



Figure S6. CPU time and memory requirement for meta-analysis with B-LORE. We compared the computational requirements of B-LORE with other finemapping methods in terms of (a) processing time and (b) maximum memory required. Along the x -axis, we vary the number of maximum allowed causal SNPs. For each point on the plot, we used an average over 20 simulations. Each simulation was a meta-analysis of 5 GWA studies with 40000 SNPs (distributed over 200 loci). All calculations were done on an Intel Xeon E5-2670 v2 processor with 8 cores. FINEMAP and CAVIARBF were allowed to use all the cores in parallel, by analyzing 25 loci in each core.