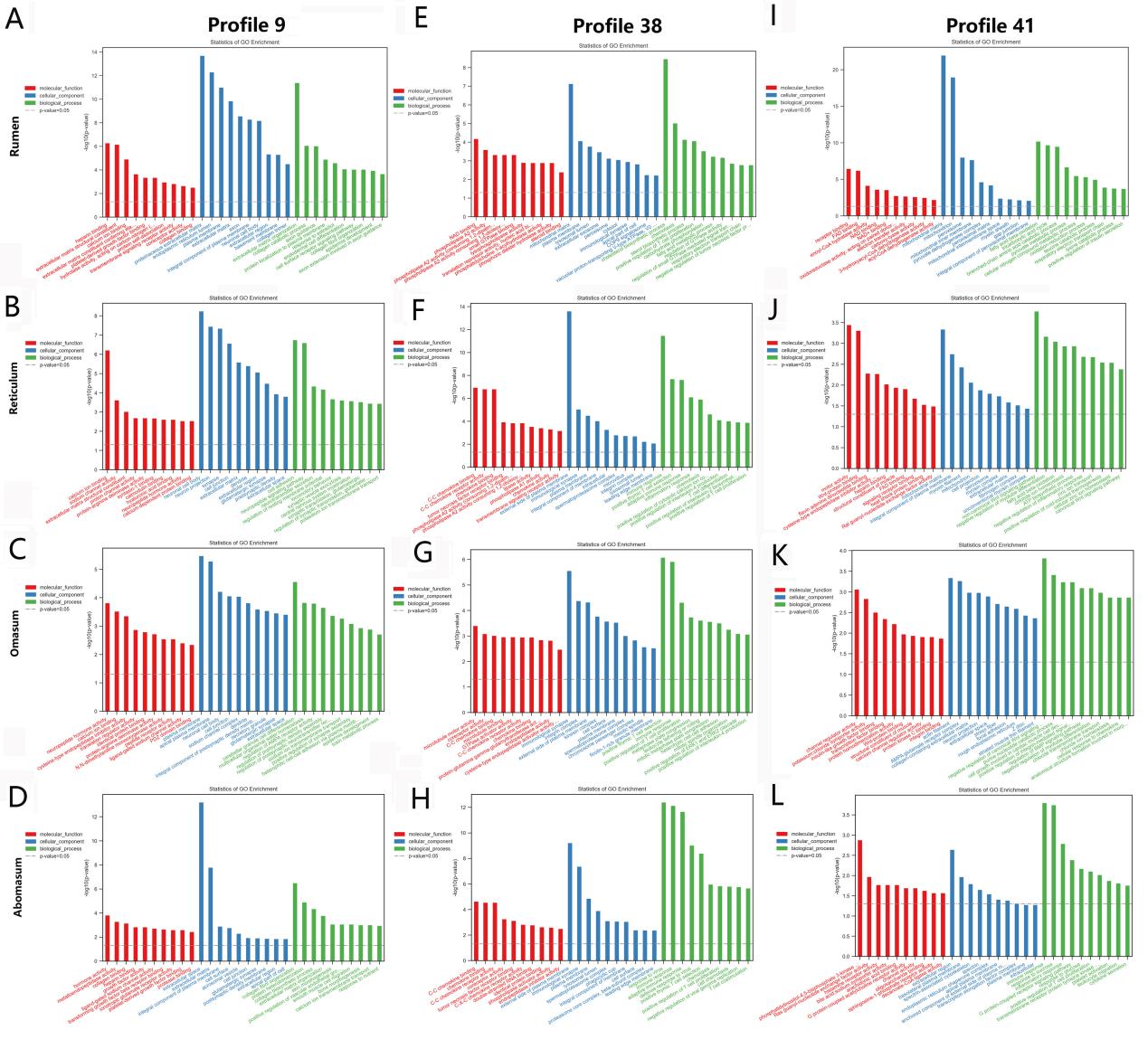
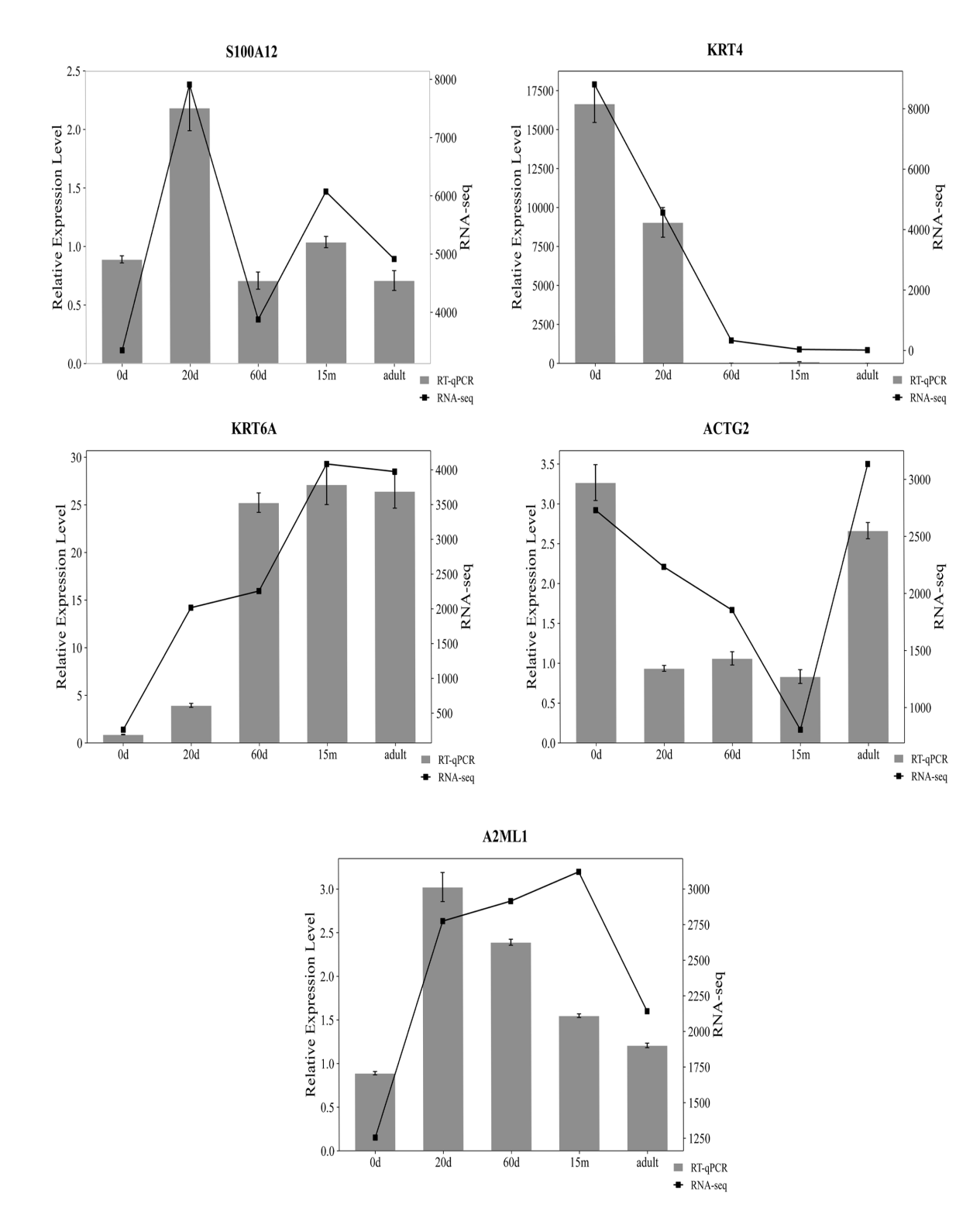
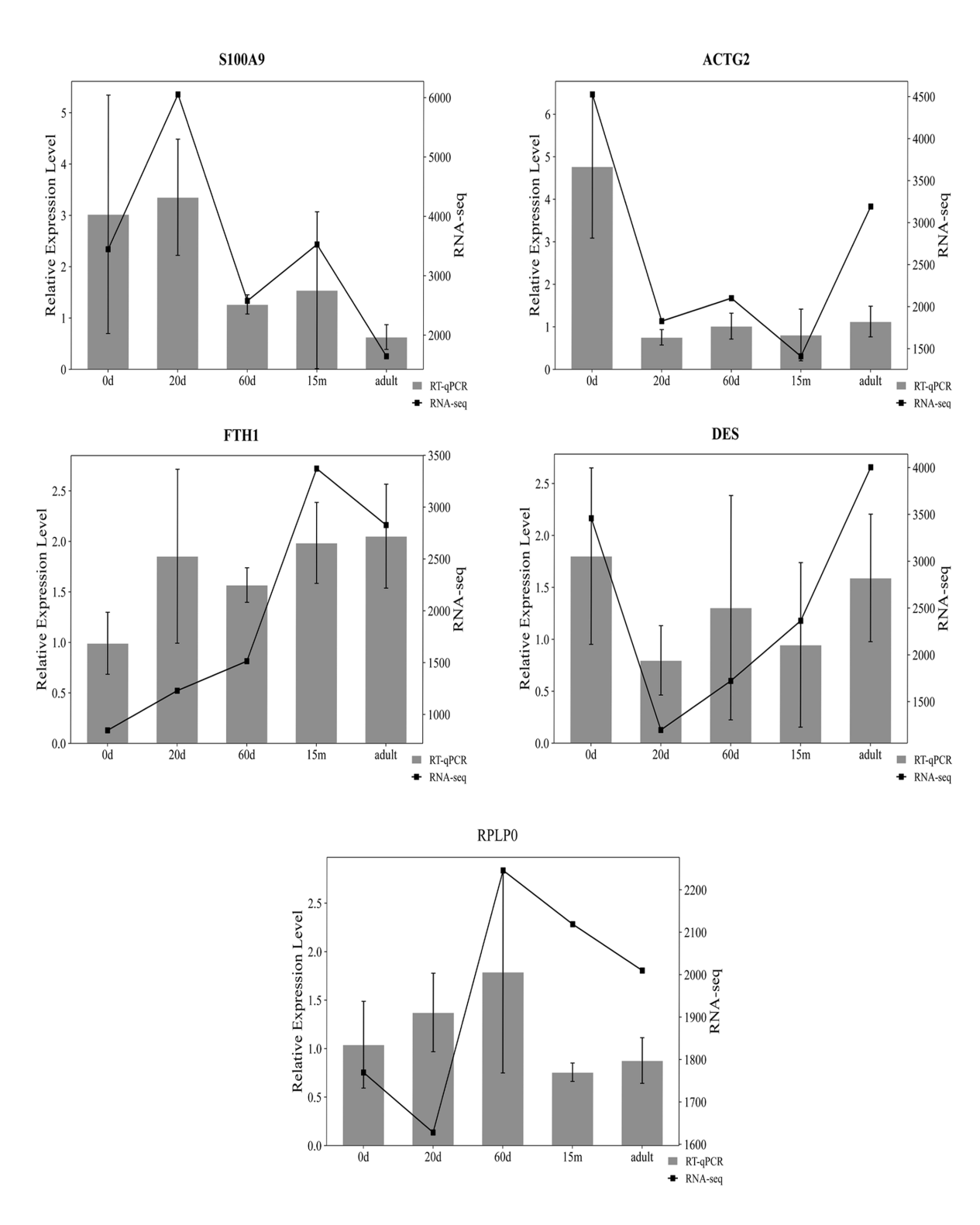
**Figure S1.** KEGG enrichment bubble plot of DEmRNAs involved in fatty acid metabolism in four closed groups.

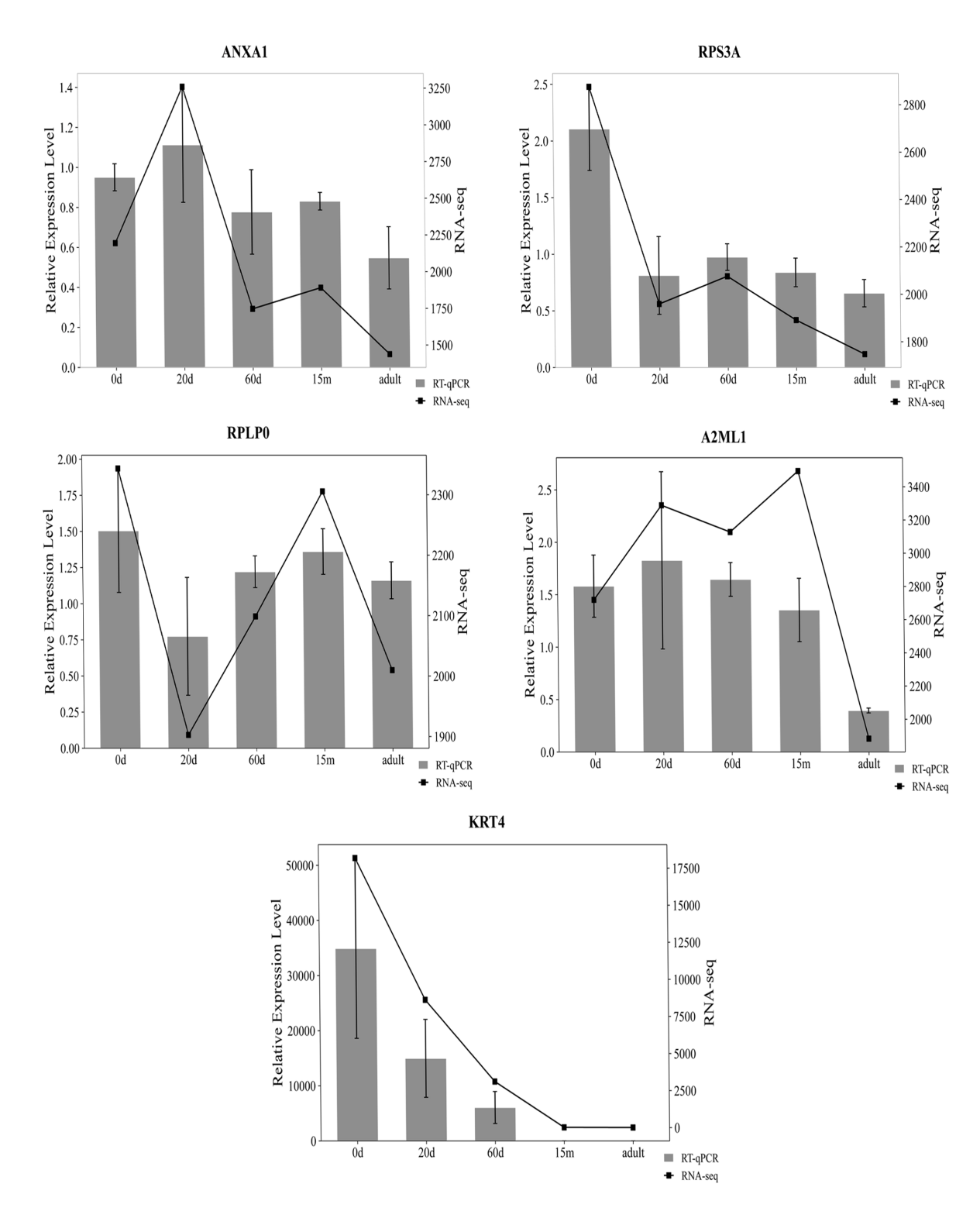


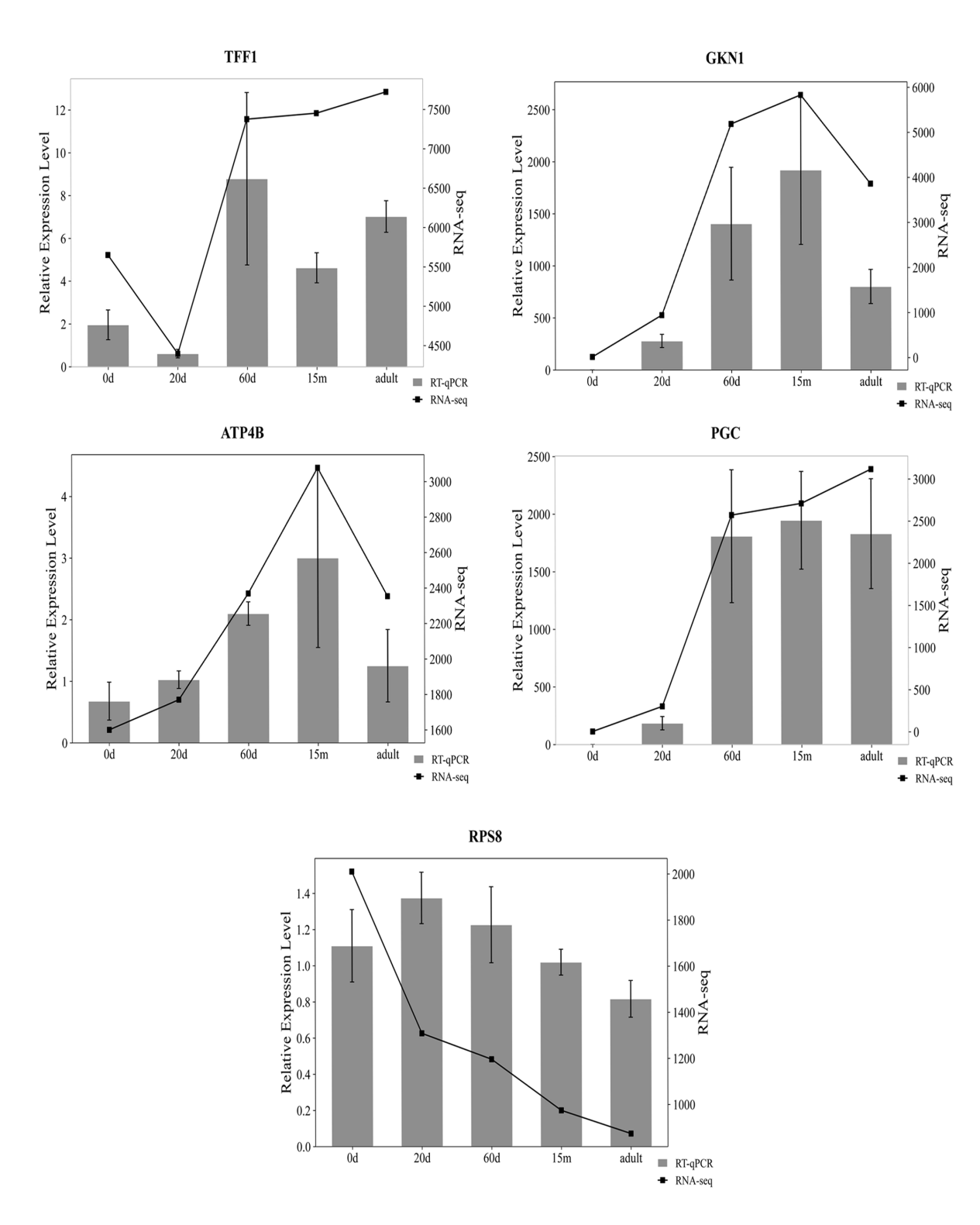
**Figure S2**. The top30 GO enrichment of profile 9, 38 and 41 in four stomachs.



**Figure S3**. Transcription patterns of *S100A12, KRT4, KRT6A, ACTG2, A2ML1* compared to expression patterns in the RNA-seq in rumen.

**Figure S4**. Transcription patterns of *S100A9*, *ACTG2, FTH1, DES, RPLP0* compared to expression patterns in the RNA-seq in reticulum.

**Figure S5**. Transcription patterns of *ANXA1, RPS3A, RPLP0, A2ML1, KRT4* compared to expression patterns in the RNA-seq in omasum.

**Figure S6**. Transcription patterns of *TFF1, GKN1, ATP4B, PGC, RPS8* compared to expression patterns in the RNA-seq in abomasum.