LINCS RNA-Seq Data Pipeline

Software version & parameters collected

RNA QC

Raw reads

FASTQ

Read QC and preprocessing

QC reports

HTML

Analysis-ready reads

FASTQ/BAM

Spliced Read Mapping, sorted and indexed

Collecting and preparing reference sequences and annotation for hg19

FASTA GTF/GFF

Mapped reads

SAM/BAM, BAI

Expression Quantification

Gene expression values (raw counts, RPKM etc)

TEXT

Post-mapping RNA-seq QC

RNA-seQC Picard

DESeq

Differential Analysis

Differentially Expressed gene list

TEXT

Data/Output Task File Format Software