Figure S1: Sensitivity, specificity and positive likelihood ratios of MSEA in capturing simulated lipid genesets across combinations of GWAS datasets, top markers included and LD cutoffs. (a) Results from GLGC GWAS. (b) Results from Finnish GWAS. (c) Results from Framingham GWAS. 20kb window distance mapping is used for all analyses.
Figure S2: MSEA signals of lipid homeostasis genes for combinations of linkage disequilibrium pruning parameter and marker filtering (top markers included). Results are from 20kb window distance mapping. Z-scores of dots with the same color in the LD cutoff plot (a) represent the values from different marker filtering settings, and vice versa in (b).
Figure S3. Performance comparison of MSEA, iGSEA and MAGENTA at FDR 5% (a) and FDR 10% (b).
Figure S4: Schematic illustration of the hierarchical structure in genetic datasets (a) and the randomization procedure that was used in the gene-permuted MSEA (b & c).
Figure S5: Schematic illustration of the weighted key driver analysis (a) and the key driver enrichment statistic (b-d).