

Table 4. Positions, genotype counts, and P - values for the mixed-model ANOVA tests of association for markers within the three trait-associated blocks. Markers forming the trait-associated blocks are indicated in bold. Results are also shown for markers interspersed with these. Some markers appear twice in the table because block 2 and block 3 overlap. Genotype counts include both members of each twin pair. The global P - value is calculated by comparing the null hypothesis of equal genotype means to the alternative of unconstrained genotype means. Dominance was evaluated when three genotype classes were observed. The additive (per-allele) substitution effect contrasting the reference and alternative alleles at each marker are shown (beta & s.e.).

Chromosome position	Marker	Ref	Alt	Genotypes 1st panel			Association 1st panel		Additive effect 1st panel		Genotypes 2nd panel			Association 2nd panel		Additive effect 2nd panel	
		Allele R	Allele A	R/R	R/A	A/A	Global	Dom	beta	s.e.	R/R	R/A	A/A	Global	Dom	beta	s.e.
BLOCK1																	
135417902	rs52090901	T	G	244	322	115	5.8E-05	8.9E-01	1.4E-01	3.2E-02	424	533	183	2.3E-03	4.7E-01	1.0E-01	3.0E-02
135417925	rs52090902	C	T	163	327	191	2.6E-03	6.5E-01	1.1E-01	3.1E-02	258	603	298	2.4E-01	8.4E-01	4.8E-02	2.9E-02
135418072	rs52090903	T	G	164	326	190	3.8E-03	7.4E-01	1.0E-01	3.1E-02	263	593	301	2.2E-01	8.9E-01	4.9E-02	2.8E-02
135418102	rs9389262	G	T	165	326	189	4.6E-03	8.9E-01	1.0E-01	3.1E-02	254	593	290	3.4E-01	6.5E-01	4.1E-02	2.9E-02
135418168	rs13208043	T	C	606	65	5	1.2E-01	6.9E-01	-9.1E-02	1.2E-01	1055	104	4	8.1E-01	5.4E-01	6.6E-02	1.5E-01
135418784	rs2183709	C	T	169	320	199	5.3E-03	1.0E+00	9.9E-02	3.1E-02	259	602	296	2.9E-01	1.0E+00	4.5E-02	2.9E-02
135418879	rs4142299	G	T	170	328	195	4.5E-03	1.0E+00	1.0E-01	3.1E-02	257	598	295	1.9E-01	8.2E-01	5.2E-02	2.9E-02
135420841	rs11154791	A	G	249	319	121	4.5E-04	7.6E-01	1.2E-01	3.2E-02	422	539	188	6.1E-04	4.9E-01	1.1E-01	3.0E-02
135422941	rs11759062	A	C	208	269	101	1.5E-04	1.0E+00	1.4E-01	3.4E-02	423	548	183	7.5E-04	4.4E-01	1.1E-01	3.0E-02
135423044	rs11759077	A	G	203	280	100	2.4E-04	7.8E-01	1.4E-01	3.5E-02	430	561	185	5.4E-04	4.0E-01	1.2E-01	3.0E-02
135424673	rs6904897	T	G	240	334	116	2.0E-05	4.4E-01	1.4E-01	3.3E-02	411	540	187	2.0E-04	4.8E-01	1.2E-01	3.0E-02
135425482	rs11758774	T	G	248	322	123	1.1E-04	6.8E-01	1.3E-01	3.2E-02	430	562	190	7.5E-04	3.8E-01	1.1E-01	3.0E-02
BLOCK 2																	
135452921	rs9376090	T	C	378	286	50	7.9E-36	1.2E-03	4.8E-01	3.9E-02	596	505	85	3.8E-40	6.6E-02	4.4E-01	3.5E-02
135453430	rs9389266	G	T	512	173	28	1.3E-03	3.1E-01	-1.1E-01	5.4E-02	-	-	-	-	-	-	-
135454075	rs52090905	C	T	581	120	4	4.0E-09	2.5E-01	-1.9E-01	1.3E-01	947	215	13	9.9E-08	3.5E-01	-1.9E-01	8.5E-02
135454329	rs52090906	T	C	582	126	4	4.8E-09	2.7E-01	-1.9E-01	1.3E-01	-	-	-	-	-	-	-
135455762	rs52090907	C	G	563	121	2	1.8E-09	1.5E-01	-9.5E-02	1.8E-01	-	-	-	-	-	-	-
135460711	rs9399137	T	C	363	290	51	4.5E-38	2.7E-04	5.0E-01	3.8E-02	588	491	82	3.8E-40	3.2E-02	4.5E-01	3.5E-02
135460947	rs52090908	T	C	619	72	0	6.4E-06	-	-3.2E-01	7.0E-02	-	-	-	-	-	-	-
135460998	rs9402684	T	C	152	334	200	2.4E-04	1.0E+00	1.3E-01	3.2E-02	-	-	-	-	-	-	-
135461381	rs9402685	T	C	358	264	46	9.4E-32	2.1E-03	4.7E-01	4.0E-02	585	493	81	2.7E-37	8.5E-02	4.3E-01	3.6E-02
135461527	rs7743042	A	G	155	349	197	1.2E-04	8.6E-01	1.3E-01	3.1E-02	-	-	-	-	-	-	-
135463989	rs11759553	A	T	364	298	54	7.6E-39	6.8E-04	4.9E-01	3.7E-02	600	486	88	5.4E-37	1.3E-01	4.2E-01	3.5E-02
135465105	rs1074849	G	A	420	242	42	7.3E-12	5.8E-01	-2.4E-01	4.4E-02	-	-	-	-	-	-	-
135465872	rs52090909	C	G	360	293	52	4.9E-38	4.0E-04	5.0E-01	3.8E-02	597	476	87	1.2E-37	1.2E-01	4.2E-01	3.4E-02

135465896	rs6930223	G	T	162	345	192	1.1E-05	4.4E-01	1.5E-01	3.1E-02	-	-	-	-	-	-	-
135468251	rs4895440	A	T	358	293	53	4.1E-39	3.1E-04	5.0E-01	3.7E-02	590	471	84	1.0E-35	2.5E-01	4.1E-01	3.5E-02
135468266	rs4895441	A	G	364	293	51	2.2E-38	2.6E-04	5.0E-01	3.8E-02	598	481	85	2.8E-36	9.2E-02	4.2E-01	3.5E-02
135468837	rs9376092	C	A	351	300	52	2.1E-38	6.8E-04	5.0E-01	3.8E-02	597	485	90	3.0E-36	1.1E-01	4.1E-01	3.4E-02
135468852	rs9389269	T	C	364	293	53	1.1E-38	6.4E-04	5.0E-01	3.8E-02	602	484	85	2.0E-35	1.2E-01	4.1E-01	3.5E-02
135469510	rs9402686	G	A	366	297	53	1.7E-38	3.3E-04	5.0E-01	3.8E-02	601	486	82	5.1E-36	1.3E-01	4.2E-01	3.6E-02
135471786	rs10484494	G	A	617	93	0	2.4E-08	-	3.6E-01	6.4E-02	1009	146	8	4.4E-05	8.4E-01	2.2E-01	1.1E-01
135473333	rs11154792	T	C	382	282	47	1.4E-35	5.7E-03	4.9E-01	4.0E-02	644	450	69	3.6E-31	5.3E-02	4.1E-01	3.8E-02
135473754	rs1411919	A	G	420	256	44	8.3E-12	2.5E-01	-2.2E-01	4.3E-02	677	418	64	1.4E-15	4.2E-01	-2.5E-01	4.1E-02
135474576	rs7766963	T	C	173	355	184	4.3E-03	4.4E-01	1.0E-01	3.1E-02	-	-	-	-	-	-	-
135476864	rs2223385	G	A	419	256	45	3.9E-12	2.4E-01	-2.2E-01	4.2E-02	672	424	64	5.2E-16	5.7E-01	-2.6E-01	4.1E-02
135477194	rs9483788	T	C	377	286	45	6.6E-29	1.3E-02	4.4E-01	4.1E-02	623	480	71	4.0E-24	1.8E-01	3.5E-01	3.8E-02
BLOCK 3																	
135473754	rs1411919	A	G	420	256	44	8.3E-12	2.5E-01	-2.2E-01	4.3E-02	677	418	64	1.4E-15	4.2E-01	-2.5E-01	4.1E-02
135474576	rs7766963	T	C	173	355	184	4.3E-03	4.4E-01	1.0E-01	3.1E-02	-	-	-	-	-	-	-
135476864	rs2223385	G	A	419	256	45	3.9E-12	2.4E-01	-2.2E-01	4.2E-02	672	424	64	5.2E-16	5.7E-01	-2.6E-01	4.1E-02
135477194	rs9483788	T	C	377	286	45	6.6E-29	1.3E-02	4.4E-01	4.1E-02	623	480	71	4.0E-24	1.8E-01	3.5E-01	3.8E-02
135479079	rs1320959	T	C	417	252	41	2.8E-11	1.0E-01	-2.0E-01	4.5E-02	-	-	-	-	-	-	-
135480316	rs52090910	A	G	608	93	2	1.4E-07	5.4E-01	2.4E-01	1.9E-01	1024	156	9	9.2E-06	5.8E-01	2.9E-01	1.0E-01
135480956	rs2026937	A	G	175	330	195	1.0E-02	2.7E-01	9.0E-02	3.1E-02	261	610	296	2.0E-01	8.1E-01	5.0E-02	2.8E-02
135484218	rs9483791	T	C	410	241	48	2.3E-11	1.8E-01	-2.1E-01	4.1E-02	688	428	65	1.5E-14	5.1E-01	-2.4E-01	4.1E-02
135484905	rs1320963	A	G	414	257	46	5.3E-12	1.4E-01	-2.1E-01	4.2E-02	680	412	62	6.3E-14	3.9E-01	-2.3E-01	4.2E-02
135485702	rs2026938	G	A	413	237	46	1.3E-10	2.9E-01	-2.1E-01	4.2E-02	688	411	62	4.2E-14	4.2E-01	-2.3E-01	4.1E-02
135487141	rs9376093	C	T	410	240	48	6.8E-12	1.3E-01	-2.1E-01	4.1E-02	690	425	65	1.8E-15	4.4E-01	-2.5E-01	4.1E-02
135487507	rs9376094	T	A	415	234	50	4.1E-11	1.9E-01	-2.1E-01	4.0E-02	689	415	67	5.3E-15	3.5E-01	-2.4E-01	4.1E-02
135488534	rs9399139	C	T	210	326	158	1.3E-01	3.9E-01	5.6E-02	3.1E-02	337	602	231	5.4E-01	3.1E-01	9.8E-03	2.9E-02
135489466	rs9321485	T	C	409	237	50	3.4E-10	2.2E-01	-2.0E-01	4.1E-02	680	422	64	1.1E-13	6.5E-01	-2.4E-01	4.1E-02
135489513	rs9321486	T	C	403	247	49	5.2E-12	6.0E-02	-2.0E-01	4.1E-02	675	438	63	1.5E-14	7.8E-01	-2.5E-01	4.1E-02
135491008	rs9494149	C	T	410	247	43	1.5E-10	1.4E-01	-2.0E-01	4.3E-02	671	427	63	1.9E-14	5.0E-01	-2.4E-01	4.1E-02
135492448	rs9376095	T	C	408	232	50	2.7E-10	1.7E-01	-2.0E-01	4.0E-02	684	421	58	3.3E-14	7.2E-01	-2.7E-01	4.3E-02
135492890	rs1041478	A	G	213	322	136	3.7E-01	6.0E-01	4.1E-02	3.3E-02	377	574	189	5.5E-01	2.9E-01	6.9E-04	3.0E-02
135493257	rs6934903	T	A	450	229	23	5.2E-23	7.1E-03	5.0E-01	5.6E-02	772	364	39	2.0E-18	7.8E-01	3.2E-01	5.1E-02
135493273	rs1569534	C	T	420	258	37	1.5E-11	2.0E-01	-2.2E-01	4.5E-02	704	391	57	1.4E-13	1.0E+00	-2.6E-01	4.3E-02
135495720	rs6929404	C	A	413	238	42	5.4E-12	1.6E-01	-2.2E-01	4.3E-02	701	391	56	1.1E-13	8.4E-01	-2.6E-01	4.3E-02
135497022	rs9385716	A	G	417	248	38	3.5E-11	8.8E-02	-2.0E-01	4.5E-02	709	391	59	3.7E-13	7.2E-01	-2.6E-01	4.2E-02