



**Figure S3. Imbalance in case-control GWAS with fixed number of controls.** We simulated phenotypes with varying case/control ratio – (a) 6500/6500, (b) 4875/6500, (c) 3250/6500 and (d) 1625/6500 respectively – using 100 loci of  $\sim 200$  SNPs, as described in the main text. All simulations used  $h_g^2 = 0.4$ . 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 100 loci and 20 simulation replicates. All methods were run with a maximum of two causal SNPs per locus. Insets schematically compare logistic model with linear model. B-LORE shows increasingly more recall over other methods with increasing imbalance, because the logistic function becomes increasingly better than the linear function to model the data.