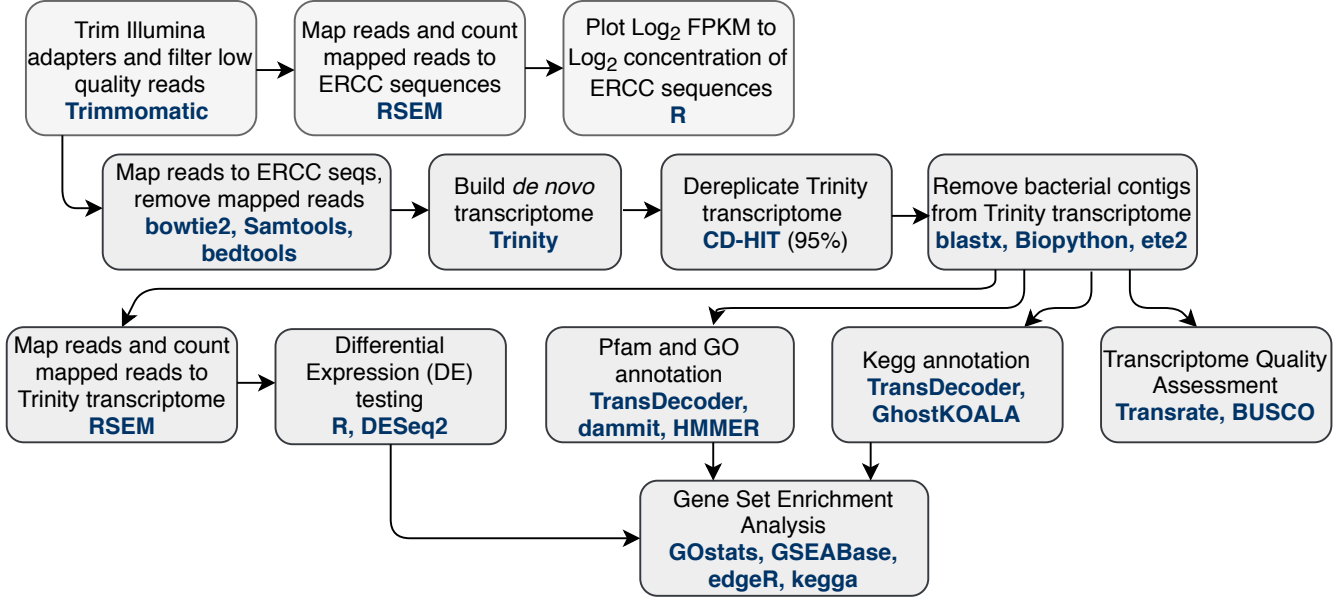
Trim Illumina adapters and filter low quality reads
Trimmomatic
Map reads and count mapped reads to ERCC sequences
RSEM
Plot Log2 FPKM to Log2 concentration of ERCC sequences
R
Map reads to ERCC seqs, remove mapped reads
bowtie2, Samtools, bedtools
Build de novo transcriptome
Trinity
Dereplicate Trinity transcriptome
CD-HIT (95%)
Remove bacterial contigs from Trinity transcriptome
blastx, Biopython, ete2
Map reads and count mapped reads to Trinity transcriptome
RSEM
Differential Expression (DE) testing
R, DESeq2
Pfam and GO annotation
TransDecoder, dammit, HMMER
Kegg annotation
TransDecoder, GhostKOALA
Transcriptome Quality Assessment
Transrate, BUSCO
Gene Set Enrichment Analysis
GOstats, GSEABase, edgeR, kegga