

**Descriptive statistics of the study populations.**

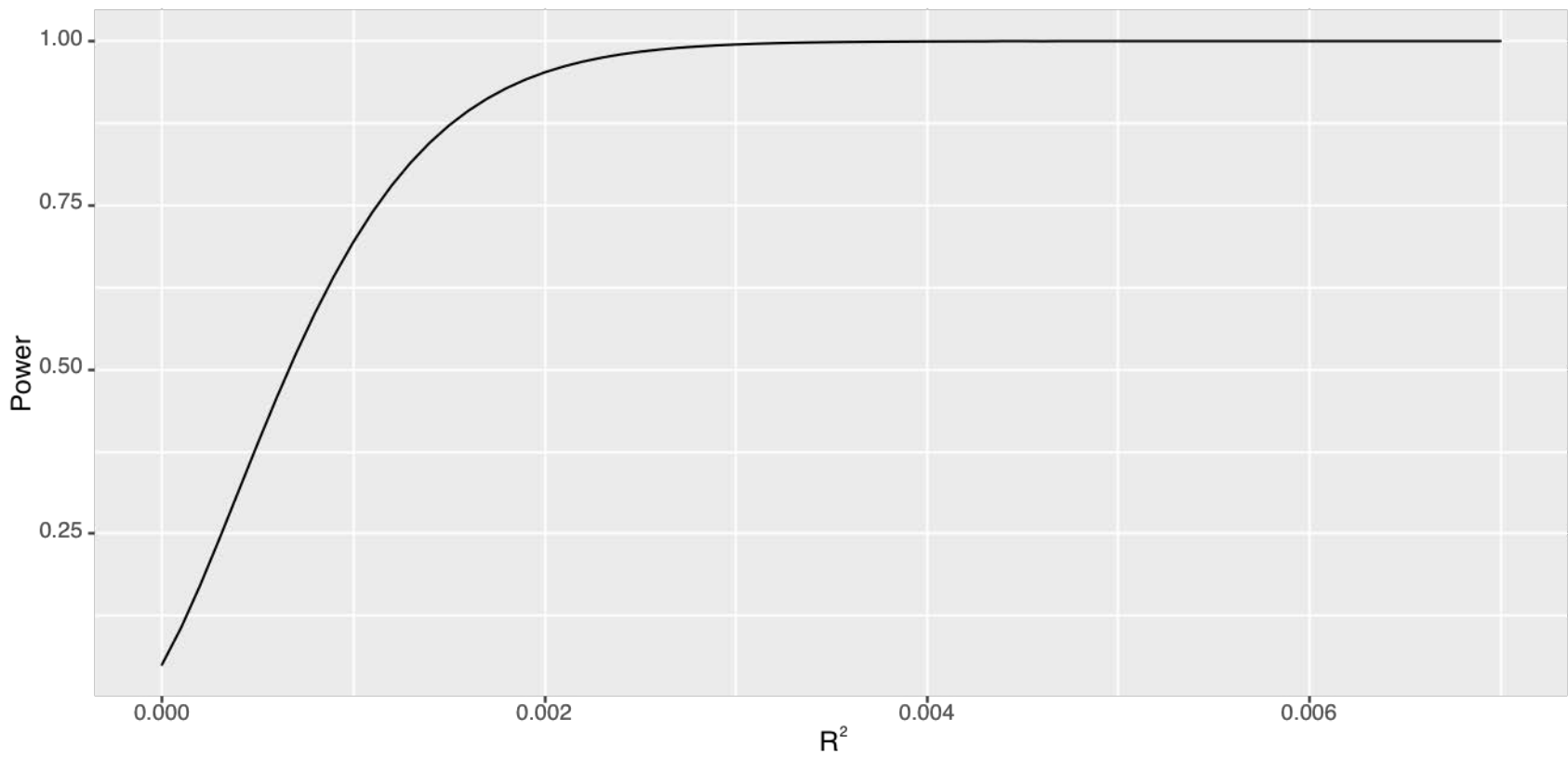
	<b>Dutch Europeans</b>		<b>Australian Europeans</b>	
	<b>(N = 10361)</b>		<b>(N = 4080)</b>	
Sex (number and percentage of male)	4400	42%	3546	41%
Age in years (mean, sd)	67.28	12.3	29.22	16.11
Height in cm (mean, sd)	169.22	10.67	167.09	9.95
Male	176.9	8.41	173.45	9.99
Female	163.54	8.35	162.69	7.15

SNPs at 14 loci significantly associated with adult height in 10361 RS subjects and exact replication in 4080 unrelated QIMR subjects

SNP	CHR	Basepair	EA	OA	fEA_RS	Beta_RS	P_RS	fEA_QIMR	Beta_QIMR	P_QIMR	Same direction	Gene	Function	Novel
rs12485899	3	41160573	T	C	0.43	-0.57	3.50E-09	0.43	0.11	0.58	FALSE	ZNF621(dist=579287),CTNNB1(dist=80370)	intergenic	FALSE
rs9838625	3	141063953	T	C	0.43	0.62	2.71E-10	0.43	0.35	0.07	TRUE	ZBTB38	intronic	FALSE
rs1265097	6	31106459	A	C	0.11	-0.89	5.39E-09	0.09	-0.54	0.11	TRUE	PSORS1C1	coding	FALSE
rs2780226	6	34199092	C	T	0.09	0.92	4.26E-08	0.08	1.12	0.002	TRUE	GRM4(dist=75692),HMGA1(dist=5486)	intergenic	FALSE
rs7741741	6	142655801	A	T	0.28	-0.60	1.72E-08	0.28	-0.67	0.002	TRUE	GPR126	intronic	FALSE
rs4272	7	92236829	G	A	0.22	0.68	4.23E-09	0.22	0.56	0.02	TRUE	CDK6	3utr	FALSE
rs6984782	8	57135889	C	T	0.11	-0.94	1.80E-09	0.13	-0.22	0.45	TRUE	CHCHD7(dist=4712),SDR16C5(dist=76682)	intergenic	FALSE
rs4931222	12	29973835	G	A	0.04	-1.36	3.05E-08	0.06	0.54	0.20	FALSE	TMTC1(dist=36142),IPO8(dist=808081)	intergenic	TRUE
rs1038196	12	66343400	C	G	0.50	-0.53	3.86E-08	0.52	-0.47	0.02	TRUE	HMGA2	intronic	FALSE
rs7159961	14	20222854	G	A	0.01	-2.66	2.68E-10	0.02	0.48	0.55	TRUE	OR4Q3(dist=6325),OR4M1(dist=25629)	intergenic	TRUE
rs1366870	15	22344879	C	G	0.02	-2.34	6.67E-11	0.00	NA	NA	NA	LOC727924	intronic	TRUE
rs2279007	19	17283403	A	G	0.23	-0.65	1.65E-08	0.25	-0.46	0.05	TRUE	MYO9B	intronic	FALSE
rs6060355	20	33890061	A	G	0.39	0.59	3.15E-09	0.37	0.42	0.04	TRUE	UQCC1	downstream	FALSE
rs10439884	21	10971951	A	G	0.02	-2.16	3.06E-09	0.00	NA	NA	NA	TPTE	intronic	TRUE

EA, OA, fEA: effect allele, other allele, frequency of effect allele

Beta: regression beta of the effect allele



**Compound heterozygous SNP pairs associated with height in RS (including those loci already detected by single SNP GWAS)**

CHR	Band	SNP1	BP1	EA1	fEA1	Major1	Minor1	Gene1	Function1	NMISS1	BETA1	STAT1	SE1	P1	SNP2
3	q23	rs1007118	140845585	A	0.01	G	A	SPSB4	intronic	10302	-0.39	-0.81	0.47	4.17E-01	rs1991431
3	q23	rs16851294	140997752	G	0.10	A	G	PXYLP1	intronic	10361	0.44	2.75	0.16	5.99E-03	rs9838625
3	q23	rs16851304	141003249	A	0.10	G	A	PXYLP1	intronic	10352	0.44	2.72	0.16	6.59E-03	rs9838625
3	q23	rs4683602	141058687	A	0.06	G	A	ZBTB38	intronic	10361	0.57	2.81	0.20	4.98E-03	rs6785073
3	q23	rs9838625	141063953	T	0.43	C	T	ZBTB38	intronic	10282	0.62	6.32	0.10	2.71E-10	rs295317
3	q23	rs726838	141072666	T	0.35	A	T	ZBTB38	intronic	10360	0.52	5.17	0.10	2.41E-07	rs6762826
3	q23	rs6784404	141073675	A	0.46	G	A	ZBTB38	intronic	10359	0.59	6.08	0.10	1.26E-09	rs1978600
3	q23	rs13095453	141074962	A	0.35	G	A	ZBTB38	intronic	10360	0.52	5.17	0.10	2.41E-07	rs6762826
3	q23	rs7624084	141093285	C	0.50	T	C	ZBTB38	intronic	10325	0.60	6.15	0.10	8.28E-10	rs1978600
3	q23	rs6440003	141094209	A	0.49	G	A	ZBTB38	intronic	10321	0.58	6.05	0.10	1.50E-09	rs1978600
3	q23	rs9821337	141096185	G	0.38	C	G	ZBTB38	intronic	10324	0.51	5.23	0.10	1.69E-07	rs6762826
3	q23	rs6764769	141100280	G	0.49	A	G	ZBTB38	5utr	10358	0.61	6.27	0.10	3.87E-10	rs1978600
3	q23	rs6763931	141102833	A	0.49	G	A	ZBTB38	intronic	10359	0.60	6.22	0.10	5.14E-10	rs1978600
3	q23	rs724016	141105570	G	0.49	A	G	ZBTB38	intronic	10358	0.60	6.24	0.10	4.51E-10	rs1978600
3	q23	rs7632381	141106063	C	0.49	T	C	ZBTB38	intronic	10358	0.60	6.24	0.10	4.56E-10	rs1978600
3	q23	rs6808936	141109321	G	0.49	A	G	ZBTB38	intronic	10359	0.61	6.28	0.10	3.47E-10	rs1978600
3	q23	rs1582874	141115219	C	0.49	T	C	ZBTB38	5utr	10358	0.61	6.26	0.10	3.90E-10	rs1978600
3	q23	rs2871960	141121814	C	0.48	A	C	ZBTB38	intronic	10308	0.58	5.99	0.10	2.17E-09	rs1978600
3	q23	rs2011092	141124607	C	0.38	T	C	ZBTB38	intronic	10339	0.55	5.56	0.10	2.82E-08	rs6762826
3	q23	rs1344674	141125186	G	0.49	A	G	ZBTB38	intronic	10348	0.61	6.29	0.10	3.30E-10	rs1978600
3	q23	rs6767899	141125439	C	0.38	T	C	ZBTB38	intronic	10339	0.55	5.56	0.10	2.71E-08	rs6762826
3	q23	rs13099193	141128804	A	0.38	G	A	ZBTB38	intronic	10339	0.55	5.57	0.10	2.57E-08	rs6762826
3	q23	rs13066993	141129999	A	0.38	G	A	ZBTB38	intronic	10339	0.55	5.57	0.10	2.57E-08	rs6762826
3	q23	rs1991431	141133450	A	0.49	G	A	ZBTB38	intronic	10348	0.61	6.31	0.10	2.93E-10	rs1978600
3	q23	rs13091182	141133960	A	0.38	G	A	ZBTB38	intronic	10339	0.55	5.57	0.10	2.57E-08	rs6762826
3	q23	rs16851397	141134818	G	0.06	A	G	ZBTB38	intronic	10352	0.45	2.16	0.21	3.07E-02	rs6785073
3	q23	rs9825379	141137035	A	0.07	G	A	ZBTB38	intronic	10361	0.35	1.84	0.19	6.60E-02	rs6785073
3	q23	rs9869102	141138833	G	0.07	A	G	ZBTB38	intronic	10361	0.35	1.84	0.19	6.60E-02	rs6785073
3	q23	rs6785073	141139330	A	0.38	G	A	ZBTB38	intronic	10361	0.55	5.63	0.10	1.86E-08	rs6762826
3	q23	rs6763927	141140366	T	0.49	A	T	ZBTB38	intronic	10361	0.60	6.17	0.10	7.00E-10	rs1978600

3	q23	rs9846396	141140968	T	0.49	C	T	ZBTB38	intronic	10361	0.60	6.18	0.10	6.51E-10	rs1978600
3	q23	rs6776991	141142391	G	0.09	C	G	ZBTB38	intronic	10360	0.36	2.17	0.17	2.99E-02	rs6789653
3	q23	rs6440006	141142691	A	0.49	G	A	ZBTB38	intronic	10356	0.60	6.18	0.10	6.78E-10	rs1978600
3	q23	rs10513137	141143430	A	0.09	G	A	ZBTB38	intronic	10358	0.35	2.11	0.17	3.47E-02	rs6789653
3	q23	rs6762826	141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	rs6789653
3	q23	rs6802753	141145473	C	0.09	T	C	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	rs6789653
5	q35.1	rs1466947	168298658	G	0.11	T	G	SLIT3	intronic	10360	-0.82	-5.30	0.15	1.21E-07	rs17070997
6	p21.33	rs11964080	30970970	A	0.03	G	A	NA	NA	10357	-0.84	-2.89	0.29	3.88E-03	rs1265097
6	p21.33	rs6457300	30998742	G	0.37	T	G	MUC22	intronic	10357	-0.39	-3.91	0.10	9.45E-05	rs2523890
6	p21.33	rs10807077	31001467	G	0.37	A	G	MUC22	intronic	10352	-0.41	-4.10	0.10	4.13E-05	rs2523890
6	p21.33	rs10947124	31001496	T	0.37	G	T	MUC22	intronic	10352	-0.41	-4.10	0.10	4.13E-05	rs2523890
6	p21.33	rs10947125	31001633	G	0.37	A	G	MUC22	intronic	10351	-0.41	-4.14	0.10	3.58E-05	rs2523890
6	p21.33	rs10947126	31001668	A	0.37	G	A	MUC22	intronic	10351	-0.41	-4.13	0.10	3.61E-05	rs2523890
6	p21.33	rs4248153	31002527	G	0.44	A	G	MUC22	coding	10323	-0.46	-4.74	0.10	2.15E-06	rs2523890
6	p21.33	rs3094670	31009486	G	0.02	C	G	NA	NA	10356	-0.96	-2.99	0.32	2.77E-03	rs1265097
6	p21.33	rs2517535	31016753	G	0.02	A	G	NA	NA	10356	-0.97	-3.04	0.32	2.41E-03	rs1265097
6	p21.33	rs2523890	31039532	G	0.36	A	G	NA	NA	10344	-0.56	-5.62	0.10	2.01E-08	rs12662501
6	p21.33	rs2233976	31079994	T	0.11	C	T	C6orf15	coding	10358	-0.81	-5.24	0.16	1.67E-07	rs12529697
6	p21.33	rs1265097	31106459	A	0.11	C	A	PSORS1C1	coding	10361	-0.89	-5.84	0.15	5.39E-09	rs12529697
6	p21.33	rs1265083	31111347	T	0.01	G	T	CCHCR1	intronic	10361	-1.35	-3.07	0.44	2.13E-03	rs12662501
6	p21.33	rs130072	31112484	T	0.10	C	T	CCHCR1	coding	10361	-0.80	-5.00	0.16	5.81E-07	rs12529697
6	p21.33	rs12529697	31125407	A	0.07	G	A	TCF19	5upstream	10331	-0.53	-2.86	0.19	4.20E-03	rs9501571
6	p21.33	rs1265180	31159345	A	0.01	C	A	NA	NA	10361	-1.34	-3.19	0.42	1.44E-03	rs12662501
6	p21.33	rs1634703	31185262	A	0.01	G	A	NA	NA	10357	-1.38	-3.28	0.42	1.06E-03	rs12662501
6	p21.33	rs1345274	31190627	G	0.01	C	G	NA	NA	10355	-1.49	-3.52	0.42	4.29E-04	rs12662501
6	p21.33	rs12662501	31190850	T	0.16	C	T	NA	NA	10360	-0.74	-5.68	0.13	1.40E-08	rs6457401
6	p21.33	rs6904669	31192796	G	0.41	A	G	PSORS1C3/HLA	intergenic	10360	0.09	0.91	0.10	3.62E-01	rs1960278
6	p21.33	rs6927461	31201803	C	0.32	G	C	PSORS1C3/HLA	intergenic	10360	0.15	1.40	0.10	1.62E-01	rs1960278
6	p21.33	rs1639106	31213317	T	0.03	C	T	NA	NA	10357	-0.94	-3.33	0.28	8.62E-04	rs4084262
6	p21.33	rs3899471	31215037	C	0.21	T	C	NA	NA	10360	-0.58	-4.90	0.12	9.58E-07	rs4248814
6	p21.33	rs4084262	31218889	T	0.17	C	T	NA	NA	10345	-0.71	-5.63	0.13	1.90E-08	rs4248814
6	p21.33	rs4386816	31247135	C	0.14	T	C	RPL3P2	5upstream	10360	-0.74	-5.40	0.14	6.77E-08	rs6457401

6 p21.33	rs7766156	31249790 G	0.21 C	G	RPL3P2	3downstream	10359	-0.61	-5.16	0.12	2.54E-07	rs6457401
6 p21.33	rs16899170	31259017 C	0.05 T	C	HLA-C	intronic	10360	-0.66	-2.87	0.23	4.13E-03	rs4248814
6 p21.33	rs16899178	31261137 T	0.05 C	T	HLA-C	intronic	10360	-0.66	-2.87	0.23	4.13E-03	rs4248814
6 p21.33	rs16899203	31266335 C	0.05 T	C	HLA-C	intronic	10360	-0.66	-2.88	0.23	4.03E-03	rs4248814
6 p21.33	rs12174774	31268965 T	0.09 C	T	HLA-C	intronic	10360	-0.51	-3.02	0.17	2.55E-03	rs4248814
6 p21.33	rs9368677	31272321 A	0.07 G	A	HLA-C	intronic	10360	-0.56	-2.87	0.19	4.18E-03	rs4248814
6 p21.33	rs9357124	31273554 A	0.07 C	A	XXbac-BPG248I3	downstream	10360	-0.56	-2.87	0.19	4.18E-03	rs4248814
6 p21.33	rs3094691	31274693 A	0.41 G	A	XXbac-BPG248I3	downstream	10361	-0.53	-5.46	0.10	4.93E-08	rs4248814
6 p21.33	rs9391764	31282138 C	0.04 T	C	HLA-C	intronic	10357	-0.82	-3.33	0.25	8.83E-04	rs4248814
6 p21.31	rs12214804	34188866 C	0.09 C	T	AL354740.29	3downstream	10295	0.92	5.48	0.17	4.40E-08	rs2744977
6 p21.31	rs1776897	34195011 G	0.09 G	T	GRM4/HMGA1	intergenic	10295	0.91	5.44	0.17	5.32E-08	rs2744977
6 p21.31	rs1759627	34197105 C	0.17 C	T	GRM4/HMGA1	intergenic	10268	0.60	4.68	0.13	2.94E-06	rs2744964
6 p21.31	rs2780226	34199092 C	0.09 C	T	NA	NA	10295	0.92	5.48	0.17	4.26E-08	rs2744977
6 p21.31	rs1150781	34214322 C	0.09 C	G	C6orf1	coding	10295	0.92	5.48	0.17	4.26E-08	rs2744977
6 q24.1	rs9389985	142653898 G	0.27 A	G	GPR126	intronic	10313	-0.60	-5.64	0.11	1.78E-08	rs262130
6 q24.1	rs2039987	142655490 C	0.28 A	C	GPR126	intronic	10314	-0.60	-5.63	0.11	1.80E-08	rs262130
6 q24.1	rs7741741	142655801 A	0.28 T	A	GPR126	intronic	10314	-0.60	-5.64	0.11	1.72E-08	rs262130
7 q21.2	rs8179	92236164 T	0.22 T	C	CDK6	3utr	10360	0.67	5.78	0.12	7.78E-09	rs17164894
7 q21.2	rs4272	92236829 G	0.22 A	G	CDK6	3utr	10350	0.68	5.88	0.12	4.23E-09	rs17164894
7 q21.2	rs42046	92252203 G	0.28 C	G	CDK6	intronic	10359	0.57	5.32	0.11	1.08E-07	rs17164894
7 q21.2	rs11767704	92256375 T	0.28 C	T	CDK6	intronic	10359	0.57	5.32	0.11	1.08E-07	rs17164894
7 q21.2	rs11771637	92260161 A	0.28 G	A	CDK6	intronic	10359	0.57	5.32	0.11	1.08E-07	rs17164894
7 q21.2	rs17688839	92263350 T	0.17 A	T	CDK6	intronic	10267	0.65	5.11	0.13	3.25E-07	rs17164894
7 q21.2	rs2282979	92264993 C	0.28 T	C	CDK6	intronic	10360	0.57	5.30	0.11	1.16E-07	rs17164894
7 q21.2	rs11765954	92280695 C	0.29 T	C	CDK6	intronic	10360	0.56	5.24	0.11	1.62E-07	rs17164894
7 q21.2	rs6948097	92281953 T	0.29 C	T	CDK6	intronic	10360	0.56	5.24	0.11	1.62E-07	rs17164894
7 q21.2	rs6954221	92283262 T	0.29 C	T	CDK6	intronic	10360	0.56	5.24	0.11	1.62E-07	rs17164894
7 q21.2	rs7804722	92288106 C	0.28 T	C	CDK6	intronic	10358	0.56	5.24	0.11	1.67E-07	rs17164894
7 q21.2	rs7793983	92485039 G	0.09 A	G	LOC101927497	intronic	10357	0.80	4.73	0.17	2.30E-06	rs17164894
9 p24.3	rs514779	1598693 C	0.03 T	C	DMRT2/SMAR	intergenic	10321	-1.28	-4.33	0.29	1.51E-05	rs10962274
9 p24.3	rs1853417	1598840 G	0.03 C	G	DMRT2/SMAR	intergenic	10321	-1.28	-4.33	0.29	1.51E-05	rs10962274
15 q11.2	rs1366870	22344879 C	0.02 C	G	LOC727924	intronic	10286	-2.34	-6.54	0.36	6.67E-11	rs1366870

15 q11.2	rs2217377	22354293 T	0.02 T	A	LOC727924	intronic	10286	-2.34	-6.54	0.36	6.67E-11	rs2217377
19 p13.11	rs11671774	17281257 G	0.23 C	G	MYO9B	intronic	10356	-0.65	-5.64	0.11	1.73E-08	rs7257450
19 p13.11	rs2279008	17283303 C	0.23 T	C	MYO9B	intronic	10358	-0.65	-5.62	0.11	1.95E-08	rs7257450
19 p13.11	rs2279007	17283403 A	0.23 G	A	MYO9B	intronic	10360	-0.65	-5.65	0.11	1.65E-08	rs7257450

---

BP2	EA2	fEA2	Major2	Minor2	Gene2	Function2	NMISS2	BETA2	STAT2	SE2	P2	NMISS	BETA	STAT	SE	P	NTEST
141133450	A	0.49	G	A	ZBTB38	intronic	10348	0.61	6.31	0.10	2.93E-10	10304	0.63	6.61	0.10	4.14E-11	172
141063953	T	0.43	C	T	ZBTB38	intronic	10282	0.62	6.32	0.10	2.71E-10	10284	-0.62	-6.65	0.09	3.05E-11	196
141063953	T	0.43	C	T	ZBTB38	intronic	10282	0.62	6.32	0.10	2.71E-10	10277	-0.62	-6.62	0.09	3.76E-11	193
141139330	A	0.38	G	A	ZBTB38	intronic	10361	0.55	5.63	0.10	1.86E-08	10361	0.65	6.81	0.10	1.07E-11	162
141363124	T	0.20	C	T	NA	NA	10360	0.29	2.37	0.12	1.76E-02	10284	-0.59	-6.52	0.09	7.44E-11	158
141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	10359	0.62	6.41	0.10	1.57E-10	157
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10287	0.62	6.44	0.10	1.27E-10	157
141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	10359	0.62	6.41	0.10	1.57E-10	156
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10255	-0.64	-6.70	0.10	2.27E-11	150
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10251	-0.63	-6.56	0.10	5.79E-11	149
141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	10323	0.62	6.48	0.10	9.59E-11	148
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10286	-0.65	-6.74	0.10	1.63E-11	147
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10287	-0.64	-6.69	0.10	2.3E-11	148
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10286	-0.64	-6.72	0.10	1.96E-11	147
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10286	-0.64	-6.72	0.10	1.98E-11	146
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10287	-0.65	-6.76	0.10	1.51E-11	145
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10286	-0.65	-6.74	0.10	1.71E-11	144
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10242	-0.62	-6.51	0.10	7.68E-11	143
141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	10338	0.65	6.75	0.10	1.52E-11	142
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10278	-0.65	-6.75	0.10	1.6E-11	141
141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	10338	0.65	6.76	0.10	1.45E-11	140
141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	10338	0.65	6.77	0.10	1.37E-11	138
141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	10338	0.65	6.77	0.10	1.37E-11	137
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10278	-0.65	-6.76	0.10	1.42E-11	138
141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	10338	0.65	6.77	0.10	1.37E-11	137
141139330	A	0.38	G	A	ZBTB38	intronic	10361	0.55	5.63	0.10	1.86E-08	10352	0.64	6.58	0.10	5.02E-11	136
141139330	A	0.38	G	A	ZBTB38	intronic	10361	0.55	5.63	0.10	1.86E-08	10361	0.62	6.46	0.10	1.12E-10	135
141139330	A	0.38	G	A	ZBTB38	intronic	10361	0.55	5.63	0.10	1.86E-08	10361	0.62	6.46	0.10	1.12E-10	134
141145315	G	0.09	A	G	ZBTB38	intronic	10359	0.37	2.20	0.17	2.77E-02	10360	0.66	6.84	0.10	8.26E-12	133
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10289	-0.64	-6.65	0.10	3.13E-11	132



141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10289	-0.64	-6.66	0.10	2.9E-11	131
141150990	A	0.38	G	A	ZBTB38	intronic	10326	0.54	5.50	0.10	3.92E-08	10326	0.65	6.73	0.10	1.76E-11	131
141149287	T	0.03	T	C	ZBTB38	intronic	10288	-0.31	-1.13	0.28	2.58E-01	10284	-0.64	-6.68	0.10	2.57E-11	129
141150990	A	0.38	G	A	ZBTB38	intronic	10326	0.54	5.50	0.10	3.92E-08	10325	0.65	6.73	0.10	1.85E-11	128
141150990	A	0.38	G	A	ZBTB38	intronic	10326	0.54	5.50	0.10	3.92E-08	10325	0.65	6.74	0.10	1.72E-11	128
141150990	A	0.38	G	A	ZBTB38	intronic	10326	0.54	5.50	0.10	3.92E-08	10325	0.65	6.74	0.10	1.72E-11	127
168643555	T	0.07	G	T	SLIT3	intronic	10316	-0.74	-3.86	0.19	1.13E-04	10316	-0.78	-6.50	0.12	8.21E-11	111
31106459	A	0.11	C	A	PSORS1C1	coding	10361	-0.89	-5.84	0.15	5.39E-09	10357	-0.87	-6.47	0.13	1.01E-10	301
31039532	G	0.36	A	G	NA	NA	10344	-0.56	-5.62	0.10	2.01E-08	10347	0.60	6.49	0.09	9.18E-11	301
31039532	G	0.36	A	G	NA	NA	10344	-0.56	-5.62	0.10	2.01E-08	10342	0.61	6.62	0.09	3.8E-11	301
31039532	G	0.36	A	G	NA	NA	10344	-0.56	-5.62	0.10	2.01E-08	10342	0.61	6.62	0.09	3.8E-11	301
31039532	G	0.36	A	G	NA	NA	10344	-0.56	-5.62	0.10	2.01E-08	10341	0.62	6.65	0.09	3.09E-11	301
31039532	G	0.36	A	G	NA	NA	10344	-0.56	-5.62	0.10	2.01E-08	10341	0.61	6.60	0.09	4.33E-11	301
31039532	G	0.36	A	G	NA	NA	10344	-0.56	-5.62	0.10	2.01E-08	10322	0.64	6.79	0.09	1.19E-11	301
31106459	A	0.11	C	A	PSORS1C1	coding	10361	-0.89	-5.84	0.15	5.39E-09	10356	-0.94	-6.71	0.14	2.08E-11	301
31106459	A	0.11	C	A	PSORS1C1	coding	10361	-0.89	-5.84	0.15	5.39E-09	10356	-0.94	-6.72	0.14	1.87E-11	301
31190850	T	0.16	C	T	NA	NA	10360	-0.74	-5.68	0.13	1.40E-08	10345	-0.53	-6.59	0.08	4.56E-11	301
31125407	A	0.07	G	A	TCF19	5upstream	10331	-0.53	-2.86	0.19	4.20E-03	10331	-0.84	-6.76	0.12	1.47E-11	301
31125407	A	0.07	G	A	TCF19	5upstream	10331	-0.53	-2.86	0.19	4.20E-03	10334	-0.90	-7.29	0.12	3.45E-13	301
31190850	T	0.16	C	T	NA	NA	10360	-0.74	-5.68	0.13	1.40E-08	10360	-0.81	-6.42	0.13	1.43E-10	301
31125407	A	0.07	G	A	TCF19	5upstream	10331	-0.53	-2.86	0.19	4.20E-03	10334	-0.83	-6.60	0.13	4.41E-11	301
31333610	T	0.15	C	T	DHFRP2	3downstream	10361	-0.69	-5.14	0.13	2.82E-07	10336	-0.77	-6.69	0.11	2.41E-11	301
31190850	T	0.16	C	T	NA	NA	10360	-0.74	-5.68	0.13	1.40E-08	10360	-0.82	-6.48	0.13	9.84E-11	301
31190850	T	0.16	C	T	NA	NA	10360	-0.74	-5.68	0.13	1.40E-08	10356	-0.82	-6.45	0.13	1.17E-10	301
31190850	T	0.16	C	T	NA	NA	10360	-0.74	-5.68	0.13	1.40E-08	10354	-0.82	-6.50	0.13	8.4E-11	301
31334852	T	0.23	G	T	DHFRP2	5upstream	10361	-0.58	-5.05	0.11	4.46E-07	10360	-0.60	-6.95	0.09	4.02E-12	301
31269874	C	0.43	C	G	HLA-C	intronic	10351	0.45	4.67	0.10	3.09E-06	10351	-0.89	-7.46	0.12	9.32E-14	301
31269874	C	0.43	C	G	HLA-C	intronic	10351	0.45	4.67	0.10	3.09E-06	10351	-0.74	-6.74	0.11	1.67E-11	301
31218889	T	0.17	C	T	NA	NA	10345	-0.71	-5.63	0.13	1.90E-08	10341	-0.80	-6.71	0.12	2.11E-11	301
31346755	A	0.12	G	A	ZDHHC20f	5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10328	-0.57	-6.52	0.09	7.32E-11	301
31346755	A	0.12	G	A	ZDHHC20f	5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10310	-0.60	-6.73	0.09	1.75E-11	301
31334852	T	0.23	G	T	DHFRP2	5upstream	10361	-0.58	-5.05	0.11	4.46E-07	10360	-0.57	-6.57	0.09	5.35E-11	301

31334852	T	0.23	G	T	DHFRP2 5upstream	10361	-0.58	-5.05	0.11	4.46E-07	10360	-0.60	-6.98	0.09	3.04E-12	301
31346755	A	0.12	G	A	ZDHHC20f 5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10320	-0.83	-6.51	0.13	8.02E-11	301
31346755	A	0.12	G	A	ZDHHC20f 5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10320	-0.83	-6.51	0.13	8.02E-11	301
31346755	A	0.12	G	A	ZDHHC20f 5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10320	-0.83	-6.51	0.13	7.86E-11	301
31346755	A	0.12	G	A	ZDHHC20f 5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10320	-0.76	-6.52	0.12	7.23E-11	301
31346755	A	0.12	G	A	ZDHHC20f 5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10320	-0.78	-6.41	0.12	1.54E-10	301
31346755	A	0.12	G	A	ZDHHC20f 5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10320	-0.78	-6.41	0.12	1.54E-10	301
31346755	A	0.12	G	A	ZDHHC20f 5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10336	-0.61	-7.00	0.09	2.7E-12	301
31346755	A	0.12	G	A	ZDHHC20f 5upstream	10321	-0.81	-5.56	0.14	2.83E-08	10317	-0.86	-6.65	0.13	3.18E-11	301
34563060	G	0.16	A	G	C6orf106 intronic	10360	0.71	5.37	0.13	8.17E-08	10296	0.78	7.41	0.11	1.4E-13	83
34563060	G	0.16	A	G	C6orf106 intronic	10360	0.71	5.37	0.13	8.17E-08	10296	0.78	7.39	0.11	1.61E-13	81
34591320	C	0.16	G	C	C6orf106 intronic	10360	0.71	5.37	0.13	8.24E-08	10271	0.60	6.41	0.09	1.49E-10	80
34563060	G	0.16	A	G	C6orf106 intronic	10360	0.71	5.37	0.13	8.17E-08	10296	0.78	7.42	0.11	1.3E-13	79
34563060	G	0.16	A	G	C6orf106 intronic	10360	0.71	5.37	0.13	8.17E-08	10296	0.78	7.42	0.11	1.3E-13	82
142853486	T	0.16	C	T	LOC15391 intronic	10287	-0.66	-5.12	0.13	3.17E-07	10255	-0.50	-6.49	0.08	8.91E-11	301
142853486	T	0.16	C	T	LOC15391 intronic	10287	-0.66	-5.12	0.13	3.17E-07	10256	-0.50	-6.49	0.08	9.19E-11	300
142853486	T	0.16	C	T	LOC15391 intronic	10287	-0.66	-5.12	0.13	3.17E-07	10256	-0.50	-6.49	0.08	8.89E-11	299
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10360	0.70	6.90	0.10	5.53E-12	133
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10350	0.71	7.03	0.10	2.27E-12	133
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10359	0.63	6.50	0.10	8.44E-11	132
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10359	0.63	6.50	0.10	8.44E-11	129
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10359	0.63	6.50	0.10	8.44E-11	127
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10267	0.72	6.62	0.11	3.91E-11	125
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10360	0.63	6.49	0.10	9.20E-11	123
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10360	0.62	6.43	0.10	1.30E-10	120
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10360	0.62	6.43	0.10	1.30E-10	119
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10360	0.62	6.43	0.10	1.30E-10	118
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10358	0.62	6.43	0.10	1.38E-10	115
92600031	A	0.07	G	A	CDK6/SAN 3downstream	10360	0.84	4.31	0.19	1.65E-05	10357	0.87	6.63	0.13	3.56E-11	135
1617716	C	0.08	A	C	DMRT2/Sf intergenic	10356	-0.66	-3.72	0.18	1.98E-04	10318	-0.98	-6.48	0.15	9.34E-11	301
1617716	C	0.08	A	C	DMRT2/Sf intergenic	10356	-0.66	-3.72	0.18	1.98E-04	10318	-0.98	-6.48	0.15	9.34E-11	301
22344879	C	0.02	C	G	LOC72792 intronic	10286	-2.34	-6.54	0.36	6.67E-11	10286	-2.34	-6.54	0.36	6.67E-11	4

---

22354293	T	0.02	T	A	LOC72792 intronic	10286	-2.34	-6.54	0.36	6.67E-11	10286	-2.34	-6.54	0.36	6.67E-11	3
17488607	G	0.17	G	A	PLVAP 5upstream	10307	-0.48	-3.67	0.13	2.42E-04	10309	-0.64	-6.75	0.09	1.52E-11	75
17488607	G	0.17	G	A	PLVAP 5upstream	10307	-0.48	-3.67	0.13	2.42E-04	10310	-0.63	-6.75	0.09	1.56E-11	74
17488607	G	0.17	G	A	PLVAP 5upstream	10307	-0.48	-3.67	0.13	2.42E-04	10312	-0.64	-6.79	0.09	1.18E-11	73

---

AA1	AB1	BB1	AA2	AB2	BB2	C0	C1	C2	SS
10392	223	1	2767	5393	2502	2721	5277	2620	TRUE
8676	1888	111	3392	5279	1925	2699	4989	2910	TRUE
8656	1901	109	3392	5279	1925	2693	4983	2915	TRUE
9452	1176	47	4075	5010	1590	3353	5207	2115	TRUE
3392	5279	1925	6908	3360	406	2230	4464	3904	TRUE
4497	4858	1319	8815	1767	91	3345	5244	2084	FALSE
3116	5387	2170	9945	652	5	2755	5357	2489	TRUE
4497	4858	1319	8815	1767	91	3345	5244	2084	FALSE
2632	5426	2581	9945	652	5	2306	5324	2939	TRUE
2755	5385	2495	9945	652	5	2420	5297	2848	TRUE
4056	4993	1589	8815	1767	91	2919	5339	2379	FALSE
2762	5400	2510	9945	652	5	2425	5312	2863	TRUE
2763	5400	2510	9945	652	5	2426	5312	2863	TRUE
2763	5401	2508	9945	652	5	2426	5313	2861	TRUE
2763	5402	2507	9945	652	5	2426	5314	2860	TRUE
2765	5401	2507	9945	652	5	2428	5313	2860	TRUE
2765	5401	2506	9945	652	5	2428	5313	2859	TRUE
2795	5360	2467	9945	652	5	2455	5285	2816	TRUE
4065	4995	1593	8815	1767	91	2925	5342	2385	TRUE
2764	5394	2504	9945	652	5	2428	5307	2857	TRUE
4065	4996	1592	8815	1767	91	2925	5343	2384	TRUE
4066	4995	1592	8815	1767	91	2926	5342	2384	TRUE
4066	4995	1592	8815	1767	91	2926	5342	2384	TRUE
2767	5393	2502	9945	652	5	2431	5306	2855	TRUE
4066	4995	1592	8815	1767	91	2926	5342	2384	TRUE
9506	1121	39	4075	5010	1590	3348	5254	2064	TRUE
9297	1329	49	4075	5010	1590	3226	5281	2168	TRUE
9297	1329	49	4075	5010	1590	3226	5281	2168	TRUE
4075	5010	1590	8815	1767	91	2925	5360	2389	TRUE
2787	5384	2504	9945	652	5	2450	5295	2858	TRUE

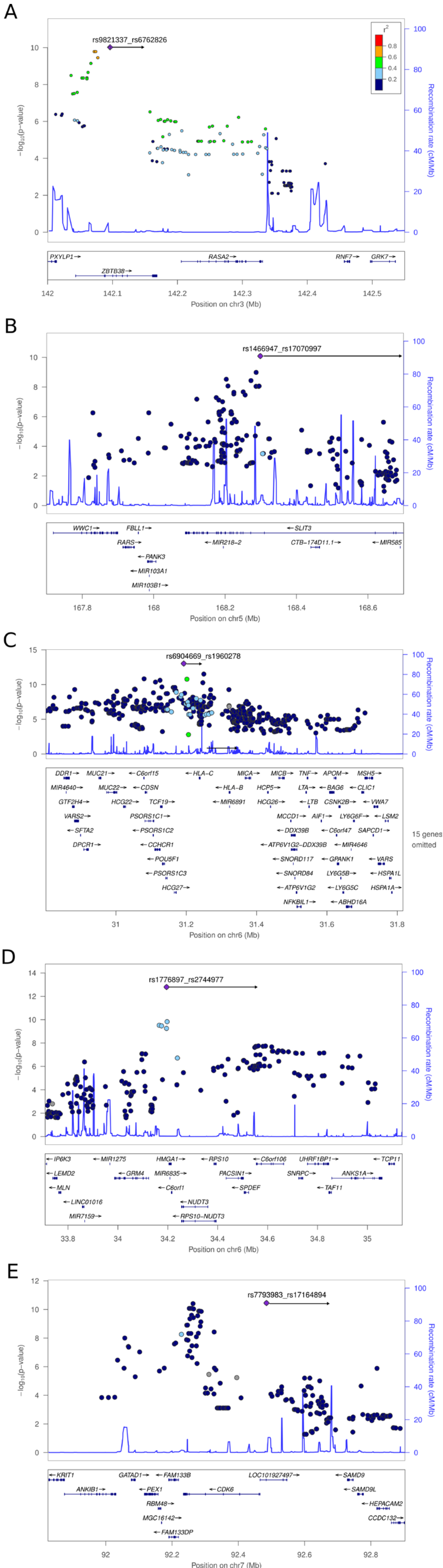
2788	5384	2503	9945	652	5	2451	5295	2857	TRUE
8810	1773	91	4064	4998	1578	2912	5351	2377	TRUE
2761	5372	2537	9945	652	5	2424	5283	2891	TRUE
8813	1768	91	4064	4998	1578	2913	5351	2375	TRUE
8815	1767	91	4064	4998	1578	2914	5351	2374	TRUE
8815	1767	91	4064	4998	1578	2914	5351	2374	TRUE
8419	2138	117	9156	1444	30	7291	2844	495	FALSE
10080	580	11	8402	2136	137	7971	2406	294	TRUE
4203	4999	1469	4376	4907	1375	1753	4007	4901	TRUE
4209	4997	1460	4376	4907	1375	1755	4009	4892	TRUE
4209	4997	1460	4376	4907	1375	1755	4009	4892	TRUE
4212	4994	1459	4376	4907	1375	1755	4010	4890	TRUE
4225	4985	1455	4376	4907	1375	1760	4013	4882	TRUE
3290	5310	2037	4376	4907	1375	1554	3567	5515	TRUE
10206	451	13	8402	2136	137	7987	2480	203	TRUE
10206	451	13	8402	2136	137	7988	2478	204	TRUE
4376	4907	1375	7479	2921	274	4193	2987	3479	TRUE
8539	2003	130	9190	1394	61	7263	3019	363	FALSE
8402	2136	137	9190	1394	61	7140	3126	382	TRUE
10419	254	2	7479	2921	274	7262	3097	315	TRUE
8641	1918	116	9190	1394	61	7357	2951	340	FALSE
9190	1394	61	7700	2730	245	6500	3601	549	FALSE
10400	272	3	7479	2921	274	7246	3109	319	TRUE
10397	271	3	7479	2921	274	7243	3108	319	TRUE
10397	269	3	7479	2921	274	7243	3106	319	TRUE
7479	2921	274	6344	3781	550	5198	3193	2283	TRUE
3673	5196	1805	3469	5213	1983	459	3216	6990	FALSE
4985	4636	1053	3469	5213	1983	733	4062	5870	FALSE
10051	606	14	7275	3067	317	6764	3449	442	TRUE
6612	3582	480	8185	2275	175	5889	2808	1945	TRUE
7275	3067	317	8185	2275	175	6511	2313	1800	TRUE
7816	2632	226	6344	3781	550	5407	3110	2157	FALSE

6695	3504	474	6344	3781	550	4517	3645	2512	FALSE
9726	927	21	8185	2275	175	7339	2999	296	TRUE
9726	927	21	8185	2275	175	7339	2999	296	TRUE
9725	928	21	8185	2275	175	7339	2998	297	TRUE
8834	1752	88	8185	2275	175	6584	3554	496	TRUE
9320	1306	48	8185	2275	175	7016	3214	404	TRUE
9320	1306	48	8185	2275	175	7016	3214	404	TRUE
3751	5158	1766	8185	2275	175	3318	4212	3120	TRUE
9843	808	20	8185	2275	175	7459	2873	299	TRUE
8813	1704	92	7617	2788	269	6426	3296	888	TRUE
8811	1705	93	7617	2788	269	6424	3297	889	FALSE
7281	2995	306	7622	2783	269	5511	3538	1536	FALSE
8814	1701	93	7617	2788	269	6427	3293	889	TRUE
8815	1701	93	7617	2788	269	6428	3293	889	TRUE
5608	4196	823	7486	2827	288	5535	1845	3189	TRUE
5606	4198	824	7486	2827	288	5535	1844	3191	TRUE
5605	4199	824	7486	2827	288	5535	1843	3192	TRUE
6418	3754	502	9319	1310	45	5686	3918	1070	TRUE
6404	3757	503	9319	1310	45	5672	3921	1071	TRUE
5440	4400	833	9319	1310	45	4818	4385	1470	FALSE
5440	4400	833	9319	1310	45	4818	4385	1470	FALSE
5440	4400	833	9319	1310	45	4818	4385	1470	FALSE
7211	3056	314	9319	1310	45	6299	3546	736	FALSE
5441	4400	833	9319	1310	45	4819	4385	1470	FALSE
5428	4405	841	9319	1310	45	4806	4390	1478	FALSE
5428	4405	841	9319	1310	45	4806	4390	1478	FALSE
5428	4405	841	9319	1310	45	4806	4390	1478	FALSE
5432	4400	840	9319	1310	45	4810	4385	1477	FALSE
8858	1722	91	9319	1310	45	7664	2723	284	FALSE
10060	570	5	9048	1547	75	8613	1831	188	FALSE
10060	570	5	9048	1547	75	8613	1831	188	FALSE
10231	357	12	10231	357	12	10231	0	369	TRUE

10231	357	12	10231	357	12	10231	0	369	TRUE
6282	3850	538	7389	2958	274	4268	4545	1810	TRUE
6285	3849	538	7389	2958	274	4269	4545	1810	TRUE
6286	3850	538	7389	2958	274	4270	4546	1810	TRUE

---

Regional plots of 5 loci with significant CH signals in RS dataset.





Compare R2 of linear models using single SNP, collapsed genotype or both SNPs as independent variables.

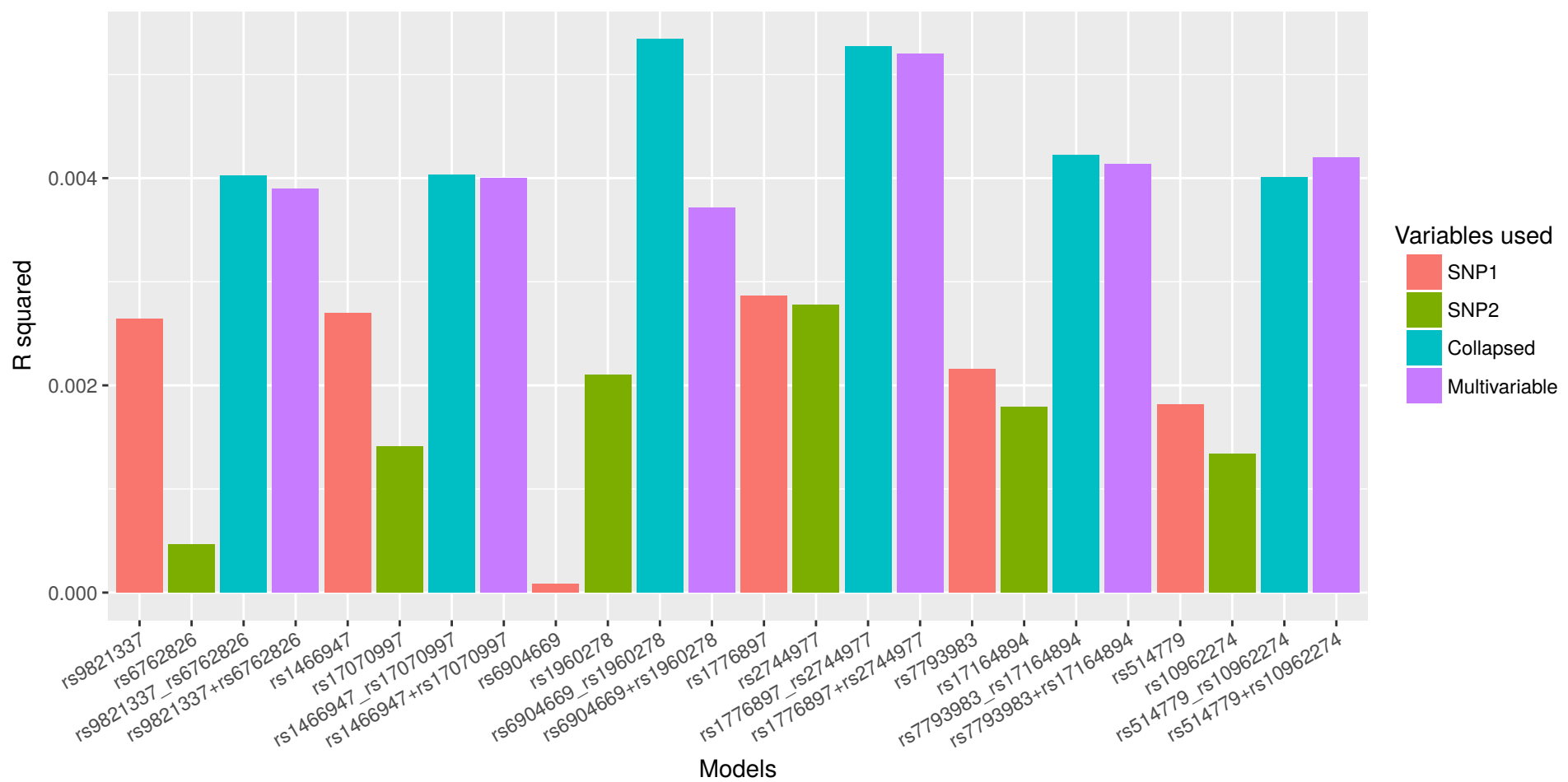
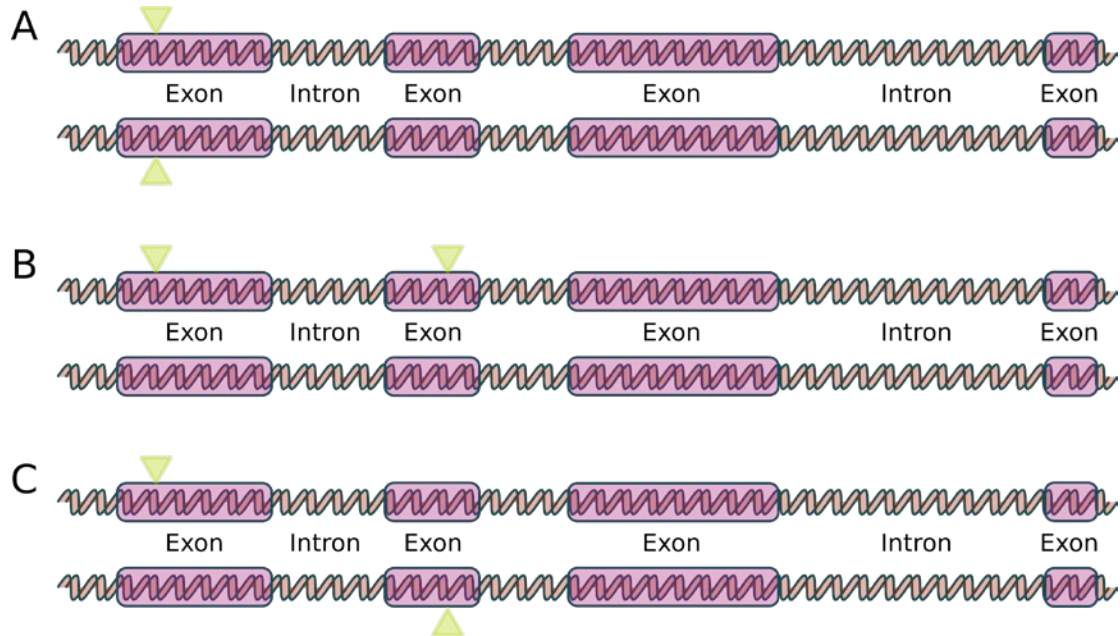


Illustration of homozygosity, double heterozygosity and compound heterozygosity. (A) Same mutation at the same position on both homologous chromosomes (homozygote). (B) Two different mutations on the same chromosome (double heterozygote). (C) Two different mutations, one on each chromosome (compound heterozygote).



**Diplotype analysis.**

SNP_pair	Cytoband	Gene	Diplotype	Mean_height	N	Total	Frequency	Has_CH	BETA
rs726838_rs6762826	3q23	ZBTB38	-1-1-	168.31	3331	10610	0.31		0.62
			-1-1-						
	3q23	ZBTB38	-1-1-	168.86	539	10610	0.05		0.62
			-1-2-						
	3q23	ZBTB38	-1-1-	169.28	2062	10610	0.19		0.62
			-2-1-						
	3q23	ZBTB38	-1-2-	168.80	521	10610	0.05		0.62
			-1-1-						
	3q23	ZBTB38	-1-2-	171.32	85	10610	0.01		0.62
			-1-2-						
	3q23	ZBTB38	-1-2-	170.98	333	10610	0.03		0.62
			-2-1-						
	3q23	ZBTB38	-1-2-	176.33	3	10610	0.00	TRUE	0.62
			-2-2-						
3q23	ZBTB38	-2-1-	169.19	2089	10610	0.20		0.62	
		-1-1-							
3q23	ZBTB38	-2-1-	169.81	335	10610	0.03		0.62	
		-1-2-							
3q23	ZBTB38	-2-1-	169.89	1282	10610	0.12		0.62	
		-2-1-							
3q23	ZBTB38	-2-1-	168.55	11	10610	0.00		0.62	
		-2-2-							
3q23	ZBTB38	-2-2-	156.90	2	10610	0.00		0.62	
		-1-2-							
3q23	ZBTB38	-2-2-	169.49	17	10610	0.00		0.62	
		-2-1-							

rs13095453_rs6762826	3q23	ZBTB38	-1-1- -1-1-	168.33	3334	10625	0.31		0.62
	3q23	ZBTB38	-1-1- -1-2-	169.19	562	10625	0.05		0.62
	3q23	ZBTB38	-1-1- -2-1-	169.49	2054	10625	0.19		0.62
	3q23	ZBTB38	-1-2- -1-1-	168.48	499	10625	0.05		0.62
	3q23	ZBTB38	-1-2- -1-2-	171.32	85	10625	0.01		0.62
	3q23	ZBTB38	-1-2- -2-1-	170.53	342	10625	0.03		0.62
	3q23	ZBTB38	-1-2- -2-2-	168.56	5	10625	0.00	TRUE	0.62
	3q23	ZBTB38	-2-1- -1-1-	169.08	2105	10625	0.20		0.62
	3q23	ZBTB38	-2-1- -1-2-	170.28	327	10625	0.03		0.62
	3q23	ZBTB38	-2-1- -2-1-	169.94	1284	10625	0.12		0.62
	3q23	ZBTB38	-2-1- -2-2-	172.41	12	10625	0.00		0.62
	3q23	ZBTB38	-2-2- -2-1-	166.66	16	10625	0.00		0.62
rs9821337_rs6762826	3q23	ZBTB38	-1-1- -1-1-	168.27	2903	10566	0.27		0.62
	3q23	ZBTB38	-1-1- -1-2-	168.71	538	10566	0.05		0.62
	3q23	ZBTB38	-1-1- -2-1-	168.72	2133	10566	0.20		0.62
	3q23	ZBTB38	-1-2-	168.05	505	10566	0.05		0.62

	3q23	ZBTB38	-1-1-	168.55	505	10566	0.05	0.62
	3q23	ZBTB38	-1-2-	171.47	87	10566	0.01	0.62
	3q23	ZBTB38	-1-2-	169.90	343	10566	0.03	0.62
	3q23	ZBTB38	-2-1-	157.90	1	10566	0.00	TRUE 0.62
	3q23	ZBTB38	-2-2-	169.27	2136	10566	0.20	0.62
	3q23	ZBTB38	-1-1-	170.27	351	10566	0.03	0.62
	3q23	ZBTB38	-2-1-	169.69	1557	10566	0.15	0.62
	3q23	ZBTB38	-2-1-	171.65	6	10566	0.00	0.62
	3q23	ZBTB38	-2-2-	168.45	2	10566	0.00	0.62
	3q23	ZBTB38	-1-2-	164.60	4	10566	0.00	0.62
	3q23	ZBTB38	-2-2-					
	3q23	ZBTB38	-2-1-					
rs1466947_rs17070997	5q35.1	SLIT3	-1-1-	169.19	7230	10555	0.68	-0.78
	5q35.1	SLIT3	-1-1-	168.59	523	10555	0.05	-0.78
	5q35.1	SLIT3	-1-2-	168.60	867	10555	0.08	-0.78
	5q35.1	SLIT3	-1-1-	168.16	176	10555	0.02	-0.78
	5q35.1	SLIT3	-2-1-	168.42	546	10555	0.05	-0.78
	5q35.1	SLIT3	-1-2-	168.23	24	10555	0.00	-0.78
	5q35.1	SLIT3	-1-1-					
	5q35.1	SLIT3	-1-2-					

	5q35.1	SLIT3	-1-2- -2-2-	165.67	3	10555	0.00	FALSE	-0.78
	5q35.1	SLIT3	-2-1- -1-1-	168.72	896	10555	0.08		-0.78
	5q35.1	SLIT3	-2-1- -2-1-	165.89	89	10555	0.01		-0.78
	5q35.1	SLIT3	-2-1- -2-2-	165.88	10	10555	0.00		-0.78
	5q35.1	SLIT3	-2-2- -1-1-	167.46	172	10555	0.02		-0.78
	5q35.1	SLIT3	-2-2- -1-2-	170.90	2	10555	0.00		-0.78
	5q35.1	SLIT3	-2-2- -2-1-	165.76	16	10555	0.00		-0.78
	5q35.1	SLIT3	-2-2- -2-2-	169.00	1	10555	0.00		-0.78
rs2233976_rs12529697	6p21.33	C6orf15	-1-1- -1-1-	169.44	7240	10606	0.68	-0.84	
	6p21.33	C6orf15	-1-1- -1-2-	168.24	602	10606	0.06	-0.84	
	6p21.33	C6orf15	-1-1- -2-1-	168.49	909	10606	0.09	-0.84	
	6p21.33	C6orf15	-1-1- -2-2-	172.79	18	10606	0.00	-0.84	
	6p21.33	C6orf15	-1-2- -1-1-	168.51	606	10606	0.06	-0.84	
	6p21.33	C6orf15	-1-2- -1-2-	167.89	54	10606	0.01	-0.84	
	6p21.33	C6orf15	-1-2- -2-1-	167.12	64	10606	0.01	-0.84	
	6p21.33	C6orf15	-1-2-	167.55	4	10606	0.00	TRUE	-0.84

	6p21.33	C6orf15	-2-2-	164.55	4	10606	0.00	TRUE	-0.84
	6p21.33	C6orf15	-2-1- -1-1-	168.14	891	10606	0.08		-0.84
	6p21.33	C6orf15	-2-1- -1-2-	166.05	75	10606	0.01		-0.84
	6p21.33	C6orf15	-2-1- -2-1-	168.23	123	10606	0.01		-0.84
	6p21.33	C6orf15	-2-1- -2-2-	174.90	2	10606	0.00		-0.84
	6p21.33	C6orf15	-2-2- -1-1-	169.68	14	10606	0.00		-0.84
	6p21.33	C6orf15	-2-2- -1-2-	169.50	2	10606	0.00		-0.84
	6p21.33	C6orf15	-2-2- -2-1-	164.75	2	10606	0.00		-0.84
rs130072_rs12529697	6p21.33	CCHCR1	-1-1- -1-1-	169.49	7356	10644	0.69		-0.83
	6p21.33	CCHCR1	-1-1- -1-2-	167.86	609	10644	0.06		-0.83
	6p21.33	CCHCR1	-1-1- -2-1-	168.30	863	10644	0.08		-0.83
	6p21.33	CCHCR1	-1-2- -1-1-	169.22	618	10644	0.06		-0.83
	6p21.33	CCHCR1	-1-2- -1-2-	168.51	56	10644	0.01		-0.83
	6p21.33	CCHCR1	-1-2- -2-1-	167.57	82	10644	0.01		-0.83
	6p21.33	CCHCR1	-1-2- -2-2-	158.50	1	10644	0.00		-0.83
	6p21.33	CCHCR1	-2-1- -1-1-	168.37	861	10644	0.08	TRUE	-0.83

	6p21.33	CCHCR1	-2-1- -1-2-	168.23	80	10644	0.01	-0.83
	6p21.33	CCHCR1	-2-1- -2-1-	168.62	109	10644	0.01	-0.83
	6p21.33	CCHCR1	-2-1- -2-2-	160.00	1	10644	0.00	-0.83
	6p21.33	CCHCR1	-2-2- -1-1-	176.50	1	10644	0.00	-0.83
	6p21.33	CCHCR1	-2-2- -1-2-	168.63	4	10644	0.00	-0.83
	6p21.33	CCHCR1	-2-2- -2-1-	163.17	3	10644	0.00	-0.83
rs1776897_rs2744977	6p21.31	GRM4/HMGA1	-1-1- -1-1-	168.79	6416	10598	0.61	0.78
	6p21.31	GRM4/HMGA1	-1-1- -1-2-	169.33	1090	10598	0.10	0.78
	6p21.31	GRM4/HMGA1	-1-1- -2-1-	169.68	569	10598	0.05	0.78
	6p21.31	GRM4/HMGA1	-1-1- -2-2-	170.49	287	10598	0.03	0.78
	6p21.31	GRM4/HMGA1	-1-2- -1-1-	169.21	1105	10598	0.10	0.78
	6p21.31	GRM4/HMGA1	-1-2- -1-2-	169.92	189	10598	0.02	0.78
	6p21.31	GRM4/HMGA1	-1-2- -2-2-	170.41	34	10598	0.00	0.78
	6p21.31	GRM4/HMGA1	-2-1- -1-1-	169.58	531	10598	0.05	0.78
	6p21.31	GRM4/HMGA1	-2-1- -2-1-	171.97	50	10598	0.00	0.78
	6p21.31	GRM4/HMGA1	-2-1-	176.78	14	10598	0.00	0.78

FALSE



	6p21.31	GRM4/HMGA1	-2-2-	170.78	14	10598	0.00	0.78
	6p21.31	GRM4/HMGA1	-2-2- -1-1-	170.21	253	10598	0.02	0.78
	6p21.31	GRM4/HMGA1	-2-2- -1-2-	171.48	31	10598	0.00	0.78
	6p21.31	GRM4/HMGA1	-2-2- -2-1-	168.35	16	10598	0.00	0.78
	6p21.31	GRM4/HMGA1	-2-2- -2-2-	167.80	13	10598	0.00	0.78
rs1759627_rs2744964	6p21.31	GRM4/HMGA1	-1-1- -1-1-	168.78	5509	10579	0.52	0.60
	6p21.31	GRM4/HMGA1	-1-1- -1-2-	168.77	827	10579	0.08	0.60
	6p21.31	GRM4/HMGA1	-1-1- -2-1-	169.38	903	10579	0.09	0.60
	6p21.31	GRM4/HMGA1	-1-1- -2-2-	170.21	517	10579	0.05	0.60
	6p21.31	GRM4/HMGA1	-1-2- -1-1-	169.29	825	10579	0.08	0.60
	6p21.31	GRM4/HMGA1	-1-2- -1-2-	169.24	117	10579	0.01	0.60
	6p21.31	GRM4/HMGA1	-1-2- -2-2-	169.38	51	10579	0.00	0.60
	6p21.31	GRM4/HMGA1	-2-1- -1-1-	169.25	983	10579	0.09	0.60
	6p21.31	GRM4/HMGA1	-2-1- -2-1-	169.84	160	10579	0.02	0.60
	6p21.31	GRM4/HMGA1	-2-1- -2-2-	171.25	54	10579	0.01	0.60
	6p21.31	GRM4/HMGA1	-2-2- -1-1-	170.13	483	10579	0.05	0.60

FALSE

	6p21.31	GRM4/HMGA1	-2-2- -1-2-	170.79	58	10579	0.01	0.60
	6p21.31	GRM4/HMGA1	-2-2- -2-1-	170.96	53	10579	0.01	0.60
	6p21.31	GRM4/HMGA1	-2-2- -2-2-	171.83	39	10579	0.00	0.60
rs42046_rs17164894	7q21.2	CDK6	-1-1- -1-1-	168.68	4813	10664	0.45	0.63
	7q21.2	CDK6	-1-1- -1-2-	169.54	289	10664	0.03	0.63
	7q21.2	CDK6	-1-1- -2-1-	169.23	1912	10664	0.18	0.63
	7q21.2	CDK6	-1-1- -2-2-	171.11	308	10664	0.03	0.63
	7q21.2	CDK6	-1-2- -1-1-	168.82	312	10664	0.03	0.63
	7q21.2	CDK6	-1-2- -1-2-	171.88	20	10664	0.00	0.63
	7q21.2	CDK6	-1-2- -2-2-	170.04	11	10664	0.00	0.63
	7q21.2	CDK6	-2-1- -1-1-	169.57	1870	10664	0.18	0.63
	7q21.2	CDK6	-2-1- -2-1-	169.81	715	10664	0.07	0.63
	7q21.2	CDK6	-2-1- -2-2-	171.09	58	10664	0.01	0.63
	7q21.2	CDK6	-2-2- -1-1-	170.43	289	10664	0.03	0.63
	7q21.2	CDK6	-2-2- -1-2-	167.32	9	10664	0.00	0.63
	7q21.2	CDK6	-2-2-	172.06	53	10664	0.00	0.63

FALSE

	7q21.2	CDK6	-2-1-	172.00	55	10664	0.00	0.63
	7q21.2	CDK6	-2-2-	176.30	5	10664	0.00	0.63
rs11767704_rs17164894	7q21.2	CDK6	-1-1-	168.65	4806	10647	0.45	0.63
	7q21.2	CDK6	-1-1-	169.29	287	10647	0.03	0.63
	7q21.2	CDK6	-1-1-	169.47	1770	10647	0.17	0.63
	7q21.2	CDK6	-2-1-	170.51	299	10647	0.03	0.63
	7q21.2	CDK6	-1-2-	169.04	313	10647	0.03	0.63
	7q21.2	CDK6	-1-1-	171.88	20	10647	0.00	0.63
	7q21.2	CDK6	-1-2-	171.52	9	10647	0.00	0.63
	7q21.2	CDK6	-2-2-	169.24	2005	10647	0.19	0.63
	7q21.2	CDK6	-2-1-	169.77	714	10647	0.07	0.63
	7q21.2	CDK6	-2-1-	170.54	53	10647	0.00	0.63
	7q21.2	CDK6	-2-2-	170.96	297	10647	0.03	0.63
	7q21.2	CDK6	-1-1-	166.60	11	10647	0.00	0.63
	7q21.2	CDK6	-2-2-	172.43	58	10647	0.01	0.63
	7q21.2	CDK6	-2-1-	176.30	5	10647	0.00	0.63
	7q21.2	CDK6	-2-2-					0.63

FALSE

rs11771637_rs17164894	7q21.2	CDK6	-1-1- -1-1-	168.69	4816	10669	0.45		0.63
	7q21.2	CDK6	-1-1- -1-2-	169.44	331	10669	0.03		0.63
	7q21.2	CDK6	-1-1- -2-1-	169.60	1842	10669	0.17		0.63
	7q21.2	CDK6	-1-1- -2-2-	170.39	306	10669	0.03		0.63
	7q21.2	CDK6	-1-2- -1-1-	168.94	271	10669	0.03		0.63
	7q21.2	CDK6	-1-2- -1-2-	171.88	20	10669	0.00		0.63
	7q21.2	CDK6	-1-2- -2-1-	167.50	1	10669	0.00		0.63
	7q21.2	CDK6	-1-2- -2-2-	170.64	13	10669	0.00	TRUE	0.63
	7q21.2	CDK6	-2-1- -1-1-	169.20	1940	10669	0.18		0.63
	7q21.2	CDK6	-2-1- -2-1-	169.89	717	10669	0.07		0.63
	7q21.2	CDK6	-2-1- -2-2-	172.43	51	10669	0.00		0.63
	7q21.2	CDK6	-2-2- -1-1-	171.09	289	10669	0.03		0.63
	7q21.2	CDK6	-2-2- -1-2-	165.43	7	10669	0.00		0.63
	7q21.2	CDK6	-2-2- -2-1-	170.77	60	10669	0.01		0.63
	7q21.2	CDK6	-2-2- -2-2-	176.30	5	10669	0.00		0.63
rs17688820_rs17164894	7q21.2	CDK6	-1-1-	168.59	6298	10577	0.60		0.72

1517066657_1517104674	7q21.2	CDK6	-1-1-	168.55	6256	10577	0.00	0.72
	7q21.2	CDK6	-1-1- -1-2-	169.19	422	10577	0.04	0.72
	7q21.2	CDK6	-1-1- -2-1-	169.51	1325	10577	0.13	0.72
	7q21.2	CDK6	-1-1- -2-2-	170.20	195	10577	0.02	0.72
	7q21.2	CDK6	-1-2- -1-1-	169.50	457	10577	0.04	0.72
	7q21.2	CDK6	-1-2- -1-2-	170.70	30	10577	0.00	0.72
	7q21.2	CDK6	-1-2- -2-1-	168.40	5	10577	0.00	0.72
	7q21.2	CDK6	-1-2- -2-2-	165.46	5	10577	0.00	0.72
	7q21.2	CDK6	-2-1- -1-1-	169.31	1340	10577	0.13	0.72
	7q21.2	CDK6	-2-1- -1-2-	171.70	7	10577	0.00	0.72
	7q21.2	CDK6	-2-1- -2-1-	170.12	275	10577	0.03	0.72
	7q21.2	CDK6	-2-1- -2-2-	172.43	15	10577	0.00	0.72
	7q21.2	CDK6	-2-2- -1-1-	171.61	171	10577	0.02	0.72
	7q21.2	CDK6	-2-2- -1-2-	173.96	8	10577	0.00	0.72
	7q21.2	CDK6	-2-2- -2-1-	169.71	23	10577	0.00	0.72
	7q21.2	CDK6	-2-2- -2-2-	167.00	1	10577	0.00	0.72

TRUE



rs2282979_rs17164894	7q21.2	CDK6	-1-1- -1-1-	168.70	4818	10669	0.45		0.63
	7q21.2	CDK6	-1-1- -1-2-	168.07	304	10669	0.03		0.63
	7q21.2	CDK6	-1-1- -2-1-	168.97	1863	10669	0.17		0.63
	7q21.2	CDK6	-1-1- -2-2-	170.38	281	10669	0.03		0.63
	7q21.2	CDK6	-1-2- -1-1-	170.40	298	10669	0.03		0.63
	7q21.2	CDK6	-1-2- -1-2-	171.88	20	10669	0.00		0.63
	7q21.2	CDK6	-1-2- -2-1-	168.00	1	10669	0.00		0.63
	7q21.2	CDK6	-1-2- -2-2-	169.70	8	10669	0.00	TRUE	0.63
	7q21.2	CDK6	-2-1- -1-1-	169.79	1917	10669	0.18		0.63
	7q21.2	CDK6	-2-1- -1-2-	173.97	3	10669	0.00		0.63
	7q21.2	CDK6	-2-1- -2-1-	169.87	717	10669	0.07		0.63
	7q21.2	CDK6	-2-1- -2-2-	172.49	54	10669	0.01		0.63
	7q21.2	CDK6	-2-2- -1-1-	171.06	311	10669	0.03		0.63
	7q21.2	CDK6	-2-2- -1-2-	168.23	12	10669	0.00		0.63
	7q21.2	CDK6	-2-2- -2-1-	170.69	57	10669	0.01		0.63
	7q21.2	CDK6	-2-2-	176.30	5	10669	0.00		0.63

	7q21.2	CDK6	-2-2-	176.30	5	10671	0.00	0.62
rs11765954_rs17164894	7q21.2	CDK6	-1-1-	168.68	4803	10671	0.45	0.62
	7q21.2	CDK6	-1-1-	169.42	306	10671	0.03	0.62
	7q21.2	CDK6	-1-1-	169.41	1848	10671	0.17	0.62
	7q21.2	CDK6	-2-1-	169.81	311	10671	0.03	0.62
	7q21.2	CDK6	-1-2-	168.97	296	10671	0.03	0.62
	7q21.2	CDK6	-1-1-	171.88	20	10671	0.00	0.62
	7q21.2	CDK6	-1-2-	168.55	12	10671	0.00	0.62
	7q21.2	CDK6	-2-2-	169.43	1940	10671	0.18	0.62
	7q21.2	CDK6	-2-1-	169.82	725	10671	0.07	0.62
	7q21.2	CDK6	-2-1-	171.33	48	10671	0.00	0.62
	7q21.2	CDK6	-2-2-	171.87	286	10671	0.03	0.62
	7q21.2	CDK6	-1-1-	169.21	8	10671	0.00	0.62
	7q21.2	CDK6	-2-2-	171.71	63	10671	0.01	0.62
	7q21.2	CDK6	-2-1-	176.30	5	10671	0.00	0.62
	7q21.2	CDK6	-2-2-					
rs6948097_rs17164894	7q21.2	CDK6	-1-1-	168.62	4773	10606	0.45	0.62
			-1-1-					

FALSE

	7q21.2	CDK6	-1-1- -1-2-	168.63	284	10606	0.03		0.62
	7q21.2	CDK6	-1-1- -2-1-	169.43	1846	10606	0.17		0.62
	7q21.2	CDK6	-1-1- -2-2-	170.49	289	10606	0.03		0.62
	7q21.2	CDK6	-1-2- -1-1-	169.72	316	10606	0.03		0.62
	7q21.2	CDK6	-1-2- -1-2-	171.88	20	10606	0.00		0.62
	7q21.2	CDK6	-1-2- -2-2-	173.36	9	10606	0.00		0.62
	7q21.2	CDK6	-2-1- -1-1-	169.28	1920	10606	0.18	FALSE	0.62
	7q21.2	CDK6	-2-1- -2-1-	169.66	720	10606	0.07		0.62
	7q21.2	CDK6	-2-1- -2-2-	172.15	62	10606	0.01		0.62
	7q21.2	CDK6	-2-2- -1-1-	170.80	302	10606	0.03		0.62
	7q21.2	CDK6	-2-2- -1-2-	165.10	11	10606	0.00		0.62
	7q21.2	CDK6	-2-2- -2-1-	170.81	49	10606	0.00		0.62
	7q21.2	CDK6	-2-2- -2-2-	176.30	5	10606	0.00		0.62
rs6954221_rs17164894	7q21.2	CDK6	-1-1- -1-1-	168.69	4805	10670	0.45		0.62
	7q21.2	CDK6	-1-1- -1-2-	169.79	305	10670	0.03		0.62
	7q21.2	CDK6	-1-1-	169.40	1858	10670	0.17		0.62



	7q21.2	CDK6	-2-1-	169.40	1638	10670	0.17	0.62
	7q21.2	CDK6	-1-1- -2-2-	170.62	271	10670	0.03	0.62
	7q21.2	CDK6	-1-2- -1-1-	168.59	297	10670	0.03	0.62
	7q21.2	CDK6	-1-2- -1-2-	171.88	20	10670	0.00	0.62
	7q21.2	CDK6	-1-2- -2-1-	168.48	19	10670	0.00	0.62
	7q21.2	CDK6	-1-2- -2-2-	169.80	9	10670	0.00	0.62
	7q21.2	CDK6	-2-1- -1-1-	169.42	1928	10670	0.18	0.62
	7q21.2	CDK6	-2-1- -1-2-	168.99	22	10670	0.00	0.62
	7q21.2	CDK6	-2-1- -2-1-	169.77	724	10670	0.07	0.62
	7q21.2	CDK6	-2-1- -2-2-	172.49	56	10670	0.01	0.62
	7q21.2	CDK6	-2-2- -1-1-	171.27	285	10670	0.03	0.62
	7q21.2	CDK6	-2-2- -1-2-	168.01	11	10670	0.00	0.62
	7q21.2	CDK6	-2-2- -2-1-	170.56	55	10670	0.01	0.62
	7q21.2	CDK6	-2-2- -2-2-	176.30	5	10670	0.00	0.62
rs7804722_rs17164894	7q21.2	CDK6	-1-1- -1-1-	168.53	4776	10609	0.45	0.62
	7q21.2	CDK6	-1-1- -1-2-	169.48	303	10609	0.03	0.62

TRUE

	7q21.2	CDK6	-1-1- -2-1-	169.39	1882	10609	0.18		0.62
	7q21.2	CDK6	-1-1- -2-2-	170.45	250	10609	0.02		0.62
	7q21.2	CDK6	-1-2- -1-1-	168.60	296	10609	0.03		0.62
	7q21.2	CDK6	-1-2- -1-2-	171.88	20	10609	0.00		0.62
	7q21.2	CDK6	-1-2- -2-1-	170.05	56	10609	0.01		0.62
	7q21.2	CDK6	-1-2- -2-2-	166.61	9	10609	0.00		0.62
	7q21.2	CDK6	-2-1- -1-1-	169.26	1887	10609	0.18	TRUE	0.62
	7q21.2	CDK6	-2-1- -1-2-	168.38	43	10609	0.00		0.62
	7q21.2	CDK6	-2-1- -2-1-	169.65	720	10609	0.07		0.62
	7q21.2	CDK6	-2-1- -2-2-	170.61	52	10609	0.00		0.62
	7q21.2	CDK6	-2-2- -1-1-	171.21	243	10609	0.02		0.62
	7q21.2	CDK6	-2-2- -1-2-	170.62	11	10609	0.00		0.62
	7q21.2	CDK6	-2-2- -2-1-	170.97	56	10609	0.01		0.62
	7q21.2	CDK6	-2-2- -2-2-	176.30	5	10609	0.00		0.62
rs7793983_rs17164894	7q21.2	LOC101927497	-1-1- -1-1-	168.87	7646	10646	0.72		0.87
	7q21.2	LOC101927497	-1-1-	169.61	558	10646	0.05		0.87

	7q21.2	LOC101927497	-1-2-	169.01	558	10646	0.05		0.87
	7q21.2	LOC101927497	-1-1- -2-1-	169.74	812	10646	0.08		0.87
	7q21.2	LOC101927497	-1-1- -2-2-	164.38	5	10646	0.00		0.87
	7q21.2	LOC101927497	-1-2- -1-1-	169.94	592	10646	0.06		0.87
	7q21.2	LOC101927497	-1-2- -1-2-	171.42	41	10646	0.00		0.87
	7q21.2	LOC101927497	-1-2- -2-1-	173.17	63	10646	0.01		0.87
	7q21.2	LOC101927497	-1-2- -2-2-	167.67	3	10646	0.00	TRUE	0.87
	7q21.2	LOC101927497	-2-1- -1-1-	169.53	754	10646	0.07		0.87
	7q21.2	LOC101927497	-2-1- -1-2-	172.07	74	10646	0.01		0.87
	7q21.2	LOC101927497	-2-1- -2-1-	170.73	83	10646	0.01		0.87
	7q21.2	LOC101927497	-2-1- -2-2-	167.24	5	10646	0.00		0.87
	7q21.2	LOC101927497	-2-2- -1-1-	170.25	6	10646	0.00		0.87
	7q21.2	LOC101927497	-2-2- -1-2-	163.70	1	10646	0.00		0.87
	7q21.2	LOC101927497	-2-2- -2-1-	173.50	3	10646	0.00		0.87
rs514779_rs10962274	9p24.3	DMRT2/SMARCA2	-1-1- -1-1-	169.25	8550	10558	0.81		-0.98
	9p24.3	DMRT2/SMARCA2	-1-1- -1-2-	167.95	670	10558	0.06		-0.98

	9p24.3	DMRT2/SMARCA2	-1-1- -2-1-	169.73	221	10558	0.02		-0.98
	9p24.3	DMRT2/SMARCA2	-1-1- -2-2-	166.22	61	10558	0.01		-0.98
	9p24.3	DMRT2/SMARCA2	-1-2- -1-1-	167.87	723	10558	0.07		-0.98
	9p24.3	DMRT2/SMARCA2	-1-2- -1-2-	167.18	41	10558	0.00	FALSE	-0.98
	9p24.3	DMRT2/SMARCA2	-1-2- -2-2-	171.85	10	10558	0.00		-0.98
	9p24.3	DMRT2/SMARCA2	-2-1- -1-1-	168.59	208	10558	0.02		-0.98
	9p24.3	DMRT2/SMARCA2	-2-1- -2-1-	165.98	4	10558	0.00		-0.98
	9p24.3	DMRT2/SMARCA2	-2-2- -1-1-	165.50	47	10558	0.00		-0.98
	9p24.3	DMRT2/SMARCA2	-2-2- -1-2-	167.08	22	10558	0.00		-0.98
	9p24.3	DMRT2/SMARCA2	-2-2- -2-1-	153.70	1	10558	0.00		-0.98
rs1853417_rs10962274	9p24.3	DMRT2/SMARCA2	-1-1- -1-1-	169.33	8603	10618	0.81		-0.98
	9p24.3	DMRT2/SMARCA2	-1-1- -1-2-	167.99	692	10618	0.07		-0.98
	9p24.3	DMRT2/SMARCA2	-1-1- -2-1-	169.04	205	10618	0.02		-0.98
	9p24.3	DMRT2/SMARCA2	-1-1- -2-2-	165.77	60	10618	0.01		-0.98
	9p24.3	DMRT2/SMARCA2	-1-2- -1-1-	167.85	708	10618	0.07		-0.98
	9p24.3	DMRT2/SMARCA2	-1-2-	167.18	41	10618	0.00		-0.98

9p24.3	DMRT2/SMARCA2	-1-2-	167.18	41	10618	0.00	FALSE	-0.98
9p24.3	DMRT2/SMARCA2	-1-2- -2-2-	166.74	13	10618	0.00		-0.98
9p24.3	DMRT2/SMARCA2	-2-1- -1-1-	169.33	224	10618	0.02		-0.98
9p24.3	DMRT2/SMARCA2	-2-1- -2-1-	165.98	4	10618	0.00		-0.98
9p24.3	DMRT2/SMARCA2	-2-2- -1-1-	166.08	48	10618	0.00		-0.98
9p24.3	DMRT2/SMARCA2	-2-2- -1-2-	169.82	19	10618	0.00		-0.98
9p24.3	DMRT2/SMARCA2	-2-2- -2-1-	153.70	1	10618	0.00		-0.98

Gene: The gene that harbors or is near to the first SNP.

N: Number of individuals in each diplotype group.

Total: Total number of individuals genotyped for both SNPs

CH: Whether the two SNPs are in compound heterozygote configuration.

BETA: Effect size of the collapsed genotype.