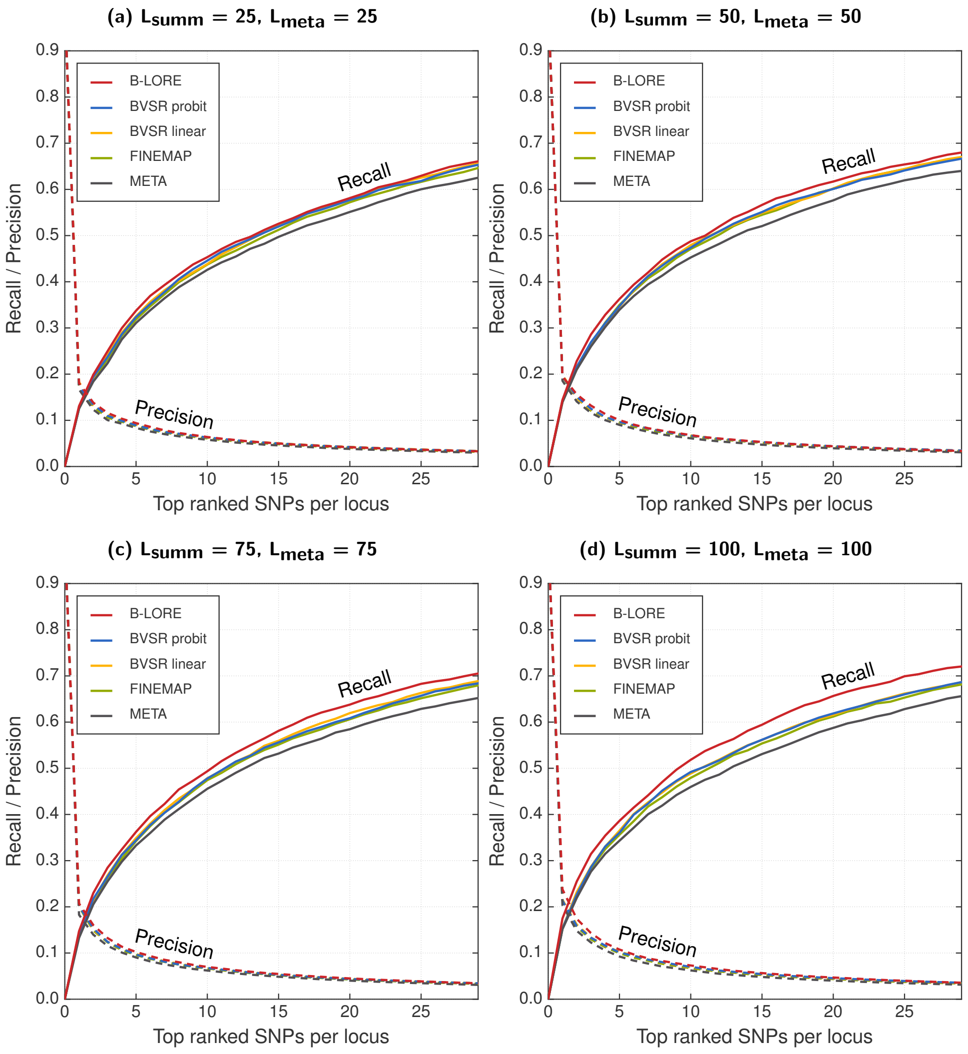

Figure S7. Impact of number of loci on calculation of B-LORE summary statistics. We simulated 13082 phenotypes using 100 loci of ~200 SNPs, as described in the main text. All simulations used $h_g^2 = 0.6$. We then used only a subset (25, 50, 75 and 100) of these loci for further analysis, and the results are shown in panels (a), (b), (c) and (d) respectively. Here, $\mathrm{L_{summ}}$ denotes the number of loci used for calculating summary statistics and $\mathrm{L_{meta}}$ denotes the number of loci used for metaanalysis. We compared the ranking of SNPs at each locus using recall (solid lines, left y-axis) and precision (dotted lines, right y-axis), which were averaged over the loci and the simulation replicates. All methods were run with a maximum of two causal SNPs per locus.