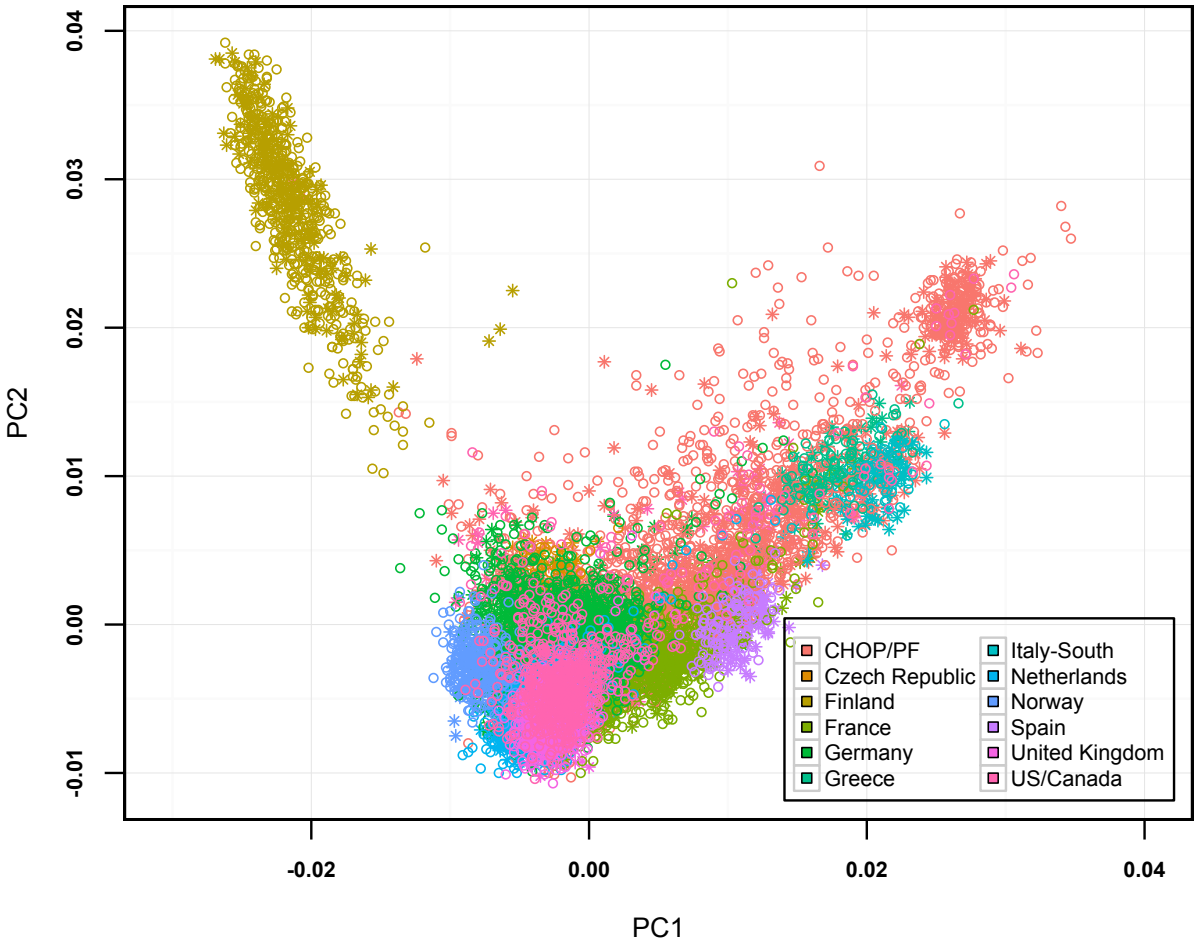
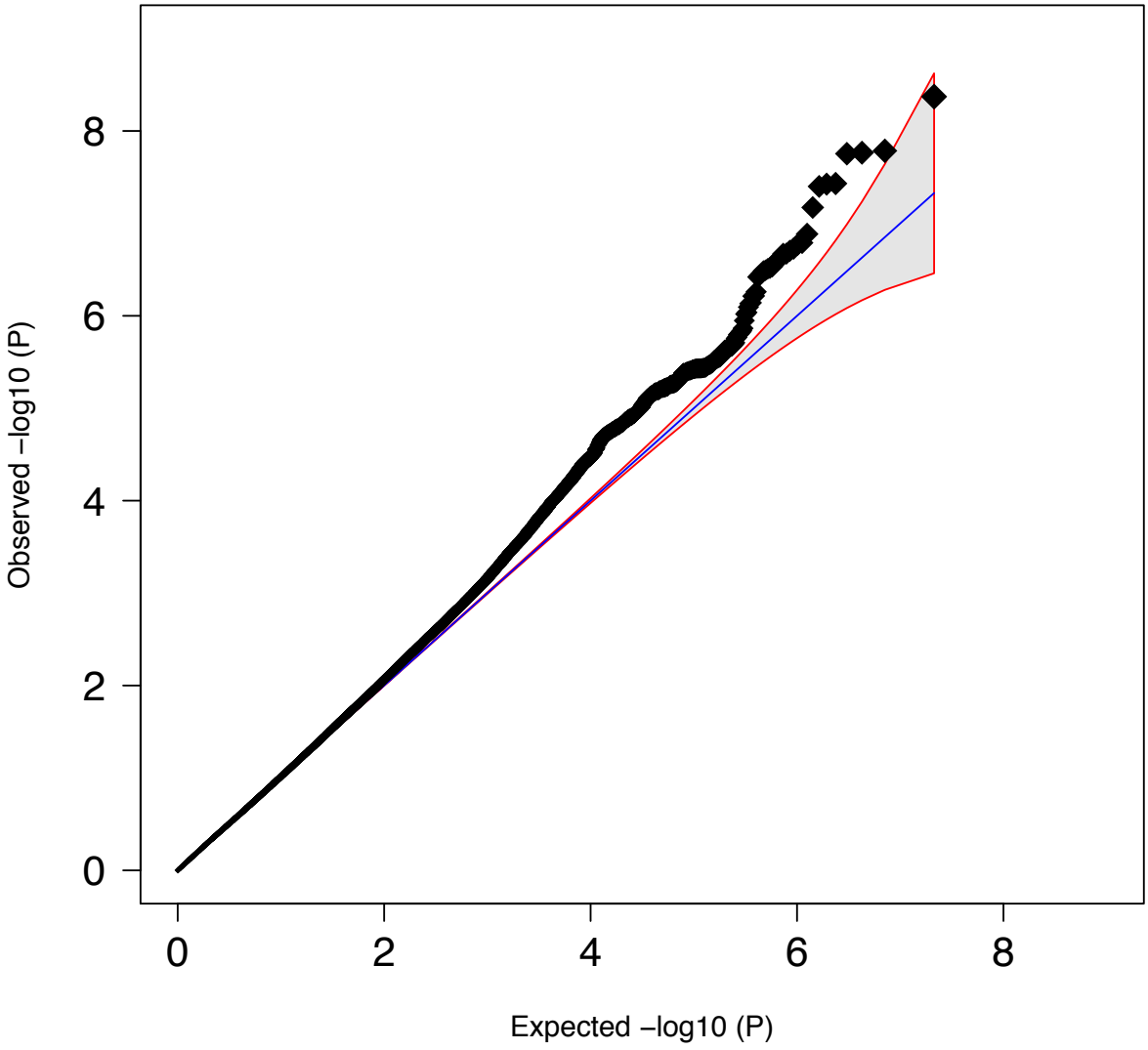
Supplementary Figure S1. **Principal components plot for all samples**. Cases are denoted with asterisks and controls with open circles. All samples are of European ancestry, and there are overlapping but identifiable clusters for each dataset. Finland is, per expectations of European ancestry populations, the most distinct among these samples.

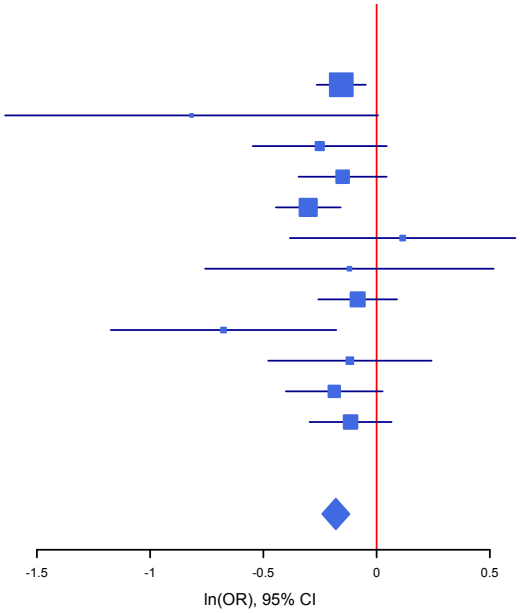


Supplementary Figure S2. **QQ plot of 10,641,224 variants with MAF>1% and imputation quality (INFO)>0.6**. 15,043,779 total variants, lambda=1.080, $lambda_{1000}$=1.008.



Supplementary Figure S3. Forest plot for top SNP rs4622308. The top SNP is a T/C variant on chromosome 12, position 56,469,185. The Q and I^2 statistics both indicate lack of heterogeneity across studies for this variant (Q=12.58, p=.32, I^2=12.59) (see Higgins *et al*., 2003).

	ngt	info	p_value	f_ca(n)	f_co(n)	ln(OR)	STDerr
CHOP / PFCG	0	0.89	0.00475	0.522(1031)	0.560(3627)	-0.156	0.0553
Czech Republic	0	0.82	0.0521	0.642(72)	0.750(41)	-0.817	0.42
Finland	0	0.87	0.097	0.495(131)	0.544(524)	-0.251	0.151
France	0	0.95	0.131	0.515(293)	0.547(979)	-0.15	0.0992
Germany	0	0.88	3.53e-05	0.507(556)	0.573(2164)	-0.302	0.073
Greece	0	0.93	0.65	0.572(70)	0.550(79)	0.115	0.254
Italy south	0	0.85	0.712	0.570(75)	0.624(50)	-0.12	0.325
Netherlands	0	0.93	0.346	0.539(348)	0.558(1362)	-0.0836	0.0887
Norway	0	0.97	0.00769	0.449(82)	0.533(315)	-0.676	0.254
Spain	0	0.96	0.521	0.501(186)	0.546(117)	-0.118	0.184
United Kingdom	0	0.92	0.0869	0.492(237)	0.532(964)	-0.187	0.109
US & Canada	0	0.92	0.212	0.529(414)	0.556(760)	-0.115	0.0924
PGC AN first wave	**0**	**0.90**	**4.25e-09**	**0.520(3495)**	**0.558(10982)**	**-0.18**	**0.0307**



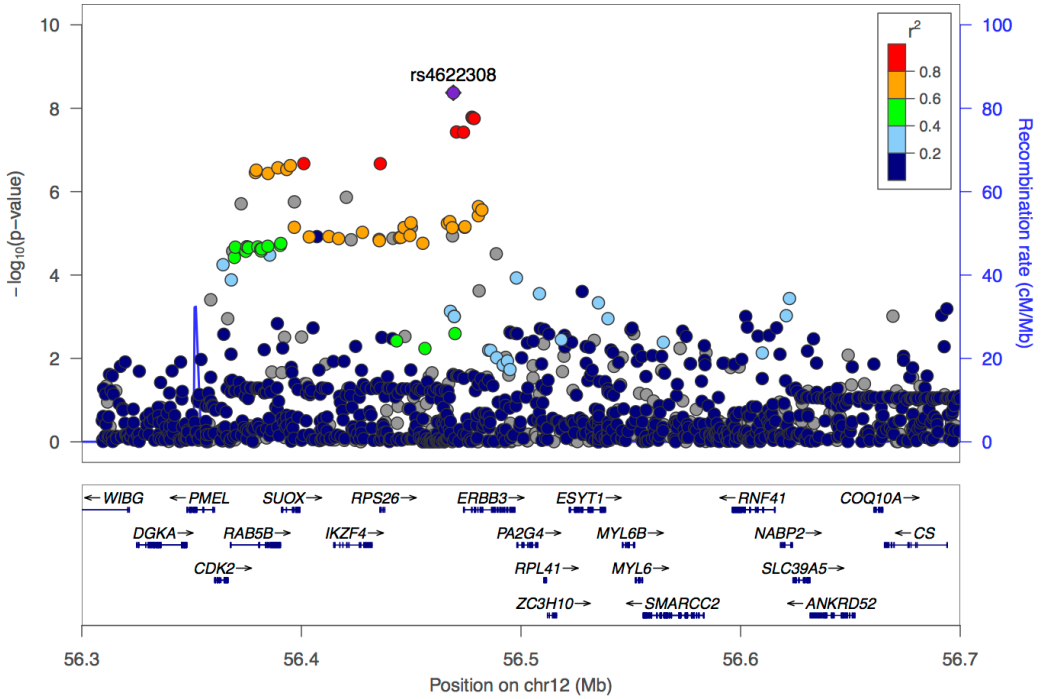
Abbreviations: ngt=number genotyped, info=imputation quality score, f_ca(n)=frequency for allele 1 in cases with number of cases in parentheses, f_co(n)=frequency for allele 1 in controls with number of controls in parentheses, ln(OR)=natural logarithm of odds ratio, STDerr=standard error.

Figure reference:

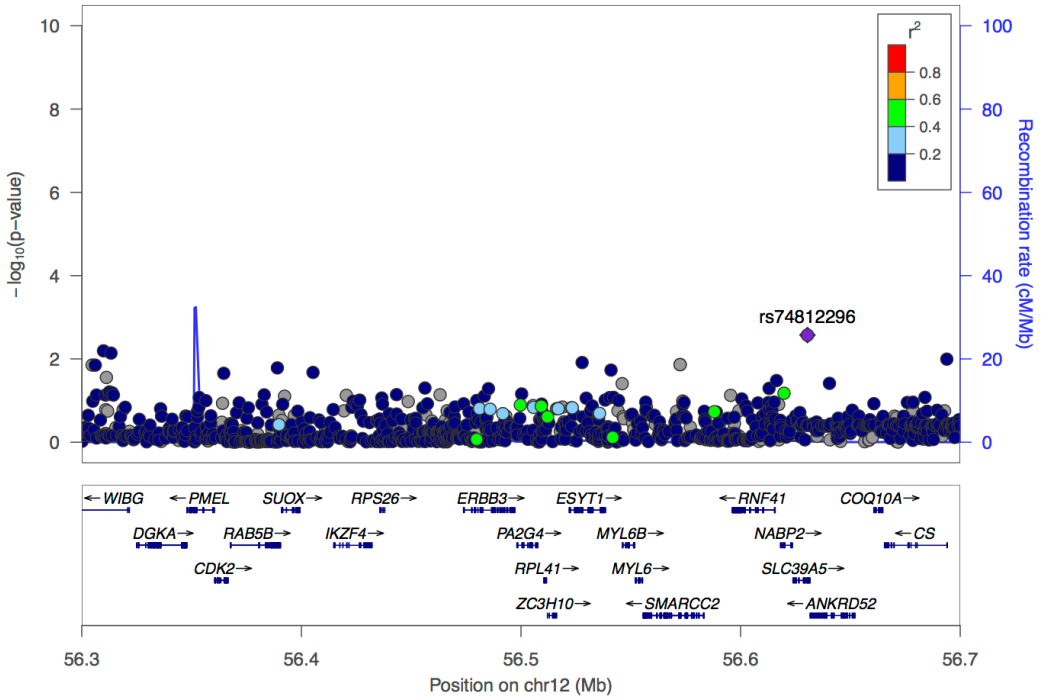
Higgins, J. P. T., Thompson, S. G., Deeks, J. J., & Altman, D. G. (2003). Measuring inconsistency in meta-analyses. *BMJ : British Medical Journal*, *327*(7414), 557–560.

Supplementary Figure S4. Results for top locus before and after conditioning on individuals' dosage data at top SNP rs4622308 are consistent with the existence of only one signal at this locus. A. Before conditioning (i.e., original analysis). B. After conditioning.

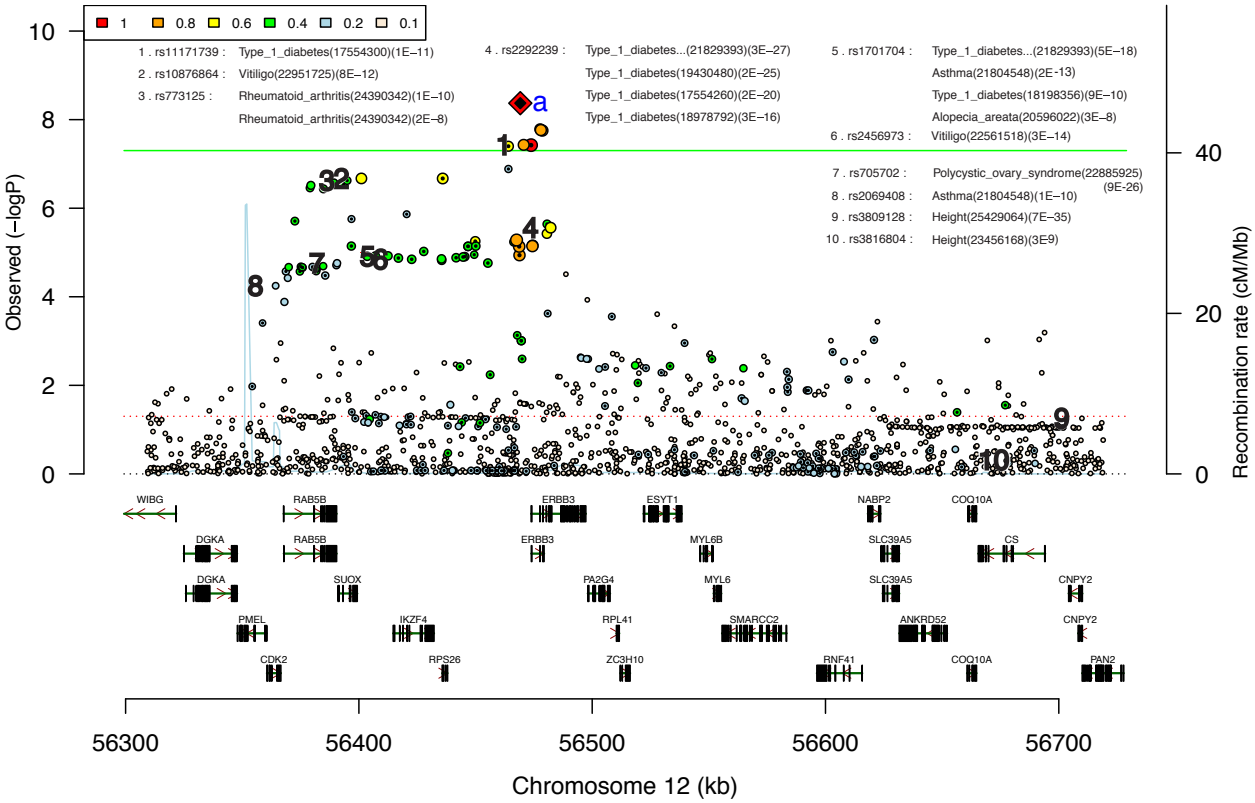
A.



B.

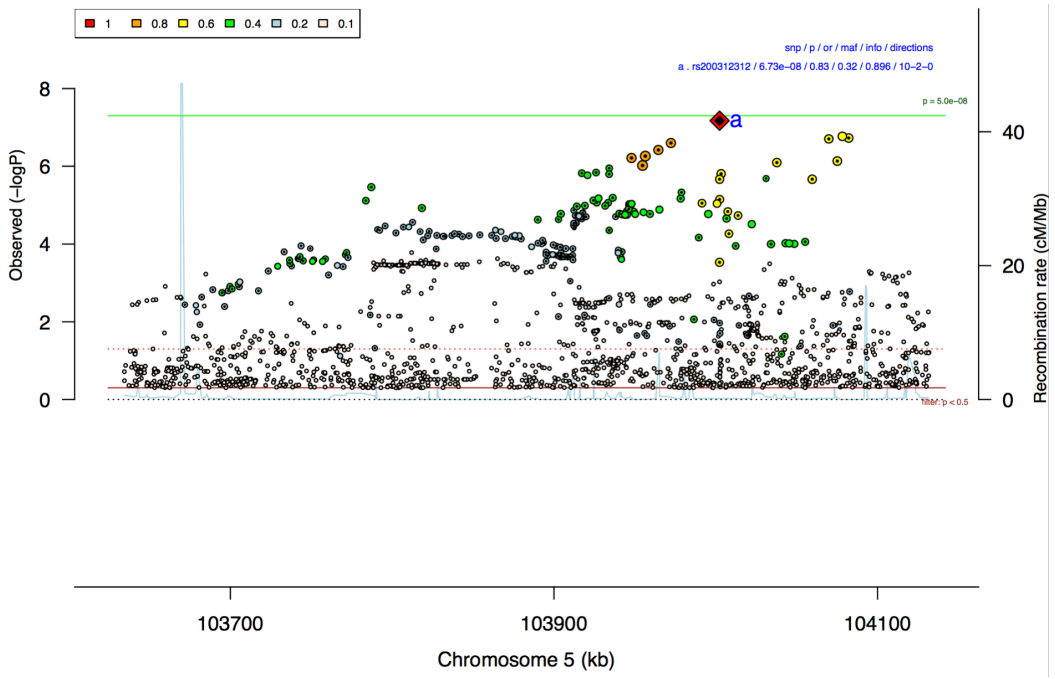


Supplementary Figure S5. Area plot for top locus with other phenotypic associations in the region. The top SNP rs4622308 is located near phenotypic associations to numerous immune-related traits.

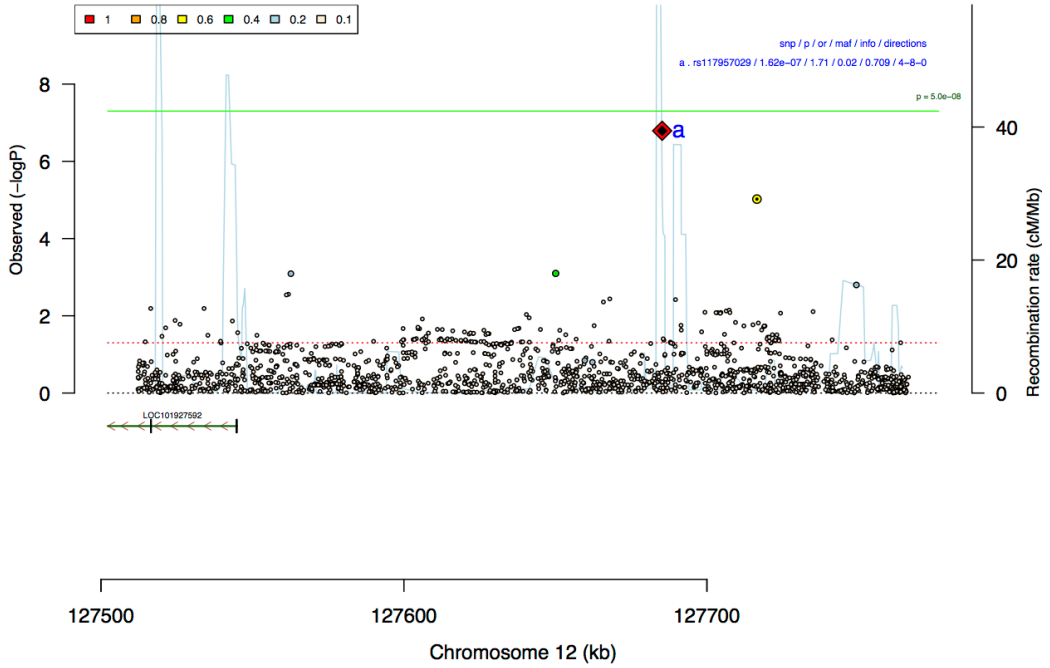


Supplementary Figure S6. Area plots for second, third, and fourth best loci. A) Second locus with top SNP rs200312312, B) Third locus with top SNP rs117957029, C) Fourth locus with top SNP rs11174202.

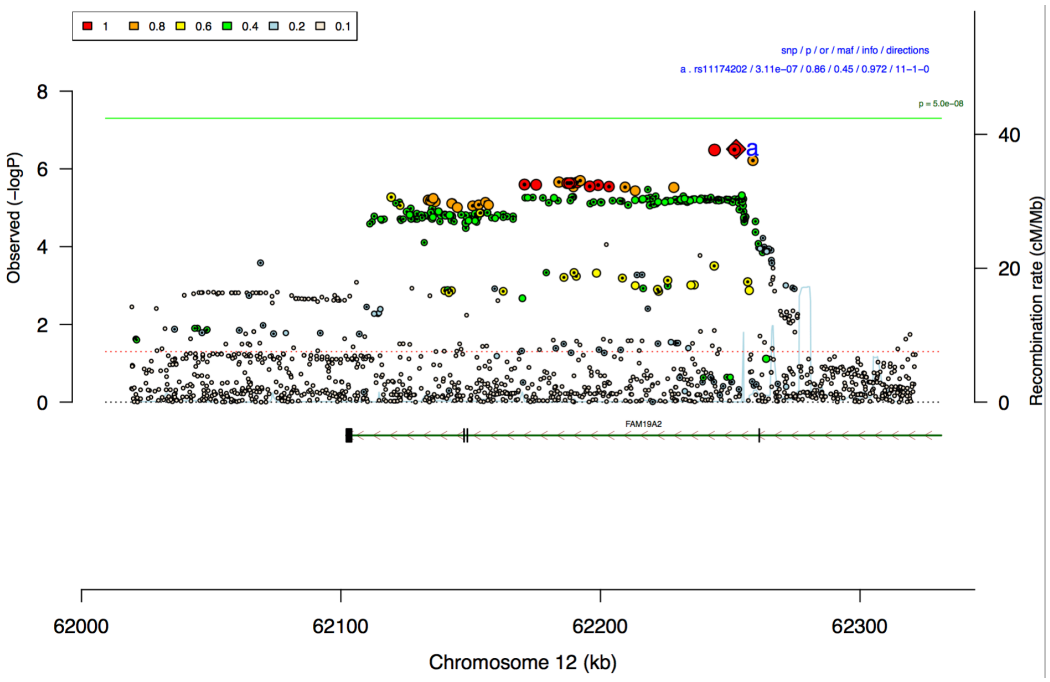
A) rs200312312 p=6.73x10^{-8}, OR=.83, MAF=.32, INFO=.90, Q=13.09, het-p=.29, I^2=15.97



B) rs117957029 p=1.62x10^{-7}, OR=1.71, MAF=.02, INFO=.71, Q=11.25, het-p=.42, I^2=2.18

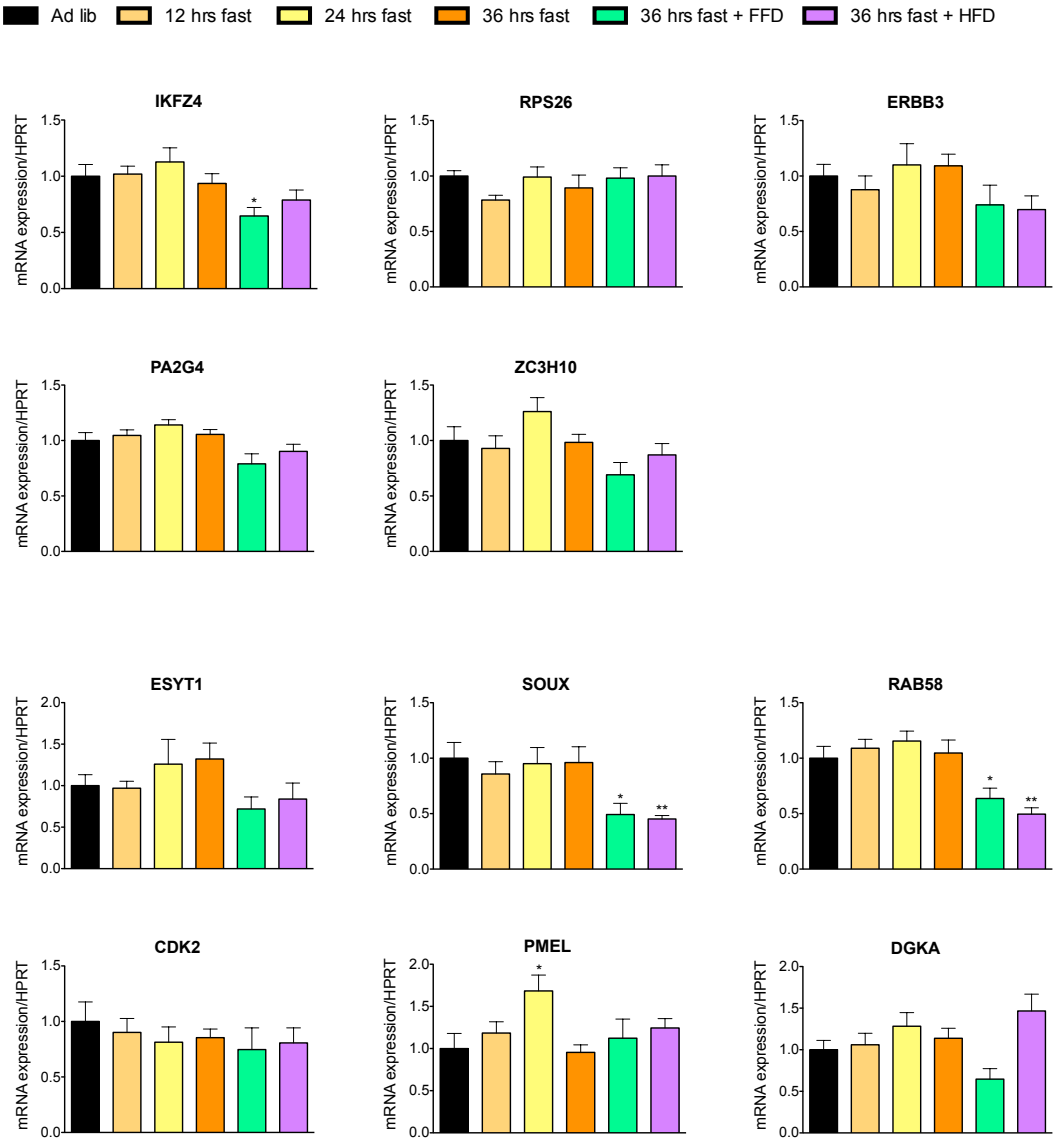


C) rs11174202 p=3.11e-7, OR=.86, MAF=.45, INFO=.97, Q=8.45, het-p=.67, I^2=-30.19

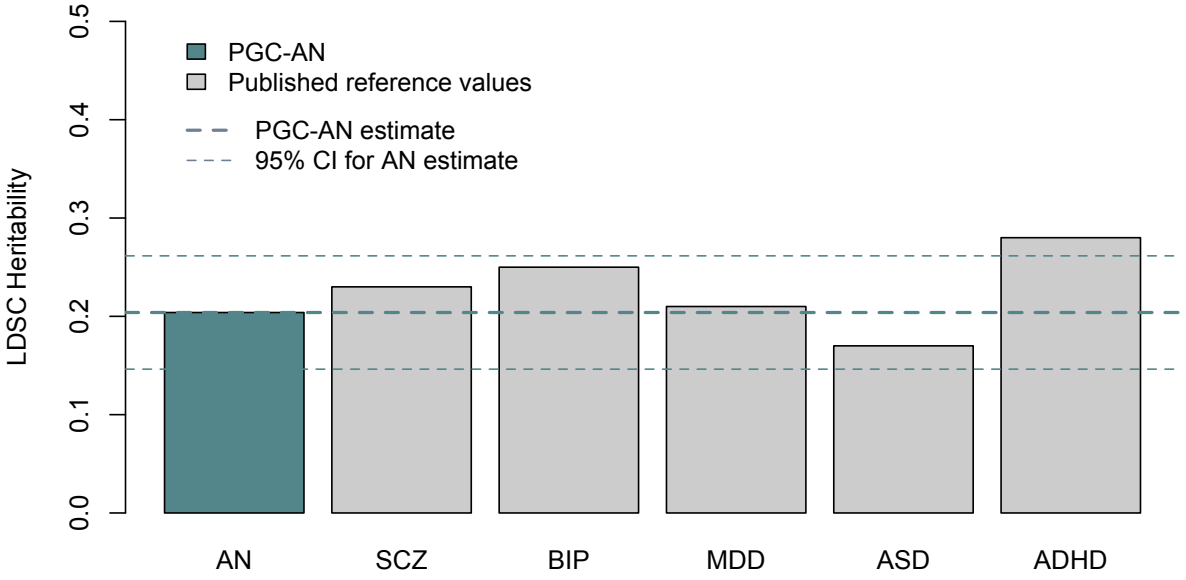


p=p-value, OR=odds ratio, MAF=minor allele frequency, INFO=imputation quality score, Q= heterogeneity statistic, het-p=p-value for heterogeneity statistic Q, I^2=heterogeneity statistic (see Higgins et al., 2003).

Supplementary Figure S7. Gene expression of the genes in the rs4622308 region in mouse hypothalamus from fasted and refed C57BL/6J mice (N=5-7 for each gene). Normalized gene expression with standard errors are shown. No changes reached significance.



Supplementary Figure S8. Genome-wide common variant SNP heritability estimate (h^2_{SNP}) for AN is comparable to that of other psychiatric disorders.



LDSC=Linkage disequilibrium score regression, PGC-AN=Psychiatric Genomics Consortium-Anorexia Nervosa group, CI=confidence interval, SCZ=schizophrenia, BIP=bipolar disorder, MDD=major depressive disorder, ASD=autism spectrum disorder, ADHD=attention deficit hyperactivity disorder. Error bars show ±1.96xSE.