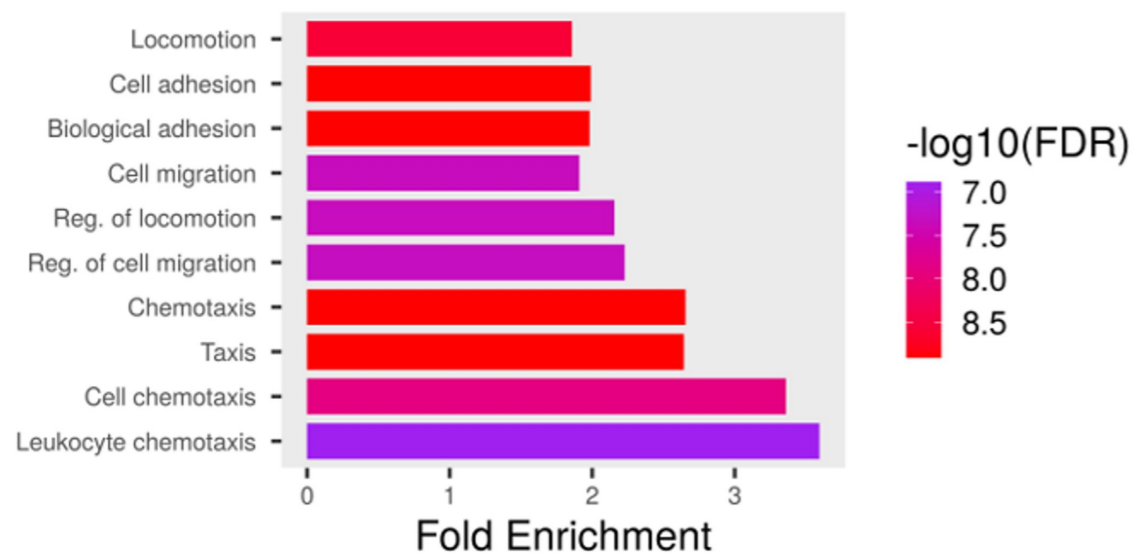
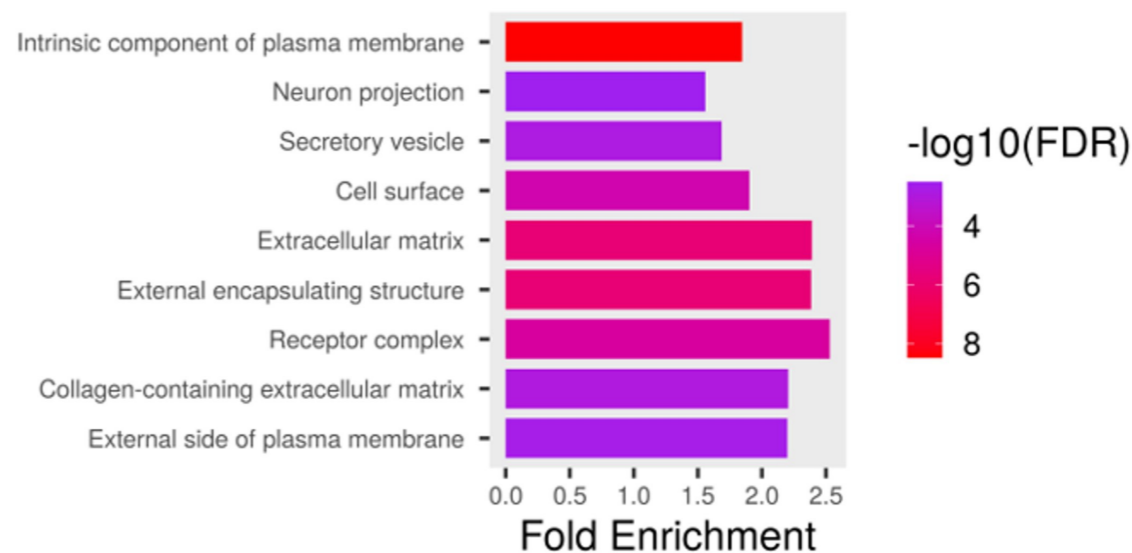


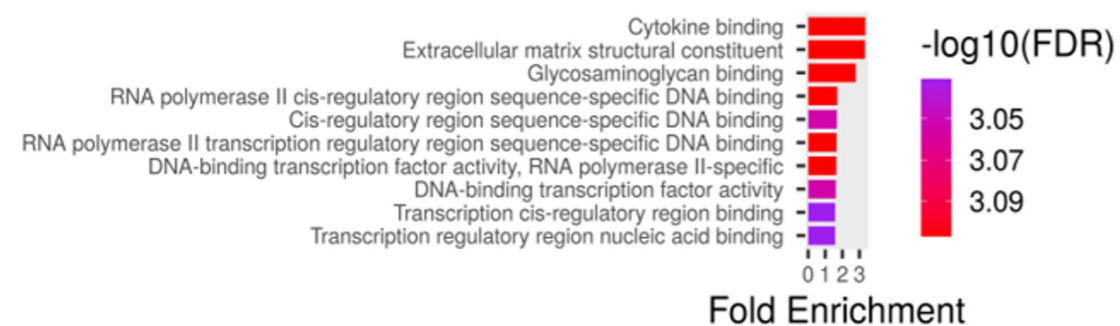
Biological Process



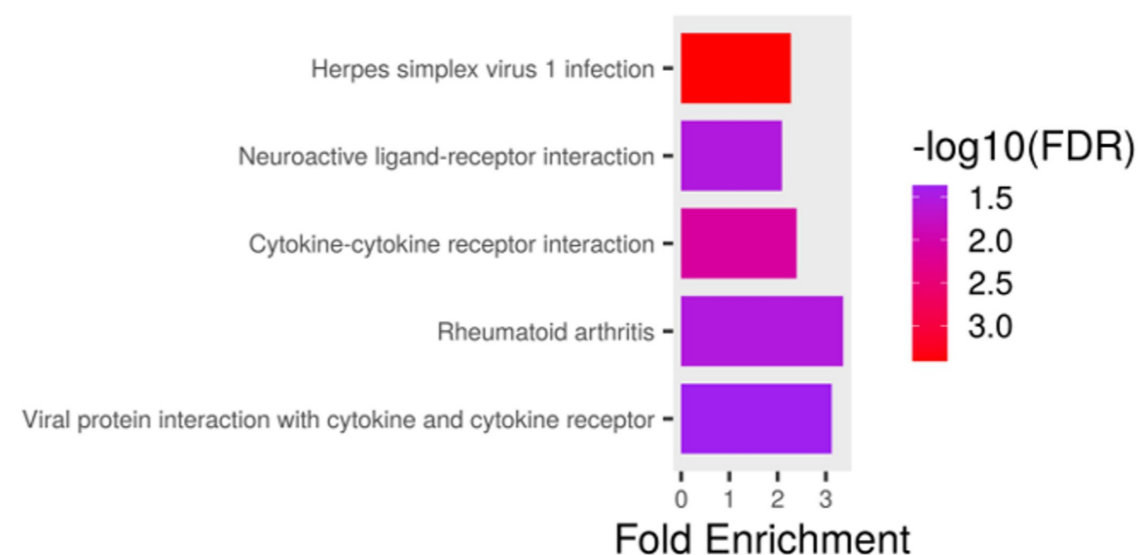
Cellular Component



Molecular Function



KEGG



Supplementary Figure 6 Gene Ontology (GO) analysis (ShinyGO (Ge SX, Jung D & Yao R, *Bioinformatics* 36:2628–2629, 2020; <http://bioinformatics.sdstate.edu/go/>)) of significantly ($p < 0.05$) upregulated differentially expressed genes (DEGs) (fold change > 1.5), common to 2 or more patients, in RNA-seq analysis of 4 patient GBM samples (D31-D34), 8-days post-chip and treated with 1 μM GSK715 vs DMSO control.