Supplementary Table 12: The lists of genes in Wild-II_vs_Wild-I_Wild-I selective sweep.

Gene ID	Transcript ID	NR ID	NR annotation
FtPinG0202106600.01	FtPinG0202106600.01.T01	--	--
FtPinG0202106800.01	FtPinG0202106800.01.T01	KNA11189.1	hypothetical protein SOVF_137480 [Spinacia oleracea]
FtPinG0202106900.01	FtPinG0202106900.01.T01	XP_010679316.1	PREDICTED: E3 ubiquitin-protein ligase Hakai [Beta vulgaris subsp. vulgaris]
FtPinG0202107300.01	FtPinG0202107300.01.T01	--	--
FtPinG0202107500.01	FtPinG0202107500.01.T01	XP_021765859.1	KH domain-containing protein At4g18375-like isoform X1 [Chenopodium quinoa]
FtPinG0202108100.01	FtPinG0202108100.01.T01	BAB08899.1	unnamed protein product [Arabidopsis thaliana]
FtPinG0202108300.01	FtPinG0202108300.01.T01	XP_010259867.1	PREDICTED: basic leucine zipper 9-like isoform X2 [Nelumbo nucifera]
FtPinG0202108500.01	FtPinG0202108500.01.T01	CBI32164.3	unnamed protein product, partial [Vitis vinifera]
FtPinG0202108800.01	FtPinG0202108800.01.T01	CBI15581.3	unnamed protein product, partial [Vitis vinifera]
FtPinG0202109200.01	FtPinG0202109200.01.T01	XP_002284273.1	PREDICTED: probable galacturonosyltransferase 13 isoform X1 [Vitis vinifera]
FtPinG0202109400.01	FtPinG0202109400.01.T01	XP_021853038.1	putative ABC transporter C family member 15 [Spinacia oleracea]
FtPinG0202109500.01	FtPinG0202109500.01.T01	CBI22072.3	unnamed protein product, partial [Vitis vinifera]
FtPinG0202109800.01	FtPinG0202109800.01.T01	XP_007041478.2	PREDICTED: peptide methionine sulfoxide reductase B5 [Theobroma cacao]
FtPinG0202109900.01	FtPinG0202109900.01.T01	XP_021729266.1	227 kDa spindle- and centromere-associated protein-like isoform X2 [Chenopodium quinoa]
FtPinG0202109900.01	FtPinG0202109900.01.T02	XP_021729265.1	227 kDa spindle- and centromere-associated protein-like isoform X1 [Chenopodium quinoa]
FtPinG0202110400.01	FtPinG0202110400.01.T01	XP_010687041.1	PREDICTED: putative D-cysteine desulfhydrase 1, mitochondrial isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0202110900.01	FtPinG0202110900.01.T01	XP_010274995.1	PREDICTED: chloride channel protein CLC-c [Nelumbo nucifera]
FtPinG0202111400.01	FtPinG0202111400.01.T01	EXB38944.1	Ankyrin repeat-containing protein [Morus notabilis]
FtPinG0202111600.01	FtPinG0202111600.01.T01	XP_026429575.1	uncharacterized protein LOC113325964 [Papaver somniferum]
FtPinG0202112100.01	FtPinG0202112100.01.T01	XP_022946447.1	pollen receptor-like kinase 3 [Cucurbita moschata]
FtPinG0202112400.01	FtPinG0202112400.01.T01	RLM97687.1	clathrin assembly protein AP17-like protein [Panicum miliaceum]

Supplementary Table 11 (Continued):

FtPinG0202112500.01	FtPinG0202112500.01.T01	XP_022730338.1	protein TIFY 10A-like [Durio zibethinus]
FtPinG0202112800.01	FtPinG0202112800.01.T01	PSR89949.1	Helicase protein [Actinidia chinensis var. chinensis]
FtPinG0303261500.01	FtPinG0303261500.01.T01	XP_021722878.1	NAC domain-containing protein 2-like [Chenopodium quinoa]
FtPinG0303262000.01	FtPinG0303262000.01.T01	XP_010667109.1	PREDICTED: protein BTR1 isoform X2 [Beta vulgaris subsp. vulgaris]
FtPinG0303262100.01	FtPinG0303262100.01.T01	KMS96320.1	hypothetical protein BVRB_000340 [Beta vulgaris subsp. vulgaris]
FtPinG0303262400.01	FtPinG0303262400.01.T01	XP_020228113.1	DNA repair protein RAD51 homolog [Cajanus cajan]
FtPinG0303262800.01	FtPinG0303262800.01.T01	XP_024950791.1	uncharacterized protein LOC102609448 [Citrus sinensis]
FtPinG0303263000.01	FtPinG0303263000.01.T01	--	--
FtPinG0303263400.01	FtPinG0303263400.01.T01	OTF91773.1	putative DNA-binding domain-containing protein [Helianthus annuus]
FtPinG0303263600.01	FtPinG0303263600.01.T01	--	--
FtPinG0303263800.01	FtPinG0303263800.01.T01	XP_018847917.1	PREDICTED: peroxisomal 2,4-dienoyl-CoA reductase [Juglans regia]
FtPinG0303264200.01	FtPinG0303264200.01.T01	GAV75697.1	zf-CCHC domain-containing protein/RVP_2 domain-containing protein [Cephalotus follicularis]
FtPinG0303264600.01	FtPinG0303264600.01.T01	--	--
FtPinG0303264700.01	FtPinG0303264700.01.T01	PNT23493.1	hypothetical protein POPTR_008G083900v3 [Populus trichocarpa]
FtPinG0303265400.01	FtPinG0303265400.01.T01	PIN07841.1	hypothetical protein CDL12_19590 [Handroanthus impetiginosus]
FtPinG0303265600.01	FtPinG0303265600.01.T01	--	--
FtPinG0303265700.01	FtPinG0303265700.01.T01	PON84111.1	Agenet domain containing protein [Trema orientale]
FtPinG0303266000.01	FtPinG0303266000.01.T01	XP_021727348.1	nijmegen breakage syndrome 1 protein-like isoform X1 [Chenopodium quinoa]
FtPinG0303266400.01	FtPinG0303266400.01.T01	--	--
FtPinG0303266500.01	FtPinG0303266500.01.T01	GAV72919.1	SUI1 domain-containing protein, partial [Cephalotus follicularis]
FtPinG0303266700.01	FtPinG0303266700.01.T01	XP_021823496.1	uncharacterized protein LOC110764782 [Prunus avium]
FtPinG0303267000.01	FtPinG0303267000.01.T01	XP_020965432.1	SAC3 family protein C [Arachis ipaensis]
FtPinG0303267000.01	FtPinG0303267000.01.T02	XP_010694650.1	PREDICTED: SAC3 family protein C [Beta vulgaris subsp. vulgaris]
FtPinG0303267100.01	FtPinG0303267100.01.T01	XP_002533224.1	WD repeat-containing protein 75 [Ricinus communis]

Supplementary Table 11 (Continued):

FtPinG0303267300.01	FtPinG0303267300.01.T01	XP_021595390.1	probable inositol transporter 2 [Manihot esculenta]
FtPinG0303267600.01	FtPinG0303267600.01.T01	XP_021742461.1	sugar transporter ERD6-like 5 [Chenopodium quinoa]
FtPinG0303267800.01	FtPinG0303267800.01.T01	KMS98200.1	hypothetical protein BVRB_4g094640 [Beta vulgaris subsp. vulgaris]
FtPinG0303283300.01	FtPinG0303283300.01.T01	--	--
FtPinG0303283600.01	FtPinG0303283600.01.T01	--	--
FtPinG0303283600.01	FtPinG0303283600.01.T02	--	--
FtPinG0303283600.01	FtPinG0303283600.01.T03	--	--
FtPinG0303283600.01	FtPinG0303283600.01.T04	XP_021720028.1	protein MAIN-LIKE 1-like [Chenopodium quinoa]
FtPinG0303283800.01	FtPinG0303283800.01.T01	--	--
FtPinG0303283800.01	FtPinG0303283800.01.T02	--	--
FtPinG0303288000.01	FtPinG0303288000.01.T01	XP_021685928.1	uncharacterized protein LOC110668858 [Hevea brasiliensis]
FtPinG0303288200.01	FtPinG0303288200.01.T01	EEF47211.1	ADP-ribosylation factor, arf, putative [Ricinus communis]
FtPinG0303288600.01	FtPinG0303288600.01.T01	CAN81634.1	hypothetical protein VITISV_034565 [Vitis vinifera]
FtPinG0303288700.01	FtPinG0303288700.01.T01	BAT96978.1	hypothetical protein VIGAN_09031200 [Vigna angularis var. angularis]
FtPinG0303288900.01	FtPinG0303288900.01.T01	OIT02660.1	pentatricopeptide repeat-containing protein, mitochondrial [Nicotiana attenuata]
FtPinG0303289200.01	FtPinG0303289200.01.T01	XP_021734520.1	polygalacturonase At1g48100-like [Chenopodium quinoa]
FtPinG0303289300.01	FtPinG0303289300.01.T01	--	--
FtPinG0303289500.01	FtPinG0303289500.01.T01	XP_022019944.1	protein SABRE [Helianthus annuus]
FtPinG0303289800.01	FtPinG0303289800.01.T01	XP_021772482.1	shaggy-related protein kinase alpha [Chenopodium quinoa]
FtPinG0303556300.01	FtPinG0303556300.01.T01	XP_021743786.1	serine hydroxymethyltransferase 2, mitochondrial [Chenopodium quinoa]
FtPinG0303556600.01	FtPinG0303556600.01.T01	XP_007018315.2	PREDICTED: CBL-interacting serine/threonine-protein kinase 8 isoform X2 [Theobroma cacao]
FtPinG0303556700.01	FtPinG0303556700.01.T01	XP_012079527.1	glycine-rich domain-containing protein 1 [Jatropha curcas]
FtPinG0303557000.01	FtPinG0303557000.01.T01	XP_010670916.1	PREDICTED: protein RCC2 homolog [Beta vulgaris subsp. vulgaris]
FtPinG0303557400.01	FtPinG0303557400.01.T01	XP_021759835.1	transcription factor RF2a-like [Chenopodium quinoa]

Supplementary Table 11 (Continued):

FtPinG0303557500.01	FtPinG0303557500.01.T01	--	--
FtPinG0303557700.01	FtPinG0303557700.01.T01	XP_022776453.1	mediator of RNA polymerase II transcription subunit 23 isoform X1 [Durio zibethinus]
FtPinG0303557900.01	FtPinG0303557900.01.T01	XP_025681225.1	vacuolar fusion protein CCZ1 homolog B-like isoform X3 [Arachis hypogaea]
FtPinG0303558300.01	FtPinG0303558300.01.T01	--	--
FtPinG0303558800.01	FtPinG0303558800.01.T01	XP_004152657.1	PREDICTED: protein BASIC PENTACYSTEINE6 [Cucumis sativus]
FtPinG0303559200.01	FtPinG0303559200.01.T01	PRQ28427.1	putative starch synthase [Rosa chinensis]
FtPinG0303559400.01	FtPinG0303559400.01.T01	XP_011083592.1	aldehyde oxidase GLOX [Sesamum indicum]
FtPinG0303559600.01	FtPinG0303559600.01.T01	CAN79684.1	hypothetical protein VITISV_003855 [Vitis vinifera]
FtPinG0303559700.01	FtPinG0303559700.01.T01	--	--
FtPinG0303559900.01	FtPinG0303559900.01.T01	XP_019103756.1	PREDICTED: lysine-specific histone demethylase 1 homolog 3 [Beta vulgaris subsp. vulgaris]
FtPinG0303560100.01	FtPinG0303560100.01.T01	XP_021613084.1	lysine-specific histone demethylase 1 homolog 3-like [Manihot esculenta]
FtPinG0303560100.01	FtPinG0303560100.01.T02	XP_021613084.1	lysine-specific histone demethylase 1 homolog 3-like [Manihot esculenta]
FtPinG0303560300.01	FtPinG0303560300.01.T01	XP_010262087.1	PREDICTED: putative pentatricopeptide repeat-containing protein At1g17630 [Nelumbo nucifera]
FtPinG0303560500.01	FtPinG0303560500.01.T01	XP_010262087.1	PREDICTED: putative pentatricopeptide repeat-containing protein At1g17630 [Nelumbo nucifera]
FtPinG0303560800.01	FtPinG0303560800.01.T01	PNX92904.1	retrovirus-related Pol polyprotein from transposon TNT 1-94 [Trifolium pratense]
FtPinG0303561000.01	FtPinG0303561000.01.T01	--	--
FtPinG0303561200.01	FtPinG0303561200.01.T01	--	--
FtPinG0303561300.01	FtPinG0303561300.01.T01	XP_022853455.1	V-type proton ATPase 16 kDa proteolipid subunit-like [Olea europaea var. sylvestris]
FtPinG0303561500.01	FtPinG0303561500.01.T01	XP_006473603.1	1-acylglycerol-3-phosphate O-acyltransferase [Citrus sinensis]
FtPinG0303561800.01	FtPinG0303561800.01.T01	XP_021759853.1	probable LRR receptor-like serine/threonine-protein kinase At4g36180 [Chenopodium quinoa]
FtPinG0303562100.01	FtPinG0303562100.01.T01	PKI50358.1	hypothetical protein CRG98_029238 [Punica granatum]

Supplementary Table 11 (Continued):

FtPinG0303562400.01	FtPinG0303562400.01.T01	XP_021743831.1	LOW QUALITY PROTEIN: kinesin-like protein KIN-7J [Chenopodium quinoa]
FtPinG0380001007.01	FtPinG0380001007.01.T01	XP_020247655.1	uncharacterized protein LOC109825253 [Asparagus officinalis]
FtPinG0380001008.01	FtPinG0380001008.01.T01	XP_021853287.1	uncharacterized protein LOC110792775 [Spinacia oleracea]
FtPinG0380001009.01	FtPinG0380001009.01.T01	XP_021719499.1	uncharacterized protein LOC110687192 [Chenopodium quinoa]
FtPinG0380001010.01	FtPinG0380001010.01.T01	XP_021835333.1	uncharacterized protein LOC110775037 [Spinacia oleracea]
FtPinG0380001011.01	FtPinG0380001011.01.T01	XP_015078360.1	PREDICTED: uncharacterized protein LOC107022192 [Solanum pennellii]
FtPinG0380001012.01	FtPinG0380001012.01.T01	XP_015078360.1	PREDICTED: uncharacterized protein LOC107022192 [Solanum pennellii]
FtPinG0380001013.01	FtPinG0380001013.01.T01	XP_026656323.1	uncharacterized protein LOC113461101 [Phoenix dactylifera]
FtPinG0380001034.01	FtPinG0380001034.01.T01	XP_010689251.1	PREDICTED: uncharacterized protein LOC104902986 [Beta vulgaris subsp. vulgaris]
FtPinG0380001035.01	FtPinG0380001035.01.T01	XP_010646217.1	PREDICTED: uncharacterized protein LOC104878131 [Vitis vinifera]
FtPinG0380001036.01	FtPinG0380001036.01.T01	XP_022878006.1	uncharacterized protein LOC111395991 [Olea europaea var. sylvestris]
FtPinG0380001039.01	FtPinG0380001039.01.T01	XP_017622027.1	PREDICTED: uncharacterized protein LOC108466183 [Gossypium arboreum]
FtPinG0380001040.01	FtPinG0380001040.01.T01	XP_021722367.1	uncharacterized protein LOC110689843 [Chenopodium quinoa]
FtPinG0380001041.01	FtPinG0380001041.01.T01	OMO74467.1	reverse transcriptase [Corchorus capsularis]
FtPinG0380001042.01	FtPinG0380001042.01.T01	XP_020247655.1	uncharacterized protein LOC109825253 [Asparagus officinalis]
FtPinG0380001181.01	FtPinG0380001181.01.T01	ABA96825.1	retrotransposon protein, putative, Ty1-copia subclass [Oryza sativa Japonica Group]
FtPinG0404200500.01	FtPinG0404200500.01.T01	XP_002274420.2	PREDICTED: UDP-glycosyltransferase 87A1 [Vitis vinifera]
FtPinG0404201100.01	FtPinG0404201100.01.T01	XP_003518323.1	UDP-glycosyltransferase 87A1 [Glycine max]
FtPinG0404201300.01	FtPinG0404201300.01.T01	XP_010650858.1	PREDICTED: UDP-glycosyltransferase 87A1 [Vitis vinifera]
FtPinG0505984500.01	FtPinG0505984500.01.T01	KRG97172.1	hypothetical protein GLYMA_19G255300 [Glycine max]
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]
FtPinG0505985200.01	FtPinG0505985200.01.T01	--	--
FtPinG0505985300.01	FtPinG0505985300.01.T01	EEF44770.1	lactoylglutathione lyase, putative [Ricinus communis]

Supplementary Table 11 (Continued):

FtPinG0505985600.01	FtPinG0505985600.01.T01	XP_010691173.1	PREDICTED: probable polygalacturonase At1g80170 isoform X1 [Beta vulgaris subsp. vulgaris]
FtPinG0505986000.01	FtPinG0505986000.01.T01	XP_026430449.1	ABC transporter I family member 20-like [Papaver somniferum]
FtPinG0505986100.01	FtPinG0505986100.01.T01	XP_006356202.1	PREDICTED: transport protein particle 20 kDa subunit isoform X1 [Solanum tuberosum]
FtPinG0505986400.01	FtPinG0505986400.01.T01	KMT00715.1	hypothetical protein BVRB_9g220010 [Beta vulgaris subsp. vulgaris]
FtPinG0505986600.01	FtPinG0505986600.01.T01	XP_021659986.1	uncharacterized protein LOC110649632 isoform X1 [Hevea brasiliensis]
FtPinG0505986700.01	FtPinG0505986700.01.T01	XP_021848213.1	probable histone H2A variant 3 [Spinacia oleracea]
FtPinG0505986900.01	FtPinG0505986900.01.T01	XP_002285258.1	PREDICTED: caffeoylshikimate esterase [Vitis vinifera]
FtPinG0505987200.01	FtPinG0505987200.01.T01	KNA21047.1	hypothetical protein SOVF_046360 [Spinacia oleracea]
FtPinG0505987600.01	FtPinG0505987600.01.T01	--	--
FtPinG0505988000.01	FtPinG0505988000.01.T01	XP_021674365.1	protein MLN51 homolog isoform X1 [Hevea brasiliensis]
FtPinG0505988000.01	FtPinG0505988000.01.T02	XP_021674365.1	protein MLN51 homolog isoform X1 [Hevea brasiliensis]
FtPinG0505988100.01	FtPinG0505988100.01.T01	PSS14124.1	Valine--tRNA ligase, partial [Actinidia chinensis var. chinensis]
FtPinG0505988600.01	FtPinG0505988600.01.T01	XP_012436134.1	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC105762782, partial [Gossypium raimondii]
FtPinG0505988800.01	FtPinG0505988800.01.T01	PSS17906.1	Nuclear pore complex protein like [Actinidia chinensis var. chinensis]
FtPinG0505989000.01	FtPinG0505989000.01.T01	XP_010691280.1	PREDICTED: coatomer subunit beta'-2 isoform X3 [Beta vulgaris subsp. vulgaris]
FtPinG0505989200.01	FtPinG0505989200.01.T01	XP_021763544.1	ubiquitin receptor RAD23d-like [Chenopodium quinoa]
FtPinG0580001914.01	FtPinG0580001914.01.T01	KYP31853.1	Retrovirus-related Pol polyprotein from transposon TNT 1-94 [Cajanus cajan]
FtPinG0580001915.01	FtPinG0580001915.01.T01	XP_021773503.1	uncharacterized protein LOC110737449 [Chenopodium quinoa]
FtPinG0580001916.01	FtPinG0580001916.01.T01	XP_015078360.1	PREDICTED: uncharacterized protein LOC107022192 [Solanum pennellii]