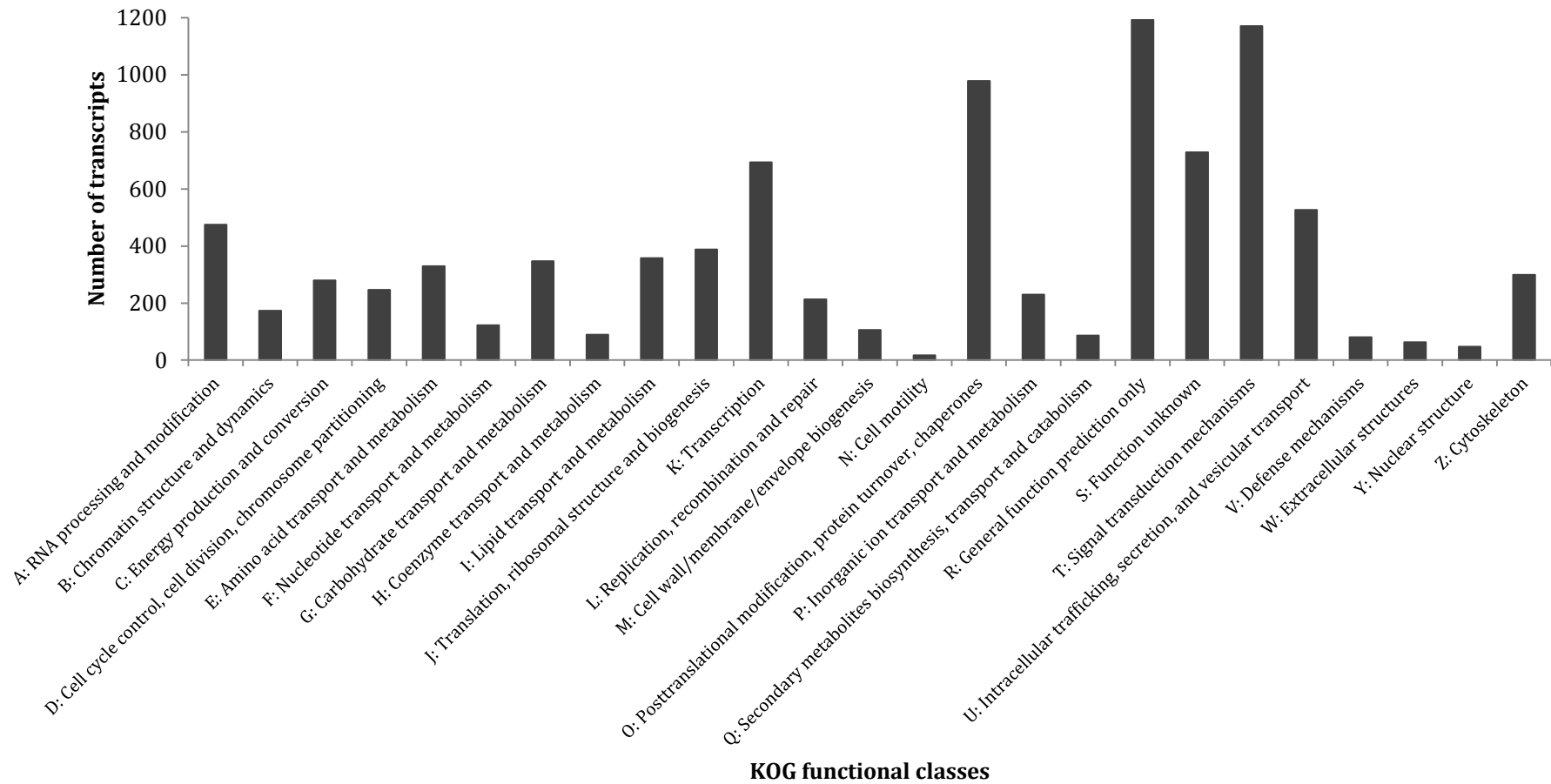
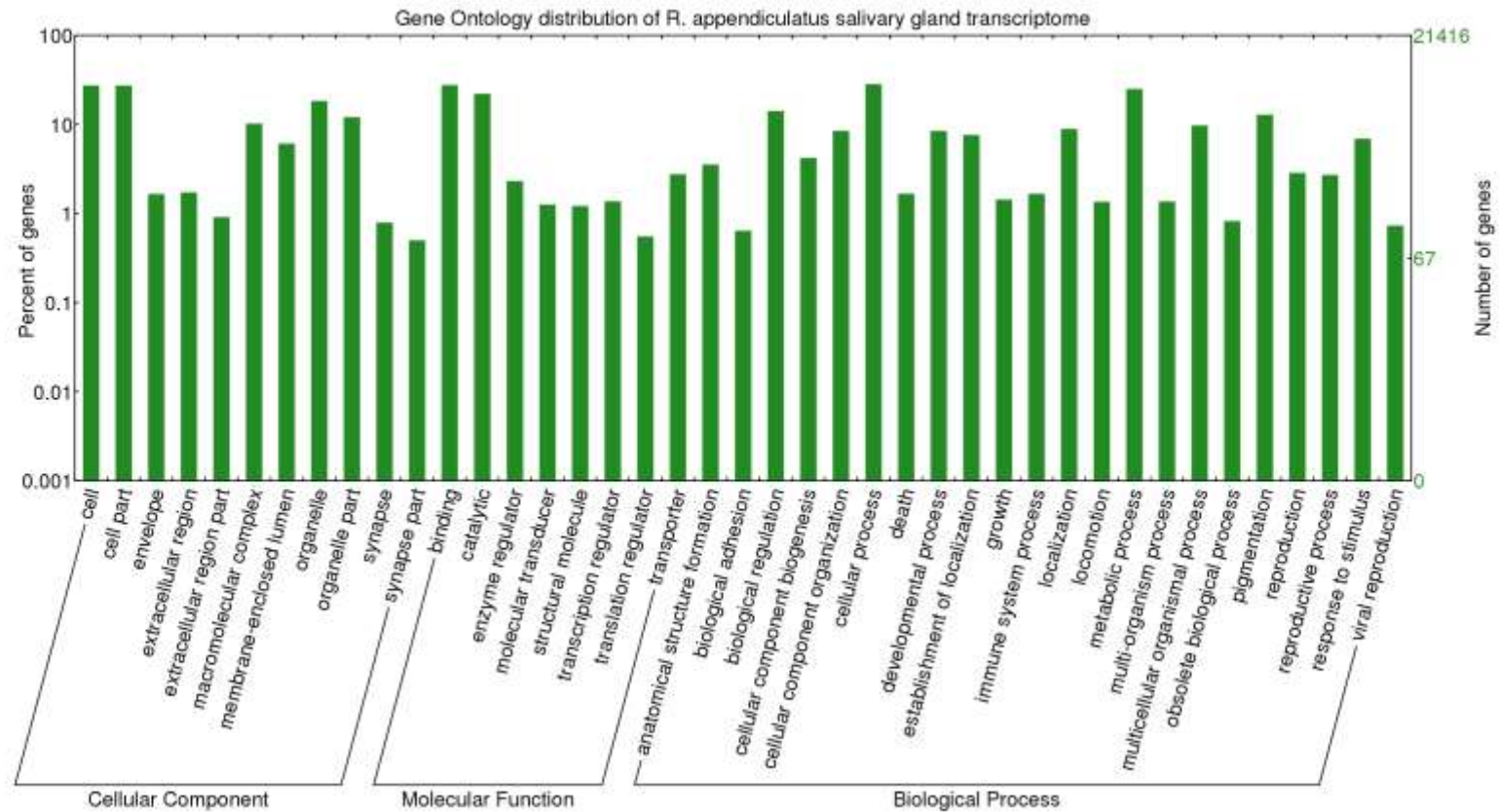


Appendix C. Supplemental Figures:

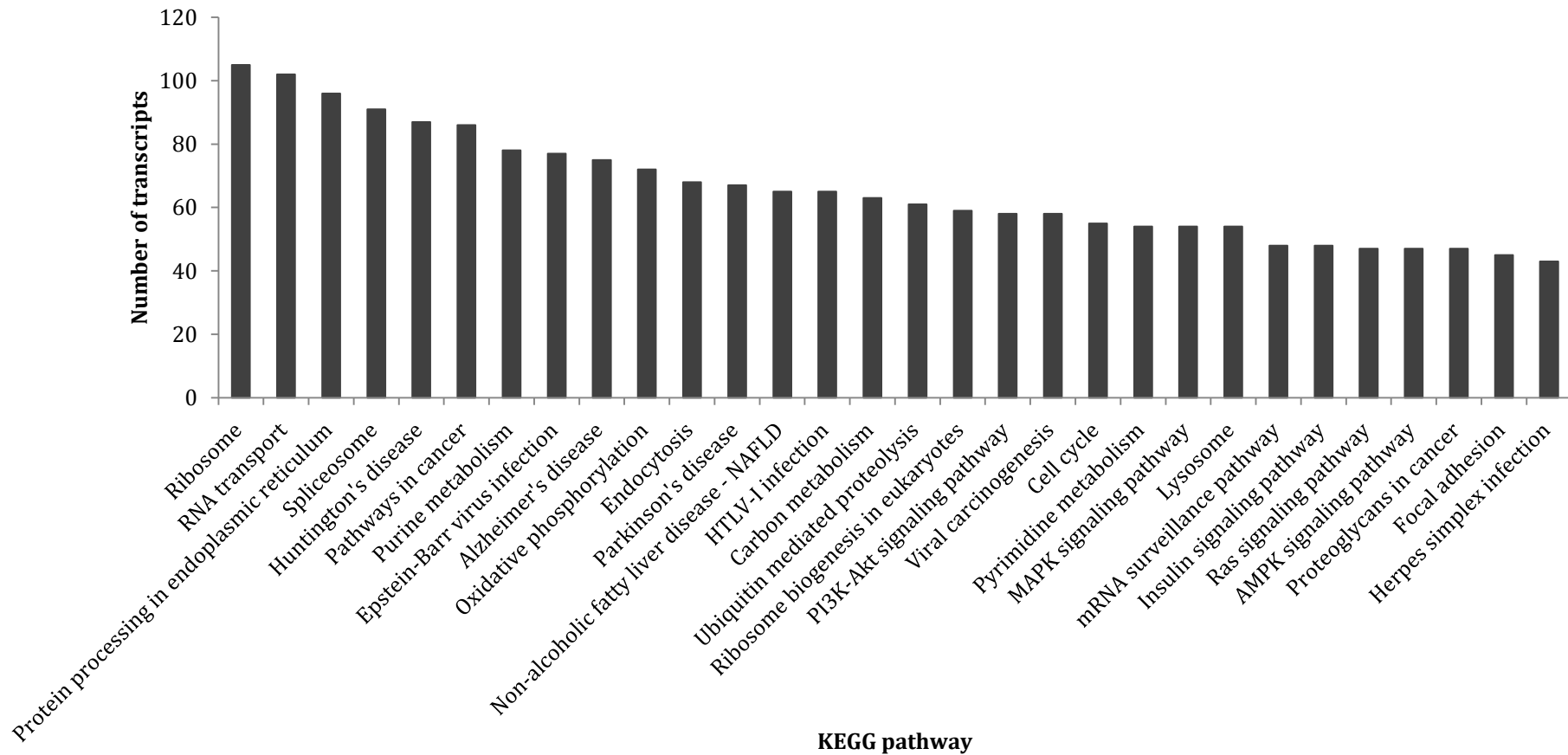
Transcriptome annotation.



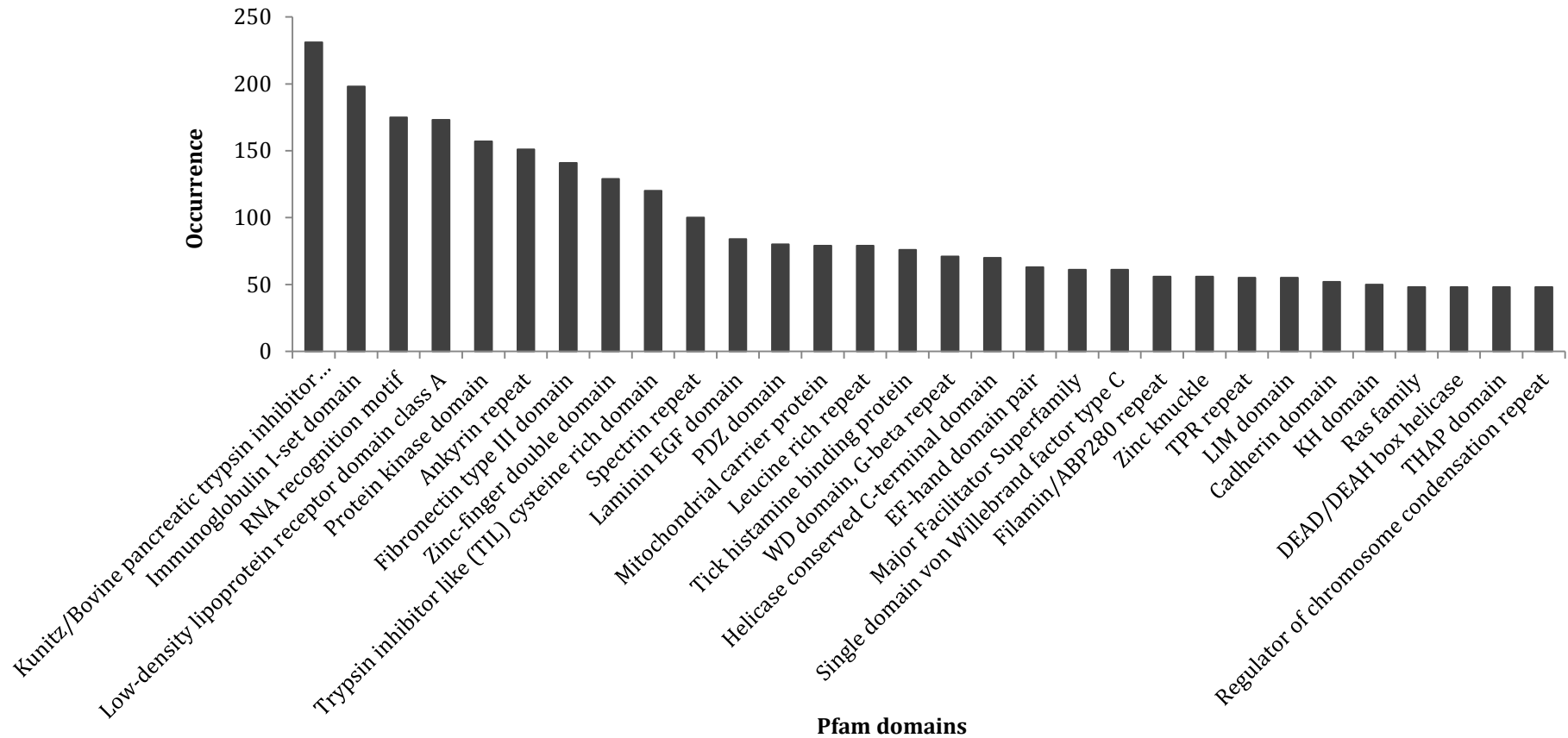
Supplemental Fig. C1. KOG functional classification of *R. appendiculatus* transcripts. Number of transcripts with a significant BLASTx result (E-value < e^{-5}) in each functional Eukaryotic Clusters of Orthologs (KOG) class. In total, 8282 transcripts obtained a significant BLASTx match and could be assigned to 25 KOG functional categories, with 3791 unique KOG terms.



Supplemental Fig. C2. Gene Ontology distribution of the *R. appendiculatus* transcriptome. Proportion of transcripts classified into different categories of cellular components, molecular functions and biological processes are indicated. Web Gene Ontology Annotation Plot (WEGO) was used to plot level 2 GO terms present in at least 100 transcripts.



Supplemental Fig. C3. KEGG Pathways identified in the *R. appendiculatus* transcriptome. In total, 4647 transcripts were assigned to 321 *I. scapularis* Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. The top 30 most abundant KEGG pathways are shown.



Supplemental Fig. C4. Pfam domains identified in the predicted proteins of the *R. appendiculatus* transcriptome. In total, 13 246 Pfam domains were identified, categorising 7630 of the *R. appendiculatus* proteins. The 30 most occurring Pfam domains are indicated.