

Supplementary Table A: SNP markers used

Marker	Sequence	Genotyping method
c1_00593	GGAGATTCAGAAGAT [A/G] GAGAGGATTTATGAG	SNPlex1
c1_02212	CCGCTAATATCCATC [T/G] GAAGAAACCCTAACT	SNPlex2
c1_02992	TTTCATGTACGTTTG [A/G] TTATACACGTAAAAC	SNPlex1
c1_04176	GACAGGTAGCCGCTT [A/C] ATGTATGTCCACGAC	SNPlex2
c1_05593	CGTTTTAGCTTTCCC [C/G] AGTTTACTTTCTTAT	SNPlex1
c1_08385	AAGTTTTTGATAGAC [G/A] AAAATTACGGATTTA	SNPlex1
c1_09782	TGTCCCTACCAATGG [C/T] GAATACGGCGAAATA	SNPlex2
c1_11160	AACAGAGTTTGGGAT [G/A] AAATGATTTCCCTTC	SNPlex1
c1_12295	TGTGAACCCTTGTCT [A/C] ACCTCTGTTGGATGG	SNPlex2
c1_13926	CGTCATTCTAAGCAC [G/C] AGATTCATGATGCAA	SNPlex1
c1_13869	AAATAACTACAATA [T/C] GTGTACAAAAGTTTG	SNPlex2
c1_15634	AGAAAGGAATAAATT [T/G] TGATTCATCTTGTGG	SNPlex2
c1_16875	AACGTCTGGTGGGAT [T/A] GGTTCACAAAGGCC	SNPlex1
c1_18433	AAACCCGACCCGACT [A/C] GGATCCGACGCAACA	SNPlex2
c1_19478	AACAGCAAACAACAC [G/C] AACCATTTTGTGATA	SNPlex1
c1_20384	CAATTTTTTTGTTTT [C/G] TTTTGTGTATGTAAC	SNPlex2
c1_22181	GACATTATGAATCAT [G/A] GAAAATTTGGAGATA	SNPlex1
c1_23381	ACACATGACTACATA [T/A] ACAAATCACAAAAT	SNPlex2
c1_24795	CCAATTTCAACACAT [C/A] TTCCTCAAATACAAI	SNPlex1
c1_25698	GTTATTGGTAGGTGA [G/A] ATTTGTTTATCAAGA	SNPlex2
c1_26993	GCGCTAGAACGAAAT [C/T] GAAAACACAAAATCG	SNPlex1
c1_28454	CCAGCCATAAGATA [C/T] GATCAACAACACTACCG	SNPlex2
c1_28667	GTTTTGGTTTTGTTG [A/G] CTCAGTGAGGATTTI	SNPlex1
c1_29898	AACTTTATTTTCTCC [T/A] GAACTATCTGATGCT	SNPlex2
c2_00593	AGATTCTTGTCAC [T/C] AAACCAAGTCCAACI	SNPlex1
c2_02365	GAGATTTAAAACCA [T/C] ATAATCAGTGGACTI	SNPlex2
c2_03041	CAACTCTTCTTCTCT [A/G] ACAGACATTTGAAGI	SNPlex1
c2_04263	CCTTGCCGACCATTG [T/G] AGACTCTCTTCAAGA	SNPlex2
c2_05588	TACTAAGTGGACACA [A/G] CCACTACATGTTCTC	SNPlex1
c2_06655	GAAAGAGATCGTGAG [T/C] CACTGTTTCGTTGTT	SNPlex2
c2_07650	TCAGATTTTGAAGAT [G/A] CGAAAACAAATCTGG	SNPlex1
c2_10250	GTTTGAGATTACTGA [C/A] ACTGAGAACTTCATA	SNPlex1
c2_11457	AGTATAGTTTATAGC [A/T] TTCTATGAAGAATAA	SNPlex2
c2_12435	ACAGACCCACTTCGA [G/C] AAATCAATCACAAAC	SNPlex1
c2_13472	CAAGGTTTACTCTGT [T/C] TAGTGTCCGATTCTI	SNPlex2
c2_15252	TTTCAGGAGGGTTTA [C/T] AACTTGAGGCACAGA	SNPlex1
c2_16837	ACATGAAAGCTCAAA [T/C] CAATTTCTATTCAAC	SNPlex1
c2_17606	TTTGTGGCCACGTC [G/C] AAACACAGTCGTTTC	SNPlex2
c2_18753	AATCTAGAGAAGTTT [A/T] TGTCTGATTCAACA	SNPlex1
c3_00580	TTTGTGCTTGTGCG [C/G] TTTGCAGTTTACAAA	SNPlex1
c3_00885	TTTTCGTATGAATCG [G/A] AATCAAGTTAGTTAA	SNPlex2
c3_01901	CATCCTCGTCTTCCT [C/G] GTCAATGTCATTGAA	SNPlex2
c3_02968	ATTGCTGAGAAACGC [G/T] TAAGCAGACATAATG	SNPlex1
c3_04141	TGTGGTTTAATATCT [C/T] TGGAATCGATCTCTG	SNPlex2
c3_05141	TGAAAACAAACCCCT [A/T] CTTAATACTTTGTAT	SNPlex1
c3_06631	GGCTCCATTTGATTA [C/A] AAAGTAGACACAAAG	SNPlex2
c3_08042	TCGGTGTGACATCC [A/T] ACAAATGCTTAGAI	SNPlex1
c3_09748	GCATTTCCCTCGAACA [G/C] CTCTCGTGCATCATC	SNPlex1
c3_10996	CATAATTTTAGCCGC [G/C] ACAGATTTTCATGAAC	SNPlex2
c3_11192	GTAATATTGTGACTT [C/T] GTGAAAATTCCTACTG	SNPlex2

c3_12647	CTTTGATTTGGAATC [A/G]	GAGCCCAAGGTTTCGC	SNPlex1
c3_14097	GCCAAGTTTCTTGAT [A/G]	TCTTGCCTGATCCAA	SNPlex2
c3_15117	GACCCTAAGCGTCCG [T/C]	CGGGAACATTCTGGT	SNPlex1
c3_16677	AGAAAAACGGTGTGG [G/A]	CCATATTCTTTTTCC	SNPlex2
c3_18180	TTTCAGATAATGTTT [T/G]	CAGGTCTTTGATTTT	SNPlex1
c3_22147	TGGAGAATCAACTTC [C/T]	CTTAATCTCAATCAG	SNPlex2
c3_20729	CTTCGCCATCTCTAC [T/C]	AAGCCCTTTGACCTA	SNPlex1
c4_00012	GATTAATTAGGAAAT [C/T]	TTGTGTTTCGTTCCG	Taqman
c4_00641	TTACTATTGTCTTGG [G/C]	TTGGTTTAAAGAGAT	SNPlex2
c4_02133	TCTGTTTCATCTAGAG [C/T]	TGCTTCTGCTTTCTC	SNPlex1
c4_03833	AATGATGGAAAAAT [A/G]	CACTTGCGGTGGTAA	SNPlex2
c4_04877	GACAAACTCCTTCTT [T/A]	GATTGGAAGCTCCCA	SNPlex1
c4_05850	CTCGCATCCACGCTT [T/C]	GAGTTCATCTCGCAA	SNPlex2
c4_06923	GATCAAGATTAAAGT [G/A]	AATTATGTTGTCCAG	SNPlex1
c4_07740	CCGTGTTAGCTAGAG [A/T]	CTTAACACGAGATAI	SNPlex2
c4_08930	CTATATAGTTGTGTT [A/T]	GGTTTAGGAATTTCC	SNPlex1
c4_10609	TGGACAGATTGCTCA [A/G]	TCTTTAGGACAAAGC	SNPlex1
c4_11878	CTAACGATTATGTAA [T/C]	ACAACAAGAGCCTTG	SNPlex2
c4_13171	AGGTTCTTCAGGCTG [G/C]	ACAGAGTGTTCCTGCT	SNPlex1
c4_14819	GTGAATGCTCTGTTT [A/C]	TAGCTTGTCTATTAT	SNPlex1
c4_15765	GGGTCAGCTCAGCTT [A/G]	GTCCTTTTTAAACGC	SNPlex2
c4_17684	TTGGAGAATCCAAAT [T/G]	ACGATGAATTGGTAA	SNPlex2
c4_18056	CATTTCCAAAATATC [A/C]	TCCTCCTCTATCAAC	Amplifluor
c5_00576	CTAAGAAATCTTAGT [A/T]	CTTCTTTCTTCATTC	SNPlex2
c5_01587	ATCCTGAATGGAGAG [A/G]	GGGAGTTCTTGACAI	SNPlex2
c5_02900	CTCGCTTGAAGCCC [T/C]	TCAGCATCAGAATCC	SNPlex1
c5_04011	AGGGGACTACAAGGC [C/T]	TTTCTTCTAGCTTTC	SNPlex2
c5_05319	TGTTGTACCTGATAA [A/G]	CCCGATGCTGTTCCCT	SNPlex1
c5_06820	CAGAAGTTGGTACCC [T/C]	GACTGTGCCTACACA	SNPlex2
c5_07442	CTGACCTTATCAAAG [G/T]	TTGCTGCGTCCATTC	SNPlex1
c5_08563	TAGGTGAATATAAAC [T/G]	AAGAGATCGAAAGTG	SNPlex2
c5_10428	GTGATTGTATGACGG [A/G]	AAGCATTGTGTGCAA	SNPlex1
c5_12699	TCAAATGTAACCATC [T/A]	GGTTGTTCTTCGGAA	SNPlex1
c5_13614	CATGGAATGCTAAAA [G/C]	TCCTCCTTGCCTTG	SNPlex2
c5_14766	GCCAAATGGAGTGGA [T/C]	TGTTGCTTGGAAAGAC	SNPlex1
c5_16368	GTCTTAAACAGCATG [T/A]	AGTGCCTCCAAGGAA	SNPlex2
c5_17570	TTGAACTGCTTGTA [C/T]	TACCGGTTTAGGTTG	SNPlex1
c5_19316	TGACATGTCCCTGAA [A/C]	TCTGCCTTTGTCTCA	SNPlex2
c5_20318	GAATTGATTTGCTAA [C/A]	ACTGGTTCATCTTCA	SNPlex1
c5_21319	ATTTCTTCTCCTCAC [T/C]	GGCGATTTCTCCTCA	SNPlex2
c5_22415	CAAACGCGCGTATT [T/A]	ATGTGATATGGCTTC	SNPlex2
c5_23116	TGAATGTTTTATATT [T/A]	TGGTTGGTACGCATT	SNPlex2
c5_24997	TGAGATCACGAGCCA [C/T]	CTCGGAGCAGAAATC	SNPlex1
c5_26671	GGTATTTTTTCGTTAC [T/A]	AATCTCCTTATACTG	SNPlex2

The marker names give the number of the chromosome followed by the physical position in kb of the markers on the chromosome (TAIR 7.0 Col-0 genomic sequence, April 23, 2007, <http://www.arabidopsis.org>). The SNPs are under brackets, the first allele is the Col-0 one. The two sets of markers genotyped together are referred to as SNPlex1 and SNPlex2.

Supplementary Table B: Microsatellite and InDel PCR-based markers

Marker	Other name	Forward primer	Reverse primer
c1_09621	CIW12	AGGTTTTATTGCTTTTCACA	CTTTCAAAAGCACATCACA
c1_11723	MSAT1.33	CTAACTAAACGCAAGCAT	GGAAAAAAGGAAGAGAAAG
c1_15927	T27K12	GGAGGCTATACGAATCTTGACA	GGACAACGTCTCAAACGGTT
c2_06280	-	ATGTTATATTTTGTGAGATTT	CTTTCTTTAATGCTATGAAG
c3_02133	-	GGTAACAAGTCTTTCGCTTCC	TGAGATTAAGGCGACAAAT
c3_07673	MSAT3.4	TGTAACATTCGCATTTTATG	CCTCTTCGGTCTATATGACT
c3_09056	MSAT3.2	AAGGTACGGCGGTGGATATTG	CGGGGATTTCTTCTTCCTGTG
c3_11208	MSAT3.32	GCACTTGCAGCTTAACTT	CGTGACTGTCAAACCG
c3_15714	-	CACGCTTTGGAGTATGACA	TGACCCAAGAAAATTATGTAA
c3_17283	-	TATTTTCAGGAGAACCAAG	TATAGTGTGAATGTTTCGG
c3_17651	MSAT3.17	GTGATGCAAACGGATAGAGA	TCAACAAAAGAGATGGCTGA
c4_00269	-	GTACACAAGGATTTTATCATGGGATTATC	GCGACTCTTTAGTAAATGCTCTACG
c4_05629	nga8	GAGGGCAAATCTTTATTTTCGG	TGGCTTTCGTTTATAAACATCC
c4_07549	MSAT4.35	CCCATGTCTCCGATGA	GGCGTTTAATTTGCATTCT
c5_09082	ICE15	CCTGCTCCTCTTTCCTTCTGCTC	CACACTAAATTATCTATCAACT

The marker names give the number of the chromosome followed by the physical position in kb of the markers on the chromosome (TAIR 7.0 Col-0 genomic sequence, April 23, 2007, <http://www.arabidopsis.org>).

Supplementary Table C: Detailed results of the QTL analyses and QTL parameters

FLO

pop.	chr	cM	Mb	LodScore	R2	2a	core pop.	chr	cM	Mb	LodScore	R2	2a
BlhCol	1	36,2	11,1	3,5	5%	-2,4	BlhCol	1	33,9	10,6	2,6	6%	-2,7
BlhCol	3	46,4	12,6	2,7	3%	1,9	BlhCol	3	45,6	12,3	2,4	6%	2,5
BlhCol	4	1,3	0,3	12,1	17%	-4,5	BlhCol	4	1,2	0,2	6,7	19%	-4,6
BlhCol	5	100,8	26,6	3,3	4%	2,1	BlhCol						
BurCol	1	40,5	13,6	4,9	6%	-3,1	BurCol						
BurCol	1	74,6	23,4	7,5	8%	-3,7	BurCol	1	74,2	23,3	4,5	12%	-4,8
BurCol	4	0,5	0,7	4,6	5%	-3,0	BurCol	4	0,0	0,6	3,4	8%	-3,7
BurCol	4	28,8	8,4	3,5	4%	-2,6	BurCol						
BurCol	5	14,3	5,9	2,6	3%	2,3	BurCol						
BurCol	5	72,2	22,2	2,3	2%	-1,9	BurCol						
CtCol	1	84,8	23,8	3,6	3%	-1,1	CtCol						
CtCol	2	34,6	9,7	6,0	7%	1,6	CtCol	2	37,9	10,2	4,2	9%	1,9
CtCol	2	70,6	18,7	2,3	2%	0,9	CtCol	2	70,5	18,7	2,4	5%	1,4
CtCol	4	68,8	16,6	4,5	5%	-1,3	CtCol						
CtCol	5	51,7	14,5	5,1	5%	-1,4	CtCol						
CtCol	5	92,8	25,8	21,2	25%	3,1	CtCol	5	92,1	25,7	8,3	27%	3,2
CviCol	1	1,3	1,0	16,6	19%	2,5	CviCol	1	1,7	1,1	4,9	13%	2,5
CviCol	2	48,7	11,4	2,3	2%	-0,9	CviCol						
CviCol	3	57,9	15,2	2,6	2%	0,9	CviCol						
CviCol	5	15,9	3,6	4,8	7%	-1,7	CviCol						
CviCol	5	38,3	9,0	10,8	13%	-2,1	CviCol	5	38,9	9,1	2,8	9%	-2,0
CviCol	5	110,4	26,1	3,5	5%	1,2	CviCol						
ShaCol	3	1,2	1,0	2,6	3%	1,6	ShaCol						
ShaCol							ShaCol	4	1,3	0,1	2,6	7%	-2,4
ShaCol	5	10,5	3,5	16,6	20%	4,4	ShaCol	5	10,5	3,5	5,3	14%	3,6
ShaCol	5	84,4	25,9	9,1	12%	3,5	ShaCol	5	79,8	24,7	2,8	7%	2,5

DIA

pop.	chr	cM	Mb	LodScore	R2	2a	core pop.	chr	cM	Mb	LodScore	R2	2a
BlhCol							BlhCol	2	66,6	18,7	2,8	7%	-15,5
BlhCol	4	3,5	0,7	9,0	16%	-22,5	BlhCol	4	3,4	0,7	3,9	12%	-20,7
BurCol	1	13,6	6,2	3,9	5%	-13,5	BurCol						
BurCol	1	37,7	13,0	3,1	4%	-12,2	BurCol						
BurCol	5	10,5	4,8	5,4	6%	-14,8	BurCol	5	7,6	3,5	2,7	6%	-15,4
CtCol	5	94,5	26,1	3,4	5%	11,9	CtCol						
CviCol	1	3,7	1,6	8,9	10%	7,9	CviCol	1	5,4	2,1	3,3	8%	7,3
CviCol	3	81,0	19,5	6,8	9%	7,1	CviCol	3	82,8	20,0	3,6	12%	8,5
CviCol	5	35,1	8,5	5,9	6%	-6,2	CviCol	5	24,9	5,9	2,3	6%	-6,0
CviCol	5	68,1	17,1	3,6	4%	-4,9	CviCol						
CviCol	5	111,1	26,3	4,9	6%	5,8	CviCol	5	108,7	25,7	2,4	6%	6,3
ShaCol	1	79,6	24,8	3,5	4%	10,4	ShaCol						
ShaCol	2	10,7	6,5	4,7	6%	-12,9	ShaCol	2	11,5	6,6	2,3	7%	-14,0
ShaCol	2	22,9	8,5	2,6	4%	-13,4	ShaCol						
ShaCol	3	19,3	11,0	3,5	7%	13,6	ShaCol						
ShaCol	4	2,3	0,2	3,9	5%	-12,4	ShaCol	4	3,1	0,3	2,4	8%	-15,5
ShaCol	5	16,6	5,2	2,6	3%	9,4	ShaCol						
ShaCol	5	85,4	26,2	5,3	7%	15,2	ShaCol						

FIT

pop.	chr	cM	Mb	LodScore	R2	2a	core pop.	chr	cM	Mb	LodScore	R2	2a
BlhCol	5	15,1	3,9	7,1	11%	-55,1	BlhCol	5	15,0	3,9	4,2	12%	-60,4
BurCol	1	39,2	13,3	6,1	6%	63,2	BurCol						
BurCol	2	24,8	10,4	3,8	4%	47,7	BurCol	2	22,5	9,9	3,0	8%	67,4
BurCol	4	0,0	0,6	3,1	3%	42,1	BurCol	4	0,0	0,6	2,6	5%	56,3
BurCol	4	29,7	8,6	4,0	4%	50,0	BurCol						
BurCol	5	8,3	3,7	22,7	28%	-133,9	BurCol	5	8,3	3,7	9,6	24%	-122,9
CtCol	5	12,5	3,8	10,4	13%	-52,5	CtCol	5	12,4	3,8	4,1	12%	-51,1
CviCol	1	3,8	1,6	9,9	13%	22,6	CviCol	1	3,3	1,5	5,1	16%	27,0
CviCol	2	83,0	18,1	2,9	4%	12,3	CviCol						
CviCol	5	109,6	25,9	3,4	5%	13,4	CviCol	5	107,8	25,4	2,4	7%	17,3
ShaCol							ShaCol	4	0,0	0,0	3,2	7%	-43,7
ShaCol	5	10,0	3,4	12,5	17%	-69,3	ShaCol	5	11,1	3,7	5,8	13%	-64,4