Additional file 8: List of loci significantly associated with days to flowering (DTF) and maturity (DTM), duration of flowering-to-maturity (DFTM) and plant height (PH) in soybean.

Traits	Loci	SNP[a]	Alleles (minor : major)	MAF[b]	Allelic effect[c] (day)	*P*-value	Candidate genes[d]	Annotation	Known-loci[e]
DTF	1	Gm01_50219219	A:C	0.08	1.2	4.5E-05	*Glyma01g37980*	Late embryogenesis abundant protein	
	2	Gm02_4465606	T:C	0.30	0.7	1.9E-04	*Glyma02g05580*	Zinc finger protein	
	3	Gm06_6074331	G:A	0.12	1.4	1.5E-07	*Glyma06g08270*	AIG2-like	
	4	Gm06_16723946	G:A	0.15	1.1	3.2E-05	*Glyma06g20310*	AtBUC2 [1]	Fflr 18-2, Ft 5-1
	5	Gm06_26933523	T:C	0.09	1.2	4.4E-05			Ft 4-2, 5-1, FT 2-1, Fflr 12-2, 4-1, 5-1, 9-1
	6	Gm07_5957056	G:A	0.17	0.9	7.1E-05			Fflr 2-2
	7	Gm07_7394287	T:C	0.17	0.8	1.7E-04	*Glyma07g08890* *Glyma07g08831*	AtAGL6 [2], GmSOC1 [3]	Fflr 2-2
	8	Gm07_11068398	G:A	0.36	-0.8	4.3E-05			Fflr 2-2
	9	Gm07_38991567	G:A	0.31	0.6	2.1E-04			
	10	Gm08_17819435	C:T	0.18	1.0	3.6E-05			
	11	Gm08_44265646	C:T	0.20	0.7	4.8E-05	*Glyma08g44640* *Glyma08g44650*	AtVRN1 [4]	
	12	Gm08_44602360	G:A	0.21	0.8	5.6E-06			
	13	Gm08_44814503	C:T	0.23	0.7	5.2E-05	*Glyma08g45680*	FAR1 DNA-binding domain containing protein [5]	
	14	Gm09_4388948	T:C	0.19	0.9	5.4E-05			
	15	Gm09_6197309	G:A	0.18	0.8	1.9E-04			
	16	Gm09_6976053	A:G	0.13	1.0	2.1E-05	*Glyma09g07980*	AtELF8/AtVIP6 [6]	Ft 3-3
	17	Gm11_1395042	C:T	0.39	0.6	2.0E-04	*Glyma11g02230*	Nucleoporin-ralated	
	18	Gm11_17274491	T:C	0.12	1.2	2.1E-06	*Glyma11g20470*	Heparansulfate 6-o-sulfotransferase 3	
	19	Gm13_39699161	C:T	0.18	0.9	8.5E-05	*Glyma13g38975*	AtCLV3 [7]	
	20	Gm14_2918117	T:C	0.14	1.1	9.2E-05			
	21	Gm14_45475177	G:A	0.08	1.2	2.8E-05	*Glyma14g36221*	AtAGL16 [8]	Ft 3-1
	22	Gm18_48177289	C:A	0.09	1.4	1.3E-05			Fflr 10-2

	23	Gm18_60868392	T:C	0.19	1.0	1.4E-06			
	24	Gm19_40662679	T:G	0.34	-0.7	6.9E-05			Fflr 15-2, 16-4, 2-3, 4-3
	25	Gm20_276793	G:T	0.14	0.9	3.7E-05	*Glyma20g00440*	Jumonji domain containing protein [9]	
	26	Gm20_23754062	G:A	0.14	1.3	1.6E-06	*Glyma20g16880*	AtEMF2 [10]	FT 2-3
		Gm20_26991347	C:T	0.15	1.4	5.5E-08			
		Gm20_27852579	C:T	0.15	1.4	5.5E-08			
		Gm20_29208847	C:T	0.12	1.4	9.1E-08			
		Gm20_29983050	G:A	0.13	1.4	9.7E-08	*Glyma20g21082*	AtAGL6 [2]	
	27	Gm20_46730763	G:T	0.05	1.4	5.6E-05	*LOC100812369*	AP2/ERF and B3 domain-containing transcription factor [11]	
DTM	1	Gm11_10152581	T:C	0.08	-1.6	5.2E-06	*Glyma11g14150*	RNA-BINDING PROTEIN	
	2	Gm16_2412662	T:C	0.47	-0.9	2.5E-06	*Glyma16g02840*	AtLEW3 [12]	
	3	Gm16_2824073	T:G	0.11	-1.2	4.3E-06			
	4	Gm16_3006858	C:T	0.19	-1.2	3.8E-06	*Glyma16g03580*	Ring finger containing protein	
	5	Gm19_45000827	C:A	0.05	-2.3	7.6E-06	*Dt1*	AtTFL1 [13]	Pod mat 13-6
	6	Gm19_47909005	A:G	0.21	1.2	1.1E-05			
DFTM	1	Gm02_49988138	T:G	0.19	0.9	1.8E-05			
	2	Gm03_1597206	T:G	0.15	0.9	8.6E-05			
	3	Gm03_5316197	T:C	0.08	1.3	9.7E-05			
	4	Gm03_11220188	A:G	0.08	-1.2	1.5E-04			Pod mat 20-2
	5	Gm03_36330058	A:G	0.49	-0.9	7.3E-06			
	6	Gm04_35149844	C:T	0.25	-1.2	4.2E-07			Pod mat 18-3
	7	Gm06_10263943	C:A	0.06	-1.6	1.9E-05			
	8	Gm06_16167243	A:G	0.07	1.6	2.3E-05	*Glyma06g19820*	Betaine-aldehyde dehydrogenase	R3 2-1, R5 3-2, R7 2-1, Pod mat 25-2
	9	Gm08_1966701	G:T	0.18	-0.9	5.1E-05	*Glyma08g02881*	Unknown	

	10	Gm08_2636067	G:T	0.12	-1.0	8.3E-05			
	11	Gm09_6970117	T:G	0.14	-1.1	2.7E-05	*Glyma09g07980*	AtELF8/AtVIP6 [6]	Pod mat 16-3, 5-2
	12	Gm09_41155181	T:C	0.31	-0.8	3.5E-06			Pod mat 27-2
	13	Gm11_9332515	A:G	0.18	0.8	1.8E-05	*Glyma11g13090*	Serine-threonine protein kinase	Pod mat 17-2, 18-2
	14	Gm12_4363882	C:T	0.08	1.4	5.7E-06			
	15	Gm15_1609497	T:C	0.08	1.2	4.0E-05	*Glyma15g02390*	Mitochondrial processing peptidase	
	16	Gm16_2412662	T:C	0.47	-0.7	4.2E-05	*Glyma16g02840*	AtLEW3 [12]	
	17[f]	Gm16_2997247	C:T	0.11	-1.0	6.7E-06	*Glyma16g03570*	WRKY family transcription factor	
	18	Gm19_45255796	A:G	0.16	1.2	6.5E-05			R5 1-2, Pod mat 24-10, 24-4, 10-4, 13-6, 4-3
PH	1	Gm04_5175822	A:G	0.06	-11.5	1.0E-07			
	2	Gm06_14889674	C:T	0.19	-4.5	4.4E-05			
	3	Gm08_42349221	C:T	0.06	-7.2	1.3E-05			
	4	Gm09_9623583	T:G	0.21	3.6	8.8E-05			Plant height 18-3
	5	Gm09_40958920	C:T	0.08	-5.8	1.6E-04	*Glyma09g34601*	AtBRX [14]	
	6	Gm09_41147947	C:T	0.14	-5.1	1.3E-05			
	7	Gm10_7796028	A:C	0.09	6.6	7.2E-07	*Glyma10g08930*	GDSL-like Lipase	
	8	Gm11_6078943	C:A	0.06	-9.0	8.6E-06			Plant height 24-4
	9	Gm12_128224	T:C	0.12	-5.6	8.7E-05	*Glyma12g00320*	AtSAC1 [15]	
	10	Gm12_8911538	G:A	0.10	4.7	9.6E-05			
	11	Gm13_36042528	G:A	0.41	3.7	6.3E-06			Plant height 17-1
	12	Gm13_36823931	G:T	0.39	3.5	1.9E-05			Plant height 17-1
	13	Gm13_42933309	C:T	0.08	-6.9	8.2E-06			
	14	Gm14_48703687	G:T	0.28	3.7	1.4E-05			
	15	Gm15_3135042	G:A	0.06	-7.2	5.0E-06			

	16	Gm15_25719454	T:G	0.05	-7.6	1.6E-05			Plant height 26-10
	17	Gm16_5773005	G:A	0.07	-6.1	4.5E-05	*Glyma16g06333*	ASB1/TRP4/WEI7	
	18	Gm16_29597918	G:A	0.07	-10.8	1.0E-08	*Glyma16g25570*	AtHAM4 [16]	
	19	Gm17_40318849	A:G	0.38	-3.7	2.7E-05	*Glyma17g36350*	Unknown	
	20	Gm17_40538815	T:C	0.12	-6.2	5.8E-06			
	21	Gm18_58462762	A:C	0.22	-3.7	6.2E-05	*Glyma18g49080*	AtPIN1 [17]	Plant height 17-3, 25-5, 26-12, 33-2, 33-8, 34-2, 34-8
	22	Gm18_60516754	A:C	0.08	-7.2	4.0E-05			Plant height 26-12, 33-2, 34-2
	23	Gm19_8629858	G:A	0.05	-9.1	1.5E-06			
	24	Gm19_44389764	T:C	0.11	-10.9	3.7E-11	*Glyma19g37180*	Pectin lyase-like [18]	Plant height 1-1, 6-1 and 10-4
	25	Gm19_45000827	C:A	0.05	-16.0	3.0E-15	*Dt1*	AtTFL1 [13]	Plant height 4-2 and 13-8
	26	Gm20_376751	C:T	0.15	4.3	4.7E-05			
	27	Gm20_35951388	C:T	0.17	-4.4	7.5E-05			

[a] Start with the chromosome number and followed by physical position of the marker on that chromosome.

[b] MAF, minor allele frequency

[c] Respect to minor allele.

[d] Genes annotated in Glyma1.1, Glyma1.0, and NCBI RefSeq gene models in SoyBase (www.soybase.org) were used as the source of candidate genes.

[e] Based on the QTL list on SoyBase (www.soybase.org).

[f] The SNP was also detected significantly associated with DTM and was clumped in the locus DTM4.

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