

Bulk mRNA Seq:

Sample quality control was performed using the Agilent 2100 Bioanalyzer or the Agilent 4200 TapeStation. Qualifying samples were then prepped following the standard protocol for the Illumina Stranded mRNA prep (Illumina). Sequencing was performed on the Illumina NextSeq2000 with Paired End 59bp × 59bp reads.

Sequencing data was demultiplexed using Illumina's BCL Convert. De-multiplexed read sequences were then aligned to the **Homo sapiens (hg38 no Alts, with decoys) /Mus Musculus (mm10)** reference sequence using DRAGEN RNA app on Basespace Sequence Hub

(https://support-docs.illumina.com/SW/DRAGEN_v41/Content/SW/DRAGEN/TPipelineIntro_fDG.htm).

Differential expression analysis was performed using DESeq2

(<https://bioconductor.org/packages/release/bioc/html/DESeq2.html>) through DRAGEN

Differential Expression app on Basespace

(<https://basespace.illumina.com/apps/14229215/DRAGEN-Differential-Expression>).