



Figure S2: Q-Q plots of the results of FaST-LMM on the WTCCC dataset. (A) Control-control analysis, 15.6% of sets have a p-value of less than 0.10. (B) Bipolar disorder, 18.4% of sets have a p-value of less than 0.10. (C) Coronary artery disease, 13.4% of sets have a p-value of less than 0.10. (D) Crohn's disease, 16.5% of sets have a p-value of less than 0.10. (E) Hypertension, 13.4% of sets have a p-value of less than 0.10. (F) Rheumatoid arthritis, 14.2% of sets have a p-value of less than 0.10. (G) Type-1 diabetes, 13.7% of sets have a p-value of less than 0.10. (H) Type-2 diabetes, 14.7% of sets have a p-value of less than 0.10. (I) Bipolar disorder with leave-one-chromosome-out GRM background kernel, 15.4% of sets have a p-value of less than 0.10. In all cases we used 100-SNP sets. In (A) through (H), we used a likelihood ratio test with 10 permutations per set and no background kernel. In (I), we used the `sc_davies` score test to improve speed with the background kernel present. In some cases,  $\lambda_{GC}$  is 0 because permutation tests result in more than half of the sets having a p-value of 1.0.