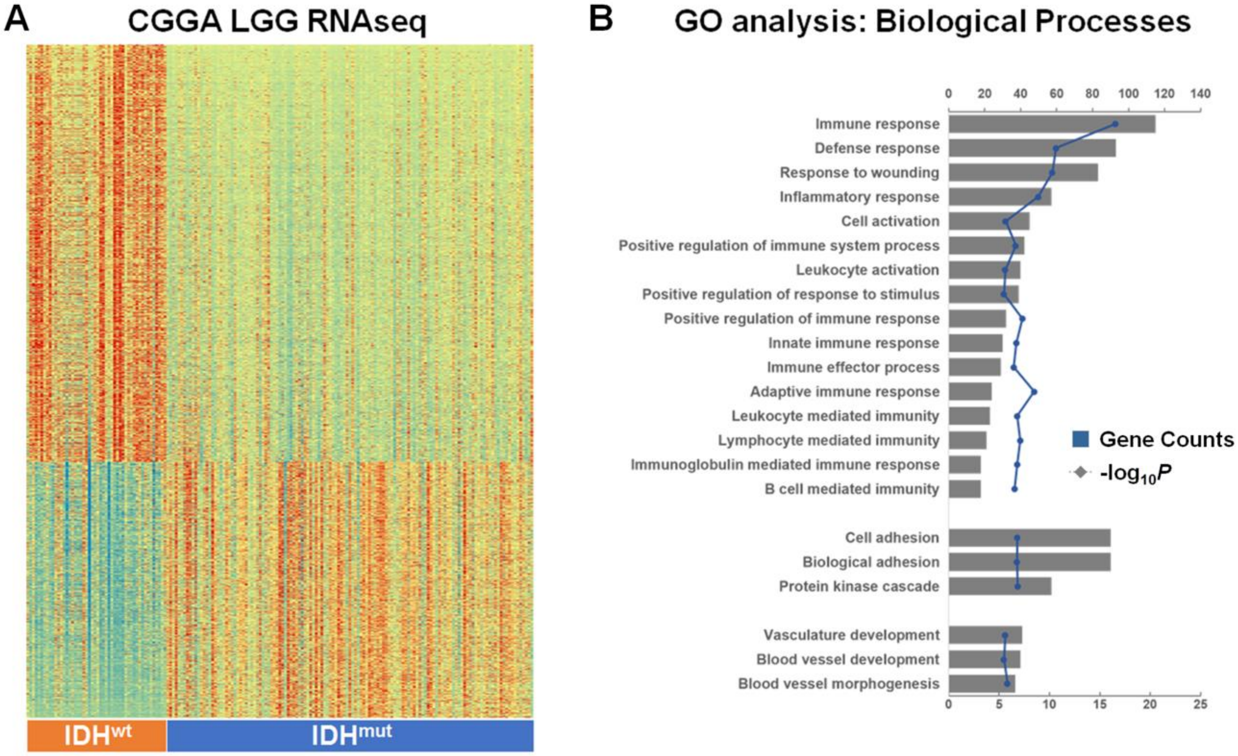
SUPPLEMENTARY MATERIAL



Supplementary Figure 1. The transcriptomic distinction between *IDH*$^{\text{MUT}}$ and *IDH*$^{\text{WT}}$ LGGs in the CGGA cohort. (**A**) Differentially expressed genes determined by the Pearson correlation algorithm. (**B**) Highly expressed genes in the *IDH*$^{\text{WT}}$ LGGs were investigated by gene annotation. The enriched biological processes included the immune response, cell adhesion, and vascular related terms.