**S1 Legends to Supplementary Tables**

Each Supplementary Table consists of 29 columns. A short description for columns is provided below:

* Column A: Name of the feature examined; in this case the Gene Name
* Columns B-E and Z-AC: Linear Total RPKM
  + RPKM or Reads assigned Per Kilobase per Million mapped reads is a normalization method for RNA-Seq experiments.
  + The RPKM method uses the signal values for each experiment and divides the total bases of target sequence by one thousand; the resulting number is then divided by the total number of mapped reads divided by one million.
  + RPKM normalization is necessary due to certain biases involved in RNA-seq such as sequencing depth and gene length.
* Columns F-I: Fold Change
  + Difference in gene expression level between the comparative groups.
* Column J: QSeqID
  + A software specific generated ID linked to the gene of that row.
* Column K: qseq\_name
  + The feature (gene) linked to the QseqID. This also matches the data in column A.
* Column L: Feature Type
  + The type of feature annotated
* Column N: Source File
  + Local pathway to template sequence
  + Includes the Accession number and Chromosome of each feature e.g. NC\_005100\_chr1
* Column O: Source Seq Length
  + The length, in base pairs, of the template sequence.
* Column P: Source Sequence
  + The template sequence on which the gene occurs (Accession number)
* Column Q: Strand
  + Strand on which the gene is located
* Colum R: Target Length
  + The target length of the fragment, equal to the end position minus the start position.
* Column S: Target Range
  + The start and end position of feature.
* Column T: db\_xref
  + Database Cross-Reference e.g. A Cross Reference of the NCBI Gene ID with the RGD ID
* Column V: gene
  + Gene Name
* Column W: gene\_synonym
  + Alternative gene names the target may have been known by at earlier times.

**Abbreviations:**

H - Hemmule

BM – Bone marrow

LN – Lymph node

BV – Blood vessel