

Meta-analysis of Northern European populations replicates rs992157
(chromosome 2q35) as a colorectal cancer risk factor

Supplementary Material

The FIN genome-wide association study (stage 1)

Supplementary Table 1: Stage 1 results for the 29 variants that were followed up based on P-value.

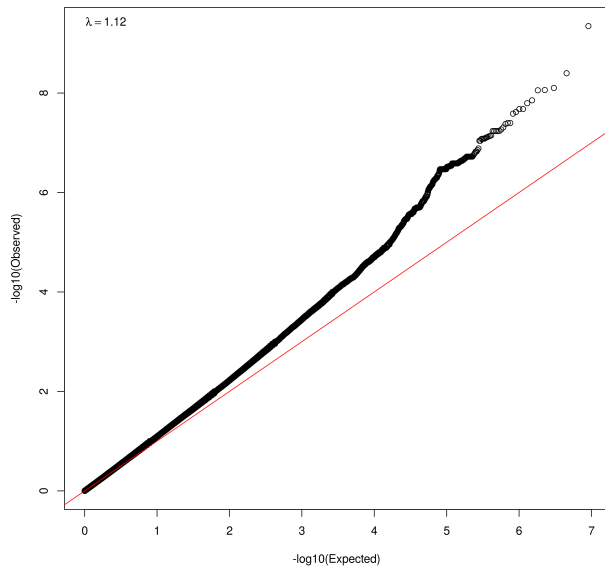
Chr.	SNP	A1	A0	A1F	INFO	r2	Beta [95% CI] LMM	P LMM
12	rs73121704	C	G	0.00860	0.927	0.940	0.109 [0.0729, 0.146]	4.07e-09
8	rs10505477	G	A	0.496	0.983	0.986	-0.0188 [-0.0255, -0.0120]	5.29e-08
12	rs73121712	C	T	0.00784	0.901	0.874	0.104 [0.0658, 0.142]	8.94e-08
18	rs182653205	T	C	0.00469	0.908	0.866	0.130 [0.0819, 0.178]	1.28e-07
5	rs150509351	T	G	0.00475	0.980	0.996	0.126 [0.0784, 0.174]	2.27e-07
18	rs148943137	A	G	0.00467	0.939	0.978	0.126 [0.0780, 0.175]	2.96e-07
12	rs117830766	A	G	0.0110	0.984	0.998	0.0838 [0.0517, 0.116]	3.14e-07
3	rs73808275	A	G	0.00891	0.948	0.903	0.0921 [0.0565, 0.128]	4.15e-07
11	rs6589219	C	G	0.764	0.984	0.987	-0.0206 [-0.0286, -0.0126]	4.34e-07
8	rs138822575	G	C	0.0283	0.941	0.943	0.0520 [0.0315, 0.0725]	6.83e-07
11	rs186867472	A	G	0.0194	0.980	0.974	0.0614 [0.0370, 0.0857]	7.95e-07
3	rs112195740	A	G	0.00759	0.929	0.985	0.0965 [0.0579, 0.135]	9.34e-07
13	rs1591602	A	G	0.479	0.999	0.996	-0.0167 [-0.0235, -0.00998]	1.17e-06
8	rs6983267	T	G	0.470	0.987	0.994	-0.0166 [-0.0234, -0.00988]	1.38e-06
8	rs111480438	A	G	0.00543	0.891	0.975	0.112 [0.0659, 0.157]	1.68e-06
8	rs113057722	C	T	0.00545	0.902	0.975	0.110 [0.0642, 0.155]	2.31e-06
14	rs117770018	A	T	0.00478	0.907	0.890	0.120 [0.0702, 0.170]	2.37e-06
14	rs185803491	T	C	0.00481	0.892	0.908	0.119 [0.0691, 0.169]	2.85e-06
11	rs7126252	A	G	0.495	0.999	0.998	0.0161 [0.00932, 0.0228]	3.03e-06
13	rs78818202	C	G	0.00807	0.912	0.875	0.0913 [0.0529, 0.130]	3.11e-06
16	rs113119427	T	C	0.0231	0.895	0.934	0.0534 [0.0309, 0.0758]	3.16e-06
16	rs111412012	C	T	0.0230	0.901	0.951	0.0518 [0.0293, 0.0743]	6.42e-06
19	rs10412919	C	T	0.0741	0.999	0.999	0.0298 [0.0169, 0.0427]	6.44e-06
19	rs10417622	C	T	0.0741	0.998	0.994	0.0298 [0.0169, 0.0427]	6.44e-06
6	rs118178707	G	A	0.0234	0.958	0.929	0.0504 [0.0280, 0.0727]	9.76e-06
18	rs11872923	T	C	0.170	0.970	0.989	0.0197 [0.0107, 0.0287]	1.85e-05
18	rs4798327	G	A	0.331	0.997	0.998	0.0155 [0.00830, 0.0227]	2.47e-05
6	6:73457627[b37]	C	G	0.0170	0.901	0.816	0.0555 [0.0296, 0.0814]	2.63e-05
4	rs1714100	A	T	0.600	0.998	0.999	-0.0147 [-0.0215, -0.00778]	2.96e-05

Abbreviations: *Chr.*, chromosome; *SNP*, single-nucleotide polymorphism; *A1*, allele 1 (alternative allele); *A0*, allele 0 (reference allele); *A1F*, frequency of allele 1; *INFO*, IMPUTE2 info score; *r2*, squared Pearson correlation coefficient between IMPUTE2 genotype dosage and MassARRAY genotype; *Beta*, estimated regression coefficient for A1; *CI*, confidence interval; *LMM*, linear mixed model; *P*, P-value; *b37*, Genome Reference Consortium human genome build 37.

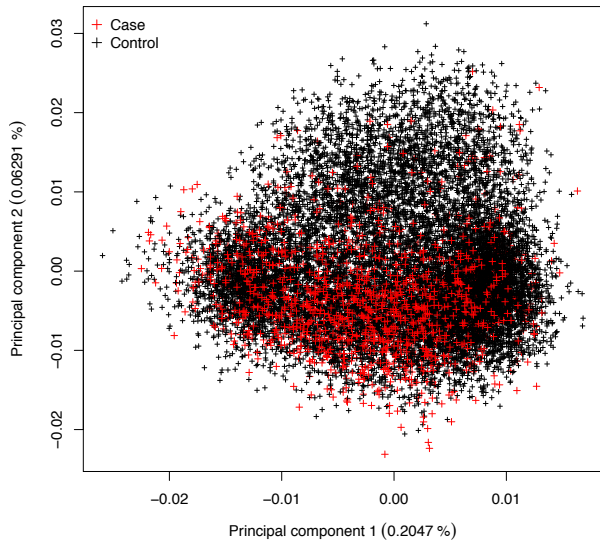
Supplementary Table 2: Stage 1 results for 38 published CRC risk SNPs.

Chr.	SNP	A1	A0	A1F	INFO	Beta [95% CI] LMM	P LMM	PMID
11	rs3802842	A	C	0.769	0.990	-0.0200 [-0.0280, -0.0119]	1.12e-06	18372901
8	rs6983267	T	G	0.470	0.987	-0.0166 [-0.0234, -0.00988]	1.38e-06	17618284
8	rs7014346	G	A	0.653	0.994	-0.0174 [-0.0245, -0.0104]	1.40e-06	18372901
20	rs961253	A	C	0.303	0.979	0.0168 [0.00947, 0.0242]	7.28e-06	19011631
15	rs4779584	C	T	0.719	0.998	-0.0144 [-0.0219, -0.00689]	1.69e-04	18372905
10	rs704017	G	A	0.683	0.951	0.0132 [0.00606, 0.0204]	3.02e-04	24836286
18	rs4939827	C	T	0.534	0.995	-0.0110 [-0.0178, -0.00421]	1.53e-03	17934461
2	rs992157	A	G	0.682	0.998	0.0116 [0.00435, 0.0188]	1.68e-03	27005424
8	rs16892766	C	A	0.119	0.992	0.0160 [0.00554, 0.0264]	2.68e-03	18372905
14	rs4444235	C	T	0.422	0.988	0.00951 [0.00267, 0.0163]	6.45e-03	19011631
6	rs1321311	A	C	0.190	0.959	0.0119 [0.00330, 0.0205]	6.69e-03	22634755
20	rs4925386	C	T	0.683	0.991	0.00899 [0.00169, 0.0163]	1.58e-02	20972440
10	rs1035209	T	C	0.159	0.993	0.0111 [0.00188, 0.0204]	1.83e-02	24737748
11	rs3824999	G	T	0.493	0.998	0.00786 [0.00112, 0.0146]	2.22e-02	22634755
3	rs35360328	A	T	0.198	0.954	0.00849 [0.00000176, 0.0170]	5.00e-02	26151821
10	rs11190164	G	A	0.266	0.981	0.00728 [-0.000356, 0.0149]	6.17e-02	26151821
14	rs1957636	C	T	0.573	0.995	-0.00649 [-0.0134, 0.000401]	6.49e-02	21655089
16	rs9929218	A	G	0.246	0.996	-0.00611 [-0.0140, 0.00175]	1.28e-01	19011631
10	rs10795668	A	G	0.296	0.998	-0.00555 [-0.0129, 0.00184]	1.41e-01	18372905
20	rs4813802	G	T	0.343	0.987	0.00516 [-0.00193, 0.0123]	1.54e-01	21655089
3	rs10936599	T	C	0.268	0.999	-0.00532 [-0.0129, 0.00231]	1.72e-01	20972440
12	rs3217810	T	C	0.139	0.825	0.00668 [-0.00302, 0.0164]	1.77e-01	23266556
1	rs6691170	T	G	0.377	0.992	0.00459 [-0.00239, 0.0116]	1.97e-01	20972440
20	rs6066825	G	A	0.259	0.971	-0.00469 [-0.0124, 0.00302]	2.33e-01	26151821
1	rs72647484	C	T	0.0901	0.982	-0.00715 [-0.0189, 0.00465]	2.35e-01	25990418
12	rs11169552	T	C	0.360	0.998	-0.00354 [-0.0105, 0.00346]	3.21e-01	20972440
4	rs35509282	A	T	0.156	0.991	0.00465 [-0.00465, 0.0140]	3.27e-01	25023989
19	rs10411210	T	C	0.142	0.998	-0.00484 [-0.0146, 0.00496]	3.33e-01	19011631
1	rs10911251	C	A	0.494	0.997	-0.00305 [-0.00976, 0.00367]	3.74e-01	23266556
10	rs12241008	C	T	0.111	0.986	0.00478 [-0.00612, 0.0157]	3.90e-01	25105248
5	rs647161	A	C	0.696	0.977	-0.00308 [-0.0104, 0.00428]	4.12e-01	25990418
12	rs12309274	G	T	0.104	0.927	0.00454 [-0.00656, 0.0156]	4.23e-01	25990418
11	rs174550	C	T	0.416	0.999	-0.00281 [-0.00970, 0.00407]	4.23e-01	25990418
19	rs1800469	G	A	0.749	0.996	0.00310 [-0.00469, 0.0109]	4.35e-01	25990418
12	rs73208120	G	T	0.0818	0.964	-0.00486 [-0.0172, 0.00751]	4.41e-01	26151821
12	rs3184504	C	T	0.597	0.865	0.00151 [-0.00538, 0.00841]	6.67e-01	26151821
16	rs16941835	C	G	0.218	0.992	0.00151 [-0.00674, 0.00977]	7.19e-01	25990418
3	rs812481	G	C	0.615	0.978	0.000500 [-0.00645, 0.00745]	8.88e-01	26151821

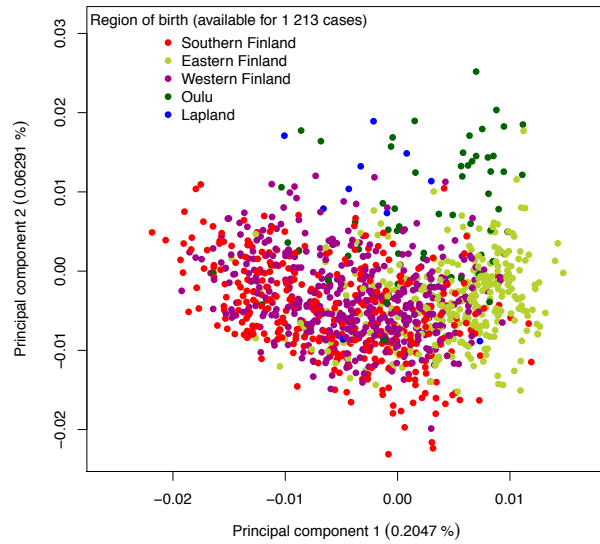
Abbreviations: *Chr.*, chromosome; *SNP*, single-nucleotide polymorphism; *A1*, allele 1 (alternative allele); *A0*, allele 0 (reference allele); *A1F*, frequency of allele 1; *INFO*, IMPUTE2 info score; *Beta*, estimated regression coefficient for A1; *CI*, confidence interval; *LMM*, linear mixed model; *P*, P-value; *PMID*, PubMed identifier.



Supplementary Figure 1: Uniform quantile-quantile plot of uncorrected stage 1 P-values based on a linear mixed model.

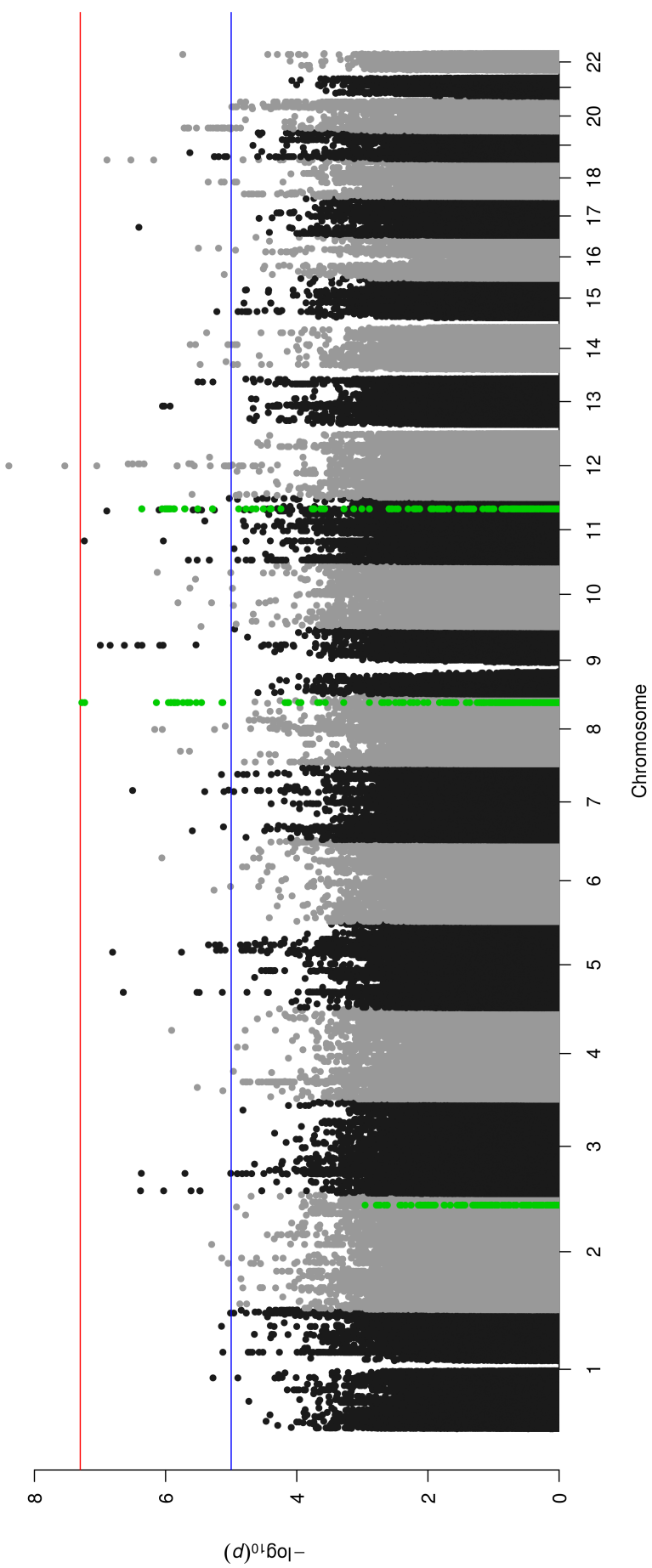


Supplementary Figure 2



Supplementary Figure 3

Supplementary Figures 2 and 3: Principal component analysis of the FIN dataset (1 701 cases and 14 082 controls).



Supplementary Figure 4: Manhattan plot of stage 1 P-values (genomic control applied). Loci that were genome-wide significant in combined analysis are shown in green.

Meta-analysis of 12 European-ancestry studies

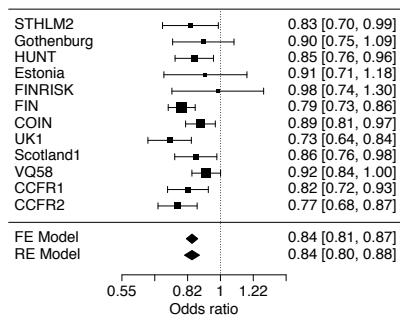
Supplementary Table 3: Results of meta-analysis of 12 European-ancestry studies.

Chr.	SNP	A1	A0	OR [95% CI] RE	P RE	OR [95% CI] FE	P FE	Phet	I2 (%)
8	rs10505477	G	A	0.841 [0.804, 0.880]	7.63e-14	0.841 [0.812, 0.871]	2.58e-22	1.4e-01	34
8	rs6983267	T	G	0.843 [0.805, 0.883]	7.45e-13	0.844 [0.815, 0.874]	1.63e-21	9.8e-02	38
2	rs992157	A	G	1.12 [1.08, 1.16]	1.50e-09	1.12 [1.08, 1.16]	1.50e-09	7.8e-01	0
11	rs6589219	C	G	0.892 [0.848, 0.938]	9.14e-06	0.889 [0.856, 0.924]	1.53e-09	1.5e-01	37
6	6:73457627[b37]	C	G	1.89 [1.39, 2.57]	4.80e-05	1.89 [1.39, 2.57]	4.80e-05	NA	NA
13	rs78818202	C	G	1.22 [0.924, 1.61]	1.61e-01	1.18 [1.01, 1.37]	3.55e-02	8.6e-03	64
8	rs138822575	G	C	1.18 [0.927, 1.49]	1.81e-01	1.28 [1.10, 1.48]	1.01e-03	5.9e-03	52
18	rs148943137	A	G	1.25 [0.890, 1.75]	1.99e-01	1.34 [1.07, 1.68]	1.04e-02	2.7e-02	53
18	rs182653205	T	C	1.23 [0.884, 1.70]	2.21e-01	1.32 [1.07, 1.62]	9.05e-03	1.3e-02	56
18	rs11872923	T	C	1.04 [0.975, 1.11]	2.42e-01	1.05 [1.00, 1.10]	3.87e-02	1.5e-01	38
5	rs150509351	T	G	2.10 [0.585, 7.53]	2.55e-01	2.89 [1.78, 4.69]	1.89e-05	4.0e-02	76
14	rs185803491	T	C	1.20 [0.878, 1.63]	2.58e-01	1.25 [0.991, 1.58]	5.94e-02	1.1e-01	39
14	rs117770018	A	T	1.19 [0.881, 1.60]	2.61e-01	1.23 [0.974, 1.55]	8.21e-02	1.6e-01	35
12	rs73121712	C	T	1.15 [0.900, 1.47]	2.62e-01	1.17 [1.01, 1.36]	3.76e-02	3.1e-03	61
18	rs4798327	G	A	1.02 [0.971, 1.07]	4.19e-01	1.03 [0.992, 1.07]	1.22e-01	2.0e-01	34
12	rs73121704	C	G	1.10 [0.854, 1.41]	4.66e-01	1.12 [0.971, 1.28]	1.22e-01	5.1e-04	67
6	rs118178707	G	A	1.12 [0.806, 1.56]	4.97e-01	1.32 [1.08, 1.60]	6.55e-03	6.0e-02	47
12	rs117830766	A	G	1.07 [0.857, 1.32]	5.68e-01	1.04 [0.918, 1.18]	5.32e-01	1.1e-03	63
3	rs112195740	A	G	1.07 [0.831, 1.39]	5.88e-01	1.06 [0.931, 1.20]	3.96e-01	5.5e-04	72
3	rs73808275	A	G	1.05 [0.795, 1.40]	7.11e-01	1.04 [0.911, 1.18]	5.74e-01	2.9e-05	76
19	rs10412919	C	T	0.988 [0.893, 1.09]	8.14e-01	1.02 [0.948, 1.09]	6.38e-01	4.1e-02	45
13	rs1591602	A	G	0.993 [0.935, 1.06]	8.29e-01	0.985 [0.951, 1.02]	3.89e-01	3.1e-04	63
19	rs10417622	C	T	0.990 [0.895, 1.10]	8.47e-01	1.02 [0.949, 1.09]	6.08e-01	4.5e-02	45
8	rs113057722	C	T	1.03 [0.733, 1.45]	8.62e-01	1.06 [0.881, 1.29]	5.18e-01	7.9e-04	66
11	rs7126252	A	G	1.00 [0.950, 1.06]	8.75e-01	1.02 [0.990, 1.06]	1.67e-01	5.0e-03	56
16	rs113119427	T	C	0.985 [0.801, 1.21]	8.84e-01	1.01 [0.904, 1.13]	8.30e-01	1.1e-03	65
11	rs186867472	A	G	1.05 [0.540, 2.02]	8.96e-01	1.56 [1.21, 2.01]	5.29e-04	2.3e-03	71
8	rs111480438	A	G	1.02 [0.723, 1.45]	8.99e-01	1.06 [0.873, 1.28]	5.72e-01	6.6e-04	67
16	rs111412012	C	T	1.01 [0.822, 1.24]	9.30e-01	1.03 [0.923, 1.16]	5.67e-01	1.1e-03	64
4	rs1714100	A	T	0.998 [0.940, 1.06]	9.40e-01	0.986 [0.952, 1.02]	4.34e-01	2.1e-03	61

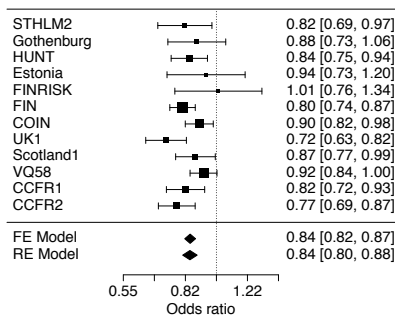
Abbreviations: *Chr.*, chromosome; *SNP*, single-nucleotide polymorphism; *A1*, allele 1 (alternative allele); *A2*, allele 0 (reference allele); *OR*, odds ratio ; *CI*, confidence interval; *RE*, random effects model; *P*, P-value; *FE*, fixed effects model; *Phet*, P-value for Cochran's Q statistic; *I2*, variance attributable to study heterogeneity under the random-effects model; *b37*, Genome Reference Consortium human genome build 37.

Forest plots for the 30 SNPs included in meta-analysis

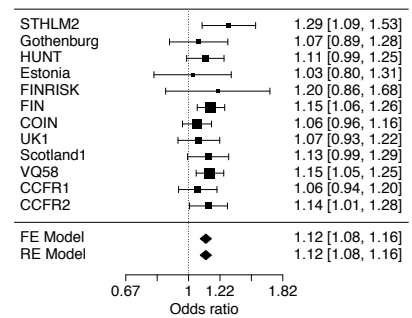
Studies with missing data or less than ten minor alleles were omitted.



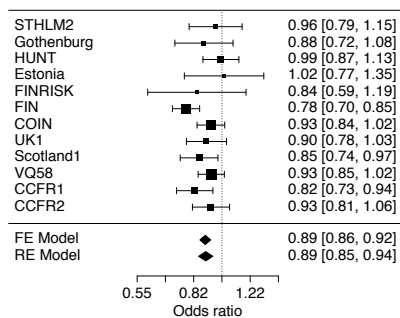
Supplementary Figure 5: Forest plot for rs10505477.



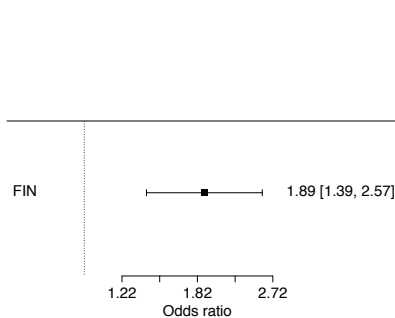
Supplementary Figure 6: Forest plot for rs6983267.



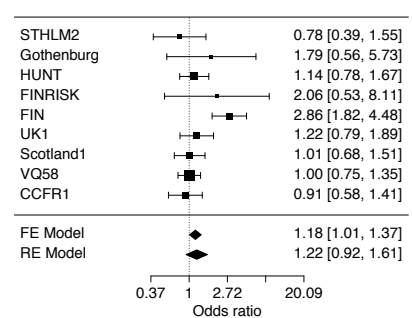
Supplementary Figure 7: Forest plot for rs992157.



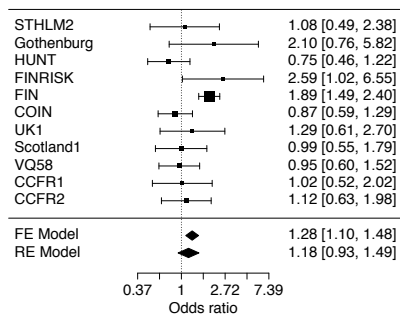
Supplementary Figure 8: Forest plot for rs6589219.



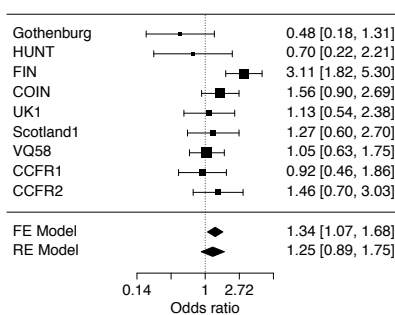
Supplementary Figure 9: Forest plot for 6:73457627[b37].



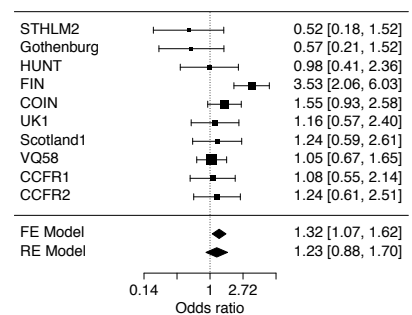
Supplementary Figure 10: Forest plot for rs78818202.



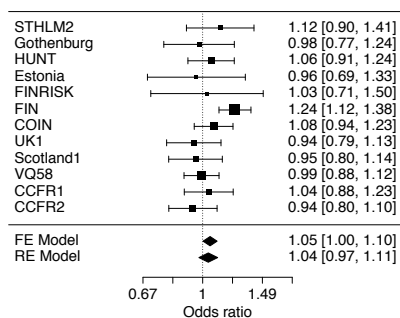
Supplementary Figure 11: Forest plot for rs138822575.



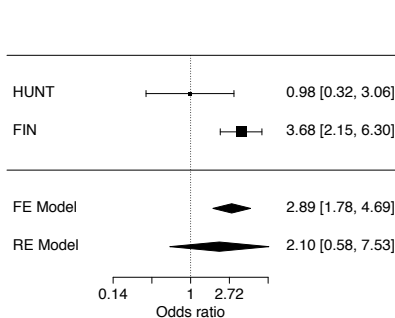
Supplementary Figure 12: Forest plot for rs148943137.



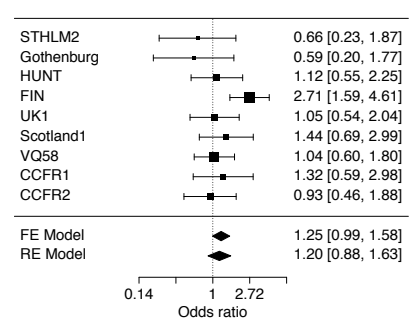
Supplementary Figure 13: Forest plot for rs182653205.



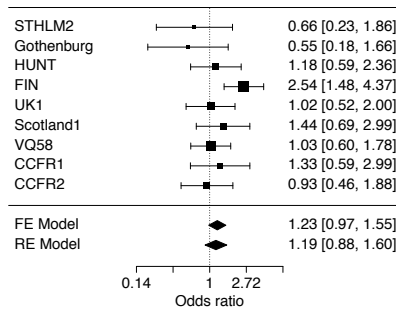
Supplementary Figure 14: Forest plot for rs11872923.



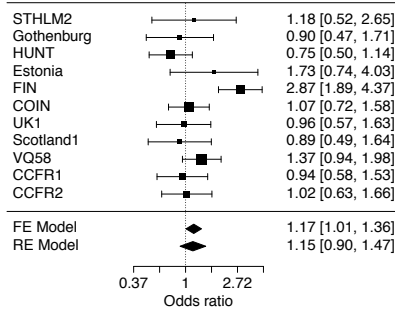
Supplementary Figure 15: Forest plot for rs150509351.



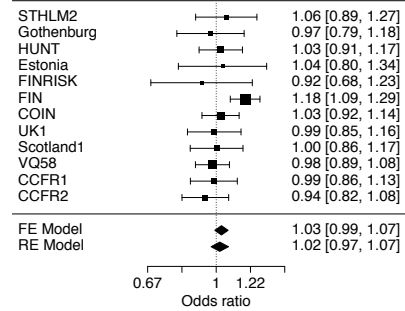
Supplementary Figure 16: Forest plot for rs185803491.



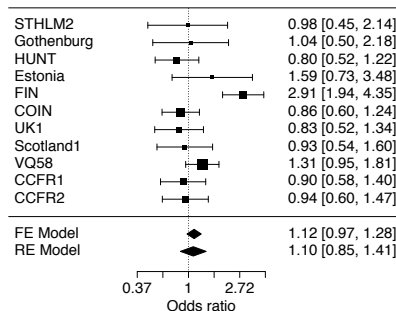
Supplementary Figure 17: Forest plot for rs117770018.



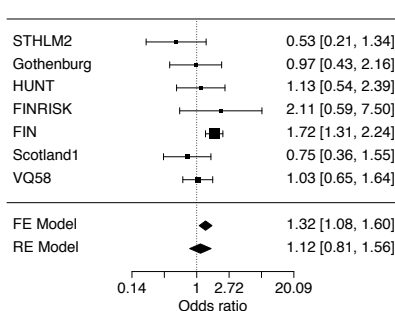
Supplementary Figure 18: Forest plot for rs73121712.



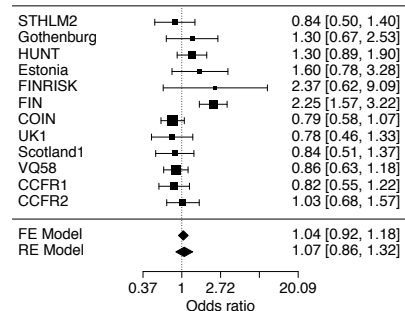
Supplementary Figure 19: Forest plot for rs4798327.



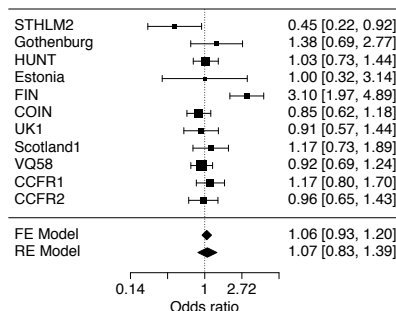
Supplementary Figure 20: Forest plot for rs73121704.



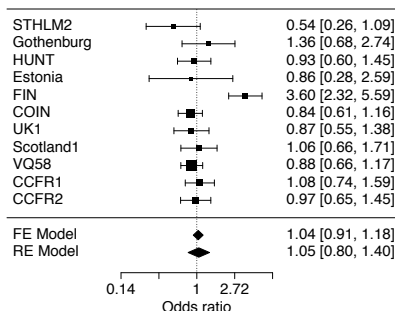
Supplementary Figure 21: Forest plot for rs118178707.



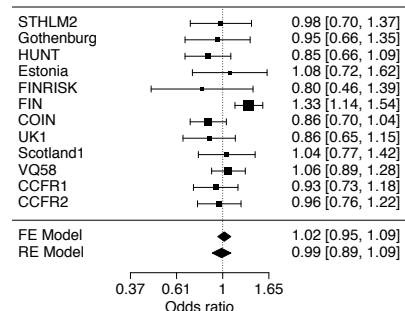
Supplementary Figure 22: Forest plot for rs117830766.



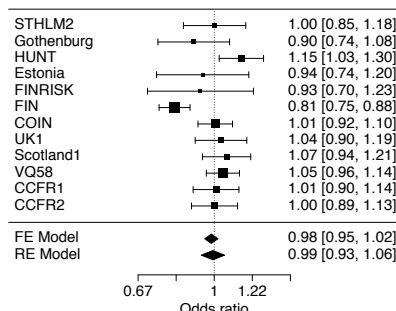
Supplementary Figure 23: Forest plot for rs112195740.



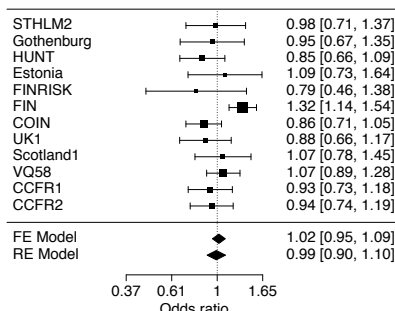
Supplementary Figure 24: Forest plot for rs73808275.



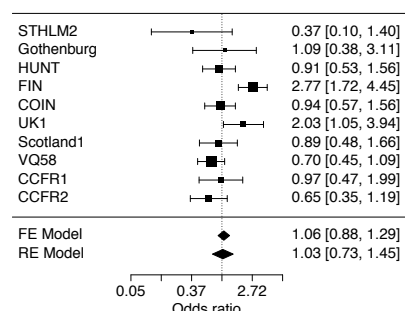
Supplementary Figure 25: Forest plot for rs10412919.



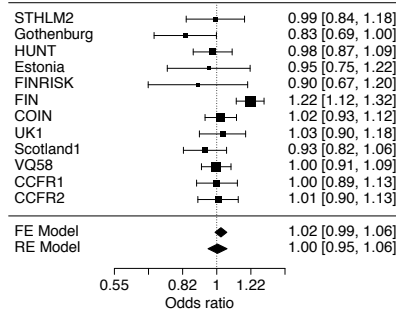
Supplementary Figure 26: Forest plot for rs1591602.



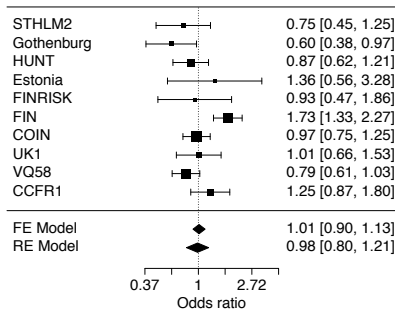
Supplementary Figure 27: Forest plot for rs10417622.



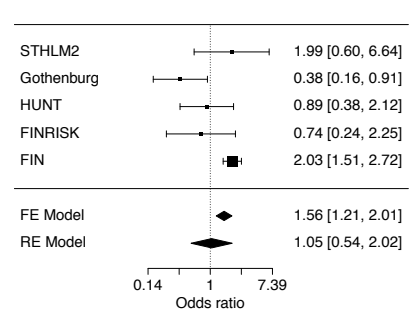
Supplementary Figure 28: Forest plot for rs113057722.



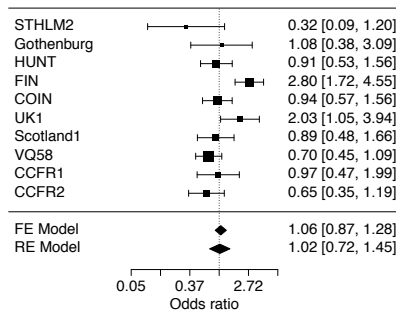
Supplementary Figure 29: Forest plot for rs17126252.



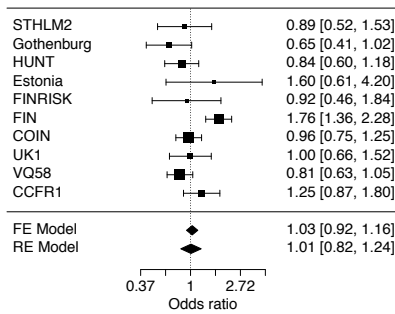
Supplementary Figure 30: Forest plot for rs113119427.



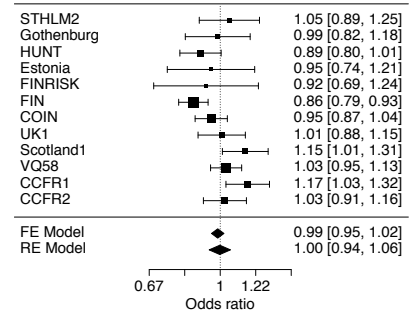
Supplementary Figure 31: Forest plot for rs186867472.



Supplementary Figure 32: Forest plot for rs111480438.



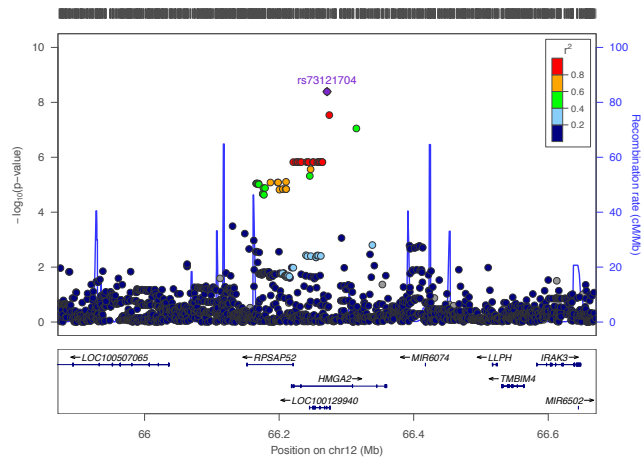
Supplementary Figure 33: Forest plot for rs111412012.



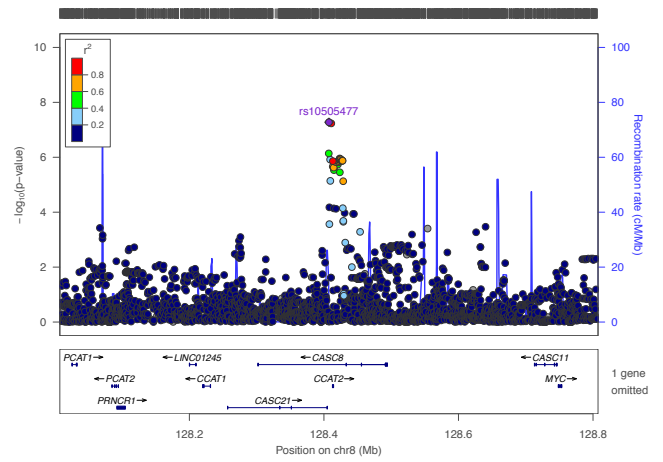
Supplementary Figure 34: Forest plot for rs1714100.

Stage 1 regional association (LocusZoom) plots for the 30 SNPs included in meta-analysis

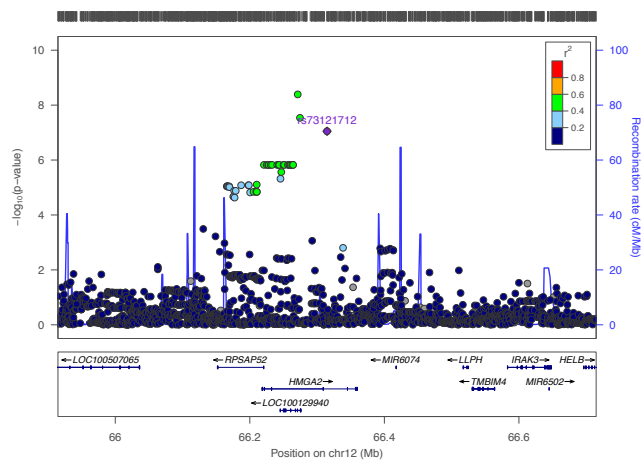
Genomic control was applied.



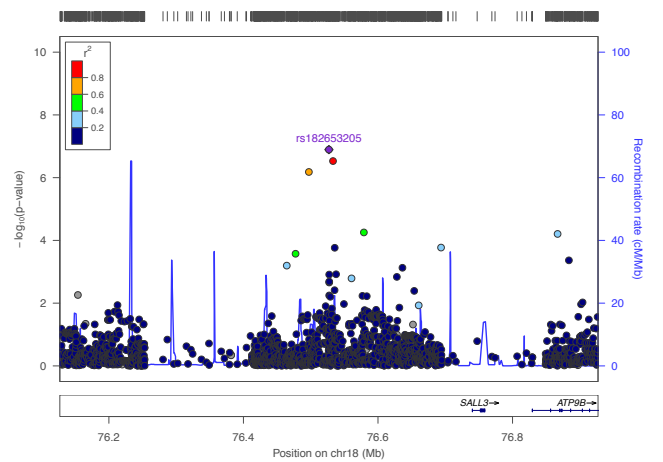
Supplementary Figure 35: LocusZoom plot for rs73121704.



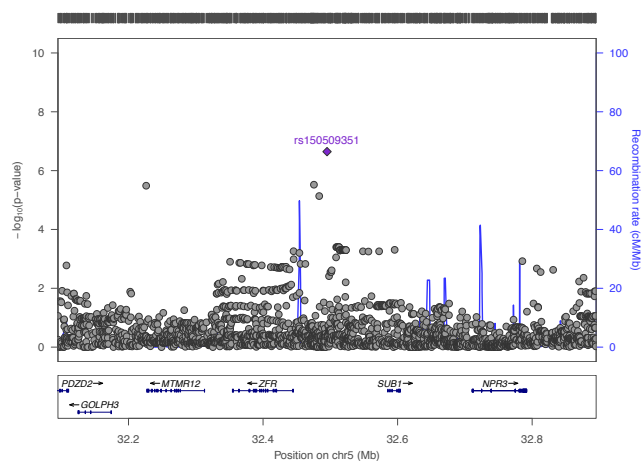
Supplementary Figure 36: LocusZoom plot for rs10505477.



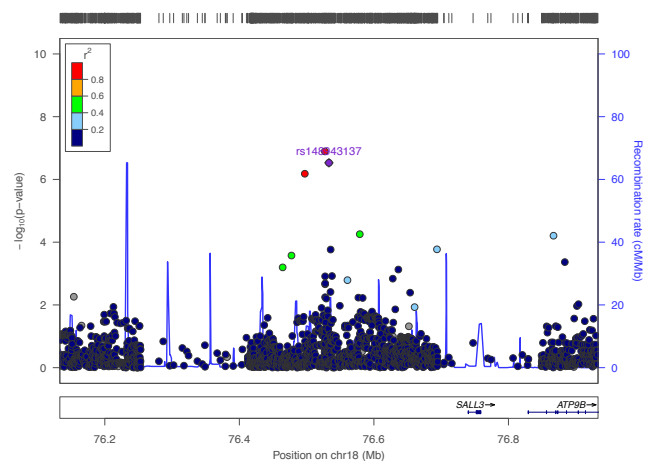
Supplementary Figure 37: LocusZoom plot for rs73121712.



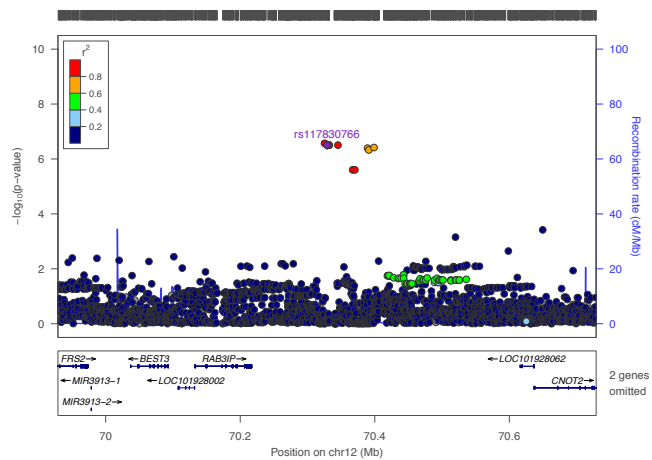
Supplementary Figure 38: LocusZoom plot for rs182653205.



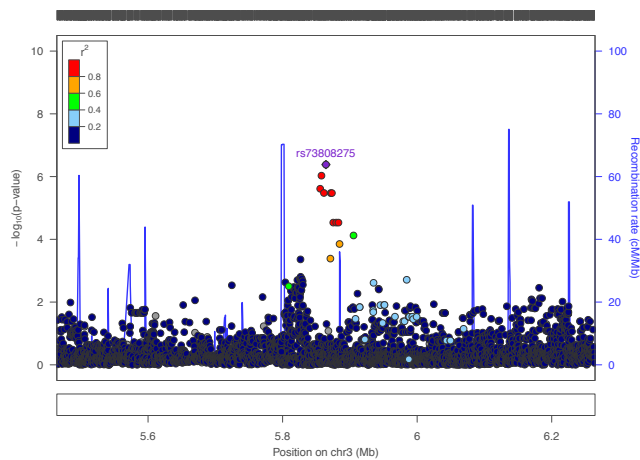
Supplementary Figure 39: LocusZoom plot for rs150509351.



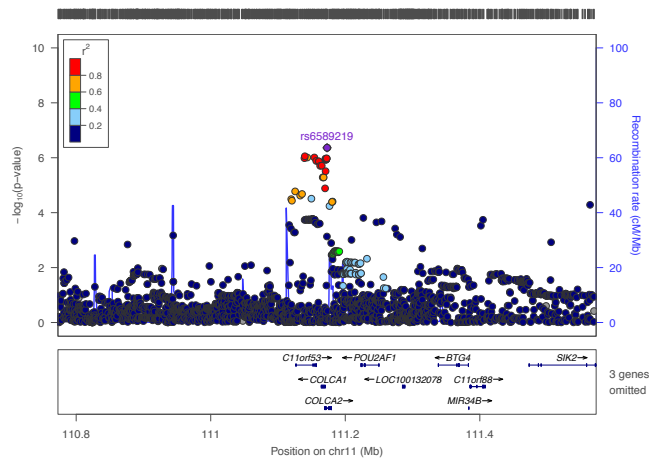
Supplementary Figure 40: LocusZoom plot for rs148943137.



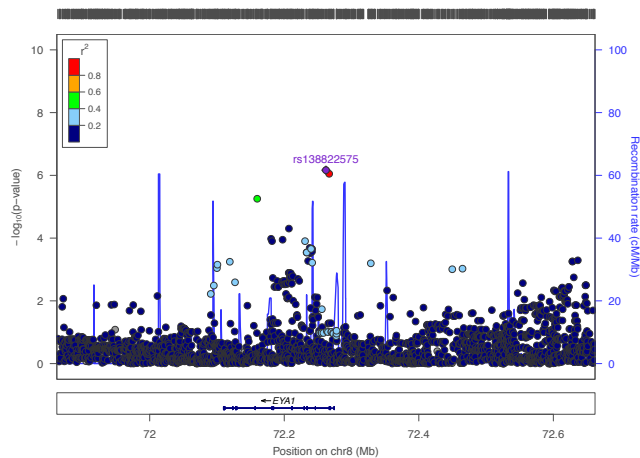
Supplementary Figure 41: LocusZoom plot for rs117830766.



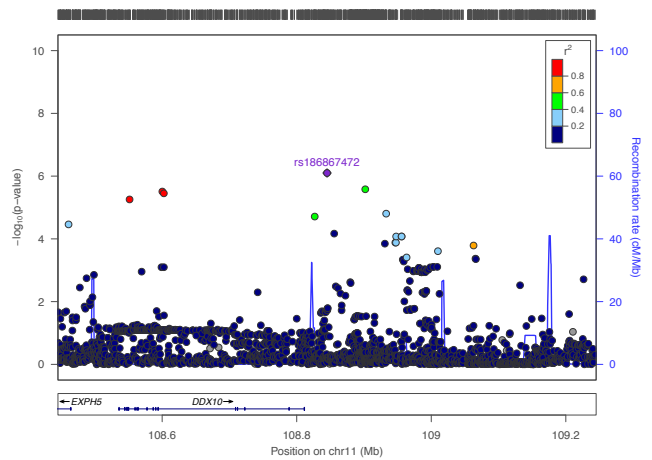
Supplementary Figure 42: LocusZoom plot for rs73808275.



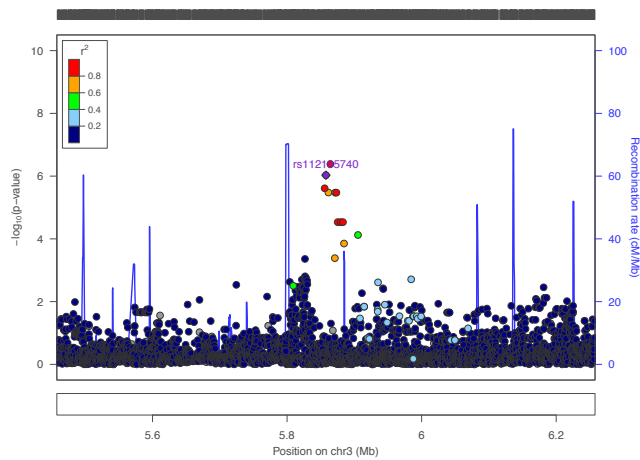
Supplementary Figure 43: LocusZoom plot for rs6589219.



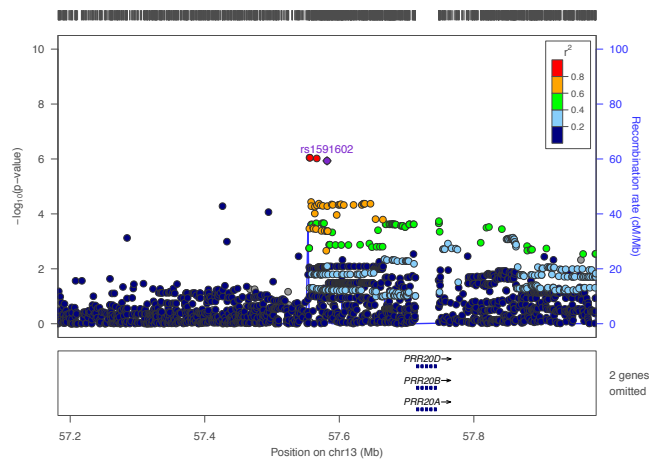
Supplementary Figure 44: LocusZoom plot for rs138822575.



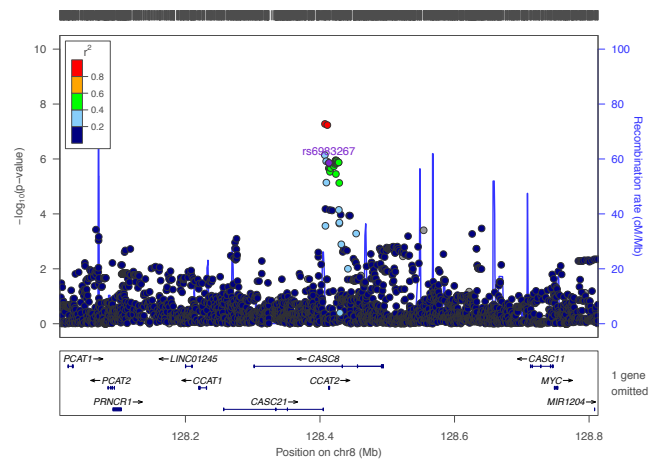
Supplementary Figure 45: LocusZoom plot for rs186867472.



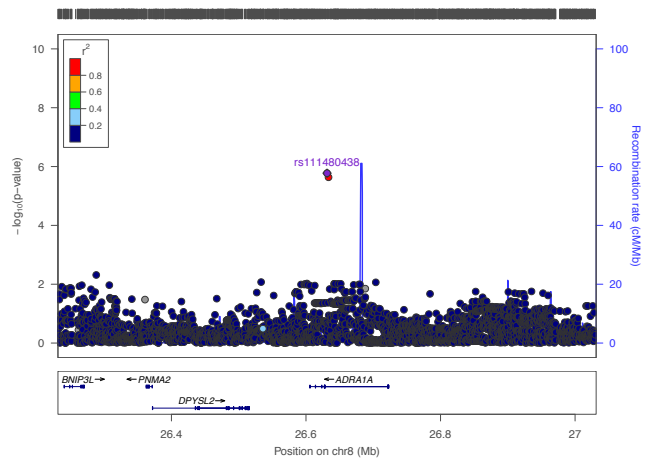
Supplementary Figure 46: LocusZoom plot for rs112195740.



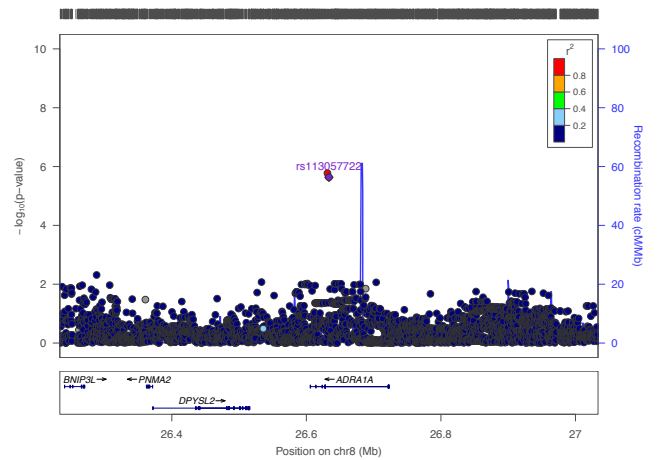
Supplementary Figure 47: LocusZoom plot for rs1591602.



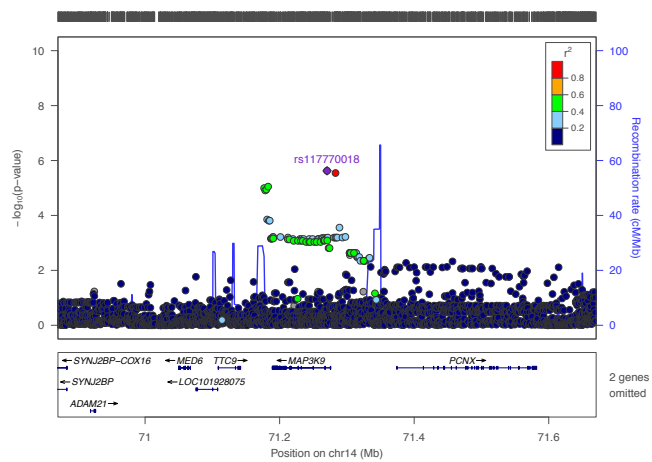
Supplementary Figure 48: LocusZoom plot for rs6983267.



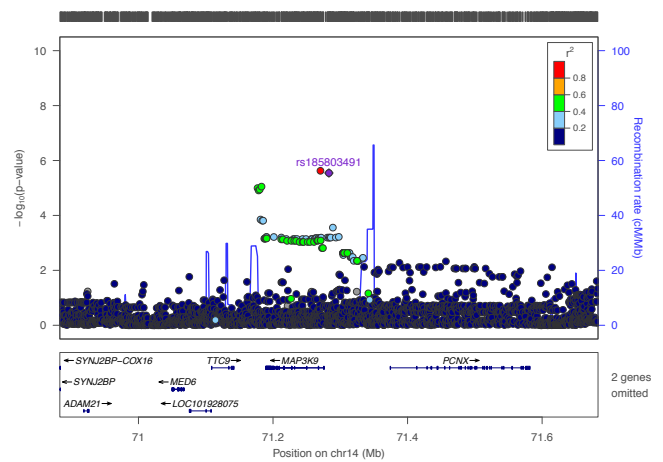
Supplementary Figure 49: LocusZoom plot for rs111480438.



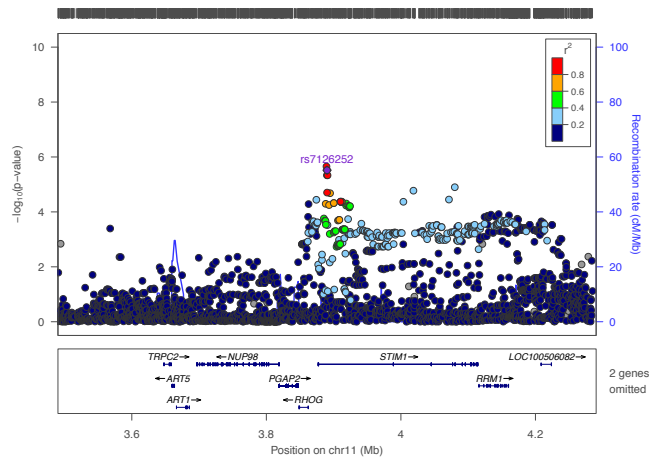
Supplementary Figure 50: LocusZoom plot for rs113057722.



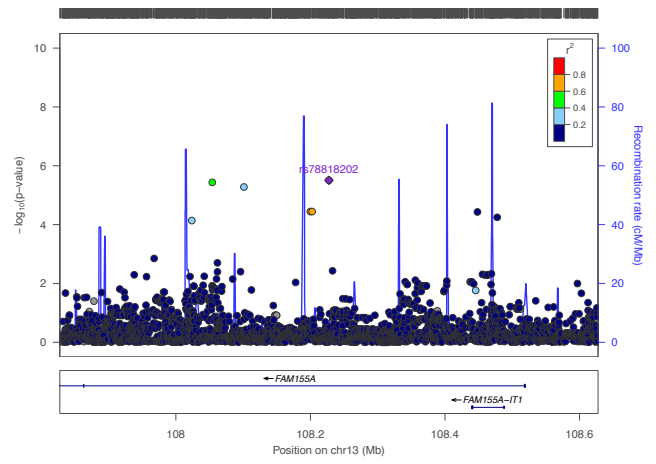
Supplementary Figure 51: LocusZoom plot for rs117770018.



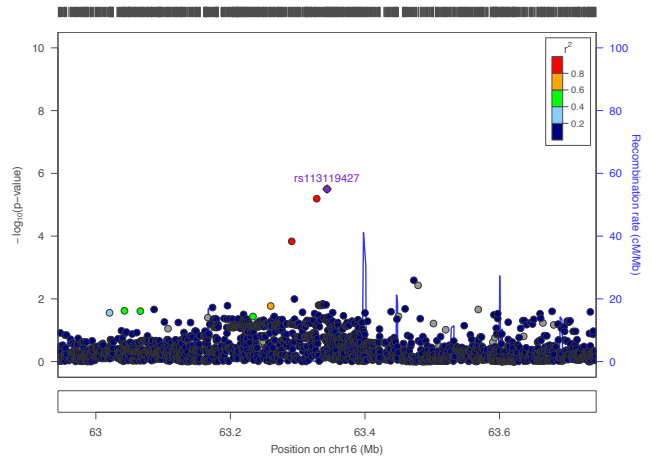
Supplementary Figure 52: LocusZoom plot for rs185803491.



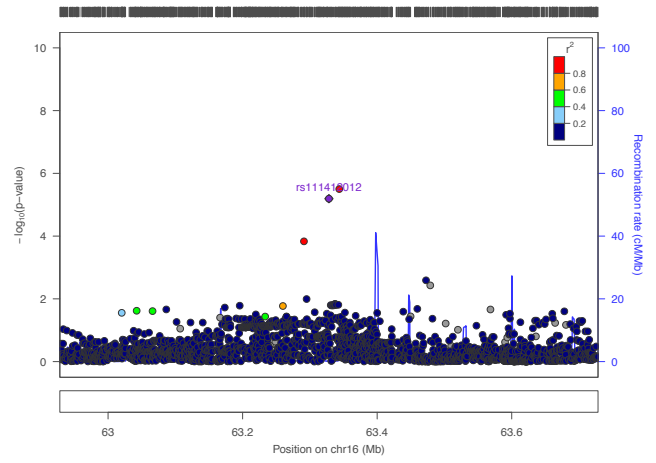
Supplementary Figure 53: LocusZoom plot for rs7126252.



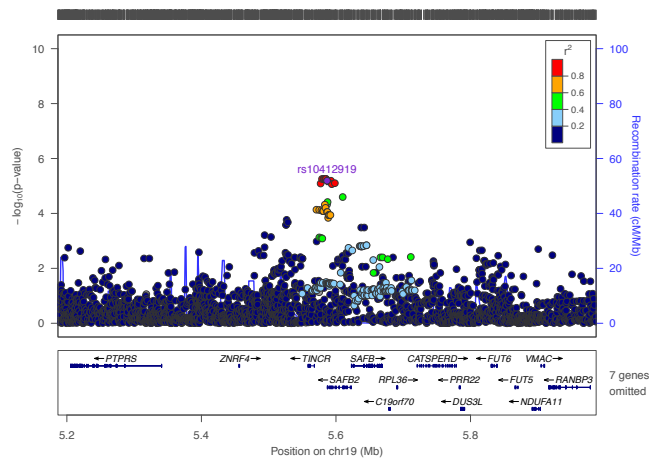
Supplementary Figure 54: LocusZoom plot for rs78818202.



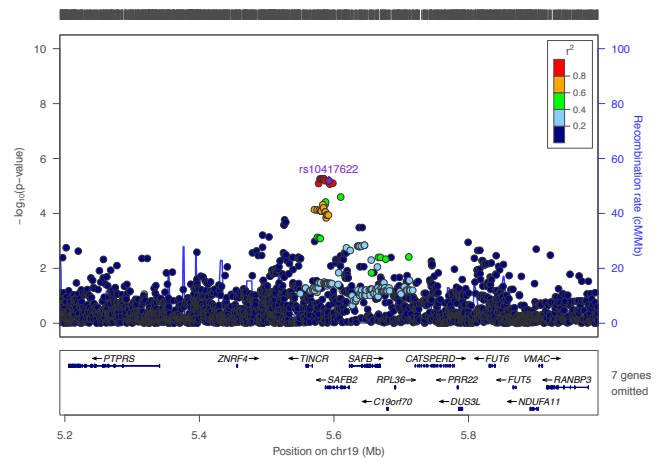
Supplementary Figure 55: LocusZoom plot for rs113119427.



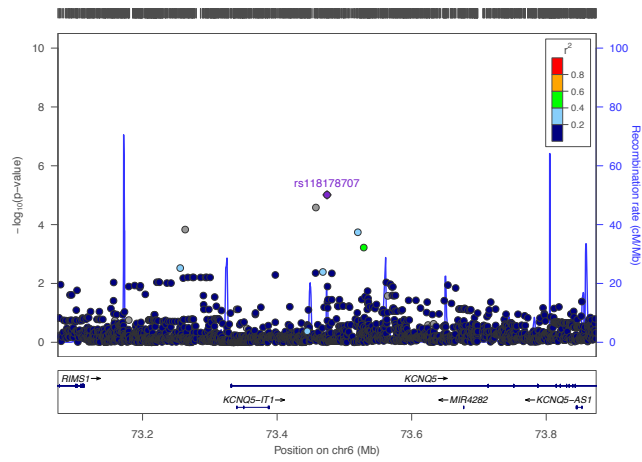
Supplementary Figure 56: LocusZoom plot for rs111412012.



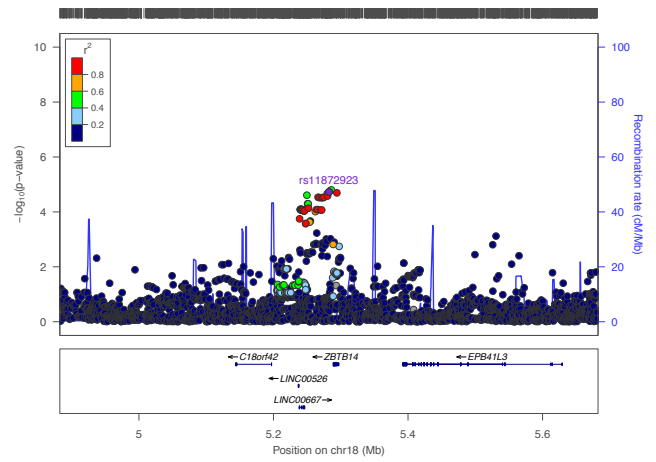
Supplementary Figure 57: LocusZoom plot for rs10412919.



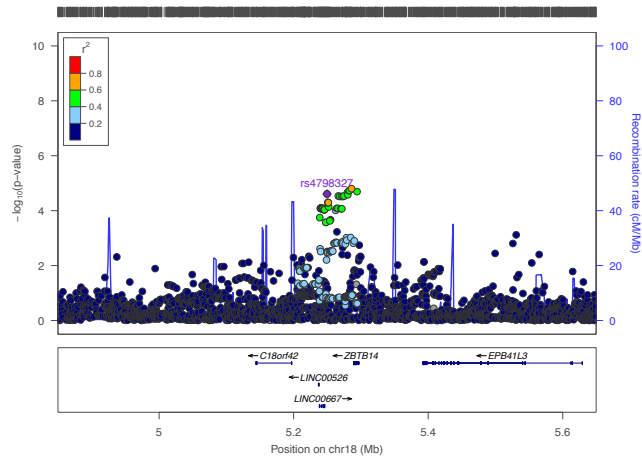
Supplementary Figure 58: LocusZoom plot for rs10417622.



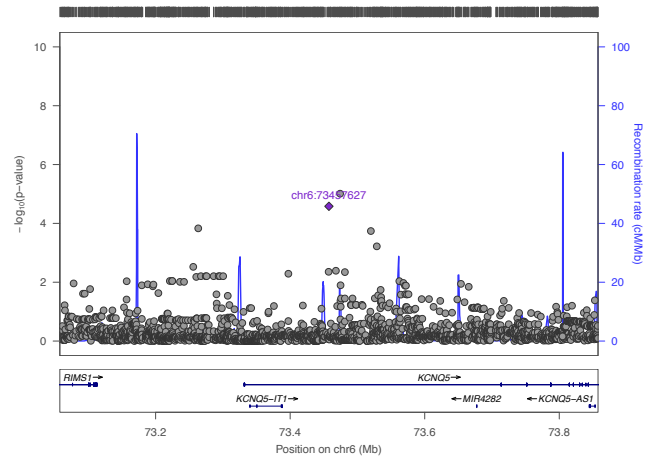
Supplementary Figure 59: LocusZoom plot for rs118178707.



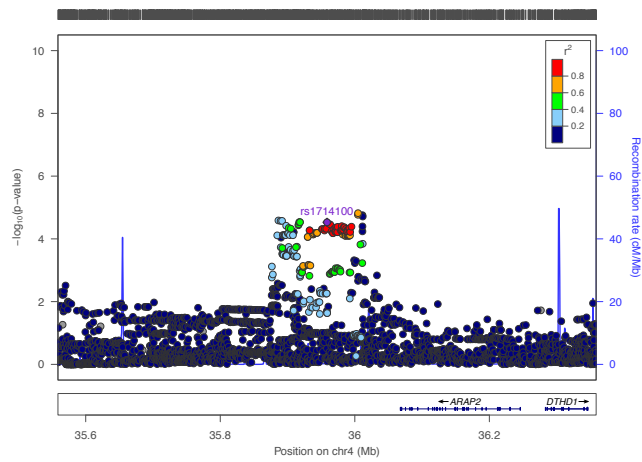
Supplementary Figure 60: LocusZoom plot for rs11872923.



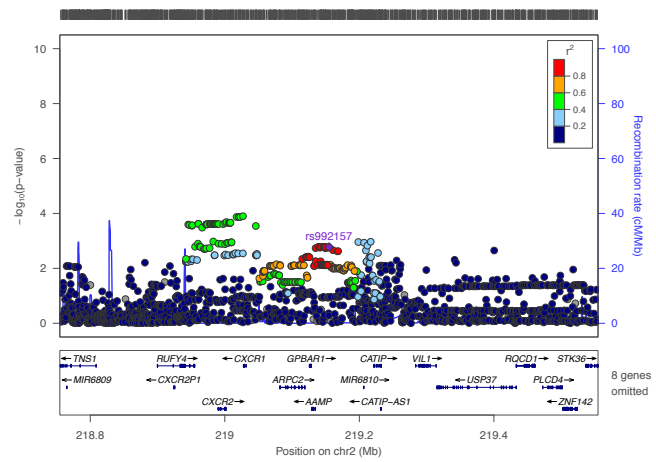
Supplementary Figure 61: LocusZoom plot for rs4798327.



Supplementary Figure 62: LocusZoom plot for 6:73457627(b37).



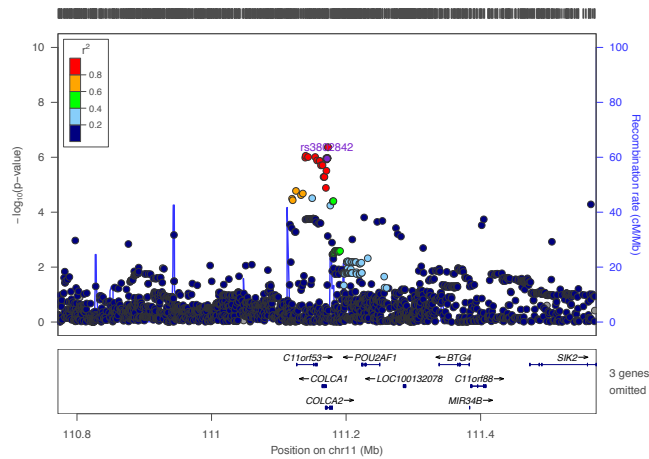
Supplementary Figure 63: LocusZoom plot for rs1714100.



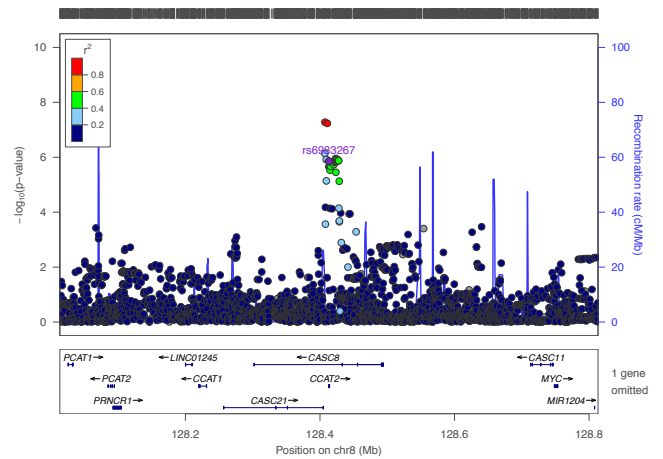
Supplementary Figure 64: LocusZoom plot for rs992157.

Stage 1 regional association (LocusZoom) plots for 38 published CRC risk SNPs

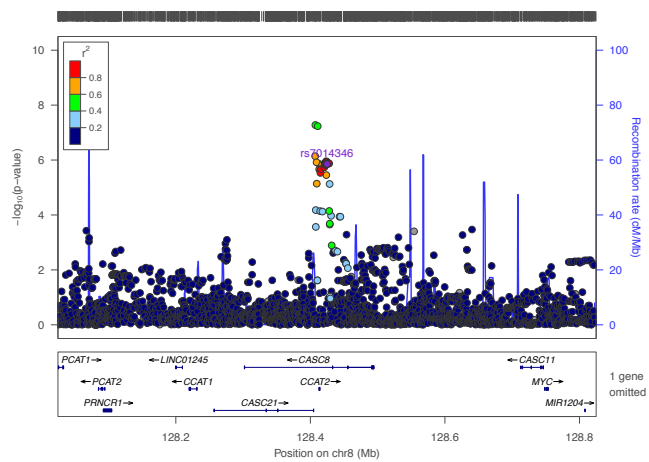
Genomic control was applied.



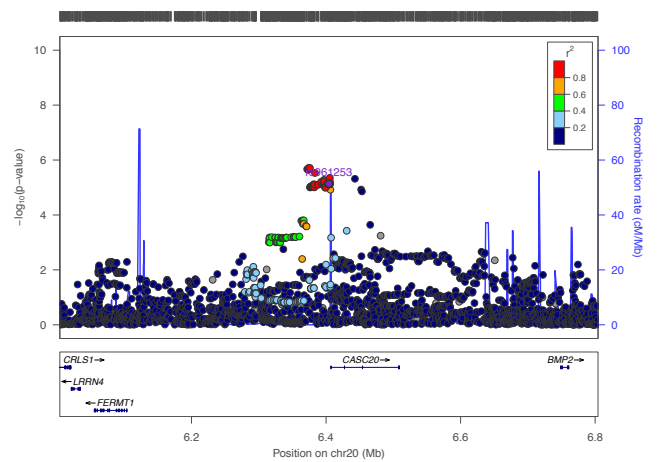
Supplementary Figure 65: LocusZoom plot for rs3802842.



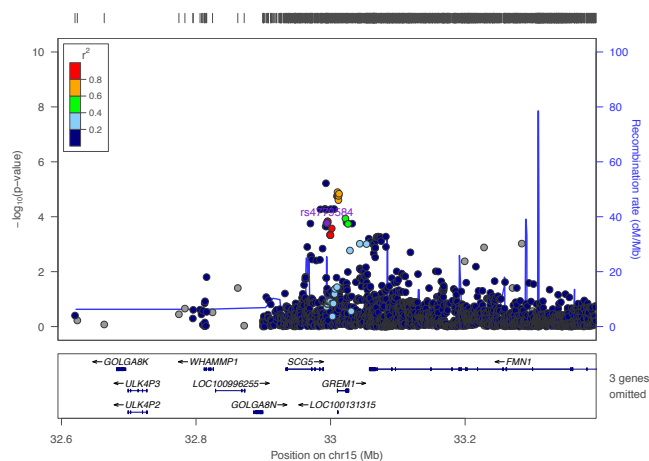
Supplementary Figure 66: LocusZoom plot for rs6983267.



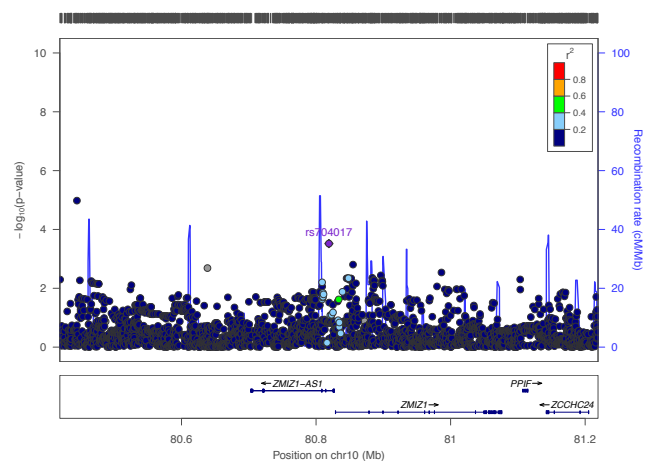
Supplementary Figure 67: LocusZoom plot for rs7014346.



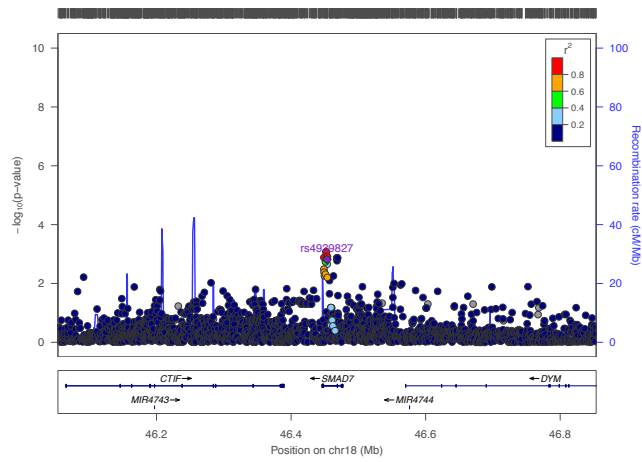
Supplementary Figure 68: LocusZoom plot for rs961253.



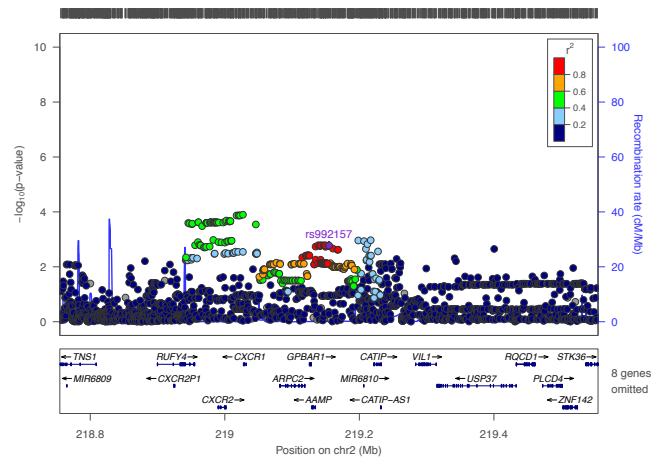
Supplementary Figure 69: LocusZoom plot for rs4779584.



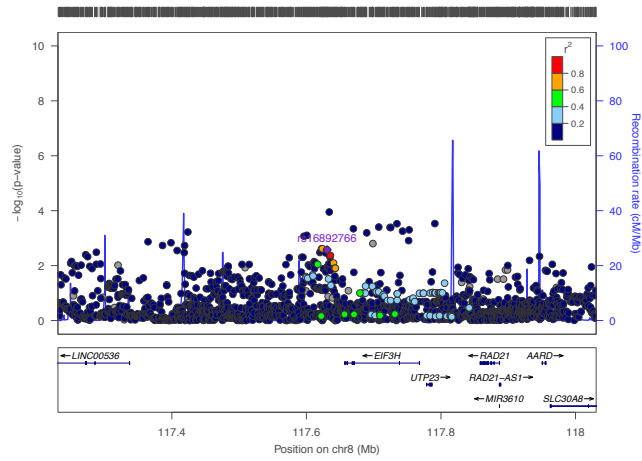
Supplementary Figure 70: LocusZoom plot for rs704017.



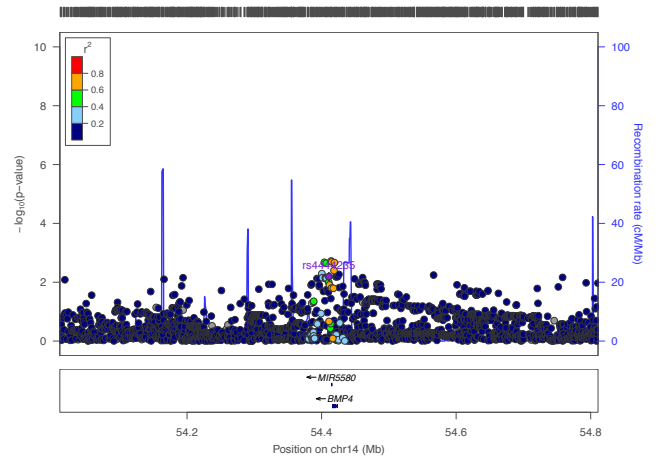
Supplementary Figure 71: LocusZoom plot for rs4939827.



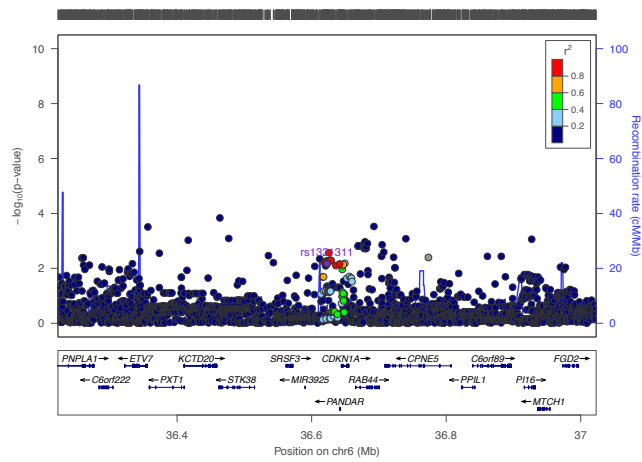
Supplementary Figure 72: LocusZoom plot for rs992157.



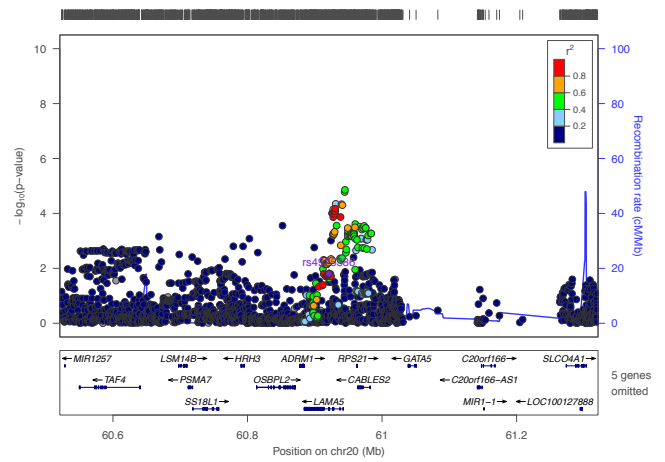
Supplementary Figure 73: LocusZoom plot for rs16892766.



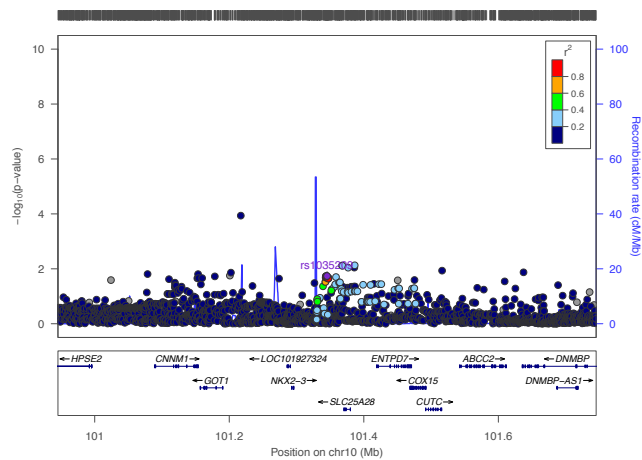
Supplementary Figure 74: LocusZoom plot for rs4444235.



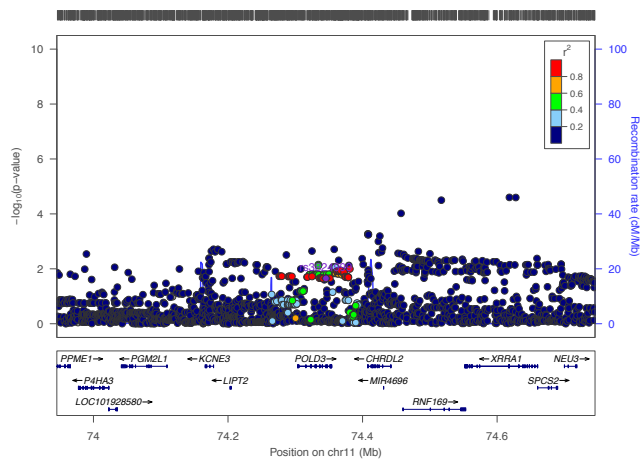
Supplementary Figure 75: LocusZoom plot for rs1321311.



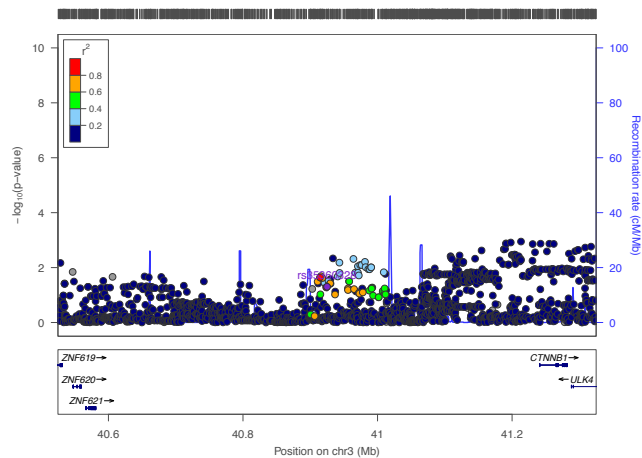
Supplementary Figure 76: LocusZoom plot for rs4925386.



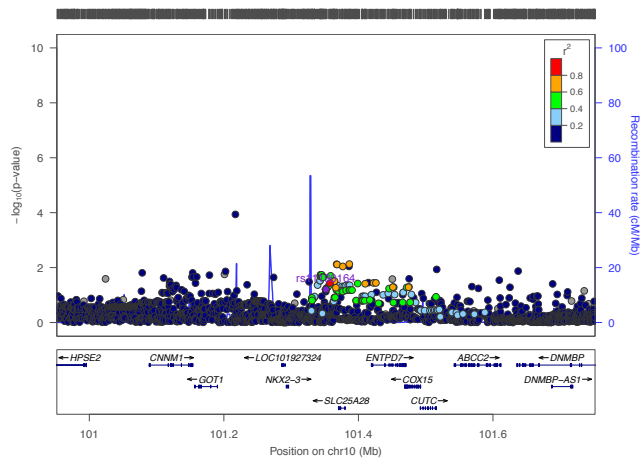
Supplementary Figure 77: LocusZoom plot for rs1035209.



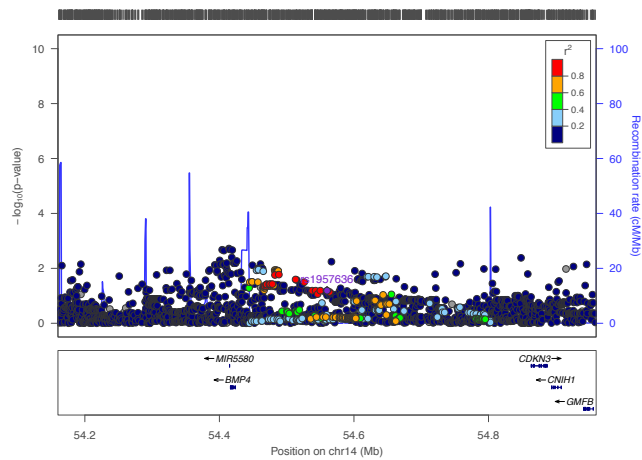
Supplementary Figure 78: LocusZoom plot for rs3824999.



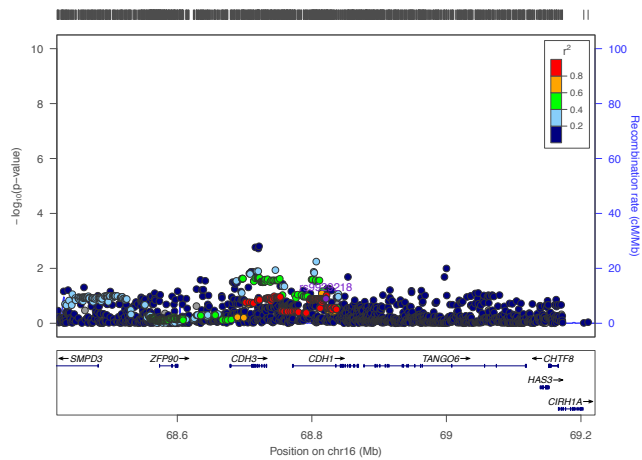
Supplementary Figure 79: LocusZoom plot for rs35360328.



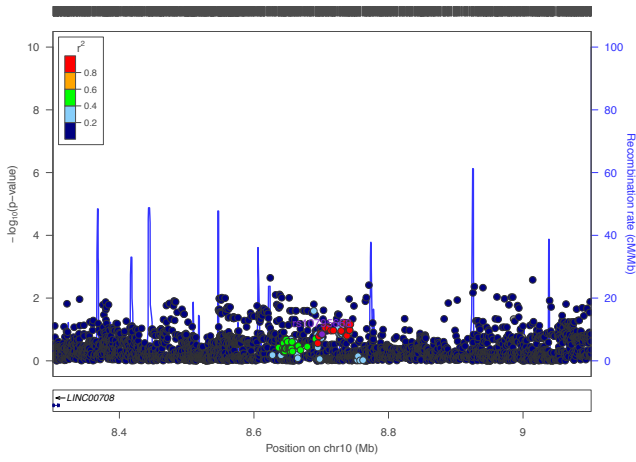
Supplementary Figure 80: LocusZoom plot for rs11190164.



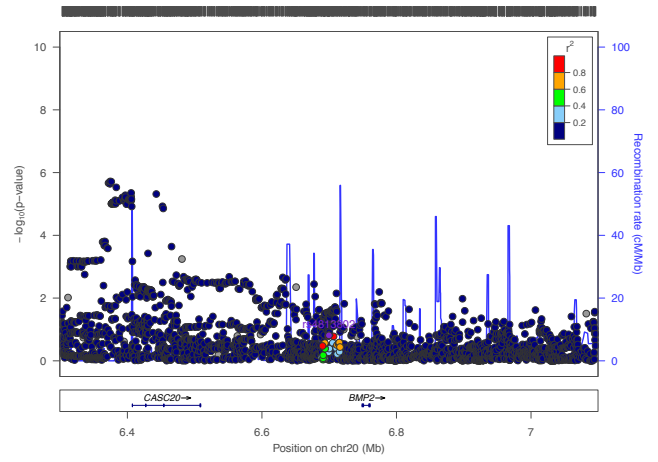
Supplementary Figure 81: LocusZoom plot for rs1957636.



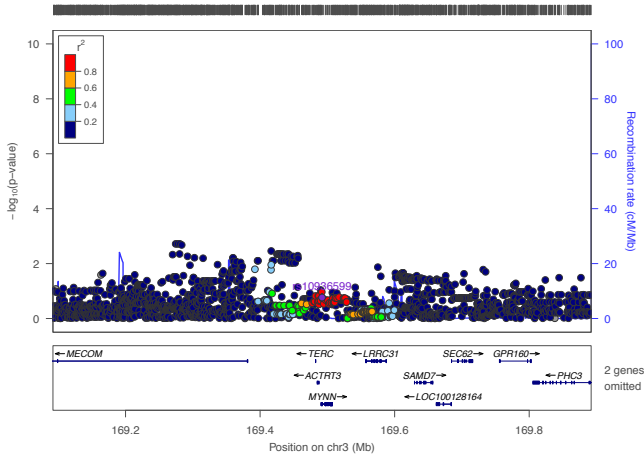
Supplementary Figure 82: LocusZoom plot for rs9929218.



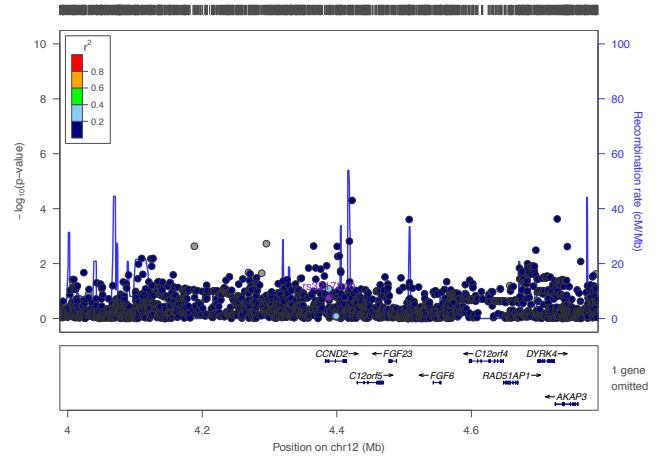
Supplementary Figure 83: LocusZoom plot for rs10795668.



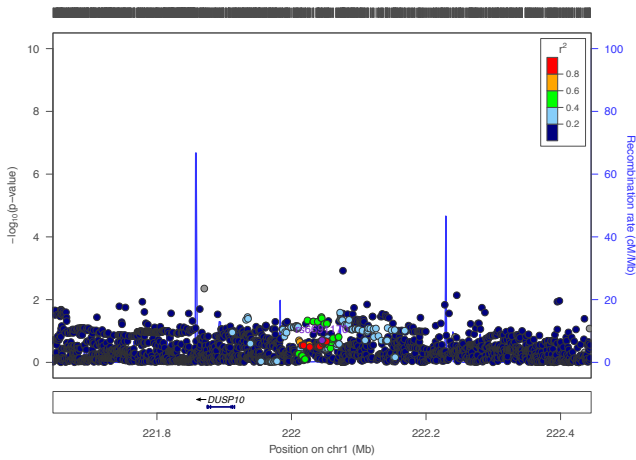
Supplementary Figure 84: LocusZoom plot for rs4813802.



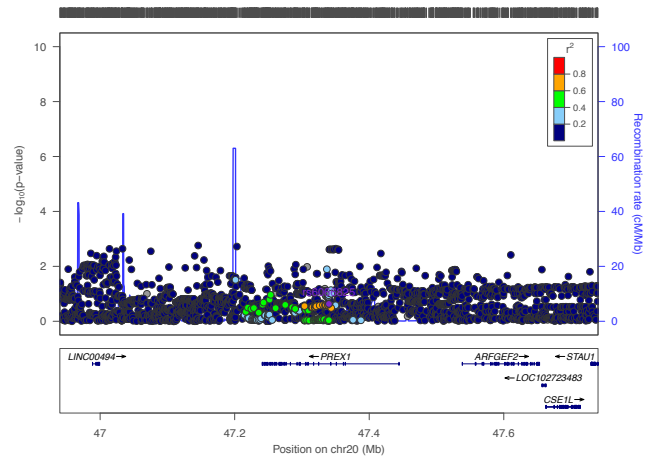
Supplementary Figure 85: LocusZoom plot for rs10936599.



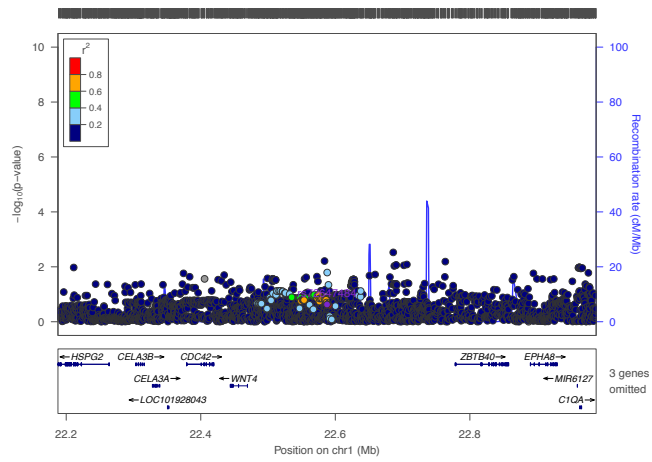
Supplementary Figure 86: LocusZoom plot for rs3217810.



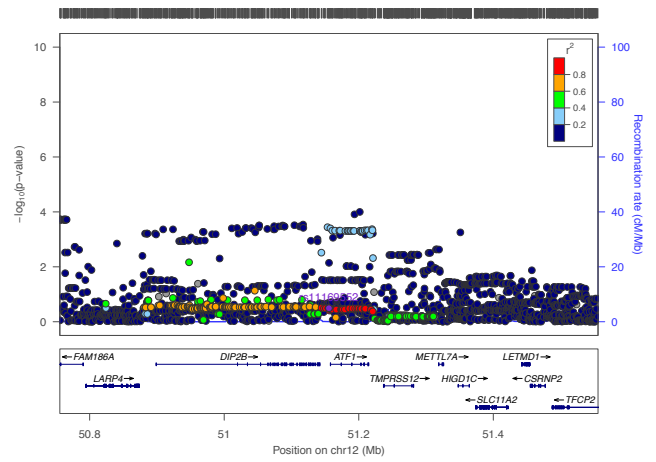
Supplementary Figure 87: LocusZoom plot for rs6691170.



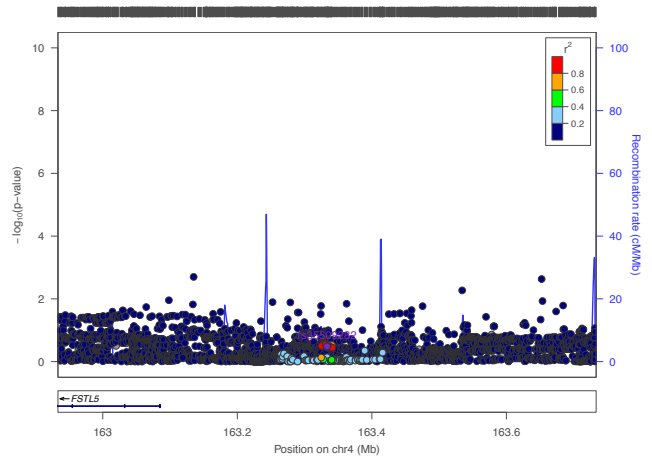
Supplementary Figure 88: LocusZoom plot for rs6066825.



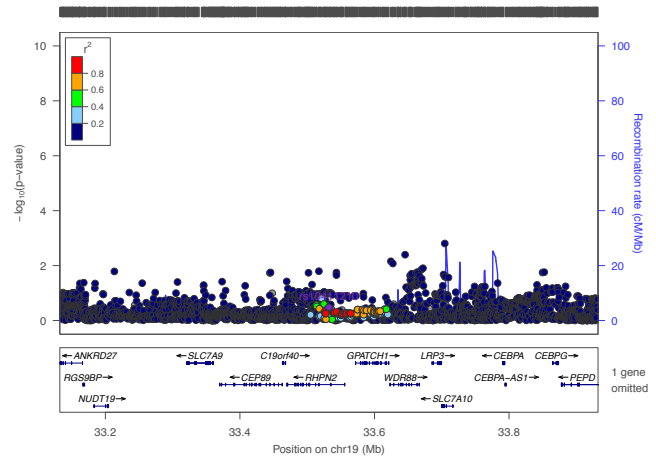
Supplementary Figure 89: LocusZoom plot for rs72647484.



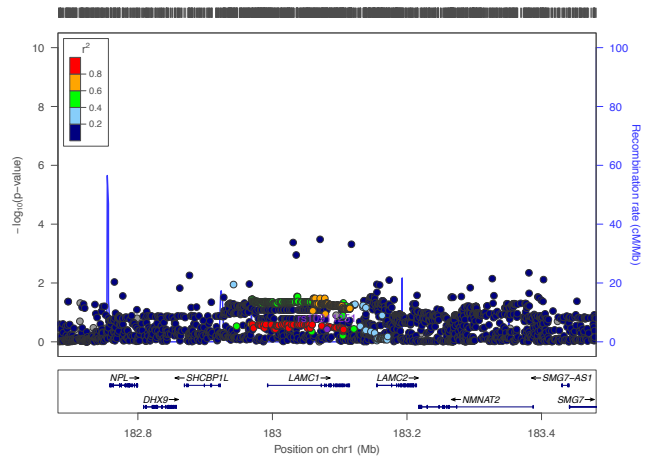
Supplementary Figure 90: LocusZoom plot for rs11169552.



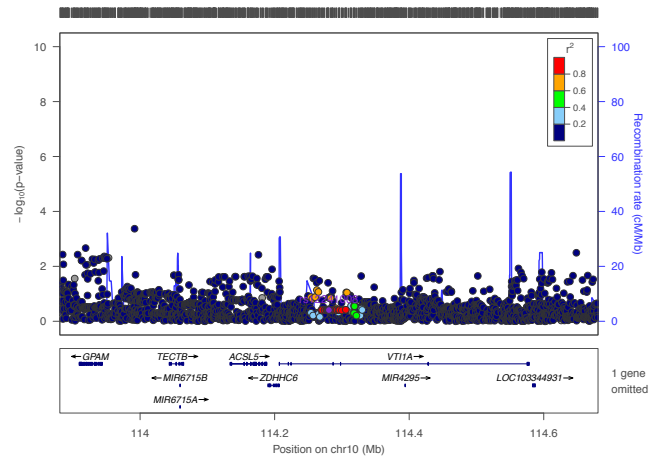
Supplementary Figure 91: LocusZoom plot for rs35509282.



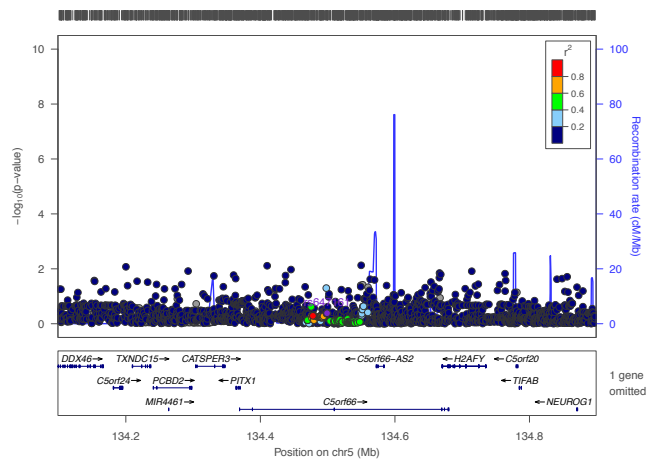
Supplementary Figure 92: LocusZoom plot for rs10411210.



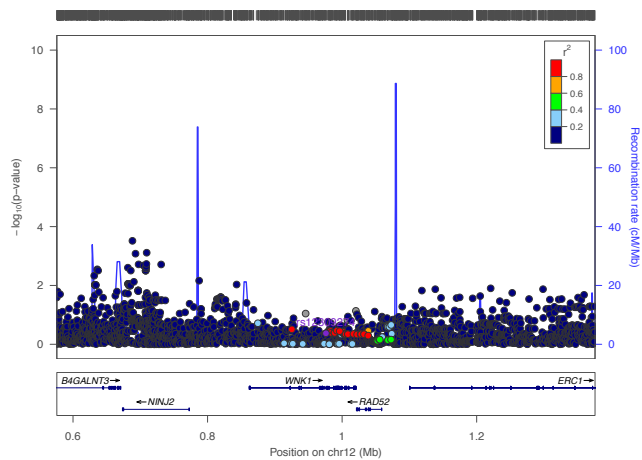
Supplementary Figure 93: LocusZoom plot for rs10911251.



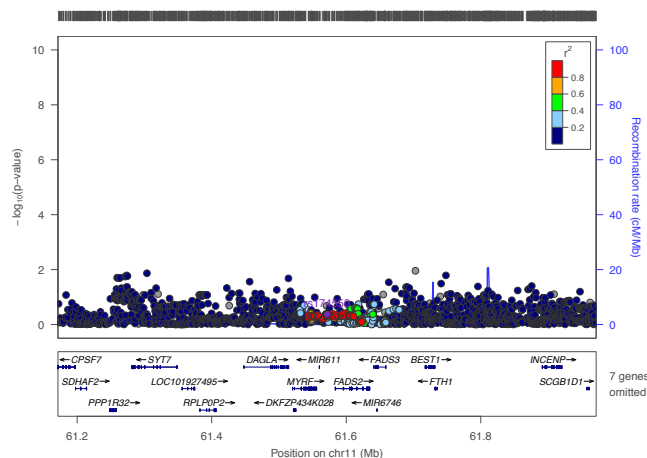
Supplementary Figure 94: LocusZoom plot for rs12241008.



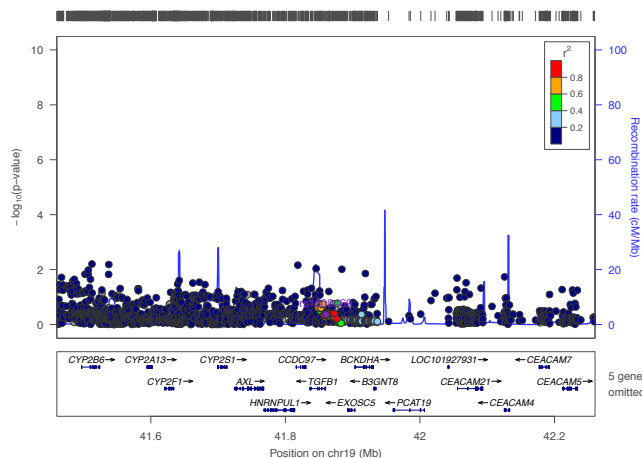
Supplementary Figure 95: LocusZoom plot for rs647161.



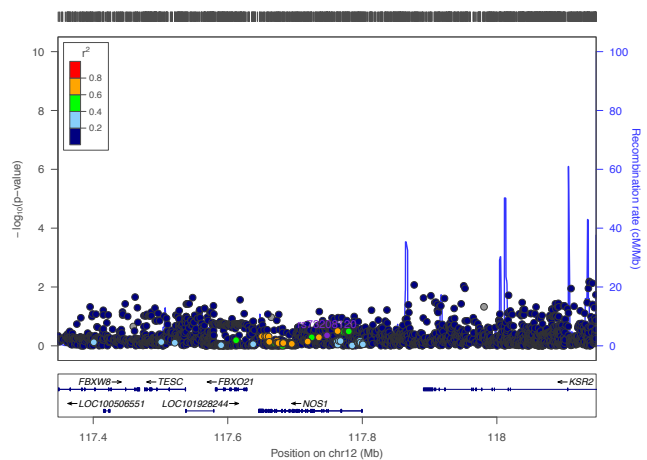
Supplementary Figure 96: LocusZoom plot for rs12309274.



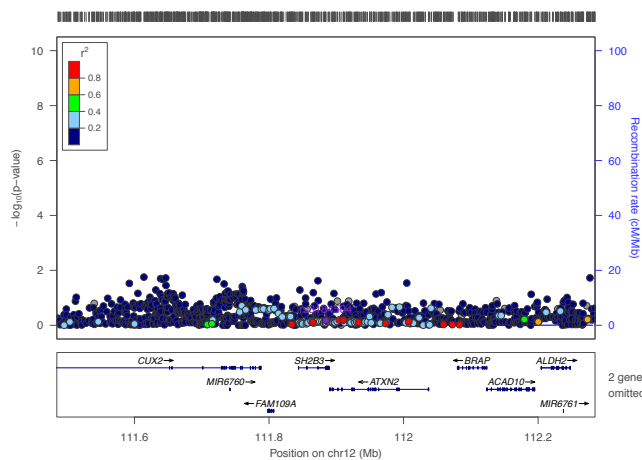
Supplementary Figure 97: LocusZoom plot for rs174550.



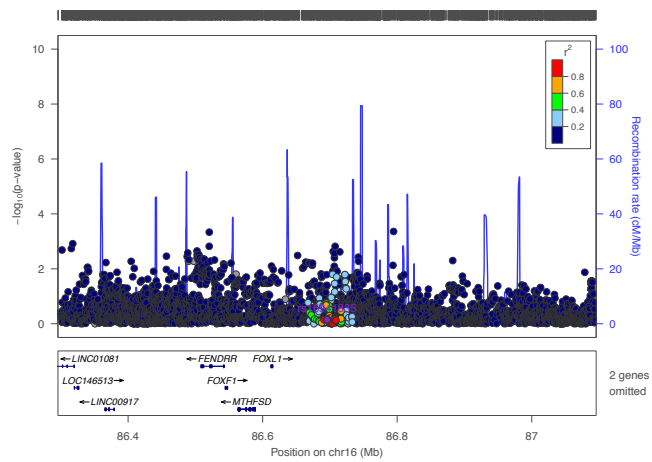
Supplementary Figure 98: LocusZoom plot for rs1800469.



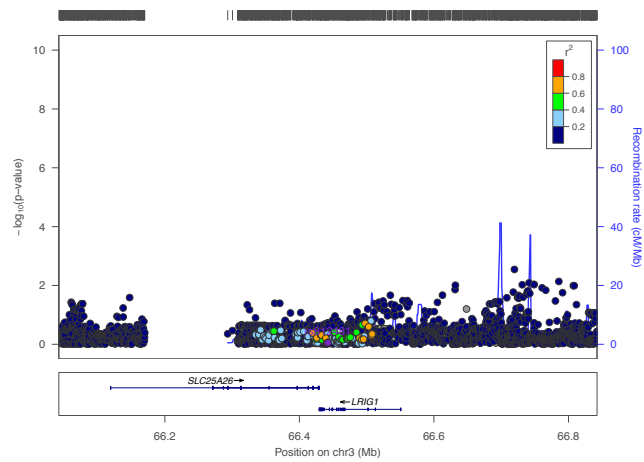
Supplementary Figure 99: LocusZoom plot for rs73208120.



Supplementary Figure 100: LocusZoom plot for rs3184504.



Supplementary Figure 101: LocusZoom plot for rs16941835.



Supplementary Figure 102: LocusZoom plot for rs812481.