

Test2

Paul Christmann

2022-07-12

The expression of all TRAs associated with a tissue cannot be used to infer organ development

In this research, we attempt to draw conclusions about the developmental state of a tissue based on the expression of genes associated with it alone. Therefore, we analyzed the share of differentially expressed transcripts above a certain expression level over time, as shown in Fig. ???A. Furthermore, we observed trends within the median expression of all differentially expressed transcripts associated with a tissue (Fig. ???B). Since both metrics only showed in miniscule changes, we hypothesized that distinct, counteracting trends in expression existed within one tissue. Thus, k-means clustering was used to determine groups of TRAs with similar expression patterns. For each of these clusters, the median expression was plotted as shown in Fig. ???C.

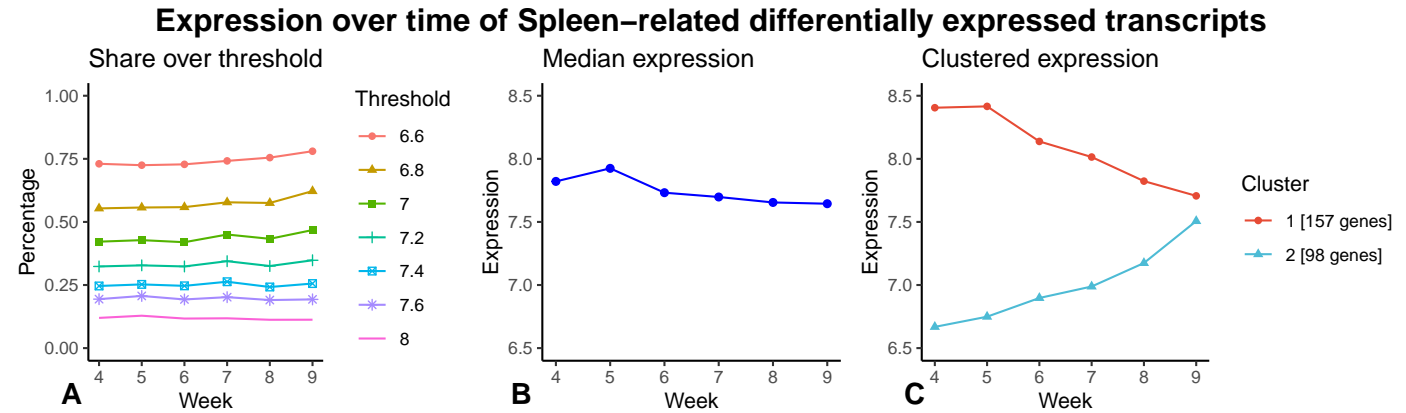


Figure 1: A. For different expression thresholds the share of differentially expressed transcripts with higher expressions than the threshold is depicted. B. The median

##Now the spleen stuff

Expression of spleen-associated transcripts

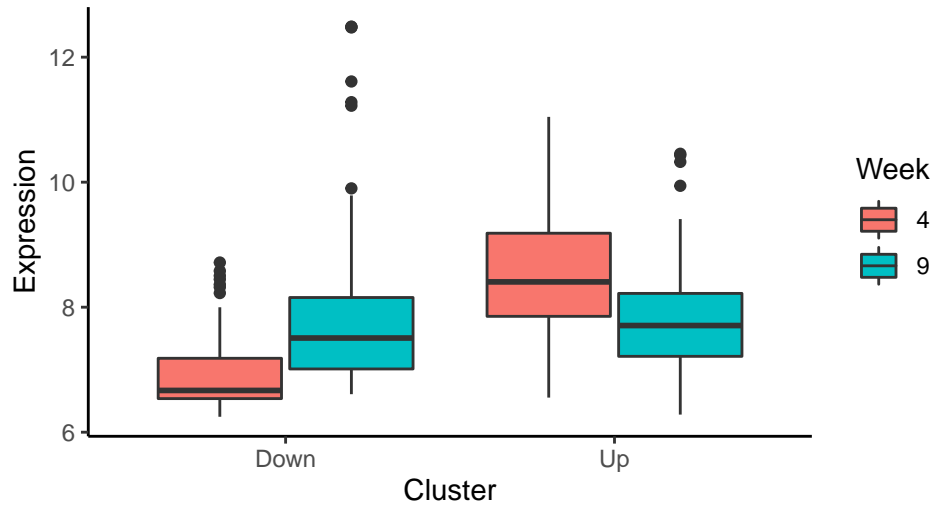


Figure 2: A further look on the expression of transcripts in the up- and downregulated clusters shows that the upregulated transcripts are close to the minimum expression level between 6 and 7 in week 4 and showing expressions between 7 and 8.5 by week 9. In contrast, the downregulated genes have very high expression levels (8-9) by week 4 and decrease to a more moderate expression between 7 and 8.5 analogous to the upregulated transcripts.

