

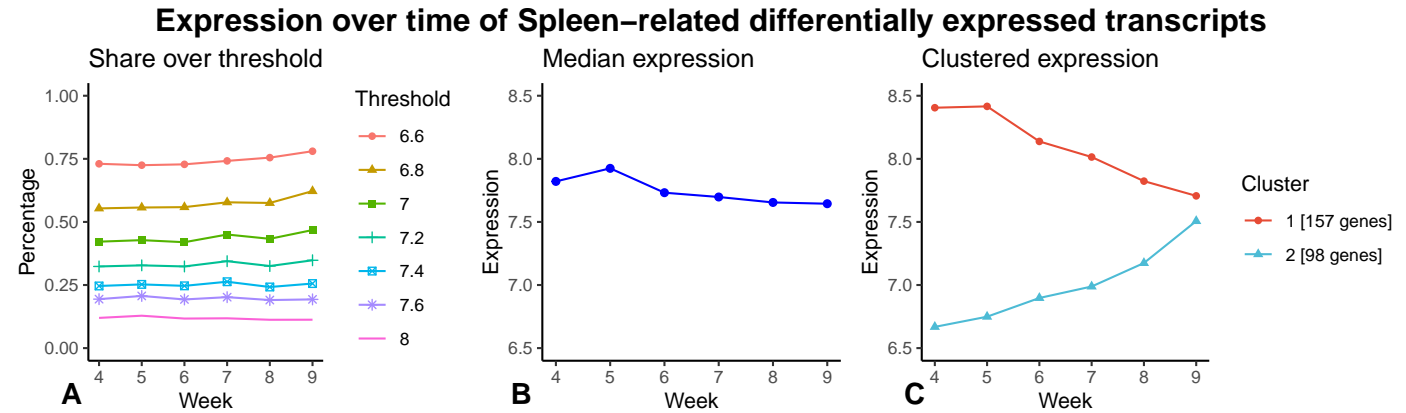
# Test2

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

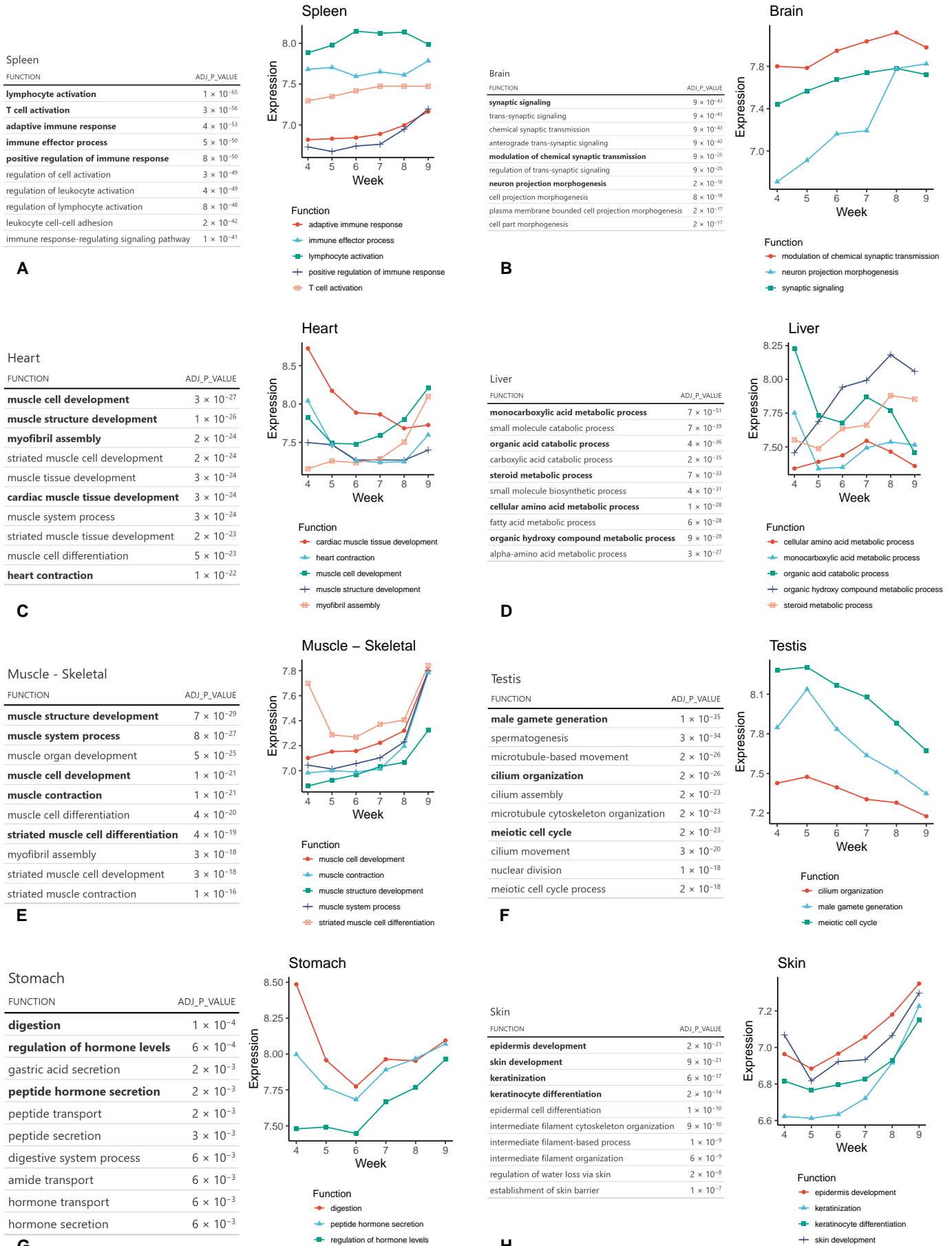
In this research, we attempt to draw conclusions about the developmental state of a tissue based on the expression of genes associated with it alone. Therefore, we analyzed the share of differentially expressed transcripts above a certain expression level over time, as shown in Fig. ???A. Furthermore, 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

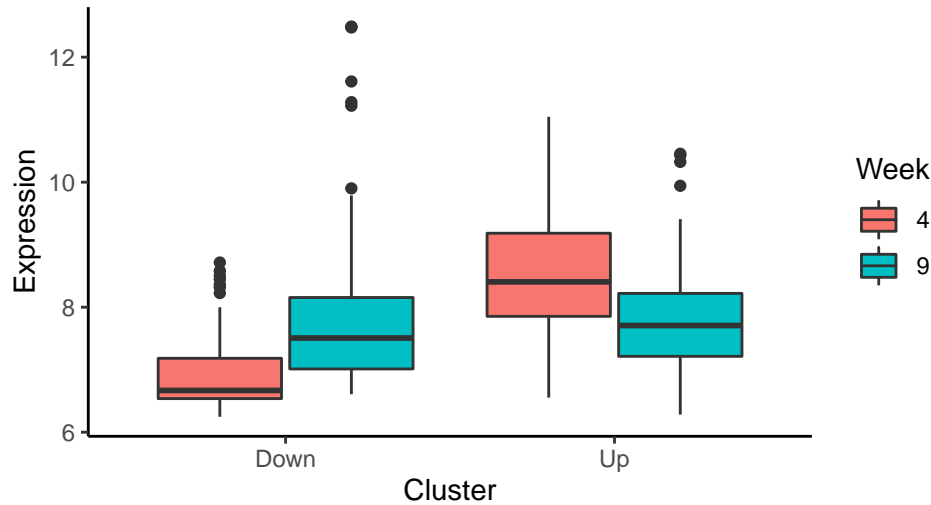
##Now the spleen stuff

## Main functions from overrepresentation analysis plotted by tissue



**Figure 2:** For eight tissues A to H, the tables show the 10 most significant results from overrepresentation analysis. There, the functional GO annotation of all transcripts in our dataset (not only the differentially expressed ones) was compared to the functions associated with all TRAs of one tissue. The significance was determined by an adjusted p-value. Of those 10 functions, up to 5 were chosen to represent different groups of functions and avoid the problem of highly related processes. For each of those, the median

## Expression of spleen-associated transcripts



**Figure 3:** 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.

