

Table S1. Genetic markers and their primers used for linkage analysis

Nr	Marker	Position (CM)	LG	Forward primer (5'-3')	Rverse primer (5'-3')	Type
1	XT01-007	0.00	A01	TGTA AACGACGGCCAGTGTAGAAGAAGAGAATACCTTTGGAG	GGAGGCACATAGAAGAGTGTGACT	SSR
2	sau_um364	1.36	A01	TGTA AACGACGGCCAGTCTACACGACGCACTCTCTCTCT	GAGCGGTAAGGGAAGTTTGAG	SSR
3	ACMP00271	23.67	A01	TGTA AACGACGGCCAGTCTACAGCTACTCTCATCTCCA	CGTCTCCACCAATGACCATA	SSR
4	XT01-019	33.08	A01	TGTA AACGACGGCCAGTCTTTGGGAGTTCAGCCGATTTCG	CTTTAGTACCATTAAAGGTTGG	SSR
5	Ra2-G09	34.63	A01	TGTA AACGACGGCCAGTACAGCAAGGATGTGTTGACG	GATGAGCCTCTGGTTCAAGC	SSR
6	BRMS-056	40.12	A01	TGTA AACGACGGCCAGTGTCAAGGCTACGGAGAGAGAG	CGTGACGCTAGAGTAATCGAGT	SSR
7	BRMS-220	40.79	A01	TGTA AACGACGGCCAGTCTGAATGTTTAGGAGTGTACTTC	TTGCTTCAGAAGGAAGGTCAGGAGA	SSR
8	XT01-025	45.11	A01	TGTA AACGACGGCCAGTCTCGGTTCGACAGATACTGC	CCTCCATTGTCAAACCACCTTCATC	SSR
9	XT01-KS40530	51.17	A01	GGAAGGTTTGACATGGTGGAC	GTTGACAGAGTAACCCCTCTGGACT	InDel
10	XT01-046	70.24	A01	TGTA AACGACGGCCAGTGTGAACAATTGAAAAGCATGA	AGCAGACCCAACCTTAGGATTGTG	SSR
11	XT01-045	70.49	A01	TGTA AACGACGGCCAGTCTATTACTTAGGGCAITTTATTTGAG	CGTAATCTGAAGCATACATTTAITGG	SSR
12	BRMS-180	71.75	A01	TGTA AACGACGGCCAGTATAAAGTCTTCTACTCACCAGCTT	AGTCACCTATCCGGCTGTACC	SSR
13	ACMP00756	72.35	A01	TGTA AACGACGGCCAGTCTCATCTTTGCCGTCTCAC	GGATTGGGTTGGTCTTCTTC	SSR
14	ACMP00617	72.82	A01	TGTA AACGACGGCCAGTAACTCAATGCTCTTCGCTCA	CCTTCTGCTCTTCCAAGAT	SSR
15	XT01-034	79.89	A01	GGTTTCGTTGTCCTATCGAGTAC	AAACATCGAAAACCTCTTCATGC	InDel
1	KBrS005A14R	0.00	A02	TGTA AACGACGGCCAGTATTCAAATCCTTTGGGTTTCATGC	GTTTCGGTATGGTCAATGTTTCAAG	SSR
2	KBrB019M05R	21.05	A02	TGTA AACGACGGCCAGTATGCAAAAGCATTGGATCTTCTCT	GTTTCCATTTGGAAGGAAACAAAAGGA	SSR
3	Bra020149	34.85	A02	CTAATACAGGCTTTGATTTCCG	ATACCCTACTCGAGGTAAGGAAAG	RFLP
4	KBrB071M18	41.75	A02	TGTA AACGACGGCCAGTACCGTGTATTTCTCGGTAAGA	GTTTATCCACAAAATGTGCTCATA	SSR
5	Bra023379	58.25	A02	CTTCGCTTTTCAAAGAGAGGATG	ATGAGAGAGTTAAACTGGTGTGACC	InDel
6	KBrH079A14F	87.54	A02	TGTA AACGACGGCCAGTATCTTCCACTTTTTCCTTC	GTTTGAGTGGGACTTGGAAITTTCCAT	SSR
1	BRMS-210	0.00	A03	TGTA AACGACGGCCAGTATTTCTGTCATGAGATATGGA	TCGGAATTGGATAAGAATTCAA	SSR
2	Ra3-D02B	29.02	A03	TGTA AACGACGGCCAGTACAGGAAACCCGTGGCTAGA	AACCCAACCTCAACGCTCTTG	SSR
3	BRMS-133	30.52	A03	TGTA AACGACGGCCAGTATGACTCTTCAAAAACGCAAAG	GATCTTGCAATAAAACCGACTTGA	SSR
4	BRMS-114	31.25	A03	TGTA AACGACGGCCAGTATCTCTTTTCTCTCTCTCTCT	TGTTCTGTATTTTATTTTCTCCGG	SSR
5	KBrH110H17R	50.67	A03	TGTA AACGACGGCCAGTACTAAGCTAGAGCTTGCACTGAA	GTTTGGGAAACAAAGGAAATGGAGAAA	SSR
6	BRMS-050	58.87	A03	TGTA AACGACGGCCAGTAACTTTGCTTCCACTGATTTTT	TTGCTTAACGCTAAATCCATAT	SSR
7	BRMS-042-2	61.33	A03	TGTA AACGACGGCCAGTATCCCGACAGCAACAAAAGA	TTCCGTTCTTTTCTGGGAATG	SSR
8	KBrH091J15R	69.71	A03	TGTA AACGACGGCCAGTACTTCCCGCAGATTTGAGTATAA	GTTTACGGTAACATCTTTGAGTAAGGTGA	SSR
9	BRMS-223	74.85	A03	TGTA AACGACGGCCAGTACTGCTTGTGCTTTTCAACG	GCTCTCAACTTGTGTTGAGTGTTA	SSR
10	BRMS-206	77.73	A03	TGTA AACGACGGCCAGTATGACTCTTCAAAAACGCAAAG	GATGACAACAACCTTCTCTGTGA	SSR
11	KBrH125H23F	83.73	A03	TGTA AACGACGGCCAGTAAAGACAAAACCTCAAAACACTA	AAGCCTTTTGAACCTCTCTGTGAT	SSR
12	BRMS-158	86.58	A03	TGTA AACGACGGCCAGTACAGTAAACAACATCACGACCA	GTTTATGATTTACATCGCGCTGCCCT	SSR
13	XT03-003	106.96	A03	TGTA AACGACGGCCAGTGTAGTTTTTCAGATTTCCGACAAC	CTCTATAGGCCCTCGTCACCAC	SSR
14	MLPK	113.65	A03	TGTA AACGACGGCCAGTGCACAAAGCATATTTGAAGAGGATC	TAACCTCCGCTTTGGCTACAGTC	SSR
15	BRMS-043	123.69	A03	TGTA AACGACGGCCAGTGGCAGTGTTTTTTCTTCAAGTGC	TTAATCCCTACCACAATTTCC	SSR
16	sau_um034	132.65	A03	TGTA AACGACGGCCAGTCTTCTTCCATCTTCACTCTCC	CTCAACTGAAGCTGCTCTCTCT	SSR
17	KBrH102J11R	151.59	A03	TGTA AACGACGGCCAGTAGCTTTGATCCATTCCCTTAGTG	GTTTCCCTCTCAGCAACACAGTACC	SSR
18	EST_0098_1343	152.55	A03	TGTA AACGACGGCCAGTAGGCTTTGATCCATTCCCTTAGTG	GTTTCCATCTCAGCAACACAGTTACG	SSR
19	KBrB054N11R	160.40	A03	TGTA AACGACGGCCAGTATCCAAACGATTTTCAATCTGCTG	GTTTGCACACCAATTTCTTCTCG	SSR
20	KBrS016H10R	163.66	A03	TGTA AACGACGGCCAGTACTTTGCTGTTGCTTAGCGAC	GTTTGTAGCAACCAATTTGCTGCATT	SSR
21	KBrH052O08F	168.42	A03	TGTA AACGACGGCCAGTAGCAGTAATCACTTTGTAGCCGC	GTTTCAATCTTTTGTCCGAACCAATCC	SSR
1	KBrH103G17F	0.00	A04	TGTA AACGACGGCCAGTACAGACAAAAGCTTCAATGCCACA	GTTTGGAGACAAAGGCTGATTCCTCCAAA	SSR
2	BRE-1_C08	10.39	A04	TGTA AACGACGGCCAGTAGAATCTATTTCTTCATCTTCCA	GTTTCACTACCAAAATCGAAAG	SSR
3	ARC1	16.31	A04	CACCATGGCCACTGATTCAGCAATG	GATCACAGGATCGTTTATGAGGTTG	RFLP
4	sau_um167	24.76	A04	TGTA AACGACGGCCAGTGGGGAAGGAGAGAGAGTTGC	CGATAGTCTCTCGATGTGCT	SSR
5	sau_um042	34.60	A04	TGTA AACGACGGCCAGTCTCCATCATCTTCTCTCTCTCT	ATGTTCTTGTGCGGCTTCTC	SSR
6	KBrB080B22F	47.79	A04	TGTA AACGACGGCCAGTAGCCTTTTGGCTTTTTCATCTGCTA	GTTTGGAGCCCAATGAAAGTGGTAGAAA	SSR
7	BRMS-276	56.39	A04	TGTA AACGACGGCCAGTACCGTTTTGCAATTTAAGAGCATT	TCACCACCACAGTATCTTCAACAATCA	SSR
8	OI10-C01	67.05	A04	TGTA AACGACGGCCAGTATGACTGTTAAACAGCGCC	CTTCTCCAACAAAAGCTCGG	SSR
9	KBrB047M10F	79.29	A04	TGTA AACGACGGCCAGTATGCTTGTCCATCTCCATAAC	GTTTGACCATGAAAGGCGTTCCG	SSR
1	Bra029671	0.00	A05	CTTCTACTGGATGTGTATAGTCCG	AGCCTATCATTACTCGGAGAGTTC	RFLP
2	sau_um014	11.66	A05	TGTA AACGACGGCCAGTGAATCTGGTTCCGGTTCAGTCT	CTCCTCATCCATCTCTCTCTCT	SSR
3	XT05-001	28.65	A05	AGAGTGACTCTCTCTTTAGCCAAC	CTGATCGTACACCTCTATCG	RFLP
4	BRE-1_F07	31.14	A05	TGTA AACGACGGCCAGTATTATCAACAGCCAACCAAAA	GTTTAGAGACTGACGGAACCTTTGAA	SSR
5	sau_um419	37.44	A05	TGTA AACGACGGCCAGTCTGCTGAAAAAGGTTACTCTGT	GGAGCCAGGTTATGAGGATTAG	SSR
6	sau_um366	41.15	A05	TGTA AACGACGGCCAGTCTTCTCTCGTATCACCCTCTCT	GCCTACGTTCTTACAGCGAGAT	SSR
7	KBrH070F21R	44.43	A05	TGTA AACGACGGCCAGTAGTTCCAAACATCTGAAACCAAGT	GTTTACTCAAGCTGCGTCCAAAAGC	SSR
8	sau_um062	49.21	A05	TGTA AACGACGGCCAGTGAACAGCAGCAGGAGGAGAC	CGAACATGGACCAAGAGAGAAC	SSR
9	KBrH059H18R	58.87	A05	TGTA AACGACGGCCAGTACCCACCTTTTCTAGATCTGTATGA	GTTTCTCCAGCTTCTCCATCTGTTTCC	SSR
10	KBrH088D21F	64.62	A05	TGTA AACGACGGCCAGTATGTTGACGGAGGCATAGACTTT	GTTTGTCCCTGGAAATGCAAAAGGTT	SSR
11	KBrH061C03F	73.01	A05	TGTA AACGACGGCCAGTATACCTGCTGCTTGTCTCTGTA	GTTTGAGATGGCTGATGCTGAAGAAC	SSR
12	KBrB075I01F	75.08	A05	TGTA AACGACGGCCAGTACCGTATTTCTCGGTAAGA	GTTTATCCACAAAATGTGCTCATA	SSR
13	XT05-004	78.50	A05	GCTTTTACCTGGAGCTTCTTCCAGG	CTAACCAAGGCCACTCCATCACG	SSR
14	BRMS-034	91.28	A05	TGTA AACGACGGCCAGTGTACAAATAACGACGGAGAGA	GAGCCAAGAAAAGGCAATAGAT	SSR

Table S1. (continued)

Nr	Marker	Position (CM)	LG	Forward primer (5'-3')	Rverse primer (5'-3')	Type
1	Na12-D04	0.00	A06	TGTAACACGACGGCCAGTACGGAGTGTATGGGTC	CCTCAATGAAACTGAAATATGTGTG	SSR
2	BRMS-077	19.08	A06	TGTAACACGACGGCCAGTCCGCCGAATTTATAGTGT	TCGATTAACCAGCTAAAATAATAATG	SSR
3	Ra2-F04	25.99	A06	TGTAACACGACGGCCAGTCCACAAACACATAAATAAGAGAGAG	AACAACATAAAGATTCATTTCCG	SSR
4	BRMS-309	45.76	A06	TGTAACACGACGGCCAGTCAAGAGCAAGTTTGAACAAACGAT	CATCAGTTCTTGATATGTAGGTGA	SSR
5	ACMP00692	52.69	A06	TGTAACACGACGGCCAGTTCGAGTTGACAGCCAAAGTAG	AACGTAACGTTCTCTTCC	SSR
6	BRMS-221	54.39	A06	TGTAACACGACGGCCAGTAAAGTCTTGACGTTGAGGAAGAA	CAGGTTCTTATGAAGACCATGCAT	SSR
7	BRMS-095	61.95	A06	TGTAACACGACGGCCAGTGCATAACCAATGTATGTCTGCT	GATCCCTAATCAAGAGACAGAGAG	SSR
8	ACMP00520	63.48	A06	TGTAACACGACGGCCAGTCCGGCTTCTAGTTGGGTAA	CGAGGCTTACTCGATGCAG	SSR
9	KBrH101E14	72.78	A06	TGTAACACGACGGCCAGTATCGAAATCAAATCAAACCGCTC	GTTTCATCAACCACGTTTTCACAGA	SSR
10	KBrH107H15R	82.90	A06	TGTAACACGACGGCCAGTACAGCGAGTGGTAGTACACGAAA	GTTTGCCTATCGTCTCTCATCTGCAT	SSR
11	EST_0098_1347	85.71	A06	TGTAACACGACGGCCAGTATCTCTCTCCGAATCCAAAA	GTTTAGCTCTGATGAGACCAGCTCTT	SSR
12	Bra026007	95.57	A06	GTGGTATGAGAGTTGGGTGTTTC	TTAGATAGAAGTGGCTCCCTGAAC	InDel
13	O110-D01	108.66	A06	TGTAACACGACGGCCAGTCTCTGCCAAAAGCAAATAGC	CTTGGCTCTCTCACCACC	SSR
1	KBrH001H12F	0.00	A07	TGTAACACGACGGCCAGTGGTGTGCTCAGGTTCAAGTAG	GTTTCTGTGTGCCATTGATCGGTAA	SSR
2	Ni4-B03	8.37	A07	TGTAACACGACGGCCAGTTGCTGTTCTGTGGAATTGTGCG	ACTTCTTTACATCTTAATCGC	SSR
3	KBrH125E20R	13.76	A07	TGTAACACGACGGCCAGTACATTCACCTTGTAGTCCGCTCAGA	GTTTAAATGTCGAAGTCAAGGTTGGGA	SSR
4	BRMS-296	16.30	A07	TGTAACACGACGGCCAGTCACTAATGTTGCTGAGAAAGAGG	TATATGAAACCGATGAAGTCTCTT	SSR
5	KBrH107O12F	25.34	A07	TGTAACACGACGGCCAGTCAATGCTGGGAAGAACTCTGTG	GTTTAGATCTCTCGCACCTCAAAA	SSR
6	KBrH106E08F	29.28	A07	TGTAACACGACGGCCAGTATCGATCCTTGGATCTGCTTGAT	GTTTAAACCGCTCAAAAAGCGTTAATTC	SSR
7	KBrS011B13F	35.78	A07	TGTAACACGACGGCCAGTAGACCAGTGCAAAATGAGGTTAGA	GTTTAAAGGGTATACAGGGGTGACGT	SSR
8	SLG	49.36	A07	ATGAAAGGCGTAAGAAAAACCTA	CCGTGTTTATTTAAGAGAAAGAGCT	RFLP
9	BRMS-298	59.47	A07	TGTAACACGACGGCCAGTCCACTGTTTTATGACTCCAGTGTCT	TGACCTGGTGAAGTATGTTGCTCGT	SSR
10	KBrB056L15	76.09	A07	TGTAACACGACGGCCAGTAGGACATCTTTTGTAAACCAA	GTTTCACTCAATCTTAATTTTGAGA	SSR
1	BRMS-033	0.00	A08	TGTAACACGACGGCCAGTGGCGAAACGAACTCTCCATGT	CCTCCTGTGCTTCCCTGGAGACG	SSR
2	XT08-028	13.50	A08	GACTCCTGTCTCTCTCTCTCTC	TGACTCCGTGAAATATAGATCGC	SSR
3	ACMP00373	18.08	A08	TGTAACACGACGGCCAGTGAAGTTGGGAGATTGGAT	GCCTCAAAGGTCATCATCAG	SSR
4	Ra2-E12	25.31	A08	TGTAACACGACGGCCAGTGTGACAGTGTCCACTTCGCG	AAGAGAAACCAATAAAGTAGAAC	SSR
5	Na12-B05	42.85	A08	TGTAACACGACGGCCAGTCAAATATCCGTCATCGGAGC	CCTGCGGATATTGAAGACC	SSR
6	KBrH077O23F	62.31	A08	TGTAACACGACGGCCAGTACTGTAAATGTGACCCCAACAAT	GTTTAGTCAAATGGCTCTCTCGCCAA	SSR
7	sau_um297	69.64	A08	TGTAACACGACGGCCAGTGGAAACACGAGTTGTCACTTA	ATGGTGAAGTGTGAAGAGGATG	SSR
8	sau_um306	87.00	A08	TGTAACACGACGGCCAGTGTACTTGGTGGTTGTTAGGCC	GTGTCCTCTCTCAGGTTCTCTC	SSR
9	EJU3	88.21	A08	TGTAACACGACGGCCAGTACTCTTTTAATCAAACAAGAAATCA	GTTTTCGGACAATGGCAGTGATA	SSR
1	KBrB016E19R	0.00	A09	TGTAACACGACGGCCAGTATGTTGAGCTGCGAATACGTTCTCT	GTTTGAGCAATCTCACCTCTCTGCTGT	SSR
2	sau_um105	1.05	A09	TGTAACACGACGGCCAGTCTTTCTAATGGGAAGCGGTAG	CTCCCTCTTCAATGACTAC	SSR
3	Bra026855	23.56	A09	GAGTGGTGTCTGAGATCATGAGG	CTAGAAGGAAGAGACAGCAGCAAG	InDel
4	ENA21	31.50	A09	TGTAACACGACGGCCAGTGGATGTTTGGAGCAGATGA	GTTGGAGACTTGGCTTTGTGT	SSR
5	Na10-B07b	44.15	A09	TGTAACACGACGGCCAGTGCCTTAGATTAGATGGTCCG	ACTTCAGCTCCGATTTGCC	SSR
6	KBrH143P19R	50.88	A09	TGTAACACGACGGCCAGTATAGACTTCCACCAAGTGGCAT	GTTTCGCATCCCAATCTTGTGAAT	SSR
7	KBrH120K23R	56.21	A09	TGTAACACGACGGCCAGTAGAATTTGGGGTCTGTACTCTGT	GTTTAAACAGACTGGGCGTTACGGAAA	SSR
8	BRMS-079	60.26	A09	TGTAACACGACGGCCAGTGGGAAGATCCCAATCAAGAAAATG	AATGACCTTGTGACCTTATCGTT	SSR
9	Bra036837	66.33	A09	TGTAACACGACGGCCAGTACTGACGTGACGTATACAGATGC	CTCCTTACGTTTTCATCATTAAAC	SSR
10	Ra2-A11	80.64	A09	TGTAACACGACGGCCAGTGACCTATTTAATATGCTGTTTACG	ACCTCACCGGAGAGAAATCC	SSR
11	BRMS-142	84.52	A09	TGTAACACGACGGCCAGTTACTTTGCTTTAATTTGCATGGAAG	TTGTTTGCATTTGCATGTAAGACTTC	SSR
12	BRMS-312	86.81	A09	TGTAACACGACGGCCAGTGCAGCAATTAAGCTTCAAGTA	ATTTCAACATGTCAGACGCTCTTTC	SSR
13	BRMS-120	93.16	A09	TGTAACACGACGGCCAGTGCAGCATAACGGCAAAAACCTCGCA	GGTACGGCAGTCTCGGTGCGTTAA	SSR
14	BRMS-154	98.45	A09	TGTAACACGACGGCCAGTATGATAGACGAAAGAAAACAAATCA	GGAACCTTCCAGACTGTACTCTC	SSR
15	KBrB060H21R	104.91	A09	TGTAACACGACGGCCAGTATGACAGGTTACATATTGTGTCT	GTTTGAAGCGCGTGAAGTCTCT	SSR
1	KBrH080A08(BrFLC1)	0.00	A10	TGTAACACGACGGCCAGTATGAACCTATTTATAGTATAGCTGGC	GTTTGTATGTTTCTCTCTTTTTCATC	SSR
2	KBrB053N06F	9.46	A10	TGTAACACGACGGCCAGTAGATCTCCATGGCTTCTTGTATGT	GTTTCCAITATAAGGCCACGAAACAAA	SSR
3	KBrH094B16F	31.28	A10	TGTAACACGACGGCCAGTACTTCTCTCGATCTCACTCTCGG	GTTTCAACTCTCTTGAACGACTC	SSR
4	KBrH006K06R	36.53	A10	TGTAACACGACGGCCAGTAAAGAGAGACGACACACACTCGG	GTTTAAATCGCAATCCCAAAAAGAGAGA	SSR
5	KBrH054N12R	43.19	A10	TGTAACACGACGGCCAGTACCATTGTAACATCTGGAAGGTGA	GTTTGTGACGAGCTTCTACACCAG	SSR
6	sau_um217	49.81	A10	TGTAACACGACGGCCAGTAAACGAAACGGTGTCAATGC	GTAAGCTCGGAACTCACTAAACG	SSR
7	BRMS-197	57.52	A10	TGTAACACGACGGCCAGTCTATTACAAGTGCACATAACCCGAAT	GCCTCAACTGTTGTTGAGTGTGA	SSR
8	sau_um433	58.30	A10	TGTAACACGACGGCCAGTAAAGTCCACAGCAGGAGATTG	GGGATGAGAAAAGACAGGTGG	SSR
9	BRMS-239	59.95	A10	TGTAACACGACGGCCAGTAAATATGCTGTAATATTCGGATT	TCTCTGATGACTCCATACTTTC	SSR
10	KBrB069K03F	61.12	A10	TGTAACACGACGGCCAGTAGCATTATTTGACAAAGAGACGG	GTTTGGGTGCGTGTGTAATCC	SSR
11	KBrB009O19R	63.23	A10	TGTAACACGACGGCCAGTACCCTGGTCTTCTTAGGTTCTCC	GTTTGAAGCCTGTTGAGTCTCTC	SSR

Table S2. *S*-haplotype segregation in F_2 population

<i>S</i> -genotype	$S_{46}S_{46}$	$S_{46}S_{55}$	$S_{55}S_{55}$	Total		Goodness of fit	
Observed	22	64	24	110	Ratio	χ^2	<i>p</i>
Calculated	27.50	55.00	27.50	110.00	1:2:1	3.02	0.2-0.4
Average of RLSICO ₂	2.22	2.51	2.49				

Table S3. Annotated genes and Arabidopsis homologues in BrSIO1

Gene ID	LG	Start	End	AGI	Description	Slide A	Slide B	Slide C	AVE
Bra004778	A05	1802120	1804421	AT2G43710	Encodes a stearyl-ACP desaturase	355.3	361.7	372.9	363.3
Bra004779	A05	1805009	1805659	AT2G43730	Mannose-binding lectin superfamily protein				
Bra004780	A05	1806494	1807130	AT2G43730	Mannose-binding lectin superfamily protein				
Bra004781	A05	1807522	1809777	AT2G43750	Arabidopsis thaliana O-acetylserine (thiol) lyase (OAS-TL) isoform oasB	272.7	287.7	333.2	297.9
Bra004782	A05	1810520	1811050	AT2G43760	molybdopterin biosynthesis MoaE family protein	123.3	118.4	163.2	134.9
Bra004783	A05	1811154	1813258	AT2G43770	Transducin/WD40 repeat-like superfamily protein	225.5	203.2	203.4	210.7
Bra004784	A05	1814778	1816787	AT2G43790	MAP KINASE 6	207.4	162.7	178.5	182.9
Bra004785	A05	1817117	1818644	AT2G43795	unknown protein				
Bra004786	A05	1822215	1825011	AT2G43800	Actin-binding FH2 (formin homology 2) family protein	343.2	339.3	349.8	344.1
Bra004787	A05	1828516	1830271	AT2G43820	Arabidopsis thaliana salicylic acid glucosyltransferase 1				
Bra004788	A05	1831237	1832659	AT2G43820	Arabidopsis thaliana salicylic acid glucosyltransferase 1				
Bra004789	A05	1837991	1839351	AT2G43880	Pectin lyase-like superfamily protein				
Bra004790	A05	1846616	1848000	AT2G43880	Pectin lyase-like superfamily protein				
Bra004791	A05	1849377	1850884	AT2G43880	Pectin lyase-like superfamily protein				
Bra004792	A05	1851396	1853277	AT2G43910	HARMLESS TO OZONE LAYER 1 (HOL1)				
Bra004793	A05	1857759	1859109	AT2G43910	HARMLESS TO OZONE LAYER 1 (HOL1)				
Bra004794	A05	1860370	1861952	AT2G43945	unknown protein				
Bra004795	A05	1863096	1865725	AT2G43970	RNA-binding protein	145.7	150.2	139.6	145.1
Bra004796	A05	1866075	1868706	AT2G43980	inositol 1,3,4-trisphosphate 5/6-kinase 4 (ITPK4)	105.7	112.6	88.8	102.4
Bra004797	A05	1868986	1870488	AT2G43990	unknown protein	26.8	25.9	26.9	26.5
Bra004798	A05	1871248	1871856	AT2G44000	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family				
Bra004799	A05	1873482	1873766	AT2G44010	unknown protein				
Bra004800	A05	1874741	1876084	AT2G44020	Mitochondrial transcription termination factor family protein	77.3	76.5	74.7	76.2
Bra004801	A05	1877612	1879360	AT2G44065	Ribosomal protein L2 family	209.7	234.3	228.9	224.3
Bra004802	A05	1881187	1889019	-	-				
Bra004803	A05	1892847	1893176	AT2G44080	Encodes ARL, a gene similar to ARGOS involved in cell expansion-dependent organ growth	98.5	114.5	104.0	105.7
Bra004804	A05	1894119	1896095	AT2G44090	Ankyrin repeat family protein	73.1	74.2	96.1	81.2
Bra004805	A05	1898162	1900945	AT2G44100	GDP dissociation inhibitor involved in vesicular membrane traffic	798.2	773.1	758.3	776.6
Bra004806	A05	1902291	1903374	AT2G44120	Ribosomal protein L30/L7 family protein	1391.5	1390.2	1443.3	1408.3
Bra004807	A05	1908181	1909470	AT2G44130	Galactose oxidase/kelch repeat superfamily protein				
Bra004808	A05	1909664	1911216	AT2G44140	Peptidase family C54 protein				
Bra004809	A05	1912514	1914621	AT2G44150	Encodes a protein-lysine N-methyltransferase. Located in ER.	92.3	88.6	81.4	87.4
Bra004810	A05	1915442	1918534	AT2G44160	methylenetetrahydrofolate reductase MTHFR2 mRNA, complete				
Bra004811	A05	1919370	1921218	AT2G44190	Encodes a novel microtubule binding protein	50.6	49.0	63.4	54.3
Bra004812	A05	1921741	1923420	AT2G44195	CBF1-interacting co-repressor CIR, N-terminal;Pre-mRNA splicing factor				
Bra004813	A05	1926040	1927962	-	-				
Bra004815	A05	1933683	1935558	-	-				
Bra004816	A05	1936960	1939048	-	-				
Bra004817	A05	1939997	1941807	AT2G44230	Plant protein of unknown function (DUF946)	96.2	86.0	85.8	89.3
Bra004818	A05	1943704	1945964	-	-				
Bra004819	A05	1947849	1950090	-	-				
Bra004820	A05	1952417	1954357	-	-				
Bra004821	A05	1965165	1969541	-	-				
Bra004822	A05	1970933	1973160	AT2G44270	Encodes ROL5, a repressor of lrx1 mutants that develop aberrant root hairs	74.2	78.7	71.0	74.6
Bra004823	A05	1974209	1976693	AT2G44280	Major facilitator superfamily protein				
Bra004824	A05	1978048	1979340	AT2G44290	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein				
Bra004825	A05	1984033	1984575	AT2G44340	VQ motif-containing protein				
Bra004826	A05	1987355	1988083	AT2G44370	Cysteine/Histidine-rich C1 domain family protein				
Bra004827	A05	1992070	1994016	-	-				
Bra004828	A05	1995264	1996025	AT2G44370	Cysteine/Histidine-rich C1 domain family protein				
Bra004829	A05	1997885	1999084	AT2G44410	RING/U-box superfamily protein				
Bra004830	A05	1999513	2001278	AT2G44420	protein N-terminal asparagine amidohydrolase family protein	41.6	42.0	44.9	42.8
Bra004831	A05	2002992	2005950	AT2G44430	DNA-binding bromodomain-containing protein				
Bra004832	A05	2006506	2008503	AT2G44440	Emsy N Terminus (ENT) domain-containing protein	47.8	56.6	46.1	50.2
Bra004833	A05	2013630	2016348	AT2G44450	beta glucosidase 15 (BGLU15)	64.3	60.3	68.0	64.2
Bra004834	A05	2020029	2022302	-	-				
Bra004835	A05	2025706	2029646	AT2G44450	beta glucosidase 15 (BGLU15).	64.3	60.3	68.0	64.2
Bra004836	A05	2035186	2039155	AT2G44450	beta glucosidase 15 (BGLU15)				
Bra004837	A05	2042204	2066541	AT2G44460	beta glucosidase 28 (BGLU28)	22.6	19.5	18.7	20.3
Bra004838	A05	2074677	2077758	AT2G44450	beta glucosidase 15 (BGLU15)				
Bra004839	A05	2080458	2083229	AT2G44490	Encodes a glycosyl hydrolase	43.2	46.4	46.5	45.4
Bra004840	A05	2086734	2089770	AT2G44450	beta glucosidase 15 (BGLU15)				
Bra004841	A05	2099727	2101689	AT2G44500	O-fucosyltransferase family protein	185.0	191.9	183.6	186.8
Bra004842	A05	2102608	2104660	AT2G44520	cytochrome c oxidase 10 (COX10)	84.6	86.9	86.4	86.0
Bra004843	A05	2105300	2106562	AT2G44525	Protein of unknown function (DUF498/DUF598)	186.7	183.3	165.9	178.6
Bra004844	A05	2107659	2109389	AT2G44540	glycosyl hydrolase 9B9 (GH9B9)				
Bra004845	A05	2111987	2113709	AT2G44540	glycosyl hydrolase 9B9 (GH9B9)				
Bra004846	A05	2116326	2118247	AT2G44560	glycosyl hydrolase 9B11 (GH9B11)				
Bra004847	A05	2124205	2124642	AT2G44581	RING/U-box superfamily protein				
Bra004848	A05	2125608	2127401	AT2G44580	zinc ion binding				
Bra004849	A05	2129746	2130591	AT2G44600	unknown protein				
Bra004850	A05	2133155	2135330	AT2G44610	Encodes a GTP-binding protein with similarity to yeast YPT6	242.5	239.0	208.8	230.1
Bra004851	A05	2136308	2136887	AT2G44620	Encodes a member of the mitochondrial acyl carrier protein (ACP) family.	518.5	491.2	524.1	511.3
Bra004852	A05	2137601	2139679	AT2G44640	unknown protein	184.6	186.0	177.7	182.8
Bra004853	A05	2139867	2141063	AT2G44650	Encodes a chloroplast-localized chaperonin 10	686.8	690.6	647.1	674.8
Bra004854	A05	2142969	2145037	AT2G44660	ALG6, ALG8 glycosyltransferase family				
Bra004855	A05	2147596	2147974	AT2G44670	Protein of unknown function (DUF581)	479.1	485.0	473.6	479.2
Bra004856	A05	2149090	2150324	AT2G44680	Encodes casein kinase II beta chain, a CK2 regulatory subunit.	137.6	137.4	140.7	138.6
Bra004857	A05	2151542	2152819	AT2G44690	A member of ROP GTPase gene family.	34.0	40.3	29.4	34.5
Bra004858	A05	2153663	2157318	AT2G44710	RNA-binding (RRM/RBD/RNP motifs) family protein	61.7	79.6	77.6	73.0
Bra004859	A05	2158462	2159370	AT2G44730	Alcohol dehydrogenase transcription factor Myb/SANT-like family protein	56.2	48.3	45.6	50.0
Bra004860	A05	2160277	2160909	-	-				
Bra004861	A05	2161320	2162135	-	-				
Bra004862	A05	2162865	2164474	-	-				
Bra004863	A05	2164973	2166282	AT2G44740	cyclin p4;1 (CYCP4;1)	102.9	110.4	121.4	111.6
Bra004864	A05	2169762	2171241	AT2G44745	WRKY family transcription factor	20.8	33.3	26.7	27.0
Bra004865	A05	2176019	2177933	AT2G44760	unknown protein	49.5	54.5	42.4	48.8

Table S3. (continued)

Bra004866	A05	2179844	2180803	AT2G44790	UCLACYANIN 2				
Bra004867	A05	2184212	2186273	AT2G44800	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein				
Bra004868	A05	2204575	2205768	-	-	-	-	-	-
Bra004869	A05	2207070	2208410	AT2G44810	DEFECTIVE ANther DEHISCENCE 1				
Bra004870	A05	2217092	2217645	-	-	-	-	-	-
Bra004871	A05	2222111	2222983	AT2G44820	unknown protein	186.4	184.1	191.6	187.4
Bra004872	A05	2228412	2231516	AT2G44830	Protein kinase superfamily protein	137.5	134.7	137.7	136.6
Bra004873	A05	2234840	2235538	AT2G44840	ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13	123.2	116.5	117.9	119.2
Bra004874	A05	2237723	2239355	AT2G44910	ARABIDOPSIS THALIANA HOMEBOX-LEUCINE ZIPPER PROTEIN 4	13.7	16.8	15.0	15.2
Bra004875	A05	2247722	2249159	AT2G44920	Tetratricopeptide repeat (TPR)-like superfamily protein	160.5	161.0	185.5	169.0
Bra004876	A05	2249958	2250774	-	-	-	-	-	-
Bra004877	A05	2252356	2257044	AT2G44930	Plant protein of unknown function (DUF247)				
Bra004878	A05	2263243	2264091	AT2G44940	encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family.	41.0	41.9	38.6	40.5
Bra004879	A05	2270073	2274586	AT2G44950	encodes one of two orthologous E3 ubiquitin ligases in Arabidopsis	71.2	78.0	73.0	74.1
Bra004880	A05	2275277	2277507	AT2G44970	alpha/beta-Hydrolases superfamily protein	131.9	125.6	123.2	126.9
Bra004881	A05	2278325	2283046	AT2G44980	SNF2 domain-containing protein / helicase domain-containing protein	24.5	28.6	27.1	26.7
Bra004882	A05	2283365	2286657	AT2G45000	EMBRYO DEFECTIVE 2766 (EMB2766)				
Bra004883	A05	2287086	2288787	AT2G45010	PLAC8 family protein	129.8	144.1	126.1	133.3
Bra004884	A05	2290046	2294328	AT2G45030	Translation elongation factor EFG/EF2 protein				
Bra004885	A05	2296232	2297251	AT2G45040	Matrixin family protein				
Bra004886	A05	2302497	2303350	AT2G45050	Encodes a member of the GATA factor family of zinc finger transcription factors.				
Bra004887	A05	2305445	2305696	AT2G45070	Sec61 Beta Subunit	932.4	956.1	1002.5	963.7
Bra004888	A05	2310343	2311104	AT2G45080	cyclin p3;1 (cycp3;1)	48.4	43.3	43.9	45.2
Bra004889	A05	2314366	2315456	AT2G45110	member of BETA-EXPANSINS.				
Bra004890	A05	2323211	2326057	AT2G45110	member of BETA-EXPANSINS.				
Bra004891	A05	2331494	2332478	-	-	-	-	-	-
Bra004892	A05	2332987	2338977	AT2G45220	Plant invertase/pectin methylesterase inhibitor superfamily				
Bra004893	A05	2344666	2347543	AT2G45240	Encodes a cytoplasmic MAP1 like methionine aminopeptidase	227.3	242.2	222.1	230.5
Bra004894	A05	2347927	2349138	AT2G45260	Plant protein of unknown function (DUF641)				
Bra004895	A05	2349797	2352347	AT2G45270	Mitochondrial protein essential for embryo development.				
Bra004896	A05	2353963	2355351	-	-	-	-	-	-
Bra004897	A05	2364883	2367127	AT2G45280	Encodes a protein similar to RAD51C	45.2	44.9	43.2	44.4
Bra004898	A05	2367652	2370453	AT2G45290	Transketolase	47.3	54.4	79.6	60.4
Bra004899	A05	2371226	2378801	AT2G45330	RNA 2'-phosphotransferase/ transferase, transferring phosphorus-containing groups				

Genes listed in BOLD are expressing in carpel based on Microarray data NASCArrays, and signal from 3 individual slides and those average are shown.

Table S4. Annotated genes and Arabidopsis homologues in BrSIO2

Gene ID	LG	Start	End	AGI	Description	Slide A	Slide B	Slide C	AVE
Bra012922	A03	21503679	21504755	AT3G49790	Carbohydrate-binding protein	37.5	35.7	42.1	38.4
Bra012921	A03	21506279	21506569	-	-	-	-	-	-
Bra012920	A03	21506932	21509115	AT3G49740	pentatricopeptide (PPR) repeat-containing protein	33.3	20.4	23.9	25.9
Bra012919	A03	21520607	21521649	AT3G49850	Encodes a telomeric DNA binding protein.	42.6	40.7	33.9	39.1
Bra012918	A03	21522066	21523153	AT3G49860	A member of ARF-like GTPase family	-	-	-	-
Bra012917	A03	21525865	21527832	AT3G49890	unknown protein	42.3	35.4	43.1	40.2
Bra012916	A03	21528338	21528778	AT3G49910	Translation protein SH3-like family protein	2606.1	2733.3	2843.0	2727.4
Bra012915	A03	21529958	21531257	AT3G49920	Encodes a voltage-dependent anion channel.	-	-	-	-
Bra012914	A03	21533867	21534508	AT3G49930	C2H2 and C2HC zinc fingers superfamily protein	-	-	-	-
Bra012913	A03	21541449	21542267	AT3G49940	LOB domain-containing protein 38 (LBD38)	62.4	54.6	67.5	61.5
Bra012912	A03	21549497	21550945	AT3G49990	unknown protein	137.9	145.5	123.6	135.6
Bra012911	A03	21570191	21571431	AT3G50040	unknown protein	-	-	-	-
Bra012910	A03	21573956	21574837	AT3G50060	Encodes a member of the R2R3 transcription factor gene family.	711.5	716.7	722.0	716.7
Bra012909	A03	21583387	21584617	AT3G50070	Encode CYCD3;3, a CYCD3 D-type cyclin.	481.9	467.3	473.2	474.1
Bra012908	A03	21588821	21591662	AT3G50110	Encodes a phosphatase with low in vitro tyrosine phosphatase activity	55.2	47.4	47.5	50.0
Bra012907	A03	21592701	21594635	AT3G50120	Plant protein of unknown function (DUF247)	-	-	-	-
Bra012906	A03	21597258	21599046	AT3G50130	Plant protein of unknown function (DUF247)	-	-	-	-
Bra012905	A03	21600007	21602471	AT3G50140	Plant protein of unknown function (DUF247)	-	-	-	-
Bra012904	A03	21609574	21611627	AT3G50120	Plant protein of unknown function (DUF247)	-	-	-	-
Bra012903	A03	21620360	21621754	AT3G50390	Transducin/WD40 repeat-like superfamily protein	-	-	-	-
Bra012902	A03	21622445	21623207	AT3G50400	GDSL-like Lipase/Acylhydrolase superfamily protein	-	-	-	-
Bra012901	A03	21630236	21630964	AT3G50410	Arabidopsis Dof protein containing a single 51-amino acid zinc finger DNA-binding domain	70.5	79.0	81.6	77.0
Bra012900	A03	21631175	21633316	AT3G50420	Pentatricopeptide repeat (PPR) superfamily protein	-	-	-	-
Bra012899	A03	21634500	21635632	AT3G50440	Encodes a protein shown to have methyl jasmonate esterase activity in vitro.	-	-	-	-
Bra012898	A03	21646727	21647884	AT3G50450	Homolog of RPW8	-	-	-	-
Bra012897	A03	21648630	21650423	AT3G50500	encodes a member of SNF1-related protein kinases (SnRK2)	178.8	185.4	183.2	182.5
Bra012896	A03	21650998	21654747	AT3G50520	Phosphoglycerate mutase family protein	120.1	133.2	124.4	125.9
Bra012895	A03	21656123	21657262	AT3G50620	P-loop containing nucleoside triphosphate hydrolases superfamily protein	68.7	61.8	52.5	61.0
Bra012894	A03	21677192	21678080	AT3G50630	Kip-related protein (KRP) gene	93.4	89.3	80.4	87.7
Bra012893	A03	21684916	21686388	AT3G50740	UGT72E1 is an UDPG:coniferyl alcohol glucosyltransferase which specifically glucosylates sinapyl- and coniferyl aldehydes.	-	-	-	-
Bra012892	A03	21689260	21690705	AT3G50470	UGT72E1 is an UDPG:coniferyl alcohol glucosyltransferase which specifically glucosylates sinapyl- and coniferyl aldehydes.	-	-	-	-
Bra012891	A03	21701000	21701975	AT3G50750	BES1/BZR1 homolog 1 (BEH1)	-	-	-	-
Bra012890	A03	21712848	21713864	AT3G50760	Encodes a protein with putative galacturonosyltransferase activity.	15.1	22.2	21.3	19.5
Bra012889	A03	21721289	21721900	AT3G50770	calmodulin-like 41 (CML41)	30.1	28.6	25.1	28.0
Bra012888	A03	21729319	21731296	-	-	-	-	-	-
Bra012887	A03	21731833	21732303	AT3G50800	unknown protein	-	-	-	-
Bra012886	A03	21735261	21735878	AT3G50810	Uncharacterised protein family (UPF0497)	62.4	74.8	60.1	65.8
Bra012885	A03	21739425	21740448	AT3G50830	cold acclimation protein WCOR413-like protein beta form	176.7	172.0	166.3	171.7
Bra012884	A03	21743712	21744839	AT3G50860	Clathrin adaptor complex small chain family protein	84.4	90.3	87.9	87.6
Bra012883	A03	21788116	21789296	AT3G50870	Encodes a GATA transcriptional regulator required to position the proembryo boundary in the early embryo.	30.0	49.1	50.4	43.2
Bra012882	A03	21799851	21803215	AT3G50890	homeobox protein 28 (HB28)	59.6	52.7	56.7	56.3
Bra012881	A03	21806412	21806831	AT3G50900	unknown protein	12.1	29.1	14.7	18.6
Bra012880	A03	21808947	21810344	AT3G50910	unknown protein	134.8	141.5	125.2	133.8
Bra012879	A03	21810726	21814469	AT3G50920	Encodes a phosphatidic acid phosphatase that can be detected in chloroplast membrane fractions.	119.6	123.1	135.3	126.0
Bra012878	A03	21819325	21820083	-	-	-	-	-	-
Bra012877	A03	21823544	21825055	AT3G50930	cytochrome BC1 synthesis (BCS1)	-	-	-	-
Bra012876	A03	21825545	21827016	AT3G50960	Encodes a protein that functions in microtubule assembly.	107.8	113.2	114.5	111.8
Bra012875	A03	21827741	21828842	AT3G51000	alpha/beta-Hydrolases superfamily protein	74.0	67.9	87.4	76.4
Bra012874	A03	21829127	21830246	AT3G51010	unknown protein	361.5	373.1	367.8	367.5
Bra012873	A03	21830934	21831338	AT3G51020	unknown protein	-	-	-	-
Bra012872	A03	21833447	21834370	AT3G51030	encodes a cytosolic thioredoxin	108.0	118.5	120.6	115.7
Bra012871	A03	21835581	21841120	AT3G51050	FG-GAP repeat-containing protein	224.6	241.3	233.2	233.0
Bra012870	A03	21842601	21844033	AT3G51090	Protein of unknown function (DUF1640)	47.3	38.6	41.7	42.5
Bra012869	A03	21844794	21846222	AT3G51100	unknown protein	174.9	164.3	172.6	170.6
Bra012868	A03	21848187	21853892	AT3G51120	DNA binding; zinc ion binding; nucleic acid binding; nucleic acid binding	105.9	101.4	99.0	102.1
Bra012867	A03	21860025	21864871	AT3G51130	unknown protein	194.6	215.8	198.9	203.1
Bra012866	A03	21867468	21874187	AT3G51150	ATP binding microtubule motor family protein	70.3	73.0	68.9	70.7
Bra012865	A03	21874550	21875635	AT3G51160	Catalyzes the first step in the de novo synthesis of GDP-L-fucose.	143.6	139.1	144.0	142.2
Bra012864	A03	21879896	21880840	AT3G51190	Ribosomal protein L2 family	-	-	-	-
Bra012863	A03	21882120	21882813	AT3G51220	Plant protein of unknown function (DUF827)	-	-	-	-
Bra012862	A03	21884085	21885545	AT3G51240	Encodes flavanone 3-hydroxylase that is coordinately expressed with chalcone synthase and chalcone isomerases.	821.2	840.4	864.6	842.1
Bra012861	A03	21887206	21888537	AT3G51260	20S proteasomal alpha subunits. Interacts with SnRK, SKP1/ASK1 during proteasomal binding of an SCF ubiquitin ligase.	425.4	398.9	393.3	405.9
Bra012860	A03	21889549	21892303	AT3G51270	protein serine/threonine kinases; ATP binding; catalytic	55.4	57.8	59.5	57.6
Bra012859	A03	21892762	21894206	AT3G51280	Tetratricopeptide repeat (TPR)-like superfamily protein	130.2	136.3	136.0	134.2
Bra012858	A03	21895239	21896289	AT3G51300	Encodes a pollen-specific Rop GTPase, member of the Rho family of small GTP binding proteins that interacts with RIC3 and RIC4 to control tip growth in pollen tubes.	61.6	52.6	63.6	59.2
Bra012857	A03	21896574	21899299	AT3G51330	Eukaryotic aspartyl protease family protein	-	-	-	-
Bra012856	A03	21904574	21904843	AT3G51370	Protein phosphatase 2C family protein	153.8	151.7	137.4	147.7
Bra012855	A03	21907338	21907726	AT3G51380	IQ-domain 20 (IQD20)	-	-	-	-
Bra012854	A03	21909542	21910375	AT3G51400	Arabidopsis protein of unknown function (DUF241)	-	-	-	-
Bra012853	A03	21913022	21913759	AT3G51410	Arabidopsis protein of unknown function (DUF241)	-	-	-	-
Bra012852	A03	21916802	21917020	AT3G51500	unknown protein	48.2	50.3	62.4	53.6
Bra012851	A03	21917365	21918998	AT3G51520	diacylglycerol acyltransferase family	122.5	119.7	125.3	122.5
Bra012850	A03	21919767	21922457	AT3G51550	FERONIA	376.0	401.5	400.2	392.6
Bra012849	A03	21923814	21925904	AT3G51580	unknown protein	51.3	49.3	50.9	50.5
Bra012848	A03	21927444	21928521	AT3G51590	Encodes a member of the lipid transfer protein family.	-	-	-	-
Bra012847	A03	21930765	21931269	AT3G51600	Predicted to encode a PR (pathogenesis-related) protein.	445.7	451.8	490.3	462.6
Bra012846	A03	21935886	21938732	AT3G51620	Tautomerase/MIF superfamily protein	86.5	92.4	95.1	91.3
Bra012845	A03	21943489	21944494	AT3G51660	Tautomerase/MIF superfamily protein	-	-	-	-
Bra012843	A03	21956417	21961018	AT3G51670	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	479.7	485.7	485.2	483.5

Table S4. (continued)

Bra012844	A03	21958056	21958801	-	-	-	-	-	-
Bra012842	A03	21966018	21967077	AT3G51680	NAD(P)-binding Rossmann-fold superfamily protein	-	-	-	-
Bra012841	A03	21972702	21974345	AT3G51710	D-mannose binding lectin protein with Apple-like carbohydrate-binding domain	-	-	-	-
Bra012840	A03	21975321	21976436	AT3G51730	saposin B domain-containing protein	572.7	536.3	516.2	541.7
Bra012839	A03	21976993	21977610	AT3G51750	unknown protein	-	-	-	-
Bra012838	A03	21979034	21982030	AT3G51770	Encodes a negative regulator of 1-aminocyclopropane-1-carboxylic acid synthase5(ACSS5)	43.9	44.7	33.4	40.6
Bra012837	A03	21987354	21988859	AT3G51780	A member of Arabidopsis BAG (Bcl-2-associated athanogene) proteins, plant homologs of mammalian regulators of apoptosis.	143.2	143.7	135.0	140.6
Bra012836	A03	21989642	21991826	AT3G51800	putative nuclear DNA-binding protein G2p (AtG2) mRNA,	910.4	862.2	1000.7	924.4
Bra012835	A03	21999149	22001348	AT3G51850	member of Calcium Dependent Protein Kinase	335.9	298.4	278.9	304.4
Bra012834	A03	22012543	22013294	-	-	-	-	-	-
Bra012833	A03	22014395	22021133	AT3G51860	cation exchanger 3 (CAX3)	189.0	184.3	180.4	184.6
Bra012832	A03	22021830	22022840	AT3G51880	Encodes a protein belonging to the subgroup of HMGB (high mobility group B) proteins that have a distinctive DNA-binding motif, the HMG-box domain.	218.6	213.7	212.6	215.0
Bra012831	A03	22023678	22028202	AT3G51895	Encodes a sulfate transporter.	363.7	386.5	370.0	373.4
Bra012830	A03	22038200	22038427	-	-	-	-	-	-
Bra012829	A03	22040320	22041629	AT3G51910	member of Heat Stress Transcription Factor (Hsf) family	143.2	140.4	129.7	137.8
Bra012828	A03	22042610	22048354	AT3G51910	member of Heat Stress Transcription Factor (Hsf) family	143.2	140.4	129.7	137.8
Bra012827	A03	22058579	22060504	AT3G51950	Zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein	667.3	644.2	633.5	648.3
Bra012826	A03	22062557	22062958	AT3G52000	serine carboxypeptidase-like 36 (scpl36)	-	-	-	-
Bra012824	A03	22064355	22067631	AT3G52030	F-box family protein with WD40/YVTN repeat domain	-	-	-	-
Bra012825	A03	22066539	22066980	AT3G52040	unknown protein	294.8	274.3	316.8	295.3
Bra012823	A03	22068270	22070117	-	-	-	-	-	-
Bra012822	A03	22071617	22074763	AT3G52080	encodes a cation:proton exchanger expressed in pollen	-	-	-	-
Bra012821	A03	22075262	22075790	AT3G52090	Non-catalytic subunit common to nuclear DNA-dependent RNA polymerases II, IV and V	560.5	596.4	607.7	588.2
Bra012820	A03	22076368	22080442	AT3G52100	RING/FYVE/PHD-type zinc finger family protein	-	-	-	-
Bra012819	A03	22081654	22082025	AT3G52130	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-	-	-	-
Bra012818	A03	22086290	22087251	AT3G52155	Phosphoglycerate mutase family protein	50.6	51.5	50.1	50.7
Bra012817	A03	22087520	22089021	AT3G52160	Encodes KCS15, a member of the 3-ketoacyl-CoA synthase family involved in the biosynthesis of VLCFA (very long chain fatty acids).	-	-	-	-
Bra012816	A03	22089446	22091224	AT3G52170	DNA binding	106.1	92.3	79.6	92.7
Bra012815	A03	22093983	22101222	AT3G52250	Encodes a protein with a putative role in mRNA splicing.	-	-	-	-
Bra012814	A03	22101545	22105804	AT3G52260	Pseudouridine synthase family protein	42.8	38.5	30.9	37.4
Bra012813	A03	22106896	22108296	AT3G52270	Transcription initiation factor IIF, beta subunit	-	-	-	-
Bra012812	A03	22109374	22110381	-	-	-	-	-	-
Bra012811	A03	22110751	22111510	AT3G52270	Transcription initiation factor IIF, beta subunit	-	-	-	-
Bra012810	A03	22111762	22113450	AT3G52280	Bromodomain containing nuclear-localized protein involved in leaf development.	-	-	-	-
Bra012809	A03	22114190	22115517	AT3G52300	ATP synthase D chain, mitochondrial (ATPQ)	1087.3	1063.0	1107.4	1085.9
Bra012808	A03	22115961	22117190	AT3G52320	F-box and associated interaction domains-containing protein	-	-	-	-
Bra012807	A03	22126348	22127526	AT3G52380	chloroplast RNA-binding protein	152.6	179.9	187.9	173.5
Bra012806	A03	22129315	22130605	AT3G52400	syntaxin protein	15.8	20.7	27.1	21.2
Bra012805	A03	22131668	22137432	AT3G52430	Encodes a lipase-like gene that is important for salicylic acid signaling and function in resistance (R) gene-mediated and basal plant disease resistance.	-	-	-	-
Bra012804	A03	22138538	22139263	AT3G52440	Dof-type zinc finger DNA-binding family protein	-	-	-	-
Bra012803	A03	22146966	22148237	AT3G52450	Encodes a cytoplasmically localized U-box domain E3 ubiquitin ligase protein	-	-	-	-
Bra012802	A03	22152538	22153290	AT3G52460	hydroxyproline-rich glycoprotein family protein	-	-	-	-
Bra012801	A03	22156349	22156975	AT3G52470	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	220.8	233.8	221.0	225.2
Bra012800	A03	22160012	22163072	AT3G52490	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein	47.6	44.7	42.6	45.0
Bra012799	A03	22174322	22175740	AT3G52500	aspartyl protease family protein	209.0	230.1	198.8	212.6
Bra012798	A03	22183180	22183584	AT4G15215	PDR13, ATPDR13; PDR13; ATP binding / ATPase/ nucleoside-triphosphate/ nucleotide binding	-	-	-	-
Bra012797	A03	22187168	22194238	AT4G15215	PDR13, ATPDR13; PDR13; ATP binding / ATPase/ nucleoside-triphosphate/ nucleotide binding	-	-	-	-
Bra012796	A03	22195037	22197102	AT4G15240	Protein of unknown function (DUF604)	21.5	23.4	17.0	20.6
Bra012795	A03	22203115	22204539	AT4G15260	UDP-Glycosyltransferase superfamily protein	-	-	-	-
Bra012794	A03	22205236	22207291	AT4G15400	Encodes BIA1, a member of the BAH3 acyltransferase family.	-	-	-	-
Bra012793	A03	22233686	22236995	AT4G15300	a member of the cytochrome P450 gene family. molecular function unknown.	-	-	-	-
Bra012792	A03	22241320	22244656	AT4G15300	a member of the cytochrome P450 gene family. molecular function unknown.	-	-	-	-
Bra012791	A03	22246023	22247577	AT4G15410	serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B prime gamma (PUX5)	183.5	144.8	163.7	164.0
Bra012790	A03	22248592	22250134	AT4G15415	B' regulatory subunit of PP2A (AtB'gamma)	83.6	89.2	79.0	84.0
Bra012789	A03	22254261	22255793	AT4G15417	RNAse II-like 1 (RTL1)	-	-	-	-
Bra012788	A03	22266555	22270612	AT4G15440	Encodes a hydroperoxide lyase. Also a member of the CYP74B cytochrome p450 family.	356.1	370.4	378.1	368.2
Bra012787	A03	22270987	22271322	AT4G15460	glycine-rich protein	-	-	-	-
Bra012786	A03	22278433	22279696	AT4G15470	Bax inhibitor-1 family protein	689.0	687.9	695.2	690.7
Bra012785	A03	22283402	22285899	AT4G15475	F-box/RN1-like superfamily protein	131.0	127.0	124.0	127.3
Bra012784	A03	22287411	22288883	AT4G15480	Encodes a protein that might have synaptic acid:UDP-glucose glucosyltransferase activity	33.9	46.0	37.1	39.0
Bra012783	A03	22290158	22293884	-	-	-	-	-	-
Bra012782	A03	22298207	22299235	AT4G15520	tRNA/rRNA methyltransferase (SpoU) family protein	98.2	94.1	101.8	98.1
Bra012781	A03	22299647	22303813	AT4G15530	Encodes a dual-targeted protein believed to act as a pyruvate, orthophosphate dikinase.	-	-	-	-
Bra012780	A03	22306772	22309183	AT4G15550	UDP-glucose:indole-3-acetate beta-D-glucosyltransferase	-	-	-	-
Bra012779	A03	22312343	22315209	AT4G15560	Encodes a protein with 1-deoxyxylulose 5-phosphate synthase activity involved in the MEP pathway.	799.0	835.5	836.8	823.8
Bra012778	A03	22315983	22316959	-	-	-	-	-	-
Bra012777	A03	22325280	22326834	AT4G15610	Uncharacterised protein family (UPF0497)	-	-	-	-
Bra012776	A03	22337080	22337502	-	-	-	-	-	-
Bra012775	A03	22340095	22341323	AT4G15610	Uncharacterised protein family (UPF0497)	-	-	-	-
Bra012774	A03	22343131	22344328	AT4G15650	unknown protein	-	-	-	-
Bra012773	A03	22347565	22347873	AT4G15660	Thioredoxin superfamily protein	-	-	-	-
Bra012772	A03	22351554	22353392	AT4G15720	Tetratricopeptide repeat (TPR)-like superfamily protein	-	-	-	-
Bra012771	A03	22356457	22357317	-	-	-	-	-	-
Bra012770	A03	22357795	22359108	-	-	-	-	-	-
Bra012769	A03	22360932	22361857	AT4G15180	SET domain protein 2 (SDG2)	-	-	-	-

Table S4. (continued)

Bra012768	A03	22362305	22362934	AT4G15740	Calcium-dependent lipid-binding (CaLB domain) family protein				
Bra012767	A03	22363915	22365639	AT4G15760	Encodes a protein with similarity to monooxygenases that are known to degrade salicylic acid (SA).				
Bra012766	A03	22366090	22366604	-	-	-	-	-	-
Bra012765	A03	22368082	22368645	AT4G15770	RNA binding	353.9	365.7	342.7	354.1
Bra012764	A03	22371466	22371801	AT4G15800	Member of a diversely expressed predicted peptide family	268.7	228.6	254.2	250.5
Bra012763	A03	22373442	22374391	AT4G15802	Encodes a protein with similarity to heat shock factor binding proteins. Involved in negative regulation of heat shock response. Becomes nuclear localized upon heat treatment.				
Bra012762	A03	22377334	22379165	AT4G15820	unknown protein	26.9	26.1	32.6	28.5
Bra012761	A03	22380010	22383776	AT4G15840	BTB/POZ domain-containing protein	65.5	69.7	68.0	67.7
Bra012760	A03	22385679	22386306	-	-	-	-	-	-
Bra012759	A03	22390060	22390823	-	-	-	-	-	-
Bra012758	A03	22391541	22395768	AT4G15880	EARLY IN SHORT DAYS 4	154.0	158.8	153.0	155.3
Bra012757	A03	22397979	22400200	-	-	-	-	-	-
Bra012756	A03	22403280	22404812	-	-	-	-	-	-
Bra012755	A03	22407515	22411960	AT4G15885	kinesin motor protein-related				
Bra012754	A03	22414390	22419755	AT4G15890	unknown protein	53.7	41.1	50.5	48.4
Bra012753	A03	22425046	22428376	AT4G15900	Encodes a nuclear WD40 protein that is imported into the nucleus.	197.5	193.1	195.5	195.4
Bra012752	A03	22429268	22432153	AT4G15920	Nodulin MtN3 family protein	103.0	107.0	93.8	101.3
Bra012751	A03	22435198	22435729	AT4G15930	Dynein light chain type 1 family protein	638.5	609.4	587.3	611.7
Bra012750	A03	22436076	22437330	-	-	-	-	-	-
Bra012749	A03	22439592	22441476	AT4G16060	unknown protein	155.9	142.3	159.0	152.4
Bra012748	A03	22450559	22450975	AT4G15990	unknown protein				
Bra012747	A03	22457311	22458730	AT4G15955	alpha/beta-Hydrolases superfamily protein				
Bra012746	A03	22459058	22460791	-	-	-	-	-	-
Bra012745	A03	22466885	22470221	AT4G16070	Mono-/di-acylglycerol lipase, N-terminal; Lipase, class 3				
Bra012744	A03	22475667	22477136	AT4G16100	Protein of unknown function (DUF789)	94.4	92.9	106.9	98.0
Bra012743	A03	22487567	22490721	AT4G16110	ARR2; ARR2 (ARABIDOPSIS RESPONSE REGULATOR 2)	36.1	43.0	32.9	37.3
Bra012742	A03	22492421	22493134	AT4G16141	sequence-specific DNA binding / transcription factor/ zinc ion binding				
Bra012741	A03	22494519	22496253	AT4G16143	Protein interacts with Agrobacterium proteins VirD2 and VirE2.				
Bra012740	A03	22500143	22500935	AT4G16143	IMPA-2; IMPA-2 (IMPORTIN ALPHA ISOFORM 2); binding / protein transporter	221.7	212.0	198.1	210.6
Bra012739	A03	22501816	22504975	AT4G16144	Encodes AMSH3, a deubiquitinating enzyme.				
Bra012738	A03	22513582	22514946	AT4G16155	dihydrolipoyl dehydrogenases	162.3	151.2	133.9	149.1
Bra012737	A03	22515311	22516483	AT4G16160	Homologous to pea OEP16 and barley pPORA (OEP16)				
Bra012736	A03	22517140	22518706	-	-	-	-	-	-
Bra012735	A03	22521491	22522159	-	-	-	-	-	-
Bra012734	A03	22522902	22527685	AT4G16170	unknown protein	199.0	169.5	274.6	214.4
Bra012733	A03	22527988	22529356	AT4G16190	Papain family cysteine protease	645.4	620.6	587.7	617.9
Bra012732	A03	22529512	22529985	AT4G16195	Plant self-incompatibility protein S1 family				
Bra012731	A03	22530232	22531190	AT4G16210	enoyl-CoA hydratase/isomerase A (ECH1A)	117.9	125.7	122.7	122.1
Bra012730	A03	22533528	22533827	-	-	-	-	-	-
Bra012729	A03	22536974	22537435	-	-	-	-	-	-
Bra012728	A03	22538822	22540554	AT4G16220	GDSL-like Lipase/Acylhydrolase superfamily protein				
Bra012727	A03	22543908	22545481	-	-	-	-	-	-
Bra012726	A03	22547001	22550278	-	-	-	-	-	-
Bra012725	A03	22553701	22554823	AT4G16360	5'-AMP-activated protein kinase beta-2 subunit protein	177.7	164.7	170.6	171.0
Bra012724	A03	22559834	22560680	AT4G16380	Heavy metal transport/detoxification superfamily protein				
Bra012723	A03	22562218	22562475	AT4G16400	unknown protein	24.5	16.0	22.0	20.8
Bra012722	A03	22562648	22563190	AT4G16410	unknown protein				
Bra012721	A03	22563364	22565755	AT4G16420	Transcriptional co-activator.	172.5	159.9	179.9	170.8
Bra012720	A03	22567864	22569234	AT4G16430	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	127.5	111.8	131.9	123.7
Bra012719	A03	22569490	22570500	AT4G16442	Uncharacterised protein family (UPF0497)	249.2	250.2	237.2	245.5
Bra012718	A03	22571225	22572303	AT4G16444	unknown protein	125.8	127.0	127.3	126.7
Bra012717	A03	22575731	22576108	AT4G16447	unknown protein	278.0	286.4	333.6	299.3
Bra012716	A03	22577486	22577899	AT4G16450	unknown protein	947.1	960.7	972.2	960.0
Bra012715	A03	22579876	22580573	AT4G16460	unknown protein;				
Bra012714	A03	22584641	22586548	AT4G16480	Encodes a high affinity H ⁺ -myo-inositol symporter.	57.0	49.2	59.1	55.1
Bra012713	A03	22587234	22588685	AT4G16490	ARM repeat superfamily protein	133.3	134.0	110.1	125.8
Bra012712	A03	22604200	22604541	AT4G16500	Cystatin/monellin superfamily protein	580.8	537.6	599.4	572.6
Bra012711	A03	22607186	22607431	AT4G16515	Encodes a root meristem growth factor (RGF).	102.2	122.4	119.1	114.5
Bra012710	A03	22608868	22609702	AT4G16520	autophagy 8f (ATG8F)	458.1	485.4	532.9	492.1
Bra012709	A03	22615941	22616609	AT4G16530	Family of unknown function (DUF577)				
Bra012708	A03	22617874	22618839	AT4G16540	Heat shock protein HSP20/alpha crystallin family				
Bra012707	A03	22621584	22622508	AT4G16540	Heat shock protein HSP20/alpha crystallin family				
Bra012706	A03	22624845	22627299	AT4G16540	Heat shock protein HSP20/alpha crystallin family				
Bra012705	A03	22629378	22632850	AT4G16540	Heat shock protein HSP20/alpha crystallin family				
Bra012704	A03	22635782	22636458	AT4G16540	Heat shock protein HSP20/alpha crystallin family				
Bra012703	A03	22642127	22650605	AT4G16566	Encodes a protein that has an unexpected bifunctional capability in vitro.	62.2	77.3	71.1	70.2
Bra012702	A03	22652381	22656889	AT4G16590	encodes a gene similar to cellulose synthase	55.7	43.2	51.8	50.2
Bra012701	A03	22662703	22663347	AT4G16610	C2H2-like zinc finger protein	96.5	117.7	105.8	106.7
Bra012700	A03	22666240	22667907	AT4G16620	nodulin MtN21-like transporter family protein				
Bra012699	A03	22674172	22675266	AT4G16640	Matrixin family protein				
Bra012698	A03	22678821	22683532	-	-	-	-	-	-
Bra012697	A03	22687071	22689558	AT4G16650	O-fucosyltransferase family protein	74.8	85.9	72.3	77.7
Bra012696	A03	22690909	22694777	AT4G16660	heat shock protein 70 (Hsp 70) family protein	186.7	177.7	208.6	191.0
Bra012695	A03	22696243	22696489	-	-	-	-	-	-
Bra012694	A03	22697449	22699659	AT4G16720	Ribosomal protein L23/L15e family protein	1979.6	2029.6	2110.4	2039.9
Bra012693	A03	22708404	22708937	AT4G16750	encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family.	15.6	15.5	17.8	16.3
Bra012692	A03	22713752	22714072	-	-	-	-	-	-
Bra012691	A03	22714414	22717327	AT4G16765	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein				
Bra012690	A03	22722231	22723763	AT4G16820	Encodes a lipase that hydrolyzes phosphatidylcholine, glycolipids as well as triacylglycerols.				
Bra012689	A03	22724348	22730873	AT4G16860	RECOGNITION OF PERONOSPORA PARASITICA 4, RPP4	12.7	12.4	16.4	13.8
Bra012688	A03	22731251	22737169	AT4G16860	RECOGNITION OF PERONOSPORA PARASITICA 4, RPP4	12.7	12.4	16.4	13.8
Bra012687	A03	22740665	22742204	-	-	-	-	-	-
Bra012686	A03	22744793	22746772	-	-	-	-	-	-
Bra012685	A03	22748498	22749631	AT4G17200	F-box and associated interaction domains-containing protein				
Bra012684	A03	22750594	22753322	AT4G17030	Encodes EXLB1 (expansin-like B1), a member of the expansin family.				

Table S4. (continued)

Bra012683	A03	22757906	22760123	AT4G17040	encodes the ClpR4 subunit of the chloroplast-localized Clp protease complex.	688.4	676.2	687.5	684.0
Bra012682	A03	22760487	22762906	AT4G17050	Encodes a protein with ureidoglycine aminohydrolase activity.	-	-	-	-
Bra012681	A03	22770001	22771524	-	-	-	-	-	-
Bra012680	A03	22775981	22781437	-	-	-	-	-	-
Bra012679	A03	22791386	22792132	-	-	-	-	-	-
Bra012678	A03	22794839	22798551	-	-	-	-	-	-
Bra012677	A03	22803983	22804240	AT4G17085	Putative membrane lipoprotein	-	-	-	-
Bra012676	A03	22804681	22806581	AT4G17090	Encodes a beta-amylase targeted to the chloroplast.	204.9	208.2	206.1	206.4
Bra012675	A03	22808866	22811066	AT4G17100	unknown protein	131.5	149.5	158.7	146.6
Bra012674	A03	22814475	22815042	AT4G17160	RAB GTPase homolog B1A (RABB1a)	-	-	-	-
Bra012673	A03	22826220	22826735	AT4G17215	Pollen Ole e 1 allergen and extensin family protein	-	-	-	-
Bra012672	A03	22831432	22833660	AT4G17250	unknown protein	-	-	-	-
Bra012671	A03	22834749	22835871	AT4G17260	Lactate/malate dehydrogenase family protein	308.5	295.5	291.2	298.4
Bra012670	A03	22837875	22839995	AT4G17270	Mo25 family protein	146.9	145.6	147.0	146.5
Bra012669	A03	22841667	22843315	AT4G17350	Protein of unknown function DUF828	72.5	66.7	76.2	71.8
Bra012668	A03	22843726	22845379	AT4G17370	Oxidoreductase family protein	22.0	21.9	27.4	23.8
Bra012667	A03	22846092	22847568	AT4G17390	Ribosomal protein L23/L15e family protein	1970.2	1845.4	2065.0	1960.2
Bra012666	A03	22850241	22851492	-	-	-	-	-	-
Bra012665	A03	22854496	22855661	-	-	-	-	-	-
Bra012664	A03	22858877	22859704	AT4G17440	Protein of unknown function (DUF1639)	-	-	-	-
Bra012663	A03	22870234	22871338	AT4G17460	Encodes a class II HD-ZIP protein that regulates meristematic activity in different tissues	404.1	411.8	389.1	401.7
Bra012662	A03	22872072	22873607	AT4G17470	alpha/beta-Hydrolases superfamily protein	-	-	-	-
Bra012661	A03	22874242	22875107	AT4G17486	PPPDE putative thiol peptidase family protein	126.5	129.9	135.4	130.6
Bra012660	A03	22876088	22877555	AT4G17510	ubiquitin C-terminal hydrolase 3 (UCH3)	189.9	192.1	200.9	194.3
Bra012659	A03	22878123	22879891	AT4G17520	Hyaluronan / mRNA binding family	261.8	283.4	308.7	284.6
Bra012658	A03	22880314	22881657	AT4G17530	AtRabD2c encodes a Rab GTPase	315.9	309.6	320.7	315.4
Bra012657	A03	22886426	22889023	AT4G17550	Encodes a member of the phosphate starvation-induced glycerol-3-phosphate permease gene family	22.9	27.3	28.9	26.3
Bra012656	A03	22890900	22892842	AT4G17600	Encodes Lil3:1 (light-harvesting-like) protein.	260.8	278.2	262.2	267.1
Bra012655	A03	22897484	22899346	AT4G17615	Member of AtCBL (Calcineurin B-like Calcium Sensor Proteins) family.	94.4	89.8	95.8	93.3
Bra012654	A03	22899921	22901861	AT4G17616	Pentatricopeptide repeat (PPR) superfamily protein	-	-	-	-
Bra012653	A03	22902680	22905495	AT4G17620	glycine-rich protein	156.9	176.7	181.3	171.6
Bra012652	A03	22906024	22908683	AT4G17640	Encodes casein kinase II beta (regulatory) subunit.	262.7	227.1	242.2	244.0
Bra012651	A03	22909790	22910427	AT4G17670	Protein of unknown function (DUF581)	396.6	379.8	388.2	388.2
Bra012650	A03	22915403	22927293	AT4G17680	SBP (S-ribonuclease binding protein) family protein	-	-	-	-
Bra012649	A03	22933529	22933996	AT4G17690	Peroxidase superfamily protein	13.7	9.7	9.4	10.9
Bra012648	A03	22947960	22948367	AT4G17718	Encodes a defensin-like (DEFL) family protein.	-	-	-	-
Bra012647	A03	22949396	22951220	AT4G17720	RNA-binding (RRM/RBD/RNP motifs) family protein	139.3	143.8	164.9	149.3
Bra012646	A03	22957393	22958909	AT4G17720	RNA-binding (RRM/RBD/RNP motifs) family protein	139.3	143.8	164.9	149.3
Bra012645	A03	22959734	22961071	AT4G17730	member of SYP2 Gene Family	193.5	195.7	188.8	192.7
Bra012644	A03	22961454	22964005	AT4G17740	Peptidase S41 family protein	102.7	112.1	126.6	113.8
Bra012643	A03	22965905	22967302	AT4G17760	damaged DNA binding;exodeoxyribonuclease IIIs	19.2	14.0	17.2	16.8

Genes listed in BOLD are expressing in carpel based on Microarray data NASCArrays, and signal from 3 individual slides and those average are shown.

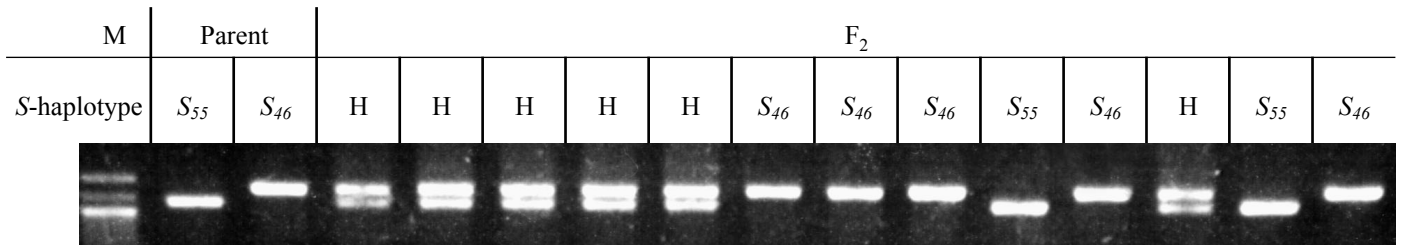


Fig. S1. *S*-haplotype analysis of F₂ plants by PCR-RFLP.

M, marker; *S*₅₅, *S*₅₅*S*₅₅-homozygote; *S*₄₆, *S*₄₆*S*₄₆-homozygote, H, *S*₄₆*S*₅₅-heterozygote.

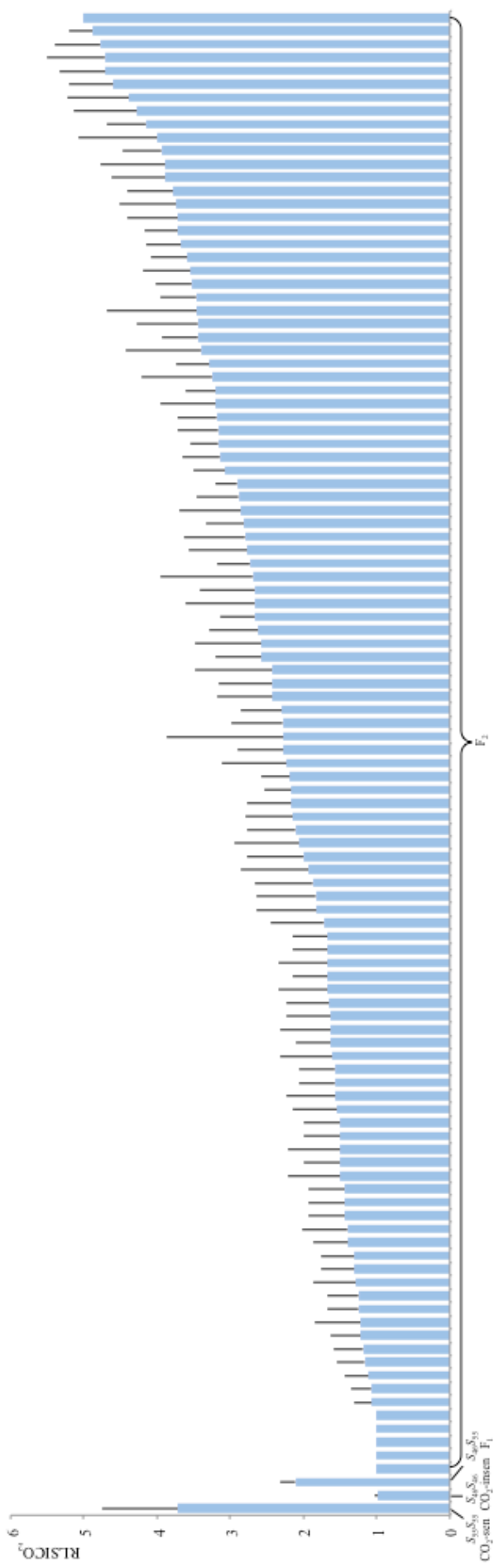


Fig. S2. RL.SICO₂ in CO₂-sensitive, CO₂-insensitive lines, F₁ and F₂ progeny based on the number of penetrating pollen tubes after self-pollination under high CO₂ conditions. RL.SICO₂ is continuously distributed and does not follow a simple one-locus biallelic Mendelian distribution.