Supplementary Table 13: The lists of genes in Wild-II_vs_Wild-I_Wild-II selective sweep.

Gene ID	Transcript ID	NR ID	NR annotation
FtPinG0100174400.01	FtPinG0100174400.01.T01	XP_010665057.1	PREDICTED: laccase-14 [Vitis vinifera]
FtPinG0100174800.01	FtPinG0100174800.01.T01	XP_010665057.1	PREDICTED: laccase-14 [Vitis vinifera]
FtPinG0100174800.01	FtPinG0100174800.01.T02	CBI29312.3	unnamed protein product, partial [Vitis vinifera]
FtPinG0100175100.01	FtPinG0100175100.01.T01	--	--
FtPinG0100175800.01	FtPinG0100175800.01.T01	XP_010061040.1	PREDICTED: 5'-3' exoribonuclease 3 isoform X2 [Eucalyptus grandis]
FtPinG0100175900.01	FtPinG0100175900.01.T01	--	--
FtPinG0100176600.01	FtPinG0100176600.01.T01	XP_010038202.1	PREDICTED: dynamin-related protein 4C [Eucalyptus grandis]
FtPinG0100176600.01	FtPinG0100176600.01.T02	KCW84558.1	hypothetical protein EUGRSUZ_B01397 [Eucalyptus grandis]
FtPinG0100176700.01	FtPinG0100176700.01.T01	KMT01843.1	hypothetical protein BVRB_9g210340 [Beta vulgaris subsp. vulgaris]
FtPinG0100177000.01	FtPinG0100177000.01.T01	XP_012075691.1	protein DETOXIFICATION 12 [Jatropha curcas]
FtPinG0100177300.01	FtPinG0100177300.01.T01	KCW60930.1	hypothetical protein EUGRSUZ_H03663 [Eucalyptus grandis]
FtPinG0100178200.01	FtPinG0100178200.01.T01	XP_019074664.1	PREDICTED: protein DETOXIFICATION 12 [Vitis vinifera]
FtPinG0100178300.01	FtPinG0100178300.01.T01	XP_021904957.1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B [Carica papaya]
FtPinG0100178700.01	FtPinG0100178700.01.T01	XP_010452888.2	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC104734904 [Camelina sativa]
FtPinG0100179200.01	FtPinG0100179200.01.T01	PSR88170.1	Fasciclin-like arabinogalactan protein [Actinidia chinensis var. chinensis]
FtPinG0100179300.01	FtPinG0100179300.01.T01	PON45785.1	hypothetical protein PanWU01x14_256600, partial [Parasponia andersonii]
FtPinG0100179500.01	FtPinG0100179500.01.T01	--	--
FtPinG0100179700.01	FtPinG0100179700.01.T01	KRH27793.1	hypothetical protein GLYMA_11G014300 [Glycine max]
FtPinG0100180000.01	FtPinG0100180000.01.T01	XP_021775558.1	transcription factor JUNGBRUNNEN 1-like [Chenopodium quinoa]
FtPinG0100180200.01	FtPinG0100180200.01.T01	XP_011093862.1	photosystem I chlorophyll a/b-binding protein 6, chloroplastic [Sesamum indicum]
FtPinG0100180300.01	FtPinG0100180300.01.T01	KZM82620.1	hypothetical protein DCAR_030189 [Daucus carota subsp. sativus]
FtPinG0100180500.01	FtPinG0100180500.01.T01	XP_021733140.1	beta-glucuronosyltransferase GlcAT14A-like [Chenopodium quinoa]
FtPinG0100180800.01	FtPinG0100180800.01.T01	BAU59407.1	cytochrome P450 81B80 [Fallopia sachalinensis]

Supplementary Table 12 (Continued):

FtPinG0100181000.01	FtPinG0100181000.01.T01	EEF52317.1	cytochrome P450, putative [Ricinus communis]
FtPinG0100181100.01	FtPinG0100181100.01.T01	XP_021592565.1	protein PIN-LIKES 2-like [Manihot esculenta]
FtPinG0100181100.01	FtPinG0100181100.01.T02	XP_010681684.1	PREDICTED: protein PIN-LIKES 2 [Beta vulgaris subsp. vulgaris]
FtPinG0100181300.01	FtPinG0100181300.01.T01	XP_021838440.1	probable ribose-5-phosphate isomerase 2 [Spinacia oleracea]
FtPinG0100181600.01	FtPinG0100181600.01.T01	KNA07972.1	hypothetical protein SOVF_166900 [Spinacia oleracea]
FtPinG0100182000.01	FtPinG0100182000.01.T01	--	--
FtPinG0100182100.01	FtPinG0100182100.01.T01	AAG50765.1	copia-type polyprotein, putative [Arabidopsis thaliana]
FtPinG0100182300.01	FtPinG0100182300.01.T01	XP_002281632.1	PREDICTED: uncharacterized protein LOC100255480 [Vitis vinifera]
FtPinG0100182600.01	FtPinG0100182600.01.T01	XP_024948696.1	receptor-like protein 14 [Citrus sinensis]
FtPinG0100182800.01	FtPinG0100182800.01.T01	XP_024948687.1	receptor-like protein 1 isoform X4 [Citrus sinensis]
FtPinG0100183000.01	FtPinG0100183000.01.T01	XP_010691120.1	PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At4g36180 [Beta vulgaris subsp. vulgaris]
FtPinG0100183100.01	FtPinG0100183100.01.T01	PON36206.1	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent [Trema orientale]
FtPinG0100183600.01	FtPinG0100183600.01.T01	XP_021728712.1	uncharacterized protein LOC110695789 [Chenopodium quinoa]
FtPinG0100183800.01	FtPinG0100183800.01.T01	XP_010666408.1	PREDICTED: uncharacterized protein LOC104883562 [Beta vulgaris subsp. vulgaris]
FtPinG0100184600.01	FtPinG0100184600.01.T01	--	--
FtPinG0100184600.01	FtPinG0100184600.01.T02	--	--
FtPinG0100185200.01	FtPinG0100185200.01.T01	AES86908.2	leucine-rich receptor-like kinase family protein, putative [Medicago truncatula]
FtPinG0180000032.01	FtPinG0180000032.01.T01	PSR88170.1	Fasciclin-like arabinogalactan protein [Actinidia chinensis var. chinensis]
FtPinG0201566500.01	FtPinG0201566500.01.T01	KMS97953.1	hypothetical protein BVRB_4g097140 [Beta vulgaris subsp. vulgaris]
FtPinG0201567500.01	FtPinG0201567500.01.T01	XP_021863622.1	putative lysine-specific demethylase JMJ16 isoform X2 [Spinacia oleracea]
FtPinG0201567500.01	FtPinG0201567500.01.T02	XP_010695040.1	PREDICTED: lysine-specific demethylase JMJ18 [Beta vulgaris subsp. vulgaris]
FtPinG0201567500.01	FtPinG0201567500.01.T03	XP_010695040.1	PREDICTED: lysine-specific demethylase JMJ18 [Beta vulgaris subsp. vulgaris]
FtPinG0201567800.01	FtPinG0201567800.01.T01	XP_002267312.1	PREDICTED: protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 1 [Vitis vinifera]

Supplementary Table 12 (Continued):

FtPinG0201568000.01	FtPinG0201568000.01.T01	XP_021742153.1	uncharacterized protein LOC110708346 [Chenopodium quinoa]
FtPinG0201569000.01	FtPinG0201569000.01.T01	XP_019167085.1	PREDICTED: elongation factor 1-delta-like [Ipomoea nil]
FtPinG0201569000.01	FtPinG0201569000.01.T02	XP_019167086.1	PREDICTED: elongation factor 1-delta-like [Ipomoea nil]
FtPinG0201569400.01	FtPinG0201569400.01.T01	XP_015575850.1	protein SPIRRIG isoform X1 [Ricinus communis]
FtPinG0201569500.01	FtPinG0201569500.01.T01	ABR16196.1	unknown [Picea sitchensis]
FtPinG0201570200.01	FtPinG0201570200.01.T01	--	--
FtPinG0201570300.01	FtPinG0201570300.01.T01	KMT13444.1	hypothetical protein BVRB_4g083500 [Beta vulgaris subsp. vulgaris]
FtPinG0201570500.01	FtPinG0201570500.01.T01	XP_019703846.1	PREDICTED: CBL-interacting serine/threonine-protein kinase 21-like [Elaeis guineensis]
FtPinG0201570500.01	FtPinG0201570500.01.T02	XP_019703846.1	PREDICTED: CBL-interacting serine/threonine-protein kinase 21-like [Elaeis guineensis]
FtPinG0201573100.01	FtPinG0201573100.01.T01	--	--
FtPinG0201573300.01	FtPinG0201573300.01.T01	PNY09734.1	putative copia-type protein [Trifolium pratense]
FtPinG0201573600.01	FtPinG0201573600.01.T01	XP_021750590.1	pentatricopeptide repeat-containing protein At5g15010, mitochondrial-like [Chenopodium quinoa]
FtPinG0201573800.01	FtPinG0201573800.01.T01	XP_021306932.1	uncharacterized protein LOC8084160 [Sorghum bicolor]
FtPinG0201838400.01	FtPinG0201838400.01.T01	XP_017980661.1	PREDICTED: BES1/BZR1 homolog protein 4 [Theobroma cacao]
FtPinG0201839000.01	FtPinG0201839000.01.T01	XP_021762758.1	mediator of RNA polymerase II transcription subunit 19a-like [Chenopodium quinoa]
FtPinG0201839800.01	FtPinG0201839800.01.T01	XP_012847480.1	PREDICTED: heparanase-like protein 1 [Erythranthe guttata]
FtPinG0201840000.01	FtPinG0201840000.01.T01	XP_024922621.1	uncharacterized protein LOC107432497 isoform X1 [Ziziphus jujuba]
FtPinG0201840100.01	FtPinG0201840100.01.T01	XP_010675324.1	PREDICTED: IRK-interacting protein [Beta vulgaris subsp. vulgaris]
FtPinG0201840100.01	FtPinG0201840100.01.T02	XP_010675324.1	PREDICTED: IRK-interacting protein [Beta vulgaris subsp. vulgaris]
FtPinG0201840800.01	FtPinG0201840800.01.T01	KMT13298.1	hypothetical protein BVRB_4g085560 [Beta vulgaris subsp. vulgaris]
FtPinG0201840900.01	FtPinG0201840900.01.T01	XP_010274424.1	PREDICTED: anaphase-promoting complex subunit 6 [Nelumbo nucifera]
FtPinG0201841200.01	FtPinG0201841200.01.T01	XP_022981173.1	alpha-1,3/1,6-mannosyltransferase ALG2 [Cucurbita maxima]

Supplementary Table 12 (Continued):

FtPinG0201841300.01	FtPinG0201841300.01.T01	XP_016169293.1	uncharacterized protein LOC107611942 [Arachis ipaensis]
FtPinG0201841600.01	FtPinG0201841600.01.T01	XP_011044080.1	PREDICTED: multiprotein-bridging factor 1b-like [Populus euphratica]
FtPinG0201841700.01	FtPinG0201841700.01.T01	XP_021773831.1	rab3 GTPase-activating protein non-catalytic subunit-like [Chenopodium quinoa]
FtPinG0201842400.01	FtPinG0201842400.01.T01	XP_021649143.1	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 7-like [Hevea brasiliensis]
FtPinG0201842600.01	FtPinG0201842600.01.T01	XP_024451454.1	uncharacterized protein LOC7465062 [Populus trichocarpa]
FtPinG0201842700.01	FtPinG0201842700.01.T01	KMT13169.1	hypothetical protein BVRB_4g085750 [Beta vulgaris subsp. vulgaris]
FtPinG0201842900.01	FtPinG0201842900.01.T01	PSS15992.1	Phosphoenolpyruvate carboxylase [Actinidia chinensis var. chinensis]
FtPinG0280000545.01	FtPinG0280000545.01.T01	XP_002885505.1	late embryogenesis abundant protein 31 [Arabidopsis lyrata subsp. lyrata]
FtPinG0280000546.01	FtPinG0280000546.01.T01	PKA63076.1	hypothetical protein AXF42_Ash007872 [Apostasia shenzhenica]
FtPinG0280000701.01	FtPinG0280000701.01.T01	XP_015078360.1	PREDICTED: uncharacterized protein LOC107022192 [Solanum pennellii]
FtPinG0302986000.01	FtPinG0302986000.01.T01	XP_021839592.1	probable membrane-associated kinase regulator 5 [Spinacia oleracea]
FtPinG0302986200.01	FtPinG0302986200.01.T01	XP_021839835.1	F-box protein At5g52880 isoform X2 [Spinacia oleracea]
FtPinG0302986700.01	FtPinG0302986700.01.T01	XP_021726740.1	DUF21 domain-containing protein At5g52790-like isoform X1 [Chenopodium quinoa]
FtPinG0302986900.01	FtPinG0302986900.01.T01	KMT16174.1	hypothetical protein BVRB_3g053340 [Beta vulgaris subsp. vulgaris]
FtPinG0302987200.01	FtPinG0302987200.01.T01	XP_021765029.1	probable polygalacturonase isoform X2 [Chenopodium quinoa]
FtPinG0302987400.01	FtPinG0302987400.01.T01	GAY45656.1	hypothetical protein CUMW_091020 [Citrus unshiu]
FtPinG0302987700.01	FtPinG0302987700.01.T01	XP_021828054.1	pentatricopeptide repeat-containing protein At3g58590 isoform X1 [Prunus avium]
FtPinG0302987900.01	FtPinG0302987900.01.T01	XP_021842697.1	probable cinnamyl alcohol dehydrogenase 1 [Spinacia oleracea]
FtPinG0302988300.01	FtPinG0302988300.01.T01	--	--
FtPinG0302988500.01	FtPinG0302988500.01.T01	--	--
FtPinG0302989100.01	FtPinG0302989100.01.T01	XP_002277375.1	PREDICTED: probable cinnamyl alcohol dehydrogenase 1 isoform X1 [Vitis vinifera]
FtPinG0302989400.01	FtPinG0302989400.01.T01	XP_002277375.1	PREDICTED: probable cinnamyl alcohol dehydrogenase 1 isoform X1 [Vitis vinifera]
FtPinG0302989600.01	FtPinG0302989600.01.T01	--	--
FtPinG0302990200.01	FtPinG0302990200.01.T01	--	--
FtPinG0302990600.01	FtPinG0302990600.01.T01	XP_021842697.1	probable cinnamyl alcohol dehydrogenase 1 [Spinacia oleracea]

Supplementary Table 12 (Continued):

FtPinG0302990700.01	FtPinG0302990700.01.T01	XP_026403817.1	DNA-binding protein HEXBP-like [Papaver somniferum]
FtPinG0302990900.01	FtPinG0302990900.01.T01	OTF96420.1	putative actin depolymerizing factor 11 [Helianthus annuus]
FtPinG0302991200.01	FtPinG0302991200.01.T01	PON44192.1	Mono-/di-acylglycerol lipase [Trema orientale]
FtPinG0302991400.01	FtPinG0302991400.01.T01	--	--
FtPinG0302991500.01	FtPinG0302991500.01.T01	--	--
FtPinG0302992200.01	FtPinG0302992200.01.T01	KYP61428.1	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Cajanus cajan]
FtPinG0302992400.01	FtPinG0302992400.01.T01	PRQ52817.1	putative RNA-directed DNA polymerase [Rosa chinensis]
FtPinG0302992800.01	FtPinG0302992800.01.T01	KOM42096.1	hypothetical protein LR48_Vigan04g229400 [Vigna angularis]
FtPinG0302993000.01	FtPinG0302993000.01.T01	--	--
FtPinG0302993000.01	FtPinG0302993000.01.T02	--	--
FtPinG0302993100.01	FtPinG0302993100.01.T01	XP_010068782.1	PREDICTED: heparanase-like protein 1 [Eucalyptus grandis]
FtPinG0302993400.01	FtPinG0302993400.01.T01	XP_010258096.1	PREDICTED: pentatricopeptide repeat-containing protein At1g26460, mitochondrial [Nelumbo nucifera]
FtPinG0302993500.01	FtPinG0302993500.01.T01	XP_015583816.1	heparanase-like protein 1 [Ricinus communis]
FtPinG0302993900.01	FtPinG0302993900.01.T01	KMT16477.1	hypothetical protein BVRB_3g050950 [Beta vulgaris subsp. vulgaris]
FtPinG0302994200.01	FtPinG0302994200.01.T01	XP_023928083.1	BAHD acyltransferase DCR-like [Quercus suber]
FtPinG0302994300.01	FtPinG0302994300.01.T01	--	--
FtPinG0302995000.01	FtPinG0302995000.01.T01	XP_024171426.1	UPF0496 protein At3g49070 [Rosa chinensis]
FtPinG0302995100.01	FtPinG0302995100.01.T01	PIN00194.1	DNA-directed DNA polymerase [Handroanthus impetiginosus]
FtPinG0302995300.01	FtPinG0302995300.01.T01	--	--
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]
FtPinG0302996100.01	FtPinG0302996100.01.T01	XP_021726699.1	uncharacterized protein LOC110693849 isoform X1 [Chenopodium quinoa]
FtPinG0302996500.01	FtPinG0302996500.01.T01	XP_021726703.1	uncharacterized protein LOC110693849 isoform X3 [Chenopodium quinoa]
FtPinG0302996900.01	FtPinG0302996900.01.T01	XP_021726724.1	probable receptor-like protein kinase At5g24010 [Chenopodium quinoa]

Supplementary Table 12 (Continued):

FtPinG0302996900.01	FtPinG0302996900.01.T02	PQQ20608.1	putative receptor-like protein kinase [Prunus yedoensis var. nudiflora]
FtPinG0302997200.01	FtPinG0302997200.01.T01	--	--
FtPinG0302997200.01	FtPinG0302997200.01.T02	--	--
FtPinG0303006100.01	FtPinG0303006100.01.T01	--	--
FtPinG0303006500.01	FtPinG0303006500.01.T01	XP_021729906.1	ERAD-associated E3 ubiquitin-protein ligase component HRD3A-like [Chenopodium quinoa]
FtPinG0303006800.01	FtPinG0303006800.01.T01	XP_010669478.1	PREDICTED: uncharacterized protein LOC104886700 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0303007300.01	FtPinG0303007300.01.T01	XP_019167504.1	PREDICTED: probable auxin efflux carrier component 1c [Ipomoea nil]
FtPinG0303007500.01	FtPinG0303007500.01.T01	--	--
FtPinG0303008800.01	FtPinG0303008800.01.T01	KHN11199.1	Vacuolar fusion protein MON1 like A [Glycine soja]
FtPinG0303008800.01	FtPinG0303008800.01.T02	--	--
FtPinG0303008900.01	FtPinG0303008900.01.T01	--	--
FtPinG0303009700.01	FtPinG0303009700.01.T01	XP_021643766.1	phosphomethylethanolamine N-methyltransferase [Hevea brasiliensis]
FtPinG0303010100.01	FtPinG0303010100.01.T01	XP_024988897.1	phosphomethylethanolamine N-methyltransferase-like isoform X1 [Cynara cardunculus var. scolymus]
FtPinG0303010100.01	FtPinG0303010100.01.T02	XP_024988897.1	phosphomethylethanolamine N-methyltransferase-like isoform X1 [Cynara cardunculus var. scolymus]
FtPinG0303010400.01	FtPinG0303010400.01.T01	KZM89363.1	hypothetical protein DCAR_023274 [Daucus carota subsp. sativus]
FtPinG0303010600.01	FtPinG0303010600.01.T01	XP_021864127.1	probable serine/threonine protein kinase IREH1 [Spinacia oleracea]
FtPinG0303011100.01	FtPinG0303011100.01.T01	XP_021600680.1	uncharacterized protein LOC110606236 [Manihot esculenta]
FtPinG0303011300.01	FtPinG0303011300.01.T01	XP_023907912.1	putative 3,4-dihydroxy-2-butanone kinase [Quercus suber]
FtPinG0303011900.01	FtPinG0303011900.01.T01	--	--
FtPinG0303012300.01	FtPinG0303012300.01.T01	XP_016458433.1	PREDICTED: putative 3,4-dihydroxy-2-butanone kinase isoform X2 [Nicotiana tabacum]

Supplementary Table 12 (Continued):

FtPinG0303012800.01	FtPinG0303012800.01.T01	XP_020537791.1	OTU domain-containing protein DDB_G0284757 [Jatropha curcas]
FtPinG0303012800.01	FtPinG0303012800.01.T02	XP_012081076.1	OTU domain-containing protein DDB_G0284757 [Jatropha curcas]
FtPinG0303013700.01	FtPinG0303013700.01.T01	XP_021725103.1	uncharacterized protein LOC110692417 [Chenopodium quinoa]
FtPinG0303013900.01	FtPinG0303013900.01.T01	XP_023887660.1	DNA replication licensing factor MCM2 [Quercus suber]
FtPinG0303014200.01	FtPinG0303014200.01.T01	XP_022720879.1	dihydroceramide fatty acyl 2-hydroxylase FAH1-like [Durio zibethinus]
FtPinG0303124400.01	FtPinG0303124400.01.T01	XP_022770622.1	11-beta-hydroxysteroid dehydrogenase 1B-like [Durio zibethinus]
FtPinG0303124600.01	FtPinG0303124600.01.T01	XP_022892059.1	HVA22-like protein e [Olea europaea var. sylvestris]
FtPinG0303124600.01	FtPinG0303124600.01.T02	KFK28245.1	hypothetical protein AALP_AA8G491100 [Arabis alpina]
FtPinG0303125000.01	FtPinG0303125000.01.T01	--	--
FtPinG0303125200.01	FtPinG0303125200.01.T01	KMT06420.1	hypothetical protein BVRB_7g160970 [Beta vulgaris subsp. vulgaris]
FtPinG0303125300.01	FtPinG0303125300.01.T01	XP_021760852.1	single-stranded DNA-bindig protein WHY2, mitochondrial-like [Chenopodium quinoa]
FtPinG0303125800.01	FtPinG0303125800.01.T01	XP_018850374.1	PREDICTED: GDSL esterase/lipase At1g71250-like [Juglans regia]
FtPinG0303126000.01	FtPinG0303126000.01.T01	KZM98589.1	hypothetical protein DCAR_014049 [Daucus carota subsp. sativus]
FtPinG0303126200.01	FtPinG0303126200.01.T01	XP_023879108.1	SCY1-like protein 2 [Quercus suber]
FtPinG0303126500.01	FtPinG0303126500.01.T01	XP_021762687.1	bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic-like [Chenopodium quinoa]
FtPinG0303126900.01	FtPinG0303126900.01.T01	XP_021288240.1	uncharacterized protein LOC110419492 [Herrania umbratica]
FtPinG0303127300.01	FtPinG0303127300.01.T01	--	--
FtPinG0303127500.01	FtPinG0303127500.01.T01	CBI19132.3	unnamed protein product, partial [Vitis vinifera]
FtPinG0303127800.01	FtPinG0303127800.01.T01	KJB64334.1	hypothetical protein B456_010G043500 [Gossypium raimondii]
FtPinG0303127900.01	FtPinG0303127900.01.T01	POO04026.1	Guanine nucleotide-binding protein, beta subunit [Trema orientale]
FtPinG0303127900.01	FtPinG0303127900.01.T02	XP_019237744.1	PREDICTED: uncharacterized WD repeat-containing protein C2A9.03-like isoform X1 [Nicotiana attenuata]
FtPinG0303139700.01	FtPinG0303139700.01.T01	XP_020268734.1	uncharacterized protein LOC109844183 [Asparagus officinalis]

Supplementary Table 12 (Continued):

FtPinG0303140000.01	FtPinG0303140000.01.T01	XP_010667260.1	PREDICTED: zinc transporter 4, chloroplastic [Beta vulgaris subsp. vulgaris]
FtPinG0303140100.01	FtPinG0303140100.01.T01	XP_002284024.1	PREDICTED: RING-H2 finger protein ATL11 [Vitis vinifera]
FtPinG0303140300.01	FtPinG0303140300.01.T01	CBK27691.1	translational elongation factor 1 alpha, partial [Trichoderma gamsii]
FtPinG0303140500.01	FtPinG0303140500.01.T01	XP_004238534.2	E3 ubiquitin-protein ligase ATL15 [Solanum lycopersicum]
FtPinG0303141000.01	FtPinG0303141000.01.T01	KDO67242.1	hypothetical protein CISIN_1g033867mg [Citrus sinensis]
FtPinG0303141400.01	FtPinG0303141400.01.T01	XP_021740299.1	purine permease 3-like isoform X1 [Chenopodium quinoa]
FtPinG0303141600.01	FtPinG0303141600.01.T01	XP_021743621.1	phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic-like isoform X1 [Chenopodium quinoa]
FtPinG0303421600.01	FtPinG0303421600.01.T01	--	--
FtPinG0303421700.01	FtPinG0303421700.01.T01	XP_008233155.1	PREDICTED: O-acyltransferase WSD1-like [Prunus mume]
FtPinG0303422000.01	FtPinG0303422000.01.T01	--	--
FtPinG0303422100.01	FtPinG0303422100.01.T01	XP_021863338.1	enoyl-[acyl-carrier-protein] reductase [NADH] 1, chloroplastic isoform X1 [Spinacia oleracea]
FtPinG0303422800.01	FtPinG0303422800.01.T01	XP_017251837.1	PREDICTED: uncharacterized protein LOC108222422 [Daucus carota subsp. sativus]
FtPinG0303423000.01	FtPinG0303423000.01.T01	PRQ29949.1	putative Myb/SANT-like domain-containing protein [Rosa chinensis]
FtPinG0303423100.01	FtPinG0303423100.01.T01	PQQ16454.1	putative inactive poly [Prunus yedoensis var. nudiflora]
FtPinG0303423300.01	FtPinG0303423300.01.T01	ADN26594.1	type III polyketide synthase [Polygonum cuspidatum]
FtPinG0303423600.01	FtPinG0303423600.01.T01	XP_010675215.1	PREDICTED: uncharacterized protein LOC104891251 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0303423900.01	FtPinG0303423900.01.T01	XP_010675238.1	PREDICTED: sucrose synthase 7 isoform X3 [Beta vulgaris subsp. vulgaris]
FtPinG0303424200.01	FtPinG0303424200.01.T01	GAV81138.1	ANTH domain-containing protein [Cephalotus follicularis]
FtPinG0380000881.01	FtPinG0380000881.01.T01	XP_021692335.1	uncharacterized protein LOC110673497 [Hevea brasiliensis]
FtPinG0380000883.01	FtPinG0380000883.01.T01	CAA73042.1	polyprotein, partial [Ananas comosus]
FtPinG0380000884.01	FtPinG0380000884.01.T01	AAN04995.1	retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa Japonica Group]
FtPinG0380000885.01	FtPinG0380000885.01.T01	--	--

Supplementary Table 12 (Continued):

FtPinG0380000886.01	FtPinG0380000886.01.T01	KNA15891.1	hypothetical protein SOVF_094210 [Spinacia oleracea]
FtPinG0380000912.01	FtPinG0380000912.01.T01	XP_010678233.2	PREDICTED: uncharacterized protein LOC104893796 [Beta vulgaris subsp. vulgaris]
FtPinG0380000921.01	FtPinG0380000921.01.T01	XP_021750654.1	uncharacterized protein LOC110716341 [Chenopodium quinoa]
FtPinG0380000922.01	FtPinG0380000922.01.T01	XP_019106659.1	PREDICTED: uncharacterized protein LOC109135685 [Beta vulgaris subsp. vulgaris]
FtPinG0380000923.01	FtPinG0380000923.01.T01	XP_010646217.1	PREDICTED: uncharacterized protein LOC104878131 [Vitis vinifera]
FtPinG0380001141.01	FtPinG0380001141.01.T01	XP_010672288.1	PREDICTED: L10-interacting MYB domain-containing protein-like isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0380001142.01	FtPinG0380001142.01.T01	XP_002513430.1	glutamic acid-rich protein [Ricinus communis]
FtPinG0403963400.01	FtPinG0403963400.01.T01	AEO97233.1	endo-1,4-beta-glucanase [Populus trichocarpa]
FtPinG0403963400.01	FtPinG0403963400.01.T02	XP_002299478.3	endoglucanase 6 [Populus trichocarpa]
FtPinG0403963600.01	FtPinG0403963600.01.T01	--	--
FtPinG0403963700.01	FtPinG0403963700.01.T01	XP_021642650.1	ethylene-responsive transcription factor ERF061 [Hevea brasiliensis]
FtPinG0403964200.01	FtPinG0403964200.01.T01	XP_002272604.1	PREDICTED: subtilisin-like protease SBT2.5 [Vitis vinifera]
FtPinG0403964400.01	FtPinG0403964400.01.T01	XP_020419056.1	probable polygalacturonase [Prunus persica]
FtPinG0403964500.01	FtPinG0403964500.01.T01	--	--
FtPinG0403964800.01	FtPinG0403964800.01.T01	--	--
FtPinG0403965400.01	FtPinG0403965400.01.T01	--	--
FtPinG0403965900.01	FtPinG0403965900.01.T01	--	--
FtPinG0403966600.01	FtPinG0403966600.01.T01	--	--
FtPinG0403967000.01	FtPinG0403967000.01.T01	XP_018815534.1	PREDICTED: high mobility group B protein 6-like [Juglans regia]
FtPinG0403967200.01	FtPinG0403967200.01.T01	XP_010104980.1	protein ENHANCED DISEASE RESISTANCE 4 [Morus notabilis]
FtPinG0403967400.01	FtPinG0403967400.01.T01	XP_010676330.1	PREDICTED: uncharacterized protein LOC104892186 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0403967900.01	FtPinG0403967900.01.T01	XP_012474863.1	PREDICTED: mitochondrial adenine nucleotide transporter ADNT1-like [Gossypium raimondii]

Supplementary Table 12 (Continued):

FtPinG0403968300.01	FtPinG0403968300.01.T01	XP_008392450.1	PREDICTED: CMP-sialic acid transporter 1 [Malus domestica]
FtPinG0403968600.01	FtPinG0403968600.01.T01	XP_021863239.1	umecyanin-like [Spinacia oleracea]
FtPinG0404863100.01	FtPinG0404863100.01.T01	XP_009334823.1	PREDICTED: probable BOI-related E3 ubiquitin-protein ligase 2 [Pyrus x bretschneideri]
FtPinG0404863300.01	FtPinG0404863300.01.T01	XP_012073565.1	cinnamoyl-CoA reductase 1 [Jatropha curcas]
FtPinG0404863500.01	FtPinG0404863500.01.T01	XP_012073565.1	cinnamoyl-CoA reductase 1 [Jatropha curcas]
FtPinG0404863800.01	FtPinG0404863800.01.T01	XP_021300687.1	protein FD-like [Herrania umbratica]
FtPinG0404864000.01	FtPinG0404864000.01.T01	XP_015887459.1	protein Simiate [Ziziphus jujuba]
FtPinG0404864200.01	FtPinG0404864200.01.T01	XP_002510588.1	expansin-A11 [Ricinus communis]
FtPinG0404864300.01	FtPinG0404864300.01.T01	XP_010692760.1	PREDICTED: E3 ubiquitin-protein ligase ATL23 [Beta vulgaris subsp. vulgaris]
FtPinG0404864500.01	FtPinG0404864500.01.T01	PIN18538.1	NADH:ubiquinone oxidoreductase, NDUFA6/B14 subunit [Handroanthus impetiginosus]
FtPinG0404864700.01	FtPinG0404864700.01.T01	KNA04357.1	hypothetical protein SOVF_200450 isoform A [Spinacia oleracea]
FtPinG0404864900.01	FtPinG0404864900.01.T01	XP_021756571.1	LOW QUALITY PROTEIN: pentatricopeptide repeat-containing protein At1g20230-like [Chenopodium quinoa]
FtPinG0404865300.01	FtPinG0404865300.01.T01	XP_021756540.1	mechanosensitive ion channel protein 6-like [Chenopodium quinoa]
FtPinG0404865800.01	FtPinG0404865800.01.T01	RDX92882.1	Choline transporter protein 1 [Mucuna pruriens]
FtPinG0404866200.01	FtPinG0404866200.01.T01	XP_008240152.1	PREDICTED: phosphoethanolamine N-methyltransferase 1 [Prunus mume]
FtPinG0404866300.01	FtPinG0404866300.01.T01	KMT16229.1	hypothetical protein BVRB_3g053860 [Beta vulgaris subsp. vulgaris]
FtPinG0404866500.01	FtPinG0404866500.01.T01	XP_019075661.1	PREDICTED: bromodomain and WD repeat-containing protein 3 isoform X1 [Vitis vinifera]
FtPinG0404866700.01	FtPinG0404866700.01.T01	PON93992.1	Peptidase S9A, prolyl oligopeptidase [Trema orientale]
FtPinG0404866900.01	FtPinG0404866900.01.T01	XP_021756518.1	prolyl endopeptidase-like [Chenopodium quinoa]
FtPinG0404867200.01	FtPinG0404867200.01.T01	KMS95442.1	hypothetical protein BVRB_008210 [Beta vulgaris subsp. vulgaris]
FtPinG0404867400.01	FtPinG0404867400.01.T01	XP_023911577.1	large proline-rich protein bag6-B-like isoform X2 [Quercus suber]

Supplementary Table 12 (Continued):

FtPinG0404867500.01	FtPinG0404867500.01.T01	XP_021976701.1	alcohol dehydrogenase-like 7 [Helianthus annuus]
FtPinG0404868500.01	FtPinG0404868500.01.T01	KNA14143.1	hypothetical protein SOVF_110090 isoform B [Spinacia oleracea]
FtPinG0404869000.01	FtPinG0404869000.01.T01	XP_021732231.1	uncharacterized protein LOC110699048 [Chenopodium quinoa]
FtPinG0404869300.01	FtPinG0404869300.01.T01	OMP11146.1	hypothetical protein COLO4_04001 [Corchorus olitorius]
FtPinG0404869500.01	FtPinG0404869500.01.T01	XP_002282626.1	PREDICTED: iron-sulfur assembly protein IscA-like 2, mitochondrial isoform X2 [Vitis vinifera]
FtPinG0404869700.01	FtPinG0404869700.01.T01	ESW25027.1	hypothetical protein PHAVU_003G001900g [Phaseolus vulgaris]
FtPinG0404870000.01	FtPinG0404870000.01.T01	XP_021838252.1	probable serine/threonine-protein kinase CST [Spinacia oleracea]
FtPinG0404870100.01	FtPinG0404870100.01.T01	--	--
FtPinG0404870400.01	FtPinG0404870400.01.T01	XP_010692532.1	PREDICTED: serine/threonine-protein kinase PBS1-like [Beta vulgaris subsp. vulgaris]
FtPinG0404870600.01	FtPinG0404870600.01.T01	KMT19257.1	hypothetical protein BVRB_1g014390 [Beta vulgaris subsp. vulgaris]
FtPinG0480001276.01	FtPinG0480001276.01.T01	XP_010045861.1	PREDICTED: probable glucan endo-1,3-beta-glucosidase BG4 [Eucalyptus grandis]
FtPinG0480001277.01	FtPinG0480001277.01.T01	--	--
FtPinG0505368300.01	FtPinG0505368300.01.T01	XP_018840155.1	PREDICTED: uncharacterized protein LOC109005598 [Juglans regia]
FtPinG0505368600.01	FtPinG0505368600.01.T01	XP_015886719.1	uncharacterized protein LOC107421883 [Ziziphus jujuba]
FtPinG0505368700.01	FtPinG0505368700.01.T01	XP_004491881.1	PREDICTED: probable galacturonosyltransferase 14 [Cicer arietinum]
FtPinG0505369000.01	FtPinG0505369000.01.T01	OVA09074.1	protein of unknown function DUF1338 [Macleaya cordata]
FtPinG0505369400.01	FtPinG0505369400.01.T01	XP_011078309.1	peroxisomal fatty acid beta-oxidation multifunctional protein AIM1 [Sesamum indicum]
FtPinG0505369600.01	FtPinG0505369600.01.T01	XP_022763876.1	uncharacterized protein LOC111309190 [Durio zibethinus]
FtPinG0505370000.01	FtPinG0505370000.01.T01	XP_021844911.1	protein SIEVE ELEMENT OCCLUSION B-like [Spinacia oleracea]
FtPinG0505370200.01	FtPinG0505370200.01.T01	XP_021844911.1	protein SIEVE ELEMENT OCCLUSION B-like [Spinacia oleracea]
FtPinG0505370400.01	FtPinG0505370400.01.T01	XP_010273709.1	PREDICTED: glucuronokinase 1-like [Nelumbo nucifera]
FtPinG0505370500.01	FtPinG0505370500.01.T01	--	--

Supplementary Table 12 (Continued):

FtPinG0505370500.01	FtPinG0505370500.01.T02	--	--
FtPinG0505370700.01	FtPinG0505370700.01.T01	XP_015879109.1	uncharacterized protein LOC107415318 isoform X2 [Ziziphus jujuba]
FtPinG0505371100.01	FtPinG0505371100.01.T01	ACZ05049.1	putative glutaredoxin [Polygonatum sibiricum]
FtPinG0505371100.01	FtPinG0505371100.01.T02	ACZ05049.1	putative glutaredoxin [Polygonatum sibiricum]
FtPinG0505371400.01	FtPinG0505371400.01.T01	XP_021814261.1	DEAD-box ATP-dependent RNA helicase 46 [Prunus avium]
FtPinG0505479500.01	FtPinG0505479500.01.T01	KNA03743.1	hypothetical protein SOVF_206180 [Spinacia oleracea]
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]
FtPinG0505480600.01	FtPinG0505480600.01.T01	XP_021718667.1	endoglucanase 2-like [Chenopodium quinoa]
FtPinG0505480700.01	FtPinG0505480700.01.T01	KNA07335.1	hypothetical protein SOVF_172800 [Spinacia oleracea]
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]
FtPinG0505481700.01	FtPinG0505481700.01.T01	GAU47808.1	hypothetical protein TSUD_404130 [Trifolium subterraneum]
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]
FtPinG0505483000.01	FtPinG0505483000.01.T01	--	--
FtPinG0505483400.01	FtPinG0505483400.01.T01	--	--
FtPinG0505483500.01	FtPinG0505483500.01.T01	PSS17963.1	Serine/arginine-rich splicing factor like [Actinidia chinensis var. chinensis]
FtPinG0505483500.01	FtPinG0505483500.01.T02	XP_010664824.1	PREDICTED: uncharacterized protein LOC100241980 isoform X1 [Vitis vinifera]
FtPinG0505483700.01	FtPinG0505483700.01.T01	--	--
FtPinG0505484000.01	FtPinG0505484000.01.T01	XP_012079565.1	long chain base biosynthesis protein 1 [Jatropha curcas]
FtPinG0505484200.01	FtPinG0505484200.01.T01	--	--

Supplementary Table 12 (Continued):

FtPinG0505485300.01	FtPinG0505485300.01.T01	KYP33548.1	ABC transporter B family member 13 [Cajanus cajan]
FtPinG0505485600.01	FtPinG0505485600.01.T01	CDP07373.1	unnamed protein product [Coffea canephora]
FtPinG0505485700.01	FtPinG0505485700.01.T01	KZV39601.1	prostaglandin E synthase 2 [Dorcoceras hygrometricum]
FtPinG0505486100.01	FtPinG0505486100.01.T01	XP_008387919.1	PREDICTED: probable BOI-related E3 ubiquitin-protein ligase 2 [Malus domestica]
FtPinG0505486600.01	FtPinG0505486600.01.T01	--	--
FtPinG0505486600.01	FtPinG0505486600.01.T02	--	--
FtPinG0580001776.01	FtPinG0580001776.01.T01	XP_015075513.1	PREDICTED: uncharacterized protein LOC107019601 [Solanum pennellii]
FtPinG0580001777.01	FtPinG0580001777.01.T01	--	--
FtPinG0580001780.01	FtPinG0580001780.01.T01	XP_021719499.1	uncharacterized protein LOC110687192 [Chenopodium quinoa]
FtPinG0580001781.01	FtPinG0580001781.01.T01	XP_021689976.1	uncharacterized protein LOC110671731 [Hevea brasiliensis]
FtPinG0580001782.01	FtPinG0580001782.01.T01	XP_019057520.1	PREDICTED: uncharacterized protein LOC104808408 [Tarenaya hassleriana]
FtPinG0580001783.01	FtPinG0580001783.01.T01	XP_010677465.1	PREDICTED: uncharacterized protein LOC104893086 [Beta vulgaris subsp. vulgaris]
FtPinG0580001784.01	FtPinG0580001784.01.T01	XP_024447839.1	uncharacterized protein LOC112325475 [Populus trichocarpa]
FtPinG0580001785.01	FtPinG0580001785.01.T01	XP_021744944.1	uncharacterized protein LOC110710909 [Chenopodium quinoa]