

Supplementary Table 1. Summary of SNP filters for melanoma genome-wide association study. "CIDR" means SNPs filtered by the genotyping center. Other filters were recommended by the GENEVA Coordinating Center<sup>20</sup>.

SNPs kept	SNPs lost	Filter
1,016,423	0	Total SNPs attempted (989,972 Autosomal, 24,103 X chromosome, 1,283 Y chromosome, 1,039 pseudoautosomal, 26 Mitochondrial  123,996 additional CNV targeting probes with only intensity information
1,012,904	3,519	SNPs that only provided intensity data (CIDR applied technical filter for complete SNP assay failure)
818,237 Autosomal and X chromosome	193,927	MAF>0.01, call rate≥95%, HWE p-value≥1 x 10 <sup>-5</sup>
740 (XY) pseudoautosomal		

Supplementary Table 2. Summary of melanoma samples and scans.

Study	Filter
Total Released	3,324
Experimental Samples	3,047 of 3,086 samples attempted (98.7%) <ul style="list-style-type: none"> <li>- 2,965 of 3,002 genomic DNA from blood Includes 2,949 of 2,965 with high quality intensity data for CNV analyses (99.5%)</li> <li>- 82 of 84 samples that underwent whole genome amplification</li> </ul>
Blind Duplicates	68 of 70 attempted
Control Samples	209 HapMap control samples (68 unique subjects) <ul style="list-style-type: none"> <li>- 129 CEPH CEU controls</li> <li>- 10 Han Chinese controls</li> <li>- 10 Japanese controls</li> <li>- 60 Yoruban controls</li> </ul> <p>CEPH CEU samples NA10851 and NA11995 were included on every plate for use in exploring approaches and reproducibility of CNV calls</p>
3,156 from MDACC	DNA samples sent for genotyping production
-41	Failed genotyping (missing > 10%)
3,115	Scans released by genotyping center including 68 blind duplicates
-11	Sample identity issues
3,104	Scans posted on dbGap
-126	67 duplicated, 20 related (IBD), 39 outliers identified by clustering and PCA
2,978	Melanoma case control data released to dbGAP
-148	<i>In situ</i> (n=138) and AMP (n=10) cases removed
2830	Eligible for analysis: 1,804 cases, 1,026 controls)

Supplementary Table 3. Results ( $p < 10^{-4}$ ) from genome-wide association analysis of melanoma with SNPs using logistic regression under a log additive adjusted for two principal components. A1 is the minor allele in top reading.

CHR	SNP	BP	A1	Number	OR	SE	STAT	P	Gene Symbol
1	rs11204754	149227878	A	2830	1.249	0.05574	3.996	$6.44 \times 10^{-5}$	ANXA9
1	rs1722784	149228493	G	2830	1.259	0.05569	4.131	$3.61 \times 10^{-5}$	ANXA9
1	rs11506	163898130	G	2830	0.6701	0.1018	-3.931	$8.48 \times 10^{-5}$	ALDH9A1
1	rs11120504	213374400	C	2830	1.244	0.05566	3.925	$8.68 \times 10^{-5}$	KCNK2
1	rs12753507	213446975	G	2829	1.249	0.05619	3.959	$7.51 \times 10^{-5}$	KCNK2
1	rs2089427	213637204	G	2828	1.248	0.0561	3.95	$7.82 \times 10^{-5}$	LOC643536
1	rs10926064	238240621	A	2828	0.7855	0.05738	-4.208	$2.57 \times 10^{-5}$	LOC645884
1	rs12733694	238284757	G	2830	1.333	0.07351	3.912	$9.15 \times 10^{-5}$	FMN2
2	rs12471713	65957786	C	2812	0.6793	0.08464	-4.569	$4.89 \times 10^{-6}$	FLJ16124
2	rs2083244	119377691	G	2828	0.7884	0.05721	-4.156	$3.23 \times 10^{-5}$	MARCO
2	rs10930182	166396434	A	2830	0.7737	0.06405	-4.005	$6.19 \times 10^{-5}$	TTC21B
2	rs2060167	166397588	A	2829	0.7721	0.06401	-4.041	$5.33 \times 10^{-5}$	TTC21B
2	rs1560594	166408044	A	2830	0.773	0.0643	-4.004	$6.23 \times 10^{-5}$	TTC21B
2	rs2304003	166422327	A	2830	0.7772	0.06442	-3.913	$9.11 \times 10^{-5}$	TTC21B
2	rs3791511	239745477	A	2830	1.435	0.09033	3.996	$6.43 \times 10^{-5}$	HDAC4
3	rs1872396	7655452	A	2830	0.7255	0.07879	-4.073	$4.65 \times 10^{-5}$	GRM7
3	rs3912449	7658162	G	2824	0.7324	0.07832	-3.977	$6.99 \times 10^{-5}$	GRM7
3	rs9790140	96158387	A	2830	0.6651	0.09942	-4.102	$4.1 \times 10^{-5}$	WDR82P1
3	rs4643673	148129994	G	2829	0.7932	0.05746	-4.031	$5.55 \times 10^{-5}$	PLSCR5
3	rs7638277	151726568	G	2830	1.259	0.05795	3.971	$7.16 \times 10^{-5}$	S x 10RP1
4	rs6823995	106483130	G	2830	0.7223	0.08212	-3.962	$7.44 \times 10^{-5}$	PPA2
4	rs17035512	106509509	C	2823	0.712	0.08325	-4.08	$4.51 \times 10^{-5}$	PPA2
4	rs17035553	106540872	A	2830	0.7341	0.07434	-4.158	$3.21 \times 10^{-5}$	PPA2
4	rs6811159	106542507	G	2830	0.7179	0.08332	-3.977	$6.97 \times 10^{-5}$	PPA2
4	rs17035584	106574235	A	2829	0.7191	0.0833	-3.958	$7.54 \times 10^{-5}$	PPA2
4	rs3898404	106575844	G	2826	0.739	0.07464	-4.051	$5.1 \times 10^{-5}$	PPA2
5	rs10940474	54916458	G	2829	1.279	0.05928	4.154	$3.26 \times 10^{-5}$	FLJ90709
6	rs3087617	31664635	T	2821	1.544	0.1098	3.959	$7.54 \times 10^{-5}$	LST1
6	rs7769019	33706620	G	2830	0.565	0.1396	-4.091	$4.3 \times 10^{-5}$	ITPR3
6	rs2495971	34037043	C	2830	1.369	0.07929	3.96	$7.51 \times 10^{-5}$	GRM4
6	rs9454109	68004709	A	2828	1.326	0.06217	4.537	$5.69 \times 10^{-6}$	RCADH5
7	rs10245068	37331759	A	2830	1.467	0.09316	4.112	$3.92 \times 10^{-5}$	x 10LMO1
8	rs2617014	4537866	A	2829	1.288	0.05565	4.544	$5.51 \times 10^{-6}$	CSMD1
8	rs2724961	4547635	A	2829	1.279	0.05584	4.402	$1.07 \times 10^{-5}$	CSMD1
8	rs10094500	4558681	A	2830	0.7783	0.05602	-4.474	$7.68 \times 10^{-6}$	CSMD1
8	rs4909616	135569749	G	2829	0.7807	0.0602	-4.113	$3.91 \times 10^{-5}$	ZFAT1
9	rs11792508	243594	A	2830	0.6563	0.09854	-4.274	$1.92 \times 10^{-5}$	DOCK8
9	rs10811582	21682017	G	2828	1.285	0.05671	4.42	$9.86 \times 10^{-6}$	LOC402359
9	rs12380505	21685893	A	2830	1.312	0.05541	4.904	$9.41 \times 10^{-7}$	LOC402359
9	rs1452658	21690795	G	2829	1.308	0.05527	4.864	$1.15 \times 10^{-6}$	LOC402359
9	rs7848524	21691432	A	2830	1.316	0.05528	4.966	$6.84 \times 10^{-7}$	LOC402359
9	rs6475552	21691674	G	2825	1.313	0.0553	4.926	$8.41 \times 10^{-7}$	LOC402359
9	rs1987458	21694873	G	2830	0.8028	0.05529	-3.973	$7.11 \times 10^{-5}$	LOC402359
9	rs896655	21696571	G	2827	0.8019	0.05609	-3.937	$8.25 \times 10^{-5}$	LOC402359

9rs2383202	21700215	G	2830	1.313	0.05537	4.919	$8.7 \times 10^{-7}$	LOC402359
9rs1335500	21701675	G	2830	1.31	0.05534	4.883	$1.04 \times 10^{-6}$	LOC402359
9rs1345026	21735756	A	2830	1.268	0.05646	4.21	$2.56 \times 10^{-5}$	LOC402359
9rs1561650	21742358	G	2830	0.7987	0.0567	-3.964	$7.38 \times 10^{-5}$	LOC402359
9rs7866787	21750639	G	2829	0.8051	0.05557	-3.9	$9.61 \times 10^{-5}$	LOC402359
9rs10121899	21760951	G	2829	0.7896	0.05677	-4.162	$3.15 \times 10^{-5}$	MTAP
9rs1341866	21761241	G	2830	0.7873	0.05683	-4.208	$2.58 \times 10^{-5}$	MTAP
9rs6475579	21761756	G	2830	0.8031	0.05562	-3.943	$8.06 \times 10^{-5}$	MTAP
9rs10757253	21762267	G	2830	0.8049	0.05561	-3.902	$9.54 \times 10^{-5}$	MTAP
9rs9886831	21763167	G	2822	0.8024	0.05565	-3.955	$7.65 \times 10^{-5}$	MTAP
9rs10757254	21765061	G	2830	0.8048	0.05569	-3.899	$9.66 \times 10^{-5}$	MTAP
9rs7021012	21765957	A	2830	0.8033	0.05565	-3.936	$8.3 \times 10^{-5}$	MTAP
9rs1440993	21768660	A	2830	0.8033	0.056	-3.912	$9.16 \times 10^{-5}$	MTAP
9rs10811615	21772164	A	2830	0.8042	0.05584	-3.902	$9.55 \times 10^{-5}$	LOC402359
9rs7863942	21774758	A	2826	0.7856	0.05679	-4.249	$2.14 \times 10^{-5}$	MTAP
9rs1345024	21775018	A	2830	0.788	0.05669	-4.203	$2.63 \times 10^{-5}$	MTAP
9rs1345023	21775139	T	2827	0.7876	0.05672	-4.21	$2.56 \times 10^{-5}$	MTAP
9rs7049092	21777262	A	2830	0.7843	0.05673	-4.282	$1.85 \times 10^{-5}$	MTAP
9rs7038708	21778081	C	2829	0.804	0.05558	-3.925	$8.68 \times 10^{-5}$	MTAP
9rs7022754	21778481	G	2829	0.7866	0.05678	-4.228	$2.36 \times 10^{-5}$	MTAP
9rs7022856	21778523	G	2830	0.8051	0.05561	-3.898	$9.71 \times 10^{-5}$	MTAP
9rs10965133	21778656	A	2830	0.7861	0.05677	-4.239	$2.25 \times 10^{-5}$	LOC402359
9rs10965134	21778782	A	2829	0.7842	0.05679	-4.281	$1.86 \times 10^{-5}$	MTAP
9rs10811617	21780067	G	2828	0.8023	0.05565	-3.959	$7.53 \times 10^{-5}$	MTAP
9rs10811618	21780142	C	2826	0.8037	0.05569	-3.925	$8.69 \times 10^{-5}$	MTAP
9rs1542075	21780669	C	2828	0.7974	0.05558	-4.074	$4.63 \times 10^{-5}$	MTAP
9rs12344842	21783177	C	2830	0.7959	0.05563	-4.104	$4.06 \times 10^{-5}$	MTAP
9rs10119693	21786791	A	2774	0.7717	0.05813	-4.459	$8.25 \times 10^{-6}$	MTAP
9rs7033503	21789598	G	2830	0.7572	0.05553	-5.008	$5.5 \times 10^{-7}$	MTAP
9rs2165408	21792469	G	2830	0.7974	0.05537	-4.088	$4.35 \times 10^{-5}$	MTAP
9rs869329	21794693	G	2830	0.7964	0.05534	-4.114	$3.89 \times 10^{-5}$	MTAP
9rs10757257	21796564	A	2829	0.7827	0.05687	-4.308	$1.65 \times 10^{-5}$	MTAP
9rs10965144	21798913	A	2827	0.7925	0.05697	-4.082	$4.46 \times 10^{-5}$	MTAP
9rs10965145	21799077	A	2828	0.7855	0.05691	-4.242	$2.21 \times 10^{-5}$	MTAP
9rs72691561	21803241	G	2829	1.244	0.05538	3.937	$8.27 \times 10^{-5}$	MTAP
9rs72691563	21803495	A	2828	1.264	0.05563	4.212	$2.53 \times 10^{-5}$	MTAP
9rs72691564	21803518	A	2829	1.246	0.0554	3.971	$7.15 \times 10^{-5}$	MTAP
9rs58377678	21803718	G	2830	0.7844	0.0552	-4.4	$1.08 \times 10^{-5}$	MTAP
9rs7023329	21806528	G	2830	0.7886	0.05512	-4.309	$1.64 \times 10^{-5}$	MTAP
9rs10114559	21806637	G	2830	0.7849	0.05567	-4.351	$1.35 \times 10^{-5}$	MTAP
9rs7023474	21806646	A	2830	1.242	0.05531	3.919	$8.87 \times 10^{-5}$	MTAP
9rs7023954	21806758	A	2830	0.7811	0.05663	-4.363	$1.28 \times 10^{-5}$	MTAP
9rs4615669	21808674	G	2830	0.7894	0.05576	-4.241	$2.22 \times 10^{-5}$	MTAP
9rs10121449	21816516	G	2830	0.7816	0.05678	-4.34	$1.43 \times 10^{-5}$	MTAP
9rs10811626	21816940	A	2828	0.7817	0.05678	-4.336	$1.45 \times 10^{-5}$	MTAP
9rs3922992	21817406	G	2830	0.7839	0.05681	-4.286	$1.82 \times 10^{-5}$	MTAP
9rs3900787	21818110	C	2829	0.7792	0.05676	-4.394	$1.11 \times 10^{-5}$	MTAP
9rs3927738	21818242	A	2830	1.259	0.05541	4.153	$3.28 \times 10^{-5}$	MTAP

10rs2797272	9125309	G	2829	0.7723	0.06348	-4.071	4.68 x 10 <sup>-5</sup>	LOC389936
10rs11001702	53773431	G	2827	0.6693	0.09232	-4.349	1.37 x 10 <sup>-5</sup>	DKK1
10rs12412902	55355079	G	2816	0.6623	0.1033	-3.989	6.65 x 10 <sup>-5</sup>	PCDH15
10rs34950775	114770071	A	2830	0.429	0.1971	-4.294	1.75 x 10 <sup>-5</sup>	TCF7L2
11rs644817	69749575	A	2830	1.609	0.1187	4.008	6.12 x 10 <sup>-5</sup>	FADD
12rs12826471	3455203	A	2829	1.412	0.07911	4.361	1.29 x 10 <sup>-5</sup>	PRMT8
13rs7995083	23043162	G	2830	1.419	0.08597	4.074	4.63 x 10 <sup>-5</sup>	TNFRSF19
13rs2202561	70442966	A	2829	0.7981	0.05657	-3.987	6.68 x 10 <sup>-5</sup>	LOC647277
13rs17691655	70445908	A	2830	0.7462	0.06431	-4.552	5.31 x 10 <sup>-6</sup>	LOC647277
14rs7150290	52220859	G	2830	1.4	0.08223	4.092	4.28 x 10 <sup>-5</sup>	ERO1L
15rs1129038	26030454	G	2830	0.6901	0.06662	-5.568	2.58 x 10 <sup>-8</sup>	HERC2
15rs12913832	26039213	A	2830	0.6948	0.06649	-5.478	4.31 x 10 <sup>-8</sup>	HERC2
16rs12445947	56357149	A	2830	0.4561	0.2017	-3.893	9.92 x 10 <sup>-5</sup>	KIFC3
16rs17827507	83202987	G	2830	0.7645	0.06175	-4.348	1.37 x 10 <sup>-5</sup>	COTL1
16rs352935	88176081	A	2799	0.8002	0.05586	-3.99	6.61 x 10 <sup>-5</sup>	CPNE7
16rs164741	88219799	A	2830	1.319	0.05877	4.714	2.43 x 10 <sup>-6</sup>	DPEP1
16rs258322	88283404	A	2829	1.548	0.08924	4.899	9.63 x 10 <sup>-7</sup>	CDK10
16rs7195043	88548362	G	2825	0.7186	0.05657	-5.841	5.18 x 10 <sup>-9</sup>	DEF8
16rs8051733	88551707	G	2811	1.41	0.05829	5.893	3.8 x 10 <sup>-9</sup>	DEF8
16rs4785751	88556918	A	2829	0.6966	0.05607	-6.448	1.13 x 10 <sup>-10</sup>	DEF8
16rs4785752	88562642	A	2830	1.354	0.05585	5.429	5.66 x 10 <sup>-8</sup>	DEF8
16rs4408545	88571529	A	2830	0.7026	0.05659	-6.238	4.43 x 10 <sup>-10</sup>	AFG3L1
16rs11648898	88573487	G	2830	1.525	0.07472	5.648	1.62 x 10 <sup>-8</sup>	AFG3L1
16rs4238833	88578190	C	2830	1.331	0.05718	4.999	5.78 x 10 <sup>-7</sup>	AFG3L1
16rs4785759	88578381	A	2830	1.36	0.05616	5.473	4.42 x 10 <sup>-8</sup>	AFG3L1
16rs9939542	88580549	C	2830	1.327	0.06159	4.595	4.32 x 10 <sup>-6</sup>	AFG3L1
16rs4785763	88594437	A	2830	1.319	0.05801	4.775	1.8 x 10 <sup>-6</sup>	AFG3L1
16rs11076650	88595442	G	2830	1.397	0.05574	5.996	2.02 x 10 <sup>-9</sup>	DBNDD1
16rs10852628	88607428	G	2821	1.393	0.0615	5.392	6.96 x 10 <sup>-8</sup>	DBNDD1
17rs16957962	9000751	G	2826	1.288	0.06051	4.185	2.85 x 10 <sup>-5</sup>	NTN1
17rs9904264	11587008	G	2829	1.334	0.06994	4.118	3.82 x 10 <sup>-5</sup>	DNAH9
17rs3744578	11589057	G	2830	1.317	0.06962	3.951	7.77 x 10 <sup>-5</sup>	DNAH9
19rs2285963	5542735	A	2830	0.6996	0.08376	-4.265	2 x 10 <sup>-5</sup>	SAFB2
19rs868878	7737047	A	2829	1.41	0.08791	3.909	9.27 x 10 <sup>-5</sup>	CLEC4M
19rs1549951	35984184	A	2830	1.249	0.05646	3.94	8.16 x 10 <sup>-5</sup>	ZNF536
19rs6510181	35984559	C	2830	1.25	0.05648	3.956	7.63 x 10 <sup>-5</sup>	ZNF536
19rs934432	36000424	C	2830	1.272	0.05634	4.267	1.98 x 10 <sup>-5</sup>	ZNF536
19rs934433	36000617	A	2830	1.27	0.05632	4.242	2.22 x 10 <sup>-5</sup>	ZNF536
19rs3745542	56279455	G	2830	1.317	0.06188	4.446	8.74 x 10 <sup>-6</sup>	KLK14
20rs17730901	16198822	A	2830	0.7204	0.08304	-3.95	7.81 x 10 <sup>-5</sup>	C20orf23
20rs4814466	16201819	A	2830	0.7175	0.08299	-3.999	6.35 x 10 <sup>-5</sup>	C20orf23
20rs62209647	31969319	C	2822	1.4540	0.09466	3.953	7.72 x 10 <sup>-5</sup>	CHMP4B
20rs6103520	41995774	A	2826	0.4188	0.211	-4.124	3.72 x 10 <sup>-5</sup>	TOX2
20rs6130484	41999382	A	2830	0.4255	0.2048	-4.171	3.03 x 10 <sup>-5</sup>	TOX2
20rs6130486	42007006	A	2829	0.423	0.2069	-4.159	3.2 x 10 <sup>-5</sup>	TOX2
20rs2284271	43038835	A	2829	0.6904	0.09484	-3.906	9.38 x 10 <sup>-5</sup>	STK4

Supplementary Table 4. Basic information of the four GWAS in the five component studies.

Data set	Breast cancer in NHS	T2D in NHS	T2D in HPFS	CHD in NHS	CHD in HPFS
Genotyping platform	Illumina HumanHap550	Affymetrix 6.0	Affymetrix 6.0	Affymetrix 6.0	Affymetrix 6.0
Sample size (Total)	2287	3116	2487	1146	1147
Hair color	1741	2377	1529	783	741
Eye color	N/A	N/A	2292	N/A	1064
Tanning ability	2166	2956	2372	1074	1110
rs12913832	Genotyped	Genotyped	Genotyped	Genotyped	Genotyped

Supplementary Table 5. SNP effects for HERC2 SNP rs12913832 on eye color, hair color and skin color in Controls.

Eye color (Frequency)	OR	P-Value	R-Squared
Blue vs Not Blue (331/694)	0.027	<.0001	0.3265
Green vs Not Green (165/860)	0.46	<.0001	0.0249
Hazel vs Not Hazel (199/826)	0.918	0.5042	0.0004
Brown vs Not Brown (312/713)	49.017	<.0001	0.4264
Gray vs Not Gray (18/1007)	0.675	0.3553	0.0009
All Categories (Ordinal Logistic Regression)			0.4955

Hair Color (Frequency)	OR	P-Value	R-Squared
Blonde vs Not Blonde (193/832)	0.271	<.0001	0.066
Red vs Not Red (38/987)	1.007	0.9805	0
Brown vs Not Brown (730/295)	1.426	0.0023	0.0093
Black vs Not Black (58/967)	3.99	<.0001	0.0452
All Categories (Ordinal Logistic Regression)			0.0997

Skin Color (Frequency)	OR	P-Value	R-Squared
Very Fair vs Not (Grades 0-3) (456/569)	0.672	0.0001	0.0144
Moderate vs Not (Grades 4-5) (389/636)	1.151	0.1718	0.0018
Dark vs Not (Grades 6-7) (158/867)	1.426	0.0078	0.0067
Very Dark (Grades 8-10) (22/1003)	1.803	0.0613	0.0032

Supplementary Table 6. Allele frequencies of rs12913832 from the CEPH Human Genome Diversity Panel.

Population	Region	Sample Size	A allele Frequency
Colombians	America	7	1.000
Karitiana	America	14	0.679
Maya	America	21	0.881
Pima	America	14	1.000
Surui	America	8	0.813
Balochi	Asia	22	0.909
Brahui	Asia	25	0.880
Burusho	Asia	25	0.880
Cambodians	Asia	9	0.667
Dai	Asia	10	1.000
Daur	Asia	10	1.000
Han	Asia	44	1.000
Hazara	Asia	22	0.750
Hezhen	Asia	9	1.000
Japanese	Asia	27	1.000
Kalash	Asia	22	0.932
Lahu	Asia	8	1.000
Makrani	Asia	25	0.800
Miaozu	Asia	10	1.000
Mongola	Asia	10	1.000
Naxi	Asia	9	1.000
Oroqen	Asia	9	1.000
Pathan	Asia	21	0.905
She	Asia	10	1.000
Sindhi	Asia	23	0.783
Tu	Asia	10	1.000
Tujia	Asia	10	0.900
Uygur	Asia	10	1.000
Xibo	Asia	9	1.000
Yakut	Asia	25	0.880
Yizu	Asia	10	1.000
Adygei	Europe	17	0.706
French	Europe	27	0.407
French_Basque	Europe	24	0.625
North_Italian	Europe	13	0.308
Orcadian	Europe	15	0.367
Russian	Europe	25	0.260
Sardinian	Europe	28	0.786
Tuscan	Europe	8	0.438
Bedouin	Middle Est	46	0.924
Druze	Middle Est	39	0.667
Palestinian	Middle Est	43	0.767
Mozabite	North Africa	29	0.897
Subsaharan Africa	Africa	105	1.000
NAN_Melanesian	Oceania	11	1.000
Papuan	Oceania	17	1.000



Supplementary Table 7. Cochrane Mantel-Haenszel tests stratifying CMM cases and controls for known CM SNP associations and *HERC2*.

	CHR	SNP	Odds Ratios Across Strata								Analysis Across Strata		
			1	2	3	4	5	6	7	8	CMH Test	Test	Breslow
			P	OR	Day Test								
P16/MTAP	9	rs1452658	0.97	1.54	1.17	1.29	1.56	1.32	0.86	1.72	3.15E-08	1.273	0.03613
HERC2	15	rs12913832	0.88	0.71	0.88	0.64	0.71	0.92	1.03	0.94	2.43E-06	0.7767	0.4241
MC1R	16	rs4408545	0.79	0.74	0.75	0.74	0.51	0.75	1.22	0.95	7.64E-11	0.7516	0.499
EIF6	20	rs619865	1.30	1.44	1.63	1.29	1.08	0.82	1.36	0.51	1.18E-06	1.387	0.3235

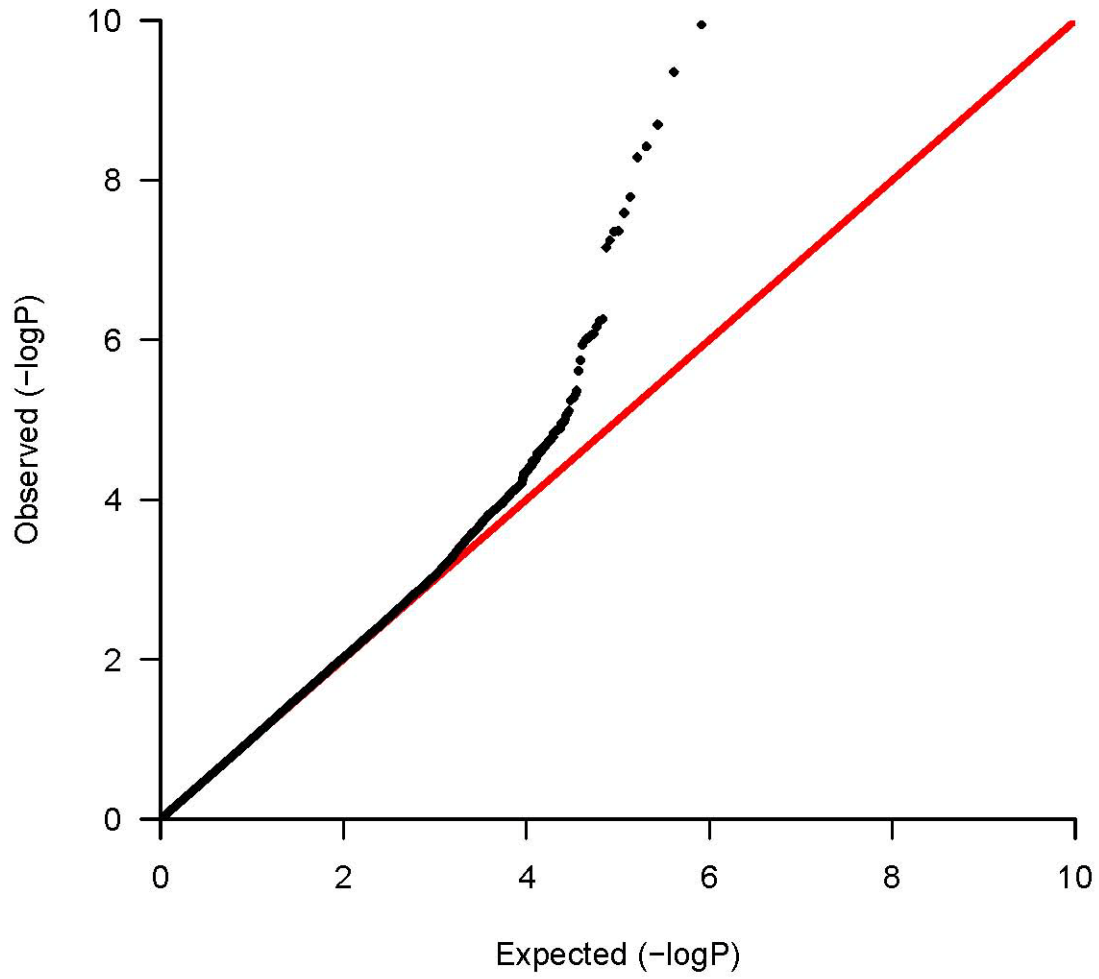
1=Irish/UK, 2=French, 3=Scandinavian, 4=German, 5=Eastern European, 6=Ashkenazi, 7=Italian, 8=German/French

Supplementary Table 8. Fixed effects meta-analysis of 10 most significant regions identified from genome-wide analysis of samples from MDACC and evaluated in additional populations. A1 is the minor allele in forward coding since some SNPs are imputed.

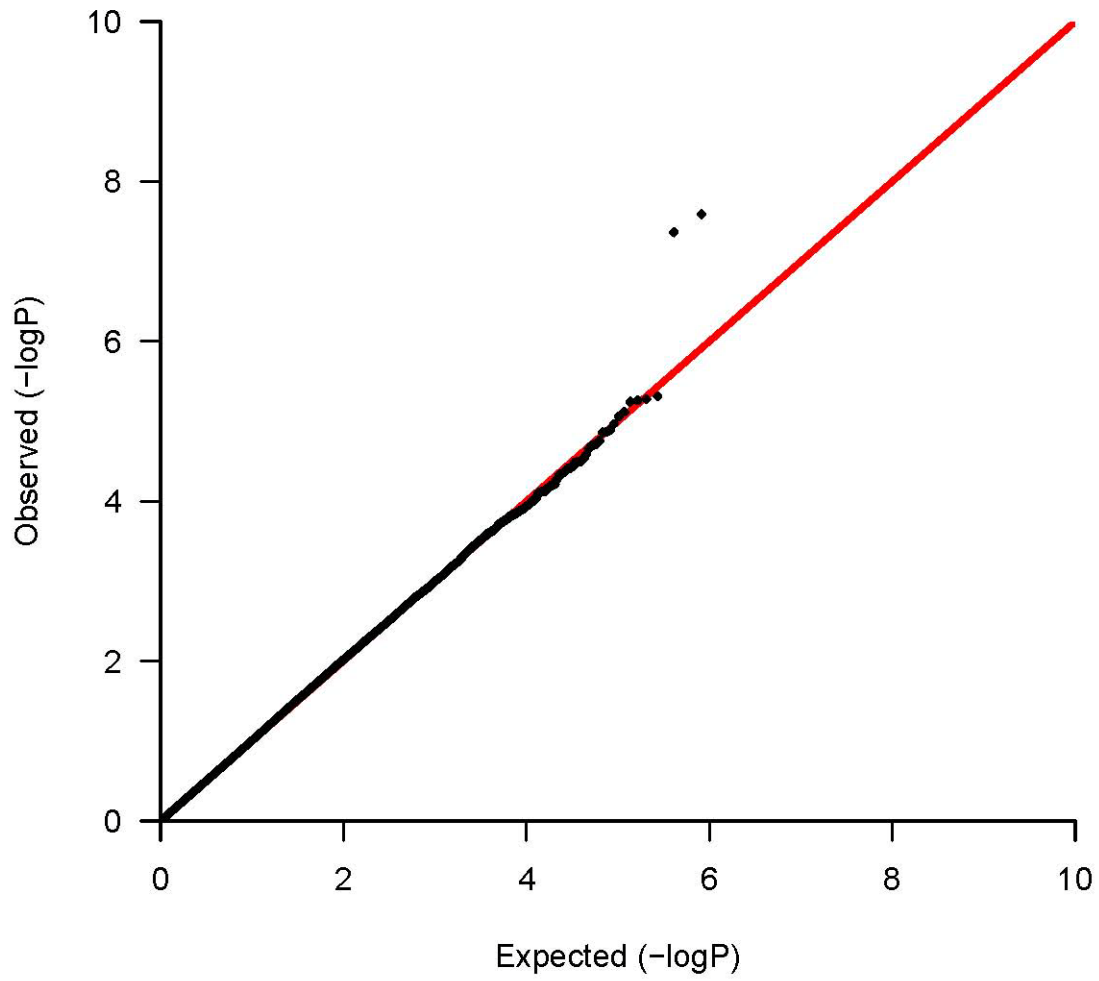
SNP	Chrom.	Coordinate	A1	MAF	Australia		MDACC		GenoMEL		Harvard		MetaAnalysis	
					OR	P	OR	P	OR	P	OR	P	OR	P
rs1722784	1	149228493	A	0.50	0.87	$2 \times 10^{-4}$	0.79	$3.61 \times 10^{-5}$	1.00	0.947	0.90	0.088	0.89	$2.41 \times 10^{-6}$
rs12038695	1	213444580	C	0.43	1.02	0.696	1.25*	$7.35 \times 10^{-5}$	1.02	0.697	0.93	0.297	1.05	0.064
rs10926064	1	238240621	T	0.38	1.04	0.340	0.79	$2.57 \times 10^{-5}$	0.99	0.785	0.99	0.832	0.97	0.167
rs2060167	2	166397588	T	0.24	0.93	0.101	0.77	$5.33 \times 10^{-5}$	1.03	0.487	1.05	0.541	0.96	0.066
rs1872396	3	7655452	A	0.14	1.18	0.001	0.73	$4.65 \times 10^{-5}$	0.97	0.480	0.95	0.592	0.99	0.754
rs3898404	4	106575844	C	0.16	1.00	0.998	0.74	$5.1 \times 10^{-5}$	0.90	0.103	0.84	0.079	0.93	0.007
rs2617014	8	4537866	A	0.46	1.01	0.734	1.29	$5.51 \times 10^{-6}$	1.01	0.725	1.05	0.471	1.05	0.016
rs12913832	15	26039213	A	0.21	0.98	0.631	0.69	$4.31 \times 10^{-8}$	0.96	0.439	0.89	0.110	0.90	$2.45 \times 10^{-4}$
rs12449476	17	11593733	T	0.21	0.93	0.267	1.33	$5.49 \times 10^{-5}$	1.00	0.920	1.12	0.169	1.05	0.088
rs6105564	20	16210545	C	0.15	0.95	0.515	0.74	$8.07 \times 10^{-5}$	1.00	0.959	1.06	0.560	0.93	0.040

\*SNP was imputed for MDACC

Supplementary Figure 1. Q-Q plot for p-values of genotyped SNPs after adjusting for the first two principal components, lambda=1.011



Supplementary Figure 2. Q-Q plot with 2 principal components and with previously identified loci around MC1R and P16 removed, lambda is 1.010.



Supplementary Figure 3: Results from Logistic Regression Analyses Before and After Adjusting for the Most Significant SNP in each Region. Legend: filled diamond – results before conditioning; open circle: results after conditioning on SNP in red diamond.

