



General Methods

RNA-Seq: Sample quality control was performed using the Agilent 2100 Bioanalyzer. Qualifying samples were then prepped following the standard protocol for the NEBnext Ultra ii Stranded mRNA (New England Biolabs). Sequencing was performed on the Illumina NextSeq 500 with Paired End 42bp × 42bp reads.

De-multiplexed read sequences were then aligned to the *reference sequence* using STAR (<https://www.ncbi.nlm.nih.gov/pubmed/23104886>) aligners. Assembly and differential expression was estimated using Cufflinks (<http://cole-trapnell-lab.github.io/cufflinks/>) through bioinformatics apps available on Illumina Sequence Hub.

Heatmaps and other figures made using the VisR platform (<https://visrsoftware.github.io/>) and (relevant app)

DNA-Seq: Standard protocol for the NEBnext DNA Ultra ii was followed.

10x Genomics 3' sc-RNA-Seq: Cells were loaded on the 10x genomics single cell controller and libraries were prepped using the Chromium Single Cell 3' Reagent v2 Chemistry kit and the standard protocol was followed for all steps.

Libraries were then sequenced on an Illumina Nextseq. 10x genomics Cell Ranger 2.0 was used to perform Demultiplexing, Alignment, Counting, Clustering, and Differential expression. This prepared data was viewed and exported using 10x Genomics Cell Loup and VisR (<https://visrsoftware.github.io/>) platform was used for CellRanger R (10x genomics), Seurat (<https://satijalab.org/seurat/>), and Monocle (<http://cole-trapnell-lab.github.io/monocle-release/>)

Heatmaps and other figures made using the VisR platform (<https://visrsoftware.github.io/>) and (relevant app)

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<http://brc.ubc.ca/next-generation-sequencing-at-the-brc/>