Table S1 List of primers used for qRT-PCR analysis

Primers used for tissue, N perturbation and leaf senescence analysis		
Name	**Sequence**	**Access number**
PtAspAT-1_qF	GCAGAGGTTGAAGGGTTTGG	Potri.005G079200
PtAspAT-1_qR	TGTAGGGTGGTCAGAGAAGC	
PtAspAT-2_qF	TCCAACCACCATAACATA	Potri.006G107100
PtAspAT-2_qR	CATTCTTGACATCATCCAT	
PtAspAT-3_qF	GGACAATGAGCCCACGAATTG	Potri.006G241500
PtAspAT-3_qR	TCCTCTATTCTCCTCCACCACTT	
PtAspAT-4_qF	GTTGCAGGCAGGGTTGAAAG	Potri.006G241600
PtAspAT-4_qR	GGCTTCAAAGAGTTTCTGGCG	
PtAspAT5-qFW	TGCACGTGGTATGGAGCTTT	Potri.006G260200
PtAspAT5-qRV	TCGGGCAATCCTTTTCAGCT	
PtAspAT-6_qF	TAGCAATGGTGCCAAGCAGA	Potri.007G088400
PtAspAT-6_qR	TCACCCAAAATGGTGCAGGA	
PtAspAT-7_qF	AGCAATCCTCCTGTTCAT	Potri.014G143300
PtAspAT-7_qR	CAGCCATTACCTTCACTTC	
PtAspAT-9_qF	TCCTCCTGTTCATGGGGCTA	Potri.018G022200
PtAspAT-9_qR	CCTCCCAGCCATCATTTCCA	
PtAspAT-10_qF	CACTGGCTTGAACACTGAACA	Potri.018G082500
PtAspAT-10_qR	AAAAGATCCCCAGAAGCGGA	
UBIC_qF	TTGCTTGAGGAACTTGAAC	Potri.006G205700.1
UBIC_qR	GTGAGGACCGATTACAGT	
β-Actin_qF	GACCTTCAATGTGCCTGCAA	Potri.019G006700.1
β-Actin_qR	ACCATCACCAGAATCCAGCA	
EF1α_qF	TCCGTCTTCCACTTCAGGATGTCT	Potri.006G130900.1
EF1α_qR	GTCACGACCATACCAGGCTTCAG	

Primers used for alternative splicing analysis		
Name	**Sequence**	**Access number**
PtAspAT-1.1_qF	ATCAGGCCCAGGTTGCATTA	Potri.005G079200.1
PtAspAT-1.1_qR	TACATTACACAGGGACGGCA	
PtAspAT-1.2_qF	ATCAGGCCCAGGGGTTG	Potri.005G079200.2
PtAspAT-1.2_qR	TACATTACACAGGGACGGCA	
PtAspAT-1.3_qF	AGGCCTTTGCAATGACTGG	Potri.005G079200.3
PtAspAT-1.3_qR	AGTGACGCTTTGGATAAACGA	
PtAspAT-9.1_qF	AGCCAACGGTTTTTCAAGTGT	Potri.018G022200.1
PtAspAT-9.1_qR	AGAGGGATTGCCTTTCTCCT	
PtAspAT-9.2_qF	GTACATCGCACAAGTGGCTC	Potri.018G022200.2
PtAspAT-9.2_qR	TCCAAGCCTCATCTTTCCCT	
PtAspAT-9.3_qF	CCAACGGTTTTTCAAGATGGCT	Potri.018G022200.3
PtAspAT-9.3_qR	TCCAAGCCTCATCTTTCCCT	
PtAspAT-9.4_qF	CCAACGGTTTTTCAAGATGGCT	Potri.018G022200.4
PtAspAT-9.4_qR	ACTTCCAAGCCTCATCTTGAGA	

Table S2. List of *AspAT* candidate genes in *Populus*

Gene	Locus v3.0	NCBI accession ID	Chromosome location	ORF (aa)	MW (kDa)	pI	CDS (bp)	Trps	Target
PtAspAT1	Potri.005G079200.1	XP_002307109.2	5829792-5834408	480	51.59	7.11	1443	3	Cp
PtAspAT2	Potri.006G107100.1	XP_024458570.1	8334612-8338470	422	46.96	7.19	1269	2	Mt
PtAspAT3	Potri.006G241500.1	PNT3347.1	25025032-25029627	479	53.31	8.01	1440	2	Cy
PtAspAT4	Potri.006G241600.1	XP_002308618.1	25030792-25035161	449	49.18	9.16	1350	4	Cy
PtAspAT5	Potri.006G260200.1	XP_024459097.1	26353269-26357505	466	51.03	8.67	1401	3	Cp
PtAspAT6	Potri.T079800*	XP_002310582.2	11464519-11467816	481	51.89	8.06	1446	3	Cp
PtAspAT7	Potri.014G143300.1	XP_002321073.3	10931994-10941223	428	47.79	8.35	1287	1	Mt
PtAspAT8	Potri.016G133000.1	PNS99394.1	13652367-13655172	304	33.11	5.66	915	1	Nu, Ex
PtAspAT9	Potri.018G022200.1	XP_002324896.1	1762470-1767522	466	50.92	8.67	1401	4	Cp
PtAspAT10	Potri.018G082500.1	XP_002324997.1	10942388-10947804	407	44.47	7.72	1224	1	Cy

Abbreviations: ORF, open reading frame; aa, amino acid; MW, molecular weight (kDa); *p*I: isoelectric point; CDS, coding DNA sequence; bp, base pair; Cp, chloroplast; Mt, Mitochondria; Cy, Cytoplasm; Nu, Nucleus; Ex, Extracellular. Note: Parameter of Potri.T079800* is deduced from both Potri.T079800.1 and Potri.T079800.3.

Table S3. Ka/Ks analysis of the *PtAspAT* gene pairs duplication

Gene 1	Gene 2	*Ka*	*Ks*	*Ka/Ks*	Date (MYA)
AspAT1	*AspAT6*	0.05	0.29	0.17	9.53
AspAT4	*AspAT10*	0.08	2.28	0.03	1.9
AspAT5	*AspAT9*	0.02	0.21	0.11	5.99

Table S4. Transcription factors predicted in binding promotors of *PtAspATs*

Accession ID	Family	Gene	start	stop	strand	score	p-value	q-value	sequence
Potri.008G073600	ERF	PpAspAT1	833	853	+	27.0735	4.65E-10	1.84E-05	TGAGGTGGAGGTGGAGGTGGA
Potri.018G028000	ERF	PpAspAT1	833	853	-	27.0147	6.24E-10	2.47E-05	TCCACCTCCACCTCCACCTCA
Potri.019G081100	C2H2	PpAspAT1	834	852	-	25.8983	9.16E-10	2.42E-05	CCACCTCCACCTCCACCTC
Potri.019G081100	C2H2	PpAspAT1	837	855	-	25.5339	1.25E-09	2.42E-05	CTTCCACCTCCACCTCCAC
Potri.018G028000	ERF	PpAspAT1	836	856	-	22.7206	9.56E-09	0.000149	ACTTCCACCTCCACCTCCACC
Potri.018G028000	ERF	PpAspAT1	830	850	-	22.4412	1.13E-08	0.000149	ACCTCCACCTCCACCTCAGTC
Potri.008G073600	ERF	PpAspAT1	830	850	+	21.9412	2.33E-08	0.000461	GACTGAGGTGGAGGTGGAGGT
Potri.006G080300	ERF	PpAspAT1	1966	1985	+	20.9062	3.94E-08	0.00156	CCACCGCCAACTAAAACGCC
Potri.015G023200	ERF	PpAspAT1	835	855	-	20.4853	5.90E-08	0.00135	CTTCCACCTCCACCTCCACCT
Potri.013G101100	ERF	PpAspAT1	829	848	-	20.3281	6.58E-08	0.0014	CTCCACCTCCACCTCAGTCA
Potri.015G082200	LBD	PpAspAT1	833	853	-	20.1719	7.00E-08	0.00277	TCCACCTCCACCTCCACCTCA
Potri.012G083500	LBD	PpAspAT1	833	853	-	20.1719	7.00E-08	0.00277	TCCACCTCCACCTCCACCTCA
Potri.013G101100	ERF	PpAspAT1	832	851	-	20.2344	7.05E-08	0.0014	CACCTCCACCTCCACCTCAG
Potri.007G067600	MYB	PpAspAT1	1879	1899	+	20.0312	7.50E-08	0.00146	TCCATTTCCTACCAACCCCCA
Potri.005G096600	MYB	PpAspAT1	1879	1899	+	20.0312	7.50E-08	0.00146	TCCATTTCCTACCAACCCCCA
Potri.008G073600	ERF	PpAspAT1	1965	1985	-	20.1176	7.84E-08	0.00103	GGCGTTTTAGTTGGCGGTGGT
Potri.015G023200	ERF	PpAspAT1	829	849	-	19.9706	8.08E-08	0.00135	CCTCCACCTCCACCTCAGTCA
Potri.017G013700	ERF	PpAspAT1	829	849	+	19.7344	1.02E-07	0.00366	TGACTGAGGTGGAGGTGGAGG
Potri.015G023200	ERF	PpAspAT1	832	852	-	19.5735	1.02E-07	0.00135	CCACCTCCACCTCCACCTCAG
Potri.013G101100	ERF	PpAspAT1	835	854	-	19.5781	1.13E-07	0.0015	TTCCACCTCCACCTCCACCT
Potri.018G021900	ERF	PpAspAT1	832	850	+	19.8438	1.16E-07	0.00458	CTGAGGTGGAGGTGGAGGT
Potri.005G233300	ERF	PpAspAT1	1960	1974	+	19.5156	1.61E-07	0.00495	CAACTACCACCGCCA
Potri.019G081100	C2H2	PpAspAT1	831	849	-	19.0339	1.64E-07	0.00159	CCTCCACCTCCACCTCAGT
Potri.015G082200	LBD	PpAspAT1	830	850	-	18.6406	1.81E-07	0.00359	ACCTCCACCTCCACCTCAGTC
Potri.012G083500	LBD	PpAspAT1	830	850	-	18.6406	1.81E-07	0.00359	ACCTCCACCTCCACCTCAGTC
Potri.013G101100	ERF	PpAspAT1	838	857	-	18.8125	1.95E-07	0.00154	AACTTCCACCTCCACCTCCA
Potri.001G154200	ERF	PpAspAT1	838	852	-	18.8594	2.15E-07	0.00852	CCACCTCCACCTCCA
Potri.018G021900	ERF	PpAspAT1	835	853	+	18.7188	2.44E-07	0.00484	AGGTGGAGGTGGAGGTGGA
Potri.005G233300	ERF	PpAspAT1	838	852	-	18.875	2.50E-07	0.00495	CCACCTCCACCTCCA
Potri.017G013700	ERF	PpAspAT1	835	855	+	18.2812	2.50E-07	0.00366	AGGTGGAGGTGGAGGTGGAAG
Potri.019G073300	ERF	PpAspAT1	839	853	+	18.7969	2.66E-07	0.0106	GGAGGTGGAGGTGGA
Potri.017G013700	ERF	PpAspAT1	832	852	+	18.1094	2.77E-07	0.00366	CTGAGGTGGAGGTGGAGGTGG
Potri.006G138800	ERF	PpAspAT1	1550	1563	-	18.3125	3.07E-07	0.0122	GGGGCCGGTGGTGA
Potri.015G082200	LBD	PpAspAT1	836	856	-	17.7188	3.15E-07	0.00415	ACTTCCACCTCCACCTCCACC
Potri.012G083500	LBD	PpAspAT1	836	856	-	17.7188	3.15E-07	0.00415	ACTTCCACCTCCACCTCCACC
Potri.001G053500	GATA	PpAspAT1	837	851	+	18.3529	3.22E-07	0.0128	GTGGAGGTGGAGGTG
Potri.016G053200	ERF	PpAspAT1	1963	1973	+	18.9219	3.23E-07	0.0128	CTACCACCGCC
Potri.005G140900	ERF	PpAspAT1	1960	1974	+	18.4688	3.59E-07	0.00713	CAACTACCACCGCCA
Potri.002G157600	MYB	PpAspAT1	1492	1506	+	17.5625	4.01E-07	0.00977	ACGTTGGTAGGTGGC
Potri.002G085600	ERF	PpAspAT1	1954	1973	+	18.2188	4.70E-07	0.0186	ATCCAACAACTACCACCGCC
Potri.014G025200	ERF	PpAspAT1	1963	1975	-	17.7344	7.14E-07	0.00947	TTGGCGGTGGTAG
Potri.010G141000	MYB	PpAspAT1	1496	1505	+	16.3558	7.22E-07	0.0287	TGGTAGGTGG
Potri.003G077700	ERF	PpAspAT1	830	850	-	16.7656	7.23E-07	0.0255	ACCTCCACCTCCACCTCAGTC
Potri.010G177100	LBD	PpAspAT1	832	852	-	16.6094	7.83E-07	0.0299	CCACCTCCACCTCCACCTCAG
Potri.008G079800	LBD	PpAspAT1	832	852	-	16.6094	7.83E-07	0.0299	CCACCTCCACCTCCACCTCAG
Potri.013G001000	MYB	PpAspAT1	1886	1900	+	16.4375	8.76E-07	0.0171	CCTACCAACCCCCAA
Potri.005G224100	MYB	PpAspAT1	1496	1516	-	16.5781	8.85E-07	0.0116	GCCTGCTCGAGCCACCTACCA
Potri.018G021900	ERF	PpAspAT1	838	856	+	16.5938	9.15E-07	0.0108	TGGAGGTGGAGGTGGAAGT
Potri.001G336700	MYB	PpAspAT1	1886	1898	+	15.9853	9.20E-07	0.026	CCTACCAACCCCC
Potri.018G028000	ERF	PpAspAT1	827	847	-	13.9559	1.05E-06	0.00693	TCCACCTCCACCTCAGTCAAG
Potri.008G073600	ERF	PpAspAT1	827	847	+	15.6324	1.12E-06	0.00677	CTTGACTGAGGTGGAGGTGGA
Potri.018G028000	ERF	PpAspAT1	839	859	-	13.6029	1.24E-06	0.00703	AAAACTTCCACCTCCACCTCC
Potri.001G154200	ERF	PpAspAT1	832	846	-	15.7969	1.34E-06	0.0267	CCACCTCCACCTCAG
Potri.008G081600	MYB	PpAspAT1	1486	1506	+	16.2812	1.41E-06	0.0425	AGTAGTACGTTGGTAGGTGGC
Potri.010G229700	NAC	PpAspAT1	785	804	-	16.5479	1.47E-06	0.0584	CTTACTTTGCAAGCAAGTTA
Potri.013G101100	ERF	PpAspAT1	1955	1974	+	15.5469	1.67E-06	0.0111	TCCAACAACTACCACCGCCA
Potri.010G177100	LBD	PpAspAT1	829	849	-	15.0938	1.86E-06	0.0299	CCTCCACCTCCACCTCAGTCA
Potri.008G079800	LBD	PpAspAT1	829	849	-	15.0938	1.86E-06	0.0299	CCTCCACCTCCACCTCAGTCA
Potri.013G001000	MYB	PpAspAT1	1492	1506	-	15.75	1.89E-06	0.0246	GCCACCTACCAACGT
Potri.019G081500	MYB	PpAspAT1	1496	1506	+	15.8617	1.91E-06	0.0551	TGGTAGGTGGC
Potri.017G082500	MYB	PpAspAT1	1954	1972	-	16.0781	1.92E-06	0.0253	GCGGTGGTAGTTGTTGGAT
Potri.007G067600	MYB	PpAspAT1	1493	1513	-	16.0625	1.94E-06	0.0192	TGCTCGAGCCACCTACCAACG
Potri.005G096600	MYB	PpAspAT1	1493	1513	-	16.0625	1.94E-06	0.0192	TGCTCGAGCCACCTACCAACG
Potri.014G074200	MIKC_MADS	PpAspAT1	1212	1232	-	15.8406	1.97E-06	0.00201	CTTTGTTTTTTGTTTCTCTCA
Potri.002G151700	MIKC_MADS	PpAspAT1	1212	1232	-	15.8406	1.97E-06	0.00198	CTTTGTTTTTTGTTTCTCTCA
Potri.001G238400	Dof	PpAspAT1	1677	1697	+	15.0938	1.97E-06	0.00821	TTCTCTTATGTTTTCTTTTTC
Potri.005G164900	MYB	PpAspAT1	1461	1481	-	15.4375	1.99E-06	0.0259	GTTGAGATGGTTGTTGAGGAA
Potri.008G073600	ERF	PpAspAT1	1549	1569	-	14.5441	2.01E-06	0.00995	GATGAGGGGGCCGGTGGTGAG
Potri.019G073300	ERF	PpAspAT1	1552	1566	-	15.6406	2.17E-06	0.0205	GAGGGGGCCGGTGGT
Potri.010G177100	LBD	PpAspAT1	835	855	-	14.7344	2.27E-06	0.0299	CTTCCACCTCCACCTCCACCT
Potri.008G079800	LBD	PpAspAT1	835	855	-	14.7344	2.27E-06	0.0299	CTTCCACCTCCACCTCCACCT
Potri.004G174400	MYB	PpAspAT1	1886	1900	-	14.3125	2.39E-06	0.047	TTGGGGGTTGGTAGG
Potri.003G077700	ERF	PpAspAT1	833	853	-	14.375	2.62E-06	0.0255	TCCACCTCCACCTCCACCTCA
Potri.007G093900	MYB	PpAspAT1	1497	1506	+	14.5616	2.71E-06	0.0532	GGTAGGTGGC
Potri.019G073300	ERF	PpAspAT1	1965	1979	-	15.2188	2.77E-06	0.0205	TTAGTTGGCGGTGGT
Potri.002G157600	MYB	PpAspAT1	1886	1900	-	15.5625	2.83E-06	0.0215	TTGGGGGTTGGTAGG
Potri.013G001000	MYB	PpAspAT1	1464	1478	+	15.375	2.83E-06	0.0277	CTCAACAACCATCTC
Potri.001G238400	Dof	PpAspAT1	1282	1302	+	14.7656	2.86E-06	0.0107	TTCTTTTCCTTTTGCTTTAAC
Potri.018G021900	ERF	PpAspAT1	829	847	+	14.5625	2.87E-06	0.0189	TGACTGAGGTGGAGGTGGA
Potri.015G023200	ERF	PpAspAT1	1963	1983	+	13.2647	2.90E-06	0.0191	CTACCACCGCCAACTAAAACG
Potri.012G031700	WRKY	PpAspAT1	1090	1100	-	16.0156	2.91E-06	0.116	CAAGTCAACGA
Potri.019G081100	C2H2	PpAspAT1	840	858	-	14.4407	2.93E-06	0.019	AAACTTCCACCTCCACCTC
Potri.001G154200	ERF	PpAspAT1	835	849	-	14.3438	2.96E-06	0.0344	CCTCCACCTCCACCT
Potri.018G028000	ERF	PpAspAT1	1965	1985	+	11.7353	2.97E-06	0.0147	ACCACCGCCAACTAAAACGCC
Potri.019G073300	ERF	PpAspAT1	833	847	+	15.0938	2.97E-06	0.0205	TGAGGTGGAGGTGGA
Potri.006G138800	ERF	PpAspAT1	1963	1976	-	15.6875	3.01E-06	0.0598	GTTGGCGGTGGTAG
Potri.001G356100	ERF	PpAspAT1	838	852	+	14.5312	3.16E-06	0.125	TGGAGGTGGAGGTGG
Potri.013G091400	bZIP	PpAspAT1	370	380	+	15.7031	3.20E-06	0.0637	ACAAGCTGTCA
Potri.013G090400	WRKY	PpAspAT1	1089	1100	+	15.7812	3.20E-06	0.127	CTCGTTGACTTG
Potri.017G013700	ERF	PpAspAT1	1550	1570	-	13.6406	3.27E-06	0.0194	CGATGAGGGGGCCGGTGGTGA
Potri.008G081600	MYB	PpAspAT1	1886	1906	-	15.4219	3.27E-06	0.0425	TGTTTATTGGGGGTTGGTAGG
Potri.001G267300	MYB	PpAspAT1	1887	1897	-	14.75	3.38E-06	0.0826	GGGGTTGGTAG
Potri.017G013700	ERF	PpAspAT1	1966	1986	-	13.5469	3.42E-06	0.0194	TGGCGTTTTAGTTGGCGGTGG
Potri.001G154200	ERF	PpAspAT1	1960	1974	+	14.0469	3.46E-06	0.0344	CAACTACCACCGCCA
Potri.003G077700	ERF	PpAspAT1	836	856	-	13.7969	3.50E-06	0.0255	ACTTCCACCTCCACCTCCACC
Potri.004G051800	ERF	PpAspAT1	834	850	+	13.1094	3.62E-06	0.0717	GAGGTGGAGGTGGAGGT

Potri.007G007900	MYB	PpAspAT1	1493	1505	+	11.2278	3.75E-06	0.0441	CGTTGGTAGGTGG
Potri.001G336700	MYB	PpAspAT1	1494	1506	-	15.1029	3.76E-06	0.0489	GCCACCTACCAAC
Potri.005G224100	MYB	PpAspAT1	1876	1896	+	14.9219	3.79E-06	0.0297	TTGTCCATTTCCTACCAACCC
Potri.008G073600	ERF	PpAspAT1	836	856	+	13.3088	3.80E-06	0.0167	GGTGGAGGTGGAGGTGGAAGT
Potri.003G077700	ERF	PpAspAT1	1965	1985	+	13.5938	3.87E-06	0.0255	ACCACCGCCAACTAAAACGCC
Potri.004G174400	MYB	PpAspAT1	1492	1506	+	14.0469	3.87E-06	0.0507	ACGTTGGTAGGTGGC
Potri.005G164900	MYB	PpAspAT1	1883	1903	-	14.7188	4.01E-06	0.0391	TTATTGGGGGTTGGTAGGAAA
Potri.013G067500	MYB	PpAspAT1	1460	1478	+	15.1875	4.04E-06	0.0768	ATTCCTCAACAACCATCTC
Potri.019G073300	ERF	PpAspAT1	836	850	+	14.5156	4.13E-06	0.0205	GGTGGAGGTGGAGGT
Potri.013G101100	ERF	PpAspAT1	1967	1986	+	14.0312	4.20E-06	0.0208	CACCGCCAACTAAAACGCCA
Potri.010G160100	WRKY	PpAspAT1	1091	1100	-	12.8842	4.23E-06	0.168	CAAGTCAACG
Potri.018G021900	ERF	PpAspAT1	1549	1567	-	13.7656	4.35E-06	0.0215	TGAGGGGGCCGGTGGTGAG
Potri.010G177100	LBD	PpAspAT1	1966	1986	+	13.5156	4.36E-06	0.0431	CCACCGCCAACTAAAACGCCA
Potri.008G079800	LBD	PpAspAT1	1966	1986	+	13.5156	4.36E-06	0.0431	CCACCGCCAACTAAAACGCCA
Potri.001G163700	ERF	PpAspAT1	1963	1983	-	13.5469	4.44E-06	0.0879	CGTTTTAGTTGGCGGTGGTAG
Potri.007G036400	Dof	PpAspAT1	1281	1301	+	14.0312	4.52E-06	0.0154	TTTCTTTTCCTTTTGCTTTAA
Potri.001G404400	NAC	PpAspAT1	788	804	-	14.2969	4.56E-06	0.181	CTTACTTTGCAAGCAAG
Potri.017G082500	MYB	PpAspAT1	1460	1478	-	14.9844	4.68E-06	0.0463	GAGATGGTTGTTGAGGAAT
Potri.002G168700	WRKY	PpAspAT1	1091	1101	-	15.1781	4.72E-06	0.188	TCAAGTCAACG
Potri.007G007900	MYB	PpAspAT1	1553	1565	-	10.2785	4.81E-06	0.0441	AGGGGGCCGGTGG
Potri.009G053900	MYB	PpAspAT1	1496	1505	+	14.7308	4.84E-06	0.173	TGGTAGGTGG
Potri.014G099900	ERF	PpAspAT1	1965	1979	-	14.9844	4.91E-06	0.076	TTAGTTGGCGGTGGT
Potri.008G073600	ERF	PpAspAT1	845	865	+	12.6765	5.21E-06	0.0206	GGAGGTGGAAGTTTTGTTGGC
Potri.003G034200	Dof	PpAspAT1	1281	1301	-	13.8594	5.56E-06	0.0169	TTAAAGCAAAAGGAAAAGAAA
Potri.007G007900	MYB	PpAspAT1	1887	1899	-	9.75949	5.56E-06	0.0441	TGGGGGTTGGTAG
Potri.016G128300	WRKY	PpAspAT1	1091	1101	-	14.7656	5.70E-06	0.223	TCAAGTCAACG
Potri.002G141200	ERF	PpAspAT1	1963	1977	-	14.875	5.76E-06	0.0762	AGTTGGCGGTGGTAG
Potri.010G181000	AP2	PpAspAT1	1281	1300	-	14.5769	5.87E-06	0.00516	TAAAGCAAAAGGAAAAGAAA
Potri.015G082200	LBD	PpAspAT1	827	847	-	12.3125	5.92E-06	0.0469	TCCACCTCCACCTCAGTCAAG
Potri.012G083500	LBD	PpAspAT1	827	847	-	12.3125	5.92E-06	0.0469	TCCACCTCCACCTCAGTCAAG
Potri.013G001000	MYB	PpAspAT1	1958	1972	+	14.5781	5.96E-06	0.0397	AACAACTACCACCGC
Potri.002G186600	WRKY	PpAspAT1	1085	1103	+	14.7344	5.96E-06	0.236	GATACTCGTTGACTTGATT
Potri.005G233300	ERF	PpAspAT1	832	846	-	13.7344	6.24E-06	0.0495	CCACCTCCACCTCAG
Potri.001G356100	ERF	PpAspAT1	1960	1974	-	13.1719	6.28E-06	0.125	TGGCGGTGGTAGTTG
Potri.011G070100	WRKY	PpAspAT1	1091	1101	-	14.7812	6.48E-06	0.258	TCAAGTCAACG
Potri.005G168700	ERF	PpAspAT1	1967	1976	+	13.5106	6.68E-06	0.103	CACCGCCAAC
Potri.004G051800	ERF	PpAspAT1	1959	1975	-	11.5938	6.72E-06	0.0888	TTGGCGGTGGTAGTTGT
Potri.017G013700	ERF	PpAspAT1	1963	1983	-	12.1406	6.88E-06	0.034	CGTTTTAGTTGGCGGTGGTAG
Potri.003G077700	ERF	PpAspAT1	1549	1569	+	12.3906	6.90E-06	0.0389	CTCACCACCGGCCCCCTCATC
Potri.002G061300	NAC	PpAspAT1	786	804	+	12.8438	7.04E-06	0.187	AACTTGCTTGCAAAGTAAG
Potri.013G001000	MYB	PpAspAT1	1955	1969	+	14.375	7.09E-06	0.0397	TCCAACAACTACCAC
Potri.018G028000	ERF	PpAspAT1	845	865	-	9.64706	7.51E-06	0.0297	GCCAACAAAACTTCCACCTCC
Potri.003G034200	Dof	PpAspAT1	740	760	+	13.5938	7.52E-06	0.0191	AAAAAAGAAAAGCAAGTACAA
Potri.013G101100	ERF	PpAspAT1	1958	1977	+	13.0156	7.60E-06	0.0334	AACAACTACCACCGCCAACT
Potri.003G150800	ERF	PpAspAT1	837	851	+	11.7812	7.70E-06	0.153	GTGGAGGTGGAGGTG
Potri.005G233300	ERF	PpAspAT1	1963	1977	+	13.3125	7.75E-06	0.0513	CTACCACCGCCAACT
Potri.005G168700	ERF	PpAspAT1	1554	1563	+	13.3191	7.79E-06	0.103	CACCGGCCCC
Potri.008G073600	ERF	PpAspAT1	1968	1988	-	11.7647	8.09E-06	0.0291	GTTGGCGTTTTAGTTGGCGGT
Potri.003G161000	ERF	PpAspAT1	838	852	+	12.3438	8.23E-06	0.327	TGGAGGTGGAGGTGG
Potri.002G157600	MYB	PpAspAT1	1464	1478	-	14.1562	8.67E-06	0.055	GAGATGGTTGTTGAG
Potri.013G090300	WRKY	PpAspAT1	1089	1101	+	14	8.85E-06	0.348	CTCGTTGACTTGA
Potri.002G193000	WRKY	PpAspAT1	1091	1098	-	15.4149	9.13E-06	0.119	AGTCAACG
Potri.013G054000	NAC	PpAspAT1	1624	1638	-	13.7031	9.23E-06	0.349	AAGAGGCGTGATGGT
Potri.008G140400	C2H2	PpAspAT1	33	47	-	14.1719	9.26E-06	0.125	AAGACGAGACAAAAA
Potri.001G004700	ERF	PpAspAT1	1547	1561	+	13.5625	9.29E-06	0.369	TGCTCACCACCGGCC
Potri.015G004100	NAC	PpAspAT1	792	806	+	14.5156	9.52E-06	0.186	CTTGCAAAGTAAGGA
Potri.012G007500	NAC	PpAspAT1	792	806	+	14.5156	9.52E-06	0.181	CTTGCAAAGTAAGGA
Potri.001G053500	GATA	PpAspAT1	834	848	+	13.5441	9.55E-06	0.19	GAGGTGGAGGTGGAG
Potri.018G021900	ERF	PpAspAT1	1962	1980	-	12.1875	9.55E-06	0.042	TTTAGTTGGCGGTGGTAGT
Potri.014G090700	WRKY	PpAspAT1	1089	1102	+	14.0469	9.88E-06	0.391	CTCGTTGACTTGAT
Potri.002G164900	WRKY	PpAspAT1	1089	1102	+	14.0469	9.88E-06	0.39	CTCGTTGACTTGAT
Potri.002G043500	WRKY	PpAspAT1	1091	1101	-	13.9375	9.98E-06	0.386	TCAAGTCAACG
Potri.014G074200	MIKC_MADS	PpAspAT10	574	594	-	19.7971	3.14E-09	3.95E-05	TTTCTTTTTCTTTTTCTTTTT
Potri.014G074200	MIKC_MADS	PpAspAT10	580	600	-	19.7971	3.14E-09	3.95E-05	TTTCTTTTTCTTTTTCTTTTT
Potri.002G151700	MIKC_MADS	PpAspAT10	574	594	-	19.7971	3.14E-09	3.90E-05	TTTCTTTTTCTTTTTCTTTTT
Potri.002G151700	MIKC_MADS	PpAspAT10	580	600	-	19.7971	3.14E-09	3.90E-05	TTTCTTTTTCTTTTTCTTTTT
Potri.001G238400	Dof	PpAspAT10	579	599	-	18.4062	1.19E-08	0.000447	TTCTTTTTCTTTTTCTTTTTC
Potri.003G034200	Dof	PpAspAT10	574	594	+	17.4844	1.74E-08	0.000327	aaaaagaaaaagaaaaagaaa
Potri.003G034200	Dof	PpAspAT10	580	600	+	17.4844	1.74E-08	0.000327	aaaaagaaaaagaaaaagaaa
Potri.010G204800	Dof	PpAspAT10	575	595	-	18.9375	1.91E-08	0.000232	TTTTCTTTTTCTTTTTCTTTT
Potri.010G204800	Dof	PpAspAT10	581	601	-	18.9375	1.91E-08	0.000232	TTTTCTTTTTCTTTTTCTTTT
Potri.014G074200	MIKC_MADS	PpAspAT10	578	598	-	18.942	2.49E-08	0.000157	TCTTTTTCTTTTTCTTTTTCT
Potri.002G151700	MIKC_MADS	PpAspAT10	578	598	-	18.942	2.49E-08	0.000155	TCTTTTTCTTTTTCTTTTTCT
Potri.010G181000	AP2	PpAspAT10	577	596	+	19.6923	2.68E-08	0.000247	aagaaaaagaaaaagaaaaa
Potri.010G181000	AP2	PpAspAT10	583	602	+	19.6923	2.68E-08	0.000247	aagaaaaagaaaaagaaaaa
Potri.014G074200	MIKC_MADS	PpAspAT10	576	596	-	18.6522	4.41E-08	0.000185	TTTTTCTTTTTCTTTTTCTTT
Potri.014G074200	MIKC_MADS	PpAspAT10	582	602	-	18.6522	4.41E-08	0.000185	TTTTTCTTTTTCTTTTTCTTT
Potri.002G151700	MIKC_MADS	PpAspAT10	576	596	-	18.6522	4.41E-08	0.000182	TTTTTCTTTTTCTTTTTCTTT
Potri.002G151700	MIKC_MADS	PpAspAT10	582	602	-	18.6522	4.41E-08	0.000182	TTTTTCTTTTTCTTTTTCTTT
Potri.007G036400	Dof	PpAspAT10	574	594	-	16.625	1.01E-07	0.00126	TTTCTTTTTCTTTTTCTTTTT
Potri.007G036400	Dof	PpAspAT10	580	600	-	16.625	1.01E-07	0.00126	TTTCTTTTTCTTTTTCTTTTT
Potri.012G081300	Dof	PpAspAT10	577	597	+	16.8906	1.06E-07	0.00199	aagaaaaagaaaaagaaaaag
Potri.003G034200	Dof	PpAspAT10	586	606	+	16.2344	1.98E-07	0.00248	aaaaagaaaaagaaaaaTAAA
Potri.001G238400	Dof	PpAspAT10	585	605	-	16.8125	2.00E-07	0.00249	TTATTTTTCTTTTTCTTTTTC
Potri.012G081300	Dof	PpAspAT10	583	603	+	16.3906	2.45E-07	0.00306	aagaaaaagaaaaagaaaaaT
Potri.001G238400	Dof	PpAspAT10	573	593	-	16.5312	3.01E-07	0.00281	TTCTTTTTCTTTTTCTTTTTA
Potri.010G181000	AP2	PpAspAT10	575	594	+	17.6538	3.60E-07	0.000913	aaaagaaaaagaaaaagaaa
Potri.010G181000	AP2	PpAspAT10	581	600	+	17.6538	3.60E-07	0.000913	aaaagaaaaagaaaaagaaa
Potri.010G181000	AP2	PpAspAT10	579	598	+	17.4487	4.51E-07	0.00104	gaaaaagaaaaagaaaaaga
Potri.017G112000	TCP	PpAspAT10	1772	1801	+	17.2152	4.69E-07	0.00922	AATGGGCGCCCACTCCTCCCGGGAGGCATT
Potri.010G101400	BBR-BPC	PpAspAT10	577	600	+	12.2031	5.78E-07	0.0171	aagaaaaagaaaaagaaaaagaaa
Potri.010G181000	AP2	PpAspAT10	573	592	+	16.5769	1.08E-06	0.00159	taaaaagaaaaagaaaaaga
Potri.010G101400	BBR-BPC	PpAspAT10	575	598	+	10.6406	1.09E-06	0.0171	aaaagaaaaagaaaaagaaaaaga
Potri.014G074200	MIKC_MADS	PpAspAT10	577	597	-	16.3913	1.10E-06	0.00134	CTTTTTCTTTTTCTTTTTCTT
Potri.002G151700	MIKC_MADS	PpAspAT10	577	597	-	16.3913	1.10E-06	0.00133	CTTTTTCTTTTTCTTTTTCTT
Potri.010G181000	AP2	PpAspAT10	1546	1565	+	16.2692	1.43E-06	0.00185	aaaaaaatgaaaaaaaaaaa
Potri.017G112000	TCP	PpAspAT10	1756	1785	-	14.7342	1.47E-06	0.0144	AGTGGGCGCCCATTGTAACGCTTTACCTTT
Potri.004G056900	Dof	PpAspAT10	577	597	+	15.2031	1.65E-06	0.0124	aagaaaaagaaaaagaaaaag
Potri.007G036400	Dof	PpAspAT10	586	606	-	14.7812	1.77E-06	0.0106	TTTATTTTTCTTTTTCTTTTT
Potri.007G036400	Dof	PpAspAT10	1892	1912	-	14.5625	2.36E-06	0.0106	AACTTTTTCCTTTTCCTTTAT

Potri.003G143000	Nin-like	PpAspAT10	1799	1813	+	14.7969	2.55E-06	0.101	ATTTGACCCTTGGCA
Potri.010G101400	BBR-BPC	PpAspAT10	579	602	+	8.32812	2.69E-06	0.0171	gaaaaagaaaaagaaaaagaaaaa
Potri.010G204800	Dof	PpAspAT10	1544	1564	-	14.9844	3.01E-06	0.00615	TTTTTTTTTTCATTTTTTTTT
Potri.008G131700	GRAS	PpAspAT10	577	596	+	14.913	3.29E-06	0.0374	aagaaaaagaaaaagaaaaa
Potri.008G131700	GRAS	PpAspAT10	583	602	+	14.913	3.29E-06	0.0374	aagaaaaagaaaaagaaaaa
Potri.001G238400	Dof	PpAspAT10	1891	1911	-	14.4531	4.04E-06	0.0116	ACTTTTTCCTTTTCCTTTATT
Potri.015G138200	TCP	PpAspAT10	1775	1784	+	14.9255	4.04E-06	0.0805	GGGCGCCCAC
Potri.003G034200	Dof	PpAspAT10	1892	1912	+	14.0625	4.38E-06	0.0149	ATAAAGGAAAAGGAAAAAGTT
Potri.014G074200	MIKC_MADS	PpAspAT10	588	608	-	14.9855	4.40E-06	0.00386	GCTTTATTTTTCTTTTTCTTT
Potri.002G151700	MIKC_MADS	PpAspAT10	588	608	-	14.9855	4.40E-06	0.00381	GCTTTATTTTTCTTTTTCTTT
Potri.010G204800	Dof	PpAspAT10	586	606	-	14.5625	4.50E-06	0.00827	TTTATTTTTCTTTTTCTTTTT
Potri.010G101400	BBR-BPC	PpAspAT10	581	604	+	6.34375	5.63E-06	0.0266	aaaagaaaaagaaaaagaaaaaTA
Potri.014G074200	MIKC_MADS	PpAspAT10	572	592	-	14.6377	5.93E-06	0.00466	TCTTTTTCTTTTTCTTTTTAA
Potri.002G151700	MIKC_MADS	PpAspAT10	572	592	-	14.6377	5.93E-06	0.00461	TCTTTTTCTTTTTCTTTTTAA
Potri.004G056900	Dof	PpAspAT10	583	603	+	14.0469	5.96E-06	0.0272	aagaaaaagaaaaagaaaaaT
Potri.007G135000	C2H2	PpAspAT10	1592	1611	+	14.4219	6.15E-06	0.117	TTATAGACGACAAAATAAAA
Potri.014G074200	MIKC_MADS	PpAspAT10	575	595	-	14.4783	6.77E-06	0.00482	TTTTCTTTTTCTTTTTCTTTT
Potri.014G074200	MIKC_MADS	PpAspAT10	581	601	-	14.4783	6.77E-06	0.00482	TTTTCTTTTTCTTTTTCTTTT
Potri.002G151700	MIKC_MADS	PpAspAT10	575	595	-	14.4783	6.77E-06	0.00476	TTTTCTTTTTCTTTTTCTTTT
Potri.002G151700	MIKC_MADS	PpAspAT10	581	601	-	14.4783	6.77E-06	0.00476	TTTTCTTTTTCTTTTTCTTTT
Potri.004G056900	Dof	PpAspAT10	1896	1916	+	13.9062	6.88E-06	0.0272	AGGAAAAGGAAAAAGTTCATT
Potri.005G168700	ERF	PpAspAT10	1836	1845	+	13.4787	7.05E-06	0.103	AGCCGCCCAC
Potri.010G181000	AP2	PpAspAT10	1544	1563	+	14.3205	7.12E-06	0.00562	aaaaaaaaatgaaaaaaaaa
Potri.010G181000	AP2	PpAspAT10	587	606	+	14.2308	7.61E-06	0.00562	aaaagaaaaagaaaaaTAAA
Potri.008G032300	C2H2	PpAspAT10	1337	1347	-	12.3281	8.17E-06	0.163	TAGTGTAGGGG
Potri.005G101800	WOX	PpAspAT10	838	847	+	13.0827	8.38E-06	0.333	CGTCAATCAA
Potri.006G129300	C2H2	PpAspAT10	1592	1611	-	13.9375	8.51E-06	0.107	TTTTATTTTGTCGTCTATAA
Potri.010G101400	BBR-BPC	PpAspAT10	583	606	+	5.1875	8.54E-06	0.0358	aagaaaaagaaaaagaaaaaTAAA
Potri.002G026700	BBR-BPC	PpAspAT10	577	597	-	4.64384	8.79E-06	0.0826	CTTTTTCTTTTTCTTTTTCTT
Potri.001G060000	TCP	PpAspAT10	1776	1785	+	13.8173	8.90E-06	0.177	GGCGCCCACT
Potri.010G204800	Dof	PpAspAT10	591	611	-	13.7812	9.02E-06	0.0111	TTAGCTTTATTTTTCTTTTTC
Potri.001G327100	TCP	PpAspAT10	1776	1784	+	13.766	9.22E-06	0.183	GGCGCCCAC
Potri.013G110700	TCP	PpAspAT10	1776	1785	+	12.3654	9.23E-06	0.13	GGCGCCCACT
Potri.012G081300	Dof	PpAspAT10	1889	1909	+	13.5156	9.75E-06	0.0261	TTAATAAAGGAAAAGGAAAAA
Potri.005G236700	ARF	PpAspAT2	1728	1737	+	15.8438	4.86E-07	0.0188	CCCGACAAGA
Potri.001G238400	Dof	PpAspAT2	155	175	+	16.0469	5.93E-07	0.00318	TTAATTTTCTTTTCCTTTTTG
Potri.007G036400	Dof	PpAspAT2	154	174	+	14.6875	2.01E-06	0.0106	CTTAATTTTCTTTTCCTTTTT
Potri.015G048300	Dof	PpAspAT2	162	175	-	14	2.05E-06	0.0765	CAAAAAGGAAAAGA
Potri.002G142200	SBP	PpAspAT2	642	657	+	13.814	2.22E-06	0.0791	ATCTACGTACCttttt
Potri.006G084200	Dof	PpAspAT2	161	175	+	14.5469	2.23E-06	0.0417	TTCTTTTCCTTTTTG
Potri.003G034200	Dof	PpAspAT2	154	174	-	14.3438	3.11E-06	0.0129	AAAAAGGAAAAGAAAATTAAG
Potri.015G048300	Dof	PpAspAT2	1663	1676	+	13.6719	4.06E-06	0.0765	AAAAAAGGGAAAAA
Potri.006G237700	GATA	PpAspAT2	846	858	+	14.9375	4.59E-06	0.182	AATCTAGATCCAG
Potri.002G228700	MYB	PpAspAT2	1252	1266	-	14.0312	4.82E-06	0.19	AATCTAAACCGAACC
Potri.006G084200	Dof	PpAspAT2	1663	1677	-	14.0312	4.90E-06	0.0609	ATTTTTCCCTTTTTT
Potri.004G078200	ARF	PpAspAT2	1728	1736	-	13.2947	5.01E-06	0.197	CTTGTCGGG
Potri.012G081300	Dof	PpAspAT2	163	183	-	14.0312	5.62E-06	0.0162	GGAGTATCCAAAAAGGAAAAG
Potri.005G122500	ZF-HD	PpAspAT2	1375	1389	+	13.1176	6.60E-06	0.123	AATTGTAATTAGTAA
Potri.014G074200	MIKC_MADS	PpAspAT2	1662	1682	-	14.4203	7.10E-06	0.00496	TGTTGATTTTTCCCTTTTTTC
Potri.002G151700	MIKC_MADS	PpAspAT2	1662	1682	-	14.4203	7.10E-06	0.0049	TGTTGATTTTTCCCTTTTTTC
Potri.012G106100	ARF	PpAspAT2	1727	1736	+	12.9531	8.93E-06	0.354	ACCCGACAAG
Potri.002G193000	WRKY	PpAspAT2	1107	1114	-	15.4149	9.13E-06	0.119	AGTCAACG
Potri.004G064300	MIKC_MADS	PpAspAT2	161	179	+	13.7059	9.47E-06	0.182	TTCTTTTCCTTTTTGGATA
Potri.014G074200	MIKC_MADS	PpAspAT3	1461	1481	-	19.8261	2.90E-09	3.95E-05	TTTCTTTTTTTTTCTTTTTTT
Potri.002G151700	MIKC_MADS	PpAspAT3	1461	1481	-	19.8261	2.90E-09	3.90E-05	TTTCTTTTTTTTTCTTTTTTT
Potri.010G181000	AP2	PpAspAT3	1462	1481	+	20.0513	1.49E-08	0.000247	aaaaaagaaaaaaaaagaaa
Potri.014G074200	MIKC_MADS	PpAspAT3	1463	1483	-	19.058	1.95E-08	0.000157	TTTTTCTTTTTTTTTCTTTTT
Potri.002G151700	MIKC_MADS	PpAspAT3	1463	1483	-	19.058	1.95E-08	0.000155	TTTTTCTTTTTTTTTCTTTTT
Potri.014G074200	MIKC_MADS	PpAspAT3	1467	1487	-	18.971	2.35E-08	0.000157	TTTTTTTTTCTTTTTTTTTCT
Potri.002G151700	MIKC_MADS	PpAspAT3	1467	1487	-	18.971	2.35E-08	0.000155	TTTTTTTTTCTTTTTTTTTCT
Potri.010G204800	Dof	PpAspAT3	1462	1482	-	18.7656	2.52E-08	0.000232	TTTTCTTTTTTTTTCTTTTTT
Potri.014G074200	MIKC_MADS	PpAspAT3	1469	1489	-	18.6087	4.79E-08	0.000185	TCTTTTTTTTTCTTTTTTTTT
Potri.002G151700	MIKC_MADS	PpAspAT3	1469	1489	-	18.6087	4.79E-08	0.000182	TCTTTTTTTTTCTTTTTTTTT
Potri.014G074200	MIKC_MADS	PpAspAT3	1459	1479	-	18.4493	6.39E-08	0.000185	TCTTTTTTTTTCTTTTTTTCC
Potri.002G151700	MIKC_MADS	PpAspAT3	1459	1479	-	18.4493	6.39E-08	0.000182	TCTTTTTTTTTCTTTTTTTCC
Potri.001G238400	Dof	PpAspAT3	1462	1482	-	17.0312	1.43E-07	0.00249	TTTTCTTTTTTTTTCTTTTTT
Potri.010G181000	AP2	PpAspAT3	1470	1489	+	18.3205	1.67E-07	0.000913	aaaaaaaagaaaaaaaaaGA
Potri.014G074200	MIKC_MADS	PpAspAT3	1465	1485	-	17.5942	2.47E-07	0.000466	TTTTTTTCTTTTTTTTTCTTT
Potri.002G151700	MIKC_MADS	PpAspAT3	1465	1485	-	17.5942	2.47E-07	0.00046	TTTTTTTCTTTTTTTTTCTTT
Potri.010G181000	AP2	PpAspAT3	1466	1485	+	17.9359	2.63E-07	0.000913	aagaaaaaaaaagaaaaaaa
Potri.010G181000	AP2	PpAspAT3	1460	1479	+	17.6667	3.55E-07	0.000913	gaaaaaaagaaaaaaaaaga
Potri.014G074200	MIKC_MADS	PpAspAT3	364	384	-	17.3188	3.59E-07	0.000629	TTTTTGTTTTTTTCTTTCCTT
Potri.002G151700	MIKC_MADS	PpAspAT3	364	384	-	17.3188	3.59E-07	0.000621	TTTTTGTTTTTTTCTTTCCTT
Potri.003G034200	Dof	PpAspAT3	1467	1487	+	15.6875	4.82E-07	0.00301	agaaaaaaaaagaaaaaaaaa
Potri.012G081300	Dof	PpAspAT3	1464	1484	+	15.8281	5.75E-07	0.00432	aaaagaaaaaaaaagaaaaaa
Potri.014G074200	MIKC_MADS	PpAspAT3	366	386	-	16.8696	6.35E-07	0.000888	GTTTTTTGTTTTTTTCTTTCC
Potri.002G151700	MIKC_MADS	PpAspAT3	366	386	-	16.8696	6.35E-07	0.000877	GTTTTTTGTTTTTTTCTTTCC
Potri.010G181000	AP2	PpAspAT3	1464	1483	+	17.0769	6.63E-07	0.00136	aaaagaaaaaaaaagaaaaa
Potri.005G231300	bZIP	PpAspAT3	1871	1885	-	17.2812	7.21E-07	0.0286	TTGGATGACGTGTCG
Potri.018G029500	bZIP	PpAspAT3	1871	1885	-	17.6875	7.53E-07	0.0299	TTGGATGACGTGTCG
Potri.010G181000	AP2	PpAspAT3	1469	1488	+	16.8974	7.91E-07	0.0015	aaaaaaaaagaaaaaaaaaG
Potri.010G181000	AP2	PpAspAT3	1467	1486	+	16.8718	8.11E-07	0.0015	agaaaaaaaaagaaaaaaaa
Potri.007G036400	Dof	PpAspAT3	1463	1483	-	15.3125	8.53E-07	0.00639	TTTTTCTTTTTTTTTCTTTTT
Potri.002G196200	bZIP	PpAspAT3	1871	1885	-	16.9688	8.91E-07	0.0354	TTGGATGACGTGTCG
Potri.014G074200	MIKC_MADS	PpAspAT3	1457	1477	-	16.4928	9.85E-07	0.00132	TTTTTTTTTCTTTTTTTCCCA
Potri.002G151700	MIKC_MADS	PpAspAT3	1457	1477	-	16.4928	9.85E-07	0.00131	TTTTTTTTTCTTTTTTTCCCA
Potri.010G181000	AP2	PpAspAT3	1468	1487	+	16.6667	9.89E-07	0.00156	gaaaaaaaaagaaaaaaaaa
Potri.014G074200	MIKC_MADS	PpAspAT3	1464	1484	-	16.4493	1.03E-06	0.00132	TTTTTTCTTTTTTTTTCTTTT
Potri.002G151700	MIKC_MADS	PpAspAT3	1464	1484	-	16.4493	1.03E-06	0.00131	TTTTTTCTTTTTTTTTCTTTT
Potri.010G181000	AP2	PpAspAT3	1458	1477	+	16.4487	1.21E-06	0.00172	gggaaaaaaagaaaaaaaaa
Potri.014G074200	MIKC_MADS	PpAspAT3	1460	1480	-	16.2754	1.25E-06	0.00148	TTCTTTTTTTTTCTTTTTTTC
Potri.002G151700	MIKC_MADS	PpAspAT3	1460	1480	-	16.2754	1.25E-06	0.00146	TTCTTTTTTTTTCTTTTTTTC
Potri.006G083000	bZIP	PpAspAT3	1869	1886	-	16.4062	1.58E-06	0.0628	ATTGGATGACGTGTCGTC
Potri.007G109100	NAC	PpAspAT3	830	850	+	16.0312	1.59E-06	0.0601	CATAACTTGTTCATGAAGTCA
Potri.014G074200	MIKC_MADS	PpAspAT3	1468	1488	-	15.971	1.72E-06	0.00181	CTTTTTTTTTCTTTTTTTTTC
Potri.002G151700	MIKC_MADS	PpAspAT3	1468	1488	-	15.971	1.72E-06	0.00179	CTTTTTTTTTCTTTTTTTTTC
Potri.012G081300	Dof	PpAspAT3	585	605	+	14.9219	1.96E-06	0.0092	gatgaaaacaaaaagaaaaat
Potri.010G101400	BBR-BPC	PpAspAT3	1458	1481	+	9.07812	2.02E-06	0.0171	gggaaaaaaagaaaaaaaaagaaa
Potri.002G125400	bZIP	PpAspAT3	1866	1883	+	16.0625	2.08E-06	0.0825	ACAGACGACACGTCATCC
Potri.002G167100	bZIP	PpAspAT3	1871	1885	+	15.7188	2.18E-06	0.0868	CGACACGTCATCCAA
Potri.014G074200	MIKC_MADS	PpAspAT3	1458	1478	-	15.7101	2.24E-06	0.00217	CTTTTTTTTTCTTTTTTTCCC
Potri.002G151700	MIKC_MADS	PpAspAT3	1458	1478	-	15.7101	2.24E-06	0.00214	CTTTTTTTTTCTTTTTTTCCC

Potri.010G181000	AP2	PpAspAT3	1459	1478	+	15.7051	2.37E-06	0.00257	ggaaaaaaagaaaaaaaaag
Potri.010G181000	AP2	PpAspAT3	363	382	+	15.6282	2.53E-06	0.00259	gaaggaaagaaaaaaacaaa
Potri.008G131700	GRAS	PpAspAT3	1458	1477	+	15.1449	2.68E-06	0.0374	gggaaaaaaagaaaaaaaaa
Potri.010G181000	AP2	PpAspAT3	1457	1476	+	15.5513	2.70E-06	0.00269	tgggaaaaaaagaaaaaaaa
Potri.008G010800	bZIP	PpAspAT3	1871	1885	-	15.3906	2.72E-06	0.108	TTGGATGACGTGTCG
Potri.010G181000	AP2	PpAspAT3	1465	1484	+	15.5128	2.79E-06	0.00271	aaagaaaaaaaaagaaaaaa
Potri.008G140400	C2H2	PpAspAT3	1035	1049	+	15.75	2.94E-06	0.112	tcaataagacaaaat
Potri.001G066900	Trihelix	PpAspAT3	1709	1726	+	14.3382	2.98E-06	0.118	agaccaaaatgccctaag
Potri.006G133000	MYB_related	PpAspAT3	127	138	-	14.875	2.99E-06	0.109	AGATATTTTTTT
Potri.007G109100	NAC	PpAspAT3	832	852	-	14.75	3.04E-06	0.0601	CCTGACTTCATGAACAAGTTA
Potri.010G101400	BBR-BPC	PpAspAT3	1466	1489	+	7.89062	3.17E-06	0.0171	aagaaaaaaaaagaaaaaaaaaGA
Potri.004G056900	Dof	PpAspAT3	1464	1484	+	14.6094	3.27E-06	0.0176	aaaagaaaaaaaaagaaaaaa
Potri.001G238400	Dof	PpAspAT3	1472	1492	-	14.6406	3.29E-06	0.0112	TGATCTTTTTTTTTCTTTTTT
Potri.008G081500	NAC	PpAspAT3	830	850	-	14.75	3.68E-06	0.142	TGACTTCATGAACAAGTTATG
Potri.001G238400	Dof	PpAspAT3	1169	1189	-	14.5156	3.77E-06	0.0116	TTTTTTATTTTCTTCTTTATG
Potri.004G074300	MYB_related	PpAspAT3	127	140	+	14.4375	3.94E-06	0.143	aaaaaaaTATCTAA
Potri.010G099100	C2H2	PpAspAT3	369	385	+	14.8438	4.32E-06	0.0814	aagaaaaaaacaaaaaa
Potri.014G089300	MYB_related	PpAspAT3	128	138	-	15.0469	4.55E-06	0.165	AGATATTTTTT
Potri.014G074200	MIKC_MADS	PpAspAT3	373	393	-	14.913	4.68E-06	0.00398	TCTTTGTGTTTTTTGTTTTTT
Potri.002G151700	MIKC_MADS	PpAspAT3	373	393	-	14.913	4.68E-06	0.00393	TCTTTGTGTTTTTTGTTTTTT
Potri.010G204800	Dof	PpAspAT3	1469	1489	-	14.5	4.77E-06	0.00835	TCTTTTTTTTTCTTTTTTTTT
Potri.008G131700	GRAS	PpAspAT3	1460	1479	+	14.3768	5.22E-06	0.0386	gaaaaaaagaaaaaaaaaga
Potri.003G097600	bZIP	PpAspAT3	1871	1885	-	13.75	5.34E-06	0.212	TTGGATGACGTGTCG
Potri.014G074200	MIKC_MADS	PpAspAT3	363	383	-	14.6377	5.93E-06	0.00466	TTTTGTTTTTTTCTTTCCTTC
Potri.002G151700	MIKC_MADS	PpAspAT3	363	383	-	14.6377	5.93E-06	0.00461	TTTTGTTTTTTTCTTTCCTTC
Potri.013G040700	bZIP	PpAspAT3	1872	1883	-	14.5638	5.93E-06	0.236	GGATGACGTGTC
Potri.008G131700	GRAS	PpAspAT3	369	388	+	14.1884	6.09E-06	0.0386	aagaaaaaaacaaaaaacac
Potri.010G204800	Dof	PpAspAT3	1468	1488	-	14.2188	6.15E-06	0.0103	CTTTTTTTTTCTTTTTTTTTC
Potri.002G023400	E2F/DP	PpAspAT3	1368	1382	+	13.3191	6.54E-06	0.26	ataaaagagccaaga
Potri.007G012100	WOX	PpAspAT3	1075	1085	-	14.4684	6.63E-06	0.179	TCATTCATTTA
Potri.010G204800	Dof	PpAspAT3	1461	1481	-	14.0625	7.07E-06	0.0109	TTTCTTTTTTTTTCTTTTTTT
Potri.006G152700	NAC	PpAspAT3	833	847	+	14.5156	7.13E-06	0.283	AACTTGTTCATGAAG
Potri.004G056900	Dof	PpAspAT3	1423	1443	+	13.8594	7.21E-06	0.0272	atcaaaaacaaaaaggataaa
Potri.015G030400	MYB_related	PpAspAT3	129	140	+	14.9375	7.24E-06	0.269	aaaaaTATCTAA
Potri.019G031600	NAC	PpAspAT3	832	850	+	13.875	7.37E-06	0.285	TAACTTGTTCATGAAGTCA
Potri.005G221900	LBD	PpAspAT3	970	984	+	13.9531	7.43E-06	0.295	TCGGAAAAAACGGTG
Potri.010G181000	AP2	PpAspAT3	355	374	+	14.2308	7.61E-06	0.00562	acaaacgtgaaggaaagaaa
Potri.003G034200	Dof	PpAspAT3	1457	1477	+	13.5781	7.65E-06	0.0191	tgggaaaaaaagaaaaaaaaa
Potri.010G204800	Dof	PpAspAT3	583	603	-	13.9531	7.78E-06	0.0109	TTTTCTTTTTGTTTTCATCAC
Potri.014G074200	MIKC_MADS	PpAspAT3	362	382	-	14.2319	8.26E-06	0.00557	TTTGTTTTTTTCTTTCCTTCA
Potri.002G151700	MIKC_MADS	PpAspAT3	362	382	-	14.2319	8.26E-06	0.0055	TTTGTTTTTTTCTTTCCTTCA
Potri.003G034200	Dof	PpAspAT3	1426	1446	+	13.5	8.34E-06	0.0195	aaaaacaaaaaggataaaagt
Potri.006G129300	C2H2	PpAspAT3	369	388	-	13.9531	8.44E-06	0.107	GTGTTTTTTGTTTTTTTTCTT
Potri.006G122100	MYB	PpAspAT3	64	78	-	14.5312	8.55E-06	0.313	TTATAATTAGGTAGA
Potri.008G107900	CAMTA	PpAspAT3	156	173	+	13.8906	8.72E-06	0.346	CCATGTTACCAGCGTGTT
Potri.010G204800	Dof	PpAspAT3	1467	1487	-	13.7969	8.90E-06	0.0111	TTTTTTTTTCTTTTTTTTTCT
Potri.010G229700	NAC	PpAspAT3	832	851	-	13.4795	9.12E-06	0.12	CTGACTTCATGAACAAGTTA
Potri.008G131700	GRAS	PpAspAT3	1468	1487	+	13.5942	9.81E-06	0.0415	gaaaaaaaaagaaaaaaaaa
Potri.008G140400	C2H2	PpAspAT3	370	384	+	14.0625	9.87E-06	0.125	agaaaaaaacaaaaa
Potri.010G181000	AP2	PpAspAT4	1776	1795	-	20.0385	1.53E-08	0.000247	AAAAAAAAGAAGAAAAGAAA
Potri.012G081300	Dof	PpAspAT4	314	334	-	17.5156	3.34E-08	0.00125	GAAAAAAGAAAAAAGGGAAGA
Potri.010G204800	Dof	PpAspAT4	316	336	+	18.5312	3.77E-08	0.000277	TTCCCttttttcttttttctt
Potri.004G056900	Dof	PpAspAT4	314	334	-	17.7812	3.94E-08	0.000742	GAAAAAAGAAAAAAGGGAAGA
Potri.010G204800	Dof	PpAspAT4	1775	1795	+	18.3594	4.91E-08	0.000301	GTTTCTTTTCTTCttttttt
Potri.019G081100	C2H2	PpAspAT4	461	479	-	20.1441	7.68E-08	0.000993	CTCTATTCTCCTCCTCCAC
Potri.007G036400	Dof	PpAspAT4	312	332	+	16.75	7.99E-08	0.00126	TCTCTTCCCttttttcttttt
Potri.014G074200	MIKC_MADS	PpAspAT4	315	335	+	17.8696	1.65E-07	0.000346	CTTCCCttttttcttttttct
Potri.002G151700	MIKC_MADS	PpAspAT4	315	335	+	17.8696	1.65E-07	0.000342	CTTCCCttttttcttttttct
Potri.015G138200	TCP	PpAspAT4	1235	1244	+	18.4043	1.97E-07	0.00785	TGGGCCCCAC
Potri.014G074200	MIKC_MADS	PpAspAT4	314	334	+	17.6377	2.32E-07	0.000461	TCTTCCCttttttcttttttc
Potri.002G151700	MIKC_MADS	PpAspAT4	314	334	+	17.6377	2.32E-07	0.000455	TCTTCCCttttttcttttttc
Potri.017G112000	TCP	PpAspAT4	1216	1245	-	18.481	2.44E-07	0.00922	AGTGGGGCCCAATGAAACTGATGTGGCACG
Potri.005G090300	TCP	PpAspAT4	1234	1244	-	19.0625	3.20E-07	0.0127	GTGGGGCCCAA
Potri.001G327100	TCP	PpAspAT4	1236	1244	+	18.6915	3.39E-07	0.0135	GGGCCCCAC
Potri.001G060000	TCP	PpAspAT4	1236	1245	+	18.375	3.52E-07	0.014	GGGCCCCACT
Potri.002G152200	TCP	PpAspAT4	1235	1244	+	18.0213	3.94E-07	0.0157	TGGGCCCCAC
Potri.010G223200	ARF	PpAspAT4	1975	1995	-	13.425	3.96E-07	0.0151	TTTGCAGTTTTTGTCGAAAAA
Potri.014G074200	MIKC_MADS	PpAspAT4	316	336	+	17.1884	4.26E-07	0.0007	TTCCCttttttcttttttctt
Potri.002G151700	MIKC_MADS	PpAspAT4	316	336	+	17.1884	4.26E-07	0.000691	TTCCCttttttcttttttctt
Potri.003G034200	Dof	PpAspAT4	318	338	-	15.75	4.36E-07	0.00301	AAAAGAAAAAAGAAAAAAGGG
Potri.001G238400	Dof	PpAspAT4	313	333	+	16.25	4.49E-07	0.00281	CTCTTCCCttttttcttttt
Potri.004G046300	TCP	PpAspAT4	1234	1253	-	12.2674	4.63E-07	0.0183	GAAGGTGAAGTGGGGCCCAA
Potri.007G036400	Dof	PpAspAT4	319	339	+	15.5469	6.05E-07	0.00566	CCttttttcttttttcttttG
Potri.017G112000	TCP	PpAspAT4	1233	1262	+	16.3671	7.07E-07	0.00926	ATTGGGCCCCACTTCACCTTCTTTTAGCAC
Potri.005G182200	MIKC_MADS	PpAspAT4	545	558	+	16.8281	7.18E-07	0.0273	ccaaaaatagaaaa
Potri.001G058400	MIKC_MADS	PpAspAT4	545	557	+	15.8529	9.76E-07	0.0387	ccaaaaatagaaa
Potri.013G110700	TCP	PpAspAT4	1236	1245	+	16.4904	9.93E-07	0.0394	GGGCCCCACT
Potri.004G064300	MIKC_MADS	PpAspAT4	542	560	-	16.0588	1.10E-06	0.0424	ATTTTTCTATTTTTGGTCT
Potri.010G181000	AP2	PpAspAT4	1781	1800	-	16.3077	1.38E-06	0.00185	AAAACAAAAAAAAGAAGAAA
Potri.014G074200	MIKC_MADS	PpAspAT4	1775	1795	+	16.1594	1.42E-06	0.0016	GTTTCTTTTCTTCttttttt
Potri.002G151700	MIKC_MADS	PpAspAT4	1775	1795	+	16.1594	1.42E-06	0.00158	GTTTCTTTTCTTCttttttt
Potri.014G074200	MIKC_MADS	PpAspAT4	317	337	+	16.1449	1.44E-06	0.0016	TCCCttttttcttttttcttt
Potri.002G151700	MIKC_MADS	PpAspAT4	317	337	+	16.1449	1.44E-06	0.00158	TCCCttttttcttttttcttt
Potri.014G074200	MIKC_MADS	PpAspAT4	318	338	+	16.1159	1.48E-06	0.0016	CCCttttttcttttttctttt
Potri.002G151700	MIKC_MADS	PpAspAT4	318	338	+	16.1159	1.48E-06	0.00158	CCCttttttcttttttctttt
Potri.010G181000	AP2	PpAspAT4	312	331	-	15.8974	2.01E-06	0.00244	AAAAGAAAAAAGGGAAGAGA
Potri.T044100	TCP	PpAspAT4	1237	1244	+	18.3269	2.08E-06	0.0825	GGCCCCAC
Potri.004G065800	TCP	PpAspAT4	1237	1244	+	17.5481	2.08E-06	0.0827	GGCCCCAC
Potri.007G011600	AP2	PpAspAT4	1206	1220	+	15.5625	2.19E-06	0.087	CCTCGACTTTCGTGC
Potri.001G375800	TCP	PpAspAT4	1235	1244	+	15.9681	2.29E-06	0.0911	TGGGCCCCAC
Potri.010G181000	AP2	PpAspAT4	319	338	-	15.6667	2.45E-06	0.00258	AAAAGAAAAAAGAAAAAAGG
Potri.002G028400	MIKC_MADS	PpAspAT4	543	557	+	15.5	2.54E-06	0.0966	gaccaaaaatagaaa
Potri.010G204800	Dof	PpAspAT4	1783	1803	+	15.0469	2.83E-06	0.00613	TCTTCttttttttgtttttAT
Potri.010G204800	Dof	PpAspAT4	315	335	+	14.9219	3.20E-06	0.0062	CTTCCCttttttcttttttct
Potri.012G081300	Dof	PpAspAT4	1781	1801	-	14.3906	3.74E-06	0.0127	AAAAACAAAAAAAAGAAGAAA
Potri.003G034200	Dof	PpAspAT4	1778	1798	-	14.1875	3.77E-06	0.0141	AACAAAAAAAAGAAGAAAAGA
Potri.005G231300	bZIP	PpAspAT4	1218	1232	-	13.4531	4.20E-06	0.0834	GAAACTGATGTGGCA
Potri.019G081100	C2H2	PpAspAT4	458	476	-	13.661	4.60E-06	0.0246	TATTCTCCTCCTCCACTTT
Potri.010G181000	AP2	PpAspAT4	700	719	+	14.8718	4.68E-06	0.0043	aaaaaaaaaagaaataaaaa
Potri.008G089000	NAC	PpAspAT4	1259	1269	+	14	4.73E-06	0.185	GCACGGAACCG

Potri.014G074200	MIKC_MADS	PpAspAT4	547	567	-	14.8986	4.74E-06	0.00398	CTTTTCTATTTTTCTATTTTT
Potri.002G151700	MIKC_MADS	PpAspAT4	547	567	-	14.8986	4.74E-06	0.00393	CTTTTCTATTTTTCTATTTTT
Potri.002G110900	GATA	PpAspAT4	1103	1117	-	14.1406	5.08E-06	0.101	TTCAGACCGTCCGAT
Potri.012G081300	Dof	PpAspAT4	321	341	-	14.0781	5.34E-06	0.0162	GTCAAAAGAAAAAAGAAAAAA
Potri.014G074100	MIKC_MADS	PpAspAT4	542	560	+	14.4375	5.50E-06	0.0988	agaccaaaaatagaaaaat
Potri.014G074200	MIKC_MADS	PpAspAT4	1782	1802	+	14.6087	6.07E-06	0.00466	TTCTTCttttttttgtttttA
Potri.002G151700	MIKC_MADS	PpAspAT4	1782	1802	+	14.6087	6.07E-06	0.00461	TTCTTCttttttttgtttttA
Potri.014G074200	MIKC_MADS	PpAspAT4	699	719	-	14.5797	6.22E-06	0.00466	TTTTTATTTCTTTTTTTTTTA
Potri.002G151700	MIKC_MADS	PpAspAT4	699	719	-	14.5797	6.22E-06	0.00461	TTTTTATTTCTTTTTTTTTTA
Potri.T044100	TCP	PpAspAT4	408	415	+	15.7212	6.36E-06	0.0843	GAGCCCAC
Potri.001G238400	Dof	PpAspAT4	1773	1793	+	14	6.50E-06	0.017	TAGTTTCTTTTCTTCtttttt
Potri.014G074200	MIKC_MADS	PpAspAT4	1777	1797	+	14.3623	7.44E-06	0.00511	TTCTTTTCTTCttttttttgt
Potri.002G151700	MIKC_MADS	PpAspAT4	1777	1797	+	14.3623	7.44E-06	0.00505	TTCTTTTCTTCttttttttgt
Potri.007G036400	Dof	PpAspAT4	1772	1792	+	13.5938	7.44E-06	0.0232	CTAGTTTCTTTTCTTCttttt
Potri.001G238400	Dof	PpAspAT4	320	340	+	13.8438	7.61E-06	0.0178	CttttttcttttttcttttGA
Potri.010G181000	AP2	PpAspAT4	1823	1842	+	14.1154	8.28E-06	0.00599	AAGAAGAAAGATGAGAAACA
Potri.010G181000	AP2	PpAspAT4	320	339	-	14.0641	8.59E-06	0.0061	CAAAAGAAAAAAGAAAAAAG
Potri.003G034200	Dof	PpAspAT4	311	331	-	13.4219	9.09E-06	0.02	AAAAGAAAAAAAGGAAGAGAT
Potri.010G181000	AP2	PpAspAT4	1774	1793	-	13.9231	9.51E-06	0.00662	AAAAAAGAAGAAAAGAAACT
Potri.013G110700	TCP	PpAspAT4	1233	1242	-	12.2596	9.82E-06	0.13	GGGGCCCAAT
Potri.013G067500	MYB	PpAspAT4	433	451	-	13.9844	9.88E-06	0.0978	CCTGGCCAACCACTCCAGA
Potri.004G056900	Dof	PpAspAT5	1045	1065	+	17.8594	3.42E-08	0.000742	TAAAGaaaaaaaaaGTGAAAA
Potri.005G122500	ZF-HD	PpAspAT5	1106	1120	-	14.5588	2.75E-07	0.0103	AAAAGTAATTAATGA
Potri.001G188800	HD-ZIP	PpAspAT5	1703	1717	-	16.7385	6.39E-07	0.0119	ATATGTAATGATGAC
Potri.010G204800	Dof	PpAspAT5	1050	1070	-	16.4375	6.42E-07	0.00262	GTATCTTTTCACTTTTTTTTT
Potri.012G081300	Dof	PpAspAT5	1045	1065	+	15.4531	9.76E-07	0.00523	TAAAGaaaaaaaaaGTGAAAA
Potri.003G034200	Dof	PpAspAT5	1048	1068	+	14.8906	1.53E-06	0.00715	AGaaaaaaaaaGTGAAAAGAT
Potri.006G084200	Dof	PpAspAT5	1053	1067	-	14.7344	1.60E-06	0.0417	TCTTTTCACTTTTTT
Potri.013G091400	bZIP	PpAspAT5	619	629	-	14.6719	6.99E-06	0.0927	GCAAGCTGGCC
Potri.002G114800	AP2	PpAspAT5	603	623	-	11.3488	7.69E-06	0.152	TGGCCCGGATACCCACGTTAA
Potri.014G106800	MYB_related	PpAspAT5	881	890	-	14.2031	8.82E-06	0.326	AGATATTTTG
Potri.014G074200	MIKC_MADS	PpAspAT5	1044	1064	-	14.1159	9.06E-06	0.0059	TTTCACTTTTTTTTTCTTTAA
Potri.002G151700	MIKC_MADS	PpAspAT5	1044	1064	-	14.1159	9.06E-06	0.00582	TTTCACTTTTTTTTTCTTTAA
Potri.014G075200	HD-ZIP	PpAspAT5	1106	1116	+	14.0781	9.22E-06	0.332	TCATTAATTAC
Potri.016G112300	MYB	PpAspAT5	1117	1137	-	13.9241	9.87E-06	0.182	AGAATTCAGGATAAGAAAAAA
Potri.001G361600	WRKY	PpAspAT5	74	86	-	14.2656	9.93E-06	0.394	AGCTTTGACTATG
Potri.010G204800	Dof	PpAspAT6	1236	1256	+	20.0781	2.03E-09	7.47E-05	TTCACtttttttttttttttt
Potri.013G001000	MYB	PpAspAT6	1214	1228	+	19.3438	1.36E-08	0.000534	CCCACCCACCTCTCC
Potri.007G067600	MYB	PpAspAT6	939	959	-	21.5625	1.51E-08	0.000596	CGCCTCCCCCACCTACTACAT
Potri.005G096600	MYB	PpAspAT6	939	959	-	21.5625	1.51E-08	0.000595	CGCCTCCCCCACCTACTACAT
Potri.010G072300	ERF	PpAspAT6	942	969	-	22.1719	2.70E-08	0.00107	CTGCTTGAGCCGCCTCCCCCACCTACTA
Potri.014G074200	MIKC_MADS	PpAspAT6	732	752	-	18.5652	5.18E-08	0.000185	CTTTTCTTTCTTTCTTTTTGT
Potri.002G151700	MIKC_MADS	PpAspAT6	732	752	-	18.5652	5.18E-08	0.000182	CTTTTCTTTCTTTCTTTTTGT
Potri.017G082500	MYB	PpAspAT6	1210	1228	-	19.2344	6.32E-08	0.0025	GGAGAGGTGGGTGGGCATA
Potri.005G224100	MYB	PpAspAT6	942	962	-	18.7031	9.53E-08	0.00373	AGCCGCCTCCCCCACCTACTA
Potri.007G067600	MYB	PpAspAT6	1564	1584	+	19.625	1.10E-07	0.00146	GCCAGCTCTCACCTACCCCGT
Potri.005G096600	MYB	PpAspAT6	1564	1584	+	19.625	1.10E-07	0.00146	GCCAGCTCTCACCTACCCCGT
Potri.013G067500	MYB	PpAspAT6	1210	1228	+	18.6562	1.25E-07	0.00494	TATGCCCACCCACCTCTCC
Potri.005G164900	MYB	PpAspAT6	1211	1231	-	17.8125	1.29E-07	0.00501	AGTGGAGAGGTGGGTGGGCAT
Potri.015G023200	ERF	PpAspAT6	946	966	-	18.7647	1.64E-07	0.00163	CTTGAGCCGCCTCCCCCACCT
Potri.008G073600	ERF	PpAspAT6	944	964	+	18.7941	1.80E-07	0.00178	GTAGGTGGGGGAGGCGGCTCA
Potri.013G101100	ERF	PpAspAT6	943	962	-	18.8438	1.91E-07	0.00154	AGCCGCCTCCCCCACCTACT
Potri.005G224100	MYB	PpAspAT6	1561	1581	+	18.0312	2.03E-07	0.00398	CTGGCCAGCTCTCACCTACCC
Potri.018G028000	ERF	PpAspAT6	944	964	-	16.8824	2.45E-07	0.00242	TGAGCCGCCTCCCCCACCTAC
Potri.004G056900	Dof	PpAspAT6	1234	1254	-	16.5156	2.95E-07	0.0034	AAAAAAAAAAAAAAGTGAATT
Potri.010G204800	Dof	PpAspAT6	723	743	-	16.9844	3.32E-07	0.00174	CTTTCTTTTTGTTTTTCCTTT
Potri.015G023200	ERF	PpAspAT6	943	963	-	17.4706	3.41E-07	0.0027	GAGCCGCCTCCCCCACCTACT
Potri.001G238400	Dof	PpAspAT6	733	753	-	16.375	3.76E-07	0.00281	TCTTTTCTTTCTTTCTTTTTG
Potri.001G163700	ERF	PpAspAT6	946	966	+	18.1562	3.78E-07	0.015	AGGTGGGGGAGGCGGCTCAAG
Potri.017G013700	ERF	PpAspAT6	946	966	+	17.3281	4.39E-07	0.00434	AGGTGGGGGAGGCGGCTCAAG
Potri.007G007900	MYB	PpAspAT6	1572	1584	-	17.5063	4.85E-07	0.0192	ACGGGGTAGGTGA
Potri.002G157600	MYB	PpAspAT6	1571	1585	-	17.3438	5.13E-07	0.00977	AACGGGGTAGGTGAG
Potri.014G074200	MIKC_MADS	PpAspAT6	724	744	-	17.0145	5.32E-07	0.000803	TCTTTCTTTTTGTTTTTCCTT
Potri.014G074200	MIKC_MADS	PpAspAT6	726	746	-	17.0145	5.32E-07	0.000803	TTTCTTTCTTTTTGTTTTTCC
Potri.002G151700	MIKC_MADS	PpAspAT6	724	744	-	17.0145	5.32E-07	0.000793	TCTTTCTTTTTGTTTTTCCTT
Potri.002G151700	MIKC_MADS	PpAspAT6	726	746	-	17.0145	5.32E-07	0.000793	TTTCTTTCTTTTTGTTTTTCC
Potri.010G181000	AP2	PpAspAT6	729	748	+	17.2821	5.38E-07	0.00117	aaaacaaaaagaaagaaaga
Potri.018G028000	ERF	PpAspAT6	941	961	-	15.2941	5.47E-07	0.00432	GCCGCCTCCCCCACCTACTAC
Potri.019G081100	C2H2	PpAspAT6	942	960	-	17.0847	5.88E-07	0.00456	CCGCCTCCCCCACCTACTA
Potri.014G074200	MIKC_MADS	PpAspAT6	730	750	-	16.8696	6.35E-07	0.000888	TTTCTTTCTTTCTTTTTGTTT
Potri.002G151700	MIKC_MADS	PpAspAT6	730	750	-	16.8696	6.35E-07	0.000877	TTTCTTTCTTTCTTTTTGTTT
Potri.004G086300	MYB	PpAspAT6	1570	1582	-	16.8228	6.46E-07	0.0257	GGGGTAGGTGAGA
Potri.003G034200	Dof	PpAspAT6	728	748	+	15.4375	7.03E-07	0.00376	aaaaacaaaaagaaagaaaga
Potri.005G164900	MYB	PpAspAT6	1412	1432	-	16.4062	7.10E-07	0.0138	GGAGATAAGTTTGGTGAAGCA
Potri.004G051800	ERF	PpAspAT6	954	970	+	16.5625	7.31E-07	0.029	GAGGCGGCTCAAGCAGG
Potri.017G082500	MYB	PpAspAT6	938	956	+	17.0938	7.43E-07	0.0147	TATGTAGTAGGTGGGGGAG
Potri.008G073600	ERF	PpAspAT6	941	961	+	16.2059	8.18E-07	0.00647	GTAGTAGGTGGGGGAGGCGGC
Potri.010G181000	AP2	PpAspAT6	733	752	+	16.8077	8.63E-07	0.00152	caaaaagaaagaaagaaaag
Potri.012G081300	Dof	PpAspAT6	1234	1254	-	15.5156	8.96E-07	0.00523	AAAAAAAAAAAAAAGTGAATT
Potri.010G181000	AP2	PpAspAT6	1237	1256	-	16.7436	9.19E-07	0.00154	AAAAAAAAAAAAAAAAGTGA
Potri.004G174400	MYB	PpAspAT6	1571	1585	-	14.75	9.83E-07	0.0386	AACGGGGTAGGTGAG
Potri.014G074200	MIKC_MADS	PpAspAT6	722	742	-	16.4348	1.05E-06	0.00132	TTTCTTTTTGTTTTTCCTTTC
Potri.002G151700	MIKC_MADS	PpAspAT6	722	742	-	16.4348	1.05E-06	0.00131	TTTCTTTTTGTTTTTCCTTTC
Potri.013G091400	bZIP	PpAspAT6	1556	1566	+	16.7188	1.08E-06	0.0429	CCCAGCTGGCC
Potri.017G013700	ERF	PpAspAT6	943	963	+	15.7031	1.10E-06	0.00869	AGTAGGTGGGGGAGGCGGCTC
Potri.005G087200	ERF	PpAspAT6	947	965	+	16.4062	1.17E-06	0.0463	GGTGGGGGAGGCGGCTCAA
Potri.004G086300	MYB	PpAspAT6	1414	1426	-	16.3165	1.30E-06	0.0257	AAGTTTGGTGAAG
Potri.001G336700	MYB	PpAspAT6	1571	1583	+	15.8382	1.33E-06	0.026	CTCACCTACCCCG
Potri.003G077700	ERF	PpAspAT6	944	964	-	15.6562	1.34E-06	0.0255	TGAGCCGCCTCCCCCACCTAC
Potri.010G204800	Dof	PpAspAT6	841	861	+	15.7656	1.36E-06	0.00499	ttttctttttAATTTCTTTCA
Potri.002G157600	MYB	PpAspAT6	938	952	+	16.3594	1.38E-06	0.0135	TATGTAGTAGGTGGG
Potri.002G157600	MYB	PpAspAT6	1214	1228	-	16.3281	1.42E-06	0.0135	GGAGAGGTGGGTGGG
Potri.010G181000	AP2	PpAspAT6	787	806	-	16.2564	1.45E-06	0.00185	GATAAAAAAAAAAAAAAAAA
Potri.019G073300	ERF	PpAspAT6	947	961	+	16.2656	1.50E-06	0.0205	GGTGGGGGAGGCGGC
Potri.018G021900	ERF	PpAspAT6	946	964	+	15.3281	1.89E-06	0.015	AGGTGGGGGAGGCGGCTCA
Potri.005G224100	MYB	PpAspAT6	1536	1556	+	15.6562	2.04E-06	0.02	GACCGCGCTCGTAACCAACCC
Potri.014G046600	ERF	PpAspAT6	951	965	-	16.0156	2.23E-06	0.0887	TTGAGCCGCCTCCCC
Potri.010G204800	Dof	PpAspAT6	731	751	-	15.2656	2.28E-06	0.00524	TTTTCTTTCTTTCTTTTTGTT
Potri.015G082200	LBD	PpAspAT6	944	964	-	14.1562	2.30E-06	0.0227	TGAGCCGCCTCCCCCACCTAC
Potri.012G083500	LBD	PpAspAT6	944	964	-	14.1562	2.30E-06	0.0227	TGAGCCGCCTCCCCCACCTAC
Potri.003G150800	ERF	PpAspAT6	951	965	+	14.6719	2.32E-06	0.092	GGGGAGGCGGCTCAA

Potri.013G114600	C2H2	PpAspAT6	944	958	-	15.2344	2.55E-06	0.088	GCCTCCCCCACCTAC
Potri.007G036400	Dof	PpAspAT6	734	754	-	14.5	2.55E-06	0.0106	ATCTTTTCTTTCTTTCTTTTT
Potri.002G110900	GATA	PpAspAT6	1485	1499	-	15.4531	2.56E-06	0.101	TCTCGGCCGTTCTTT
Potri.007G093900	MYB	PpAspAT6	1571	1580	-	14.6027	2.60E-06	0.0532	GGTAGGTGAG
Potri.003G077700	ERF	PpAspAT6	947	967	-	14.2812	2.74E-06	0.0255	GCTTGAGCCGCCTCCCCCACC
Potri.019G081500	MYB	PpAspAT6	1571	1581	-	15.6277	2.77E-06	0.0551	GGGTAGGTGAG
Potri.008G081600	MYB	PpAspAT6	1214	1234	-	15.5781	2.83E-06	0.0425	TTCAGTGGAGAGGTGGGTGGG
Potri.013G101100	ERF	PpAspAT6	940	959	-	14.6562	2.89E-06	0.0164	CGCCTCCCCCACCTACTACA
Potri.012G081300	Dof	PpAspAT6	839	859	-	14.5938	2.94E-06	0.0117	AAAGAAATTAAAAAGAAAAAA
Potri.010G181000	AP2	PpAspAT6	727	746	+	15.4231	3.00E-06	0.00284	gaaaaacaaaaagaaagaaa
Potri.010G101400	BBR-BPC	PpAspAT6	727	750	+	8	3.05E-06	0.0171	gaaaaacaaaaagaaagaaagaaa
Potri.012G081300	Dof	PpAspAT6	725	745	+	14.5469	3.11E-06	0.0117	aggaaaaacaaaaagaaagaa
Potri.002G069500	bZIP	PpAspAT6	1556	1567	-	15.7812	3.16E-06	0.126	TGGCCAGCTGGG
Potri.007G007900	MYB	PpAspAT6	1547	1559	-	11.7215	3.23E-06	0.0441	TGGGGGTTGGTTA
Potri.017G027400	bZIP	PpAspAT6	1556	1566	+	14.9589	3.70E-06	0.14	CCCAGCTGGCC
Potri.018G021900	ERF	PpAspAT6	949	967	+	14.0469	3.76E-06	0.0213	TGGGGGAGGCGGCTCAAGC
Potri.001G267300	MYB	PpAspAT6	1572	1582	-	14.5312	4.21E-06	0.0826	GGGGTAGGTGA
Potri.014G074200	MIKC_MADS	PpAspAT6	785	805	+	15.0145	4.28E-06	0.00385	GttttttttttttttttttAT
Potri.002G151700	MIKC_MADS	PpAspAT6	785	805	+	15.0145	4.28E-06	0.0038	GttttttttttttttttttAT
Potri.004G086300	MYB	PpAspAT6	941	953	+	15.2405	4.39E-06	0.0581	GTAGTAGGTGGGG
Potri.013G114600	C2H2	PpAspAT6	1574	1588	+	14.5625	4.43E-06	0.088	ACCTACCCCGTTTAA
Potri.010G181000	AP2	PpAspAT6	1241	1260	-	14.8462	4.77E-06	0.0043	TGTAAAAAAAAAAAAAAAAA
Potri.019G081100	C2H2	PpAspAT6	939	957	-	13.4915	5.06E-06	0.0246	CCTCCCCCACCTACTACAT
Potri.010G177100	LBD	PpAspAT6	946	966	-	13.0312	5.60E-06	0.0443	CTTGAGCCGCCTCCCCCACCT
Potri.008G079800	LBD	PpAspAT6	946	966	-	13.0312	5.60E-06	0.0443	CTTGAGCCGCCTCCCCCACCT
Potri.014G074200	MIKC_MADS	PpAspAT6	1237	1257	+	14.6667	5.79E-06	0.00466	TCACttttttttttttttttt
Potri.002G151700	MIKC_MADS	PpAspAT6	1237	1257	+	14.6667	5.79E-06	0.00461	TCACttttttttttttttttt
Potri.013G067500	MYB	PpAspAT6	938	956	-	14.7188	5.82E-06	0.0768	CTCCCCCACCTACTACATA
Potri.003G034200	Dof	PpAspAT6	836	856	-	13.8125	5.87E-06	0.0169	GAAATTAAAAAGAAAAAAAAA
Potri.004G174400	MYB	PpAspAT6	938	952	+	13.7656	6.00E-06	0.059	TATGTAGTAGGTGGG
Potri.001G336700	MYB	PpAspAT6	940	952	-	14.7941	6.01E-06	0.0587	CCCACCTACTACA
Potri.010G006800	ERF	PpAspAT6	956	963	-	14.7596	6.17E-06	0.246	GAGCCGCC
Potri.013G001000	MYB	PpAspAT6	1571	1585	+	14.4375	6.72E-06	0.0397	CTCACCTACCCCGTT
Potri.010G181000	AP2	PpAspAT6	1390	1409	-	14.359	6.92E-06	0.00562	AATGAATAGAAAAAAAAAAG
Potri.017G027400	bZIP	PpAspAT6	1555	1565	-	13.411	7.03E-06	0.14	GCCAGCTGGGG
Potri.010G181000	AP2	PpAspAT6	723	742	+	14.2949	7.26E-06	0.00562	aaaggaaaaacaaaaagaaa
Potri.010G181000	AP2	PpAspAT6	786	805	-	14.2692	7.40E-06	0.00562	ATAAAAAAAAAAAAAAAAAA
Potri.001G154200	ERF	PpAspAT6	952	966	-	12.4688	7.70E-06	0.0611	CTTGAGCCGCCTCCC
Potri.017G082500	MYB	PpAspAT6	1567	1585	-	14.2344	8.12E-06	0.0642	AACGGGGTAGGTGAGAGCT
Potri.019G081100	C2H2	PpAspAT6	948	966	-	12.6186	8.26E-06	0.0356	CTTGAGCCGCCTCCCCCAC
Potri.013G101100	ERF	PpAspAT6	946	965	-	12.8281	8.46E-06	0.0335	TTGAGCCGCCTCCCCCACCT
Potri.013G001000	MYB	PpAspAT6	938	952	-	14.1719	8.48E-06	0.0415	CCCACCTACTACATA
Potri.007G007900	MYB	PpAspAT6	1215	1227	-	8.41772	8.49E-06	0.0561	GAGAGGTGGGTGG
Potri.009G053900	MYB	PpAspAT6	1572	1581	-	14.2788	8.70E-06	0.173	GGGTAGGTGA
Potri.011G167600	MYB	PpAspAT6	1570	1584	-	13.8438	8.74E-06	0.337	ACGGGGTAGGTGAGA
Potri.018G028000	ERF	PpAspAT6	950	970	-	9.20588	9.08E-06	0.0326	CCTGCTTGAGCCGCCTCCCCC
Potri.002G193000	WRKY	PpAspAT6	1447	1454	+	15.4149	9.13E-06	0.119	AGTCAACG
Potri.001G094800	ERF	PpAspAT6	956	963	-	14.5426	9.25E-06	0.369	GAGCCGCC
Potri.007G036400	Dof	PpAspAT6	721	741	-	13.3906	9.28E-06	0.0267	TTCTTTTTGTTTTTCCTTTCC
Potri.002G198100	MYB	PpAspAT6	1572	1581	+	14.5	9.61E-06	0.383	TCACCTACCC
Potri.008G081600	MYB	PpAspAT6	1571	1591	-	14.0938	9.75E-06	0.0951	GTCTTAAACGGGGTAGGTGAG
Potri.014G025200	ERF	PpAspAT7	10	22	-	19.2344	1.53E-07	0.00304	GAGTCGGTGGTGG
Potri.004G056900	Dof	PpAspAT7	275	295	+	16.375	3.61E-07	0.0034	ATaaaaaaaaaaaaGTGCATG
Potri.016G053200	ERF	PpAspAT7	10	20	+	16.9219	9.88E-07	0.0196	CCACCACCGAC
Potri.018G021900	ERF	PpAspAT7	9	27	-	16.2969	1.09E-06	0.0108	TTGTTGAGTCGGTGGTGGA
Potri.008G073600	ERF	PpAspAT7	9	29	-	15.5147	1.20E-06	0.00677	CATTGTTGAGTCGGTGGTGGA
Potri.015G004100	NAC	PpAspAT7	1281	1295	+	16.4062	1.57E-06	0.0614	CTTGGCTGCTAAGCA
Potri.012G007500	NAC	PpAspAT7	1281	1295	+	16.4062	1.57E-06	0.0599	CTTGGCTGCTAAGCA
Potri.002G141200	ERF	PpAspAT7	10	24	-	16.75	1.60E-06	0.0318	TTGAGTCGGTGGTGG
Potri.005G140900	ERF	PpAspAT7	7	21	+	16.5469	1.66E-06	0.022	GATCCACCACCGACT
Potri.002G026700	BBR-BPC	PpAspAT7	1003	1023	-	9.32877	1.75E-06	0.0657	TTAATTCTCTATCTCTCTCAA
Potri.005G233300	ERF	PpAspAT7	7	21	+	15.4219	2.39E-06	0.0237	GATCCACCACCGACT
Potri.002G085600	ERF	PpAspAT7	1	20	+	15.6719	2.40E-06	0.0317	AGCAATGATCCACCACCGAC
Potri.010G101400	BBR-BPC	PpAspAT7	995	1018	+	8.20312	2.82E-06	0.0171	gaagaaaattgagagagatagaga
Potri.019G073300	ERF	PpAspAT7	9	23	-	14.8281	3.46E-06	0.0205	TGAGTCGGTGGTGGA
Potri.018G028000	ERF	PpAspAT7	9	29	+	10.8676	4.39E-06	0.0193	TCCACCACCGACTCAACAATG
Potri.019G073300	ERF	PpAspAT7	12	26	-	14.3125	4.64E-06	0.0205	TGTTGAGTCGGTGGT
Potri.010G229700	NAC	PpAspAT7	1278	1297	-	14.4658	5.31E-06	0.105	GTTGCTTAGCAGCCAAGAAA
Potri.002G009700	Nin-like	PpAspAT7	1219	1233	-	14.5882	5.74E-06	0.228	GAAGCAGCAACAGTT
Potri.014G099900	ERF	PpAspAT7	12	26	-	14.6562	5.74E-06	0.076	TGTTGAGTCGGTGGT
Potri.006G080300	ERF	PpAspAT7	13	32	+	14	7.02E-06	0.0927	CCACCGACTCAACAATGTAA
Potri.002G113300	TALE	PpAspAT7	1221	1240	+	13.6667	7.07E-06	0.0501	CTGTTGCTGCTTCTTACTGC
Potri.010G204800	Dof	PpAspAT7	584	604	+	14.0312	7.26E-06	0.0109	ttgtcttttttgtttttattt
Potri.006G138800	ERF	PpAspAT7	10	23	-	14.3594	7.46E-06	0.0989	TGAGTCGGTGGTGG
Potri.002G026700	BBR-BPC	PpAspAT7	1001	1021	-	4.91781	8.04E-06	0.0826	AATTCTCTATCTCTCTCAATT
Potri.002G026700	BBR-BPC	PpAspAT7	999	1019	-	4.84932	8.22E-06	0.0826	TTCTCTATCTCTCTCAATTTT
Potri.017G084600	Dof	PpAspAT7	283	292	+	11.4655	8.53E-06	0.332	aaaaaaGTGC
Potri.011G169300	WRKY	PpAspAT7	215	222	+	13.9362	8.85E-06	0.353	
Potri.002G061300	NAC	PpAspAT7	1275	1293	+	12.1406	9.43E-06	0.187	TTCTTTCTTGGCTGCTAAG
Potri.007G012100	WOX	PpAspAT7	1031	1041	+	14.1139	9.55E-06	0.179	ACAATCATTCA
Potri.010G176600	NAC	PpAspAT7	1278	1298	-	13.5312	9.64E-06	0.382	TGTTGCTTAGCAGCCAAGAAA
Potri.002G141200	ERF	PpAspAT8	530	544	-	19.3906	9.35E-08	0.00371	ATGTGTCGGTGGTAG
Potri.014G025200	ERF	PpAspAT8	530	542	-	19.5625	1.04E-07	0.00304	GTGTCGGTGGTAG
Potri.014G099900	ERF	PpAspAT8	532	546	-	19.5625	1.31E-07	0.0052	ACATGTGTCGGTGGT
Potri.005G140900	ERF	PpAspAT8	527	541	+	19.2344	1.81E-07	0.00713	TCACTACCACCGACA
Potri.003G034200	Dof	PpAspAT8	486	506	+	15.9062	3.40E-07	0.00301	TAAGAGaaaaagaaaaaaaaa
Potri.014G074200	MIKC_MADS	PpAspAT8	486	506	-	17.3043	3.66E-07	0.000629	TTTTTTTTTCTTTTTCTCTTA
Potri.002G151700	MIKC_MADS	PpAspAT8	486	506	-	17.3043	3.66E-07	0.000621	TTTTTTTTTCTTTTTCTCTTA
Potri.003G040100	C2H2	PpAspAT8	581	598	+	18.3125	4.24E-07	0.0162	AACGACACGACaaaaaaa
Potri.003G036900	C2H2	PpAspAT8	581	598	+	18.3125	4.24E-07	0.0162	AACGACACGACaaaaaaa
Potri.006G080300	ERF	PpAspAT8	533	552	+	18.2969	4.48E-07	0.00887	CCACCGACACATGTCATATC
Potri.010G204800	Dof	PpAspAT8	481	501	-	16.6562	4.96E-07	0.00228	TTTTCTTTTTCTCTTATTCCT
Potri.012G081300	Dof	PpAspAT8	483	503	+	15.8906	5.25E-07	0.00432	GAATAAGAGaaaaagaaaaaa
Potri.007G135000	C2H2	PpAspAT8	581	600	+	17.9844	5.56E-07	0.0211	AACGACACGACaaaaaaaTA
Potri.010G181000	AP2	PpAspAT8	481	500	+	16.641	1.01E-06	0.00156	AGGAATAAGAGaaaaagaaa
Potri.006G129300	C2H2	PpAspAT8	581	600	-	16.8281	1.21E-06	0.0455	TATTTTTTTGTCGTGTCGTT
Potri.005G125600	C2H2	PpAspAT8	581	597	+	16.875	1.30E-06	0.0494	AACGACACGACaaaaaa
Potri.005G233300	ERF	PpAspAT8	527	541	+	16.4219	1.34E-06	0.0177	TCACTACCACCGACA
Potri.008G032300	C2H2	PpAspAT8	1454	1464	+	13.0625	1.66E-06	0.0661	CAGTGGAGGGG
Potri.002G085600	ERF	PpAspAT8	521	540	+	16.2031	1.75E-06	0.0317	ATTGTCTCACTACCACCGAC
Potri.010G099200	C2H2	PpAspAT8	581	596	-	16.2603	1.85E-06	0.0703	TTTTTGTCGTGTCGTT
Potri.010G181000	AP2	PpAspAT8	487	506	+	15.8718	2.05E-06	0.00244	AAGAGaaaaagaaaaaaaaa

Potri.010G099100	C2H2	PpAspAT8	581	597	+	15.9844	2.22E-06	0.0814	AACGACACGACaaaaaa
Potri.010G181000	AP2	PpAspAT8	405	424	+	15.7308	2.32E-06	0.00257	aagaaaaaaaataaaaaaaa
Potri.004G056900	Dof	PpAspAT8	483	503	+	14.875	2.43E-06	0.0152	GAATAAGAGaaaaagaaaaaa
Potri.002G114800	AP2	PpAspAT8	1233	1253	-	13.9767	2.59E-06	0.102	GCACACAGTTCCCAAGTATTT
Potri.014G074200	MIKC_MADS	PpAspAT8	1577	1597	-	15.5217	2.69E-06	0.00254	CTTTTCCTTCTGCTTCTTCCA
Potri.002G151700	MIKC_MADS	PpAspAT8	1577	1597	-	15.5217	2.69E-06	0.00251	CTTTTCCTTCTGCTTCTTCCA
Potri.016G112300	MYB	PpAspAT8	93	113	+	15.2278	3.65E-06	0.135	aagaatgaggataaaaatcaa
Potri.014G074100	MIKC_MADS	PpAspAT8	51	69	+	15.1094	3.66E-06	0.0988	tatccaaaataagaaaaga
Potri.019G073300	ERF	PpAspAT8	532	546	-	14.7188	3.69E-06	0.0205	ACATGTGTCGGTGGT
Potri.008G131700	GRAS	PpAspAT8	487	506	+	14.7101	3.93E-06	0.0374	AAGAGaaaaagaaaaaaaaa
Potri.004G228800	ARF	PpAspAT8	535	542	+	14.9186	4.42E-06	0.176	ACCGACAC
Potri.003G121200	ERF	PpAspAT8	530	544	-	15.3906	4.54E-06	0.18	ATGTGTCGGTGGTAG
Potri.009G055700	MIKC_MADS	PpAspAT8	49	67	-	14.7188	4.79E-06	0.185	TTTTCTTATTTTGGATACT
Potri.016G053200	ERF	PpAspAT8	530	540	+	13.5	5.79E-06	0.0767	CTACCACCGAC
Potri.014G074200	MIKC_MADS	PpAspAT8	480	500	-	14.5652	6.30E-06	0.00466	TTTCTTTTTCTCTTATTCCTC
Potri.002G151700	MIKC_MADS	PpAspAT8	480	500	-	14.5652	6.30E-06	0.00461	TTTCTTTTTCTCTTATTCCTC
Potri.004G065800	TCP	PpAspAT8	617	624	+	15.5192	6.36E-06	0.127	GGCACCAC
Potri.010G181000	AP2	PpAspAT8	409	428	+	14.4231	6.60E-06	0.00562	aaaaaaataaaaaaaataaa
Potri.001G238400	Dof	PpAspAT8	395	415	-	13.9531	6.82E-06	0.017	TTTTTTTTCTTGATCTTTTTG
Potri.008G131700	GRAS	PpAspAT8	489	508	+	13.9855	7.19E-06	0.039	GAGaaaaagaaaaaaaaaCT
Potri.010G181000	AP2	PpAspAT8	486	505	+	14.2692	7.40E-06	0.00562	TAAGAGaaaaagaaaaaaaa
Potri.017G082900	ZF-HD	PpAspAT8	1482	1496	-	13.1618	7.66E-06	0.288	TTTAATTACTAATTA
Potri.002G113300	TALE	PpAspAT8	1579	1598	-	13.48	7.81E-06	0.0501	CCTTTTCCTTCTGCTTCTTC
Potri.008G131700	GRAS	PpAspAT8	481	500	+	13.8116	8.26E-06	0.0393	AGGAATAAGAGaaaaagaaa
Potri.014G074200	MIKC_MADS	PpAspAT8	404	424	-	14.2029	8.46E-06	0.0056	TTTTTTTTATTTTTTTTCTTG
Potri.002G151700	MIKC_MADS	PpAspAT8	404	424	-	14.2029	8.46E-06	0.00553	TTTTTTTTATTTTTTTTCTTG
Potri.010G204800	Dof	PpAspAT8	408	428	-	13.7812	9.02E-06	0.0111	TTTATTTTTTTTATTTTTTTT
Potri.010G101400	BBR-BPC	PpAspAT8	483	506	+	4.82812	9.69E-06	0.0366	GAATAAGAGaaaaagaaaaaaaaa
Potri.014G074200	MIKC_MADS	PpAspAT9	378	398	+	18.3333	7.82E-08	0.000185	ttttttttttttttttttttt
Potri.014G074200	MIKC_MADS	PpAspAT9	379	399	+	18.3333	7.82E-08	0.000185	ttttttttttttttttttttt
Potri.014G074200	MIKC_MADS	PpAspAT9	380	400	+	18.3333	7.82E-08	0.000185	ttttttttttttttttttttt
Potri.014G074200	MIKC_MADS	PpAspAT9	381	401	+	18.3333	7.82E-08	0.000185	ttttttttttttttttttttt
Potri.014G074200	MIKC_MADS	PpAspAT9	382	402	+	18.3333	7.82E-08	0.000185	ttttttttttttttttttttt
Potri.002G151700	MIKC_MADS	PpAspAT9	378	398	+	18.3333	7.82E-08	0.000182	ttttttttttttttttttttt
Potri.002G151700	MIKC_MADS	PpAspAT9	379	399	+	18.3333	7.82E-08	0.000182	ttttttttttttttttttttt
Potri.002G151700	MIKC_MADS	PpAspAT9	380	400	+	18.3333	7.82E-08	0.000182	ttttttttttttttttttttt
Potri.002G151700	MIKC_MADS	PpAspAT9	381	401	+	18.3333	7.82E-08	0.000182	ttttttttttttttttttttt
Potri.002G151700	MIKC_MADS	PpAspAT9	382	402	+	18.3333	7.82E-08	0.000182	ttttttttttttttttttttt
Potri.014G074200	MIKC_MADS	PpAspAT9	383	403	+	17.942	1.48E-07	0.000328	ttttttttttttttttttttg
Potri.002G151700	MIKC_MADS	PpAspAT9	383	403	+	17.942	1.48E-07	0.000324	ttttttttttttttttttttg
Potri.010G181000	AP2	PpAspAT9	378	397	-	17.6282	3.71E-07	0.000913	AAAAAAAAAAAAAAAAAAAA
Potri.010G181000	AP2	PpAspAT9	379	398	-	17.6282	3.71E-07	0.000913	AAAAAAAAAAAAAAAAAAAA
Potri.010G181000	AP2	PpAspAT9	380	399	-	17.6282	3.71E-07	0.000913	AAAAAAAAAAAAAAAAAAAA
Potri.010G181000	AP2	PpAspAT9	381	400	-	17.6282	3.71E-07	0.000913	AAAAAAAAAAAAAAAAAAAA
Potri.010G181000	AP2	PpAspAT9	382	401	-	17.6282	3.71E-07	0.000913	AAAAAAAAAAAAAAAAAAAA
Potri.010G181000	AP2	PpAspAT9	383	402	-	17.6282	3.71E-07	0.000913	AAAAAAAAAAAAAAAAAAAA
Potri.002G113300	TALE	PpAspAT9	532	551	-	18.3333	3.73E-07	0.0064	GTTCCGCCCCCCCTCCCGGG
Potri.002G113300	TALE	PpAspAT9	530	549	-	18.2667	3.92E-07	0.0064	TCCGCCCCCCCTCCCGGGTT
Potri.002G113300	TALE	PpAspAT9	533	552	-	17.9333	4.99E-07	0.0064	TGTTCCGCCCCCCCTCCCGG
Potri.001G188800	HD-ZIP	PpAspAT9	1280	1294	-	16.7385	6.39E-07	0.0119	ATATGTAATGATGAC
Potri.001G238400	Dof	PpAspAT9	54	74	+	15.6406	1.01E-06	0.00474	TTCTCCTATTTTTACTTTATG
Potri.002G113300	TALE	PpAspAT9	534	553	-	16.3867	1.42E-06	0.0137	TTGTTCCGCCCCCCCTCCCG
Potri.010G204800	Dof	PpAspAT9	378	398	+	15.3438	2.11E-06	0.00516	ttttttttttttttttttttt
Potri.010G204800	Dof	PpAspAT9	379	399	+	15.3438	2.11E-06	0.00516	ttttttttttttttttttttt
Potri.010G204800	Dof	PpAspAT9	380	400	+	15.3438	2.11E-06	0.00516	ttttttttttttttttttttt
Potri.010G204800	Dof	PpAspAT9	381	401	+	15.3438	2.11E-06	0.00516	ttttttttttttttttttttt
Potri.010G204800	Dof	PpAspAT9	382	402	+	15.3438	2.11E-06	0.00516	ttttttttttttttttttttt
Potri.014G074200	MIKC_MADS	PpAspAT9	384	404	+	15.7391	2.18E-06	0.00216	tttttttttttttttttttga
Potri.002G151700	MIKC_MADS	PpAspAT9	384	404	+	15.7391	2.18E-06	0.00214	tttttttttttttttttttga
Potri.010G181000	AP2	PpAspAT9	384	403	-	15.7179	2.34E-06	0.00257	CAAAAAAAAAAAAAAAAAAA
Potri.005G139700	bHLH	PpAspAT9	406	414	-	15.1702	3.19E-06	0.127	CCCACGTGA
Potri.001G015900	EIL	PpAspAT9	350	370	+	15.4051	3.21E-06	0.127	TTGTCTAGGTACTAGGTCAAT
Potri.015G023200	ERF	PpAspAT9	534	554	-	12.8824	3.46E-06	0.0196	CTTGTTCCGCCCCCCCTCCCG
Potri.001G188800	HD-ZIP	PpAspAT9	1727	1741	-	15.2769	3.52E-06	0.0437	ATATGTAATGATGGC
Potri.010G137600	bHLH	PpAspAT9	407	421	+	15.4375	3.59E-06	0.143	cacgtggggtgtccg
Potri.007G036400	Dof	PpAspAT9	53	73	+	14.1875	3.75E-06	0.014	TTTCTCCTATTTTTACTTTAT
Potri.014G074200	MIKC_MADS	PpAspAT9	961	981	-	15.058	4.12E-06	0.0038	TTTTATTTTTTTTCTTTGCTT
Potri.002G151700	MIKC_MADS	PpAspAT9	961	981	-	15.058	4.12E-06	0.00375	TTTTATTTTTTTTCTTTGCTT
Potri.005G207200	bHLH	PpAspAT9	406	413	+	15.9559	4.42E-06	0.176	tcacgtgg
Potri.015G106900	LFY	PpAspAT9	452	470	+	13.2059	6.00E-06	0.119	cacggcccactggacatcc
Potri.015G106900	LFY	PpAspAT9	452	470	-	13.2059	6.00E-06	0.119	GGATGTCCAGTGGGCCGTG
Potri.T044100	TCP	PpAspAT9	162	169	-	15.7212	6.36E-06	0.0843	GACCCCAC
Potri.014G066500	bHLH	PpAspAT9	406	413	-	14.8191	6.57E-06	0.262	CCACGTGA
Potri.006G084200	Dof	PpAspAT9	60	74	+	13.7344	7.29E-06	0.068	TATTTTTACTTTATG
Potri.009G064700	bHLH	PpAspAT9	1925	1933	-	15.1489	7.36E-06	0.293	GCCACTTGT
Potri.003G207200	bHLH	PpAspAT9	1925	1933	-	15.1489	7.36E-06	0.293	GCCACTTGT
Potri.002G149000	LBD	PpAspAT9	533	551	-	13.9219	7.61E-06	0.301	GTTCCGCCCCCCCTCCCGG
Potri.005G001800	bHLH	PpAspAT9	406	415	-	14.8594	7.82E-06	0.312	CCCCACGTGA
Potri.010G204800	Dof	PpAspAT9	960	980	-	13.9375	7.88E-06	0.0109	TTTATTTTTTTTCTTTGCTTT
Potri.010G204800	Dof	PpAspAT9	383	403	+	13.9219	7.99E-06	0.0109	ttttttttttttttttttttg
Potri.002G113300	TALE	PpAspAT9	531	550	-	13.16	9.25E-06	0.0509	TTCCGCCCCCCCTCCCGGGT

Table S5. Conserved motifs of AspATs deduced by MEME analysis

Name	E-value	Sites	Length	MEME best matched sequences	AA Residues	Function of AA residues
Motif 1	1.10E-185	8	50	TYRYYDPKTKGLDFQGLLDDIKAAPSGSFVLLHACAHNPTGVDPTPEQWE	N	PLP binding site
Motif 2	3.30E-154	7	50	WSHILKQIGMFTFTGLNPEQVDFMTKEYHIYMTSDGRISMAGLSSKTVPY	Unknown	Unknown
Motif 3	2.20E-114	7	41	RVKSQLKLIARPMYSNPPVH**G**AS**I**VAAILGDPDLFNEWTVE	G I	homodimer interface
Motif 4	5.90E-153	7	50	PFFDVA**Y**QGFASGSLDADAQSVRMFVADGGELLVAQ**S**Y**AK**NMGLY**GER**VG	Y S AK G[N]ER	PLP binding site; catalytic residue; Homodimer interface
Motif 5	1.80E-151	8	50	IKENRVATVQCLS**GTG**SLRLGAEFLARYYPQSQIYIPSPT**W**GNHHNIFRD	GTG W	Homodimer interface; PLP binding site
Motif 6	2.30E-145	8	50	PAPEDPILGVTEAFLADPSPKKLNLGVGAYRTEEGKPVVLNVVRKAEQLL	Unknown	Unknown
Motif 7	2.60E-30	7	21	KAMADRIISMRQKLFDALSAR	Unknown	Unknown
Motif 8	9.80E-32	7	21	PIEGLAAFNKLSAQLLFGADS	Unknown	Unknown
Motif 9	5.30E-20	2	50	HPRLLVLSDEIYEHIIYAPATHISFASLPGMWERTLTVNGFSKAFAMTGW	Unknown	specific for Iβ members，Unknown
Motif 10	1.40E-17	2	50	KEENGISYKPDQILVSNGAKQSIYQAILAVCSPGDEVIIPAPFWVSYPEM	Unknown	specific for Iβ members，Unknown
Motif 11	7.90E-16	10	11	LNILCSDADVA	Unknown	Unknown
Motif 12	1.40E-13	2	50	VPVIRLAAGEPDFDTPVVIAEAGINAIREGFTRYTPNAGTQELRVAICQK	Unknown	specific for Iβ members，Unknown
Motif 13	3.50E-13	2	50	FYLFIDFSSYYGAEVEGFGKIEDSDALCRYLLDQAQVALVPGVAFGDDSC	Unknown	specific for Iβ members，Unknown
Motif 14	1.30E-09	2	50	QEILKGKARLGSGSVSTLFNKEKGNPFIKKKSFGRISMTVAVNVSRFEGI	Unknown	specific for Iα-C AspAT，Unknown
Motif 15	1.30E-08	2	50	HCFYFKPLEATRRSQLSRISVVVKAESRSEEMQLDISLSPRVNAVKPSKT	Unknown	specific for Iβ members，Unknown

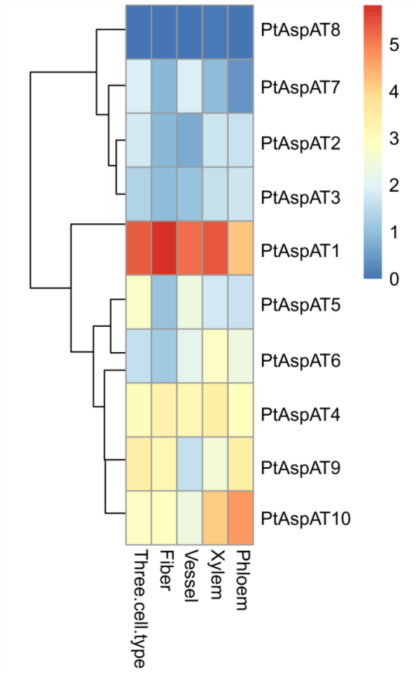

Figure S1. Transcriptomic analysis of *PtAspATs* in vascular tissues. Data was collected from GEO Datasets (GSE81077), including phloems, stem differentiating xylems, vessels, fibers, and a mixture of three cell types (fibers, vessels, and ray cells). FPKM (fragments per kilobase per million reads) values of *PtAspAT* genes were transformed by log2 and displayed in heat map.

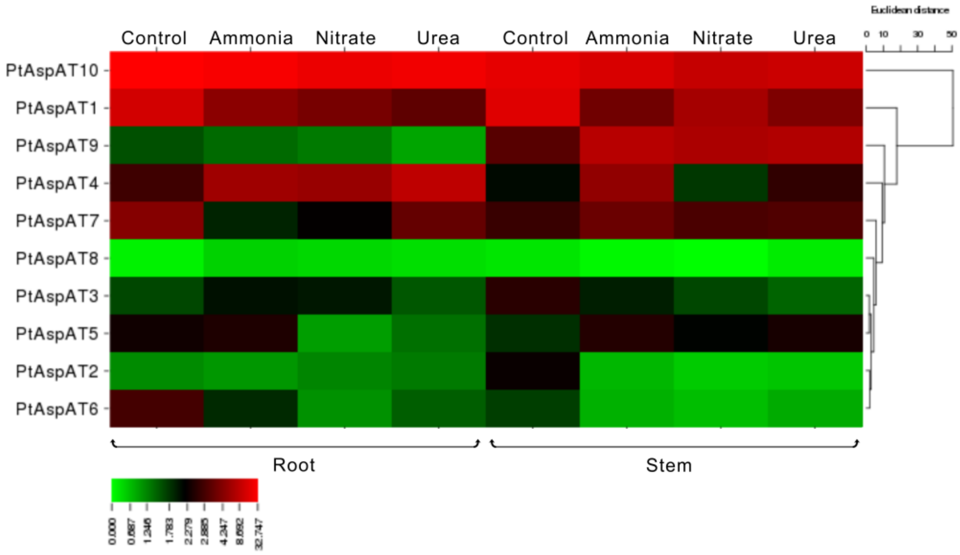

Figure S2. Transcriptomic analysis of *PtAspATs* in response to various nitrogen resources. The RNA-seq results were given in FPKM (fragments per kilobase per million reads) expression values.

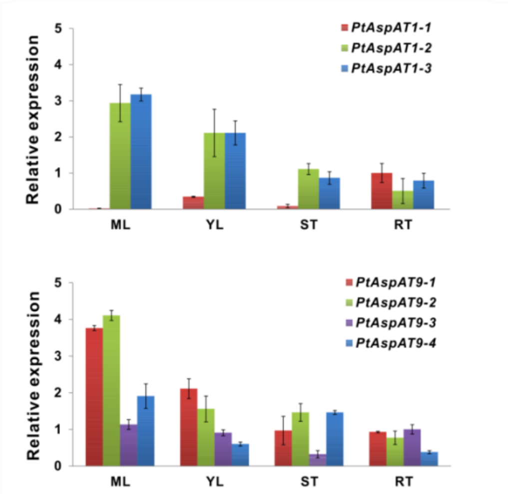

Figure S3. Expression analysis of the transcript variants of *PtAspAT1* and *PtAspAT9* in different tissues. Expression was evaluated by qRT-PCR. Samples were harvested from ML (mature leaves), YL (young leaves), RT (roots) and ST (stems). Data represent mean values ±SE of at least three independent biological replicates for qRT-PCR. *PtActin*, *PtUBIC*, and *PtEF1α* were used as reference genes.

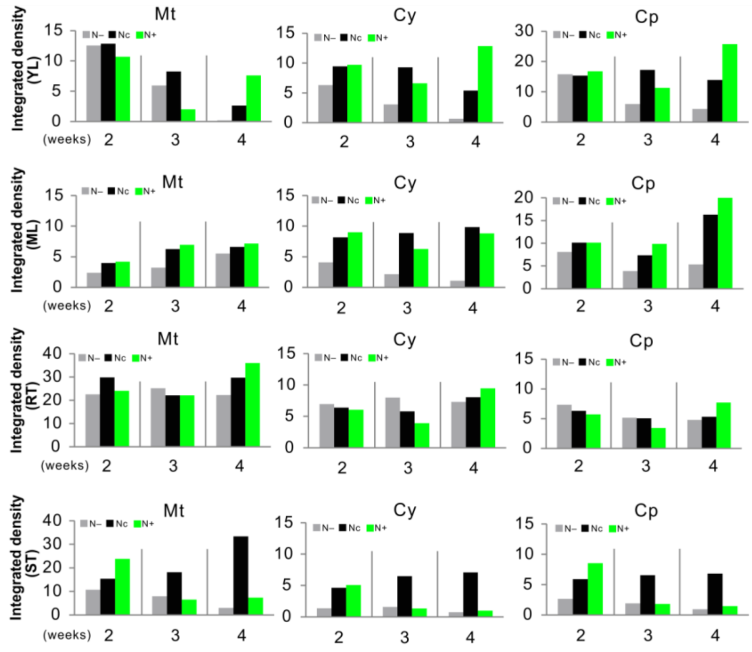

Figure S4. Effects on enzyme activities in various tissues of *'Nanlin895'*. Enzyme activities were assayed by in-gel analyses under 0 mM (N-), 2 mM (Nc) and 10 mM (N+) nitrogen treatments for 2-4 weeks. Samples were harvested from YL (young leaves), ML (mature leaves), RT (roots), and ST (stems). Mt, Cy, and Cp indicate mitochondria, cytosol and chloroplast, respectively.

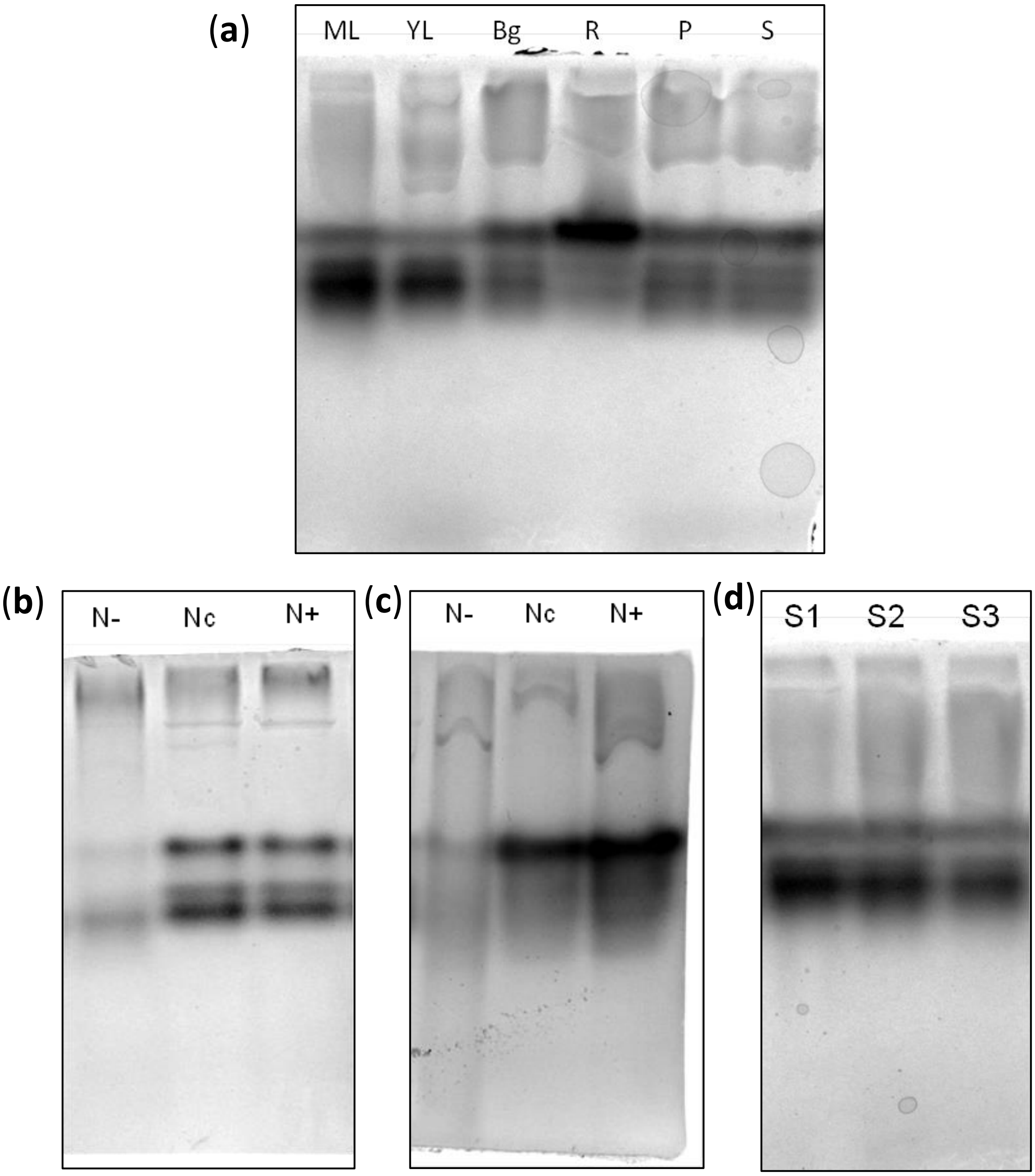

Figure S5. The entire native PAGE gel images showing AspAT activities that were compatible with Figure 8. (**a**) Gel activities from different tissues (**b**) N treated plant leaves (**c**) N treated plant roots (**d**) seasonal senescent leaves from poplar plants.