

Table S1. List of 198 putative genes with annotation function within the two most significant flanking regions of chromosomes 3 and 13 of soybean mapping populations.

Traits	Chr.	Flanking region	Gene name	Description (function)
AD RV LAD	03	Gm03:829023.. 3365988	<i>Glyma.03G010700</i>	RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBS
			<i>Glyma.03G011200</i>	AT HOOK MOTIF DNA BINDING FAMILY PROTEIN
			<i>Glyma.03G017900</i>	UDPGALACTOSE/UDP GLUCOSE TRANSPORTER 2
			<i>Glyma.03G020300</i>	SERINE/THREONINE PROTEIN KINASE AURORA3
			<i>Glyma.03G013700</i>	DOWNSTREAM TARGET OF AGL15 2
			<i>Glyma.03G011000</i>	BR SIGNALING KINASE 3-RELATED
			<i>Glyma.03G008600</i>	SIGNAL PEPTIDE PEPTIDASEL IKE 4
			<i>Glyma.03G010200</i>	PLANT PHOSPHORIBOSYLTRANSFERASE C-TERMINAL (PRT_C)
			<i>Glyma.03G014900</i>	ATP-DEPENDENT RNA HELICASE DDX47-RELATED
			<i>Glyma.03G009900</i>	FBOX/KELCHREPEAT PROTEIN SKIP4-RELATED
			<i>Glyma.03G013300</i>	MYB-LIKE DNA BINDING PROTEIN MYB
			<i>Glyma.03G021300</i>	EPIDIDYMAL MEMBRANE PROTEIN E9-RELATED
			<i>Glyma.03G009800</i>	ACYLCOA THIOESTERASE
			<i>Glyma.03G016000</i>	BON1-ASSOCIATED PROTEIN 1-RELATED
			<i>Glyma.03G021700</i>	SERINE/THREONINE PROTEIN KINASE AURORA3
			<i>Glyma.03G025900</i>	GENOMIC DNA, CHROMOSOME 3, P1 CLONE: MDJ14-RELATED
			<i>Glyma.03G019400</i>	AGAMOUS-LIKE MADSBOX PROTEIN AGL13-RELATED
			<i>Glyma.03G029800</i>	AXIAL REGULATOR YABBY 1-RELATED
			<i>Glyma.03G022900</i>	PROTEIN BOI2
			<i>Glyma.03G027000</i>	PLANT PROTEIN OF UNKNOWN FUNCTION (DUF247)
			<i>Glyma.03G025400</i>	ZINC FINGER PROTEIN 183
			<i>Glyma.03G029100</i>	PECTINESTERASE/PECTINESTERASE INHIBITOR 17-RELATED
			<i>Glyma.03G011900</i>	HELITRON HELICASE-LIKE DOMAIN AT N-TERMINUS (HELITRON_LIKE_N)
			<i>Glyma.03G025500</i>	PROTEIN S-ACYL TRANSFERASE 13-RELATED
			<i>Glyma.03G018300</i>	POLYNUCLEOTIDYL TRANSFERASE, RIBONUCLEASE H-LIKE SUPERFAMILY PROTEIN
			<i>Glyma.03G017200</i>	ALTERNATIVE SPLICING FACTOR SRP55/B52/SRP75 (RRM SUPERFAMILY)
			<i>Glyma.03G012000</i>	FAS-ASSOCIATED PROTEIN
			<i>Glyma.03G029200</i>	PECTINESTERASE/PECTINESTERASE INHIBITOR 17-RELATED
			<i>Glyma.03G022800</i>	CALCIUM BINDING PROTEIN CML24-RELATED
			<i>Glyma.03G027500</i>	TRANSKETOLASE/GLYCOALDEHYDE TRANSFERASE
			<i>Glyma.03G024300</i>	CHITINASE/POLYBETAGLUCOSAMINIDASE

		<i>Glyma.03G028900</i>	PECTINESTERASE/PECTINESTERASE INHIBITOR 36-RELATED
		<i>Glyma.03G028000</i>	ARGINASE/CANAVANASE
		<i>Glyma.03G024000</i>	ATP-DEPENDENT RNA HELICASE DHX37-RELATED
		<i>Glyma.03G022300</i>	4 HYDROXYTETRAHYDRODIPICOLINATE SYNTHASE/DIHYDRODIPICOLINATE SYNTHETASE
		<i>Glyma.03G029000</i>	PECTINESTERASE/PECTINESTERASE INHIBITOR 17-RELATED
		<i>Glyma.03G020800</i>	C2 CALCIUM/LIPID BINDING ENDONUCLEASE/-EXONUCLEASE/PHOSPHATASE-RELATED
		<i>Glyma.03G013500</i>	ROP GUANINE NUCLEOTIDE EXCHANGE FACTOR 2-RELATED
		<i>Glyma.03G019600</i>	TRANSCRIPTIONAL COREPRESSOR COMPONENT
		<i>Glyma.03G027400</i>	3PHOSPHOSHIKIMATE 1 CARBOXYVINYLTRANSFERASE/EPSP SYNTHASE
		<i>Glyma.03G028700</i>	ACETYL COA-BENZYL ALCOHOL ACETYL TRANSFERASE-LIKE PROTEIN-RELATED
		<i>Glyma.03G016600</i>	HOMEODOMAIN (HOMEODOMAIN)/START DOMAIN (START)
		<i>Glyma.03G022700</i>	ATHOOK MOTIF NUCLEAR LOCALIZED PROTEIN 18-RELATED
		<i>Glyma.03G012200</i>	PROTEIN SAY1
		<i>Glyma.03G026600</i>	PROTEIN OF UNKNOWN FUNCTION
		<i>Glyma.03G030100</i>	CYTOCHROME P450 71B21-RELATED
		<i>Glyma.03G027200</i>	PROTEIN KINASE DOMAIN (PKINASE)/LEUCINE RICH REPEAT (LRR_8)
		<i>Glyma.03G017100</i>	ARMADILLO/BETACATENIN REPEAT CONTAINING PROTEIN-RELATED
		<i>Glyma.03G016200</i>	BON1-ASSOCIATED PROTEIN 1-RELATED
AD		<i>Glyma.03G012800</i>	KDEL LYSASPGULEU CONTAINING-RELATED
RV		<i>Glyma.03G027800</i>	PPR REPEAT (PPR)/PPR REPEAT FAMILY (PPR_2)
LAD		<i>Glyma.03G018500</i>	ARSENITE-TRANSPORTING ATPASE/ARSENITE-TRANSLOCATING ATPASE
		<i>Glyma.03G024500</i>	CHITINASE/POLYBETAGLUCOSAMINIDASE
		<i>Glyma.03G024700</i>	SULFATE TRANSPORTER 3.3-RELATED
		<i>Glyma.03G028400</i>	PLANT PROTEIN OF UNKNOWN FUNCTION (DUF641) (DUF641)
		<i>Glyma.03G026400</i>	EXOCYST COMPLEX COMPONENT SEC6-RELATED
		<i>Glyma.03G013600</i>	ADENOSINE-DEAMINASE (EDITASE) DOMAIN (A_DEAMIN)
		<i>Glyma.03G021200</i>	GERANIOL 8 HYDROXYLASE/CYTOCHROME P450, FAMILY 76, SUBFAMILY C, POLYPEPTIDE 4
		<i>Glyma.03G029600</i>	AUXIN REGULATED PROTEIN-RELATED
		<i>Glyma.03G015400</i>	EXTENDED SYNAPTOTAGMIN-RELATED
		<i>Glyma.03G023700</i>	PROTEIN KINASE DOMAIN (PKINASE)/LEUCINE RICH REPEAT (LRR_1)/LEUCINE RICH REPEAT (LRR_8)

		<i>Glyma.03G014500</i>	DEHYDROGENASES WITH DIFFERENT SPECIFICITIES (RELATED TO SHORT CHAIN ALCOHOL DEHYDROGENASES)
		<i>Glyma.03G019300</i>	MADSBX PROTEIN SOC1
		<i>Glyma.03G009400</i>	PREDICTED CA ²⁺ -DEPENDENT PHOSPHOLIPID BINDING PROTEIN
		<i>Glyma.03G014800</i>	AUXIN RESPONSIVE PROTEIN (AUXIN_INDUCIBLE)
		<i>Glyma.03G013100</i>	MITOCHONDRIAL RIBOSOMAL PROTEIN S33
		<i>Glyma.03G012900</i>	KDEL LYSASPGULEU CONTAINING-RELATED
		<i>Glyma.03G026100</i>	EXOCYST COMPLEX COMPONENT 3
		<i>Glyma.03G026700</i>	PPR REPEAT (PPR)//PPR REPEAT FAMILY (PPR_2)
		<i>Glyma.03G019500</i>	PROTEIN Y45F10A.7, ISOFORM A
		<i>Glyma.03G013400</i>	REMORIN, NTERMINAL REGION (REMORIN_N)
		<i>Glyma.03G020400</i>	CYTOCHROME P450, FAMILY 704, SUBFAMILY A, POLYPEPTIDE 1
		<i>Glyma.03G028800</i>	METHIONINE AMINOPEPTIDASE 1
		<i>Glyma.03G025800</i>	GENOMIC DNA, CHROMOSOME 3, P1 CLONE: MDJ14-RELATED
		<i>Glyma.03G009200</i>	MEDIATOR OF RNA POLYMERASE II TRANSCRIPTION SUBUNIT 12
		<i>Glyma.03G015700</i>	FAST LEU-RICH DOMAIN CONTAINING
		<i>Glyma.03G023500</i>	AT HOOK MOTIF DNA BINDING FAMILY PROTEIN
		<i>Glyma.03G020100</i>	EXPRESSED PROTEIN
		<i>Glyma.03G027900</i>	PREDICTED METALLOPROTEASE WITH CHAPERONE ACTIVITY (RNASE H/HSP70 FOLD)
		<i>Glyma.03G021100</i>	RIBOSOMAL RNA PROCESSING PROTEIN 36 HOMOLOG
		<i>Glyma.03G018200</i>	POLYNUCLEOTIDYL TRANSFERASE, RIBONUCLEASE H-LIKE SUPERFAMILY PROTEIN
		<i>Glyma.03G016400</i>	BON1-ASSOCIATED PROTEIN 1-RELATED
		<i>Glyma.03G016700</i>	METHYLTRANSFERASE PMT13-RELATED
		<i>Glyma.03G019100</i>	SUBTILASE FAMILY PROTEIN-RELATED
		<i>Glyma.03G022200</i>	LITTLE ZIPPER 1 PROTEIN-RELATED
		<i>Glyma.03G029900</i>	CYTOCHROME P450 71B21-RELATED
		<i>Glyma.03G015100</i>	DTDP4DEHYDRORHAMNOSE REDUCTASE
		<i>Glyma.03G025300</i>	ABSCISIC ACID RECEPTOR PYL10-RELATED
		<i>Glyma.03G009500</i>	TRANSCRIPTION FACTOR MYC1
		<i>Glyma.03G016500</i>	SHAGGY-RELATED PROTEIN KINASE BETA-RELATED
		<i>Glyma.03G027600</i>	DNA REPAIR PROTEIN RAD51 HOMOLOG 3
		<i>Glyma.03G019800</i>	GIBBERELLIN 20 OXIDASE 1-RELATED
		<i>Glyma.03G029300</i>	ENTH/VHS/GAT FAMILY PROTEIN
		<i>Glyma.03G015600</i>	CELL DIVISION PROTEIN FTSY HOMOLOG, CHLOROPLASTIC
		<i>Glyma.03G017500</i>	RING FINGER DOMAIN CONTAINING
		<i>Glyma.03G023100</i>	LOB DOMAIN CONTAINING PROTEIN 19-RELATED
		<i>Glyma.03G021900</i>	GROWTH REGULATING FACTOR 9

			<i>Glyma.03G021800</i>	NADHUBIQUINONE OXIDOREDUCTASE
			<i>Glyma.03G017000</i>	FBOX PROTEIN PP2A13
			<i>Glyma.03G020500</i>	MEMBER OF "GDXG" FAMILY OF LIPOLYTIC ENZYMES
AD	13	Gm13:2752708	<i>Glyma.13G175000</i>	DUF679 DOMAIN MEMBRANE PROTEIN 7
RV		3..43496306	<i>Glyma.13G310900</i>	RING ZINC FINGER PROTEIN
LAD			<i>Glyma.13G172800</i>	RAS-RELATED PROTEIN RABA1G
			<i>Glyma.13G171200</i>	RIBOSOMAL RNA PROCESSING PROTEIN 7-RELATED
			<i>Glyma.13G165200</i>	40S RIBOSOMAL PROTEIN S11 FAMILY MEMBER
			<i>Glyma.13G177300</i>	MITOCHONDRIAL ARGININE TRANSPORTER BAC1
			<i>Glyma.13G159900</i>	SMALL NUCLEAR RNA ACTIVATING COMPLEX, POLYPEPTIDE 1
			<i>Glyma.13G226900</i>	PROTEIN OF UNKNOWN FUNCTION (DUF1685) (DUF1685)
			<i>Glyma.13G172200</i>	APOPTOSIS INHIBITOR 5
			<i>Glyma.13G175600</i>	DROUGHT INDUCED 19 PROTEIN (DI19), ZINC BINDING
			<i>Glyma.13G162300</i>	UBIQUITIN SPECIFIC PROTEASE
			<i>Glyma.13G178200</i>	NON-SENSE-MEDIATED mRNA DECAY PROTEIN
			<i>Glyma.13G173500</i>	2HYDROXYISOFLAVANONE SYNTHASE/ISOFLAVONOID SYNTHASE
			<i>Glyma.13G172700</i>	HOMEODOMAIN (HOMEODOMAIN)
			<i>Glyma.13G173600</i>	O-METHYL TRANSFERASE
			<i>Glyma.13G170700</i>	POTASSIUM TRANSPORTER 8
			<i>Glyma.13G161400</i>	XYLOGALACTURONAN BETA-1,3-XYLOSYLTRANSFERASE
			<i>Glyma.13G167600</i>	SOLUTE CARRIER FAMILY 35
			<i>Glyma.13G167500</i>	GLYCOSYLTRANSFERASE 14 FAMILY MEMBER
			<i>Glyma.13G162500</i>	ARP2/3 COMPLEX 21 KD SUBUNIT
			<i>Glyma.13G176400</i>	POLYUBIQUITIN 3
			<i>Glyma.13G168600</i>	PROTEIN FARNESYLTRANSFERASE SUBUNIT BETA
			<i>Glyma.13G160400</i>	HYDROPHOBIC SEED PROTEIN (HYDROPHOB_SEED)
			<i>Glyma.13G166000</i>	HISTON ELYSINE N-METHYL TRANSFERASE, H3 LYSINE9 SP
			<i>Glyma.13G173100</i>	HISTONE H3
			<i>Glyma.13G167100</i>	PEROXIDASE 25
			<i>Glyma.13G167900</i>	RIBOSOME BIOGENESIS REGULATORY PROTEIN
			<i>Glyma.13G196900</i>	DNA DIRECTED RNA POLYMERASE V SUBUNIT 1
			<i>Glyma.13G168800</i>	PLASTOCYANIN-LIKE DOMAIN (CU_BIND_LIKE)
			<i>Glyma.13G175100</i>	SOLUTE CARRIER FAMILY 35
			<i>Glyma.13G224000</i>	MOLECULAR CHAPERONES GRP78/BIP/KAR2, HSP70 SUPERFAMILY
			<i>Glyma.13G165700</i>	EQUILIBRATIVE NUCLEOTIDE TRANSPORTER 8
			<i>Glyma.13G174800</i>	PROTEIN KINASE FAMILY PROTEIN

			<i>Glyma.13G166200</i>	FBOX-LIKE (FBOX-LIKE)//LEUCINE-RICH REPEAT
			<i>Glyma.13G265400</i>	RING BOX
			<i>Glyma.13G244500</i>	PROTEIN OF UNKNOWN FUNCTION (DUF707) (DUF707)
			<i>Glyma.13G174900</i>	RECEPTORL IKE PROTEIN KINASE HSL1
			<i>Glyma.13G268600</i>	PLUG DOMAIN OF SEC61P (PLUG_TRANSLOCON)
			<i>Glyma.13G159800</i>	BED FINGER-RELATED
			<i>Glyma.13G169000</i>	CALCIUM HOMEOSTASIS REGULATOR-RELATED
			<i>Glyma.13G174300</i>	XBOX TRANSCRIPTION FACTOR-RELATED
			<i>Glyma.13G168700</i>	2HYDROXYACID DEHYDROGENASE-RELATED
			<i>Glyma.13G190400</i>	LEUCINE-RICH REPEAT CONTAINING PROTEIN
			<i>Glyma.13G176700</i>	PROTEASOME SUBUNIT ALPHA TYPE1
			<i>Glyma.13G172000</i>	IQDOMAIN 9 PROTEIN
			<i>Glyma.13G172500</i>	ZINC FINGER FYVE DOMAIN CONTAINING PROT
			<i>Glyma.13G169700</i>	BIDIRECTIONAL SUGAR TRANSPORTER SWEET4-RELATED
			<i>Glyma.13G165500</i>	RING FINGER DOMAIN CONTAINING
			<i>Glyma.13G336600</i>	EXPANSINA6
			<i>Glyma.13G337300</i>	SCARECROW-LIKE PROTEIN 14-RELATED
			<i>Glyma.13G330900</i>	CHITINASE
			<i>Glyma.13G332000</i>	COPPER TRANSPORT PROTEIN ATOX1-RELATED
			<i>Glyma.13G328800</i>	NODULIN (NODULIN)
			<i>Glyma.13G337100</i>	PROTEIN TBF1
			<i>Glyma.13G338100</i>	MULTICOPPER OXIDASE
			<i>Glyma.13G329500</i>	PROTEIN NRT1/PTR FAMILY 2.1-RELATED
			<i>Glyma.13G334200</i>	RNA AND EXPORT FACTOR BINDING PROTEIN
			<i>Glyma.13G329000</i>	DOF ZINC FINGER PROTEIN DOF1.1-RELATED
			<i>Glyma.13G338300</i>	ZINC/IRON TRANSPORTER
			<i>Glyma.13G343600</i>	PROTEIN FARNESYLTRANSFERASE/FTASE//PROTEINGERANYL GERANYL-TRANSFERASE TYPE I
			<i>Glyma.13G335600</i>	ACTIN
			<i>Glyma.13G338000</i>	DVL13-RELATED
			<i>Glyma.13G335900</i>	PHOSPHATIDYLINOSITOL NACETYL- GLUCOSAMINYL TRANSFERASE SUBUNIT P DOWN SYNDROME CRITICAL REGION PROTEIN 5-RELATED
			<i>Glyma.13G337500</i>	SCARECROW-LIKE PROTEIN 11-RELATED
			<i>Glyma.13G329700</i>	ETHYLENE RESPONSIVE TRANSCRIPTION FACTOR RAP27
			<i>Glyma.13G330400</i>	FLIPPASE KINASE 1-RELATED
			<i>Glyma.13G341500</i>	DNADAMAGEREPAIR/TOLERATION PROTEIN DRT100-RELATED
			<i>Glyma.13G336100</i>	OUTER ENVELOPE PORE PROTEIN 161, CHLOROPLASTIC
			<i>Glyma.13G331300</i>	RECEPTORL IKE PROTEIN KINASE HERK 1

		<i>Glyma.13G330600</i>	KINESIN MOTOR PROTEIN-RELATED
		<i>Glyma.13G334300</i>	HISTONE 2A
		<i>Glyma.13G332700</i>	60S RIBOSOMAL PROTEIN L23A
		<i>Glyma.13G331700</i>	EXOCYST COMPLEX PROTEIN EXO70
		<i>Glyma.13G330300</i>	RING FRINGE-RELATED
		<i>Glyma.13G338700</i>	PROTEIN TOC753, CHLOROPLASTIC-RELATED
		<i>Glyma.13G333300</i>	METHYLCPGBINDING DOMAIN CONTAINING PROTEIN 1-RELATED
		<i>Glyma.13G342700</i>	ANTHRANILATE PHOSPHORIBOSYL TRANSFERASE-LIKE PROTEIN
		<i>Glyma.13G338200</i>	ZINC/IRON TRANSPORTER
		<i>Glyma.13G333200</i>	TRANSCRIPTION FACTOR MYB48-RELATED
		<i>Glyma.13G342500</i>	ETHYLENE INSENSITIVE 3-LIKE 3 PROTEIN
		<i>Glyma.13G341600</i>	PROTEIN FAR1-RELATED SEQUENCE 4
		<i>Glyma.13G331900</i>	60S RIBOSOMAL PROTEIN L35
		<i>Glyma.13G330800</i>	CHITINASE
		<i>Glyma.13G333800</i>	HISTONE 2A
		<i>Glyma.13G339700</i>	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10
		<i>Glyma.13G341100</i>	PROTEIN TYROSINE KINASE (PKINASE_TYR)//TPR REPEAT (TPR_11)
		<i>Glyma.13G338400</i>	RING ZINC FINGER PROTEIN
		<i>Glyma.13G338600</i>	DNAJ HOMOLOG SUBFAMILY C MEMBER
		<i>Glyma.13G342000</i>	HISTONE H3
		<i>Glyma.13G340400</i>	E3 UBIQUITIN LIGASE BIG BROTHER
		<i>Glyma.13G340900</i>	PROTEIN ZNTB
		<i>Glyma.13G335300</i>	E3 UBIQUITINPROTEIN LIGASE XBAT31-RELATED
		<i>Glyma.13G333100</i>	AQUAPORIN TRANSPORTER
		<i>Glyma.13G333900</i>	HISTONE 2A
		<i>Glyma.13G341400</i>	AGC (CAMP-DEPENDENT, CGMP-DEPEN-DENT AND PROTEIN KINASE C) KINASE FAMILY PROTEIN
		<i>Glyma.13G343000</i>	GLYCOSYL HYDROLASE
		<i>Glyma.13G340100</i>	ORIGIN RECOGNITION COMPLEX SUBUNIT 1

Table S2. List of SNP variations between ‘William 82’ and ‘PI366121’ along with the genes underlying the most significant root QTL genomic regions.

Position	Gene	Ref	ALT	Effect	Start	End	Strand
Chr03:1040647	<i>Glyma.03G010700</i>	A	T	3_prime_UTR_variant	1,037,842	1,042,141	+
Chr03:1789064	<i>Glyma.03G017900</i>	T	C	Upstream gene variant	1,787,790	1,800,965	+
Chr03:2075749	<i>Glyma.03G020300</i>	G	T/A	Upstream gene variant	2,074,821	2,078,561	-
Chr03:1393538	<i>Glyma.03G013700</i>	G	T	Missense variant	1,393,484	1,393,734	+
Chr03:831779	<i>Glyma.03G008600</i>	C	G	Downstream gene variant	830,451	838,408	-
Chr03:1496887	<i>Glyma.03G014900</i>	G	C	Downstream gene variant	1,494,708	1,502,910	-
Chr03:2805098	<i>Glyma.03G025900</i>	G	A	Synonymous variant	2,804,898	2,805,383	+
Chr03:1981263	<i>Glyma.03G019400</i>	A	G	Intron variant	1,977,661	1,985,026	-
Chr03:2413616	<i>Glyma.03G022900</i>	C	T	Missense variant	2,413,172	2,413,671	-
Chr03:1738562	<i>Glyma.03G017200</i>	G	A	5_prime_UTR_variant	1,735,158	1,738,810	-
Chr03:3186369	<i>Glyma.03G029200</i>	T	G	Synonymous variant	3,185,979	3,188,159	-
Chr03:3022150	<i>Glyma.03G027500</i>	C	T	Synonymous variant	3,022,087	3,022,240	-
Chr03:3151051	<i>Glyma.03G028900</i>	G	A	Intron variant	3,148,672	3,152,887	-
Chr03:3072041	<i>Glyma.03G028000</i>	G	C	Missense variant	3,071,857	3,072,066	-
Chr03:3165706	<i>Glyma.03G029000</i>	C	T	Intron variant	3,164,736	3,166,769	+
Chr03:2124946	<i>Glyma.03G020800</i>	A	G	3_prime_UTR_variant	2,124,895	2,135,692	-
Chr03:2009608	<i>Glyma.03G019600</i>	G	C	3_prime_UTR_variant	2,007,617	2,009,871	+
Chr03:3010747	<i>Glyma.03G027400</i>	C	T	Missense variant	3,010,213	3,018,498	-
Chr03:3128983	<i>Glyma.03G028700</i>	A	G	Missense variant	3,128,776	3,130,648	+
Chr03:2998840	<i>Glyma.03G027200</i>	A	G	Missense variant	2,997,332	2,999,026	+
Chr03:1295079	<i>Glyma.03G012800</i>	A	G	Intron variant	1,292,400	1,298,429	-
Chr03:1852211	<i>Glyma.03G018500</i>	A	C	Intron variant	1,849,093	1,855,316	+
Chr03:3109886	<i>Glyma.03G028400</i>	T	C	Missense variant	3,107,378	3,110,786	+
Chr03:2902943	<i>Glyma.03G026400</i>	C	G	Intron variant	2,892,021	2,904,360	+
Chr03:1385095	<i>Glyma.03G013600</i>	CA	C	Intron variant	1,379,993	1,390,392	+
Chr03:2171360	<i>Glyma.03G021200</i>	G	A	Downstream gene variant	2,170,567	2,172,891	-
Chr03:3253737	<i>Glyma.03G029600</i>	T	C	3_prime_UTR_variant	3,253,478	3,255,163	-
Chr03:1452530	<i>Glyma.03G014500</i>	C	T	Missense variant	1,452,354	1,452,677	-
Chr03:2490109	<i>Glyma.03G023500</i>	C	A	Intron variant	2,486,847	2,493,916	+
Chr03:2061229	<i>Glyma.03G020100</i>	A	C	Missense variant	2,057,797	2,063,029	-
Chr03:3053137	<i>Glyma.03G027900</i>	T	C	Intron variant	3,048,805	3,061,575	-
Chr03:2164039	<i>Glyma.03G021100</i>	C	T	Splice region variant	2,162,406	2,167,712	+
Chr03:3029835	<i>Glyma.03G027600</i>	A	G	Splice region variant	3,029,154	3,033,239	-
Chr03:2043655	<i>Glyma.03G019800</i>	T	G	Synonymous variant	2,043,161	2,043,723	+
Chr03:3225850	<i>Glyma.03G029300</i>	T	C	Synonymous variant	3,225,772	3,226,185	-
Chr03:1547374	<i>Glyma.03G015600</i>	A	G	Upstream gene variant	1,539,775	1,548,226	-
Chr03:2286654	<i>Glyma.03G021900</i>	G	T	Intron variant	2,285,871	2,289,619	-
Chr03:2092471	<i>Glyma.03G020500</i>	G	A	Intron variant	2,091,153	2,093,117	+
Chr13:28686299	<i>Glyma.13G172800</i>	G	C	Missense variant	28,683,493	28,686,774	+
Chr13:28537151	<i>Glyma.13G171200</i>	T	C	Intron variant	28,536,983	28,540,336	-
Chr13:29123039	<i>Glyma.13G177300</i>	C	A	5_prime_UTR_variant	29,122,910	29,128,171	+
Chr13:27561946	<i>Glyma.13G159900</i>	T	C	Upstream gene variant	27,560,735	27,566,769	+
Chr13:28613474	<i>Glyma.13G172200</i>	A	G	Downstream gene variant	28,612,286	28,620,441	-
Chr13:27774334	<i>Glyma.13G162300</i>	G	T	3_prime_UTR_variant	27,773,991	27,778,719	-
Chr13:28672639	<i>Glyma.13G172700</i>	T	A	Missense variant	28,671,831	28,675,231	+

Chr13:28488019	<i>Glyma.13G170700</i>	G	C	5_prime_UTR_variant	28,487,838	28,494,611	+
Chr13:27700711	<i>Glyma.13G161400</i>	C	T	Downstream gene variant	27,698,462	27,701,365	-;
Chr13:28211158	<i>Glyma.13G167600</i>	T	G	Synonymous variant	28,210,440	28,212,300	+
Chr13:27786625	<i>Glyma.13G162500</i>	A	T	Upstream gene variant	27,785,225	27,788,045	-
Chr13:28303515	<i>Glyma.13G168600</i>	G	A	Missense variant	28,298,272	28,304,199	-
Chr13:27606195	<i>Glyma.13G160400</i>	C	T	3_prime_UTR_variant	27,606,020	27,608,359	-
Chr13:28720934	<i>Glyma.13G173100</i>	C	T	Synonymous variant	28,720,656	28,721,572	+
Chr13:28182349	<i>Glyma.13G167100</i>	T	A	Missense variant	28,182,121	28,182,399	+
Chr13:28240930	<i>Glyma.13G167900</i>	T	G	Upstream gene variant	28,240,381	28,243,803	+
Chr13:31057839	<i>Glyma.13G196900</i>	T	G	Downstream gene variant	31,055,891	31,072,513	+
Chr13:28317204	<i>Glyma.13G168800</i>	C	T	Upstream gene variant	28,316,886	28,317,715	+
Chr13:28970569	<i>Glyma.13G175100</i>	A	C	Downstream gene variant	28,969,904	28,975,782	+
Chr13:33685460	<i>Glyma.13G224000</i>	T	A	Missense variant	33,684,833	33,686,902	+
Chr13:28928217	<i>Glyma.13G174800</i>	A	G	Synonymous variant	28,927,266	28,928,267	-
Chr13:28096911	<i>Glyma.13G166200</i>	G	A	Intron variant	28,093,807	28,097,420	-
Chr13:35388368	<i>Glyma.13G244500</i>	T	A	Upstream gene variant	35,387,923	35,395,610	+
Chr13:28938817	<i>Glyma.13G174900</i>	A	C	Synonymous variant	28,938,189	28,940,823	-
Chr13:28305241	<i>Glyma.13G168700</i>	C	T	Splice donor variant	28,305,098	28,310,222	+
Chr13:30403159	<i>Glyma.13G190400</i>	G	T	Missense variant	30,402,029	30,409,606	+
Chr13:28595304	<i>Glyma.13G172000</i>	T	C	Upstream gene variant	28,593,222	28,598,072	-
Chr13:28645033	<i>Glyma.13G172500</i>	G	A	Synonymous variant	28,644,819	28,649,188	-
Chr13:28367052	<i>Glyma.13G169700</i>	A	T	Intron variant	28,363,094	28,367,579	-
Chr13:28031079	<i>Glyma.13G165500</i>	A	T	Downstream gene variant	28,030,788	28,034,710	+
Chr13:42993020	<i>Glyma.13G336600</i>	A	G	Synonymous variant	42,991,934	42,993,435	-
Chr13:42797618	<i>Glyma.13G334200</i>	T	C	Missense variant	42,794,878	42,801,645	+
Chr13:42918068	<i>Glyma.13G335600</i>	T	A	Synonymous variant	42,916,206	42,918,785	+
Chr13:42423055	<i>Glyma.13G329700</i>	C	T	Intron variant	42,422,213	42,426,774	-
Chr13:42503906	<i>Glyma.13G330400</i>	A	G	Intron variant	42,494,484	42,509,495	+
Chr13:43326463	<i>Glyma.13G341500</i>	C	A	Missense variant	43,325,404	43,326,510	-
Chr13:42581208	<i>Glyma.13G331300</i>	A	T	Synonymous variant	42,580,671	42,582,344	-
Chr13:42523190	<i>Glyma.13G330600</i>	A	T	Missense variant	42,523,075	42,523,280	-
Chr13:42807826	<i>Glyma.13G334300</i>	A	T	Synonymous variant	42,807,791	42,808,000	+
Chr13:42687849	<i>Glyma.13G332700</i>	C	T	5_prime_UTR_variant	42,687,782	42,689,387	+
Chr13:42740451	<i>Glyma.13G333300</i>	A	T	Synonymous variant	42,739,408	42,742,467	-
Chr13:42713462	<i>Glyma.13G333200</i>	C	A	Synonymous variant	42,713,045	42,714,681	-
Chr13:43333456	<i>Glyma.13G341600</i>	T	C	Missense variant	43,331,375	43,335,735	-
Chr13:42650050	<i>Glyma.13G331900</i>	A	G	Splice region variant	42,648,871	42,650,712	-
Chr13:43295111	<i>Glyma.13G341100</i>	C	A	Downstream gene variant	43,292,117	43,296,459	-
Chr13:43246090	<i>Glyma.13G340400</i>	G	A	Splice region variant	43,244,791	43,246,867	-
Chr13:43284804	<i>Glyma.13G340900</i>	A	G	Upstream gene variant	43,282,672	43,286,972	-
Chr13:42711332	<i>Glyma.13G333100</i>	G	A	Missense variant	42,711,023	42,711,397	+
Chr13:43311794	<i>Glyma.13G341400</i>	C	A	Missense variant	43,311,148	43,312,308	+
Chr13:43447450	<i>Glyma.13G343000</i>	G	C	Missense variant	43,447,390	43,451,125	-
Chr13:43217945	<i>Glyma.13G340100</i>	T	A	3_prime_UTR_variant	43,210,673	43,218,069	+

Table S3. List of candidate genes showing high expression in the root with annotation descriptions.

GENE NAME	ANNOTATION DESCRIPTION
<i>Glyma.03G013700</i>	DOWNSTREAM TARGET OF AGL15 2
<i>Glyma.03G008600</i>	SIGNAL PEPTIDE PEPTIDASE-LIKE 4
<i>Glyma.03G022900</i>	GUANYL-NUCLEOTIDE EXCHANGE FACTOR
<i>Glyma.03G029100</i>	PHOSPHOENOL-PYRUVATE DIKINASE-RELATED
<i>Glyma.03G027500</i>	TRANSKETOLASE/GLYCOALDEHYDE TRANSFERASE
<i>Glyma.03G028000</i>	ARGINASE/CANAVANASE
<i>Glyma.03G027400</i>	3PHOSPHOSHIKIMATE 1CARBOXYVINYLTRANSFERASE/EPSP SYNTHASE
<i>Glyma.03G028700</i>	TRANSFERASE ACTIVITY, TRANSFERRING ACYL GROUPS OTHER THAN AMINO-ACYL GROUPS
<i>Glyma.03G027200</i>	LEUCINE-RICH REPEAT RECEPTOR-LIKE PROTEIN KINASE
<i>Glyma.03G027800</i>	PPR REPEAT (PPR)//PPR REPEAT FAMILY (PPR_2)
<i>Glyma.03G028400</i>	PLANT PROTEIN OF UNKNOWN FUNCTION (DUF641) (DUF641)
<i>Glyma.03G014500</i>	DEHYDROGENASES WITH DIFFERENT SPECIFICITIES (RELATED TO SHORTCHAIN ALCOHOL DEHYDROGENASES)
<i>Glyma.03G020100</i>	NUCLEOTIDYLTRANSFERASE FAMILY PROTEIN
<i>Glyma.03G021100</i>	RIBOSOMAL RNA PROCESSING PROTEIN 36 HOMOLOG
<i>Glyma.03G027600</i>	DNA REPAIR PROTEIN RAD51 HOMOLOG 3
<i>Glyma.13G172800</i>	GTPASE RAB11/YPT3, SMALL G PROTEIN SUPERFAMILY
<i>Glyma.13G172700</i>	HOMEODOMAIN (HOMEODOMAIN)
<i>Glyma.13G168600</i>	PROTEIN FARNESYLTRANSFERASE SUBUNIT BETA
<i>Glyma.13G167100</i>	PEROXIDASE 25
<i>Glyma.13G224000</i>	HEAT SHOCK PROTEIN 70 KDA
<i>Glyma.13G168700</i>	2 HYDROXY-ACID DEHYDROGENASE-RELATED
<i>Glyma.13G190400</i>	LEUCINE RICH REPEAT CONTAINING PROTEIN
<i>Glyma.13G172500</i>	ZINC FINGER FYVE DOMAIN CONTAINING PROTEIN
<i>Glyma.13G334200</i>	RNA AND EXPORT FACTOR BINDING PROTEIN
<i>Glyma.13G341500</i>	LEUCINE-RICH REPEAT RECEPTOR-LIKE PROTEIN KINASE
<i>Glyma.13G330600</i>	KINESIN MOTOR PROTEIN-RELATED
<i>Glyma.13G341600</i>	PROTEIN FAR1-RELATED SEQUENCE 4
<i>Glyma.13G331900</i>	60S RIBOSOMAL PROTEIN L35
<i>Glyma.13G333100</i>	AQUAPORIN TRANSPORTER
<i>Glyma.13G341400</i>	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) KINASE FAMILY PROTEIN
<i>Glyma.13G343000</i>	GLYCOSYL HYDROLASE
<i>Glyma.13G340400</i>	RING FINGER DOMAIN-CONTAINING

Table S4. List of candidate genes with various tissue/organ-specific values in soybean from the ePlant soybean transcriptome data.

Gene name	Root	Root tip	Root stripped	Root hair (24HAI)	Leaves	SAM	Flower	Green pods	Nodules
<i>Glyma.03G008600</i>	10.02	5.56	10.11	7.50	15.63	16.72	21.05	22.55	2.39
<i>Glyma.03G029100</i>	1.85	0.00	0.52	0.56	0.00	0.76	0.00	0.00	0.27
<i>Glyma.03G028000</i>	1.58	1.55	382.18	156.61	2.13	52.94	4.74	0.68	0.00
<i>Glyma.03G028700</i>	2.37	0.31	0.78	0.00	0.36	1.77	0.30	0.00	0.00
<i>Glyma.03G027200</i>	0.00	0.00	0.00	0.00	0.36	0.00	0.00	0.00	0.00
<i>Glyma.03G020100</i>	34.28	19.78	23.32	16.66	24.86	52.43	48.63	32.80	50.80
<i>Glyma.03G021100</i>	4.48	5.25	1.04	5.28	4.97	7.35	4.45	1.37	5.05
<i>Glyma.03G027600</i>	4.48	8.03	5.44	4.72	7.81	8.87	6.52	6.83	1.86
<i>Glyma.03G022900</i>	10.81	37.39	14.77	10.00	5.33	29.38	6.52	15.03	0.80
<i>Glyma.03G027500</i>	239.20	364.97	164.79	170.49	27.70	136.53	37.36	225.48	57.71
<i>Glyma.03G027400</i>	51.95	36.78	51.56	44.43	17.40	40.78	9.19	40.31	15.69
<i>Glyma.03G028400</i>	17.41	14.52	18.14	14.72	10.65	19.00	11.86	14.35	15.96
<i>Glyma.03G014500</i>	13.98	9.89	4.40	8.89	1.07	0.76	0.30	0.68	0.80
<i>Glyma.13G172800</i>	2.64	5.56	3.89	5.55	1.07	2.53	3.56	2.73	2.13
<i>Glyma.13G172700</i>	0.00	0.00	0.00	0.28	0.00	0.00	0.00	0.68	0.00
<i>Glyma.13G168600</i>	8.44	17.61	19.69	8.89	9.23	16.97	10.67	13.67	16.49
<i>Glyma.13G167100</i>	1.85	0.00	2.33	0.28	4.26	0.25	2.08	1.37	0.00
<i>Glyma.13G168700</i>	32.70	3.71	25.65	21.94	18.47	34.45	265.97	210.45	4.26
<i>Glyma.13G190400</i>	2.11	3.40	0.52	4.17	2.13	3.29	1.78	1.37	1.60
<i>Glyma.13G172500</i>	2.64	3.09	0.78	3.05	20.24	0.00	1.48	0.00	0.27
<i>Glyma.13G341500</i>	10.02	202.42	364.56	36.37	125.36	44.07	423.42	101.13	0.27
<i>Glyma.13G330600</i>	9.23	33.99	7.00	10.83	13.85	30.90	11.56	11.62	41.22
<i>Glyma.13G341600</i>	3.96	6.80	5.70	7.22	7.81	6.84	9.19	4.10	5.58
<i>Glyma.13G333100</i>	61.18	10.82	14.25	21.66	12.78	78.52	37.66	14.35	2.13
<i>Glyma.13G341400</i>	27.95	10.82	4.66	49.15	2.84	2.79	13.05	5.47	5.05
<i>Glyma.13G343000</i>	0.26	0.00	0.00	5.55	0.71	91.95	3.85	0.68	0.00
<i>Glyma.13G334200</i>	117.62	266.39	115.04	112.73	94.82	155.28	136.69	110.69	58.77
<i>Glyma.13G331900</i>	14.77	43.57	27.98	30.27	7.46	17.98	2.37	8.88	6.91
<i>Glyma.13G224000</i>	134.50	0.93	155.46	12.77	64.63	68.39	30.84	211.82	50.53

Table S5. Distribution of SNP markers mapped on soybean chromosome/linkage groups

Chromosome	Linkage group	No. of markers	Distance (cM)	Density SNP/cM
1	D1a	56	188.56	3.37
2	D1b	88	293.83	3.33
3	N	61	246.62	4.04
4	C1	65	226.36	3.48
5	A1	71	220.26	3.10

6	C2	62	211.06	3.40
7	M	83	233.44	2.81
8	A2	81	262.07	3.24
9	K	65	212.68	3.27
10	O	78	215.62	2.76
11	B1	50	219.89	4.40
12	H	59	281.99	4.78
13	F	96	224.18	2.34
14	B2	70	172.16	2.46
15	E	71	198.24	2.79
16	J	63	180.02	2.86
17	D2	62	233.71	3.77
18	G	86	198.24	2.30
19	L	82	240.27	2.93
20	I	59	167.50	2.84
Total		1408	4426.70	3.14
Average marker and distance/chromosome		70.4	221.33	3.14

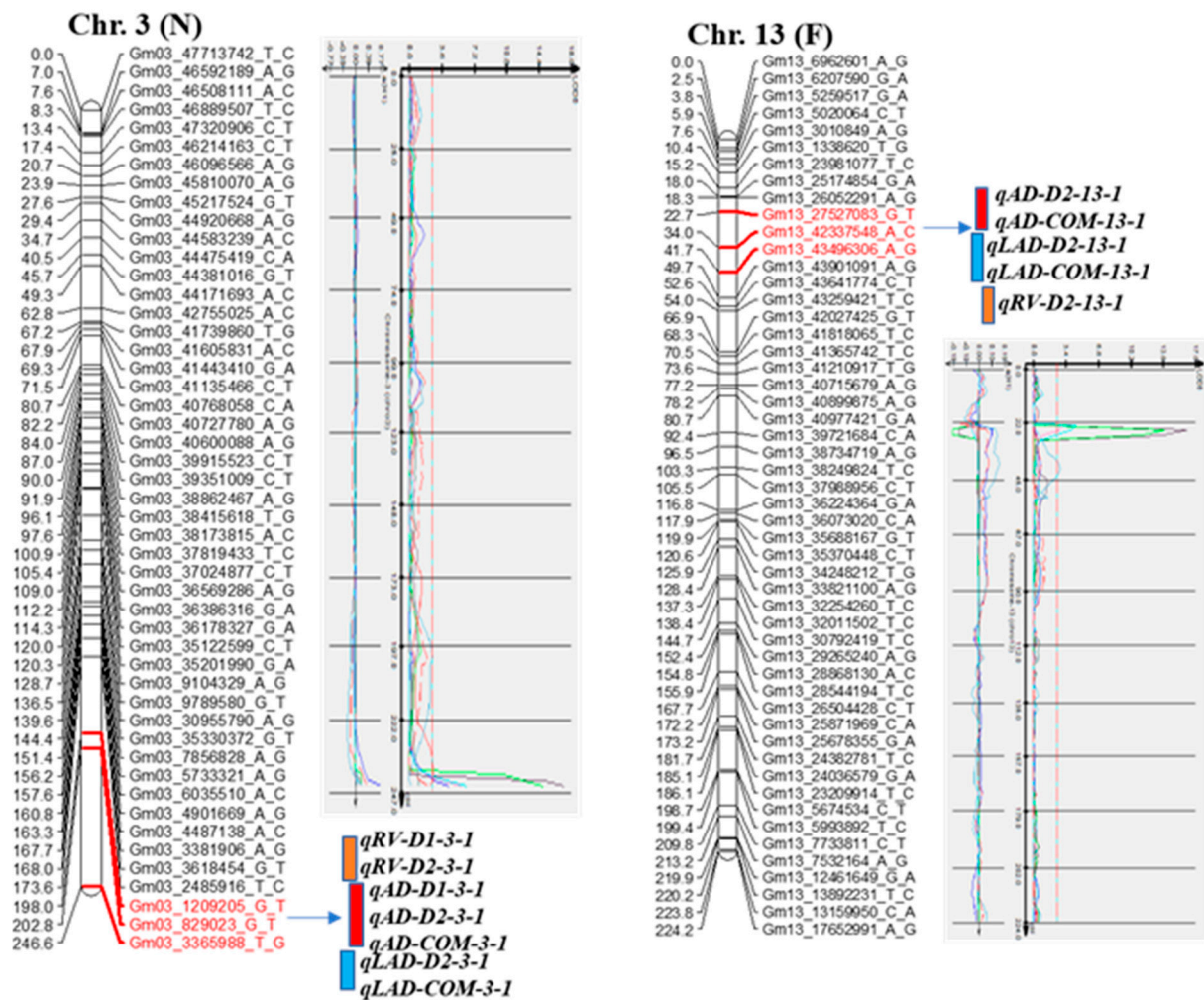


Figure S1. The most significant QTL regions with LOD distribution curve on chromosomes 3 and 13. Chr:

chromosome; AD: average diameter; RV: root volume; LAD: link average diameter. D1, D2, and COM indicate environment 1, environment 2, and combined environments, respectively. Different colors indicate different QTLs within same region.

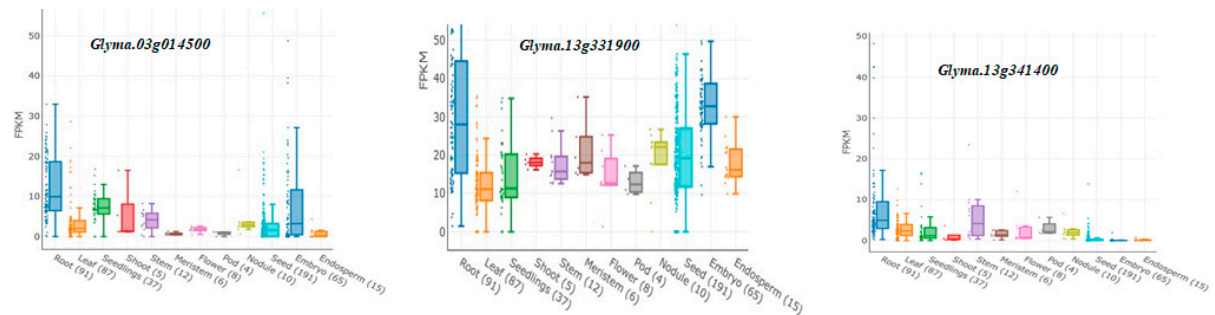


Figure S2. Expression patterns of three candidate genes across twelve different soybean tissues/organs (web-based publicly available RNA-Seq soybean libraries '4085') (<http://ipf.sustech.edu.-cn/pub/soybean/>). FPKM: fragments per kilobase of transcript per million mapped reads. The blue colored bar on the left indicates the expression level in the roots.