	3	12	CAAGCTCAAACTCCACTATTGCT	63.044	GtACACTGTCACTGTGGACCTCTG	63.045	132
HM_0835	contig32212	TAC	3	15	TTCACTCaATTCATGcTCTCTCT	62.602	GGATGTGGGTCTGAATTGGATAG	62.887	129
HM_0836	contig47781	GAG	3	12	CTTTGGACTCATCGTCTGTCTG	63.01	ATGGCCGAAGAGGTACTAAAAAG	62.91	157
HM_0837	contig46605	CCG	3	15	AGACTAAGAAAGAAcGGGACCACC	63.092	aTAAACCTCAACCACTGCTCTGC	62.949	118
HM_0838	contig18976	GAA	3	12	TCCCATTTCTCTTCTCTTCTCC	63.053	GAATGCTGCAATTCATCTACTCA	62.632	120
HM_0839	contig03031	AGA	3	12	TCGtGTACCACTAAATGGAGAA	62.126	CtATGTTCACTCTGATGCTGGCT	63.057	138
HM_0840	contig27518	TCT	3	12	GATACGGCTCTCTTTTCAAGCTC	62.757	GTTACCATGACATCTCTCAAGGG	63.102	143
HM_0841	contig40200	TAT	3	15	aTTCCAGTACGCTTCACTAAcCa	62.962	CAAGaAGTGGAGAGGCTGcTG	63.702	130
HM_0842	contig03181	GAA	3	24	AGATtgTAGTtAcACCGCAGAGGG	62.835	CATCATATTCCTGtGCCATTCT	63.432	153
HM_0843	contig17421	GGA	3	12	GTGGTGGTGGCTGTGGATCT	63.399	ACCACCAAGTAAACCACTCACTCTC	62.91	125
HM_0844	contig09794	TAA	3	12	AGCCATTCAAACTCAACaCGTAG	62.44	AACGTGAGTGCTTGGTCTGGTTC	63.027	137
HM_0845	contig39749	CCA	3	12	CACCGCAAGTTTCAAGTCAAAATC	62.968	TACTTGTAgGgHtCTTGGGCTGT	62.103	97
HM_0846	contig21373	TTC	3	15	CACCAATTAATTGAACGAAGGAAG	62.906	TGCAGAACTTaGCCCTaAAACA	62.236	123
HM_0847	contig09031	CGG	3	12	GAGGAGGAGGGATTGGATgTACAC	63.483	CACCaAATGCCCTAATCGAAGAC	63.948	117
HM_0848	contig47481	CTT	3	15	GtGCCATATGaGaaTTTGTCTC	63.037	TGAAAAAGACAATAATGTCCAGTCT	62.04	83
HM_0849	contig18171	TTC	3	12	CcaCTTTTGGATTATAGGAGATTG	62.798	GGATGTTCTTGAATcTCTCCAA	62.773	134
HM_0850	contig46341	GAA	3	15	GAACCGATAAAACCCCAACTTTC	62.992	AATCACAACATTTCTTTGGACGCC	62.634	122
HM_0851	contig10095	TCA	3	12	CCTCAtGGtATcTcAgATGgTC	63.102	AGTCTAcTTTTAAATTTGGTGTTCGG	62.104	101
HM_0852	contig18239	TGA	3	12	GCAGGGGATGTTCTTGAAGAGTTA	62.91	gGGagGAGGATCTAATGGAGTACG	63.374	157
HM_0853	contig13705	GTG	3	15	GGATGCTCCAAGAATCATCTGTG	62.802	CCGAAGCAGAGAAATCTCAAAAT	62.919	106
HM_0854	contig35013	AGA	3	12	GCAAAATTCGACAAAGACCTAa	63.647	ACGaAACGAAGAACTACGACCATC	62.838	148
HM_0855	contig04809	GGT	3	15	TCACTGAAATTGGGGGAgAATTTA	62.884	CACGCTTATCTCTGCCACTACT	62.936	100

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0856	contig29854	TAG	3	24	GCTTGCTAAATTTGTTGGTCTT	60.182	CTACCACACTACTGCTCTaTaccctt	60.095	159
HM_0857	contig37250	TCT	3	15	GATGAAGCTCCACTGACCACACTA	62.829	GCTGAATATGCTTCTCCGCTACT	63.051	157
HM_0858	contig42094	AGC	3	12	TGCTCTGGAATTGCTTCATCTCA	63.362	CACGAGTTGTGCACATATCCAGc	62.975	143
HM_0859	contig05734	CTT	3	15	TGCTCATTTACCAATTcAgTCTTGC	62.645	CATGTAGTTGAATTTAGCTGCAAGTAGG	62.545	148
HM_0860	contig34696	TGA	3	12	CTCTCAAAATCCCCAATGTTCAT	63.419	CATATcCTTcCAGTCAACTCCAC	63.102	111
HM_0861	contig15199	CCA	3	12	AGAAgAAACACAgAGCCCAACAAC	63.036	GAGTGGTGGTCTTTTGGTAGTGG	63.12	141
HM_0862	contig39180	ACC	3	12	CTTTCTGGCTAaGAAATGAGCTGC	62.851	GTTGTGGAAGCTTATGGGATCG	63.028	158
HM_0863	contig35250	CTG	3	15	tCCaCActGtGaaGAGCTCTAG	62.918	GGTCTGCATCTTCTCCCAAGTAT	62.701	154
HM_0864	contig38948	CAT	3	12	CTCATCATCAAACTTCAAACTCGG	62.921	AAATCCCAACCAACAACCTAGAT	62.983	153
HM_0865	contig18587	ATG	3	12	aCAACgACCGTTGATtCTTTTAT	62.923	CAACGATGCTGGTTGTAACTATG	62.756	145
HM_0866	contig20015	TTA	3	12	TCCGTGAAATCAAAGTCTCTCTCC	62.897	AACATCGGAGAGCAACAATCTACC	62.827	108
HM_0867	contig22591	ATT	3	18	GGAGCTGAAAGGGTCTCCAACATAT	63.193	CTAAACCCCAATaTCAACCACTCa	63.002	145
HM_0868	contig02486	ATG	3	12	GCgTTTGTAGTAATTTGGGGTGG	63.652	CTTCCGTGAATTTCTATCGCATG	62.839	127
HM_0869	contig17961	TTG	3	12	GCACCTGAATTGAAGGAGTGATT	62.813	CACACTCTGAATCGAAGaGAAAG	63.04	140
HM_0870	contig35054	CAT	3	12	TTCAcAGTGTGTCTCTCAAGCTCC	62.947	AGAGTTCAAAATCGGTCAAGAGTG	63.124	144
HM_0871	contig31946	GCT	3	15	TCGATTTTTAGTGCTTCTGTGTGA	63.068	TCATTCAATTCCAGATCTTCTCCA	63.196	155
HM_0872	contig21871	TCC	3	12	ACCTTGGGAGGAGTAATAACCA	63.074	AGTTGATAAGGAAGGGAAGAACGG	62.98	99
HM_0873	contig10671	GTG	3	15	TTGGTTGGTCCCAATATAATCC	63.941	ATTTCCGAGATtctCtTCTTTCCC	63.188	120
HM_0874	contig30420	CAC	3	15	CAACAAGACATAAATCTGGCTCT	62.839	GAGaGAAATAGCGGTGGTAGTGGT	62.015	99
HM_0875	contig29904	CGC	3	12	TGACGAAAACACTAGGCTAGGAATG	62.823	TTACCTAAAGATTTTTCCGGCGAT	63.101	134
HM_0876	contig03408	TTG	3	12	AGAGAGGAGGGTCTGTCTGTGTT	62.974	TCTTcCTcCTCacCTCTCCTCTcT	63.161	131
HM_0877	contig47617	GTG	3	21	TCTCTGATCTTGGAAATTTGGGAC	62.773	TTCTCCACCAATTTCACTCTCTCC	62.987	102
HM_0878	contig33127	TGG	3	15	TCTTTCTCTCTCTCGAGTTGG	63.32	AGCGAGTAGATCACATCTTGAT	63.474	113
HM_0879	contig43405	GCA	3	15	GTTATCTGGTGGTCCATCTCATC	62.994	GAATCCgaCCATGCTCAATAGTA	63.237	147
HM_0880	contig44348	AGA	3	21	ACCTCTGAGAACTGGCTCTCGTIA	62.922	CCACAGAACTCGAAGaAACTAGGG	62.937	128
HM_0881	contig42201	TCA	3	12	TTATCTTCATCACCATCACCATC	63.24	ATGACAACAAGAAACAAGaAGcCC	62.824	152
HM_0882	contig50252	TTG	3	12	AATGGAGGAAGAGGAAGGAAGA	62.948	GGCGGTAACACATACAAGCGTAAG	62.978	132
HM_0883	contig20357	TCG	3	15	TGCACAACTACATATTTCCGAGCA	62.959	AGGAAGAAACCTTCAAAAGCTGC	63.308	149
HM_0884	contig07058	TTC	3	12	GTGAAATGGACTTTGTGCAACAC	62.858	ATGTGAAGTGGTGTCTGGAATTGA	62.922	112
HM_0885	contig34562	TCA	3	21	GAGAATCAGGAGTGAACACAGGAG	62.871	GCCAGTTCTCTCAATCATAGAA	62.9	139
HM_0886	contig28839	ACC	3	12	CTTATCTCTCTCCCTCCATCTCA	63.972	GTTCTCAAAGGGCAGAGATGGTTT	64.014	158
HM_0887	contig37549	TTG	3	12	AGGATCACCAAGGTGTCTTCTGA	63.43	GAAATTTCTTCAGCTCTCAGGAC	63.589	160
HM_0888	contig05468	CGG	3	12	GTCAAGTTCGGAAGACAGAGG	62.895	AAATGTCAACAATAGAGGCTCCCA	63.121	155
HM_0889	contig43451	TCT	3	12	AATTTCTCtCtTTTTCCGAATCTC	63.904	gaAGAGaAAGCAGAGGCAAGAGG	63.199	144
HM_0890	contig04378	TTT	3	12	AGTCAACTCTTACCTCcGCTTTGG	61.988	AGAGaGTAAAAATGTCGGCAAGc	62.849	99
HM_0891	contig20148	AAC	3	21	CaAGCaGAGTTTGATGtaTtATG	62.933	CAAGATTGCTTAGTcTCTTGTCa	62.026	119
HM_0892	contig16932	GTG	3	15	AAAGAAgGAAATGCTGGTACTGGA	62.411	GCCTTCACTGTTTGGAGATTCTCT	63.311	153
HM_0893	contig05440	GGC	3	12	CATAGAAAAACAATcGCTGCTCT	62.947	GGaAGaAGAGaTACCAGGGAGG	62.659	84
HM_0894	contig35814	GAA	3	18	CTTTTGGCTTAAACAATCTCTTTT	62.718	ATTAGGGTTGTGCTCGAGTTCA	63.239	151
HM_0895	contig34058	GAA	3	15	GGAGAAGTCGGCGGTGTATAAAT	63.602	TATACTCTCTTCGCCGTCTCGTC	63.146	157
HM_0896	contig38603	GAA	3	12	CTTTTGAACAAAAGTTGcActc	63.234	ACGAATATGAATCAAGTGCCTGC	63.456	128
HM_0897	contig28949	TGT	3	12	TTCAATGTGATTTTCGGTCTTGA	62.931	CAGAAAAAGAGAGTTGagaGGGA	63.085	131
HM_0898	contig31855	TTC	3	12	AcgTtCTCTATCTTCTGCTGTC	63.141	TGGCAGAAATGTTCAACAATATC	63.063	138
HM_0899	contig01528	ACC	3	15	GACCACTACCACCACAATTCAG	62.799	CAGCATCTTCAGATAATCTCCGT	62.913	143
HM_0900	contig18933	CAC	3	21	ATACATCTCTCTCCCTAGGCATCT	63.295	ACTTCGGATTGCTTTAAACAGGTGA	63.239	103
HM_0901	contig51131	GAA	3	18	GGGTGTGTAAAGGATCTGTTTGGTC	63.014	CAGTCTCCAATCCCTATTCCCTTT	62.863	109
HM_0902	contig19203	ATC	3	12	TGATGTTTCAACCAAGACATCAAC	63.256	GGGATTTCAGGAGGTATAGAGAGA	63.266	144
HM_0903	contig05004	GTA	3	12	ATATTAAAGCGTTGAGACACTCGGG	62.742	AAATGCAGCTTATGGAGTAGTCGC	62.975	132
HM_0904	contig27982	TGA	3	18	TAGATCATGTGGGTGAATACAGGA	62.791	aAAGCTCAATTTCCGAGTATCCA	62.328	91
HM_0905	contig23234	CCA	3	18	aCTACGtTCCCATATCCCTAAC	62.504	ACTTCTGgATATGGTGGTGTGGT	62.912	114
HM_0906	contig02350	TTT	3	12	AATTTCTCTATTCTTGAGATGCCG	63.013	CCGAAATTAAGAGCTTGGTTAGCCT	62.932	159
HM_0907	contig33222	TCT	3	12	AAAGTGGACAGAGCACTTGGAC	63.249	GCCAACACAGACACTTATGCAAC	62.989	117
HM_0908	contig34358	ACC	3	12	CATCAATATGCTCCATACCCATT	62.902	TGGaCAATCTGTGAAGATGATGT	62.911	137
HM_0909	contig01917	GAA	3	12	TTCTCGGATCAACAAATCCAAAT	62.899	TAAGCCCAAGTCAAGTCAATTAGGG	62.714	101
HM_0910	contig18687	CGG	3	12	GTTCTCGGTCAAGAACCCAAAC	62.121	ATTGTTTTCGGAAGGTTAACCGAT	63.004	160
HM_0911	contig35890	GAG	3	12	TTATTTCTCTATTGGTGTTTGGG	63.097	ATCATCTCCCTCTCTCTCTCATC	63.262	99
HM_0912	contig18276	TCT	3	24	TAATTCAGACCACTCTTCACTCT	62.368	aAGTTGAAGAGAGAAAGGGAACCG	63.28	160
HM_0913	contig50904	TTA	3	12	aCTAATCATTTGGATTGAAGCAGAAAA	62.397	CGaAGGTTGGTTAGTCTCTCGGA	62.905	157
HM_0914	contig06640	TTT	3	12	GAAAGGGAGAGAAAAACCAAGGTG	63.47	CGCATGATCGAAGAGGGAAGAGA	64.067	133
HM_0915	contig01473	GAC	3	12	GCAACACAGAGTTGTGAGCGTAGT	62.986	GAGGTTAAGAGCTcGGTTCGACA	63.238	121
HM_0916	contig14494	CCA	3	12	ATTACCACTACTGCTCTCCGCTC	63.917	TTAGAAAGcCATATTCTCGGACAGG	63.636	159
HM_0917	contig24342	AAG	3	12	GGGAACCTGGGAAGGTAGTGAAGT	62.983	GGTTACTCTCCAATTGGGTACTCT	62.992	134
HM_0918	contig14301	ATT	3	18	CACCTCAAGCTTTTGCTcGTGTTG	62.516	TGaAGAGAAATgGTGATgAAGa	62.144	127
HM_0919	contig26137	TGG	3	12	CAGCAGAAGATGATGTTGGTTG	63.048	CTTCAATGGGCTGTAGAGAAGCAT	63.035	115
HM_0920	contig12250	TCT	3	12	CACCAAGCTAGTCACTTCAACT	63.033	TAACAGTGGTGTCTTGTGCAAT	63.087	155
HM_0921	contig16643	GCC	3	12	TCAAGTTAAATGGATCGAGGGTGA	62.896	ACGAGCTTCTAGGCTTTGATTCCC	63.313	120
HM_0922	contig21942	GGC	3	15	GCAACAGAGTAAGCTGTTTGGTT	62.959	GAAATGGTTTGGGAGGAAAGAAATC	62.971	153
HM_0923	contig15405	CCT	3	18	CaAGTCTCAAGACACTTGATCT	63.124	TCTTCCAGCTCTCTGGAGATCTA	62.754	160
HM_0924	contig19426	GCT	3	24	GAACCTTGGGAGCTGACTCTA	62.908	CgTtGGCCCTAAAAAGAAAGGAAT	63.475	92
HM_0925	contig03137	ATG	3	12	GAGAAGACGAAGGTGCAAGACTTG	62.909	TCTTGAAGCAAAATCCGGTATGGA	63.113	138
HM_0926	contig14710	TGG	3	12	CaAGCTCCGAGTCTGTAGGGTAC	62.624	ctATTgATGAAATgGACACCC	62.691	160
HM_0927	contig40355	GTG	3	12	ATCATTTGGGGTAACAGAGGAAT	62.974	GTGGAGGAGTGAGAAAAGGGaTCT	63.278	141
HM_0928	contig11518	CAT	3	15	AAGGACCTAGTAAGCATCTCCTCC	62.891	TCAATTGTGcTCCAGCTGAGATAG	62.948	157
HM_0929	contig13175	GCT	3	15	GGAACATCCAGGAATACCATCA	63.19	CTCTTGGGTTTCTGTTAGTTGc	62.945	114
HM_0930	contig08230	ATT	3	12	GAAACGATGCTGATTAGGGCTTG	61.305	aAAGATGATGAgTTGTTaACAGAGTG	61.136	150
HM_0931	contig11716	TGG	3	12	GAATCTGAAACAGCTTGGGAGAA	63.009	GAGATGAATCGTTGAATCTCGCT	62.916	95
HM_0932	contig32671	TGG	3	12	ATGTCAGCCAAACCTCTCTcAAC	63.027	ATCCAGCAAGAGTGAACACTAcC	62.925	119
HM_0933	contig51113	GTA	3	15	AATCTCAGTGGCAAGTCAAGAAg	63.124	AATCACCAGAAAAGACTAcCacC	63.594	126
HM_0934	contig40393	GAG	3	24	TCGTGGAGGTGATCTTTAGGTTT	62.411	AAAAATAGCCGAATAATACCTCTCG	62.648	118
HM_0935	contig04798	TAC	3	15	TCCCTTCCCTcGTAAATAATAA	62.875	GTTGAGCCCAACATAGAGAGTAGG	62.497	103
HM_0936	contig02138	TCT	3	15	CACCAAGTCTTTGATGCTTCCAT	63.648	TCAACAGTTTGTGATCTGAACAGAA	63.059	118
HM_0937	contig17284	CCT	3	15	TGATCTCAAAATCCAAGACAATCC	63.514	TTGAGAGTTGTGAGAATGGaATCg	62.698	116
HM_0938	contig11764	CTG	3	12	ATTtGAAGcGATGAGACCCAAa	63.108	CagTAGCTCTCTCaAATatTGCATGG	63.427	99
HM_0939	contig32279	ACC	3	12	CAACTACTTCTCAGGAGGCCCTT	63.292	GGTTCAAGGGCGGTAGAGAT	62.635	129
HM_0940	contig29897	CTG	3	12	CACCTTTACTTGGGAGCACCAAC	63.12	GCAAgTCTGAgGCTAGCACTTCTT	62.653	105
HM_0941	contig17820	CAG	3	12	GtagTGGGAAATACCTTcGGTt	62.61	TTTGAGCCAAGGGCATGTAGTAT	63.043	140
HM_0942	contig05519	GGA	3	12	CTGATCTGAGCGGTGAAGCACTAGC	62.838	ACTCTCTCaTCTCTCTcTtGCTT	63.077	146
HM_0943	contig10817	CTT	3	12	GTCTTGCTAATGGGTCTGCATCTT	62.949	CAcCCCAAGTCAAGAAAGGGGT	62.778	119
HM_0944	contig24442	TTT	3	12	GCCATAaTCACTGAAACGgTCAaT	63.346	GAGGACGAAGAAGAATTACGCAAA	62.935	130
HM_0945	contig05251	TCT	3	18	CGGTGGATAAAAGTGAAGGAACAC	63.019	GGAAAGCAAGAGCAAGAAACAAGA	63.225	119
HM_0946	contig14265	AAC	3	12	TTATCGAAAACCCAGAAAAATTGG	62.331	GGTCTTGAATCGAAAGAGGCTAT	63.093	153
HM_0947	contig02531	CAA	3	12	AAATaccAaAACCTCAAAaCCCC	63.285	GAGACCCAGCTCTCTGTTCTGta	63.238	101
HM_0948	contig43260	CAT	3	21	aGAACCAATGCTGATGtaACaCt	63.027	GGGTAACTCTTTCTTGTGGACc	63.078	139
HM_0949	contig25602	AGA	3	12	CTCGCAATTACCTTGAATAATGCC	62.957	CTAGAAGCTGATTCCGGTAGGA	62.907	146
HM_0950	contig37948	CAC	3	12	CTCACCAATCTTCCCAACaTAG	62.894	TGGGAGGTGATAGTGGTAGTGGT	63.01	98

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_0951	contig35429	CTT	3	24	CCCCACcACATATTCAATACTC	62.593	TTGGATTACAGGTTACAGGATCACT	63.204	157
HM_0952	contig22633	TGT	3	18	GGTCAGGTTTGAATCAGGGGTAG	62.897	TCATCTGCTTACTTCTCCTCTCA	62.821	156
HM_0953	contig36042	CCA	3	12	AAAGaCTTTcTGCTCTAGAICTTCTCTCA	60.835	CCATGACCACATGTTTCACTAGTC	61.826	145
HM_0954	contig08860	TAA	3	12	CAACAACAAACCTTCGGAAGAA	63.517	GTTTGGGTCGTTCAATTTTAGGTG	62.823	136
HM_0955	contig19732	TCA	3	12	ACCTCCGACTtaTCTCTGACTCcA	62.678	ATGAGCAAGCAAAATGTAATGGGT	62.95	93
HM_0956	contig15868	TCA	3	24	CGTTGtcGTCGTCTACCTTATGTG	62.969	CTGGCTTGCTGTAgGAAACCTCTA	63.138	136
HM_0957	contig13174	TCC	3	12	CCATGGCCtAAATACTCATCTTTTC	62.925	CTGCAAAACCAACAGAGCCTTAGT	63.053	127
HM_0958	contig25605	TGA	3	12	GGATGCTGAtGAGGACtCGTACT	63.031	CATCAAGTCCACCGTACCAATa	63.141	155
HM_0959	contig30368	AAG	3	12	AAAATCGATGAGTTCGACATGACA	62.938	AATGTCGTGTTTACGGTGAATCT	63.048	95
HM_0960	contig00200	GGT	3	12	CAGTtHGTTGATTGTTGGGTTCT	62.724	AAATTGGCATCACTCACCATC	63.264	160
HM_0961	contig14810	TGA	3	12	CTCTCTCATCATCATCCACAATGG	63.005	TATTTGTAATGGGGCAGTGGAAAC	63.126	131
HM_0962	contig30237	CAA	3	30	CGGTGCTTACTGAACTCCCAATC	63.231	TGGcTtcGtCTgtTCTTGTaTGA	63.163	110
HM_0963	contig29644	CAC	3	12	ACTCAGTGACCGAACTGCCTTAG	62.064	ACTATTACAATGGTGGCTTGACCC	62.425	128
HM_0964	contig05920	TGA	3	12	GAAGAGTTCGTTGATAGAGACCGC	62.727	AGGAGATTcAgTTCGTCACAAC	62.912	144
HM_0965	contig09216	TTC	3	15	AATATTGTGCTAGACGGGAGGt	63.208	CTGAaAgTGAAACGAGAAAGAGG	62.582	128
HM_0966	contig35399	CTG	3	12	CTACAAAACtGgTTTCGTGTCT	62.943	caactgaagagatggaGGAGCAT	63.115	149
HM_0967	contig00595	TTC	3	18	ATCCTGATCTTGTAATCTGTCTCC	63.007	CTGAAGAGTTGAAGCCGCTTTT	62.191	156
HM_0968	contig15974	TGA	3	12	TTAGAAATGGAGCGTGTGATGAG	62.397	GGCTGTCTGAACCACTCTCT	63.012	158
HM_0969	contig27787	ATG	3	18	TATGGGCTTCGAGATCGATTGTAT	63.025	tccaaggcttctgtctgtcaatg	62.592	126
HM_0970	contig34654	CAC	3	12	aGGGAGGGAGAGTGTGAGACCTA	63.808	TTATTATCGTTTCCAGTGATGGG	63.101	160
HM_0971	contig38468	TGA	3	12	GTAACGAAGTATTGGCAGGAAT	62.634	TGGATCTGCAACATTGTATCAACA	63.596	110
HM_0972	contig18672	TTC	3	24	TCTTCTCTGCTACTCTCGTTCGG	63.125	CCAACtTTCCCACTTCTCTCT	63.172	128
HM_0973	contig08411	ATT	3	15	aGCCACCGGTcTACAATGATCTTA	63.133	CTGATGAAGATGGGTGTGACAAAG	63.026	154
HM_0974	contig34232	TGA	3	12	TGAAaAagTTGAACCCAAaATcTG	63.403	AATTTCTCACTCTAGcAAACCCC	62.995	138
HM_0975	contig06721	TAC	3	15	TAGTTGCTGATTGAGGAGGAGTC	63.115	CTCCTTATACTTTCACTGCGTCG	63.343	155
HM_0976	contig30524	CTT	3	15	CCGTACTACAGTTCCTCTGACG	63.339	TGTTGGCTTAGTTCCTCTGATTT	62.944	112
HM_0977	contig04170	AAG	3	15	GGAAGAAGTGGAGCAAGAAATGA	63.009	TCAAAGCTTTTGTGACTTGTGG	62.641	141
HM_0978	contig36688	TTC	3	12	CTCATTTGATCAAAACAGTGAAC	62.948	TTTATTTTGGAAATGGGTTTTGTG	62.905	150
HM_0979	contig20855	CCA	3	12	CCTCTACTCTCTCCCTCCATC	63.786	AGAGAACCCCTcCTTGTCTCTGGT	62.974	129
HM_0980	contig12715	AGA	3	12	AGCAaCATTTTGTGCTACTCTGTGA	62.896	AAGTGCCAAGTTCACATATTCAA	62.922	116
HM_0981	contig48760	AGT	3	12	GAAGAAACtGCAATGACGTCAC	63.166	gTTCTtTTCGATCCTCTTTTTCa	62.99	87
HM_0982	contig09956	TCA	3	12	TGATCCACGAACtGAGAAATGTTG	62.607	AAGTTTGTTCATGGATGAGCTTC	62.813	145
HM_0983	contig07981	TGA	3	21	GGGCGCTTATTAGGCTTTTCTTAA	62.944	GAGGACGTAAACGCATAATTGAGG	63.043	136
HM_0984	contig13548	GAA	3	12	AgTATCCTCtCCGAGGTAAATGG	62.876	aagatttcaaatTCtagtctccc	62.903	160
HM_0985	contig10718	ATC	3	12	GATAAGATTGTTCCGTTTTCTGGC	63.138	TGCATGATGATGAAGATGaaGATG	62.255	117
HM_0986	contig05870	TGA	3	21	CGGTAGGTTGGAAGAGACAGAAAT	62.228	AGGTGCTTCTCATCAGCTCCTAA	62.824	129
HM_0987	contig44891	CGC	3	12	CCTCTGTTTGAATCTTCACTCGGT	63.01	TAATGGAACCAACAGGCCATAAC	63.126	137
HM_0988	contig25373	TGG	3	18	TTGAACAACTTCAACATGGTGGT	62.724	GGTTTTGCATAGCCCTCaTATTa	63.332	137
HM_0989	contig41963	ACT	3	15	AACTcGACTGCATaGAAcTGCT	62.752	GAAATcGCAAAATCGCTCATCCG	63.13	159
HM_0990	contig38103	AAG	3	12	ATGGAGAAGAAATGGGAAGGGAAC	62.865	CTTCTTTGCTTCAATTTTGGAAAC	62.329	92
HM_0991	contig00859	GAG	3	12	TTTTAAACGCTCGTCAAAAGCATC	63.647	TAAATAAGCATGGATGATCCCCGT	64.567	156
HM_0992	contig32170	GGA	3	12	GATGCTTCAGTGAGGAGTGTGAAT	63.017	GATaTGCtGAGGCGACTGTATTCC	63.253	134
HM_0993	contig15839	AGA	3	15	CCTTTGATTCCTTGTTCCTGAAG	62.383	AGTTTCCACTcAGCAcCATGC	62.579	136
HM_0994	contig20735	CGA	3	18	cagAAGAACCAACCCACCAATCA	63.364	TTCTCAATTTCTTACGAGCAGGG	62.919	116
HM_0995	contig21477	AAG	3	12	CTGAAAGTCAACCTTCACTTAAC	62.61	TGCGAGAGGCATACCTTACTCTCT	62.838	103
HM_0996	contig42762	GTG	3	18	GTTTGTGTGCTCTTGGAGGAG	63.132	CCTAAGACACCATCTCCACCTGTT	62.793	158
HM_0997	contig51790	GTA	3	30	TTGgaGAAGAGATCCAAGTTCTCG	63.199	TCTGaAGGAATCTGTAgTcGgGG	63.837	160
HM_0998	contig06920	TCA	3	12	GTTCAGGGGCTTGAAATAGtCTA	62.839	ACCGGAAATTGCAAACTACTACGA	63.051	118
HM_0999	contig39586	GTG	3	12	GTGCCAAAAATaAGTCCAAATC	62.854	GAGGCTGAGCAGCGTAAGATCA	63.166	143
HM_1000	contig39950	TAT	3	12	TGTGATTATTTCGAGATTGTGGC	63.321	GGACGGCTCTGTTAAGTGGaATAA	62.729	157
HM_1001	contig43960	GGT	3	12	CAGTACGAGATTGCTTCTCGGTT	63.044	TGAATCTACACACCACTACCCAGG	62.382	122
HM_1002	contig34967	TCT	3	12	GTGATTTTCTCTCAGGCTCCAA	63.006	GGGACATTGATGAATGTCTGATG	62.687	140
HM_1003	contig20065	TTC	3	12	CTCAAAaTCTTCTcACCCcTcT	63.164	AAGAGAATAATACCCCACTCCCAAC	62.866	95
HM_1004	contig31882	CTT	3	24	CATCAACAGGCTCTAGGATCAACA	62.712	GGTAcCAcATCATCAGACCAACGAG	62.937	91
HM_1005	contig06370	GGC	3	15	GTCAACTCTCTGTCTCACCgAa	63.01	GACACCATGTATATCGACTCCCC	62.802	119
HM_1006	contig12273	AAT	3	12	AAAAAGACTGCTCAACTTTAAGTCCC	61.552	ATTTCAAATTACCTCTTGTGGCT	61.752	121
HM_1007	contig32714	AGT	3	12	ATTGACACAGGGATCAACAGGTGA	62.726	AACAACGTCTCTGCTCTCATCTCC	63.141	152
HM_1008	contig31860	GAA	3	12	CTCTCCTCTTGGCAATCTTCTCA	63.104	CAGCCTTCTACCAACCAATCATCT	62.811	130
HM_1009	contig36339	TCA	3	15	tcCTTAATGTCAAGCTTtcTcTc	62.826	CTCcaGAAATgTGGTGATTGAG	63	130
HM_1010	contig13896	ACT	3	12	CaACAGTGAGCAAAATGAACAAa	62.321	GCCACTATTATGGAAGTTCATCC	62.94	132
HM_1011	contig09658	TCT	3	15	ACCATCAACATAAAGCaTAAGCA	61.881	cGTACCCCTGAAATGGAAATTG	62.573	107
HM_1012	contig06635	TGC	3	12	CCAGTATATCATGGAGaAAAGGCG	63.018	CACACATAACTTGGCATTAACCG	62.756	160
HM_1013	contig19416	ATC	3	24	ATAAATTGTGGGGAAGAGTctGGT	62.983	TCTTGGTTACAGGCGTTACAGGTT	63.15	157
HM_1014	contig36340	CTA	3	15	TGAAGATGAGGAGACGAGAGGT	62.991	TGCATATGGATTGAAATGGaAAaA	62.425	147
HM_1015	contig19363	TAT	3	18	TGATTCTCTCTCCATTTCTGTG	63	GCTACAGCTTGGAAACCAATTA	63.532	129
HM_1016	contig01899	CAC	3	18	AGAGAGAAAAATGGCATGACTTCA	63.431	GATAGCAGTGGGAGTcAGAAGAGG	62.795	147
HM_1017	contig40774	CAT	3	12	TATTGTTCTCCAGTTTCCCTCTCA	63.3	tGACACaCAATGGGAAGATGACT	62.922	87
HM_1018	contig29672	GGT	3	15	TGAGTAGTGGGATGACATGTGGA	62.934	CaGGCcAGtTATCAtcAAAGAAg	63.214	154
HM_1019	contig07522	TTC	3	15	ATCCAGGTGACAGACAAATCGAAG	63	cCGAAGAAGAAGAGGAAGATGATG	62.67	124
HM_1020	contig08411	TCT	3	15	TGCTGAACGGAAAGTCTGGAGTAT	63.45	CAGGTTTCAGGGAAGAAGAAACAGA	63.094	131
HM_1021	contig08862	TTC	3	12	CACGTATTCTCTGGAACATGCA	63.498	CCTCAAGCTGATAAATGAAACGCT	62.947	94
HM_1022	contig09469	GGT	3	12	AATTTGTTGAAAGTGAATTTGGCG	63.334	AATGATTACAGCCTTGACCTGTC	62.713	134
HM_1023	contig16725	GGC	3	12	GGTACCATATCCcCGCACT	63.104	ATGGACCCGTCTGCGCATATC	64.043	159
HM_1024	contig41283	TCT	3	12	TTGGAGTCTTTGATTGCTGATCTC	61.948	CACTGCACCAATATGAGAAATGC	62.861	157
HM_1025	contig25674	CTG	3	12	GTCCAAATCTTCAGAGTCTGGAT	63.017	TCAACTTTTGAACAGCTACGCC	62.957	112
HM_1026	contig14849	TGA	3	12	GTTGGAGAAGCAAGCAACCTCTA	63.031	GATATGCCaATGACAAAGCTACG	62.875	86
HM_1027	contig07779	GGC	3	12	CTcTgTgTgTGTGCTGCACT	63.09	TTTAAAGGaAGCgaTGAAGCAGC	63.043	109
HM_1028	contig36220	AGT	3	12	GGACGATCCAGAGTAGGAGACACA	64.001	aAGATCTGGAGGCGAGTGTACAAg	63.137	147
HM_1029	contig45559	TGT	3	12	CTGCTTCCATTTCTTGTCTCTGT	63.031	GAATGTGGAAATCTCTCTGTgGG	63.204	126
HM_1030	contig05212	TCT	3	15	GTGACAAcGaATTGCTAGAGTGT	62.324	TGTGCAATCTTGTATGTTTGGG	63.055	152
HM_1031	contig27586	GTT	3	18	TGTTGTTGATGCTGATGAGTCTGA	63.076	GAGTCCACAGTACCCAGCTACACC	63.141	135
HM_1032	contig27844	ACC	3	12	TCTGCTGTCTTAATCACCTCGTCG	62.958	ACACTCGAGGAGAAACaAAATGG	62.809	134
HM_1033	contig08214	CGT	3	12	CAATCGCTGCTCAGGAcTATCAT	62.834	aaGACGAGtGcgAGtTGAaATG	63.115	115
HM_1034	contig41942	TTG	3	12	TCTCTAATTTTCTCTCCGTTTC	62.875	CAAAAGAAcTGAAGAGGAAGCCAC	62.619	109
HM_1035	contig37225	GAT	3	24	CCTAGTTTGGCTCAAAACATCTCC	62.411	ATCCGGTTTTATCTCAACCACTT	63.09	160
HM_1036	contig29889	CCA	3	18	TGCAAGTATGATTCTGGTACTGG	62.621	gGGTCGtAGTGGTGGTGGTTAT	63.227	93
HM_1037	contig07250	AGG	3	12	AACAAGCTTACATCAGGTGgAGGT	62.411	CgaAGTTcCaTcGtCTTTTCTCT	63.119	121
HM_1038	contig30111	TCA	3	18	AATTAAGTCGATCGCAAAAGAGT	63.406	GATTGGAAAGTACAATGGGTGCTC	63.026	139
HM_1039	contig10469	TCC	3	12	TCTAaTgATcTcAGtTGGGAGC	62.9	aAAaACTTGGAAATcCTTTCGGGA	63.08	144
HM_1040	contig39730	AGG	3	15	AGTGCTCAGCAGGAATGATCTCA	63.556	CACCTCTCTCCACCCCTCTTACTC	63.808	116
HM_1041	contig31960	TAT	3	12	CTGCTCATATAAAGTGTGCTGGG	63.006	cTTTCAAAACGCTACTCTCTCAAA	62.929	154
HM_1042	contig16039	TCT	3	12	AAGATTTCCCAACcTACAACAT	62.983	GAAAGATTcCaTtGAcGAAGTTGG	63.108	99
HM_1043	contig02234	GGC	3	15	GGGTTTGGAGGATAGACGAaA	62.783	CACCCAGCTCGTGTCTCAGt	63.837	113
HM_1044	contig00251	GGT	3	15	GGCGTATTCTTGAGACACTCTTT	63.141	TATCTCTCAACACGGGGTACTAA	62.811	92
HM_1045	contig05751	TGG	3	12	GTTTGAGTGGGAGTAGGGGTTCT	62.983	CGGAGCAAGtAGTGAGTTATGGG	63.234	145

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1046	contig02677	CCT	3	12	AACCCCTCTATCTCCGAATAC	62.878	TTGGTGGTTGGGAATTACGTTAAG	63.118	138
HM_1047	contig03753	TCG	3	12	ATCACGCCACAGGTCACTTTTACG	63.549	ACAATCCGACGACCAAAAAc	63.232	90
HM_1048	contig36555	TTC	3	12	TCACCTTCTCTCAGTACTTCTCC	63.21	AGAAGAAGACGAAAGGAAAGAG	63.599	134
HM_1049	contig00057	GCC	3	12	CCATTTGCTTATCTGACAGTACT	63.563	GCTTATAAGAAGATGGTGGTGGG	63.981	145
HM_1050	contig03332	TTC	3	12	CGGCACTATTCTGAATcTCAACT	62.839	AAGAITGGTTAGaAGATCgGAGGC	63.093	138
HM_1051	contig21496	TGA	3	12	CCACTCTCCACATaGAACCAaAGG	63.208	TcATCAGCTCCTTAATCCCTCTC	62.889	136
HM_1052	contig06862	GGC	3	12	TGAGATTGGAGAAGAGAGGTGAGG	63.301	GGCAGAGTTTACAGAGTCAATC	63.242	142
HM_1053	contig05550	TTC	3	12	TAAACTCGTGTGAGGACCACTCT	63.338	ATTGGAAAGTTTGGGATTGGATTG	63.206	159
HM_1054	contig49999	CCA	3	12	ACCCAAGTATaAGTCCGCCACC	63.431	gTagACTgGGGTGGTGAGAGTG	64.344	131
HM_1055	contig00075	CCG	3	12	AAGCTCTCTCAGCGGTAGAAATC	63.517	GTGATAGACCTAGGGGAAACTGG	63.381	90
HM_1056	contig22675	TCT	3	12	CCATTACTGGTTGgTgAGGAGTC	63.111	CCTAGGCGAtaAGGCCAAGAAG	63.409	117
HM_1057	contig48151	GAA	3	12	TCTCTCCGAACCTCTCAATAATT	62.571	CCAGCTATCTGTCTCACTCCCACT	63.236	160
HM_1058	contig14010	GAG	3	12	ACGATCTTGAAGTGAAGTCCGAG	64.004	CaAAACTACGCTCTTACCCGTC	63.15	146
HM_1059	contig00870	TCT	3	12	CTATTGGCGCTTGAAGTAGAGG	63.132	GAAAGAGCATGGGCTGAAAGATTA	62.925	102
HM_1060	contig13697	TAG	3	15	cgTTacGTtACGTtCGTtTtaGTT	62.448	CaAAcACGTCGATGaTcTGTGTTc	62.948	121
HM_1061	contig00614	TAT	3	12	ATCTTTGAAGCTGGTCTGATGCT	62.727	GGCAGATcACCATTTTCATCAACTA	62.397	143
HM_1062	contig18556	GAG	3	12	TAATGGATTCTGagAGATCAGACA	63.146	ATTgaACaTCTCGGACAACATTC	63.437	151
HM_1063	contig01633	TGT	3	18	AAGACCTATATCCGTTCCGAGAG	62.983	CCGATCATCATCTCACTCAATCC	62.98	110
HM_1064	contig06136	TCT	3	24	AAGAAAAaCCCAAGAAACAGTCCA	62.299	TTGCCATTTGAgaATCAAAgAAT	63.009	88
HM_1065	contig05950	TAC	3	12	AAAAAGggTtCTGTCTGTAGCCA	62.452	AgGGAgGGTtTtTtTTCGCTTTT	63.249	108
HM_1066	contig15207	CTG	3	15	GcTcTTTcTCTTGTcATCTcTAT	63	AGCCTTCATcTGAATGTgTgATT	63.234	148
HM_1067	contig50404	TGG	3	12	AGCTAGGGTTCCTGGGTAACCTGG	63.001	ACGTCTCAATCTCTTGTCTCCAC	63.141	110
HM_1068	contig04560	ATC	3	12	TAAAGGCTTAGCCCTGGAGATAGG	63.092	CAAAATCAACAACGAAACCTTTGA	62.326	113
HM_1069	contig24642	GAA	3	24	AATTTACACCGATTCCACACAAC	63.133	TTCGTTCTGATTTCTCTCTCTC	63.009	106
HM_1070	contig42015	TAC	3	12	AGTAaTgaTtTGAGGcCAcAatCC	62.51	AATGGATCTGATGGACAGTCAAAA	61.932	148
HM_1071	contig01113	GGT	3	12	GTGTTGAAGAAGCTCGTGTATG	62.339	GcTTGATCTCTGATcCACTGCTACT	63.146	144
HM_1072	contig45888	AGT	3	21	AGTTGTACGTACGCTGGGATATGA	61.939	TAAATAGAaGcATaCAACAACCTCATCCa	61.329	80
HM_1073	contig03692	CGG	3	12	TTTGGTATGAGCTGTGAGAGAG	63.04	CGCTCTAGTGAAGAAGATCCGAG	63.133	103
HM_1074	contig45548	CTT	3	18	CCCTCGCGATTGTCTCTTTGAAT	63.022	GTGACTGAAACTgaAAGGGAAACC	62.382	160
HM_1075	contig03017	TCT	3	12	atGgctCgaCaCTTCTTTCTTTT	63.031	GATCGatTGcATTATGAACGTGAC	62.75	159
HM_1076	contig51727	GCT	3	12	AATCTCATCGAGGTAGTAGGCTG	62.327	CAACAACCACTCAACAATTTACG	62.641	150
HM_1077	contig33421	CCA	3	15	GACGCTTTTAACCCCAAGTGT	62.959	AGCGTTGTCTGACCAGAGTAAGG	63.146	153
HM_1078	contig12220	CAA	3	12	TTCTCAACATTTCTCTCCAAGC	63.009	AGAATTGGGATCATGGTGTCTGT	63.004	115
HM_1079	contig17786	TCT	3	21	AGAGGTGAGATCTTATCTGGGCGT	63.72	AATGAAGTTTGACGAAGATGTCC	62.936	156
HM_1080	contig25633	TCG	3	12	AGCGAGAATGCTTTTGACCAATC	62.926	CGACACTaCAACAATCAAAAGCT	62.979	91
HM_1081	contig49618	TCT	3	21	ACCATGGTAGAGTCTCTGAGCG	62.8	CgTACGCTaACTCGAGaGaaATC	62.646	160
HM_1082	contig14716	GAA	3	12	aGGTTTGGTTCTTCAAGTCTTTT	60.721	AGATGCTTGATACTCCAAGTgTgTTTT	60.687	141
HM_1083	contig02705	GTG	3	12	GTGAGCAGAGACAGTAGGAGGAG	63.015	CTCAACCTCAACTCAACTCAAC	63.437	120
HM_1084	contig38987	TTC	3	12	TGAATCTTGCCATTACCCAAGT	62.922	ATaCAAGGGAATGCTGAAAATGGA	62.912	109
HM_1085	contig24098	GGT	3	15	GAGGAGAAAGCAgACTCTGGAAAT	63.396	CCAGAAATGTTCTTTCTCTACCA	62.991	158
HM_1086	contig32593	TTC	3	12	GTCTCTTTGTGCTAATGACCACGC	64.331	GGTGGTAAACAGGATCATCAAGAA	63.419	155
HM_1087	contig18303	CGG	3	12	ATTCGCAaCAGGcTCTTAGACTC	62.995	CGTACAGTgTCTCTCTCTGAAGC	62.119	154
HM_1088	contig07930	CTT	3	21	ACCTGAACAAATCAACcTTTGAA	62.996	GGAGaAaCaGaAaCAGAAcCAGA	62.997	135
HM_1089	contig00468	CTA	3	24	TAAaATCCcAaACCTCTCTCTC	62.958	TGCGGTGTAGCTAGCAGTGAAT	63.1	158
HM_1090	contig07004	AGT	3	18	CTGTGcaGTTGTCTCAaGTTGTG	62.852	TCAGCaCCAAGACCTCTTATTCTC	63.115	151
HM_1091	contig00637	TGG	3	12	TCTTGTAGAGGTGTGTCTCcGT	63.449	GTCCCATCTCATCTCTCCAgTa	62.874	160
HM_1092	contig24186	CAT	3	18	TTGTGAGCCACCATTAAGAAAGTgA	63.048	CCAAAATTTTCAAGTCCCAATGACC	62.8	141
HM_1093	contig05868	GAA	3	12	CAAGAAGCTCAAAATCAAACTCtCa	62.044	GGTCGAGAGcCATAATGAGGTAGA	62.913	109
HM_1094	contig21613	TCT	3	15	AATAGCTGAACCCCAAGTATGA	63.034	GaAGAAGAGTGACTGcAAGGAAA	63.225	160
HM_1095	contig45504	TGT	3	15	GTGAACCTGGTtGGGCGGTG	63.286	TCTCTTCTACCAcCAGTACCGTCC	62.909	119
HM_1096	contig11970	GCT	3	18	GCTTGTGTGTGCTGGTGTAGAAG	63.288	GCAACAAGGAGGGTTTATCATGCG	63.97	159
HM_1097	contig22196	CGC	3	12	CGTGACTTCTCTGTGACTGTGT	62.947	GTGAACAACCCAGTTCACTTCT	62.807	137
HM_1098	contig08535	AGA	3	12	GGATCAATTCTGTAGAGCTCTCTCA	63.013	CTGTTTATGAAAGGAACCTCACGGC	63.239	121
HM_1099	contig21462	CGG	3	12	TCCTCGCTCTCCCTCTTATTAC	63.184	GTCTATTGGTGGAGCTGAAGTGC	63.468	109
HM_1100	contig06799	TGA	3	12	AGGCGACTTCTCTCTCTTGTG	63.105	GATCTCAAGAGTCAAGACCCAGA	63.202	143
HM_1101	contig25717	TCG	3	12	CAGCAGGAAATAGGGTTGGCTTA	62.744	CACGCTTTCATATCTTTGCAATTG	63.081	138
HM_1102	contig34614	CGG	3	15	CTTCGAGAACTGACGCTCTTCG	62.905	CACAGTGTGATAGACCCCAAAATG	62.71	111
HM_1103	contig35686	GAA	3	15	GACGACGATGATTTGAATCCTCT	63.007	TTGGTTTTCAAATCCCAgTCTC	62.592	147
HM_1104	contig39084	GTT	3	12	TTGTAGTAGTCATCAAAACCCGGG	63.319	AACAGAGAGAATTTTGGAAAGCT	62.626	140
HM_1105	contig04773	TCT	3	24	AATACATGGGGTACGGGACACTTA	62.619	CAATTGACACCAATTCATACGA	63.046	157
HM_1106	contig40410	TGG	3	15	AAaAGaGGGTTTCCCAAGTGAGAC	63.08	TGGAGACAGAAAGCTTCACTCT	62.71	158
HM_1107	contig41531	GAA	3	24	AAACCTTCCCTAAACCAAGACG	62.804	TACTGTTTCATGCTCTCTCTTCCC	62.798	142
HM_1108	contig15821	CCT	3	12	TAAGCCTCGTCCAATCGATTCTTA	63.221	CTGATCTGCCGAGATCATCTGT	63.762	147
HM_1109	contig24295	TCT	3	12	CTGTCTTGTGTTGAcTCTCTCT	63.02	AGCAACCAAGCTGAATTCAGAGC	63.048	117
HM_1110	contig46174	TCA	3	12	ATCTTCATCATACCACCCCAcT	62.901	TCAAGGTCTGAAGTGAACGATGAG	62.919	108
HM_1111	contig04464	TCC	3	21	AGCTGTGCCTCAAGTGTCTGAATC	63.073	ACACACCACAGCAGTCacC	63.227	108
HM_1112	contig09402	GAA	3	12	AAAATGAGGGAGTGTCAAGTGAAGC	63.027	tGTGctCCCCAaCTaTACTAAcGg	63.546	156
HM_1113	contig05984	AGC	3	12	GCCAGTTTGTAGTTGGGAGGTTGA	63.432	GGCTCAGCATCAGTCCCTCTTAT	64.13	122
HM_1114	contig12247	TCT	3	12	GGAAGAGATTGTGAGGAGGTGAA	62.987	GTCTTTTGAATCTCAGAGAGGCTG	62.898	127
HM_1115	contig04800	TGA	3	18	TACGGTGTGTGACGGCATCTATAA	64.666	CATGGCGAGTACCAGATCAGATG	64.047	130
HM_1116	contig17432	ACA	3	12	GACATGACtGAggCTCACATCTTA	62.817	gaAGGCTTGACGACCTCTCTATTG	62.712	155
HM_1117	contig49135	TCT	3	24	CCTCCAAATCAAAATCTCTGACG	63.202	GCTGTTGAAAAATGCATTGAGAAAT	62.667	151
HM_1118	contig25376	TGT	3	12	TCGTCTCTGTGATCACTTCTGGTC	63.035	TTCGTCTCTGTCTCAGCAATGTC	63.057	96
HM_1119	contig31065	CTG	3	12	GATGATGACATCGGTTGAGAAGTG	63.033	gGGACTTCTTGGAAGAGGaaAGTGA	63.164	128
HM_1120	contig42388	TGT	3	18	AACAATTTTGGCAACTTGAAGAGA	63.027	TCCCGATTGATATGAAAGAAAGA	63.092	119
HM_1121	contig20274	TCT	3	15	TTCTCAATTTAGCCTTCACTGCC	62.935	aAAGAAAAATGCGCAAGTGGATA	63.05	130
HM_1122	contig08715	ACT	3	12	CCTCCATATTTACCTCTCCAAA	62.758	ATGATAAAAAAGCAGTACCCGAT	62.94	120
HM_1123	contig24996	TGG	3	12	CATTAGTGGGACCATCATTCAG	62.67	ACTTTACAGCGCTGATGTATTGCC	62.647	123
HM_1124	contig35903	TGT	3	12	GTGTGATCATCGAGGTAATAGG	62.786	GACATGTCTCTGAGCGATTTC	63.278	158
HM_1125	contig13753	GGC	3	12	TAAACCTTGGCAAGAAAGATCG	63.63	AGCTCTGAAACTTCAATCTCCCA	62.698	121
HM_1126	contig03804	GGA	3	12	TACCTTTGTTGCTGTAGGAAg	63.048	TaCACACAAGGACatGAGaCACC	63.386	146
HM_1127	contig31156	GAG	3	12	GcGTTGGTgGcATAGAAgATAG	63.353	GCTgaAAATTAAGGTGCTAGAAATGG	63.384	104
HM_1128	contig49922	TTC	3	15	CACCACCAATCTCTTCACTcTCT	62.884	CAITGCTAATTGGGTATgTGAAG	62.664	96
HM_1129	contig01755	CCG	3	12	AaCCTAGATTTCAAACTCCACCA	63.189	GTGTTcGGTGGTTTACGAGGTC	63.984	147
HM_1130	contig51291	TGT	3	21	GTCTTTTGAAGTCCACCAACCC	63.023	TGGTGACCGTAGGGATATcaTgT	63.643	107
HM_1131	contig20751	AGA	3	24	TTGCAAAACAATTTGGGTGTTCTA	62.649	ACACTAACAGCATGTTTCCCGAAT	63.048	159
HM_1132	contig47380	TGG	3	30	GACTCAACGACTGTGGGCTCT	63.984	CAAATCGTTACTTCTAGGGTCCG	63.199	143
HM_1133	contig26234	TCT	3	24	ATGTGACTTCTCAACAAAATCCGT	63.128	CGCACATGCTCTACTCAAACTc	62.651	137
HM_1134	contig21404	CTT	3	21	CtGAGTCGcTCTGTTTCAACTTT	63.245	AAAGCATTCAAAATCATAAACCCA	62.722	106
HM_1135	contig06738	CCA	3	21	TAGTTGTTGCCACCATCAACTTTC	62.956	CTGTTTTGGAGATGGAGGATATG	62.983	136
HM_1136	contig00959	GTT	3	12	AGCTCCCAATTGATGACTCTTCT	62.992	GGATTCTAAGAGGTCAAAAGGCT	63.494	117
HM_1137	contig50421	CTG	3	18	TGAAGTcGACTGAGgATATTGTT	63.217	GTCATCaAGagCTATGAAGCCGAT	63.042	94
HM_1138	contig49439	TCG	3	12	GCTACGATCTACGCGTAAACaCT	62.985	CAATCGACATTTCTGTTCTCATCG	63.038	139
HM_1139	contig00179	TCA	3	12	CaTCTCTCGTCATCATCATCTGC	63.146	AGTACCGGAGGCTACTTACGAGA	63.61	110
HM_1140	contig33191	AAT	3	18	AAGGCCAAAACATCAAGTTCAGAGT	62.512	CTTTAAAGCAATTTGATGTGcagG	63.014	145

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1141	contig11235	AGA	3	12	GTAACCTTCATGACTTCGACAGGG	63.225	ATGATGCAACCCAGATCCACATAC	64.21	121
HM_1142	contig06479	TCT	3	12	CAAGGTTCAAATCGGACACCTCT	62.895	GGTCAAAACCATATCTTTTGCTCCT	62.821	149
HM_1143	contig21371	GTG	3	12	CGTAGGAAGTCGGATAAGTAGTC	62.523	cCTTTCTTTGAgcCaAGTcCtT	63.187	130
HM_1144	contig26071	GTG	3	12	TTCTCAGAATTCACCTTAGCG	63.117	TTAGTTGTACGTGCTTGGGAAGAG	62.893	143
HM_1145	contig02111	GGA	3	12	CACCAACAAATTCATACCCATT	62.909	GGTTACGTCTCAATCTCTGCAGAT	62.827	83
HM_1146	contig32464	GAT	3	15	TCATCTGAGAAATGGTGATGATTC	62.443	CCCCAAACTTCTgaATTGAATCTG	63.091	136
HM_1147	contig18485	CAC	3	12	CCCcAAGGTTgTtGGTTATTTT	63.179	TGGGTGTGTTTAgAAGCTGGTTT	63.138	153
HM_1148	contig18174	GGA	3	12	GGACCCCAATATCAATTGTTCAA	62.996	CAGTCAACATTTTCTTGCCAGTGG	63.057	109
HM_1149	contig14418	CAA	3	15	CAAAACCGGAGTGAATCAGAAATC	63.108	TgGGTGTATGATTTGTGAATTGT	62.807	132
HM_1150	contig13565	TTG	3	12	TCCTCTAATTTCTCTCGgTTTC	62.875	CAAAAGAAtcGAAAGAGAAGCCAC	62.619	109
HM_1151	contig19602	TTG	3	12	TTAGTTCTTTTGGCGGAGATGAAA	63.216	AACTGCTGCTCTTGTCTTCCACT	62.949	87
HM_1152	contig23069	TCT	3	12	GATGACGAATCTTGAGAAGCCAGT	63.133	atTCtTccTgTGAGAGGTTTGG	62.15	131
HM_1153	contig00982	CTC	3	12	TGCTATCtGACTGGGAGCACTTC	62.829	GcTTGATgAGGGGAGTGGAAGATAC	62.484	116
HM_1154	contig01173	TTC	3	12	CTTTGATAGTGTAAATCTGGCGGG	63.027	CAGTGAAGGCCAAGAGAAAGAAAG	62.806	152
HM_1155	contig45655	ATG	3	12	CAGCGTTGGGGTTTAAGATAGAAC	62.247	GTAGATAGTGACCGCAGTCTGTGC	62.442	139
HM_1156	contig06459	AAT	3	15	AaTgaCTTCCATgaCAAGCCAAAT	63.026	GAGTCTTTGAGGCCATCACTCAAT	63.017	142
HM_1157	contig46329	CGG	3	12	GTTGGTAGGAATTCGGAAGGTGTG	63.225	TAGTACCGATCAAGACAAACCGTCC	63.549	140
HM_1158	contig14328	ACG	3	15	CTTGATCTCAACATGAAGCCGAT	63.754	GATCTGAAGCTCAAGAAACCCaaA	63.009	156
HM_1159	contig45788	AAG	3	12	TCCTGAAGAACACAGAAGCAGGTT	62.736	TGTTGAGCTCTCTTCAACATGAgac	62.185	160
HM_1160	contig28096	TCT	3	12	CCAAAGCAATTTCAAGTTTCTGAAT	62.921	CTTCGGAAGAAGACACACAACTG	62.942	153
HM_1161	contig21337	CAC	3	15	AATCCGgTAGCATACCCAAATG	63.115	AATTTTCCAATCCAGTTGCTCTG	62.921	110
HM_1162	contig52040	ATC	3	12	TAGTCTCTCTCCCTCGTCCAC	63.105	CCaaatgATGTACAAGCaGCACCTC	63.078	128
HM_1163	contig36475	CTT	3	18	GgAGGTATCTGGAAACCaGACCT	62.974	ATgTTGACACTGAAGGCAAAAGag	62.933	129
HM_1164	contig35154	TCT	3	12	ATTGTGTCGGAATCAAAACCaTTTC	63.223	ACCTCTGCTCTTGCCTAGACTTT	63.117	126
HM_1165	contig06846	AGA	3	12	AGTATTGGACGGCTCTGTGGAAAA	63.019	CTTCACACATTCAAGATCAGGTGg	63.026	109
HM_1166	contig30173	CTT	3	12	TCTGcTTTTAGTACCATCTCGC	62.947	TGTTGATGTCAcAgacACAGAAGG	62.478	156
HM_1167	contig09688	ATG	3	15	ATCATACGGACCAAAATATCGGTGT	62.622	GCAGCAGTGATATCAGTTTCAACG	63.194	152
HM_1168	contig06482	GGC	3	21	TACACAAACTCATTTGAATGTCCCC	62.175	ATCTGAGAGTGACGAACGTAAGCC	63.154	123
HM_1169	contig24514	GAA	3	12	TAGTTGTGAAAAAGCCAAAGATGCC	63.648	TAACCACACGCTCTCATCagTTCCG	63.493	150
HM_1170	contig33748	AAG	3	12	GGTGCTCTCACTCGAAACTCGT	63.04	AAATGACTGATCATCTCCCTGCTC	63.007	153
HM_1171	contig10312	AGA	3	15	TTGCTTCGTCTAACCACTCACAA	63.172	AAGATTTCaAACCCTGGGCACTATT	63.301	134
HM_1172	contig34499	ACC	3	18	GGTGGTTGGGAATgAGgAGATACA	62.584	CAATTTTATGCTGGGATGGTGAA	63.046	99
HM_1173	contig41351	GAA	3	12	AAGAGACCCAGAAAGGATCTGAG	63.372	TTTTCTAcTtCCcCCCAcCTTC	63.164	83
HM_1174	contig00061	CCA	3	12	CCCCTaCtTTCTCTTCCACCTC	63.354	GAAGAAGGATTGCAAGGGTGAGTT	63.002	129
HM_1175	contig15684	TGG	3	24	GGTAGAGCTCTGGTTTCTCATCTGT	62.228	AAAAATTTTCAAAACATcCtCccc	62.397	114
HM_1176	contig37678	CTC	3	12	GGAAATGCCGTTTCCAGAAATCTa	62.533	CTAAGCCAGTTTAAAGGGTGCTGa	62.941	156
HM_1177	contig23760	CAA	3	12	TCATCATTTCTGCCAAAAACAGAA	62.932	TCTGAATGAGAAAGACTCCTTTGG	63.085	135
HM_1178	contig05684	TGA	3	12	ACAATGGTCAAACTGGCTGTAAT	63.048	TGTTATTGCAATTACAAGAGCCA	62.761	144
HM_1179	contig12287	AGA	3	15	ACGCTTGGTAATCTGGCTGAATAA	63.158	TGTGCGCTTTTCTCGGATATTTA	63.026	139
HM_1180	contig05449	GCC	3	12	GATTTGAATCTGAATTCGGTGTGG	62.923	AAGAGAAGCACAGTATCCGGAGG	63.122	112
HM_1181	contig36998	CCA	3	24	GGGTGGAAATCGTGTATTGAAAAAG	62.813	GCCACCTGAAGAAACTACAAGCTC	62.739	123
HM_1182	contig15262	CAT	3	12	CAACAAATTCAGGCTGTCTACAA	63.367	GAGGATGATGATGAGGATTATGCC	62.997	106
HM_1183	contig05578	CCA	3	12	AATTAGGCAATTGCCATGTCTCT	63.035	CGGTTATGACCTCCTCTAGCTCCT	63.297	143
HM_1184	contig03859	TTC	3	12	TAGAAAGAAATCAGGTGTCTCGCC	62.91	TTGCCAGAGTGGTTCaAttTTT	63.027	84
HM_1185	contig27648	CAC	3	18	ATTTTATtTcAAACCTCTCACCGT	62.9	GgaATAGTGCTAACGTGAACAGGG	63.142	145
HM_1186	contig33838	GGT	3	12	AAaAGaGTCAAAATCGAAGGCTGA	62.619	CCAGGGATGCCCTCTCATGACTCT	63.189	148
HM_1187	contig33615	GTA	3	12	TGGCTGTGAACACTAATAGCAGCA	62.982	ATCAATGCACAAAGAGTAATGCGA	62.975	120
HM_1188	contig05623	ATC	3	21	TCTACGTCCAAACCaCATCTTGA	62.931	ATGATTATGATGTTGGTGCAATG	62.837	130
HM_1189	contig07790	TTC	3	12	CtCcACCAGTCTCTCTTCATGCT	63.34	AGTACGAAAATGAGAGGCACGAG	63.044	139
HM_1190	contig07324	GAA	3	12	ACAATCGACGgAACTGAAGTGA	63.148	GACTGTCTTCATCTTcaACGGCT	63.141	82
HM_1191	contig43767	CGT	3	12	AAATTGGAGAAGAAATGAGCGGACT	63.601	GTCTCCAATTGAAGCGTGACGAC	64.324	117
HM_1192	contig06914	AGG	3	12	AGAATTGAACCCCAACACAGACCT	62.824	GTCTCAGATTCAAACTCCATCCCC	63.073	143
HM_1193	contig01221	TTC	3	18	GTCTTTGATTTTGGTGTGCTCT	62.824	AGAGCCCTGGGAAGTGAAGAAGA	63.08	147
HM_1194	contig01408	AGA	3	18	AGAAGATGATTGGTGGTACGAGGA	63.217	tgttGTGgggtttTGAGGAAGTATG	63.233	157
HM_1195	contig22897	CTT	3	12	GCAGTCAGCATTTCAATCAATGTC	63.073	AATTAGGGCTTTAGATGACGAGGC	63.019	157
HM_1196	contig20695	CCA	3	15	ATAAACCCCTCGACCAAGAAACCTC	62.888	TCCTCTTCCACTCTCCTCTCTC	63.389	132
HM_1197	contig30422	TCA	3	21	TCCAATTTCACTTCAAAATCAAA	62.703	CCCATTTGCTCTTGAGAAATTAACCT	61.914	155
HM_1198	contig25571	ATG	3	15	tcGTCCTCCGCTGTAGCTCTACTC	62.281	ATATCGACTACTGTCTCCGCCATC	62.829	136
HM_1199	contig50059	GGT	3	21	TACGATTGGAAATCTGGTGTCTG	63.242	GATTGCAACTCACCACTCAACTC	63.061	129
HM_1200	contig22581	AGA	3	12	CAATTGGAGGATTGTCTCTCAACC	63.204	TCTCCACACTATCCTCaAACATGG	62.473	131
HM_1201	contig00978	GGA	3	12	TCAGGTGTGGAATTCAGGTTCAAA	63.034	CTCCAGAGAGGACTCAAAACGAGT	63.223	147
HM_1202	contig10865	AGC	3	12	CACGAATCAGTCACTACGACGATC	63.278	GAATGGCTTTTGGTATCTgAAAGTG	63.129	145
HM_1203	contig12305	TAC	3	12	AATTAATAGACAATGCCACCAGC	62.451	CTGGTCTGTgcTTTTGTTTTCacC	62.171	102
HM_1204	contig06141	CAC	3	12	TGCTACTAGGGTTTCTGATGGGG	62.811	GAGCTCAACTTTTACCAAGGACAT	62.838	156
HM_1205	contig46985	GGT	3	12	TCTGTACACCTGaaagaatCCAA	62.039	CACCTACAGGAAGAACGACCAGT	63.033	110
HM_1206	contig00331	AGA	3	12	AACAGCATTCACAACAGAAACGAG	62.753	CGCAGTATGCATTAGTGGTTCTTG	62.982	122
HM_1207	contig20194	TCA	3	15	CAGAAAGAAaCAAAACGATGAATAA	61.694	ATGATCCGATCGAAACTGGTAATC	62.496	106
HM_1208	contig28844	GAA	3	15	GTTCCCTCTTTTGTCTCATCTCT	62.876	GTTTGTCTCTCTCTCTCTCTCTC	62.863	119
HM_1209	contig12020	CGG	3	12	CGAGGTTCTGGAATTCaAGcTc	63.123	CGAGaAAATTGtTCGgGTAGtGc	62.166	119
HM_1210	contig03013	TTC	3	15	GCTCTTCTGATAATGGCGCTAGAC	62.759	CTTCTgaAGACCAAGAGTcCaCACA	63.027	117
HM_1211	contig38759	GTG	3	12	AAGAGCAATGATGGCACAAgGTGA	63.078	CATcCCTGTgATTTTAATACAGCAGC	63.057	146
HM_1212	contig37032	ATG	3	12	CTGGGATGcTCCAATCTTGAGAT	63.766	CAATTGCGAACTAGGACTAAGCGA	62.932	106
HM_1213	contig17566	CGA	3	12	TCTGTGTACGAGcCAACCTTAAC	63.664	GAGGATCGGCCACTACGAGAG	63.465	159
HM_1214	contig25566	TCT	3	12	TGAGATACCTGAAAGTCCCTGGC	62.91	AACTTGgggGTTcGagATCTGAGT	62.589	81
HM_1215	contig14878	TTC	3	12	ccTCTCTCTTTCTTCAAGGCTTC	62.98	TAAAGTCTCAATGGCGGACTCAAT	63.03	108
HM_1216	contig21643	ATG	3	12	ATCATATGGTCTAGTGGAGgAGG	63.303	TGCTACTGCTACTGctacTGTgcr	63.353	159
HM_1217	contig09121	AGC	3	12	TGCAGTATCCTTAAGTCTGCAAG	62.883	TTCTAGTTGGATGACCTTTTGGG	62.591	160
HM_1218	contig29429	AGA	3	12	AAGATATTTCACTaTGCTCAAGGGCA	61.545	GGTAGCTAACGTGGAGCTTGAGA	62.103	160
HM_1219	contig48925	GAA	3	12	CGATTAAATGCTGGAAAGGTGGT	63.438	TCCATCTACTATTCAACCGTGGCT	63.133	137
HM_1220	contig08918	GCT	3	12	AGGCTGAGCTCTCAGTCTCTCTT	63.42	TCAGTGGCATGGAAATCAGAGTA	63.038	120
HM_1221	contig13079	CGT	3	12	AGGTGGTATGCTGGGCTTAATC	62.712	CCTCTCTCATGCTCCTCTCTCTC	62.887	137
HM_1222	contig18276	CTT	3	18	CTTCTCTTTTCTATCTCAGTCTG	62.683	GAGGAAGAGAACAATGGAGTGGaA	62.987	145
HM_1223	contig17307	CAC	3	12	CCACTTCTCTCTCTTTCTGGCT	63.387	CAGTGAACAAATGGCCCATGGAA	63.242	146
HM_1224	contig45194	GAG	3	15	AGAGGAGAGGAaTGAAGATTGGGAG	63.365	ATCTGcCGCTCAATTGTCTATAA	63.034	115
HM_1225	contig43565	GCG	3	12	TCTCATGTTGGCATTTTCAAGGA	62.832	tCTATCCCCTCTCTGTTCTCTCCA	62.504	128
HM_1226	contig48601	TCT	3	18	CACAGCCAAACTGACAGAGAATGA	62.958	GAGAAGATTCTCAAGATTCCGaAGA	62.754	147
HM_1227	contig11231	CCA	3	12	TATTGATCCAGTGACCATGATTGC	63.15	GCATCTATATCTAGTGCAgGTGGGA	62.745	126
HM_1228	contig07730	CCG	3	21	GTTTTGGGGTCCATAGAAGAAAGC	63.289	TCAACCCaACAAACAGCaATaACAC	63.176	157
HM_1229	contig09991	TTC	3	12	GAACCTCTGATATTTCGCAAGAA	62.815	GGAAGCAACAGGAaAAGGAAGGTT	63.098	97
HM_1230	contig20266	TCC	3	18	TTCTTGATATACGGCGACTCGACT	63.456	AATGAGGTAGAGaAAGGGCGGAA	62.703	126
HM_1231	contig32159	CTT	3	21	GTCAAAGGAATTTTGTGTGAGG	63.117	CAAAAGTGAGACTGAGAGCAGCAG	62.958	159
HM_1232	contig24845	AGA	3	21	TTTTCTCTCCAAAACTCCACAA	62.999	AGGGTTTTTCTTAACATCAGATGGG	62.702	153
HM_1233	contig31987	CCA	3	15	ATACATCTTAGCCATCTCTGCCAC	63.574	AGTATCACCGTTCGGTTGGATATG	64.181	158
HM_1234	contig29260	AAG	3	24	TGCAATAATGATTTCTGTGTGGG	63.046	GCCTCACGAGTCTTGTCTTGT	63.15	141
HM_1235	contig01540	TTG	3	24	GAGGAAGAAGATGTTAACTGGGCG	63.601	GACCTTCCAATGTTCCCAATTATT	63.271	140

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1236	contig10892	CAT	3	12	CCATTGTCATTGTCTCATCACC	62.332	AATTCCTCTCTATAGCTCCTCT	62.858	80
HM_1237	contig31359	CTT	3	12	AAGGCTtaaaaaGTGCaCATTCa	63.146	CataGaAgaAGGTACgATGCACGA	62.643	96
HM_1238	contig17530	CCG	3	12	GATGACAAAGaAaGATGAAGACGGT	62.901	gtACAGAAAATTGGGTGCATCAGG	63.009	124
HM_1239	contig04792	ACC	3	18	CTGGTAGTGTCTCTCTGGTGGGT	63.011	TTCAGAACACAGCGTTAATGGGAT	63.009	154
HM_1240	contig11816	TCT	3	21	TAATTCCTGACTTTCCCAAGGAAT	62.98	AAGAGAGAAAGGCAAGGACACAGA	62.909	122
HM_1241	contig30573	AGT	3	15	1GGAAGAATGGGGATAAAGGAaAat	62.959	CTCTATCATCAATGCCCTTGACA	62.7	141
HM_1242	contig40778	CTC	3	24	GctCTTCCAgTctATCaTCTCTCa	62.382	AACCTGGAaAAcAaGAaAgATGcTG	62.921	125
HM_1243	contig18587	TGA	3	12	GATCAAAAGGACTGTGTGAATTGG	62.996	GGAGGCTCATCATCATCTTCTCTCT	62.249	135
HM_1244	contig36012	CCA	3	15	TATGGCGGATAAGATTGAAATGC	63.231	CCCAACAACACACCTTAgCTACC	63.041	121
HM_1245	contig49604	CTG	3	15	AAGGGATGTGAAGGATTGAGATT	63.27	AACGATCTCTCTCCATCaCAAAA	63.118	117
HM_1246	contig33479	CTC	3	12	CTGGTCCACAGTCAGTCCTAGCTT	63.244	CGAGGATAGCCTTTGACTGAAGA	63.117	160
HM_1247	contig02852	CAC	3	12	GGTCCTCTTCAGCCAGACAAGTAA	63.124	ACaGTGTTGAGTCGCTGGGT	62.67	159
HM_1248	contig11787	ACC	3	12	AATATGTGGTGAGCGAACCTTCA	63.121	ACCCAGCAATGATTAAAGGCTTCTT	63.06	124
HM_1249	contig34847	AGG	3	18	TGTCCGAGTCCGAAACACTAGTAA	63.184	ATACATTTCACATGGACTGCATCG	63.172	159
HM_1250	contig32155	AGA	3	12	TTTCTCAGTGGGAAGAACAGGGT	64.118	CCATTCAAAATTTTCAACCCAgAa	63.192	157
HM_1251	contig05591	GGT	3	12	ACGAGCTTCCAATCTGATGATACC	62.929	AATACCTCGCTCTGTGCCATTACA	63.353	121
HM_1252	contig18999	TGG	3	12	CTCCACCAAAACAGAACCATTAT	62.397	CGAAACCTAGATGGAGAAGAAGA	62.171	137
HM_1253	contig36626	CGG	3	12	AGTGTCTCACTCTCCAGTGCTTC	63.005	GATTTGATAGTGGGACCACTGAG	63.102	150
HM_1254	contig11307	CAT	3	24	TCTAGGTGAAATTTGGTCCACCAT	63.419	CgGGGGAgaTAATGAGGAAGATAG	63.254	145
HM_1255	contig16220	GGA	3	12	GCCGAGAGATGAGAAGAAGAAG	62.989	GATGACAAATCgTCGTCAATGGTA	63.159	141
HM_1256	contig26311	GAA	3	12	ATCGATGAGGACGAGGAGGATAG	62.979	ATCCTAAACTTGACACTCGCTTC	62.838	158
HM_1257	contig02998	CGA	3	12	ATATTCTCCGACGCTCACCTTT	63.398	GTTGTGGTGAGGAAGTCTTCGTT	62.922	146
HM_1258	contig30879	CCA	3	21	aTCATCCTCACTCAAGCTCCATTC	62.791	CtGTGaAAAGAAgTTGTTCTCGG	63.426	139
HM_1259	contig44061	TCA	3	21	ATCATCTCTCCATCACCACATCT	63.211	GGAGGACCGGCTaAAGAAACAAGTA	63.89	113
HM_1260	contig24602	AGA	3	12	TACTCGTCAGCTTCAATTGCTAAC	62.858	GGCGTAGTGTCTCTACTCTCcaGC	62.752	98
HM_1261	contig14415	GGT	3	12	GTGGACATTAGGTTACGGATGGAC	62.813	TTTCTTTCTGTGTCAGTGCTGA	63.377	136
HM_1262	contig04923	GTG	3	15	GTCTCAGGAACTAGTGAAGGACG	62.691	CTCCTTGGTaTCTACTCCCTGCT	63.189	92
HM_1263	contig33700	TCT	3	12	GCCCATTAGATGAATTTCCACAG	62.912	AAACCTAGtCCTAGATCGAACG	62.992	95
HM_1264	contig33418	CTT	3	12	ATAGAACAGAGGcTCCCCATCTT	62.686	TACATTATCAGGAGACCCACTCA	63.016	160
HM_1265	contig28210	GTG	3	15	AAGGGTTATGTGGTGGTTTGCAT	62.912	CACCCTCATGGACACTACCACTC	63.045	134
HM_1266	contig22974	GAA	3	21	TGAaTTTATTTTCAAATGGGCTCG	63.211	GAGCTTTATGCAAAATaATACGGGc	62.981	113
HM_1267	contig10801	TGG	3	15	cTccGATTtTAAaaggGGTTaATGc	63	TTTAGGATCAGAGGTGAGGACGAG	62.984	158
HM_1268	contig03887	AAG	3	18	ATATCTCTCTCGAACCCAACAGT	64.331	ACTGTAGCGACTTTCAGAGACCCA	63.677	115
HM_1269	contig23920	CAT	3	12	TTTatGTcTcCAACTTGcCTcCA	63.048	TTCTGGGaTtGtGATGtGTTTT	62.907	126
HM_1270	contig31486	TTC	3	12	TGCATATTGTCTGGCTCTATTGAA	62.972	TTCCGAGtCTGTACTGAAGAAGC	63.238	134
HM_1271	contig45940	TGC	3	21	AATTcCaGtTCTTCCGGTGTATT	63.184	TGCATACGCTTTTCTGATTTCa	62.982	151
HM_1272	contig11762	GAA	3	12	CCACCATACTCCAAAAGATCATCC	62.887	GAATAGGTCTGCTGCTGTTGTACC	63.048	132
HM_1273	contig43451	TCT	3	18	TCTTCTCTTTGTCTCTGCTTc	62.483	cCATGAAGACATAGCTAACACCGA	62.528	105
HM_1274	contig41525	CAG	3	15	AAAGTAGCGAGCagaTtGAGCATC	63.273	TGcTtgaCTGAAGGTGCTGATAG	63.962	145
HM_1275	contig17974	CCG	3	12	CTCTTCTCACTCTCGAAACCTG	62.892	TCTCtTAAAGTTTGGCCCTTTCC	63.18	153
HM_1276	contig15798	GCT	3	12	GaTgTcCaATtCcTGCTGtTAAaC	63.026	TCTCAGGTcATTGGATATgGagGt	63.093	135
HM_1277	contig09428	CAT	3	12	CACATCTGATGAAGATGATGCCA	63.358	AGGCaagaaTCAAAATGCTAGGGT	63.406	151
HM_1278	contig19309	TGA	3	30	CGATAAAGATCTTCGcAGGTGACT	63.035	CTCCTCTATGTGATCCTCTTAA	62.897	140
HM_1279	contig01934	TTG	3	12	AATTCCTATTATAGCCCTTGGTGT	62.903	ACATTGGGAGCTACAAAGAGTCCA	63.338	138
HM_1280	contig11532	CTC	3	15	AAGAACAAGGGAGTGGTGAATTTT	63.285	AAACCTAGAAAGAGGTAAAGCCCA	62.609	133
HM_1281	contig03295	ACA	3	18	ATtCTGCaCaTCCAAaCaAGAAcA	62.948	gtgggtggggaagcttaactcTGTc	63.887	147
HM_1282	contig16937	GCC	3	12	GTGTAAGAAGTTCTCTCAAGAGGGC	63.296	TTAATTCAGGAGAAACCAATgaCG	63.204	149
HM_1283	contig08137	GGA	3	12	GTGCGAAAGAAAGAACCACTAGa	63.142	AGAGTTGGGTGATGaGAAATCGT	62.382	138
HM_1284	contig21733	CCT	3	15	CATCATATATGCAGACCCTCCAA	62.925	GCGGAAGATGAGGAAGaAGAAGa	63.308	132
HM_1285	contig50547	AGG	3	15	GAGGTGGGAGAAAGATCCCAAT	63.777	AACAACATCCCAAAACACCAcAC	63.042	106
HM_1286	contig41841	GAA	3	12	TTCCACATCCaCTTTTCGATACT	63.009	CTGAAAGTTGCTGGGAAGTTGAGT	63.133	118
HM_1287	contig22310	GAT	3	15	GAAaAaTCCGATGTGGGATTTCAA	63.105	AAACCCaAAACAGATCACCATCAT	63.014	141
HM_1288	contig24212	ACC	3	12	AGCAGCAGACATAACCACTCTTGA	63.186	TGAAAAGAGTcAGTgATTGGGAAGG	62.811	142
HM_1289	contig02081	TGC	3	12	GatttCTCAAGAGGAGGGAAGG	62.755	GTAAGGTAGGGGAAGAGGCGAG	62.898	121
HM_1290	contig31112	ATC	3	12	TGCTTCATATCCTCAAGATCTCC	62.889	ATTGAGCGATTGAGAGGGACATTA	63.223	138
HM_1291	contig18906	GTG	3	12	CTTTCAcAGCGTCTCTGACTCTT	63.258	TGTCTATCATGCAACTCCaACcAT	62.833	122
HM_1292	contig18295	ATA	3	21	CGAAAACCaCAGAACCTCATAC	63.747	AATGAGCAAGAGAGTGAAGCTGG	63.044	140
HM_1293	contig12948	CAC	3	24	TGTCTGCTCtCAGCTATaATGAa	62.14	TGTAATAGCCATATGGAGGATGGG	63.105	151
HM_1294	contig28135	GAA	3	12	GCGTTTAGGATACTCGGCTCAAA	62.839	GATACTCAaCTTTTCCCCATTCC	63.069	92
HM_1295	contig00669	GGT	3	12	TATCGGTGAACACATCGGAATC	62.939	CCATTGTGTTCAACATACTCTcG	62.828	148
HM_1296	contig46830	GGA	3	18	TCTCGAAGAACTGTGCTTACAAAT	62.27	CCCAAGAAAGATAGGCAATTcGTA	62.813	145
HM_1297	contig28304	TCA	3	12	CTGTGGCTTCGGTCTCACTCTCT	62.922	TGAAAATCGAGGCGAGCACTaTAAa	62.264	92
HM_1298	contig33727	GCT	3	21	CTCACCTTCAAGATGGCAAGAAT	62.91	AAAAcAGCTTTCTTCCACcAGAGA	62.71	127
HM_1299	contig18793	TGG	3	15	1cGGTAATGTGTTGTTGGGAGTG	63.259	CAGAGCCGCTAACAGAGAaAAATg	63.546	86
HM_1300	contig21803	ACT	3	15	ATGATACAATCTCAGaAAACCCAT	62.916	GGTGTcAGAGAAGTGGAGCTATCC	62.694	145
HM_1301	contig01869	TGT	3	15	CGATACTCTGTCATGATCCAAATTA	63.163	TATTGGAAGGCAACAGGAACAGAT	63.121	152
HM_1302	contig18118	GAA	3	12	TACGATTGAAGAAGCAAGTCCGGA	63.038	TCCACATCTTCTCCaCaATCTCAT	62.119	95
HM_1303	contig26098	TTC	3	12	TcGtTACCATTGTAGCATGACAC	63.308	ATGTcAgCGAGAAGATTTGAAGC	63.15	127
HM_1304	contig13281	TCA	3	24	TAAAGCTTACGCTCTTCTGTGTC	63.17	GTTGACAACGACGATGATAACGAC	62.861	155
HM_1305	contig21530	CAC	3	12	CTCCAATGAAAGTCAACAATGcAG	63.048	GTGGAATTCAGGTGGAAAGAGTG	63.006	141
HM_1306	contig39796	ATG	3	21	GATGGgtTcttcTTGgaGATACAG	62.353	AACCTCTCACTCTTCAACCAATCG	63.01	128
HM_1307	contig25268	GTG	3	15	CTTCTCCACATTAGCACTCCCAT	62.811	TGCAATATCAAAAGGcAGATGTTG	63.27	147
HM_1308	contig00134	GTG	3	12	GAAAGACATGGTTTATGCCTTTGG	62.922	ATCTCATCCCAATCATTTGCCTTAG	62.594	147
HM_1309	contig43952	GAA	3	15	TGAAACAATCGTCAAAaGACCTGA	63.034	AGTGTCAAGCTCAGTTGGAACTT	62.719	134
HM_1310	contig29583	CCA	3	12	GAGAACATATGTCgATTCTTCGAA	62.9	TGGAGAATCAGATGCGTaCaAAa	62.946	158
HM_1311	contig17469	TGA	3	12	AGTGATTGGAGATTGAGATTGGG	62.672	TTTTCTAGAGAGTGAAGCAACCC	62.2	90
HM_1312	contig20992	TAG	3	12	TATCGGATAGTTGGAATGGGAAA	62.696	GcAGTACCACCTCTTCAAATCAC	63.242	152
HM_1313	contig14488	ATC	3	12	CTCGTCCAGATTtCTcTATTTTGG	63.202	TATCAGAAGGAATTGGGACcAGAG	62.771	135
HM_1314	contig20915	TGA	3	21	AGaGATGATGTTGTTGTGGCAT	62.927	TCCATCTACTAAGTCTCGGTTGCC	62.923	156
HM_1315	contig22751	AAG	3	12	AGTtATTtGGGCTTCCCAAGACTC	62.995	TATTATGACCCTGATCGACCCAAG	63.305	159
HM_1316	contig04187	CCA	3	12	CAGAAGCTCAACAAGACCAATCCA	62.828	CGGTAGATtCCGAAGGcATAGAG	63.314	115
HM_1317	contig23130	TCT	3	12	AAGAACCTGTCAAGGCTTCCATTG	62.921	TAGTATGGGAAGTTGAGGcACAG	63.641	117
HM_1318	contig51328	TTG	3	12	TCAAGAAGAGGGTAGGAGGAGGTT	62.86	GACAATCGTACAGTCTTGcAGAA	62.741	158
HM_1319	contig16782	TAC	3	15	AGTCTCTCAAGTTTCTCACTCAGC	63.02	TtGcAGCGACATTTTGCTTCACTA	63.081	124
HM_1320	contig29638	CAT	3	12	CAGAGTCTTTAAACCTCCGAAGGA	62.894	AAGTGCTTCTCAACCTGCAcACTG	63.09	113
HM_1321	contig19490	TGT	3	12	TGAATTCACTTTATGCTGGTTTG	63.146	ATATCAGTGCAAGGCGcATTGTTG	63.273	155
HM_1322	contig19682	ATC	3	12	CTCCTGTGATTCTTCTGGCTCACT	63.34	CCCTTAAAGCGTTCagAGtTTTT	63.01	148
HM_1323	contig48051	TGT	3	12	GCACCTCTAACCTTGAACCTCGAA	63.031	CTGCTCAcACTACGACGCTTTAAc	62.483	160
HM_1324	contig38205	AAT	3	21	gaATTTCACTGctCAAGTCTTCAGA	63.024	TCTCATTCAGTGATGTTTGGGA	62.907	114
HM_1325	contig24713	AGA	3	30	TCCCGAAATTTAGAAGGTGACAAA	63.002	GTCTCGAGTTcATGCAACACAGTT	62.858	151
HM_1326	contig00674	TCT	3	12	AGCTTCATCAGTCAACCAaATTC	62.813	ACCGATTGATCAGCTGAAAGAGTT	62.613	139
HM_1327	contig22117	CGC	3	18	ACTTCTTCAACCTCGCTCACTcC	63.309	CGGTGATGAATGTTGGGCTTCTA	63.439	153
HM_1328	contig25428	CTA	3	18	GATTTCATCGGAGATAGTGGTT	63.584	CTGAGCTAAgGCCTTCAAAACAGA	63.234	122
HM_1329	contig40442	GGT	3	15	GAGGCGCTACTTGAGAAAATTGAA	62.826	CGTTGAAAATCCTCACAGAGAACC	63.325	142
HM_1330	contig04743	ATC	3	12	ACATAGTTATCATGTGCCGCCCTA	62.828	CCCAACCCAGGTTGAGTAATTTAG	62.821	127

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1331	contig06274	CAC	3	15	GgTGCAATTATTCATAACCGGAAGA	63.225	ATTGATCAAGCCATAAGGGAGTTG	62.607	153
HM_1332	contig31936	TGG	3	12	CaAaCAATcACCCACTTTCTCTCT	62.895	AAGACGGGTtAGGGATACTAaAgCG	62.922	141
HM_1333	contig05868	TCT	3	12	AATCTCAAACTCTTCTCCCAATC	62.865	TTGTTGTTTCGCTTTTGGGTtATT	62.852	158
HM_1334	contig08758	GAT	3	12	AGTTACAAGCGGACAAGAACCATC	62.838	TTTCACTAGGTTTTTGGTCTCTCA	63.1	129
HM_1335	contig52037	AGC	3	21	ATAGCTGTCAAGTGGAAAGTGGAG	63.023	GTTGCCGtTtCIATCTCaCaTcT	62.827	122
HM_1336	contig03452	TGG	3	18	CCAAATAGTAGTtGGCTCCATGAC	63.022	TGGCTCTCTCTAATTtCTTCTCTC	63.172	142
HM_1337	contig29744	TTG	3	12	GGAGTGAGAAAGTGAGAGGACGAAG	63.001	ACCAGAACCAGAGATTtCAATTTCa	62.996	112
HM_1338	contig39482	CAC	3	12	GCATCTCTCCACcATTACAGACT	62.915	IGGtTtTgGGAGGAGCaAAGAT	63.747	151
HM_1339	contig20628	CAC	3	12	GAATGAATCCAAAGCTTtGATGG	63.009	TGAGGTcAGACtTTGATGTGtTTTG	62.62	128
HM_1340	contig19242	CTC	3	12	AAGGCCACCAAAACAGTATCCACTA	63.031	CTGCACCACTCAATAAGAAGCTCA	62.744	160
HM_1341	contig39626	GTG	3	18	TCCATTACTGCTGTCTCCaCAAA	63.048	GACTACCACtACCACTCTCtCaTc	63.411	90
HM_1342	contig12146	TGG	3	15	GGTGGCTTTATGTACTCCaCAAG	63.031	AtTtCtCTCTCTCCCTCAAAcCAc	63.071	132
HM_1343	contig01235	TCG	3	12	GTGTAGTCTTCTCGTCTGCTCTCC	63.583	CTTCTCCAACCTTCTGTGACGAT	63.01	95
HM_1344	contig49027	GTG	3	15	ATGGGTtGGATgAATcAGAAACCTG	63.419	aCAAAAAcAAAAAGCAGAAGCAGC	63.076	138
HM_1345	contig32910	TCT	3	15	ACTTCCAACCTCACCAAAcCAAC	63.564	AGGAAATGGGTTCTCAAGCTCTG	63.086	157
HM_1346	contig38474	CAT	3	12	cACCAGCAtATgAATATCgTGAA	63.05	TGCTAGAAAGAGAAGTgGGATTGaA	62.619	132
HM_1347	contig21645	ATT	3	12	TTTTtGGGAATCTTTTTCTCCGAT	63.163	ATATCGGAATAGTcGCCGGACTT	64.098	151
HM_1348	contig15581	TCA	3	12	ATATGCATCGTcAtGtCaTCAcT	63.173	CTCTCTCTCTGAGTtCAACAGTC	62.882	95
HM_1349	contig33060	TTG	3	12	TAAGGTTCTGATCGCCATaACCAT	62.925	TTCAGTCACAAATTGGCTCTACCA	63.048	151
HM_1350	contig39925	GAG	3	12	GCTGAGGACGAGGAGAGGT	63.347	aATCTAGtCTCtCAcAcCCTCAATC	62.988	159
HM_1351	contig51305	TCT	3	21	TACAACCTCAAGGAATGTTcGAGG	63.629	TCTCATCTTCAACCACCATtGAA	62.907	132
HM_1352	contig25976	GGA	3	18	GTTTCGCTCGAAGATGTGGATT	63.758	CGAGCTGAACAACTCTCTaATGTT	62.933	138
HM_1353	contig08932	TCC	3	15	GGCAGATCACTACTtGAAGCAaAGG	63.341	TCTTGTCTTCTGCTGAAGTGACGAG	63.168	158
HM_1354	contig13876	GTC	3	21	ACAATAACAATATGGGGGgACG	62.922	TGCTTTTGATTCTTCTTCCAaAG	62.906	132
HM_1355	contig24648	CCA	3	12	TAACCTtcttCTTCCGAATCCGT	63.293	AAGAcCTACTCTGGGtTCCGATG	63.616	160
HM_1356	contig25782	ACC	3	12	CCATTTTATGATTCTCGGGAAGAG	63.113	GGCGGTTACTGGTAATCCtCTTT	62.82	110
HM_1357	contig15921	TGT	3	15	CTGATGTTGGGCACTCTCTCTt	62.9	ATCAACAACCCaAAACCTACCTC	62.992	124
HM_1358	contig03041	GAG	3	15	CTATTGACCGTtAATTCTGCGgAG	63.027	ACAAAAcAAGACCTCTCCACCTT	63.5	121
HM_1359	contig46210	AGA	3	12	AACCCCAAGCAACCAcCAAAAGT	63.008	GAAACAGaAGACACTGTTTGACGA	62.739	159
HM_1360	contig27687	GCT	3	12	CAAGTTGGTATGGAAGAGTGGAG	63.003	GCAGTTcAGATAAAAGTGTGAGGC	63.248	128
HM_1361	contig12686	CCA	3	12	AGAAAAATGTTCTTCACTGCGCAGG	62.716	AATAGAGTACCgCCTtCTCAGGCT	62.926	108
HM_1362	contig15675	CCA	3	15	GCTGTTGTTGGCAAAATTACCAT	63.256	GAAGAAGACGGTGAATTGAGGAG	62.584	111
HM_1363	contig32014	TCC	3	12	ATCGGAAGTCTCAGATATTGCAGG	62.913	cGTCGGATGTGAGCTATTAAACC	63.043	89
HM_1364	contig15695	GGA	3	15	CGAAaTGCAAAACCTAGAATCCCT	63.014	ATTTCAATTGGTcAGATtGGGA	62.789	157
HM_1365	contig39160	TCT	3	21	cAGtGACGGAGATGAACtGCTCA	62.812	GGCATTCACTgAGcTGGGTcGtT	62.925	124
HM_1366	contig25925	CTT	3	12	ATCTCTTGTGtGATGGGATcG	63.526	GGATGCTATTGAACAGACAATCCCTG	63.135	120
HM_1367	contig27856	GAC	3	18	TCACCTCATCTCCCAATCTTCTC	62.977	CCTCATTTGGATGTTGCTAGtGATG	63.006	118
HM_1368	contig28654	TGT	3	15	CGCCATACAAGCTCACTACTACC	63.263	GGTGAATGTGAAGAAAGGTTTG	63.006	99
HM_1369	contig20810	TTT	3	12	TACTAGGACCACTGTGCTGACTG	62.958	CCATTATTGTTGATGTTGCATCTGA	62.861	116
HM_1370	contig45684	GTG	3	12	TGTcAGAATcATATCTGTcGCTG	62.951	AAGTTcAGAAGTTGATCCAGTGGG	62.095	102
HM_1371	contig06981	TGT	3	12	TGTTGACCTGCTGAATGAATTGT	62.948	agCAGCAACAATGAATCATCAAC	62.544	151
HM_1372	contig23064	TTT	3	12	tGCACTATTtctGTTTTCCTtC	62.716	CATAGATTGAAGCTCCtCTTCCa	62.996	153
HM_1373	contig37591	TTT	3	12	TCAATtCtTTTGTACCATCGCTT	63.03	ATCCTTAATGGGTCGGATGAGATT	63.073	119
HM_1374	contig27475	TCC	3	18	GTCATTGcAGACCTCCCACTTTAC	63.026	AAATTCCTGGAGGATATGACCCT	62.964	146
HM_1375	contig30154	GAA	3	18	GGGATGTTTTTGGTGTTCAGCTAC	63.035	CTCCCAATTCTCTCTCAATCT	63.156	150
HM_1376	contig33326	TAC	3	15	GCTACAATCACTGAATCTCTCTG	63.031	TCAAAcAATTGGCATTCAAGAAGA	62.932	86
HM_1377	contig19577	CCG	3	12	CTCCATAGAAATTGCAACCGAAAC	63.03	GAAAAAGAAAGTAAAGAATCCGCA	62.628	147
HM_1378	contig28789	AAG	3	12	GATCGAGAAAGAGTGGAACAAGGA	63.093	AGAACATGTTCTGATGAGGTTGCG	62.827	133
HM_1379	contig03942	TAG	3	15	ACCATCAAAACCAAGCAGCATAAT	62.95	CCACATTCACTGTCTCTCTGGA	62.798	120
HM_1380	contig14269	ATG	3	12	GAGGATAGCCAgCTTTGTATGATACA	61.25	AGaAGGATCAcAATAGCAGGAAGC	62.213	160
HM_1381	contig02690	CGC	3	12	GATTTCTCAAACTCCATGAACCG	63.108	TGTGATGGTCTACTCGTTCTGAT	63.057	128
HM_1382	contig41559	CAT	3	15	CTTCATCATCATATTCTGCTCTcA	63.249	CAAAATGTCGAGGAGTGAGGATTC	63.318	155
HM_1383	contig41418	TGT	3	15	CTCGATATTCCGATGTcAGGATG	62.897	GaAAAGAGtCCCGAAGGACTC	62.874	136
HM_1384	contig10737	TGA	3	12	TTCCTTCTTCTCCCTCTCCCAT	62.958	TTAACGGAGGCAAGTTCATCGTAT	63.043	148
HM_1385	contig29957	TCA	3	12	ACCTAGATCctCGCTCTTtCaTc	63.295	CgGATtCAAAATCAGAAGTGTcG	63.023	131
HM_1386	contig22234	TCT	3	15	CCCTTAATGCCTATcCTTCTCTG	63.273	CACCTGCAATTTTCAAGCAATAA	63.278	82
HM_1387	contig08580	ACC	3	12	AAGTGGTGTGTTGGAAGTGTCTG	62.732	AGAAAGAAAGAGTgGtTtggggGT	63.5	121
HM_1388	contig25439	GTG	3	18	GCAGGTGAACCTCAgTGGGTAG	63.275	AACCCATGCTCACTCAAAcCAAT	63.189	155
HM_1389	contig02124	AGG	3	21	GACAAGGCTAATGAAGTCATGCTG	62.323	TGGTGTAGAGGGAGTcGAATTAGC	62.923	147
HM_1390	contig09630	CGC	3	18	CATCCCTCTCTCTCTCTCTTAG	62.945	GGGGCTAGGGTTTTGAGTAGTAA	62.806	131
HM_1391	contig51309	GGT	3	12	GTACCAAACTCGGAGGAGTGAAT	62.571	TACTCTTCGAGGGGTGGATGG	63.541	151
HM_1392	contig27921	TCT	3	12	GATATCTTCGGGATTtTCGAGATG	62.609	CTCTCTCTGGTGGCTCTTTTATT	63.086	138
HM_1393	contig50511	TCT	3	36	AGCTTACAATAATGAAGATCGCG	62.761	GTCAAAcCAAAAGCTGAGCAAGAA	62.972	128
HM_1394	contig20633	GAA	3	24	GCAGACTTCGAGGAGTGGAGT	63.335	CtAACAAATTCAACCAATTGAGCG	62.922	113
HM_1395	contig16237	CGC	3	12	AAaTCGAAGcTcGTGTTGCTTG	63.031	CTAcCAAGGAGTGAGTTTCAATGG	62.314	125
HM_1396	contig17489	TGG	3	18	ATGTTCTTTCAAGTGGCTCTGAT	62.498	GTaCAAAcCAcTcGtTAAAAcCG	62.847	148
HM_1397	contig27465	TCC	3	21	TCTATAAGATGATAGGAGTGGGG	62.507	TCATCAGAATGAATCCTCTCTCTC	62.967	126
HM_1398	contig09491	CTT	3	12	AATTCTCTTGCTAATGGCGATTCT	63.305	TcCCCAACAACAACCTAAAGGTA	63.003	139
HM_1399	contig05127	GAA	3	15	CCACAACCTGACTGACCAATTAG	62.93	ATTTCCCTTCGGTGATTACCAAGT	63.049	141
HM_1400	contig44455	TCC	3	12	CTTCTCTCTCTCTCTCTCTTCAT	62.639	GGTTTTGAGGTGTTGGAAGTAGAC	63.115	103
HM_1401	contig19413	CCT	3	15	AAGAATGGACTCTACCACTGGC	62.925	CATTTTGAAGCTGTAACCTCTGACG	63.25	150
HM_1402	contig36558	TCT	3	18	TTTtGGATGGAGGAGATGATGCT	63.196	GAGGGTACCACCTACCTCTGCCAC	63.343	134
HM_1403	contig52182	TGT	3	30	ATCTGGCAGTAGGCTTCAACATAT	63.368	CAAAACCACCATCTCTTTTCGAG	63.21	133
HM_1404	contig45886	CAG	3	12	GATtGTTCAAGCAGATGGGGATC	63.016	GGGTTAAGCCATCAgTTGCTAAGA	62.839	113
HM_1405	contig30251	GAA	3	12	AGACGATGAGAATGcTAAAGTGGG	62.923	CTTCGGGTCTACTGCTACTCAAA	63.028	158
HM_1406	contig38266	ACT	3	12	GCTTTTGGCTTAAATAtcCTCC	62.358	TGGGATACAAATATGGGAAGCAT	62.626	128
HM_1407	contig41771	GAG	3	12	CtCtTTCCCTcATCTCTTCTTTC	62.755	TAGTaCGGTCTACAGCTTCATCCA	63.051	153
HM_1408	contig35018	TCT	3	21	GGCAGTGAGTCCCTCTTCAAACT	62.5	AATTGCAGAAACACAAAAcCAACC	63.348	159
HM_1409	contig19946	AGA	3	30	ATCAAAcAGAAATCCAGATTTTTCA	62.107	CCACCACCTCTCTAGTtTTTCTCA	62.993	160
HM_1410	contig39188	ATC	3	12	AATTGGTtGAATATGACCGTCTGT	63.219	GAAcAGGAACAATCAgAGCATGA	62.714	147
HM_1411	contig13599	GTA	3	12	TGAAGACTGTGACTGTAAAGTGGTC	61.85	CCCTTTTCAAAACCGCaGtAAGA	62.65	147
HM_1412	contig27897	CCT	3	12	ATCTGTGGATGAACCTAAAGTCTG	62.512	ATCAGGTGCATTAAcGCTAAcCC	62.647	130
HM_1413	contig06617	TTT	3	18	AtgTCTCTTATCTCTCCAGCGTG	63.128	GATGTCAAGACAAAGATGACGTG	63.164	99
HM_1414	contig31159	GTT	3	12	AGAAAGTTAAAGGGAACAGTGAAGG	63.076	CTTTTACCCTTTTctGTCCCAAc	63.176	103
HM_1415	contig38704	CTG	3	15	GCCTTGTCTCAAAATTCAACTCCAC	63.353	AAGAAGACAGGCAAGTGCAAAAC	63.057	95
HM_1416	contig07982	CGC	3	12	CtGtTtGCTTTTCAcAaAcCc	63.006	TGCTAGTAGTGTGAAGaTCTGGCTG	62.339	134
HM_1417	contig19923	GAT	3	12	ATTCCTCTCACTCTCTCTGCCCTT	62.986	AACACAGCGACCTACTCCATCAT	63.255	154
HM_1418	contig10104	AGG	3	12	CGAGGAAGATTcAGAGTAGTCCA	63.325	GATCAAAcGATGCTGCCAATAT	63.565	131
HM_1419	contig04324	CGC	3	12	CCAAACACCTGAGAGAAATTCCAC	63.212	GATGTgGTGATTAGAtTTTtGGG	62.817	130
HM_1420	contig08631	GAA	3	18	TCCGTTATGATCAAAcATTGGAA	62.511	TAGACACCAaAAcCAAAcCAACCT	62.918	125
HM_1421	contig01821	CCA	3	15	GACCCACCAACACCAcATAAc	63.475	AGGTCCCACTAGATTGATGCTTG	62.811	144
HM_1422	contig26638	CTT	3	21	tGTTCACTGTAAAGCCCAATTCT	62.932	ACCTTTGATTtCAAACTGCGAGTG	63.762	121
HM_1423	contig04005	TGA	3	24	TAATATCTATCCATTCTGCTGCCG	63.227	ATAgGtGTTGTTGAGGTTGAAGGCT	63.616	154
HM_1424	contig22448	CTA	3	12	TCAACCATTTcAGAAACCACTCA	62.918	CATCATCGAAATGAATGAAGCAG	62.935	142
HM_1425	contig31381	ATC	3	12	TAAGATCCAAcCAAGGAaACCA	62.894	GTCaAGGATCCAGATTTCACAAAG	63.204	153

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1426	contig08023	AGG	3	15	AtttAGGCTGTGTTTCGGATTG	62.545	ATCTGGTCTAACTCGGTCCCAACT	63.506	147
HM_1427	contig19363	TGA	3	12	ATGATTTTGGATTGGGTTTGGT	63.005	AAGACCCATCATCAGAGCAAGAAC	63.017	83
HM_1428	contig44599	TCT	3	12	CATCTCCTTCTCATCACTCCAAT	62.874	CGTTTTCGTTTCACTCTCTCTCT	62.508	152
HM_1429	contig04041	GGT	3	15	TTGGTACTAAAGCCGGTGAAAGAA	63.13	CAATGATGTGAAGAACCTTTGGAA	63.128	143
HM_1430	contig01234	CGG	3	15	CaaTTGTCGGTGTAGGTTTGGT	62.711	CaCagAATCaAGCCTaCGaCACC	62.412	136
HM_1431	contig25878	TTC	3	24	CAGAAATTCATCGTCTCTTGGCT	63.022	AGCGTTCAAGGACTGAGAATGAAG	63.238	116
HM_1432	contig01390	GGC	3	12	AGCACTTCTCTCACAGTCTCTCC	62.486	ATGGGTTGCTGATTAGCAACCACT	63.06	152
HM_1433	contig38163	GAA	3	12	AACCTCATCTCAGAACTgcAATC	63.017	GGTCCGGAaAACTATATCTCTCT	62.81	90
HM_1434	contig18760	TCT	3	24	CAAACGTCGGGAACAAAGAGGTAT	62.822	gTgGGAAGCCCTAGTCCCTAGATa	62.983	109
HM_1435	contig31703	TCA	3	12	TTCAAATCTCTCCATTATCCCCA	63.083	GAAGAAGCAGTGGCAGCATCTAAT	63.162	153
HM_1436	contig21035	GCT	3	15	GAGAGATTGGGTCTCTTGCATTT	63.104	CACAACATAGAAGTGGTCAAAAGAA	62.555	152
HM_1437	contig19366	GTC	3	15	CGGGCTCTCTCTCTCTCTaCaC	62.835	TCAATTTCACTCTCGTTCCACATGA	62.921	80
HM_1438	contig21842	TGT	3	18	ATCCAGCAACCAAGACGATTCT	63.446	AATAACAGCTTTCCGATAAAGTCGG	62.771	157
HM_1439	contig05983	ACC	3	12	TGCTCTCTCTCaCTGCTCCGtc	62.24	TCGGATTGAGTTTgATATGGCT	63.021	115
HM_1440	contig16277	CAG	3	18	CAACAATTCACACGCAACTCTAG	63.057	GTAATTGGCaGGAGCTTGTGCTT	62.838	93
HM_1441	contig17465	GAT	3	12	ACAGCCTGGTGAACCACTAGAAGG	63.033	CGTGTGGACCTAACTGAAGGTT	62.721	158
HM_1442	contig25499	TCT	3	12	TTGATCCCAAGgCaTAAaCTCT	63.121	TAACAACCAAGTAcGAGGAGGAGC	63.646	108
HM_1443	contig07891	TGG	3	15	TCAAAGaCcGaAaCCGTATTATGc	63.339	GGTGATGAGAAAGTGGTGGTGCT	63.792	145
HM_1444	contig13762	TTG	3	12	TTTGACAGCTTTTGAAACAGCATT	63.189	ACAAGTGGAAAGATATCGAGGGAA	63.341	98
HM_1445	contig00434	TTC	3	15	CTCTCTTGTGGGAGCAATCTCT	63.124	GGGTAAATGTGGAGAAAGTCGATG	63.009	125
HM_1446	contig00161	CCA	3	18	CTACTGGCATTTCAAAGAACAT	62.619	GTAGAAAATGGCGGTTTGGGTAAT	63.3	150
HM_1447	contig28838	TTC	3	18	TCATTTCTGGGAGCTTCTCAATC	63	TTGGCAATTCTGGATTCAATTTCT	63.009	148
HM_1448	contig52059	GGT	3	12	GAGAGCCATCTCCAGAAGGTTTTA	62.2	CCCATTaAAACCAcCAACACATT	62.919	147
HM_1449	contig28017	CAC	3	12	TGCTTCTGAGTGATGAAGAAGACG	63.159	GGATGCAATGCAGCAATAAGTGTA	63.3	149
HM_1450	contig13738	GAG	3	18	AAAGGAGGAGTAGagCTGAAGGA	63.08	CTCAGTTGCCAGTGTACTCAG	62.428	88
HM_1451	contig04218	TCT	3	15	TGGAATCAAGAAGTGGTATAGTGG	62.473	TTCTGAGTCTGCTCTGAGGT	63.119	158
HM_1452	contig43150	CGG	3	12	GGGTACCATGTCTGAAGACGAAC	63.128	GATCATGTTATTGGTCTGGCAGTG	62.833	111
HM_1453	contig31237	GAT	3	18	AATTGAAAACCCGTCTTCTAGC	62.912	AAACTACATTAGGGTgCAGTTgg	62.645	158
HM_1454	contig10845	AGA	3	18	GCTACGGgAAGAAAAAGTAGGGAA	63.001	GTAGCAAACTCCTTCCAGTTCCAA	62.921	160
HM_1455	contig28918	CTT	3	18	TTAATCGCTATGGTCTGCTCAAGC	62.579	aTAACGGTAAACAACGAGAAcCCAA	62.836	119
HM_1456	contig18587	AAG	3	12	TTCTTTCCTTGGAAACAATGGCATC	63.524	CTAATCTGTCTCAGGTCCTGCTCG	63.653	141
HM_1457	contig29276	GAC	3	12	ATTTCAATGCAACAATCAATTCAG	62.785	GTCAAAAAGGTTATGATCTCACCG	63.123	148
HM_1458	contig01256	ACC	3	12	AGCAAGAAAGGGTTCCACTACC	63.005	AGCCTAACAGAGGAGGAAAAATGG	63.086	116
HM_1459	contig40928	CAA	3	12	IGTTtGGATTTTTGGATTtTGTC	63.101	TATAAcacccAGAgacCTTgCAT	63.022	113
HM_1460	contig12749	TCG	3	12	TGAACAGCTACAGATGAAGCaCa	63.184	GTGGAGGGAGAGTGAATGATGGGC	63.611	148
HM_1461	contig48277	TTA	3	15	tGgaTAATGcTtCaGaCAGGGG	63.561	TcTTTTAGCATaCaCTGCCACTCG	62.985	155
HM_1462	contig13573	CTT	3	15	TGGTGCTCTGAATCTAATTCCTC	62.9	GTTCCAAACCCAAACCCCTaCTAC	62.792	146
HM_1463	contig11927	TTC	3	18	AGACCACCTTGTCTTGGATTTT	63.285	CTCACACTCTCGTGGTCCATTCT	63.106	131
HM_1464	contig15685	ATA	3	24	ATTCCTTCGACAGAGTCAATCCA	63.318	TGGCGTAACCTCATTTTCAACATA	62.65	106
HM_1465	contig34044	GAA	3	15	GAGAGcATATCATTTATCGAGGTCCA	62.721	GTGCGTATCTCTGGAAGATGTGG	63.444	86
HM_1466	contig19926	CCT	3	12	CCCATCaTtctGTCTTCTCGTCT	63	CTTAATGGCAATGGAGGGTatcAA	63.209	98
HM_1467	contig02638	TTC	3	12	TCTTGCTTCTAGTgCaAaCCTTtL	62.67	CTAAGCAGAACTCTgCAGGTGACA	63.181	138
HM_1468	contig00108	CGG	3	12	AACCACCAGAACCATCACAGtCTC	63.792	GGGAATCGAAATCCTTCAACAG	63.085	132
HM_1469	contig03896	GAG	3	12	AACAAGTTTCTAGTGTGGTGTGTTG	62.882	GAATCACCACCGTTTCATCTCTCT	62.901	126
HM_1470	contig40425	TGG	3	12	TTTCCAATATATACCTTGTGGTGG	63.002	GGTTTGGTAGCCCTATGTGAAGTG	63.031	93
HM_1471	contig29365	GGT	3	15	GTTGCTAACGTAGACGGTGGATT	62.659	AAACCTTCACTACCGCTACGCTC	62.764	151
HM_1472	contig37031	TCA	3	15	ATCACCGTcATACCCCAAAAC	62.993	CGATGGaGAaAATGATGAAGATGA	62.471	142
HM_1473	contig13715	AGA	3	12	CAGAGAGAAGAATTGGGGAAGAAG	61.842	TGAATCTCAACTCTTTCAATTTCTGA	61.674	159
HM_1474	contig06679	CTT	3	12	GAATAGAAGACACGCCGATaTGG	63.034	TGTgTTATaAGGAcTgTtTgGC	62.464	95
HM_1475	contig46308	AAC	3	15	TTGCAAAATCATGTGATCTCCCTCT	63.121	AGGTGCGAAGGAGTAATAGATCCC	62.999	125
HM_1476	contig20488	CAC	3	15	CATTGGTCTCTCTCGATCCATAC	63.209	GGATCAGAGGTTGGAGTTGATGTT	62.784	114
HM_1477	contig44319	AGT	3	24	GCCTTGGAAACCGTAAATCTCAcT	63.804	CATCGCCGGACTTATCAAAATTC	62.809	93
HM_1478	contig03394	TTC	3	18	ACTAACCATGTCAACCATGGCACT	62.095	ATTATTCTCACTCCCTCCTCACC	62.964	130
HM_1479	contig01520	GAT	3	12	GGAGACGATGAAGAAGAGAACGAA	63.217	AGTGTGACTCAACACCTCGACT	62.805	99
HM_1480	contig10037	GGT	3	15	CTAAAGTGGTCATTGGAGTGATG	62.945	GAGGAATCAAGAGGAGATGAGC	62.759	91
HM_1481	contig30907	GGA	3	12	CaACTCCCAATCAAGATCAAAAGC	63.129	AAGGATGGGATCTTGTGGAACATA	62.887	146
HM_1482	contig22504	GAA	3	15	CCCAAAGAGATGAATAATTTGGAA	62.492	TTCTGTCATTCTCTTATTAGCTTCA	61.495	156
HM_1483	contig34900	ACC	3	12	aGACTTCTCAACCGCTTCTCTCT	63.105	ATCGTGGTCTTGGTCAAAAGAACT	62.7	158
HM_1484	contig28242	CCT	3	12	TCACTActCTCACTCTTCACTGCC	63.362	TGTGATGAGTGTGGTGGGATCTT	62.815	116
HM_1485	contig47730	GAA	3	12	ACTAAGATATGTGGGCTGAGTGG	62.824	GGGAATTaAAATCCATCTCGAT	63.275	158
HM_1486	contig35407	CAT	3	15	GATGCCGAGAGTGTCTTAGAGCAT	63.26	AAGAGGTAGtGGTGAAGTCACTC	62.909	119
HM_1487	contig29911	CAT	3	15	TCTAaCTTCCACAAGCCCAAGCAT	63.053	TGCCATCAAAATTCAGTGGGATAC	63.159	143
HM_1488	contig37010	CTT	3	21	TTGTATACACAGCATCAAAACCA	62.534	ACCTGAAGAAATCATGTCCAGAGGA	63.424	147
HM_1489	contig16064	TCT	3	18	ACTCCAATTCTTCCGAACAAGAAC	62.824	AAAATGGAGAGACTCGGAAAAAGC	63.196	150
HM_1490	contig43257	TTC	3	12	TtCCGACATCCTCaAATGTCTAT	63	GAAGATTATCCGAATGTGGATTGC	62.918	83
HM_1491	contig06809	CAT	3	12	AAGAAATCAACTGTCAtagCAAGCG	62.971	ATTACCTCGTGCATCTTCAACCA	63.133	156
HM_1492	contig37155	CAT	3	12	AGGCTGCTGTGTTGTGGTGGT	63.081	GATCCTTTCTTGGCTTCCAACACT	64.014	138
HM_1493	contig21860	AGA	3	15	GTTCAAGACCGGATCTTTCTCTTA	63.022	AAAgCCAAATCATCAACCAATCTT	63.99	81
HM_1494	contig34980	GAT	3	12	TTGTGTCTGAATTTGGAGTGAGGA	63.132	GCTATGAAGCGAGGTTACCAAGAA	62.947	80
HM_1495	contig30995	CAC	3	12	AATCCCTCTTGTGATGAAGAATTC	62.855	GGGGAAATGAAGAAGAGGGAGATA	62.949	158
HM_1496	contig41121	TGG	3	18	TCTGCTCATTTCTGGAACAATTC	62.631	ATGGAGACGAGAGGACCAACAG	62.88	85
HM_1497	contig15012	CAA	3	12	AAGAACAAGCAGTtagCTTCCCAA	62.645	TCTCGATTCTTTTGGAGATTAC	62.887	139
HM_1498	contig03157	CCT	3	15	GCAAGCCTGAGGAGGTAATGATA	62.828	TGGATAATTCACGGGTTGATAG	63.209	136
HM_1499	contig00745	GAA	3	15	TCAACCTGAAAAGaGGAGAGGAA	62.669	ATTTCCCTTCCATTCAACCC	63.262	102
HM_1500	contig32191	GAG	3	15	TGATTTTATGAAGATTATTCGAGC	60.324	TCTGCGACCAATATGAACACTCTA	61.021	106
HM_1501	contig11681	TTG	3	12	GGTCACAACTCATTGAgCaCAGA	62.692	CAAAATGAAGTGGCAACAAGAACAG	63.057	141
HM_1502	contig22847	CTA	3	12	GGAGTCGTGATCTTGAGAGGTTA	63	AAGTAcCAAAATAGCCATCCGA	62.935	117
HM_1503	contig25633	GGC	3	12	TGATCGATTTTTCAACCACAAc	63.13	TGAGAATGATCAATTGAGGACCAA	62.896	155
HM_1504	contig38191	TGG	3	12	GCAATTGTAGGATCGGGTGTGCT	62.713	TTATCTTCAACCAACCaCATGG	63.025	152
HM_1505	contig22373	TCT	3	12	TTCAAGTCTGCTCTCCAAAGaGt	62.698	AAGGAGATTGAGAGAATGGGGTG	62.884	90
HM_1506	contig18641	GTC	3	12	TGCTTCACATCAGCTCTCAACTTG	62.842	AAAACCCTAGAACCAACAAGCTCC	63.005	98
HM_1507	contig03781	CGG	3	21	CGACCTTTTGGTCTGGATGAAGT	62.71	TTCAAGAAATTCGCTATTGCTTTC	62.842	145
HM_1508	contig35802	TGA	3	12	TGTGGCAAGCTGTCTGATTTCT	63.385	TTCTACTTCCCACTTCCGTCTCAC	63.01	136
HM_1509	contig22258	TTG	3	21	CAGTGATTGAGCAcTACCTCTCT	63.023	AAAAGACAGCAAAAGAGCCAGAGA	62.933	121
HM_1510	contig49272	GCC	3	12	CCATCTcAgAAATtAGaCaAaCa	62.514	ACTGCAGAGGTCTTCTTgTAAG	61.812	133
HM_1511	contig46596	GCT	3	12	GACATCATCATCGAGACATCATC	62.906	CTCCGCAACCTCAACTTTCAGAAC	63.482	95
HM_1512	contig10844	CTT	3	12	AATcGTGCTAATGATGATCGGTCT	63.029	TCGGATATACTGCAGATTGATGGA	62.823	145
HM_1513	contig31553	CTC	3	15	CtTTCTCTCCCACTTTTCTCT	62.275	AATCCGAGTTGCAAAATGAAGTT	63.146	90
HM_1514	contig14015	TGG	3	15	CTGAACCTGCACATTTCGCTACTG	62.883	TGCTTTACTTTTTGCTCTCCAC	63.051	122
HM_1515	contig15029	TTC	3	15	TCTTAGCTGCAGCAATTGACTAATT	61.776	GACTTTGACAATGGTTACTTTGGC	62.041	87
HM_1516	contig14316	TGA	3	12	TGGATTTTtGGTGAATTGATGATG	62.909	CGTTCAAGAAAGCTGTGGATACT	62.933	154
HM_1517	contig45708	AAG	3	15	CTCtcGTGAaATcCAaAaTACTCc	63.009	TcGtaACTCTCTGCATCTaAGGGTT	62.751	115
HM_1518	contig38761	ACC	3	12	CTCTCGAGCTTTTAAATACCGA	62.954	cTCAACCAAAAGTTTGAATCAATC	63.006	110
HM_1519	contig21525	TGG	3	18	CAAAGATGAAGCGGTGACGTATC	62.323	GGGGAATTATCTCCAAGTCATCA	62.468	156
HM_1520	contig06738	GCC	3	12	TAGTTGTTGCCACCATAACTTATG	62.956	CTGTTTTGGAGATGGAGGATATG	62.983	136

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1521	contig00076	CAC	3	15	CGAGGCTTCTCTCTGGTCTACA	63.332	GTATGCTTTCTGTTTACTTCGGGTG	63.051	154
HM_1522	contig45473	AGC	3	12	CAAGAAAGGGCAaCTTGAAGaCAT	62.921	TGATAGAGGAGAATGTCTGGaGG	62.996	94
HM_1523	contig26767	TCG	3	12	CTTCTTcGGCTTCATCTCTCTCTC	62.811	GAAGCTCaGAAAGCAGCAATCTCT	62.741	153
HM_1524	contig06899	ATG	3	12	CAACACTACACCTCAGAGCAGAA	62.944	GCAAAAGGAGGAATATGCTGAGAAA	62.925	156
HM_1525	contig44704	AGA	3	12	lACTGGGTGGACtCgagTGAGTT	63.449	CATCTTGTCaTcAtcCTTCCtCT	62.874	148
HM_1526	contig09285	GAA	3	12	CTAGGcCATAGATCGAAcAgAAGS	62.619	TTTGCTaACAAATCTGCAACTGGa	63.068	87
HM_1527	contig33958	TCC	3	12	CTGCCTCTGAAGCAaCTTCTCTCT	62.821	TTATTTCTGACAGTTGAGGAGGAAA	63.101	119
HM_1528	contig23841	ACA	3	15	CAACAACATGACCAAAATTCaA	63.055	TGCACCTTGCAGTAAGACCTaAGA	62.555	150
HM_1529	contig18223	ACA	3	15	GAATCAAAACCATCTTCATCATCCC	62.879	ATTGTTGATTtTAAGGGGCCaAGAC	63.487	148
HM_1530	contig19394	TCT	3	15	GAAGAGATCGTcAGGGGTGAGAG	62.991	ACAGAGaGACGACGTTTTTGAGT	63.588	149
HM_1531	contig34888	CTG	3	12	GAGGAGAGAAGAGGCTCCATaAC	62.977	TAGGGTTTGTCTGTTTCATTTTGG	63.317	124
HM_1532	contig28568	TCA	3	12	CCCATTTCTAGTTTCATCTCTGg	62.27	CTAAGGAAGCAAGaATGACCCCTT	63.086	128
HM_1533	contig05331	GAT	3	12	GCGTGTGTTCTCTATGTGAACGAT	62.652	TGGCGAAACTAGTATGAGCCACTT	63.36	145
HM_1534	contig48616	TTC	3	12	CTCAGtGAGTtATGCGCGCTG	63.172	GTACAGATTCTCGTTTTCGCGAG	63.239	156
HM_1535	contig12020	TGT	3	12	CTGATTTTCTGCAATTTGGAGTTAC	63.03	TCGATCTCACCACTTTTCTCAAC	63.632	124
HM_1536	contig04040	AAG	3	12	AGCAGAGTGGTCAGaAGCAGTTTT	62.949	aAAATCaATTGTTGTACCCCTCC	63.278	137
HM_1537	contig18550	GAG	3	12	TGTGTGCTTAATTATGTGGTGGTGA	63.501	TATATTGAAaATGCCATGTGGcTG	62.959	159
HM_1538	contig22572	TTC	3	12	TCCCATGAATTTCTTCTGTTTCT	63.108	TCTcCGATcCAGTTGaAAGGTAG	62.894	119
HM_1539	contig42553	ATC	3	24	CATGAGTGGACTACTAGAGATTGATG	61.574	ATgGAgGAGTACTGCTATcCC	62.011	116
HM_1540	contig34150	GTT	3	30	GGCTTGGGAGAGGAGGATAGTAG	62.983	AGTTATGAGGAGTtACGTCCGCaG	62.946	149
HM_1541	contig32801	GGA	3	18	AGTGTGTACAATCAATTGGACGGA	62.726	AGCAACTTTGGTGATGACATGGTA	62.844	149
HM_1542	contig05616	TCA	3	12	ATGCTCTTCTGGGTATCAGACAT	63.361	GTtACTGACGAAGTGGTGCTTTT	62.848	132
HM_1543	contig17952	AAG	3	12	CAGTGATGGTGAACACGAGATTG	63.006	GcGTTTAcACTTCgACCAc	62.808	84
HM_1544	contig19760	CTT	3	18	TcGtCTCTCTCTAGGCTTTTCA	62.714	AAGTGGAAAAATCTGAGCaaAAAA	62.329	135
HM_1545	contig37440	GTG	3	36	CACGCTATTAGGTTATTCGGCATT	62.489	CaAAAGAgGAgGTCAATGGtTc	63.303	142
HM_1546	contig05131	AGA	3	12	GGTTTGTGAGGGCAGATCAGATAG	63.331	TTTCCAGTCTTGCTGTGATAGAG	62.993	156
HM_1547	contig46472	TTG	3	12	CACGGACTTGAATAGGAGGAGAGA	63.098	CCGAGACTTAGCACTTGAAGAAG	62.82	160
HM_1548	contig18624	GAG	3	18	TAGGATGTGCAGGAACAGGATTG	62.473	ACTCAATCTCGCGATGAAGAAA	63.341	146
HM_1549	contig00864	ATG	3	15	GCACCTCTCTCCGAACATTCA	63.022	ATGAAGCGAAcGCTACTCTaATc	62.164	111
HM_1550	contig29092	GAA	3	18	ctGGGAGAGAAAGATCAACCAAAA	62.881	ATCACGACTCTCAACTCAAGCTC	62.295	125
HM_1551	contig40165	CAT	3	12	AACTGGAGGGAGATCTTGAGTtc	63.278	AGTAAGGGATTCCGAGAAGATTG	62.961	110
HM_1552	contig22276	TGG	3	18	GGAAGAGGACGAAGAGTTTGtGA	62.997	CTGACCaCGAAACATGTCAATTA	63.15	124
HM_1553	contig45495	GGT	3	15	TGAGTTGGAGTGTGTTGTTGGT	62.944	TCTTATTACGCaATGCCCTCAC	63.438	125
HM_1554	contig35441	TTC	3	12	CCCCAACTACTTCTCTTCTGACT	63.185	TGGGtGTTTTTCAGCAAGTAGTGA	63.057	99
HM_1555	contig29668	GTG	3	21	GCtCAAAAATGtACCAACAACAG	62.867	ATTGAGAAGCAATCTCGAGCAAGT	62.84	146
HM_1556	contig23977	TCA	3	12	ACTTTTCAGATTCCATGGCTTCAC	62.813	GTCAAAATCCCAAGCAAGaCAAC	63.035	121
HM_1557	contig00385	CTT	3	12	TCCTTGAACCTTTGCTTGCTATC	62.935	CAGAAAAAGGGTATGACTTGCAACC	63.856	158
HM_1558	contig29308	CGG	3	15	ctCGCCATTATACCATTCTCATCC	62.915	GATCaAACCTcCTCACTCCCT	62.974	146
HM_1559	contig07729	CCA	3	12	ACtCTtAACTCACTTGACCCAA	62.327	TTTAGTACCCTTAcCAATGCCACG	62.558	160
HM_1560	contig02041	CCT	3	18	cGATCTAGCTATCGCTTTCGACAT	63.058	GAGGAGTTGGGTGTAGaAGTgG	63.408	108
HM_1561	contig21479	GCT	3	12	ATAGCTTCTCAACATTTGCTCCCA	63.341	TCAGATCAAGGGGGTACTATCAT	63.125	159
HM_1562	contig15167	TCA	3	15	TCCTCAACTCTCATGCTATAGTCG	62.712	GGTCTATCTCTCCCAATCATAGGT	62.661	160
HM_1563	contig11046	GCC	3	12	CGAGGATTCCACCTCTAGGGTTAT	62.876	AATCTTCAATTTCTCCCAATTCA	62.077	127
HM_1564	contig39612	CGT	3	12	ATCCAATGATTTCTTGTTGGTCTG	62.913	ATACTCGAAGACGATGAGGTGAGG	63.014	117
HM_1565	contig08844	GGT	3	12	CTCTTGAGGCTCCCACTTTATT	63.086	CCACCGGCTCACTCTATGCTCTT	62.824	130
HM_1566	contig16171	AGA	3	12	CAGATGAATACCAAAAGgAAAAcC	61.19	AGCTACTAGCATGAGCAGACATGG	62.132	159
HM_1567	contig35294	AAC	3	12	AAAGTCATCAACATGAACCTCCCTC	62.784	CAACGTGTATGCAACGATCTGATT	63.296	123
HM_1568	contig04915	CCT	3	12	GGTgTGTtTGACCTTCTTGTTCTC	62.807	GCAAGCTTGATGATGAGACTGAAG	62.623	122
HM_1569	contig27314	CTC	3	12	TCAAAATGCTGTCTTCTgTCCA	63.15	GTGGAGATGAAGTTGGGTTG	63.515	154
HM_1570	contig06981	TTG	3	24	TTTGTGCTGCTGTTGATTCAITTT	62.972	CAGTTGCAACaCAAGATTCaGGAC	63.181	160
HM_1571	contig38998	CTA	3	12	CTCTCGTCAATTCTGATTCATCT	63.196	aGTGATTTGCTCAAGCACAAAAGC	63.997	129
HM_1572	contig13668	CAT	3	12	CTTCACTCTCTCACTACCTCATC	62.874	GATGAAGATTCTCGGGTGAAGAG	62.571	157
HM_1573	contig43910	AGT	3	12	tGAAATCTCGGCTATTGGATcTc	62.804	CCCATTCTGGAaACTTCTaAGCA	63.015	157
HM_1574	contig16681	TGG	3	12	AGCATACGAATCCCAATAACAA	62.735	CTTGCTCTCTCTCTCTCAITTT	62.2	155
HM_1575	contig42630	ACG	3	12	AaTCTTGAGATCAAACTCGGTG	62.798	GATaATcGCTACGGAITCTGTG	62.218	157
HM_1576	contig16807	TCT	3	18	TGCAATCCACTAGATTCTTCGGA	63.305	tTTTGCCGGAATTGAATCTTAGC	62.568	154
HM_1577	contig47443	CAT	3	12	tAGCTCGATGAaCTCAGGCTCATT	63.444	CAAGTGTAAGTGAaATCTTCGGGG	63.113	122
HM_1578	contig25006	ACT	3	15	CGATCATCTTCCtCTCTTCCGAC	62.686	GACATCCAGCTTTGGAGAATgG	63.112	155
HM_1579	contig04313	CTT	3	12	TCACCCAGTTTaaCTTCCAATC	62.495	CACATACAGCAGCTGTGtTTTTAC	62.087	92
HM_1580	contig03779	TAT	3	18	TCTTTCGATTCTTCTGCTTTTGC	63.138	ATTTATGaATCTTGCGGtTtCC	63.385	107
HM_1581	contig09370	AAG	3	21	GAAGACTCCAAGCAGCATCGTTT	63.141	TTAAGCATGaAAAGGCTCaAAAGC	62.957	152
HM_1582	contig01072	CGA	3	12	GATGCGAGTTGCAACTCTTTG	63.178	CAAGGACGAGGTCTGAAGATCA	63.689	149
HM_1583	contig09549	GAG	3	15	TGATGAATTTGAATTGGGGTTAGG	63.089	CAACAATGGCAAGACTCTCTTTT	62.921	98
HM_1584	contig04117	AGC	3	12	ACTTCTTACGCCCTCAAAATGAAT	63.509	GAGGTACCACTCGTTAGCCCTAT	62.913	101
HM_1585	contig36776	ATC	3	12	GAGCTGTATAGtACTGGgCGAAT	62.953	GAGATGCTGAAGACACAGAAGAA	63.057	118
HM_1586	contig10967	TAG	3	12	GgGaACCTACCTGGTGTATGAG	63.01	AATCctTTGCTTCCATCTATGCTC	62.986	147
HM_1587	contig29587	TCA	3	12	ATTCTGTGTTGTTTCTCGTTTCTCC	62.712	GGTCAGGTGAGGCTACGACAAGT	63.028	87
HM_1588	contig08442	GAA	3	12	CTTTCGCTCCATTTCATAGATC	63.237	tTCGTTCAAGCTACTCCAAAGC	63.051	89
HM_1589	contig20321	CTC	3	12	AAGCCACACAGATGTGTTGAAGaa	63.173	TTGGGagGAActTtACGtGTTAT	63.019	128
HM_1590	contig04964	CAT	3	30	aCaTCATCGTcATCGTCAAC	60.807	TCCGAGCCATGAAaTAAGAATTA	61.065	126
HM_1591	contig07910	CTT	3	12	ACACACCATCAGGCTTTATTTCTCC	62.713	GTACAGAGGACGACAGATGAAGGT	63.154	144
HM_1592	contig22691	TTC	3	12	GTTTGGGGTTTTCAGAGAGTCGTT	63.91	AAAAATaGTCAGGTGGGTTGGTC	63.488	101
HM_1593	contig01398	AAG	3	12	TTCCAGAATTAATCAAGCCCAAA	62.908	TCTTCAGCTTATCTTTGATTACGGC	63.046	133
HM_1594	contig49686	AGG	3	21	TTCTCTCCACGATAGTCGAATC	62.9	AACAAGCAATGATTTTGCTCTCC	62.62	137
HM_1595	contig03014	GTT	3	24	CATGTTGTTGtGATTTGAGGAGC	62.948	GaTaGTGcCTTGcATTGATTC	62.94	157
HM_1596	contig23101	TGG	3	12	ACCCTAACATCACCGGAGGACTA	63.1	AAATTCATCAACACAAGTCCCAc	63.331	135
HM_1597	contig23346	CCG	3	12	ATCAGATCGAGAAaCTGATCGAc	63.007	GGCGcTAGaTTaAGcAgTTTTGA	62.969	136
HM_1598	contig08609	ACA	3	12	GGATGTTGTTCTGATGACCTGATG	62.911	ATGTGGGGCTGAATTTAATTTTCA	62.722	151
HM_1599	contig05662	CTT	3	12	GGGGATcACCATTTTCTCTCTc	62.865	ATGAAGtTcAAAGCACTCAGCC	62.841	130
HM_1600	contig34184	CTT	3	18	ATAAGCATCCATGGAATCCAGAAA	63.012	GAGaAAGAGAATTCGtTTGGGG	63.366	151
HM_1601	contig23941	ACC	3	18	TATATGTGGCGGAAGATCAGCATC	62.646	AGAGAGAAGATGGGTTTCGAGGT	62.876	109
HM_1602	contig37985	TTC	3	15	TAAAAaCACAGAATTCGGaACCTG	62.932	GACATGGGAGTTAATTGGAGATGG	62.887	100
HM_1603	contig24834	CAC	3	12	AagAGAAATGAAATGCTGACCTGC	63.039	CCTCAGAAaACTTATTCTCATGG	62.609	86
HM_1604	contig33652	CCA	3	12	AAAAGTGATGAGCTGATGAGGGAG	63.115	TTGTTGTAGCCAATAGGTTGGTCT	62.956	153
HM_1605	contig39167	CAG	3	12	TTCAACAACAGCAGtTCTTCTATC	62.962	CTCgACCAATCTTCTTCTCTCT	63.022	135
HM_1606	contig04808	ACC	3	12	TTTTTGGGATGATGAaAATTGAGG	62.789	ATTGAGAAGAGAGGGATTTTGGT	62.673	136
HM_1607	contig01999	CTT	3	21	GgATTTTCATCTCTTGATATCCCC	63.06	TTGTTGACGAAGAAGAACGATGAG	62.828	139
HM_1608	contig17279	CCT	3	15	CCTCCAGCTAGTGAAGGTGCG	63.472	TTCTAGCAATCCAATCCAAACCTc	63.121	96
HM_1609	contig21140	TCC	3	12	TTACCAAAATCCGAATCTCACGAC	63.432	AAAGTACGCCAAAGCCAAAGActc	63.046	155
HM_1610	contig06693	GAA	3	12	AGGATGCAGATAAGCATAGCCTTG	62.841	CTCTTTTGTCATCTTCCACCACTT	63.01	132
HM_1611	contig13563	GTG	3	12	ACTCAAGCTCTGATGAaAATTGGCC	63.027	CaGAATCTCTCTTCCaACGACTT	62.267	116
HM_1612	contig29414	TGG	3	12	GAACAGCCAATTCAGGTCTTCTCT	63.027	CTGTCAACCATaTACCTCCACa	63.146	137
HM_1613	contig32972	CAT	3	18	CTTCACTCTTCTTCCATtctt	62.968	GTCGACgGTGATAgTGAATGGAGAT	63.675	156
HM_1614	contig21643	GAG	3	21	GAGTAGCCACAGCGATTGATTG	63.17	ATTTTCCGGGTTGATTTTGATTT	62.799	160
HM_1615	contig38698	GAA	3	12	ATTCACCGAGATTTCATACCCA	62.691	TCTTACTCTGGCAAAAGGGCTAgG	63.028	134

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1616	contig39596	ACC	3	21	ACTAGGCTTAGCCACACACCAT	63.275	gatatGCCACCACCTGTTGAGTCC	62.927	150
HM_1617	contig02137	CAG	3	12	GGCTCTCTCTCTCCAGATTAT	63.212	AAAATCCCGCAGAAATGACTAAAC	63.138	151
HM_1618	contig21865	TTC	3	12	AGACTAACATCGACGAGCTCGC	63.154	ATTGAAGAAAGGGAATGGAGGAAG	62.958	97
HM_1619	contig13368	ATC	3	24	TCTGGGCTTATCATCTCTTCGC	62.937	AGCAGCTCTGAAGGAGATGAAGAG	62.809	151
HM_1620	contig15733	TGC	3	18	CCGAAGcACTACTACAGGCTGATT	63.057	TCAGTGATGAGAGAGGCTCTCGT	63.141	141
HM_1621	contig47749	GTT	3	24	ATCTTCTGGGTGCTCTGAGGAACAC	63.005	TCCGAATATCTCTCAGATGCTTCT	62.706	129
HM_1622	contig33762	TTC	3	12	TCATTGCGTAATTGCAATTTGTTG	63.503	CCAAAAGCAAAATTTACTATCCAACACC	63.824	152
HM_1623	contig16477	CAA	3	12	ATGAATCGGCATCACTATCAACT	63.029	GATTGGATGGATTCTGGTTAATG	63.498	131
HM_1624	contig06637	TTC	3	24	AGTGGGGCGCTAATTATCATATC	63.401	GGAAGAAAGGAAGATTGGGTTGT	62.876	160
HM_1625	contig05023	CGC	3	12	CTATTGAGGAAAGACCAAGAGGG	63.459	AAACCCAGAAATGCAATAGCAGA	63.138	146
HM_1626	contig01273	TCG	3	18	CTGAAACCCCTCAGTTTACGATT	62.631	AAACTTTCGTTGGAAAACGATCAC	62.633	149
HM_1627	contig01192	CGT	3	12	ACCTCGTTGTTGCTCAGGTGTC	63.862	CaAAACGCTTCTCTCTCTCTCT	63.199	140
HM_1628	contig27233	CTT	3	12	GGAAAAaCTAAaaGCCAATGCAAA	62.567	CTTGGTGTTGGGCAATATTGAACCT	63.366	132
HM_1629	contig02870	GTA	3	15	CACATTGGAAGCTTgCTCAATAGTT	62.971	CCGTCCCAAGTCAAAAATGAGACT	62.71	147
HM_1630	contig12526	ATC	3	12	TACTCCGAAGAACACCAACCAAT	63.019	GAGAATGAGAGATTGGGTCTGGT	62.994	143
HM_1631	contig00864	TCT	3	21	AGGgTTAGgTCTTCTGCTGCTCT	62.899	CTACTTTCGCTctCTCCACAATg	63.543	143
HM_1632	contig08728	CCA	3	12	AAGTCGGTCTTCGACACTCTGTTAC	63.05	AGTGATCTCACCCTTGGTGAACCT	62.471	141
HM_1633	contig12783	ATG	3	21	CCAGTTATGATCAACGACATCGAA	63.257	CATCTCCACTTACTCTCTCTCTG	62.663	126
HM_1634	contig01862	TGA	3	18	TGAAGTGTGTAAGTCTCAATACGG	62.642	GATGGACTTCAGAGCGTTGAGAAT	63.133	158
HM_1635	contig02844	TCT	3	24	ATTCTGCTCTCTCTCAGCTGCTTTC	62.512	TGATGGAGCAGATAGAGGTTTGTCT	62.842	151
HM_1636	contig02205	CAA	3	12	CCATcACCAATTTCAACAACTTCA	63.137	TTAGAGCCGTTAAGATAGGCCACC	63.789	120
HM_1637	contig16337	CCA	3	15	TATGTTGGACAGTGTCTCCGACTC	62.707	CCCAACATGGCCGAGTAGTAGTAg	63.138	152
HM_1638	contig14161	CGA	3	15	CTCCACGAATATTGCTGTGAGATG	63.051	GaCGAAATGTCAAATTCAGACCTC	63.013	151
HM_1639	contig01107	GTG	3	15	TGGGTGTGTCGATGATCTCAATAG	63.362	AAAACAATCGGCTCTGTGTTTTTG	63.546	151
HM_1640	contig00334	GGT	3	12	TTCTTTGTAAGTAACCAACCGCTAC	63.45	CTTAATCTTCACCAACGGCGTACT	62.754	96
HM_1641	contig32220	CCG	3	12	TGAGGAAATCGAGGAAATGTTGT	63.108	AGCCATTTTTCCAATCGTCAaATA	62.829	121
HM_1642	contig22169	CCA	3	15	AGTACCTACCGGCCACCGATTAG	64.503	ATCGTAGTGGAGCAGTGGTACTGG	63.789	92
HM_1643	contig47179	CTG	3	12	CATGACCAAGTTCTGTTTGTGCAT	63.395	CTGCTTATACGGATCTTCATTGGG	63.018	141
HM_1644	contig31915	TCT	3	12	CTTCTAACTGTTCCAGCCAATGGT	62.822	GCATACTTGAAGCTaAAGGGGTGT	62.877	110
HM_1645	contig16694	GAA	3	18	AGGCAAGAGGCTTGAGGTGAG	63.239	CATAGCTCGAACCTTCTCTCTCTG	62.824	97
HM_1646	contig00316	GCC	3	15	CACCATACGTGGAACCACTAAGG	62.606	CAAAACCTCAATTGGAATCTTCG	63.002	151
HM_1647	contig40811	CCT	3	15	GAGTGcTCAaAgGAAcAGcAC	63.565	AGTCAACACCACcAGACCaAT	62.922	143
HM_1648	contig00183	TTC	3	12	CCACGACTTCTCTAGTGTTCGTC	63.564	ttccAAGGCAATCAAAcAATCAT	63.728	111
HM_1649	contig00864	TCG	3	12	GCCGAAGGCTTCTTCGATTCT	63.455	GAGAAGTCAcCaTCTGCTGTCG	63.289	154
HM_1650	contig30933	CTC	3	12	ATGCTTACATGGCACTCTCTAGC	62.856	TTCCGTGATCTCCATAGCAAAAGAC	63.754	159
HM_1651	contig24625	CCG	3	12	GACTCCGTctcccACTCACTCTC	63.911	GTTTCTTgTGAGGAGGAAAGACC	63.593	134
HM_1652	contig43372	CAT	3	18	TATATAAGCCAGCATGCAATCGAaA	62.781	CATCAATgGAgggTGATGatga	62.996	152
HM_1653	contig36339	TCT	3	12	ACCACAGATTCAACAACTTCATT	63.014	TAGTGATGGAATTGAGAGAAGCCC	62.9	157
HM_1654	contig47342	GAT	3	24	GACAGAGACTGCGATGAAGGGAT	63.031	GTCTCCTGTTCCAAAACCTTAaCT	62.983	151
HM_1655	contig35256	TCT	3	12	TAGCAGTGGGTGTGTTTTCTCT	63.345	ACCGGAGTATCcaTCTAAACAGCA	63.133	119
HM_1656	contig04981	AGA	3	12	TACCCTTTTCCCAATTGCTTTGTA	62.825	GTACgTGCTCTATCTCTCGCTGTG	62.665	115
HM_1657	contig16491	TCA	3	15	TAAAAACCTTGGGAGGAGGAATTG	63.545	TGATGAGGAGATTCTGCTCTGGT	63.656	159
HM_1658	contig21236	AAG	3	12	TGATCCACTTCTCGGAGATTTTC	62.773	CTTCTCATGAGTGAAGTGCAAGGA	63.04	152
HM_1659	contig05525	TGG	3	12	GGTGACCTGAAGGTGTCTGTA	62.91	CACCCAGAAAGATATCGAAGACGA	63.735	118
HM_1660	contig01827	GGT	3	15	CGGTGGGTCTTATTATAGAGCGG	62.064	CAGCAATCGTCAGCTAATATGCTC	62.368	137
HM_1661	contig01353	CTG	3	12	AGACATTCTCGAGAGTGGCAATTG	63.643	CAtcCCAGATGCAAGACTATCTCT	62.8	156
HM_1662	contig40704	TGG	3	12	ATAGGCCAGGTCTTGTCTCTCT	62.698	AAACaCAGAGTGTAACTCTCCGCG	62.838	160
HM_1663	contig30530	ATC	3	12	ACATGCAATCCCATATTCCATCAC	63.97	AAAGAAGAAATGAATCACTGCTG	63.039	128
HM_1664	contig12113	TTC	3	12	TCCtCTGAaTCTcCTCAgAATG	63.209	ATTGATGCTGCTGtCTCTAGTg	63.261	144
HM_1665	contig30432	AGA	3	12	AGGGGAAGACCCAGAAAACAAATAG	62.873	GGTGGTGGTaGTTTCAATCTGAAT	62.599	108
HM_1666	contig00136	CTT	3	12	CTCTTCTGCTCAGCTCCTGTATC	63.027	ATGGTTGTGATTTTGAAGTGGTATG	62.924	116
HM_1667	contig23128	CAT	3	12	AGctGTGTtACTCcgCTGAAaAaC	63.069	atacgctattcaggctttgttga	63.15	90
HM_1668	contig36644	AGA	3	21	ATGGAGGAACcctaTGCTGTGATA	63.013	GCCTGGATTGTTCCACATAGTACG	63.15	135
HM_1669	contig03433	CTG	3	12	GCCCAAAAGAGTAGGAGAAAATAG	62.715	GGCCCTTAATGAGTGATGTGGTAG	63.022	104
HM_1670	contig15090	TGG	3	12	TTGTGTATGATCAGGACGACGACT	63.057	GACCCaCTCTCTCACCATCTCATC	63.325	156
HM_1671	contig39611	TCG	3	12	TCTCTACATACCACTGCGACCTGA	63.278	ACGATGACTCGATGAAGCAcAACA	63.164	105
HM_1672	contig39958	TCT	3	12	AGTATCTCTTTCGgATTCTCGGAC	62.986	CCCGAAGAAGAAAGAGGAGGAGTTA	63.364	132
HM_1673	contig47716	GAA	3	21	TtTtcGACaATCGTtAGAAAGGgAA	63.109	GAAATACTACaCCGGTtTGAGCG	63.051	145
HM_1674	contig12052	TTA	3	12	gACGATGATGATCCATGATGATa	63.5	TAtACGGAaCAcAAACCACTcGGT	63.762	117
HM_1675	contig03007	GAC	3	12	GAGGCGTaGgTGATGGCAAC	62.926	GAGTCCCTctTGACCAGCTCT	63.429	137
HM_1676	contig45370	CGA	3	12	TAAGATCCAAATCGGACAACTGGT	63.009	CTCTCTCGAAGGAAACCAATTCT	63.273	115
HM_1677	contig32256	ATC	3	12	CGCTCTCTAATATTGCGCTCTAA	63.062	AAGTTGCAAAATgGGATGGAAGAA	63.018	137
HM_1678	contig38243	CTT	3	18	GGAGAGATTTCGAAGCCATCTCTA	62.9	TCTTCAcACCACTcTATCTTtAGCA	62.383	92
HM_1679	contig22948	TGG	3	15	AATGAGTGGTCTTCCCAATCAGAA	63.204	AACGAgGCTCTCTCTGTTCTGTC	63.343	146
HM_1680	contig04771	GGA	3	12	CAGGTTGAGAAGAAGAGTCGGAAG	62.892	TATGACAGGTGTTGAATCTCCCAA	62.803	101
HM_1681	contig15807	ATC	3	12	GCATTGACCTAGGATTCAACAAA	63.426	CGATCAATCTGAGTCTCTGTCAT	62.665	156
HM_1682	contig09954	CTT	3	12	GGCATACCAAGCTTCACTCTCAT	62.915	TTGTGACaGATTGCAcCaaAAA	63.403	80
HM_1683	contig32008	AGG	3	12	CGGCTAGATTGAACCAACAGAGAA	62.815	TGTTGGAAGCTGTTTGTGGAGATA	63.163	119
HM_1684	contig03295	GAT	3	24	AAGTTGGAAGAGAGATTGGGATTCT	63.071	ATTCTCAACAAACcCCCTTTGAA	63.006	157
HM_1685	contig22489	TTC	3	30	ATCATCTTCCACCTGGATGTATTG	62.173	GAAAGTAAAAGGAGCAACAGGAG	62.535	132
HM_1686	contig13650	CTA	3	12	AAGAACCTTCAAAATGGGCAATA	63.96	TGTGCTTtaCTGGATCAAGTGGTGT	63.067	123
HM_1687	contig40645	CGC	3	15	GGgATAAGGCTTGGGATTAAAACTC	63.256	ATaGGTCTGcAGATCTCTCACCg	63.128	145
HM_1688	contig28105	TTC	3	12	TAGCTCATCGCAcAGaGATTGAAG	63.065	aGAAAGAAcAaACCaCGGTAAAGGA	62.313	128
HM_1689	contig44546	TTC	3	15	TGGAAAAAGTTACACAGATTCAATCAC	61.703	GGGTGCTGAAGTGAATCAATATAATC	61.375	120
HM_1690	contig29758	CTC	3	18	TCTTGACTCGCAcCTCTCTCTCT	63.023	TTTGAGGAACAGaAgTCTTgGaCC	62.997	99
HM_1691	contig43945	CAT	3	15	AAAGGATTGGAAGGCTGCTGTT	63.544	ACACATGACCACTTCTCTGCTT	63.033	158
HM_1692	contig04534	CTC	3	18	AAGTGAAGTGAAGTCTGGTGAGG	63.023	AgGAGAAAGGGAAGGTGATAGAGA	62.85	151
HM_1693	contig11030	CCT	3	15	AACAAGTCTCTCAACAAATCGGAC	62.712	AAGAATGTTGATTGCGATGCACTA	62.975	135
HM_1694	contig26466	CAC	3	18	TTCAGAAAGACGATGGGAAGTTCA	63.15	ATCAAGTTcAGAAACCTGcAGCCAT	63.468	136
HM_1695	contig09546	CCA	3	12	CGAACTAGGCACTCCCACTTTCAC	63.561	ATTGCACTCAGCAATTGGATTGT	63.824	121
HM_1696	contig49580	ACC	3	18	TCGTAAAGTTCCTCAACTATCCCAA	63.837	ATTATCGCGATCGGATTCAAC	63.539	158
HM_1697	contig21517	CAC	3	12	GCAACAACAGCACTATTGATTCTC	63.309	ATCATGGTAcTGAAGGGGTgAAGA	63.102	117
HM_1698	contig21078	GAA	3	12	AaTGAGgAAGCTTTGCTGAATTg	62.935	CAcCTTCTctTCTGATCTCTGTTc	62.996	129
HM_1699	contig00451	GCC	3	15	AGGATAACCAAGACCCAGCCATC	63.639	TCTTTTACCAGTTGCTCTTCTCTG	63.015	143
HM_1700	contig17807	TCC	3	15	AGAGATCAcAGCATCCCAATCATCA	63.146	TCTAGAAGGTAACTAGCTCCGCG	63.308	114
HM_1701	contig28643	GTT	3	21	TTcccGGCAATCTTAACTTTTATT	61.529	AtTATCCGGAACAGCTCCAAATAG	61.748	129
HM_1702	contig27791	AGA	3	12	ATACCTCTGGGTTTCACTACCGG	63.583	AAGCAAAATCAGTGGTGACTGAGG	63.879	102
HM_1703	contig19969	AGC	3	12	GCCTGAATACCACTACCAAGCa	63.45	ACAAGAACGGTaAATAGGAAGcCC	62.82	135
HM_1704	contig20876	CTT	3	24	TGGGCAAGTATGTTGTTGGGA	62.955	AGTGAGTGTGGGAGGTAGTTGAC	62.91	143
HM_1705	contig43451	TCT	3	24	AAATTTCTCtCTTTTCGAAATCTCC	63.904	gaAGAGaAAGCAGAGGCAAGAGAGG	63.199	144
HM_1706	contig14496	AGG	3	12	gATCAGAgATcTGcCaTCTGCATT	64.007	TGCTAGTCCGATCTCATCTTAcCA	63.168	133
HM_1707	contig31012	TCA	3	24	ACCAATTGGAGAGCTCGATAACTTG	62.923	CCGCTTGAATGCTTATATACAGGG	62.945	83
HM_1708	contig07771	TTA	3	12	CTGCCCTCTTCAAAACaATTAC	63.092	GAGaagaagAAGAGTGAAGTGGGG	63.908	100
HM_1709	contig46154	TCT	3	36	TTCTTCTCTCTTGGCTTTATTGG	63.75	ACATTCACCGAGCTTGTAGTCAGT	63.583	151
HM_1710	contig18303	TTG	3	12	gAAGGTGAGAAAAATAGCCGGAGT	63.102	GGCTCTGTTCCAAATCAGATCTTC	62.586	120

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1711	contig34005	TCT	3	12	ACTTCTGGAATCCTCTCCAAACC	63.071	tATGGAAAGAGCAGAGCAGAAGG	63.227	119
HM_1712	contig51856	TTG	3	12	CTACAGATCGAAACGCAATGATG	62.959	AAAAGCAAAATCAATcaAAACCA	62.827	99
HM_1713	contig11871	GCG	3	12	CACCAAGTACTCTCGAGGGTCTC	63.539	GTTGGTCTCTGCAACATCTTCT	64.01	112
HM_1714	contig25068	GAG	3	12	GAAGACaACCGAATACAGGAAA	62.606	CTGACCGACTGTCTTCATCTTTC	63.546	116
HM_1715	contig01237	ACA	3	12	ATTAATCTCTCTTCGAGGGCGAC	63.2	gAGCAAAATCTGGGATCATTTG	63.529	157
HM_1716	contig01775	GGT	3	12	GTAATTTTTGGAGTGGCAACAACCG	62.823	TTTTTGCAAGCTCAACACCAAAATG	63.373	127
HM_1717	contig36956	TCT	3	12	ACTCTTCACTCTTCAAATCCAGCCA	63.431	TTCCGTTGATAATTCGTCAGAGGAT	63.121	148
HM_1718	contig02720	TGT	3	12	ACTTCATCTAAGCTCGAATCGAGCC	62.326	AATGCAGAACCAATTCACAGTTTCA	62.948	114
HM_1719	contig21901	GAG	3	15	GTAATCGGACGCTGATTGAGAG	63.028	CCATCGCTGTTATCATCTCTTCT	62.913	130
HM_1720	contig35851	TCA	3	12	GGGGATGAGTCAATGTTGAGAGAG	63.424	AAACCAAGCCTAAACACCACTT	63.013	158
HM_1721	contig32578	GAT	3	15	TTACTATTGCGGTATCCATCTCTCG	63.327	ACAAGCATGGAATAGGAGGCTATG	62.731	158
HM_1722	contig08422	CGA	3	12	TTGAAAAAGTCAAGGGCAATCAAAT	63.018	TCAGATTCTGAATTCACCTCATTCa	63.015	118
HM_1723	contig30166	TTA	3	12	CTCATTTTGAAGGCAATACCAaT	62.619	AGACAAGTACAAGGGTAAATGTCAGAA	61.674	102
HM_1724	contig00213	CGT	3	15	CCATTATCAGAACAAATCGAACCC	62.802	GTGGTGGTGGAGGATGAAGAAG	63.103	86
HM_1725	contig33693	AAG	3	24	TCACCTCTTGACCCCTTTTGAGC	63.019	aACCTAGaAAcAACATcCCCTc	62.78	136
HM_1726	contig21274	TCA	3	21	ccaaccccttCTaaCTGCTCTT	63.094	aagggTgTgttGAGGATGTTGAT	63.014	142
HM_1727	contig25426	CTT	3	21	CTAGGGTTTACGCGTCTCTTCT	63.211	cCGCaAhtCTCTCACTTTCTTCT	62.811	156
HM_1728	contig47869	CAG	3	18	AGGGTTTTAACTCGTATCATCGACA	63.009	GTGAAGGCAAACTATCTGGAGGA	62.91	113
HM_1729	contig08131	TCA	3	12	TCCTCAGCTCGTAATATGCTCTCG	62.831	GATATGCTTCATGTGATGGTGAGC	62.958	146
HM_1730	contig25496	TGT	3	21	GAGGCTTGTCTCGAGCTCGAC	63.851	CTGAGCCAACCTTCTCGAGGC	63.701	126
HM_1731	contig09310	GTG	3	12	TGGGTTTGgTTTTGTAGAGAGA	63.1	AGtCCtCTGTaCtCCCAACG	63.901	134
HM_1732	contig00849	CCA	3	12	ACATTTGTTCATCAGCAGGCTTC	63.777	AGGACTAGGCCGAAGAAGAGTAA	62.898	140
HM_1733	contig15725	TAA	3	12	CTAAITGAGCTTTGAGGGTGGCa	62.629	TCTACTTCACTCTTGTITGCAATT	62.764	106
HM_1734	contig32378	TTC	3	12	TCAATATCTCTGCTACCAAGGGC	62.718	ACCCTGTTTGGCAAAAACAAGTAA	62.941	85
HM_1735	contig01695	TCT	3	12	CATCATCAGCAAAAATGTGATCC	62.721	AAACTCTGAGTCTTGGGAGCTT	62.996	133
HM_1736	contig11285	GAA	3	18	AATCGTTAACCCCAATGCTCTC	63.31	GTGGAAGCACCCAGATGATGATA	63.358	160
HM_1737	contig07754	CTA	3	21	AGTCATTCAGTCCCCCTTTTGAT	63.219	GTGAGCCTGTCTAGAGCCCATAAA	63.035	103
HM_1738	contig16658	GAC	3	12	GATTTCTCTGGTTCGTTCTTCGAG	62.698	AGAACAGCCATGGTTTCGTAAGT	63.263	152
HM_1739	contig31594	ATT	3	18	AaTtGtGaAGAGAGTGGTGAGG	62.895	AAAAGCCTTCTCAACGACAAAC	63.057	89
HM_1740	contig14327	CTG	3	18	GAGGAGCTAGTtTCTGCTGCTGT	62.653	GATGACCGCATGAATCTTTACAT	63.339	114
HM_1741	contig10143	CAA	3	12	GCAAAAGTCTCTCGCAATTAAGA	63.043	CTTGCAAAATGGAAGAACACCCAC	63.957	159
HM_1742	contig07874	GTG	3	12	TAACCGGAGAGAAGTAGAGAGCGa	62.921	GAGaTACCCTTTCTcGTCTGTA	63	63
HM_1743	contig40142	ATG	3	12	AATTGGAATGACGATCGATGAAC	63.327	ACAgAGATGGGAAGGTGCAATCTA	63.331	140
HM_1744	contig42204	CAG	3	30	GTGAGGAGATTCTCTCGCAAAAT	62.214	ACATGTTGTTTCCGGTGTAATTGA	62.528	151
HM_1745	contig07685	CGT	3	12	GGTGGTGAATGATTCTATGTGGC	62.702	TCCATCTCTATGCCAAATGTGTTCT	63.112	131
HM_1746	contig03445	AGA	3	12	AAATTTGAATTTGTGAGGGGACAG	62.495	GCTCATCTTCTCTGCTCAAGTGT	62.243	98
HM_1747	contig22660	AGA	3	12	AACCAAGGCAAGAGGGTCTAGT	62.899	TGAGCTTCGCTTCTTCTATTCa	62.439	129
HM_1748	contig12129	TGG	3	12	CTACGCCACCTTTACATAGTTGC	63.064	GATATTTCCAGGGGACaAAACAT	63.271	121
HM_1749	contig49268	CGA	3	12	AGTCACCTTCTCTTGAAGGGTTGC	63.01	GATACTGGAGAGAAGGAGGCCAAT	63.185	99
HM_1750	contig18324	AAG	3	12	GAGTGTGAGTCTGTGTCGTTGCT	63.066	AGCGTGCAATTTTGTGTTTCT	62.841	96
HM_1751	contig30711	ATC	3	12	TGTCGTATCTCAGGGTGgAAGAT	63.102	TATACGATGAAAGGACAAATGCCA	62.638	85
HM_1752	contig22416	GGT	3	12	GCAAGAGTATCAAAATATGGTGC	62.735	CaAgTgTGGGAAGITTTCAAGa	62.623	153
HM_1753	contig33051	GAG	3	12	GGAGCTTGAGACATTTGAAGAAGC	62.827	agttttCCACCTTCTCTCAACAA	62.483	101
HM_1754	contig33858	GCT	3	12	ATTTTGTCTTTCTGCTCTCGTG	63.031	CTCACAATGGTCCAGTaaCAAC	62.827	89
HM_1755	contig36198	GCC	3	15	TCGTGACAGAGTCGAACACATAGA	62.158	AACaACCTTAACTCCCATACGAA	62.716	148
HM_1756	contig05135	TTC	3	12	GTCCGCAAAACCAACTCTTTTGAT	62.712	CAAGATGGAGTGAAAGCTCTgaTT	63.115	135
HM_1757	contig31681	GAT	3	15	CTCTAAACAAATCACTCTCCGCA	62.894	CTAGGCATCGATGATGAGGTCAAT	63.651	156
HM_1758	contig23751	ATC	3	12	GTAGACAAGTTGAGCaAGGGTGGT	62.935	TGATAAGAAAAGCtCAATCGGCT	62.546	126
HM_1759	contig29645	GCA	3	12	CTCTCGTCTGCCATCACTACTCT	62.325	CAACAACATTTCTACCACCACTGC	62.856	158
HM_1760	contig35970	ATC	3	18	CGATCCTCTCTAATACTCgTGGG	63.108	GCCATCGaAGGIAGAAGAACTGA	63.022	139
HM_1761	contig14735	AAG	3	12	AAGCTCGAGAACCCCTTGAGAAAAC	63.404	TaCCCTCTCTTCTCACTCTTcg	64.314	122
HM_1762	contig27384	TTC	3	15	CCACCTTGTGTGATTCATCCATCT	63.318	AGTGCCATTAAAGCCCAAAAGTCT	63.412	95
HM_1763	contig17408	GTC	3	12	GAAGTCTCTCCAAGGAGATCCG	63.788	GCGGAATTTCCATCGTAGAAGGT	62.915	89
HM_1764	contig51035	TTC	3	12	TGTGTTGCTGCTCTTCTCGTGT	63.332	AAAGTCAGTGATCTCTGTAGCCGc	63.268	127
HM_1765	contig01937	CAT	3	12	CAAGAATTCAGCAAACTCAGGGT	62.921	CACAATTTGACGAAGACATTGAGG	62.931	147
HM_1766	contig32107	TCT	3	15	TCTCGAGTGTCTTGAATTAaGTG	62.869	AAGAAGaAGaGtGacTGCaAgGGa	62.909	151
HM_1767	contig08942	ATC	3	18	TTTCCATATTTTTGTCTGCAACCC	63.221	ATGGAGGTTCAAACTACACGGCT	63.263	149
HM_1768	contig03927	TGA	3	12	CGAGATGGATGGTGTGATGATGATA	63.123	ATATATTCTGTGATCGCAGGCTT	63.17	108
HM_1769	contig07503	GGC	3	12	GATCATGGTCAATGTGTGTTGTTT	63.047	TGCTATaTCTCTCATGCAATCAC	62.516	83
HM_1770	contig20100	AAG	3	21	cAAaCaCCCCaGaCTGaCACTA	62.501	TTCACTGTTAGAGGTGTGGTgG	62.501	148
HM_1771	contig14755	TCT	3	18	AACACAATCATCTGTCCACCTTGA	62.922	AATATTGCGGCAAGTAAGAAGCAG	62.877	91
HM_1772	contig48539	CCT	3	12	TaGAAAACTTTTcACCGACaCgAT	63.129	GCCGTGGtGAACTTAGAAATATC	63.058	119
HM_1773	contig19506	TGT	3	12	TGGTCCGAGTAGCTGATTATCATT	62.915	ATTCAAGGTACAATCCCTGTCGAA	63.009	156
HM_1774	contig10920	GGC	3	12	GCagAGAGTTCGCAATACGTTCACT	62.94	cCCCCAATTTCTACTACACTCTCG	62.299	146
HM_1775	contig45707	ATT	3	15	GACCCTTGAGATCTTGGCTTAAAT	62.986	CAACAACAACGACCAACAACA	63.112	155
HM_1776	contig31525	AAG	3	12	AATTGATCGAAGCaGAGAAaAAT	62.342	CCTAGCCCTAAGAGGATTTTCAGC	63.005	154
HM_1777	contig40342	AGA	3	15	CTGTTTCTATTTTGAAGTGGGGG	62.798	ACAATCTCCACACATCGATTCACT	62.043	90
HM_1778	contig24008	CAG	3	15	CTATACAGgTCATCTTCATCAGCCC	62.312	AATTCCGTTCTCTGAGACAGTGT	63.01	103
HM_1779	contig26877	GAG	3	12	GTACGGAACAGAGTGCCATAGAAG	63.251	ATGaTAgTGTcGTCTGCAACTCTC	63.031	160
HM_1780	contig49212	AGT	3	12	CTCGCTAAATGTGTAATTCCTCCG	63.134	AATTTCTCAACAATCTCTCCCC	62.865	142
HM_1781	contig40671	ATG	3	21	GGTATtCGGAGgATGAaATAGGG	62.971	GTGAGCCTaATCTTAATCAATgCGC	63.142	142
HM_1782	contig14470	TCT	3	15	GCAGaATTCTGATTTTCCACTCT	63.774	AACAAGCCCTGAAGGATGAGATT	63.494	131
HM_1783	contig35829	GAA	3	12	GAGTGAAAGCTCATCACAAGCAAA	62.962	CAACCATCGTCTCAACTCTTCTT	63.01	102
HM_1784	contig34139	TCT	3	21	CCTCTAGAGCTCAGATGTGTGCT	63.353	agCAGaCCTGTGtTGTCTTTT	62.525	120
HM_1785	contig43226	TCT	3	15	ACTGTACTCAAGTCCCACTTGAG	63.011	GTCCTAGCTCGAAGCAGAGGGAG	63.799	138
HM_1786	contig49450	CAT	3	24	cTAAAgTAGGGTGGTGGAGGT	64.731	GTGATCCAGATGCTGCAACCTT	64.771	95
HM_1787	contig34192	CAG	3	12	CACAACCACCAATCCCAATAATCT	63.108	GCCACCAAGGTCTTATACGTTAC	62.851	130
HM_1788	contig24162	GGT	3	18	GCTCTTTAGTCCCAATCTTGACGA	63.022	AATCAGAATCAGAACCCTTCATCG	62.786	141
HM_1789	contig30234	ATC	3	12	TTtCtCAGTGTAGCAATGTGgAA	63.163	GATGACCGGTGATGCAATCTCTTCT	62.827	152
HM_1790	contig51531	GTC	3	15	AACAAGGCATCAAAATGAGAAGTCC	62.813	AATCCTcGTCCTTaACTCTGGTC	62.984	88
HM_1791	contig24768	TGA	3	15	TTTGCAAGATGATCTTGAGTGTGG	63.164	AGTGGATCTTAgTCTGATCAATG	63.013	154
HM_1792	contig08290	CGG	3	12	ACCATCTCTTTTCAACTTTCTCC	62.876	GAAATCAGGAGGACAAGCAAGAA	63.009	120
HM_1793	contig05517	CCT	3	12	TAATTGGCAAAATACCCGAAGATG	63.118	GATACTGATGTGGGATTGTTTC	63.016	147
HM_1794	contig31915	GCG	3	15	ATTGGAGAGAGCACTTTGAAAG	63.133	CTAGCCaTTTaCACTGCTTGCT	62.96	118
HM_1795	contig30812	GAA	3	12	TTCTCTCGTTTATtCTTGGGAC	62.919	CgaTctCTGtCTCCGtTTCTT	62.2	92
HM_1796	contig38087	TGA	3	12	CAAGGAGTTTCTGTTCCAAGTGT	62.906	TAGCCGTTCTCTGAATCTACGTC	63.035	153
HM_1797	contig06789	TGC	3	12	AATCAATTCATGAGCAGAAACC	62.608	TTTGCAACTATTGGTATGGATTG	63.046	148
HM_1798	contig11243	TTC	3	18	GAATGCTTGTGAGTCACCATCTCT	63.443	ACGACCAAGAGACCaGaAA	63.211	156
HM_1799	contig26856	TCC	3	15	ACACCGTCTCTTGATGATCTCT	63.322	ACCTGTTGACTCGATTGGTGAAGT	63.353	159
HM_1800	contig46384	GAA	3	12	AGaGTACTTGGAAAGTCCCTGTG	62.296	CATTAGGAGGATTTGAAATGTCCG	62.896	143
HM_1801	contig09241	GTG	3	15	TAATGACAATTGACCTGCAACAC	63.168	GGTCTCTcCTCGGtACCGT	62.995	154
HM_1802	contig36306	AGC	3	12	AGGGTGAATGTGTGACTCCAAAT	63.014	CAAGGCTATGTTTGAAGCAAGTTGA	62.756	101
HM_1803	contig14573	TGA	3	12	AGACCTCTGTGATCCCACTTGAC	63.005	TGAAGAAACAACAACCTCAATCCCA	62.918	155
HM_1804	contig27154	GAA	3	12	GTATTCTGtGcCAaATcTGTGTC	63.046	gGGATctACAGATGtAGTGCTGg	63.23	105
HM_1805	contig34982	ATC	3	15	AGTAGAGGGCCAGGAACAATAATC	62.995	GGGCTTTGTTGTGATGAAGCTATT	62.744	101

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1806	contig35299	ACT	3	12	CTCAGCCTCTCGTCTTCTCATTC	63.014	CCTCTGTCAAAGTctCCCAAGaAAA	63.094	109
HM_1807	contig27124	GTC	3	12	ATCGATTTTCTCTATGACACCG	62.607	GCTGTTTAGCAGGATTTGgAGTGA	62.839	91
HM_1808	contig33351	GGC	3	15	TGTAGCGACGAGAAATGACTCAG	62.958	AAGaTaAAAAATGTGGaACAAAGGGC	62.643	103
HM_1809	contig38155	GTG	3	12	TGGGAGGCCATATATAGGAGTTT	62.983	ACTCCAAGACTCtCTACCAtcACCA	62.589	111
HM_1810	contig30130	AAT	3	15	CTTTGACAGATTGAGCTCCCACC	62.598	CTTGACAAATCTGCCCCATTAC	62.826	139
HM_1811	contig45870	TCA	3	24	CTGTTCCGGACAGAAGATGAGAGT	62.181	TCCAACGAAGAAGAACAAACAGAA	62.295	150
HM_1812	contig01292	TGG	3	12	ATATTCCcTTTCTCTCTGGGCT	63.432	AGGTTGAGCTTTACGCCTTTTAC	63.138	128
HM_1813	contig02239	GGT	3	12	TCTTGCTCTTGTTTATGACTCTC	63.142	ATTGTAGCCAAGTCAACAGCCCTA	62.251	82
HM_1814	contig01584	TGA	3	15	TGTGAACAAACTGTGTGGAACCT	62.944	CAGGCTTAGAACGTTACGGTGAGA	63.862	141
HM_1815	contig00721	TCT	3	12	CTCCACAGTTTCTCTCAAGCTC	62.909	CTCTAGGACCAAAATCGAAACCTT	62.98	158
HM_1816	contig00952	AGT	3	12	ATACCTGTGgTAATTGACAGGTGGT	62.221	TTTGAGAACTTTTGCTTCTGGGAG	63.113	112
HM_1817	contig29246	GGT	3	15	aCTACCCtCTGGTtATtGGTTg	63.482	GGTtAGtGGGTcAaaCagCAATTC	63.035	127
HM_1818	contig01257	AGA	3	15	TTTGACGGAGTTTGGTAAAGAAC	62.809	CTGAACCTGCTATGGAGTCTCTCT	62.795	147
HM_1819	contig29210	CTC	3	21	TGGATTCTATGATCTCAAGAGGG	62.873	AAGTGAATTTTGcAGGCATTTCA	62.946	129
HM_1820	contig16948	AAC	3	12	TGTGTGtGTtTTATTCGgTTACA	63.373	TTGAAAAAATTGAAGGAaaaaATTGA	63.007	160
HM_1821	contig24555	CTT	3	15	AATTTCATTGAGATAACCATCGC	62.424	TCGTTTAAACCGTGAACAGCTTT	63.138	156
HM_1822	contig45317	GAA	3	21	GAGTCTGCGCCTAGTTGGTAGAAA	63.154	GGTTTGGAACTCTGTGAgaATGCC	63.026	160
HM_1823	contig29271	GTG	3	15	CTGAGCTGAGCAGATCATCAAA	63.061	AATCGGTAGGGTTTTCaAACATTT	62.9	141
HM_1824	contig41906	GTG	3	12	aGcaTCAACAACAAACATtCTCA	62.948	AAAGAgGGAAGTAtGgTTTCTGCG	63.89	137
HM_1825	contig18237	AAC	3	12	CGATGCTCGCTCTTATCATCAG	63.168	AGGAAGGCTCGGTAGTGTATGTA	62.624	95
HM_1826	contig00493	TCT	3	15	gCAGAATGGTCTTTCATGTTTT	62.62	CAAGAGAttacCCATGcCCAATTAC	62.815	123
HM_1827	contig33124	GAT	3	12	CATCAACTGGAAACACCAACAAG	62.826	GGTTTGCAGAGAGtGATCGATAG	63.556	150
HM_1828	contig03982	AGA	3	12	GATGgAAAAACAGAGGACTGAAGA	63.217	AAACAAACAGAGCAATTCAAGAAAGC	63.071	123
HM_1829	contig27601	TGA	3	12	TGCTGGAGAAAGaGAAAGAGtGAGA	63.122	TGGCACCTCCTTACTCTCTTGTGA	63.432	152
HM_1830	contig34090	GGA	3	15	GaGAGGTGGCAGTGGTGTC	63.14	CAGAAATGTGTGGAACCCCTAGATG	63.017	127
HM_1831	contig03696	TGA	3	12	AGTACTTCAACCTCATGGCTCAC	62.925	GCTTAGGAcCTCTGATCAATGGAA	62.9	80
HM_1832	contig24757	TTG	3	15	GAGGATCGTTCGGATAATCTCCT	62.977	CAAAACCTCGAAGAAGTcCTCTTT	63.28	153
HM_1833	contig22499	TGG	3	12	GCTGAAGATAGGATGATTCAGGGA	62.889	CAGAGCCAAAACCTTAGCTCTACA	63.138	86
HM_1834	contig39674	ACC	3	12	CATTTTACCCtCTGtAGgACCC	63.285	AGtGAATGCCATGGGTgGTAGTAg	63.45	157
HM_1835	contig29290	ATT	3	15	GACTTCGATCGTCTTCTCCACAT	63.017	GTATTGCACCAAGGAAATAGGG	62.826	109
HM_1836	contig49602	CAT	3	12	TAaAGCCACAAGTtCTCTCCAG	63.015	ACTCAATAGTtGGCCGCTCTCTa	63.338	84
HM_1837	contig11889	TTT	3	12	TTTGTAGTTTGAAGTTTCGGTgCT	62.946	ATCATTGACGTCTTAGAcHCCCA	63.217	156
HM_1838	contig14966	TGG	3	12	AAGTGATGGGTCTTATGCAATCC	62.51	ACCATAGCCACCTCCCATGTAAc	63.333	154
HM_1839	contig03098	CCA	3	12	GATGGTCTAGGAGtCGCAcAATTT	62.94	ACGGTACGACATGCTTCTTTGTG	63.375	139
HM_1840	contig13118	GGT	3	12	GGGGAATATGAGAAAGATGGGAC	63.06	CATCTTCTATCCTTCGCTCACCA	63.377	142
HM_1841	contig15457	GTC	3	12	cTGGTCTCAACACAGTCTCTCAAT	63.259	CtCTCAAAcCTGCTCGaCG	63.382	114
HM_1842	contig16811	TCA	3	18	TaaGCAAAATTCACAAGGAGGAA	63.109	TATGAGAGCTTTGATgTACGTGG	62.528	142
HM_1843	contig03857	TAC	3	12	TCCAGTTTGATCAACCAAAAAATC	63.305	GGGTTTGGGTTTCTGTATCAGA	63.302	153
HM_1844	contig02876	TGG	3	21	CGTGGAaaTtAGAGTTTGGGTTTG	62.916	CATACAATGCCAGTAgCagTCAACC	62.741	129
HM_1845	contig39239	TGT	3	12	GAAgAGTTGGGGTGAGTGAATCTC	62.561	GATCGcCACCAATTTCaTAACTc	62.928	103
HM_1846	contig51852	TGC	3	18	CTCTTCTCTGGAGGAACCTGTTG	62.892	CTAGAAAAACCATCTCTGtccag	63.32	149
HM_1847	contig27130	CTT	3	12	CCTTCCGAGTCTCATTTCTGACAG	63.117	GGTGCcAATTGGAACCAAAA	63.017	123
HM_1848	contig46041	ACC	3	12	GTAGACGAAGGAGGCGTATTGGT	62.826	TCCAATGACGAGTAgAaGATgTG	62.593	156
HM_1849	contig15238	TGC	3	15	AATTTGCCATCTCCTGATTCAAAG	62.705	GTCCGGTCTTGGTAgaaAACTGTGA	62.809	135
HM_1850	contig32743	TCT	3	12	CTGCTGATTCTGGAGGACATAACC	63.331	AAATCGCTCATCGGTTGTAATGTT	62.95	142
HM_1851	contig39674	ATC	3	12	TTCAAGCTtATGCCCATCATCTCT	63.018	GTCtGaAATTAcCATTTGGcAAGG	62.922	160
HM_1852	contig04249	TTT	3	15	CCCTCTATTGACAGGACAgATAGAT	62.997	gATGTGGACCAAGTGAAGaTCAA	62.473	134
HM_1853	contig46021	ATC	3	12	TGACCATCAaCAaCATCATCATCA	63.404	AATTCAATGACTTGATGGTGCTCT	63.55	151
HM_1854	contig09901	TAC	3	12	AATTCAATGGGTGTTTCAACGAGT	62.923	TCAGCAATTAATTTCTCTGTGCCA	63.059	138
HM_1855	contig29229	GAT	3	12	TTTCTGAATGTCATcGAGGTGAA	63.025	TCAGATcCACATCCCACTACTCA	63.016	152
HM_1856	contig35793	AGG	3	15	agAAGGTGGGTcGgAGAGAACATA	64.432	CCCACAATAAGACAGTgTACGCC	63.566	112
HM_1857	contig47388	TTA	3	12	gCGAGGGCTATTAGATGAGAAGACA	63.146	GATATGGGGATGATGAGaAGAACG	62.99	146
HM_1858	contig06295	TCA	3	12	GAACTCCCTAACTCACTGAGCTGC	62.939	AAcAGCAcGAAGAGAcGAAGAAG	63.357	118
HM_1859	contig41009	CAT	3	12	GCGTTGAACTGAAGACGAGAAAT	63.048	ATGATGACATTGATGAACGACGAC	62.828	141
HM_1860	contig16459	GGA	3	12	GGTGAAGGAGGAGTGGgAGTC	62.364	AGCTCTGCTCTCCACCTATCT	62.06	146
HM_1861	contig24183	GAT	3	21	TGGATTaGtAGCTcCGTAATTGAA	63.038	TTCTCTGAGTTcATCACCACCATC	62.679	157
HM_1862	contig01589	TAT	3	21	ATGAACATTCTcGgTgTGAATT	62.913	ACGCCACGTTACCGTTTATG	62.843	117
HM_1863	contig03819	ACC	3	12	TCCCAAGAATGAAGCCGTAATAA	62.92	GCATGGTAAGATGCTTGTATGACG	62.988	109
HM_1864	contig04730	ATC	3	24	GTtAcATTCTTGTGGGAGGATGAT	62.572	AGGATGATGATGGGAGTGTAGAT	63.111	123
HM_1865	contig49936	AAG	3	15	CCAAGACAACAAAGAAATCTGTGC	62.958	TTTTCTTGCCACAAGGATGtTTT	63.027	129
HM_1866	contig50197	GTC	3	15	CGGAGATCTTGAAATGAAGACGAAG	63.525	AcTGTGCTGCTgCAaACTCTGT	62.575	155
HM_1867	contig18236	GGT	3	12	GTAAGGGCTGTCAGAGGATGATT	63.105	CtAAccctaATCACCGCACTACT	62.835	125
HM_1868	contig10493	TAT	3	12	GGGAATTcAGGTGTGAGATCATTT	62.572	AGTCATGTTGACAGAAACCATCA	63.164	92
HM_1869	contig03992	GGA	3	12	TCCCAACCAACTCTTCACTTTCA	62.177	TTTAGTACTTCCAGTTTGTCTCG	63.048	107
HM_1870	contig12647	TTT	3	21	ACCaTCTCCATCTTGTGCAATAA	63	TCTCTACTCTAATTCTCAGcCcG	62.425	145
HM_1871	contig08146	GGT	3	12	GAACAATCACAGGGGAGTCTGAGT	63.005	TACTTCTCTCTCCAACTCGCT	62.922	99
HM_1872	contig04314	TTT	3	12	TTCTGCTCTTCTCTCACTTCAAC	63.111	CGGAGATTCTACAAGCAAGACCAT	62.923	159
HM_1873	contig37134	ATC	3	12	GTACATGCTCAGTTCCTTTCGc	62.55	cCactccTtTctAtgtcCAATTCTcCA	63.013	106
HM_1874	contig26492	AGA	3	12	GAGAGCTCCATTCAGATTCTCTTGA	62.484	CCGAGTTGGGAACCTAGAAGAAAG	62.187	158
HM_1875	contig07333	GTG	3	12	CGGCTTTATGAGCTTtAGGTAGCA	62.966	GGATCAATCCATcCGaAcCtaAG	62.975	155
HM_1876	contig00771	CTG	3	12	TGTGAGACATCTCTGAATGGAGAGC	62.926	TGcATTTCACCTCAATCCAAATCA	62.807	156
HM_1877	contig10333	GTG	3	12	GTGCTGAAGAATCTTtAAGCGCA	62.86	TCCTATTGTCTCATGTCCCTTGC	63.643	139
HM_1878	contig13665	ACC	3	12	CAAAACCGGATGTAAGATGTGAGAG	64.068	GTCCTcGACTACATCATCAAAAGG	63.217	92
HM_1879	contig10085	TCA	3	12	TGTTCTCATCATCTCTCATCTCA	63.113	GAGGATACAAGGGGCTCGAAAT	62.878	155
HM_1880	contig17931	GAC	3	12	CTTTACCTTCATCAACCCCACTGAC	63.111	AGCTCATGCTCTGCTCTGTGAAG	63.403	144
HM_1881	contig31630	TCT	3	30	AATGATTGAGTCTCTCTCCGTGCG	63.115	GAGTGTGATTGCAAGGGAACCTCT	63.027	104
HM_1882	contig32341	CCA	3	12	TCTCACCGGAGGACAGAGAGATAC	63.215	CACCacCTCTCTGCTCGATATAA	62.382	150
HM_1883	contig32831	GAA	3	15	tAgcAaaaGGGTTtCaGCCATAa	63.034	cccTGGATTtGATTcCATTGTATAA	63.08	108
HM_1884	contig12331	TTA	3	18	TCGATCTTCACTCCGAATATGTCA	63.028	GGTTCCAGTGCTGCTTTCTGTATT	62.949	156
HM_1885	contig06384	ATC	3	12	AACTGGGGTCTTACTGGTTGAGT	63.403	CCCCTACTTCAAGAAAGGCTCAAT	63.086	158
HM_1886	contig22710	TAG	3	24	TAATGGAGTCAAAAGGTGGAGAGG	62.782	GGAGTACGcAGCAGATCTGAATTT	63.051	146
HM_1887	contig41793	TTT	3	21	ACGATTTTGAAGTGTGATATGGCT	63.039	AAAGCCTCAaAgTTCaAGTCACCA	62.438	140
HM_1888	contig20983	GTT	3	18	ATTTGATCTGCATCAACGAAC	63.393	AAAGaAGAACCGGtTATTtCGAC	62.808	116
HM_1889	contig39364	CAC	3	15	lCTTCATCAATTGTCACCTCTTCA	63.123	ACTGATAACAGAAATAGCGCGAC	62.867	125
HM_1890	contig49916	TAT	3	12	TGCAACCATATCACTCCTTTTGT	63.046	GAGATGCATGGAATtGAATCTGTG	62.927	137
HM_1891	contig34587	GGT	3	12	CAGGATCTCAACCCCTAGACCTCA	62.984	TCTCCATCAGATCAGCTACTACG	62.844	155
HM_1892	contig32559	ATC	3	12	CAATTAACAGCTAGATCGCACTCA	62.643	TTTTTCTCTTCACAAAAGGATGcC	62.813	140
HM_1893	contig01951	GAA	3	12	TCAGACCTGAAGAAGAAGCTGTGA	62.812	TTTGTCTCTCTGCTCTCTCTGTT	62.71	159
HM_1894	contig36851	GAA	3	15	TCACTAAATTCGCTTtAGTTGAGCG	62.947	CAACGGTCACAAATTCCTCTCTCT	63.325	141
HM_1895	contig04542	CTC	3	15	AGCACTCTGtGTTTGTtTTCTC	62.946	GTCACCTTGAAATGGGTGAATCTG	63.106	155
HM_1896	contig19087	CAT	3	12	CaTATGGTGTCTTCTGCTCAAC	62.844	GATTTTCAGGTTAGACCAAGTGGG	62.299	141
HM_1897	contig15922	GAA	3	15	GAACCCCTTCATCTACCTCCAC	62.974	TGAAGATCAAGAAGGGAAGtCTA	63.401	140
HM_1898	contig38700	ACC	3	12	CACACAAGaaactaaGCTTCGaaaa	63.799	TCCAAGATCAAAACAAAGCCTAAA	63.109	89
HM_1899	contig44561	GAA	3	12	AGTGCGAAAGAACATGAAGGAATC	62.926	AAATACCGATCTCACCACCTCAA	63.009	120
HM_1900	contig24846	TCC	3	12	CTTTAAGGTACCTGAGCGCAAGA	63.048	AACCCCTTACGATTTTACTCTGTC	63.114	144

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1901	contig08687	AGA	3	12	CATCTTCTCCAAGCAGTACAGCAA	62.958	GCCGAAGAAGAGGAtcATGTC	63.639	137
HM_1902	contig36910	CAT	3	18	ACACTTCTGGTTGGTAAAGCTTGC	62.959	TGCAGAGTTAGGAGAAACCTTGGA	63.531	122
HM_1903	contig44560	CAG	3	12	TCCAATAATAGGGACAAACCATGC	63.329	GTTTGGGACTTGATAAAATTTGGCA	63.221	156
HM_1904	contig20831	GGC	3	15	ACAGAAAGGGCAAGCTTCATCTG	63.044	ACCGGAACCGTGTCTCTCTcTAC	62.91	138
HM_1905	contig35458	ATC	3	12	GTGTTGAGAGCTCAAAACCATCT	63.027	TCCTAGCTCAATCATCATCAACA	63.028	87
HM_1906	contig00148	TTC	3	12	CTGGTTTTCTTCATACCCACTTG	63.003	TCAGGAAGAGTTTTTCAAGAACCG	63.003	155
HM_1907	contig22213	TTG	3	12	TCCTCTAATTTTCTCTCGgTTTC	62.875	CAAAAGAAATcGAAAGAGAGCCAC	62.619	109
HM_1908	contig23553	CAC	3	12	TACCTTTGAGAGGTTGTGTGCATC	62.622	TGGACAATAAGGAGATGGTTGCTT	63.009	150
HM_1909	contig42984	ATC	3	24	CCTCAAAACaGACTCTGCTGCTAa	64.804	GAACaGcAGTATcTcGcAGGGTAA	63.879	153
HM_1910	contig05253	TGG	3	15	GCATCACTAGaAaGAACCAACCTGA	62.935	TcCCACACATATTgaACCAATCTC	62.211	144
HM_1911	contig20236	CCT	3	15	TTCTGTAGACATCAATCAAGCCA	63.038	TATTCCTTGAATATGCTCGAACCC	62.718	107
HM_1912	contig13394	CAG	3	12	GATGCAGGAGATGATAAGGAaGga	62.889	CAGCTTGCTGTACACATAAACCCAC	62.985	107
HM_1913	contig40052	AGT	3	30	TTTGAaaTTGAATTcACAATCCCC	63.092	CACCTGCTGCTGATCATCATACTT	62.743	157
HM_1914	contig12602	TTC	3	12	CCGTTAGTGCAATCTCATCGGTAT	63.45	TcTACCACCTTCTGAATCACTCCG	63.856	113
HM_1915	contig41832	CAT	3	12	GCATTCTCTCTGGTGGTTTAAAG	63.239	AAATTGGCTGAACAGAAAGTTTGC	62.851	142
HM_1916	contig22870	TCT	3	12	ATGGTGgGAGACTGGTcTaCTGTC	62.899	GcCAAGTGATGAACAATAATCAGGA	63.441	100
HM_1917	contig26707	CTT	3	12	GGACTGTCAACCTTGTCAAGACG	63.261	ATCTCTAGGATGGGAGCTTGGCT	63.623	157
HM_1918	contig22242	TCG	3	15	GATGGCATCTGACCAATATCC	62.661	GATCTGAACACACGGCTGAGATTT	62.926	158
HM_1919	contig19000	CCA	3	12	CCAAATGTTCCGAATTCCTAGCT	62.798	TTTAGGGTTTACGAGGTTTGGGT	62.998	142
HM_1920	contig45216	GAT	3	15	ATGAATGACATGGCTCTTTGGATT	63.016	CTCTCACTCTCGATCCCTCTCACT	62.991	106
HM_1921	contig27739	GCA	3	12	gTgAGGCACTGCCATAAAAAAGaC	63.256	AGCCACGACAAGATTGTTAAAGCTC	63.06	133
HM_1922	contig17091	GGC	3	12	TATGACATGAAGCTGAGAATTGGC	63.6	TGAAGCAACCTCGAAGTAGAACAC	62.869	116
HM_1923	contig06524	CTC	3	15	ATCTTACGCCGACGAAGTCTCTC	62.925	ACACTACTAGCCCCATGAATGGAA	62.822	88
HM_1924	contig04559	TTA	3	15	CTTTTCaTGtGCaTaTGgTgTa	62.946	TTGCTGCTTCTCTCACTTTAAAC	62.541	132
HM_1925	contig13022	GAA	3	12	AGATAGACAAGCACTGTAAcCGCC	62.962	aAATCAAGTGTTCAGGGTTTGGAA	63.006	143
HM_1926	contig12488	TCA	3	12	CCTCAATATCAGCCTCAGTGACCT	63.014	ATCAATTCTTGGTGAAGGAGGAA	63.318	146
HM_1927	contig06260	GCT	3	12	TTGTCCTGCTAATTAGTCTCTCT	62.823	AGATCCACCGTTTATGGTATATGG	63.112	129
HM_1928	contig18151	GCG	3	12	GAAGTGGTCTCGAGGTTCTCTCTG	63.137	CTCGGGTGACCTCTCCATTG	62.977	82
HM_1929	contig29396	TCA	3	21	CATTGAATGTGCAAAATCTCTCAAA	62.485	TCCTAGTAGCTGCaAAATCTATCGG	62.108	82
HM_1930	contig02497	AGT	3	15	ATGGTCTGGTTGACAAATTCGGA	63.009	TGGTTAGCAATTGAGTGAATGGGA	62.731	151
HM_1931	contig03692	GAA	3	12	TTGCACTCTGTAATAGGGGTAAa	63.122	TGACCAGATAATGAACATCATGCG	63.15	115
HM_1932	contig50275	CTT	3	15	CAATCCAAAGGTAGGCTACTCCA	62.714	TGAaAACCGACCAATTGAAGAAGAA	63.034	93
HM_1933	contig41045	ACC	3	15	GATCAaTGgATTGCTTTGAAAC	62.915	TGCAGATGAAGCACAACCTTAATa	62.959	95
HM_1934	contig06392	GAG	3	12	AAGATCAGTTGTGGGGTCTCTCATC	62.784	CTCCACCACTACCAGACCACTAA	63.646	155
HM_1935	contig11788	ACT	3	12	ATTCGTCCTTAATcTGTCTCCG	63.683	TGTTCTGCTGAATCTCAACAATGA	63.392	144
HM_1936	contig15259	AGA	3	24	GAAGTGGAGATGAAGAAGGATGGA	62.977	GaAAAGcGACTCTGTAaAAACCT	63.11	107
HM_1937	contig41949	CGG	3	12	TATCCATCTCCTCAAGCTCTGACC	63.106	CtCtTcCTCCTCaCTCtCTTCCCT	62.611	153
HM_1938	contig34532	ATC	3	12	ACAGCGgCTGATAGCTTcCaC	63.962	ACAATGCTCTGTATGGTGGTgaTG	63.283	154
HM_1939	contig50564	AAT	3	24	TACAAGACTGCCAGGGTTGTGAAG	63.754	GtGTGGGTGTGGGTGTCTGAT	63.153	148
HM_1940	contig01509	TCG	3	24	ACATGCTTTTTCTACTGTGTATCCC	62.713	GAAGACaGAAATCAACACCACTAC	62.045	138
HM_1941	contig52082	AGG	3	15	TCCCTGAACTATACtCTTGAAa	63.083	ATgGAGCTCaAgcCTAGTGTCAIT	62.627	94
HM_1942	contig51631	GCT	3	24	ATTTGTGCTCTGTGCTCTGCTCT	63.583	ttCtTCTCTAGTCTCACACTGCCA	62.739	138
HM_1943	contig35334	AGT	3	12	ATAGCGTCTCAGATCCAAaAGTGC	63.051	CTAAACAAGaAAATGGTTCGGCAG	63.13	144
HM_1944	contig29352	CTC	3	12	TACTCtCATCTCTCTCCACATCC	62.874	AGGGTTGTGATTGGTTGAGATGTT	63.014	134
HM_1945	contig52351	CTA	3	30	CAGAGCTTTAGAAATGTTTCCGTA	62.932	CgACGGGGTTTCaATTAAAGAAATA	63.282	145
HM_1946	contig08362	CCT	3	12	ACTCAAGTCAATGGGTGATCTGTC	62.397	GGCATTGAATTTGTTCAAGAAGGAC	63.125	117
HM_1947	contig30922	CAA	3	12	ATATCCAGGCCCAACTCTGAAGAG	62.811	CCTATGTtGGAACCTTTGGAGC	62.411	96
HM_1948	contig07665	TTC	3	12	TGAATTCTCTGTTCTCTCTTGGT	63.212	GAGCTGAATTGAAAGGAGGAAAC	62.523	101
HM_1949	contig14726	CCA	3	12	CTTGAATGGGgATCTCTTTTCTT	62.958	TTGGGAAGAAGTGAAGAAGTTGG	62.892	111
HM_1950	contig11417	AAG	3	12	CGAGCAATGGGATCTCTTGTATT	62.729	ATCATCATGACTGTGGTGACCACT	62.928	143
HM_1951	contig26905	GGT	3	12	ATCTCTACTCCACGAACCTCTCC	63.29	CAACCTAGAGCAAAATCTGGCG	63.252	160
HM_1952	contig32846	GCG	3	12	cTAcACTCCGACCTCTGCTTC	62.569	GAGCGTAGGCTCAAAAGTTGGTGT	62.972	116
HM_1953	contig49000	GGT	3	12	ATTGAAaGAGCAGGAACAGAGCG	63.232	GACTCCATCTCCACTCTCACTcTc	62.754	96
HM_1954	contig18468	GAA	3	24	GAATCGAAGAAGGAACGTGATTG	63.219	TTCAATTTTCACTCTCTCAATGG	63.397	118
HM_1955	contig06317	ATG	3	12	GTAGCTTCACCAAGTCCAGTTTTC	63.474	AAGCCTAAAGCGCGGATTAACCTAC	63.058	135
HM_1956	contig12866	ACC	3	12	GAAATACCCAAAGGTTGGGAAAG	63.962	AGCTAATGGGAGGGGAAATAGGTC	63.823	147
HM_1957	contig22503	TTC	3	12	TCAGTCACACTCTCTTGAACCT	62.612	CCCAGAGCCAGAACTAGTAACCA	62.918	126
HM_1958	contig44673	TAT	3	12	GATGaGgAGGATGGTGTGAAGAG	63.424	TCATGGAAGCAAGAGTAcTCAATG	62.514	160
HM_1959	contig01692	TCG	3	15	AGCACTAGCTGTCGAAGTTCCACCT	62.848	TcTGTGGCaATCATTCTGCTACIC	63.719	144
HM_1960	contig02153	AGT	3	12	TGAAGGGATTAGAAAGGAGGGAAG	63.05	GGATTCAACTGCCACTGTTTTAG	63.129	158
HM_1961	contig24082	GCG	3	12	GAAATTTGGGTTTCTCTGCGGAAT	63.476	TTCTGATCTCGCTTGTCTCACT	62.712	117
HM_1962	contig06842	TTG	3	12	TTGATGATGAAGGAGGAATTTTCA	62.315	CCTCACAATTTGGGCTCTCTACTA	62.907	92
HM_1963	contig06643	TTG	3	18	ATGCTCTAATTTTCACTTCCACCA	62.922	AGAAAACCCAGCCCAAGTTTATTC	62.808	144
HM_1964	contig16378	ATT	3	12	CCACCATTCCCTTTTCAACAa	62.764	gAGTTTAGCCACACCAAGAAGAAa	62.728	139
HM_1965	contig11817	ATC	3	12	GTTCATCAGCCACAGTTACGACAC	63.085	TCAATGCACTGACATTAAAGACAA	62.857	151
HM_1966	contig09889	AGA	3	12	AAATTGACCTCCGATGAAGTGC	62.923	CGACTATAGATTGGAGATTTTGC	62.342	84
HM_1967	contig24739	GCA	3	12	ACCACAACCTCAAGGAGAAGCAAG	63.133	CAGTGGCCGGCATGATATTAGT	63.262	146
HM_1968	contig49977	GAA	3	24	AGTTGATGCAAGAGGATCCGAAG	62.897	TCGGAGTGTCCAGTTCTTCTTCT	62.793	134
HM_1969	contig38372	GAT	3	15	CTTGAGAACACGCTTCTTGAGGAGG	63.007	AATGCTCTATAACGAACCCCAT	63.007	98
HM_1970	contig29195	TTC	3	12	TtTAAICGcAGTTTCTTACCgTTT	61.407	ACTGAcGAAATGCAACAGAAGAG	62	141
HM_1971	contig11455	GTG	3	15	GTTTAgTTGGGGTTGACATGGTTAG	60.869	TTTCAATCCAAgGTTTTACTTTCA	60.239	136
HM_1972	contig06154	GAG	3	12	GATCGGAGGAGAGGAATTGAATG	63.288	ACTTATcGCCGACTCTTAAGT	62.839	87
HM_1973	contig12006	GAA	3	18	AACACTCCAGCAGTGGAAATCTGT	63.043	CATCTCCAACAAGGGGACCTTCTC	63.408	117
HM_1974	contig11786	TTC	3	18	ACCACTACTCTGACCCCTAGTCT	63.086	AATCAAAATGGAAGAGGATGGTGAA	62.987	158
HM_1975	contig14509	GAG	3	15	GAGGATTGCTCTCTCTATGCTGAA	63.125	CCTACCAAGAAGACCTTTCCGTTT	62.989	138
HM_1976	contig05181	ATG	3	24	ACGTGTTGAagAaGAAAGAAGAACG	63.263	ACATACATGCTGCGAGTTCGCTA	62.975	123
HM_1977	contig32535	TGC	3	12	TAGCATATGCGAAGAGCAATCTTG	62.777	CATCTGATTATATCTTCTTGGCG	62.817	150
HM_1978	contig45573	GAT	3	15	TTCTGGAATCACAAGAATTGGCTa	62.946	TAGGTGGCATAGCTTCTTAGGATG	62.935	160
HM_1979	contig33270	TCT	3	24	CATGCTTTTTCCGATATCTCTATGG	63.023	GCCATTGAAGGTGAGAAGAACAAT	62.813	142
HM_1980	contig14942	GCG	3	12	AGATGACTTTTAAACGCTAGAGCC	62.179	CCATCATCATCAACTCAGCTCC	63.13	157
HM_1981	contig12430	CTT	3	12	GACCTTTCTGAGACCCcACTTAC	63.495	GGTCTGAATTCCTCTTTTGGTCA	62.784	149
HM_1982	contig38129	AGC	3	12	AGCGGTTGaaTTACTTGCATCAAT	63.058	TGCAGAGACGACTTCTCTCTCTAT	62.912	145
HM_1983	contig22455	ATC	3	12	GcCtaGATAATTCTCGTCTTGGg	63.383	AACTGTGATTGTAAACGTTCCCG	63.343	154
HM_1984	contig44436	CCA	3	30	GAGGGGCTTGTATTGATAGCAGAGA	63.125	GCTCAACCTCTCTCTGTGAATTATG	63.331	153
HM_1985	contig08980	GCG	3	12	GGGAGTGGAGCTTAAATTTCCC	63.473	TACTGAGAGCTTCTAGACCTGGGC	62.512	155
HM_1986	contig04039	TTC	3	18	AATAATCAACCTTGGACCCACTC	63.482	ACTAAcCAGCAAGGCGAGGC	62.826	103
HM_1987	contig03856	TCG	3	12	AAATGAAGTCATCGGAGGTGAGAG	63	CAGACCAAAATCACTCCCCaAG	62.993	151
HM_1988	contig16525	CGG	3	12	CAGAAATGAGTGGGAGCTTTGG	63.225	CCACACCCGAATCTCAAACTAC	63.019	135
HM_1989	contig02994	TCT	3	21	CCTCCAATCAACGACGGATAGATA	63.414	TAGTACTCGGACGAGCTGTATGGA	63.189	156
HM_1990	contig26149	CCA	3	18	CAAGAAaTcAGGcCAAGTCAaAG	63.13	ACTATTAGCAATCCAACACCCAC	63.256	152
HM_1991	contig03376	TGG	3	12	AGAGTAGGGTTTTTCTGAGGGGTG	63.189	ACAACCTCTGcGATCTCTGTC	63.04	120
HM_1992	contig38055	TTC	3	18	ATTTGTGAATGCATTTCCTCATT	62.817	TAAAGTGAAAGcGCTTCTGAAGG	62.929	117
HM_1993	contig21033	CTA	3	18	TGATTTCTCGGTGCTCAAGAGAAG	63.406	CCACACATGTAGCGTCAgaTAAGC	63.091	156
HM_1994	contig05060	TCG	3	12	CGAGTACGTTCTCTATgAAGGGGA	62.907	GGAGATGTCACAGTGAAGTCGATG	63.269	111
HM_1995	contig35930	GGT	3	12	GTGTTTGGAAATGGGGGATTTATT	63.075	AACTTTGCCAATGGCTCTCACT	63.227	149

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_1996	contig17183	CCT	3	12	GAGCAATTGCAAGAGTTGCAG	62.57	CTGAGGTTATCTGCTGAGATGGGT	63.014	138
HM_1997	contig26537	TGG	3	18	CCATTGAGGCTTACGCTACCTCA	62.631	TACTTGTGAAGCTCAAGCAACAC	62.869	159
HM_1998	contig09235	CTT	3	18	AAGCTTCAGCTAAGATGGTTTCTC	61.043	TTGTGTTGATGGATTACGAGGATT	61.771	110
HM_1999	contig14026	TCA	3	12	AGCATATCTGCTGTTTGTGGGT	63.158	TCgTGGGAtATcGTTAgCTGAAT	63.043	106
HM_2000	contig20709	ACT	3	12	AATTTGACTTCCCTGATgCACAAT	63.026	GAAGGAGTTGGAATGATTGAGAGC	62.586	142
HM_2001	contig20280	CCA	3	12	TAGGCATCGGAAGAGGGTAACTT	63.389	GTTAGGGAGCTGCTATGGTGTGAT	62.84	90
HM_2002	contig19797	ATA	3	18	GGTGGAAACCGaCAATGTATTCTT	62.411	GGCCATATGCTACAGATCTGAAC	63.142	129
HM_2003	contig10310	GTG	3	12	GgTGTGATAGTATGATGGTGGGT	64.232	GTTATGAGGAGCTGTGAATTTGC	62.248	148
HM_2004	contig01385	CCA	3	12	CTCAAAACCTTATGGTGGACACA	63.21	ATAGATTGGGGTTAGGTTGGT	63.816	138
HM_2005	contig40956	TAA	3	12	CAAGAAAAGCCAGAGCTGTAGTGA	62.853	TATCAAAAGCACTTCTGCTGTTTG	62.642	113
HM_2006	contig00891	AGA	3	24	aCaTCTCGATCCTCCGATCAG	62.761	TTCAGATCATCAGAGGTACGCCTT	63.444	160
HM_2007	contig44717	TGG	3	15	AAGAATCAATAAGGGCTTCCAT	62.986	GTACCCACATCGAGGGTGTGTTG	63.256	146
HM_2008	contig39444	GAA	3	15	ACaGCAGTCAAACTCAAGCAAAAT	63.256	TGTATGTAATTCTTATCTGCCCCG	62.489	91
HM_2009	contig31567	TGA	3	12	ATCTGTTGAAAGGGGTGAAGCCAA	63.129	GGGAATCACTAACTCTcCCCCA	62.763	110
HM_2010	contig25640	TTA	3	15	CTCTCTCTCaATGCTCaTTCCT	63.059	ATAGGCAATGATGTACGGCAAAAT	62.863	146
HM_2011	contig12873	TTC	3	21	CTCACTGGCGAGTCTTATCAAGT	63.137	GAGAAATTTCCATGGCAAGAACg	63.219	136
HM_2012	contig50321	TCG	3	15	AGTTGACGGTGTGATGAACCTTGA	63.053	CACCACTTGCATATATTGGCAGAA	63.171	122
HM_2013	contig28845	CTC	3	12	AATGCTTCAGATTCATCTTGGC	63.039	GATGATTGCTTCGGGATGTATTCT	63.248	106
HM_2014	contig21763	GAA	3	15	AAGAAATCGATGATGAAGGCGCA	63.121	AATTGGACTTGAACACTTTCTGGC	62.824	126
HM_2015	contig05808	AAG	3	12	GCCTGCTTGAAGATTGATCTGGT	62.949	ACAAAGGATGAGCTAGCAATTA	62.342	120
HM_2016	contig01629	CGG	3	15	GTAGAGGGAAGATGAGGAAGGGg	63.561	TTCAATATTCCCCCAAAACcAc	63.184	160
HM_2017	contig31943	TTC	3	15	CCCAACCATCTTAGCTATCCAAA	63.421	aCCgaAAAGGGTCACTGTTTGtTA	63.028	116
HM_2018	contig48192	GAA	3	12	CAaTTTCGCAGAAACCTTAGAAT	63.676	CaAAAtaTGCACTaGAtTCTCCa	63.036	138
HM_2019	contig01796	GAA	3	15	AACCGATCAATGGGATGATCTTG	63.211	TTCACTTCTCTTTTGCTCTCTTCA	62.919	125
HM_2020	contig24108	TTG	3	24	GTGTCTGGGCTGAGTCAGACTGTA	63.06	GAGGAGCTATGGATCAGAAACCA	62.9	149
HM_2021	contig43871	CAT	3	12	aTtCTGCTCATAAAGcACATc	62.929	TTTCGAGatGGATCAATCAAAAT	62.889	149
HM_2022	contig15333	GCT	3	15	CGAGCATATCCATCTCAGATTCC	63.216	CCTCAACTCAACCTCAAGAGAA	63.094	155
HM_2023	contig37574	CTT	3	12	CAAACGAGACCTTCTTGATATAC	63.239	TTCAGGAAGAGGAGATCAAGATTG	63.076	145
HM_2024	contig47426	TCC	3	12	ATTCTGTATGCCAATCAACCTCCG	63.341	GAAATACCGGCTCTCAGTCGATA	62.828	154
HM_2025	contig17112	GTG	3	18	GAGGCGTATGATTAACGGAATTGTG	63.043	GTCACCACTCCCTCAATTCaATA	63.419	96
HM_2026	contig14597	CAT	3	12	AACCTTCATCTCCTACTACCGGAAC	63.81	GAGGAAGTGGATTTTGAGGAGGT	63.071	112
HM_2027	contig13039	GAG	3	21	CGTGTGATCACTTGTGAACGGGC	63.357	TTACAGcTTGCaAAGAGATTTGA	63.179	146
HM_2028	contig32854	CTC	3	15	CCCAATACAGGAAGACTCGTTGT	62.71	GTGCAGCAGTGCATAGTACAGAGG	63.433	99
HM_2029	contig33441	TCA	3	12	GAGTGGCTTCTTGAAGCTTTTCT	63.804	ACGGTTTGAATGTGGATCATTTCT	62.913	160
HM_2030	contig08837	TCT	3	12	TAaAGAGAAGACATGAACCTGCC	62.91	aTTAAGTTCGCTCAICTCTTTCT	63.007	153
HM_2031	contig07739	ATG	3	24	CCCAACTTCTTCTCTCTGCTG	63.007	GTTTGAGTCAGTCCGGAAGAGAA	62.907	150
HM_2032	contig14720	ACC	3	15	GAGATAAAGAAAGGAAGGAGCGA	63.278	CtGTTTATCCAATCaCAAAcAg	62.856	135
HM_2033	contig45680	TGA	3	15	GTTTGGGTTAGGTTTGAAGGTCT	62.791	ATGGAGCGCAATAGTAGAAGAGGa	62.634	128
HM_2034	contig00154	AAC	3	15	GAAACACATCACTTCAAGAGGCA	62.726	gaaggagtttcttgggtgttctt	63.08	159
HM_2035	contig51759	TAC	3	12	ATAGTTTGAGGGATGAATTTGGCA	62.912	GGCAAGAGTATCTaACAAAAACAATGG	62.321	154
HM_2036	contig09465	CGG	3	18	GAGATGcAGCCCATTAAGAAGAAg	63.334	TACGTCTCCGACAGATCTCAAAc	63.876	155
HM_2037	contig31636	ATC	3	12	GCTTCTCTGATCTTCTTCACCA	63.217	GCCAGTGCATGCAACATTAATAGA	63.3	110
HM_2038	contig35917	AGC	3	15	CAGTGGGGTGTATAGCTTTGAGA	63.641	ATATACTAGCAGCATGGAGCGGAG	62.963	151
HM_2039	contig04010	TCT	3	12	CGTCAATTACGCTCTCTGTCTT	63.044	TCAAGCGGAGACAGGTGAGC	64.029	150
HM_2040	contig28407	GAT	3	18	GTCACTCaGACGAACaCTTGCATCT	62.858	aATTTCACTGTCCATAcCCCCtTc	63.482	87
HM_2041	contig26894	CAC	3	15	ACaGAGGCTGaCCaCAaGAaAAC	62.935	ACAGGaGGTTTaaTGGCtaTgGGT	63.102	111
HM_2042	contig20647	ACA	3	18	CTAGTCGGAACCAATTTGAGAGA	63.006	ATCAACAACAACCTCGTCTCTCTC	62.912	133
HM_2043	contig16036	GTG	3	12	GTGCTACTGGAGTGTCTCACACAT	62.872	GGACGTTTAAACCTGCTCATCTCT	63.804	160
HM_2044	contig41621	TCT	3	15	TTCACTCTAGCAATCTCTCTCC	62.693	TACGAGGACATATCGGTTGTTATG	63.072	134
HM_2045	contig01543	CCG	3	18	CAGCCTGATTGCTGAGGTACTA	62.829	CAATTGCTCTCTCTCAGTAGTGT	63.137	156
HM_2046	contig14812	AAT	3	21	CCCTAATCTGCCTTCTATGTGA	62.703	AATGCAAAATAGGGTTTgGGTAGG	63.284	158
HM_2047	contig42537	TGG	3	12	aTcGAGAGCTGTTGTTATGGTTAGG	62.633	TCTCTACTCGCTCTTACGTCTG	63.345	103
HM_2048	contig46455	TCG	3	12	TGGTGTGGTGTGGTCAACTTAT	62.621	AAACaAAAAAACAATCCCCCC	63.183	107
HM_2049	contig03273	TCA	3	12	GGTTTTGAAGGGTGTTCCTGATG	63.006	CCAACATATCCCTTTCTCACAGAAT	63.325	147
HM_2050	contig40652	CCA	3	12	GACATTAGGCATCTTCTAGCCAA	62.828	aCACTGGTGTCACTgGAACGAT	63.047	146
HM_2051	contig27017	ATC	3	12	TCTTTTTTGTGCTTGTGCTTCA	62.642	AGCGGATTTCGGTTCATCATCTTA	63.034	99
HM_2052	contig25059	CGC	3	18	ATGGACGAGAAGCTGATACAGaGG	63.128	ATCATCGAACCAATGATTGAAG	63.368	153
HM_2053	contig05508	CAG	3	12	AACTTTTTGCCCATTACAAATGCG	62.384	GCTACCCTAGCTTTGCAAGTCTCTG	62.959	155
HM_2054	contig49520	ATA	3	12	CCAGCAGAAAGGGGACAAAAA	63.538	cTTGCACTAGGAcCCTGaATGaAa	62.894	159
HM_2055	contig16950	CCA	3	15	CGTACTCTCATGCCATTACATA	62.225	ATGTGCTGTGCTTTTGTGAGA	63.189	158
HM_2056	contig13908	GAA	3	12	GAAACTCCACAGATCTGCTCTCT	62.472	tTCTTCTGCTTCTTCTCTCTCTG	62.62	98
HM_2057	contig32725	AGG	3	15	TTTGATTCTCTTTAGCAGCAGGG	62.919	GAGACTGGAGGAATCTTGGTCA	62.987	89
HM_2058	contig14810	ATG	3	15	ATCTGGGATCAACATTCAAACT	63.293	ACTGGTTTGTGTTGCGTGTGTTGT	62.943	113
HM_2059	contig10152	TTC	3	18	AAAAGAGCTCTCGAACTCGAAcT	63.213	CCAcCTCGaITTTGATGAATGTT	63.317	114
HM_2060	contig12640	CAG	3	12	GCCCTTTTTGCTTCAACAGTTCTA	62.944	CGTGATTTGGTTTTGTGTTTTT	63.13	101
HM_2061	contig33739	GAG	3	12	AAGAGCTTTCGTATTGcATCTCT	62.312	AAATAGAACTCCTCGTCAATCCCC	62.878	113
HM_2062	contig00796	GGT	3	15	TAATAGTCTCGGCAATAGCCTTG	62.746	CATTCTATGGGAAGAATCACCAAG	62.983	117
HM_2063	contig28532	CGA	3	12	TcAtATTTTCACTCATCATCGCG	61.533	AGGTGAAGTTTATGTTCTCCGAGT	62.526	120
HM_2064	contig30055	TAC	3	18	ATGGTTTTTGATCATGGAGAGACG	63.532	ACTTCTCACTGAITGCTcAaCC	63.027	152
HM_2065	contig09805	CTT	3	12	GGAGGGAACAGAAACACcATAA	62.696	TCCGTTGAACAGACTCAGTTAT	63.45	158
HM_2066	contig29337	TCC	3	12	TCGACCGCTGTATTGCTATTAT	62.854	GTTTACGCAATTGATGGATTCCC	62.642	120
HM_2067	contig14966	GGT	3	12	CAAAGGAcCTTCCATGATTGTAAC	62.996	GTTAGTTGAATTGCCAcCAGAACC	63.035	156
HM_2068	contig16239	TGG	3	15	CAGTAAAGGGTAAGCGTCAAAAGCG	63.266	GATGTGGGAGATGGAATTGaAgaA	63.514	153
HM_2069	contig14064	AAG	3	18	AAACCAACCAACCATGAATTAAG	63.108	AGCCTCAAGAACCTCTGGTaaAAA	63.588	135
HM_2070	contig25319	CAT	3	15	CATTGTATCCCACTGATCTCTCT	63.093	TGGTCCTATGATCATTTCTGGCTC	63.413	157
HM_2071	contig27263	CTT	3	15	TCCTCTCGAGTTTGATCTTATCG	62.996	GAAATTGAAGGTGTTTCGGAATTG	63.117	86
HM_2072	contig49620	GAG	3	12	CCGCGCGTGTATaTAATCTCAAAAA	64.043	GGCCCCCATCACTACTTTg	64.958	149
HM_2073	contig49136	GCC	3	24	GTGCGGAAGTAGTCAcATTGTTCT	62.219	TATTTTCGATGCTCAAAACCTTAA	62.92	136
HM_2074	contig32169	ATT	3	12	GAAAGTACAGAGACTTTGTCCACg	63.345	TGGAAGAAATAGTGAaAcaAGAGG	62.727	152
HM_2075	contig34387	TGC	3	15	GGCGTGTGCTGTGCTGCTGT	63.945	CAGGCTTCTTTCGCTAcCCCTAT	62.992	137
HM_2076	contig33554	GCA	3	12	GTCAATGAGGACATAATCCAGaC	63.016	AGGGAAGGCTACTTGGCCAG	62.879	83
HM_2077	contig09551	CAA	3	12	TCGGTAACCTTCATTGAATCTGTT	63.019	TTACaGATAGCTGTTGCTGCTGGT	62.353	137
HM_2078	contig29643	TTC	3	18	ATCATTTGGATTGGGAGAGATCAGA	63.187	TGCATTAGAGTCCGCTACAATCAA	62.845	143
HM_2079	contig13495	CAA	3	12	TGACTCCAATTATGTTCCAAACTC	63.159	TAATATCTGCAGAAAGATGCCACCA	62.949	155
HM_2080	contig02614	GAG	3	12	TGAGGATGAGTGACAAATGGGTA	62.803	CTCCAAAGCAAGTTCTTGTTTCA	62.921	92
HM_2081	contig35480	GAG	3	30	TTAGGgTTTGcAGAGGAGAGAGGT	63.802	CACAGCAATGGCTAGACTCTCTT	63.25	95
HM_2082	contig44018	GTG	3	15	GAGGGTAGTCTTGATGACGGGTG	63.238	TTCCAACAAACATCTTCAATTCA	62.703	158
HM_2083	contig16967	CTC	3	12	ATCCATGGCGACTCTaCATTTCAAT	63.029	CTTGCCGCTAATTAACTCCGATAA	62.462	107
HM_2084	contig02575	TGA	3	12	AAGAGATCAAAAGCAGACGAATGTT	62.613	GGGTTTTCTGCACATTAGACGAC	63.146	160
HM_2085	contig51089	GCC	3	12	GTATTTTGGGCACATACCGATCAA	62.962	GcCCAcCTGaATCTCAACTaTAC	63.133	150
HM_2086	contig12563	TGA	3	12	CTCCGAAGCTACTCAaagGAAGTCG	62.931	AATGATGAATGGATGCCCAAAATA	63.41	160
HM_2087	contig11887	CGC	3	12	CTCGAGAGTCCAATTGTTATGAAC	63.231	GGAAGAAGCTGTGGGTTTAAACAT	63.7	159
HM_2088	contig43850	GAT	3	18	AGATAGATAAGCAGCGCTCTCAA	62.667	CTCTGCTGACTGATCTGTTaCAA	62.119	135
HM_2089	contig19466	AGG	3	12	TCGGGTTgAAAGaGGGACTCTAT	63.476	TAATCCAAGTCgCTGAAATTGc	64.465	155
HM_2090	contig33870	TTC	3	24	GATGCTGACTGTGGGTATCTCTCT	62.915	AGAGAACAGCAAAATGaaAATTGg	62.826	157

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2091	contig29853	GAA	3	18	CTTTTCTGGGTGAATCCTCATCTG	63.3	ATAATAGCTTCCCACAGTGGCCA	63.034	141
HM_2092	contig40907	TTC	3	18	CAGTTCAAATGTCTCGaaGAAACC	63.117	CGAATGCCTCTATTTCTcAcaCTT	63.028	123
HM_2093	contig24308	TTC	3	15	TTTGAAGAACCCTTTGATTTCAG	62.688	tTCTTGctTtCAAtTgGAGGAGAG	63.104	143
HM_2094	contig37993	GAC	3	12	GGAGATTTCACAACACTTGGGAAGC	63.365	tactaatgagtggctgaaacgcaa	62.969	159
HM_2095	contig05573	TCT	3	30	TACCCTCCCAATCATCAACAATC	63.198	GGTTAAGAGTGGAGTGAATGTGGC	63.242	122
HM_2096	contig27585	GGT	3	15	GATTTCGTGATCGGAGATGAATCG	63.961	atGGCGATCTCAGctttTACATC	63.042	144
HM_2097	contig33686	TTG	3	12	AAGAcgATATgCTCCTCGATGAAT	62.411	CcaAAACATTTTACCTTCACACTTatCa	61.556	138
HM_2098	contig12314	CCA	3	12	CAAAACAAGCAACAGAACCAACAA	63.38	GAGATCCCCAAGAGTGGAGGTATT	62.964	141
HM_2099	contig16021	CAT	3	12	TTCaTTtCATGTTCATCtCcTCT	62.987	ACTGACGATTCTTTCAACTCTGGG	63.01	132
HM_2100	contig50818	TCA	3	12	CATCCACTGCCACTACTACCCTCT	62.922	AGGATTGATTTTGGAAATGGAAGC	63.575	83
HM_2101	contig41140	GAG	3	12	TATTCACATCCCCAACTCAATCG	63.91	CTGTAGCCAGCACTGcCac	64.287	106
HM_2102	contig19412	ACG	3	12	TCTTGTGAGCAGACTCAATCGTC	63.057	AGGACTATCGTTGTCTTCGAGCAG	63.25	156
HM_2103	contig10120	CTT	3	12	ttGACAGGAAGTACCAGAGGTTCC	62.895	CAGAAGACGGTGAAGAAGAGGGAAG	62.892	100
HM_2104	contig19451	GAG	3	12	CGGACGATTCTGATCTTAGGAGG	63.212	CAACTCTcCGATTTCATCCTCTC	63.519	101
HM_2105	contig38814	GCA	3	12	CGGAACACTCGCTGATATAATGC	63.048	caacaccaagctacatgatcaaa	63.265	150
HM_2106	contig14701	TTC	3	12	ATTTCCAGTCAATACCCACAGAT	62.813	CCATGAAGATTTCTGTTGATGACA	63.244	123
HM_2107	contig26514	TTC	3	12	TTCAATTTGCATATTCACAACCTTC	62.384	aATTTTGTAGTGGGAGTACTTGGG	62.621	146
HM_2108	contig17285	TTG	3	15	TGGGAATGGAGTCTAGGGTTTGA	62.993	ATAATTAAATCAACAATGGCGAGG	62.25	111
HM_2109	contig37495	CAT	3	15	TCTTCTCTCCCACTTCTCTTCTCT	62.958	GCTTGCTTGAAGATcTGAATAATC	62.622	159
HM_2110	contig03877	GAT	3	12	CCGAGATTATGGACACTAGATGG	62.996	ACTGATCCAAACAAGAACCCACAT	63.014	142
HM_2111	contig09873	TCT	3	12	GATCAACAATTTCCGgTGAATAA	63.317	CCCCAAGAAGCTGTGAGTCTGAAT	63.124	123
HM_2112	contig05492	TGA	3	12	GATCGTCATTCTGGTCCCTGTAG	63.217	TCCCATTTCTCAGaAGaATCAGAGC	63.209	134
HM_2113	contig01302	GAT	3	12	GATTGGTGAGCTTTTCTGCTTGAT	63.039	TGAATTTGGTGCAATGAAGAACAT	62.733	107
HM_2114	contig35776	TGG	3	24	ATGGACTTTGGGACATAATGTGT	62.673	TCTCAACTTCCCTATCTCCACCAC	62.884	90
HM_2115	contig08985	TCC	3	12	TCTTCCACTGCTATTAgTGACCTT	63.338	TgTGATTGTGACTCAtCaGAATGG	63.349	159
HM_2116	contig29736	TTC	3	24	TCATCTTGATTGGCCCTTTCTCTC	63	AGAATAGAGAGaTTCcCaCacCCC	62.964	132
HM_2117	contig38749	GGT	3	15	TGAGTAACAGAGTTGGTGGTGG	62.501	CAAAATCCCTCTCCAGTCTCAAA	62.881	138
HM_2118	contig11040	TTA	3	12	TGGtTTGGACTTTGATCATTTCTT	62.996	gGTGTGTCcCAATTTTATcTCTTC	63.1	153
HM_2119	contig38596	CAC	3	18	GATCGAATTGCTGTTTCTGATTC	63.228	ATCACCATTCTTCTGAGTCACTgG	63.649	159
HM_2120	contig23777	TCT	3	21	CAGAGCTATGGGAaCAAAATGG	63.014	CATCTCTCTTGGAAATCGACTGAT	62.99	95
HM_2121	contig14225	TTG	3	12	TCAATAATCTGGTAATCGGGCTTG	63.316	AACGACAACGACCCTCAATTACT	63.15	159
HM_2122	contig03985	AGA	3	12	AACTTtCATGTGgCTGTCTCT	63.767	CAGAATCACCAGTCaCGAAATCAC	63.044	159
HM_2123	contig10322	TCT	3	15	TGCTTTGCCTTCATTGAAAATACA	62.859	GTCCACAATtGGTACTCGAAATC	62.913	159
HM_2124	contig09741	AAT	3	15	ATtATCAAAATCCGagTTTCTGcC	61.745	aaattaccgTTGCTACacATTATACA	61.013	95
HM_2125	contig51246	GAA	3	15	TGTCCTCTTTTGTCTCTCATCT	62.876	GTTTGTCTCTCTCTCTCTCTCTCT	62.863	119
HM_2126	contig10535	GAA	3	15	GTATCAGGGAATCTGGAATGGACG	63	AAGCTTGATCTTGGAGAGCC	63.209	136
HM_2127	contig22635	TTC	3	24	GCTTCACAAATCAGCTCTTGTCT	63.343	AGAgagGGGAAAGAGATGGAAAGA	62.948	153
HM_2128	contig07661	GAA	3	12	GAGGTCAGGCACACTTTTAGGTTC	62.512	CACTTTTTgCcaACaCATCTGCTA	63.386	154
HM_2129	contig16152	TTG	3	24	GCTCAGCAGAGATTtGGTTTTC	62.634	ACTGATGAGATGGAGAAATCACCC	62.994	115
HM_2130	contig15645	AGA	3	15	AGAGCATAAAATTTGAACGGCAGTC	62.854	AACGgTTTGAACGTTTTTCTCT	63.303	156
HM_2131	contig03880	GAG	3	15	CAGAGACTTCAAGCTGGTACGACA	63.063	TTCaAGCCAAAGCTCTCTATCC	63.133	153
HM_2132	contig14738	TAT	3	15	ATCAGTGTAATGAAGAGGGAGACA	63.331	AGCTGGGTCTCTAGCTCTCTCTGTC	62.926	142
HM_2133	contig14223	TGA	3	15	TattttCTCAGCAGGAACCACTCT	62.91	ATTCTCTGTATTTGCTGCCCCAA	63.034	141
HM_2134	contig15076	TGA	3	12	TGCTGGTGTGTTGGAGATGTAGT	63.067	TCAGAAGAATCCAGTGCAGACAAG	63.04	133
HM_2135	contig49787	TCA	3	18	AGTTTTCTCTCTCTGCTCTCGT	63.105	CAAGACTTGGAAATGGTTCCCTGA	63.618	115
HM_2136	contig11898	CTC	3	18	ACAGACCAGCTCTCCATAaTTGG	62.811	TGGGAAAGaAGAACCATCTCAAA	63.312	144
HM_2137	contig32714	CTA	3	12	TGCAAGCCTATGTTGGTTATTGA	62.761	CGAAATTCACCTGATTCTGATTGT	61.978	132
HM_2138	contig15879	AGC	3	12	GATAAACCAAGCTGCTCAGTCCA	63.035	TTGCTGAGCAGAAAGAGTGAaCTG	63.07	137
HM_2139	contig34956	CCA	3	15	tCACCAAAAGCTCTCTCTCTCT	62.883	CATATACAGAGTCTCGGGCGTTTA	62.579	148
HM_2140	contig21985	TCA	3	18	CTTCAAAATCCCCAATATACCCA	63.089	TGAAAAGAGGTTGGTTGTTTTCTC	62.795	135
HM_2141	contig06206	GAA	3	15	ATTCAATCAATGGGAAGaGGAGC	62.802	TTTTGGCACCATAAGGATAGAGAAT	62.912	132
HM_2142	contig45646	GAA	3	21	TGGAAGAGGAAGAGAACAACCTTG	62.172	TcaAAAAATAAGATgGTTTCgGCT	62.157	136
HM_2143	contig24825	CGG	3	15	TTGTTCTCTCTCTCTGTGCAACAC	62.947	TTCAAGAGAAAAAGCTACAGATGC	63.043	122
HM_2144	contig17274	ACC	3	15	TGCAAAACCCAACCACTCTATCCA	63.002	AAGCACATTAAAGCGTTTGTGG	63.379	133
HM_2145	contig46947	GAT	3	15	GACGGAGGTTTTGACAAGATGAT	62.7	GATGATTGAAGCAAGTTCCCTA	63.42	127
HM_2146	contig26227	GCA	3	12	GATCAtCACCAATCTCTCTCATC	63.088	aaTCTTACAACGCAACCAACCA	62.77	142
HM_2147	contig00693	CCG	3	12	ATCAATCTCTCTCAATTCTGACCT	62.977	CGGAGAAGAAGCTGGTGAAGATT	63.215	143
HM_2148	contig12489	CTC	3	15	AATCTTCAACCTCTGAACCAACCA	62.907	GGGATGGGTGATCAGTAGCAATA	63.322	152
HM_2149	contig26104	CGG	3	12	GTCTCGGACGTAGTTTGAGTTG	62.276	TTTCAGGATACTGGGTTTGaACT	62.842	133
HM_2150	contig32162	AGA	3	12	agCAAAACAATCATTAATCTCTGCA	62.318	GAAgAATAGATCTTCCGCGCAGT	63.2	133
HM_2151	contig32078	TCC	3	12	GaaTCCAGTTTGAGGAAGCATCAC	63.336	GTTGATTGATGAAGCTgAGGGACT	63.017	154
HM_2152	contig16761	CCA	3	12	CaCCACcACcCAAGTACaAgTCT	62.474	gTGTTGGGGGAGAGTGGTaa	63.322	127
HM_2153	contig17683	ATC	3	12	GCACTAGCAACTTTGGAAGCAAT	62.972	GGTGATACTGGAGAGCAATGTA	62.543	99
HM_2154	contig10679	AAG	3	15	tCAAGTGTtTtTgAGAGGGaAAaA	63.198	ATaCaAACGCTTCTCTCTcCCGT	63.404	133
HM_2155	contig38879	ATT	3	15	AAGTAATCCGAGTATGACGTGGA	63.022	CCAACATcCaaTCAcTActAtcAA	62.343	160
HM_2156	contig28951	TGT	3	15	ATGTCTTCAGCAGGTATCCCCAA	63.121	AACCGTCAAGcGAGAATCATTA	63.121	154
HM_2157	contig41597	GTG	3	12	GGCATGACTTtGAACATCATTTTG	62.733	GCAGCTGCCTCAGTAGAAGAGAAA	63.573	103
HM_2158	contig20552	GTA	3	15	TTGTTTCGGAATAAAATGGTCCAG	63.204	GTCGTTAAAAACAGAGTTGCAAGt	62.848	130
HM_2159	contig02113	GAG	3	12	GAGAACTGTGAATCGGAATCGTCT	63.017	CtCTTTGCTTTCTCCGCCAT	62.908	80
HM_2160	contig05491	TCT	3	18	TCTCTTCTCCAACAGTCTTCTGTC	63.327	aAAGAAAAGAGAGTGAGACCAAC	62.397	117
HM_2161	contig25817	AGA	3	15	CCTTACTGGGCAAGTATCAGTTCa	62.74	GATcCTCTGGTGTtTTATCTGCG	63.231	141
HM_2162	contig01845	CTT	3	12	TTTAGAAgCCcGGAAGAGTAACC	63.001	GATAGATCTCAGCGGCAACGAAG	63.331	138
HM_2163	contig30510	CGA	3	12	CCAGTGAACATGGGATTTCTCTCT	63.204	CAGGTAGTAGATAGTGGGATCATGGG	63.098	114
HM_2164	contig13710	TCT	3	30	CCAAAAACCAACCACTCTCTCT	62.906	cCCAATGGGcAtTACCGtATATAAT	62.838	158
HM_2165	contig25110	GAT	3	21	ATCGAGCTTAGGGTACGCAAGC	62.953	ATCATCATGAATCaACCACAACAC	63.037	119
HM_2166	contig44854	TCT	3	24	AGCGTCTCTCTTCTCAAGTCTGA	63.023	cGTTTGTGAGAATtATGAGCACG	62.969	130
HM_2167	contig18738	CTA	3	18	TCTGAGCGATTAAAGAAGAAGACA	62.643	TGAGTGGTGGTCTCTAACATAA	63.176	159
HM_2168	contig01666	GGT	3	18	TTGAGTAAATTTCTGGAGGAACCA	63.202	AGCTGAAGTGGGTGTCTCTAACT	63.154	154
HM_2169	contig33468	TCA	3	12	CCAAAAAGgGgCAACATCATAAg	62.825	AAAAATTTGgaAGAGGAGGACGAAG	63.074	155
HM_2170	contig39576	AGA	3	15	CCCCAGTtATTCTTTTGTGGGTT	63.372	TTTGGGATTTCTCTTGTATCTCT	62.877	160
HM_2171	contig06551	GAC	3	12	CACCACAGACAAGAAGAAATACAG	62.438	CTtTTTGGTGTGAAGTCTGCTG	63.78	97
HM_2172	contig02346	GAA	3	12	TGAGTGTGCTGTAAGATGTTTGGGA	63.057	AGCACACAACCTAAAATCAGCAAA	63.189	122
HM_2173	contig29223	TAA	3	15	CCAGGTATGTAATCTATGGTGCCA	61.188	TTTTTCTcCTAGGCTAATACACAAA	60.67	119
HM_2174	contig43135	CAG	3	12	CAGAAAAGATTGTTTGGCACTGT	63.057	CAACAAATATCGATGAtGGGGTTT	63.009	92
HM_2175	contig36635	TGC	3	12	TCAGATCGGCAGTTGTGAAGAAG	63.154	gTACAGGCACTCTATGTGGAGT	63.053	124
HM_2176	contig51642	TGG	3	12	GTATTGGCTCTCTTCCAAGC	63.211	ACTCTCTCATCAcCaacCAcCa	63.146	160
HM_2177	contig11042	TCT	3	12	ATCGTAGTAATATTCTGCGCCTG	62.573	TTTCTTGAGATGTTCGAAGAAGG	62.993	148
HM_2178	contig12900	GCT	3	12	CcACCAGCATTTTATAGATGATGA	62.311	AGaGAAATGTTGGTATTgTTGGG	62.977	125
HM_2179	contig17710	TTC	3	45	CGACCAAACTCTCTCTCTCTCTCT	62.793	CAAGAAGTGATgCTCATCAGAA	62.817	153
HM_2180	contig14451	TCT	3	15	CTTTCTCAGCATATGGGTTTCTG	63.214	TTGAGGAAGTGCATGAGGAAAAAG	62.993	113
HM_2181	contig40852	TCT	3	12	TTCTGCTACTTGTGCTCTCTCT	62.922	CAGGAGAAGCAAACTCTTAACCA	63.015	130
HM_2182	contig05338	CGT	3	12	CGACTAAAGCTCGATTCTGTCTCC	62.824	TTCAAGCAATGCAACCAATACCC	63.339	151
HM_2183	contig43719	ACC	3	12	AGATCTCTcTtAacgAGGTCCACAG	64.128	CTTGAAGCTCTGGGGGAGAC	63.867	152
HM_2184	contig31201	TTC	3	12	CCTCCGACATATCTCTGTTTCTC	62.469	TCCCAAGGAAGAAACTCGTTAAA	62.316	117
HM_2185	contig13024	TGG	3	15	AGAGGTAAGGTAGGTCTGGAGCG	63.213	GTGTGAAGACAAATCAACACGAG	63.053	120

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2186	contig15443	TGG	3	12	CGATCTGGATCGTCTGGTCC	62.985	AAACCACCTCCACAGAAAGTACAC	62.705	145
HM_2187	contig21642	GTG	3	12	GGGGAAGGCGTTATTACCTGTATC	63.007	GATCCTcctgctactgctaCTGCT	62.54	159
HM_2188	contig34811	CCA	3	15	TCATCAACCGCTCTCTGACTCAAC	62.815	TGAAGAACATATGGAGTGTGAGG	62.712	160
HM_2189	contig15606	ATT	3	15	CTGTGAATCTTCTTCCGGTGAT	62.798	TTTGAATTCGGTCCATCTCTGAT	63.099	147
HM_2190	contig26267	GAA	3	12	AgcAGTTACTCtCGATGCAAAAG	63.154	TGTTTGCTTGTGTTGAACCTGT	62.969	136
HM_2191	contig03260	GCT	3	12	CTGCTAATGCTACTGCTCTGGCTT	63.383	TTCTTTTGCTGAGCATCAAGTCTG	63.061	145
HM_2192	contig29247	GTG	3	12	AATTTTCGATTGCGTGTGTACCG	63.346	TAGCTGCTTTTCAACCaCCAAAT	63.146	140
HM_2193	contig23102	GAT	3	12	TTCTCTCTGTTGGAATCAGCTGG	62.798	TGGAGcTGAGAAGAAAGAAACG	63.222	135
HM_2194	contig13615	ATC	3	21	GGATATGGGTTAGGTTGGGTTTC	62.795	CGATCAACAATCAGTTACAGGGTG	62.828	142
HM_2195	contig16522	TCT	3	12	TCCTGTTCATGCTCTTCTCTCC	62.987	ATTCTTTGTCGACGACTTCTTG	62.921	103
HM_2196	contig25794	CTT	3	30	TGATCTTGACAGAGGAATGAGCTG	63.03	GTTTATGGATTGATTCAAGCTGGC	63.037	156
HM_2197	contig22367	TCT	3	15	AGTGGGATTACGCTTTTCAGGACC	63.81	GCAACTGCAACGCATGTATAAGAC	63.015	154
HM_2198	contig09032	CTG	3	12	GATTTAGAAAGGAATGGCTGGT	62.797	TTTGGaACTGTCGAGATTGGTACA	63.048	141
HM_2199	contig39749	CCA	3	15	ACAAAGTCAAGATCTCTCTCCTC	63.186	TGAAGGGTAATAGTAATGGTGCGG	63.228	118
HM_2200	contig28372	GAT	3	21	GATTCGAAGAAATGGGACAACAAG	62.996	GAAACAGTgACAGAGGAAGCAGC	62.475	104
HM_2201	contig36212	TCT	3	15	CCCTCTGGTCTTGTCAATACCCT	62.793	ACGAGTCAGAGaCGaAAACCTT	63.681	152
HM_2202	contig47651	TTG	3	18	GcaTTAACCACCACTCAATCTTGT	63.244	CCaATGTcCTCTCTGCTGTACT	63.023	158
HM_2203	contig22150	AAG	3	12	GCAAAAGGCACTTTTCTGCTGTT	62.841	GACGTTAAAGGTCAATTCTGCAACT	61.974	137
HM_2204	contig15112	CGT	3	18	AGGGGATGTAGAGATGAGGAGAGG	63.265	GaGAAATACAGAGATGACCGTggG	63.444	157
HM_2205	contig51957	TCT	3	18	CTCTCAAACTCTCTCAGAACTCT	63.172	CCACGTTACAGACCAACACGAAAT	63.172	159
HM_2206	contig20970	CCG	3	15	gTCCGTGATCTTCTCATCTTAC	63.443	GAATAGGAAGGAGAAAGCAGAGGC	62.999	136
HM_2207	contig34701	AAG	3	12	AAGAAGAGAAAAATTTGAGGGAGAA	61.151	TTTAAGAGTCCATTGGTCTCTCC	61.786	88
HM_2208	contig42526	ATT	3	18	TTCTTGCTCAATCTCAGaagCaGA	62.831	CAAGGGGAAGAGATCATCAAGAAG	62.556	127
HM_2209	contig47226	TTC	3	15	TATAGCTCCCAGCTCTCACTGAC	63.035	GCCCAACTACCAAGAAACAGAAACA	63.653	113
HM_2210	contig02105	GAA	3	15	GACCCAGTAGAGTTCTGGCTCAA	63.124	TGTTGCTGAGGATTGCAATTGAT	62.938	155
HM_2211	contig13845	GAG	3	12	AGGTCTCTGGTTCGATCTTCAAT	63.599	AAAtaCATCTCCaCTCAACACAAAA	63.035	145
HM_2212	contig24202	TGC	3	18	GGTCCGTTACACAAGAAACAAAGG	63.028	CATTTCACTGCATTATGTCGGTA	63.059	83
HM_2213	contig27536	GGT	3	18	TGATGAACaAaCTTTAGGGGAAGGA	63.091	CGATTAGCTCgCTACACTCTCC	62.659	155
HM_2214	contig27823	TCT	3	12	CAAGTTGGTGCATCTcAGTCTcT	63.231	GGACATCCAGGTACaAAGGAAAAA	62.495	126
HM_2215	contig43315	GAC	3	12	GACAACTTGAGTGAGGCGAGTG	62.314	ATCTCAGGGGAGATGAGAGAAC	63.283	80
HM_2216	contig28199	TTG	3	12	CCTCCCACTCTAATGATCctCTT	62.853	GTTgGAATTGGATCATCTTCTCTG	62.987	134
HM_2217	contig03157	ATG	3	21	CGGTGTCAaCAACAACATCTCTAA	63.159	TAGcCTGgCATCgTAGTAgGtTA	62.146	122
HM_2218	contig44928	GGT	3	12	TTGGCATCTGACTCTCAACAaGg	63.04	CTGGTCTTAAcAACCTAGAGCC	62.622	142
HM_2219	contig00770	CTC	3	12	ACCTTCCATAGAAGTGCTGTCAAC	62.925	GTCTGAAAGAGGTTTGAGTTCGAG	62.793	119
HM_2220	contig12423	TTC	3	15	TTTTCTCTTGAAGGTTTGAGATG	62.881	TTTAACCAaCTCCCAaATTACCG	63.171	159
HM_2221	contig08186	TCA	3	12	TCAATTCCATCCCAAGAAAAATa	62.683	TCTCAAGCAATTGATGAGATTGGAA	63.132	159
HM_2222	contig04491	CGG	3	12	ATCCACTCCGTAGAACaACTCTGGA	63.217	CAGAGACAGAGAAGAGCGCAITTC	63.014	142
HM_2223	contig32457	CTT	3	12	GGCTTCTTAAAGTCTCCAaGcGT	63.319	AACTGCATACACTCAGTCACAGGC	62.872	144
HM_2224	contig49262	TAC	3	12	TGGTAAAAAGGGGTCAAGAACATA	63.618	TCCaAAAAAGAACTCATCGTCTCTG	63.017	140
HM_2225	contig26019	GAT	3	12	AATTAGCTGGTGAATGgTATGATG	62.293	AATGACaATAATGCCCTgAACAC	63.236	92
HM_2226	contig30771	GAT	3	12	TGGTGATTGTCTGAGTGCTCTCT	62.937	TATCTTCGGCAATTCTTTaTCCCA	62.911	148
HM_2227	contig43613	TGT	3	12	CAGAAGCAAGCATCAAGaGACAG	62.739	CaAgGTACCTcCAGCAGCAGTA	62.841	134
HM_2228	contig07403	GGC	3	12	GCAaCATGTCCAAACCAATTGTAA	62.959	AgAAGGATaTGCTGACTCAcCACC	62.915	158
HM_2229	contig08317	TTA	3	12	CAGAAATAGGGCTcAAACAGCTC	63.341	TGTCACATTCGCATTCTGTITTT	62.859	143
HM_2230	contig14613	TTC	3	12	TCCAGTCACTGCTTACACTCTTT	62.427	AGGACAGTCGAGTTTCAGAAAGCAT	62.823	142
HM_2231	contig14664	GAG	3	12	ACTGATCGAGTCTTCTATCCCAT	62.368	CTTCCAAAACGTCAATTCTCATCT	62.91	145
HM_2232	contig00552	TCT	3	15	AATTTTGTACATTGACGCGAAAC	63.15	GACCCTCTGTGACTGCTCCTCTTA	63.106	155
HM_2233	contig14887	CCG	3	15	GAAACACAAAACAACCTCTCGTCC	63.238	TACTGTTATGCGGGcAGGGTTTIG	63.445	153
HM_2234	contig30107	GAT	3	30	TGGGAGCAAGCATGTATTCTAT	63.034	CTTTCGTAATTCATTGTTcaCCC	63.845	97
HM_2235	contig20124	TGA	3	18	GGTCTTTTGGTCTCGAGGTGATA	63.419	CCCGTCAATcTCTCTCTTTCGAC	62.712	131
HM_2236	contig26152	CCG	3	12	CCTCTCAACCTCCACACATCTAT	62.782	TTCGTTATCGTCTCGACTCTCTCC	63.022	145
HM_2237	contig01876	CAC	3	12	ACTGGGATTGTgagCTGATCACTG	63.544	GGTTgATTACAGGTGTgGTGaAAAT	63.331	160
HM_2238	contig38482	CCA	3	15	ACCAACCTCACACAACACTGAT	62.95	GACtTTTGGGGTGAGATTGAGCTA	62.91	106
HM_2239	contig33107	CTT	3	15	TTTGACCaCTGATGAATTGGAAAC	62.509	GTCAAGGTTCTGCTCTCTGCTAC	62.939	140
HM_2240	contig36177	TTC	3	12	ATTCTTCTCTCTCGTGTCTTTT	62.715	TGGTGTTAAGGtGATGTGTGATTG	61.948	111
HM_2241	contig51664	TCT	3	15	TCITTTATTTCCCAATTCACCA	62.695	TAGTGCTAGATCGAAAGGAAGAGG	63.129	83
HM_2242	contig14078	CTT	3	18	CCACTCTTCTCAGCTGTCTTCACT	63.133	GGAGGAGACTACAGAGGTGGTGAA	63.106	158
HM_2243	contig01201	GTG	3	12	GTGGTGGAATAATATGTGGCGAAC	63.553	AtTcCTcCAcCACTTgCTCCTcTA	64.539	115
HM_2244	contig05411	CTT	3	21	ATTCACTTAATAACCGAGCCACT	62.26	ATCGAAGATTGCGTTAAAAATTCG	62.568	155
HM_2245	contig02848	CTG	3	30	AACCTTCCAATTCAACACAAGGA	63.006	gSAITTCtAAGGGGTcAGAAAGCAT	62.986	138
HM_2246	contig32832	TGC	3	24	TCATTTCTCTGTTGCTCATCTCA	63.025	CTGAAAACGAGGATGCTATGGAGT	62.923	85
HM_2247	contig16386	CAT	3	24	GCTCTTCAAAATCGAAAGATCCCT	63.188	CATGCAAGGATTGAAGAAGTGCTA	62.958	157
HM_2248	contig33429	AGC	3	24	GCTTGAAGAAACTGACGTTTTCG	63.45	CGAAGGGAATTTGCTGTCAATTATC	63.021	154
HM_2249	contig23757	TGC	3	18	CTTGAGATTAGTTTCAAGGAGGTCTg	62.61	GACTTGGTGGACGAGATTGCTACT	63.04	116
HM_2250	contig31404	CTT	3	15	TGATAGAACTGACCAATTGTCG	63.426	TGTTAGTTGcAGaGaAAGGaaAAA	62.45	131
HM_2251	contig38813	GAT	3	15	GCAGAAaGGTTCAaTGACAGTAGT	63.171	TCTGATTTGACTGTCACTCCGA	63.251	132
HM_2252	contig05429	TTC	3	12	GTTTCTTCTACTTACGGCTCGCG	62.826	tggggaAAAaggaAAAGAAAGAAA	63.246	124
HM_2253	contig26860	TTC	3	12	TCAGTAGAAGAAAGAAaGAAAGCCTG	61.995	GACGACAGTGCCCAATTAaTGTT	62.536	120
HM_2254	contig22060	GTC	3	24	GAGGACATGGGTTTGAATTTAAG	62.996	CCGAGTCAAACTCGTAATAAATCG	62.827	101
HM_2255	contig10763	ATG	3	12	tcGCCAAGTTTATCTCAACTTCC	62.826	AAGTTCtTCTTACATGTGGCTCG	62.933	143
HM_2256	contig34305	TGA	3	15	GAAACGACAGCACTCATAGCACTT	62.827	atcatCACTGTGActcGCTcAATc	62.835	113
HM_2257	contig30187	CTT	3	12	GTAGTTGGCCATGAGAGTAATGGG	63.022	ATACACCAAGCCCAAGAGATCAA	63.121	155
HM_2258	contig22393	TCT	3	12	AAGAACGACAAGaGGTTGATGGAG	63.01	ctTCAGcATTGAAGAGaGaaAAGC	62.923	87
HM_2259	contig06494	GTG	3	12	GAACCAACCAACCAAGCATGTTTAT	63.244	CACCACCGCTGGACACTACTT	62.462	140
HM_2260	contig16050	GGT	3	15	CCTTCGACTTCTCCGCTTATTC	62.799	CAAGGAATACCAAGGGGTTGAACT	63.576	126
HM_2261	contig04414	CTG	3	12	GAATGTTCTCGAGGATCAAGTCGT	63.017	ATTTGAACATTGGGAGATGGATCA	63.728	157
HM_2262	contig20801	GGC	3	12	cAACAATCCCAATAAGCTCTCTTTC	62.552	GTCCaAGTCCaAGAGAGTGACC	63.546	160
HM_2263	contig00237	ACC	3	21	gTTAAACATGCCACCaCCAAaAaCT	63.251	AGGTGGACTGTTAGGGTgAgGagG	62.98	87
HM_2264	contig02142	AGT	3	12	TGAGATCAACGTTTTTGGGATACAG	62.397	TAAAGTGAGAAGGATCGGTGTTTG	61.676	158
HM_2265	contig42694	TAA	3	12	ATAGCCGTGATGTCAAGTCTACGG	63.048	TGGaAggaaAAGATTGAATGACTG	62.702	150
HM_2266	contig31272	GGT	3	15	CgCTAACGATGATAGTTTCGAGTTC	61.436	AGTACGAGATGGAACGTTTCTATAAT	62.788	109
HM_2267	contig20305	AGA	3	24	CTCTACATCCATGCTTTTGAGCC	63.341	TaTCTGGTGTGCTGATCTAcCCCTT	64.206	148
HM_2268	contig08940	TTC	3	12	TGTGCATTGCAATGAAAAaTAACC	63.063	AAAACTTtTcACTcCTTgTGTCG	63.794	129
HM_2269	contig05033	TTC	3	12	CTTCTCCACGCTGCTTCACTTCA	63.04	CTGTTTTGAGGTTACAGAGCAAT	62.933	131
HM_2270	contig01217	TTC	3	15	CATGATTATGAAGAAGCCAAAGGG	63.005	CGATGTGAAGGagTGTCAAGCTAA	62.842	144
HM_2271	contig34584	TCT	3	12	GAGAGAAGCGATTCTGCCTTAaAa	62.342	AGTGGAATCTTCACTCACGAAGG	63.01	133
HM_2272	contig36258	CTT	3	15	CAGTATCTCTGCCCAATCGAGAA	62.913	CTGATGACCAGAAGCTGAGAAATG	63.146	149
HM_2273	contig41729	GAT	3	24	GcATCCCTAACGCTTTTAACACCA	63.444	CCTGGCACTGGTAAGACATCCATA	64.388	137
HM_2274	contig26922	AGA	3	21	TACCAgTcGAAATTTGTGTGTTG	63.273	AtTTAACTGgGCGGAGATCGATAG	63.785	107
HM_2275	contig47370	ATG	3	30	GCTGGATTCTAATCGGGCTCAACT	63.019	TCTAACATCCCAATTCGACACTCA	62.921	127
HM_2276	contig32832	TCA	3	12	ATaTGGTgGCTGATTGTGCACTTC	63.456	GGGTGGAAGTATGaAGAAAGATGA	63.747	133
HM_2277	contig42904	GAA	3	15	TCCCAAAAATTTTAAGGCCAAATT	62.811	GATTGGATAGATAGAACGATGCGC	63.041	104
HM_2278	contig19657	CAT	3	18	ACTGAACATTCCCGGTGTTTACAT	62.824	AATTTGATTGTGGAACAAATTGCC	63.13	157
HM_2279	contig16057	TCT	3	18	CTTCCactTCGATTCTTCTCTCAA	62.993	GAGAACAGCACCGAATCCGA	63.627	124
HM_2280	contig13165	GAT	3	12	aGAGATCGTTGGTCaAGGATGAAG	63	CGTTTTGCTCAATTTCTGTTGCG	63.023	156

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2281	contig23830	TCA	3	12	CTCTCTCCACAATAAATCCGATGG	63.095	GTGGTGCAATTTTCTGAACCTGTG	62.958	90
HM_2282	contig11887	CAC	3	12	GCACCGCTCGTCAATAATCAATTC	63.076	GAGcCGaAGAAATGGAGGAGaT	63.084	153
HM_2283	contig16933	AGA	3	18	AGAAAGACCAaAaGgaGAAaAaTGGG	62.968	TGTCaACaCaCTTgaATCaTCgTc	63.398	105
HM_2284	contig07919	CAT	3	12	TGCTGTATCCCGTGTAAATCTACTG	62.781	AAGGAGAGAGGGAAATGTAAATgGG	62.863	105
HM_2285	contig04533	ATC	3	12	CCGGGCTACTAACCAAACTCCTCT	62.896	ATGGCTGGTGTGTAGTATTGGT	62.838	158
HM_2286	contig26734	CAT	3	12	GACATTTCGTACTGTTTCCGAGGT	62.912	ATAGAGTGCAAGCTCAGCCtGTTT	62.864	139
HM_2287	contig21645	GAG	3	12	GGGtGGgTTTGAAGTaTGTATTGC	62.731	TTCAcCaACTGtTtCtCTGCTCA	62.287	159
HM_2288	contig22730	TGA	3	18	AAGAAGAGCCATTGGTGCTTTAT	63.406	AATgGCgGAgGGtTTTGAAT	62.476	96
HM_2289	contig36534	GAG	3	36	TGTTGaTCCAGaTTCATCAATgTg	62.687	AGCATTTACagGAAGAGAAAGcCC	63.208	150
HM_2290	contig27171	TGC	3	12	TGCCCCCTCTGCAGAAATTAAGAAC	63.022	CAACTCGTCAGCTTCTCTTAAGCG	62.946	160
HM_2291	contig10879	ACC	3	15	AAGACCTTGACGGTGAGAGGTG	62.919	AAAACCTTCCTTTGTCCATTTCaA	62.109	160
HM_2292	contig25205	CAC	3	21	CTAATTGCCTCTCTCATCTCTCCA	62.996	CGAAGTACACACTGTCCCAATCGa	63.389	126
HM_2293	contig24748	CTT	3	24	AATCTGGACTAAAgTTTCCCTTGC	62.995	aAGAGGGGAGAGAcCAACcAG	63.288	90
HM_2294	contig07631	AGG	3	12	ICTTTAATTCTGCTTCTCATGCTCT	63.245	ATAGATGATAAGACCTCCCTCGC	62.865	118
HM_2295	contig26600	TCT	3	12	AACCGACTCTCTCATCGACTTCAC	63.017	TGCAAGAGACAGAGAAACAAGCAAC	62.991	120
HM_2296	contig16192	GGA	3	12	ATTaTAACTGTGGGTCTCCGGT	62.903	ACCAaCTCTACAAGATCCGGTG	62.336	112
HM_2297	contig19848	CAG	3	18	TAATGACTTCCGACGAATCTCTat	63.112	ACCTGACGAGTTGTTGGAGAGAAG	63.231	116
HM_2298	contig28039	GCC	3	12	AGTATGAGCAGCCAGCTCGAG	62.838	ATCGATGACaGAAGACGACGATG	62.476	159
HM_2299	contig00394	ACC	3	15	TCTTTATCTACACCCTCCCCAA	62.993	GTGGAGCTCTCGTTTGGAGC	63.601	82
HM_2300	contig03486	TCT	3	21	GGTCTATCTCCCTGGAGTACGCT	62.986	aAGAGAAACTGAGAAACAACcAGG	62.166	133
HM_2301	contig00196	AAG	3	15	GGTCAAGAGCTCCTACAAGCTTCC	63.929	CCTTGGTAGCAGTCTTAGGCTTGG	64.495	140
HM_2302	contig29804	CAA	3	24	GAGAAATGCCACGACTCATCTCT	63.017	AATTCAGAGATTGGAGCTGTTTG	62.91	132
HM_2303	contig19477	CTT	3	12	ACACAGCTTCCAAGTACTTTCCT	63.027	TGGIAATTTCAAACTCAAGCCAA	62.637	152
HM_2304	contig20720	GTG	3	15	GGTCATTGTTCATCGGAATTGA	63.121	TCAACCAGaAAGAAcCAACTTGGA	62.367	154
HM_2305	contig22451	CAC	3	12	TACtGTTtCTCtCACTCACTCCAC	63.649	TCTAGTGAAGAAAGTCCATCAGCC	63.115	129
HM_2306	contig32340	AGG	3	36	GTCATTGAATCCAGACAATCCTCC	63.097	TATCTCGATCCAGCCAGTCTAACCC	62.913	157
HM_2307	contig46071	GGT	3	15	ACTCGATTGTCACCAAGACATAA	62.962	AGAcAGACAGAGAGGCCATAGTCG	63.353	115
HM_2308	contig29409	ATT	3	12	GAAAGTTTTCTGGCGAGAGTGGA	63.031	GTTGGGATGGAGGAGAAATaAGT	62.769	144
HM_2309	contig08886	ATC	3	12	TGGGAGATTATCTCGGTGAAACAT	63.009	TTTTGTGATCATTTGATGAGGGC	63.262	160
HM_2310	contig30175	TCC	3	12	CTCAGGACCCCTCTTCAATCAATG	63.3	AGTTAATTGAATCCGATGACGACG	63.438	128
HM_2311	contig21895	TCT	3	15	ATCCATAGCGGGACACAATAAAAA	62.948	ATGACGATGGAAGAAAGAACGAGC	63.017	137
HM_2312	contig24358	AGG	3	24	GTAAGAGGCATATTTTAAACCCCG	62.911	GAACCTTTATGTCAAGCTCGCAa	62.975	138
HM_2313	contig11188	CAT	3	12	CTCCATAGGgTCTCTAATGGgTT	62.767	TACACACAACACCAGTTCATGCTG	63.22	134
HM_2314	contig10781	GGT	3	15	TCCAATGGGAGATGTTCTCGAGAG	62.984	GGGATTCAACAACACAACATACA	62.934	159
HM_2315	contig12994	GAA	3	21	CTCCaAgTGTTCGACGAAGAACT	63.133	CAGCTTCTCTTCAATCCGaCAAT	63.022	92
HM_2316	contig28225	CAC	3	12	CATAGAGCTGCGAATCAGTCACAT	62.861	CTCAAGTTCAAGCGCAAACTCC	63.487	114
HM_2317	contig29581	GAA	3	21	TGGAAGAAACTGGAAATGGGTTTA	63.002	TCTCaTCCAGAAAGGAAATCagC	63	95
HM_2318	contig18168	GAA	3	12	CTTGATTGGGTAAgGGGTcAGAT	62.383	CtTTACCTTgtGCCcATTGAAGAT	62.619	151
HM_2319	contig34333	CAC	3	12	CTTCTCTCTCTCTCAACAGCAG	63.007	GAGGAACATTGGAGACCTCATCAT	62.772	131
HM_2320	contig08997	AGA	3	15	GAGACGAACAAGAATTAACGACAaA	61.839	CACCCACTTCTCTCTCTGTTTCT	62.397	117
HM_2321	contig05567	ATC	3	12	AgAAAGGCAATAaCTTCCCATgA	62.912	CTTGTTATGGCTGCCCAAGTAaAC	63.051	103
HM_2322	contig09207	ATC	3	18	GAAGACTCACTGCAAAACCTCCAA	62.809	TTATCTGcCGTAAAGATAGCGCA	63.142	142
HM_2323	contig13687	CTT	3	12	TCCTcGCATACtGtTTGAGATTC	62.728	GaGGAGAGATcCgAAGGAGGAG	62.938	141
HM_2324	contig41216	GTG	3	12	AACTCCAGCGTAATTACATTCCCA	62.935	CCTATCAGAAGACCGGTGGCT	62.772	155
HM_2325	contig38256	CAC	3	12	GATTCCCAACCAACCACTCACTA	63.15	GGCGCTCTGTTTTGTTGAATT	63.535	89
HM_2326	contig03868	CTT	3	12	TGCAAGACCTTCAaAaCAACATCA	63.034	AAAGAGAAACTCTGGTGAAGCAa	62.822	122
HM_2327	contig13997	GCT	3	18	TGACACACTCCCTCCACTATCTT	63.327	GTGAATCTGGCGAGACTACTGTGA	62.951	157
HM_2328	contig49117	CGA	3	12	CaGGGagAGCGTCGGAGATAC	63.465	GTACGGTCTCTTCTCTCAGCTT	63.518	122
HM_2329	contig00786	TGG	3	12	GATATCGAGGAGTGTGGAGAGTT	63.075	GGGCCATGATGGAGAGTTCA	63.358	141
HM_2330	contig07470	CAA	3	18	TGCGAACTATGCTCTCAGTTTCT	62.712	GTACAATCGTCCGCTGACTTCTCT	63.683	113
HM_2331	contig17541	CTT	3	12	CTTTCTCAAGTTCATCTCCACCG	63.42	CAAGGATGGTATCCATGCAAGTCT	63.544	159
HM_2332	contig27201	TCT	3	12	ICTTCGGTGTAGTtTgcGaaCATTA	62.969	TATACCTCACTCCaCTCCAaAGC	62.811	156
HM_2333	contig09284	CGC	3	15	GTTTAlCcTCTCCGAATACGGGCT	64.71	GAAAGGGAAAGAAACCgAAGAGG	64.482	143
HM_2334	contig26665	ATC	3	12	TTCCGCTAGGAAGAATGGTTTAA	63.034	GCAAGGTGTCTAGCCATGAGAAT	62.94	148
HM_2335	contig45847	ATG	3	12	GAAGATGAAGAAGAAGCGCTCTG	62.811	CTCTcTcCAAAcCCCTcACTCaTa	62.984	131
HM_2336	contig22210	TAC	3	36	TTTTAACTTCCACTTTGGTCCGA	63.011	AAAGAAGAGGCGAGCTGaCaATA	63.781	156
HM_2337	contig10229	TCT	3	12	TGAGCATACTTGAGAGTGCCATTG	63.719	AGCAGTAATGGTGATCAGGGTGT	63.141	146
HM_2338	contig29644	TCT	3	24	GGAAACAGCCATCTTCTTTCTCTCT	62.603	TAACAAGAGAGATGGACACACCCA	63.026	95
HM_2339	contig32770	TAG	3	12	ATCTGATCTGAGGTTgGTGGGCT	62.994	CGCAAGGAATGGAACCTACACTCT	62.933	146
HM_2340	contig00672	TTC	3	12	GTGGGTCTCTATGTGTTTCGCTAGA	62.923	GTCCGAGAGATCTGTGCCTATGTT	63.031	151
HM_2341	contig14598	GAA	3	15	AAgaGAGTCTTTGGGCGAGC	63.014	TcCaaAcCCCTATCTCTTTTCTC	62.958	122
HM_2342	contig40901	ATC	3	12	AGCGATAaCcCGTATCTTTCTCT	63.093	aagacacaaacaggcatgtcaaaa	62.958	136
HM_2343	contig16949	TCG	3	12	CTCGCACTAGAACTCGTGAAGGT	63.044	CATCGATCCCACTATATATTGTTGATT	63.028	153
HM_2344	contig27537	AAG	3	12	TGGTCAAGAATACTCCAGAAAGGTA	63.091	TGacCaTTTcTTTAACTTccCaA	62.894	135
HM_2345	contig27572	TGT	3	18	ATTCTGATTTTGTGtGtGCTGCTG	62.657	GGGATTTATGGGCAGATGAATTTT	63.275	93
HM_2346	contig32481	TGA	3	15	TTCTCCCACTAACCAACTCTGA	63	AagaTGGGTGAATTTTGGGAAT	62.878	92
HM_2347	contig42401	ACC	3	15	CTAACCTTAATGCCAAAGCCCAT	63.486	TAGAGGACTAGCTTGACCAcCACc	63.023	150
HM_2348	contig18190	TCA	3	15	CATTtTtCGCTtCTTCTCTCTCT	62.714	AATTGGGATGATATTCTGGGTCa	62.679	159
HM_2349	contig44276	TGC	3	21	CATTCTGTGCCCAACTTTGT	63.109	AATTAAGCAAGGGAACAACAGCa	63.146	136
HM_2350	contig04739	GAT	3	12	AAGTCGATTTGGCTCAAAAGAAC	62.833	CTTCAACATCTCTGCGCTATGCTT	63.035	100
HM_2351	contig02596	ATA	3	12	CCCTAAACTAAATTAAGATTCCCA	62.479	TgGAggGCTTTCTTAAATGTGAAC	62.716	90
HM_2352	contig03942	TCT	3	21	TCTTCTAGGTGCCCTAAACTGTGG	62.918	ATCATCTAGCAGAAGAAGACCGGA	62.7	156
HM_2353	contig03030	GGT	3	21	CTGGTGGTGGATGCTCTCTTTTT	63.86	CCTCTCATCTCTCAGTCgGAGTC	62.991	112
HM_2354	contig32323	GGT	3	12	AATCGACTTGGTTGAGGATTGAAG	62.798	AATTCCTCATCTTTGAACTGACGA	63.108	141
HM_2355	contig22088	GCG	3	15	TGTCACACTACTACTTTTTCGCCA	63.07	ACACGTCGAAGACGGGTAAATCAT	62.949	146
HM_2356	contig43671	TCG	3	21	CTCTTCTCGACTTCTCTCAACGTC	62.909	CTCCGGTTCACTCTGTAGATGATG	62.26	152
HM_2357	contig51206	TCT	3	24	ATATATGAATGCCACGAGGTTGT	62.733	AGAAATaGtcGGAGTCGAGTCAa	62.598	146
HM_2358	contig09244	CTC	3	12	TGGTGAAGCTTCTGATTAGACGTG	62.842	TgGGTTTAAGaAAAGATGAGGAGG	61.887	151
HM_2359	contig39537	TCA	3	12	ATTGTGCTTCAGCTTATCCCATCT	62.733	GTTAAAGGTGCGCTCTCAGAAAGa	63.251	133
HM_2360	contig26747	TTG	3	12	AGCTtgatgaactccgtattg	62.947	TTCAAGTACGTATTACATtctggtgct	62.359	136
HM_2361	contig47272	TAC	3	24	TGTCTCATCTTCTCGAACACTTG	62.945	AAATTTTGATCAGATCGaCGAGGAG	62.9	125
HM_2362	contig17499	AGG	3	12	GATAAGTAACCGAGGGCGTAGGAT	62.822	ATGAAGAAGAcctACCACACCA	63.111	134
HM_2363	contig30870	TTG	3	12	GCAATAGGATTGTTGGTTGATGC	63.758	GGGGTCTGTAACAGTGAGAAGCTG	63.564	83
HM_2364	contig31640	CCA	3	12	GgaAAGGaTtaTTTGCTCGAAGTCA	62.815	CTGTTCCGCCACTAGTAGCATTGT	63.784	137
HM_2365	contig19543	GAT	3	12	CGGAAGAAGACGATGATACAGAGA	61.95	gCtTcTcccaAAATGCTGtCTAT	62.213	110
HM_2366	contig46310	CTC	3	18	GAGTAAGTTTGAATTGGCCACTCG	63.256	CaAGCAGACAGACGAGCAGATAAGA	62.649	133
HM_2367	contig32794	CTC	3	15	GcctGACTCACTCACTCACTCACT	62.365	cGTAGaACAAGATAGTAAGAGTAGCGAA	61.663	140
HM_2368	contig16537	GGC	3	12	GACGCTGAACCTGATGCAIATGTA	63.517	AGAGTcTAAACCATGGCGAATCTG	62.923	117
HM_2369	contig09568	GAT	3	18	TATGATAAGCAACCACTTACCCCA	62.525	CATCGGAAGCTACATGTGCTGATA	63.499	133
HM_2370	contig21122	GTG	3	18	ACTGTTGAATTCTCGgTGTCTCT	62.912	CTCGCTCTTGTGCTCTCTTTTC	63.739	147
HM_2371	contig38267	ATC	3	18	AGGGTTTGGATCTGCGGTTGTTC	62.992	ATCACTCATCACACATCAATGGC	63.272	115
HM_2372	contig24960	TCT	3	12	AGCTGGGACTTGATCTCCAATatg	62.8	TCGACAaCTTTACaCatCAGGGA	62.921	152
HM_2373	contig20765	AGC	3	12	AACTTTGGGATGTTCTTCCCTCT	62.876	GGCCTTCTTACGAGAGTGGTCT	63.408	116
HM_2374	contig43855	TCT	3	21	TCCGGTGAAGAGAAcATAACTGA	63.154	GAATGTGTGAATGACAGTTTCAa	63.27	139
HM_2375	contig18703	GAT	3	18	TGgACACAATTGGGTCaCaTAAAC	63.168	CCCATTCCTTATTACACCAATTCA	62.993	120

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2376	contig50060	TGT	3	12	CTTCACAGCCATATAACACCTCC	63.022	ATAACCACTTCATCAAAACGCACC	63.353	152
HM_2377	contig40975	ATC	3	15	CTTGTTGGCTGTGTGGAATACAG	62.945	GAAGCTCaaAAACCTTCAAGGACA	63.019	134
HM_2378	contig43321	GAA	3	18	CATTGCTTGGTGAATAATGTTGTA	63.055	CCTCTGGAATAATCTCATTGTTG	63.091	94
HM_2379	contig48915	CAC	3	12	CTTGGAACAATTCTCTCCAAATC	62.996	GACTCAAATTCAGCACAGCATCAG	63.401	154
HM_2380	contig00223	TTA	3	15	TGCCCTTAAGCTGTAAACACAAAGA	63.257	AATTCATCTTCGCAAGCAAG	63.643	154
HM_2381	contig37518	ATC	3	12	CACAGTGGCATTAAAGTCTCTCCA	62.724	gGGTTTGATTCACATCTGCTGAC	62.8	150
HM_2382	contig37983	CCG	3	12	TCAAATTAATAATCaaCAAAATCC	63.092	TATGATAGAGGGGAGGACATGGAA	62.974	147
HM_2383	contig02782	CCA	3	12	CACGTGCTATTGTGGCCCTATC	63.022	ATTCTCTGTAGACCGGGTTTGG	63.791	106
HM_2384	contig07236	CCA	3	12	GAGGCGTTGTCCATCTTCATAAAC	63.137	CTTCGATGATGTGCAGCTGAG	63.3	160
HM_2385	contig39288	CGC	3	12	GTCTTGTATGGCTCTATCATCTT	63.042	tTCaTATCATCATCAACGCCATC	63.044	148
HM_2386	contig01253	GGC	3	12	CACCACCTCCAAACGATaGAAAT	63.219	AATGAAAGTTTCGGTCTCTGTTCA	63.227	136
HM_2387	contig17305	CGC	3	12	ACTCTGCTTCAACCCATCAATCTC	63.017	GGTAGGACGGTAGCTGGAATTTCT	63.008	130
HM_2388	contig29338	GAG	3	12	AGAGAAGTGACATTAACTGGAGGCA	63.561	CCCTACAAAACCTATGCTGAGGT	63.693	122
HM_2389	contig36402	GGC	3	15	GGACAACAACATCTCTCCCCAT	63.531	tTAGGGTTGGAGaGaAATCAACTG	62.782	143
HM_2390	contig34968	AAG	3	15	TCGGAAGAATAAATGAAGAAGAAA	62.237	ACTGACTCTGgaATTGGGATGTCT	62.397	160
HM_2391	contig04233	CCA	3	12	GGTTCACGATTTTCATCGTTAGTT	63.462	TTAGACgGTGACCCAGAGAAGCTC	63.01	89
HM_2392	contig23641	GAG	3	12	CAAGACCAAGGAAGAACTCGTAA	62.905	TATATGGGACTTCTTCGGGTTCAA	62.896	159
HM_2393	contig00606	TCT	3	12	GGCTGAgaAGGTCaAAGATTGAA	62.91	CACACTGTTTAAATGGGGTGAGCC	63.031	128
HM_2394	contig40475	TTC	3	30	AGTCTGATATGGAGGATGACCGAA	63.209	ATCTCCGGAAGAACAATTTTCCG	63.877	160
HM_2395	contig30812	TGT	3	12	GAGCAATTCCAGATGGGACTAAAA	62.705	GTATCGTCTACGGATGGAATGGAC	62.916	109
HM_2396	contig44686	AGA	3	12	CAGAGAGAAGAATGGGGAAGAAG	61.842	TGAATCTCAACTCTTTCTTTCTGA	61.674	159
HM_2397	contig01257	GGT	3	15	GGCACTTTTAGTCAcAGTCC	62.439	ATTCAAATGCTGTGACCGAGTA	62.936	150
HM_2398	contig48123	GTG	3	12	TGAGCAATTTTGGAGTCTTTGATG	62.615	CTCTATCTCACTCATCTCCACG	62.784	149
HM_2399	contig31056	CTT	3	12	GATAAAGTCTGTTTCTCTCGCA	62.716	AAGAACATGAGCGCTCAAGAATTT	62.425	157
HM_2400	contig07270	TCA	3	12	CTGaTCAACCTTTTCGATTCT	63.772	tttttgaatttgagaagtgagg	62.798	118
HM_2401	contig15798	TCA	3	15	GCAATTCCGtTCTCaGGTAGTTA	62.729	CAAAGTTGGGTTTCTCTCAATGG	63.1	145
HM_2402	contig26237	ATC	3	12	TATAAGCCCTCTAAACCCAAAA	62.986	AGTGCATGCAAGGCCACAGATA	63.078	131
HM_2403	contig01155	ACA	3	12	aCCCCaCACATGGAATCAACAGAT	62.912	ATGAGAAGAAGACGGAGACTCTGTG	63.34	144
HM_2404	contig21021	GTT	3	12	GCTGTTGTTGGAAGAGATGGTTT	62.824	CCaTCTCTCAGATCTTTCaACGG	63.413	121
HM_2405	contig01694	CAC	3	12	AGCTAAGACAAGCGTCTCTCAAGA	62.946	GTCGACCACTTGAATAACAAAGCG	63.146	157
HM_2406	contig11869	TTT	3	15	CcACCAACGCTTAATAAACTGAA	63.329	CATTTTGAAGCTAGGGTTAGGGT	62.806	135
HM_2407	contig02821	TTC	3	18	CGGATTCAACAATAAGGGACTACG	62.919	CGATTTCTGATTTCTCACTCATC	63.112	87
HM_2408	contig19142	GGT	3	21	AATCTTCATCAACAGCTTTGGGAG	62.91	TTACCCACATGTGAAAGAAAGCaA	62.843	137
HM_2409	contig04041	GAC	3	12	CTCTGAGACCAACCTCCATTGAT	62.884	TCACTACTCTCTCCCAAGTCCC	63.106	160
HM_2410	contig14718	CTG	3	18	GTCACCATTTGATGCGTTGTGATG	62.844	AATAGGCCATGGATGAATCAGAAC	62.496	124
HM_2411	contig02341	GCC	3	12	TACAATCTCcACCACTCCACCAC	62.276	GCAATAGTGGAAAGGCAAGAAAGA	62.935	160
HM_2412	contig10188	CAT	3	12	AGAAAGAGCTTCTCCGAAAAGTGA	62.102	TCAATATATGAATTGATGGCGTGC	62.966	159
HM_2413	contig15295	TGG	3	12	AAAAaCCTTtCTGACCGTGGTTt	63.199	TtTCTCTCTCTCAGAGCCAGTTA	62.997	139
HM_2414	contig02520	TGC	3	12	AAGCTATCGTCTCGTCTGATCTC	63.718	AGTGATCGTCTCTGgaAGTCaC	62.898	146
HM_2415	contig20146	CCG	3	12	TGCGTATTCTCGACcACCGTC	63.033	AgaCGATCTGGAAGTCCCAAAAC	62.886	137
HM_2416	contig39016	ATC	3	18	CTCAAGGTTGAAGAACCATCTc	62.598	TGTCAGAATTGGAGTGATAAGGCA	63.038	141
HM_2417	contig22621	TCT	3	12	TATTtTTTCGAGTCTCTCTGCGC	63.027	AAGCATGTTAGGGAGATGCAAGAG	63.035	132
HM_2418	contig00161	TTG	3	12	TCTTACGGCAAGAACAATCAAAA	62.956	TTGACGCAATTACAATAACAACG	62.978	144
HM_2419	contig04967	TGA	3	12	CCAGTGTGAATAGAGGACGAGCTT	63.137	GGAAACTCTGAACAACCTTAGCAA	62.921	85
HM_2420	contig01634	TTG	3	18	TAGGGAATGAGGAGGAGACGACGA	62.795	CTGCTCTCTGTTGATGCTTGAGA	63.074	158
HM_2421	contig00652	CCT	3	21	GTGTACGGGATCAACCTCTGTGAT	63.794	ACATTCTTGCTGTTGTTGACGAGA	63.291	146
HM_2422	contig36082	GGT	3	15	CGTGATCGTCAAGATTGAGAATTG	63.038	AACCTGAATATACCAAAACACCCC	63.285	80
HM_2423	contig39430	CAT	3	12	ATTCACAAACGCCCCAAGCAATAA	62.95	CGGGAACCAATcGTAGATAATGA	63.209	138
HM_2424	contig47187	CCT	3	12	TCTTATGATCAGCCCTTCTGTTT	62.815	AGCAATTCATTTGGGTTGTAGGA	62.922	127
HM_2425	contig24108	TAG	3	12	CTCTATCAACCACTGAaaaaCCAG	62.993	TTTGATCTTCATCTCATCTTCTCA	63.015	124
HM_2426	contig04412	GAC	3	18	ACCTTGTGGAaGaaGAACCTCACG	63.02	ATCATCTCTCTCTcGTCTCTCT	62.265	152
HM_2427	contig05202	GTT	3	12	CATGGAGGCCATTAGTTATCGAAC	62.925	CGATGAGCTTGTAAATCAAGCTT	62.947	113
HM_2428	contig10724	GAA	3	12	TTCTTCAACCACTCTCTATTTTC	62.784	GTACTCGAGAGCTAGGGTTGTGCG	62.752	139
HM_2429	contig18276	TTC	3	12	TAATTCAGACCACTCTTCAACT	62.368	aAGTTGAAGAGAGAAGGGAACCG	63.28	160
HM_2430	contig42485	AGA	3	24	AGCAGGGTTGTATAGGAATAACA	62.935	AGTTCTCTCAACTTTGGGCTCC	62.266	96
HM_2431	contig03866	TCT	3	12	TCATCTGGAGTTTCTCTcCATC	62.977	agtaaggagagaaccccttaggg	63.106	127
HM_2432	contig08920	GAC	3	15	GACCCCAAAATCAACACGATAG	62.897	AAATTTGGTGAAGTTTTCaATGC	62.888	114
HM_2433	contig15849	CTT	3	12	TTGTAGGGACATGATACGACTGG	62.502	GCTTCTGCTCAATGGCTAGGATA	63.046	91
HM_2434	contig24945	GAT	3	12	TCTCTACACTCTCGGCTGTTGTG	63.063	gTCACTCACTCGAGGCAACTTAC	63.356	142
HM_2435	contig35432	TCA	3	12	TTGCAACACTACAAGAAcTGAA	63.172	ttaattttcttggatcaacc	62.301	151
HM_2436	contig00221	GAG	3	12	TTTGAACCTGGGTGTAGGAGAGAG	62.993	CATCGATcAcAcCTCCAATTTTC	62.819	134
HM_2437	contig31683	CTT	3	12	CATCAAACTTCTCGTGTACTGCT	62.14	ATTGCAAGGTAGAGTGACCAAGG	62.822	159
HM_2438	contig40883	TTG	3	12	GGTTTGATTGTTGTGACCACTCTC	63.558	TTGAATCAAAATCAACCAAGaGAA	62.703	80
HM_2439	contig30440	CTG	3	21	CTCACAGTTTCAAGAATTGTCCG	62.192	CACAACATAAGACCTCTTTGGAG	62.482	156
HM_2440	contig06656	TTC	3	18	ATCTCAGTTCCCAATCTTTTGCTG	62.91	GAAGAAGATGGAGAGGAGAGTCA	62.427	132
HM_2441	contig15211	CCA	3	12	GAAGGTTGTACACGGAACAGAG	63.138	GATTACGCAAGTCAATCAGTTCA	62.529	110
HM_2442	contig17163	CTC	3	12	TATATTCTCTCTCTCTCTCGCC	63.176	GCTAGGGACATGTTTGAATTGGAAC	63.026	111
HM_2443	contig25519	TCA	3	12	GTCAGATAGCTCAATTCCGCACT	63.051	ACCACCAATTCAGTCTACGaAAG	62.71	127
HM_2444	contig35340	TTC	3	12	ATCTGAGGCACTCATCTCAAGT	62.694	TGACCACTGTGATGTTTCTCTTA	62.601	121
HM_2445	contig01888	TGC	3	15	AGCAAAATGATCGAATCTTtCtCG	62.935	GATCGTcGCCCTATCATCTAAC	63.118	106
HM_2446	contig16389	CCG	3	12	CGAAGTCCGACTCTCTCTGTTTC	62.909	GAGAGGGTCAAGCTGGAACAGG	63.475	143
HM_2447	contig23918	CTT	3	36	TAAGGCAATTGTTTGACGACCTT	63.039	GTTATGTTTGGAAATTGCGCAT	63.227	141
HM_2448	contig05831	TGC	3	15	CTGACTGAAGGAGATGTGAAAGCA	63.04	GTTGTTTGCAGGATCAAAACAGT	63.561	142
HM_2449	contig45833	TCT	3	12	TTGcTATTTaCTAGTTTcTaGGGTGA	61.561	TAGGATACGGAGACGCTAGGATA	62.328	152
HM_2450	contig08040	AAC	3	12	ATTGGTATTGAGAGTATTGGGCT	62.903	GTCAACTGGTGAAGTGTCCAATTG	62.933	150
HM_2451	contig12774	TCT	3	18	AGCTAAAGGAAGGaGGGAATGAATG	63.078	ATGTTATgCTTCATATGCTCGGT	62.953	158
HM_2452	contig46312	AGA	3	12	TTAGAAaCcGCCATTTTTCAGAGA	63.216	GAAACAGCAAGCCCAATGTGAG	64.16	119
HM_2453	contig34161	GGT	3	18	TTGGgATAATtGgTGAaAcCaG	62.097	ACATGtTTGGCTTaTGGAAAGAA	62.922	87
HM_2454	contig36908	TTC	3	12	TGAAATTGGTTTTGAAGGTTGGTT	62.811	AGtGTaGAGACCAaACCAAGCAAGG	63.033	142
HM_2455	contig29292	TCA	3	12	TGATGTGAAATGAAGCAAGTGGT	62.948	CATTAAAGAcTTCaCcaAGTGGTTT	62.737	136
HM_2456	contig45394	ACA	3	12	CGGACATAACGAGCATACCAATTA	62.161	GCTGTAGTcATcAGACCTGTGCTG	62.255	94
HM_2457	contig36494	GTT	3	30	CCACTCTGAGTcctGACAAGTTGA	63.027	AATTGCAAGAGAGATTGTgTCTCT	62.926	146
HM_2458	contig25974	GAG	3	12	TaTAGGGATCGAATGTGTGCGTTT	62.815	CACTTTGCCTCTCTTTCTCATC	62.698	149
HM_2459	contig14553	TTC	3	15	GATTGAGCTTGGGATGAGAAGAA	63.236	AGCTCGTCTGAGGATGATTGGAAG	63.23	158
HM_2460	contig01874	CCT	3	15	CACATGAGTATGTTCCGCTGTAGC	62.975	AAGGTGAAATTTGAAGAACCCACA	63.006	90
HM_2461	contig06270	GGT	3	15	AGTTTGGAACTCATCAAGCAAT	63.146	TGAACCTCTCAGACCTAATGACG	63.856	156
HM_2462	contig17958	CTT	3	12	CGAAGTAGGTGACGAAGTTGGATT	62.822	TTCTGTTTCTCTGCTTCAAAAC	63.019	150
HM_2463	contig50148	CCT	3	21	AGAATCAGAAGAGTACCACCACG	62.909	TGaGAAACAAATATGGCAAGGGT	62.922	130
HM_2464	contig30209	CTG	3	15	GGCTGAAGTGTGCGAGATCTCA	63.166	TCCATCGAGTTCAACTCTTCTTCC	63.102	144
HM_2465	contig03428	CAA	3	36	AACCATCAAAACAAATcaACCAG	63.214	AACTTTTGGATGCAAAATAGGGGT	63.004	138
HM_2466	contig20869	TTC	3	24	CCCTGTTTTTCCCCCTTCTTCTAT	63.598	CCGAAACGTTGGTCTCATCTTCTA	63.739	129
HM_2467	contig12332	TCT	3	15	CcACATGAAATGTGGAAGTTTCTC	62.996	TTGACAGCTGTTGAGGTGATTAG	62.958	137
HM_2468	contig11830	ACC	3	21	GAGCCTTCAACAGATCTGATGTT	62.926	TGGTAGAAGGAATGAATGCAAGT	63.121	146
HM_2469	contig01106	CAC	3	15	gATCAAAACCAACCCAAAcAT	63.097	gTGATTAGGAAGTTGAGGTGGC	63.242	156
HM_2470	contig48312	AGG	3	12	AAGCGGGGTATCTGTTGTTTTTT	63.115	CCCTTTACACAGCCCATATGATT	62.815	158

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2471	contig42560	AGC	3	12	CATatCGTCATCGCTCTCTCTTT	63.026	ATCATTGGTGGAGGTGGTGGT	63.699	147
HM_2472	contig12887	GTT	3	15	GACCATTTGTTGAAGTCTTTGGG	63.006	GGAAGTCCAAGTcCAAGTTGAAGa	62.997	154
HM_2473	contig38103	AAG	3	12	ATGGAGAAGAAATGGAAGGGAAAC	62.865	CTTCTTCTTCTTCAATTTTGGAAAC	62.329	92
HM_2474	contig16142	GGC	3	12	GCgATGGTCAAGAAGTTATGGAG	63.231	TCAAATCCTCGGGCTATAAAATCCA	62.911	100
HM_2475	contig40130	CTT	3	12	GCTCATCAAGAATGgCAAGAAAG	63.438	GAgGGGAATTGGTTAGAGAAGAA	62.958	121
HM_2476	contig42096	CAA	3	24	ATCTCATCGTCAACCATTTTCATC	63.431	ATTAACTGATCGGGATCAGAAGA	63.112	122
HM_2477	contig11545	GTT	3	12	CATTGGGAATTTAGTTTGTGGGAg	62.798	CTGTTTGATCAAAATCTCTGACCC	63.009	143
HM_2478	contig09262	GTC	3	18	GTCTCCATCTTCAGCTTGGTCTTC	62.798	GGCTTCTCTCAGGAGACtACTcC	62.939	100
HM_2479	contig38373	TCA	3	15	tATTTCACCTTCcACTTCaAgCtC	62.91	AGaTCTCTACTCATCAGCCGCATC	63.252	143
HM_2480	contig02347	TGA	3	12	GGAGTGGCTTCTGCTAGTATCT	63.205	TTCTCTTCTTCTTGAAGATaGCCAA	62.919	152
HM_2481	contig35362	GTC	3	12	TTCTTCTGTTAGCGCTcTTCTTC	62.425	TCACGAGGTCTCAAAATTTTCCAAT	63.108	104
HM_2482	contig41219	TGC	3	12	TGATGAAGATGAAGTTGACCGAGA	63.243	ACCTCCAAGAAGAAAGTGTGGAG	63.115	157
HM_2483	contig34824	TCC	3	21	CTGAAGTTGAGCTCTCTTCGCT	62.411	AGTTATAGCTCTGCTTCgGACTCG	62.341	112
HM_2484	contig15882	TTT	3	12	AATTGAATCAACTCTTTCGTCTG	62.841	tTtGctaaAAAGCaAGAGCAATC	62.957	126
HM_2485	contig17919	ATT	3	15	GAGgCGgTtGtTtGtTATtGATTAg	62.935	TGGAGAAACCatCTTAATCTCTCG	62.894	118
HM_2486	contig05359	GTT	3	12	ACGTCAACCCtAAGGAGAAAAATC	62.888	CTACTGAAATGCTGGTGTCAATG	62.945	144
HM_2487	contig18921	GTG	3	12	CAAACTAGCTCGGGTCTTCAAAA	62.919	CAGATGGATCTGTACTATTCTGGC	63.125	114
HM_2488	contig26361	CTC	3	12	TTTTCTCAATCTCTCAATCGGTAA	62.993	GTAGTCAGTGGCGGAGAGTTCAG	63.677	158
HM_2489	contig02060	CTT	3	18	TTAAGTTTCTTCAATTAGCAGCCG	61.032	TGAGCAAAcAATAAAGGTGTACGGA	60.897	130
HM_2490	contig22988	CTT	3	15	AGaCTCGGAAGTGAATTGTgACTCC	63.123	AGcAAATaGATcAACCcAAAcAa	62.922	126
HM_2491	contig14509	GAA	3	15	CGAGGAGTTTATGCCAGATGAGAT	62.913	TTTCTGCAAAAGAGGACCTACTTA	62.508	104
HM_2492	contig46150	TCG	3	12	TACATTGTCAGAGAATCAGATGG	63.486	GGGGTAAGAGAAAGTGTGGTGAGA	62.895	160
HM_2493	contig00804	ACA	3	12	agTAGATTGCCAGGAaTCAGGCAG	62.936	acGAGGAGCAGAACCTTGAAGTGT	62.823	147
HM_2494	contig09414	GAA	3	12	CGAGCTCAGGAGGAGAAAGTAGATG	63.01	TTGTTGCTCTCATCTCCAAGAAA	63.141	91
HM_2495	contig05711	TCA	3	15	CATGGTTTAAcTGAACTcGCTCC	63.019	AGAAATGTTACCGGAcGAAAGGAT	63.196	135
HM_2496	contig39945	TCT	3	12	TCTtGTtGAATtGTGTGTCATGG	63.137	GTTCTACTCTCTCAAGCCTGTT	63.201	145
HM_2497	contig19078	CAA	3	15	TGCGAATTTGTTATACCTAaGAACCC	62.585	TTCTTCTATCTCTTtGCTTTCTCT	62.69	141
HM_2498	contig34258	TCT	3	12	AGGAGGAGCTGCTTCTATCATCA	62.813	CAAAACCCAATTTCTCATCTGGTC	62.996	152
HM_2499	contig44449	TGC	3	21	GAGACATAGGACCCACATTGAACC	63.004	GGAGTTATGAGCAACAGCAAAACC	63.256	159
HM_2500	contig21482	TAA	3	12	CTTCTCTGCTTCAaCCAGTGCTA	62.222	CTTGTCCTAGTGGTGGCTtAIt	63.044	124
HM_2501	contig08371	ATG	3	12	CGATCACAGCGAATCTTCTCTC	63.355	CTCGATCGACATGTTCAACG	62.817	139
HM_2502	contig35218	ATC	3	12	TATGAGTTTCATCAAGGGGAGAGA	63.293	TACAGACCCAGTACCTCATCCAT	63	106
HM_2503	contig34157	CGA	3	12	ATTGATAGTGCTTCCCAGAGTCT	63.505	GAcCGATCAGTTTtCAACCACAAG	64.079	139
HM_2504	contig14917	TTG	3	30	TACCAGCAGCAGCATCTACaCTGT	62.455	AGATGATATcGTCCaACCGCTTTTA	63.034	128
HM_2505	contig07188	ACG	3	18	GTTGACGAGACGAATATCGGAAAC	63.137	AGCGTCCATCCAGGAAGAGTC	62.997	141
HM_2506	contig14936	TCC	3	12	AAAAATTGATTCCAaCTCTCTCTCT	62.988	AGtCTTTTCAAGAGTCTGAGTGA	63.456	97
HM_2507	contig36104	GCG	3	12	ATCCATCCCACTAGTACCAGCAAC	63.68	TTTGTGATGTATGGTAaCtCC	63.018	132
HM_2508	contig32242	GGA	3	12	ACCTTCAATGTGGTATGATTGGG	63.108	AAGCATGAATCTGGAAAACCTCG	62.826	87
HM_2509	contig16593	AAT	3	12	CAAACTCGATCCAATCTCACTAAT	61.549	GCAGTtTTTtATCTGCTTCTATCTCT	60.591	123
HM_2510	contig34263	GAG	3	12	GTACCAAAAGGACCCCTGAAAG	63.072	GCTTTATGGGTACTCTCAACAACG	63.142	135
HM_2511	contig16892	GGC	3	15	gCTGCTCGGTACGAaATGaGAAT	62.867	CTCTCTCCAAaATCAGAGAATCC	62.455	121
HM_2512	contig38853	CTT	3	12	CACCTAGGAGTCCCGaTCTTTTt	62.971	GTAATtTTGCTgGGGaTGGATTA	63.109	151
HM_2513	contig01487	CGG	3	12	AGGTTTAGGTTTCCaATGACAGGC	63.7	ACAACCCAATGGAATCACTCTAC	63.23	159
HM_2514	contig35862	AAG	3	24	CCAGACCAGACTGATCACAAGTIA	62.69	TTTTGCAATTTGAACCCCAATTTc	63.026	110
HM_2515	contig03868	ATC	3	12	tTCGAATGAaACCTTAATCCAGAA	62.993	GATGAaAGCAACGACAACAACAAC	62.975	122
HM_2516	contig18784	AGA	3	21	CtCtTtCATAGCTCAACAGCTTC	62.824	gACGCTCCACAGCTTCTTGAAGT	63.05	138
HM_2517	contig20458	GGC	3	12	CATTGAGGGTAGAACGGTCAATTC	63.009	AGaAACCCCAaATCCCACTATAA	62.703	102
HM_2518	contig29892	TTG	3	12	AGCATGTGATTtGAGAAcCATGTG	63.388	AAATgCTCTCAATtGCAACTTCTTC	62.841	139
HM_2519	contig17295	GTG	3	24	GACTCTCTGAAGCTCTCTCTCC	63.402	CAAAACCTTAACCAACCAACTC	62.893	144
HM_2520	contig17626	CCA	3	15	ACAAAACCACTTCACAaACCTTA	62.918	GaCGGGGTGACTAAGGTAGGT	62.664	152
HM_2521	contig09244	CAC	3	12	GACCCCTGTTCCACCATCTGAaAC	63.023	GGATGAAGAAGTGGTGTGCTAA	63.648	142
HM_2522	contig11565	CAC	3	18	CGCTATGTCAAGAGGCAAGAGTTA	62.156	ATGGATTGTCCATCTCAAGTGT	63.004	151
HM_2523	contig20193	AGA	3	12	TGCTACCTCAGTAGGATTTCCGG	63.019	CTTCTCTGTTCTCTCTGcTCTA	62.597	134
HM_2524	contig35034	ATC	3	12	TGACAAGAGATTCCACCGCTACTT	63.225	GCCTTCAAGGGATGAGCAAACT	62.925	104
HM_2525	contig03798	GTG	3	12	CgATACAGAATCACTTGTCTCT	62.698	TATGaAGTCTCCCACTCCtCA	63.3	100
HM_2526	contig24707	ATC	3	12	CAGAGGCCAAAGTCAATGTCACTA	62.724	TACAGGAAGGAGGAACAGGAACAGG	62.993	147
HM_2527	contig15685	CTG	3	12	ACTTATCGCCCTCaTACGTTTCAA	63.043	AATGAGATGACAACGAGGAaAAGG	62.798	133
HM_2528	contig27949	CCG	3	15	TCTTCAGAGCTAGGAGGAGATGA	62.987	GAttTccCTCGGcTCTCAIt	63.839	92
HM_2529	contig31894	ATC	3	21	ATGAAGAAGCAAAACCACTATG	62.922	TTTATGCCATCTCTGGAAGCAT	63.13	126
HM_2530	contig20458	GGT	3	24	GCTGGGTCTGATCTGGGTTCT	62.869	CAGAAGAATCTCCACCACCACT	62.895	152
HM_2531	contig20377	TTT	3	12	CAATTTACACAATCTCGGACAAC	62.883	CCCCGGATTATTGCTACTTACTCT	62.514	157
HM_2532	contig15329	AGC	3	12	TATATACAATGAaAGCCCTCCCC	63.271	AGAAAGAGAAAACCTTCATGGCT	62.793	102
HM_2533	contig41454	TCT	3	15	TCTTCCACACTCTCCCTTATCA	63.3	ATTTGGTACAAATCCtGGGTGGT	63.689	138
HM_2534	contig40138	TCT	3	24	CTTCTGTTGATCTAGGAGCTAGGG	63.576	CaACAGCGAGaGAGCAAACTTA	62.827	117
HM_2535	contig45922	AAG	3	18	GATTAGGGTAACAATAGCAACGCG	62.09	TTCTCTCTTTTATTCGtATTCGGAG	61.299	137
HM_2536	contig48544	AAG	3	15	GTTCCTCTTTTGTCTCTATCTCT	62.876	CTCTCTCTCTCTCTGCTCTCTCT	62.873	135
HM_2537	contig23365	TCC	3	21	CATCAACTCTCTCTCACTGGTT	62.895	TATGGGAGGAGAGGTTGAGAGAAT	63.576	115
HM_2538	contig14411	GGT	3	18	AAGGaTAGGGGTGGAaATAGGGT	63.14	GTCGAGTTTCCTGGAACACAGAT	62.695	150
HM_2539	contig03484	TGA	3	12	TTTATCTCTCAGAAGCTGAACAGC	63.133	TTCAAAATCAGAGACTCCACTCCC	62.987	130
HM_2540	contig32310	GAT	3	12	AATGCCGTGGATTATGTAATCTG	63.041	GTCGCAATCCAGCTCAATAAAAC	63.154	110
HM_2541	contig11255	GCT	3	15	GTCTTGTAGGCTCTACATCTCT	62.484	TCTATTCTCCGACTCATCTCTCG	62.987	142
HM_2542	contig09306	GGT	3	18	GGaGAAATTTCAATGCTGCTTAA	62.735	CAAAAGGAATCAGCAATCTTGACA	62.615	154
HM_2543	contig17623	GGT	3	18	ACGTGGGAGaGGTTTGTGATAAG	62.822	TCTGCAACAATGAACAATATGGC	63.397	98
HM_2544	contig10992	GAT	3	12	ACAGAGGTGCATCTTCAATCTCT	62.812	ATTGGTCTTCCAACCATGAAGAAG	62.684	121
HM_2545	contig34189	GGC	3	12	AGTCGGAcTCCCTCTtTtCTTTC	62.666	TCTCTTGAACCCAAATCAACAT	62.996	138
HM_2546	contig28786	GAG	3	12	AAGAGGAAaAGACCGAAATGAG	63.074	ATTTTaAgTTGTGCTCCATGCT	62.987	145
HM_2547	contig32027	GAG	3	15	TGGTCTTCTTCTGATTGAGCTTCT	62.811	TCTGTATAAcCaAGTGAACCCA	62.71	96
HM_2548	contig21951	CGC	3	15	AATGAAGAGATGGTTGCTGATTC	62.802	AAGTtTtGTGCAAGGCAAAATCT	63.563	128
HM_2549	contig44126	TGC	3	15	TTGTAGGACATGATCATCTGGTG	63.243	ATCAAAAGGaCATGATTTTGGGAC	62.383	85
HM_2550	contig21383	TTA	3	12	cGCaTAaCACtGtGATTCTTCTT	62.755	TATTTTtGGGATAACCCCAcCAAG	63.002	106
HM_2551	contig23673	AAG	3	12	ACATCATCCGATCGCTGTTtCA	63.029	TTAACAACAACATGcCTCATGAAC	63.168	98
HM_2552	contig03233	ATT	3	12	TCCATATAGCGTTTCTTGACAGCA	63.072	TAGGTTGGCCAATCATCTACATT	62.815	138
HM_2553	contig43630	TGG	3	15	AATTGGAAGAAGACAAGGCTCTGA	62.698	TGTTTAAAGCTGCTCCCACTTCTC	63.142	150
HM_2554	contig00026	TGG	3	12	TCTGATCCACCAACCAATCACTCC	63.419	CGTCAGATCTACGATCTTTACGGC	63.353	152
HM_2555	contig41769	GCC	3	15	AGTGAGACCAAACTCAAGCTCAAC	63.027	GCAATGAGCAATGCTaCAAGAAAA	62.679	110
HM_2556	contig41137	CAC	3	15	AAGAAGATcCACTTGTCTTTTGC	63.048	ATATGCTCTTCTTATGCGCCATC	62.765	101
HM_2557	contig26422	TCT	3	18	GTACTTGTTCACACCTTCCCGCT	63.362	GCGGCAAGAACaAGAAATACAA	63.754	96
HM_2558	contig45172	GAT	3	12	GACACGGAGAAATTAATGCTCTG	63.231	tCGACAAGTTATGCTCTCTGTAg	62.958	143
HM_2559	contig38997	TGG	3	12	CTCTGCTCTCTTTCAGACGCTCT	62.909	TTTTCAATTTGGTTGCTCTCGT	63.03	100
HM_2560	contig01968	TCT	3	12	TCCACCATTTCCACGATAGTTTCT	63.009	GCTCAGAGATTGACGGGTCTTAA	63.022	155
HM_2561	contig17601	GGT	3	12	CTCTGCTGATCTGTATCTCAAGCA	63.044	TGGTGCTCTTGTGACAATCTCAA	63.038	135
HM_2562	contig23482	CTC	3	15	TTTTCTCGGTTTGTCTTCTCTG	63.023	TGGTAGAAAGAACTCAATCTCTG	62.894	113
HM_2563	contig04616	CCA	3	12	GTTGCTTGCATATTTCCCACTAAC	63.035	TTCTTCGAGAAGTAACGAGAGGG	63.125	143
HM_2564	contig20639	TGG	3	12	TCATCTTTAGCTGTTTGAGATGCG	62.859	GGAACATGGGTTTACTCAACCTG	62.907	153
HM_2565	contig28829	CGC	3	15	ACTCGACCTCGAGAGTGATTGTCT	62.913	aTCACTTGGAGAGATaGAAGCGA	62.7	117

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2566	contig31481	TGG	3	12	AATGGACCTGGAGGATAaTAGGGA	63.057	CAGCATATCCACCTCCTCATACC	63.751	139
HM_2567	contig05485	GTG	3	18	GTTGGGCTTGAGGTACATAATGG	62.826	CAAACTACCACTTCGATCATCCC	63.009	154
HM_2568	contig00692	ATC	3	15	aCctcAaTATCTcGcGTCCAC	62.595	TCCTTGATACCTTTAAcCCTGAGG	62.823	82
HM_2569	contig110611	TGC	3	21	gCATGGAAAGTGATGAAGTTAAG	63.121	CTTCAGAAACAGCAGCAACATCAT	62.858	149
HM_2570	contig37015	GTG	3	12	CCCCACTCCTCTCTGTTCTTAC	63.586	AAITTCaAITTCcAATTTCCAC	63.167	87
HM_2571	contig43797	TCA	3	15	TTGGGAATTTGACTCTAGGACCTG	62.782	AGAGAGGAATTGAGGGAAGCTGAT	62.977	111
HM_2572	contig03002	TCT	3	12	TTGAGTGTTTCcATCTCTTGATGC	62.714	TCGTTTCCGGAAGTAITAGAGAG	63.006	159
HM_2573	contig03275	AAG	3	12	CGaAcGAGTTAGTGATCCaACAAT	63.549	AAAGGTGCTCTCCTCaTGAAATG	62.917	137
HM_2574	contig08498	CTT	3	24	TATTAATGgTGGGCTGAGGTTGTT	62.826	GAAGTTGATGATCCAAAGCAATCC	63.116	132
HM_2575	contig17950	GCT	3	12	GTCCCTAAcACTGGTAACCTGGTG	63.02	TGCAGTTGCAGCAAGTAATcCTT	62.57	150
HM_2576	contig05392	GAT	3	12	TTGGATTTTAGGTTTTGTTGAGAA	62.052	GTGGAGGTTCAAGGAAGAAACAAGA	62.997	158
HM_2577	contig41212	TCA	3	12	ATTCCTCATCGTCACCACTAAGCTC	63.031	TGAGGATGAATTTGATGCAGAAAGA	63.132	100
HM_2578	contig46203	AAG	3	15	CCAAAGACAAACAGAAACATGTGC	62.958	CTTCTTTCCCTTGAACCTTCTCCC	62.765	87
HM_2579	contig43248	TGT	3	15	tccACtGAAaGCAACTCCAAaAaT	63.227	CTTGATGTgGAACATGGGTGTGA	63.034	135
HM_2580	contig31709	ACC	3	12	AaCATCAaCAACCTTaGAGACGA	60.047	GaGTTTCAGaAGTGAGaAITGAG	60.761	82
HM_2581	contig46768	TCT	3	15	GTCACTCCCTTCcGATCCACATA	63.211	AGCAGACTGGATAGAcCAACGAG	63.137	152
HM_2582	contig13900	ATG	3	21	TTCTTGGTTAGTAGGTTCTGCTCTC	62.809	TCTCTCgaGACAgGTTcCTCTAA	62.882	150
HM_2583	contig15793	CCG	3	12	CGGATTTCCACCAACTATAACAG	63.027	AAAAaGtCTCGCCGCAAAATTTAG	62.911	111
HM_2584	contig01542	TCT	3	15	TATCATCTGCATGATGTCCAAACC	63.032	GGGAAGAAAGAGGAAGGAAGAAG	62.244	138
HM_2585	contig46721	GTG	3	15	TGAGAGAAgTAGGTgTGTGGTTG	62.703	CTAcCCTCTATCTcTCTCGCTC	62.589	81
HM_2586	contig110641	ATT	3	21	CaGATGGaAaTTTGTCTTACAA	63.517	AGTGCTTGTtctgaattctgggAG	63.124	119
HM_2587	contig03003	TAG	3	12	TTGGAAATCATTACATTAATCCCACT	60.949	TaAAGCTATGGATGGTTTgGTGA	61.822	128
HM_2588	contig07875	CAT	3	12	ATGTGGATGCCAAATCTCAACT	63.026	CCCAATGGCAGAAATGAAATAA	63.106	118
HM_2589	contig14792	GTA	3	15	TGATGACAGAGCGTAATAGACTGAA	62.491	GATAGGAGTGAGTCTCTGCCGAAG	62.912	144
HM_2590	contig40868	TTG	3	15	TCCTTCTTCAGCTGATCTCCGAC	63	TGTCAAATGtTCATGCGTTACAA	62.566	114
HM_2591	contig37684	ATC	3	12	GCAATTTAAGTCGACTCACTGCCT	63.06	GAGCCCTTCTGTAGCTAATGGA	63.035	117
HM_2592	contig27739	GCT	3	12	ATTTGAACtCGAGGTGTGCTGACC	63.027	GTACAAGCTGGCTGCTGCTTTTT	62.959	160
HM_2593	contig00315	CCA	3	12	aaTATGGCAATAACGAGGTCCAG	63.021	ATGGGAACaACGAAGAgGATGT	63.104	160
HM_2594	contig04987	TTC	3	18	CCAATCATCCCAATCTGTCTCTC	62.987	AgCtCTCAAACTCTCACTCCACaC	63.017	128
HM_2595	contig01589	GAA	3	12	TCGGAGATTGAGCAGAGCATGTG	63.063	CTAGCCATTTTCTCAACTCTCCCA	63.006	139
HM_2596	contig04666	GGT	3	12	AGGGATTCTCTCATGTGGTGGGTT	62.974	CTGACTTGcaATTGGcTGACAAC	63.076	124
HM_2597	contig09460	CTT	3	12	TCCTCAATTCCTCAACTCCCTG	62.771	CTCAATCCGCAAAACCAATTTCTAC	63.03	129
HM_2598	contig03356	TTA	3	15	TCGGGTTTAGTTGTTGATGTGATCT	63.033	CAGCAATGGTAGCTCAATGGTA	62.453	130
HM_2599	contig05862	TCT	3	15	GACGATGATGCTGTGGGTGTTTAC	62.861	TGGGGAAACAAAGAGCAGTAAGAG	63.015	146
HM_2600	contig05338	CAC	3	15	CGTTGAGGTCAAAAATATGCACGT	62.856	TCGGAGTCTTGAGACTTCCAAT	62.892	149
HM_2601	contig41319	TCA	3	12	TcTcACACCTCTgaTGCAACAAT	63.057	GaTTCTGTGATGATCaGGGTTT	63.339	136
HM_2602	contig36348	TTC	3	12	ATTTGATTGAGGCGTCTTCTCCT	62.598	GaACTTCACTGCTGTAGGCTCCTAC	62.94	155
HM_2603	contig19691	CCT	3	15	CCCTTCctTTCATCTTCTCTTC	62.948	TGGAAGAAACAGTAGAGGGAGCA	63.214	139
HM_2604	contig38108	ACT	3	12	TACCAAGCTCACATCTCTCTTTC	62.91	TGAAGGGGAATATTGGATTGTATG	63.08	147
HM_2605	contig05657	TTC	3	30	AAaAGAGAAAGGGGAAGAAAGAGG	61.613	TGAATCTGAATCGACGAAGAAGAA	62.382	147
HM_2606	contig23633	AGT	3	18	AGTTTCGCAATCGAATTTAGCAAA	63.05	GAAGCTGTGAGATCTTGCATGAA	63.177	125
HM_2607	contig14241	AAG	3	12	ACACCCTAACGATATAGTCCAGC	62.661	AAAAAGGGTTGCTTAAACTCAAAATG	61.966	150
HM_2608	contig27255	GAA	3	12	AAGAGCTCTCGGATGAAATCCC	63.093	ATCACACCCACGAGAGGGACTA	63.117	103
HM_2609	contig03149	AGA	3	15	TTGCAAAATCGGAATAGAGAGATCG	62.899	TTTAGAGAAATCTTCGCAATTCGG	62.827	96
HM_2610	contig19087	TTC	3	12	TcATCACTCTCTCAATCTCATGCT	62.914	ATTGCAAAATGGAGATGTGAAGAT	63.016	134
HM_2611	contig03506	AGA	3	15	CTCGgCATCAAGAAAGTTAGAA	62.919	ACCATCGATCAACATCTCAACGTA	62.833	154
HM_2612	contig46734	ACA	3	12	GACATCACTGGCATCAACACAG	62.847	GaAAAGGCTCAGAAATGAAGAGAGA	63.009	100
HM_2613	contig11687	CCA	3	15	TGcTACCCtTCAaTCCAATTAAC	62.729	AACCTTCGAAAcGTTTGGGTTTGTA	62.941	136
HM_2614	contig25793	TCT	3	15	ATCATCTGTCATCATCGGTATCCTT	62.906	TACTACTGCCAGCTGTTGCTGaC	62.999	127
HM_2615	contig48482	CCT	3	18	TAATCTCTCTTGAGGTTGGGCAC	62.91	TCAGTAATCCTCTCCAAAGTCCAA	63.3	129
HM_2616	contig02061	AGT	3	12	GACTGCAAAATTTGACCTGGATCTT	62.813	tGTGTTTCAGAGAAATCAAGGGGA	63.132	152
HM_2617	contig43424	CCA	3	12	GC GGCTGATGAGGCTTCTTATTA	63.154	ATGGTgGAAGAAATTTGGAATCTCA	62.996	111
HM_2618	contig09045	TCA	3	12	CTGCCAATTAAGATGGTGGCTAAA	63.428	aAGATGATTGGAATTTTCGCAAGC	62.655	137
HM_2619	contig00012	AAG	3	12	TtCCAATAACGAAATCAGAAACGCT	63.138	GCACATCACTCTCTgTTACCTCT	62.925	120
HM_2620	contig18555	GGT	3	12	AGTTTTTGATCAGAGACCAATCG	62.798	CGAGAACATGATCGATGAGTACGA	63.598	131
HM_2621	contig32348	TGA	3	12	CCCAATGATGATGACCAAGGGTTAT	63.099	TATCCAGAACCAAGCTTTTTTACC	62.684	135
HM_2622	contig20486	CTT	3	12	ATCCTCTGCTGCTTCACTCTTTT	61.829	GGACACCAACACCATCTCAITTTa	62.715	143
HM_2623	contig40786	TCT	3	30	CAATCATCATCACCATCATCTTCA	63.005	TGGTCATGATCAAGAAATACAAAAa	62.758	159
HM_2624	contig32644	TCT	3	12	GGCCATTGTAGAACAGAAAGCATTT	62.744	AATCGTTGCAGAGGAAGATCAAG	62.022	142
HM_2625	contig32471	AGA	3	12	GTCAaTAATGCCTATATGGCGAGC	62.966	TCGACCAGATAACCTTCaGAATCA	63.217	114
HM_2626	contig41500	AGA	3	15	ACCGTTTTGACTGTTCTGTTGTTT	63.146	CTGAGACGAAGCTATGGAGGCTAT	62.327	125
HM_2627	contig23424	CAT	3	12	aCATCAATCTCAAGTTGGGAGAA	63.204	CCAATGCCTGTTGTTCAAGaTTA	62.514	138
HM_2628	contig18397	TGT	3	15	TAAGAACAAATCCCAAAATTTCA	62.695	TTGAAGAGATTGGTCAAGAGGAGG	63.085	159
HM_2629	contig40867	GTA	3	12	TAAACTACGTGCGTAAGATTCGGC	63.566	CACCTGGAGACAGAAAGAACACCA	63.027	154
HM_2630	contig11040	AGG	3	15	TCTGTTTTCTGTTTCGATGCTACA	63.068	CCCAACTTTACACTCGGTTTgaC	63.028	89
HM_2631	contig39329	TCA	3	24	CACAAACCAACTTTCCAAACTCT	62.708	CACCACTAAGGGCAGTACCAAAAC	63.041	160
HM_2632	contig05469	ACA	3	18	ATTTCCAAACCAATTaAcAaCCc	63.084	TGTTGGTAGAACTGAGGGAATGGT	63.111	139
HM_2633	contig22633	TCT	3	18	TTATCCACAGAACTCTCTCGCC	63.022	GATTGATTTGTTGATGAATgTGAA	63.137	96
HM_2634	contig12831	ATT	3	12	TAAACaGATTATCGCCCAAAaAGG	62.449	AATCCAAGGCTGACTCAGTTTGT	62.512	87
HM_2635	contig05363	GAT	3	12	GATAAGGGCGGTTTTTGTGATTA	62.357	TAATTCAAGCAACCCAGTCAACCT	63.129	129
HM_2636	contig45625	TCA	3	12	TCTGTTCTCTCTGCTCTCTCTCC	62.643	GGTGACTGGTAATGAGAAATGGG	62.897	132
HM_2637	contig11902	CTA	3	12	ATCTAGATCTTGACCGTCCaCTG	62.898	AAGAGAAGaAAGATCCAGCAGCA	63.128	81
HM_2638	contig20974	CTT	3	12	TTGTCGTTGAGCATCAATCTTAAT	62.007	AAGTGATTGGTCTTTGaTCTCTCG	62.813	157
HM_2639	contig50303	ATC	3	15	TGGGTGAACACATCTGTTTTGTT	62.724	AAACCCaAGAAAAACCCATaGAA	62.977	141
HM_2640	contig33538	TCC	3	15	CACGAATCAATCCAAACAAAGAAC	62.831	ATTTCTCAAAATCGGGGAATCTC	63.679	102
HM_2641	contig47514	CCG	3	12	CTCTATCACCCTCCCACTCT	63.341	ACGGCGGTAATTCACAGAATAGAG	62.742	87
HM_2642	contig06753	CCG	3	12	AaCCACACCCaAaCACAaATAGC	63.251	GGCTTTGAGTACTGaTGGGCTGT	62.925	154
HM_2643	contig38105	TTC	3	15	ATaCAATGCAGCTCTGAGATGTG	62.743	CcATAGATTCCATACAAACAGGCC	62.815	117
HM_2644	contig33618	TGA	3	12	AACTGTTTTGATTGTTTGGTGCTT	63.044	CTTGACTTGAAGGTCCCTACTGGA	62.993	138
HM_2645	contig50760	GAT	3	18	aGGTAGGGTTTTGGGTTTTGTTGT	63.001	TTCCATTCTTGCTATGCTTCTCT	62.62	120
HM_2646	contig33746	GAA	3	15	GTcTaTcTGATGATGTTTgTCG	62.951	CTTCTTTTTTGTGGCTGGCTTAG	62.739	155
HM_2647	contig05294	TTC	3	12	TCTTCAGACGCTTAGCAGATTTT	62.851	ACTTTAACAGACTGTGGATGCC	62.725	133
HM_2648	contig28360	CCT	3	15	ctcGATATGACCCCTTGAACCTG	63.117	CAGGATGAAATTAAGCCaCTATGGA	62.532	125
HM_2649	contig10643	CTT	3	12	TTGTTcATcAcGCTGATGAACCTG	62.948	TGCTTGGGaaAaCAAGCTCTGTGA	63.141	147
HM_2650	contig21810	TCG	3	15	TGTCGGAAGATTCTGCTCTTTTTT	62.813	TACAACAGCGTAGCGATCTCaATC	62.774	134
HM_2651	contig34546	GAA	3	12	AATAAGGAGCCCACTAGTGcG	63.751	TTTTTCAACCTTCACTaAITTgG	63.299	137
HM_2652	contig14848	ATT	3	12	GGCTTCATCTTGAaTCTCTCTA	61.994	TCCTAGAGAGCCTTGGACTAGCAA	62.921	116
HM_2653	contig48643	CAA	3	12	TCAAGTGTCTAAAAGTTCACAAATTAGC	60.447	TAGGTACCCAGTTCATATCCCAAG	60.928	145
HM_2654	contig00782	GAC	3	12	TcGAGACTGTGAaAGAGTCTGA	62.69	ATTCAACCTCACTCACTCACAT	62.128	85
HM_2655	contig33944	AAG	3	12	AGCTGAAATATCTTGCCCTTGAA	62.438	ATTGAACCCCATCTTGTGAAGGTA	62.897	154
HM_2656	contig47782	ATC	3	18	GATTTGCGTTCCTCACTAGGGTCT	63.294	GGAGCAGAAATGGTCTTGAAGATGT	63.017	101
HM_2657	contig25426	TCA	3	12	GGCTCATATGTCGCTTTTACIGCT	62.975	CGAACCTGTAACATACGCGGAAT	63.675	144
HM_2658	contig03219	TTC	3	12	ACTAGACAAACTGCACCTGATCC	63.04	GAACGTGCCGCTAGTTCTGTAAT	62.877	96
HM_2659	contig35312	TTG	3	24	gATTAGATGAATGACGAAGGTGGG	63	ATCGATCGAAATCTTCAACCAT	63.016	154
HM_2660	contig03698	TTG	3	15	AAGTTCAGATTGCAACCTTTTGAG	60.988	GAAGACAGACAGAAAGATGACTACAG	60.258	147

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2661	contig40665	CGT	3	12	CCAGAAAGCCAGTAATATGGTGG	62.919	TCGATTCATGGAGGTGCAATAGAT	63.103	153
HM_2662	contig40943	GGT	3	12	GAGTTGGTGGACTTGGAGAGTGAG	63.666	ACtTtCCCTATTTTCTCCACC	62.755	160
HM_2663	contig17433	CCG	3	12	AAAAGCaACCACTCCACCTC	62.663	AACtGGAATTAAGCGAGTGACGAT	62.439	95
HM_2664	contig37614	GAT	3	12	CCAAAGAAAGCGAAGAGGAAAGAT	63.285	GACTATCAAAAGcCTTcCCAACCA	62.91	136
HM_2665	contig18429	ATC	3	12	TAAACTGCAATTCGATCCAACT	63.03	TTGAGAATGTAGCCCTAGGATTG	62.813	157
HM_2666	contig20698	GGA	3	12	CGGTTGTAATGCCACATGTAGAGA	63.278	ACATCCCAACTCTTCAACCCAGA	64.21	112
HM_2667	contig11432	GAA	3	12	TCTGTTTctCCTGATtGGTTTTc	62.784	GACTACTGATGGATCGAATTTGTGG	63.024	144
HM_2668	contig31630	GGT	3	15	AAGTCCTGCATtAAGGCCATTTTT	63.21	ACTGATTGCAACAATCAAGcCCTA	63.231	116
HM_2669	contig36207	CAC	3	12	GGAAGTCCTCTGTACGGAATAGTT	63.008	TGAAGTTCATGATGGAGAGCACTCA	63.113	159
HM_2670	contig41064	TAC	3	12	ATCGAATTCCTACGAAGACCTC	62.986	ACCACTGCACTGGTAATCTCAA	63.042	119
HM_2671	contig09743	CAT	3	21	TCCTCGTCATCATCAAGaaGTTG	62.698	GACACCTGGAGATGGTGAAGTTG	63.129	130
HM_2672	contig04456	GGT	3	12	GTTCTTTGTAGAGGTCGGTGGAGA	63.01	ATCAACAATGACTTCCCTCTGCTG	63.763	110
HM_2673	contig32384	ATG	3	12	AACGTCCTATTCTTTCTCGGAAT	63.289	GTTGACTGATGGAAGGTTTTCTGG	63.212	145
HM_2674	contig39040	TTC	3	21	TTGGAGTTCTCATCATCTGCTCTG	63.03	TTGCGTTGATGTTTTTCTCGATT	63.018	150
HM_2675	contig08966	GTT	3	12	GGTTATAACGGAAGTCGTCAAACG	62.944	ATTATGTTGTGAAGAGCAATG	62.366	127
HM_2676	contig02920	TAG	3	12	AaTTGCAAGTGAaATtGAAGGCAT	63.046	CATTGAGTAGCTCCGCTCTTGAC	62.623	95
HM_2677	contig12888	GTG	3	21	ACTGAGGTTGCTGATCTGAAGCTG	61.612	GAAGAAGGGAAGGACAGAGGAGT	62.553	91
HM_2678	contig33924	AGA	3	15	GCAGAGGTTCAACTTCTTCTTCG	62.822	CAACCAAAACAAGTTATGCCAA	62.164	127
HM_2679	contig02779	TGC	3	12	CCCTCAATCATATACTCACGGCT	62.62	AGTCTGAAGAgGGTTGAGAGGA	62.86	94
HM_2680	contig03080	TCT	3	12	AACAGAATCTCTATTCTGcCTTG	62.91	GGAAGGAGGAGGAaATTGAGATG	62.958	103
HM_2681	contig08750	GGA	3	12	gATCTGAGAACTTTTGACGCGAC	63.678	GCTTCTCGAACCATATCAATGCCT	63.051	152
HM_2682	contig21006	CTT	3	15	AAACTCTCGAATCATCATCTCCG	62.9	CcAaACCTTAAAGGCTTCAATT	63.183	155
HM_2683	contig52285	GAA	3	21	GGGTGGCTTAATGATGCTCGAAAC	63.026	CTCAGAAGAAATACCAAGTTCCAC	62.368	137
HM_2684	contig42584	CCA	3	15	CAGATGGGTTGGTTGAAGAGAA	63.618	TGATGTCTCTCACCAATGGAGGTA	63.016	126
HM_2685	contig01270	AAG	3	12	GCAAGGACCACACCAATAAaAC	62.731	TTCTGGGAGaAAACAGCTTCTTG	63.113	130
HM_2686	contig19051	ACG	3	12	aAATAGCCGTGTAAGAGGCTCTC	62.536	CAAGATCGTCTCTGGGTCAAATC	63.318	118
HM_2687	contig44512	TTG	3	15	TTGGCTTAGCAAAACCACTTTTC	62.944	CCATAAACCAATCCCATATCACA	63.706	138
HM_2688	contig37678	CCT	3	12	TATCTCtATCTATCTCTCAAA	63.074	ctGGTGTTTCTGCTTGTGTAAC	63.028	155
HM_2689	contig21026	CCA	3	30	TTCTACATCACCACCAATATCCc	63.099	ACTTGGAATTTGTCATCGGAGAAGT	62.382	142
HM_2690	contig31549	CTG	3	15	ctGACAATCAGTTCGCAATATCGAC	62.951	aTgaAgGaCaAgGATGATgagg	62.874	136
HM_2691	contig43596	AGG	3	15	AAACTAATCTGCAACCCAAAGGA	62.233	GTGGTGAATCAGATATAAAGCCG	62.925	158
HM_2692	contig05719	TTC	3	12	TAGTACTCTCCAAATTTCTCAGGc	62.823	AGCATAAAACCGAGTATTTCGGG	62.928	118
HM_2693	contig32078	GGA	3	12	CAACTGACTTCTATTgCTTCAACC	62.438	GATTGGTAGGCATCTTCTCAGCAT	62.929	134
HM_2694	contig25641	TCA	3	24	GATTACCACcATAATGATGACCCG	62.438	TACTGCGACTGCTATTCTGCTACTC	62.989	159
HM_2695	contig11592	TGA	3	18	ATCTTAGTCTTCAAGTCTGCCAC	62.94	GTTTCAGGATGGACCTCTCTCGTA	63	160
HM_2696	contig11076	ATC	3	24	TaTtCGCGaGgGTGGAGTTAAGTA	63.134	ATGCGATGTTTGTCAAGaGAAATG	62.529	120
HM_2697	contig20522	CTT	3	12	CTTCCACACTGAAAGCCTCAaAT	62.921	CAAAAGACCTTTTAGCAAAACCA	62.821	102
HM_2698	contig13578	TGA	3	15	AAGTACCACCTGACCTGCCACTTC	62.935	GaAgTgATaATGGGAAGCATCCAG	63.112	149
HM_2699	contig40106	GGA	3	12	TTCTGGTGGTCTATGTGTTGGTG	62.827	CATGAATCTCACTCTCACCAG	62.865	158
HM_2700	contig28470	AGA	3	12	TGAACCAACGAAGCAAGAGCAAAA	63.159	CCTCTTCATCACTTTCACTGGGT	62.884	159
HM_2701	contig01325	GGT	3	12	ATTAAGAGAGATCAACCGACGGC	62.719	TCGATTCTTCTCAcCCAACCAaA	62.896	153
HM_2702	contig32433	GTG	3	18	CTTCTGATGCCAGCACTTAGCGAT	63.146	GGTGGTACAAgTTAAAGGGGCTCT	62.696	137
HM_2703	contig26372	GTA	3	12	CAaACCCCTTCTCTaTCTCTGTT	62.98	GTCaAAAACGaTCCGCTCTCTACT	62.949	151
HM_2704	contig25057	CCA	3	21	TTCTGTCAAAGTGGATTCGTTGAA	63.034	ATCAGATCTCTCAAAGTCAAGGTG	62.884	105
HM_2705	contig03695	CTT	3	18	CTTCTCTTTTTCATCTCAAGTCG	62.683	GAGGAAGAGAAcAATGGAGTGGAA	62.987	145
HM_2706	contig26479	TTC	3	12	TGCGAATTTGTAATAAACTGTGG	63.167	GTAAGGATTGTGcCCtTAcTcG	63.119	159
HM_2707	contig35611	ATG	3	15	TATGGGTCTCAAGaAaCCAAGCTC	62.91	ATGTTTCACCAcAaCAGCaCAa	62.856	96
HM_2708	contig01492	TTC	3	15	GAATTTCCAGAAATCCGTATCTCTC	63.168	ACCGATGAAGAAGAAATCAAGGA	62.383	147
HM_2709	contig38167	TCA	3	18	GTGTTCATATGCGTAGGGCTCTT	62.757	TCGAAATTTGGGAATGATTGAAGT	62.899	153
HM_2710	contig21033	AAC	3	15	CtCACTGAgCTTCAACAATGGC	62.253	AGAGTTGGGATTGGAGAGAAAGG	63.164	138
HM_2711	contig47398	GGC	3	21	TGAATCATCTTCATCTCTCTCTC	62.967	CACGTTTCAAGTGTGTTGTTGTG	62.734	133
HM_2712	contig14451	TCC	3	12	ctccaagtccctttCATCATCTTT	62.705	GATGAGGAAGAGAGTGGTGGTGAT	62.994	118
HM_2713	contig35407	TGA	3	12	TTACAGCTGATCAAGAAAGCGATG	62.859	TCAACTTGTAGTGCTCTGTGAGC	63.081	160
HM_2714	contig20037	CTG	3	12	GGAATCGTCAGGACTAAaCGAGA	62.91	TGCCTTTTTCAGGAATGCTAGAAG	63.027	136
HM_2715	contig04385	CTA	3	12	CGATTGTTGACTATGGGTGCAAA	63.15	GCTTTACGAGCCGTTTATACCGT	63.617	101
HM_2716	contig20640	CTC	3	12	GGTGAGATGAAAGAGTTGAAGGA	62.987	GTATTGTATTGGAGGTGGCCGTAG	62.839	128
HM_2717	contig01359	AGG	3	12	ACGGgTTGAACATTGGATGTGAAT	62.824	GCCATATGGGATTGTGCTATTGT	63.037	111
HM_2718	contig28626	GAT	3	12	CTGTTTCCGACTGATGTAAAGAcA	62.842	TCACTTGTGGTGAAGCAATAAAA	62.956	153
HM_2719	contig37273	TAG	3	24	TCAGTCACGACTGTCTTCCAATA	63.146	CCACTTTCAAAGGCTCAGAACAT	62.921	159
HM_2720	contig30300	GAT	3	15	GCGGATGAGTAATACAGACAACCC	63.039	AGCCCTAACAGTAACAGCAACAGC	63.082	119
HM_2721	contig05143	GGC	3	12	ATGTGGTGGGCGCTATTGTAACT	62.949	TTCCAACCTCCAGGCTTATTATC	63.569	158
HM_2722	contig07861	CAT	3	12	AGCTTCTGCATCATATGGCTCTC	63.154	GCCTTGTGCCAACTGTAAATAAG	63.051	99
HM_2723	contig26506	ATT	3	12	TCCTTGAGAATAAACTAAAGGGG	62.717	TCACGAGTTGACCTTGTACTCAATG	62.634	158
HM_2724	contig36375	TCT	3	24	GTTCAAGTCGGACACTGCTCT	63.035	CCGAGGTGGTGCAGTACTACTCTA	62.708	153
HM_2725	contig14503	CAT	3	21	ACTTGTCTTTCTCTTGGCAtGc	63.048	gGGGAAAgGGTAGGGGTACTACAT	63.534	146
HM_2726	contig24328	CTT	3	12	GCTGGTAAACCCCATCATCAGTAG	63.022	CGGAGTTGGATGAGAACTCAAGA	63.957	150
HM_2727	contig11545	TGA	3	12	CCATCCACTGGAGATTtTGAATT	62.884	cGTCTATGACcACcATCTcTct	63.119	141
HM_2728	contig20776	GGT	3	12	AAGGAGCAAGGGGAGGTAGATATG	62.983	AGAACCTCCACGACTACCAACATC	62.809	131
HM_2729	contig31056	TGA	3	12	TGGTATGGTGGTATGATGATGAGG	62.91	CTCTCTACCCAACATGAAaATGG	62.993	120
HM_2730	contig05000	CTT	3	12	TCTCATGTCTACTGGGgCTTTTGT	63.338	TGAGGAAGAAGAGGAAGTGGAGA	62.868	155
HM_2731	contig07399	CAC	3	12	cGACATGtTACcTCAcAGaAAcAC	62.947	CTTTTGGAGAATTTCTCAGCAC	62.71	149
HM_2732	contig27418	CTT	3	15	TCATCaAcATCCCTTTCTCTGAT	63.196	GGGTTTGAATACTGGTGTAGCTC	63.158	128
HM_2733	contig32988	TTC	3	12	TCAGATGTCTCCACATACCTTCA	63.016	GAAGATCAATGGTCCAAATCCAAG	62.987	80
HM_2734	contig43009	GAT	3	15	TCTGGAAGATGAATATCTCTTGGC	62.693	GGAAAGTTCAcCTCCAGTAaATTG	63.31	129
HM_2735	contig06259	TCT	3	12	CAAGAAGGAGAAAGGCTCAATTG	62.907	ACTAACTTCTTCCGATCGACATC	62.94	109
HM_2736	contig25044	GGC	3	15	TAGGATTTTCTGTTTTGATGATGA	62.959	AACTAGACTCCGACTCCACCAAC	63.003	132
HM_2737	contig33962	CTT	3	12	CACcAAcATCCCACTAATTCCAT	63.108	TAATGGGGTGGTGTtTAAaATTGG	62.812	131
HM_2738	contig49341	GGA	3	12	AGCAATGATCTCTCTTTCGTAGG	62.425	gTGAATCAAAAGTCAGGCC	62.911	148
HM_2739	contig09256	TTG	3	18	GCGGTCTTGATCTCTCTTGA	63.005	CacAACCCCTTCTTTTGTtTTC	63.015	139
HM_2740	contig36696	GCC	3	12	ATCTCCAaATCAcCAACATGGTCT	63.323	TTGGGTAGTGAGGTAAAGCTTCTCG	63.028	134
HM_2741	contig09519	CCG	3	12	AATTGAATTGAaACTCCGCGCTC	62.903	CAAAATCaCCGTCCCTTCGATA	63.218	121
HM_2742	contig08752	TGA	3	12	GTGATCTGCTATGCTTGTGGTG	63.078	GTACTTTTGTGTCGGTGTAGC	63.076	145
HM_2743	contig46676	TCT	3	24	TCTTCTCATCTTTCTGCATCTCTC	63.209	TTACTTATTCTCAGCCTGTTGG	63.735	159
HM_2744	contig45808	ACT	3	18	GCTGTACTCGTAGCTGCTTCAaCa	62.999	GAACAAACAAACAACTAgGgGG	62.714	117
HM_2745	contig22415	TTC	3	18	TCAATTAGGTTTTCTGTCGCCCTA	63.014	GATTaACGATCAGGGCGAAaATACT	63.02	111
HM_2746	contig13807	CAC	3	12	GACATACaGcCGGAAaGTACGAC	63.158	aGCTAGAGCaAGCTCtTtGgGTT	63.134	157
HM_2747	contig29184	GAG	3	18	CCTGTTGgAAaAcCTTtGCTTtCT	62.977	tTCTtCAcGCAAGgTtCTCTCT	63.759	82
HM_2748	contig07944	TGA	3	18	TCAAGTCATCATGTATTGTACATGCTC	62.505	AGGAAGGaaGaCCTCCAGAAGAAA	62.958	116
HM_2749	contig49502	ACC	3	15	CATGATGAGAAATGAGGCAAAATACC	62.926	gaGCTATAGACATGGTGGTGTGCTG	62.122	128
HM_2750	contig37650	CTT	3	15	AGAAATCCAATCTCAAACTGTC	63.685	CGAGaActgattctgcactc	63.619	134
HM_2751	contig03005	ACC	3	12	TATCTCTcCAcGgATATcCaG	63.52	aAgGCTGATATAGGGTTTGGCTTT	63.221	133
HM_2752	contig04941	ATC	3	15	TCAGAGTGTCAATTTCTGACTGCC	62.741	CTGAGTTCATCTCTCTGCTGTA	62.711	109
HM_2753	contig16077	GCT	3	12	ACATGGGGGGAaAGATAGAGAGAG	63.059	CCTTAaAGAGACCCATCATCATCA	62.593	149
HM_2754	contig42011	TCT	3	18	TCCTTGTCTTGTCTCTcTcATCA	62.351	GAAGGAGGAGGATGTtGTTTCTTA	61.955	114
HM_2755	contig33361	CTC	3	15	GGTGTCGCTGATGACTTTTgaTA	63.196	GGGTGTTTTCAAGGATGGGAT	62.455	157

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2756	contig43001	CTG	3	12	TTATTTGGGTGATGAAAGAGAAACg	62.532	CAACAGAGTAGAGGGTGGGTTCAC	63.334	156
HM_2757	contig14706	TGG	3	12	CTTACCAACCCCAAAAGAGCAAT	63.372	TGATGTTTCCATGTGGTGACAAAG	63.045	156
HM_2758	contig03083	TCC	3	15	AATTCTCTCCCTCCCACTATACAC	62.964	ATGTGATGATGTTGAcAcCAATg	62.924	93
HM_2759	contig22295	ACC	3	12	TGCACATTCTCTCTTCTGTATGA	63.038	CAACCAATGGCATTTCAGTTTCT	62.397	106
HM_2760	contig25254	TCA	3	12	ACCTTAGCCTCAAGTTTCCCATTC	62.995	TATTTTTCGGGATACCAAGCTGAT	62.948	134
HM_2761	contig40111	GAA	3	15	CTTTAGGCAAGGCTTCAGTTTCATA	62.932	CATGCCATTACAGCCTATTGTGTG	62.859	112
HM_2762	contig05032	TCA	3	12	CCAAAGAGCTTCTGTGTCACTCT	63.124	TAGAAGATCGTATCATCCACGCA	62.949	126
HM_2763	contig37780	GAA	3	12	gCATCgtcAaTaTTATCGTCCAGA	62.325	AAATTGaaAAACAATTCGGACCT	62.992	92
HM_2764	contig18205	CCA	3	12	TGTTTCCCTATGGGAACCTCTGGTA	62.993	AACCACCAACACATCACTCACTG	63.393	120
HM_2765	contig14518	GCG	3	12	TTGCCAAATATTGCTGAACAATCG	63.174	TGCTGGGCACAAGTGTAGTAGAA	63.184	153
HM_2766	contig36874	CCG	3	12	AACAATATCGTAGCCATAACCGgA	62.748	GAGATTGATGCGAACCATTAGACCC	63.129	143
HM_2767	contig46335	AGA	3	15	AGTTCTCCGGTGAGTTTCTGTGT	63.452	CTTTCACAGACCTTGAACCTCAAT	62.895	146
HM_2768	contig12668	TAA	3	12	CTCTCTAGCAACTAGGAAGCAGGGG	62.118	GCATTCTAAAATTCAAGGGGCTT	62.824	128
HM_2769	contig38398	TGC	3	15	CTCTCTTCTCTGCCATGAACtC	62.698	TGTTCTGTCTAAAATGATGAACACG	62.355	138
HM_2770	contig09848	ATT	3	12	CGTATACCCAAgTAAATGACTGGC	61.999	GAAATTCACAGACTCCAcGTTTT	62.509	148
HM_2771	contig40408	CTT	3	12	TGCATCAAC:TGCTTCAGTAAATC	62.645	TGATTGAAGCTGaaAAACAAGCAG	62.856	119
HM_2772	contig10838	CTC	3	12	CTGCTTCAAAATATTCAATGGCCTC	63.13	GGAGTAGAGCAGCGAGATTTCATA	63.137	152
HM_2773	contig12511	ATG	3	12	AATTCAAGCTCACCCACCAATCT	63.242	AGGCTTCTTCATGGTCTGTTTCAG	63.124	113
HM_2774	contig03478	TTC	3	12	TATACGGAGCTGCTTTTCCAGAAC	62.947	AcTCCATTCAcCGGTGTTGATGAT	63.121	156
HM_2775	contig28296	TTC	3	24	CtaATTCTCTCTCAAAATCACTCca	62.566	TCAAGCTTGGTTTCAATCACTTCT	63.219	156
HM_2776	contig48700	GAT	3	15	ATCAATTTGAGGGACATTCTTCCA	62.987	TCTGCCAAAACATAACTCGAAACA	62.956	155
HM_2777	contig05046	CTT	3	12	AACTGCATGCTCTGGTTGTAGGAT	63.368	CCAGCAAAATCAAGTAATCAAAAGAGG	63.302	159
HM_2778	contig10426	CCT	3	12	TCCAGTCATTTCGggATTGAT	62.987	TTCAGGGGAGtCTTTAGCTGATG	63.006	98
HM_2779	contig50258	ACC	3	15	TCTCCATGAAATACAGCCAGTCA	63.038	CCCTCTTCTCTCTACCTTCCA	63.256	159
HM_2780	contig12371	CTA	3	15	TGGCAATAGTCTCAGCAATGCTCT	62.847	GTGTTGGAAGTACTGGAAGGTGCT	62.935	140
HM_2781	contig05532	CAG	3	12	TCATGGTATTCTGCCATAAGCAG	63.163	GCAGAAATGGCTAATGCAGAAAAG	63.351	145
HM_2782	contig48235	GGT	3	12	AAGGTGATGTTTGGGCAATATC	63.236	TTATGCATACTTATGGGGGACTGC	63.237	144
HM_2783	contig16459	CGG	3	15	AGGAGATAGGTGGAGAGGCAAGAG	63.495	CCGACTTCGAATTcACAATCTCTC	63.431	104
HM_2784	contig02872	CAT	3	12	TCTCTCCAATGTCTTCTTCCAC	62.987	AAGCCGAGTGATTAATGTGAATGTT	63.039	103
HM_2785	contig14838	TGT	3	12	TCATGACCTCTGTTGTCTTGTGT	63.053	AGAGaGCGATCGTCACTTCTGTAT	62.928	99
HM_2786	contig10607	TTC	3	18	CTTTGTCTTCTTAAGCGCGAAGA	63.036	TCAGATCCAATTGATTcAaACCTC	62.987	99
HM_2787	contig24648	TGT	3	12	AATTCAAGATTCTCACTCTCTGCT	63	GGTAGCAATGAAGAACAATTTTCG	63.03	128
HM_2788	contig51080	CCA	3	12	CACCACCCAAAGTATAgTCCGC	62.817	GGTGGTGGtGAGACTGTGTAGAcT	62.91	152
HM_2789	contig31837	TGA	3	12	AAAGGAGAAaCGATCAAGGtTCC	63.196	aAcTGAATCTTCaTtGcCTCCaA	63.219	127
HM_2790	contig16969	CCA	3	12	TCTAATAGTTGGGTGCTTCTCGC	62.729	TGACTTTAACGCACTTCATATGGC	62.468	143
HM_2791	contig05485	GAT	3	12	CTGAaCAATTGgCCATAGATGAAT	63.322	ATTATTCAACAACCAACCCCAATC	63.013	144
HM_2792	contig43121	TGG	3	18	GTGGTGGAAATTTATGTGGCAAA	62.934	TTTACTCTATcCCCCAATCCACA	62.787	145
HM_2793	contig28261	TGA	3	21	GATGTGGGgAGGAGAACTAGGAT	62.964	TTTTGTTGCTGTATGATCTCGATG	63.474	135
HM_2794	contig45771	GGT	3	15	AGGAAGATAGTGGCTTGGAGAGA	62.712	ATCCTCTGTGTCTGCACTCCATC	62.914	126
HM_2795	contig41698	CTC	3	12	CGCGAGTTCTGTTTTCTGTACT	63.053	GGCCTACTaATAGGAGGAAGACGA	62.914	148
HM_2796	contig06999	ATC	3	12	TCTTCAGCACTGGGCAATATAATCA	62.949	CTGAGGGTCTGtTGTATTTGAGT	63.01	124
HM_2797	contig27756	CCA	3	12	ACATCCCTCTCCCTCTTTCTGTCT	62.764	AGTATGGTGAGGATGCTCTCAAGG	63.014	151
HM_2798	contig46751	TCT	3	12	TTTGGGTAGGAGACTGTTGTTTT	63.028	TTCGAAAAGGGTTAAGATTTCAGAAG	62.182	133
HM_2799	contig04074	CGA	3	12	GTTTGAAgAggACAATGGCGaC	63.141	AAGTCGAGGTCCGAGTCTGAAGT	63.78	121
HM_2800	contig32049	GTT	3	12	TGAGACTCTTGAAGGGTGGTTTTAG	62.993	TACTCTTgGAACGCTCTTCTCAcC	63.238	108
HM_2801	contig13308	TTC	3	12	TTCCTATTGATTTCATTTTCATCC	63.084	TAGCTTCTTCACTACGCGGAGAG	63.348	130
HM_2802	contig15697	GGA	3	18	CCTCCTCTATTCtTCCAAAGAAA	63.05	TTGGACCTACGGAAGAGGTAATTG	62.823	158
HM_2803	contig02035	GAG	3	15	TTGAGCAGCCAAAaTtGGTTAAT	62.945	GTGCAATTGGCAcAATTAAGTCTCT	62.455	112
HM_2804	contig07352	AAG	3	12	TCAATCAAAAaCGTtTCAATGACG	63.154	TAGCACCATGATCACTCAATCGCT	62.338	126
HM_2805	contig14067	AAT	3	12	ATGACTGAATTTAGGAGTCCGTCT	62.698	TcAATGAAGaAAAgGAATGGGAAA	62.98	120
HM_2806	contig03392	TTC	3	12	GAACAaCAGCTTTTGAAGCCATCT	63.048	GTCGTcTCCAAGTGTTCCTTCTGT	63.036	105
HM_2807	contig07590	CTG	3	15	AATCGGAGCAACAGCACTTATTTC	62.854	TCCGTTCGGTCTAAACACTCAGAAG	63.015	143
HM_2808	contig03554	CAA	3	15	GGAAATTGGGAAAaTCTCTATCTCC	63.334	TTGGTGTGGtTTGGTGATaGTTG	63.044	160
HM_2809	contig116159	TTC	3	12	TGGGAAGAACTCTTGTCTATCTCT	62.773	AGAGTACTGTGCAgAaCAAAATgGc	61.91	96
HM_2810	contig22787	TGC	3	12	CTCTCGAGCTGACAAAGATGACAC	63.64	TAGTTAGATGCTTCGCTCTCAGG	63.239	107
HM_2811	contig22058	TTC	3	15	GAGATGAaGAGAGCGGATCTGAA	63.093	GTTGATCTGTTCTCTGTGAAGCCA	62.937	148
HM_2812	contig35387	GCT	3	15	ATTGAAGGGGgAAATGAaAgAATC	62.77	TAAGAAGAAACACGACGATGGACA	63.048	81
HM_2813	contig35919	GCT	3	12	TGGGCTCCATcGTtTTCAGaATt	63.121	TCCATAATCAGACATGTTGCTGT	63.257	119
HM_2814	contig18233	GGT	3	15	GGCTATCTTCCGTTTGTGCTACTGA	62.947	CTTCCGAGAACGCACTACCAAGAT	63.023	92
HM_2815	contig30354	ACA	3	12	CTTCTGCTCTTTTGATGACCTGG	63.531	TGTGAAAACAACCTAAAAAGTGGa	62.928	146
HM_2816	contig28372	TAG	3	15	GTGGTTTTGAGATTTTGGAGGATG	62.996	CcAaCAAAATCACTCTCACTTCA	62.592	149
HM_2817	contig38851	TCT	3	12	cGAAACaAcTGGAGgAGTCTtTl	62.282	CAGGGGAaAcCTAGTcCATAGAT	62.767	94
HM_2818	contig12908	TGG	3	12	GTTTTTCCtGTTTTCTCGCTTTCA	62.932	TCAAACCTCTcCAAAcCAATCaAAAA	63.013	153
HM_2819	contig02737	TTC	3	12	CTTTTTCTTGGGTAAGCTTTTT	62.998	AAATTGAGCTTTTACTTCCAGCA	62.451	155
HM_2820	contig16334	TGA	3	12	CGATATCTGGGCTTAGGCTTTTCT	63.107	CATCACCACTGTTGAAGCTACC	63.042	103
HM_2821	contig00719	GGC	3	12	AAGATTCCAGTGATTGAGCGAGC	63.051	CTCCGCTCTTGTGCTGGATAG	63.474	147
HM_2822	contig31723	GGA	3	15	TTCGGACTCGGATTCTGATAACTC	62.9	TCTGACTCTCACAAGAACTCACTG	63.027	123
HM_2823	contig16352	TGA	3	36	TGAGAGCAAAATCCAAACATCTAC	62.645	TCTAGATCTcCACTCAATcTcCCA	63.285	154
HM_2824	contig33271	CCA	3	18	TTGAGAAGAGCATAGTGGTAGGGG	62.907	TtGgGATGTTGAGTCTGCTTTGG	63.743	107
HM_2825	contig29458	CAT	3	12	aTACCCCTCATCAATACCCcCG	63.203	TaTtAGGTTGGAaAgGGGGAaCaAT	62.875	113
HM_2826	contig15234	ACT	3	12	GCTCcaACCATCTAAGTCTGACC	63.133	ATTGCTTCTAaAgAAGGGCTTTGc	63.221	153
HM_2827	contig05936	TTC	3	24	CAAGTTCATGGACATAGCCTTTCC	63.121	cCCCCATTGTAACGAAGGAACCTT	63.576	134
HM_2828	contig10813	TTC	3	12	ATTTAAAGGTTTTGTCTGGGCAATG	62.437	CCAATCACAGTTTATGTCGACAG	62.324	157
HM_2829	contig07408	ATC	3	12	GgtCAcTTTCTCTCGTTTAcCaATC	62.199	GGTGCTTAACAAGCTTGAACACA	63.688	118
HM_2830	contig05933	TCA	3	12	GTATATGCCCTCAGTGAATAGCGG	63.046	GATGAAGGCATTTTTGAATTGAGC	63.134	158
HM_2831	contig38324	TTC	3	12	AcccATCAACTCTAAATATCAATTCTT	60.642	TGAcTCACTATAGAGCTcCaAaCa	61.162	116
HM_2832	contig22749	CTT	3	12	GATTCTCTTGTGGAAGcCTTGtG	63.438	AAGCTGTTTTTCAAGCTTTCGGTA	62.571	131
HM_2833	contig27510	GGC	3	12	TCACATTCACTGCACAGACTTCA	63.076	GTTTCTCAGCGGAGAGAGCATTAG	62.936	126
HM_2834	contig38671	CCA	3	15	ACTTTCTGATCTTCAAGAAAGTCC	63.29	GAACTCGATGATGGTGGAGTG	64.057	147
HM_2835	contig23959	CAC	3	12	ATAGCATAAATCCGGCTTACACCA	62.854	AAGCAATgCTGAGAAATGAAGCC	62.941	158
HM_2836	contig18109	TTC	3	12	TCACATTCACTATCTTCTGAGCG	62.948	TTGGAAGATCTTTATTACACAGCA	63.059	158
HM_2837	contig13875	ATG	3	12	GAGGGATAGAGACAGAGTGGGA	62.99	CTCTATcACAGtAcCCtTCCCAT	62.865	148
HM_2838	contig14055	TGG	3	18	GCGATTTCGTAATCCCACTACTCT	62.425	CTTTTCCGACTCACTCCCAATTAC	62.299	155
HM_2839	contig26648	GTG	3	12	TTGCTCTCCGTTCTTTGAAGTAAG	63.015	ATAAAACCAAGAACTCGCATCC	62.608	150
HM_2840	contig45251	TCT	3	15	CagCAGAGACTTGAAGGGTAGTTT	63.146	CAACAGACTAGAGATgGGGAgGAA	62.984	133
HM_2841	contig51424	CCT	3	18	AAaCAGCcaTGACTCGCTCG	63.796	cGCAATGGAGCGCGATtAgAG	64.79	88
HM_2842	contig03089	TGC	3	24	ATACACAGTGATTGGCTGTCCAAC	62.412	TTATTACCATgGATATGGCTGTgG	61.919	113
HM_2843	contig10438	GTG	3	18	ATATTGGTGGTCTCAGTCTCGGT	62.798	AGAGCAGCTCGGAAAGTATGTTG	63.154	157
HM_2844	contig29978	AGT	3	15	TTTTATGACAGGCAATCAAGGGAT	62.912	ATAAAAGCAATGaAGGCaACGAAA	63.05	87
HM_2845	contig02215	ATC	3	12	TATTCAAGAGCagTACATCGAGCA	63.283	CCCTcTTTTAGCCTCATTTGTTT	63.005	152
HM_2846	contig38498	CTT	3	12	CTGTGACAGTATCGTCTTCTCC	63.1	GATTGATAAGGTTTTGTGGCAG	63.03	110
HM_2847	contig15251	CGA	3	15	CAATCAACAACAGCTCCATAGAGC	62.962	GCGAGCTATCagGGTgaAGAAAG	63.256	128
HM_2848	contig09313	GAA	3	12	TCTGAATTTAAGAAAaCAGCAGAGTG	63.133	cGACGAACCTACAACTaAAACCa	63.265	128
HM_2849	contig06596	AAG	3	15	CaaGAAaGAAAaGTaGCAAGCAACA	62.228	TCTCGCGGTAGACTATTATCCCA	63.126	109
HM_2850	contig00011	CCG	3	15	AGCCACTGGTCAAGTATGAAGCTG	62.949	TAAGATCCGAGGGAGAAGAGATCA	62.658	125

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2851	contig06996	CAT	3	15	TTGTCTGGAAAGGAAATCATCATCA	62.896	TGCAAGGAAGCTCTaAGTTTGTCT	62.862	115
HM_2852	contig11240	GCT	3	15	AGGCTGGTAAAGGAAATCTGGAC	62.995	ATGATGCCAATTCCTCTGTCTCTA	63.112	100
HM_2853	contig11649	TAT	3	12	AGAGAGTTGGTCTCAGAGAGGG	62.52	CCGATCACTTCTCTCTCTCTCA	63.098	149
HM_2854	contig18255	TGA	3	15	GTGATTGGGGTATTGCTCTTT	63.487	AAGTGTAGTCCCATTCCATGAAA	62.897	127
HM_2855	contig42762	GTA	3	15	TGGTAATTGGGTGGTAGTTTGG	63.011	TCATGGTGAAGTACTCTAACTAGCTGG	62.32	137
HM_2856	contig02182	CGG	3	12	CATATTGTGTGGAACCTCTGCTCC	61.966	TTGGTCTTGTCTAGAATATCACCC	62.607	123
HM_2857	contig16844	TGA	3	12	CCAATGgTGGAAATAAAGTCCAGAG	62.993	AGTAGtGTCAACATGGGCACTCaAA	62.844	137
HM_2858	contig45387	GAA	3	15	TGGGGGTGTGTGATGTCAGATAGT	63.01	AACCAAGTCCCAAGCTCAAAACAC	63.036	111
HM_2859	contig28504	TTG	3	21	CAGTCATCACTTCAACAATCTCC	62.922	AACAGCAACAGCAACATGAAGAAG	62.869	99
HM_2860	contig23365	ACC	3	12	TATATTATGACCGACCAATACCCC	61.922	AGGAGGAtGCTCTTgtTGTG	62.921	100
HM_2861	contig22226	CTT	3	12	AACTCTTCAACCTTcGCTTTTT	62.726	CAGTTCTGGGAATGCAGatGATA	62.51	153
HM_2862	contig05812	TGA	3	12	ATAATGGACGGCTGTGATCTGTT	63.039	aAACCTTCACTCAGCTGCTTcAc	63.255	92
HM_2863	contig02383	AGG	3	12	AATGTGAGGTGTGCAACACAAAAAG	62.635	GGGCTTAAACCTCAcAAAAACACA	63.439	154
HM_2864	contig11012	CCG	3	15	CTCTCAAAATCCCCCTATTCAAC	63.16	GCGGAACACCTCAITCTTACaAAA	63.54	157
HM_2865	contig26417	TAA	3	12	ACGtTTGAATATTATTAAGCAGC	62.451	tTAtTGC AAAATCATGATGGGT	63.416	147
HM_2866	contig17136	ACT	3	12	TCTTTCTCCCCCTTCTCATCT	62.755	TTGTCCATCAAATTCACATCTGC	63.262	124
HM_2867	contig18313	GGT	3	12	gTCCAGTCGGTGGTGGTGT	63.262	TCTCAATACCCAAACCTTAACCTT	63.074	135
HM_2868	contig00114	CTT	3	15	TGCAACACCTGTAGGATGAGAGAA	63.265	TTTGATCTCTCAACAAAATCTCC	62.897	128
HM_2869	contig00671	CTT	3	15	GgAATAaGGGgAATTtgTGTAAa	63.255	TTGGCTATTATTCTCGgGAAATG	62.437	153
HM_2870	contig07058	GTT	3	12	AATCCACCATTTGTCAATACTGCCT	62.926	TTTCTtTcTtCtCCCTTCACTC	62.968	153
HM_2871	contig17983	ACC	3	12	ccaTTAACCTCTGTAaCTGgaCCG	63.015	TGCTGAGGTcGAAGAAGTTAGAT	62.712	159
HM_2872	contig51301	TGT	3	12	aTTAGGGTTCGGTGTGGCTTTAG	63.589	GAAACAGGTGGAGGATGAGAAAGA	62.987	155
HM_2873	contig02753	TAT	3	12	TGAGCGTTTGTATTGGTTTAAAT	62.839	AGATTTTTTCCGATTGAGTTGTG	62.712	118
HM_2874	contig09918	ACT	3	12	TGACATTCCTGTAGGAGCACTCT	63.102	GTAACCTGCATCTCTGAACACAGA	62.741	135
HM_2875	contig35388	TCA	3	12	ATCCTCATCGTCACCACTCAAGCTC	63.031	TGAGGATGAATTTGATGAGAGA	63.132	100
HM_2876	contig01909	CAC	3	15	CGCGTTATCATCTTCTCTACAT	63.766	aATcATTTTTaAgGGCGTGAAAT	62.914	147
HM_2877	contig14741	CTG	3	15	TCTCATGTTCGGGACAATTAACAA	62.717	ATGAgTAGCAGCAGAGGAGGAAGA	63.027	139
HM_2878	contig44573	CTT	3	12	TGCTTCCGgtGTtATTtAAAGAAa	63.034	GATACCTAGCAAAATGCGGATCAACC	63.05	143
HM_2879	contig01918	TCA	3	12	GATGTGTCACTGCCATTGGATA	63.381	CTCCAAAGATGTTGGTCCCAAG	64.042	156
HM_2880	contig03911	TCT	3	12	CGCCAACTCTATAGAGCATTTTCT	63.084	AGAATCGCCTTAATAGTCGGGAAG	63.004	158
HM_2881	contig42827	AGA	3	15	AAGAGTTCGACaAGagaaATGgGA	62.698	tgGTTCTCTGTCTAGCTcTCG	63.554	157
HM_2882	contig21515	GAG	3	12	ATGTTTGACATCGCTGCTTGATA	62.975	CTCTCTCTTGGGTCCAATCAA	63.094	133
HM_2883	contig23554	GAA	3	12	AGCACCCAACTCTGTCTTCTC	63.036	AGCTCCGAAGAGCTTGTATCTCT	63.02	101
HM_2884	contig38239	CCT	3	12	TCACCTTCAACCCATCAACTACAA	63.026	CAAAAGAGAGACGGTGATGACTT	63.01	145
HM_2885	contig23654	TCT	3	15	GACCAAGCAACATATGACTTCTCC	63.248	GGAGGTAGAGGAAGAGGAAGAGGA	62.639	90
HM_2886	contig32717	TCT	3	12	TAAGGAATCCATGGAAGAGCTCAG	62.996	TATCTTCAAACTCTTTGCGCAGC	63.043	106
HM_2887	contig12929	ATC	3	15	ACCAGGAAAACCGATAGTAGTGA	63.225	TAGTCCCAAAATGGGTAATAATGC	63.041	82
HM_2888	contig00760	TCT	3	15	CcATGTGAaAAATCAATCTTCTGT	62.294	AAGAGTGAGCTGTAAGGGAaAAcC	63.201	90
HM_2889	contig34126	TCC	3	18	GTGACACCGTGAATTTCTCTATTG	62.831	AGAGAGTTTTcCAGATCCAAATCG	62.07	107
HM_2890	contig27900	GAA	3	15	CTCTTCTAGAACCACCTCCCAAT	63.068	GGTCGTCTTcCTCTGTTTTCTCTC	62.998	127
HM_2891	contig36558	TTG	3	21	TTTgATtCTTgAATTGAGAGGTT	63.96	TACTCACAACCAcCAAAACAACG	63.167	98
HM_2892	contig30280	TCC	3	12	GCCTCACTTCTCTTGAACACTT	63.027	GTACTGAGGAGGATGAGGAGGGG	63.629	146
HM_2893	contig49802	TTG	3	15	CCATTGAACCTTCTCCATCAACT	62.684	GaATCGATCGTCAGGAGATACAG	63.55	141
HM_2894	contig04057	GAC	3	15	AGAGTCAcGAaGAAaCGGCACCTG	63.146	TCCTTTATGCTCTATTTCCCTCTC	62.993	156
HM_2895	contig33166	CGA	3	12	TTTAAACTCGAACTGTGCCCAGA	63.21	ATCTACGAAGCGCAACAATTTCT	62.439	159
HM_2896	contig31592	GTC	3	15	CCGTTTTAGAGTCTCAACAACCT	63.02	taTagATACaTgCGGcTGCAGAT	63.971	133
HM_2897	contig01108	TTG	3	12	ATGTCTCGACTCAAGCTCTGTCT	63.032	TAAGAATCAACAATGGTGAAGCGA	62.946	153
HM_2898	contig26311	GGT	3	12	AGAGATGAGTCAAGAGGTGGTGA	63.662	CCGGAaAATCTGTCTTTCTCTCA	62.919	125
HM_2899	contig28475	AGA	3	21	ATCAATAAACAAGATCCCCATAGCC	62.693	AGTGAATCGGATGTTGtGAAGAT	63.12	143
HM_2900	contig12724	GGT	3	12	GTGCTGATGTACAAACGGATCCAA	63.181	CCACAATGTTTTCATGCTTACAA	63.055	103
HM_2901	contig03089	ACC	3	12	TCACGGTAATGCTAGCTCTCTTAg	62.944	GATAAAGATGGTCAGCCCAAAATG	62.912	151
HM_2902	contig06065	CGA	3	15	ACTAACCCCTAACCTAGCCCAAT	63.26	AATCAGTAACATTCGACGAGAGC	62.94	160
HM_2903	contig15732	GTG	3	12	CTCTCGACCACTGGTCTCTGTT	63.02	GGGTCTCTGACTACAATGTCTCT	63.918	114
HM_2904	contig20040	CTT	3	15	AAAACAACCCAGAGTCTCAACAC	61.888	GAGGGGTgTAGGGTCTCTCAGTAT	62.876	113
HM_2905	contig15632	TCT	3	12	tAGTCGATGCGAGGATGCTTATC	62.95	CGATAAACGAGGAGTGAAGAAGGA	63.006	135
HM_2906	contig52474	TGT	3	24	TCAAAGCTGAACCTATAAGACACCA	62.37	TGAcATGGGATTTCAAAACAGTAGTCA	62.86	137
HM_2907	contig33362	GAG	3	12	GGCTGATGCTCAAGCTAGAGATA	62.834	CGATCCCTAGGTGACAACTCCTA	62.795	138
HM_2908	contig40555	ACT	3	12	AAGGACCAATCAATCTCTGGGT	63.278	TTTAGATCGAGCAGGTGGTAAAGC	62.947	139
HM_2909	contig09727	AGG	3	12	TAAAGAAAGCAGCATCTGGCTGA	62.555	CTTGCCGGCTTCTTCAAG	62.188	115
HM_2910	contig00204	TGG	3	15	GCAATTTGTAGTAAAGGGCAAGA	62.652	TTACATGCCACTAGTCCCAATGAC	62.309	133
HM_2911	contig27173	TCT	3	12	AATCGCTATAGCCGAGCAAAATC	62.858	TGTCAAGCCCAAAATACAGAGG	63.471	128
HM_2912	contig33623	AGA	3	12	CTCTCGAACTCAATGACTGTCCCA	62.919	CTAGATGTGCGCTTGATTGTCG	62.11	111
HM_2913	contig19516	TCA	3	30	TGCATACAATTTAAGATGTACCACAG	62.318	GGATTTTTCATGTATATTCTGGTAGCC	61.329	137
HM_2914	contig40710	CCA	3	24	TGTTTCTCTCGCCCTTAAACAACAC	62.836	TCATCATCTGAATTTGACAACGCT	63.055	104
HM_2915	contig39674	ACC	3	15	AACCCCATCAATTATCTCATTTcC	63.067	tGGGcTACCTcaGAGGgTaAAAAAT	63.285	108
HM_2916	contig15773	TGC	3	15	AACCTGTGGAGGGTACTGGTGAC	63.67	tCCCCCATTTGaTaAGATGATGT	62.887	149
HM_2917	contig36300	CCA	3	21	CACCTACCACTCgaTACCAACAAT	63.338	GGTGgAAGGGGTgGTAaAATTAGAG	63.18	157
HM_2918	contig18976	GTG	3	12	tGTGTGTGTGTGTAGTGTGG	62.955	CCAATTACaAGAAATTCCAATGCC	62.722	159
HM_2919	contig09648	GGT	3	15	TTGGGACATCATCAAAACAATCAC	63.028	TTGAGTCATGACTCTCTCAGAGCC	62.045	158
HM_2920	contig14712	GAA	3	12	TGAGTGTTTTTGGTGATGAGAC	62.487	cATGAGATcCaAaACCAGTATCC	62.887	160
HM_2921	contig28555	GTG	3	12	TTGGTCCAACCTTGAAGAGATAA	63.091	AACCTTCCACCATGTTAGCCCTT	63.203	99
HM_2922	contig02936	TGT	3	12	ATGGAATTTTCAGAACAGGAACCA	62.996	GTTACACAAACCCCTGAACAAACC	62.822	147
HM_2923	contig03226	GGC	3	12	ACCATCTTCgAaGCAATCATCAAT	63.129	ACACAGATCCAAACAATcCTCATT	63.004	87
HM_2924	contig25623	GCT	3	12	AAGAGTGCTCAACCTTTGAACCAG	63.133	AAAAGCCTGATGAGATTTCTGTGG	62.91	146
HM_2925	contig14980	TGG	3	15	GGTCAGGCTACCATCTGAGTTCAT	62.915	CCATAAGTGCCAAACACCATTTCT	63.134	127
HM_2926	contig20872	GAG	3	12	ATGGACTGTACAGCTGGAGACTT	63.249	CCACACTACaACAATGACCACTC	62.827	140
HM_2927	contig12134	ATC	3	12	CTGGTCTGATGATGAGAGAGTCCA	63.006	GCCATAGTGATACAGCAAAAGGG	63.043	115
HM_2928	contig08290	TCA	3	12	ATCGTTGAGTGTGAAAGAAaGCG	63.87	CGGTTGATGCTGATTTgtGGTTTT	63.134	137
HM_2929	contig40961	TGA	3	12	TGAGAATTGGGTCTATCTCTGAAT	62.987	GATGCCCATGGATAGATCaGaAc	63.007	159
HM_2930	contig37347	TCG	3	12	GGAAATCATGGTGAAGGTAAGAA	63.317	CTGCTATCTCCGTCTACTCGTCC	62.725	158
HM_2931	contig13575	AAG	3	21	TGTTGGAGAGACAGCAAAATCAG	62.919	ATGATGATGACTAGGCAACCTTG	62.923	157
HM_2932	contig41062	AAG	3	15	CCAAGACAACAAGAAACATGTGC	62.958	TTCTCTCTTAACCTCTTCCCTTGA	62.045	84
HM_2933	contig01391	GAA	3	12	GAAGAATCGCATCATCATCTGAC	64.21	CAGTCCGTAGCTTcTcAAATTTCA	63.848	133
HM_2934	contig45608	ACT	3	15	AGTGGTGCAGAAAGCTAGTGGTTG	63.146	CTAGAAACCCAGAGATGGACACG	62.598	160
HM_2935	contig15997	GAG	3	12	CAGATGATGAGGGTGAGAGGGTGA	62.677	AATCAGAATCATCAGAATGGCGTT	63.129	159
HM_2936	contig05154	TTC	3	12	ATTTTTGCTCTGTTTTCCCTGTTT	63.296	GaGAACCCCTGTTGCACTTCTTA	62.022	160
HM_2937	contig30050	ATT	3	15	TTTGCCAGCTAAAGCCAATATTGT	63.146	tCgTTTTgGGATTTATCGAgAGAC	62.705	150
HM_2938	contig04454	CTC	3	12	GACACCTTTAAAAGATCCAAACC	63.078	ACGGTTGTGGTGTGTTTTTTCT	62.943	111
HM_2939	contig02579	ACC	3	12	GAGGACTTCTCCTGAGGTGAC	62.986	CTGATGGTgAAAAGaCACAATGAT	63.388	121
HM_2940	contig38139	ACT	3	12	TCGTCTGCACGACTCATTTGAC	63.623	CAGGATACTCagTCTCTGTTGAAATGG	63.513	126
HM_2941	contig20735	AGA	3	12	CTGAGAGCGAGTTACAGTGGTCA	63.063	CTCTTCAAGCAAAATCAAGCTTCT	63.031	124
HM_2942	contig00605	GGA	3	12	GGTGGTGTGGATCTCGATCTTTA	63.532	AATCCTAATCTCTCCACCAGGAAT	62.971	104
HM_2943	contig08797	CAC	3	15	ATGTCCTACTGTCATCATCATCTGC	63.515	GaaaGaaaGAGAACTGCCTCCA	63.019	125
HM_2944	contig14855	TCT	3	12	CCTCACTTCAACCTCAACCTTAC	64.324	CGGTGATAGTGAaAATGCATCTGA	63.372	149
HM_2945	contig50844	TCT	3	15	CAAAAGTTTTCAAGCTGTGTGAG	63.326	AACTTAGCAAGGCAAGAAACCTTA	62.522	137

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_2946	contig41072	TTC	3	15	cGGTCCcTaGgATgTAaAGATGA	62.784	aAGAAAGAGAGAGaAAGAGAGgaAGAGG	62.608	124
HM_2947	contig39272	CAT	3	21	GTCTCTTCACAGACGGAGAAATTA	63.022	TAAGAAAAAGTGCCTCAACCAATGC	63.439	159
HM_2948	contig12362	CCA	3	15	GTCTCTCAACaGTCTCTGCATCAAA	62.937	AAATTTCCGGATGGTGAGAGAAAT	63.176	142
HM_2949	contig45841	GAC	3	15	CGACATCGTTATTCACTTCTGACG	63.061	GAGATATGACGATTATGATGGGGG	62.681	147
HM_2950	contig06893	CAG	3	12	GtCAACACCAGCTTTaACACCTCC	63.25	CATGGAAATATATGATCCGCGTCT	63.23	133
HM_2951	contig23771	TGA	3	15	AAGTTGAAAGAGGGGGTTGAAGAG	63.172	TTCAAGCAGCAATAGGATCAGTC	62.847	110
HM_2952	contig16423	CAT	3	18	AATGAGTCCCTCTTAACTTCTCA	63.204	GGGAAGAGAACGAGGGTTTAAATG	63.273	124
HM_2953	contig04233	GCG	3	12	CATTgATCTATtCGGGTAGTGGGA	63.305	AGTTTGGGGATGAGACTGAAGTTG	62.895	132
HM_2954	contig20437	TGG	3	12	ATGGATCTTTGAGGCTACAGTGAC	62.816	TTTTCTCTCACACAGAGTTGTGG	62.81	120
HM_2955	contig12228	CCA	3	18	AATGAAATAAAGGCCTCTCTCCG	63.676	GAATCATCCCTCAAAATTCACCAAG	62.987	125
HM_2956	contig47600	AAG	3	36	TCCAGATCTTAAGCCCAATaCGTGA	62.11	GGCATAGAAATCTTGGCTTCTCA	62.925	156
HM_2957	contig30625	GGA	3	12	AAAGCCCCGAATTAACATCTTCC	62.631	CTTCCAACTTCCGCTTGTGTATT	62.741	153
HM_2958	contig50276	AGA	3	12	AaCACACATACGAGGAAAGAGGA	63.019	CCGATGACACACTCTAAACACAT	63.348	146
HM_2959	contig42836	GGT	3	12	GTGAGTTTGGAGGAGGATCTTT	63.062	GTCGAAGaCAAGAGaAGCTCGAA	63.45	135
HM_2960	contig02872	GAG	3	15	ACCGATTTCATCAACTCGTTTTT	63.778	CTAAGGAAGACGCTCAAGCG	62.945	145
HM_2961	contig39019	CTT	3	12	ACAAACAGGcTTGAcAGaATAGGC	62.949	tGAACaACCCATATTTTGATGGAC	63.206	152
HM_2962	contig03098	GGT	3	21	CAGAGAAGCATTTGTCTAGGCCATT	63.035	ACACCTTCTCCAGAAACAGCAATC	63.027	135
HM_2963	contig22931	GTG	3	12	CCGAGTACaGATGCTTGAATATG	62.125	GCAGGCAATGTAAGCTCTCTTA	63.055	134
HM_2964	contig25853	CAT	3	12	CAATGAAAGGTTTTGTCATTCTCC	63.018	GTCGCTCTGGTTTGAAGGAACT	63.126	133
HM_2965	contig52105	GTT	3	12	TAAATCATAGACCATCGGATGACG	63.163	ACCAGGGTTTTGGAAGTGAAGAT	63.285	159
HM_2966	contig09501	TCT	3	18	AAGGAACTGTTTGCCGAGAGTAT	63.511	TAAATTTTAGCAATGGCGGAAGA	62.943	156
HM_2967	contig00007	GTT	3	15	AAaTCTGATGTTGtTGTGCTTgA	62.948	GATATGATGGAATTTGGGAAAAACG	62.602	159
HM_2968	contig32942	TCT	3	12	TAAAGACCACCTGTTTCCGAGAAG	62.905	GCAGATTGAGGTGGATGAATTAAC	63.016	116
HM_2969	contig04902	TCT	3	15	ATCGACGACGaGTGTCtGTAAgt	63.48	GTTAAGAGATTGTCGAGGGATG	63.142	124
HM_2970	contig37199	TCA	3	18	ACATTGCTTTGCGAGACTCTTTTT	62.659	GAAATCAATCATGATACCTGTGG	62.901	157
HM_2971	contig27174	TGG	3	12	GTCTCGCTGAGAGATCAATAGGA	63.222	CGTGGTATGGGAGGAGGTAT	63.293	115
HM_2972	contig10603	TAC	3	12	ATCAGGATTAAGGTGGTGGCTGA	62.91	GTGGATACCAAGATTCACCTGGAG	63.102	138
HM_2973	contig01499	AAG	3	12	GGTTTCGTGAAGAAGAGAACCA	63.796	ATGACATGCTCAGCGGATAAGATA	62.979	156
HM_2974	contig15060	GAA	3	12	GCCATGcGTGTTTTCTCTTTCTA	62.935	TCCTCTCCATCACTGTCTCTTTCC	63.202	123
HM_2975	contig44365	TGA	3	21	GATTGTgAaATTTGGTGGTATTCC	63.639	TCACAATCTCAATATCATCTCGTCAa	63.044	128
HM_2976	contig40728	TGC	3	24	ATTGGCCcTGAGAGCTGTCTCa	63.767	AACaGCCtTCACAGAAATTCGAG	62.933	135
HM_2977	contig23656	CCC	3	12	gtTATACCCGcTaCTAcGCCcAc	62.961	ATTGATATGTCTTGCAACCAACT	62.926	156
HM_2978	contig17150	TGA	3	12	AGGAAGATACCAAGAGGCCAAGTT	62.899	TtATCATCaTAGTGCTTGGCGTg	63.283	155
HM_2979	contig04216	ATC	3	12	CACCTGGATGTGAATCTGCGGTTG	62.922	TTACaACtGCTTCTTCTCCCTTGG	63.015	126
HM_2980	contig14352	CTC	3	21	GCAGTGATGAGTTGTTGAaaaaGA	60.68	AGaACCTTTTCTAcCTGCTTTTCG	61.3	160
HM_2981	contig38090	AAG	3	15	TTTGTCGCTGTGTTCTGAATCAAT	62.948	TtAAACCTAGAAAGGaaACCTCTg	62.779	110
HM_2982	contig03867	ACC	3	12	AATTCACTTTCGCAATTTctCCA	63.009	GAAAGTGACAGGCCCTGTGATTA	63.648	116
HM_2983	contig09104	GAT	3	18	ACCAACAAGACCTTGAATATGGA	63.006	AGGACTCAACAACCAACAACAA	62.944	82
HM_2984	contig13539	TCT	3	12	AATATTCAGTTGATGTGAGGGGA	62.887	TcCAcCaATGGAAGTAAGAAATGA	62.588	155
HM_2985	contig00553	TAC	3	12	CCATATCTTAGTGTCCATCAACGG	62.884	TTGTACACCATCCATCAACCTGCC	63.065	148
HM_2986	contig21638	GCA	3	15	CTGGTGTCTCCACTCTTATGGG	63.208	TGCACAGAAGTAGATTgGGATTCA	63.038	114
HM_2987	contig42278	CTT	3	12	CAATTCAACTTTTGGCAAACTCT	63.027	GGTGATAAGCAAGCGGAAAGATAC	62.356	150
HM_2988	contig29565	CGT	3	12	AGAGATGGAGCTGTACGTCAGT	62.721	ACCATGTTTCAGGCAATTTCTCAT	63.026	154
HM_2989	contig31458	TGG	3	24	TGAAGGATCTGATGAGTGTCTCTG	63.03	ATCGTTCAAGCTTTCTAAACCCCTT	62.623	121
HM_2990	contig01506	TCT	3	12	GGATTTTCAGTTTTTGGCTTTTC	63.187	CATCAATATCTCAGACCCAGATG	62.924	149
HM_2991	contig21643	AGC	3	12	GAGGAGGGTTGATCTTCATCTTgA	62.977	ACgGACgGCTCtACTTTGATCTG	62.946	112
HM_2992	contig16761	CCA	3	12	CACCACCCAAATGTAAGTCCCG	62.817	GGTGGGGTGGaGACTTGTAGACT	62.91	152
HM_2993	contig14309	AAT	3	12	TGAACCAAAACAACTcGAAAAATAA	62.669	TGTTGGAGGATGAGATCGAGAAAT	63.311	154
HM_2994	contig43497	TGG	3	15	cAIGGTTGTGtACTGaCTCCAAAA	63.259	CCAActGtGACACtCACACc	64.188	149
HM_2995	contig50586	GGC	3	12	TTTTAGCCGCAACAGAAAGAAAA	62.357	TCAAAGCTTATCTAGACCGGTTG	62.823	124
HM_2996	contig16056	TGC	3	12	TTTTTCACTTCTCTTCTTCCGACG	63.239	CCTCATCTACAAGATGACCCGCTT	62.698	133
HM_2997	contig20869	GGA	3	15	TATTTCTGCTGTTCTTCTCTCCG	62.919	AAAATCTACAACACGCTCTGCTCC	62.838	97
HM_2998	contig48700	GCA	3	18	AAGTGgAAAAAGCAAGAGgAAAG	62.998	ATTTGCTGTATATCACTCGCCCC	62.523	116
HM_2999	contig01428	GTC	3	15	TGAGACGATTGAGATTGTGAGTC	62.926	AGTCCAAGCAACTACGaAAACGAC	62.959	141
HM_3000	contig23649	GGT	3	15	TGgTAGGgTTCGATTAAAGAGAC	63	AACaAgACCCtAtCaAAACACCA	62.907	112
HM_3001	contig00435	AGA	3	12	TCGGATGACCTTAGATTGTTGTGA	62.921	AGAGTCTCCAAGGAACATGGTGAG	63.106	112
HM_3002	contig09570	GGT	3	21	GTGGAGGGTAAATGTGCTCTGTG	63.111	CGAAGCTAGGGTTCACTCTCTTA	62.313	155
HM_3003	contig20045	CCA	3	15	GACCAGGTTCTCCAACTTCGTAAC	63.128	TCACACAATTCAAAAGGAAGTGGA	62.918	129
HM_3004	contig40725	GGC	3	12	CAATTCAGAGGGGGAGgTAGTGG	63.364	CTTAAATCAGAAACCAACAGAGCG	63.331	85
HM_3005	contig05996	GAA	3	12	CaATTGTTTGAAGTTGtGTGTA	63.103	TTCTcTCCAATTCCTTCTCTTCC	63.053	114
HM_3006	contig11392	ATC	3	21	ATGCTTATGAAGGCTGATACGCTG	63.772	TGAAAACGTCTTCTAGCTGGTG	63.851	134
HM_3007	contig15238	CAA	3	15	CTCTACACACAGCATCTCCAGC	62.736	ACTGTGGAGGTACATTTGATGGT	62.912	153
HM_3008	contig11004	GTG	3	12	ATCTCTCACAGTGTGACTGACTG	63.06	CTCACCACTCAAAACCAACTCAT	63.553	125
HM_3009	contig13808	GCA	3	12	GCAAAACAATgCTTTAGaagCA	62.579	ATGAAGGTGCTGCTGGTGAAAC	62.679	146
HM_3010	contig13581	TCT	3	18	GATGAAACTTCACTCTCTCCATCACA	63.027	TGGAGGAGAGGAAAAATgtGaAA	63.19	122
HM_3011	contig32748	GAG	3	18	AAATGTGTTAAGAGTGACGCCGAC	63.664	CaAAGGCTATCCAAAGCaCAAAA	63.526	149
HM_3012	contig22669	GTG	3	12	ATAGAAGAGAGGgCCGAgaaGAAG	62.685	CCATTATCATCCCTTCAAACTCca	63.048	150
HM_3013	contig05757	GAA	3	15	GTAGggCAAAaAGGGCTGAGACT	63.122	GATCCGAGGTGcGATGATACAGCAT	62.829	125
HM_3014	contig27762	GAA	3	12	ATCTGGCGAAGACTAAGATGATGg	62.913	AAGTCTCTCATGGTCATGGGTTTC	62.784	152
HM_3015	contig36551	AGA	3	24	TACGAGGAGAAATGGGATGAAGAC	62.786	GCTCTCTCTCTTTCATgGTACG	62.898	149
HM_3016	contig10173	GAA	3	12	GACCAAGCTCAGTCTTACTTCCCA	63.124	GGATtAcGCTATTGCACTGGAGT	62.94	121
HM_3017	contig12347	GAA	3	12	ATGGACTGCATTGACTGAAAGCA	63.078	TcCACTACATCTTCTCTGCTTCC	63	119
HM_3018	contig20647	AGA	3	15	ACAATCACTACTATTCGAGGCGGA	63.244	CGTTTGAAGACGATGTTGTTCTGT	62.635	151
HM_3019	contig17547	TGT	3	15	AGCTTCTGAACCTTGTGCGAATC	63.118	tTtACAGAAAAcCCCTACCAgGC	63.578	130
HM_3020	contig24162	TGT	3	12	GGCAAGAAACTCGAGCTCTCTACA	63.462	AACATAGACGAAGACGGCATCAAC	62.949	100
HM_3021	contig34055	ATG	3	12	TTTTGTATCAATCCGTACGAGAA	62.946	TTCCCTCACATCAATATCTCAT	62.876	134
HM_3022	contig43151	GGT	3	15	AAAAGTGACAGAGATTGAGTCCGT	62.626	gGCACAGTCTCTTCACTAGTGT	62.953	134
HM_3023	contig29332	CAC	3	12	CTTCTCAGCTCCCTTAATCAAAAC	63.583	CAAAAAGAGCGACACTGCTCTCT	63.159	157
HM_3024	contig34271	TCT	3	12	CACGAATTTCTGCAATCTCTCTT	63.022	TGATCTTGAAGAAAGAGAACGAGC	63.331	113
HM_3025	contig29489	CTC	3	18	CGGcCTCCCTATCACTATCACTa	62.705	TTCAAGTCTGATCAAAACGAGAAG	62.698	149
HM_3026	contig07599	GCA	3	12	GTATTCTGCCCAAGAGGATGAGT	62.915	ATTGTGGACATACGAGTCAAGTA	62.975	104
HM_3027	contig12465	TGA	3	12	ATGATCAAGGACTTGTGGCACTTT	63.242	ATCAACCAaCAACCTCACTGAT	63.014	149
HM_3028	contig32181	CTT	3	12	AGGTAAAAAGGATACCTGGAGTGCC	62.901	GATGACGGACACtGagAGAAAAAT	63.017	143
HM_3029	contig21927	TAC	3	15	TCAACAACCTcGAGACTCATCATCC	62.803	CTCATCTGAGGAAAGTCGAAGCTC	63.014	84
HM_3030	contig18963	GAA	3	15	TCTACTCCAAAACGCTGaGAAACC	63.031	GGACATGGAAGGATGAGATTGAAC	63.097	138
HM_3031	contig17602	ATC	3	15	ATTCCCACTTGTCTTCTTTTGG	63.671	TTGCCAGACCGGATTTGGAGaTA	63.944	126
HM_3032	contig09523	GTC	3	12	GTGTTTCGTGCACATCATCTGC	62.956	GCAAGAAGAACACTTCCCAATTC	62.411	160
HM_3033	contig08766	GGC	3	15	AGTTGAGGAGATTGAGGAAGGTT	62.764	cTAITTCaACcCCCaAAATCaA	63.097	157
HM_3034	contig17704	CGG	3	15	TGGAAGAGAAGACACGACAAATG	62.71	CCCTGTAAACCAATTTCTCTGTCC	63.111	128
HM_3035	contig28915	AGG	3	12	CCGATCAATCTCATTTGGTATCTCT	62.99	CAGAGCTGTCTGGTTACCTCCATT	63.023	92
HM_3036	contig26497	TGC	3	15	CAACTTGTCTCTGAGGAGGCTGTT	63.347	TCCTCTTCACTCAACGCTACCA	63.015	150
HM_3037	contig18043	CAC	3	12	ACCATCGTATTAGCACCACATCT	62.94	GGGAGTGTGAGCGATTACTGTGT	62.723	95
HM_3038	contig19076	GTT	3	12	AATTTTGCATCTACTCGCCATGA	63.341	AACaAGAAAGGGCAATTAGGCTC	63.016	158
HM_3039	contig01293	CTA	3	12	ATACACTTCAGACCCGACTTCTC	63.04	TTAGATTGGAAGACGCTTTTGAC	62.935	136
HM_3040	contig45006	CAT	3	18	TGTATAACAAGCAATTCGCCAAC	62.287	CCCAAGAGGGTAAATGGGAAGACT	62.873	158

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3041	contig29182	AAG	3	24	GACCCCTTTGAGCTTAAATGGAGA	63.002	ATGATTTACTCCGTGGTGTGG	63.227	151
HM_3042	contig08854	ACT	3	12	ATGATGATCAATCTGGCAATCTCT	63.007	CTGATTGTGAATTTGACTTGGAGC	62.931	107
HM_3043	contig32867	TGG	3	15	TTCaCAATTTCTCTCTCTCTCG	62.993	GACGAACGCTTCACTCTCCA	63.627	155
HM_3044	contig19443	TAA	3	15	CCATGTAAGTCTGATGTTTTCAGGA	62.279	ACTCTATGAACAAGGCTCTGTGC	63.04	117
HM_3045	contig36275	TAC	3	15	ACAGATGATGGTTCATACATGCG	63.172	accacCTCAATATCTCAAGCAA	63.121	140
HM_3046	contig30286	TCT	3	18	CTAACCTGTAACCTCGAGGCCATT	63.797	GAGTGAGAGTGGTGGTGTAGTA	63.06	125
HM_3047	contig46000	CGC	3	21	CTCATCAGCTTCAAATCTTATCA	62.814	AAAAGCGGAAGTCTACGATGGAG	63.02	140
HM_3048	contig08353	CAA	3	12	ATGAGGATTCACCTCTGAAACTCG	63	CAGCAAGCATAGGAGCTAAGGTGT	63.166	133
HM_3049	contig16788	TGT	3	24	AGTCTTAGAGGtTGTGTGTggg	62.805	gTCATCAATATGCAAAGCACTCCC	63.016	150
HM_3050	contig39685	CTT	3	12	CCTCTCTTCCAAGCAACAAC	64.394	GGGTAAGTGAGAGGCCAAATC	64.438	133
HM_3051	contig05291	AGA	3	12	GGATCACCCATCAaCAaATATGAA	63.01	GGCAAGATCATTAGCACTGAAAT	62.733	144
HM_3052	contig28126	CAT	3	12	TCTCCGATCTCTGTTCGAGTTT	62.698	CCAACTAAGCAAGGCTGAAATTA	62.744	139
HM_3053	contig43311	TTC	3	12	CCAAACACGGTCAAAATCATCG	63.492	TATCATAACAATCTCGGATCGGA	63.713	119
HM_3054	contig25229	CCA	3	15	CGTTACAGATCTGCTTCCCAAGT	62.933	TACTCTTTTGACTCGTTGGAGGg	62.905	120
HM_3055	contig09272	CGG	3	15	AAAGTCAAAgtCGTGGGAGG	62.77	AATGGtGcCTTTGATGATACATT	63.15	160
HM_3056	contig02013	CGG	3	12	GGGATTTTGACACGGTTGTCTTC	62.923	TtCGGTGTATAAATCCACCTTCG	63.421	134
HM_3057	contig08112	TTA	3	12	CTGTTCAAGGAAGAGTGTACCTG	61.417	CGAGACACTGCTAGAGCTTAACGA	62.353	148
HM_3058	contig44939	GAT	3	15	GCCTCGTTAGGcTGTCTGTACT	64.35	CTTTGAAAGCGTTGAAAGTGAGAA	63.948	151
HM_3059	contig16227	TGG	3	15	CACCACACCGTTATGACTTTCT	63.444	GCAGATCTCTTGGTGTGTTTCTCT	63.027	148
HM_3060	contig29702	CAT	3	18	AGTTGGTTTCACTTTCACACCTCT	62.807	AGAAAGCAGGTGGTGTGGGTGAT	63.15	102
HM_3061	contig43253	GAA	3	12	ACCAAAGAGGAAGAAATGAGGg	62.968	CTCTCCTCTTCTTCGAGCCTTT	62.791	147
HM_3062	contig11646	ATC	3	12	CTCTTCGCTTCGTTGTATAGACT	63.263	GGAACACAGGATTTAGCATCTGG	63.121	125
HM_3063	contig01799	GTG	3	15	TCGAGATTTGAAGAGGACAGGTG	62.919	GTCTTCTCTCTCTCTCTCTCAAC	63.064	145
HM_3064	contig18279	ATC	3	15	CTGCAAGGTAgCtCCATTAAAGAA	62.932	GGAATTGcaTTCTCTCTGCTGATT	63.029	153
HM_3065	contig22320	AAG	3	12	cAcCATCTTCTGgAGGTCTCTT	62.884	CGCTTTCACAAATTCATCACTCC	63.044	129
HM_3066	contig39424	TGA	3	15	TCGAGGATAAGCAAAACACTCTC	63.022	ATCCAGAACCAGTTAATAgGCGA	62.233	159
HM_3067	contig26989	CAT	3	15	CAAGAACCACAAATTCGACCATA	63.204	AAATGACCAAAgGGTCTTCTctC	63.071	147
HM_3068	contig06054	CAT	3	24	TGATGGATCTAACTCAACATCCGA	62.91	TGTTCCAAGTGAAGATGGGTATGA	62.803	145
HM_3069	contig21830	GAT	3	18	TCGATTACCAACAAAGCAAAAGT	63.039	TGCTTGATTGATGCAAAATTTCTTG	63.369	126
HM_3070	contig42141	AAC	3	12	TTTTCTCAACCAACCAACAGATTGA	63.036	ATTTGCATCTTTGCGCTGCTATT	63.358	156
HM_3071	contig00201	TGC	3	12	TGTCATAGgTGGATATCTCGATCC	63.315	TaggGGCTGGGACGCTCTAT	64.029	158
HM_3072	contig19926	TGC	3	15	TTTTGTGGAAGCTCTTCGGAAT	62.922	ATTTACTATGGCGGATGAGACGAT	62.134	152
HM_3073	contig02069	GGC	3	12	CCTTCTCAAATAGATGTTGCCTCG	63.324	TCCATCCGAATGTGTGATTGATAC	63.032	147
HM_3074	contig35434	CTC	3	15	GAAGTGGGTTTGAGGTCTAGAAGAA	62.997	GACAATCGAAGAGGAAAGACAGGA	63.102	139
HM_3075	contig14897	CTT	3	12	CCcCATCTAAAGTTTTCGCTCTAC	63.086	TCATTGCCTAGTACAAATGACAGC	62.659	125
HM_3076	contig01365	CGC	3	12	CAAGTCGATCCGATATGTGAAG	62.908	CTCGGAAGAGAGGAGGGAATC	63.735	127
HM_3077	contig41027	AAG	3	12	AGGTGGTGTCAACACAAAGCTGTA	63.077	CGGTTCTCAAGTcCCactATTTTG	63.113	152
HM_3078	contig43451	TCT	3	18	AATTTCCtCtTTTTCGAATCTCC	63.904	gaAGAGaAAGCAGAGGACAAAGAGG	63.199	144
HM_3079	contig24372	TCA	3	18	GAATACCTCTCGAGCAGCGTCCAT	64.115	AATCCCAAGTCAAGaAGGGTGaAT	63.489	157
HM_3080	contig06070	CTT	3	12	ACTCAaATcAGCTACGcGTCTAC	62.89	GAGAGCGAATCACAGAGaGaaAAGA	62.612	112
HM_3081	contig49753	AAG	3	24	GAAGAACCTTTTGAGGGGTGTTGT	62.992	CACATCaAAATCTCAATCCCTTCC	62.957	131
HM_3082	contig03865	TAC	3	12	CAAACGAACAGCTAACTCACAC	63.051	TTAGTCCGCTCACTGTTGTGTTA	62.886	84
HM_3083	contig01076	TTC	3	12	GGTCCAATGAGTCTTAGCATGTT	62.713	TACTAGTCCCCAAACCCACAG	63.405	142
HM_3084	contig01530	GTG	3	18	CTAATCGTGGTTCCTTGCATTT	62.729	TCCAGCAAACTCCATATATCCAG	63.223	160
HM_3085	contig08796	TCA	3	12	CATGAGGAACCTGATCAATAAGGC	63.112	GCTCGGTTCTAATATGCGGATGTC	63.158	144
HM_3086	contig33756	ATC	3	18	CAAAaGAAaTCTAGTTCACAGCA	62.811	CTTTATCCCAAGGATTTGAATTG	62.884	122
HM_3087	contig20596	TTC	3	15	CAGAGGCCATCTCTTTCTCTTct	63.18	CAAAAGCAGTCAGCAGTgTAAGCTC	62.78	150
HM_3088	contig00391	CCG	3	12	ACCGGTGATGGCTATAACAGAAAA	62.935	TAAGTTGATTTCGGACTGGGTGTG	63.415	103
HM_3089	contig02071	CTT	3	15	TCTCtCTGAAACaTtGgTTTTG	63.747	AGATGCACATCTCtTAAGcCCAC	63.146	141
HM_3090	contig16896	GAT	3	15	GATGGTGATCTAGAAATTCGCGCT	62.816	AATCCaAGcAAGaCagaagaCGAT	62.613	112
HM_3091	contig31083	TGG	3	15	GTGGCAGAGATTGGAGATTACAGAG	63.656	TCAGGCACAAACCTACTACTTCTC	62.822	158
HM_3092	contig07485	GGA	3	21	TGTTTATGATGGTGTAGCTCGAA	62.731	gCAAGTACCGCTACTAGTCAAAAGT	62.972	128
HM_3093	contig13752	GAA	3	24	CTGTCCAAAATCGGAAGCAATAAA	63.416	ACATATCACCCTTAAGAACCTCAGTCCA	62.45	133
HM_3094	contig27114	GTG	3	12	CAAAGAGTTTGGATCGAATGAGG	63.202	GCAGAATGGATaAGATTGCTTTCT	62.438	159
HM_3095	contig22348	TCG	3	15	GCTAGAAGGGAGAGAGGAAGGGA	62.863	CTGCGATTAGAGTGAAGGGACTA	63.019	101
HM_3096	contig36630	GAG	3	12	GTCTCGAGTGctattGGGTTGTGT	63.798	CACCCTCTCACACTCACCTACTT	63.011	150
HM_3097	contig30825	TCT	3	24	GCCCAATTGTGTATTATTCAaCAA	63.026	GAATCCATTATATCGCAATTTGGA	63.011	119
HM_3098	contig21025	TCA	3	12	TCAGCACCTTGAAATTTTCTGAT	63.219	TTGTTAGATGGAGAAATTAATGACGGA	63.022	151
HM_3099	contig46620	TTC	3	12	TCTTATTCTTTCTCAGACTGCCG	63.117	GGAGCTCAATgGAGATATCGaAGA	63.003	127
HM_3100	contig43022	TGA	3	12	ATGATGCTGATGTGGAAGTCAAAA	62.938	GGAGCTTCTCTCTGCTCTTTCT	62.999	135
HM_3101	contig25813	CAT	3	18	TACCCACATCACCAAACTCAATA	63.579	GACGGTCATGTTGATGACTCTGAT	62.586	140
HM_3102	contig33099	TGG	3	12	GGTACGTGAGATGGGTTTtGAAG	63.019	TCCACAGACATAGTCAACGGTACAA	62.828	141
HM_3103	contig31411	GAG	3	12	GgcTTTGAAAGTCTATGTGAGGCG	62.727	ATGTgCGTTTGCTCATTTTTCAT	63.026	113
HM_3104	contig22533	CTC	3	12	ATGAGAGTGAGGAGAGGCCCAAT	63.44	TTGCTtATTCAACACAAACACAGA	62.864	145
HM_3105	contig26227	ATC	3	24	ACTTTTGCTCGTATTTCTCTCTC	63.102	AGTAGGCTCCATTCTCTCTCTCTC	62.44	108
HM_3106	contig16250	CTC	3	12	TTCAAGCAAGAAAGGAGTGCTACC	63.142	CAAGcCAATGTTAGTTCAGATGG	62.945	116
HM_3107	contig09141	AGA	3	24	CGCTTGTGAAGGTAGAAAAGTCTG	63.053	ATCAAGCTaAAATAGCAAgGacccC	62.915	157
HM_3108	contig30603	AAG	3	21	GgTCTTGAGCGGTGTGTCAGtAG	63.373	GAGGGAGaAAAGAGaAAAGTGCGC	62.888	155
HM_3109	contig40095	GAG	3	12	CAGAAGCTCGAAGCTGTGTGAAAT	63.251	CTAGtTTAAGTCTCAGTCGAGcC	62.873	155
HM_3110	contig05442	CAA	3	18	TtTgagTgAGAGAGGAGAGGAGA	63.079	ATCCATTGCTGTTGATTTCGAT	62.736	120
HM_3111	contig28076	GAT	3	15	AGAGGAGCTTAATTTTCCCGAG	62.504	TtGTTAGGCGAGTGAAGTGTGAA	63.048	143
HM_3112	contig31693	TTC	3	36	TGAATGACCTGTAcAATTTTAcGCA	62.676	AACTAGTAATAAtcCTGCCCCGTG	62.464	158
HM_3113	contig15842	CAG	3	15	CATCGCAATAcCAATcAACATTC	62.962	AAAACCTTCATCATCAGCCAAATGC	63.553	109
HM_3114	contig33409	AGA	3	15	ATAcTGCATTGTGACACCAACCT	62.936	ATGTGCTGCTTTCAATGGC	63.41	147
HM_3115	contig23411	TGT	3	15	ATGTCGCAACGGCTCTGTACTC	62.966	TCAATTCAcATCATCACCATCTCT	63.24	102
HM_3116	contig01116	GAA	3	15	AGTGGTGAAGGAGGAGTACTGTG	63.011	CATCATCTCCCTAGGCCAATAAT	63.47	132
HM_3117	contig31592	CTT	3	24	TTTGTCTtGCTGCAAAACAGCAT	63.189	TGTGATCATTGCAAAAGGAAGaG	63.141	144
HM_3118	contig10191	TGG	3	12	gTATAAAACACCAAGTGCCAGCG	62.871	TCAGAGTAATGGAAGCTTTAGGCG	63.039	158
HM_3119	contig36086	TTC	3	15	TCCAGTCAACCAACAGTATTTCAT	62.726	ATAGCAGTTGAGAGCAGGAAAGGA	62.824	106
HM_3120	contig27076	CCA	3	18	AcGAGATcTCCCTTCTTGCTAT	63.612	CACAACCGTCAACCACTAATAA	62.843	137
HM_3121	contig05274	AAC	3	18	GAAGGAAACTGATAGTGGTGTGG	63.111	TACCTTTTGCAAGTTCACCTACAG	62.737	160
HM_3122	contig43022	GAT	3	15	ATGATGCTGATGTGGAAGTCAAAA	62.938	GGAGCTTCTCTCTGCTCTTTCT	62.999	135
HM_3123	contig13834	TGA	3	18	TTTGATTGGAATTTTCGTCAAGT	63.299	CTCATCATCTCGTGATTCAATG	62.91	113
HM_3124	contig11010	CCT	3	12	CCCCATCTCTTCTGTATCTCTC	63.059	TGAACCTAGtGtGGGATGATGA	63.016	114
HM_3125	contig28648	CAA	3	12	TCACATAAATCGTTGACCTTGGGT	63.019	GCCAGCCTTCCTAACCTAAGTATG	63.114	157
HM_3126	contig26114	TCA	3	15	TAaCCAAaTAcTgAGATGGAAGG	63.312	TATGATCTCTCAGCGAACAATGG	63.117	84
HM_3127	contig02033	CAT	3	18	GGAAGACTTCAGCTTCCAAATG	61.431	GGGTgATGGTGAGTCTCTTGTGA	62.351	112
HM_3128	contig25742	TCA	3	18	ACTGCCATTGaCAAACTGTGAaA	62.958	GAGGATGATGATGAGGaAAAGGa	62.761	160
HM_3129	contig15673	ACC	3	12	TAATGAGAAGCGGTGATcAGgAGGT	63.022	TCTGTTAGCGGAACATGTCTGTG	63.664	149
HM_3130	contig08536	GGT	3	12	AGGAAATGGGTCaCAAGCTTTTAC	63.7	CTATTCAACCATCATTTCCGCTCT	63.67	132
HM_3131	contig13216	CTT	3	12	ATCGATATGTGGAACAAGGGGAA	63	CCAAAGCTGATcATATCGGaaaaa	62.72	135
HM_3132	contig13997	GAA	3	12	ATCATTTGATGCTGATTTCGacGA	63.046	GGTATGAAGGAGTcAGCAAGCTC	63.356	118
HM_3133	contig26255	GGA	3	12	GGAGAACATCGAGCTCATCCAGTA	63.873	CCATAGCCAGctCATCCACT	63.697	104
HM_3134	contig09198	GAG	3	15	CCGACGTCCATTTGTTAGAGAG	63.222	CTCTTATCCTCAAAAGCATCCCA	62.8	137
HM_3135	contig40538	AGT	3	18	AAAAGTTGATTGGGAAGAGAAGGC	63.09	CCGGTCAACTGTAAACCTTATGCT	62.548	123

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3136	contig16277	CAA	3	12	CAGCAACaAagTCATTITTCaAa	63.373	CTGAGGTTGCTGTGaAATTGTTG	63.057	150
HM_3137	contig00349	TGT	3	12	AGATTTGGTGGTGACGATTTTGT	62.923	GGATTTTCATGGGGAACAAAAGAG	62.094	106
HM_3138	contig23728	TCT	3	21	TTTTAAGTtGCGGGTCAAAATAGG	63.126	ATCAGATCGAGAGAGCGAGAAGA	63.12	154
HM_3139	contig31712	TGC	3	12	TAAATGCTCGTCAACGTCTCAA	63.068	TCTGTCAATCAATACACCCCTCT	63.102	116
HM_3140	contig05232	AGC	3	12	GTTCGTGAATTAGCCTTCAGAA	62.86	CAAACTGCATAGCCTAGAGGAA	62.955	122
HM_3141	contig26609	TCT	3	15	CAAGTACTCTCACCTTTGCCACT	63.033	TTATTATAGCTGCGGGAGTTCTCG	62.852	145
HM_3142	contig01583	CAC	3	21	AAAAAGAGCAACGCTAATGGGT	63.99	CCCAAGTTGGAAATGTTGAGAAA	63.403	147
HM_3143	contig11880	TCG	3	15	CAATTCTCTCAACATTCCTCATC	62.987	GGGACTTGAACCTGATGAAGAGA	62.987	143
HM_3144	contig40716	CCG	3	12	CTTGATATCCACTCGACTCCAC	63.217	GTGGTATgGAGGATACGCTg	62.794	141
HM_3145	contig22980	TCT	3	12	GATCCAgTCCAGTTGcAGTTCTAT	62.901	TAGTTCTGTGCGCTCAACAAAGTC	62.985	128
HM_3146	contig26768	TCA	3	30	ATTTGTGGTGTGGATCTATGGCT	62.926	CTGTGCAGCTTCCCCTATAAAT	62.944	150
HM_3147	contig03116	AGT	3	21	TTGTGTGGgATTCTTTCTAATGG	63.3	TAACACAGTTGcAaACACCCAAAC	63.184	137
HM_3148	contig43308	GTC	3	12	GGTAACCGAGAGATGTGGAATCTG	63.217	GCCGACAAGGTGGAATATTGAATG	63.179	145
HM_3149	contig37481	CTT	3	15	GTGCGGAATGACATTTACAAACAG	62.872	ATTTcCacTcCacTcCAATCATA	62.887	152
HM_3150	contig05211	TAT	3	12	AATGTAATCAAGATTGTTGATCTTTCG	60.117	GAGCCAAGCCACAACTCTAAATT	60.976	132
HM_3151	contig03974	CGG	3	12	CGTCCCTTCagTCCCTTAAATA	63.556	GATGATTGAGGAAATCTCGAAGGA	62.876	136
HM_3152	contig32745	GGT	3	12	CTAATTTTGGAGTTGGGCAACAT	62.437	CCCTCTGATgtTaAGCCCTGAAAA	62.714	151
HM_3153	contig29426	TTC	3	18	GTTTGGTACGcAGTGACTTTTTC	63.154	GGAACTCCTAGTCCCTAGATCGAA	62.961	122
HM_3154	contig02137	CTA	3	21	CGGTATTGgATTCTCTGTGATCc	63	CGAGGAGAAAATCTCCACTTTGAA	62.993	136
HM_3155	contig02908	TCC	3	18	TTTTGGAACCTCAATCTCCACCTA	63.091	TGCATGACACCTCAGGACCTAATA	62.934	120
HM_3156	contig25097	TCG	3	12	CAAGTCCCTTCTTTGAGGGTC	63.392	GGGTAAACAATTAGGGTTTCTCG	62.989	149
HM_3157	contig38105	GAG	3	18	ATCATCTCTGACGAAAAGCATA	63.223	AaATCGAGTCAGGCGAATTAAG	62.839	144
HM_3158	contig48078	TCT	3	24	ACCATCATTTTCCACTTCTCATC	63.316	TATAGGGCTAGGGTTTTTGGGTTG	62.737	156
HM_3159	contig31987	GGT	3	15	AGAAACGGTTGGAGTCAAAGTCTG	63.02	CATCTGCTTCTCTCTCTCCAAAC	62.898	138
HM_3160	contig34704	GAT	3	12	GGGGACCAAAATCATGAAGGTAT	63.271	TTCAACCGATCAACAATGAACAAC	62.954	137
HM_3161	contig23679	TCA	3	18	GACCCCTTGAATTAAGAACTACCC	63.078	AGagAGTGGGAAAGGGTGAAGAT	62.764	117
HM_3162	contig36118	TTG	3	18	GGGTTTGGTCTCACATTTTGTtG	63.338	ATGAGCTTAGCCCTTTTTCGAATC	63.111	148
HM_3163	contig45960	GAC	3	12	TTGTACGTTGAAATGCTCGAAGAA	63.068	GAGTGAAGTGCTCTACCGGACCTA	63.137	115
HM_3164	contig47227	GTT	3	21	AAaGaaTCATTTTGGACGCATCAAC	63.444	AaTgGAGAACATTTCTTCCGCAAC	63.318	148
HM_3165	contig46797	CTT	3	18	CTTCTCCGAACATCTGCAAACTCT	63.02	ACTGCTCGCTTTCGAAGATAAATG	62.947	154
HM_3166	contig10359	ATC	3	12	TCATAGTtATgCTAGTcGTGCCA	62.763	ACTACAGcGCAcAaACCATCTAcA	62.869	152
HM_3167	contig38715	AAG	3	12	CTGCACCACTATTAGACAACAG	63.168	ATACATCGTTCGGTTGATTGGAAG	63.329	144
HM_3168	contig28948	GTG	3	15	GaGGGgTgTcGTAATTGCTGTAGT	62.851	ACTATTGGGCCAACCACTCTACAA	63.031	145
HM_3169	contig18725	GAA	3	36	CCTTAATCTTGACcAGAcagAGCG	63.32	TTCACTTCTCGTTCTCTCTCGTCC	63.009	122
HM_3170	contig07831	TGT	3	12	TAACAGGaTGTGTTATGTTTCCG	63.216	GCTCACCTACTAGCTTCAACACCC	62.639	148
HM_3171	contig45068	TCG	3	12	CAACTAAACATCCATTAGAGACACGC	62.289	CACAACCTCAGTGTGATcTCTCAGC	61.67	122
HM_3172	contig21690	TGC	3	15	GAGAcAaGAGATGcGTGAAATCG	62.397	CGGTAGAcTACCGGATGCAATAC	63.071	110
HM_3173	contig37173	GAT	3	15	GGAGATCCAAAGTCTCCCATTTCT	63.062	AAATCAATGTTCCATCATCACCC	63.103	155
HM_3174	contig17015	CGG	3	12	GGTGTGCTGAAATGCGTTCAA	63.148	GAATCTCTGTTTGTGTGAAGAC	62.306	118
HM_3175	contig11335	AAG	3	18	GgGTCTTtCTTGTTGTTTCTCTCT	63.08	CAATCTCTCAACGACATATTCCC	63	139
HM_3176	contig38175	GCA	3	12	CACAAGATAATGGTTGTTGGTTGG	62.513	TCCtaTCTCTGcTCTCTCACACA	62.815	160
HM_3177	contig43833	TTC	3	15	TGGGACATTTTGGCCCAATAAG	62.993	GATTTGGAAACGCTGAGCTGTAA	63.677	159
HM_3178	contig51600	TTC	3	12	CTTTCTCTGCTTCAAGAACTCCG	63.044	TTCCCTCGAGAGCTGTAATAACAT	63.009	159
HM_3179	contig02854	ACC	3	15	TCAAAAaTCCAGCATGGATTCAGA	62.821	CAGTGTGcTaGTAATgTGTgATG	62.757	126
HM_3180	contig16762	CCA	3	12	CACCACCCAAAGTATaAGTCCCG	62.817	gGGGTGGTGGAGAGTGGTAGA	63.565	128
HM_3181	contig29401	GAC	3	15	AGTAGCGCAACCAATTAGCTGAT	63.28	CATGTTTCATGACGAAGAAGAGACT	63.025	139
HM_3182	contig01118	TTC	3	12	CGGTTATATTATCATCTCGGTGG	63.422	GGTACAAGTTGTCTCACTAGTGTGCG	63.569	152
HM_3183	contig52363	GGA	3	18	CTCCTCTGCATCATCTGGGTATT	62.8	CCACTTCACAGCTACTCTTTCCAT	62.822	141
HM_3184	contig24021	TGG	3	12	GTCGAATGGTAATGTGGGTGT	63.133	TcCAAGCACAATTCAGATGAAC	63.471	158
HM_3185	contig04242	GAG	3	18	AGTGTGGGGAGGGCTACAGATT	63.32	TTGAGTACTTGAAGGTGATTCCCA	63.115	146
HM_3186	contig14000	TTC	3	12	GAGTCTCCATTTTCAAGTGGTGT	63.027	AGTTCAATCAAAAGTGGGAGAG	62.936	153
HM_3187	contig21757	TCA	3	21	AGCCTATCATCTTCAATCGCAAC	62.843	GAGTGAAGTCGTTTCAACCCCTAA	62.921	160
HM_3188	contig43754	AGA	3	12	GAAGAGTGTCTTGAGGGCAAGAAc	62.925	CCCTAAGAATCGAAGTCCCAATA	63.552	156
HM_3189	contig29290	CTC	3	12	TCGATCGGTGTTATgTTCATCC	63.322	TTTTCGGAAAGATCAACCTCTCT	63.366	82
HM_3190	contig23735	CCG	3	12	GTTCTGCCATCAATCAATAAACC	62.706	AATCCAAGAGAACATCAATGAGGG	62.672	151
HM_3191	contig14523	CTT	3	15	AAACCCAGAACCACTCTCAATAT	62.983	GGAGTTTCATGcTTTTCAGAGA	63.009	100
HM_3192	contig13751	CCT	3	12	TTCTAATACCAAGTTTCTGTGGC	62.619	ATGATGGGGAGATCATGATACGG	63.112	113
HM_3193	contig45405	TGA	3	21	GCAAAACCCGGAaTGAAGAAATCA	63.327	GTCCTCTTTTGAGAACTCCGGTCA	63.01	121
HM_3194	contig47501	GGA	3	15	ATGCTCTCTGAGAAATGGTGAGAC	62.994	GTCATGCTGTGTTGTTGTTGAG	63.983	104
HM_3195	contig28926	CTC	3	12	CTTCTCGCTTTTGTAGTGAAG	63.761	CAAGAAGGAAACAGTTGGTCTGGT	62.906	148
HM_3196	contig27023	AAG	3	24	TCACATTTTGTCAACCATTGATT	62.5	TCAATAGATaACACTACCAATTCaAc	61.685	108
HM_3197	contig30256	TCC	3	12	GGTAGCTCTTCTTCGTACGAT	63.008	AGAGAGATCATGTTGTTGCTGCT	62.045	82
HM_3198	contig51368	GGA	3	15	GGACCCAGTTCACGTTGAG	63.008	TCTCTCTCCCTCTcCCCTCT	63.829	160
HM_3199	contig22621	CAT	3	21	TGATTTTGTGGTCTCTCTCTCC	62.802	GTGTGTTTACTGCATCCACCTTTG	62.856	156
HM_3200	contig44738	CGA	3	15	CAGTGAATCTCTGGGTTTCgAACT	63.01	cagaccggagaccctaacaatCT	62.883	148
HM_3201	contig10411	CCG	3	15	CCAATCTACTTACAGCGTCACCA	62.541	AGAcGTCGTTGAGGAgTACTTTGG	63.033	156
HM_3202	contig02880	GAA	3	15	TCGTAAGGATTGGAGGATTCATA	63.095	GAGGGGACTCACTCAGATCAATGT	62.994	122
HM_3203	contig13293	TCA	3	15	GGAGAATGAATCAGGTGTTATCGC	63.129	CGGCTGATTGATACCCAAAT	63.226	159
HM_3204	contig03836	AGA	3	21	GAGGGAAaAGTCTCTGCTGAGAA	63.019	CTCTCaaGCTCATCACCGCAAGT	63.362	89
HM_3205	contig38943	TGC	3	15	AaTGTCTGAGGCAAAAGTCC	62.925	TAGATCCAGACCaCAACAACAGC	62.622	159
HM_3206	contig06062	CGG	3	15	CCAGATTTACAGCCTATTGCTCA	63.421	TAATCGTTGACTGCTCATCTTCA	63.154	156
HM_3207	contig42463	TTC	3	12	ATGTAGCCGACCTCTTCTCTCT	62.999	GGAcACAGCAGGGGAAATcAG	63.016	125
HM_3208	contig25020	GAA	3	12	AaCTTACCACATCTGTTTCTCTCA	63.111	AAGAAGTcgTggtAATGAAGCCT	63.511	102
HM_3209	contig22920	TGT	3	12	CTTGTTCTTCCACCAAGCTCACT	63.115	aAAACAAACCTTTTTCACAGCAAA	63.036	138
HM_3210	contig13312	TCT	3	12	GGAGCCTTTGAAGAACCTTACTCT	62.793	CTGGGTTTGGTAGAGATATGGTGG	62.894	151
HM_3211	contig12629	TCG	3	18	aCACCAACAGCTCTCTGATtTCA	62.856	AATTTGATcTCTcTCAAGTTTC	62.974	136
HM_3212	contig28096	TTC	3	12	GTCGAAACATTGGCTTTAGACACC	63.146	GGACAATGAAATCCAAATcgaAA	63.201	138
HM_3213	contig00604	TGC	3	18	CAATTGCTGGTGGTGGTGTACTT	63.275	CCAACAGTACCCGAACCTGAATAA	63.319	133
HM_3214	contig09742	AGA	3	15	CGAGGAAAGGAcCAGGACtAAAGTA	63.107	AaCaTAGACAATTCaCaAAATGGc	62.356	122
HM_3215	contig25264	AGA	3	12	CTTtttGCTTtGtTGTGCTGTG	62.975	AGAGCATCGAATGTTGACAGTGAC	62.846	145
HM_3216	contig12590	AGA	3	18	AAGATGACACTGcAAGcCAAGAG	63.055	CGTCTAGGGCTCATTACCACTTC	62.936	135
HM_3217	contig47779	GAG	3	18	AAGATACTCTTCCAGGCAAGTG	62.999	ATTGTATGAGGAAGCTGGCACTGT	63.368	155
HM_3218	contig10416	ATT	3	18	TGCTGCTCATATACCTCTTAGCA	63.307	CGATTACAGAAGGAGTGAGCAACA	62.842	154
HM_3219	contig46872	GAT	3	24	AACCTTAATGTCCGACTCTTTGCT	61.944	CTCTACGTCACCACTGTTGATCT	62.706	133
HM_3220	contig42576	TGA	3	15	TCATGGCACTATAAGATGGTGTG	63.154	CCACAACAAGATGTCAAGATTGG	62.948	93
HM_3221	contig00689	TCC	3	12	TCCTGaGTCCGGaCaaATTAaaaa	63.002	GaCTGCGagTTAGCAAGTGAAGG	63.675	146
HM_3222	contig37020	TCT	3	15	AAGCCTCAACAATGCATATCAACCT	63.15	ACTGAAGGAGGAGGAAAGAAAGAA	62.958	127
HM_3223	contig29560	GAA	3	12	IGAAAATGGCTTCTGATTCTCTC	63	AGTACAAGACACCCAAACCCAAA	62.918	151
HM_3224	contig01951	AAG	3	15	TCAGACCTGAAGAAAGAGCTGTGA	62.812	TTTGTCTTCTCGTCTCTCTCGTT	62.71	159
HM_3225	contig28910	TTG	3	21	TCGTAATCTTCAACTCTCTGGAAC	62.91	GACATTAGGCTTTCCACTAGGGCT	63.114	143
HM_3226	contig25478	ATA	3	12	TCATTAAACGAGAATCATTAGAGTG	60.364	TtCaAAACTCTTGTATTGAgATCTGg	60.058	160
HM_3227	contig13440	CAT	3	21	CCAGTGATTGAGACGCGAAG	64.254	CCATTCTCAGACTCGAGCAGTTC	63.774	148
HM_3228	contig03943	CCA	3	21	aTCAATCTCTCTCTGCTCCAC	63.986	GTCTCGTGGGAAGTCTGAAGATA	63	127
HM_3229	contig21041	CTT	3	12	CGTTGGTGAACCTCAGCAAGAGATA	62.842	CTCCAGCAACAAATGGAAGAGG	63.225	154
HM_3230	contig31282	TCA	3	24	CTCTGTTGCAACCATTTCTCAACC	63.325	TTTTTCGATACATACAGTTGCCGA	62.761	160

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3231	contig00542	GAC	3	12	GGGTATTAGGGTTATGCGCCTC	62.915	CATCGGTCTGaAACCACTATcct	62.698	148
HM_3232	contig15523	TCT	3	12	CGCTATCGCTCTATCTCTCCAA	63.138	GAGCACAGaGATGAGIacGAAGA	63.071	141
HM_3233	contig45980	TGC	3	12	CATCGATGATGACGACACTCT	63.722	GCTGTGGACCGTAATACCAACAGT	63.474	108
HM_3234	contig18669	GAT	3	12	AATGTTAAAAcgtTGGATTGGCG	62.342	GAGTtgTGATCTCGAACCACTT	63.027	128
HM_3235	contig31008	CTT	3	18	GCTTCCTGATCTCTAACTTTCCG	63.481	TGAGGAGCTAGAGCATGAAGATGA	62.714	139
HM_3236	contig46882	TCA	3	12	CACCACCCTCCCTATCTCTCTTT	63.068	GAGACAAGGGAAGGGAAAGGAC	63.573	120
HM_3237	contig27039	TTG	3	12	ATACACTGTACAacGTCCTCCGAT	62.838	ACTTAGCGCAGaAGAAATCAAAcG	63.064	159
HM_3238	contig29245	CTC	3	12	AACCATTTGAAAGATGATCTCCAGAA	62.987	gGAGATTGGAGGacTTGGGTTTAT	62.769	146
HM_3239	contig09618	TCA	3	12	CCATTGGAGAAcACAGaGaaACC	63.212	CaTTACAGGGCAATGAATTTTGTG	63.376	154
HM_3240	contig19291	GAT	3	18	GATCTCCAGATCTCGCTTTTCTG	63.544	GTCTATGGAGGCTTGTTCGCTCT	63.04	147
HM_3241	contig01821	CCA	3	12	GTCTTGGAAATGAAAAACCCACC	63.838	GGTGGCGATTaTGGTGTGATAAT	63.037	160
HM_3242	contig33144	CTT	3	12	CTCTCCAGAGAAATCTCTCATCGT	62.77	GTCAGAAAGaGATTTGGaACgGaaA	63.111	102
HM_3243	contig45047	TCT	3	24	CACAGTTGTTGAATGATCTCTCTCAG	62.839	GaaAAGTtacTgGaAggGaAaccc	62.397	136
HM_3244	contig14423	TCT	3	12	TCGTAACACTACTGTTcCaATAGCATGT	62.359	AGTcCcGtTGAAATTTCTCTCTC	63.181	94
HM_3245	contig05837	GGA	3	15	AGTGTCTCTCCATCTCTCTGAA	62.871	CATCTTCTGCCAATCaATCTTCT	62.786	145
HM_3246	contig09342	ATG	3	18	GAAGTCCCACTGgATTAAGAGC	63.289	gCATgCTCAATtCaATCATCATC	62.842	109
HM_3247	contig19477	TGA	3	30	TGGTGTCTGCTGCTTGATAATACT	62.269	TGATCAAAcAAGATTGGGGACTAA	61.861	160
HM_3248	contig23957	TCT	3	15	CACCTCAAAcCAATCTCTCAAGCA	63.006	CCAAATCACCAATTATCAAGCA	62.046	129
HM_3249	contig30946	CTC	3	12	GCaGAAACAGCTCTCGGTTgaTA	62.185	TAAACAAATAGGAGCAGGAGGA	63.091	155
HM_3250	contig17688	GAA	3	12	ATCTCTCAGCTCTCTCTTTGGCTC	63.72	agGtATGtCgTGGAATTTGGTA	62.921	105
HM_3251	contig29762	CGG	3	15	ACGTGCTTCTCTCACCTCTCG	63.141	GATGAATCGaAGCTCATCTGAGTg	62.489	159
HM_3252	contig26293	CTG	3	12	GCTAGTCGAGCTGACGGGAATTA	63.97	ATCTCACCACTGTCAAATCTCGAG	63.01	100
HM_3253	contig33758	AAG	3	12	AGCATCGCAATTGAATGGATAAA	63.732	CTCTAACCTTCATCCCAATTCT	62.863	160
HM_3254	contig08025	CAC	3	12	TGTCGTTGCAACTGACCTAGTA	63.07	ggTGGGATTGATAGTGaCaTGCTC	63.349	143
HM_3255	contig23824	CAC	3	12	GCTCTATTACGTACCAAGCCTC	63.268	CAGACATTGACTTTTcAaGaaAAACG	62.37	159
HM_3256	contig11271	TCT	3	21	GATACTGGCCAAaCaCGGTAATC	62.841	AAAACGGaAGTCCAAAGAAATGA	62.22	131
HM_3257	contig48129	GCT	3	24	AAGTTCTGTGAGGgTTTGATGAGG	62.895	tCctTTTCAACATctCTCCACTC	62.987	126
HM_3258	contig17205	TCA	3	15	TGGTGATGGAAATGTTCTAGACA	62.803	TgaGAATTTTCTCCAGGAGACAG	63.085	135
HM_3259	contig09403	AGA	3	15	AACAACAAGAAATGAGCCCTTT	63.296	TTTTTCACTGCTTTAGAGTTGGG	62.821	89
HM_3260	contig06293	ACC	3	12	TACAAGCTCTGAGGCTTCAAACT	63.133	CGCAACATTCTAGGGTTCTCTATT	62.729	155
HM_3261	contig02206	GTG	3	15	TCTGGTTAACGATTGATGAGTGA	63.038	CACCTAAATTCCTCAAAATCCCA	62.996	134
HM_3262	contig18156	AAG	3	12	TATTGCTTTTGGAAATaGGGATGC	62.45	CACAAAACAATGAGCTTctTCTTCA	62.954	148
HM_3263	contig13545	TTC	3	12	TATTATTTTCTGGCCGTTGTG	63.126	AGGATGCTTATGGATGATGAGGag	62.789	136
HM_3264	contig41767	GCC	3	12	GTAAGTATACGTTGCTCTCGCCAC	63.06	aACTTACCATCTTATGTCaATgGg	62.328	154
HM_3265	contig14916	CCA	3	15	CAATGTGGAACAACCTCAAGTCAAC	62.933	AGGGTGGTCTTGCTAAGATCAATG	62.811	133
HM_3266	contig19137	CGA	3	18	TTTCTCGCTCTTCAACTCATCAT	63.318	CGAGTGGATGAGAGAACTCGGTATC	63.323	145
HM_3267	contig04118	ACC	3	12	GCTTTCTGTATCTGAACCTGGAAA	63.009	GCCACCACAAGTCACCTATGAAC	62.938	140
HM_3268	contig28016	ACC	3	15	CTGATTTGAGCAAGaAaCAAGGAT	63.022	AGCCATAAGTGAAGGGTGTCCAA	63.031	139
HM_3269	contig36258	ATC	3	12	CTCTCTGCTCTCTCACTCTGACAT	63.34	GACTACCTCCGAATCGAaCTGAAC	62.498	88
HM_3270	contig28884	TAC	3	15	CGGTGAAGGAAGTGAaCTCAACAA	62.619	TATCAACTTAGCAAGAtcgCCAC	61.921	94
HM_3271	contig40962	GCT	3	12	AAGCATCAGATTAACTTGCGCCG	62.854	AAGCCAAAGTACCTGCTAGAGCC	63.331	133
HM_3272	contig36730	ATC	3	15	TCCATCGTCACTACCATCATCTC	63.253	CCCTCTGAGAGATGCAgTTGCTTA	63.129	88
HM_3273	contig01432	TTC	3	12	GGGTTGGAAATGCTGATGAGATA	63.42	TTGAGGGATCATCAAATTCATCT	62.977	142
HM_3274	contig19742	GAT	3	21	TCCAACCATGCACATAAAGAGATG	63.038	CTCGGGTGGTGGTTCTATTACAAA	63.319	160
HM_3275	contig01039	GGA	3	21	CTTGGGATCATTCACCATGTGCTA	63.362	CGTGATGGGATCGAAATAGTAAT	63.237	93
HM_3276	contig37481	CCT	3	15	CCACAaCTCGCTGCTACTCTTCA	62.724	TGACCTTGGATCATTGACTTcCC	63.419	98
HM_3277	contig11558	GAA	3	15	CAAGGTATCAATTGTGGTGCAAAA	63.055	CGATTTCACTGCTAGCaAAAGT	63.064	141
HM_3278	contig06417	GAT	3	24	CGCTAGTCTTCGATCTCTTTGCG	62.851	CGAATCATCAACGGCtctCTCT	63.849	106
HM_3279	contig01074	GAC	3	15	ATGGGGGACAGGAaGAAAGTAG	63.068	GTAAGCGCATCTCTCAATGACG	63.341	105
HM_3280	contig14882	CCA	3	12	AACCAaCTGTTCCATCATAGAGCG	62.713	CTaTAATTTGTCTGTGGTGGTGG	62.642	118
HM_3281	contig07952	GAG	3	12	GAGAGGAAGGGTTTGAGAAAGCT	63.486	GAGTGGTGGTGTCTAGGATACG	63.03	131
HM_3282	contig21615	ACT	3	12	CAATTAAGCTTAACGACCCATCAT	63.03	TGTTCTGAGTACAGAAAGCGAAGA	62.739	141
HM_3283	contig00329	GAG	3	15	GAGTGAGATCAACGGCTGAC	63.178	GACCAGaAAACCGTCAATCTTCC	63.206	146
HM_3284	contig00179	TCG	3	12	GTGTTGGTGTAAACAGCTCTCTCC	63.236	TATGTCTGACTACTCTCTCAGGCCA	63.954	153
HM_3285	contig15571	ACC	3	12	ATTTTCAgCTCAAAcCTAGGAGG	63.086	GAGACGTCAATGAGGGGTTGTATC	63.12	83
HM_3286	contig09414	TCA	3	15	ATtCTTTTgTgAGCTGTGGTGCTG	63.773	ATTAGATCCGTAGGAGCGTTGCT	63.52	133
HM_3287	contig23340	TTG	3	12	GCATAGGACAAGTCTCAACCAATT	62.713	TGGAGATTATAGTCTCAACAGCA	62.294	99
HM_3288	contig08452	TTC	3	12	CaAGGcTTACCTCAATCATCTCT	62.085	ATCTCTGCTCTTGATCGCTCTCC	62.577	91
HM_3289	contig37964	CAC	3	12	GCAGCTGTGTAaAAACCCaAaTA	63.339	CAATGCTGCTGTTAGTGTTCGAGT	62.883	123
HM_3290	contig37224	GAA	3	24	GAGCATTGGGAAGAAGATCAGAA	63	TCGATTAAcAATGAGGGTTAGGG	62.41	125
HM_3291	contig01407	AGA	3	18	AGAAGATGATTGTGGGTACGAGGA	63.217	CACCCAATCAAGTACCCTATCTCT	62.584	123
HM_3292	contig37768	CTC	3	12	TTTTGCTCTCTTCTTCTCTGAAC	62.949	TGAGTTTGACTGGGAACCTGATGA	63.132	136
HM_3293	contig36013	TCT	3	12	ACCCaAAAGACTAAcAACTCC	62.78	AATGGAAaAcTCTGTTTGGGTTG	62.508	134
HM_3294	contig23186	GGC	3	12	ATTTCTGTTGTTGACGGAGGATGT	63.128	ATCAATCTCTCTCTCTCGCAAC	64.013	122
HM_3295	contig17270	TAC	3	15	TtGTCACTAAGATgAaAcCAAAATCG	62.558	gAgGATTATGATGAGTAATGGcGG	62.915	105
HM_3296	contig00967	GAG	3	12	TATGTAGAGAGGAGcAAACCCACC	62.698	CCTCTCACTCTCTCTCTCTCTC	63.161	152
HM_3297	contig11075	GAA	3	15	ATCAaAGCATCTGTTATGGGCACA	62.861	GaAGGGACGCATCACTAGaGAA	63.022	149
HM_3298	contig45501	GTG	3	12	TGAAATTGAAATCTCTCTTGGcAT	63.009	TCCACATCGTCCCTACTATTCTC	62.686	124
HM_3299	contig41279	GAA	3	12	TACCAaAgATGATCCACATGTTCT	63.042	aCCAaCTCaAGTgaATTCTTCCGA	63.325	134
HM_3300	contig44408	AAG	3	12	TGATTATGAGTAATACCGAACGAGGA	62.933	TTGATAGGCTGATGTGTGGATTTC	63.159	122
HM_3301	contig48790	GTT	3	21	AGAGCCAATGATGTAATTGGGAGA	63.112	AcCTCTCTCTCATCTCTCTTCTG	63.077	139
HM_3302	contig41620	ATC	3	15	TTCTCATCAAGCTTATCCCAAG	62.8	GaAGGAGAAGGAGAAGGAGAAGGA	62.738	126
HM_3303	contig21571	GAT	3	15	TaaGAAATTGacGACCCGATTCAT	62.912	GATGACGTTTTTGTGTCCATTG	62.629	155
HM_3304	contig06287	GTA	3	15	TCATTGTGAGGAATACGATGAGGA	62.91	GCGCACTCaCTAACTCATTAT	62.757	154
HM_3305	contig38476	TGT	3	12	ATGTCAATTATCATGAACGTTCGCA	63.607	CCAGCaGACAGACTAAACGGTGA	62.75	144
HM_3306	contig00624	CCT	3	12	TTGCTGATCTCGAAACAACCTCACT	63.057	GAAATGTCTGCTGATTGAGAGACC	63.336	114
HM_3307	contig37015	ATC	3	21	CCATCTCTGCTTCTGATCTCTCC	62.887	TTGTGTGATGATcCTTCTCTCTC	62.977	137
HM_3308	contig03936	GTG	3	21	AGTGGAAAGAGGGTAAGAAAGTGG	63.076	GACCCGCAACATTTTGTAACTCT	62.646	87
HM_3309	contig12225	CTC	3	12	TAGAGGAATGGATAGGAATGGCAG	62.897	CgGAAGGAAGGAAAGTGAAGAT	62.236	121
HM_3310	contig45509	CGG	3	12	ACATATTGTGGTGTTCACACCT	62.685	AATCTACTTTGGGGATGTGGGTT	62.983	139
HM_3311	contig09205	AGA	3	12	TCGGCTAGACATTCTTGGACATGG	63.019	GCTGAGGGTcAGAAATCCAGTAA	62.91	120
HM_3312	contig09760	TCA	3	12	TAAGGcATTtACCAcATcCGCTC	62.854	CAATTTCAcGAAcAAATcCAAAAG	61.939	144
HM_3313	contig31687	ATG	3	12	CAAGCAAACTCGAATTTCTCATCA	62.731	TGACACTATTATGTTGTGGCATCAAT	61.781	98
HM_3314	contig14055	TCT	3	12	GGCTCCCAAAAGGTTCTGAAGAT	62	GCATAAATGTCAACAGCAATGAGC	62.992	107
HM_3315	contig08062	CGA	3	12	GAGAAGCTCTGTGATGTCAGTGT	62.599	GAGAGCTATGTGAGTGTGGAGATG	61.63	147
HM_3316	contig19834	CTG	3	12	GGACTCGAACTTGTGAGCTCTCTC	62.925	CGATCTCGCaTaAAACGCCAT	63.365	137
HM_3317	contig13670	GAA	3	12	ATCAGTCAAGCAACCACTCTAAG	63.023	AGTgcTTGAAGGAAATGATGGAG	62.91	131
HM_3318	contig36774	TTC	3	18	CGTCTCaIaTGcATTCTCTGCa	63.465	ATTTTCCtCTCTTAATCTcACCG	62.971	101
HM_3319	contig30229	CAC	3	21	GGCATACTTGGATGTTCTTCATC	63.016	GATAGGGTGGTCAATTGTGGAGTT	62.484	159
HM_3320	contig03518	GTG	3	12	TCAGCAACAGGATCTGATTGGA	63.038	GGCTTCTGTGCTCTCAACGGAT	63.04	156
HM_3321	contig02203	GTG	3	12	CGAAATTGGAGAAGATTGGAGAA	62.787	CAACACAGACTTCAATGGCAGAT	63.272	133
HM_3322	contig15813	AGT	3	24	AAAGGGACCTACCAATCTCTTGG	63.076	TcAGATGAAATGAGGATGTgaCG	63.132	142
HM_3323	contig37688	TCT	3	24	ACTATTCTTCTCTCGCTGTCTc	63.102	ACTGTGACTGTGACTGTGACCC	62.932	155
HM_3324	contig29879	CAA	3	15	ATGTGTGCGTCTCCAaCATGTaaC	63.309	acggtagcagcagataaagaagag	62.933	122
HM_3325	contig21752	GGT	3	15	AGTTTGATAGTGGGTGCAACATGG	63.438	CGATCTCAcGTTTTCTCAACCTCA	63.117	116

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3326	contig131282	GGT	3	15	CGATGTTGATGGGATTTCTAGGG	62.8	GTCACCAAACTTCACTCACACC	63.06	160
HM_3327	contig06952	GGT	3	12	cTGATTGCAAGCTTGAAcCCCTTA	62.919	aACTACTACTGcCGCAAGGTCAAC	62.972	137
HM_3328	contig05790	TCA	3	12	GGATGCTAGATTGATCAGCGTCT	62.816	GAAGATAAACCAAGGCGCAAGACT	62.995	160
HM_3329	contig13026	CTG	3	12	TTTTGTCAAGATCAGGGTCAGTG	62.81	ATGGTGATGATGATTGGTTCCT	62.789	142
HM_3330	contig33421	TTC	3	12	GAGGAAAGTCAAAGCTTCTTTCC	62.888	AATGGTGAAGGTGGACTTGAAGAG	62.895	96
HM_3331	contig46631	TGA	3	12	CTCTCTACTCTGCTTCTCTCGG	62.995	CGCAGCAAACTATTGACAAACAG	63.081	150
HM_3332	contig11764	GAT	3	12	CAATGGCcGAAATACTCAAGAATC	63.021	CCCAAACTTTAGTCTTCAAGCC	63.176	140
HM_3333	contig10796	TGA	3	12	GGCAGTTTCAGAGATGTGAAGAGC	63.794	AgGTTCTAGGGATTGCTTTGGAC	62.995	145
HM_3334	contig30289	TGA	3	12	TATATGGGTTCAGAAATGTGCAAG	62.211	ACCCTTCATCAAGGAATCAACAT	63.004	141
HM_3335	contig39879	TCA	3	12	ttaacctctctggATTAAGCATCG	62.626	TCGATTGGATAACATTCTCCGT	62.912	154
HM_3336	contig33331	TCC	3	15	CAGAAGTAGATCCTCGCTGTGCT	63.25	GGACGACGACAGAGTTAATGAAGA	62.935	90
HM_3337	contig37637	CTT	3	12	GTCAACTTGGTCTCTGTCTGATT	63.027	TTGAGAAGGATCTCCAGAAGAAGC	63.199	142
HM_3338	contig47284	ATA	3	15	ATTGATATCAGACTCATGCCACAGC	62.639	GGGTATTATCACCACCTGCTTAC	62.926	124
HM_3339	contig47542	AGG	3	12	AATTACCAATAATCCAAACCCCA	62.41	TGCGACTGCCACTATTATGATTCT	62.138	157
HM_3340	contig49823	ACAAAA	6	24	AAaAGCAGCAACAATCTTACGAC	62.864	cTctTTGTTTCCAGCTGATAATCG	63.324	152
HM_3341	contig46826	AAAAATA	6	24	AAACAGGAAACGATTGAAAGCAAA	63.134	AAGTCGTCTTCTCTCTGCTCGC	63.688	119
HM_3342	contig06712	CTCTGC	6	30	AAATCACCAACGACCACTCTCTC	62.912	GTAAGCGAAGAGGCTAAATCGT	63.13	158
HM_3343	contig26351	ACCACA	6	30	AACAAGCAGCGCTTGAAGGCTTAC	63.275	CACAACAAGCTCTTGTACTCCAGC	62.307	145
HM_3344	contig04858	AATCAA	6	24	AACCAACCAATCGCAATCAAAA	62.629	TTATGGGTAATCGGAGGAGGATT	62.971	153
HM_3345	contig05166	CGGGGG	6	24	AACGAATTTGAGATTAGGAAGGGG	62.783	tCTCGCTGCTCTCTATCTCTC	62.982	134
HM_3346	contig23500	CTATTC	6	30	AACGGTTCTTCTCTTCCAAAG	62.995	GCCCTTTCAAGTCTCACTGAACAT	63.027	152
HM_3347	contig34678	CTCCTA	6	24	AACGTGAAATGGAGTAACCGTTG	62.521	TCTCTCCTTAGGCTTTTGATTG	62.109	155
HM_3348	contig46571	AATCGA	6	24	AACTTTTCTCAGCTTCTCCATCG	63.008	GTTGAGCACTTTCAGGAGTTTTCG	63.573	119
HM_3349	contig48362	GATGAA	6	24	AAGAAACGTTGTGAATCTCAGGC	62.936	GaAAATGCACTGATGGTCTGTTG	62.948	152
HM_3350	contig48544	TTGGGC	6	24	AAGAAGCAGAGGAGAAGGAGGAG	62.873	TGGACATGAAGAGACCGTCTAGT	63.443	113
HM_3351	contig05555	TGGTGA	6	24	AAGCTTGTAAAGGAAGCCGATAAGC	63.233	TGTCAATGGTTCTCTGTTgAAA	62.918	129
HM_3352	contig33904	ATATAG	6	48	AAGGCATTTTGTCCAGTTAGAGA	62.633	cCTAGCAAGGGGATaGTAACACTG	62.448	140
HM_3353	contig13472	CGCCGT	6	24	AAGGTTGAGAAATGCCCTTcCAGG	63.285	CTCTAGAAATCcaAGGAAGAGCC	62.69	137
HM_3354	contig36446	AGCCTG	6	24	AATACCAAGCCCAATTAAACCAAGT	63.394	GACTCaCAAATCGAACTGCTGCTA	62.975	131
HM_3355	contig40866	CACGCC	6	36	AATCAAAAaAGGgGTGGCCTTTc	62.797	CACAAGAATTTATGCGACCTTc	63.03	119
HM_3356	contig11271	TTTTCT	6	24	AATCCCATCGATCACCTTCAGATA	62.99	AGGCCCAAGAGAAAATTTCAAAC	62.9	114
HM_3357	contig49159	CGGAAG	6	24	AATGGAATCATCTCTGAAGACCA	63.012	ATAGAACAAATTCATcCCCTTc	62.573	140
HM_3358	contig15246	CGCATT	6	30	AATTACGACGAAACCTCCCTcgT	63.404	TGTGACTCTGAGGTCGATTTTGAG	62.919	146
HM_3359	contig15066	CTCTTT	6	24	AATTGCAAGGCTCTTCTCTCTTT	63.008	GTCATTCTCTCAACCTCTCTCT	63.278	106
HM_3360	contig07729	TCAACT	6	24	ACAAACTCTCTCACTAAGGCCACG	62.425	AGAGGAAGTGATCAGTGGTGAAG	63.141	148
HM_3361	contig35963	GGTGCT	6	24	aCATATATATTGaaGTGGCGcGT	62.953	GATCTGCCACGAACACGACAC	63.178	114
HM_3362	contig25439	GAGGGA	6	24	ACATTCTGCTGCTCTCGAAGATC	63.358	GATGGTGAATAGAACCGATCACC	62.903	137
HM_3363	contig01302	ATGAGA	6	24	ACCACAGGAAGAGATTAGAGGGC	63.193	GTTTCTGCTCTGATGAATCCGTTT	62.813	146
HM_3364	contig44572	AGGGTT	6	30	ACCAGGaTACGGGTAGTAAGGAgg	62.791	AAATTACGGCGAACAGGTACGTT	62.958	113
HM_3365	contig01469	GAAGAG	6	30	ACCTTCGGACATCATTTCAACGAA	63.121	GTGTACAACTAGGGTTTCCGATG	62.921	116
HM_3366	contig09917	TCACAC	6	24	ACGATTCAATGGTTTCTACACTAA	60.212	TGTGAGTCCCAAGTACTACTAAGAAA	60.504	160
HM_3367	contig34510	TGGGGT	6	24	ACGCTaTGTGAGTATGagCTGTG	63.002	ACTCGAGGAGTAGGAgGACATCT	62.977	135
HM_3368	contig29169	AAGTTG	6	36	ACGTGCTCTTCGAGTAATAAAAGC	62.179	TCTGTCTCTCAAACAAATTTCA	62.918	129
HM_3369	contig52324	CAGAAC	6	30	ACTAGGGTCTTCAACACAGCTCC	63.93	TGGATTGATGATGGTTAGGAAGT	63	158
HM_3370	contig06389	CATTCC	6	24	aCTTATGTTCTGgTGAAGgATTG	63.549	cgaatgggaactctgactctctat	63.128	158
HM_3371	contig05182	TGATGT	6	30	ACTTGGTGACAGGGAATCTACCAA	63.111	AGCACATTCTAGCACCAACAAGAG	64.001	155
HM_3372	contig10209	TGGTTC	6	24	AGAACTTGGTgTTGAGAGAGTCG	63.365	ATACATTGGATCGGAgGTgGAAGT	64.013	160
HM_3373	contig07201	GGAGAT	6	24	AGaAGATTGGAaATGGAAGAggaG	63.156	GCATGATAAGGGGTAGGTGATGTT	62.411	151
HM_3374	contig11526	CGCTCT	6	30	AGaAGCAACGGAGGTGTTATCTG	62.933	ATGaATACCCtATcTCTCTCTC	62.954	125
HM_3375	contig00458	TTAGGG	6	30	AGAGGACGCTGCTGTTCTATGAaT	62.741	AACGTGGTTGTTCAAGATGTGGTC	62.427	130
HM_3376	contig42149	GATATA	6	24	AGATAAACTCAATTGTGGGCAAC	62.523	CAGCAGCTTAATCTTGGGATCAG	63.432	116
HM_3377	contig06103	GATTTT	6	24	GAGTTCAACAATCACTTCTLCGGC	62.926	GGGTGGGTTATACATCAACgTaT	62.922	95
HM_3378	contig27952	GATTTG	6	24	AGATTGCAAAATGAGAAGAAAGC	62.312	CAGACACCACAACCAACACACAG	62.747	139
HM_3379	contig37250	GTTGCT	6	24	AGATTGTTCTTGTGCTTGTGCTG	62.869	GCCATCTAATGCGGTTAGTACTCG	63.178	153
HM_3380	contig49092	AACCAA	6	24	AGCTCATGTATGCCGAATTGAT	62.05	cCACTCAAGTATCATAGATTGATTT	62.729	160
HM_3381	contig12600	TCCTCT	6	24	AGCTTCCATCTCATCTTCTCTGG	63.106	TGGAGGAAGAGGTTGagTATGAGG	62.984	149
HM_3382	contig48389	TCCTCT	6	24	AGGAaAGTAATTCATCCCTCGGCT	62.878	TCAAAGGTAaAAAGGTaCAgagg	63.459	139
HM_3383	contig20636	GGGTCA	6	24	AGGATTGATTGAGATTGgAGGGT	63.27	AAATGTCTGTTTTTTGGGCTCT	63.296	131
HM_3384	contig07433	AATGGG	6	30	AGGGCATATGAGTCAATTTCAACC	62.701	GCACCTGAATCAACCACTTATCT	63.228	104
HM_3385	contig47533	ATGGGA	6	30	AGGGTTTATGTTGTTCGATGAGA	63.009	CAACAGTCAcCAAGCTCAcAaCT	62.852	107
HM_3386	contig28856	ACAAAA	6	24	aGGTTGAAATGTGAATTTTCCCG	63.273	CGTACCITGCTCTTCTCTATTACG	62.508	148
HM_3387	contig23728	GCAGTA	6	30	AGGTACATTGGACGAAGGAAGAAG	63.01	TTTTCTGCTAGTAGGTAGGCCCC	62.91	147
HM_3388	contig00031	GGACCG	6	30	AGGTCCAGcCTCATATGCTAC	62.815	GCACGGGTAGCAACAGTcTc	62.829	148
HM_3389	contig06597	TTGGCT	6	30	AGTAGAAGGGCTTGCACTTGGAGT	62.899	AAACCTTCTCTTCTTCCCTTGT	62.804	103
HM_3390	contig03225	TTCTCT	6	24	ATAACAGCAAAACAACCCGGAAT	62.851	CCATCAGTTGGTGAACACAGAAAC	62.933	146
HM_3391	contig30008	TGACCC	6	36	ATAATACCTTGACCAATGGGAC	63.261	TATATGGATGTTGAGCCGGGTAGT	62.828	114
HM_3392	contig20857	ATTACT	6	30	ATACGAAAGCTTCAATGGCATGAT	63.158	GAAAGAgGaAAGAgcAAGAgGGG	63.177	99
HM_3393	contig11629	CTTTTC	6	36	ATATCCCTATCagTgTgATCCCa	62.775	AGGAGAAGGAAGAAGGTGAAGGAAA	62.958	127
HM_3394	contig32152	GTCTGT	6	24	ATCAGAGGAATAGAGAGGCCAGT	62.879	ATCTTCATcTCCCACTGTGATA	63.093	120
HM_3395	contig47345	TAACTG	6	24	ATCAATACTGGGTCCTCTCTGc	61.574	GTCCCACTAcGATGTCATCAAG	61.798	134
HM_3396	contig29665	CCTTCA	6	42	ATCCAATATCCCTGTTTCCAGT	62.974	AAAAACAACCTCCCTGCTAcACAT	62.936	230
HM_3397	contig44478	AAATCC	6	24	ATCCCACTCAAGCTTTTACCAAT	62.995	GTTATGACGATGGCATGGGTATT	63.037	145
HM_3398	contig13663	GGTGCT	6	24	ATCTTGGTGTGATGATGGTATG	63.017	TCTCtTGGTCAcCAATgGAGGAT	63.424	94
HM_3399	contig13545	TGAGGC	6	24	ATGAGCTTCTCATGATTCTCGGT	62.6	TGCCCAAGATGAGAGAAGATTTA	63.005	143
HM_3400	contig00715	ACTCGC	6	24	ATGAGGAATCGAGAACTACGACG	62.923	TCCTTCAAGCACTACGCTCTTC	63.124	139
HM_3401	contig25866	ATCTAA	6	30	ATGATCAGATCGACGGTGTAGATG	62.489	agCCActctTCTATCAAAcAaAAc	62.824	150
HM_3402	contig45872	TAGGGT	6	30	ATGATCTGTCTGGGTGAGAAAC	62.901	CTTCTCTCGGCTCTCTCTATT	62.983	95
HM_3403	contig25526	CACCTC	6	24	aTGTGTTACGGCTTGGTCTTCAT	63.048	CTCCACCATCAATTAATCCAAGG	62.993	153
HM_3404	contig30571	GTTCAT	6	36	TTACTTTCTGGGTGGTTCAGGT	63.189	TGGGTAGTGAATCAGATGTGGGA	62.803	113
HM_3405	contig09543	ACCTTA	6	42	ATTCACATGGTATCAGAGCCTCC	62.701	GTCgGCTAGTGTGAGGATAGGGT	62.913	134
HM_3406	contig26620	AACCCAG	6	24	ATTCAAAAGGTTCAAAGAGTGTG	62.809	AGAAGTTATCCCAATGGCTCAA	63.084	124
HM_3407	contig36366	AATCTC	6	24	ATTCCTCTCGCTAATCGAATTC	62.998	TGAAGAGAGACACAATGGTACGA	62.207	159
HM_3408	contig26677	TTCTCT	6	24	ATTTTCAACCCCTGCTTTCTCtC	63.071	AGCGGTGGAAGACATATTCAAGA	63.231	129
HM_3409	contig02203	TAACCC	6	30	ATTTCTGCTTCAACGTCAGTCCAT	63.242	GGGAGTTTTTGTGATGAGAGCTTT	63.09	97
HM_3410	contig07763	TGGCGT	6	30	ATTTCTCCACACCGTCAAGGActa	63.225	CGTCCATCAGATCCACAGTTATGA	63.362	144
HM_3411	contig41290	CCGTGT	6	24	ATTTGTTGTGTGcGAGTACTGCTG	63.298	AccgTATACTGGAActGAcGTCT	62.54	135
HM_3412	contig08580	CATTTC	6	24	ATTTTCCATTCAAATGCCAACAT	62.828	AAATTACCAACCAAGGCGTAAT	63.016	137
HM_3413	contig41729	GGGTG	6	24	ATTTGGGCTGAATAGGAGAGAG	63.078	GAATgSATCTCTCAACCAAAAC	62.761	137
HM_3414	contig30985	GAGTCC	6	30	ATTTGTCACTCTTTTCCAGATGA	62.996	CaACTCTCAACTCAACTCCAACt	63.437	148
HM_3415	contig34936	AGAAAT	6	24	CAAAATCGCAcActCCATAGCTTA	62.566	CAITTTGTTGATTTTCGATCGT	63.221	140
HM_3416	contig19652	AATCAA	6	30	CAAAACCAAAATCTATAGCAGGAG	62.22	AGAATTTAAGGCACTCCCTGTTC	62.995	143
HM_3417	contig09480	AAAAAT	6	24	CAaAGCAACCAACAAGTATCAAA	62.34	CCCTTTTGTATCTGTTGTTGAGAG	62.411	160
HM_3418	contig03413	GTCTCT	6	24	CAACAGCTCCCAACAACGTATTA	63.285	GCAAGCTCCAGCTCTCTCATATTA	63.046	158
HM_3419	contig28393	TTGTGA	6	24	CAACTACTGTGTGcGCTCTCTGT	62.986	CAITTCATCGAAcATCGTCACT	63.365	147
HM_3420	contig48758	CACAGG	6	36	CAATCAGaacTACAgaAATGTGTCC	62.229	GTCACGACGCTAAAAGCTGAC	62.285	125

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3421	contig13491	TCTTCA	6	24	CAATCCCCTCATCTTCTCTCTT	63.156	ATGATCCCGCTGCAATAGTAAT	62.929	138
HM_3422	contig12004	CTCTAT	6	24	CAaTGGCAGATATACAGAGGTGg	62.629	ATcaAACCACTCCCAcAAGATTGAT	62.789	121
HM_3423	contig47788	CAGATT	6	30	CAATTTTTTGTGATTGCGAGCTAC	62.972	CACACCCACAATTTCAAGAACAAA	63.146	146
HM_3424	contig47425	CACAAA	6	30	CACAAATCTTTAGTTCCTGCAAAaCA	63.602	TCGACACGCTTTAAcAAATCTCTTC	62.958	160
HM_3425	contig01258	TCATAG	6	24	CACAAATCATCAAGTCTGTTCG	62.948	TGGAGCATTTGATCATCTTGAaaa	62.922	157
HM_3426	contig10539	TGATCG	6	48	CACGAGATTAGCAGGCTCTCTTC	63.45	GATCATGTGCATATGGATTGGTCA	62.902	159
HM_3427	contig16196	GCTGTT	6	24	CACCATGTTATTGCCTAGACCTCC	63.022	TTCACTTTCAGATGTTACAGCAGC	62.858	131
HM_3428	contig00626	CTAACCC	6	24	cAcTCTTAAAGTTTACTTGGGgATGc	63.291	CCCATTTTCCAGAcCAAGTTTGATA	63.3	159
HM_3429	contig31965	CAGCAA	6	30	CACTTTCAAGCATCTCAGATGAAGA	62.817	GAAGAAGCAGCTTGGAGCTGAG	62.922	154
HM_3430	contig20442	TGGGGT	6	30	CagAGGAATGTCTGAAGAGAGGGT	62.337	AGGAGCTCTCAAGACTACTGCAa	63.036	149
HM_3431	contig42885	AATCAA	6	24	CAGCAGATTTTACGAATCGTCG	63.057	GAATTTcACAAACCTATTGCGAGC	63.154	146
HM_3432	contig42306	GATTTT	6	24	CAGCCAATCGAGGAGAAAGTATg	63.324	CCCAtcGGATGTTTCAGTGTTTAG	63.837	114
HM_3433	contig52567	AGATCG	6	24	CAGCTTACATTCTCGTCAACAGC	63.194	GAAGCCTTTTGGATGTCACCTCTC	62.809	148
HM_3434	contig20369	GCTCTC	6	24	CAGTCTTGACAGATGTTGTCGG	63.272	ATTTGAAATGAGCTCAGACAGCC	63.039	157
HM_3435	contig40302	TCTCTA	6	24	CATAATCCGTCAAAGGTTCCAAa	63.204	CTCGACTCTCTAGACCCAGTgTCC	62.896	160
HM_3436	contig19877	TCCCAT	6	36	CATCGCAATAATCTGTTTCTCCC	63.021	GATTTCATCTGGGAGTCGAATTG	63.099	141
HM_3437	contig52092	GGCGAT	6	24	CATCGCTCTCTcAtGGCTGAC	64.542	ACACCAACGCCATCGTCAIT	63.654	159
HM_3438	contig12595	ATCGTA	6	24	cACTGTCTGTgTGAaCTCTCTG	63.267	CCTCTTCAcCCCAATTTCTTTTAT	62.677	142
HM_3439	contig27936	GACTCG	6	24	CCCCTTTAAATTTAAACTCGGCT	63.08	CTAGTTTGGACTCTGAGTTGGGGA	62.993	134
HM_3440	contig27936	TTCTCT	6	24	CCGAGAGAAATGAATTCGTATTTT	62.72	TAATAATGATCGGATGTGGGTTTC	62.999	151
HM_3441	contig01977	GCGGTG	6	24	CCGCACTTGATACACTAGGTTTG	62.043	ACAGTACCGAAACTACCCCTCCTC	62.996	148
HM_3442	contig24635	GTGATG	6	24	CCGCTATGTGTGATGGGTTAATCT	63.341	CTAATGTTGGTGGCATCCCTAATC	62.815	157
HM_3443	contig15524	ACTATT	6	24	CCTCATGTCTTGTGATTTGTTGCT	62.622	AtTTTGCATAGCCGGATGATAGTG	63.344	153
HM_3444	contig36014	CAATCC	6	36	CCTCATTTCTCAGGTTATCATGc	63.112	GAGGGTTCCTAAGTGTTCGCTTT	63.005	159
HM_3445	contig11816	CTCACT	6	30	cCTTCTcTcGcCTCTaTtAT	63.067	CTCGAAGAGGAAGGATGATTGCTA	62.996	139
HM_3446	contig24549	GGTTGA	6	42	CCTCTTCTCTACTTGAAGGCTCG	62.116	GGCCATAACCAACACAGATGAT	62.204	130
HM_3447	contig10211	GATGGA	6	30	CtCGAAaAtAATcAGGAGATGGA	62.566	AATTTcAGAAAGTTGGAaACCC	62.876	140
HM_3448	contig23289	TCTTCC	6	24	CTGGAGTCTCTCTCCAACAGTCT	62.882	ACgGgAGaGAAACCAATGTCCTTA	63.18	90
HM_3449	contig00245	AATTCC	6	24	CtTcTAACTCTCTCtCCtCCAttc	63.617	AGGAGAGGaaAGaAGGTTTcCAGAG	62.651	82
HM_3450	contig02178	TATATC	6	24	CGACGACGAAGAACAAGTTTATG	63.337	CGGAACACTCTGATTATCAAGCG	63.021	122
HM_3451	contig21754	TGAATC	6	30	CGAGCTTATGTCAAACACAACAGG	63.07	AGTCGAATTTTCAAAGCGTTCCT	63.504	154
HM_3452	contig46571	GGACTT	6	30	CGATCGGAGTATTATAGGcCaTt	62.745	TGcGCAAAAGAGAGTAAGAAATC	63.043	139
HM_3453	contig34340	AGAGAC	6	30	CGATGAGGACTCATCAaGAAaAGC	62.536	TGGTTTTGtGgAaTTCTAAGGTG	62.437	134
HM_3454	contig40506	GTGACT	6	30	CGCATGACTGAGTATTcGAaATG	62.959	TTACGCTAAATGGGAGGAGGTAGC	63.789	132
HM_3455	contig28976	GCTTACT	6	24	CGCTCCAATGTTTGTCTCTATCT	62.937	CCGAGTTTGAaAATCCATGGACAA	63.409	145
HM_3456	contig14260	TTCGGA	6	30	CgGaATATACAAATCCGAACcAAa	63.005	GATCCGAATCCGAcacAAAATATC	62.806	108
HM_3457	contig47754	GGAGGT	6	36	CGGATGTAAGAATCGGAATCCA	64.231	GCCTACACACCGCAACAGAGAC	64.334	156
HM_3458	contig11512	TCCCTA	6	24	CGGTcAGAGTcATTGCTCTATCA	62.831	GacCGTGAACGTGGTAGGGA	63.257	158
HM_3459	contig48075	TGGTAT	6	24	CGTCATTTTcGGTGGGTTGTAGT	63.444	ATCATTTTtGAATGGACAATTCCG	63.105	123
HM_3460	contig07763	AGATCC	6	24	CGGTACGACCCCTCTATCTCGTA	63.653	CACACGAACTTCTCAGCAATACA	63.609	147
HM_3461	contig30553	TTTTTG	6	30	CGTTGTgTtgaagttttgttttg	61.892	GCTCAACAATGTTCAACAGCTTCA	62.657	120
HM_3462	contig20381	TGCTAA	6	24	CTACATCGATCTTTTtGCTGCT	62.759	ITGGAAgTTGGAACAActAGatCTG	61.948	118
HM_3463	contig26293	ATTTTG	6	24	CTCACAATGcACGcATTtTCTAAC	62.985	AAATTAAGTTTGCATTCGGTGG	62.437	110
HM_3464	contig18449	CCGCCT	6	30	CTCACTctGATCTCTCTCTCATC	62.859	TTCAAATCGAAGCAACAAAGATCA	63.046	134
HM_3465	contig48832	TCTCTA	6	24	CTcATATCTCTAtcagTCTCT	63.201	TGAGcACCCCTGATTTGACTTTgA	63.048	85
HM_3466	contig16984	CTCTCG	6	30	CTCTCTCGACAGTCTCTCAACTCT	63.023	TGAAGGAAGAGgAaGATcATCAGG	63.076	134
HM_3467	contig18920	GGTTTG	6	24	CTGTTTTCATCCGAGTGTGGAG	63.249	CTGTGTTTGAACCTCGGAACCTT	62.82	122
HM_3468	contig07032	CTGCCT	6	24	CTCTCTCTCCCACTCTcCTCTCT	64.806	GTCGTAGAGGTGCTCCGAAGG	64.528	152
HM_3469	contig31767	CTTGCA	6	24	CTGCAAGTCTGTGATCTATTGG	63.265	GCaGGAAaATTATGTGAGAAAGCG	63.245	151
HM_3470	contig13941	TGACGA	6	24	TCGcAGGTAAATTGAACTCTCGT	63.154	CTGTCACTGGTTTGGGTTTCAGT	63.658	107
HM_3471	contig38883	CTATTT	6	24	CTGCTCGTGATTTATGCTACTT	63.249	GATAAGGTCTCCACAAGGTTTCCA	62.684	117
HM_3472	contig36418	CTTCTA	6	24	CTGCTGGGTTTCTTCAAAATTCTC	62.508	CATTCACTCCCTCTCTTTCTCT	62.863	157
HM_3473	contig21866	TACCAA	6	30	cttctgtctctctctcagagt	63.208	CCAGTCTCTCTCTGCTTCAAC	62.909	145
HM_3474	contig19743	AGCACT	6	24	CTTGCTGGATGAGAaAATGGAA	63.834	CCATTCCAAaACCACTCTAGATT	64.593	149
HM_3475	contig13367	AGACCC	6	24	CTTTCAAAGCCTTGTCTGCTTA	63.036	ATTaAGAAATGGCATCGGgTCAa	63.021	97
HM_3476	contig32050	TCTTTC	6	24	CTTTCTATTACCTCTCGCTGCTG	62.741	AGTGATAGCGGTTTGGAGGAGAG	63.113	141
HM_3477	contig01018	TGGAAT	6	24	CTTTTGGGGAGATTGATGTTG	62.894	TAATCCCTCAGCTTCACTCTATT	63.009	131
HM_3478	contig03943	GAGGAA	6	30	GAAAGAAAGGAGCAACAGCAAGA	63.225	CTGTGTTTCTCGACGACATTG	63.057	125
HM_3479	contig06066	AATTTG	6	24	GAAAGAAAGTGACTCTcATCCGAC	62.68	aAGGAGAGAAaATTGGAGGGAATG	62.958	104
HM_3480	contig36981	ATCGCC	6	30	GAAGCAATTTCGAAaAcgAaTCTCT	63.121	TCTGGTGGTGGGAATGAAGATAGT	63.102	127
HM_3481	contig21039	GGTCGG	6	24	GAAGGTGAAGTGAAGTCGCATTG	63.267	ACTACTAGAAAGATCGCATGCTGG	63.048	157
HM_3482	contig09524	CTAGAT	6	24	GAATCGATACAGTTGGAGGACAGC	62.547	CAGTACTGAGTAGGGAATGGACAGT	61.977	150
HM_3483	contig44824	TGAAGG	6	30	GAATTTGGAAGTCTCAATGAATG	63.117	GAGTCACCCCTCTCTCTTCTCA	63.186	147
HM_3484	contig48221	TCTTCG	6	30	GACTCTCTCTCTCTCACTCCACCG	63.919	TCCGGTCTCTAGGTTAGCAAT	63.389	158
HM_3485	contig44781	GAGGGA	6	30	GACTGTGGGAGgAAGAGGAACAG	63.645	AGCGTCaACCACTCATACCTCTCT	63.04	116
HM_3486	contig10821	TGGGTT	6	24	GAGAAGAAGTGGAGGGGATTGTT	63.071	ACAGACACACAACATgGAAGAAc	62.49	141
HM_3487	contig08934	CCGTCT	6	24	GaGaGGAAcAGaAGGAGGAGAGa	63.692	CGGGGACAGAGAGAgGATACG	64.134	146
HM_3488	contig03128	GCAAGG	6	24	GAGATAGAGGAACGAGGGTgGACA	63	AGAATCTTCTGTTGCATCTTGCT	62.727	140
HM_3489	contig01940	TGGGAT	6	24	GAGGAATTCCCAATTTCTTGGAGT	62.865	CCCAATTACCTCCGATGCTTTTCT	62.91	119
HM_3490	contig07700	GTGTGT	6	24	GAGGATggttGGTTGTGTGCTG	63.537	ACAATCTCTTCCCAAAACCCCTC	62.769	146
HM_3491	contig17272	CGACGG	6	24	gAGGCTCTGTTTtTGGAAGAGACA	63.225	AAAGGCTGTCTGAAGGTACTGGAC	63.025	160
HM_3492	contig34143	CCTAAA	6	36	GAGGgTTGACCAGACTGAGATGAT	62.994	TGATAGTTGTGAAGGCGATAACGA	62.959	154
HM_3493	contig09921	GGGAGA	6	24	GAGTAGAGGGGAGGAGGAAGAGAA	62.639	TCTCTgTACTCTCAATTGAAGcC	63.343	107
HM_3494	contig37195	AGCAGG	6	30	GATAAGTATCTTtGGCGATTGCG	63.053	CCGATACATTCTACGTGCTGCATA	63.295	157
HM_3495	contig00456	GAACAT	6	24	GATAATTGGAAGTTCGGCTCCTCT	63.093	GAAGGTTTcGAATAAATCCCTCTG	63.072	155
HM_3496	contig43168	GCCAGT	6	24	GATACCTGACCCCTCTCCAATACC	63.39	GTATGGAACCTGGAACCTGGCACTG	63.042	148
HM_3497	contig38782	TCATAC	6	24	GATCACCCACAGACTTGGAACTAA	62.711	TTAGCGAACGATACGAAGAGGAAG	63.039	126
HM_3498	contig35485	CTCTCG	6	24	GATCTCTTCTTCTTCAATGGCCC	63.584	ATACACCGATTGGTAGTAGCCAGC	62.661	147
HM_3499	contig42730	TGAATC	6	36	GATGACGACGAAACACAATCAAC	62.847	CAGAGTCCATTTCCTGGTTCTGAT	62.884	107
HM_3500	contig19145	CTGAGG	6	30	GATGCTGGTCTTCAATAATTGGC	63.037	AAGcAGCTAATCAAAACCCAgTTG	62.849	145
HM_3501	contig18085	GCGGAG	6	24	GATTGGTCTACATAGCGCTCTTCC	62.537	GGAACAAACGACCACTCTCTCT	63.256	151
HM_3502	contig04246	AGTCTC	6	24	GcCaAAAAAGAGAGTgATGTGATGA	62.742	GTGTTGAAGAAAGCGCTATTTTTG	63.252	82
HM_3503	contig02066	GGTGTA	6	24	GCACCTCAGATTTGGTGTTCAGA	63.747	TCAAGAGCTGTTAGGAGGTGAaAGA	62.821	118
HM_3504	contig27383	GGGTTT	6	24	CATTGGAAGAAGAGATGAATCGG	63.322	AcCTTTTCAATTTCCCAAAAtcC	62.41	105
HM_3505	contig13549	ATAAAA	6	24	GCATAAGGCCAAATATCATCCAA	63.126	TGCGGATGACTATTATGCAAGTGT	62.875	110
HM_3506	contig17411	CTCTTT	6	24	GCCCCACCTCTTCTTCTCAACTAT	63.193	GTTTTTGAaAATGAATCGAAGCG	63.083	120
HM_3507	contig21386	GGAGTG	6	36	GCCTGTTTGAGAGACGAAGAAGAG	63.023	TTCTACTGCTTTCaAAGTCCCGC	62.957	147
HM_3508	contig09422	AGGCAT	6	24	GCSCGCTGTCTATTAGCTATTAT	62.925	TAAAGCAAGCCCTATCCCTATCC	62.812	85
HM_3509	contig25006	TCATCT	6	30	CGGcCTATTATTCTCATACAGT	62.746	GTGCTCAGAAGGAGGAAGATATGC	62.715	140
HM_3510	contig12144	GAGTTT	6	24	GCGGTTAATTTCAAGTTTATGtcTGA	62.695	CCCAGTCTTCAATTTCCATAg	61.863	158
HM_3511	contig08611	GATGAA	6	24	GCTAGGGTTAGTGGGATGACTGTG	63.238	AtTTTTCTGTgAGtTTTCAgGc	63.54	152
HM_3512	contig39951	GGCTGA	6	24	GCTcATTAAATGGAaCgATTGGAC	62.928	TCATTTAGACTGTGCAACAGCAGC	63.857	151
HM_3513	contig16986	TCTGTG	6	24	GCTGGGTCTGGGCTCACTATAGAAG	62.497	CCAACATAAATGGGTTTCTGTGTC	62.907	139
HM_3514	contig04784	GCCGTT	6	24	GCTGTGGATGTGGTgAGGATATT	62.382	TAAGCAGTGGCTATACAGGTGcAG	62.783	125
HM_3515	contig35058	CCAAGT	6	24	GCTTCTcATCAaCaCcaCTTCT	63.027	TAAATGCTCTTCTCTGGGCT	63.378	153

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3516	contig34845	GGATGT	6	24	GCTTGCAACCAGCAATAAAAAAT	62.773	GCCAAAGCGAACAACTGAAAGTAG	63.462	149
HM_3517	contig33057	TCAAAA	6	24	GCTTTCTCCCAAAATCCAATATC	63.079	TGAACCAACCAAAATTTGATCTCG	63.137	146
HM_3518	contig28282	TTGGAA	6	24	GCTTTGTTGGGATTTTCAGAT	62.62	CATCaAAGCATTTTCACCTcTAcC	63.121	136
HM_3519	contig43400	ATACAT	6	24	GGAAAGGAATTTGGGGTgAAACTTA	63.459	CAACATCGATCCCTTTCTCAACT	62.786	149
HM_3520	contig31113	GGCTTA	6	42	GGAAATAGATTGTAGGAAGGGCACC	63.188	AGCAGCACATAATCAGACACAGC	63.112	117
HM_3521	contig10673	CACCTGC	6	24	GGAATAGTGGTTAAAGGGGGCAAC	63.004	GATGAAGAATCGAAGAAAAGGGGT	62.974	116
HM_3522	contig38515	GTGCTG	6	24	GGAACTCAACCTTCACAAAaactGG	63.006	TTGtTgagTACACTGAGCGATTGG	63.609	134
HM_3523	contig23202	CTTGAC	6	24	GGACATTGctCTGACTCTGAAGACT	63.04	CAGAAAGTTGCGAAGAAAACCaG	62.325	124
HM_3524	contig34617	ATATGA	6	30	GGACTGGATTTTAATGGCAACAA	62.828	GACACACTGTCAAGCGAAATTCAAG	63.291	155
HM_3525	contig12783	TGAAGA	6	30	GGAGGAGTAAGGTGGAGATGAAGA	62.133	GCGTATGcTCCTGTTGTCTAAGAG	61.618	160
HM_3526	contig13590	AGAACC	6	42	GGAGGAGTAATAATCATCATGGTTGg	62.903	CTAGGGGATGAGGAAAAAGACTGG	63.459	135
HM_3527	contig44545	TTTCATC	6	24	GgAGTCTGTTTCTCATTTTCgAG	62.584	TcGAATTTGCaTGATAGTGAATCG	63.263	105
HM_3528	contig09910	ATTGGA	6	30	GGATGCGAAGAATCAAAATCAAG	63.117	GGATCgCTGCAAAATGAITCTTAA	63.533	145
HM_3529	contig17091	GGAGAA	6	24	GGCAAGAAAAaagTGCAAGAGAA	63.03	ctGCGCTTTCCATTTCATATAC	62.948	132
HM_3530	contig11468	AAGATG	6	24	GGCCATTACCAAGAAATTTGAAG	63.03	GGAACTTTgGATTCTCATCATCA	63.514	115
HM_3531	contig35622	ATCCCT	6	36	GGGGATCCATGTGATATGTAGAATG	62.595	CTATTGAGTTTGTGATTGGGATCG	63.005	160
HM_3532	contig36544	CATCTT	6	24	GGGTAGTCCGACTCATCATCATCT	62.786	GCTTGGATTGCCCTTaAgAAAGTT	63.016	152
HM_3533	contig21155	GGATTA	6	36	GGGTCCAATAAACACCACTGTTCT	63.544	ATTCTGGCCTTTTAAAGAGCAACC	63.016	126
HM_3534	contig33490	ATACAG	6	36	gggTgGaatGACGATGACATTATT	63.116	AAGCTATtATTcCCTTCacCCC	63.621	134
HM_3535	contig13750	CTCTTC	6	24	GgGTTGTGGGTTTTTGAACAGA	63.225	CAAACTCAAAcCAGTGCCAGAGA	62.81	134
HM_3536	contig42032	TTTAGA	6	24	GGTCTCTCTAGCATAGCGATTCA	62.26	TTGTTGACTTCTCTGTGTGTTTTGA	62.383	118
HM_3537	contig00220	TTTGGG	6	30	GGTGACAGGTGGAGAGACGG	63.119	AGTTATGACTCTCGATCCCCGAG	62.989	89
HM_3538	contig52078	CTCAGC	6	24	GATCGGGTgCaATTAATGGGG	63.311	AGTCGGTTGTGGTAGTGGCTATGT	63.138	138
HM_3539	contig49980	AACCTC	6	24	GTCAGGACACTCCTCTCGCAGT	63.295	tTCTGCTATCGGtaAAATCTTCAA	63.124	159
HM_3540	contig29512	ATCAGA	6	30	GTCCCAACCATCACCATCTCTTC	63.004	ATGGGTTTGGAAATTATAACCAAGG	63.072	108
HM_3541	contig18794	AGATAC	6	30	gTCTTTGTCTCCCTAATACGCT	63.008	GCAAGGACCCAAAGCTCTACATA	62.839	143
HM_3542	contig09563	AAGTTC	6	24	GTCCTTGAAGAAAGAGGTGTCGGA	63.111	CAATGGGIAAACCaGtCTCTGATGA	63.321	134
HM_3543	contig37505	GGACAG	6	24	GTGCTAaTAGGTGAATGGAGGCaC	63.15	AITACGATCATGCTTCGAAACGT	63.15	120
HM_3544	contig26207	GGAGGT	6	24	GTGGAGGTGGTgaCGAGAC	63.001	TTACTATCTCCACACCCTGGTTTA	62.811	101
HM_3545	contig14073	CCCTTG	6	42	GTGGTTTACGGGAGCAATGCTAc	63.048	GGGCCAAATTGTCTGATACaAAAA	63.221	139
HM_3546	contig46256	GCGAAT	6	30	GTGTAGACCGCACATGAGAAACAG	63.186	ATTGATTTCCTCGAGCTCTCATC	63.596	156
HM_3547	contig24396	CCATTG	6	24	GTGCTTGTATTATTTGTAAGTCCG	62.935	TGCTCTCCCAATTATCCCTATCA	62.996	132
HM_3548	contig48544	TCATTT	6	30	GTTCCCTTTTTGTTCTCATCTCT	62.876	CCTCCTCTCTCTCTGCTCTCTCT	62.873	135
HM_3549	contig23153	GGTGAC	6	24	GTTGCTGGTGAAGAGGTAACATT	62.725	CCAGTgTgTgGATTCACTCTTCT	63.649	90
HM_3550	contig34634	TGTGTT	6	24	GTTGCTTTTTGGGTTCTGTAAAGC	62.37	AACITGTACTCTGTGCGGAGC	62.951	148
HM_3551	contig04829	TGGGTT	6	24	GTTTGCTCTGGTTGTGTCTCTC	63.35	CTTCCCTGTATAGCATCGCAC	63.042	160
HM_3552	contig49598	TGGGCA	6	30	GTTTGCTGTGTTTGTGAAGATGG	62.958	ACCACACATACCATCATACCCG	63.022	159
HM_3553	contig49726	GGGATT	6	24	TAAGGTTTCATCTGCTAAGTGGGG	62.714	TGAAGAGATCAAGTGATGGACAgG	62.786	130
HM_3554	contig50529	CTCCCA	6	42	TAATAAACCCACCAACGCAACTG	62.956	CAATTGTTCTTTCTAATCACGCC	63.03	158
HM_3555	contig27465	CGTCAA	6	24	TAATGGAAaAACCTCCACTCTGG	63.519	GGATGAGGATGAAGATGAAGATGA	62.776	160
HM_3556	contig47819	CTTTCT	6	30	TACCCCATGGACGTTGTCTAATTC	63.219	GATCAATCACTACCCACaAaAgA	62.473	145
HM_3557	contig15659	CTATTC	6	30	TACTCTCTGGTCCCAAGCTACACA	63.049	TCATAAGAGaAgACGAGGGGAATg	62.884	142
HM_3558	contig47847	GGCGGT	6	30	TAGAACATTTTGGTGTGGTGTG	63.159	CCCTATAAGTTGCAAAAGTGGGTG	63.015	109
HM_3559	contig18231	CCCCAA	6	30	TAGCTAGAAATTAACAGCGCICC	61.984	GTTTTTAAGTCGAGTGTGTGAGTGG	61.304	100
HM_3560	contig39941	TCTTGA	6	24	TAGGCCCTCATGATTGCTAATACC	63.322	AAGATGACTCAACTGAGAAACCCG	63.01	142
HM_3561	contig41479	CTGCAA	6	24	TATAAATCTCAAGCACAAGCGCAG	62.788	TTTTTCAGGTGTGATGGTGATGAT	62.7	86
HM_3562	contig02388	TCCTCT	6	24	TATAAATCTCCATTGTTGCTGCCCT	63.034	TAGACAGACTGAgGtGAGAGACCG	62.241	142
HM_3563	contig24098	GAGGTG	6	24	TATAGAAGGTTGTGGAGCTGGAGG	62.907	CAGGGTAgTATCTCCGcCAGTT	62.81	152
HM_3564	contig21545	TCTTGT	6	24	TATCAGTGGTCATGATTGGCTCAT	62.822	TACACTCTACCCACAACCTCCA	62.71	157
HM_3565	contig04932	AGTTGA	6	30	TATCGACGGTGGAGAGAATTGAGT	63.331	GGTTGGGTCACTGTCTAATGCT	63.684	155
HM_3566	contig41734	GTTGGG	6	36	TATCTATCGATCAGAGGAGGgaGg	62.038	tccgcaagcccaatagtagt	63.026	141
HM_3567	contig48866	ACGAGG	6	24	TCAaAGGAAGGAAGGACAGATTGT	62.71	TCGATTTCGATCTCTCTTCAACC	63	155
HM_3568	contig11341	TCGCAA	6	36	TCACCTCAACTCCACCAAACTCA	63.367	CTCGAGGTTGATTGTTGATGTTCT	63.941	159
HM_3569	contig36643	GTCACG	6	36	TCATAATCAGCATCAGCACTCTG	63.481	TTAGATGGGCGGAATATCATGTT	62.925	134
HM_3570	contig40593	TCACCC	6	24	TCATCTGACACCTTTGAAGAAGGA	62.351	CCAATGGaAattaTgaGGcTCTG	63.005	157
HM_3571	contig13001	ATCTTC	6	30	TCATCTCAGAATCTTCAGAACCAAA	62.508	GGAGATATGGCAAGCAATGTTCT	62.733	150
HM_3572	contig37866	TTCTCC	6	36	TCCAAGTTCAACACAGATCCTTT	63.212	GCTTCTGTTTGTGAGTTGGAATCA	62.726	126
HM_3573	contig09929	GGTGGA	6	24	tCcaGAAGTGGTCAAGAGaAGGT	62.677	ATACCTCTCACCCaGGCCTC	62.665	160
HM_3574	contig04798	ACGACA	6	24	TCCTACTCTATGTGTGGGCTCAA	63.425	TCCTCTCGACACGAATATGATGA	63.028	93
HM_3575	contig05605	CACCTC	6	30	TCCTCTCCATCCAAACTCAATCTC	62.977	AagSGTGAGGGTTATACCGGC	63.41	126
HM_3576	contig30900	AGACCC	6	24	TCctcTGAAACTGcTgGTTTCATC	62.152	GAAGATGTCAAGATTTCGAGCTTCA	63.135	137
HM_3577	contig25615	TGATCT	6	24	TCTAATATACATACATACCACCACGG	61.352	AAGAAGGTGACCGACCTTCAATA	62.299	159
HM_3578	contig37989	TTTCATC	6	36	TCTCCCACTGATTCTTCCAAGATACT	62.698	CATCACAGCCACAGATTGA	61.905	158
HM_3579	contig26433	CTACCG	6	24	TCTCCGATACCTTTTGTGCAAAAT	63.03	TACCACTCATCTCTGCAAGTTCT	62.609	153
HM_3580	contig04002	GACAGA	6	30	TCTGATCCGAATCGGGAAAAat	63.917	CTTTTCCAGgAGTTGAGGAgAG	63.626	158
HM_3581	contig17824	GATGAA	6	36	tctGcTCAACTCAATACcAGtG	62.944	TGTTGGGACATTTTgATTGGAGA	62.601	127
HM_3582	contig25944	AGTTGT	6	24	TCTTCCAGTACAGATTAGTCGCGC	62.946	AAAAGGCTTCAGACAAATGCAAAAC	62.851	145
HM_3583	contig46010	CTTTTC	6	30	TCTTGTGTTCTGCTCGGGGATTT	63.019	AGGCGAAGAGACTATCCACAGGG	63.297	111
HM_3584	contig23725	TCTGTC	6	30	tGAaATTAGGCacTtATGATGAaCc	62.438	TCCAAAATGATCgGGTCTAGGTTCT	63.104	102
HM_3585	contig48566	TCGGAA	6	24	TGAATTGAACCgAGTTATCTGCAGA	63.038	TTTGAATGAGTCCATTAGTCCG	63.409	154
HM_3586	contig40575	GCACCG	6	24	TGAATTAGTACCTCCTCTGCACC	63.549	CGCTGTGAGTCTGATACCGTTG	63.159	143
HM_3587	contig38290	CACCTT	6	24	TGAGATcCAATCATCTGTCTGCTG	62.701	GTGCGTGGACCTACGTAAGGTAA	63.462	101
HM_3588	contig05829	TGGAGG	6	30	TGATAATGACCCACACATCCAAC	62.924	AtTAGTCCAACCTTATGTGCCAGC	62.647	160
HM_3589	contig07738	TTGGGG	6	24	TGATAATGATGAACAGGCCCAACAG	63.257	TcATGAATCgGGTgGATtGATaTaa	62.397	129
HM_3590	contig14359	TGGAGG	6	24	TgATCTGGTCCAACCTCCGATTAT	63	AGCGTCAACAATCTCAGCTCTCTT	63.053	142
HM_3591	contig30136	TGAAGG	6	42	TGATCTTGATCTGCAACAGCAGCAT	63.394	TCAAAAGaAAATCAAGAAATGGTCAA	62.932	135
HM_3592	contig31531	GATGGC	6	36	TGATGATGCTAAACCTAAAACGCA	62.872	CGAAGAAGctGaAgGAAGcGTTA	63.343	143
HM_3593	contig18180	TGTGGG	6	24	TGATTCTACGGTGACCGGTTCT	63.016	AGAAACAACTGAAGTGGTGAAGGC	63.036	109
HM_3594	contig47840	ATCCCG	6	24	TGATTCTCTCGCAAAAGGATTAC	62.815	TCTAGACCTAGACCTGCTCTTGG	62.382	130
HM_3595	contig19766	TTGTGG	6	24	TGATTCTGATCTGGGTGCAAGG	63.667	TCCTTCATAGACCTCATCTCCACC	62.874	158
HM_3596	contig27705	CTTGGA	6	24	TGCCAGAACACGTCTACTGTAATG	63.504	TCTTCAGAGaGTAAAAATGGCGC	62.919	88
HM_3597	contig44573	AGCCTG	6	30	TGCTTCTCTATCTGCTGAGCCATT	63.777	CGTCTCGAGAgAgaggTCTACAG	62.906	140
HM_3598	contig32067	TTCTGA	6	24	TGGAGCTTTGAATCGTTGAACCTT	63.336	CGTTTGTGCCCTaAAAACGAATAC	62.862	107
HM_3599	contig30141	TTGAGA	6	24	TGGGTTAAGATTGAATGGATGGG	62.993	ATTGCAATTCAGTTAACGCCCTC	62.55	137
HM_3600	contig34949	CAGAGA	6	24	TGGTGAAGTGAAGCAGAGAGAAGA	62.812	AGGTTCACTCTTATTCTTCCAA	62.269	143
HM_3601	contig50731	CTGTGC	6	24	TGTGGGTTTGTGATTTCTCTCTC	63.751	GATcCGTCTCAGCTCTCACTC	63.898	80
HM_3602	contig13636	TGGGTG	6	24	TGTGTCTCATTTTCAGAGGTGTC	62.692	TATATTCTcCaAACAcCGCTTgct	63.15	136
HM_3603	contig09900	TTTGTG	6	24	TGTGTTGGAGTCTGCTGCATATT	63.078	CTTGAGCAGTTCATGGACAACACT	62.841	131
HM_3604	contig50367	TCCAAA	6	24	TAAAAaCAATACCACGATTACGC	62.333	GCCAAATCAGTCTGGAAGAGAA	63.009	87
HM_3605	contig49756	ATGTAG	6	36	TTATCCCAACAATATCCCAAGGC	63.117	CAGTGCTGGAGCCGTCTTCTTACT	63.677	141
HM_3606	contig31567	GAGAGA	6	30	TtATTAGIATTGTCATTCCGCCCT	62.981	CTTGcGTTGTGTAtTctCGCT	63.534	145
HM_3607	contig38465	GGGTGT	6	24	TTCAaTAAACACTTGAACACAGA	62.843	GATTGAGACCTTAATGTTCTGCG	63.03	160
HM_3608	contig00616	TTCCGG	6	24	TTCAaTTCACACAGCACTCCATC	62.609	TAAAGATGCACCAAGTCTTTCAGG	63.03	141
HM_3609	contig28773	TCCTGT	6	24	TTCCAATTGAGAGGTAGGATGCTC	62.9	CAGTCAACaAAACAGATGAACAG	63.036	132
HM_3610	contig10465	GTTACG	6	24	TTCCGGTGAAGTTCAAGTTCAAG	63.732	ATCGTGTGCAATCCGATAACAGT	62.926	118

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3611	contig28242	CCAGAC	6	30	TTCTCTCCTCTAAAGATACCCACC	62.863	ACCCTaaGTCGGGTCTAGGAGTG	63.089	143
HM_3612	contig30411	TTTGTG	6	24	TTCAAGGTGGCAGTTGTCATTAT	63.043	TACACTTCTCTACCACCGGAGGAC	62.909	137
HM_3613	contig35268	CGCCAT	6	48	TTCTGTGTATGCCGAGGATAAAAT	63.021	ACTGGCTGTCTAGGACcTCTTcat	62.899	160
HM_3614	contig39879	AAAAAT	6	24	TTCTTCATCGTTCTTCACATCTGC	62.833	TATCAGTTCTCTCACTGTGTcCCC	63.649	115
HM_3615	contig07564	TGGGTC	6	24	TTCTTCTCTCGTCATTTCATGT	63.108	TCCCTTAGCTCAGTCAGCTCTCTC	62.809	154
HM_3616	contig12075	ATTTTT	6	24	TTGAAAGCTCCTGATTGTGGAAAT	63.219	CATAGTGTCTCAGCTTcCtcat	63.035	135
HM_3617	contig20124	CTTCGC	6	24	TtgAAGAAcGTaggATTAcgAGGC	62.839	TGAAGCTAGTGTCTGTCATGAAAGG	62.943	131
HM_3618	contig09097	AGTGAC	6	24	TTGATATCGAACATCGTTCACTCG	63.257	ATGGCTACCAGTGTCACTCCACT	63.365	149
HM_3619	contig30187	GCGGAG	6	24	TTGATCTTCTGGGCTTGGTGAT	63.121	AATCGACAATGTGAAAGCGAAGAT	63.248	148
HM_3620	contig17308	GGGTG	6	30	TTGATTCAATTTTGTGATTGTGG	62.919	CGAACCCGTCAGCGAGAcTA	63.773	158
HM_3621	contig23862	GGGTG	6	30	TTGGTGAGGTTGTTGAATGAAGA	62.918	GTATGTACACGTTAAACATGGCGGA	62.985	148
HM_3622	contig28453	TTGAGA	6	42	TTGTTGCACTGTCTTGTTCCTG	62.945	AATCATcCaAcCCAAACACAGAAT	62.8	131
HM_3623	contig26166	CACAGG	6	36	TTGTTGCAATCTTGAACACCAATT	62.744	AGaATCAGAGCTCTCACAGCAaT	62.928	156
HM_3624	contig23726	TGCTGA	6	30	TTTCGATATCATCAAGGTAAGGC	62.737	AAGATCGTAGCATTGACAGAAGcC	63.051	87
HM_3625	contig13615	TTTAGG	6	36	TTTCTCTTTTGGGGGTCGATTT	63.163	GGATTcATgGAAAACTCCCTTAT	62.573	96
HM_3626	contig32152	GCTCCT	6	24	TTTGCAACTTGATGTTACCTTGA	62.843	GTACACAACCAACCTCTCCACC	63.023	155
HM_3627	contig37036	AGGAGC	6	30	TTTTTTCATCACTCAACCTGTCATC	62.514	TACAGATGGCAGATaAAAAGGGGA	63.005	147
HM_3628	contig43549	CGAGCC	6	30	TTTCTGCGCTCGTGTCAAAGAT	63.165	TCAAGCTCCaAGIAAGATATGcCa	62.241	148
HM_3629	contig49460	TTTGGA	6	24	TTTTGGTGGTCTCCAACCTCCT	63.197	AGGCACAACAGTCCAAGATTAG	62.729	112
HM_3630	contig42049	AGGT	4	16	AAAAATCCAAACAAaGGGAAAAA	62.1	CGCTGTCTCAGAATCTCTCTCT	63.014	160
HM_3631	contig27424	TATT	4	16	AaaCAAAATGGGCATCAGAAGGATA	62.912	TGAGaTTTGCTCGGTGTGAATA	62.946	142
HM_3632	contig46758	TTCT	4	16	AAACTCATCAAGATGCTTACCGC	62.854	TGTAATGAAGGTGTGATGCTGATGG	63.257	119
HM_3633	contig20015	ACAG	4	16	AATACACTCGTGTCAAATAACCG	62.343	TTCTCTCAGGATGAGTTTCTCTGTG	62.015	113
HM_3634	contig26699	TTGC	4	20	AAATAGGAGGGGAAATACATCGC	62.81	GACACaGAAACGAGAGTGACCAga	63.045	122
HM_3635	contig12166	AGCT	4	16	AAATCTAGCTACACGAAACGcG	62.862	TGGCTCATAACCCCAATAGGAAT	63.764	144
HM_3636	contig46162	TATG	4	16	AACAAGGCTCTCAATCATATGGC	62.733	CCTTCAATTTTgACtCTTCACG	63.21	94
HM_3637	contig31933	TTTA	4	16	AACCAAACTGCGCTAACTGTTA	63.166	TGATATTTGCCACAGAGAGCAAG	62.744	153
HM_3638	contig27515	GCAT	4	16	AACCAACCACTTAATGGTAGCGC	62.645	AGTGATGGATTGCCAAGAGCTC	62.914	82
HM_3639	contig23135	TTTC	4	16	AACGGGAAGTGTTCCTTCTCTCTC	63.189	GATGCGGAACAAGATGATAATGTG	62.735	100
HM_3640	contig09838	GATC	4	16	AACTGATACAAaATGGACACTcG	62.44	GGCCAACTCCTGATGCTATTAAg	63.01	116
HM_3641	contig21997	ACAA	4	28	AAGGGAAGAATAATGCAATATCaAGC	61.944	TAGGtTGAGATTGTGAACGTGTG	62.538	157
HM_3642	contig19204	AAGA	4	16	AAGTAGTCTGCTCTCAGTGCAC	62.779	CCTGATTCAATTAATCCCGACCA	63.101	143
HM_3643	contig35606	TAGG	4	16	AAGTcTCAACAAAAGATgCGAaG	63.031	TcCTCAATTGGTAGGGATGTTTg	63.3	96
HM_3644	contig03433	AGGC	4	16	ACAAaGCAGCAAAAGGACCATAAA	63.146	ATGAGCAGCTGTCACTCACTTGT	63.318	112
HM_3645	contig17501	ATTT	4	20	ACATTGGTGACcTGTATLcAGT	63.027	TGCTAATAAAAGTGATCATATCGGGCa	62.979	137
HM_3646	contig15895	TGAT	4	20	ACCCTAGAGAGAAAATCGTCGTCA	62.598	GATCGAAAGTGcTtTCaTAaAAA	62.628	159
HM_3647	contig49165	CTGC	4	16	ACCCTTGCcAtaTTATTGTTTCg	62.264	ACAAACAACAGAGACGCGAATTA	62.156	138
HM_3648	contig10936	TGTA	4	16	AcCGAGTtTGTGAGAGTCAATTG	62.798	ACtCTCGTcTtTTCTTCgGTCA	62.71	144
HM_3649	contig18057	ATAC	4	28	ACGAACGACCACAGATTGTGAAT	62.936	AGCCTAGATTCTCTTGGTCTGGG	63.285	105
HM_3650	contig02048	CTAT	4	20	ACTCATTTGTCACTCCCAACCT	62.901	GCAATACCTAAGAGTGGAAAGAGGGA	63.1	122
HM_3651	contig05933	CTTT	4	16	AGAAAAaCCaCTTGAACAGCAATTG	62.82	CCTCACATATAAGAAGCTCGGAGGA	63.009	148
HM_3652	contig14244	ACAT	4	28	AGATTGATTtAgGcGgTgTGATA	62.925	CCATAGCCCAACCAAAATaCGATA	63.13	126
HM_3653	contig32781	AGTG	4	28	AGCCTTGCAAGTCGACAAATTAAG	62.947	GATGGTGGTGGGTAATAAGAAAA	63.005	135
HM_3654	contig44794	AAAC	4	20	AGGTGCCAAAGCTAGAGTTTCAGA	63.057	AAAATCaATGAAGCAAAAGCCCT	63.3	154
HM_3655	contig39100	ACAT	4	16	AGGAGgAgAAAGCTATTGGCCAAAT	62.717	TTCTCTGCTGGTCAGATATTGATT	63.112	106
HM_3656	contig27882	ACGA	4	16	AGTAAACTCGAATATTTGGGGCG	63.486	TGTCTcTGAATTGCAACTCTCG	63.014	159
HM_3657	contig42200	GTCT	4	20	AGTCTCAGGCAACACAGTGGCT	63.392	TGATCGATTGAATCTCGTACGA	63.05	92
HM_3658	contig23694	AAAG	4	16	AGTTTCGTTTTGGGATTTCAGAGT	62.618	AGAGAGTTCATCTGGCTTCAATCG	63.23	107
HM_3659	contig21909	GTTT	4	16	AGTTTTGTTGCTTGATTGGAGAG	63.031	ACTGCCACGTCTTGTCTATCTCT	63.04	147
HM_3660	contig42048	TACA	4	40	ATACATCACAACTCTCAGCAAGC	62.441	TgGTAAAGGTCCTCAGAGATGATA	62.313	158
HM_3661	contig30951	AAAC	4	16	ATAGTCCACAGTCCAGACACACA	63.045	AAGGGCCTAATACCTAGTATGGCT	62.558	137
HM_3662	contig09041	TACA	4	16	ATCAATGGGGATTGGGTAAGATT	62.774	TGAAATAATTGGATGACTTTTCTATCC	62.651	142
HM_3663	contig02061	ACAA	4	16	ATCACCATGTCTAGGCTCAACAA	62.086	AAGCTATGGCTATGGCTACAACG	62.543	158
HM_3664	contig42398	AAAT	4	20	ATCCAAaATCTTACaaaCCCCcA	63.655	AATGaAGCTCGAGTGAGCAAAAA	63.552	106
HM_3665	contig29302	ATAC	4	32	ATCTTCAGATATGGGATCACAGG	62.558	CAATGATTGTTGCTCCATTCTCTA	61.588	157
HM_3666	contig21035	GCAT	4	16	ATGACAGTCTTAGAGGCAATCGG	62.923	GACTCATCTTCACTTTCAGAGCA	62.152	126
HM_3667	contig21810	AAAT	4	16	ATTGGAGgAAAGATTAaAACCCGA	63.072	CTTgTGGTCTTCTcTGGTGAAT	63.01	102
HM_3668	contig39374	TGAG	4	24	ATTGGGATGGTAGAATCAACAGC	62.713	AACaCATCATCAATCATcAACCC	63.011	160
HM_3669	contig36908	AAAT	4	20	ATTGTGCAATTTgTTCAGT	62.839	AAGAAGaATTAAACTTgGGGCTCG	63.001	156
HM_3670	contig05772	CAAT	4	16	aTTTCCAATCAAAACCCAGATT	62.878	GCAAGCCAAGAGAGAGATCAAG	62.923	148
HM_3671	contig35554	AATA	4	16	ATTTTTAACTGGGAACcTgATCG	62.315	AATCAgGaTaAAAGACTCAAAATGGGA	62.331	95
HM_3672	contig13862	TAAA	4	16	CAAAACCCATCTTAAATATTTGCTCC	63.016	TGGCAAGTGGTGTGGATTAGTATG	62.167	159
HM_3673	contig25298	ATAC	4	20	CAAACTCAGATCGGAAGaAAaGc	62.619	TGTcTcTCTCTGCTCTTCACTCT	62.736	85
HM_3674	contig33158	TGCT	4	20	CAAACTCAAGAAGATGGAGACCC	63.204	CCCTCTCGGAAGATTGTTGAATTT	63.709	113
HM_3675	contig13648	AAAG	4	16	CAAAGTCTCATCTTAAAGTCCCTTC	62.828	aAGGTGCaAAAGTTTTGACTAAGaAA	62.703	116
HM_3676	contig17811	CAAT	4	16	CAAGGCTCTTAAATGTGATGTACC	63.026	TCTATCATGTGATGTCGCAAGTCA	62.855	150
HM_3677	contig07083	AAAT	4	16	CACATTTCACACTCGAAACAAAG	62.942	GGGTTTTGATTTTCCCTCATTTTC	62.971	93
HM_3678	contig01267	AAAT	4	16	CACCACCATCTACTACTCTCTCT	62.793	GTTTCTTGAACAAAGCCATGTGGT	63.561	111
HM_3679	contig38516	GAGC	4	16	CACGACATCTCTCAAGTCTCAA	62.798	CGGTCTGAGaGGTAACCCCTCTCT	63.197	159
HM_3680	contig07569	GTGA	4	24	CACCATCTCAAATACACGCATA	63.059	TTTCCCATTTCtTCTCTGTGA	63.19	150
HM_3681	contig23140	AGAT	4	16	CAGCTCGACTCTGCACAAAGaTAA	62.642	AAACGACTAATTACGGAGACACGC	62.768	125
HM_3682	contig03806	TTTG	4	16	CATTAGTCGCCATTGAATCTCTGA	62.617	ATTTTCaATTCCaATTCaATCC	63.16	156
HM_3683	contig11340	AGTG	4	28	CATTCTCTATTGCGTTCTAGTTCGAT	62.324	AGGATTTTTGCAATGCTTTGTGTT	63.055	120
HM_3684	contig51366	CTCC	4	16	CCACCACAGTCTTTATCTTAGCG	63.234	CAAAATACAACTACTCACGGGCCA	63.25	105
HM_3685	contig10360	AAAT	4	16	CCATCTTAGGAAGCGAGCTTAATA	62.064	ATCTAAAGGAGaCAAAcTGGGCG	61.969	160
HM_3686	contig00785	ATAA	4	16	CCATCTCAACCACTTTTCTCTTG	63.1	CATGTAAGGATTTGTGTTGAATCTACC	62.958	146
HM_3687	contig07401	TAAT	4	24	CCATTGAGTGTGTGAGGAATTTCA	62.382	ATCTcTtTGGTAGTAGTGGGTGC	61.901	159
HM_3688	contig29328	AAAT	4	16	CCCAACCCCTAACTCAAAATACCC	62.875	GTTATACCTTTCCGCTCTTGTCT	63.028	128
HM_3689	contig12671	AAGA	4	16	CCCAATTCAACCAATTAACCAAA	62.905	AgTGGGCTCAAAAGaAATAcCTA	62.122	107
HM_3690	contig01832	ACAT	4	32	CCCAATTCAATCTCTAaTCTTCTgC	63.189	CCACCAAACTCGGAGTAAACCTT	62.597	145
HM_3691	contig37960	GGCC	4	16	cccgactactcaactctagcaat	62.946	GCAATCTAGTGTGCTCTTTTCACT	63.154	90
HM_3692	contig12925	AAAC	4	20	CTCAaCGTATAATCAACTCCACAAAA	62.496	TAAATTTCAAAAGCGGCTCTCTAC	62.734	160
HM_3693	contig51473	TTAT	4	16	CCTGAGCTATGGCAAGTCTTAGA	63.129	TGGCTGcTtTTTCAATTAAAGTgT	63.146	134
HM_3694	contig31369	AAAC	4	16	CTCGCTTTTCTCTCGgTTAcTT	63.199	CTGTGTTGGGTAGGaACTGTGAGC	62.355	144
HM_3695	contig23301	TTTA	4	16	CTTTTCTTAAAGATCGCCATTGAA	62.919	GCTATgGTGGAaCATCTTGTGAAC	63.026	91
HM_3696	contig32620	GGCT	4	20	CTTTGAAATTTCTGGATGTGACC	62.996	ATTGTTTGGGAAGGTGCTTTAGCA	63.129	149
HM_3697	contig19481	GAGG	4	16	CTTtGGTCTGCaGgAGAGATAGA	63.212	CTCTCTCCCCCaCTTCTGTCT	63.301	115
HM_3698	contig09773	TCTT	4	20	CGACCTTTACCACTCTGATGATA	62.728	aAATcCATACTGGACAAGGGGATT	62.974	146
HM_3699	contig20219	TTTC	4	16	CGACGTGCTTCCCTTATGTTTTT	63.129	CAATAGGCTTTGGAGTGATTGGTT	62.665	208
HM_3700	contig41117	AAAT	4	16	cggtaccagatttaactactcaaa	62.676	accacaattttgattgatcggtt	62.851	88
HM_3701	contig33356	AAAC	4	16	CTACACCAAACTTTTGTCTCGCT	63.663	GATGGCCTTTTTCATCAAGAGTG	63.121	96
HM_3702	contig38396	CGTT	4	16	CTGCTATAAaTAAcCGGCTCAAC	63.074	ACGTTTCTCTTACAGCGAAAGCAC	63.179	121
HM_3703	contig14780	GCTC	4	16	CTCTCTGTCTGTTGATGAACCT	63.01	AGTATATAGctcTAGTGGCCgGg	62.924	131
HM_3704	contig14961	TGAA	4	16	CTGAGAGGTTGACAGAAGACACCa	63.027	GGGCACTCTGCCCTAGaTAAAACT	63.114	93
HM_3705	contig46800	CTCA	4	16	GAAAACAaTTCaAGTGCACCTCT	63.006	CGTCGATTCTGATCATCaATAA	63.15	141

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3706	contig40708	TCTT	4	28	GAATGAACCTCACCATTCTGCTGTA	62.609	CTaTAGCTGCTcCACTTTGCCAAT	62.96	149
HM_3707	contig20015	CTTC	4	20	GACACTTTCCACATTCTCGATTT	60.73	ACtTACatTCACITTCTCTCCTCAtcC	60.279	159
HM_3708	contig11070	TATG	4	16	GACATCACCATTATGCAACAAACCAC	62.743	TcAcCTtCAGCTCCAATACATACAA	61.825	124
HM_3709	contig30780	CGAG	4	16	GAGGAAAAGGAAAGGGAAGATGA	63.053	CACATCACACATCCACAcCTCATA	62.949	157
HM_3710	contig30782	CGAG	4	16	GAGGAAAAGGAAAGGGAAGATGA	63.053	CACATCACACATCCACAcCTCATA	62.949	157
HM_3711	contig30783	CGAG	4	16	GAGGAAAAGGAAAGGGAAGATGA	63.053	CACATCACACATCCACAcCTCATA	62.949	157
HM_3712	contig10972	TTCC	4	16	gaggggcTTtAAAGATCCGAAGAAT	62.225	CATggaAAAAcCACTACGGaAGAAA	62.544	120
HM_3713	contig13759	TAGA	4	32	GAGGTCCGAGAAAAGAGGCTATAC	62.795	CAGCCTGTAGCTTGAAATTGTGAG	62.44	119
HM_3714	contig13195	GAGT	4	20	GAGTGCACAAAATGAAGAAGTGTCTCA	62.084	TTTTTCAACACCTGGACATgACA	62.587	156
HM_3715	contig09336	GGAG	4	16	GATGGAATTGCGATTGGAGTAACAC	62.928	CCCAGACCTCaACaCATCAATTACTT	62.611	116
HM_3716	contig13075	GTTT	4	16	GCAAGTGAGTCCCTATTCCAACTG	63.338	ATGGCCAAATTGTTCCAAATCTTTA	62.722	160
HM_3717	contig35782	ATCT	4	20	GCACCTCACAGATTGCAAAAACAA	62.643	GGATGCCCTCCGCTaTTaTGtAgA	62.642	94
HM_3718	contig27331	TTGG	4	16	GCATGGATGTTCTCTGAATTTGT	63.334	TAcACTaGATGGCCCTTTAcCACC	63.563	113
HM_3719	contig06496	GATT	4	16	GCCATTGATTTGTGATTGGTt	63.13	TTCCAGACACCTTCTCTGTGTTT	62.483	80
HM_3720	contig20080	TTAT	4	16	GCCCAcAACCACTAACAAA	60.597	AATGAAGCTAAATTCTCTCTCATAAGG	60.067	145
HM_3721	contig12377	TAAA	4	16	GCCTTGGAGAAAGGtCtCaTtATt	62.986	ATGGATTGGACGATTCTAGGGTT	63.081	148
HM_3722	contig41614	TTTC	4	16	GCTGATTCTGTAATGTTGGACCT	62.713	TGCTTCACAGGTTCACTCTGTGTT	62.206	158
HM_3723	contig10849	AAAT	4	20	GCTGTCAATGATTGTCTGGTTTA	63.397	AAAAACATCATCACCCGAAGAGAG	62.798	159
HM_3724	contig17674	AATA	4	16	GCTTACCAATGATTAGAGCCAAC	63.223	GCCAGAGTCCAATGACTaTTTGTG	63.121	155
HM_3725	contig03048	GCAG	4	16	GCTTGACCAATCCCAATATgAAG	63.846	ACTTGTCTCTTCAGTAGTCAACgTG	63.25	158
HM_3726	contig26780	ATAA	4	16	GCTTACGTGATCTCTGCATCGTA	62.774	ATCATCAACGAATGATCTGCACAA	62.927	159
HM_3727	contig40603	TCTT	4	24	GCTTTAGCATGTCTGTTTGTGCTA	62.814	TCTGCTCTCACTCACTCTCTTCC	63.792	138
HM_3728	contig36538	GTGA	4	16	GgaGAAGACTGGtCTCAAGATTTCA	63.217	GGCTTCATTGTTGTTGTCaGaATC	63.236	132
HM_3729	contig00159	TAAA	4	16	GGATCCCATGAACATTTGAGATT	62.572	GTTTCGAGTAATGCTATGCTTCCC	62.356	82
HM_3730	contig02613	GAGT	4	24	GGATGAAGCCATTGACGATATGTT	63.339	TGTGATTGAGAAGCAGAGGCTGTC	62.937	105
HM_3731	contig11647	TCTT	4	16	GGCTTAAAAGGGGTGAATTGGGAC	63.004	CCCTCCTAGTCTGCTCTGTGAA	62.139	152
HM_3732	contig43030	TTGG	4	16	GGGATGTTTGTGATGGAGAGGAT	63.796	CCCAcACaACCAATCACTCAAT	63.134	80
HM_3733	contig09849	AAAT	4	16	GTTTAGCCTTGAGTCAAAACCGG	64.168	CGTTCTTTTgAAACCGGaCAAAAT	64.361	119
HM_3734	contig12089	TATC	4	20	GGTTTCAATCTCGAATCCCAAAAT	63.47	CTGACTCAATCTCTGCTCAcCCC	63.662	160
HM_3735	contig05737	TTGT	4	20	GTACTTGTGGGTTGTCAAAATCG	62.739	GCAGGCATTAGAACCACAAATTA	63.399	109
HM_3736	contig31545	AAAT	4	16	GTCACCTGCCAGGAATCAAAATTC	63.026	CTTGTACCGGCTTTGCTTATAIT	62.665	152
HM_3737	contig03785	GGGT	4	20	GTGCAAGCTCGTACCAAGG	64.295	CTCTcCCCCAcTCTCAAAAC	64.419	160
HM_3738	contig26809	GTTT	4	16	gtcTGAGGATTGTGCGATGTTATG	62.951	CGCTATTGTGACTGTGCATGTTg	62.774	158
HM_3739	contig17530	AAAT	4	16	GTGACCGTTAGgATTAGCCTTTAC	62.729	AAGAGCCTGTTTGGGTTAGCTTTT	62.739	159
HM_3740	contig14945	AAAT	4	20	GCTGTGTTGTTTATTGCTCTTCC	63.133	GCCCTAACTATGACAATGgGAATG	62.815	159
HM_3741	contig42533	AATA	4	16	TAGGCAAAATCCTTTGCAACATAA	63.034	CacCAaAAGAGcAAAGGGGTATCT	62.907	129
HM_3742	contig31368	GTCT	4	16	TATGTGGTACCATTTCGCTTTTC	63.126	ACACAGAcCaGACACAGACACAGA	62.263	99
HM_3743	contig39726	TTAT	4	16	TCAAACAGATATCCAATGTtCcAaGA	62.922	GCCTGATTAAgGAAcTGATTGAA	62.705	134
HM_3744	contig23145	AAAT	4	16	TCACAATTTTACCTgGaGAAAGGCA	62.112	AGCTGACATGCACGTGATTAGGTTT	61.392	130
HM_3745	contig42404	AAAC	4	24	TACATCTCTGAGATCAACAAACAA	61.801	GACTGATGGAAAGCCGTAATTT	62.788	157
HM_3746	contig50489	ATAA	4	16	TACATTGGCTCAAGGCATACTA	62.959	CTTGACAAGCAGCTaAAAGGGTA	62.834	81
HM_3747	contig24629	ATAC	4	20	TCCACTGTAAAACATCTGGAGGCTT	63.129	TGTACTTGATGTGGGTAATCTGTCTGA	63.055	82
HM_3748	contig47596	GATT	4	24	TCCATTTCGAAACAAATTAACCG	63.115	TCTACCAATCTGCCCAATTGATTT	62.912	156
HM_3749	contig03295	TTTC	4	16	TCCCTAAATGTTTGGTAAGcTTTtC	61.951	TGCCCaTAGCTTAGTGTGAGTAGG	62.856	139
HM_3750	contig37745	AACC	4	16	tCtTCCcTcTTATCTACAACCA	62.27	ATGTTCAAAGTGGAGGAGAGATG	62.884	127
HM_3751	contig46349	GATT	4	16	TCCTGTCTCTCTCTGGAATTAG	62.057	TTCTGCTGTTTCTACTTcAGGCTGC	62.576	128
HM_3752	contig23185	TGTT	4	16	tCGTACAAATCTTACCCGAACACA	62.754	TAGACACAACCACTCTcCCAGTGA	63.026	145
HM_3753	contig32253	GGTT	4	24	TGCTCATCCCTAAACTCAGAATCG	63.735	CTTCAGGAGCTTTGAGCTCATCTT	63.462	156
HM_3754	contig36856	TGTA	4	24	TCTATGAATTTCTTGGGAAAGCGA	63.209	CTCACTCTCGTTTCACTCAATTCA	62.919	159
HM_3755	contig07963	ATAG	4	16	TCTGATTATACCCATCGAAGACG	63.414	TcGaCTGAAAAGaAAAGCAGAACA	62.527	105
HM_3756	contig02180	CTTC	4	16	TCTAGATGATTCTTCTCTGCGCC	63.108	GAGAAAGAGCAAAAGCATTGACG	63.773	108
HM_3757	contig13603	CTTT	4	16	TCTTGTACGCTCTTCTCAaATCT	62.522	GCATTGCGTTGAAATCTAGAGAG	63.45	135
HM_3758	contig26495	TTGA	4	16	TCTtCAATTCGGAATCAItGgc	63.854	CGGCCAGTAgGtTTAAAGTTGTG	63.044	160
HM_3759	contig26488	AAAT	4	16	tGAAGATCTACATCATCGACAAACC	61.283	AGaATTGACCTCAAGTCTTTtCCTT	60.299	123
HM_3760	contig19880	ATAG	4	16	TGACCAAGTCCAACCTCAATATCA	62.803	CTCTTTTCTTTCACTCTCTGTGTG	61.906	133
HM_3761	contig21333	TTTA	4	24	TGAGAGACTaTTAAcAATGGCGGC	63.654	AATGTGcCAATTTTGGaATTtTTTg	63.026	153
HM_3762	contig06505	CATC	4	16	TGAGTGTGCGCTAcTTCTTGATG	62.842	CCTATCTTGGAACATGCTGGAAAAA	63.517	152
HM_3763	contig44011	ATGA	4	16	TGCAaAGgTGTaGTGTTTGTG	63.303	TTGATGctTACATGCAcTCCAAT	62.861	160
HM_3764	contig41735	ATTT	4	20	TGGACATACATGtCAAGCAGAG	62.397	TGAaATGCTTTCATGGAAATTG	62.146	151
HM_3765	contig34840	TGTA	4	20	TGGGAACGTGAAGGGGTACAACTA	63.003	CAGAGGcAGaACAACAGAAAACT	63.133	123
HM_3766	contig30582	TTTA	4	16	TGGTTGAGTAATATTGGAGAGCGT	62.261	AAAAAGCTCAATGGTCAITTCcAA	63.018	145
HM_3767	contig29381	CAAT	4	32	TGTTCTTcACTTGTCAACATCCC	61.316	CGGGGATGTTATCAITCTTAITCtC	61.162	160
HM_3768	contig29815	GTAT	4	16	TGTTTtAIGTACGCACTTCTGCG	63.068	TGCTCTGGAGTCTGGACTACATCTT	62.822	152
HM_3769	contig24395	ATTT	4	20	TTAACCGGTACAAGATgGcCACC	61.874	GCTGTTcAGGCGATAGTACTTTT	62.179	111
HM_3770	contig29707	AATA	4	16	TAACTTGCTTACCAAAAGACCA	63.023	ATGTGATTGCTAATGCCCTGTT	62.963	147
HM_3771	contig16383	ATAG	4	28	TTCAATCAAGCAACCACTACTGTC	62.381	TGGAGATTGAGGTACCTTTATATGTG	61.405	122
HM_3772	contig36558	AATC	4	16	tTtTtCCcTCACTCctCTTATTCT	62.949	CAGCTGAAGCTcACAGAAAGAAc	62.002	105
HM_3773	contig40007	ATAC	4	20	TTCTTTGgCaATAGGTCAaCaC	63.432	GAAtaaatCAACAGccCTCTccCT	62.986	160
HM_3774	contig16468	GAAA	4	16	TtGAaTTGCAaATAGTGGCCACC	62.16	ATGtCGTTTTCTGtttccTCGtC	62.824	116
HM_3775	contig18081	AAAT	4	16	TtGAGGGAAGGACAGaGAAACAC	62.997	TTTTTcACCGTcCAAAAAATTCAA	62.635	150
HM_3776	contig08867	TACA	4	24	TtGATCTCTTCTcTCCAgCTtCAg	63.313	ATTGTCGGAGGTCCAATTGTTGAT	62.813	96
HM_3777	contig13481	TTTA	4	16	TtGCTACGTACTACTGATGGGTA	62.982	TCCAAGTgtTAAGTGCTCTGCAA	63.285	156
HM_3778	contig31998	AATA	4	16	TtGGTACTCTCTGAAAAATCGATTAA	62.551	TGTGCTCCCTTGTtTAATTTTCTC	62.742	239
HM_3779	contig36799	CTAG	4	16	TtGGTGATGTAGGAAGACTGTT	62.972	CtctccAAGACGCaGACActacat	63.89	152
HM_3780	contig11620	CATT	4	16	TtGTATATGATGATGGCTCTCTCG	62.311	TAGGTCAACcAGAGGGGAGAGTTG	62.993	131
HM_3781	contig05675	TTTC	4	16	TtTGGTTTAAAGCACCAGTAACCA	62.44	TACCAcGATTCAcATTGCAITt	62.493	136
HM_3782	contig04544	TTTA	4	16	TtGtTCATGTTCTTGGTTgAACT	62.088	ACCCTAcAAAAATGAACCTGACGA	63.019	130
HM_3783	contig28169	AAAT	4	20	TTTATGTTTTCTcGTGTTgtCTCA	62.956	AcCcaATGATACGAACCAcAGAT	62.813	150
HM_3784	contig10323	AGCA	4	16	TTTGAATCTAACAGCTGGGCTCT	61.688	CaATTCAAGATTCAAGATTGAaATT	60.876	136
HM_3785	contig46172	ATCA	4	16	TTTGAATCCAAACGAGAATGGAC	63.305	TTGATCATTAGGTGAATgAgTTGGA	62.922	131
HM_3786	contig11613	ATTCA	5	20	AAAAAGTTTCAAAAAAGGGCAAG	62.998	CAAAATTGCAaTAAGGACCCATTCA	62.132	136
HM_3787	contig41789	AAAGA	5	20	AAaCAATaCATCAAAAGAcTCCAAaAa	62.234	ATTGCTAGaAATTGGCAGCTGTG	62.759	151
HM_3788	contig46020	TGTGC	5	20	AAACTCGAGTCAATTCATCACCGT	63.242	TGTTTCCACTTATTCGGAGAGGAG	62.894	151
HM_3789	contig02210	GAATC	5	30	AAaTCAACCGGATGAAGGACTGGTA	63.009	TGCTTTAAACCGTCTCTTTTCTCA	63.118	115
HM_3790	contig46783	TCTGG	5	25	AAATGAAGTCGACGCTGCAACTAT	63.377	GGACTTCACCTTCACTCTGCTTTT	62.912	127
HM_3791	contig44195	AAAAG	5	20	AaCAGGAAAGAAATCTGCAAAACA	61.308	CaAAAAAGAAAGTAACCCCAaA	61.246	128
HM_3792	contig35579	TAACT	5	20	AaGAAGCAAGTGTGGAGAGCAAGt	62.949	ATATGGctccTTGACgGTGTGTAT	62.94	140
HM_3793	contig20078	ATAAA	5	20	AAGCTtCACAAACTACCATCTCTC	63.027	tGtTTTTGTTTACCTTGGGAAGGa	62.904	148
HM_3794	contig45600	GGAAA	5	20	aaGGGGCTACACTGATCAAAACCTC	62.838	GGCTGTGATTCCAATATCCCT	63.52	119
HM_3795	contig23935	TGATC	5	20	AAGTAGGCCAGTTGTCCCTCG	62.785	TTGGCaAtTTGTATAAGCTAGTCGG	62.592	117
HM_3796	contig00392	GACCT	5	20	AATaaaCTGATTGGCAcctcCTT	63.196	CAAGTTACCACAGCAaagCTATC	63.251	122
HM_3797	contig27878	GAATT	5	30	ACAGAGAAGCCCAAAACCTTAGTC	63.201	TTcAGGAGTAAGGAGGTGGATACG	62.795	154
HM_3798	contig51826	TCAAC	5	35	AcCaAGGTTcTctCTTgGTCACATAG	62.793	GACTaAAGGtAcTAGGCaAGGAg	62.598	138
HM_3799	contig34285	ATTGA	5	20	ACCAAtGTCCGATGCCTTAGATa	63.013	tatcgctgtgtcgtattgcttc	63.868	160
HM_3800	contig13615	ACTCA	5	20	ACCTTCAACAAAGTCCAATCAACC	62.807	TGAGTCCAAGGAATTGGAAAAAG	62.881	141

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3801	contig49783	GTGGT	5	35	ACGGCTCTACATCTTCTTTGTGG	62.933	CGTTTCAGAGGGAACCTGTTGATCT	63.01	126
HM_3802	contig36526	ACTAT	5	20	AGTAATAAATAGGGGCTCCCAAA	61.329	CATCGTTGCTTATACGTTCTTCG	62.093	104
HM_3803	contig14441	CGGTT	5	20	ATaCAACACTTAATTTTaGGGGTGAAC	60.197	AATAAGCTAAATCGAACCGAAC	60.965	143
HM_3804	contig18579	GGAAA	5	20	ATATCCAAAGGCTCACACAACACA	62.844	AGACGACGaCCCTATCACAACTTC	62.925	104
HM_3805	contig32959	TGATC	5	20	ATCACTCAAGATTTCGATTGGAACA	62.053	CGAACAATTTCAATTCTGCTTTCA	62.425	92
HM_3806	contig50556	TCTCT	5	25	ATCTTCTAAAGTACGGGAAGCACG	63.076	AAGAGTGACTACTGCAAGGGAAGC	62.425	145
HM_3807	contig32172	CTTTT	5	20	ATCAAAATTTATTCAGGAGCACCG	63.339	TTCTTTcaAACGGAAGaGAAAGG	63.954	137
HM_3808	contig32824	ACAGA	5	20	attcAAAAGTGGAAAaTCTGgTGA	62.996	ATGCTGTTTTTGTGCTCTTCA	62.982	92
HM_3809	contig03563	GTGGG	5	20	CAAAAGTGTCCACACAGGTGTAA	62.109	TATCTCTGTGTCAAAACACCGACA	63.048	151
HM_3810	contig23163	TTTTA	5	20	CAAACGATGATTTTATGAAAAaTGCAAG	62.963	GGATGCCAATCaATTGTgATTITA	63.929	158
HM_3811	contig52539	TTTCT	5	30	CAAGATTGCAAGAGAGCTTTGGT	63.142	ggcagtgaacctttgtTGAGTAGAGA	63.148	95
HM_3812	contig48704	TTTGG	5	20	CAGGCTTAGATTCTTTGGGACCTT	63.086	TCGTAGAATCTCTCAITTCATTTCa	63.007	157
HM_3813	contig33076	CTTTT	5	20	CAGTCCCATCCTGTGAAAaTgTTC	62.897	TGAAACTCTCTCACCTCTCTGCTCT	63.119	147
HM_3814	contig10346	AAGAG	5	20	CTAGAGTAGCAGTGGGGCTTAGA	63.15	ggGGACgGaAAATaCTaAcCATCaT	63.282	148
HM_3815	contig10673	TTTTT	5	25	CTGCTTTCCATGTTGATTTTGAT	63.426	GaAAATagGGGTAAgAGGGGGAT	62.757	101
HM_3816	contig17480	CTTTT	5	20	CCTTGCTAGCCAAACAAAGAAAA	62.847	GGTCATTGATCACCTGTTCAATT	63.323	141
HM_3817	contig29026	TTTCC	5	20	CTTTTATGAGCCCATCTCTTAT	62.606	TTTCATCACCTcACCTCaATTTCAT	62.887	159
HM_3818	contig24667	AAATC	5	20	GACCTTAGCGAAACGATTAACT	62.665	AACATCTGAATCGaAAACCGACaT	62.982	152
HM_3819	contig33987	AAACG	5	20	CGCAAAATCGCACAGATaTaaCA	63.187	CGATGGACATTgCCTCTTAATTCT	62.718	149
HM_3820	contig52450	GAAAA	5	20	CGCGCTGCTCTAATAAGTTTAA	60.989	GCTCTaCCcCACACCAATTC	60.52	117
HM_3821	contig42650	AAGGA	5	20	CGtCTCTTCGAGTTCTGTTAGTG	63.548	AATggGaCAACAATTAACcACaAG	63.117	158
HM_3822	contig46455	TTTCT	5	20	CTACCCAGTAGAAGGTCTATGTGC	63.238	ATCAGCATATATTCCGCCaGGAAAG	62.642	153
HM_3823	contig18252	TTTGG	5	20	CTCCATAATTTTCTAGGTTGCCA	62.519	TACATCTCaCCCTAACCCAAATTC	62.383	135
HM_3824	contig06199	TTTAT	5	20	GAAAGACAGCAGGTTaaCAAACT	62.848	tCGaTGAATTTGAAACtGcACGcG	63.397	123
HM_3825	contig35232	GTAAT	5	20	gAaGTCTCTCGTATTGTTGAAGAA	63.121	TCTgaATAGTcCCCTcTCTcAcGac	63	93
HM_3826	contig21888	TCTGT	5	20	GAGAAAGAAaGGTGTCTCTGTGTA	63.01	CgctCCTCTCTCaagtCTG	62.691	138
HM_3827	contig19370	TTTCT	5	25	GAGCCACTTGTGTAGCTTTgAAT	62.949	CTAgGCgaAagtGaAAAGGATCaA	62.919	116
HM_3828	contig29905	GGATT	5	25	GAGGGATTCTGATTGTAGACGAGA	62.9	GTTGGAGAAGATCTCCCATTTCTCT	63.062	114
HM_3829	contig33906	GGCTA	5	20	GaTAGCAGATCGaCGGCAAGT	63.182	GATGAGAGATAGTTCCTCTGCTCT	62.715	101
HM_3830	contig01009	GCCCC	5	20	GATTGCAATTTCCCATTTTGT	64.059	CATGACACGTTCAITGGTTCTCAC	63.841	99
HM_3831	contig34988	ACAAA	5	20	GCAACAACAACCAAAATAGAGA	62.426	GCTTCTCGGATTTGTATATTAAACAC	62.361	155
HM_3832	contig36478	TTAGT	5	20	GCAATTAAGTCACTGTGAaTGTGA	63.397	tATCAAAAGCTTGGCaTTTGTTCg	64.349	108
HM_3833	contig06125	AAAAT	5	20	GCGACAGCACCAATATTTCAATTT	63.356	ACCAATCAGGCATTGACAGGATAC	63.45	80
HM_3834	contig07196	GAGAT	5	20	GCGGTTGTgaTTACAGACATCT	62.609	TCTTAGTTGATTCaATATTCAGCTCA	62.497	138
HM_3835	contig14222	AAAAA	5	20	GGCACAAGTACGAATTTCTATCTT	61.492	CCAgGTCtGGTTTTgtCtaTTTCT	61.052	160
HM_3836	contig46444	CAATC	5	20	GGGTGATTGATGAGAGaACGAAC	63.222	GCCTAAGGAGATAGaAAATCGAGGA	62.331	159
HM_3837	contig35537	CTTTG	5	20	GGTTTGTTGTTCTCTGATCCTCT	62.912	AAGTCgCGGGAATAAGCaAATA	63.039	132
HM_3838	contig41661	TTCTC	5	20	TCCAACATGATGAGAAAACTCa	62.907	ccTTTGGATTGAGAGAAGTGGAga	63.085	103
HM_3839	contig39839	TTTTT	5	25	TCCATGGTAACGAGAGaGAAAA	63.091	GCAGATTGTTTAGGCTCTGTTTGG	63.348	114
HM_3840	contig15324	TGTAA	5	25	TCTATCATCTCATCTCTCCAAAA	62.368	AACCCaCACATTACACTCCAAACA	62.621	145
HM_3841	contig26953	TTTCT	5	20	TGCATTCTTACCACCATCTCTCC	62.786	GaAAAAAGGTgtCCATTTCATTG	62.8	140
HM_3842	contig33487	TTCTC	5	20	TCTCTGCACTGTGTGTGTCTG	62.975	TTaTTATTTTGGAGGTGGGGAAG	63.25	138
HM_3843	contig29329	AAAAA	5	20	TGAaTtGCATGAATTTTCCAGA	60.436	ATCTCTCTACGAGGACCATCATTG	60.858	120
HM_3844	contig09906	TTGGT	5	20	TGAGCATATAGCTCTGATCGTgc	62.877	ACATGTGCATCGGAGATGGTCTAA	63.057	132
HM_3845	contig19941	AATGT	5	20	TGAGGTCTCTTGGGTCATTTGGAT	63.093	CCCTTTTcTCAACTCAGCAGTCaG	63.758	107
HM_3846	contig07302	TGGGT	5	20	TGATTGATGATTCACTCGTAATCAGA	63.044	CTCAAAAGGAGTTCACCTCTACCA	62.993	109
HM_3847	contig39631	GAACA	5	20	TGCAGTGCAAGTAgAGGTATaCaCa	63.098	gATCATCATCATGTGCTCTCTCCTT	63.775	130
HM_3848	contig42593	GGTGC	5	25	TGCCTGATTCAACCTCTTACTT	63.338	TTTaaCGAGACTcCGCCC	63.548	130
HM_3849	contig13784	AGCAA	5	20	TGGAACCTAAAATGGGTTGGGTATG	63.002	TTTGTAAATTTGGGTGACTTGAAAGTTG	62.52	157
HM_3850	contig39144	TTCCA	5	20	TGGCTATTCACTAACTAGAGAGGG	60.039	AGGTGATGAATgAAACAAGTAGCA	60.062	131
HM_3851	contig02477	TAGAA	5	20	TGTTGAGACTTACACTCCGTTGGA	62.121	TCCAGCTCTAAACCAATCAACAA	62.112	143
HM_3852	contig15679	TTTTT	5	20	TAAAGACTTTTGGAGGACAGAAA	60.475	TGCATAAAAAGGTACAATACAATGAAA	60.072	85
HM_3853	contig31764	AAAAA	5	20	TTCAAACTcAAAGCTCaTgTCAAC	62.726	GGCCATGTGTCAAAACACTTGTAA	63.176	143
HM_3854	contig23741	TAAAA	5	20	TTGTTGTGCTTTGATTTTAAACC	63.228	TGAGACGTTCACTTTTGAGACAGG	62.93	144
HM_3855	contig13507	TTTTA	5	20	TtGACCTATTATACATATTTGTGAGc	60.791	TGTTGGAATCTGTAGATTGCAAT	61.049	124
HM_3856	contig42982	AAGAA	5	20	TtGaTTGGGAGTtggAGAGaGAAG	63.085	tTTCATCTaAGTgGGGATAGAATGGT	62.239	113
HM_3857	contig28884	CTGCA	5	20	TTGTCTTATACCGGGGAAACCT	62.989	GTGTaAATtATTTGGAGCCGCTTG	62.957	151
HM_3858	contig26166	TCTGT	5	20	TTTCGGCAAAAAAaCAACTCTT	63.142	GAGCCGATTGATTGATTGAGAGAT	62.906	107
HM_3859	contig30656	TCTCT	5	35	tttCTGATTGATTCCTTTCCGAGTC	62.912	GGACTCTGGATTTCACCTCTGCA	63.017	133
HM_3860	contig02176	TAGAA	5	25	TTTGTGTGTAAaGGATTCCGGT	62.823	TCAAGTCTATCTCAAAACCAACaAAA	62.276	142
HM_3861	contig36621	AATAA	5	20	TTTTACAATGATCTCTCTGGTCC	62.593	GGGGAGTGTGACAATTTCTAAAG	63.001	143
HM_3862	contig00674	TTTGT	5	20	TTTtAGTTCCtCTTTGAAAGGT	62.49	ACATTTCCaCATTTTGAAGGAaaa	61.957	125
HM_3863	contig44141	TTCAATTTTG	9	36	TtATCACTTCTCTCGATCTCCA	62.279	GAAGATGGcCCTCaAGaAAACaC	62.716	126
HM_3864	contig16051	TC	2	14	AAaAaGGACGATTGTGcTTCCAT	63.991	ActGGTGAgtGTGTGAGAAAGATT	63.141	139
HM_3865	contig16404	AG	2	12	AaaaaTCAATTTGCTAATCCGAACC	62.561	AAAAATAAAATTTGGTCCGCACT	62.853	96
HM_3866	contig29866	AT	2	14	AAAAATCTCTCTCGTTTCGCTC	63.301	TAAACAACGATTGAATAGGGTGg	63.109	136
HM_3867	contig34724	AC	2	16	AAAACCAAAaCCATCGGAGATAA	62.839	cCAgtGTCTCGTAGCTTTTCAAGa	63.063	157
HM_3868	contig51240	CT	2	14	AAAACCATCAAACTaGAgTgCT	63.035	GAGGaAGtTgTgTTAgGGTCTgt	63.092	96
HM_3869	contig50524	AG	2	32	AAAACCTTAaTtTgTCAATCCGG	63.273	AAGCaAGAGGAGTTTCCGTATACC	63.102	138
HM_3870	contig16082	AT	2	16	AaaaCGaaGTATcGACCTTGGC	63.644	AcCaCAACaATtGTTGATTGATCG	63.026	113
HM_3871	contig10068	AG	2	16	AAAACCTGCGTTTATGCTTTCCACTG	62.966	TGGAGCTTGTGcCACTGTGAATA	62.969	146
HM_3872	contig42910	GA	2	16	AAAAGAAAaTGGGGATgAAGCAAT	63.087	TaCaCTTcCTaCCCaAAAGCAA	63.023	102
HM_3873	contig01310	AG	2	14	AAaAGAGaAaGAAAGGGGAAGAGG	63.415	GGAGGTCCCTATTATTAATTGTTTTC	63.15	109
HM_3874	contig36604	TA	2	12	AAAAGATGGCCGGAATTCATCT	63.099	TtctTGATCaATTCtGTTTCGTTg	62.731	94
HM_3875	contig21871	TC	2	16	AAAAGCGGTTCGAGTCTCTCAGTA	62.645	CAATCaAAACAaCaCAGCaAgag	63.057	109
HM_3876	contig08323	AG	2	12	AAAAGCTGTCAAGAAAGAACGC	62.452	CTTCCAATCTCAACACCTTCAACT	62.906	159
HM_3877	contig44811	GA	2	14	AaaaGGTaGAGAGAAGGTGCTGAAA	62.086	TCAAGCAACCAAGTATTCTTCAC	62.726	102
HM_3878	contig26099	CT	2	12	AAAAGTCAGCTCTCTCTGTTGCC	63.297	GATCCCAATCCAGTTCATCTCTCT	63.792	121
HM_3879	contig40985	TG	2	14	AAaAGTTGCTCCAATCTCTGCC	63.024	CTGCTTTTGTtCtAGCATCgGTT	62.957	117
HM_3880	contig30789	TC	2	24	AAAATCTCTGTGTGCGCTGTACc	62.838	TGAAACATgGAAAAAGACACTGTAA	62.918	82
HM_3881	contig43870	TC	2	12	AAAATTTGATTCTCCGCAACTT	63.198	AGACCAcTtCAACAAATTTCCCAT	62.585	131
HM_3882	contig42816	TC	2	14	AAACAaCACTGCCTATCTCTAa	63.129	agggtTCTCTGTTGCGTcAAaTcT	62.526	112
HM_3883	contig42653	AT	2	16	AAACAAATCCAAGAAACCCACAA	62.811	GTGATGAGCTGCGATTGGTAAAG	63.17	114
HM_3884	contig11694	TC	2	12	AAACAaGctTCGAACGATATTCT	62.854	TTGGAGCATATGATGTGTTTGGG	63.046	112
HM_3885	contig21934	CT	2	12	AAACAGAGAGGAAGTTCTCATGGC	62.281	TCCCTCATCAATCTCATGATTCAA	62.885	112
HM_3886	contig25853	AG	2	20	AAACCAAGCCTCTGCTCACTCTC	63.11	TCATCCCAACCACTAAACCTAGACA	63.017	96
HM_3887	contig37009	AG	2	14	AAACCTaGAAATTTGGTTTGGGA	62.977	TTTTTCCATTTCACTACCAATAACAGT	62.119	86
HM_3888	contig37986	GC	2	12	AAACCTAGCTTGCCTCAATCTAC	62.924	GGGCAATTACCAITTTAGGAGGA	63.368	123
HM_3889	contig09432	TC	2	14	AAACCTAATCGTGTGATGATTGA	62.912	TTCACTCTTTATGAGGGCTTCAG	63.006	138
HM_3890	contig33003	AG	2	32	AAACCTTcAGGTTCATCAAGTCCA	63.212	ACtCTGACTTcCCAACCTCTCTC	63.092	151
HM_3891	contig31990	AG	2	14	AAaCGAAGACAGAGAGAGaAaC	63.24	TCTCTTCTCTTCACTCGAGCTTT	63.035	107
HM_3892	contig27263	GA	2	12	AAACTTGGATTGTTTCACTGCTCT	63.048	CCACCAGAAATACAAACCCAAAG	62.808	132
HM_3893	contig45844	GA	2	14	AAAGAACTCTGGGATGACGACTCT	63.002	GTCACATTCTATGGGGTCTCGaAC	63.004	127
HM_3894	contig42738	AG	2	20	AAAGAATTGAGAGAAACGCACAGC	63.158	CCCCATCTCACTCACTGTaAG	63.199	159
HM_3895	contig29282	GA	2	24	AAAGACACGaGcAGACCGGAGC	62.96	AGCTTGAATTTTCTGTTGAGTTG	63.031	144

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3896	contig02659	TC	2	16	AAAGACGGGGTGATATGCAATAGA	62.925	GGGACTCTCAAGGATTTCAAG	63.165	134
HM_3897	contig35621	TC	2	12	AAAGAGCCCTAGATGTCAGATGATG	63.026	ATtgcGCCATTAAAGTAACACAGA	62.957	126
HM_3898	contig51562	CT	2	16	AAAGAGTCCAaTCAGTCACTCACG	61.94	TCTCAATTcACtCCCTAAAGTCCC	61.955	108
HM_3899	contig36690	AG	2	20	AAAGATTAGCGAGGACCTTGAA	63.481	AgGClTTAAGAAACTACTCCCCC	64.009	160
HM_3900	contig23786	TC	2	20	AAAGCAAGACGAAGGACATAAGGA	62.522	CTACTAItACITTaCCITCgGTGGagG	61.831	140
HM_3901	contig17083	AG	2	32	AAAGCATTTCTTCAGAGTTGGTG	62.921	CCCTTCtAcGTtTCTCTaCaTt	63.18	151
HM_3902	contig19522	TC	2	12	AAAGCTCAAGTGCTCTGAGAGAA	63.137	TcTCCATCTGATcAaAAACCAAG	63.613	94
HM_3903	contig15390	GA	2	12	AAAGGAaGgAGGGAGTAGCACTAGc	62.616	GAAAGATTATGCGCCTTCaAAAA	61.654	129
HM_3904	contig25569	GA	2	16	AAAGGATTATcAGTGGGTTCCG	63.47	CACACATTACACACTGCTGACTGC	63.019	100
HM_3905	contig16159	CT	2	12	AAAGGCTTCTAGCTGAGATGGAT	62.904	CTCACACCTATTGATAAGACGGGG	63.006	108
HM_3906	contig06343	AG	2	12	AAAGTGAACCTGTTGGGTTTgT	63.122	GTCTCTTGACAGCCCTCATTTG	63.352	119
HM_3907	contig06445	TG	2	20	AAAGTGCTCTCAAAAGTCAAAACCCA	62.328	GCCTTATTGCACTGTTGtGTGa	62.556	147
HM_3908	contig31048	AG	2	12	AAATaCTTGGCGAGAACTTCAACA	62.922	TCACTAATTGTCAACAACACAGTCA	62.661	134
HM_3909	contig16582	TG	2	12	AAATAGTCTTGTAGGCCAAATCGT	63.301	TTGAGATTATATACGTTCTCTTTCA	62.348	151
HM_3910	contig21237	GA	2	12	AAATATTAGCGAAGATGCCACTGC	62.56	TCCAATCTCATCCACAGTCAAGAA	63.123	148
HM_3911	contig14395	CT	2	14	AAATCAAAACCTTGACAGACCAcT	63.035	AGAGTCAgAGGTGAgAAGGGTga	62.882	129
HM_3912	contig42043	GA	2	16	AAATCAGAATTGCAAGACCCAC	62.7	aAcTcGACCAcCACCcAaCc	63.272	146
HM_3913	contig08732	CT	2	20	AAATCATTTCTGCACAACTTCTCG	62.529	CGAAGATCACTAGCTACAGACTCA	62.307	103
HM_3914	contig15266	CT	2	14	AAATCTTTGAGGGCCaCTTCAATC	63.79	ATGtTGGAACCTGCTCTGTTGAGA	63.4	160
HM_3915	contig36895	GA	2	12	AAATGGAGTAGAAGACCAATGAG	63.865	CCTGTGGCTTTAGAAAGAGCAAGAA	63.234	152
HM_3916	contig07050	GA	2	16	AAATGGTCACTGAAAGCTGTAGCC	62.949	TaGtAGaACCaCCGATCaAAACCC	62.508	143
HM_3917	contig44807	AG	2	16	AAATGTGAGCGGAAGATTGAAGAC	62.926	ClCTaCaAACCACTCTCCGaGGC	63.677	97
HM_3918	contig44060	AC	2	14	AAATTTATAGAAAACAGAAAAGGGGG	62.039	TCAGCTGATTCTTGATTGTGATTTC	62.841	146
HM_3919	contig25250	TG	2	12	AAATTCATAAAGCCCAATGATGC	62.328	GACTCGGATGACACCAAGAAAG	62.444	155
HM_3920	contig09708	CA	2	16	AAATTGCAAAACCGATAACGAGAA	62.945	TCACACCCGAAAGTTAGGGTTTT	63.028	152
HM_3921	contig46066	GA	2	16	AAATTTCAAAAACATCAAAATTCGg	62.264	GGATCCGAACGATTGTTATAGTGG	62.815	143
HM_3922	contig15768	AG	2	12	AAATTTGAATCGAGTAGAGCTCGG	63.055	GCTATgAgTCTCTaAAAgAGGCACC	62.741	140
HM_3923	contig32052	AT	2	14	AAATTTTCAAAACCAATTAACCC	60.495	TTTtctTTTCATCCCTATCTATGTGTG	60.187	117
HM_3924	contig31252	TA	2	12	AACAAGAGCTTCGgATGAATTTCTG	62.826	GATTTTGGAGATTCTTGCTCTGGA	62.705	153
HM_3925	contig52220	TC	2	14	aacaaccaactgcttattgtaC	63.263	gAGaAATCgAAGTaGAGAGCACTAGCA	62.777	80
HM_3926	contig17105	TC	2	16	AACAAGCAAAAAGAACTGATGATCC	61.942	CGGtaGTTGGGTAGAAAGACGAGA	62.918	142
HM_3927	contig08384	TG	2	12	AACAAGGAATCGTCAATCACTGC	63.55	TCCTTACCAGATCTCGACTCTCAG	63.089	93
HM_3928	contig26208	AG	2	24	AACaCAGAGCACTGAGAGTCTGGA	62.825	TTTTGAAGTTGCTCACAGTCTTCG	62.955	139
HM_3929	contig29366	AT	2	16	aaCACCCTACGCTGCTAATTTGAA	61.981	TTTTGATTTTACTCTCATGAATGGTC	61.672	136
HM_3930	contig18490	TA	2	14	aaCaCcTcAACAAGAAAGAGtGtG	62.648	ACATTGCTGAGaAGAAAGAACTGCT	63.048	127
HM_3931	contig33201	TC	2	20	AACACCTCAACCAATTTcGtGAAC	62.598	GTCGTCTGGGgAGGAGAGAT	61.622	99
HM_3932	contig48698	GA	2	16	AACACCTTAGTCTGCCAACAGAGG	63.033	ATGCAACCAAGTCAACAGACAC	63.533	91
HM_3933	contig23733	AG	2	16	AaCactTGGTCCATCAGGAAAAGA	63.212	AAAGCAAGaAAGATTATCTCCCA	62.495	156
HM_3934	contig46232	AG	2	30	AACAGAAcAaaagaCCGGAATGAA	63.117	GCTGCTGCTTCTAGGTACATCTC	62.853	106
HM_3935	contig15573	AG	2	12	AACAGAGGATTCAACAAGTGAGGC	63.027	TTCAATcCcatCTCTCACTCTCT	62.977	148
HM_3936	contig41568	CT	2	14	AACAGCAATATGAAAGATCCCCC	63.482	CTATTGAATTCaCtCAATTCGGC	63.021	94
HM_3937	contig45105	TA	2	14	AACAGCCCAATTGAACAATTTTA	62.733	TTCAATTTTATAGATCTGCTTCTAcCA	61.776	97
HM_3938	contig44311	CT	2	20	AACAGCGCCGTGATCTTCATAC	63.618	ATCGAGCTCATACAGAAAGACGA	63.556	88
HM_3939	contig12065	CT	2	24	AaCAGTATTGGATTTTCTGGGAA	62.922	CGGTTGGIACCAAGTAATCTGAC	63.031	147
HM_3940	contig24162	AG	2	12	AACCAAAATCTAGCTTTTGAGCC	63.799	GATTTCTGCCATTGATGAGTTAGC	63.352	151
HM_3941	contig28352	TG	2	12	AACCAAGGGTTCGCCATTATACT	63.016	GCAACTCTCTcATCTCTGgAAcT	62.472	121
HM_3942	contig43268	AT	2	12	AACCaCaCAATTAAGAGATTTCACAA	60.252	CATCAACTCCCTCTCTCTTATG	61.161	136
HM_3943	contig06959	TC	2	12	AACCACATCATCTCCCACTTTCTC	62.784	ATACTGAATTTCCCTCTGGAAGCC	62.986	144
HM_3944	contig46074	CT	2	16	AACCACCTTGAACCGTAGTCTGAT	63.15	TCtCTTTGTcTGGTTcGTAGTaGcG	63.16	151
HM_3945	contig19488	TC	2	14	AACCATAAAGCCCTGAATTTGGGT	62.903	TCCATTATGAGAAACagCAAGAA	63.141	157
HM_3946	contig22308	AC	2	20	AaCactCTGTtTcAACAIAACCCA	62.741	GGCATTGGCTCCtTTATTACTCC	63.202	157
HM_3947	contig37294	TC	2	20	AACCCACTCAAGCAAAACACAACT	63.258	TAGAGGATTGGTTGACTTGGCAT	63.121	92
HM_3948	contig13004	GA	2	12	AACCATAAAGCAACAACACAGG	63.354	GCAAAATGGCAAAAAGATGAGT	62.851	137
HM_3949	contig28654	GA	2	12	AACCCCAATTCACCATTTCTCT	63.078	CGTCTTTTGTCTCCCACTTTTG	62.809	155
HM_3950	contig14428	AG	2	14	AACCTAGCTAGCACCGAGAGAGT	63.13	GGATAAItTAcTcCCCCtTTG	63	144
HM_3951	contig15977	AT	2	12	AACCTTTTAACTCATTTTCCCA	61.458	TTGATTCCCTTACTGACtTTTGA	62.22	86
HM_3952	contig24997	TC	2	14	AACGCAAAAAGTCTCCAACCTCAC	62.922	GTTGCAGACACAGTGAGAGAAAGC	63.751	85
HM_3953	contig43058	GA	2	16	AACCTCTGATCTGCTCGTAATAG	62.923	TCCATCAAAACTTGCACTAgACA	63.048	82
HM_3954	contig31139	TC	2	12	AACCTTGAAGCCCTCAATTTCACT	63.285	AGGAGGGGCTTTAACTATCACa	63.285	160
HM_3955	contig45296	TC	2	24	AaCCTTTTCGGGGTACTTTGATTc	62.703	GAGTGAGGAACAGAGGGTTGAGAC	62.779	159
HM_3956	contig30393	GA	2	32	AACGAAAAAAGGTGAAGCAGAAG	63.041	TGAItTGTACACtTCTCCATCTCT	62.699	154
HM_3957	contig28202	AG	2	14	AACGACGATGAGAAAGACGAAGAC	63.141	GtCaAAGAGACACTAGcGAggCTT	63.275	93
HM_3958	contig36219	CT	2	16	AaCgTtAcCCcTAcTtCtAAACCTC	61.775	TTcAGATcAGTCAACCGAAAGaTG	62.698	144
HM_3959	contig39392	TC	2	12	AACGTtGCTTCTTGAACAAGAACCC	62.946	cTGAGGTTGGTACTTGAItTGCT	63.023	148
HM_3960	contig42590	AT	2	14	aaCtAaCaTACATGCAACATGCAc	62.313	TCAItTGcATaATAGaGtCTTGcATC	62.796	124
HM_3961	contig32714	GA	2	12	AACCTAGCATGAGATTGAAGAGC	63.051	TCAACTCGGACAAAAGATTTCa	63.034	90
HM_3962	contig28427	AT	2	20	AACACTGtGaCAAAATaGGGAGCCG	62.862	AAGACACTGAATGGAAAGaAgCACc	63.027	160
HM_3963	contig04840	TG	2	16	AACTAGGAAATTCAGGGTCGGAAG	62.98	GAACCGCAAAATCTCAGAGGTAAg	62.522	127
HM_3964	contig10188	AT	2	16	AACATTATTCTTCAACAACAAACCCG	61.781	GCaAACTACATGATTACATAcCaAAcA	61.448	115
HM_3965	contig43322	TC	2	16	AACCTCATGAGATGCCCTTCAAA	62.397	TCATCTATTCACTGGGAGTTTCA	63.132	125
HM_3966	contig41467	TC	2	16	AACCTGCTGCCAAATAAACTCCAA	63.146	GGGCTTAATgAGTTATGcAgGGAT	63.597	107
HM_3967	contig51331	TC	2	12	AACCTGGTCATAAACGCCATTACT	62.972	CACaCCAGAGcTAgGGITTCAGAT	63.023	99
HM_3968	contig32809	CT	2	12	AaCTTGCCATGTACACGTTCTCT	63.375	ATAACCCACAGATCTTCAACCAA	62.897	131
HM_3969	contig01290	AG	2	12	AACCTGTTTCTGGCAGTCCACAGT	63.474	CCCATTTGCTCATACATTCTCACT	63.544	113
HM_3970	contig01096	CT	2	24	AAGAAAAACGAGCCAAACAAACAG	62.954	AGGAGCAGTGAGAGAAAGAAgAA	63.023	109
HM_3971	contig44289	GA	2	20	AAGAAAAAGGATGAGGAAGGAAACAA	62.596	TCCACAGTCAAACTCACAAGCCTA	63.272	121
HM_3972	contig26156	AT	2	12	AAGAAACTGGGGTCTCATTGTGA	63.212	GATCTCTcCaaaCCACACAAc	64.1	158
HM_3973	contig40561	TG	2	14	aagaagaagcagaagggcatttCc	63.005	tcctactaaaccccttagattcCtCTC	63.152	109
HM_3974	contig00196	GA	2	20	AAGAAGCTCCAGTGAAGAAAGGCT	63.017	CAGGACTACCCCTCTCACAGACAA	62.892	160
HM_3975	contig43487	AT	2	16	AAGAAGATTCTCCCAACAaCGAatG	62.798	TGTTTGGCGGCTTGAAGAAATACTC	62.759	116
HM_3976	contig27825	GT	2	20	AAGAAGGCCATAATAGCAACAAAT	60.668	ATAAGATGGAATAcAaTATTcAgCA	60.024	109
HM_3977	contig32491	AG	2	20	AAGACGACATCGATATCTCCGAAC	62.816	ATACGAAGTGGGAAATGAAGAAA	63.138	141
HM_3978	contig05490	GA	2	12	AAGAGaAGGAGAACAAATGtGTC	63.002	TTTTTAaCtCATaGACGCaGCCa	63.081	88
HM_3979	contig50531	GA	2	12	AaGAGAGTGAGAAaAGGGAGGcCAT	62.986	ACACTAgTAGCCGACGATCaAAGG	62.946	94
HM_3980	contig41431	AT	2	12	AaGAGCAAAATTCACCAAAATGC	62.654	GCTCACTCAgagTATGATGAGAGA	62.026	144
HM_3981	contig42160	AG	2	14	AAGAGCCATGGCGCAAGAAATTAT	63.509	CAGATGcTAgATCCCTCTTCTCA	62.996	115
HM_3982	contig01189	TA	2	16	AAGAGGACgAAACGAAGAGGAAGT	62.996	AAGAGAGAAAGAGAGAgAgGGGCA	63.177	149
HM_3983	contig42487	GA	2	24	AAGAGGCTAAAGGCTTCCTGAAT	62.055	GACaCaTAAAcTTCtCtTcCTCTCT	61.132	156
HM_3984	contig00345	CT	2	16	AaGAGTGCGAaATgTCTCaCaC	63.06	cAAAGATCAAAATTGTTCCCAAGG	62.894	85
HM_3985	contig39585	AG	2	16	AAGATCCACAAACCCACTTCAAA	63.006	CTCTTTTCTAGcCGCTCaCAAGTC	62.946	108
HM_3986	contig37131	AG	2	14	AAGATCGATCGGCGCCACTTTTAT	63.399	CCAATTCTTTCTCCCAATTTATCA	63.391	119
HM_3987	contig29588	AG	2	16	AAGATCGGTTGGATCTCTGTGTC	62.901	AAAcCAACGAAACATTGACGAGTT	63.044	102
HM_3988	contig26630	AG	2	16	AAGATCAACCTTTGGTCTGCCA	62.411	AGAAGGGTATTCTGGAGGTGGAG	63.068	117
HM_3989	contig05538	CT	2	24	AAGATCTCGAAAGGCTATGCC	62.12	CCCCACTAGTCTTCTCTGTCA	63.107	106
HM_3990	contig20365	GA	2	12	AAGATGGAAGTGGaATCGGTTGTG	63.653	ATCGCAAGGTTCAATTGGTTCTCTa	63.231	135

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_3991	contig23924	CT	2	20	AAGATTAAAGGTTCCGGAAATCGTC	62.797	TTGCaGAtTATTGCCITCTCCAAT	63.13	159
HM_3992	contig00240	TA	2	12	AAGCAAAAGAAAAAGTCAAAATCCCC	62.9	GATATGTGCACACCACCACCATAG	63.506	98
HM_3993	contig20561	TC	2	14	AAGCAAAATAGTCTTTCCTATATCTACA	61.051	TCCAACCTTCACACTCttgttthA	61.88	139
HM_3994	contig36673	GA	2	12	AAGCAAAATCTCAGCAAGCAAAATCT	62.757	AGAGGAAGAGCATCAACAAGTTCG	63.238	159
HM_3995	contig06313	TC	2	24	AAGCAAGCAACAATCAATCCTAAGC	62.963	GTTGAACGaAGCAGAGAAGAGGAG	63.023	90
HM_3996	contig02366	AG	2	12	AAGCAGAGAATCGACTGATTTTGG	63.022	CAGCTCTCGAACTCTGCCAAT	63.15	147
HM_3997	contig11350	AG	2	12	AAGCAAAAGCAAGCAGAATTGTAG	63.064	CCCAAGTGATTAATGGAAATGTCA	62.08	113
HM_3998	contig50966	AT	2	14	aaGCCTAcTGAGAACATTCCTCAA	62.411	TCTCTCATGGCTGGTCTATGTG	62.712	109
HM_3999	contig29151	CA	2	16	AAGCCTCTATGGGGTCTCTCACT	62.889	CATTCCCAAAACATCAATCAACAA	62.919	144
HM_4000	contig16113	GA	2	16	AaGCGGAAGAAGCAAGAAAGAAaG	63.599	CTTATGCTCTGGGATTTGCAACG	63.841	150
HM_4001	contig32058	AC	2	16	AAGGAaTgGTGgAGAGAGCACTAA	62.598	TTTGTGAACAGTGGGAGGTTTT	63.015	98
HM_4002	contig08092	AT	2	16	AAGGTACAGATCTACGGAGAGGCG	64.121	GCAGTgGCaCacCTTAAATTTCTGT	63.129	158
HM_4003	contig39027	GA	2	16	AAGTGACTTGGTGAACCTGTAAC	62.807	CACACATATACGCATACAGAGTTTCTGA	62.622	96
HM_4004	contig36464	AG	2	16	AAGTGAGtGCCCTCaatGTCTTC	63.027	GTCTCTGGtTtCtCTCcatTcCt	63.278	139
HM_4005	contig25736	GA	2	12	AAGTGATGTGTGTGTGTGGTGG	63.168	TTCTGtTtCtACTGACTGCTCTGC	63.413	150
HM_4006	contig00726	TA	2	12	AAGTGCAAAAAAGAGCTGCCTACG	63.076	GCAGTTTACCACTGGGTTGaAGT	62.737	135
HM_4007	contig11463	GA	2	20	AAGTGGCCATTTCGTGACCAACTAA	63.129	CTATCTCTtCCtTCGaAGaCC	62.767	148
HM_4008	contig18376	TC	2	32	AAGTGGTAATCCCCCAATTGACTCT	62.974	AccCCCAATTAGAAGGaTCTGTgt	63.181	112
HM_4009	contig24156	TC	2	20	aagttctcgtGAgTcgTGAgtGCTG	63.819	accctataatcccTaAGCCaCA	62.992	113
HM_4010	contig16902	AG	2	16	aagtttagggttgatggttttggC	63.492	ACCACCCAGTAATCTCTCTGTCT	62.724	101
HM_4011	contig27901	CA	2	14	AATagCCGATCACAAAACCgAAac	62.634	CAATTTCTCTTCAGTGTGAGCAT	62.858	154
HM_4012	contig23184	AG	2	12	AATCAAAAGCACCCAGAAAGCAGac	63.027	caACAGGcaCCTTctatcCTCTGT	63.023	148
HM_4013	contig48377	GA	2	14	AATCCAAACTCTCCAATTCCAACA	62.996	CTTTCACACAACTTcCacAGTCg	63.155	154
HM_4014	contig19791	GA	2	12	AATCCAATCTCCcAAACAGAGAAT	63.278	CAGTGGCAGAGTGATTTGGTATGTC	63.057	119
HM_4015	contig16350	TC	2	16	AATCCAATCTGGGTCTCTCtCtCt	62.954	ACACCCATTAAAGGGCATTTTTCa	62.944	94
HM_4016	contig09418	AG	2	20	AATCGAATTCACACATTCAGGAT	62.903	AAAAATAGCACACCTCGTCAATC	62.634	137
HM_4017	contig46227	AG	2	12	AATCGaTCTGTATCTCTCGAACGC	63.042	GTATATCTATGGCCTTGGCCCTCC	63.103	141
HM_4018	contig41674	TC	2	32	AATCGCTTCTCAGAGTGGCTATC	63.051	ACTCGCGTTTCAGCAGaCAAAAT	63.401	147
HM_4019	contig25848	TG	2	12	AATCGTGGTCTCAAAACATCAAAAT	63.026	GAAAAGAGCGTAGCGTAAGTCTTGA	62.397	160
HM_4020	contig21214	GA	2	14	AATCTGACACTAGACGTGCGGCaAT	63.368	CCATCCACATCTTCAATACACAA	63.128	154
HM_4021	contig07784	AG	2	14	AATGAAACTTTTGAATTTGTGGCG	63.334	AACCCCTTCTCATTTCCTCTCTg	63.164	104
HM_4022	contig110331	AG	2	14	AATGAATCGAAATTCGAaCCTGA	63.009	AATTAGTCTTTTTCCGAGATcC	62.903	136
HM_4023	contig02532	GA	2	16	AATGACTCGAGACATGTTGAA	63.164	CATTTCTCTCTCTCCACAGAT	62.798	116
HM_4024	contig03654	AG	2	14	AATGCAATATCTGGATGGGAACAT	62.82	TGCTTAGTATGTGAAttCCGGGT	62.935	135
HM_4025	contig15676	TA	2	16	AATGCGCTGTTTACCCACACAT	62.936	GTGTTGTGCTGTATACTTGGCT	62.985	127
HM_4026	contig25180	AG	2	16	AATGCTACCAATCTTCCGATCAA	63.021	TGGGTGTGcATTTTCAATCAGTA	63.581	118
HM_4027	contig14003	AG	2	12	AATGCTATTTTAAACCGAGCAACGC	62.786	TCCAACAGAAACaAGGaAAATCCTC	62.784	124
HM_4028	contig48441	CT	2	12	AATGAAAAAGgAaAGGACTCTCTG	62.968	taACGAGAATTGACTGTGACCAG	62.724	88
HM_4029	contig17538	TC	2	20	AATGGCCCCAGTATTTCTCTCAT	63.878	GCCTTGCTACAGAGACAAGaAAA	63.142	151
HM_4030	contig08693	TA	2	14	AATGGCGCGAAATAGGAATTAAG	62.536	AGCGGTGTACTGATGCTTGT	63.171	149
HM_4031	contig15896	GA	2	12	AATGTGGGAAaCTCGAAATCTCAA	63.117	TCGAGATCAATCATTCTCaGAAA	62.821	83
HM_4032	contig00383	AG	2	16	AATTaCAAAaATTTGCAAGAGCCA	62.945	ttcaagaaaaaacaaagggttctCt	62.714	106
HM_4033	contig52121	CT	2	16	AATTATCCATCTCGTCTCCACATT	62.83	TCGATTGTAGGCTGTAGCACAAAG	62.77	141
HM_4034	contig07869	AG	2	16	AATTCATTTCCTCCAGGTGATT	63.069	gAGGCaGAACCCCTTAATTCAGT	62.995	144
HM_4035	contig28579	CT	2	16	AATTCCCATGGCATATTGAACAC	63.025	GAACCTACCGACCGTACCTGC	63.032	102
HM_4036	contig40412	TC	2	14	AATTTGACCACTTGATGTGATGG	63.198	GGGATGTTGTGTTGTGGTAACCTG	62.621	137
HM_4037	contig15884	CT	2	12	AATGTAaAaCAACAAATCCACCGG	63.122	GCTTCCAAAGCTGATAAGAGTGT	62.453	112
HM_4038	contig06588	TG	2	16	AaTgCGCaCgaAGGTTtgAAATTA	63.03	ATCGGCCATCtcttCTGTAATGAG	62.913	120
HM_4039	contig06114	AG	2	12	AATTGGAATAACTATGACGCCACT	63.039	TGAAACAAgTCaAAAATTGGGTTc	62.437	152
HM_4040	contig01092	AG	2	12	AATTGTGAACCGTGAATAATGGCTG	63.444	GTCACtCtTTAGaACCAACCCCT	62.983	81
HM_4041	contig43861	CT	2	12	AATTGTTTTATGGAGCAAGCATGG	63.339	TTATTCCTTTCAAACTCTCGAACG	62.613	148
HM_4042	contig46358	CT	2	12	AATTTCAACGACGATGAAGCAAT	63.968	CTGAGCTTCATTGGTCACACAA	63.493	159
HM_4043	contig01959	TC	2	12	AATTGGCAGAGAGCTTAGGTGTG	63.044	GTGGGAGGAAAGAGAGACAGAG	62.882	154
HM_4044	contig37425	TC	2	20	AATTTTGGGTaCACAATCTCAG	62.056	ACACAATCTTTTGGGTGcACTTTT	63.044	133
HM_4045	contig30432	AT	2	14	ACAAAAAGGAAGAGCGCATCAA	63.336	TCTgGTCTTAGTGATTGCCACTG	62.724	87
HM_4046	contig10712	GA	2	12	ACAAAAAGGCGAAATCAGAAaAa	63.027	CGCGGATaCTCGAGGTAAg	62.932	153
HM_4047	contig34499	GT	2	20	ACAAAACTCTCAATCGAAAGCAGT	63.256	CTCTGCTCTCTCTGCTGCCATA	63.551	148
HM_4048	contig35623	CA	2	16	ACAAaCGGAaAaCaGAAAGCAAAA	63.142	GcCTcTCAaAGATTACAGACAAcT	63.163	98
HM_4049	contig47773	GA	2	24	ACAAAGGAAGGAAaAaAGCTTCAC	63.098	TCTCTCTCTCgtCTcCTCCTcCT	63.273	132
HM_4050	contig20592	CT	2	16	aCAAAATACACaCtCtCTCCCC	63.702	AGATAGAGATTGAACCGGACATCG	62.8	92
HM_4051	contig06678	AG	2	12	aCAAAATTCATACCCAGAGGCCA	62.815	GACACGTATCGGTGGGTAGAGAG	63.238	124
HM_4052	contig23552	CT	2	20	ACAACAAAAGACATCAACAAAGCCA	62.958	TGCaAAAAAGATTGAaAATGGTGTG	63.154	136
HM_4053	contig39905	TC	2	14	ACAACCTCAAAACTGGACCTGTGG	63.658	CTGTCTCGAaAATTTGCCGCTC	63.597	96
HM_4054	contig21532	CT	2	14	ACAAGAAaGgGgTTTTCAATCAttCaA	62.461	TGGTTGTCTCTGCTTTATGTTGGA	63.048	96
HM_4055	contig49044	GA	2	20	ACAAGaACACGAACCTGGGTCTTC	62.922	CGTCTTACACTCATCGTGAATC	62.118	94
HM_4056	contig05453	TA	2	12	ACAaGACCTTAGCAAGAAAAaCC	62.071	AAGCAAAAGAAATCATACCTTCTCCTT	61.456	135
HM_4057	contig15401	AG	2	16	ACAAGTAGCTGAGACAGACGCCAT	63.708	GCTCTGGTTTATCTTCTTcggAcC	63.601	115
HM_4058	contig50164	AG	2	16	aCAATCGATGgTGaCaGaaAGTCA	63.044	AGATCACCCCTCTGCaAAGaAATACG	62.923	158
HM_4059	contig08559	GT	2	16	ACaATCGGCAATAATTTGGCTTTC	62.37	ATgCTGaAtAGCAATTTTGTGac	61.382	148
HM_4060	contig30687	AG	2	12	aCACAACAAAATCACTCTCAACGA	62.842	CCCTTTGTTCAATTTCTCGTCTGT	62.809	150
HM_4061	contig09012	AT	2	14	ACACAGgttGGGTtTGATTTCTGTT	63.023	ATCCATTtgggtTTTTCCAAATTC	63.167	159
HM_4062	contig32780	AG	2	12	ACACAGTACTCACGGGCTCTTT	62.539	GGAAAcACTCCCTTTCATTACaC	62.085	87
HM_4063	contig22036	AG	2	14	ACACTAGTAGACGCTGCCATGACC	63.086	GTCCGAGAAATCGAACTgaATCTG	63.431	138
HM_4064	contig22340	AC	2	16	ACACTTCGACCACTTCTCAACT	62.589	TGAATTTCAAACCAACGAGGTAT	61.853	126
HM_4065	contig41537	AG	2	16	ACAGAACTTACCACTCGGAGATGG	62.909	GCTaTACGaAACCAAAATCgCAAG	63.062	89
HM_4066	contig07466	AC	2	12	ACAGAGATCCCAAGCAACATGAC	64.023	GAGGTGTCCCTTGATTTCATCAGA	63.747	85
HM_4067	contig39843	AG	2	14	ACAGAGGGAAATCTCAACAGCAC	63.027	CACCACTACCAaACTACTCTCTc	63.334	156
HM_4068	contig36761	AT	2	14	ACAGATACAGGTACgAAGAAgGCG	62.946	aCTcTtaCTCTcTCCCCtCtct	63.344	97
HM_4069	contig16998	AG	2	12	ACAGCTTcTtTAAACACTGTCCc	63.005	TTATCATGATGCAATATTCTCCG	62.115	133
HM_4070	contig46030	AC	2	12	AcATAGTCTCGACCTGGATTTCG	62.811	ATCTCAACAGAGATTGCATTTGT	63.234	130
HM_4071	contig38817	TG	2	16	ACATCTGTGTGAGAAATGATCGAAA	63.055	ATGACGACGACGTATTGAGTTCT	62.864	150
HM_4072	contig33959	AG	2	12	ACATCTGTAGGGGTTAATGGCGTAG	62.633	GGAAATAAGTTCACAGAACAGACGTC	61.822	156
HM_4073	contig41883	CT	2	12	ACATGGTGATTTGGCTATGgAAGT	62.926	GACGAGCTCCATGATGATTTCTCT	63.124	145
HM_4074	contig03791	TC	2	16	ACATTGATGTTTCTCTGCACT	63.137	ATTTTCACTGATCTGCGAGCTGCG	62.142	155
HM_4075	contig17233	TG	2	16	ACATTGTACCCGACCaCTTGAAC	63.343	CgaTCTcTCTTTTTATTCaATAACCC	62.47	156
HM_4076	contig20053	CT	2	16	ACATTTTTGGGAAATTGCTGAAT	63.775	CAAAAGCaAAAGaACgACAGAA	62.867	90
HM_4077	contig49988	TC	2	14	ACCAAAaTTCGATGAATGATGTC	63.216	TAGTCTCATCTCAATcCaACcG	62.592	156
HM_4078	contig21204	AC	2	14	ACCAATGGAAGGAATCAACaCATC	63.323	ATCTCCCTCTCAGACAGCATGAAG	63.128	135
HM_4079	contig13859	AT	2	14	ACCAAAATACAGAGGTTTCCACAA	62.739	AAAAAGATATTCCAATCTTCTCTACA	61.783	156
HM_4080	contig03751	CT	2	12	ACCACAATTTGAAGGAGAAATTCG	62.606	tCAGTGGAACTTGGAAATGGACATA	62.803	156
HM_4081	contig05245	CT	2	12	ACCACaCTCTCTCTCTCTCTCTC	63.502	AGGGTTTTGGAGAGGAGTACTTG	63.076	130
HM_4082	contig34750	TA	2	12	aCCACCACTCTGCTCTCATAGtc	63.137	ttgtCaATACCCGcCTCAAGTAT	62.935	149
HM_4083	contig33479	TA	2	12	ACACGACGATCTGGTCTTTAGAA	63.338	GAGGCTGGAATTTGAATGCAAAAG	64.154	160
HM_4084	contig06602	CA	2	16	ACCACTCTTTTGACACCAATTTGT	63.023	GAGGATTGAGGATTGAGAGTTATTTT	62.258	157
HM_4085	contig02195	CT	2	16	ACCACTGaGAGTCTCCCActtC	63.21	ACAGTTCTCGAGATCAGAGGAAGC	62.59	160

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4086	contig32666	AG	2	16	ACCACTTCTGTACCCCAACATTA	62.809	GACGGGTTTGATATTTCTTCCgt	63.487	156
HM_4087	contig18614	AC	2	14	ACCAAGAAAACCTTGTGCAAGACAC	63.036	GAGAAGAGGTTGGGACCTGGTAGT	63.186	154
HM_4088	contig02483	AG	2	12	ACCAGAAAGACGAGGACCTGAT	63.537	CACCTCaCaAACCACTCTCTcACG	63.342	109
HM_4089	contig25802	CA	2	14	ACCAGAATTCcAAacTTCAATCCA	62.996	GTGTCTGAAAACGGACCGAACTAc	63.25	157
HM_4090	contig39158	TC	2	16	ACCAGATCTGAGGATGTCTCCTG	63.096	GAGAGAATGACGGAGCTCAAGAG	63.014	114
HM_4091	contig24456	TC	2	16	ACGAGCGTGTAGATTCTGTGTTT	63.263	ACGAGTGcCCCCCTTTTACCAT	62.882	80
HM_4092	contig27863	AC	2	20	aCAGGGGTCAAGTTCACCAATAAA	62.907	CCTGACCAGGCTcCTaAACTACAT	62.003	155
HM_4093	contig02900	CT	2	12	ACCATCACTCGTTTTCCTTCTCC	63.071	GGCCAGATCAAAATATCAGTCACCC	63.016	92
HM_4094	contig26876	AC	2	24	AcATCCAAATTGtGtGtCCG	62.072	AGATGGAAGtGATCTCGAGCTTG	62.215	148
HM_4095	contig40272	CT	2	16	ACCATTCCTGTCTGtTTCAGAT	63.128	CCGTCAACAACAATCAATTAGTCG	63.711	149
HM_4096	contig33461	CT	2	20	accnaaaacccaaactacTTTCGAT	63.098	CTCTTCTCTCCCTCTCCATTGAC	63.906	155
HM_4097	contig35113	AC	2	12	ACCCAAAGTTCAGTGACTCATCAAG	61.816	CCAGTTTCAAGTTCTCTGTGACC	61.411	159
HM_4098	contig15613	GA	2	12	ACCCAcGTAAAGACAACCTCACG	63.488	GAGGAGGAAGTGGAGGACGACG	62.496	99
HM_4099	contig31159	AG	2	14	ACCCATATCCATTACTCCGGTTCT	62.986	CAGCGTTTGTGACATTGAGAGAAT	62.741	126
HM_4100	contig17669	TC	2	16	ACCCATCAATTCCATCAGTGCACT	63.004	tgcagtgcagatGCTTTATTAGA	63.184	151
HM_4101	contig02126	TC	2	12	ACCCATGAGAAGCCATTAAACAGA	63.121	AAGTCTAGATGGTGTGACCTCG	62.909	132
HM_4102	contig15997	TC	2	24	ACCCAcTCTCTGTcCaATCTGATT	64.483	CGGACTTGAGGGAGAAAACGTaAT	63.786	87
HM_4103	contig30244	GA	2	20	ACCCGGCAaTTTAGAGTGAGAGAT	63.505	GTCaAGAACGAAAGAAACCATCCAT	62.7	118
HM_4104	contig11542	AC	2	20	ACcTAGATTGGTTTGcCTGCTT	63.404	AcCCTCaAAAGGAAAAGTTAGcCc	63.918	130
HM_4105	contig08461	AT	2	12	ACCGATGGTACCGCAGAGTTAATA	62.947	CCAATTTCTTTcCTAGACCACTC	63.968	156
HM_4106	contig25191	AG	2	14	ACCTAAAGTGgCATCAATGTGCTT	63.158	GACTGCGATTAAAGGACCACTCT	63.015	156
HM_4107	contig01676	AG	2	16	ACCTACAAGCTCCGTAACAATGGTG	63.566	AGAACGTGaCTAACCGGaGCG	63.825	145
HM_4108	contig31539	AC	2	20	ACCTAGaCAACAATAATTGTGCGTTC	61.974	TCgACATTATTTCTGTACGTGTCTG	62.596	104
HM_4109	contig09675	CT	2	16	ACCTGAAGagCTCGGATGTTGTAG	63.023	CgaAGAAATTAgaATGcAGAGAGGA	62.233	148
HM_4110	contig29752	AG	2	14	ACCTGTCTGATGAcTtCTCTACC	63.005	TTCaACTCcaACCTTAAACCGTA	62.916	127
HM_4111	contig50506	CT	2	20	ACCTTCTCTCTCTCACGGTTC	63.083	TGCGTTTCTGTATAGAATTTGCGAG	63.655	157
HM_4112	contig43685	TG	2	14	ACCTTGAGTTGACCTCAGTTGGG	62.805	tTCTCTAGACATAcCCAcCaAGC	62.811	141
HM_4113	contig29759	GT	2	12	ACGAAGAGAGATTGGGAGGGAGAT	62.865	TGAGAAGGAATTTGAAGAAGACGC	63.121	139
HM_4114	contig37383	AG	2	12	ACGAGATTTGAGGATTGAATGGA	63.099	CagTAAGGAGTAGCAATTTCTgTCaA	63.043	146
HM_4115	contig03978	GA	2	14	ACGAGGCTTCACTACTCTCAACAAC	63.04	ATATCAgGGCgaAACCTCTCACTC	64.023	111
HM_4116	contig50475	GA	2	24	ACGATCAACGAGTTAATGGACAGG	63.549	GGTTTGTTCGAGACATCGACCTAT	62.713	101
HM_4117	contig34219	TG	2	16	ACGATGATTCCATCATCTAGCTCT	62.916	AAAATTGATCTGAACAACGCCTTC	62.731	155
HM_4118	contig23468	AT	2	16	ACGCAACTAAATCTTGAACCAAA	63.039	TGCCCCAACCACTATATTCTCTA	62.909	148
HM_4119	contig00948	TA	2	14	ACGCAAGcTAGgTAGAGtCaCAA	63.578	AAGaAAAGCAGCAGTTGCAAGACT	62.972	145
HM_4120	contig14336	AG	2	14	ACGCAGCAAAACaCATATAGCAAGA	63.11	GAATGTTGCGGTCTTTTCAGTTT	63.244	150
HM_4121	contig09173	AG	2	12	ACGATGATGAGTAGTCCCGAG	63.883	GATCTCTGCaACTTtGcCTCTCTC	63.031	155
HM_4122	contig39128	CA	2	14	ACGCCATGTTTAATGCAACAGTTT	63.776	CCTaGaAAAACCCCTATTCCAGCTT	63.074	95
HM_4123	contig05651	GA	2	16	ACGCGATTTTGATtACCTGTGTT	62.96	GAGaAGTGAAGaAGaAGGGAGGG	63.161	121
HM_4124	contig30139	CT	2	12	ACGGATCGTAGATGAATTTCTTCC	62.733	TTTCCCAAGCTCAACTATCGATCT	63.121	158
HM_4125	contig38711	CA	2	12	ACGTcTACCACCTCTTTTCCGACG	63.05	TCTTGTTCTCATGCTAGTGAATTG	63.083	132
HM_4126	contig02351	CT	2	12	ACGTTCTCTCTcTcGTGGTGGT	63.452	AAGaGaAGAGTgTAGGCGCAGTA	62.848	113
HM_4127	contig08194	AG	2	12	ACGTTGATTGTCTCATCTCAGTTCCA	63.044	GCCTTCAAGATCATCAAAAGaCGA	63.854	144
HM_4128	contig10217	AG	2	24	ACTACAGGCTACAGCCaATGTGTA	62.134	ACATTGGGAGACGACGATATCACT	63.133	124
HM_4129	contig35847	TC	2	14	ACTACTCCacGAGCCaCAAGGTC	64.019	TCCCAAGTTCATCTGCTACACAA	63.048	103
HM_4130	contig18819	TC	2	14	ACTAGcGTCTCTTCACTCTCATT	62.526	AtGTGaAGGaGTCcCCGtTCTA	63.202	147
HM_4131	contig22815	TA	2	12	ACTAGGTCAGTGTCCTAAAGTCC	63.063	ATCAGCaCAAAAGAGCcaCACAA	62.958	115
HM_4132	contig37600	CA	2	20	ACTATCaTGCACCAACACGAC	62.338	TTCAACTCCGCTCATCaAACCTC	63.022	156
HM_4133	contig15701	GA	2	16	ACTCCAATTGtGCCAACTACTC	63.456	TGTTTGTAGTCTTCTCaGCTcTCTc	62.853	127
HM_4134	contig37902	GA	2	16	ACTCCGTCCTGAAGTGTCTAGTG	63.128	aTaACCAAAATaCCTCTCCCTCT	63.14	151
HM_4135	contig40885	TC	2	12	ACTCTCAATTtTGTAAACGTGGC	62.646	ACCAGAAGTGTGATTGTTGTGCT	63.25	102
HM_4136	contig08176	AG	2	12	ACTCTTGGCAACATGATCAAAAT	63.026	TCATACTGAAGAAGCCCACTCTCC	63.115	112
HM_4137	contig10542	GA	2	12	ACTCGATGGCGACAGTGAAGAAA	63.561	ATCTACACACTTGCAATTGACCGA	62.962	86
HM_4138	contig27509	CT	2	12	ACTCTTCTCCCTCACCACTCTCT	63.183	TTCGAGTTGGTTTCTGTTCAAGTG	62.809	144
HM_4139	contig16241	AG	2	20	ACTGAAATTCGATTTCtCGTTGC	62.841	TCATTTCaGTCCTTaACCTCA	63.035	115
HM_4140	contig45543	GT	2	12	ACTGAGCAGGCCATTACTCTGTCT	62.837	CAcCCACATAGTTTCTGATCTTG	61.953	115
HM_4141	contig51310	TC	2	14	aCTGATCgTAGGTTTtGaCAAGCc	62.838	tTgagaggaggagagaaactaaa	63.554	127
HM_4142	contig35531	AT	2	16	ACTGCTGTAAATCCGTTGACACAA	62.869	GAATAGGTTTCAGCTCACAGAAGGA	62.214	138
HM_4143	contig03382	GA	2	24	ACTGGAGTGTGGCATTGTAGTGA	63.067	tctCtTCTCTcTtCCTcGaaAc	63.581	116
HM_4144	contig01083	AG	2	12	ACTGGATCTAGCAAGAAGGGGTG	63.014	aCTCAcGAcTACCAGTAgCATCAGCG	62.174	99
HM_4145	contig24940	TA	2	12	aCTGGCACTGTGCACATTTTAAG	63.065	CAAcCAACaACTCaCtTTTAGCATC	62.466	125
HM_4146	contig35259	TC	2	20	ACTGTGATCGTCTGTtGcttCATC	62.846	ACGCCATTGAACCTTTGAGAGTAGC	63.06	112
HM_4147	contig25266	AG	2	16	ACTTCACCCAGTAAACCCCAAGA	63.12	CTAGTCCCTCTCTTCTCTCTGCT	62.886	144
HM_4148	contig43326	GT	2	20	ACTTCATCATCCaAAGAACCAACA	62.922	AtTTGATCTGTGTGAGATTGCTGT	62.979	157
HM_4149	contig29348	TA	2	12	ACTTCgCAaATCCCAATTCaAAGC	62.655	TCACTCTCAATCTGGCATCTCaAc	62.926	160
HM_4150	contig04647	CT	2	12	ACTTGAGGtCtTCTCTCGCtAT	63.109	TcCAcAcTtGACATCACTCTCTC	62.909	155
HM_4151	contig24888	TC	2	12	ACTTGAAATCTTATTGACCCCC	62.585	TTGAGGGTGAGTAAGAGACAAGGG	62.993	149
HM_4152	contig25652	GT	2	14	ACTTGGGGTTTATGTGCTGTTGT	62.946	GCTTaAAATTTCTTCTGGGGAACA	62.82	119
HM_4153	contig00083	TC	2	24	ACTTGGGTCTCTCAGTCAATTTCG	63.01	tTATCTTAAAGTGCAGAcCCGCaG	62.823	109
HM_4154	contig19951	GA	2	16	ACTTGTTTGATCTTCcTCAAGTGC	63.027	CTCTCGGTACAAAGGGTTCTTCT	63.482	85
HM_4155	contig37238	TC	2	14	ACTTGTTTAGCAGACCTTTTTCG	62.058	TGAGTAACATAATTCAATGCGGTTAGG	61.843	135
HM_4156	contig36036	TA	2	12	ACTTTAACACGCGCATACAGAAAT	62.972	ATCTGACCCTCTCAATCTCTCT	62.954	108
HM_4157	contig38191	AG	2	12	ACTTTCTTCTACCACCACCAATTG	62.597	AGAGAGTGAGAAGAAGCAACCCA	62.909	158
HM_4158	contig30450	CT	2	16	AGAAAAATGATTGGTGGGTACGA	62.813	TCTGACCCTTTcGtATCATCAIT	63	135
HM_4159	contig22156	AG	2	14	AGAAAAATGGCAAcGGACAACCTTT	64.096	TAAGTCTCTTCTTCTAGATCCGGC	64.206	87
HM_4160	contig09818	GT	2	20	AGAAACACTGCAGAGGTCTCTTGG	63.347	TTcTTAATTGGGTGgGGAACCT	62.977	153
HM_4161	contig34507	TA	2	12	aGAAAGCTTCCGTGTTCTGGAGAC	63.506	CATCCAGCTCTCAATGTGTTTTCA	62.514	141
HM_4162	contig29244	AG	2	14	AgAAAGGgGTGGAGAAGAGAGAAA	62.958	AGTAAGAGAGTAGGCGGAAGGTGG	63.304	113
HM_4163	contig17173	GT	2	16	AGAAAGAAACGaCTCACATTATATGCAC	62.068	CAATAAACCATTAACGAGAAACGCC	62.746	116
HM_4164	contig05184	CT	2	12	AGAAAGATGACGATGATGATGCTGA	63.267	ATAGTTGAGAAATTTGGAGCGAAG	62.947	130
HM_4165	contig24128	CT	2	14	AGAAAGCAACATACATCTCTCCG	62.923	AATTTTAGGGTTTgGAGGgtGTGT	62.992	120
HM_4166	contig41808	AG	2	20	AGAAAGTGGAGACCTTCTCGACCA	62.882	cttccacgttcttccaaCTAc	63.026	88
HM_4167	contig26006	GT	2	16	AGAAATAAGAGAGCTTCAGAGGGCA	62.1	ACTACTCTTAcCacTAACaCaACCAAC	61.224	146
HM_4168	contig29228	CA	2	12	aGAATGAAaCAAAATCAATCCcTg	62.481	CACCAAGATCAATACTGGACCG	62.801	92
HM_4169	contig43217	CT	2	20	AGAAATGCATGATATGCAACACTGT	63.288	CACCTCTTCTTCCCTCtTctTCC	62.958	138
HM_4170	contig03900	TA	2	14	AGAAATGGAAGTTGGGAAACCAAT	63.078	caactttactgttccgccaTCAAT	63.444	93
HM_4171	contig42790	GC	2	14	AGAAATTCGgTACCAAGGAAGCAG	62.933	CTGAAGAAGCCAAAGCTGAAGAAG	63.028	156
HM_4172	contig06574	GA	2	12	AGACAGTGAGGTGGAGCTTGAGAT	62.913	ACCTCTGCTAACTACATCATCGGC	62.953	103
HM_4173	contig38199	TC	2	24	aGaCATCGcAAaAGGGTTcAATA	63.03	CTGAGCAGAATAAGAGGTGcCAI	63.035	157
HM_4174	contig40972	TC	2	16	AGACATTGTGTGAGGTTGATTGGT	63.771	GcTCCCGCTACCAITAAITTTGT	63.503	80
HM_4175	contig20530	CT	2	14	AGACCAAGGCTTTGATATGAGTG	62.811	GAAAAGCTTGCTGTAAAACCCAGA	62.944	123
HM_4176	contig21505	TG	2	24	AGACCACTTTTACAAGATGGCCCTT	63.404	TTTGAAAGAGAAACAgGGCAAGaAC	63.019	82
HM_4177	contig00608	CT	2	20	AGACGAGAGATGAGACGCCATACT	62.826	gTCGCGCTTACAGAAAGGAGAAAG	62.835	81
HM_4178	contig49742	AG	2	20	AGACTCAAAAGTCAGCAAAAGGAGA	62.909	CATTCTGACCAACCAACCcAGTA	63.325	134
HM_4179	contig34540	GA	2	20	AGACTCGCTTCTTGCATTGATT	62.851	TCAGTACAGAAAcCTCTTTCATCGC	63.046	156
HM_4180	contig51877	GA	2	12	AGACTGAGaAGAGGGTCTGCTGC	63.69	aCTTCTgtCTTcCaCCTcCC	63.083	129

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4181	contig02099	GA	2	14	AGACTGTGTAGGGTCCGATCTTTC	62.061	CCTAACCCAAACATCTCATCT	62.584	113
HM_4182	contig02547	CT	2	12	AgACTgTlCtACaAAaTCCAATACC	60.065	AATCAATTgAgAGCAAAATGGAAAC	60.968	143
HM_4183	contig14859	TC	2	16	AGACTTGTAACTGCTTGGATGCC	62.949	ATTCACTACCTCCAAACACAACTCAA	62.712	120
HM_4184	contig34926	AG	2	12	AGACTTTCTGGCAACTCcGACATA	63.45	AAGcTCTGCTCTGaAATCCCTCT	63.205	142
HM_4185	contig03311	GA	2	16	AGAGAAATCAACGAGGAGAAACGA	62.811	GTCTtCtTcTgTCCACACATCG	63.376	87
HM_4186	contig04656	TC	2	12	AGAGAAGCCAAGAGAAAGAAAGCC	62.806	AAGTGAATGATGGGACGGAACCTTA	63.009	142
HM_4187	contig31919	GA	2	12	AGAGAAATGTACTTGAATCGCCAC	62.129	TCTGCTcttcATCTGATCTTAC	63.013	124
HM_4188	contig04307	TA	2	14	AGAGACAACCGTTACCAATCTACCA	62.23	AAGAGAGTTACCATCATGCCCAAG	62.811	147
HM_4189	contig14023	TC	2	16	AGAGACACGCTCTTTTGAATTTG	62.834	TGCTCTCTGCTcCGCATTTTATG	63.456	115
HM_4190	contig32077	TC	2	24	aGAgACACgaggCAAGAAACg	63.159	TGGCTTATCACtGAGAGCTCTGA	62.487	121
HM_4191	contig51254	AG	2	12	AGAGAGAATTAGCTGCTGCCTGAG	62.739	AAAACtTTCAGgAACTcACcaAC	62.723	128
HM_4192	contig49164	TG	2	12	AGAGAGCAGAGAATTTGGATTGCA	61.613	tTGGATCCTCATgATCATCTCTATG	61.508	123
HM_4193	contig36718	GA	2	12	AGAGAGGGGgAGAGAAATGGAAATTG	63.372	ATCTCaCaAAcCCTaACCATTCGA	62.897	129
HM_4194	contig35390	AG	2	14	AGaGAGTGCTGAGATCGAGAGAGG	62.899	CTAGAcACAgCCCAATTAACGTCC	63.142	88
HM_4195	contig08417	AG	2	12	AGAGATCTCTCAACTTCGCCATT	63.596	TGAAGTGAAGTGAAGTGAACCCAG	62.81	123
HM_4196	contig14502	TC	2	14	AGAGATGAGAGAAATGGCGAGAGA	63.004	AACAAGAAgACGAAGAAAAACCCC	62.992	132
HM_4197	contig32807	AG	2	14	AGAGATTTGGGTGTTGGAAATTGAA	62.996	GAAAACAAGCTCCGAAGAACTCTGA	63.121	131
HM_4198	contig40073	AG	2	24	AGAGCACTCAAGTACCAAAaTGC	62.949	TGAGGTTCAAGAAATGGGAAGTATT	62.298	153
HM_4199	contig36007	TC	2	14	AGAGCAGCCCATGAATGAATGTG	63.142	GgTATGAGAGAAGACCGCTAAAA	63.055	96
HM_4200	contig16903	TG	2	14	AGAGGCAAGAGTGGAATCGAGAAG	62.575	GCTGGTTGCCCATCTACGATTCT	63.15	159
HM_4201	contig09686	AG	2	20	AGaGGCAGAGTGATGAAAAACCaG	63.124	AAAGGAGAGCCCTaTAAGTTCAATCA	62.741	144
HM_4202	contig28884	GA	2	24	agaggccgaGAGAGTGTGTG	60.608	CGCTCTTCTTGACCAATATCTTTG	61.302	152
HM_4203	contig15329	AC	2	14	AGAGGGGAAGCTCTTCAACTGTGA	62.677	CACCTGTAGAAACAAGGCAATCT	63.044	135
HM_4204	contig17205	TC	2	14	AGAGGTGGCTCAACCCCTCTTAAT	62.899	TTTCACTGGGCTGGTGTGTTT	63.138	87
HM_4205	contig21460	AG	2	12	agAgtGAGAGAGGTGTGAaTGGTGG	63.106	AAACCATTTTggaGAAGGAAGAGG	62.968	101
HM_4206	contig44568	GA	2	14	AGAGTGAGTGGAAATCGAAGGATTG	63	cCCCTTcACCAATCTAItTCTT	62.677	100
HM_4207	contig34225	TG	2	12	AGAGTTCAGAGCTCAAGTGCCAT	62.939	GACACTCCTCAACTTCACACCTCA	62.921	160
HM_4208	contig25070	GA	2	12	AGATACaAgGAGGAAGTTGCAAAAGA	62.739	CTGTGGaTgaGTTgAGTAgGGGG	63.083	159
HM_4209	contig01119	TC	2	14	AGATCGTAATTGTTGCTTTGTCCC	62.634	CACATTaAATACACACATTTCGCTG	62.605	119
HM_4210	contig45697	TA	2	12	AGATCTTTTCGgCaTtGGTTCAATA	63.021	GCTTCATTCTCTGCACCAATAaA	62.44	134
HM_4211	contig02152	GA	2	16	AGATGTTGAAATCACCAGTGGCT	63.242	GTTATCGGTTCTCTCTGCTCTG	62.598	160
HM_4212	contig44334	AG	2	20	AGATTAGCGCAGAAACaAGGAAG	63.086	TAGCGaACTCCAGCTAGACCAATTC	63.146	145
HM_4213	contig03335	CA	2	12	AGATTCCATTCCAGAAACAGCAC	62.813	CGCAACAGGCCATAAAATAGTTC	62.957	121
HM_4214	contig39552	AG	2	20	AGATTCTTCCCATTTGCAATTCA	63.009	acTaATgaATCCCACTCTCTCTCC	62.964	88
HM_4215	contig44214	AG	2	32	AGCAAAaTtAAaGgAACCAAGTTG	61.77	ACAItTcTGTgTAGCAcATTgACa	60.96	133
HM_4216	contig46090	GA	2	12	AGCAAAAGTAACCTCTCGCTGAA	62.835	TTCTCAACAGAGCGAAATTCATCA	63.257	155
HM_4217	contig03294	TC	2	16	AGCAACAGACCAAGTGAAGCTCGT	63.764	GCCCAITTTTAgCAAAAGTGAACA	63.543	157
HM_4218	contig35725	TG	2	24	AGCAATGCGCAATACAGAAGAAT	63.273	CCCACCTCACTCACTCCAATATT	62.793	89
HM_4219	contig36482	GA	2	14	AGCAATTTTGACAGGATCTTAGTTG	62.839	GACTCTCCCTCAACACCATCAAC	63.649	152
HM_4220	contig26284	TC	2	16	AGCACTCGATGACGACGAACATTA	62.532	CCCTGAAGATTTTTGAATTTCTGTG	63.002	147
HM_4221	contig26900	GA	2	16	AGCACTTTTACCCTATTTGACGA	63.239	CCTACCTCTCTCTCAcCAAAc	62.575	117
HM_4222	contig49848	AG	2	24	AGCAGCACAGCTTAAAGAAACAAGT	62.875	ATCAACaTTGCAATCTCTGCTCTG	61.964	142
HM_4223	contig47294	TC	2	12	AGCAGCTCAACAGTCTCTTATCG	63.362	ACCTCATGAAACGGATCCAAAAG	63.516	151
HM_4224	contig43040	AC	2	12	AGCATAAAAaCaCgACGAAGAACC	62.755	TTGAGATTATTTTGAAGAATCTCATGG	61.951	106
HM_4225	contig37966	AG	2	24	AGCCATGAATGATTCTTAAGCCAA	63.13	GaAACTCACTCTCTcCTCGTGTG	62.899	91
HM_4226	contig13000	CA	2	20	AGCCCTGAAGAGATCATcTGAACAC	63.017	CTGACTTGAATTAAGCTGTTTCTCT	62.23	150
HM_4227	contig27238	TG	2	48	AGCCTCCACTCGCAAGCAAAATAG	63.044	TGACTTCACTCTaCCTCCTcCaT	62.56	145
HM_4228	contig44228	GA	2	24	AGCGAGGTTTGAGATACCAATCag	63.035	AgGCTCTTATCTTTaCacCaGCGa	62.536	117
HM_4229	contig04799	AT	2	14	AGCTACTGgTtAAaAaGccAaTATACA	60.876	AcGATCCAAATAGCACACATTCTAT	61.799	110
HM_4230	contig30810	CT	2	14	agCTcAGGCTTAGGCTTAAcGATT	62.948	CATGCTCTCAGTTTTGGAACCTCAA	62.828	137
HM_4231	contig06779	AG	2	16	AGCTCTGTCTCTCCCTTGATGA	62.898	AcACCAAGaATACgATTCctctacc	63.494	147
HM_4232	contig08832	TC	2	14	AGCTGCTAACCTTGGTGGCTTTG	62.958	CGTCTATCTTCCCTCTCTTCTCT	63.074	90
HM_4233	contig09423	TC	2	30	AGCTGGTTTTCTTCCCTGGACTAC	63.201	GGCAGTGGAGCAAACTCTaTGAAG	63.45	128
HM_4234	contig50223	TC	2	14	agCTGTTGAATACTTTGGGAAGaa	62.508	ACTCTGTTTcCacCTGAAGTGTCT	62.719	157
HM_4235	contig12950	TA	2	12	AGCTTCAAGATCTGCAAAAGCTCAT	62.953	AaCtCTCTCATCTTCCGATCGTT	63.709	159
HM_4236	contig27484	GA	2	24	AGCTTCCGCTTCAATCTTTCTCT	63.406	TACCCTcCTccCTGtACTTTCTc	62.683	139
HM_4237	contig38833	CT	2	16	agGAAaCTGCaACTGCAAGAGAG	63.357	GAAAGAAAGATTGgAGGTTGGCT	63.09	118
HM_4238	contig08694	TC	2	14	AGGAAATCTCTCAATCGCTCGTCA	62.397	ggggtcataATACAAGTCGaAcCG	62.826	155
HM_4239	contig32450	GA	2	14	AGGAAAGGGGCTCTCAATAAGAC	62.972	AGCCCTTATTTCTCACTCTCCCTC	62.48	130
HM_4240	contig02037	CT	2	20	AGGAAAGTGAAGGAGACGATGATG	63	CTCtGGaGaGAAaAgGCAGAGTT	63.598	150
HM_4241	contig27803	GT	2	20	AGGAAAGAAATGCTTGATCTGCA	63.438	TTTGTACCCTCGGCAAGAAcTAC	62.741	97
HM_4242	contig11972	AG	2	20	AGGAATAGCATCTCCCTGTCACCT	63.505	ACATTTGAGCCCTCTCTTTGTT	63.499	118
HM_4243	contig26513	AT	2	14	AGGACAAACAGAAATGGACTCCG	62.698	AGcCTTACGAAgGGTCAACCaAc	62.823	159
HM_4244	contig24986	AG	2	16	AGGACGAAGGCACATATGACATA	61.905	CCCAACaaCAAACTATCTATGGGC	62.826	158
HM_4245	contig31016	AG	2	12	aGGAGGAGAGAAAGAGAgAACCa	62.958	gtacggaggaaacccaagtagctt	62.924	121
HM_4246	contig06764	CT	2	14	AGGATAATCACCTGGTCCGCTAAT	63.2	TCGGAGACTCATATTTACACGCCAA	62.959	155
HM_4247	contig24328	GA	2	14	AGGATAGAAAGGCAAGTGCCTGA	62.824	TATCATCCACCTAGGcCTGTGAT	63.013	151
HM_4248	contig21414	AG	2	12	AGGATAGAGATGAGCGAGATCTCT	62.98	TCACtTGTCACTcctcATCACACT	63.155	136
HM_4249	contig24466	AG	2	14	AGGATGCTCAGCAGAAATGAAGC	63.139	TCTTaCaAAATCTTATCgTgTCG	62.758	105
HM_4250	contig11492	TG	2	12	AGGCACGCTGAATGGTATAGTA	62.937	CAGAAGTACCAGCCTATTTCTCA	62.724	158
HM_4251	contig04396	CT	2	20	AGGCATAGAGCCTTAACTTCGAG	63.219	CTAAGAAAGACGAAGTGGGAGGTG	63.132	160
HM_4252	contig38266	TC	2	14	AGGCCGTGGTATGATCACATCT	62.94	TTAGTTCGTTTTGTAGGCaAGGC	62.874	153
HM_4253	contig12640	TC	2	16	AGGgAAGCAGATGAGAAGGAATT	62.782	GaATAGAGGGGACCTTTGGAGAGA	63.156	150
HM_4254	contig25681	TC	2	12	AGGGACAAGAAAGTGTGATGAC	63.027	CTTAATTGAGAGAAATCCAGTGGC	62.451	160
HM_4255	contig07114	GT	2	12	AGGGCTCCGAAAAATATGAGTTG	63.676	CAGAACATTAAAGGcAGTTTGGa	63.63	158
HM_4256	contig10567	TC	2	16	AGGGCTGGATGTAAcCTATTCCGG	63.584	aaCaAGAGAAAGcCTATGATTGGG	62.911	147
HM_4257	contig37860	AT	2	12	AGGGCTCTCTTCTCATGATCTTA	62.62	CtaAAACCTTGTCTcCTTcCC	62.49	157
HM_4258	contig12510	TC	2	16	AGGGGAAGTGAGGGTTAGGGTACT	63.547	TGTCTcCTTTCTATCTTGCTTGAC	63.249	154
HM_4259	contig13640	TA	2	12	AGGGGACCACTATCAAGATCAaTa	62.887	CcATGGAGGCTCtCAGATAAGGTA	62.67	150
HM_4260	contig43456	TC	2	24	aGGGgCTAGCGTTACATATTTT	63.221	TCACAGAAATCCAAGCTTGAACCA	62.132	107
HM_4261	contig19577	TC	2	12	AGGGGGCATAGTGTCTTCGACT	63.437	atttccTCCaaaccTAgACTGC	63.995	130
HM_4262	contig30830	TC	2	20	AGGGGgCGGATtAGAAATGTATAG	62.618	TGCTCTGTGATTATTTCTCCGC	61.787	147
HM_4263	contig19863	GA	2	16	AGGGTTGAGAGGTCTGAATTAGGG	63.068	CTATcCAGaAAATAGCTCCGCC	63.107	92
HM_4264	contig01294	CT	2	16	AGGTCTATCCAGCACTTCTTAGGC	62.929	GAgGATAcCAAGCGCACGTGAT	62.087	144
HM_4265	contig26206	TC	2	12	AGGTGGAGGTGAGGAGAGTAAC	63.186	TTTCTGTGAAGTGAATGACACAG	63.219	112
HM_4266	contig29704	GA	2	12	AGGTGGGATGGTTTAAAGATTGGA	62.974	CAGAgGtGtTTTCTCTCACTTCAGTC	62.733	128
HM_4267	contig45820	CT	2	12	AGGTTTCTGTACTCGAGGAATCCA	62.483	AAAGAcCaAACCCCTAAATTCACCA	62.013	155
HM_4268	contig07676	AT	2	16	AGTAACCGTCTCTCATCTCCACAG	62.909	TCCGCCATTCTCACTATTCTCTCT	63.013	159
HM_4269	contig46373	TC	2	14	AGTAAGCGTAgCGGTTCTCTCTCT	63.533	GAgGATAcCAAGCGCACGTGAT	63.223	140
HM_4270	contig07796	CT	2	14	AGTAGCAATCTTTCGGAATTTGTC	62.854	TTCTGTCTCTCAATCGTCTTCT	62.698	160
HM_4271	contig37063	GA	2	24	AGTCCACCATGTCTTCTTCAATCC	62.784	ACTGAGAgGAAGCGAGAGAGTGAG	62.91	123
HM_4272	contig47063	CT	2	24	AGTCCGTAAGTGAAGGACATCGAG	63.035	tTAGTGGTCTTgTtTAGGgAGGG	63.664	143
HM_4273	contig33982	GA	2	12	AGTCTAGTTGTGTGGCGGAA	63.146	AAACGGTCTCCATTcCACAATTT	63.888	134
HM_4274	contig21368	AG	2	12	AGTCCAGGATTCGATGATAGTGGT	62.382	ACCTTcATcCACTCACTGTACCC	61.557	96
HM_4275	contig21912	AG	2	12	AGTCTCCACAGAAATCATGACGAG	63	TCCAAATATATAGCCCTCTCAC	63.271	96

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4276	contig45441	GA	2	12	AGTGAAGAGTGATCGGATTGGGTT	64.345	aCACTCTCCTCCACTACCCACCTC	63.93	160
HM_4277	contig31453	CA	2	12	AGTGACGgCATcATTCTCTACTG	61.878	CCGCTTCGgTTTTACATATGTGTT	62.451	142
HM_4278	contig48451	GA	2	14	AGTGAGCCaAGTAGTGGTGGT	63.372	CTGCTCTGCTCTGCTAAAACCaAG	63.873	80
HM_4279	contig37472	TC	2	20	AGTGATCCATTTCCTCAAAATCC	63.365	TATATCTCTCTCCAACCAAGCaAg	62.703	132
HM_4280	contig05248	AG	2	20	AGTGGTAGCCTGGAAGGGAaTAG	62.992	TCTCgGTTCCACACITGaAATACA	62.931	86
HM_4281	contig09864	AT	2	16	AGTGTaGCAACATGcTCTCATGC	62.889	GaAGTGTGTTTGCTTCTCAGCa	62.869	143
HM_4282	contig31780	GT	2	16	AGTGTTCCAAAGCCCaATTGA	61.765	TTTGAATCAaCAAGGATGGTGCA	62.629	105
HM_4283	contig13716	TC	2	20	AGTGTGTTTATGATGGTGAaTTGcTG	62.426	CACCaAAACAAATACACCGAGAAA	62.227	91
HM_4284	contig22931	GA	2	24	aGTgAaGTcGaGAGAGGgAaAaa	61.757	ATCATCCCAACTGCTCTTTG	62.701	99
HM_4285	contig06284	CT	2	12	AGTTGGTAGTTCAGATGCTTCG	62.933	CAACAGCTCCTGATTCCAAATCTT	62.91	114
HM_4286	contig10587	GA	2	20	AGTTTCATCAAGTCCATCTCTCGG	63	TgTCTGTAcCacTTAgTTgTgCA	62.423	150
HM_4287	contig23278	AT	2	12	AGTTTCaATGCAAAATAAATTCATAG	61.008	GCCTTCGATGTAGTGATGAAATTTG	62.007	152
HM_4288	contig00136	AG	2	20	AGTTTGAGAGGTGAGGAGAAGGGT	62.974	AGGTGTGTGAGTGAGACTACCGAG	62.961	145
HM_4289	contig04245	TC	2	14	AGTTTGATTcAGAGTGGTGGTGG	62.598	CAGTGTGAAGATCGGAAGTGGTGT	62.72	129
HM_4290	contig30854	CT	2	16	ATAAAAGTCAACACTCCGCTCCG	62.822	TCaCACAGAGGTGGGAGaAGTAA	62.261	92
HM_4291	contig02679	CT	2	12	ATAAACCTCAAAcTaCGTcGCC	62.654	CCATGACCTAAGTGTGGTGTGCA	63.259	131
HM_4292	contig02916	CA	2	12	ATAAGCACATCATGCAAAACATTGG	63.076	ACTTTATGGTTGGCCTGTGATAC	62.536	149
HM_4293	contig02433	TC	2	12	ATAAGCTCTCCCAATCTCACAAT	63.188	GGAGGAGTCAACCGATAGTTTACCA	63.696	151
HM_4294	contig37352	AT	2	16	aTAATACAAAGCCGTAGACCAC	61.572	TTTCGTCAATGTGATAGTTCAAT	60.757	121
HM_4295	contig11686	AT	2	14	ATAATCGCTGCCATTTCCTGAT	63.05	TCCTATCTTCACTGcCGCATC	62.137	154
HM_4296	contig46272	TC	2	24	ATACATgTcGAaATCCTTCGCCA	63	AAAACTTagTGGCACAACCAAA	62.941	157
HM_4297	contig17272	TG	2	12	ATACATTGACGGGTCTGCATTTT	62.841	GGCCACAACCTCATCAATCTCTTT	62.813	137
HM_4298	contig04126	AG	2	20	AtaCCATtACaCTGTGaCaGAGG	63.225	ATCTCGAAAGAACAGAGACAGCC	63.358	158
HM_4299	contig35165	AG	2	12	ATACCCATCAACGAtcaagaacta	62.925	TGATTcCACCATGaaAaCCTAAT	62.897	100
HM_4300	contig45737	AG	2	32	ATACGAGGCAATAGAACAGCTCCa	63.353	AAGaATCTTACGTGcGAGAGGACA	62.712	137
HM_4301	contig26356	GA	2	16	ATACGGGGCTTATCTTATCGACG	63.492	TATTTCCCAATCTCCTGACC	63.36	150
HM_4302	contig10960	TG	2	24	ATAGAAGCAGTCGCATTTTTTCAG	62.947	CTTACTAACCCaACCAaCtAcG	62.046	156
HM_4303	contig12122	GA	2	12	ATAGACATTcGATGaCCCGTAGGA	63.013	CTGCTCTCCTCTGGAAACAATC	63.525	153
HM_4304	contig19996	AG	2	14	ATAGAAGAGGGAATTTGGAAGTCGG	62.971	cACAcTcAGAGTCTcgaaAAG	62.596	105
HM_4305	contig25768	AG	2	14	ATAGGTCTGGAGCTCTCCACAAA	63.225	GTCACAGCAAAACCTaCTaGACCG	62.563	156
HM_4306	contig26778	TA	2	12	ATATCTCGGATTGCTTTCGATTCA	63.121	AAACCTACCTCACCCTACCAAT	63.058	104
HM_4307	contig05362	TG	2	16	ATATCTGCAACTGCTGACTCTCC	62.94	CCCTCTTGITTTTTCTACTTGGC	63.404	160
HM_4308	contig27289	AC	2	12	ATATGAACGATTCTCGACCCATGT	62.802	GAGCCGaAGaACagagGAAGTAC	61.901	122
HM_4309	contig22711	GA	2	16	ATATGACTGGTAAGATGGGGCCG	63.608	AGGAGAAAAGGaCaAAACAgTCC	63.08	151
HM_4310	contig49019	TC	2	20	ATATGGCTCTCATCTTGGCTCTG	63.026	TCTCTTTcACATaAAAGaAGGAA	62.526	136
HM_4311	contig01715	TG	2	14	ATATGGGcAGTGATTTCCTCATTA	62.616	TAGGCCTATAGCCCAcCaAgAAGT	63.4	115
HM_4312	contig48134	GA	2	14	ATACaAGCCGTcATTtCTCTCT	62.613	ACCCTAGATAGAAGATCGATgGGG	62.865	91
HM_4313	contig04304	CT	2	12	ATCAaCCACaTaCATAGCCCTCc	62.411	AGAGAAAGAGCTATGTCCTGCC	62.265	106
HM_4314	contig28002	AG	2	14	ATCAaTAGAACTTCCAGTGGGTGG	62.584	AAAAGaACGcCTGAGTTCCTAAC	63.11	124
HM_4315	contig43136	AG	2	16	ATACAAAAATTCAGATGCTTTGCG	62.529	TTTTAGTTTTcACATGGGATGCG	63.113	160
HM_4316	contig44683	AC	2	12	ATACCAAGTTcACCAACCAACCC	63.338	CGTGGTAAATGATgGTgATgATG	62.938	145
HM_4317	contig29908	TG	2	14	aTcCaCaTTCCaATcCaCctG	63.125	CATCATTTTCTCTGATCCGCTCTC	63.54	150
HM_4318	contig28278	AG	2	20	ATCAGAAGTGGGCTATGATTTTG	63.438	CTCCCTGCCATTTTGTTCaA	63.329	160
HM_4319	contig44190	TC	2	20	ATCAGAGATCAAGGGCTGAGTTG	63.115	GAITTCtGATCTcAggGAGGG	63.378	156
HM_4320	contig33618	GA	2	20	ATCATCTTGTAGCGCTTTCATCAT	63.029	CACACTCATTTTcTcATGCTTTG	63.048	137
HM_4321	contig21364	AG	2	14	ATCACTtATTTtACCaAGCCCC	63.498	CGGAGGAACCAAAACATCTCTCT	63.747	119
HM_4322	contig33795	GA	2	30	ATCATTTCAAGGATGGGgAAGg	63.36	GCAGACTCCATTTCGGGTATATCA	63.432	105
HM_4323	contig43523	CT	2	16	AtcATTgATGATCCCTCCGActA	62.99	TCTCTCAAGCTGTCTGTGAATCG	63.159	155
HM_4324	contig25989	CT	2	16	ATCCAAATAGTAaCCTTCGGGTGG	63.378	AACaAAAAATTCAAAACCAAGCAC	63.252	105
HM_4325	contig15630	GA	2	16	ATCCAATACCTGATTCTACTGCG	62.731	TcTcAGAACTCCAGCTCTgATaACAT	62.004	159
HM_4326	contig33496	CT	2	16	ATCCCAACATTCCTTCAAAACAGC	62.824	gGGTTCgTTGAGTCTGATGTTGG	63.233	122
HM_4327	contig39775	GA	2	20	ATCCATAGATGAAGTGGCAGAGGa	63.103	TaGAGTGAGaAAGTTGGGAGGGTG	62.993	147
HM_4328	contig09002	TG	2	14	ATCCATTAGCCAGAGACTCCAATG	62.8	AGCTGCTGGAGATTTTAgGGITTT	62.728	158
HM_4329	contig01740	CT	2	16	ATCCCATTTTAGCTTTCAAAACC	63.282	GTGCTTATCAGCCATTAGCCCTC	63.158	113
HM_4330	contig22528	AC	2	14	ATCCtCAGAATTGTAATGGATG	62.368	ACATCCCTCTGcTGTGTGATGT	62.077	139
HM_4331	contig18693	CA	2	14	ATCCGAATTCCTCATATACACC	63.275	TaTgCCaAttTTTaTgTCTCGT	62.842	105
HM_4332	contig28185	TG	2	20	ATCGAAACTGGTTTAGCCATGAaA	63.03	GGGACCAgGAGGAATTCAAAATAC	63.069	117
HM_4333	contig22589	AG	2	16	ATCGAAGCAAAATTCATCACAC	62.518	GTGATGGACACAGGATTTGAGTTG	62.922	150
HM_4334	contig26330	AG	2	20	ATCGAAGCGAACTGTCACAAAATC	63.039	CACCTCGAGTTaAATCAaATTCTG	63.241	94
HM_4335	contig03048	GA	2	14	ATCGAAGgAGaCAGAAcAAAGTG	63.124	CTATCTGCTCACCACTcCTCC	63.331	137
HM_4336	contig49707	TG	2	16	aTCGATGGGATCTAGGCTGGTTaT	63.192	CATGGTACGATCTCCATTACTCT	62.9	132
HM_4337	contig07265	GA	2	12	ATCGATTTTCGGGGAGAAaAT	62.977	AcTTCGATATCTGCTTCTCATC	63.042	89
HM_4338	contig16014	AG	2	16	ATCGCCAGTTTGAAGACAAGAGAT	62.626	CtAcCGCTCcaCTCTACtACTCT	63.209	142
HM_4339	contig25177	TG	2	16	ATCGGAAAGGTGGTCAAACTCAG	62.798	ACAATCACTGGATTTTCTGCACT	63.242	145
HM_4340	contig22633	AG	2	16	ATCGGAAATGGGAGGAGATTAGAT	62.369	aAGaGaACCCCAaAACGacTAAG	62.989	159
HM_4341	contig22176	TC	2	16	ATCGGCTCTCCTCTCTGCTCTCT	63.096	AAGGCTCTCaCATAGCTGATGGTGT	62.857	114
HM_4342	contig28217	CT	2	20	ATGATATATGTGAGGACTCACCTC	62.715	cGaACGAcACAGAGATtACTGTAGGA	62.956	141
HM_4343	contig26975	TC	2	12	ATGCTCTCTCCcTTACTCCGAAGA	63.799	CTGACTGGAGGAGATTGACCGT	62.88	143
HM_4344	contig14783	AG	2	20	ATGCTCTTGTGCTGATTCTGAAGC	63.039	TGTaCaCaAAACCGAcCcaTA	63.581	85
HM_4345	contig05855	GA	2	16	aTcTACaGGaAGCTGATTTCcG	63.888	ATGCGGCTTTTTAAGGAATGATGA	63.021	149
HM_4346	contig13896	CT	2	40	ATCTCATGCGATATTGTCCCAAAC	63.339	aACGAACGAACgaagAacGaAg	62.828	144
HM_4347	contig40150	TA	2	14	ATCTCCATTGTcATGcAaGTGGTT	63.12	GCAAAcACaCaAATATACACACGC	62.656	149
HM_4348	contig35937	CT	2	12	ATtCTCTTTCTCCCTCTCTGgTgT	62.964	GAGAGACGATGAgCGATGagACG	63.796	149
HM_4349	contig42433	TC	2	12	ATCTCGACGACGACGAAGTAGAGA	62.912	AGAGACGaACTGGAGaAGTCAAGG	62.471	155
HM_4350	contig05020	TC	2	12	ATCTGAAAGATGAAGATCTGGTcC	60.008	CTGTTCACTCTCTATTGCTCTCTCAA	60.667	157
HM_4351	contig03134	AG	2	16	ATCTGACGCTTCACTCTCTGTAT	60.681	CCCCAcTtAACTTAcCTTCTACT	60.494	159
HM_4352	contig25964	AT	2	14	ATCTGTTTGGAGTCAGGTGAGAGA	63.43	CCCCAAATCGCTATTTAAGTGTG	62.837	152
HM_4353	contig12411	AG	2	16	ATCTTCCAATCACCGTGACAAAT	62.913	AGaGTTgGGAGTATAcCCCTGGAG	62.971	149
HM_4354	contig00362	AG	2	14	ATCTTCTAGTGGAAAGCGCTATTG	62.923	CTAcTCTCTCTCCCTCTcCC	62.692	88
HM_4355	contig35771	GA	2	14	ATGAAAAACAACtGATCGCCTAC	62.634	GGTTCACTAACTCCCTCTCTGT	63.186	148
HM_4356	contig22534	AG	2	14	ATGAAAAAGAAGGAGACCTTTTGC	63.09	TCACTTTTcAGCTTcACagATCC	62.937	155
HM_4357	contig32590	CT	2	12	aTGAACATCCAAATTCGCGGTT	62.937	TTGATTTGGAGAAATTAGGGAGCC	62.72	88
HM_4358	contig44298	TC	2	24	ATGAACCTGTCACTTCACCCGAAT	63.12	TtCTTCTCTTGTGATTCATGT	63.108	113
HM_4359	contig18294	TC	2	20	ATGAGATTAAAGCTCCTGAGTCCG	64.11	AGTGGAGGAgGGAggtgcttAGGT	64.93	153
HM_4360	contig16515	AC	2	12	ATGATCGcTCAAAaGAGACTTCAT	62.6	TTTCTGATTGtCTCTCTGtCaAA	61.692	100
HM_4361	contig01136	TA	2	20	aTGATCGTTAAATACCCACcAcCa	63.426	TTGATTCTgATtGTCTCTTCAAG	63.644	157
HM_4362	contig46861	TC	2	14	ATGATGAGTCGTCTCGTCAAAAG	63.876	GTGGTGGGTTTACGAATTTGTTGT	63.142	154
HM_4363	contig23339	GA	2	12	ATGATGCTAAACGTGGCTTGAAC	63.268	AGTAGGCCcAGGAAAAGATTTTG	63.094	158
HM_4364	contig15255	TA	2	16	aTGCACAGAATCAGCAAGAGAAGA	62.623	CATGGATGATATAaCATGATTCcAA	61.991	160
HM_4365	contig41791	CT	2	12	ATGCACATAAAACCAAGAACCCCA	62.826	CTCATAGAGGGCCAGTGAGATGTT	63.014	84
HM_4366	contig48315	CT	2	14	ATGCCAAACCTCAAAATTTGGTCC	64.187	CACCAACCAcCTcATAATCAATC	63.632	154
HM_4367	contig25974	AT	2	14	ATGCCATAGCCGAACACTTAAAT	63.027	AATCTGGTTgAAGAAATCCTGTTG	62.798	148
HM_4368	contig39687	AT	2	12	aTGCCTCATCAAGAACCTCCATTA	63.112	GTGCTGCTGTGTTTTGGAAGAAT	63.781	159
HM_4369	contig39674	AC	2	16	aTgGAACaCaCAAGGTACAAT	62.712	AGAAGAGGCAGAAcAGAGCGATA	62.936	146
HM_4370	contig04880	GA	2	20	ATGGATGACGaAAATGaGGAAaA	63.099	ttgtccatgaacattgtctta	62.931	130

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4371	contig41474	TG	2	16	ATGGCAAAAATTCTTGAACGTCA	62.937	tTGCCCTGTGGGAATaTTATGGT	62.628	108
HM_4372	contig45149	AG	2	14	ATGGCAATTCAAAGTCTTGTTGAT	63.026	CgGGCTTTCAGITTCaAaATCT	63.001	141
HM_4373	contig18997	AG	2	16	ATGGCCATCAATCTGACCTAAAG	62.607	AAATTTTCTCtCTtTcttGCTTCG	61.823	119
HM_4374	contig12872	AT	2	20	ATGGGTCGACGACATTTTAAAC	63.236	ATCGTTTGTCTGGATCAACATTGC	63.565	141
HM_4375	contig33191	AG	2	16	ATGGTAAGAAAGAGGCAACACACA	63.129	CACCGAcGtCaAcCTCtaCTCTT	63.033	151
HM_4376	contig04317	AG	2	14	ATGGTAAGGCTCGTAACCTCTCTC	63.008	TCaCTGTAGCTCTCTccTGCTCCT	63.132	154
HM_4377	contig19360	GA	2	12	ATGGTCTCTGTAATGTGAGGGCCA	63.022	TTTGAcATgGGTCTCGTACTCTCA	63.146	106
HM_4378	contig01915	AT	2	14	ATGGTCTGCTCAAGTGTCTCAAGA	62.532	AAAAAGGAGCTACAGCGTGC	62.95	134
HM_4379	contig35906	TA	2	12	ATGGTCTGCGGATCTCAAGTAT	62.312	ATTCAATCAGCTTcCCCAATCA	62.902	129
HM_4380	contig22366	AG	2	14	ATGTAATATTCCGAATTGGCCCT	62.814	CCGTACATGTCAATTGAATTTGG	62.311	101
HM_4381	contig34610	GA	2	12	ATGTACACCAAGAGTGGGTCTGT	63.132	gaattcttgaTCTTCgTCCCTc	63.584	142
HM_4382	contig00474	CT	2	16	ATGTAGCCGGAGAAAGCCATT	63.223	CACGCACATCCATACACAACACTA	63	114
HM_4383	contig01028	TC	2	20	ATGTGCAAGTACACCTGGGATT	63.002	GCTCAGTGTGTGTGtCGACITTT	62.689	112
HM_4384	contig34177	AT	2	12	ATGTGATTGATGATCAAAACGAG	62.609	TagGtATTGAATTGaAgCCTcCA	63.005	155
HM_4385	contig16341	CT	2	20	ATGTGACTGATCAATCCCTCATCA	62.9	TGTAAGCGCTGCAATACAGaAAA	63.099	103
HM_4386	contig19741	TG	2	14	ATGTGCTTTCAAGGTAGAGAAA	62.411	TAATCCCTACCAATGTCCCAAC	63.108	160
HM_4387	contig38775	AC	2	16	ATGTCTCCACTTCAGGATCTCTCG	63	gGTcCaCCTTAGATTGTCCACTA	62.584	156
HM_4388	contig46977	GA	2	14	ATGTGTCTCTGAATTTCTCCGAC	62.7	ACCTCTACTACTTCGCTCAGCCT	63.13	160
HM_4389	contig18511	AG	2	20	ATGTTTGTGGTTTACCGTCAATTG	64.064	aGTgGAGGAGGCGGgaGAT	64.832	106
HM_4390	contig23001	GA	2	12	ATTAAGAAATCCAAATGCAAGCAGC	62.582	CCATCCCATCATATAATCTCTT	62.354	160
HM_4391	contig34315	CT	2	12	ATTAAGGAACCAATCCCACCTGT	62.983	AAAGTTGGAGGAATTGCTAGAGG	63.086	136
HM_4392	contig49666	AT	2	16	ATTAAGtGTAGTcATGtCCaGAG	60.216	AAATaTAGGCTGTATtGCTGCCa	61.13	114
HM_4393	contig35189	AG	2	16	ATtaCAAAACACCTCGCTCAATA	62.935	CACATAAAATaCCCCaAcGTc	62.716	156
HM_4394	contig40850	AG	2	14	ATTAACAACCTGGAATCGCTGAAT	63.039	CCTCaAATATACACTcCACCCA	63.194	96
HM_4395	contig45200	TC	2	14	ATtACAGCGGATGATGAGCTGAAG	63.876	CCTCGGATCGTCACTGTGTGT	64.807	122
HM_4396	contig26111	AC	2	14	ATTAACATTGACGCAAGACCAAT	62.95	GAAATGTGAATTGTtGGGGTAA	63.005	144
HM_4397	contig29899	AC	2	32	ATtAcCtTCGACGCGcACAc	63.431	ATTACCCGTCTGAGATCAATACCC	62.586	122
HM_4398	contig07305	TG	2	12	ATTAGGGTTTCTGGGGAGGTTAT	61.361	TCTGTATCCTGTCAATTTCTTAAT	60.946	143
HM_4399	contig02237	GA	2	12	ATTATACAGAAAGAGGCCCCa	63.084	CCGCTTTAAAAAGTCAGCTTGT	62.662	147
HM_4400	contig30062	CT	2	16	ATtATTCCTCTTCTTTGTGCTG	62.797	GgGTAAACCGGTAGCAGTATAGCC	63.198	92
HM_4401	contig40265	TC	2	20	ATTATtGGGtTCTCTGCTTTCCG	63.796	TCaCAACCCATCTAcCaTAcCCTC	63.318	112
HM_4402	contig07513	TG	2	16	ATTCGATTCTGACGTGCTGATG	63.368	CTCACATAACCTTCCAGAACACC	63.111	118
HM_4403	contig27852	TC	2	16	ATTCCTCtTTCAGTCTCTCaATC	63.062	TGCTGCCACAGATTATTAGGGTT	63.043	149
HM_4404	contig46658	TC	2	12	ATTCCTTTTATGAGGACCAATGAA	63.175	ACCTGAGAAACAAACAATGACCA	62.958	111
HM_4405	contig42504	TC	2	16	ATTCGAATTCCTCGGGCAT	62.994	GGGGGTTCACACAGATCTaAg	63.063	144
HM_4406	contig16647	AG	2	12	ATTCGGAAGTAGGGAGAGAAATCG	63.078	CCCAATTTTCAACAATGAGTTC	62.8	127
HM_4407	contig36675	AG	2	16	ATTCGTCTTGCTCTGTACGGTAA	63.251	GAGTcCCCTAcCcccaAAAA	63.367	88
HM_4408	contig08217	AC	2	16	ATTCGTCTTCGCGAGTCAAAATC	62.841	CCATTGACTAGcAAtTTGGTTGa	62.326	131
HM_4409	contig25842	AG	2	20	ATTCCTGCCGGAACCTGTGA	64.017	aCCAACCTCTCAATCTCTCTCGAGC	64.349	80
HM_4410	contig02192	TC	2	20	attctctgccccaaacatcagag	62.91	GGGTaAgGATCAGCAGACTGAGAA	63.115	119
HM_4411	contig20182	GA	2	16	ATTCCTCTCTCAAAATCGCAGCA	63.45	CGATCTCTGCAACAATGGGATT	63.438	157
HM_4412	contig28923	AG	2	16	ATTCCTTTGCTCATtGATgACCC	62.608	TAGGGGTTTGTGATTGGAGATG	63.091	117
HM_4413	contig30286	TA	2	12	ATTCCTTTCTCTCGCCATAAC	62.903	ACCAAGCTACCCTCAcTcCTCTC	63.099	146
HM_4414	contig00540	TC	2	14	ATTGACAGAAAGCTATTGCCTACC	62.94	GGGTAgTCCCTAAAGGGCCTAAG	63.432	99
HM_4415	contig43118	AC	2	14	ATTGATACCTCCAAATTCACCGAA	62.802	gGTCaTAAATCTCTGTTTACTGGG	62.011	131
HM_4416	contig13510	GA	2	12	ATTGATTGAGGAGCTTTAGGAGG	63.078	AAACcctaACAGATCCTtCaAAC	62.78	129
HM_4417	contig09729	AG	2	12	ATTGCCGATGAGAGGTAAAGCAAA	63.231	AGCCTACCCACCACTACCaAAAA	63.017	97
HM_4418	contig08206	AC	2	12	ATTGCTTTGaCaAAGGCGGATaG	63.15	ATcCCCGGTAATGTTAGTCAAAAT	62.797	115
HM_4419	contig12326	TA	2	12	aTTGGGATGTGATTGTTTTCACA	62.5	GCCAACATTGGAGGATTATTGG	62.616	118
HM_4420	contig12744	GA	2	14	ATTGGTgTGTTTTAGAGGAGGAGG	62.933	AAAGGCGACACCAATTCACCTACC	62.536	152
HM_4421	contig39247	GA	2	16	ATTGTCACAGCTGgTGTGTAATG	62.965	TCAAAATGATGtGTTTGGAAATGC	63.05	117
HM_4422	contig23218	TC	2	14	ATTGTGACGTCCCAAGTTCACCTC	64.112	CgGTAGTCTcCACGAATCaATCTC	63.331	116
HM_4423	contig29961	GA	2	12	ATTTAAGACACCCATGAGCTGAG	62.811	TTTTCAAAATCCAGTAGAGCGAG	62.606	113
HM_4424	contig16132	AT	2	12	ATTATCATCAGGACATCCGCGAG	63.432	CCTaATGGACTTATAGGCAACAGGT	62.727	98
HM_4425	contig29029	AG	2	12	ATTTCAAATCGGAAGTGGAGTGAG	62.798	GCTATTGCTcTCCCTATTGCTTa	63.046	148
HM_4426	contig42040	GT	2	16	ATTTGCAAGCCAACTCTTATGGC	63.801	GTCTTGTTCACCTGAAGCTGTGA	63.067	157
HM_4427	contig04330	TA	2	12	ATTTGATTCGAGCAACTTTTGTG	63.055	AAACTCAITGAGCTAGAGACTCCC	62.213	159
HM_4428	contig32126	TG	2	14	ATTCGggTTTGGTCTGAAATC	63.192	CCTATTGTTTATCTGAACTGCTGC	63.078	124
HM_4429	contig03114	TC	2	12	ATTCGTCTCCAATTCATTTCA	62.899	CATGCAAAAGCGACAGATGAAC	63.076	134
HM_4430	contig36585	CA	2	12	ATTCCTTGCATCATAAGCATGcG	63.562	TTTGAttttGATCTGTCAgCAGcC	62.958	87
HM_4431	contig06767	TC	2	14	ATTTGAGCTATgCCTTTCCTCT	62.717	GAAGaAGTGGATGTCCCAAGAGA	62.987	138
HM_4432	contig05910	TA	2	14	ATTTGtCCATGATCTGTAATGA	61.989	CAACACCCCAATTGGTTCTACTG	61.191	125
HM_4433	contig26521	AG	2	24	ATTTGTCTCTCACAACATAAACCC	60.37	GTTTCACCTCTGTACTAGtCaACCA	60.025	152
HM_4434	contig23026	GA	2	12	ATTTTTGGCGaAaGATTGAACAa	63.134	CATTCTCCCATCATATCCCTACA	63.186	133
HM_4435	contig01831	TC	2	20	CAAAAACACCAATGTCTACCCAT	63.117	ATAGAAGCAAGCACAAgaGCTG	62.251	137
HM_4436	contig06306	AT	2	12	CAAAAATACAAAAACCCCAAGT	62.234	ggCAGTCAAGccCATAATAATTT	62.451	160
HM_4437	contig20349	AT	2	12	CAAAAATTCAAAATCAATTTGGC	62.634	acacggttgatttccatgttttc	63.231	159
HM_4438	contig18171	TC	2	20	CAAAAATTTGGgAaGAGAGGCTT	62.989	TTTGTAGAAAGGCCAAATTTCCA	63.109	112
HM_4439	contig43065	TC	2	14	CAAAACGtATCTCGCCATTAAATT	62.463	GtgGGGAGACGAGTAgTGTGTT	62.821	155
HM_4440	contig05874	AT	2	12	CAAAACACCTGTGcTTCCTAcAa	63.499	TgtCGTTCTGTGCTCTCTCATG	62.842	121
HM_4441	contig19798	AG	2	12	CAAAcATTATcTACGAGACCCG	63.104	GGTTCGTAGAAACAAAGTGAATGG	62.968	151
HM_4442	contig25569	GA	2	20	CAAACTCATGATTACAGTtGgC	62.856	AGTGGATGATGGCTGATATTGGAT	62.906	122
HM_4443	contig47740	GA	2	16	CAAAACCTCGAAAGTGAAGATTG	63.1	TAGTTCGTGACAGACCTCaAAAC	63.155	134
HM_4444	contig33738	CA	2	12	CAAAcGGGCTCTTAATGGATGTT	62.451	GATTTTGACAAACTTTACCTCTGC	63.055	145
HM_4445	contig44305	GA	2	20	CAAACTCGaTACATAAaGATTCCAA	60.772	CCTTCTCATGTCTCTGACCTTCC	61.637	143
HM_4446	contig25130	TC	2	16	CAAACTGAGACGACGGCTATTGAAC	64.309	aACACCCGATTATCAGGACG	63.339	147
HM_4447	contig19287	AT	2	12	CAAAAGCAGATAACCCaATCA	62.514	ACCTATGCCATCACAACCAAG	63.336	158
HM_4448	contig10870	TC	2	12	CAAAAGCAGACTCGTGAAGCTCT	62.412	GCGATGGAGGTAAAGTGAGAGTA	62.923	146
HM_4449	contig10640	AG	2	16	CAAAAGTCAACAATGTAACACCCG	62.845	CCGaACAACTATtccCTGTTTTG	62.916	141
HM_4450	contig30451	AG	2	12	CAAAAGTATCTGAACCAACCAAC	62.933	ATTCAACTTACCCGGCAATATCT	63.007	148
HM_4451	contig43585	GT	2	14	CAAAATTTTAGGAAGaCaATCTCATC	62.384	TGTATTTTTGTCTTTTTGTGGc	63.322	154
HM_4452	contig25092	CA	2	16	CAAACTATCACAGGGTTTACGGC	62.935	CGAAGTTGATGAGGAAGAGAGAA	62.993	97
HM_4453	contig06531	AG	2	12	CAAACTCGAACTCACTGGTAgCGA	62.842	CCAATCATATCAGCAACCTGCTC	63.069	82
HM_4454	contig48415	GT	2	16	CAAAATGGGCTCTGTAAGAGAGAA	63.006	ACTCTCTCACCATTTtaccCTCC	62.964	106
HM_4455	contig14451	AG	2	12	CAAAATGTCTCGGCTATTGATTACT	63.438	TCTCTCTGTCAgTGAATTGCTGTG	62.949	154
HM_4456	contig00667	GA	2	16	CAAAATTAAGGGAAGGCCACTCT	62.897	TCCGATaAAGAAATAGAAACCCAGA	62.359	82
HM_4457	contig02533	GA	2	12	CAACAAACGGGTACAGATAGAGTT	63.554	GCTCTCATCTCAATGTTCTCTCTC	62.904	139
HM_4458	contig41505	GA	2	20	CAACAAATGTATAGGGACCGT	63.227	cCTCtCTGCATGcCaACATAACT	64.001	143
HM_4459	contig43955	TA	2	16	CAACAACTGAAATGCAACATAGC	62.861	GCCAAGAGTGAAGTCAACATGTCA	63.735	153
HM_4460	contig21426	GA	2	14	CAACACCTCTCATGAAATTAAGC	62.922	gTGACtCTTCTGTTTCAACCACT	63.15	135
HM_4461	contig41127	AG	2	14	CAACCAaAaCCCACTTTAAACAAC	63.427	AaCCATCAcCTTCTTAACgGTTT	63.098	151
HM_4462	contig13522	AT	2	12	CAACAGGGTTTCTCTTATCTCC	61.476	GAAACCAaTACCACATAcTAcATTGA	60.603	148
HM_4463	contig24215	AT	2	16	CAACCGCAACAATTGAACAACAGC	62.754	AGCTCCTCTTCTATACACGACG	63.166	130
HM_4464	contig42859	GA	2	12	CAACCTTGTCTTGTAGCATTATG	62.965	CCCAAAAGCAGATTGTGCATAGT	63.552	107
HM_4465	contig39023	TA	2	12	CAACgTtAGcGTGTTGATGtc	62.492	CCTGAATAGGTTTATCCCAAGC	63.092	129

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4466	contig16470	AG	2	12	CAACgTTGATGTGAAGAAAGATG	62.931	GAGAGAGTTCATCAATgGCgGTAG	63.444	117
HM_4467	contig11235	TC	2	12	caacTaaTCCCCCTcCTCTCAT	62.863	TGATTTGTTTGAAGTGTGGGTAGa	63.038	155
HM_4468	contig01808	AG	2	12	CAACTGTCCAGAGAGACGCTGA	63.063	CATCTGGAAATTAATCTTTTCCACCG	62.896	156
HM_4469	contig43355	CT	2	20	CAACTTAATGTCTCTGGCACT	63.053	aCTTTATTCACITTTGcGGaGG	62.715	149
HM_4470	contig38255	CT	2	24	CAACTGGCCAGGTAAACATTGTC	63.859	ACCTCTGCATCTCTGCAACACAG	63.06	144
HM_4471	contig01810	CT	2	20	CAACTTTGTAAAGTGGAGAGATCAA	61.948	CgAAGGaaAAGTTGGaaAAGATGTGT	62.809	134
HM_4472	contig16987	TG	2	12	cAAGAAATGGTTCCTTTGTTTc	62.109	TCTCgCTcTcTCTCTATCAAA	62.897	159
HM_4473	contig09949	TG	2	16	CAAGCAAGCTCATCTTTTGTGTA	62.856	AAATCATTCTGTTTGGCTTCTCTTG	62.826	149
HM_4474	contig04619	TC	2	16	CAAGCgAgATTTTGACAAGGATA	63.625	gGGaCgGATtGATtTgGTACtTT	63.383	123
HM_4475	contig16457	GA	2	12	CAAGCTCAAAATCTGTGTTTGGAA	62.628	AcCCAATCTTATGGGTCTTGTatGA	62.887	140
HM_4476	contig08326	GA	2	16	CAAGTCATCTAGACCATAGTGTCCG	62.341	AGGCTTTGCAATTTGATGCTTCTAC	62.963	136
HM_4477	contig45959	TC	2	12	caagtgcaccaagtctacACCTAGC	63.468	TTGtTGGaAgGTGTGTAGGAAAGAAA	63.123	123
HM_4478	contig33201	GA	2	12	CAATCAACCAATTCATCAACAAAC	62.486	TCTTCTTCTTCTCCGCTCTGTATC	63.022	153
HM_4479	contig06980	GA	2	14	CAATCCCAATTTCTGACTGGTTTC	62.996	CTCCaCTCAGCAGTCAAGTACaCac	62.505	96
HM_4480	contig48861	TA	2	14	CAATCGACTGATGAGAGAACCAAA	62.698	GAGTCGCaACCAATTTCTATtCC	62.928	121
HM_4481	contig17298	CT	2	14	CAATCTTCACTTGCCTCTCTCAA	63.006	TTCCATTGGTGATGAGATTCaAGA	62.896	152
HM_4482	contig10219	GA	2	12	CAATGTGTTTAAAAACCCtcGTATG	60.828	TCTCTCTTATATTCCaAGCACTCA	60.597	154
HM_4483	contig02022	GT	2	12	CAATTAACATATAAACCCACaCcaaa	62.859	CTCTAAGGCGCTGACAGAATTTGA	62.823	130
HM_4484	contig50498	GA	2	12	CAATTGGATTACCCACACCTTAA	63.002	TTATCCCAATGAACCTCAAAACAA	62.703	154
HM_4485	contig008581	GA	2	16	CAATTGTCTTTATGGAAGGGAAg	62.906	TGCAAGACAGCACTGGTAGTGAAT	63.304	128
HM_4486	contig50536	CT	2	14	CACAAATTTCTCATGAACCTCC	62.996	GGACGACAATGTTTTGCTGATATG	62.746	118
HM_4487	contig27641	GA	2	14	CACAAGCTCAATCAATAGGCGTTA	62.566	AGTCAAGCATACATCaAGAcGTgc	62.771	89
HM_4488	contig48034	GA	2	24	CACAATTTGATTCTTAGGTTTGG	62.798	GCAACTAGCAACTAGCTAACGCaA	62.137	158
HM_4489	contig01460	TC	2	12	CACACCTCaCATTGGCTCAaC	63.906	AGACTGAGAGGaAGAAAGTGCAGa	63.236	124
HM_4490	contig26693	AC	2	20	CACACCTCTACGATCTTTTGCCT	62.933	CTGTAGGGTGTGTCTGATGATTGC	63.04	145
HM_4491	contig35333	CT	2	16	CACACTGAACCTGCTGGATGTTAG	63.168	GCCAAACCATGAAATCAAGCTATC	63.037	124
HM_4492	contig44925	AG	2	12	CACAGAAGCTATACAAAGgTGCC	63.067	GGGAAACCCCTTAAAAACAAACAC	62.093	143
HM_4493	contig03843	TC	2	12	CACAGTTCATAATTTCTCTGTCTCTG	61.008	AGGCGAGAGGTCCAGAAATC	60.735	99
HM_4494	contig31082	TC	2	12	CACATCGTCTTTATCGAGATTCC	63.112	TGGAAAGACCAAAACACACAAGT	62.969	114
HM_4495	contig05646	GA	2	12	CACATTGAATCAGCTTTCACCAAG	63.048	TCTAAAGGGTGTCTTCTCTTCCA	62.795	147
HM_4496	contig43580	GA	2	14	CACCAAGGTGTGTAGTCAGATGC	63.067	ATCCATCAACACCACTACCAAGT	62.901	132
HM_4497	contig03183	CT	2	16	CCAATTTTATCACAGCAAGGTG	62.742	CTGAGTGAGAGATTGAgGAGAGG	62.049	112
HM_4498	contig49099	TC	2	12	CACCACAAATACAGGAATCAACa	63.034	GGAGcGAAAAcAgAGAAcCaATa	62.826	121
HM_4499	contig34645	AT	2	16	CACCACATAAGACCAAGAGAGCTG	62.454	TCGCCaAAATTTAAACaaTCaCa	62.561	142
HM_4500	contig09181	TC	2	12	CACCATACTCTCAACCTCtccca	63.413	GGTCCCACTCAaAGGGTAACAC	63.997	127
HM_4501	contig36453	AC	2	12	CACCATGAGGTGTGAGCTGATTAC	63.057	CACACTCAGATATGTACACACGCT	62.56	154
HM_4502	contig33027	AG	2	12	CACCATACCATGTATCTCCCAT	63.099	ATATCAGTTCACACTGGCTTCC	62.713	151
HM_4503	contig03962	AG	2	12	CACCATCAATAAAAATTGGGAA	62.896	GCTCAATTGAATTTGATCTTcGTTT	62.848	131
HM_4504	contig39142	AC	2	20	CACCGTTCTCTTGTaTCTCATGTT	63.444	GcCAGgGTAAAGATATTGTaAtgGAGT	62.755	160
HM_4505	contig21205	TC	2	20	CaCCGTGTGCTAGAACCCACaCAGC	64.434	aCaGaAAGcAcCACCACGc	63.545	80
HM_4506	contig11479	TC	2	16	CACCTAACGGAGGCTGCTAGTATG	63.354	TcCAGAGGACATATAGTGAAGGAGAA	62.831	139
HM_4507	contig36032	TC	2	20	CACCTAAATGAGTGAACAAACGCG	62.978	TTCTGGTATGTGGGTTTGATATGG	63.016	109
HM_4508	contig46213	GA	2	24	CACCTGAAACTGTGCTGTGAAGA	62.969	TTTGATCAACCAAAAGTACCACAA	62.649	122
HM_4509	contig34568	CT	2	16	CACCTCTCTGATGCCATCTCTCT	63.332	CCCCTTAAcCTCTcCatTtCcIA	62.768	154
HM_4510	contig46382	TC	2	16	CAGGAGACGACATTTTCTCTCTCT	63.438	gATGCGCTTCTCTCTCTGCTCT	63.312	90
HM_4511	contig30350	AC	2	40	CACGTACATGCCATGAATAGAAA	63.059	GGGTGACCAAGAGCTCaAGAGT	63.226	149
HM_4512	contig10975	CT	2	14	CAGCTCTATTGGTCTTTTCTCATG	62.872	CAAGATCCTcCAACACTCATGC	63.139	151
HM_4513	contig46306	CT	2	20	CACCTCGCTACTATTCGCAATTC	62.96	agccctgaaccaactctcttatt	62.698	116
HM_4514	contig15686	TA	2	16	CACGAAAAATGTCTCATCTCGG	63.026	AGGCGAAATATTACAGCGATCAAC	62.668	154
HM_4515	contig01797	CT	2	14	CACGAACTCTCTCTCTCTCTCAC	62.677	AACTAGATGAGCTAACGGAAACC	63.008	153
HM_4516	contig25960	TC	2	14	cactgaatgaacccccggtt	62.056	TCCTTCGAAGCAGaTAATTAAGGG	61.941	94
HM_4517	contig34024	TC	2	16	CACCTGAGAGGCAATCTCTGTAAG	62.842	TCTCTGTtaAAGAGaCAGgTtTGTG	62.134	148
HM_4518	contig39384	AG	2	14	CACGTGTTGTAAGAACAGcAGcAG	63.177	tTCCATcCACCAGAgTgTACCAATA	62.698	156
HM_4519	contig10830	AG	2	20	CACCTTGCCCAATTTCAAAATCTTA	63.311	CTCTCTCTCTCTCTCTCTcTcTgT	62.846	97
HM_4520	contig42958	AC	2	14	CACCTTGGCTTAAGGTGCTTTGC	63.354	GTTTGTGGCTCTCTCATCGTTT	62.936	129
HM_4521	contig32111	AT	2	12	CACCTTGGTAAAGTCTGATGCTGA	62.756	ATCTccCtGAGTACGaAgagCCT	62.999	88
HM_4522	contig10828	TA	2	12	CAGAAACCCCTAACAACTCAACAAAG	62.169	CAGTAGTTTTCGCGAGAATTCAAAG	62.369	147
HM_4523	contig41394	GT	2	14	CAGAACCCCTTTTCTATTACAGA	62.591	GAATTTAGCATGAGAAGGAGGTGG	62.397	117
HM_4524	contig35654	AG	2	12	CAGAACTAGTGCAAGCACTACcAA	62.867	GTTGGATCTCTCGGAAGTCTTCT	63.181	146
HM_4525	contig18910	AT	2	12	CAGaGATTGGCCCTTTTATCTA	62.8	TcCGTATGGTGTATATGGGATTTT	62.533	120
HM_4526	contig35638	AC	2	12	CAGAGCCTAGTTTGGCTCAACTTA	63.138	TAAcTTCCCCAAATCTGTTCGTG	63.019	134
HM_4527	contig39099	TG	2	12	CAGAGGCCAAGTATGCTAAGGCA	63.051	AATGTgGTcCAAGACTGACAAcCAC	62.49	95
HM_4528	contig24498	AC	2	12	CAGAGGCCAATCTTCGTTATTGTA	63.529	CAAAATTCAGCTTTTGTCTGTC	63.24	128
HM_4529	contig43868	AT	2	16	CAGAGGCCCTCATCACTTAATCT	62.983	GGTATCTCTTGTaAAAcCCTCgTGA	62.83	125
HM_4530	contig27789	TC	2	14	CAGAGGTTTCTTCCCTACCcAAGT	63.076	GTTTgGAGACTGGAGAGTAGATTGA	63.201	106
HM_4531	contig37208	CT	2	16	CAGAGTGTTCGCAATATTGCA	63.323	ATTCATCTCTTCTATcCGTCTG	62.802	111
HM_4532	contig43787	GA	2	16	CAGAGTTGAGTGAGTCATTGTTGGA	62.825	TCACAAACACACTCTCCACCTCC	62.705	95
HM_4533	contig18728	AT	2	14	CAGATATTGGTGGTGGTGGTAAT	63.009	GAATACCAAAACCTCGAAACCTCC	63.078	141
HM_4534	contig12120	AT	2	12	CAGATCAAAACCAACcATCAGAC	62.922	gCCGCGGTTGTCTCTTAGATATT	62.842	158
HM_4535	contig37919	TG	2	24	CAGATGAATGTGgtCTTTTATGTTt	62.588	AGAGAAAGGGGCTCAGTCACCTT	63.198	149
HM_4536	contig04561	AG	2	14	CAGCCATGACTGATGACGAATGA	63.486	AgTtTgGGAACcCCgTAcCCTa	63.865	134
HM_4537	contig50048	TC	2	32	CAGCCCCATACATGAGAAGACTA	63.636	acgtaacgaacgaacgtaacgaga	64.086	159
HM_4538	contig29637	CA	2	12	cAGCCTCTCCCATTAaAgAAACATT	62.911	TGGACCGCTGTgTCACTAGCAGTA	63.278	160
HM_4539	contig08030	GA	2	14	CAGCCTTCAGAGCTCTTATTGTGA	63.04	AGTCCCTCGTTaAAACCCCAAAAC	62.714	143
HM_4540	contig04195	AG	2	14	CAGCTGAGCTTTAGGCTGTGT	63.173	aattccatgaattgttccggtg	63.009	157
HM_4541	contig32715	TC	2	32	CAGCTGATATATGTCGGACAATGG	62.733	CCGCGATTCAATTTGATTATCACT	63.332	145
HM_4542	contig20940	TC	2	12	CAGgAGGAAGACAGACTCCTCAA	63.309	GTGATGCCCTGAATTCATTCTCT	62.802	158
HM_4543	contig00977	TC	2	12	CAGGCTCAAGGCCATCTTATTAT	63.683	GGCTCGGTTACACATCTTTGACT	62.838	157
HM_4544	contig43289	CA	2	20	CAGGGCAGAAAATTTCAAAACAA	61.451	GCTACTCTTATTTTCTcTCCATtTct	61.037	151
HM_4545	contig46157	TC	2	16	CAGTACAGAGGTGGGCCAGTA	63.582	CCTCTTCAACATACATAcGTCG	62.842	154
HM_4546	contig15209	TA	2	14	CAGTACTAGTTGGGCTCTGTATGA	61.16	CATCTTTTTCaAAGCACAATATA	60.407	155
HM_4547	contig37172	TC	2	12	CAGTCCGAGCCCTCCTCTAAT	62.857	ACACAAATcCTCAATTTCAATCACCT	62.188	147
HM_4548	contig02559	AG	2	14	CAGTCTATAACGGCATCACTGGAG	62.206	CgAGACTACTCGTAgcCCTCtct	61.704	148
HM_4549	contig06062	TC	2	12	CAGTGCTATTAATTCATTCAAACCCc	62.935	GTCAGTgGTCTGTCTGTCTTCT	63.593	136
HM_4550	contig14554	AG	2	12	CAGTGTGCATTGAAgTGCATTGAA	63.227	CTGTTCTCGGAACATCGGAATTC	63.318	154
HM_4551	contig12537	TC	2	20	CAGTGTGACATCTGAGACAGCTT	63.06	AGCagGAACCGCTTGTCTTCTATT	63.515	125
HM_4552	contig45830	CA	2	14	CAGTTACAGCATCTCTCAATTTCTG	62.191	CAGTGCCTCATATACACCAAAATATA	61.434	154
HM_4553	contig07318	TA	2	16	CAGTTGGATGGAAcCTTAAACCaG	63.003	AcCaCCTTCTCTTTTGGTCATT	63.285	140
HM_4554	contig03537	TA	2	12	CATACCCCAATCCATCTTCCCAA	62.983	gTGACAGCTaGACATcCaAgATA	63.751	146
HM_4555	contig23747	TA	2	12	CATACCTTCCGACCTCTCTGTCa	62.898	CTCTCGATGACCACTTTAGGGA	62.894	160
HM_4556	contig08634	GT	2	12	CATAGTCTCAACGACcCTCCAC	63.225	CGAATGGGATGAAACCAAAAGAT	63.317	119
HM_4557	contig05899	AG	2	20	cATATCGCTCAaCTCCCAACAA	63.379	CACACACGaaAACGCaCTT	63.305	81
HM_4558	contig36693	CT	2	12	CATATTCAAGCTGCAACTCTCTCT	63.035	TTCTGTGATGGACTGTGGGTG	63.055	124
HM_4559	contig38651	GA	2	12	CATCACTCCGATCTGCTTCAA	63.687	AAAACTGGATCAACAGGTCCAA	63.006	148
HM_4560	contig04309	GA	2	14	CATCATGCTGTGATGTTGTACG	62.836	aAACATTGGAGaAAGATGGATCA	62.987	88

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4561	contig01645	CT	2	16	CATCAtcTTCCtGGAaTAaGgaGc	62.383	AATTCAGaTgAgGCAAAaAaCC	61.634	91
HM_4562	contig22723	AC	2	16	CATCCAAcAAATTTTGAACCCCTC	62.8	AATTGAATGGGTTTTACCAATTG	63.005	124
HM_4563	contig25785	AG	2	14	CATCGAATGCTTAGGGTTGgaTTC	63.021	GTAGTCGGAGATCGCTAGACCG	62.488	119
HM_4564	contig33154	AT	2	12	CATCGCTAGTTCGGGAAGGATTTA	60.799	AGGATCaATTgGATCACTCAATCT	60.21	91
HM_4565	contig32637	CT	2	14	CATCTTCATATCTCCGTCACATC	62.674	TTAcTATAGTGGTCGACGCTTTC	61.785	110
HM_4566	contig14149	GT	2	14	cATGAACCCATTGTTGGTcATT	62.934	TGGATTTCCTGCTTTTGTAGTTCAT	63.231	154
HM_4567	contig51398	CA	2	16	catgacttGTTCAAaTaaccacgc	63.761	GTCAAATTTGCTCaTGGATTgGaT	63.327	133
HM_4568	contig32763	CA	2	12	CATGATTGCTCTGTTTGGTTTCTG	63.048	ACGAAGCAGTCTCTGAAGGCAAC	62.75	82
HM_4569	contig06191	TG	2	14	CATGTCGGGgAaTACTCCATTAaA	63.101	GATGGAGcCCTTACATGHTTCG	62.91	159
HM_4570	contig05119	TC	2	16	CATGTTGCGAGCAaTAaCAAGTTC	62.985	AAAgAaGGGgAgGGAaAGAAAG	63.222	146
HM_4571	contig06181	CT	2	14	CATTACTGTCGATCTCCGAAAAA	63.517	TCCACAACCTCTCCCTCaAGAAAC	62.997	159
HM_4572	contig10820	TC	2	16	CATTCCCTCACCCTTCTTCACTCC	62.455	GgaTTgCAAAcACAACACAGAA	63.278	124
HM_4573	contig30763	TC	2	16	CATTCTAGCAAGAAGCAGATcCcA	63.02	cgTgtcaaataccgaatccGAT	63.456	109
HM_4574	contig37976	CT	2	12	CATTCTGTCTGCCCTCTCTTTGT	63.124	ATACCACATAGGACATCCACCCT	63.084	133
HM_4575	contig32006	CT	2	12	CATTGATGTCTACGACTTGGTG	63.181	CGTGCAATgTcAGACTCCATGA	63.303	142
HM_4576	contig15532	GA	2	16	CATTGCAGTTCATCTGGTATGCTT	62.543	TGTGGTGAGGGTgTAGTCAAACTC	62.598	132
HM_4577	contig37218	TA	2	16	CATTGTCAACCGCATATGTGTTTA	63.804	CTTCCCTTCATACACAGAGTCT	63.023	91
HM_4578	contig23323	AT	2	16	CATTTCACCTTAGGAATGCTCTTCT	60.517	TGTGTTGTTACATaaAGTGTGTTCTTG	60.621	148
HM_4579	contig44169	CT	2	14	CATTTCATCATATCGCTCAGCTTG	63.063	GGAACgACGAACacCaaAA	63.131	141
HM_4580	contig40868	TC	2	20	CATTGTAAATGGCTGAaAGAGGG	63.014	GTTGAGTGCCTTCGCTGTTTC	63.411	128
HM_4581	contig29009	CT	2	24	CATTTTAAGGAcGCCATTTTGTa	63.126	ttGGAGTTGGATCTGTAAGAGATGA	62.411	151
HM_4582	contig39547	GA	2	20	CCAAACCAACAACAAATACACCA	62.829	GTGcCAATGTAGCTCTAAGTAGGA	62.07	154
HM_4583	contig39568	CT	2	80	CCAAATGATTGCGCAACAAAGAAAG	62.93	TTTAGAAATCAAGCGAATTGGGA	63.013	159
HM_4584	contig16408	AC	2	14	CCAAATGTCAAGTCCGCAATTTGA	63.068	CCAAGTGTCAAGTCAAAATACAGCTT	62.789	98
HM_4585	contig27161	TA	2	16	CCAAACAAACaAaTGTCCCACTT	63.214	gTGAAGATGATGGATgAACAcTcGt	62.614	157
HM_4586	contig03219	AG	2	12	CCAAACACAGAAAAACCTTaTG	62.808	TAGTCACTTCATCGGCATTCaAA	63.163	160
HM_4587	contig45029	AT	2	16	CCAACACCTGTTTACACATCAAA	63.159	AAGGCTAGGATGAGCTTTTGGAC	63.208	103
HM_4588	contig39569	AG	2	12	CCAAGTCTCTGCTACAAAGAAaAGC	62.955	gAGTtGTTTcgggtTTTcaACAATC	63.022	123
HM_4589	contig05561	AT	2	16	CCAATAAGAAAGTCTGACATTTAAAC	61.767	TGAATTTTGCCAATTTCCCTTTA	62.725	142
HM_4590	contig42853	TA	2	12	CcAATCCCACTGTATGTGAATGA	62.705	taccgaaaaacttttggaaattg	62.331	120
HM_4591	contig48168	TC	2	16	CCAATCTCATATGCAAACTCTCT	61.136	TtAcGACCAAGaTCAACTcCGAA	61.433	131
HM_4592	contig09539	AG	2	24	CCAATTCAAGATCCGAAGCAAAAG	63.091	TCTCATTTTCTCTTCTCAACCAC	62.987	126
HM_4593	contig27212	TA	2	12	CCAATTGgACAGAAAAGTAAAGTCA	61.788	TTTCATTTTCCaAGCAATTGTGTA	61.788	123
HM_4594	contig01450	TC	2	12	CCACACACCAACACATCTGTAT	63.053	TGAGGTAACTGCTCTCAATGAAGCT	62.606	139
HM_4595	contig40469	TC	2	16	CCACACACCAAGGAATTTCAAAC	62.739	CTcACAATTTCAATTcAGAAGCC	63.219	87
HM_4596	contig00742	AT	2	16	CcACACATATTACAGGAGAGCTAGaA	61.881	GATGGGTTGAAATCAGAAGAGAGG	62.455	152
HM_4597	contig26198	TC	2	16	CCACATCAACACCGAAGTCTCTT	63.766	AcTgGAACcAAAGGAAGAcAcAG	62.906	119
HM_4598	contig43862	TC	2	20	CCACCAATTGCTCACAATTCCTA	64.247	ATATACACACGCCGCCGACA	64.484	156
HM_4599	contig20892	AG	2	20	CcACCAAGTCTCTTCTTGTTGTA	62.737	GAGCTCTCATCTCAGCTCTCTCT	63.036	140
HM_4600	contig33744	AG	2	24	CACCCCAACAATCTTCACTTTA	62.907	TTGTACACTACTGCaCaCATCTCTCa	62.995	92
HM_4601	contig34426	AG	2	20	CCACCCaCATGGGTAAAACCTAA	63.21	tTTTGTCCATTGAAGCAAAATGA	62.735	138
HM_4602	contig38076	AC	2	12	CCACCTTATCTGCTATTGGAAT	63.322	CCCAGTTGAGTGGATGATGACTAA	62.743	141
HM_4603	contig13219	AC	2	12	CCACGAATCAGGTGAAAGAAAAGT	62.809	TTTTcTcaATTcAaaATCCCCGT	62.887	144
HM_4604	contig06524	TC	2	14	CCACTAGACTGCTcCTCACATTT	63.023	TCACCTAATCGAGCATTCACACAT	62.951	93
HM_4605	contig08696	CT	2	20	CcACTCTCCCTCTTCTCTCAATTA	63.974	GAGAGGCGGacCAAGaCAGAG	63.704	84
HM_4606	contig33928	TC	2	20	CCAGAAAAaTTGGCAAGACATTT	62.532	AcCAGTTGGTAGTCAAGAACGACc	62.032	81
HM_4607	contig46139	AG	2	20	CAGACAGCAATGGCAATACTACT	61.72	GATCCTTTTCCATTTACAGATTCA	60.965	100
HM_4608	contig07326	GA	2	14	CcAGATCTAGCCAAAGTATTGAGGG	62.397	CCAGAGACCCAATCAACGAAGAA	62.993	119
HM_4609	contig11504	CT	2	12	CCAGATGAAGGATTAGCCACTCTC	62.585	GAGCTGCAGAGGTGAAGGAAGAG	63.036	128
HM_4610	contig52024	AG	2	24	CAGCAGCTATGAATAGTGAATG	63.085	TGTGCTgCGAGTTACCAAGATCTA	63.29	148
HM_4611	contig24517	GA	2	20	CCAGTATCGTACTCGAGCTAGGG	62.535	CTTCTCGACCATCATGTCCTC	62.991	131
HM_4612	contig35494	TC	2	14	CcAGTTCACTCTCCAACAACCTCT	63.115	cagGctcTCTCTCTCTTTCTCTC	63.08	94
HM_4613	contig09880	AG	2	24	CCATAAGTATCCGCATCTCTGCT	62.841	AgTCTCGAGAGTatCGCTCCCT	63.203	142
HM_4614	contig30603	AT	2	14	CCATACCCCACTACTGTAAACCCAA	62.93	TGCACAGATCTCAATAgTACTTCCA	63.251	154
HM_4615	contig12920	GA	2	12	CCATACTGTtCAATTTCCAACCTT	61.564	TTAGAAACGGATTCCACATATCCA	61.688	141
HM_4616	contig08639	TC	2	16	CCATAGAAGCAATAACCCCAACT	62.522	TATGTACGTTCTCTCAATTGGACA	62.615	154
HM_4617	contig49267	GA	2	14	CCATAGaCTCTGCTGCAAGGTT	63.023	CaGAACCGGAAGTCAACAGAC	63.237	91
HM_4618	contig18891	AG	2	16	CCATATCCAAACCAAGCAACAAA	63.097	GGGTTTGTATCATCaATTaTTGCG	62.617	82
HM_4619	contig37745	TC	2	16	CCATATCTCAAGAAACGGAATCGC	63.034	CGAAGCTCAGGTCAATaTTCTcC	62.509	128
HM_4620	contig36918	AC	2	20	CCATCAAGAAATCGATGCTCAG	61.875	AGGAGTATGTGTTATGtTctGTTGGT	61.49	154
HM_4621	contig37793	TC	2	20	CCATCACTGATCCACCTTCTTCT	62.884	GAGATCGGTGCTGGTAGGTGAT	62.681	130
HM_4622	contig05575	CA	2	14	CATCCAAATGATGATGAATTTGA	62.898	tTGAAGATTCTCATTGCCATTTT	62.91	81
HM_4623	contig19889	TC	2	14	CcATCAtcAtTaaTGAAAGAGCT	63.569	AGAGAAGTTTTTCAACCACTGCC	62.824	153
HM_4624	contig37499	AG	2	16	CCATGAAGAAATCACTTTTGGGA	63.391	AACATAACAACAACAAGAACGcAA	62.795	88
HM_4625	contig03623	AC	2	14	CCATGAaTGCAAGAAGTAAAGATAA	60.744	AACAACATAACAACGTCAGCGAG	61.627	140
HM_4626	contig18388	GA	2	32	CCATGTCGTCTGTGTATGATT	63.283	TCgaaaCAGTAGAATTaAcCacTCTcG	63.043	118
HM_4627	contig31925	GA	2	12	CcATGTtCtCaTTCACTCAACATA	63.015	CTCTAgGATTCTCACTAGTGGCAcG	62.736	151
HM_4628	contig35662	GA	2	12	CCATTAAAGGCCAAACAAATGaaGA	63.311	CCTTCAACCCTaTTTgGATCTaA	63.552	130
HM_4629	contig20176	AG	2	20	CcATTCAAGaGACTGATtCCACtC	62.884	agtctttaacctcaatcatccgc	63.801	91
HM_4630	contig26818	GA	2	24	CcATTCTCCGACATGTTCTCTCT	63	CaAATaCCCTCGTtTCTCTcAc	62.299	155
HM_4631	contig37741	AG	2	14	CCATTCTCTAAACAACCTGGTGCC	63.129	CTACGCAAGGCTCCTCTTTTATC	63.595	131
HM_4632	contig48169	TC	2	12	CCATTCTCTATATTCCATCTCCCA	63.285	ACACAATCGaAaAcCACAACCTC	63.45	110
HM_4633	contig51011	TC	2	80	CCATTGTGTTCTCTGCTTCTCT	63.124	GGGAAATTAACACGGAAAAATCAA	62.237	240
HM_4634	contig07183	GT	2	16	CCATTGTTAAACCCATTGGAGAAA	63.097	tTcATTCTCTCCATcCCTCAATC	62.977	138
HM_4635	contig44253	GC	2	14	CcATTTCGCGAAGTCAATAATA	63.11	CAGTTCATTTCTCGGCAAACTT	63.041	122
HM_4636	contig00639	AG	2	12	CcAATGAATAAGGAGAGAGCA	62.8	GGGCTCTCTCAGTTGTTTCTGT	62.296	106
HM_4637	contig08754	AG	2	14	CCCAACAGATAATTACCAGTGAGTGA	62.535	TCTATTcATTCTGTAGTGGATTgG	61.579	91
HM_4638	contig46470	GT	2	16	CCCACTAGGATCAAACTCAATTAACA	62.652	TGAGATCCCAAGATCTACCGTAT	63.125	155
HM_4639	contig11468	AG	2	20	CCCACTCATCTCTCTTCTTCTT	63.164	CGATTCTCTCTCTCCGATCTCT	63.816	145
HM_4640	contig17189	TC	2	16	CcAGATTCAACAaGaATCCAATC	62.987	GAGATCGTCACaAGCATCTCTGTA	62.847	124
HM_4641	contig37382	TC	2	32	CcAGTGATTCAAAATgACTCTCC	62.397	GAGTTTACTGCAATTGGGAGGATG	63.121	141
HM_4642	contig48173	TC	2	14	CCCAaGAAAAACCAAGATTCTCC	63.16	CaCaAAAAACCACTTCGATTCTCT	63.117	157
HM_4643	contig37020	TC	2	24	CCCATATCGTCCAATTTACTCCAA	63.101	GAAAGATTGACAGGGAAATATGGGA	62.468	124
HM_4644	contig36143	TC	2	12	CCCATCAAGGTAAAGAAAGTGAC	63.121	GCAACGGATAGATTGGTAATGGA	62.225	216
HM_4645	contig05976	GA	2	20	CCCAATGAAGTTCTCAATTTGTGC	62.922	CGTTTTTGGCACAATGATATCAAAATC	62.593	156
HM_4646	contig36006	TC	2	16	CCCAAAATCAaACCTTAGAACCTT	62.689	ATTCTCGGATTCAAAAAACCTaGC	62.903	152
HM_4647	contig44713	CT	2	32	CCCCAGATCCGCTAGTAAATACC	63.095	GTACTTCGAGGAGAGGACACAAG	62.691	141
HM_4648	contig02158	GA	2	12	CCCCATAGCTCTGCTCTCTCT	63.089	TATcTtCCAGAGCTCAGCACTC	63.343	149
HM_4649	contig24398	AG	2	12	CCCCATTACTGTATTCTTTTGCCA	63.216	GGAGCACTATTCTCTCTCCAAAC	62.885	155
HM_4650	contig50361	AG	2	12	CCCCaCTGTATTAGTGAGAAATG	62.993	GACTCTTCAAGCAACCCCC	63.231	148
HM_4651	contig38322	GA	2	24	CCCAATGAaAaTtAAAACTCAAA	62.224	ATGTTGTGAAGGCGCCCTTCTTT	62.517	145
HM_4652	contig45082	AG	2	24	CCCTCTATGcccTAATCAGAATAC	62.331	CtAGTAgaACCGTGGAGTGCCaAT	62.835	135
HM_4653	contig25859	AG	2	12	ccccttGGTgATTAGCTAGagAG	61.708	TTTTTGGGACCTTGAGTGTACGA	61.913	124
HM_4654	contig14199	AC	2	16	CCCTAACACCAACAATCAAAACA	63.044	CGCATaTCTCTCTCCAATCCATC	63.216	151
HM_4655	contig37751	GA	2	20	CCCTAATTTGtGGAACTAGATAAGAA	61.865	ACCAACAACAAATCAAGCTATCG	62.412	160

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4656	contig37366	AG	2	16	CCCTACATATCGCTCTCGGACTA	62.826	CGATCCTCTGTTTtctCACACTC	63.546	122
HM_4657	contig29411	TC	2	14	CcCTCAAAATcaccTACAAGTTTg	63.003	CCTACTTCGGAACAgGACTCGTGT	63.033	157
HM_4658	contig03781	AG	2	12	CcCTCACTCCTCAATAAATGTTGc	63.121	ACCACCACCACTGCaAAACA	62.432	159
HM_4659	contig34922	CT	2	16	CCCTCTCAAGCCCTTATTCAAAACA	62.811	TAAACGCCAACAAAAAGGATTGAT	62.839	125
HM_4660	contig36362	CT	2	16	CCCTCTCTAATTCcctACCTCCc	63.512	TCATTGTTGCTgTTGAGATCTGGT	63.164	99
HM_4661	contig01281	TC	2	14	CCCTGTTGTTTCATCTCTCTGCTT	63.124	TcaTTCTCATGCTCTTCACTGAG	63.03	151
HM_4662	contig44712	GA	2	14	CCCTTACTTTGGTCTGATTTTGGa	62.591	TtAAATAcTCTCGCTTGCCTGCT	62.784	135
HM_4663	contig19334	TC	2	12	CCCTTCTCTGACTCTGGGTAGTG	63.228	TGATACATAGAGGCGTTTCTGCTA	62.959	111
HM_4664	contig20368	TC	2	24	CCCTCTATCAATTTCTCGCTTT	62.992	CTGCACaAgGTTTTCCaITCTGTA	62.527	153
HM_4665	contig31427	AG	2	16	CcCTTGTTGAGaTcgataaagaga	62.69	cccttctccagtttcaGTGttc	62.483	96
HM_4666	contig15778	TA	2	12	CCCTTTTCATAaGATTGACTAACTACA	62.031	GGCaGTTTCGGTAAgAACAAAAGT	61.961	137
HM_4667	contig48112	GA	2	20	CCCTTTTCACTGCTTGTTCAATC	63.108	AGaGaaAACGAggGaTAccCagAC	63.084	157
HM_4668	contig48195	AG	2	14	CGGAAGGGGTTTCTTAAaAACaTAA	63.359	GCTATCCTCTGCGCTCTCTCT	62.458	119
HM_4669	contig15849	CT	2	16	CGGAATTCAAGAGCATCTAGGAAA	62.909	ACTGAAGCTTTTTGAGATTGCGCG	62.957	156
HM_4670	contig00535	CT	2	16	CGGAATTGGATCTTCAAGAGTAA	62.505	TAGCTGCTCTTcACTCCACTACC	63.25	110
HM_4671	contig45746	TC	2	14	CcGaGATTgAGAAAACCTGAAAAA	62.798	GCAGCTTAGAATCAGCAGTCATTG	62.557	159
HM_4672	contig35952	GA	2	16	CGGATACAGCTGGTGAACCTTTTc	62.933	GATTTCCTCATCCACTTCGGAGTAG	63	87
HM_4673	contig36011	AG	2	16	CGGATGTTAGCGAATTCTCTCTA	63.422	aCCACCaACaCaACITTTCTGCT	63.564	117
HM_4674	contig39749	AG	2	12	CGGCACCAATTACTATTACCcTTCA	63.228	TCTTCTCACTcTCTGCAATGCC	64.2	159
HM_4675	contig25380	CT	2	12	CGCATTTTtAGtCATGTCTCTCT	63.231	TCGATGCTGTTTGTAGTTTCTTTC	62.935	148
HM_4676	contig26163	AG	2	16	CGGCATTACTCTTATGCTGTTCT	62.166	CCTTTTCaAtTTTACCATcTCCC	62.968	116
HM_4677	contig00062	AC	2	14	CCGCTAAATAATCATCACACCA	63.059	CCCCGTGTCAGGAGGTAITTTAC	63.074	143
HM_4678	contig04353	TC	2	12	CGCTACTTTTtAGTTGCTTCA	62.859	GATGGAGAGGTTGCTGAgGaAGTA	63.115	114
HM_4679	contig30285	CT	2	16	CGCTTCTCCAGATAGATACCTCC	63.589	aAAACaGAGTgGAAGGGGc	62.634	108
HM_4680	contig44567	CT	2	20	CGGAATTTCAGCATTTGAAGATG	62.607	gCCCAACTCTAGTGAGAGAAAGTTACA	62.676	126
HM_4681	contig05666	GA	2	12	CGGAGACTATGTCGTGGAAGTAG	63.332	TACTCATCTCCACATCTTCACCA	63.016	154
HM_4682	contig18650	AC	2	20	CGGATAACACTTTCACACACTGA	63.377	TCTCACCACCTCACTTGTCTTGG	62.81	141
HM_4683	contig00615	GA	2	16	CGGTGCTCAATTCAAGAAATC	63.015	ACGACATACGTCtCTcTgGTgCT	63.595	83
HM_4684	contig13605	TA	2	14	CGGTGCTGCTTGTCTATGTTC	62.946	CATATTGATTCGAGCTTGATCGC	62.779	135
HM_4685	contig06600	GA	2	12	CGGTTTGACATATTCTTCTGCTG	63.336	CaAAATCAACTTCAAGCCCTAGCC	64.279	152
HM_4686	contig16505	AT	2	12	CcGTATTGAAGgtGCATAAACCA	63.068	AGAGGGGCGACTGACAAAGAAGATA	62.598	144
HM_4687	contig23750	TG	2	16	CGCTCGGAGATGCTCTAAATAACA	63.636	TGCTAGTATTGAGCAAGTTGCATTG	62.703	149
HM_4688	contig36870	TC	2	20	CGCTCGGTGGATCACATAGAAT	63.223	AAGGGAGAgGGGTAAACGAATCAG	63.068	157
HM_4689	contig12803	AG	2	20	CcGTTGGATGCTGAGAGAGTAA	62.815	CtGCTCTGCTTCTCTCTcCaG	62.065	84
HM_4690	contig12803	AG	2	14	CcGTTTGGATGCTGAGAGAGTAA	62.815	CtGCTCTGCTTCTCTCTcCaG	62.065	84
HM_4691	contig30293	CT	2	20	CTAAATCGGAATATCATTTCcC	62.777	GATGATACTTGAATGAcGCCAA	62.325	90
HM_4692	contig38152	CT	2	12	CtACcTCTCCCAACaCAACAAG	63.216	TTTGATTGGAGGAGGATGAAGAG	62.871	126
HM_4693	contig40113	CT	2	30	CCTACGAACAGCTTACGCTCTCT	62.466	GAAAATTGGAGAAcTCGAAGCAGa	63.121	135
HM_4694	contig42577	CT	2	16	CCTCAAAATCTACCAaAcATCACC	60.945	CCACAATATTATTAGTAGCAATTTTCG	60.352	129
HM_4695	contig01874	AG	2	24	CCTCAAGTTTTGGTCTGAAAACAG	63.218	aCGTGGATGATTGGGIATTCCTC	62.393	96
HM_4696	contig44115	TG	2	12	CtCTCAATATTTTGGGCCATTTT	63.375	GCCTTTTGAAGCAAGGTGTTGAATC	63.353	108
HM_4697	contig13999	AG	2	16	CTCACTTGTGTTGATGAAGACCG	61.913	TTGCAATTGGCGTTAGATATACCA	62.575	159
HM_4698	contig01597	CT	2	14	CCTCCAaAcCAGCACAGTTCCTCT	63.133	ATATCAAGCAATcGaCAACCCCTc	62.622	160
HM_4699	contig07424	CA	2	14	CTCTCATAGCCACAaTgAAcTCT	62.811	TCAGCTTCCTTATTTCATGCTCT	62.925	149
HM_4700	contig25609	TG	2	14	CTCCCTAACTCCAATTCCTATTG	63.156	GcCCCAATTTTCATATTCAATCAA	63.008	106
HM_4701	contig30318	TC	2	12	CTCCGCTCTGTTCTCTCACTAA	63.22	CTCTCATGCTCTCTCTCTCTCC	63.085	104
HM_4702	contig20719	TG	2	16	CcCTCAAAAGaCcaCTAGGCAAT	62.992	GCCTCTaAAACAGTACaAATCATATGGC	63.244	129
HM_4703	contig13159	CT	2	24	CCTCTAACCTCTGGTGTCTCTCT	63.391	ACACaACaCAACACATatGCaG	63.139	85
HM_4704	contig39206	GA	2	14	CCTCTCTTCAATTCAGCACCTG	63.531	TCaTTTGTCCCCAAATTGaAAAC	63.101	160
HM_4705	contig46259	TC	2	20	CCTCTCTCTCTCTGGCATTTGAA	63.104	CCACACAGAGATCACACATCaAGA	62.463	108
HM_4706	contig47000	AG	2	16	CtCTtGTTGatGgTTTGTGAGc	63.968	TAGGTCTCTCAACAGCTTCTATGTG	63.12	111
HM_4707	contig34885	AG	2	20	CCTGATTATGACAGCACCTTCTCT	62.633	ACTCCaAGTCCCaAGTcCT	63.4	157
HM_4708	contig37186	TC	2	20	CCTGTAACATGGCAGTGAGACCA	62.621	CTTCTCAGATTGAAGcCAGCTTG	61.744	158
HM_4709	contig34961	GA	2	24	CCTTAAACTATTCTCTGCTGCCCC	63.285	AGACTTcAGCGaCaCTCCCTCTC	63.518	150
HM_4710	contig42840	CT	2	24	CCTTACCACGCTCAGTCATCTT	63.023	AGTGTGAGTCGATCAGAGcAgAA	62.722	80
HM_4711	contig28961	CA	2	16	CCTTAGACCAAAACAGGCTCTGG	63.216	CAAAATTGGAAAGTGTGATTTGAT	62.225	153
HM_4712	contig13688	TA	2	16	CCTTATCCTTTCCCACTAGAGA	62.955	TCAGTTTGCTTTAAACACACAGCGT	63.21	154
HM_4713	contig31260	AC	2	16	CCTTATTAAACACCACTGAGC	62.826	GTTCTGATTGTTGAGTAGTAGG	62.897	90
HM_4714	contig23085	CA	2	20	CtTcACATTtGCTcTCAATt	62.607	TGAGTGCAGCTAGTAGCGAGaGAA	62.985	135
HM_4715	contig08632	TA	2	12	CCTTCCcACTTCTCACTCTCTT	63.378	GCAAAATTTCAAGCTCTGATTAC	63.346	155
HM_4716	contig11045	AG	2	12	ccTTCCTCGaaCGAAACGTAAAAAC	64.077	AGTGTCTGTTGGGATCTCTGTT	63.353	137
HM_4717	contig05074	AC	2	24	CCTcGAATCCcCAaGAAAAATA	62.505	TTTGATTGGACTTGGAGGTTTGAT	62.996	134
HM_4718	contig10483	TC	2	14	CtCTtTAATTGATGCACTGAGGc	63.341	CTTATTCTCCGCTCTCCATCTCA	62.884	128
HM_4719	contig15578	AG	2	14	CCTTGAaATgAAATtGGTCTGG	63.014	ATGcCCaTTAAITCCACACAT	63.533	111
HM_4720	contig42084	GA	2	14	CtTGTCTtCTTTGtGTCTATT	62.696	CCATTaAAGaTCCTATGtGcCTCC	63.278	116
HM_4721	contig05214	AG	2	14	CCTTGCTTTCCACAGATCTcCTc	62.664	CaAACTCTcCTGTTTCTGCTGTA	62.905	151
HM_4722	contig10663	TA	2	14	CCTTGTGCACTTGTTTTCTCATAT	62.657	GAAGTAGGCCaGcGCTAGTAAT	63.073	88
HM_4723	contig04154	AC	2	16	CTTTTACCCTCCAACATCTCCTT	62.873	cCAATCCGAAAATTAGGGTTTCTC	63.072	151
HM_4724	contig14728	AC	2	12	CGAAAAGaAaCAAAATAGTTAAGGCA	61.081	TTTGTTTGGGTTTATGAGGTGtT	61.88	88
HM_4725	contig42835	AT	2	16	CGAAAGGTGCCATACCTTCTTAT	63.584	GACGGCTTGGAAAGATCAAGTc	63.434	98
HM_4726	contig21074	CA	2	16	CGAAACACAAAAGTTGCTAAACAGC	62.285	ACCGATCTCAACAGCTTCTCaAG	62.215	143
HM_4727	contig14643	AT	2	14	CGAACATAATAGCCAATCTCAC	62.925	CAAGGTAATCCCACCTTCTCTTCA	62.907	134
HM_4728	contig22541	CA	2	12	CGAACCGATTTCAAAATTTACCAT	62.251	GcGCGACTTCTACTTCACTGTGA	62.251	157
HM_4729	contig34630	CA	2	12	CGAAGACTTCAACTTTTCCACAA	61.971	GTGGAAGGAGGAATGAAAAGATGA	62.773	128
HM_4730	contig17082	TC	2	12	CGAAGAGATTCACTGGTGCATATA	62.712	TATTGAGGCTATTCTAGATGGGCG	62.75	138
HM_4731	contig35690	TA	2	12	CGAATAGAACTGAAACGAGCCAA	63.439	CGATCAAAACACCAACaAACTGAG	62.942	115
HM_4732	contig46988	CT	2	16	CGAATCGCTCTTTCTTAAAGCAACT	63.327	AACGGAGGATAGGATCATCGGTAG	63.685	141
HM_4733	contig03576	AC	2	12	CgAATGAgTtTAAAGGGAaCATGG	62.906	CATTCTGATTCTGAGCTTCATCC	63.425	157
HM_4734	contig03525	GA	2	16	GGAATGGATTAAAGATTGGCATAG	62.817	AGGCTACAGAGCCAAATCaACAAAT	62.439	134
HM_4735	contig37888	AG	2	20	CGACAAATGAGGAAaATTTtAGGG	62.996	TAGGTAAATTTTGTGGTGTGGC	63.24	89
HM_4736	contig43296	AG	2	16	GACATCTCTCACTCACTTGGCTG	62.516	TcTGATTGACAGTtGAAAAGATTCTGA	62.535	143
HM_4737	contig28532	TC	2	12	CGACCAATCTCACCTTCTCAAGT	63.01	GATAAACCCGGTATCCCTCAGAAC	63.081	111
HM_4738	contig49680	CT	2	16	GACGCTGACATCTTCTTTTCTT	63.031	GCCCTCAGAATCAATTACAGAGCA	63.865	102
HM_4739	contig00666	CT	2	20	cgAcGTGtccCTCACTCACTACT	63.462	GAGCTAGGGTTTCTGTGATTGGAA	62.91	81
HM_4740	contig30915	AC	2	16	cgActccttttaccaggattacACaaC	63.612	AACCTGCTAGGGCAACATCAATCG	62.949	150
HM_4741	contig08960	TA	2	14	GACTGTAGTCATGGCGTTAGGT	62.636	TCATCTTTTCTAGAgGGAAGAGCAT	62.055	131
HM_4742	contig37620	GA	2	16	CGAGAAAGCAAAATAAcCAaTTAAGGA	62.757	TGAgGGTtGCTAgcCATTACtTC	62.839	155
HM_4743	contig21687	AG	2	14	CGAGAACCAGGACCATGCTCT	63.113	ACGTTCAGcATTtTAGGGTTTCA	63.039	134
HM_4744	contig01822	AG	2	20	CGAGATCAACCATGACTTTTGACG	62.945	TGCTCTCTCATTTCTAGATTGCGCT	62.174	129
HM_4745	contig25073	TA	2	24	CGAGATTGAAATtGGGAgAaTGTG	63.202	CcTtTcCTCTCTTCAACCTgGA	63.256	154
HM_4746	contig20904	GA	2	12	cGAGGTtGATtCTTGCAACTACTA	62.629	CACAATCACAGATACTCACTGAACCC	63.15	145
HM_4747	contig03365	GA	2	12	CGAGTCTTCGaGAAAGATTGTAGC	62.824	ATCATCTTCGGCAATTCATCTc	62.906	131
HM_4748	contig15330	AG	2	20	CGATAcacGCCaGAAaCAATCTCT	61.462	AACCTGAGCGGAAGAAGAACTAAC	62.355	114
HM_4749	contig17362	TC	2	16	CGATAGTTACCCAACCAAGTACCA	63.222	TTCTAcCACGGTtCATTCTCTC	62.798	150
HM_4750	contig10891	TC	2	24	CGATTCTGTGATGAGACTCTCCA	62.276	GTGAACATAAGACAAAATGTACGTTGC	61.412	127

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4751	contig04603	TC	2	16	CGATTATTACAATAGCTTCTGCTGCG	63.089	AAACGGaATAAACAGTGTGAGGGA	63.019	141
HM_4752	contig14630	CT	2	20	CGATTCTCCGTGAATATGTTCTTC	63.219	CTTgCAITaCTCAAAATGGcTC	63.245	136
HM_4753	contig20035	TC	2	16	CGATTGCTAGGGTTTCTGTAGGTG	63.234	tAGTGCCagTGGAGAGATGCATTA	63.168	122
HM_4754	contig45466	TC	2	12	CGATTTHGAAGGTGAGGAAGAAGA	62.993	GTagTaACGAAGCaACtTcCTG	63.258	98
HM_4755	contig20191	AG	2	20	CGCAGATCCAATCTCTGTAAAT	62.533	aATCTATTCTCTCTCTGTGCTGC	63.247	124
HM_4756	contig50984	GA	2	14	CGACGCCCTTACATGAGAAGATAA	63.743	CTATCACATGTGCTGTGATTGGG	63.707	136
HM_4757	contig16406	AC	2	16	cGCCATCAAAcCaGTAAACAAATG	62.662	TATTCCGATTTGTGGGTTTTTCG	63.022	133
HM_4758	contig21853	GA	2	16	GGCCATCGATATTATCAACaCAG	62.652	AGctcCGTTTGTCTACGTTTCaTC	62.949	122
HM_4759	contig41664	CT	2	14	CGCCCTATCAACTCTCTCATATCTT	62.914	GCATTGATGGAGATCTCTGAAAA	63.739	135
HM_4760	contig10977	AG	2	16	CGCCGAGATCaGACATATCAAACT	63.766	TcCTCTCTTTCTCTTCaAcTTC	63.261	150
HM_4761	contig35294	AC	2	16	CGCGATTAGGTTAATTAGGGACAC	62.077	ACaAAACACCTTGATcaATTGCC	61.319	157
HM_4762	contig25754	AT	2	16	CGCTACTCTCGGGAAGTTCAATAGT	62.946	cTCCCTCGTTCTCAACaCaAcT	63.901	129
HM_4763	contig41042	TG	2	16	CGCTCTCTCTCTTGTGTTCTTACT	63.392	CTCTCCCACTCTGGAAGaTAACCA	62.984	127
HM_4764	contig13371	CA	2	24	CgcTCTTAAcCcaCaCCTcTtAT	63.797	TAACAAGaGTCCCAAGAAAGCCAA	63.319	109
HM_4765	contig18179	TC	2	16	CGCTCTCTTCTAGCTCAAAATCCAT	62.247	TGATCAATCGAATTACGATAAGCG	62.355	147
HM_4766	contig35568	AG	2	14	CGCTGAGTTTCTCTGATGATTCTT	63.022	GAGAGaAacGTCTcCCACCG	62.145	123
HM_4767	contig40384	TA	2	14	CGCTGTTTGTGGGTATTATACATT	63.146	aATTGGATgAGGAAATTTAGGGGA	62.959	145
HM_4768	contig08143	AG	2	20	CGGAATCTCTGTTGGAATTTGTA	63.204	ACTGAATACTTCTGACACTGAACC	63.154	154
HM_4769	contig46416	AG	2	12	CgGAGGAGTTGTTGGGATTATAGT	63.682	GTCACATGCATCTcCACCTCTCT	63.137	80
HM_4770	contig31619	CT	2	12	CgGATAAcAGCAaTATCATCCcTC	62.915	GAGATTAGAGTTTTCGCCATGGAA	62.815	132
HM_4771	contig04441	AG	2	14	CgGATCGGCAGAACTATaGAGA	62.922	GCCtCGGAAGAGATATAGGAGaT	63.204	144
HM_4772	contig07275	AG	2	12	CGGCAIATTGACAACCTGATAGGG	62.718	CCATGGTAGAACAGGATTcAGAGG	63.199	160
HM_4773	contig37995	AG	2	24	CGGCcATCTTCATTAGTCTTCTA	63.03	CTCAgAGTCACTCAAGGCaCaC	63.624	94
HM_4774	contig22783	TG	2	14	CGGCGTCAATaACGTGTTGTTTa	62.991	tcaccgtgaCtagcatTAaagagaga	63.366	88
HM_4775	contig23396	GA	2	16	CGGCTGAGATTAGAATTAGGAGCA	63.03	cTCTCaATaTcCTCCCTaCaACA	63.001	103
HM_4776	contig14480	AC	2	24	CGGGGAATTTGAATTTCTAGGAG	63.159	taAAATaCGGAACaCTCAgGGcaT	62.935	123
HM_4777	contig03823	TG	2	12	CGGGTATACATTGTCATCTCTACT	63.13	CAAAcCATCAATATGTTCTGCACC	62.631	158
HM_4778	contig01383	TC	2	14	CGGTACTGGGTGACTGTTTTCCT	62.919	GTCaAGCTCTCCACATTCATACCA	62.609	93
HM_4779	contig23732	CA	2	14	CGGTAcTTAAATTCATGGCGGATA	63.13	TCCATCCAGTTACTACTTCAAAACCC	62.726	122
HM_4780	contig14812	TG	2	20	CgGtTAGGtTTTGCTCaCtGtTc	63.142	ATCTTCTCTCTCCCTCTTGATCGT	62.865	155
HM_4781	contig11365	CT	2	14	CGGTGTAGACGAAGGTCTCG	60.843	CACCTCTCTCATCTTAACTTTACAGG	61.134	138
HM_4782	contig46136	AG	2	16	cGTTACAGTGTCTGAATTTAGGG	63.036	TGGATTTTAGCCGAAGTAAGGtCa	63.122	122
HM_4783	contig07284	CT	2	14	CGGTTGAACAAAACAGAAATTGAA	62.326	AGAATGGGACAGAGATTTCTGCAT	62.484	154
HM_4784	contig32741	TC	2	20	CGTACTCATACACCCCTCTCCAC	63.124	AGTaATTGATTGGGACGAATTTT	64.089	93
HM_4785	contig03344	GA	2	14	CGTAGGATTGGAGGATGTCAATAG	62.996	ACTGAGAAATCaAACCAATGCTCT	63.219	135
HM_4786	contig48740	GA	2	12	CGATAtgaTGGATTGATTCGATT	62.249	TTTaGGGTACCAAAAACCAATCCC	63.171	102
HM_4787	contig36676	TC	2	14	CGTCACTGTCTCTCTCGGAACCT	63.023	tTGCACTGTGcAAGaGAACCTCAAC	62.972	84
HM_4788	contig27160	GA	2	14	CGTCCGAAGAAGTTCTcTATCCA	63.006	TGTTTATgAgAGACaAGCAGCCA	63.5	132
HM_4789	contig15940	GA	2	16	CGTCCGGTTTTTGCAAAATTATAG	62.76	AACaAGCCACCAgAAACcCTAAT	63.203	113
HM_4790	contig32031	AG	2	16	CGTCGGTTATTCAAACTCTGTCT	62.631	AGACCTCACTCTCCGgTAAATTC	62.768	143
HM_4791	contig46124	TC	2	30	CGTCGCCTCTCAACTAGAACTGT	63.258	tTtcTctGtcGtTtTTCaAcTc	62.907	159
HM_4792	contig33675	GA	2	16	CGTCTACACCTCTCACTCGCACTC	62.505	TTTCAAGcCTCAACaCACAAGATC	62.739	102
HM_4793	contig07208	CT	2	14	CGTCTCATAGACCCTCACTCACT	63.119	CTTCCATGAACAAAGTCAGAAATG	63.048	155
HM_4794	contig03831	GT	2	16	CGTGAGTCCCAAGGTCTATACAAA	62.411	CTTTTGcTTTCTTTTCCCTCTCT	62.503	139
HM_4795	contig14684	AG	2	14	CGTGATTATATGCTCTGGCTACT	62.667	CTCAACCTCAAAAAGaCaAAACGA	62.641	134
HM_4796	contig40540	TC	2	20	CGTGAAGAAGAAAGACATCTTTGG	63.42	ggggatctaattcctctgtttca	63.013	157
HM_4797	contig46172	GA	2	14	CGTGAAGATTGTTGGTGGACTGAGA	63.377	aATgGaATgGaTcCTCTGTGATG	63.692	100
HM_4798	contig33086	TC	2	16	CgTTAACGATATCATCTGGGTCAA	63.059	cAAcCTCACTCaGCCATATCAAITA	63.223	148
HM_4799	contig41398	GA	2	12	CGTTAGAATCGTGGATTGGTAG	62.919	CGGCTCTTTTCTGTAATGTTGTT	62.859	110
HM_4800	contig03140	CA	2	20	CGTTCAACATCTCAAAACACACAA	63.206	CATCTCTCAATTCCTCTCTCTCT	63.156	144
HM_4801	contig23017	TC	2	20	CGTTGTGCTGTaATCaCGGATT	63.146	CACATCTCTCTTGAAGACCAAAACC	62.212	109
HM_4802	contig20958	TG	2	12	CGTTTgGtTGAACCCtAcAcCCtG	62.916	aATTTCaAACCCtAcAcCCtG	63.995	143
HM_4803	contig15971	TC	2	24	CTAACACCGGCTAGTTTCATCAGG	63.234	TTAAATTGCCCAATTTGTTGTCC	63.026	141
HM_4804	contig12323	GA	2	12	CTAACATACCAAACTCAGGGCAG	62.919	AAATGTCTTGGGGATTAAAGCACT	62.797	108
HM_4805	contig07266	TA	2	12	CTAacGATCGCTTCTGTGAATGA	62.744	ATTAGCACCGATCAAAcCTCTCTG	62.923	117
HM_4806	contig05702	GA	2	16	cTAATCCGGTTAGGGTTTCTGTGT	62.701	tCCAAGtGTcCCTTccatTctAc	62.684	121
HM_4807	contig26445	AT	2	12	CTAatCCTCGCAAAATTCaCACCC	62.922	ATGGGAGGAATTGCTGACTaCaAa	63.121	93
HM_4808	contig32516	TC	2	12	CTAATTGGCCATGAGTTGAAAGGT	62.619	TGGTTAGGTGGTTAGAGTCAAGGG	62.695	130
HM_4809	contig43175	GA	2	16	CTACAAcTcCGCTGGAATGCTCT	62.946	TCCTaAAAACACATACATAAGCAGCA	62.168	141
HM_4810	contig38029	CT	2	12	CTACAAGCTCGCTATTCTCTCAAC	63.468	CAGATGGAGAGGgAAGAAAGTTCA	63.085	86
HM_4811	contig34036	CT	2	20	CTACAATGGATCAGCTCAGAAACC	63.331	AGGTTCTTTCAAATcTcCTcCaC	63.071	138
HM_4812	contig28773	TC	2	24	CTACCGCAAGCAaATGCTTTGAA	63.471	ATAgGGAATGCaAGACAGCAAGAG	63.035	114
HM_4813	contig41903	GA	2	24	CTACGATTTCCGCAAAAGTGATCC	63.121	TCTGCACCTCTCCCACTTATCAC	63.876	141
HM_4814	contig20098	AG	2	24	CTACGGTGGCTAGTACTCTGGTGG	63.352	GGGTCTCTGTGGTTGAAGTTAAcag	62.411	138
HM_4815	contig41557	AG	2	20	CTACTGAAATAAAGgTAGCcGCCA	62.757	ATCTCGaACCTAAGATCTCCCTC	63.185	135
HM_4816	contig03959	AG	2	20	CTAGAACAGAATCAAAACGGGA	62.811	ATGATGTaAAAAGGGAGCGCTGT	63.196	110
HM_4817	contig33126	AC	2	32	CTAGACAATCCCAAAACAGCTTGC	63.348	TGTTGTTTCTATTGTTGCaGAAATGCG	63.456	145
HM_4818	contig11604	TG	2	14	CTAGAGAAGGGCATGAGTACAGGG	62.597	GGGCAAAAGTCATataAAAATCTCCA	63.452	98
HM_4819	contig34492	AG	2	20	ctAGGGAAGGGTTTTAagCGTCACT	63.106	GGGATCTTTCTGAATGTTCTTCCA	62.773	160
HM_4820	contig30438	GA	2	12	CTAGGGTTTGTGGGATTGGGATT	63.273	aAtaCaCAATCTcGTGTgCCACC	63.353	131
HM_4821	contig06405	TC	2	24	CTATCACCACTGGAATCTGATCG	62.805	GggtgtGGGtTgTATTTCaTtTC	62.607	160
HM_4822	contig37695	TC	2	16	CTATCAGAGCTTCCCTTCCAACA	63.006	GCACATCTCATTTgGTgTtCTC	62.084	80
HM_4823	contig28938	GA	2	12	CTATCCAACCCAGACGAGTGTT	60.415	TTGCTcATcccCatcaCTaC	60.126	149
HM_4824	contig12684	TA	2	12	CTATCCATTCAcTACCCTCGCAAC	63.133	ATGAGTGGAGCAGAGCTGGTAGAG	63.468	115
HM_4825	contig26796	TC	2	12	CTATCGCCAGCTCGAATAAAGCTA	63.062	CAAAACAACAAGAGAAACAGCGA	62.754	156
HM_4826	contig32145	AT	2	16	CTATCTgaTCTGGATTTCCTCAAC	63	GAGCTGCTCATgTAATATcTcCCC	62.411	132
HM_4827	contig39878	CA	2	12	CTATGATGGGCAcCATACGTACA	63.176	TGTTTGAAGCTTTGTGTGAAGGAA	63.159	112
HM_4828	contig00597	AG	2	12	CTATGCTTCATTAACTCTCTGGC	62.255	TGAGATCGAGGATGAACCACTCA	63.137	158
HM_4829	contig41439	TA	2	14	CTATGgAGAGCaACACATGCaCaC	63.057	TGGACCTGTACATGGTTTTATcCC	63.108	153
HM_4830	contig08247	AG	2	16	CTATTTGGTTTACAGCGAGTGCG	63.079	TCCTTTCTGCTCTTcGgGCG	64.017	156
HM_4831	contig11177	CT	2	14	CTCAAAATCCCACTGTCACTGACT	62.884	GAAAGACaCaAAAGGAGCAGAg	62.71	131
HM_4832	contig43228	GA	2	16	CTCAATAAAGCTTCTCTGGGTGC	62.824	ATaAAACCCCTcCTTCTcATT	63.045	153
HM_4833	contig20425	GA	2	16	CTCAATACCAAACTGGTTTCCCA	63.307	AAATaCGTTTCCCTCTATCCAGAC	62.598	148
HM_4834	contig17136	AC	2	12	CTCACTCTCTGAATCTCCGGGTA	62.907	CATTGCCGAAGAAGAAACCATAC	63.03	123
HM_4835	contig21819	TC	2	16	ctCATCATCAACACATCATGgGA	63.243	cCTTAGGGTCAGAGAATTGGGCTAT	62.983	99
HM_4836	contig01079	CT	2	12	CTCATCCATCTCTCTCTCTCTCT	62.271	GAACCTTGAAGCTTGAAGTGAGAC	62.809	112
HM_4837	contig47513	CT	2	12	CTCATCTCATCTCTCTCTCTCTCT	62.271	GAACCTTGAAGCTTGAAGTGAGAC	62.809	112
HM_4838	contig42157	TC	2	16	CTCATCTCGAAATCTCTCAACGA	62.934	aCCTGCTaTGCTTgATCTCTTTC	63.051	156
HM_4839	contig00603	AG	2	32	CTCAGGAGGGAGTTTGTATGTA	62.782	AcTtTtTgGTcCacacATaCCCAT	62.712	160
HM_4840	contig33263	CT	2	12	CTCCATCTctGTCTTCCACCACT	63.106	tGATTTGGGTGAAAAGaGGAaAA	62.989	151
HM_4841	contig48053	CT	2	14	CTCCATCTGTGATGAAATTTCT	60.665	AaCTGTGACATACATATAAGAAAGGAA	60.671	90
HM_4842	contig08364	TG	2	24	CTCCCTTCGTGCTTATGAATCT	62.923	cCCAACcCaAAACCAACGAATA	63.118	105
HM_4843	contig01842	AC	2	14	CTCCGATCAGAGACTAGGTGCTA	62.031	CCACTCCAGAGTCAGAAACACAAA	62.81	128
HM_4844	contig36690	TC	2	12	CTCTCTTCAAGCTCAGCACTCTT	62.821	CGGATACGCTCTTGAATAGATTG	63.126	90
HM_4845	contig42415	TC	2	14	CTCTTGGAAATGCGGTAACAAAC	63.019	AGTTGAAGGATTGACGAACAACC	62.712	143

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4846	contig01171	CT	2	14	CTCGAATCGCAGGAGATTACTCAT	63.026	taacacagCAACACAGCaCAG	63.263	90
HM_4847	contig22590	CT	2	12	CTCGATACCCAGGTTCACTACCAT	62.598	GATGTGAGCGAGGTAGTGAGGAGT	63.254	148
HM_4848	contig37171	TC	2	16	CTCGGATCTAGAGAGTTCTGTGCG	63.027	ggtttgtagtCAATAgGGTTTCG	62.028	158
HM_4849	contig42579	TC	2	12	CTCGGGTTTACGTTTACCTCCTC	63.292	GAAAGAGCAACAGATCGAAACCTA	63.022	82
HM_4850	contig46815	TC	2	16	CTCGATCGGACATGGTAGGACTC	63.462	CTAAAGGGCTTCGGAAGTCAACC	63.482	139
HM_4851	contig42396	TC	2	14	CTCGTCATTTTCCACAGCTATGT	62.923	AAAGCGGGAGcgtTTTAAGTAGag	63.021	125
HM_4852	contig05265	AG	2	12	CTCGTTGCGATCTCACAATGTTCA	63.078	GCGaAATCaAAGAGGAGCaCAA	63.796	127
HM_4853	contig42411	CT	2	12	CTCTCATCATCAGCAACAAGCAGT	63.071	GtTGAAGAAGAGGAGAGTGAACCAA	62.997	136
HM_4854	contig43572	TC	2	14	CTCTCCACAAAGAAAGGCTGTA	63.015	TGGATTTTGAGCAGGCTAGTTAG	62.839	135
HM_4855	contig42163	CT	2	12	CTCTCCCTCTCCCTCTCTCC	63.021	GAATGGGAATTCAGAGCAGTGA	63.42	106
HM_4856	contig06681	TC	2	12	CTCTCCTCCACAGTCAGTCAACA	63.027	TGATCAGAAACAGCAATGTCAACC	63.494	151
HM_4857	contig04752	CT	2	12	ctctctctctgctcccaacatc	62.046	CTgagaGCAAGTGACTgagtagcg	62.972	95
HM_4858	contig15850	AC	2	12	CTCTCTCGGTGACGCTCTCTCT	62.883	GAAAAGAGGAAAAATGGGGTGAC	63.172	124
HM_4859	contig03932	TC	2	30	CTCTCTTCAaCtTCGTCTCCATCC	62.782	CaAAATTTCTgGTTCTCTCTgG	62.383	119
HM_4860	contig49605	AG	2	12	CTCTGAAGTCTCGGTGTGTCACT	62.7	GGCATGTGGAACTACTCTGGATA	63.544	113
HM_4861	contig15208	TC	2	14	CTCtGTCTGAAAAAGaGcTCTCA	62.397	AGTCCAAATcAGAAAATGCAGCTC	63.039	145
HM_4862	contig12984	CT	2	20	CTCTCTTCCAAACCAAAACCAT	62.67	AAATTCaAGTGAAGAcGTGCAGAcAg	62.635	115
HM_4863	contig45715	TC	2	12	CTCTTTCTCTCTTACCCGAAGCC	62.992	TTTCGATCTGCTACAACCTCTTCG	62.026	138
HM_4864	contig33962	GA	2	16	CTGAAGACACCATGATTGCACTG	62.947	aAAATGTAACTCTCGGTTCTCACCG	62.619	145
HM_4865	contig34712	AG	2	14	CTGACAGAGGATACACAGCATTC	62.275	GTAATTGcGTGTATGTAGTGTGCC	62.757	157
HM_4866	contig06747	GA	2	20	CTGAGATGGGAAGCATCAGACATA	62.7	ATCTCTaCTCTCTGtGCCAT	61.782	90
HM_4867	contig04152	TC	2	20	CTGAGCTCCCTTGAAGTTTCCA	63.006	GTGGTCGCTTTTGAGCTGATTCT	63.06	140
HM_4868	contig37557	AG	2	12	CTGAGGGTGTGATGAGATCTTG	62.413	tcaattccctCTCATTTATCTCTCAA	62.527	160
HM_4869	contig23164	AG	2	14	CTGAGGTTTGTGAGTGGTTTCCGA	62.905	CcATCCCTATCacCCTCTCTCT	63.059	88
HM_4870	contig11764	AG	2	12	CTGATGTCACGCGTAAAGTTGTG	62.839	ACGTGTTTCCGAAATCTCTGTAc	63.027	125
HM_4871	contig01970	TC	2	14	cTgaTtTcTGATtTtTCTCTCC	63.459	CCCaCATCATGATCAAACTTTCAA	63.128	150
HM_4872	contig18545	AG	2	14	CTGCAATAGAGGAGGAGATTTAGG	62.702	ACTCaACAAAATCACCACAAACCC	63.338	116
HM_4873	contig15931	CT	2	16	CTGCATATAAaCAAGGTGACGAGC	62.269	tcCCGGGTTTAAaAGTTGtATTG	63.118	136
HM_4874	contig46599	GA	2	12	CTGCATCGAATGAATGAGAAGAGA	62.924	GGATCACAGGTTATGGCTCCTC	62.101	142
HM_4875	contig06678	TC	2	16	CTGCATCGCTAGAGAAGGGAATTA	63.03	TATACCaTAAaCTCCCAAGTccc	63.266	125
HM_4876	contig45104	AC	2	16	cTGCCACAAACAAATTTGAAa	62.067	TATaTATGCTGGGTTTGGTGGGT	62.533	160
HM_4877	contig19803	GT	2	16	cTGccTCTTTTtAGCaTACGATT	62.877	GAGcAlCTtTcCaCCaATTACG	63.009	113
HM_4878	contig27015	AG	2	16	CTGCTAAACTTTCATTCCCACTG	61.314	GGAATTAGTACTGCTGCCITTTTG	60.507	143
HM_4879	contig04824	GA	2	16	CTGCTCATGATGACATGACTGTGA	63.559	ATaACCAcACTTATTGCCAGTT	62.936	132
HM_4880	contig05368	TC	2	20	CTGCTGGAACATAATTTCTGTGCTG	62.44	ACCcATCACTTGGTCATCTCaTa	62.58	154
HM_4881	contig12095	GA	2	12	CTGCTTTAACCAAGTGACGAGAGGT	63.146	TTGAAGATAGCTCTTAGCGCGAGT	62.972	148
HM_4882	contig04248	AG	2	12	CTGCTTTTCTGTGTGTTCTCTT	62.931	CTCTCCCGCTCTCCCTCT	63.628	88
HM_4883	contig04869	TA	2	16	CTGGAAGATGGGTGTGCTTAAC	63.129	tcagaagatcTAATCAGGAAGCC	63.013	88
HM_4884	contig50576	AG	2	12	CTGGAgaGAATGGGATTAGGGATT	62.853	CTTCTCTCaaACATcCCACtCAG	63.527	94
HM_4885	contig28973	TC	2	14	CTGGAGAGAGCGCATTTGTATgaC	63.444	GtaAGGGAGaAGGAGcGTTTGA	63.955	158
HM_4886	contig14172	TA	2	14	CTGGGCATATTATAGCGGAAAAACA	63.234	cCTCAGTATTTTCTCTCATGCACA	62.514	145
HM_4887	contig02323	AG	2	14	CTGGGTCTCTCTCGTTTTCATCT	62.597	CTACGATTTTcCaAAcCaAGTCCAG	63.113	104
HM_4888	contig10106	AG	2	16	CTGTCCTcATAGCCTTaGtTgC	62.536	GTTTCTGTCCATACGCTCATTTC	63.137	159
HM_4889	contig22158	AG	2	16	CTGTGACAAAAAGAACCGCAAGAC	62.531	tTTGCGTTTgGTTTgTgTACTACTA	62.662	138
HM_4890	contig05603	TA	2	14	CTGTGCAATCACCTCAATTGTTTC	62.948	TTCAATgGGGAGAGGTCACTaAAA	63.091	148
HM_4891	contig29305	AG	2	12	CTGTGGTTGATGATGACGAAGAAG	63.146	TCTTGAAACCTCaAAcAAGCATCa	63.15	148
HM_4892	contig05230	AC	2	14	CTGTGTCCACAATTCAAAGCATTC	62.948	ATCAGAGATTCCCAATTGAAGAaC	62.916	155
HM_4893	contig02733	TC	2	12	CTGTCAAGGGTTCTTCCAATCTG	63.308	CCCCAATTCATATCTTACACCA	63.194	105
HM_4894	contig35715	CT	2	12	CTTAGAACGCCCTAGCATcACATT	62.851	GTATGATTGgTgTGATTGGGGT	63.013	106
HM_4895	contig02028	CT	2	20	CTTAGACTTTCGCCCAATTTTAGG	63.28	AGGGTTTCCaAAAACGATTGAGa	62.823	154
HM_4896	contig25913	TC	2	16	CTTATCAGTAATCGTCTGCGAAGC	61.552	CcTtTAgTAcATTTCTTCAcTACcAG	60.954	114
HM_4897	contig47672	GA	2	12	CTTcAGGGGgAGAAaTgAgTgT	62.869	CCCTTTTGTACAATTTCTTcCT	62.689	146
HM_4898	contig04068	TC	2	14	CTtCaTtCGctCATTcATTCaTg	62.935	CCAcCgtTGAAGAGaAAACaGAGa	63.732	117
HM_4899	contig07216	AT	2	16	CTTCCAAGTGTCTCTCCCAAT	61.567	ACCTCTTCCCAAGGATGATTCTCA	62.455	104
HM_4900	contig04825	GA	2	14	CTTCCACAAACAGCTGAGGCTT	63.04	tTTCTCTCTCTACATTTCTcCCCTC	62.613	150
HM_4901	contig06383	AG	2	12	CTTcATGCTTCTCTCTCACTC	63.799	ACCaACCAACCACTTCTCTCTT	63.5	155
HM_4902	contig38393	TC	2	12	CTTccGGCCATATTTTCTCTCT	62.992	AGATgGGGGATTACATGAGGAAGT	63.173	123
HM_4903	contig33574	AG	2	12	CTTCTCTCAACTCTCGGCAACAT	63.124	GCaAGATCGGTGTATGATCGtTT	63.456	147
HM_4904	contig13711	GA	2	14	CTTCGAAGTgGTgAGTATGGAAG	63.32	TCCAATCTCATCACTGTGTTTGT	62.933	148
HM_4905	contig00891	TC	2	24	CTTCGCAAGTAAATGATGAAGAGCC	63.45	TCTCTCTAGACTCTCTGCGAGGC	62.809	145
HM_4906	contig03381	TC	2	16	CTTGTCTCTCATCTCTCTCAAC	63.525	TCTCTTAcTCTCCCCCTCCATC	64.1	137
HM_4907	contig30014	AC	2	20	CTTCTCCAACATCTCTCTCTCGG	63.413	AAAATTTGGCCTTCAACACAGTCAT	63.035	107
HM_4908	contig31768	AT	2	12	CTTCTCCATCTGAAACTGTAGCGC	63.543	TGTTGCGGTTCTTAAACGAAGATT	63.146	89
HM_4909	contig32608	GA	2	20	CTTCTCTCTCTCAATGCTGTGT	63.01	TCCATCTACGATTGCTAGTGCaAA	63.072	133
HM_4910	contig49912	CT	2	20	CTTCTGATGTCTTTTAAACAGGGC	62.451	CGAaCaAGGCATagcTATATAAACTGG	62.36	140
HM_4911	contig48434	AG	2	20	CTTGAGCAAGGTCTGCTACGCT	63.5	CgCACACaGTTACACATACACTC	62.893	143
HM_4912	contig02989	TC	2	12	CTTGATCTTGAAGAGAGACCGGA	62.894	GACGTAGAAGCAGGAGTTCGAAGAA	63.022	136
HM_4913	contig49381	TC	2	20	CTTGCTTTCAGTTTCAGGCTATCT	63.142	TTGAAGACGagaaacGTATcCAGT	62.327	137
HM_4914	contig37752	CT	2	14	CTTGCTTTGTCTTACCGCTCTCAG	63.057	AATTTGGAAGACGACTCCGACAC	63.767	123
HM_4915	contig39627	TC	2	16	CTTGGATGATCTCTCAAGCTCTT	62.9	ACAGGCACTTCTCTCaGGcTT	63.897	123
HM_4916	contig00940	AG	2	24	CTTGGCTCAGACCCCCCTTTT	64.678	CATCCGtTgATGAATCTGA AAC	63.842	117
HM_4917	contig08793	AG	2	14	CTTGGTGATGCCCTGGATGTTAT	64.284	TCTCTGGATcAccCTCTCa	63.311	138
HM_4918	contig22753	AT	2	12	CTTGTAAATTTTCAAGTGAAGCAAC	63.129	AATGTCAgATGGGACTaGGAACCA	63.102	148
HM_4919	contig03221	TC	2	12	CTTGTGATCTCGGCTAATCCATCT	62.913	TAGAGAGGaTaAaCgTgGTGGGA	63.104	138
HM_4920	contig46705	GA	2	14	CTTGTTCCTCTCTCTCTCTGTGCG	62.892	AAGACGGTGaCaTcCAGACTCTCT	62.793	98
HM_4921	contig52394	AG	2	20	CTTGTGTGAAGTACAGGGAAGGG	63.216	AGACACAGCAAAATCATCAACAGC	62.757	145
HM_4922	contig00493	TC	2	14	CTTTCAGTTTCCCATGACACCTCT	62.895	ATCATGAGAATTGGAGTTGCAGG	63.643	151
HM_4923	contig14847	GA	2	20	CTTTCAGCCATTAATCAAACTGT	63.014	TTCCgACTTTCGAATCTCTCAGAT	62.698	98
HM_4924	contig04381	TC	2	12	CTTCTGTTTTCaAACTGATTGCG	63.018	GAGAGaAAACGGGAGAgTACTAgGAGAG	62.599	118
HM_4925	contig15497	GA	2	16	CTTTCGCTTTTTCAGTGAGATCAT	62.91	AACCTCaAAaCCTaACCCCaAAAG	62.7	101
HM_4926	contig36092	AG	2	14	CTTGTCTTGAAGAGATGcACACAA	62.839	AGCaAcaaAAGaAAGaTcCCATT	63.289	147
HM_4927	contig01765	CT	2	14	CTTTGTCTCGAGCTCTCGATCT	63.549	GGCAACTGCAAGTAAAGTTGTAGc	63.187	156
HM_4928	contig04768	TC	2	12	CTTtGTGtTGCCCTCCACAC	63.036	CTTCTGATCAACCGACACTCAGA	62.919	159
HM_4929	contig19689	GA	2	16	CTTTTCTGAAAGGGGATGGTTTT	62.781	CTGTTTTCATTAACCTGCTATTTTG	62.039	142
HM_4930	contig15203	GA	2	14	CTTTTGATCGAATGGAATTTTCGG	62.804	aagactgagctgactgattgattg	62.872	159
HM_4931	contig23831	GA	2	16	CTTTTGTCTGCTCAAGGCAAAAT	62.769	GCCAGACTCGGTAgAGATGTGGAAA	62.923	101
HM_4932	contig05640	GT	2	12	CTTTTGTGATCAACAAcggagaa	62.513	CGTGTCTTCTCTCTCTCACTGc	61.776	158
HM_4933	contig45753	TC	2	16	GAAAAAGCAAGCTCTCTGATCCG	63.348	CTGCGAATTTCTTCTGAGGAGAG	62.907	96
HM_4934	contig00436	TC	2	12	GAAAAAGTAGGCTAGTCCGAAGCT	62.543	CACATCTGCAAAAGTATCAAACTGG	61.927	97
HM_4935	contig24200	CT	2	14	GAAAATGAGGACCTGAGGAGAAc	63.313	GCACACgGTCTCTTCTCTCTCTC	62.925	100
HM_4936	contig09667	AG	2	12	GAAAGCATATACCTGGTGAGGAAACA	62.947	CAACCTAATGGCTTCAGATATGG	62.909	152
HM_4937	contig15542	CT	2	16	GAAAGCGATGAAGTGAAGAGGTA	63.022	aagtccaacaaactgagggg	63.452	142
HM_4938	contig41296	GA	2	16	GAAAGGAaCAGGACCTaGGGTGAT	62.974	GAACTGTCTACGATCTGaAAaTtGAT	63.026	144
HM_4939	contig00685	AG	2	12	GAAAGTACTGTTTCCAGCGATGT	63.06	ACAACCTACACATACCAGCACCT	63.05	123
HM_4940	contig25887	TC	2	12	GAAATGGAAGCTTCTAGGGTTTGGT	62.995	CACCAATTTCTCACCTTAGACTCC	62.368	147

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_4941	contig34800	AC	2	16	GAaATGTCGAGACAGCAAACCTCa	62.844	GGAGGTTGCGAGATAGGAGTGAA	63.115	105
HM_4942	contig16646	TC	2	12	GAACAAATGAATCCATGACCCCTC	62.889	TATTGCGGAGAGGGATAGATTGAG	62.802	127
HM_4943	contig04471	AT	2	14	GAACAGTGAGCTGATGATCGGAAGT	61.809	TCCCTCTCtGtATTCACAAAGT	62.469	143
HM_4944	contig02688	TG	2	12	GaACATGCTTGGACAATCTCTTCA	62.714	AGGAGCAGGTCTTATACCTGGTCTCT	62.914	80
HM_4945	contig32382	AG	2	14	GAACCAAAATTTGAAGAGCGTAA	62.639	GAAGAAAGAACGAAGAGGAAAAGG	62.044	159
HM_4946	contig22066	TG	2	20	GAACCCGGATGTCAAAATTCGAATA	63.105	ATCTGTCTGATGTTGTTCTGGGTT	63.014	143
HM_4947	contig09483	GA	2	12	GAACGGGTGAGTAATCAAGCAAC	63.146	atTTCTACCTCCAGTGACCTCTCC	63.193	151
HM_4948	contig16876	TA	2	16	GaACTCTCAAAAAGCTGGAGTgC	62.838	GGGTTTGTGATGGAGAAGTCTGTT	62.795	152
HM_4949	contig29053	GA	2	16	GAACCTGAGAAGGGGGTTGAACCT	63.08	gGaAaCtATCTGaACCAATCaAtc	62.889	103
HM_4950	contig08820	GA	2	14	GAACCTCGAAACCCATGCCCTAA	63.001	TTATACCGAACATTgACCaATccC	63.009	113
HM_4951	contig34101	AG	2	24	GAACCTGAGCTCCATGATCTGGTT	63.017	AaCCTTGAATGAATccCCAATC	63.365	138
HM_4952	contig24642	TA	2	12	GAAGAAATCACGAACGAACCTCA	60.637	TTGCTGTATTTCATGCTGTTGTGATG	60.572	160
HM_4953	contig16651	AG	2	16	GAAgAAATCACTCAACACAAAACA	62.67	GAAGCAATTGTTGAAAAGAGGAGA	63.009	127
HM_4954	contig46200	TC	2	16	GAAGAAGCAAAATTTCTCCAC	62.411	CCTcCCCTCTCTCACTCAcCTAT	63.273	97
HM_4955	contig36423	AG	2	14	GAAGAAGCATTTTCCCTCTGA	63.009	TCTCTACACTCAITTCaAgACCaACCAC	62.278	95
HM_4956	contig04679	AG	2	16	GAAGAAGGTTCCAAGGGTTGAAT	62.876	TCCaAAATCTCATTgGCCTACaT	62.912	90
HM_4957	contig00163	AG	2	16	GAAGAGTGGTTGTAGACTGCCAT	63.04	TCTTCTTTCCtctccCATTCtCt	62.948	122
HM_4958	contig22425	TC	2	14	GaAGATaACATCTCtCtTgTGCa	62.9	AgCAACACtACCAAGTCTCtCt	62.639	80
HM_4959	contig30688	GA	2	12	gAAGCAACACACtGcCAAAATAG	62.156	GAAGAGAAgACaAGCagATTGaGac	61.221	87
HM_4960	contig23915	AG	2	20	GAAGCAACATTTCTCTGGTCTCT	62.1	tTACCACCACTCTGCAACTGAAC	62.635	97
HM_4961	contig52320	TG	2	14	GAAGCCTCTCCACCAACTACTCA	63.124	CAGAAGAAAGACAGCAAGAAgagg	63.007	153
HM_4962	contig31176	AG	2	20	GAAGGAAGCTTAGCTCCGGTATTC	62.822	TAAGAACACGACAGACgGagGg	63.69	157
HM_4963	contig40840	GA	2	14	GAAGGAGATAAaGTGAACCAATCA	62.808	TGTGAACCGCATGTACAAGCaAc	63.518	156
HM_4964	contig24694	AG	2	14	gAAGATTCTGAGTTGTTGGGA	62.784	ACTCTCCTCtGtCCACtCTCCTC	63.297	116
HM_4965	contig33811	AT	2	12	GAAGGGTAGTGTGGGAGTTGATT	63.482	CTTAATGATGATCGGAAGAGTCGG	63.206	135
HM_4966	contig37432	AT	2	12	GAAGGTGTGccATTGTTTAAATCC	62.848	gcCATTGcAGATCATGtaaAAGGT	63.456	157
HM_4967	contig29268	CT	2	20	GAAGGTTGATGATGGAGGAGATGG	62.876	TTTTTAggGGTTTTTcGGTcAttT	62.897	147
HM_4968	contig35157	AC	2	12	GAAGTCATAAATTTGATGAGCAC	62.211	TCATGtctaAGGTcatGTctctCtC	62.9	109
HM_4969	contig23104	GA	2	12	GAAGTCATGAAGACTCTGTGCGT	63.123	CTCTCTCCTTTCTCTCCACCA	63.285	124
HM_4970	contig06484	TC	2	12	GAAGTCGATTCCAAGTAGCTGGTC	62.613	CTAtTAACtCtCtTaAGCGTGGcG	62.397	146
HM_4971	contig38692	GA	2	20	GaAGTGGGTTgTGGAGTGAAGAT	62.795	CAGCTCTTGCAAGCTGGTTCTTATAC	62.78	93
HM_4972	contig19058	CT	2	12	GAAGTGGTTTGAACCTGAGTCCAC	63.34	CCCCTagTcaATTcAGGTTGTTGA	62.714	107
HM_4973	contig08424	GA	2	14	gAaGTTGATGAGACCGAGAGTGT	63.241	ACCAACCaCaAAACCaAATTCAA	63.523	140
HM_4974	contig04510	CT	2	24	GAAGTTGCAGAGAAATGAAGGGAA	63.009	AAACCaGACaACCAACtCcAGg	63.638	128
HM_4975	contig42035	CT	2	20	GaATCACTATTGCGAGGATTGCC	62.484	TGGAAAATTATGaTGGAGGTTGtG	63.111	133
HM_4976	contig33620	CA	2	16	GaATCATCaAATTAAACCaGAAATCA	62.46	tGTGTTCTGATCTGGGTTTGATGA	62.907	144
HM_4977	contig48334	TC	2	14	GAATCCTTCACTCCACATGCTACC	63.016	TATAGGCACACAACTGTTCCGACG	63.398	141
HM_4978	contig03042	AT	2	16	GAATCGAACACCTCTCTCTCTCA	63.102	GCTGGTtCTGTgCTTTCTTTCT	62.341	143
HM_4979	contig04871	AG	2	16	GAATCGCCGAGATACACAGATAG	63.236	TaGtCCgTAgTCTCAACGTTTTCT	62.645	147
HM_4980	contig20546	AC	2	12	GaATCTctCtGtGGTCTgTGCTA	63.071	GGTGTTTGAAAAAGTTctGCTGCT	63.057	122
HM_4981	contig41337	CT	2	14	GAATGAGAAAGTGACCTTGCCTTG	64.299	ATACCAATcCCCAAACTCAACATA	64.261	159
HM_4982	contig13629	AG	2	12	GaATGCAATTtGgATGAAGGTAg	62.912	ACTcTtCTCTGTCTCAITCacGg	63.223	124
HM_4983	contig32723	GA	2	16	GaATTAGGGCTTGATGAACCTGT	60.707	tTagCTGCAGcCGCaTATAct	60.041	88
HM_4984	contig11667	AG	2	20	GAATTCAAAGCTTCTCGGGTCTT	63.196	TCCTCAACAGaaAGAACCTTtCC	63.984	160
HM_4985	contig21335	AG	2	12	GAATTGACTCCGAGGTGAGGGGTT	63.084	CTTCTCTTCAACCAATTCaCCAA	62.592	156
HM_4986	contig48263	GT	2	24	gAATTGAGGAGTGAAGAGGAGAT	63.062	AAtaGGGTgGaAAtaGACGaCCG	63.481	114
HM_4987	contig41216	CT	2	16	GAATTTGAAGGTGGAGAGATGG	62.987	CaACCaAAACCaAcGaACaCtGa	63.164	152
HM_4988	contig01490	AG	2	16	GAATTTGTCTGCGATCTCCAAGTA	61.787	AAACTTACTCGAAAGACGCTCTCC	61.539	108
HM_4989	contig09444	CT	2	12	GACAAAACATCATCCCCAACAC	63.643	TAAACAAAACGGACTTTTATGCGG	63.237	134
HM_4990	contig19999	TC	2	14	GACAAAATTGAAGGTTATCCGGTG	62.813	catcaaaaCCAATcCTGAAAAGAGaG	61.856	155
HM_4991	contig37904	AG	2	12	GACAAATCGAGAGCACTCTGACAA	63.057	CCTCCACtTcAtCtGtCTCtCa	63.321	134
HM_4992	contig39640	TC	2	12	GACCAACATTCGCTCAAGAGAA	62.784	aCGGTACgTCTAGGGGGAATAAGa	63.192	106
HM_4993	contig03756	GA	2	16	GACAATGGAAATTAATGGCCAAAG	63.213	TATAAACGAAAGACTGACCTCCG	62.839	111
HM_4994	contig19520	TA	2	12	GACACGACACGAATACGATGAGaC	63.075	TAGTGCATTaAGaTCTtTCCCG	62.823	154
HM_4995	contig29287	TA	2	14	GACAGAAGAGGGGcAACGTATTTA	62.729	GattatCCgATCCCtCCTAGTCA	62.468	122
HM_4996	contig36391	AG	2	16	GACATGtCccTCTCtTCTGTa	62.884	ATCGAAGATCTGGTTCTGGTCTGT	63	145
HM_4997	contig43672	AG	2	12	GACCACATGAGATGGACAGAAATG	62.911	CTGTCAAGCATCTCAGATTCAACa	62.843	80
HM_4998	contig40325	GA	2	12	GACCAGCTAGTGTGGTGTGTTGT	63.077	CgTATCAATCGATCAAAAGGCT	62.607	160
HM_4999	contig20632	TC	2	16	GACCATGCGATTGTGATGTGAG	62.951	TAggaTTCCCTACCTcCCTACCA	62.767	144
HM_5000	contig23453	AT	2	14	GACCATGAACCATATAACCAAGC	62.72	AAGATCaATGAGctGATGTGAATGA	62.188	88
HM_5001	contig08642	TC	2	16	GACCCCAAACTTTTTCACATAGT	63.115	GTTGAGAGAGGACAGGAATGAAGC	62.798	111
HM_5002	contig13541	CT	2	24	GACCTCTCTTCTGCGGTTCTC	62.9	TATCCTATAACaACCTTAgcCGC	62.559	103
HM_5003	contig21135	TC	2	12	GACGACCATAAGGAAGTACACCC	63.027	GGTTTGATGaAGATTCTTATGCGG	63.021	85
HM_5004	contig22810	CT	2	12	gACgACCTtCtCtGCTTCAACAC	62.599	TCTCTATCCTcGACTCGTCACTCA	62.692	154
HM_5005	contig41862	GA	2	14	GACGAGCTGTCAaGTTGTGTTGT	62.869	GAATAGAGGATGTGGTGAGAGacc	62.25	144
HM_5006	contig23995	AG	2	16	GACGATGCTTCGCTCAACATCTA	63.835	ATTCCAATCATTGCACTCTGTT	63.026	112
HM_5007	contig26491	GA	2	16	GACGATGGGTTCTTGGAAGTTATG	63.009	GTTCCGATTGAAGGTTTaCAAAAT	62.451	130
HM_5008	contig36701	AG	2	20	GACGATGTTGTTGTAGCTGAATGC	63.095	TCAAACACAGATTCaCAtctctctc	63.027	140
HM_5009	contig15323	AC	2	12	GACGCACTTgaGtcttTCCAAC	63.15	TGGTGGTGACTCTCAGGTCTGTGA	63.259	138
HM_5010	contig10040	TC	2	20	GACGCCATTAAAGTCAAAACGTAG	63.051	CTCAACAGAAACGAGGAGGAAGA	63.208	144
HM_5011	contig00029	TC	2	14	GACGCTATAGATGCGGAAGTGTt	62.867	GAAAAAgCCTCTCAACTcCAACACT	62.661	101
HM_5012	contig25159	CT	2	12	GACGGAGATGAAGCTCTAGTtGC	62.84	TTGTATTAAACaCcaCAACaCAGC	63.134	146
HM_5013	contig28009	CT	2	16	GACTCAAAACCTCTCTCACTTCT	63.285	AATGGGTTTTTGAAGGTAGTGGTT	62.992	143
HM_5014	contig12418	TC	2	24	gaCTCACTACCACTCGTAAAGCCAA	62.958	AAACAAAGACTACGAAGCATAAACCC	62.043	131
HM_5015	contig24807	AG	2	20	GACTCCATAGTGTGGTTTTCCGAG	63.225	GTTTGGGTGGGTGGACTTATTTCT	63.783	150
HM_5016	contig14130	AG	2	16	GACTTCAATTGTCTCCCTTTCTCT	63.181	CGTGGTTGtTACTTTCAITTCACGA	62.875	107
HM_5017	contig17396	GA	2	14	GACTTGATCTGCACTCTCCATT	63.017	TCTCATTCGcAGAAATCCC	63.426	126
HM_5018	contig09914	AG	2	30	GACTTTGAGTTTGTCTGCCATTTT	62.851	CTCTCTCTGTTAcGtACCTCTCa	63.12	92
HM_5019	contig27633	AT	2	14	GACTTTTCAACACAGACCTAAAGTT	61.34	GGTTTGCTAGTAAGGTGCAAGT	62.247	159
HM_5020	contig21513	CT	2	16	GAGAAGGAATAGCTTGTGAGCGAG	62.936	CTACAAAGAAAGTGCAGAACGAGc	63.568	143
HM_5021	contig31285	AG	2	16	GAGAAGTCGAGTCTGTgAGAGGAC	62.888	GAGCTGTGAACAGCCTTGAAGCT	63.036	114
HM_5022	contig49022	CT	2	20	GAGAAGTTGGAGTGAGAGTGAGC	63.018	CCAATACAGATTGGCCTTAATTCG	62.827	158
HM_5023	contig23565	CT	2	14	GAGAATGTTTGATTTCCCAACacc	62.9	GGATCTGaAATTTTGTGCGATAGG	63.021	148
HM_5024	contig43341	AG	2	20	GAGACGATGATGAAGAACGAGCTC	63.905	CACCTCTGACTCTCTGtCACTCT	63.573	123
HM_5025	contig28039	TC	2	24	gAGACGTTGGATTCTCTTCTCCA	63.102	ACGGGGAAAAAGGGAATGACTCTT	63.275	105
HM_5026	contig31487	GA	2	16	GAGACTGAGAATCTGAGAGAGCGG	63.995	gCGCAATTCTTTTCACTCTCACAT	63.133	87
HM_5027	contig33077	GA	2	24	GAGAGAAGTCGCCATTAGCTCTG	62.936	TGCTTTGGCATATGAATTAATGA	62.549	110
HM_5028	contig04317	CT	2	16	GAGAGAGCTGAGATGgGATGAG	60.751	GTtGtGcGAGTgtGAGAGtGA	60.088	95
HM_5029	contig05876	GA	2	24	GAGAGAGGTGGTTTGTGACTTGT	63.015	aAgTtCCCTcTCTCTCTGtGtCt	62.455	122
HM_5030	contig47906	CT	2	20	GAGAGATCAAAACCTCCCTAGCTG	63.302	AGtTCaATCGAGcCtGAGGAG	64.199	160
HM_5031	contig01511	TC	2	14	GAGAGCGTATTGcCTTGGAAGAG	62.824	AGGGCTAAACACCAACATCAACAG	63.554	124
HM_5032	contig15020	GA	2	14	GAGAGGAAACaCGAGACTCAACA	62.815	TCTCTCTCTATACAGTCTGCCGC	63.356	115
HM_5033	contig28259	CT	2	24	GAGAGGAGGTTGCTATTTCACACT	63.181	TCTCACACTCTTCCaccCAAAAT	63.204	138
HM_5034	contig49108	GA	2	12	GagaGgGgaTtgaGgagAaatgAT	63.053	GAGCTCTCCAAGAAATCTTCCAc	63.807	148
HM_5035	contig15490	AG	2	14	GaGAGTGAGGAGGTTGTTGGGT	63.015	CTTTCTGATTCATCAcCACCAT	63.419	127

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5036	contig20409	AG	2	12	GAGATAGGGTACCGTGAACCTCCA	62.698	GacCCCCtTtTaTCGACAGCTCT	63.084	129
HM_5037	contig06617	AG	2	16	GaGATCTATGGGAGTgaTCGAAcG	63.323	TCGAAAGCTCATGAGGATACATCTC	63.037	147
HM_5038	contig03070	TA	2	14	GAGATCTGTAGGCGCAGCAGTAGT	63.392	ATcCTGCTcCTCTCAATTAATTC	62.868	138
HM_5039	contig27030	AG	2	12	GAGATTGCTTTGCTCAAGaAaCa	63.043	TTgtcGcGATcTAATGATTAATTT	62.904	98
HM_5040	contig02074	TC	2	16	GAGATTGATTCTGTAGCGTTTGG	63.138	CgTcACGATcTCaTAaaaaAa	62.677	136
HM_5041	contig22784	AG	2	16	GAGATTGATTTTTTGAGGCCATAG	62.203	CgAAAtacCACTaTcCaAAACACAC	62.087	80
HM_5042	contig49494	GA	2	20	GAGCCGTTGTCCATTTTAACAGC	63.146	ACGTATCACCATCATCAGATCCCT	63.007	149
HM_5043	contig38690	AG	2	14	GAGCTAGGCGGATCCAGTTTTTA	63.635	AcCAcTTCACCAAcCcaAAcTtTa	62.918	157
HM_5044	contig30809	CT	2	12	GAGCTCAGTCATGATGTCTACCGA	62.94	CCtTCTTCATCCAaCaAACCAAG	63.1	113
HM_5045	contig04419	TC	2	16	GAGCTCTCACTCTTGAGTTCCGAC	63.137	GaAACCACTGACTGTGAGGAGGAT	63.005	155
HM_5046	contig49405	AG	2	24	GAGCTTAGCAGCAGAGTCTTTGG	63.057	CClTTTTGCTGATTTTGTCTGTCT	62.944	131
HM_5047	contig34118	CT	2	20	GaGCTTATCCAGTcCaAGGGC	61.169	ATTGGAGATTTGAGAGATGGAAGG	61.937	101
HM_5048	contig01593	TC	2	12	GAGCTTCTTCAGACTGCAAGCTCT	62.604	GGGGAAGTGGtATGAGaAAGAGA	62.982	145
HM_5049	contig15149	AG	2	14	GAGGAACGACAGAGGAGACAAAG	62.909	cTcTgtGTGTAGTAGTTGGCCTGA	61.916	95
HM_5050	contig06733	TA	2	16	GAGGAACCTAGCAATCGGTTCAC	63.356	CTCTCACTGTCTTCAATTGGGTGT	62.921	157
HM_5051	contig00465	GA	2	14	GAGGACCTCTGAAGGCATCG	63.232	aACACAGACATaAAACCAGGCC	63.441	110
HM_5052	contig36494	AG	2	14	GaGGAGATTTCTTTTCTTTGGA	63.053	GaTTCCTTTGATTTCTTcGTTTTG	63.185	104
HM_5053	contig19383	TC	2	24	GAGGATCCGAATAGAACGAACCTGA	62.9	TTTaaAAGTGTGTGCGGTTGT	62.812	95
HM_5054	contig41476	GA	2	16	GAGGATGAACGAAGATCTGAGAGC	62.715	AACaAAGtACTGaCAGaGcGcG	62.015	135
HM_5055	contig39781	CT	2	24	GAGGGAATAGAGTGGGAGGAAGG	62.85	gtAGGGGTacggttaggtacgTT	62.341	95
HM_5056	contig42021	AG	2	12	GAGGGAGTACCGGAATCGTAGTT	62.901	CTGCACCTGTTATTCTCATCATCG	63.051	134
HM_5057	contig43044	AG	2	12	GAGGGCATTGGATGTAGTCTCTGT	62.915	TAAGCACCaaAaTcCCAaCTcT	63.129	154
HM_5058	contig37146	AC	2	14	GAGGTTTCAAGCTCCCTCAAGAT	62.999	ATGGAAATTTTCACAGAAATAAGCG	62.533	144
HM_5059	contig13584	AG	2	14	GAGGTTGGATATGAAGGTTTgGa	62.468	TCTATcTTTcTATGtAAACCCCAACA	61.568	138
HM_5060	contig48132	TC	2	16	GAGTACCTGTGGCTCCCACTCA	62.811	gCGTACGTACTCAcACTCTAGAGCG	63.012	126
HM_5061	contig46255	AG	2	12	GAGTCCGAAGAGAGAAGCAGAAA	62.598	GCAGCtGAACAGATAGAAGTGAGG	61.773	153
HM_5062	contig15447	GA	2	20	GAGTCGTCGGTTTGGAGAGAAGAG	62.909	TAGTTCATTGGGAATTCACCTGG	63.3	132
HM_5063	contig34529	CT	2	12	gAGTGAACGAAGaATGATGGGAT	62.89	gGGAGATACATATTGAGAGAgGGGA	62.867	84
HM_5064	contig07161	AG	2	14	GAGTGCCAATCAATTAGGGTTTCA	63.426	ACaAAACAGACCCATCCCTTAAC	63.488	153
HM_5065	contig19599	AG	2	12	GAGTGGAGTAAAGAGGGAAGGAGG	63.91	CgGaATTCCaATTgTGTCCATCTA	64.139	156
HM_5066	contig31687	AG	2	14	GAGTGACACCCCAAGATTTA	63.243	CGTAGATAGGGATGGCTGTAGTG	63.129	119
HM_5067	contig00843	CT	2	14	GAGTTCGAGTGGCAATTTTGtAA	62.311	aTAGCAGCAAAAGCaCAAGGCT	62.672	117
HM_5068	contig46080	CT	2	14	GAGTGGGTCTTTTGTCTCTCca	62.997	ATTGTCTCTCTCCCTCTTcCAC	63.278	159
HM_5069	contig32458	AG	2	14	GATAACAGGAGGAAGCGAGAAACA	63.022	CTGCTTGCTGCTTCTCaTcaac	63.619	123
HM_5070	contig48115	TC	2	16	GATAGCATCTATAGGCGATGCTCG	63.146	CTCCGATCAATGCAGAGATCATATT	62.721	133
HM_5071	contig30658	CT	2	20	GATAGTTTTCCGAATTTGTCTGCG	63.03	gAGaAAGAGcGctaatacCACCG	63.447	148
HM_5072	contig12881	AG	2	20	GATCAATCGAACtCATCACAAACA	63.368	GCGTTTCACTGATACCTCGACTGT	63.91	93
HM_5073	contig30798	TC	2	32	GATCATCTTCGCCTTCACTTTGAT	62.916	gGagGaTGATGAGaAAAGaTAGGG	63.356	154
HM_5074	contig27535	GT	2	12	GATCgCTGTGTGAGAGTTGAAAAG	62.517	TCtGTCTCTTTTaTCCCTCTCTCT	61.715	127
HM_5075	contig33563	AG	2	12	GATCGGCTCAATGTGCGaTAACAC	62.942	GCCAACTAATTTGATTTTCGTCA	63.433	160
HM_5076	contig27706	GA	2	12	GATCTGATCACAGAGCTGTCTGG	62.585	GCAAAggggcCTAAaATcTCTCT	62.169	150
HM_5077	contig04754	AT	2	12	GATCTGTGATAACCTACACACTTCT	61.01	ATCTACGCTTGTCTGACTAATGA	61.436	143
HM_5078	contig18733	AG	2	16	GATGAAAAaGtaGCAAGATGGCA	61.735	CCAGGGAACCTAACCTCTCTCTAC	62.575	90
HM_5079	contig22952	TG	2	16	GATGAAAAAGGTCATTTGTTGGC	63.125	aAAGGaaAAATCTAgCCtGcATC	63.007	115
HM_5080	contig39765	TG	2	20	GATGAGGCGATGGTGTAGCTTAGT	62.953	GATCTTCTCATcCCCTAACCTCA	62.853	144
HM_5081	contig10626	TG	2	16	GATGAGTTTGTATGACGGCTTTTG	62.872	CCTAACTCTCTAGTGTGACGCCG	63.56	119
HM_5082	contig24203	GA	2	16	GATGCAAAACATCTTGTCCACAGAC	63.061	TTTAATCACCGATAGCTTGTGACG	62.566	138
HM_5083	contig32229	CT	2	16	GATGGAGTGAGCAGTTGTCTTGA	62.937	ATCCGTGGTATCAATCAATCCTG	63.211	107
HM_5084	contig17299	TC	2	12	GATGGCCAAAATTGAACAGAGAC	63.125	GCAGAGCAGCGTGAGTAGTACTAGAG	62.314	92
HM_5085	contig32614	AG	2	14	GATGGCTGAGATGCAACACTCTT	63.017	AACCACTCCGACGAAGGCTC	63.945	123
HM_5086	contig01458	AT	2	16	GATGCTCTCCATTGCAAAACaAG	63.954	ATcCCCACTcCCCTTCTATCAC	62.964	123
HM_5087	contig29605	TC	2	14	GATGTTTTGATTTTGCACAAATGCC	62.915	GAAAGGATTTCTgaCAGGGAACac	63.309	129
HM_5088	contig16893	TA	2	16	GATTATGTGCTCCAAACTATGCG	62.94	GAAGctTTTGACTAGCGCTCACAC	63.803	124
HM_5089	contig05268	CT	2	24	GATTCCTCTCTgTATCTCaGcCc	62.637	ACATTACCGCGCAAGTTCATTTT	62.936	108
HM_5090	contig18979	TA	2	14	GATTCTGGCACTGTGCACTATGTT	62.652	AATgGaAAGAAATgGACCaACTTCA	62.996	151
HM_5091	contig48410	GA	2	20	GATTCTTGATATCCGAAGCCTGA	62.804	TCCaTAAATTTATCTCacTTATCCCTg	62.65	139
HM_5092	contig12836	AT	2	16	GATTGATCAAGAAGCTGGTTTgGc	63.125	CGATTCTcTCAAAACCATaCAAGC	62.356	157
HM_5093	contig13518	TA	2	16	GATTGTCATGACGATAGAACACAT	63.306	TTCCTCAACAGGTTTGTcATCTC	62.692	127
HM_5094	contig23420	GA	2	12	GATTGGATGGTGGTGATGATGA	62.902	CAACCCAAGAAATTCATAACCCA	63.097	150
HM_5095	contig29008	AG	2	16	GATTTCGAaCAAAAaTGCACATCA	62.258	TGTGTATGCAACTATgtCTCTGAAGC	61.869	131
HM_5096	contig33172	CT	2	20	GATTTCTAGAGTTTGGTTCCTGCG	62.522	GTCGACTGCAACAATCAITTTGTGT	63.414	116
HM_5097	contig15880	AG	2	12	GATTTGGGAAGTACAGTTACTCGG	63.009	TTTTGTCTATGAGcACCCCTaA	63.014	152
HM_5098	contig07071	CT	2	20	GcAAAGATGAAGAGATGTGcTGTG	63.181	CCATGTTTTACCaATCTcCCCA	63.002	114
HM_5099	contig07520	TC	2	20	GCAAAATACACACCTTTCAACAC	62.755	GAAAGTcCCACCGaAGTGAAGTAA	62.798	140
HM_5100	contig13826	AT	2	12	GCAAAATCGCAACTCTCTACCAA	63.754	TGTTGCTgGGTTTGTGTCTTCTA	63.057	152
HM_5101	contig42059	TC	2	12	GCAACGAGAAGAAGCCACATTAGT	63.06	AACTCacaGACGCTGAGACAC	64.002	153
HM_5102	contig20908	TC	2	24	GCAACTTCACTCTTCTCCAGTTGT	63.036	ATTCAACAATCAGTTGTGCTTCTCC	62.813	106
HM_5103	contig05170	TA	2	12	GCAAGATTATCTAAaAGGCCCA	63.589	CAATCACTCGTTCAGAGGATAA	62.629	132
HM_5104	contig49067	CT	2	14	GcAagCCTACCTCCGCTTCA	63.834	CCAATCaCCATCTTCTTTGAACC	62.996	134
HM_5105	contig21909	TC	2	12	GCAATAACACTGCAATCTGAGACG	63.194	TgGaAAGTGGAACATCACTCTTTG	62.592	154
HM_5106	contig14701	AT	2	12	GCAATAAGTGCAGCAAGTTTCA	63.175	CTGTGATCCATGTAAAGTGGATGT	62.503	159
HM_5107	contig41854	GA	2	14	GCAATCTCCTTGGTACTCATTCG	63.231	ATGAATCAACCAACCAATCGAAAC	63.223	148
HM_5108	contig42966	CT	2	16	GCAATGATGAATCGACATGAGAG	63.046	ACAACAATCCAAACaTCAGCAAG	62.426	95
HM_5109	contig13795	AG	2	16	GCACACAATCAATTTTCGAATTTG	63.237	TTGTTGTCTCTCCaAACTTCTC	62.907	143
HM_5110	contig42776	AG	2	12	GCACATGAACCTCTCATCTCTCT	63.017	cCTTCAAACTATCTCCCTATGTTCA	62.605	123
HM_5111	contig14897	GA	2	16	GCACATTGAAGTGAAGCATCAC	62.979	GCGAAATCTGTCTGTCTGTGTCT	62.615	157
HM_5112	contig28590	TA	2	12	GCACAGTCCAGAGAAAATCAGa	62.91	ATTCCaCTTTTCThGGTGGATT	63.069	119
HM_5113	contig50074	AG	2	12	GCACCTGTGAACCTCAGATCTACA	63.747	AGAGATCGGAAAACATGATTCGAG	62.9	112
HM_5114	contig17960	TA	2	16	GCAGAAAACAGACATGACAGAAA	62.726	TCAGAACTTTAAATTTGAATCTGATGC	61.975	147
HM_5115	contig29746	GA	2	16	GCAGAAATAGCTCATTGTGGAGC	63.468	TTGGTCAAAITCTGGAACCTGGT	62.907	91
HM_5116	contig32174	TC	2	16	GCAGAGTGCATcATcTGTgtGAG	62.651	AACTGCACAGTTTGAgtTTTGTG	62.78	92
HM_5117	contig37819	AC	2	12	GCAGATAAATAGCCCTAGAAACCCC	62.436	cCTTTTCTAATTCGGTAGAGAGAAGc	62.227	146
HM_5118	contig27753	TC	2	14	GCAGATTCAAATCTCATGAGCAAA	62.735	TTAGaAgCTGGTGATGTaAATTggG	62.545	96
HM_5119	contig24681	AG	2	16	GCAGCATCTGGATTGTGATGTGT	63.078	CTTCTACGATATCGCGTTCCTG	63.24	97
HM_5120	contig37249	GA	2	12	gCAGCCTGAAAAGTGTTCATATT	62.744	TGTTAACAGCTGCAAAATATGGG	62.273	91
HM_5121	contig02362	TC	2	20	GCAGCTCTCTTAGAGCCATTGAG	63.048	TCATCCGCTGCTAAACCCCTAC	62.617	111
HM_5122	contig26890	TC	2	12	GCAGTAATGAGCTTcGCTTATTGG	63.362	GGaAaCTCATGGtaGGTGCTAGA	62.811	158
HM_5123	contig09863	CA	2	12	gCATCACACTCTcGCTCcTtTA	64.1	AAGAGTCCGGAATTTTGAAGATA	63.456	133
HM_5124	contig04506	AG	2	16	GCATCTTTTGGAAaGAGGAAGAA	62.108	AAACCTACCAAGCAAAACCCC	62.072	80
HM_5125	contig11947	TC	2	14	GCATGAAAATGGGATCGAAaTGAAT	63.222	GaAcaACaCaTtTAgAGCtTTTgAGaa	62.233	136
HM_5126	contig34490	TC	2	32	GCATTGATAAGCCCCAGATGCAT	63.654	cCTcCTGTCTTCAgtAGGTTTGT	63.099	111
HM_5127	contig42160	TC	2	12	GCATTGCACGTTAAACCACATGTAT	63.001	TTCTCGaACGGAAGGTGaGa	63.228	134
HM_5128	contig19169	TG	2	14	GCATTGTAGAACTgaCCTGTGCC	63.242	TTTTTTGATCACTACTCTGGGGA	62.798	120
HM_5129	contig07932	GA	2	24	GCATTTCTCAGTAGGTTTCATCGCT	63.051	GGCGACACTGTTCACTACTCTTCA	62.961	100
HM_5130	contig13388	TC	2	12	gCCAaCCAAAaCCCTAACTCTCT	63.289	AGTTgaGGGGAATTCATTGATGG	63.397	151

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5131	contig33317	TA	2	20	GCCAAACTGTCTGAGAAACAAAGTCA	62.947	TTGTGCTAAAGTCAATCCGACC	63.54	109
HM_5132	contig42952	AC	2	14	gCCAAACGAGCTGGAACTAGTCTAA	62.933	CCCATCAACCTCAAACTTTTCATC	62.996	143
HM_5133	contig01481	CT	2	12	GCCAACTTCTCACACAGACCAATA	63.668	atTTGTTTGTCTCGAGTGTCTGTG	62.793	152
HM_5134	contig34187	AC	2	20	GCCAAACACATACAAGCAGGTACA	62.556	TGATTGGTGAATTGaACGAAGTG	63.252	156
HM_5135	contig50756	CT	2	12	GCCACAGAAGAACTTGTCTACCAG	63.566	AGGATCGTGGAGTCGGAGAGT	63.657	127
HM_5136	contig40983	GT	2	16	GCCACTAACTTCACTCGCTCACT	62.838	GTTACACGCTCACTAACTGCG	63.194	149
HM_5137	contig37434	GA	2	20	GCCATCGGATTTTAAAGGGTTT	62.448	TGCAATTACTTCAATATCACCCACA	61.722	121
HM_5138	contig26169	AG	2	14	GCCATGAACGCTGTAAATCCTTAG	63.15	TGCTCTGCTACCTCTCCACTTAT	62.725	101
HM_5139	contig35033	TG	2	12	GccatGcGAACTTTCAATATCTTT	62.655	TGCGAGGAATGTAACTAGATCGTG	62.643	124
HM_5140	contig34762	AG	2	16	GCCATGGATTGAGTTCTGCTGTA	63.643	CTaCTCTCTCTcCTCCGTCTCT	62.86	160
HM_5141	contig00603	TC	2	16	gCCATTATCACCTTTGTCTCCATC	63.016	GGTGAGCCAAAATTTCTTGATTGAT	62.608	137
HM_5142	contig33541	TC	2	16	GCCATTGCCTTGATATATCTCACACT	63.63	TGAGATTGTTTGTGAAGTCAATTTGA	63.05	145
HM_5143	contig26444	GA	2	12	GCCATGTAAATGAACAGTGTGG	61.62	TCTcTCAGATCACTCAATTTCTGATT	60.94	92
HM_5144	contig36885	AG	2	14	GCCCAACACTCCATAATCAAAAG	62.922	TCTCTTCACTGGCAGATTGTGAG	63.04	131
HM_5145	contig12445	CT	2	14	GCCCACTCTCTCCTCTCTTC	62.966	CTccGCGAAATTTCTCAITGTAA	63.521	120
HM_5146	contig22369	AG	2	12	GCCCATCAATTCCTCACTAGAA	62.607	GGAACAGTACAGacGGAACAGAA	62.834	120
HM_5147	contig15718	AT	2	14	GCCCTGATCAACCTAAACCAAA	63.574	TCTTTTGTGTTATTGAAAAGGCTCA	63.224	127
HM_5148	contig22793	TC	2	14	GCCTAAGCCCTATGTATCTTCT	63.103	GGGAgTCATCAGCATCTTCATCA	63.705	148
HM_5149	contig28556	CT	2	12	GCCCTCAGCCTTCTAGCTCTAGT	62.832	GGAGGAGAGCTTTGTGTTATCGAA	63.022	129
HM_5150	contig27693	CT	2	16	GCCCTTCAGGCTCTCATCTCTGTA	63.115	TGCTCTTGCTCTGTGTTGTGAG	62.969	129
HM_5151	contig30838	GA	2	12	GCCGAAACACTACATTTACGCTT	62.864	ACCAcCaCTTTCaTCTCTCT	63.119	139
HM_5152	contig14969	AG	2	20	GCCGAAAGCTACAACAGTACAACA	62.683	AACCACTACCAAGATCTAGCTCTCT	62.282	160
HM_5153	contig14713	AG	2	12	GCCGGAGAGAAATCTGaGAAgT	62.59	TATATGGGCTATCCCACTTCT	62.988	156
HM_5154	contig07732	TG	2	32	GCCGGAGATTCTTCTGACATA	63.735	TCTTCATCTTCACTTCCAAACA	62.907	159
HM_5155	contig23032	AG	2	16	GCCGGTGAGGaaGATGATTGA	62.471	TAAACaCTCCCAACATCTGCA	63.048	90
HM_5156	contig03688	GA	2	16	GCTTAACACTCGGAACCTCTTT	63.11	GCATCTTTCACTCTGCTCTT	62.841	80
HM_5157	contig19409	TC	2	12	GCTCAACAGTATTTCTATGACGA	62.529	TCTCGAACcCACTAcAGAGTACAGATT	62.747	149
HM_5158	contig51704	TC	2	16	GCTGCTTTGATCTCACTTCTCTC	63.031	TGTGCTTTTAcCAAAATGAGCTTGA	63.068	151
HM_5159	contig29442	TA	2	14	GCCTTAATAACCCATATCCCAAT	62.242	GGAAAGTCATCaCAATCAATTTGAAAA	62.438	158
HM_5160	contig35582	GA	2	16	GCTTAGACTCGGAAGTGAAGTCT	62.526	CTCACTCTGCTCTGCTGCTaTAAT	62.117	104
HM_5161	contig06469	AG	2	20	GCTTGGTGACTGTGGTGTGTC	64.082	cGCCgGTATCTTcTAcCCCT	63.616	135
HM_5162	contig17403	GA	2	16	GCGAAAAGGaaGATAAGAGGAGAT	62.41	TcattTCAAAcCTGaTTTGATCC	63.297	160
HM_5163	contig27775	AG	2	16	gCGAACGCCATTTTAAATGTAGG	62.957	TCTTCATCACTTCAATGCGAAAA	63.046	87
HM_5164	contig26277	AG	2	16	GCGAAGAGGAGGAGTTCCTTAG	62.992	ATTGTCCaCaAAGCCATCAGATT	63.55	142
HM_5165	contig22497	TA	2	12	GCGAAGTCGCTGCTATCTCATAT	62.775	cGaATCTAGGGTtActCaTcATTTCG	63.221	125
HM_5166	contig34192	GA	2	24	GCGAATTAGCCAAATAGAGAAGA	62.842	GCACCTaaAACCAACcCCCACTAA	63.343	160
HM_5167	contig19800	TC	2	12	gCGACGgTATAATCACTTCCATTC	62.94	cCACTGAGATTGcAGATAGTGGTC	63.353	92
HM_5168	contig48250	AG	2	12	gCGATATCCGTAGTAGAGGCAAGA	62.95	TCCAGTCATCAgGTATCaAACCCt	63.102	149
HM_5169	contig29834	AG	2	14	GCGaTGAAATGCAATTTAAAGGGT	62.37	GCGCGTGATTTCATATTTATCTC	62.954	143
HM_5170	contig47102	AG	2	16	GCGATGAGGTAGAAGATGAGAAAA	63.013	ACAGcCTTCTaTgTTAgCTTCC	63.114	145
HM_5171	contig14113	AG	2	16	GCGATGCTCAAAACACATGATTA	63.288	CTacCATTTTCAcGTTTCAcCTc	63.019	154
HM_5172	contig07307	TC	2	14	GCGATTTCcAagaggAATAGATCA	62.804	TGAATCTTATAGGATCTGAGCGCG	62.928	141
HM_5173	contig37850	GA	2	12	GCGCCAGTGTGAGTAGTGTAGTTG	63.324	CTCCCTcATCTCTAAACCACTCA	62.797	131
HM_5174	contig05272	TA	2	14	GCGCGTGTGTAGAAAAAGTGTGA	63.534	TCAATTCCAGTTTCAATTTCTATGC	63.33	157
HM_5175	contig44532	TC	2	16	GCGCTGcCTCTCATCTCTCTAC	64.256	AGGAGCAAAACCCAAAGATGATT	63.289	80
HM_5176	contig39109	TG	2	20	GCGCTTTCaTTTAAACGaaTATTAGAA	62.816	TATTCCTTCCATGGAAGCCAGT	63.121	159
HM_5177	contig03137	AG	2	16	GCGGCCGATAGAAGTAAcCATAG	64.08	CGGAAAACTGTTTCTGTCTTTC	63.204	144
HM_5178	contig45155	AG	2	16	GCGTAcATAcTCCGTTTCTCTCATC	63.15	CgGTGTtTCTTCTCaATTCaAGt	63.543	138
HM_5179	contig17420	AG	2	12	GCTAACCTTAATCCTAAGATGACGC	62.744	GCTCTTACTGGGCCCTTATGT	62.924	114
HM_5180	contig16826	TC	2	32	GCTAATAACTTCTTCTCTCGCG	62.822	CACATCACCGGaaAAGGTAGTCA	63.377	152
HM_5181	contig35829	TC	2	20	GCTACAATTGACGAGAATGATCCC	63.129	gtCCACTTCCATCacaAATTCA	63.256	140
HM_5182	contig04642	AG	2	14	GCTACATCTCTGATCTCCCTCT	61.762	TTCATTCACTGACTAATCAATTTCTCTG	61.124	112
HM_5183	contig45620	CT	2	16	GCTACCTCAACCTCAGATCAGCAT	63.146	ATGATTTCCTCTCTCTGCGGTTC	63.062	131
HM_5184	contig32118	TA	2	12	GCTACTCTGCTCCACTTGGCAAC	63.375	gcACAcCgGCCATaAACTATACa	64.059	154
HM_5185	contig04639	AG	2	12	GCTACTGTACCTCTCTcaTAGCC	62.627	CAACTCTcCAAAcaAGTAGGTTCTCA	62.134	121
HM_5186	contig52029	CT	2	16	GCTAgTAAAGCACCACATGAATCC	63.15	AATTTcCTCAATGtGATTGTTC	63.334	123
HM_5187	contig42643	GA	2	12	GCTAGTCTGCTGATGTCTCTTATGC	63.108	TTAATTTTGtGAgACCTTGCAATTG	63.278	128
HM_5188	contig37446	TC	2	12	GCTAGTGCAACAAGTAACCAACG	63.109	aAGCATCAAGGTGgaAAGAAAGA	62.508	105
HM_5189	contig46487	TC	2	12	GCTATCCAcCTTCACTCTCTCA	63.873	GAAATCTAGGCTTTTGAAGTcGGGT	63.102	82
HM_5190	contig15429	CT	2	12	GCTCAAAATATACTCTCAAGTCTACGC	61.219	GAATCCCAATCGACTCAGAGAG	61.452	141
HM_5191	contig36416	AG	2	16	GCTCAAAACATACATCTCCCAAG	62.713	ACATTGATGAGGTCTGGAATGACA	62.911	155
HM_5192	contig37307	CA	2	16	GCTCCAATTTCAaCCACTTTCT	62.824	tAAATTTTTGtGGGTCTGTgT	62.714	127
HM_5193	contig04732	TC	2	16	GCTCTGCTCATACTGTTATGGCT	63.064	GACGGAGAGAAACTaGCAcAGGAG	62.922	87
HM_5194	contig01134	TC	2	16	GCTCGAAaCCCTAGGATTGCACTTC	62.636	ACTCGAGTtTTCAGAGCATTTG	63.583	87
HM_5195	contig27993	CT	2	16	GCTGAAGCCAATTCtACCTTTt	63.016	TtGTCAATTTGTTAGAGGAGaCC	62.798	124
HM_5196	contig41553	TC	2	20	GCTGCACAGTTTGAGAGATGGT	62.952	CTcAGTAcCCCAATGcCATAGA	62.411	158
HM_5197	contig33804	GA	2	14	GCTGGAAATGAGTGAAGCAAAATCAT	62.953	CACCTGAATATCGTGcaAAGCTCC	63.17	156
HM_5198	contig51157	AG	2	12	GCTTCAAGTCgTCTCTTTTTCAG	62.822	CGGAAAGTtACCGCACAGTCTCT	63.033	160
HM_5199	contig48863	AT	2	14	GCTTCAATATCAGATCTAGCCCA	62.817	TCTCGTTGGAAGATTtAGAGCTG	63.227	140
HM_5200	contig20233	TC	2	14	GCTTCACTGTGACTGGAGGAGTAG	61.724	GACCAATCTaAAATTCaCGTATCG	61.969	127
HM_5201	contig48114	CT	2	12	GCTTGTGGAAGCAAGCAAAAGTAAg	62.571	ttgactgtATTGATGATGAACAGcG	63.265	120
HM_5202	contig00682	GA	2	14	GCTTTGTGGAGTGTGAGAGGAT	63.027	AAACGAACCTCTCTGTCTGTCCACC	63.132	153
HM_5203	contig31523	TC	2	12	GCTTTTTTCTCAAGTGGGAATAGG	62.219	CTCGATCAAAaTACAGCAGGCT	62.933	159
HM_5204	contig28249	CA	2	24	GgAAACACaCaATTACTCTCAATTTCa	61.703	TTGGTGCTGCAATTGTAAATGTC	62.354	130
HM_5205	contig06058	TC	2	16	GGAaAcCAGGGCAGGGAATTCaT	64.519	GCATTGGGGATCGATGAAGTTT	64.29	81
HM_5206	contig40322	TC	2	16	GGAACACTCTCACATAGTCCCTGA	62.884	GGTGAgaAGacTGAATtGATTgGGT	61.962	116
HM_5207	contig39582	TC	2	12	GGAaAaTAATgtCCAAaCCaCAT	62.106	AgcCCCCCTCCACATATTtTACT	62.132	150
HM_5208	contig23832	AC	2	16	GGAaATCAACCTTTTtTACCTTCC	62.212	ATTGACCATCTGACCAAGAAATc	63.004	116
HM_5209	contig23150	TA	2	16	GGAaATGTTCCTCTGCTCCCTTA	62.91	TcATAGCCGATGATTTCACCCCTc	62.706	158
HM_5210	contig43146	CT	2	14	GGAaATTACCAAGCAGCAACTCTA	62.729	aAgGaAgGAATTTGGGtTCTtG	62.781	135
HM_5211	contig09258	AG	2	14	GGAACGTGAGTGAAGAAACACCCA	63.432	TCTTGTCTTTCATCACTGAgCCA	63.37	151
HM_5212	contig51991	TC	2	20	GGAAGACATATTTCCGGCGATA	63.311	CCCCAGCAGCTAAATATAGAGA	62.639	138
HM_5213	contig00867	AG	2	16	GGAAGaCGCAGAAGATGAAGTTGT	63.141	TATCTAGTTGGTGGTGGTTCG	62.28	99
HM_5214	contig29436	AT	2	16	GGAAGATCTCCGAGCTAAATACCC	62.599	TCTCCATTTCCCAATTTCTATCAC	62.468	155
HM_5215	contig25957	GA	2	16	GGAAGATTTCTTTGGCGATCAAG	63.307	TGAATTCGAGGTGgaGAAGTGCTg	63.04	116
HM_5216	contig15307	AG	2	16	GGAAGGAAGGAaAGAAAGAGAGAA	61.879	AGCCTTCTTCAAAAGCTCACTTCT	62.793	154
HM_5217	contig29471	CT	2	12	GGAATTAGAGATTGAGCACCACAA	62.815	AAGGTCGTTTtAGAGGCGATTTC	63.016	117
HM_5218	contig24341	GA	2	16	GGAATTTGATGTTAGGCTTAGG	63.084	TCTCGAATTTGcTtATCCAATCGt	63.13	118
HM_5219	contig28910	CT	2	20	GGACACAAAGTTTtGGAAATTGA	63.312	GtAcACAGAGAgGGAGGGAAGAGT	63.4	140
HM_5220	contig45546	AC	2	12	GGACAGATGCTACACATAGAGTCATAGA	61.22	TAACCTCTATGCCAAACAGACTTA	62.011	140
HM_5221	contig39169	TC	2	20	GGACTAGAATCGAAACCAAGGTGA	62.798	GGGATATTCTCTCTGccCAAACTc	62.986	94
HM_5222	contig12500	TC	2	16	GGACTCGAAATGGATTTGAAGAA	62.691	CCCAAGACAGAGCAACAGTAAG	62.412	109
HM_5223	contig14013	AG	2	16	GGACTCTCAATCCCTTGAAGTCT	62.231	GGTTTGAATTTGGTTTGTGAGTGA	62.294	159
HM_5224	contig13195	TG	2	16	GGACTTGGTTTTCTCCATAGCTGA	62.91	CCGATCATTCATACTGTTGCTCAC	62.951	112
HM_5225	contig00373	GA	2	12	GgACTTGCTTGAGTTCATCctt	63.027	GTCAAAACGAGCTTgGAGAGATc	62.809	144

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5226	contig49038	GA	2	12	GgAGAGAAGATCGTTTACGGCTA	63.035	CATAACCAGCaGCTCCATCAACTA	62.643	91
HM_5227	contig01550	GA	2	12	GGAGAGACTCGGATCAGATGAGAA	63.312	CCTTCGTTTACCCCTACACTTCac	63.233	148
HM_5228	contig28681	AG	2	16	GGAGAGAGTGTGAATGGGTGAAA	63.751	CCAGTCGCTgTaAGCCATTTG	64.018	139
HM_5229	contig14972	GA	2	12	GGAGAGGTATTTGCTGATGACTGC	63.462	ATCTAAACAAAGCCTTCGATCAGCA	63.341	160
HM_5230	contig47156	GA	2	12	GGAGAGIATAGAGgCAGACCcATT	61.164	GaAAAGCTAACTgTGGGaGTTaAAGTT	60.73	87
HM_5231	contig06801	AG	2	12	GGAGATACAGAGAAAGTGGGgAT	62.964	TACGATTCcCaAAATCATcCaAAC	63.105	126
HM_5232	contig43854	AG	2	16	GGAGATCCCCCATGTTTTAGAGA	63.662	ATTGTGGAATGATTTGGGATTCaa	63.506	148
HM_5233	contig13486	AG	2	24	GgAGATGAAaGgATGTAGATGAaAa	62.147	TCCATTTTCATGCATCAGTACGTAAA	62.664	150
HM_5234	contig45642	TC	2	16	GGAGATTTTAGGGGTGGCATTAG	63.084	gGAGTGCACAAAGACAAITGAAA	62.528	142
HM_5235	contig01074	AT	2	12	ggagcAaTaTATCTGTGTATGTGaGGG	63.041	TTTCGAGATTCAAAcCAGGAAG	62.787	133
HM_5236	contig06355	AT	2	12	GGAGCCCTAGTTTCAAAaCaCAAA	62.728	AAGtaCCGGTGAATTTgTAAGAGc	62.202	142
HM_5237	contig38721	AG	2	14	GGAGCTAAAAGATTCAAAGCAAGC	61.887	TTTTTAITCTTCGGATGATTCACATAGT	61.438	117
HM_5238	contig49862	TC	2	14	GGAGCTTCTGTTACTGCTCCATT	63.037	TTGGAgTcTTCGTTcAAGTCATCTC	63.126	112
HM_5239	contig20805	AG	2	14	GGAGgAGGTATATCGTTTTCCaAg	63.172	AACAGTTTTGATCCATTTCCTCGA	62.996	83
HM_5240	contig25884	TC	2	12	GGAGGaGTGAaGTTCGTGAATTG	63.438	CGCaTAATaCAACCCATTTGGGA	63.026	107
HM_5241	contig33856	GA	2	14	GGAGGGgtAGAGTTCcTaATg	63.285	GagGtTGACATGaTAGCCTTGAC	64.221	80
HM_5242	contig42042	TG	2	16	GGAGTGGTTCAATTTTGTATGAG	62.996	CCCTcATTCcCTcTCTcACTCTCT	63.591	106
HM_5243	contig45115	GA	2	16	GGAGTCTCATATGAAGCAGGAAGA	62.9	GGCGACACTTGAACCTCACATCA	63.726	149
HM_5244	contig16782	AG	2	12	GGAGTCGTTGCAGAGTATGTGGA	63.726	CTGATCTCCCCATCGAATCTCTAA	62.873	134
HM_5245	contig19108	CT	2	32	GGAGTTGAGATCTCCAGCTGCTaa	63.343	GTGTTGATTGAATCTGTGACATCTG	62.949	123
HM_5246	contig14108	AG	2	12	GGATACAGAGAAGCGGGATGTAG	62.411	AAGATTTTAGGCTGCTGATTGTTG	61.999	80
HM_5247	contig46208	AC	2	12	GGATAGCCTGTCTGCTTGTAAAG	62.853	TGTTGCaTAAATGCGCTGACTCAA	62.946	129
HM_5248	contig00225	TC	2	32	GGATCCAAGTAGAAGCTTCAGGT	63.193	GacGACgAAGcAAGcAAGAGaG	63.602	107
HM_5249	contig37064	TG	2	12	GGATCCACATCTGGTTTCTGTGA	62.366	ACCACCGTGcCTaCaAAATACTG	63.354	84
HM_5250	contig27046	TC	2	12	GGATCCAGAGGGGAGTAATCTT	62.94	CTGaATCTCTTATCTCTCGTAGGC	62.279	158
HM_5251	contig08461	CT	2	12	GGATGTGACAAATACATCACACG	61.615	TAAACTGCTTGCCTTTGTGTCC	61.773	123
HM_5252	contig13871	AG	2	16	GGATTATATCTTTCAAACTGGC	62.105	TAACTTTCTCAGCAAGTCAGCA	62.528	100
HM_5253	contig20237	GA	2	20	GgATTGAGAGAAGAAGTGGTGGT	62.046	CTGTCTCTGTCAGGgTTTTCTAT	61.988	120
HM_5254	contig45346	AG	2	12	GGATTGAGCAGAGTAGGGCTATGA	63.026	TCTaAAACTGTCTTCTGGCACCC	62.921	120
HM_5255	contig27483	TC	2	16	GGCAATTCATCTGATTTCCAGAC	63.116	CCGCTaCTCaaAActtAcCAGaC	63.747	131
HM_5256	contig16995	AG	2	16	GGCACCCCACTAAaTACCAGT	62.439	TAGGGTTTGGCAAGAACTTGAAA	63.224	117
HM_5257	contig38902	TC	2	14	GGCACTTCTAAATCTCAGTCAGGT	62.357	ACAACATGGTTGTAATgGCATCag	63.065	115
HM_5258	contig34633	TC	2	16	GGCCAAAGAGTCTGAAATGCTTAC	62.536	TGGAATTGGTtAGTTGGATTCaAGA	62.908	147
HM_5259	contig37691	TG	2	16	GGCCACACATGAaAGTGTGATGT	63.191	GCATGGCAGATAAAITCAACACaa	63.175	118
HM_5260	contig14837	AG	2	12	GGCCATTTTTTCAACTCCCTATGCT	63.396	CAAGTCTCCCTCTTCCGTACAAA	62.905	89
HM_5261	contig04615	AC	2	12	GGCCTTCTCCTCTCACAAAA	62.866	GATGCTTACGGTGGATTGTTTG	62.732	119
HM_5262	contig39805	TC	2	14	ggCCTTTTACTACCACTTTTCcG	63.201	TGCAGCTTGATTAGctCTCTTAGC	63.54	142
HM_5263	contig08329	AG	2	20	GGCGGAGAAGACAGACAGTACAGA	64.232	GACATCTCGATCGCaCaGTTc	64.325	103
HM_5264	contig04853	AT	2	14	GGCTCCACATAGAAGCAAGAGGTa	63.035	GAGCTCTCTCACTCAACTCCACAA	62.366	141
HM_5265	contig20240	AT	2	16	GgCTCTCaattctgcttttaCG	62.824	TACTTTGCACACTCCAGGCATAAA	62.969	140
HM_5266	contig05794	CT	2	12	GGCTTCTTCACTCTCCATCTGAA	63.209	CCATCGTCTGTAATGGAGGCTAC	63.133	160
HM_5267	contig49531	GA	2	12	GGCTTCTTGGTCTTCTGTTGTCT	63.027	ACTACTTACTTTAGCGAAGCGGTC	62.41	160
HM_5268	contig26842	AG	2	30	GGCTTGAAGAAGTGAATTCATGG	63.219	ACGCACTAACCAcCCGAcCC	63.362	121
HM_5269	contig43186	TA	2	12	GGCTTGAACCTCAGTCAAAcATT	63.781	TGAGTTTTCAGTTTCACTTCTGTC	62.972	117
HM_5270	contig14566	GA	2	14	GGGACGAGTGAGGAGATTAACAGAG	62.678	CCACCACaTaAAATCACACAAA	62.829	122
HM_5271	contig45919	GT	2	16	GGGACGGAATGGGAATTAATAAa	63.07	AGTTGCCCTTGGTCCAAGTGTTC	62.737	99
HM_5272	contig18864	GA	2	12	GGGAGAAATTTAGGCGATGagTGT	63.696	CAAAACCATACATTGATACACCA	62.717	147
HM_5273	contig05814	GA	2	12	GGGAGAGACAGAcAgGATTAGAAATG	63.003	TACTTCTCGCACACTCTGAAAGC	62.236	121
HM_5274	contig32352	TC	2	12	GGGATCAGCTTATTCACACACTCC	63.234	TGGCCCTGTAGTGAGAGaAAAT	62.633	150
HM_5275	contig11012	GA	2	16	GgGAtGgTtGCATAAACACTATGA	62.108	TCTATTTTGGaAATCACAAAGTTCaA	62.065	105
HM_5276	contig18416	AG	2	12	GGGCTTTATAGTCTTTGTGGTGGG	63.983	CcAaAcCCTCTCAATTaAaCCIC	63.168	131
HM_5277	contig34821	CT	2	12	GGGgAAaAGcATTaGAGAgTgGA	63.164	CATCGAAGATGATGGAGATGGTG	63.914	158
HM_5278	contig45439	CT	2	16	GGGgAAATTTGGGTTTTTCTCc	63.842	GCCCaAAAGaCcaAAAGCaaACTA	64.461	97
HM_5279	contig29096	CA	2	12	GgggaCCCAaAaTAAaAaCACA	62.035	GCCTGTgCaTTTGTtTAITTTTc	62.137	149
HM_5280	contig09096	AG	2	16	GGGGACGTaCTGcATtGttttt	62.612	CACCACCAACAACCGcTATCTAC	62.843	115
HM_5281	contig50887	TC	2	12	GGGgaGGGAagTaGCTTTTTCaTa	62.888	ACCACACCACTTGCCATCATTTT	62.693	124
HM_5282	contig06087	AT	2	14	GGGGGATAGAGAATCGAAAAaAa	63.558	TCCACACTTGCTCATATTaTACACA	62.772	155
HM_5283	contig16079	AG	2	12	GGGGGtAgAATTAGGAATTTTTGTG	62.985	ctTCTCTCTCTTCACATCCCCC	63.679	131
HM_5284	contig26690	TA	2	12	GGTCCCTCTCTCTCTCTGTHC	62.863	AAAAAgacAGaCGAGAGTGCAaTAc	62.575	105
HM_5285	contig01261	CA	2	16	GGGTCTCATCTGTGAGTGGtTTT	62.795	GaAAGaCAATGTGATGtAgGCCAG	63.164	132
HM_5286	contig34206	TC	2	16	GGGTgAATTGAGAGATGtTtTtG	62.996	ctAcTAAACCTGTAAAGCCaCTgc	62.383	147
HM_5287	contig15658	CT	2	16	GgGTGcTtATaAGGGTGGATTAAGA	63.476	AAGATGCACAAAGTTTCCACATGTC	62.518	110
HM_5288	contig13667	CT	2	14	GGGTTCAAGATGGTCTCACTCTT	62.046	GAAATAGAGTGTGTGAGAGAAAGATG	61.9	146
HM_5289	contig21156	GA	2	14	GGGTTCTgAAATGAAGGTTTGA	62.703	TTGGTGGAAGTGAGTGGGTATT	62.907	159
HM_5290	contig07494	CT	2	14	GGGTTTATACACTCCCCAcTCTC	63.181	ACTCTTTATTTCGCACATTCCACC	63.552	81
HM_5291	contig02241	AT	2	12	GGGTTGTGTAGTGGACCAAGTT	62.511	GCCCAATgAACTATACAAATGTGTC	62.87	151
HM_5292	contig42674	AG	2	16	GgTAGTGAGGTGGTTTTGTTGGAG	63.12	CaCACATCTTTGTGCTCCATATC	62.833	105
HM_5293	contig49534	CT	2	32	GGATATTGGTATCGCATAGCTCAC	62.953	gggACACACATTTCATCGACTACT	62.626	125
HM_5294	contig03625	AC	2	12	GGTCaTACATTAAACCGCAGCA	63.181	GGcTACTTtaAATgCaGTGTTG	63.051	157
HM_5295	contig25405	AT	2	12	GGTCGAACCAATAAATCCGTACA	63.126	ATCTGGcTCTGTTCAATTGGTAG	62.923	159
HM_5296	contig25233	GA	2	14	GGTCGTGGTGAGTAGGAACTTTA	62.71	AAGTTCAGTTCaCCCTAAACCC	62.791	117
HM_5297	contig38658	AT	2	16	GGTCGTCTATCTTGAAGaGAGTA	61.982	CACCCACGGAATCTATtGTTTct	61.045	100
HM_5298	contig24318	AG	2	14	GGTCGTGATGAAAGAGAAAGAGAG	62.898	TTCACTCACCACACTACCGACTCAGA	63.38	125
HM_5299	contig34317	TC	2	16	GGTCTGGTTCTCTTCAaAcCATC	63.106	CCTCTCTTATCAGGGAAGCTGACa	63.212	100
HM_5300	contig45596	GA	2	12	GGTGAGGGcTtGATTCTGAAAAA	63.728	CACCACCGACCTCAcCTAAAGTAT	63.607	116
HM_5301	contig14408	AG	2	16	ggTGAGTTAGGAAGTGGCGATG	63.137	ttttcttctctctctctgtttca	62.868	157
HM_5302	contig46997	CT	2	14	GgTGATTCTTCAAGTTTGAGCTGT	63.027	ACAAAACTACTCGAGAGGGGAGAGG	62.223	120
HM_5303	contig43233	AG	2	24	GGTGTGGAATCCAGTTCATCTT	63.553	ctctcgctcCaaCTaCaCTC	63.349	152
HM_5304	contig45893	AG	2	12	GGTTAAGTGTCTCTTCCGACCA	62.809	aCTAtCTTTTGTcACCGCCAA	62.921	113
HM_5305	contig41449	AG	2	12	GGTTACAAGGGATgAaTTTGATG	62.691	TGAGTCTCGGAACCTGTGAGAAGC	62.17	150
HM_5306	contig40046	TA	2	14	GGTTATCCAAATTCGATCAGCTTCT	62.733	TGCAACTGCAATGATAAAGAAAGCA	63.083	106
HM_5307	contig08886	AG	2	12	GGTTCGACAGAGATCTGGTAGAG	62.912	TCAAgGGaaATgAAAGACAAgA	63.19	95
HM_5308	contig43040	AG	2	20	GGTTGAAAGAGGGAACAAGAGTGA	62.997	TTTTCTTTGGGCTTTATTGTGGA	62.918	93
HM_5309	contig27339	GA	2	16	GGTTGAGGTAGAGATGGAGCAAAA	62.91	AGaCTGCCTcTACCCaCTCCTCTT	63.099	100
HM_5310	contig39015	AG	2	12	GGTTGGTGCAATAAACAGAAAAAGC	63.055	TTTTaAGaGAGGTTTTTAGGCGcG	63.02	131
HM_5311	contig00148	GA	2	12	GGTTtGGATTCAAGGGGTTTTAG	62.977	CTCaTATcTCCGATTCTCTCTCA	62.873	126
HM_5312	contig19453	GA	2	14	GGTTTTCCAGGGCTAAAAGGAATA	63.475	TACaGTCTgTgTGTGTCAITCA	62.492	114
HM_5313	contig32602	CT	2	12	GTAAcCaaCCAaGAGAGACCcAT	63.702	GctTAGAGATGAGGCTGTGGTGT	62.925	88
HM_5314	contig23485	AT	2	14	GTAAcGACAAATTAACCAATCCCG	62.639	GTGGAAcCACACAGCTTAAGTCCT	62.935	131
HM_5315	contig00524	GA	2	20	GTAAGTTTTCTGCTGATCTGATTGC	63.248	TTCTactgttcCaAcCCaAcG	63.338	156
HM_5316	contig06402	GT	2	12	GTAAGTTTTCTGCTCaATGGTTTGC	62.947	CaAAACACACATGAAAGAACTCG	63.037	126
HM_5317	contig03331	TC	2	20	GTAATTCAAGCAATTTGGTCTGGG	62.922	GAcTAACCTTTCTCTGGATTGcG	62.522	157
HM_5318	contig03292	TC	2	24	GTACAACGTCCCTCTCTATGTC	62.281	TGGAAGATCGGAGAGAAACaAAT	62.495	160
HM_5319	contig37494	TA	2	14	GTACACATAGTCGGCTTACCCTAT	63.268	CACCAAAATTAACCAAAAGcACC	63.641	97
HM_5320	contig50802	AG	2	12	GTACATCTTGGGAAGGCTTGTT	61.832	ACGAATTTTGGCTCATCCC	60.905	150

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5321	contig08109	GA	2	12	GTAGAAGGTTTCGAAGGTGGAGGAG	63.695	TTCCATGAGAGTCCCTATTCTGTC	62.786	134
HM_5322	contig02627	TC	2	12	GTAGATATGGTCGCGCTGTTTGAG	63.133	ACAGGTAGCGAGAACAGAGTAGCG	63.381	120
HM_5323	contig24599	AG	2	12	GTAGATGGTGGTGTCTGGAGATCAT	63.675	ACCTCTTCTCTCTCTCTCTCCCT	63.441	144
HM_5324	contig17507	AG	2	12	GTAGCTCGTCAGTGCACGTAgtcc	64.588	CATCATACACAtcACGTTGCATCA	63.902	159
HM_5325	contig02053	AG	2	12	GTAGGTGGGTGGATTTTCTGTGT	62.907	AGAAAAACCAATCCAATCTCTCTCT	62.563	121
HM_5326	contig16902	AG	2	14	GTAGGTGGTCGAGAGGGGCT	62.868	CCATAGCTCAGGATTCATTCCTTT	61.896	148
HM_5327	contig22032	CT	2	16	GTATCGAATTCCTGTGCGAGACC	64.205	GCTACCTCACAAGTCACaCACAA	63.633	159
HM_5328	contig04877	TG	2	12	GTCAgAAACAGTGGCTTGGAGATT	63.036	GGCTTTTCTCAATTCTCTcACat	62.813	141
HM_5329	contig28815	TC	2	12	GTCCCCCAaCTCTCCACCTT	62.963	CtATaCAAGCGAAACGaCgaCT	62.754	99
HM_5330	contig28007	TC	2	12	GTCCGATTACTGGAGCAGAAG	62.473	TAGAAAAGGGGAAGTAGTGTGG	62.782	129
HM_5331	contig47980	CT	2	14	GGCTTTCCTCTCTCTCTCTCTC	63.055	CaAGATCATCATCCACAGTACCCA	63.243	143
HM_5332	contig03987	GA	2	20	GTGGAATATCCACACACCAGACAT	62.274	AcCacCTTAAACTCACACTACTTCA	61.467	80
HM_5333	contig48603	GA	2	16	GTGCGCaGAGATTTCAGGGTTT	63.102	ATATCAGAAACCACACAAACATCA	62.594	142
HM_5334	contig35236	GA	2	16	GTGCGCTCATCTCAGTATTGTCT	63.051	GACGGTTCGAATCATGTCCT	62.767	144
HM_5335	contig16315	CT	2	16	GTGCTCAGCGTtaTCGTTGTGT	63.293	TGGATTATCGAItATAGAGCGAGAG	62.295	95
HM_5336	contig16402	AC	2	24	GTCTCACTCTGGAGTCTTTTCCC	63.816	TTTATTAGGTTTATGGTTCGGcCC	63.189	150
HM_5337	contig26490	CT	2	12	GTCTCGTCTCCGCTTTCTCTCTC	62.993	GAGAGTGGGGAACCTCTCaAAACa	62.997	86
HM_5338	contig28318	TG	2	14	GTCTCTCCATTGGAGTTGGAGTT	62.046	ACATGCACAAACACCAAACTCAGT	62.755	130
HM_5339	contig21011	GA	2	24	GTCTGACTGAGAGCTGAAATGCAA	63.177	aACACAGGCATTATTGCAITTCGT	62.95	138
HM_5340	contig40983	GT	2	12	GTGAACAGAGAGGTGTTGTGTGC	63.305	CACACaCTCGAGCAGTGAACTAGG	63.52	158
HM_5341	contig40983	GT	2	16	GTGAACAGAGAGGTGTTGTGTGC	63.305	CACACaCTCGAGCAGTGAACTAGG	63.52	158
HM_5342	contig30433	GA	2	12	GTGAACCTTAGTATTGCTTAACCTCA	62.043	AGCCTCCATTTCTCACTCTCTCAC	62.472	158
HM_5343	contig13570	GA	2	14	GTGAACCTCCGGAAGAGAGAGT	63.396	TACTCCAAcCTTaAcCcaACTTCA	63.003	87
HM_5344	contig07921	GA	2	20	GTGAAGAGGAGTTCtGAAAGAGC	62.061	TCTCTCTCTaTaAtCCTTTCTcTCTC	61.595	107
HM_5345	contig22319	GA	2	12	GTGAAGCTGTGTTGTCTGCAATT	62.769	ATCGTTTGGAGTGACCACTATCAT	62.802	157
HM_5346	contig49706	TC	2	14	GTGAAGTAAGCAGAGGAACCTCGC	62.851	CTCTCTCACTCAAACTCGGCACAAT	63	141
HM_5347	contig18421	TC	2	16	GTGAAGTGTGAaCAGTGAACCTCA	61.559	AAGAGTGAAGAGAGAAtGGGCAGT	61.958	88
HM_5348	contig29691	AC	2	14	GTGACACCCAaTTgAGAGAAAAC	63.115	GACaATTCCTAAGTAGGGTTCGTG	63.009	137
HM_5349	contig27821	GA	2	24	GTGACTTTCTGGCGATTCAATTTT	62.731	CgTGTGAGAGACGCAAGAGCTCT	62.116	84
HM_5350	contig23559	TG	2	16	GTGACTTTGGAAATTGGCATCGT	63.346	AcITTGGTTACCCAACCTGAATTGC	62.536	108
HM_5351	contig52061	CT	2	20	GTGAGTGAATATGAGGCCCTCAAA	62.607	taccgtttctgattttgtcTTCCT	62.497	160
HM_5352	contig46127	GA	2	14	GTGATGGCCAAAGAGAGATGAAC	63.336	CTTGAAGAGACTTTCAGCAGCCTC	63.137	81
HM_5353	contig45977	GA	2	14	GTGCAGAGACCCCAATATCTCTTA	62.8	TGAATTGAAAGAGAAACGAGAGGG	62.993	131
HM_5354	contig07614	TG	2	16	GTGCATAGCCTAAGGAATGAAGGA	62.828	CTCTCTTACCTCACTcCCCTCCA	63.16	119
HM_5355	contig05173	AC	2	12	GTGCGGATACACAGACACAGAGT	62.979	CCACCTCTCTTcCACTACgaACAT	62.909	115
HM_5356	contig40366	GA	2	16	GTGGACAGCaAAGGTAATAACCG	62.896	TGCTCCTATCATGGGACTACTTCA	62.175	160
HM_5357	contig12886	AT	2	14	GTGgACGGaATACTTTGTCAAAAC	62.309	TGGGTATATATgGAGTGTGTGCTc	63.246	83
HM_5358	contig47859	GA	2	16	GTGGAGTTCGAGCGAGAAG	63.58	GaCCCCGTaCTaACgAAACCaAaC	63.901	96
HM_5359	contig44616	TC	2	12	GTGGGGACACGTCATCTCTACCTA	63.661	GAGCAGTGAaCTTGTcGGAGAAATC	63.68	152
HM_5360	contig09159	TC	2	14	GTGGGTGAaCTAATCGAAGGTGAG	63.225	TCACCAAACTGTTGCTGTGATTT	62.958	147
HM_5361	contig09112	TC	2	16	GTGGGTGTTGTTGTTTCTGAAAC	62.921	CAAAATACAGGCGtctTGGTAgtC	63.142	153
HM_5362	contig14764	AG	2	14	GTGTAATTGCGGGAATTTTGTGTA	62.064	TTCaATATCgGAGGCTGTCTCTCT	62.7	120
HM_5363	contig05885	AC	2	14	GTGTACCTcGAGAATGCaCAaC	61.93	AATGGAAATgAGGAgAGACTTtGG	62.863	97
HM_5364	contig16119	TC	2	32	GTGTAGAGGTCGGCCTTTCATTG	63.338	CATGAGTGACGAGAGACaAGCAT	63.174	145
HM_5365	contig38697	TA	2	16	GTGCGGCAAGCAaCaCAACTAAT	63.575	TCTACAGATgGGAGTCAATTTTGG	63.106	109
HM_5366	contig07234	GA	2	12	GTGTCTGATGGTGCCTGTTTAG	63.161	GCACCAaCTTcttCTATCTCCA	63.115	131
HM_5367	contig13661	AG	2	12	GTGTGgaTTAATGAGCGGAACCTC	63.137	AGAGACAGCGAAcTCTCACTTTTC	62.604	111
HM_5368	contig41106	GC	2	12	GTGTTGATTCCAAGATTTCCAAGC	63.125	ACgGTCgaaAGaAGaGaaAGaGTT	62.804	140
HM_5369	contig24003	GT	2	14	GTGTTTGATTGAGATGATGAACCG	63.055	TTGAAGTCAAGAACTGTGACCAG	62.93	81
HM_5370	contig01886	CT	2	24	GTGTTTGGGAGTGAGAGACAGTGA	62.921	GGTTCGTCTTACTTGCGAACCAT	63.552	150
HM_5371	contig15047	AG	2	12	GTAAAGATACCGAGTCTCCAGCG	62.548	TCTCTACAAACCACTTACCACCA	63.036	160
HM_5372	contig08168	GA	2	16	GTTAAGAGGAGGAAGGgagAGAG	62.971	TCTATGCTCCAGCGGCTGTTTTAT	63.15	142
HM_5373	contig07581	AG	2	14	GTTAGGGTTGAACGTgATGAACG	63.019	CCCTCGGCTCTCTCAATaACAGTA	63.019	80
HM_5374	contig04172	GA	2	14	GTTCAAACACATCCCGATTAGA	63.317	ATATGTatCTCCaCGGCTCTCTCT	62.829	113
HM_5375	contig30652	AC	2	14	GTTCACATACaTGCATGGACAAA	61.882	CTGCTCTGtTTCaAaATGCGTA	62.549	109
HM_5376	contig42374	AG	2	12	GTTCATCTCAATGCGCtCAATTTC	63.116	CATCTcCCAACCTCTGCTCTCTCT	63.11	134
HM_5377	contig11276	AC	2	20	GTTCCTCAATATAGACATCaACGC	62.83	TTATCAAACTCTCTGTTCCGCCAT	63.021	129
HM_5378	contig04352	TC	2	16	GTTCGGAAGTATAGCTCGATAGC	62.478	aTCCAAACACGTCACCTCCAGCT	63.353	147
HM_5379	contig17234	TC	2	12	GTTCGGAAGGATCATGAGCTTTT	62.903	AAcCTAAAGGCCGTTCACTTATCG	63.691	129
HM_5380	contig00274	TC	2	16	gTTCCTCCcCTCaTTCCTCT	62.714	GTTCTCTGCCATGATCTTTGAGT	63.017	146
HM_5381	contig42312	AG	2	14	GTTCGAaCCTTAaTCCCTCGTAaCC	63.196	CGGTGatGATTITTAATTTGATCT	62.37	117
HM_5382	contig11390	AG	2	20	GTTCGACGAATTGCTTCCCTGAT	63.326	CATATGctTtGaaAaCaTctaAcCC	62.935	83
HM_5383	contig33733	TC	2	20	GTTCGTCACTCTCTTTGGCCCTAC	62.626	GAGAGAAGAGAAACAGAAAGAGCG	63.137	140
HM_5384	contig03685	TA	2	12	GTTCGTGGTGGATTGTTGAACATA	64.16	TTTGGGAATGATGACAAATGAA	63.449	156
HM_5385	contig11392	TC	2	16	GTTCCTCTGATCTTGGCATCTCT	62.786	aCACaCaAACACaCaAAGGaCACA	62.637	145
HM_5386	contig05252	GA	2	32	GTTCCTATCGTAaCGACAGGCCAT	62.647	cttcgcagtagacctcttctctt	63.001	155
HM_5387	contig21277	GA	2	20	GTTCCTTGGAAAGGTTaTTTGGtCa	62.495	TCCTGGTATagCaCAACTaACCCA	62.943	117
HM_5388	contig01053	AG	2	16	GTCTTTGGGgAGGGAACCATTT	64.512	TCTGATCTCGTCCCTTTGTAAATG	63.625	145
HM_5389	contig39497	TG	2	12	GTGGAACCACTGTCTGTTGAAC	63.45	ATTCCGTCCACTTGACTGAcITTC	62.912	152
HM_5390	contig42568	AG	2	16	GTGAGAGTGAAGCTTCGGTTATG	63.45	tTCAcGCTTaCGTaCCCTCTcCTc	63.901	93
HM_5391	contig12391	CA	2	20	gTgAGgAaTCcGgTCTgTCT	62.7	TTGACCAAGCTGTGCTCAATTGTGA	62.969	159
HM_5392	contig13275	CT	2	12	GTGATAAGGTCTCTGCACTGAAT	62.827	CCTTATCGCTACTCAAGATCGCAT	62.95	146
HM_5393	contig11348	CT	2	20	GTGGCTTAaCAGATGGAGCAAGT	62.949	ATTGATAGAAATGTGAGCAGCGC	63.565	122
HM_5394	contig38977	TC	2	14	GTGCTAGATTTTCTGCAACACCC	63.256	CCACTAGCTTCAACaCaAAACACAC	63.077	148
HM_5395	contig35366	GA	2	12	GTGCTCTCCGCAATTTAGAGAGA	63.022	CATCTTAGACAGACCCAATGCCTC	63.331	156
HM_5396	contig25279	AG	2	12	GTGTTTTGACAGAGGAAGTTTGT	62.835	AAGCCTCTGCTCTCACTTCTCT	63.42	139
HM_5397	contig50539	TC	2	20	GTTTAAGGATGTGACCGATCCAAA	63.317	ATTTTGTGCGcGTTaAAGaAAAC	63.497	119
HM_5398	contig26253	CA	2	12	GTTTATTTTCGGACATGCaCTACA	63.196	TGCAGGGCCAAGTTAAATATGTCT	63.043	150
HM_5399	contig13879	TC	2	16	GTTCGAAACCCCTGAaAAAGCGT	63.024	GGGAAACAAAGGTTAGTTGGTCT	62.791	132
HM_5400	contig45361	CT	2	16	GTTCGGAaTTTcCAAAaAGCCcTA	63.565	ACAgAAACAGAGAcGgAGaAggG	63.208	112
HM_5401	contig47768	TG	2	12	GTTCCTTTTGGCAGACGACTGATAC	63.256	TgTCTCTCaAAATCAaCTATACCA	62.356	129
HM_5402	contig02421	TC	2	24	GTTTGAATTGGGGATTGTAGGAG	61.996	GACAcCCGGAaAACTCTGTGT	61.36	80
HM_5403	contig31721	GA	2	14	GTTCGACACGACATCTCTGTTAT	63.462	TCGTTGCTTaAACGCTATCACCTC	62.863	148
HM_5404	contig22034	TC	2	12	GTTCCTACCTTCCCAATAGCGCC	61.975	TTCTGTTGTGGAGGTGAGAGTTTG	62.81	99
HM_5405	contig51183	TG	2	16	GTTCCTGGAATTTCTCCGCTGGTATT	63.383	CTAGCCTCAGCTCCAATCTTTTCA	63.227	157
HM_5406	contig05475	TC	2	20	TAAAAaTAGCAaTCTTTGCGCAT	62.969	GAGCTCAAGAAATTCAACTCCGA	63.121	156
HM_5407	contig00830	GA	2	20	TAAATGCTGGCGATAAATAGCA	62.792	GTCGATTCTCTGCCGCTCTG	62.365	120
HM_5408	contig32779	GA	2	32	TAAACGGCTTcAGCTGCACAT	63.086	GTTCCTTCAGGGGTTCCATTTATC	63.069	146
HM_5409	contig25701	AG	2	12	TAAaCGTACACCGTGAaACAGGa	62.754	CCTAAGGGCTTGAAGGGTTAAAGA	62.986	136
HM_5410	contig25775	GA	2	12	TAAACTTTTTGGAGTGGGTGAGGA	63.1	AACCTGCGAAACCTTACGATCATTC	62.744	132
HM_5411	contig29379	TC	2	12	TAAAGATGTGAGATGTGAGGGGCG	62.9	TGCTTCTGtATTTCTTTGATaTcTG	61.922	99
HM_5412	contig38338	AG	2	12	TAAAGTAAGTGAACCCATGTGGCA	63.027	TTTcTCTCAaATCTGtcCTCTTCA	63.407	151
HM_5413	contig10844	AG	2	24	TAAATTCGGAATACTAAGATGGC	62.616	CTTAACTgCACTCTACCTGCTCG	63.578	129
HM_5414	contig12529	CT	2	24	TAAACAAATCTGAGGCGAGCA	62.947	ATCCAAAGcaaccccttttctctt	63.289	160
HM_5415	contig27675	GA	2	14	TAaAGAAACaAGTCGGCTTCAAC	63.031	TAAAGTTTTTGAAGCCCCATCCA	62.825	112

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5416	contig45634	AG	2	16	TAAGAATTTTACGCAACGCAATC	61.547	TATTTCACTCCTCTGTCTCTGCTTTg	61.448	80
HM_5417	contig42675	AG	2	12	TAATCTlGgTGgTgTTTTGGGgt	62.618	cccatTTtcagagcttcaactcaat	62.91	136
HM_5418	contig10105	AG	2	16	TAATCCAAAGGAGCAATGTTCCaA	63.602	AGCCATACCACAGGCTCCTAATA	64.095	158
HM_5419	contig01007	TC	2	14	TAATCGCACTCCTCATCAATGAA	62.935	TGCTTTGATTTTTCIAAAACGTGAGA	62.397	122
HM_5420	contig15711	GA	2	16	TAATCTCGAAGAGGAGGAAAGACGa	62.784	CTCCGACTACATATGGCAACATCA	63.27	131
HM_5421	contig28795	CT	2	20	TAATTTATCGTGGGCGAAAGGACTA	62.933	CAGAGGCCATTaAAAAATGGATTGA	63.304	150
HM_5422	contig21572	CT	2	14	TAATTTCCATAGCTCTGCTGCTCA	64.246	GACGCTCGAAACAGAAACAGAAAGT	63.263	127
HM_5423	contig04274	TC	2	16	TACAACCAAGTCCTGTGCTGATGA	62.945	TaCCEAACTTaGCTCAGcCTCTG	63.138	129
HM_5424	contig50492	CT	2	20	TACAACCTCACCATCGATCTCaa	62.921	GGAGCTGGAGGATCACACTACTAA	62.8	153
HM_5425	contig41026	AT	2	14	TACAATCCaCACAaAGCcACTTG	63.259	CAACaATTTTCGAGGGTgGATaAAA	63.204	149
HM_5426	contig48107	TC	2	12	TACAATTGAGCGGTTCTCTGTCT	63.45	GAAAGAGGGAGATTACAACATGGCA	62.91	159
HM_5427	contig50331	AG	2	16	TACCATTGCGCTACCTCCAATC	63.564	gGGGCTCTaTaAcGtCtGCTTCTA	62.96	94
HM_5428	contig42356	CA	2	16	TaCCCATTAAGTTCGACAGACAT	63.133	GGGTcCAGCTACCTTTGTCTCTT	63.813	116
HM_5429	contig42049	AG	2	14	TACGTACAGAGTGAGgATGACGGC	61.912	TTTAATAAACaAgGTcCCCTcgc	62.519	124
HM_5430	contig03323	TC	2	20	TATATACGACGCGCTTCAACCTT	63.064	ATGGTGATTGAGAGGAAATTGGA	62.987	158
HM_5431	contig46061	TC	2	12	TACtCTTtTtCTTCTCccGCTCT	62.992	GGGATGATGATCGTAGGTACAGGT	62.484	109
HM_5432	contig01619	GA	2	20	TacTcGAGCGGTAGTCTCTGtTA	63.45	GAAAAGCAATGACCCTTcCC	64.048	108
HM_5433	contig11666	CT	2	14	TACTGGTTCTGGCTGCAAGAGTG	62.944	TTCTGCTTTTgAcAACCCAGTGTA	62.942	129
HM_5434	contig32097	TC	2	12	TACTGTGGCACTGTGGGAACTTTA	62.955	TAACAGCATATGAGCAACATGCAa	62.692	119
HM_5435	contig20750	TG	2	20	TACTTGCTTCTGAACAAAGAGGG	63.015	TAGGCATGaAAAGAGaAAcAGGGA	63.312	91
HM_5436	contig08455	TC	2	12	TAGAAaGTTTTTAAGACCTTCCGCG	63.882	CAGTAAGTCAGAGTATCGAGTGTT	63.014	116
HM_5437	contig36924	AG	2	14	TAGACCATGCAAGCAACACtTAC	62.556	GGTTaAAACtTcTTTCgATTGGG	63.08	93
HM_5438	contig37384	CT	2	16	TAGACTCCGgTACCGTACACCTTC	62.723	GGCAGCATACATAATCCCAATCTC	62.931	112
HM_5439	contig18732	GA	2	14	TAGAGAGAAatGAGaAGAGCctG	62.469	aGTCTTCTtTtAcTcCATGtCC	62.974	94
HM_5440	contig39219	TG	2	16	TAGCATCTCAAAACCATAGCATGA	62.949	AATAAAACAGCCAGTTTCTGGTGC	62.755	102
HM_5441	contig24445	TG	2	14	TAGCCACAGCAATAACAGGAAATG	62.453	CCCCCTTTAAcGtTTGTAAATG	61.803	147
HM_5442	contig51852	AG	2	24	TAGCTTCATCTTGGTGCTTCTTC	63.133	GGGCTAGCACTAGCACTTGTGAT	63.073	146
HM_5443	contig40571	TA	2	24	TAGGACAAATCGGAAATCTGATGA	61.961	CCTGTTgATtTCTCTgGcTACTA	62.714	159
HM_5444	contig15134	AC	2	12	TAGGACGATCACCTGCACGTATTA	63.051	TTATTcACCCATTCTCTTGAATGC	63.213	135
HM_5445	contig41651	CT	2	14	TaGgATTCAACTGACTCACACGCTC	62.488	tTCAgAGAGCAGAGAGAttgGTCA	62.8	80
HM_5446	contig32622	GA	2	20	TAGGGTCAAAATGAATGTgTtGGA	62.814	ACGAAATAGaAATCCCGTCTCC	62.797	153
HM_5447	contig12334	CT	2	16	lAGGGTTTTTCCcATTCTCGATcT	63.383	CTGGGTAGATTGTTGATTGGtgG	62.798	147
HM_5448	contig01178	GA	2	20	TAGGTGCCCTTTGAAGCTTAATCA	63.228	CTCCCaAGTACAAGAAATtGcc	63.95	116
HM_5449	contig08861	TC	2	12	TaGTTATAGGGTGgGTGGCTTTGA	62.919	ACaGAAGAACaCaAACaAGGGGT	62.296	90
HM_5450	contig20532	CA	2	12	TAGTTTGAAGAGCACTGGCTTCCTT	62.835	AAGaAACAGCTCAAGCGAAAGAGA	63.044	130
HM_5451	contig33322	CT	2	20	TATAATGCATTCAACCCCGAAAC	63.029	GAATCGaAGACaCTCCcATTGaA	62.565	125
HM_5452	contig47891	TC	2	20	TATACAGTCTTCGCTCTCCCC	62.899	CACCAATGTAGCACTAGGAGAG	62.967	146
HM_5453	contig11295	GA	2	12	TATACTGGGTGTTCAAGCAATGGA	62.731	CTAGatGAGtGTACtCtCTCGC	61.917	110
HM_5454	contig20137	TA	2	12	TATACTTgAaCTCCACACCGGACa	62.828	TCGCTaATACCTTGAAGagcGAGT	62.536	144
HM_5455	contig14515	GA	2	12	TATATCTCTTggaCGggtTCTG	62.592	CTCTCTCACCTGTGACGTGCTCTA	63.041	154
HM_5456	contig41803	TC	2	16	TATCTCCCACTTGGGTGTGTAT	62.798	TCTCTTCTCTCctAAAGTtCCTCC	62.452	136
HM_5457	contig25155	CT	2	14	lATCGtGCTCCcAaCTCTgTTC	63.584	GTGCTAGGGTTTTTCAATTGTGG	62.932	159
HM_5458	contig23153	GA	2	16	TAICTCTACACGCGAAAAaTCGCT	63.362	CTGTCTCTCCCTTCATCCGAC	63.759	85
HM_5459	contig13102	CT	2	24	TATGATCGACGTTTTGCTTAGTGC	62.58	AGCtTCAGAGCTTGAGATTGAtT	62.953	152
HM_5460	contig38503	CT	2	16	TATGCTCCAACCTCCAACGTGTTGA	63.048	CGCGGTAGATTTGCTAGAGGTGTA	63.758	111
HM_5461	contig24913	TA	2	14	TATGATCTGAATTAGAAGGGGGGcG	64.241	CCAATCCCAAAATCCCAATACTCT	63.36	118
HM_5462	contig17350	TC	2	12	TATTCTATCCcACCTCTCAATCAaCA	62.588	TCtATCGCACTTCCGCTCAATTTT	63.03	128
HM_5463	contig46269	TC	2	40	TATTCTTCCCCACACTTTCGCACAT	63.009	TGGGTTTACTTACGAGGAGGATGA	63.104	106
HM_5464	contig02259	GA	2	16	TATGACGAATGAATCCAAAGCA	62.737	ATCaATTcCCCCCTCCCTACTTTT	63.23	129
HM_5465	contig09782	GA	2	24	TATTGCCATTTTTGcCaCATCTT	63.632	aTTGCTctatTctTGATCCATG	62.706	86
HM_5466	contig12966	TC	2	12	TATTGGCTCTCTGTTGAAAAAGCG	62.826	TCCATTGGAAACaAACATCGAATAA	62.511	146
HM_5467	contig34017	AG	2	16	TATTGTGGGAGCTGGGTGGTATTCT	63.108	aAAAAATCAGCCAGCTGCATCTaAT	62.465	118
HM_5468	contig45942	GA	2	12	TCAAATCTGTAAGAAAGTAgcCAATGG	61.121	tCCAAAGCTGCaAATAAAAGAGA	61.467	104
HM_5469	contig33155	GA	2	14	TcAaCAATGTCCCTTGTGTAGTG	62.712	AcACCCCTGTAGTGCAtTTGTT	62.946	137
HM_5470	contig30003	TC	2	12	TCAAAGGACACTCAAGACCCATT	63.212	GCTCAAAAGaAGaAAAAAGCTgG	63.023	93
HM_5471	contig11371	TG	2	12	tCAAAgGTGGGAAAGAGAGAGaG	62.669	TCCTTCATcCTTACgTCTTCGTCT	62.91	117
HM_5472	contig47945	AC	2	24	TCAAACAACCTTAAAAATTTTCAACA	60.907	AgGGATATGAGATaATAAAcCCAcATA	60.405	147
HM_5473	contig01349	TC	2	16	TCAAACAaTGGTTTCTCATCctTtC	62.996	CCTTTCCAAGaGCTCTGCATTT	63.852	97
HM_5474	contig46840	CT	2	16	TCAaCACaGcATCGTCTCTTtC	62.937	TACTTGATCTTGCTTCGGCTACCT	62.646	133
HM_5475	contig12759	AT	2	14	TCAACtCAaATtGTCTCTGcGA	63.265	AGCTGATCAgGGGAACCGAT	63.21	134
HM_5476	contig12857	CT	2	16	TCAATCGCTGAGATCTTCCCC	63.789	CAGTATGAGAGGAGAGAGAAATA	63.065	90
HM_5477	contig38615	GA	2	16	tcAATGgAGGAGTCGTGATgTAAa	62.921	CcATCTTTCTTACCcATgGAGGc	63.278	157
HM_5478	contig39235	CT	2	16	TCAATTTGATGGAAGCATTTGTGG	62.932	TAgGGaAATGAATTgGATGATGGa	63.593	85
HM_5479	contig42453	GA	2	24	TCAATTTCTCAGCAcCAACCAAA	62.943	cTCTCTGCTTatCTCTTgGTCAc	62.016	105
HM_5480	contig45557	GA	2	12	TCACAAAaAGTAAAGAACATTAATcACG	62.607	TCCGAAGCTGCAAAATAAAAGAGA	63.428	141
HM_5481	contig15069	AG	2	16	TCACTATAAAAGGTAGTGACCAGG	62.725	gTACTTGAAGAAGCTTCAACCGa	63.031	108
HM_5482	contig00925	TA	2	12	TACCTCTCTAATCCCCAATCTC	63.3	ACAAAGCAACTcCCACAACTCTCTC	63.027	102
HM_5483	contig29948	CT	2	16	tcactattcttcaactctcccc	62.337	AATACTAGGATGTGAGCAGcCTGc	62.84	101
HM_5484	contig28678	AC	2	16	TCACTCAACTACTCATAGGGAATGTCA	62.341	CAATTCAAGGTAcCTCTCTCTGTT	61.873	148
HM_5485	contig09026	GA	2	20	TCACTTAGAGCTGGCGGTACATCA	62.44	TTTGTGGGTATGGCTTATTATGG	63.022	151
HM_5486	contig18152	CT	2	12	TCAGAAAGCaCcaAAGTTGTGAaA	63.159	CTAACTAGGGCTTCGAAACAGGGA	63.975	92
HM_5487	contig19825	GA	2	32	TCAGAAAGAGATCTCGGCTTCAACT	63.014	TGAgTCATTcGTTctACCAcctcC	63.025	127
HM_5488	contig34608	TG	2	14	TCAGCGTGTtTgATCATCTATTCT	62.173	TGATCAGTCTTTgGGTtGtTtT	63.006	112
HM_5489	contig17712	AG	2	14	TCACTCTCAACATTGATATCCCT	63.112	CAGTACGAGCTTccaTTCTCTC	63.027	155
HM_5490	contig50583	AG	2	12	TCAGGTATATGCGTCTGAGAGCTG	62.962	cATTTCcCAATAATTGTGTGCTTCA	63.134	137
HM_5491	contig05564	AC	2	12	TCATACCTACcTtTCTCTCTCCC	62.863	ATTTGtGGGGGTGAAATTTATGTG	62.909	82
HM_5492	contig46996	TC	2	14	TCATCAAGCTAAGCAAGAGTCCCC	63.133	aAACTGCTTGTtTCTAgGAAAGTTCA	62.867	107
HM_5493	contig36073	GA	2	14	TCATCATTTGAGTGAAGAGAGATGA	63.113	CATTGCATCTACATTTTcGATCC	63.736	146
HM_5494	contig49761	TC	2	24	lCATCTTTAAATGcTgTTTTGGgt	62.922	TAATCTGCTTACACTGCAATCCA	62.959	99
HM_5495	contig17542	GA	2	12	TCATGCTTTTCAAGCTCTTAAATC	62.925	gGGGTTTGAACAGGTtTgATCTCT	62.795	142
HM_5496	contig27039	AG	2	14	TCATTGCGGTCTGAGGTTTATGA	62.845	CAGACTGATTGACtGATtTgTG	61.9	160
HM_5497	contig36265	AG	2	14	TCATTGTGCCATTTTCTGAGACAT	62.938	cCATCACACTCAcAACTaCATaCC	62.848	151
HM_5498	contig48728	GA	2	16	lCATTTCAcCtTCGCTgATCTTCC	63.013	AlTTTCAcATTCCCAACTCTCTCG	62.798	102
HM_5499	contig33733	TA	2	12	TCATTTGGGATACAAATTCGGGA	63.392	GTACTcGTTTtGAGCTGGGATTTC	63.035	132
HM_5500	contig33459	AG	2	16	TCCAATCTGCAAAATGAAATGAA	62.723	cCCCTaCAGACTGTGTTCTCTCT	62.065	133
HM_5501	contig14530	TG	2	20	TCCAACAGCTCAAGAGTGAACAG	63.04	cTCCCCAAcTTTTCTaAAACAC	63.176	85
HM_5502	contig13282	CT	2	14	TCCAAGAGGCAAGTCTTTGgAGTA	63.531	aGATAGGTTGAACCCGGATGACT	63.29	152
HM_5503	contig20845	AT	2	12	TCCACAGCTCTTATGTCCCTCTA	62.426	AGAAACTAGTtagCAACTTGcAGCAIT	62.096	156
HM_5504	contig21532	AG	2	14	TCAACACAGAGACATTTTCTTA	63.048	GTGTTTTCAITCTTgGGTGtG	62.91	108
HM_5505	contig24925	TA	2	14	TCAACCCCACTAAGGTATTTTCTG	62.494	TGAACCTGGATTGCTACTTTTCAT	63.121	88
HM_5506	contig06026	TC	2	20	TCCAGAAcATgTtgggaatttca	63.662	GTTGTGGAaAATgGGAATGaAAG	62.8	143
HM_5507	contig52534	TG	2	16	TCCAGATCAGTAAcAAAGCAGAGAA	62.324	ATTCCCGAAATTCCAATGTTTcIT	62.983	139
HM_5508	contig39952	TA	2	12	TCCAGCACTTAATACACGGGAT	63.046	AACGCTCTGAATCTGAACAAAGC	63.048	144
HM_5509	contig17095	AC	2	14	TCCAATAACAGCTCACAAGAGAT	63.338	ATATAACGCTAATGGTgcCCTGAA	62.854	129
HM_5510	contig27381	TC	2	14	TCCATCTCTACACTTGTtTgTCT	62.397	tTTCGTAgaACAGTATCGGGATT	62.935	80

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5511	contig03595	CT	2	20	TCCATCTTTCCACGAAACAATAACA	62.717	GAAGGCCAAAACCTGAAATTCACC	63.11	150
HM_5512	contig36357	TG	2	20	TCCATGTATTCTCTCTCCAGCTC	63.106	CATGATgCgCaCAACTACAGccTAC	63.091	106
HM_5513	contig25254	GA	2	14	TCCATTGACAGACGGAAGTAGAGA	62.367	TTTTTAACCCCTTTTCGTTTCCTC	62.706	147
HM_5514	contig43745	AC	2	12	TCATTCTTGATTTAGGGGTTGTG	63.3	TGCAAAATCATaAGGAAGACATGCCA	63.801	140
HM_5515	contig25150	CT	2	14	TCCcAAAAGGAAAAAGaaGAAAGAA	62.603	GGTTATAAgTgGGGATGTGAGCA	63.329	87
HM_5516	contig01464	AT	2	16	TCCCATATATCATACGCAAAACACG	62.861	GAAAGAGAAAAACGGATGACCAaA	62.703	139
HM_5517	contig03367	GA	2	12	TCCCATTTTAGTATACCCGGTTCC	63.175	AAAAACCTTTATAGGATCTCAGCCG	62.9	115
HM_5518	contig31217	AG	2	20	TCCCAAAAAATCAAAATCAAA	62.8	AcCCGTACCTCTATCTGCTATCTCA	63.115	97
HM_5519	contig29069	TC	2	16	TCCcTAACTGAATTTCTGAATGCG	62.705	CAAAATGTCTGGGATGAAGAAGTAG	62.343	142
HM_5520	contig00875	AT	2	16	TCCcTGGAACcAGAAATATCA	62.884	AAAAGAAAAATTGCCGGAATAA	62.91	152
HM_5521	contig07091	AT	2	12	TCCGAAATCTGAATCTTTCTCGAT	62.328	TTTGAACCTCCACTCGTACTGTGA	62.412	151
HM_5522	contig33768	TC	2	14	TCCGAAACACTTGATACCATCAACAT	62.726	AGCAGCTTGGCAGAGcTATAAGa	62.972	123
HM_5523	contig28508	AC	2	16	TCCGACATATAATCTCTTGGCATCA	62.626	GATgATATGATCACTGAACcCCC	61.659	136
HM_5524	contig25681	CT	2	16	TCCGACTACTGCTTcTCTCaCTCA	62.827	GaAAAGaGAGGGTGTCTCGATGGA	62.987	147
HM_5525	contig24240	TC	2	16	TCTATAGCAGCTTCGCAACTAC	63.067	AAATAcGACCGAGaGAGaACACAC	62.838	114
HM_5526	contig00456	AC	2	12	TCCtCTATTTCaCTCTCTaTATCA	60.824	GATTGCTGATTGTTGTTCTCCATT	61.56	139
HM_5527	contig47318	GA	2	24	tcttgacctttgttctactcactg	62.81	tgttgggagtagcgaatcatttt	62.813	121
HM_5528	contig19701	GA	2	12	TCCTTAAGGTACgTCTCCCAaCa	63.113	CAATCTGAGCTCCCTcTCTCAAAC	62.898	93
HM_5529	contig51363	GA	2	14	TGcTTCCAATTCCACTCATCATTT	62.987	TATACACTTaAAACcCCCCAcgc	63.146	152
HM_5530	contig39565	TA	2	16	TCTTCTCATTTTCAAGAATTTCCA	62.98	TTGATTGGAATAAGGTTTGGTG	63.097	134
HM_5531	contig12693	TC	2	20	TCCTTgTTCtCTCTCTCTCCCT	63.273	TCACTctcccTTAGATTCGTG	62.894	89
HM_5532	contig12609	TC	2	24	TCCTTcCTGCaATTCTTTTCTG	63.104	AAAGACGAGTGAGCAAGAGTTGT	63.812	108
HM_5533	contig14570	CT	2	12	TCCTTGACCTTATCTTTCTCCCT	63.156	GGAAAAGGAGAGATTAAAGTCCCG	62.584	102
HM_5534	contig04263	GA	2	12	TCCTTGGCTAAATGAAAGCTCTG	63.027	CCCCCTTCTCTCAAAACCTCAT	63.068	139
HM_5535	contig05852	TC	2	12	TCGAACACGCGCATAGCTACTGA	63.085	GcTGAGCTGACtCTAGGTAGACA	62.506	141
HM_5536	contig28098	AG	2	20	TCGAACAGCTCAATCAACTCTTTC	62.086	ATCgGAGACAAAAATCAAGCTCTC	62.198	132
HM_5537	contig26767	AG	2	16	TCGAaCTTtGAGAGCTTtCTTCC	63.129	TgaCTCTCtCAhTATCGTtccC	63.861	106
HM_5538	contig43599	AG	2	12	TCGACAAACACTCGTATCTGTCAT	63.078	AAATCAGAtCTCCCTCTCCAGTG	63.27	154
HM_5539	contig10805	AG	2	16	TCGACTGAATAGGAAGGtGAGAC	63	ACTCGAGTTCGGAATCTCTCAaAA	62.909	136
HM_5540	contig39071	TA	2	12	TCGAGAGAGGAGATTGAATTTGA	62.593	CCAATCCGaATTcAGGTAAATATCA	62.236	156
HM_5541	contig16266	TC	2	12	TGgaGTCTTCTAAAGCCCAACG	63.031	AgGaTtCTGTAGACGaATTGCG	62.836	117
HM_5542	contig19780	CT	2	20	TCGAGTTCAAGAGACTTGCACATA	62.411	GACGGGaCCGTTCTGTAGTAC	61.966	115
HM_5543	contig14046	CT	2	14	TCGATGCCAACTAGTCTACTGCTG	62.872	GGCCaCTGaATCCACTTTTGTAG	63.129	123
HM_5544	contig36076	GA	2	12	TCGATTTCGAATTTGAAGTCTCTT	62.495	CTgTcGggGCTAtgTATAAGTTG	62.932	105
HM_5545	contig46911	CT	2	16	TCGATTCTTTCGTTGTAGAACTG	62.705	AATGAGCaAAGAATCCCAAAATACA	62.912	147
HM_5546	contig04339	AG	2	12	TCGATTAGAGGAGTCCAAGAACG	63.006	TCTCTATCCGCAAACTCTCCGTA	63.126	142
HM_5547	contig40349	CT	2	16	TCGATTTTGGGTCTTCAAGGTAA	63.002	ATcCTTTATTTTTCAGTCCAGCCG	63.676	121
HM_5548	contig46350	TC	2	32	TGcCACTCTTTCTCTTaCTTaCTT	60.75	TGAGAGAGGGAATATTGAGACAA	61.289	113
HM_5549	contig46294	GA	2	16	TGCGTCTTCTACTCAATCCATCAA	62.397	CCTCAAAATCCAAATGaCTAAACCG	62.906	123
HM_5550	contig30380	AT	2	14	TGCTTCTCaGcTAAGAAATaCGC	63.055	aAAGAAAGAAATaGTCTGacCgAgTTG	62.37	136
HM_5551	contig15447	GA	2	12	TGCGTTGAAGTTAAAAAGCGGAG	62.954	GACACCTCTTCTCTCAAAACGGAC	62.693	138
HM_5552	contig27386	AG	2	12	TCGGTGaGACGTGATGACGAAT	63.152	AAGTTCTCTGTCTCTCACTTCCG	62.604	124
HM_5553	contig15508	TG	2	16	TCGGTTGAaCccAGTGATATAGGT	62.91	TTCACTGTATTTTGGGCTACCAgG	63.216	144
HM_5554	contig09676	CT	2	20	tGCTCACCAATAGtaGGCTTCTC	62.923	ATGGAGTTAAACAGGTGGTGTGGT	62.922	138
HM_5555	contig27689	AG	2	14	TGTCCTCAACTTCTAGTGTTCAAA	62.192	TATCTCGCACTCAAGaCAGTGGT	62.951	145
HM_5556	contig14369	GA	2	32	TCGTCCCAAGGATGTGATATAAAC	63.211	ATCCAACACAGcCCTAAATCAAAA	62.922	157
HM_5557	contig51173	AG	2	16	TCGTCCGACATGTTCTTAGAGAG	61.969	aTATACTTTTACACGGTGTCTTGc	61.568	89
HM_5558	contig01826	AG	2	12	TCGTGTTGGTGTGTTCTCACTAT	62.972	CaTaAcTTCCAATATACCTCGCTGc	62.198	131
HM_5559	contig12001	TG	2	14	TCGTTGGAGATGACAAGTTACAGC	62.741	AATTCTCTGGTGAAGGTTTGGTT	63.285	145
HM_5560	contig17439	AC	2	12	TCTACCACAAGACACAGGTTCC	63.653	GCTCAGGTTTTCTGTAGCTTTGG	63.246	152
HM_5561	contig46174	GT	2	16	TCTACTCTCTTTCATGAGCAATCA	62.786	CacCaCaCaCaCACTACACCAAA	62.982	156
HM_5562	contig43023	TG	2	14	TCTAGCTTCTTCAACCATCTGCTC	63.022	GTGAGTcGtTcCCCTGTGTTGTAT	62.612	117
HM_5563	contig12814	TC	2	12	TCTAGTGATGGGGTTTATGGCTT	62.122	CCTCTGTGCTCTATGCTAATGGC	62.523	83
HM_5564	contig11090	TA	2	12	TCTATCATATCAGGCCCTCTCAC	62.789	GCTACTCAACGTCTCTCGGATA	63.035	149
HM_5565	contig13511	TC	2	24	TCTATGAATGTTCTGTTCGCTC	62.549	AGGTTTGGTGAGCTTACAGAGAG	62.919	126
HM_5566	contig35539	CT	2	20	TCTATCTCTGTAATAACACCAACA	61.986	CTTCTCAGGTTTAAATCGACGACAT	61.704	159
HM_5567	contig00983	AG	2	24	TCTCAAAGCTTcTGAACaCaAGTT	62.006	TAATTTGTCCCTCTCGCTCACT	62.522	106
HM_5568	contig41431	AG	2	12	TCTcTGAACCCCTGAGAGAAAGG	63.085	GTGTACATATCCGAGGAGCTTGG	62.91	158
HM_5569	contig36360	AG	2	14	TCTCCGAaAaCTTCAATTTCAAAG	62.798	AATCTCAAAATGGGGAGcAAAAGT	63.184	145
HM_5570	contig40260	TA	2	12	TCTCTAGTtGtGTTGGTtTGA	63.036	gtttcggaggtaaaatctcattcc	63.176	139
HM_5571	contig15688	TC	2	24	tCtCTCtCtCTCTCTCAGCTTCAa	63.079	TTGAGAGATTGTTCCATGGGGAT	62.887	112
HM_5572	contig19620	CT	2	14	TCTCTACCaATCACCTCTCTCTC	63.096	AATCCAACCAACAGaAGaTcAGG	62.684	93
HM_5573	contig17411	AG	2	20	TCTCTCAAGGGAACAATAGCATTC	62.9	cTCTCTCAACATCATCTTTCATCA	62.564	115
HM_5574	contig03300	AG	2	14	TCTCTGGAGGAAGAAGGAGGATT	62.948	CTTCGCTGCTCTCACATACtTTT	63.044	122
HM_5575	contig04035	GT	2	12	TCTCTGTGCAATCTCTGATCGTA	63.375	AAGAAGTAATAGCGGAGAGCAGCC	63.233	126
HM_5576	contig16465	CA	2	14	TCTGAACGATAAAGGCATCACaA	62.946	GAAGAAGAGGGAGGGGAACaA	62.968	136
HM_5577	contig51191	TC	2	24	TCTGAACAATGTGGTGTTCGTCT	63.053	GGAAATCAGTGTGTTGGAGCGAG	63.45	141
HM_5578	contig08157	AT	2	14	TCGAATTTCTGGAACAGTGACTCAA	63.444	TTACGCGAATAATCAAGTCGGAT	62.948	93
HM_5579	contig21329	TC	2	14	TCTGCTTTTGTCTGGTAAGTTGA	63.068	atctccctcttctagtcttgg	62.466	109
HM_5580	contig13709	TC	2	24	TCTGGAGTGAAGATCAAGGAGATT	63.424	CCAATTgCTCaAcTTCTAGCTTC	62.633	158
HM_5581	contig18110	TC	2	12	TCTTACTCTTCTCCCATTCGAG	63.006	GGATTACGAGCTGCTCAAGAGAG	62.755	160
HM_5582	contig20051	TC	2	12	TCTTCAAATCGTCAACCAATCTC	62.594	GTGACTGAGTCCGATTCCGAC	63.247	159
HM_5583	contig10697	TA	2	14	TCTTCACTGGATGAACAGaAGC	62.937	CGAGCACCTTAtATTgTCTcT	62.851	132
HM_5584	contig43254	GA	2	12	TCTTCTATCTATCTCTCCGACG	63.204	CAACCTCTACACTCTCGAGCACa	63.063	117
HM_5585	contig31605	CT	2	12	tCTTCCACCGTTGAaTCTTCACC	63.537	CTTCACAGCTTCTTCAACACAGa	62.955	154
HM_5586	contig00191	AG	2	16	TCTTCTCCGAAGAAGGTTTCAGA	62.984	AAAAACCCCTACAGTTTCGTTTGA	62.139	120
HM_5587	contig10949	AT	2	12	TCTTCTCTGTTCACTGAAAACC	62.997	TGGGTTTCATGCATCTTTTGATT	63.108	145
HM_5588	contig23457	TC	2	20	TCTTCTGATACGTCTTACCCCaC	62.522	TGGATTGAAATGCACCTCTCTCATT	62.173	129
HM_5589	contig01133	GA	2	14	TCTTCTGTTCTCTTAAATCAACCG	63.006	CTCTGATCCCGCAGATTCAa	63.606	125
HM_5590	contig24923	GA	2	12	TCTTCTGCCTTGTATTATCGTTC	62.815	tccatttcacagtgCTTGAGTAA	63.048	125
HM_5591	contig22120	TC	2	12	TCTTCTTCAACAATCAACGCAATT	63.065	TGACTGGAACAAACATCCACGTT	63.019	115
HM_5592	contig24155	TC	2	20	TCTTCTTCCAGTCGTCTCTCAGT	63.001	AGCCACCACAATCGTTTACICATT	63.048	82
HM_5593	contig45625	AG	2	14	TCTTCTTTCGCTTGAATCTCATC	63	CTaATAAATCCCAATCaGCTCtCC	62.423	101
HM_5594	contig48735	GA	2	12	TCTTTAGTCACTCTGAAAGCATCG	63.146	TCTGAATTGAACATCGTAGCCaAA	62.946	152
HM_5595	contig51220	GA	2	16	TCTTtGAGGGGAATTTTGAATTT	63.06	cCAcATcCacATgTAACTGCTCT	62.517	129
HM_5596	contig30354	GA	2	12	TGAAAATGTATCAGCGAGTCTCG	62.744	TTCCAAGCaAAACCAACTCTTTTC	62.823	156
HM_5597	contig02472	AG	2	14	TGAAACAGAGCATAGTCGAGAAGAGA	62.946	ATTGTGAaAaCCACGTTGATAAAC	63.244	160
HM_5598	contig47164	AG	2	20	tgaacactgtcttgagatcagtc	62.937	ACCAATATGGAGTAAATCATTcccc	62.317	134
HM_5599	contig33542	AG	2	16	TGAAACCTTTGATATCGCTTTGGT	63.03	TGTAATCTCGCAITTACTTCACAAAG	62.255	130
HM_5600	contig19076	GA	2	14	TGAAACCGGAAGAGGTGGGTA	63.113	TCTCTTGTAGCTCCTAAGGTGGG	64.092	86
HM_5601	contig01901	AG	2	24	TGAAATGTGTGAGGCTCTGAaCTT	62.397	CCCTcCCTCTCTcTACCAAC	61.486	84
HM_5602	contig28751	GA	2	12	TGAAcCAcCTTAAAAAGcAACAATCA	62.843	CTAACACACTTGGTGGTGGTGTg	63.723	160
HM_5603	contig01107	TC	2	16	TGAACACCTTCAAAACaTCTTCAAA	62.012	AGATTTGTTTGGTTTCGGTGGAT	63.011	111
HM_5604	contig10816	AG	2	12	TGAACCGATAAATGAAGCAACTGT	62.024	ATCTCCACCTCCGTAACCTCAACT	61.568	108
HM_5605	contig31363	AG	2	12	TGAAGAGAATTAGAGAGATTGGGAAa	62.988	TGGACATTTGTTCTGTTTGGGTA	62.614	105

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5606	contig43649	AG	2	12	TGAAGAGAGTTGAGAAAGAGGCCA	63.856	CATTGGACTCCCAAACTgAGTcAc	64.21	128
HM_5607	contig18157	AG	2	20	tGAaGATGGCCcGAATTAGATAGA	63.105	TCCTcTCTCTCCGACTcTcACAT	62.991	87
HM_5608	contig25025	AT	2	12	TgAAGCAAA TTCTcTTACCCAA	63.216	GCTTTGGGACATTCACTGATCATA	62.997	157
HM_5609	contig22200	AT	2	16	TGAAGGACTTTCAcAAAAAATTGGA	63.013	AGTGTAaATCTATCaTTCcGcGCC	63.493	160
HM_5610	contig07498	GA	2	16	TGAAGTTACATAcTCTCGGATGA	62.845	TCATCTCTCGGCTGCTTTAATC	63.125	100
HM_5611	contig42705	AT	2	12	TGAATCAATACTGTAAATTCcAAAGC	60.87	tggttctTGATTTCTCTAAcCTTTg	61.279	158
HM_5612	contig10963	CT	2	12	TGAATCCTGTCTACGCTCATCTCA	63.375	TCCGTATGTGTAAAGtcGAAGCGAT	64.084	100
HM_5613	contig42082	TA	2	14	TGAATCTCACTTTTGATTGGGT	62.899	CCCAGTTTCACTCATTCTCTAGC	62.598	141
HM_5614	contig13081	AG	2	14	TGAATGTcAGCCcCTTTCTATT	62.912	GGCCTTCATTCTcTTTTCAT	63.772	127
HM_5615	contig38176	CT	2	12	TGAATTGACACTGAGGATTGCTG	62.744	CCTTCACGTCATGAGACACAGAGA	63.141	82
HM_5616	contig38373	TC	2	16	tGAaTTTGATCCGTGACTGTGAGT	63.044	GATCCCCGgAAAAcACAATTC	62.444	88
HM_5617	contig18941	AG	2	12	TGACACAGaAGGGGAGAGAAaAGc	63.225	AtTTaACcAGTTTcAAcGcggAC	63.447	157
HM_5618	contig20225	CT	2	16	TGACATGtTTTGGAATAAATTTG	62.919	aAAACCTTAGcCAAcTCTCCAGGG	63.094	126
HM_5619	contig41608	AG	2	12	TgaCcGGAGACTCCAAAGTATAGTc	63.01	TcTCTcTCTACCTCTCTCTCaA	63.079	160
HM_5620	contig37706	CA	2	12	TGACTCAAGAGCGGAGAAATCCC	63.022	AGATTAGAATGTGGGTTTGGGT	62.983	151
HM_5621	contig09367	AG	2	12	TGACTTTGACCATTCTTGGTTCA	63.141	GACTCGACCTCCGTGACAGTA	63.837	139
HM_5622	contig01659	GA	2	20	TGAGaCAATAAAATACCGAGGCG	63.428	CtGCTCTCTCACTCTCTCact	62.791	132
HM_5623	contig21604	TC	2	16	TGAGAATATAAGTGTGGAGGGCT	63.112	ACtGACAGCAGGGAGACACAGAT	62.575	125
HM_5624	contig30484	TG	2	12	TGAGACCACCTCAAAAAATGCAGA	63.048	gcACCTCAcTcTCCcATATCAT	62.904	144
HM_5625	contig37937	GA	2	12	TGAGCATTAAAGATGACGACGAAa	63.059	GGAAACCAACTAGAACATCTCGTca	63.046	87
HM_5626	contig06936	GA	2	12	TGAGCGACTAGCACAAACCTTTC	62.985	AATAGGGGCGAGTGAGAGAAAAAG	63.192	158
HM_5627	contig02487	TC	2	20	TGAGGAGGAAGAAGAGAGCAAGTG	63.539	CgCTCATCCAAAGTTCAAAATCA	64.448	98
HM_5628	contig42706	AG	2	14	TGAGGCATGTGGTAATAAATCTTT	63.043	TTTaAGAAcCAATAAGTTGCGCCA	62.933	149
HM_5629	contig17597	TG	2	14	TGAGGCTTGTAGTTGGTCTATG	62.656	ATATGaAACTCATTGCTCACTGGC	61.697	123
HM_5630	contig21230	GA	2	14	TGAGGGAAgTAaCTGTGcCAATT	63.129	CATATaCaAAATGGcTTTGGCCT	63.154	148
HM_5631	contig06680	TC	2	20	TGAGTCCAAGTAGGGAAGTGAGAcc	63.106	GAGAGAGGGGTTGGAGAAAGAGAGA	63.692	157
HM_5632	contig01259	TC	2	12	TGAGTcGtCGTGAATCTACTCGTA	61.231	ATGACTCATCAGACACGTCCA	60.577	137
HM_5633	contig12861	TC	2	12	TGAGTCTcCTCTTTGTTTCACT	62.677	AGGTAcCTTTTcTcCCCTTGGAT	63.431	135
HM_5634	contig08193	GA	2	16	TGAGTCTTCCACCAAGTTTTCGAG	62.93	CaATaCaCACTGTCTCTcCCCT	62.793	141
HM_5635	contig43240	CT	2	16	TGAGTCTTCAAGCAACTATAACCCA	62.327	tCTGAaAGCAGCTCAATaCTCGAAG	62.324	140
HM_5636	contig36294	AG	2	14	TGAGTCTTGGTCTCGAAGTGAa	62.69	GCTTTGAAGACACACCCTCTCT	63.249	149
HM_5637	contig24509	GA	2	16	TGAGTTGGAAGTTCTTCTGGGG	63.848	ACTCTcTccCTcTCTCCAGTCC	63.711	82
HM_5638	contig28092	CT	2	20	TGATAaGTGGGTCCATGCTTTTaT	60.912	TTGCAAAAGACGTAGTCTCTCaa	60.586	146
HM_5639	contig34854	AG	2	16	TGATCGAAATgATTGGAGCATGA	62.935	cGAAACCTgttAAGGCTCAGTTTgt	62.943	113
HM_5640	contig27435	GT	2	14	IGATCTTTCAAGGAGCAAGAACT	63.014	CAATTGCGTGTgaaTGTGAATATg	62.337	158
HM_5641	contig10893	TG	2	20	TGATGATGATTGGAGATGAGGAAG	62.55	CaAAAAcCAAAATACCCCAAAAc	63.459	159
HM_5642	contig21846	GA	2	14	TGATGGTAACAGTGGATGGTATT	62.594	CCCCAAACtACcAGCATCagTAgA	63.531	118
HM_5643	contig01789	GA	2	16	TGATGTATCGCTTAAAGTTTGGG	63.322	AATTTCtCaCCaACcAACAGCTC	62.824	91
HM_5644	contig09333	GT	2	12	TGATTaCACTTCACTGCACTGCC	63.628	GGGTTTTTgTAgAAATTTCAgGGG	62.977	124
HM_5645	contig48090	AC	2	12	TGATTCGCTAGTGAACAAATGAGTG	62.689	ctgaCACTGTGGTCCACTAGAAg	62.966	127
HM_5646	contig05421	AG	2	16	TGATTGAAaAGAGACACATCCAT	62.819	CacaAACACTTCGGAATAGGaAAGT	61.851	101
HM_5647	contig37061	AG	2	32	TGATTGaaTAAATTTGCTGAGTGTG	63.158	AGTGCTCTcTCCATCGTTACGC	64.116	131
HM_5648	contig14971	TA	2	12	TGATTTCGAACaAaTACTGTCAATACAT	60.077	AACTACTGGGGAGGATTATTCTGG	60.918	120
HM_5649	contig02124	CT	2	16	TGATTTCGtATAAATTTCTCGAGCCA	62.278	cGACATAATTACcggAGACGAAAG	63.027	154
HM_5650	contig41915	TA	2	12	TGCAAGCAACCTCTAATTgTAAGAG	63.859	GaTctTgGaaATgGaaAgTAGGGC	63.282	158
HM_5651	contig14786	AT	2	16	TGCAATTGAAACAGAGCTTATCACA	63.712	AAGGTACGTATGcCTcCTCTTcC	63.008	160
HM_5652	contig51978	AG	2	14	TGCAGAGTGAGTACGTGTAGGTGG	63.077	AGTGCTAATTCCCAAGAACCCGaaA	62.299	137
HM_5653	contig22085	GA	2	16	TGCAGCATCAGTACAGAAATGcC	63.623	TTCTAGGGATTGCATTACcAGGT	63.121	127
HM_5654	contig05967	CT	2	12	TGCAGGAATTATTCTCGAAGATCAG	62.923	GcCCaATAGCAATAGcTGTAGATGA	62.774	140
HM_5655	contig15147	GA	2	12	TGCAGTATGAGATAGGGGCTTGA	62.924	CTcCCCTCTCCCTcCTCTCT	63.239	90
HM_5656	contig46167	GA	2	12	TGCAGTCTCATAATCTCCCTCCAT	63.323	CTcTaaAATCgctTTTCCATTCTCT	62.992	125
HM_5657	contig48091	GA	2	14	TGCATCTATAAACTCTGAACCGGA	62.11	ATCCCCAAATCAACCAACACAGAGA	62.996	139
HM_5658	contig33090	AG	2	20	TGCATCGaAGGGGATTAATGTT	62.925	GlCTTCGCTCTcTcTCTCcTaT	63.312	128
HM_5659	contig43430	TA	2	12	TGCATCTATGATACCAAGTGTACGAAA	62.888	tGTTTTGGAATCAGCAAAATGAGA	62.932	144
HM_5660	contig03550	AG	2	20	TGCATCTCTTTGCGATATCAGA	63.27	GagGaACTAgGGcACAGcTtaTc	63.718	96
HM_5661	contig11435	GA	2	16	TGCATTGCATTCAACATATCTCTAA	63.474	cgtTCaGgGAATTCGaGaAGACT	63.317	114
HM_5662	contig10919	TA	2	16	TGCCATGAATCTAAATCACCACT	61.889	GCACCTGGGTTATTGATTACTTTG	60.937	156
HM_5663	contig12395	TA	2	12	TGCCCTTGAATACTCCAAGTTAAT	62.233	CCATGGGTACATAGCAATGTGAAA	62.946	130
HM_5664	contig36029	AG	2	14	IGCCTATTATTATGGCTctGcCAG	62.684	cGgtTAcCCCCtAAAcCTCaAAC	62.998	98
HM_5665	contig07745	TC	2	16	TGCCTCTCTCGtTCTTTGtAaTc	63.022	AATCAATCAAAATCACCGGAAG	63.317	105
HM_5666	contig18406	CT	2	14	TgCgaaaaTGTCTATGAAGtTTTTG	63.456	TGcCCGTtTCTaACAAGcCAAACT	63.354	159
HM_5667	contig05886	TC	2	16	TGCGACTACTaGtACACCGGTTTC	62.767	AGAGTTGGGAGTTGTGTGCTCAGT	63.703	118
HM_5668	contig12486	AG	2	16	TGCGaTCTGAGAGAGATTGGAAG	62.071	ACTTTTcTaTCGCAAGCTCAGAGT	62.03	190
HM_5669	contig27917	TC	2	12	TGCGcTCTCTcTGAGcATGATtT	62.864	GACCTCCGCTTGAACGTATAGAGA	63.035	88
HM_5670	contig15726	GA	2	16	TGCGGCTCTACTGTAAGAAAGCTA	63.663	TcCTCTcTgtTATcTCTCTCTCTC	62.788	111
HM_5671	contig34692	TA	2	16	TGCTACAAaGTTTCAATTTTTAGGgC	62.781	ATTCCAAAGTGGGTAACTTTTGGG	63.372	135
HM_5672	contig10183	AG	2	16	TGCTAcTCAgAAAAAGGGGTAAGT	61.625	CATCATCTCTcTCTATCaCCTTCTG	62.228	140
HM_5673	contig45815	AC	2	20	TGCTATGGAGGTTTTTGAAAGGTA	63.014	TGCTCATCAATAAATGACCAACAAa	62.538	157
HM_5674	contig41945	TC	2	14	TGCTATGTAGTCACTCAGTCCCTC	63.544	cccaCTACAATcCAAGCTTCACT	64.022	160
HM_5675	contig25318	AG	2	14	TGCTCTGgCCTTATCATCTAAg	62.922	ttaaactgCgCACTtCtTcTcT	62.754	148
HM_5676	contig41524	AG	2	12	TGCTTATGACCTGATGAGATGA	63.028	CgGTTCaCaAAAGTCTGAAAATCC	63.117	90
HM_5677	contig32616	TC	2	14	TgGAaCTTcAAaCCCTCTGTATC	62.684	GGCCAGCTTTTGAAGAACAAAGA	63.019	88
HM_5678	contig05148	AG	2	16	TGGAAGAAAGGATCCATCATAGGAA	63.074	tccccctTctTCACTTCTTaAcC	62.968	92
HM_5679	contig23364	GA	2	16	TGGAAGCTTTTGAAGGACTCTTTTG	63.113	CTCAGAGGCTAGCAGTAGCACAC	63.912	148
HM_5680	contig37631	TC	2	32	TGGACCTCACTATCTCAGCTAC	63.014	AGTGGGTGTtAcCACATACCTTGG	63.233	155
HM_5681	contig34636	AG	2	12	TGGAGAGAAAGAGTCAAGCAACC	63.225	AGCGAATGGACTCTCTTTCTCTCT	63.096	157
HM_5682	contig25545	GA	2	12	TgGAAGCAAGAGATCATTTGGAAG	62.828	GATCAACAGTAACTCCCaATTC	62.793	93
HM_5683	contig26286	GA	2	16	TgGAAGaATTTGAGATTGGAGAGAG	63.076	ATCgATATCTGtTCAaAAAcGTC	63.346	149
HM_5684	contig12622	TC	2	14	TGGAGTTGCAAAATTTTCTGCT	63.347	CAAACTGAAATTCACCGTATCg	62.716	152
HM_5685	contig40530	AG	2	12	TGGATTCAATAATCATTTCCAAACC	62.986	ATGAAGCTGGACATGGCTCTCT	63.672	151
HM_5686	contig16107	CT	2	24	TGGATTGGGAATTTATAGTGGTGG	62.993	GGAAACCATTTGTGCTCACTCGA	62.692	157
HM_5687	contig12114	GA	2	14	TgGCAATATCATCTCTCTCTGAT	63.103	ATGGCAGCTTCTCATaATTCTCG	62.937	138
HM_5688	contig25079	TG	2	12	TGGCATATTTTAAAGCATTTCCAGG	63.222	GCCTTTGCTCTTTTGTATGTGGa	63.648	160
HM_5689	contig33896	AG	2	12	TGGCATTTTACTACCTCTCTTCC	62.619	TGcACcAGCGAGTCTCTTAGTtT	62.835	123
HM_5690	contig23536	AT	2	12	TGGCtTCTCTCAAGAGGAAAcTA	62.508	TTCTGTTATGaAAACCGCAAAATT	61.971	138
HM_5691	contig44091	AG	2	16	TGgCGaAGGAGGATGTAGTGTGT	62.624	TCTCTTCTCTcTcCTcTCTGtTCT	62.763	103
HM_5692	contig30965	TC	2	12	TGGCTCTCAAAATTCaAaCTCCTC	63.009	TTTGAGATGGGTTGTGTTTGTGTTG	63.146	160
HM_5693	contig44097	GA	2	24	TGGGAACCAAAATgAAGAGAGAA	63.19	CAAACTCAAGCTTcGCTAGAATCTCA	63.148	145
HM_5694	contig46267	AG	2	20	TGGGAACGCTGTGATGCTGA AAAAC	63.762	CTcCaGtTCTGTTCCGATTCTCC	63.525	159
HM_5695	contig04586	GA	2	16	TGGGACGATTTTCAAAACCACTT	63.529	TATTGACACGACTTTaAACGCTTc	63.555	145
HM_5696	contig25839	CA	2	12	TGGGAGgTAAATTAACGAGTTTGA	62.798	ATATCTCCCTCACCACTACCC	63.579	87
HM_5697	contig37952	GA	2	12	TGGATTCTGTAAGATGAGAGAAAT	63.311	CTCtCTCAGAGTCTGGGAGTTGG	62.984	136
HM_5698	contig18394	AC	2	20	TGGGACCGGCTCATTAAGTGTGA	64.698	CGGCAACCTACATCAAAATa	62.987	158
HM_5699	contig36479	AG	2	24	TGGGATGACTCAGATCCTTCCAT	63.093	CAAGCaACAACATAATTcCTTGAAG	62.37	120
HM_5700	contig46504	AG	2	12	TGGTGCCATTTTAgAGAAAGAAA	63.109	ccaactccactctaagTCaAt	62.895	149

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5701	contig44803	TG	2	14	TGGGTTaGAAAGAGGTAATTcGaCC	62.807	GGGCTaaACtCTGCaAAAACTCCT	63.016	157
HM_5702	contig26832	GA	2	12	TGGTAGaAGGCTGAGAGGATTTGG	62.907	CGaAGTTCAGAGTAcCTTCAaTaG	62.438	144
HM_5703	contig25028	AG	2	14	TGGTATGTAAATGAGGGTTTTGg	63.002	GGGTatTAAGTTCGAACAGCAGACAGA	62.755	152
HM_5704	contig31487	AG	2	14	IGGTCCTCGAAATAGCCATTGT	63.03	GGCTCCTCAGATTCTCAGTCTCTC	62.23	144
HM_5705	contig44200	CT	2	16	TGGTGAAACCAACAGTAGCTGGAA	63.036	TTACATTgCCTAATGGCCCTAATC	62.357	153
HM_5706	contig16050	CT	2	16	TGgTGAGCCACACATATTTTTgt	62.643	CAGAAGTATAGCTGACACCCGCT	63.057	156
HM_5707	contig37206	TC	2	14	TGgTGGaAGGATCAACTGATTCAA	63.132	CGAGGTaATGTTCAAGaCAATAGGG	62.139	83
HM_5708	contig49493	TC	2	24	TGGTGGTCGAATGTAAATAAAGGG	63.109	GGTCGACCACACTGACTCTCTCT	63.355	157
HM_5709	contig42445	GA	2	12	TGgTTCGACTCAACAAATTGAGAA	63.034	AAGCTAGAAGTTTTATCACC GCC	63.028	148
HM_5710	contig20773	TC	2	14	TGGTTGGATCAaATGgTTTCTt	62.8	tTGAgGCAACACCTTCATACAAAA	62.843	117
HM_5711	contig03619	AG	2	12	tGgTTTTagCTACAAaTTgCTGgG	63.434	CTCTCTactTCCAATCCAAGCTc	62.712	94
HM_5712	contig26356	AC	2	16	TGTAACCAACAATTACGAGCCCTAG	62.487	GAGGCGTTGATAGGCTTAGCATTT	63.041	153
HM_5713	contig18208	TC	2	20	TGTAAgGAAGATCTCCAGCAaGATT	62.509	TCCAGCACACTACAGAGGGTACAA	63.168	157
HM_5714	contig02754	GA	2	14	TGTAATCTGAGACACTAGCATTTTTG	62.876	CACCTCTCaCaTaAAGGCAATTCAA	62.859	107
HM_5715	contig51442	AG	2	12	TGTATAGGCTCTGGTGTTGGGTTT	63.031	AATTCTgTGAAGATGaAgTGTGGT	63.128	156
HM_5716	contig00811	TA	2	12	TGTATAGGCTTGATTTCGAGAGCTT	62.585	TGGA AAAAGaAGATCTCAGGCATC	63	143
HM_5717	contig42218	AC	2	16	TGTCaAGATTAACCTGGAATGGACA	62.841	GCCTTGaATTATAAGGCaATGagG	63.114	143
HM_5718	contig39739	AT	2	14	TGTCACATTTGTTCTCTCATGTCCT	63.256	CacAcAGACaCaAgaCACACTcTc	62.263	81
HM_5719	contig12319	AG	2	16	TGTCAGTTGTCACTGGTGCACATA	62.755	GTGGCTCTGGTTCACTCTCAGC	63.747	157
HM_5720	contig30584	CT	2	12	TGTCATCTTCAGACACCTTCGAG	62.919	TGATTGGTTGAGAAGTCACAGAA	63.132	159
HM_5721	contig09542	GA	2	12	IGTCCCGAATGCTTTAGAATGTg	63.009	AGTCTTCGtCATCaCacCTCTTc	63.123	120
HM_5722	contig39410	AG	2	24	TGTCGATCaTCTGaAGACTGAAGC	63.047	TCCAGATATAGCAATTGCGTTC	63.142	105
HM_5723	contig13808	CT	2	24	TGTCGACTGCTGCTCGAACATTT	61.984	GaAAAGcCCTctTCTACTGGGAG	62.886	140
HM_5724	contig25918	GA	2	12	TGTCAAATTTGCTGCTCTCGGA	62.528	GTGATcCTGATTGAAAGTTGGGAG	63.204	83
HM_5725	contig25918	TC	2	32	TGTCGTGATATCGTCAAAATCCG	63.27	TATATACTAcCACCACCCACCA	63.312	110
HM_5726	contig15426	CT	2	14	TGTCCTCCCATAGTCCCGTAAAA	62.906	TcATTGGTTTTaCCCATTTgTc	63.005	112
HM_5727	contig47926	TG	2	12	TGTCCTTTCTTgTgTgCATGTT	62.958	CTCTGTCAACATGATCTGAcACC	63.146	133
HM_5728	contig39658	TC	2	20	TGGAATCGATCGAAGTGAAGAG	63.03	TTCaAcCTCAAGaCCTTCgAGA	63.42	149
HM_5729	contig06103	TC	2	14	TGTGAACCTAAAGTTCTCTCTGGG	63.015	GTGCTGTTTTGCAAGTCTAGTGT	63.792	142
HM_5730	contig12412	AG	2	12	TGTGATCGGATTTGATAGTTTCA	63.462	ATCgATTGAATACTCTGcTc	62.733	153
HM_5731	contig39470	CA	2	24	TGTGCAAGATTAGAAaAGCAAAAGG	63.05	TGCTTAAGCTGTTGTATGTGGTG	63.398	160
HM_5732	contig14757	AC	2	16	TGTGCTACTGAGTCCAAATTCATCA	63.063	GIATTAGAAATGtCTCCCAcC	62.974	146
HM_5733	contig21271	CT	2	16	TGTGGCCGTTTATACAGTTTCTT	62.944	CCAACTCTTCAGTTTCAGTTTCA	62.916	150
HM_5734	contig43036	GA	2	20	TGTGGTCTTTGTATATGCTTCTG	60.414	TTGTAGAGGGaAGTCTTGATCTGc	61.114	149
HM_5735	contig07961	AG	2	12	TGTGGTCTCTGTAGAGGTTTGAA	62.074	TTCTGTTTcTaaTgCTCCGTTc	62.826	109
HM_5736	contig12615	TG	2	12	TGTGGTTTTGCTCCTGTTAGAT	63.129	TTAGTCATGGTTGCCTAGCgTTG	62.656	103
HM_5737	contig22421	AG	2	16	TGTGTTTTGAaTTTTCGAATCAGATG	63.334	GTACTTaccCCaCCCCACC	63.854	126
HM_5738	contig01713	AT	2	16	TGTTACTGCTATCCACCaCCAC	63.291	TGCAGTTACCACTATGTAACCCA	63.486	129
HM_5739	contig48986	CT	2	20	TGTTAGCTTCTTCATCACTCTCC	62.91	GCgTTGGTGGTgAgTTTTAAAAAG	63.048	138
HM_5740	contig26678	GA	2	16	TGTTATTTATTACTCaCTTTGTGAtggg	62.237	GcCTCAATgtTAcCttaaAACTG	61.734	85
HM_5741	contig14742	AG	2	16	TGTTCGAATGAGAGAGAGAAAGGG	63.199	ATTTTACACAGAGTGCAGAGCC	63.06	154
HM_5742	contig35277	AC	2	14	TGTCGGCATaAGGCTTAAaATc	62.568	ACACTCGGATGCTAACaCAATGA	62.962	156
HM_5743	contig36191	CT	2	20	TGTTCTTCACTGCTTGTATCTCG	62.962	CACACGaACAGTACaCaAGAGGA	62.51	153
HM_5744	contig32713	CA	2	12	TGTTGCACCTCTTGTAACTCTCA	63.048	ACAAGATCACCATCTCACTCTCCC	62.994	123
HM_5745	contig09585	CT	2	12	TGTTGGaaGGCTCTTCTCTTTTG	63.113	GAGGCAAGAGTAGATTGACCAAGG	62.598	147
HM_5746	contig37551	AG	2	16	IGTTGTTCTcTtCTGTGGTG	62.739	CCCTcACCTCaAcCaTcTTCTT	63.068	100
HM_5747	contig31225	GA	2	20	TGTTtctGAcTcTGTGtCTGAG	63.272	GAGATTGGAACCCACATATCGAAC	63.016	155
HM_5748	contig11609	TC	2	14	TGTTTCTTGAAaAGGCAATTGgT	63.027	cTaCAATCGaACAGTCACTcCTG	62.397	138
HM_5749	contig06817	CT	2	14	TGTTTGCTCTGTGGCTATCAAT	63.078	GACCgAAAGAGAAaAGACCaGc	62.699	142
HM_5750	contig37954	TC	2	20	TGTTgTTTGTAaCTCTGTTTGTGga	61.143	TCGAGaAAATCGCAAAATCAAT	60.903	160
HM_5751	contig33523	AC	2	14	TTAAaAGAAAGTGTCTGGATAggaga	61.071	GTGGCaAAGTGAgGTAGATgCTTA	61.822	118
HM_5752	contig18238	CT	2	14	TAAACGTCTCTCGACTCGCC	62.934	TGAGCTGTTTGAGAAATAgGGT	63.121	94
HM_5753	contig12475	GA	2	14	TAAACATCATGAATTGGGGGAAAC	62.996	GGGAGGTTGaAAAGGAGTgAGCT	62.316	150
HM_5754	contig38056	AG	2	16	TAAAGaGAACCTGGGTAGGCTTCATC	62.863	AGCTGAGAAGCACCGATTATATGG	62.841	117
HM_5755	contig52580	TA	2	12	TAAAGCATAAACACGCACTATGCC	62.41	CACTGTTCACTGCGACCTATATC	62.975	85
HM_5756	contig26310	AG	2	16	TAAAGCGCAAGTACAAATTTCCAG	63.537	cccaaaaaacactttaaatatgagagg	63.087	145
HM_5757	contig38783	CT	2	14	TAAATCCAACGACCGGACTTAATG	63.216	GAGAATAAGATAAGTGTGGACTCGGC	62.65	150
HM_5758	contig11986	AG	2	20	TACAAACCTCGaACCTCACTCT	62.382	ATGGCATGTGGTCTGAGGaATAGT	63.133	133
HM_5759	contig23148	AG	2	16	TACAgTATCACTGGGgTTGgAT	63.022	GAACTTGATCTGTATGCCCTACC	63.15	118
HM_5760	contig27421	TC	2	12	TTACAGTGAACAATTGGAGGGCTT	63.129	TCCTTCAAAATGCTCTTGATT	62.315	137
HM_5761	contig43509	TC	2	24	TTACATCGCAGAGTTGAGAGTTCTG	62.958	GCTGCTACTGTaCGAAACCaCT	62.191	155
HM_5762	contig18313	AT	2	14	TTACCCATGCAAAATAcCtCTT	62.922	aaATTCTCTCCAAGTTTGGGCT	63.61	148
HM_5763	contig29420	GA	2	20	TTACTCTTCTGGGgTACTTGTCTCA	63.003	AGGaAgGACAGTAgGACattCTT	62.913	152
HM_5764	contig08585	TA	2	12	TACTGCTGCAACAAGGGTGCACA	63.272	CCCACTTCACTCTcTGACCTTA	62.993	109
HM_5765	contig05332	AT	2	12	ttaCTTCAATCAATCGGAAaAGa	62.993	TACGCTTCCCATTTAGAAGCTGCG	63.852	122
HM_5766	contig38560	AG	2	14	TTAGAAGCAATGTGTGCTCAGAC	62.858	TGTTTCTGCTCTCTCTTcGgAT	62.811	146
HM_5767	contig20002	TC	2	16	TAGCGCTTTGCTCTCTCTTTCTTC	63.051	CATCAACCACTACCTACCAAAAT	63.009	152
HM_5768	contig26711	TC	2	20	TTAGGGCTTGAAATGTTCTCTCG	62.919	AGACTCTCGGATTCTTGgGTGTG	62.589	125
HM_5769	contig51194	AG	2	16	TTAGGGGATGTTTAgGTTgTggaga	62.993	TCTATTCTTCCCTCTcTCTCGCT	62.983	96
HM_5770	contig48799	AG	2	12	TTAGGGTTTCATAGGCAAAATc	60.519	GGGTAACTGTaCACCTTGTGCTC	60.287	160
HM_5771	contig40087	AG	2	14	TAGTCCACCTTCACTTGCACTT	63.345	AcAGCACAaAATGGGGTTGTTTTA	63.241	152
HM_5772	contig39330	AT	2	16	TtaGtGAAATTaGGGcCAGATgGa	63.005	GTGCGCTCATGTCAAAGTaGGAAT	63.789	155
HM_5773	contig01921	TC	2	12	TtaTAAAGTTATCGATaGgGcGGG	62.483	CTGGGATGGAGTTATCCAACCTGT	62.584	151
HM_5774	contig18346	TC	2	20	ttaTAAATTCAgATACCCCGACg	62.237	CGGAATAGTGTGCGCAATgaa	63.144	154
HM_5775	contig11351	TA	2	16	TTATagTtGTTGGGTGGCGTATgta	60.524	TAAATCAACACAATCAACAGGTGC	61.145	142
HM_5776	contig35089	AG	2	24	TATCAACTGTGTTTTGGAGCGAT	63.03	CAAGTTTTCTCaTAGCTCACAG	63.184	160
HM_5777	contig19437	CA	2	12	TTATCCCACTAATACCAACACG	63.014	CTATCCAGCGTTTGGTCTGACAA	63.456	125
HM_5778	contig11451	TC	2	14	TTATCCgCTCTCAGATCCAGAGAAc	63.013	ATAGATCCTCTTGGCTCCGAGAAA	63.578	113
HM_5779	contig13712	AT	2	16	TtATCTTTCTTTGGGCAACAATT	62.049	tTTTTgGaAAATGAGAAGGCTACA	61.24	134
HM_5780	contig52146	AT	2	20	TTATGGATCGGgaGTGTTAcAaCc	63.219	AACATGCGTGCAAAATAGGAAGG	62.665	138
HM_5781	contig15558	AC	2	20	TTCAAAACCTAAAGGGAGaGAACC	62.968	GTTCTCACTCTCACTCTcAcCa	63.234	120
HM_5782	contig41141	AT	2	12	TTCAACTaGTCATAaGTCATACACG	62.423	tCCGatTCTGataCTGTCTcTgAcC	63.015	142
HM_5783	contig03973	CT	2	12	TTCAAGACAGTTTTGGGAAGGAAG	62.892	CTGAGATCGAGCAACTCAGACA	63.053	135
HM_5784	contig02320	CT	2	24	TTCAAGTTCTGCGCACTAGACCC	62.724	TTCACTAATCTAATcCCACCGGTT	62.011	82
HM_5785	contig29176	GA	2	24	TTCAATGAAGaAGcTgTGCGACAC	62.962	CTCAGATCTaATTcCTcCCGTT	62.971	115
HM_5786	contig31989	TC	2	12	TTCAGCATCTCTCTCAAAACCC	62.897	cCaAAAGTTGGGGAATCTTTTTC	63.068	95
HM_5787	contig25853	AC	2	16	TTCAAGACATCTGGTGATACCAAA	62.803	tTTGCaGtGTTCTTGAGTTGTGt	63.181	141
HM_5788	contig39273	GA	2	16	TTCAAGATAGTGTCAATGGAAAGTCT	62.439	ATcCTCCGTTgGTTCTcTTTTCT	62.983	102
HM_5789	contig48978	GA	2	16	TTCAGATATCTCTATTCAACAATTGCC	62.574	gaCCAGTGCTTTGgCTGATTAACT	62.949	115
HM_5790	contig29592	GA	2	14	TTCAAGTGGCTCTCTATTCTTCTCT	61.704	AgGCTTTTaCaAACTaGTTGCACTTT	60.955	133
HM_5791	contig27852	GT	2	14	TTCAATGCTCAAGTGTCCCAAGAT	63.121	TAcACGGAAGAAAGcGAGATTGTT	63.129	138
HM_5792	contig12006	AT	2	12	TTCAATGGCTGAATTGTATAGGC	63.332	CAACAACAACATTTGGTTGGAAGa	63.146	80
HM_5793	contig49576	CT	2	20	TTCAATGGATGACAGAGTCAAAC	63.743	CCACTgCCCTCAAAATaCAATaa	63.216	140
HM_5794	contig26427	CA	2	16	TTCAATTaATTACACACTCCAACACA	61.765	AATTGTGTGATTGGTTGATGTC	62.123	96
HM_5795	contig34288	AG	2	20	TTCAATTAAGATTTGACAGAACTACA	60.414	CTGCTTTTTGTACTAGATTTCTTAGC	60.51	119

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5796	contig24309	GT	2	16	TTCCATCGACATCCATAACTTTCA	62.705	CGCAGGTTCTGATTCTTGATTTA	63.625	150
HM_5797	contig08438	AG	2	32	TTCCATGTACTCGAAATCGACAA	62.832	CACAGTCGCAGTCACACTCTTCTT	63.192	157
HM_5798	contig42772	CT	2	24	TTCCCACTGTTTCGCTACTTCATT	63.019	TGTTGACTGCTGTTCCCGAAATTA	62.729	99
HM_5799	contig25100	TA	2	12	TTCCCCAAATTCCTCATATCTCA	62.873	TTGGAGATACATTGCTCGGAAAT	63.021	80
HM_5800	contig11861	AT	2	14	TTcgaACCTTCAATATTCACAGT	63.009	TTACCTTTTTCGATCTGTAACCA	63.025	115
HM_5801	contig30296	TC	2	12	TTCCGATCTGAGAAATgTGGAAT	63.099	ATTGCTATTTCACAGCAGCAAAAG	63.552	153
HM_5802	contig33998	GT	2	12	TTcGGAATTTGTGAGAACTTCAT	63.108	ATGACAAGGGCCCTCAAGATTATT	63.196	152
HM_5803	contig04484	AT	2	20	TTCTGATCTCTCTGCAATAGCTC	63.125	TcAAATTAACATCTCTGATTGTGTC	62.678	144
HM_5804	contig42595	CT	2	14	TTCGATCACCACTATTTTAACTC	62.813	ctTACCCTCGGACGTAAATCTCG	62.411	87
HM_5805	contig20780	TC	2	20	TTCGATTGTTGACTCATTTGGTG	62.943	AGGTTGTGTGAGAgGAGAAATGaG	62.118	120
HM_5806	contig04570	TG	2	16	TTGCTCTGCTAGTATTACTGTGC	63.067	TCTCTGCGACTCAATCTCCACAC	62.951	157
HM_5807	contig46369	GT	2	12	TtGgTATGgTAgTTGACCGAAAC	63.336	ACACgATTACTCTCGTTTCTCTTgG	62.822	159
HM_5808	contig20735	GA	2	12	TtCTAaGACTGAGACACCGAAGC	63.238	TTTGGTTGTAGTTTCAATGTCCC	62.132	143
HM_5809	contig25141	AG	2	14	TTCTAAGTGTGTCCATTCTGcGA	63.163	tTtCtAtcTtATCTCTCATTTCTcACC	62.359	126
HM_5810	contig09369	AT	2	12	TTCTACTAGCTGGTTTCGATTGA	62.241	TTCAATCTTGTAATCCAATTGTGG	62.181	152
HM_5811	contig22879	CT	2	12	TTCTCACAAGATCTCTCCCACTC	62.987	AACCTGCACAATACAGATcCACA	62.833	117
HM_5812	contig27795	TC	2	12	TtCTCCAATCTCTCTCACTCCCTTG	63.085	GCAACCAAAACAGATCTCAAAATGA	62.514	108
HM_5813	contig18403	TC	2	12	TTCTCCATTTCTGGTTCTCTAGAC	62.987	TGAcTgTGAcAcATGTATAAGAGTGG	62.531	133
HM_5814	contig17903	GA	2	12	TTCTCTCCATTCAAACTCCACAGT	63.204	TGGCTTCaATAGAGACAGCTCAG	62.206	134
HM_5815	contig00227	GA	2	16	TTCTGAAAGACAGAGCTCGAAGAA	61.639	GGAAGACAATCGAGAGCTaATAACTG	60.935	154
HM_5816	contig45269	CT	2	24	TTCTGTACATCCATCACTCCTTGC	62.609	GCCAAGaGACATTGAGTGTGTTT	62.824	160
HM_5817	contig00413	TC	2	20	TTCTTCGTCTCTGCTTcTCTCTTC	63.338	AgTGGCGGTTCTGTTCAATGAT	63.033	133
HM_5818	contig11816	TC	2	16	TTCTCTTTTTTCCCTCTGCTGTG	63.003	GagTGAGGAGGATaATAGGAGGcg	63.589	158
HM_5819	contig50496	TC	2	20	TTCTTGAATTCGAAACGGGTAGTC	62.716	tCTGATCTGTCACATCTCCACCTT	62.334	151
HM_5820	contig24734	TC	2	14	TTCTTTGTTGACTGACTCAACGG	62.723	TgGAGACAGAGACGAGAGATACCTG	63.337	130
HM_5821	contig39591	AG	2	14	TTGAAAGTGgATGTAGAAGGGAA	63.091	CAACTCaAcCaCCACTTCACAT	62.397	154
HM_5822	contig07960	AC	2	24	TTGAAATCAAAATCATTTCCCAACA	62.497	cCtctCTCTCACTCTCATCATgTA	61.887	139
HM_5823	contig21524	GA	2	12	TTGAAGATCGgAAATGGAAGAAAA	63.089	CAITCTCATCATCACTACCATCGC	62.941	134
HM_5824	contig03125	TC	2	12	TTGAAGCTGTGTAAGACATTTTCAGC	61.923	GAAGCCAGAAAGGTTAAAGAAATTTGAT	62.312	109
HM_5825	contig07230	TG	2	16	TTGAaTTGTTTCTCCTCTcTtGCG	62.813	cCAcATCAITCAACAATCAACAAC	63.481	103
HM_5826	contig40905	TC	2	14	TTGAGTCCCTCTCAAGGATAATTT	61.526	AAAAAGaAGTGAGGCAATGTAATGTT	60.617	144
HM_5827	contig07294	AG	2	12	TTGCAATTcaAGTAAGTAATCTCG	62.258	CGGCTAACTTGTGTTTAATGCTTC	62.292	121
HM_5828	contig34794	AT	2	16	TTGCACAAaTGATAAGTACGGTACAA	61.739	CTTTCCCTTAITCCCTCCCAT	62.652	94
HM_5829	contig38762	CA	2	20	TTGCACGACTTATGTTATCCAA	62.65	ACACCAGAGCAAAAGAGGAGAAAGA	62.909	153
HM_5830	contig50322	GA	2	16	TTGcAGTGcAGGTAGTAATTTGg	62.656	cCATCAATCCTCTTTTGTCAACAC	61.95	110
HM_5831	contig31660	AC	2	16	TTGCCATAAATTTTACAGGAATG	63.013	ATAGCCAAACTTCAACAAACGGAA	63.039	146
HM_5832	contig46281	TC	2	14	TTGCCcATGAACCTGATAACAAa	62.637	CAGTgATCATCCCAcTGATCAAA	63.349	153
HM_5833	contig04754	TC	2	20	TTGCTGTGTTTGTGGGTTCTCTAT	63.129	tTGaATaAAgGAAGGGAGAGCa	62.41	99
HM_5834	contig38654	TC	2	14	TtGCGAAATGgAATAAGAAACTGaa	63.036	CTTCGATCATGCGgTAgGTTTT	63.532	133
HM_5835	contig10708	CT	2	32	TTGCGCCATTACAATTTAGAATTG	63.238	TAcCCtAcCCTaAccctaAccCaA	62.883	89
HM_5836	contig38991	CT	2	16	TTGCTTCTAAGATTCAAGCATTCA	62.325	AAATTCATATGCTGtGgGAATGTG	62.108	99
HM_5837	contig29873	GA	2	12	TTGGAATGTAAAAAGGGGAGAA	62.023	ACAgTGCTATTAACTCACTCCCAACA	62.753	106
HM_5838	contig38551	TA	2	14	TTGGAAGAAAAAGGGTAaCTCaAGAA	60.67	GTCTCGCAAGAAATGAGATCTCTAC	60.616	98
HM_5839	contig11164	AG	2	16	TTGGAAGTTGAAAAACAGAGACC	61.709	aCCTCTATcCCACCTACATtGtCa	60.991	158
HM_5840	contig20913	TC	2	24	TTGGAGAGTAAGAGGGCGTTTCTG	63.125	GTAcGTaACgAAACGAGCAGCAG	64.086	91
HM_5841	contig13302	TC	2	16	TTGGCAAGTTTtGACAGTgATGTT	62.958	GCCTCGTcCAATTTTTCTTTGTTT	63.687	126
HM_5842	contig09185	AG	2	12	TTGGCTACAATTTGTGATTGAGA	62.832	cgTCAGCAAAAATCTCTCATCT	63.022	81
HM_5843	contig35351	GA	2	16	TTGGGGCTgTtTtCAGACCAATT	63.106	TTCTGTTTCTCCTCTCTtCCCCA	62.669	156
HM_5844	contig04450	TA	2	14	TTGGGTTTtGTTGGATTCAGAA	62.823	TCTGAgAGGGAATCTCTCAATTTG	63.076	146
HM_5845	contig03039	CT	2	12	TTGGTGTTCCTTAATGTGTTATTC	62.757	CTTTGCAAGCAAAATCACTTCTTT	62.944	106
HM_5846	contig25125	AG	2	12	TtGGTTACACGTTTGGTCTTCGTA	62.754	CCCTCAAGAGCgGTACGGTAcTAcT	62.931	147
HM_5847	contig16056	GA	2	30	TtGGTTCTTCACTACTCGCACTGT	62.427	ATAACACCTTCCCTTGTCTCTGT	63.189	156
HM_5848	contig36904	GA	2	12	TtGGTtGAACAATCTTGTCTGGA	62.918	AGGTTTCTTGTGGAACAAATCAGC	62.824	111
HM_5849	contig09051	AG	2	16	TtGGTTTGAaTcATGCGTACTCTGT	62.7	cCTCAATAAaCAGAGGCCAgCTT	62.341	108
HM_5850	contig49332	CT	2	16	TtGTcTCTTTTcTCTATCgAA	62.481	AACGATGATGATATGTGTGCGGT	62.625	151
HM_5851	contig02675	CT	2	12	TtGTcTAGAAATCTCCATTCTCCACC	62.995	CCAAACACACTCAAAAACAGCCCA	63.28	160
HM_5852	contig00902	TC	2	12	TtGTCTtCTtCAcAAaTCCaA	62.012	TTTTTGGGTTGTAGTGGGATCAT	62.897	143
HM_5853	contig11691	CT	2	12	TtGTTAAATACATGTTTGGCGCA	63.384	GgTTACATtTgGtGTGCAAAATGA	62.959	160
HM_5854	contig41417	AG	2	16	TtGTCTCTGTTCTTCGCAATAAT	63.03	TtGAGAAGGCTTTTtTtATACCCA	63.034	80
HM_5855	contig04778	CA	2	12	TTGTGAAGGTCAAAAGCACCC	63.148	TATGGGgAGAGTCTCCTTTgAGT	63.369	106
HM_5856	contig25562	GA	2	12	TTGTTGGGGATTATCGTAGAGGAA	62.896	CTCAAAACCAAGAACCTCTCACT	63.115	153
HM_5857	contig18999	TC	2	16	TTGTGGTGCTCACTGCTCAATG	63.398	CCAATCAATAAAGGGGAGaAAAG	63.056	94
HM_5858	contig23385	GT	2	16	TTGTGTTGATGTTGATCTCGTAA	61.621	GTTGTCAACAGCATCTGCATA	60.747	153
HM_5859	contig41008	AG	2	16	TtGTTTGGAGCAAACTCGTAAGT	63.245	ACCTAAGCAACAACAGGGCTACAG	62.956	131
HM_5860	contig23454	TG	2	14	TTGTTGGGTTTGGGCTTTTGAC	63.214	GGCTTGAACATTATGGCTGAAC	63.046	128
HM_5861	contig47294	CG	2	12	TTGTTGTGTGGAAGTCCATTGTC	63.265	CGCCCTATCCCTaAcTtCTCTCT	62.41	153
HM_5862	contig33331	GA	2	16	TTTAGAGagCAGTTTTTGGAGCGAT	62.742	TcCTCTTATaAAATCaAgCTcCTCTC	61.797	152
HM_5863	contig16879	GA	2	24	TTTAGAGAGTTGTAGTGCCTCGG	63.028	TCTTCTCTCAATCTTCCCTCCA	62.657	104
HM_5864	contig18802	GA	2	16	TtTAGGGTTTTtCTCAACCGCA	62.93	ACAATCATaCcaAAcGAgTGTCA	62.726	93
HM_5865	contig37942	AT	2	20	TTTATATACTAACCCGGCTGGAGC	62.696	CCGTATTACCATCTCTCACTTTG	63.027	101
HM_5866	contig42469	TA	2	12	TTTaTCACATGCCCAATGCAAAAT	62.665	CTGGTATCGACTCTcTCTCTCT	63.384	118
HM_5867	contig11462	TA	2	14	TTTATGTTGAATGgTCTCGCAAA	62.748	CTTGTtCTTCTATTTTcAATGCTTG	61.748	142
HM_5868	contig44616	AC	2	24	TTTCAAAATCAACTCAGTGCTTCG	62.758	GCaATTGTAAAGCATCGTCACTCT	61.834	134
HM_5869	contig37414	CA	2	14	TTTCCCAAAAAGAGAAAAACCACT	63.268	caCAGGCATAgGAGTCATAGAG	63.325	128
HM_5870	contig34527	TC	2	12	TTTCCCTCTGAAACCTGTGCTTC	63.019	ATTTTTCAAGGGGTTGCAATTTGAT	62.983	131
HM_5871	contig14231	CT	2	12	TTTCCGGTAAACATTTCTGTTGGT	62.823	TCACATACAATTTAAAGAAAGCCAA	62.496	113
HM_5872	contig13469	AG	2	16	tTtCtGgAgAaGCTAGAGCGTA	62.836	TcCCGCCAATcAtAcAATcTtTg	63.316	93
HM_5873	contig15376	TC	2	16	TTTGGACTAATTTGGGGTCTGGTT	63.019	TCCTAGACCTGGCAATTTTGTATC	62.828	130
HM_5874	contig32847	TG	2	16	TTTGGCCCATTTGTTGTTAGTT	62.743	CATCTCTCCAGTTCTGTGCGTATT	62.032	137
HM_5875	contig06796	GA	2	12	TTTGGGGAaAaTGAAGTTCGTAA	62.918	AGCTATGATGCTTCTCTGACAG	63.462	119
HM_5876	contig18535	CA	2	16	TTTCTCGAGCCGCTTAACTAAAG	62.859	TGCACTTgATCTCTACTGGTCTCG	62.064	156
HM_5877	contig13712	AG	2	20	TTTCTcTGTGTTGCTCTCTCTGC	63.019	CCTCTCTTGGATcCTCTCTCAC	63.906	134
HM_5878	contig36872	TC	2	20	TTTCTGCTATGTCATaTTCAGGC	62.567	tAACCAAGAGCTTAAACAGGgC	61.986	123
HM_5879	contig28631	GA	2	12	TTTGAACAACCCCAAGAAAAACCT	63.015	AtCTCTCGCTcCTcCTCaTAATTTCT	63.085	129
HM_5880	contig37211	AG	2	12	TTTGAAGAAAAATGCTCTGACTGTCA	60.966	tGgGTTgTGAACCTGgTtTACTGAT	61.865	105
HM_5881	contig44518	CA	2	16	TTTGACTTTTtGAAATtTGGGGA	62.989	ACaAAGGGTAGTTGTGTCATCG	63.444	106
HM_5882	contig50969	GA	2	40	TTTGATTTTTAGACATGGTGTGTC	62.225	CTcCTCTCTcTCTCTCTGtCa	62.545	121
HM_5883	contig30668	TG	2	14	TTTGACACAAACTCTGCTCAACT	62.958	GATGCGATTATCTTTaTGGATCTGA	62.663	158
HM_5884	contig16723	AG	2	20	TTTGGCGAGATTACGTTGATTCT	63.138	CATTtTGCACACTTCTAGTTTCC	63.129	158
HM_5885	contig11808	CA	2	12	TTTGTACAGTCAAGACACCCAC	63.612	ACTTTGAACAGGGGTTTCACTc	62.78	90
HM_5886	contig03938	AT	2	20	TTTGTCTGTGTTTCAATCATCTCA	60.449	CATTCAITTTCTCTTgATTCTCTC	61.411	89
HM_5887	contig00059	TA	2	14	TTTGGAGTGGTCTGAGATGTCAAT	62.136	tGtTtTtGtGAGTTGAGACACACA	61.877	146
HM_5888	contig48707	AG	2	12	TTTGGCTGCTGCTCAGACATACT	63.515	TcCTCTCTaAACataCaaACgCA	63.144	91
HM_5889	contig10164	TC	2	24	TTTGGGAAGAAATGATTCGGTAGA	62.993	CTTTTGTAGCTTCGCTTGTCTCAT	63.17	149
HM_5890	contig38641	CT	2	16	TTTGGGAGTTTCTGTTCAATTTTT	62.919	gaacAAAAACaTTCGGGATAAGA	63.327	141

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5891	contig48013	AG	2	20	TTTGGGCTCTTTGATAGGGAATGAT	61.996	cctCCAAATACAATaCaAAATCCA	62.144	81
HM_5892	contig15352	AC	2	14	TTTGTCACGACAGCATCGAAGACAC	63.036	CCaAAACaAAACaAAACCaAAAA	63.016	159
HM_5893	contig03262	CT	2	12	TTTGCTCTTCCCTCTCTCTCCAA	62.669	GTCTCTGGGCAAGAAAAATGAGTC	62.599	111
HM_5894	contig43447	CT	2	12	TTTGTTCTCTGACATCACCCTTGT	62.088	GGATTGAAAAATATCAGACTTACGTTGG	62.207	115
HM_5895	contig01688	TC	2	16	TTTGTTtacTCTtATGIAGGGCCg	62.681	ACGCTCTGAAACCACCTACAAAAAG	63.069	97
HM_5896	contig14892	TA	2	12	TTTCAAAATCAACATCAGGCGCTCT	63.219	GTAAGCTCCCTCTCTGTGGGGTGT	63.023	150
HM_5897	contig13249	AG	2	12	TTTTCAGGAATGTTTCAGGTTGAGG	62.892	ATTTCCGTTCTGTTCCACTCTACTG	63.044	144
HM_5898	contig39151	GA	2	12	TTTTGAGGAAGTGGGGTGTGAATTT	63.006	CTCTAGAACCCCTTTGTGCTCAACC	62.61	121
HM_5899	contig36751	TG	2	14	TTTTGGTGCAAGTTTTCCTTTCaT	63.027	CACGTCCAAAGaAATGACTCACAC	63.053	129
HM_5900	contig24473	TA	2	12	TTTTTAATCAGCTCAAGGCTCTCCA	63.322	GGGCACCTTATTAGAGAGCTTTTG	62.622	158
HM_5901	contig06379	TG	2	12	TTTTTACACTCAAGGTCCTCGCTC	63.031	CGCTTTACCTCTActACAGCAATG	63.154	127
HM_5902	contig32730	TG	2	14	TTTTTAAGCAAGTGAAATGTCTCA	62.859	aCATgGGTGagGATcttATGTgCT	63.133	152
HM_5903	contig39036	TA	2	14	TTTTTGAAGCCCTAATCATCGGAAA	63.013	TGCAGGTAACTGAATCTCTGTTTG	62.527	94
HM_5904	contig43607	AG	2	14	TTTTTGCACTTACTCTCTCCAAGA	62.437	AATACGATCTGAAGGTCGACGAAG	62.923	138
HM_5905	contig41175	AC	2	14	TTTTTGGAATCTGCTGATTCTCC	62.813	GGTGCAATTGTTGTTATTGTCTACA	62.289	137
HM_5906	contig01323	AAT	3	12	cAaTATGGAAGGaGAGGtAAGAAA	62.897	AGGAAGAAGAAACAGCAGAGGCTT	63.213	159
HM_5907	contig42822	AAT	3	12	cagaaaaaggttaacaagatcccaaa	61.757	TGTGCTACTTCTCTGGGTGTTCT	62.637	114
HM_5908	contig10965	AGC	3	12	gtagtatgcaccgctactggAAG	63.263	ATCACAGGAGTCAATTGCTGC	62.564	160
HM_5909	contig05961	AAC	3	12	TTTGATTTGgACATGTGCTGATGG	62.932	CaCAACTGTTGCTGCTCCTCTTT	63.041	102
HM_5910	contig18547	GAT	3	12	CCATGTTATTAAGGCGGGAAgtc	62.629	ACCgACACACTACTACCAAAA	62.931	137
HM_5911	contig14389	CAA	3	24	TCcTGAAGAAATTTGGGAATGAA	62.98	TGAATTTTATCATGGCTAtcGTTGC	63.252	114
HM_5912	contig31203	CAG	3	12	GCAATCATcGACcCtCagAGAC	63.364	GcCGTCGACCTTGCTATGAC	63.056	99
HM_5913	contig51917	TCT	3	15	GGGCATaTgtTgTAGCCAGAGTtc	63.15	AATCGITGCAGAGGAAGATCAAG	62.022	121
HM_5914	contig44675	TTT	3	12	cGaTGTATGATCCTGTaCCgT	63.231	gGACAGGACGGGGtaGAATAGAc	63.29	154
HM_5915	contig20221	ATT	3	12	TGCGTAACATATTTCCaACTCA	62.65	GTATGttTTGGGTGATcATTGc	63.541	97
HM_5916	contig39399	CTT	3	12	TCAaTACCATCACTTTCcTcTc	62.672	CCaAAGAGCAGAGGAATTGAAGAA	63.104	111
HM_5917	contig35905	CAT	3	15	atctcctaaccaccacaaaccc	63.488	TGATGAGGAGTGACAGAAATTGAG	63.03	117
HM_5918	contig25525	CTG	3	12	aCAAAAACAAAGgATCCACAACCAT	62.811	AAGTTCacCTCCTAGTCTTTGGG	63.076	109
HM_5919	contig12309	TAT	3	12	TGCGTAGAGATCAGAATTGCCAACA	63.27	GGGTTTGGCAATGAAGAGGTTTTAT	63.487	148
HM_5920	contig29488	GTT	3	12	ccgagattgatttctcgagagt	62.053	CAAAATCCCAAACTGTACCAACT	62.907	139
HM_5921	contig19474	GGT	3	21	gtgtactactccagcaggacagg	63.462	catctcatcttctctctcacc	62.651	84
HM_5922	contig22383	CCA	3	12	CTCTCTCTCTCTCAATCTCTCT	63.593	AAACGACGTGCTGTGTGGAGATT	63.307	131
HM_5923	contig33120	ATC	3	15	ATGAGgAGGGACTCTCTCACCTTT	62.964	caTcCGCAGCAGCAAGTATaATAA	62.272	85
HM_5924	contig28362	GTA	3	30	GACGAGAGGtAcGgTaCGGGtAg	63.235	CCCAGACACCAAGGAGTAGAATATC	63.194	121
HM_5925	contig07905	GTG	3	12	ccaaggagctcttcaacgtca	62.8	CCTcAGGTACTTCTCTCTGCTCT	62.281	98
HM_5926	contig12750	CGG	3	12	catactctcatcgaggtgacgag	63.189	GGAGTGAATGGACCGTTGAG	64.039	139
HM_5927	contig22290	TAA	3	12	cTtHCGCgTGAAGGTTGTATT	63.491	agGTTTCAGCTGCTGCACTTAT	62.661	151
HM_5928	contig00533	AAG	3	12	aacttaagattggcagagaagaaaa	62.497	CCATTTTCTCCACGCAATAAAAGA	63.416	156
HM_5929	contig21445	AGA	3	15	agtttCGgattcaaaattccaca	62.909	gcacttggctattacaattgctg	62.093	107
HM_5930	contig27714	TCA	3	12	TTCTAgggCTTCTCAAGCTTCT	63.098	gagtggtgagcttgttttGTTgAA	62.799	95
HM_5931	contig24389	CAC	3	15	gtattcagaaccatccaccctc	63.004	TagAGtGatTTTTCGGIGtcatc	63.532	132
HM_5932	contig41635	GAA	3	21	GAGAcagggAGGGAAGAAAGAACT	62.553	CTGCTGCTCTGCCATCTTTATCT	63.256	99
HM_5933	contig28105	CAG	3	15	TGCGATtTCattGtctctaaat	62.912	GGAATCATAGcGtTTACaGGGAc	62.83	157
HM_5934	contig39750	GAT	3	15	GggATTGTGAGTGTCTTGGATAA	63.419	GTAGTTTGAATTGCGGTAGTGGCT	62.768	140
HM_5935	contig21515	TTA	3	15	tattctgaagggaaggaagaaat	63.254	TGGAGATGAGGAGCTTAAGAGGACTG	63.212	146
HM_5936	contig17478	AGA	3	12	GAAcCaAacTcAaCAGTgATCGg	63.028	TCgTCGtCTGTCTCaCTGatTT	62.397	160
HM_5937	contig22046	TGG	3	12	GGgTtHCCGTTTCTcTcGAT	64.502	AATTTCAATCCGACTCTCTGCTCT	62.142	138
HM_5938	contig42480	GGT	3	15	GGGGTGgTGGAGAATAAATGAA	62.189	AAGAGTACTCAcCacCTcCacCAG	63.011	153
HM_5939	contig40563	GTG	3	21	GGAGTCAGAGAGCAATGGAGAGAG	63.11	TctCATCTCAACAGTATctcCC	62.775	159
HM_5940	contig14433	TAG	3	15	GTCTGTATCgCAaAgAATCAAGGg	63.231	CCGCACTGAAGCCTAAAAAGACTA	63.048	116
HM_5941	contig04202	CAC	3	12	tGgATiATACAACTTCTTcAaCaAg	62.472	ATGATCTCAGGTTCCGAGGGAG	62.782	81
HM_5942	contig40842	ACA	3	12	TCACTCTCAGGTTCTCTATTTC	62.987	AATCGATTCTATTGCCCAAGTACA	62.925	118
HM_5943	contig35982	GAG	3	15	TGCAATGGATTGCTTTTGTGTTT	62.933	GCCACCGTTATgTcGTTAATATC	62.655	154
HM_5944	contig17005	TGA	3	12	AAACaagggtTCTAAAGCGTAGG	62.919	AGATAACAGATTGTTTCTCGCG	62.729	102
HM_5945	contig08316	GTG	3	12	TTTTATTGGTgctGGAGAAGAAT	63.219	CTTCTTCAGTCCCACCATCTCTA	62.984	135
HM_5946	contig14109	GAT	3	12	GAGATCTCGGGGAGGATCTGa	63.224	CaCTtCTcATTAGCCAAGCTCAcA	62.958	142
HM_5947	contig01551	GTT	3	24	CTTCAAAAACCCTaGTTTCCAAG	62.821	CGTCTCTGCTAGAAACACAGCTA	62.982	146
HM_5948	contig40653	GTA	3	12	AGgACCAAAACACAgTCAcAcATA	62.827	ATTTTAAAGCATGCCACTACCGAT	62.09	159
HM_5949	contig22383	TCC	3	21	ctctctctccaccctctc	62.447	GcgACTGATCTGTGGTGGTAT	62.463	98
HM_5950	contig45523	TCT	3	12	GAAACAGCGGATAAGtCAACCTCT	62.827	AGCaAgGAGAAGaGGAGGAAGG	62.531	134
HM_5951	contig03100	AAG	3	12	aaggccagtaaccagctacacac	62.861	ttCGAAGGAAGCAATTTCAATCT	62.424	137
HM_5952	contig03649	CTT	3	36	GTGTTTATgTTTGGGGGtGTGTT	63.031	TTTGCAACCATATTTCTCTCTGT	62.922	151
HM_5953	contig15046	AGA	3	21	agcactgatcacagagaccacac	63.017	AGTCgGAGGAATCCAGAACACAC	63.108	137
HM_5954	contig13700	CAT	3	12	ttttcttgtagccagAGtcagaaga	60.891	GTACTTAGAAGAACTCCACCCCC	60.596	110
HM_5955	contig31722	CTC	3	18	cgaagAAGACAAACCAACACTCTC	62.292	GGCTGCTCTGATCTATGGATCT	62.929	124
HM_5956	contig37433	CAC	3	12	TTTATTTCCCTTgaTtTGCTATT	63.009	ATGaATCGGAGaACGAAGACGAC	63.877	86
HM_5957	contig27445	TCT	3	12	GTAaAagCAAGCTGTAGAGgTCCA	62.957	gGAGaAGCaAGAGGAAGGAGAAAG	63.177	94
HM_5958	contig22245	CTT	3	18	gagctctgttcgctgtaagt	64.287	ttcgaagaagtggtgaagcagagt	63.778	146
HM_5959	contig33757	AGA	3	12	GATAATATTACGCCACAGGAGGagg	63.109	CAACAGGGGAATGTCCATaAAAGA	63.3	100
HM_5960	contig14597	GTT	3	12	GGTGTCTGAATGGTGGTACAG	62.799	CTTACCACCTCTCAAAACCCaTT	62.696	103
HM_5961	contig08363	GAT	3	12	tcGTGTCTTCTCTGCTATggTg	62.842	aATTTCTCTGGAAGCTTCTGCT	63.008	84
HM_5962	contig12695	TTC	3	18	TAACTGTAGATGGTACTCGgCTg	62.739	TGTaAAAGTgGTGGGCTCACTT	63.12	108
HM_5963	contig48581	TGA	3	24	TGAGGAAATGcAGAGAAGAGAGg	63.313	CTTCTCATTTcCAACCAATCACT	62.987	82
HM_5964	contig29266	AAG	3	12	aaaaagggaaggaagagaagaaca	62.765	AGATTGAACCATGCCAACCACTT	63.035	155
HM_5965	contig05326	CGG	3	12	GGTAATGcGCTTCCCTGAGATAG	63.238	AACTATTTCTTCCCAACCTGCC	62.808	145
HM_5966	contig13757	AGA	3	12	TTTGGGGTgAAAGCAaCTTTCTa	63.118	gaAGaAAAAcctctTgGGGAGTA	62.968	159
HM_5967	contig15477	GCC	3	12	CTAAGAAAGAGgCGGCCAACTA	63.025	CTGACGCTTTTATTGAGAGTT	62.698	160
HM_5968	contig01381	TAA	3	15	AGTATCCATAGATGAAGATGGCGg	62.608	aAAAAGGGAATTTGAGAGGTTTG	63.098	144
HM_5969	contig05415	TTC	3	12	CtCTGTCTTCTCTGTCTcGTGCT	63.231	CACCATCAAAACCAAAACTCTc	63.006	158
HM_5970	contig06394	ACC	3	12	CcAAcAAATTAAGAAATgCTGaAcA	62.488	CCATGGCCTTTcCAAGTCTAAT	61.515	149
HM_5971	contig35521	GCC	3	15	gctcgactacgataaaggaaaga	62.137	GTCGaAACCAAGGTTTCTCTGTT	63.005	113
HM_5972	contig21273	GAC	3	12	AGAGAGGAAgAGGATTGCGtgATA	62.7	GATGACGAAGAAAACGACTCACT	63.027	155
HM_5973	contig16988	GAA	3	18	TGGGGAGTAGAAGgTGAAGTTGc	63.107	TGGcTCTAGCCATTTCAAACCT	63.133	102
HM_5974	contig09552	TAA	3	15	TggTGTCTTCTGATGTTCTCTGCT	62.692	TTAACTTGAATTTCTGGTtCC	63.221	107
HM_5975	contig43407	TTA	3	15	gACACTATTATtGcAGCgAgggga	62.495	TTGAGAGCGGGTATATGTTTGTG	63.322	160
HM_5976	contig26056	GGA	3	12	AGGTGAGAGAGGgAGGAAGG	63.264	CtCAAACTCTCGATCTCTCCA	62.353	93
HM_5977	contig00305	TGG	3	12	CATGagAAAcTACGTGGAGGAGG	63.3	CACCGGTTATTATGGTgCCAATAC	63.339	155
HM_5978	contig08336	ATA	3	21	TCACTGTCAATtACcaaaCaaTAGGA	62.952	TCCTCGCTGGCTCTCAACTATAG	63.051	160
HM_5979	contig35982	CAC	3	12	aCCGAGACATTGGAGATTaCAgGa	63.217	GTAATTGCGcGcCAAACTCATAG	62.96	92
HM_5980	contig20349	AGA	3	12	tgtaattcccaacgtgatataacagaga	62.955	AGAATCCCaAATGTCTAGGCAAA	63.121	149
HM_5981	contig30134	GAA	3	12	GAAAAaGaGgAAGCTGAAGGGAAA	63.273	AATCTcCTCAATTgGATCCCTCTC	63.053	149
HM_5982	contig00182	GCG	3	12	AAGACgGCAAAATTggAAGC	63.686	CCATCACCTCTcTtTGTGCTCC	63.189	84
HM_5983	contig28444	AGG	3	12	TGAAGTTTTGgAaTCCACTGACAA	62.918	TTGGACTTTAGTAGGTGGCGAGAG	63.028	111
HM_5984	contig37767	TCA	3	12	catcagcttctcagcttttctct	63.031	GAAGATGGGTCAAGTGAAGTGAAGT	62.994	123
HM_5985	contig21692	GAA	3	24	CCGAAaAaGGAAcGAAaAaTaGA	63.548	GTTATTGTCCTcCTTTGTGGTTG	62.829	128

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_5986	contig26127	TAC	3	12	tggacatctctctgttcaGTTTgT	63.235	GaAGaAAATCCCAAGCAATTGAG	62.315	123
HM_5987	GD20F4R02FWVRH	TGA	3	15	CCCTCTCAAGTACTCTACCACCGGA	63.007	GTCCTTAAGGGGAAGAGGTGCACAG	62.61	108
HM_5988	GD20F4R02H018X	AAG	3	12	CCCTCGCTCTCTTTCTCTCTCT	62.762	TACCCACTTAAGTTTGGCGGAATA	63.036	148
HM_5989	GD20F4R02I36IT	GTG	3	18	CCATGGTTACTGCCAACGCTAGT	64.51	GTTGCCCAACACCACCAC	64.683	99
HM_5990	GD20F4R01B2WC7	AGA	3	24	AACAAAGCAAGAAAGAGGTCCC	63.098	TGTCCCACTGTGGTACTGTTGTC	63.159	144
HM_5991	GD20F4R01ED9RY	AAG	3	12	TATCAGAAGTCCACTTGCCCTCAT	63.331	TTTTAAGGGATTGGTTGGTTTGA	62.706	140
HM_5992	GD20F4R01A8242	AGA	3	21	CCTTGGTGGCACTTTCAGTTATTCT	63.129	CAATCCCCCTTGGATTTTCTATT	63.156	126
HM_5993	GD20F4R01AFR60	CCT	3	18	GGGACTTGTTATGATGATCTGGC	63.016	AGGGAAATCTCTTCATATCTCG	62.961	153
HM_5994	GD20F4R02HEQ9S	TCA	3	15	CTGGCTTTAAATCAGCATCTCTTG	63.122	AAAATCAAAAGTTGATCAAGGTGG	62.495	146
HM_5995	GD20F4R01BKS5D	TCT	3	12	AACATACTGCCAAACACTCTCCC	62.725	GCACCGAGAAGAAGCAGATAGTG	63.671	157
HM_5996	GD20F4R02G3B59	CTG	3	12	ACCAAGTCCCTGTGCTGATATCTC	62.925	TGCTCTACACTGCCATTCTGCTAC	62.989	125
HM_5997	GD20F4R02I1W79	TCT	3	12	ATCCACCTCCGGCACAGACT	64.329	CACCAAGTTACATAGTGTGGGAA	63.389	134
HM_5998	GD20F4R01A842D	TTA	3	12	TTTACCCTACGTTTACCGTTTAA	61.817	TTTTGTTTGTGTTTCTGTTCTTCG	62.802	216
HM_5999	GD20F4R02HQRXI	GAA	3	15	GAATGGCTCTGAGAAATTTGAAA	62.802	TTTGAGTGGGTCCATCAATGACTA	62.803	129
HM_6000	GD20F4R02HTSTW	ATT	3	15	TTGTCCACACTGTTTGTATTAGG	63.044	AACGAGCAGAAATTACAGCGTTAGG	62.969	157
HM_6001	GD20F4R01A4XTY	AAG	3	12	CGTGAGAGGGGAAAATAGAGAGAA	62.171	CGCTTTTCAATGGAAATTTAGAG	63.122	117
HM_6002	GD20F4R02JGGFR	TTG	3	12	GTGGATTATGGCAATGGTAATGGTT	62.937	GTGCAGCTTCAACAACAACAGTCT	62.989	91
HM_6003	GD20F4R02JOW61	TTT	3	15	TCCACCTTGTCTTGGCATTTACT	63.129	GTCACATAAGGATACGGTGGAAAG	62.91	92
HM_6004	GD20F4R01DKV0N	CTA	3	15	TGGCAATAGTCTCAGCAATGTCTC	62.847	GTGTTGGAAGTACTGGAAGGTGCT	62.935	140
HM_6005	GD20F4R01ATQJO	GAA	3	12	GCAGTATCGTGTATGAGAAGAGCAT	61.021	TTTTTGGTTCTTCTTCAATCTGCT	60.17	204
HM_6006	GD20F4R01A43OR	CTT	3	12	GCATGTGACCTTCTTGGCAAGACT	62.949	AAAGAAGAAGAGGAAGAGGGGTCA	62.958	117
HM_6007	GD20F4R02G8AQN	TTA	3	12	CGTAAGTCTGCCCAAGTTATGCTT	62.862	GGCAAAACCACAAATCAATTTTTA	63.026	106
HM_6008	GD20F4R01CJZRL	TCT	3	12	GGTGAGCTTGTCTTACTAGTGTCAA	62.858	CCGAAGTTCACTAGATTTCACCG	63.214	146
HM_6009	GD20F4R01B4OYE	CTA	3	12	ATCTTTCTCCGACTCTGGGT	60.074	GAAGAAGAAAGAAAGGATATACGGA	60.194	152
HM_6010	GD20F4R02H3L6I	GGC	3	12	GGAAGCGGAGCTCAATTTATAGT	63.019	GCCTCGTCTTCACTTGTCTTGTAT	62.145	152
HM_6011	GD20F4R01A0DUZ	TTC	3	18	GACTTGCTCACAAGGCAAGTTTTT	63.057	TTAGGAGGAGATGGCTGAACAAG	63.006	155
HM_6012	GD20F4R01AEVLN	CCT	3	18	GGGACTACCTCGAAACTTGAA	63.776	AGTGTGTTGTTGTTGTCATGCTG	63.402	131
HM_6013	GD20F4R01D780D	AAG	3	12	AGGACACCATGTGGTCAAAATTTTC	63.331	CAAAAGTTTGGTGTCTTCTGACG	62.942	132
HM_6014	GD20F4R01D0L7K	AGA	3	15	CACATAACACCCATAGGGAAG	62.905	CGTCGATGTGAACCTTTTACTGCTG	63.184	152
HM_6015	GD20F4R02JIJ9H	TCT	3	12	ATATGGGTGGCGATCAATGTATTCT	63.028	TGGTTCATCAAAACTATGGTACG	62.34	106
HM_6016	GD20F4R01EC5BM	AGC	3	12	GTTCTTTGAGAAGATCGGCAAGA	63.121	AATAGTTTGGGAGCAAGAACGAGT	62.672	123
HM_6017	GD20F4R02GF26A	CTT	3	12	TAGCTGGATAATTTCCAAGGCAA	63.026	AGGAGAAAGAAGAAGGACCGAAGA	63.068	144
HM_6018	GD20F4R01EOJYI	GAA	3	12	GGACTCAATGTCCAAGTGATATGG	61.826	ATTCTCATTTCCCTTTTGAAGAAC	62.679	159
HM_6019	GD20F4R02F075R	CAT	3	12	TACAAAACTCAGATTTCTGCCAA	63.068	TGAATCAAAAAGCATCAAGTTCA	62.932	137
HM_6020	GD20F4R02J0PAH	TGA	3	12	ATGCTCTCAAGTTAACCTTTTCCA	62.922	GCTTCGTGGTATTTCTCAAGTCT	62.54	139
HM_6021	GD20F4R01C2Q8S	GAA	3	18	AGTGGAGGAGACAAGAGGAGGAT	62.964	GCTTTCTGATGGTACTCAACGCT	63.06	123
HM_6022	GD20F4R02GF26A	ACA	3	12	TAAATCCGAATTGTGATGCTCAAC	62.533	CGATCCTCTCCATCCCTGAATTT	62.961	154
HM_6023	GD20F4R01CLXMW	TGA	3	12	GGGCTGGTAATGATGGTTATTTGA	63.117	AAGTACAAGTCCAACGACCAACCT	62.425	143
HM_6024	GD20F4R02JWZ5W	ACC	3	15	TTAAACATCAATTTTGGCTGCG	63.234	CTTTGTTATGTGGGATGCACTGT	62.324	146
HM_6025	GD20F4R02FZ789	TGA	3	12	CATCAACATCACCCAGAACTAC	63.718	ATTCAATGGTGATATTCAACCCAGG	63.108	147
HM_6026	GD20F4R01DL65V	ATC	3	24	TCACCTAACATCCAGATCAGCAAG	63.038	ACGATCACGATCAGGATTTCTTCT	63.349	100
HM_6027	GD20F4R02FXC2B	CCA	3	15	GAATTCACCCCAAGCACTAAG	63.123	GTACACCCGGTACATCAGGTGCTA	62.339	112
HM_6028	GD20F4R01AMEY7	ACT	3	12	CATGACCACATCAATCCTATCCCT	63.311	CTGTGAAGTTGAGAGAGCAATGGA	63.04	121
HM_6029	GD20F4R02IX1T3	TCT	3	12	GTGAGGAAAACCTCAATGGAGGAA	62.784	TTCACGAGTGTATACCAAGCAAA	62.969	123
HM_6030	GD20F4R01A8KHH	GAT	3	12	GCACGGTTTTCTCTTCAAAACAA	62.947	CTTCACCAAACTCTCAAGGGCTTA	63.015	160
HM_6031	GD20F4R01EDN7G	ATC	3	12	AATCAAATTCCTATCCCTGGTAAG	63.36	GATGAAGAAGAGGACACTGGTGGT	63.005	130
HM_6032	GD20F4R01DAWUT	CCT	3	21	CGGGCTAAACACTCGTGGATGATG	64.065	TAACACAGATCATGGTACTTGGCG	63.278	157
HM_6033	GD20F4R01ARQEL	CCA	3	12	TAGCTTGCCATTAGAAACCTCTGCT	63.055	GGGTGGTGGAGACTGTACTTAGG	62.282	128
HM_6034	GD20F4R02JM8RJ	TCT	3	15	CCAATACATTGCTTCAAAATGCC	63.527	AGCATTCTCTCCATTTCTATCAG	62.9	157
HM_6035	GD20F4R02JYYN8	GTG	3	21	ATTCTACCAAACTCCCTGAAGTCC	63.696	CTCCAGTGCCACTTCTTCTCAACT	63.347	149
HM_6036	GD20F4R02F088J	TTG	3	18	TTGTTTTGCTGTGATATCTTCCA	62.946	ATCGGATTCAATCTTTGATTTGGT	61.992	137
HM_6037	GD20F4R02GY2PS	TTG	3	24	GATGAATCGACGATAGACCCCA	63.016	CAATTCAAAACCTCTCCCAATCA	63.397	150
HM_6038	GD20F4R02J0FID	AGC	3	18	AGGAGTAGGAGAGGGGAAATGATG	63.059	TCTCGGTAAGTCAATCGGAGTAGG	62.907	153
HM_6039	GD20F4R01CC2GX	GAA	3	18	TTTTGGTGATGAATCTCCCAACT	62.996	GCGAGTTGAGTGAGCAAAAATGTA	62.772	145
HM_6040	GD20F4R01C8HRD	TCT	3	21	TAAGCACAGAAGGAGGAAGAAAGC	62.425	TAGAAGAAGGGGAAGAAGAAGACG	61.481	113
HM_6041	GD20F4R01C39X9	GGA	3	12	GAAGCTTCGGTTGAACACGAT	62.714	TTACGAGTCTTCTCGAGATTGCTCT	63.244	131
HM_6042	GD20F4R01CJ9LH	GAA	3	21	TGAATCCGATGATAATCTTGCAG	62.411	GAAGCCATGTTTGGCAGTCTCTAT	62.94	138
HM_6043	GD20F4R01D7NUY	AAG	3	12	TCCTGACTATACCTCTCTACCCC	62.767	CGCTCGGTACTGGTTATCAGCTCT	62.946	143
HM_6044	GD20F4R02F1980	TGG	3	12	AACAGATTAAGGTGGAGTGTGGGC	62.925	GTGGGGATTGATACCAATGATACG	63.42	135
HM_6045	GD20F4R01AX2IS	AAG	3	12	TTTTCAAACTCTTTAGAACAACTCA	60.028	GCACACTCTTAACAGCCAAAGATT	61.015	97
HM_6046	GD20F4R01DAEFT	TAC	3	24	CTGTATCCGAGGAGAGCTTCGTA	63.129	GATTTGTGATCGACTGCGAAAAATA	62.44	135
HM_6047	GD20F4R01CUZK4	AAT	3	12	GGCAAGTCAAAATAGCAAAACAGC	63.268	GTAACACCAAGCACTCAAAAGCC	63.166	131
HM_6048	GD20F4R01DU5HC	ACC	3	15	GATTGATCTTCAATGGGAATCGAC	62.993	TGGCCACATCAACCAATCAATAA	63.25	109
HM_6049	GD20F4R01B73YB	GAT	3	12	TTCTGGTCTTGGTAATGTGCTGA	62.31	TACCCTACGTCACCTTGTGCTTT	63.15	82
HM_6050	GD20F4R02F6WVI	TCT	3	12	GGAGAACAGAGAGTCGCAATGTTT	63.141	GTGTGAGGCTATGGAGGAGATTGT	62.915	116
HM_6051	GD20F4R01DENEW	CGC	3	18	AAAAACAACGCTTTGATCAATGTT	62.947	TCGTGTGTATAGGGTTGAGTAGTTCA	62.196	113
HM_6052	GD20F4R02GLTDH	GGA	3	12	TTTTACCGTACGTGTTCGATCAT	63.648	AACCCCTCCGATCTGAAGAAGAAT	64.542	133
HM_6053	GD20F4R02FMW5F	ATT	3	15	TGTTTGTCAAGTTCACATGCTTCA	62.864	GAGACACTCCCTAAAGAGGCTTGG	63.802	145
HM_6054	GD20F4R01A9D4A	CCA	3	12	ATGCTCTTATGGCCCTCTG	62.671	AGGAGCTGAAGATGAGGAAGGAGT	63.19	101
HM_6055	GD20F4R02ITWQV	CCT	3	12	ACCATCTTCAAAATCCACATCAG	63.419	AGAAGTGAACATGAAGATCTGGCG	63.988	126
HM_6056	GD20F4R01ANP1Y	GTG	3	21	CAAGCATTTTGTGCTGCTCGTAGT	63.076	AACGGTCAAGACTCAACAAAAT	63.369	138
HM_6057	GD20F4R01CED5Q	CGG	3	12	AGAGGGGTTAAGTACGAAGCGAT	62.636	CTTTTAATGGACTCTCCGAACCTT	62.98	140
HM_6058	GD20F4R02G03MA	GAA	3	12	TTCCATTGTACAGCCATAAACCC	63.126	ACTTAGCTGCCACCCCAATCAT	64.088	97
HM_6059	GD20F4R01B8KY0	AAT	3	12	GTACTTGGTTCCGAGGGCTATTTC	63.196	ACCTGTTGCTGGTTTTTGTATGT	63.166	109
HM_6060	GD20F4R02H9TOX	GAA	3	12	CATCTCTTCTGGAATCAGCTGAT	62.99	CAGAGCTATGGGAAACAAAATGG	63.014	86
HM_6061	GD20F4R01DI26U	TCA	3	15	TCAAGCTTGTAAATCGATCCAGTA	63.136	CGATCTCAAGGACCAAGGTAATA	62.592	155
HM_6062	GD20F4R01C6SKH	TTA	3	12	CCTCACCATCAGGCTTATGAGATT	62.8	AACCAAGAAAAAGGAGTTGTCGT	63.399	159
HM_6063	GD20F4R02HKL2X	TGA	3	24	TCCGATCAATTTTGTGGGTATAAA	62.542	GGCAGAGTATCAGTCAATCAAGA	62.965	157
HM_6064	GD20F4R02FQB8Y6	TCC	3	12	ATTTCAGCTGTGGGACCAACAG	63.71	CTATCACTGGCCCTCTTCTTCA	63.006	157
HM_6065	GD20F4R01A393S	ATC	3	12	ATGACGAAGGGACATGGACATAAC	63.336	CGTCATCAGAATTTGGCTACGCTT	62.96	133
HM_6066	GD20F4R01DQGBX	AGC	3	12	CATTAGCAAGGATGAGGGGAAAAA	62.811	GTTGAATTTTCAATCCGATGGTG	63.62	98
HM_6067	GD20F4R01EIM6Y	GCA	3	12	ACCTTCTGCTCGAACATCAGAGT	62.823	TAATCCTTTATCTGAAGCTGGCCC	63.775	152
HM_6068	GD20F4R02GN17M	GTA	3	12	TTGATGCTCTCTCTTTGTGTGT	63.173	TGATTTCTGTCTTCAAAATCCGCT	63.108	141
HM_6069	GD20F4R02H6BOO	TCC	3	12	AAGAAACTGCAACTTGTTCGAT	62.425	CGAAATTCATCTTGTAAAGGGG	63.034	142
HM_6070	GD20F4R02GULYK	CCA	3	15	GACCTCGAAACCGTAACACAGG	63.146	CCGTATAATCATGGGCAAAATTGAG	63.621	134
HM_6071	GD20F4R01DLG98	ATC	3	21	TTTACCACACAAAATAAGTGGGTTT	61.018	CAGGATTCAATTTTCTCCTCTGT	61.313	121
HM_6072	GD20F4R02GIKJ	TCC	3	12	GCATCTCTCAATCATCATGACCTT	62.915	GAAGAGGGGAGATACAACGTCAGA	63	149
HM_6073	GD20F4R01EOWI9	CAA	3	15	AGTCCCAATGTCAATGGACTTAA	60.945	AGGTTGATGATTTGCTGTAATTGTG	60.12	82
HM_6074	GD20F4R01C3XZC	AAG	3	12	TTTCCAGGGTTTAAAGCTTCAAGT	63.015	ACTAAGGGCTGTTTCGATGTTGTC	62.838	157
HM_6075	GD20F4R01B3A1I	TCA	3	12	TGCTCATCTGTCATGCTTCTTACT	62.397	AAACACTTAGTTGCAACCCGGGAAT	63.203	137
HM_6076	GD20F4R02GZLID	AAT	3	18	TCAAATTCAAAGGTTTAGACAGCAA	62.162	TTGGGTACTGCTCTTTTAAACAAA	62.187	104
HM_6077	GD20F4R02FLW10	TTC	3	12	ACTCTCTGAGTTCATCCCAAAA	61.35	AATGGTTAAGTTGGGTAAACATAGAAA	60.904	105
HM_6078	GD20F4R01A8W0V	TTA	3	15	CAATGGTAATTTTCAAGAAATCTCA	63.297	CAAAACAACATTTTCAACCAATT	63.014	108
HM_6079	GD20F4R01AOZSD	ACG	3	12	CGCAAGAACTATTACTGACTCGCA	62.883	ATTCCAGAGACTCGACCAATCAG	63	133
HM_6080	GD20F4R02HXNRC	TCA	3	15	AGGGGGTGGTTTTAATATCTCCAA	62.875	GCTGACCTGCTCATGAGTCAAT	63.146	157

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6081	GD2OF4R02FXN2M	CCG	3	12	CCTCAATCTCAACCTCATCCAAC	63.204	GAAAGTTGAGTGCTCTTCGCC	62.609	105
HM_6082	GD2OF4R01AVG00	GAT	3	24	CCCTAAACCCAAATGTGAATGAA	63.097	CTGACTAGGATGTGATGTCGAACG	63.159	113
HM_6083	GD2OF4R02GRJDA	GCG	3	15	TCCTGTTTGAGCTTTCTAGGTGC	63.142	CTACCTCGTGCCTCTACACC	63.44	120
HM_6084	GD2OF4R01DUSWY	GAA	3	24	GCGGTTTTGGTAGAATGTTGTTG	63.747	GCGATCAATTCATCATCACATC	63.706	125
HM_6085	GD2OF4R01A8QCM	TCT	3	24	TTAAAAGGGCTGATTATGGTCTCTC	62.72	AAACCACAGAAGGTGAAGGTGAAG	62.906	90
HM_6086	GD2OF4R02HBEUK	CTT	3	15	AAGAGAAATTTGGGGGAATCAAAA	63.06	GGGAAACCTAGATTAGCAGCAGT	63.114	119
HM_6087	GD2OF4R02I95YN	TAA	3	12	TTGCGCTTTATGATTGTTTCAGGT	63.03	AAAACCTAAGGAGGGTTTGGGAG	62.859	132
HM_6088	GD2OF4R01CWNQJ	AGT	3	12	CTACTGATCCAAAGGAGGAACACC	62.368	AGGCAACAAACATAGAGGAACCA	63.129	158
HM_6089	GD2OF4R01ALNL7	CTG	3	12	TGAGGATTGTGTGTCTTTCATCC	62.473	GCTCAGATGCTCTCATGGTCAAC	62.476	141
HM_6090	GD2OF4R01DW0II	GAG	3	12	CCGAGATTCAATAATTTGCCGAA	63.304	TTGGGATTAGTTTCTGCAATGCTT	63.138	159
HM_6091	GD2OF4R01C36RN	TGT	3	12	ATCTTGGAGGCCACAGAGAGTATG	63.014	AGACCCAGTCCAAACCACTAAAGA	62.382	141
HM_6092	GD2OF4R01BCHA0	CCG	3	12	ATTTGAACTCCTTGCTCTCTCTCT	62.986	TTTGAGCTATGTTCTGCTGGGAG	62.958	156
HM_6093	GD2OF4R01A53JD	GAT	3	12	TGGAACAACCTCTCCAATACAATG	62.279	GCTGAGATCATGAAGTTTCTCTCAA	63.024	135
HM_6094	GD2OF4R01AENZE	TTG	3	12	TGATAACAATGGATTGTCAATTTTATT	60.128	GCCAACTCTCGAACCATACTACTAA	60.911	153
HM_6095	GD2OF4R01CL4WX	CAC	3	12	AGTCACCCACTCTTTTGGAGTG	62.906	GCAGTGAATCTATTCCATTTGCT	62.733	117
HM_6096	GD2OF4R02F7PL3	AGA	3	12	TCAATGAATCAATGCCCTAGAAAA	61.903	AGATTCTCTTTTCTCATCTCTGCAA	61.014	91
HM_6097	GD2OF4R02HMMQK	TTG	3	15	ACATTTACGAAAGTGCTGATGGT	64.111	AACAGCATGTTCTCGAAACCTCAT	63.356	92
HM_6098	GD2OF4R01CM3QT	CCT	3	18	TGAATTGAGCTCTGTTTGGGGTA	63.048	CGAAACAGTCAGGAATAAGAAATGGA	62.715	115
HM_6099	GD2OF4R02I0FNN	CCA	3	12	AGACAATCTTCTCCACTCTCTCT	62.964	GATACAATGAGGATAAACGGAAGCC	63.113	154
HM_6100	GD2OF4R02I1LMD	GTG	3	15	TCAAAAACCTCCCAACTACAATGTTCC	63.498	TTAGCATTTTCTCATATTGGCGG	62.234	152
HM_6101	GD2OF4R01DICQ5	ATC	3	12	TCCCTCAGTGTGGTCATGTAGTA	62.919	TACGATGATTGCTTCATCAGGTTT	62.515	120
HM_6102	GD2OF4R02IGKYL	AGA	3	12	CTATTTGGGAGAATGACAGGTGGT	62.584	ACTCTACAGTTTCTCTCCATCGC	62.295	147
HM_6103	GD2OF4R02I8VO9	GCG	3	15	TGAACACACCGTCACTTCTCAC	63.295	GAGGTGGCGGAGACAAGTT	63.821	151
HM_6104	GD2OF4R02HUH0N	CCA	3	12	CACGTTGTTACAGCATTAAGACTA	63.406	TTGAACATGGAATTCGTCAAGTGT	62.831	81
HM_6105	GD2OF4R01EYUZA	GGT	3	15	TTCTCATCTCTCATCTCTCTTG	63.076	TACTACTTCTCAACCACTATGCA	62.843	83
HM_6106	GD2OF4R02GFQ5D	TTG	3	12	GAATCGCATCTTGACATTTAAAGG	63.021	GCTCAATCTTGGAAGAAAGAAATGG	62.495	112
HM_6107	GD2OF4R02F1QN5	TTC	3	12	TCCAGCTAATGACCCCAACTATGT	63.022	GGATTGGGAAAGTTAGAGAAGGAGG	63.621	114
HM_6108	GD2OF4R01D5W4W	TTT	3	15	TGGAAGACATCGAAAAATAAGTTAATC	60.135	TGAAGAAAGGGGAATTAATTAAGAA	60.77	238
HM_6109	GD2OF4R02I8W09	GTC	3	18	CGAGAAGTCAGCTGTGATGTGG	63.295	CCCACGAGGTCATTCATACATAG	63.735	121
HM_6110	GD2OF4R01C2G50	GAA	3	12	CGATTTGTAGTTTTCACAAACCTCT	63.512	GTACGATATATAGCCACGGTCGGA	63.249	139
HM_6111	GD2OF4R01BRNGR	ATC	3	12	TCCACCGTTTGTGAAATTTTGT	63.63	GGACAATATGCTACTCTGATGG	63.013	115
HM_6112	GD2OF4R01BB0XW	TGA	3	30	CCACCACTTTTGAGAGATGAGAGC	63.431	GGTCTCATGTGATCAACTCGACT	63.269	97
HM_6113	GD2OF4R01EI6RQ	TGA	3	12	TCAAGGAAAGTGGAATATAAAGTTGG	62.753	CCTCATCGTCATCACTTCTCTCT	63	114
HM_6114	GD2OF4R02F520G	ATG	3	15	CATTGCTGATACAAGAAAGAAACGA	62.664	GAAAAGAAAGACGATTCGGATGAA	62.802	133
HM_6115	GD2OF4R01A0IQD	CTC	3	12	TTGAATGTGCTGGTGTCATTAATC	63.042	ATGATGTACCGTGGATCACTGTG	63.164	148
HM_6116	GD2OF4R01DHA6Y	TTA	3	15	GTGGACTCTCAATGCTGATTT	62.813	GTTTGTCTGCGATGTTGTGATGAT	63.407	136
HM_6117	GD2OF4R01AZB4L	TAA	3	12	AACACAACATCGAAATCACTCT	62.913	GATCATATGAGAGTTGGTTGGGT	62.47	103
HM_6118	GD2OF4R01AUKQI	TTC	3	12	AAGATGCTTGATGTCATGAATGA	62.261	GATGAAGCGAAGCAACATAAAGT	62.963	216
HM_6119	GD2OF4R01BMRNB	CCA	3	12	CCACACAGACACATCGAATC	63.775	CTCACAGTGACATCGGAAGGTT	63.034	149
HM_6120	GD2OF4R02JPHK5	TCT	3	15	CCGCTATTTCTTCAATCTACGC	62.933	GAAACACAAAAAGGTGATGAATGG	63.02	156
HM_6121	GD2OF4R01CXW76	TAG	3	24	ATCCGACACGCTATTATAGGGCT	63.019	TGAAAACATGTGTTTGGGAAGAA	62.715	110
HM_6122	GD2OF4R01B0CTJ	CTG	3	15	CCAGGACTCGGAAGCACTTTTA	63.083	ATCAGGAGGAGGCTAAGAGCAAG	63.499	123
HM_6123	GD2OF4R01BAMVO	CGG	3	12	TAGATCTAGAGGCTTCCGACCA	62.684	TCTCTCAGTCTCTATAACCTCG	62.984	137
HM_6124	GD2OF4R02FTP2Z	TCA	3	12	GCTAGTGCTACTTGAGGTCTGTA	62.961	ATAGGCAAAATAGCGCGAAATACA	62.981	146
HM_6125	GD2OF4R01B40YE	CAT	3	30	TGACTTTTGGGATCACTTGTGTA	62.918	TGAAACACTTCACATAGCTCTCG	62.842	105
HM_6126	GD2OF4R02I1QWC	CCA	3	12	CTTTGCTCTGTAATCCAATCTCA	62.828	CTGAGCAAACTTGGAGATGAAA	62.615	122
HM_6127	GD2OF4R02JVDI8	AAT	3	24	CGAAGCCAATGCAATAAATCTAGAA	62.696	TATTTGAACTGCTGGCCAAATCT	63.138	158
HM_6128	GD2OF4R02IA5KZ	GCG	3	15	CATCTCATTCTCTCTCCAAATC	62.441	AACATTTGAACGCTGAGGCTGC	62.965	158
HM_6129	GD2OF4R02JUM8N	GTA	3	12	TGAGAGAGGAGATGTTTCCCTTG	63.085	CCACACCTTACAAATTTACAGGAA	62.343	105
HM_6130	GD2OF4R01AZZBK	GAT	3	12	ATTGTCACTCTGATGGAATGCTG	63.388	GCAGCTAAATTCACCGAGCTAAA	62.969	147
HM_6131	GD2OF4R01CW3VO	AAT	3	15	CTTCTAATTTCAAGTCCCTTATTTGA	62.051	TGAAATTCCTCAGTGGAATGAA	63.025	160
HM_6132	GD2OF4R01D1CMVZ	TCT	3	60	TTCACTAATAGTCTCTCTGGCTGC	63.035	AGGGCGGATAGCTCGAAATACAA	63.402	150
HM_6133	GD2OF4R02HC1LE	GCA	3	12	ACTACGAGGTTGACGAGCGAAC	62.951	CGGCGCAACTACTCTCTCTAGC	62.959	140
HM_6134	GD2OF4R01AF4FA	TAT	3	12	TAGTTAGAGCTGTTTGGTCAGCC	63.044	TTCAAGTTTGTGGTGGCTTTT	63.027	153
HM_6135	GD2OF4R01DI7LG	TCA	3	18	GCTCTCTATCATGTCTCCATCGT	63.021	CCTGCTGATGATGACCACTTG	62.919	121
HM_6136	GD2OF4R01AF264	AAG	3	12	CAGGGTCTTCTCATTTTCTGCTA	63.006	AAAGAAAGATGGGTTCCAAAGCTC	63.09	97
HM_6137	GD2OF4R01W67Z	TGC	3	12	AGAGGAAGAAGTGTGGAAAGTTTG	62.166	GACTCTACAGAGTGAGGCTGAGGC	63.15	105
HM_6138	GD2OF4R01CZ2L7	GTT	3	12	TGCTCAAAACAAAACTAAAAACAA	62.772	AACCTGAAGCAAGAAAGTAGCAG	63.162	151
HM_6139	GD2OF4R02IGEPB	TCT	3	12	TCTGATTTTCTCTCTGCTCCGTC	63.009	ATTTCTACCGCAATCTATTTTGT	63.029	131
HM_6140	GD2OF4R01CS2XJ	ACA	3	15	GTGCAGCTTCAACAAACAGTCT	62.989	TGTGATTTGTCATGGTAATGG	62.717	93
HM_6141	GD2OF4R01ALD5Z	GAC	3	12	GAGCACGAGCAGGTTCAACAAG	63.427	CTCTGTTGTCAAAAACCTCTCTGT	63.02	152
HM_6142	GD2OF4R02IWEW2	GCT	3	12	GCACACTGGATTATCCAGGAC	64.076	TACTCGCAACGCTATCCCTATTGT	63.162	135
HM_6143	GD2OF4R01BVW75	TCA	3	18	AATCTCGGCTAAATCATGTGAAG	62.718	ATTTGAAAGTGAAGATGGAGGGTG	62.684	147
HM_6144	GD2OF4R01D18D6	ATG	3	12	GCTACGCAAAATATGCTGCACTTT	62.786	TGTAACAATGAGCAACCAATCAC	62.934	143
HM_6145	GD2OF4R01C5H6M	TTC	3	18	TTCTTTTGTGTGATGTGATGCGT	63.834	GTGTATAACCAACGATCCGAAAA	63.126	150
HM_6146	GD2OF4R01AKGNK	TTC	3	12	ATGAATCAATAAGGGTGACATGGG	63.099	GGACAACAGAATGGAAGATTGAG	63.204	132
HM_6147	GD2OF4R01D4RIC	TCT	3	12	TTTGGGTGTGAAAAATGAAATTCG	62.032	TGATCAACTACAGAAGAAITTCACAGAA	61.611	157
HM_6148	GD2OF4R02JZTJB	CTT	3	12	TGAGGAAACAAACGATTGGTGATA	62.717	CAGTCTTCTTTCTCTTCGATCCG	62.795	158
HM_6149	GD2OF4R01EZUQX	GCT	3	12	AGTGCACTCGGCTAAAGGAGTCT	62.726	TCTGAAACAACAGATCGACGTTA	63.048	116
HM_6150	GD2OF4R02HN106	TTC	3	15	GCCTCTCATCTTCATCATCTCTCT	62.249	GTAGCAGGTACGTGGAGCAAAACT	62.861	138
HM_6151	GD2OF4R02H5X08	GTG	3	18	CAGTGTGGGATGTTTGAAGTAG	62.93	CTCAATCTCCCAACCATAACAGAC	63.102	141
HM_6152	GD2OF4R01A4SOY	TTC	3	12	TCGTGATGATGAATCATTTCTTTCG	63.371	ATAAGCTGAACGAGACGAAGCTG	63.263	99
HM_6153	GD2OF4R02GEFQX	ATT	3	12	CAGGTCAATTATCAACGATCCAA	63.15	ATCGAGCTCTGTGTTCTCTCACA	62.722	145
HM_6154	GD2OF4R01C3CC0	TAA	3	12	CTGTGCTGCTTCATCTTTAACT	63.044	ATGCTAGGTTTTCGCAAGGTTTT	63.217	133
HM_6155	GD2OF4R02FPGIT	GCA	3	12	ATTTTCTAGCTTCTTTTCCCGC	63.89	AGAGCTGTTGGATGACACTGGAG	63.033	135
HM_6156	GD2OF4R01EX7O6	ATT	3	12	AAGTCTCGTCTGTGATTGTGATCG	62.829	ACGTTGTCGAGAAGAACGAGAGAA	63.778	155
HM_6157	GD2OF4R01EEFFQ	ATG	3	21	TGATGAGAGGATGGATTGATTGA	62.885	CGCATCTACTCAGAAAGCAGTT	63.154	128
HM_6158	GD2OF4R02GNVWA	GTG	3	12	GATGTAAGCAAGAGAGGTGGGTGG	63.338	TGCAGTGATCAATTTTGTGACTTTATG	63.369	156
HM_6159	GD2OF4R02GHC6M	TGA	3	30	ATCAATGGACTGTTGATTCGGAAC	63.437	TTATCTGAGTGGGTGTGATGGCA	62.707	105
HM_6160	GD2OF4R02IRIKQ	TTC	3	36	TTCACTCATGTTGTCGAATCCC	63.138	TATTGTCGAAATAATTCACGCTCG	62.369	105
HM_6161	GD2OF4R02I0Z93	TGA	3	12	GGGGCACAAATTGAGATTCAATTAT	62.314	TTCTCGTTGTGGTGTCTTGAAA	63.044	132
HM_6162	GD2OF4R02GGSWP	TTC	3	21	GTTCTTTTGGGTGCGGTATTATG	63.665	ATTGTTACTGGGTTCCCAATTTT	62.795	121
HM_6163	GD2OF4R01A7JJP	TGA	3	21	AGAGGTCAGGCTTGGAAAGATAC	63.193	CATCTCAAGCTCACTTCTCTTCC	62.898	142
HM_6164	GD2OF4R02HC1HX	TTA	3	12	GGACGAGTAAATCTGACCGTAATG	63.022	ATCCACAGGTTGTTATGGCTAAT	62.744	117
HM_6165	GD2OF4R02F4DO3	GCG	3	12	AGAGTGTGATGAACCTGAGAATGGC	61.934	CCACTCTCTCCGCTAGATACAACC	62.382	156
HM_6166	GD2OF4R02I25NJ	GTG	3	12	GTCAGAGACTTGAATGGAGAGCC	62.798	CAACTCCACTCACTCTCTCTCTC	62.882	145
HM_6167	GD2OF4R01B4H84	TGA	3	12	GAGTCTAAGCTGAACCTCGTTTGG	62.723	ATTCGTTGGAGTAAGGCAACATC	62.713	154
HM_6168	GD2OF4R01CHJCI	TCT	3	15	CTACTGGCAATTTCTACCTGCTT	63.044	CATGCTGTTGATGATATGGGAG	62.934	152
HM_6169	GD2OF4R01A7DMO	AAG	3	18	CCAAAGTCAAAAACGAGTTAAAT	63.528	TTGATGATGTGTGGGCATAATGTT	63.378	118
HM_6170	GD2OF4R02IUFWF	TGG	3	12	TGCACTTGTAAAGGTGTTTCACCG	63.614	AGAGGAATATCTGGCTCTCGCT	63.1	113
HM_6171	GD2OF4R01DUQDI	CTT	3	12	CCAAAACCTAGGTGTGATGCTCAT	63.031	ACGTTTTAGGGGGTTTAAAGGGAT	63.064	155
HM_6172	GD2OF4R02IXVDH	ATA	3	12	TTAATTAGGAACCAAGCACTCCCA	63.014	CGCATCTACATGATCAGCTCTTGT	63.283	113
HM_6173	GD2OF4R02G0U4T	TGA	3	12	TATGCTCTTCACTTACGAGGCAAT	63.15	GTCAGCGTAGAAGCTGAATCAAT	63.051	81
HM_6174	GD2OF4R01D0XF5	GAA	3	24	AACATTTAATGAGAGTGAACCGGG	62.508	ATTTTGAAGGACTTTAGTGGGAGG	62.873	84
HM_6175	GD2OF4R01EV44F	TGC	3	21	ATATGCTGCGCTTGGTTACTCAG	64.611	ACAGCAACAGCAACAGCAACAAC	64.792	160

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6176	GD20F4R02IGWXZ	AAT	3	12	CCCATCAATGGAATCACCTAATC	62.679	CACAAGTGCTCACCAACTCTTT	62.852	151
HM_6177	GD20F4R02D22U	GAA	3	21	CATTTTTGAGGTTTTCTATACATTTCA	60.062	ATTGATCAGTTTCTTGGTCTGCACA	60.04	140
HM_6178	GD20F4R02HRY57	TTG	3	12	GAACGTGGAACACATCTGTTGGTG	62.933	CATGTTGGAGTTAATCAACGAGGA	62.397	133
HM_6179	GD20F4R01BGVV6	GAA	3	12	CACCAAGGAGACGCAAAAAAGAG	63.405	CCATTGCTGTTGAGTTCCTTACC	63.019	157
HM_6180	GD20F4R01CHSDJ	ATC	3	12	CTGAAAAAGCAATCATCAACGCA	63.381	TGAAGTTGATGCAAAAGCAAAATGT	62.972	122
HM_6181	GD20F4R02GN1H5	GAT	3	15	GAGGAGATCATAGGAGGAGTTGGT	62.964	TCAAGGTCTGCTCTTTGTGAGCTATT	62.625	93
HM_6182	GD20F4R01D81L6	AAT	3	12	TTTGCAAAAGGGTACTCCTTGATGT	63.129	CAAGAGGGAGAAATGCTCTGGTTA	63.006	155
HM_6183	GD20F4R01C1DWJ	CAA	3	18	ATTGTGCATAATAACCAACACC	62.937	CTGCTGCACAGCTAAATTTTTTCAA	62.786	109
HM_6184	GD20F4R01E16RQ	TGT	3	12	CCGATTCTGCAAGTCGTTAAAGT	62.849	CCTCTCTCCAACTTCATCACCAT	62.884	146
HM_6185	GD20F4R01BNFM7	GAA	3	12	AGAAAAAGGAGAACCTACCTCGTCG	63.292	AGGAGACTGAGTGACGATAGTGGC	63.254	150
HM_6186	GD20F4R02199H0	ACC	3	12	GATCTTCGGATGCAATGATTTGGAC	63.129	AATTCATTGATTTGGGAAACATT	63.668	95
HM_6187	GD20F4R01BC2Q8	GAT	3	21	CGGTGATTGACCTTGATATGGTT	63.329	TTCAACAGGCCACTATCCTCTAC	62.872	123
HM_6188	GD20F4R01AG9LM	TCT	3	12	ATTTCAAAACAAAATCTTCCCG	63.363	GCCGAGAAACAAAGAAAGAGTGAG	62.822	152
HM_6189	GD20F4R01ALJCG	GTG	3	12	TTATTGGGATGTGTGAATTTGGT	63.414	CTCGTCAATTAACCTCTCTCTCGG	62.696	157
HM_6190	GD20F4R01BN6J7	TGT	3	12	GAAATGGAGATGGAGATTTTGTG	63.116	CATTGTCTTAAACTTTCTCGGGG	63.13	129
HM_6191	GD20F4R02JKSP3	TCA	3	12	ATTACAAAATCCTCGAAGCCACC	63.696	CAAGACCATTGACAGCTCTCTATT	62.884	143
HM_6192	GD20F4R01DQ5O4	TGA	3	12	AAGCTGATTAGTCAGTCATAACAGACG	62.333	AGCCTAACGTACGGAAAAAGAGG	63.021	95
HM_6193	GD20F4R02F1D0B	CTT	3	18	TCATCATCACCACTCATGATT	62.911	CGATCCGTGTTATCTAAGGGATG	62.909	106
HM_6194	GD20F4R01BGE4A	TTT	3	15	CAAATCTGGTTAAATCATCTGCAA	63.325	ACTCAATGGACATTCAAGAAAGGA	63.204	121
HM_6195	GD20F4R02JV5LZ	TAT	3	12	TTTGGGGCTGATTGAAATTTATCA	61.251	GCATGCTAATAATTGTTGCTGCAT	62.089	125
HM_6196	GD20F4R01EQG93	TCT	3	18	AATTGGAATCGCACTAACACAAAT	62.95	TTGAAAGAGAAATGACAGTTGAGGAA	62.521	83
HM_6197	GD20F4R02FUC88	GGC	3	12	CTTCTATTGTAAGCCGACAGACA	63.63	TAGGCTCAACTCCCAGGATTT	64.39	88
HM_6198	GD20F4R02HG6HQ	GGA	3	12	CTCTTTTTACGATAGTGTTCCG	63.044	ACCCTCCGATCTGAAGAAAGAT	63.579	134
HM_6199	GD20F4R02JK6MK	GAA	3	12	TGTTAGTGCTCTCACAATGAAGTCG	62.868	CAAACTTAAACACGAAACCCCTTG	62.926	131
HM_6200	GD20F4R02HAP7J	CTC	3	18	TCGGGATGCATATCTGTTAGGAAA	62.996	CAGTGCCTTCGTAGATAGTGGTCA	62.739	142
HM_6201	GD20F4R02I0UF7	AAT	3	12	TGAGTCGGTGTGTTTTCTACAGTC	62.72	GCTTTTCGGAAATTTCTAGTGTTCG	63.405	111
HM_6202	GD20F4R01AOPU0	TCT	3	12	AGCAGCATCTGTTCTGTCTGAAGTA	62.532	TTAGGGTAGTCAGGCGCATCATG	62.716	90
HM_6203	GD20F4R01AUWLM	ATC	3	21	GGCATATTTCAGCAACAGACTCCT	62.94	ATTGTCAGAGACAGTCTGCGTTG	62.961	147
HM_6204	GD20F4R02IR371	AAG	3	12	GGATATTTTTCTTCCCAACAAA	63.255	GATCAAACTCCAAAGCCTGAAAA	62.813	139
HM_6205	GD20F4R01D1H24	ACT	3	18	GGGGTACTCTGATTGGAGAGAGC	63.505	ACAGAGCGTTGATGTTGTAATGGA	62.962	116
HM_6206	GD20F4R01AWDBN	ATT	3	15	TCGAGGTAAGAAATCTAAATTTGGT	60.546	TGGTGACAAATGACAAATGAAGAA	60.482	160
HM_6207	GD20F4R01D2MTA	ACG	3	15	GGCAGTGGTAAGAAAGAGAAAA	62.836	CGGATGATGTCCTGTCACAGACT	62.693	118
HM_6208	GD20F4R01EB8S3	TTC	3	24	CAGTCGGAAGTCAGAACAGAGT	63.231	ACTGGTTCGAAGAAAGACAAATCG	62.921	121
HM_6209	GD20F4R01B9S02	GAG	3	12	GTAATAATCCGATACCTGGGTGAT	63.365	AGCTATTTGTTCTATGGGCGACTT	63.246	157
HM_6210	GD20F4R01C7854	TGA	3	15	TCGTCTGTGATGATGACTCTTT	63.172	CAACCTCCATCTGTTTCTTCAAT	62.684	143
HM_6211	GD20F4R02JH2C5	ATA	3	12	AAAAAGGACGCGCAAGTAAAAATA	63.864	AGGACACATAAAATGTGACGGAGG	63.438	80
HM_6212	GD20F4R02ILT8K	CTG	3	12	TGTAGTTGTCTGATGAAGGGTGTGA	62.828	GTCCTACACCAATTCACAGTCTCA	63.228	107
HM_6213	GD20F4R02HXIEB	CTT	3	12	TGAACCATGAATCCCAGAGATT	62.987	ACGACGATGACTCCAGTTTCTTTC	63.027	121
HM_6214	GD20F4R01B919M	GCC	3	15	TCTCTAACTCCATGCTCAACACCC	63.763	TAAGTGATAGCAGCAGTGAACGAG	62.972	110
HM_6215	GD20F4R01DTGTD	CAT	3	12	AAAAACCAAGAACACAGCCACTG	63.595	GATATTTGTCACTCTTTCTGTTGG	63.009	143
HM_6216	GD20F4R01BQFX4	TCA	3	12	CAGGTTCCGAATTAAGTCTCTAG	63.32	TCATGAGTGATGCGATGATGATT	63.824	86
HM_6217	GD20F4R02JUZUH	CGG	3	12	CTGGAGATCTCTTTTGTGACGTCA	63.04	CTCTGGGAGACCGTCTGCAT	62.758	146
HM_6218	GD20F4R01BTBGV	TGG	3	12	TTAGCGTCTACGCTGATCCAT	63.067	GAGTTGAAGAAAGATTGCCAAGGA	63.009	160
HM_6219	GD20F4R01EUDTD	TGT	3	12	GCCAAAAAGCATTTTATACATTG	61.12	TCAACTTGAATCTCTCTAATCTGCT	60.217	111
HM_6220	GD20F4R01DBC5H	TTG	3	12	GTGCTGTTTGGCTTTTAGTTTT	62.766	AAACGACATCAGCAACTACGACAA	63.087	90
HM_6221	GD20F4R01AID30	GGA	3	15	ATTTTCATCAGAGATGATGCGAGG	63.639	ATAGCAGCAACAGGAGAGCAAT	62.853	155
HM_6222	GD20F4R02GD3PR	TCA	3	15	ACAGAATCAACATCTCAACCTCTC	62.784	GACTCTTGGACAGATGGTGGCTAT	63.775	115
HM_6223	GD20F4R02G2CX8	GTA	3	21	GCCAACTCGCTATTCTGAAGATT	62.854	ATCTTCCGTCAATGTCCTTCTCTT	63.386	142
HM_6224	GD20F4R01CYN1T	TGT	3	12	CTTCTGCAACCACTGCCTAAGAT	63.044	GTTGGGCTACTGCTCTGTGATT	62.949	113
HM_6225	GD20F4R01COC24	GAA	3	12	TGTGAATCTTTGCTTGTGTTCTG	62.955	GGGAAATCCCATCTCTATTCTTC	63.361	122
HM_6226	GD20F4R02JW4YM	GCT	3	12	ATGCTTATACAGCAAGCAAGGAC	62.867	AGGACAATTACGCCATAAGTGGAA	62.935	105
HM_6227	GD20F4R01AFDUH	AGG	3	12	GAGGGAAGAGAGTGCCCTAGAAG	63.08	AAAGCAAGCAATCTTCACTCTCTC	62.312	144
HM_6228	GD20F4R02F7N44	AAT	3	12	ATAAATGCAGGAACAAGATGAGGC	62.733	GGAATGATAACTATCTGCTACTGCCC	61.844	135
HM_6229	GD20F4R01AVO13	TCA	3	15	GCCTGAGTCTGAAGAACTTCAAGG	62.909	TAGGTCGTGCTGTGATTAATGCT	63.504	155
HM_6230	GD20F4R02HHQ4N	GAT	3	12	ATGTTGTTGTATGTTGCTGTGA	62.872	TTTGTCCGTCACTGAGTGAATAA	62.717	154
HM_6231	GD20F4R01B1QW9	TGG	3	12	GTTAGCGGAAGCTAACCAAGGAAG	63.6	CCACACAATCAACCAACCAACT	63.27	157
HM_6232	GD20F4R01CEJEA	TGA	3	12	CACTAACTTGGGGGTTTGTAGTG	63.003	TGTTATGTGTGATGGCGATAAAG	62.959	115
HM_6233	GD20F4R02GLF7M	GAT	3	18	TTCTTGATCTTGTGAAATGGTGA	63.141	AAGCCCTTATCTTCTTCTTCCCC	63.242	103
HM_6234	GD20F4R02HCM7A	AAG	3	12	CTACGCTGCGAACCACATTTCAT	63.609	CTTCTTGCTGGTTCGAGTATTT	62.957	129
HM_6235	GD20F4R01EORQM	TCT	3	24	AGTCCTGTGATCCCTTCTCTT	62.876	ACCGTTCTTACACAAGAGGAGC	62.131	153
HM_6236	GD20F4R01CGNEY	TTG	3	18	CTCGCATCTCTAATACCAAGATT	62.718	CGAACCAAACTTACAATCTGATC	62.813	157
HM_6237	GD20F4R01A278J	TTC	3	12	ATCCAGGGAAGGAAACATGATGC	63.591	AAGAGTCTGGATCGCTAATCCCC	63.075	160
HM_6238	GD20F4R02HUEJW	GTA	3	30	TGGCAAGTTGTTGATGAAGAAAGAA	63.15	GGAGTACCAAAACCTCTCAGAAAT	62.974	151
HM_6239	GD20F4R01EJFCW	CCA	3	15	CCACCATCTGCTGCAATTAC	64.741	GATGGTAATAGTGGTGGCGATCC	63.755	108
HM_6240	GD20F4R01DOJ1N	CAA	3	12	GCTCGAAGTGTGAGCATGAAGAA	63.057	TTAGTTGTTGGGTTTGTAAAGTCTGGA	62.197	110
HM_6241	GD20F4R02KLGNN	GTT	3	15	GGTAACAGCAGCATATTGGTCAT	63.358	AAACCAACAGGAGAAACAAACA	62.853	150
HM_6242	GD20F4R01EELGJ	CTT	3	12	TTACGCGACACTTTCTACTGTG	62.619	TTACATTCTTCTCTCTGTTGACC	61.818	148
HM_6243	GD20F4R02ILA6U	GCG	3	12	GGAGAGGCTGAGAAGAGGACATC	62.982	TGCTGGAGCTAGAGTTTGGAACTT	62.835	105
HM_6244	GD20F4R01B4XZL	GAA	3	21	ATCTGGTCTGGTCTTTTGTAGCAG	62.838	CAGAACCAATTAATCTTGGATCG	62.896	150
HM_6245	GD20F4R02HEFGA	TTC	3	12	TTGGTCTTTGGATGTGAATGTA	62.601	GCTGCCATCAATAAACCACTAGAT	62.635	130
HM_6246	GD20F4R02FODTF	TTC	3	24	CTCGGACCACTGCTTTTT	63.672	ATCAAAATCAACAAATGCGGATACA	62.685	159
HM_6247	GD20F4R02J1KGI	CCA	3	12	TTTATCATGGTATCAAGGCCACCC	63.117	AAGCCTGTGAGGGCTGTAGGT	63.558	124
HM_6248	GD20F4R02IW60E	CTT	3	15	GCCTTTGGTTATAGGAATTTGGGCT	62.734	TGTTCAACCAACCATAGGAACCT	62.932	153
HM_6249	GD20F4R01CFUGM	GTT	3	12	AGCCTTCTTTTCTTTTACACCC	63.024	AACAAACCTAAGGCAACACAGC	62.766	139
HM_6250	GD20F4R01B1WE	AAT	3	12	ACATTTGTTGATTTTAAAGTGCCA	60.932	GTCATCATTTGACTATGGATTGCG	61.751	82
HM_6251	GD20F4R01B86VZ	AGA	3	12	CGAGTCTCGGGAAATCTTATG	63.005	TCTAACTCGAAACCAACACGACA	63.057	128
HM_6252	GD20F4R01D92KY	TTC	3	12	AAACCGATCTCTTTTCCAAACC	63.462	ATGTGAAGGACTTTGATTGGGTGT	63.014	99
HM_6253	GD20F4R01BFT1D	TGA	3	12	TGGTTCCAAGTTTTTCTTTCTATGA	63.038	TTGGCCTTTATGGAGTTCACTGT	62.485	160
HM_6254	GD20F4R01CEZPY	CTT	3	30	TGTACGAGTGAATACACGATGG	63.163	TCCAATTCACAATATGCTTACCCAA	62.639	155
HM_6255	GD20F4R01ECATQ	TGT	3	18	GCCTTTGAAGCTGCTGATTATTGT	62.963	GGTGAAGAGCAATGAAGAAAGAA	63.009	108
HM_6256	GD20F4R02IXVSK	TCG	3	12	CGAGAAATTCGGAACCTCGTAGTC	62.522	TATGCTCTTAATTTGAGGAAGGG	61.941	96
HM_6257	GD20F4R02FZNCS	GAT	3	15	ATCTGGCGAGCAATTAATCAAA	63.034	CTTGCAAACTACCTGCTAGTTCAA	62.756	114
HM_6258	GD20F4R02FNXN0	GAA	3	24	TAGGGTTTGCTTTTTCAGTTCT	62.028	GATTCAAGCCCTAGATTACTGCTCC	62.731	113
HM_6259	GD20F4R01EOBAF	ACC	3	12	AGACCACAAACCTCTTACGTCT	62.709	GGCTAACCAATGAGGAAGCCAGATA	62.828	110
HM_6260	GD20F4R01CHEX5	CAT	3	12	GAACCTGCTCGAGTCGGAATCTA	63.133	AGATATGGATGAAGATGCCGAAAA	63.012	116
HM_6261	GD20F4R01A0BT0	AAG	3	15	AAAAAGAGCAAAAAATGGAAG	61.864	AAAGTGATGTGATAGCTTGGGGG	62.522	98
HM_6262	GD20F4R02F5WWT	ATA	3	12	ACAACAATGGTTCGACACTGAGAA	63.173	TTCAATTTGTAGATTTTGCTGTA	62.859	119
HM_6263	GD20F4R02LUX8	GAT	3	12	ATCAATGTGTCTGTGCAATGTG	63.105	GTATCTGACCTACATTGGGCTCCT	62.727	155
HM_6264	GD20F4R02I61A7	GAA	3	12	GGTGAAGAAACCACTGACAGAACT	63.036	CCTTCAATGACCAAGCTATGCT	63.053	116
HM_6265	GD20F4R02H0HUX	TTC	3	12	TCATCGCAATAATTAGCTTCGGTT	63.053	TGCAGGCTACTAACACGGTATCTC	63.263	94
HM_6266	GD20F4R01EUAKU	TTC	3	30	ATTTTGATAGGCAACGGGACATTG	63.329	GTTCAATGGCTACCAAGTACCAAC	62.936	139
HM_6267	GD20F4R01EP7C6	AAT	3	12	TCCACCATTTACTCTGCGGATTT	63.009	TTGTTTGAAGACGGTGATGTG	63.091	154
HM_6268	GD20F4R02J1JNS	TCA	3	12	CCTCTGCGATCAATAGATCAGGTT	62.8	CCTAGCGAAGCGAAATTTTGTAA	62.772	116
HM_6269	GD20F4R01DT4W4	AAG	3	15	ATTACCCATATTTGCCTTCCATT	62.995	CCGAGTGATCTATTGCTGCTTT	62.312	127
HM_6270	GD20F4R02G4UJG	TAT	3	12	ATGCCCATTTGAATTGTGCTACT	62.95	TACTATTCAACGCCATAAGCGG	63.334	100

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6271	GD20F4R02GJXLR	TCG	3	15	TTTTCGTCATCTTCATCATCTTCG	62.602	AAATCTAAAGATATCGCTGCCCT	63.519	116
HM_6272	GD20F4R01BOGS3	CTT	3	12	GGCCCTTGCTTCTCTATAATATCTC	62.905	GTCCATGTCCAAAGTTGAAACCAT	63.331	101
HM_6273	GD20F4R01A1C6V	ATC	3	12	CTAGCCGACGAATCATGAGGAGA	63.121	CTCTCTAATCATTGACTGGACCAT	62.571	142
HM_6274	GD20F4R01EV9K2	AAT	3	12	CGTGGAGACACTTTGGAGAAAAAT	62.809	GGCTCTCTAATTTGGTTGAGAGGCT	63.41	113
HM_6275	GD20F4R01A8242	AGT	3	18	ACTACTGATAAGCTGAACCTGAAGTAGCA	60.398	ATGGCGTCTCATAGTCTCTTCT	60.511	157
HM_6276	GD20F4R02IV3LW	GGT	3	12	TTTAGGTTGGGTTTGGTGGTATTG	63.011	TCTAGGAGCAAGAGAAAGTCATAGCC	62.648	88
HM_6277	GD20F4R021C4S	TCT	3	15	TCAGAACTCACCAGATGTGCTAAA	63.048	GAGAAGCAGATAGAAGCAGAGGAGG	62.411	158
HM_6278	GD20F4R01COZJ9	CTG	3	21	TCAAGTTGATGCTGTTGACGAGAA	62.04	CACCTTGACCACATCTCTCTCTTT	62.004	173
HM_6279	GD20F4R01BXV4N	TTC	3	15	AAAACCTACCTTCCCATACCCAA	62.885	ATAGCTGCTGAGATTGAGGGAGA	62.813	143
HM_6280	GD20F4R02G6XBT	TCT	3	30	TCTTCCCTCTTAATTTCTCTCCC	62.958	GGAATTAGCCCCCTACTCAGCCTA	63.004	133
HM_6281	GD20F4R01D21XZ	CTC	3	12	TTGTACTTGATGCAAAACCTGCCTC	62.772	TGTGTTCAAGAACTGAAGCGAAAG	62.955	149
HM_6282	GD20F4R02G11X8	CAT	3	15	GACTCCTCAGCTTCTCGATACCA	63.23	AATGTTACGGATGATGGATTGCTT	62.813	143
HM_6283	GD20F4R02HW50R	GTC	3	12	CTAACCACTTCGTGAAGGCCATAA	62.834	GACTTGACCACATCCAAAAGAGAAA	62.619	126
HM_6284	GD20F4R02GT4U4	TCT	3	45	CGAAGCTGCCTACACAACATCTA	62.77	ATTCACCTGAGAGGGAAATGGAAT	63.27	135
HM_6285	GD20F4R01CAZIS	AGA	3	21	ACACCAATCTTGAGATTTAGGGCA	63.121	CGCAGATCAAAAGGGTTAAGAGAA	62.919	159
HM_6286	GD20F4R01AZW2	CGA	3	12	CTCTGTGAAAAAGACTGCCTCTGC	63.89	TGGAGAAGGACTAGGTCTCCTATCG	63.282	160
HM_6287	GD20F4R02JGVX	ACA	3	12	GAGAGAACAACAAGCATTTTGTGTA	61.999	TGTTCTCGGTTTGAACCTTCAACTTT	61.521	157
HM_6288	GD20F4R01BACBX	ATG	3	12	CATCGAGGTGGCTCTTATGGATAG	63.219	CGAGCCAGTGATAAAATCCCAATA	63.316	103
HM_6289	GD20F4R02F3AXR	TTC	3	15	AAAGCTTCATTTTACTCCTTGCC	63.016	TCAAAGATGAAGAACTGGAGAAGAAGA	63.003	130
HM_6290	GD20F4R01A5CUN	TGA	3	12	TCTCGATTTCGTTTGTATTGATGA	62.959	CTTCTCGCTTCTCGTGGATAAAAA	62.927	112
HM_6291	GD20F4R01CCR6P	TGA	3	15	GTCCGATACATTTGACGATGATGA	63.15	AATTGACACGCTGCTAATTCTG	62.759	80
HM_6292	GD20F4R01B8QCH	AAG	3	12	GGTGAGATGATAAAGATGCAAA	62.632	CTTCTTCACTGGAGCCTTAGCCTT	63.505	159
HM_6293	GD20F4R01CFA7D	TGA	3	15	ATGAGGAGAATCATGTGGTGACA	62.9	ACCTTCTGCTGACGTGGAC	62.655	96
HM_6294	GD20F4R02H5B7E	GAC	3	12	GTGTTGGTACCGTAATTTCTGCGAC	62.96	ATCACCAACAACCACTCAACTGTTG	63.159	157
HM_6295	GD20F4R02F4MFT	TTG	3	15	CGCGATTTCGTTTGTGATTAT	63.134	GACTAGTCGGTGGTTGTGATGATG	62.937	135
HM_6296	GD20F4R01BYVGT	ACG	3	12	CGACTAACTACGTAGGACCGACC	62.341	TTAAGGTAAACGACGACCGACCTA	63.036	160
HM_6297	GD20F4R01AWGA7	GCC	3	12	CAGCTCTCTGTAGCGATCTTCC	62.843	AGCTATCGCGTGAAGGCGTATG	62.861	133
HM_6298	GD20F4R01C252V	GTA	3	12	GGGGGTTATAAGAGCCCTATTITT	62.697	CTTTTATTTTAAACCCATCTCATTTGT	61.838	132
HM_6299	GD20F4R01ERIOI	ACC	3	12	TTTATCCACACTGTTACCAACAGG	63.159	ATACTGTGAGGCGTAGGAGACGAG	63.15	106
HM_6300	GD20F4R02JHT9K	GCC	3	15	GATTGAAGGACGCGGATGATG	63.232	TTATCTCGTAGGGTTTTCGACAAA	62.932	160
HM_6301	GD20F4R01DL4UP	TCT	3	12	CTAGAGCAGAAAAGGGAAGAAAGG	62.791	ACGCGAAGACAAGAGACAAAGAA	63.357	147
HM_6302	GD20F4R01LY77	CAT	3	12	TCCACTTCGTTACATTCCAGTCAA	62.931	TACATCTGAGCAGGAGACAAGCTG	62.045	151
HM_6303	GD20F4R02JRQSO	TCT	3	12	TAGCCCGTGTTTCTTCATTGT	63.039	TCAAGTAGCTGAAGCTGAGATGG	63.03	112
HM_6304	GD20F4R02I0VZ	AAT	3	12	CAATCCAGACCAATTAATTTCACA	63.134	CCCTCTTTGGACATATTTAGCCTG	62.22	121
HM_6305	GD20F4R01ENN3W	GAT	3	24	GACAGAGACTGCGCATGAAGGGTAT	63.031	CCCTGTTCCCAACCACTCACTAAA	63.459	131
HM_6306	GD20F4R01APIHX	AGG	3	18	AAAGAGAATCTGGACGAGATGGTG	63	CCCTCCTCTCTTCTACGACTTGA	62.368	126
HM_6307	GD20F4R02IU4H	AGC	3	15	AGGATTCCATGATGACCATGAA	62.99	CCAGCCATTACCTTCGGTAAGAA	63.584	132
HM_6308	GD20F4R01APXU8	CCA	3	12	CCTCACTTCGGCTTTTATATCTG	62.329	GGATATAATTGTGTGACGGACCC	62.608	83
HM_6309	GD20F4R01C1700	CTT	3	30	CCAGATTTCGTAAATGCTTGCTT	62.839	CTTTGAGGAATGGAGGAAGTCAA	62.881	143
HM_6310	GD20F4R01AE2E4	GTG	3	12	ATGGAATGATGACGACATGATG	63.032	GGGTTTGAGTATGAACCAAGTGA	62.522	152
HM_6311	GD20F4R02J38A7	TCG	3	12	TTGTAGAGTGCTAGTTTCGGCTCC	63.154	TTACGATCAGGATCCGAAGAACT	63.231	107
HM_6312	GD20F4R01EFMNV	CAT	3	12	GCAACAATGTGGATGAACAACTG	63.761	TCTATGACGGTAGCTCATTGTGGA	63.051	122
HM_6313	GD20F4R01DZTWH	TTC	3	12	TCCCTTCTCTTCTCTGAGTTCT	62.958	GATCAATTTGGTTCCGCGTTTT	63.227	143
HM_6314	GD20F4R02G955M	TAA	3	12	TGACTAACTGTATTCCTCCCTTT	62.186	GATATCTCTGTAGCAGCTTGAGGG	62.634	146
HM_6315	GD20F4R02JTNBU	CAT	3	18	ATCAAAATATTCACAATGGGTGTC	63.025	TTCTATTTGAGGCCACAGGTGATT	63.121	158
HM_6316	GD20F4R01D1SMX	GAA	3	21	CGATGTCAAGATCTAAAGTCGAC	62.635	AAGGGTTTTTACAGGACGAGGAAG	63.094	121
HM_6317	GD20F4R02HW5UY	ATT	3	12	GGGCCAGCAGTTCAATTACTCTA	62.839	TCAATAAAGTGGACGAGGGAG	62.592	155
HM_6318	GD20F4R02HS928	CTT	3	12	TGAACCTCACTCAATGGTGGAGA	63.132	AGCCTGCATACACTCTTCCATACC	62.84	136
HM_6319	GD20F4R02H3DVG	CTT	3	12	ATCCAGTGGTCTTAACTCAGC	63.918	TGCTCGAATCCAATTAGAGCTAC	62.937	160
HM_6320	GD20F4R02JOLZC	TGG	3	18	GGCCGATATGATGTTTATTTCCAA	63.02	CCACACGCTTGAAATCATAAGAA	63.517	144
HM_6321	GD20F4R02HLZ93	ATG	3	15	TTGTGATCGTTGGTTTGTACTGTT	62.872	ATCATCACCATTACCAATAACAT	63.431	96
HM_6322	GD20F4R02F7W2P	TGG	3	12	CAATCTTTTGTATGAGAGATGTGT	62.699	TTATAGGTGGGACACCTGTGACAA	62.71	160
HM_6323	GD20F4R01EP3QL	AAG	3	12	ATGGGTAAAGTACACGGATGCTA	62.947	GTGAGAAACGACGGTTGTATTGC	62.963	136
HM_6324	GD20F4R02FK0B3	GAA	3	15	TCACGTACCTTGGCAGCAATCCTA	63.061	AGATGGGGTGAGATCATGCTCT	63.315	91
HM_6325	GD20F4R02GXJDP	GGA	3	18	AGGCAGAGACATTAGATGCGAAAG	63.146	ATCTATGGCTCCCAACATCTCCT	63.391	101
HM_6326	GD20F4R01AYI5B	TCT	3	15	GGAAGAAGATGAAGAAAGGGGAAA	63.053	AAGAAGAAGACAAGAGCAGAGCGC	62.639	138
HM_6327	GD20F4R01DQTUL	CTC	3	15	CAACCTGCTTCTCCTCTTACAAC	62.411	TTTCTCTCTGAATCACAAGAGG	61.64	89
HM_6328	GD20F4R01CB2M1	CAG	3	12	CTTCAAGTTTCAGACGACGATC	62.508	TGAGTTACCTGAGTTACCGGTTGA	62.09	83
HM_6329	GD20F4R01B191I	TTC	3	15	AGTGGTACGTTATCAGACGCTTGG	62.455	TTGATGAACATACACACTCCGAA	61.638	124
HM_6330	GD20F4R02F07PA	AGC	3	12	CCAACATAGCTCACAACAACAAC	63.273	AACAGATCTCTTTGGCTGTTTT	63.4	144
HM_6331	GD20F4R02HBND0	ATG	3	15	TTGTGATCGTTGGTTTGTACTGTT	62.872	TCACCATCATCACCATCACCATA	63.266	100
HM_6332	GD20F4R01DIUCZ	CTT	3	15	GCATTTGAGCACATGAGGTTTTG	62.156	TTTTCTCCATTGAAAGGGTAAATTG	61.585	137
HM_6333	GD20F4R02HD9KI	AAG	3	12	GTGTGCAAGGTTTATCTTTGGC	63.055	CACCAAGGCTTATTGTCTACTTCC	62.37	137
HM_6334	GD20F4R01BLCHR	GGA	3	12	ATTACAGTCTTTCGCGTATCGTC	62.757	GGAACCTGGAAGCATCAGAAAGAGA	63.217	101
HM_6335	GD20F4R02H7I2G	TTG	3	12	ATTACTTCTGCCCCCATGATA	62.925	ATCCATAAAGGCATCAATCGAAA	62.819	102
HM_6336	GD20F4R02H369G	ATG	3	12	TAAAGCATGAGTGGGTGATCTGA	63.038	TGACCAATCAAACTCATTTGGG	63.113	98
HM_6337	GD20F4R02J12BS	AGG	3	12	ACCTATGTGACTCAGTGAGGAGG	63.236	TGAATCAACTTGCTTTTCTGACGA	63.179	128
HM_6338	GD20F4R02F80H4	ACG	3	12	GCCTGGGGTACCTATCAGTTGAC	63.118	AGACTTCAAATCCACCTACGTT	63.297	160
HM_6339	GD20F4R01CETOF	CGG	3	12	TCGATGAATTTGAGGATTCAAAG	63.5	CAAACCTCAAAGGCTACGACGAC	64.294	148
HM_6340	GD20F4R02H7QKQ	TCT	3	12	TTTCTCTTCTTCTTCTGTTCTCA	60.045	GAGAAGCATTCAGTGTGTAACAC	60.782	110
HM_6341	GD20F4R01EBD02	TCT	3	18	ATAAAGATCAACAATCTCGGTGG	62.508	AAGAACAATTACAATCCACCCAGC	62.523	110
HM_6342	GD20F4R01DYKAN	ATA	3	12	TTTGCGTTTTCCTCTTCAATTTA	63.022	CAAAAGTTCCAAGACAATTTGCG	63.336	132
HM_6343	GD20F4R01B12WW	ACA	3	12	GGCGGGGAGATGAAAATATAAAAC	62.904	AGGCCAAAATGTCTCAATGTTAATGG	62.451	153
HM_6344	GD20F4R02HUX3D	AGC	3	12	CAACCCAAACAAAGTGTAAAGACA	62.355	TGTACATCGTCTCTGGAAGTTGTTCT	61.442	132
HM_6345	GD20F4R02G8R8X	ATT	3	12	TGTTGTAAACACAGCAATTTCCAA	61.61	CATAGTTGTTTTAGTTGGGTTGC	61.913	160
HM_6346	GD20F4R01DHFZX	AGC	3	12	ACAAGTCTGGATAGTGGGCAAG	63.023	TAATTATCGGATCTGGGCTAAGA	62.923	117
HM_6347	GD20F4R01EF937	TTC	3	12	TGCAGGCATGATCTATACGAATC	62.646	GTGGTTTCTGAATGTTGGGTATTA	63.018	157
HM_6348	GD20F4R01D3H50	AAT	3	12	ATTATAGTAGCTCCCCCACCACAA	62.992	GGGGAGACTGACGATGTTGTATC	63.12	86
HM_6349	GD20F4R02F21BJ	GTA	3	21	AGGACGAGCAGACAAATGATGTAT	63.247	CCTACTAGCCACGTTGCTGT	63.484	128
HM_6350	GD20F4R02HKD65	TAA	3	12	CATTGTATTTCTTTGACCCCAAC	63.097	ATTTTCTGCAACTCTTGGAATTC	62.841	141
HM_6351	GD20F4R02IEOJ4	CAA	3	12	TCTGGACCATATAGGCAACATCA	62.719	CCTATCAGGACGCAAGGCTCTAAA	63.039	114
HM_6352	GD20F4R01CG2AC	CTT	3	12	GATCCACAGAGGAGTGTAAAAAA	62.91	ATTGCAAGGCAAAATGTTAAAAAG	62.945	133
HM_6353	GD20F4R01BX22I	TCT	3	12	AGTTTCTCATCTTCCAGGTGTGC	63.899	AGGTAGTTAAGAGGCCAGAAATG	62.992	152
HM_6354	GD20F4R01EPOI1	TCT	3	12	GAAAGACCAACACCTGCGAGAT	62.679	CTGGAACTGATCAGACCAATAAGCC	63.331	103
HM_6355	GD20F4R02FXU32	AGA	3	12	CCCTTTAGTGAAGAGAGGCCATTG	62.508	CACITTTGGTGGTGTTCGAGAAC	62.944	154
HM_6356	GD20F4R02GGMLO	ATC	3	15	CTGACAGATGCTTCTCTGAGCTT	63.57	GGGTTGGCTTACAACGGTAATT	63.307	143
HM_6357	GD20F4R01BW6LN	ACA	3	15	TTTGAATCTGCCCAAAATATACC	62.344	TGAATTTGAAATGTTCTTTGTGCT	62.04	111
HM_6358	GD20F4R01B3NO6	AGA	3	12	TGAAAACATCCATGAGAAAGGACC	63.52	ACTGTCTCAGGACCTCCATCTCT	64.178	135
HM_6359	GD20F4R01B3GXT	CAA	3	12	CATAAGTATCGGCCCCACTAAACC	63.103	TTCCAGGATCAGGTGTTGGATTAT	62.887	157
HM_6360	GD20F4R01D1CRH	CTT	3	12	TCTGGAACAGTACTCCCAAGATTC	62.895	AGGCTGTGGATGACTATGACTTC	63.031	159
HM_6361	GD20F4R02JNGTF	CAG	3	15	TGCTGCTGTGTATGATGACATCA	62.881	ATGTTAGGCCATCAAGAAAATGGA	62.112	129
HM_6362	GD20F4R01ALLPL	GGC	3	12	CAAACGCAATGTTCTGACCTTC	63.165	TTAAGTCTCCCTACTCTTCTCCC	62.181	148
HM_6363	GD20F4R02JQ6UF	GTT	3	12	TCCCCATAGGGTGGGAAATCTC	64.054	CACGGGCAAAAGCAAAATCTC	64.01	115
HM_6364	GD20F4R02JJDZW	CGA	3	21	CAACGACAGCATGGAAGAAAGTA	62.756	GAGATCTCCGTATCACTCCAAG	62.469	133
HM_6365	GD20F4R01DVTKB	TCT	3	21	CCAAGTAAATCCCAAGGTCAAG	63.01	ATGGATTGTTGGTGTCTGTAATGG	63.108	130

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6366	GD2OF4R01B66KC	AGC	3	12	AAAGTAAAGCAGTCCAGTCCAGG	62.118	GATATGTGGGGTTTGGTTCCATT	62.988	141
HM_6367	GD2OF4R02IEEMM	CAT	3	12	ATCATCATCTTCGACGCTTTCATT	63.241	GATTGGAGTTCATACGACGCTCTT	62.94	120
HM_6368	GD2OF4R02GJTAB	CAA	3	12	GTAGTCTGGAGACTTCGGTTCGAG	62.807	GCTCAACCTCTCCCTCTTTTATC	62.782	115
HM_6369	GD2OF4R01D1E5O	ATC	3	12	TCCTTCATTAGCTCTCTCTCTTCATTG	62.461	ATGGAAGGACTTGCCGAAGTTAAT	63.301	158
HM_6370	GD2OF4R02GNG3W	GGC	3	15	GTTAGTGTGGTTTCTTACGGGGG	62.044	CCAAGAGCAACAAGAGAGAAGAGG	63.007	157
HM_6371	GD2OF4R01C9FB0	CAT	3	12	AAGCAGCTAAACGCTGTGGTTGGTT	62.397	AATCCAGCTGAACGACAAAGCTAAC	63.06	130
HM_6372	GD2OF4R018XK2L	AAT	3	12	GCTTCTTCGTACACAGCAACTGA	62.985	TCATTGCAGGAAGACATCATCTCT	62.701	101
HM_6373	GD2OF4R01DYURN	TAA	3	12	TGAAACTGACCTTAAGTACAGGGG	62.695	ACTAAAATGTGGGGGTGGTCTCTT	63.189	125
HM_6374	GD2OF4R01D53A1	TCT	3	15	CCCTGGGAATAAACTCTCAACTCA	62.782	AGTGAGAAAAGTAGAGAGGGAGCCT	63.198	95
HM_6375	GD2OF4R02IP13X	TTC	3	12	TCAACAATTTTCGAGTTCCTGTCT	62.324	AGAAGGAAGAGCATCTTGAAGGA	61.97	136
HM_6376	GD2OF4R01EB49M	TAC	3	12	GAGGAGGGTTTCAAGCTTTTCAAT	63.09	ATACCAGAAATGGAGGGGAGAAAA	63.16	147
HM_6377	GD2OF4R01CJL9B	TGG	3	24	AACTCTCAGCTCTGTGAATGTCC	63.241	GGGTCCCAACCACTATACATCAT	63.128	129
HM_6378	GD2OF4R02INHHE	TGT	3	12	CTCTCGTCTCTTGTGTGCATCT	63.124	AAGGTGAAGTCGATCATGTGTTC	63.018	112
HM_6379	GD2OF4R01BAOCE	TTC	3	12	AATCAAGTCTATAAATGGGCCGGT	63.007	AAAATCTGGCCAGTTCAAATTTCA	63.018	137
HM_6380	GD2OF4R02IJ21L	GGT	3	12	TCAATTTGCTCCTCAAAGATTGGGT	62.996	ATCTCTCTACCCCTCTCTCACCTG	62.977	136
HM_6381	GD2OF4R02G6GHR	TAA	3	12	TCACATGATCCAGAGAGTCAGGTA	61.066	ACCCTTTTCTACCAATTTCTGACA	60.261	146
HM_6382	GD2OF4R02G9BSO	ATA	3	12	TGTGTCTGTAATCCAAATCTCAATG	62.226	GGTATTTCTCATTTTGGTCTCTCCA	62.808	153
HM_6383	GD2OF4R02H808L	CTT	3	12	AAAGGGAAGAAAGCGAGTCAAA	63.47	CGAAGGAAGAGATCGAAGACGAAG	62.907	99
HM_6384	GD2OF4R02CPPL	GAA	3	12	CTAGAAACGCTAAAGTTTGCCGCC	63.271	CCACGTTCTCGACGATTACTACCT	62.835	140
HM_6385	GD2OF4R02HWD6J	TGG	3	12	ATGGTAGCGGTAGAGATCATGGT	62.411	CTATCACCACCACTCCACTCC	62.992	151
HM_6386	GD2OF4R01AKIQI	CAT	3	12	CTTGAGAGATTTCATCGGTGATTGA	62.685	ACACAATCCTTCGGAAGCAAAATAG	62.729	131
HM_6387	GD2OF4R01AVUNM	TCG	3	12	TCGAACCTCCGATAAAGAGACCA	63.525	GACCACATCGTCCCAAGAAG	63.938	159
HM_6388	GD2OF4R02H0PVN	AAT	3	12	CGAAATGTATTTTGGTGTGAGATT	63.339	TGCTCTTCTCTTCAAGCTCTCTTT	63.137	127
HM_6389	GD2OF4R01A6Y1	TCA	3	12	CGTCGACAGTTTCTTCTCTGTTT	62.931	AGGTAACAGTGTGCGAAAACAAGT	63.174	157
HM_6390	GD2OF4R01AWQBK	CTT	3	12	AAATTGCCCTACTCTTTCATCGT	63.301	AACGACGAAGACCAAGAAACAAC	63.036	120
HM_6391	GD2OF4R02HY871	CTT	3	15	TGAGGCACCGAGTACACCATCTA	62.958	TGACTGAAAATCTCGATGGGATGA	62.921	160
HM_6392	GD2OF4R01CS3YY	ATC	3	12	CGAACATTGTTAGGGCTTGAAC	63.039	GTTTCGAGCAATGGATAACAACC	62.937	156
HM_6393	GD2OF4R01DMGBJ	GAA	3	15	CGGTGAACACTGCTGAATGACAA	62.989	TTGAGCTCTCTTCTTGGATTG	62.906	137
HM_6394	GD2OF4R02IPFLK	GAC	3	12	CACAGGCGATGTAATTTGTTGAG	62.856	AGCTGAGGAAGAGAACTTGTGTGC	62.526	139
HM_6395	GD2OF4R02JSBOG	GTG	3	12	TGAGTTTGGAAACGTAGGTGACAA	62.942	CCACTCTCTCTACTCGAGCATCA	63.173	81
HM_6396	GD2OF4R02H1BPZ	GTG	3	12	ATCCCTAAATGCTCACTCTGGTA	63.022	ACCAACACTCATCATCGGATCAC	62.274	125
HM_6397	GD2OF4R02JWW4Z	GGC	3	15	CAGGATTAGTATCCACGAGCA	63.278	CTTCATCGTCTAAGGATGGGAAGA	62.884	119
HM_6398	GD2OF4R01C7FZC	GAT	3	30	GGGGGAATTTAGGGTTAGGGTTAG	63.042	TCTGACCCCAAAAAGCACTCAAGA	63.407	124
HM_6399	GD2OF4R01CT90E	GTA	3	15	TACGGGCGAGGATAGTAATAGCG	63.535	ATCGGAAGTAGGTCAACAATGTGCT	63.255	212
HM_6400	GD2OF4R02GWYVJ	TTG	3	15	GGCATATCGTTTTCTTGGATCT	62.622	AATTGAACATTTCTTTCGGGGATT	62.983	138
HM_6401	GD2OF4R01BQZWY	ATG	3	12	CAATACCCATTCCACATCATCGG	63.512	TCTTTGTTGAAGCTCCTCATCCG	63.117	155
HM_6402	GD2OF4R01BBVW2	ATT	3	18	GATTTGCTGACTCTTCACTCACCC	63.242	AGGCAAAAATTTGACGACTTAAT	62.304	146
HM_6403	GD2OF4R01BYG07	ATA	3	12	AAATTGAGAAACATCAGAGAGGC	62.926	TCTTTGCTGCTTATGGTTGCTG	63.701	130
HM_6404	GD2OF4R01B6SCQ	TTC	3	12	CCACTTTTCAGTTGAGTATTTTCCA	60.734	ACAAAAATCATACCAACCATGATCA	61.652	137
HM_6405	GD2OF4R01CWM66	CTT	3	15	TACTGTTTCCACCAAGGATCTGA	63.026	AACAGATGGGAGGATTAATGAACA	62.897	138
HM_6406	GD2OF4R02IVGD5	AAT	3	15	TCCAAGTTATCAATGTTTCGGAATG	63.218	TAGATTTGTTGGTTGGATGGTCTCC	63.419	145
HM_6407	GD2OF4R02HMIHZ	TCG	3	15	TGGTTACCTCTTGGGATTTTGA	63.091	ATCTTCTCTCCAGAACTCACCC	63.278	156
HM_6408	GD2OF4R02JXY14	CTC	3	12	CACCTAAACCTCGAACCAATCAAG	63.113	CATTCAACGGGTATGACAAATCAAC	62.932	103
HM_6409	GD2OF4R01B30BB	TCT	3	21	TTGGAATTCGACAGCTCTGACTCT	63.661	CCGTGGATCTTACAGAGGAAGAAA	62.894	127
HM_6410	GD2OF4R01EJEO6	TTG	3	12	TCCGATCTTTTCACTTGGCTTTTCT	62.897	CCCAACAACAACCACTCTACAAC	62.621	90
HM_6411	GD2OF4R02FURGV	GGT	3	15	GATTTGTGGCAGATGGAACACTC	63.035	ACGACAATCCCTCAACCTCAG	63.691	104
HM_6412	GD2OF4R02ITX77	ATC	3	12	GCAAGGCAGATATTITTCGACATC	63.037	GGCAAGGGCATGACAAATATAAAG	62.842	101
HM_6413	GD2OF4R02HF90L	TCT	3	12	ATGATCCGCCAAACGAATATCTCT	63.127	TCACAACCTCCCACTAACCAATTT	62.907	159
HM_6414	GD2OF4R02GLE3C	TGG	3	12	ATGTGACCAACTCACCATCTCG	62.922	ACTTGTTCACAAACGATCTCG	63.612	139
HM_6415	GD2OF4R01B8NFS	GAC	3	12	TAGATTTCTTGGGCTCTTTCACCA	63.312	TCCAAATCTCAAAATCACCAGACA	62.907	146
HM_6416	GD2OF4R02ITQU5	TCA	3	12	GCCCTCATCATCGGTATCAATATC	62.8	AGGAATACAAATGACGAGCAGAA	62.922	92
HM_6417	GD2OF4R01CGZTT	CCA	3	12	GAACCCGTCATTCTCTGTATAGTG	63.022	TCAAAGTGCAAAATGTGACAAATCA	62.641	135
HM_6418	GD2OF4R02J20L3	ACC	3	12	ATTTTAGGAGTGTCCGTCATCAT	63.039	ACCAAGAGTTTCTGAATCAGTCTCG	63.124	153
HM_6419	GD2OF4R01A2NP1	GAG	3	12	GAGCGAGGGAGGATGAGAGTAGT	63.739	TTAAGAACAAAGTGAGAGGCTGG	63.006	86
HM_6420	GD2OF4R02JQK2A	TCT	3	24	AGATTTGACCTCGTCTCTCTCTT	62.876	TATAGCTGAACAGATTGGGGCAT	63.034	122
HM_6421	GD2OF4R01BQGU8	GTG	3	12	GAAAGAGGTTCCGAGGATGTG	63.203	CTCTCAAGACTCTTTACCAACCC	63.28	80
HM_6422	GD2OF4R01CHX71	TCT	3	12	GATGAGCTCCGAGACTGTTCATT	63.133	AAACTATTATACCAACCCGCGTAA	62.759	126
HM_6423	GD2OF4R02HIOIK	ACC	3	12	GGTTCATTCAATTTCTTCAATGCT	62.608	CAACACCCAGGAATCTCAATCTTC	63.009	121
HM_6424	GD2OF4R02GQDNC	AAT	3	12	GCACACTGCCCATAGATAAAAAT	62.451	CGGTAGAAGTGAACATTTGGCTGAT	62.933	158
HM_6425	GD2OF4R02JQBXC	CGA	3	12	GACTCAATCTCCACAACGCC	64.185	GAGGTTCAACCTCGAGTCTTTG	63.36	90
HM_6426	GD2OF4R02FH77R	CCA	3	18	AAATGGGGCTAGTCTCTGAGAC	63.193	TGATGGAGGAGAGTTCTAACAAGC	62.9	86
HM_6427	GD2OF4R01D83YA	TGA	3	12	GCTGTTGCTGCTACTGCTTTCTT	63.608	ATACGAGAAAGTGAAAGGGGGAAG	62.98	154
HM_6428	GD2OF4R02IKKAP	TTC	3	18	AAACAATGCAATGAGCGTAACCT	63.174	GGCTTGCTCGACATTTAGTTTCA	63.365	115
HM_6429	GD2OF4R02HCBUM	TTC	3	12	TGGCACAAGATTGGGATATTTCT	63.152	TTTGAATTTCTGCTACAGGATGAGC	62.949	155
HM_6430	GD2OF4R02GGR1I	CAT	3	18	GAGCTCTTGTGATGTTTGTGCTC	62.949	AAGGAAGGAATTAATTGAAGAGGAAT	61.981	160
HM_6431	GD2OF4R02GYB8U	CAT	3	12	AATAATGTGTAGTGGTCAGCCGGT	62.949	GAGAGGACCATCACAATTTCTTGT	63.204	141
HM_6432	GD2OF4R01DUBZ1	AGA	3	15	ATTTCTGAATGCACTGGGCTTTT	64.197	GCAAACTTCTAGGTAGAATCGGAA	63.676	160
HM_6433	GD2OF4R02JGD8	AGA	3	12	GTACTATGCTCTGTTGGGCGACT	62.962	CTCCTCTTTTCTTCTCTTTTCTG	62.36	154
HM_6434	GD2OF4R02HLB1T	TTC	3	12	ATATAAAACCGCACCATGCGAATA	63.342	GGAGGAGAAGGAGAACGCGCA	64.032	129
HM_6435	GD2OF4R02H6PRL	TCT	3	15	AGTGTTCTAAATCAGACCAACGAGT	62.559	AACATTGATAATGAGGCCATGGAG	63.322	142
HM_6436	GD2OF4R01D0YIX	CCT	3	15	TAGCAAAAGGACGCTCATCACTA	63.582	TGAAATAGGGGTGACTATCCGAGA	62.983	88
HM_6437	GD2OF4R01D3HJX	GGT	3	12	TGAACAGGGTTGAGAAAAGAGTGA	62.367	GAAAAAGTTTGAATTTGAGGCAA	62.626	135
HM_6438	GD2OF4R02GYX52	AAT	3	15	ATCTTCCCGGATTTTCTAAGCAAC	62.903	GGGTTATCGCAATCTCTCTCTT	63.093	144
HM_6439	GD2OF4R01CTZSU	TTG	3	12	TTAAGGTGTTGCTCTCACACCTC	63.345	TCTAAAGTCAAAATGGCAGTGGAAA	63.132	148
HM_6440	GD2OF4R01E1D1V	CAC	3	15	TGAATGCACAAAGTCTCAAATTC	62.514	TACTTAGAAGGAGAGGCGGTGTG	63.028	108
HM_6441	GD2OF4R02G962K	TAG	3	12	TGAGATGATGCTCATGAAGTGT	61.044	TTTCACTTACAGCTACACACAATG	60.782	111
HM_6442	GD2OF4R01A00ZV	TGA	3	15	GTGTAGAAGGAGAGAAAAGGGGAG	62.86	GTAGAGGCAATGAAAAGAGGAGAT	62.986	160
HM_6443	GD2OF4R01DAJUI	TCA	3	12	GCTTCTCAGGTCTCAGATTTCCAC	63.709	AAACATCGTCAAGGTCCGTTTCTA	63.129	131
HM_6444	GD2OF4R01EJBVA	TTA	3	15	TTTGTGTTGCAATGCTTATTTCTG	61.372	TGCAAAAGAAAGATGGAATTTAAAG	61.045	152
HM_6445	GD2OF4R01CX0NO	TTC	3	12	TGAAGAGTTGAAGTCTGTTACATTTGTT	60.795	TTAGTAATCCCTGGTCCATCAACA	61.759	104
HM_6446	GD2OF4R02HNN3	CTA	3	12	GAGAGGTTGAGGATGAGGAGGAG	62.844	CAGCGTCACCTACACAACCAATA	63.285	158
HM_6447	GD2OF4R01A7H9L	AGC	3	12	GTGATTCGATTCAGATGATGATG	62.795	ATTTCTTCTCTGCTGCTTGATG	63.133	150
HM_6448	GD2OF4R02GNA0W	GGT	3	15	GTTGTTGAAGAGAGCAGCAGGAG	62.828	CAAAAATGGAAGCAAAAGTAAGCG	63.146	94
HM_6449	GD2OF4R01ERXK6	CCA	3	12	AGGGAGAAAAATTTGATGTTGGAT	63.069	GTCCGACTCTGGTCAAGTCTTCAT	63.123	122
HM_6450	GD2OF4R02JAXOD	AAG	3	21	GAGAAGCAACAGGAAGGTGAAGAG	62.793	ACGGTAGAACCTGATACCAACGACA	63.133	145
HM_6451	GD2OF4R01C3UPL	TTC	3	12	CGATTTTCTTTTGAATCTTTTGGC	63.134	ATCATCATCACCAGCAATTACAGC	63.172	146
HM_6452	GD2OF4R02GASPP	TCT	3	15	AAGCCTCAACAATGCATATCAACT	63.15	CCAGAAAGAGAAAGGAAGGAGAA	62.49	115
HM_6453	GD2OF4R01EAJCG	CCA	3	12	TCCTCACTCTCTCCGTTGTCTCT	63.001	ATCTGATTTCTGACAGTGTGGTG	62.584	127
HM_6454	GD2OF4R01CI0DJ	GCC	3	12	GCTCTTGAACCTGTGAACACGACA	62.972	GATTGGGTGCTGAATGGTTGTC	62.665	148
HM_6455	GD2OF4R01DGXF1	CCA	3	15	CATTCTATGACAGGCGATTGG	62.919	AGAAATGGAGACTAAGAACAAAGTGG	62.237	151
HM_6456	GD2OF4R01A3G22	CTC	3	12	TACAACGCGATCTGCTGATCAGC	62.989	CTTCTTTTCTACCAAGCAGGGACA	63.015	151
HM_6457	GD2OF4R01AKDA3	TTT	3	12	TCTTCAGGAATTTGGTTTCTTCA	63.19	CCCATTAGCAGCTCTTACAGTGT	62.536	99
HM_6458	GD2OF4R02JGGRF	CTG	3	15	GTGGTAATGGCAATGGAATGGTT	62.937	GTGCAGCTCTCAACAACAAGCTCT	62.989	91
HM_6459	GD2OF4R01BU3VV	CAC	3	12	GAAATCCAACATGGTATCAGAGCC	63.016	GTGTGGTGGTATAGATGATGTGG	62.488	102
HM_6460	GD2OF4R01B8SEX	GAG	3	18	CTGAGAAAGCTGTTGAGTATCCA	62.088	AATCATCTCATAGCCTTTTCTCT	62.787	155

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6461	GD20F4R01ALO1D	TTG	3	12	AGTACTTGCCACGCTTGGTAT	63.156	CATTCTTCTCATCATATCGTCC	62.99	86
HM_6462	GD20F4R01BICIYK	CTT	3	30	CTCCAAATTTTCAATCCCC	63.677	TTCCGAAATCGTACTGGTTAACTGA	63.037	159
HM_6463	GD20F4R01ASW79	GTG	3	21	CTGGGGATAGTGGTGGTGT	63.211	TCTGAGATCTGGGCTCGCTCTAC	63.332	127
HM_6464	GD20F4R02HAS5H	TAA	3	12	ACACCACAGGTTCTGGAATATG	61.534	TGTTGTCTTCTTCTATTGGTTATTG	60.791	118
HM_6465	GD20F4R02FNJXS	GAT	3	12	GGAATCTCAATCTCTCCGCTGA	63.013	ATGTACAATCTGGTGGCTCATAA	62.833	156
HM_6466	GD20F4R01EZ89K	CGT	3	12	AATCTCTAAGCCACTTGGTTTTG	62.957	ATATATACTGGGCCCATCTCAGCA	62.928	117
HM_6467	GD20F4R01EC04R	ATG	3	21	TGTAGCTTCATTGATGATCCGGC	63.388	CCATTCTCTCTCTCAAATTTTC	63.254	158
HM_6468	GD20F4R01BCH9C	AAT	3	12	GTCTGAGGGCAGGATAGAATTG	63.308	ACACAACACGACAGGGATACGTT	62.842	138
HM_6469	GD20F4R01ETC1W	TCT	3	12	CTGGCTTGACTTTGTTTGACTCTG	62.516	TACGAAAAACCCGTAATGCAAACT	63.142	156
HM_6470	GD20F4R02HCEDT	CAA	3	15	AAGGCCTTTAAAGCTCGCTGTTA	63.355	AATCGTGTAAAGTCTGGTGTGCAA	62.972	121
HM_6471	GD20F4R02GM42S	GAT	3	15	TAGGCTTGGTGATGAAAGGGTAAA	63.014	TCATCCAGTCATCAGATTGTTGT	62.911	94
HM_6472	GD20F4R02HE40O	AGA	3	12	GAGAAGTTGGTTGGGAGGAAGATT	63.071	AGACTGAAGTTTCAAGCGCAGCG	63.053	108
HM_6473	GD20F4R01CN69B	TCT	3	12	ATTTTGTTCACAACTTCTCGGAGG	63.543	AAGCAGCAGTGTTCACGCAC	63.241	117
HM_6474	GD20F4R01BQ3W0	TCT	3	12	GTAGCTAGCCGATCGATGAGTGT	63.064	TAGTCCAGTGGTCACAAGATGGA	63.026	114
HM_6475	GD20F4R02JNOE6	AAG	3	15	GAGAAATGCAACCAAGCTCAAAATC	63.346	GATTTGGCCCATACATGAGACTTT	62.51	157
HM_6476	GD20F4R01EDDUU	AAC	3	12	ACTCAAGATGACAGTGGGAAAAA	63.212	TTGTGCCCTTCTCAGGATTATCTC	62.9	129
HM_6477	GD20F4R01D4VXD	TGG	3	12	AGACTTGGAGTGGTCTGGATGAGG	63.011	ACCACCAACATCCCTAATTCCTCT	63.181	119
HM_6478	GD20F4R01BWCMI7	GGT	3	12	GTCCTAGCTGAGCTGGGAATTTT	63.208	ATGGATGTCTGAGTATGAAGCGT	63.247	112
HM_6479	GD20F4R01A8D3M	GAT	3	15	TGGTGTTCATTCATGATGATGAGG	63.025	CATCATCTTCCACCAACAAAGAAAC	63.38	158
HM_6480	GD20F4R01CFJ24	TGA	3	18	CCAAATGCCAAGAGCAACCTTAT	62.652	TGAAGAACCCGAAAGAAAAATGTCA	63.12	103
HM_6481	GD20F4R02JGK44	CTT	3	21	TCATCTCTGCTTTGATTGCTGC	62.746	GCAATAAGAAAAAGAAAGTAGGGGA	62.397	139
HM_6482	GD20F4R01C707X	GAT	3	24	GTTAGAGCTCACCAGGGTAAAGAT	63.008	TTCTTCTTCAGCTTGTGCTTGAAC	62.221	145
HM_6483	GD20F4R01DB9XF	ACC	3	12	GGATAGGGAAGAAAGGAAAGCAAA	62.98	TGGGAGTAGGTTTGGTGAAGAGAA	63.1	149
HM_6484	GD20F4R01EGT5Q	GCT	3	18	TTAGGCGTTTACTTTCACGTGTC	61.675	CTAATTGGAGACATCTCTCTCCG	62.509	159
HM_6485	GD20F4R01EYPET	TCT	3	12	GTCTCATGGTGGTCTTTTCTATC	63.106	TATCATGATCGTTTGAGACACTGGG	63.362	98
HM_6486	GD20F4R02GDIA5	ATC	3	12	GAATTCTCTCCGCTCTCTCAAA	62.887	GGATGATGGGATTCAGAACCTTG	62.887	144
HM_6487	GD20F4R02HRWMD	AAT	3	21	TTAAAGCACAGTGTGCTGTTGGT	62.982	TGGCGGAGTACTTCTTTCTTTTTCT	63.113	141
HM_6488	GD20F4R02IE4QN	CCA	3	12	CACCACATAGCTTACCCATTTAG	63.848	GGGATTACAGTTGAGAATTGTGGG	62.897	143
HM_6489	GD20F4R02H15P6	CTT	3	12	GCTGCTTTCCGAGATTTGGAATTA	62.842	TGACGAAGAAAGATGATGGTGAAAA	63.025	87
HM_6490	GD20F4R01AGFX9	ATG	3	12	GGCAAAATTAGATTGGTTCATTGA	62.829	TTTGTCAAATGAATTCCTTTCTCTTG	61.894	115
HM_6491	GD20F4R01EFWM6	AAG	3	21	TTAACTCTCTGCTCTTGTCTAC	62.729	CCAACTTAGAGACTTCATCTCC	63.581	149
HM_6492	GD20F4R01B5SEQ	AGA	3	12	TTTCAGTTTCTCTGCTGCTGAT	63.341	CCGACGATAAAATTTCACTCTTATCC	63.37	139
HM_6493	GD20F4R01BMRNB	CCA	3	15	CTTCCGATGTCACTGTGAGCC	63.158	CGAGCTCGTTTGACATTGAATATG	62.959	150
HM_6494	GD20F4R01C279Y	CAG	3	12	TACCTCCAGGACTACGGTGCT	63.58	ACAGCATCAAACTAGTACTGCTGC	63.08	133
HM_6495	GD20F4R01APO7F	TTC	3	36	TGCTGCTTTCCAGTCTTCTATCATC	61.905	GAGAAGAAAGAACTCAAAACAGAGGTGA	61.57	113
HM_6496	GD20F4R01A675W	CAT	3	18	TTTGCTCTCTAACTTGGCAGCTT	62.862	AGGAGGGGAAGCCTTCTCTGTGTT	62.972	149
HM_6497	GD20F4R02JG65O	TTC	3	18	TCTGCTGGATCAACCAAGTATAAA	62.717	CAAGAAATGGGAGAGAAAGATCAAG	62.556	125
HM_6498	GD20F4R01CVJEW	TCC	3	12	TGCTTTCAAAGTGCTCAAGTCAG	63.07	GCAAGAAGGGAAATCCTCAAGTT	63.09	139
HM_6499	GD20F4R02III8S	CGC	3	12	GCTGTTAGTTGAGCAATTACAGAG	62.455	ACGCCACAGTGTAACTCATCATGT	62.979	125
HM_6500	GD20F4R02HALWX	CAT	3	12	CTCTCTAAGGTTCGTAGCAAAATG	63.106	GGTTTCAATGAAGAGGTGACCGC	64.062	116
HM_6501	GD20F4R02JUIAO	GGA	3	12	TTGCAAGTTGATAGGAGTCCGAGAT	62.598	TGCTCACCCTCGTATTTACTCTCA	63.061	102
HM_6502	GD20F4R01CRIHW	GAC	3	18	ACTGAATTTGATAAGGCCACTCCA	63.121	GTCTGATGATTTCTCTGCTGCTG	63.896	88
HM_6503	GD20F4R02GR8YS	GTT	3	12	GCTGCTGGAGAAGCTGTGAG	62.708	CGTTGGATCAACAACAAGTACC	62.739	117
HM_6504	GD20F4R02FM1A5	CAC	3	12	TTTCTCCATTTTCTCTCTCTCACA	62.494	CTGGAATAGATGCCCTAAGAGGT	63.09	123
HM_6505	GD20F4R02HGFMI8	AGG	3	12	TCAAATCTGAAGAGAGGGGCTTGG	63.085	TCAACATCGTCTCTACTCTACAGC	62.951	118
HM_6506	GD20F4R02IGRIF	ATC	3	12	CACCAGCAATAATTCGACCAGTTT	63.444	GCTGGAGGAAATCAATTGGAAGT	63.79	159
HM_6507	GD20F4R01B12NY	GAA	3	24	AAAACGAACAAAACTCAACACACAA	62.78	CAACCGTAATTAATATTTCGGGCCA	62.943	157
HM_6508	GD20F4R01A1JLLO	AGT	3	15	AGGCGAACAACATCATGATAAAAC	62.746	AGAATGTGTTCTGTATCGACTGCAA	62.236	136
HM_6509	GD20F4R02HYIEJ	ATG	3	12	TTGAAATGGAGTAGTGTGGTGGT	61.845	CCAAGTCTAGTCTTGATTCTATCTTG	61.113	97
HM_6510	GD20F4R01ESE3X	GAA	3	12	GGATTTCAACAATAACCAAACTTAACA	60.681	GGTGTCTGACTCTTCTTTTCTTCTTC	61.035	81
HM_6511	GD20F4R02HD25S	CTT	3	21	GACCCAAGCGAAATGAGAGAAGTA	63.022	ATGTTTCTCTCTGTTGGGAAAAA	63.006	130
HM_6512	GD20F4R02J2V2A	TTC	3	12	TGTTACATAGCAGCAATGATTTCTCTC	61.135	TGTTGTCTCATGATGCTTTACAAA	61.762	123
HM_6513	GD20F4R01C11AL	GAA	3	15	TTCTCATAGGAGATGCCTCAAAAG	63.125	AAATACTCATAAATCCCAAGCTGCTG	62.857	149
HM_6514	GD20F4R01CT4RB	AAT	3	12	CTTGAATCTTCTTCTGCTGGATCT	63.219	GTGGAAGGAAGGAAAGGAAGAAG	62.765	153
HM_6515	GD20F4R01A38OQ	AGA	3	12	TCAGTCACTACTGATCATGGTCC	62.57	TTTCTAGTAGACTCCACCGCAAC	62.933	146
HM_6516	GD20F4R02JRG1N	GGT	3	15	CTCAGGAAGGGGGATTTGTTCATT	62.657	GAGAGTAGATAATAGCAGGTGACGAACA	61.74	138
HM_6517	GD20F4R01B7PM1	TGT	3	12	TGCTGCTCGTTATCCATCTCGTA	62.959	AAGCAACCCAGCTACTACAACAACA	62.982	131
HM_6518	GD20F4R02FGS6S	TTC	3	12	TCTTCAATTTCTTTTCTTCTTCTCA	62.629	TTCAACAAGTTTGTGGCAATGTCTT	62.958	130
HM_6519	GD20F4R01EBYML	TTC	3	12	TCTGAACATTTGTTTGTCTTTCAG	62.355	TTTCTTGACATAGCACGAGTGT	63.202	140
HM_6520	GD20F4R01CSPGV	CAT	3	12	TATCATCTTCATCATGCTCATCGG	63.241	TGTTCTGAGCATGGCAGTCTATTCT	62.847	136
HM_6521	GD20F4R01CICQ5	AAT	3	12	CCACAAGGTTGTAGGAAGACTGTAAA	61.87	CCCCTAACCTACGCCAAATTAATCT	62.641	158
HM_6522	GD20F4R02HHSV4	CAT	3	18	TAAATTTGGAGCTGGTACTCCAC	62.619	AAGCCATGGATATTGATCAGTTGTT	62.037	153
HM_6523	GD20F4R02JHF9N	TCT	3	12	ATAACATCTCCGGAATATCAGCCA	62.915	AGAACAGACAAGACAAGAGCAAGG	62.311	125
HM_6524	GD20F4R01B1IXO	AAG	3	12	CCTCGGTAGAACGCGATGTGAAGA	63.129	AGTCGCACAACAGCTATTGAATG	62.671	159
HM_6525	GD20F4R01ASDEZ	TCT	3	12	AGTTTTGGCAATGCTCTGCTTTCT	63.048	GAGTGAGTCGTCGGGTGTC	63.14	95
HM_6526	GD20F4R01D0VDQ	AAC	3	12	TTACTCTTCTTCCCTGATTGGTG	62.782	GTCTTCAATGGTGTGAATTTCCCT	62.585	128
HM_6527	GD20F4R01AHPYQ	ATC	3	12	TAAGCTGTGGGAAACGAATGATGA	62.946	TACGATGGCGGACTTATACTCGAT	63.046	160
HM_6528	GD20F4R02HCNCJ	GGT	3	12	GTCTTAGCACTTGTGTGAGAGGGG	63.564	AAGCTTTTCTCATCATCAACAGCCC	63.906	139
HM_6529	GD20F4R02HATTO	AAG	3	15	TGTTAAGGTGAAAACTGGGTTGA	62.966	TTTACATGGCAGAACACAAGAGAA	62.843	129
HM_6530	GD20F4R01A1PHR	GCA	3	12	TGAGCAGCAGCAACCAATAGAAAA	62.843	AGCTCGAAATTAGTCACTGCTCAGC	63.162	87
HM_6531	GD20F4R02HNO4R	TGG	3	12	AAAGGTTGGGCAACAATACCTGTGT	62.946	ACGGTCTCTGACTAAATACCCGAT	63.102	118
HM_6532	GD20F4R01ASRTW	TTG	3	15	CGTATGATTGGTGCAGTTGAACAG	62.945	TGTACCACAATCTCAAGCTGCCTA	63.176	152
HM_6533	GD20F4R02HPUMI	TGA	3	12	TTGTTTCTGATCATCCACCTTGG	63.034	TTACCACCAACCAATTTCAAAAAA	62.425	157
HM_6534	GD20F4R01DRP2J	TCC	3	18	GGCACATAACCAAGTTCAACATTAA	62.972	TATGCTTTCTAATTGGTGTGTCAT	62.076	155
HM_6535	GD20F4R01B8LR4	AAG	3	24	AGTGGTCTCAACAACCAATCCGAA	63.019	ACCATCATATGAAGTAAGCTCCCG	62.62	160
HM_6536	GD20F4R02F8BCE	ATA	3	12	ATCAAAATCAAAACCCCTTGAATCT	63.078	GAAGAGGATCTTCAAGGCAAGTGT	62.281	131
HM_6537	GD20F4R02HJ2YV	TCA	3	12	ACTCATCTTCAGAGCATGTAGGGC	63.146	CAACCACAACCAAGAGCAAGAAG	63.257	130
HM_6538	GD20F4R01DQF4U	GTT	3	18	CATTTCATATCCACCAAGAGAGG	62.983	ATGGATCCAACAACAATCTGGAT	63.004	150
HM_6539	GD20F4R01B0APA	TGA	3	12	GTATAAGACACGTGGTGATGGTGG	62.622	TGTAAGTAAATACGCTTAAACATGCC	63.436	80
HM_6540	GD20F4R01BV5OL	GGT	3	12	GTTGATTGGTGTGTTGGTGTGA	63.048	CCACCACCTCACCTTACTTTCAAC	63.12	108
HM_6541	GD20F4R02I7BEW	CCA	3	18	TTCAAATAACATACACCAACGCTC	62.009	TGCACTCGTTAGTTTGTCTTCTCT	62.754	123
HM_6542	GD20F4R02HU56L	GGT	3	12	AACCATCATAAATTTGTTGAGGAGGA	62.01	AGTACCAGTGCAAAATCAAGCTCC	62.949	141
HM_6543	GD20F4R01DKKAO	CAC	3	15	ATGAACCATCATGGACTGAGGAAAT	62.994	GCTCCGACGCTATAGTAGAATCA	63.058	99
HM_6544	GD20F4R02H5XZE	TTC	3	15	CTGTGATCTCAAACTTGGGCTGCTT	63.053	CAACTAACAAAGACAACAACAACACC	62.117	139
HM_6545	GD20F4R01BVUD2	AAT	3	18	ATCTTTTTTCCACGAGGTGGC	62.603	TGAAATGTCAAGAGGTGAGTGT	62.276	119
HM_6546	GD20F4R02IE1JF	AGC	3	12	CATATCATCTTCAATTTCTCCGGC	63.012	ATATCCACCCCAATTCAGTTCTT	62.974	105
HM_6547	GD20F4R01C423H	GGT	3	12	GTAATAATTACATCGCCACCTTT	63.3	ACTAGCTTACTATCACAGCCCC	63.02	152
HM_6548	GD20F4R02GKJXF	CGG	3	15	CCTTCCCCCATAGGAACATAAAT	62.397	AGACCACCACTGTTTGAAGT	63.023	83
HM_6549	GD20F4R01EDCL3	TGA	3	12	TGGAATAATAGGATTATCAGCGG	63.309	TGTTGCTGGTGTCTTCTACCAAG	62.54	148
HM_6550	GD20F4R02ILXR1	CAA	3	12	CGGAGTGTCTTCTGCTGGTAAC	63.456	AAATCCAAGAGCTGAAGCTTTT	62.82	149
HM_6551	GD20F4R02JULFJ	CAA	3	12	TAATAAACCAAGCTGGAATCACC	63.018	ATTATACGGCTGGGACTGCATTT	63.123	136
HM_6552	GD20F4R02GK9FE	ACA	3	12	GAACTTACAACACCATTAAGAGGGG	62.908	AGCCAAAATGTCTCAATGTTAATGG	62.451	101
HM_6553	GD20F4R01CORJX	TCC	3	12	GTCTTCAGGCCAATCTTCTCTC	63.599	CAATATGATCAAGGGCAAGTCTCC	63.112	115
HM_6554	GD20F4R02JHYIQ	TTC	3	12	GCATTATGATGTTATCTTATGTTAGCC	62.173	AAGTCGGGTTATACAACACCAACC	62.327	108
HM_6555	GD20F4R01DAWCI	TTG	3	15	GTCTTCCATTTGGTGGAGC	63.247	CTACACCTCAACTACCTCTCGAC	62.397	82

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6556	GD2OF4R01BWFBH	TGA	3	12	CGACAGAAATGGAAAAATGGTCTT	62.606	ATGCTCTAGTGTGCCCATATTCT	63.064	158
HM_6557	GD2OF4R01BF66R	TGA	3	30	ACCTTGGAAGAAACACATGCTCAAT	63.035	GGACAGGGGAGCTCGAATTTACAATA	63.484	154
HM_6558	GD2OF4R01AWL4X	TCC	3	12	GACCACCTCTTTTCTTGGCTTACC	63.098	TGTGTTTTCTATCATCATGCCAAC	63.159	111
HM_6559	GD2OF4R01AY4JC	GCA	3	24	ATGACACGTTTTGATCTCTCATGC	62.625	TGCTCACTCCTGCTCGTCTCTCT	62.896	145
HM_6560	GD2OF4R01B21M2	ATA	3	15	TCAGCTGCATGTTTCTCTATCCA	63.27	ATTCCATCTTGTGGTTTTGATTGG	63.206	158
HM_6561	GD2OF4R01E4Q1F	TAC	3	12	CTTTAGACATGTGGTGGCATGGC	62.962	AAAGGGGGGAATTTCTCTCATAGC	62.986	130
HM_6562	GD2OF4R02JDW0	AGA	3	15	GATTGTATAAATTTTTTGCAAGGAA	60.084	GGCTCTCAAAACACAGCTGTTACT	61.07	134
HM_6563	GD2OF4R01CG4W9	GTT	3	12	GACGTAATCTTGGACCTTCAATTTCA	62.755	GCTGTAGCTTTGGGTACATGGAA	63.552	157
HM_6564	GD2OF4R01CXHPI	GAT	3	18	CAGGATTGAGTCTGAGGATGATAA	62.899	CCTCCACCTAATGCATATCGAATC	62.915	160
HM_6565	GD2OF4R02FLG17	ATA	3	12	AGCACAAATAGGGATGACAAGGAA	63.121	TAAGCTTGATCACCATAGCCACAG	62.643	147
HM_6566	GD2OF4R01A0DZS	CAT	3	12	TCATATCTGTTGGACTTTGAAGCA	62.126	GAAGGGGAGCATTTTCGTTAATTT	62.721	156
HM_6567	GD2OF4R01DH48L	TTC	3	18	ATAGACATCCCTTCGACCAAAAAA	62.108	TTGGAAAAAGTCAATTTGTTCAATCC	62.424	113
HM_6568	GD2OF4R01AR5UI	AGG	3	12	CTATGACACCTCCGTGCAAGCTC	63.537	GGTCTTAATCTCTCCCTCCACTGT	62.974	99
HM_6569	GD2OF4R02JINUD	GAT	3	12	AAGGGATCTGTGTACGAGGCTTT	63.511	CAACTTCATCAATGTTCTCAACGG	62.931	134
HM_6570	GD2OF4R01AE1TE	AGT	3	18	AATTCTGTGGTCAAGATGGTGGT	63.014	ACGACAATTTCACTCATCTCTCTC	62.901	128
HM_6571	GD2OF4R01A3TSQ	TAG	3	15	GCATCGGGCTCTCAAGGAGT	63.134	GGTTGGACTCAAGTAGCCTTCA	62.921	155
HM_6572	GD2OF4R02GR19F	TCT	3	12	TTTATGATTCTCGGCAATCTAGC	62.737	CTCGTTAGGACGCAAGGATTAC	63.043	143
HM_6573	GD2OF4R02FK6D	TTC	3	12	AAGTCATCGACAGTGGAGCTTGT	63.137	GCCTCAAGAAAAAGAGAAAGTCA	62.299	104
HM_6574	GD2OF4R01DKNXH	AGA	3	12	GCTCGTTAGAGCATATCCTTTTGT	62.291	CTCAGCCATATTGCTTTTCTGTTTC	63.245	135
HM_6575	GD2OF4R02HIVQ3	TGT	3	12	ATTGGGTGGAGATGTTAATGGTGT	63.108	TTGCACCTTCATCATCAATGAATC	63.254	83
HM_6576	GD2OF4R01CMO7F	AGA	3	15	GGGAGAGGTTGTTCAAGTGTGTTG	63.22	TATTTTTCCACGCAATATTTTCGG	63.033	145
HM_6577	GD2OF4R02F8K92	GAT	3	12	TGAGCTAGATGATGAAGTGTAGGTCG	63.057	CAAGACTGTCACTGGTTCATCAGG	63.259	121
HM_6578	GD2OF4R01CXH81	TCA	3	12	ACTCTCGAGATGCTTCATCACCTT	62.812	AGTGAAGAGGTGGTAGCGAAGTT	61.819	109
HM_6579	GD2OF4R02J49IN	TAT	3	12	CTTCCATCTCAGACCTCATTTTTCG	63.431	AAAGAAGTTCATCCCACTTGCTG	62.921	131
HM_6580	GD2OF4R02JCD4X	GAA	3	12	CTATTCTGAAGATCTCGGGGGT	62.971	GCTGGTTGCTATCTCTTTAGTTTGG	62.474	106
HM_6581	GD2OF4R01ET19P	AGC	3	12	GGAATGGTGGAGAAACATGTTAGG	62.897	ATTTGCTCTCTCATCTCTGTTGC	63.039	116
HM_6582	GD2OF4R02HQAKA	ATT	3	12	CCAGTTTATGTTTTCAGCCGACT	62.571	GAACAACTCCATCAATATCATCAA	62.356	151
HM_6583	GD2OF4R02HBLKQ	TTA	3	12	GGCTAGCTAATTCACCAACAGGAA	62.839	AAGAAGGAAGCTCCACCACTCAAC	62.922	155
HM_6584	GD2OF4R02IQACO	TTA	3	15	CATCGACGTAACCGTAGTTCTTCC	63.142	CTCCACATATAAGATCAGCGAGCC	63.125	126
HM_6585	GD2OF4R02IOWOM	CAC	3	12	AGCCACCAACAGTTCAACCTACAT	63.15	ATGGATTATAGGGCTCGGATGTT	62.998	144
HM_6586	GD2OF4R01E2JFO	CCT	3	15	TTTTACATCGAAGGGAACATTTCG	63.327	GTCGATCAGCATCTCAATGTGAC	63.025	104
HM_6587	GD2OF4R02G2HFU	AAG	3	12	AAAATCTGACGTAAGAGGGAAGG	63.103	GGAAAGATGTTTGGCGAGTTTAGA	62.882	95
HM_6588	GD2OF4R01CY3LN	TCT	3	15	TTTCTTATCTCTCTCTGCTTTTG	61.943	TCGAATTTATAGATTAAACAGGGTTCA	61.394	144
HM_6589	GD2OF4R02J04UE	CTA	3	15	GGAAAGCCCTCTCTCTTCTTCAT	63.268	ACGACGGTGGTGGTAAAAATTATG	63.039	110
HM_6590	GD2OF4R01B8S0Z	TGT	3	18	AATTAAAGCAGCACAGTGGAATC	63.57	TCACACCTATTCTGCTACTCTGCT	62.755	140
HM_6591	GD2OF4R01CYS5D	AGG	3	18	GTTCTATCGGATGCCCAATCAGTG	63	CCAGCACCTACTACCACAATGAAA	62.426	130
HM_6592	GD2OF4R02IY84Q	GTG	3	12	TCCTCGAGGGAGGATTTATGAGAT	62.756	CCATGAACCAAGCATCTTTTCTCT	62.822	127
HM_6593	GD2OF4R02IR77A	TTC	3	12	TGAAACGAGAGGTTACCAAAAGGA	63.21	AATGAAGATATTGGCGAAGGAAG	63.672	158
HM_6594	GD2OF4R01C4W8B	AGT	3	15	AAGCTCCAAGTTATTCCAAACAAAC	62.262	CAGTTCATGTCATTTCAACACATC	63.15	105
HM_6595	GD2OF4R01D17KS	GAT	3	12	TGGAACTCATGTTGTAATAAGACA	61.894	TTGGATTATCGGCATCATTTCTTT	62.819	151
HM_6596	GD2OF4R02HWF70	AAG	3	12	AATACCACAGCAACAAACAAAGGA	62.856	TGCTTGGTGTAACCAAAATGCCTAA	62.773	87
HM_6597	GD2OF4R02J4QM2	GCG	3	12	AAGGTTTTGAGGTAAATGACGGGC	63.036	CCCTCTCCACCTCTCTACACATA	62.882	124
HM_6598	GD2OF4R01ECH21	CAG	3	12	ACATCCAGACGCAACATACAAAAA	63.019	GGTGACTTGGTCTTTATGGTTTC	63.115	117
HM_6599	GD2OF4R01D2007	CTT	3	18	GGTTGAATCTGAGAGTCTCCACT	63.027	ATATTCACTATTGGGCTTCCATTCT	63.125	158
HM_6600	GD2OF4R01BJ5S3	TCA	3	12	TGAAGTTGGTTTTCTCATTTGCTT	62.919	CTGCAACATCAACCAAGAAAAATC	62.859	121
HM_6601	GD2OF4R02HGD3V	TTA	3	12	TCTAACCTAGGCCAGCTTTCTCTCT	63.005	CAGAAGATGGCATCAGAAGGAAAT	62.9	155
HM_6602	GD2OF4R01CZ1AK	GCT	3	21	CGTTGAAACAGAGAAGATGTTGA	62.71	CAACAAAAACAGCAACAGACAGTAGC	62.33	128
HM_6603	GD2OF4R01BJ883	TCA	3	12	AAGGAAAAGCTTAAATGACAGAGGG	63.103	GTAAGTCCAGCCACCACTCTCTCT	63.003	150
HM_6604	GD2OF4R02IE5RM	CCA	3	12	AACCCCAATCAAGGAGATGAAGAT	63.27	GTAGTGGCAAGGTAGTGGTG	62.919	113
HM_6605	GD2OF4R02IS37Z	TGC	3	12	GATGACAAAGAAAACTTGTTCGCG	63.244	CATGTGACCCATGTTTGTGCTGCT	62.838	155
HM_6606	GD2OF4R02HKMWM	GTG	3	21	GTGGAGGAAGGGAAGTGTGTTCTA	62.895	AACCTCTCTACCAACACTTCTCTC	63.186	119
HM_6607	GD2OF4R01C8JHU	TTG	3	12	TTTTCCAATATCTGAACCACTCGC	63.216	GGTTCTAAAGGCGACGATGTTTGT	62.755	150
HM_6608	GD2OF4R02G2QUO	GAC	3	12	CACCTTTCAGGAGTACGGTGTGTC	63.233	GATTGAAATGTGTGATAGCAATGAGG	62.95	123
HM_6609	GD2OF4R02IXMOI	AAT	3	15	AACTAAACCAAGGCGGATGCTAA	62.836	CACGATTGCAATTCACCAATTCAT	63.159	120
HM_6610	GD2OF4R01A0MH1	TTA	3	12	TAAATCCAGGAAGCTGCTAGTCT	62.947	GATTCTCCGAGCCCTCATATC	63.296	146
HM_6611	GD2OF4R02JGBWP	CAC	3	15	CTGGGATCATGGGTGAGTTAAAG	62.993	GTTACCTAGATCAAGGGGAGCTG	63.488	160
HM_6612	GD2OF4R01BAP7	AAG	3	12	AATTATGCGGTCCCAATCTCTCT	63.007	GGAGTTGATTGCAAGTCGGATAC	63.039	122
HM_6613	GD2OF4R01C4EBJ	GTG	3	12	CAGTCAACCACTGGAAAGCACTGC	62.933	AAAAACCAACGACAGCCCACT	63.148	120
HM_6614	GD2OF4R01AUX9L	ACC	3	24	CATACCTCTCCCTCCTCATAC	62.975	CATGGATGGACAGGAACATAATGG	63.724	152
HM_6615	GD2OF4R02HJU3L	CAT	3	12	CATGTGCTTTCCACAAATTTGTTA	63.055	CGATCGATGAGAGAATACAGAGACAA	63.035	160
HM_6616	GD2OF4R02JCVAJ	TGT	3	12	TTACAGCTTCATCGATCACCACCT	62.844	TCAACCAACAGTCGATTACACGAG	62.527	136
HM_6617	GD2OF4R01COE0U	GTT	3	12	GATCCAGCTGAGAGAAGAGCAGAC	63.031	GGTTTCTCTGAATCGGCAAGATTA	62.815	146
HM_6618	GD2OF4R02HSY03	AAT	3	15	CCATAAGCTGAATCTGCTCAACCT	63.035	CTGTATATGATGCTTTCTGTGGGC	62.875	143
HM_6619	GD2OF4R01BT487	ATC	3	12	CTGTGATCCCTTATCATCTGCTG	62.859	GATGAGGACAAATGAAGGCTGAT	63.007	100
HM_6620	GD2OF4R01B5W4J	AGC	3	12	AGCCACCCATCTATTGAAACTGAA	63.121	GTGTGAAGTTGCTCTGTGATTGCT	62.979	160
HM_6621	GD2OF4R01AVOON	AGA	3	15	GGGGAAGCGACGATACATAGAATA	62.533	CTCTTTTCTCTCTCTCTCGCA	62.696	139
HM_6622	GD2OF4R01BL4FJ	ACA	3	12	GTCATGCGAGGAATACCAATTA	63.117	TTGAGTGATGTTCTCGGGAATTTT	63.088	148
HM_6623	GD2OF4R01A17QD	AAG	3	12	TCTGAGGTGGGTATGAGAAGGAC	62.884	CTCCTCAAGCCCAACATCAAAAC	63.129	151
HM_6624	GD2OF4R01DIWVB	ATG	3	12	AATTATTTTGGTGTGGTATTGCG	62.945	CTCTCACCATTCCAAGCATATTAT	63.544	151
HM_6625	GD2OF4R01CGKAP	GCC	3	12	ACCTCATCTAGTCTCCACCCTG	63.001	GCTTCTTCTGCCATTTTCTTTT	63.107	142
HM_6626	GD2OF4R02H859G	GCC	3	12	GCCTGGATTGAGAGAAGAAAGAT	63.081	CTCAATTATCGAAACCTCCACCTG	63.104	127
HM_6627	GD2OF4R01C7263	ATG	3	12	CCCCAAGATGATGATTCTGTGTT	62.481	TGATTTTGGTGGTCAATTTTGATA	63.357	101
HM_6628	GD2OF4R02JGGFR	TGT	3	18	AACTGCGGTAAAGTTTGTGGTAGC	62.779	GAACAAACGACAGCAGCAGAG	62.145	137
HM_6629	GD2OF4R02FUUB8	ATC	3	12	GCTGCTCTTTGCTAGTGGTTTA	63.064	CCAAGAACATCCAATGGAAATGAT	63.198	150
HM_6630	GD2OF4R02HJHHH	ATC	3	12	TCATCATGTGCAACATCACTTTCA	62.588	TGGTCGATATAACTATCAGGCTTT	62.198	158
HM_6631	GD2OF4R02FUOGE	TTG	3	15	TCGTATCTTTTGTAAAGATTTCCGT	60.595	TTTAACATGACGTTCCCTATTCCC	61.409	138
HM_6632	GD2OF4R01ECLVP	CCG	3	12	TGAAATTTCTCTCAAGAAAGTTGA	62.494	ACCTATGATCGATCTCCGATG	62.428	159
HM_6633	GD2OF4R02G7IBQ	TTC	3	18	CTTCTCATGGCTTCTCTCTCAT	63.278	ATGGTCTGCTCGAAGGTAGTCAAA	63.225	112
HM_6634	GD2OF4R02HBE06	ACT	3	15	ATGGATTCTGCTCTTTGCAACTCG	62.91	GAACAAACAGGCTGATGTGAAGT	62.736	147
HM_6635	GD2OF4R01DALD9	GGT	3	12	GTGGGCACTTTGACACCACTTAT	63.462	CACAATGAGTGAAATCTTGGTGC	62.948	148
HM_6636	GD2OF4R01D4PAK	GTA	3	15	ATGGGTGTTGAGGATCTAGACGA	63	ACCCGACCACTCATTACCATTA	63.696	123
HM_6637	GD2OF4R02FK60F	TTC	3	18	TTATACCACTCTCCCAAAATCT	62.875	CCCTTCAAGCACTGAAAAGACA	63.84	139
HM_6638	GD2OF4R02HV5RP	AGT	3	12	AATTTTAAAGGGTTGGAGATGGC	61.62	TGAAACAGAGAATGAGAAATCTCAA	60.835	105
HM_6639	GD2OF4R02GUFBV	GAA	3	15	CATCATCAATTTGCGCTTATTA	62.369	TTGCTCACATTAGTAAGTTTCTTCTC	61.526	91
HM_6640	GD2OF4R01DNHSY	TAC	3	15	AGAAAGGAGGACTCGACCTGTTAT	62.778	CCGAAGGACAAATACATTTGACAAG	61.895	149
HM_6641	GD2OF4R02FWF1Z	TTC	3	12	ACAAACCAAACTCATCTCCCA	63.006	TATGAACCTTTTATCCTAATGCGAG	62.44	152
HM_6642	GD2OF4R02G0UO2	TGC	3	12	CATGAAATTTGGCATCTCTTCC	64.024	CGAACCTACCTCACACTGCAAC	63.17	129
HM_6643	GD2OF4R02FMQ56	AAT	3	12	TAGTCATGCCACAGTTTGTCTGT	63.087	TGCACCTGCTAAATCGCTATGAAA	63.091	121
HM_6644	GD2OF4R02I3O49	GCG	3	12	TTTTTGTGAGGTTTGTGATTGT	62.339	TTCTCCAGAGACTTCATCTTCCA	62.336	102
HM_6645	GD2OF4R01AR3CC	TCC	3	15	TAGATAGCAAAACGACCTTTTCT	62.759	GGGAGAGAGCGAGAATACTAGAGAGA	62.032	87
HM_6646	GD2OF4R01E2G2U	GTG	3	12	TTTACCTTCAATAGCGGTGGTGT	62.944	CCACCTTCAACCTGGAAGT	62.736	102
HM_6647	GD2OF4R01B0988	GTT	3	15	ATGCGTAGCTTTACTTTTCTGCTG	62.99	AAATCCAATCAACACAGCAACAG	62.426	129
HM_6648	GD2OF4R01DNIPE	TCT	3	15	GCACCTGCTGATTTTCTCTTACT	63.171	AAACCTAGTCCCTAGATCGAACG	62.992	139
HM_6649	GD2OF4R01EJL9J	TGT	3	12	GTGGAGATCGACAATATTGGGAC	62.903	CAAACTGCTTGAACCTGAACCTCAA	62.742	83
HM_6650	GD2OF4R01CC434	CGT	3	12	CAAGACAAGGTATGTAATCATCCGC	62.949	AACCCACCACAACATAACAACATCA	62.621	142

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6651	GD20F4R01B91C4	ACC	3	12	ACGAAAGAGGAAGATTGTGACGAAG	63.124	GACGATGATTCTGGAGTTGGTTCT	62.901	154
HM_6652	GD20F4R01EP01C	CTG	3	12	ATCGATCTCTGTTCCGTTGGTAA	63.121	AATTAGAGCAACCCAGAGGAAGGT	62.698	156
HM_6653	GD20F4R01EMC2U	GAA	3	15	TCTTTCTTGAGAGCCTATTGGGTG	63.006	GGCACGACATAAGGTACAAATACCC	62.744	150
HM_6654	GD20F4R01C5Q9T	GAG	3	12	GGGAGGAGGAGGATTCCACAATATA	62.68	CCTAACGGTATGGTTGTGCCA	62.93	93
HM_6655	GD20F4R02G1H1A	GTC	3	12	TATGGTACATCCAAATCCACCTT	62.815	ACTGAATAGCAACCCGCTGCTAGA	63.468	112
HM_6656	GD20F4R02F3JUX	TTA	3	15	TTAGTACACGTGTCTGGTGTG	63.204	GACCAGCTCTCGAGGTCACTG	62.534	158
HM_6657	GD20F4R01EXNZU	ATC	3	12	ACTTGAACAAATGATCTCCCAAT	63.026	TCATCGTTAGCCCAATGTTTATCA	62.638	134
HM_6658	GD20F4R01B5CNQ	TCA	3	24	GGACCACATCTTCAATCTCGTCTT	62.901	GGGCTGAAGTGAAGCTAGGTAGA	62.327	142
HM_6659	GD20F4R01DHX0W	CCG	3	15	CGGGTGGTCTTCTGTCTCTCT	62.57	GATTTGAAGATTATCGCTGCTGT	62.953	146
HM_6660	GD20F4R02GSAH9	CTT	3	30	TTGCACTTATCATTTTCCAAAGA	62.932	CAGCTGAATTCAACCTCTCTGCA	63.04	127
HM_6661	GD20F4R02J46ZT	TCA	3	15	TCAAACAAATGGAATGGATCAGAA	62.691	TGATGATGCTAATGATGATGGTC	63.141	145
HM_6662	GD20F4R01A0JQD	ATA	3	15	CGAATGATCTCTCTCACTGTGTT	61.921	TGTCATAAGAATTAGATTGCTGATT	60.977	97
HM_6663	GD20F4R02J70K	TGC	3	12	CTGTGAATCTGGGCAAAATTAACG	62.837	GCTCAACAGCGCTCAACAAACAC	62.157	134
HM_6664	GD20F4R02HPKQ7	AGA	3	12	TGAGAGCTATGACCCGATAAATGG	63.524	GGTTGTAGTGCCCTCTCTTGA	62.921	149
HM_6665	GD20F4R01AYY3Q	CTT	3	12	ACACCCTTAACTCAATCTTGAAA	62.813	AAACCACCAAGTGACAAGGGTAA	62.918	132
HM_6666	GD20F4R02FJM7A	AGA	3	12	GAACATTTTGGAGGTGTTTTCGAC	63.022	GTGTGGTGTGTTATTATTGGGC	62.546	158
HM_6667	GD20F4R01CS7WU	TCA	3	18	ATATACCTCAGGGTCTCTGGCTC	63.088	GAGCATCGTGAAGGAGGATTATGAT	62.805	111
HM_6668	GD20F4R02B1LYVE	ACC	3	15	TGGGTGGAGTAGAAGCTAGAGTCA	62.459	AAATTGGTGAACTGTGAGATGTC	62.444	149
HM_6669	GD20F4R02J74XY	GAT	3	12	CAGAGCATTGGAAAATGAAGATGA	62.602	CATCGGAGGAGAAAAAGAGAACT	63.273	119
HM_6670	GD20F4R02FISBQ	ATG	3	12	CTCTAGATCATGCTGCACAACC	63.272	CTCTCATTTGCTAACCTCTCAC	63.217	158
HM_6671	GD20F4R01D4D49	CTC	3	15	GTTCAAGGAGACCTGCGAAGAC	62.57	ATGGTGTGTGAAGACTCAGTGGAG	62.81	159
HM_6672	GD20F4R01BYK9G	GAG	3	15	CACCAGCAGATATCATCTTTGC	62.833	AACTGATCGTGTCTAAGGTGGACG	63.778	83
HM_6673	GD20F4R02JREW0	TTG	3	15	CGATGGGAACCTAGGTGGGTA	63.2	AAGGTTTGAAGCAAGAAAGACAG	62.921	122
HM_6674	GD20F4R02F7P9A	CCA	3	12	ACTACCCCTCACTCATCTTTCCC	62.974	TAGAAGACAGATGGTGTGGTGAC	62.584	152
HM_6675	GD20F4R01E026Z	CCT	3	18	TGTACACATGATTTTCTCGCACT	62.962	TCTCTTCTCTTTCAACCTTTCACG	62.542	147
HM_6676	GD20F4R02GH708	TAT	3	15	TAGATGAGGGGATGAAGCTTTGTT	62.397	GACCTGAAAAACAGAGGTCTCACAA	63.022	135
HM_6677	GD20F4R01BD42W	AGC	3	21	TCATTGACAAGAAACCCCAAGT	63.204	AAGATGCTTCTCGAATTTCCCAAGT	63.601	160
HM_6678	GD20F4R01DA4L8	AAG	3	12	GTGTGGGCACTGTTGATCACTA	63.205	CCATGGCACTCATGAATCAAGTTA	63.257	130
HM_6679	GD20F4R01BHD8P	AAG	3	15	TGGACCACTGATGATATCTCGTG	63.362	TAAATTGGGCATTCTCTCACGTA	63.827	108
HM_6680	GD20F4R02LQ6Z	ACC	3	12	GAAGACAATAACAATTTCCCTCT	63.179	TGTCCTCAAACTTTGAACATCAGAA	62.918	104
HM_6681	GD20F4R01DOCA7	GAT	3	12	GATGTGGGAGAGTTATGAACGGC	63.137	ACACTTCATCTTCCCAAAAACCT	63.285	97
HM_6682	GD20F4R02HHGLN	GGT	3	24	TTCTTTTCTCTCGTCAAGTATG	62.691	ATAACTCCGATTGTGTGGTGAC	63.343	142
HM_6683	GD20F4R01DOPZW	GTG	3	12	TCAAACCAATAACCAAAATTTCCC	63.005	AGCTGAAGCATCAACATCATCAAG	62.847	149
HM_6684	GD20F4R01D4EVK	CAC	3	18	ACTACCTTAAACCTAACCAACAGCG	63.707	AATGCAATGAACAGTAGCGATGAA	62.975	147
HM_6685	GD20F4R01B3ZVW	GAT	3	15	ATCATCGGCTGCTGCTTTTCT	63.251	TGTTTGGGTCAAAATACCAATACC	63.018	121
HM_6686	GD20F4R01CWMPPW	TTG	3	12	TGTATATCTGGGCTGTGTATGC	63.237	TCATCAAATTCACAAACCCCAAC	63.038	108
HM_6687	GD20F4R02JIKF5	GAA	3	21	CAAGAAGACGACAAACAGACGAA	62.839	ACTAGGGTTCTTGTGAGTCCCC	62.884	126
HM_6688	GD20F4R02H4J2O	ACC	3	18	GAGCGACTACGGTGAAGGAGAG	62.692	CATTATGACGGGTGTAATGGTG	63.242	121
HM_6689	GD20F4R01E068M	TCT	3	15	TGCTTCTTTCAGGCGATAGTACC	63.035	TAGACCACCAAGTACCACTGAGG	63.758	97
HM_6690	GD20F4R02J0CZH	TTG	3	12	TAAGGTTCCGACAACCTGTGATTGA	62.931	GACTTACGAGCTGGGTGAAGAGAA	63.031	125
HM_6691	GD20F4R01B9P52	ATC	3	12	ATTGCTCTCATCGTCATCATCGTC	62.489	ACCTTGACTTTGGAGGATCTGATT	61.53	158
HM_6692	GD20F4R02IKZGT	TCA	3	12	TGCACTGATCTTCTTGTCTATGA	63.243	CAGATGAATTAAGCTGGGCTCTG	63.432	159
HM_6693	GD20F4R01ASSJT	AAG	3	12	GAAGATGAGCGAGCACTTGGTAT	63.051	TGGCTCTACTTCACTCGTCTTTC	63.022	88
HM_6694	GD20F4R01B26JA	TGA	3	15	ATCTTAGTCTTGAATCTCTGCCAC	62.94	GTTTCAGGATGGACCTCTCTCGTA	63	151
HM_6695	GD20F4R01DPB7Y	TGG	3	21	AGGCAATGTCAACGATTTGGAGT	63.048	ATGCCACCTATTATCTCCGATCT	63.192	137
HM_6696	GD20F4R02GSN3R	TAA	3	12	ACAGACCCCTCTGATCCAAATACA	62.029	ACTCGAAAAATTTGATATGCCAGA	61.128	145
HM_6697	GD20F4R02GNEWT	TCT	3	12	CCTTCAAGCTCTCTCATCTTCCAC	62.898	CTTGATTAGAGAACCAATGCAGGG	63.214	143
HM_6698	GD20F4R02J4XR3	TGT	3	12	AATCTCAGGCCAATAAGGGCTTT	63.385	AGAACACACATGCGCTAGAGGTAG	63.892	159
HM_6699	GD20F4R01B08G5	TTA	3	12	GAGGGGGAGGTGTGAGAGTTGTA	62.895	GAGACAGCATGTCTTCCCTTTCT	62.281	141
HM_6700	GD20F4R02L0TA	ATG	3	12	AAAGCAAAAGTGAATGTGATTTCA	63.041	AACTTGCTTCAAGTTGATGGTG	63.036	144
HM_6701	GD20F4R02JUFM0	CAT	3	12	TAATTGCGAGCTGCTCAAGTCTTCT	62.96	AATTGCTTCTTGTCAACGTCTTCA	61.977	141
HM_6702	GD20F4R01ET9J	TGC	3	15	CTTCGCTGTCAGAGGTCTTCT	63.475	AGAGAAATCCTTCAGAACTCCGA	62.779	87
HM_6703	GD20F4R01CD8D0	TTT	3	15	TCTTTTCTTCTTCTGCTACTGCT	62.933	CAATCAAGGAAAGGAAATGCTCA	63.614	157
HM_6704	GD20F4R02H94PL	AGA	3	12	CGATTGAAAGGAAGCAGATGAGTT	63.022	TTGGTTACTCTCTTCTGCAACCA	62.261	143
HM_6705	GD20F4R02ICWDN	AAT	3	21	GTCGATTATACCCGACAACCAGG	63.739	TTTATCCAAGAAGAATCCAGAGC	63	113
HM_6706	GD20F4R01CBO1N	GGT	3	12	ACCTTGGATGAGAATTTGGGAAAT	63.069	TGGTCCATACTTCAAATCAACACTC	62.737	112
HM_6707	GD20F4R01B3WCF	GTT	3	12	TGGGCATTTGAACCTGATTATTT	62.722	CAATCAACAACAAGATCGTCAACA	62.181	129
HM_6708	GD20F4R02GOTKJ	GGT	3	12	AATTTCAACCTCAAACTCTCTCT	63.071	TGAAAAAGGAGCAGAGAAGAATG	62.881	119
HM_6709	GD20F4R01E0ZLX	GAC	3	12	CTTTCAGCATCTTTGAGAGGCTAT	62.312	CCCTCATTTATGATGATTTCGA	61.32	125
HM_6710	GD20F4R02H90RB	GTC	3	24	GAGGACATGGGTTTGAATTTGAAG	62.996	CCGAGTCAAATCGGTAATAATCG	62.827	104
HM_6711	GD20F4R01CPY7P	CAT	3	15	CTCAAACTCTCAAAGGCCATCTT	62.91	AAGTACATGTCACACGAGGAGGT	63.48	159
HM_6712	GD20F4R02HNYLP	GTT	3	36	TTTGACACGACAAATCTAGGACA	62.931	AAGGAATCTGTTGTGGCTATGGAG	62.811	144
HM_6713	GD20F4R01EU2SA	AGG	3	30	TAGGGTTTCTGGTCAGAGAAAAGT	63.482	GCTGCAGAGTAGTGTGAGGCTCG	62.639	160
HM_6714	GD20F4R01BEBUO	TGA	3	12	TCATAGCTGAAGTGGATGAATGGA	63.028	CATAAAGTAAAGTTTGGAGGCA	63.238	114
HM_6715	GD20F4R01A9WZF	TGT	3	15	GCAAGATTGTACGAAAATCGTGAAC	63.069	AATTAACCAATATGCACGACACCC	63.046	119
HM_6716	GD20F4R01C2GAW	TCA	3	15	TTTATTTGGCTCAGCATCTTCTTC	62.925	TGGTTTCGCCACATATCTTCTAT	62.925	153
HM_6717	GD20F4R01D898G	TTG	3	15	GAGTATTGGGAAGCATAGTGGTG	63.022	CTCCAATTAACCTGCCAATTCAC	63.03	146
HM_6718	GD20F4R02JXY14	GTT	3	12	ATCTTTAGCAGCATCAGCAGCAG	63.08	CAACAACAACGAATACAGGGACAA	63.159	83
HM_6719	GD20F4R02F4T5O	GGC	3	12	GGCGAAGAAGGGTTTCTCTAATA	62.992	GGAAAAACAACGAAAGCAGAAGAA	62.932	150
HM_6720	GD20F4R01C4GKG	GAG	3	15	AATTACCTATGCTTTCGCAAGCA	63.062	GATCACAACTATCTGTTTCCCCC	62.068	130
HM_6721	GD20F4R02GH3PM	CTC	3	12	AAATGAGTCTCTCTTGCCTCTCT	62.986	TGATGGAGAAACAGAAAAGCTTCC	63.009	104
HM_6722	GD20F4R01D4ELZ	CCA	3	12	TGTTCAACCTAACCTCAGCTCAA	63.222	ATCTGGTTTGGTGAGATGGTGATT	63.004	122
HM_6723	GD20F4R02HCB0M	TGA	3	12	TCTCGCATCTATCGCATGATTAA	62.962	GAGGAGGATTTCAGCTTCACTTA	63.125	97
HM_6724	GD20F4R02G5OZM	CCA	3	12	GCGATCACTCTTTTGGTTGTCT	62.936	CAAAAGTCTGTTGAGCACTCTCAG	62.718	160
HM_6725	GD20F4R02F188O	CTT	3	12	AAATCCATAGGCTCAATCTGTGAC	63.023	ACAGAGGACTGAGAATGGAACCTG	63.241	142
HM_6726	GD20F4R01B3WCF	TTG	3	18	TGGGCATTTGAACCTTGATTATTT	62.722	CAATCAACAACAAGATCGTCAACA	62.181	129
HM_6727	GD20F4R01BCH90	GCT	3	12	TAAAGACGTGTTGGTACTCCGTT	63.041	CTTCTGGTTTCAACGGCATCAGT	62.933	134
HM_6728	GD20F4R01CZP0C	TGG	3	12	TGTTTAATGATGAGGTTGGTGATG	63.025	TCATTTATGATCCCCAACCAAGT	63.198	102
HM_6729	GD20F4R01DKD2A	TCT	3	24	AAGAGCTGTGGTTGATGAGTGG	63.033	GTTTCGTGTCAGACATGGATTACG	63.044	104
HM_6730	GD20F4R01AIWII	AAG	3	12	ATACCGTCTCTTGGTGGCTACCT	62.228	TCACCATCATCTTCACTTTGTTCT	62.473	157
HM_6731	GD20F4R02JIT3F	CTT	3	21	TGGAAGTGGTAACTATGAGTGT	63.129	ATGGGTGGTTGTACGAAAGAAGAA	63.019	149
HM_6732	GD20F4R01EF8V1	GAT	3	15	AAAGAAGGAATCAATGGAAGGTG	60.68	TTCTCTATCTTCATCACCATCTTCT	60.041	123
HM_6733	GD20F4R01B9VDZ	ACC	3	12	ACAGAGATGCACAATGATTGCTTT	62.219	TGTGCAAACTTGGTAGTGAGTACA	62.98	144
HM_6734	GD20F4R01ADH11	CAT	3	15	AGGAGTGATGCTCTTGGGATTTCT	63.017	AGAGGTCTCGGGGATCAATTAAT	63.283	130
HM_6735	GD20F4R01CRLU3	TAC	3	15	ACATGGGACATAGGCTAAAAATAGCAC	62.68	GTCACATGATTTTTGGGAGCTTA	63.426	125
HM_6736	GD20F4R02G01L5	GGT	3	12	CGTAGGCTTGGAAACAGTCTCTTA	63.028	TGGTGGCTCCACTACCTCCA	63.992	114
HM_6737	GD20F4R01DF238	GAG	3	21	GATTGAGGTTCTAAGCTGCTCCAA	63.133	TCATCTTCACTCTTGGATTAAAGCA	62.485	149
HM_6738	GD20F4R02JGWY	AGA	3	15	TTTTTACCATTGAAGGAGGGAAG	63.168	ACCTGTTACTTGGCTAGGAGTTTC	62.911	152
HM_6739	GD20F4R01ESOUQ	CTA	3	15	TGGGCTCGGAATGTTCTTCTTCTA	63.216	TGACAAATACCGAGATCGATACCA	62.719	126
HM_6740	GD20F4R02G6WGP	TAC	3	12	GAGAAATTTCCGGTTTGGTGAGT	62.685	CAATTCGGTGGAAGAAGAGACAT	62.798	87
HM_6741	GD20F4R01B8TY2	TGA	3	12	GATGATGGTGTGATGGTGTGATG	63.037	AAGTGCAATTAAGGATCTGCTCG	62.839	120
HM_6742	GD20F4R01DYSTJ	CAT	3	12	CTTCTTCTCAATTGTCATCACCAC	62.136	AAGATGACCAAGGTGAAGTTCAGG	62.895	123
HM_6743	GD20F4R01C2UXC	GAA	3	15	TGGAAGAATGAAGAAGAAAGGGA	62.467	GCTTCTCATCTCTGCTACTACGCC	62.966	144
HM_6744	GD20F4R01EP92T	GAT	3	12	TGTTCTTATAGTGATGAGGTGGCG	62.528	GTCCCATATTGAAACCAACCAAGG	62.703	153
HM_6745	GD20F4R01DV52Q	GCG	3	12	GCACGAGCCCAATCGTAGTG	64.013	GGGTGAGGGTTTCCATCGTATC	63.847	117

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6746	GD2OF4R01D5B31	TGG	3	15	TAGGAGCAGGACATGCACAATAAA	62.959	TCCTATGTTACCATGTGATGCGAC	63.172	146
HM_6747	GD2OF4R01D54Q6	GAT	3	12	GAGCTTCCAAATGTGCGATGAAGAT	62.916	ACTTGTCCGCTCGTCCCATC	63.586	89
HM_6748	GD2OF4R01BQ38Z	AGA	3	12	AACATCAGCCAAATGAGGGAGCAG	63.035	CTGGGTTTCCGTTTTATTGTTA	62.252	105
HM_6749	GD2OF4R02FX11H	CCA	3	12	TCTCAGTCACTTGGAAAGAGTGAT	62.599	AGATAGGGGTAAAATGGGAATGGA	62.866	113
HM_6750	GD2OF4R01BE1EA	TTA	3	15	AATTGTTCTTTTCTCCCCCTTTT	62.521	TGACTGAGTTTGACGGAGAGAAAT	63.438	131
HM_6751	GD2OF4R02H4LNS	TTT	3	12	TCTAAAAATCGTAGGCTTAGGCG	62.198	CGAAATTTTGATCCTTGATTGGAG	62.993	189
HM_6752	GD2OF4R01E2JFO	CTC	3	12	CGAGGTATTTTCAGGTTCTCTTCC	62.411	TTAGATTGTGAACGGGATCGATT	62.912	101
HM_6753	GD2OF4R02JG6LR	AAG	3	12	ACAAAGAGTTTCACAATCAAAATCAAA	61.352	ATAATGTTAGGTTTTGCGGATTGG	62.264	111
HM_6754	GD2OF4R01DVZ2Z	AAG	3	12	TCCCATACTACAATCAAAATGGG	62.993	CTTCTCTCTCTCTCCCGGTGAT	63.483	148
HM_6755	GD2OF4R02IDB49	GGT	3	12	CCCTAAACTCTCGTACACGACAT	62.723	CGGTGACATTCAAAATCCACTAA	62.212	160
HM_6756	GD2OF4R01EMUW1	TCT	3	12	TACTTTTGTGCTGATCACCCTGTA	63.081	GACTGAGATCACAACCTTTGGTGG	62.35	96
HM_6757	GD2OF4R01ED7BU	CTT	3	12	TGCTGTCAATCTTCTCTCCCTGTG	63.133	TTAAAGAAAGCAGGGCAACAGACTT	62.645	95
HM_6758	GD2OF4R02G28GC	CGC	3	12	CAACCAATTCCTCGTCTCCG	62.874	GAAGGATTAGATCCGAGGTTC	63.358	136
HM_6759	GD2OF4R02J5J34	TAT	3	12	GCTCGAAGTCAAGCAATGTTAAT	62.854	GTTTGAACTTGAGCTTTTGGGCTT	63.057	93
HM_6760	GD2OF4R02GYOMN	TGA	3	12	ATGATTTTGGTTGTTTACCTTGGC	62.342	GATGAAATGATACCTCGGTGGTC	62.903	128
HM_6761	GD2OF4R01EFDYY	AGG	3	36	CCTTACCTCGAGGACACGAC	64.174	TCTTCTCGACGAGTAAATGCCA	63.531	144
HM_6762	GD2OF4R02IYVJH	CCA	3	12	CACCTCCGGTAAGGAACTAGGTTT	62.896	GGGTATTTCGAAGCTAGGATTTCG	63.305	150
HM_6763	GD2OF4R02FTWAO	ATC	3	12	ATAAACTTGACTTCGACATCCCA	63.009	CCAACCTTCGAAGCTGAATTGAAG	63.319	112
HM_6764	GD2OF4R02I05RS	GGT	3	12	AATTGCTTATGGGGGATTGGTGA	63.278	TTCTTCTATGCTGCTGATTGATT	63.009	130
HM_6765	GD2OF4R01AEC3M	CGC	3	12	CAGCCAGTTGCAAGAAGGATAAC	63.354	CACAGCCACTGAAACGCTCAC	64.038	141
HM_6766	GD2OF4R01B6G6Z	TGG	3	12	GTGCGGTTGTCTCTCAGATGG	63.158	CTCTGAAGAAGACGCTCATTCAAC	63.774	154
HM_6767	GD2OF4R01ECR6F	CAC	3	12	GGAAAAGGAAAGGAAACACTGAGA	62.072	AGAATGGGGATGGAATAGGACATA	61.864	115
HM_6768	GD2OF4R02IMZV1	TTT	3	21	TGCTGTAAAATCTCCCTCATTTTC	62.716	AAAAAGAGCGCTTTAGGCC	61.739	146
HM_6769	GD2OF4R02JN1OQ	CAA	3	12	CCTCAAAAGACTCACCTCAAAAG	62.582	TGAGCAACAACCTCAACAATAAATG	62.355	142
HM_6770	GD2OF4R01CBBJ2	AGC	3	12	GGAAAACAGGTAATTTGTGGAGCA	63.432	GAAATCCAATTTGTGGGGAACAC	63.661	151
HM_6771	GD2OF4R01A529Q	AAG	3	12	ATGAGATGATCGCAACCAATAAAG	63.432	GTTGCAGATGATTGTTGATTGAG	62.938	157
HM_6772	GD2OF4R01EYVGG9	TCT	3	15	CAGAATTTTACTGGCCCATGAAG	63.014	ATATCAATGCTCGGATGATGAACA	62.723	89
HM_6773	GD2OF4R01CLM7E	TCC	3	15	TCACTGAGCAGCAGCAGTAGTAG	63.311	GACGACCAGATCAGAAAGACCTTAA	63	113
HM_6774	GD2OF4R01AHDG1	GTG	3	18	AAACATATCTCAGCAGGAGGATTGA	62.298	GGCATTTACGTCAAAGTGGGAATC	63.146	100
HM_6775	GD2OF4R02H875F	ACC	3	12	CACCTTGAGCACTTTGACGACCT	62.867	ACCTGGACACTTTGCCAGAGAT	63.446	91
HM_6776	GD2OF4R02JZYNH	AGG	3	21	GATGATGAGAGCAATGAAGTCGTG	63.275	CTTCTCTGCTGCTGTTTGGTAT	63.881	159
HM_6777	GD2OF4R01CNBSZ	TTT	3	12	AGAAAGGGGGAAGAAGACGAAGA	62.98	TCGTGAAGAAGAAGTCGAAGATCG	62.425	118
HM_6778	GD2OF4R01B9F13	TAA	3	12	TTGCAATTTGGTTGTGTGGTTAT	63.391	TCAGGATGCTTAGAGCTTCGTTTT	62.742	133
HM_6779	GD2OF4R01AONHW	AAG	3	21	TGCTTAATTTTGGCTCATCTTGT	63.138	TGGCAAAAACGCTATAGAGCTAGAA	62.604	160
HM_6780	GD2OF4R02JXU17	GTG	3	12	GTCAAGAGACTTGAAATGAGGACCC	62.798	CAACTCCACTCTCTCTCTCTCTC	62.882	145
HM_6781	GD2OF4R02H96ML	CCA	3	12	TGCGCAAGTGACCAAACTCAC	63.528	GTTCAACATGTGGTAGGACTGGGC	63.15	126
HM_6782	GD2OF4R01COK5C	TTG	3	12	GTTCGAAGGCTTGGGCTGAT	63.81	GAGTCAACGTGGTGGTTCC	62.893	128
HM_6783	GD2OF4R02GZHTZ	CAA	3	15	TCTTCTTGAAGCATGCCACATT	63.341	GGTTGCTCTCTCTCTCTGAGT	62.411	115
HM_6784	GD2OF4R01CCWYI	TTT	3	12	ACAGAGACAATCGACACAACAAA	63.053	GGGGAAGAAAAGAGACAACAAGG	63.47	142
HM_6785	GD2OF4R01D33VL	AAT	3	15	CAAAAGAAATTAACGAAATCAATTTCA	61.76	TTCTAAAAATATCGAATGTAGGCATT	61.256	102
HM_6786	GD2OF4R02I1K74	TTT	3	12	CGCGTCTCTCTCTGGTAGTTATC	61.782	TGAACCAAGATTCAAATCTCGAC	61.652	146
HM_6787	GD2OF4R01A4J09	ATA	3	12	TGGAACCAACATTTTAAGTGCATA	62.637	CCAACAACACTTCTACCTGCTCTA	62.426	135
HM_6788	GD2OF4R02GCKJM	CAC	3	12	TGCAAAATTTGGATAAACCACTTCC	63.221	GTTTTCTTGGAGGAATTTGGTGG	63.962	160
HM_6789	GD2OF4R02I6SUT	GTT	3	12	AACAAAAGACGACCAACCACTAAG	62.721	TTGGAATACCATCTCCATGAGT	62.887	118
HM_6790	GD2OF4R02HEK05	GAT	3	12	ATTAGGCCAAATGTAGGAGAAGAA	63.13	TGGTCTTAGAGGCAAAAAGAAAGAA	62.605	160
HM_6791	GD2OF4R02H90KT	GCC	3	12	ATCGGGTACTTGGGTTAGTAGGA	63.086	ACTCAGCAGCAGAAAGAGGAATA	63.328	129
HM_6792	GD2OF4R02JQBSV	AGA	3	21	GATCACACACATCAGAAGAATCG	63.033	CTCCTCTGCTGCTGCTGCTATT	62.933	138
HM_6793	GD2OF4R01AUND7	TTT	3	12	AAATCAAAATCCAAATGCTCTCGG	63.317	AGAAGAAGCAGAAGCAGAAGCAG	62.848	99
HM_6794	GD2OF4R01CGAZS	CAT	3	18	TCTTCTTCTCTCACTTTGTATCC	62.987	CGCGAGTAGTACCACAGATTGTA	62.883	132
HM_6795	GD2OF4R01AMDHN	AGC	3	12	TTTGCTCTGTACAAAATCACCAGC	63.386	CGCAAGAAAAGCAGAAGTCGTAAT	63.064	154
HM_6796	GD2OF4R02IQ09U	GGT	3	12	CTCATGGTTGTGGCTGATCTTGT	63.168	ATATCTCTGATCTAGGGGGCTTC	62.989	105
HM_6797	GD2OF4R02HNSN4	ATG	3	12	TGGATGATAATGAGTTGATGTGGG	63.015	ATCAACCCCAAGAGTGATCAATA	62.912	85
HM_6798	GD2OF4R01APU4W	TAA	3	12	CAATGGTCCCTAGAAATCTCTCG	62.912	AAATCCCAAGAGCTTCTCATGTT	63.499	135
HM_6799	GD2OF4R02I2J2	CAT	3	15	AGTAGTTGAGTTCAAAGCGGCAC	62.884	ATTCTCTCAACATATGAGGCGACG	62.917	152
HM_6800	GD2OF4R02IVREV	ATC	3	12	GATCACGTGAGATGAACACAGCTT	62.846	AATGAAGAAGATCACGCTCAACC	62.926	92
HM_6801	GD2OF4R02F1Q11	TTT	3	12	AAGCCTCTATATTGGGATTTGCT	62.905	CGGCTAGGGTTTGTGATTTCTTT	63.89	153
HM_6802	GD2OF4R02F680F	AAT	3	15	AGAATGGGCAAAAATGACTTCTC	62.813	TTGCTTCTTGTGATTTGTCTATT	62.831	154
HM_6803	GD2OF4R01A785Q	TGG	3	15	AGGTTGAGTAGGGTTCCGACAT	62.81	CCTAACCAACCTTAAACCATCAC	62.809	134
HM_6804	GD2OF4R02HNNQE	TCA	3	12	AATCTCAGTCTCTCTCTGCTCT	63.19	AGTGGATGAGATGGAGTTTACCGA	63.217	134
HM_6805	GD2OF4R01BW3CN	TAA	3	12	TTTCTCATAACCAAACTGAATGAA	62.065	TTCCAGATCTTAAACTCTTGTGG	61.122	193
HM_6806	GD2OF4R01A7RRH	CTT	3	12	CTGATCTTTCTCTCGAATCTCGC	63.655	TGAAGTTGAGGGAAAATTTGTGAAA	63.013	86
HM_6807	GD2OF4R01AKAXI	GGA	3	18	GAAGAATCGTACCCAGATTCTTCT	62.878	AGCAAGAAGGATCGAACAACAAAG	62.936	92
HM_6808	GD2OF4R02JWYJN	AAT	3	15	AACTTCACCTGTTTCTGCTGCAAG	62.135	TTCTTCTCACCTCTCTCTCTT	62.958	102
HM_6809	GD2OF4R02HATND	ACT	3	12	AACCTTTCTTTTTCGACATGCTCA	63.336	TTTCCATAAATTACAACGTGTTAGCGA	62.984	95
HM_6810	GD2OF4R01AVZTU	TCT	3	12	AGCCCCCTCTCTTATCTTTTCT	62.959	AGCTTCCATGGAGGTTTTGAATCT	63.494	112
HM_6811	GD2OF4R01BU0YZ	TAT	3	12	TGACAATCTATTAGCAAAATTTGCT	62.034	TACTGGAGTCGTTGTGATGACTC	62.707	146
HM_6812	GD2OF4R02IKMI1	GGT	3	15	GAGCCAGAAATCATCTAGCGAAAA	63.034	TCTCTCAGGAACACAGCAATATACC	63	134
HM_6813	GD2OF4R01AY451	TGA	3	15	GGATAACCAACATTTGAAAGCTGGA	63.648	ATTCTCTGTATTTGCTGCTCCCA	63.034	108
HM_6814	GD2OF4R01CGZ2O	CGG	3	15	ACCAATCTCAAACTCATCCGACAT	63.12	CGATCTCTCATCTCATCAACGA	63.019	160
HM_6815	GD2OF4R02HNLH1	GGC	3	12	AAAAACTCAGCAGTCAAAAGTAGGTCG	63.231	AGAAACCTTTCTTCCCCGC	63.826	111
HM_6816	GD2OF4R01CW4UY	TCA	3	12	GCTCGAGTTCTTCAATGACAGATA	62.965	TGGCAGAGACCTCAAGAAGAAAG	63.309	139
HM_6817	GD2OF4R02I4VL3	TTT	3	12	GGCCTCTGTCTAACCCCTCTGTA	62.999	CGCCAATTCAAGAAGAGAAAAAGA	63.014	82
HM_6818	GD2OF4R01B8CTK	TCA	3	12	GACAACATGATTGAGAGGGGCTAC	63.234	AAGATGAGATGAAACAGAGGAGC	63	128
HM_6819	GD2OF4R02HF7C9	TGG	3	12	ATTAAAGTGGGTTGGTGAAGTGG	63.233	CTCAAAACCCCGATACACATCAT	63.219	116
HM_6820	GD2OF4R02GR34N	GGT	3	24	ACTGACGATTGGGATGATGTGTTG	63.27	AGTCTTCCGCAATGATGTCATCTT	63.349	90
HM_6821	GD2OF4R02F3LCS	TAT	3	12	TGGGATTGCAATCTATATGCTTGA	63.729	TCCACTCTACCCACCATGATCTT	63.102	146
HM_6822	GD2OF4R01AVFPJ	AAT	3	15	TCAGAAGAGCCACATGAAACAAAA	63.15	ATATGTCATTTCAGCACTCACGA	62.951	86
HM_6823	GD2OF4R01B2EUH	CTG	3	12	ACAGTTGCAAGACCTTCAGGTACA	62.307	AGCAACACATTTGGTATCACTGCG	62.652	159
HM_6824	GD2OF4R01EUAPZ	TTG	3	12	AACCTTGAAGATTCACTGCTCAC	63.796	ATCGTAAGCTCTTCTCACCAACA	63.45	101
HM_6825	GD2OF4R02HTAX9	TGA	3	12	AAAGATCAGCAACAAGTTCTCTCG	63.031	GCTCTGCGATTACGTACAGGCT	62.962	156
HM_6826	GD2OF4R01B7OQB	TTT	3	15	CACGGGTTCTGAGACTTCTGTAT	62.909	AACTCTCAAGAACTTCGAAAGACCC	63.189	91
HM_6827	GD2OF4R01AMM9F	AGT	3	12	CACCTGAACCAACAAGAACCAAT	62.397	TTAATACTCAGACGACCGGATCT	63.353	159
HM_6828	GD2OF4R01AHJ6H	ATC	3	12	GGTTGTCAATGTTGGCAGTAGATCA	63.388	GATCAGATCGGTCTCGAGGACTT	63.209	155
HM_6829	GD2OF4R02F7G5S	GGT	3	12	ATTATGGAATGGAAATGCTCGAA	62.819	TGTCATAATACATCATCAACCAAA	62.273	120
HM_6830	GD2OF4R02HMU21	ATG	3	12	GGAACGATGAGGATGATGGAAA	63.321	ATCATCATCAACAAACCAACCA	63.021	118
HM_6831	GD2OF4R01DUF0N	GTA	3	12	CCCCAATCCCAAGTATAGTCTAT	63.429	CTTCCGTAATAATTTTCACTCAAA	62.453	211
HM_6832	GD2OF4R02IACDW	ACC	3	15	TGTTCTCTGATCATCAACCTTGCTA	63.87	GTGTTGATTTTGCAATGCTCTTC	63.865	159
HM_6833	GD2OF4R02F46IZ	TTT	3	12	GACGGTTCTACCTTTACTCCG	63.223	CGTTGGTTGTTTGGTAATGAGTG	62.41	153
HM_6834	GD2OF4R01D88EG	TCT	3	12	CAGCTTCAGCTTCTTAGATCCACC	62.824	CTTCGAATTTCTCTACGTTCCAA	63.006	159
HM_6835	GD2OF4R02GTNDE	CCA	3	12	ACTGGACACCGGTGGATGATAAC	63.242	GAATAGGAGGTCGTTGTTGACT	62.809	100
HM_6836	GD2OF4R02H17EE	AAT	3	12	GACCAACAGAGGCTATGTAAAGT	62.536	GAATCCCACTACAGACACTGAAAC	62.026	156
HM_6837	GD2OF4R01AWFJQ	ATT	3	15	CCCTCGATGTAGAAAAGCTGCTTC	62.215	GGCACTCACAAGAGAGCTAAGAGG	63.036	157
HM_6838	GD2OF4R01DAFPC	TTG	3	15	TTGATTTGTTTCTTCTCATCATC	62.311	TGCTACGGATACTTCAACATTTCA	62.845	158
HM_6839	GD2OF4R02FVPD2	TTT	3	12	AGGTGAGACGAAAGAGCTTACCT	63.009	GGTGAGGAGTTGGAAGATTCTCT	63.278	146
HM_6840	GD2OF4R01EQ4XG	AAT	3	15	AAACTTTCCCAATCAACCATTTCAA	62.8	TTGGTTGTCAGGTTGGAATCTAT	62.897	129

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6841	GD20F4R02HSOW1	GTT	3	18	TGAGATGACGATTCTGTTGAAAGG	62.698	ACCCCAACAAAGTCGCAGTTATAC	62.549	154
HM_6842	GD20F4R02J0C0	TGT	3	18	TGGAATTAGAGAGCCATTGAGGAG	62.996	GAGATGGAAATGGAGAAAGAGCA	63	151
HM_6843	GD20F4R01CU1IN	AAT	3	12	ACCCAATACAATGGAAATCTCCAAA	62.691	GGGTGTTGAAGTGAGGGAATAAAA	62.495	153
HM_6844	GD20F4R01ATUHW	TAG	3	15	GCAGTGGTGATGCATAAGGAGATA	62.529	GGATGTGTTGGATATTGTGATGGA	62.913	134
HM_6845	GD20F4R02ISUD5	TCA	3	24	CCTGGCACTGGTAAGACATCCATA	64.388	GCATCCCTAACGCTCTTTAACACCA	63.444	137
HM_6846	GD20F4R02FKU47	TTC	3	15	TTTTGCTTTTGTAACTGTGCTCTG	61.874	AAACACAAACGAAAGTACCCAAAAA	60.969	114
HM_6847	GD20F4R02ILNMP	AGA	3	18	CTTCCAACTGCTTTTTCGTGATCT	63.031	GGAAAGACACTTCTCGGAGATGAAA	63.102	130
HM_6848	GD20F4R02FTJX5	TAA	3	12	CATGTCCACTGAAATTTTACCACA	62.127	TCATCAATTACAAACCAACCAACA	62.397	133
HM_6849	GD20F4R02HXZ53	ATT	3	12	ACGTGGCCATTCTCAGTTTCTCAA	63.239	GGTTTCAGTTTCGGTTTTTTGTTTT	62.652	95
HM_6850	GD20F4R02I37I8	GCA	3	15	CAGTACTGAGCACTCCAAGTTGA	62.944	TGGGTAAAAATGATAATTGGGCTG	63.013	129
HM_6851	GD20F4R01DHE03	AGA	3	18	AAAGAAGAAGTAAGCAGCAGTCCA	61.976	TGCTCATCTTTGTTGCTCTTC	62.962	114
HM_6852	GD20F4R02GTIOX	TGC	3	12	AGAAAGTTGAGGGGACCAAGTTT	63.48	TTAATTTGAAGTACGCCGCACATT	62.957	150
HM_6853	GD20F4R01BEPKU	TCT	3	12	AGTTAGTCTCCAAGTCTCTACCG	63.304	TTCTAGTAGTCACTGCTTCTCTTG	62.842	82
HM_6854	GD20F4R01ARPRY	TTG	3	15	TTAGAGTTGGGTGCATCATCAGAA	63.038	CAAGAAATCCCAAAACATGCTTC	63.018	87
HM_6855	GD20F4R01DLTBE	TCT	3	24	TTTATCTCTCGCTCTTCTTCTATC	62.804	CTCCTCTCTCAACCTTCCACAA	62.993	140
HM_6856	GD20F4R01D46H8	GGC	3	15	GACAGTCTCTCGCTCCACAGT	63.269	GAGACGGAACTCTACCGGAATGT	63.918	83
HM_6857	GD20F4R01BGX05	ATG	3	12	TGATGATCAACATAATGGCGAAAA	63.462	GGGATAACTCTTGTCATTAAATGTG	62.993	136
HM_6858	GD20F4R01C3IYL	CCA	3	12	ATGATGCCACCACTCAAGTCTT	63.132	TGGGATAGAGAGAAAGCAATGGAA	63.305	120
HM_6859	GD20F4R02ISV2	CTT	3	15	CTTTTGGAGAAAAATTGGCTACG	63.13	TTGAGGAGACTATGGACCACTATC	63.644	104
HM_6860	GD20F4R01CYC3Z	CTT	3	24	CATCTGCTGTATTCGGAGATCTCT	62.913	GAGTTTAAACGACGTGAAGACGAC	63.362	109
HM_6861	GD20F4R02IBBYT	TCT	3	15	TTTTTGCCATTAGGTGTTTGC	63.146	CGCCTTCTATTCCTTGTCTTCT	63.001	92
HM_6862	GD20F4R01ARKEF	TTA	3	12	TTGCTGATGCTCTTAAAGGTAGG	63.146	TGTCATACATGCTGCTAAAGCT	62.185	128
HM_6863	GD20F4R01DZU0K	TGG	3	12	AGGCCCAAGTTGATTGTGGATT	62.884	AATGATAACTCATCAACCCACCG	63.219	126
HM_6864	GD20F4R02GQ3K0	CAA	3	12	AATATTCAACGACAGACTCGGCTC	62.94	CAAACTCGCAGAAATTTGGAGATGA	62.615	134
HM_6865	GD20F4R01A7H0A	ACC	3	12	CATTAACTACTGACTCATGAATGCTT	61.948	ATGCTATATTTCCGCAACTTCTTG	62.654	121
HM_6866	GD20F4R01CUJ0Q	AGA	3	12	GCTACGTACACACAAGTTGGTGCTT	63.717	TGCTATGGTATGTGGTATGACTG	62.866	131
HM_6867	GD20F4R01B9ERE	GCT	3	12	CCAGATCCCAAACTCTATGTCA	63.513	CGGTCAGATATTGACTAATCGCT	62.856	103
HM_6868	GD20F4R02IEP4T	GGT	3	12	GAATTTTCGTGCAACAGTTAGGTGG	63.129	AACTTTTTTCTCATAGCCGCTTC	63.119	92
HM_6869	GD20F4R01EZSJI	GCA	3	12	TCTTCAAGAAAACGGAGACGACAG	64.179	CTGAGATCGAGCATGGAATGTATCC	64.2	115
HM_6870	GD20F4R02GP3GP	CCT	3	12	ATCATTAATCCCAATGCTTCCCTT	62.986	GTGTAATCAGTTGCAAGAGGGTCC	62.949	152
HM_6871	GD20F4R01D7Y5H	GAA	3	21	TCAAGTCAATCTGTAACCAACCAAT	62.918	TTGATGTTTCTCATCTCATCATC	62.367	125
HM_6872	GD20F4R02HJUID	CGT	3	12	GAAACTCACCTGATGTGCGCAAT	62.838	AGAGAAAGAGACCCCAACCAAC	63.015	120
HM_6873	GD20F4R02HYSS5	CTT	3	12	TTGTGTCTGATGGAAGAGCACTGT	63.4	AACACGGAACTGCATCTAATGTT	63.048	130
HM_6874	GD20F4R01A8F7X	TCA	3	12	GAGTGAGGCTTCAGACCAAGAGAC	63.018	GTCACCAAAATGCACCAAAAGAG	62.958	118
HM_6875	GD20F4R01EVVJI	AGA	3	18	GGAAATCATCTCTCTGTGTAAG	63.204	AACCAACGCTCTAGGGTTTTCAAT	63.098	158
HM_6876	GD20F4R01B667V	CAG	3	12	CTCGAAGTACACACCACTGATGAC	64.095	TTTGATGACGTTTTTGTGGCCTTT	63.154	100
HM_6877	GD20F4R01BSGG5	CTT	3	15	CTCTTCCAAACAGTCTTCTGCTC	62.793	GAGTCCAAAGCAGGAACCTTA	62.767	117
HM_6878	GD20F4R01DBXLW	TCT	3	12	TTCTAATGGGTATGAGAAAAGTGTG	60.907	TAAATATCATGCCATCCCAATGAC	61.898	130
HM_6879	GD20F4R01DUBN4	AGT	3	12	AAAAATAGCCATGATGAGAAGCCA	63.13	GCATCTAGTGAATAGTGGTCCAA	63.117	127
HM_6880	GD20F4R01EQLMM	GAA	3	12	TACGATTGAGAAGACAGTGATCGGA	63.038	TCTCTGGGAATGGACTTCTCATC	62.977	130
HM_6881	GD20F4R01AE3Q8	ACA	3	12	TGAGAACACTGCAAGTCTTGAAC	62.947	AAGTTGCTCTCAGGTGGAGATG	62.999	109
HM_6882	GD20F4R02ICF9E	TGA	3	15	GACTAGGTGGTGTGTAATTTGGG	62.907	GGTTATTTTGTGTTACCAAGTAGG	62.909	117
HM_6883	GD20F4R01CJT3N	CAT	3	24	ATGTGGTAGATCTTTGGGAGGTCA	63.102	CCACCATTTTTGAGAGATGAGAGC	63.431	127
HM_6884	GD20F4R01AQN73	CCA	3	12	TGGGTTTTCAAGAAAAGGTGAGAG	62.892	TACTCACTGAGGGGGTGTATTTGT	63.111	133
HM_6885	GD20F4R02HXCJX	TCA	3	12	ATTCGAAGGATATCCGAGTCTGGAT	63.073	GGACTTGGTGATGATGTTGTTGAA	63.256	100
HM_6886	GD20F4R02HXHZD	TGA	3	12	AAGGATATGAATCCGAGATGACGA	63.103	CATTAACTACGCTGTCGACCAACC	62.753	135
HM_6887	GD20F4R01A0DY4	TCT	3	15	GCATTTTTCAGGGTTTGAACAAG	63.027	TTCAATAGAGCTAAACATGGCGTG	62.566	92
HM_6888	GD20F4R01ANFTU	CAC	3	12	CCCAATCTGAAATCCATATCCAA	63.292	TCTCTTTTGGGAATAGTGGGATGA	63.083	116
HM_6889	GD20F4R01C652Y	AAT	3	15	CGAGAACCCTTTACCAATCTT	63.682	GATGATTGAGACCTTTTCTCTCA	62.773	116
HM_6890	GD20F4R01AVCGA	TTC	3	12	CACGTGATTAGACTCTGATAGCAACA	62.086	ATTTTCCCGCAAAAATAGGACC	62.397	160
HM_6891	GD20F4R01EE4Z9	ACT	3	15	AACCTCTGGAACCTCTTCCCAACC	63.08	GGGATATCTAGGAGAAGCAGGAGG	62.769	158
HM_6892	GD20F4R01CYFZ	AAG	3	12	AAGGCAATGACAACGACCAAGAAT	63.256	GAGGCTGAATGAGCACTTACTTA	62.947	152
HM_6893	GD20F4R01BG3PA	AGT	3	12	TGAAGTTTCATTTTCAGATGTACCAAGA	63.224	CTGAGGAGCAGAAAAATCAAAA	62.906	154
HM_6894	GD20F4R02JR6NF	GCA	3	12	ATCTAATTGCTTTGCTTGTCCAAAG	61.636	CGTGACGCTTCTTAAACAACTCAT	62.569	108
HM_6895	GD20F4R02HQ05I	ATG	3	15	TGTGATCGATCCCCCTTAATCTA	62.886	AAAAAGGCAACAGATGTTAGTGG	63.45	86
HM_6896	GD20F4R02H5N00	TTC	3	15	GCTATGGTGAACCTTATCTCCCC	63.188	ACATATGAAGGGCAATGAAAGGGA	62.912	126
HM_6897	GD20F4R01AV7M0	AGA	3	15	GAAAAGGATAAGCTCCCTCTTTG	62.69	TATGTGCTGAACATGTTGATTTGG	61.991	156
HM_6898	GD20F4R01DWYAS	TCA	3	12	GCATCCCTAACTGTAACAACAGCA	62.556	CATTCAAAACGAGCTGGTAAAC	63.039	114
HM_6899	GD20F4R01D48EZ	ATC	3	12	GATCCTGGTTAAACACGGGAAAAA	62.424	GAAATTGAAGACGATGACGATGAC	62.067	151
HM_6900	GD20F4R02HPM28	CAT	3	15	TAATTTGTCCAATACGCGACAC	62.369	GCTTCTGTGATTTGGAGAAAG	62.698	111
HM_6901	GD20F4R01EKI2Z	CAG	3	15	CTTCATTGCTTCTTCACTCATC	62.9	ATTGTAGTGGTGGCCTTACTCCA	63.031	154
HM_6902	GD20F4R01EPN86	TTC	3	12	GGTGACAGACTTTTCAAGTGCTT	62.949	GGAGTTAGCGCCCAATTTTATTC	63.116	112
HM_6903	GD20F4R02HU05P	TTC	3	12	GTATTAGGCATTAGCAGACGCCAG	63.374	TGGGAGATTCTCGAATCTGAAA	63.194	96
HM_6904	GD20F4R02G0J78	ATG	3	12	TGCATTCTCTTCTTCTGTAGCCC	63.133	ACACTCTGGCAGCTTTGAGAGATT	62.949	155
HM_6905	GD20F4R02IK824	TGT	3	12	TCGAGGAATTAATTAATGTTGGTG	62.264	TCGTGATCAATCATCTCAACAACA	62.715	156
HM_6906	GD20F4R02HIRUD	GAA	3	12	CGCAACTCGAGCAGCTTATCTAA	64.06	CAGTTGCTCAGTTGCGAAGACATT	63.171	152
HM_6907	GD20F4R01DJV1R	ACA	3	12	TTGGGCGAAATTTACCAAGTCTA	61.668	CTTTTGCTTTGTTGTGTCAGATCA	62.288	157
HM_6908	GD20F4R02HBVUC	GGA	3	12	ATATCAGAAAAACAAAGCCACCA	62.922	TCTCTCTCTTCTCGGCTACTCT	63.071	153
HM_6909	GD20F4R02IR09J	TTC	3	18	TAGAAGAACCAAGCATGCACAAGCC	62.119	TCCAAAAATTAACAACCACTTAACCTG	61.496	145
HM_6910	GD20F4R01EFEA0	CTT	3	21	AATAAACGCGTGATCTTTAATGGC	62.489	CCTAATGCAACAGAAAGCATGTGTG	63.061	127
HM_6911	GD20F4R01A2EUH	ATA	3	15	GACCACATCTCAACTGCAATGAT	63.45	TTTTTGATTGTGCGGAGAAAAAG	63.515	159
HM_6912	GD20F4R02IEJ23	CAT	3	12	TTCCAGCCCACTCTACACATTTATC	62.633	ATGGTAGTGGAGAAGGTGGAAATG	62.584	129
HM_6913	GD20F4R02G53S5	CTA	3	15	TCATCAGGTTCACTATCCAAAGCA	63.038	TGGAAATAGTAGTGGCAGTGGTGA	62.945	121
HM_6914	GD20F4R01CG8TR	TCA	3	12	CTTGATGATTTTGTGTTCTTG	62.242	AAACAACCTCTAGAGAAGAGTGTGG	61.614	157
HM_6915	GD20F4R02FXOWN	GGT	3	12	TGATGAAACATGAGGAGGAGGTGGC	63.418	CTCCTCTCCATCACCACCG	62.977	80
HM_6916	GD20F4R01CY6RK	TGG	3	15	CACACTAAGTGGCATGGAAAAACC	62.829	AGAGAAGACCTGTTTTCCGAAGGT	62.886	81
HM_6917	GD20F4R02FWQ0R	TAT	3	21	CTGCTTGGATCAAAACTCACC	63.227	CAAGAAGACGAAGACGATTATCC	62.397	85
HM_6918	GD20F4R02HZW6B	CGG	3	12	CAAGGACATGAGAAGAGCCATGAT	63.873	GGATGGGTATAGTGTGCTGTGTG	63.356	133
HM_6919	GD20F4R01AWQBK	TTC	3	18	CTTCTCTGCTCATTCGTGTTCTT	62.921	CTTCAAAATTTACCAACACGACG	62.916	149
HM_6920	GD20F4R02FVEON	TTC	3	12	GATTGTTTGGGTGAAAGGAGAACT	62.712	TCTGACACCTGTGGAATTTAGGA	62.057	95
HM_6921	GD20F4R01AQR8T	ATG	3	24	AACAGAGACGCTTTCACATCATC	62.827	ATGATTGTGTTGATCTGGGCATC	63.228	146
HM_6922	GD20F4R01BYVGT	CTA	3	15	TTAACCTTTTTCCCTAACCCGAA	62.983	GTAACGGTACTAACGAAAGGGGGA	63.487	136
HM_6923	GD20F4R01DHH3C	TTC	3	12	ATTACATCTCCCAATGTATCCG	62.999	TATAAAGACAGACCTGGGGTTCA	62.993	106
HM_6924	GD20F4R01D42MT	AAT	3	12	GAGGAAGTGAATTTGCTGCTAATG	63.45	CGGGAACATGCAATTTGGAACGTAT	64.38	102
HM_6925	GD20F4R01E2HYP	TCT	3	24	GCATACCTGAAGTTAGGGGTGTGC	63.158	CGAAGTGAAGTCAATTTGGTGGT	63.543	110
HM_6926	GD20F4R02GJIZ3	CCA	3	12	CTACCCCAACAAAGCAAAAAGG	63.23	TTCAAGTAGTGCCTCTGTTGTTC	62.869	146
HM_6927	GD20F4R01CF03G	ATG	3	12	CATTATCTCTGCGATGTTCTGTTT	63.339	CATCATTCATCAATCCCGTAATCA	62.912	129
HM_6928	GD20F4R02HHU7X	TCT	3	15	GCTTTCTGTAATGCTCTCTCTCT	63.302	GAGCAAGAACATAGAGCGGAAGA	63.244	95
HM_6929	GD20F4R01D42MT	GTG	3	12	CGTTTTCGACACTTCTTCAAC	62.197	GAAATGCAAGATCTCAAGTGGGT	62.813	116
HM_6930	GD20F4R02I6V2W	CAT	3	12	ATAACGTCGGGTTGAGGTTCAATTA	62.826	TTGTTTGTTCATCTCTTCTTGAAC	61.963	160
HM_6931	GD20F4R02H9B7X	AAG	3	12	GAAAAAGTAAACCAACAAAGGCA	62.544	CATGCCAGGCTCAATATATTTCT	62.533	127
HM_6932	GD20F4R02IWPPT	CAA	3	18	GTCAACATTTTCTTCTCAACCC	62.9	TCGTCGAGTAAGTGTGTTTCATC	62.622	116
HM_6933	GD20F4R02H74Q	GGT	3	12	TGATTTCCGAGGACTCATGAATTT	63.099	ATCACCAGACCTTGACAGACCAT	63.228	139
HM_6934	GD20F4R01ALKN6	GAA	3	12	CTCAACTCAACGCTCTGTCTATC	63.498	GGTGGGATGGAGAATTAGGAGATT	62.758	106
HM_6935	GD20F4R01ALON8	TCT	3	18	ACAGTACTCGCATCACAACCAACA	62.972	GCTGATACGGAAGACGCTGTATTCT	63.166	150

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_6936	GD2OF4R02IKJKR	GTG	3	15	CATAGCACCGTCTGAGAGGTAGT	63.036	TTCTCACACGTTAATGGAACTCA	62.931	142
HM_6937	GD2OF4R01BIR52	CCG	3	15	ACGGAGGACTCAGTCACAGTTACC	63.028	CTACATCCACATGCACCTCTCTT	62.898	130
HM_6938	GD2OF4R01D2L7J	GAA	3	18	TGGGATTGGAAAGAAAATCTCAA	62.98	CTTTTGGCGTGGTCTTTCACTAGA	63.015	150
HM_6939	GD2OF4R01A0GVE	TCC	3	12	TCCAGAAGAAAGTCATGTGGTGAA	63.132	AACAAAAGATGGGAAACCATGAAA	62.8	150
HM_6940	GD2OF4R01DYGNH	TAT	3	12	ACAACAGTGGGCTTTTGCTTTTG	62.859	CATACAACACATCCACATCCACT	63.044	117
HM_6941	GD2OF4R01CZ4IK	CAA	3	12	GATTCCTTTTACTGTGACGGCAACC	62.312	ATTGTGTGATGTGGGAATTGTGAA	61.399	119
HM_6942	GD2OF4R02IV0QK	TCT	3	30	TGGTAAATCATGTTGCTTGTGTA	63.581	GGAAAGAGCCAGAGGATGATTATGA	62.889	145
HM_6943	GD2OF4R01EEFY5	TGT	3	12	TGATTTTTGAGCTGATGGGTTTTT	63.018	GCACAATGCATGTGAACATTAAGA	62.126	97
HM_6944	GD2OF4R01C0SJC	CTT	3	12	TTCGCTCTCTCTGTTTTCTGTGTC	63.019	AGAAGAAGAAGCTGCGAAGAAGCTG	62.737	139
HM_6945	GD2OF4R01EJH18	AAT	3	12	AAGCCAGAGAAATCAAAAGGGAAC	63.09	ATGGGTTGGACCTAAGACCAAAAG	63.576	160
HM_6946	GD2OF4R02JLN85	TAG	3	12	TGCTTTTTCTTTGATGAAGTCAAG	62.095	ATGATTTCCGAATAGGACCAAAACA	62.802	150
HM_6947	GD2OF4R02IW4L8	CTC	3	12	CGGAGATTCTGTGTAATCTCGAAGG	63.214	ACTGCTACTGTGGCGACACTCTG	63.712	159
HM_6948	GD2OF4R02HMEBM	GAT	3	12	CGCAGGCTAAAAACCTCTTCCAC	62.477	CTATCATCTAATGGGGACATTGCT	62.804	121
HM_6949	GD2OF4R01EJEO6	GTT	3	12	TTAATGGAGTTTGGGAAATGGTG	63.097	AAAGCTGAAGCTTCTGAAGACGAA	63.044	118
HM_6950	GD2OF4R01CR8XL	TAC	3	12	AGAAAAGTTACTCGACAGTGGACGC	63.163	TTTCAATCCACGTTACAGACTCT	63.009	153
HM_6951	GD2OF4R01CZYGE	ATC	3	15	AACCTCTCTCCGCTCTACTGTGT	63.009	AGACAGACAGTTGTATGCCCGAC	62.751	122
HM_6952	GD2OF4R02GMNFI	TTA	3	12	GGATGTTGACATCTAATCTCTGACA	62.536	GTCCCTCTCTCAAACCTGGTCTCTG	62.882	121
HM_6953	GD2OF4R02IOJOP	TGA	3	15	AAATCCCAAACTTCATCTCAACGA	63.108	GAGTTGGAGGGTCACTCTTTTGTG	62.437	134
HM_6954	GD2OF4R02IBY3K	CTC	3	12	TGTCATGTGCATCATCAAGGATT	62.687	TTTGGGAAATTAATAGGCCACC	63.178	104
HM_6955	GD2OF4R01CSAV4	ATT	3	12	TAGGGTCTATTTTGTGAACACCCC	62.397	TGGTACGTTATACAATGCATAGGAA	61.975	135
HM_6956	GD2OF4R02J0R98	GGT	3	12	AAGAGATTGGAGAGGCTGTGGTGTG	63.106	AACCTCACCTGAGCTGTCTGG	63.017	146
HM_6957	GD2OF4R01AQV19	TCA	3	18	CTTCTCAATCGATGCTTCCAAT	62.815	GATCAACACAGGTGTATTGAACCA	62.175	145
HM_6958	GD2OF4R02G430T	TCT	3	12	TCTTCAGATTTACCTCGTCTTCA	61.433	TTATCAACTGAATCACCGTCAACA	62.188	152
HM_6959	GD2OF4R01EARAI	GCC	3	18	TCAAGTCTCTCAATGATTCTCCC	62.773	CCAATTCTGAGTTCGCAATTCTGAT	62.786	139
HM_6960	GD2OF4R01AY15B	TTC	3	12	GGAAGAAGATGAAGAAGGGGAAAA	63.053	GCGAAGCAAGAAGACAGAAGAAG	63.044	116
HM_6961	GD2OF4R02H46VF	GTG	3	12	AGTCTCTTCTCTGGGTGTCAATGG	63.106	CCCGATATTTAGGGGTGTTCTCAT	62.888	148
HM_6962	GD2OF4R02F97DV	TAT	3	12	GGGTGATTAATTTGACCAACCAA	63.005	TTCAAAATGTAAATATGCTTGCCC	62.307	114
HM_6963	GD2OF4R02JPXFE	TGA	3	12	TAATTTATCTGATCGGCCACTTCT	62.52	AACTTCTCATGTATCATCTCCAGC	62.081	128
HM_6964	GD2OF4R02HAWV8	TGA	3	15	TACAGACCAGGATACCTCATTCAT	63	TATGAGTTTATTCAAGGTGCGGAGA	63.154	127
HM_6965	GD2OF4R01DUD6Z	TAC	3	12	CTTATGGCTCTTCTTGACATCGT	62.923	ACTTGGGCGAGTACTGTTCAATTGTG	62.531	131
HM_6966	GD2OF4R01DEKOC	GGT	3	12	GATGGTGTGGAGGGGACTATAGA	63.993	CATCACCACTCTCAGCGTACTATT	63.338	94
HM_6967	GD2OF4R021RIA	CTC	3	12	ACTTGTCTCTGCTTCTCTCTCT	63.42	GGCAGAAGTTGGAGTCAAGTCTA	63.238	124
HM_6968	GD2OF4R01BT8CC	CTT	3	18	ATGAAACAAGCAAAACCCACATCT	63.035	TATGGAGCAAAAGAAACCTTGAA	63.109	110
HM_6969	GD2OF4R02J0FB8	ATG	3	15	TTTGATCGTGGTGTGTGTACTGTT	62.872	TCACCATCATCACCATCACCATTA	63.266	100
HM_6970	GD2OF4R01DOVF9	TCT	3	15	TTGAAGCTTTTCATGAACAAAAA	62.036	GGAATTGGGTTTGTATTAAACCTT	62.41	92
HM_6971	GD2OF4R01DUWYU	GAT	3	12	TCTAACAGGTATGTGGTGGTCTG	63.272	AATTAGCAACATCATCTCAGCCG	63.565	127
HM_6972	GD2OF4R01ERMWC	CGC	3	12	CCAAACAAGTATAGTAGGAGGGAG	63.216	ATCAATCAATGATGACCCAAATCC	63.094	118
HM_6973	GD2OF4R01DV3HG	AAG	3	18	GTGCAATGAAATGGATGAATTTT	61.221	AGGAGGAAGTAATCAAGAGAGCC	60.586	111
HM_6974	GD2OF4R01DBP9X	TTG	3	21	TCCGATCTCTCAACTCTCTGGAAC	62.91	CATTTAGGCTTTCCACTAGGGCT	63.013	143
HM_6975	GD2OF4R01CWLVS	TAG	3	12	TTGATGCGCATGAATGTGTGTGT	63.069	CTAGATGCCAATCCCTTAAAGGAC	63.178	99
HM_6976	GD2OF4R01DXO21	GAA	3	12	GCCATGGGCATAAATGAAGAAAA	62.081	ATTTCCATCTCTCTCAGCTCTT	62.977	157
HM_6977	GD2OF4R01B73YB	TGT	3	15	TGGATGATTGCTGTAAACATCAAA	62.857	GCCAACGACAACAATCAACAATAA	63.072	133
HM_6978	GD2OF4R01CLS5W	TAA	3	12	AAGTGCTTATGCTCTGAAGGTTG	62.822	GTGACCTTCATCAGCCAGCTTAAT	62.94	125
HM_6979	GD2OF4R02G2OFX	TGT	3	15	GATGATCCGTAGCTATCATCCGC	63.972	ACTATAGCTCAGGAAACACGAGC	63.057	124
HM_6980	GD2OF4R02HPB2G	GTG	3	21	CAATAATGGCGTATGATGGTGGT	63.471	CTCTCTGTGTGAGATCTGGGTCG	63.597	160
HM_6981	GD2OF4R02H5JPV	ATT	3	15	TCAATTTTCAAGCCAAAAGAAAA	60.319	TGCTTATTTGAATGTAGGACAGT	61.168	84
HM_6982	GD2OF4R02H49LK	TGT	3	18	CGCTTTAAACCGCTCTGTATGTTA	63.248	TTAACCCACAGCTCTCTCGAGTTC	63.031	110
HM_6983	GD2OF4R02JRN5M	GAT	3	12	TGGGACGGATTAGGAGACTAGAA	63.095	TGACATACGGCTGTCACTAACTC	63.506	138
HM_6984	GD2OF4R01DW63N	CGC	3	12	ATGGTTGAAAAGGAGCTAGGAGT	62.698	ACTCTCTCCATCGCAACCACTC	63.025	136
HM_6985	GD2OF4R01BIT50	TCT	3	21	GGGAGCTTACCTGATCTCTCTCT	62.977	AATCCCAAAATAAGAAAGGCCAAA	62.989	159
HM_6986	GD2OF4R01C7I8B	GAT	3	18	GCTCCTGTACCTACATGGCACTT	62.851	TCAATGTATTTCTCCCTAGTCCAACA	62.138	159
HM_6987	GD2OF4R02G06AR	AAG	3	12	AGGGGGGACAAACAGTCAATGT	62.999	TGATGATCCCTTTTGTATGGAACA	62.588	157
HM_6988	GD2OF4R01AQWIK	CAC	3	12	AATGTCAAGCGTATGCTAACCCACA	62.858	CTGTCTCAGCAACATCGCTACTA	62.972	109
HM_6989	GD2OF4R02I8Z15	CTA	3	15	ACAAATCATCATCGCTCTCGTCAA	62.938	CGGTTACGGTTTACGTTTAGGTTAGG	63.816	93
HM_6990	GD2OF4R01EFH81	ATG	3	18	ACACCCCCCTGGAATATCTCTCAT	63.173	GCTGAATCCCCTTACATGTTCC	63.026	85
HM_6991	GD2OF4R01A3M6U	CCA	3	12	GTAGGGTGGTGGTGTGATTTCTCC	62.912	CACAATCCCCTTCAACATCAATT	63.732	80
HM_6992	GD2OF4R01DX5X1	CTA	3	21	CACCATGGTGTGATTCAGTTACAA	63.034	ACTCTGAGGATGTTTGGGAACAAG	62.895	146
HM_6993	GD2OF4R01CKFC6	GTT	3	21	TTCTCATCTCTTCATGGTGATCC	63.743	GAATTTTGGCCGAGAATGAAAG	63.103	119
HM_6994	GD2OF4R02HLCI4	CTA	3	12	TCTTAAAACTCACCGCGGAAAC	62.836	GCATGAATCAGTGATTTCTAAACTC	62.383	80
HM_6995	GD2OF4R01CBPAV	GGT	3	12	CCCGTTACTGATCATTACGCTCTT	62.923	CAATTATCACAATGACACATGGGG	63.244	146
HM_6996	GD2OF4R02IBS2O	TAA	3	12	CATTTGGCAGCTTGGAAATGAAGA	63.521	TTTCCCAATTTCTTGCTACTTGT	62.619	155
HM_6997	GD2OF4R01DDGFE	GGT	3	12	CTGAAATCGAGGATTTTGGCCAC	63.948	CGTCTTGTGCTTCTGCTGCTACTA	63.096	153
HM_6998	GD2OF4R01ATHZK	GTA	3	12	AATTTGTCATTGCTTCATCTGGGT	63.026	CATTAAACACAGAATGGCTATTGG	62.745	103
HM_6999	GD2OF4R02GPL09	ATC	3	12	TGGGATTTCTTGGAGACTCTTTTG	62.993	TAGTGATCGATTTCGCGCTAGAG	62.922	123
HM_7000	GD2OF4R01CFD7F	TTC	3	12	TGATTTGATCAATGACTACTTCAGAGC	63.051	CTCCATTAACTCCCATGATGAGT	62.571	156
HM_7001	GD2OF4R02FZS9D	TTC	3	18	TGCAACTCCCTGTAATATTTCGT	62.122	AAGGTGGAGGTGATGACATTGATT	63.004	98
HM_7002	GD2OF4R02H99LF	CTC	3	15	TTAGGAAAAACAACCTTACGGCTC	63.001	CGGAGGGGAGTTAGGAAATGAGTA	63.765	133
HM_7003	GD2OF4R01DN2L9	AGA	3	12	ACAGAATGGAAACCTTGTGAGTGT	63.236	AGGACCCAGCAGTGTATTTTCAAT	63.048	130
HM_7004	GD2OF4R01EPL4P	TCA	3	12	TGCTCCAAACCTTCAATAATCTCA	62.832	AATGGCACCAGTGAATAAATCAGC	63.456	153
HM_7005	GD2OF4R01CM45R	TGG	3	12	GTCTGATTTCCGGAGACCCAAAG	63.525	TCACAGTTGGGACTTATCAACAACA	62.841	148
HM_7006	GD2OF4R02JWAEJ	GAG	3	12	CAACCATAGGACGACGAGATAGGA	62.897	AATCTTAACCTGTGCAAAATTTCCCT	63.099	109
HM_7007	GD2OF4R02IK1O1	GGT	3	15	TGGCTCTCTACATCGGATGGATA	64.051	CGATGTAGTAAAGGGTCGATACGC	63.055	124
HM_7008	GD2OF4R02IIA40	TCT	3	12	CCAATCGATTGCGGATCAATAAT	63.332	CGACTAGGATGATGAACAATGACAA	62.412	113
HM_7009	GD2OF4R02HQ71J	TGC	3	12	TTGAAGTACCTTTATGAGAGCG	63.039	ACTTTGATGGTCAGGCTACAGCTC	63.154	136
HM_7010	GD2OF4R01EGS06	TTG	3	12	TGGCTATCCAATGCATCACTCTA	62.949	TGTGTATCTCTGCCAAATAGAGAA	63.038	125
HM_7011	GD2OF4R02JVQ07	GAA	3	12	CAATTACACTCCGATGTCATT	63.336	GCTGCAAAATTTGTTGGTTCTA	62.467	113
HM_7012	GD2OF4R02HZPH4	AAT	3	21	CCCCAAATATAAACAGCATTGA	61.184	GTGGAATCTCTGCACACCATATT	61.456	133
HM_7013	GD2OF4R02GY2DO	GGA	3	12	CACCTGAAACAGAGAGATGACCG	63.335	TCTTAACTCTCTTAACTTCAATGCTC	62.421	127
HM_7014	GD2OF4R02GUA8V	TGA	3	24	TCTAGCAATTCTGAGCGCTGTGA	63.072	GTATCGTCTACGGATGGGAATGGAC	62.916	146
HM_7015	GD2OF4R01CGAJJ	GGA	3	12	AAAGGAGATCAGCTCTTGGGAGT	62.986	GTAGCTCAAACTCTGCTCTTGTG	62.633	128
HM_7016	GD2OF4R021XP5	GTC	3	12	GGAAGCTCAACAACAGCAGAGAAG	62.946	AGGAGCTCATCTTGTGAGTCTCT	62.928	127
HM_7017	GD2OF4R01CVP82	GTC	3	12	TCTTCTTGAAGTATCTCTGCGG	64.163	CTACCATCTCTCGATCCTCGAC	63.531	135
HM_7018	GD2OF4R02FN8PR	TGG	3	12	TGATCCATCTTTGTTTGTGCTGTG	63.252	GACCAAGGTTACCATCATCATCAC	62.61	152
HM_7019	GD2OF4R01ANAND	AGG	3	15	ATTTTGCAGAGGGTGAATCGTAA	63.03	CTGCGTGCAGAGTCTTCTTCT	63.159	130
HM_7020	GD2OF4R021Y25	TTC	3	12	TGCGCACACAGTAACACTCTCTC	62.961	AGCATAAGCCCTTGTGCTCG	63.815	131
HM_7021	GD2OF4R02F694B	ACA	3	12	ACCATAAAGGGGGAAGAAGA	60.173	AAAAAGAGCAAAATGCTCAATTG	60.82	95
HM_7022	GD2OF4R01EMSAY	CGC	3	24	GGCGAATTTGGAGATTCTCTCTT	63.188	CCGATGAAGCGATAAGATTGTAGAG	62.451	97
HM_7023	GD2OF4R02J2983	ATG	3	24	CCTAATGGGTGCTCGTATTATT	62.438	CTCATCATGCATCATCATCA	62.145	159
HM_7024	GD2OF4R01AU7JY	GGA	3	15	CTTCTTTTACCGTACGTTTCCG	63.044	AACCCCTCCGATCTGGAAGAAGA	63.503	130
HM_7025	GD2OF4R02HQKE9	GTG	3	12	TGTGCTAAGAGCACTCCAACGC	62.96	GAGGTCTGAGCAGCGTAAGATCA	63.166	118
HM_7026	GD2OF4R02FYOW7	ATT	3	12	GACTCAAGCAAGTGAAGACGCA	62.236	AATTGGTGTGTTTCCGACAAGT	62.933	154
HM_7027	GD2OF4R01DS746	GTG	3	15	ATGGTAGATTGACGTTGGAAGGAA	63.009	AGCCAAATTCAGATATCTCCAGC	62.718	146
HM_7028	GD2OF4R01AS03Z	CAC	3	15	AAATCTTGAAGCCCTCTACACTC	62.986	TGAGGTAATTTCTCACTCATTTG	62.605	100
HM_7029	GD2OF4R02HONK0	ATC	3	12	GGAATCTGTATCATGTGCATCG	62.735	ACACGATCAATGGAATACAGCTCA	62.951	126
HM_7030	GD2OF4R02115MI	TTC	3	12	TGCCCGCTTAAATGGATATTAG	63.026	TTGAATGGAAACTCTGATGTCCTC	62.799	147

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7031	GD2OF4R02GV7FZ	AAG	3	12	CTCTTCCATTTTCTTTCCCTTA	62.861	CAGCACACTAGCCATCTTTCTCTT	63.044	119
HM_7032	GD2OF4R01A052J	TAT	3	12	GAGATGGAATGTTGATGAGAGGAGA	62.992	AGCTCAAGGGAAGTACATGCAAAAC	62.949	146
HM_7033	GD2OF4R01BUE8T	ATC	3	12	CTGGTTCCACCATTAATACAA	62.21	TGCTGAAGACATCGGTGATAAAGA	63.154	145
HM_7034	GD2OF4R01CBO1N	ATG	3	12	CCACAAGAGGTTGAGGAGATTTCAT	62.884	TCATATCATTTGTCACCTGCATCC	63.381	158
HM_7035	GD2OF4R02F76KW	TCT	3	12	ATATCCCTGTCCACCACAACAAAT	62.7	GAAGAAACCCAGGAAAGGAAGAAG	62.873	146
HM_7036	GD2OF4R01EP7NR	AAG	3	18	CAATTGAAATGGGGTTACACAGAAT	63.206	ATAGCTTGGGTTTAGGGCATCACT	63.313	135
HM_7037	GD2OF4R01BL50O	TCT	3	12	CGACAGACATGATTGGAATAATGA	63.244	ATCGACAGAAACACACCACAAGA	63.053	86
HM_7038	GD2OF4R01DYJ4D	CCA	3	12	CCTCAGTAAGTACAGCACTCAA	62.918	GTCCTGAGCCACCTGATGGA	63.627	130
HM_7039	GD2OF4R02GRWX5	TCA	3	12	CTTCAGTCAGCTCACCATTGACCT	63.25	CCAGTTCACTGAAAGAGAGGAC	62.677	155
HM_7040	GD2OF4R02JNLGY	TGT	3	12	ATTTGCAGATCAAAATGTTAGGGA	63.952	CGACCTGAAACAAGACGGTGAC	64.18	84
HM_7041	GD2OF4R01DOH43	GTC	3	21	TGGAGAATATATCGTATGGGCAGC	63.337	ACAACACCCTACCTCCATAATCA	62.798	153
HM_7042	GD2OF4R01CS2PH	AAG	3	15	GCTAGAGGAGCATGAGGAGAATGA	63.336	CTAAAGATCCGATCCGGTTAGCTT	63.004	106
HM_7043	GD2OF4R02IL2P7	AAT	3	15	TTAAGGGTCCATTTTGTAAACATTGC	62.278	ACGTTGTGATTTTGTGTTTCCAGT	62.933	130
HM_7044	GD2OF4R02HYKFR	GAA	3	12	AAATTTTCGCTTCCTGATCTCT	63.211	CAGCTTGATGCTACTTTACAGAAAGAAA	62.446	149
HM_7045	GD2OF4R02FN84P	CAA	3	12	ACCCATTACAATAGACGCCAACCC	63.137	AGGTTGTCCATTTCAGTCTGATGT	63.128	130
HM_7046	GD2OF4R02GGB22	GAT	3	12	GTGGTGACATTGCAAGAAATTGAG	62.948	TTTCTTCTCAGGGTGTAAAGCTC	63.031	95
HM_7047	GD2OF4R02IAB34	TCC	3	12	ACTACATGCTCCCTTATCAACCAC	62.613	GAGGTGGAGCTGATAGCCACAT	62.805	147
HM_7048	GD2OF4R02DYXIH	GGA	3	15	GCAATGGGGATAAGAAATCATCAG	62.902	ATTCAATTTCTCAGGCAATGTCTG	63.137	118
HM_7049	GD2OF4R02HXD74	TGA	3	24	TCGGATTGATCCATTGTATCTCTT	62.791	ATTTTCTCTATCATTCTCGCGCT	63.608	130
HM_7050	GD2OF4R02GOE6D	CCA	3	12	TTTGTTTTTCTCTGGACAGGAAGC	63.019	ATGGTGAGGACATGGTGGA	63.613	132
HM_7051	GD2OF4R0188F2C	TCA	3	24	AAACCAATAAAAGTTGGTCTTAGAAAA	60.089	ACGATGAAGATGAAGATGAAGAGG	60.965	129
HM_7052	GD2OF4R02G1GAI	TCG	3	18	AGTCGCTGCTCTGCATTATCATCT	63.697	GAATCTCGTGGGTGTTTCAAG	63.002	128
HM_7053	GD2OF4R02JXWNF	ATG	3	12	CTGGTGATGCAACTGAGATCTCTA	62.712	CCTTAAGAGGGTGATCAAGCTCA	63.006	87
HM_7054	GD2OF4R01AJRTN	TTA	3	12	AAGCCTTAGTGATTACTGCTTTTT	61.196	AAAATCTATAGAGTGGAGAAGCCGAA	61.91	97
HM_7055	GD2OF4R02G4XPO	CCA	3	12	ATTTTGGCCCATTTGACTATCTTT	62.995	ATCTTATATGGTGGGTGGAGTTGG	62.844	119
HM_7056	GD2OF4R02HJZDU	GAA	3	12	AGGAAGAGGAAGAACTAATTTTTGGG	62.347	TTTGGTTACATATTTCCACACCTTG	63.132	80
HM_7057	GD2OF4R01AZ80O	AAG	3	12	CAAAAGTTGGGAGGGGAAAGTATTC	63.168	CTGCAGAACTCTGATCTCTCGCTT	63.456	130
HM_7058	GD2OF4R02JNL55	TTC	3	12	GGCCATGAACTAATGCTCTTCACT	60.748	ATACTAGTAATAACCCGTGCCCGT	61.114	108
HM_7059	GD2OF4R01DUBW3	TCT	3	12	TATTTTGAGCACGTAAGAGGGTGG	63.329	ATTTTGGAACTAGCCATGCAAAAC	63.456	142
HM_7060	GD2OF4R02F3WB6	TGT	3	12	AAAAAGGCTTGACCTCATCATCAC	62.813	AAACCCGTTAAAAAGGACACAGT	63.106	106
HM_7061	GD2OF4R01AHSSX	TCG	3	12	TGCGACTGAGTCTCTGCTGTAAAC	62.985	GTTTCAGCAGATGCAGGTCTTAT	62.94	121
HM_7062	GD2OF4R01B89E5	GCT	3	12	CCCAAGCTTGAGAAAGTTTAAAG	63.015	ATTCTCAGCTGCTTCTCTCTCT	63.205	143
HM_7063	GD2OF4R01DWSWD	CTG	3	12	CTTGTTGAGCATGCTCTCTCTACT	63.25	ATCTCTGTATGACCAAAACCCCA	62.897	146
HM_7064	GD2OF4R02F6UW8	AGG	3	15	GATCAATATATCATTCCAGGCCGA	63.21	TGGTACCACAATGAGGGACTACT	63.238	131
HM_7065	GD2OF4R02JX9Q	GGT	3	12	GTGGAGAAGCAGTCGCTAGTGG	63.373	CTTATGTGTGCTGCTTCCATCT	63.148	96
HM_7066	GD2OF4R01AKQ8A	AGC	3	15	AAGCAAGGTTTACCTCATGCTCAG	62.933	ACAGAAGTTGGCATCAGTTCCTTC	63.027	149
HM_7067	GD2OF4R02HB4U2	TGC	3	18	CAGGTTTGTAATAAGCAGCCCAA	63.434	TCCGCTACTTTCTCAGACCATCT	62.712	103
HM_7068	GD2OF4R02I9NY9	AAG	3	12	CCCGACATACAGGCTTATTAACAT	63.309	TTGTTGTTCTAAGGCGAAAGTG	62.687	147
HM_7069	GD2OF4R02GLTDH	GGA	3	15	TTTTACGTCAGTGTTCGAGTATC	63.648	AACCTCCGATCTGGAAGAAGA	63.503	133
HM_7070	GD2OF4R02F0529	GTT	3	15	ATGCCAGACAGCTCACTTGATGAT	63.907	TCATCGTCAACGGTCTAGATTCA	63.038	159
HM_7071	GD2OF4R01C05JC	TCT	3	12	TTGCTCTCTCTGTTTTTCTGCTC	63.019	AGAAGAAGAAAGCTGCGAAGAAGCT	62.737	139
HM_7072	GD2OF4R01E1DFX	CTT	3	24	TGAACTCAAACTTCAATGTGGAA	62.918	CACCATGGGAACCTGTAATCTGTA	62.176	147
HM_7073	GD2OF4R02HJCU6	TTC	3	21	AATCCGGCGACAGTACTCTTCTT	62.612	AAAATTGGAAAGGAGGAGGATAGAA	61.656	106
HM_7074	GD2OF4R02GXJ3N	CTC	3	12	ACCACCGTCCACATCTCTCTC	63.586	GTGTGTCAGTTGGATCAGAGGTG	63.155	125
HM_7075	GD2OF4R02IAXDO	CGT	3	15	CACCTCTCTGCTGCTCTCTCT	63.376	TACGGTACGGTACGGACGGA	63.502	206
HM_7076	GD2OF4R01AH189	TCT	3	12	CGAACATATGAACCTCTGCAAG	62.324	CTTTCCGAGCTTGAGAGAGGC	62.895	80
HM_7077	GD2OF4R02G0FOE	CAT	3	24	ATCACCAAGATGAGTAGGAGCCAC	62.915	TGGTAAGCTACCGTTTGGGAAGA	63.13	157
HM_7078	GD2OF4R02G3K0K	TTC	3	15	AAGGAGAGCATGGTGACCGTATTA	63.133	ACTAGCGAGGAGGAGACTCCAGAC	63.739	121
HM_7079	GD2OF4R02J0H6	TTC	3	12	GCTTCCGCTCTCTGAATCTATTT	63.111	GTTGCTGTTGATGAAGACCTGTT	63.672	80
HM_7080	GD2OF4R01AE70S	AGA	3	15	AGAAGAAGCAGCAAGCTGCGAGAG	63.801	CTAACTTAGAAAGCGTCTGCTCG	64.572	106
HM_7081	GD2OF4R02HTL5O	CTG	3	12	CTGAAGCTGCTGATCTCTGCTCTG	62.947	AATTGGTTGTAATGTCTGGTTCGG	63.227	143
HM_7082	GD2OF4R01CHX71	CTC	3	15	AAGGTGATCTGAGCGCTCTCT	60.216	GTGAAGGTGTGAACCTGGAAGAGTT	60.958	101
HM_7083	GD2OF4R02J5V76	TGG	3	12	GGCCCACTAAATTTGAACCTTAA	63.375	GTGATGATTGTTGAATGGGTGGT	63.021	133
HM_7084	GD2OF4R02G1HIA	TTC	3	15	TGAAAGTTTTTCTCTCACTCTCTG	62.437	TAGAAAGGGCAATTACCAAGTTGA	63.014	130
HM_7085	GD2OF4R01EVTGW	TGG	3	12	TAAATGGAGGAGGAGGTGATGGA	62.974	CTTACTATTACAAATGCCACCCG	62.969	151
HM_7086	GD2OF4R02F7YJM	CCA	3	12	ATCAGAGCCACCAAAATACCATC	62.926	AGGTGTTGGGGTGATGTAGAAGAG	62.793	121
HM_7087	GD2OF4R01CLRJ4	CTT	3	18	AGTTTTGGATAGCATGTTTGAAGG	62.619	CACCTTAAATGGCAACAGCATCAAG	62.969	122
HM_7088	GD2OF4R01CHK11	CAT	3	15	GGATTGAGGAAGCAATGAATGAGC	62.586	TGATGATGAAGATCAGAACCAAGA	63.113	150
HM_7089	GD2OF4R01AYI5B	TCT	3	12	GGAAAGAGTGAAGAGGGGGAAAA	63.053	GCGAAGCAAGAGACAAAGAAGAAG	63.044	116
HM_7090	GD2OF4R02HE47Y	CAC	3	12	CCATCTAACCCGCAAAATCAACATA	64.028	CGATTGATGTGCTAGCAGTTTTG	63.081	123
HM_7091	GD2OF4R01DYX1T	CTT	3	12	CGTCATGCTTGGAAACCAATAA	63.15	CATGTTTCTCTATGAAACCCGAC	62.804	116
HM_7092	GD2OF4R01A5NBN	CAT	3	12	TAGCGGTTTCATGCTCAAGTAGT	62.643	GATGAACAGGAGGAGAACCTTAGA	62.672	108
HM_7093	GD2OF4R02G3O0Y	ACC	3	12	ACCACCACATCTCCGAGCTA	64.174	CTCGTAAAAATGTTGCTTTGGT	64.598	154
HM_7094	GD2OF4R01E1OK5	GAT	3	12	AGAAAGGGTATTGAAGTGGAAGGG	62.873	TCACCATTTATGCTCATGCTCTCT	62.595	125
HM_7095	GD2OF4R01EX6ZK	ATC	3	12	ATATTGACTGGAGGATGGAAGGT	63.173	AGGACCGAAGGAGAAGACGATAAC	63.193	158
HM_7096	GD2OF4R02GFJFO	TCC	3	12	TCACTTGTTCCAAGTAACCTCTT	62.696	AGGCAGCTGGTGATATGACAGAGA	63.678	150
HM_7097	GD2OF4R01A8F7X	ATC	3	15	CTCAACCATTCATGGGTTGTTTT	63.214	CTCCACACAGAGGAAGAACCTAA	62.993	93
HM_7098	GD2OF4R01DFX9L	TGG	3	12	GTATACCCCTTGAAGGCTCTCAAGC	62.198	CGGAATGATCATCAAGAATACCC	63	128
HM_7099	GD2OF4R01EGWLP	TCC	3	15	GTCCTTTGAGATCTGTTGGAAGC	62.599	CGGGAGTAAGTCTGAGTGAAGGAA	63.107	160
HM_7100	GD2OF4R01AZV57	TCT	3	15	CGTTGCTAAGCATGATGAGTTGCT	62.134	TACGGGTACGGCTAGGGTATGTTA	62.757	145
HM_7101	GD2OF4R01D25NP	TGG	3	12	TGAGGATACATAGGTTGAGAGGGA	62.455	CGCCTTCTCTACTGTTCTCTCT	63.399	130
HM_7102	GD2OF4R02ITV11	CAA	3	12	AGTGTGAATCTAACAGTAGCAGCAG	62.287	GAAACATACAACCTGCGTCTGTG	62.972	128
HM_7103	GD2OF4R01EXJ58	GAG	3	12	AGCTTGACGCTCTCATCCAATAC	63.051	CGACTTCTCTGTTCACTCAGAT	63.223	117
HM_7104	GD2OF4R01ATPPI	CTC	3	15	CATTATCGAGGAGAAAGCTTTGAGC	62.546	CGAGAAAAGCGAAGATAAGAGGGA	62.329	138
HM_7105	GD2OF4R02ISILE	GGT	3	12	CTAGAATCTCTGCTCTGCTGCTCG	63.035	CGAAGTAATCAACATGCCCCCT	63.807	159
HM_7106	GD2OF4R01EBPXX	TCG	3	12	TCTAAGGACACAAGTGGGTTTTCC	62.696	GTCGGTTAGATCCGAAGTGTCTA	62.811	130
HM_7107	GD2OF4R01C9JXN	TTC	3	18	CATCTTCTCCACGATGATGGTT	62.458	GGAGGCTATACCGTTACACCTTT	62.728	103
HM_7108	GD2OF4R02JOEBU	GTT	3	12	TGGAGAGTGAATGTGACTCTGAG	62.919	GCTGTTCTGTTAGTGCTCGGAGTT	63.163	157
HM_7109	GD2OF4R01CW5F6	TCT	3	15	AGTCTTAAACCTGGCATCTCTCC	63.193	ATCACGAGAATGACTCTTTGTCC	62.901	103
HM_7110	GD2OF4R01D0334	TCG	3	12	GTGGTCGCCCTCTCATCAT	64.685	TTCTCTTGTCTCAAGCCCTTCT	63.899	131
HM_7111	GD2OF4R02H5E71	AAC	3	12	CACACGTACATCATGTGACAAACA	62.891	TTGTTGATTTTGACCTAAGATCA	62.832	129
HM_7112	GD2OF4R01BFPWU	CAC	3	12	CCCCAACCTTATATCATCTCTCCA	63.369	GATTGACGGTGGTGATGAGGTT	63.358	109
HM_7113	GD2OF4R02GURP7	CTT	3	12	ATGGAGGAGGCCATGGAAAC	63.435	TACAACCACTCTCCAGCCATTGA	62.731	81
HM_7114	GD2OF4R02JFVQW	ATC	3	12	ACGACGAACACGTTTGAAATTTCT	63.154	GAATCAGATGATGACGACGATGAG	63.146	154
HM_7115	GD2OF4R01D3KX1	TCT	3	48	AAAGCCCTAATCACCATTCAACA	63.129	TGAGTGAGATTGAACCCAAACG	63.459	116
HM_7116	GD2OF4R01DL4UP	TCT	3	15	CTAGAGCAAGAAAGGGAAGGAGG	62.791	CGACACGCAAGACAAAGAGAC	63.743	151
HM_7117	GD2OF4R01AUJLP	GTG	3	21	ACCGAAGAGTGAGAGATCTGGCTA	62.912	CACCACTCAAAACCTGATTTCTCT	62.895	140
HM_7118	GD2OF4R02JIIET	CAT	3	18	CTTGCTGATTTTTGATGCTCTT	62.935	GTTTACTGCATCCACCTTTGGTGT	63.462	156
HM_7119	GD2OF4R01EXVEV	AAG	3	12	AGCTCGAAGATGTCAAGAGCAAC	62.29	CTCACTTTTGCATTTGATTCTAC	62.219	143
HM_7120	GD2OF4R01EJWL7	AAT	3	12	CTCTCCACAACCGAAGAGAAGTA	63.107	CAAGAAGTGACTGCTACCCGAGTT	62.146	107
HM_7121	GD2OF4R02HAYLO	GAT	3	24	TCAATCACACGACAAAGGAATTG	63.252	GGCTGGTAAAGAAACAAATATCACA	63.596	158
HM_7122	GD2OF4R02HZWZF	GCG	3	12	CCGATGATAGATCGGAGTTGCT	62.687	ATTATCATCCAGGCGCACAATATC	63.246	142
HM_7123	GD2OF4R01DR6VE	GCG	3	12	GATGTCAAGTCCGATTTGGGTAAT	62.397	GTCACGCTCTGAGATCATCTTCTTC	62.058	157
HM_7124	GD2OF4R02GUV5J	TTC	3	12	TGAAATCTTGCCATTTACCAAGT	62.922	ATACAAGGAAGTCTGAAATGGA	62.912	105
HM_7125	GD2OF4R01AVOON	TTC	3	12	GAGGAAGAACCTATGTTGACGAG	62.598	CGTTCATGAGGGATATAGTCCAGA	63.52	144

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7126	GD2OF4R01C05JC	TCT	3	12	TTGCTCTCTCTGTTTTTCTGGTC	63.019	AGAAGAAGAAGCTGCGAAGAAGCTG	62.737	139
HM_7127	GD2OF4R01BQJ54	GAA	3	15	ACAACATGATGGACAGTCGATTGAA	63.044	TTTATGCAAGATTAATACGCCGCTCT	62.969	106
HM_7128	GD2OF4R02ICGE4	AAG	3	12	TGTGGAAAGCGCATTAATATTATTGTT	62.787	GAAGCTCCCCACAAACTCTTTTT	63.098	145
HM_7129	GD2OF4R02F13VT	TTC	3	24	CACCTGGGCTACCTCTCTCTTTT	62.088	GACTGGTAGGGTCCCCTTAGAGATT	62.996	91
HM_7130	GD2OF4R02I4NWR	AGA	3	12	TAGCAGTCCGATTCTCACATGAT	63.154	CAGCATTTGTATAAACTCCTCGCC	63.15	149
HM_7131	GD2OF4R01DBS15	TCT	3	18	ATGCGAACCTCCAGTCTCTCTCTG	63.238	TATCCGCGACCTTAAGAATACCAA	62.933	141
HM_7132	GD2OF4R01CTY0X	AGA	3	12	CATCTCAATCAACAAACCCAAAAGA	62.437	TGGCAATGGGCTTAATATTCTCTG	62.357	128
HM_7133	GD2OF4R01D8AIB	CTT	3	15	GTCTCCATGGTGTGTGGAGAG	63.129	TCAACCTTAGCAATGACCCCACT	64.073	157
HM_7134	GD2OF4R02G3RBJ	ATT	3	15	CGTGATAAAAGGAAGCCACATCAG	63.07	TAGACTGGAGGTCAATTGGGTTCT	62.368	158
HM_7135	GD2OF4R02IBS53	TAA	3	12	CTTCTGTCTCTACTCCACCGT	63.033	GAGGAATGCCGTGATGTTATTTCT	62.928	140
HM_7136	GD2OF4R02J13V6	CCG	3	24	ACTCTGGGCTGCTCTCTCTCT	64.129	TGGAGGAGCAGCTTTATCAGAAAC	63.133	107
HM_7137	GD2OF4R01ECEKF	AGA	3	12	ACTCATGAATAGTCGGGAGAGGC	63.006	AGATTCTGATGACGAGGTGATCC	62.89	122
HM_7138	GD2OF4R02IBA3P	CAC	3	12	AAAACACCATCAATCCATGAATC	62.8	ACTCTGCACCTTGTCTCTGCTT	62.834	114
HM_7139	GD2OF4R01D78FB	GAA	3	18	ATGGGCTGACTTACCAATGAGAAC	62.713	TTGATCATATTCAAGGCTCAATCG	62.411	134
HM_7140	GD2OF4R01B58U	TAC	3	12	TTCTTGATCATCATCTCACCCGT	63.033	GATCTGTTTCATGAGTCAGACGAGC	63.392	89
HM_7141	GD2OF4R02JCB4	TGA	3	12	GGGAGCAACCTTAGAAGTCACTCA	63.124	AGAACATTATCCAGCTGTGACCG	63.267	125
HM_7142	GD2OF4R01DA6DH	GGT	3	12	TATCCAGAGAAACATCGGGCTCT	62.446	TCCAGTGAGATTGAATGGGTACA	62.803	133
HM_7143	GD2OF4R02I28YG	TTC	3	12	ATATAAACCTCGAAATCCCTCGC	62.723	AATCAGCAGAATTGGAGAAACCTG	62.91	154
HM_7144	GD2OF4R02FYP8W	TGT	3	15	CTTCTCCAACCTGTTTCACTGCCT	63.133	AATCGCTACCTGACATATTGCAT	63.062	124
HM_7145	GD2OF4R02H0JV2	CCA	3	12	CTGAGAAAGAACTCATGGAGCACA	62.919	ATGGCTATAATGGGCTTCACTCTG	62.731	138
HM_7146	GD2OF4R02H0S6P	CAG	3	15	TTAGGGGTTCTTCAAGGTCACAA	63.1	CCACCAGCTCCACTACCATTTTAC	63.031	150
HM_7147	GD2OF4R02G637U	AGA	3	12	TTAGTGTGATAAGGCGGTGTGTC	62.44	ATTCAGTATTCCCAAGGCAACTA	63.121	85
HM_7148	GD2OF4R02G2C8X	CCT	3	15	TGAGTGATGTTGGTGTGTGAGTT	62.933	ATAGTTTGGTTGGCAGTTGGTGAT	62.936	120
HM_7149	GD2OF4R01C88RK	GCC	3	12	CACAGACTCGCCTCTTCTCACTT	63.462	GCGGAGCTCAATTTCACAGTAACA	62.783	157
HM_7150	GD2OF4R02I26L	ATT	3	15	TTTTCGGAATTTTATAGTCTTCTGTG	60.263	GTACAACCCCAATTACATTTTCAA	61.019	111
HM_7151	GD2OF4R01BCV36	GAG	3	12	GAAGGGAGAGAAAAGGGAAGAAGA	62.549	CGTGGTCATGTCAGCCTATTATT	63.341	101
HM_7152	GD2OF4R02GRD3D	AAG	3	18	CAAAACGGAATAAAGCAAAAAACA	62.409	TTTTTAGGGGCTCTGGAGTCTGC	62.896	128
HM_7153	GD2OF4R01D2F20	GTT	3	15	GGCGGAGAGGTTTTTATGACTGGT	63.017	TACCTTCTCACTCTTGTTCGGC	63.031	142
HM_7154	GD2OF4R02FM462	TCC	3	21	CACAGCCCTAGAAAGCTCCTCAT	63.227	AGTGATGGTACGACGGGTGATGAT	63.896	99
HM_7155	GD2OF4R01CLZTX	GAA	3	12	GGACGTACATATTAGGCAACAAGA	61.536	GTTCCTTATTTTGTGAGCCAAGC	62.356	114
HM_7156	GD2OF4R01A5F6Q	ATC	3	15	CTTGCAAAATATTCTCTCCATCC	62.033	AGAAAGGTGTTTGAAGGTGTGCC	62.835	140
HM_7157	GD2OF4R01DBYNQ	AGA	3	15	TTTGTCCGAACCAACATCGAATTG	62.942	TCATCATATAATCATCATCGAATTG	62.013	126
HM_7158	GD2OF4R02ILRCR	CTT	3	18	GTTCGATCTGTTATTTCTGTGTCC	63.013	GCAGAGGAATTTGTGGTGGTAAC	63.035	153
HM_7159	GD2OF4R01CNRCM	TCT	3	12	TCAATATTTTGGCTCCGGATATGT	62.724	TTCTCCTCTTATGGTATGCCTCA	63.206	105
HM_7160	GD2OF4R01AVJ16	ATG	3	18	AGCTGGATCTGGTGGTGGTAT	64.105	TGGCCAAACATTTTGGGTGACTAT	63.54	156
HM_7161	GD2OF4R02F36PZ	TCA	3	15	TTGATCGAAAGCAAGAAATGAACA	62.932	TCAACAATCCTGTGGTAGTGTTC	62.244	118
HM_7162	GD2OF4R01E2ZVR	CTT	3	30	CCATCCCTAGACATGTCGTTTTTC	63.009	ACATCTGCAGTGTTCGACTGTGAG	63.998	96
HM_7163	GD2OF4R02H504J	TCT	3	12	AACTGGTCACAAAATCTCTCAAC	62.598	ACGCGATCTTCGAGATACGTAAC	62.867	157
HM_7164	GD2OF4R01B6PCL	CAT	3	12	TTCTCAATCTTGGGTCCAGC	63.671	ATGAAGGAGTTGGAGAGTGTCTGC	63.241	144
HM_7165	GD2OF4R01BG5UX	TGC	3	12	TGACATCTCAGGTTGAATTTGTCT	62.291	AACCTCTAAAGTGAAACCTCAGCGG	62.23	134
HM_7166	GD2OF4R02ID3CA	ATA	3	12	TTTGAGGGATTCAAGTTGAGAAAT	60.333	ACACCAATTCTTTGTGGATTTTCT	60.396	159
HM_7167	GD2OF4R02G2N02	ATT	3	18	AAGTCACATAGATTGACGATTACATGA	61.265	ACAACCTGGCACAACATCAAAAT	62.122	146
HM_7168	GD2OF4R01C4OQ1	GGT	3	12	GTACGCGATGAATTATTGCAAGT	62.354	CCTCGTGAAGATACTGGGTCAATT	62.909	105
HM_7169	GD2OF4R01B98G9	GAT	3	12	GAATGAGAGAAAGAGAAAAGGGC	62.878	ATCCCATCTCAACCAACTTCTCT	63.078	90
HM_7170	GD2OF4R01BUIQ5	TTC	3	24	AATCTCTCTCTGCGCAACTTAT	63.188	TTCAAAGCTAGTCAAAGAGTGCGA	62.656	128
HM_7171	GD2OF4R02HRAUQ	AAC	3	12	TGTGGGAATTCATTAATGGTGTG	63.034	GTAATGATCCTCTCTCTGACGCC	62.7	111
HM_7172	GD2OF4R02HDNYK	CTT	3	12	AGTGCGTATTGACTGTCTCTCCCT	63.04	AAGGTCCAATTAAGACGTTGGAA	62.124	101
HM_7173	GD2OF4R02H2S6D	CCA	3	15	TCTCAATCCCCCACTCCCTT	63.049	GGGGAGAGGAGTTGGTTGAATC	63.286	140
HM_7174	GD2OF4R01BMLXY	CCA	3	15	AGCAACATCATGTGTAGTGTGTC	62.412	ATGATGTACTGCAGCTTGATAGCG	62.788	131
HM_7175	GD2OF4R01AJJUN	GTA	3	15	AAAGAGAGTGTTAATGTGCGTGAAA	62.397	CAATTGGTTTATAGGCGAAAAATGA	63.218	86
HM_7176	GD2OF4R02G3SK6	CAT	3	15	TTATGAATCAAGCGAAGAAACGG	63.521	TGATTTTCATGATTTTACCACGGA	62.691	115
HM_7177	GD2OF4R01A4WDJ	TCT	3	12	AAGCAGAAGGTGGTTGGCAT	63.139	GACCTTGGGAAGGAGAACTGATGA	62.977	86
HM_7178	GD2OF4R01EVN6E	AGC	3	12	CACTGCTGGATAAATCTTGTGTGC	62.339	TTTCATTAAGATGGGTCAACAAAG	63.3	160
HM_7179	GD2OF4R01AXHIW	CCG	3	12	CCACCATCACTCTGTGATCAAG	62.894	AGTTGCTGATAGATGAGTCGGTCC	63.031	149
HM_7180	GD2OF4R01D7J7V	TGG	3	12	AGGCTAGGACAGCATAGGAGGCT	63.012	AATAAGCTAGAGCGACCGTAAGCA	62.691	156
HM_7181	GD2OF4R01CQPPU	CCA	3	12	TTGACCAAAACCGCTACTGTACT	63.15	TTCTCTGTGTACATCCGATGCTG	63.841	145
HM_7182	GD2OF4R01BLQ64	TCT	3	12	CTTCAGCTGTGCTAAAGCAACAA	62.991	ACGCTACTCAAAGATTCAACGGAC	62.949	142
HM_7183	GD2OF4R01EKK1I	AGG	3	12	TAAGCAGGAGCAGTATTGATCA	63.184	GTGGTTTTCTGTGAGAGGGGTG	63.775	157
HM_7184	GD2OF4R01AUHKN	TCT	3	12	GATTAGTCTCTCAATGGCTCCGAAT	63.798	GAGCTGAGTTCAAACTCCTCTCA	63.443	100
HM_7185	GD2OF4R02J6CDC	ATC	3	12	CAAGAGCGGTGCTGAATTAATAG	63.24	AATTTCAAAGACACCGTGATGATG	62.294	142
HM_7186	GD2OF4R02F18DD	AGC	3	18	AGAAACGCGAAACAAACGAAGAAA	63.247	TTTCTTTCTCAAGGACCTTCGTG	63.003	113
HM_7187	GD2OF4R02HGGHQ	GGA	3	15	CTTCTTTTACCTGATGTTGCTCG	63.044	AACCCCTCCGATCTGAAGAAGA	63.503	135
HM_7188	GD2OF4R02JYJMK	TGA	3	12	GGCATGGTGATGACTAGCTATTGT	62.138	GGGTGATCATCATGGTTGTAAGAA	62.158	94
HM_7189	GD2OF4R02JSWBL	TCT	3	12	TGCTAGCCCTAGACACATATTGGA	63.148	TTTGTGGTGAAGGTTTAAATGCA	62.551	147
HM_7190	GD2OF4R02F171V	AAG	3	12	ATCATGTCTATGTATGGATCGGC	63.233	TAAACATTCCACTAAGCATGCCA	62.761	115
HM_7191	GD2OF4R02I1HB1	CTT	3	15	AAATGCGATGAACATTCCTGTTTT	62.937	AGAAGGAGGAAGAAGAAGGGAACA	62.958	132
HM_7192	GD2OF4R02GBJTD	TAA	3	12	TGGATCCAGGAGTTTAGGAGTTTG	62.782	CTCGAGTTGTGTTATTTATGATTGGTT	61.803	160
HM_7193	GD2OF4R01D80HW	TCT	3	12	ATGCTCACTGACATCAACCAATTC	62.382	AATCAGGATGAAGCTCGTAACCTT	62.439	126
HM_7194	GD2OF4R01AH4XH	TCT	3	36	TTCTTCCAAAAATCCCTCTCGT	63.08	GAAGAAGACGACGACAGACAGTA	63.081	101
HM_7195	GD2OF4R01AJ7J	TCC	3	12	TTGGCTGTCTCTCTTCAACTTC	63.225	AATGGAGGAGAAAATCCGAAAAA	63.366	130
HM_7196	GD2OF4R02JO8P1	TGG	3	21	GCTCTCTTGTTCAGAGTCAACCTC	63.018	AAAATGGGTACAGATGACGGAAGA	63.009	137
HM_7197	GD2OF4R01B4X8B	AAG	3	15	TCAAAGAGAATTGAACAAAGAAGGG	62.998	TTGCGATTGCTCTTTAACTTAA	63.138	153
HM_7198	GD2OF4R01B9RLP	CGG	3	12	AAAAACCACTCATCCCTCG	62.056	TTCTTAACCTCAAAACCTTAGCCATC	61.255	144
HM_7199	GD2OF4R02FKW48	AGA	3	12	CAAAAGTTGGGAGGAGTAGAATTC	62.61	TATTCCTTTTCCCGCTCTCTTCT	63.278	150
HM_7200	GD2OF4R02H873S	AAT	3	12	CGTGAATGTTGGGGTGGAATTTA	63.817	AAGGAACGATTGCCAAAGATTCAA	63.03	148
HM_7201	GD2OF4R01DYB2T	GCT	3	12	TCTGCACCGCTGATAGAGCTTTT	63.781	TACGCCGCTGCTCTGACTTTTAT	64.387	84
HM_7202	GD2OF4R02HGB3J	AAC	3	18	CAAGACACAATACCAACTCACTTG	62.059	TAGCCGACAGTACCTTTTGTTC	62.957	136
HM_7203	GD2OF4R02I628H	GTG	3	12	TTACACTGACATCCCTTGAGAGACA	63.026	CACATGCTTTTGTGATGACTCCAC	63.078	105
HM_7204	GD2OF4R01CCMBO	TAA	3	12	TTCTGTATTGTTCTTCTCTCTCT	61.476	TGACAATTTTTGTATCAATTTGTGTG	61.162	109
HM_7205	GD2OF4R01EZPET	AAAGGC	6	30	AAAATCAACAGTGAACCAAGAAA	62.139	CTATCCCAATGATTCCTATGCTA	62.397	123
HM_7206	GD2OF4R02IC3LZ	TGGTAT	6	24	AAAATGGCATTACGGGTCTCAGG	63.141	TTTGGATACAAACATTTTTCGATGG	62.932	151
HM_7207	GD2OF4R01BNTWZ	GTTGAA	6	48	AAAGAGGGAATTTTGGAGAAAGCG	62.992	CAAATTAAGCGACCCAAAGTCATC	63.03	145
HM_7208	GD2OF4R02IXPY1	ACAAAA	6	24	AAATGGAAAAAAATTTGCGCC	63.139	AAAGGCAAAAAATAGAAAAACGAAA	62.311	151
HM_7209	GD2OF4R02GJ3CD	AGGCAC	6	24	AACAGAAATTTTGGAGCAGCAGAG	63.142	CTCTCAACATGAGATTGTGCTCTCA	63.829	89
HM_7210	GD2OF4R01ANOR7	GTGGTT	6	24	AACGTGATTGACGAGGTGAGAAT	63.242	GCTTTTGCAAGAGACACTGAAACA	62.972	132
HM_7211	GD2OF4R02H8CCZ	CAACAC	6	24	AAGGAGAAACAGGTTGATCAGCAG	63.124	GGTGATGCTAGAAGATCTGTCGCT	63.26	109
HM_7212	GD2OF4R02J3J28	TATATG	6	24	AATACCAATTCGACAAACCAACCA	63.428	CTTTTCCGAGAAAGAAATGACCC	63.261	139
HM_7213	GD2OF4R02FSM6H	ATGAAT	6	24	AATACCATCCGACAAACCAATCT	62.974	AAACGTGCGCTCTTTATATCAC	62.502	105
HM_7214	GD2OF4R01C392I	ATATAC	6	24	ACCGAAAAAAGTTGAGAACAGCTTC	62.229	GACAAAAACCGGCAACTCCAAG	62.921	104
HM_7215	GD2OF4R01C2FRG	ACTGAA	6	24	ACCGAAATCACTACAGAGGCTGAG	63.137	AGTCTCAGTGTGGCCTTCAAAATC	63.027	99
HM_7216	GD2OF4R01DBJAX	AAAAATA	6	24	ACCTCCATTTACCAATGACATGC	62.217	CAATTTCTTGTTCGCGAGTTATC	63.03	144
HM_7217	GD2OF4R01A7HYE	AAATCA	6	30	ACTGGAGGAAAAATGCAAAAGACA	63.227	TTGTTGATGTAAATCGAGTGTTCG	63.379	143
HM_7218	GD2OF4R01DJ1XP	GAGTGT	6	30	ACCTTCACACCACTCATCTCTCC	63.015	ACCACTGTGCGGGTATTCTTACAT	62.949	121
HM_7219	GD2OF4R01CZ14B	TGAAAC	6	24	AGAGCACTACTCAAAACCTCAACC	62.195	AGGCATATATCTCCGCTCATCTGAA	61.323	155
HM_7220	GD2OF4R01DIU62	TTTTCT	6	24	AGTGGTAAAAATCAAGGAGTCGGT	61.409	ACAAACGAAGAACAAAGTAGACCTAAC	60.662	134

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7221	GD2OF4R02GJQVD	TACATA	6	24	ATACACAGATATATTCCCGCTGCG	63.142	TGCCCATTAATTCACATCTCATT	63.499	160
HM_7222	GD2OF4R01DVFK4	TAAAAA	6	30	ATAGGGGGTACCACAATCCCGATA	63.569	TGTGACTGAGACTTCAAAATTCAGC	63.057	156
HM_7223	GD2OF4R01A66TO	AGAATT	6	30	ATATATGAAAAACACAGGGGGAGG	63.266	CGAAGTTCAGCGAGGTATGAGAC	62.291	150
HM_7224	GD2OF4R01CEOLH	ACAAAA	6	24	ATCTTGCTTTCCAATGGTTGTCT	62.62	GGGTGTTTAATGGTTTTAGGTTTGG	62.729	154
HM_7225	GD2OF4R02IKQTA	GGAGCT	6	30	ATTCAAGAATCTGGGCAATCCAT	63.988	TGGTGTCTGCACATAATTTGCTC	63.397	83
HM_7226	GD2OF4R02G36Q0	TTCTCT	6	30	ATTCATGCTTTGACCCACAAGTTT	63.035	GCTTTTTGGACACAGAAGATGATG	62.19	138
HM_7227	GD2OF4R01AXX3S	GGGTCT	6	24	ATTGTTTTTGGATGATCCGACAGT	62.913	CTCATTCCCACACTACAGCTTTC	63.388	152
HM_7228	GD2OF4R02H2MHO	ATGCAC	6	24	CAAAAAATCTTAAAGTGAAGGAAGAGA	60.758	TTTGTCTTCTACCTAATGGGTTTCAA	61.184	151
HM_7229	GD2OF4R01BNMPD	AGAGTG	6	42	CAACAAAAACCCCTCTCTCTTGTG	62.424	ATCAGTCTCTCACTCTCACAGGGG	63.329	134
HM_7230	GD2OF4R01EKSJD	CTCTTA	6	24	CAACTCCAGATGA AAAAATCTG	63.048	AACAATGCCCCAAGAGAATCTCT	62.788	139
HM_7231	GD2OF4R01B772L	AAAAAG	6	24	CACAAAAATCGATACAGGGTAAACA	61.275	CTGGCTAAACTCAATATTCGGACC	62.233	160
HM_7232	GD2OF4R02HQ8EL	TTTTCT	6	24	CACAGTGAATGAAAGGAACCTTAA	61.748	TCCATTGCAAAAGAAAATAGATTAGAAA	60.881	153
HM_7233	GD2OF4R01DPNTD	ATTTTT	6	30	CCGTAATGTATGGCTACCGAAT	63.15	TCATAAGTACGAAAGACCACTTCAACC	62.854	99
HM_7234	GD2OF4R02GMJYC	CCAAAT	6	24	CAGAGTACCTGGACAGGCCACTAT	62.922	GATTTTAGTGCCAAAGATTGGTG	62.922	149
HM_7235	GD2OF4R01CZCS1	CAACTC	6	24	CAGCTTGCAGAGTAGAAGGAAGAC	62.946	TCATGTGTTAAGTCTCCAGACGCAC	62.948	148
HM_7236	GD2OF4R01DYA56	AAATAA	6	24	CCAACGATTATCCCAAAATAA	60.876	ACAATTTGTTTTGATTGTAGCAACTT	60.33	154
HM_7237	GD2OF4R01D4STG	ATCTGT	6	24	CCCAAAAGCTCTCATACATCTCTCG	60.637	TCCCCTAATACGCTGTCCATAG	60.344	134
HM_7238	GD2OF4R01D8XQ4	ATATAC	6	30	CCGTATCGAGATCTCATGTGCAAC	63.385	GTCCTCCTTGAATCGCTTAACTT	63.102	149
HM_7239	GD2OF4R02JGH64	TCTTCC	6	24	CTCATCTGCCTCAGATTTTGCACT	63.035	AGGGGAGGGTACATTAGGAATTGA	63.065	109
HM_7240	GD2OF4R01CF9MN	GAACAG	6	30	CCTTGTTCATGACTAGCACCTCTT	63.023	ACTCGGAATTAGCACATCGGAC	62.595	159
HM_7241	GD2OF4R01EKTTP	ATGGAG	6	36	CGATCGAATACGTACGGAGGTAAC	62.947	ATTAATTCTCTATCCCTCGCTCGG	62.995	143
HM_7242	GD2OF4R02FVZ53	CGAATT	6	24	CGATTATCGAAGCTTTGGATTTCA	63.516	TTCGAATTCACACCACTTCAATT	62.909	98
HM_7243	GD2OF4R02FLF03	GTCTCT	6	24	CGAGGAGAAATTCGTCATATAGTT	62.607	GCAACGTTTGTGGAGAGTAATCAA	62.452	158
HM_7244	GD2OF4R02IAQD5	AAAAAT	6	24	CGTTCACTGGGGAATAATCATC	62.791	CTTTTCTATGAGAGCCCTTCGAT	62.992	142
HM_7245	GD2OF4R02JEFBJ	CATCTC	6	30	CGTTGTACCTTGGATGCTCTCTTT	62.958	AGACATTTATGCCCTGTCTATTGG	63.329	88
HM_7246	GD2OF4R02GWSDN	CAACCC	6	30	CTCTAGACAGATTGAAAAACCC	63.369	GTGTGTAGCGACTGTGAAGCTTTG	63.427	133
HM_7247	GD2OF4R01CYMRW	CTGTGG	6	24	CTGAGCTCTGTTGTGAGGAATAA	63.049	ATCTCTCTCTCCACCCCACTCT	62.964	96
HM_7248	GD2OF4R01AR4SL	CATTC	6	48	CTTCCATCAAGACCAATAACCCCTA	62.481	CAGAGGACTATGCGGACTTTGATT	62.923	111
HM_7249	GD2OF4R01EYLSI	TCTTCA	6	24	CTTCTCTCTCTCTCTCTCTCGG	63.16	AGAGAGGACAGGGCAGACATTCTT	64.049	150
HM_7250	GD2OF4R01BR0V7	CTGTGA	6	42	CTTTATAGGGCCGCGCTCTG	63.101	TGGTGGATCTATGCTTTTGTCTCA	63.038	136
HM_7251	GD2OF4R02J6BII	ATTTTT	6	24	GAAACTTTTCAGAAATTTGGGGG	63.068	AAAGAGGGCTTGTAGCTCTCAGA	63.999	111
HM_7252	GD2OF4R01D88GT	AACCGA	6	24	GAACCGAAATTTACACACTCCGA	63.432	AATGGTTCGGTTCAGTGTGTTTT	62.933	85
HM_7253	GD2OF4R01CV1IA	TATACA	6	24	GAATAACAGTCAGCTCTGCGGAT	63.051	CTCTCTCGTCTGAAATCTCTCCG	62.997	103
HM_7254	GD2OF4R01DLKUH	TCTCGG	6	24	GAATTGAAATGAACTGCAACACGC	63.057	CACCATCTACATCTTATTTCTCGCG	62.37	130
HM_7255	GD2OF4R01CNT6P	TTTCTG	6	30	GACCATGGCGGTGATCTCAAT	63.229	CATGGAGGTTCAAAATTATAAGCGA	62.463	147
HM_7256	GD2OF4R01DXAW2	TATATG	6	24	GAGCTCATGCACTGGAGCTG	62.022	AGGACAATTTTCAGGGGTACAAAA	62.013	154
HM_7257	GD2OF4R01ES2GF	TGGAGG	6	24	GAGGAGGAGGTGGTAAAGGCTTAT	62.208	CCTCCACTATTTCTCTAGACCC	62.562	124
HM_7258	GD2OF4R02J49P	TAGAAG	6	24	GATGTGCAAGCCAGAAGAGTTT	63.048	ACAGGGACGGTAAGATTAGGGGTG	63.201	123
HM_7259	GD2OF4R01BVSKO	TGGAGG	6	24	GGAGGAGGAGGTGGTAAAGGCTTAT	64.919	CCACTAGACCTTCTCCGCGG	64.375	103
HM_7260	GD2OF4R01CFFLW	GTCTGT	6	30	GGCACACAAATTTGGGACTACTGT	63.462	CAGAGTTCCCGGACTGACCTC	63.451	142
HM_7261	GD2OF4R02HYTBM	TCTTCA	6	24	GGGATTTTCCCAAAAGCTGTCT	62.773	TGAACGTCAAGCTGAAGGAAGAA	62.724	154
HM_7262	GD2OF4R01CMGCM	GGGTGC	6	30	GGGTTGGGCACACATCTCTC	62.881	GACACATACGTATAGGATGGCAAC	63.673	144
HM_7263	GD2OF4R02IDLIT	ATCGAG	6	36	GGTTTCACTGAGGGCTATGACAAT	62.713	ACCACCAACCAACTACCTACGTC	62.525	132
HM_7264	GD2OF4R02FNDXR	TGTGAT	6	24	GTAATTGTTCAACTTTACCCGCGAA	63.346	GGCAATCTCTCTTGAACACCTTA	62.91	110
HM_7265	GD2OF4R01DJMZI	AAAAAT	6	24	GTGAAAAATGGTGAATTCACACTC	60.834	TTCGAGTGAATTTTATTTGTGCTTAA	60.495	154
HM_7266	GD2OF4R01B489L	ACAAAA	6	30	GTGAACATGCTCAAGAAGAAAGCA	62.962	GAAGGATTGGGCTTGACAGCATT	62.744	129
HM_7267	GD2OF4R01CDNUD	CAATGG	6	24	GTGCTGATCAGAGGAAACAGAGG	63.661	AGCTTGTTCAGAGGATGTTTCAAT	63.468	141
HM_7268	GD2OF4R01BZVKO	CTACCA	6	30	GTTCTTATAGTCTCTGATGCCAG	63.133	GCGCATAGGACACAAAATTAGCA	63.396	160
HM_7269	GD2OF4R01ASEND	AGGCGG	6	36	TATACAAACTAGCCGACCTCTG	62.728	GTGATGTGTCAGGAAACCAAG	62.933	156
HM_7270	GD2OF4R01A8NV8	AAAACA	6	30	TCATGGGAGGTTACTAATTATCCCTA	60.525	TAATTGTCGGGATTTCTATCTTG	61.194	151
HM_7271	GD2OF4R01CF19T	TATATG	6	24	TCATTTTCCCATCAAAATATGACAA	62.425	CACCTCAGTGTCTCGGTAAATGGG	62.93	118
HM_7272	GD2OF4R01BW4V9	TTCTCA	6	24	TCCATTGGGCTGAGAAATCTTTT	63.196	ACCAAGGAACATTGGAGCAAAATA	62.922	160
HM_7273	GD2OF4R02FHT00	TCACAC	6	24	TGCACACAAACAAACAGATCAA	62.741	TGTGTGTCGAGTGTGAGTGTGAG	62.468	133
HM_7274	GD2OF4R01BZLF0	GGAGAG	6	42	TGCTAAAAGAGAAATGATTACGGAGA	62.484	TTTGATTGAAGGGAGCTCTACAC	62.91	100
HM_7275	GD2OF4R02H055S	TCTCTA	6	24	TCTCTATTGATCAGCTTCCCAAC	63.013	AAGAGAAAGCCATGGTGTGTTAG	62.822	156
HM_7276	GD2OF4R01B9PBN	TTTTCT	6	24	TCTTTCTGATTGGTGTGTTGCTGT	62.206	TCAAAATAGAATGATGAGCTACCA	63.062	154
HM_7277	GD2OF4R02I614V	TTGTGT	6	48	TCTTTGTGCTGTTTTCTTGCTG	62.754	CTAAGTTGAGCCCAACCTTAGGTC	63.493	160
HM_7278	GD2OF4R01DAQ00	TTTTCT	6	30	TGAAAAACCTTTGGCAGCTAAAAA	63.134	ACAGTTTTTAAACCAACCCCATAG	63.28	99
HM_7279	GD2OF4R02G5PI6	TTTGCT	6	24	TGAAGACAAATCTCAGAGTGCAG	63.04	CATCCATACATTTTGGGAAAAGGA	63.089	159
HM_7280	GD2OF4R01CHF6S	TGTTGG	6	24	TGACTGTGTCATCTCAGTCACTAA	63.076	ATTTTACCCCAACCAATACCAAT	62.514	83
HM_7281	GD2OF4R01BYD83	CTTCAT	6	24	TGAGAAATGCTCACTATAGACTTGTCC	62.489	GCGTTACTGGGATCTAGTGTTC	63.268	160
HM_7282	GD2OF4R02JBNVJ	GGCTCT	6	24	TGAGCTCAATCCGATGATGA	60.315	GTATATGAGGGGGAAAGATGGATT	60.598	138
HM_7283	GD2OF4R02FSKLI	GTTTCT	6	24	TGAGTAGGAAAGGTGTTTGTAGG	62.793	TGATCATCCCAAGATTATTCACGA	62.693	109
HM_7284	GD2OF4R02G9GRZ	TTTCTT	6	36	TGCCGTCTTTTGTGCTTTCTATT	63.252	CGAGTTTTGAAAAGCAAGAAAAGG	62.558	104
HM_7285	GD2OF4R02JXS01	GGATTC	6	24	TGGACCTTACGAATCTGATACTGG	62.619	ACAGCTCACAGTCAGCCACTTATG	62.975	153
HM_7286	GD2OF4R01ARQUL	TGAAGA	6	24	TGGATAATTGTTGCCATGACAGT	63.171	CATGTAACCTGTCATTTTCATTCA	63.182	99
HM_7287	GD2OF4R02G3BKH	TATCTA	6	24	TGGGGATGGTAGTGCTAGCAATAT	62.828	ATCAAGAGGAGGATCCCTCGTAAG	63.169	147
HM_7288	GD2OF4R01ALD8S	CAAACT	6	24	TGTAGCAGCATCAACATCTGACCT	63.304	CCCTTAACTTGTCCCTCTGTT	63.562	133
HM_7289	GD2OF4R02GMSDP	TAAAAA	6	24	TGTGTTTTGCAAAATTCAGCAATC	63.283	GGGCCAATTTAATAGCAAGAA	62.463	150
HM_7290	GD2OF4R01CGFCK	AAACCA	6	24	TGTTGTCAATAAATGTGCGTTTGG	63.175	TCAGGGTTTGTGATGATGAGTCGG	62.619	119
HM_7291	GD2OF4R01EL0UU	CCGTGC	6	24	TTATGTCAGCTGTCAAGTTCGTA	62.77	GGATGAGATGTTTCTCTCTCTCT	63.062	158
HM_7292	GD2OF4R02HSEVN	CGGGGG	6	24	TTATGTTGGTTAGGGTGGGTGAC	63.117	TCTTTGGTTTTGTGATAGGATGG	63.307	148
HM_7293	GD2OF4R01EEZL6	CATCTC	6	24	TTCACTGTGCGGTGAATTTGTC	63.3	TGGCCACAAAAGAGTGAATTAATA	62.941	152
HM_7294	GD2OF4R01BDHZQ	CAGAAG	6	30	TTCTCTTCAGAATTCAATCTCTCC	62.397	GTACCTTGAACCCCACTTCT	63.086	96
HM_7295	GD2OF4R02H2U45	ATGTCC	6	24	TTTTTCTTTCAGGAACATGACCA	62.051	TTTGTAAAGGTAACCACTCATCAC	61.241	156
HM_7296	GD2OF4R02HCC4B	AAAT	4	16	AAAAACACAAAAGGATGGGAGAAATA	62.181	TCACACTCTTTAGCTCTTTGTTTTG	63.14	140
HM_7297	GD2OF4R02JNLLN	AATA	4	16	AAAAACACCGTGAATCTCTATGA	62.922	CCCATTTTCTGCATAACATCTCC	62.912	90
HM_7298	GD2OF4R01DWECX	ATAA	4	16	AAAAACCCCTTGAATACCGGACTT	63.192	TTTTTGCATCACTATCTCGATTTTT	63.123	119
HM_7299	GD2OF4R01C7NKM	AAAC	4	24	AAAAACGACTTATCTCTTTTCTCTTTT	60.338	TTAAACCAAGGTTGTTTTGAACTT	60.669	227
HM_7300	GD2OF4R01EBF8P	TGTT	4	16	AAAAAGTATTAGAAGGATACATCGAGAA	60.86	GTGATTTATGTTGTTTTCGCGC	61.579	147
HM_7301	GD2OF4R01D5174	AAAT	4	16	AAAAAGTCTGCTGTGTTTTGCTC	63.057	AGCTGTTTGAATCACGAATGCA	62.872	160
HM_7302	GD2OF4R01CV25M	ACAA	4	24	AAAAACTGAATTCGCGCAACAA	62.839	CATTCACTTCCGTGAGGAGAGAT	63	128
HM_7303	GD2OF4R01BGMT9	TCGA	4	16	AAAAATTAACCTTCCGATGGCTCT	63.312	ACTGTTGGAGGAGGAAAAATGATCT	62.59	141
HM_7304	GD2OF4R01BR20U	AAAT	4	20	AAACAAAAAGAAATAATGACAAATGGA	62.064	GGGGGCAAGTTCACAAATTTT	62.248	140
HM_7305	GD2OF4R02I601W	TCCA	4	16	AAACAAAAAGGAAGGAATGACCC	62.876	CTCTTTTGGCGATGGAATCTTAT	62.947	128
HM_7306	GD2OF4R01EP0H9	AAAG	4	16	AAACATGCATACACAAATGGAA	60.508	CCCACTACTCTACTTCACTATCC	60.618	159
HM_7307	GD2OF4R01E0WDC	TTTA	4	16	AAAGTACATGGGGTAAGTGCAAA	62.836	CCAACGCAATAGACTGTCTACCA	62.541	154
HM_7308	GD2OF4R02I14TE	ATAA	4	20	AACCCAATTCACTTTTGTATCT	63.078	ATTGTTTTGTTGCGAAAAATGCC	63.245	145
HM_7309	GD2OF4R02H7680	AAAG	4	16	AATTACAACCATGATTCATGTCC	63.003	TTCTCATGTTTCTGTTGCAAGTG	63.173	150
HM_7310	GD2OF4R02HRVH7	TAAA	4	16	AATTGTGTAAATCCAATCGCAC	63.353	TCTGCTGGAATGTTTTTCTGGTT	63.227	158
HM_7311	GD2OF4R02F9YF6	TATG	4	16	ACAAACCCCTCAAGGCTAAATCACT	61.523	GTAGCTATGAATGTGATCATCCGTACA	60.532	135
HM_7312	GD2OF4R01CNA1U	AAAT	4	20	CAAGTGAACCAACCCAAAGAAA	63.015	AGCTCAACAACTGCTAAGATTGG	63.044	118
HM_7313	GD2OF4R02GCK52	AAAT	4	16	ACAATAGCACGGAAGAAATGCCAA	63.231	TTCAAGTCACTGGATTTTTCGTA	62.956	96
HM_7314	GD2OF4R02H4EIQ	AAAG	4	16	ACAATTTCTTCAAGGCCAAACAA	63.027	CGGTTGTTGAAGTTAGAGGTTCCG	63.23	149
HM_7315	GD2OF4R01C74PV	TCAA	4	20	ACACCAACCAATGAAGCTCAAAAT	63.035	GGCGAGTAGGGTGTGATGTATGTC	63.039	102

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7316	GD2OF4R01B6GOC	AGTG	4	16	ACACTGACGTAACAGAGTGCAGAAA	63.311	TTTATTGTTGGGTCCCATGTGCT	62.703	128
HM_7317	GD2OF4R02GNBLR	TCTT	4	16	ACATGTGTTGGACACCAAGTAT	63.514	ACAGACAATTACAAAGGCCACACC	63.462	126
HM_7318	GD2OF4R02HRUGD	TCGA	4	20	ACACCACCGCTTAATAGTGTAA	63.873	AGGCATTCTGCTCAAGGGTTTCTA	64.509	103
HM_7319	GD2OF4R02CAHH	CAAA	4	16	ACCCGTGATAGTAGGGTGTATC	62.439	CACAAATTGATTAAGAGTTAGAGGG	61.676	158
HM_7320	GD2OF4R01B1P4A	TCCG	4	16	ACCGAATATTACTCCACCTGCAC	62.536	TTTCTTTTCAAGATTCTCACCCC	62.798	91
HM_7321	GD2OF4R01ACXW8	AAC	4	16	ACCGTAACGTACCAACCAATCTA	61.724	CGTCTCTCTGTACGAGACTCACT	61.34	112
HM_7322	GD2OF4R02GO6X1	ATAC	4	20	AGAAAACGAAGTGAACCAATGA	63.117	CCGATTTTAAAGAGACTGCAAGGT	62.729	158
HM_7323	GD2OF4R01EYEH	TTCC	4	16	AGAAGATGAAGCTGTATGGCTGT	62.727	CTCGTCTTTAGGACCCCTCACTCT	63.391	159
HM_7324	GD2OF4R01C6OVD	AAAT	4	16	AGAGAGGGAGAAGATGTTCCAAAC	63.278	GGCTATCCACTTTGATATTCTTAGCCT	63.193	160
HM_7325	GD2OF4R01A188S	AGAC	4	16	AGAGGTTCAATGCCAACAGATG	63.027	ATGCCAATGCTGTTCTTTTCAAT	63.046	101
HM_7326	GD2OF4R01B9GK2	AACA	4	16	AGATCACACCTTACAACTCACCCC	62.484	TTGTTGTAGCTCTCCCTTTTGTG	61.813	134
HM_7327	GD2OF4R01A15X6	ATAG	4	20	AGGAAATACTCACTCTCTGCAACG	62.933	ATTACGGGGACCTTTCTCTCTCT	63.739	141
HM_7328	GD2OF4R01EV229	TTTA	4	16	AGGAGGGTGATAATGGGTTTCAA	63.866	CATGGATGAATGGATGATGTCAA	63.897	145
HM_7329	GD2OF4R02JM0DV	ATTT	4	16	AGGCTAATTACCAATCAATCCCT	63.188	TAGAATGGCAACCAAGTTGTCTCT	63.129	140
HM_7330	GD2OF4R02J075O	ATAG	4	16	AGGGTTGGACTGAAACAGAAAT	63.285	CGCTTCGGACTCAATTTATAGGTG	63.134	118
HM_7331	GD2OF4R02FKK5R	TACA	4	20	AGGGTTTTATTACACCATAGGCA	62.826	TCAGCGTGAATAATGTGCTCTC	62.76	91
HM_7332	GD2OF4R01CS9QW	TGTT	4	20	AGTGTGAGAACTGTTGGCGGTG	63.893	GGCCCTAAATTTTGTCTCTCTCA	63.665	131
HM_7333	GD2OF4R02G9RL8	AATA	4	16	ATACAAGCACCAACCACTAAAGC	62.659	ATCGTGATGATCAGTGGAAATGTG	62.82	113
HM_7334	GD2OF4R02H22R6	TTTC	4	16	ATAGCGACAGATCAAGGAAAGGA	62.509	TTCTTAAGAGAGTTGTGCTCCCCA	62.993	123
HM_7335	GD2OF4R02H4NY2	CAAC	4	16	ATAGCGCATGTTTGGCTCAATTT	62.903	TGTTTAAGCTTTGGAACTTCTCTC	62.028	91
HM_7336	GD2OF4R02IR1AY	TTTA	4	16	ATATCACTGTCCCCCATGTTGAC	62.118	GGCAGATTAAAGTACGCGATG	62.964	160
HM_7337	GD2OF4R02IZIR5	TATT	4	16	ATCACAGAGTACGGGGACAAACAT	63.027	GCCTTTGGTCTGCTCTTTTAATG	62.451	128
HM_7338	GD2OF4R01AGSRE	TGTA	4	16	ATCTCTCTCTTTCTGGATTGGGA	63.459	GGTTCATTTCGATCACCATAAT	62.944	137
HM_7339	GD2OF4R01AUBW1	TAAA	4	16	ATCTCTGTGTTGGGATCAAAATTA	62.802	GTCCCATCTGATGCTCTTTTGTG	62.838	102
HM_7340	GD2OF4R02HD9FO	TCGA	4	16	ATCGGATCGATTGTGCTCTTTTG	62.693	CCATCTCAACAGCTAAATGCTCGG	62.911	113
HM_7341	GD2OF4R01B910L	AAAT	4	16	ATGTTGACGAGAAAGAAATACCCCT	63.196	ACTGCATAAAGGTTGCAGAGTTCA	62.339	132
HM_7342	GD2OF4R02GMH03	ATTT	4	16	ATTAATAAAGGACGCGAAATGGCT	63.127	GAACACCTTTTCTTTGTTGGCT	62.91	131
HM_7343	GD2OF4R02GJDZ0	AAGA	4	16	CAAAATCTGAGAAGATGCAAAATC	61.262	AAATTCGTAAACCTTAGATTTTCC	61.168	153
HM_7344	GD2OF4R01A5QXW	TCGA	4	16	CAAGCGCTCGAGTAATCAAAGTT	63.064	TTACACAATAATGTTTCTGCTCGT	62.995	109
HM_7345	GD2OF4R02FL7DV	AAAT	4	16	CAAGTCTCTGCTGATGTAACCA	63.03	GTTCGATCAGGATTTGTCTCT	62.962	131
HM_7346	GD2OF4R01C8BTL	ACAA	4	24	CAATATGCGGAAGCTCTATAATC	62.938	CAAGTCGTAGACACAATGTTAAGCTGT	62.035	120
HM_7347	GD2OF4R02JN23K	AAAG	4	16	CAATCGAAACCAATCTAAAGCCAC	63.03	TTTCAACTAGACACTCCCCCTTG	62.793	158
HM_7348	GD2OF4R02H1G93	CAAA	4	28	CACAATGATCCATCAGGATAGTGT	62.924	AGGCAAAACCATGAATAAGTGAGG	62.619	159
HM_7349	GD2OF4R02H2MFO	AACA	4	16	CACAGATATGGCTAAAAGTGCCAA	62.453	TTGCATCTTTGTTTATAGGGCAAC	63.439	155
HM_7350	GD2OF4R02F3M20	AAAT	4	16	CACCAAAATGAAGCTCAATTC	63.311	TTTCACTCATCTCAAAATTTTCCA	63.004	155
HM_7351	GD2OF4R02FPJFO	TACA	4	28	CACGGAACAATAAACCAACGAAA	63.064	GGAGGTGATTCTCTCAACCTTTT	63.071	147
HM_7352	GD2OF4R01AU9FB	GCCA	4	16	CACATGTGCTGGATTAAAGGGGC	62.077	GTGAGGAGAGATATTATTGTTGGG	62.887	84
HM_7353	GD2OF4R02IAXDO	ACGT	4	32	CACCTCTCTGCTGCTGCTCTCT	63.376	TACGGTACGGTACGGACGGA	63.502	206
HM_7354	GD2OF4R02IAXDO	CGTA	4	16	CACCTCTCTGCTGCTGCTCTCT	63.376	TACGGTACGGTACGGACGGA	63.502	206
HM_7355	GD2OF4R02IAXDO	CGTA	4	28	CACCTCTCTGCTGCTGCTCTCT	63.376	TACGGTACGGTACGGACGGA	63.502	206
HM_7356	GD2OF4R01BGA3D	TCTT	4	16	CAGAACCTCTTGATCACACAACCTG	62.176	AAATAGGTTCTTGTCTTATGAC	61.484	149
HM_7357	GD2OF4R01EFLTV	AAAT	4	16	CAGTGCCTCTCCAGTACCTAA	61.791	TAGAAGAAGTTGGGCTGCTGTG	62.645	150
HM_7358	GD2OF4R01BIUHC	TTTA	4	16	CAGTTGTGCTCAAGAACGGTTTAA	62.654	TCACAAAGGTTGAAGACATGGTA	62.814	134
HM_7359	GD2OF4R02JTB8	CTTT	4	16	CATGAGACAAGAGATGTCATTC	62.832	CCACACCTTTGCCCAATATAAGAG	62.919	132
HM_7360	GD2OF4R02JFA7N	TTTC	4	16	CATGATTCAAAATTCACAAACAA	62.943	ACTTTTGGCATTTTCCACAAAC	63.044	131
HM_7361	GD2OF4R02JNX24	ATAA	4	16	CATGGGAGCATATATCAAGAAAAA	62.344	TTTGTAAATCCACCTTTGTTGCT	62.932	100
HM_7362	GD2OF4R01DRLNG	AAAT	4	16	CACAACTTAGGGTTGACAACTGTG	62.636	GGGGAAGTTGTGAAGTTGTCAATTA	62.922	158
HM_7363	GD2OF4R02GE91V	CTGC	4	20	CCAAAGAAGCTGTGCTGACTCTC	62.828	CAAAATCAGACAATGCTGGACAG	63.048	135
HM_7364	GD2OF4R02FQAGL	CAAT	4	16	CAAACCTTCTTAATCTCTAGC	63.534	AGGATGTGGTGAATAGTGGTTGT	62.912	82
HM_7365	GD2OF4R01EQAN5	ATTT	4	16	CCAATGCATGGTCAAAAGTGGAA	63.046	CGCTGATTTCTTAAAGTTGCGTGA	62.172	149
HM_7366	GD2OF4R02GZGK8	AATT	4	16	CCACACCCCTTAGGCTTAGTTTT	62.816	TGCTTGGGCAAGCTTATTACT	63.348	139
HM_7367	GD2OF4R02HLOFH	AATA	4	16	CCACACACAAGCTCCCTCTT	62.472	TTTGACACTTGTACCATGCATCT	62.844	136
HM_7368	GD2OF4R02IRMW2	AAGA	4	16	CCACGATAGAACTATGAAGTTGC	61.923	TATGGTGGCATTTTGAGGATGAA	62.525	111
HM_7369	GD2OF4R01ELQOF	AACA	4	16	CCAGTAGCTGGAATGTGATTGTTCT	63.144	TGGAGGAAGATGGATGATCAAGAA	63.394	154
HM_7370	GD2OF4R02FTXVP	TTTA	4	20	CCCTATTCTCTTGAGCATGTGTG	62.811	TGAAGGCTGGTACTTTTAACGAAA	62.292	145
HM_7371	GD2OF4R02JNL6R	AAGA	4	16	CCCTCTAGTTCTGCTCTGGAAG	62.906	GTAATTGGGACCTCTCAATTTCCGT	63.589	139
HM_7372	GD2OF4R02FQU85	CTAT	4	20	CCGGATCAAAACATCAACATCA	63.15	CTTTCATAGTCGATGCAACAGAGA	62.831	129
HM_7373	GD2OF4R01CBGB2	TCAC	4	16	CTATCTGTTGTTGCTCCAAATAC	62.152	GAGCTATTTGGTGTGTTTGAT	61.552	133
HM_7374	GD2OF4R02FUONI	ATAA	4	16	CTTTTCTCAACTCTCAATTTGCTG	63.42	GCTGACTTCCCGGATACTAAAT	62.81	151
HM_7375	GD2OF4R01B8TPX	GATC	4	20	CGAACTACAATCGATTACATCCA	63.257	TTGTGTTTCAGGTGTGCTCTCTC	62.947	84
HM_7376	GD2OF4R02IMU6O	TTTA	4	16	CGCACCTTAAATCTCACTTTTGTG	62.37	CCACGGATAAACCAATTAGAAAGC	63.022	155
HM_7377	GD2OF4R01BOKEN	AAAC	4	20	CGTGTCTGCTTGGAGATTAGAG	62.309	GATAAACAAGCACGATGCAATAA	63.203	112
HM_7378	GD2OF4R02F8NJS	ATAC	4	16	CTACATACAAGCAGCGGCACATAG	62.77	TGTTGGACACCATTTGCTATTATC	62.291	159
HM_7379	GD2OF4R02HCGD5	TAAA	4	24	CTACTTTAAACACAGGGGGTGA	62.507	TAAATTTCTCTTTGTTGCTCGCA	62.723	160
HM_7380	GD2OF4R01E1JZ2	GTGG	4	24	CTATGCTCTGCTGGGGTAGATG	63.039	TTTTGATCTTCTAGCTGGGGAC	63.877	87
HM_7381	GD2OF4R01BFDNU	GATT	4	16	CTATGCTTCAAGCTTCACTCTG	62.542	TAAGGCGAGGAAGTATAAAGCCC	62.923	155
HM_7382	GD2OF4R02I68BP	ATAC	4	24	CTCACATTGTCCTCTCACTCTCT	62.895	CACGTATATCCGCAAGAACCCAT	63.341	151
HM_7383	GD2OF4R02FSA5Y	CTTT	4	28	CTCCAAATGCTTCAACAAAAAC	63.027	GTCTTCGCAAAAGTCAAAAGTAA	62.439	149
HM_7384	GD2OF4R01AG643	AAAT	4	16	CTGTTCAAGCATCAACCTCCCTCA	62.724	GGAAGGTGCTGCTGACTACTATT	61.901	142
HM_7385	GD2OF4R01AESM9	TTAA	4	20	GAAACGAGCTAAGGAAGTGGTCA	63.031	TTGCTTGGTTAATTGACGAAAAGG	62.756	123
HM_7386	GD2OF4R02GP7WV	ACAT	4	40	GAAAGTTCACTAATTAATGGCGTG	60.177	TCCTGCTAGATGCAAGTACTCTC	60.402	122
HM_7387	GD2OF4R01C1PHD	AACC	4	16	GAAATCTATTGTCATAAACCCAAA	60.711	CATGGGTTCAATGAGAGCTCTAC	61.096	86
HM_7388	GD2OF4R01A0BBK	GATA	4	16	GAAATGGGAATTCACCAATCACTA	61.246	AATGTGTAAACAATTTGTAGCAGAGGT	60.452	156
HM_7389	GD2OF4R02I9QQ9	AAAT	4	16	GAACTTTAAGGCATCAACATCCA	62.921	TTGATTCCTGTCAAGTTACCAACA	62.814	126
HM_7390	GD2OF4R02JOEAT	TTTA	4	16	GAAAGGACCTAGACCAATTTCTC	62.563	TTGCTGAAATGATGGATTTTGTG	63.146	160
HM_7391	GD2OF4R01DFFO4	TAAA	4	16	GACACGAGACACAATCTCAATG	63.164	AAACCTTTTACTTTCTGATTCTTCC	62.408	99
HM_7392	GD2OF4R02G5WYF	AAAC	4	16	GACCTAAAAACACACAAGCAAGCA	62.67	GATCTGTATGGAGTGGTATCAATG	61.841	106
HM_7393	GD2OF4R02H4VQO	TGGT	4	20	GACCTTCTCCTGAACCTGTGCTAC	63.546	TCAACTACAACCTTCAACCAAAAC	62.722	103
HM_7394	GD2OF4R01ARCAI	ATAC	4	24	GAGTGGTTAAGCAACCAACACATA	63.336	TGATGGGTGCTTCTTCCAATAAGG	63.513	100
HM_7395	GD2OF4R01D88LH	TTTC	4	20	GATCAAAATCAAGTGGGTTTAC	62.9	GTTGTCATTACAAACACACCCCT	63.238	153
HM_7396	GD2OF4R01A9ROL	TTTA	4	16	GATGTTGACAGTTATGCTCGTTA	62.468	TGTATAGACATGATTAGTTTGCTCTGA	62.106	142
HM_7397	GD2OF4R02IDBIB	AAAT	4	16	GCAAAAACGATATGATGTTATGAAA	61.552	TGCTGAAAGATATGGGTGTAGCAT	62.022	142
HM_7398	GD2OF4R02J115J	TGTA	4	28	GCAAAATCTAGACCAAGATAGAATTG	61.8	AAGTTGGTGTGCTATGCAATTTG	62.369	152
HM_7399	GD2OF4R02G2G72	TTAT	4	16	GCAATTGCTAGTCCGATTGTGAAC	63.058	ACCATTGGAGAGTTCCTGGATA	63.194	105
HM_7400	GD2OF4R02FJPY2	TTTA	4	24	CGCGTAGAGAACTACAGGTTTACG	62.848	GTTCACCTCTGCTGAGGCTTTGG	63.345	155
HM_7401	GD2OF4R01B419A	AAAT	4	16	CGGTGACGATACCCATATTCAACA	63.181	CACAAAGTAGGATTACTCTGGGATG	63.199	141
HM_7402	GD2OF4R01B9M5Z	AATA	4	24	GCTATTCTGCTTTCTTTGCTT	63.221	GCTTAAACACCTTTTGGTACAG	63.247	139
HM_7403	GD2OF4R02JCXH3	TTAT	4	16	GCTCTGGAGTTTGGGATCTATT	62.986	GTGACTGCATTTTGCATTACAG	62.872	126
HM_7404	GD2OF4R02IUNC0	TAGT	4	16	GCTCTTAATGGCCCCCAATTAT	64.285	CCATTCTTGGTATTCTCTGGATT	63.36	99
HM_7405	GD2OF4R01ANLR2	CTAT	4	24	GCTTGAGTCTGAGCTTCACTCTC	62.727	TGCAATTCAATAAGGGAACAATCTG	63.325	87
HM_7406	GD2OF4R01CGLAS	ATAA	4	16	GGAATCCACGTGAACCATACATA	62.294	TGCTAAAAGGCTATTGTATGCTCG	61.827	102
HM_7407	GD2OF4R02IOWMY	AAAT	4	16	GGAGAAATGGAGCAACATCAAAAC	63.125	TTGATTTGGGAAATTTAAGGACC	63.357	123
HM_7408	GD2OF4R01A11LA	CATT	4	16	GGAGAATCATCATCAATTTCCATT	62.354	AACGTTTGTGATCGTATGAGGAGG	62.633	121
HM_7409	GD2OF4R01DPAHK	AAAT	4	20	GGAGTTGGATACACGTCAATGCT	63.567	GTTCTTTGGGTGCTGCAAGTTCTT	63.036	126
HM_7410	GD2OF4R02HIIDX	CATA	4	24	GGCGCTCAAGTGACATAAGACTTT	63.06	TCTCATGTTTGTGATGAATGCTG	62.289	117

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7411	GD2OF4R02HARGW	TATG	4	32	GGGTACACCCGAATGGAATAAGT	61.487	TTCCATTGAAACAAAATATTCTCC	60.712	157
HM_7412	GD2OF4R02IG33K	TACA	4	16	GGTCCTAAACAATTCGAGAAAACAA	62.558	CGGTATGTATGCAATGTGTAAATATCAA	62.009	149
HM_7413	GD2OF4R02H2789	TTAT	4	16	GGTTTCATACTTCCACCGCTTTT	62.425	CTAGATCCCTTCAATTTTCCGACA	62.621	149
HM_7414	GD2OF4R02GCW6X	GTTT	4	20	GTAAAAGCATTCCAAACGACAAGG	63.039	TGCATATCTGTACGCAAAGGAAGA	63.072	95
HM_7415	GD2OF4R02IZXH4	AGAA	4	16	GTACACACATTTGTTTGGCAATC	62.774	AAATTTGATCAGATGCTCCGCTGTT	62.913	149
HM_7416	GD2OF4R01CXN2	TAAA	4	16	GTATCAAGTGGCGAAGGCAAGTAA	63.659	AATCAATTCGCAACCTGCAATACT	63.115	136
HM_7417	GD2OF4R01ENDJ7	AGCT	4	16	GTCAATATTCATTGGATTGTGCTCT	63.228	GTCAAATTTGGGGAGATGAGGAAGT	63.578	110
HM_7418	GD2OF4R01DUIY6	GATA	4	20	GTTGTTTGCACATTAGGGACATGA	63.168	TCCATTTCTTGTGATTCACATCA	62.821	142
HM_7419	GD2OF4R02HSDS1	CATC	4	16	GTTGTGTTGCTTGTAGTCTGCGAT	62.783	ACCAACTGGAGTCTGCTGAATTTT	62.512	156
HM_7420	GD2OF4R01ETAN8	TTGC	4	16	GTTGTTGCTTCAGAACCATCTTT	62.824	GACCAAAATTTTCTTGGGTTCTCT	62.691	160
HM_7421	GD2OF4R02I73KE	TATG	4	20	GTTTCTTAAGGCAAGGCGCTAAT	63.046	GTCCTTTTCCCTAATTTGATCG	63.072	106
HM_7422	GD2OF4R01BLVNE	AATA	4	16	GTTTTGTTTGGTTTGCAGATTGA	62.34	AATGTTATTACGCAAAAGGAGGA	62.852	113
HM_7423	GD2OF4R01C62PX	TTTA	4	16	TAAAAATGATGAGTTGGAGCTGGG	63.517	AAAAATCCCAATTAACCAAGTGCT	63.004	106
HM_7424	GD2OF4R01CR4F6	CCGA	4	16	TAAACCAACCGGAACCCCTAAAAG	63.365	CAAGTGTAGGGGTGTAATCGGCT	62.921	144
HM_7425	GD2OF4R01EWBGD	AAAT	4	16	TAAAGACGCTCATGTTGGACAAA	60.729	TGGTAACATTTGAATATCAGCAACA	60.621	153
HM_7426	GD2OF4R02H9H79	AGTG	4	16	TAAACACGAATAGTTGGCTTTGA	64.04	AGGCATATTTGTCAGCGAGTCATT	63.261	145
HM_7427	GD2OF4R02FR7VJ	CTGT	4	16	TAGAGCCTAAATACCAAGGACCG	62.044	AATAAACATTTGGACCTCTCTCCA	62.17	107
HM_7428	GD2OF4R01ECQJ	GTAC	4	16	TATTCGATCTCAGTCTGGTGTG	62.712	CCCTACCTTTCTCTCTCTTCCA	63.058	143
HM_7429	GD2OF4R02GF29U	AATT	4	16	TCAATCAAGCCCTAATTTCTCTGA	63.101	TGGTAGTTTTGTGTTCTGTGACG	63.462	127
HM_7430	GD2OF4R02F7WJ	AACC	4	16	TCCAACAAAATTTTCAGATAGAATACA	60.453	TATTCATGAACGAGCAGCATCGAG	60.633	151
HM_7431	GD2OF4R01B109U	TTTA	4	16	TCCAGAGTAGTGAATAAGGGTTCACA	62.327	TGTGTTTCTGGGTCAATTGATGTT	62.712	138
HM_7432	GD2OF4R02J6CNN	AAAT	4	16	TCCGAAACCAACCAAGCTAAGGA	63.21	TGACGCGAAGCTAGAAAAAGAGG	63.234	142
HM_7433	GD2OF4R01DHW07	AAAT	4	20	TCCGCAATCCCAATTGGAGCAAGAA	63.209	GTTTTGCAAGGCATTATTGGTTTC	62.854	124
HM_7434	GD2OF4R01BMA4P	CGTG	4	24	TGAAAAACCAATCTTGAGGAAAA	62.989	CGTTGGTTAAACATCTACTCCCG	62.919	151
HM_7435	GD2OF4R01B0SYT	TTTG	4	28	TGAAAAATGGCGGAAATCTTTAA	63.022	CCGGCACTTAAGTCTCGTATGAA	63.641	124
HM_7436	GD2OF4R02I040L	AAAT	4	16	TGAAACCGACACAGACATTAACAA	62.931	TTCAGTGGTGGTGTGCATTATAAA	62.565	125
HM_7437	GD2OF4R02GV70R	TTCT	4	16	TGAAAGAATTTTGACAAGTGAAGTGA	62.37	TGCTTTCGACAGAATGCTAGAGG	63.05	89
HM_7438	GD2OF4R01BTKK3	TGTA	4	32	TGAAATTTGACTTATCTGGACACACA	60.793	ACGTTTGAAATTTGATTTGTGAAGTG	60.551	184
HM_7439	GD2OF4R01EYBYN	ATAA	4	20	TGAACCTATCTGCGCCCTTATTTT	63.084	GGAGCAAAATTTGAACATAGCAGTTG	62.212	158
HM_7440	GD2OF4R02JHP80	TTTA	4	20	TGACGGTCAAGTCTAATATCTCAGC	62.724	TGCGAGTTCTATAATTTGTTTTGG	62.259	193
HM_7441	GD2OF4R02GXB19	ATGG	4	16	TGACGTGACTGGCTCTCTGTTTAC	62.753	CTCAGTGCCGAACCTACTCGTTCT	63.258	158
HM_7442	GD2OF4R01BP2OW	AGTG	4	16	TGAGCTGCACACATAGCTGAAT	62.455	AATGAACCTCCCTCTCTGGTG	62.869	112
HM_7443	GD2OF4R02H8TD8	AAAC	4	16	TGATCATCTCCAAAGCTTCATCA	63.132	TTCTCTAAGGCTCTGGTGTGG	62.993	147
HM_7444	GD2OF4R01BDU88	AAAC	4	16	TGCAAGGAAAGAAACCCAGTTTAA	63.118	TATCGAGCTGAAGGAGTACTTGGG	63.019	150
HM_7445	GD2OF4R02JCTD4	TGAA	4	16	TGCATTGAATCTATGTTTGGTGCTC	63.154	TCACACTAGGCTCTCTTGGCATC	63.338	158
HM_7446	GD2OF4R02FV796	ATAC	4	32	TGCCAGCTGGTACCTACATTAATA	60.69	CACCTCAAAGATGATACAAGTACCG	60.346	148
HM_7447	GD2OF4R02IMSUT	TTTG	4	16	TGCTCTGTTTGTGGTGAGAAAA	63.159	CGAAATGCACTCTTAATCCGAG	63.122	154
HM_7448	GD2OF4R01C5BCS	TAAA	4	16	TGCTCTCTCCACCGTAAAAATAGA	63.122	TAATAATGATGCCGCTTAGGAGA	63.029	145
HM_7449	GD2OF4R02GIS31	TTTC	4	16	TGGATCAGATGATTGGAAGCTG	62.486	TGAGGGGGTGTGTTGTTGATGTT	62.918	147
HM_7450	GD2OF4R02HMH1L	CAAA	4	20	TGGGTGCTTTTGACAACTCTCTT	63.345	GGGTGAGGCTCCTTAAGAGCAAA	64.101	100
HM_7451	GD2OF4R02FSZXE	AAAC	4	16	TGTCAAAACAGCAAAAGAACATC	62.528	ATCGGAAGTGCATTAATTTTGT	62.937	223
HM_7452	GD2OF4R02HHQD5	AACA	4	16	TGTCGTACAGATAATACGCGAGA	61.009	TTATCGTTTTTGTGGTGAAGATG	61.06	144
HM_7453	GD2OF4R01C7WHN	AGTT	4	20	TGTTGATGGGCTAGACACACATTT	62.844	ATGTCCTAATTTCCACGACAGA	63.121	159
HM_7454	GD2OF4R02FL88F	AATA	4	16	TGTTGTAGCAAGGACCTACCAA	62.955	ACATTGAATTTCCAGCTCTCGAG	63.648	109
HM_7455	GD2OF4R01AREXQ	TAAA	4	16	TTACCACTTTCTTAGCCCAACAA	63.023	TTTGATTACCAAAACCAAGGGAATG	63.097	84
HM_7456	GD2OF4R01BGMCF	AAAG	4	16	TTCAACTTGGTTTTCTGGACACA	62.928	GCTTCCAATTCATTCATACAAATG	62.736	158
HM_7457	GD2OF4R01EBW8L	ACAT	4	28	TTCAATCTGCTCCCTTAATTTTCA	63.101	AAAGACATGCTCCGCACTAATAA	62.935	146
HM_7458	GD2OF4R01CQWQ6	AAAT	4	16	TTCTGAACAAAATGATTATCAACCGA	62.839	TAGGCCTCGTTTATGTGCTAGA	63.45	156
HM_7459	GD2OF4R01DMVIV	AAAT	4	16	TTCTTCCACCAATAAACATCAAA	62.72	TATTGAAAGGCCAACTAATCATGC	63.439	160
HM_7460	GD2OF4R01C4M9K	TTAT	4	16	TTCTTAGTTGATGGTGCAATGTC	62.412	ATGTCACTATGTACCCATCACGA	62.609	106
HM_7461	GD2OF4R02HAHZ7	AAGA	4	16	TTCTTTCCCTTTTCTTCCCTT	63.499	TTCTTTTCTATTGCTCATCGTT	63.126	105
HM_7462	GD2OF4R01EVONS	AAAT	4	20	TGGAAGGAAAAATACCAATACAAACA	62.865	TTGCGACTGAGAAAGGATACAGAT	63.341	110
HM_7463	GD2OF4R02IERO2	ATTT	4	16	TTGCAGTCACTTACATCTCTGGG	62.724	CCCAATACTCTCCCTGTTTGA	62.591	93
HM_7464	GD2OF4R02G5BID	AGAT	4	32	TTGCCACATGAATTGATGATACCT	62.618	TGAGGATCAGATGTTGCCATTTA	62.821	123
HM_7465	GD2OF4R02FN620	CAAA	4	20	TTGTTGACGCTGAAACATGTCTA	61.904	TGCCCTTAGTTTCTCTTCTTCTC	61.194	132
HM_7466	GD2OF4R02IVF08	TTTC	4	16	TTGTTTGGTAATCGTTTCCCTTTT	62.919	TTCCGATTCGGTTTGTAAATTTCT	62.989	240
HM_7467	GD2OF4R01EQ7WL	ATAC	4	20	TTTCAAGACCCCAATCTCATGA	62.884	GTAGCTCGACTGCCTCAAACTTC	62.851	150
HM_7468	GD2OF4R02HFUJ2	GTTT	4	20	TTTCCAGCTTGAGAGATCAGACG	63.134	AAAAAGCACAATTACGGAGTGAT	63.067	157
HM_7469	GD2OF4R01AFSOW	TTTC	4	16	TTTCTGGGTTTCTACTTGCAAAA	63.118	GGTTCTTAGATCCAGTGTGGCAAT	62.713	148
HM_7470	GD2OF4R02FW7ZN	ATAG	4	16	TTTGATTTTGTCTCTCTCGCTC	63.009	CAAATTCACACGGAATCTGTTG	62.942	151
HM_7471	GD2OF4R01BNAIZ	ATAG	4	28	TTTTGGCTACACTCTCAGCTTTT	62.645	TGCAACAATGAGATGCATAGAGA	61.988	95
HM_7472	GD2OF4R01A7Z3N	TTCGG	5	20	AAATGGTTTGATAGGTTGTATGTCGG	62.308	GGAAACTTAAAAATCGGTTTTCGG	62.997	140
HM_7473	GD2OF4R01D96WM	TTTGG	5	25	AACACAAAGGATTCATACAGCCGAT	63.039	AACCTACTCTTTGGCAATGGTT	63.227	100
HM_7474	GD2OF4R01CV8QN	ATTTT	5	20	AATAAAACCACTCGCTCAACAGC	63.069	TGATCTGGTTGTTGGAATGCAAT	62.7	107
HM_7475	GD2OF4R01APV1C	TTTTA	5	20	AAGGAAAGAAAAGGGAATGATT	61.547	TTTTGATTTGTCATGCAATTTCTT	61.005	158
HM_7476	GD2OF4R02GYVIF	AAAAAT	5	20	AATCACAGCTAGAGTCGCTGAAAA	62.767	TGGTCAAATGCATGATTTGGAAG	63.036	157
HM_7477	GD2OF4R01BD2LX	CATAT	5	20	AATCGAGGTGGGTCAAATGAGTA	63.009	TCATCCCTCTACTTTGATTTCCGGA	62.219	144
HM_7478	GD2OF4R02HPXAC	AAAAAT	5	20	AATGGAGAAAAGAAAATAGGGTGA	62.318	TTCCCTAGTATTTCCCTCCATGCT	63.278	148
HM_7479	GD2OF4R01CFYIU	TTTTTA	5	20	AATTGAAGCTTAGAGCTAATCCCG	61.876	CTTTTCAGGCAACCACTTTTAG	62.343	137
HM_7480	GD2OF4R02G074A	AAAAAT	5	20	ACAAAAGACCCAAAGGCACTTTGA	62.932	TTTCACTGCCCTTCAAAGTACC	62.728	149
HM_7481	GD2OF4R02IRRO1	AAACA	5	20	ACAAATCACCAACCAATGTTTTC	63.121	CAGACCTCGAATATGCAAGTTT	62.933	160
HM_7482	GD2OF4R01EFQF9	ACCGA	5	25	ACAGTAGGGGTGTTCAAAACCAA	62.918	TCCAAAAATGGTACGTGGGAGTAA	63.618	159
HM_7483	GD2OF4R02JPJY2	TCITT	5	25	ACCCGGAAGTTTGTGTTAATGTT	61.946	AAAAAGATAGATATCGACCCGAGTAAA	61.753	157
HM_7484	GD2OF4R02GT6AP	AGAAA	5	20	ACTCTAGGGCTGTGTTGTGCTCAC	62.935	TTCTCACTATTTCTTGGCAACC	62.716	108
HM_7485	GD2OF4R02HCY05	TGTTG	5	20	AGGAGCTCTTCCCATGTTTCTG	63.1	TCACCAATAAACAGAACTTAGGCAAA	62.2	88
HM_7486	GD2OF4R02H8IKB	TTCTT	5	20	AGGAGTTTCTTCTCTGGCAGCT	63.506	TTTGAAGAGCAGAAAACCTTTGT	62.521	147
HM_7487	GD2OF4R02H03PA	GGTTG	5	20	AGTTATGGGTAGACCTGGCAATG	62.522	CTCTCTGTAACCTCTCTCGAGTG	63.02	146
HM_7488	GD2OF4R02GRLZ5	GGGTTG	5	20	ATAATTCCGCGAGCTGATTAGACA	63.142	ATCAAACTTTTGGACAGTCTCCCT	62.266	141
HM_7489	GD2OF4R02I7H4L	TCITT	5	20	ATCTCCAAATTTAGTCCAAAACGA	63.108	GCTTTGCTTTTCACTGTGATTT	62.755	146
HM_7490	GD2OF4R01A3V0R	AAAAAT	5	20	ATGTTTGTGAAGGGCTGGAATTTGA	62.922	TTCTCTGAGAGTCTTTTGTGG	62.881	101
HM_7491	GD2OF4R01CWT6M	GGTTA	5	25	ATTAATCTCTGCTCCGCTCCCTA	63.172	ATGGGTCAACGATTTTCTTCC	63.477	85
HM_7492	GD2OF4R02G7W10	TTTTG	5	20	CAAGAATTTGAGTTGCTGTCCA	62.628	TGGAATATGATCACAATAACACA	62.525	83
HM_7493	GD2OF4R01CVZ8A	AAAAAT	5	20	CAATTGCCAGGCTTAATTTGACA	64.132	TGCCGATATTAAGCCCAACTACTCATT	63.756	157
HM_7494	GD2OF4R01AD50N	TTCTA	5	20	CACAGCCCCATGATCTATTCTTC	63.031	TGAGATTGATGGCTTTTGTGTT	63.018	105
HM_7495	GD2OF4R01A3L8G	CGAAC	5	25	CATGCAAGTGTAAAAACGAAACCGA	63.386	TACTTAGGGGTGGAAGGTTGTTCA	62.798	85
HM_7496	GD2OF4R02JRQDU	CGAAC	5	25	CATGCAAGTGTAAAAACGAAACCGA	63.386	TGGCAATACTTAGGGGTGAAATG	63.216	89
HM_7497	GD2OF4R02H3JC1	ATAAA	5	20	CATGGTATCGGTTGATGTTTGA	62.932	CCCAATAACAAATCAATCCACTCT	62.204	124
HM_7498	GD2OF4R01BLW55	TTTTT	5	35	CATGCTATTGGAGCAATTTCTGA	63.244	AGGTGAAAAAGAAATCAACCGTCA	63.117	150
HM_7499	GD2OF4R01B64PX	AAACC	5	20	CCACCAATTAATCACAACACGAGAA	63.142	AAAAATGATCATAACGACCCCT	63.325	145
HM_7500	GD2OF4R01AYYNT	GGGGG	5	25	CCCTTAACCTTATAGCTCTCCC	63.226	GTTGCTCAAAGGGGGAAGGAAG	62.569	157
HM_7501	GD2OF4R02GKAHQ	TTTTT	5	25	CCCTTAGTTTCTGCTCATGTTA	63.322	AGGGAGTGTAAAGGCTTTGTTGGT	63.41	133
HM_7502	GD2OF4R01CLSWX	GATCC	5	25	CGAACATGATAAGTCTCGGAT	62.495	TCATGCGATTTAATATTGTTCAA	61.826	98
HM_7503	GD2OF4R01DCOZW	CTCCC	5	20	CCGAGATACAAAATATCGAGGCTG	63.126	GAGCGAGAGTTCTCTGAGAAAGG	63.023	110
HM_7504	GD2OF4R02JHN8Q	AAAAG	5	20	CCTACATTCAGTGGGTAGCAGAA	63.641	AGTGCCATTATCAATTCATGGAGC	63.45	92
HM_7505	GD2OF4R02F2UET	AAAAT	5	20	CCTTAATCACACAGGCAACATGAA	63.265	GAGGTGCTTACTCCAAACAGCAT	62.838	106

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7506	GD2OF4R01A1410	TTTAT	5	20	CGAATCATCTTGAGTTGACGATCAAA	62.947	CATTGGGCTCAATTTTGTGCGTAT	63.233	116
HM_7507	GD2OF4R01B51JT	AAAAAT	5	20	CGGCCTTTCACTCCAAATACAG	63.021	TTGGTGAGAAAACCTGAGAAAATAGGA	62.551	129
HM_7508	GD2OF4R02F2JIN	AAAAG	5	20	CGTTTCATTACACTTAAGCTCTCT	62.933	CTCCTCTACTGCTGGCATGAAC	63.25	95
HM_7509	GD2OF4R02IWS2D	ACCTC	5	20	CTAGCTAGAGATCTTCAACCCAGG	61.641	ATGGCTGGTTGTATTGTGATGA	62.631	130
HM_7510	GD2OF4R02U572	AAAAC	5	20	CTGCTGCAGTTTAGCAAACTCGT	62.884	AACATAAACGACTTCAGATCCACG	62.645	160
HM_7511	GD2OF4R01A2JUN	ATTTT	5	20	CTGGGGATAAAGAAAGACAGGTT	62.873	CTCTCTACGGGTACCCCTCTTTT	63.068	101
HM_7512	GD2OF4R02JNODM	GTATT	5	20	CTTCCATGCATATAAAGGGTCACTG	62.933	CGCATGTCCAATCTATTCCAAC	63.438	158
HM_7513	GD2OF4R02JPDL5G	AGGGT	5	20	CTTCGTCTCAGATCAATGTTCTCT	63	TTATGATGTGGCCACAAATGAGAG	63.257	146
HM_7514	GD2OF4R01BEF74	TTATT	5	30	CTTTGCATCCGCTCTCTAAATAC	62.451	GTACATGCTTGCTCATTTGATTGG	62.861	160
HM_7515	GD2OF4R02IYZEM	ATAAG	5	20	GAAGATCCAGTGGAAAGAGTCA	62.987	TGACATGTAACCTTGATTGCTTCA	62.775	139
HM_7516	GD2OF4R01ANXP2	TTTCT	5	20	GAAGCGCTCACAAAACAAAGAAT	62.96	TGGTTGATAGGGAAAAACATGAGA	62.057	96
HM_7517	GD2OF4R02FJU2R	TTGGT	5	20	GAATCAGGTTCTGGGAGATGTCAG	63.424	CCTTGTCGCCAATCATAGGTTGT	63.325	106
HM_7518	GD2OF4R02I1B6KLC	GGTGG	5	30	GACAGGCTATCTCAATTTACCCCG	63.095	TACCTACAGGGGATGACAATTTCC	62.383	123
HM_7519	GD2OF4R01CH5CG	CAACT	5	20	GACCGAGTAATCTCATATTAGGACG	61.479	ATCAGAATGGACAGGATTGTGTG	62.366	124
HM_7520	GD2OF4R01EUKZL	GGAGT	5	20	GAGATGAAGTGGAGTAGGAATGGG	62.353	AGTAGGAGTGCCTATTCCTCAAC	63.015	136
HM_7521	GD2OF4R01C7NNP	GCTCG	5	20	GAGCTTGAGCAGATCTTACCAAA	63.133	TTGTGATTAGGGCTTCAACCTCTG	63.739	126
HM_7522	GD2OF4R02JKDHE	CTTTT	5	20	GATCGGATTAGCTTATTCTATAGCTTTT	61.543	AGCCTGTTGCGAGTTGGCTTTTA	62.411	160
HM_7523	GD2OF4R01EL12L	CCGAG	5	20	GCACTCTATCAAACTTGGCCGAT	62.827	TTAAAAATCAATTCAAAAGCTCGCG	62.66	82
HM_7524	GD2OF4R02I4RHW	ATTTG	5	20	GCGCATTGAAGTCAACCGTTATC	62.977	TGCAATTTCTCAGCAGCAAAACTA	63.29	118
HM_7525	GD2OF4R02GG2QG	TTTAT	5	20	GGAGTCTTCGTGCTATGCTGGAT	62.953	ATCGCTAGCTGACTATGGAGTTCCG	63.158	160
HM_7526	GD2OF4R01CM4I7	AAAAG	5	20	GGCTGAGCTCTTGAAATTTTACT	61.476	CCCTTTTGTTCTATTTCATTGTCTTC	60.567	160
HM_7527	GD2OF4R01AJ7H5	AATAA	5	20	GGTCGGGATCCAGGTAAGTATAACA	63.392	CCCCCTCTATTATTAATGTACGCA	63.2	115
HM_7528	GD2OF4R02JBGLY	GTACG	5	30	TACCGGGTTCAACCGGAAGT	62.895	CCGTTACGTACCGTTCCGTTCC	63.691	203
HM_7529	GD2OF4R02HDQV2	CCGAC	5	20	GTCAGGGTGTGAGATCAAGTCACC	63.332	TCAAAGAGAAAAGAGGAGGCATTG	63.104	159
HM_7530	GD2OF4R01DM1NL	AGAGA	5	20	GTCGACCGAGCTCTGAAATATAG	64.297	ACAAGTGGAACTGTGCAAAAGAAA	63.336	93
HM_7531	GD2OF4R02G2HBN	AATCA	5	20	GTTTGATTTCCTGCTTTCGTTTA	62.532	CAATTCCAATTCCCTTCTGTGTC	62.996	156
HM_7532	GD2OF4R02HMV7B	CGACA	5	20	GTTTGCTTCACTCGGTAGAGAAA	63.031	TGTGTCGTCGATCTTATCGTGCT	63.091	149
HM_7533	GD2OF4R01EPAD5	AAAAAT	5	20	TAAAAATGCTGAAACTCTCGCAT	63.138	CCACTATTGGTACAACATCTGGAACCT	63.535	123
HM_7534	GD2OF4R02IOKHO	GGGGA	5	20	TAAGGTCGATCAATTTCAAGAGGG	62.69	ACCCAATTTGAGTTTGGTTGTTTG	63.222	141
HM_7535	GD2OF4R01DX7FE	GGGTT	5	25	TAAGTTGAAATGAGTGGCCCTTG	63.129	TAGATCCGGACTGGATACGCAC	63.475	110
HM_7536	GD2OF4R02HHMBP	AATAA	5	20	TAATTGCAAGAGCAATGAACTCA	63.171	TGTTGAAGATTAAATGGCTCGGT	63.03	99
HM_7537	GD2OF4R02JX8PU	TCATA	5	20	TAGTGTCCCAACCGTAGTACTAT	62.91	TTCAAGAGGATGGAAAGTAGAGGA	62.556	143
HM_7538	GD2OF4R01ES0TM	TCGGT	5	20	TATGAAATAGGGGTGAAAGTCGG	62.41	TAGGGGTGAAAGTTGATAACCGAA	62.906	130
HM_7539	GD2OF4R02J0TE1	AATAG	5	20	TCAAATCATGTCAAAACACTCCGT	62.831	AAAAAGTGGTCGGATTGTCAAGA	63.117	96
HM_7540	GD2OF4R01A537T	TTTTT	5	20	TCAGGCAATCTTACTATCACTGCG	62.853	CACCTGTAGTGACCCATTGTCAT	63.267	155
HM_7541	GD2OF4R01CR86N	TTTTT	5	25	TCCTCACTGCTTCTCTATGAACA	62.294	TATGGTCAGGACAGAAAATGCTA	62.959	155
HM_7542	GD2OF4R01BEX26	AAAAG	5	20	TGAAGAGAGAAACGTCTCAGGGG	63.107	CGGTTTCTGTTTCTCTCACTGTC	63.479	85
HM_7543	GD2OF4R01BSG3L	CGGGG	5	25	TGCATTAATAACTGCTTTTCAATTT	62.89	CGCTTAGTAATAACCCCTCCCC	63.081	143
HM_7544	GD2OF4R01BYV87	AAGCA	5	20	TGGTAATAGGCATACCATTTGGCC	63.041	AACCTATCTTGGTCCCTGCTCT	62.698	86
HM_7545	GD2OF4R02JMH7V	CTCAC	5	20	TGGTAATATAGCAAGACCAACAA	61.951	AATGGGTATATAGCAAGGAGCAC	62.635	114
HM_7546	GD2OF4R01EECN3	ATTTT	5	20	TGTTGTTCACTGCTCTTGTACTTCA	62.492	TCTTAAGTCTCCCTTTTGCAACC	63.201	107
HM_7547	GD2OF4R01C4BMP	GTGGA	5	20	TAAAGGTTAAGAAGTGGCGCTACG	62.872	GTTGCGAGAGCTGACAAAACAGT	63.083	121
HM_7548	GD2OF4R02IQGUH	ACCCA	5	25	TTCATGATGATGATGTTTTTCC	61.354	TCTGGTTCGCTGTTGTAGT	60.931	129
HM_7549	GD2OF4R01C20W0	TAAAA	5	25	TTTATGATCCGGATCGAAATCT	62.902	TTTTGGAAGGATATGGTGTGTT	62.703	105
HM_7550	GD2OF4R02J36HC	GAGTG	5	20	TTTCTTCAACCTAGATGATCGTGG	62.782	AAATTTGAGGAGGCTGTTCCCT	63.479	155
HM_7551	GD2OF4R02JWSBM	GAAAA	5	25	TTTGTTCTTTGACATAGTAGAGG	61.558	TCTTTCTATTTTCTTCAATTTTCC	61.222	111
HM_7552	GD2OF4R01DMA2Z	TTTTT	5	25	TTTTCGCGATATTTTATTTTCC	63.087	AGATTAAAGGCTCTGTTGGCTGCT	63.721	133
HM_7553	GD2OF4R02GVRWR	GAGAG	5	20	TTTTCTAGATCGAGGTTGGGG	63.589	CGTGCCCTCTCTCTCTCTCTC	64.018	160
HM_7554	GD2OF4R01BERPY	TTTTT	5	20	TTTTCTGGTCAAAATGCCAATCTT	63.018	ACTACAAAAATTCTGCAGCGAAG	62.957	90
HM_7555	GD2OF4R02H97MN	TTTCT	5	35	TTTTCTTTTCAAAACAGGGTTGA	62.999	TGGATTGAGAGAAATCGGAGAGAA	63.191	119
HM_7556	GD2OF4R02IUKAC	TAAAAAA	7	28	CGTTCATGTTAAATCTAAGGTTTCAGC	63.309	GGCCAAACAAATTAAAGCCCAATTTTA	63.973	159
HM_7557	GD2OF4R01A3NR9	TTGTGCTG	9	36	ATGGTTGGGACAGGAGATAATCA	62.887	CAAAAATTGGAAAAGGAGGAATCA	62.492	138
HM_7558	GD2OF4R01ENM7E	TACGTTACG	9	36	TACGTAAGTTCGGGTTACGTCATG	63.255	GTTACGGGTTACGGTTAGGTACGTT	62.499	150
HM_7559	GD2OF4R01AP87K	AGAGCCAGA	9	36	TTCATGTTAAGTGTGCTTCCAA	62.843	GATCAGGAAAAGACAGTGGCAGAT	63.017	153
HM_7560	GD2OF4R01B9BAQ	ACCTTTCCGGCA	12	48	AAAACTCAGAGCTGCTTCAGAGGA	62.923	GGAATCTGTTGTAAGCTCTCCAG	62.598	142
HM_7561	GD2OF4R01C1AY4	CT	2	14	AAAAACTTTCTTACCGCTCCACA	62.356	GGGAATTTGAGAAAAGACGGATT	62.785	93
HM_7562	GD2OF4R01DXS8	AG	2	16	AAAAAGAAAAAGAAAGAACACACA	61.694	AAGGATCTCCTTTCTCAAGGTTCA	61.828	80
HM_7563	GD2OF4R02HWPIG	AG	2	16	AAAAAGAAATGATGCAAAAGAGCTA	61.829	AATCAATCACTGCTGGGTCACTC	62.695	126
HM_7564	GD2OF4R01EPUZT	AC	2	16	AAAAAGACGACGGGGAAGTGTG	62.382	GGGCATTGGTATGATTCCATCTT	62.217	146
HM_7565	GD2OF4R02JXLUC	TG	2	14	AAAAAGAGACCCAAATGACACAA	63.006	ACACAGTCGCAACTGTAACAATC	62.665	109
HM_7566	GD2OF4R01DMYB4	AC	2	16	AAAAAGAGAGTAGAGAAACCAACCA	62.844	TCCTAGGCGACTAAGCATTTGGTAA	63.24	135
HM_7567	GD2OF4R01C0Z3H	CT	2	16	AAAAAGATCTGTGCTTTTCTGCT	62.151	CCTGGCTGACCGATTATCAACTAT	62.62	144
HM_7568	GD2OF4R02H9ITT	CT	2	16	AAAAAGATTTTCCCAATCGAAAG	60.925	TTTTAGTTACTTGGTCTTTAGGTTT	60.131	91
HM_7569	GD2OF4R02I2ZC3	TC	2	16	AAAAAGCTTTCTTGTGTTCTCG	62.153	GTCGGAATCACACGAATAGGAGT	62.851	125
HM_7570	GD2OF4R02FY5J5	AG	2	12	AAACACTGAACCTAAAAAGGCC	62.818	AAGCCCAATTGTAATTTGAGGTCC	63.487	93
HM_7571	GD2OF4R01CQ33N	AT	2	14	AAAAACCTAACAGCAACGATTCG	62.571	CCTCTCAGGTTTGACAAATTTCTACT	63.187	146
HM_7572	GD2OF4R01BMH7N	AG	2	16	AAAAAGCTAGTTTAAATGATGGCAGACG	62.984	CCCAATTCATGTTATGGAGTGGT	63.108	150
HM_7573	GD2OF4R02IBL6Y	AG	2	12	AAAAGTAAGAGGGGCTCTGATCGGT	62.806	CCCTACGCTCTCTCTTCTCTAC	62.898	127
HM_7574	GD2OF4R02HKLOG	AT	2	12	AAAAGTCAGCAAGAAATCTTTCAA	60.903	TGAGATAATGTACATACGTGATGCG	61.126	97
HM_7575	GD2OF4R01B870I	AT	2	12	AAAAGTGAATACATGAGGGGGTG	60.382	ATCATCATTTGATTGAAGCCAC	60.205	154
HM_7576	GD2OF4R01BNLO8	AG	2	12	AAAATCCAATTAGGTGTTTTC	62.41	GACTCCGCTCTGTCTCAACTTGA	63.019	155
HM_7577	GD2OF4R01AKSPF	AG	2	14	AAAAATCCACGGCAATTTAGTCAT	63.785	AGAATGCCGCAAGAAAGACATTAG	62.947	156
HM_7578	GD2OF4R01A20QZ	AG	2	20	AAAATGAAAAATGGGGAAACCAT	62.696	GTCAGATCGGACGAAGACTATTG	63.331	156
HM_7579	GD2OF4R02HGO9Y	AG	2	20	AAAATGAAAAATGGGGAAACCAT	62.696	AACCCGCAAAATCAATTTCTATCA	62.829	83
HM_7580	GD2OF4R02G2I60	AG	2	12	AAAATGAAATACATGTTGCTACAAACA	61.12	GATGGAGAGAACTGGAGAGGAGAG	62.094	113
HM_7581	GD2OF4R02GILLH	AC	2	20	AAAATGCTCTCAGTTTGATCTGATGG	60.735	TTTGTTAATCCCAATGATGATATG	60.595	133
HM_7582	GD2OF4R01B9W16	TC	2	20	AAAATAGATCCCATCAGAACCCC	62.573	TTTGCAATTTGCTGCTCTTTTCT	62.313	99
HM_7583	GD2OF4R01ARTJ1	AT	2	20	AAACCCGTGAGCTTCTCTATACC	63.008	TTTAGTCAGGCTGCACAAGGTAGA	62.44	142
HM_7584	GD2OF4R02GZ8XR	TA	2	14	AAACCTCAATCTATTGCAATAAAG	61.004	CTCACTATTGTTGCACATTTTGA	61.258	122
HM_7585	GD2OF4R01CKB4U	AT	2	12	AAACGGGCCATTTATACACAC	63.046	TGTCATTTCTCTAGCGACCTTTG	63.848	128
HM_7586	GD2OF4R02H7SUM	TA	2	12	AAACTACTCTTGTGGTGCAGCT	62.652	ACTCTGCCCTCTCTGCTTATAC	63.314	136
HM_7587	GD2OF4R01DE97M	GA	2	16	AAACTCTGCTTACTTGTGTGCTG	63.076	ACACCACTTCGCTGACTCT	63.492	92
HM_7588	GD2OF4R02JB0Z3	GA	2	24	AAAGAAAAATGGACAGAACAGACGC	62.948	GGATCAACGTAATAATCGCAGAGC	63.158	104
HM_7589	GD2OF4R01CH1KC	AT	2	16	AAAGAAAGACGAGAGTGGGTAGGC	63.11	TTTCATGACTGTCACATACACTTTGAAC	62.589	148
HM_7590	GD2OF4R01BW4D0	TG	2	20	AAAGAAAGCACTTCAGGCTAATTTCA	62.766	TATTTGTCAATCAGAGCAGAGCA	63.27	159
HM_7591	GD2OF4R01DIOJV	AT	2	14	AAAGAAATGTACAATTTGAGTGGGT	60.998	CCCCCTCGTAACACTCTATACTCT	60.604	120
HM_7592	GD2OF4R01CSGBH	TC	2	16	AAAGAGAAAGAGGCAAGCCCTTA	62.91	GGAGAAATCATCCACCTCTACAGAT	62.979	110
HM_7593	GD2OF4R02IHR4W	AG	2	14	AAAGAGACAACCTTACTCCCCGAG	63.185	TATACCTTGCTCCGACTCGGATT	63.244	142
HM_7594	GD2OF4R02JHOCD	AC	2	12	AAAGAGCAGAAAACCAACTCATCTC	62.114	TGGGTTGAAGTGCAAACTTGAATA	62.843	111
HM_7595	GD2OF4R02IBD8R	AC	2	12	AAAGATTTTAGGCCAATGCAACAA	62.945	GAAAGGCTCAGATGGAGAGATT	63.185	156
HM_7596	GD2OF4R01C0D6O	AT	2	12	AAAGCGAACACAGCTCTGTAATCT	62.851	TTCTCAGCAACGATCATTTCAAAA	63.046	110
HM_7597	GD2OF4R02HC6Y9	AG	2	14	AAAGGATATCCAGGCTCAAACT	63.476	GTTGATCGGAAATAGGGGTTTCAAC	63.885	112
HM_7598	GD2OF4R01B1120	AC	2	16	AAAGGGAAGAAATCTTGATTTG	63.09	GGGTAGAAGTTTGAAGAGAACTCCA	62.33	136
HM_7599	GD2OF4R02FUMVH	GT	2	14	AAAGGGATTTTGAGATCTGTGTGC	62.813	CATGTGATGTGATGAACACAGGA	63.062	145
HM_7600	GD2OF4R02GAHWN	TC	2	16	AAAGTCGATTAGGATGTCCCAACA	63.009	ATTGCAAGTCTTGTGTTTATGG	63.336	124

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7601	GD2OF4R02G7M96	TG	2	12	AAAGTGACATCAAGTCGAACCACA	63.053	CCCAACCATCGTTATACAAGAACC	62.716	131
HM_7602	GD2OF4R02GET40	CT	2	12	AAATAAAAATGGGAAGCAAGACA	62.099	GCTAGCATCTGTAATCCCCCTTTT	62.915	102
HM_7603	GD2OF4R01AH450	GA	2	14	AAATACATGCTCTCTGCTTTGG	62.652	TCCTTTGTTAAAGTAGTATCTCCAGGT	61.874	133
HM_7604	GD2OF4R01B8HVH	AC	2	12	AAATCAGCACAAACAATGCAGAAA	62.972	TTAACTTGTGGACAGCCTTGGAAAT	63.129	107
HM_7605	GD2OF4R01CCGEI	AG	2	20	AAATCAGCATGGGGGATCCAGT	63.962	TATTGCAACCGCTAATTTAGTGCC	63.36	153
HM_7606	GD2OF4R02HH9V4	CT	2	16	AAATCATTCCCCAACCCCATTT	63.064	CAGATCTACGGGGGATAGTGAGAA	62.784	121
HM_7607	GD2OF4R02DKM5	AT	2	16	AAATGGTAATTTCAATGCACAGACC	62.356	TGAAACTCTTGATGAACAGGCGA	63.163	143
HM_7608	GD2OF4R02JD9K	AG	2	20	AAATTGGGGATCAGCAATCAAAAT	63.99	GGTGCAATTATCAGGTGGAAATAGC	63.15	150
HM_7609	GD2OF4R01AXAOS	AG	2	12	AAATTTGGGACGTGATTGAGAAAA	62.909	TTTTTGGGACAAAAGCCTTGTA	63.118	133
HM_7610	GD2OF4R02JUOD	AT	2	16	AACAAATCCCAATACATCAACTGTG	60.512	ACGAAAGTCTCAGGAGATCGTA	61.492	121
HM_7611	GD2OF4R01D8XQ4	AT	2	20	AACAAATTTTGTATGCTCCCGT	62.923	TCGCACTGATCAGCATTGATTAT	62.965	113
HM_7612	GD2OF4R01C8I2	TC	2	20	AACAACCTTCTGCAACCTTCTTG	62.931	TAATTTGAATGCACAAAAGGCGAG	62.369	148
HM_7613	GD2OF4R02HIBSO	TC	2	14	AACAATCTCAGCAGCTCTCTCCAT	62.928	TCTAAGACCCCAAGCTCTTGGTGA	63.531	102
HM_7614	GD2OF4R01ECA7N	AG	2	24	AACACCATAGATCCCAATCAAGAA	62.28	TTGATGCGTGAAGATCGTAACAGGG	62.676	111
HM_7615	GD2OF4R01B0244	TA	2	12	AACAGCGCAGTTACTCTGTCT	62.962	TGATTTCAATTCATACACAAGCCC	63.235	114
HM_7616	GD2OF4R02W46F	AC	2	20	AACAGGATCAATAATTTGGGGTGA	62.691	TATTTTGACATGGTTCAGCATTG	63.046	141
HM_7617	GD2OF4R02FM2EO	GA	2	12	AACAGTTTTCAGCTGGTGTGTACA	62.982	TTACCTCAAAACACACCTTCTCT	62.696	107
HM_7618	GD2OF4R01AZDMV	GT	2	12	AACAGTTTTCTCACTGTTTGGTGT	62.665	AGTAGACTGTGTTGGTCTCTCCCA	62.574	93
HM_7619	GD2OF4R02JF06Q	TA	2	12	AACATCAATTTTAAAGTGGCGGT	63.99	CCATGAGGTGTGTATCTGATGATGG	63.66	117
HM_7620	GD2OF4R01B9518	CA	2	12	AACATCACAGAATCATGGATCACAC	62.274	TGGTTCAGAATAGTGACCCACTCA	63.026	157
HM_7621	GD2OF4R02IK20B	AC	2	16	AACCAACACCTCTCTGAGAAAA	62.78	GTGTGGGAGTGCTTCTACTCCAT	62.925	149
HM_7622	GD2OF4R02I9QT0	TC	2	14	AACCACATACAATCCCTGTGTCA	62.607	TGATGAAGCCGAAATAGGTAGGA	63.113	83
HM_7623	GD2OF4R02IBTSH0	GA	2	14	AACCGCTGATATGTGAAGAAATGG	62.742	CTCAAAACCTTAAACGAAACCT	62.804	109
HM_7624	GD2OF4R02FWLKB	TC	2	12	AACCATATAAGCCGTAATTTGGT	62.903	GGAGTCTGACTTTGCTCGTAGCC	63.562	137
HM_7625	GD2OF4R01DTOWP	AC	2	12	AACCAAAATCATGAAGTCAAAAA	62.8	CTAAGTCTCATCTCTCATTCGCG	62.7	151
HM_7626	GD2OF4R02INRCU	CA	2	20	AACCTAAACAAACCCCAAGGCAC	62.726	CAGAGCGTTTCAGGATACCTTGT	62.933	80
HM_7627	GD2OF4R02IGINL	CT	2	14	AACGAAGATGAAGCTCTATGACGG	63.035	GGGGAAATACACAAAAACAAGG	63.659	121
HM_7628	GD2OF4R02H874P	CT	2	16	AACGTCAACAATCAAGTCTGGGTG	62.871	ACAGAGACAGAGACAAGGCAAGG	63.347	133
HM_7629	GD2OF4R02FUZMH	AG	2	14	AACCTCAAAACCAAAATGAGCGCAT	64.095	TCTCTCTCGGTCTTCCCTCTAC	63.483	104
HM_7630	GD2OF4R01B104G	AC	2	20	AACCTCACAGCAGCTTCAACTGTA	62.663	ACGGCTCAGATGCTTTTGTAGAG	63.154	159
HM_7631	GD2OF4R02FNV4E	GA	2	12	AACCTGAAGAGTTTAAAGTGGTACGAT	60.897	TGATCCATCTCAATATATTITTGACA	61.792	83
HM_7632	GD2OF4R01AH5GD	GA	2	16	AACCTAGCTAATCCCAACGGGCTC	63.028	AAGTTTTCTAGGCCATCTCTGCT	62.909	152
HM_7633	GD2OF4R01AZR5B	TG	2	12	AACCTGTTTTCAGACAGAGAACGCC	63.15	GACCATGTCAGACAGGAGATCCA	62.9	117
HM_7634	GD2OF4R02HYHEA	AT	2	16	AAGAAAAACATCTCCCAACAACCAT	62.085	TCCTACTTAGATCTGTGCTAAATCTGCT	61.345	127
HM_7635	GD2OF4R01DMADO	AG	2	32	AAGAACCCATCAAGGTCAACAAAA	63.006	GAAAGTTGGTGTGAGGAGGA	62.799	141
HM_7636	GD2OF4R01AIBCO	TA	2	16	AAGAACTATGAAACCAATCGCGA	63.03	GTGTACCATCATTGAAACCAACA	62.934	113
HM_7637	GD2OF4R02HIU70	AG	2	24	AAGAAAGAACATTCAAATGCGATGG	63.535	GATCGGGGTTGAGTCTATTACCT	63.589	119
HM_7638	GD2OF4R02F9ICO	GA	2	20	AAGACCAAGCCCTTAAAGAGAGA	62.886	GAATCTCAACCCCAACAC	63.791	89
HM_7639	GD2OF4R02I9332	GA	2	20	AAGATGTTTGTGAGCAGCGGTAGT	63.486	GTTTTCGCTCTATTTCCTCACTCT	64.014	119
HM_7640	GD2OF4R02IBO8R	GA	2	12	AAGCAAACTCAGCAAGCAAACTCT	62.757	AGAGGAAGAGCATCAACAGGTCG	63.238	159
HM_7641	GD2OF4R01AX721	AT	2	16	AAGCAAGTTGGACCAAAAGGT	63.212	TTTGGACCATCTCTGTTTGTAC	62.437	140
HM_7642	GD2OF4R02G5FN	AG	2	16	AAGCAATCAACTGAGACCATCGG	62.923	AGAAGGTCCTCTCCCTCC	63.134	108
HM_7643	GD2OF4R02IQ70X	AT	2	12	AAGCATTTGCTGCGAGTTCATC	63.839	CTTGCCACCATCTCACAGAAAC	63.067	147
HM_7644	GD2OF4R01C8CJ1	TA	2	16	AAGCCCTTAAAGTTGAGACAACCA	62.425	ATTTGCCACCAATTAATCCCTTG	63.278	142
HM_7645	GD2OF4R01AXX8X	AT	2	14	AAGCGTCGAAGTGTCTTCTCATAC	62.949	GCATGTATTGCCCTCTATTGATGAT	63.138	113
HM_7646	GD2OF4R01CCJ07	GA	2	24	AAGCTGATCTGATCTGTAATGCC	60.964	ATCACTCTCTGTTGGTGTGTGA	60.999	129
HM_7647	GD2OF4R01BFMAH	AT	2	12	AAGCTGGTAACACCTCTAAAGTG	62.145	CCACCACCATCTACTACTGCTA	62.764	155
HM_7648	GD2OF4R02IDR5	TA	2	12	AAGGAAGGTTTGAAAGATGAGCGG	63.001	ACACAACATGCGATAGTGCATGAT	62.265	135
HM_7649	GD2OF4R02I8RTB	TC	2	12	AAGGAATCAATCTGCTCTCATCTTC	62.988	TGCCATTGGATATGATGTTGAGTT	62.618	152
HM_7650	GD2OF4R01A6HD9	GA	2	12	AAGGAGCAATAAGTTTGGGGCTG	61.225	ACTCACCACTCTCTTAATTATATCC	60.391	91
HM_7651	GD2OF4R01EZEAV	AG	2	12	AAGGAGTTCGGAGGAGAGAAAAAT	63.074	TGTCCTCTTGAATAGACCAAAAA	62.894	140
HM_7652	GD2OF4R01AS2WL	GT	2	12	AAGGCTTGTGATGATGTGTTG	63.861	ATTTCTGCTGACCGATTGCTACAT	63.15	154
HM_7653	GD2OF4R01BYC9D	CT	2	16	AAGGGAACAAGTGAAGGGATAAGG	62.873	AAAAGTAGAACAATGACTTGCAACG	61.938	127
HM_7654	GD2OF4R01DDOYU	GA	2	16	AAGGATGATGATCAAGCATGAA	62.897	TCATCAAGTTTGGCAATGTCCTT	62.948	135
HM_7655	GD2OF4R01A1PT9	AG	2	14	AAGGTATCTCCCTAGTTAACGCC	63.008	GGTAGGGCAGGTGTAATCATGT	62.205	93
HM_7656	GD2OF4R02HQF63	TG	2	24	AAGGTGGAAGATGAGAAATCGGTG	62.895	CGTCTACTTTCTTTCTCTCC	63.296	90
HM_7657	GD2OF4R01CWF04	AG	2	16	AAGGTTCAAACCTGCTACACCTTG	62.833	TGTTTTTAATTCCTTGACGTTGG	62.512	157
HM_7658	GD2OF4R01BLG2L	GA	2	12	AAGTGGAGGCTTAAATGACTGA	62.522	GTTGAGTGTGTTTGTGCTGCT	62.835	117
HM_7659	GD2OF4R02GOCR8	AG	2	24	AAGTGGGTATCCACGCTTAAAGT	63.215	TTCCCACTGATGACCTCTCTACTA	63.199	137
HM_7660	GD2OF4R02IRVGF	GA	2	14	AATAGCTTGAGGTGTGTCATC	62.713	TTCTCAGCAGACTCAAACTCTCT	62.898	140
HM_7661	GD2OF4R02HUKP4	GA	2	12	AATAGTTTCGACGAAGGGAGAGAGG	63.285	TCTGTTTCTGAATCATGCTCATC	62.58	121
HM_7662	GD2OF4R02G2OHQ	GA	2	12	AATATCAAAAGAAATGTAAGAGTGTG	61.94	ACCAATCTTATATTTCTCAACAAGG	61.046	80
HM_7663	GD2OF4R02FU4C4	AT	2	16	AATCAAAACCAACACAGACCCCA	63.006	AAGAGCAGAGACCAAGACCAAC	63.249	143
HM_7664	GD2OF4R01CWRLN	AC	2	24	AATCAAAACCAACCATTTTACC	61.14	TTTCTATATCAACACACCTCAAGTCTG	60.215	82
HM_7665	GD2OF4R01BWJKH	AG	2	12	AATCAATCTTGTGCGTGACCCAT	62.813	ATTCGATATCTCTCCGTCTTG	62.718	137
HM_7666	GD2OF4R02IX4YJ	TC	2	12	AATCAATCTCAACCAACCACTT	63.014	AGGCTGCAAACTCAGAAGAGAAAGA	62.923	98
HM_7667	GD2OF4R01CQYNS	AC	2	16	AATCACAATTAAGCTCAATTTGGG	62.424	CCCTACCGGATCTCATCTACATA	62.481	151
HM_7668	GD2OF4R01CVF30	CT	2	16	AATCCCAACGCTTTCTTACTCTTT	62.623	AAGACAGGAGCGTTTTAGTTC	63.11	80
HM_7669	GD2OF4R01BFP3A	GA	2	20	AATCGATCGGTATGATGTTTGGT	62.94	AATTCGAAAACCGAATGTGAAGAC	62.62	119
HM_7670	GD2OF4R02F8K72	AT	2	16	AATCGTAAAGTTGTGCTTTGCTC	62.864	CCAACACGATCAAGTCAATGCTAA	63.379	126
HM_7671	GD2OF4R02HU18S	AG	2	12	AATCGTAGTGTCTGAGATGGGAAG	62.923	CATCTGCTCTAATTCCGCTCTC	62.622	80
HM_7672	GD2OF4R01AH8XF	AG	2	12	AATCGTTCAAAGGATGAAAAATG	63.327	ATAAAAAATTTGGCGACGAAAAAGA	63.852	96
HM_7673	GD2OF4R01B772L	CT	2	14	AATCTTATATTTGGGCACAGGTGCG	62.438	CCCTGTATCGATTTTGTGTCTGT	61.467	156
HM_7674	GD2OF4R02IZUY	TC	2	12	AATCTTCACTCACTGTGCAATGG	62.622	AGTGGACAAGATGTGTCTCTCGTG	62.935	131
HM_7675	GD2OF4R02ISAXS	TA	2	16	AATGCAAGGAAAAACAAAGAGAAA	60.471	CCTACTACCTTCCGGTACTTCT	60.283	160
HM_7676	GD2OF4R02JV1AG	CT	2	24	AATGCTCAGTCATTGCCAACAA	63.509	GGTGGTAGCAACAAACCATCTCT	63.035	116
HM_7677	GD2OF4R01BXTHO	CT	2	16	AATGGACAATTTTACCCTCTCA	61.996	GCAATGTTGGAGTTTCTCAATTTT	62.62	86
HM_7678	GD2OF4R02GZGQG	CT	2	12	AATGGGAGAGAGTCACTGTATGTC	63.04	GTGAAGCCAAGGTAGTCCCAAGTA	62.822	129
HM_7679	GD2OF4R02IE31Z	AG	2	14	AATGGTAGGTCACTTCTCAGGGTT	63.189	CGCCGGAATCAACGAATAC	62.584	147
HM_7680	GD2OF4R01EJXYT	GA	2	12	AATGCTCCAGAAATGGAATGCTAC	62.51	GCAATTAACAACCAACGCTTAGGAA	63.444	144
HM_7681	GD2OF4R02JCKWQ	GA	2	20	AATGTTTCTCCCAAGATGATTGA	62.789	CCAAAAAGAAAAAGAAATCTCA	61.882	144
HM_7682	GD2OF4R01CP25W	AT	2	16	AATTACATTTATCAGCATCGCCAG	63.344	CAAAATCAAGCTTTAGTGGGTGG	63.023	121
HM_7683	GD2OF4R02GEMN4	GA	2	24	AATTATGGCCGCAATGCAATAATA	63.345	CGTCGCTGCTCAATTTACTGTG	63.293	160
HM_7684	GD2OF4R01D19H	GA	2	14	AATTCACGAATTTGCTTAATTTCT	60.831	GGACTCTCGCATTACTCACTGACT	60.252	87
HM_7685	GD2OF4R01C1NS0	TG	2	14	AATTCAGTGAAATGCAATAACACA	61.752	TTCTATTTGTAATCGGGCTGCTG	62.5	88
HM_7686	GD2OF4R02I1LIC	AG	2	16	AATTGATGATTTTCAATGCGGCT	62.918	CACACTCTCAACATCTCTCAATC	62.136	124
HM_7687	GD2OF4R02GDUD4	AT	2	12	AATTGGGTTCACTACACGGTCAT	62.824	AATTTCCAGCTTTCCATGTTTGA	63.018	141
HM_7688	GD2OF4R01C032Y	GT	2	14	AATTGTCTCCAGGACATAACCT	63.398	CTCTCTGTCAATCTCTGCTCAC	63.897	153
HM_7689	GD2OF4R01C7MO3	TA	2	16	AATTTTGAATGCTTCCAAGTCTC	62.841	CTCTGCCCAAGAGAAATATGGTC	62.397	159
HM_7690	GD2OF4R01BLO8O	AG	2	16	AATTTTACGCAACCACTCAACT	62.981	CCTTTTTAAAGTTTCTGGAGGGGA	62.871	112
HM_7691	GD2OF4R01DOW7F	AT	2	16	ACAAAGCCACTCTAGGTTTCTT	63.005	ATCGCCACCATGTCTGATAGGTA	62.82	108
HM_7692	GD2OF4R02F194S	AT	2	16	ACAACTTTAAGATGCGCATGCAAT	62.95	TTGATTTGATTACGCAAAATGAC	63.163	123
HM_7693	GD2OF4R02HB9G8	CT	2	14	ACAAGCAAGCTCTTGTGACATTA	62.455	TTTTTTTATAGGGGACGTGAG	63.401	85
HM_7694	GD2OF4R01EE3KW	AC	2	16	ACAAGTAAGTCCCAACTGTTGTA	62.018	TTGGGCTGCTCTGTGAAGTATTTG	61.644	159
HM_7695	GD2OF4R02I32R0	AG	2	16	ACAAATCCCAAAAAGAAAGTTGTG	61.677	GTTAGGCTGTTGTGACTTTGTGCG	62.251	103

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SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7696	GD2OF4R01AF3YG	TC	2	20	ACACACTCTTGAGTCTAACGCC	63.05	AATCCGATAGTTTGGGAAGGAATG	63.465	92
HM_7697	GD2OF4R02HUPI7	GA	2	16	ACACAGAAGTTGATGATGCCAAA	62.948	CGTAGGTACTTCAATTAACAGGCCG	63.048	122
HM_7698	GD2OF4R02FR8VT	AC	2	20	ACACCAATTATCACTGTGTGCAAT	62.638	AAAGGAATCACAAAGAAATCACTGC	61.942	107
HM_7699	GD2OF4R02GK0L3	TC	2	20	ACACGAATCAGACAACCTCCTACAGA	61.442	GGTGGGAGGTATCATTTTATACCA	62.204	149
HM_7700	GD2OF4R02ISR21	AG	2	40	ACAGAGGTCATGGTCTCTAACATTTTC	63.764	CACCTCCCTCCCTCTCTCTC	64.68	205
HM_7701	GD2OF4R01COO1N	TA	2	20	ACAGATAACAAACAAATCACCGCC	63.353	TTTGTTTTAGTATGTGTATCTCAGCGA	63.161	142
HM_7702	GD2OF4R02H4P1J	GT	2	12	ACAGCAATTCAAATGTGACAGATGC	61.565	ATCTTTCGTCTCTTGTGAGGAAGC	62.214	146
HM_7703	GD2OF4R01DD6DX	AC	2	12	ACAGCCAATAATAGCAAAACCCAA	62.852	AAAGTTTTTGGCGTGTGTCTCTC	62.946	147
HM_7704	GD2OF4R01DL4JQ	CT	2	16	ACAGCCTTAAGTCTCGAAGCAATG	63.154	TCGCGGGCGTAACCTAAGTATAGTC	62.784	131
HM_7705	GD2OF4R02FP2ZS	GA	2	14	ACATAGTGATTGGCCCAACAGTAA	62.885	AAAATACCTCAAGAAATCTGACGGG	62.844	124
HM_7706	GD2OF4R02H46KK	GT	2	16	ACATGACGAGGCTACTCCAAACAT	63.255	ATTCGCCCAATAGTAGCCATTT	62.903	120
HM_7707	GD2OF4R02GIUN4	TA	2	12	ACATGGTTGGGTGCTTAGAAGATG	63.549	ATATGGCCTTTTGCCCAACATAAA	64.438	158
HM_7708	GD2OF4R02H3ZWL	AT	2	12	ACCAATTCTGGCAATGCACTTGA	62.846	CATTTCATCCGTGCTCTCTCTT	62.826	157
HM_7709	GD2OF4R02GF1VT	AT	2	16	ACCCAAATCCCAACAACTACTCTG	61.37	TGTAGTATATCGTAGGAATGGAAATG	60.843	147
HM_7710	GD2OF4R01A6MNP	AT	2	16	ACCCACCAATGCAATCTTTTAGAGC	62.744	AAATTGCAGCTATACACCCCAAA	62.852	113
HM_7711	GD2OF4R02ICWXV	AC	2	16	ACCTCTCCCCAAACACTAATCTC	62.983	TTCTCTGCTGAACATAGTTTCTCTCT	62.264	125
HM_7712	GD2OF4R02GNMNY	AT	2	14	ACCGAAATACATCAATGGATCGG	63.021	CATGGTGACGATCTCTCTACAG	62.958	150
HM_7713	GD2OF4R02JYFCA	CT	2	14	ACCGAGCTAAGAATCTTCCGAC	63.208	TGGGAATCAGTTTTATCAATGCC	63.213	102
HM_7714	GD2OF4R01AXKSJ	GA	2	14	ACCGTTGAACGATCAAAATTC	62.718	CGCATTAATACCAATGGGGTG	62.355	158
HM_7715	GD2OF4R01BX23Q	TG	2	14	ACCGTTGACACGCGATAGAAATTA	63.043	ATGGCTCCGTATGGGCAGAT	62.948	122
HM_7716	GD2OF4R01C1AMA	TA	2	14	ACCTCGTTAGTGGGCTCTGTATAA	62.425	TTTGGGAAGCACACATTACATTT	61.739	82
HM_7717	GD2OF4R02HBKS4	AG	2	24	ACCTGCATAGAAAAAGCCCAAT	62.719	CCGTTACAACGGTGGAAAAATAGA	62.224	160
HM_7718	GD2OF4R01BVC1N	TG	2	12	ACCTTTGATCAGTTTGTATCTCTCG	62.798	TGGATTACTGGTTGACCCCTTCT	62.897	149
HM_7719	GD2OF4R02G3P29	AC	2	12	ACGAAACAGAAATGAAACCAAA	61.878	TTATGAACCATTTTATATCGGTTTTGA	60.907	151
HM_7720	GD2OF4R02JWEE	TA	2	12	ACGAAATCAATGAACCAACATAG	61.286	TTGACTATCTATTGCAACCTTAACCTCA	60.717	127
HM_7721	GD2OF4R01EYPV5	AG	2	12	ACGACACAGGATCCATTTTCACT	63.128	AGTTGCTTCTCTCAACGAGTTGCT	63.063	134
HM_7722	GD2OF4R02GBDM5	AT	2	14	ACGATTCTGAAATCAACCAACT	62.009	CCTCTCTACCCGACTGTCTCTC	61.842	157
HM_7723	GD2OF4R01ETTAV	AC	2	20	ACGGAGCTCGAAATTAACCTTTAGC	62.924	GAAAAAGGTGAGTCTTATTCGCGA	62.826	148
HM_7724	GD2OF4R02IBD7W	TC	2	14	ACGGACTCTTCTAGTCCACCATG	63.04	TCCTGATGGAAATTTGAACCCATC	62.481	94
HM_7725	GD2OF4R02JLX8K	TC	2	16	ACGGAGTACATACTAAGTACACJG	63.202	CTTCTAATCAGCAGGCAACCAAC	63.348	156
HM_7726	GD2OF4R01EXQIB	AC	2	12	ACTAGTCGCTGACGAGTGTTTTA	62.252	AAAGATAATCTGAGCTCCGCTCC	63.093	149
HM_7727	GD2OF4R02HLRQB	GA	2	14	ACTCCAAATGATGCTCTAATGGC	60.205	AGTATACGTTGGAGGAGTAAAAACAA	60.155	100
HM_7728	GD2OF4R02HDFM3	TC	2	16	ACTCCATAAGGGAAGAGGTTGG	63.791	GGTGACAAACACAGACAAACAA	63.209	93
HM_7729	GD2OF4R01AU1F6	AG	2	20	ACTCCGTTTTTGTGGAATATCCAG	62.619	TGCAGTCACACACTCACCTTCAT	63.109	111
HM_7730	GD2OF4R01BR6GJ	CT	2	12	ACTCTACCACTCTGCTCTCTCTG	62.485	TCCGGTACGCTACAAAGAAAGTC	62.822	158
HM_7731	GD2OF4R01BCX0A	GA	2	20	ACTGGGTACAGCAATGGATCTT	62.214	GTCGTCAGCATCACCATTC	62.797	83
HM_7732	GD2OF4R01ELFTJ	TA	2	14	ACTTCCATCACTCTGCTCAATTC	63.017	ATCTAAGACGTTCAATGGACGAGC	62.94	148
HM_7733	GD2OF4R02H8TXO	TG	2	12	ACTTCCGAATGATGAGAAGTTGG	62.798	CTCTCAACTGCCTCTCCATCTCT	62.575	156
HM_7734	GD2OF4R01BNGX3	CT	2	12	AGAAAAGAGACTTGAGTCCATTCATT	60.064	GCTGGTTGGAGAAGTTGAAGTAAT	60.063	160
HM_7735	GD2OF4R01AV4VL	AG	2	16	AGAAAAGAGAGATAGAGAGACGGG	62.466	ATAAAGACTTTTTCTCTCGCCC	62.239	112
HM_7736	GD2OF4R02GGPQH	GA	2	20	AGAAAAGTGAAGGTTGACTGCTCTT	62.818	ATAGAGACGCTGGGATCTCTCACT	63.72	114
HM_7737	GD2OF4R01CA57Z	AG	2	14	AGAAATGCCTACTAGGACACCCCTC	63.096	CACAAACCAACTCTCTACACCAACA	62.586	140
HM_7738	GD2OF4R01C5KXR	AG	2	16	AGACAAATCCAGTTGTGACCACCT	63.236	AAGAAGAAAGTTAGGACCGCTCT	62.923	120
HM_7739	GD2OF4R01B8LR4	TC	2	14	AGACATTAATCCCTTCCACCAT	62.974	GTTTCTTGGTGGTTTTCGGATTA	62.424	133
HM_7740	GD2OF4R01CRMME	GA	2	12	AGACGATGCTGGAGAAATGAGAG	63.23	GTGTTCTGCAGATGCCCTTCC	64.185	112
HM_7741	GD2OF4R02IEWJ1	GA	2	16	AGACTGACAGAGGGTCTATAGGTGG	63.001	CTTTTTACGTTTGTGATGCAATCT	62.545	130
HM_7742	GD2OF4R01EL16W	CA	2	12	AGACTTATCTTGGCTCTCAAGTC	60.142	TTTCTAGTTTTGTAGAATGTGTATCCG	60.212	98
HM_7743	GD2OF4R01EXP1K	AT	2	12	AGAGAAAGAAACAGCAACAAACA	63.444	TACTGTGCCCTCTCTCACTACAAG	63.87	80
HM_7744	GD2OF4R01ECNEE	TA	2	12	AGAGACAGAGCAATGCTAACGATG	61.998	CGAGACGTTCTGTGTATGTGTGA	62.23	88
HM_7745	GD2OF4R01C9WTC	CA	2	16	AGAGAGAACCTGAAAGTGCTGAA	62.909	AAAAGGAATGGCTCACCTTTTGT	63.296	131
HM_7746	GD2OF4R01ENC88	CA	2	12	AGAGAGTGAGAGGAGGGTTTTGTG	62.974	TTCTCTTTCTTCTTCTTCAGTCCA	61.974	106
HM_7747	GD2OF4R01B8M7U	AC	2	12	AGAGATCCATTGTTTCAACACCA	62.922	GACCGAGGAGATTGCTGCTCTTA	63.23	123
HM_7748	GD2OF4R01CYLHQ	CT	2	14	AGAGCAACAAACAGCATGAGATG	62.858	AAAGAAGGGTAAATCAAGAGGTTTCT	62.563	160
HM_7749	GD2OF4R02JATRD	CT	2	16	AGAGCCAAAAATAGTGAATGCTCGC	61.247	CCAGGTGATTTCTATCTCTGTGCC	62.17	116
HM_7750	GD2OF4R01CD24Q	GA	2	20	AGAGTAACAGAAACCCCGCTCT	62.899	TCTTCTCATACCTTACGTAGTTGGG	62.032	96
HM_7751	GD2OF4R01DQ48J	GA	2	16	AGAGTTAGGGTTTCCAGAGGTTGG	63.076	CTCTCAATCCCTGATCTCACAT	63.215	86
HM_7752	GD2OF4R02HMGGU	CT	2	12	AGATGGACGCGAGAAATCTGTGAG	63	GTAAGCGACGACCTCCAACAGTAG	63.468	125
HM_7753	GD2OF4R01A8HAT	AG	2	12	AGATGTAAAGCCCTAAATTAATCGAAA	61.712	CACACACCTCAATCTAAACCTCA	62.487	159
HM_7754	GD2OF4R02IKU08	TG	2	16	AGATGTTTGTGAGAGGTCAACAGTGA	62.652	AGTCAATTTCACTAACTGACCCCA	63.111	157
HM_7755	GD2OF4R02IGA2S	GA	2	16	AGATTAATCTCCACCACTAACCC	60.811	GGAATACTTACTGAGCTGTTCTTTTT	60.024	114
HM_7756	GD2OF4R01BC99L	TG	2	20	AGATTGGGAGAAACAAAGAACCC	62.598	CAGTCCGAGCTCTGCTGTTTTAGT	62.935	116
HM_7757	GD2OF4R01AJP1G	TC	2	12	AGATTTCCCATTTCAACTCTCAT	63.069	CAGTCCGAGCTCTGCTGTTTTAGT	63.033	134
HM_7758	GD2OF4R01BM7YK	TA	2	20	AGATTGTATGATGATGAGTGAACA	62.293	CGTCTCGTACGCTATTACTAGT	62.958	150
HM_7759	GD2OF4R02GMVPR	CA	2	12	AGCAGAAATGGGACACTGAAATTTG	63.242	AGGTGATCACTCACCAATTTGT	63.014	158
HM_7760	GD2OF4R01DHYEX	GA	2	12	AGCATACAAGAACACCAAAACCC	62.536	TGCTCTTTCTTAAAGCCATGGAA	63.322	114
HM_7761	GD2OF4R01DQCPE	TG	2	20	AGCATGTTTTGTTTTGTTTTTGG	62.397	ACTGTTAAAAAGTAGGAGGTTGGG	62.789	105
HM_7762	GD2OF4R02H794R	TG	2	14	AGCATTACCACTTAAGAAGCAACC	62.744	CTGCATCTCGCATTTGACATTTT	63.188	102
HM_7763	GD2OF4R01B013U	GA	2	12	AGCCACCTCTGGCAGTATATACAC	62.84	ACCCAAACATGACCATCAAAATAG	63.108	143
HM_7764	GD2OF4R02J1W7T	AG	2	16	AGCCACTGAACTCTCTCTGTTGCG	63.255	TCTCCACCACTAACCAAGTAGC	62.516	154
HM_7765	GD2OF4R01A1QMB	TC	2	20	AGCCATTACGCTAACTAGGGTTTT	61.386	GCAATATCAGAGACTGCGCAGAG	61.581	120
HM_7766	GD2OF4R02HJV6P	CT	2	12	AGCCCTATAAAGGGGATGCTTTG	64.562	CAGTTGGAGAACTCTGGACAACAT	63.649	104
HM_7767	GD2OF4R02F2TEP	AT	2	14	AGCCCTAGTTATCCCCAATGAAA	63.084	TGGTAACGTTTTCTGCGACCTAT	63.051	90
HM_7768	GD2OF4R02HE7A1	GT	2	16	AGCCTCCGAATTTCTCAAGAAATC	63.188	ATTTTCTGTAAGAACTGCCCTCTC	62.912	115
HM_7769	GD2OF4R02GHCGB	GA	2	16	AGCCTGAGGGTAAGGCAATAGG	63.174	CTAGTTCTACGGGATCACTCAC	62.856	111
HM_7770	GD2OF4R02JPSQE	TC	2	12	AGCCTGTGAAGAATGGGTGATT	63.219	CCAAACGAAGCTTAATAGTGATGG	63.027	155
HM_7771	GD2OF4R01E4V0C	CA	2	20	AGCCTTTGAAGCAATAGCCTTTGT	63.617	CTAACTGAGGGATCAGTGACGGT	62.909	110
HM_7772	GD2OF4R02IZONU	GA	2	16	AGCGAAAGGCTGAAAGAAATTACC	63.119	TACGTTTTCGTTAGTTGGGTCG	63.336	147
HM_7773	GD2OF4R01D3VY5	TG	2	20	AGCTCTGAGTCTGCAACCAAAAC	63.263	AGAGGAAAGAGGGCAACAAACT	62.804	156
HM_7774	GD2OF4R01AOP6L	AG	2	12	AGCTGCATGACAGTCTCTCTTCC	63.474	GCCCTTACTAGCACTTCTACAT	63.029	159
HM_7775	GD2OF4R01D8FFR	GA	2	12	AGCTTCACAAATAGAGAGGGGGG	63.086	CCTGTCAAGCTCATTAATCTGGT	62.811	89
HM_7776	GD2OF4R02J97N	AT	2	16	AGCTTTTATCTTTTATGTCGCGCT	62.47	CGAATCGTAAGACGAAATGAAGT	62.947	151
HM_7777	GD2OF4R01B1ZKL	GA	2	14	AGCTTTCTACTGCTATTCTCGCC	63.428	AAAAGACATTGACAGCCCACTCCC	63.799	96
HM_7778	GD2OF4R01AOV1D	AG	2	14	AGGAGCAACTTACATTCCAAAGC	62.055	AACTGTGCATTATGTAATCACCTGGG	61.481	158
HM_7779	GD2OF4R01BXCXY	AG	2	16	AGGAGGTAGAAAGTGAACATCAG	62.933	ACACTCTCGTCTCTGTCGATTT	62.913	91
HM_7780	GD2OF4R01EAX7O	TG	2	12	AGGATAATGACCTTGAGGAGGACC	62.964	CGTACCTAGTCTTCCCGCTCT	63.111	90
HM_7781	GD2OF4R01A51HL	TA	2	16	AGGATCCAGTGGTTGAAACAGAA	63.212	AATGATTGAAAAATGGATCCAAAG	63.105	155
HM_7782	GD2OF4R01AKKGG	GA	2	16	AGGCAGCAAAAGCAATTAATCAA	63.154	CTTTAATCAACTCTCGCCGAGC	63.235	155
HM_7783	GD2OF4R01AF3E8	CA	2	12	AGGCATATGATCCCCGTATCTA	63.014	TGGCTATGCAAGTGAATACGAAAA	62.872	123
HM_7784	GD2OF4R01D0PCE	GA	2	12	AGGCCATTTTTGAAAAGGAGATT	62.89	TCTGGGTTTTCTGTCTCTTTTTG	63.003	160
HM_7785	GD2OF4R02HJCZJ	AT	2	12	AGGCTAAGAGAAATCAAAATGGGAA	61.967	TCGATGGTTGTTTCAATCTTGAAC	62.397	224
HM_7786	GD2OF4R02J5KX7	TC	2	12	AGGGGAGGAATATCTCTTCAAG	62.572	CCCTTTAATTTTCTGAACTCTTTGG	62.564	146
HM_7787	GD2OF4R01DM5HL	GA	2	40	AGGGGTTTCACTCCACAGTTCTA	62.382	TCAATACGCCACTTATCGAAAGAC	61.636	95
HM_7788	GD2OF4R02J9P7T	CT	2	16	AGGTCCCCCTAGACTTTGTATGAC	62.974	AGCGCGCCACAGACTACTTTAG	63.087	160
HM_7789	GD2OF4R02F2AEL	GA	2	14	AGGTGTCAGTGCAATAATGCAGA	63.078	AATAGGGCGATAAGGCACATAACA	62.854	130
HM_7790	GD2OF4R02IWQRK	GA	2	14	AGGTTCACTTGTGGAGATCTTGG	60.788	GAACCCAGGAATGACCTTGTG	60.74	84

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7791	GD2OF4R02IZMBP	AG	2	14	AGTAAACTGCACCTCTGGAGTCGG	63.146	CAGCAGGTTGGTAAGGCTTCTCT	63.235	80
HM_7792	GD2OF4R02JNF80	AT	2	14	AGTACCTCTTGGAGGGCTTCTCT	63.846	AATAGACGATCCAACGACCACAAC	63.456	155
HM_7793	GD2OF4R02JHPIV	TC	2	16	AGTAGGAGTTGTGATCTCTGCTG	62.639	GCTCATATTTTACCCAGTCATCTTAGC	61.694	141
HM_7794	GD2OF4R018XEJZ	GA	2	12	AGTATTGCCACCCCTACCTAGCAC	63.721	TGTTGGTAAACGAACAACATACCG	63.093	108
HM_7795	GD2OF4R02HDF1C	AG	2	12	AGTCAAAAGCCCTCGTTTCTCTT	62.911	GACTAGATTGACGACACACAGAT	62.771	114
HM_7796	GD2OF4R02FU67R	GA	2	14	AGTCCACTTTTATCTCTGTGTGGC	60.922	TTTTTCTAAACTGTGTCTCGAACCTTT	60.514	105
HM_7797	GD2OF4R02G2QJ5	TC	2	16	AGTCGAGTCTCTCCACAAACGAT	62.707	CAGGTTCAACCACCAATCTCTATTATTG	63.1	133
HM_7798	GD2OF4R02FNIWN	TG	2	16	AGTGAAACTGCTCCAAACTCAAC	63.036	CGTCCATCATTCTTTCTAAGAGG	62.383	130
HM_7799	GD2OF4R01A73SD	AC	2	16	AGTGATATGACCGGCAAGAAGAC	62.827	TGTGAGAGCTCACACATTTGTTTGT	63.174	155
HM_7800	GD2OF4R02HO53Q	AC	2	12	AGTGACACAGCTAACTTTCTTGGG	63.053	TTGGGTTTATTGGCAGTACAATTTTT	62.769	114
HM_7801	GD2OF4R01C1P93	CA	2	16	AGTGGTGCTAGAGACACACCACAA	63.299	TTTTCCCTTAACTATGGAGGAG	62.768	92
HM_7802	GD2OF4R02F8YF	TC	2	24	AGTGTTTTCAGTGTCTGCTTTTTCG	61.954	TGTTTGGTAGTGTCTACGTCTGCG	61.757	80
HM_7803	GD2OF4R02F5RG2	CT	2	12	AGTTATCCAAATGTTGGGTTTCA	62.922	ATGGTTATCAGTCTGCTCTGCTT	63.039	150
HM_7804	GD2OF4R02IAWPW	AT	2	14	AGTTCCCACTCTACGTCTATCCC	64.76	CTGTCACGACGCACTCTACTA	64.985	159
HM_7805	GD2OF4R01CQXAY	CT	2	14	AGTTGCTCTCTCTTTGTGCATCT	62.939	CTCCAGACCAAGAGAAATGGAAG	62.569	112
HM_7806	GD2OF4R01EO5MS	AC	2	14	AGTTGGTAGTAGCTAGTGTGTCAC	62.141	AGCTTTCATAAGGTGTAGAGGCC	63.114	99
HM_7807	GD2OF4R01E11LC	TC	2	16	AGTTTACGTTTGGCTGCTCTTTTG	62.966	TTTGTACCGTAGAGACCAATAACCA	62.615	128
HM_7808	GD2OF4R02J4WUN	AT	2	16	ATAAAATGCATCAAAAGCAACAGA	61.949	GCATGGAATTCAGGTGTATATCTTCAT	61.06	149
HM_7809	GD2OF4R02FU1NK	AC	2	14	ATAAATCACTGTCTCCGCTTTGA	62.233	CCTAGAACGATGGTCTCTTTGACA	61.849	97
HM_7810	GD2OF4R02GPTOA	CA	2	14	ATAAGGGCAGGAATGTCTGGAT	62.891	CAAGCAAGAGTATAAGAAAGCAGATTG	62.005	92
HM_7811	GD2OF4R01ATR8N	GA	2	20	ATAATTTCAAAATCCAGCGTCCAG	62.533	TGAGTTCGATCTCGAAGATTGTTG	62.817	156
HM_7812	GD2OF4R02JQI6	CA	2	20	ATACAACAGCTTCTCATCTCGCC	63.051	AAATAACTGCTGGAGACGGATTG	62.729	136
HM_7813	GD2OF4R01DQ59O	GT	2	32	ATCTTGGATTCATTGTAGTGCGCT	63.039	ATTGTTGGTTTCAAGGAACCTTG	63.044	156
HM_7814	GD2OF4R02INTXC	TC	2	16	ATAGAAGAGCCATTGAATTCGAC	62.937	TCCGACCACCAATACCACCTATT	62.921	113
HM_7815	GD2OF4R01AOWU7	AT	2	12	ATAGCAAAACCGCAACATTAAGA	62.957	TTGCTTTTCTTCTCTCATACCC	62.593	147
HM_7816	GD2OF4R01EABCD	TG	2	20	ATAGCTACTGAAACAAAGGGGTGC	61.958	CGGTTTATTGTAATCATGCTTTGC	62.787	84
HM_7817	GD2OF4R01D4X7Z	TA	2	14	ATATATGAGACCTTTTGGGCTG	63.007	TCTCTTCTGCTCAATCATCTGTG	62.908	151
HM_7818	GD2OF4R02F3I12	GA	2	12	ATATCTAAATGGTGGCTGCTGCT	63.111	CGTGTTCAGTACCTACTTCTCTCTCT	62.694	113
HM_7819	GD2OF4R01AE6G7	TA	2	14	ATATGACAAATCGGGGGTGTCTAA	62.826	GGTAGTCATTGCTGGAGAGAGAGA	63.115	109
HM_7820	GD2OF4R01EXE6X	TG	2	14	ATATGCCCATCATGCAACAGTT	62.558	AGGTAGGAGGCTCTAATGTTCTGT	62.711	129
HM_7821	GD2OF4R02J4NFV	AC	2	12	ATATGGAAAGTTCACAAAGAAAGCAA	62.409	GCACATCACATGAATGTTGACT	63.288	80
HM_7822	GD2OF4R01D7MG5	GT	2	32	ATATGGAATTTCAATGACCAACCG	63.009	TCCTTCTTGGTAGCTTTTCTTACA	62.249	117
HM_7823	GD2OF4R01AM4RH	AC	2	16	ATATGTGTGATGTGCGGTGTGTAT	62.366	TTGTATTTAGCTGAAATATCAGTGCC	61.939	127
HM_7824	GD2OF4R01CYKHS	CT	2	14	ATATTCACCAATCCAAATGTTGCC	63.025	CTCTCACCTCTTCTATTTACAGTT	63.01	155
HM_7825	GD2OF4R02HWW7U	GA	2	24	ATCAAAAATCACGGCTCTCTAC	62.622	AAAGAAAACCACTCTTCACTCTAAATC	61.685	132
HM_7826	GD2OF4R02GRP5A	CT	2	14	ATCAATCATTTGCAACCAATGACA	62.412	TGTAATAATAGTCGTTTCCGGT	62.944	81
HM_7827	GD2OF4R02IMOOQ	TC	2	16	ATCAGCTAACAGGCTCTCGTACAC	62.962	TTCCATCTTGTACTCTGGCATCC	63.643	130
HM_7828	GD2OF4R02F0MIX	CT	2	16	ATCATCTGAGATAGAGCCACAG	60.983	GGGGAACGGAAGTTACTATCTA	60.13	143
HM_7829	GD2OF4R01B342N	AT	2	12	ATCCAAAACCAACCAATCTCCAT	62.8	GGAAACCAAGGTTGGTTTCAGAA	62.598	131
HM_7830	GD2OF4R01AMYL	AT	2	12	ATCCATTCAACCCGTTTCAACTAA	62.813	CTAGGGTTTCAGGTCCTAGTGCTG	62.609	135
HM_7831	GD2OF4R01BQUCR	AT	2	14	ATCCCCCTCTACTGTTTCAAGCTC	63.178	CGCAGATCTGGAGTACTGTCTCT	62.937	134
HM_7832	GD2OF4R01DXOPK	AG	2	14	ATCCCTGTGAGAGCAATGAAGCAC	62.94	TGCATTTCTCATGTGTATGTTCTTT	62.96	127
HM_7833	GD2OF4R02JD6O4	CA	2	16	ATCCTCTTTCCCACTAGCCAAAG	64.005	GAAAGATCTTGTGGCAGACACC	63.343	106
HM_7834	GD2OF4R01B4NYX	AC	2	16	ATCGGTGGTAGCAAAATCCAATA	62.735	TTCAATTGAGCATTGATCTGGAAC	62.5	109
HM_7835	GD2OF4R01EQHIL	TC	2	12	ATCGGTTGAAGAGCAAGGAAGCA	62.811	CCCTAAGCAACCAACTCTCCAAT	62.822	81
HM_7836	GD2OF4R02GHJP4	AG	2	20	ATCGTAATTCAGATGTGCTCACTC	63.678	GCAGATCCAGGACTCGCAATTA	63.699	93
HM_7837	GD2OF4R02IBXRB	AG	2	16	ATGCTCTCCCAACACTCTTCACTT	62.589	ACATCTGGAATTTCTCAACGAAGC	62.926	156
HM_7838	GD2OF4R02FRDXF	AC	2	12	ATGCTCTGACTCAGGCTTTTAAGA	62.712	ATGGTGACAATGCAATGTTTCTG	63.168	160
HM_7839	GD2OF4R01AVCF5	CA	2	16	ATCGTTTGGCTCTCTAGTTTIT	62.623	CACCAAAAGCGAATGTATGAAAGA	62.439	158
HM_7840	GD2OF4R02JG9J5	GA	2	32	ATCTAGGAGATTCTCGCACTGG	63.104	TGATCTCTTGGTAGTGTGTTTTCG	62.606	156
HM_7841	GD2OF4R02FOLRG	AG	2	32	ATCTCCATAGCTCAAGCTCTACAG	63.242	CTCTAATTTGGTTGAGATTGGTGG	62.993	125
HM_7842	GD2OF4R01B6I5D	GA	2	12	ATCTCCGCTAATATCATCTGCTAA	63.162	ACGACCACTACACCAAACTACG	63.462	109
HM_7843	GD2OF4R01BXS1A	TA	2	12	ATCTCTATGGTGTGCAAAATCTCG	63.655	GAGACAACCTACAGCAGGAAGGTGC	63.696	141
HM_7844	GD2OF4R01DNMIY	CT	2	12	ATGAAGACATGGGTTGTGATGTA	62.922	TGACGTTTCAATAGCCGATCTGA	62.959	160
HM_7845	GD2OF4R01CTRRO	TA	2	14	ATGAATAAGAGATCCGCAAAACG	62.641	TAAATGAGCTCCAATGACCAGGAT	63.112	144
HM_7846	GD2OF4R02GSV8Z	GA	2	16	ATGACGACGTATGGATCACTGCTA	62.965	TCCTTTTCTATTGTTATCTCTGTCTA	62.411	157
HM_7847	GD2OF4R01A7WVD	GA	2	16	ATGAGCCATATCATCTGCTGTT	62.94	CGGTCAATCTTATTTCAAGTTCTGC	63.318	137
HM_7848	GD2OF4R02FV2Q	AG	2	14	ATGAGGAGAGAGGGATGGACTTTT	62.753	TTTTTGGCAGATCTTGGGTTGTAT	62.922	155
HM_7849	GD2OF4R02JG6PT	CT	2	24	ATGAGGGTTACACACAATCACCC	63.23	CTCAGCTTCTAGATCCCAAGCTC	63.804	106
HM_7850	GD2OF4R01B1X7C	AT	2	16	ATGCAACACAAGTTTTCTCAGCAG	62.869	ATGCATGGGGTAGTTAAGTCTGA	63.022	125
HM_7851	GD2OF4R01BCT7B	GA	2	30	ATGCATTACTGCGTTATAGGGGTC	62.681	TAGTCTCAACACGTAACCCGTA	63.645	112
HM_7852	GD2OF4R02H6DWQ	GA	2	16	ATGCCCAACCAAAATTTGAAG	63.128	GGTCTGTCTTCGGATCTCGACTA	63.115	110
HM_7853	GD2OF4R01DA9Y0	TG	2	20	ATGGCTGTAAACGAGAAGTGAGGAC	62.925	ACGAAATTTGAAGGGAATAGGTAGC	61.999	128
HM_7854	GD2OF4R02GGH77	TC	2	12	ATGGGCAGAGGAGTAGTAAACAG	63.023	CCGAGAGAGTTGTGAGGGTT	62.863	98
HM_7855	GD2OF4R02JD1LY	CT	2	24	ATGGGTCCCAATTGTGTACTTTT	61.817	AATAATTTACGGTTTCTGTACTACG	61.071	126
HM_7856	GD2OF4R01D1D2U	CT	2	12	ATGGTTACGGTGCTTTCTGTCTG	62.838	AATATACCATCCGTTGCCCTCAAC	62.298	99
HM_7857	GD2OF4R02G4JRB	AC	2	12	ATGTATGGGCAGACAACTTCCAT	63.039	TTTAAGACACCGTTTGTACAGGGG	63.326	123
HM_7858	GD2OF4R01C5I7O	AC	2	16	ATGTCTGTCCAAATATCCCATCAT	62.7	CCACTGAAACCTTCCCTCATGTC	63.212	97
HM_7859	GD2OF4R02G2CTE	AG	2	16	ATGTCTTCACTCTCTTGTCTGCT	62.939	CTGCTTCTATCCCTAACCCACG	62.041	118
HM_7860	GD2OF4R01BJR6U	GA	2	16	ATGTGATAGTGTGAGTGAGCGAGC	62.982	AGAAATCTCTTCTCTATCCCTCCC	63.029	104
HM_7861	GD2OF4R01A27ER	TG	2	14	ATTAGACCAAGCATGTGTGGAAAT	62.926	AACCCAAACGGAATACTACCTCTC	62.61	157
HM_7862	GD2OF4R02G52ND	AC	2	14	ATTATACCAAGGGGATGATGCAAA	62.616	CCTTATGGTGGATTGATTGCTTTT	62.424	123
HM_7863	GD2OF4R02GA7AW	TG	2	16	ATTATTTGAGGGGAAGTTGACGCA	63.971	GTATTCCACACGGCGACGAC	64.904	159
HM_7864	GD2OF4R02HDOZJ	TA	2	14	ATTCAACTCGCAAGGAGAAATACG	62.839	ACTCCACATTTCTCCCTTAAACC	62.78	153
HM_7865	GD2OF4R02G3BNO	CA	2	20	ATTCAAGCAGCAGCATGTAATTT	63.166	TTGACCAGTTGGCAGATTGGAATA	62.832	105
HM_7866	GD2OF4R02GTLMR	GA	2	12	ATTCCAGGGAGTAGATCGAAATCA	62.269	CTTCTATTGCTTTTCGGGACTTC	62.606	115
HM_7867	GD2OF4R01EBQHU	TC	2	20	ATTGACAGAAGCTATTGCTTACC	62.94	AGGGATTCCCTAAAGGGCCTAAG	62.965	105
HM_7868	GD2OF4R01AGWDF	GA	2	16	ATTGAGTCTTAAAAATAGAGAAAGCG	61.687	CCGGCACTTTCTAAAGCTGTATGTA	62.369	80
HM_7869	GD2OF4R01AWDYK	TA	2	14	ATGTGTTGAAACCAACTCCATTT	62.137	GGTTTGTCTGATAAATGAGGGGAA	62.519	156
HM_7870	GD2OF4R01D16I4	TG	2	16	ATTGGAAACTGGCTTCAAGATCA	63.219	CGAATTTAGGGGTACAGGATCTC	62.992	132
HM_7871	GD2OF4R02GMPAD	AT	2	12	ATTGGAAAGCATGGCATTTTCTAT	62.739	CGAGTTGTTGACAAATTTCTCTCT	63.611	105
HM_7872	GD2OF4R01AGSAX	AT	2	14	ATTGTTATGCCAAAGCATCAAGT	62.95	TGGGAGAAAATGATATGACCCTAT	62.887	155
HM_7873	GD2OF4R01BSU1I	CA	2	16	ATTATGATTTGGGACGACGACAG	62.96	AACAAGCCCTTTCATTGTGTGATT	63.035	80
HM_7874	GD2OF4R01COYAN	GA	2	16	ATTTCATGAATCCAGCTCATCTT	62.903	AGTAACGCACAACCTAGTTCTATTG	62.006	92
HM_7875	GD2OF4R02IGN47	GT	2	12	ATTTCCGTCAAAACCGTACAAAG	63.321	GGCTTGATCTCCTTATCTCCCTC	62.772	124
HM_7876	GD2OF4R02F5QOI	GA	2	16	ATTTCGAGGAGTATGGAGTGTTT	62.881	GTACACCTTCTGCTCTCTCGGTA	63.023	125
HM_7877	GD2OF4R01CGNDM	AG	2	20	ATTTTCGTTATTTCTTCAATGCC	63.385	AAAGACGGAGAGAGACTAAGGAAGC	62.914	119
HM_7878	GD2OF4R02I1NIV	TG	2	14	ATTTGAAACGGGACTCTGAGTGT	63.392	GTGGCATCGAACCTTCTCAAT	62.58	94
HM_7879	GD2OF4R01DD8JZ	AG	2	16	ATTTTATTGCATTTTCTGACCCC	63.186	GAAACAAAACCAACTCCCACTCC	64.101	92
HM_7880	GD2OF4R01D12Z2	GA	2	14	ATTTTGTGATTTTCTTGGGGGAT	62.868	ATCGTCCATTTCCCTCTTTTCTT	62.673	144
HM_7881	GD2OF4R01B2N96	GA	2	16	CAAAAACACTTATGAACCAACAGCA	62.369	GGTGTATTATGTGAGAGCAAGATCA	61.722	97
HM_7882	GD2OF4R02H8CXT	AG	2	20	CAAAAACAAACCAAAACCAACAA	62.055	TGTATTCTTATACATCATATTGCG	61.209	110
HM_7883	GD2OF4R01C17ZE	CA	2	14	CAAAAACCTCTCAATGTATATCGC	62.932	TGTTACTGCTCTTCACTTATACCC	62.659	157
HM_7884	GD2OF4R02GK6Y	CA	2	16	CAAAAGGACACCACTTATTCAA	63.137	CAAAAATGTTTGGCCATCTGTA	62.148	156
HM_7885	GD2OF4R01DLKSH	TA	2	12	CAAAATATCATTTGCAGCAACAA	62.956	TCCCGAATTTTACAGCAACCAAC	63.324	145

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7886	GD2OF4R01A9880	AC	2	20	CAAAATCAAAGTACTGCACAAAGCA	62.675	TTGTTGACCTTTCAGCTTATCTTCC	62.958	85
HM_7887	GD2OF4R01D4NTK	TC	2	12	CAAAATCATCATACCAACCAATAAAA	61.235	AGTCTCCCTCTCCGTGAAATGT	61.408	93
HM_7888	GD2OF4R02JOVXE	GT	2	12	CAAAACAAACAGACACATCCCAAA	63.146	CACACATGTACAGAAGCACAGCAC	63.019	148
HM_7889	GD2OF4R02JZNYO	GT	2	12	CAAAACAAACAGACACATCCCAAA	63.146	CACACATGTACAGAAGCACAGCAC	63.019	148
HM_7890	GD2OF4R02IR95F	AG	2	24	CAAAACAAAGCTGCTCCCTACATT	62.849	CGCTCATGCATACTCTATGTCC	63.192	126
HM_7891	GD2OF4R02JHPBS	CT	2	16	CAAAACACGATCAATGCACAGAAA	63.265	GTTTGTGTTGGTTGGTTGGTAG	62.726	160
HM_7892	GD2OF4R02GG9LG	AG	2	14	CAAAACATAAATCAACGGTTAGGGG	62.625	CGCTGCTCTCTTATTTGGTAATCA	63.529	111
HM_7893	GD2OF4R02FMIQA	GA	2	16	CAAACTAAGAGCCGTGAGGTAGA	63.028	CCCTCATTGGACTATGTAACCAAG	62.894	125
HM_7894	GD2OF4R02IQ3NT	GA	2	14	CAAGATGAGTTTTGAGGGGTGAAG	61.336	GAAGACCATTCTAGTTTTGTACTTTTG	60.91	116
HM_7895	GD2OF4R02GJSRA	CA	2	20	CAAAATAGCATCTACCACTAATACCC	61.201	CGTGGGTGAGTACGATTTTATTA	61.369	90
HM_7896	GD2OF4R01CDR4C	TG	2	12	CAAAATCAAAACAAAGGGTCAAGGTC	63.006	CGTAAATCTTTCTATACCTTACCCCC	62.351	128
HM_7897	GD2OF4R02JSP7	AT	2	16	CAAAATGAGTCAGTGATGGAAATCG	62.921	CAAAACGCTTCAACGAGTCCAC	63.06	125
HM_7898	GD2OF4R01BPDK3	CT	2	12	CAAAATGCTTCAACACATTTTCTCA	62.628	ATTTTAGAGCTTCAAGCGGAGAC	63.313	86
HM_7899	GD2OF4R01ASIP0	AG	2	14	CAAAATGATGTAATGGGTGTATTGAA	61.178	GGGATTCTCGAGGTAGTCAGTATC	60.699	131
HM_7900	GD2OF4R02IOQG6	AT	2	14	CAACAAGCAACACATCTCATCT	63.388	CGCTCTACTCTTGATTTTCTCTCCTT	62.836	124
HM_7901	GD2OF4R02I68X0	GA	2	20	CAACATGCAGATGAATGTGCTAAA	62.233	AGATAATAAGGGGAAGAGAACC	62.132	144
HM_7902	GD2OF4R02HP7JA	AT	2	12	CAACCAAAAAATCATTCACAAACCT	62.315	GTTTAAAGTAGGAGGTCTGGCTCG	62.601	152
HM_7903	GD2OF4R02ID85GO	CT	2	14	CAACCATCAAGTACAGTGTCTGT	63.173	ACATGACAAAGTCAAAAGGAAGGG	62.696	130
HM_7904	GD2OF4R02I8AGG	AT	2	16	CAACCTACTCAAACTAGCAGTCTG	61.392	TGTGCTATCTCAAGTGTGGTTAAG	60.93	159
HM_7905	GD2OF4R02FZCQU	TA	2	16	CAACTGATCTACGCCCTGTTC	64.032	TTGGAAAACTAGTTCAGTGCCT	63.246	148
HM_7906	GD2OF4R01D4RF5	AG	2	12	CAAGAAAAGGGAAGGTGTGAGGAA	62.892	CACCTGACCTCTGTGTACTGCTCT	63.244	124
HM_7907	GD2OF4R02JPGK5	AT	2	12	CAAGAGATCTCTGTAATCGCCAAT	62.828	TTGGGATATTGGATCAACAGTTG	62.08	135
HM_7908	GD2OF4R01AOJNN	GA	2	20	CAAGCCCTTAAAGAGGGACAGATA	62.013	GGATCTTCAAGCTGAATCTCAA	63	98
HM_7909	GD2OF4R01B18LE	AT	2	14	CAAGCCGCACATGATTTTAGA	62.307	TGGGTATGCCATATAAACAATTCG	61.864	132
HM_7910	GD2OF4R01B5HYP	GA	2	20	CAAGGAGCAACATGCACTTA	62.326	GAATACAGTTTCAAGCTTCCAGG	62.411	135
HM_7911	GD2OF4R02IH7Z5	AC	2	16	CAAGGAGAGAAGAGAATCACCCA	63.085	TTGTAGCCGACTTGAAGAATGTG	62.642	94
HM_7912	GD2OF4R02HYW5E	AT	2	16	CAAGGAGATGAAGCAGAACACGAT	63.988	TAACCCAACTTCAAGCAGAAAAGG	63.528	159
HM_7913	GD2OF4R02GMH2H	GA	2	24	CAAGGGGTATTGAGCTTACCTGTG	63.125	CTTTTCTCTTCCAAACAACT	62.88	94
HM_7914	GD2OF4R02GDY5G	AT	2	16	CAATCGGCCAAATGTGATCTCAAG	62.845	AGCTCAGTGGTTTGTTCATTTTTG	62.635	134
HM_7915	GD2OF4R02HVB8W	TA	2	14	CAATTATGAAATGCTTCTCCCTCG	63.095	AACCATGGGAGTTCAAGACAGG	63.633	95
HM_7916	GD2OF4R02GKYEY	TG	2	16	CAATTGTAGGTTGTGCTTGTGTTG	62.754	AAACAAGCTAGTGACCTGTTTGGG	62.833	111
HM_7917	GD2OF4R01DOVHO	GT	2	16	CAATTTAATCTGAGCAGAGTGGG	63.014	AACCTGATCAGCGAAGAAAGGTAA	62.522	144
HM_7918	GD2OF4R01AMWJC	TC	2	16	CAATTTTGGCAGATCTACTTTGC	63.138	TCCTGTATCTCGCTTCTCTCTCA	63.102	95
HM_7919	GD2OF4R02FYB5T	AG	2	16	CAATTTTGGCGAATAGCTTCTCT	63.879	ACCTGCCATACCTTTTCCGCT	62.184	100
HM_7920	GD2OF4R02J4HTX	TG	2	16	CAACAAATAAAAAACACATGGGGA	62.829	CTTCTCTCCCTACCTACTTAT	62.944	95
HM_7921	GD2OF4R02GTC5O	CA	2	12	CACAATGCCAATACGACATCTTA	63.059	ATGCTCTGTTTGTGAATGTGCAA	63.946	159
HM_7922	GD2OF4R02HE4UZ	CA	2	16	CAACAATCCACATAGACTTCCA	62.487	AGTTATGGGCTGCCAGTTTCTAT	63.313	152
HM_7923	GD2OF4R01AZZ1E	AC	2	20	CACAGTCTCTGGAAGACGTACAA	62.824	ATTACGCTCTGGATCCATGTTGT	63.039	142
HM_7924	GD2OF4R02H9CKR	AT	2	12	CACAGTTTGCTCGTTTAAAGT	62.752	GTTTGTACCGTGTAAAGTGTGTG	62.75	145
HM_7925	GD2OF4R02JOCAO	CT	2	16	CACATACAGGACCGGCTAGCTACT	62.959	ATACCTTCTCTTGACTGTGCGGT	62.909	99
HM_7926	GD2OF4R01CRIT6	TC	2	16	CACATCTTTTGACCAACCTTCT	62.895	CGTACCAACGGGAGCTGTAAATA	63.236	135
HM_7927	GD2OF4R01B8FE0	GA	2	16	CACATTTGTGGGACATTTTCTG	62.614	CCCTTTATCCCTTGAACACACA	62.41	158
HM_7928	GD2OF4R01C14L3	GA	2	14	CACAGTACACCTTCTGATGATGC	63.04	AATTTTCCCTCACCTCATTTTTC	62.679	108
HM_7929	GD2OF4R01ATPKX	AG	2	12	CACCATAGATCTGATCGAAACCC	63	TCCTTCTCTCTTCCAGAAATGTTGC	62.313	153
HM_7930	GD2OF4R02GM99G	AG	2	16	CACCCAGTTGAAGATCTGAACAAA	62.592	CCATTTCTATCACTTTCGGTCCAC	63.009	160
HM_7931	GD2OF4R02JWUFK	TG	2	16	CACCGAAGCTTTCAACATCTTTCT	63.031	TGTTTGTCTCTTCTCCCTCGTC	63.111	139
HM_7932	GD2OF4R02JW768	CA	2	12	CAGGGATGGTTCAAAAGTACACA	63.159	AGCACCAACTGTATCTCGAACTC	63.04	135
HM_7933	GD2OF4R02G2YRK	CT	2	12	CAGCTTATAGTTCGCAAAATTTGAGT	62.657	GCTTCAGCAGTTGTCTGGTAAAGTT	62.272	158
HM_7934	GD2OF4R01DEUOQ	TA	2	16	CACTAAAACCTTGTCTTCTGCTG	63.154	GCACAATTTAGTGCAATGGTAGT	62.254	156
HM_7935	GD2OF4R01C874N	TC	2	16	CACTAGCCGAGTACAATCGTAGCA	62.783	GTGGTTGTGATTTGTGTGACCA	62.947	135
HM_7936	GD2OF4R01CEWF6	GT	2	16	CATCGTGAAATCTCTTTTCCGT	62.921	TCCTGCTACTGTATCTGATCCC	62.8	160
HM_7937	GD2OF4R01BLHLG	AG	2	14	CACTGAACCTACGGAACATCGAA	61.446	TTTTAGTCTCAGCTGTGTACACTCTC	60.68	117
HM_7938	GD2OF4R01ASQ8K	CT	2	12	CACTGCCAAAATAAAACAAATTC	61.918	TCCTTTGGGTGAGTGAACATAGAA	61.063	141
HM_7939	GD2OF4R01APZV1	GA	2	16	CATCGCAATGCGATCAACTGTAG	63.093	CTTTTCAATCTCCAGCCCTCT	63.078	146
HM_7940	GD2OF4R02GDM4H	AT	2	16	CACTGGAACCATGAATAATGCTG	62.731	GATTTTGTAGTACGCACATTCACG	61.868	160
HM_7941	GD2OF4R02H983	CT	2	12	CACTTGGCATGGTTAATTTCTCT	62.922	CGCTAATTCAGGTTGTTGAAGAGAG	62.644	130
HM_7942	GD2OF4R01D9R2T	GA	2	14	CACTTGTGTGCTCCAAAGTATGTC	62.958	CCAATTGGTTCTGGTATGCTCTT	62.619	91
HM_7943	GD2OF4R01DMHFE	CA	2	14	CACCTTAAACCAACAAAGACGAG	63.121	CAGTAAGTGCTGCTCAATCTCT	63.044	138
HM_7944	GD2OF4R01AZH1X	AT	2	16	CATTTGATAGTGTGGGTCTCTCT	63.023	AACCTGCTTTCATATTACATCTC	62.51	141
HM_7945	GD2OF4R02JTYSD	TA	2	20	CAGAACGATCAGTTTGAAGTGG	62.382	GTAACACTCTCGCTCTCTGCTC	63.167	142
HM_7946	GD2OF4R01BGYE1	AC	2	16	CAGATGATGGTTCTCACTGATGG	63.016	TGTATGCAGGATTTGTCAGCAGTT	63.078	140
HM_7947	GD2OF4R02G3I62	AT	2	20	AGCAAGGATTTCAAGCAAGTATTC	63.341	TGGAAGCAACAATCGTAGAACATC	62.529	140
HM_7948	GD2OF4R01BDBPX	AT	2	14	CAGCAATAGCTGGAATGTTTGA	62.552	AAGCTTAGGAATACACACGACAC	61.752	105
HM_7949	GD2OF4R01BJTVW	AG	2	20	CAGCACTCTCTTACTGATCGTT	63.137	TAACCTTCACTCCACCACTATTG	63.202	112
HM_7950	GD2OF4R02FUZBY	TA	2	12	CAGCCAAACGTGGGTACTGTAT	63.354	GGCTTGAAGTTGAACCGATAAAA	62.639	125
HM_7951	GD2OF4R02G2OZG	AC	2	20	CAGCCCATCTTTCGACATCTTATC	63.334	AAACTCTGTTTCAAAATCCGCA	63.134	134
HM_7952	GD2OF4R02JXE8E	AG	2	14	CAGCGAATAAAGAAAGTCAAAACAAA	61.315	CAAAATTGATTAAAGTCAAGCTGTG	62.255	101
HM_7953	GD2OF4R01DVD1H	AG	2	16	CAGTACATTCACCAAGACACCAA	63.259	TGTGAAATCGAACCGTAGAATCA	62.832	105
HM_7954	GD2OF4R01BYD7Y	GA	2	12	CAGTAGAGAAATGGAGTCCGGAGA	63.098	CACCAAAACCGAATCACTACTCG	62.944	99
HM_7955	GD2OF4R01BZE51	AC	2	12	CAGTCAATCAACTCGTACATTTCA	62.426	TTTCAGTTAAGTCAATTATCTCCAAA	61.732	114
HM_7956	GD2OF4R02ICY3	AT	2	12	CAGTCAATAAGTGAAGACATTTGC	60.914	CACCTCCCAAGTGAACAAGATA	61.748	156
HM_7957	GD2OF4R01BUJXG	GA	2	14	CAGTCAATCAAGTATGTGATGTG	62.633	AAAGACACTACCGCTGTGACAA	63.05	141
HM_7958	GD2OF4R01CD8WT	GA	2	12	CAGTGTGATTTGGCAAAAATGAGG	62.814	CTTTTACCACGCTCAACCACTC	63.233	113
HM_7959	GD2OF4R02ILEAD	GA	2	24	CAGTTACACGATGACAGAGACCG	63.168	CACACACCAACCACTACACAATTT	63.063	128
HM_7960	GD2OF4R01BDBMT	AT	2	16	CATAAATCTTATGCTCTCTTGGG	62.371	ATAACACAGATGCAAGTCCAACTC	62.652	121
HM_7961	GD2OF4R02FZN2P	CA	2	12	CATAAATCTTTCGCAAGCTCTGTT	62.849	AGGGAACCTGGTTCTCTGTTGTT	63.292	91
HM_7962	GD2OF4R02H5SLP	AT	2	12	CATACACACGAAAAGGACATTGA	63.15	TTTTCCCGTAGTAAACCGGAATA	63.715	124
HM_7963	GD2OF4R01DOT2F	TG	2	12	CATACCCCATGTAGCATTTTGA	62.946	TCACATTTCAAGCTTAGTTTTCG	62.756	104
HM_7964	GD2OF4R01BCQEU	CT	2	12	CATATTTTACAGGCTTAGACAGAGCA	63.064	TGAGGGGGAGGTTGTGAGAGTTA	63.208	142
HM_7965	GD2OF4R01CWDNF	AC	2	14	CATCAGTGACCAACTAGATGGGG	62.919	ACACCTCCAATTTTCTCGTGTCTA	63.239	101
HM_7966	GD2OF4R01AVB9T	CT	2	14	CATCATCTGCAAGACAAACCAAT	62.412	AGCTATAGATACATGAATCGACGATGA	61.445	114
HM_7967	GD2OF4R02G80JT	CT	2	14	CATCATGTTTTATGAGCACTGAGG	60.896	AAAAAGGAAGAGAAGGCAATG	60.114	151
HM_7968	GD2OF4R01CHV8D	TG	2	16	CATCCCCCTCCCCATATAAAAA	62.945	AATGGTCTTATGGCAGTGACAGT	63.141	151
HM_7969	GD2OF4R02INDRA	AG	2	12	CATCTTGGTTTACACCTCTCTCT	61.873	AAATAGCTTCTTCTCTGCGCATA	62.489	145
HM_7970	GD2OF4R01BHA8C	CA	2	12	CATGCAAAATGATGACACAAATAA	62.78	ACATGTGTGATTTGTGCAAAAGG	63.074	135
HM_7971	GD2OF4R02HGM0H	AT	2	12	CATGGAGCTCCCTTAAATATGAT	62.733	GGCCGACCTACCTCTCTTAGACT	62.507	150
HM_7972	GD2OF4R01AMIS5P	TA	2	12	CATGGGATGGGCAATTTACTA	62.814	CGCCCTCATGACCAATAAGTGT	63.341	160
HM_7973	GD2OF4R02FZCEZ	AC	2	16	CATGTCCAGCAAGAAACAAGGATA	62.514	GTCATCCCTGTCCGATCTTTT	62.673	131
HM_7974	GD2OF4R01AUA2Y	AT	2	12	CATGTTTCCGATTTCTCTCTGAT	62.786	AAGCTCGGAATACACCGGTAAAG	63.044	153
HM_7975	GD2OF4R02ILF2B	AT	2	16	CATTTCTCATGCACTGATGATG	63.083	AGAGTTGGTGTGGGAAATCTCAA	63.212	159
HM_7976	GD2OF4R02IBF8Z	CT	2	14	CATTTCTGATTTGGTCAATTTTGA	62.832	CATATTGGGCTAACTCTCACACC	63.022	129
HM_7977	GD2OF4R02HERGU	AG	2	14	CATTGAACAGAGAGACAAACATTGA	62.753	GACGGGCAATAGTGCTCTCTG	62.236	83
HM_7978	GD2OF4R02HERGU	AG	2	14	CATTGAACAGAGAGACAAACATTGA	62.753	GACGGGCAATAGTGCTCTCTG	62.236	83
HM_7979	GD2OF4R01ECM3X	AG	2	16	CATTGTGGGTTAGTGAGGAGTGTG	62.93	CAGACAAAGGCCAGATGTAAGAA	63.03	127
HM_7980	GD2OF4R02IFAJU	TC	2	12	CATTTCTTATGGGAAGGATGGAA	61.707	CGCTCTTCTATTGAACATTAAT	60.728	143

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_7981	GD2OF4R01AN1E	CA	2	14	CATTTTCCAATTGCTCCACATTC	62.706	ACAAACCTTTTAAATGCGTGTGA	61.871	133
HM_7982	GD2OF4R01AHLZ3	TG	2	16	CCAAAAGGGCCAAAACATGTATAA	63.022	GTAACCCGATGCTGTTCCATTGTT	63.353	154
HM_7983	GD2OF4R01C874N	GT	2	16	CCAAAAGGGGCTAGAGAAAAGA	63.077	ACTAACAAATTGCCACCAATTAACC	62.247	81
HM_7984	GD2OF4R02H5O4Y	AT	2	12	CCAAAGAATGAGCTAGAGACGGAT	62.199	TCAATTGAGACGAATCGGTAGTGA	63.038	122
HM_7985	GD2OF4R02GXPGH	AT	2	14	CCAAAGGACTCAATCCACAACCTC	63.212	GCCAACTTTTCTTTTCCCTTGT	62.91	145
HM_7986	GD2OF4R01DN48P	TG	2	16	CCAAAGGGTTTCTTAATTGGGAT	62.501	GGGTTGGTTATCATCTCTATAAGGC	62.295	94
HM_7987	GD2OF4R02HFB14	AC	2	16	CCAAATTAAGGGATCTTGCCCTACT	62.795	TTGGTACGTAGGTATGTGTCCA	62.555	148
HM_7988	GD2OF4R02GMT0A	AT	2	12	CCAAACAATTAACACCGCAATTTT	63.942	GATGTTGAAATCAATGGTGATGGA	63.018	159
HM_7989	GD2OF4R01C9MIQ	TC	2	12	CCAACACACATAACTCTGGGACAC	62.827	TAGCAGAGTAATGGGATTCGAGA	63.317	106
HM_7990	GD2OF4R02H681X	TA	2	16	CCAACCTTTTGAGCTGTGATTTG	63.014	CATCTTTCCCAATCCTTTAATGT	62.514	146
HM_7991	GD2OF4R01B2KOG	CT	2	12	CCAACGGTAACCCCAAGTTTACT	63.39	CAACGAGTTTCATCTCTGTCCA	62.919	121
HM_7992	GD2OF4R01EE6QJ	GT	2	14	CCAACGTAGAAAATACACGAGTTGC	60.432	GACATCACAGATATCAACAATGTGGT	61.264	112
HM_7993	GD2OF4R01E473C	AG	2	16	CCAACCTTGAAACAACCACTGGAAGA	62.605	CCACTATTTTCTCGCAACCTCATCT	62.923	83
HM_7994	GD2OF4R01ETMDC	TA	2	20	CCAAAGAGATACCGCTATACCAACA	61.525	ACAATTGATTGAATGTTGAAGTCAG	60.637	151
HM_7995	GD2OF4R01CH6VA	GA	2	14	CCAAGATAGAGCGGAAAAGATGA	62.909	GAAGAGACCAATAAGGACACTGCC	62.498	146
HM_7996	GD2OF4R02FMUYO	AG	2	20	CCAATCAAGTGCAATTTCTGTTC	63.367	CTGTGTTCTGAGCTTCACACCTT	62.943	108
HM_7997	GD2OF4R01BLC4E	CT	2	16	CCAATCATGTGCCATTTATTTTGA	62.835	GGCGTGATCAGACCACTCTAGTT	63.04	117
HM_7998	GD2OF4R02IFTWH	CA	2	24	CCAATCTCAAAATTAAGCAACAAG	63.014	AATCTTTTCTTTGTAACAGAAATGGTGA	62.371	142
HM_7999	GD2OF4R02GEFQX	GA	2	16	CCAATGAATTGACAAAATCCGGAT	63.105	TCTACTTCACTTTCTTACACCTTCC	62.237	126
HM_8000	GD2OF4R01B4TIV	GA	2	24	CCACAATAGATCATCGAATGCACA	63.249	TCGTAATCGTAATCGTAAGTCCAAAT	62.334	153
HM_8001	GD2OF4R01AOOAC	AT	2	12	CCACACAGAAAAAGTGGAAAGACA	62.605	AGGCATGTAATCCCAATCTCAACT	62.198	157
HM_8002	GD2OF4R01CRU3I	AG	2	20	CCACCAACAACATAAATGGTTCA	62.829	TCAATTTTGAATTTGATCGGTAGTCTC	62.745	147
HM_8003	GD2OF4R01DYMQD	GA	2	40	CCACCTCATCAATCAATGTGTATC	62.382	CGTACCTACGGTCTGCTCTACTA	61.744	160
HM_8004	GD2OF4R02GMKT3	TC	2	16	CCACCTCTCCCACTTCTCTCATTT	62.15	CTGTCTCATGTGATTGCTGAGGAT	62.817	99
HM_8005	GD2OF4R01C8MKO	CA	2	20	CCACCTGAAAATGGCAATGAT	61.985	GGCTCTACTGTGTTTGAATGTCCA	61.621	159
HM_8006	GD2OF4R01EU08G	AT	2	14	CCACGAGGAATATTACATTGCACA	63.059	GAATTGAGACACACTAAACACACAA	62.546	124
HM_8007	GD2OF4R02GS9A8	AT	2	12	CCACTCTTGGAAATGACCAAAATTC	62.996	CTCATTGTCCGTCGGTTAATGTA	62.226	158
HM_8008	GD2OF4R02G9OCD	AG	2	20	CCAGATTTGAGAGAACTGCTTTAGG	61.836	ATTCTATAATGCGAAGCTGGTTGG	62.654	98
HM_8009	GD2OF4R02HP7JA	GT	2	12	CCAGCCTCCACAATAATTAACACAA	63.311	GGGAGGCTCTGTGCAAGAAATGAAT	64.013	129
HM_8010	GD2OF4R02INDYK	GA	2	30	CAGGTTTTCTCAAACTGTGCACAC	63.332	AGTGGGTAGTGTGTTCTACCAACG	63.569	137
HM_8011	GD2OF4R01ANE9T	TC	2	16	CCAGTAAAGATACCTCCCAAC	63.074	TTGCTTCTGTCAGATCTACCAATTA	63.184	125
HM_8012	GD2OF4R02HWMK6	CT	2	12	CCATACAACCTTTACAGACCAAA	63.21	GGGTATACCGCCAGTTAGGATCA	63.341	86
HM_8013	GD2OF4R02ITPNH	AT	2	16	CCATAGCTTCTCAATGTCAATTCG	63.136	ACACGTAATACTTGACATTACATGCG	62.358	80
HM_8014	GD2OF4R02HEB1V	AG	2	16	CCATCCCAACACACTCTCTCTCT	63.341	CTCCATGTGAATGGCAATGTAGA	63.257	90
HM_8015	GD2OF4R01CZSU1	AT	2	12	CCATCTGACTATCAGTCTACATAAAGA	60.302	TCTTGATCTGACTTTCTGGGTAAAAA	60.707	155
HM_8016	GD2OF4R01DK4XK	AG	2	14	CCATGCTATACCATCCCAACAT	63.231	TTGATTGTAACATTGCTGGGAGA	62.946	148
HM_8017	GD2OF4R02H470C	AG	2	32	CCATGTACACTTACACCAAAATCT	62.071	GAACCAACCAACTAGTAACCCGAA	62.521	174
HM_8018	GD2OF4R02FOE9I	TA	2	12	CCATTAAGGTTGTGATCTTGATACGA	62.451	CTCTTTTACGGACAGGTAGAGAG	62.791	115
HM_8019	GD2OF4R02I2R1E	TA	2	12	CCATTAACCCAACCTCAATACACAAC	62.079	TCACCTAAGTATGTTGTGGTGCA	62.769	89
HM_8020	GD2OF4R01AV57D	AG	2	20	CCATTGGTGGTGGTGTGATTGTGA	62.729	AGCAAGAAGACCAAACTCATTTCT	61.911	145
HM_8021	GD2OF4R02F07YN	AG	2	14	CCATTTACAGTGACAGTTGGCGAC	62.955	GCTTGGGTACGTTTGGTACGCTCTA	63.462	84
HM_8022	GD2OF4R01EXNWA	CT	2	16	CCATTTCAATATCTCTCTGGCAC	63.021	CTCTGATGGGTCTTCCATAACCG	63.006	147
HM_8023	GD2OF4R02FYAWC	TG	2	12	CCCAAAACCAATCTCTGCCAATA	62.993	TCTCAGCTCTTCACAAACTGAAAA	62.606	137
HM_8024	GD2OF4R02GF48D	GA	2	14	CCCAAAAGCTAAGTTTTTCAACAGC	63.138	ATGAATTTGCAGCTCTTGGCTTC	63.979	157
HM_8025	GD2OF4R01BWP80	AT	2	20	CCCAACAACAAATTCATCATATAACC	62.424	AATCTCAATCTTGAGGTGCTGG	62.91	156
HM_8026	GD2OF4R02FVL5I	GA	2	20	CCCAACATCTTTTTCTCGGTACAT	62.508	CTCTTGCAGGATGTAACCACTAA	62.811	156
HM_8027	GD2OF4R01EHU5	TA	2	14	CCCAATATACATACAGGATAAACC	62.022	CCCTCGTAGACTCCCAATTAAGT	61.888	115
HM_8028	GD2OF4R02IG7Y8	TG	2	14	CCCAATGAAAACTACCAAAAAGC	62.932	CTAGAGATCGCTGTTCCAGCAAT	63.035	111
HM_8029	GD2OF4R02HKDDG	AC	2	40	CCCAATTAGAAAGGTGGAATGAA	62.397	CATCAGCTGTAAGGTCTCTTAATACTG	61.867	125
HM_8030	GD2OF4R02GEME5	GA	2	12	CCCACTTTGTTGACCACTCAATG	62.723	GGAGGAACCTGAGTCACTTGAAAA	62.997	147
HM_8031	GD2OF4R01AQB6I	AG	2	16	CCAGATTAGGAAAGCAAGCTGAA	62.701	GGTTTTGGTTTCTGTCACTAGCT	62.048	139
HM_8032	GD2OF4R02GR92J	AT	2	14	CCCAATTGATTTCAAGCTTTTATG	62.814	TGTTGATATGTTTATGAGTTGGAAGCA	61.868	107
HM_8033	GD2OF4R01DAIY4	AG	2	32	CCCAAAATCAAAAATCAAAAATCACA	63.185	CCCGACTAACCAAACTACATACACA	62.547	105
HM_8034	GD2OF4R01EZHC1	AT	2	12	CCCATGTTGTTTGTGATCTCTCA	64.047	GGCTCCAATCCCTCATCTGTTAAA	63.569	125
HM_8035	GD2OF4R02F27MT	TC	2	14	CCCCCTCCGTTATATTACCGTTTA	63.086	CAATGGAGGTAGTAAGGTTGGTTG	62.905	144
HM_8036	GD2OF4R02JRMH5	AG	2	40	CCCGGCGATAGTCAGATACAACCT	63.652	CTCTCTCTACTACTACTACTCTCT	62.706	170
HM_8037	GD2OF4R01DS24B	GA	2	14	CCCTACACCAAGGCTCTCTCATATA	62.907	TATAGATATGTGTGCGGAGTGTG	62.263	99
HM_8038	GD2OF4R01D29D7	TC	2	14	CCCTACCAACCAAAATGATATATT	62.108	GGTCTGTGTTCAAAATGGTAGTGA	61.486	100
HM_8039	GD2OF4R02GBXOR	AT	2	12	CCCTAGGTTTAAAGCAATTTGGG	62.905	TGTTCTGCTTCAACAGTTGGAATA	63.048	139
HM_8040	GD2OF4R01A823C	TC	2	16	CCCTTCGCCATCATATACAGTTTC	62.925	GTTGGTTGTAGTGTGTCGCTT	63.301	87
HM_8041	GD2OF4R01DSB7U	TG	2	12	CCGAACAATCATCTGCAAAATTA	62.244	GATCCAGCTCCGAGAACATAAGTC	62.234	135
HM_8042	GD2OF4R01DPR8B	GA	2	14	CCGAAGAAATGGACATCTTCAAG	63.202	CCTTCTAATGGCTCATCTCCAAGA	63.996	122
HM_8043	GD2OF4R01ASJYK	GA	2	12	CCGAATCAAAATGACGATAGAACA	62.959	AGTCCGGTGAGGTTTCTTCTCTCT	63.828	129
HM_8044	GD2OF4R01C8988	AT	2	20	CCGAATTAAGAGGTTACAGACACC	63.051	CATCGACTTCACTTCTTCCGAAT	62.91	129
HM_8045	GD2OF4R01EF9KG	CA	2	16	CCGAGACCATTCCTCTTCTTCTT	63.273	TATAATTAACCTACGCCACCCAA	62.554	139
HM_8046	GD2OF4R02JQHL0	GA	2	20	CCGATTTCTGATTTAATGCTGGA	63.41	AGCTTTTGTCTCCAGATATGCCAG	63.035	82
HM_8047	GD2OF4R02IT4AA	AG	2	14	CGCCCATCGTAGAAGCACTTTTA	63.641	TTCTTGAAGATTGAAAAAGCGAAG	63.014	154
HM_8048	GD2OF4R02J38DG	TA	2	16	CCGCTAAACACCTCAAAATTTGA	63.329	GCTGCCTTGCTAACCTCTTGAC	62.623	159
HM_8049	GD2OF4R01ARSX5	AC	2	14	CCGGAGTGATCATCATTTATAGA	62.367	TCCGTAATAACATGAATAATTGCTCG	62.32	104
HM_8050	GD2OF4R02G10ZF	TC	2	12	CCGGTACTTTCTGGGACCTTAA	62.809	GAAGCAGAGAGTTTGAGAGGGAGA	62.678	99
HM_8051	GD2OF4R01CH46E	GA	2	16	CCGGTATCAGTCAATAAGCAAC	62.716	AATTTGGTTTACCACTTAACCGG	63.28	117
HM_8052	GD2OF4R01DTRM5	TC	2	12	CCTAAGCAAACTAATCTCCAGCTCT	62.831	TTGGATCCGTGCTTTGAATATGA	62.705	93
HM_8053	GD2OF4R01AUZQK	GA	2	20	CCTAGATGATATCCGAAGGTTGGG	63.275	ATTCGAATCATTCACAGCTCTCT	62.916	135
HM_8054	GD2OF4R01EWUJG	TA	2	16	CCTATCTCAGCTAGCCCTGCAAAAT	64.105	CGGGACTTGCTGTGATCATATTCT	64.509	192
HM_8055	GD2OF4R01EHOZ8	GA	2	12	CCTATGACAGTTCAAGGAAGAAGCA	63.03	CAAAACAAAAACCAACCAACACACA	62.113	147
HM_8056	GD2OF4R01BEI13	AG	2	12	CCTCGTGGATCGAGAAATGATGT	62.923	TAGCCGCTCTCAAGTAACCAACA	63.247	159
HM_8057	GD2OF4R01CWTPY	AG	2	16	CCTCTCTCATATCATATCCAATTTCC	61.527	TTAGAGAGTTAATCAAGCAACG	60.982	80
HM_8058	GD2OF4R01EC5JI	AC	2	12	CTTGCCCAACTCGGATTAATAATTAG	63.019	AAGTCCAGGTTCTGTGTTCTCCAT	62.471	125
HM_8059	GD2OF4R01BD00X	TA	2	12	CTGCTCTACAGGATGAGAAATTA	63.636	ATATAGAGAGATCAGGTGCGGGTG	62.813	132
HM_8060	GD2OF4R02JARZA	CT	2	20	CTTTCACATTAATTTCTTCTTCAACA	62.741	GAGAGAGGACCAATATGTGTTGCC	63.234	149
HM_8061	GD2OF4R02J18DA	CT	2	14	CTTGTCCATGTGATGCTCTCTGT	62.003	CACAGCACTTGTTTCTATCATCA	61.357	153
HM_8062	GD2OF4R01EOHLW	AT	2	12	CTTGTTCACCTTAAGAGCTGACC	62.61	ACCATGGCTACTATCTGGGTGTT	63.171	135
HM_8063	GD2OF4R01A1BEH	AG	2	16	CTTTTCCAAGCAAGCACTAAAAA	62.847	GACTCTAATGGTCCGACAAAGCAT	62.827	132
HM_8064	GD2OF4R02JVR3R	GA	2	24	CGAAAAGGCCATCATTAAGAAAGC	62.942	TCCAAAATACCAACCGAAAAGAGA	63.002	145
HM_8065	GD2OF4R02G3TRI	GA	2	16	CGAAAGAGAAGGTAGCAATGGG	63.309	AGTAGCATGTTAGTGCTCCATAACCC	62.869	82
HM_8066	GD2OF4R02G26EC	CA	2	16	CGAAATCTTTTCCGAAAAGGGTA	63.548	GCATTGCTGCTCTGATTTAAGGT	62.963	144
HM_8067	GD2OF4R02G4A8D	GT	2	12	CGAAGTCTATAAAGCGGACATCCA	63.421	TCGGTCAGAGTTTCTCTATTTATCC	63.089	123
HM_8068	GD2OF4R02GFFRZ	AC	2	16	CGAATTCACACAAGCTTTACCTCA	62.642	TTATGTCATGAATTGCAAGTGGTT	62.631	156
HM_8069	GD2OF4R02JVL2W	TC	2	14	CGACAATACCCCTAGGACATATACA	63.206	GGAGAGCTGCTACGGTAGAAATTTG	62.446	141
HM_8070	GD2OF4R01CRDOB	TA	2	12	CGACTAACCAATACCGAGATCCAA	63.421	GACCGATGACTTCACTGTAAACC	63.242	160
HM_8071	GD2OF4R02G4VB5	GA	2	24	GAGGACACTACACAATGACAAACAA	63.498	CTTCTCCATCTGAACCAAGAGCTC	62.898	153
HM_8072	GD2OF4R01CDLWB	CT	2	20	CGAGTCAACGACTAGCAATTTCT	63.154	TGTTGCATATAAATGGAGTGGTGG	62.946	146
HM_8073	GD2OF4R02HQ5BF	CA	2	20	CGATGTCTGAATCTGCGCTCTCT	63.449	GGCGCTACAAACCGTAGAGATAGA	62.96	129
HM_8074	GD2OF4R01CQ7D4	AC	2	14	CGATTGGTATCTTCAATCTCACA	62.382	CCGGTACTACTGTTTCCCTCTA	62.795	150
HM_8075	GD2OF4R02GOVFD	CA	2	12	CGCAGCAAAAGATATACACACAGA	63.504	TGCCACCTTTTATTTCTTTCCAA	62.918	132

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_8076	GD2OF4R01C0DXC	AG	2	24	CGCCAAGTAAAGAAATGGAATATG	62.93	CCCTCCAACTCTGCTCTCTTCAG	62.984	104
HM_8077	GD2OF4R01AHK5D	CT	2	24	CGCCAAGTATACATCCCATATCTC	63.133	TGTAGAACGACGTGGTTGAGAGAG	62.944	95
HM_8078	GD2OF4R02GP9G4	TG	2	16	CGCCATGTACGTGCTGATCTTT	63.503	AGAAAATTCGGGGCTGAAATGTGA	63.96	108
HM_8079	GD2OF4R02JG4B8	AG	2	24	CGCTCTTTTGTCTTAATCAAAATT	63.675	ACTGTTCTTCTTCGGAGTTGTGTG	63.02	127
HM_8080	GD2OF4R02GZGSP	TC	2	12	CGCTGAATATCGGAGAATCGTACT	62.841	GGTATTGTCTAATAGCGGCCCTC	63.214	154
HM_8081	GD2OF4R01DBCYT	TA	2	14	CGCTGCAAAAATCAAAACATACAA	63.182	ATATGTATGCACCAACCCAAATGC	63.865	105
HM_8082	GD2OF4R02IPXWH	GT	2	24	CGGAAAAATCACAGGCAAAAGAGT	62.741	AGAAAAATGCAGCGCATATAGATGA	63.021	117
HM_8083	GD2OF4R018YL7T	GA	2	14	CGGAAATCACATCAATAGGAGATG	61.858	TTCTCAAAATTTTCAAGAGGAAAAA	60.879	160
HM_8084	GD2OF4R018QUZE	TC	2	12	CGGAGATGAGCCTTTTAGTTACCA	62.823	CTAATGGCTGACCGCTGTACTGTTG	62.969	139
HM_8085	GD2OF4R0182UHK	AG	2	16	CGGAGTCCATGGAGATTTAGTAGT	62.686	CCCTCCCAACTCAAAATAGTACA	62.494	102
HM_8086	GD2OF4R01ASM6V	TA	2	12	CGGATTGTTGAATTTGAATACCGT	63.126	ATTCTTTGTTGCCGTTCTATCA	63.138	139
HM_8087	GD2OF4R02JFBWF	AT	2	20	CGGCGAATCATCTCTCATATCTA	63.416	GACAAGACTATGAAAGTCGGGAT	62.94	151
HM_8088	GD2OF4R02GIE6M	AC	2	16	CGGCGTGAATACGAAATAGAGAGT	62.851	GAACGAGAACGACTCTCTCAACCT	62.486	115
HM_8089	GD2OF4R02IOXEE	TC	2	12	CGGCTTCTAGCAGTAGTACTGCAC	62.804	AGTTTCCCTCTCAGTTCCAAATTC	62.876	100
HM_8090	GD2OF4R01D3A63	AT	2	14	CGGGGTACATCGTCAATATAGAG	63.743	TCCTTGCAATTTTAGGGTTTTCA	62.918	135
HM_8091	GD2OF4R02G066C	GT	2	14	CGGTGGGGTGAACCATATAGAAAT	64.075	GATCTCAGATGCTGTTGTGTGTC	63.302	139
HM_8092	GD2OF4R01CH69I	AG	2	12	CGGTTTCATGAAGAGTGAGAAAGTT	63.01	TCTCACTCTTAAACCTCATAGCC	62.811	86
HM_8093	GD2OF4R01BH61N	GA	2	16	CGTAATTTTGTCAATCCCAATTTT	63.94	GGCGACTTCCAAGGATTTGCT	63.754	108
HM_8094	GD2OF4R02HV2RI	AC	2	16	CGTAGCATTTTGAACAACAGAGCAT	62.556	AAAGATTCAACATTTTCAACAGGTCAA	62.152	132
HM_8095	GD2OF4R01AULPP	TA	2	12	CGTCCAAAGAGAAGGAACCAAAA	63.713	TGATTTCCACAAGTTGGACTCATTT	63.02	114
HM_8096	GD2OF4R01EZ37F	GA	2	16	CGTCCAGTTTITAGACTTTTCCAA	60.837	ACTCTCTCTAGTTCGCTACTTCTCTC	60.229	119
HM_8097	GD2OF4R02IMOQM	AT	2	16	CGTCGCTAAAAGGTTTGTTCGT	62.769	GGAAAACTGCAAAATACCATATGC	63.545	133
HM_8098	GD2OF4R01C66XB	AT	2	16	CGTCTGTTGTTTACGGTTTTCACA	62.619	TCCATTAACTGCAACACTGTCACC	63.395	139
HM_8099	GD2OF4R02JDRG6	TA	2	16	CGTGCAAAAGCACGTACTCTAAGAC	62.483	ACACCTTTAACAGAGCTGGGTTTG	62.833	120
HM_8100	GD2OF4R02G1Q18	CA	2	12	CGTGCTTGTCTTCCAGAAATTA	63.63	GCACCTTCAACAGAAATTTGGAAGG	63.227	95
HM_8101	GD2OF4R02JVA0A	CT	2	20	CGTGGGGCTATATATGTTCAAAT	63.15	GAGAGAGCGTAGATCTGACGGG	62.713	112
HM_8102	GD2OF4R01CS4JK	AC	2	16	CGTTTAAAGGGGTGCTAGATGTG	63.036	CTGCCACATTTCTTGAATGGAATA	62.311	136
HM_8103	GD2OF4R01APLYZ	AG	2	20	CGTTTGGTTACCGAGAAATATGAG	63.023	CCCGAGAAATTTTGGCTAATTTGAT	63.47	157
HM_8104	GD2OF4R02FIW02	CT	2	14	CTAATTTCTACCCCAACCCAGCACC	63.031	GAGGCGAGATAGGGAGAGAAGAG	63.181	112
HM_8105	GD2OF4R02HHX9K	GA	2	12	CTACACCCCAAGCATCTGTATCT	62.712	GGGTCTTTGAGATATTTTCTCGG	63.266	117
HM_8106	GD2OF4R01AMT2S	AG	2	32	CTACACTACTGTCCGAGTGAGGG	63.329	CGGTACGGTACGGAACCAAACTA	63.243	141
HM_8107	GD2OF4R02J8BIQ	TC	2	16	CTACCCCTCCACTAACACATCAT	63.01	GGGAGAGTTGTATATCCCAAACTAGAA	62.129	113
HM_8108	GD2OF4R01BS4JW	GA	2	20	CTACCTGTATCAGTTGGCATCAG	62.088	ACTTTTGTCAAAGTTGGTACATGCT	61.437	87
HM_8109	GD2OF4R01CYS8R	AT	2	16	CTAGAATGGTTAGAGGGAGGCGACA	62.907	TCACTCTGCACCATCAAGAACTGA	63.5	130
HM_8110	GD2OF4R02GROAE	TA	2	16	CTATCCAGCCCAACACTCTACGTGT	61.793	AAAGCCCATATAAAGCGGTCAAAA	62.746	127
HM_8111	GD2OF4R01C2ZTW	GA	2	12	CTCAATATGTACAATGCGCGGAAA	62.147	TGTCACTATTGTTGCTGCTCTTCA	63.078	151
HM_8112	GD2OF4R02JUI9SY	TC	2	12	CTCAATTCGACGTCCAGAACAC	62.276	GTGTTAGAGTGACCAAGGTTTGCT	62.935	117
HM_8113	GD2OF4R02J6BYS	GA	2	20	CTCAATTTGTTGCTTATGAGAGT	62.729	GAAGACGACAAAAACAAATAGTTATCCA	61.89	107
HM_8114	GD2OF4R01DSCGM	AT	2	12	CTCAGCAGCACCACAAATCTCT	63.829	GGTACTACCAAGTGCCAAAGATCACA	63.569	80
HM_8115	GD2OF4R02I51QM	TC	2	24	CTCATGGATAGATTGATGGCCCT	62.594	GCTATAAGCAACTTCCCTTTTCTC	62.54	129
HM_8116	GD2OF4R01E0SKC	TG	2	12	CTCCAACTTTTTCATCTCCCTGTGA	62.782	GCAAGTTGAAATGATAGGCTGACA	62.645	92
HM_8117	GD2OF4R01AKIYL	TC	2	24	CTCCCTCTCTCTCTCTCTCTC	64.112	CGCTAAACTTCTTATTTGGACTGCG	63.416	120
HM_8118	GD2OF4R02IOWWF	AG	2	20	CTCCGAAACCTTCTATAATCGCT	63.004	TTTTTCTGTAGGGTTAGGGTTTGTG	62.64	158
HM_8119	GD2OF4R01EMO3I	TG	2	24	CTCCGGTTTTCATCTCTATCTTC	61.57	TTTTGGTTAGTCAGATAGAAGTACGACA	60.759	96
HM_8120	GD2OF4R02HI2TG	AG	2	14	CTCTTACTGTCAACAATCAAGAG	61.472	TGTTCCCTCTCTATAGTCTCTGCT	61.091	140
HM_8121	GD2OF4R02HEMO1	AC	2	16	CTCTCTTCTGCTACAAAGTTCTGTG	63.053	GCAGTTATGTGTTCTTAAGTGGCGA	62.671	149
HM_8122	GD2OF4R02JOELV	CT	2	16	CTCTCTAACCTCATCGGTACGCTC	62.725	GGGAACCTTCTGTTCTGTGATTCT	61.985	155
HM_8123	GD2OF4R01CM1O3	GT	2	16	CTCTCTTCGATCCCATCTCTCTCT	63.477	AGCTACTCACCACCTCGCAAACTCT	62.962	150
HM_8124	GD2OF4R02JF4Q3	GA	2	20	CTCTGAGAGTGGGAGTCTCGTGAAG	61.971	CTTCTATTACACTTCTGCTGGAGA	61.969	80
HM_8125	GD2OF4R02F0SER	TC	2	16	CTCTGCAACTAACCAACAGTGGAA	62.737	GGGTTATTTTCCCTTCTAATCCCT	62.757	126
HM_8126	GD2OF4R02FYYXO	CA	2	12	CTCTGCAACTCTCCATCTCTGG	63.992	GTGAATTGCGAGCAATCAAGAAAT	63.553	158
HM_8127	GD2OF4R01C99HX	TA	2	12	CTCTGCAATTAGCATTTTCCCT	60.587	TGCTACTTCATGCAATGGCTATATACT	61.441	159
HM_8128	GD2OF4R01AS4VG	TC	2	16	CTCTGTCAAATCTGAAACCGGGT	63.02	GGTTAGAAATTAGGTGACCATTCGAG	63.127	117
HM_8129	GD2OF4R01I9LWK	TC	2	16	CTCTCTTTCTGTTTCACTTCGACA	62.955	ATGTAGATGAGCAACGGCTAAAGG	62.851	94
HM_8130	GD2OF4R02HTTH8	AG	2	12	CTCTTGCACATTTTGAGCTCCATT	63.867	ATTCACAAATTAATCGGCACCTCG	63.339	150
HM_8131	GD2OF4R01EVJ0B	CA	2	20	CTCTTTAAATTCATCTCGGCCG	63.207	AGAAGGATGTTGAATTTGGGTTTG	62.495	92
HM_8132	GD2OF4R02INQES	CT	2	24	CTCTTTACTCGGCTGTGGCATCT	64.095	AGCGATCAACTTCCACAACAACCT	63.362	99
HM_8133	GD2OF4R02JDQ5R	CT	2	20	CTGAACCAAGTGTGCTGTTTCTCA	62.81	AGACGAGAAGGAACGGACGACTA	63.657	122
HM_8134	GD2OF4R02HMTG6	TA	2	14	CTGAATTCCTCATGATGAACGTC	63	ATCCAGATGGGTTGAATTTACAT	62.789	122
HM_8135	GD2OF4R02JITLQ	AT	2	12	CTGAGCTCTCTCAATCCCAACT	63.34	TGTTCTCAACGTGTAATGTCGGT	62.856	159
HM_8136	GD2OF4R02JRCV7	AG	2	24	CTGATTTCTTGCTTTCAATTTGAGG	64.265	CGTCAACAAGCAACCCGAAAC	63.878	80
HM_8137	GD2OF4R02J3DGB	GA	2	40	CTGACGGTCCCTGAATCTTG	63.121	CGTAACGTACTCCCTCTCTCTCT	63.197	107
HM_8138	GD2OF4R01AUCNR	AC	2	24	CTGCATTTCTGTGGGAGTACAA	63.471	TCATTTTGTGCTGTATGCTTTTCA	62.962	152
HM_8139	GD2OF4R02GP9GS	AT	2	12	CTGCGCTAACCAAGCATCTTCA	62.869	TTCAATCAATGGATTATGACGAGGA	62.612	145
HM_8140	GD2OF4R01CNOTJ	AT	2	12	CTGCTCCAACCTCAAGCTAATTGA	62.642	TGCATCTGAAAGATGGAGGAGATT	63.425	159
HM_8141	GD2OF4R02FLJCL	TC	2	14	CTGGAAGGCTGATCTTTTGAAC	62.508	TAGAATTGCTTGAATCTGCTTTG	62.026	149
HM_8142	GD2OF4R02H4C38	TG	2	20	CTGGTCACCTCCGAGTCTGTCT	63.121	CTCTTCTCCAATCTCCACCCACTA	62.984	93
HM_8143	GD2OF4R02GX1NE	AG	2	16	CTTAAAAACCTTTCTCCAAACCG	63.175	ACATCTCTCAGACCAAAACCAAAAC	62.795	138
HM_8144	GD2OF4R02JQWDT	CT	2	16	CTTAAAGGGCGGTGAATAGCAA	62.524	TATGCTTTAGGTAGCGATGGATTG	61.574	153
HM_8145	GD2OF4R01DMDFB	TG	2	16	CTTAATTCGACCATCTCGTGACTC	62.412	GTTAGAAAGCATGCAAGGACAGGT	62.949	154
HM_8146	GD2OF4R01BU8L7	AG	2	16	CTTAGAATCCATCTCGGAAACCT	62.971	ATTCAAGTTCTTCCATCGATCCAG	62.786	148
HM_8147	GD2OF4R02JU2SA	TG	2	16	CTTAGTCTCTGCTGATTCGGTCAA	62.088	GCAAAACATTGCCCTTATTGTCTC	63.046	128
HM_8148	GD2OF4R02JEVAI	AT	2	14	CTTCCATCACTACACTCGGA	61.24	AAAAACTACCCACGTATTGCAATTC	60.496	170
HM_8149	GD2OF4R01DHRQV	AT	2	14	CTTCTATTCTTGGATTGGCTAATTC	60.913	TCTATTATTGGGCGTGAATTTCAA	61.753	156
HM_8150	GD2OF4R02ISGFO	AT	2	20	CTTCTCAGCTCCATGCTTTCTAGC	63.048	CCTCAGGGTTAGGAAAGTCTGTAAA	62.164	138
HM_8151	GD2OF4R01BG8QS	AG	2	12	CTTCTCATATCATCAAAACCGACC	63	TCAAACCACTTTTCAAGTTTCA	62.928	124
HM_8152	GD2OF4R01DR36S	CT	2	12	CTTCTCTCCATAACTCAATGCGCT	63.146	AGGGGTAGACTCAGCAGATACTTGAA	62.829	127
HM_8153	GD2OF4R01BOHQ2	AT	2	14	CTTGAACATTTGGTGGTATCATGC	61.908	TTTGTAAAAAGACTCCAATCAGATCA	61.429	125
HM_8154	GD2OF4R02HROWC	CA	2	12	CTTGCCCTCTTCAAAATCTGATGTC	62.91	GGCCAAGATCATTTGTATGATCAT	62.474	135
HM_8155	GD2OF4R01BILOY	GA	2	30	CTTGCGGATTACGGTTTGAATAGGA	63.428	TTTGTTATTGGGTGACGACCACTC	63.227	158
HM_8156	GD2OF4R01AYHK0	CT	2	16	CTTCTCTTCTCATGCTCCGCTGT	62.98	TTTGTTCAGTTGCTCGCTTACAA	63.187	98
HM_8157	GD2OF4R01AKI7H	CA	2	12	CTTTGAGTAGGTACCTGCTGCTGT	63.033	TCTCAGAAAAACAACTAGTCGGCA	62.426	140
HM_8158	GD2OF4R02HLKSW	TC	2	12	CTTTGATAAGCCGAACCTCTCTTG	62.618	CACCTCTCGCTACACATACACA	61.637	143
HM_8159	GD2OF4R01EY1Z3	TC	2	12	CTTTGGCTATGGTGAATCTTCAAGG	63.214	GCATCTCACTCTCACACAAACACA	62.639	129
HM_8160	GD2OF4R01CISAA	CT	2	20	CTTTTCATCCATAAATCTGCCAAC	62.922	TCAGCTCCAATCAAAACAAAAACA	62.943	139
HM_8161	GD2OF4R01B2BA0	TC	2	24	CTTTTCCAGGTGTTTTCTCTCTCA	63.003	TGCATGTACATCAGGCAAGAGAT	63.296	121
HM_8162	GD2OF4R02ILIFW	AG	2	16	CTTTTCTCTCTCTCTCTCTCTCTC	62.571	ATTAGTATCTCCCTCTCTCTCTC	63.128	96
HM_8163	GD2OF4R01D520K	GT	2	16	CTTTTGTGTCGGAACATCGGTTTT	63.331	GAGCGTCCATGTTTTCATACAATCA	63.275	153
HM_8164	GD2OF4R02GHFTJ	TA	2	12	GAAAAACCTGCGAGATCGGAGAGTA	63.022	GCCCCTAGGTCTAAGGTCAAGTT	62.901	151
HM_8165	GD2OF4R01CVECF	AG	2	16	GAAAAAGAACCAAAAGTTGGGAGG	63.268	CGCCGACTTGTCTATTGTCTCAAT	63.769	123
HM_8166	GD2OF4R01A6UNO	TC	2	16	GAAAAATTATGTGCTGATGCTGTC	62.877	AAATCACCTCTTTTCTCTCATATCCAG	62.732	135
HM_8167	GD2OF4R01BNK07	TG	2	16	GAAACCATGTCTGTGCGTGTGATG	62.947	ATGCTCAGCTTTTGAAGTCTCTT	62.938	147
HM_8168	GD2OF4R01EDG3G	CT	2	12	GAAATCTTCAGGTTGGATGATGG	62.987	CGATAAGCATGTCAGAGAGATACAA	63.065	110
HM_8169	GD2OF4R02GHYRF	AG	2	20	GAAACAACTTTTTCGAGAGGGAGA	63.019	AGTTCTCTCTCTCTCTCTCTCTC	63.647	150
HM_8170	GD2OF4R01EH8QN	TA	2	16	GAAACCGGATTAAGTACAGTCTCT	63.04	GAGAGAGGAGGAAGGAGGAGAGA	62.937	131

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_8171	GD2OF4R02JIOKJ	CA	2	16	GAACCAAAACGCTGCTCTCTTC	62.725	CGGTGTTGTGGGTTCAAAACT	63.246	89
HM_8172	GD2OF4R02GIED3	TC	2	12	GAACCAACTTTTACCATTCTCGAT	62.523	TCTGCATTTCCATCAGCTTCATTA	63.05	137
HM_8173	GD2OF4R02JUM49	GA	2	12	GAACCTAAGCATGAGGAACGCGT	63.919	TAACCTGAACAATTCACCCCTTCC	64.49	115
HM_8174	GD2OF4R01A5UG2	AT	2	12	GAACCTTTTCTGCACCAATCACT	62.824	ACCCTAGCTCTGTTTAGATTCTGGA	61.978	139
HM_8175	GD2OF4R01ET60U	AG	2	20	GAACGTGAAGCTTAGAAAGTGGA	63.031	GGCGATGCGTGTATAAGATTCTATC	62.916	116
HM_8176	GD2OF4R01DGTZK	TA	2	12	GAAGAACGATTTTACAGACAAAGCA	62.946	AGTCCTTGCCAGCATTTCTCTCT	62.193	96
HM_8177	GD2OF4R01EU6AI	TG	2	12	GAAGAAGAGGGGAGAAAGAGTG	62.958	TCATTGTTACGAAAACGTTTAATCTCA	62.052	145
HM_8178	GD2OF4R02I4KIE	AG	2	20	GAAGAGTAGTTGCATGGCCAGATT	62.94	CACCAACATAAGACTCCTCTCTCTACA	62.204	111
HM_8179	GD2OF4R01B2GV9	AT	2	14	GAAGATAAGCAGGGCTCTTAATGC	61.553	TGCAATGTTTCTGAAGAAGATATGATT	60.619	152
HM_8180	GD2OF4R01EPTD1	AG	2	12	GAAGATTAGAGGCTTTGAGAACACA	63.236	CCGATCCGATTAGAGGATCTGAA	63.712	108
HM_8181	GD2OF4R01AWYU2	AG	2	14	GAAGCGCTCTTCAAACTCATATACA	62.98	GTTTCTACCTCTCGAACCCACAC	63.33	98
HM_8182	GD2OF4R01DIUYP	TG	2	12	GAAGCTGGACACACGAAAGGATAT	62.838	GGCTTATTCAAGGATGTTTAGGGG	63.084	140
HM_8183	GD2OF4R02I9R9B	GA	2	24	GAAGGACTCTCTCTCTCGTAATC	61.924	CGTAGCTTCTCATCAATCACCACCTA	62.528	123
HM_8184	GD2OF4R02GSDSK	CT	2	16	GAAGTGTAAGCAGCACTCCATCTC	63.356	AGAGAATATAGCATTTTGTGCGGG	62.761	155
HM_8185	GD2OF4R01C7L77	AG	2	12	GAAGTTGAATTCACGCTTGGGTC	63.022	AAAACCCCAAGAAGAAAATGAGGC	62.9	155
HM_8186	GD2OF4R01DALZO	TG	2	12	GAATACAAATCTCTGTGTGCGTGC	63.095	TCACCTTCTCCCGTGTCAAGTAT	63.225	147
HM_8187	GD2OF4R01AKJNW	CT	2	12	GAATGCGTACCATCTCCCTATAAA	63.225	GAAAGGGCTCTGGTTATGGAGTTT	62.995	148
HM_8188	GD2OF4R02F3AXR	CA	2	14	GAATTTCTTTTCCCAATGAAAGGC	63.179	GAACCTCATCTCTCTCTCTTTTC	62.852	82
HM_8189	GD2OF4R02IZEMI	GA	2	14	GAATTGAGTGGTCAATGAAGAGCA	62.714	AGTTTCTCATCTCTCTCCCTGGT	62.764	101
HM_8190	GD2OF4R01WVK6	TA	2	12	GAATTGGTCCACCAAGACAACAT	63.331	AAGAAAGATATTGCGTGGATTGTGA	63.044	159
HM_8191	GD2OF4R01BVS1A	TA	2	16	GAATTTCTGAGAGAGAGTGAAGAAA	60.581	TTGTACGGACATCAAGCTGTAGTG	61.463	130
HM_8192	GD2OF4R02F731X	TC	2	16	GACAGGAGGAACACAGTGGAGTG	63.373	ACCATTACACCAAAAGGCCAAAG	63.343	123
HM_8193	GD2OF4R01ADNOS	TA	2	12	GACCAAAATGTTCTATTCTCCAGTG	62.056	CAAAATCCCTTCGGAGGCTAGA	62.761	138
HM_8194	GD2OF4R01CG17E	GT	2	12	GACCAAAACAAACAGACACATCCC	63.876	ATAGTAGCAGCAGCATGCGCACAG	64.755	116
HM_8195	GD2OF4R01CJTSU	TA	2	12	GACCGAAGGTGTCTTCAACAGCTA	62.933	TGCTAAAGACATGTTTTCGGACT	63.239	88
HM_8196	GD2OF4R02GE1HW	AG	2	16	GACCTTGTTCGAGCAAAAGATATG	63.239	CTAGTGTGCCCGTGTGCTCTATC	62.974	152
HM_8197	GD2OF4R02J1TKN	CT	2	16	GACGTAGTGTCTCTGATTGGCTCTC	62.787	CCACACTACAAGAACATAGGGCGT	63.566	100
HM_8198	GD2OF4R01DGR1B	AT	2	14	GACTACTTTGGGATGCTCTGCATT	62.94	CGGTGCTTCTAGCTATGTGGTTA	63.652	92
HM_8199	GD2OF4R02JHXFE	AC	2	14	GACTGCAGGAATTTGGTCTTTGTTC	63.343	CTAAGATTGGGTGTGGCAAACTCAC	63.856	149
HM_8200	GD2OF4R01D7Y29	CT	2	16	GACTGGTTCTCCACCACTATTC	63.004	AGAGGTACGACGGGGAGGAG	62.85	109
HM_8201	GD2OF4R02H9RFS	GA	2	20	GAGAAAAATCAAAACCCACCGAT	63.476	CACCTTCTAGCAGATGGAGCG	63.474	134
HM_8202	GD2OF4R01EOMNS	AG	2	30	GAGAAGAAATCGAAGAGGAGGA	63.308	TTCGATTGATTCTGCTCCG	63.601	104
HM_8203	GD2OF4R02G5JGU	AG	2	16	GAGACTCCCTCAAAGGAACAAAC	61.653	GATCTTATTATCATCCACTTCTATT	60.748	156
HM_8204	GD2OF4R01ED1AQ	AG	2	12	GAGAGAAATGGAGGGGAGAGACC	63.055	CTCTTCTCTCGTATAGATTGTTCG	62.522	85
HM_8205	GD2OF4R01AMUV9	CT	2	14	GAGAGAGTTTCCACCATTTGAAAGA	63.102	ACCAACATGAGATAGGCAGGAGAG	63.014	155
HM_8206	GD2OF4R02J2QOV	TC	2	20	GAGAGCTAACTATTGCTGCTGGGA	63.035	GCTGTGCAGACTCCAACATTAATA	62.657	156
HM_8207	GD2OF4R02HFOJM	AG	2	24	GAGAGTCTCTATCCAAAGTCCAA	60.095	AATGACATGACCCACACTTCTCTT	61.009	110
HM_8208	GD2OF4R02JBNVJ	GA	2	12	GAGATCTGGAGCGCAAAACCTG	62.349	AACCTCCACCAAAATAAGCTTCC	62.425	84
HM_8209	GD2OF4R02FUE9C	AG	2	12	GAGCGAAAGTGAGACTTATGAGCT	63.268	CACCTGATCATCCCTCTGTCCATT	63.644	84
HM_8210	GD2OF4R02GMX8D	TC	2	16	GAGCTCTTCCCAATTAGCGAAATA	63.025	CTACCTGGAAGTTTGAAGGTTGC	62.425	121
HM_8211	GD2OF4R01DVPGB	TG	2	20	GAGGAATCCCTCATTAGAAACTCTCTG	62.981	AGTGGGAAATGGGTGAAAAGAAAT	63.078	146
HM_8212	GD2OF4R01EVS7C	CT	2	20	GAGGAGCAGTCCCATCTCTCACTA	63.332	CTCTATCTGCTTTTGTGCTGTT	63.044	110
HM_8213	GD2OF4R01ASCQJ	TG	2	20	GAGGGAAGTTGTAGCTTACACACA	63.879	CCATTACCAACTGTTTCATCACCTT	63.325	150
HM_8214	GD2OF4R02JT306	CT	2	12	GAGGGAGGAAGAGGCATCGAC	63.639	TCCGGAAGATAGTATGGTGTTCG	63.421	149
HM_8215	GD2OF4R02GKELB	GA	2	20	GAGGGGACACTTCTCTCAATTT	63.071	AAGTGTTCGCTTCTACTCCACGAG	63.033	158
HM_8216	GD2OF4R01BGUWJ	CT	2	12	GAGTAAGCTGCTCCCTCTCAAGATG	62.598	CCGTCACTTTGAAATTCATTAGC	63.03	118
HM_8217	GD2OF4R02FHUPY	GA	2	12	GAGTCTTGAGGGTGAGACTTGGTC	62.779	ATTTCACTGCGGCTCTCT	62.68	142
HM_8218	GD2OF4R01D2U34	GA	2	16	GAGTGTGGTGTGACAGGAGATA	62.584	TGGATTCTCTCTCATCTCTTGGC	62.298	122
HM_8219	GD2OF4R01EIKSC	CT	2	16	GATATCAAAAGACTGAGCCAACTG	62.425	CCAAGTTGGTGCCAGCAATCC	62.762	80
HM_8220	GD2OF4R02FNNOK	TA	2	16	GATCAACCACTTATTCATAGGGA	63.198	AAACTACATATCTGCGCAATGGT	62.972	107
HM_8221	GD2OF4R01DDNEH	CT	2	20	GATCAGTCATCACTCTGCTCTCT	63.492	GAGATGGAGAGGTTGCTAGCAGTG	63.672	113
HM_8222	GD2OF4R01A6I43	AC	2	12	GATCTTCTCAGCTTTGTTTCACG	62.309	CACATGAGGTTCAAGTGAATCAAT	62.366	154
HM_8223	GD2OF4R02FNYHW	AT	2	12	GATCCCTCATAAGAGGGGCTCTGT	63.185	CGAGATCTTCAAGTGAACCTGAGCA	63.159	130
HM_8224	GD2OF4R01A5A03	AG	2	12	GATCTGGAGAGAGTATTTGGCTCG	62.7	ATTTCTTATCAACCGCTCTCTTC	62.903	133
HM_8225	GD2OF4R01AU1IJ	TA	2	14	GATGAGGCGAAATCGATTCACTT	63.642	CAGAATGAATGTCACATTACGGA	63.257	94
HM_8226	GD2OF4R01BQ54B	TA	2	14	GATGATGCGAAACCTACCAAGATTC	63.129	CCGACTATAACACACAAACACACA	63.081	113
HM_8227	GD2OF4R01D03MU	TA	2	12	GATGCTGGTGATCAATAGGGTGA	62.293	GTGTCTGTGTGGGTATCTGAGGG	63.019	158
HM_8228	GD2OF4R01DWSYN	AG	2	20	GATGGAGATCCCAAGAGAAAGTTT	63.062	GACACCCAGTACACACCAAGTTC	62.95	134
HM_8229	GD2OF4R02I8E13	CA	2	24	GATGGGTGATGGCTTAAAGTGATT	62.51	GCACAATTGTCAATCTCTGTCTC	62.274	94
HM_8230	GD2OF4R02IHLRG	GT	2	12	GATGTTGCTGTGAATTTGCTCGG	63.954	CACCTGCACAAATCACAAGCTTTA	63.116	146
HM_8231	GD2OF4R02I6H6J	AT	2	16	GATTAGGGTTTGAGAGCAGAAGGG	63.583	CTACCTGCAACGCTTTCGAATTTT	62.849	130
HM_8232	GD2OF4R02FYP0B	AC	2	16	GATTGCGAGGACTTTGAAGACCAA	62.897	TGCTCGGTGGTGATCATAGACTAA	62.934	121
HM_8233	GD2OF4R01D10O2	TG	2	14	GATTTCTACTGATTGAGGTCAATG	62.189	ATAGGGTGGTCAAGACACTGGTA	63.01	83
HM_8234	GD2OF4R02GQQH8	TC	2	12	GATTTCTGTGGGTAACCTGGATGG	63.111	GATTGCTGAGAGAAAGCGAAGGTA	63.244	137
HM_8235	GD2OF4R01BU8RG	AT	2	12	GATTGCGGCAATTTCTCTTAT	63.524	ACCTGGGAGAGAGCTAAAGCCTAA	63.005	157
HM_8236	GD2OF4R01DC3J6	AC	2	12	GATTTAAAGACTCATTGGCGCG	63.132	TCTCTTCCAGAAAACACAAACAA	62.177	160
HM_8237	GD2OF4R01D3Y0D	AG	2	12	GATTTATCACAGCGCGGAACAGTA	63.654	ACCAACCCCTCTCTTACACAG	64.65	150
HM_8238	GD2OF4R02H61KM	AT	2	12	GATTTGGTGGAAAGCTCTGTGTAT	62.813	GTCACCTCAAGACAATGGTAAGCA	62.622	173
HM_8239	GD2OF4R02IDOMI	AG	2	12	GATTTTCTACGAGGACTATGGG	63.172	ATTTTGAACCTTCAACCCCTGACAAA	63.006	155
HM_8240	GD2OF4R01A5M64	GA	2	20	GCAAAATATTTTGAACCCCAACA	63.026	TTGATGCTCAACAACCTAGCTATCC	62.853	98
HM_8241	GD2OF4R01AQ5KE	AG	2	24	GCAAACTTGGAAAGCTGTCTTAAG	63.246	TCTTTCTAGCATCTCACTCAGCA	62.528	201
HM_8242	GD2OF4R02HZVMU	GA	2	12	GCAACTGCATCTACACCACTATG	62.975	GGTCTCTGTTTCTCTCTCTTTA	63.074	155
HM_8243	GD2OF4R01C2ANO	AG	2	16	GCAAGAAAAGCACTTCATCTCTGT	61.271	GCAACGTTGTTCTGTACTTCTGG	62.237	109
HM_8244	GD2OF4R02IRMOQ	CA	2	16	GCAAGTACCTTTTCTTGGAAACA	62.728	GCACATAAATCAAAATCCCAAAACC	62.22	149
HM_8245	GD2OF4R01C745R	AT	2	16	GCACCTCAAGCATACACACCTA	62.195	AAAACCCCAAGCCATAAAGCTAAA	63.109	143
HM_8246	GD2OF4R01E2JYP	AG	2	12	GACGCCCCCAAAATAGATTGTAA	62.463	GGTGCATTTGGGGTATTTTATT	63.044	124
HM_8247	GD2OF4R02JX4CT	TG	2	14	GCAGTCAAAAGTCATAACCAACC	63.035	CATATACAATTTGGACACGCGCT	63.186	115
HM_8248	GD2OF4R01CCJ6D	AT	2	14	GCATACCTGTACTTTTTCGCGTGT	63.158	TACCATCTCGTTGGACCACTAAT	62.91	160
HM_8249	GD2OF4R01B795T	GA	2	48	GCTGACAGACGATGACTACTACT	61.481	GTAACGGGTACGGGTACGGTAGTC	60.9	96
HM_8250	GD2OF4R02HDS1V	GT	2	14	GCATGTCAATGCAGGTAATGGA	63.175	CATTTCACAAATCACAACCTTCCA	63.377	149
HM_8251	GD2OF4R01CXNLF	GA	2	14	GCATTAAAGTCAATCAGAGGAGCA	62.73	GGGGCCCACTAGAATTAACCAAA	63.135	160
HM_8252	GD2OF4R01BU1CP	AT	2	16	GCATTTGAAGCCTCTCGATATAC	63.026	AAGTTCGAATGTTAAGGGTGACCA	63.019	125
HM_8253	GD2OF4R01EO4FI	AT	2	12	GCCACAAGCGTTCATTAATAACAA	64.246	TAACACAACCAATCGTCTTTGAC	63.29	100
HM_8254	GD2OF4R02H4YR7	AT	2	16	GCACATATTTGGGGGTTTGTATTA	62.829	CAAGAAAGATCAGCTCTCATGGT	63.115	99
HM_8255	GD2OF4R01E59H3	TG	2	12	GCACAGTACCTTGGAAAGTATACAA	63.348	CCCCATCAGTATGTTTCATAGGCT	62.112	159
HM_8256	GD2OF4R01C26DR	TG	2	12	GCCATAAATCAAGAAATGGCTAA	62.45	TCATGTTGTTTATCTTGCACAATG	61.991	144
HM_8257	GD2OF4R01COKEB	TA	2	16	GCCATCTCAACATACCAAGTATT	61.478	CAAGCAACTGAGAGAATTTGAAAT	62.041	160
HM_8258	GD2OF4R02G9WVB	TA	2	12	GCCCAACACACATACATATCAT	63.873	TTATCACTGCGGTGTTAGCCAAGG	64.466	119
HM_8259	GD2OF4R02F2U3V	TA	2	16	GCCCCATTAATTTGTGTTTGTG	63.428	TAGGGGTGGGTGTGTTTATATTG	62.906	85
HM_8260	GD2OF4R02JKDWA	TA	2	12	GCCCGGATTAAGGTGCAAAATATA	61.459	TCAAATTTTCAATTTTGTCTCTACA	60.504	146
HM_8261	GD2OF4R01E5SUPP	CT	2	16	GCCCTGATTCTGTTTCAATTACCA	63.426	AATACAATCCCAACCTTCTCTGCC	63.696	137
HM_8262	GD2OF4R01AX3O8	TG	2	24	CCGCTGATTGACAAGAAAGAAAG	63.336	CCCACCTGCAAGAAACATACCATA	63.427	159
HM_8263	GD2OF4R02F3FOZ	AG	2	14	GCCTCTGCTCTAAATCCCAAAAT	63.007	CGTTGAAAGCACAAAAGTTTTC	63.142	142
HM_8264	GD2OF4R02GRXGD	GA	2	16	GCCTTGGTGTCTTAGTTCTTCA	62.944	TTCATTTTAAACCTTAACCCGCA	62.748	127
HM_8265	GD2OF4R02FWOIG	CT	2	16	GCCTTTTACAACCAAGATCACA	63.432	CGAGGCATAAAGAGTGAAGAGGA	63.117	145

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_8266	GD2OF4R01D3DXD	TC	2	12	GCGAGCTTTTCACTATGATGTCT	63.051	AGATGAAACGAGAAAGGATGTGC	62.827	112
HM_8267	GD2OF4R01EKRIA	GT	2	24	GCGATTCCAGAGGAAAGAAGAAT	63.188	TGCACATAAACCTACTCAAAACCAA	62.872	125
HM_8268	GD2OF4R02GMO8I	GT	2	16	GCGTCTCCATTTTAAAGCAGCTA	62.566	GAACAGCTGAACCGAAGATCAAT	62.926	142
HM_8269	GD2OF4R02GCN85	AG	2	16	GCGTCCACACATTTTGTCAAG	63.818	TGCCACTTAATAGTTTGGTCGCT	62.944	100
HM_8270	GD2OF4R01ATUF1	CT	2	12	GCTAAAAAGTTACGACAACCCCA	62.558	CACCCCAAAACAGTATATGAGC	62.826	111
HM_8271	GD2OF4R02IOW8X	AC	2	16	GCTAAAGAGATGGCCCAATACAGA	62.828	AGGTAAAAATCCATTTTGGCTTT	63.123	128
HM_8272	GD2OF4R01EHIOC	AG	2	14	GCTAAATTCAAACGAGAGCTCAA	63.043	TTTCTCTGTTGATGCACTTTTCTT	62.342	150
HM_8273	GD2OF4R01CQ1RF	CA	2	16	GCTAGTAAATGGATGACGGGGGT	62.717	AGATGCATGTTTTCGAATCAAGA	62.962	136
HM_8274	GD2OF4R02GLEVF	TG	2	14	GCTATAGAGCTAGGCGACAGGTT	63.336	TGTTGTCGGTATGCTACAGGATG	63.278	152
HM_8275	GD2OF4R02G16TE	TA	2	16	GCTATTTTGGACCTTAACGATGT	62.655	TGGATTCACTTTCTGCACTTCA	63.141	158
HM_8276	GD2OF4R02GNJQ9	TG	2	24	GCTCAATATGTAGGCATTGGCATA	62.271	CCAGTCTGTGGTTTGTATCCTATTGT	61.656	124
HM_8277	GD2OF4R01DRDN9	AC	2	14	GCTCCCAATGGTTCGAGTATTTT	63.487	ACAGCCAGACTTGCACATATACC	62.851	130
HM_8278	GD2OF4R02IRXSD	GA	2	12	GCTCGATTGAGAGATGACGGGGT	63.124	CAATCAACTCCCAACCTCTCGAG	63.808	142
HM_8279	GD2OF4R01ARL4H	CT	2	16	GCTCTTCTACACCTCTCCCTAT	62.383	AACCACTGACATGGTGGATTCTT	63.128	104
HM_8280	GD2OF4R01EUASO	CA	2	16	GCTGATATGCTAAAAGGTTAATCAGCA	62.893	ATGTCGCTTTTGTCCCATAGATA	62.925	138
HM_8281	GD2OF4R02I4VK5	TC	2	14	GCTGCTCCCACTGTCTGGAT	63.963	TTGTTGGTTATGGAAAAATTGTGACC	63.028	147
HM_8282	GD2OF4R01AZTRA	GA	2	16	GCTGCTGGAGTAGACTTTCAAGTT	62.425	ATTTGAAACCCCTTTTGGCTG	63.397	86
HM_8283	GD2OF4R01BNYEZ	CT	2	12	GCTGGTGAGTACAACAATCACCG	62.869	TTATTGACGCTTTTGTGATTGACG	63.778	152
HM_8284	GD2OF4R01B4ZL5	CT	2	16	GCTGTTTGTGTTGAGAGAGGGAGA	63.225	AATGAGAATGATGACGTCTGCTG	62.477	102
HM_8285	GD2OF4R01DZ423	CT	2	16	GCTTAATTTGCAACCTTTGCACTC	63.268	TTAATAAGATCGGGTGCCTCTCTG	62.821	119
HM_8286	GD2OF4R01CNW2V	GA	2	12	GCTTCAGTGTCCAATCAACAATATACA	61.856	TCTCTCCCTCTCAAAATTAATCCCA	62.706	152
HM_8287	GD2OF4R01D125G	TC	2	16	GCTTCTCTCTCTCCATTTTCTCT	63.075	TGTGGTTGTTATGATTTGGGTGAA	63.354	150
HM_8288	GD2OF4R01CJ3K	TC	2	14	GCTTCTTAAACATTTTGTATCCCCC	63.087	CAAACTACTGAAACGAAGCGATT	62.849	110
HM_8289	GD2OF4R01E1XW3	AG	2	16	GCTTTACTTCATGAGGCAATCTCC	62.523	AATCTAGGGTTTGGTCTACTCCGC	63.008	158
HM_8290	GD2OF4R02GZS57	AG	2	12	GCTTTGTCAAAATCACTTCGCT	62.96	TAAAGTCCACTTCCAGCTTTTGT	62.871	110
HM_8291	GD2OF4R01BLVIU	AT	2	12	GGAAAAGAACAAACAGGGGATAG	61.323	TGCTCTCACTCTCTAGGCTATAAATC	61.625	98
HM_8292	GD2OF4R02F1BVG	AG	2	14	GGAAAGAGAGTAGTGGAATATGGG	60.571	TGTTCTCCATTATAGGAGGTGTACG	60.625	157
HM_8293	GD2OF4R01BNX8Y	AC	2	14	GGAAAGTGGACATAATTTGGGA	62.495	AAACTCGTTTGAAGCTCTGGAGT	62.75	155
HM_8294	GD2OF4R02JYNDM	GA	2	14	GGAAAGGGGAAAACTCATAGAGGA	62.958	GCTCCACTCTCTCTCCCAAC	62.626	139
HM_8295	GD2OF4R01B3Z2B	TG	2	16	GGAAAGTCTTTCTTCAACTCTGTTT	60.696	TGCGTCCATGTATCTCTCTTTTCT	60.484	160
HM_8296	GD2OF4R01CB51K	TG	2	12	GGAAATTTTGTGTTGGCAAGGGG	62.899	TTGGTAGAGTTGAATCTCCCACT	62.368	93
HM_8297	GD2OF4R01BEM64	GT	2	14	GGACAGCAAGTCTTCACTGACAC	63.204	ATTGTTTTCGCTCATACACAGT	62.824	128
HM_8298	GD2OF4R01A7WHG	GT	2	14	GGACATATGAAAGTCATAGTATTTTGG	62.075	TTCAACATGAGCAAAAGAGTGC	62.962	151
HM_8299	GD2OF4R01ADLUN	GA	2	24	GGACTAGAATTGCTGAGTTCGTCG	63.561	CTCTCGCTCTCTATCTCGTCACT	63.804	81
HM_8300	GD2OF4R02LQJB	GA	2	14	GGAGAGAGGTGGAGATGAGAGAG	64.145	GGCCCAACAATATTTCCCTCTAAA	63.368	125
HM_8301	GD2OF4R01C1XYG	GA	2	24	GGAGATTCTCTGATTAATATGGAT	60.696	TTGGTCAGACTCTAATCGAGATTTAC	60.391	93
HM_8302	GD2OF4R01D2I4K	TA	2	12	GGAGCACCAAGAAGCTATATCTGCC	62.425	GTTCAAGTTTCAGGAGCAGCAAA	63.039	150
HM_8303	GD2OF4R01ELWRI	AG	2	16	GGAGCTTGAATCTCAGGAATTTT	63.081	GATCTGTTTCGCATAGATCTGTT	62.816	125
HM_8304	GD2OF4R02J1VHS	TC	2	20	GGATGAACCGCTCATTCAGTTTAC	63.137	AGCCACTTTGTAGGCGTCTTACC	63.921	119
HM_8305	GD2OF4R02HXK2G	AT	2	12	GGATGCATAGAACAACAAATAGCA	63.353	CGCCCTCTAATGTCTGCACCTAAT	63.898	137
HM_8306	GD2OF4R02HJLJK	AG	2	16	GGATTTCATAGCTGTCTTACAGAG	63.353	TTAGCTTGAATCATTGGGTCTGT	63.121	116
HM_8307	GD2OF4R01BYYDF	TA	2	12	GGATTTCACCAAGAAGGTACACACA	62.487	CAAGTCACTGCAATTTCAAGAAAA	61.759	110
HM_8308	GD2OF4R02H5FQB	CT	2	12	GGATTTCTCTCTCTATTCAGGGAA	62.949	AAATGGTTCTCAATTTTGGGAA	62.467	143
HM_8309	GD2OF4R02H06IP	CA	2	12	GGCAGAACAAATTTTCTTAATCA	60.658	ATGTGCTCTTCAACCAAAATGTCT	61.581	154
HM_8310	GD2OF4R01D9HSQ	GA	2	12	GGCAGATCGAGCTTGTCTTTCTTG	63.45	CAGGTAAATGAGTTTGGTCTTCCA	62.617	90
HM_8311	GD2OF4R02GQCP4	GA	2	12	GGCCACACCACTTTAGAAAAAT	62.737	TGACGGTCTAGAATATTTGATGCTC	61.887	138
HM_8312	GD2OF4R02IKIFX	AT	2	14	GGCCACTATTGTGATCTTTTATGTCG	63.021	CTCGAGTTCGCTCTTTTAACTCTAA	62.094	134
HM_8313	GD2OF4R01BDTMI	CA	2	12	GGCCGCAATAAGTCTGAATAGTA	62.654	AACATTATGCAATGACGAGACAC	63.198	108
HM_8314	GD2OF4R01D7UBR	CT	2	14	GGCTATGCGCTTAAACAACCTCT	63.708	AAGGTGCTGTTGTTTACAAGCAA	62.982	85
HM_8315	GD2OF4R02GUOSR	GA	2	24	GGCTTTTAAACAAGAAATCTGGG	63.19	CGAGGTCTAAACGAAAGTTGTGGT	62.833	82
HM_8316	GD2OF4R01BAGB6	TA	2	12	GGCGAGATCTATTTCTTTTCTTCA	62.074	AGGTTGTGCTTGGCTCTGATACC	62.925	119
HM_8317	GD2OF4R02IN96P	GA	2	16	GGCGTGTCTTATCCAAATAGAGGA	62.718	CGCTTTTATCTCTCTGAGATTGT	63.022	125
HM_8318	GD2OF4R01EP7C3	TA	2	14	GGCTCATCACTCAGTGTCTTGAAT	63.042	CACGTGCGCTTACCTAGTACACAC	63.122	157
HM_8319	GD2OF4R01DSM6Z	CA	2	16	GGCTGAACATATACCTTTTCCACC	63.196	ATACCTGCTCTTTCGGAGTTAG	63.098	83
HM_8320	GD2OF4R02FUO8N	TC	2	16	GGCTTCATTACCCAGTTCATTCA	63.426	CCACCTCAGAGAAACGTAACCC	64.196	129
HM_8321	GD2OF4R02F07RR	TC	2	20	GGGAAATCTTAATACACTGGGCA	62.533	CGTGACTTTTTCTCTTACACCCA	62.929	136
HM_8322	GD2OF4R01CUPWX	TC	2	12	GGGAAATTTGAAAGATCAAAAGGG	63.06	GAATTAAGAGAGGGGAGATGTGGG	63.362	124
HM_8323	GD2OF4R01A6N7D	GA	2	14	GGGACGTCATTATATATTTAGAGAGG	60.647	CATTGCTGATTCAATGAGGTAA	61.234	144
HM_8324	GD2OF4R01DBY1I	TG	2	16	GGGCAAAAGGGGTGATGTTTCAGTA	63.336	GTGTGACCAACCAATACCAAGTG	62.827	125
HM_8325	GD2OF4R01ADKR6	GA	2	24	GGCGGATTCTGAGAAAAATACAGA	62.815	CCTAAAAACCCCTACCCCTACTCT	62.953	96
HM_8326	GD2OF4R01CR8YY	AG	2	16	GGGGAATTAAGAAGAAATTCGACCA	63.558	ATTGAAATTTTGTTCATGTGGGG	63.005	151
HM_8327	GD2OF4R01ESSL8	AG	2	12	GGGGTGTGTACTTGTAAACCTGCT	62.525	GAATTCCTCATTTTGGCTGCTAT	63.393	135
HM_8328	GD2OF4R01BV6JK	AT	2	16	GGGGTTCATCTGCAATGAAGTCTA	63.541	CTCGATGATGGCAATAGAACACTG	63.051	129
HM_8329	GD2OF4R01CBVSF	GA	2	16	GGGTCAACCTCTCATTTCAATTG	62.691	TCCAGGAATCAAGGTGAGAGTCT	62.987	129
HM_8330	GD2OF4R01ANNZC	GA	2	16	GGGTGGATTATCTTATTTTGGGA	62.502	TACTCTAAGGGCCCTTCTACCC	62.969	160
HM_8331	GD2OF4R01BMQLD	AC	2	16	GGGTTAAAAAGCATGTGTGAGAGAA	62.741	AACAGGACCTTAAGTTTACGCAGC	62.085	118
HM_8332	GD2OF4R02I3APY	TG	2	30	GGGTTCCCAAGATGACACGAA	63.336	GCTATCTACTACAAGCAAGCCCA	62.96	125
HM_8333	GD2OF4R01EFUJH	TA	2	12	GGGTTCTGTGTGACCTGTTTGTAT	63.35	CAATTTGAAAAATGTAAACAGAGC	62.743	143
HM_8334	GD2OF4R02GVOFI	AC	2	32	GGGTTTCTGGAAGTGTTTGAGAG	62.483	TCTTGTCTTCTCTCTTCTCTG	62.497	160
HM_8335	GD2OF4R02JPDYP	GA	2	20	GGTAAGGTGGAGCGGAAGAGG	62.336	ATGATTTACCCAGACCTTGCCT	63.102	106
HM_8336	GD2OF4R01CCO4P	CA	2	12	GGTAACCAACAAACGGAACACT	62.438	CTGTTGGATGTTTGGATGTTTAGG	63.142	149
HM_8337	GD2OF4R01B17VW	AG	2	12	GGTAGGGTTGAGTTGATGGAGTTG	63.111	CTGAACCTTCCCTCTCTCTCTCT	62.651	85
HM_8338	GD2OF4R02GQQUI	AC	2	12	GGTCAATAACTTGCACGGAACCTT	62.646	GAGTAAAAATGCAATCACCGCAAT	63.356	85
HM_8339	GD2OF4R02GKZOK	AT	2	16	GGTCCAGATATAGTTGCAATGGA	63.322	CCAAACGATACACACAATCACACA	62.864	123
HM_8340	GD2OF4R01C5XMA	AC	2	16	GGTCCGTTTGTAGACCTTGTGTA	62.741	TAGAAAAGCGTAATGATGTGCG	63.445	116
HM_8341	GD2OF4R02IQD3S	GA	2	12	GGTCGAAAGAAAAAGCAGATCAAA	62.922	TGACGACGAGAAAATATAAATGGC	63.243	147
HM_8342	GD2OF4R02GJ5GF	AC	2	12	GGTCTCATGGATGAATCAGCTCT	63.007	ACGACGAGTGAATGAACTTTT	63.263	88
HM_8343	GD2OF4R02G803O	AG	2	14	GGTCTCTTGTGTGAGAAAAAGTTA	62.2	TTTGCTAAGAAAAACGAGGACAA	62.929	152
HM_8344	GD2OF4R01DV9XA	AG	2	16	GGTCTGAACAGAAATAGAGGGCT	63.193	GGCAGCAGAGGTATCACTCACTCT	63.371	95
HM_8345	GD2OF4R01DYVSU	AG	2	14	GGTCTTCAAAAGGACCTGGAAAGT	63.08	CGCTACGATCTATCTAATCCCT	62.903	95
HM_8346	GD2OF4R02FTN8A	GA	2	16	GGTGAACACTAGATTGTCTCTCT	62.998	CTTCTCAATGATTGGGATTTTGG	62.884	146
HM_8347	GD2OF4R01EB99E	GA	2	12	GGTGAGAGAATTCATTGGGTTTG	62.996	TTTGGGTTCTGTGTAACCTGGTCT	62.508	124
HM_8348	GD2OF4R02IDAA8	AC	2	12	GGTGATTAATGATGCACGTACCA	62.962	TTCCGTTCAATCTATCACTTCCG	63.517	103
HM_8349	GD2OF4R02GX2I	GT	2	16	GGTGTGATCAACATGGGACTTCTT	63.553	TGCGCCGAGTGATACTACCTTGT	64.195	115
HM_8350	GD2OF4R02I4O7S	AC	2	20	GGTTCCCTGAATGATCAATGCTAA	63.42	CCGGAAGTTGATTTTACATGGC	62.746	152
HM_8351	GD2OF4R01ASVC	TC	2	12	GGTTGGAACCTCAAGCGAACT	60.655	TTTAGGCTGATTTGGATACGAAATTAT	60.619	125
HM_8352	GD2OF4R01COH57	TG	2	16	GGTTGATCTCTTATTCACAACCT	61.783	GTGTCGTTATGGCTTTTGGTTCT	62.646	157
HM_8353	GD2OF4R01BVY1X	TA	2	16	GGTTTAACCTCTATGTTTACTCTAAGCG	60.325	GATGGTGAATCATGTAACTCTC	61.205	196
HM_8354	GD2OF4R01AZLBV	AG	2	12	GGTTTTAGAGATGGGAGGTTTA	61.861	TGTGACGGTTCATCTTATAATTTC	62.288	152
HM_8355	GD2OF4R01DYCR1	AG	2	20	GTAAGTTGCTGTGTTGGCAGATG	63.087	CTTCCCTCTGGAAAACTGACTCT	63.172	150
HM_8356	GD2OF4R01CSU7X	AT	2	14	GTAAGTCTATGCTCATCTCGATG	61.961	GATCTGGAGAAATTTACAGTCCGA	61.895	157
HM_8357	GD2OF4R02GXO4Y	AT	2	16	GTAACCCAAAGGGAGACCAAG	63.072	ATATCATACACTAAGTACGCCCTCC	62.766	80
HM_8358	GD2OF4R01EF3ZR	TA	2	16	GATCTCTCTGCTGATTTCCCAAT	62.974	CTGCAATGATCATCAACTGGGA	62.5	131
HM_8359	GD2OF4R02FYQPO	TC	2	32	GTAAGTGTCAACCTTCCCAACAG	63.077	ATTGTTTCTACGCCCTCTCTCTC	63.302	96
HM_8360	GD2OF4R02HWA6	CT	2	16	GTAAGAGCTTCACTGGCTCCCTC	62.913	AGTCAATTGAAACCAACGAGAA	63.019	88

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_8361	GD2OF4R02GTJXQ	AT	2	16	GTAGATCACCTACCGTTGCCCT	62.712	ACATCTCAACCTACATCCCTCAT	62.147	141
HM_8362	GD2OF4R02I07EL	CT	2	20	GTAGACCCGTAGACATTAGTCGCA	62.685	AGAGGGGTATCACAGTGGTGTGT	63.365	146
HM_8363	GD2OF4R01EZ3EI	CT	2	12	GATGCTGGATGGGGTAGTTCACAG	63	AGGCAGACGAGCAGAGAAGAAATA	62.936	154
HM_8364	GD2OF4R02J0G3G	CA	2	12	GTATAAAATCCGAGTGTTCAGGG	62.826	AAGCATGTGAGACAATACATCGGA	62.951	144
HM_8365	GD2OF4R02HYOT5	TG	2	20	GTATCTCTCCGACCCCATGATT	62.558	AAGTAAATTTCTGCCACATCTCG	62.729	158
HM_8366	GD2OF4R01EY9B3	AC	2	14	GTCAAAATAGGCCGTGAGTACCAC	63.048	TTTGTGAACCTTTTGTATTGGGG	63.106	134
HM_8367	GD2OF4R02HE3SV	GA	2	12	GTCAACATTGCTTAGTGAGGACCT	62.949	CGCGGCACTACCTTCTCTATT	63.856	136
HM_8368	GD2OF4R02F809C	AT	2	16	GTCAATAGGCGACATTATTCTCGC	63.05	CACGTCTACTCATGGTAATGGGTGA	62.575	146
HM_8369	GD2OF4R02G6PKS	TA	2	12	GTCAATTGCGAAGATGATCACAGT	62.504	ATAACAGATCGGAAGTCAAGGG	61.802	132
HM_8370	GD2OF4R01BTBG2	GT	2	12	GTACAGTGTGTGAGACCAATATT	62.291	AGTATTTTGTGGGGTAGGTGTG	62.299	110
HM_8371	GD2OF4R02JXAN7	GA	2	12	GTGACCGTGGTGTCTTTT	63.416	GAATAGGTGGAGCTTTGAAATGGC	64.197	137
HM_8372	GD2OF4R01BER1U	AG	2	12	GTACATCAGTGGACTCCGAAAC	63.148	TTGCATCTCATCTCTTTTCTCTTC	62.331	150
HM_8373	GD2OF4R01EUNON	AC	2	12	GTCCACGGAGAAAGCAGAGATTA	63.022	CACATGCTTCAGTCTTTTCTCATG	63.181	136
HM_8374	GD2OF4R01B1BPN	TA	2	14	GTCCGCGACAAGAAGTGCTGTG	63.427	TCACATATCATTTGAAAAACCTGTG	63.134	81
HM_8375	GD2OF4R01BE3ON	GA	2	20	GTCTCTGTTTGGGCTACTTCTCA	63.124	TCTCTCAAATGTGCTCTCTGAA	62.593	145
HM_8376	GD2OF4R01DPWMS	AT	2	12	GTCTAAACATAGGTACGCCCTGA	62.633	TTCAAGAGTGTTTATGGATATCAGCA	62.199	141
HM_8377	GD2OF4R01B0OW5	AG	2	12	GTCTCACAGCTATGATCGGGAGTT	63.031	AACCTCGCAATCAGGCTCTTCTTTT	63.815	100
HM_8378	GD2OF4R02JE5DJ	TC	2	20	GTCTCTGGTGACCCCTAAGATGAT	63.327	GACTGAACCACTGTTTTACACCCC	63.023	155
HM_8379	GD2OF4R01C3KM1	TG	2	12	GTCTCTGTTTCATTGTAGGGGACC	63.106	TTGCAATTAACCTTTGACTTGTAGTGT	62.289	80
HM_8380	GD2OF4R02H1W4N	GA	2	14	GTGAAGGATTGTAAATTTGCGCT	62.559	GCAAAATTTGTGCAACTCTCACCA	63.5	136
HM_8381	GD2OF4R02JU43P	AC	2	16	GTGAAGGCTTAGGCCAATAGGTTT	62.924	CCAGCTTGAGGGAGGTGTTAAAG	63.417	117
HM_8382	GD2OF4R01D6SOL	TC	2	12	GTGACAGCTATGGTGTCACTCTC	62.381	TCGAAGGGAGTCTAGATAGAGATCAA	62.056	134
HM_8383	GD2OF4R01BT6KF	TA	2	14	GTGACCAAGATGTCTTCTCCATA	63.644	TGGGTCACTTGACTATAATGTCTACGG	63.517	107
HM_8384	GD2OF4R01CKF7F	TC	2	16	GTGAAGGAATGAGTGTGGATTTC	63.106	GAGTGGGAGGACTTGAGAATGAGA	63.202	112
HM_8385	GD2OF4R01EJL3K	GC	2	14	GTGAGTGTGTCTCCAATGGTGTG	63.974	ATGAACACCACTCATGACAG	63.266	139
HM_8386	GD2OF4R01EZ24Q	GC	2	14	GTGAGTGTGTCTCCAATGGTGTG	63.974	ATGAACACCACTCATGACAG	63.326	139
HM_8387	GD2OF4R02G2ZM	AG	2	14	GTGCACATTTACTGAGGAGCAGAC	62.412	CCTTCGGGTATTTGTTGTCACTC	63.019	126
HM_8388	GD2OF4R01BMHM3	AT	2	12	GTGCATAATGAACCTGGGATTA	60.373	CCGACAATTGACAACCTAGGAAAAG	61.198	160
HM_8389	GD2OF4R01C263R	AG	2	12	GTGCTCGTGTGGTAGAGAAAGT	63.05	TGCTCTCATCTCTACCCCTCTTCA	62.583	116
HM_8390	GD2OF4R01BEY5N	TG	2	14	GTGCTCGCTCTTATCTTTGCTT	63.071	AAAACCAACGTTTGTCTTCACT	62.933	111
HM_8391	GD2OF4R02GEIWK	AT	2	14	GTGCTGAAGGGATATGGAAGTTTG	63.121	CTGAAGCTACTGGGGAAGTGTGAT	63.023	131
HM_8392	GD2OF4R02GM1NG	AG	2	24	GTGCTTAATACATGGAATTTCCGC	63.058	GCTAGCACAGAGCCCTCTTC	62.804	109
HM_8393	GD2OF4R01A0I6V	GA	2	14	GTGGAGAGACGAACGACATGTTT	63.786	TCCTCTCAAATCAACACCACAA	62.918	111
HM_8394	GD2OF4R02FSVNL	TA	2	12	GTGGGGTGTGGTGTGTTTGTC	62.397	GGAGAGGGTGGTGTGACTATGTTT	62.693	160
HM_8395	GD2OF4R01AVLJ4	AG	2	24	GTGGTGTGTTCTTCCGAATGTT	63.161	AGTTTTCTACATGGGATGGGTGCG	63.416	109
HM_8396	GD2OF4R01E1VDK	AC	2	12	GTGGTTTGGGAGGTGACTGTG	63.918	CACTTTGGTAATGTTTGGGCACA	63.064	116
HM_8397	GD2OF4R01D0S5E	GA	2	16	GTGCTCTTCACTCAACTTCTCGT	63.132	CACGAGGACCATGAAATTTTGAAT	63.317	110
HM_8398	GD2OF4R01DBKD5	CT	2	16	GTGTCGATGAATCACGAAAACCT	63.556	AGACTTGGATGGCAAGCAAAATTA	63.138	104
HM_8399	GD2OF4R02JQGE8	GA	2	12	GTGTGAACCTTTTGAAGATCCGGT	62.912	GACGTGTTTTCTCTCCCCCTAC	63.392	153
HM_8400	GD2OF4R02FYFXF	TG	2	14	GTGTGGTGTGATGTTGTGCGG	62.517	ACACACTCACTGCCACTGTACTC	62.979	101
HM_8401	GD2OF4R02F6KRO	AG	2	20	GTGTGTTTGTCCGAGAGTTTGAT	61.651	TTTCTCTCACCATTTCTCTTTCT	60.778	126
HM_8402	GD2OF4R01A0W5D	CA	2	16	GTATCAAAATACGAAAACCTGGCG	62.972	CAATGAATTATGAACAGATTGGACGA	63.233	131
HM_8403	GD2OF4R01EZXBV	AG	2	20	GTATGGATGAAATGGCCAAAAAG	62.722	AATCCCTCTTGTGTGAGGTCTCT	62.764	151
HM_8404	GD2OF4R01CCOXV	TC	2	12	GTATGTAGCCCAACACAACTG	62.753	TCATGAACCCACATAACTGGGAGA	62.803	127
HM_8405	GD2OF4R01BPXOW	GA	2	20	GTCCAAAAAAGTCAAGGCTGAAA	62.823	CAATCACTTACAGGAGTTTAGGGC	62.313	137
HM_8406	GD2OF4R02HP2YQ	TG	2	12	GTCCCAATTTTCAAGTCCAAAGC	64.085	CTCTGTCTCTTATTTCCCCAGCA	63.212	150
HM_8407	GD2OF4R01D70RF	CT	2	16	GTCTAAATGAAATATAGGGCTCG	61.401	GGAGAAGTAAACCTTGAAGAAAAAGAA	61.5	85
HM_8408	GD2OF4R02JADAG	AC	2	16	GTCTTGAGAGCTCCAGATGGAAA	63.217	CATGGATAGTGAATGTCAGCTTGT	63.181	105
HM_8409	GD2OF4R01EB8JB	GA	2	24	GTTGATTTCGCGAATAAATCGTC	63.046	TACGACGACATACTCTCTCTCTC	63.014	148
HM_8410	GD2OF4R02GHHQZ	TC	2	12	GTGGCTGTGAGAAAAAGACAGT	63.036	CTGAGTAGATCGGGCATTTGAACT	63.223	107
HM_8411	GD2OF4R02G095P	GA	2	16	GTCTTGAGTCCATCCCTGTCTAC	62.25	GCTTCTAGCAGCAACAACTAAGTG	62.791	123
HM_8412	GD2OF4R01BOVVP	GT	2	12	GTCTTGTTTGAGCAGAGAGGGT	63.012	GAAGCTCAACACCCCTACAC	63.126	116
HM_8413	GD2OF4R02HYGZ9	AG	2	16	TAAAAAGGGTGAATATGTGCTCT	63.039	TTCTTAATTTCTCTGACCTCACGC	63.022	100
HM_8414	GD2OF4R01CWRWA	GA	2	16	TAAAGATCTGTCAATGTGGGGGT	62.897	TTTTGGGCTCTGAAGAAAAATCAT	63.126	136
HM_8415	GD2OF4R01C257R	TC	2	14	TAAATGACAGCTACAACCTACGCC	62.671	GAAGGCTCTGTTCTAGTGTGTTG	61.786	83
HM_8416	GD2OF4R01DWI93	AT	2	16	TAAATTAATTTCCATCTCCGCCAC	62.533	ATCATCAGAGAGATTCTTCGGCAG	63.222	138
HM_8417	GD2OF4R01A9717	TC	2	16	TAAACAATTTGCTATGCTCTGGA	63.014	GCGAATGCTCAACCTACCAAAATA	63.445	86
HM_8418	GD2OF4R01DNWQF	TC	2	12	TAACTTAATCATCAAGCGCTCTC	62.937	TGGCAGAAAGAGGAAGAGAAAGAG	62.583	99
HM_8419	GD2OF4R02HUJUF	TC	2	14	TAAAGTCAATGGGCTTCTCAATTG	62.519	CCTAATCTATGCTCTTAGGCAAA	62.932	125
HM_8420	GD2OF4R01B2ZBR	TA	2	14	TAACTGGGTGAACCGACTCAT	61.631	TTCCCTAAGATAGTGTCTGATAGTTC	61.419	190
HM_8421	GD2OF4R02HCPMX	GA	2	16	TAAATTAATGAGTCCGTGGTGGT	62.112	TCCTAAATCCTCTCTCAATCTCT	61.215	82
HM_8422	GD2OF4R01CQ8NO	TG	2	14	TAAATTTGGACCAATGTGGGTTT	62.519	GTTAGGTGGGAATGTTTGGGTA	63.117	142
HM_8423	GD2OF4R01DLQLY	AG	2	24	TACAAAAGTGAGAGAGTGGAGGCA	62.502	CCACCAAGGCGTCTTCTACATC	63.137	134
HM_8424	GD2OF4R01D8SDE	AT	2	16	TACAGCAAGAAAAACCCCAAGTA	63.023	CGCCATAATCTTATGATCACATCG	63.635	99
HM_8425	GD2OF4R02IC8Q9	AC	2	16	TACATCCCAATTTGAGCAGCTA	61.832	TGTGGGTATGATTTTGTATGTTAATG	61.09	123
HM_8426	GD2OF4R01B0ZEU	AG	2	12	TACCACCAAGTCAGCAACCTACAA	62.955	AGCCTCACTATGTAATTTGCCCT	63.313	154
HM_8427	GD2OF4R02FPQ76	AG	2	20	TACCAAAATGCAATAATCCCAATC	62.913	CTTTTGTGGTGTGATGCTCGGTC	63.019	142
HM_8428	GD2OF4R02IBDKA	AT	2	14	TACCCATCTTTGGAGAGCAAAAT	63.121	CCATATCTCAACCTTCCACCATTA	63.194	122
HM_8429	GD2OF4R02F6669	TA	2	16	TACCGAAGCTCCGCACTTCTCTAA	63.222	GCTCTGTTCTTGATCAGCTCTTG	63.887	144
HM_8430	GD2OF4R01EIVNE	TG	2	16	TACCTCTTTCATCATGACCTCTC	63.102	GCTCGGTTGTGGCTCGTGT	63.541	157
HM_8431	GD2OF4R02F48NW	AT	2	14	TACTAGCACTTTGGCATCTTCTTC	62.839	TTTTCTATATGGACAATCGCGTG	62.258	143
HM_8432	GD2OF4R01AWTUZ	AG	2	12	TACTTCTCTGTTCACTTGGGGCT	62.61	GAAATCTTGGTCTCGGTCTCTA	63.022	126
HM_8433	GD2OF4R02ITW0Z	AT	2	12	TAGACGGCACTTCCCAATTAAGAA	63.122	CTCATCCCAAAATTTCTTTGTC	62.996	146
HM_8434	GD2OF4R02JBE5I	GA	2	14	TAGACTCTTTGGGTCACTGGGAG	62.993	CTTATGTTCAACGCTTCTCCCTT	63.682	103
HM_8435	GD2OF4R02HHBPJ	CT	2	24	TAGCAGCCATATTGAGCTTCTC	63.046	TCATATATACACCCACCGAGCTC	63.223	108
HM_8436	GD2OF4R01A01HB	AG	2	24	TAGCATTTTGTAGTGCAGACCTGA	63.176	CCTCTTAATCTCCTCTCTGCTTT	62.89	123
HM_8437	GD2OF4R01DQ9OF	AG	2	12	TAGCCAATAAGAAGCAATGGA	63.026	ATTATTTTGGCCAAATCGGGTAG	63.189	133
HM_8438	GD2OF4R02ISZ44	GA	2	20	TAGGAATCAGGTGGCGAGATCG	61.361	TCATATATCTATCTGCTTCCGCTCA	60.835	155
HM_8439	GD2OF4R01B85NV	CT	2	16	TAGGGCACTCTCACTATCCGTTTC	62.718	ATGCGACTTTGTTCTTTGTTGGT	63.154	142
HM_8440	GD2OF4R02F1BCS	AC	2	12	TAGTAGCTCTTCCCAACCCATCTC	62.102	TAAATGGAATTCCTCATTAACCA	62.588	134
HM_8441	GD2OF4R01DSFLC	TA	2	20	TAGTGCTGTTGCTGTTGTTCCAA	62.966	AGGTGTTCTTGTGACGAGACCGTGA	62.307	160
HM_8442	GD2OF4R01EY27D	AG	2	14	TAGTTTCAGGCACAGCTCCTCTC	63.036	GGAAATTTCTCGTACGCTTTTCT	63.016	154
HM_8443	GD2OF4R02JJKWD	TC	2	14	TATAACCAACCATCACTCCCAAC	63.108	TTGGTGGCCATAAACCCCTTAGAT	63.092	114
HM_8444	GD2OF4R02GCP5I	TC	2	16	TATATGAGGTTTGGAGAGGGGGCT	63.176	TTTTGTGGGAAACCGTAGAAGAA	63.011	117
HM_8445	GD2OF4R02H4MBL	TC	2	14	TATATGCAAGTCTGCAAGTCAAC	62.565	TAAAGTGAAGATGCGAGATCGAC	62.084	93
HM_8446	GD2OF4R01DARRB	CA	2	16	TATATGGGGAATTTGATTCGCAAC	62.913	TTCTGGGGTTAGTTGGGGTTATCT	63.074	160
HM_8447	GD2OF4R01EWZMS	GT	2	16	TATCGCATGGTGCTTAAATCTGA	62.861	CCACCAAAAAAGAAACGTAACAC	62.834	156
HM_8448	GD2OF4R01D0G57	CT	2	16	TATCTCAAGAGCAACCAACCAAC	63.048	AGAAACCCATGAAGAAACCACTT	63.285	113
HM_8449	GD2OF4R02HBZA2	CT	2	14	TATCTCAATCTCAACACCTCACCC	63.644	GTTTTAGGTAAACGATTGCTCCAGC	63.051	129
HM_8450	GD2OF4R02FN3A8	GA	2	20	TATCTCGTACCGGTTTTTCGCTTA	63.046	AATCAATTTGATCTGGGAGATTCT	62.354	146
HM_8451	GD2OF4R01AE9W8	AT	2	14	TATGGGCTTTCTCACTCTCGCAAC	62.815	GCTGTATCTCTCTCTCTCTCTCT	62.667	142
HM_8452	GD2OF4R01B5DSQ	AG	2	14	TATGGCTCCATGATTGCTTTTCT	63.42	AAATGCTTTGGGCTGTTTACTGA	63.146	135
HM_8453	GD2OF4R02FTO6X	TC	2	14	TATGGGCTTGTCTCATCTATTTTA	61.641	TACTCCAATGACGAACCAAAATG	62.211	141
HM_8454	GD2OF4R02HS5TQ	CT	2	12	TATTACACATGGGATTTGCTCTC	62.815	ATAGCTTGAAGAACCTGCAAAATG	62.839	106
HM_8455	GD2OF4R02J2KFF	AC	2	24	TATTCCTACTCTCGAGTTATTGAT	61.004	CTGCAAAACCAATACAAAATAACAAA	60.67	160

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_8456	GD2OF4R02IDFT5	TG	2	14	TATTTACGCCACTGAAGCAATCAA	62.872	ATGAAGATTTCATCCCTTTTGAG	62.705	157
HM_8457	GD2OF4R01C3BA2	GA	2	20	TATTTTCAGTGCTTCTGTGCTTT	61.441	GTCCGTCGTAACCTACCTCCTC	61.256	98
HM_8458	GD2OF4R01CD0L1	TA	2	12	TATTTGGCAACAACCTCCCTTAT	63.768	TCTATTGTAGGGGGTTCCTGTG	63.42	87
HM_8459	GD2OF4R01BC7B0	AT	2	16	TCAAAAAACAAGTGCCAAAAAACA	62.953	GACTTTGGATGTTAATCGATGGG	62.802	146
HM_8460	GD2OF4R01A4D6Y	AT	2	20	TCAAAAAACAATCAGTGGCTTGAA	62.943	CTTTTACGTCTTTGGAACGACAC	63.138	148
HM_8461	GD2OF4R01BQKQ1	GA	2	16	TCAAAACCACTTCTAGTTTCGAGAT	60.352	GTACACAGTCTTTGCTTCCTCCTC	60.44	87
HM_8462	GD2OF4R01D0830	AG	2	14	TCAAAATCAACTTCCCAAGATCAA	63.004	CAAGTTCGTTGCCAAGAATAGGT	62.741	148
HM_8463	GD2OF4R01A38F7	CT	2	12	TCAAACTACTCTTATCTCCCTCACA	62.61	CTTTGAAGCTGGGCTTACTATGA	62.932	150
HM_8464	GD2OF4R01CBF3	TG	2	16	TCAAATTCGTAGTGTGGTGCAAT	62.872	GACGCATCAATCCTCCTCGAAAG	63.54	125
HM_8465	GD2OF4R01CX755	AC	2	16	TCAAATTTAGGGAGCATCAACAGACT	60.694	TCCCATCCTCTTTCTTGAGTTT	61.574	160
HM_8466	GD2OF4R01BYRWD	CT	2	12	TCAACCTATCATTTGCATCAAGAAA	61.935	TTTGATGAGGTGTGTGTGTGAGAG	62.592	80
HM_8467	GD2OF4R01C6Z1E	AC	2	14	TCAACTAAAACTCCTCTACGTAACCG	62.148	GCCTCCGATCTCTAAAAGTATCCA	62.828	159
HM_8468	GD2OF4R02HGS81	GT	2	20	TCAAGGCTCAAAATGACACAAGGT	63.129	AACGTACGAGGATATTTTGAAACG	62.631	116
HM_8469	GD2OF4R01BM245	CA	2	14	TCAATACTAATAGCAACACGGCA	62.875	CCCAATGTGACAGTGATATCTT	62.515	158
HM_8470	GD2OF4R02G0ED5	TA	2	12	TCAATTTGGGTGTTGTAATTTTGA	62.51	CTAGACCTTCATCCACAGATAGG	62.353	141
HM_8471	GD2OF4R01AETH2	AG	2	20	TCACTTAATCCTTTGCAAAAAATCG	63.416	TGCAGAAGACATATAGTTCGAG	63.074	129
HM_8472	GD2OF4R01D721B	CA	2	14	TCACTTCACAGAGAAACACACT	62.366	AATTTGTGTTTACGCACTGTTTAAATT	61.383	159
HM_8473	GD2OF4R02JINT10	AT	2	14	TACGAATAGAGTGTGCTGATAA	63.072	CACCATGATTCTTAACAGGTTC	62.897	109
HM_8474	GD2OF4R02JJUC6	CT	2	12	TCACTGCTCTCTACCTTCATCA	63.383	CGATCTGGGATGGTTTGTAGTAGT	62.686	95
HM_8475	GD2OF4R02JTK6C	AT	2	16	TCACTCAACTCTGTAATTAACAAATCAA	61.229	GAATCGGTCCAACAATAACATACTA	62.17	160
HM_8476	GD2OF4R01EVVDK	GA	2	12	TCAGAACCGATCTCAGCTTTATCA	63.038	CGCCGTGATACCTCTCTCATATA	62.829	148
HM_8477	GD2OF4R01CP7V4	AC	2	32	TCAGAAATGCCACTATAGCAAAAA	63.059	ACGGGTAAAGGAACGTATTCCCTA	63.001	160
HM_8478	GD2OF4R02G5N6H	GA	2	12	TCAGAGCCAATCAGCAATTTTGTA	63.059	CAGCAAAAGGTGGCTTTTATCTGG	63.142	102
HM_8479	GD2OF4R01AYQNM	AG	2	12	TCAGATCATCATTCATGCTTCGT	63.046	CGTTCAATACAAAACCCACAACA	62.953	132
HM_8480	GD2OF4R01C9J79	TA	2	16	TCAGATTAAAGCTACAGACGACA	63.29	AGAGTGATCCATCCAGGAGTAA	62.353	130
HM_8481	GD2OF4R01ESGBM	AG	2	14	TCAGCATCTACACAACATCCGTA	61.778	TTCATCTGTATCTCAAAAAATCAATC	60.935	112
HM_8482	GD2OF4R02HUYB6	AG	2	40	TCAGCCTACAGTAGAACCTTTACACA	61.646	ACTACTACTACTCCCTCCTCC	61.377	132
HM_8483	GD2OF4R01AKV2D	AC	2	16	TCAGGGCAAAACAGATGATGAGATA	63.028	CGTCTCTTCTACGACCCAAGAGT	63.01	121
HM_8484	GD2OF4R02HMHZ	AG	2	12	TCATAATTTTCAAGTCTTTTJAGGGA	62.408	ATGGTGGTATACCGTTCATGGTG	62.818	138
HM_8485	GD2OF4R02JEBW8	AC	2	24	TCAATACCAAGTCATCAACCATATA	62.589	TTCTGGCATGAAATTTTGTGTTCT	63.018	95
HM_8486	GD2OF4R01BDXE0	TC	2	12	TCATAGGTCTTTATCAAAATGTGGA	61.955	AGACAGAAGGGTCTTGGTGTGTTTG	62.906	130
HM_8487	GD2OF4R02F28F0	TC	2	12	TCATATTTATCAGCGCTTTCTCGC	63.545	AGAGATAGAGAGGAGCGTACGAG	62.707	121
HM_8488	GD2OF4R02HUSK8	TC	2	12	TCATATTTATCAGCGCTTTCTCGC	63.545	AGAGATAGAGAGGAGCGTACGAG	62.707	122
HM_8489	GD2OF4R01DPLY9	AT	2	16	TCATCAATGAACATCAAAACCAAGT	61.789	TGGGTAAAAGTTTACTTGATCGCAT	62.092	127
HM_8490	GD2OF4R01BDWYW	TG	2	20	TCACTCCCTGTGAGTCAATGATTT	61.096	ACCTCTTCAAAATTAATCTAAAGGACCA	60.211	124
HM_8491	GD2OF4R01DI39T	AC	2	16	TCATCCGGAAGAAACAATCTCAT	63.099	GTGATTTTGGATCGGTTTCTTTTG	62.909	101
HM_8492	GD2OF4R01AKB6K	AC	2	14	TCATCCAGGTTCAAGTCGTGTAAGA	62.438	CTCAGTAATGGTCTTTCTGGGTT	62.71	151
HM_8493	GD2OF4R01AQJMY	TA	2	14	TCATCGATTATCACACTGCAATA	62.629	ATCATCCATTATTTGGAGCGGTAA	62.724	137
HM_8494	GD2OF4R02JL6L	TA	2	12	TCATCTCAATTTGGTAGATTGGGAA	62.898	TTTGCCATTATAGGAAAAACAATG	63.115	138
HM_8495	GD2OF4R01CWPYM	CT	2	14	TCATGCCATGTATTATTTGCTACT	63.066	GATAGAAACAGAAAGTGACCCGTCC	63.407	133
HM_8496	GD2OF4R01AXGY4	CT	2	12	TCATGTTCCCTCTACTCAAATTA	62.787	TCGTCAAGCATCATGTGATCAATAC	62.691	153
HM_8497	GD2OF4R02JXU6A	CT	2	14	TCATTTGGGTTGAATCATTCACAG	63.128	AGAGAAGAGGACAGACCCACAGAG	63.271	140
HM_8498	GD2OF4R01AJI75	AT	2	20	TCATTTTTCAGAGATCTCAAAATGGAA	62.264	ATCGTTTGTCTGCATGTCGTAGA	63.078	153
HM_8499	GD2OF4R01AX6RM	AC	2	16	TCATTTTCTCTGCACATACAGC	62.645	TCATGGGTAAAAACTCAAAAGATAGTG	61.793	127
HM_8500	GD2OF4R01EKS7T	AG	2	16	TCAAAAACAGGAACCTTAAACCT	63.176	CGCTTCTAAGAGGTTGCGAAATTTT	63.103	156
HM_8501	GD2OF4R01AVXIL	TA	2	20	TCCAATATATATCTGATTAATTCGGGT	61.165	AGGAAACTACGTCTAGTCGGTTCG	62.132	137
HM_8502	GD2OF4R02F3L2J	GT	2	20	TCCACAATTTTGTCTTAATGTCG	62.439	TTGTGCAAGAACTGTTCTCTTTTTC	62.848	102
HM_8503	GD2OF4R02HYKK0	GA	2	30	TCCACCTCATCTACAGCTTCTCTCC	63.115	ATAGCAGGCGTGATGTTGGG	63.278	96
HM_8504	GD2OF4R02HAPAY	TC	2	16	TCCATAAATATCTCAATATCCCTTGA	62.904	AGTTGGGTTTCGGTATTGGGAT	63.776	115
HM_8505	GD2OF4R02HF19G	TC	2	14	TCATCTCCCTCTCCTCTAACTCT	63.365	ATTCTCAATCGCTTTGCTCTCT	63.812	159
HM_8506	GD2OF4R02HUCZH	CT	2	32	TCAATGTGGGCTTCTAACTAATGG	63.421	GAAACGAAACGAAAGAGGATGATG	63.348	155
HM_8507	GD2OF4R02J3N39	TC	2	12	TCCCAATCTCAACCTCTCTTTTA	62.369	GTGGAAGGGAATGGGATAAGAAC	63.069	150
HM_8508	GD2OF4R01C2K2K	AG	2	16	TCCCAAGTCTGGAAATTTTAATC	61.232	CAAAATGATGTTTTGTATCATTTGTTT	61.329	87
HM_8509	GD2OF4R01AH9U	GA	2	14	TCCGCAAGCTACGTTTACAGAGAG	63.138	CTCTCTGCTTCAACCTCTACGAAA	63.125	83
HM_8510	GD2OF4R01DD2M6	TA	2	12	TCCCGTTCAAGTTACATACAACCA	62.628	GACTATAGCATTTCAAGAATAACCCA	61.86	149
HM_8511	GD2OF4R01B9U5Q	AT	2	14	TCCGAAACATGAAAGGAAGGATAA	62.993	GGGGCGTCTGTTCCATACAT	62.069	130
HM_8512	GD2OF4R01AL12X	TC	2	12	TCCGAATTTCAATCTCTGTCTCT	63.093	GAAACTAGCCCTGTTTATTCTGTGGA	62.934	81
HM_8513	GD2OF4R01AMJXA	CT	2	12	TCCTCATATGTTCACTTCTCCCAA	63.106	TCAGCAGGCGGTGTAACGTGTATT	63.1	157
HM_8514	GD2OF4R01BNSN6	CA	2	14	TCCTCCAAAGAGGTTTGGTTACAC	62.696	TTTAACCATGTGTTGTGATTTCGG	62.943	158
HM_8515	GD2OF4R01C8GXP	CA	2	14	TCCTCCACTATCACCCCAACATAG	63.413	AAACGGATGTGCATAATGTTTGAA	62.553	131
HM_8516	GD2OF4R01EFA9R	TA	2	12	TCCTCTAAAGACCCCTCCATTTCT	62.659	AATTTCACTCGGGTCTTCTGTGTA	62.298	91
HM_8517	GD2OF4R02GJVU6	AG	2	20	TCTGGAAGCAACCAATCAAAAGTGA	62.411	TTGTTGCGGAACGTACTCTCTCCTC	63.148	80
HM_8518	GD2OF4R01CPFT9	GA	2	12	TCCTGATTGCAAGACATGTGGTTTA	63.048	CAAAATTCACAACTACACACCA	62.324	159
HM_8519	GD2OF4R01EMOTB	AT	2	16	TCCTTTTCTAGCTTCTCAATTTTGC	61.688	CCATGCAGCTGTAGTACATTGTGT	61.367	132
HM_8520	GD2OF4R02G6N0D	CT	2	20	TCGAGAATAGTTTTTGTACGGTTAGC	62.091	TAAATGAGATGGGAAATGGAGG	62.383	104
HM_8521	GD2OF4R01AHGOV	CT	2	12	TCGATGTTGAAAGATTCTAATGTTTG	62.545	CAGTGCAACATATCCAATTTGCT	63.296	131
HM_8522	GD2OF4R01BV4M7	TA	2	16	TCGATTATGGTGATTTTATACAAA	61.561	GGAAAGGGAAGTGACTAGGCTTAAA	61.242	155
HM_8523	GD2OF4R02HBX4C	GA	2	12	TCGCGGTGAAAGTCGAATCT	63.761	ACCAAGTCTCTCCACTCACACAG	64.137	152
HM_8524	GD2OF4R02DGPOM	TA	2	20	TCGCGTATCAAAAAAATAAGGAGC	62.606	ACATGCAAGCCATTCACTGTGATG	62.556	142
HM_8525	GD2OF4R02JB8DM	AT	2	14	TCGGGTGAAAAATCTATGGAAGAG	62.505	GTGGCATTGATATGCGTTATTTT	63.057	96
HM_8526	GD2OF4R01B1XZW	AG	2	12	TCGTCTTCAAGATATTATGGACACA	61.444	AGTCAGCAACATGATCAACCTCTC	61.934	187
HM_8527	GD2OF4R01CVNQK	AC	2	16	TCGTGTAGATGATATAAGCTAATGCAA	60.393	TAGTACTAGGGTCCCACTGTGT	61.021	139
HM_8528	GD2OF4R01A7AJL	AG	2	12	TCGTTGACATACAAGCCCTCATGTA	62.14	GATGGTTCTTAATCCCACTGGTCT	61.75	160
HM_8529	GD2OF4R01CUM8H	AT	2	12	TCTAACATTTACATCACACACAGC	62.055	TTTTTCATTTTGTGCGAAATTTG	61.264	152
HM_8530	GD2OF4R02JIMZC	AT	2	14	TCTACTATACACCCACACCCACACC	63.248	TGCCAATGCAACAATTAATGAC	62.972	105
HM_8531	GD2OF4R01EQZ3D	AG	2	14	TCTAGGATGAAGAACGCAAAACACA	63.163	CTTAGTTTGAGTGTGTGGGTGTGG	62.941	156
HM_8532	GD2OF4R02HKP5R	AG	2	16	TCTAGTCTCTCACATGGGGTTTC	62.884	CTCTCTAGTCTCTCCCTCTCTCG	62.535	146
HM_8533	GD2OF4R01AXAX9	AC	2	24	TCTATCACTTGGGTGGCAATAAAA	61.822	TTGTAGGACATTATGTTGATTTCCTC	61.773	120
HM_8534	GD2OF4R02H2TH9	GA	2	12	TCTATGGCTTTTGAAGCTTCTTCC	62.233	TCATTTGCTAGCACTCTCATTTCC	61.905	158
HM_8535	GD2OF4R02H7FER	CT	2	20	TCTATTCAATCCAACTCGAGTCCC	63.787	GTCAGTGTGGTAGGTCTCCCATC	62.91	80
HM_8536	GD2OF4R01EWWY7	AT	2	12	TCTCATGCTGCAAGCTTATTTT	61.266	CATATGCCTCTTTTAACTTTCTCTTTC	60.369	108
HM_8537	GD2OF4R01EDWMJ	AG	2	12	TCTCAAGAACATTAACATCTGCG	63.743	CACACAAAGCCATTAAAGCACAG	62.979	95
HM_8538	GD2OF4R01B0A2E	AT	2	12	TCTCATATCTGATAAGAGCTGCCA	63.441	GGAAGCAAGTCAGTCGTACCAAG	63.456	113
HM_8539	GD2OF4R01DK3QR	AG	2	20	TCTCATGTTTAAAGTGCCCTCTCC	62.91	TCCCTCTCTCTTAATCTCTCTCT	62.13	151
HM_8540	GD2OF4R01AD30V	TG	2	16	TCTCTACGCCCACTAGTGGATTA	63.227	CCTTAGTAGCCCTGATTTTACCTG	62.828	142
HM_8541	GD2OF4R02FSXV	GA	2	14	TCTGAATCTGTGTCAGTTGTGAAGC	62.937	AGGCTTGACCTTGTCTGTGATTA	63.338	149
HM_8542	GD2OF4R02I66TB	TA	2	12	TCTGACTATTAAAGATTCTCTGCCC	62.039	ATCCACACTTTGTGAAATCAACGA	62.831	153
HM_8543	GD2OF4R01EQ1WP	CT	2	24	TCTGCAACTATATCTCTCTTTTGAT	63.58	GGGATGCGAGTTCCCATAGATAG	63.101	80
HM_8544	GD2OF4R02HU3DI	CA	2	20	TCGTGATTGTATCTCAATTTCTCTGC	62.747	CGAATAAAATCACATGTAGATGGTCC	61.873	123
HM_8545	GD2OF4R01DQTCX	TC	2	14	TCTGTGAGCAACGAAGACAATAAT	62.324	TCATCTGAATTTGTCTCTCTCCA	62.336	106
HM_8546	GD2OF4R01EN2AV	CT	2	16	TCTGTTGCTCTGTGTGACAGTCT	63.199	GGAGAGTTGTTGGGTGCTGTTTGA	63.233	124
HM_8547	GD2OF4R01EJ6V7	AT	2	16	TCTTACCCTCTCAACACTCAGCAA	62.502	TGCATGTGATGCTGTGGTTTATC	63.41	126
HM_8548	GD2OF4R02G6OP4	TA	2	16	TCTTCAACGACTAGCTGAACAACAA	62.339	CGTGAGCTTCTCACTACTCTCTT	62.397	120
HM_8549	GD2OF4R01AJK0I	AT	2	16	TCTTCAGGGAAGTTTAGGGATCA	62.369	CTTCTCAACCCCTTTTGATCT	63.1	146
HM_8550	GD2OF4R02IKG2R	AT	2	12	TCTTCAGTCCCTCTTTTATCGGAG	63.117	GGAGTCATGATGTGATGTAGTGG	62.803	148

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_8551	GD2OF4R01DUKU0	GA	2	20	TCCTCAGTTGGAGGCTTTTCAGTT	62.71	TAGCCAGCTCAGACCTCAAATCTT	62.824	138
HM_8552	GD2OF4R02FU4YD	TG	2	14	TCCTCCAAACCCAGAAAATTCACAA	62.989	CACAACCGTCCAATATCACTCAA	63.15	150
HM_8553	GD2OF4R01CLFMO	AG	2	24	TCCTCCAAATACCAAAGCTCACAA	62.112	GGTGCTCTCTGGCTTTGTACTCTC	62.939	148
HM_8554	GD2OF4R01EXIDW	AG	2	14	TCCTCTCTTGTGAACACCACTG	62.81	CAATGTTTCTCTGCCTACAACCT	63.239	143
HM_8555	GD2OF4R02GAFTH	TC	2	16	TCCTTGACATCAGGACCTCTCTCTC	63.202	GGATCTTAGCTGACTCTTGCCTT	62.341	125
HM_8556	GD2OF4R02GUNFM	TG	2	16	TCCTTGACATGGGTTTTCAGTTTGT	62.397	CCACACTTGCATAAGCAACTTAGAA	61.79	113
HM_8557	GD2OF4R01B8TEQ	AC	2	16	TCCTTGACTTGGTGGGTCAAGAAGC	61.639	ACACTCCACTGGAAAGTCACTCTG	60.966	145
HM_8558	GD2OF4R02HJ03P	AG	2	20	TCCTTGAGCAACAATCAAGCATGAA	61.275	GAATGTCCACTGGTTCGCACTC	62.028	159
HM_8559	GD2OF4R02H5RS5	GA	2	16	TCCTTCCCAAACCTCATCTTCAGG	62.881	CATTTATAAAGCAGCAGCTTCCC	63.062	119
HM_8560	GD2OF4R02GVRWR	GA	2	14	TCCTTTTCTAGATCGAGGGTTGGG	63.859	TCCTCTCCTCTCTCAAGTCAA	63.079	132
HM_8561	GD2OF4R02HQ048	TA	2	12	TGAAAACACCCACCACCTATCTA	63.728	TGCTCGTCGATGTTCTTATCTCTG	62.948	155
HM_8562	GD2OF4R02IL6GZ	TA	2	12	TGAAACCCCTCTCACTTCTCTCTCC	62.479	CACATCCGCTGAAAATTTGAAACCA	62.475	135
HM_8563	GD2OF4R01E2T4J	TA	2	16	TGAAAGCAATAGGTAGCAGCAGTTC	63.078	GGGTTATTAAACCAAGCGACATG	62.438	83
HM_8564	GD2OF4R02IP7BR	TA	2	14	TGAACACTATTTTGGGAGGGAAGG	62.591	AGTGTGCATATTGTGATCCAGCTT	62.757	131
HM_8565	GD2OF4R01EH01R	CA	2	16	TGAACATGGTGAATGGACGCTACA	63.061	CATGCATTGACTGTTGCAATTCTA	62.233	223
HM_8566	GD2OF4R01BUP95	TA	2	16	TGAAGCTTTTTCATCAAAACACAGA	62.241	TTCAGGGAAGGAACCTTGTGTAAG	63.198	121
HM_8567	GD2OF4R01B0I5K	CG	2	12	TGAAGGAATTTGAGGAAATTTGGAGA	63.182	GACACCGTGGTGACTTTACAGTTG	62.958	135
HM_8568	GD2OF4R01HLYL7	AG	2	16	TGAAGGGCAACTACACAGTCACAT	63.067	CCTCACTCTGTCACTCTCAAGGTATG	62.717	159
HM_8569	GD2OF4R01EC44D	AT	2	12	TGAATTTGTAGTACTAGCTGAATGA	60.546	TTTGAAACAAGAACCAAGAAAT	60.355	112
HM_8570	GD2OF4R02G58KJ	AT	2	12	TGAATTTATGGGGAACCTTCTTGAAA	61.163	GGAAAGCCAGAAATAAATGGAAAC	61.276	131
HM_8571	GD2OF4R02GGD0D	CT	2	16	TGAATTTCAAGGCAATCTTCAAAA	61.921	GGAGATACGATCTGTTGGTTTCTC	62.902	89
HM_8572	GD2OF4R01DQGSZ	AT	2	14	TGACAAATGATTAAACACAGACCGT	62.726	GCAGTCATCTCTCATTCATTATGC	63.255	118
HM_8573	GD2OF4R01CULJ8	AT	2	16	TGACATGGTCTATGATGCTGTTTT	62.646	ACCTTTCTGTTGGTTGCTGTTTT	62.933	112
HM_8574	GD2OF4R01ASKWO	TG	2	12	TGACGATGAAACAGTTCCCAAAAT	62.717	TTCTATCTCGGCAACATCACACAT	62.951	155
HM_8575	GD2OF4R01HNG2	AC	2	12	TGAGACCTTATCTTGTCTGTGGTCC	62.91	CACGACACTTCACGGACACTATTC	63.067	159
HM_8576	GD2OF4R01DD9TV	AG	2	14	TGAGAGATATGAGAGAGTGGCTGC	62.274	CACCTAAGCCAAATGCCCTGTATG	63.142	114
HM_8577	GD2OF4R02GQDF5	AG	2	12	TGAGAGCCAAAGGTAATCCCAAGTA	63.214	ACCAGAACTCCATAACTCCAGAA	62.368	86
HM_8578	GD2OF4R02IPEG8	CT	2	12	TGAGCAGTCCCACTCTCTCTCTTT	62.898	GAGCTAAGATTGACCCGAGTGTGT	63.154	152
HM_8579	GD2OF4R01C7QBX	AT	2	14	TGAGCAGTTCAAGTTCATTCACTCT	62.397	TGAGAAAGAACGGGTGTGTACAT	62.221	111
HM_8580	GD2OF4R02GU68N	TA	2	12	TGATAAATGGGACCTCTGAAGTGG	62.211	GTGCGTTGGATGTTTCTCATTCTA	62.529	154
HM_8581	GD2OF4R02IO5IR	TA	2	14	TGATCTCAGCAGATGCCAAATCAAC	63.028	ACATCACAGTATTCTATCGCCGTG	63.051	155
HM_8582	GD2OF4R02G5AKL	CT	2	24	TGATGAAATGGGCTGTGAGAGTGA	63.038	CCACATTATTACAGAAATAAACCCGACA	62.348	149
HM_8583	GD2OF4R01EJL9J	TA	2	16	TGATGAGTCCTGTGTATATGCG	62.196	TTCACTTTGTCTCTCAGGTAGCTC	62.555	102
HM_8584	GD2OF4R02IHLCY	CT	2	24	TGATGGAAACCCATCACTCTTAAC	62.383	GATGGAGTCGTGACATTTAGTGTG	61.524	143
HM_8585	GD2OF4R01ELRSW	TG	2	12	TGATGTGAATTTGTGATGTATTTTGTG	61.057	TTACTATCTTTATCTGCCACCCACC	61.67	85
HM_8586	GD2OF4R01BTSFX	CT	2	12	TGATTTCTGTAAGTATTTGATGGTGA	60.167	GCCTGTAAGTCTGACAGAGCTTAT	61.127	110
HM_8587	GD2OF4R01DFS41	TA	2	12	TGATTTGATGTCATGTTTTCCTT	62.614	CACAATCTATACATAGACCCACACAGA	61.626	157
HM_8588	GD2OF4R01CH1A9	TC	2	14	TGATTTTCTCCAAATGTGCTCTTC	61.771	CTTTTGTGCCATTGATGAGACT	62.713	83
HM_8589	GD2OF4R01DHQC7	CT	2	12	TGCAAAAGACTCTCTTAGGCAAAA	61.644	GCCTAAGATCGAAAACATACGAGAA	61.983	119
HM_8590	GD2OF4R02JAP65	AG	2	16	TGCAACACCTCAAGTTAGTTGGTTG	63.16	AATTACGGGGTTCTTCACAATTTGA	62.194	144
HM_8591	GD2OF4R02G24DB	AT	2	14	TGCAATCTTTCCACAAATCTCCAA	62.832	AGGATCGGAGGAGGTAATAAGCAC	62.999	139
HM_8592	GD2OF4R01CZ5E1	TG	2	12	TGCAATCTTTTAAAGAACTGAAGCAAA	62.542	AATAGGAAGATCCGATGCTCTGTG	62.913	153
HM_8593	GD2OF4R02HELDE	AG	2	12	TGCAATCTTGTGAAATTAAGTGG	63.367	TGCTAGTGGGTTCCATTCTCTCT	62.598	112
HM_8594	GD2OF4R01DKK2X	AC	2	12	TGCACAAAAAGATTTAGGCCATTC	63.433	AGGTCACTCATTTTGTGGGTCTC	62.585	83
HM_8595	GD2OF4R01EAP8E	AG	2	12	TGCAACATGCCAGCTGTATAGTTTA	62.485	CGATCATCGCTGATGGTGATAG	62.813	121
HM_8596	GD2OF4R01CDR5K	TG	2	14	TGCATCACCTAAAAGTATGACCGA	62.845	TGGGAGTCTGTACGGTATCTCTTG	62.502	131
HM_8597	GD2OF4R01AWZ4U	TA	2	12	TGCATCGTGTATGATCACTCACTCT	62.169	TGTTGTTTAATGTTTCTGCAAAATGA	62.795	133
HM_8598	GD2OF4R01A6UL	GT	2	16	TGCCAAAAGACTGTTGTGAGTTGA	63.159	AAGGAGTGTTTGAAATTTGGTTGG	62.508	86
HM_8599	GD2OF4R02FL4TZ	AT	2	16	TGCCCAACAACTAGTGACTCTGCG	62.869	CATGTTTGTCTCTGTTGTTGGTCA	63.169	147
HM_8600	GD2OF4R01DAFT7	CT	2	12	TGCCATGGATGTAGCAATTAAGAGA	62.949	GTCTCTGAGAGAGGCAATGGAA	63.022	81
HM_8601	GD2OF4R02JH5G2	CT	2	12	TGCTCAAAATAGATGCATATTGCC	61.285	TCCACCAATTTGCAATGGTAGTTT	61.62	126
HM_8602	GD2OF4R01DJ6WB	GT	2	12	TGCTGAGGGGAGAAGTACTTTTGG	63.015	CTTCTCGCGTCTCTTTCTCTTTT	63.395	140
HM_8603	GD2OF4R02IRMD5	AC	2	20	TGCTTCTTGGCTTTAAATCATTAA	63.026	TACTTGAGACAGAAGGGGAGGTTG	62.993	149
HM_8604	GD2OF4R02GWVH3	AT	2	12	TGCTTGTATTGTTTCTTAATGTCACA	61.942	TTTTCAAAAATCGAGAGTGCAGTG	62.742	130
HM_8605	GD2OF4R01CC3OF	CT	2	12	TGCTTTAGGAGTTGTATCTTGCCA	62.241	CTCTAGGGTTTCAAGTCTAGGCCA	62.201	137
HM_8606	GD2OF4R021FKJ	AG	2	24	TGAAAAAGAACCAAAAATGGAAAA	62.824	TGAAAAACAAGAGGAGGGTTATATCG	62.73	110
HM_8607	GD2OF4R01A15OR	AG	2	32	TGGAAGTGAGTGAACAATCTGTTGA	62.013	TACCTCCCTCTCTTACGTTT	62.503	153
HM_8608	GD2OF4R01EVFXA	TC	2	12	TGGAATGTATCATGAACAATAGGG	62.807	CTTCTTTGCTTCTACATGCACT	63.044	153
HM_8609	GD2OF4R01AE86G	GA	2	16	TGGAATTCATCACTCAACACCAT	62.7	TGAACCTGGATGAAGGTTTGTATGAA	62.932	131
HM_8610	GD2OF4R01BBDJZ	GA	2	12	TGGACGAAAGAGATAAACACAGCA	62.294	GAGCAGCTCTCATCTCTCTCTC	62.075	83
HM_8611	GD2OF4R01A1TC9	TC	2	12	TGGAGAGAAAGCAAGAGAAATGG	63.104	TTCTTTTCTCCCTACGGATCTCT	62.767	93
HM_8612	GD2OF4R02HEN6D	GA	2	14	TGGAGATGATATACGGGTTGGACT	62.9	TAAACCAATTTTCAAGGCCACAA	63.068	138
HM_8613	GD2OF4R01DEYLA	AT	2	20	TGGAGGTTAAGTCAGACGAATGAA	62.176	TCTATCCAACTGATAATAGCTGCCA	62.291	117
HM_8614	GD2OF4R01AX45M	AC	2	16	TGGAGTGAAGCGATAAATAGTCA	62.11	CCACAGCAAGAGACATTTTTCATA	62.514	157
HM_8615	GD2OF4R02FZWM4	CA	2	20	TGGCAACAATTCAGTCCCAAAAATA	62.637	GGAGGTCAACCAATAAACCTCAT	63.482	131
HM_8616	GD2OF4R01A9EV9	AG	2	16	TGGCAACCAATCAAGCCTTATATC	63.332	AAAATTAGCGAAAAGACTCAGGCG	63.119	119
HM_8617	GD2OF4R01EZ0FS	TC	2	12	TGGCACTAATGAGAGAGGTGAAGAA	62.294	TGTATATATGTGCGTGTGGTGA	63.226	86
HM_8618	GD2OF4R01EC80H	AG	2	24	TGGCGAGAAGACAGATGTAAAGAGA	63.383	TGCATGTCCATTTTGTAACTCTCA	62.857	158
HM_8619	GD2OF4R02JP9HX	TA	2	14	TGGCGGTCTTATAGATATTGCG	63.082	CAATAGAGGAGAGTGTACAGCGCC	63.672	135
HM_8620	GD2OF4R02IUI8C	GA	2	14	TGGCTGTATACAAACATCAGCTCT	62.975	ATCCACTCAACTCTCGAATTGGC	63.017	121
HM_8621	GD2OF4R01EN2KF	AG	2	12	TGGCTTGTGTTTATTTCTTAAGGGG	62.531	TCTTTAACAGGGCATCAAGAGGAG	63.006	155
HM_8622	GD2OF4R02HJLJN	AT	2	16	TGGGTATAACAGCATCATTTGCCA	63.474	CCTGAATGACAAAATGAAAGGGTT	62.495	121
HM_8623	GD2OF4R01B3OM7	CT	2	12	TGGGCTTTTGATGCTGTTTGTAGA	62.367	TTGAGAGAAAGAGGTCAGTCATGG	62.015	133
HM_8624	GD2OF4R01BA7OG	GA	2	12	TGGGTTTTTAATCATCTTTGCTTTC	63.478	CAGCTTCACTCGATTTTCACTCT	63.23	131
HM_8625	GD2OF4R02HKRKS	AG	2	14	TGGTGAACATGAGTATGCTTTCCA	63.048	CTCCTTTTCTTCTCACACACCC	62.677	104
HM_8626	GD2OF4R02GKYWF	TA	2	16	TGGTGGTGATGTTATCTTGCAAT	62.631	ATGTCACATAGCTCCCTCACTGCT	63.589	93
HM_8627	GD2OF4R02JZD1I	AC	2	16	TGGTTAATGTAAATGCGCGTG	62.88	TTGTTTCATGTGTTCTACAAGTTGGTT	62.101	86
HM_8628	GD2OF4R01E0893	GA	2	24	TGGTTTTTACCAACAGGTTCAATTC	62.343	CCGGCTTCAGTCTCTAGTAACC	62.597	104
HM_8629	GD2OF4R01DBIIM	CA	2	16	TGTAAGATGTATACACACCGGCACA	62.249	TGGCTTTGGTTTTGTAAGTCACTCT	62.741	82
HM_8630	GD2OF4R02JLX19	CT	2	12	TGTAACCTCACCTCTCTTTGTGCC	62.895	AGCAAGGTGGTGGATGACTGTAG	63.778	115
HM_8631	GD2OF4R01A7UNS	GA	2	16	TGTACATCGTCTCATCACTGCTCC	63.262	TCATAAGCAATTTCCCACTCTCTC	62.9	91
HM_8632	GD2OF4R01AHMKW	AT	2	12	TGTAGCTTCACTGCTCGGAGAA	63.05	AGACATTAAAGATGAATCGTCGGC	62.733	139
HM_8633	GD2OF4R02GQ55O	CT	2	16	TGTATAAATGTCAAAATGCCCC	62.923	ACTTGGGTTTTGGGTTACGAGAT	63.098	86
HM_8634	GD2OF4R01BH5OM	TA	2	16	TGTATCGATTTGGGGTTTTCAGTCT	63.009	TGAGGGAACCAATACCAACCACT	62.907	159
HM_8635	GD2OF4R01DIP3W	AC	2	16	TGTATGGAACACAAATAAGGCGAA	62.65	GTACAAACCCCTCAAGATGAGA	63.649	156
HM_8636	GD2OF4R02HDIAM	GA	2	14	TGTATGTCAGACCTCTCTCGATG	62.8	AGTTCTCAAGCCCTCTTCTCTGT	63.105	84
HM_8637	GD2OF4R01D2M7V	TC	2	16	TGTATTGCGGCAAGTAGCTGAGA	63.29	CCTGGTACATACCTGGTTCCAAAC	62.809	155
HM_8638	GD2OF4R01CY9N8	GA	2	12	TGCTCTGCTCACAAGCTCTTACA	63.272	TTAGTAGTGGGATGCACAGTTGACA	62.97	158
HM_8639	GD2OF4R01CLE11	AT	2	14	TGTGACAGGCAATGAAGATCCAAA	62.832	GCACACTACCCCTAGCGTAACCTGA	63.784	92
HM_8640	GD2OF4R02H7J76	GA	2	40	TGTGAGAGTGATTTTTTGGTGAATGA	62.933	CCGAACCAAGAAACAACTACTTA	63.433	148
HM_8641	GD2OF4R01EVL4V	GT	2	16	TGTGAGTGGTGGTGACATGTGTAG	63.204	AGTAGAGACTACCAACCATGGGC	62.823	120
HM_8642	GD2OF4R01AQLXZ	TA	2	12	TGTGCGAGAGTGAGAAATTAAGCA	63.278	TCCTCCCTACCAATAAGTACTCTC	63.07	91
HM_8643	GD2OF4R01B1VJO	GA	2	14	TGTGCGCATAGATAAAAACAGGAA	62.872	CTTAATCTCCATTGAAGCCCTCA	62.8	133
HM_8644	GD2OF4R01ATVOR	TG	2	12	TGTGCTCTTTCTCTCTCTTCTGCC	63.45	CAAAGTACCAACCACTGCTACC	63.041	99
HM_8645	GD2OF4R01AU380	GA	2	20	TGTGTGTTTGCTAACCCAGAGAG	62.737	TTTTCTTCTCTAGCCGGAGAGT	62.992	137

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_8646	GD2OF4R018VDK9	TA	2	16	TGTTGTTGAGACTGAGAGCTTGACA	62.494	TCGTTCTTTGTCTTCATTTACAGATTG	61.908	108
HM_8647	GD2OF4R02F0088	TG	2	16	TGTTGTTGATGTTTCGAAAGGAAGA	63.034	GTGCCAGTGTGCCACTGTATATGT	63.322	129
HM_8648	GD2OF4R01EVBNV	AG	2	14	TGTTAAAAATTAGAGAGCGAAGTGAACG	63.061	AGCTCAGCTTCTAGCAATGTGGT	62.864	116
HM_8649	GD2OF4R01EGNWA	CA	2	14	TGTTACCAAAATTCGCCAGCTTAT	62.746	TGATCCACTTCCCAAGAGTCAAAA	62.351	153
HM_8650	GD2OF4R018MB4B	AC	2	24	TGTTCTAGGATGAAAAATCCCCAG	62.579	TCCTTCGTGTAGTAGGATAGCAAGC	62.18	145
HM_8651	GD2OF4R02IK80D	AG	2	12	TGTTGTGTAATGTTGGATGGAACA	62.289	CTGACCACATACCCCTCACCA	63.123	84
HM_8652	GD2OF4R018YHX0	CT	2	16	TGTTTAATGCGATTATTGGCTCC	63.238	CCGCAAGAAACAGCAAAAAGTAG	63.347	88
HM_8653	GD2OF4R01CU02N	TA	2	12	TGTTTCCAGAAGAAATGGTGCACA	62.918	CCAAGCGCAAAAGATAGAGAGAAA	63.134	138
HM_8654	GD2OF4R02H5W0N	AT	2	12	TGTTTGTCATCTATTATTGGTATGACG	63.175	GCGGTGCAACATCTCTTATAGGCT	62.243	142
HM_8655	GD2OF4R02IUJ8F	GA	2	12	TGTTTTCAATGGCCAATACTATGA	61.673	TGTGCAGGATGAGAAGAGATCAAT	62.366	157
HM_8656	GD2OF4R01AECUJ	AG	2	12	TGTTTTTGGGACAACTTCCACATT	63.739	GACTGCCCCACGATTCCCA	64.499	157
HM_8657	GD2OF4R01AQ532	TA	2	12	TTAAACACCCCACTGTTGGATTGAT	61.488	ACTAAGTTCCTCAACAGTACCTCTCA	60.895	80
HM_8658	GD2OF4R02ILQ4L	TC	2	14	TTAAACCAAAACAGAGCCTTAGCCA	63.236	ATCTGTGGTTCAGTTTGGTGGTC	63.558	159
HM_8659	GD2OF4R02IGWOK	AG	2	12	TTAAATTGAGAGACCAAGAGGCG	62.919	ATTATTCCCTCATCCATTGTCTCT	62.964	91
HM_8660	GD2OF4R01EEFW8	AG	2	12	TTAACCTCAATGTGGCAAAACAAA	61.711	GAGGAACCCAGGACTAATCAACA	62.684	145
HM_8661	GD2OF4R02JNLQU	TC	2	12	TTAAGACAGCCATTGACATTGAA	61.952	GTCCAAGTGCGCATAACTCATAA	62.468	84
HM_8662	GD2OF4R02HZDSU	AT	2	16	TTAAGTCTAAAAGAACCCACGGCG	63.68	CTTCACTTCACCCACTCTCCATC	63.102	146
HM_8663	GD2OF4R02GWIPR	AG	2	12	TTAATAAAGATGGAGCGACCAAAA	62.92	TCCTGTAGTTCCTCTCTCTTCTCTC	62.331	135
HM_8664	GD2OF4R02JGKR6	TA	2	12	TTAATGCGAAGGGCTAACAGGGCT	62.571	TGCGCATGCACATAATATCTCTCT	63.092	106
HM_8665	GD2OF4R02IMTLA	AT	2	16	TTACCTTGGCTTCCATTATCACACT	62.151	ATGCTCTATATATTGCATGGGGA	62.726	122
HM_8666	GD2OF4R02FJZC8	TA	2	12	TTACGGTACTGCTAATTCGGAACC	62.558	AAGTAGCACAGCCCAACTAATGC	62.877	151
HM_8667	GD2OF4R01CFQJ1	AT	2	14	TTACTTTGGTTTCATCGGGCTTTA	62.93	TGGTAACCTGCCAATATGGAGCTCT	63.022	108
HM_8668	GD2OF4R02H7N2B	AC	2	12	TTAGACCAAAATGAACCCCAACAA	61.712	TTCTGAACTCAAGCACTAAAACCAA	62.477	143
HM_8669	GD2OF4R02IEFSN	TC	2	14	TTAGCAGCTTGGCTCTCTTAATTG	63.146	GGCAAGCTAGTGGATCCGAA	63.682	93
HM_8670	GD2OF4R02S0IP	TC	2	24	TAGGTTTTCAGGGATGAGGTTTGA	63.091	GGTGATGGAGAGTAAGACAAATTGAG	63.404	159
HM_8671	GD2OF4R01ELB9V	GA	2	16	TTAGTTATTGGGTGAACAAACGCA	62.882	AATACAAAATGCACACATACACCCC	62.961	131
HM_8672	GD2OF4R02F0048	TA	2	20	TTATGGTGAATTAGGCGATACACG	62.049	CTCTGCTTCAATACCAACGACCT	62.933	106
HM_8673	GD2OF4R02GJYTS	GT	2	14	TTATGTTTGTCTTGCTGTGGC	63.391	ATCTTTTCCACTGGATTATGGCT	63.188	123
HM_8674	GD2OF4R02GTR86	AT	2	14	TTATTGCTCCAATTAACTGTGGC	63.339	TGAATCGGACTAACCACCACTTCT	63.009	160
HM_8675	GD2OF4R01AZPBJ	CT	2	14	TTCAAAACCAACCACTTACATCATC	63.028	CTTTGTGTTTGTGAGTCAATGGG	62.826	160
HM_8676	GD2OF4R01CKZ9Q	AG	2	12	TTCAATGGTGGTGAAGCTGATGT	62.844	GGAAACCGCAACTACTACGACTCT	62.411	127
HM_8677	GD2OF4R02CFMY82	TA	2	12	TTACACACACTCCCAATTGTGATT	62.631	TCAAAATCGTGAATGTGTAGATCA	61.741	126
HM_8678	GD2OF4R01AP4WN	GA	2	14	TTACATAATGAAGTTGACGCCAC	63.283	CACCTACACTAGAAGCTAATCCACG	62.567	95
HM_8679	GD2OF4R01EP7C6	TG	2	20	TTCACTGTCTCTTCAAAAATCCGT	61.347	CACCTTCTCTATTAGTAAGCTAAGTGGGC	60.537	153
HM_8680	GD2OF4R02I1MUJ	TC	2	24	TTCAAGTTGTTTTCACATGGGGAT	63.735	TGTGTGTTTTCGCTCCTCAATGTTC	63.383	100
HM_8681	GD2OF4R02IHLFD	AC	2	16	TTCATCATCCCACTAATAGATCGG	63.107	GTCTCCGGAATCATGGCAAGTAT	63.541	117
HM_8682	GD2OF4R01BAG4A	AG	2	14	TTCATCGCTTGTGTTGATCTGTCT	62.833	GTACCCGTCATCCCAACCTCA	63.097	84
HM_8683	GD2OF4R02HBR8H	TC	2	14	TTCAATAAAGCCTCAATCCACAAA	61.921	CAAGAGCATTTGTTTCGAAAAGT	62.836	143
HM_8684	GD2OF4R02FJYFP	CA	2	12	TTCAATTGATGGAGGACCAAAAATA	62.588	GACGCCCTTTTAGTAGCCTGAC	62.536	160
HM_8685	GD2OF4R01AJF9M	GT	2	14	TTCCAGAGAAATGATCTCAGGG	62.771	ACCCTGACTCTACTTCTGTTGAG	62.538	153
HM_8686	GD2OF4R01DF3XC	AG	2	14	TTCCATCTTCAAAATTTCTGGAG	62.676	ACACAAGACAATTTCTCCGGC	62.803	146
HM_8687	GD2OF4R02GEDPJ	GA	2	14	TTCCAGCCCTAGACACTGACGAC	63.12	TGAACCACTAAGCTTCTGCGC	63.378	122
HM_8688	GD2OF4R01D7AAE	TG	2	24	TTCTCTGAAACCTCTTGTGTTGG	62.892	CTCTCATGCACACATACCCCTTTG	62.945	139
HM_8689	GD2OF4R01AOHDX	CT	2	14	TTCTCTCTATCTATTCTGCCCC	62.737	GGATTGTGAAAAGAGGAACCTTGA	62.784	137
HM_8690	GD2OF4R01D90P1	CA	2	20	TTCTTTTCAAAAGAAATATTAGGG	60.921	GGCACAACCTGATCTTCTGTTTCA	61.753	115
HM_8691	GD2OF4R01COR0P	TA	2	16	TTCGAAGGTTTCTGGTTTCAGAG	63.003	TTCTCCAGAGTCCAGAGAGCATTT	62.898	142
HM_8692	GD2OF4R01EFZOL	AT	2	12	TTCGATGAGAAACCAATATACAAA	61.807	TGTATCATGCTTTTCTCTGTACAGCT	62.035	189
HM_8693	GD2OF4R01BNGKV	GA	2	24	TTGCTCATACTGTTTCATCCTTCA	62.921	AATGTCTGCTACGGTCTGCACAT	63.193	108
HM_8694	GD2OF4R01DVOLN	GA	2	20	TTGCTCTCTCTGCAATTTGTTTA	62.226	CCGTTCCGGTCAGTCATTTT	62.187	99
HM_8695	GD2OF4R01AOTOU	AC	2	12	TTGTTTGTGTTTACGTGACACACC	62.683	CAAAACAGGTTGGTTTGTCTTCC	63.015	91
HM_8696	GD2OF4R02I8OW7	GT	2	14	TTCTAAATAGCTCTGTTCTCGG	61.958	CCCAATAGAGAACAGAACACAGCA	62.724	89
HM_8697	GD2OF4R01AW83X	TC	2	16	TTCTACAGGCTCTTGGCATTCTAC	63.035	CAACACACTGATAAAGAGTGGCCTT	62.847	149
HM_8698	GD2OF4R02G3LYE	GC	2	12	TTCTCTACACCTCAATTAATGCCAA	62.171	TCATTTAAGCTTGACCAATCCCTT	62.219	124
HM_8699	GD2OF4R02IGEL3	AC	2	16	TTTGACGCTCATTTGTGACGAG	63.651	GGAGAAAAGCTGGATTGGTGTATA	62.705	122
HM_8700	GD2OF4R02JSS5O	CA	2	12	TTCTCTTATGTCCACGACGACTC	62.741	TTCTCAATCATCTAAATTTCTCTCC	61.957	97
HM_8701	GD2OF4R01EYKK1	AG	2	24	TTCTCTTTTGATTGTTCTCTCGG	63.725	CTTCCCTCCCTCTCTCTGAC	64.68	107
HM_8702	GD2OF4R02JZKW	TC	2	20	TTCTTCTCTCTCTCAAAATGGGTA	63.009	GGGAGTCTTCACTTCAATTGGGTA	62.684	137
HM_8703	GD2OF4R02G2F7O	GT	2	32	TTCTTTGATAGCCCAACACATCC	62.412	TTTACCGTAACGCGAGAGAAGAAC	62.741	147
HM_8704	GD2OF4R01A5FPJ	TG	2	16	TTGAAAACATAACCATACGACCCC	63.018	TTCTACTAATTCGCTTCTGTTGCT	62.571	135
HM_8705	GD2OF4R01CE9GO	GT	2	20	TTGAAACAGCTGCGCATAG	62.381	TCTGACAAGAGTTGCATAAATACTACA	61.491	93
HM_8706	GD2OF4R02JDH9J	GA	2	16	TTGAAATCATTTCTTCCACTTGT	62.996	CAAACTAGTACCTTCCACACCA	62.799	149
HM_8707	GD2OF4R02G23TD	GA	2	14	TTGAAACACTTCTCCCATGTCTAA	63.048	CCTCTTTTCTTCCACAGTCTCCA	63.309	157
HM_8708	GD2OF4R01AE4NH	AG	2	12	TTGAACAGCTCTTCTTGAACACT	61.467	GACATTCATTAAAGTGACATGGCT	61.456	131
HM_8709	GD2OF4R02IK343	GA	2	16	TTGAACGAGGAAATATCCATAATCA	62.296	CCGCTCACTATCAATGCACATATC	63.037	128
HM_8710	GD2OF4R02H0GCE	CT	2	14	TTGAGAAAATGATCTCTCAATCAC	61.105	GGATGCAAAATAACAGCAATACAT	61.254	142
HM_8711	GD2OF4R01D1SQT	CT	2	16	TTGACTCTCTTCTCTCCACAAA	62.695	ACCACCACTAGTCGAAACAACACT	63.036	131
HM_8712	GD2OF4R02GFXL2	GA	2	12	TTGAGGAGTTGGAGAGAGGAGAGA	63.079	ACATGTTCAACAGAGAGAGGGTT	63.023	110
HM_8713	GD2OF4R02FRF2G	CT	2	12	TTGAGGCTAAAAATGGGGGAAAT	62.989	TGACCTCGTAGCTCTTATCTCTCT	62.912	159
HM_8714	GD2OF4R02IYC3T	AC	2	16	TTGATCTTTTCTACTGTTCCGAG	62.727	GCTCCAATGCTACATATCTCTCCA	63.541	121
HM_8715	GD2OF4R01CEONM	AG	2	14	TTGATGGAAACCTAGAGGAGGAG	63.974	GCTTAGTCTAAGTGGGACTCCAAGA	63.306	160
HM_8716	GD2OF4R02ICEOC	AG	2	12	TTGATTTGAATGGGGTTTCAACT	63.092	TGACTGTCTCTCTCTCCCATCTC	63.202	105
HM_8717	GD2OF4R02GP2V2	GA	2	16	TTGCACAATCCAAGAGAAGTTGT	62.206	TTTAGACCCCTTTCCCTCTCTGCT	63.18	196
HM_8718	GD2OF4R01A88JG	CT	2	12	TTGCACATATTTGGCCTTCCAT	62.842	TCTCAGGCTCTCTGTGAACCTTT	62.909	84
HM_8719	GD2OF4R01C8MSX	GA	2	16	TTGCACTGATTTCTCAACTTACA	63.048	GCAGAGGTAGGTGTCTGTTTTC	62.512	111
HM_8720	GD2OF4R01DG25S	AT	2	12	TTGCCATATTGATTCATGTTACT	60.786	GTGTTATAGGTAGCAGGCCCC	61.058	160
HM_8721	GD2OF4R01DVN1L	AT	2	16	TTGCCCTAACGACTTGGAGAATAA	63.122	TCTCTCTCTCTCTCAACTTCTCTCA	62.69	147
HM_8722	GD2OF4R02JC3PT	TA	2	14	TTGCCTTAAAAAGTAATTATTCTAGC	60.642	TAAACAACAGGTAAAGTTGGTCGG	61.435	156
HM_8723	GD2OF4R01AZAQ2	TC	2	14	TTGGATCTTCTTCTGCTTGCAATC	63	TTCACTCCATACCACTTTTGGAACT	63.206	114
HM_8724	GD2OF4R01ADIARF	CA	2	20	TTGGATGAAATGACTCAAAACCC	63.305	CTCTGCTTTTGTGGCTCTTGTGTT	63.15	127
HM_8725	GD2OF4R02HL8QP	AG	2	20	TTGGCATGACTGTGAGTGTGTTG	62.214	AACATTTGAATCAGAGGTGCAAGC	62.926	143
HM_8726	GD2OF4R02JL59R	AT	2	16	TTGGGCCCACTTCTTAACCACTTA	63.014	TGCTCTCTCTTTTGTCTTTGCT	62.957	141
HM_8727	GD2OF4R02G10AE	CT	2	12	TTGGGTTAGTTGGTAAACAGAGCA	63.046	CCAGCACTGTGCAACTATGGC	64.032	141
HM_8728	GD2OF4R02JXLBK	TG	2	16	TTGGGTTTAGCAACAGATTGAGA	62.112	TTTGCTTTATTACATGCGAACACA	61.675	143
HM_8729	GD2OF4R02I4KPT	AG	2	16	TTGGTGCACTTCAGCACTTCTTA	63.068	TAGACCCAAATCTGCAAACTCAAA	62.112	157
HM_8730	GD2OF4R02H84XY	TA	2	12	TTGTACGCGAACCACTACAAGAAA	62.979	TCAATGCTCATGATGGTCACTGTT	63.711	160
HM_8731	GD2OF4R01HY26O	AC	2	24	TTGTGCAACCAAAATCTGAATAACC	62.225	CACATTCGTGTTGACGATTCAAA	62.305	133
HM_8732	GD2OF4R01EXRIN	AG	2	20	TTGTGCACTCTGTTTGTATTGG	63.055	CTTTTCAATCTTTCAGCGCTTACC	62.343	86
HM_8733	GD2OF4R02HZ7MW	TA	2	12	TTGTGCTGAAATCTGGCATAGTG	62.339	GGAATGGAATCAATACAAAGGAGA	62.618	149
HM_8734	GD2OF4R01B2YV	GA	2	16	TTGTGCTGTTTCTGTTTCTCTG	62.856	TCACTGCCAAATCTGGAGTTCTG	62.712	91
HM_8735	GD2OF4R01AJ6XT	TG	2	16	TTGTGTGCACATTGAAAGCAAGT	61.872	GCATTTCTTTTAATTGTGCTGTT	61.621	160
HM_8736	GD2OF4R01DEVJS	TC	2	12	TTGTACTTCTGCTGTTCTCTCC	63.031	AAATGTTAAGGGCGCTGTTTGGTT	63.013	100
HM_8737	GD2OF4R01B9GIA	CA	2	12	TTAACATTTGGTGATCTCTCGCAC	62.529	CACCAAGACCAAAATGCTCAAGTC	62.826	80
HM_8738	GD2OF4R02HUEAZ	GA	2	12	TTTAAGATTCTGTGGGGGTGAGA	63.091	GGTATTTTTCTTGTATCGCTTCC	63.191	137
HM_8739	GD2OF4R02IN1ID	TG	2	12	TTAATTTGGTCACATGTGGGTACG	62.843	GAGAGAAGAAGTTGTGTTGGGGAA	62.997	115
HM_8740	GD2OF4R01DS226	TA	2	12	TTTACAGCGAATTGGATTCAGTTTT	63.03	ATAACATCCAGATTGCAACACA	62.631	141

Supplement Table 1 Details of 8,780 EST-SSR markers developed from transcriptome of two hydrangea cultivar, Veitchii and Endless Summer

SSR ID	Contig/Singletons	MinMatch	Type	Length	Forward Sequence	LeftTM	Reverse Sequence	RightTM	ProductSize
HM_8741	GD2OF4R01AQYNJ	CA	2	14	TTTACCATGTTCAAATTCACACGC	63.072	TTGTGTAATAAAGGGCGTTTATCCA	62.877	87
HM_8742	GD2OF4R02FTB4I	TG	2	14	TTTACCTGGAAAAATCTGTGAAGGC	62.716	ACAACACCGTCATAGCCACCTATT	62.949	104
HM_8743	GD2OF4R02H2AA1	AT	2	20	TTTATCAATCCAAGCTGGCTCTGT	63.341	CCAGCGCTCCTGTAAGTTTATGT	62.862	96
HM_8744	GD2OF4R02HDQP	GA	2	14	TTTATTGCCAATCTTTATTGTGTC	62.307	AGGGGTGTGAAATTGGATCTACA	62.897	146
HM_8745	GD2OF4R02J0KW	TA	2	14	TTTATTTATGCATTGGCTGTATG	60.447	CGACCACTACTTTGGGTGTGTAT	61.386	143
HM_8746	GD2OF4R02FL045	AC	2	16	TTTCAACACTTCAGAAATACCAGACTAAG	60.45	TGTTTGTATTGTGAGATTGGTTACTTTC	60.843	155
HM_8747	GD2OF4R01CCH5K	TA	2	16	TTTCAGCATGTCTTCTCGCTTTA	63.171	CATCCAAAAAATGTGTACTCGC	62.958	92
HM_8748	GD2OF4R02HTDQL	TC	2	12	TTTCAGGTTCTGGACTCTCTTTCTC	62.601	CGTGAAATAACATGAGACTGCG	62.869	130
HM_8749	GD2OF4R01A3F85	GA	2	24	TTTCATCATCGATTCCCATCTTTT	62.889	TCGAAATTTATAGAAGGTCGAGG	63.006	103
HM_8750	GD2OF4R01CSSLE	AT	2	14	TTTCATTGTTACTTTATGCCCGC	63.126	CGTGCAACGCACGTATTGTATTA	62.919	152
HM_8751	GD2OF4R01BENLJ	AC	2	16	TTTCTGCAAAACCTACCTAACA	63.023	ACGAACAAGGCTTCGAGGTTACTA	62.548	156
HM_8752	GD2OF4R01AIHPB	GA	2	24	TTTCTCTCCACCTTAGTGACACACC	62.92	ATTCTTGAAGACCCCTTTCTTTGC	63.09	157
HM_8753	GD2OF4R01DUQTG	TA	2	12	TTTCTCTCTCATAGTTGCCCTTG	62.811	GCCACTACACAACTTGCCCTTTT	62.737	120
HM_8754	GD2OF4R01DI3WS	GA	2	32	TTTCTCCCTCTATTAAAGGTTCTCAGG	61.493	AAAAACCAACCCCACTTACCTTC	60.799	82
HM_8755	GD2OF4R01CUNEG	AC	2	14	TTTCTGAAATCTGAACAGGAAGTGA	61.453	AACCTGGAATCTTGTTCAGTGATT	60.615	125
HM_8756	GD2OF4R01BPII0	AC	2	20	TTTGATTTTGATATTCCTGCCCAA	63.599	CAGTAATACACATGCGGGTGTAA	62.969	89
HM_8757	GD2OF4R02GF2K7	AT	2	16	TTTGCAATTCCTCTTTGATTTTGA	63.024	CAATTCAAAACAAATCTCAGCTCCC	63.219	119
HM_8758	GD2OF4R01CCUQK	TA	2	12	TTTGCAGAGGTTGTATATCTGAA	63.154	TACATCAGCGCCTCTCATTTATT	63.142	149
HM_8759	GD2OF4R02IG7IL	AG	2	12	TTTGAGAGACAGAAATGAGGGTTC	62.784	ACCCTTCGGTACTTTTCTCTCG	63.094	111
HM_8760	GD2OF4R02I4RC0	TA	2	12	TTTGATAGCACCAATTTGAACCT	62.922	AACCTTAACAGAGCCGATCGTAC	62.949	124
HM_8761	GD2OF4R02FTGGT	AG	2	14	TTTGGCAAATATTACACTAACCAAGTTGA	62.887	ATGGATTTCAAGTTGGGGTGTAGT	62.983	107
HM_8762	GD2OF4R01CH9C1	TC	2	14	TTTGGGGGTAGTTCGCAAAATAA	62.646	TTTGCAAAATTTAATACCCAGGA	61.66	157
HM_8763	GD2OF4R01DK989	TA	2	12	TTTGGGTCCATAAAATTTCTCCCT	62.968	AGCAAAACATAAAGCTTGAAAGGC	62.105	140
HM_8764	GD2OF4R01AM79N	AT	2	12	TTTGTTAATACCTTTCTCTGTGCG	62.016	CTACGATCCGACTGTCAAAACAGA	62.724	140
HM_8765	GD2OF4R01DNC7O	AG	2	12	TTTGTAGATAGGGCAATGAGCG	63.532	TTCGTCTCTCCTCCTAATTGGT	63.476	147
HM_8766	GD2OF4R02IACOV	TC	2	12	TTTGTGCATAAGTTGCAAAACATAAA	62.734	ACCAAGCTAACCTGAACAAGACG	62.943	134
HM_8767	GD2OF4R01AN33M	AC	2	12	TTTGTTCACAAAGTTCAAAACCT	63.015	CCCCAAGAAAGAGAAAAAGGAAA	62.962	153
HM_8768	GD2OF4R02JZW09	AG	2	14	TTTACCTTCAGAACACCCCTAG	62.617	CTCACTTCACAGGAGGATGTTT	62.793	91
HM_8769	GD2OF4R02IWKYJ	AT	2	20	TTTTCACAGAGCTGAAAAAGTGAAG	62.276	GCCTAAACCAATCTGCAAGATAAA	62.641	147
HM_8770	GD2OF4R01B4HSC	AG	2	20	TTTTCACAAAGAAACAGAAACC	62.605	AGGCCTTCGTTGAATTTGTCAAT	63.34	118
HM_8771	GD2OF4R01CYEXG	AT	2	16	TTTTCCTCTTTAATTCGGATTGT	62.887	CCACCCAGTCGGTAGTGATAC	62.786	145
HM_8772	GD2OF4R01D46JE	AT	2	16	TTTTCGAATCGGATGAAGAATGTT	63.009	CGAATTTTCGTTGTTTTCTTTTCG	63.031	112
HM_8773	GD2OF4R01EOLL1	AT	2	12	TTTCTTTTACCTTTGACGCTGG	62.742	AACCAATCCAGTTCATAGTCCCAA	62.897	93
HM_8774	GD2OF4R02ICNZL	TA	2	14	TTTGGCTGACTCACTCCCTACAT	63.338	ACAAGCAGAAAGAACTCACACACG	62.972	102
HM_8775	GD2OF4R02JGXDE	GA	2	14	TTTGGCTTAATTGGTTGAGGAGA	63.109	GAGTCCGATGTCATTTACAAAGCC	63.137	91
HM_8776	GD2OF4R01AZC8Y	AC	2	14	TTTTTAAACTGCAACAGGATCA	60.038	TTTCTTTTCTCCTCATAGCATTT	60.913	88
HM_8777	GD2OF4R01BBQ9Q	TA	2	12	TTTTTAGGGAATTAGGGTTAGTTTCAG	61.358	CCCAACCTGCGACACTAATTAAA	62.326	95
HM_8778	GD2OF4R02IMUXP	TA	2	12	TTTTTCCCCCTCAATGTAAGT	60.892	CTATTTTTCGAGTTTGAATCCGT	61.752	128
HM_8779	GD2OF4R02GPFKS	AT	2	16	TTTTTCTCCGGAAGCACACAGTAT	63.239	ACTGGACTTTGTGGTCGGAATAAC	62.821	151
HM_8780	GD2OF4R01DVT3A	TA	2	14	TTTTTGAAGTCTGTTTAAAGATCCG	60.047	TGAAATCTTACCAATTTGTTCCACA	60.606	116