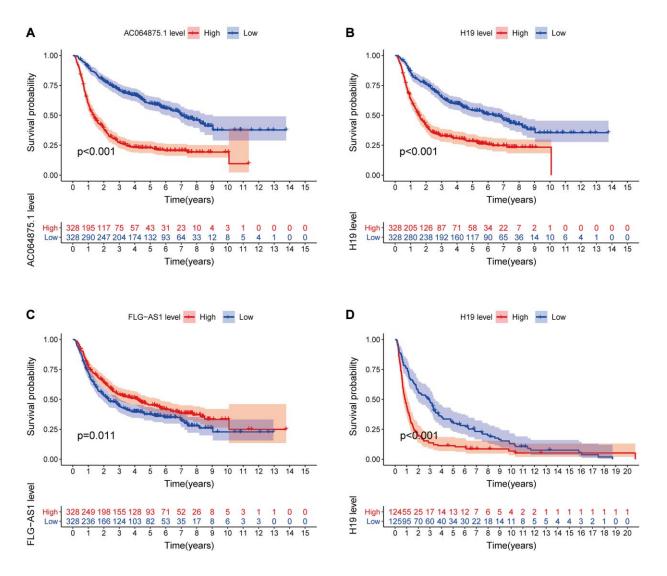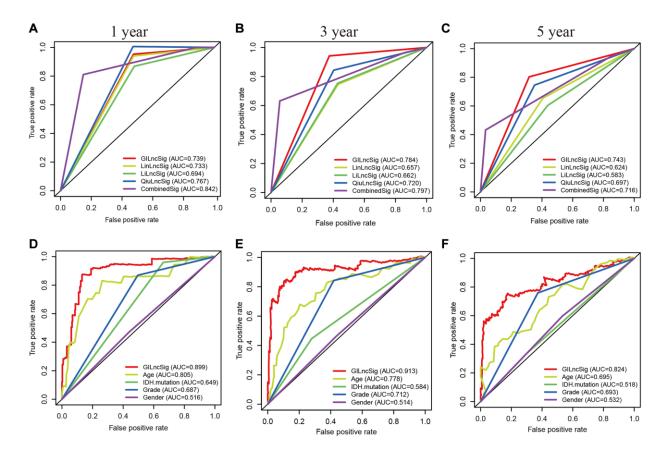# SUPPLEMENTARY FIGURES

Supplementary Figure 1. (**A**–**B**) Overall survival probability of patients with high expression levels of AC064875.1 and H19 in the CGGA mRNA-seq-693 dataset was significantly lower compared with that of patients with low expression levels ($p < 0.001$). (**C**) Overall survival probability of patients with high expression level of FLG-AS1 in the CGGA mRNA-seq-693 dataset was significantly higher compared with the low expression level of FLG-AS1. ($P < 0.05$). (**D**) The overall survival probability of patients with low expression level of H19 in the GSE16011 dataset was significantly higher compared with the OS of patients with high expression of H19. ($p < 0.001$).

Supplementary Figure 2. (**A**–**C**) As the ROC curves showed, the CombinedSig signature could increase the prognostic power for 1 year and 3 year survival rate compared to other four independent signatures. (**D**–**F**) Receiver operating characteristic (ROC) curve analysis shows that the prediction of 1 year, 3 year and 5 year in the prognostic accuracy of clinicopathological parameters such as age, gender, IDH status and grade and GILncSig signature prognostic risk score.