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Supplementary Material

Identification of quantitative trait loci governing biosynthesis of phospholipids in soybean

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Supplementary Table S1. Common polymorphic SSR markers in F₂ populations I (JS20-34×AVKS215) and II (JS20-98×AVKS215)

S. N.	Chr	Marker Position	Marker Name	S. N.	Chr	Marker Position	Marker Name	S. N.	Chr	Marker Position	Marker Name	S. N.	Chr	Marker Position	Marker Name
1	1	5.25	Sat_332	53	7	48.86	Sat_244	105	11	100.88	Sat_123	157	16	43.01	Satt380
2	1	5.93	Sat_413	54	7	51.6	Sat_253	106	11	102.56	Satt359	158	16	44.49	Sat_361
3	1	17.52	Satt184	55	7	53.54	Satt245	107	11	125.74	Sat_331	159	16	65.04	Satt244
4	1	40.87	Satt531	56	7	56.29	Satt220	108	12	46.95	Satt442	160	16	69.3	Sat_396
5	1	48.14	Satt342	57	7	60.05	Satt323	109	12	67.17	Satt253	161	16	75.13	Sat_224
6	1	49.07	Satt532	58	7	61.04	Satt702	110	12	73.46	Sat_158	162	16	89.43	Sat_394
7	1	62.37	Satt580	59	7	66.99	Satt175	111	12	81.04	Satt302	163	16	89.48	Sat_395
8	1	66.39	Sat_106	60	7	76.41	Sat_288	112	12	85.79	Satt637	164	17	11.77	Sct_192
9	1	69.91	Satt468	61	7	80.97	Sat_422	113	12	89.09	Satt293	165	17	57.07	Satt154
10	1	70.69	Satt436	62	7	85.35	Satt697	114	12	104.37	Sat_180	166	17	69.3	Satt397
11	1	75.25	Sat_036	63	7	95.45	Satt551	115	12	105.74	Satt434	167	17	75.29	Sat_292
12	2	40.04	Satt701	64	7	130.76	Satt308	116	13	1.79	Sat_390	168	17	79.23	Satt389
13	2	46.92	Sat_254	65	7	140.69	Sat_330	117	13	2.23	Satt325	169	17	85.15	Satt226
14	2	52.61	Satt296	66	8	0	Sat_383	118	13	3.11	Sat_387	170	17	99.04	<i>GMHSP179</i>
15	2	59.61	Satt266	67	8	36.77	Satt177	119	13	3.35	Satt569	171	17	128.73	Sat_220
16	2	74.02	Satt611	68	8	60.59	Satt424	120	13	3.63	Satt586	172	18	0	Satt163
17	2	75.29	Satt005	69	8	67.86	<i>AW132402</i>	121	13	3.95	Satt030	173	18	3.7	Sat_210
18	2	76.1	Satt282	70	8	84.08	Sat_129	122	13	16.08	Satt252	174	18	12.54	Satt688
19	2	100.89	Satt172	71	8	84.09	Sat_199	123	13	44.42	Satt516	175	18	15.63	<i>AW734137</i>
20	2	102.6	Sat_069	72	8	115.93	Satt421	124	13	57.77	Sat_103	176	18	27.48	Sat_315
21	2	137.97	Satg001	73	8	128.44	Satt209	125	13	59.6	Sat_297	177	18	33.26	Satt324
22	3	28.52	Satt009	74	8	131.97	Sat_294	126	13	62.79	Sat_229	178	18	34.87	Sat_403
23	3	29.28	Satt641	75	8	145.57	Satt409	127	13	71.41	Satt510	179	18	43.38	Satt394
24	3	32.85	Satt530	76	9	30.28	Satt102	128	13	72.97	Sat_317	180	18	53.42	Satt303
25	3	36.86	Sat_084	77	9	43.35	Satt544	129	13	75.97	Sat_120	181	18	56.18	Sat_094
26	3	45.14	Satt080	78	9	47.38	Satt337	130	13	103.51	Sat_197	182	18	56.52	Satt533
27	3	58.38	Sat_033	79	9	50.8	Satt673	131	13	111.89	Satt554	183	18	57.32	Satt564
28	3	70.6	Satt549	80	9	50.94	Satt617	132	13	116.91	Satt657	184	18	59.83	Satt504
29	4	24.11	Satt396	81	9	54.97	Satt559	133	13	119.19	Satt522	185	18	61.42	Sat_260
30	4	90.11	Sat_311	82	9	56.62	Satt273	134	13	124.88	<i>AW756935</i>	186	18	63.28	Satt400
31	4	92.99	Sct_191	83	9	58.01	Sat_044	135	13	130.64	Sat_090	187	18	66.55	Satt012
32	4	94.62	Sat_235	84	9	61.67	Sat_043	136	14	12.56	Sat_264	188	18	68.67	Sat_164
33	4	122.63	<i>AI794821</i>	85	9	78.68	Satt475	137	14	51.45	Sct_034	189	18	69.87	Satt517
34	4	123.79	Satt338	86	9	80.12	Satt260	138	14	56.96	Satt416	190	18	73.42	Sat_143
35	4	132.46	Satt164	87	10	42.29	Satt347	139	14	66.24	Sat_355	191	18	76.77	Satt288
36	5	19.38	Sat_344	88	10	49.71	Satt420	140	14	78.66	Sat_009	192	18	80.38	Satt612
37	5	46.45	Satt050	89	10	54.68	Satt585	141	14	90.3	<i>AW620774</i>	193	19	27.92	Satt523
38	5	52.32	Sat_407	90	10	59.43	Satt345	142	14	97.92	Satt560	194	19	29.62	Sat_405
39	5	57.79	Sat_171	91	10	63.81	Sat_282	143	15	32.1	Satt651	195	19	53.67	Sat_150
40	5	66.8	<i>SOYNOD26A</i>	92	10	67.93	Sat_341	144	15	32.27	Satt212	196	19	64.66	Satt448
41	5	69.21	Satt619	93	10	93.37	Satt331	145	15	34.2	Satt598	197	19	106.37	Satt513
42	5	78.45	Sat_267	94	10	106.03	Satt581	146	15	35.79	Satt573	198	19	115.07	Sat_245
43	5	93.23	Satt236	95	10	119.5	Satt243	147	15	39.77	Satt606	199	20	18.5	Satt571
44	6	3.15	Satt681	96	10	129.8	Sat_190	148	15	42.74	Sat_172	200	20	21.9	Satt419
45	6	30.8	Sat_062	97	11	0	<i>BE806308</i>	149	15	44.27	Satt268	201	20	31.94	Satt614
46	6	69.67	Satt305	98	11	14.32	Sat_272	150	15	44.93	Satt151	202	20	36.03	Sat_219
47	6	99.18	Sat_076	99	11	32.51	Satt509	151	15	46.65	Satt045	203	20	46.22	Satt354
48	6	107.59	Satt277	100	11	46.39	Satt197	152	15	70.23	Satt231	204	20	50.11	Satt270
49	6	115.1	Sat_142	101	11	53.41	Sat_128	153	16	11.74	Satt249	205	20	65.62	Sat_104
50	6	117.46	Sat_238	102	11	57.91	Satt519	154	16	15.69	Satt287	206	20	74.26	Sat_418
51	6	121.27	Satt307	103	11	64.91	Satt298	155	16	15.95	Satt674	207	20	92.52	Satt623
52	6	151.91	Satt357	104	11	73.77	Satt597	156	16	33.88	Satt693	208	20	98.39	Sat_420

Chr – chromosome number; Marker position in cM

Supplementary Table S2. Candidate genes for phospholipid biosynthesis annotated on SoyBase (<https://soybase.org>) within QTL regions

S.N.	Chr	Marker Interval (Physical position in bp)	QTLs Name	Candidate gene (Physical position in bp)	Encoded Enzymes
1.	2	Satt282-Satt172 (24281724-43443700)	qPC-2.1 ^{II}	Glyma.02g181300 (30974188-30982074)	Lysophosphatidic acid acyltransferase
				Glyma.02g188800 (35266321-35270969)	Phospholipase D
				Glyma.02g215100 (40116603-40118606)	Phosphatidate phosphatase
				Glyma.02g189600 (35576153-35584255)	SAM-dependent Methyltransferases
2.	2	Satt172-Sat_069 (43443481-46353789)	qPC-2.2 ^{II}	Glyma.02g249300 (43682559-43685068)	Glycerol-3-phosphate acyltransferase
				Glyma.02g250400 (43786923-43791698)	SAM- dependent Methyltransferases
				Glyma.02g263500 (44905409-44909750)	SAM- dependent Methyltransferases
				Glyma.02g295000 (47306160-47312036)	CDP-DAG synthase
3.	5	Sat_344-Satt050 (5158878-34005141)	qPA-5.1 ^{II} qPI-5.1 ^I qPI-5.1 ^{II} qPC-5.1 ^I	Glyma.05g070000 (7308307-7313710)	SAM-dependent methyltransferase
				Glyma.05g127200 (32014213-32017922)	SAM-dependent methyltransferase
4.	5	Satt619-Sat_267 (35971621-37612480)	qPI-5.2 ^I	Glyma.05g131100 (32411641-32419257)	Glycerol-3-phosphate acyltransferase
				Glyma.05g134300 (32701637-32706863)	CDP-diacylglycerol biosynthesis
				Glyma.05g164100 (35507006-35512721)	Lysophosphatidic acyltransferase
				Glyma.05g168300 (35880140-35891738)	Phospholipase D
5.	6	Satt305-Sat_076 (11336632-16007854)	qPA-6.1 ^{II}	Glyma.05g191200 (37681814-37696898)	Phosphatidylinositol synthase
				Glyma.05g221700 (40115849-40120124)	Phosphocholine cytidyltransferase
6.	6	Satt307-Satt357 (46820673-50509807)	qPE-6.1 ^{II} qPA-6.2 ^{II} qPC-6.1 ^I qPC-6.1 ^{II}	Glyma.06g154800 (12624685-12630456)	SAM- dependent methyltransferases
				Glyma.06g255600 (43638890-43639726)	Glycerol-3-phosphate acyltransferase
				Glyma.06g283400 (47132958-47137448)	SAM-dependent Methyltransferases
				Glyma.06g283600 (47144786-47149722)	SAM-dependent Methyltransferases
				Glyma.06g301100 (49013527-49014231)	SAM-dependent Methyltransferases
				Glyma.06g291200 (48005588-48006624)	DAG-TAG Synthase
				Glyma.06g291300 (48016841-48019943)	DAG and TAG synthase
Glyma.06g309300 (49782967-49789474)	Choline/ethanolamine kinase				

S.N.	Chr	Marker Interval (Physical position in bp)	QTLs Name	Candidate gene (Physical position in bp)	Encoded Enzymes
7.	7	Sat_422-Satt697 (34896625-37079608)	qPI-7.1 ^I	-----	-----
8.	8	Satt421-Satt209 (34051955-42191059)	qPA-8.1 ^I	Glyma.08g300700 (41877139-41882242) Glyma.08g309200 (42818069-42821065) Glyma.08g325300 (44333579-44336247)	SAM-dependent Methyltransferases Glycerol-3-phosphate acyltransferase Phospholipase D
9.	9	Satt337-Satt673 (21181211-33969806)	qPA-9.1 ^{II}	Glyma.09g113300 (23022119-23022442) Glyma.09g115800 (25250447-25256732) Glyma.09g119200 (28544565-28555723)	Phosphatidate cytidyltransferase Phosphatidate phosphatase Glycerol-3-phosphate acyltransferase
10.	9	Satt617-Satt559 (34441819-37762947)	qPE-9.1 ^I qPA-9.1 ^I	Glyma.09g144200 (35794124-35801051)	SAM- dependent methyltransferases
11.	10	Sat_341-Satt331 (38715763-44031226)	qPE-10.1 ^I qPE-10.1 ^{II} qPA-10.1 ^I qPA-10.1 ^{II} qPI-10.1 ^I qPI-10.1 ^{II} qPC-10.1 ^I qPC-10.1 ^{II}	Glyma.10g150200 (38559852-38564099) Glyma.10g178600 (41181744-41185579) Glyma.10g181400 (41487272-41492543) Glyma.10g183200 (41621187-41628008) Glyma.10g200500 (43127338-43129956) Glyma.10g221200 (45255043-45261362) Glyma.10g268300 (49080298-49087091)	Phospholipase D SAM-dependent Methyltransferases SAM-dependent Methyltransferases CDP-DAG Synthase Kinase and Cytidyltransferase family Protein Choline/ethanolamine kinase Phosphatidylserine synthase
12.	11	BE806308-Sat_272 (199131-2719123)	qPE-11.1 ^{II}	-----	-----
13.	11	Satt197-Sat_128 (8898878-10011521)	qPC-11.1 ^{II}	Glyma.11g120600 (9200478-9204544) Glyma.11g121200 (9252726-9255419)	Lysophosphatidic acyltransferase SAM-dependent methyltransferases
14.	11	Sat_128-Satt519 (10011307-13984515)	qPE-11.2 ^{II} qPI-11.1 ^{II} qPC-11.1 ^I qPC-11.2 ^{II}	Glyma.11g150800 (11842709-11846206) Glyma.11g161400 (14879180-14885665)	SAM-dependent methyltransferases Phosphocholine/ Ethanolamine cytidyltransferase
15.	12	Satt253-Sat_158 (25888292-33865980)	qPI-12.1 ^{II}	Glyma.12g161600 (30282037-30283669) Glyma.12g163500 (31643018-31654015) Glyma.12g177300 (33594800-33605403)	Phosphatidylinositol synthase Glycerol-3-phosphate acyltransferase CDP-DAG Synthase
16.	12	Sat_158-Satt302 (33865805-35083099)	qPA-12.1 ^I qPA-12.1 ^{II}	-----	-----

S.N.	Chr	Marker Interval (Physical position in bp)	QTLs Name	Candidate gene (Physical position in bp)	Encoded Enzymes
17.	13	Satt325-Sat_387 (8587948-11102091)	qPE-13.1 ^I qPE-13.1 ^{II} qPA-13.1 ^I qPA-13.1 ^{II} qPI-13.1 ^I qPI-13.1 ^{II} qPC-13.1 ^I qPC-13.1 ^{II}	Glyma.13g035300 (10955343-10962062)	SAM- dependent Methyltransferases
18.	13	Sat_229-Satt510 (28912864-31802559)	qPE-13.1 ^I qPE-13.1 ^{II} qPA-13.1 ^I qPA-13.1 ^{II} qPI-13.1 ^I qPI-13.1 ^{II} qPC-13.1 ^I qPC-13.1 ^{II}	Glyma.13g134500 (24696109-24705068) Glyma.13g137800 (25048422-25053352) Glyma.13g189900 (30337066-30343138) Glyma.13g323400 (41791841-41798858)	Phosphatidate phosphatase Phosphatidate phosphatase Choline/ethanolamine kinase Phosphatidate cytidyltransferase
19.	15	Satt598-Satt573 (13653981-16632923)	qPE-15.1 ^I qPC-15.1 ^I	Glyma.15g152100 (12613312-12626308) Glyma.15g157500 (13208021-13213532) Glyma.15g157700 (13215542-13218745) Glyma.15g184600 (18484786-18485815)	Phospholipase D Phosphocholine cytidyltransferase SAM- dependent methyltransferases SAM- dependent methyltransferases
20.	16	Satt674-Satt693 (1559992-6325780)	qPA-16.1 ^I qPA-16.1 ^{II}	Glyma.16g051200 (4908821-4920565) Glyma.16g051300 (4923435-4935752)	DAG synthase DAG synthase
21.	17	Satt389-Satt226 (13771477-26354928)	qPE-17.1 ^I	Glyma.17g152700 (12736004-12742355)	SAM- dependent methyltransferases
22.	18	Satt394-Satt303 (11427068-21906282)	qPE-18.1 ^I qPC-18.1 ^I	Glyma.18g119600 (14861975-14867035)	SAM- dependent methyltransferases
23.	19	Satt448-satt513 (42119600-49223661)	qPC-19.1 ^I	Glyma.19g165700 (42686038-42691597) Glyma.19g165700 (42686038-42691597) Glyma.19g175600 (43561808-43569019) Glyma.19g204500 (46069891-46075375) Glyma.19g218100 (47082133-47085750) Glyma.19g233400 (48321642-48325912)	SAM- dependent methyltransferases SAM- dependent methyltransferases Phosphatidate phosphatase Phosphatidate phosphatase Glycerol-3-phosphate acyltransferase DAG and TAG synthase

Chr – Chromosome Number