Supplementary Materials: Identification of Differentially Expressed Genes between "Honeycrisp" and "Golden Delicious" Apple Fruit Tissues Reveal Candidates for Crop Improvement

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Table S1. Subset of differentially expressed transcripts from differential display study, confirmed via qRT-PCR, from apple genome release 1.0.

Gene Model ID	Gene Model ID
MDP0000200646	MDP0000172863
MDP0000037251	MDP0000180389
MDP0000875654	MDP0000523205
MDP0000296716	MDP0000138340
MDP0000128468	MDP0000166116
MDP0000712586	MDP0000220601
MDP0000618650	MDP0000237908
MDP0000920333	MDP0000273484
MDP0000152947	MDP0000286959
MDP0000883284	MDP0000292888
MDP0000253074	MDP0000320533
MDP0000213808	MDP00005772242
MDP0000547450	MDP0000697474
MDP0000310811	MDP0000233229
MDP0000232309	MDP0000255887
MDP0000161275	MDP0000901731
MDP0000176723	
MDP0000304285	

Table S2. BLAST output from Blast2GO against the nr-database using sequences of apple genome (v1.0) predicted genes against sequences with highest similarity to sequenced differential display fragments. SeqName—name of sequence from apple genome predicted gene set, Description—annotation, Length—length of query in base pairs, *e*-Value—expected value, Sim mean—percentage of sequence identity. Differential display fragment-to-apple genome predicted sequence correlations performed using UCLUST at default parameters in global alignment.

SeqName	Description	Length	*e*-Value	Sim Mean	GO Terms	Enzyme Codes List	InterPro Ids
MDP0000547450	unc93-like protein	1389	0.00E+00	82.35%	C:membrane; P:transport; P:cellular process	-	IPR011701 (PFAM); IPR016196 (SUPERFAMILY); G3DSA:1.20.1250.20 (GENE3D), PTHR23294 (PANTHER), PTHR23294:SF0 (PANTHER), tmhmm (TMHMM)
MDP0000172863	protein	1824	0.00E+00	76.95%	F:nucleotide binding; P:response to biotic stimulus; C:nucleus; P:signal transduction; C:membrane; P:cellular amino acid metabolic process; P:cellular protein modification process; F:receptor activity; F:kinase activity; P:response to stress; C:plastid; C:plasma membrane	EC:2.7.11.0; EC:2.7.10.0	IPR000719 (PROFILE); IPR001245 (PFAM); IPR002290 (SMART); IPR011009 (SUPERFAMILY); IPR020635 (SMART); PR00019 (PRINTS), G3DSA:1.10.510.10 (GENE3D), G3DSA:3.30.200.20 (GENE3D), G3DSA:3.80.10.10 (GENE3D), PTHR24420 (PANTHER), PTHR24420:SF428 (PANTHER), PF13504 (PFAM), PF13855 (PFAM), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM), SSF52058 (SUPERFAMILY)
MDP0000316244	probable adp-ribosylation factor gtpase-activating protein agd15-like	1596	2.20E−87	73.65%	P:signal transduction; F:binding; F:enzyme regulator activity	-	IPR001164 (PRINTS); IPR002068 (PFAM); IPR008978 (SUPERFAMILY); G3DSA:2.60.40.790 (GENE3D), PTHR23180 (PANTHER), PTHR23180:SF31 (PANTHER), tmhmm (TMHMM)
MDP0000320533	proteasome assembly chaperone	390	8.10E−61	78.20%	P:catabolic process; P:lipid metabolic process; P:cellular process; C:intracellular	-	IPR018788 (PFAM); PTHR31051 (PANTHER)
MDP0000161275	mitochondrial substrate carrier family protein	978	1.80E−177	89.30%	C:membrane; C:mitochondrion; P:transport; P:cellular process; F:transporter activity; C:plastid	-	IPR018108 (PFAM); IPR023395 (G3DSA:1.50.40.GENE3D); PTHR24089 (PANTHER), PTHR24089:SF22 (PANTHER)
MDP0000232309	transmembrane bax inhibitor motif-containing protein 4	759	4.50E−117	80.35%	C:membrane; P:cellular component organization; P:transport; P:cellular process; C:intracellular	-	IPR006214 (PANTHER); PTHR23291:SF24 (PANTHER), tmhmm (TMHMM)

Table S2. *Cont.*

SeqName	Description	Length	*e*-Value	Sim Mean	GO Terms	Enzyme Codes List	InterPro IDs
MDP0000875654	hydroquinone glucosyltransferase	1419	0.00E+00	79.50%	P:secondary metabolic process; P:biological_process; P:catabolic process; P:biosynthetic process; P:transport; P:response to stress; C:intracellular; P:cellular process; P:response to abiotic stimulus; P:cell death; P:response to external stimulus; P:cellular amino acid metabolic process; F:transferase activity	EC:2.4.1.218	IPR002213 (PANTHER); G3DSA:3.40.50.2000 (GENE3D), PTHR11926:SF15 (PANTHER), SSF53756 (SUPERFAMILY)
MDP0000883284	PREDICTED: uncharacterized protein LOC100248602 [Vitis vinifera]	606	1.60E−04	76%		-	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
MDP0000237908	metallothionein-like protein	201	4.10E−26	79%	F:binding	-	no IPS match
MDP0000310811	cysteine protease inhibitor	501	8.20E−56	81.55%	P:biological_process; P:protein metabolic process; P:catabolic process; F:enzyme regulator activity; F:hydrolase activity	-	IPR000010 (PFAM); IPR018073 (PROSITE); IPR020381 (PRODOM); G3DSA:3.10.450.10 (GENE3D), PTHR11413 (PANTHER), PTHR11413:SF3 (PANTHER), SSF54403 (SUPERFAMILY)
MDP0000584042	protein	951	0.00E+00	80.60%	P:biological_process; F:molecular_function	-	IPR006904 (PANTHER); PTHR16007:SF5 (PANTHER), SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
MDP0000443265	---NA---	366	-	-		-	no IPS match
MDP0000606453	probable nitrite transporter at1g68570-like	1743	0.00E+00	80.25%	C:membrane; P:transport; F:transporter activity	-	IPR000109 (PFAM); IPR016196 (SUPERFAMILY); IPR018456 (PROSITE); G3DSA:1.20.1250.20 (GENE3D), PTHR11654 (PANTHER), PTHR11654:SF57 (PANTHER), tmhmm (TMHMM)
MDP0000255887	tir-nbs-lrr resistance protein	3138	5.80E−90	54.15%	F:nucleotide binding; F:ATP binding; P:signal transduction; F:nucleoside-triphosphatase activity; F:ADP binding; P:defense response; C:intracellular	-	IPR000157 (PFAM); IPR000767 (PRINTS); IPR001232 (PANTHER); IPR002182 (PFAM); IPR011333 (G3DSA:3.30.710.GENE3D); IPR016072 (PFAM); IPR016073 (PFAM); G3DSA:3.40.50.10140 (GENE3D), G3DSA:3.80.10.10 (GENE3D), PTHR11165:SF47 (PANTHER), SSF52058 (SUPERFAMILY), SSF52540 (SUPERFAMILY)

Table S2. *Cont.*

SeqName	Description	Length	*e*-Value	Sim Mean	GO Terms	Enzyme Codes List	InterPro IDs
MDP0000138340	nac domain ipr003441	639	3.00E−40	59.90%	P:response to biotic stimulus; P:response to abiotic stimulus; F:transcription factor activity, sequence-specific DNA binding; F:protein binding; P:transcription, DNA-templated; P:multicellular organismal development; F:obsolete transcription regulator activity; P:response to endogenous stimulus; P:response to stress; C:nucleoplasm	-	IPR003441 (PFAM); PTHR31989 (PANTHER), PTHR31989:SF0 (PANTHER)
MDP0000200646	nac domain ipr003441	705	1.20E−38	61.20%	F:transcription factor activity, sequence-specific DNA binding; F:protein binding; P:transcription, DNA-templated; P:multicellular organismal development; P:response to stress; C:nucleoplasm	-	IPR003441 (PFAM); PTHR31989 (PANTHER), PTHR31989:SF0 (PANTHER)
MDP0000618650	nac domain ipr003441	1494	0.00E+00	74.05%	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; C:cytoplasm; P:multicellular organismal development; C:nucleoplasm	-	IPR003441 (PFAM); PTHR31079 (PANTHER), PTHR31079:SF0 (PANTHER)
MDP0000128468	abscisic acid stress ripening protein homolog	627	1.10E−12	62.75%	P:response to stress	-	IPR003496 (PFAM)
MDP0000296716	ethylene-responsive transcription factor rap2-7-like	1392	1.40E−132	64.15%	P:biological_process; P:transcription, DNA-templated; P:multicellular organismal development; P:post-embryonic development; P:anatomical structure morphogenesis; P:reproduction	-	IPR001471 (PRINTS); IPR016177 (SUPERFAMILY); PTHR32467 (PANTHER), PTHR32467:SF0 (PANTHER)
MDP0000234325	wwe protein-protein interaction domain family protein	1908	0.00E+00	60.85%	P:embryo development; P:biological_process; P:signal transduction; P:post-embryonic development; P:anatomical structure morphogenesis; P:biosynthetic process; P:transport; P:response to stress; P:cellular process; P:reproduction; P:response to biotic stimulus; P:carbohydrate metabolic process; C:nucleus; P:response to abiotic stimulus; F:protein binding; P:cell death; C:cytoplasm; P:response to endogenous stimulus; P:cellular component organization	-	IPR004170 (PFAM); IPR012317 (PROFILE); IPR022003 (PFAM); G3DSA:3.90.228.10 (GENE3D), PTHR32263 (PANTHER), PTHR32263:SF0 (PANTHER), SSF56399 (SUPERFAMILY)

Table S2. *Cont.*

SeqName	Description	Length	*e*-Value	Sim Mean	GO Terms	Enzyme Codes List	InterPro IDs
MDP0000037251	cinnamyl alcohol dehydrogenase-like protein	1083	0.00E+00	88.60%	P:secondary metabolic process; F:nucleotide binding; P:response to biotic stimulus; P:cell death; F:catalytic activity; P:catabolic process; P:cellular amino acid metabolic process; P:metabolic process; P:biosynthetic process; F:binding; P:response to stress; P:cellular process	EC:1.1.1.90; EC:1.1.1.195	IPR002085 (PANTHER); IPR002328 (PROSITE); IPR011032 (SUPERFAMILY); IPR013149 (PFAM); IPR013154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020843 (SMART); G3DSA:3.90.180.10 (GENE3D), PTHR11695:SF261 (PANTHER), SSF51735 (SUPERFAMILY)
MDP0000580900	porin voltage-dependent anion-selective channel protein	846	1.60E−157	82.45%	P:biological_process; P:generation of precursor metabolites and energy; P:catabolic process; P:transport; C:vacuole; P:cellular process; C:plastid; F:transporter activity; C:plasma membrane; P:response to biotic stimulus; P:carbohydrate metabolic process; C:cell wall; C:membrane; C:mitochondrion	-	IPR001925 (PFAM); PTHR11743 (PANTHER), PTHR11743:SF14 (PANTHER)
MDP0000129664	3-ketoacyl- thiolase	2067	0.00E+00	91.55%	P:secondary metabolic process; P:protein metabolic process; P:catabolic process; P:signal transduction; P:metabolic process; P:biosynthetic process; C:nucleolus; C:vacuole; P:response to stress; P:cellular process; C:plastid; C:plasma membrane; P:response to biotic stimulus; C:peroxisome; P:response to external stimulus; C:membrane; P:lipid metabolic process; P:response to endogenous stimulus; C:mitochondrion; P:cellular amino acid metabolic process; P:cellular component organization; C:cytosol; F:transferase activity	EC:2.3.1.16	IPR002155 (PANTHER); IPR016038 (G3DSA:3.40.47.GENE3D); IPR016039 (SUPERFAMILY); IPR020610 (PROSITE); IPR020613 (PROSITE); IPR020615 (PROSITE); IPR020616 (PFAM); IPR020617 (PFAM); PTHR18919:SF15 (PANTHER)
MDP0000180389	disease resistance protein at3g14460-like	4335	0.00E+00	57.25%	F:ADP binding; P:defense response	-	IPR000767 (PRINTS); IPR001611 (PFAM); IPR002182 (PFAM); IPR025875 (PFAM); G3DSA:3.40.50.300 (GENE3D), G3DSA:3.80.10.10 (GENE3D), PTHR23155 (PANTHER), PTHR23155:SF138 (PANTHER), SignalP-NN(euk) (SIGNALP), SSF52047 (SUPERFAMILY), SSF52058 (SUPERFAMILY), SSF52540 (SUPERFAMILY)
MDP0000286959	dentin sialophospho protein	5976	0.00E+00	58.55%	C:plasma membrane	-	PTHR31267 (PANTHER)

Table S2. *Cont.*

SeqName	Description	Length	*e*-Value	Sim Mean	GO Terms	Enzyme Codes List	InterPro IDs
MDP0000220601	zinc finger ccch domain-containing protein 53-like	2217	0.00E+00	63.40%	F:nucleic acid binding; F:binding	-	IPR000504 (SMART); IPR000571 (PFAM); IPR012677 (G3DSA:3.30.70.GENE3D); G3DSA:4.10.1000.10 (GENE3D), PTHR24009 (PANTHER), PTHR24009:SF0 (PANTHER), PF14259 (PFAM), SSF54928 (SUPERFAMILY)
MDP0000901731	---NA---	471	-	-		-	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
MDP0000152947	wound-induced protein	603	2.00E−59	66.90%	P:response to biotic stimulus; P:biological_process; P:response to stress	-	no IPS match
MDP0000689999	protein disulfide isomerase	1503	0.00E+00	85.30%	P:embryo development; P:cellular homeostasis; P:biological_process; P:metabolic process; P:post-embryonic development; P:cellular protein modification process; C:endoplasmic reticulum; P:biosynthetic process; C:vacuole; P:reproduction; P:response to stress; P:cellular process; F:molecular_function; C:plastid; C:plasma membrane; C:thylakoid; P:carbohydrate metabolic process; P:response to abiotic stimulus; P:cell death; F:catalytic activity; C:cell wall; C:membrane; F:transferase activity	EC:5.3.4.1; EC:2.4.1.119	IPR005746 (PRINTS); IPR005788 (TIGRFAMs); IPR005792 (TIGRFAMs); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR017937 (PROSITE); PTHR18929 (PANTHER), PTHR18929:SF32 (PANTHER), PF13848 (PFAM), SignalP-NN(euk) (SIGNALP)
MDP0000166116	acyl:coa ligase acetate-coa synthetase-like protein	1659	0.00E+00	83.65%	C:peroxisome; F:catalytic activity; P:biosynthetic process; P:cellular process	EC:6.2.1.26	IPR000873 (PFAM); IPR020845 (PROSITE); IPR025110 (PFAM); G3DSA:2.30.38.10 (GENE3D), G3DSA:3.30.300.30 (GENE3D), G3DSA:3.40.50.980 (GENE3D), PTHR24095 (PANTHER), PTHR24095:SF29 (PANTHER), SSF56801 (SUPERFAMILY)
MDP0000304285	xanthine uracil permease family expressed	1728	0.00E+00	75.15%	P:transport; C:plasma membrane; P:cellular process; F:transporter activity	-	IPR006043 (PANTHER); PTHR11119:SF8 (PANTHER), tmhmm (TMHMM)
MDP0000920333	protein phosphatase	315	2.40E−52	89.50%	P:signal transduction; P:cellular protein modification process; P:biosynthetic process; C:plasma membrane; P:response to stress; P:cellular process; C:cell; P:response to biotic stimulus; C:nucleus; P:response to abiotic stimulus; P:cellular amino acid metabolic process; P:cellular component organization; F:hydrolase activity	-	IPR001932 (G3DSA:3.60.40.GENE3D); IPR015655 (PANTHER); PTHR13832:SF188 (PANTHER)

Table S2. *Cont.*

SeqName	Description	Length	*e*-Value	Sim Mean	GO Terms	Enzyme Codes List	InterPro IDs
MDP0000213808	probable ubiquitin conjugation factor e4-like	3189	0.00E+00	77.75%	P:carbohydrate metabolic process; P:protein metabolic process; P:catabolic process; F:catalytic activity; P:cellular protein modification process; C:cytosol; P:biosynthetic process; P:cellular process; C:intracellular	-	IPR003613 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); IPR019474 (PFAM); PTHR13931 (PANTHER), PTHR13931:SF2 (PANTHER), SSF57850 (SUPERFAMILY)
MDP0000253074	abscisic acid stress ripening protein homolog	702	8.20E−10	59.71%	P:response to stress	-	IPR003496 (PFAM)
MDP0000697474	reverse transcriptase	453	7.50E−25	88.10%	F:nucleic acid binding; C:Golgi apparatus; P:biosynthetic process; F:transferase activity; F:binding; P:DNA metabolic process	EC:2.7.7.49	IPR013103 (PFAM); PTHR11439 (PANTHER), PTHR11439:SF127 (PANTHER), tmhmm (TMHMM)
MDP0000292888	gyf domain-containing protein	5529	0.00E+00	59.50%	P:response to endogenous stimulus	-	IPR003169 (PFAM); G3DSA:3.30.1490.40 (GENE3D), PTHR14445 (PANTHER), PTHR14445:SF23 (PANTHER)
MDP0000233229	protein	2328	0.00E+00	68.50%	P:biological_process; F:molecular_function	-	tmhmm (TMHMM)
MDP0000523205	protein	1041	0.00E+00	81.85%	P:secondary metabolic process; P:response to biotic stimulus; F:catalytic activity; P:metabolic process; P:cellular amino acid metabolic process; P:biosynthetic process; F:binding; P:response to stress; P:cellular process	EC:1.14.11.9	IPR002283 (PRINTS); IPR005123 (PFAM); G3DSA:2.60.120.330 (GENE3D), PTHR10209 (PANTHER), PTHR10209:SF55 (PANTHER), PF14226 (PFAM), SSF51197 (SUPERFAMILY)
MDP0000378585	at4g03420 f9h3_4	1122	1.40E−173	83.25%	P:biological_process; C:cellular_component; F:molecular_function	-	IPR008507 (PFAM); PTHR31343 (PANTHER), PTHR31343:SF0 (PANTHER)
MDP0000572242	probable xyloglucan glycosyltransferase 12-like	2202	0.00E+00	83.45%	P:carbohydrate metabolic process; C:membrane; P:biosynthetic process; F:transferase activity; P:nucleobase-containing compound metabolic process; C:plasma membrane; P:cellular process	EC:2.4.1.12	G3DSA:3.90.550.10 (GENE3D), PTHR32044 (PANTHER), PTHR32044:SF0 (PANTHER), PF13641 (PFAM), tmhmm (TMHMM), SSF53448 (SUPERFAMILY)
MDP0000281279	protein	2601	0.00E+00	57.65%	C:mitochondrion; F:binding	-	IPR001752 (PRINTS); PTHR24115 (PANTHER), PTHR24115:SF169 (PANTHER), SSF52540 (SUPERFAMILY)
MDP0000712586	protein scai-like	708	1.10E−05	69.54%	P:biological_process; C:cytosol; F:molecular_function	-	IPR022709 (PFAM); PTHR21243 (PANTHER), PTHR21243:SF10 (PANTHER), SignalP-NN(euk) (SIGNALP)
MDP0000176723	acyl:coa ligase acetate-coa synthetase-like protein	420	1.70E−74	89.10%	C:peroxisome; F:o-succinylbenzoate-CoA ligase activity; P:ubiquinone biosynthetic process	EC:6.2.1.26	no IPS match

Table S2. *Cont*.

SeqName	Description	Length	*e*-Value	Sim Mean	GO Terms	Enzyme Codes List	InterPro IDs
MDP0000876817	---NA---	198	-	-		-	SignalP-NN(euk) (SIGNALP), tmhmm (TMHMM)
MDP0000273484	skp1-like protein	633	5.10E−61	61.70%	C:nucleus; C:cytoplasm; C:nucleolus; P:ubiquitin-dependent protein catabolic process	-	IPR001232 (PANTHER); IPR011333 (G3DSA:3.30.710.GENE3D); IPR016072 (PFAM); IPR016073 (PFAM); IPR016897 (PIR); PTHR11165:SF47 (PANTHER)

Table S3. Forward and Reverse primer sequences designed based upon predicted gene sequence from Apple Genome (1.0).

Gene Model ID	**Primer**	**Sequence (5′->3′)**
MDP0000037251	Forward	GCCACTTGACCTCCATGTGTTTCC
MDP0000037251	Reverse	TCTTAGCGAGACGCTCCATTGCTG
MDP0000128468	Forward	CCACAAGCATCTCAAGCACCTC
MDP0000128468	Reverse	GAAAGCAAATCCACCCGAACC
MDP0000129664	Forward	GGATAAGTCCGGGATGCCTGAC
MDP0000129664	Reverse	CAATGCGTTGCAGTGCTACTCAC
MDP0000138340	Forward	GTCCTCTGGCGCCTGAAGAAC
MDP0000138340	Reverse	TGGCTCTGCAATCACGTCACTTAC
MDP0000152947	Forward	GATTACCCCATTGGCGACAGTC
MDP0000152947	Reverse	CGACCCACCAGTTCTTGATGC
MDP0000161275	Forward	GAGATGGGAGAGTCCTGCTGCC
MDP0000161275	Reverse	GCCCTTGTATTTCATCTTGCCATC
MDP0000166116	Forward	GTGGAGGTGGAGTCGGTGCTG
MDP0000166116	Reverse	CTCAATGATCTCCTTCTCCGTCG
MDP0000172863	Forward	GAATTGGTGACTGGACAGAAGCC
MDP0000172863	Reverse	CTGCAAAATCTCATCATCGTGACC
MDP0000176723	Forward	CATTCGTGAGCTTGAAGAGTGAGG
MDP0000176723	Reverse	GGAAGCTCGTCCGTAAACACCAC
MDP0000180389	Forward	TGTCCAAAGCTAGCATCCATTCC
MDP0000180389	Reverse	CGCTCTCAAAGCAAGACAGAACC
MDP0000200646	Forward	GGTCAGATTCAAMCCCACTGATGAGTT
MDP0000200646	Reverse	TCTGGGAAGAATGCAGGAAGATCG
MDP0000213808	Forward	CTTTAATGAAGGATCCAGTTATCTTACCGTC
MDP0000213808	Reverse	CTGTATCCTTGCCTTTAATTCATTGTCTGG
MDP0000220601	Forward	CGATATCGGTGATTTGCTGGAAG
MDP0000220601	Reverse	GAAGTCGCCAAGTTTATGTTAGCAGC
MDP0000232309	Forward	GCTGTGGTTGCATCCTTGACTG
MDP0000232309	Reverse	GGCACCATATATGGCATTAGTTGTAGG
MDP0000233229	Forward	GCATCGCCTTAGCTTTCTTACCTG
MDP0000233229	Reverse	CCAAATTCCGAGTCTCTGCTGCG
MDP0000237908	Forward	GAAACAGCTACGACTTGGTGATCG
MDP0000237908	Reverse	GTGACCACAGGTGCAGCTCACAC
MDP0000253074	Forward	CAGTTGCAATCAGGAGAAGAAATGAG
MDP0000253074	Reverse	GAAGGCAAATCCACCCGAACCAACT
MDP0000255887	Forward	AATATTCTGGCAAACTTCCTTTAACTCTG
MDP0000255887	Reverse	CCTCACGAAGCCACAATTGACTACGT
MDP0000273484	Forward	CAAGACCCTTTTGGACCTGACTTG
MDP0000273484	Reverse	CGACGAACTTCCTCCTCTTCCTC
MDP0000286959	Forward	GAACGACCTCAAACAGATCTCCATG
MDP0000286959	Reverse	CTTCAAACGTCTCAAGTCTCTGACAAG
MDP0000292888	Forward	AGGAGTTGCTACCGGCTGATGTC
MDP0000292888	Reverse	GGTCCACATCCCCAACATCTGC
MDP0000296716	Forward	GCGAAGGGCGACTTCAGTTCC
MDP0000296716	Reverse	CAATGGTGGATGGTGATCTGATGTC
MDP0000304285	Forward	TTGTCTCGAACACCACCCCG
MDP0000304285	Reverse	CAAGCGTGTTATCCAGCAGCG
MDP0000310811	Forward	CCAAGGTTCCGCCAACAGC
MDP0000310811	Reverse	CAGATAATGCATAGTGCCCGAAACC
MDP0000320533	Forward	TCAACGTGGCTGTAATCTTCGG
MDP0000320533	Reverse	GAGAAAGCATTAACGGCTTTGAGG
MDP0000523205	Forward	GGTTGCAGGTCCTTAGAAATGGC
MDP0000523205	Reverse	GGTGCTGGACAGTAGAAAGTTGGG
MDP0000547450	Forward	GAGCCTTGGCGGATGACTCTG
MDP0000547450	Reverse	CTAGCAACGGATAGCTCACGGTG

MDP0000572242	Forward	GAGAAGCCAAAGCATCAAAGGG
MDP0000572242	Reverse	AGAAGGAGGAATGCCAATGCC
MDP0000618650	Forward	CCACCACACCTCCATCATTCTTG
MDP0000618650	Reverse	CCTATCTCCCATCTTATGATGCTGTTG
MDP0000697474	Forward	CTAAACGATCCTCCGCCGC
MDP0000697474	Reverse	GATCATCATGATCGCCGCTCC
MDP0000712586	Forward	GAGTCGAAGAAATGCTGTTGAACTTG
MDP0000712586	Reverse	CTCCATAACTTTCTCTGTCCTATTCACTCC
MDP0000875654	Forward	TCGTAAATGGTGTACCTCTTGTTGC
MDP0000875654	Reverse	CGCTTACCTTCCTCGCCTTCC
MDP0000883284	Forward	GGTGGAGGAGGACTTGGAGGAG
MDP0000883284	Reverse	GGAAGTGCATGGAGAAATGAATCG
MDP0000901731	Forward	GCAAAGATGGATGAGTTGGGTGAG
MDP0000901731	Reverse	GGGAATTGCGGAATTGGAAGG
MDP0000920333	Forward	TACTGATGTTCTAATCCTTGCCAG
MDP0000920333	Reverse	TCTAACAACAACGCATGAAATATCATC

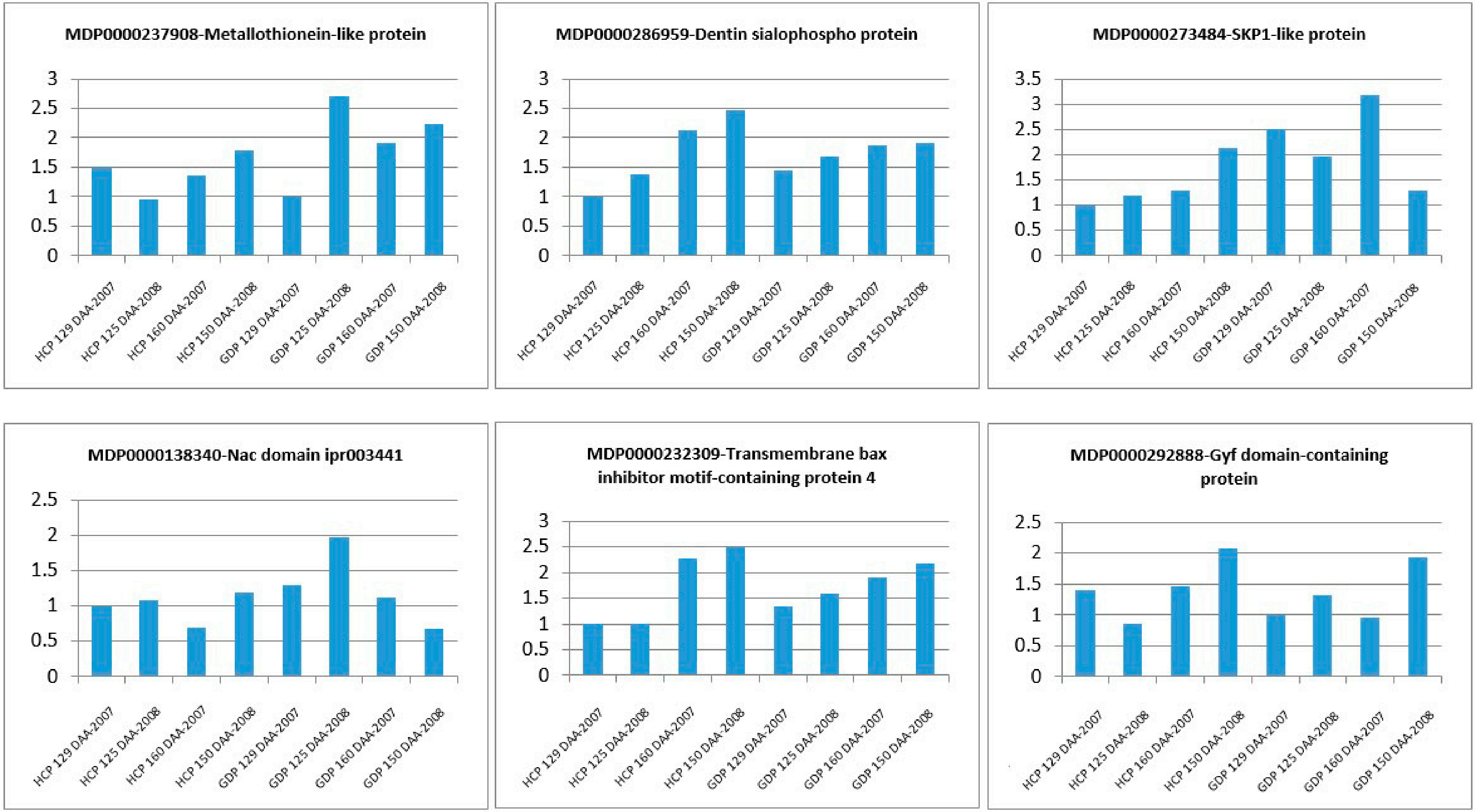
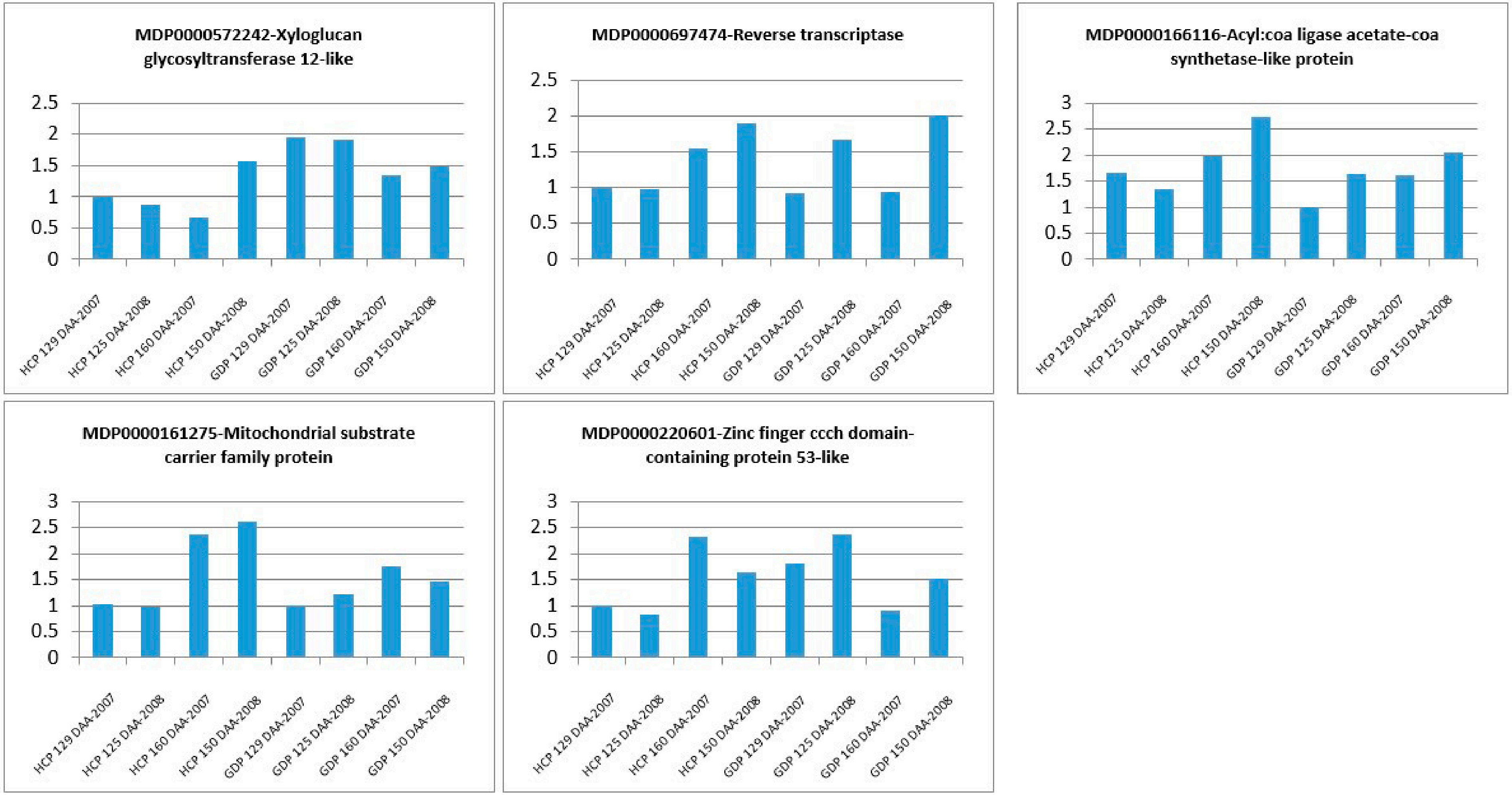


Figure S1. *Cont.*



MDP0000572242-Xyloglucan glycosyltransferase 12-like

MDP0000697474-Reverse transcriptase

MDP0000166116-Acyl:coa ligase acetate-coa synthetase-like protein

MDP0000161275-Mitochondrial substrate carrier family protein

MDP0000220601-Zinc finger ccch domain-containing protein 53-like

Figure S1. Low differential expression of genes identified with differential display. Samples with 0 to 3-fold differences in expression relative to the control were classified as low differential expression. Expression is separated by sample tested and plotted against fold expression relative to the β-tubulin control expression.

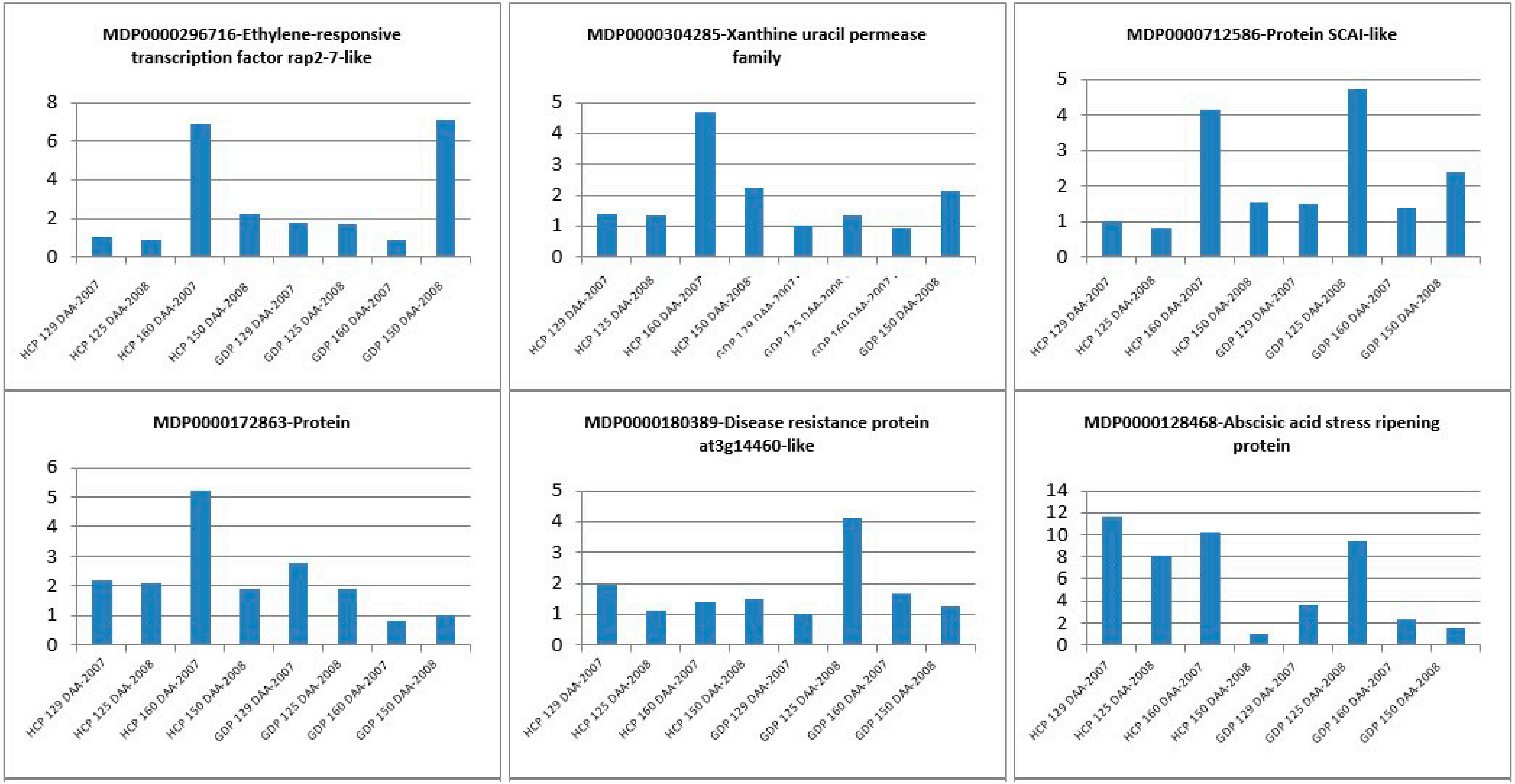


Figure S2. *Cont.*

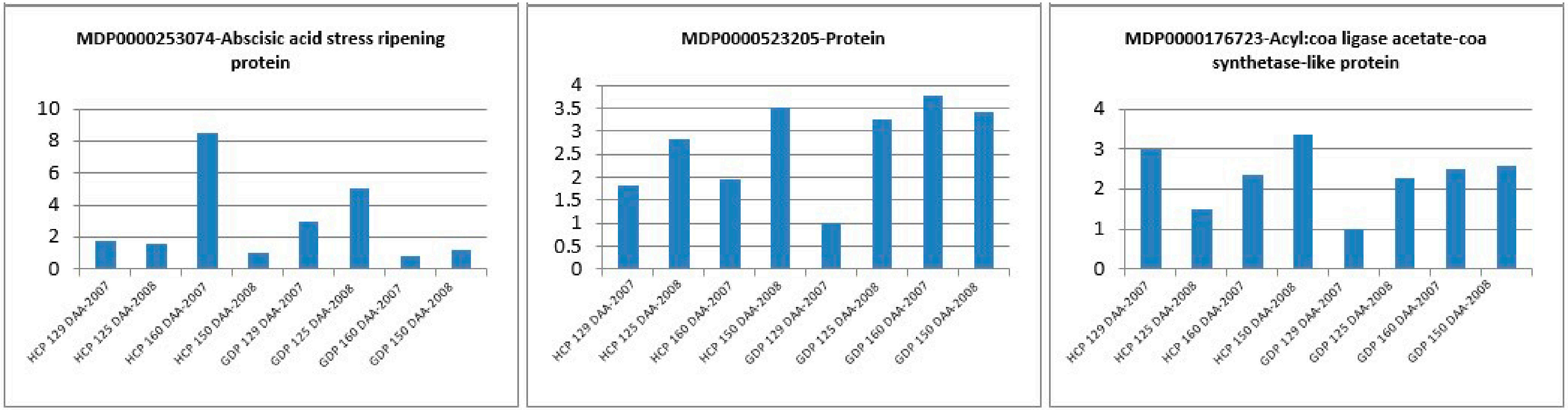


Figure S2. Seasonally-variable differential expression of genes identified with differential display. Samples with over 3-fold differential expression between samples, but not consistent between seasons were classified as seasonally-variable. Expression is separated by sample tested and plotted against fold expression relative to the β-tubulin control expression.