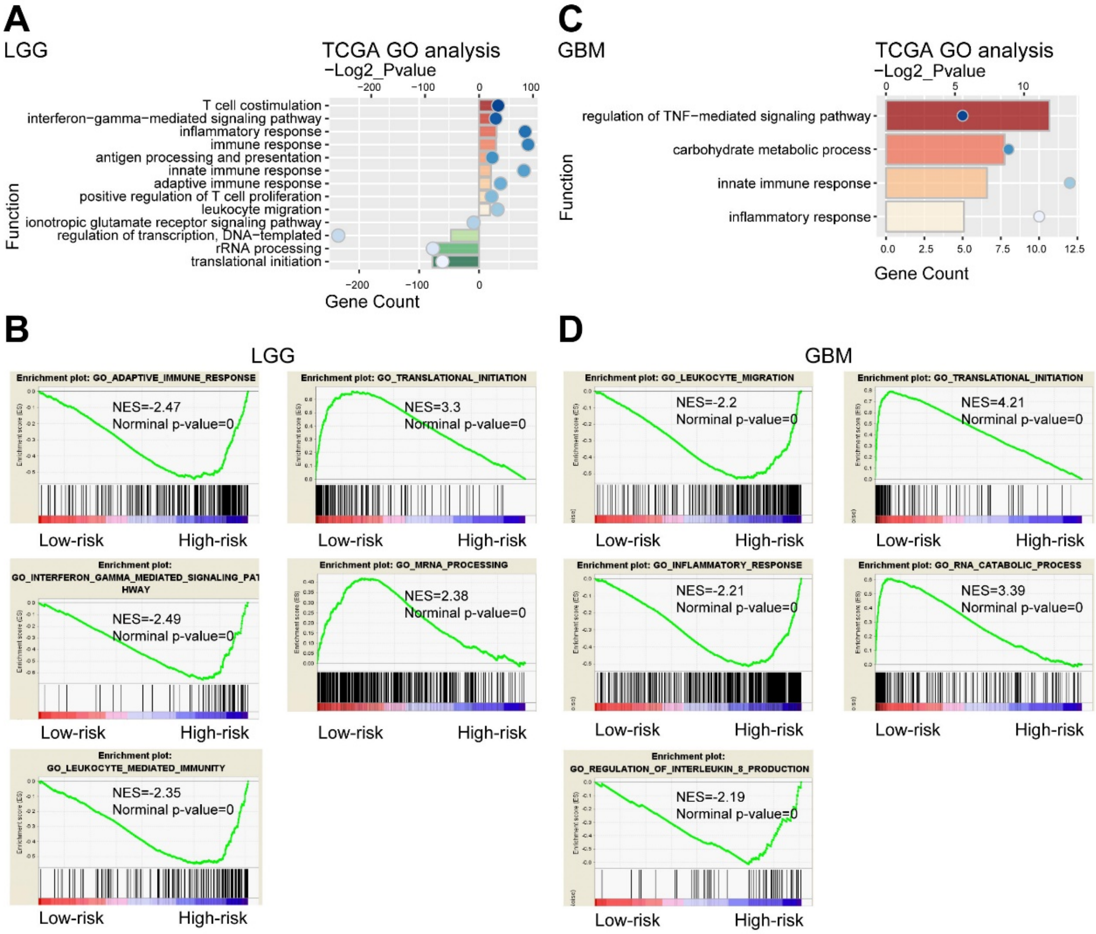

Supplementary Figure 9. Functional analysis of the 29-gene signature in LGG and GBM of TCGA cohort. (**A**) GO annotations based on the top 2000 genes positively and negatively associated with the 29-gene signature in LGG. (**B**) GSEA analysis based on the median value of risk score in LGG. (**C**) GO annotations based on the top 2000 genes positively and negatively associated with the 29-gene signature in GBM. (**D**) GSEA analysis based on the median value of risk score in GBM.