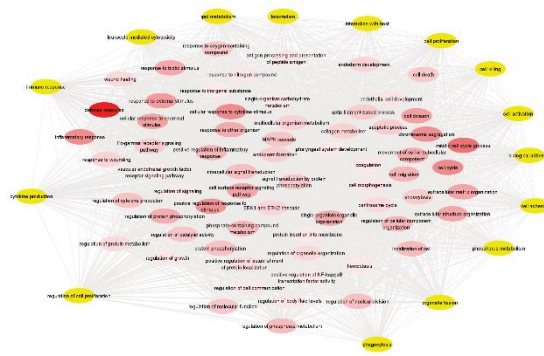


A



B

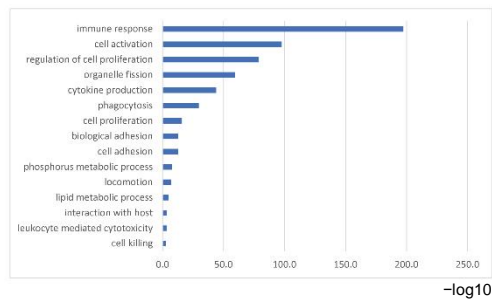


Figure S1: Enrichment analysis of Gene Ontology (GO) biological processes (GOTERM_BP_FAT) among canine PCa DEGs summarized and visualized using REVIGO. **(A)** Bubble plot of the GOs. The color and size of circles indicate the \log_{10} of the false discovery rate (FDR) and the frequency of the GO term, respectively. Representative terms are highlighted with yellow oval circle **(B)** Bar chart summarizing the biological processes. The height of the bars denotes the sum of the $-\log_{10}$ FDR of the individual biological processes clustered together by REVIGO and represented by the respective terms on the x-axis.