Supplementary Table 10: The lists of annotation genes in cultivated-wild selective sweep.

Gene ID	Transcript ID	NR ID	NR annotation
FtPinG0100252000.01	FtPinG0100252000.01.T01	XP_019075186.1	PREDICTED: probable nucleoredoxin 3 [Vitis vinifera]
FtPinG0100252100.01	FtPinG0100252100.01.T01	XP_021849646.1	transmembrane protein 18 [Spinacia oleracea]
FtPinG0100252400.01	FtPinG0100252400.01.T01	XP_010676478.1	PREDICTED: protein SENSITIVE TO PROTON RHIZOTOXICITY 1 [Beta vulgaris subsp. vulgaris]
FtPinG0100253700.01	FtPinG0100253700.01.T01	XP_021748807.1	dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic-like [Chenopodium quinoa]
FtPinG0100254200.01	FtPinG0100254200.01.T01	XP_019075186.1	PREDICTED: probable nucleoredoxin 3 [Vitis vinifera]
FtPinG0100254400.01	FtPinG0100254400.01.T01	XP_010691236.1	PREDICTED: 3beta-hydroxysteroid-dehydrogenase/decarboxylase-like isoform X2 [Beta vulgaris subsp. vulgaris]
FtPinG0100254800.01	FtPinG0100254800.01.T02	XP_023913187.1	probable transmembrane ascorbate ferrireductase 2 [Quercus suber]
FtPinG0100254800.01	FtPinG0100254800.01.T01	RLW26382.1	putative transmembrane ascorbate ferrireductase 2 [Quercus suber]
FtPinG0100255000.01	FtPinG0100255000.01.T01	XP_021760032.1	protein decapping 5-like [Chenopodium quinoa]
FtPinG0100255700.01	FtPinG0100255700.01.T01	XP_010660444.1	PREDICTED: protein CROWDED NUCLEI 1 isoform X2 [Vitis vinifera]
FtPinG0100256000.01	FtPinG0100256000.01.T01	XP_021689782.1	protein GAMETE EXPRESSED 3-like isoform X4 [Hevea brasiliensis]
FtPinG0100256300.01	FtPinG0100256300.01.T01	XP_015933649.1	uroporphyrinogen decarboxylase 1, chloroplastic isoform X1 [Arachis duranensis]
FtPinG0100256600.01	FtPinG0100256600.01.T01	XP_021763495.1	probable endo-1,3(4)-beta-glucanase ARB_01444 [Chenopodium quinoa]
FtPinG0100256700.01	FtPinG0100256700.01.T01	XP_021800103.1	putative UPF0481 protein At3g02645 [Prunus avium]
FtPinG0100663300.01	FtPinG0100663300.01.T01	XP_023899032.1	heparan-alpha-glucosaminide N-acetyltransferase-like [Quercus suber]
FtPinG0100663500.01	FtPinG0100663500.01.T01	RDX72110.1	Aquaporin PIP2-7, partial [Mucuna pruriens]
FtPinG0100664000.01	FtPinG0100664000.01.T01	OMO74529.1	mRNA splicing factor SYF2 [Corchorus capsularis]
FtPinG0100664300.01	FtPinG0100664300.01.T01	XP_010266936.1	PREDICTED: uncharacterized protein LOC104604334 [Nelumbo nucifera]
FtPinG0100664600.01	FtPinG0100664600.01.T01	XP_010690345.1	PREDICTED: probable ubiquitin-conjugating enzyme E2 23 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0100664800.01	FtPinG0100664800.01.T01	XP_021753051.1	probable ubiquitin-conjugating enzyme E2 23 isoform X2 [Chenopodium quinoa]

Supplementary Table 10 (Continued):

FtPinG0100665000.01	FtPinG0100665000.01.T01	XP_022857690.1	probable ubiquitin-conjugating enzyme E2 23 isoform X2 [Olea europaea var. sylvestris]
FtPinG0100665400.01	FtPinG0100665400.01.T01	PQQ14470.1	DDB1- and CUL4-associated factor 8 isoform X1 [Prunus yedoensis var. nudiflora]
FtPinG0100665600.01	FtPinG0100665600.01.T01	XP_018854196.1	PREDICTED: mechanosensitive ion channel protein 6-like [Juglans regia]
FtPinG0100665800.01	FtPinG0100665800.01.T01	PHT71678.1	Heterodimeric geranylgeranyl pyrophosphate synthase small subunit, chloroplastic [Capsicum annuum]
FtPinG0100667400.01	FtPinG0100667400.01.T01	XP_010690268.1	PREDICTED: cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG5 [Beta vulgaris subsp. vulgaris]
FtPinG0100671400.01	FtPinG0100671400.01.T01	XP_010690264.1	PREDICTED: probable serine/threonine-protein kinase At4g35230 [Beta vulgaris subsp. vulgaris]
FtPinG0100671800.01	FtPinG0100671800.01.T01	PSS31547.1	protein of unknown function DUF632 protein [Actinidia chinensis var. chinensis]
FtPinG0100706600.01	FtPinG0100706600.01.T01	PSR86411.1	Adaptin ear-binding coat-associated protein 1 NECAP-1 protein [Actinidia chinensis var. chinensis]
FtPinG0100706800.01	FtPinG0100706800.01.T01	XP_021770157.1	protein CHROMATIN REMODELING 8-like isoform X1 [Chenopodium quinoa]
FtPinG0100706800.01	FtPinG0100706800.01.T02	XP_021770157.1	protein CHROMATIN REMODELING 8-like isoform X1 [Chenopodium quinoa]
FtPinG0100707200.01	FtPinG0100707200.01.T01	XP_021729666.1	FAD-linked sulfhydryl oxidase ERV1-like [Chenopodium quinoa]
FtPinG0100708000.01	FtPinG0100708000.01.T01	XP_010680162.1	PREDICTED: signal recognition particle receptor subunit alpha [Beta vulgaris subsp. vulgaris]
FtPinG0100873600.01	FtPinG0100873600.01.T01	XP_021768107.1	expansin-like B1 [Chenopodium quinoa]
FtPinG0100873700.01	FtPinG0100873700.01.T01	PON75367.1	LIS motif containing RING-type zinc-finger protein [Parasponia andersonii]
FtPinG0100873900.01	FtPinG0100873900.01.T01	XP_021768097.1	regulator of nonsense transcripts 1 homolog [Chenopodium quinoa]
FtPinG0100874500.01	FtPinG0100874500.01.T01	GAV86133.1	Med7 domain-containing protein [Cephalotus follicularis]
FtPinG0100874500.01	FtPinG0100874500.01.T02	GAV86133.1	Med7 domain-containing protein [Cephalotus follicularis]
FtPinG0100874800.01	FtPinG0100874800.01.T01	XP_010664169.1	PREDICTED: uncharacterized protein LOC100260794 [Vitis vinifera]
FtPinG0100874800.01	FtPinG0100874800.01.T02	XP_010664169.1	PREDICTED: uncharacterized protein LOC100260794 [Vitis vinifera]

Supplementary Table 10 (Continued):

FtPinG0100875700.01	FtPinG0100875700.01.T01	PSS09672.1	DNA-directed RNA polymerase II subunit RPB2 [Actinidia chinensis var. chinensis]
FtPinG0100876200.01	FtPinG0100876200.01.T01	XP_017972739.1	PREDICTED: beta-amylase 3, chloroplastic [Theobroma cacao]
FtPinG0100876600.01	FtPinG0100876600.01.T01	AAP52850.1	retrotransposon protein, putative, Ty3-gypsy subclass [Oryza sativa Japonica Group]
FtPinG0100877200.01	FtPinG0100877200.01.T01	XP_011070262.1	decapping nuclease DXO homolog, chloroplastic [Sesamum indicum]
FtPinG0100878100.01	FtPinG0100878100.01.T01	XP_008238533.1	PREDICTED: protein transport protein SEC16B homolog [Prunus mume]
FtPinG0100878400.01	FtPinG0100878400.01.T01	XP_017973320.1	PREDICTED: serine/threonine-protein kinase EDR1 isoform X1 [Theobroma cacao]
FtPinG0100879100.01	FtPinG0100879100.01.T01	XP_019265997.1	PREDICTED: uncharacterized protein LOC109243506 [Nicotiana attenuata]
FtPinG0100879900.01	FtPinG0100879900.01.T01	AOM81064.1	mother of FT 2 protein [Oxybasis rubra]
FtPinG0101091500.01	FtPinG0101091500.01.T01	XP_021727022.1	polygalacturonase 1 beta-like protein 3 isoform X1 [Chenopodium quinoa]
FtPinG0101091700.01	FtPinG0101091700.01.T01	XP_021842913.1	polygalacturonase 1 beta-like protein 3 [Spinacia oleracea]
FtPinG0101092400.01	FtPinG0101092400.01.T01	XP_021640326.1	ubiquitin-like-specific protease 1D isoform X6 [Hevea brasiliensis]
FtPinG0101093000.01	FtPinG0101093000.01.T01	XP_006483831.1	equilibrative nucleotide transporter 1 isoform X2 [Citrus sinensis]
FtPinG0101093300.01	FtPinG0101093300.01.T01	XP_010682574.1	PREDICTED: probable xyloglucan endotransglucosylase/hydrolase protein 33 [Beta vulgaris subsp. vulgaris]
FtPinG0101093800.01	FtPinG0101093800.01.T01	XP_010682575.1	PREDICTED: aldehyde dehydrogenase family 2 member B7, mitochondrial isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0101094100.01	FtPinG0101094100.01.T01	XP_021742290.1	spermidine synthase 1-like [Chenopodium quinoa]
FtPinG0101094400.01	FtPinG0101094400.01.T01	XP_021769688.1	protein SCO1 homolog 1, mitochondrial-like [Chenopodium quinoa]
FtPinG0101094500.01	FtPinG0101094500.01.T01	XP_021742193.1	probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 [Chenopodium quinoa]
FtPinG0101095100.01	FtPinG0101095100.01.T01	XP_010689261.1	PREDICTED: uncharacterized protein LOC104902996 [Beta vulgaris subsp. vulgaris]
FtPinG0101095300.01	FtPinG0101095300.01.T01	XP_010682592.1	PREDICTED: AP-1 complex subunit gamma-2 [Beta vulgaris subsp. vulgaris]
FtPinG0101095300.01	FtPinG0101095300.01.T02	XP_010682592.1	PREDICTED: AP-1 complex subunit gamma-2 [Beta vulgaris subsp. vulgaris]
FtPinG0101096000.01	FtPinG0101096000.01.T01	XP_002521029.1	transcription factor PAR2 [Ricinus communis]
FtPinG0101096100.01	FtPinG0101096100.01.T01	XP_021842862.1	WAT1-related protein At3g28050-like [Spinacia oleracea]

Supplementary Table 10 (Continued):

FtPinG0101096500.01	FtPinG0101096500.01.T01	XP_021726959.1	WAT1-related protein At1g70260-like [Chenopodium quinoa]
FtPinG0101096700.01	FtPinG0101096700.01.T01	PSS13576.1	Proline-rich receptor-like protein kinase [Actinidia chinensis var. chinensis]
FtPinG0101097000.01	FtPinG0101097000.01.T01	XP_017604038.1	PREDICTED: protein ALTERED XYLOGLUCAN 4-like [Gossypium arboreum]
FtPinG0101098200.01	FtPinG0101098200.01.T01	XP_007044533.2	PREDICTED: cyclin-D1-1 isoform X1 [Theobroma cacao]
FtPinG0101098400.01	FtPinG0101098400.01.T01	XP_024195280.1	zinc finger protein 5 [Rosa chinensis]
FtPinG0101098600.01	FtPinG0101098600.01.T01	XP_015063482.1	PREDICTED: tubulin-folding cofactor A [Solanum pennellii]
FtPinG0101099000.01	FtPinG0101099000.01.T01	PSS02538.1	WRKY transcription factor 14 [Actinidia chinensis var. chinensis]
FtPinG0101099500.01	FtPinG0101099500.01.T01	NP_001233804.1	protein phosphatase 2A catalytic subunit [Solanum lycopersicum]
FtPinG0101100000.01	FtPinG0101100000.01.T01	XP_021747188.1	probable inactive receptor kinase At1g27190 [Chenopodium quinoa]
FtPinG0101100100.01	FtPinG0101100100.01.T01	XP_021752477.1	wall-associated receptor kinase 4-like [Chenopodium quinoa]
FtPinG0101100600.01	FtPinG0101100600.01.T01	EEF30134.1	30S ribosomal protein S20, putative [Ricinus communis]
FtPinG0101100800.01	FtPinG0101100800.01.T01	PON53755.1	Germin [Trema orientale]
FtPinG0101100900.01	FtPinG0101100900.01.T01	GAV81325.1	TPX2 domain-containing protein [Cephalotus follicularis]
FtPinG0101101200.01	FtPinG0101101200.01.T01	XP_021731173.1	formin-like protein 4 [Chenopodium quinoa]
FtPinG0101101400.01	FtPinG0101101400.01.T01	XP_024990448.1	two-component response regulator ARR5-like [Cynara cardunculus var. scolymus]
FtPinG0180000046.01	FtPinG0180000046.01.T01	XP_018479560.1	PREDICTED: uncharacterized protein LOC108850544 [Raphanus sativus]
FtPinG0180000259.01	FtPinG0180000259.01.T01	XP_012572980.1	PREDICTED: uncharacterized protein LOC105852393, partial [Cicer arietinum]
FtPinG0180000260.01	FtPinG0180000260.01.T01	XP_010667599.1	PREDICTED: uncharacterized protein LOC104884611 [Beta vulgaris subsp. vulgaris]
FtPinG0180000261.01	FtPinG0180000261.01.T01	XP_018511976.1	PREDICTED: uncharacterized protein LOC108870789 [Brassica rapa]
FtPinG0180000262.01	FtPinG0180000262.01.T01	XP_010668282.1	PREDICTED: uncharacterized protein LOC104885285, partial [Beta vulgaris subsp. vulgaris]
FtPinG0180000265.01	FtPinG0180000265.01.T01	PWA90654.1	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Artemisia annua]
FtPinG0180000267.01	FtPinG0180000267.01.T01	XP_010690668.1	PREDICTED: uncharacterized protein LOC104904171 [Beta vulgaris subsp. vulgaris]
FtPinG0180000268.01	FtPinG0180000268.01.T01	XP_012436425.1	PREDICTED: uncharacterized protein LOC105762969 [Gossypium raimondii]
FtPinG0180000269.01	FtPinG0180000269.01.T01	XP_010687130.1	PREDICTED: uncharacterized protein LOC104901276 [Beta vulgaris subsp. vulgaris]

Supplementary Table 10 (Continued):

FtPinG0180000272.01	FtPinG0180000272.01.T01	XP_008382472.1	PREDICTED: uncharacterized protein LOC103445254 [Malus domestica]
FtPinG0180000300.01	FtPinG0180000300.01.T01	XP_018459795.1	PREDICTED: uncharacterized protein LOC108830698 [Raphanus sativus]
FtPinG0180000301.01	FtPinG0180000301.01.T01	XP_012842863.1	PREDICTED: uncharacterized protein LOC105963045 [Erythranthe guttata]
FtPinG0180000302.01	FtPinG0180000302.01.T01	XP_017622027.1	PREDICTED: uncharacterized protein LOC108466183 [Gossypium arboreum]
FtPinG0180000409.01	FtPinG0180000409.01.T01	PNX74094.1	copia LTR rider, partial [Trifolium pratense]
FtPinG0201347000.01	FtPinG0201347000.01.T01	XP_021725536.1	carbon catabolite repressor protein 4 homolog 4-like isoform X1 [Chenopodium quinoa]
FtPinG0201347300.01	FtPinG0201347300.01.T01	XP_010677519.1	PREDICTED: LRR receptor-like serine/threonine-protein kinase FEI 2 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0201347800.01	FtPinG0201347800.01.T01	PON94653.1	Galactose oxidase, beta-propeller [Trema orientale]
FtPinG0201348000.01	FtPinG0201348000.01.T01	XP_024021552.1	actin-related protein 5 [Morus notabilis]
FtPinG0201348600.01	FtPinG0201348600.01.T01	XP_019190423.1	PREDICTED: actin-related protein 5 isoform X1 [Ipomoea nil]
FtPinG0201348800.01	FtPinG0201348800.01.T01	XP_010677463.1	PREDICTED: protein ENHANCED DISEASE RESISTANCE 2 isoform X2 [Beta vulgaris subsp. vulgaris]
FtPinG0201349200.01	FtPinG0201349200.01.T01	XP_021903103.1	transmembrane protein 45A [Carica papaya]
FtPinG0201349700.01	FtPinG0201349700.01.T01	XP_022889493.1	exportin-T-like [Olea europaea var. sylvestris]
FtPinG0201350100.01	FtPinG0201350100.01.T01	XP_022889493.1	exportin-T-like [Olea europaea var. sylvestris]
FtPinG0201350400.01	FtPinG0201350400.01.T02	XP_003612633.1	MOB kinase activator-like 1A [Medicago truncatula]
FtPinG0201350400.01	FtPinG0201350400.01.T01	XP_025696921.1	MOB kinase activator-like 1B isoform X1 [Arachis hypogaea]
FtPinG0201350500.01	FtPinG0201350500.01.T01	XP_010665021.1	PREDICTED: protein BREVIS RADIX [Vitis vinifera]
FtPinG0201351000.01	FtPinG0201351000.01.T01	XP_011092622.1	mechanosensitive ion channel protein 10 [Sesamum indicum]
FtPinG0201351100.01	FtPinG0201351100.01.T01	CAD27443.1	vacuolar ATPase subunit B [Mesembryanthemum crystallinum]
FtPinG0201351400.01	FtPinG0201351400.01.T01	XP_012075071.1	probable methyltransferase PMT21 isoform X1 [Jatropha curcas]
FtPinG0201352000.01	FtPinG0201352000.01.T01	XP_021862357.1	probable polyamine transporter At1g31830 isoform X3 [Spinacia oleracea]
FtPinG0201352200.01	FtPinG0201352200.01.T01	XP_018491746.1	PREDICTED: ubiquinol oxidase 1a, mitochondrial [Raphanus sativus]

Supplementary Table 10 (Continued):

FtPinG0201371900.01	FtPinG0201371900.01.T01	AHH29648.1	tocopherol cyclase, partial [Juglans regia]
FtPinG0201372100.01	FtPinG0201372100.01.T01	XP_021714870.1	probable glycosyltransferase At3g07620 [Chenopodium quinoa]
FtPinG0201372300.01	FtPinG0201372300.01.T02	XP_012840247.1	PREDICTED: zinc finger CCCH domain-containing protein 5 [Erythranthe guttata]
FtPinG0201372300.01	FtPinG0201372300.01.T01	XP_021723422.1	zinc finger CCCH domain-containing protein 5-like isoform X1 [Chenopodium quinoa]
FtPinG0201372700.01	FtPinG0201372700.01.T01	XP_020548571.1	glucan endo-1,3-beta-glucosidase 14 [Sesamum indicum]
FtPinG0201373000.01	FtPinG0201373000.01.T01	XP_022869684.1	protein RADIALIS-like 3 [Olea europaea var. sylvestris]
FtPinG0201373300.01	FtPinG0201373300.01.T01	XP_010648493.1	PREDICTED: nuclear pore complex protein NUP85 [Vitis vinifera]
FtPinG0201373800.01	FtPinG0201373800.01.T01	XP_002515173.1	protoporphyrinogen oxidase 1, chloroplastic [Ricinus communis]
FtPinG0201373900.01	FtPinG0201373900.01.T01	OVA11353.1	Protein kinase domain [Macleaya cordata]
FtPinG0201375400.01	FtPinG0201375400.01.T01	XP_010654518.1	PREDICTED: protein FLX-like 3 [Vitis vinifera]
FtPinG0201376200.01	FtPinG0201376200.01.T01	GAV78074.1	Fasciclin domain-containing protein, partial [Cephalotus follicularis]
FtPinG0201376400.01	FtPinG0201376400.01.T01	XP_010671758.1	PREDICTED: DNA replication complex GINS protein SLD5 [Beta vulgaris subsp. vulgaris]
FtPinG0201376400.01	FtPinG0201376400.01.T02	XP_010671758.1	PREDICTED: DNA replication complex GINS protein SLD5 [Beta vulgaris subsp. vulgaris]
FtPinG0201426000.01	FtPinG0201426000.01.T01	XP_021772394.1	transcription factor bHLH149-like [Chenopodium quinoa]
FtPinG0201426100.01	FtPinG0201426100.01.T01	XP_020572871.1	rab9 effector protein with kelch motifs-like isoform X2 [Phalaenopsis equestris]
FtPinG0201426400.01	FtPinG0201426400.01.T01	XP_021863353.1	ABC transporter D family member 1 [Spinacia oleracea]
FtPinG0202114900.01	FtPinG0202114900.01.T01	XP_021750041.1	protein bem46-like [Chenopodium quinoa]
FtPinG0202114900.01	FtPinG0202114900.01.T02	XP_021750042.1	protein bem46-like [Chenopodium quinoa]
FtPinG0202115600.01	FtPinG0202115600.01.T01	PON84439.1	Telomeric repeat-binding factor [Trema orientale]
FtPinG0202116200.01	FtPinG0202116200.01.T01	XP_021714690.1	threonine synthase, chloroplastic-like [Chenopodium quinoa]
FtPinG0202117000.01	FtPinG0202117000.01.T01	ASZ85199.1	protein phosphatase 2C 16 [Hylocereus polyrhizus]
FtPinG0202117600.01	FtPinG0202117600.01.T01	KHG17950.1	Glycylpeptide N-tetradecanoyltransferase 1 -like protein [Gossypium arboreum]

Supplementary Table 10 (Continued):

FtPinG0202118300.01	FtPinG0202118300.01.T01	XP_002281323.1	PREDICTED: uncharacterized protein LOC100266443 [Vitis vinifera]
FtPinG0202118700.01	FtPinG0202118700.01.T01	XP_021277363.1	BTB/POZ domain and ankyrin repeat-containing protein NPR1-like [Herrania umbratica]
FtPinG0202119700.01	FtPinG0202119700.01.T01	OMO69628.1	Thioredoxin [Corchorus capsularis]
FtPinG0202119900.01	FtPinG0202119900.01.T01	PSS15518.1	Malonyl-[acyl-carrier protein] O-methyltransferase [Actinidia chinensis var. chinensis]
FtPinG0202120100.01	FtPinG0202120100.01.T01	XP_006363940.1	PREDICTED: L-ascorbate oxidase-like [Solanum tuberosum]
FtPinG0202120400.01	FtPinG0202120400.01.T01	XP_021714131.1	protein CELLULOSE SYNTHASE INTERACTIVE 1-like [Chenopodium quinoa]
FtPinG0202120600.01	FtPinG0202120600.01.T01	XP_002281012.1	PREDICTED: NADPH-dependent 1-acyldihydroxyacetone phosphate reductase [Vitis vinifera]
FtPinG0202121000.01	FtPinG0202121000.01.T01	XP_010680953.1	PREDICTED: CASP-like protein 5C1 [Beta vulgaris subsp. vulgaris]
FtPinG0202121300.01	FtPinG0202121300.01.T01	XP_021679725.1	GDSL esterase/lipase At2g23540-like [Hevea brasiliensis]
FtPinG0202121600.01	FtPinG0202121600.01.T01	ACH63241.1	ethylene esterase-like protein [Rheum australe]
FtPinG0202148300.01	FtPinG0202148300.01.T01	XP_010652849.1	PREDICTED: transcription factor TGA1 isoform X3 [Vitis vinifera]
FtPinG0202148300.01	FtPinG0202148300.01.T02	XP_010652849.1	PREDICTED: transcription factor TGA1 isoform X3 [Vitis vinifera]
FtPinG0202148600.01	FtPinG0202148600.01.T01	XP_011097618.1	alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial [Sesamum indicum]
FtPinG0202149000.01	FtPinG0202149000.01.T01	XP_012469440.1	PREDICTED: succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial isoform X1 [Gossypium raimondii]
FtPinG0202149100.01	FtPinG0202149100.01.T01	XP_011003098.1	PREDICTED: ornithine decarboxylase-like [Populus euphratica]
FtPinG0202149300.01	FtPinG0202149300.01.T01	XP_021746809.1	single myb histone 6-like isoform X3 [Chenopodium quinoa]
FtPinG0202149600.01	FtPinG0202149600.01.T01	XP_022843794.1	ADP-ribosylation factor-like protein 8a [Olea europaea var. sylvestris]
FtPinG0202150400.01	FtPinG0202150400.01.T01	XP_021889780.1	enoyl-[acyl-carrier-protein] reductase, mitochondrial [Carica papaya]
FtPinG0202151900.01	FtPinG0202151900.01.T01	XP_008392865.1	PREDICTED: 60S ribosomal protein L26-1 [Malus domestica]
FtPinG0202152100.01	FtPinG0202152100.01.T01	XP_010666091.1	PREDICTED: tyrosine/DOPA decarboxylase 1 [Beta vulgaris subsp. vulgaris]
FtPinG0202152900.01	FtPinG0202152900.01.T01	XP_021714443.1	BTB/POZ domain-containing protein NPY4-like [Chenopodium quinoa]
FtPinG0280000492.01	FtPinG0280000492.01.T01	XP_010687071.1	PREDICTED: uncharacterized protein LOC104901222 [Beta vulgaris subsp. vulgaris]

Supplementary Table 10 (Continued):

FtPinG0280000493.01	FtPinG0280000493.01.T01	XP_018819453.1	PREDICTED: uncharacterized protein LOC108990059 [Juglans regia]
FtPinG0280000754.01	FtPinG0280000754.01.T01	XP_010064836.1	PREDICTED: uncharacterized protein LOC104451992 [Eucalyptus grandis]
FtPinG0280000758.01	FtPinG0280000758.01.T01	PRQ19855.1	putative nucleotidyltransferase, Ribonuclease H [Rosa chinensis]
FtPinG0302580200.01	FtPinG0302580200.01.T01	PON88622.1	Equilibrative nucleoside transporter [Trema orientale]
FtPinG0302580200.01	FtPinG0302580200.01.T02	XP_018805882.1	PREDICTED: equilibrative nucleotide transporter 3-like isoform X2 [Juglans regia]
FtPinG0302580600.01	FtPinG0302580600.01.T01	XP_024950987.1	pentatricopeptide repeat-containing protein At1g06270 [Citrus sinensis]
FtPinG0302580800.01	FtPinG0302580800.01.T01	XP_022876520.1	cytochrome b6-f complex iron-sulfur subunit 2, chloroplastic-like [Olea europaea var. sylvestris]
FtPinG0302580900.01	FtPinG0302580900.01.T01	XP_010681128.1	PREDICTED: nucleolar protein 14 [Beta vulgaris subsp. vulgaris]
FtPinG0302581200.01	FtPinG0302581200.01.T01	ALT31507.1	MYB7 [Fagopyrum tataricum]
FtPinG0302581400.01	FtPinG0302581400.01.T01	XP_010653853.1	PREDICTED: serine/threonine-protein kinase STY8 isoform X2 [Vitis vinifera]
FtPinG0302581600.01	FtPinG0302581600.01.T01	EXC22895.1	putative leucine-rich repeat receptor-like serine/threonine-protein kinase [Morus notabilis]
FtPinG0302581800.01	FtPinG0302581800.01.T01	EEF46636.1	(R)-limonene synthase, putative [Ricinus communis]
FtPinG0302581900.01	FtPinG0302581900.01.T01	XP_002515689.1	monoterpene synthase [Ricinus communis]
FtPinG0302582100.01	FtPinG0302582100.01.T01	EEF46636.1	(R)-limonene synthase, putative [Ricinus communis]
FtPinG0302582800.01	FtPinG0302582800.01.T01	XP_007223387.2	heat stress transcription factor A-5 [Prunus persica]
FtPinG0302583100.01	FtPinG0302583100.01.T01	PSS21410.1	ESF1 like [Actinidia chinensis var. chinensis]
FtPinG0302583800.01	FtPinG0302583800.01.T01	KYP50337.1	Xyloglucan endotransglucosylase/hydrolase protein 9, partial [Cajanus cajan]
FtPinG0302583900.01	FtPinG0302583900.01.T01	OMO61979.1	Sugar/inositol transporter [Corchorus capsularis]
FtPinG0302584500.01	FtPinG0302584500.01.T01	XP_002276175.1	PREDICTED: fasciclin-like arabinogalactan protein 21 [Vitis vinifera]
FtPinG0302584800.01	FtPinG0302584800.01.T01	XP_021651067.1	indole-3-acetic acid-amido synthetase GH3.6-like [Hevea brasiliensis]
FtPinG0302585000.01	FtPinG0302585000.01.T01	XP_011089272.1	protein CNGC15b isoform X2 [Sesamum indicum]
FtPinG0302746400.01	FtPinG0302746400.01.T01	XP_023902957.1	ankyrin repeat domain-containing protein 2A-like [Quercus suber]
FtPinG0302746600.01	FtPinG0302746600.01.T01	RLW29401.1	ankyrin repeat domain-containing protein 2b [Quercus suber]

Supplementary Table 10 (Continued):

FtPinG0302747100.01	FtPinG0302747100.01.T01	PRQ29577.1	putative glucan endo-1,3-beta-D-glucosidase [Rosa chinensis]
FtPinG0302747300.01	FtPinG0302747300.01.T01	XP_021743351.1	ABC transporter C family member 2-like [Chenopodium quinoa]
FtPinG0302747700.01	FtPinG0302747700.01.T01	XP_021728895.1	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK3 [Chenopodium quinoa]
FtPinG0302748100.01	FtPinG0302748100.01.T01	XP_021773241.1	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK3 [Chenopodium quinoa]
FtPinG0302748700.01	FtPinG0302748700.01.T01	XP_017983502.1	PREDICTED: BTB/POZ domain-containing protein At1g30440 isoform X1 [Theobroma cacao]
FtPinG0302748700.01	FtPinG0302748700.01.T02	XP_017983502.1	PREDICTED: BTB/POZ domain-containing protein At1g30440 isoform X1 [Theobroma cacao]
FtPinG0302748700.01	FtPinG0302748700.01.T03	XP_017983502.1	PREDICTED: BTB/POZ domain-containing protein At1g30440 isoform X1 [Theobroma cacao]
FtPinG0302749000.01	FtPinG0302749000.01.T02	PWA74495.1	HAD-like domain-containing protein [Artemisia annua]
FtPinG0302749200.01	FtPinG0302749200.01.T01	PSS02627.1	Cation-chloride cotransporter like [Actinidia chinensis var. chinensis]
FtPinG0302749700.01	FtPinG0302749700.01.T01	XP_002268531.1	PREDICTED: WAT1-related protein At3g45870 isoform X1 [Vitis vinifera]
FtPinG0302750000.01	FtPinG0302750000.01.T01	PSS28906.1	Coiled-coil domain-containing protein [Actinidia chinensis var. chinensis]
FtPinG0302750400.01	FtPinG0302750400.01.T01	PSS17865.1	Pentatricopeptide repeat-containing protein [Actinidia chinensis var. chinensis]
FtPinG0302750900.01	FtPinG0302750900.01.T01	XP_021725756.1	nucleoprotein TPR-like isoform X2 [Chenopodium quinoa]
FtPinG0302750900.01	FtPinG0302750900.01.T02	XP_021725756.1	nucleoprotein TPR-like isoform X2 [Chenopodium quinoa]
FtPinG0302751600.01	FtPinG0302751600.01.T01	OMO52409.1	Pyridine nucleotide-disulfide oxidoreductase, class-II [Corchorus capsularis]
FtPinG0302751700.01	FtPinG0302751700.01.T01	XP_012067578.2	fasciclin-like arabinogalactan protein 14 [Jatropha curcas]
FtPinG0302752000.01	FtPinG0302752000.01.T01	XP_019430808.1	PREDICTED: beta-glucuronosyltransferase GlcAT14A-like [Lupinus angustifolius]
FtPinG0302752600.01	FtPinG0302752600.01.T01	XP_021741196.1	probable polyribonucleotide nucleotidyltransferase 1, chloroplastic [Chenopodium quinoa]
FtPinG0302753000.01	FtPinG0302753000.01.T01	XP_003555016.2	GDSL esterase/lipase 7 isoform X1 [Glycine max]

Supplementary Table 10 (Continued):

FtPinG0302807100.01	FtPinG0302807100.01.T01	KYP62091.1	Tuftelin-interacting protein 11 [Cajanus cajan]
FtPinG0302807600.01	FtPinG0302807600.01.T01	XP_011039030.1	PREDICTED: transcription factor MYC2 isoform X2 [Populus euphratica]
FtPinG0302807800.01	FtPinG0302807800.01.T01	XP_020205460.1	transcription factor MYC4-like [Cajanus cajan]
FtPinG0302808000.01	FtPinG0302808000.01.T01	PSS03906.1	Transcription factor like [Actinidia chinensis var. chinensis]
FtPinG0302809300.01	FtPinG0302809300.01.T01	OVA16139.1	Peptidase C26 [Macleaya cordata]
FtPinG0302809600.01	FtPinG0302809600.01.T01	AJD87472.1	cytochrome P450 CYP76AD16 [Cleretum bellidiforme]
FtPinG0302810000.01	FtPinG0302810000.01.T01	XP_010693635.1	PREDICTED: uncharacterized protein LOC104906563 [Beta vulgaris subsp. vulgaris]
FtPinG0302810300.01	FtPinG0302810300.01.T01	XP_021744340.1	ribonuclease H2 subunit B-like [Chenopodium quinoa]
FtPinG0302810800.01	FtPinG0302810800.01.T01	XP_021640036.1	CBS domain-containing protein CBSX5-like [Hevea brasiliensis]
FtPinG0302810900.01	FtPinG0302810900.01.T01	XP_010686525.1	PREDICTED: splicing factor U2af large subunit B-like isoform X3 [Beta vulgaris subsp. vulgaris]
FtPinG0302811100.01	FtPinG0302811100.01.T01	XP_021740558.1	stem-specific protein TSJT1-like [Chenopodium quinoa]
FtPinG0302811300.01	FtPinG0302811300.01.T01	XP_021726413.1	putative serine/threonine-protein kinase isoform X1 [Chenopodium quinoa]
FtPinG0302811900.01	FtPinG0302811900.01.T01	XP_021276897.1	LOW QUALITY PROTEIN: pentatricopeptide repeat-containing protein At1g77170 [Herrania umbratica]
FtPinG0302812200.01	FtPinG0302812200.01.T01	XP_021293630.1	RNA polymerase II C-terminal domain phosphatase-like 1 isoform X1 [Herrania umbratica]
FtPinG0302812300.01	FtPinG0302812300.01.T01	XP_010646902.1	PREDICTED: uncharacterized protein LOC100249879 [Vitis vinifera]
FtPinG0302812500.01	FtPinG0302812500.01.T01	XP_023550671.1	50S ribosomal protein L27, chloroplastic [Cucurbita pepo subsp. pepo]
FtPinG0302812700.01	FtPinG0302812700.01.T01	XP_015900774.1	exosome complex component RRP42 isoform X2 [Ziziphus jujuba]
FtPinG0302812700.01	FtPinG0302812700.01.T02	XP_015900774.1	exosome complex component RRP42 isoform X2 [Ziziphus jujuba]
FtPinG0302815600.01	FtPinG0302815600.01.T01	XP_022715923.1	serine carboxypeptidase-like 31 isoform X2 [Durio zibethinus]
FtPinG0302815800.01	FtPinG0302815800.01.T01	AFO63288.1	bZIP9 [Tamarix hispida]
FtPinG0302816700.01	FtPinG0302816700.01.T01	XP_021616320.1	FGGY carbohydrate kinase domain-containing protein isoform X1 [Manihot esculenta]

Supplementary Table 10 (Continued):

FtPinG0302816900.01	FtPinG0302816900.01.T01	XP_010694375.1	PREDICTED: inactive protein RESTRICTED TEV MOVEMENT 2 [Beta vulgaris subsp. vulgaris]
FtPinG0302817100.01	FtPinG0302817100.01.T01	XP_018812445.1	PREDICTED: uncharacterized protein LOC108984832 [Juglans regia]
FtPinG0302817800.01	FtPinG0302817800.01.T01	XP_010671528.1	PREDICTED: lipoyl synthase 2, mitochondrial [Beta vulgaris subsp. vulgaris]
FtPinG0302818100.01	FtPinG0302818100.01.T01	XP_021740494.1	katanin p80 WD40 repeat-containing subunit B1 homolog isoform X1 [Chenopodium quinoa]
FtPinG0302818900.01	FtPinG0302818900.01.T01	XP_008364461.2	PREDICTED: midasin-like [Malus domestica]
FtPinG0302819100.01	FtPinG0302819100.01.T01	GAV80132.1	AAA_5 domain-containing protein [Cephalotus follicularis]
FtPinG0302819300.01	FtPinG0302819300.01.T01	XP_024931658.1	midasin-like [Ziziphus jujuba]
FtPinG0302819700.01	FtPinG0302819700.01.T01	XP_010654485.1	PREDICTED: midasin isoform X1 [Vitis vinifera]
FtPinG0302819900.01	FtPinG0302819900.01.T01	XP_024971455.1	midasin isoform X4 [Cynara cardunculus var. scolymus]
FtPinG0302820100.01	FtPinG0302820100.01.T01	XP_021720498.1	midasin-like [Chenopodium quinoa]
FtPinG0302820300.01	FtPinG0302820300.01.T01	XP_022715212.1	midasin isoform X14 [Durio zibethinus]
FtPinG0302820500.01	FtPinG0302820500.01.T01	XP_010654485.1	PREDICTED: midasin isoform X1 [Vitis vinifera]
FtPinG0302820700.01	FtPinG0302820700.01.T01	XP_023881016.1	midasin isoform X3 [Quercus suber]
FtPinG0302821200.01	FtPinG0302821200.01.T01	XP_013733270.1	glycine-rich cell wall structural protein-like [Brassica napus]
FtPinG0302821800.01	FtPinG0302821800.01.T01	XP_021615637.1	(+)-neomenthol dehydrogenase [Manihot esculenta]
FtPinG0302822200.01	FtPinG0302822200.01.T01	XP_021653044.1	(+)-neomenthol dehydrogenase-like isoform X1 [Hevea brasiliensis]
FtPinG0302822300.01	FtPinG0302822300.01.T01	XP_021901055.1	probable serine/threonine-protein kinase PBL18 isoform X1 [Carica papaya]
FtPinG0302822500.01	FtPinG0302822500.01.T01	XP_015943332.1	quinone oxidoreductase PIG3 [Arachis duranensis]
FtPinG0302822700.01	FtPinG0302822700.01.T01	XP_010268800.1	PREDICTED: quinone oxidoreductase PIG3 [Nelumbo nucifera]
FtPinG0302823100.01	FtPinG0302823100.01.T01	XP_002268954.2	PREDICTED: transmembrane protein 184 homolog DDB_G0279555 [Vitis vinifera]
FtPinG0302823500.01	FtPinG0302823500.01.T01	XP_023900610.1	probable ADP-ribosylation factor GTPase-activating protein AGD5 isoform X1 [Quercus suber]
FtPinG0302831400.01	FtPinG0302831400.01.T01	XP_010677149.1	PREDICTED: serine/threonine-protein kinase SAPK3 [Beta vulgaris subsp. vulgaris]

Supplementary Table 10 (Continued):

FtPinG0302831500.01	FtPinG0302831500.01.T01	XP_021765757.1	chlorophyll a-b binding protein CP29.1, chloroplastic-like [Chenopodium quinoa]
FtPinG0302831800.01	FtPinG0302831800.01.T01	XP_010096714.1	nudix hydrolase 1 [Morus notabilis]
FtPinG0302832300.01	FtPinG0302832300.01.T01	XP_021768475.1	chaperone protein dnaJ 13-like [Chenopodium quinoa]
FtPinG0302832500.01	FtPinG0302832500.01.T01	XP_006350990.1	PREDICTED: polyubiquitin-like [Solanum tuberosum]
FtPinG0302832900.01	FtPinG0302832900.01.T01	XP_010683074.1	PREDICTED: ATP-dependent 6-phosphofructokinase 2 [Beta vulgaris subsp. vulgaris]
FtPinG0302833600.01	FtPinG0302833600.01.T01	XP_010685243.1	PREDICTED: berberine bridge enzyme-like 4 [Beta vulgaris subsp. vulgaris]
FtPinG0302833700.01	FtPinG0302833700.01.T01	XP_021821169.1	L-lactate dehydrogenase B-like [Prunus avium]
FtPinG0302834400.01	FtPinG0302834400.01.T01	XP_006478407.1	2-oxoglutarate dehydrogenase, mitochondrial-like [Citrus sinensis]
FtPinG0302834500.01	FtPinG0302834500.01.T01	XP_004297048.1	PREDICTED: uncharacterized protein LOC101298011 [Fragaria vesca subsp. vesca]
FtPinG0302834700.01	FtPinG0302834700.01.T01	XP_021908276.1	GDP-mannose 4,6 dehydratase 1 [Carica papaya]
FtPinG0302834900.01	FtPinG0302834900.01.T01	XP_012079677.1	alcohol dehydrogenase-like 6 isoform X1 [Jatropha curcas]
FtPinG0302835100.01	FtPinG0302835100.01.T01	XP_023877711.1	probable receptor-like protein kinase At2g42960 [Quercus suber]
FtPinG0302835100.01	FtPinG0302835100.01.T02	XP_023877711.1	probable receptor-like protein kinase At2g42960 [Quercus suber]
FtPinG0302835500.01	FtPinG0302835500.01.T02	PSS17635.1	Acetylxylan esterase A precursor [Actinidia chinensis var. chinensis]
FtPinG0302836100.01	FtPinG0302836100.01.T01	OMO49665.1	Phospholipid/glycerol acyltransferase [Corchorus capsularis]
FtPinG0302837000.01	FtPinG0302837000.01.T01	XP_010688885.1	PREDICTED: callose synthase 7 [Beta vulgaris subsp. vulgaris]
FtPinG0302837400.01	FtPinG0302837400.01.T01	XP_021609324.1	probable glucuronoxylan glucuronosyltransferase IRX7 [Manihot esculenta]
FtPinG0302837600.01	FtPinG0302837600.01.T01	POO01140.1	Xyloglucan endotransglucosylase/hydrolase [Trema orientale]
FtPinG0302995100.01	FtPinG0302995100.01.T01	PIN00194.1	DNA-directed DNA polymerase [Handroanthus impetiginosus]
FtPinG0302995500.01	FtPinG0302995500.01.T01	AFO83616.1	APETALA3-like protein [Fagopyrum esculentum]
FtPinG0302995800.01	FtPinG0302995800.01.T01	XP_021765055.1	LOW QUALITY PROTEIN: scarecrow-like protein 8 [Chenopodium quinoa]
FtPinG0302996900.01	FtPinG0302996900.01.T01	XP_021726724.1	probable receptor-like protein kinase At5g24010 [Chenopodium quinoa]
FtPinG0302996900.01	FtPinG0302996900.01.T02	PQQ20608.1	putative receptor-like protein kinase [Prunus yedoensis var. nudiflora]
FtPinG0302997500.01	FtPinG0302997500.01.T01	XP_021765112.1	cytokinin hydroxylase-like [Chenopodium quinoa]

Supplementary Table 10 (Continued):

FtPinG0302997800.01	FtPinG0302997800.01.T01	XP_012090212.1	sec-independent protein translocase protein TATB, chloroplastic [Jatropha curcas]
FtPinG0302998400.01	FtPinG0302998400.01.T01	XP_019449673.1	PREDICTED: putative transporter arsB [Lupinus angustifolius]
FtPinG0302998900.01	FtPinG0302998900.01.T01	XP_008234212.1	PREDICTED: uncharacterized protein At3g49055 [Prunus mume]
FtPinG0302999100.01	FtPinG0302999100.01.T01	XP_002272855.1	PREDICTED: ABC transporter B family member 26, chloroplastic isoform X4 [Vitis vinifera]
FtPinG0303464800.01	FtPinG0303464800.01.T01	XP_021772712.1	MDIS1-interacting receptor like kinase 1-like [Chenopodium quinoa]
FtPinG0303464800.01	FtPinG0303464800.01.T02	XP_002270291.2	PREDICTED: probable aminopyrimidine aminohydrolase, mitochondrial isoform X2 [Vitis vinifera]
FtPinG0303465600.01	FtPinG0303465600.01.T01	XP_021734750.1	ammonium transporter 1 member 2-like [Chenopodium quinoa]
FtPinG0303466500.01	FtPinG0303466500.01.T01	XP_009369494.1	PREDICTED: uncharacterized protein LOC103958897 [Pyrus x bretschneideri]
FtPinG0303466800.01	FtPinG0303466800.01.T01	OMO87820.1	SWEET sugar transporter [Corchorus olitorius]
FtPinG0303467200.01	FtPinG0303467200.01.T01	XP_019104252.1	PREDICTED: serine/threonine-protein kinase CDL1-like [Beta vulgaris subsp. vulgaris]
FtPinG0303467300.01	FtPinG0303467300.01.T01	XP_023917751.1	rab escort protein 1-like [Quercus suber]
FtPinG0303467800.01	FtPinG0303467800.01.T01	RLW15752.1	U-box domain-containing protein 33 [Quercus suber]
FtPinG0303467900.01	FtPinG0303467900.01.T01	XP_010674196.1	PREDICTED: putative F-box protein PP2-B12 [Beta vulgaris subsp. vulgaris]
FtPinG0303589600.01	FtPinG0303589600.01.T01	OMO75233.1	PetM of cytochrome b6/f complex subunit 7 [Corchorus capsularis]
FtPinG0303589800.01	FtPinG0303589800.01.T01	XP_010664618.1	PREDICTED: B3 domain-containing protein Os01g0723500 isoform X1 [Vitis vinifera]
FtPinG0303590100.01	FtPinG0303590100.01.T01	XP_021856248.1	thylakoidal processing peptidase 1, chloroplastic-like [Spinacia oleracea]
FtPinG0303590300.01	FtPinG0303590300.01.T01	XP_021726664.1	LOW QUALITY PROTEIN: nucleobase-ascorbate transporter 3-like [Chenopodium quinoa]
FtPinG0303590800.01	FtPinG0303590800.01.T01	XP_021718731.1	LOW QUALITY PROTEIN: probable disease resistance protein At4g33300 [Chenopodium quinoa]
FtPinG0303591400.01	FtPinG0303591400.01.T01	OMO74881.1	Thioredoxin-like protein [Corchorus olitorius]

Supplementary Table 10 (Continued):

FtPinG0303591800.01	FtPinG0303591800.01.T01	XP_015885429.1	protein MIZU-KUSSEI 1 [Ziziphus jujuba]
FtPinG0303591900.01	FtPinG0303591900.01.T01	XP_002284264.2	PREDICTED: dipeptidyl-peptidase 5 [Vitis vinifera]
FtPinG0303592500.01	FtPinG0303592500.01.T01	XP_010667609.1	PREDICTED: uncharacterized protein LOC104884621 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0303593000.01	FtPinG0303593000.01.T01	XP_022773627.1	polyadenylate-binding protein RBP47-like [Durio zibethinus]
FtPinG0303593300.01	FtPinG0303593300.01.T01	ADP20180.1	mutant gag-pol polyprotein [Pisum sativum]
FtPinG0303593900.01	FtPinG0303593900.01.T01	XP_010684140.1	PREDICTED: uncharacterized protein LOC104898734 [Beta vulgaris subsp. vulgaris]
FtPinG0303594300.01	FtPinG0303594300.01.T01	EOY14522.1	Succinate dehydrogenase 5 [Theobroma cacao]
FtPinG0303595100.01	FtPinG0303595100.01.T01	XP_018827570.1	PREDICTED: uncharacterized protein LOC108996256 [Juglans regia]
FtPinG0303595700.01	FtPinG0303595700.01.T01	PSR99759.1	Transmembrane protein like [Actinidia chinensis var. chinensis]
FtPinG0303596100.01	FtPinG0303596100.01.T01	OVA03687.1	GTP binding domain [Macleaya cordata]
FtPinG0380001156.01	FtPinG0380001156.01.T01	XP_004506381.1	PREDICTED: uncharacterized protein LOC101512433 [Cicer arietinum]
FtPinG0380001190.01	FtPinG0380001190.01.T01	PNY14872.1	ribonuclease H, partial [Trifolium pratense]
FtPinG0403695900.01	FtPinG0403695900.01.T01	XP_021753672.1	probable serine/threonine-protein kinase At1g54610 [Chenopodium quinoa]
FtPinG0403698000.01	FtPinG0403698000.01.T01	RLW51031.1	pentatricopeptide repeat-containing protein [Quercus suber]
FtPinG0403698100.01	FtPinG0403698100.01.T01	XP_008233855.1	PREDICTED: probable xyloglucan galactosyltransferase GT17 [Prunus mume]
FtPinG0403698600.01	FtPinG0403698600.01.T01	XP_010656978.1	PREDICTED: dihydroorotase, mitochondrial isoform X1 [Vitis vinifera]
FtPinG0403699000.01	FtPinG0403699000.01.T01	XP_020540100.1	ADP,ATP carrier protein 3, mitochondrial [Jatropha curcas]
FtPinG0403699200.01	FtPinG0403699200.01.T01	PSS14467.1	Mitotic checkpoint serine/threonine-protein kinase [Actinidia chinensis var. chinensis]
FtPinG0403699300.01	FtPinG0403699300.01.T01	XP_021642502.1	putative E3 ubiquitin-protein ligase RING1a isoform X2 [Hevea brasiliensis]
FtPinG0403699700.01	FtPinG0403699700.01.T01	EEF44395.1	Nonspecific lipid-transfer protein 3 precursor, putative [Ricinus communis]
FtPinG0403700100.01	FtPinG0403700100.01.T01	XP_021894296.1	probable protein phosphatase 2C 58 isoform X1 [Carica papaya]
FtPinG0403700500.01	FtPinG0403700500.01.T01	XP_017639190.1	PREDICTED: zinc finger CCCH domain-containing protein 2-like isoform X1 [Gossypium arboreum]
FtPinG0403701800.01	FtPinG0403701800.01.T01	XP_006372753.2	transcription activator GLK1 isoform X1 [Populus trichocarpa]

Supplementary Table 10 (Continued):

FtPinG0403701800.01	FtPinG0403701800.01.T02	XP_021848304.1	transcription activator GLK1-like [Spinacia oleracea]
FtPinG0403702100.01	FtPinG0403702100.01.T01	EEF44371.1	Protein SIS1, putative [Ricinus communis]
FtPinG0403953900.01	FtPinG0403953900.01.T01	OMO63959.1	CTP synthase [Corchorus capsularis]
FtPinG0403953900.01	FtPinG0403953900.01.T02	OMO63959.1	CTP synthase [Corchorus capsularis]
FtPinG0403954200.01	FtPinG0403954200.01.T01	XP_011041610.1	PREDICTED: uncharacterized protein LOC105137530 [Populus euphratica]
FtPinG0403954400.01	FtPinG0403954400.01.T01	XP_021768823.1	casein kinase 1-like protein 10 [Chenopodium quinoa]
FtPinG0403954500.01	FtPinG0403954500.01.T01	XP_002277335.1	PREDICTED: serine/threonine-protein kinase 19 isoform X1 [Vitis vinifera]
FtPinG0403954900.01	FtPinG0403954900.01.T01	XP_013717716.1	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 4-like [Brassica napus]
FtPinG0403955300.01	FtPinG0403955300.01.T01	XP_021769866.1	patellin-4-like [Chenopodium quinoa]
FtPinG0403955500.01	FtPinG0403955500.01.T01	ABB77213.1	11S globulin-like protein [Actinidia chinensis]
FtPinG0403955800.01	FtPinG0403955800.01.T01	XP_021854998.1	chromatin modification-related protein MEAF6-like isoform X1 [Spinacia oleracea]
FtPinG0403955900.01	FtPinG0403955900.01.T01	XP_011078309.1	peroxisomal fatty acid beta-oxidation multifunctional protein AIM1 [Sesamum indicum]
FtPinG0403956100.01	FtPinG0403956100.01.T01	ACH63222.1	actin depolymerizing factor [Rheum australe]
FtPinG0403957100.01	FtPinG0403957100.01.T01	XP_021864615.1	bidirectional sugar transporter SWEET4-like [Spinacia oleracea]
FtPinG0403957300.01	FtPinG0403957300.01.T01	XP_021864615.1	bidirectional sugar transporter SWEET4-like [Spinacia oleracea]
FtPinG0403957900.01	FtPinG0403957900.01.T01	XP_021757713.1	bidirectional sugar transporter SWEET7-like [Chenopodium quinoa]
FtPinG0403958100.01	FtPinG0403958100.01.T01	XP_021864615.1	bidirectional sugar transporter SWEET4-like [Spinacia oleracea]
FtPinG0403958400.01	FtPinG0403958400.01.T02	XP_021757709.1	protein NLP6-like [Chenopodium quinoa]
FtPinG0404044100.01	FtPinG0404044100.01.T01	XP_021866543.1	putative pentatricopeptide repeat-containing protein At2g01510 [Spinacia oleracea]
FtPinG0404044600.01	FtPinG0404044600.01.T01	XP_018807572.1	PREDICTED: serine/threonine-protein kinase EDR1-like isoform X1 [Juglans regia]
FtPinG0404045400.01	FtPinG0404045400.01.T01	PON82288.1	Multi antimicrobial extrusion protein [Trema orientale]
FtPinG0404046000.01	FtPinG0404046000.01.T01	PON82288.1	Multi antimicrobial extrusion protein [Trema orientale]
FtPinG0404046300.01	FtPinG0404046300.01.T01	XP_010261209.1	PREDICTED: bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase-like [Nelumbo nucifera]

Supplementary Table 10 (Continued):

FtPinG0404046300.01	FtPinG0404046300.01.T02	XP_010261209.1	PREDICTED: bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase-like [Nelumbo nucifera]
FtPinG0404046500.01	FtPinG0404046500.01.T01	XP_010251068.1	PREDICTED: uncharacterized protein LOC104593060 isoform X1 [Nelumbo nucifera]
FtPinG0404047000.01	FtPinG0404047000.01.T01	XP_010695655.1	PREDICTED: DExH-box ATP-dependent RNA helicase DExH3 [Beta vulgaris subsp. vulgaris]
FtPinG0404048000.01	FtPinG0404048000.01.T01	XP_018478119.1	PREDICTED: 60S ribosomal protein L11-2-like [Raphanus sativus]
FtPinG0404048600.01	FtPinG0404048600.01.T01	XP_019055261.1	PREDICTED: granule-bound starch synthase 1, chloroplastic/amyloplastic isoform X1 [Nelumbo nucifera]
FtPinG0404051200.01	FtPinG0404051200.01.T01	XP_010663543.1	PREDICTED: transcription factor DICHOTOMA [Vitis vinifera]
FtPinG0404052800.01	FtPinG0404052800.01.T01	XP_023913092.1	histone deacetylase 15 isoform X1 [Quercus suber]
FtPinG0404056500.01	FtPinG0404056500.01.T01	XP_011008350.1	PREDICTED: ras-related protein RABA6a [Populus euphratica]
FtPinG0404057600.01	FtPinG0404057600.01.T01	XP_018821437.1	PREDICTED: arabinosyltransferase XEG113 [Juglans regia]
FtPinG0404057800.01	FtPinG0404057800.01.T01	OMO67967.1	Zinc finger, RING-type [Corchorus capsularis]
FtPinG0404057800.01	FtPinG0404057800.01.T02	OMO67967.1	Zinc finger, RING-type [Corchorus capsularis]
FtPinG0404058800.01	FtPinG0404058800.01.T01	XP_017645864.1	PREDICTED: uridine-cytidine kinase C-like isoform X1 [Gossypium arboreum]
FtPinG0404059300.01	FtPinG0404059300.01.T01	XP_018825667.1	PREDICTED: protein CWC15 homolog [Juglans regia]
FtPinG0404059300.01	FtPinG0404059300.01.T02	XP_018825676.1	PREDICTED: protein CWC15 homolog [Juglans regia]
FtPinG0404060800.01	FtPinG0404060800.01.T01	AYA22044.1	UFGT41 [Fagopyrum tataricum]
FtPinG0404061000.01	FtPinG0404061000.01.T01	AYA22044.1	UFGT41 [Fagopyrum tataricum]
FtPinG0404061200.01	FtPinG0404061200.01.T01	BAP90367.1	UDP-glycose: glycosyltransferase UGT89G1 [Fagopyrum esculentum]
FtPinG0404061600.01	FtPinG0404061600.01.T01	AYA22044.1	UFGT41 [Fagopyrum tataricum]
FtPinG0404061900.01	FtPinG0404061900.01.T01	AYA22044.1	UFGT41 [Fagopyrum tataricum]
FtPinG0404062900.01	FtPinG0404062900.01.T01	XP_002267092.1	PREDICTED: dof zinc finger protein DOF5.4 [Vitis vinifera]
FtPinG0404064400.01	FtPinG0404064400.01.T01	XP_021608269.1	probable caffeoyl-CoA O-methyltransferase At4g26220 [Manihot esculenta]

Supplementary Table 10 (Continued):

FtPinG0404065200.01	FtPinG0404065200.01.T01	XP_018846507.1	PREDICTED: probable flavin-containing monooxygenase 1 [Juglans regia]
FtPinG0404067500.01	FtPinG0404067500.01.T01	XP_010695247.1	PREDICTED: tip elongation aberrant protein 1 isoform X2 [Beta vulgaris subsp. vulgaris]
FtPinG0404067500.01	FtPinG0404067500.01.T02	XP_010663461.1	PREDICTED: uncharacterized protein LOC100251831 isoform X2 [Vitis vinifera]
FtPinG0404068100.01	FtPinG0404068100.01.T01	XP_010695245.1	PREDICTED: zinc finger CCCH domain-containing protein 55 isoform X2 [Beta vulgaris subsp. vulgaris]
FtPinG0404068500.01	FtPinG0404068500.01.T01	XP_019082048.1	PREDICTED: uncharacterized protein LOC100246698 isoform X2 [Vitis vinifera]
FtPinG0404069500.01	FtPinG0404069500.01.T01	XP_007037593.1	PREDICTED: transcription factor TCP5 [Theobroma cacao]
FtPinG0404070000.01	FtPinG0404070000.01.T01	XP_010030753.1	PREDICTED: uncharacterized protein LOC104420646 [Eucalyptus grandis]
FtPinG0404087800.01	FtPinG0404087800.01.T01	EXB39215.1	Cysteine synthase [Morus notabilis]
FtPinG0404087800.01	FtPinG0404087800.01.T02	EXB39215.1	Cysteine synthase [Morus notabilis]
FtPinG0404088700.01	FtPinG0404088700.01.T01	PON80852.1	camphor resistance CrcB family protein [Trema orientale]
FtPinG0404089100.01	FtPinG0404089100.01.T01	XP_021760516.1	fluoride export protein 1-like [Chenopodium quinoa]
FtPinG0404089300.01	FtPinG0404089300.01.T01	XP_010678474.1	PREDICTED: 18.5 kDa class I heat shock protein [Beta vulgaris subsp. vulgaris]
FtPinG0404091700.01	FtPinG0404091700.01.T01	XP_023549818.1	DNA-directed RNA polymerase II subunit 4-like [Cucurbita pepo subsp. pepo]
FtPinG0404091900.01	FtPinG0404091900.01.T01	XP_019199551.1	PREDICTED: DNA-directed RNA polymerase II subunit 4 [Ipomoea nil]
FtPinG0404092800.01	FtPinG0404092800.01.T01	XP_002281994.1	PREDICTED: cyclic dof factor 3 [Vitis vinifera]
FtPinG0404094700.01	FtPinG0404094700.01.T01	XP_020419191.1	pentatricopeptide repeat-containing protein At3g47530 [Prunus persica]
FtPinG0404095000.01	FtPinG0404095000.01.T01	XP_025012362.1	malate dehydrogenase, chloroplastic [Ricinus communis]
FtPinG0404095300.01	FtPinG0404095300.01.T01	XP_010693235.1	PREDICTED: 60S ribosomal protein L34 [Beta vulgaris subsp. vulgaris]
FtPinG0404095600.01	FtPinG0404095600.01.T01	XP_018826587.1	PREDICTED: putative pentatricopeptide repeat-containing protein At1g74580 [Juglans regia]
FtPinG0404096200.01	FtPinG0404096200.01.T01	XP_010681353.1	PREDICTED: uncharacterized protein LOC104896316 [Beta vulgaris subsp. vulgaris]
FtPinG0404172500.01	FtPinG0404172500.01.T01	XP_017971007.1	PREDICTED: ATP-dependent DNA helicase homolog RECG, chloroplastic [Theobroma cacao]

Supplementary Table 10 (Continued):

FtPinG0404173000.01	FtPinG0404173000.01.T01	PWA89375.1	ribonucleotide reductase 1 [Artemisia annua]
FtPinG0404173100.01	FtPinG0404173100.01.T01	AES76571.1	nodulin MtN21/EamA-like transporter family protein [Medicago truncatula]
FtPinG0404173400.01	FtPinG0404173400.01.T01	AAK70407.1	pol polyprotein [Citrus x paradisi]
FtPinG0404173500.01	FtPinG0404173500.01.T01	XP_009601533.1	PREDICTED: auxin efflux carrier component 3-like isoform X2 [Nicotiana tomentosiformis]
FtPinG0404476900.01	FtPinG0404476900.01.T01	XP_022864680.1	protein JINGUBANG-like isoform X2 [Olea europaea var. sylvestris]
FtPinG0404477200.01	FtPinG0404477200.01.T01	PON59436.1	Isopenicillin N synthase [Parasponia andersonii]
FtPinG0404477800.01	FtPinG0404477800.01.T01	XP_021737868.1	probable glycerol-3-phosphate dehydrogenase [NAD(+)] 1, cytosolic [Chenopodium quinoa]
FtPinG0404478600.01	FtPinG0404478600.01.T01	XP_010670380.1	PREDICTED: uncharacterized protein LOC104887448 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0404478800.01	FtPinG0404478800.01.T01	XP_010670354.1	PREDICTED: serine/threonine-protein kinase D6PKL1 [Beta vulgaris subsp. vulgaris]
FtPinG0404479400.01	FtPinG0404479400.01.T01	AAY42864.1	thioredoxin H [Nicotiana alata]
FtPinG0404479600.01	FtPinG0404479600.01.T01	XP_023880018.1	protein arginine methyltransferase NDUFAF7, mitochondrial isoform X2 [Quercus suber]
FtPinG0404480000.01	FtPinG0404480000.01.T01	XP_008457481.2	PREDICTED: methyl-CpG-binding domain-containing protein 5 [Cucumis melo]
FtPinG0404480100.01	FtPinG0404480100.01.T01	GAV76934.1	Aldose_epim domain-containing protein [Cephalotus follicularis]
FtPinG0404480400.01	FtPinG0404480400.01.T01	XP_021721379.1	binding partner of ACD11 1-like [Chenopodium quinoa]
FtPinG0404480800.01	FtPinG0404480800.01.T01	XP_016716068.1	PREDICTED: L10-interacting MYB domain-containing protein-like [Gossypium hirsutum]
FtPinG0404481100.01	FtPinG0404481100.01.T01	XP_010685074.1	PREDICTED: uncharacterized protein LOC104899556 [Beta vulgaris subsp. vulgaris]
FtPinG0404481300.01	FtPinG0404481300.01.T01	XP_010693230.1	PREDICTED: ATP-dependent 6-phosphofructokinase 5, chloroplastic [Beta vulgaris subsp. vulgaris]
FtPinG0404513000.01	FtPinG0404513000.01.T01	XP_021808490.1	indole-3-acetic acid-amido synthetase GH3.6 [Prunus avium]
FtPinG0404513200.01	FtPinG0404513200.01.T01	XP_021756372.1	histone-lysine N-methyltransferase ASHR2-like [Chenopodium quinoa]

Supplementary Table 10 (Continued):

FtPinG0404514000.01	FtPinG0404514000.01.T01	XP_021737727.1	histone-lysine N-methyltransferase ASHH1-like isoform X1 [Chenopodium quinoa]
FtPinG0404514400.01	FtPinG0404514400.01.T01	AUS89428.1	sulfate transporter [Sesuvium portulacastrum]
FtPinG0404514400.01	FtPinG0404514400.01.T02	AUS89428.1	sulfate transporter [Sesuvium portulacastrum]
FtPinG0404514500.01	FtPinG0404514500.01.T01	PSS31658.1	Low affinity sulfate transporter like [Actinidia chinensis var. chinensis]
FtPinG0404514900.01	FtPinG0404514900.01.T01	XP_008233986.1	PREDICTED: uncharacterized protein LOC103332977 [Prunus mume]
FtPinG0404515200.01	FtPinG0404515200.01.T01	XP_021729477.1	heavy metal-associated isoprenylated plant protein 24-like [Chenopodium quinoa]
FtPinG0404515400.01	FtPinG0404515400.01.T01	AFY26883.1	F-box family protein [Morella rubra]
FtPinG0404515600.01	FtPinG0404515600.01.T01	XP_024449939.1	protein NETWORKED 1D isoform X3 [Populus trichocarpa]
FtPinG0404516000.01	FtPinG0404516000.01.T01	XP_010664285.1	PREDICTED: centromere-associated protein E [Vitis vinifera]
FtPinG0404517800.01	FtPinG0404517800.01.T01	XP_015578697.1	pentatricopeptide repeat-containing protein At1g71420 [Ricinus communis]
FtPinG0404518400.01	FtPinG0404518400.01.T01	XP_004290467.1	PREDICTED: ras-related protein Rab7 [Fragaria vesca subsp. vesca]
FtPinG0404518400.01	FtPinG0404518400.01.T02	XP_004290467.1	PREDICTED: ras-related protein Rab7 [Fragaria vesca subsp. vesca]
FtPinG0404518800.01	FtPinG0404518800.01.T01	PRQ24550.1	putative initiation factor eIF-4 gamma, MA3 [Rosa chinensis]
FtPinG0404519100.01	FtPinG0404519100.01.T01	XP_010523588.2	PREDICTED: uncharacterized protein LOC104801906, partial [Tarenaya hassleriana]
FtPinG0404519600.01	FtPinG0404519600.01.T02	PIN25287.1	putative unusual protein kinase [Handroanthus impetiginosus]
FtPinG0404519600.01	FtPinG0404519600.01.T03	PIN25287.1	putative unusual protein kinase [Handroanthus impetiginosus]
FtPinG0404520400.01	FtPinG0404520400.01.T01	XP_002264732.1	PREDICTED: exocyst complex component SEC6 [Vitis vinifera]
FtPinG0404521100.01	FtPinG0404521100.01.T01	XP_010261009.1	PREDICTED: peroxidase 12-like [Nelumbo nucifera]
FtPinG0404521500.01	FtPinG0404521500.01.T01	XP_010683356.1	PREDICTED: putative methylesterase 14, chloroplastic [Beta vulgaris subsp. vulgaris]
FtPinG0404521500.01	FtPinG0404521500.01.T02	XP_010683356.1	PREDICTED: putative methylesterase 14, chloroplastic [Beta vulgaris subsp. vulgaris]
FtPinG0404521800.01	FtPinG0404521800.01.T01	XP_008219076.1	PREDICTED: uncharacterized protein LOC103319326 [Prunus mume]
FtPinG0404522000.01	FtPinG0404522000.01.T01	XP_021732215.1	gamma-tubulin complex component 5-like isoform X2 [Chenopodium quinoa]
FtPinG0404522300.01	FtPinG0404522300.01.T01	XP_018849478.1	PREDICTED: queuine tRNA-ribosyltransferase accessory subunit-like [Juglans regia]
FtPinG0404522300.01	FtPinG0404522300.01.T02	XP_017980821.1	PREDICTED: queuine tRNA-ribosyltransferase subunit qtrtd1 [Theobroma cacao]

Supplementary Table 10 (Continued):

FtPinG0404522300.01	FtPinG0404522300.01.T03	XP_022718362.1	queuine tRNA-ribosyltransferase accessory subunit 2-like isoform X4 [Durio zibethinus]
FtPinG0404522800.01	FtPinG0404522800.01.T01	PSS32451.1	Transmembrane protein like [Actinidia chinensis var. chinensis]
FtPinG0404522800.01	FtPinG0404522800.01.T02	PSS32451.1	Transmembrane protein like [Actinidia chinensis var. chinensis]
FtPinG0404522800.01	FtPinG0404522800.01.T03	PSS34390.1	Transmembrane protein like [Actinidia chinensis var. chinensis]
FtPinG0404523300.01	FtPinG0404523300.01.T01	PSR85302.1	Alanine--tRNA ligase [Actinidia chinensis var. chinensis]
FtPinG0404523800.01	FtPinG0404523800.01.T01	XP_021613140.1	beta-amylase 7 isoform X1 [Manihot esculenta]
FtPinG0404525000.01	FtPinG0404525000.01.T01	XP_021850025.1	U-box domain-containing protein 33-like isoform X3 [Spinacia oleracea]
FtPinG0404525500.01	FtPinG0404525500.01.T01	XP_024024022.1	U-box domain-containing protein 33 [Morus notabilis]
FtPinG0404525900.01	FtPinG0404525900.01.T01	XP_012836150.1	PREDICTED: uncharacterized protein LOC105956795 [Erythranthe guttata]
FtPinG0404526400.01	FtPinG0404526400.01.T01	XP_010663715.1	PREDICTED: origin of replication complex subunit 5 [Vitis vinifera]
FtPinG0404884300.01	FtPinG0404884300.01.T01	XP_021277916.1	receptor-like protein kinase HERK 1 [Herrania umbratica]
FtPinG0404884700.01	FtPinG0404884700.01.T01	XP_021741717.1	nuclear pore complex protein NUP205-like [Chenopodium quinoa]
FtPinG0404885300.01	FtPinG0404885300.01.T01	XP_010669557.1	PREDICTED: uncharacterized protein LOC104886760 [Beta vulgaris subsp. vulgaris]
FtPinG0404885700.01	FtPinG0404885700.01.T01	XP_019434094.1	PREDICTED: 60S ribosomal protein L19-3-like [Lupinus angustifolius]
FtPinG0404886100.01	FtPinG0404886100.01.T01	XP_019434094.1	PREDICTED: 60S ribosomal protein L19-3-like [Lupinus angustifolius]
FtPinG0404886400.01	FtPinG0404886400.01.T01	AAB68819.1	ethylene receptor [Rumex palustris]
FtPinG0404886800.01	FtPinG0404886800.01.T01	XP_021889215.1	chaperone protein DnaJ-like isoform X3 [Carica papaya]
FtPinG0404887000.01	FtPinG0404887000.01.T01	XP_021865774.1	kinesin-like protein KIN-14I [Spinacia oleracea]
FtPinG0404887200.01	FtPinG0404887200.01.T01	XP_018824788.1	PREDICTED: nicotinamide adenine dinucleotide transporter 1, chloroplastic-like [Juglans regia]
FtPinG0404887600.01	FtPinG0404887600.01.T01	AYM45134.1	flavonol synthase [Fagopyrum tataricum]
FtPinG0404887800.01	FtPinG0404887800.01.T01	BAU59409.1	cytochrome P450 82an1 [Fallopia sachalinensis]
FtPinG0404887900.01	FtPinG0404887900.01.T01	XP_012575216.1	PREDICTED: uncharacterized protein LOC105852922, partial [Cicer arietinum]
FtPinG0404888400.01	FtPinG0404888400.01.T01	XP_010683547.1	PREDICTED: probable terpene synthase 6 isoform X2 [Beta vulgaris subsp. vulgaris]

Supplementary Table 10 (Continued):

FtPinG0404888500.01	FtPinG0404888500.01.T01	KHN16363.1	Cytochrome P450 82A4 [Glycine soja]
FtPinG0404888800.01	FtPinG0404888800.01.T01	XP_004509679.1	PREDICTED: mitochondrial uncoupling protein 5-like [Cicer arietinum]
FtPinG0404889100.01	FtPinG0404889100.01.T01	XP_019156461.1	PREDICTED: cytochrome P450 81E8-like [Ipomoea nil]
FtPinG0404889400.01	FtPinG0404889400.01.T01	EEF47309.1	ATP binding protein, putative [Ricinus communis]
FtPinG0404889700.01	FtPinG0404889700.01.T01	XP_021763261.1	vacuolar protein sorting-associated protein 2 homolog 3-like [Chenopodium quinoa]
FtPinG0404890000.01	FtPinG0404890000.01.T01	XP_019076869.1	PREDICTED: glutathione gamma-glutamylcysteinyltransferase 1 [Vitis vinifera]
FtPinG0404890100.01	FtPinG0404890100.01.T01	PSR89747.1	Tetratricopeptide repeat protein like [Actinidia chinensis var. chinensis]
FtPinG0404890600.01	FtPinG0404890600.01.T01	XP_021722219.1	multiple organellar RNA editing factor 2, chloroplastic-like [Chenopodium quinoa]
FtPinG0404890700.01	FtPinG0404890700.01.T01	XP_010695523.1	PREDICTED: uncharacterized protein LOC104908140 [Beta vulgaris subsp. vulgaris]
FtPinG0404890900.01	FtPinG0404890900.01.T01	XP_010668250.1	PREDICTED: uncharacterized protein LOC104885245, partial [Beta vulgaris subsp. vulgaris]
FtPinG0404891100.01	FtPinG0404891100.01.T01	XP_010668250.1	PREDICTED: uncharacterized protein LOC104885245, partial [Beta vulgaris subsp. vulgaris]
FtPinG0404891800.01	FtPinG0404891800.01.T01	XP_010670227.1	PREDICTED: UPF0496 protein At3g19330 isoform X2 [Beta vulgaris subsp. vulgaris]
FtPinG0404892000.01	FtPinG0404892000.01.T01	XP_018827295.1	PREDICTED: probable inactive histone-lysine N-methyltransferase SUVR2 isoform X2 [Juglans regia]
FtPinG0404892700.01	FtPinG0404892700.01.T01	XP_018858586.1	PREDICTED: tetratricopeptide repeat protein 4 homolog [Juglans regia]
FtPinG0404893000.01	FtPinG0404893000.01.T01	PON54579.1	Alcohol dehydrogenase class III/S-(hydroxymethyl)glutathione dehydrogenase [Trema orientale]
FtPinG0404893400.01	FtPinG0404893400.01.T01	XP_008234035.1	PREDICTED: U6 snRNA phosphodiesterase [Prunus mume]
FtPinG0404893400.01	FtPinG0404893400.01.T02	XP_008234035.1	PREDICTED: U6 snRNA phosphodiesterase [Prunus mume]
FtPinG0404893600.01	FtPinG0404893600.01.T01	PWA72580.1	myb/SANT-like domain-containing protein [Artemisia annua]
FtPinG0404893700.01	FtPinG0404893700.01.T01	OMO85257.1	Isochorismatase-like protein [Corchorus capsularis]
FtPinG0480001301.01	FtPinG0480001301.01.T01	PNX90017.1	retrotransposon gag protein, partial [Trifolium pratense]

Supplementary Table 10 (Continued):

FtPinG0480001304.01	FtPinG0480001304.01.T01	XP_015078360.1	PREDICTED: uncharacterized protein LOC107022192 [Solanum pennellii]
FtPinG0480001305.01	FtPinG0480001305.01.T01	XP_015078360.1	PREDICTED: uncharacterized protein LOC107022192 [Solanum pennellii]
FtPinG0480001317.01	FtPinG0480001317.01.T01	XP_012572980.1	PREDICTED: uncharacterized protein LOC105852393, partial [Cicer arietinum]
FtPinG0480001333.01	FtPinG0480001333.01.T01	XP_012572980.1	PREDICTED: uncharacterized protein LOC105852393, partial [Cicer arietinum]
FtPinG0480001334.01	FtPinG0480001334.01.T01	XP_021891236.1	cysteine synthase-like [Carica papaya]
FtPinG0480001335.01	FtPinG0480001335.01.T01	PNX74094.1	copia LTR rider, partial [Trifolium pratense]
FtPinG0480001338.01	FtPinG0480001338.01.T01	XP_015078360.1	PREDICTED: uncharacterized protein LOC107022192 [Solanum pennellii]
FtPinG0480001339.01	FtPinG0480001339.01.T01	ABA96825.1	retrotransposon protein, putative, Ty1-copia subclass [Oryza sativa Japonica Group]
FtPinG0480001378.01	FtPinG0480001378.01.T01	XP_016732634.1	PREDICTED: uncharacterized protein LOC107943393 [Gossypium hirsutum]
FtPinG0480001499.01	FtPinG0480001499.01.T01	PNY02521.1	putative retrotransposon Ty1-copia subclass protein [Trifolium pratense]
FtPinG0480001565.01	FtPinG0480001565.01.T01	EEF33591.1	conserved hypothetical protein [Ricinus communis]
FtPinG0505235000.01	FtPinG0505235000.01.T01	XP_010099839.1	protein indeterminate-domain 2 [Morus notabilis]
FtPinG0505235200.01	FtPinG0505235200.01.T01	XP_024980048.1	ankyrin repeat-containing protein ITN1-like [Cynara cardunculus var. scolymus]
FtPinG0505235500.01	FtPinG0505235500.01.T01	XP_021847883.1	DNA-directed RNA polymerase III subunit RPC5 [Spinacia oleracea]
FtPinG0505236100.01	FtPinG0505236100.01.T02	XP_002271463.2	PREDICTED: splicing factor U2af large subunit B isoform X1 [Vitis vinifera]
FtPinG0505236100.01	FtPinG0505236100.01.T01	XP_024035990.1	splicing factor U2af large subunit B isoform X4 [Citrus clementina]
FtPinG0505236500.01	FtPinG0505236500.01.T01	XP_021275127.1	splicing factor 3B subunit 4 [Herrania umbratica]
FtPinG0505236800.01	FtPinG0505236800.01.T01	XP_018826453.1	PREDICTED: transcription repressor OFP7 [Juglans regia]
FtPinG0505236900.01	FtPinG0505236900.01.T01	XP_023893245.1	probable polyol transporter 6 [Quercus suber]
FtPinG0505237100.01	FtPinG0505237100.01.T01	PHT97903.1	Proline-rich receptor-like protein kinase PERK1 [Capsicum chinense]
FtPinG0505237300.01	FtPinG0505237300.01.T01	XP_021718463.1	U1 small nuclear ribonucleoprotein 70 kDa-like [Chenopodium quinoa]
FtPinG0505237700.01	FtPinG0505237700.01.T01	XP_021890494.1	lysosomal Pro-X carboxypeptidase [Carica papaya]
FtPinG0505238000.01	FtPinG0505238000.01.T01	XP_010547498.1	PREDICTED: cytochrome P450 90B1-like [Tarenaya hassleriana]
FtPinG0505238000.01	FtPinG0505238000.01.T02	XP_010547498.1	PREDICTED: cytochrome P450 90B1-like [Tarenaya hassleriana]

Supplementary Table 10 (Continued):

FtPinG0505399000.01	FtPinG0505399000.01.T01	XP_021745887.1	RNA polymerase II C-terminal domain phosphatase-like 3 isoform X1 [Chenopodium quinoa]
FtPinG0505399200.01	FtPinG0505399200.01.T02	XP_002266814.1	PREDICTED: uncharacterized protein LOC100259104 isoform X1 [Vitis vinifera]
FtPinG0505399700.01	FtPinG0505399700.01.T01	XP_018816313.1	PREDICTED: exonuclease mut-7 homolog isoform X2 [Juglans regia]
FtPinG0505400500.01	FtPinG0505400500.01.T01	XP_024035615.1	LOW QUALITY PROTEIN: uncharacterized protein LOC112096422 [Citrus clementina]
FtPinG0505400700.01	FtPinG0505400700.01.T01	XP_023891908.1	ATP-dependent DNA helicase Q-like 1 [Quercus suber]
FtPinG0505400700.01	FtPinG0505400700.01.T02	XP_023891908.1	ATP-dependent DNA helicase Q-like 1 [Quercus suber]
FtPinG0505423400.01	FtPinG0505423400.01.T01	XP_021846522.1	histone-lysine N-methyltransferase ATX3 isoform X2 [Spinacia oleracea]
FtPinG0505424600.01	FtPinG0505424600.01.T01	XP_010669540.1	PREDICTED: BTB/POZ domain-containing protein POB1 [Beta vulgaris subsp. vulgaris]
FtPinG0505424800.01	FtPinG0505424800.01.T01	XP_021612918.1	protein BPS1, chloroplastic-like [Manihot esculenta]
FtPinG0505425400.01	FtPinG0505425400.01.T01	XP_021641130.1	probable serine/threonine-protein kinase At1g01540 [Hevea brasiliensis]
FtPinG0505425500.01	FtPinG0505425500.01.T01	XP_024017103.1	ubiquitin-like protein 5 [Morus notabilis]
FtPinG0505456100.01	FtPinG0505456100.01.T01	XP_022724304.1	receptor-like serine/threonine-protein kinase SD1-8 [Durio zibethinus]
FtPinG0505456700.01	FtPinG0505456700.01.T01	XP_021846807.1	receptor-like serine/threonine-protein kinase SD1-8 isoform X1 [Spinacia oleracea]
FtPinG0505457000.01	FtPinG0505457000.01.T01	XP_023929787.1	Golgi to ER traffic protein 4 homolog [Quercus suber]
FtPinG0505457000.01	FtPinG0505457000.01.T02	XP_023929787.1	Golgi to ER traffic protein 4 homolog [Quercus suber]
FtPinG0505457200.01	FtPinG0505457200.01.T01	XP_008370922.1	PREDICTED: zinc finger protein ZAT12-like [Malus domestica]
FtPinG0505457500.01	FtPinG0505457500.01.T01	XP_013617706.1	PREDICTED: uncharacterized protein LOC106324252 [Brassica oleracea var. oleracea]
FtPinG0505458800.01	FtPinG0505458800.01.T01	XP_021771330.1	28 kDa ribonucleoprotein, chloroplastic-like [Chenopodium quinoa]
FtPinG0505461900.01	FtPinG0505461900.01.T01	XP_010660457.1	PREDICTED: nuclear pore complex protein NUP98A [Vitis vinifera]
FtPinG0505462200.01	FtPinG0505462200.01.T02	XP_019237283.1	PREDICTED: probable RNA 3'-terminal phosphate cyclase-like protein [Nicotiana attenuata]

Supplementary Table 10 (Continued):

FtPinG0505462200.01	FtPinG0505462200.01.T01	OIT22528.1	putative rna 3'-terminal phosphate cyclase-like protein [Nicotiana attenuata]
FtPinG0505462400.01	FtPinG0505462400.01.T01	XP_010669901.1	PREDICTED: uncharacterized protein LOC104887023 [Beta vulgaris subsp. vulgaris]
FtPinG0505462900.01	FtPinG0505462900.01.T01	PRQ58876.1	putative mitochondrial carrier protein [Rosa chinensis]
FtPinG0505463300.01	FtPinG0505463300.01.T01	KHG01533.1	Transmembrane 70, mitochondrial [Gossypium arboreum]
FtPinG0505464000.01	FtPinG0505464000.01.T01	XP_008232685.1	PREDICTED: 4-hydroxy-tetrahydrodipicolinate synthase, chloroplastic-like [Prunus mume]
FtPinG0505464100.01	FtPinG0505464100.01.T01	XP_023887334.1	alpha-taxilin isoform X2 [Quercus suber]
FtPinG0505464500.01	FtPinG0505464500.01.T01	XP_021826862.1	RNA pseudouridine synthase 5 [Prunus avium]
FtPinG0505469700.01	FtPinG0505469700.01.T01	XP_002315117.3	probable E3 ubiquitin-protein ligase ARI8 [Populus trichocarpa]
FtPinG0505472400.01	FtPinG0505472400.01.T01	XP_021767663.1	transcription factor RAX3-like [Chenopodium quinoa]
FtPinG0505472600.01	FtPinG0505472600.01.T01	XP_021839117.1	zinc finger BED domain-containing protein RICESLEEPER 2-like [Spinacia oleracea]
FtPinG0505472800.01	FtPinG0505472800.01.T01	XP_021836529.1	branched-chain-amino-acid aminotransferase 2, chloroplastic-like isoform X1 [Spinacia oleracea]
FtPinG0505473400.01	FtPinG0505473400.01.T01	XP_006433683.1	branched-chain-amino-acid aminotransferase 2, chloroplastic isoform X2 [Citrus clementina]
FtPinG0505474000.01	FtPinG0505474000.01.T01	XP_021640344.1	branched-chain-amino-acid aminotransferase 2, chloroplastic-like [Hevea brasiliensis]
FtPinG0505477900.01	FtPinG0505477900.01.T01	XP_021602555.1	cysteine-rich receptor-like protein kinase 10 isoform X5 [Manihot esculenta]
FtPinG0505478300.01	FtPinG0505478300.01.T01	XP_010664782.1	PREDICTED: protein IQ-DOMAIN 32 isoform X2 [Vitis vinifera]
FtPinG0505478500.01	FtPinG0505478500.01.T01	XP_010664782.1	PREDICTED: protein IQ-DOMAIN 32 isoform X2 [Vitis vinifera]
FtPinG0505478700.01	FtPinG0505478700.01.T01	XP_010271420.1	PREDICTED: zinc finger CCCH domain-containing protein 6 isoform X1 [Nelumbo nucifera]
FtPinG0505479100.01	FtPinG0505479100.01.T01	XP_023900991.1	auxin-induced protein 6B-like [Quercus suber]
FtPinG0505479700.01	FtPinG0505479700.01.T01	XP_010692720.1	PREDICTED: filament-like plant protein 4 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0505480300.01	FtPinG0505480300.01.T01	XP_021682540.1	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1-like [Hevea brasiliensis]

Supplementary Table 10 (Continued):

FtPinG0505480600.01	FtPinG0505480600.01.T01	XP_021718667.1	endoglucanase 2-like [Chenopodium quinoa]
FtPinG0505481300.01	FtPinG0505481300.01.T01	XP_020219050.1	putative HVA22-like protein g [Cajanus cajan]
FtPinG0505481300.01	FtPinG0505481300.01.T02	XP_020219050.1	putative HVA22-like protein g [Cajanus cajan]
FtPinG0505481600.01	FtPinG0505481600.01.T01	PWA89720.1	zinc finger, CCHC-type [Artemisia annua]
FtPinG0505482000.01	FtPinG0505482000.01.T01	XP_018833440.1	PREDICTED: uncharacterized protein LOC109000876 isoform X1 [Juglans regia]
FtPinG0505482600.01	FtPinG0505482600.01.T01	XP_019174208.1	PREDICTED: snakin-2-like [Ipomoea nil]
FtPinG0505482800.01	FtPinG0505482800.01.T01	XP_021718762.1	putative ER lumen protein-retaining receptor C28H8.4 [Chenopodium quinoa]
FtPinG0505496000.01	FtPinG0505496000.01.T01	XP_012073667.1	metallocarboxypeptidase A-like protein TRV_02598 [Jatropha curcas]
FtPinG0505496400.01	FtPinG0505496400.01.T01	PSS17166.1	Acyl-activating enzyme 1, peroxisomal like [Actinidia chinensis var. chinensis]
FtPinG0505497000.01	FtPinG0505497000.01.T01	PSS19873.1	Dolichol-phosphate mannosyltransferase subunit 1 like [Actinidia chinensis var. chinensis]
FtPinG0505497400.01	FtPinG0505497400.01.T01	PSR99517.1	1,4-alpha-glucan-branching enzyme like [Actinidia chinensis var. chinensis]
FtPinG0505497800.01	FtPinG0505497800.01.T01	XP_002270675.1	PREDICTED: BTB/POZ domain-containing protein At2g30600 [Vitis vinifera]
FtPinG0505497800.01	FtPinG0505497800.01.T02	XP_002270675.1	PREDICTED: BTB/POZ domain-containing protein At2g30600 [Vitis vinifera]
FtPinG0505498000.01	FtPinG0505498000.01.T01	PON90459.1	Cyclin [Trema orientale]
FtPinG0505498300.01	FtPinG0505498300.01.T01	ACH63223.1	catalase [Rheum australe]
FtPinG0505498800.01	FtPinG0505498800.01.T01	XP_010061179.1	PREDICTED: Niemann-Pick C1 protein isoform X1 [Eucalyptus grandis]
FtPinG0505583000.01	FtPinG0505583000.01.T01	XP_021770837.1	protein GAMETE EXPRESSED 2-like [Chenopodium quinoa]
FtPinG0505583300.01	FtPinG0505583300.01.T01	EEF45564.1	multidrug resistance pump, putative [Ricinus communis]
FtPinG0505583300.01	FtPinG0505583300.01.T02	XP_002516950.1	protein DETOXIFICATION 55 [Ricinus communis]
FtPinG0505583700.01	FtPinG0505583700.01.T01	PSR85119.1	Ubiquitin-like-specific protease [Actinidia chinensis var. chinensis]
FtPinG0505583900.01	FtPinG0505583900.01.T01	XP_010645901.1	PREDICTED: pentatricopeptide repeat-containing protein At1g71490 [Vitis vinifera]
FtPinG0505584400.01	FtPinG0505584400.01.T01	EOY28575.1	Cysteine-rich RLK 10 [Theobroma cacao]
FtPinG0505584600.01	FtPinG0505584600.01.T01	OMO63810.1	putative glycosyltransferase 2 protein [Corchorus capsularis]

Supplementary Table 10 (Continued):

FtPinG0505586000.01	FtPinG0505586000.01.T01	XP_010259642.1	PREDICTED: uncharacterized protein LOC104598988 isoform X4 [Nelumbo nucifera]
FtPinG0505586700.01	FtPinG0505586700.01.T01	XP_018460460.1	PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g29720 [Raphanus sativus]
FtPinG0505587200.01	FtPinG0505587200.01.T01	OTG31904.1	putative calcium-dependent lipid-binding (CaLB domain) family protein [Helianthus annuus]
FtPinG0505911100.01	FtPinG0505911100.01.T01	GAV80138.1	Abhydrolase_6 domain-containing protein [Cephalotus follicularis]
FtPinG0505911900.01	FtPinG0505911900.01.T01	XP_010660394.1	PREDICTED: uncharacterized protein LOC100246403 [Vitis vinifera]
FtPinG0505912100.01	FtPinG0505912100.01.T01	ACD01043.1	polygalacturonase-inhibiting protein [Knorringia sibirica]
FtPinG0505912500.01	FtPinG0505912500.01.T01	ACD01043.1	polygalacturonase-inhibiting protein [Knorringia sibirica]
FtPinG0505912700.01	FtPinG0505912700.01.T01	XP_010671147.1	PREDICTED: transcription factor IIIB 90 kDa subunit isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0505912700.01	FtPinG0505912700.01.T02	XP_021846297.1	transcription factor IIIB 90 kDa subunit [Spinacia oleracea]
FtPinG0505913500.01	FtPinG0505913500.01.T01	PSS30596.1	Leaf rust 10 disease-resistance locus receptor-like protein kinase [Actinidia chinensis var. chinensis]
FtPinG0505914000.01	FtPinG0505914000.01.T01	XP_009345691.1	PREDICTED: delta(7)-sterol-C5(6)-desaturase-like [Pyrus x bretschneideri]
FtPinG0505914600.01	FtPinG0505914600.01.T01	XP_018500360.1	PREDICTED: uncharacterized protein LOC103936628 [Pyrus x bretschneideri]
FtPinG0505914800.01	FtPinG0505914800.01.T01	AAG00995.1	putative glucose translocator [Mesembryanthemum crystallinum]
FtPinG0505915000.01	FtPinG0505915000.01.T01	PSR87819.1	Methylesterase [Actinidia chinensis var. chinensis]
FtPinG0505915500.01	FtPinG0505915500.01.T01	CAD21856.1	putative ribulose 1,5 biphosphate carboxylase small subunit percursor [Rumex obtusifolius]
FtPinG0505915800.01	FtPinG0505915800.01.T01	BAT16785.1	Os12g0291066, partial [Oryza sativa Japonica Group]
FtPinG0505916000.01	FtPinG0505916000.01.T01	CAD21856.1	putative ribulose 1,5 biphosphate carboxylase small subunit percursor [Rumex obtusifolius]
FtPinG0505916200.01	FtPinG0505916200.01.T01	XP_022879839.1	3-ketoacyl-CoA synthase 6 [Olea europaea var. sylvestris]

Supplementary Table 10 (Continued):

FtPinG0505974900.01	FtPinG0505974900.01.T01	XP_021739219.1	protein SYM1-like [Chenopodium quinoa]
FtPinG0505975400.01	FtPinG0505975400.01.T01	XP_024190057.1	LOW QUALITY PROTEIN: probable polygalacturonase At3g15720 [Rosa chinensis]
FtPinG0505975900.01	FtPinG0505975900.01.T01	XP_010673405.1	PREDICTED: cation/H(+) antiporter 28 [Beta vulgaris subsp. vulgaris]
FtPinG0505976700.01	FtPinG0505976700.01.T01	XP_019103096.1	PREDICTED: phosphatidylinositol-glycan biosynthesis class X protein [Beta vulgaris subsp. vulgaris]
FtPinG0505977500.01	FtPinG0505977500.01.T01	OMO80483.1	Ubiquitin system component Cue [Corchorus olitorius]
FtPinG0505977900.01	FtPinG0505977900.01.T01	GAV91404.1	GLTP domain-containing protein [Cephalotus follicularis]
FtPinG0505979000.01	FtPinG0505979000.01.T01	XP_024971299.1	tubulin-folding cofactor B [Cynara cardunculus var. scolymus]
FtPinG0505979100.01	FtPinG0505979100.01.T01	XP_021747294.1	U3 snoRNP-associated protein-like EMB2271 isoform X1 [Chenopodium quinoa]
FtPinG0505979400.01	FtPinG0505979400.01.T01	XP_010655735.1	PREDICTED: serine/threonine-protein phosphatase 6 regulatory subunit 2 isoform X1 [Vitis vinifera]
FtPinG0505979500.01	FtPinG0505979500.01.T02	XP_023923092.1	kxDL motif-containing protein 1-like [Quercus suber]
FtPinG0505980300.01	FtPinG0505980300.01.T01	XP_021764149.1	WPP domain-associated protein-like [Chenopodium quinoa]
FtPinG0505980500.01	FtPinG0505980500.01.T01	XP_021722574.1	LOW QUALITY PROTEIN: WPP domain-associated protein-like, partial [Chenopodium quinoa]
FtPinG0505980700.01	FtPinG0505980700.01.T01	GAV72919.1	SUI1 domain-containing protein, partial [Cephalotus follicularis]
FtPinG0505980900.01	FtPinG0505980900.01.T01	GAV72919.1	SUI1 domain-containing protein, partial [Cephalotus follicularis]
FtPinG0505981800.01	FtPinG0505981800.01.T01	XP_015573816.1	receptor-like protein 9a isoform X1 [Ricinus communis]
FtPinG0505982200.01	FtPinG0505982200.01.T01	XP_024952380.1	receptor-like protein 1 [Citrus sinensis]
FtPinG0505982300.01	FtPinG0505982300.01.T01	XP_006490131.3	receptor-like protein 14 isoform X2 [Citrus sinensis]
FtPinG0505982600.01	FtPinG0505982600.01.T01	XP_021736426.1	pentatricopeptide repeat-containing protein PNM1, mitochondrial-like [Chenopodium quinoa]
FtPinG0505984800.01	FtPinG0505984800.01.T01	XP_012437760.1	PREDICTED: putative cyclic nucleotide-gated ion channel 13 isoform X1 [Gossypium raimondii]
FtPinG0505985000.01	FtPinG0505985000.01.T01	XP_022733945.1	cyclic nucleotide-gated ion channel 1-like [Durio zibethinus]

Supplementary Table 10 (Continued):

FtPinG0506012900.01	FtPinG0506012900.01.T01	XP_007041944.1	PREDICTED: type III polyketide synthase B [Theobroma cacao]
FtPinG0506013300.01	FtPinG0506013300.01.T01	XP_010658410.1	PREDICTED: patatin-like protein 6 [Vitis vinifera]
FtPinG0506013700.01	FtPinG0506013700.01.T01	PON64158.1	Mediator-associated protein [Parasponia andersonii]
FtPinG0506014100.01	FtPinG0506014100.01.T01	XP_021837257.1	U-box domain-containing protein 4 [Spinacia oleracea]
FtPinG0506014700.01	FtPinG0506014700.01.T01	GAV62521.1	Pkinase domain-containing protein [Cephalotus follicularis]
FtPinG0506015000.01	FtPinG0506015000.01.T01	XP_023912652.1	26S proteasome non-ATPase regulatory subunit 9-like [Quercus suber]
FtPinG0506015300.01	FtPinG0506015300.01.T01	XP_021858121.1	kinesin-like protein KIN-UC isoform X2 [Spinacia oleracea]
FtPinG0506015600.01	FtPinG0506015600.01.T01	XP_016716016.1	PREDICTED: alpha-mannosidase I MNS4-like [Gossypium hirsutum]
FtPinG0506016000.01	FtPinG0506016000.01.T01	PON78075.1	POLLUX-like ion channel [Trema orientale]
FtPinG0506016300.01	FtPinG0506016300.01.T02	XP_011458877.1	PREDICTED: protein PHLOEM PROTEIN 2-LIKE A10 [Fragaria vesca subsp. vesca]
FtPinG0506016300.01	FtPinG0506016300.01.T01	PSR99928.1	Protein PHLOEM PROTEIN 2-LIKE like [Actinidia chinensis var. chinensis]
FtPinG0506016600.01	FtPinG0506016600.01.T01	XP_021754697.1	U-box domain-containing protein 30-like [Chenopodium quinoa]
FtPinG0506016700.01	FtPinG0506016700.01.T01	EOY15685.1	FKBP-type peptidyl-prolyl cis-trans isomerase family protein [Theobroma cacao]
FtPinG0506016900.01	FtPinG0506016900.01.T01	XP_002283413.1	PREDICTED: serine carboxypeptidase-like 2 [Vitis vinifera]
FtPinG0506017300.01	FtPinG0506017300.01.T01	PSR99921.1	U3 small nucleolar RNA-associated protein [Actinidia chinensis var. chinensis]
FtPinG0506017800.01	FtPinG0506017800.01.T01	XP_010272905.1	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial [Nelumbo nucifera]
FtPinG0506018800.01	FtPinG0506018800.01.T01	XP_010272772.1	PREDICTED: uncharacterized protein LOC104608456 [Nelumbo nucifera]
FtPinG0506019600.01	FtPinG0506019600.01.T01	XP_012851604.1	PREDICTED: uncharacterized protein LOC105971303 [Erythranthe guttata]
FtPinG0506020200.01	FtPinG0506020200.01.T02	XP_012068258.1	3-oxo-Delta(4,5)-steroid 5-beta-reductase [Jatropha curcas]
FtPinG0580001633.01	FtPinG0580001633.01.T01	XP_015075513.1	PREDICTED: uncharacterized protein LOC107019601 [Solanum pennellii]
FtPinG0580001636.01	FtPinG0580001636.01.T01	ABM55240.1	retrotransposon protein [Beta vulgaris]
FtPinG0580001707.01	FtPinG0580001707.01.T01	XP_018625026.1	PREDICTED: uncharacterized protein LOC104092482, partial [Nicotiana tomentosiformis]

Supplementary Table 10 (Continued):

FtPinG0580001718.01	FtPinG0580001718.01.T01	ABM55240.1	retrotransposon protein [Beta vulgaris]
FtPinG0580001719.01	FtPinG0580001719.01.T01	XP_015078360.1	PREDICTED: uncharacterized protein LOC107022192 [Solanum pennellii]
FtPinG0580001720.01	FtPinG0580001720.01.T01	AAW28577.1	Putative gag-pol polyprotein, identical [Solanum demissum]
FtPinG0580001740.01	FtPinG0580001740.01.T01	XP_016727824.1	PREDICTED: uncharacterized protein LOC107939044 [Gossypium hirsutum]
FtPinG0580001761.01	FtPinG0580001761.01.T01	XP_004506381.1	PREDICTED: uncharacterized protein LOC101512433 [Cicer arietinum]
FtPinG0580001766.01	FtPinG0580001766.01.T01	XP_019107186.1	PREDICTED: uncharacterized protein LOC104903782 [Beta vulgaris subsp. vulgaris]
FtPinG0580001769.01	FtPinG0580001769.01.T01	XP_015078360.1	PREDICTED: uncharacterized protein LOC107022192 [Solanum pennellii]
FtPinG0580001776.01	FtPinG0580001776.01.T01	XP_015075513.1	PREDICTED: uncharacterized protein LOC107019601 [Solanum pennellii]
FtPinG0580001790.01	FtPinG0580001790.01.T01	PWA34357.1	myb/SANT-like domain-containing protein [Artemisia annua]
FtPinG0580001792.01	FtPinG0580001792.01.T01	ABO36636.1	copia LTR rider [Solanum lycopersicum]
FtPinG0606848100.01	FtPinG0606848100.01.T01	XP_021841972.1	putative pentatricopeptide repeat-containing protein At5g08310, mitochondrial [Spinacia oleracea]
FtPinG0606848600.01	FtPinG0606848600.01.T01	XP_024642268.1	LOW QUALITY PROTEIN: uncharacterized protein LOC25497180 [Medicago truncatula]
FtPinG0606848900.01	FtPinG0606848900.01.T01	XP_010043898.1	PREDICTED: protein NRT1/ PTR FAMILY 8.3 [Eucalyptus grandis]
FtPinG0606849500.01	FtPinG0606849500.01.T01	XP_023918465.1	calmodulin-binding transcription activator 4 [Quercus suber]
FtPinG0606849700.01	FtPinG0606849700.01.T01	XP_021290394.1	transcription factor bHLH128-like [Herrania umbratica]
FtPinG0606851000.01	FtPinG0606851000.01.T01	XP_002528284.1	PI-PLC X-box domain-containing protein DDB_G0293730 [Ricinus communis]
FtPinG0606851400.01	FtPinG0606851400.01.T01	ABM55240.1	retrotransposon protein [Beta vulgaris]
FtPinG0606851700.01	FtPinG0606851700.01.T01	XP_019105734.1	PREDICTED: uncharacterized protein LOC104895764 [Beta vulgaris subsp. vulgaris]
FtPinG0606851900.01	FtPinG0606851900.01.T01	XP_019105735.1	PREDICTED: uncharacterized protein LOC104895764 [Beta vulgaris subsp. vulgaris]
FtPinG0606852100.01	FtPinG0606852100.01.T01	XP_008228155.1	PREDICTED: uncharacterized protein LOC103327594 [Prunus mume]
FtPinG0606853000.01	FtPinG0606853000.01.T01	XP_010693531.1	PREDICTED: protein phosphatase inhibitor 2 isoform X2 [Beta vulgaris subsp. vulgaris]
FtPinG0606853300.01	FtPinG0606853300.01.T01	XP_023894199.1	spermine synthase [Quercus suber]

Supplementary Table 10 (Continued):

FtPinG0606853600.01	FtPinG0606853600.01.T01	XP_021761970.1	glutathione S-transferase U8-like [Chenopodium quinoa]
FtPinG0606854400.01	FtPinG0606854400.01.T01	EEF51480.1	DNA binding protein, putative [Ricinus communis]
FtPinG0680002173.01	FtPinG0680002173.01.T01	XP_012842863.1	PREDICTED: uncharacterized protein LOC105963045 [Erythranthe guttata]
FtPinG0680002176.01	FtPinG0680002176.01.T01	XP_010424030.1	PREDICTED: uncharacterized protein LOC104709061 [Camelina sativa]
FtPinG0707219300.01	FtPinG0707219300.01.T01	XP_021717642.1	heat stress transcription factor A-6b-like [Chenopodium quinoa]
FtPinG0707219700.01	FtPinG0707219700.01.T01	XP_021692011.1	guanine nucleotide-binding protein subunit gamma 2-like isoform X1 [Hevea brasiliensis]
FtPinG0707220200.01	FtPinG0707220200.01.T01	XP_016484142.1	PREDICTED: ADP-ribosylation factor-like protein 5 [Nicotiana tabacum]
FtPinG0707220500.01	FtPinG0707220500.01.T01	XP_021721091.1	transportin MOS14-like [Chenopodium quinoa]
FtPinG0707220500.01	FtPinG0707220500.01.T02	XP_021721091.1	transportin MOS14-like [Chenopodium quinoa]
FtPinG0707220700.01	FtPinG0707220700.01.T01	APO15847.1	korrigan [Sesuvium portulacastrum]
FtPinG0707221300.01	FtPinG0707221300.01.T01	XP_021823099.1	glycerophosphodiester phosphodiesterase GDPD1, chloroplastic-like [Prunus avium]
FtPinG0707221500.01	FtPinG0707221500.01.T01	XP_002276230.1	PREDICTED: pentatricopeptide repeat-containing protein At4g15720 [Vitis vinifera]
FtPinG0707221500.01	FtPinG0707221500.01.T02	XP_002276230.1	PREDICTED: pentatricopeptide repeat-containing protein At4g15720 [Vitis vinifera]
FtPinG0707221700.01	FtPinG0707221700.01.T01	XP_017971309.1	PREDICTED: E2F-associated phosphoprotein [Theobroma cacao]
FtPinG0707223200.01	FtPinG0707223200.01.T01	XP_021754418.1	CTL-like protein DDB_G0274487 isoform X1 [Chenopodium quinoa]
FtPinG0707223500.01	FtPinG0707223500.01.T01	XP_016730384.1	PREDICTED: glucuronoxylan 4-O-methyltransferase 1-like [Gossypium hirsutum]
FtPinG0707223800.01	FtPinG0707223800.01.T01	XP_021754679.1	AP2/ERF and B3 domain-containing transcription factor RAV1-like [Chenopodium quinoa]
FtPinG0707641700.01	FtPinG0707641700.01.T01	KHN21611.1	40S ribosomal protein S2-4 [Glycine soja]
FtPinG0707642100.01	FtPinG0707642100.01.T01	XP_010666756.1	PREDICTED: uncharacterized protein LOC104883885 [Beta vulgaris subsp. vulgaris]
FtPinG0707642400.01	FtPinG0707642400.01.T01	XP_017977930.1	PREDICTED: leucine-rich repeat receptor-like tyrosine-protein kinase PXC3 isoform X2 [Theobroma cacao]
FtPinG0707642800.01	FtPinG0707642800.01.T01	XP_002308948.3	protein N-terminal glutamine amidohydrolase [Populus trichocarpa]
FtPinG0707643600.01	FtPinG0707643600.01.T01	XP_023902085.1	heat stress transcription factor B-3-like isoform X2 [Quercus suber]

Supplementary Table 10 (Continued):

FtPinG0707644200.01	FtPinG0707644200.01.T01	XP_021741018.1	protein MIZU-KUSSEI 1-like [Chenopodium quinoa]
FtPinG0707644500.01	FtPinG0707644500.01.T01	KZV46381.1	glutamyl-tRNA reductase 1, chloroplastic-like [Dorcoceras hygrometricum]
FtPinG0707644800.01	FtPinG0707644800.01.T01	XP_011048083.1	PREDICTED: agamous-like MADS-box protein AGL18 [Populus euphratica]
FtPinG0707817600.01	FtPinG0707817600.01.T01	XP_020224552.1	GRF1-interacting factor 3-like [Cajanus cajan]
FtPinG0707818600.01	FtPinG0707818600.01.T01	XP_002267268.2	PREDICTED: probable L-gulonolactone oxidase 6 [Vitis vinifera]
FtPinG0707818700.01	FtPinG0707818700.01.T01	XP_019081159.1	PREDICTED: protein LHY isoform X3 [Vitis vinifera]
FtPinG0707820000.01	FtPinG0707820000.01.T01	XP_021748823.1	serine/threonine-protein kinase ATG1a-like [Chenopodium quinoa]
FtPinG0707820200.01	FtPinG0707820200.01.T01	KHG12105.1	Ribosome production factor 1 [Gossypium arboreum]
FtPinG0707820600.01	FtPinG0707820600.01.T01	KMZ73246.1	Protein phosphatase 1 regulatory subunit 11 [Zostera marina]
FtPinG0707821400.01	FtPinG0707821400.01.T01	PSS31813.1	Protein TIC 40 like [Actinidia chinensis var. chinensis]
FtPinG0707821600.01	FtPinG0707821600.01.T01	XP_010679738.1	PREDICTED: ATPase family AAA domain-containing protein 3 [Beta vulgaris subsp. vulgaris]
FtPinG0707821800.01	FtPinG0707821800.01.T01	XP_018816194.1	PREDICTED: E3 ubiquitin-protein ligase RNF170-like isoform X1 [Juglans regia]
FtPinG0707822100.01	FtPinG0707822100.01.T01	XP_021760411.1	patellin-3-like [Chenopodium quinoa]
FtPinG0707822600.01	FtPinG0707822600.01.T01	XP_010256479.1	PREDICTED: uncharacterized protein LOC104596850 [Nelumbo nucifera]
FtPinG0707823000.01	FtPinG0707823000.01.T01	XP_010679642.1	PREDICTED: histidinol dehydrogenase, chloroplastic isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0707824100.01	FtPinG0707824100.01.T01	XP_010062000.1	PREDICTED: calcium-dependent protein kinase 11 [Eucalyptus grandis]
FtPinG0707824300.01	FtPinG0707824300.01.T01	XP_010677683.1	PREDICTED: uncharacterized protein LOC104893259 [Beta vulgaris subsp. vulgaris]
FtPinG0707825000.01	FtPinG0707825000.01.T01	XP_021849646.1	transmembrane protein 18 [Spinacia oleracea]
FtPinG0707825200.01	FtPinG0707825200.01.T01	XP_021760460.1	sucrose transport protein-like isoform X1 [Chenopodium quinoa]
FtPinG0707825600.01	FtPinG0707825600.01.T01	EEF48427.1	Auxin response factor, putative [Ricinus communis]
FtPinG0707836300.01	FtPinG0707836300.01.T01	XP_021890273.1	serine/threonine-protein kinase Aurora-2 [Carica papaya]
FtPinG0707836500.01	FtPinG0707836500.01.T01	XP_021297355.1	ferredoxin-dependent glutamate synthase, chloroplastic [Herrania umbratica]
FtPinG0707836700.01	FtPinG0707836700.01.T01	EEF48565.1	conserved hypothetical protein [Ricinus communis]

Supplementary Table 10 (Continued):

FtPinG0707837200.01	FtPinG0707837200.01.T01	XP_015060186.1	PREDICTED: cytochrome c oxidase subunit 6b-1-like isoform X2 [Solanum pennellii]
FtPinG0707837400.01	FtPinG0707837400.01.T01	XP_010664347.1	PREDICTED: alcohol dehydrogenase-like 1 [Vitis vinifera]
FtPinG0707837600.01	FtPinG0707837600.01.T01	XP_012446473.1	PREDICTED: 14-3-3-like protein [Gossypium raimondii]
FtPinG0707837700.01	FtPinG0707837700.01.T01	ACQ99190.1	flavanone-3-hydroxylase [Fagopyrum tataricum]
FtPinG0707838000.01	FtPinG0707838000.01.T01	XP_025613151.1	14-3-3-like protein [Arachis hypogaea]
FtPinG0707838100.01	FtPinG0707838100.01.T01	XP_021677811.1	40S ribosomal protein S6 [Hevea brasiliensis]
FtPinG0707838500.01	FtPinG0707838500.01.T01	XP_021740247.1	protein EXORDIUM-like [Chenopodium quinoa]
FtPinG0707838800.01	FtPinG0707838800.01.T01	XP_004299654.1	PREDICTED: protein EXORDIUM-like [Fragaria vesca subsp. vesca]
FtPinG0707838900.01	FtPinG0707838900.01.T01	XP_004299654.1	PREDICTED: protein EXORDIUM-like [Fragaria vesca subsp. vesca]
FtPinG0707839100.01	FtPinG0707839100.01.T01	GAV63592.1	UDPGT domain-containing protein [Cephalotus follicularis]
FtPinG0707839300.01	FtPinG0707839300.01.T01	XP_002285767.1	PREDICTED: 7-deoxyloganetin glucosyltransferase [Vitis vinifera]
FtPinG0707839500.01	FtPinG0707839500.01.T01	XP_002285767.1	PREDICTED: 7-deoxyloganetin glucosyltransferase [Vitis vinifera]
FtPinG0707839700.01	FtPinG0707839700.01.T01	XP_017981739.1	PREDICTED: 7-deoxyloganetin glucosyltransferase [Theobroma cacao]
FtPinG0707839900.01	FtPinG0707839900.01.T01	XP_010060020.1	PREDICTED: 7-deoxyloganetin glucosyltransferase-like [Eucalyptus grandis]
FtPinG0707998300.01	FtPinG0707998300.01.T01	XP_026445908.1	calmodulin-like protein 1 [Papaver somniferum]
FtPinG0707998500.01	FtPinG0707998500.01.T01	XP_010254574.1	PREDICTED: KH domain-containing protein HEN4-like [Nelumbo nucifera]
FtPinG0707998700.01	FtPinG0707998700.01.T01	KVH93381.1	K Homology domain-containing protein [Cynara cardunculus var. scolymus]
FtPinG0707998900.01	FtPinG0707998900.01.T01	XP_010680385.1	PREDICTED: kinesin-like protein KIN-14R [Beta vulgaris subsp. vulgaris]
FtPinG0707999600.01	FtPinG0707999600.01.T01	XP_006466346.3	8-hydroxygeraniol dehydrogenase-like [Citrus sinensis]
FtPinG0708000200.01	FtPinG0708000200.01.T01	XP_021810803.1	phosphopantothenate--cysteine ligase 2-like [Prunus avium]
FtPinG0708000600.01	FtPinG0708000600.01.T01	OVA04924.1	Protein kinase domain [Macleaya cordata]
FtPinG0708000800.01	FtPinG0708000800.01.T01	AEF30420.1	flavones 3-hydroxylase [Fagopyrum tataricum]
FtPinG0708001200.01	FtPinG0708001200.01.T01	XP_022741471.1	salicylate carboxymethyltransferase-like [Durio zibethinus]
FtPinG0708001600.01	FtPinG0708001600.01.T01	XP_023518474.1	salicylate carboxymethyltransferase-like [Cucurbita pepo subsp. pepo]
FtPinG0708002200.01	FtPinG0708002200.01.T01	XP_022962782.1	salicylate carboxymethyltransferase-like [Cucurbita moschata]

Supplementary Table 10 (Continued):

FtPinG0708043500.01	FtPinG0708043500.01.T01	PSS30271.1	Shikimate kinase [Actinidia chinensis var. chinensis]
FtPinG0708043700.01	FtPinG0708043700.01.T01	XP_010652857.1	PREDICTED: uncharacterized protein LOC100264638 isoform X1 [Vitis vinifera]
FtPinG0708044100.01	FtPinG0708044100.01.T01	RDX63673.1	putative inactive receptor kinase, partial [Mucuna pruriens]
FtPinG0708044300.01	FtPinG0708044300.01.T01	XP_021736621.1	pentatricopeptide repeat-containing protein At4g39620, chloroplastic-like [Chenopodium quinoa]
FtPinG0708044500.01	FtPinG0708044500.01.T01	XP_019106331.1	PREDICTED: pentatricopeptide repeat-containing protein At2g22070 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0708044700.01	FtPinG0708044700.01.T01	XP_021759310.1	kinesin-like protein KIN-14E [Chenopodium quinoa]
FtPinG0708044900.01	FtPinG0708044900.01.T01	PSR86829.1	Xanthine dehydrogenase [Actinidia chinensis var. chinensis]
FtPinG0708045200.01	FtPinG0708045200.01.T01	XP_010673619.1	PREDICTED: E3 ubiquitin ligase BIG BROTHER [Beta vulgaris subsp. vulgaris]
FtPinG0708045300.01	FtPinG0708045300.01.T01	XP_021728954.1	outer envelope protein 80, chloroplastic-like isoform X1 [Chenopodium quinoa]
FtPinG0708046200.01	FtPinG0708046200.01.T01	XP_021727622.1	probable L-type lectin-domain containing receptor kinase S.5 [Chenopodium quinoa]
FtPinG0708047000.01	FtPinG0708047000.01.T01	XP_002280674.1	PREDICTED: uncharacterized protein LOC100244641 [Vitis vinifera]
FtPinG0708047200.01	FtPinG0708047200.01.T01	XP_021863733.1	serine/threonine-protein phosphatase 7 [Spinacia oleracea]
FtPinG0708048000.01	FtPinG0708048000.01.T01	PON90522.1	Hydroxymethylglutaryl-CoA reductase [Trema orientale]
FtPinG0780002614.01	FtPinG0780002614.01.T01	PWA90654.1	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Artemisia annua]
FtPinG0808974900.01	FtPinG0808974900.01.T01	XP_019076333.1	PREDICTED: probable apyrase 6 [Vitis vinifera]
FtPinG0808975200.01	FtPinG0808975200.01.T01	XP_015873361.1	NADH--cytochrome b5 reductase 1-like [Ziziphus jujuba]
FtPinG0808975500.01	FtPinG0808975500.01.T01	XP_021720620.1	molybdopterin biosynthesis protein CNX1-like isoform X1 [Chenopodium quinoa]
FtPinG0808976200.01	FtPinG0808976200.01.T01	XP_022988492.1	serine/threonine-protein kinase TOUSLED-like isoform X2 [Cucurbita maxima]
FtPinG0808976700.01	FtPinG0808976700.01.T01	XP_021720606.1	ubiquitin carboxyl-terminal hydrolase 12 [Chenopodium quinoa]
FtPinG0808977300.01	FtPinG0808977300.01.T01	XP_007015617.2	PREDICTED: outer envelope protein 61 [Theobroma cacao]
FtPinG0808977700.01	FtPinG0808977700.01.T01	XP_021715634.1	E3 ubiquitin-protein ligase RHF2A-like isoform X1 [Chenopodium quinoa]
FtPinG0808977900.01	FtPinG0808977900.01.T01	XP_023512203.1	fasciclin-like arabinogalactan protein 17 [Cucurbita pepo subsp. pepo]
FtPinG0808978200.01	FtPinG0808978200.01.T01	PSS09433.1	Succinate dehydrogenase [Actinidia chinensis var. chinensis]

Supplementary Table 10 (Continued):

FtPinG0808978300.01	FtPinG0808978300.01.T01	XP_010685472.1	PREDICTED: uncharacterized protein LOC104899879 [Beta vulgaris subsp. vulgaris]
FtPinG0808978600.01	FtPinG0808978600.01.T01	XP_021754119.1	RNA-binding protein NOB1-like [Chenopodium quinoa]
FtPinG0808978900.01	FtPinG0808978900.01.T01	XP_011044607.1	PREDICTED: probable receptor-like protein kinase At1g49730 isoform X1 [Populus euphratica]
FtPinG0808979200.01	FtPinG0808979200.01.T01	XP_021715651.1	dnaJ protein homolog ANJ1-like [Chenopodium quinoa]
FtPinG0808979800.01	FtPinG0808979800.01.T01	XP_021715659.1	J domain-containing protein spf31-like [Chenopodium quinoa]
FtPinG0808979900.01	FtPinG0808979900.01.T01	XP_024452016.1	transcription factor LHW isoform X2 [Populus trichocarpa]
FtPinG0808980300.01	FtPinG0808980300.01.T01	XP_010088638.1	aluminum-activated malate transporter 2 [Morus notabilis]
FtPinG0808980700.01	FtPinG0808980700.01.T01	XP_021720550.1	NDR1/HIN1-like protein 10 [Chenopodium quinoa]
FtPinG0808980900.01	FtPinG0808980900.01.T01	XP_021715674.1	NDR1/HIN1-like protein 1 [Chenopodium quinoa]
FtPinG0808980900.01	FtPinG0808980900.01.T02	XP_021715674.1	NDR1/HIN1-like protein 1 [Chenopodium quinoa]
FtPinG0808981700.01	FtPinG0808981700.01.T01	XP_022752529.1	transcription factor E2FB-like isoform X2 [Durio zibethinus]
FtPinG0808981900.01	FtPinG0808981900.01.T01	RLW16559.1	transcription repressor ofp6 [Quercus suber]
FtPinG0808982200.01	FtPinG0808982200.01.T01	XP_021735190.1	ubiquitin-conjugating enzyme E2 variant 1D-like [Chenopodium quinoa]
FtPinG0808982400.01	FtPinG0808982400.01.T01	XP_021715682.1	NAC domain-containing protein 89-like [Chenopodium quinoa]
FtPinG0808982600.01	FtPinG0808982600.01.T01	XP_021720533.1	centrosomal protein of 83 kDa-like isoform X1 [Chenopodium quinoa]
FtPinG0809022500.01	FtPinG0809022500.01.T01	XP_021283809.1	homeobox protein knotted-1-like 2 [Herrania umbratica]
FtPinG0809022500.01	FtPinG0809022500.01.T02	XP_021283810.1	homeobox protein knotted-1-like 2 [Herrania umbratica]
FtPinG0809023100.01	FtPinG0809023100.01.T01	EEF52233.1	heat shock protein binding protein, putative [Ricinus communis]
FtPinG0809023500.01	FtPinG0809023500.01.T01	XP_002285486.1	PREDICTED: probable xyloglucan glycosyltransferase 12 [Vitis vinifera]
FtPinG0809023700.01	FtPinG0809023700.01.T01	XP_002283504.2	PREDICTED: growth-regulating factor 1 [Vitis vinifera]
FtPinG0809023900.01	FtPinG0809023900.01.T01	XP_008347595.2	PREDICTED: basic leucine zipper 43-like [Malus domestica]
FtPinG0809024100.01	FtPinG0809024100.01.T01	XP_003635085.1	PREDICTED: thioredoxin-like protein HCF164, chloroplastic [Vitis vinifera]
FtPinG0809024300.01	FtPinG0809024300.01.T01	XP_021728473.1	U-box domain-containing protein 4-like [Chenopodium quinoa]
FtPinG0809024600.01	FtPinG0809024600.01.T01	XP_008444563.1	PREDICTED: putative transcription factor bHLH086 [Cucumis melo]

Supplementary Table 10 (Continued):

FtPinG0809025100.01	FtPinG0809025100.01.T01	XP_002285152.1	PREDICTED: 3-oxo-Delta(4,5)-steroid 5-beta-reductase [Vitis vinifera]
FtPinG0809025600.01	FtPinG0809025600.01.T01	PON90588.1	LOW QUALITY PROTEIN: hypothetical protein TorRG33x02_136430 [Trema orientale]
FtPinG0809026200.01	FtPinG0809026200.01.T01	XP_021691577.1	DUF724 domain-containing protein 2 isoform X1 [Hevea brasiliensis]
FtPinG0809027000.01	FtPinG0809027000.01.T01	XP_002285152.1	PREDICTED: 3-oxo-Delta(4,5)-steroid 5-beta-reductase [Vitis vinifera]
FtPinG0809027200.01	FtPinG0809027200.01.T01	XP_023910558.1	protein DCL homolog, chloroplastic [Quercus suber]
FtPinG0809027600.01	FtPinG0809027600.01.T01	XP_010688678.1	PREDICTED: kinesin-like protein KIN-4A isoform X2 [Beta vulgaris subsp. vulgaris]
FtPinG0809058900.01	FtPinG0809058900.01.T01	XP_021772666.1	probable carboxylesterase 18 [Chenopodium quinoa]
FtPinG0809059200.01	FtPinG0809059200.01.T01	XP_010674331.1	PREDICTED: T-complex protein 1 subunit gamma [Beta vulgaris subsp. vulgaris]
FtPinG0809059400.01	FtPinG0809059400.01.T01	XP_004509307.1	PREDICTED: thioredoxin domain-containing protein PLP3B [Cicer arietinum]
FtPinG0809059600.01	FtPinG0809059600.01.T01	XP_018809407.1	PREDICTED: uncharacterized protein LOC108982470 isoform X1 [Juglans regia]
FtPinG0809060200.01	FtPinG0809060200.01.T01	XP_021734647.1	fatty acid amide hydrolase-like isoform X1 [Chenopodium quinoa]
FtPinG0809060500.01	FtPinG0809060500.01.T01	XP_023907344.1	protein DOG1-like 3 [Quercus suber]
FtPinG0809061200.01	FtPinG0809061200.01.T01	XP_020111358.1	amino-acid permease BAT1 homolog [Ananas comosus]
FtPinG0809061600.01	FtPinG0809061600.01.T01	XP_018827727.1	PREDICTED: amino-acid permease BAT1 homolog [Juglans regia]
FtPinG0809061700.01	FtPinG0809061700.01.T01	XP_019417755.1	PREDICTED: RNA polymerase II transcriptional coactivator KIWI [Lupinus angustifolius]
FtPinG0809062000.01	FtPinG0809062000.01.T01	XP_021859846.1	farnesylcysteine lyase [Spinacia oleracea]
FtPinG0809063400.01	FtPinG0809063400.01.T01	OMO76281.1	t-SNARE [Corchorus olitorius]
FtPinG0809063500.01	FtPinG0809063500.01.T01	ADV02769.1	putative low temperature and salt responsive protein isoform 2 [Ipomoea batatas]
FtPinG0809063700.01	FtPinG0809063700.01.T01	XP_010674511.1	PREDICTED: LOW QUALITY PROTEIN: pleiotropic drug resistance protein 3-like [Beta vulgaris subsp. vulgaris]
FtPinG0809064000.01	FtPinG0809064000.01.T01	XP_021664714.1	S-adenosylmethionine synthase 1-like [Hevea brasiliensis]
FtPinG0809064000.01	FtPinG0809064000.01.T02	XP_021664714.1	S-adenosylmethionine synthase 1-like [Hevea brasiliensis]
FtPinG0809064100.01	FtPinG0809064100.01.T01	XP_021691414.1	WAT1-related protein At1g09380-like [Hevea brasiliensis]

Supplementary Table 10 (Continued):

FtPinG0809064300.01	FtPinG0809064300.01.T02	XP_021623320.1	ADP-ribosylation factor [Manihot esculenta]
FtPinG0809064300.01	FtPinG0809064300.01.T04	XP_020254978.1	ADP-ribosylation factor 1 [Asparagus officinalis]
FtPinG0809064300.01	FtPinG0809064300.01.T03	XP_016705457.1	PREDICTED: ADP-ribosylation factor 2-B isoform X1 [Gossypium hirsutum]
FtPinG0809064300.01	FtPinG0809064300.01.T01	XP_015072238.1	PREDICTED: ADP-ribosylation factor isoform X1 [Solanum pennellii]
FtPinG0809064800.01	FtPinG0809064800.01.T01	AAM96868.1	fagopyritol synthase 2 [Fagopyrum esculentum]
FtPinG0809065300.01	FtPinG0809065300.01.T01	XP_021853446.1	AP-3 complex subunit mu [Spinacia oleracea]
FtPinG0809065500.01	FtPinG0809065500.01.T01	XP_002277327.1	PREDICTED: putative pentatricopeptide repeat-containing protein At1g56570 [Vitis vinifera]
FtPinG0809065700.01	FtPinG0809065700.01.T01	XP_021734488.1	DUF724 domain-containing protein 6-like [Chenopodium quinoa]
FtPinG0809066200.01	FtPinG0809066200.01.T01	XP_018813114.1	PREDICTED: protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic-like isoform X1 [Juglans regia]
FtPinG0809066400.01	FtPinG0809066400.01.T01	XP_021821287.1	NHL repeat-containing protein 2 isoform X2 [Prunus avium]
FtPinG0809067000.01	FtPinG0809067000.01.T01	XP_021805750.1	LYR motif-containing protein 4 [Prunus avium]
FtPinG0809067400.01	FtPinG0809067400.01.T01	PON41632.1	HAUS augmin-like complex subunit [Parasponia andersonii]
FtPinG0809067500.01	FtPinG0809067500.01.T01	XP_015572386.1	cytochrome c oxidase subunit 5C [Ricinus communis]
FtPinG0809067900.01	FtPinG0809067900.01.T01	XP_021734456.1	transcription initiation factor TFIID subunit 9-like [Chenopodium quinoa]
FtPinG0809068200.01	FtPinG0809068200.01.T01	XP_018807886.1	PREDICTED: nicotianamine synthase-like [Juglans regia]
FtPinG0809068900.01	FtPinG0809068900.01.T01	XP_021853254.1	calreticulin [Spinacia oleracea]
FtPinG0809069200.01	FtPinG0809069200.01.T01	XP_021772765.1	pentatricopeptide repeat-containing protein At1g09190-like [Chenopodium quinoa]
FtPinG0809069900.01	FtPinG0809069900.01.T01	PIN09428.1	Serine/threonine protein kinase [Handroanthus impetiginosus]
FtPinG0809070500.01	FtPinG0809070500.01.T01	XP_022895871.1	calmodulin-binding protein 60 C-like [Olea europaea var. sylvestris]
FtPinG0809070700.01	FtPinG0809070700.01.T01	XP_021772798.1	dnaJ homolog subfamily B member 3-like [Chenopodium quinoa]
FtPinG0809071000.01	FtPinG0809071000.01.T01	XP_019104455.1	PREDICTED: uncharacterized protein LOC104890385 [Beta vulgaris subsp. vulgaris]
FtPinG0809071200.01	FtPinG0809071200.01.T01	XP_019080615.1	PREDICTED: uncharacterized protein LOC100240780 [Vitis vinifera]