

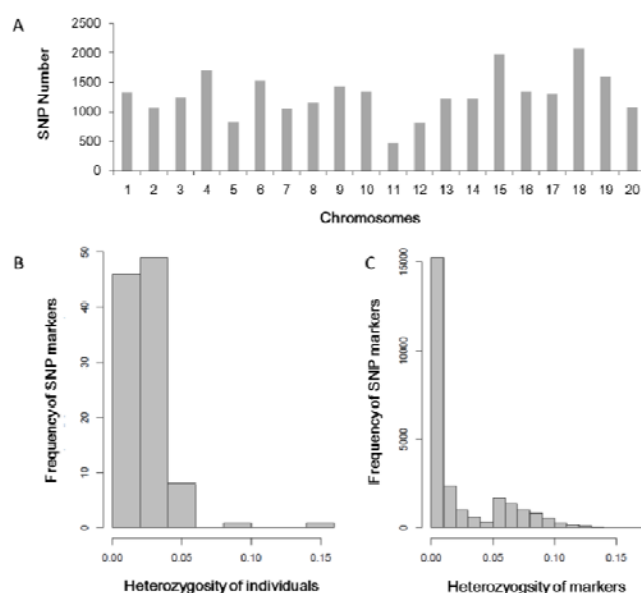
**Appendix A** Phenotypic variations in hexanol content in seeds of various soybean accessions.

**Appendix B** Source and phenotype data of 105 soybean accessions.

Name	Country	Latitude (°N)	Longitude (°W)	Hexanol content		
				Harbin(ng.ml-1)	Shenyang (ng.ml-1)	Gongzhuling (ng.ml-1)
SN1	China	48.29	128.08	91.46	149.00	49.70
DN1068	China	48.29	128.08	600.05	1060.64	143.42
Datenhei	China	39.19	116.285	347.29	371.54	178.59
Z20	China	40.145	116.275	756.26	947.19	240.05
Ken22	China	48.29	128.08	870.68	876.49	287.60
L-9	America	41.83	92.905	699.23	280.83	307.63
TF8	China	40.845	121.995	610.10	699.24	353.61
Heimodou	China	43.35	126.285	644.09	534.53	355.07
B1484	China	48.29	128.08	1076.16	1381.82	358.68
HYoutai	China	43.35	126.285	1713.37	507.18	401.55
H04-1824	China	48.29	128.08	638.64	2635.31	421.85
DN43	China	48.29	128.08	1043.63	2730.03	427.37
K29	China	48.29	128.08	139.41	26.49	140.35
Douludou	China	43.35	126.285	707.23	3516.83	440.56
KJ23	China	48.29	128.08	212.01	1149.87	446.27
ZZ00-683	China	40.145	116.275	367.11	1316.18	451.45
S29	China	48.29	128.08	739.93	729.53	451.70
NF11	China	48.29	128.08	412.72	904.41	460.39
Z95-5388	China	40.145	116.275	421.98	1359.25	548.77
DY2004-5	China	43.35	126.285	567.99	653.32	575.62
JD33	China	40.845	121.995	1057.21	2009.51	576.65
DN46	China	48.29	128.08	820.91	3821.75	581.58
B4834	China	48.29	128.08	207.72	702.50	583.59
HF37	China	48.29	128.08	1924.43	523.19	586.62
HF45	China	48.29	128.08	3082.00	994.11	587.82
HF50	China	48.29	128.08	724.70	788.47	594.43
Ken14	China	48.29	128.08	2152.34	966.70	604.09
4five-star	China	39.19	116.285	623.18	678.28	618.98

S30	China	48.29	128.08	769.09	1532.59	624.29
SN8	China	48.29	128.08	2994.66	1166.70	627.02
Yapiche	China	48.29	128.08	1653.80	569.61	643.76
B1361	China	48.29	128.08	1622.53	684.68	651.05
Jshanmoshi	China	43.35	126.285	320.02	1248.92	651.05
Big black	China	36.225	118.31	591.50	1382.53	665.93
J89	China	43.35	126.285	284.62	725.64	690.33
Cse	China	43.35	126.285	846.84	654.89	696.63
Harvest10	China	48.29	128.08	407.93	1382.25	703.96
Z30	China	40.145	116.275	672.56	547.47	708.82
HN51	China	48.29	128.08	868.66	980.02	714.81
JN21	China	43.35	126.285	905.26	866.53	714.81
DN48	China	48.29	128.08	291.76	1637.46	715.07
DN49	China	48.29	128.08	552.88	865.79	716.39
ZD35	China	40.145	116.275	489.52	550.47	727.71
KB1	China	48.29	128.08	604.03	1096.28	738.07
Sui20	China	48.29	128.08	306.94	1693.07	739.05
Z03-5179	China	40.145	116.275	965.35	2130.38	743.37
Z03-5334	China	40.145	116.275	902.38	2189.48	760.15
L-28	Canada	43.4	79.25	696.43	1099.15	766.36
JD17	China	39.19	116.285	1100.00	585.90	770.35
DN L-13	Canada	43.4	79.25	1069.94	711.22	772.92
HH18	China	48.29	128.08	877.38	2273.63	774.47
SN10	China	48.29	128.08	994.63	157.34	783.32
HF11	China	48.29	128.08	818.55	692.74	787.49
Nova	Italy	41.54	12.3	486.57	1002.53	788.40
Tiefeng31	China	40.845	121.995	703.96	958.48	805.02
LP03-11	China	48.29	128.08	315.69	1617.29	808.33
S03-3952	China	48.29	128.08	913.92	3309.56	832.04
JL47	China	43.35	126.285	370.45	1457.42	838.05
HN55	China	48.29	128.08	497.82	1075.40	845.81
Fenshou6	China	48.29	128.08	1326.43	969.62	855.67
L-57	America	41.83	92.905	938.46	454.80	871.82
S03-3046	China	48.29	128.08	710.29	786.71	888.02
L-10	America	41.83	92.905	1414.94	706.17	905.14
B1873	China	48.29	128.08	598.53	736.58	911.56
TD50	China	40.845	121.995	609.87	1215.59	921.66
ZD27	China	40.145	116.275	788.54	539.35	955.83
Domaka Tolisa	Yugoslavia	46.3	14.3	254.25	1043.90	962.42
Tejia	China	40.845	121.995	551.43	558.70	964.77
Ken18	China	48.29	128.08	781.09	530.19	985.27
HuaJiang4403	China	48.29	128.08	1177.83	448.97	1014.25
BD16	China	48.29	128.08	1506.33	606.20	1014.88
HF47	China	48.29	128.08	621.75	876.28	1041.85
K04-8579	China	48.29	128.08	752.30	721.26	1068.95
HH48	China	48.29	128.08	1202.12	2817.43	1122.54
L98072	China	40.845	121.995	704.05	624.09	1126.99
Suinong4	China	48.29	128.08	935.25	780.43	1136.26
S05-7304	China	48.29	128.08	1049.10	571.65	1142.03

HN44	China	48.29	128.08	211.44	692.55	1166.97
HF35	China	48.29	128.08	693.57	1741.13	1172.21
Xian3	China	48.29	128.08	3562.82	1943.44	1173.69
DN594	China	48.29	128.08	2320.70	1117.61	1176.76
Heinong33	China	48.29	128.08	816.49	1372.17	1182.43
LD3	China	40.845	121.995	763.39	1047.59	1185.40
Stone	China	39.19	116.285	811.80	4257.93	1204.28
Hujiao03-286	China	48.29	128.08	971.60	511.09	1211.53
TD52	China	40.845	121.995	349.34	431.85	1235.10
K30	China	48.29	128.08	1733.48	2839.24	1241.97
HN48	China	48.29	128.08	1127.69	1262.61	1298.44
DN07-909	China	48.29	128.08	471.14	1325.94	1309.53
DN42	China	48.29	128.08	984.39	518.41	1317.61
Aika166	Rumania	44.23	26.1	487.08	2024.91	1344.43
LD23	China	40.845	121.995	958.15	269.96	1376.00
BF9	China	48.29	128.08	885.39	1678.48	1422.89
Xian2	China	48.29	128.08	1158.01	627.60	1469.67
MF1	China	48.29	128.08	965.16	1887.81	1612.32
Heersong2	Ukraine	50.28	30.29	525.91	530.82	1652.77
HF55	China	48.29	128.08	2110.56	537.06	1661.36
HF25	China	48.29	128.08	744.42	607.73	1865.66
JN20	China	43.35	126.285	739.75	1030.08	1978.70
Small yellow	China	37.385	112.235	679.94	2258.11	2034.93
JY94	China	43.35	126.285	517.39	749.69	2202.16
MD14	China	44.49	111.695	1167.79	1336.90	2472.17
HF29	China	48.29	128.08	3569.55	671.95	3177.13
LongX1	China	48.29	128.08	118.95	979.08	3487.88
L-21	America	41.83	92.905	658.50	562.38	4959.26



**Appendix C Genotyping information of 105 accessions.** (A) SNP distribution across 20 soybean chromosomes. (B) Heterozygosity statistics of the individuals in the association panel. (C) The heterozygosity statistics of SNP markers.

Appendix D Peak SNP and beneficial allele associated with hexanol content in soybean seed

## identified by GWAS

Peak SNP	Chromosome	Position	$-\log_{10}(P)$	MAF	$R^2$		Location	High alleles	Low alleles	Average hexanol content of popula
rs7949610	1	7949610	3.44	0.07	0.18		Shenyang	A	G	1062.94
rs7434004	2	7434004	3.37	0.06	0.18		Shenyang	C	A	1067.23
rs1635582	3	1635582	3.96	0.05	0.29		Harbin	A	C	854.54
rs7354971	4	7354971	3.96	0.07	0.29		Harbin	A	C	814.60
rs46985091	4	46985091	3.42	0.12	0.20	0.16	Shenyang Gongzhuling	C	T	1046.73
rs34810214	5	34810214	3.55	0.06	0.27		Harbin	C	A	987.96
rs37095787	6	37095787	3.67	0.07	0.20		Shenyang	C	A	1090.56
rs9050779	7	9050779	3.43	0.04	0.27		Harbin	C	G	833.80
rs7850306	8	7850306	3.86	0.19	0.29		Harbin	G	C	809.91
rs7850698	8	7850698	3.62	0.16	0.28		Harbin	T	C	797.00
rs34283785	8	34283785	3.44	0.07	0.27		Harbin	G	T	840.78
rs7850289	8	7850289	3.41	0.16	0.27	0.17	Harbin Shenyang	A	G	968.23
rs5956376	10	5956376	4.09	0.04	0.26		Gongzhuling	A	G	912.94
rs21274416	10	21274416	3.56	0.05	0.19		Shenyang	A	C	1059.21
rs39423632	10	39423632	3.39	0.10	0.17	0.20	Shenyang Gongzhuling	A	C	1016.07
rs30339809	12	30339809	4.73	0.06	0.29		Gongzhuling	A	C	874.96
rs16906415	13	16906415	4.24	0.04	0.23		Shenyang	G	T	1070.26
rs20179963	16	20179963	3.55	0.05	0.23		Gongzhuling	G	T	902.14
rs31452203	16	31452203	3.36	0.47	0.18	0.20	Shenyang Gongzhuling	A	G	936.39
rs26461853	17	26461853	3.45	0.05	0.19		Shenyang	T	G	1065.15
rs6997906	18	6997906	5.29	0.09	0.36		Harbin	A	C	798.35
rs45823655	18	45823655	4.17	0.06	0.23		Shenyang	T	C	1038.53
rs39204566	19	39204566	3.39	0.06	0.27		Harbin	C	A	836.17
rs39007334	19	39007334	4.16	0.05	0.26		Gongzhuling	A	G	900.58
rs34553027	19	34553027	3.41	0.06	0.18		Shenyang	G	A	1078.47

## Appendix E Gene models in the flanking regions of four stable QTNs.

Chr.	Peak SNP	position	Gene model	Start	End	Functional annotation
			Glyma.04G197300	46933093	46935391	Heavy metal transport/detoxification superfamily protein
			Glyma.04G197400	46949919	46952545	fatty acyl-ACP thioesterases B
			Glyma.04G197500	46955006	46958396	fatty acyl-ACP thioesterases B
			Glyma.04G197600	46972049	46973585	HVA22 homologue E
4	rs46985091	46985091	Glyma.04G197900	46997022	47003489	DEK domain-containing chromatin associated protein
			Glyma.04G198000	47006819	47010367	HXXXD-type acyl-transferase family protein
			Glyma.04G198100	47015967	47016915	SAUR-like auxin-responsive protein family
			Glyma.04G198200	47040135	47043213	tapetum determinant 1
			Glyma.04G198400	47063998	47066834	Nodulin MtN3 family protein
			Glyma.04G198500	47074408	47077440	Nodulin MtN3 family protein
8	rs7850289	7850289	Glyma.08G101000	7754858	7756331	HXXXD-type acyl-transferase family protein
			Glyma.08G101100	7762803	7770986	SRP72 RNA-binding domain
			Glyma.08G101200	7777648	7781453	Ribonuclease inhibitor
			Glyma.08G101300	7783123	7787744	myo-inositol oxygenase 4
			Glyma.08G101400	7786430	7788380	Restriction endonuclease, type II-like superfamily protein
			Glyma.08G101500	7801199	7808033	multidrug resistance-associated protein 3
			Glyma.08G101700	7809420	7812331	multidrug resistance-associated protein 14
			Glyma.08G101800	7815034	7818607	Ankyrin repeat family protein

			Glyma.08G101900	7820506	7822709	lysine histidine transporter 1
			Glyma.08G102000	7828786	7831334	Cation efflux family protein
			Glyma.08G102100	7832596	7835793	NAD(P)-binding Rossmann-fold superfamily protein
			Glyma.08G102300	7852398	7860539	DEAD/DEAH box RNA helicase family protein
			Glyma.08G102400	7861186	7864074	Acid phosphatase/vanadium-dependent haloperoxidase-related protein
			Glyma.08G102500	7867338	7870782	Remorin family protein
			Glyma.08G102600	7873501	7880615	Protein kinase superfamily protein
			Glyma.08G102700	7881635	7885788	Protein of unknown function (DUF3537)
			Glyma.08G102900	7886865	7892029	PLAT/LH2 domain-containing lipoxygenase family protein
			Glyma.08G103000	7893965	7899813	urease
			Glyma.08G103100	7902820	7907892	ARM repeat superfamily protein
			Glyma.08G103200	7918306	7932242	glucosidase 1
			Glyma.08G103300	7934866	7944355	Zn-dependent exopeptidases superfamily protein
			Glyma.08G103400	7945667	7949720	Galactose oxidase/kelch repeat superfamily protein
			Glyma.10G159300	39341911	39347622	Nucleolar histone methyltransferase-related protein
			Glyma.10G159400	39348892	39350723	Seed maturation protein
			Glyma.10G159500	39351821	39383657	ARM repeat superfamily protein
			Glyma.10G159600	39390360	39392641	HXXXD-type acyl-transferase family protein
			Glyma.10G159700	39402685	39409102	cysteine synthase D1
			Glyma.10G159800	39411242	39416676	cysteine synthase D1
			Glyma.10G159900	39419546	39422127	exoribonuclease 4
			Glyma.10G160000	39422646	39424482	DNA-binding storekeeper protein-related transcriptional regulator
10	rs39423632	39423632	Glyma.10G160100	39434399	39435558	DNA-binding storekeeper protein-related transcriptional regulator
			Glyma.10G160200	39436452	39439106	Cytidine/deoxycytidylate deaminase family protein
			Glyma.10G160300	39440769	39442935	Ribosomal protein S24e family protein
			Glyma.10G160400	39451122	39454920	with no lysine (K) kinase 1
			Glyma.10G160500	39484183	39489346	zeta-carotene desaturase
			Glyma.10G160600	39489751	39493062	Uncharacterized conserved protein (DUF2358)
			Glyma.10G160700	39494523	39495680	Plant protein of unknown function (DUF868)
			Glyma.10G160800	39497701	39498093	Calcium-binding EF hand family protein
			Glyma.10G160900	39514267	39516118	Plant protein of unknown function (DUF868)
			Glyma.10G161000	39522164	39526626	N-MYC downregulated-like 1
16	rs31452203	31452203	Glyma.16G152900	31358542	31362310	ARM repeat superfamily protein
			Glyma.16G153000	31363737	31366379	NDH-dependent cyclic electron flow 5
			Glyma.16G153100	31368331	31370455	Transducin family protein / WD-40 repeat family protein
			Glyma.16G153200	31375013	31381634	TCP-1/cpn60 chaperonin family protein
			Glyma.16G153300	31387861	31392064	UTP:galactose-1-phosphate uridylyltransferases; ribose-5-phosphate adenylyltransferases
			Glyma.16G153400	31393061	31398041	glutamate dehydrogenase 1
			Glyma.16G153600	31420465	31421069	arabinogalactan protein 14
			Glyma.16G153800	31441158	31444423	novel cap-binding protein
			Glyma.16G153900	31445530	31449234	copper/zinc superoxide dismutase 3
			Glyma.16G154000	31450077	31455500	tubulin alpha-3
			Glyma.16G154100	31458458	31459539	related to AP2 11
			Glyma.16G154200	31463230	31469750	syntaxin of plants 131
			Glyma.16G154300	31472047	31475600	shikimate kinase like 1
			Glyma.16G154400	31477476	31484052	GC-rich sequence DNA-binding factor-like protein with Tufelin interacting domain

Glyma.16G154600	31484987	31489298	fucosyltransferase 13
Glyma.16G154700	31491889	31496125	Tryptophan/tyrosine permease
Glyma.16G155000	31513389	31517035	plasma membrane intrinsic protein 2
Glyma.16G155100	31522889	31524889	plasma membrane intrinsic protein 2
Glyma.16G155200	31533926	31545061	Pleckstrin homology (PH) and lipid-binding START domains-containing protein

## Appendix F Gene-based association study on hexanol content of soybean with 71 candidate genes

Marker	Chromosome	Location	P value	Gene	Variation region	Position
Gm04-46999425	4	Shenyang	3.71E-03	Glyma.04G197900	intronic	46999425
		Gongzhuling	0.003164			
		Harbin	0.004206			
Gm04-46952822	4	Shenyang	6.11E-04	Glyma.04G197400	intronic	46952822
		Gongzhuling	0.003016			
		Harbin	0.00321			
Gm04-46955929	4	Shenyang	0.005211	Glyma.04G197500	intronic	46955929
		Gongzhuling	0.005692			
		Harbin	0.006357			
Gm10-39346715	10	Shenyang	9.18E-06	Glyma.10G159300	intronic	39346715
		Gongzhuling	3.82E-04			
		Harbin	0.00321			
Gm16-31361247	16	Shenyang	1.14E-05	Glyma.16G152900	intronic	31361247
		Gongzhuling	1.67E-04			
		Harbin	0.001497			
Gm16-31391214	16	Shenyang	9.17E-05	Glyma.16G153300	intronic	31391214
		Gongzhuling	4.32E-04			
		Harbin	0.003016			