Supplementary Table 11: The list of selected genes.

ID	Name	Chr	Position (bp)	Weighted_F_{ST}	$\log_2(\pi_W/\pi_C)$	NR id	NR annotation	InterPro IDs	InterPro Description
FtPinG0101098400.01	ZPF5	Ft1	58520001-58720000	0.608080	8.308004503	XP_024195280.1	zinc finger protein 5 [Rosa chinensis]	IPR013087;IPR036236	Zinc finger C2H2-type | Zinc finger C2H2 superfamily
FtPinG0201347300.01	LRR	Ft2	5520001-5720000	0.532166	6.681980099	XP_010677519.1	PREDICTED: LRR receptor-like serine/threonine-protein kinase FEI 2 isoform X1 [Beta vulgaris subsp. vulgaris]	IPR000719;IPR001611;IPR003591;IPR008271;IPR011009;IPR013210;IPR017441;IPR031071;IPR032675	Protein kinase domain | Leucine-rich repeat | Leucine-rich repeat, typical subtype | Serine/threonine-protein kinase, active site | Protein kinase-like domain superfamily | Leucine-rich repeat-containing N-terminal, plant-type | Protein kinase, ATP binding site | LRR receptor-like serine/threonine-protein kinase FEI1/2 | Leucine-rich repeat domain superfamily
FtPinG0201348000.01	ARP5	Ft2	5560001-5760000	0.537238	7.090701249	XP_024021552.1	actin-related protein 5 [Morus notabilis]	IPR004000;IPR027664	Actin family | Actin-related protein 5
FtPinG0201372300.01	CCCH	Ft2	6620001-6820000	0.579476	6.718341271	XP_021723422.1	zinc finger CCCH domain-containing protein 5-like isoform X1 [Chenopodium quinoa]	IPR000571;IPR009145	Zinc finger, CCCH-type | U2 auxiliary factor small subunit
FtPinG0201376200.01	FLAs	Ft2	6620001-6820000	0.579476	6.718341271	GAV78074.1	Fasciclin domain-containing protein, partial [Cephalotus follicularis]	IPR000782;IPR033254;IPR036378	FAS1 domain | Fasciclin-like arabinogalactan protein | FAS1 domain superfamily
FtPinG0202115400.01	MYB	Ft2	47360001-47560000	0.543661	6.903447869	KMS96851.1	hypothetical protein BVRB_8g199270 [Beta vulgaris subsp. vulgaris]	IPR001005;IPR005818;IPR009057;IPR017930;IPR036390	SANT/Myb domain | Linker histone H1/H5, domain H15 | Homeobox-like domain superfamily | Myb domain | Winged helix DNA-binding domain superfamily
FtPinG0202115600.01	MYB	Ft2	47360001-47560000	0.543661	6.903447869	PON84439.1	Telomeric repeat-binding factor [Trema orientale]	IPR001005;IPR005818;IPR009057;IPR017930;IPR036388;IPR036390	SANT/Myb domain | Linker histone H1/H5, domain H15 | Homeobox-like domain superfamily | Myb domain | Winged helix-like DNA-binding domain superfamily | Winged helix DNA-binding domain superfamily
FtPinG0202117300.01	MYB	Ft2	47380001-47580000	0.545511	7.416619026	PHT43010.1	hypothetical protein CQW23_17035 [Capsicum baccatum]	IPR001005;IPR005818;IPR009057;IPR017930;IPR036388;IPR036390	SANT/Myb domain | Linker histone H1/H5, domain H15 | Homeobox-like domain superfamily | Myb domain | Winged helix-like DNA-binding domain superfamily | Winged helix DNA-binding domain superfamily
FtPinG0202149300.01	MYB	Ft2	48520001-48720000	0.565374	8.151689847	XP_021746809.1	single myb histone 6-like isoform X3 [Chenopodium quinoa]	IPR001005;IPR005818;IPR009057;IPR017930;IPR036388;IPR036390	SANT/Myb domain | Linker histone H1/H5, domain H15 | Homeobox-like domain superfamily | Myb domain | Winged helix-like DNA-binding domain superfamily | Winged helix DNA-binding domain superfamily
FtPinG0302584500.01	FLAs	Ft3	2260001-2460000	0.576774	7.320274445	XP_002276175.1	PREDICTED: fasciclin-like arabinogalactan protein 21 [Vitis vinifera]	IPR000782;IPR036378	FAS1 domain | FAS1 domain superfamily

Supplementary Table 13 (Continued):

FtPinG0302747300.01	ABCC2	Ft3	7900001-8100000	0.583337	8.371872552	XP_021743351.1	ABC transporter C family member 2-like [Chenopodium quinoa]	IPR003439;IPR003593;IPR011527;IPR017871;IPR027417;IPR036640	ABC transporter-like | AAA+ ATPase domain | ABC transporter type 1, transmembrane domain | ABC transporter, conserved site | P-loop containing nucleoside triphosphate hydrolase | ABC transporter type 1, transmembrane domain superfamily
FtPinG0302751700.01	FLAs	Ft3	7900001-8100000	0.583337	8.371872552	XP_012067578.2	fasciclin-like arabinogalactan protein 14 [Jatropha curcas]	IPR033254	Fasciclin-like arabinogalactan protein
FtPinG0302807600.01	MYC	Ft3	9700001-9900000	0.514097	6.639781692	XP_011039030.1	PREDICTED: transcription factor MYC2 isoform X2 [Populus euphratica]	IPR011598;IPR036638	Myc-type, basic helix-loop-helix (bHLH) domain | Helix-loop-helix DNA-binding domain superfamily
FtPinG0302808000.01	MYC	Ft3	9700001-9900000	0.514097	6.639781692	PSS03906.1	Transcription factor like [Actinidia chinensis var. chinensis]	IPR011598;IPR036638	Myc-type, basic helix-loop-helix (bHLH) domain | Helix-loop-helix DNA-binding domain superfamily
FtPinG0302995500.01	APETALA3	Ft3	16480001-16680000	0.535297	6.931321935	AFO83616.1	APETALA3-like protein [Fagopyrum esculentum]	IPR002100;IPR036879	Transcription factor, MADS-box | Transcription factor, MADS-box superfamily
FtPinG0302995800.01	GRAS	Ft3	16480001-16680000	0.535297	6.931321935	XP_021765055.1	LOW QUALITY PROTEIN: scarecrow-like protein 8 [Chenopodium quinoa]	IPR005202;IPR030013	Transcription factor GRAS | Scarecrow-like protein 8
FtPinG0403954700.01	NAM	Ft4	10940001-11140000	0.541615	7.609860381	KMT09915.1	hypothetical protein BVRB_5g121330 [Beta vulgaris subsp. vulgaris]	IPR003441;IPR036093	NAC domain | NAC domain superfamily
FtPinG0403956300.01	AP2/ERF	Ft4	10960001-11160000	0.530647	7.327373713	KMT10356.1	hypothetical protein BVRB_5g121050 [Beta vulgaris subsp. vulgaris]	IPR001471;IPR016177;IPR017392;IPR036955	AP2/ERF domain | DNA-binding domain superfamily | AP2/ERF transcription factor ERF/PTI6 | AP2/ERF domain superfamily
FtPinG0404479200.01	LOB	Ft4	40860001-41060000	0.572700	6.811754523	CAN76952.1	hypothetical protein VITISV_040518 [Vitis vinifera]	IPR004883	Lateral organ boundaries, LOB
FtPinG0404513600.01	AP2/ERF	Ft4	42300001-42500000	0.524963	6.690727164	PKI72042.1	hypothetical protein CRG98_007588 [Punica granatum]	IPR001471;IPR016177;IPR036955	AP2/ERF domain | DNA-binding domain superfamily | AP2/ERF domain superfamily
FtPinG0404518400.01	Rab7	Ft4	42480001-42680000	0.517268	6.636335376	XP_004290467.1	PREDICTED: ras-related protein Rab7 [Fragaria vesca subsp. vesca]	IPR001806;IPR005225;IPR027417	Small GTPase | Small GTP-binding protein domain | P-loop containing nucleoside triphosphate hydrolase

Supplementary Table 13 (Continued):

FtPinG0505478700.01	CCCH	Ft5	29100001-29300000	0.517963	6.771213693	XP_010271420.1	PREDICTED: zinc finger CCCH domain-containing protein 6 isoform X1 [Nelumbo nucifera]	IPR000571	Zinc finger, CCCH-type
FtPinG0505481600.01	CCHC	Ft5	29480001-29680000	0.518719	7.44183458	PWA89720.1	zinc finger, CCHC-type [Artemisia annua]	IPR001878;IPR036875	Zinc finger, CCHC-type | Zinc finger, CCHC-type superfamily
FtPinG0505497800.01	BTB/POZ	Ft5	31000001-31200000	0.548461	6.752898621	XP_002270675.1	PREDICTED: BTB/POZ domain-containing protein At2g30600 [Vitis vinifera]	IPR000210;IPR011333;IPR022041	BTB/POZ domain | SKP1/BTB/POZ domain superfamily | Farnesoic acid O-methyl transferase
FtPinG0505979100.01	WD40	Ft5	52140001-52340000	0.546553	7.427665132	XP_021747294.1	U3 snoRNP-associated protein-like EMB2271 isoform X1 [Chenopodium quinoa]	IPR001680;IPR015943;IPR017986;IPR019775;IPR020472;IPR036322;IPR039241	WD40 repeat | WD40/YVTN repeat-like-containing domain superfamily | WD40-repeat-containing domain | WD40 repeat, conserved site | G-protein beta WD-40 repeat | WD40-repeat-containing domain superfamily | Ribosomal RNA-processing protein Rrp9-like
FtPinG0506019300.01	LOB	Ft5	53380001-53580000	0.518554	7.941287965	OAY23018.1	hypothetical protein MANES_18G045200 [Manihot esculenta]	IPR004883	Lateral organ boundaries, LOB
FtPinG0707223800.01	RAV1	Ft7	3960001-4160000	0.572757	7.441129123	XP_021754679.1	AP2/ERF and B3 domain-containing transcription factor RAV1-like [Chenopodium quinoa]	IPR001471;IPR003340;IPR015300;IPR016177;IPR036955	AP2/ERF domain | B3 DNA binding domain | DNA-binding pseudobarrel domain superfamily | DNA-binding domain superfamily | AP2/ERF domain superfamily
FtPinG0707839100.01	UGT6	Ft7	41080001-41280000	0.585302	7.357676688	GAV63592.1	UDPGT domain-containing protein [Cephalotus follicularis]	IPR002213;IPR035595	UDP-glucuronosyl/UDP-glucosyltransferase | UDP-glycosyltransferase family, conserved site
FtPinG0707839700.01	UGT2	Ft7	41080001-41280000	0.585302	7.357676688	XP_017981739.1	PREDICTED: 7-deoxyloganetin glucosyltransferase [Theobroma cacao]	IPR002213	UDP-glucuronosyl/UDP-glucosyltransferase
FtPinG0808982400.01	NAM	Ft8	43660001-43860000	0.627668	6.891971504	XP_021715682.1	NAC domain-containing protein 89-like [Chenopodium quinoa]	IPR003441;IPR036093	NAC domain | NAC domain superfamily
FtPinG0809023700.01	GRF1	Ft8	45040001-45240000	0.553649	6.766725255	XP_002283504.2	PREDICTED: growth-regulating factor 1 [Vitis vinifera]	IPR014977;IPR014978;IPR031137	WRC domain | Glutamine-Leucine-Glutamine, QLQ | Growth-regulating factor
FtPinG0809060500.01	DOG1	Ft8	46180001-46380000	0.527643	6.990619934	XP_023907344.1	protein DOG1-like 3 [Quercus suber]	IPR025422	Transcription factor TGA like domain