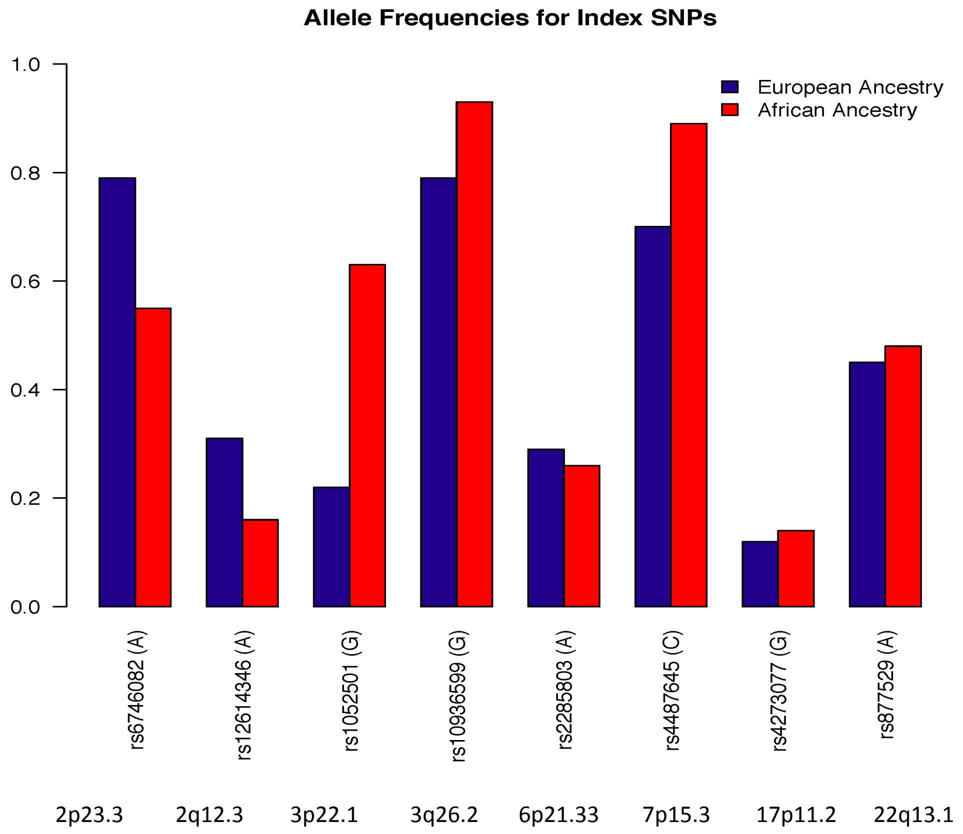
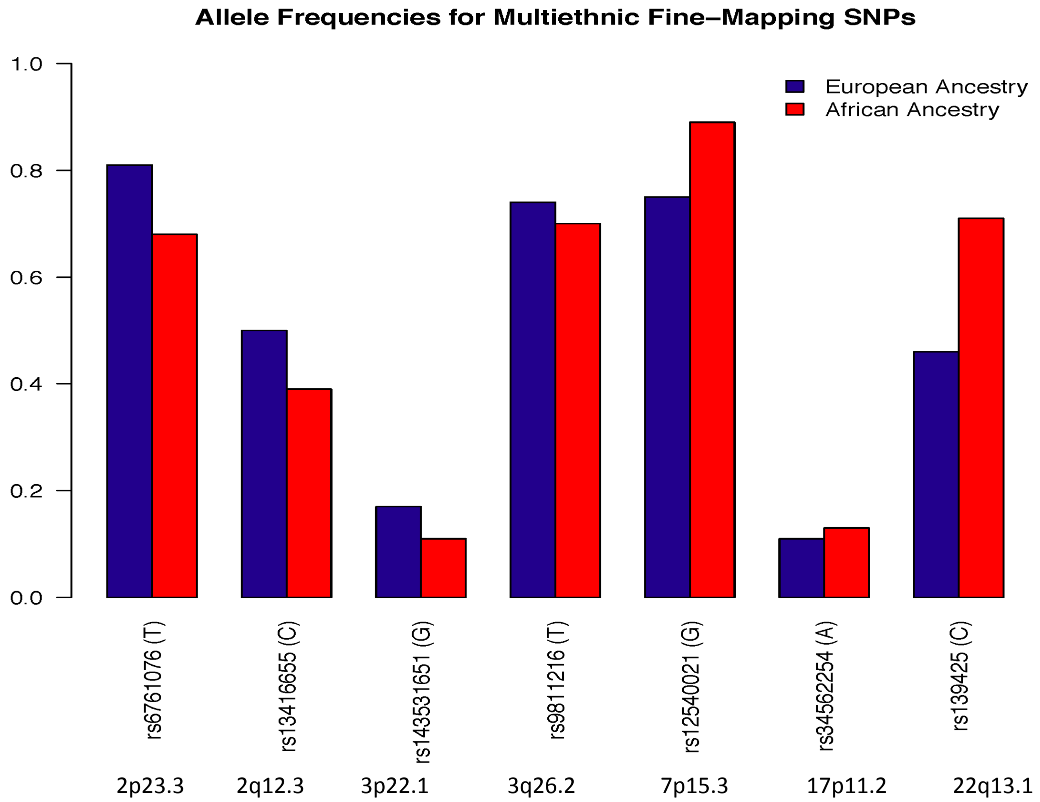
Supplementary Figure 1a. Allele frequencies of index SNPs observed in subjects of European and African ancestry.

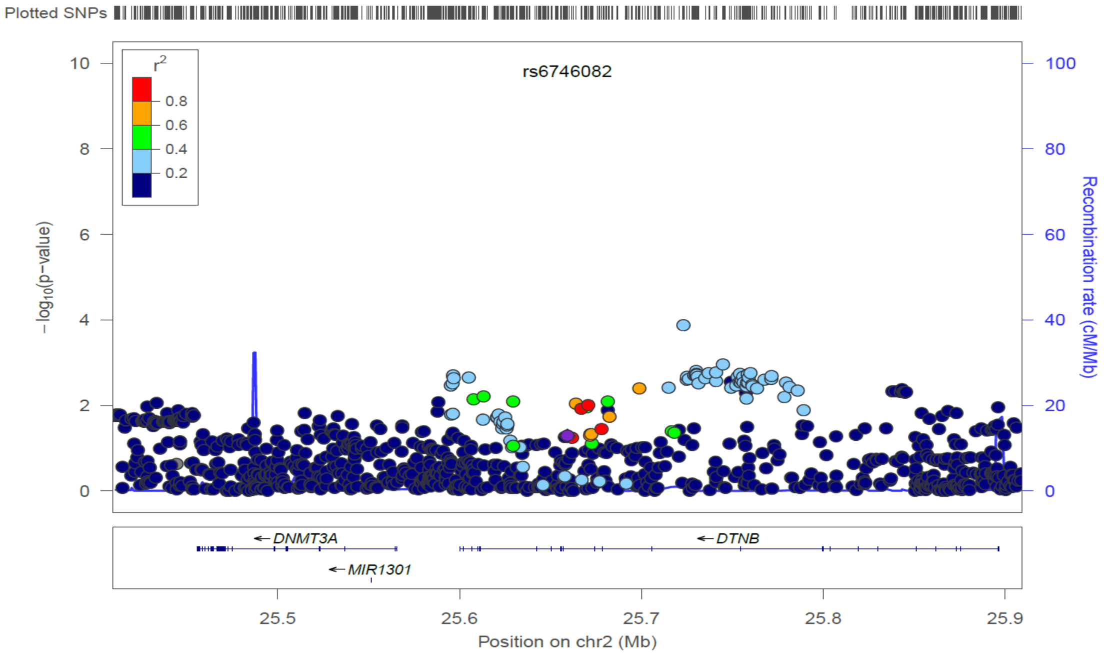


Supplementary Figure 1b. Allele frequencies observed in subjects of European and African ancestry for the most significant SNPs from the combined meta-analysis in two populations.

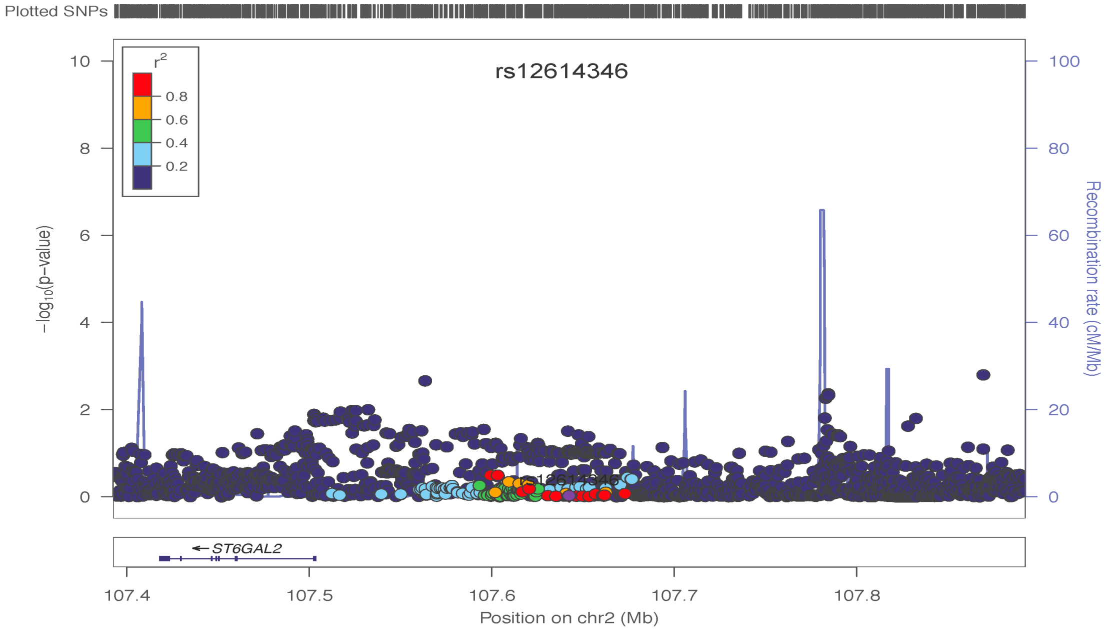


Supplementary Figure 2a. LocusZoom plots for the eight regions for subjects of European ancestry. (1KGP EUR reference)

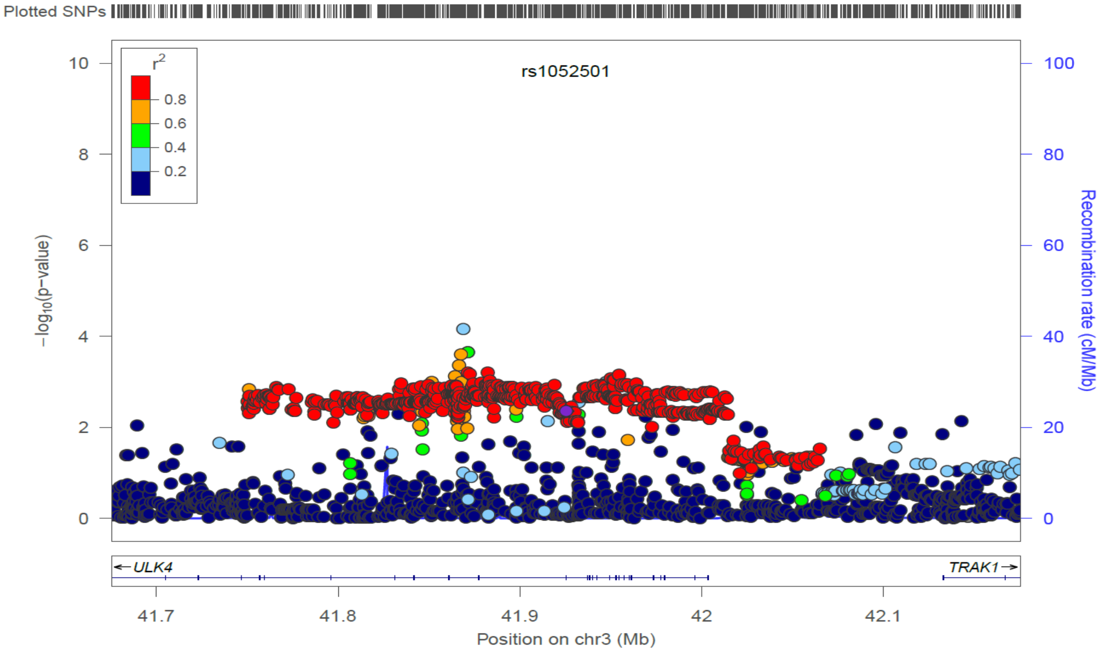
2p23.3



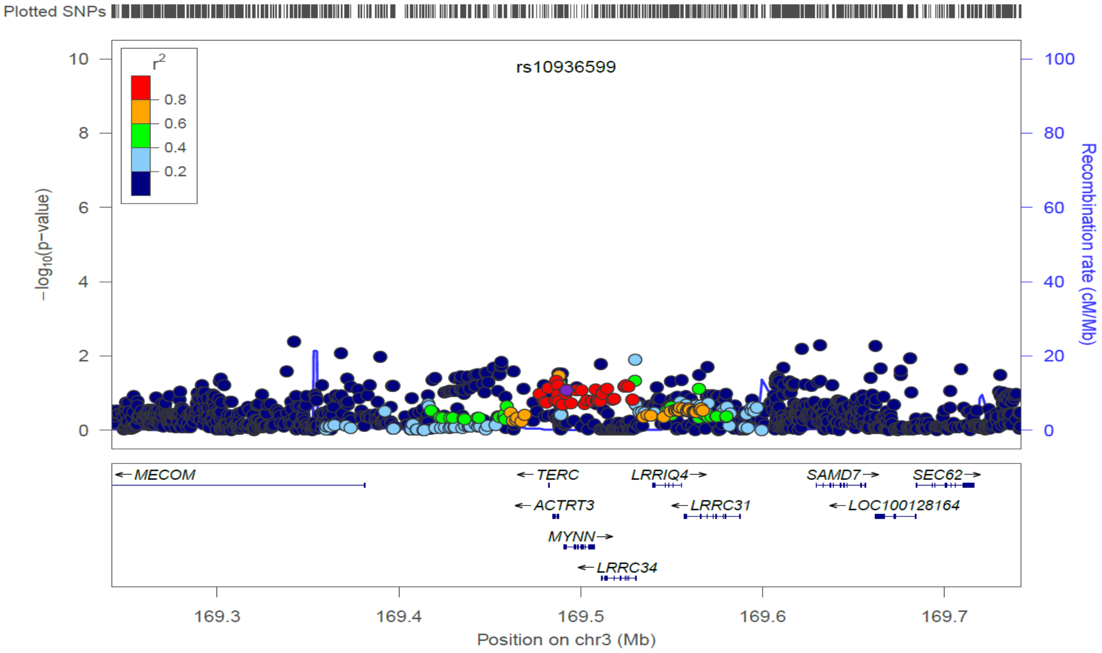
2q12.3



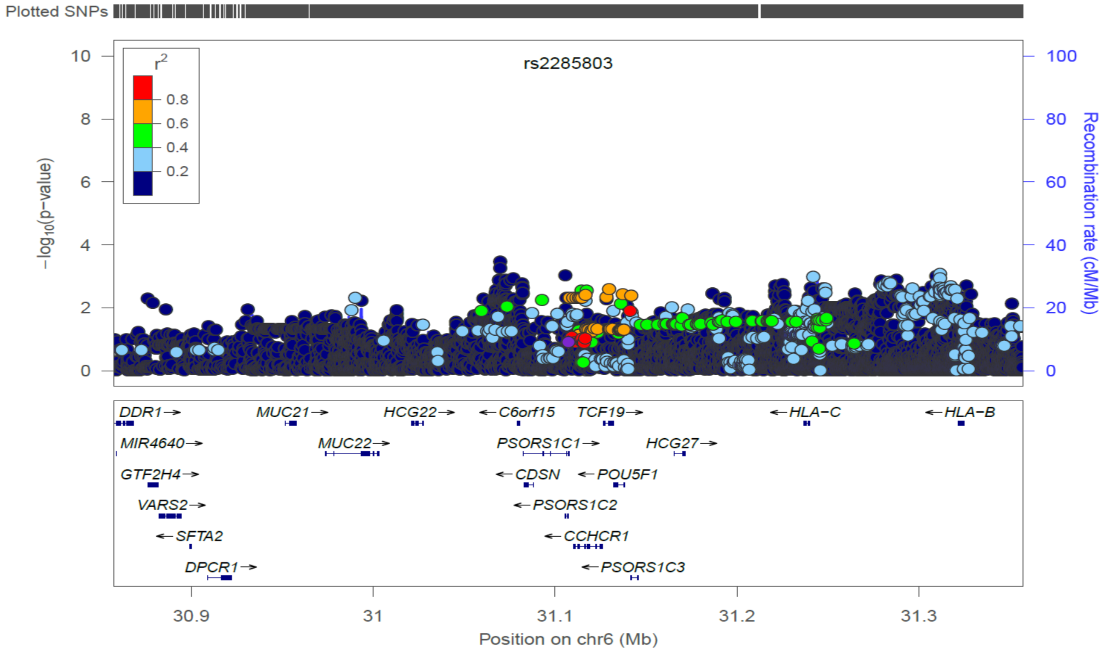
3p22.1


Plotted SNPs
rs1052501
r2
0.8
0.6
0.4
0.2
-log10(p-value)
10
8
6
4
2
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
ULK4
TRAK1
41.7
41.8
41.9
42
42.1
Position on chr3 (Mb)

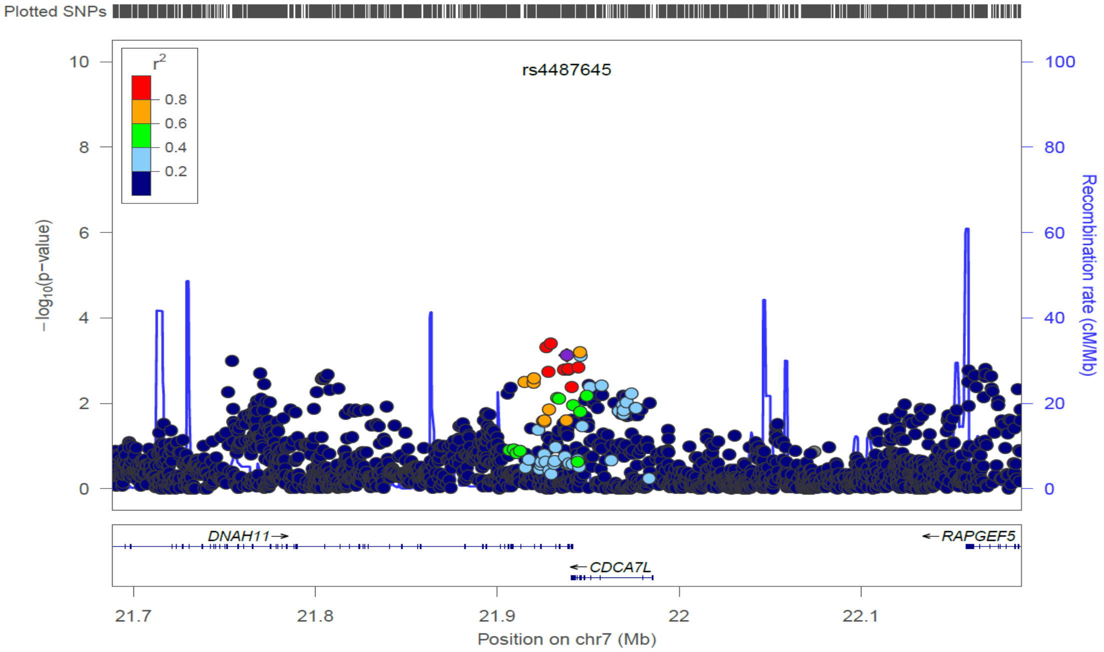
3q26.2


Plotted SNPs
rs10936599
r2
0.8
0.6
0.4
0.2
-log10(p-value)
10
8
6
4
2
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
MECOM
TERC
ACTRT3
MYNN
LRRC34
LRRIQ4
LRRC31
SAMD7
LOC100128164
SEC62
169.3
169.4
169.5
169.6
169.7
Position on chr3 (Mb)

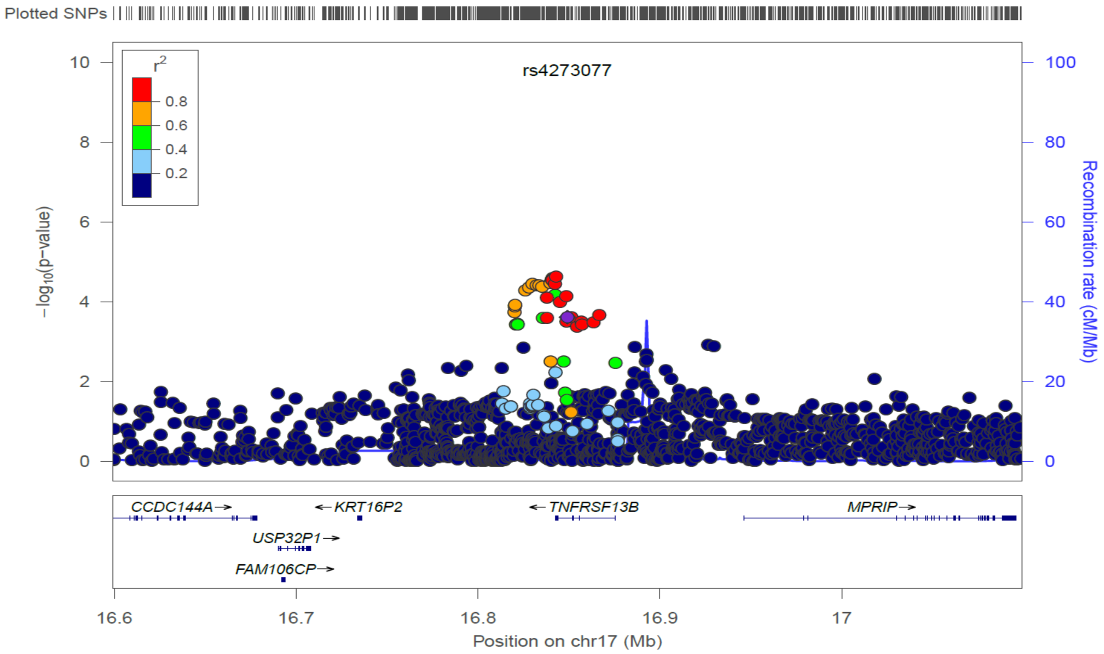
6p21.33



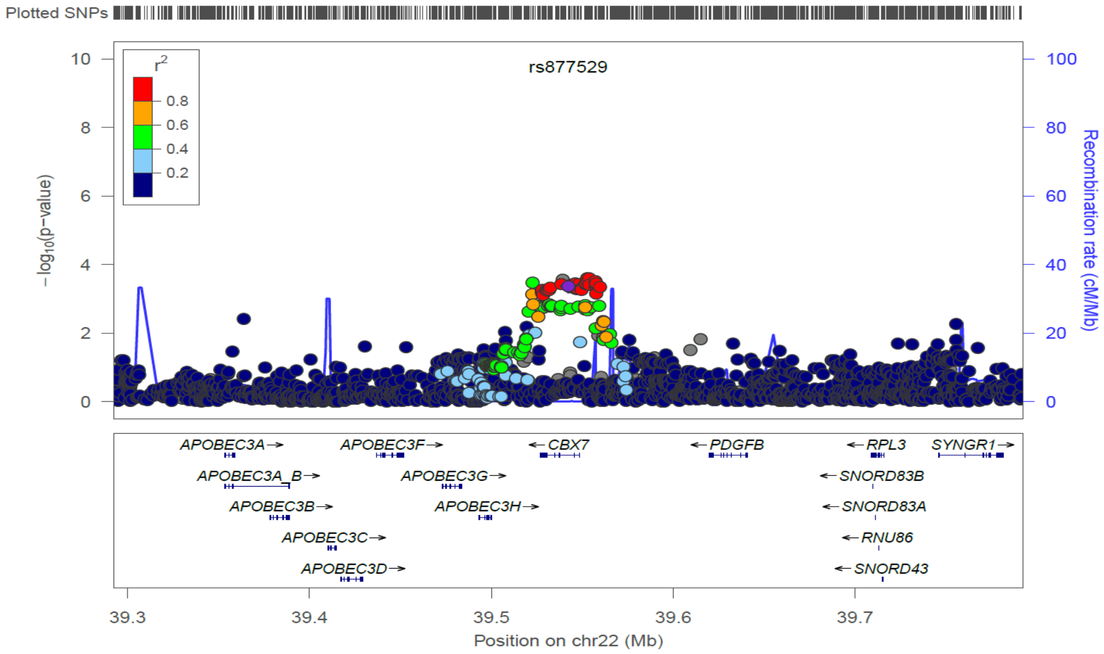
7p15.3



17p11.2

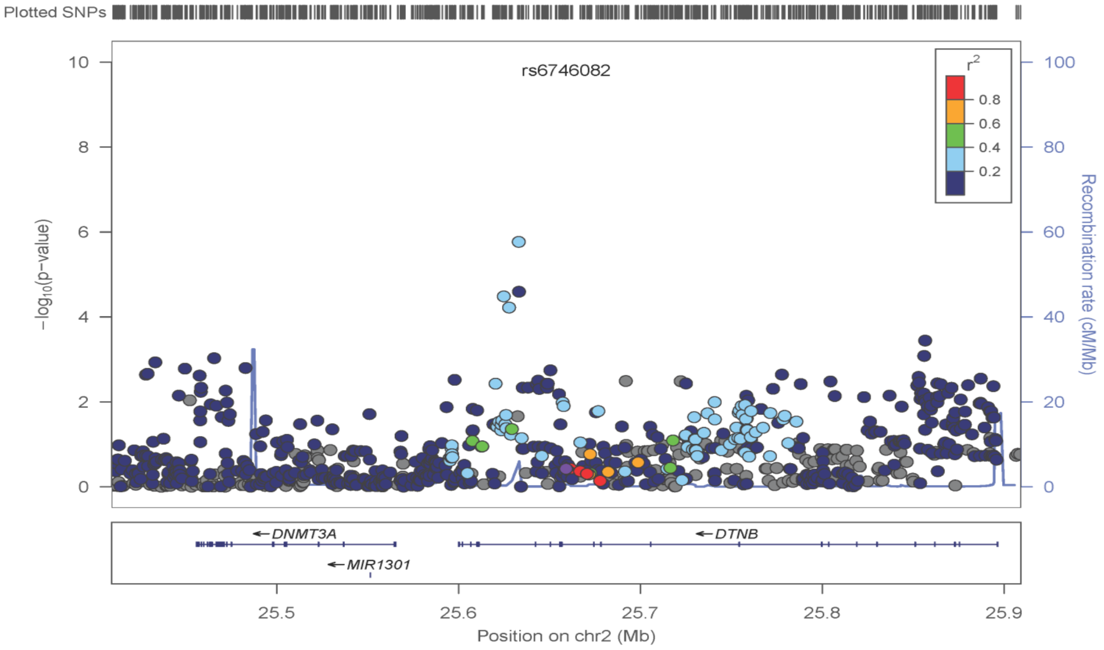


22q13.1

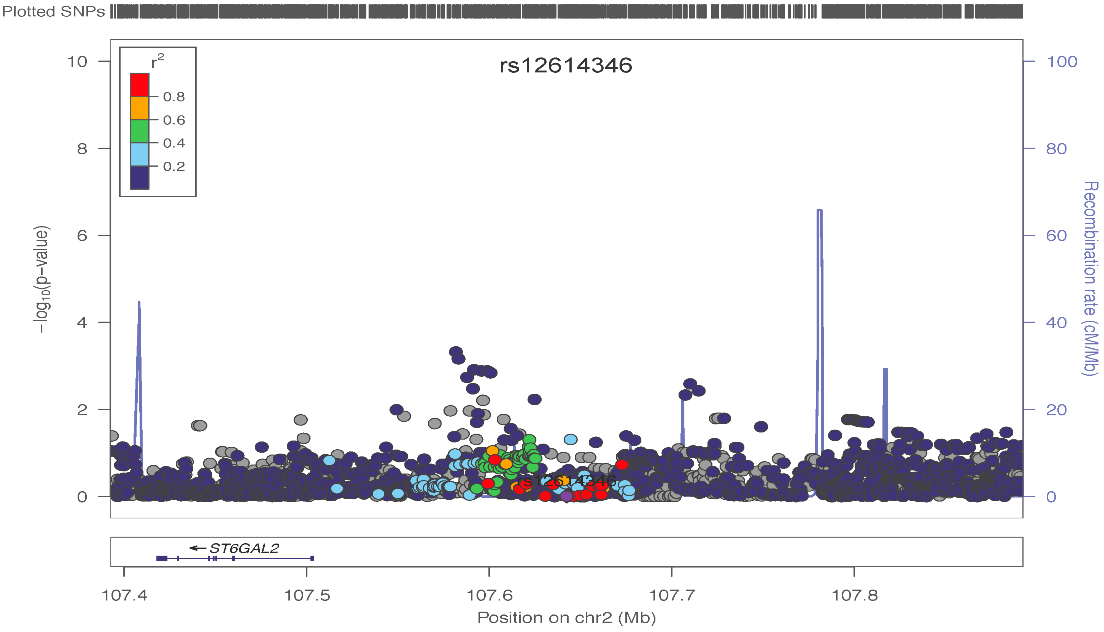


Supplementary Figure 2b. LocusZoom plots for the eight regions for subjects of African ancestry. (1KGP EUR reference)

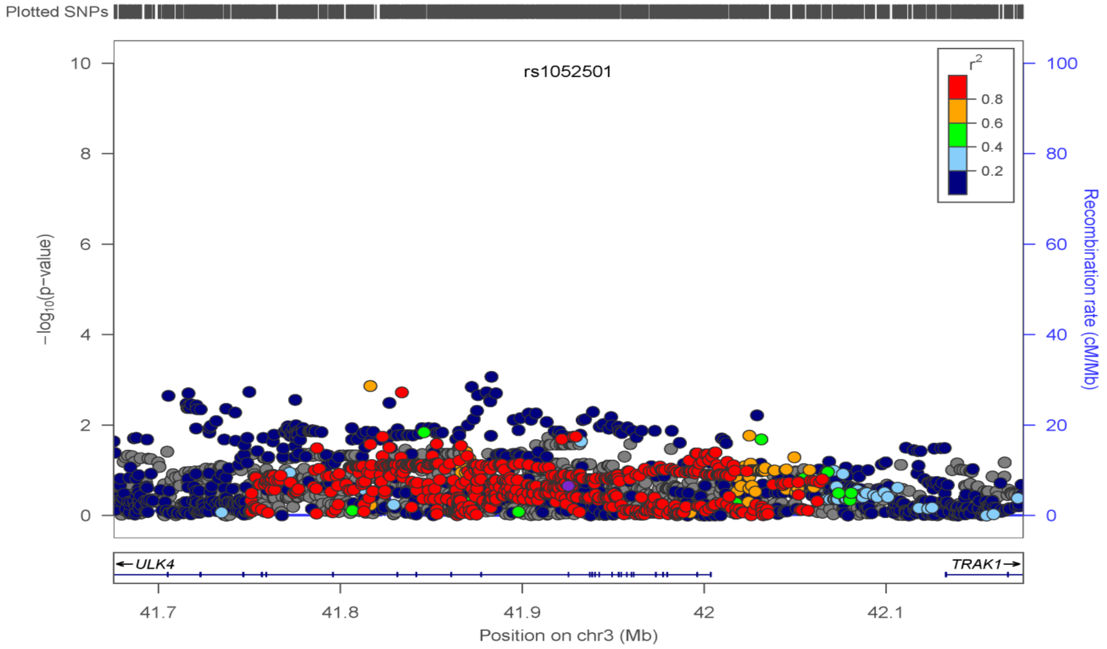
2p23.3



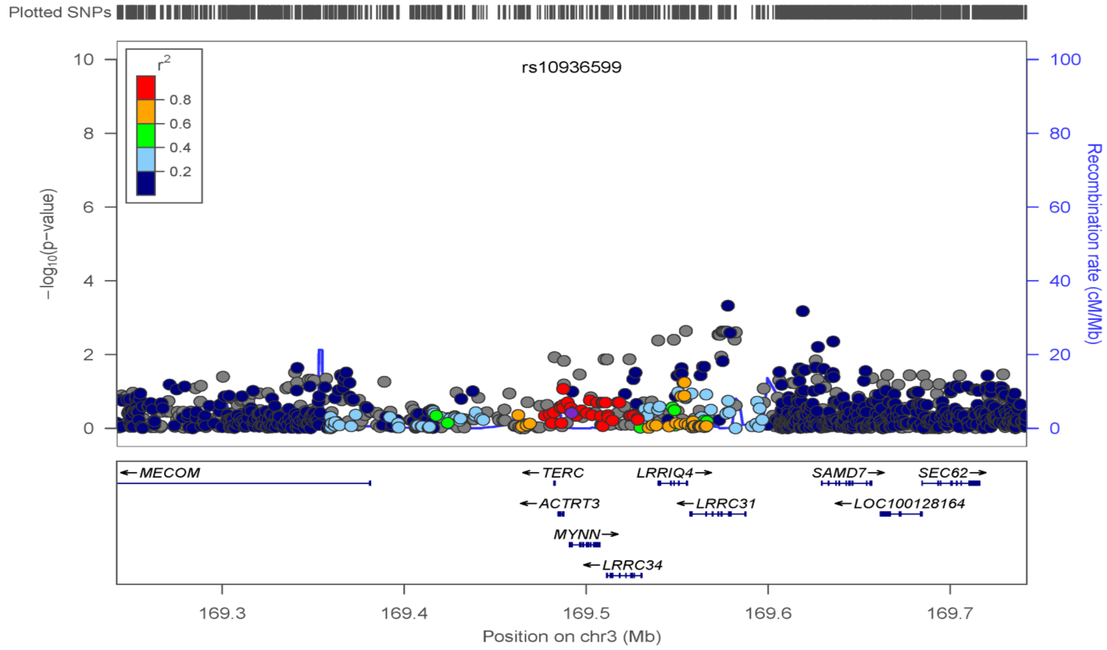
2q12.3



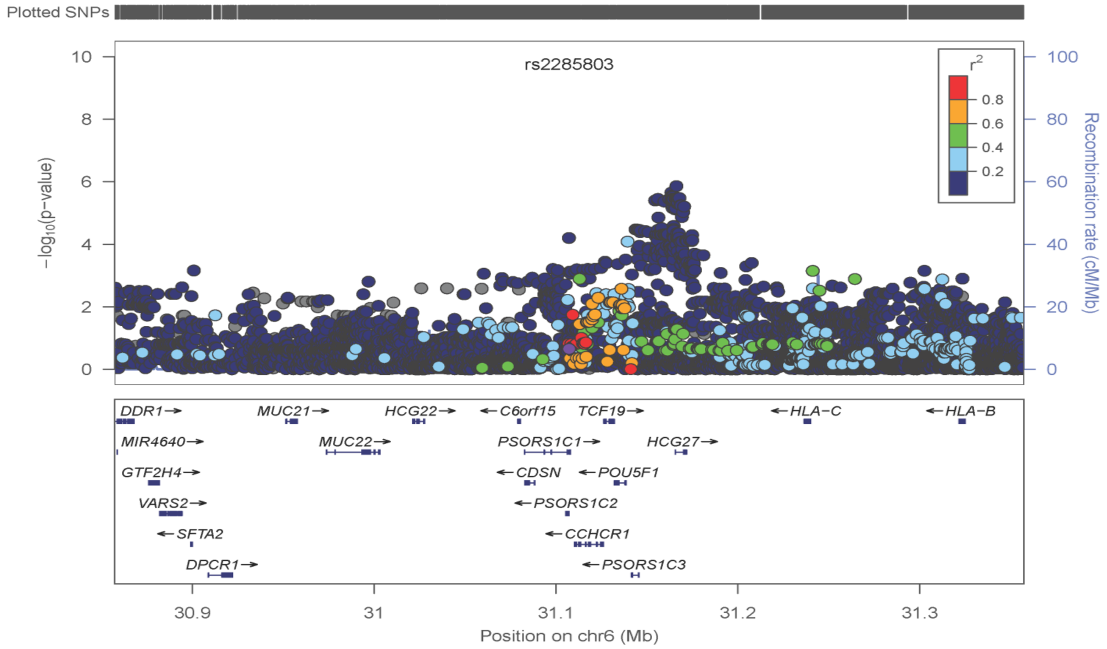
3p22.1


Plotted SNPs
rs1052501
r^2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
←ULK4
TRAK1→
41.7
41.8
41.9
42
42.1
Position on chr3 (Mb)

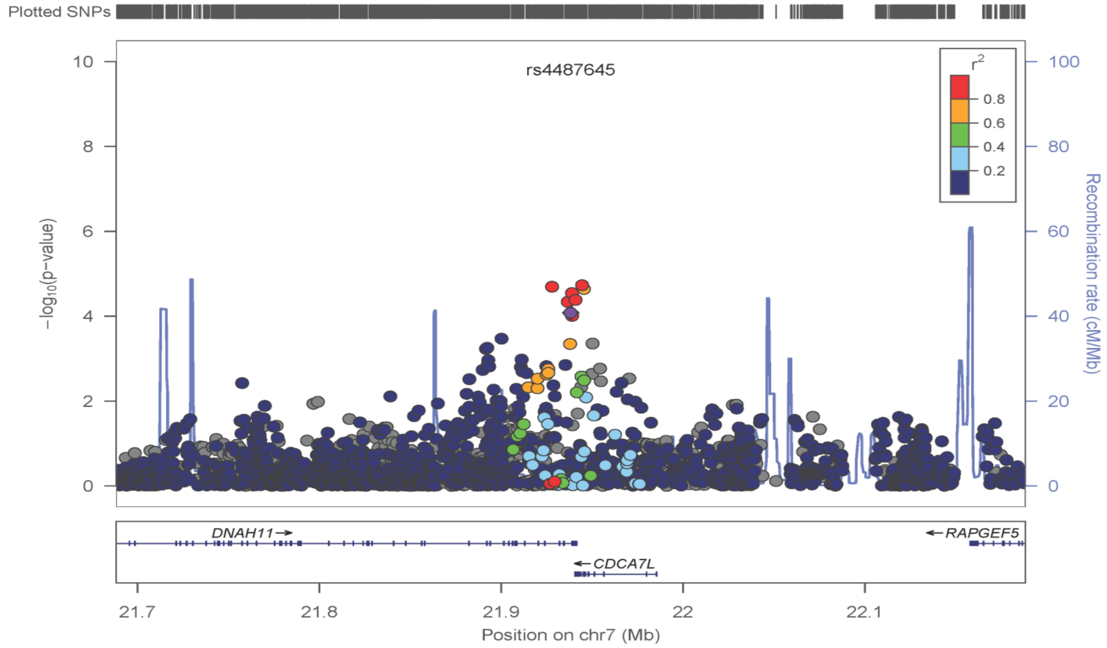
3q26.2


Plotted SNPs
rs10936599
r^2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
←MECOM
←TERC
←ACTRT3
MYNN→
←LRRC34
LRRIQ4→
←LRRC31
SAMD7→
←LOC100128164
SEC62→
169.3
169.4
169.5
169.6
169.7
Position on chr3 (Mb)

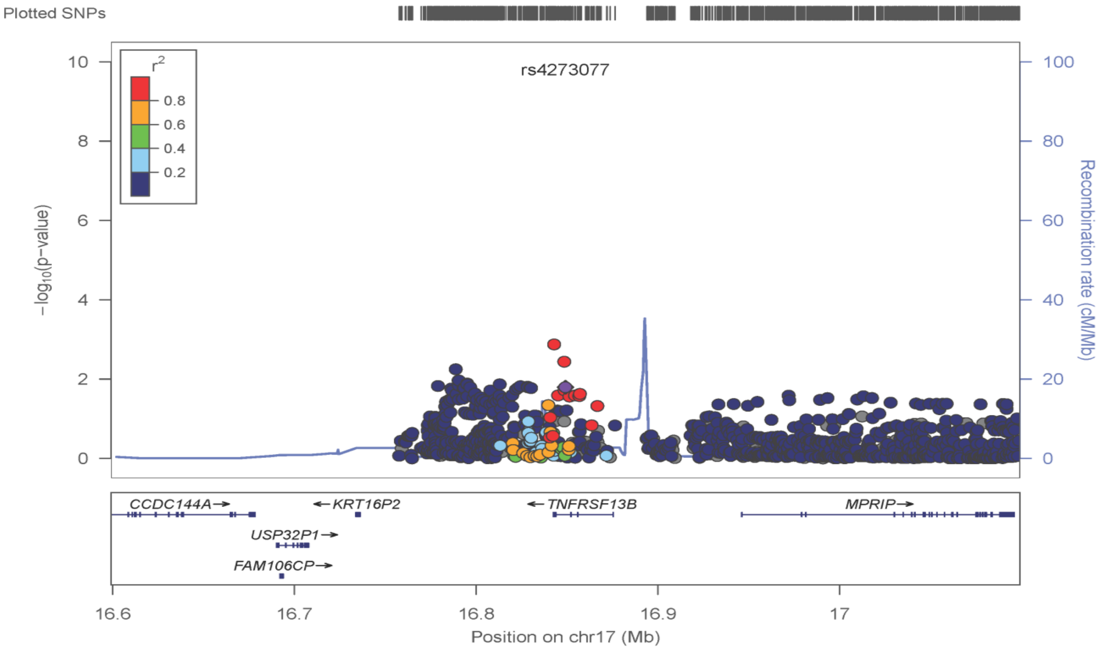
6p21.33



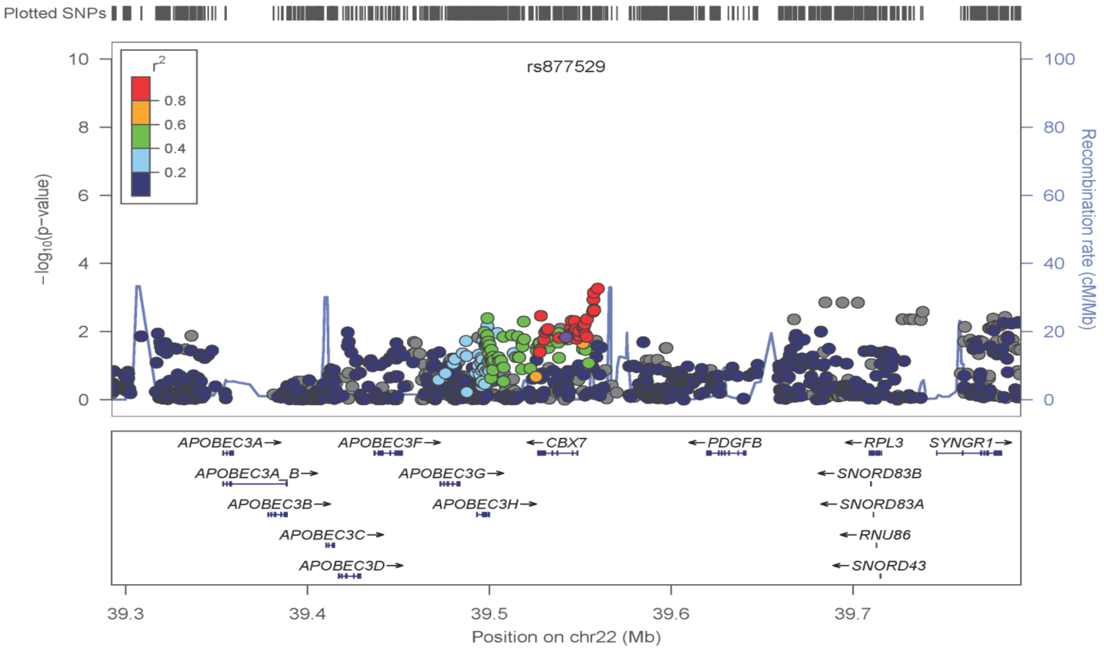
7p15.3



17p11.2

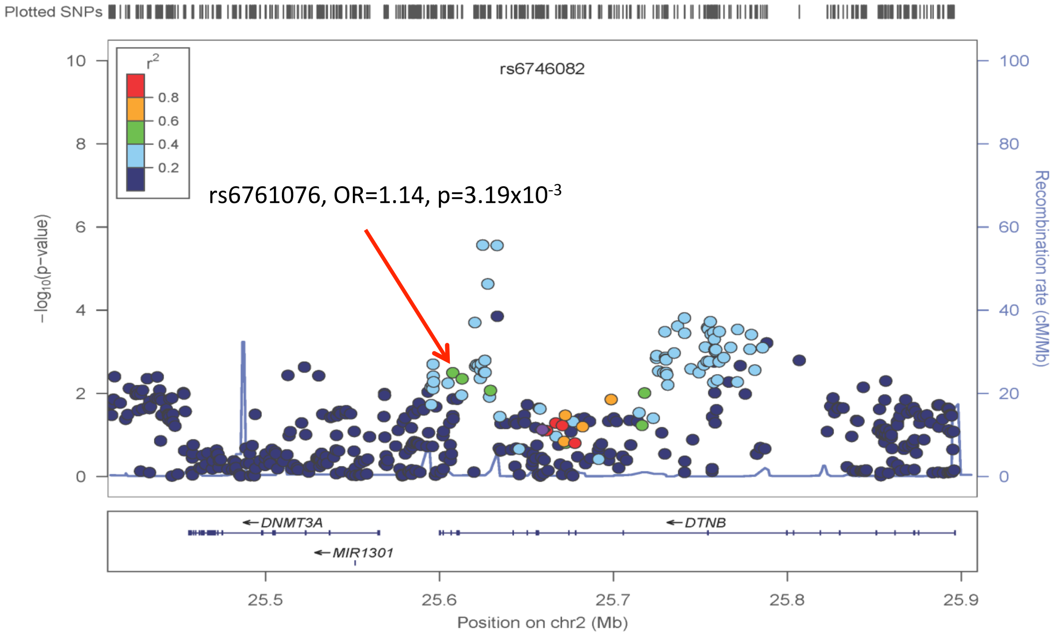


22q13.1



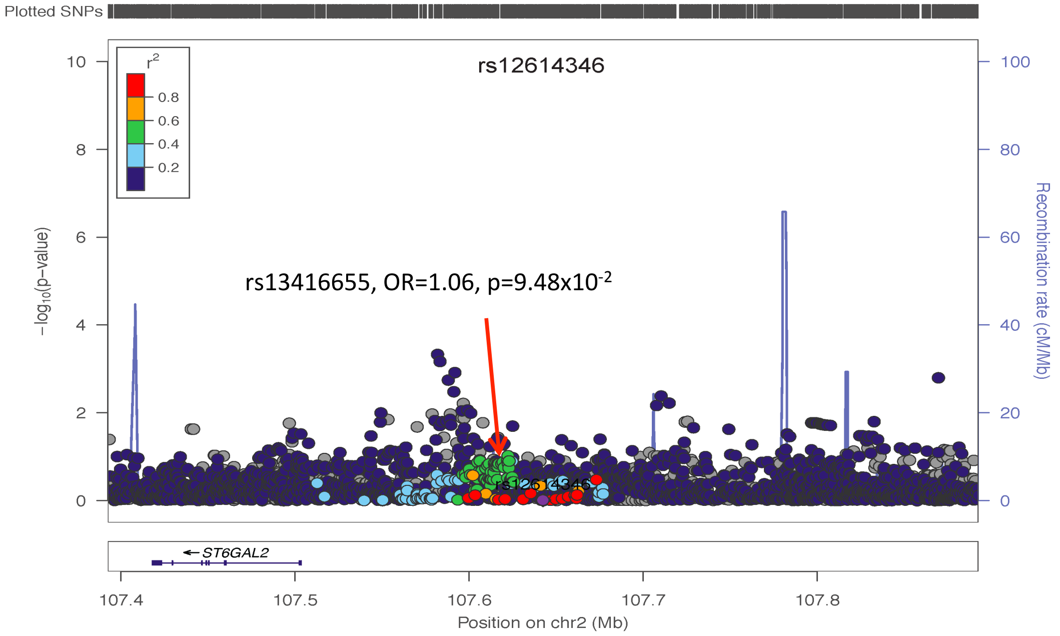
Supplementary Figure 3a. LocusZoom Plots of European and African ancestry combined meta-analysis with LD calculated in relation to the index SNP (1KGP EUR ref). The most significant Group A SNP in each region is labeled.

2p23.3



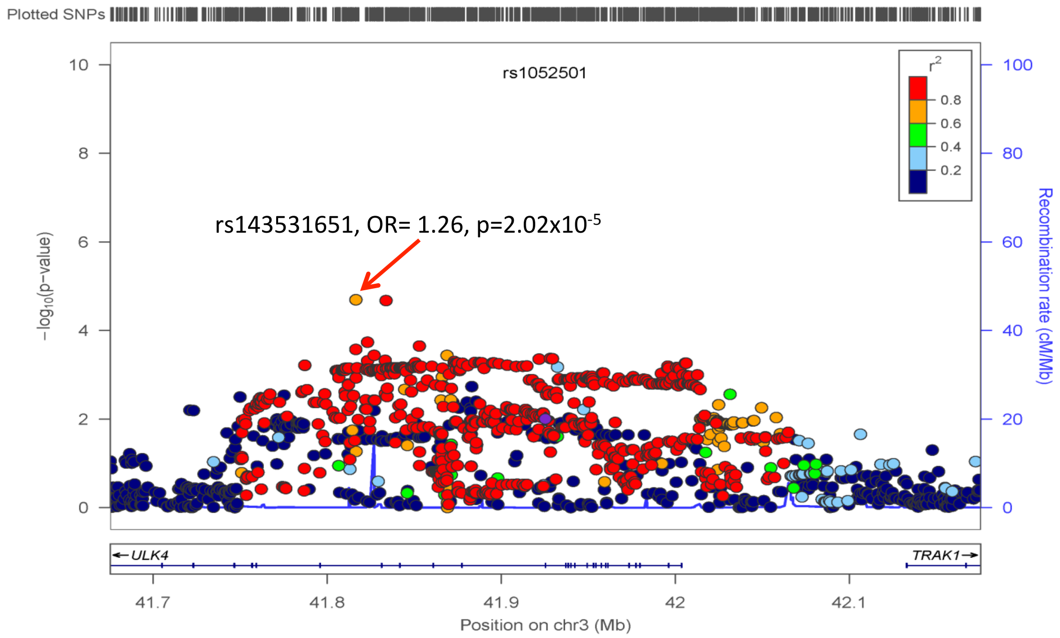
rs6761076, OR=1.14, p=3.19x10^{-3}

2q12.3

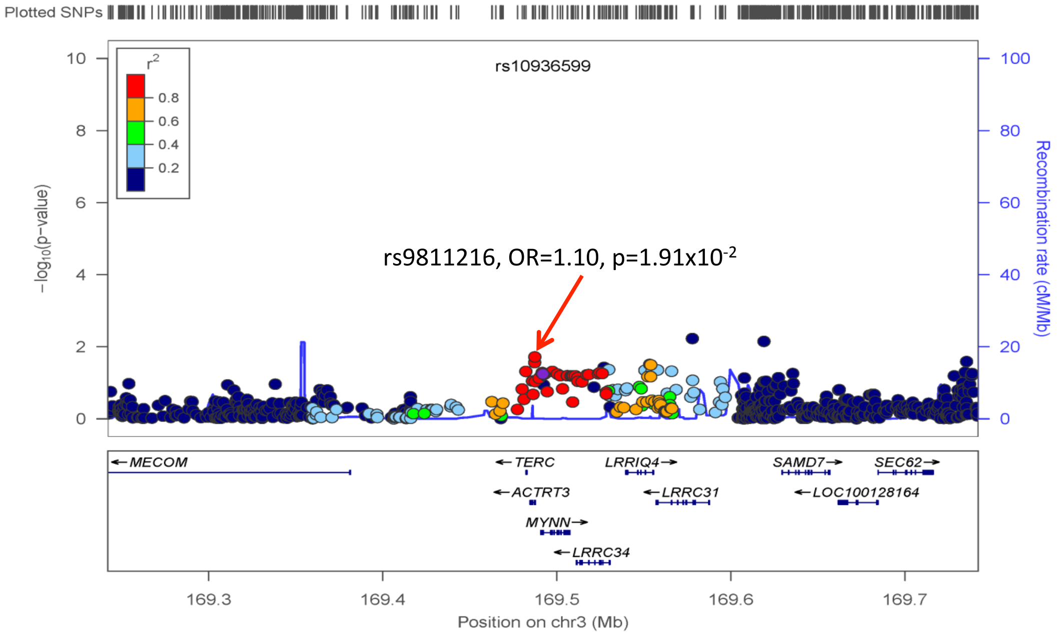


rs13416655, OR=1.06, p=9.48x10^{-2}

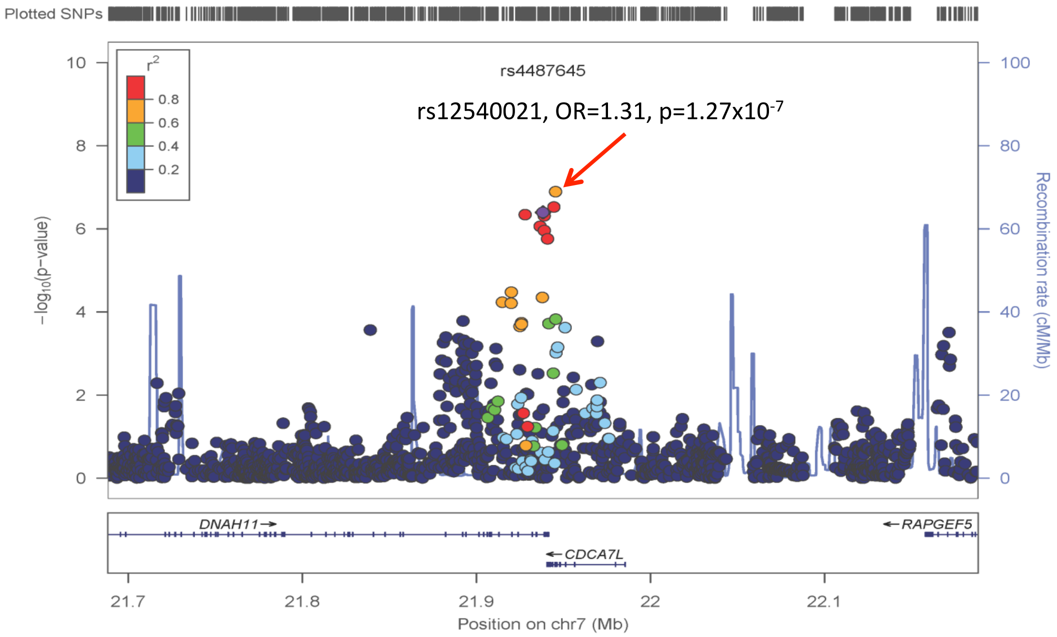
3p22.1


rs143531651, OR= 1.26, p=2.02x10^{-5}

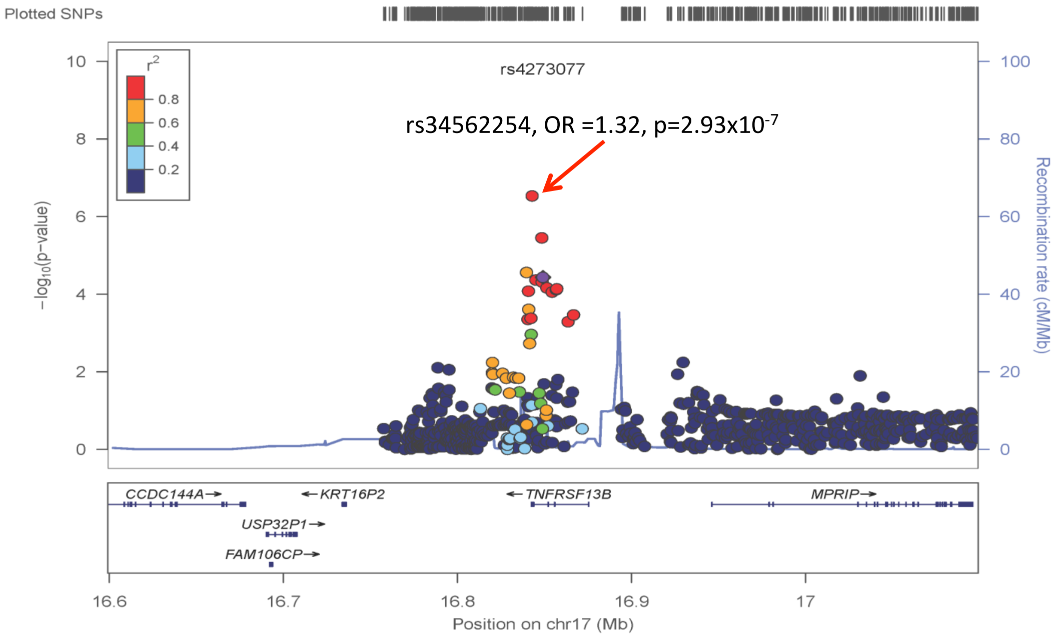
3q26.2


rs9811216, OR=1.10, p=1.91x10^{-2}

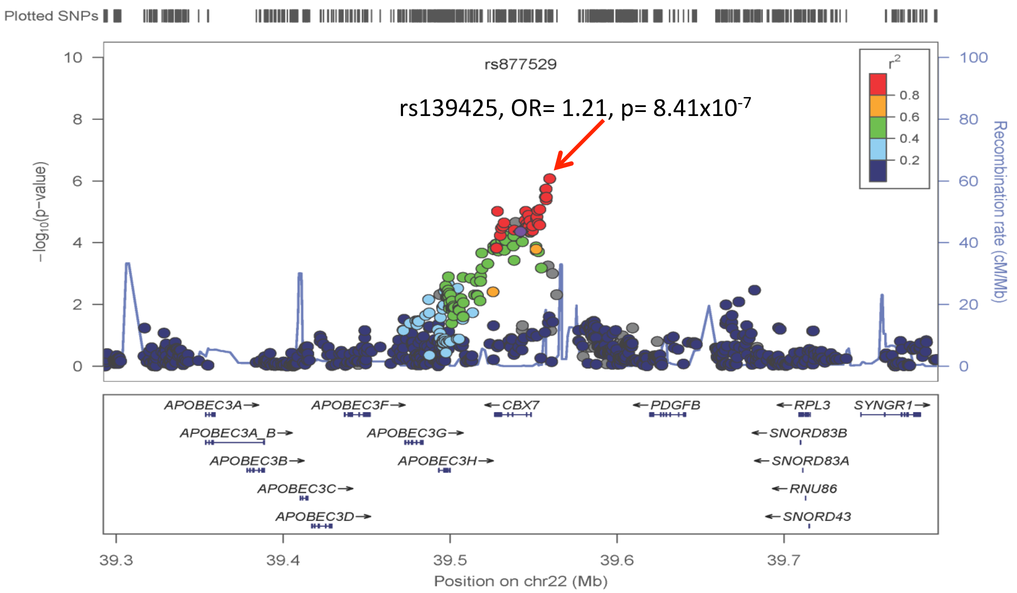
7p15.3


rs12540021, OR=1.31, p=$1.27x10^{-7}$

17p11.2


rs34562254, OR =1.32, p=$2.93x10^{-7}$

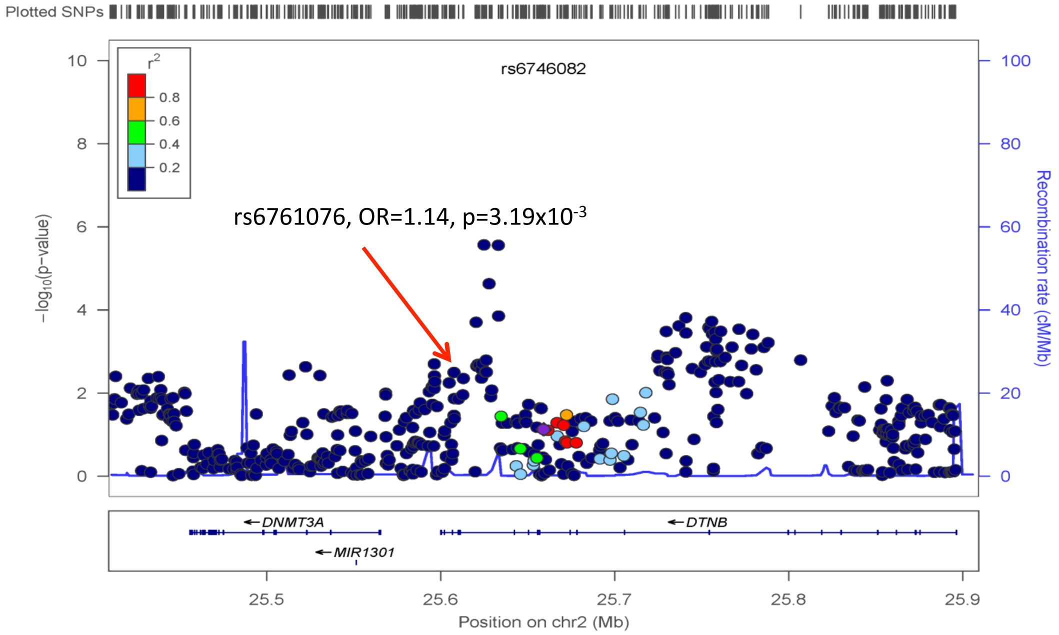
22q13.1



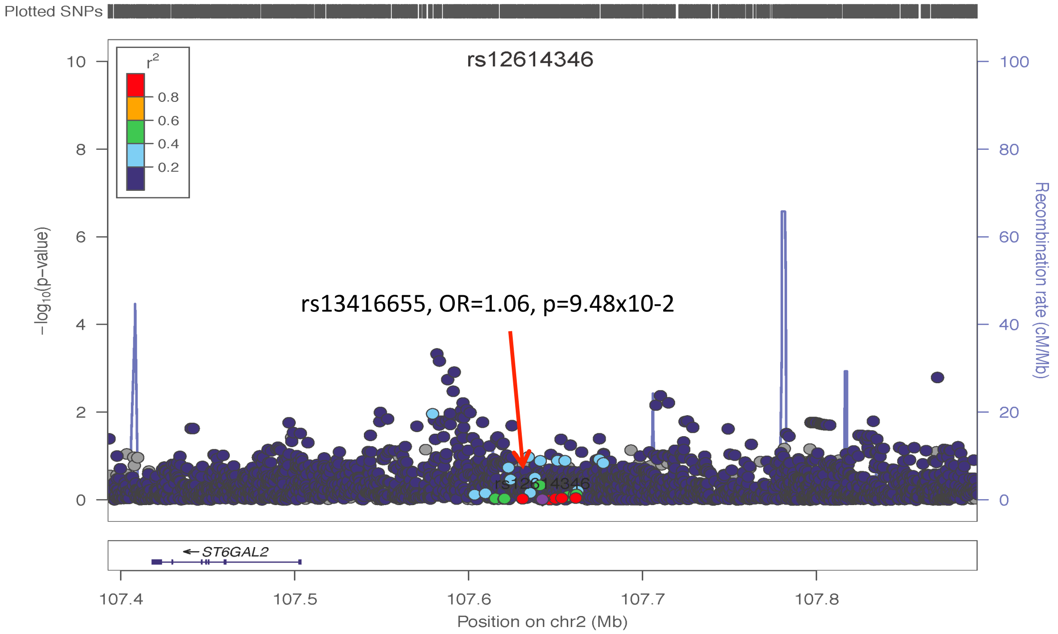
rs139425, OR= 1.21, p= $8.41\text{x}10^{-7}$

Supplementary Figure 3b. LocusZoom Plots of European and African ancestry combined meta-analysis with LD calculated in relation to the index SNP (1KGP AFR ref). The most significant Group A SNP in each region is labeled

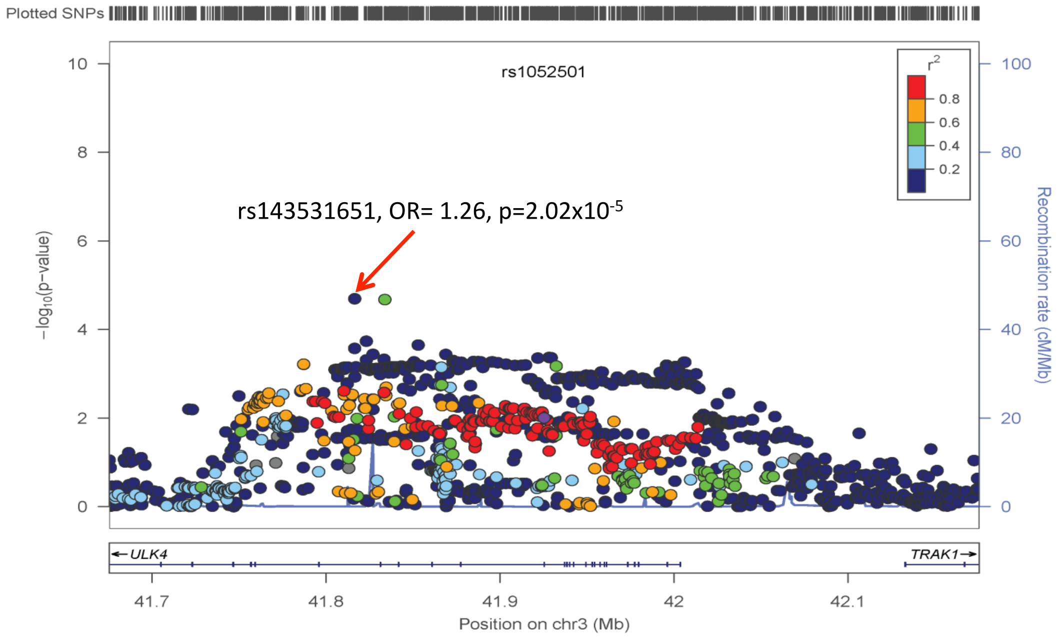
2p23.3



2q12.3

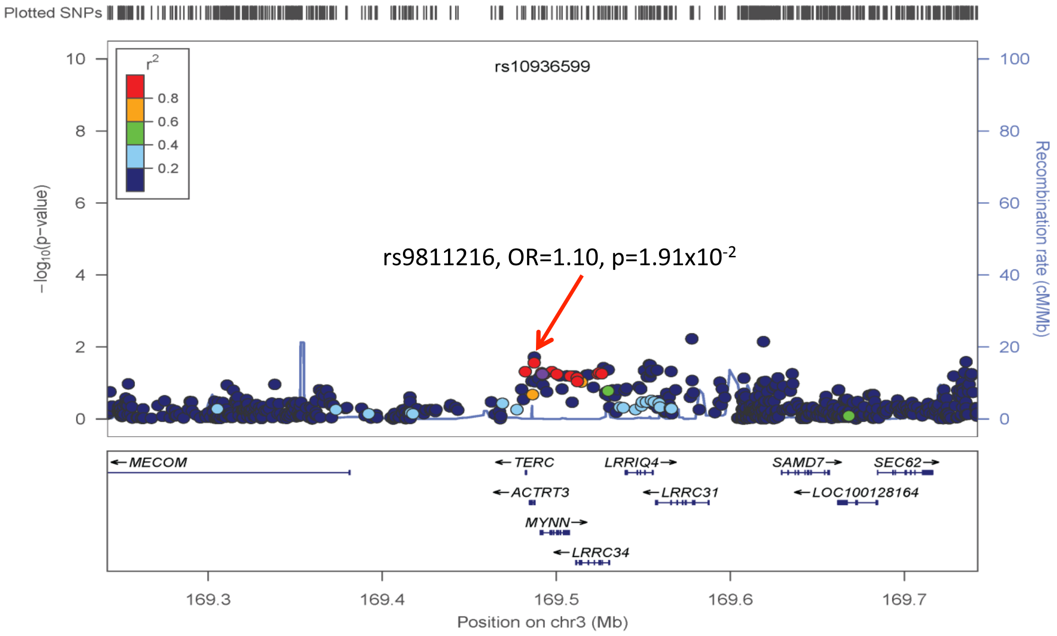


3p22.1



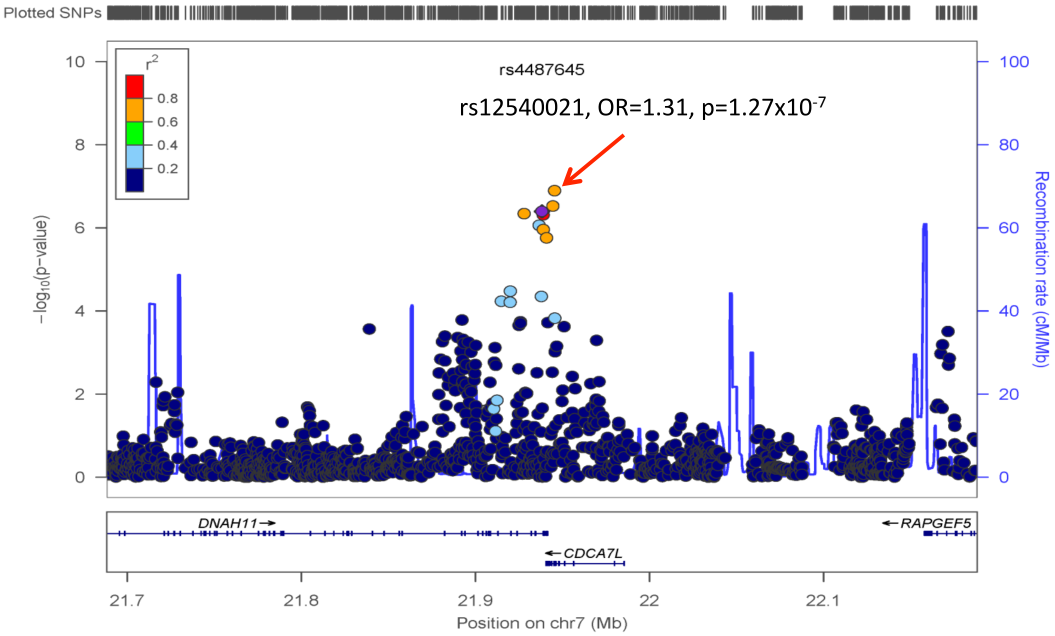
rs143531651, OR= 1.26, p=2.02×10^{-5}

3q26.2

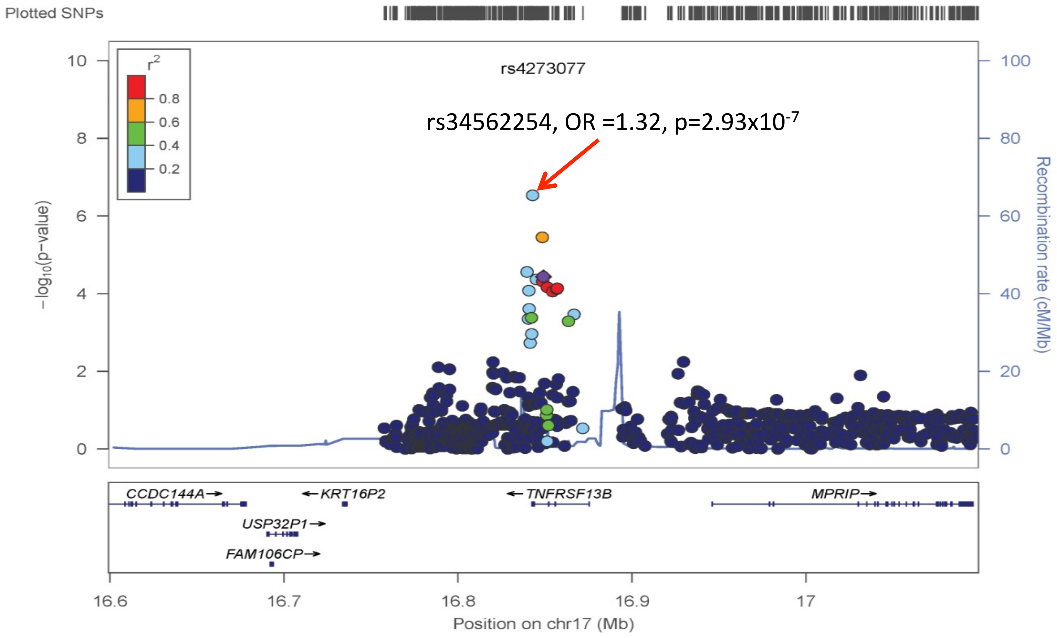


rs9811216, OR=1.10, p=1.91×10^{-2}

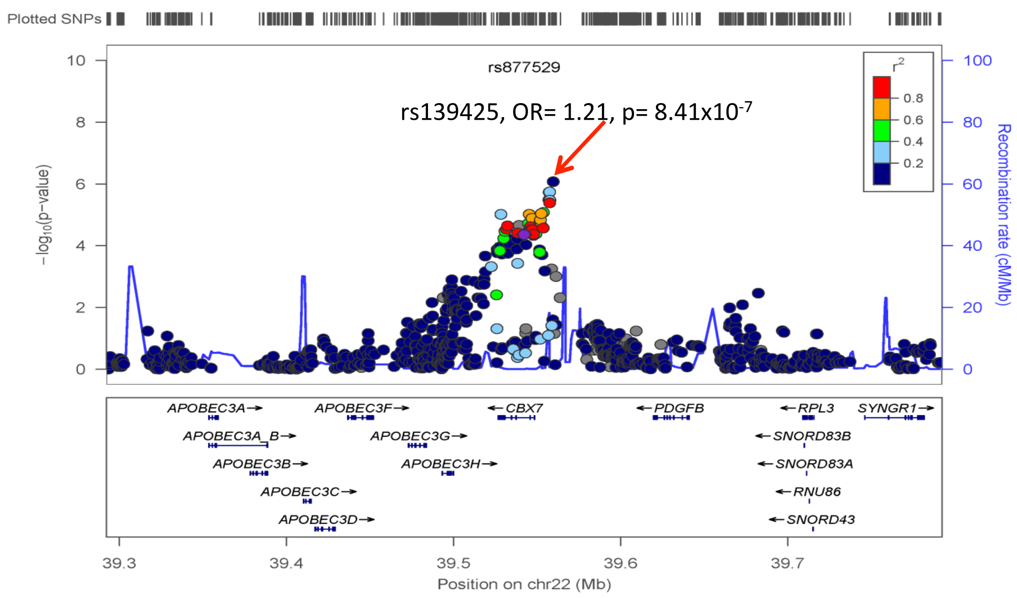
7p15.3


rs12540021, OR=1.31, $p=1.27 \times 10^{-7}$

17p11.2


rs34562254, OR =1.32, $p=2.93 \times 10^{-7}$

22q13.1



Plotted SNPs
rs877529
rs139425, OR= 1.21, p= 8.41x10-7
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
APOBEC3A
APOBEC3A_B
APOBEC3B
APOBEC3C
APOBEC3D
APOBEC3F
APOBEC3G
APOBEC3H
CBX7
PDGFB
RPL3
SYNGR1
SNORD83B
SNORD83A
RNU86
SNORD43
39.3
39.4
39.5
39.6
39.7
Position on chr22 (Mb)

Supplementary Table 1. Imputation quality by region in subjects of African ancestry.

SNP	CHR:BP	Typed[a]	Imputed[b]	info > 0.8[c]	info < 0.8[d]
rs6746082	2:25659244	27	2006	884	1122
rs12614346	2:107642482	42	2971	2396	575
rs1052501	3:41925398	22	3438	2777	661
rs10936599	3:169492101	34	2910	1492	1418
rs2285803	6:31107258	125	10229	9358	871
rs4487645	7:21938240	78	4174	2669	1505
rs4273077	17:16849139	22	2574	1125	1449
rs877529	22:39542292	34	3967	1322	2645

[a] Number of genotyped SNPs within +/- 250 kb of the index marker

[b] Number of KGP imputed SNPs with MAF>1%

[c] Imputed SNPs with info > 0.8 and MAF >1%

[d] Imputed SNPs with info < 0.8 and MAF >1%

Supplementary Table 2. Significance thresholds for eight regions derived from 1,000 permutations using African ancestry case-control data.

		N SNPs[a]		**Significance threshold**	
SNP	**CHR:BP**	**Group A**[b]	**Group B**[c]	**Group A**[b]	**Group B**[c]
rs6746082	2:25659244	14	870	7.60×10^{-3}	5.04×10^{-6}
rs12614346	2:107642482	59	2337	4.85×10^{-3}	7.19×10^{-6}
rs1052501	3:41925398	711	2066	1.48×10^{-3}	5.60×10^{-6}
rs10936599	3:169492101	70	1422	2.41×10^{-3}	7.62×10^{-6}
rs2285803	6:31107258	52	9306	5.46×10^{-3}	1.03×10^{-6}
rs4487645	7:21938240	26	2643	4.44×10^{-3}	3.43×10^{-6}
rs4273077	17:16849139	36	1089	3.93×10^{-3}	5.79×10^{-6}
rs877529	22:39542292	58	1264	2.87×10^{-3}	2.50×10^{-6}

[a] Total number of SNPs (MAF>1% and INFO>0.80) within +/-250 kb of the index SNP

[b] SNP correlated with the index SNP at r2≥0.50 (based on the 1000 Genomes EUR populations)

[c] SNP correlated with the index SNP at r2<0.50 (based on the 1000 Genomes EUR populations)

Supplementary Table 3. The most significant associations in subjects of African ancestry (r2≥0.50 with index in KGP EUR).

SNP	CHR:BP	A1[a]/A2	Freq in EAs[b]	Freq in AAs[b]	OR[b] AA	P-value AA	r2 with Index in Region[c]
rs679112	2:25718052	A/G	0.75	0.58	1.09	$8.10x10^{-2}$	0.25 / 0.53
rs13416655	2:107621925	C/T	0.50	0.39	1.10	$4.90x10^{-2}$	0.13 / 0.52
rs143531651	3:41816589	G/C	0.17	0.11	1.27	$1.37x10^{-3}$	0.02 / 0.79
rs9833035	3:169553498	G/T	0.78	0.69	1.10	$5.67x10^{-2}$	0.13 / 0.61
rs113704463	6:31113052	G/A	0.29	0.40	1.15	$1.27x10^{-3}$	0.38 / 0.57
rs56249828	7:21944607	T/C	0.68	0.89	1.41	$1.85x10^{-5}$	0.71 / 0.85
rs34562254	17:16842991	A/G	0.11	0.13	1.25	$1.33x10^{-3}$	0.33 / 0.90
rs139425	22:39559742	C/G	0.46	0.71	1.21	$5.45x10^{-4}$	0.18 / 0.95

[a] Risk allele

[b] Frequency and OR for A1 allele

[c] r2 metrics based on 1000 Genomes Project AFR/EUR populations

Supplementary Table 4.The most significant associations in subjects of European ancestry (r2 ≥0.50 with index in KGP EUR).

SNP	CHR:BP	A1[a]/A2	Freq in EAs[b]	Freq in AAs	OR EA	P-value EA	P-het EA	R2 with Index in region[c]
rs4665791	2:25698847	G/A	0.83	0.57	1.24	$3.99\text{x}10^{-3}$	0.42	0.38 / 0.61
rs4676096	2:107603011	A/G	0.34	0.19	1.06	$3.18\text{x}10^{-1}$	0.48	0.30 / 0.86
rs28581706	3:41871397	C/A	0.13	0.35	1.41	$2.23\text{x}10^{-4}$	0.43	0.29 / 0.55
rs55735727	3:169488148	A/T	0.74	0.89	1.16	$3.49\text{x}10^{-2}$	0.80	0.26 / 0.66
rs112941857	6:31129642	A/C	0.21	0.13	1.27	$2.56\text{x}10^{-3}$	0.71	0.05 / 0.62
rs6948632	7:21929452	G/T	0.69	0.60	1.24	$4.00\text{x}10^{-4}$	0.63	0.03 / 0.90
rs34562254	17:16842991	A/G	0.11	0.13	1.45	$2.39\text{x}10^{-5}$	0.37	0.33 / 0.90
rs139413	22:39553772	G/A	0.49	0.46	1.22	$2.49\text{x}10^{-4}$	0.72	0.92 / 0.99

[a] Risk allele

[b] Minimum frequency observed in meta-analysis of four studies

[c] r2 metrics based on 1000 Genomes Project AFR/EUR populations

Supplementary Table 5. Potential transcription factor binding motif disruption or improvement from matching motifs of SNPs and correlated proxies from the combined African and European ancestry fine-mapping analysis.

seqnames	start	end	rsnames	REF	ALT	snpPos	motifPos	geneSymbol	dataSource	providerName	providerId	seqMatch	pctRef	pctAlt	scoreRef	scoreAlt	Refpvalue	Altpvalue	alleleRef	alleleAlt	effect
chr3	41923000	41923009	rs73081392	G	A	41923009	1	BARX2	HOCOMOCO	BARX2_si	BARX2_HUMAN	ccattaaaaG	0.958586874	0.98947081	6.850509362	7.06493625	0.000198364	1.53E-05	0.141732283	0.645669291	weak
chr3	41923002	41923015	rs73081392	G	A	41923009	7	MEF2A	HOCOMOCO	MEF2A_f1	MEF2A_HUMAN	attaaaaGtaatga	0.756832794	0.864359595	9.361218757	10.67408994	0.001212995	8.57E-05	0.022628057	0.915672288	strong
chr3	41923002	41923013	rs73081392	G	A	41923009	5	MEF2D	HOCOMOCO	MEF2D_f1	MEF2D_HUMAN	attaaaaGtaat	0.768123488	0.868697489	7.206174183	8.114537669	0.000806153	5.64E-05	0.094736842	0.905263158	strong
chr3	41923295	41923309	rs17217536	A	C	41923300	6	PROP1	HOCOMOCO	PROP1_f1	PROP1_HUMAN	cgggaAttaacatcc	0.857697797	0.76722871	5.451705075	4.911008949	9.04E-05	0.001106552	0.775280899	0	strong
chr3	42002753	42002763	rs55916855	A	G	42002761	3	EGR1	HOCOMOCO	EGR1_f2	EGR1_HUMAN	actcccgcAcc	0.822072194	0.894181244	9.376286354	10.18764115	0.000494003	7.56E-05	0.093113305	0.828280374	strong
chr3	42003365	42003376	rs73071261	C	A	42003369	5	INSM1	HOCOMOCO	INSM1_f1	INSM1_HUMAN	ggtaCggggtcc	0.723980381	0.834254129	10.00640574	11.50651833	0.001464248	9.58E-05	0	0.971311053	strong
chr7	21938226	21938242	rs4487645:T	C	T	21938240	3	IRF3	HOCOMOCO	IRF3_f1	IRF3_HUMAN	tcaaggtttcacttCtc	0.85801921	0.949263496	10.23300185	11.28949295	9.56E-05	5.02E-06	0.084832905	0.892030848	strong
chr7	21938228	21938241	rs4487645:T	C	T	21938240	2	PRDM1	HOCOMOCO	PRDM1_f1	PRDM1_HUMAN	aaggtttcacttCt	0.83507868	0.865112233	12.98205447	13.442246	8.78E-05	3.47E-05	0.204807165	0.729927123	weak
chr7	21938229	21938242	rs4487645:T	C	T	21938240	3	IRF2	HOCOMOCO	IRF2_f1	IRF2_HUMAN	aggtttcacttCtc	0.880141866	0.960014143	11.44457306	12.46620463	7.29E-05	5.32E-06	0.088041683	0.880263311	strong
chr7	21938229	21938243	rs4487645:A	C	A	21938240	4	IRF8	HOCOMOCO	IRF8_si	IRF8_HUMAN	aggtttcacttCtct	0.913588669	0.87349348	9.255198574	8.861705822	3.80E-05	0.000114241	0.445471349	0	weak
chr7	21938230	21938241	rs4487645:T	C	T	21938240	2	IRF1	HOCOMOCO	IRF1_si	IRF1_HUMAN	ggtttcacttCt	0.915569097	0.977147255	11.76483884	12.54688339	7.07E-05	6.74E-06	0.139289145	0.825168108	weak
chr7	21938230	21938241	rs4487645:T	C	T	21938240	2	IRF9	HOCOMOCO	IRF9_f1	IRF9_HUMAN	ggtttcacttCt	0.754471365	0.876571361	6.951202401	7.999798438	0.000887096	3.70E-05	0	1	strong
chr7	21938231	21938247	rs4487645:A	C	A	21938240	8	GATA5	HOCOMOCO	GATA5_f1	GATA5_HUMAN	gtttcacttCtctctta	0.752858474	0.973780687	5.447741911	6.946189372	0.011908525	2.37E-06	0	1	strong
chr7	21938232	21938247	rs4487645:A	C	A	21938240	8	IRF4	HOCOMOCO	IRF4_si	IRF4_HUMAN	tttcacttCtctctta	0.893357671	0.848920981	9.871931615	9.39233731	2.99E-05	0.000165682	0.489848023	0.000346661	weak
chr7	21938232	21938241	rs4487645:T	C	T	21938240	2	IRF7	HOCOMOCO	IRF7_f1	IRF7_HUMAN	tttcacttCt	0.812180887	0.967494127	6.584012729	7.815514654	0.001771927	1.53E-05	0	0.897435897	strong
chr7	21938234	21938253	rs4487645:T	C	T	21938240	14	IRF5	HOCOMOCO	IRF5_f1	IRF5_HUMAN	tcacttCtctcttaatttta	0.70282668	0.790148342	9.169317022	10.21791306	0.000381842	2.12E-05	0	1	strong
chr7	21938236	21938245	rs4487645:A	C	A	21938240	6	GATA1	HOCOMOCO	GATA1_si	GATA1_HUMAN	acttCtctct	0.803132382	0.985940798	8.820857536	10.80851961	0.002171516	3.34E-05	0	1	strong
chr7	21938237	21938244	rs4487645:A	C	A	21938240	5	GATA2	HOCOMOCO	GATA2_si	GATA2_HUMAN	cttCtctc	0.743889122	0.998387426	5.572283727	7.425911805	0.016372681	1.53E-05	0.009275054	0.988365742	strong
chr22	39528439	39528447	rs79503	A	G	39528440	2	FOXP3	HOCOMOCO	FOXP3_f1	FOXP3_HUMAN	aAtctggtt	0.968092838	0.82583522	6.079840328	5.216017718	4.20E-05	0.001609802	0.875	0	strong
chr22	39530851	39530862	rs139386	T	C	39530859	4	ARNT2	HOCOMOCO	ARNT2_si	ARNT2_HUMAN	ccatgccaTgtc	0.740860677	0.941338091	4.994084863	6.293668646	0.007395029	8.19E-05	0	0.944785276	strong
chr22	39530851	39530862	rs139386	T	C	39530859	4	XBP1	HOCOMOCO	XBP1_f1	XBP1_HUMAN	ccatgccaTgtc	0.808484327	0.954849351	11.11193184	13.10525928	0.000777721	2.41E-05	0	1	strong
chr22	39530854	39530875	rs139386	T	C	39530859	17	ZBTB7B	HOCOMOCO	ZBT7B_si	ZBT7B_HUMAN	tgccaTgtctacccactcaact	0.762953969	0.802306263	8.962172907	9.404825421	0.000293925	7.23E-05	0	0.693181818	weak
chr22	39542285	39542299	rs877529	G	A	39542292	8	ELF2	HOCOMOCO	ELF2_f1	ELF2_HUMAN	gcccaggGagcgtaa	0.773096957	0.930361182	6.974155176	8.321289817	0.001888129	3.05E-05	0	1	strong
chr22	39542287	39542296	rs877529	G	A	39542292	6	ELF1	HOCOMOCO	ELF1_f1	ELF1_HUMAN	ccaggGagcg	0.783397567	0.97932729	7.164488805	8.927300637	0.004446983	4.86E-05	0.011412268	0.988587732	strong
chr22	39542287	39542295	rs877529	G	A	39542292	6	ETS1	HOCOMOCO	ETS1_si	ETS1_HUMAN	ccaggGagc	0.720305155	0.967785677	5.749660836	7.683343594	0.016174316	5.34E-05	0	1	strong
chr22	39542288	39542295	rs877529	G	A	39542292	5	ETV4	HOCOMOCO	ETV4_f1	ETV4_HUMAN	caggGagc	0.814577724	0.982289508	5.065824605	6.083897327	0.003326416	6.10E-05	0.120448179	0.879551821	strong
chr22	39542290	39542300	rs877529	G	A	39542292	3	PAX6	HOCOMOCO	PAX6_f1	PAX6_HUMAN	ggGagcgtaaa	0.709765442	0.875078745	5.626392352	6.887095001	0.004620552	8.42E-05	0.076659879	0.915160946	strong
chr22	39544957	39544970	rs139398	C	G	39544970	1	HIVEP2	HOCOMOCO	ZEP2_si	ZEP2_HUMAN	ggggtttccaggaC	0.941287294	0.886883441	5.126975875	4.843325687	1.03E-05	0.000172962	0.62628866	0.038659794	weak
chr22	39547879	39547898	rs1005300	C	G	39547891	13	SP3	HOCOMOCO	SP3_f1	SP3_HUMAN	gtgctcgggtggCgtagagg	0.82303755	0.881244496	8.119308501	8.6629343	0.000482903	8.22E-05	0.034939759	0.719277108	weak
chr22	39547883	39547893	rs1005300	C	G	39547891	9	KLF1	HOCOMOCO	KLF1_f1	KLF1_HUMAN	tcgggtggCgt	0.834879604	0.949269436	7.853557164	8.887415264	0.00058651	5.22E-05	0	0.910891089	strong
chr22	39547884	39547893	rs1005300	C	G	39547891	8	KLF4	HOCOMOCO	KLF4_f2	KLF4_HUMAN	cgggtggCgt	0.840086497	0.970276354	8.374187072	9.651458376	0.000898361	5.15E-05	0.011830758	0.905316671	strong
chr22	39547885	39547901	rs1005300	C	G	39547891	7	PURA	HOCOMOCO	PURA_f1	PURA_HUMAN	gggtggCgtagaggggg	0.783881358	0.827709656	4.618115305	4.860039677	0.000384059	8.53E-05	0.151515152	0.626262626	weak
chr22	39547889	39547905	rs1005300	C	G	39547891	3	MAZ	HOCOMOCO	MAZ_f1	MAZ_HUMAN	ggCgtagagggggcagg	0.789431886	0.8329674	8.243800665	8.687304218	0.000253748	5.68E-05	0	0.657947686	weak
chr22	39547955	39547963	rs6001455	C	T	39547962	2	NFATC2	HOCOMOCO	NFAC2_f1	NFAC2_HUMAN	acttttcCa	0.990872692	0.79895623	9.926437857	8.032547293	3.43E-05	0.002750397	1	0	strong
chr22	39547955	39547963	rs6001455	C	T	39547962	2	NFATC3	HOCOMOCO	NFAC3_f1	NFAC3_HUMAN	acttttcCa	0.993253655	0.802966558	8.569456203	6.961239698	1.14E-05	0.002285004	1	0	strong
chr22	39548014	39548027	rs5995688	A	G	39548027	14	NR2E3	HOCOMOCO	NR2E3_f1	NR2E3_HUMAN	gagttcaaaacccA	0.828681559	0.781515081	8.333629598	7.881421292	4.30E-05	0.000193715	0.733503717	0.077369888	weak
chr22	39549412	39549433	rs12158877	T	G	39549426	15	RREB1	HOCOMOCO	RREB1_si	RREB1_HUMAN	tgggcgctaggtgcTtagtggg	0.797742617	0.761499809	9.787880902	9.356502313	4.78E-05	0.000175868	0.730200468	0.237594388	weak
chr22	39549521	39549527	rs139405	C	A	39549526	6	MECP2	HOCOMOCO	MECP2_f1	MECP2_HUMAN	cccggCg	0.939344531	1	8.667185451	9.224246552	0.000854492	0	0	0.575068761	weak

Supplementary Table 6. Functional overlap for fine-mapping SNPs that were significantly associated with multiple myeloma risk in the combined African and European ancestry analysis.

chromosome	start	end	name	CD20_RO01778 DNASE HYPERSENSITIVE SITE	CD20_RO01794 CTCF SITE	CD20_RO01794 ENHANCER REGION WITH ACTIVE MARKS	CD20_RO01794 DNASE HYPERSENSITIVE SITE IN ENHANCER REGION WITH ACTIVE MARKS	CD20_RO01794 PROMOTER REGION WITH ACTIVE MARKS	CD20_RO01794 DNASE HYPERSENSITIVE SITE IN PROMOTER REGION WITH ACTIVE MARKS	CD20_RO01794 DNASE HYPERSENSITIVE SITE	MISSENSE	3' UTR	GENE
chr3	42003368	42003369	rs73071261	0	0	0	0	0	1	0	0	0	
chr3	42003697	42003698	rs73830585	0	0	0	0	0	1	0	0	0	
chr3	42002760	42002761	rs55916855	0	0	0	0	0	1	0	0	0	
chr3	42001846	42001847	rs73071259	0	0	1	0	0	0	0	0	0	
chr3	42004427	42004428	rs55953604	0	0	0	0	1	0	0	0	0	
chr3	41923008	41923009	rs73081392	0	1	0	0	0	0	0	0	0	
chr3	42005165	42005166	rs60966614	0	0	1	0	0	0	0	0	0	
chr3	42004680	42004681	rs4434125	0	0	1	0	0	0	0	0	0	
chr3	42004881	42004882	rs56290987	0	0	1	0	0	0	0	0	0	
chr3	41831202	41831203	rs17215589	0	0	0	0	0	0	0	1	0	ULK4
chr3	42004426	42004427	rs56201224	0	0	0	0	1	0	0	0	0	
chr3	41923299	41923300	rs17217536	0	1	0	0	0	0	0	0	0	
chr3	42001986	42001987	rs7639859	0	0	1	0	0	0	0	0	0	
chr3	41952851	41952852	rs35263917	0	0	0	0	0	0	0	1	0	ULK4
chr7	21939031	21939032	rs56333627	0	0	1	0	0	0	0	0	0	
chr7	21936697	21936698	rs75341503	0	0	1	0	0	0	0	0	0	
chr7	21928078	21928079	rs57104699	0	0	1	0	0	0	0	0	0	
chr7	21944606	21944607	rs56249828	0	0	1	0	0	0	0	0	0	
chr7	21938239	21938240	rs4487645	0	0	0	1	0	0	0	0	0	
chr7	21939088	21939089	rs55714084	0	0	1	0	0	0	0	0	0	
chr7	21940959	21940960	rs7971	0	0	1	0	0	0	0	0	1	
chr7	21945562	21945563	rs12540021	0	0	1	0	0	0	0	0	0	
chr17	16848564	16848565	rs4500785	0	0	1	0	0	0	0	0	0	
chr17	16842990	16842991	rs34562254	0	0	0	0	0	0	0	1	0	TNFRSF13B
chr22	39547961	39547962	rs6001455	0	0	0	0	0	1	0	0	0	
chr22	39530131	39530132	rs139385	0	0	0	0	0	0	1	0	0	
chr22	39547020	39547021	rs139403	0	0	1	0	0	0	0	0	0	
chr22	39549425	39549426	rs12158877	0	0	0	0	0	1	0	0	0	
chr22	39530858	39530859	rs139386	0	1	0	0	0	0	0	0	0	
chr22	39547200	39547201	rs139404	0	0	1	0	0	0	0	0	0	
chr22	39549525	39549526	rs139405	0	0	0	0	0	1	0	0	0	
chr22	39547890	39547891	rs1005300	0	0	0	0	0	1	0	0	0	
chr22	39546144	39546145	rs139402	0	0	1	0	0	0	0	0	0	
chr22	39545395	39545396	rs139400	0	0	1	0	0	0	0	0	0	
chr22	39544969	39544970	rs139398	1	0	0	1	0	0	0	0	0	
chr22	39539298	39539299	rs71813239	0	0	1	0	0	0	0	0	0	
chr22	39542291	39542292	rs877529	0	0	0	1	0	0	0	0	0	
chr22	39548026	39548027	rs5995688	0	0	0	0	0	1	0	0	0	
chr22	39546073	39546074	rs139401	0	0	1	0	0	0	0	0	0	
chr22	39528439	39528440	rs79503	0	0	0	0	0	0	1	0	1	
TOTAL				1	3	19	3	2	8	2	3	2	