

Table 1. Classification, available accessions, ploidy level, accessions evaluated and their geographic origin.

Species - Spooner Classification [2]	Species - Old Classification	Number of Accessions Available from GRIN	Ploidy Level	Number of Accessions Tested	PI Number Tested	Origin
<i>S. stipuloideum</i>	<i>S. circaeifolium</i>	14	2X	3	498116	Cochabamba, Bolivia
					498120	Santa Cruz, Bolivia
					545974	La Paz, Bolivia
<i>S. chacoense</i>	<i>S. chacoense</i> subsp. <i>chacoense</i>	174	2X	2	197760	?
					320293	Salta, Argentina
<i>S. candolleanum</i>	<i>S. bukasovii</i>	176	2X	3	265863	Puno, Peru
					365321	Huanuco, Peru
					458379	Apurimac, Peru
<i>S. acaule</i>	<i>S. acaule</i> f. <i>acaule</i>	424	4X	3	175395, 472661	Argentina
					473481	Huancavelica, Peru
<i>S. demissum</i>	-	164	6X	3	160208	Mexico
					230589	Huanuco, Peru
					498232	Apurimac, Peru
<i>S. microdontum</i>	<i>S. microdontum</i> subsp. <i>microdontum</i>	116	2X	2	458355	Jujuy, Argentina
					498123	Chuquisaca, Bolivia
<i>S. okadae</i>	<i>S. venturii</i>	16	2X	1	458368	Salta, Argentina
	-		2X	2	498130	Cochabamba, Bolivia
	-				320327	Salta, Argentina
<i>S. tuberosum</i> subsp. <i>andigenum</i>	<i>S. stenotomum</i> subsp. <i>stenotomum</i>	1006	2X	2	195204	Cuzco, Peru
					283141	Colombia
	<i>S. phureja</i> subsp. <i>phureja</i>		2X	3	320355, 320377	Narino, Colombia
					225710	Cauca, Colombia
	-		4X	3	546023	Potosi, Bolivia
	-				607886	Cuzco, Peru
-			281034	Mexico		

Table 1. Cont.

<i>S. boliviense</i>	<i>S. megistacrolobum</i>	222	2X	26	283082	Bolivia		
					283133	Ecuador		
					275149, 435077, 500029	Salta, Argentina		
					500030			
					458347, 458348, 473110, 473112, 473113, 473124, 473129, 473130,	Jujuy, Argentina		
					473138, 473141, 473144, 473149, 473160, 558094			
					545899, 568986			
					597689	Tarija, Bolivia		
					597705, 597706, 597736	Oruro, Bolivia		
						Potosi, Bolivia		
<i>S. vernei</i>	<i>S. vernei subsp. vernei</i>	36	2X	18	320332	Catamarca, Argentina		
					230468, 458373, 473308	Tucuman, Argentina		
					458374, 473306, 473310, 473311, 500045, 500062, 500063, 500065,	Salta, Argentina		
					558147, 558148			
					500067, 500069, 558149, 558150	Jujuy, Argentina		
	<i>S. vernei subsp. ballsii</i>				2X	5	458369, 473303	Jujuy, Argentina
							458370, 458371, 458372	Salta, Argentina
-	2X	1	500066	Jujuy, Argentina				

Table 2. Folate Concentration (Mean \pm SE) in ng g⁻¹ dry matter per accession. In bold are individuals with folate concentrations higher than 1500 ng g⁻¹ dry weight.

Plant Introduction Number	Species	Number of Individuals Tested	Individual Measurements	Mean \pm SE	%DM
R. Burbank	<i>S. tuberosum</i> subsp. <i>tuberosum</i>	3	1276-915-929	1040 \pm 118	26
498116	<i>S. stipuloideum</i>	3	907-1115-1118	1046 \pm 57	25
498120	<i>S. stipuloideum</i>	3	304-553-532	463 \pm 65	25
545974	<i>S. stipuloideum</i>	4	415-824-1119-882	810 \pm 127	23
197760	<i>S. chacoense</i>	3	591-653-653	632 \pm 17	36
320293	<i>S. chacoense</i>	4	478-240-1198-408	581 \pm 183	37
265863	<i>S. candolleanum</i>	3	1367-508-481	786 \pm 206	25
365321	<i>S. candolleanum</i>	1	918	918 \pm n.d.	19
458379	<i>S. candolleanum</i>	1	1023	1023 \pm n.d.	19
175395	<i>S. acaule</i>	4	461-562-562-1017	651 \pm 108	22
472661	<i>S. acaule</i>	4	480-490-517-1014	625 \pm 113	23
473481	<i>S. acaule</i>	2	632-757	695 \pm 44	25
160208	<i>S. demissum</i>	4	749-455-487-556	562 \pm 57	23
230589	<i>S. demissum</i>	2	410-631	520 \pm 78	22
498232	<i>S. demissum</i>	4	760-737-669-455	655 \pm 60	30
458355	<i>S. microdontum</i>	3	703-694-650	682 \pm 13	32
498123	<i>S. microdontum</i>	2	913-767	840 \pm 51	36
320327	<i>S. okadae</i>	3	876-548-629	684 \pm 80	35
458368	<i>S. okadae</i>	3	611-1317-991	973 \pm 167	34
498130	<i>S. okadae</i>	3	723-660-806	730 \pm 34	38
195204	<i>S. tuberosum</i> subsp. <i>andigenum</i>	4	410-836-499-794	635 \pm 92	24
225710	<i>S. tuberosum</i> subsp. <i>andigenum</i>	1	2337	2337 \pm n.d.	22
281034	<i>S. tuberosum</i> subsp. <i>andigenum</i>	4	565-1030-1126-506	807 \pm 137	18
283141	<i>S. tuberosum</i> subsp. <i>andigenum</i>	3	468-457-711	545 \pm 68	18
320355	<i>S. tuberosum</i> subsp. <i>andigenum</i>	2	853-1400	1126 \pm 193	28
320377	<i>S. tuberosum</i> subsp. <i>andigenum</i>	2	2198 -1038	1618 \pm 410	17
546023	<i>S. tuberosum</i> subsp. <i>andigenum</i>	4	985-700-333-626	661 \pm 116	21
607886	<i>S. tuberosum</i> subsp. <i>andigenum</i>	4	404-553-622-361	485 \pm 53	21
275149	<i>S. boliviense</i>	4	566-561-602-515	561 \pm 15	24
283082	<i>S. boliviense</i>	1	934	934 \pm n.d.	23
283133	<i>S. boliviense</i>	4	891-1102-1097-351	860 \pm 153	27
435077	<i>S. boliviense</i>	3	421-652-630	568 \pm 60	26
458347	<i>S. boliviense</i>	3	779-1393-525	899 \pm 210	21
458348	<i>S. boliviense</i>	4	585-759-666-679	672 \pm 31	23
473110	<i>S. boliviense</i>	4	362-456-651-611	520 \pm 58	18
473112	<i>S. boliviense</i>	4	517-897-450-688	638 \pm 87	20
473113	<i>S. boliviense</i>	1	869	869 \pm n.d.	20
473124	<i>S. boliviense</i>	4	630-547-456-610	561 \pm 34	20
473129	<i>S. boliviense</i>	4	816-997-722-584	780 \pm 75	21
473130	<i>S. boliviense</i>	4	411-526-512-751	550 \pm 62	24

473138	<i>S. boliviense</i>	4	1265-787-512-745	827 ± 137	21
473141	<i>S. boliviense</i>	4	460-524-630-385	500 ± 45	23
473144	<i>S. boliviense</i>	4	473-355-222-449	375 ± 49	22
473149	<i>S. boliviense</i>	4	628-523-826-780	689 ± 60	24
473160	<i>S. boliviense</i>	4	557-352-706-347	491 ± 75	22
500029	<i>S. boliviense</i>	4	684-461-610-622	594 ± 41	26
500030	<i>S. boliviense</i>	4	541-494-575-671	634 ± 32	24
545899	<i>S. boliviense</i>	4	647-426-1033-780	721 ± 110	22
558094	<i>S. boliviense</i>	3	350-473-542	455 ± 46	21
568986	<i>S. boliviense</i>	2	684-888	786 ± 72	19
597689	<i>S. boliviense</i>	4	570-1099-723-822	804 ± 96	22
597705	<i>S. boliviense</i>	4	332-749-366-707	539 ± 95	20
597706	<i>S. boliviense</i>	4	484-567-551-623	556 ± 25	23
597736	<i>S. boliviense</i>	4	713- 1947 -539-777	994 ± 279	33
230468	<i>S. vernei</i>	4	1377-1072-1416- 1911	1444 ± 150	24
320332	<i>S. vernei</i>	4	1137-846- 1985 -1105	1268 ± 215	28
458369	<i>S. vernei</i>	2	1197-1002	1099 ± 69	22
458370	<i>S. vernei</i>	4	1207-1062-1073-817	1040 ± 70	20
458371	<i>S. vernei</i>	4	1940 -786-881- 1601	1302 ± 242	22
458372	<i>S. vernei</i>	4	1450- 1801 -1023-1110	1346 ± 154	23
458373	<i>S. vernei</i>	2	1316-1145	1230 ± 60	26
458374	<i>S. vernei</i>	4	891-838-851-908	872 ± 14	25
473303	<i>S. vernei</i>	3	1623 -1099-774	1165 ± 202	21
473306	<i>S. vernei</i>	3	1968 -1307- 1703	1659 ± 157	18
473308	<i>S. vernei</i>	1	1117	1117 ± n.d.	25
473310	<i>S. vernei</i>	3	649-973-1058	893 ± 102	21
473311	<i>S. vernei</i>	3	1589 -1309-1122	1340 ± 111	23
500045	<i>S. vernei</i>	2	1361-826	1093 ± 189	26
500062	<i>S. vernei</i>	2	1287-818	1053 ± 166	25
500063	<i>S. vernei</i>	4	469-1282-776-725	813 ± 147	22
500065	<i>S. vernei</i>	3	829-1105-835	923 ± 74	25
500066	<i>S. vernei</i>	3	1178- 1722 -1372	1424 ± 112	20
500067	<i>S. vernei</i>	4	1219-1370-961-1035	1146 ± 280	22
500069	<i>S. vernei</i>	3	970-948-1294	1070 ± 91	24
558147	<i>S. vernei</i>	2	1117-1150	1133 ± 12	23
558148	<i>S. vernei</i>	4	853-974-1312-959	1024 ± 86	26
558149	<i>S. vernei</i>	4	1268- 2211 - 1688 -1355	1630 ± 185	24
558150	<i>S. vernei</i>	2	909- 1620	1264 ± 252	22

Table 3. Folate concentrations of samples used in real time quantitative RT-PCR reactions. Folate values for *S. tuberosum* subsp. *andigenum* and *S. vernei* were previously published in Robinson et al. 2015. Data are means \pm SE from 3 or 4 technical determinations.

Sample	Folate concentration (ng/g DW)
BRR1 12	2373 \pm 29
BRR1 27	471 \pm 20
BRR3 56	326 \pm 21
BRR3 90	2952 \pm 277
Tbr 225710.3	2336 \pm n.d.
Tbr 546023.4	626 \pm 21
Vrn 558149.3	1688 \pm 18
Vrn 500063.1	469 \pm 16
Fol 1-3	1667 \pm 113
Fol 1-5	810 \pm 269
Fol 1-6	2137 \pm 473
Fol 1-11	911 \pm 67

Table 4. Ct values, $2^{\Delta C_t}$ values, and fold change in GGH1 expression in high and low folate genotypes as determined by real time quantitative RT-PCR reactions. Data are means of 4 technical determinations.

High Folate Genotype	C_t Value	Low Folate Genotype	C_t Value	High/Low 2^{-DeltaC_t}	Fold Change in GGH1 Expression
BRR1 12	31.74	BRR1 27	34.18	0.189/0.018	10
BRR3 90	40.44	BRR3 56	36.71	3.33E -05/4.53E -04	0.1
Tbr PI 225710	29.66	Tbr PI 546023	38.84	3.00E -02/1.55E -02	2
Vrn PI 558149	35.33	Vrn PI 500063	40.78	6.25E -02/1.29E -04	481
Fol 1-6	32.01	Fol 1-11	35.41	7.10E -03/4.76E -04	15
Fol 1-6	32.01	Fol 1-5	39.82	7.10E -03/8.07E -05	88
Fol 1-3	30.90	Fol 1-11	35.41	1.13E -02/4.76E -04	24
Fol 1-3	30.90	Fol 1-5	39.82	1.13E -02/8.07E -05	140

Table 5. SNP information for consensus maps used in QTL analysis. Number of SNPs from each parent are presented, along with the number of codominant markers, group length, the total number of SNPs per linkage group and marker coverage.

Linkage Group	SNPs from Parents		Number of Codominant markers	Group Length (cM)	Total SNPs per linkage group	Marker Coverage (markers/cM)
	USW4s#3	Fol 1.6				
1	59	7	2	98.177	68	1.44
2	22	15	9	124.182	46	2.69
3	51	2	3	165.488	56	2.95
4	49	4	4	140.512	57	2.40
5	29	6	4	123.679	39	1.65
6	36	6	4	113.482	46	2.67
7	24	5	10	59.681	39	2.58
8	52	0	0	126.636	52	2.43
9	48	4	2	157.314	54	3.41
10	51	1	3	113.187	55	2.05
11	58	4	6	101.767	68	1.41
12	51	8	5	107.182	64	1.67
Total	530	62	52	1431.227	644	2.22

Table 6. Top 10 SNPs in common from marker association and QTL single marker analyses.

SNP_ID	CHR	POS	R-squared trend
solcap_snp_c2_53198	chr00	29279410	0.114572486
solcap_snp_c2_48372	chr03	39255217	0.105971323
solcap_snp_c2_48371	chr03	39255236	0.105971323
solcap_snp_c2_48369	chr03	39257162	0.105971323
solcap_snp_c2_35234	chr03	40992986	0.105971323
solcap_snp_c1_6875	chr03	41994529	0.103532909
solcap_snp_c2_10688	chr04	71592216	0.108221677
solcap_snp_c2_28223	chr07	51604961	0.10388895
solcap_snp_c2_18680	chr07	55283766	0.114219648
solcap_snp_c2_48597	chr09	778420	0.109861634

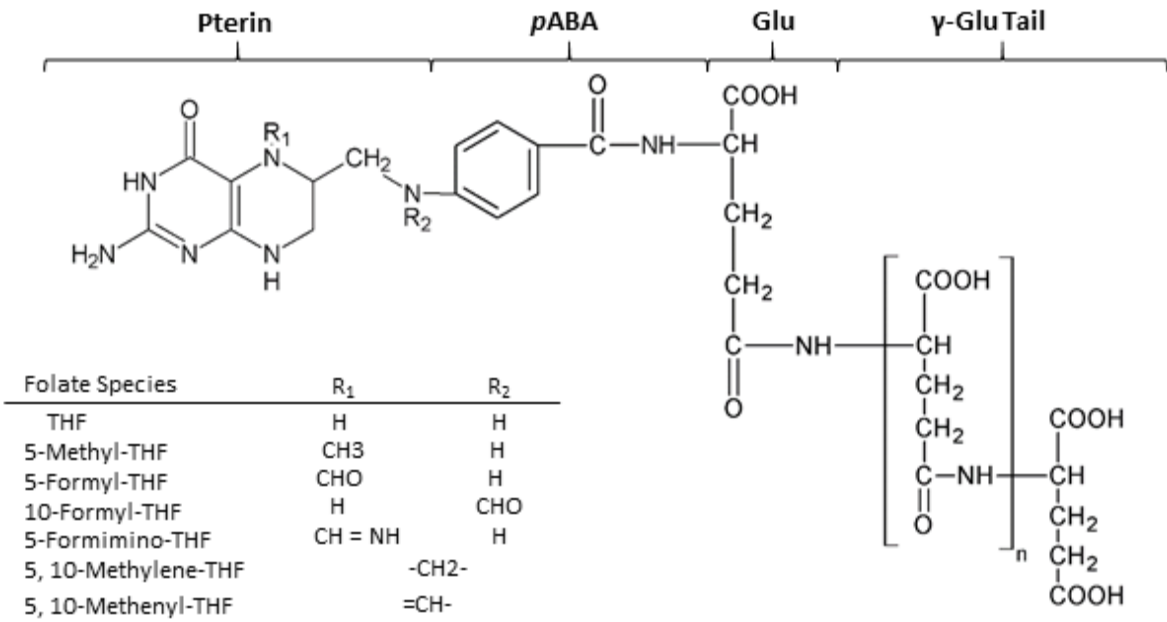


Figure 1. Structure of folates. Folates are made of a pterin, *p*-aminobenzoate, and glutamate residue. A gamma-linked polyglutamate tail of up to eight residues is attached to the first glutamate.

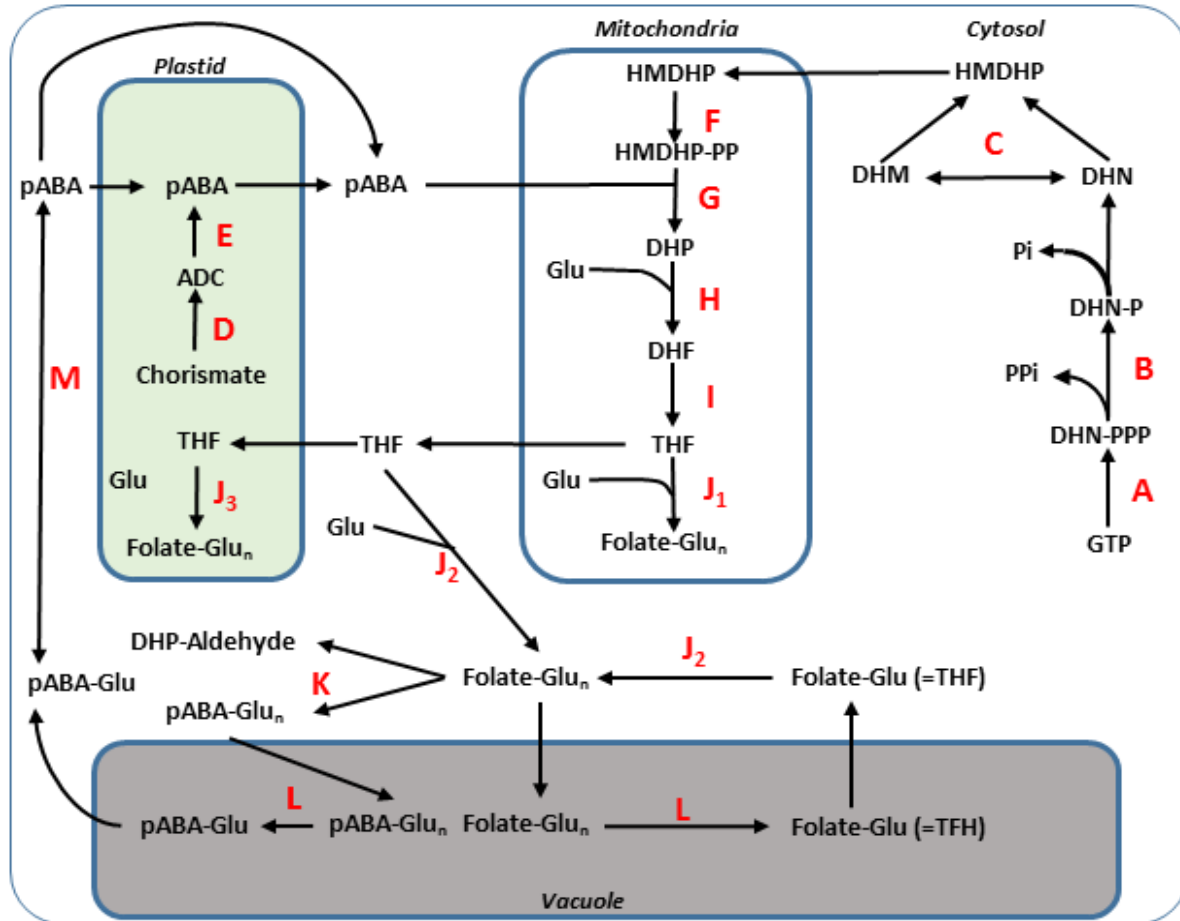


Figure 2. Folate biosynthesis pathway in plants. Enzymes involved in folate biosynthesis are listed by letter. A. GTP cyclohydrolase 1, B. DHN-PPP diphosphatase, C. DHN aldolase, D. ADC synthase, E. ADC lyase, F. HMDHP pyrophosphokinase, G. Dihydropteroate synthase, H. Dihydrofolate synthase, I. Dihydrofolate reductase, J_{1,2,3}. Folylpolyglutamate synthase. K. Oxidative degradation. L. Gamma Glutamyl Hydrolase 1. M. *p*ABA-glu Hydrolase or UDP-glucose *p*ABA glycosyl transferase. Abbreviations for chemical species follow: *p*ABA, para-aminobenzoate; ADC, aminodeoxychorismate; HMDHP, hydroxylmethyldihydropterin; DHP, dihydropteroate; DHF, dihydrofolate; THF, tetrahydrofolate; DHM, dihydromonapterin; DHN, dihydroneopterin.

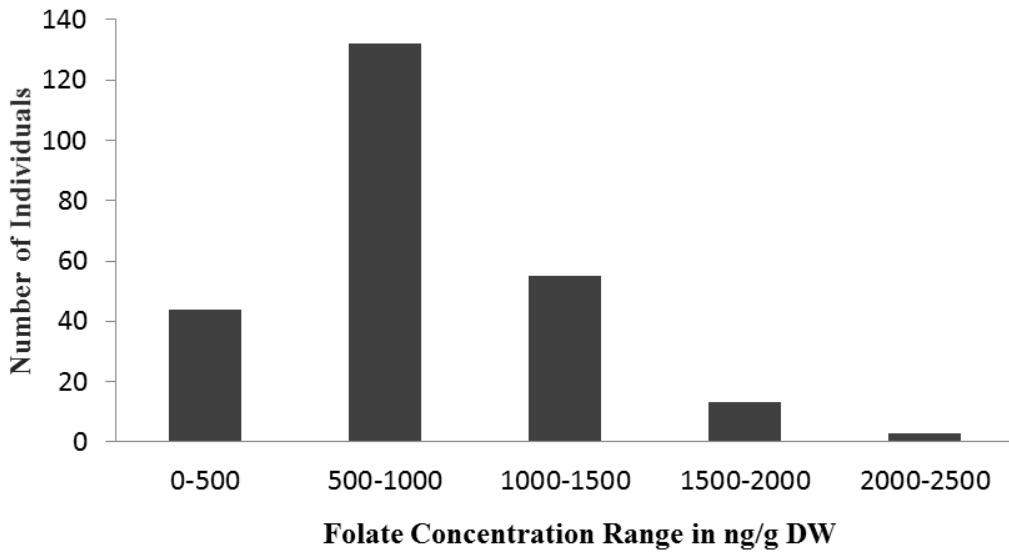


Figure 3. Histogram of number of individuals within folate concentrations brackets.

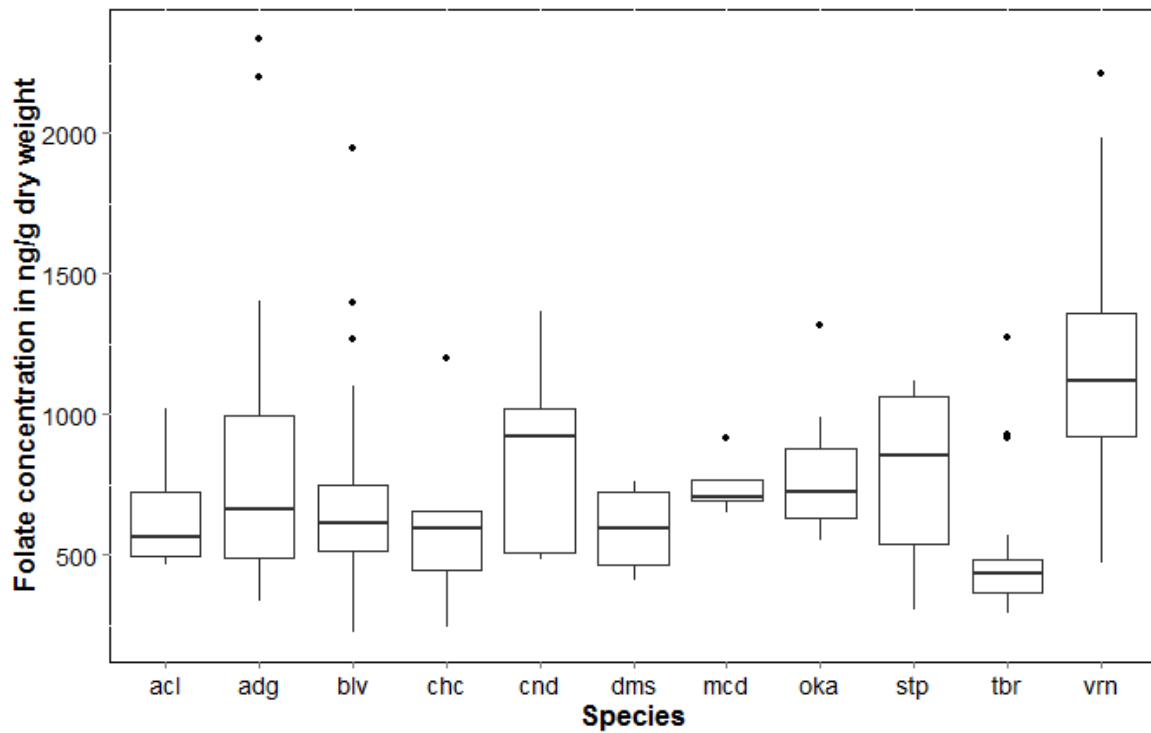


Figure 4. Box and whisker plot of folate concentrations by species. acl, *S. acaule*; adg, *S. tuberosum* subsp. *andigenum*; blv, *S. boliviense*; chc, *S. chacoense* subsp. *chacoense*; cnd, *S. candolleianum*; dms, *S. demissum*; mcd, *S. microdontum*; oka, *S. okadae*; stp, *S. stipuloideum*; tbr, *S. tuberosum*; vrn, *S. vernei*. For *S. tuberosum*, data for two varieties, Russet Burbank and Yukon Gold, each in three biological replicates, were used.

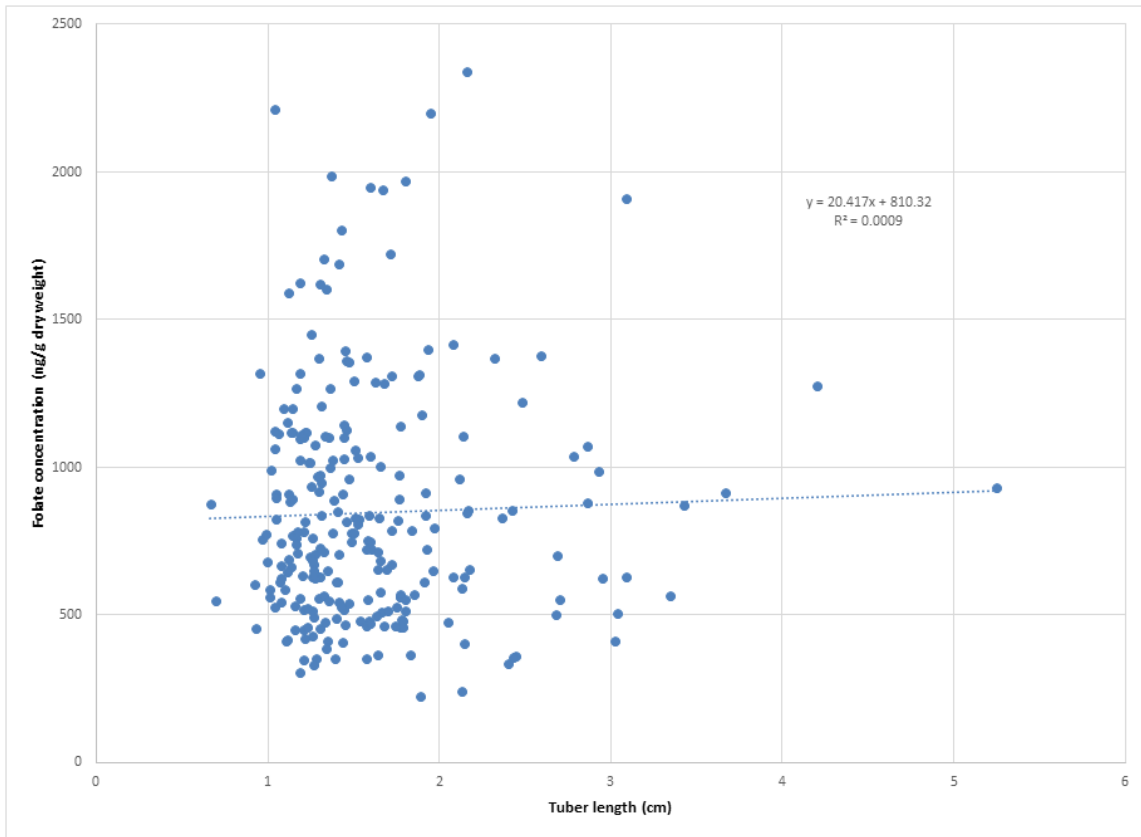


Figure 5. Relationship between folate concentration and tuber length.

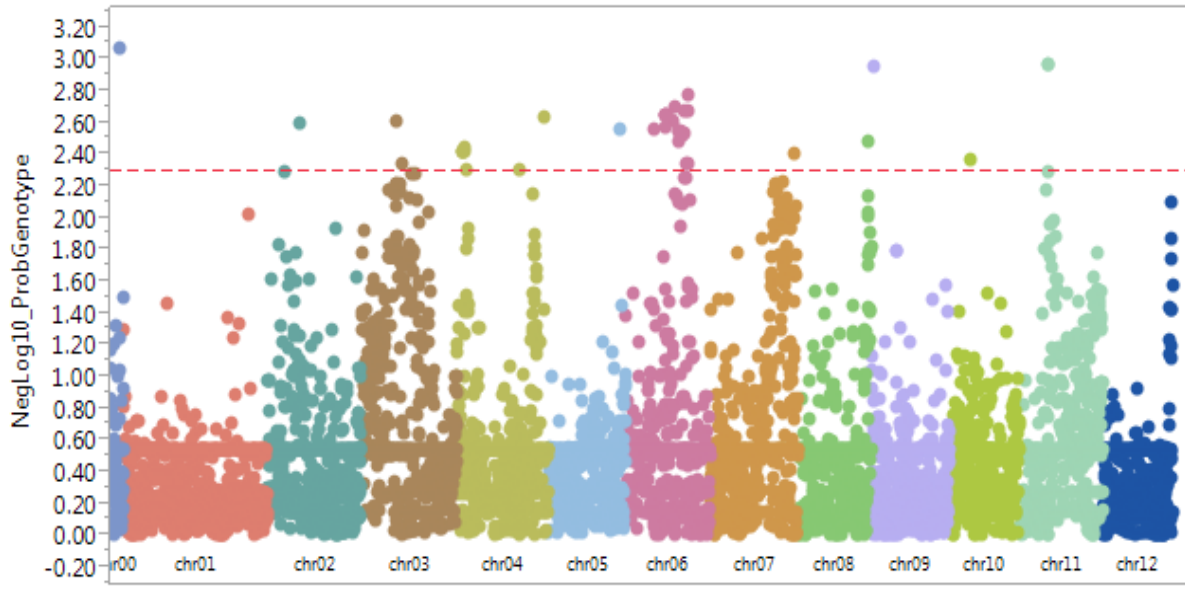


Figure 6. Manhattan plot of SNP-trait association results.

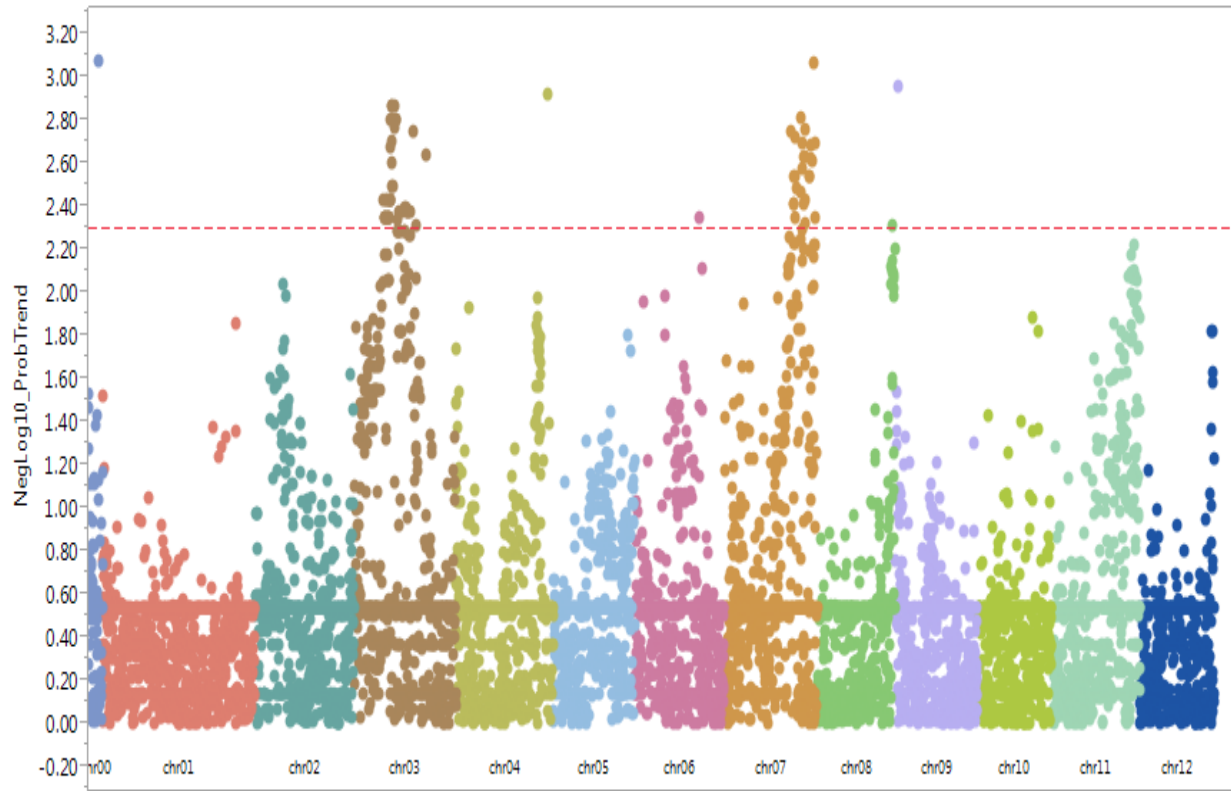


Figure 7. Manhattan plot of QTL single marker analysis results.

Appendix A. 1. Alignments of GGH (A) and EF1- α (B) sequences and primers used in qPCR reactions. GGH1, GGH2 and GGH3 transcripts sequences from the DM genotype were aligned in order to design primers specific of GGH1. EF1- α sequences from four genotypes were aligned to design primers within highly conserved regions.

A

			GA
DM-GGH1	978	CAGTGCCGCGAGAAGTGCTCGATAGTCTCATATACAATTACAATCCCACTTATCGTGGGA	
DM-GGH2	1018	CGGCTACCAGCAAAAGTGCTTGACAACCTCATCTACAATTACAATCCCTTCTTATGCTGGGA	
DM-GGH3	893	CAGAAGCTCAAAAAGTACTCGACAATCTCATCTACAATTACAATCCCACTTATAGTGGAA	

		Fwd	
		AGGCAGGGAAGGGTTATG	
DM-GGH1	1038	AGGCAGGGAAGGGTTATGACGAGGTTATCTCTTCACTCCGCAATCTTCCTCGAGCTCTA	
DM-GGH2	1078	AGGTTGGGGGAGTTTGGAGGAGGTTACCTCTTCACTCCGCGTCCACCTTGAGCTCTC	
DM-GGH3	953	AGACTGGGAAAGGTTACGATGAGGTTACGTTTCAA.....CAGTCATGCTGTGAACCTA	

		Rev	
		CAACTGCACAATCTTATTGATGC	
DM-GGH1	1098	TGTAGAGAAAAAACACCCAGTTTAATTGAGCAATAACC	AACTGCACAATCTTATTGATGC
DM-GGH2	1138	TGTAGATGCAAGTGAAC.....TGCAAAGCATTGAC..	AAATGTCATGATCAAAGA..TTAT
DM-GGH3	1008	A	

B

		Fwd		
		CTGGTATGGTTGTGACCTTTG		
DM	766	CAGTTGGTTCGTGTTGAGACTGGTGTGATCAAGCCTGGTATGGTTGTGACCTTTGGCCCTA		
Kuras	814	CTGTTGGTTCGTGTTGAGACTGGTGTGATCAAGCCTGGTATGGTTGTGACCTTTGGCCCTA		
Desiree	838	CAGTTGGTTCGTGTAAGAGACTGGTGTGATCAAGCCTGGTATGGTTGTGACCTTTGGCCCTA		
CIP800928	269	CTGTTGGTTCGTGTTGAGACTGGTGTGATCAAGCCTGGTATGGTTGTGACCTTTGGCCCTA		

DM	826	CTGGTTTGACAACCTGAAGTCAAGTCTGTAAGAGATGCACCACGAAGCTCTCTGGAGGCA		
Kuras	874	CTGGTTTGACAACCTGAAGTCCAGTCTGTTGAGATGCACCACGAGCTCTTCTGGAGGCA		
Desiree	898	CTGGTTTGACAACCTGAAGTCAAGTCTGTTGAGATGCACCACGAAGCTCTTCTGGAGGCA		
CIP800928	329	CTGGTTTGACAACCTGAAGTCAAGTCTGTTGAGATGCACCACGAAGCTCTTCTGGAGGCA		

		Rev		
		GGTGACAATGTTGGGTTCAA		
DM	885	CTCCCTGGTGACAATGTTGGGTTCAATGTTAAGAATGTTGCTGTTAAGGATCTTAAAGCG		
Kuras	933	CTCCCTGGTGACAATGTTGGGTTCAATGTTAAGAATGTTGCTGTTAAGGATCTGAAGCG		
Desiree	957	CTCCCTGGTGACAATGTTGGGTTCAATGTTAAGAATGTTGCTGTTAAGGATCTGAAGCG		
CIP800928	388	CTCCCTGGTGACAATGTTGGGTTCAATGTTAAGAATGTTGCTGTTAAGGATCTGAAGCG		

Appendix A. 2. Comparison of high and low fol lines based on RNA-Seq analysis. Genes involved in folate biosynthesis are listed with their corresponding PGSC genecodes and pseudo counts for those genes as shown in 2 replicates for each individual. Log2 (fold change), p-values, and q-values are calculated for each comparison. Highlighted in yellow are Log2 (fold change) >2 or <0.5 AND p and q values <0.05. In red are pseudo counts =< 4.

Comparison fol 1-3 over fol 1-5		Pseudo Counts				Log fold change	p-value	q-value
Gene name	PGSC Genecode	fol1.3_Rep1	fol1.3_Rep2	fol1.5_Rep1	fol1.5_Rep2			
5-formyltetrahydrofolate cycloligase	PGSC0003DMG400024570	239	270	213	227	0.210162133	0.527197844	0.902897321
GTP cyclohydrolase I	PGSC0003DMG400020105	223	234	180	248	0.094583369	0.781551987	1
dihydroneopterin triphosphate diphosphatase	PGSC0003DMG400030259	51	38	26	49	0.24691474	0.590848847	0.930384261
DHN aldolase	PGSC0003DMG400029847	158	157	172	184	-0.176525413	0.610692198	0.942300517
DHN aldolase	PGSC0003DMG400007623	1	5	0	0	Inf	0.057874193	0.336079292
aminodeoxychorismate synthase	PGSC0003DMG400009777	194	220	217	211	-0.047980029	0.892843362	1
aminodeoxychorismate lyase	PGSC0003DMG400018587	13	16	13	10	0.334419039	0.634903638	0.954498308
dihydropteroate synthase	PGSC0003DMG400028362	64	68	70	81	-0.19401062	0.630412645	0.952178017
DHF reductase	PGSC0003DMG400000736	614	629	642	733	-0.145605322	0.643141703	0.957387976
folylpolyglutamate synthase	PGSC0003DMG400002352	209	235	275	274	-0.306246473	0.353007111	0.810238924
folylpolyglutamate synthase	PGSC0003DMG400027193	601	487	382	378	0.517607233	0.102221952	0.469350918
UDP-glucose-pABA glucosyltransferase	PGSC0003DMG400025862	201	219	133	158	0.529370175	0.119488108	0.514484372
γ-glutamyl hydrolase	PGSC0003DMG400007066	399	390	67	57	2.66968518	7.52624E-14	1.87451E-11
γ-glutamyl hydrolase	PGSC0003DMG400021256	746	744	670	652	0.172590154	0.581888603	0.924121067
γ-glutamyl hydrolase	PGSC0003DMG400035974	3	3	0	0	Inf	0.057874193	0.336079292
Comparison fol1 1-3 over fol 1-11								
Gene name	PGSC Genecode	fol1.3_Rep1	fol1.3_Rep2	fol1.11_Rep1	fol1.11_Rep2	Log fold change	p-value	q-value
5-formyltetrahydrofolate cycloligase	PGSC0003DMG400024570	235	266	68	75	1.808795456	3.48909E-07	3.87704E-07

GTP cyclohydrolase I	PGSC0003DMG400020105	215	232	50	59	2.035946696	2.57E-08	4.05E-08
dihydroneopterin triphosphate diphosphatase	PGSC0003DMG400030259	43	40	8	12	2.053111336	9.74E-05	6.05E-05
DHN aldolase	PGSC0003DMG400029847	140	155	45	33	1.919168925	6.80E-07	6.97E-07
DHN aldolase	PGSC0003DMG400007623	2	5	0	0	Inf	0.034740023	0.014400558
aminodeoxychorismate synthase	PGSC0003DMG400009777	196	222	60	77	1.609327049	7.27E-06	5.72E-06
aminodeoxychorismate lyase	PGSC0003DMG400018587	16	17	4	2	2.459431619	0.001351139	0.000693394
dihydropteroate synthase	PGSC0003DMG400028362	66	70	14	18	2.087462841	6.05E-06	4.86E-06
DHF reductase	PGSC0003DMG400000736	601	637	168	122	2.093886509	3.22E-10	9.36E-10
folylpolyglutamate synthase	PGSC0003DMG400002352	215	236	64	82	1.627159064	4.76E-06	3.91E-06
folylpolyglutamate synthase	PGSC0003DMG400027193	594	496	131	116	2.141745188	1.95E-10	6.12E-10
UDP-glucose-pABA glucosyltransferase	PGSC0003DMG400025862	206	218	35	34	2.619395998	9.65E-12	4.65E-11
γ-glutamyl hydrolase	PGSC0003DMG400007066	389	402	14	23	4.418080519	2.10E-27	2.87E-25
γ-glutamyl hydrolase	PGSC0003DMG400021256	745	739	220	238	1.696071589	1.68E-07	2.04E-07
γ-glutamyl hydrolase	PGSC0003DMG400035974	4	3	0	0	Inf	0.034740023	0.014400558
Comparison fol 1-6 over fol 1-5								
Gene name	PGSC Genecode	fol1.6_Rep1	fol1.6_Rep2	fol1.5_Rep1	fol1.5_Rep2	Log fold change	p-value	q-value
5-formyltetrahydrofolate cycloligase	PGSC0003DMG400024570	228	215	213	234	-0.012968133	0.976440827	1
GTP cyclohydrolase I	PGSC0003DMG400020105	174	202	180	247	-0.183503408	0.588503825	0.959300236
dihydroneopterin triphosphate diphosphatase	PGSC0003DMG400030259	32	59	26	53	0.204013892	0.658529831	0.980673513
DHN aldolase	PGSC0003DMG400029847	112	144	172	178	-0.451211112	0.193302466	0.660848388
DHN aldolase	PGSC0003DMG400007623	0	2	0	0	Inf	0.543778007	0.934686923
aminodeoxychorismate synthase	PGSC0003DMG400009777	207	215	217	213	-0.027093661	0.942834668	1
aminodeoxychorismate lyase	PGSC0003DMG400018587	128	137	13	12	3.40599236	3.74E-14	6.83E-12
dihydropteroate synthase	PGSC0003DMG400028362	52	59	70	85	-0.481708539	0.224763347	0.714464784
DHF reductase	PGSC0003DMG400000736	282	430	642	739	-0.955764173	0.002592872	0.037492358
folylpolyglutamate synthase	PGSC0003DMG400002352	192	143	275	275	-0.715270523	0.031820521	0.236799396

folylpolyglutamate synthase	PGSC0003DMG400027193	540	602	382	382	0.579918107	0.067032847	0.374038218
UDP-glucose-pABA glucosyltransferase	PGSC0003DMG400025862	96	121	133	159	-0.428273326	0.227842244	0.719070979
γ -glutamyl hydrolase	PGSC0003DMG400007066	201	205	67	59	1.688055994	3.19E-06	0.000135241
γ -glutamyl hydrolase	PGSC0003DMG400021256	445	499	670	637	-0.469400376	0.135698427	0.562766861
γ -glutamyl hydrolase	PGSC0003DMG400035974	3	8	0	0	Inf	0.004604042	0.058152786
Comparison fol 1-6 over fol 1-11								
Gene name	PGSC Genecode	fol1.6_Rep1	fol1.6_Rep2	fol1.11_Rep1	fol1.11_Rep2	Log fold change	p-value	q-value
5-formyltetrahydrofolate cycloligase	PGSC0003DMG400024570	217	221	60	70	1.752419247	1.12E-06	1.46E-06
GTP cyclohydrolase I	PGSC0003DMG400020105	173	211	47	66	1.764783538	1.49E-06	1.87E-06
dihydroneopterin triphosphate diphosphatase	PGSC0003DMG400030259	34	64	10	12	2.155278225	2.08E-05	1.82E-05
DHN aldolase	PGSC0003DMG400029847	113	150	46	29	1.810100299	3.63E-06	4.02E-06
DHN aldolase	PGSC0003DMG400007623	0	1	0	1	0	1	0.341896713
aminodeoxychorismate synthase	PGSC0003DMG400009777	209	214	54	74	1.724513853	1.77E-06	2.16E-06
aminodeoxychorismate lyase	PGSC0003DMG400018587	130	127	3	3	5.420662048	5.48E-22	2.20E-20
dihydropteroate synthase	PGSC0003DMG400028362	54	62	11	25	1.688055994	0.000255889	1.73E-04
DHF reductase	PGSC0003DMG400000736	266	447	154	131	1.322940157	7.38E-05	5.65E-05
folylpolyglutamate synthase	PGSC0003DMG400002352	193	141	63	72	1.306888695	3.21E-04	2.12E-04
folylpolyglutamate synthase	PGSC0003DMG400027193	526	621	123	120	2.238837172	3.21E-11	1.87E-10
UDP-glucose-pABA glucosyltransferase	PGSC0003DMG400025862	87	122	35	32	1.641269942	4.57E-05	3.67E-05
γ -glutamyl hydrolase	PGSC0003DMG400007066	200	204	16	24	3.336283388	5.14E-16	8.50E-15
γ -glutamyl hydrolase	PGSC0003DMG400021256	446	527	217	260	1.028450539	0.001442543	0.000843685
γ -glutamyl hydrolase	PGSC0003DMG400035974	4	9	0	0	Inf	0.001773404	0.001021976

Appendix A. 3. Gene IDs corresponding to Arabidopsis, tomato, and potato sequences for the folate biosynthesis related genes.

Gene name	Genebank ID Arabidopsis	Genebank ID tomato	PGSC Gene Code	CHR	Start Pos.	End Pos.
5-Formyltetrahydrofolate cycloligase	ATG513050	LOC543718	PGSC0003DMG400024570	3	53.57 Mb	53.5732 Mb
GTP cyclohydrolase I	ATG07270	LOC543831	PGSC0003DMG400020105	6	58.2183 Mb	58.222 Mb
Dihydroneopterin (DHN) triphosphate diphosphatase	AT1G68760	Solyc03g043860.2.1	PGSC0003DMG400030259 (Nudix Hydrolase I)	3	6.3019 Mb	6.3032 Mb
DHN aldolase	AT3G11750 AT5G62980 AT3G21730	LOC544263	PGSC0003DMG400029847 PGSC0003DMG400007623	10	58.0069 Mb	59.00975 Mb
Aminodeoxychorismate synthase	AT2G28880	LOC543912	PGSC0003DMG400009777	4	11.3513 Mb	11.35325 Mb
Aminodeoxychorismate lyase	AT5G57850	LOC778238	PGSC0003DMG400018587	4	32.0905 Mb	32.0927 Mb
6-Hydroxymethyl-dihydropterin (HMDHP) pyrophosphokinase/dihydropteroate (DHP) synthase	AT4G30000 (mitochondrial) AT1G69190 (cytosolic, only in Arabidopsis)	Solyc05g012090.2.1	PGSC0003DMG400028362	11	42.62765 Mb	42.6322 Mb
Dihydrofolate (DHF) synthase	AT5G41480	LOC101257178	PGSC0003DMG400002352	5	0.6923 Mb	0.6949 Mb
DHF reductase	AT2G16370 AT4G34570 AT2G21550	LOC101267455	PGSC0003DMG400000736	6 1	38.181 Mb 86.1386 Mb	38.18745 Mb 86.1451 Mb
Folylpolyglutamate synthase	FPGS1: AT5G05980 FPGS2: AT3G10160 FPGS3: AT3G55630	LOC101250507 LOC101246415 LOC101257178 = DHFS	PGSC0003DMG400027193	5	48.2082 Mb	48.21565 Mb
UDP-Glucose-p-aminobenzoate (pABA) Glucosyltransferase	AT1G05560	Solyc12g098590.1.1	PGSC0003DMG400004573	12	59.38865 Mb	59.391 Mb
γ -Glutamyl hydrolase	AT1G78660 AT1G78680 AT1G78670	Solyc10g007410.2.1 Solyc07g062270.2.1 Solyc07g062280.2.1	PGSC0003DMG400007066 PGSC0003DMG400021256 PGSC0003DMG400035974	7 10 7	52.4544 Mb 2.484 Mb 52.4594 Mb	52.459 Mb 2.4875 Mb 52.46275 Mb

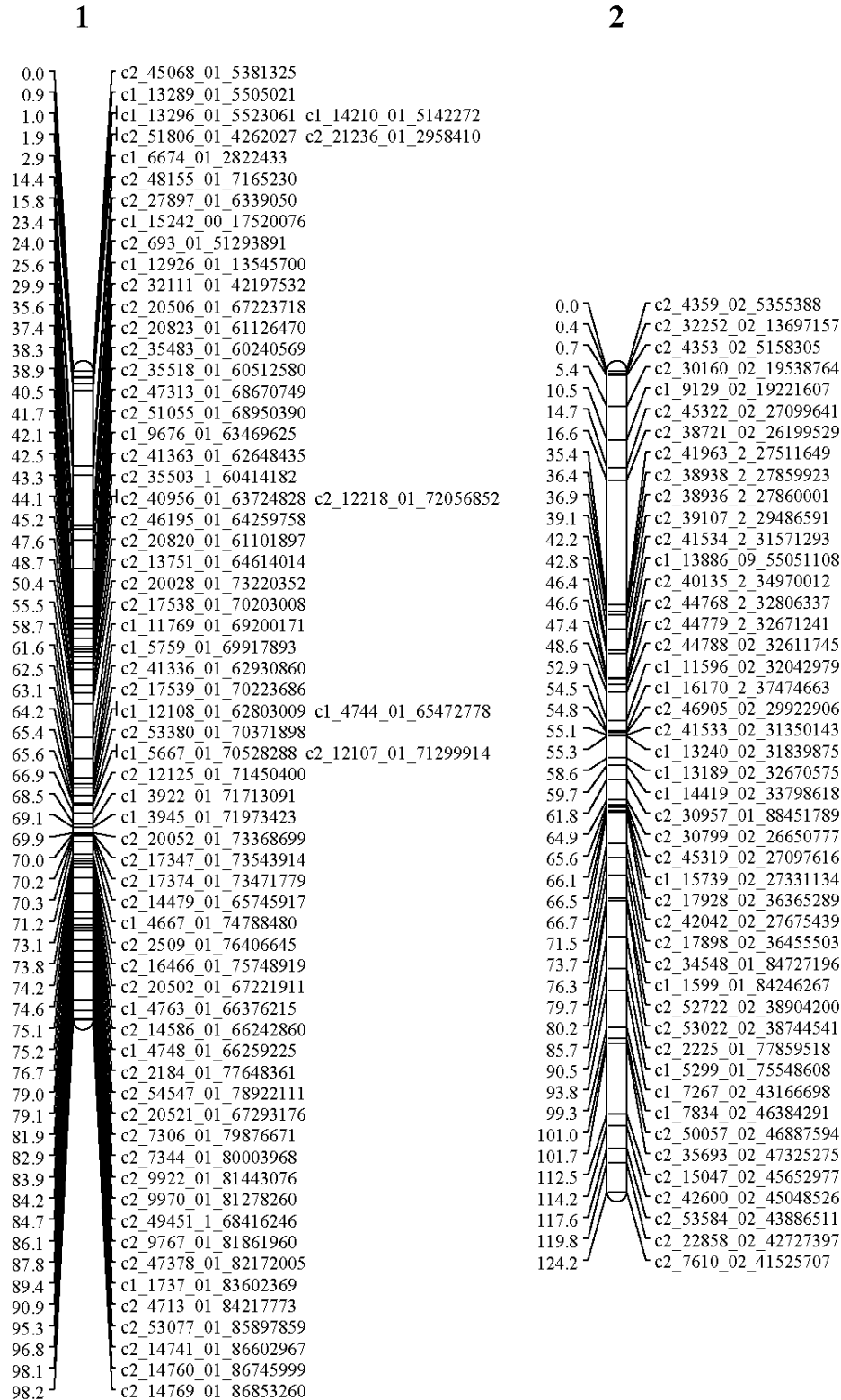
Appendix A. 4. Percent heterozygosity for progeny individuals and parents used in SNP study.

Sample	--	AA	AC	AG	AT	CC	CG	GC	GG	TA	TC	TG	TT	%He
Foll6	404	2028	50	217	10	2584	4	5	2670	14	178	40	1916	5.3
USW4S3	210	1442	356	1341	55	1821	37	28	1842	68	1274	292	1354	34.8
BRR1	380	1830	157	648	27	2310	15	12	2317	37	561	138	1688	16.4
BRR101	371	1735	189	713	25	2255	20	20	2317	36	653	139	1647	18.4
BRR103	362	1833	142	559	22	2329	14	14	2412	26	566	109	1732	14.9
BRR106	338	1711	213	786	36	2167	24	22	2221	43	770	180	1609	21.2
BRR107	384	1818	160	621	27	2306	17	15	2360	29	570	136	1677	16.2
BRR109	344	1789	195	748	20	2223	18	16	2256	30	681	141	1659	18.9
BRR110	353	1766	181	724	26	2277	24	19	2260	32	651	161	1646	18.6
BRR111	354	1750	190	677	28	2249	19	16	2341	35	641	155	1665	18.0
BRR112	368	1648	204	826	30	2181	22	19	2230	37	813	193	1549	22.0
BRR113	345	1725	196	742	24	2207	27	18	2278	35	711	174	1638	19.7
BRR116	353	1794	168	637	25	2297	23	10	2368	28	588	132	1697	16.5
BRR117	300	1711	232	837	24	2146	20	14	2190	38	821	199	1588	22.3
BRR12	306	1794	185	643	26	2305	18	10	2363	28	605	126	1711	16.7
BRR120	355	1814	161	637	27	2294	19	14	2321	30	603	149	1696	16.8
BRR122	265	1702	220	822	36	2175	28	22	2230	41	790	168	1621	21.6
BRR124	346	1881	137	529	22	2316	14	13	2412	23	513	118	1796	14.0
BRR125	368	1800	165	669	25	2288	16	15	2307	28	605	153	1681	17.2
BRR126	295	1781	182	747	36	2246	20	23	2289	33	657	147	1664	18.8
BRR127	468	1668	201	728	32	2226	24	17	2276	35	717	161	1567	19.8
BRR128	301	1723	208	762	28	2246	26	19	2274	37	662	159	1675	19.4
BRR129	300	1739	199	765	29	2217	18	16	2268	34	746	180	1609	20.2
BRR131	323	1761	182	731	30	2238	22	12	2296	33	682	147	1663	18.8
BRR132	577	1575	209	808	33	2183	26	18	2228	38	763	177	1485	21.7
BRR133	314	1748	186	762	22	2233	24	14	2283	37	703	167	1627	19.5
BRR134	310	1622	245	926	33	2142	27	23	2183	41	811	200	1557	23.5
BRR136	280	1626	247	911	33	2111	26	26	2177	44	868	205	1566	24.0
BRR138	295	1723	208	827	28	2184	22	21	2207	27	754	183	1641	21.1
BRR139	294	1741	199	767	29	2220	18	16	2269	34	745	180	1608	20.2
BRR14	297	1731	206	795	29	2169	23	18	2233	37	776	178	1628	21.0
BRR141	320	1794	193	670	24	2272	18	13	2320	33	635	160	1668	17.8
BRR142	330	1751	185	731	24	2265	17	18	2300	35	694	145	1625	18.9
BRR144	285	1784	191	708	32	2273	22	17	2291	37	650	164	1666	18.5
BRR146	319	1722	187	776	32	2225	20	21	2239	38	724	189	1628	20.3
BRR15	346	1725	211	791	28	2183	28	18	2219	41	736	178	1616	20.8
BRR16	292	1589	238	979	39	2126	33	15	2126	47	899	225	1512	25.2
BRR19	403	1835	157	579	24	2288	16	11	2373	36	612	127	1659	16.1
BRR2	322	1653	238	891	37	2139	22	19	2186	43	817	196	1557	23.1
BRR22	404	1788	166	639	25	2313	17	19	2354	32	585	108	1670	16.4
BRR24	352	1746	184	704	33	2221	23	17	2294	32	672	167	1675	18.8

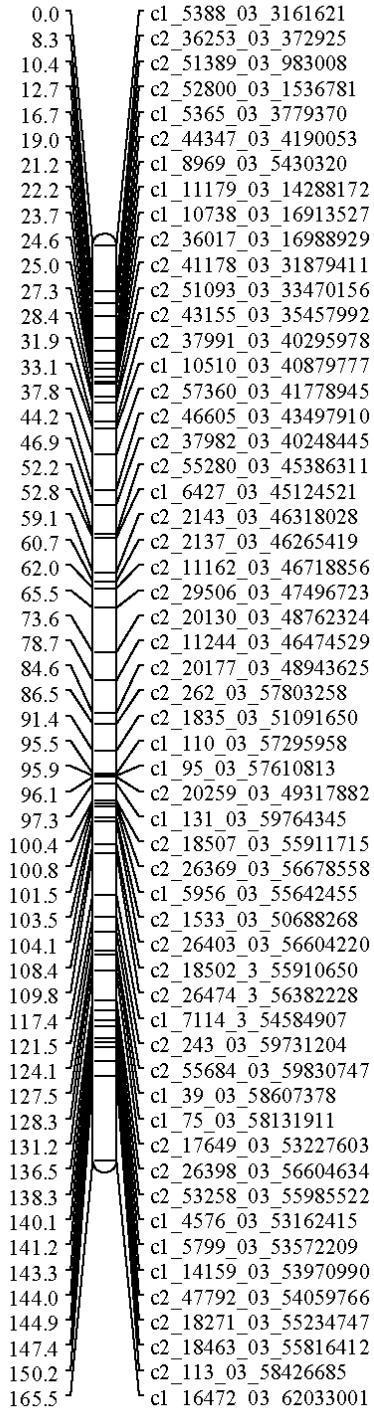
BRR27	490	2001	51	207	12	2556	7	6	2646	17	199	37	1891	5.6
BRR3	289	1723	224	822	37	2153	27	20	2206	40	797	166	1616	21.7
BRR32	319	1689	225	915	26	2079	25	16	2103	47	885	219	1572	24.1
BRR33	366	1821	168	636	25	2251	11	13	2328	26	641	140	1694	17.0
BRR37	330	1707	225	831	36	2163	25	19	2202	37	771	181	1593	21.7
BRR38	336	1735	181	717	23	2229	23	19	2298	43	695	171	1650	19.1
BRR39	290	1633	249	943	31	2123	26	24	2148	39	849	198	1567	24.0
BRR4	337	1740	183	722	27	2242	18	14	2285	31	690	172	1659	19.0
BRR40	345	1827	157	588	22	2308	18	12	2378	30	560	129	1746	15.5
BRR41	320	1661	207	846	35	2206	23	22	2213	40	754	185	1608	21.6
BRR42	325	1737	201	805	30	2141	24	24	2234	36	795	182	1586	21.4
BRR43	319	1678	244	891	37	2108	19	18	2143	47	873	211	1532	23.9
BRR44	359	1807	152	679	29	2276	16	17	2305	28	607	154	1691	17.2
BRR45	342	1848	169	598	25	2266	19	11	2371	30	587	115	1739	15.9
BRR47	264	1611	244	966	45	2077	31	19	2150	42	945	220	1506	25.5
BRR48	337	1710	191	769	28	2225	24	16	2281	40	714	166	1619	19.9
BRR49	308	1698	221	847	24	2175	20	21	2216	44	787	174	1585	21.8
BRR50	314	1864	147	602	24	2312	16	16	2366	23	575	137	1724	15.7
BRR51	328	1715	224	807	33	2207	20	12	2248	30	693	169	1634	20.3
BRR52	359	1856	119	542	25	2391	13	10	2450	28	462	94	1771	13.2
BRR53	945	1416	255	1009	40	1894	29	20	1935	43	943	219	1372	27.9
BRR54	326	1738	187	775	30	2224	17	15	2250	40	706	151	1661	19.6
BRR55	316	1650	231	896	35	2153	33	19	2178	41	854	178	1536	23.3
BRR56	323	1662	224	889	36	2178	18	17	2181	36	787	197	1572	22.5
BRR57	344	1720	178	750	21	2240	17	19	2287	38	698	152	1656	19.2
BRR58	311	1745	201	801	31	2155	24	14	2203	40	781	192	1622	21.2
BRR6	561	1958	54	227	14	2554	7	3	2637	18	194	37	1856	5.8
BRR60	356	1745	184	720	30	2268	19	19	2308	34	643	140	1654	18.3
BRR61	349	1711	216	816	23	2194	22	12	2216	35	726	184	1616	20.8
BRR62	329	1791	168	714	26	2273	23	13	2307	33	667	134	1642	18.2
BRR63	355	1857	142	594	21	2308	18	15	2356	30	569	141	1714	15.7
BRR66	341	1791	183	634	27	2290	26	16	2347	29	580	149	1707	16.8
BRR68	861	1417	289	1135	49	1829	32	26	1868	44	1034	214	1322	30.5
BRR69	289	1722	194	817	33	2233	29	15	2239	33	687	153	1676	19.9
BRR7	337	1745	189	724	31	2251	20	12	2309	29	676	140	1657	18.6
BRR70	357	1781	173	684	31	2287	13	7	2330	25	604	136	1692	17.1
BRR71	350	1856	140	585	24	2356	20	14	2378	27	543	105	1722	14.9
BRR73	352	1805	176	696	31	2244	21	16	2285	32	672	152	1638	18.4
BRR78	328	1755	182	727	20	2260	21	13	2328	33	661	142	1650	18.4
BRR8	328	1641	234	894	31	2157	23	24	2187	40	805	199	1557	23.0
BRR80	906	890	471	2074	75	1178	51	32	1160	93	1819	433	938	54.8
BRR81	336	1611	239	895	36	2140	30	24	2184	39	857	199	1530	23.7
BRR83	341	1656	212	833	25	2210	21	17	2257	38	755	169	1586	21.2
BRR85	380	1752	189	702	29	2254	25	14	2322	34	629	128	1662	18.0
BRR88	299	1670	214	920	29	2131	22	21	2169	43	851	203	1548	23.4

BRR90	416	1751	178	662	28	2301	17	15	2318	38	605	148	1643	17.4
BRR91	589	1717	199	700	26	2213	24	13	2232	33	629	154	1591	18.7
BRR92	383	1802	174	678	22	2231	23	17	2293	36	682	127	1652	18.1
BRR93	871	1441	265	999	39	1909	33	24	1964	39	946	215	1375	27.7
BRR95	320	1677	227	932	32	2079	31	17	2126	45	863	194	1577	23.9
BRR97	411	1776	168	658	25	2276	20	19	2308	30	579	137	1713	16.9
BRR99	364	1781	168	671	26	2266	21	16	2316	34	655	140	1662	17.7

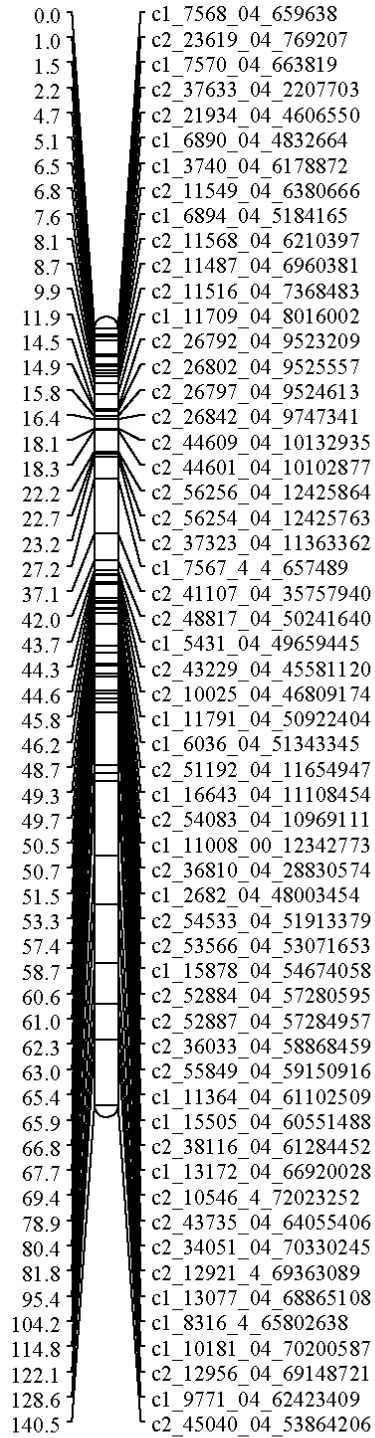
Appendix A. 5. Consensus Linkage Group Maps



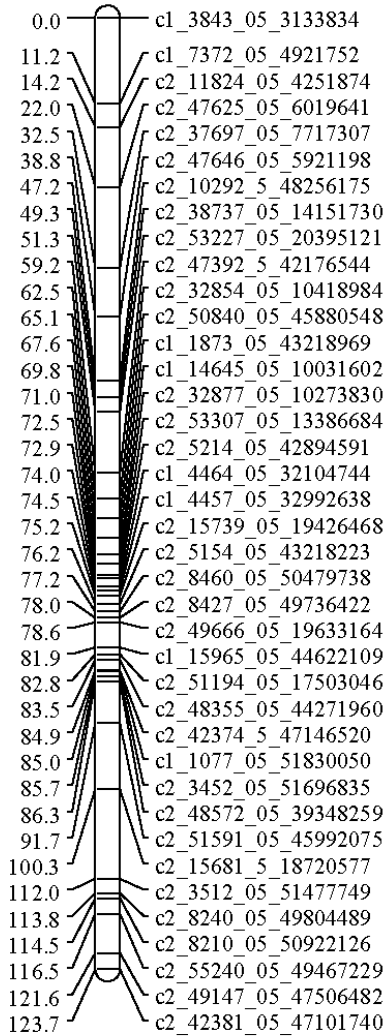
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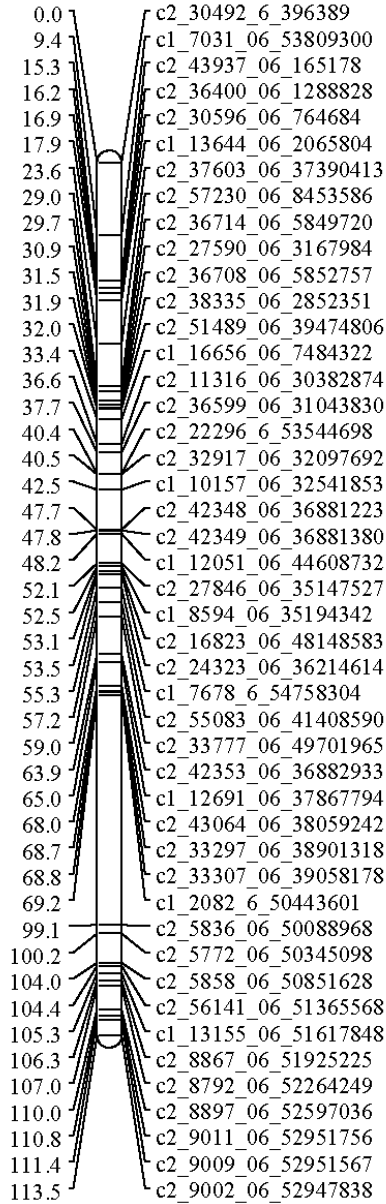
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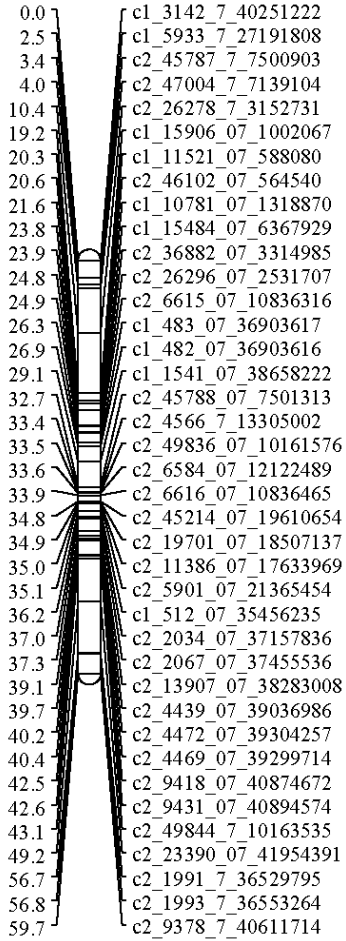
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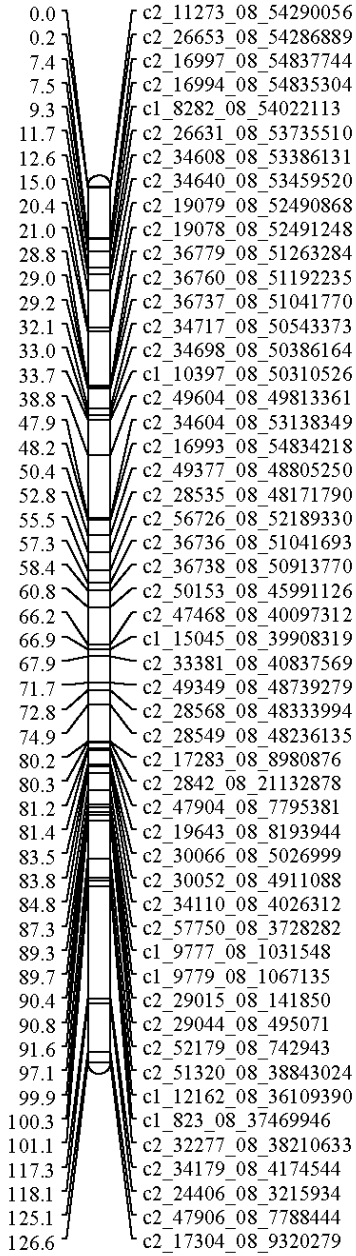
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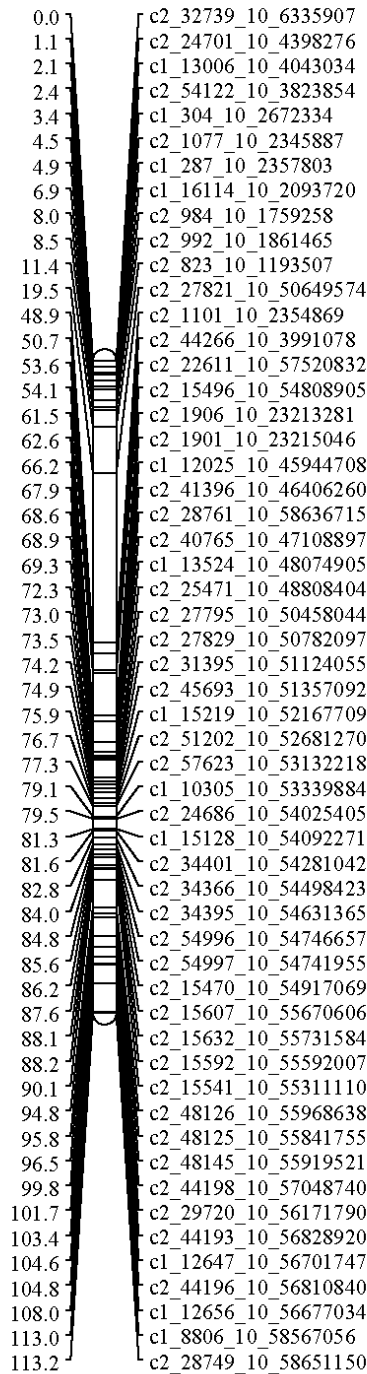
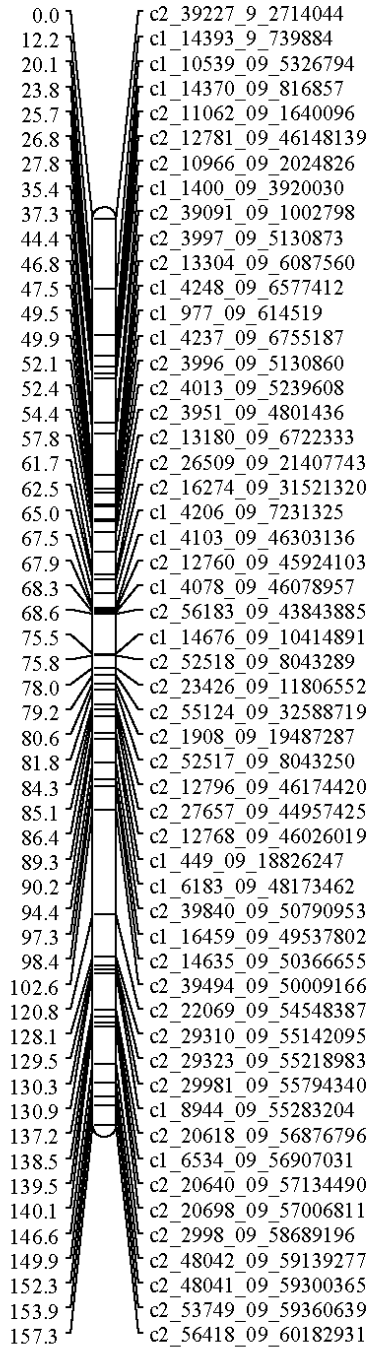


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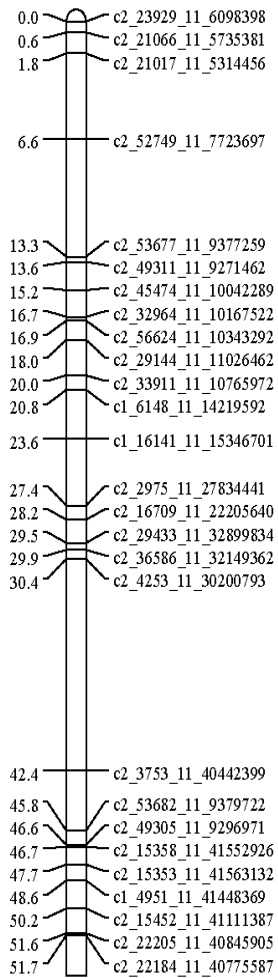


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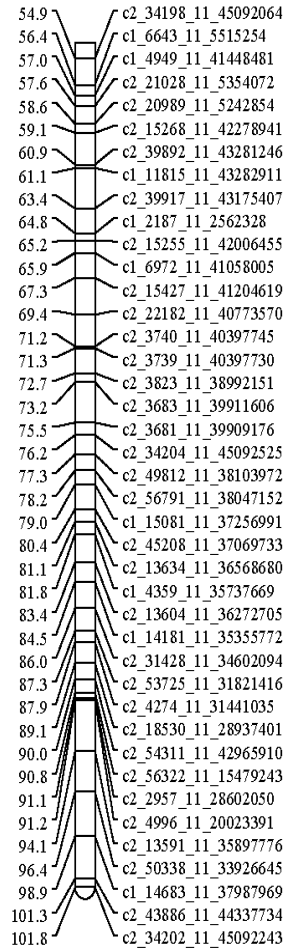




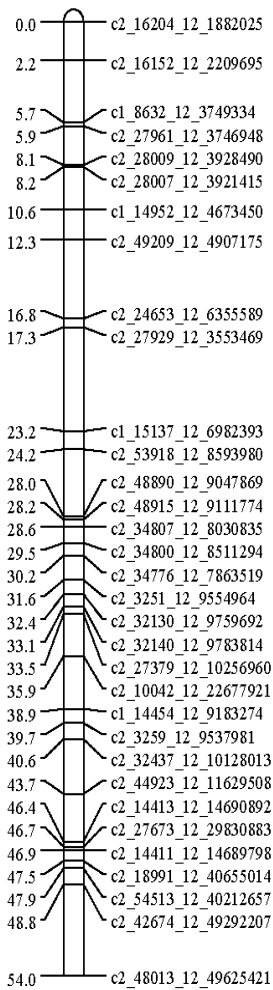
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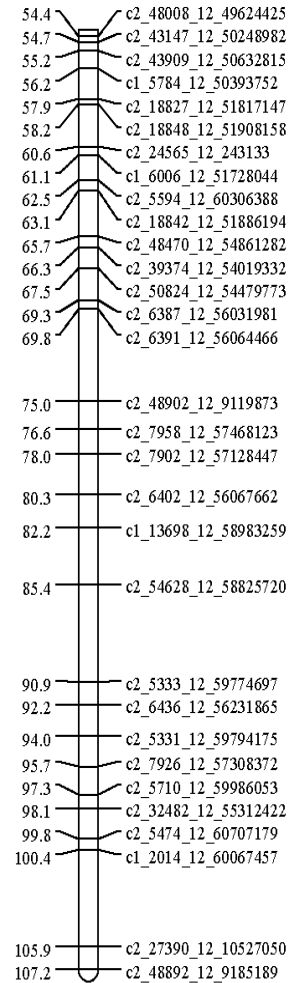
11 [2]



12 [1]



12 [2]



Appendix A. 6. USW4s#3 linkage group SNP data

Linkage Group	Number of SNPs	Group Length (cM)	Marker Coverage (marker/cM)
1	56	104.21	1.86
2	49	153.48	3.13
3	56	103.55	1.85
4	59	79.04	1.34
5	31	147.28	4.75
6	49	96.99	1.97
7	59	112.31	1.90
8	53	121/46	2.29
9	51	90.03	1.77
10	48	68.36	1.43
11	72	83.57	1.16
12	59	68.89	1.17
Total	642	1229.213	1.91

Appendix A. 7. Fol 1.6 linkage group SNP data

Linkage Group	Number of SNPs	Group Length (cM)	Marker Coverage (marker/cM)
1a	6	28.9	4.81
1b	5	25.1	5.02
2a	9	105.9	11.8
2b	5	28.4	5.68
3	4	19.9	4.97
4	5	62.2	12.4
5	4	51.5	12.9
6a	8	44.4	5.55
6b	3	11.1	3.7
7	4	61.1	15.3
8	2	4.4	2.2
9	6	41.6	6.9
10	3	24.2	8.1
11a	4	25.4	6.35
11b	3	35.7	11.9
12a	7	86.8	12.4
12b	4	45.6	11.4
Total	82	702.47	8.57

Appendix A. 8. SNPs identified by marker trait association.

SNP ID	CHR	POS	F-value genotype	Neg. Log10 probability Genotype	R-squared Genotype	Std. Error Trend
solcap_snp_c2_53198	chr00	29279410	11.9	3.072	0.114572486	0.056772
solcap_snp_c2_21661	chr02	25508015	6.39	2.5986	0.123225032	0.023611
solcap_snp_c2_43267	chr03	34373409	4.41	1.827	0.088311115	0.042481
solcap_snp_c2_43256	chr03	34491679	4.22	1.7527	0.084876762	0.045321
solcap_snp_c2_43253	chr03	34493653	4.22	1.7527	0.084876762	0.045321
solcap_snp_c2_55460	chr03	35334246	4.22	1.7527	0.084876762	0.045321
solcap_snp_c2_43165	chr03	35563675	4.22	1.7527	0.084876762	0.045321
solcap_snp_c2_43168	chr03	35566030	4.22	1.7527	0.084876762	0.045321
solcap_snp_c2_43169	chr03	35567091	4.41	1.827	0.088311115	0.042481
solcap_snp_c2_35332	chr03	35939787	4.22	1.7527	0.084876762	0.045321
solcap_snp_c1_15926	chr03	36151220	4.41	1.827	0.088311115	0.042481
solcap_snp_c2_30741	chr03	36334363	4.22	1.7527	0.084876762	0.045321
solcap_snp_c1_9292	chr03	36528674	4.22	1.7527	0.084876762	0.045321
solcap_snp_c2_57012	chr03	36939832	4.22	1.7527	0.084876762	0.045321
solcap_snp_c2_52496	chr03	37489785	4.22	1.7527	0.084876762	0.045321
solcap_snp_c2_52494	chr03	37495967	4.22	1.7527	0.084876762	0.045321
solcap_snp_c1_7139	chr03	37699819	5.21	2.1438	0.102811642	0.035402
solcap_snp_c2_36467	chr03	38142166	4.41	1.827	0.088311115	0.042481
solcap_snp_c1_10879	chr03	38177443	4.41	1.827	0.088311115	0.042481
solcap_snp_c2_38047	chr03	38662974	4.41	1.827	0.088311115	0.042481
solcap_snp_c2_38054	chr03	38711501	5.26	2.1604	0.103563891	0.045503
solcap_snp_c2_38058	chr03	38756280	9.67	2.6023	0.095072403	0.023467
solcap_snp_c2_48378	chr03	39198646	4.53	1.8773	0.090628535	0.046556
solcap_snp_c2_48372	chr03	39255217	5.39	2.2137	0.105980172	0.042581
solcap_snp_c2_48371	chr03	39255236	5.39	2.2137	0.105980172	0.042581
solcap_snp_c2_48370	chr03	39255317	5.26	2.1604	0.103563891	0.045503
solcap_snp_c2_48369	chr03	39257162	5.39	2.2137	0.105980172	0.042581
solcap_snp_c2_48368	chr03	39257271	5.04	2.077	0.099771544	0.045613
solcap_snp_c2_48389	chr03	39312775	4.53	1.8773	0.090628535	0.046556
solcap_snp_c1_16679	chr03	40197844	5.27	2.1641	0.103730931	0.039886
solcap_snp_c2_35234	chr03	40992986	5.39	2.2137	0.105980172	0.042581
solcap_snp_c2_42312	chr03	41530089	5.26	2.1604	0.103563891	0.045503
solcap_snp_c1_6875	chr03	41994529	5.26	2.1604	0.103563891	0.045503
solcap_snp_c1_6850	chr03	42019542	8.45	2.3399	0.084126956	0.047216
solcap_snp_c2_46597	chr03	43481994	4.29	1.7809	0.08618407	0.042533
solcap_snp_c2_20309	chr03	44661865	4.29	1.7809	0.08618407	0.042533
solcap_snp_c2_25654	chr03	45603662	4.31	1.7867	0.086452367	0.048311
solcap_snp_c2_25662	chr03	45979293	4.31	1.7867	0.086452367	0.048311
solcap_snp_c2_11147	chr03	46806099	4.27	1.771	0.085726204	0.047471
solcap_snp_c2_29665	chr03	46924861	4.27	1.771	0.085726204	0.047471

solcap_snp_c2_45914	chr03	47769763	4.27	1.771	0.085726204	0.047471
solcap_snp_c2_20164	chr03	48882551	5.13	2.1103	0.101291801	0.038327
solcap_snp_c2_1533	chr03	50688268	4.76	1.9673	0.094763007	0.030338
solcap_snp_c2_22466	chr03	54580832	4.92	2.0287	0.097572091	0.029048
solcap_snp_c2_31688	chr04	3816447	5.9	2.4105	0.114839537	0.041585
solcap_snp_c2_31717	chr04	3888182	5.9	2.4105	0.114839537	0.041585
solcap_snp_c1_9546	chr04	3905183	5.9	2.4105	0.114839537	0.041585
solcap_snp_c2_31732	chr04	3924918	5.9	2.4105	0.114839537	0.041585
solcap_snp_c2_21946	chr04	4567755	5.9	2.4105	0.114839537	0.041585
solcap_snp_c2_21936	chr04	4595286	5.99	2.443	0.116293159	0.040112
solcap_snp_c1_6749	chr04	64973061	5.63	2.3056	0.110128993	0.040587
solcap_snp_c2_10688	chr04	71592216	6.47	2.6289	0.124570969	0.040132
solcap_snp_c1_2799	chr05	49778404	6.28	2.5542	0.121251633	0.089952
solcap_snp_c2_42350	chr06	36881392	6.28	2.5542	0.121251633	0.089952
solcap_snp_c2_49048	chr06	41926673	6.51	2.6436	0.125220769	0.03849
solcap_snp_c2_49052	chr06	41927092	6.51	2.6436	0.125220769	0.03849
solcap_snp_c2_43135	chr06	42626082	6.31	2.5669	0.121819261	0.038639
solcap_snp_c2_57014	chr06	42746310	6.51	2.6436	0.125220769	0.03849
solcap_snp_c2_57017	chr06	42759644	6.51	2.6436	0.125220769	0.03849
solcap_snp_c2_37770	chr06	43114810	6.51	2.6436	0.125220769	0.03849
solcap_snp_c2_25926	chr06	46018319	6.43	2.6107	0.123761602	0.036897
solcap_snp_c2_46184	chr06	47027778	6.65	2.6974	0.127599934	0.038372
solcap_snp_c2_52583	chr06	48405097	6.25	2.5446	0.120827029	0.038722
solcap_snp_c1_15372	chr06	48416425	6.25	2.5446	0.120827029	0.038722
solcap_snp_c1_15371	chr06	48416539	6.25	2.5446	0.120827029	0.038722
solcap_snp_c2_31214	chr06	48529862	6.07	2.4742	0.11768825	0.036001
solcap_snp_c2_31139	chr06	48874844	6.25	2.543	0.120757212	0.038788
solcap_snp_c2_35897	chr06	49305939	6.2	2.523	0.119864882	0.038912
solcap_snp_c2_35893	chr06	49406412	6.2	2.523	0.119864882	0.038912
solcap_snp_c2_35889	chr06	49407305	6.2	2.523	0.119864882	0.038912
solcap_snp_c2_5869	chr06	50109162	6.21	2.5267	0.120031302	0.038922
solcap_snp_c1_2109	chr06	50109778	6.21	2.5267	0.120031302	0.038922
solcap_snp_c1_2060	chr06	50219978	6.21	2.5267	0.120031302	0.038922
solcap_snp_c2_5772	chr06	50345098	6.59	2.6731	0.126525808	0.039186
solcap_snp_c2_5858	chr06	50851628	5.73	2.3454	0.111918957	0.037799
solcap_snp_c2_41406	chr06	51183356	5.73	2.3454	0.111918957	0.037799
solcap_snp_c2_41405	chr06	51183805	6.84	2.7691	0.130759267	0.066581
solcap_snp_c2_56141	chr06	51365568	6.58	2.6685	0.126322111	0.039148
solcap_snp_c2_19804	chr07	48956963	5.26	2.16	0.103548579	0.032548
solcap_snp_c1_10457	chr07	49665986	5.29	2.1744	0.104199155	0.028685
solcap_snp_c2_35049	chr07	49745280	5.4	2.218	0.106175191	0.028939
solcap_snp_c2_35053	chr07	49746796	5.29	2.1744	0.104199155	0.028685
solcap_snp_c2_35078	chr07	49839630	5.4	2.218	0.106175191	0.028939
solcap_snp_c2_35094	chr07	49918098	4.74	1.9602	0.094436865	0.029363
solcap_snp_c2_26003	chr07	50150805	5.29	2.1724	0.104110688	0.02911

solcap_snp_c2_26011	chr07	50151997	4.92	2.0272	0.09750429	0.029628
solcap_snp_c2_28223	chr07	51604961	5.44	2.2308	0.10675491	0.033719
solcap_snp_c2_28238	chr07	51779684	4.68	1.9336	0.093216016	0.029638
solcap_snp_c2_28244	chr07	51780403	4.9	2.0199	0.097168353	0.031158
solcap_snp_c2_42763	chr07	52191007	5	2.062	0.099091151	0.034835
solcap_snp_c2_12404	chr07	52544646	4.86	2.004	0.096442781	0.031925
solcap_snp_c1_16636	chr07	52759623	4.38	1.8177	0.087881833	0.035102
solcap_snp_c2_12529	chr07	52792811	4.2	1.7442	0.084482011	0.035224
solcap_snp_c2_12531	chr07	52795452	4.86	2.004	0.096442781	0.031925
solcap_snp_c2_12549	chr07	52913969	4.39	1.8192	0.08795369	0.03398
solcap_snp_c2_12565	chr07	52958673	5.16	2.1228	0.101856715	0.032732
solcap_snp_c2_16846	chr07	53783075	4.66	1.9287	0.092990221	0.032925
solcap_snp_c2_16843	chr07	53822702	4.67	1.9293	0.093018274	0.034998
solcap_snp_c2_18544	chr07	54839197	4.82	1.99	0.095802978	0.033871
solcap_snp_c2_18549	chr07	54860473	4.98	2.0508	0.098579298	0.034938
solcap_snp_c1_5981	chr07	55130142	4.83	1.9936	0.095966161	0.036247
solcap_snp_c2_18680	chr07	55283766	5.87	2.3974	0.114252092	0.030794
solcap_snp_c2_18684	chr07	55284214	5.03	2.0716	0.09952956	0.036105
solcap_snp_c1_8821	chr07	55855903	4.25	1.7644	0.085421723	0.036769
solcap_snp_c2_16159	chr08	55853675	6.08	2.4767	0.117801382	0.032199
solcap_snp_c2_48597	chr09	778420	11.35	2.9582	0.109861634	0.097527
solcap_snp_c2_7747	chr10	43000239	5.79	2.3654	0.112817145	0.041107
solcap_snp_c2_49303	chr11	9312026	7.36	2.9626	0.139226259	0.030447
solcap_snp_c1_15658	chr11	9380301	7.36	2.9626	0.139226259	0.030447

Appendix A. 9. Potential QTLs identified by QTL single marker analysis.

SNP ID	CHR	POS	Std. Error trend	F-value trend	Neg. log10 prob. trend	R-squared trend
solcap_snp_c2_53198	chr00	29279410	0.056772	11.9	3.072	0.114572
solcap_snp_c2_43267	chr03	34373409	0.042481	8.87	2.4308	0.087923
solcap_snp_c2_43256	chr03	34491679	0.045321	8.48	2.3456	0.084367
solcap_snp_c2_43253	chr03	34493653	0.045321	8.48	2.3456	0.084367
solcap_snp_c2_55460	chr03	35334246	0.045321	8.48	2.3456	0.084367
solcap_snp_c2_43165	chr03	35563675	0.045321	8.48	2.3456	0.084367
solcap_snp_c2_43168	chr03	35566030	0.045321	8.48	2.3456	0.084367
solcap_snp_c2_43169	chr03	35567091	0.042481	8.87	2.4308	0.087923
solcap_snp_c2_35332	chr03	35939787	0.045321	8.48	2.3456	0.084367
solcap_snp_c1_15926	chr03	36151220	0.042481	8.87	2.4308	0.087923
solcap_snp_c2_30741	chr03	36334363	0.045321	8.48	2.3456	0.084367
solcap_snp_c1_9292	chr03	36528674	0.045321	8.48	2.3456	0.084367
solcap_snp_c2_57012	chr03	36939832	0.045321	8.48	2.3456	0.084367
solcap_snp_c2_52496	chr03	37489785	0.045321	8.48	2.3456	0.084367
solcap_snp_c2_52494	chr03	37495967	0.045321	8.48	2.3456	0.084367
solcap_snp_c1_7139	chr03	37699819	0.035402	10.02	2.6783	0.098237
solcap_snp_c2_36467	chr03	38142166	0.042481	8.87	2.4308	0.087923
solcap_snp_c1_10879	chr03	38177443	0.042481	8.87	2.4308	0.087923
solcap_snp_c2_38047	chr03	38662974	0.042481	8.87	2.4308	0.087923
solcap_snp_c2_38054	chr03	38711501	0.045503	10.63	2.8056	0.103533
solcap_snp_c2_38058	chr03	38756280	0.023467	9.67	2.6023	0.095072
solcap_snp_c2_48378	chr03	39198646	0.046556	9.15	2.4921	0.090479
solcap_snp_c2_48372	chr03	39255217	0.042581	10.9	2.8643	0.105971
solcap_snp_c2_48371	chr03	39255236	0.042581	10.9	2.8643	0.105971
solcap_snp_c2_48370	chr03	39255317	0.045503	10.63	2.8056	0.103533
solcap_snp_c2_48369	chr03	39257162	0.042581	10.9	2.8643	0.105971
solcap_snp_c2_48368	chr03	39257271	0.045613	10.13	2.702	0.099227
solcap_snp_c2_48389	chr03	39312775	0.046556	9.15	2.4921	0.090479
solcap_snp_c1_16679	chr03	40197844	0.039886	10.44	2.7657	0.101876
solcap_snp_c2_35234	chr03	40992986	0.042581	10.9	2.8643	0.105971
solcap_snp_c2_42312	chr03	41530089	0.045503	10.63	2.8056	0.103533
solcap_snp_c1_6875	chr03	41994529	0.045503	10.63	2.8056	0.103533
solcap_snp_c1_6850	chr03	42019542	0.047216	8.45	2.3399	0.084127
solcap_snp_c1_9150	chr03	42895402	0.045378	8.22	2.2899	0.082043
solcap_snp_c1_9161	chr03	43024161	0.045378	8.22	2.2899	0.082043
solcap_snp_c2_45698	chr03	43326301	0.045378	8.22	2.2899	0.082043
solcap_snp_c2_46597	chr03	43481994	0.042533	8.62	2.3774	0.085694
solcap_snp_c2_46603	chr03	43498325	0.045378	8.22	2.2899	0.082043
solcap_snp_c2_20309	chr03	44661865	0.042533	8.62	2.3774	0.085694
solcap_snp_c2_55284	chr03	45388822	0.045378	8.22	2.2899	0.082043
solcap_snp_c1_8079	chr03	45435790	0.045378	8.22	2.2899	0.082043

solcap_snp_c2_25654	chr03	45603662	0.048311	8.7	2.3936	0.086372
solcap_snp_c2_25662	chr03	45979293	0.048311	8.7	2.3936	0.086372
solcap_snp_c2_11147	chr03	46806099	0.047471	8.61	2.3741	0.085556
solcap_snp_c2_29665	chr03	46924861	0.047471	8.61	2.3741	0.085556
solcap_snp_c2_45914	chr03	47769763	0.047471	8.61	2.3741	0.085556
solcap_snp_c2_20164	chr03	48882551	0.038327	10.36	2.7507	0.101251
solcap_snp_c2_1533	chr03	50688268	0.030338	8.31	2.3086	0.082822
solcap_snp_c2_22466	chr03	54580832	0.029048	9.84	2.6388	0.096594
solcap_snp_c2_10688	chr04	71592216	0.040132	11.16	2.9186	0.108222
solcap_snp_c2_41405	chr06	51183805	0.066581	8.48	2.3463	0.084394
solcap_snp_c2_19804	chr07	48956963	0.032548	10.38	2.753	0.101346
solcap_snp_c1_10457	chr07	49665986	0.028685	8.8	2.4165	0.087325
solcap_snp_c2_35049	chr07	49745280	0.028939	9.36	2.5372	0.09236
solcap_snp_c2_35053	chr07	49746796	0.028685	8.8	2.4165	0.087325
solcap_snp_c2_35078	chr07	49839630	0.028939	9.36	2.5372	0.09236
solcap_snp_c2_35094	chr07	49918098	0.029363	8.49	2.3483	0.08448
solcap_snp_c2_26003	chr07	50150805	0.02911	10.24	2.7249	0.100176
solcap_snp_c2_26011	chr07	50151997	0.029628	9.12	2.4842	0.090149
solcap_snp_c2_28223	chr07	51604961	0.033719	10.67	2.8142	0.103889
solcap_snp_c2_28238	chr07	51779684	0.029638	9.05	2.4702	0.089565
solcap_snp_c2_28244	chr07	51780403	0.031158	9.56	2.5795	0.094125
solcap_snp_c2_28290	chr07	52001357	0.035317	8.24	2.293	0.082171
solcap_snp_c2_42763	chr07	52191007	0.034835	10.09	2.6923	0.09882
solcap_snp_c2_12404	chr07	52544646	0.031925	9.82	2.6344	0.096413
solcap_snp_c1_16636	chr07	52759623	0.035102	8.78	2.4111	0.087103
solcap_snp_c2_12529	chr07	52792811	0.035224	8.39	2.3261	0.083551
solcap_snp_c2_12531	chr07	52795452	0.031925	9.82	2.6344	0.096413
solcap_snp_c2_12549	chr07	52913969	0.03398	8.87	2.4305	0.087912
solcap_snp_c2_12565	chr07	52958673	0.032732	10.41	2.761	0.101678
solcap_snp_c2_16846	chr07	53783075	0.032925	9.37	2.5383	0.092408
solcap_snp_c2_16843	chr07	53822702	0.034998	9.38	2.5417	0.092547
solcap_snp_c2_18544	chr07	54839197	0.033871	9.74	2.6191	0.095773
solcap_snp_c2_18549	chr07	54860473	0.034938	10.04	2.6821	0.098397
solcap_snp_c1_5981	chr07	55130142	0.036247	9.7	2.6087	0.095342
solcap_snp_c2_18680	chr07	55283766	0.030794	11.86	3.0635	0.11422
solcap_snp_c2_18684	chr07	55284214	0.036105	10.09	2.6923	0.098823
solcap_snp_c1_8821	chr07	55855903	0.036769	8.48	2.3468	0.084418
solcap_snp_c2_16159	chr08	55853675	0.032199	8.32	2.3115	0.082942
solcap_snp_c2_48597	chr09	778420	0.097527	11.35	2.9582	0.109862
