Here are the violin plots from the 1000 GEMMA permutations.

One plot for each phenotype.

x axis is 1 = single smallest p-value for any SNP in one permutation run.

2 = second smallest SNP/ run, etc.

GEMMA runs a total of 237,878 SNPs after missingness & MAF cutoffs, so the 2500th SNP is close to top 1%.

y axis is SNP p-score. Note that I switched to the log10 scale rather than log2.

The p-values are very consistent across all 15 phenotypes. What do you think we should use for thresholds?

I've attached a couple of Manhattan plots on the log10 scale for comparison.

Do Gemma and bigRR find the same genes for the same traits?