Supplementary information for: Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array.

Supplementary Table 1: Number of cases and controls by study and population

No	Study	Genotyped samples			Samples included in final analysis (after QC and without samples genotyped in previous scans)					
					European			African/Mix Af		
		Co	Ca	Total	Co	Ca	Total	Co	Ca	Total
1	CAPS	677	1,197	1,874	271	408	679			
2	CPCS1	2,777	872	3,649	2,657	841	3,498			
3	CPCS2	798	306	1,104	762	255	1,017			
4	EPIC Germany[1]	302	244	546	302	228	530			
5	EPIC Greece[1]	23	25	48	23	25	48			
6	EPIC Italy[1]	97	70	167	97	69	166			
7	EPIC Netherlands[1]	20	17	37	18	17	35			
8	EPIC-Norfolk	1,136	528	1,664	1,111	511	1,622			
9	EPIC Oxford[1]	51	34	85	51	32	83			
10	EPIC Spain[1]	107	97	204	105	94	199			
11	EPIC Sweden[1]	299	231	530	289	219	508			
12	ESTHER	334	322	656	318	313	631			
13	FHCRC	707	683	1,390	637	604	1,241	51	57	108
14	IPO-Porto	88	187	275	66	183	249			
15	MAYO	391	614	1,005	384	601	985			
16	MCCS[2]	1,233	389	1,622	1,180	359	1,539			
17	MEC	895	890	1,785	597	586	1,183			
18	MOFFITT	138	490	628	100	414	514	30	41	71
19	PCFS[2]	13	1,409	1,422	3	1,326	1,329			
20	PCMUS	145	152	297	140	151	291			
21	Poland	472	453	925	359	438	797			
22	ProMPT	2	187	189	2	166	168			
23	ProtecT	1,498	1,624	3,122	1,474	1,563	3,037			
24	QLD	94	187	281	87	186	273			
25	SCCS	510	545	1,055	0	0	0	488	525	1,013
26	SEARCH	1,290	1,468	2,758	1,244	1,371	2,615			
27	STHM1	2,330	2,056	4,386	2,224	2,006	4,230			
28	TAMPERE	2,769	2,836	5,605	2,413	2,754	5,167			
29	UKGPCS	4,314	4,900	9,214	2,193	2,859	5,052			
30	ULM	506	609	1,115	354	603	957			
31	UTAH	256	454	710	254	440	694			
32	WUGS	0	998	998	0	0	0			
	Total	**24,272**	**25,074**	**49,346**	**19,715**	**19,622**	**39,337**	**569**	**623**	**1,192**

[1] Subsets from the international EPIC study

[2] Studies from the Melbourne group

Co =Controls

Ca= Cases

Supplementary Table 2: Disease-specific odds ratios for Indolent and Aggressive disease each versus controls and case only analysis (Indolent *vs.*Aggressive) using samples with Europeans ancestry.

Marker	Indolent	Aggressive	Case only analysis	*P*-value
rs1218582	1.06 (1.03-1.09)	1.08 (1.02-1.14)	1.01 (.96-1.08)	.55
rs4245739	.91 (.88-.95)	.91 (.85-.97)	1.00 (.98-1.29)	.97
rs11902236	1.07 (1.03-1.11)	1.06 (.99-1.13)	.99 (.93-1.05)	.69
rs3771570	1.14 (1.09-1.19)	1.02 (.95-1.10)	.90 (.83-.97)	.007
rs7611694	.90 (.87-.93)	.94 (.89-.99)	1.05 (.99-1.11)	.12
rs1894292	.92 (.89-.95)	.90 (.85-.95)	.99 (.93-1.04)	.65
rs6869841	1.08 (1.04-1.12)	1.04 (.97-1.12)	.96 (.90-1.03)	.26
rs3096702	1.08 (1.04-1.11)	1.05 (.99-1.11)	.98 (.92-1.03)	.41
rs2273669	1.08 (1.04-1.13)	.99 (.92-1.08)	.90 (.83-.97)	.01
rs1933488	.89 (.86-.91)	.91 (.86-.96)	1.03 (.97-1.09)	.30
rs12155172	1.10 (1.06-1.14)	1.16 (1.09-1.24)	1.04 (.97-1.11)	.27
rs11135910	1.11 (1.06-1.16)	1.10 (1.02-1.19)	1.01 (.93-1.09)	.82
rs3850699	.91 (.88-.94)	.94 (.88-1.00)	1.02 (.96-1.09)	.43
rs11568818	.91 (.88-.94)	.92 (.87-.97)	1.01 (.96-1.07)	.62
rs1270884	1.07 (1.04-1.11)	1.02 (.97-1.08)	.94 (.89-.99)	.03
rs8008270	.89 (.86-.93)	.89 (.83-.96)	1.01 (.94-1.09)	.71
rs7141529	1.08 (1.05-1.12)	1.11 (1.05-1.17)	1.03 (.97-1.09)	.31
rs684232	1.10 (1.07-1.14)	1.10 (1.04-1.16)	.99 (.93-1.05)	.73
rs11650494	1.14 (1.08-1.21)	1.20 (1.08-1.33)	1.04 (.94-1.16)	.41
rs7241993	.92 (.89-.95)	.92 (.87-.98)	.99 (.93-1.06)	.79
rs2427345	.93 (.90-.96)	.97 (.91-1.02)	1.05 (.99-1.11)	.11
rs6062509	.90 (.87-.93)	.85 (.80-.90)	.94 (.89-1.00)	.07
rs2405942	.89 (.84-.94)	.82 (.74-.90)	.92 (.83-1.02)	.10

P trend for difference in the per-allele OR (see methods).

Supplementary Table 3: Geometric mean PSA levels by genotype in controls (Samples with European ancestry)

Marker	Geometric mean PSA (95%CI)			P-value[1]
rs1218582	AA	AG	GG	.64
	1.95 (1.85-2.05)	1.93 (1.85-2.01)	2.08 (1.93-2.24)	
rs4245739	AA	AC	CC	.49
	1.97 (1.89-2.05)	1.95 (1.85-2.04)	2.05 (1.82-2.27)	
rs11902236	GG	GA	AA	.89
	1.95 (1.87-2.02)	2.00 (1.90-2.11)	1.91 (1.70-2.11)	
rs3771570	GG	GA	AA	.98
	1.98 (1.91-2.05)	1.95 (1.84-2.06)	1.73 (1.42-2.04)	
rs7611694	AA	AC	CC	.23
	1.95 (1.86-2.05)	2.00 (1.91-2.09)	1.90 (1.77-2.04)	
rs1894292	GG	GA	AA	.70
	1.93 (1.81-2.04)	1.98 (1.90-2.06)	1.99 (1.86-2.12)	
rs6869841	GG	GA	AA	.0001
	1.90 (1.83-1.98)	2.03 (1.93-2.13)	2.36 (2.05-2.68)	
rs3096702	GG	GA	AA	.26
	1.92 (1.83-2.01)	1.96 (1.87-2.04)	2.13 (1.95-2.32)	
rs2273669	AA	AG	GG	.87
	1.97 (1.91-2.05)	1.93 (1.81-2.04)	2.00 (1.57-2.42)	
rs1933488	AA	AG	GG	.12
	1.97 (1.88-2.07)	2.00 (1.91-2.09)	1.86 (1.71-2.00)	
rs12155172	GG	GA	AA	.10
	1.92 (1.84-1.99)	2.05 (1.94-2.16)	2.01 (1.75-2.26)	
rs11135910	GG	GA	AA	.84
	1.94 (1.87-2.01)	2.02 (1.90-2.13)	2.11 (1.34-2.88)	
rs3850699	AA	AG	GG	.39
	1.97 (1.88-2.05)	1.96 (1.87-2.04)	2.02 (1.82-2.22)	
rs11568818	AA	AG	GG	.08
	1.95 (1.84-2.07)	1.93 (1.85-2.01)	2.06 (1.93-2.19)	
rs1270884	GG	GA	AA	.02
	1.88 (1.76-2.00)	1.97 (1.89-2.05)	2.05 (1.92-2.17)	
rs8008270	GG	GA	AA	.07
	2.01 (1.93-2.08)	1.87 (1.77-1.97)	2.05 (1.69-2.42)	
rs7141529	AA	AG	GG	.36
	2.05 (1.92-2.18)	1.95 (1.87-2.03)	1.91 (1.80-2.03)	
rs684232	AA	AG	GG	.43
	1.98 (1.89-2.08)	1.96 (1.88-2.05)	1.92 (1.76-2.09)	
rs11650494	GG	GA	AA	.77
	1.97 (1.91-2.04)	1.91 (1.76-2.06)	2.19 (1.52-2.86)	
rs7241993	GG	GA	AA	.66
	2.00 (1.91-2.08)	1.90 (1.81-2.00)	2.07 (1.87-2.26)	
rs2427345	GG	GA	AA	.48
	2.03 (1.93-2.14)	1.91 (1.83-1.99)	1.97 (1.82-2.13)	
rs6062509	AA	AC	CC	.35
	1.99 (1.90-2.08)	1.95 (1.86-2.04)	1.91 (1.73-2.09)	
rs2405942	AA	AG	GG	.60
	1.98 (1.91-2.05)	NA	1.91 (1.79-2.03)	

[1] Test for trend in log (PSA) by allele dose.

Supplementary Table 4: Family history-specific odds ratios (Samples with European ancestry)

Marker	No Family history	With Family history	Ptrend[1]
rs1218582	1.06 (1.03-1.09)	1.05 (.99-1.11)	.81
rs4245739	.91 (.88-.94)	.95 (.89-1.02)	.42
rs11902236	1.07 (1.03-1.10)	1.08 (1.01-1.15)	.85
rs3771570	1.11 (1.06-1.16)	1.19 (1.10-1.29)	.04
rs7611694	.90 (.88-.93)	.92 (.86-.98)	.46
rs1894292	.92 (.89-.94)	.89 (.84-.95)	.30
rs6869841	1.07 (1.03-1.11)	1.10 (1.02-1.18)	.86
rs3096702	1.07 (1.04-1.11)	1.03 (.97-1.10)	.56
rs2273669	1.06 (1.02-1.11)	1.12 (1.03-1.22)	.18
rs1933488	.89 (.87-.92)	.87 (.81-.92)	.80
rs12155172	1.10 (1.07-1.14)	1.12 (1.05-1.21)	.30
rs11135910	1.10 (1.05-1.14)	1.17 (1.08-1.27)	.03
rs3850699	.92 (.89-.95)	.86 (.80-.92)	.07
rs11568818	.91 (.88-.94)	.90 (.85-.96)	.85
rs1270884	1.07 (1.03-1.10)	1.08 (1.01-1.15)	.95
rs8008270	.89 (.86-.93)	.91 (.84-.98)	.93
rs7141529	1.09 (1.05-1.12)	1.10 (1.03-1.16)	.93
rs684232	1.10 (1.06-1.13)	1.14 (1.07-1.22)	.23
rs11650494	1.14 (1.08-1.21)	1.17 (1.05-1.30)	.17
rs7241993	.92 (.89-.95)	.93 (.87-.99)	.88
rs2427345	.93 (.90-.96)	.99 (.93-1.05)	.26
rs6062509	.89 (.86-.92)	.88 (.82-.94)	.86
rs2405942	.88 (.84-.93)	.85 (.76-.95)	.52

[1] *P* for difference in the per-allele OR (see methods).

Supplementary Table 5: Age-specific odds ratios for each SNP (Samples with European ancestry)

Marker	Age at diagnosis (years)					Ptrend[1]
	<55	55-59	60-64	65-69	70+	
rs1218582	1.05 (.99-1.13)	1.07 (1.02-1.13)	1.07 (1.02-1.12)	1.08 (1.03-1.13)	1.04 (.99-1.09)	.46
rs4245739	.90 (.84-.98)	.91 (.85-.96)	.92 (.87-.98)	.94 (.89-.99)	.90 (.85-.95)	.54
rs11902236	1.11 (1.03-1.19)	1.05 (.99-1.12)	1.03 (.98-1.09)	1.06 (1.01-1.12)	1.11 (1.06-1.18)	.07
rs3771570	1.20 (1.10-1.32)	1.12 (1.04-1.20)	1.08 (1.01-1.16)	1.14 (1.07-1.22)	1.09 (1.02-1.17)	.05
rs7611694	.85 (.79-.91)	.89 (.85-.94)	.92 (.88-.96)	.90 (.86-.94)	.94 (.90-.99)	.02
rs1894292	.90 (.84-.97)	.92 (.87-.97)	.89 (.85-.93)	.92 (.88-.97)	.93 (.88-.97)	.32
rs6869841	1.18 (1.09-1.28)	1.09 (1.02-1.16)	1.11 (1.05-1.18)	1.04 (.98-1.10)	1.03 (.97-1.09)	.01
rs3096702	1.10 (1.02-1.18)	1.12 (1.06-1.18)	1.06 (1.01-1.12)	1.07 (1.02-1.12)	1.02 (.97-1.07)	.005
rs2273669	1.01 (.92-1.12)	1.12 (1.05-1.21)	1.06 (.99-1.13)	1.06 (.99-1.13)	1.09 (1.01-1.16)	.73
rs1933488	.86 (.80-.92)	.89 (.85-.94)	.88 (.83-.92)	.90 (.85-.94)	.89 (.85-.93)	.70
rs12155172	1.12 (1.04-1.21)	1.11 (1.04-1.18)	1.07 (1.01-1.13)	1.11 (1.05-1.17)	1.13 (1.07-1.20)	.53
rs11135910	1.12 (1.02-1.22)	1.12 (1.04-1.21)	1.11 (1.04-1.19)	1.12 (1.05-1.20)	1.06 (.99-1.13)	.37
rs3850699	.88 (.82-.95)	.93 (.87-.98)	.91 (.86-.96)	.90 (.86-.95)	.93 (.88-.98)	.63
rs11568818	.92 (.86-.99)	.94 (.89-.99)	.87 (.83-.91)	.91 (.87-.95)	.93 (.89-.98)	.85
rs1270884	1.08 (1.01-1.16)	1.08 (1.02-1.14)	1.07 (1.02-1.12)	1.08 (1.03-1.13)	1.05 (1.00-1.10)	.45
rs8008270	.84 (.77-.92)	.88 (.82-.94)	.90 (.84-.96)	.93 (.88-.99)	.88 (.83-.94)	.14
rs7141529	1.08 (1.01-1.16)	1.09 (1.03-1.15)	1.11 (1.06-1.17)	1.08 (1.03-1.13)	1.07 (1.02-1.12)	.65
rs684232	1.21 (1.13-1.29)	1.16 (1.10-1.23)	1.07 (1.02-1.13)	1.08 (1.03-1.14)	1.06 (1.01-1.12)	.0002
rs11650494	1.20 (1.07-1.35)	1.08 (.98-1.19)	1.19 (1.10-1.30)	1.12 (1.03-1.22)	1.14 (1.05-1.25)	.12
rs7241993	.88 (.83-.96)	.87 (.82-.93)	.94 (.89-.99)	.93 (.89-.98)	.95 (.90-1.00)	.02
rs2427345	.93 (.87-1.00)	.91 (.86-.96)	.95 (.90-.99)	.96 (.92-1.01)	.92 (.88-.97)	.09
rs6062509	.86 (.80-.93)	.85 (.81-.91)	.89 (.85-.94)	.90 (.85-.95)	.91 (.86-.95)	.12
rs2405942	.83 (.74-.94)	.82 (.75-.90)	.89 (.82-.97)	.88 (.81-.96)	.93 (.86-1.01)	.89

[1] 1df trend test for trend in OR by age, using case only analysis

Supplementary Table 6. Genes in flanking regions of 23 novel tagSNPs

#	Chr	tagSNP	Genes in Intersection. LD R-squared 0.2 or 250KB flank.	Additional genes in 1MB Flank
1	chr1	rs1218582	*ADAM15, ADAR, CKS1B, DCST1, DCST2, DPM3, EFNA1, EFNA3, EFNA4, FLAD1, KCNN3, LENEP, LOC10050, LOC100505666, MIR4258, PBXIP1, PMVK, PYGO2, SHC1, SLC50A1, ZBTB7B,*	*ASH1L, CHRNB2, CLK2, FAM189B, FDPS, GBA, GBAP1, HCN3, IL6R, IL6R, KRTCAP2, MIR555, MIR92B, MTX1, MUC1, PKLR, RUSC1, RUSC1-AS1, SCAMP3, SHE, TDRD10, THBS3, TRIM46, UBE2Q1,*
2	chr1	rs4245739	*LOC127841, LRRN2, MDM4, PIK3C2B, PLEKHA6, PPP1R15B,*	*CNTN2, ETNK2, GOLT1A, KISS1, NFASC, NFASC, REN, SOX13,*
3	chr2	rs11902236	*C2orf48, CYS1, GRHL1, KLF11, MIR4261, RRM2, TAF1B,*	*ADAM17, HPCAL1, IAH1, ODC1, SNORA80B, YWHAQ,*
4	chr2	rs3771570	*ANO7, ATG4B, BOK, BOK-AS1, DTYMK, FARP2, HDLBP, SEP2, STK25, THAP4,*	*CXXC11, D2HGDH, GAL3ST2, ING5, LOC200772, MTERFD2, NEU4, PASK, PASK, PDCD1, PPP1R7, SEPT2, SNED1, THAP4,*
5	chr3	rs7611694	*ATP6V1A, BOC, KIAA2018, MIR4446, NAA50, SIDT1, SPICE1, WDR52, WDR52-AS, WDR52-AS1,*	*GRAMD1C, GRAMD1C, KIAA1407, QTRTD1, WDR52, ZDHHC23,*
6	chr4	rs1894292	*AFM, AFP, ALB, ANKRD17, COX18, LOC72804, LOC728040, RASSF6,*	*CXCL1, CXCL6, IL8, PF4, PF4V1,*
7	chr5	rs6869841	*BOD1, LOC285593, STC2,*	*ATP6V0E1, BNIP1, C5orf47, CPEB4, CREBRF, CREBRF, NKX2-5, SNORA74B,*
8	chr6	rs1933488	*FBXO5, MTRF1L, RGS17,*	*MYCT1, SYNE1, VIP,*
9	chr6	rs2273669	*ARMC2, CEP57L1, FOXO3, LACE1, LINC0022, LINC00222, SESN1,*	*CCDC162P, CD164, MICAL1, PPIL6, SESN1, SMPD2, ZBTB24,*
10	chr6	rs3096702	*AGER, AGPAT1, ATF6B, BTNL2, C2, C4A, C4B, C6orf10, CFB, CYP21A1P, CYP21A2, DOM3Z, EGFL8, FKBPL, GPSM3, HCG23, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1, HLA-DRB5, HLA-DRB6, LOC10029, LOC100293534, LOC10050, LOC100507547, MIR1236, NOTCH4, PBX2, PPT2, PPT2-EGF, PPT2-EGFL8, PRRT1, RDBP, RNF5, RNF5P1, SKIV2L, STK19, TNXA, TNXB,*	*C2, C4A, C4B, C6orf25, C6orf48, CLIC1, DDAH2, EHMT2, HSPA1A, HSPA1B, HSPA1L, LOC100293534, LSM2, MSH5, MSH5-SAPCD1, NEU1, SAPCD1, SLC44A4, SNORD48, SNORD52, STK19, VARS, VWA7, ZBTB12,*
11	chr7	rs12155172	*ABCB5, RPL23P8, SP8,*	*ABCB5, SP4,*
12	chr8	rs11135910	*EBF2,*	*BNIP3L, DPYSL2, PNMA2, PPP2R2A,*

13	chr10	rs3850699	*ACTR1A, ARL3, AS3MT, C10orf32, C10orf32-AS3MT, C10orf95, CNNM2, CUEDC2, CYP17A1, FBXL15, LOC100505761, MIR146B, PSD, SFXN2, SUFU, TMEM180, TRIM8, WBP1L,*	*C10orf26, CNNM2, ELOVL3, GBF1, NFKB2, NOLC1, NT5C2, PITX3,*
14	chr11	rs11568818	*BIRC2, BIRC3, MMP10, MMP20, MMP27, MMP7, MMP8, TMEM123, YAP1,*	*C11orf70, LOC100288077, MMP1, MMP12, MMP13, MMP3,*
15	chr12	rs1270884	*LOC255480, TBX5,*	*RBM19, TBX3,*
16	chr14	rs7141529	*ACTN1, RAD51B, ZFP36L1,*	*DCAF5,*
17	chr14	rs8008270	*DDHD1, ERO1L, FERMT2, GNPNAT1, GPR137C, PSMC6, STYX, TXNDC16,*	-
18	chr17	rs11650494	*ZNF652, ABI3, B4GALNT2, FLJ40194, GNGT2, IGF2BP1, NGFR, PHB, PHOSPHO1,*	*ATP5G1, CALCOCO2, FAM117A, GIP, NXPH3, SLC35B1, SNF8, SPOP, TTLL6, UBE2Z, HOXB13, PRAC,*
19	chr17	rs684232	*DBIL5P, FAM57A, GEMIN4, GLOD4, NXN, RNMTL1, VPS53,*	*ABR, ABR, C17orf97, FAM101B, LOC100506388, MIR3183, RPH3AL, TIMM22,*
20	chr18	rs7241993	*ATP9B, SALL3,*	*NFATC1,*
21	chr20	rs2427345	*ADRM1, C20orf15, C20orf151, C20orf166, C20orf166-AS1, CABLES2, GATA5, GTPBP5, HRH3, LAMA5, MIR1-1, MIR133A2, MIR4758, OSBPL2, RPS21,*	*C20orf20, CDH4, COL9A3, DPH3P1, LOC100127888, LOC100652730, LSM14B, MIR1257, NTSR1, OGFR, PSMA7, SLCO4A1, SS18L1, TAF4, TCFL5,*
22	chr20	rs6062509	*ABHD16B, ARFRP1, C20orf195, DNAJC5, EEF1A2, GMEB2, LIME1, LOC100505815, MIR1914, MIR647, MIR941-1, MIR941-2, MIR941-3, MIR941-4, PPDPF, PRIC285, PRPF6, PTK6, RTEL1, RTEL1-TN, RTEL1-TNFRSF6B, SAMD10, SLC2A4RG, SRMS, STMN3, TNFRSF6B, TPD52L2, UCKL1, UCKL1-AS1, ZBTB46, ZGPAT, ZNF512B,*	*ARFGAP1, BIRC7, C20orf201, CHRNA4, COL20A1, FLJ16779, KCNQ2, LINC00176, MIR3196, MIR4326, MIR941-2, MIR941-2, MIR941-2, MIR941-3, MIR941-3, MIR941-4, MIR941-4, MYT1, NKAIN4, NPBWR2, OPRL1, OPRL1, RGS19, SOX18, TCEA2,*
23	chrX	rs2405942	*GPR143, LOC100288814, SHROOM2, TBL1X, WWC3,*	*CLCN4,*

Regions were defined by either SNPs r2<0.2 or a 500kb window, using whichever boundary was the furthest. For pathway analysis we also used the genes from a 1 Mb window.

Supplementary Table 7

HOXB13 hits (rs138213197, rs11650494)

Analysis performed in subset of CAPS comprising 1927 cases and 987 controls. Markers explored under a dominant genetic model in logistic regression analysis.

Correlation: r^2=0.001, D'=0.056

Association:

				Univariate		Mutually adjusted	
Marker	Alleles	MA	MAF	OR (95% CI)	*P* value	OR (95% CI)	*P* value
rs138213197	C/T	C	0.017	2.77 (1.59 to 4.84)	0.00034	2.75 (1.57 to 4.80)	0.00038
rs11650494	G/A	A	0.062	1.28 (1.00 to 1.64)	0.046	1.28 (1.00 to 1.65)	0.048

MA minor allele
MAF minor allele frequency

The University of Michigan recently completed a GWAS for 931 men of European descent diagnosed with PrCa prior to age 56 years. Twenty-three of the affected men were determined to carry the *HOXB13* G84E mutation, all on the same founder haplotype; rs11650494 was not directly genotyped. Genotype imputation was performed, using MACH, resulting in predicted high-quality genotype scores at rs11650494 (r^2=0.97) and a proxy genotyped SNP rs7216993 (r^2 = 0.83 with rs11650494 based on 1000 Genomes) was identified. Twenty-two of the 23 G84E carriers were homozygous for the common *non-risk* allele at rs11950494 (unambiguously predicted based on imputation) and rs7216993 (Lange and Cooney; *personal communication*). These findings indicate that the association of rs11650494 with PrCa is not due to confounding with *HOXB13* G84E and that multiple PrCa susceptibility variants in the *HOXB13* region may exist, conferring different risks.

Supplementary Table 8:

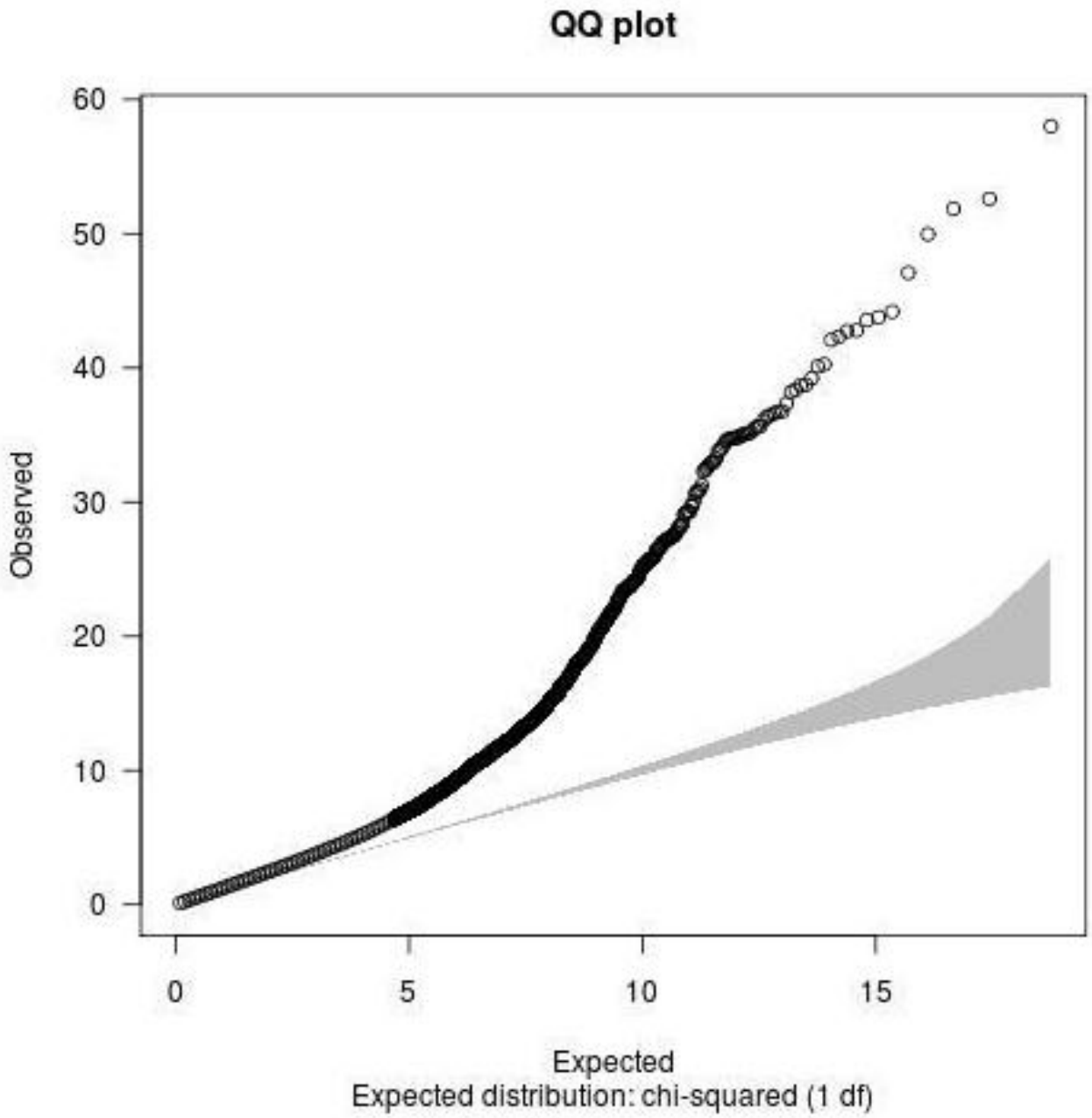
Relative Risk Estimation Using 68 known PrCa susceptibility loci*

Percentiles	RR	RR
< 1%	1 (baseline)	0.16 (.11-.24)
1-10%	2.15 (1.43-3.23)	0.35 (.32-.39)
10-25%	3.31 (2.22-4.94)	0.54 (.50-.58)
25-75%	6.10 (4.11-9.07)	1 (baseline)
75-90%	10.35 (6.95-15.42)	1.70 (1.60-1.80)
90-99%	16.14 (10.83-24.07)	2.64 (2.48-2.82)
>= 99%	26.88 (17.54-41.20)	4.40 (3.74-5.19)

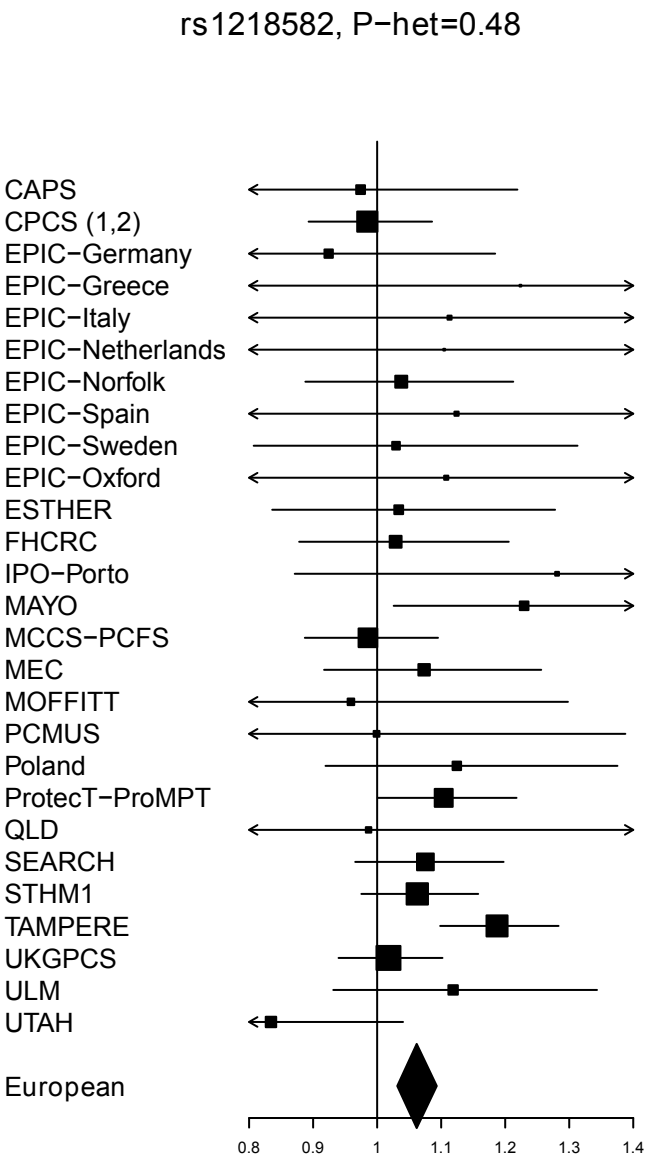
* PRACTICAL European samples in iCOGS were used for risk estimation and for 9 out of 68 SNPs, a proxy with r2 greater than 0.76 was used.

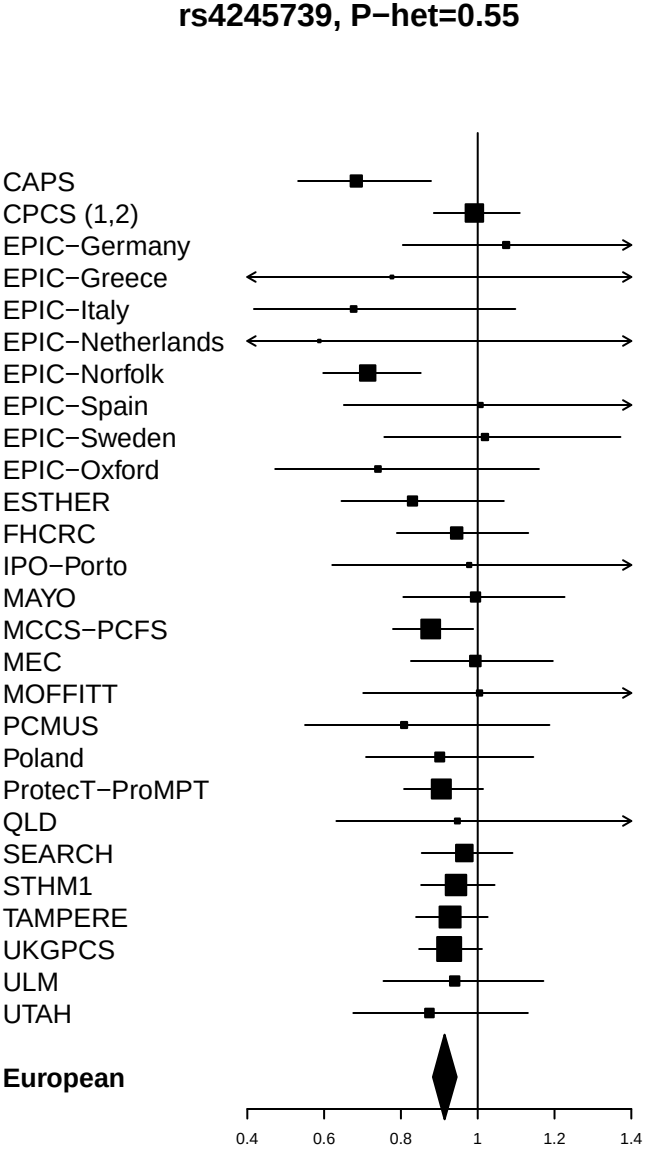
Supplementary Figure 1

This shows the Quantile-Quantile (Q-Q) plot for SNPs selected from combined GWAS excluding fine mapping and candidate SNPs

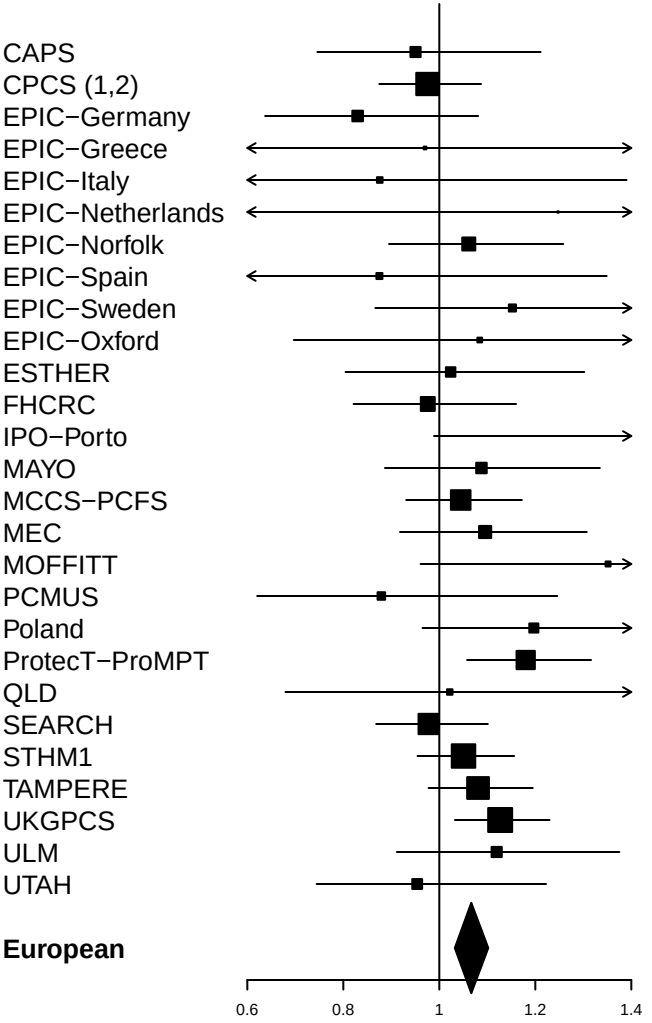


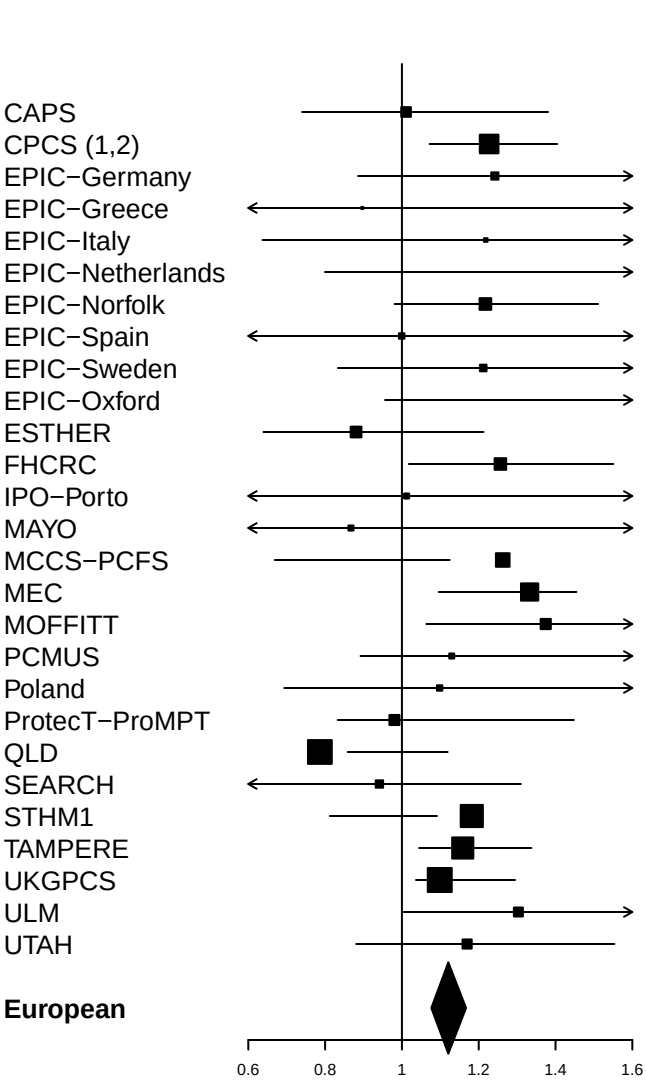
Supplementary Figure 2 - Forest plots showing the point estimates and 95% CI in each study for each of the 23 new loci. The size of the square reflects the size of the study.



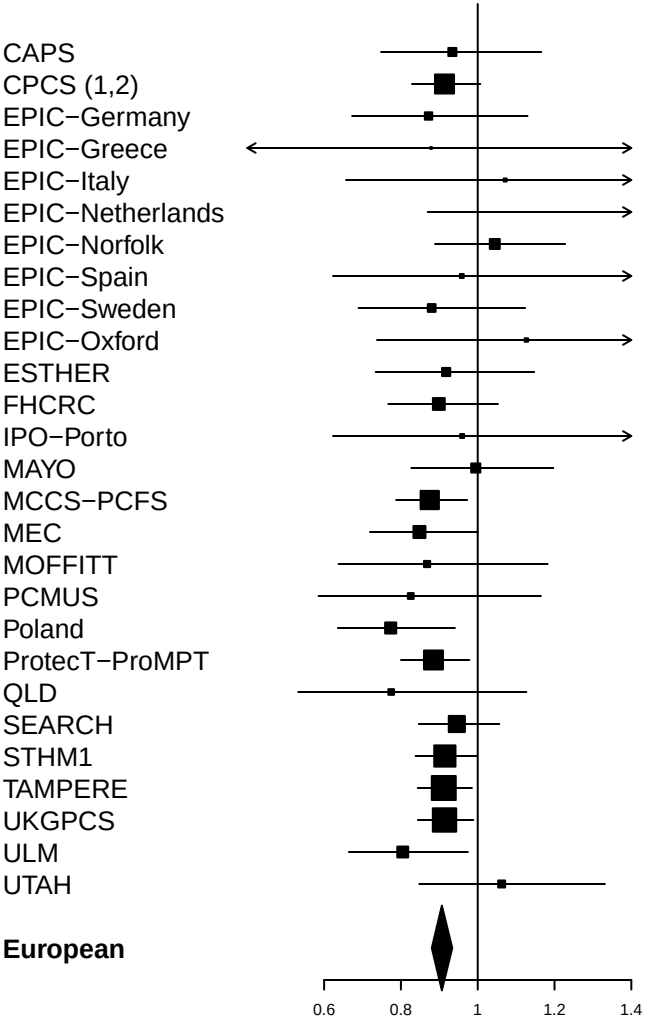

rs4245739, P−het=0.55
CAPS
CPCS (1,2)
EPIC−Germany
EPIC−Greece
EPIC−Italy
EPIC−Netherlands
EPIC−Norfolk
EPIC−Spain
EPIC−Sweden
EPIC−Oxford
ESTHER
FHCRC
IPO−Porto
MAYO
MCCS−PCFS
MEC
MOFFITT
PCMUS
Poland
ProtecT−ProMPT
QLD
SEARCH
STHM1
TAMPERE
UKGPCS
ULM
UTAH
European
0.4
0.6
0.8
1
1.2
1.4

rs11902236, P−het=0.52

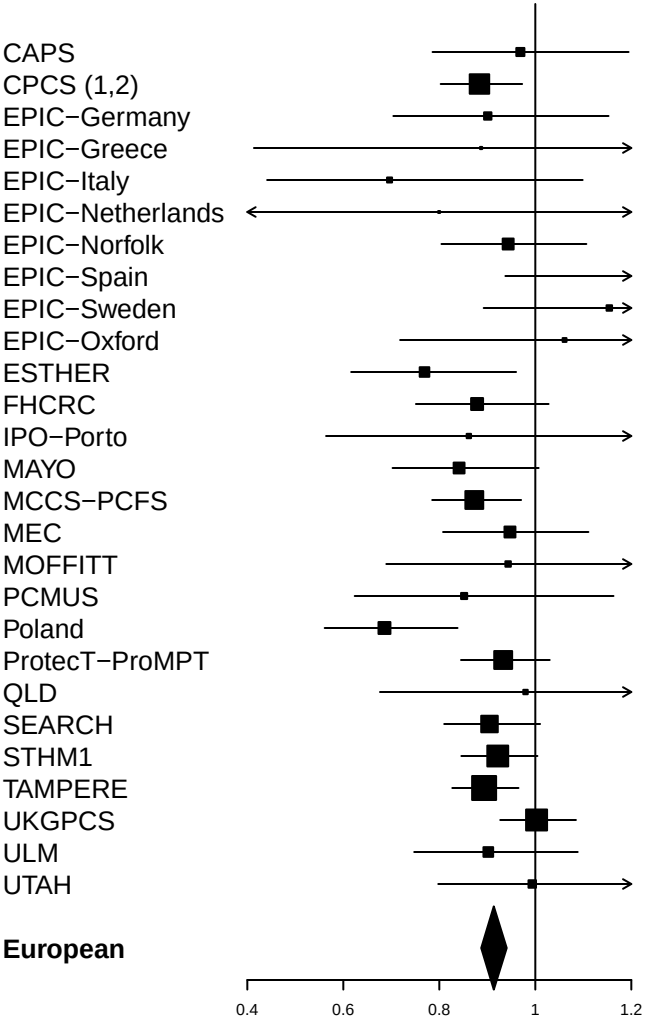



rs3771570, P−het=0.12
CAPS
CPCS (1,2)
EPIC−Germany
EPIC−Greece
EPIC−Italy
EPIC−Netherlands
EPIC−Norfolk
EPIC−Spain
EPIC−Sweden
EPIC−Oxford
ESTHER
FHCRC
IPO−Porto
MAYO
MCCS−PCFS
MEC
MOFFITT
PCMUS
Poland
ProtecT−ProMPT
QLD
SEARCH
STHM1
TAMPERE
UKGPCS
ULM
UTAH
European
0.6
0.8
1
1.2
1.4
1.6

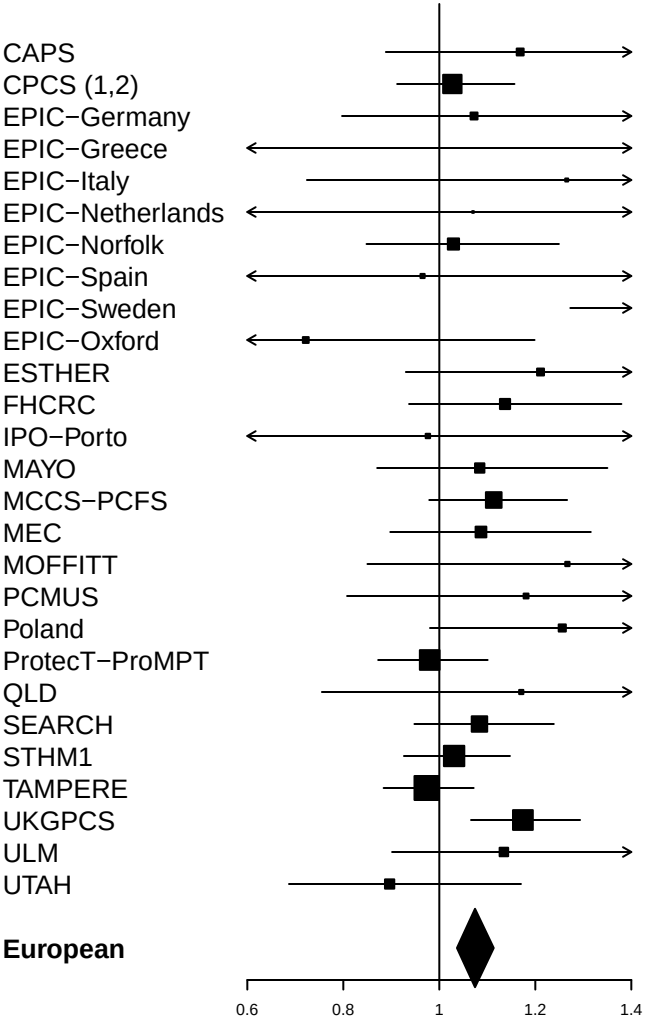
rs7611694, P−het=0.87



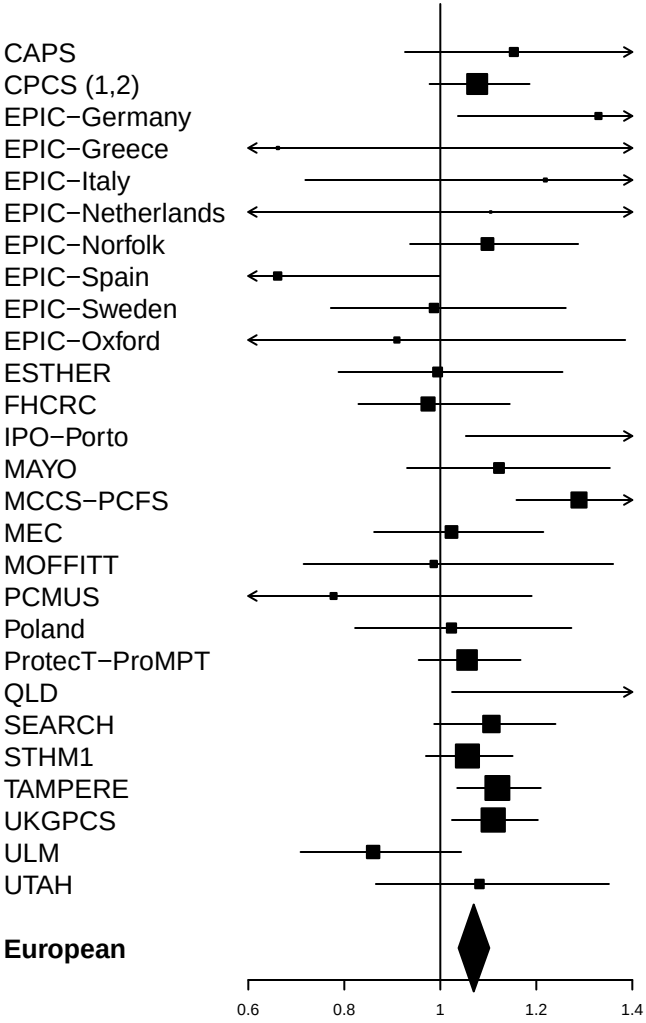
rs1894292, P−het=0.29

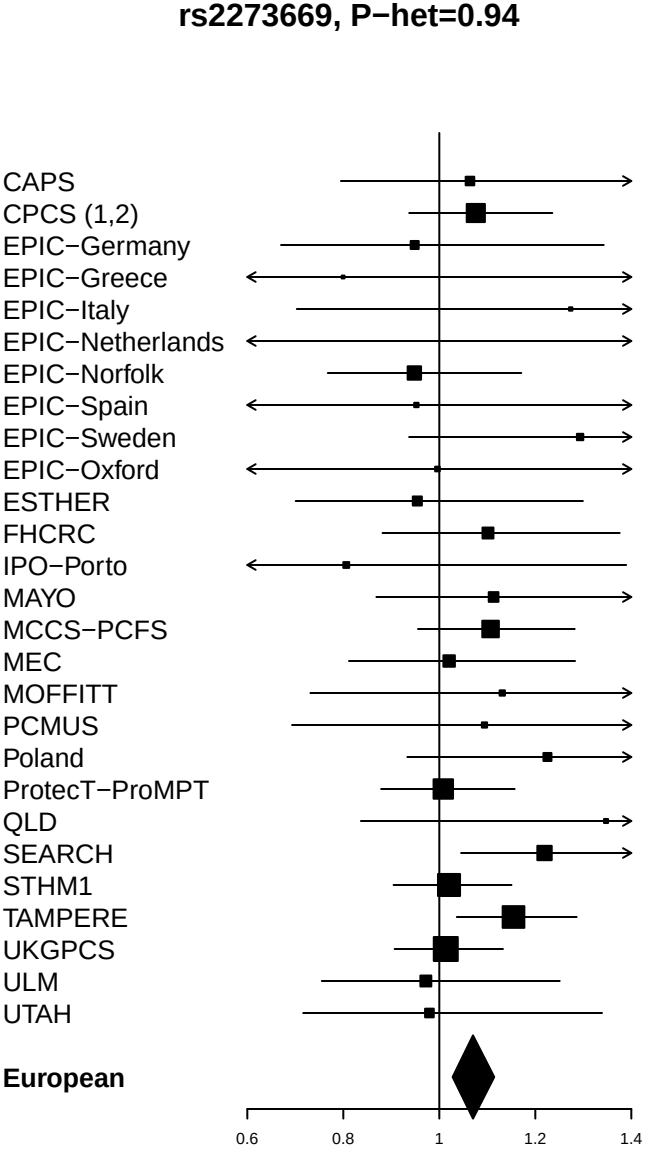


rs6869841, P−het=0.29

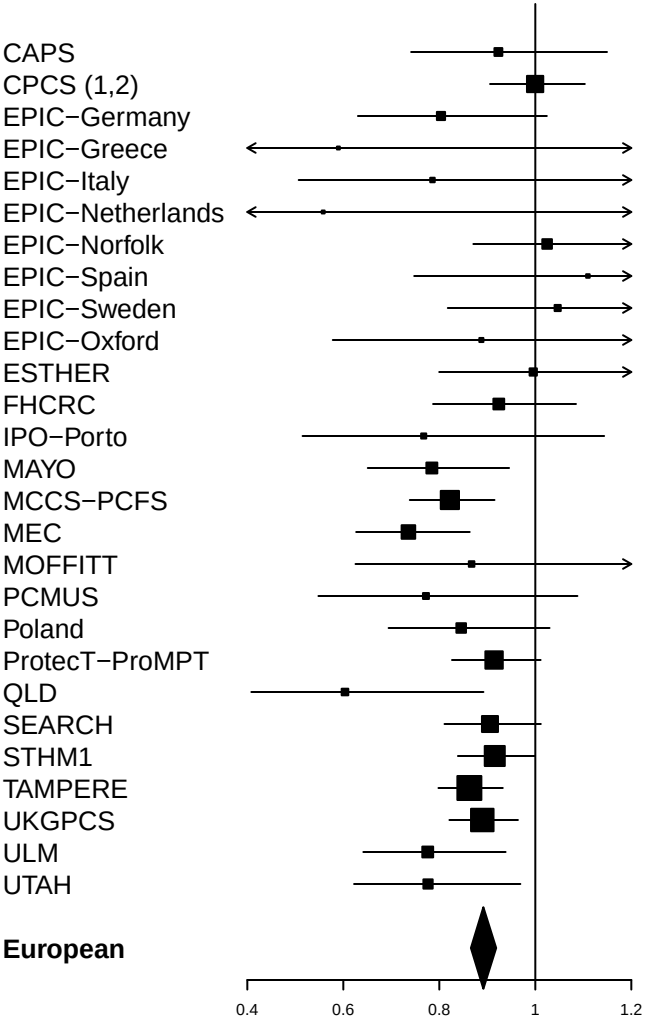


rs3096702, P−het=0.04

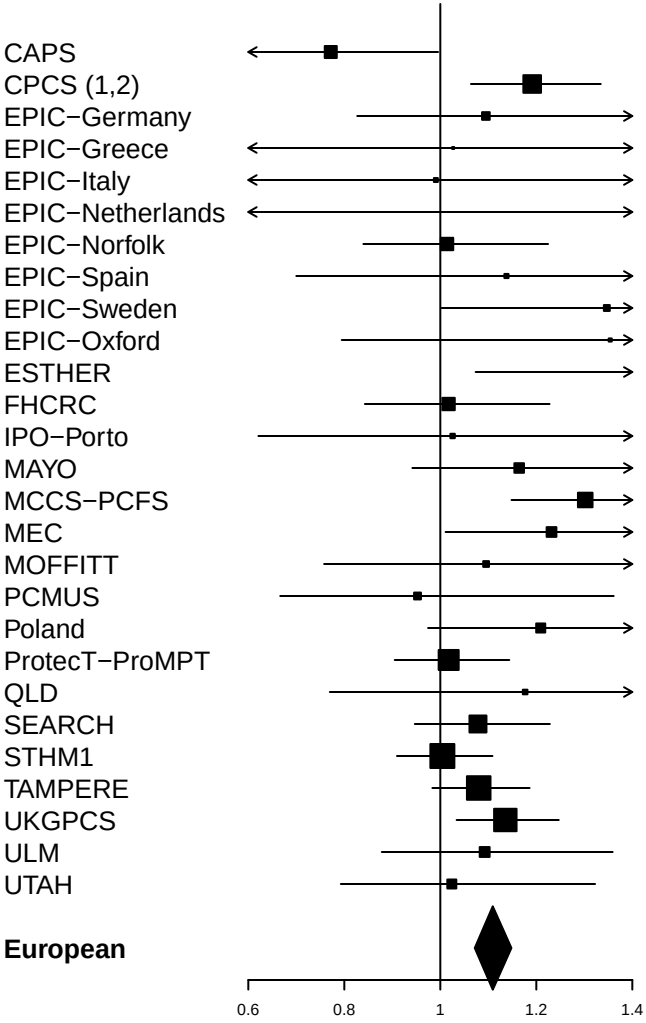



rs2273669, P−het=0.94
CAPS
CPCS (1,2)
EPIC−Germany
EPIC−Greece
EPIC−Italy
EPIC−Netherlands
EPIC−Norfolk
EPIC−Spain
EPIC−Sweden
EPIC−Oxford
ESTHER
FHCRC
IPO−Porto
MAYO
MCCS−PCFS
MEC
MOFFITT
PCMUS
Poland
ProtecT−ProMPT
QLD
SEARCH
STHM1
TAMPERE
UKGPCS
ULM
UTAH
European
0.6
0.8
1
1.2
1.4

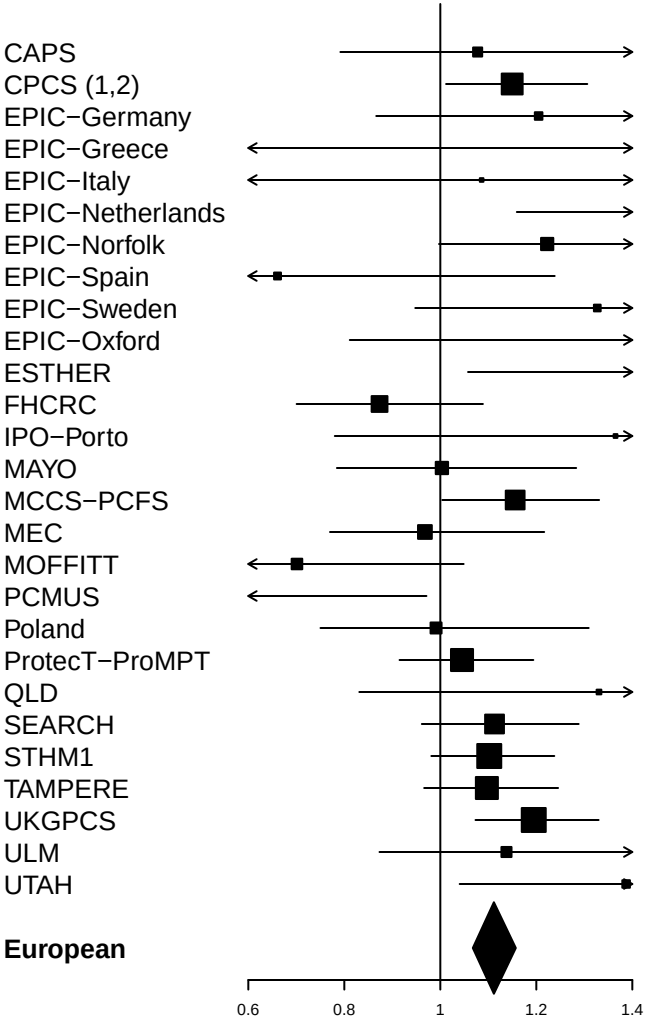
rs1933488, P−het=0.12



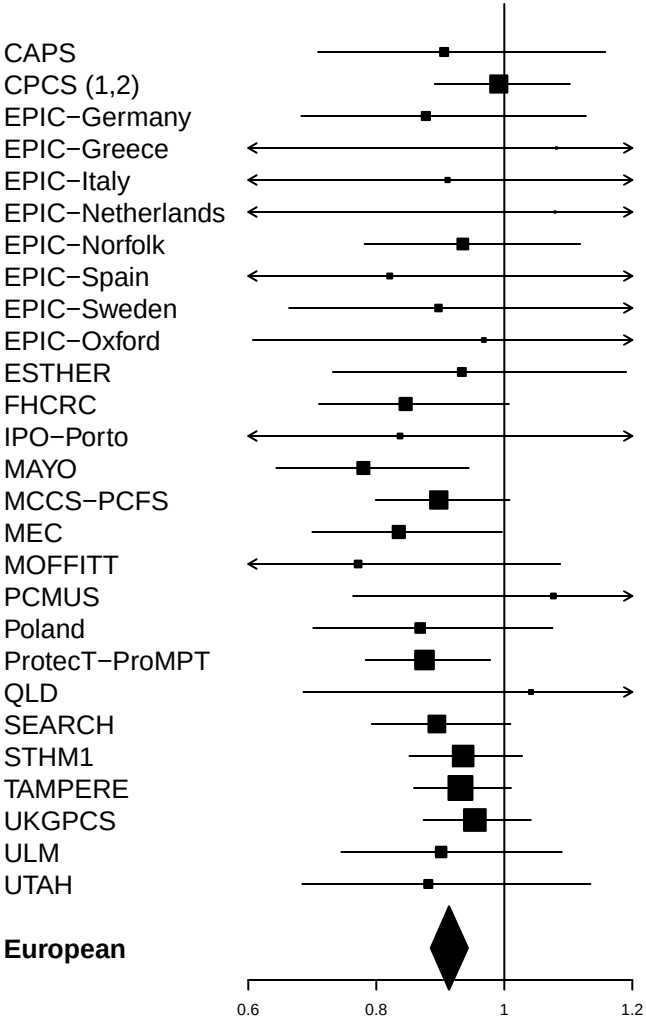
rs12155172, P−het=0.14



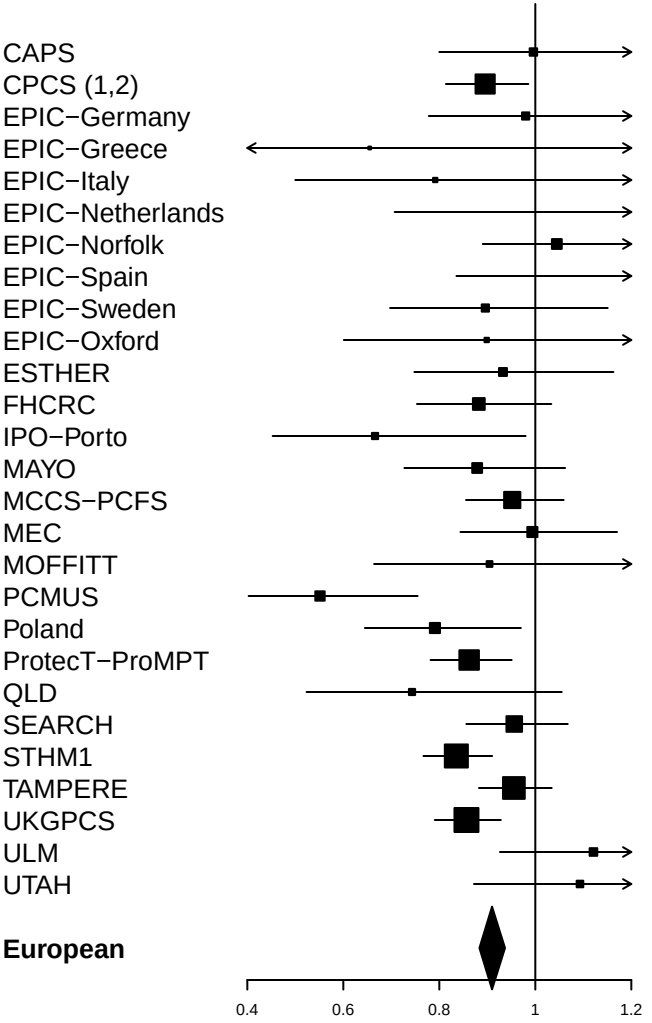
rs11135910, P−het=0.06



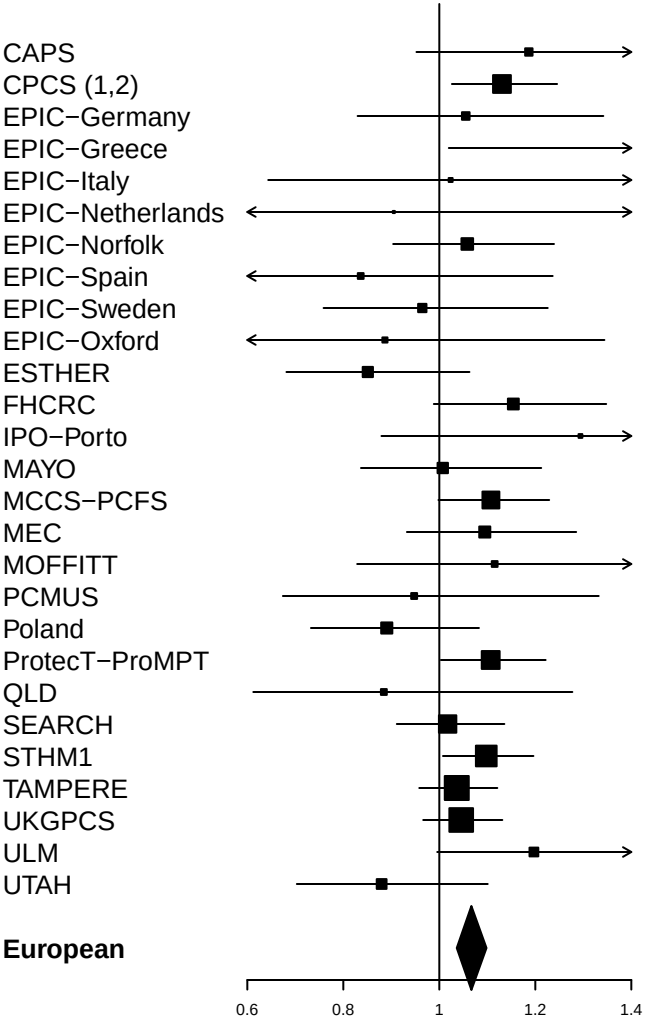
rs3850699, P−het=0.99



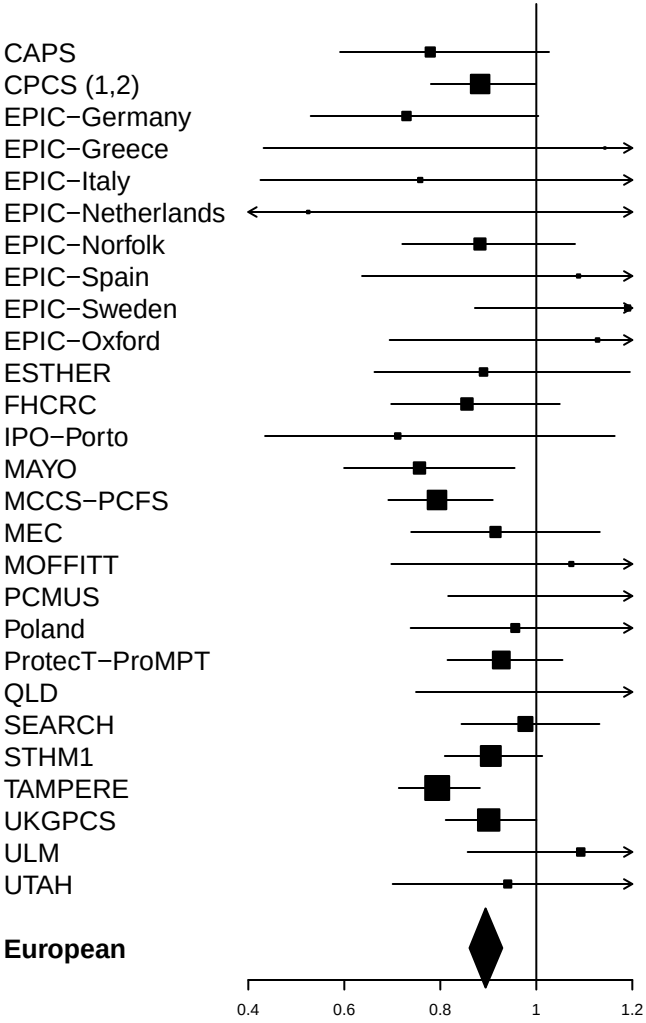
rs11568818, P−het=0.02



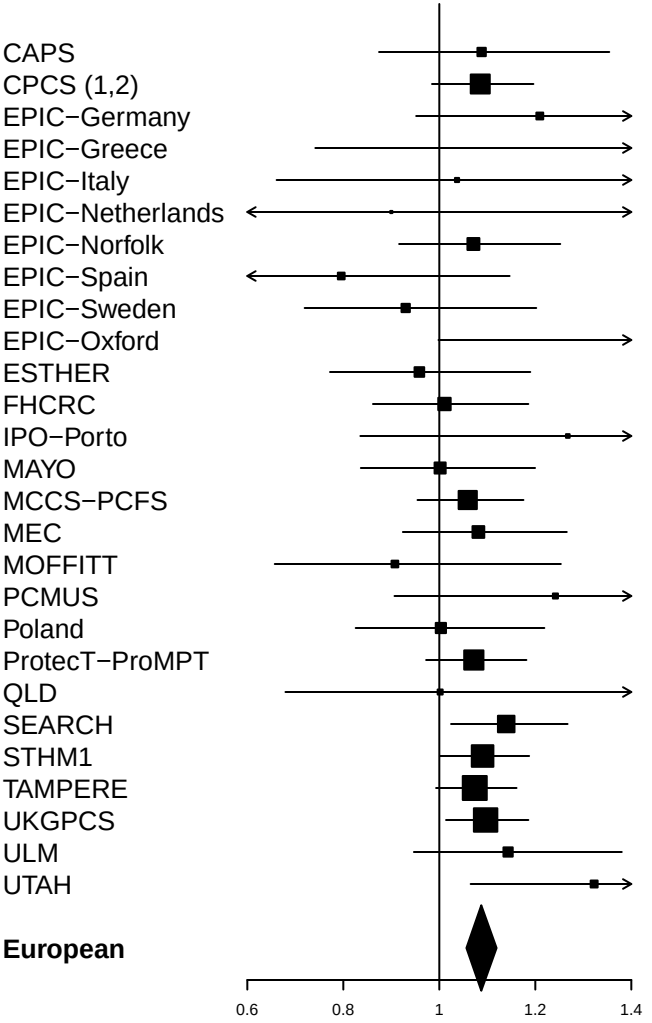
rs1270884, P−het=0.39



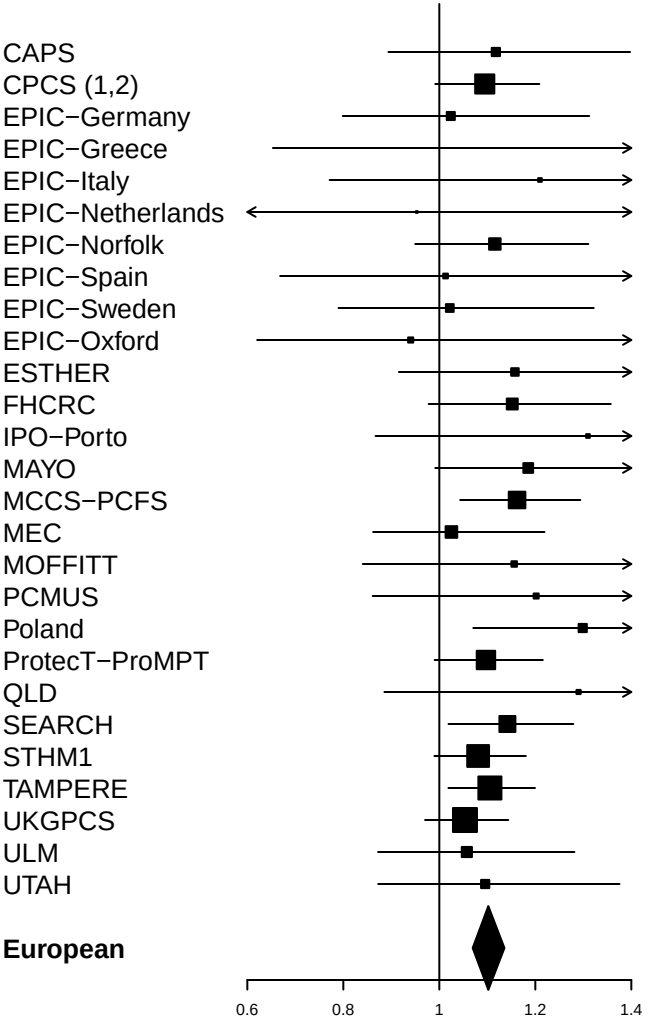
rs8008270, P−het=0.33



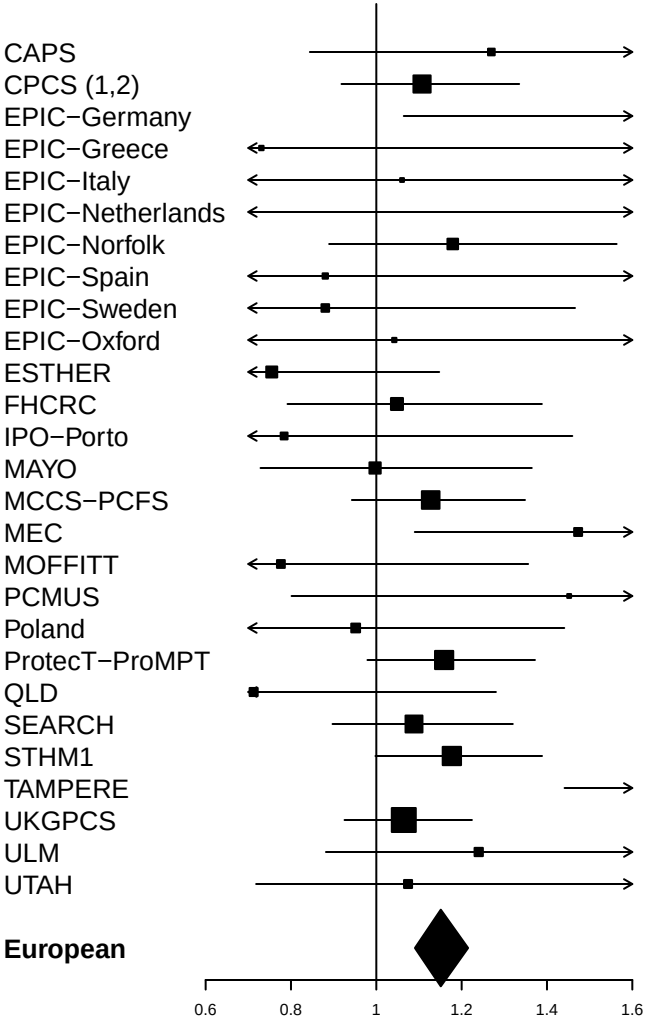
rs7141529, P−het=0.81



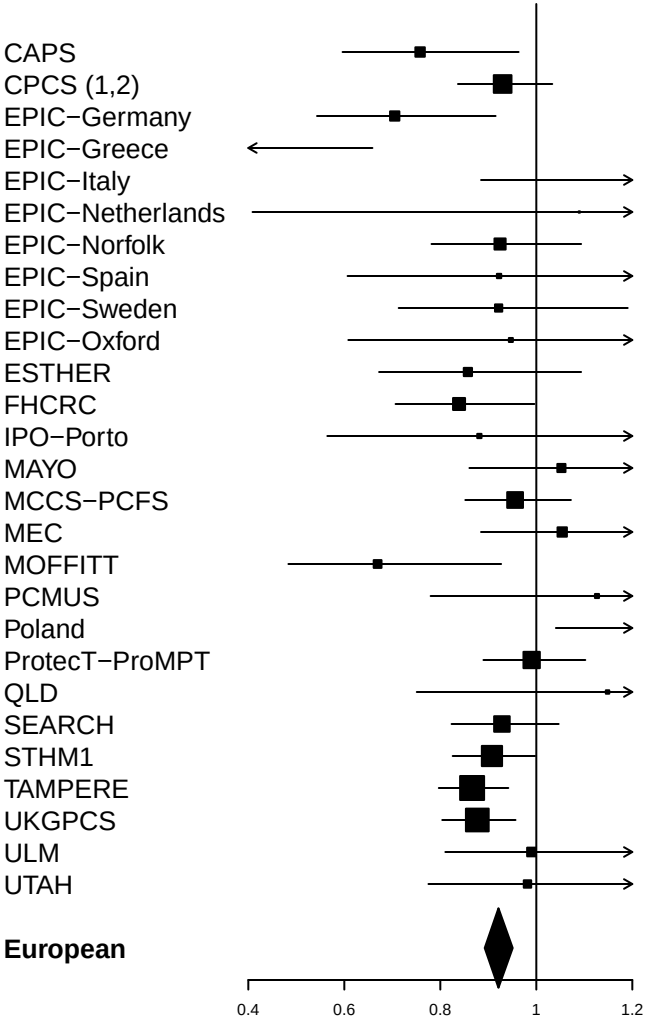
rs684232, P−het=0.99

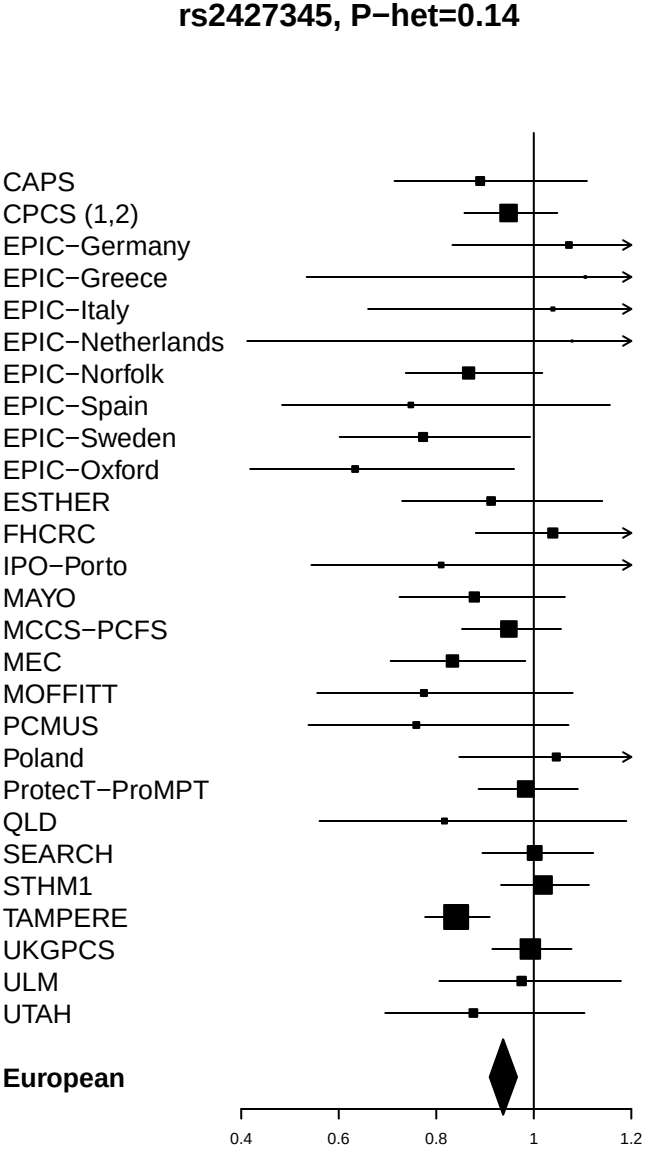


rs11650494, P−het=0.02

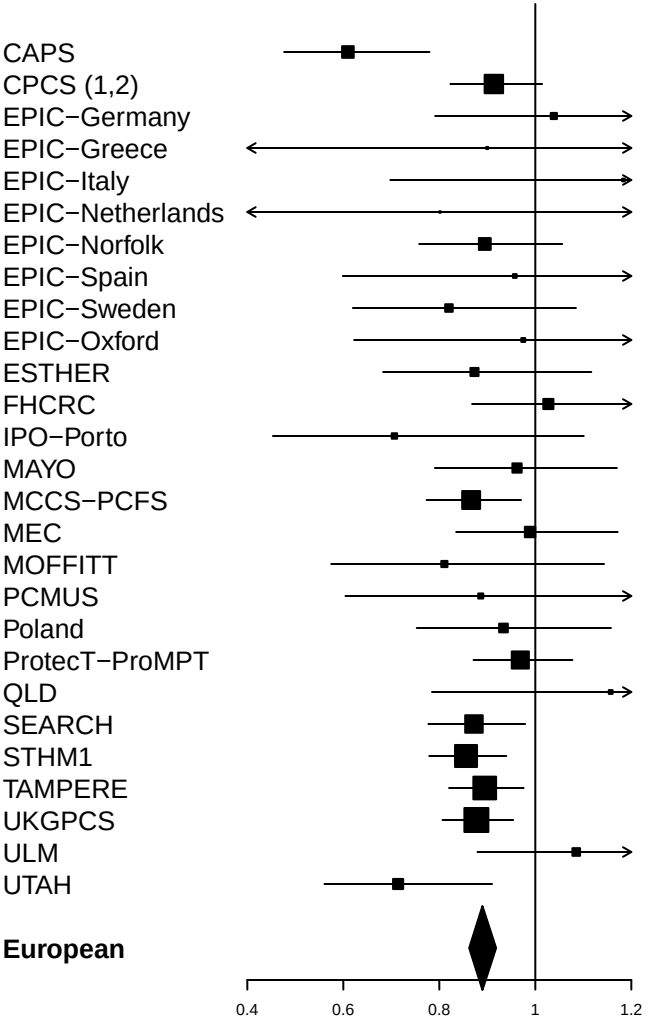


rs7241993, P−het=0.01

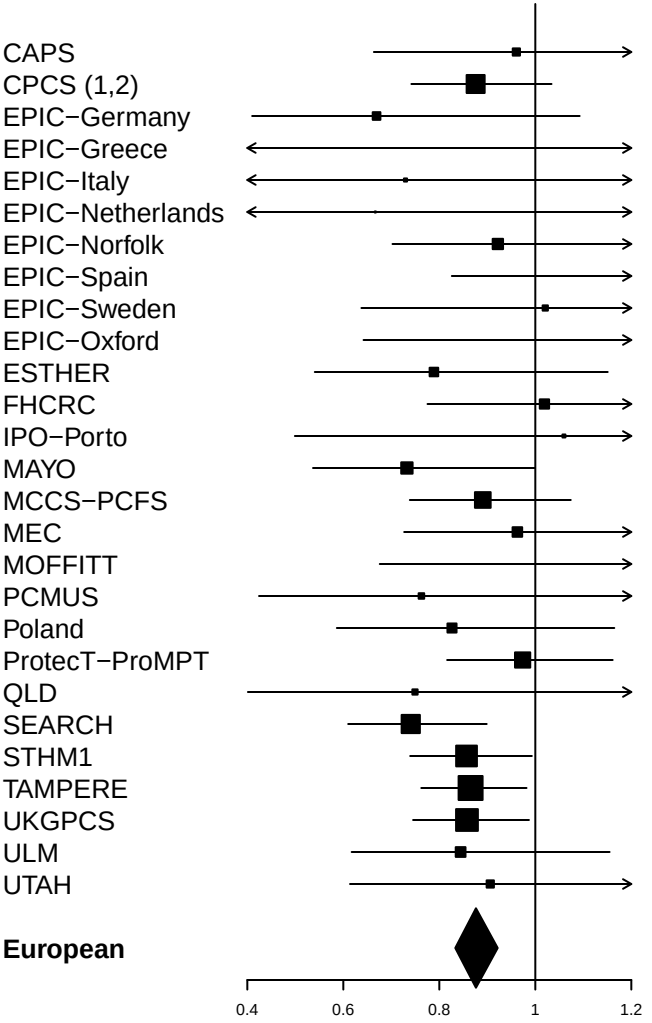



rs2427345, P−het=0.14
CAPS
CPCS (1,2)
EPIC−Germany
EPIC−Greece
EPIC−Italy
EPIC−Netherlands
EPIC−Norfolk
EPIC−Spain
EPIC−Sweden
EPIC−Oxford
ESTHER
FHCRC
IPO−Porto
MAYO
MCCS−PCFS
MEC
MOFFITT
PCMUS
Poland
ProtecT−ProMPT
QLD
SEARCH
STHM1
TAMPERE
UKGPCS
ULM
UTAH
European
0.4
0.6
0.8
1
1.2

rs6062509, P−het=0.25

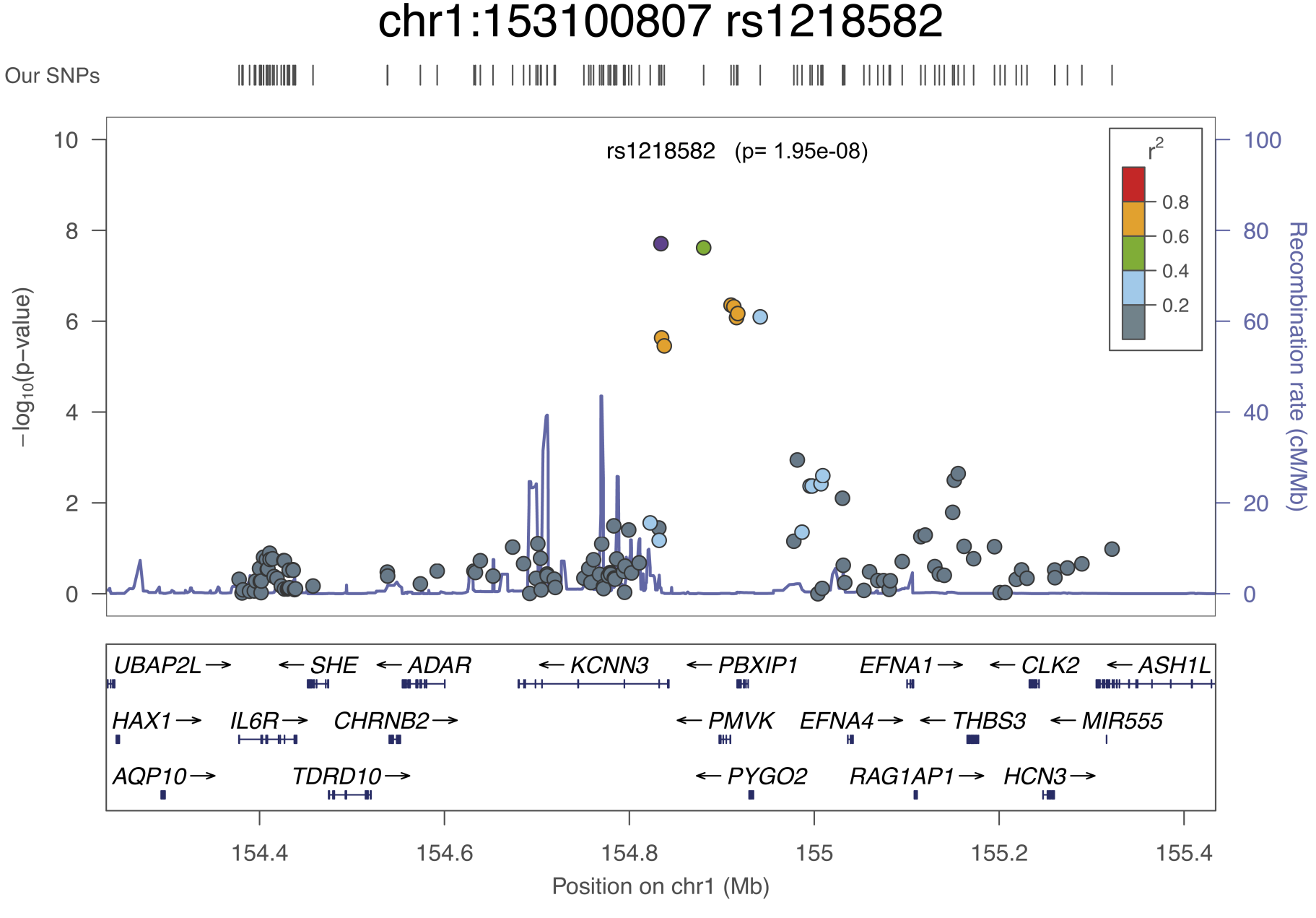


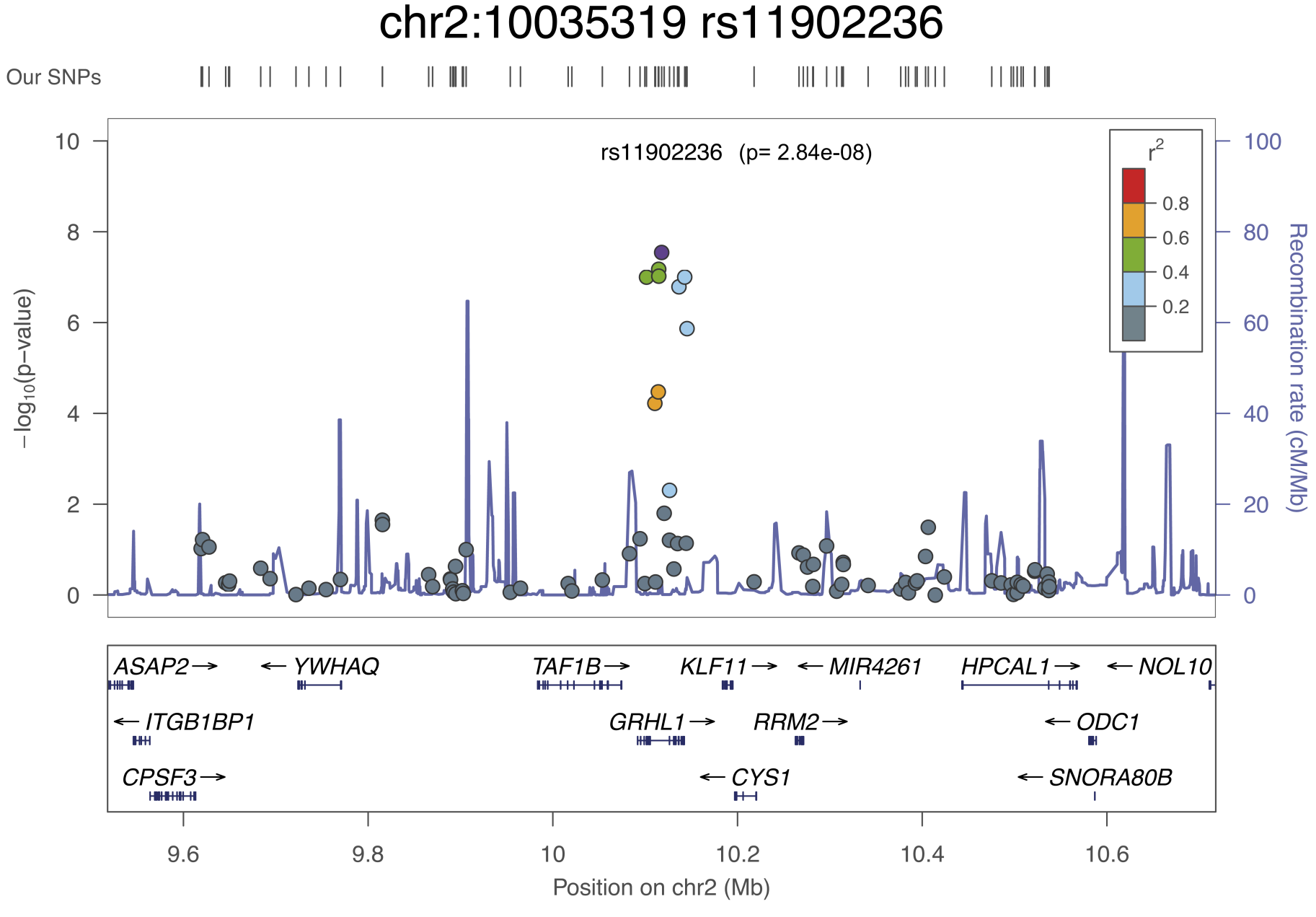
rs2405942, P−het=0.91

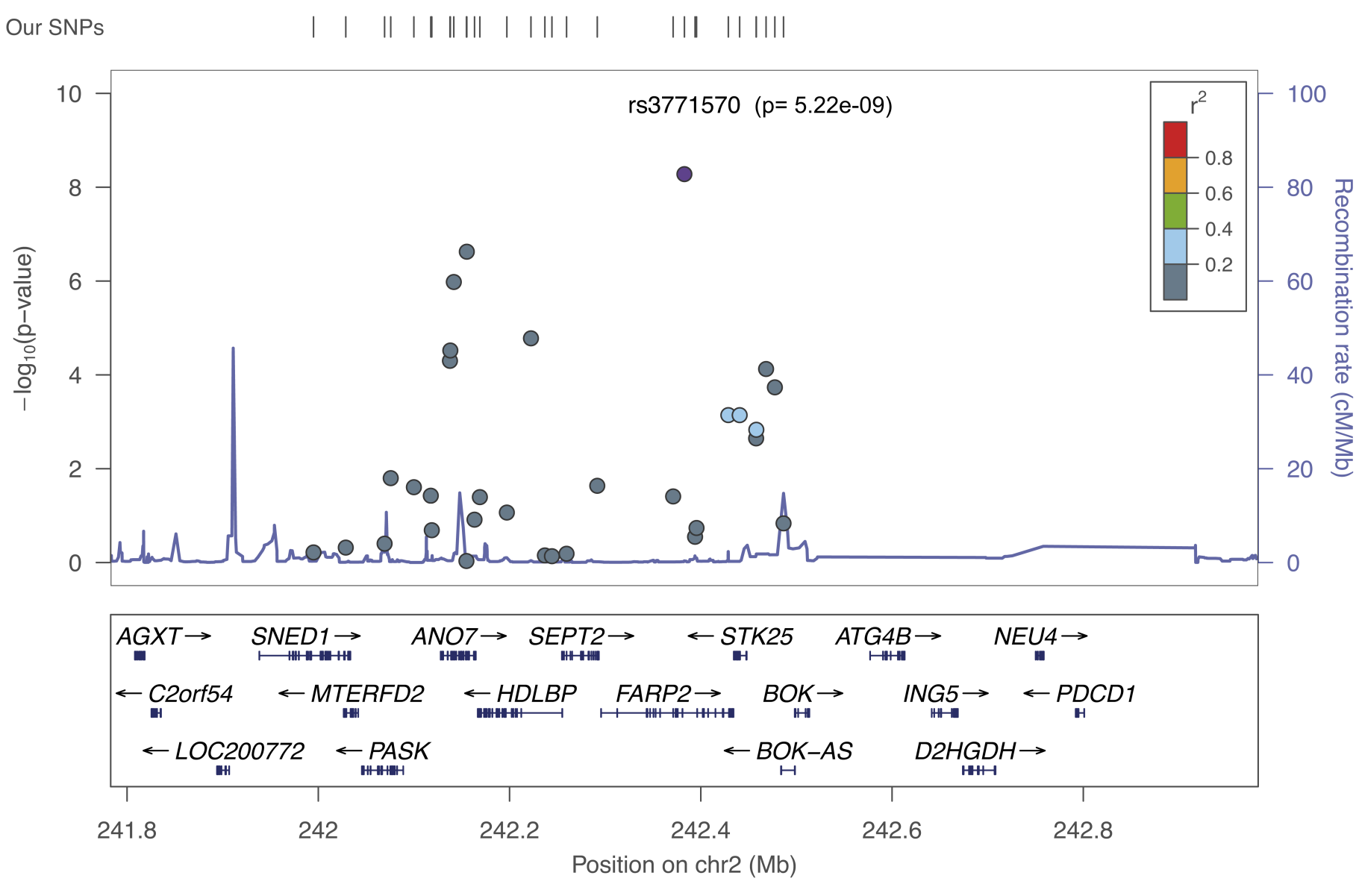


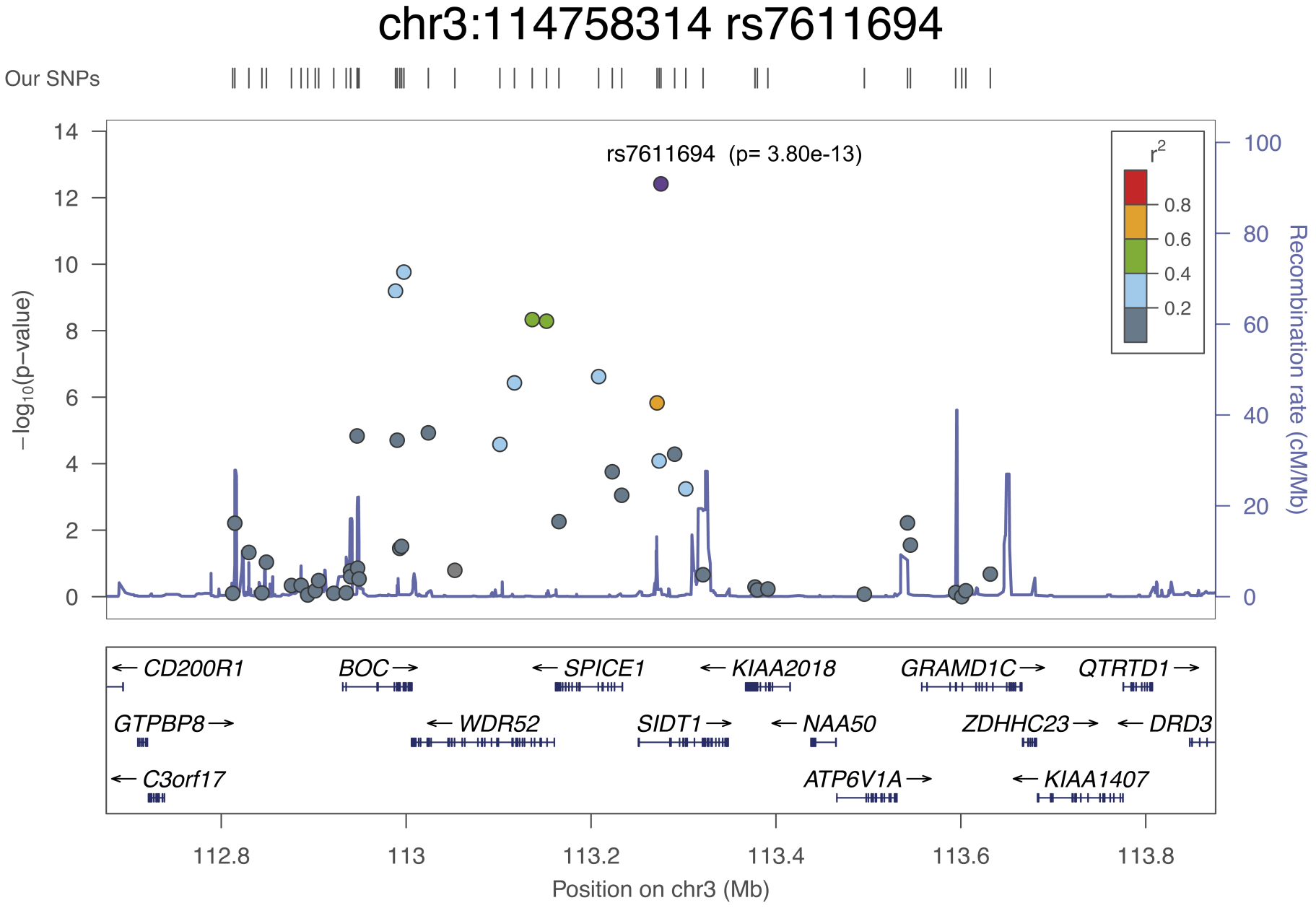
Supplementary Figure 3 (19 SNAP plots)

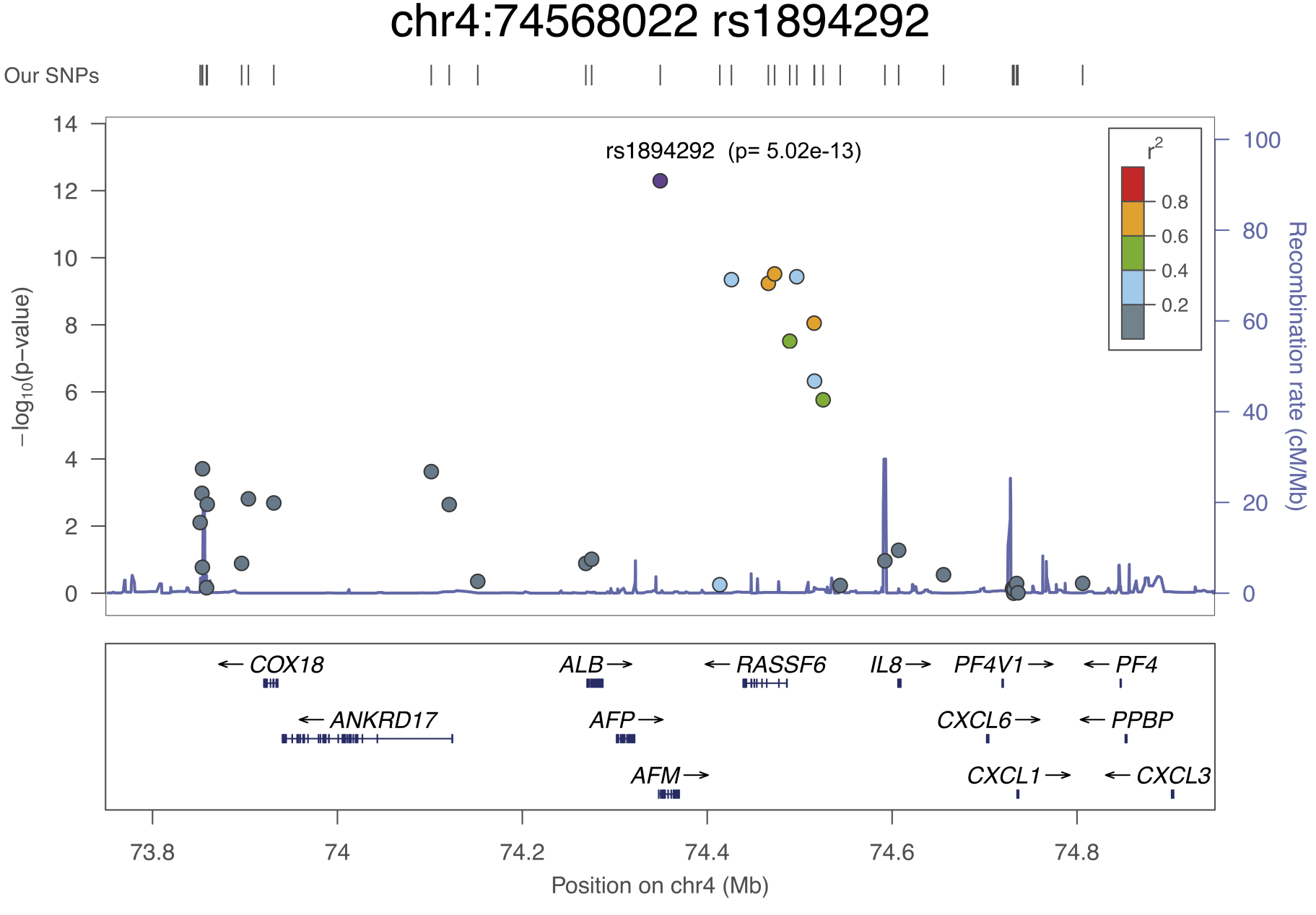
Regional plots of the 19 associated SNPs detailed in Table 1 excluding those shown in Figure 3. Plots show the genomic regions associated with PrCa and $-\log_{10}$ association *P* values of SNPs. Also shown are the SNP build 36/hg18 coordinates in kilobases, recombination rates and genes in the region. The intensity of red shading indicates the strength of LD (r^2) with the index SNP. Plots drawn using locus zoom command line options (University of Michigan) http://csg.sph.umich.edu/locuszoom/

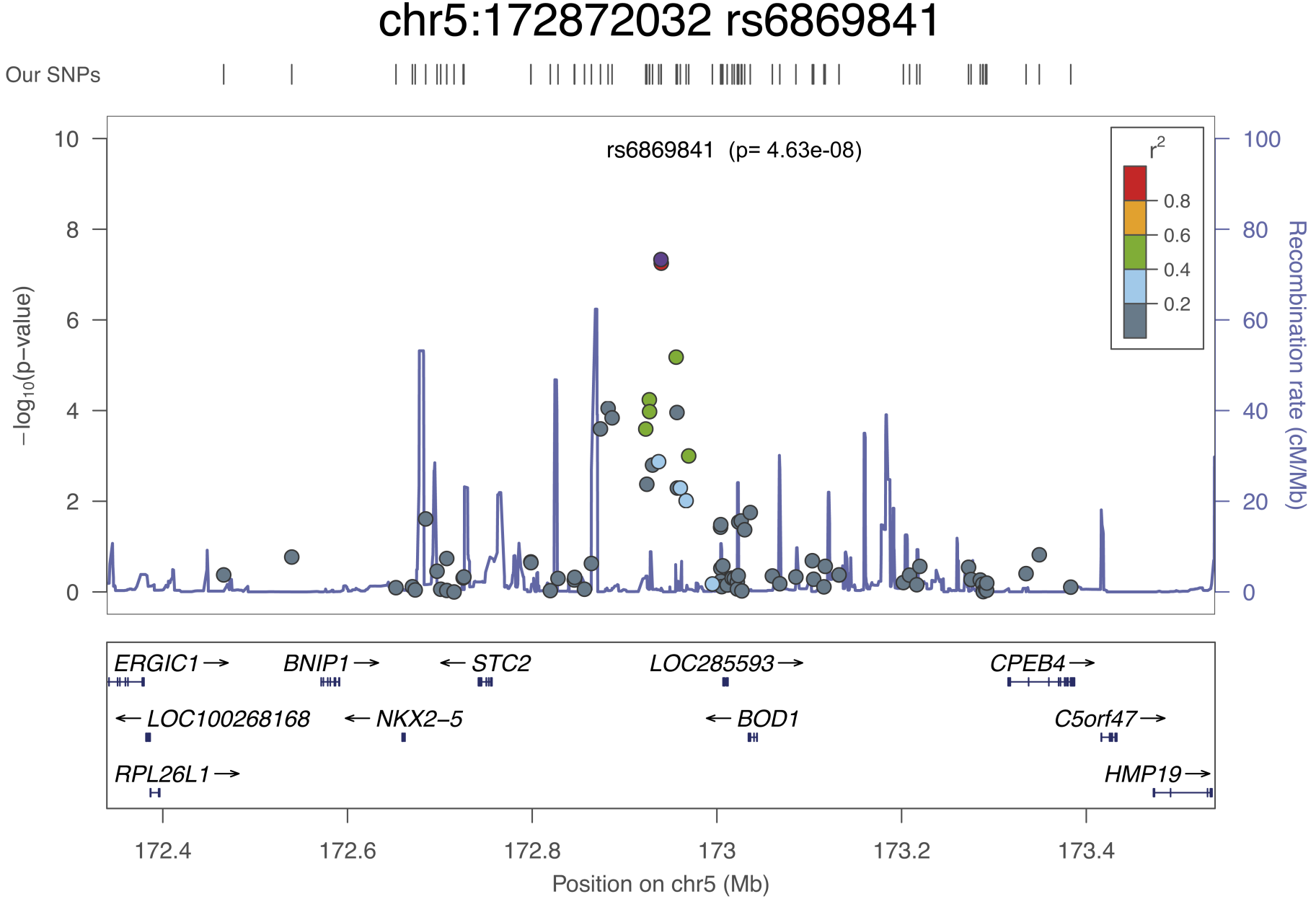

chr1:153100807 rs1218582
Our SNPs
rs1218582 (p= 1.95e-08)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
UBAP2L
SHE
ADAR
KCNN3
PBXIP1
EFNA1
CLK2
ASH1L
HAX1
IL6R
CHRNB2
PMVK
EFNA4
THBS3
MIR555
AQP10
TDRD10
PYGO2
RAG1AP1
HCN3
Position on chr1 (Mb)

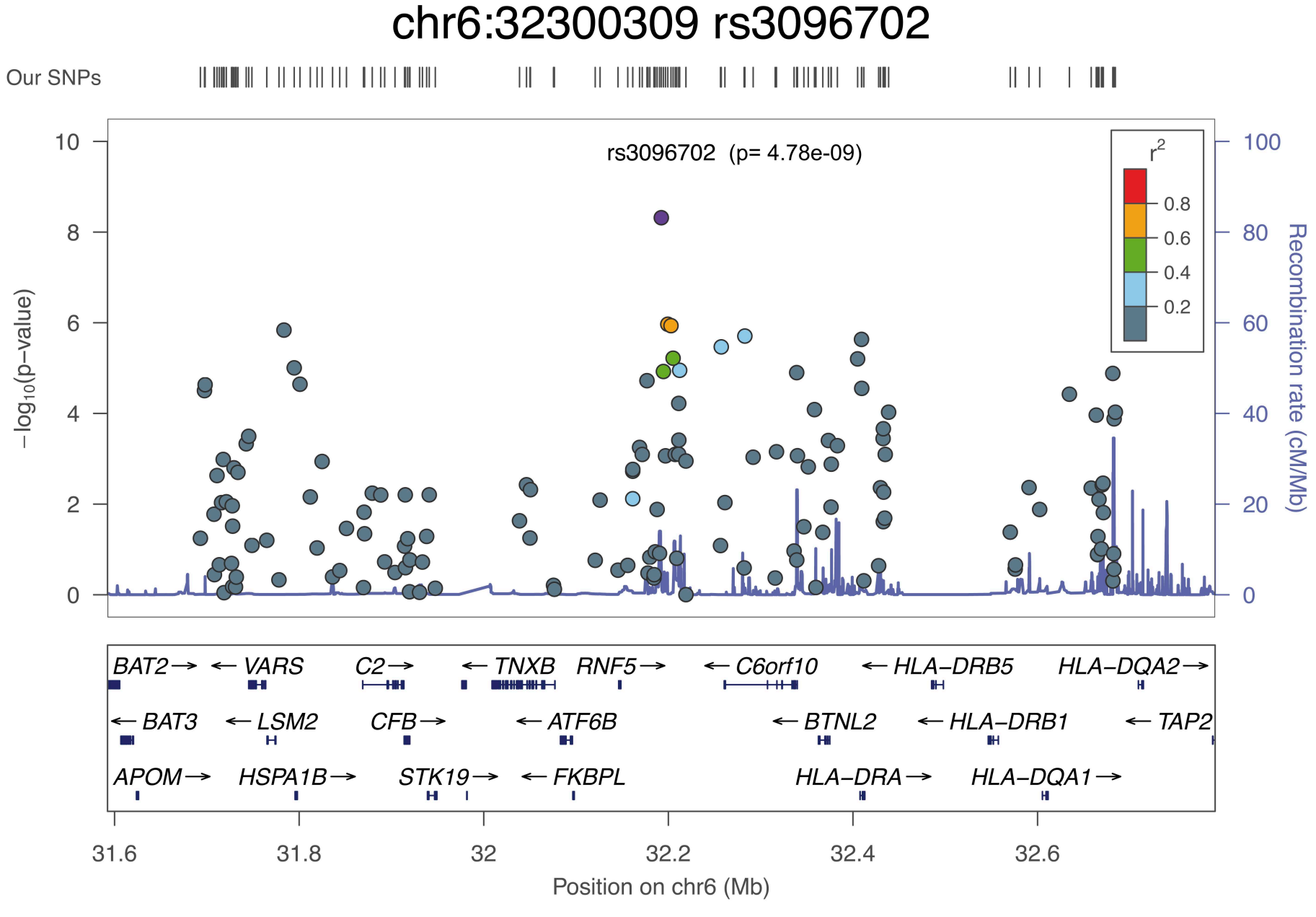

chr2:10035319 rs11902236
Our SNPs
rs11902236 (p= 2.84e-08)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ASAP2
YWHAQ
TAF1B
KLF11
MIR4261
HPCAL1
NOL10
ITGB1BP1
GRHL1
RRM2
ODC1
CPSF3
CYS1
SNORA80B
Position on chr2 (Mb)

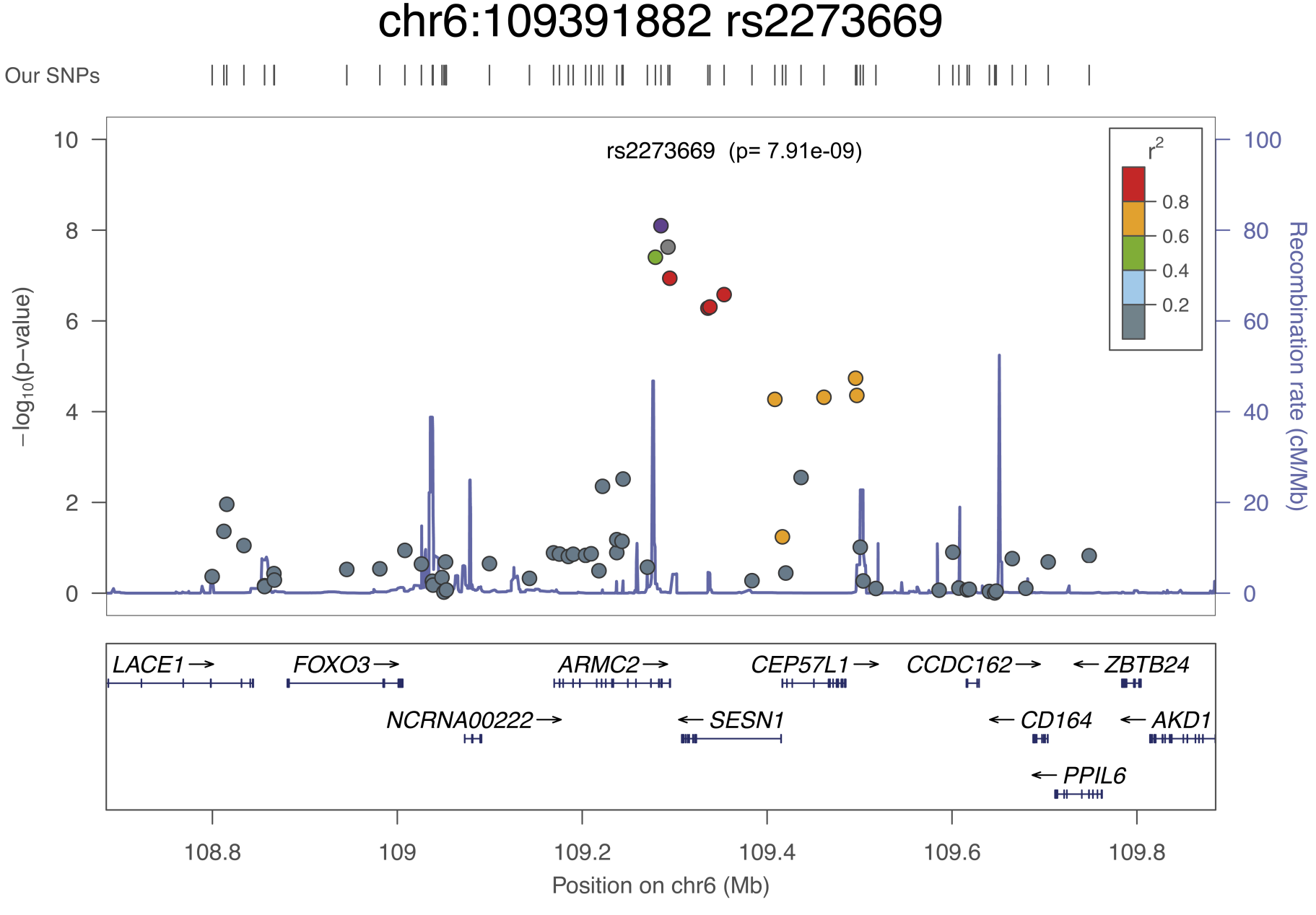

chr2:242031537 rs3771570
Our SNPs
rs3771570 (p= 5.22e-09)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
10
8
6
4
2
0
100
80
60
40
20
0
AGXT→
SNED1→
ANO7→
SEPT2→
←STK25
ATG4B→
NEU4→
←C2orf54
←MTERFD2
←HDLBP
FARP2→
BOK→
ING5→
←PDCD1
←LOC200772
←PASK
←BOK−AS
D2HGDH→
241.8
242
242.2
242.4
242.6
242.8
Position on chr2 (Mb)

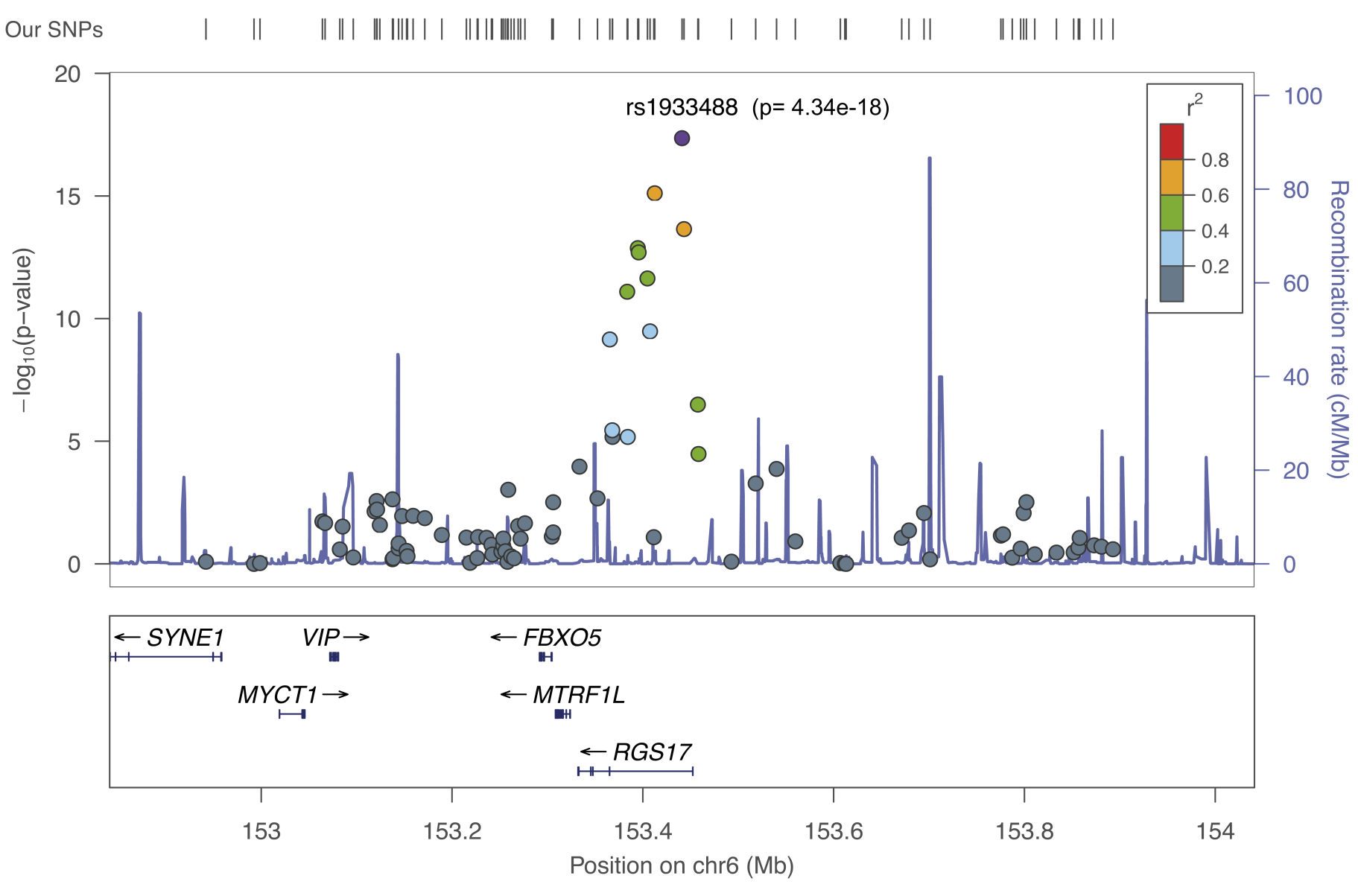

chr3:114758314 rs7611694
Our SNPs
rs7611694 (p= 3.80e-13)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
CD200R1
BOC
SPICE1
KIAA2018
GRAMD1C
QTRTD1
GTPBP8
WDR52
SIDT1
NAA50
ZDHHC23
DRD3
C3orf17
ATP6V1A
KIAA1407
Position on chr3 (Mb)

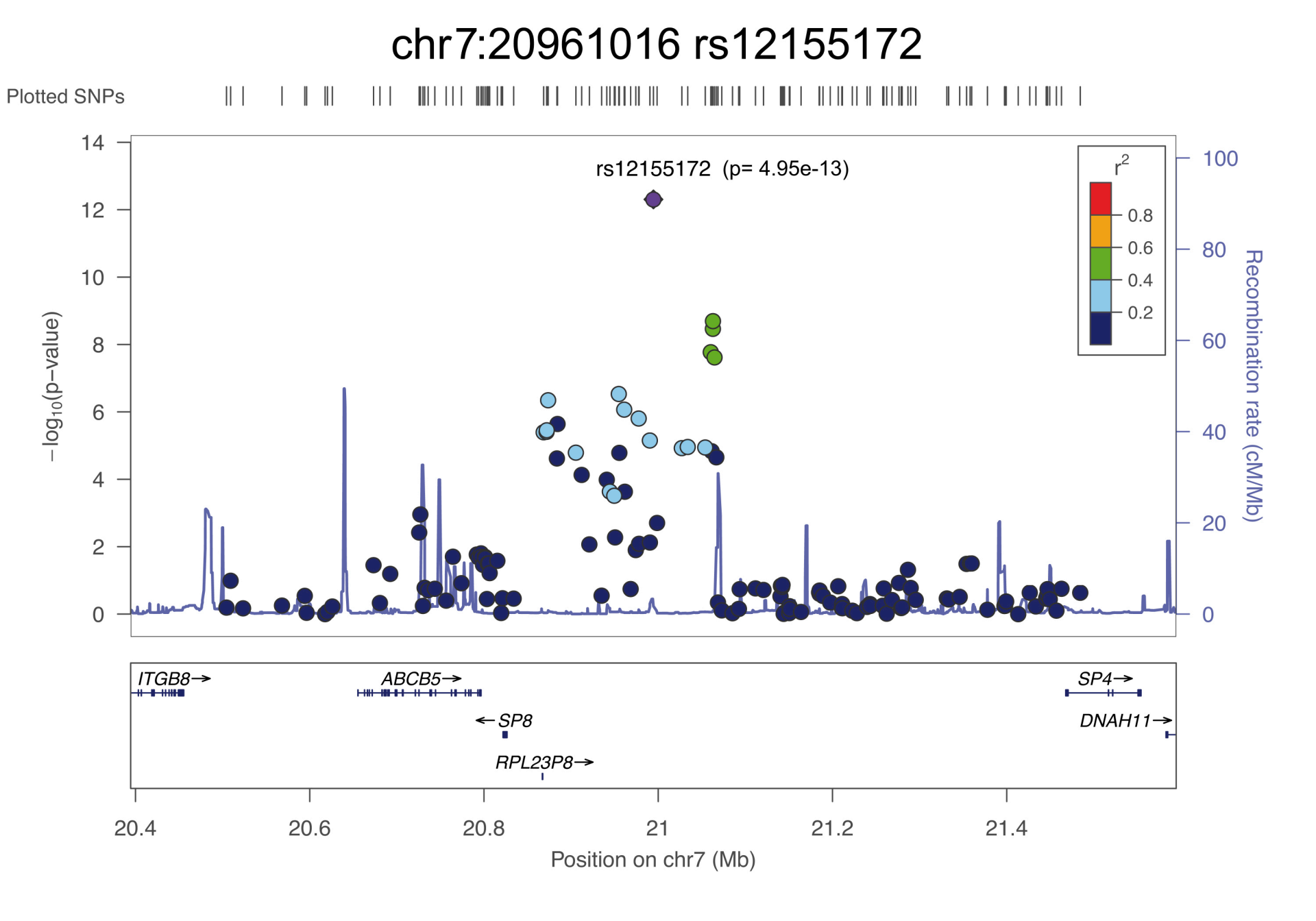

chr4:74568022 rs1894292
Our SNPs
rs1894292 (p= 5.02e-13)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
COX18
ALB
RASSF6
IL8
PF4V1
PF4
ANKRD17
AFP
CXCL6
PPBP
AFM
CXCL1
CXCL3
Position on chr4 (Mb)

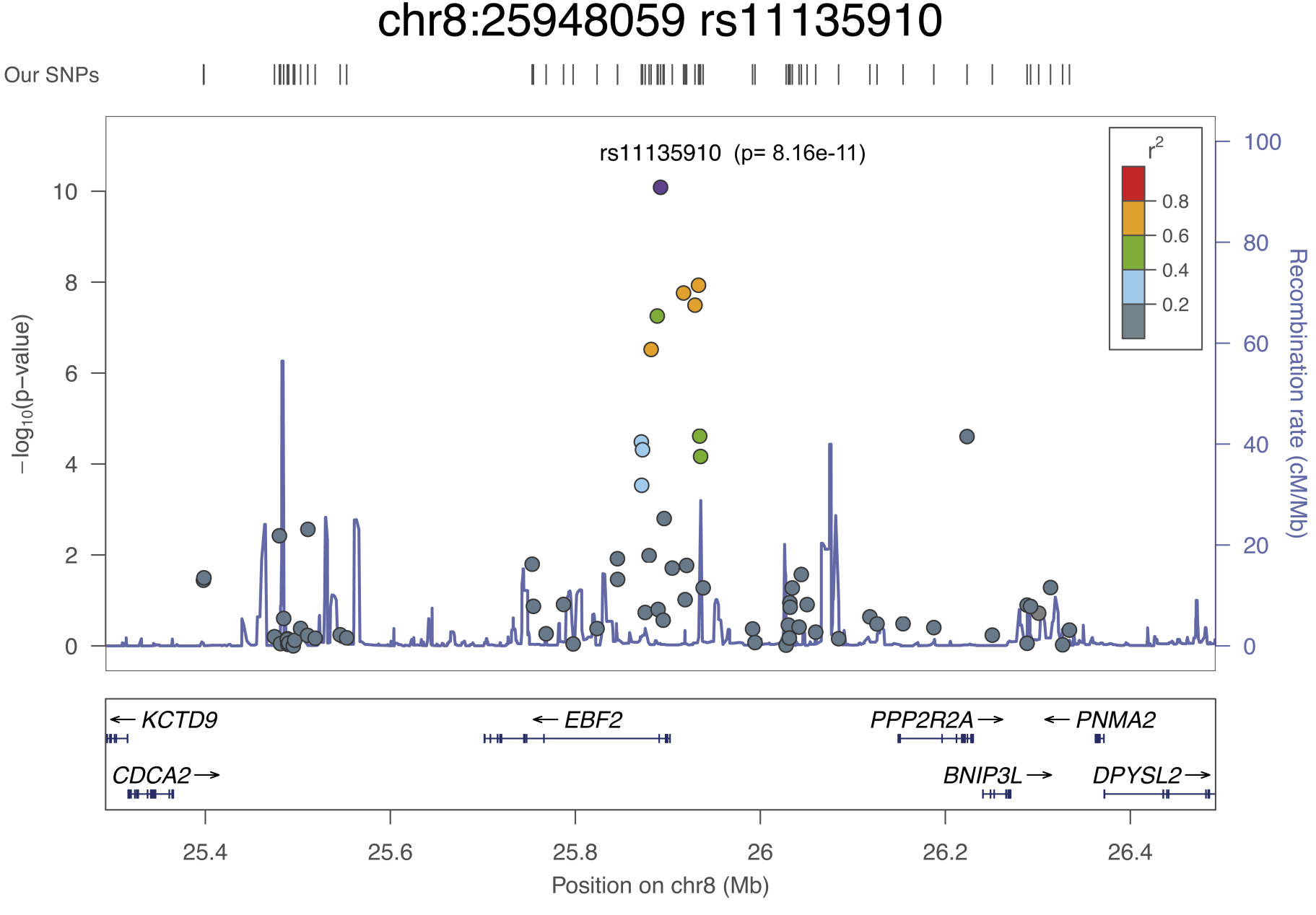

chr5:172872032 rs6869841
Our SNPs
rs6869841 (p= 4.63e-08)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ERGIC1
BNIP1
STC2
LOC285593
CPEB4
LOC100268168
NKX2−5
BOD1
C5orf47
RPL26L1
HMP19
172.4
172.6
172.8
173
173.2
173.4
Position on chr5 (Mb)

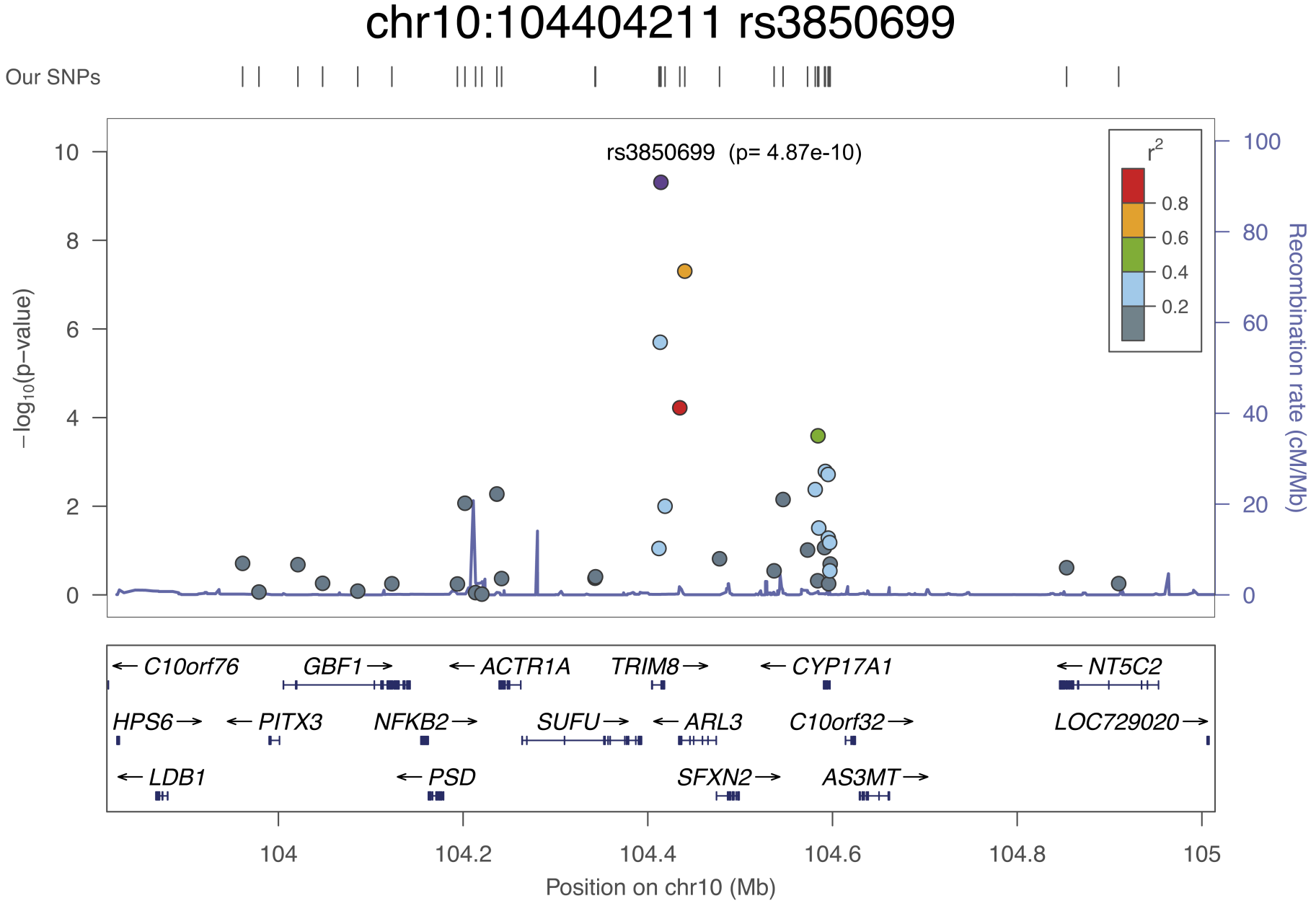

chr6:32300309 rs3096702
Our SNPs
rs3096702 (p= 4.78e-09)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
BAT2→ ← VARS C2→ ← TNXB RNF5→ ← C6orf10 ← HLA−DRB5 HLA−DQA2→
← BAT3 ← LSM2 CFB→ ← ATF6B ← BTNL2 ← HLA−DRB1 ← TAP2
APOM→ HSPA1B→ STK19→ ← FKBPL HLA−DRA→ HLA−DQA1→
Position on chr6 (Mb)

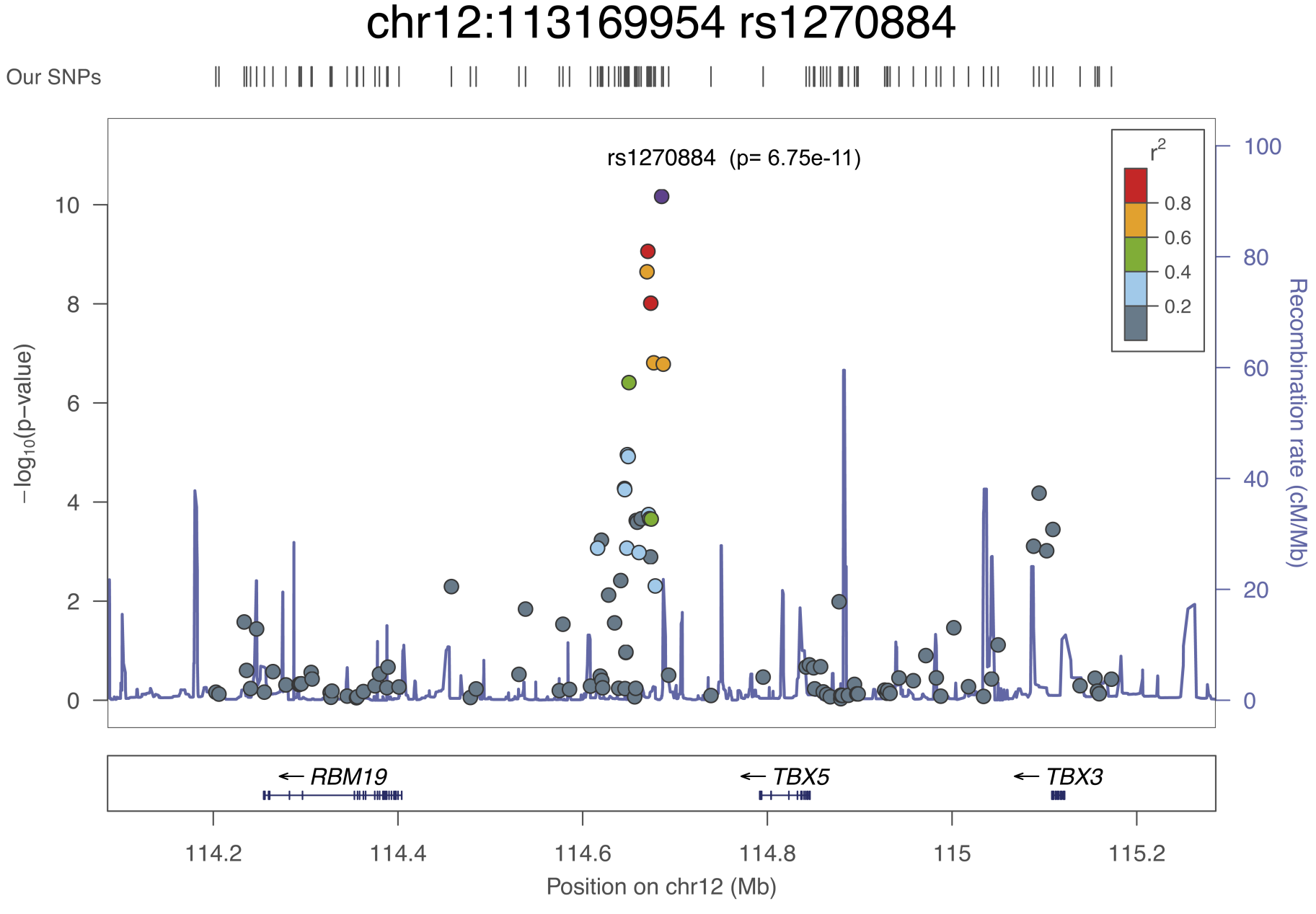

chr6:109391882 rs2273669
Our SNPs
rs2273669 (p= 7.91e-09)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
LACE1
FOXO3
ARMC2
CEP57L1
CCDC162
ZBTB24
NCRNA00222
SESN1
CD164
AKD1
PPIL6
Position on chr6 (Mb)

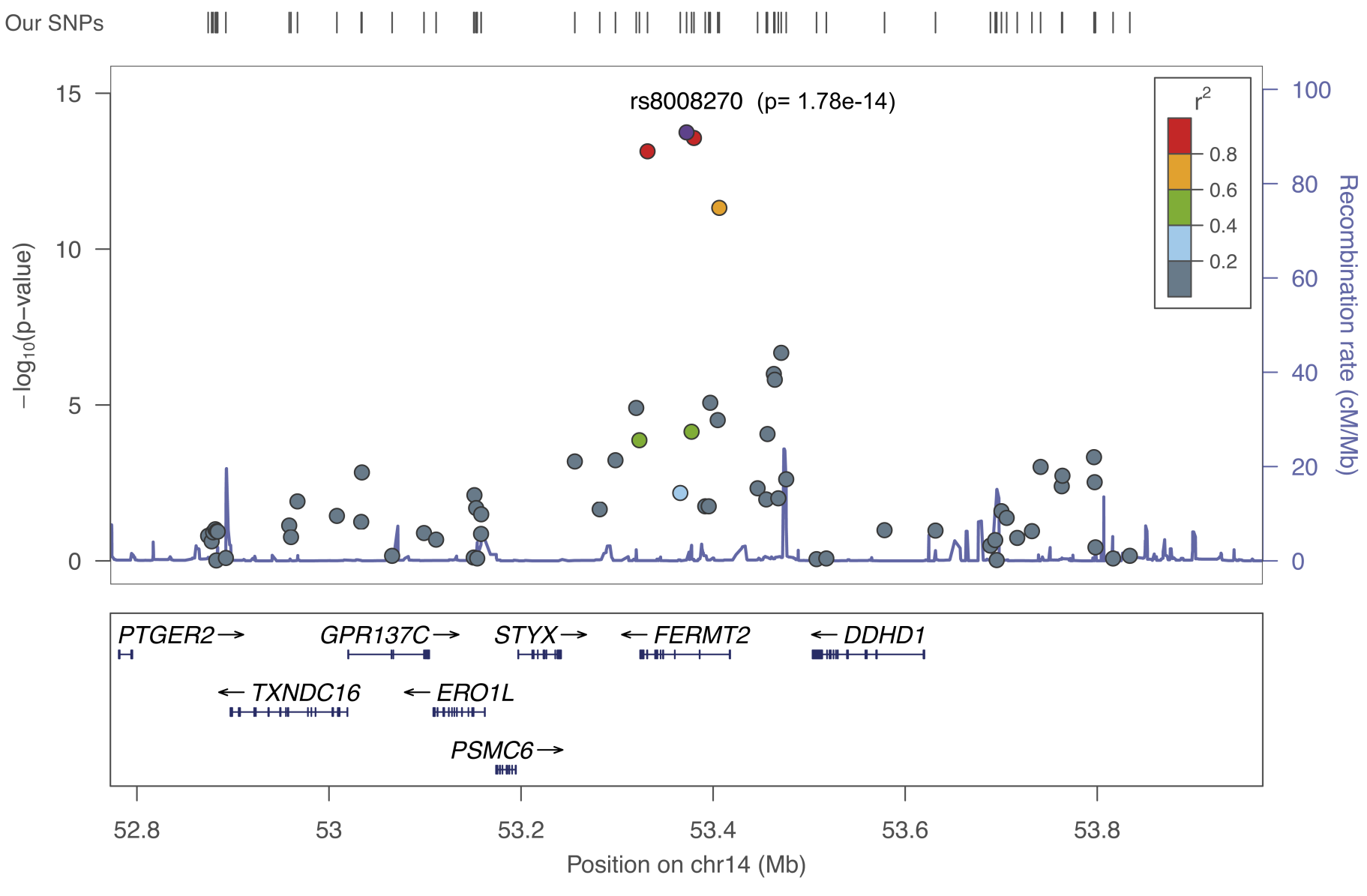

chr6:153482772 rs1933488
Our SNPs
rs1933488 (p= 4.34e-18)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SYNE1
VIP
FBXO5
MYCT1
MTRF1L
RGS17
Position on chr6 (Mb)

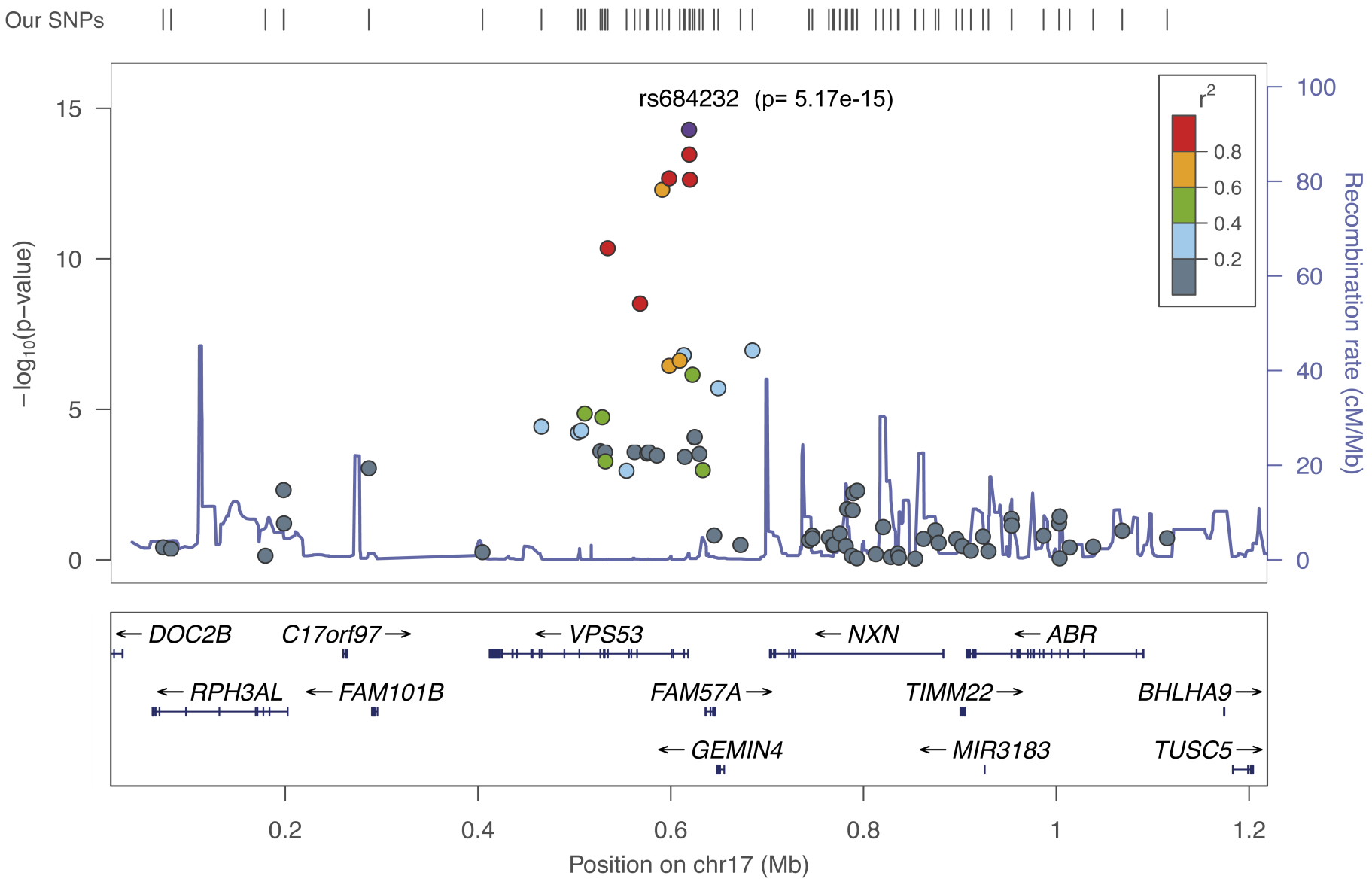

chr7:20961016 rs12155172
Plotted SNPs
rs12155172 (p= 4.95e-13)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ITGB8
ABCB5
SP8
SP4
DNAH11
RPL23P8
20.4
20.6
20.8
21
21.2
21.4
Position on chr7 (Mb)

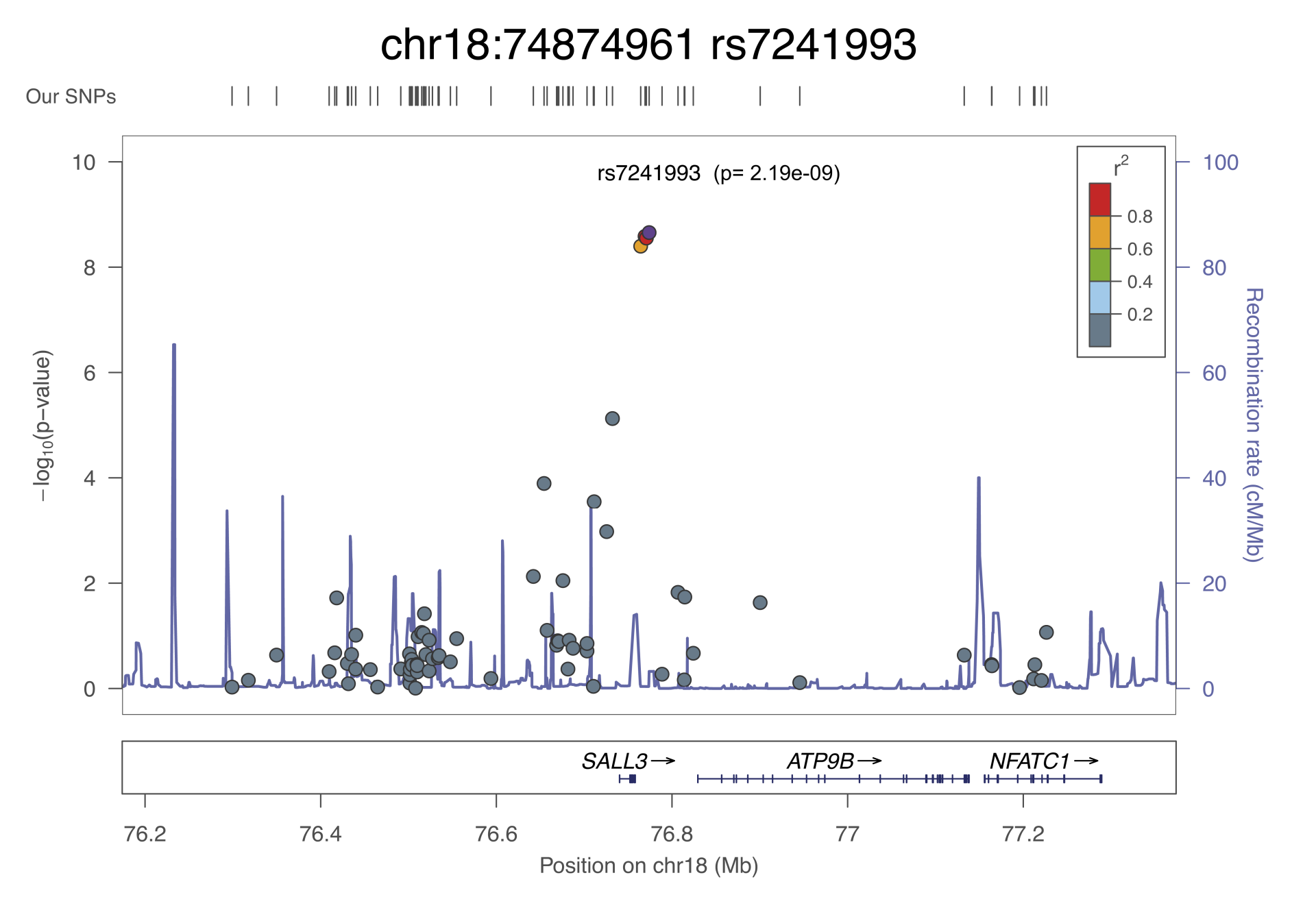

chr8:25948059 rs11135910
Our SNPs
rs11135910 (p= 8.16e-11)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
KCTD9
EBF2
PPP2R2A
PNMA2
CDCA2
BNIP3L
DPYSL2
Position on chr8 (Mb)

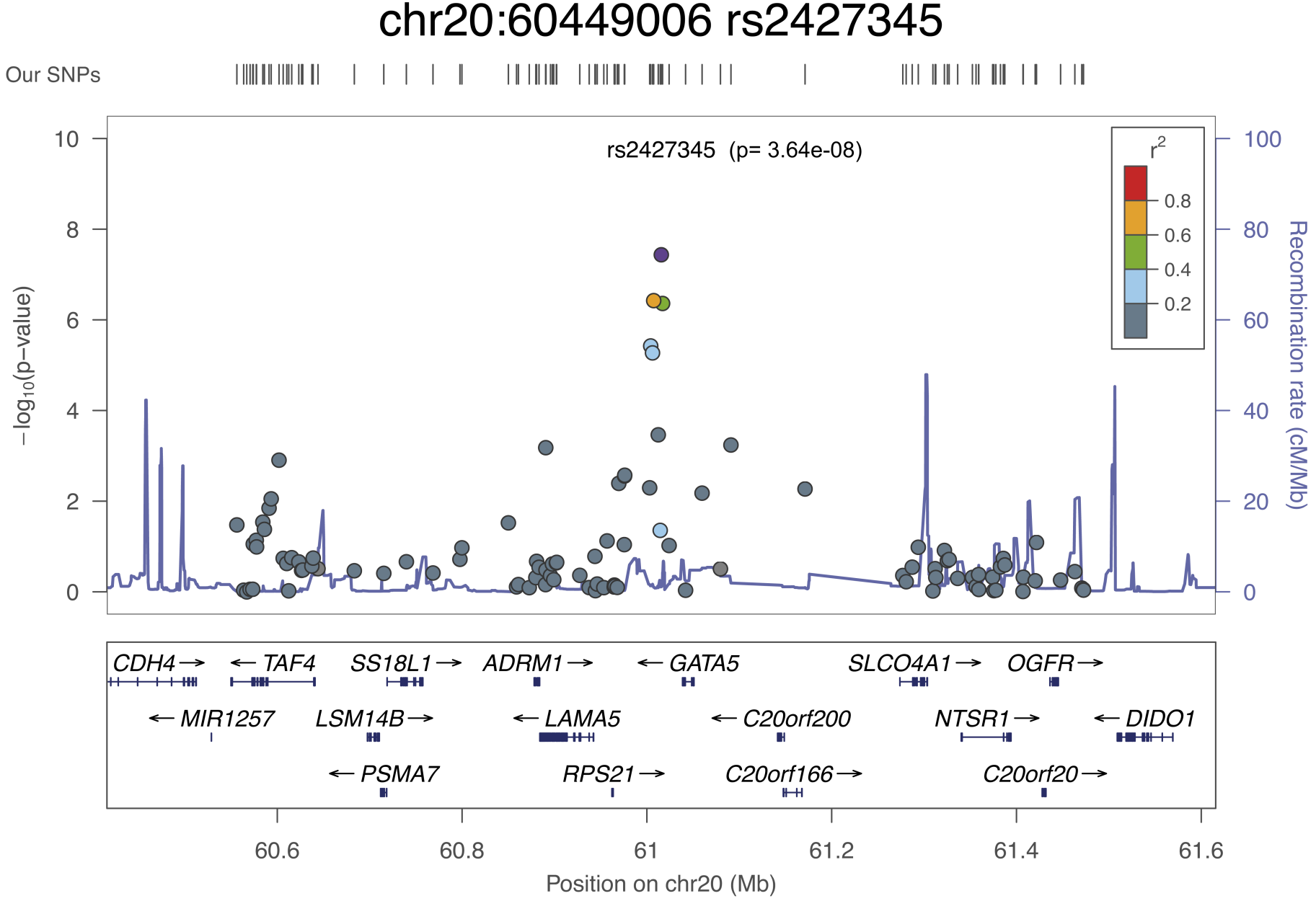

chr10:104404211 rs3850699
Our SNPs
rs3850699 (p= 4.87e-10)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
C10orf76
GBF1
ACTR1A
TRIM8
CYP17A1
NT5C2
HPS6
PITX3
NFKB2
SUFU
ARL3
C10orf32
LOC729020
LDB1
PSD
SFXN2
AS3MT
Position on chr10 (Mb)

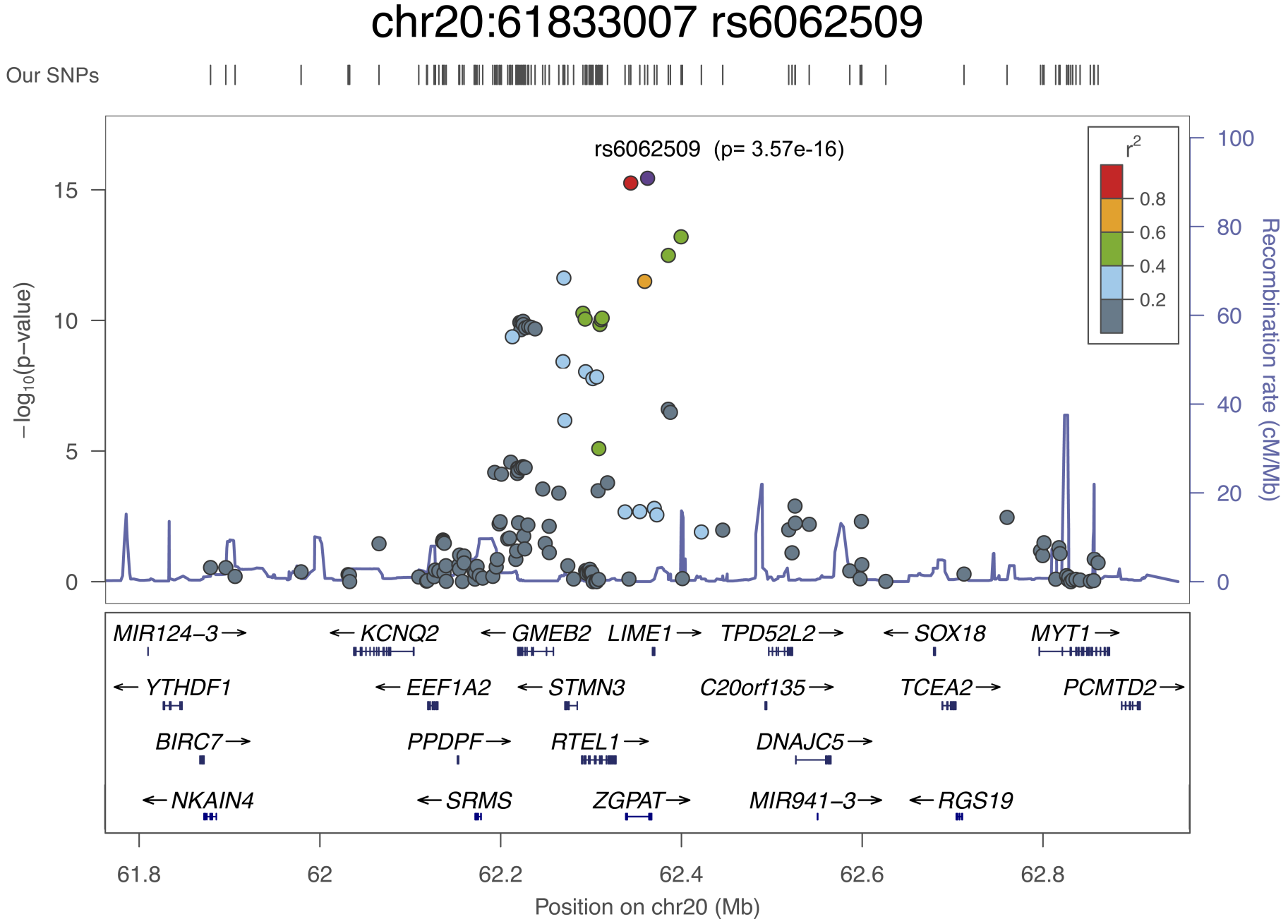

chr12:113169954 rs1270884
Our SNPs
rs1270884 (p= 6.75e-11)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
RBM19
TBX5
TBX3
Position on chr12 (Mb)

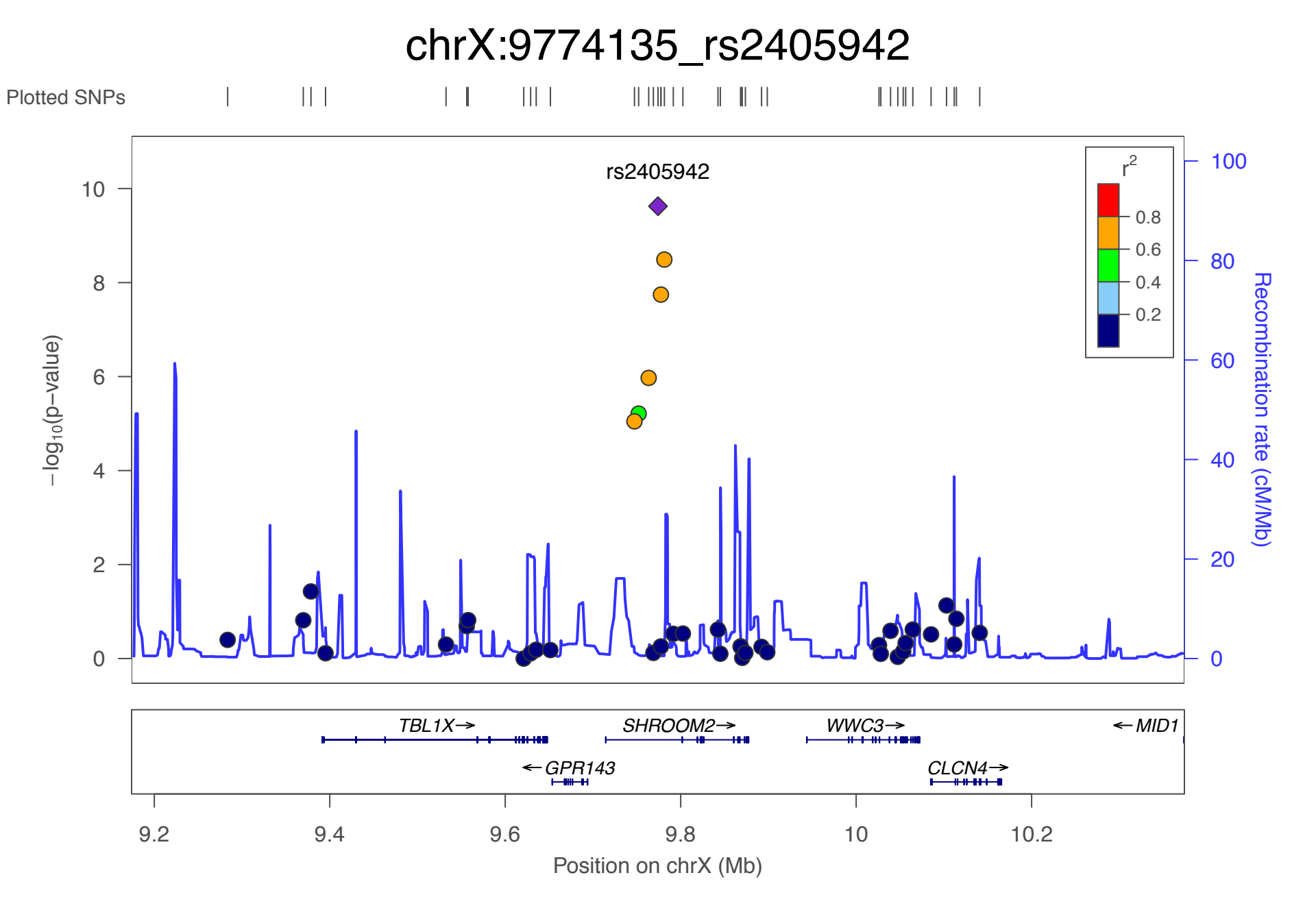

chr14:52442080 rs8008270
Our SNPs
rs8008270 (p= 1.78e-14)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
15
10
5
0
100
80
60
40
20
0
PTGER2
GPR137C
STYX
FERMT2
DDHD1
TXNDC16
ERO1L
PSMC6
52.8
53
53.2
53.4
53.6
53.8
Position on chr14 (Mb)


chr17:565715 rs684232
Our SNPs
rs684232 (p= 5.17e-15)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
DOC2B
C17orf97
VPS53
NXN
ABR
RPH3AL
FAM101B
FAM57A
TIMM22
BHLHA9
GEMIN4
MIR3183
TUSC5
Position on chr17 (Mb)

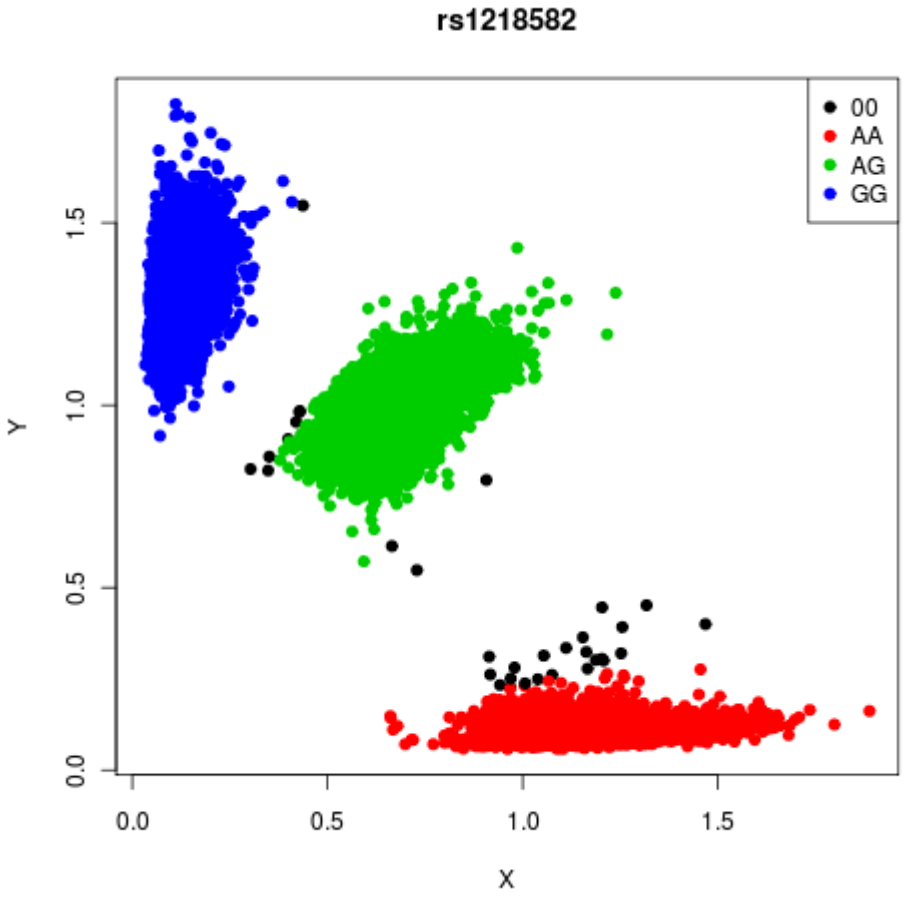

chr18:74874961 rs7241993
Our SNPs
rs7241993 (p= 2.19e-09)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SALL3
ATP9B
NFATC1
76.2
76.4
76.6
76.8
77
77.2
Position on chr18 (Mb)

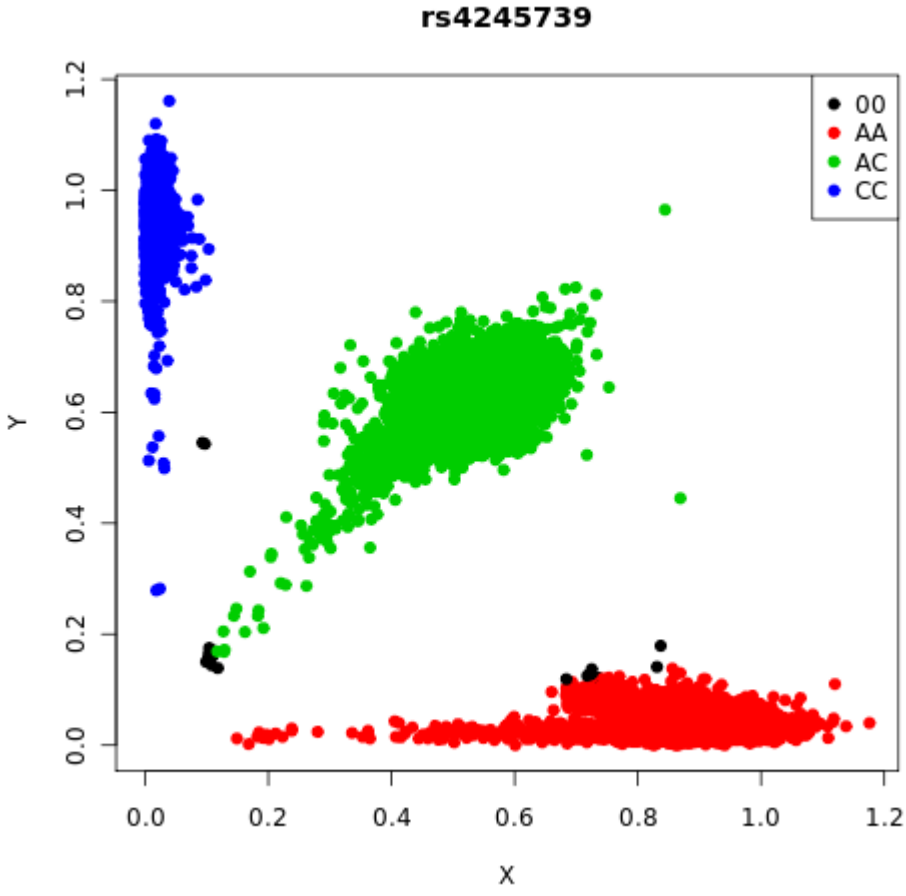

chr20:60449006 rs2427345
Our SNPs
rs2427345 (p= 3.64e-08)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
CDH4
TAF4
SS18L1
ADRM1
GATA5
SLCO4A1
OGFR
MIR1257
LSM14B
LAMA5
C20orf200
NTSR1
DIDO1
PSMA7
RPS21
C20orf166
C20orf20
Position on chr20 (Mb)

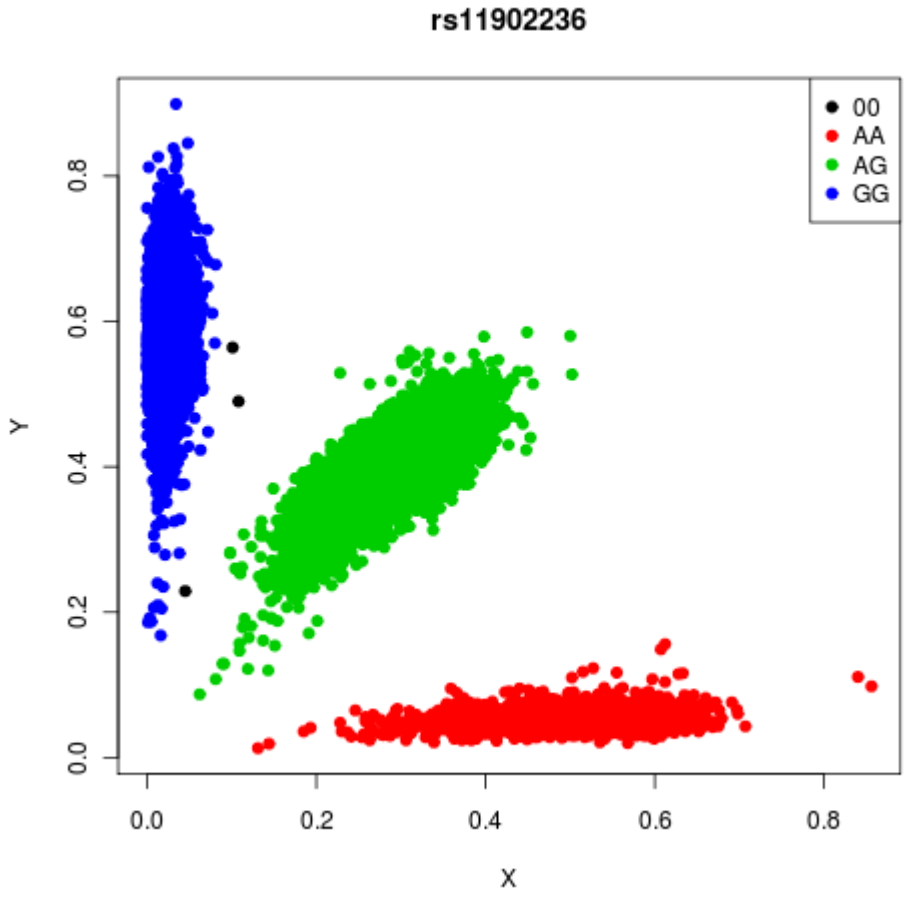

chr20:61833007 rs6062509
Our SNPs
rs6062509 (p= 3.57e-16)
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
MIR124−3
KCNQ2
GMEB2
LIME1
TPD52L2
SOX18
MYT1
YTHDF1
EEF1A2
STMN3
C20orf135
TCEA2
PCMTD2
BIRC7
PPDPF
RTEL1
DNAJC5
NKAIN4
SRMS
ZGPAT
MIR941−3
RGS19
Position on chr20 (Mb)

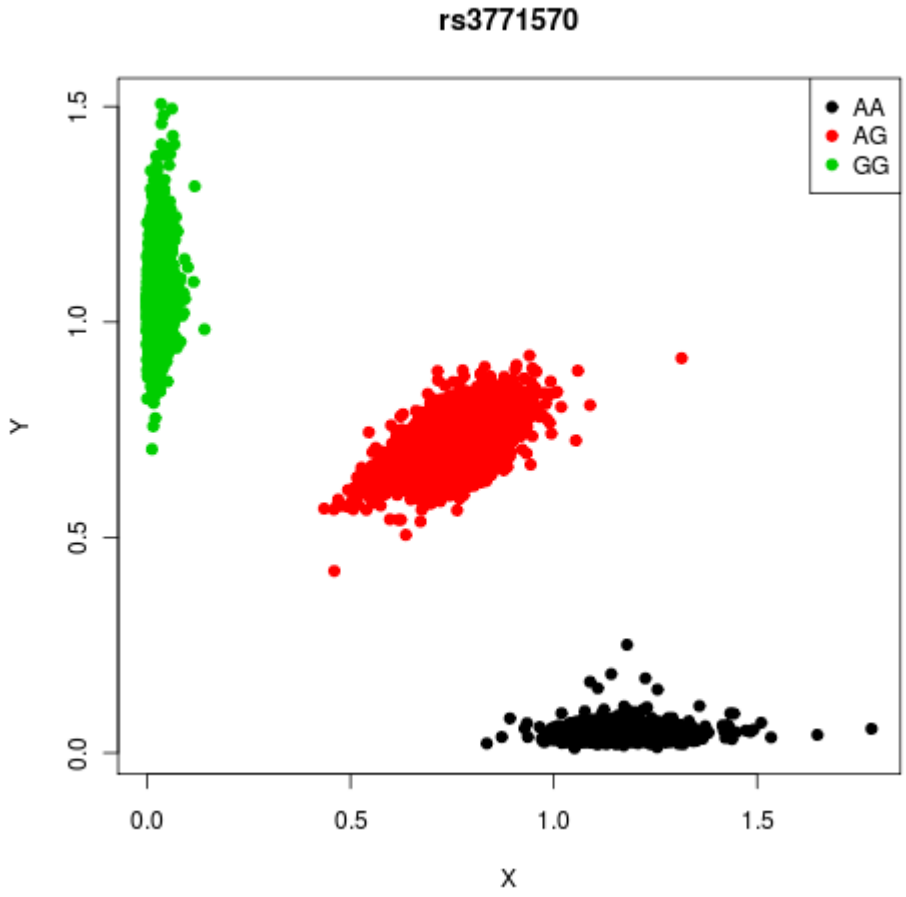

chrX:9774135_rs2405942
Plotted SNPs
rs2405942
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
TBL1X→
SHROOM2→
WWC3→
←MID1
←GPR143
CLCN4→
Position on chrX (Mb)

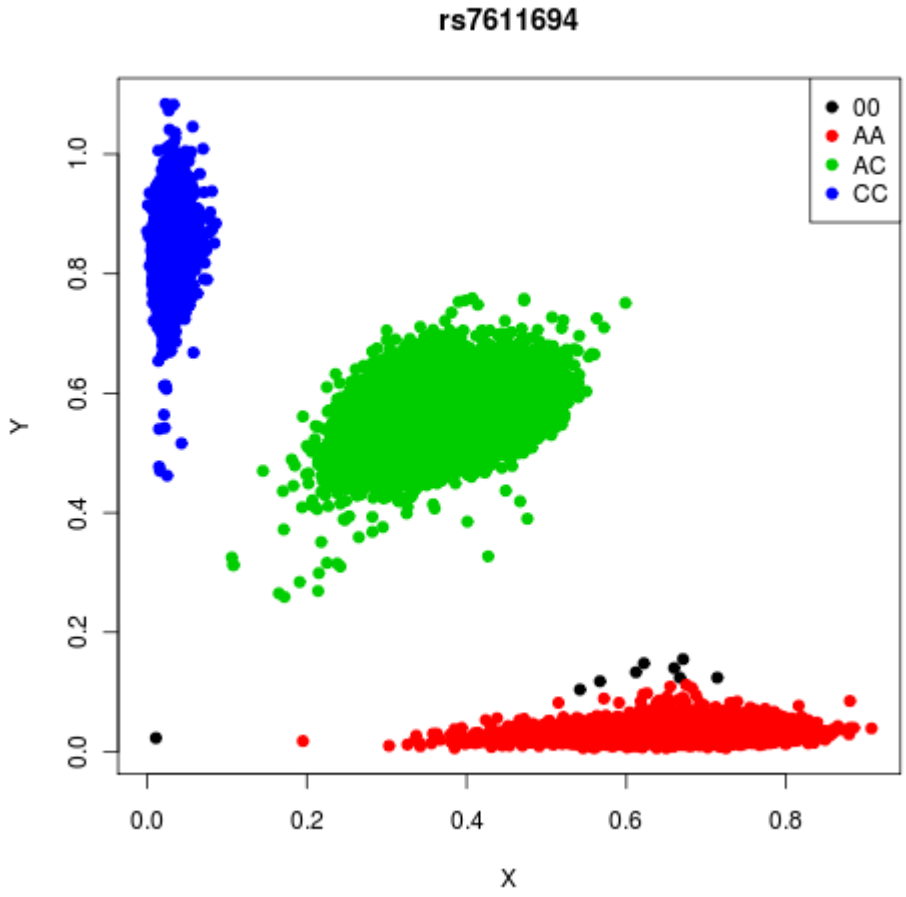
Supplementary Figure 4 - Cluster plots for each of the 23 new loci in iCOGS

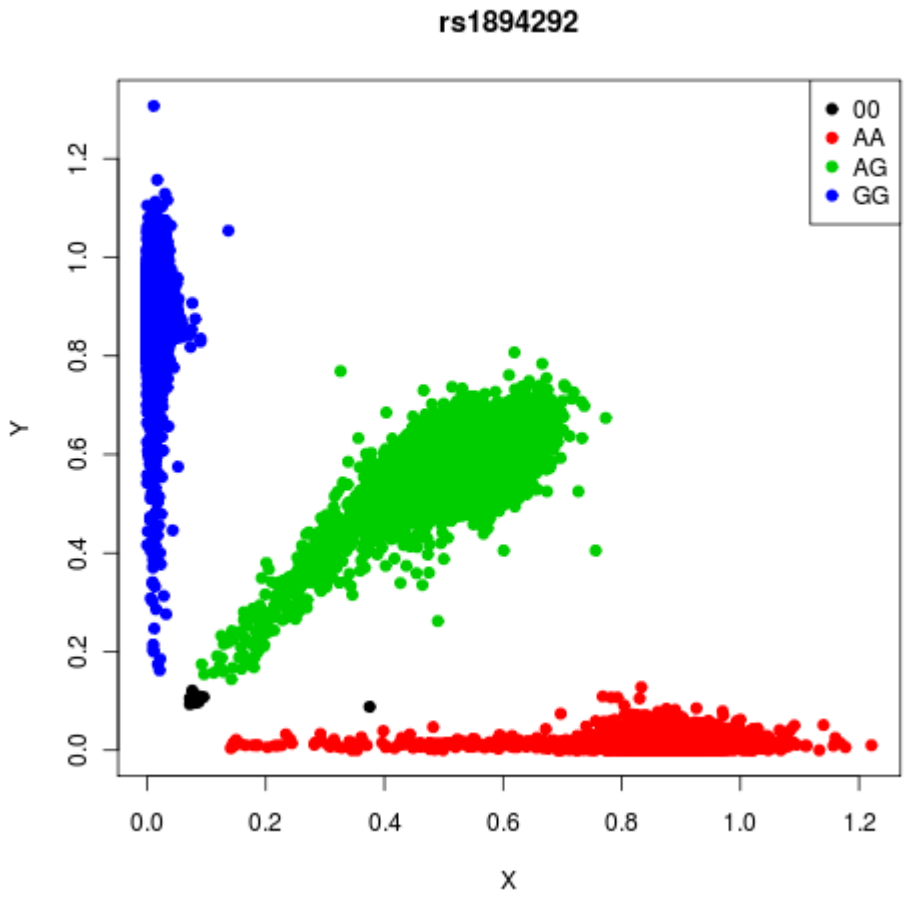


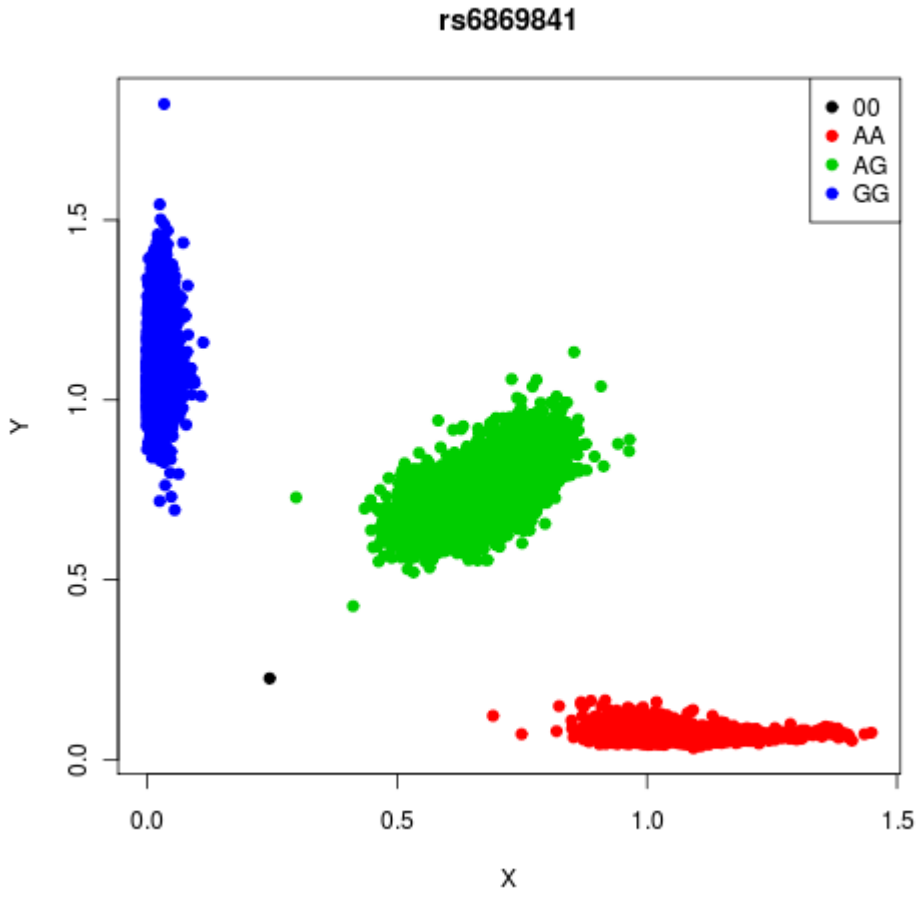


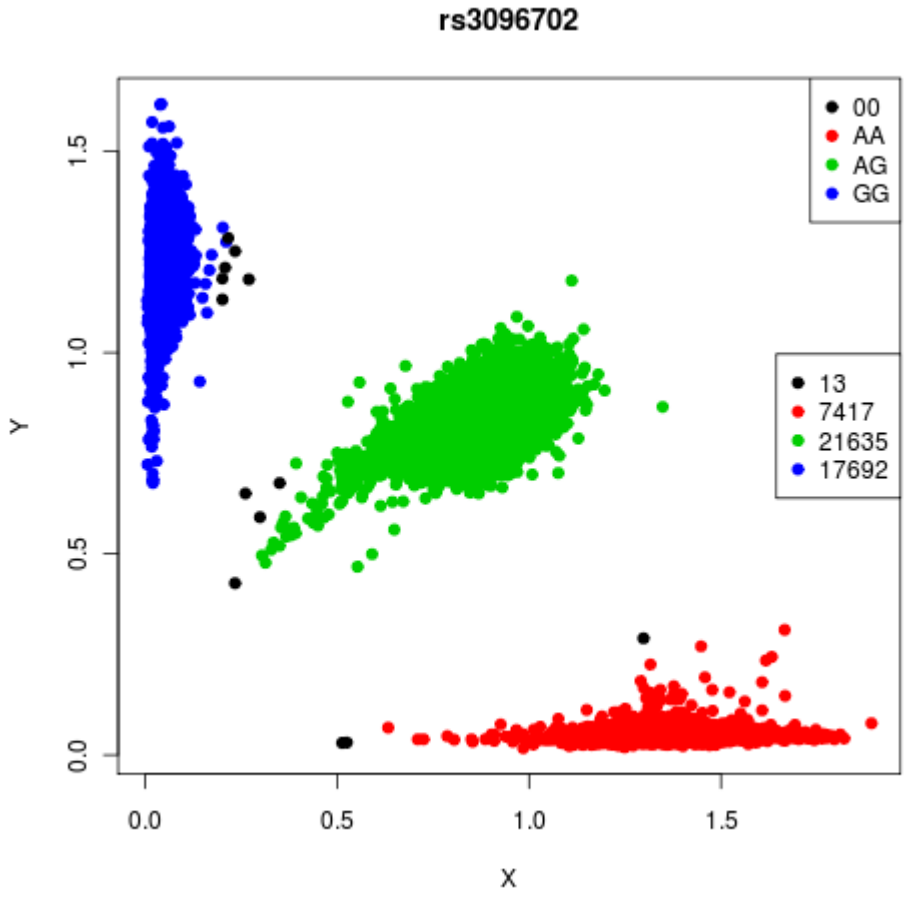

rs11902236
00
AA
AG
GG
Y
X
0.0
0.2
0.4
0.6
0.8

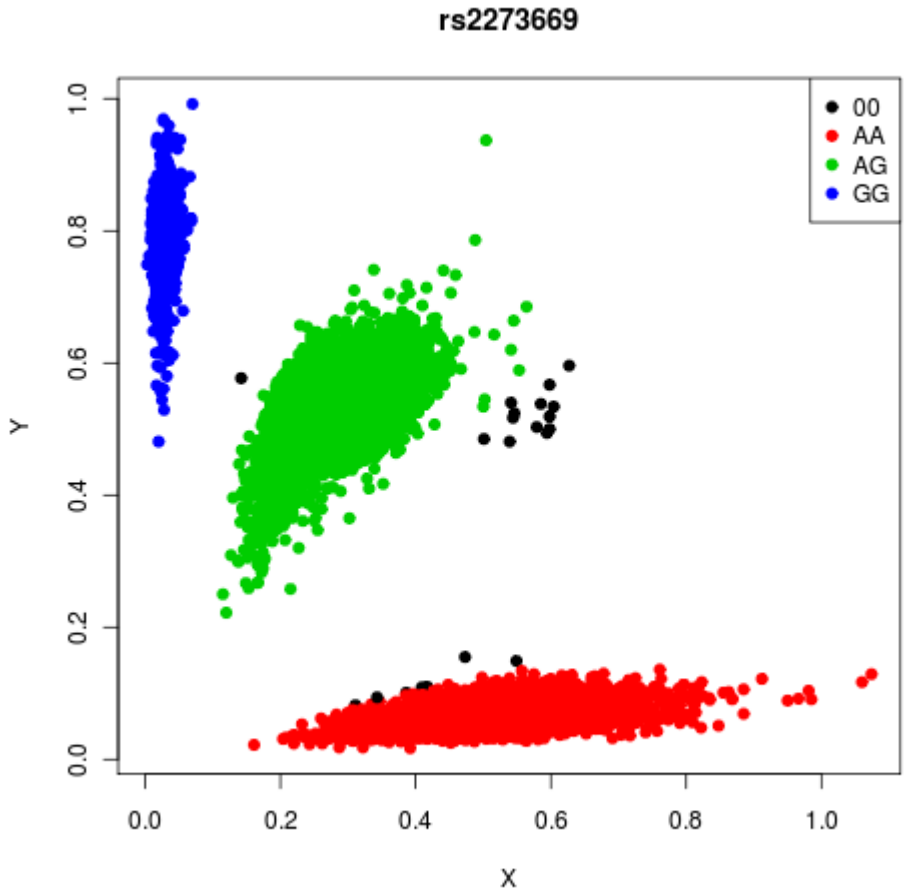

rs3771570
AA
AG
GG
Y
X
0.0
0.5
1.0
1.5

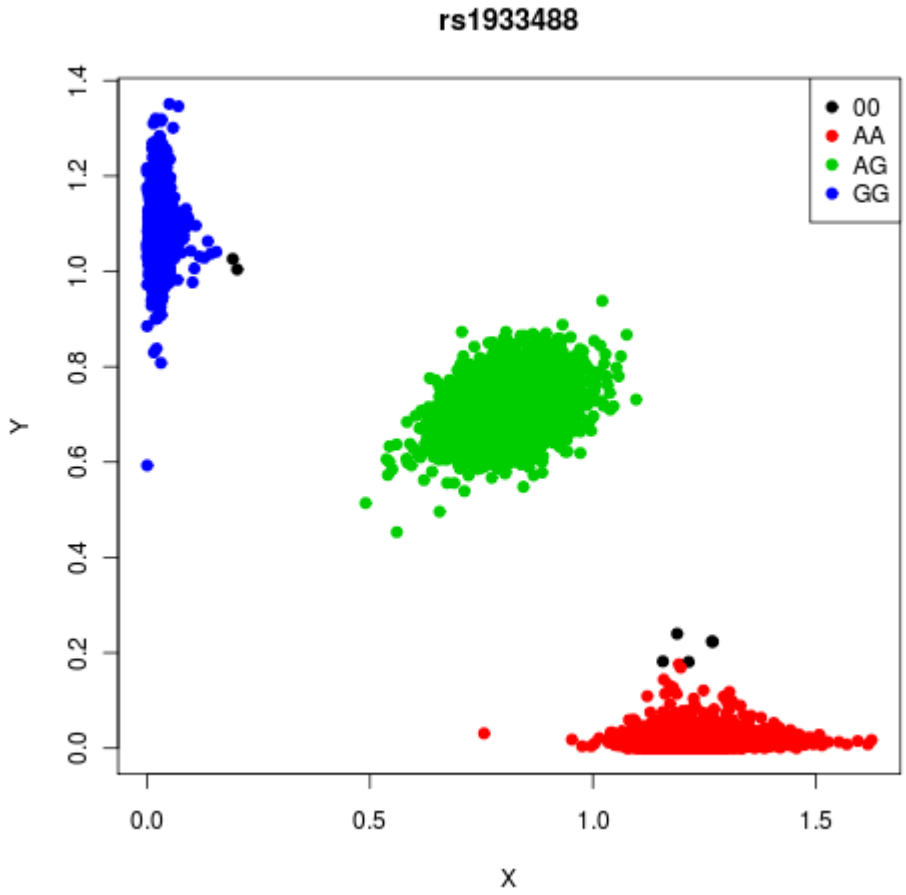

rs7611694
00
AA
AC
CC
Y
X
0.0
0.2
0.4
0.6
0.8
1.0

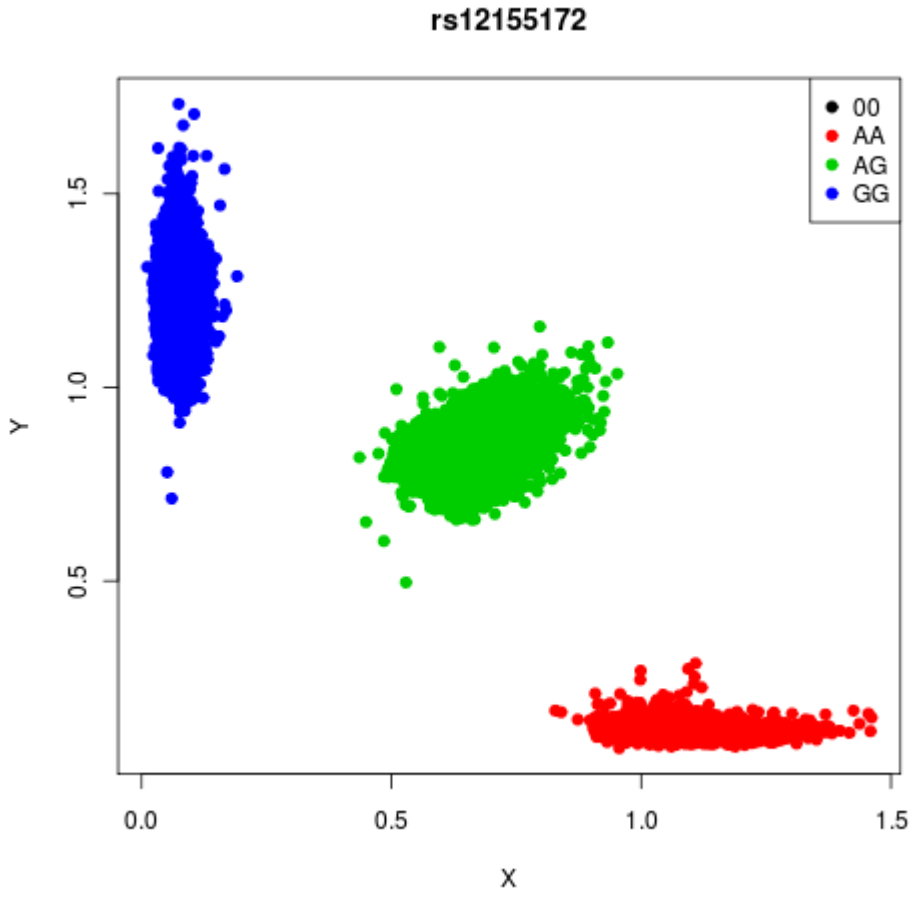

rs1894292
00
AA
AG
GG
Y
X
0.0
0.2
0.4
0.6
0.8
1.0
1.2

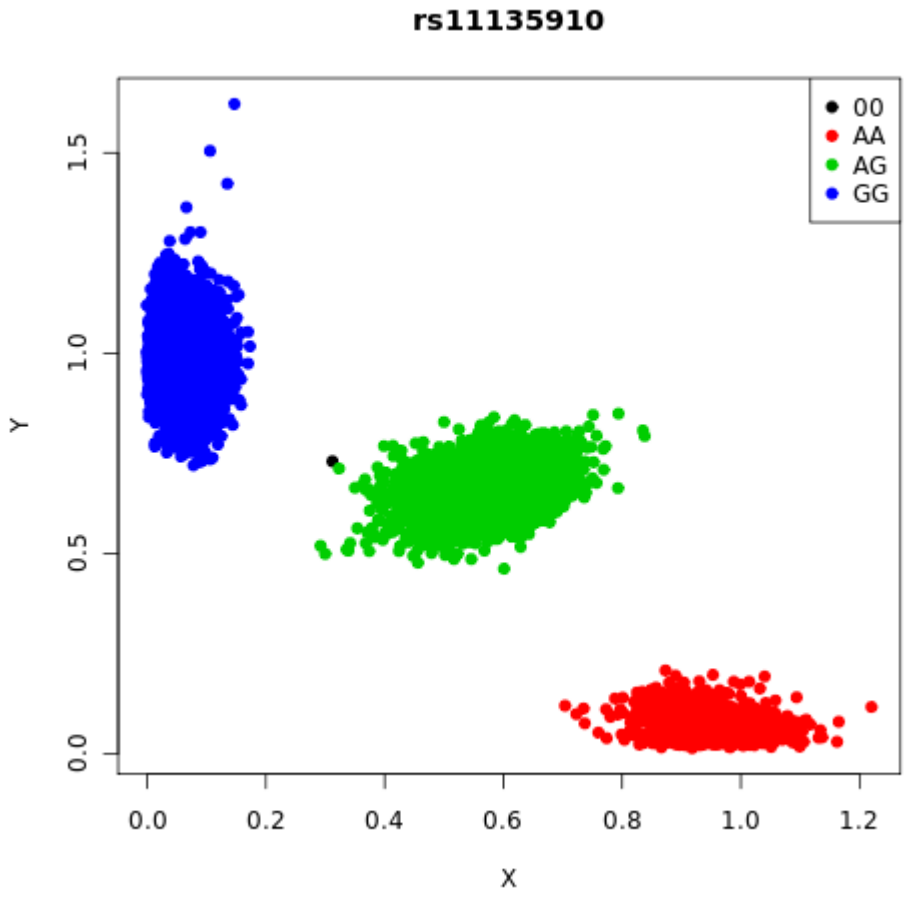

rs6869841
00
AA
AG
GG
Y
X
0.0
0.5
1.0
1.5

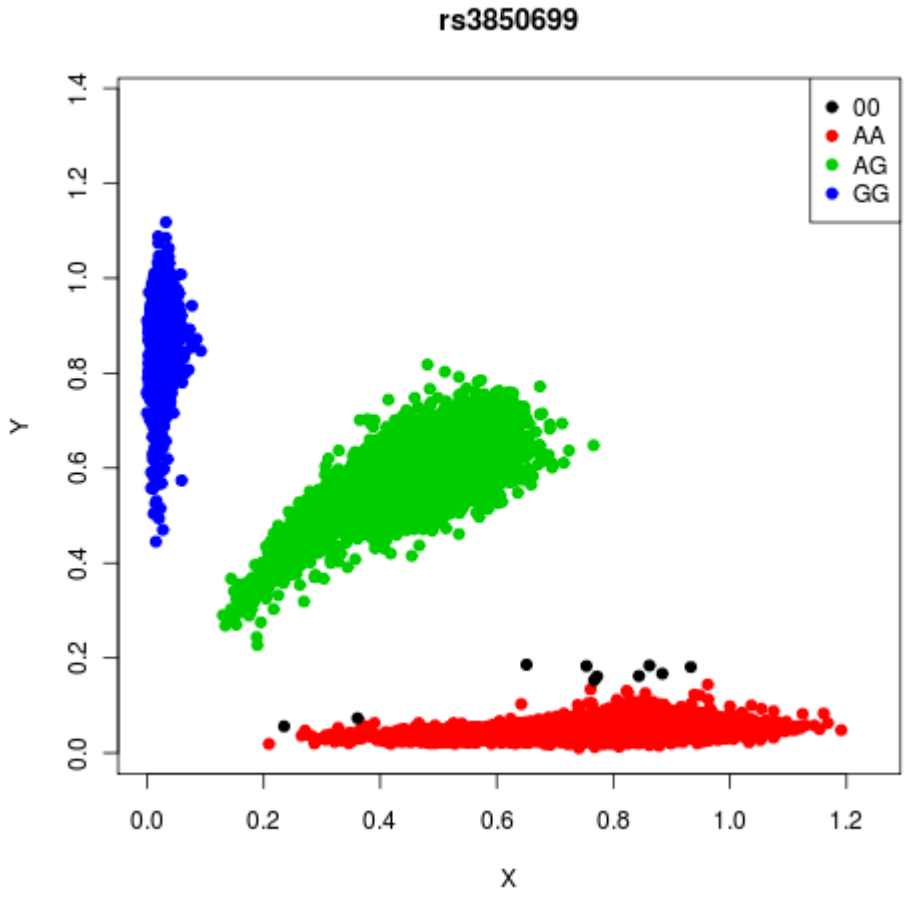

rs3096702
00
AA
AG
GG
13
7417
21635
17692
Y
X
0.0
0.5
1.0
1.5

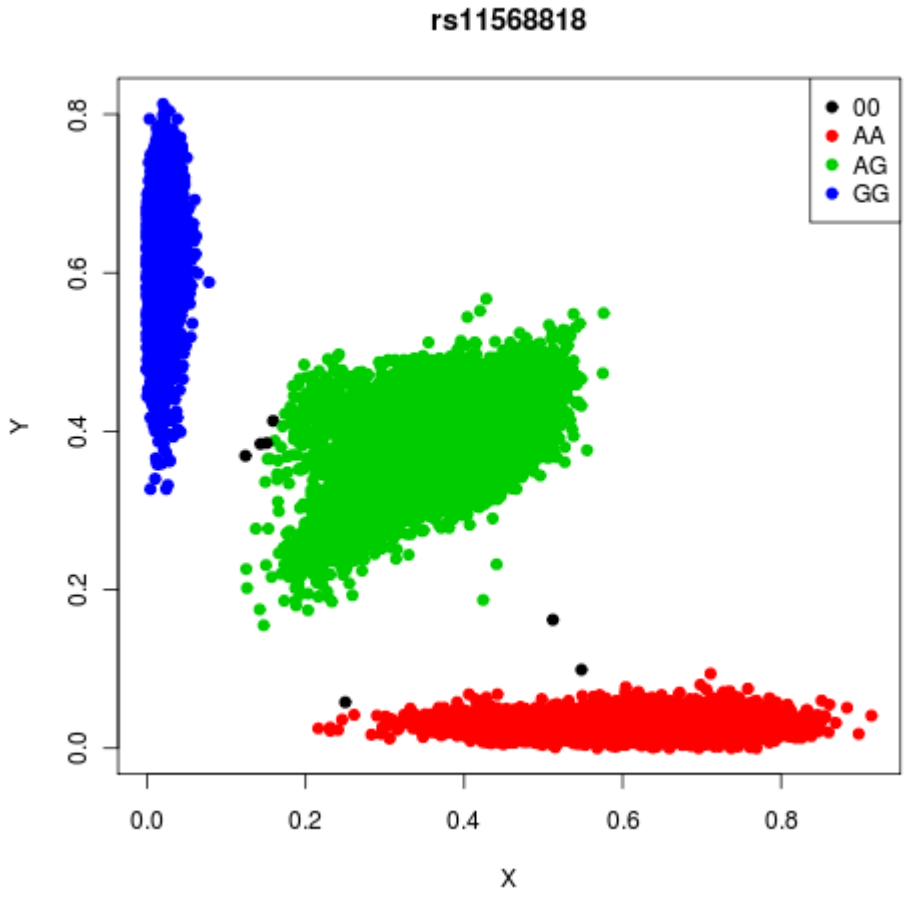

rs2273669
00
AA
AG
GG
Y
X
0.0
0.2
0.4
0.6
0.8
1.0

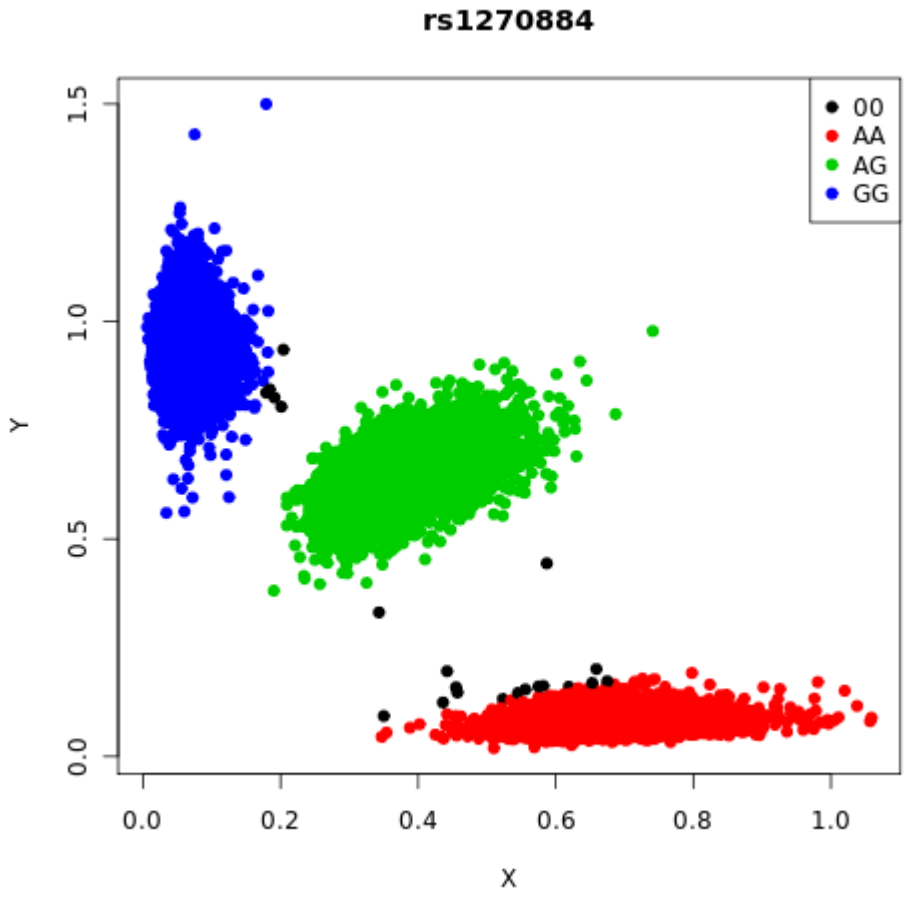

rs1933488
00
AA
AG
GG
Y
X
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0.5
1.5

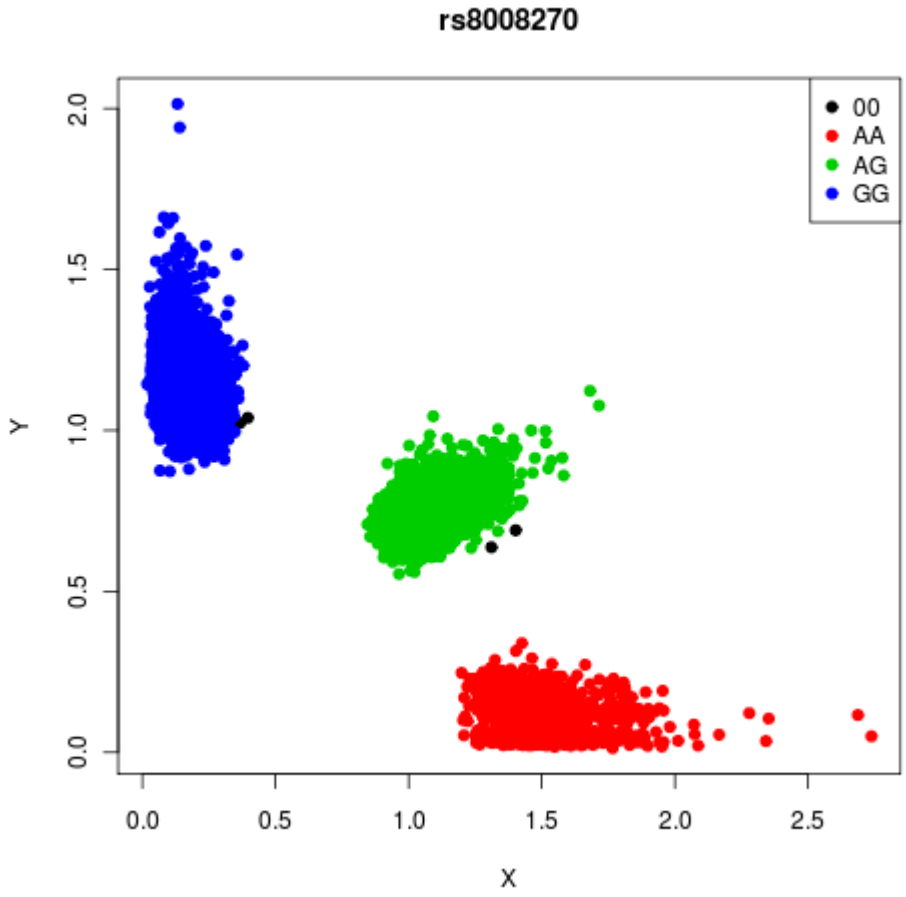

rs12155172
00
AA
AG
GG
Y
X
0.0
0.5
1.0
1.5

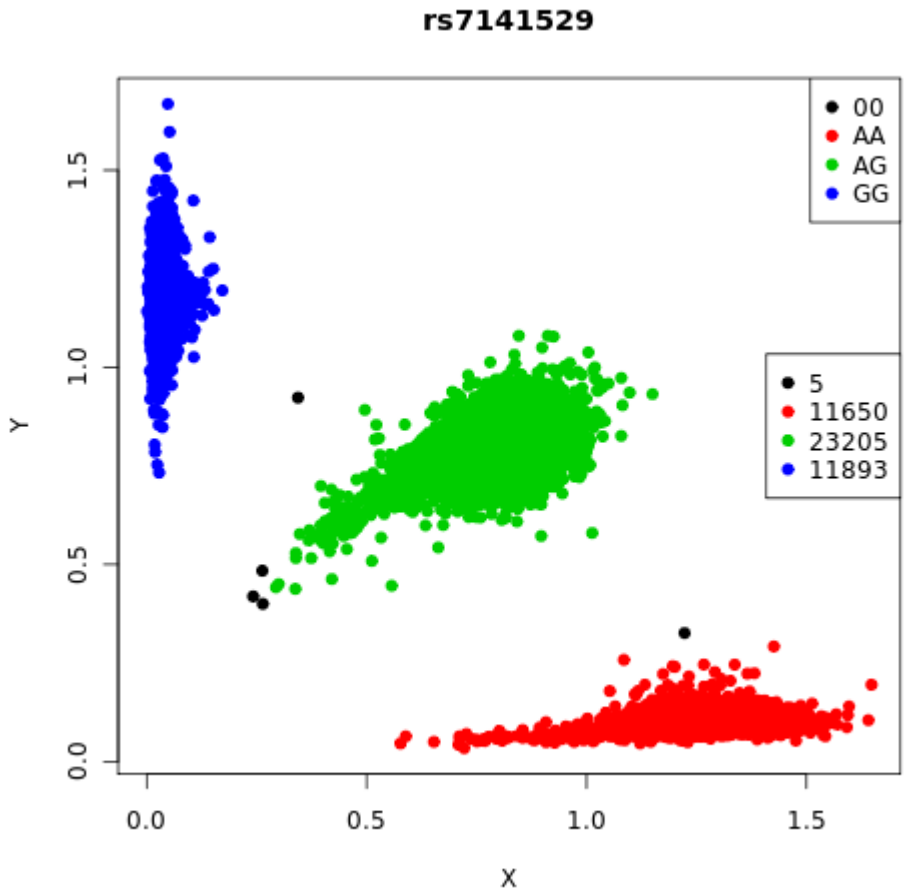

rs11135910
00
AA
AG
GG
Y
X
0.0
0.2
0.4
0.6
0.8
1.0
1.2
0.5
1.5

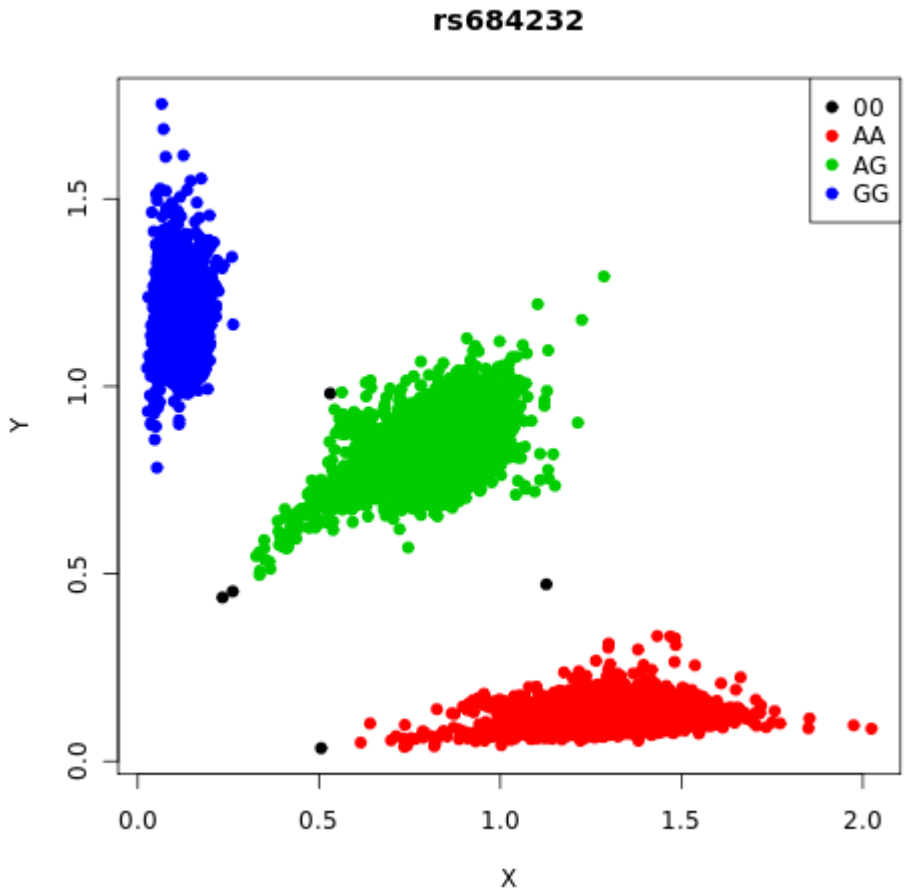

rs3850699
00
AA
AG
GG
Y
X
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4

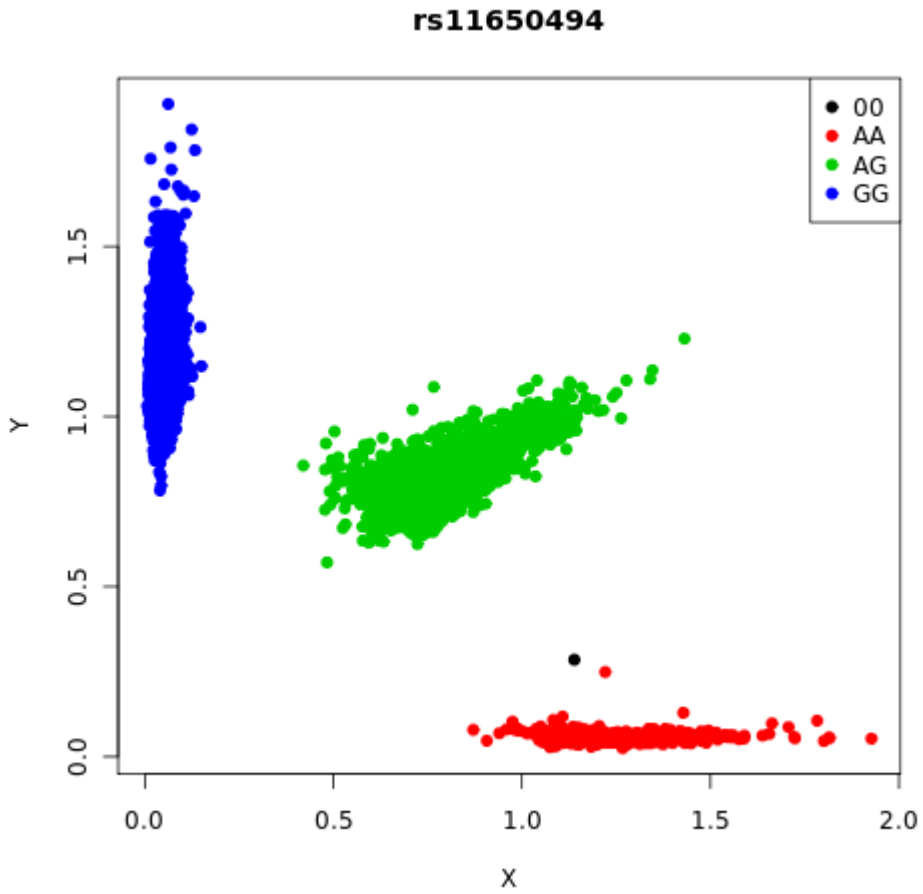

rs11568818
00
AA
AG
GG
Y
X
0.0
0.2
0.4
0.6
0.8

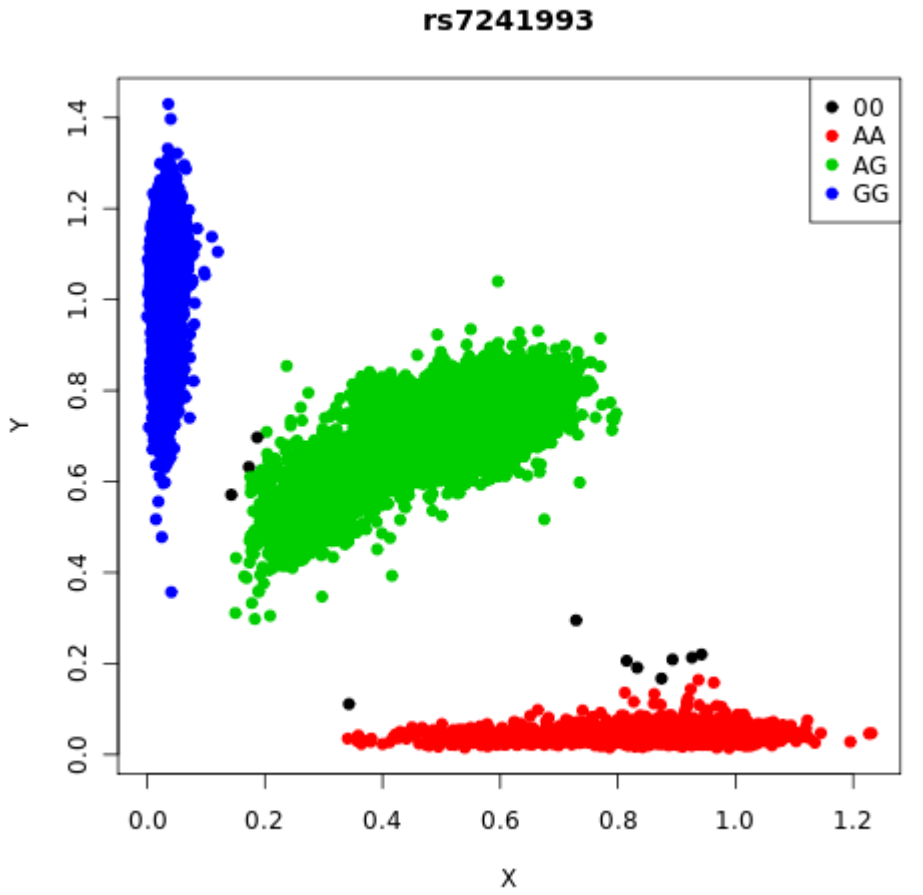

rs1270884
00
AA
AG
GG
Y
X
0.0
0.5
1.0
1.5
0.0
0.2
0.4
0.6
0.8
1.0

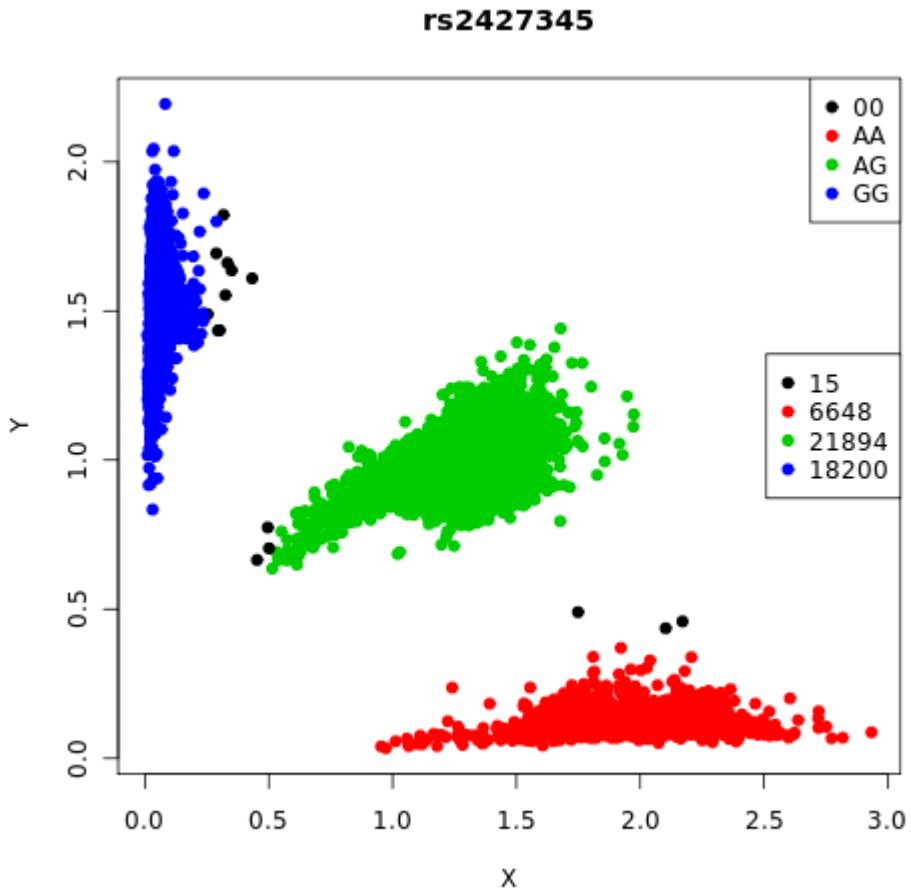

rs8008270
00
AA
AG
GG
Y
X
0.0
0.5
1.0
1.5
2.0
0.0
0.5
1.0
1.5
2.0
2.5

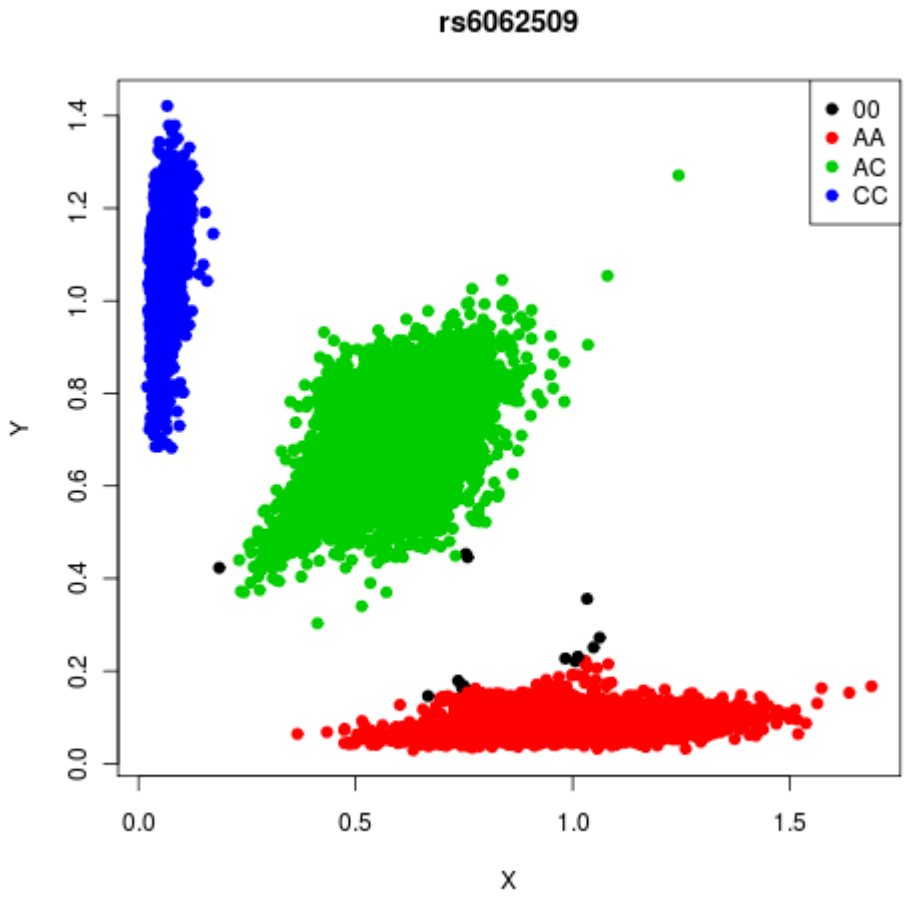

rs7141529
00
AA
AG
GG
5
11650
23205
11893
Y
X
0.0
0.5
1.0
1.5

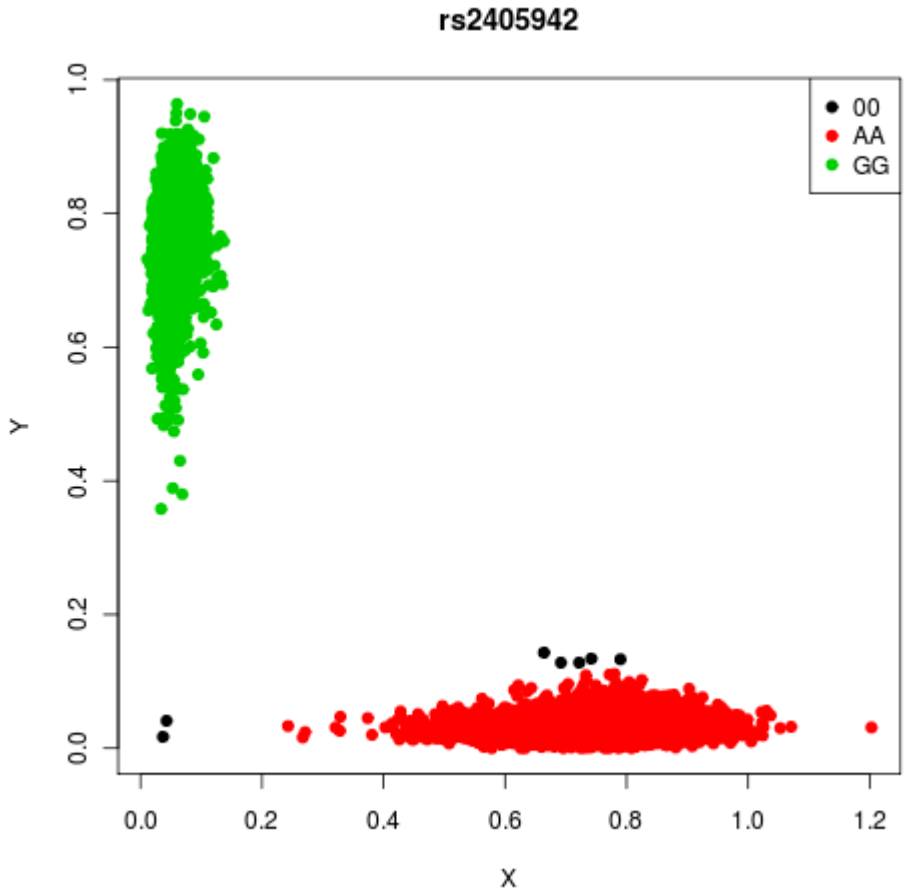

rs684232
00
AA
AG
GG
Y
X
0.0
0.5
1.0
1.5
2.0


rs11650494
00
AA
AG
GG
Y
X
0.0
0.5
1.0
1.5
2.0


rs7241993
00
AA
AG
GG
Y
X
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4


rs2427345
00
AA
AG
GG
15
6648
21894
18200
Y
X
0.0
0.5
1.0
1.5
2.0
2.5
3.0


rs6062509
00
AA
AC
CC
Y
X
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0.5
1.5


rs2405942
00
AA
GG
Y
X
0.0
0.2
0.4
0.6
0.8
1.0
1.2

SUPPLEMENTARY NOTE

Description of four GWAS and the PRACTICAL Consortium groups

All studies were approved by the appropriate ethics committees and informed consent was obtained. A list of the groups is in Supplementary Table 1.

Combined GWAS

Stages 1 & 2 UK:

A GWAS based on genotyping of 541,129 SNPs in 1,854 individuals with clinically detected (non PSA-screened) prostate cancer (cases) and 1,894 controls. 43,671 SNPs showing strong evidence of association in stage 1 were followed up by genotyping a further 3,268 cases and 3,366 controls from UK and Melbourne in stage2[1, 2].

BPC3:

Breast and Prostate Cancer Cohort Consortium (BPC3), is an NCI sponsored study combining 10 large prospective cohorts with biospecimens to conduct research on gene, environmental, and gene-environment effects in breast and prostate cancer etiology (http://epi.grants.cancer.gov/BPC3/). An advanced prostate cancer GWAS, where cases were defined as either a Gleason score ≥8 or tumor stage ≥C, was undertaken across 7 cohorts using the Illumina 610K SNP array for the majority of subjects. In total 2,473 advanced prostate cancer cases and 3,534 controls were included in the analysis following QC[3].

CAPS:

Cancer of the Prostate in Sweden (CAPS), a population-based prostate cancer case-control study with 3,030 cases and 1,960 controls who donated blood samples during 2001-2003 (http://ki.se/ki/jsp/polopoly.jsp?d=13809&a=29862&l=en).

CGEMS:

Cancer Genetic Markers of Susceptibility (CGEMS; http://www.cgems.cancer.gov/) is a GWAS consisting of 1,117 prostate cancer cases and 1,105 controls of European ancestry nested in the

Prostate, Lung, Colorectal, and Ovarian (PLCO) Cancer Screening Trial. Cases were oversampled for aggressive prostate cancer (Stage 3 or 4 or Gleason ≥ 7)[4].

Groups with samples genotyped using iCOGs

CAPS

The study population has been described in detail elsewhere[5]. Briefly, we identified and recruited biopsy confirmed prostate cancer cases from four out of six regional cancer registries in Sweden, diagnosed between July 2001 and October 2003. Clinical data including TNM stage, Gleason grade and PSA levels at time for diagnosis were retrieved through record linkage to the National Prostate Cancer Registry. Control subjects, who were recruited concurrently with case subjects, were randomly selected from the Swedish Population Registry and matched according to the expected age distribution of cases (groups of 5-year intervals) and geographic region. Whole blood was collected from all individuals for extraction of genomic DNA.

CPCS1+2:

The CPCS (Copenhagen Prostate Cancer Study) 1 + 2, Copenhagen, Denmark

The Copenhagen Prostate Cancer Study 1 included 872 unselected patients recruited with prostate cancer between 2008-2011 from Herlev Hospital, Copenhagen University Hospital, Herlev, Denmark. The Copenhagen Prostate Cancer Study 2 included 306 unselected patients with prostate cancer recruited in 2010-2011 from Rigshospitalet, Copenhagen University Hospital, Copenhagen, Denmark. PSA is not routinely screened for in Denmark, and cases are therefore mainly clinically detected. Controls were 2,777 (CPCS1) and 798 (CPCS2) prostate cancer free men from the general population, whom participated in the Copenhagen City Heart Study. Diagnosis of prostate cancer was confirmed by fully trained pathologists. All participants were white and of Danish descent. Participants filled out questionnaires, gave blood samples for DNA extraction and gave written informed consent.

EPIC: European Prospective Investigation into Cancer and Nutrition

The European Prospective Investigation into Cancer and Nutrition (EPIC) is a prospective study designed to investigate both genetic and non-genetic risk factors for different forms of cancer. Study participants were almost all white Europeans. Approximately 500,000 individuals (150,000 men) in EPIC were recruited between 1992 and 2000, from 23 centres in 10 European countries. Overall approximately 400,000 subjects also provided a blood sample at recruitment. The methods of recruitment and details of the study design are described in detail elsewhere[6].

In brief, study participants completed an extensive questionnaire on both dietary and nondietary data at recruitment. The present study includes 1673 prostate cancer cases matched to 2153 controls based on study center, length of follow-up, age at enrollment (±6 months), fasting and time of day of blood collection (±1 hour). The prostate cancer subjects were from 8 of the 10 participating countries: Denmark, Germany, Greece, Italy, the Netherlands, Spain, Sweden and the United Kingdom (UK). France and Norway were not included in the current study because these cohorts only included female subjects. All participants gave written consent for the research and approval for the study was obtained from the ethical review board from all local institutions in the regions where participants had been recruited for the EPIC study.

ESTHER

In the ESTHER study, patients with a first diagnosis of prostate cancer at age 50-75 years were recruited in hospitals and medical practices in Saarland, a state located in southwest Germany, from 2001 to 2003. Controls were selected from participants of a general health-check up within the same age range (and frequency matched to the cases by 5-year age groups) who were recruited in general practices in Saarland in 2000-2002. Cases and controls who were almost exclusively of European descent, filled out a detailed standardized questionnaire on life time history of potential risk factors and had a blood sample taken, and medical data were extracted from medical records.

FHCRC: Fred Hutchinson Cancer Research Center, Seattle US

The study population consists of participants from two population-based case-control studies in Caucasian and African American residents of King County, Washington (Study I and Study II), which have been previously described[7]. Incident cases with histologically confirmed prostate cancer were ascertained from the Seattle-Puget Sound Surveillance, Epidemiology and End Results cancer registry. In Study I, cases were diagnosed between January 1, 1993, and December 31, 1996 and were 40-64 years of age at diagnosis. In Study II, cases were diagnosed between January 1, 2002, and December 31, 2005 and were 35-74 years of age at diagnosis. Overall, 2,244 eligible prostate cancer patients were identified and 1,754 (78%) were interviewed. Blood samples yielding sufficient DNA for genotyping were drawn from 1,457 (83%) cases who completed the study interview. A comparison group of controls without a history of prostate cancer, residing in King County, Washington, was identified for each study using random digit telephone dialling. Controls were frequency-matched to cases by five-year age groups and recruited evenly throughout each ascertainment period for cases. A total of 2,448 men were identified who met the eligibility criteria and 1,645 (67%) completed a study interview. Blood samples were drawn and DNA prepared from 1,352 (82%) interviewed controls.

IPO-Porto, Porto, Portugal

The IPO-Porto prostate cancer study includes patients with clinically localized prostate adenocarcinoma consecutively diagnosed and treated with open radical prostatectomy at the Portuguese Oncology Institute – Porto, Portugal, since 1999. The project involves sample collection of peripheral blood, urine and fresh-frozen tumour tissue. Relevant clinical data, namely Gleason grading, clinico-pathological staging and PSA level at diagnosis, are obtained from medical records. After QC 183 cases and 66 controls of European ancestry were analysed.

MAYO, Rochester, Minnesota, US

The Mayo Clinic study consisted of clinic-based cases, including 476 affected men from 185 families with prostate cancer, 445 men with sporadic prostate cancer, 199 with aggressive (Gleason score > 7) prostate cancer, and 500 population-based controls. The controls (all males) were randomly selected from a sampling frame of Olmsted County, Minnesota, provided by the Rochester Epidemiology Project. The methods used to ascertain familial and sporadic prostate cancer patients, as well as controls, have been described previously[8]. All individuals from the Mayo Clinic study included in this report were of self-reported European descent.

Cancer Council Victoria Prostate Cancer Program, Melbourne

The Cancer Council Victoria's Prostate Cancer Program includes three studies: the Melbourne Collaborative Cohort Study (MCCS) and the prostate Cancer Family Study (PCFS). Cases and controls (and informative families) from these studies have been used for several stages of this research effort, beginning with the UK and Melbourne stage 2 GWAS.

The MCCS is a prospective cohort study that includes 17,154 men who were aged 40 and 69 years when recruited between 1990 and 1994. MCCS participants are regularly linked to the Victorian Cancer Registry and the Australian Cancer Database to ascertain incident cases (1582 by end of 2008) including men diagnosed in other states of Australia. A random sample of MCCS participants who were not diagnosed with prostate cancer during follow-up provides a control group.

The PCFS is a population-based family series of 1428 men diagnosed with prostate cancer before the age of 56 years and 256 men diagnosed after the age of 55 years who were recruited in Victoria between 1998 and 2010. Cases were ascertained using the population-based Victorian Cancer Registry, and family members were approached after gaining the consent of each case. Altogether, 77% of cases agreed to participate.

MEC: Multiethnic Cohort

The Multiethnic Cohort Study is a population-based prospective cohort study that was initiated between 1993 and 1996 and includes subjects from various ethnic groups -African-Americans and

Latinos primarily from California (mainly Los Angeles) and Native Hawaiians, Japanese-Americans, and European Americans primarily from Hawaii. State drivers' license files were the primary sources used to identify study subjects in Hawaii and California. Additionally, in Hawaii, state voter's registration files were used, and, in California, Health Care Financing Administration (HCFA) files were used to identify additional African American men. All participants (n=215,251) returned a 26-page self-administered baseline questionnaire that obtained general demographic, medical and risk factor information. In the cohort, incident cancer cases are identified annually through cohort linkage to population-based cancer Surveillance, Epidemiology, and End Results (SEER) registries in Hawaii and Los Angeles County as well as to the California State cancer registry. Information on stage and grade of disease are also obtained through the SEER registries. Blood sample collection in the MEC began in 1994 and targeted incident prostate cancer cases and a random sample of study participants to serve as controls for genetic analyses. This nested prostate cancer case-control study in the MEC consists of 890 invasive prostate cancer cases and 895 controls. This study was approved by the Institutional Review Boards at the University of Southern California and at the University of Hawaii and informed consent was obtained from all study participants.

MOFFITT: Moffitt Study, Tampa, Florida, US

This is a hospital-based incident study of 638 patients with primary adenocarcinoma of the prostate. They were recruited from 2002 to 2009 at the H. Lee Moffitt Cancer Center (Tampa, FL, US) and James A. Haley Veterans Affairs Hospital (Tampa, FL, US). Ninety-five percent of the case subjects who were asked to participate in the study agreed. All cancer cases were histologically confirmed by the Department of Pathology at each institution. The controls consisted of 147 subjects who were visiting the Lifetime Cancer Screening Center, which is affiliated with the H. Lee Moffitt Cancer Center or VA hospital. All control subjects were male and had had no previous diagnosis of cancer. The control subjects were frequency matched to the patients by age at diagnosis (± 5 years). Eighty-three percent of the control subjects who were asked to participate in the study consented. Non-genetic risk factor data for the present study were obtained through in-person interviews with the patients and controls at enrolment. The questionnaire covered demographic information, family history of cancer (i.e., whether they have one or more first-degree family member with prostate cancer), medical history, and detailed tobacco consumption. For the patients, data on cancer stage, Gleason score, and prostate specific antigen level were abstracted from the medical records. The subjects were asked to provide a blood or buccal sample after the interview as a source of genomic DNA.

PCMUS: Bulgaria

The Bulgarian sample of prostate cancer patients consist mainly of newly diagnosed cases, which are histopathologically confirmed. The patients (N=150, age range 39-93) are of Bulgarian origin. Transrectal biopsy was performed at the Urology Clinic, Alexandrovska University Hospital, mainly because of an elevated PSA. Some of the patients were referred from other centres to the tertiary university hospital after being previously diagnosed with prostate cancer. A small subset of patients had previously had definitive treatment (mainly radical prostatectomy) and they were called retrospectively with invitation to join the study. The control group is matched to the patients by sex, age, and ethnicity. It consists of two groups: (i) 72 healthy males, age range 54-87, presenting to our institution with lower urinary tract symptoms caused by benign prostatic hypertrophy (BPH) who had a PSA <3.5. The majority of them subsequently underwent surgical treatment with histological verification of the BPH; (ii) an additional healthy control group of 78 anonymous males matched to the prostate cancer patients by age and ethnicity, but with no PSA data.

POLAND

Polish case-control series included 458 men with prostate cancer, diagnosed in north-western Poland between 1999 and 2009 at the University Hospital in Szczecin. Study participants were unselected for age and family history. The mean age of prostate cancer diagnosis was 68 years (range 41–90 years). The control group included 476 cancer-free adult men from the same population (age range, 24–89 years; mean 63.1) taken from the healthy adult patients of five family doctors practicing in the Szczecin region. These individuals were selected randomly from the patient lists of the participating doctors.

ProtecT/ ProMPT, UK

The ProtecT[9] (Prostate testing for cancer and Treatment) trial is an NIHR-funded, UK-wide study of community-based PSA testing followed by a randomised controlled trial of prostate cancer treatment (radical surgery, radical conformal radiotherapy and active monitoring: ProMPT). Over 200,000 men between the ages of 50 and 69 years, ascertained through general practices in nine regions in the UK, were approached and over 100, 000 attended for PSA testing and, when PSA was 3.0ng/ml or more, for prostate cancer diagnosis. Over 95% of recruited men were of white ethnicity. For this study, after QC, 1563 cases identified by PSA screening within the ProtecT study were analysed. Controls with normal PSA levels (<3ng/ml) were selected from the same GP register and 5 year age band as the cases (n=1474 after QC were analysed).

QUEENSLAND: Australia

Caucasian patients were accrued through the Queensland node of the Australian Prostate Cancer BioResource (APCB), where cases were recruited through local urologists at the time of diagnosis (n=186 after QC). All cases had histopathologically confirmed prostate cancer, following

presentation with an abnormal serum PSA and/or lower urinary tract symptoms. Controls comprised healthy male blood donors with no personal history of prostate cancer, were recruited through Queensland University of Technology from the Australian Electoral Commission (n= 87, age range 54-90 years).

The Southern Community Cohort Study (SCCS)

The SCCS is a prospective cohort of African Americans and non-African Americans which during 2002-2009 enrolled over 85,000 residents aged 40-79 years across 12 southern states (www.southerncommunitystudy.org)[10]. Recruitment occurred mainly at community health centers, institutions providing basic health services primarily to the medically uninsured, so that the cohort includes many adults of lower income and educational status. Each study participant completed a detailed baseline questionnaire, and nearly 90% provided a biologic specimen (approximately 45% a blood sample and 45% buccal cells). Follow-up of the cohort is conducted by linkage to national mortality registers and to state cancer registries. Included in this study are 545 African American prevalent and incident prostate cancer cases and 510 African American male controls.

SEARCH

Prostate cancer cases were identified via the Eastern Cancer Registration and Information Centre, East Anglia, UK. Incident cases <70 years at diagnosis are recruited. Controls are men attending general practice who are frequency- matched to cases by age and geographic region.

STOCKHOLM: Sweden STHM1

The Stockholm-1 (STHLM1) study invited men without a history of prostate cancer who had undergone prostate biopsy between 01.01.2005 and 31.12.2007 in the Stockholm area. In total, 7035 men were invited and 5241 (75%) consented to participate in the study by donating a blood sample and completing a questionnaire regarding life-style factors and family history of prostate cancer. Record linkage to the Regional Cancer Registry and the Stockholm part of the National Prostate Cancer Registry revealed information about incident prostate cancer cases in the cohort including tumour stage and grade of diseased men. For the present study DNA was available from a total of 2126 prostate cancer cases and 2403 unaffected men.

TAMPERE: Finland

Total of 8744 Finnish samples were sent to for typing. Of these, 2960 unselected cases and 165 controls (PSA < 4 µg/ml) were collected in Tampere, Finland and all are of Finnish origin. The mean age of diagnosis was 68.7 years (range 36-94). The patients were diagnosed with prostate cancer in 1993-2008 in the Tampere University Hospital, Department of Urology. Tampere University Hospital is a regional referral center in the area for all patients with prostate cancer,

which results in an unselected, population-based collection of patients. The other unselected set of samples were 5522 samples collected in the Finnish arm of The European Randomized Study of Screening for Prostate Cancer, which was initiated in the early 1990s to evaluate the effect of screening with prostate-specific–antigen (PSA) testing on death rates from prostate cancer. This sample set includes 1106 Finnish cancer cases and 4416 controls. These men were born in years 1933, 1937 and 1941 and were randomly assigned to a group that was offered PSA screening at an average of once every 4 years or to a control group that did not receive such screening. In addition to these two sporadic sample sets, 97 familial cancer cases (mean age at diagnosis 70 years) from Finnish prostate cancer families were genotyped.

UKGPCS

Blood DNA from prostate cancer cases was collected from cases throughout the UK aged $\leq$ 60 years at diagnosis and a systematic series from the prostate cancer clinic at The Royal Marsden NHS Foundation Trust. Diagnosis is confirmed from medical record or death certificate. 60% are clinically detected.

ULM: Germany

Cases were recruited in two different ways. Familial prostate cancer probands (index cases) were ascertained from all over Germany. They were advised by their attending physicians to contact the Clinic of Urology of Ulm. The positive family history was then verified by reviewing medical records or death certificates of family members. In each case, only one member of each family (e.g. the proband) was enrolled in the present study. Sporadic cases, who reported no relatives affected with prostate cancer, were almost exclusively collected at Ulm during their course of treatment (e.g. radical prostatectomy) in our Urology Clinic. The control group consists of 213 age-matched healthy men and 295 population controls of unknown disease status.

UTAH, US

All 455 prostate cancer cases were drawn from the set of sampled prostate cancer cases belonging to extended Utah high-risk pedigrees. All cases were selected to have kinship coefficients ≤0.0156 with any other case included from the high-risk pedigree set. The 256 controls were selected from other high-risk pedigree studies as: 1) not related to a prostate kindred, 2) not having cancer, 3) not having a first degree relative with prostate cancer.

WUGS: St. Louis, Missouri, US

The Washington University Genetic Study is a prospective study designed to investigate both genetic and non-genetic risk factors for prostate cancer progression. A hospital-based series of 1901 patients with newly diagnosed prostate cancer, who were treated for prostate cancer

between August 2004 and August 2011. All patients had biopsy-proven adenocarcinoma of the prostate. From this cohort were selected 990 consecutively treated patients from August 2004-March 2010, with available blood DNA and environmental data.

UKGPCS, ProtecT and PRACTICAL co-authorship list

The UK Genetic Prostate Cancer Study Collaborators

Mr Z Abbasi,
Mr M Akhlil Abdul-Hamid
Mr Paul D Abel
Professor Paul H Abrams
Dr Fawzi A Adab
Mr Andrew Adamson
Mr A Adeyoju
Mr Naveed Afzal
Mr Ernest K N Ahiaku
Mr Munir Ahmed
Mr Mohammed L Al Sudani
Dr Christopher Alcock
Dr Zulfiqar Ali
Mr David J Almond
Dr Roberto Alonzi
Dr Amir S M Al-Samarraie
Dr Al-Samerraie
Mr Waleed Al-Singary
Mr Al-Sudani
Mr John Anderson
Mr Steven Andrews
Mr Henry Andrews
Mr Iqbal Anjum
Mr Ken Anson
Dr Nicola A Anyamene
Mr Ike Apakama
Dr F Aparcia
Mr J A A Archbold
Dr D Ash
Dr Richard F U Ashford
Dr A Azzabi
Mr David Badenoch
Dr Amit Bahl
Mr M J Bailey
Mrs Karen Bailey
Mr Andrew J Ball
Mr G Banerjee
Dr N Barber
Dr Jim Barber
Dr Baria
Mr Douglas G Barnes
Mr J Bashir
Mr Pradip Basu
Mr Christopher A Bates
Dr N A Bax
Mr D Baxter-Smith
Mr Amar Bdesha
Mr Christopher J M Beacock
Professor Ronald P Beaney
Mr Ralph Beard
Mr John D Beatty
Mr Rupert Beck
Ms Gail Beese
Dr Sharon Beesley
Mr C Richard W Bell
Mr James Bellringer
Dr Richard Benson
Dr Beresford
Mr Christopher R A Bevis
Dr Rajanee Bhana
Mr S Bhanot
Dr A Bhatnagar
Mr R I Bhatt
Mr Brian Birch
Dr Alison Birtle
Mr M Bishop
Mr C Shekhar Biyani
Mr A R E Blacklock
Miss Rosemary Blades
Dr Peter Bliss
Dr David J Bloomfield
Miss S Boddy
Professor C M Booth
Mr Pradeep Bose
Dr Michael C Bott
Dr David Bottomley
Mr Nigel R Boucher
Dr J Bowen
Dr Mark Bower
Mr W G Bowsher
Mr P J R Boyd
Mr F James Bramble
Mr Simon F Brewster
Mr Tim Briggs
Dr Cathryn Brock
Dr Sue Brock
Mr Stephen Bromage
Mr Richard Brough
Dr Richard Brown
Mr Stephen Brown
Mr Richard Brown
Mr Tony J Browning
Mr N Bryan
Mr Neil A Burgess
Mr Nicholas Burns-Cox
Mr Paul C Butterworth
Mr D Cahill
Mr P S Callaghan
Mr John Calleary
Dr M Calleja
Dr Frances Calman
Dr Philip Camilleri
Mr Alister Campbell
Miss Andrea Cannon
Dr Dawn M Carnell
Mr T W Carr
Mr Simon Carter
Mr Charles J M Carter
Dr Adam C Carter
Dr Bruce M Castle
Mr David Chadwick
Mr Rohit Chahal
Dr P Chakraborti
Mr Chappell
Mr C Charig
Dr Anula D Chetiyawardana
Mr Christopher Chilton
Mr F I Chinegwundoh
Dr Irene Chong
Dr Ananya Choudhury
Mr Wai-Man Chow
Mr Timothy J Christmas
Dr Mark J Churn
Mr Noel W Clarke
Mr Jorge Clavijo-Eisele
Dr M Coe
Mr N P Cohen

Mr C Coker
Dr Trevor Cole
Dr David J Cole
Mr O Cole
Mr Gerald Collins
Dr Matthew Collinson
Mr I Conn
Dr C Connell
Dr Audrey Cook
Mr Peter Cooke
Mr Graeme Cooksey
Mr L Coombs
Mr Robert F Copland
Mr Andrew J Cornaby
Mr P A Cornford
Mr Corolis
Mr John Corr
Mr C B Costello
Mrs N Coull
Dr Richard Cowan
Mr Robert Cox
Dr C Coyle
Mr Jeremy Crew
Mr John C Crisp
Dr W Cross
Mr W Cross
Dr Dorthe Cruger
Mr Malcolm Crundwell
Mr Cummings
Mr Nazeer Dahar
Dr Francis N Daniel
Mr J Darrad
Mr Pallon Daruwala
Mr Gautam Das
Mr Shibendra Datta
Dr S Davidson
Dr Joseph Davies
Mr Owen W Davison
Mr Guy Dawkins
Mr Chris Dawson
Mr Alan R De Bolla
Professor David Dearnaley
Mr Ken M Desai
Dr George P Deutsch
Mr John Dick
Mr Andrew J Dickinson
Dr Jeanette Dickson
Mr Michael Dinneen
Dr Sanjay Dixit
Dr H Jane Dobbs
Mr A Doble
Dr David Dodds
Mr Alan Doherty
Mr P Donaldson
Dr M Dooldeniya
Dr S Fiona Douglas
Mr Drake
Dr Gill M Duchesne
Mr Peter Duffy
Mr Michael Dunn
Mr W D Dunsmuir
Dr Sajid K Durrani
Mr Alan C Eaton
Professor Diane Eccles
Mr B Eddy
Mr C D Eden
Mr J Edwards
Mr Jeremy Elkabir
Dr P Tony Elliott
Mr B W Ellis
Dr R Ellis
Dr A El-Modir
Mr Andrew W S Elves
Dr Christine Elwell
Mr Mark Emberton
Dr Louise Emmerson
Mr Roland C D England
Mr R D Errington
Professor D Gareth Evans
Dr Alison Falconer
Mr Derek Fawcett
Dr C Featherston
Dr Carolyn J Featherstone
Mr Jeremy Feggetter
Dr C Ferguson
Dr D Fermont
Mr Michael Ferro
Mr Matthew Fletcher
Dr A Folkes
Mr Trevor F Ford
Mr Paul W Foster
Dr Kevin N Franks
Dr Olivera Frim
Dr Joanna Gale
Mr Christopher Gallegos
Mr James S Gelister
Dr Ghana
Dr Stephanie Gibbs
Mr Hugh Gilbert
Mr David Gillatt
Dr John Glaholm
Mr Jonathan M Glass
Mr James Glenister
Dr Thomas D Goode
Ms E M Gordon
Mr Richard L Gower
Dr John Graham
Mr Damian Green
Mr Jonathan Greenland
Dr Robert Grieve
Mr Thomas R L Griffiths
Mr Sandy Gujral
Dr Nishi Gupta
Mr Riza Murat Gurun
Mr Peter J Guy
Mr Neil Haldar
Mr N Halder
Professor F C Hamdy
Dr C Hamilton
Mr John Hammonds
Mr S J Hampson
Mr Damien C Hanbury
Dr P D John Hardman
Dr Stephen J Harland
Mr John M Harney
Dr Peter Harper
Dr Sarah Harris
Mr D Harris
Mr G S M Harrison
Mr D R Harriss
Mr N Harvey-Hills
Mr Simon Hawkyard
Dr Catherine M Heath
Mr Michael Hehir
Mr Giles O Hellawell
Mr David Hendry
Mr Mike Henley
Dr Ann Henry
Dr John Hetherington
Dr Tamas Hickish
Mr James A Hicks
Dr Serena Hilman
Mr Richard Hindley
Mr John R Hindmarsh
Mr John Hines
Dr M Hingorani
Mr Edwin T S Ho
Professor Shirley Hodgson
Dr U Hoffman
Mr David Holden
Dr A Hollingdale
Mr Graham W Hollins
Mr Simon A V Holmes
Dr Gail Horan
Professor Alan Horwich
Professor Peter Hoskin
Mr Graham P Howell
Mr D Hrouda
Dr Robert Huddart
Ms Liz Hudson
Dr Rob Hughes

Mr Michael Hughes
Mr Owen Hughes
Dr Caroline Humber
Mr John W Iacovou
Dr A Ibrahim
Mr John A Inglis
Mr Stuart Irving
Mr C Irwin
Dr Louise Izatt
Mr Victor Izegbu
Mr Basharat Jameel
Mr Michael J James
Professor N James
Mr R Lester James
Mr Pradip Javle
Dr P Jenkins
Dr Sameer Jhavar
Dr Gareth Jones
Mr Chris R Jones
Dr David A Jones
Mr J Joseph
Dr Shelagh Joss
Mr Amir Kaisary
Dr Alexandre L Kaliski
Dr G Kapur
Mr O Karim
Dr Stephen J Karp
Mr F X Keeley
Mr Anand R Kelkar
Mr J P Kelleher
Mr John Kelly
Dr Sue Kenwrick
Mr F Khan
Dr Vincent Khoo
Ms Rachel M Kimber
Mr R Kinder
Professor Roger S Kirby
Professor David Kirk
Dr Peter Kirkbride
Mr Magdi M Kirollos
Mr Roger Kockelbergh
Mr Philip C W C Koenig
Mr Gordon G Kooiman
Dr O Koreich
Mr Anthony Koupparis
Mr Mohamed Kourah
Dr Sigurd Kraus
Ms Magda L Kujawa
Mr Ravi Kulkarni
Mr M Kumar
Dr Ian H Kunkler
Professor H Kynaston
Dr Katherine L Lachlan
Dr Robert Laing
Dr Fiona Lalloo
Mr M Lancashire
Mr Stephen E M Langley
Mr Marc Laniado
Mr T R Larner
Mr Maurice W Lau
Mr W T Lawrence
Miss Anne Lawson
Mr Pieter J Le Roux
Professor Mary Leader
Mr J O Lee
Ms L Lee
Ms A Lee
Dr R John Lemburger
Dr Priscilla Leone
Dr Jason Lester
Mr Hing Leung
Mr J Lewis
Mr D Christopher Lewis
Mr Thomas Liston
Dr Jacqueline Livsey
Mr S Lloyd
Dr Imogen Locke
Mr Richard Lodge
Dr John Logue
Mr Mark Longmuir
Mr Malcolm G Lucas
Mr C J Luscombe
Dr Anna Lydon
Mr Michael Lynch
Mr Naing N K Lynn
Mr James P A MacDermott
Mr Ruaraidh P Macdonagh
Mr Macdonald
Mr Sanjeev Madaan
Dr Kudingila R Madhava
Dr Joseph Maguire
Professor E R Maher
Dr Rana Mahmood
Dr Graeme H M Mair
Mr Peter R Malone
Dr Stephen A Mangar
Mr Mark Mantle
Mr I Mark
Mr Robert Mason
Professor M D Mason
Mr Matanhelia
Mr Shyam Matenhelia
Mr Philip N Matthews
Dr J McAleese
Ms Donna McBride
Mr Jonathan McFarlane
Mr McGrath
Mr Craig McIlhenny
Mr Paul McInerney
Mr Gregor McIntosh
Dr F McKinna
Dr Duncan McLaren
Miss Esther McLarty
Dr Rhona McMenemin
Mr Alan McNeill
Mr T A McNicholas
Mr Robert N Meddings
Mr A David Mee
Dr Lucinda Melcher
Mr Memon
Mr Pravin Menzes
Mr Marek Miller
Mr Robert Mills
Mr S Mitchell
Dr Natasha Mithal
Dr Anita Mitra
Ms Gillian E Mobb
Mr Leslie E F Moffat
Mr Mokete
Dr Julian Money-Kyrle
Mr Bruce Montgomery
Mr Martin P Moody
Mr Roland Morley
Mr Sean B Morris
Professor Patrick Morrison
Dr Diana Mort
Mr Amir H Mostafid
Mr Hanif Motiwala
Mr Gulzar Mufti
Mr Gordon Muir
Mr Faiz Mumtaz
Mr Michael Murphy
Mr Keith W Murray
Dr Alexandra Murray
Dr Shirley Murrell
Dr D Muthukumar
Mr Harry Naerger
Mr Siva Namasivayam
Mr Vinod Nargund
Mr Nawrocki
Mr Donald Neilson
Dr A Nethersell
Mr Julian Barwell
Dr Jacqueline C Newby
Dr Hugh Newman
Dr R Newton
Mr Neil Oakley
Mr P J O'Boyle
Mr J O'Brien
Mr Tim S O'Brien
Dr H O'Donnell
Mr Neil O'Donoghue

Mr E O'Donoghue
Mr Chris Ogden
Mr Hemant Ohja
Professor Tim Oliver
Mr Eng K Ong
Mr P O'Reilly
Dr J S O'Rourke
Mr David Osborn
Dr Peter Ostler
Professor Joe O'Sullivan
Dr J Owen
Mr Edward Palfrey
Dr Miguel Panades
Dr Niki Panakis
Mr M Pancharatnam
Mr Michalakis L Pantelides
Dr U Panwar
Dr Omi Parikh
Dr Chris Parker
Mr Christopher H Parker
Mr Bohdan T Parys
Dr Sarah Pascoe
Mr Anup Patel
Dr Joan Paterson
Mr S Pathack
Ms Jhumur Pati
Dr Helen Patterson
Dr Pattu
Mr A Paul
Dr Heather Payne
Dr David Peake
Dr I Pedley
Mr A Pengelly
Mr Amjad M Peracha
Dr Matthew Perry
Mr Raj Persad
Mr John Peters
Mr N H Philp
Mr T Philp
Dr Lisa M Pickering
Dr Katharine Pigott
Mr R Plail
Dr P Nicholas Plowman
Mr Richard D Pocock
Mr A J Pope
Mr Rick Popert
Mr Tim Porter
Mr John M Potter
Mr Christopher Powell
Dr Thomas B Powles
Mr Krishna Prasad
Mr Seshadri Sri Prasad
Mr J W Prejbisz
Mr Stephen Prescott
Dr Andrew Protheroe
Mr Khaver N Qureshi
Dr Nigel Raby
Dr Narasimhan Ragavan
Mr Palaniappa G S Raju
Dr Prakash B Ramachandra
Dr R Raman
Mr Abhay Rane
Dr Julia Rankin
Mr Y Rao
Mr Hari L Ratan
Mr Ramachandran Ravi
Dr K Ravishankar
Dr Read
Mr Paul J Reddy
Mr Peter R Rimington
Dr Peter A Ritchie
Dr J Trevor Roberts
Mr Andrew Robertson
Dr Angus Robinson
Dr Anne C Robinson
Mr Lee Q Robinson
Mr Mark A Rochester
Mr P B Rogers
Mr Tomas P Rosenbaum
Mr Neil Rothwell
Mr Carl Rowbotham
Mr Rowe
Dr Kathryn Rowley
Dr Deborah Ruddy
Mr John Rundle
Dr John M Russell
Mr P G Ryan
Dr A Sabharwal
Dr Anand K Saggar
Dr Ali Samanci
Mr Vijay K Sangar
Mr M F Saxby
Mr Hartwig Schwaibold
Dr John E Scoble
Dr Christopher Scrase
Mr Selim
Mr Henry Sells
Mr Krishna K Sethia
Mr David C Shackley
Dr Shaffer
Dr Nihil Shah
Dr D Shakespeare
Dr Sue Shanley
Mr Neerah K Sharma
Dr Denise J Sheehan
Dr Elizabeth Sherwin
Dr Poh Lin Shum
Dr LucySide
Dr Norma Sidek
Professor Karol Sikora
Dr R Simcock
Mr Andrew M Sinclair
Mr Pravin Singh
Dr M Siva
Mr Michael F Smith
Mr James Smith
Dr Michael Sokal
Mr Graham M Sole
Mr Mark J Speakman
Dr Alexander Spiers
Dr Thiagarajan Sreenivasan
Dr Narayanan N Srihari
Mr Srinivasan
Mr Rajagopalan Sriram
Dr John N Staffurth
Dr D Stewart
Dr Andrew Stockdale
Mr Mark A Stott
Mr M J Stower
Mr John R Strachan
Professor Nicholas S A Stuart
Dr Elaine Sugden
Mr Duncan Summerton
Dr Santhanam Sundar
Mr S K Sundaram
Mr Gokarakonda Suresh
Mr Shabbir Susnerwala
Mr Kuchibhotla S Swami
Miss Stephanie J Symons
Dr Isabel Syndikus
Dr Saad Tahir
Dr J Tanquay
Dr John W Taylor
Dr J W Taylor
Mr T Terry
Dr Robert J Thomas
Mr Stephen A Thomas
Mr Alan Thompson
Dr Alastair H Thomson
Dr A Thurston
Dr Owen Tilsley
Mr Stuart F Tindall
Dr K Tipples
Dr Tong
Mr Hamid Toussi
Dr Elizabeth W Toy
Professor Richard C Trembath
Mr David N Tulloch
Mr Kevin J Turner

Mr James Tweedle
Dr C J Tyrell
Mr N Umez-Eronini
Mr Graeme H Urwin
Mr Justin A Vale
Dr Van As
Dr Nicholas Van As
Dr Subramaniam Vasanthan
Mr Sean Vesey
Dr Maria Vilarino-Varela
Dr John Violet
Mr Jaspal Virdi
Dr Robert Wade
Dr Katherine Waite
Mr E M Walker
Mr Roger Walker
Mr David M A Wallace
Mr Nicholas A Watkin
Mr M E Watson
Professor J H Waxman
Mr Brian Waymont
Dr Andrew Weaver
Mr Ralph J Webb
Mr Andrew Wedderburn
Dr Paula Wells
Mr G D Wemyss-Holden
Mr P M T Weston
Dr Duncan Wheatley
Mr P Whelan
Dr D Whillis
Mr Adam D Wilde
Dr Vicki Wiles
Dr Marie Wilkins
Mr John H Williams
Mr Simon Williams
Mr Michael Willis
Mr Michael I Wills
Mr Richard Wilson
Mr J R Wilson
Mr Mathias H Winkler
Dr Marcus Wise
Mr Simon Woodhams
Professor C Woodhouse
Dr Cathryn Woodward
Dr Woolf
Mr K A Woolfenden
Dr Jane Worlding
Mr Mark Wright
Dr James P Wylie
Dr Chris Wynne
Ms Angelika Zang
Dr A Zarkar

The UK ProtecT Study Collaborators

Prasad Bollina, Sue Bonnington, Lynne Bradshaw, James Catto, Debbie Cooper, Liz Down, Andrew Doble, Alan Doherty, Garrett Durkan, Emma Elliott, David Gillatt, Pippa Herbert, Peter Holding, Joanne Howson, Mandy Jones, Roger Kockelbergh, Rajeev Kumar, Peter Holding, Howard Kynaston, Athene Lane, Teresa Lennon, Norma Lyons, Hing Leung, Malcolm Mason, Hilary Moody, Philip Powell, Alan Paul, Stephen Prescott, Derek Rosario, Patricia O'Sullivan, Pauline Thompson, Lynne Bradshaw, Sarah Tidball.

THE BPC3 and PRACTICAL CONSORTIUM (in addition to those named in the author list)

UK Genetic Prostate Cancer Study and The Prostate Cancer Research Foundation Study

The Institute of Cancer Research & The Royal Marsden NHS Foundation Trust, Sutton UK

Stephen Edwards

Cyril Fisher

Charles Jameson

Elizabeth Page

The ProtecT Study

Paul M. Brown

Anne George

Gemma Marsden

Athene Lane

Michael Davis
The UK ProtecT Study Collaborators – as above

CAPS SWEDEN
Jan Adolfson
Pär Stattin
Jan-Erik Johansson

AUSTRALIA (Melbourne)
John Pedersen

AUSTRALIA (Queensland)
Australian Prostate Cancer Bio Resource-QLD node:
Peter Heathcote
Glenn Wood
Greg Malone
Pamela Saunders
Allison Eckert
Trina Yeadon
Kris Kerr
Angus Collins
Megan Turner

Australian Prostate Cancer Research Centre-Qld, Institute of Health and Biomedical Innovation, Queensland, University of Technology, Brisbane, Australia:
Srilakshmi Srinivasan
Mary-Anne Kedda
Kimberly Alexander
Tracy O'Mara

BULGARIA PCMUS study
Medical University – Sofia,
Department of Urology
Elenko Popov

Molecular Medicine Center and Department of Chemistry and Biochemistry

Darina Kachakova
Atanaska Mitkova
Teodora Goranova
Gergana Stancheva
Olga Beltcheva
Rumyana Dodova

Department of General and Clinical Pathology
Aleksandrina Vlahova
Tihomir Dikov
Svetlana Christova

DENMARK
CPCS1
Department of Urology, Herlev Hospital, Copenhagen University Hospital,
Herlev, Denmark
CPCS2
Prof. DMSc Peter Iversen. Department of Urology, Rigshospitalet,
Copenhagen University Hospital, Copenhagen, Denmark

GERMANY

EPIC-BPC3
Department of Epidemiology and Biostatistics, School of Public Health, Imperial College, London, United Kingdom

Hans Wallinder,
Sven Gustafsson

ESTHER
Saarland Cancer Registry, Saarbrücken, Germany
Christa Stegmaier

Ulm
Department of Urology, University Hospital Ulm, Germany
Manuel Luedeke
Mark Schrader

Institute of Human Genetics, University Hospital Ulm, Germany
Josef Hoegel

Department of Urology, Technical University Munich, Germany
Kathleen Herkommer

PORTUGAL

IPO-Porto Study

Department of Pathology, Portuguese Oncology Institute, Porto, Portugal
Rui Henrique

Department of Genetics, Portuguese Oncology Institute, Porto, Portugal
Carmen Jerónimo
Pedro Pinto
Joana Santos
João D. Barros-Silva

SWEDEN

CAPS

Carin Cavalli-Björkman,
Ami Rönnberg Karlsson,
Michael Broms

FINLAND

The Finnish Cancer Registry
Liisa Määttänen

MAYO

Lori Tillmans
Shaun Riska
Liang Wang

MEC-BPC3

Department of Preventive Medicine, Keck School of Medicine, University of Southern California, Los Angeles, CA, USA:
Stram Dan

Epidemiology Program, University of Hawaii Cancer Center, Department of Medicine, John A. Burns School of Medicine, Univerisity of Hawaii, Honolulu, HI, USA:
Kolonel Laurence N.

MOFFIT
Julio Pow-Sang
Hyun Y. Park
Selina Radlein
Maria Rincon
James A Haley VA Hospital, Tampa, FL, USA
Babu Zachariah

The COGS-Cancer Research UK GWAS-ELLIPSE (part of GAME-ON) Initiative This is the prostate component of these initiatives

ACKNOWLEDGEMENTS

This work was supported by European Commission's Seventh Framework Programme grant agreement n° 223175 (HEALTH-F2-2009-223175), Cancer Research UK Grants C5047/A7357, C1287/A10118, C5047/A3354, C5047/A10692, C16913/A6135, and The National Institute of Health (NIH) Cancer Post-Cancer GWAS initiative grant: No. 1 U19 CA 148537-01 (the GAME-ON initiative).

BPC3: This work was supported by the U.S. National Institutes of Health, National Cancer Institute [cooperative agreements U01-CA98233-07 to David J. Hunter, U01-CA98710-06 to Susan M. Gapstur, U01-CA98216-06 to Elio Riboli and Rudolf Kaaks, and U01-CA98758-07 to Brian E. Henderson, and Intramural Research Program of NIH/National Cancer Institute, Division of Cancer Epidemiology and Genetics].

CAPS: we would like to thank all urologists and other persons involved in the planning, coordination, and data collection of the CAPS study.

We would also like to thank the following for funding support: The Institute of Cancer Research and The Everyman Campaign, The Prostate Cancer Research Foundation, Prostate Research Campaign UK (now Prostate Action), The Orchid Cancer Appeal, The National Cancer Research

Network UK, The National Cancer Research Institute (NCRI) UK. We are grateful for support of NIHR funding to the NIHR Biomedical Research Centre at The Institute of Cancer Research and The Royal Marsden NHS Foundation Trust.

The FHCRC, Mayo, MCCS, Tampere, UKGPCS and Ulm groups are part of the ICPCG supported by NIH Grant No. U01 CA089600-04.

The Prostate Cancer Program of Cancer Council Victoria also acknowledge grant support from The National Health and Medical Research Council, Australia (126402, 209057, 251533, , 396414, 450104, 504700, 504702, 504715, 623204, 940394, 614296,), VicHealth, Cancer Council Victoria, The Prostate Cancer Foundation of Australia, The Whitten Foundation, PricewaterhouseCoopers, and Tattersall's. EAO, DMK, and EMK acknowledge the Intramural Program of the National Human Genome Research Institute for their support.

The QLD research is supported by The National Health and Medical Research Council, Australia Project Grant [390130, 1009458] and Enabling Grant [614296 to APCB]; the Prostate Cancer Foundation of Australia (Project Grant [PG7] and Research infrastructure grant [to APCB]).

We would like to acknowledge the support of The University of Cambridge, Cancer Research UK. Cancer Research UK grants [C8197/A10123] and [C8197/A10865] supported the genotyping team. We would also like to acknowledge the support of the National Institute for Health Research which funds the Cambridge Bio-medical Research Centre, Cambridge, UK. We would also like to acknowledge the support of the National Cancer Research Prostate Cancer: Mechanisms of Progression and Treatment (PROMPT) collaborative (grant code G0500966/75466) which has funded tissue and urine collections in Cambridge.

We are grateful to staff at the Welcome Trust Clinical Research Facility, Addenbrooke's Clinical Research Centre, Cambridge, UK for their help in conducting the ProtecT study. We also acknowledge the support of the NIHR Cambridge Biomedical Research Centre, the DOH HTA (ProtecT grant) and the NCRI / MRC (ProMPT grant) for help with the bio-repository. The UK Department of Health funded the ProtecT study through the NIHR Health Technology Assessment Programme (projects 96/20/06, 96/20/99). The ProtecT trial and its linked ProMPT and CAP (Comparison Arm for ProtecT) studies are supported by Department of Health, England; Cancer Research UK grant number C522/A8649, Medical Research Council of England grant number G0500966, ID 75466 and The NCRI, UK. The epidemiological data for ProtecT were generated though funding from the Southwest National Health Service Research and Development. DNA extraction in ProtecT was supported by USA Dept of Defense award W81XWH-04-1-0280,

Yorkshire Cancer Research and Cancer Research UK. The authors would like to acknowledge the contribution of all members of the ProtecT study research group. The views and opinions expressed therein are those of the authors and do not necessarily reflect those of the Department of Health of England. The bio-repository from ProtecT is supported by the NCRI (ProMPT) Prostate Cancer Collaborative and the Cambridge BMRC grant from NIHR.

We should like to acknowledge the NCRN nurses, data managers and Consultants for their work in the UKGPCS study.

The CGEMS and PLCO studies were funded by the Intramural Research Program of the Division of Cancer Epidemiology and Genetics, National Cancer Institute, NIH.

The Mayo group was supported by the US National Cancer Institute (R01CA72818).

The MEC was support by NIH grants CA63464, CA54281 and CA098758.
The Moffitt group was supported by the US National Cancer Institute (R01CA128813, PI: J.Y. Park).

The USC study was supported by the US National Cancer Institute (R01CA84979) and by the California Cancer Research Program (99-00524V-10258).

The San Francisco Bay Area Prostate Cancer Study was supported by the California Cancer Research Fund (99-00527V-10182).

The Tampere (Finland) study was supported by the Academy of Finland Grant 116437 and 126714, The Finnish Cancer Organisations, Sigrid Juselius Foundation, Reino Lahtikari Foundation and The Medical Research Fund of Tampere University Hospital (# 9L091). The PSA screening samples were collected by the Finnish part of ERSPC (European Study of Screening for Prostate Cancer). Linda Enroth is thanked for technical assistance**.** Riitta Vaalavuo and Liisa Määttänen are thanked for their work with databases.

The FHCRC studies were supported by grants RO1 CA056678, RO1 CA082664, and RO1 CA092579 from the National Cancer Institute, National Institutes of Health, with additional support from the Fred Hutchinson Cancer Research Center. Genotyping was supported by the Intramural Program of the National Human Genome Research Institute, National Institutes of Health.

The Department of Medical Epidemiology and Biostatistics, Karolinska Institute, Stockholm, Sweden was supported by the Cancer Risk Prediction Center (CRisP; www.crispcenter.org), a Linneus Centre (Contract ID 70867902) financed by the Swedish Research Council, Swedish Research Council (grant no K2010-70X-20430-04-3), the Swedish Cancer Foundation (grant no 09-0677), the Hedlund Foundation, the Söderberg Foundation, the Enqvist Foundation, ALF funds from the Stockholm County Council. Stiftelsen Johanna Hagstrand och Sigfrid Linnér's Minne, Karlsson's Fund for urological and surgical research. We thank and acknowledge all of the participants in the Stockholm-1 study. We thank Carin Cavalli-Björkman and Ami Rönnberg Karlsson for their dedicated work in the collection of data. Michael Broms is acknowledged for his skilful work with the databases. KI Biobank is acknowledged for handling the samples and for DNA extraction. Hans Wallinder at Aleris Medilab and Sven Gustafsson at Karolinska University Laboratory are thanked for their good cooperation in providing historical laboratory results.

The PCMUS study was supported by the Bulgarian National Science Fund, Ministry of Education, Youth and Science (contract DOO-119/2009) with additional support from the Science Fund of Medical University - Sofia (contract 51/2009; 8I/2009).

SCCS is funded by NIH grant R01 CA092447, and SCCS sample preparation was conducted at the Epidemiology Biospecimen Core Lab that is supported in part by the Vanderbilt-Ingram Cancer Center (P30 CA68485). Data on SCCS cancer cases used in this publication were provided by the Alabama Statewide Cancer Registry; Kentucky Cancer Registry, Lexington, KY; Tennessee Department of Health, Office of Cancer Surveillance; Florida Cancer Data System; North Carolina Central Cancer Registry, North Carolina Division of Public Health; Georgia Comprehensive Cancer Registry; Louisiana Tumor Registry; Mississippi Cancer Registry; South Carolina Central Cancer Registry; Virginia Department of Health, Virginia Cancer Registry; Arkansas Department of Health, Cancer Registry, 4815 W. Markham, Little Rock, AR 72205. The Arkansas Central Cancer Registry is fully funded by a grant from National Program of Cancer Registries, Centers for Disease Control and Prevention (CDC). Data on SCCS cancer cases from Mississippi were collected by the Mississippi Cancer Registry which participates in the National Program of Cancer Registries (NPCR) of the Centers for Disease Control and Prevention (CDC). The contents of this publication are solely the responsibility of the authors and do not necessarily represent the official views of the CDC or the Mississippi Cancer Registry.

The Keith and Susan Warshaw Fund, C. S. Watkins Urologic Cancer Fund and The Tennity Family Fund supported the Utah study. The project was supported by Award Number P30CA042014 from the National Cancer Institute.

The ESTHER study was supported by a grant from the Baden-Württemberg Ministry of Science, Research and Arts.

The authors would like to acknowledge the contribution of the entire staff of the genotyping unit under the supervision of Dr. Sylvie LaBoissière as well as Frédérick Robidoux from the McGill University and Génome Québec Innovation Centre.

John Hopper is an Australia Fellow of the NHMRC. A. Spurdle is an NHMRC Senior Research Fellow, J. Clements is an NHMRC Principal Research Fellow, and J. Batra is an NHMRC Training Fellow.
We should like to thank all the patients and control men who took part in this study.

Reference List

1. Eeles,R.A. *et al.* Multiple newly identified loci associated with prostate cancer susceptibility. *Nat. Genet.* **40**, 316-321 (2008).
2. Eeles,R.A. *et al.* Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. *Nat. Genet.* **41**, 1116-1121 (2009).
3. Schumacher,F.R. *et al.* Genome-wide association study identifies new prostate cancer susceptibility loci. *Hum. Mol. Genet.*(2011).
4. Yeager,M. *et al.* Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. *Nat. Genet.* **39**, 645-649 (2007).
5. Zheng,S.L. *et al.* A comprehensive association study for genes in inflammation pathway provides support for their roles in prostate cancer risk in the CAPS study. *Prostate* **66**, 1556-1564 (2006).
6. Riboli,E. *et al.* European Prospective Investigation into Cancer and Nutrition (EPIC): study populations and data collection. *Public Health Nutr.* **5**, 1113-1124 (2002).
7. FitzGerald,L.M. *et al.* Sequence variants of alpha-methylacyl-CoA racemase are associated with prostate cancer risk: a replication study in an ethnically homogeneous population. *Prostate* **68**, 1373-1379 (2008).
8. Schaid,D.J., McDonnell,S.K., Blute,M.L., & Thibodeau,S.N. Evidence for autosomal dominant inheritance of prostate cancer. *Am. J. Hum. Genet.* **62**, 1425-1438 (1998).
9. Donovan,J. *et al.* Prostate Testing for Cancer and Treatment (ProtecT) feasibility study. *Health Technol. Assess.* **7**, 1-88 (2003).
10. Signorello,L.B., Hargreaves,M.K., & Blot,W.J. The Southern Community Cohort Study: investigating health disparities. *J. Health Care Poor Underserved* **21**, 26-37 (2010).