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Supplemental Information

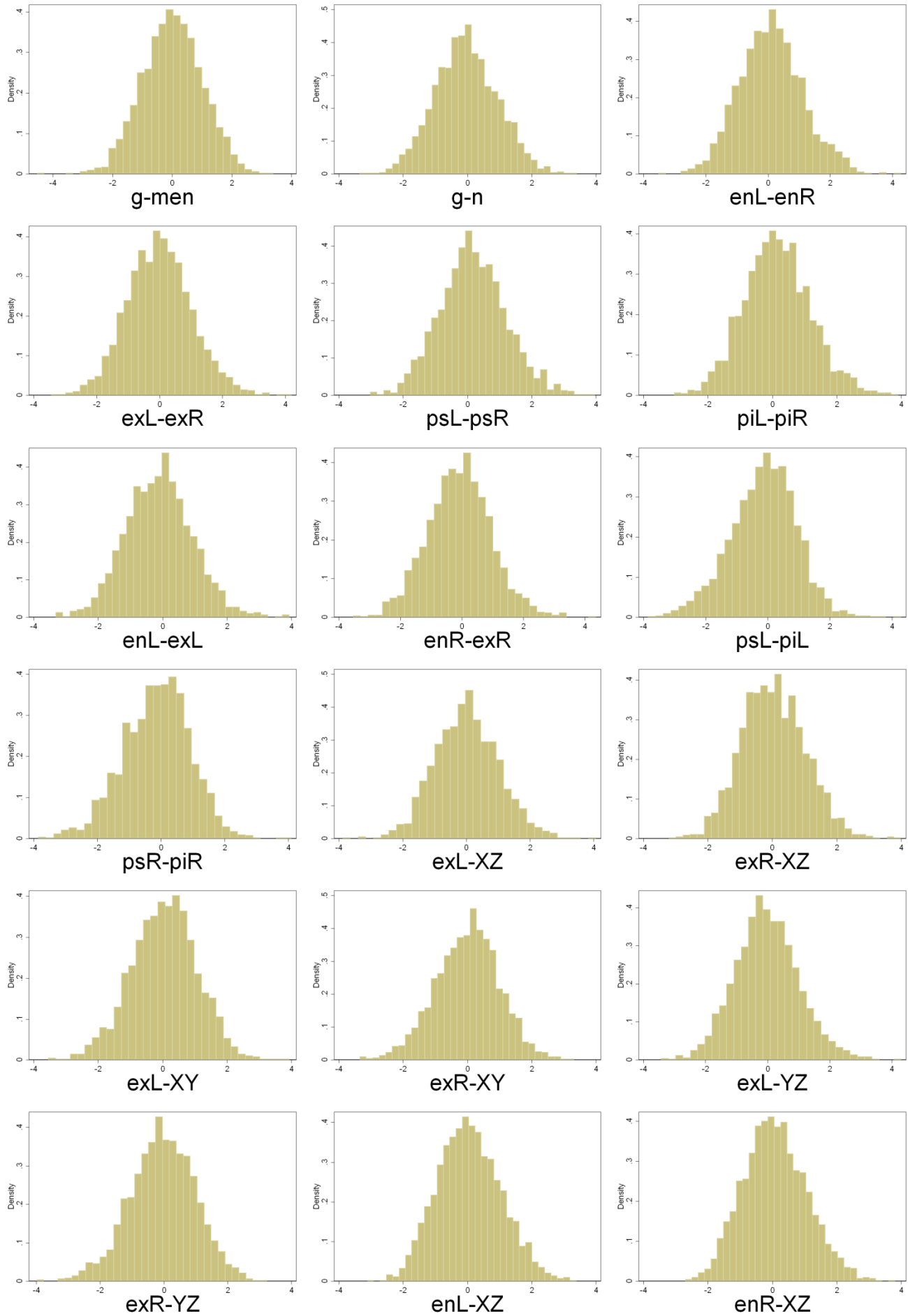
Genome-wide Association Study of Three-Dimensional

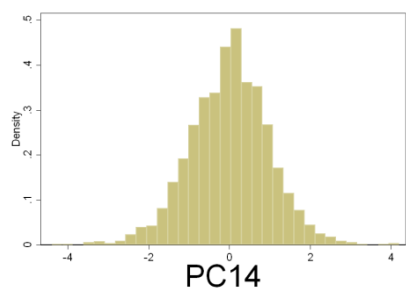
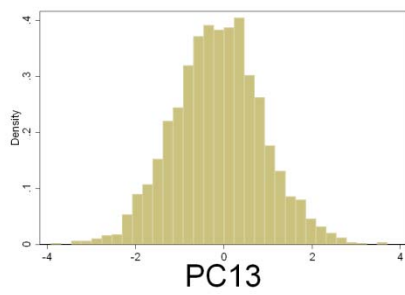
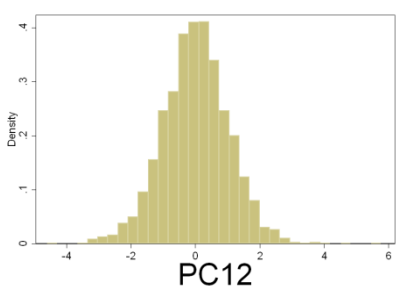
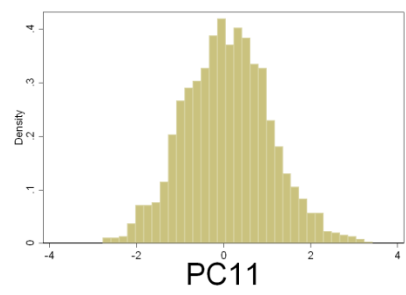
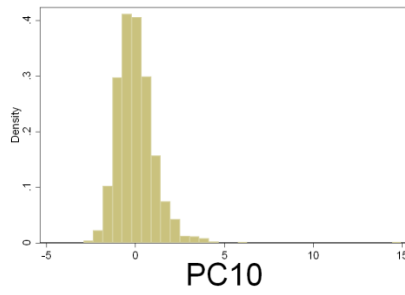
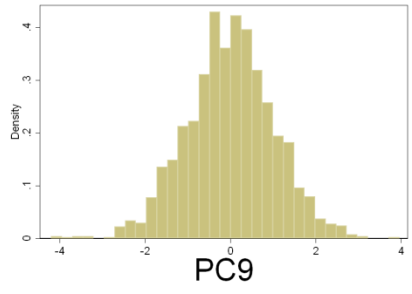
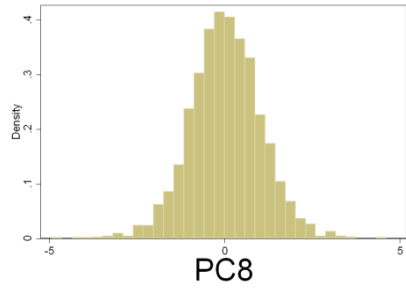
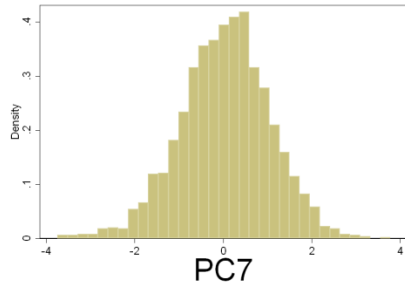
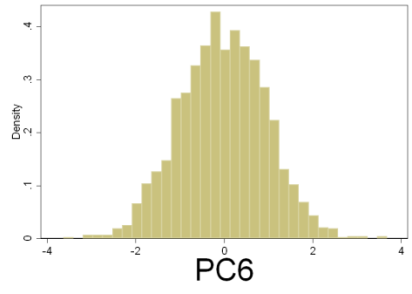
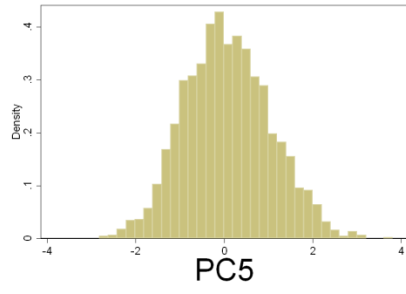
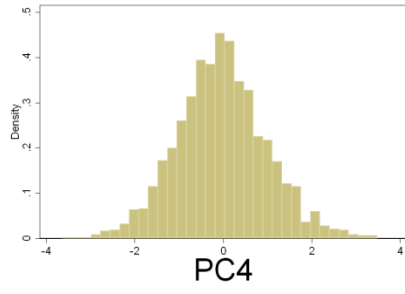
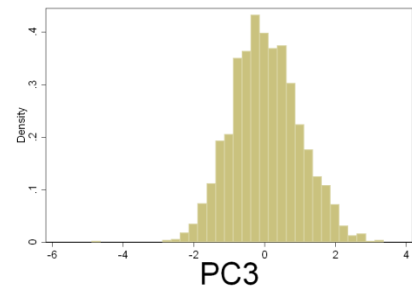
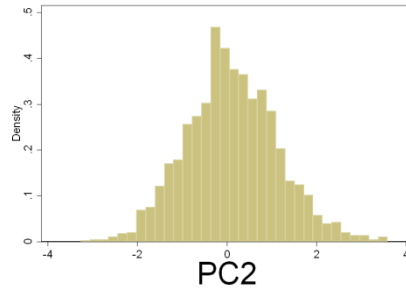
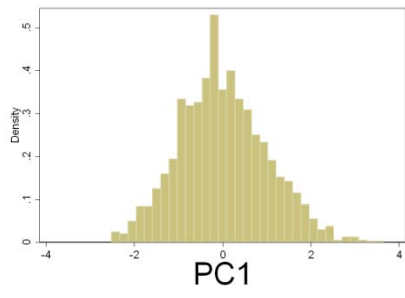
Facial Morphology Identifies a Variant

in *PAX3* Associated with Nasion Position

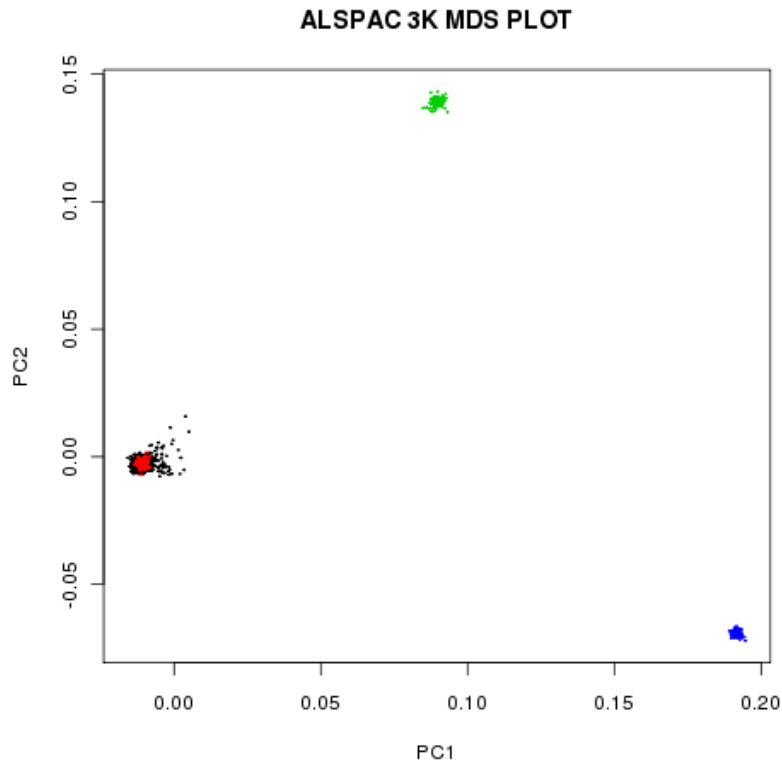
Lavinia Paternoster, Alexei I. Zhurov, Arshed M. Toma, John P. Kemp, Beate St. Pourcain, Nicholas J. Timpson, George McMahon, Wendy McArdle, Susan M. Ring, George Davey Smith, Stephen Richmond, and David M. Evans

Figure S1. Distributional plots for the 54 distances and 14 principal components in the discovery sample.





a.



b.

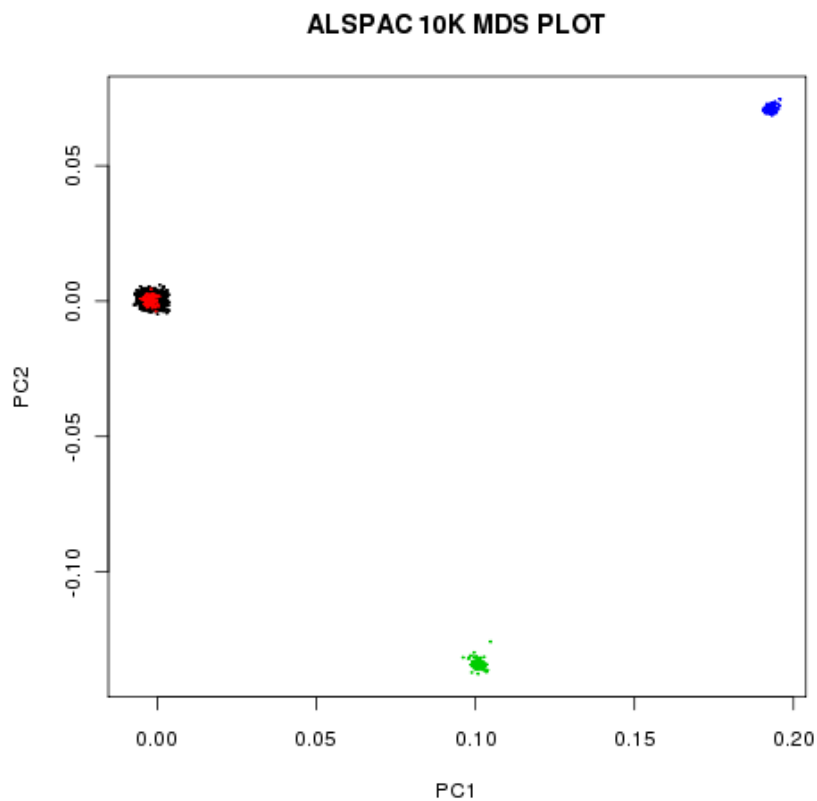


Figure S2. Multidimensional scaling (MDS) analysis plots for the individuals included in the (a) discovery and (b) replication analyses. Black points are the current participants, red points are the HapMap CEU individuals, green points are the Hapmap JPT/CHB individuals, blue points are the HapMap YRI individuals. As can be seen by the clusters of included individuals a less strict exclusion criteria was applied in the discovery sample (and EIGENSTRAT PC1 and PC2 were included in the analyses as covariates). Stricter ethnicity exclusion criteria were used for the replication sample and so it was not necessary to adjust for EIGENSTRAT values in the analyses.

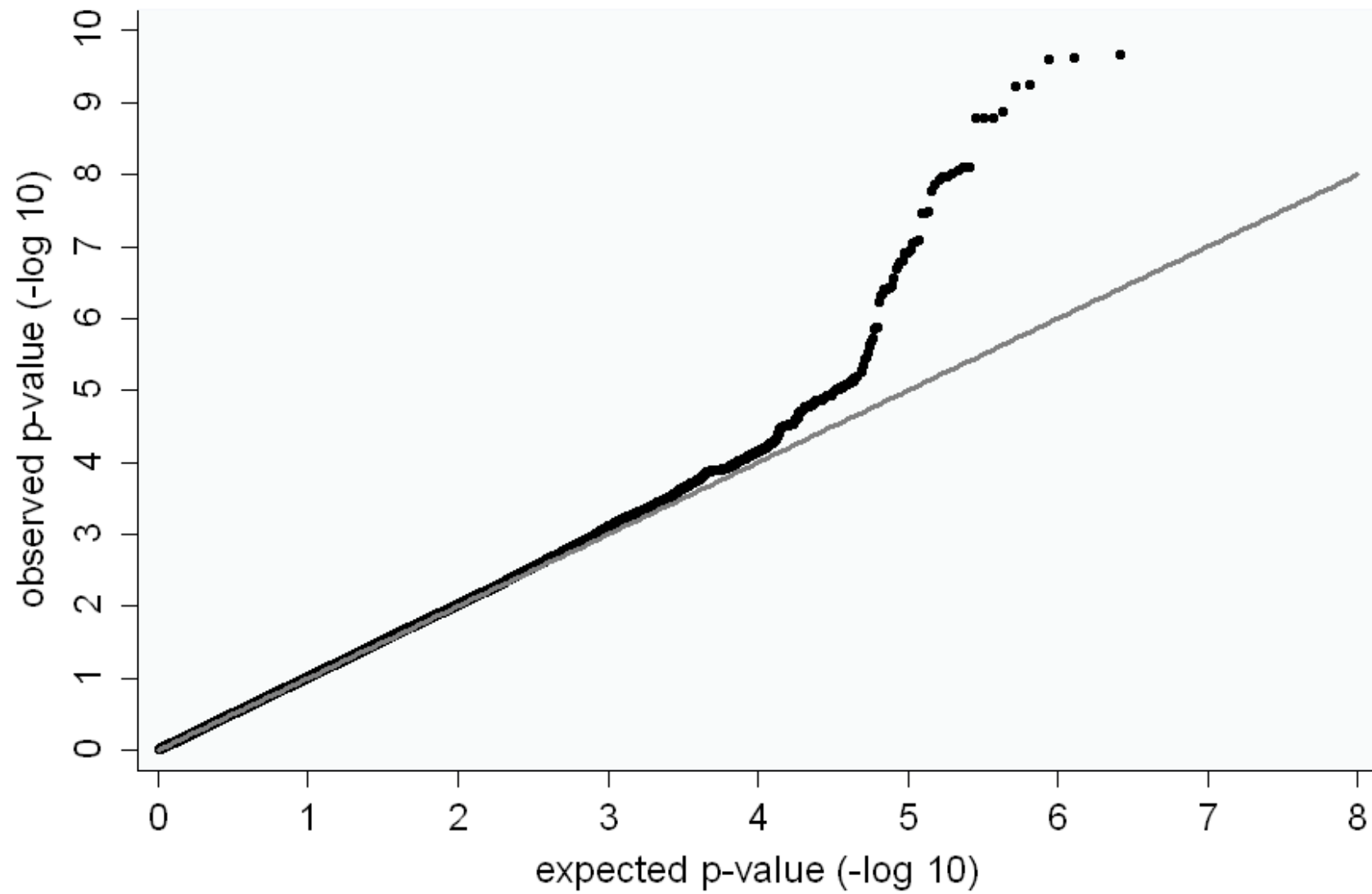


Figure S3. QQ plot for the n-men GWA. Lambda=1.02

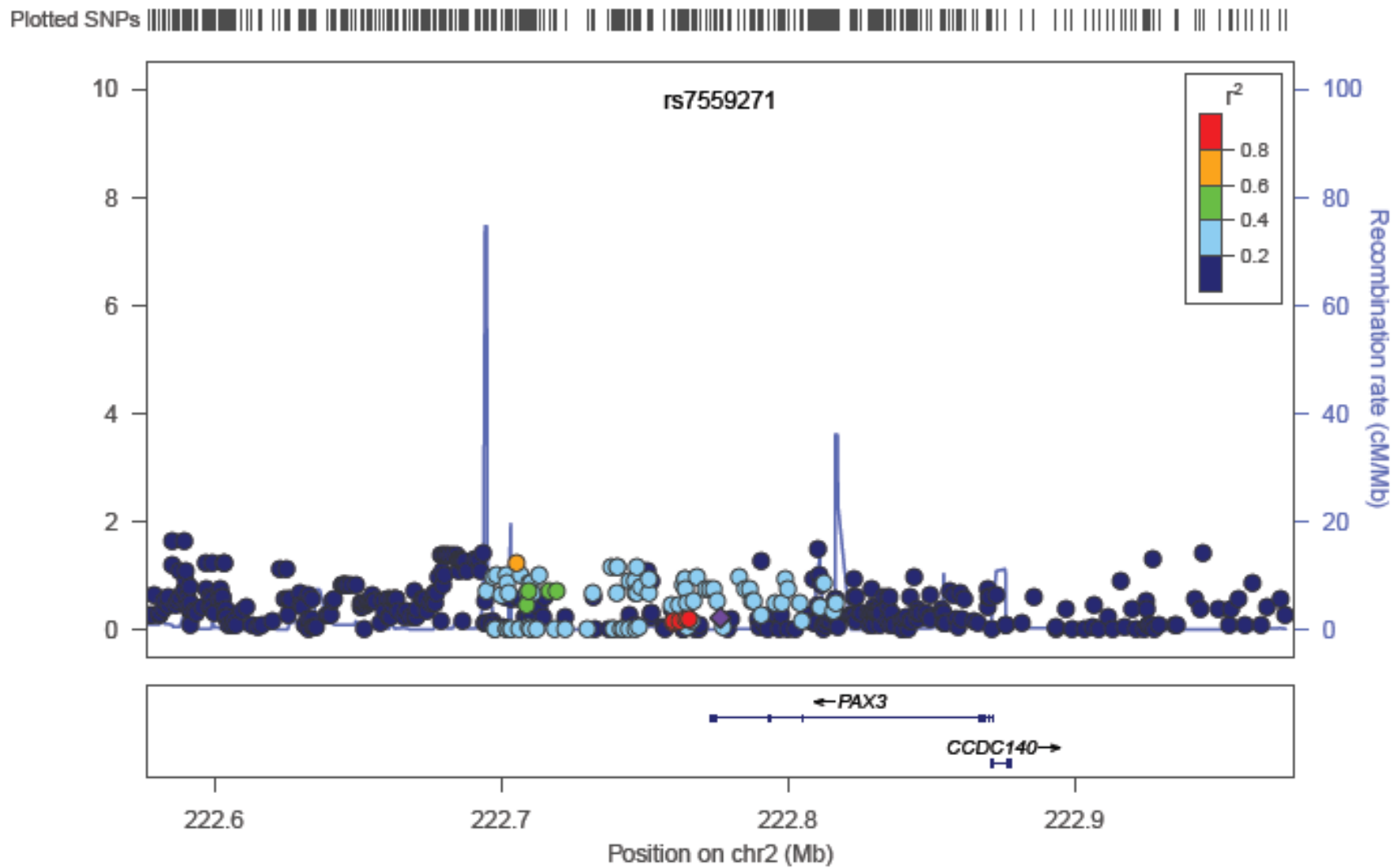


Figure S4. Association plot of the region surrounding *PAX3* for the inter-canthal width (enL-enR).

Table S2. Principal Component Analysis (a) of Landmark Data and (b) brief description of the principal components extracted for the total sample.

a.

PC	x-y-z	Principal Components													
		1	2	3	4	5	6	7	8	9	10	11	12	13	14
PC1	lsy	-.851		.260							.186				
	cphRy	-.843		.243			.102			.126					
	cphLy	-.841		.240			.107			.137					
	enLy	.834	.138	-.112	.165	-.200	-.155								-.105
	enRy	.829	.160	-.108	.153	-.176	-.180						.106		.116
	pgy	-.822	-.155				-.187								
	chRy	-.816	-.190		-.214										
	chLy	-.814	-.180		-.221			-.100							
	piRy	.810			.154	-.151	-.256						.125	-.100	.168
	piLy	.808			.165	-.170	-.254						-.137	-.104	-.162
	psLy	.792					-.278						-.123	.332	-.126
	psRy	.783					-.276						.112	.335	.181
	liy	-.769	-.124		-.386										
	exRy	.759			.189	-.210	-.309						.145		.197
exLy	.748			.194	-.173	-.313						-.184		-.220	
gy	.644	.223			.308	-.130							-.192		
ny	.620	.132	-.468		.123							-.145			
PC2	psLx	.143	.939							-.125					
	psRx	-.139	-.939							-.116					
	piLx	.144	.933							-.135					
	piRx	-.150	-.932							-.127			-.126		
	enRx		-.837			.129				-.168				.219	
	enLx	.102	.830			-.108				-.126				-.225	
PC3	exRx	-.192	-.810						.123				-.116	-.391	
	exLx	.184	.768						-.123	-.148		.140	.432		
	alLz	.209		-.798		-.101	-.171	-.130					-.136		
	alRz	.220		-.786			-.152	-.144					-.132		
	snz	.347		-.706	.260	-.144		-.150					-.113		
PC4	prnz	.404		-.690		-.253	-.138	-.204					-.185		
	liz	.295		.562				-.239							
	lsz	.368			.863			-.102			-.163				
	cphRz	.391			.861	-.112		-.110						-.109	
PC5	cphLz	.388			.861	-.117									
	pgz	-.151		.271	-.788		-.195	-.321							
	gz	-.103	.198	.176		-.858							-.148	.158	
	nz		.157	-.163		-.822	.103						-.299	.167	
	piRz	-.374		.352	-.245	.673						.114	-.120		
PC6	piLz	-.376		.349	-.242	.659			.117		.114	.105	-.111	.119	
	enLz	-.469		.244	-.191	.521	.154		.111		.105		-.139	.274	
	enRz	-.458		.250	-.185	.485	.167			-.105			-.140	.321	
	prny					.120	.821						.106		
PC7	alLy	-.284					.791		-.108						
	alRy	-.299					.768								
	sny	-.226		.184			.722						.162		
PC8	chRx	-.123	-.128								.196				
	chLx	.139	.145								-.205				
	chLz	.203		.230									-.124		
	chRz	.195		.225									.145		
PC9	snx								.940						
	prnx								.906	.167				-.139	
PC10	gx										.974				
	nx										.967				
PC11	cphRx	-.164					.183				.809		.312		
	cphLx	.147					-.199				-.768		.422		
	alLx	.266	.321		.158	-.163	-.219	.266			-.488	.188			
PC12	alRx	-.275	-.332		-.162	.158	.219	.265			.481	-.189			
	psLz	-.275		.207		.101	.219		.109			.805	.109		
PC13	psRz	-.288		.237			.209		-.116			.784	-.125		
	lsx												.942		
PC14	exLz	-.307	-.252	.278	-.172	.369			.166	.105			.161	-.618	
	exRz	-.320	-.290	.287	-.186	.368	.109		-.129	-.118			-.146	-.598	
PC14	pgx								-.180					-.153	.926
	lix								-.104					.486	.775

The highlighted cells (coefficients > 0.5 in magnitude) indicate landmark coordinates that contribute greatly to the facial variation; non-highlighted cells (coefficients < 0.5 in magnitude) indicate landmark coordinates that have less effect on facial variation (coefficients in the range 0.1 - 0.49 in magnitude are presented and coefficients < 0.1 in magnitude are not shown).

b.

Principal Components	Percentage of variance
PC1 , Face Height	28.8
PC2 , Inter-Eyes Distance (Face Width)	10.4
PC3 , Prominence of the nose	6.7
PC4 , Protrusion of the upper lip relative to the chin	5.3
PC5 , Prominence of the eyes relative to the nasal bridge	4.8
PC6 , Vertical height of the nose	4.4
PC7 , Ratio of the mouth width to mouth depth	4.0
PC8 , Deviation of the nasal tip and columella base	3.6
PC9 , Horizontal asymmetry of the nasal bridge	3.2
PC10 , Philtrum-to-nose width ratio	2.7
PC11 , Prominence of the upper eyelids	2.4
PC12 , Horizontal asymmetry of the upper lip (philtrum)	2.3
PC13 , Facial flatness (outer canthi depth)	1.9
PC14 , Horizontal asymmetry of the chin and lower lip	1.7

Table S3. Discovery results for all associations with $p < 5 \times 10^{-7}$. Associations taken forward to replication are shaded grey.

Trait	SNP	Chr	position	Allele 1,2	Allele 1 freq	R2	Beta (allele 2)	SE	P-value
g-men	rs12146102	1	114601393	A,G	0.9062	0.8141	0.283	0.055	2.74E-07
g-men	rs6666714	1	114596380	C,T	0.9073	0.8371	0.281	0.055	2.82E-07
enL-exR	rs3828294	2	207338149	A,G	0.2572	0.9902	0.171	0.034	4.64E-07
exL-exR	rs4716593	7	155704176	A,G	0.3727	0.9992	-0.164	0.032	2.65E-07
exL-exR	rs4717020	7	155704226	A,G	0.3727	0.999	-0.164	0.032	2.68E-07
exL-exR	rs4717021	7	155704640	C,T	0.6272	0.9987	0.163	0.032	2.76E-07
exL-exR	rs12050594	15	48560028	A,T	0.869	0.8501	-0.254	0.05	3.62E-07
psR-piR	rs4375631	15	85239778	C,T	0.0625	0.4648	0.504	0.1	4.31E-07
exR.yz	rs4716593	7	155704176	A,G	0.3727	0.9992	0.165	0.032	2.30E-07
exR.yz	rs4717020	7	155704226	A,G	0.3727	0.999	0.165	0.032	2.33E-07
exR.yz	rs4717021	7	155704640	C,T	0.6272	0.9987	-0.165	0.032	2.40E-07
exR.yz	rs2901850	2	77637083	G,T	0.8246	0.9463	-0.207	0.041	4.58E-07
enL.xz	rs9907335	17	62359090	A,G	0.5217	0.8718	-0.137	0.026	1.61E-07
enR.yz	rs10862567	12	81946483	A,T	0.6875	0.963	0.181	0.033	4.43E-08
enR.yz	rs10746265	12	81944579	C,G	0.3126	0.9701	-0.18	0.033	4.76E-08
enR.yz	rs892540	12	81941606	C,T	0.6881	0.9779	0.179	0.033	5.43E-08
enR.yz	rs2020370	12	81942025	A,G	0.6871	0.9937	0.176	0.033	6.02E-08
enR.yz	rs10862569	12	81947239	A,T	0.3428	0.871	-0.182	0.034	9.68E-08
enR.yz	rs10862568	12	81946655	A,G	0.3432	0.8938	-0.178	0.034	1.22E-07
enR.yz	rs11115550	12	81946617	C,T	0.6565	0.9142	0.175	0.033	1.50E-07
enR.yz	rs10862566	12	81946435	C,T	0.6564	0.9187	0.174	0.033	1.56E-07
enR.yz	rs4374000	12	81945470	A,C	0.3436	0.9192	-0.174	0.033	1.57E-07
enR.yz	rs10862545	12	81939361	A,T	0.6586	0.9095	0.175	0.033	1.63E-07
enR.yz	rs10862548	12	81939850	C,G	0.6576	0.9212	0.173	0.033	1.73E-07
enR.yz	rs7965643	12	81938025	C,T	0.6445	0.894	0.174	0.033	1.74E-07
enR.yz	rs17740709	12	81947471	A,G	0.7991	0.8368	0.216	0.041	1.75E-07
enR.yz	rs10862560	12	81943799	C,T	0.6562	0.9341	0.172	0.033	1.81E-07
enR.yz	rs11115544	12	81943635	A,G	0.3438	0.936	-0.171	0.033	1.84E-07
enR.yz	rs11115545	12	81943731	A,G	0.3438	0.9353	-0.171	0.033	1.84E-07
enR.yz	rs11115542	12	81943390	A,G	0.3439	0.9425	-0.17	0.033	1.95E-07
enR.yz	rs3913351	15	85556598	A,G	0.4223	0.9984	-0.161	0.031	2.37E-07
enR.yz	rs7176553	15	85549546	A,T	0.5773	0.9863	0.161	0.031	2.81E-07
enR.yz	rs12101402	15	85543102	A,G	0.5774	0.9839	0.161	0.031	2.83E-07
enR.yz	rs17796608	12	81938282	C,T	0.2131	0.8633	-0.203	0.04	3.52E-07
n-men	rs7559271	2	222776530	A,G	0.6156	0.9956	0.169	0.027	2.20E-10
n-men	rs6741414	2	222765382	C,G	0.3841	0.9926	-0.169	0.027	2.42E-10
n-men	rs10209141	2	222764612	A,C	0.3839	0.9914	-0.169	0.027	2.55E-10
n-men	rs10178871	2	222762245	A,G	0.6179	0.9881	0.166	0.027	5.75E-10
n-men	rs11677206	2	222760227	C,T	0.382	0.9884	-0.166	0.027	6.07E-10
n-men	rs10176525	2	222747296	A,T	0.2395	0.9647	-0.191	0.031	1.37E-09
n-men	rs986430	2	222740886	G,T	0.7605	0.9676	0.19	0.031	1.65E-09
n-men	rs986429	2	222740643	A,T	0.2395	0.9676	-0.189	0.031	1.65E-09
n-men	rs1370926	2	222738746	C,G	0.7605	0.9676	0.189	0.031	1.68E-09
n-men	rs6730989	2	222787588	A,G	0.154	0.9986	-0.21	0.036	8.05E-09
n-men	rs2578449	2	222788436	A,G	0.154	0.9986	-0.21	0.036	8.07E-09
n-men	rs2855268	2	222775163	C,G	0.8459	0.9962	0.209	0.036	8.77E-09
n-men	rs7597751	2	222767149	C,T	0.8458	0.9938	0.209	0.036	9.81E-09
n-men	rs10209300	2	222764744	A,G	0.8458	0.9923	0.209	0.036	1.07E-08
n-men	rs7590866	2	222795573	A,G	0.1541	0.9974	-0.208	0.036	1.11E-08
n-men	rs13410020	2	222811181	A,G	0.1488	0.7776	-0.236	0.042	1.22E-08
n-men	rs17401668	2	222797983	A,G	0.8459	0.997	0.206	0.036	1.40E-08
n-men	rs1549773	2	222804212	C,T	0.8459	0.9971	0.205	0.036	1.71E-08
n-men	rs6728938	2	222762001	C,T	0.8452	0.9884	0.202	0.037	3.38E-08
n-men	rs1430655	2	222811792	A,G	0.111	0.932	-0.238	0.043	3.57E-08
n-men	rs10169326	2	222759746	A,G	0.1548	0.9879	-0.202	0.037	3.59E-08
n-men	rs1438605	2	222751581	A,G	0.855	0.9405	0.209	0.039	8.23E-08
n-men	rs10211404	2	222747424	A,G	0.1451	0.943	-0.209	0.039	8.99E-08
n-men	rs13388386	2	222812662	A,G	0.8886	0.9778	0.225	0.042	9.08E-08
n-men	rs10210971	2	222747139	C,T	0.8547	0.9495	0.206	0.039	1.12E-07
n-men	rs7607981	2	222740246	C,T	0.8546	0.9522	0.205	0.039	1.24E-07
n-men	rs7608778	2	222731823	C,T	0.1455	0.9523	-0.205	0.039	1.27E-07
n-men	rs13385121	2	222710949	A,G	0.8543	0.95	0.204	0.039	1.62E-07
n-men	rs10932943	2	222709305	A,G	0.1458	0.9459	-0.204	0.039	1.72E-07
n-men	rs6749789	2	222702465	A,G	0.1461	0.9325	-0.204	0.039	1.88E-07
n-men	rs11886961	2	222700162	C,G	0.8535	0.9162	0.205	0.039	2.03E-07
n-men	rs6757456	2	222695072	C,T	0.1461	0.7332	-0.226	0.044	2.75E-07

n-men	rs7588554	2	222782895	A,G	0.5819	0.9975	-0.137	0.027	3.72E-07
n-men	rs1438607	2	222768195	A,G	0.5815	0.9941	-0.137	0.027	3.77E-07
n-men	rs10208761	2	222764220	A,C	0.5809	0.9901	-0.137	0.027	3.92E-07
n-men	rs10498131	2	222764049	A,G	0.4191	0.99	0.137	0.027	3.92E-07
n-men	rs2894450	2	222705348	A,G	0.6015	0.9848	0.137	0.027	3.93E-07
n-men	rs1013262	2	222799023	G,T	0.4182	0.9916	0.136	0.027	4.67E-07
n-men	rs13023573	2	222763470	A,C	0.5792	0.9844	-0.136	0.027	4.86E-07
sn-men	rs4832657	2	16590220	C,T	0.7276	0.9604	0.154	0.03	2.68E-07
sn-men	rs6761778	2	16580947	C,T	0.7281	0.9796	0.152	0.03	2.87E-07
sn-men	rs2067702	2	16582375	A,G	0.7281	0.9791	0.152	0.03	2.87E-07
sn-men	rs7573656	2	16598913	A,G	0.2737	0.9129	-0.157	0.031	3.01E-07
sn-men	rs7552	2	16597409	A,G	0.7095	0.883	0.156	0.031	3.25E-07
sn-men	rs5007483	2	16597006	G,T	0.7318	0.9242	0.155	0.031	4.42E-07
prn-sn	rs12532887	7	88040653	A,T	0.0136	0.406	-1.059	0.197	7.16E-08
prn-all	rs11738462	5	61049533	A,G	0.1701	0.996	0.204	0.036	1.77E-08
prn-all	rs12521924	5	61046695	A,G	0.17	0.9978	0.204	0.036	1.77E-08
prn-all	rs13154578	5	61049025	A,T	0.83	0.9967	-0.204	0.036	1.77E-08
prn-all	rs13159935	5	61046869	C,T	0.17	0.9983	0.204	0.036	1.79E-08
prn-all	rs12514378	5	61046957	C,T	0.17	0.9985	0.204	0.036	1.80E-08
prn-all	rs1982862	3	55039780	A,C	0.1249	0.7971	0.258	0.046	1.82E-08
prn-all	rs13160822	5	61043203	G,T	0.8485	0.809	-0.231	0.042	4.55E-08
prn-all	rs7704929	5	61007579	A,G	0.809	0.9726	-0.189	0.035	8.25E-08
prn-all	rs11746049	5	61008040	C,T	0.8115	0.9816	-0.188	0.035	8.43E-08
prn-all	rs13175459	5	61021456	A,G	0.8108	0.9972	-0.186	0.035	8.46E-08
prn-all	rs11750644	5	61009820	C,T	0.1888	0.9937	0.187	0.035	8.50E-08
prn-all	rs11747208	5	61009334	C,G	0.1888	0.9933	0.187	0.035	8.50E-08
prn-all	rs1501845	5	61012367	A,G	0.8112	0.9989	-0.186	0.035	8.51E-08
prn-all	rs11740126	5	61026710	A,G	0.1894	0.9967	0.185	0.035	9.45E-08
prn-all	rs13156637	5	61037146	A,G	0.8102	0.9952	-0.184	0.035	1.08E-07
prn-all	rs12520360	5	61035117	C,T	0.1898	0.9954	0.184	0.035	1.08E-07
prn-all	rs11748959	5	61034436	A,G	0.8102	0.9955	-0.184	0.035	1.10E-07
prn-all	rs4700430	5	61033066	A,G	0.1898	0.9957	0.184	0.035	1.12E-07
prn-all	rs13163936	5	61031899	A,G	0.1898	0.996	0.184	0.035	1.14E-07
prn-all	rs6870236	5	61031633	C,T	0.8102	0.9961	-0.184	0.035	1.15E-07
prn-all	rs13186555	5	61030794	C,T	0.8103	0.9967	-0.184	0.035	1.18E-07
prn-all	rs11747263	5	61030624	C,T	0.1897	0.9967	0.184	0.035	1.19E-07
prn-all	rs11743702	5	61030585	A,G	0.1897	0.9969	0.184	0.035	1.20E-07
prn-all	rs4855096	3	180798461	G,T	0.5364	0.9956	-0.139	0.027	3.32E-07
prn-all	rs9831673	3	180796256	C,T	0.5426	0.9765	-0.141	0.028	3.32E-07
prn-all	rs6790272	3	180772123	A,C	0.4637	0.9896	0.14	0.027	3.34E-07
prn-all	rs7630170	3	180812289	A,G	0.5364	0.9971	-0.139	0.027	3.34E-07
prn-all	rs9883607	3	180813386	A,G	0.4636	0.9977	0.139	0.027	3.35E-07
prn-all	rs9816801	3	180762075	C,G	0.536	0.9791	-0.14	0.027	3.45E-07
ls-cphL	rs10822139	10	52462200	A,G	0.689	0.9708	0.169	0.032	1.04E-07
cphL-cphR	rs10822139	10	52462200	A,G	0.689	0.9708	0.156	0.031	4.90E-07
chL-chR	rs4717019	7	155703821	G,T	0.3941	0.955	-0.166	0.031	5.96E-08
chL-chR	rs4717018	7	155703260	C,T	0.606	0.9547	0.166	0.031	6.02E-08
chL-chR	rs4717017	7	155703058	A,G	0.403	0.9535	-0.163	0.031	1.04E-07
chL-chR	rs6698642	1	19128258	C,T	0.8352	0.9992	-0.208	0.04	2.32E-07
chL-chR	rs4717023	7	155707483	A,T	0.3693	0.9968	-0.155	0.031	4.06E-07
chL-chR	rs4716593	7	155704176	A,G	0.3727	0.9992	-0.154	0.031	4.75E-07
chL-chR	rs4717020	7	155704226	A,G	0.3727	0.999	-0.154	0.031	4.78E-07
chL-chR	rs4717021	7	155704640	C,T	0.6272	0.9987	0.154	0.031	4.84E-07
chr-li	rs9599075	13	65624171	A,T	0.7905	0.8865	0.188	0.037	4.04E-07
ls-men	rs12997119	2	16597765	C,T	0.2246	0.9136	-0.156	0.03	2.52E-07
li-men	rs7158989	14	54655311	C,T	0.9035	0.954	-0.224	0.044	3.99E-07
pg-n	rs3012485	10	17064855	A,G	0.0964	0.9972	-0.231	0.045	3.14E-07
pg-n	rs3012486	10	17064965	C,T	0.0964	0.9964	-0.231	0.045	3.14E-07
pg-n	rs3012487	10	17065000	C,T	0.0963	0.9956	-0.231	0.045	3.15E-07
pg-n	rs3012490	10	17065651	C,T	0.0963	0.9948	-0.231	0.045	3.15E-07
pg-n	rs3012488	10	17065113	A,T	0.9037	0.9951	0.231	0.045	3.15E-07
pg-n	rs3012491	10	17065672	C,T	0.9037	0.9943	0.232	0.045	3.16E-07
pg-n	rs3012493	10	17065834	C,T	0.0962	0.9912	-0.232	0.045	3.19E-07
pg-n	rs1801229	10	17064621	A,T	0.0964	0.9971	-0.231	0.045	3.19E-07
pg-n	rs1801231	10	17064509	A,G	0.9036	0.997	0.231	0.045	3.25E-07
pg-n	rs3012484	10	17064410	C,T	0.0963	0.9954	-0.231	0.045	3.51E-07
pg-n	rs2932895	10	17064381	A,T	0.0962	0.9952	-0.231	0.045	3.55E-07
pg-n	rs2942365	10	17064223	A,C	0.0962	0.9946	-0.23	0.045	3.68E-07
pg-n	rs2942364	10	17064031	C,T	0.9039	0.9943	0.23	0.045	3.76E-07
pg-n	rs1512702	10	17063674	G,T	0.9039	0.9939	0.23	0.045	3.85E-07
pg-n	rs3012494	10	17066390	A,G	0.0949	0.9706	-0.233	0.046	4.02E-07

pg-n	rs3012482	10	17063663	C,T	0.096	0.9932	-0.23	0.045	4.05E-07
pg-n	rs3012480	10	17063570	C,T	0.9041	0.9926	0.23	0.045	4.25E-07
pg-chL	rs463498	21	43150483	C,T	0.9347	0.9819	0.326	0.061	7.55E-08
pg-chL	rs4148974	21	43196789	C,T	0.9472	0.9768	0.365	0.068	7.65E-08
pg-chL	rs460128	21	43147076	A,T	0.0645	0.9837	-0.324	0.061	1.08E-07
pg-chL	rs2839603	21	43197575	C,T	0.0674	0.9723	-0.312	0.06	2.05E-07
pg-chL	rs11203166	21	43216705	A,G	0.9322	0.9523	0.314	0.06	2.12E-07
pg-chL	rs2321769	6	79494679	G,T	0.548	0.999	-0.154	0.031	4.27E-07
pg-chL	rs9350774	6	79518322	A,G	0.5481	1	-0.154	0.031	4.27E-07
pg-chL	rs9350776	6	79520564	A,G	0.5481	1	-0.154	0.031	4.27E-07
pg-chL	rs1180825	6	79490569	G,T	0.548	0.9987	-0.154	0.031	4.28E-07
pg-chL	rs3918524	6	79515816	A,G	0.4519	0.9999	0.154	0.031	4.28E-07
pg-chL	rs7740607	6	79498009	C,T	0.548	0.9991	-0.154	0.031	4.28E-07
pg-chL	rs9352628	6	79514166	G,T	0.4519	0.9998	0.154	0.031	4.28E-07
pg-chL	rs9359343	6	79513450	A,G	0.4519	0.9997	0.154	0.031	4.28E-07
pg-chL	rs7743640	6	79510794	A,G	0.5481	0.9996	-0.154	0.031	4.29E-07
pg-chL	rs9352627	6	79512305	C,T	0.4519	0.9997	0.154	0.031	4.29E-07
pg-chL	rs9448542	6	79501084	A,C	0.4519	0.9995	0.154	0.031	4.29E-07
pg-chL	rs2321772	6	79532909	G,T	0.452	0.9994	0.154	0.031	4.31E-07
pg-chR	rs9350774	6	79518322	A,G	0.5481	1	-0.156	0.03	2.42E-07
pg-chR	rs9350776	6	79520564	A,G	0.5481	1	-0.156	0.03	2.42E-07
pg-chR	rs3918524	6	79515816	A,G	0.4519	0.9999	0.156	0.03	2.43E-07
pg-chR	rs2321769	6	79494679	G,T	0.548	0.999	-0.156	0.03	2.43E-07
pg-chR	rs9352628	6	79514166	G,T	0.4519	0.9998	0.156	0.03	2.43E-07
pg-chR	rs1180825	6	79490569	G,T	0.548	0.9987	-0.156	0.03	2.43E-07
pg-chR	rs7740607	6	79498009	C,T	0.548	0.9991	-0.156	0.03	2.43E-07
pg-chR	rs9359343	6	79513450	A,G	0.4519	0.9997	0.156	0.03	2.44E-07
pg-chR	rs9448542	6	79501084	A,C	0.4519	0.9995	0.156	0.03	2.44E-07
pg-chR	rs7743640	6	79510794	A,G	0.5481	0.9996	-0.156	0.03	2.44E-07
pg-chR	rs9352627	6	79512305	C,T	0.4519	0.9997	0.156	0.03	2.44E-07
pg-chR	rs2321772	6	79532909	G,T	0.452	0.9994	0.156	0.03	2.45E-07
PC6	rs507798	5	84846956	C,G	0.3687	0.9334	-0.157	0.031	4.8E-07
PC6	rs612777	5	84847479	A,G	0.6313	0.9335	0.157	0.031	4.8E-07
PC6	rs413927	5	84848924	C,T	0.3687	0.9335	-0.157	0.031	4.8E-07
PC6	rs488160	5	84849976	A,G	0.3688	0.9335	-0.157	0.031	4.8E-07
PC6	rs800837	5	84853165	A,G	0.6312	0.9336	0.157	0.031	4.8E-07
PC6	rs1697833	5	84853946	G,T	0.6312	0.9337	0.157	0.031	4.9E-07
PC6	rs405852	5	84854071	C,T	0.6311	0.9338	0.157	0.031	4.9E-07
PC6	rs373272	5	84854412	A,G	0.3689	0.9338	-0.157	0.031	4.9E-07
PC6	rs395495	5	84856749	C,T	0.3689	0.9338	-0.157	0.031	4.9E-07
PC6	rs576581	5	84858101	A,G	0.6311	0.9339	0.157	0.031	4.9E-07
PC6	rs596598	5	84858153	C,G	0.631	0.934	0.157	0.031	4.9E-07
PC6	rs425542	5	84858536	A,T	0.369	0.934	-0.157	0.031	5.0E-07
PC6	rs414692	5	84858565	C,T	0.631	0.9341	0.157	0.031	5.0E-07
PC7	rs4780055	15	30955652	C,T	0.7365	0.9747	0.17	0.034	4.0E-07
PC7	rs4780056	15	30956048	C,G	0.2635	0.9745	-0.17	0.034	4.0E-07
PC7	rs8026174	15	30956497	A,G	0.2635	0.9744	-0.17	0.034	4.0E-07
PC7	rs8030979	15	91794785	C,T	0.7328	0.8568	0.183	0.036	4.6E-07
PC10	rs11122837	2	121428330	A,G	0.9766	0.3007	1.019	0.191	9.6E-08
PC10	rs11689760	2	121428730	A,C	0.0234	0.3004	-1.019	0.191	9.6E-08
PC10	rs2084234	2	121427325	G,T	0.9766	0.3007	1.018	0.191	9.7E-08
PC10	rs12711536	2	121426256	C,T	0.0234	0.3016	-1.016	0.191	9.7E-08
PC10	rs10864866	2	121425133	A,G	0.0234	0.3041	-1.011	0.19	9.9E-08
PC10	rs11681136	2	121425561	A,G	0.9766	0.3041	1.011	0.19	9.9E-08
PC10	rs12711535	2	121426006	C,T	0.0234	0.3034	-1.012	0.19	1.0E-07
PC10	rs11122835	2	121424629	G,T	0.9766	0.3061	1.006	0.189	1.0E-07
PC10	rs1466042	2	121419389	A,G	0.0234	0.3064	-1.005	0.189	1.0E-07
PC10	rs4848658	2	121423860	C,T	0.0234	0.3061	-1.006	0.189	1.0E-07
PC10	rs2166565	2	121408947	A,G	0.0235	0.3105	-0.995	0.188	1.1E-07
PC10	rs7816288	8	53271417	C,T	0.9891	0.4249	1.333	0.257	2.1E-07
PC10	rs10206938	2	121391708	A,G	0.9762	0.3488	0.912	0.176	2.2E-07
PC10	rs935428	2	121390883	A,G	0.9762	0.3491	0.91	0.176	2.3E-07
PC11	rs970797	2	176820065	G,T	0.5783	0.9996	-0.159	0.029	7.6E-08

Table S4. rs7559271 results for the 14 principal components.

PC	Beta	SE	p-value
1	-0.007	0.026	0.784
2	0.024	0.030	0.434
3	0.048	0.028	0.087
4	0.004	0.029	0.900
5	0.095	0.025	2E-4
6	0.012	0.029	0.689
7	-0.011	0.030	0.717
8	0.000	0.031	0.997
9	-0.008	0.031	0.788
10	0.027	0.032	0.403
11	0.130	0.029	6E-6
12	0.015	0.031	0.624
13	0.009	0.030	0.764
14	0.001	0.030	0.974

Betas are shown according to the G allele