Supplementary Tables

Supplementary Table 1: Heritability Estimates

Phenotype	h^2_{obs}	h^2_{obs} SE	Sample Prevalence	Population Prevalence	h^2_{liab}	h^2_{liab} SE
Crohn's	0.763	0.043	0.285	0.0032[5]	0.405	0.023
Ulcerative Colitis	0.416	0.042	0.254	0.0025[5]	0.227	0.023
Schizophrenia	0.994	0.015	0.447	0.010[6]	0.555	0.008
Major Depression	0.342	0.028	0.493	0.150[6]	0.409	0.033
Bipolar	0.951	0.039	0.443	0.010[6]	0.531	0.022

LD Score regression heritability estimates for phenotypes that did not employ any GC correction (GC correction at the individual study level will bias the heritability estimate downwards). Standard errors were obtained as in table 1. These are estimates of the heritability explained by all 1000 Genomes SNPs (h2(1kG)), obtained by multiplying the regression slope by M/N, where N:=sample size and M is about 15 million. If the average rare SNP in 1000 Genomes explains less phenotypic variance than the average common SNP, then a smaller value of M would be more appropriate, and the estimates in this table will be biased upwards. Relaxing these assumptions in order to obtain a robust estimate h2(1kG) is a direction for further research; however, we note that the LD Score regression intercept is robust to these assumptions. We report heritability on the observed scale (h^2_{obs}) and also transformed to the liability scale (h^2_{liab}) using the prevalence estimates listed in the prevalence column. For some phenotypes (*e.g.,* Crohn's disease, which has been increasing in prevalence[5]), it is difficult to obtain accurate prevalence estimates, so liability scale heritability estimates should be interpreted cautiously.