SUPPLEMENTARY TABLES AND FIGURES

Supplementary Table 1. All SNPs with $p < 5 \times 10^{-6}$ in the meta-analysis, sorted by chromosome and position. The most significant SNP at each locus is highlighted in yellow.

MarkerName	A1	A2	Freq1	FreqSE	MinFreq	MaxFreq	Effect	StdErr	P	Direction	HetISq	HetChiSq	HetDf	HetPVal	SNP	CHR	BP
1:19761429	a	g	0.1987	0.0098	0.1868	0.2068	-0.1265	0.0269	2.51E-06	--	57	2.325	1	0.127	rs12136530	1	19,761,429
1:19761435	a	t	0.1986	0.0098	0.1868	0.2067	-0.1261	0.0269	2.70E-06	--	56.4	2.295	1	0.130	rs12136534	1	19,761,435
1:163151841	a	g	0.47	0.0036	0.4665	0.4738	0.0887	0.019	3.17E-06	++	20.5	1.258	1	0.262	rs4291481	1	163,151,841
1:163156524	a	g	0.4701	0.0039	0.4664	0.4743	0.0892	0.019	2.72E-06	++	29.6	1.42	1	0.233	rs10753606	1	163,156,524
1:163158828	t	c	0.5305	0.0034	0.5269	0.5337	-0.0887	0.0191	3.47E-06	--	41.2	1.702	1	0.192	rs10753607	1	163,158,828
1:163159496	a	g	0.4697	0.0037	0.4662	0.4736	0.0884	0.019	3.20E-06	++	38.5	1.626	1	0.202	rs7355070	1	163,159,496
1:163160051	t	c	0.5362	0.0029	0.5335	0.5394	-0.0903	0.0192	2.62E-06	--	48.4	1.938	1	0.164	rs10753608	1	163,160,051
1:163160337	a	g	0.4699	0.0034	0.4667	0.4735	0.0883	0.019	3.25E-06	++	39.2	1.645	1	0.200	rs10753609	1	163,160,337
1:163162067	a	g	0.53	0.0033	0.5265	0.5331	-0.0884	0.019	3.15E-06	--	38.9	1.637	1	0.201	rs2662775	1	163,162,067
1:163165029	a	g	0.5293	0.0038	0.5252	0.5329	-0.0894	0.019	2.54E-06	--	42.5	1.738	1	0.187	rs2662776	1	163,165,029
1:163166676	a	g	0.4704	0.0027	0.4678	0.4733	0.0892	0.019	2.59E-06	++	36.7	1.581	1	0.209	rs2999967	1	163,166,676
1:163166723	a	c	0.4701	0.0031	0.4672	0.4734	0.0889	0.019	2.78E-06	++	38.1	1.617	1	0.204	rs2999859	1	163,166,723
1:163168299	a	g	0.5303	0.0026	0.5275	0.5328	-0.0888	0.019	2.88E-06	--	37.6	1.602	1	0.206	rs2999965	1	163,168,299
3:9214817	t	c	0.9516	0.0029	0.9498	0.9563	0.2381	0.0514	3.58E-06	++	45	1.819	1	0.178	rs76153987	3	9,214,817
3:84136391	t	c	0.0926	0.0055	0.0863	0.0973	-0.1562	0.0334	2.98E-06	--	0	0.739	1	0.390	rs138894667	3	84,136,391
3:84147443	c	g	0.0921	0.005	0.0864	0.0965	-0.1619	0.0335	1.38E-06	--	13.9	1.162	1	0.281	rs9863067	3	84,147,443
3:84147864	t	c	0.9043	0.0008	0.9035	0.9052	0.1524	0.0323	2.35E-06	++	44.2	1.792	1	0.181	rs7625182	3	84,147,864
3:84148161	t	c	0.0961	0.0004	0.0957	0.0965	-0.1519	0.0322	2.39E-06	--	45.4	1.831	1	0.176	rs7637167	3	84,148,161
3:84152266	a	g	0.0961	0.0004	0.0957	0.0965	-0.1517	0.0322	2.43E-06	--	45.8	1.844	1	0.175	rs9847846	3	84,152,266
3:84153365	a	g	0.9039	0.0004	0.9035	0.9043	0.1518	0.0322	2.42E-06	++	45.8	1.846	1	0.174	rs9819662	3	84,153,365
3:84154174	t	c	0.9045	0.0002	0.9043	0.9047	0.1506	0.0323	3.07E-06	++	43.5	1.768	1	0.184	rs4392427	3	84,154,174
3:84156439	t	g	0.9038	0.0003	0.9035	0.9042	0.1514	0.0322	2.54E-06	++	46.5	1.871	1	0.171	rs6791832	3	84,156,439

MarkerName	A1	A2	Freq1	FreqSE	MinFreq	MaxFreq	Effect	StdErr	P	Direction	HetISq	HetChiSq	HetDf	HetPVal	SNP	CHR	BP
3:84157679	t	c	0.9082	0.0055	0.9035	0.9146	0.1603	0.0338	2.16E-06	++	24.2	1.319	1	0.251	rs73842687	3	84,157,679
3:84157681	t	c	0.9082	0.0055	0.9035	0.9146	0.1603	0.0338	2.16E-06	++	24.2	1.319	1	0.251	rs73842688	3	84,157,681
3:84160822	t	c	0.9038	0.0003	0.9035	0.9042	0.1513	0.0322	2.61E-06	++	46.9	1.885	1	0.170	rs9829344	3	84,160,822
3:84162671	t	c	0.0948	0.0018	0.0928	0.0965	-0.1505	0.0326	3.99E-06	--	50.1	2.003	1	0.157	rs11924771	3	84,162,671
3:84167120	t	c	0.096	0.0003	0.0957	0.0963	-0.1506	0.0322	2.99E-06	--	47.2	1.895	1	0.169	rs11923494	3	84,167,120
3:84168160	a	g	0.9046	0.0012	0.9035	0.9059	0.1504	0.0325	3.78E-06	++	50.4	2.015	1	0.156	rs13093168	3	84,168,160
3:84171529	c	g	0.9057	0.0024	0.9035	0.9084	0.1536	0.0328	2.91E-06	++	43.5	1.77	1	0.183	rs34575837	3	84,171,529
3:84172631	a	t	0.0955	0.0002	0.0953	0.0957	-0.149	0.0323	4.03E-06	--	47.8	1.917	1	0.166	rs74568637	3	84,172,631
3:84178038	a	g	0.0955	0.0001	0.0954	0.0957	-0.1493	0.0323	3.88E-06	--	49.5	1.979	1	0.160	rs77090875	3	84,178,038
3:84179229	a	g	0.9039	0.0004	0.9034	0.9043	0.1504	0.0322	3.09E-06	++	51.6	2.067	1	0.151	rs4390938	3	84,179,229
3:84179935	t	c	0.0961	0.0005	0.0957	0.0966	-0.1501	0.0322	3.22E-06	--	52.2	2.093	1	0.148	rs9818881	3	84,179,935
3:148481023	a	g	0.0257	0.0001	0.0256	0.0259	-0.3254	0.0689	2.33E-06	--	0	0.86	1	0.354	rs79019069	3	148,481,023
7:11705786	t	c	0.0164	0.0007	0.0155	0.0169	0.4121	0.0805	3.06E-07	++	0	0.093	1	0.760	rs116864947	7	11,705,786
7:11728276	c	g	0.9805	0.0001	0.9805	0.9806	-0.3948	0.0797	7.35E-07	--	0	0.079	1	0.779	rs139521481	7	11,728,276
7:11760783	a	c	0.9832	0.0005	0.9828	0.9839	-0.4077	0.0816	5.88E-07	--	0	0.085	1	0.771	rs140407951	7	11,760,783
7:27519118	a	g	0.5087	0.0055	0.5037	0.5147	-0.0918	0.02	4.26E-06	--	0	0.182	1	0.670	rs6462018	7	27,519,118
7:77917038	a	c	0.6433	0.0024	0.6408	0.6456	0.0923	0.02	3.88E-06	++	0	0.977	1	0.323	rs798338	7	77,917,038
7:138820245	a	g	0.9733	0.0009	0.9723	0.9741	-0.3146	0.0605	1.99E-07	--	0	0.085	1	0.771	rs28526625	7	138,820,245
7:138822895	a	t	0.0267	0.001	0.0258	0.0278	0.302	0.0608	6.71E-07	++	0	0.014	1	0.905	rs7809243	7	138,822,895
7:138825446	a	g	0.9736	0.0011	0.9723	0.9746	-0.3163	0.0607	1.92E-07	--	0	0.119	1	0.730	rs12114023	7	138,825,446
7:138826304	a	g	0.9743	0.0004	0.9739	0.9746	-0.325	0.062	1.59E-07	--	0	0.036	1	0.849	rs13221853	7	138,826,304
7:138827527	a	g	0.9766	0.004	0.9746	0.9848	-0.3741	0.0741	4.37E-07	--	4.6	1.049	1	0.306	rs59018042	7	138,827,527
7:138839426	a	c	0.9758	0.0014	0.9743	0.9771	-0.3193	0.065	9.03E-07	--	0	0.074	1	0.785	rs117684722	7	138,839,426
7:138846477	a	g	0.0256	0.0003	0.0253	0.026	0.32	0.061	1.55E-07	++	0	0.108	1	0.743	rs6944116	7	138,846,477

MarkerName	A1	A2	Freq1	FreqSE	MinFreq	MaxFreq	Effect	StdErr	P	Direction	HetISq	HetChiSq	HetDf	HetPVal	SNP	CHR	BP
7:138850967	a	g	0.9742	0.0006	0.9736	0.9747	-0.3215	0.0611	1.42E-07	--	0	0.116	1	0.733	rs60580184	7	138,850,967
7:138857309	t	c	0.9739	0.0009	0.9728	0.9747	-0.3141	0.0608	2.40E-07	--	0	0.214	1	0.644	rs4732357	7	138,857,309
7:138858270	t	c	0.9742	0.0006	0.9735	0.9747	-0.321	0.0611	1.50E-07	--	0	0.114	1	0.736	rs28415898	7	138,858,270
7:138859884	a	g	0.0258	0.0006	0.0253	0.0265	0.3209	0.0611	1.51E-07	++	0	0.114	1	0.735	rs58013295	7	138,859,884
7:138861003	t	c	0.9742	0.0006	0.9735	0.9747	-0.3209	0.0611	1.52E-07	--	0	0.115	1	0.735	rs7787241	7	138,861,003
7:138861715	t	c	0.9746	0.0001	0.9745	0.9747	-0.3265	0.0622	1.55E-07	--	0	0.097	1	0.756	rs10248900	7	138,861,715
7:138871278	t	c	0.9743	0.0004	0.9738	0.9746	-0.3203	0.0612	1.65E-07	--	0	0.122	1	0.727	rs61049683	7	138,871,278
7:138872067	t	c	0.0262	0.0009	0.0254	0.0273	0.3207	0.0617	1.98E-07	++	0	0.121	1	0.728	rs2249153	7	138,872,067
7:138884934	a	g	0.9802	0.0064	0.9736	0.9864	-0.4172	0.0876	1.93E-06	--	0	0.884	1	0.347	rs7385468	7	138,884,934
9:116131695	a	g	0.2089	0.0054	0.203	0.2139	0.1333	0.0241	3.35E-08	++	0	0.196	1	0.658	rs10121150	9	116,131,695
9:116143097	t	c	0.1234	0.0004	0.1231	0.1239	0.1674	0.0365	4.45E-06	++	0	0.427	1	0.514	rs34000674	9	116,143,097
9:116151191	a	g	0.3051	0.0197	0.2735	0.3174	-0.1764	0.0233	3.91E-14	--	82.1	5.599	1	0.018	rs1805313	9	116,151,191
9:116153900	a	g	0.3744	0.0057	0.3684	0.3798	0.096	0.0194	7.87E-07	++	57.3	2.344	1	0.126	rs1139488	9	116,153,900
9:116154099	t	c	0.9237	0.0037	0.9179	0.9261	0.3068	0.0471	7.17E-11	++	94.1	16.919	1	3.90E-05	rs8177800	9	116,154,099
9:136141870	t	c	0.8172	0.0167	0.8039	0.8383	0.1211	0.026	3.11E-06	++	0	0.207	1	0.649	rs2519093	9	136,141,870
9:136146597	t	c	0.7461	0.0129	0.7344	0.7603	0.1035	0.0222	3.02E-06	++	0	0.366	1	0.545	rs550057	9	136,146,597
9:136149399	a	g	0.8162	0.0166	0.803	0.8369	0.1191	0.0258	3.88E-06	++	0	0.284	1	0.594	rs507666	9	136,149,399
9:136149830	a	g	0.8161	0.0165	0.8029	0.8368	0.1191	0.0258	3.87E-06	++	0	0.285	1	0.594	rs532436	9	136,149,830
9:136155000	t	c	0.8159	0.0168	0.8025	0.8368	0.1201	0.026	3.84E-06	++	0	0.212	1	0.645	rs635634	9	136,155,000
18:12909504	a	g	0.9283	0.0136	0.9252	0.9875	-0.2584	0.0495	1.75E-07	--	0	0.386	1	0.534	rs144653651	18	12,909,504
19:33877523	c	g	0.2636	0.0056	0.2576	0.2688	0.1021	0.022	3.37E-06	++	0	0.003	1	0.954	rs8111027	19	33,877,523
19:33878039	a	g	0.265	0.0063	0.2582	0.2709	0.101	0.0219	3.93E-06	++	0	0.024	1	0.877	rs3556	19	33,878,039
19:33880000	c	g	0.2646	0.0046	0.2597	0.2689	0.1004	0.0218	4.24E-06	++	0	0	1	0.993	rs3786893	19	33,880,000
19:33884341	a	g	0.3025	0.0122	0.2889	0.3135	0.1049	0.0213	8.64E-07	++	0	0.046	1	0.831	rs16968074	19	33,884,341

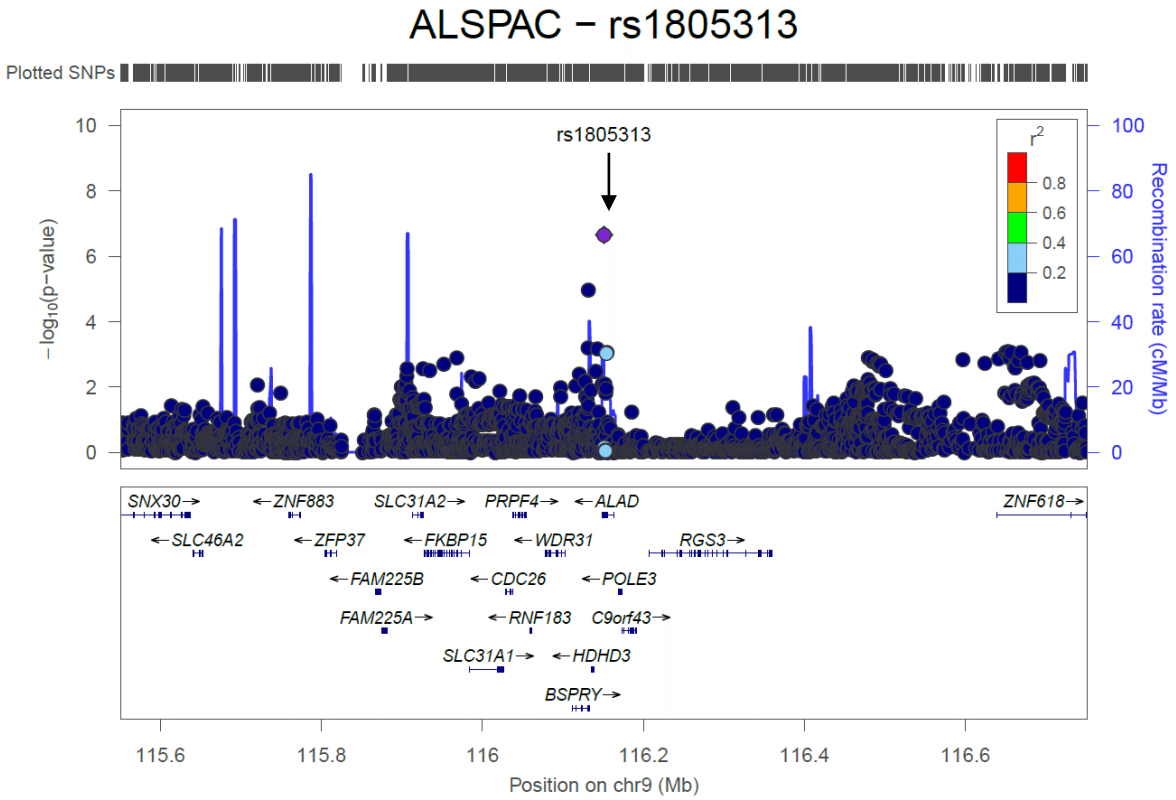
Supplementary Table 2. Demographic characteristics of study participants for the Australian (QIMR) and UK (ALSPAC) studies.

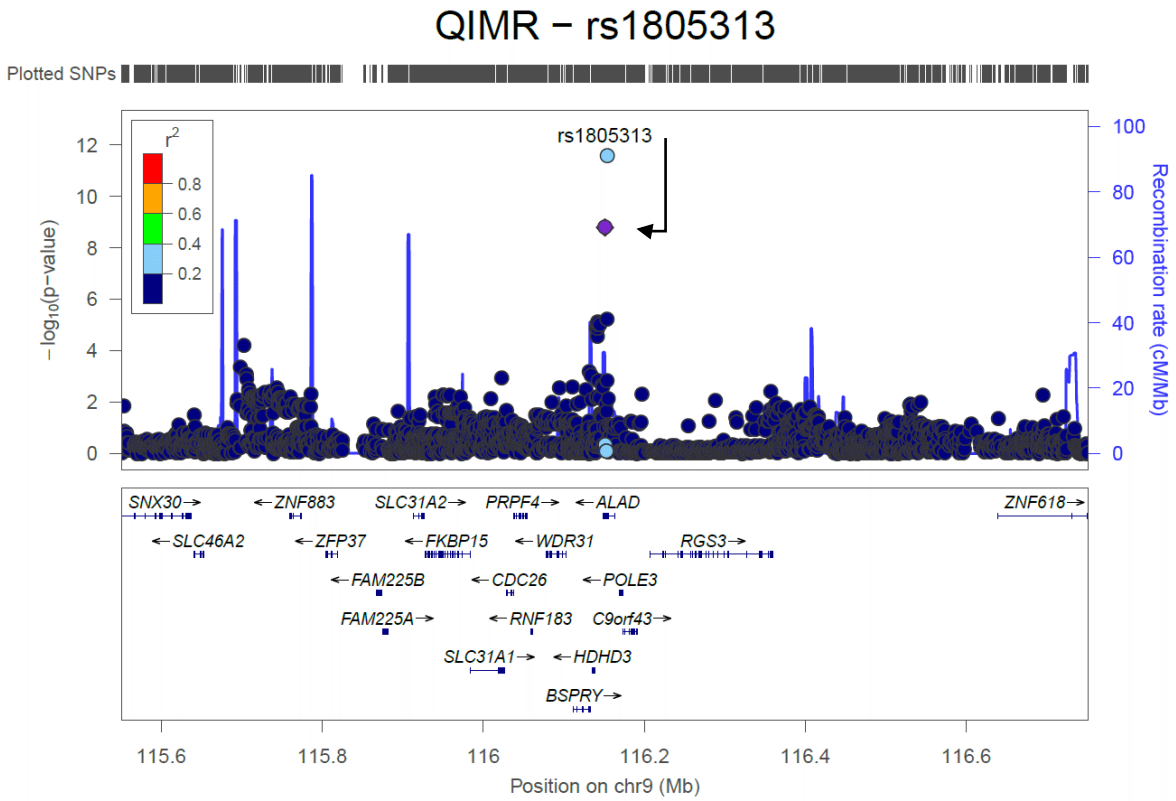
Study	**QIMR**		**ALSPAC**
Date of recruitment	**1993-96**	**2001-05**	
Source of recruitment	Adult twin-pairs resident in Australia	Adult twins, their first-degree relatives and spouses, resident in Australia	Population of Bristol and Avon county
N with phenotype and genotype data	1570	1104	
Sex (percent Female)	66%	50%	100% (all pregnant at time of blood collection, median gestational age 11 weeks)
Age (mean ± SD)	46.0 ± 11.8	49.0 ± 13.0	28.4 ± 4.8
Smoking status (percent current smokers)	20%	27%	32%

Additional information about these studies and characteristics of participants is given in:

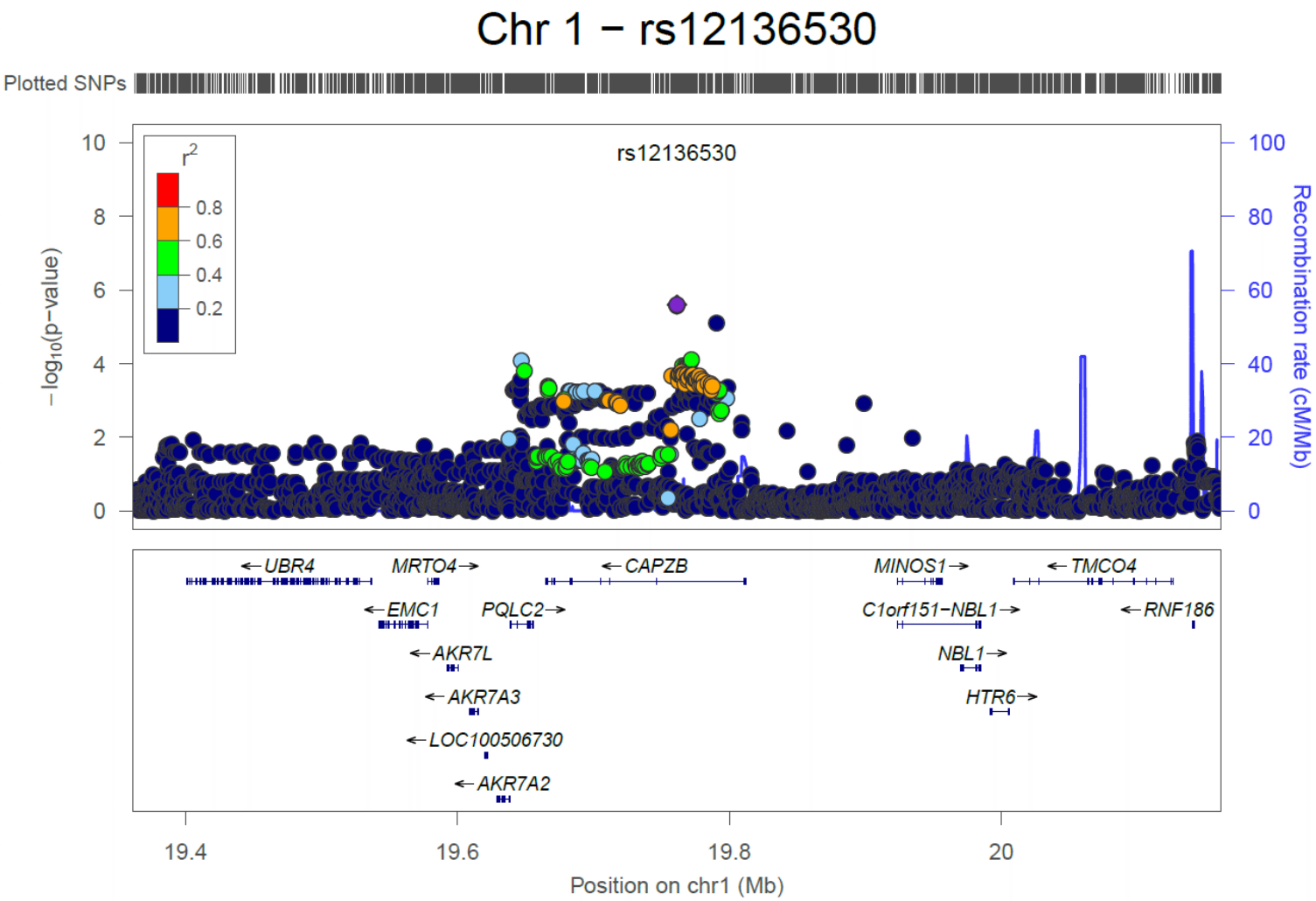
1. Whitfield, J.B., Dy, V., McQuilty, R., Zhu, G., Montgomery, G.W., Ferreira, M.A., Duffy, D.L., Neale, M.C., Heijmans, B.T., Heath, A.C. *et al.* (2007) Evidence of genetic effects on blood lead concentration. *Environ Health Perspect*, **115**, 1224-1230.
2. Heath, A.C., Whitfield, J.B., Martin, N.G., Pergadia, M.L., Goate, A.M., Lind, P.A., McEvoy, B.P., Schrage, A.J., Grant, J.D., Chou, Y.L. *et al.* (2011) A quantitative-trait genome-wide association study of alcoholism risk in the community: findings and implications. *Biol Psychiatry*, **70**, 513-518.
3. Fraser, A., Macdonald-Wallis, C., Tilling, K., Boyd, A., Golding, J., Davey Smith, G., Henderson, J., Macleod, J., Molloy, L., Ness, A. *et al.* (2012) Cohort Profile: The Avon Longitudinal Study of Parents and Children: ALSPAC mothers cohort. *Int J Epidemiol*. **42**, 97-110.
4. Taylor, C.M., Golding, J., Hibbeln, J. and Emond, A.M. (2013) Environmental factors predicting blood lead levels in pregnant women in the UK: the ALSPAC study. *PLoS One*, **8**, e72371.

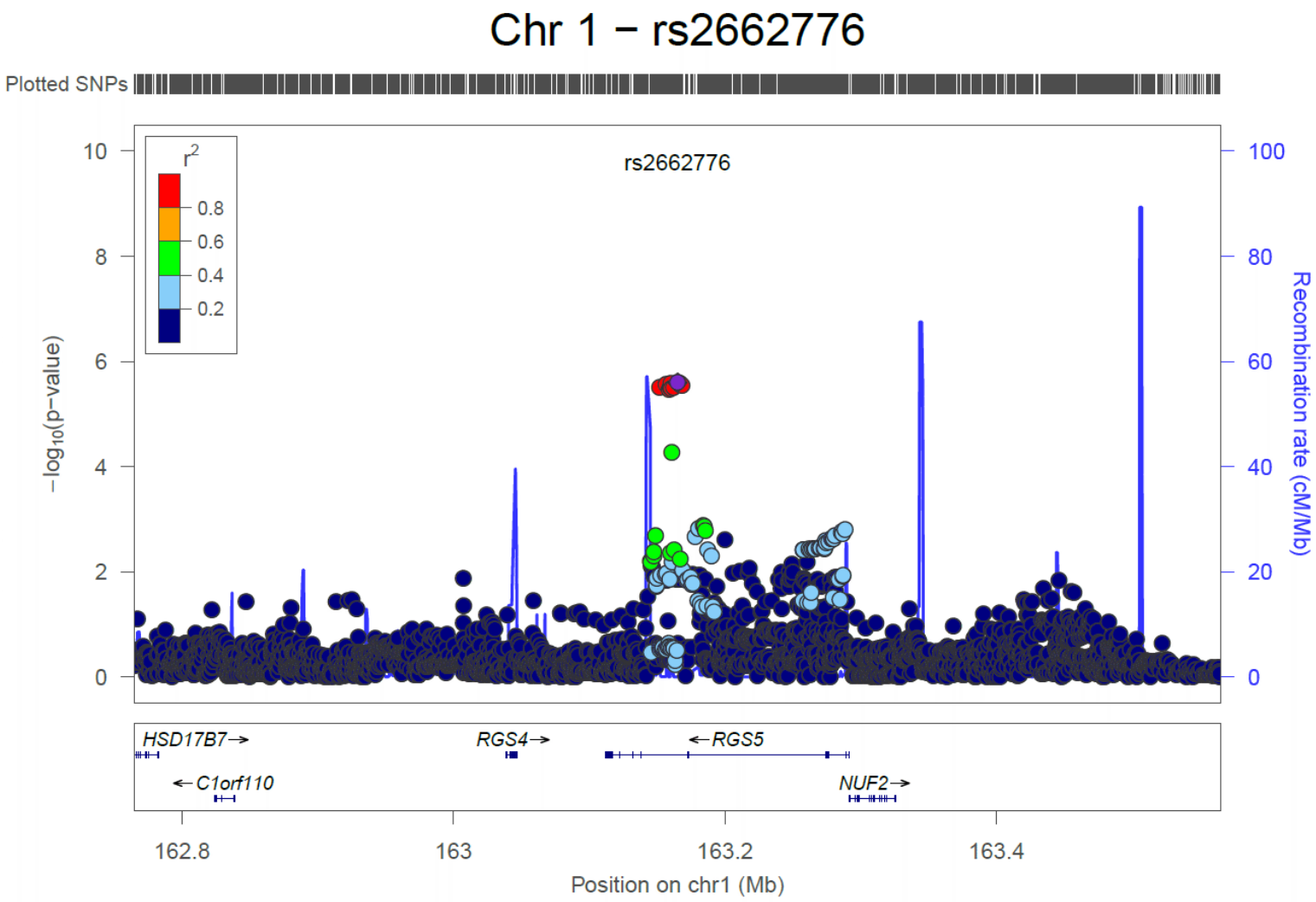
Supplementary Figure 1.Regional plots for the chromosome 9 (ALAD) locus, showing 1000G-imputed results for ALSPAC and QIMR separately.

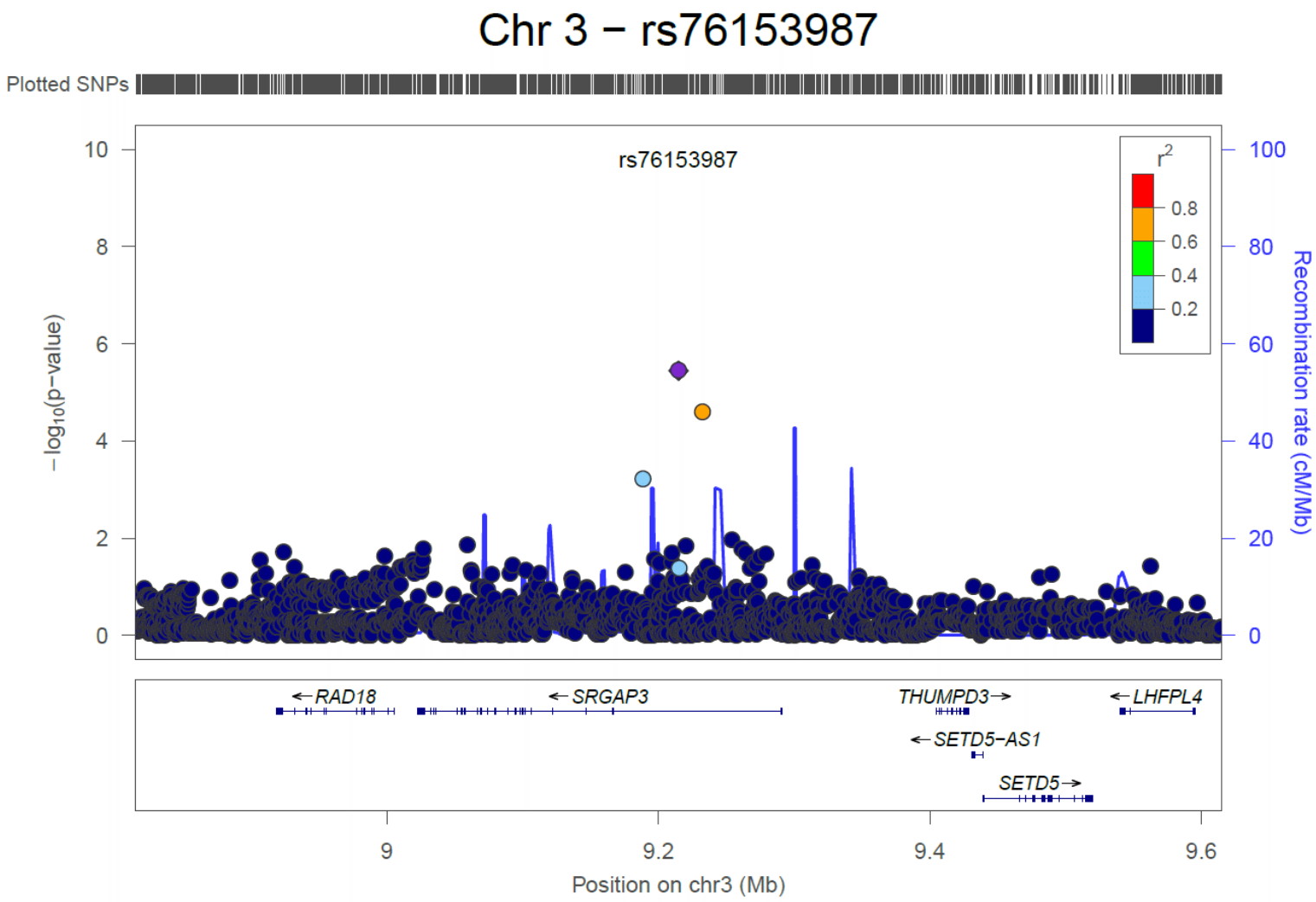




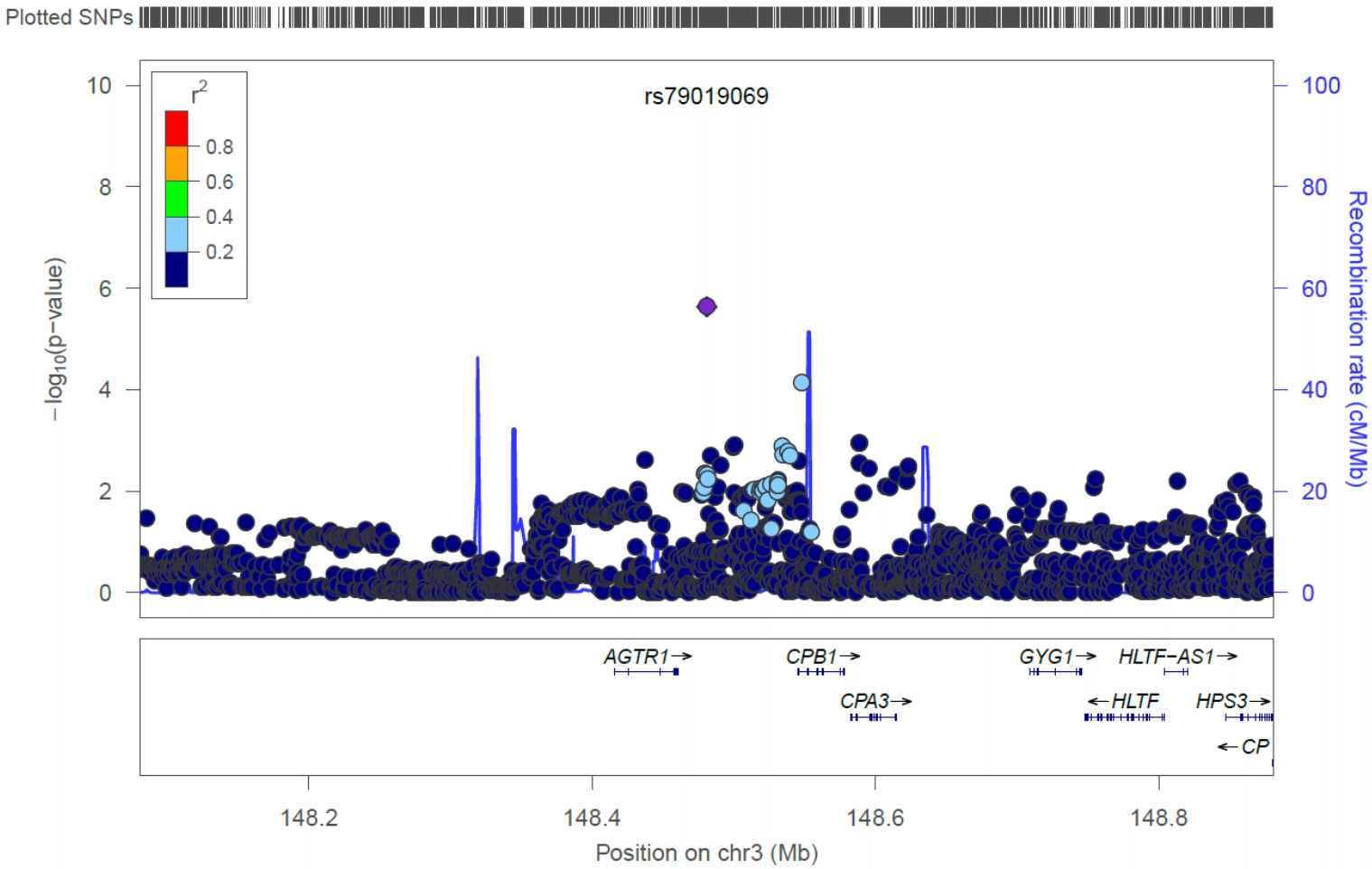
Supplementary Figure 2. Regional plots for the suggestive loci from meta-analysis of 1000G-imputed results from ALSPAC and QIMR. For details of the most significant SNP at each locus, see Table 1.

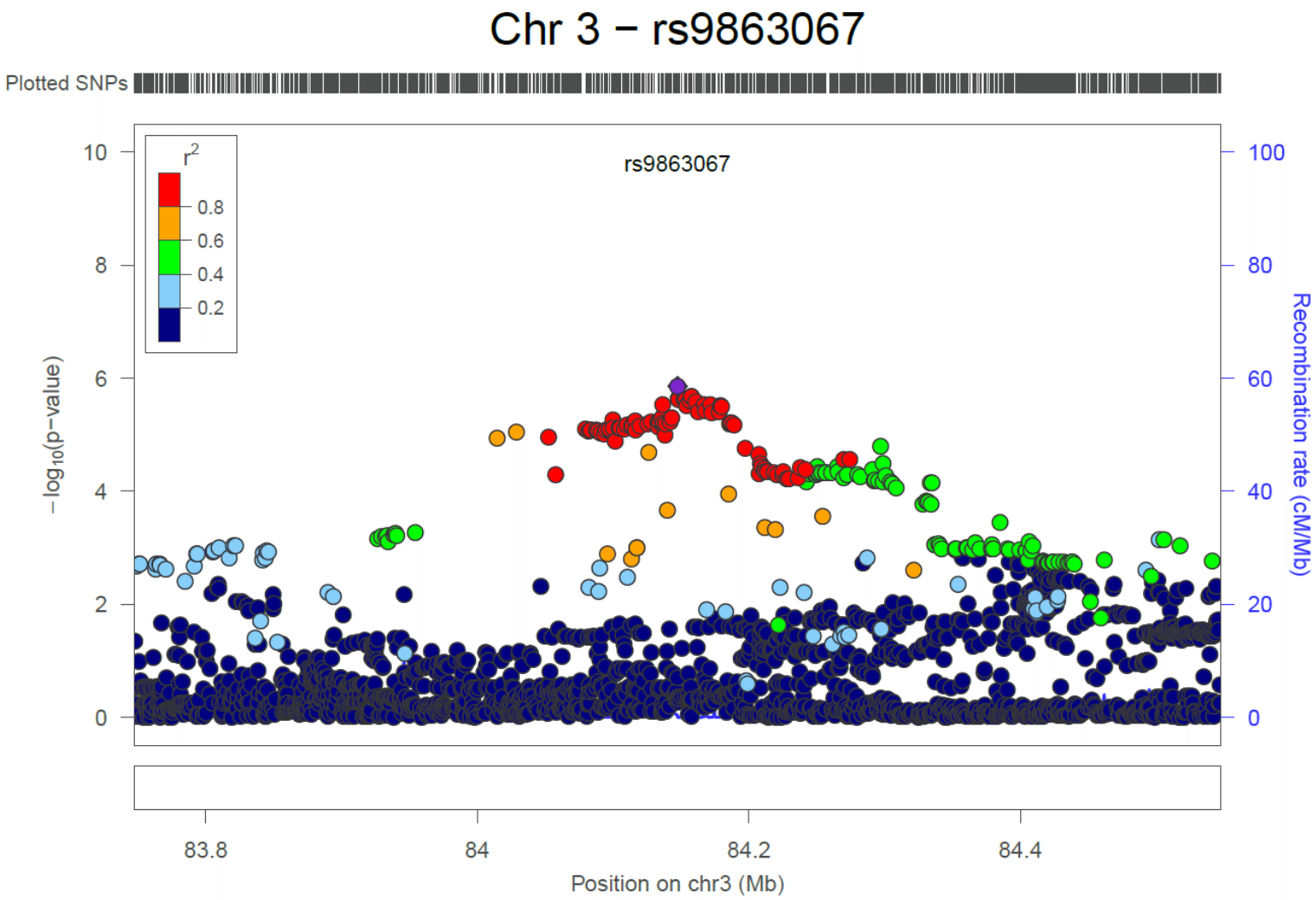


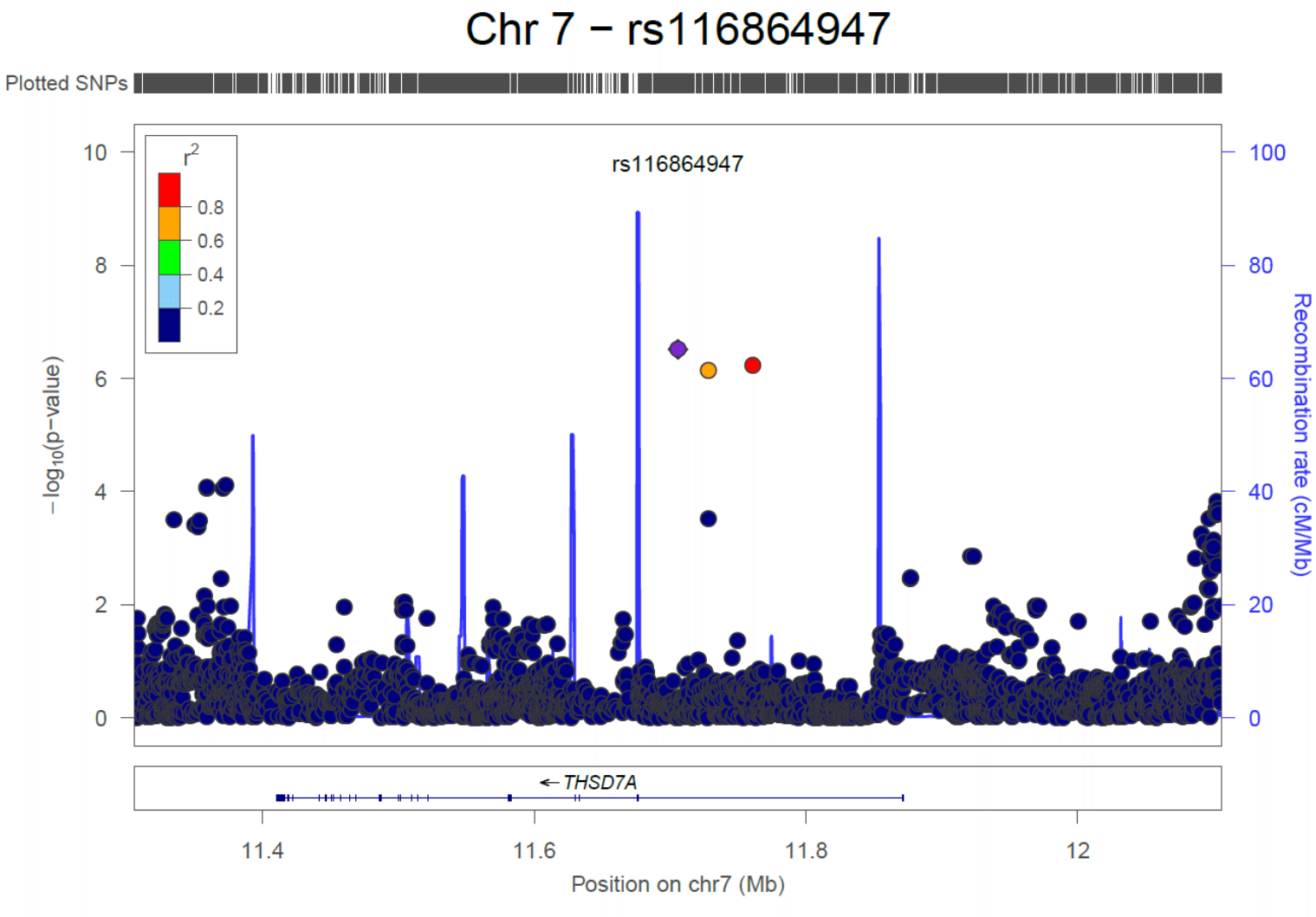

Chr 1 – rs2662776
Plotted SNPs
rs2662776
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HSD17B7
RGS4
RGS5
C1orf110
NUF2
162.8
163
163.2
163.4
Position on chr1 (Mb)


Chr 3 – rs76153987
Plotted SNPs
rs76153987
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
RAD18
SRGAP3
THUMPD3
LHFPL4
SETD5−AS1
SETD5
Position on chr3 (Mb)

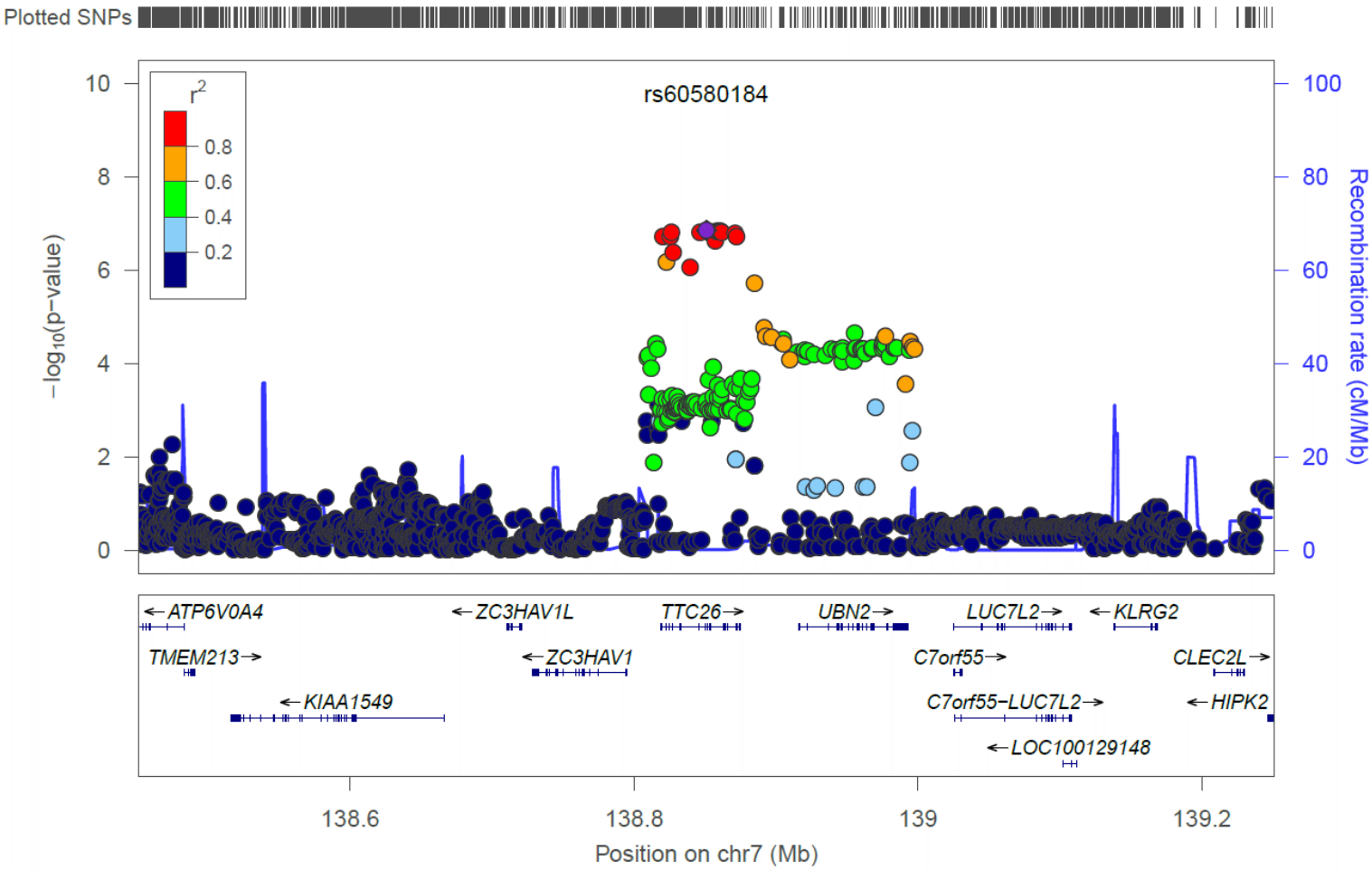
Chr 3 – rs79019069

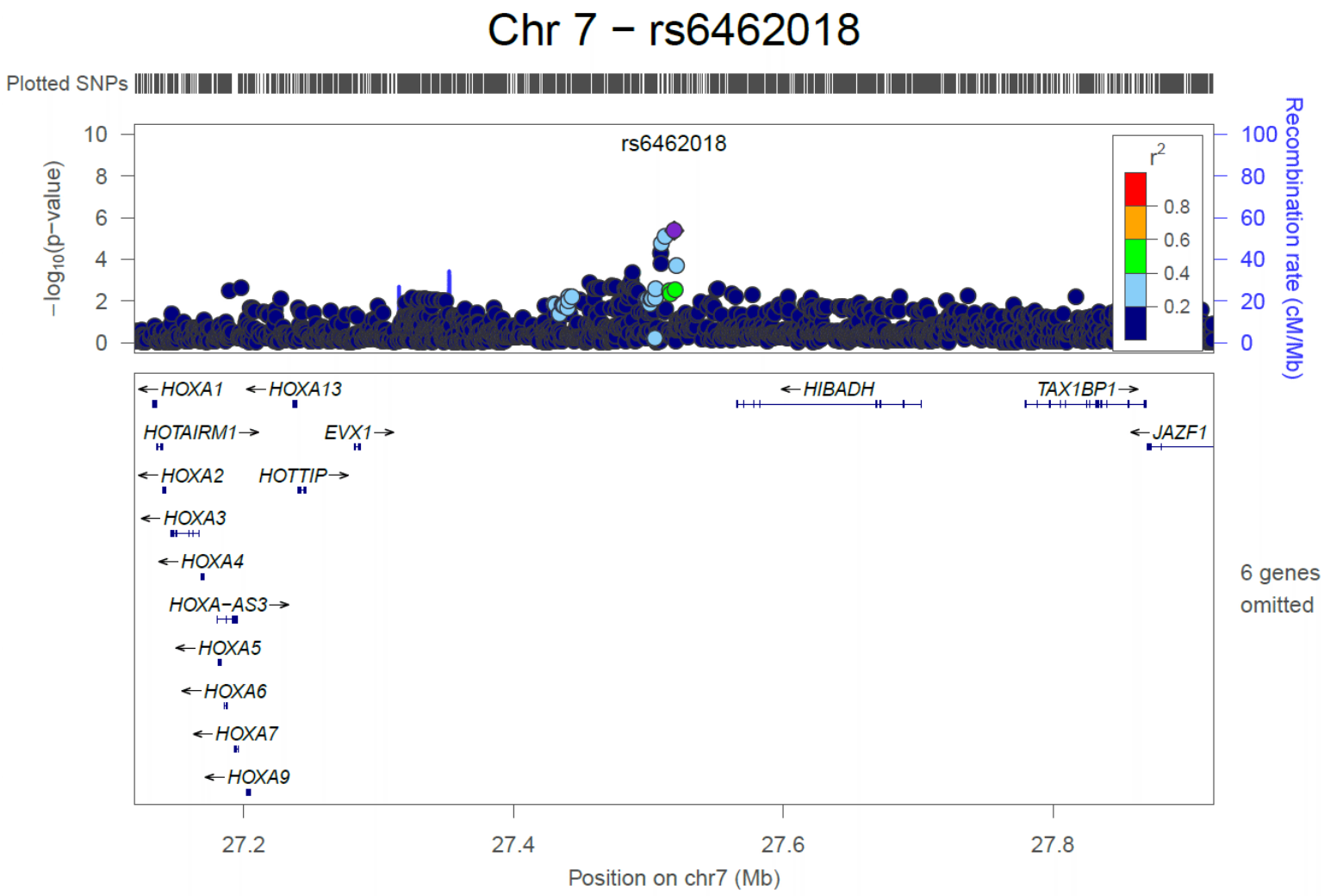


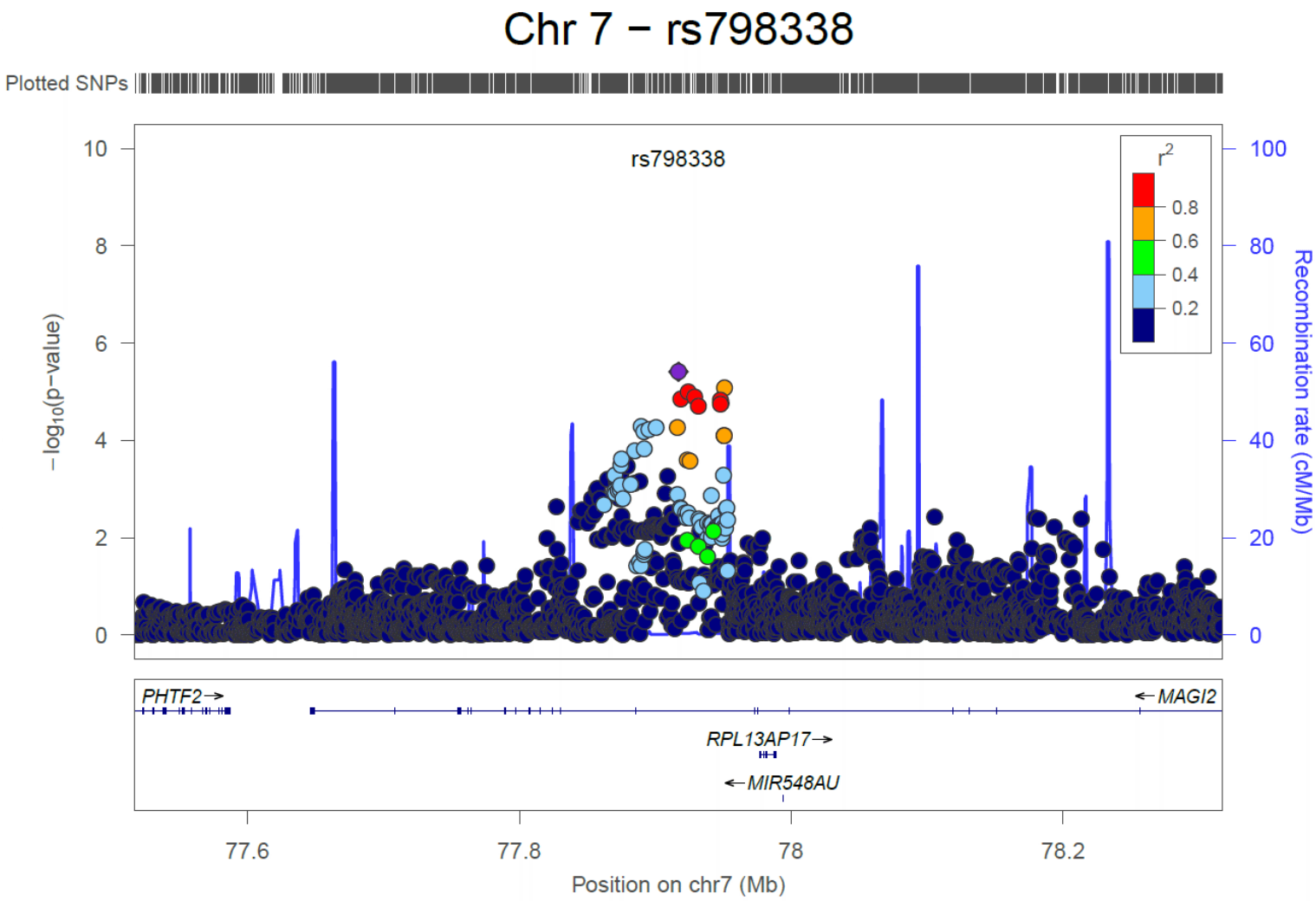

Chr 3 – rs9863067
Plotted SNPs
rs9863067
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Position on chr3 (Mb)
83.8
84
84.2
84.4
0
2
4
6
8
10
0
20
40
60
80
100

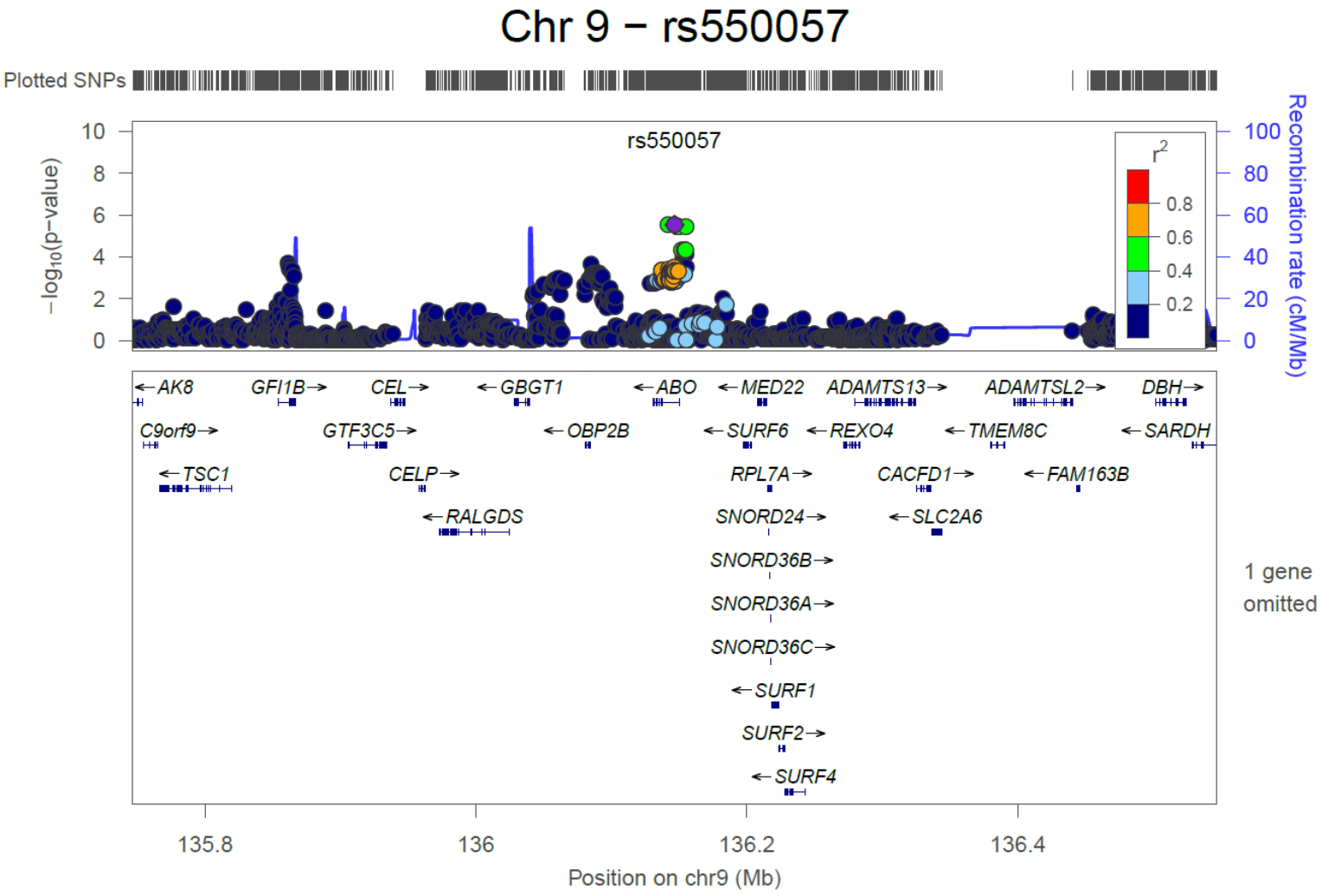

Chr 7 − rs116864947
Plotted SNPs
rs116864947
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
THSD7A
Position on chr7 (Mb)
11.4
11.6
11.8
12

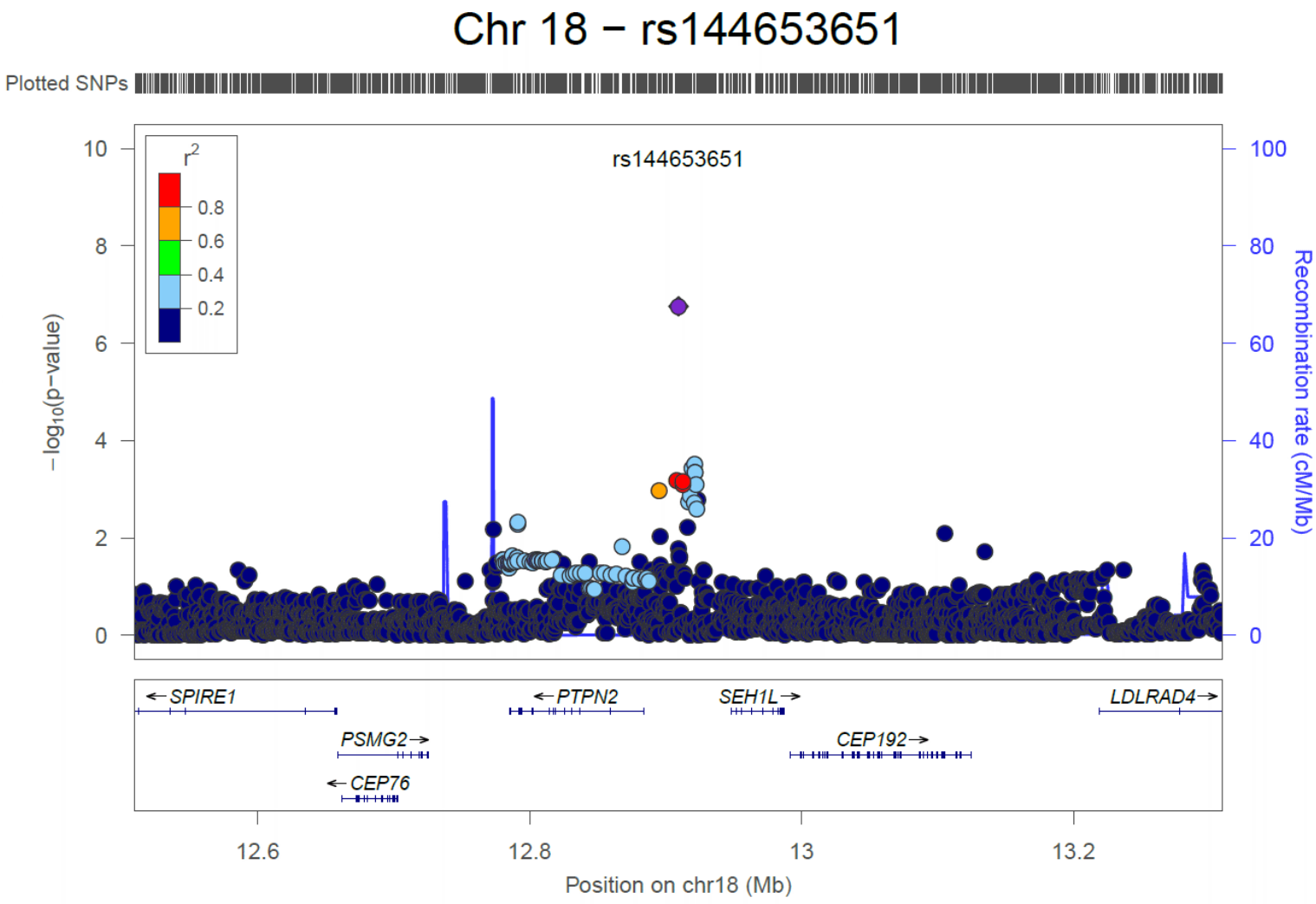
Chr 7 – rs60580184

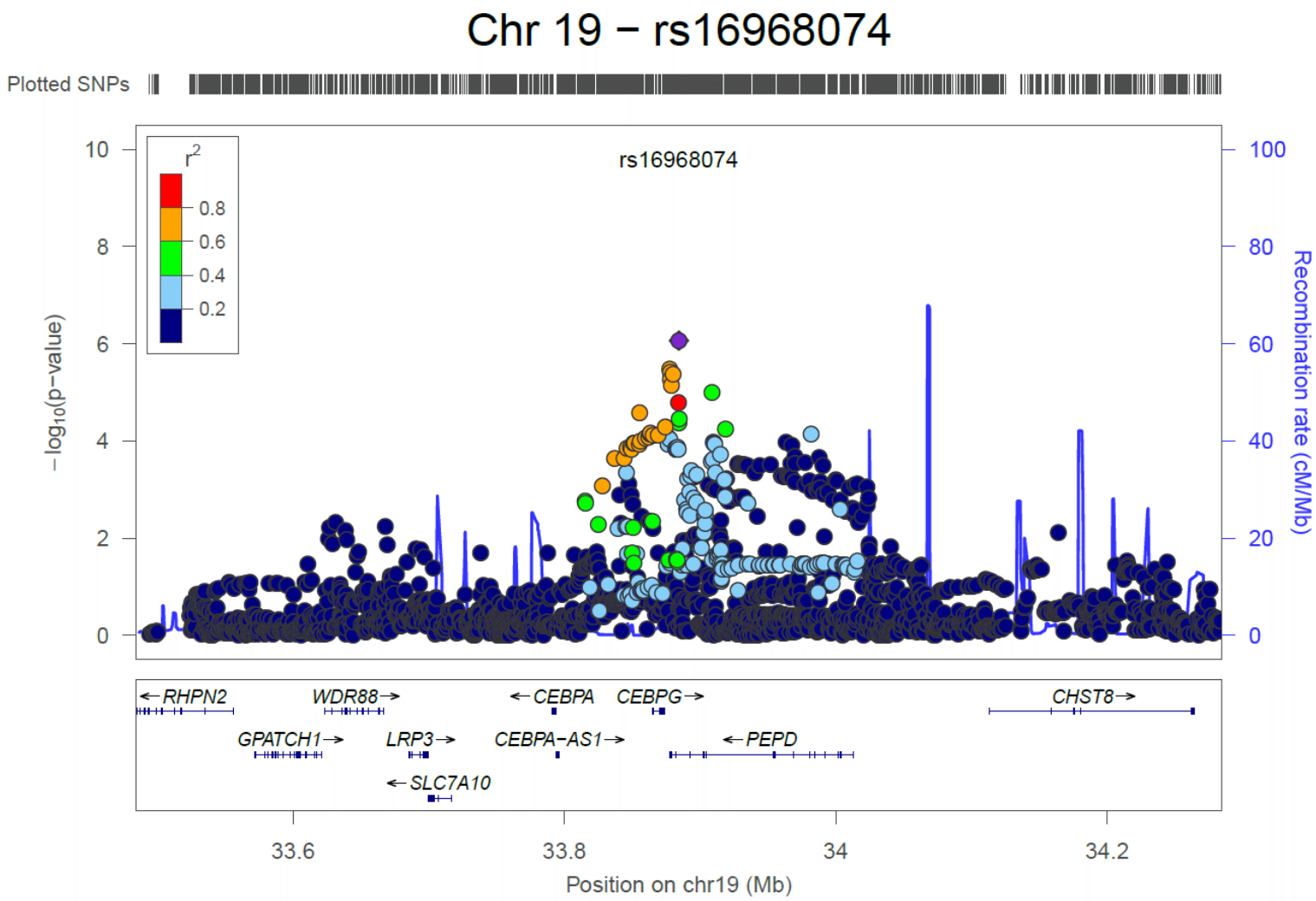



Chr 7 − rs6462018
Plotted SNPs
rs6462018
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HOXA1
HOXA13
HIBADH
TAX1BP1
HOTAIRM1
EVX1
JAZF1
HOXA2
HOTTIP
HOXA3
HOXA4
HOXA−AS3
HOXA5
HOXA6
HOXA7
HOXA9
6 genes omitted
Position on chr7 (Mb)


Chr 7 – rs798338
Plotted SNPs
rs798338
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
PHTF2
MAGI2
RPL13AP17
MIR548AU
77.6
77.8
78
78.2
Position on chr7 (Mb)


Chr 9 – rs550057
Plotted SNPs
rs550057
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
AK8
GFI1B
CEL
GBGT1
ABO
MED22
ADAMTS13
ADAMTSL2
DBH
C9orf9
GTF3C5
OBP2B
SURF6
REXO4
TMEM8C
SARDH
TSC1
CELP
RPL7A
CACFD1
FAM163B
RALGDS
SNORD24
SLC2A6
SNORD36B
SNORD36A
SNORD36C
SURF1
SURF2
SURF4
1 gene omitted
135.8
136
136.2
136.4
Position on chr9 (Mb)


Chr 18 − rs144653651
Plotted SNPs
rs144653651
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SPIRE1
PTPN2
SEH1L
LDLRAD4
PSMG2
CEP192
CEP76
12.6
12.8
13
13.2
Position on chr18 (Mb)


Chr 19 − rs16968074
Plotted SNPs
rs16968074
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
RHPN2
WDR88
CEBPA
CEBPG
CHST8
GPATCH1
LRP3
CEBPA−AS1
PEPD
SLC7A10
33.6
33.8
34
34.2
Position on chr19 (Mb)

Supplementary Figure 3. Conditional analysis. Chromosome 9 *BSPRY-ALAD* region, results adjusted for effect of rs1805313; meta-analysis of ALSPAC and QIMR data.