A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling

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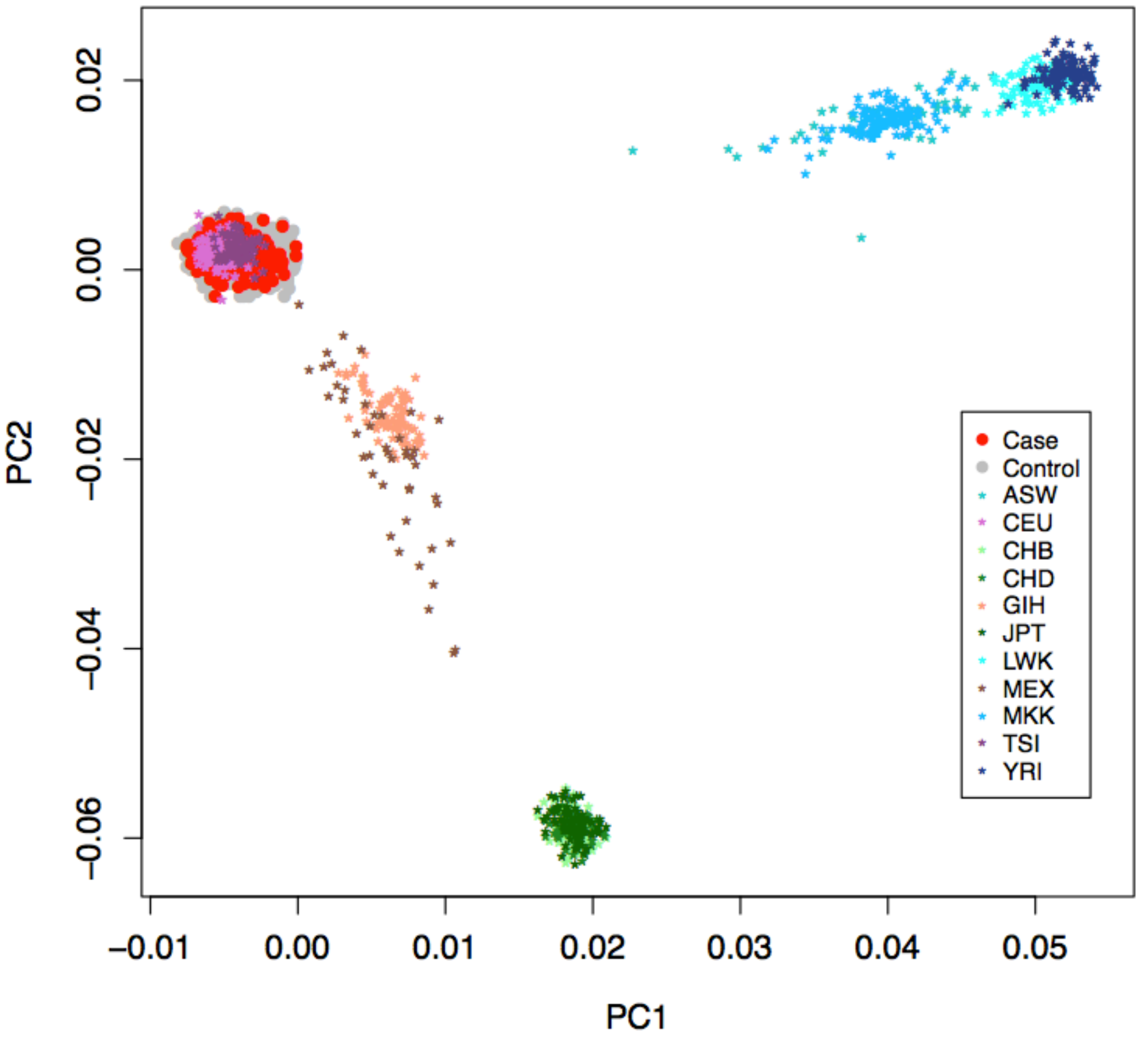
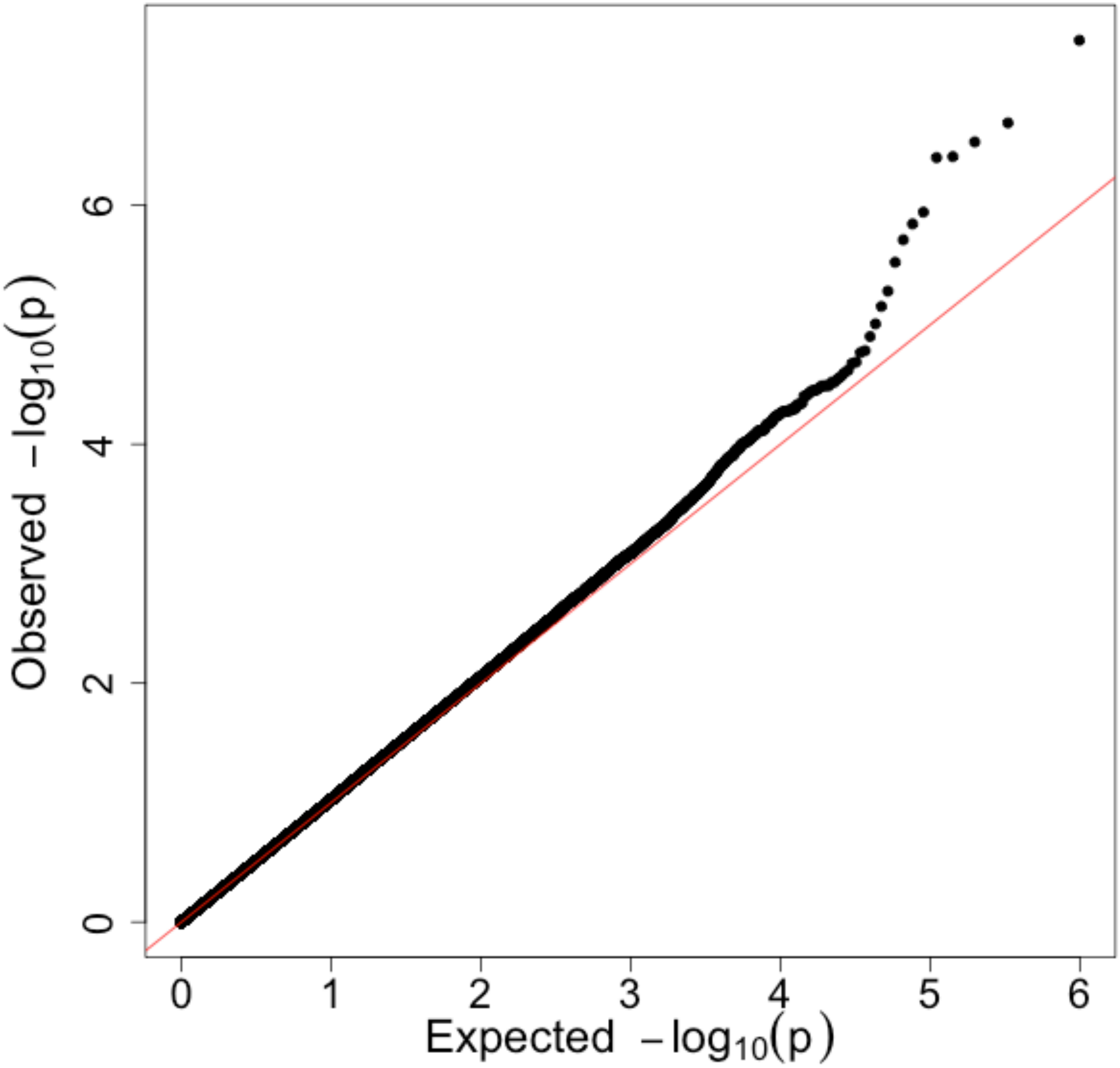
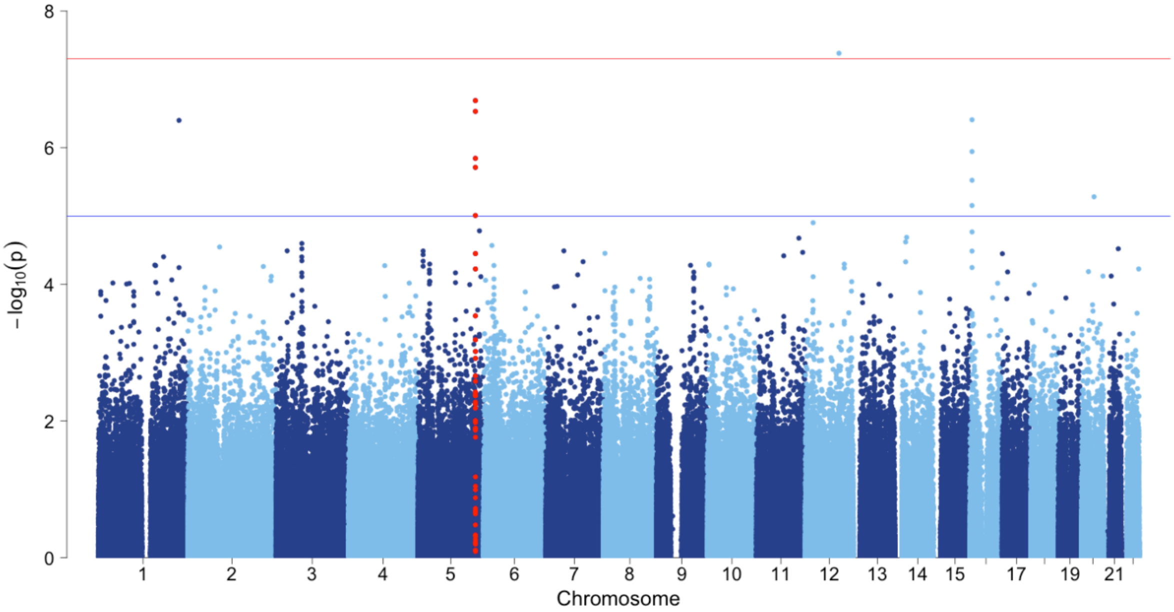
Supplementary Materials



Supplementary Figure 1. Principal component analysis of all genotyped subjects (CHOP) together with 11 HapMap 3 populations (CEU, YRI, CHB, JPT, etc.).



Supplementary Figure 2. The quantile-quantile plot of $-\log_{10}$ *P* values for genome-wide association tests on SNPs.



Supplementary Figure 3. The Manhattan plot of $-\log_{10} P$ values versus genomic coordinates for whole-genome SNPs

Supplementary Table 1. Summary of the cases/controls in this study.

Cohort	Age (onset age for case and assessment age for control)			Number (all females)
	Mean	SD	Median and lower to upper quartile range	
Case	16.2	3	16 (14-18)	692
Control	18.3	5.7	19 (13-23)	3570

Supplementary Table 2. Association results for the genotyped SNP (*P* < 1e-5)

Chr	Postion	Marker	MA	OR	SE	L95	U95	P
1	224794913	rs7535525	C	1.869	0.1234	1.468	2.38	3.99E-07
5	158270225	rs7707918	C	0.7115	0.07062	0.6195	0.8171	1.43E-06
5	158274071	rs1978706	T	1.36	0.06948	1.186	1.558	9.83E-06
5	158296996	rs2072495	A	0.7147	0.07057	0.6224	0.8207	1.94E-06
5	158310631	rs929626	C	0.7004	0.06855	0.6123	0.8011	2.04E-07
5	158332380	rs17543752	C	0.6927	0.0716	0.602	0.7971	2.94E-07
12	94031881	rs2196426	T	2.821	0.1891	1.947	4.086	4.15E-08
16	5794312	rs9941024	C	0.7301	0.07	0.6365	0.8375	7.02E-06
16	5802062	rs7200175	C	0.7234	0.06931	0.6315	0.8287	2.99E-06
16	5808871	rs7205418	A	0.7074	0.07112	0.6154	0.8133	1.14E-06
16	5819274	rs2043633	G	0.6958	0.07149	0.6048	0.8004	3.91E-07
20	34987833	rs6072022	T	1.37	0.06915	1.197	1.569	5.23E-06

Abbreviations: Chr, chromosome; MA, minor allele; OR, odds ratio; SE, standard error; L95, lower 95% confidence interval; U95, upper 95% confidence interval; P, *P*-value

Supplementary Table 3. Association results for the imputed and genotyped SNPs (P < 1e-5)

Chr	Postion	Marker	A	B	MAF of cases	MAF of controls	OR	SE	L95	U95	P
5	158261163	rs17715065	C	T	0.53422	0.466544	0.762527	0.0596573	0.679419	0.8558	3.21E-06
5	158267423	rs891905	T	C	0.352788	0.423768	0.741204	0.0619748	0.657498	0.835566	5.94E-07
5	158267473	rs891904	G	A	0.354273	0.424982	0.742336	0.061951	0.658571	0.836756	6.57E-07
5	158267958	rs4546365	C	T	0.351897	0.420824	0.747279	0.0619485	0.662837	0.842478	1.24E-06
5	158267974	rs4594837	A	C	0.354772	0.424097	0.746656	0.0619808	0.662421	0.841602	1.06E-06
5	158268426	rs6875710	C	T	0.356245	0.427103	0.742286	0.0620044	0.658617	0.836584	6.05E-07
5	158269081	rs10052777	T	C	0.354449	0.424859	0.743282	0.0618283	0.659417	0.837813	7.64E-07
5	158269591	rs62385360	C	T	0.353125	0.423698	0.742509	0.0618038	0.65867	0.837019	7.31E-07
5	158269734	rs17715535	G	A	0.353157	0.423708	0.742583	0.0617925	0.658737	0.837101	7.40E-07
5	158270225	rs7707918	A	C	0.354046	0.42423	0.743887	0.0617308	0.659934	0.838519	8.57E-07
5	158272130	rs3981205	T	G	0.403985	0.331666	0.73215	0.0604776	0.650573	0.823957	2.87E-07
5	158274071	rs1978706	T	C	0.401012	0.330812	0.738406	0.0603584	0.656046	0.831106	6.63E-07
5	158274491	rs17643057	A	G	0.352488	0.423298	0.741653	0.0617845	0.657882	0.836091	6.77E-07
5	158275318	chr5:158275318:I	A	AT	0.400819	0.33074	0.738758	0.0603854	0.656352	0.831509	6.84E-07
5	158275319	chr5:158275319:I	T	TA	0.404647	0.333972	0.737764	0.0605715	0.655601	0.830223	5.17E-07
5	158275601	rs2033448	T	A	0.400573	0.330403	0.73839	0.0604198	0.656016	0.831108	6.51E-07
5	158276323	rs6871291	A	G	0.400737	0.330564	0.738423	0.0604148	0.656051	0.831138	6.53E-07
5	158290225	rs61045787	C	T	0.352265	0.423462	0.740433	0.0617845	0.656791	0.834727	5.91E-07
5	158294657	chr5:158294657:I	T	TTC	0.400329	0.329969	0.737693	0.0604251	0.655385	0.830337	6.05E-07
5	158296996	rs2072495	C	T	0.353324	0.423109	0.74495	0.0617349	0.660842	0.839762	9.87E-07
5	158299860	rs9313794	G	C	0.413681	0.48877	0.737978	0.059745	0.656752	0.82925	2.82E-07
5	158300126	rs10866709	C	T	0.347181	0.419483	0.735976	0.0620553	0.652599	0.830006	3.62E-07
5	158300798	rs31196	C	A	0.474766	0.405173	0.75357	0.059199	0.671303	0.845918	1.69E-06
5	158305076	rs17543640	T	A	0.346598	0.419209	0.734911	0.062077	0.651627	0.828839	3.22E-07
5	158310631	rs929626	A	G	0.40896	0.486134	0.731402	0.0598673	0.650788	0.822002	1.27E-07
5	158310882	rs1469069	T	G	0.411613	0.488136	0.733567	0.0597614	0.652779	0.824354	1.69E-07
5	158317804	rs7737500	G	C	0.343225	0.418128	0.727247	0.0622212	0.644676	0.820395	1.32E-07
5	158318147	rs7724989	T	G	0.342984	0.417901	0.727145	0.0622357	0.644573	0.820295	1.31E-07
5	158319479	rs62385377	G	A	0.343069	0.417805	0.727707	0.0622575	0.645075	0.820924	1.39E-07
5	158319915	chr5:158319915:D	AT	A	0.342837	0.417485	0.727916	0.0622616	0.645248	0.821175	1.43E-07
5	158320876	rs1422797	T	A	0.338522	0.41248	0.728941	0.0630488	0.645933	0.822616	1.38E-07
5	158320877	rs1422798	C	G	0.33705	0.411775	0.726267	0.06309	0.64349	0.819692	1.02E-07
5	158321121	rs1422799	C	G	0.346617	0.421629	0.727709	0.0624015	0.645252	0.820703	1.17E-07
5	158332380	rs17543752	T	C	0.34104	0.416106	0.726234	0.0622497	0.643668	0.81939	1.23E-07

5	158333692	rs6556370	T	C	0.407546	0.33459	0.730975	0.0602879	0.649646	0.822486	2.49E-07
5	158343969	rs7736883	A	G	0.341567	0.416081	0.728012	0.062408	0.645269	0.821366	1.41E-07
5	158367249	rs62385385	T	A	0.341941	0.415807	0.730045	0.0623702	0.647086	0.823638	1.82E-07
5	158381512	rs1081073	T	A	0.436377	0.505998	0.755879	0.0592025	0.673144	0.848784	2.18E-06
5	158381663	rs1081071	T	C	0.34374	0.414091	0.741118	0.0623102	0.656979	0.836034	6.71E-07
5	158410081	rs12153593	C	G	0.393853	0.329299	0.755623	0.0603488	0.671125	0.850761	4.82E-06
5	158418490	rs10447210	C	T	0.393163	0.329132	0.757241	0.0603845	0.672539	0.852609	5.68E-06
5	158424391	rs10040979	G	A	0.375723	0.312745	0.756107	0.0606211	0.670782	0.852285	7.07E-06
5	158424451	rs10061082	A	G	0.375727	0.312733	0.756049	0.0606554	0.670731	0.85222	6.95E-06
5	158433339	rs67265526	T	C	0.34896	0.412493	0.763421	0.0615749	0.676986	0.860891	8.67E-06
5	158435950	rs9791127	T	C	0.376104	0.312904	0.755436	0.0608298	0.670202	0.851509	6.05E-06
5	158442930	rs6894893	T	C	0.393934	0.328758	0.753518	0.0605642	0.669251	0.848395	3.59E-06

Abbreviations: Chr, chromosome; A, coded allele; B, uncoded allele; MAF, minor allele frequency; OR, odds ratio; SE, standard error; L95, lower 95% confidence interval; U95, upper 95% confidence interval; P, *P*-value