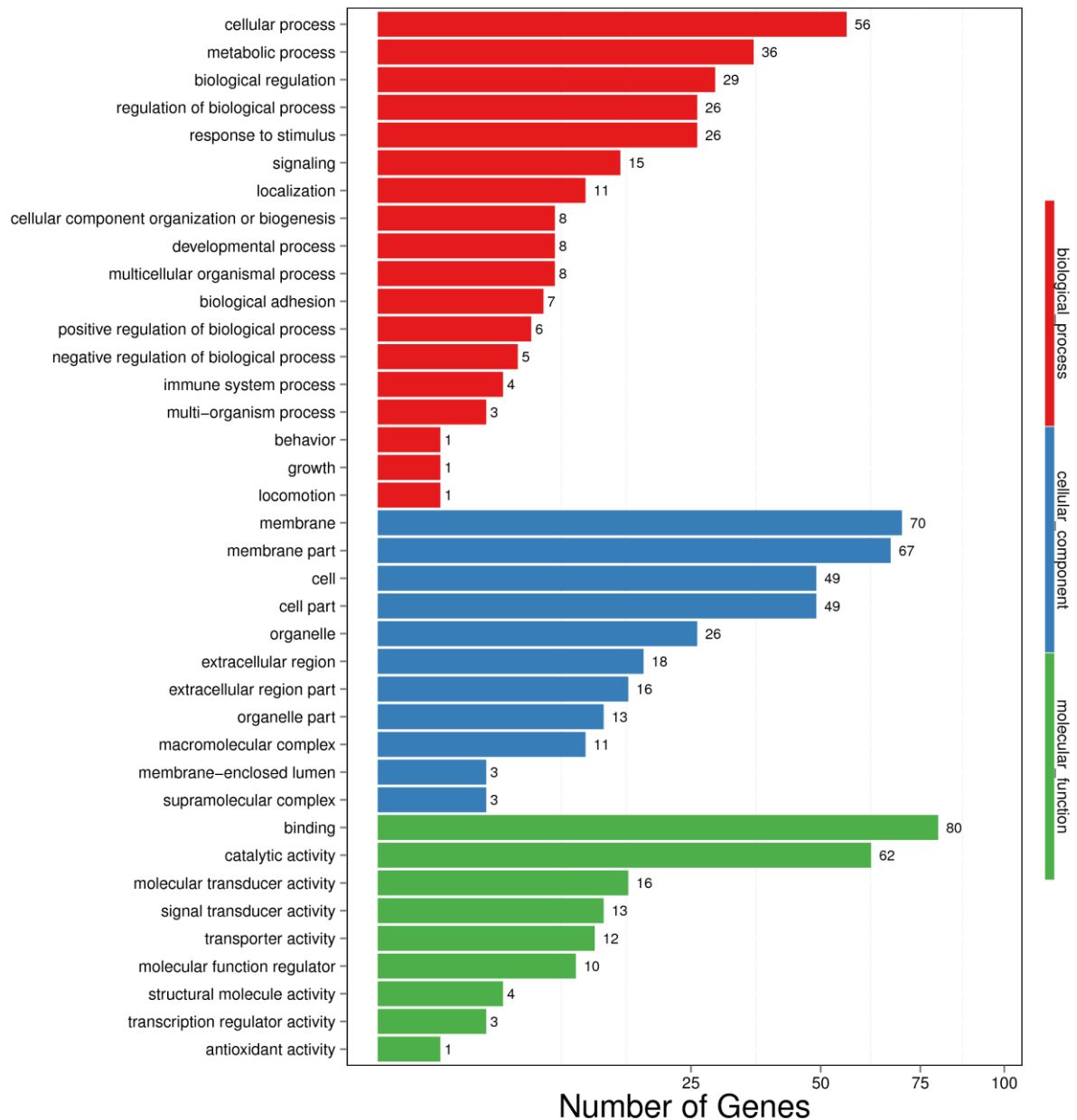
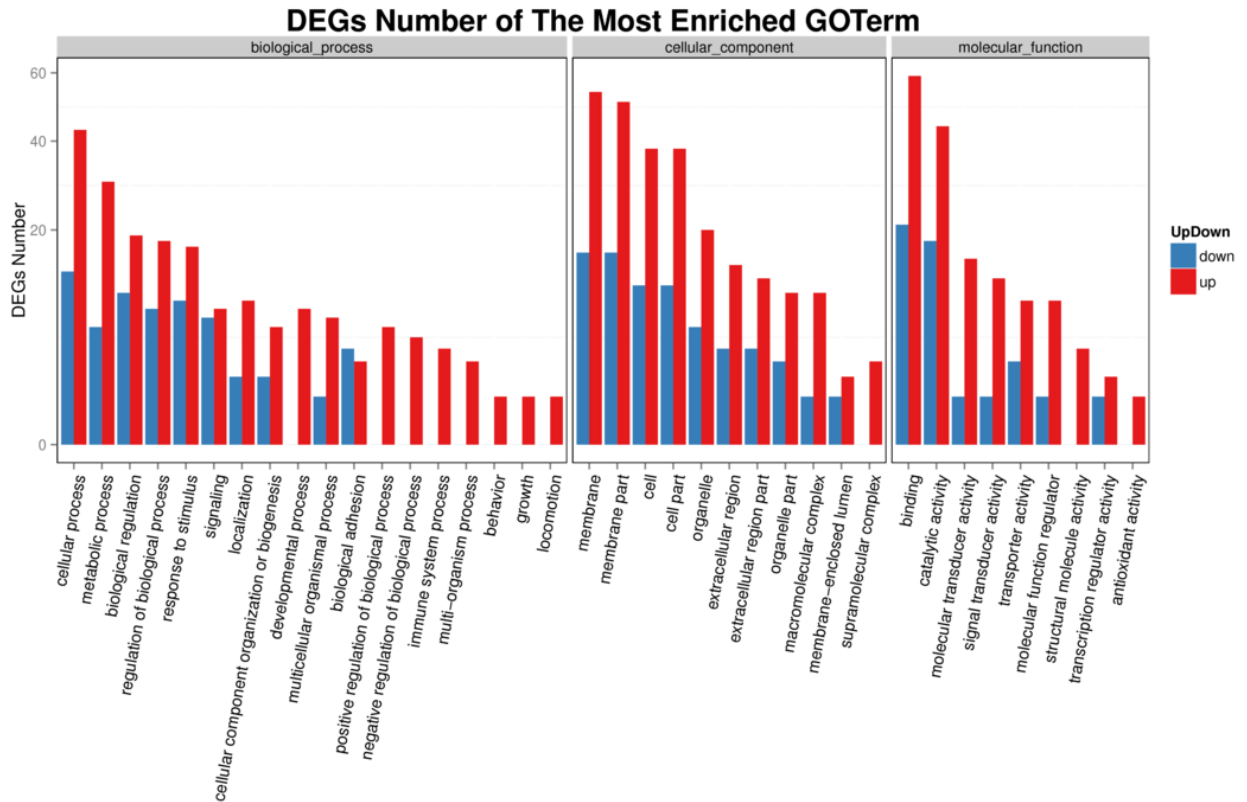
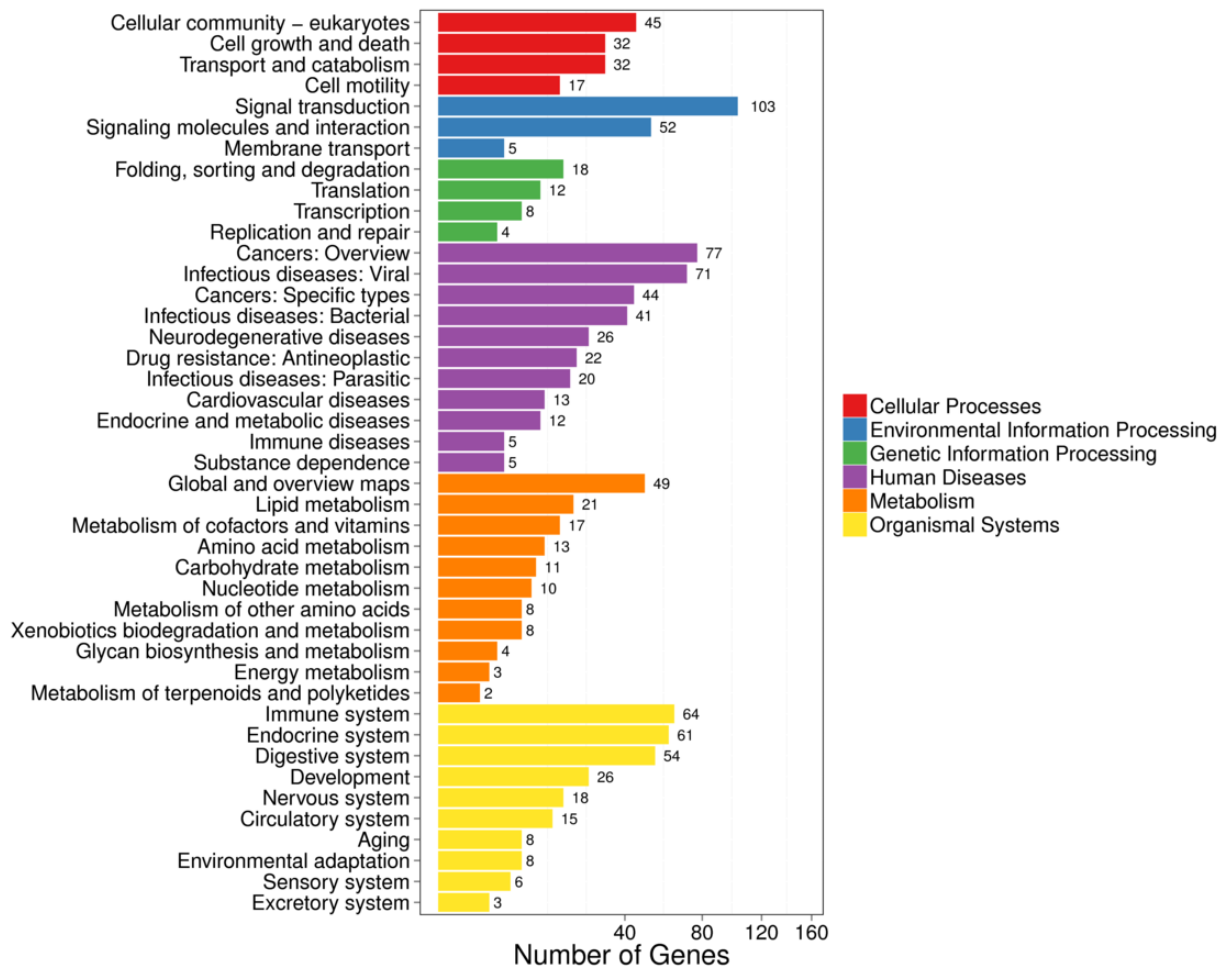




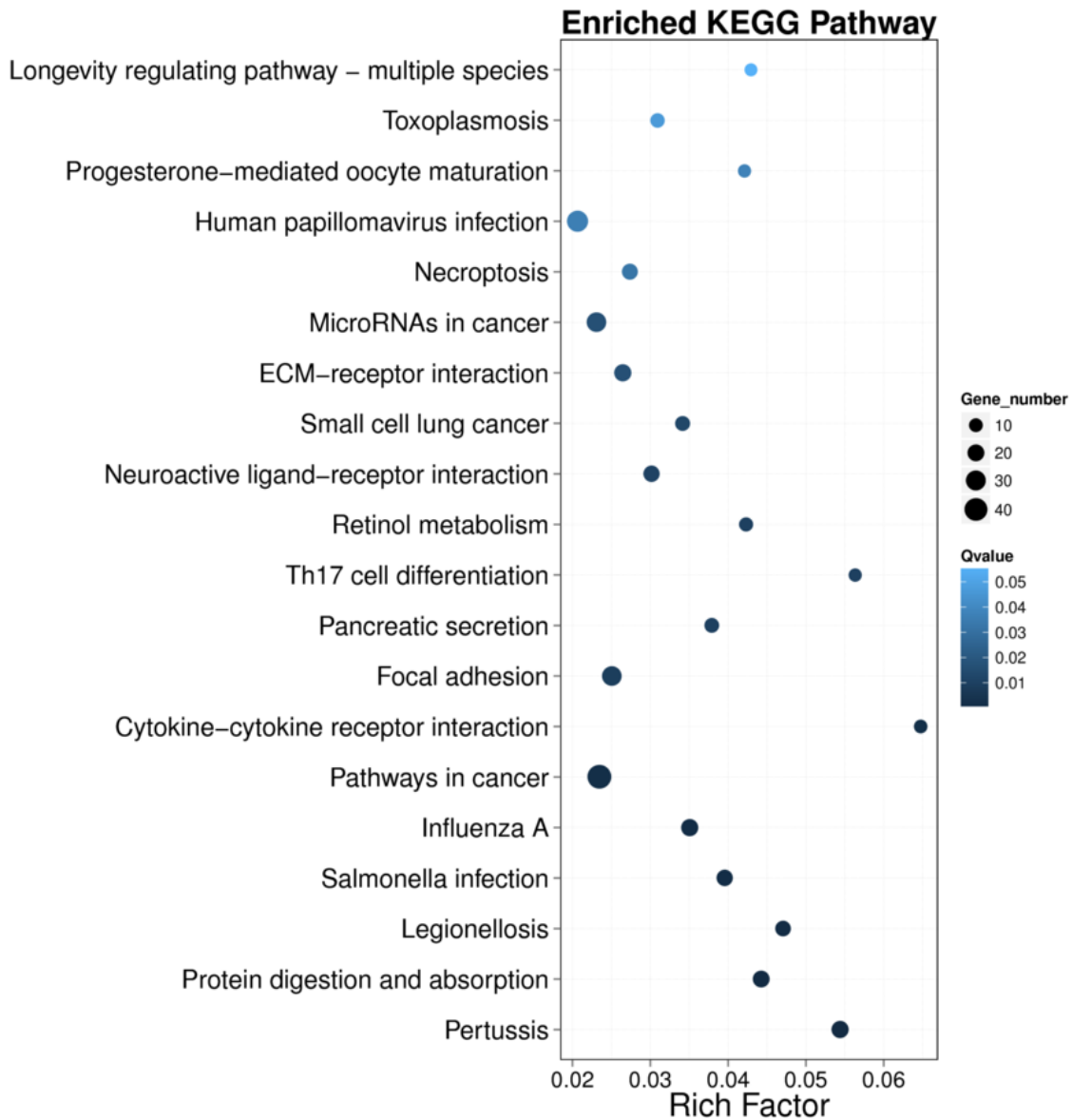
Sup. 5.1. Distribution of DEGs in gene ontologies (GO): the X axis represents the number of DEGs and the Y axis represents GO terms. GO are divided into three categories, represented by different colours.



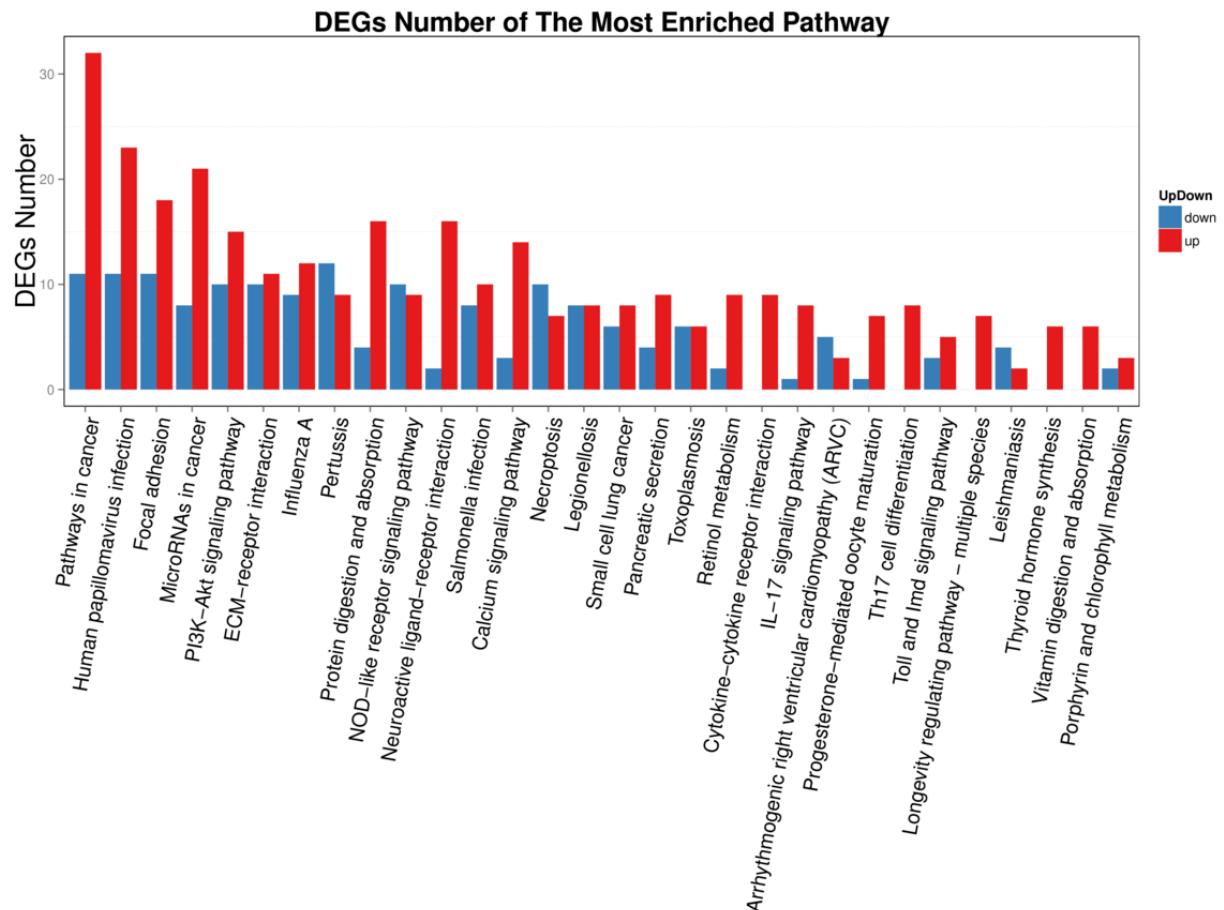
Sup. 5.2. GO distribution of up-regulated (red) and down-regulated (blue) genes: the X axis represents the terms of gene ontology and the Y axis represents the number of unigenes.



Sup. 5.3. Distribution of DEGs in KEGG pathways: the X axis represents the number of DEGs and the Y axis represents KEGG pathways. Pathways are divided into seven main categories, represented by different colours.



Sup. 5.4. The 20 most enriched KEGG pathways. The X-axis represents the value of the enrichment-rich factor, which is, for a given pathway, the number of annotated DEGs versus the number of annotated unigenes, and the Y-axis represents the different KEGG pathways. The colour of the dots represents the q-value, which corresponds to an adjusted p-value ranging from 0 to 1: a lower q-value means a greater significance. The size of the dots represents the number of DEGs in the KEGG pathway.



Sup. 5.5. KEGG pathway distribution of up-regulated (red) and down-regulated (blue) genes: the X axis represents the pathway terms and the Y axis represents the number of unigenes.