



Figure S8 Summary of ASE read depth across tissues and gene sets. Data from version 6 of the GTEx Project. (A) Histogram of read depth across tissues. ‘Combined’ (shown in black) refers to combined-tissue ASE (reads spanning each ASE site in a single individual are summed, regardless of the tissue in which they were sampled). The nine best-sampled GTEx tissues are included. ‘Blood’ (shown in red) are ASE measurements from whole blood alone. (B) Histogram of read depth for combined-tissue ASE across high- and low-*pLI* genes.