



**Supplementary Figure 5:** Correlation of RNAseq with qPCR **Left:** Validation of RNAseq results (Fig. 3) with qPCR showing the log2(foldchange expression) of 18 genes. For qPCR, Datapoints each represent one biological replicate (n=10), which is the mean of technical replicates (n=3). Bar height represents mean of biological replicates, error bars show standard deviation of biological replicates. **Right:** Correlation between qPCR and RNAseq in terms of log2(mean foldchange expression per gene). Each dot represents one gene shown in the barplot to the left. Genes measured with qPCR that showed no differential expression in RNAseq were set to have a log2(FC) = 0. Shaded area shows the confidence interval of linear regression. Correlation coefficient ( ) was calculated using Spearman's rank. N = 18 genes. FC = fold change expression.