

Normalization method	Description	Accounted factors	Recommendations for use
TPM	counts per length of transcript (kb) per million reads mapped	sequencing depth and gene length	gene count comparisons within a sample or between samples of the same sample group; NOT for DE analysis
RPKM/FPKM	reads per kilobase of exon per million reads mapped)	sequencing depth and gene length	gene count comparisons between genes within a sample; NOT for between sample comparisons or DE analysis
DESeq2's median of ratios	counts divided by sample-specific size factors determined by median ratio of gene counts relative to geometric mean per gene	sequencing depth and RNA composition	gene count comparisons between samples and for DE analysis ; NOT for within sample comparisons