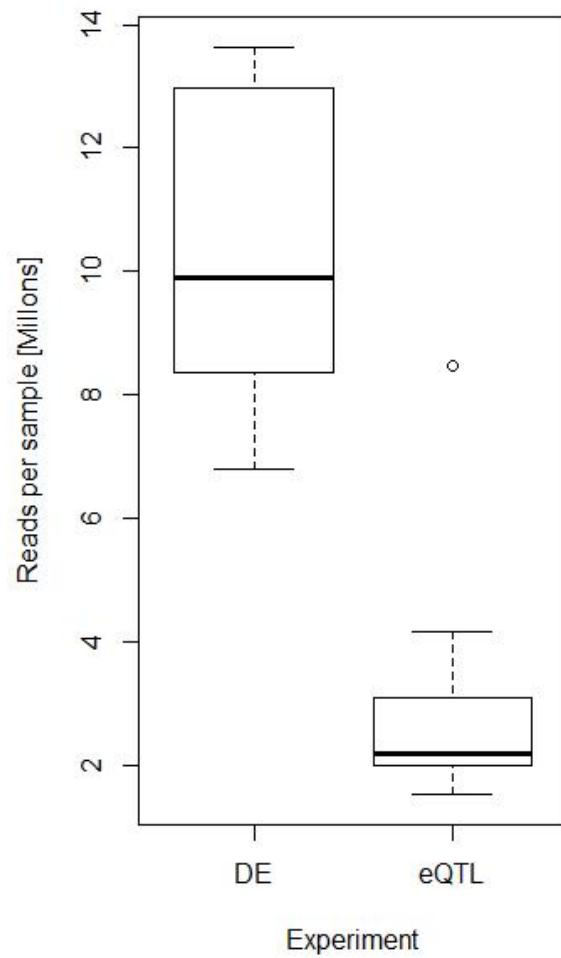




Supplementary Figure S1: Distribution of number of quality reads per sample for differential expression (DE) and eQTL studies. Libraries containing 12 and 24 barcoded samples were pooled for DE and eQTL, respectively. For each study, a RNA-Seq library was prepared according to (Zhong *et al.*, 2011) and single-end sequenced in separate lanes on a HiSeq2000 (Illumina Inc, USA).