

Figure S2

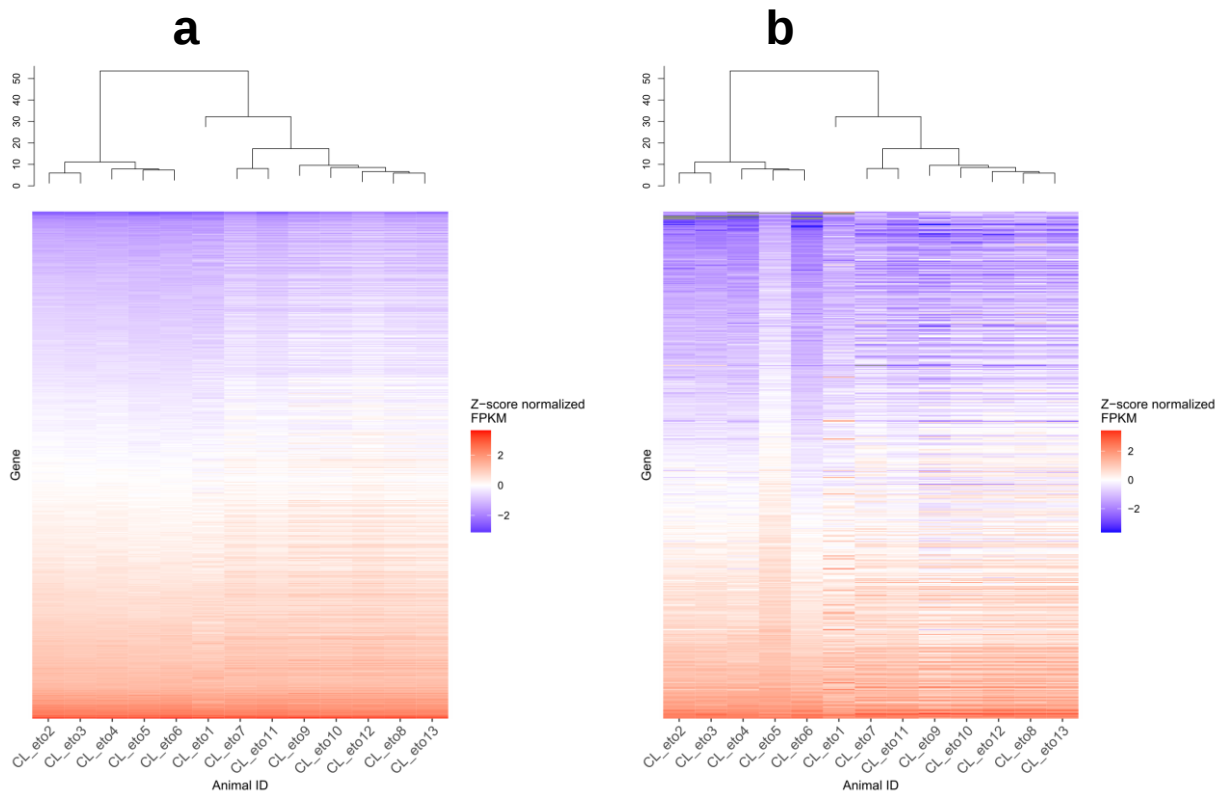


Figure s2: Two heatmaps showing the expression levels of the 1152 differentially expressed genes (DEGs) together with a cluster analysis of the individuals (shown on top of each heatmap) based on the DEGs. Here, the CL_et01 animal was included in the differential gene expression analysis. **(a)** DEGs with small (< 50%) fold-change differences (641 genes). **(b)** DEGs with large fold-change differences (511 genes). Genes with > 50% differences in fold-change were classified as highly differentially expressed genes. Note: for the cluster analysis, all 1152 differentially expressed genes were used.