For analysis, raw reads were demultiplexed using bcl2fastq (\*\*\*Note, this was performed by the sequencing core, so I am unaware of the version\*\*\*). Quality filtering and adapter removal were performed using cutadapt-1.16 with the following parameters: “ -m 20 -a 'AGATCGGAAGAGCACACGTCTGAACTCCAGTCA' -A 'AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT' ” Processed/cleaned reads were then mapped to the *Mus musculus* reference genome sequence (GRCm38, mm10) with STAR-2.5.2a given the following parameters: “--genomeDir {path to mm10} --sjdbGTFfile {path to mm10 gtf} --readFilesIn {trimmed fastqs} --readFilesCommand zcat --outSAMtype BAM SortedByCoordinate. The subread-1.6.2 package (featureCounts) was used to derive gene counts given the following parameters: “-s 1 -p -B.” Differential expression analysis and data normalization were performed using DESeq2-1.30.0 with an adjusted *P* value threshold of 0.05 within an R-4.0.3 environment.