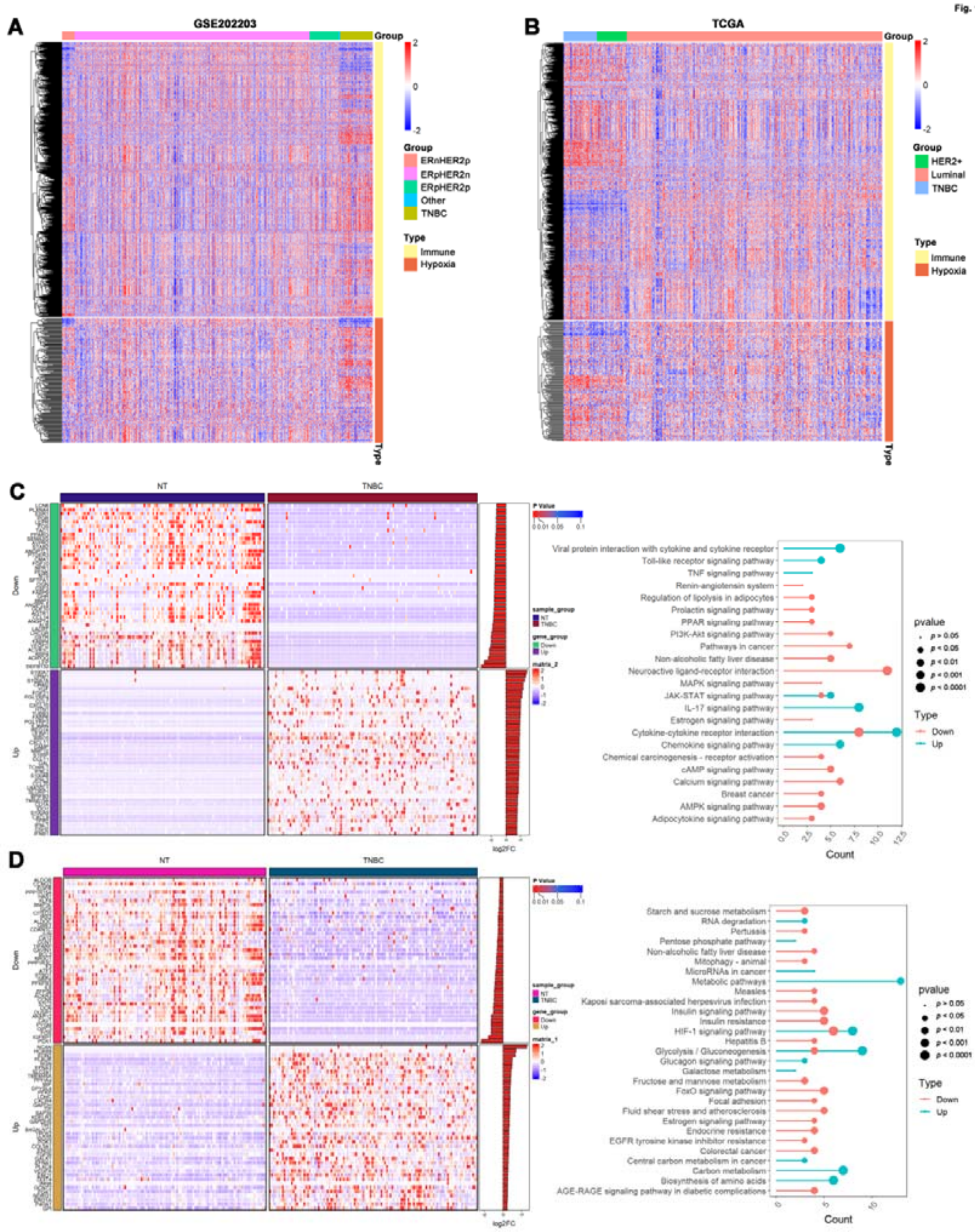
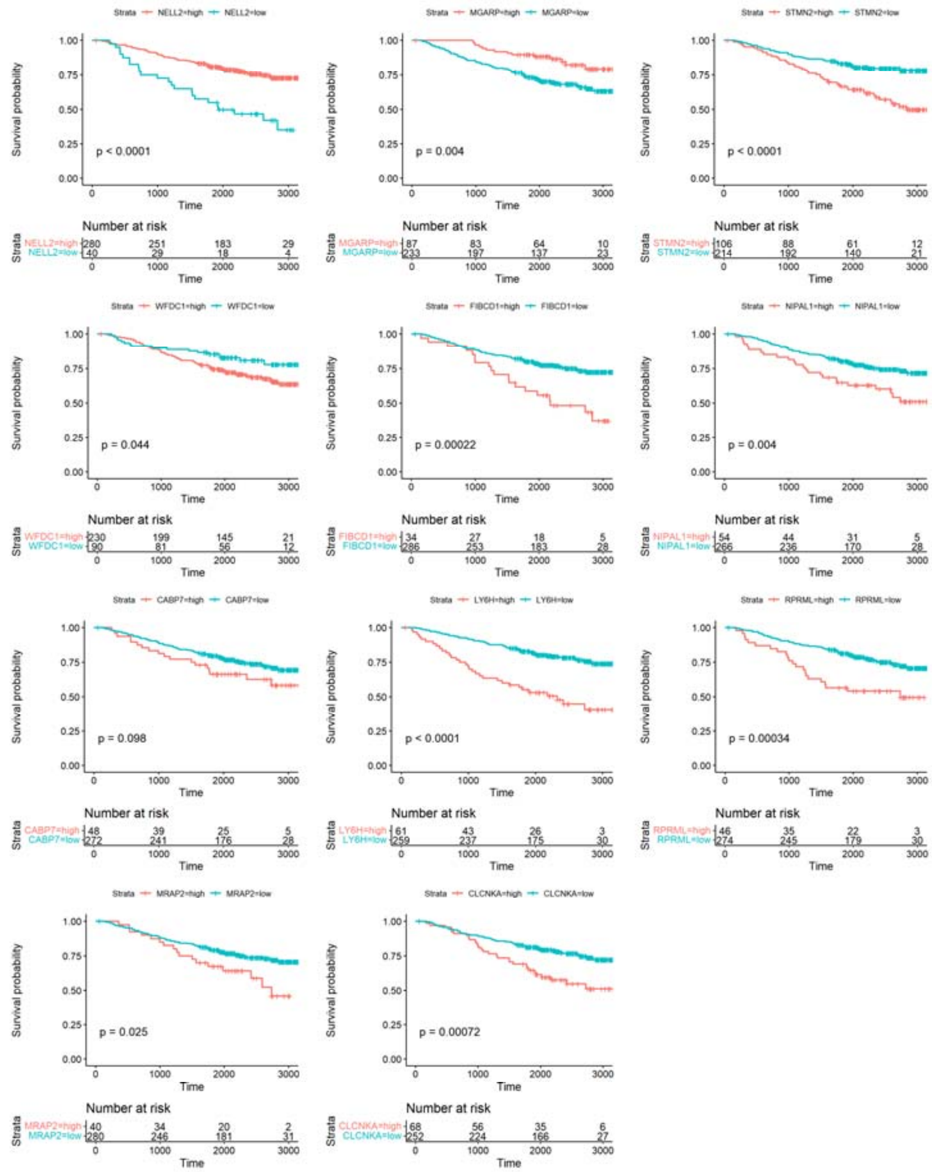
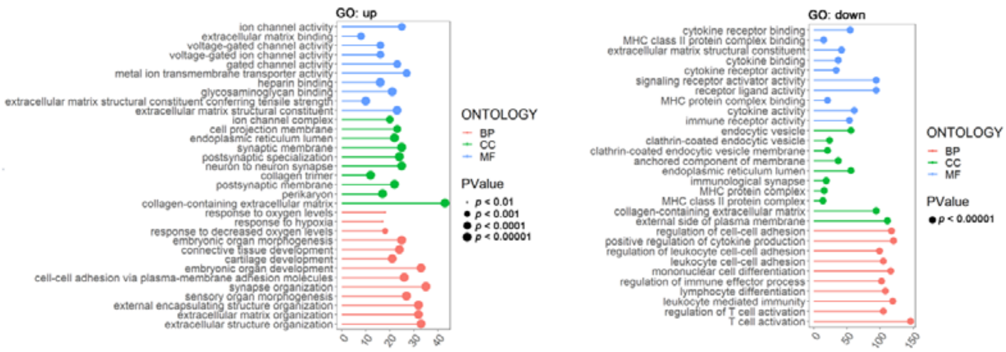


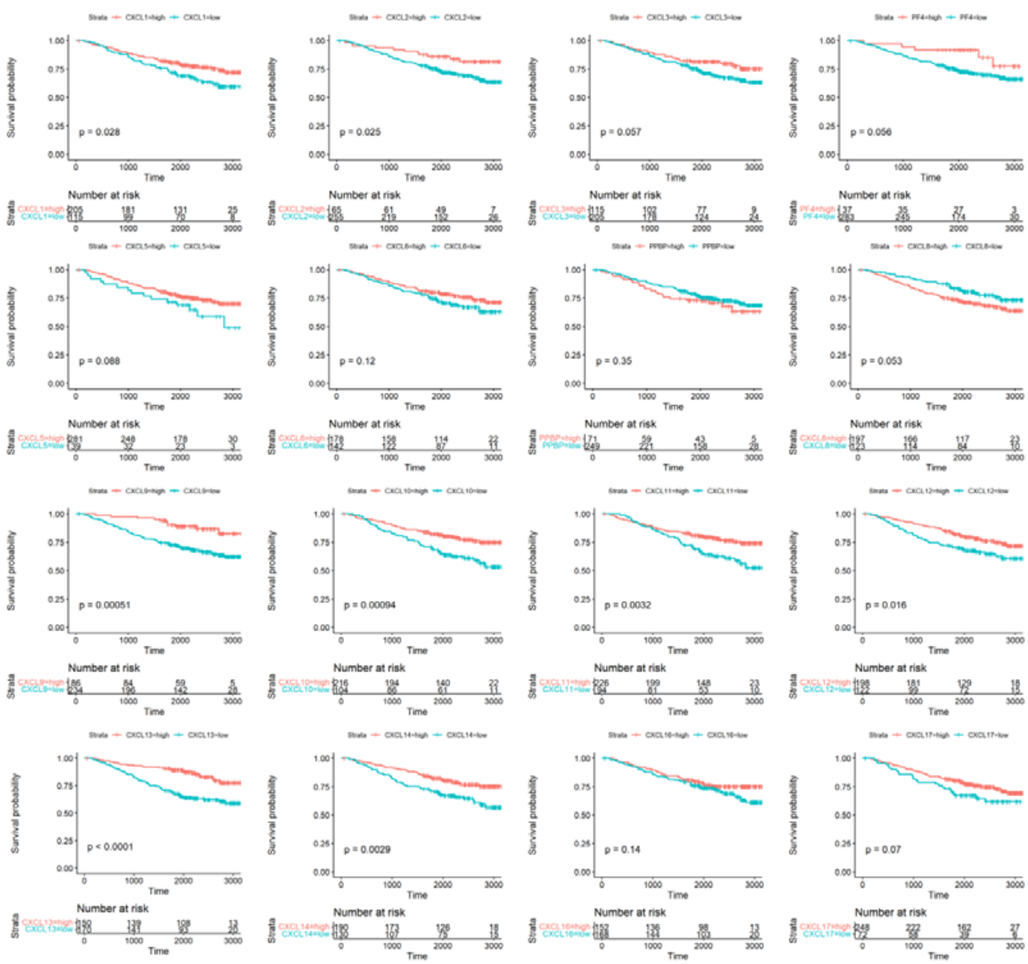
Supplementary Figure 1. (**A**, **B**) Heatmap of immune and hypoxia genes in TNBC versus other types of breast cancer. (**C**) Heatmap and KEGG functional enrichment analysis of immune-related DEGs in TNBC versus normal tissues (NTs). (**D**) Heatmap and KEGG functional enrichment analysis of hypoxia DEGs in TNBC versus NTs. Transcriptional data of (**A**) and (**B**, **C**, **D**) were download from GSE202203 and TCGA respectively.



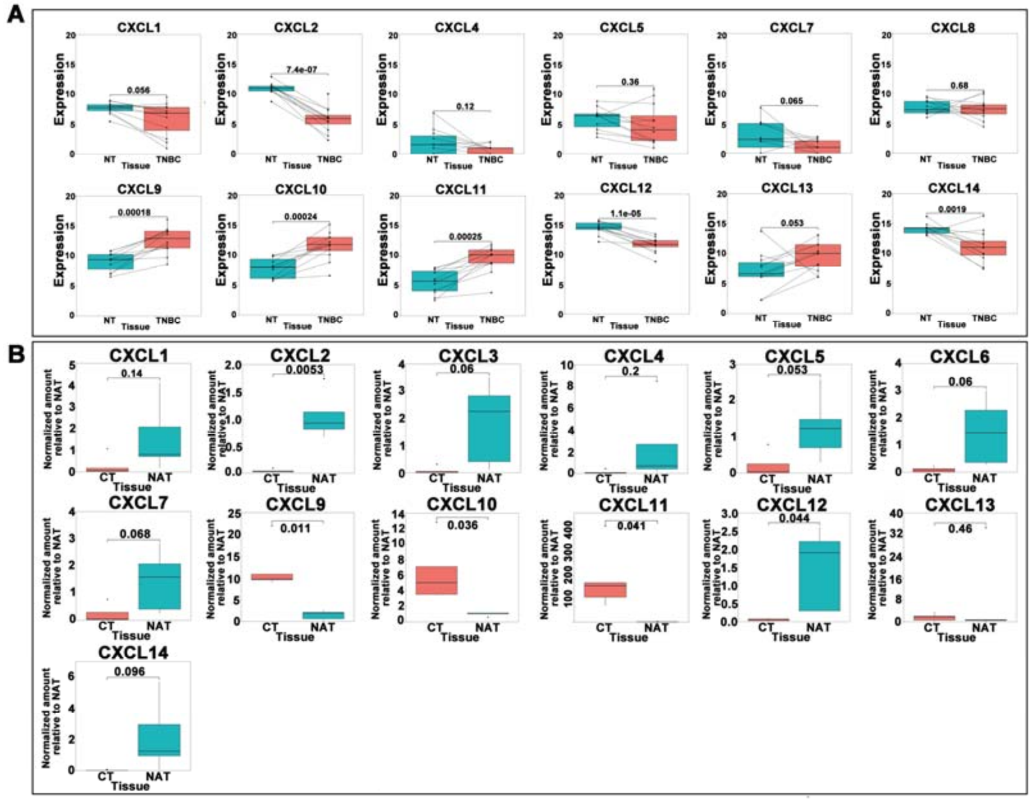
Supplementary Figure 2: Kaplan-Meier survival analysis for patients grouped into high or low expression of model genes.



Supplementary Figure 3. Functional enrichment analysis of DEGs correlated to model genes were conducted: GO functional enrichment analysis of DEGs between high- and low-risk groups.



Supplementary Figure 4. Kaplan-Meier survival analysis for patients grouped into high or low expression of CXC chemokines.



Supplementary Figure 5. Analysis of mRNA levels of CXC chemokines in TNBC versus normal samples. (A) The transcription of CXC chemokines in TNBC and paired NT (data from TCGA). (B) The transcription of CXC chemokines in TNBC and NAT (results of qRT-PCR).