

Suppl. Fig. 1. The protein–protein interaction (PPI) networks (A) and the co-expression networks (B) of differentially expressed pyroptosis-related genes between the recurrent and non-recurrent samples.

The purple and red nodes represent the genes that were significantly downregulated and upregulated, respectively, in the recurrent samples; the white nodes represent the genes with no changes in expression level. The red and green edges represent significantly positive and negative correlations, respectively.