

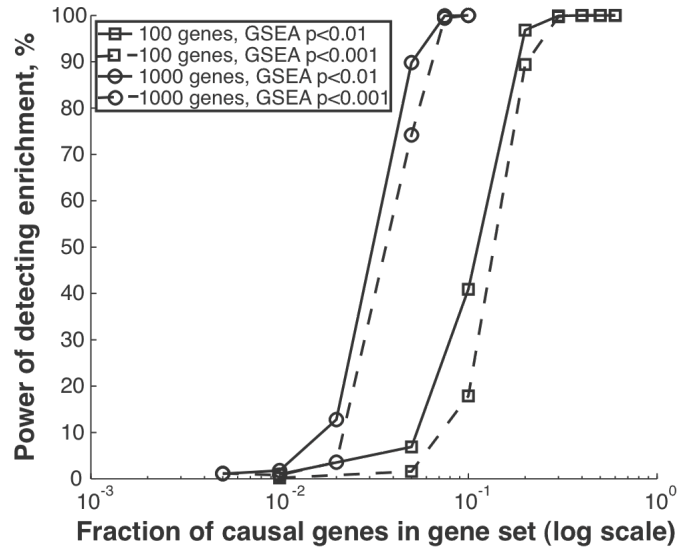
Figure S9

Figure S9. Power of MAGENTA as a function of gene set enrichment significance threshold. We compared the effect of two p -value thresholds used to call a gene set significantly enriched in a given simulation run, on the power of MAGENTA to detect gene set enrichment. The two cutoffs tested were: $P_{gs}^{GSEA} < 0.01$ (solid line) and $P_{gs}^{GSEA} < 0.001$ (dashed line). P_{gs}^{GSEA} is the nominal enrichment p -value for gene set gs . Power is plotted as a function of the fraction of causal genes that were randomly assigned a SNP with a modest effect size equivalent to 1% power of detecting an association at genome-wide significance (p -value $< 5e-8$) using single SNP analysis. Two gene set sizes were examined: 100 genes (squares) and 1,000 genes (circles). Power appears to decrease only slightly with a more stringent GSEA p -value threshold. Note the x-axis is on a \log_{10} scale.