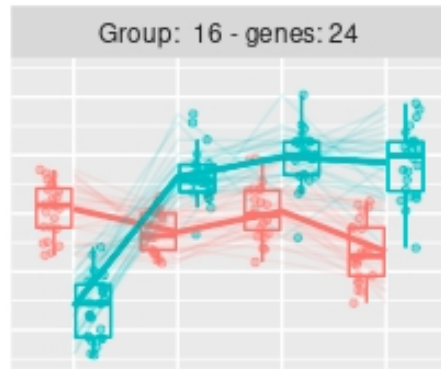
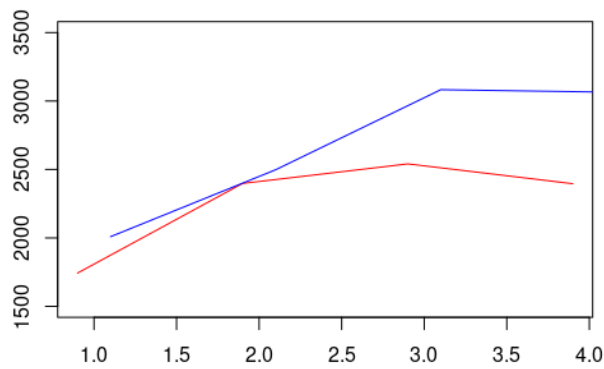


DEGpatterns output for Group 16 genes across four time points:



Compare to a plot of means for the same genes from the same DESeq2 normalized counts:



To confirm the issue: if we use `scale()` to compute a Z-score from the normalized counts, we see the same trend pattern from DEGpatterns.

