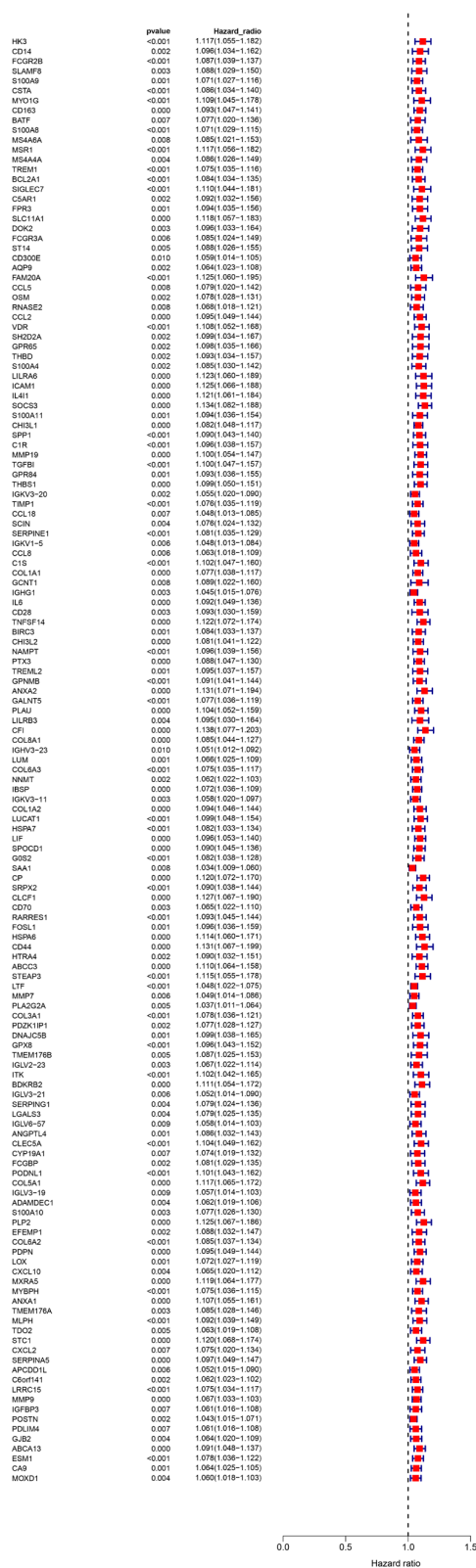


**Figure S1** Volcano plot of DEGs between immune hot versus cold GBM subtypes. Volcano plot visualizing DEGs identified between immune hot and cold GBM subtypes. The x-axis represents  $\log_2$ [fold change (FC)], with positive values indicating upregulation in hot tumors and negative values indicating upregulation in cold tumors. The y-axis shows  $-\log_{10}$ (p-value) for statistical significance. Dots are color-coded: red (significantly upregulated in hot tumors,  $\log_2\text{FC}>2$ ,  $P<0.05$ ), blue (significantly downregulated in hot tumors,  $\log_2\text{FC}<-2$ ,  $P<0.05$ ), and gray (non-significant genes). Horizontal dashed line marks the significance threshold ( $P=0.05$ ). The plot highlights enhanced expression of immune activation genes in hot tumors and suppressed IRGs in cold tumors.



**Figure S2** Forest plot of prognostic IRGs in GBM patients. Forest plot displaying hazard ratios (HRs) and 95% confidence intervals (CIs) for candidate IRGs identified through univariate Cox proportional hazards regression analysis.