README

The scripts provided here were used for RNAseq analyses in the publication <<enter citation here>>. *RNAseq\_scripts* generate the data required for *Plotting\_scripts* to make Figure 1 and Supplementary Figure 1.

Source data can be downloaded from Array Express (<https://www.ebi.ac.uk/arrayexpress>), accession number E-MTAB-14687.

Metadata = sdrf.tsv

Raw counts matrix = rawcounts.csv

TPM matrix = tpm\_PC0.001\_log2\_genesymbol\_dedup.csv

To make:

Figure S1A: RNAseq\_script\_1 🡪 RNAseq\_script\_2 🡪 IPA upstream regulator analysis 🡪 RNAseq\_script\_6 🡪 Gephi network visualisation

Figure S1B: RNAseq\_script\_1 🡪 RNAseq\_script\_3 🡪 IPA upstream regulator analysis 🡪 RNAseq\_script\_7 🡪 Gephi network visualisation

Figure S1C-D: RNAseq\_script\_1 🡪 RNAseq\_script\_4 🡪 IPA upstream regulator analysis 🡪 RNAseq\_script\_8 🡪 Plotting\_script\_FigureS1C-D

Figure S1E: RNAseq\_script\_1 🡪 RNAseq\_script\_5 🡪 Plotting\_script\_FigureS1E

Figure S1F: RNAseq\_script\_1 🡪 RNAseq\_script\_5 🡪 Plotting\_script\_FigureS1E 🡪 Plotting\_script\_FigureS1F

Figure 1A-B: RNAseq\_script\_1 🡪 RNAseq\_script\_9 🡪 Plotting\_script\_Figure1A-B

Figure 1C: RNAseq\_script\_1 🡪 RNAseq\_script\_9 🡪 Plotting\_script\_Figure1C

Overview of analysis scripts:

RNAseq\_script\_1: Prepare data and differential gene expression analyses

RNAseq\_script\_2: SARtools DeSeq2 analysis (TST\_D2 vs saline) and prep for subsequent analysis

RNAseq\_script\_3: SARtools DeSeq2 analysis (TST\_D7 vs saline) and prep for subsequent analysis

RNAseq\_script\_4: SARtools DeSeq2 analysis (all TST vs saline) and prep for subsequent analysis

RNAseq\_script\_5: SARtools DeSeq2 analysis (D7 vs D2 within integrated TST response) and prep for subsequent analysis

RNAseq\_script\_6: Correlation analysis of upstream regulator target genes (TST\_D2 vs saline) and prep for Gephi visualisation

RNAseq\_script\_7: Correlation analysis of upstream regulator target genes (TST\_D7 vs saline) and prep for Gephi visualisation

RNAseq\_script\_8: Correlation analysis of upstream regulator target genes (all TST vs saline) and calculation of module scores per sample

RNAseq\_script\_9: Module analyses