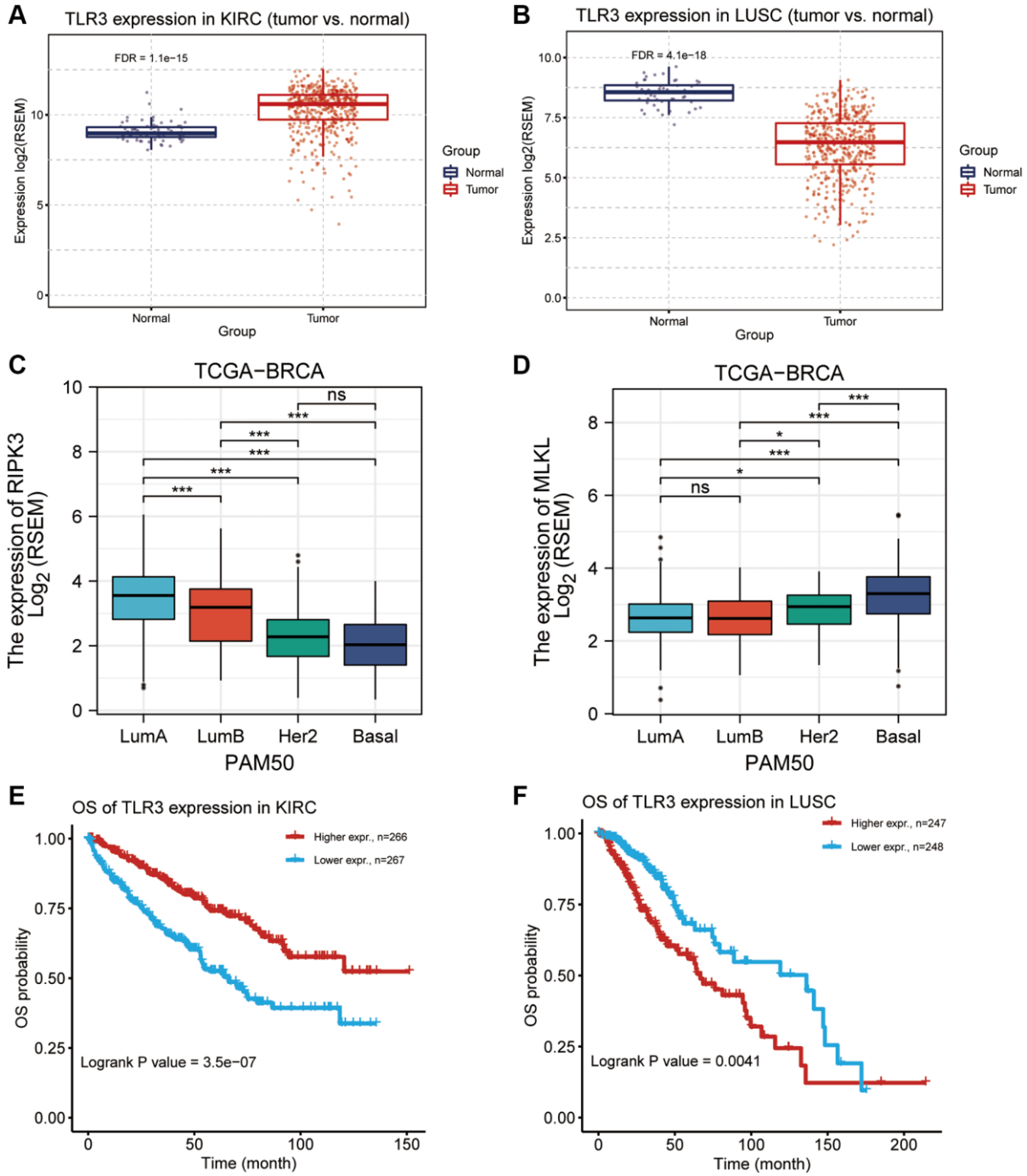
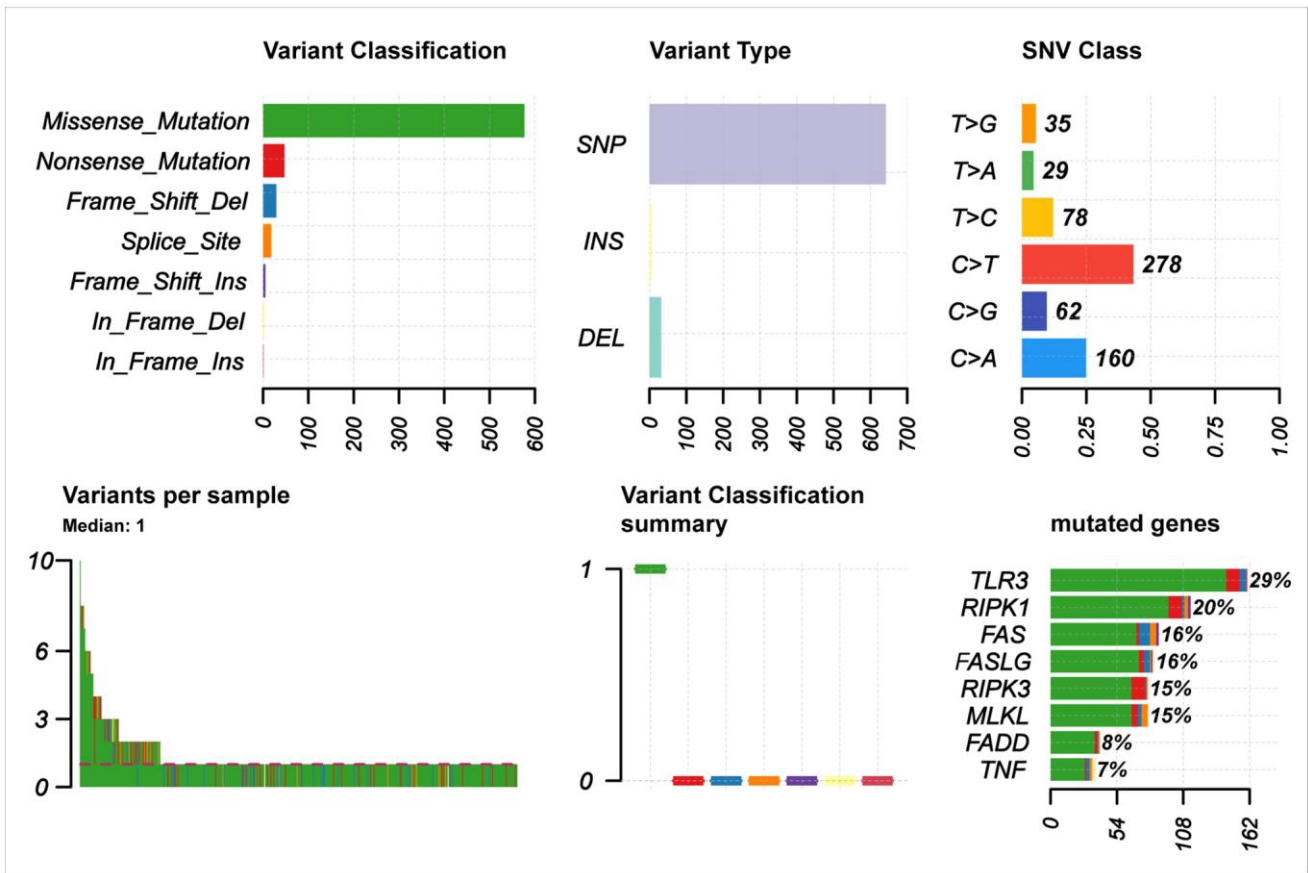


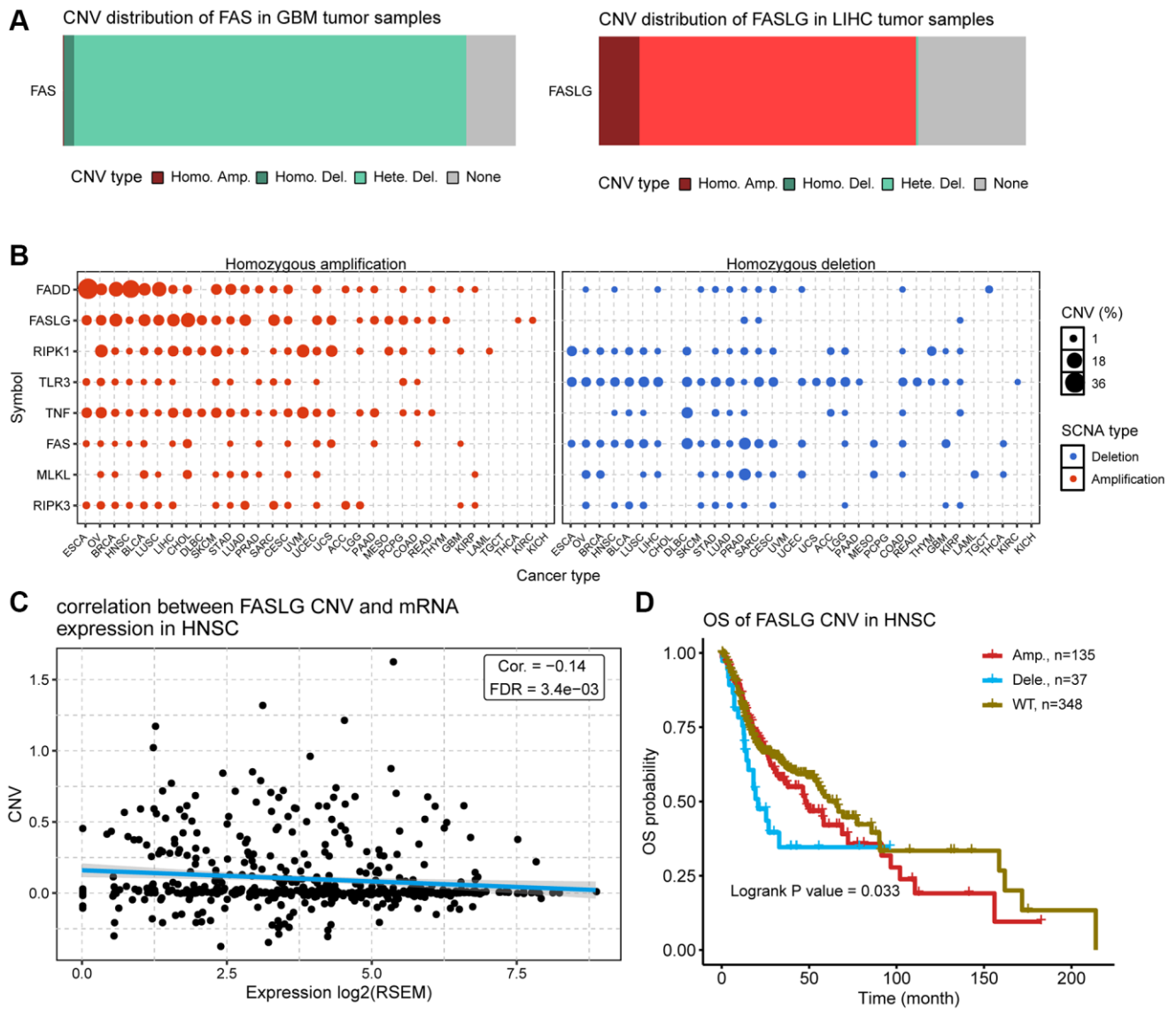
SUPPLEMENTARY FIGURES



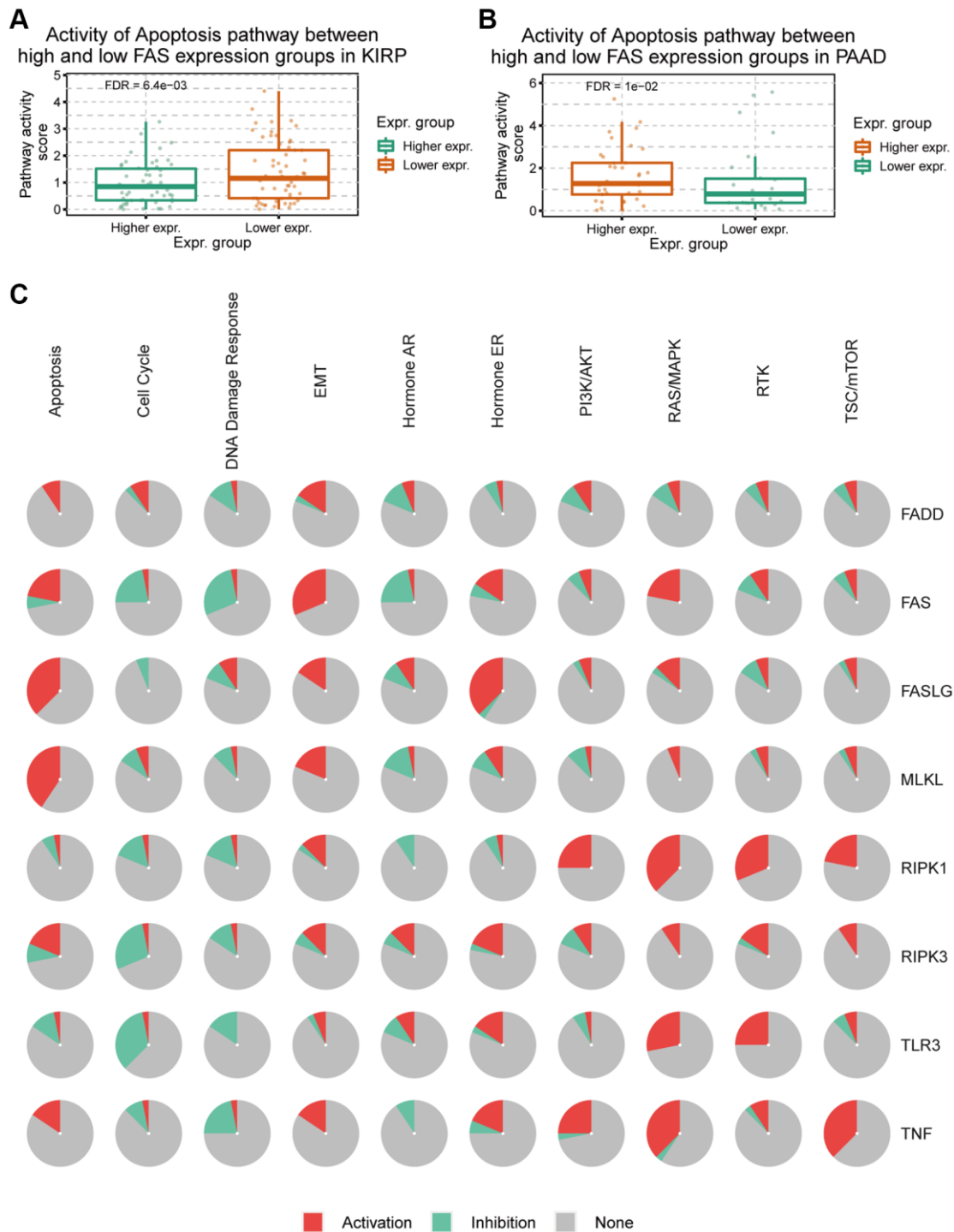
Supplementary Figure 1. (A) The differential expression of TLR3 between normal and tumor tissue in KIRC. (B) The differential expression of TLR3 between normal and tumor tissue in LUSC. (C) The expression of RIPK3 in different BRCA subtypes. (D) The expression of MLKL in different BRCA subtypes. (E) Kaplan-Meier curve between high and low expression of TLR3 in KIRC. (F) Kaplan-Meier curve between high and low expression of TLR3 in LUSC.



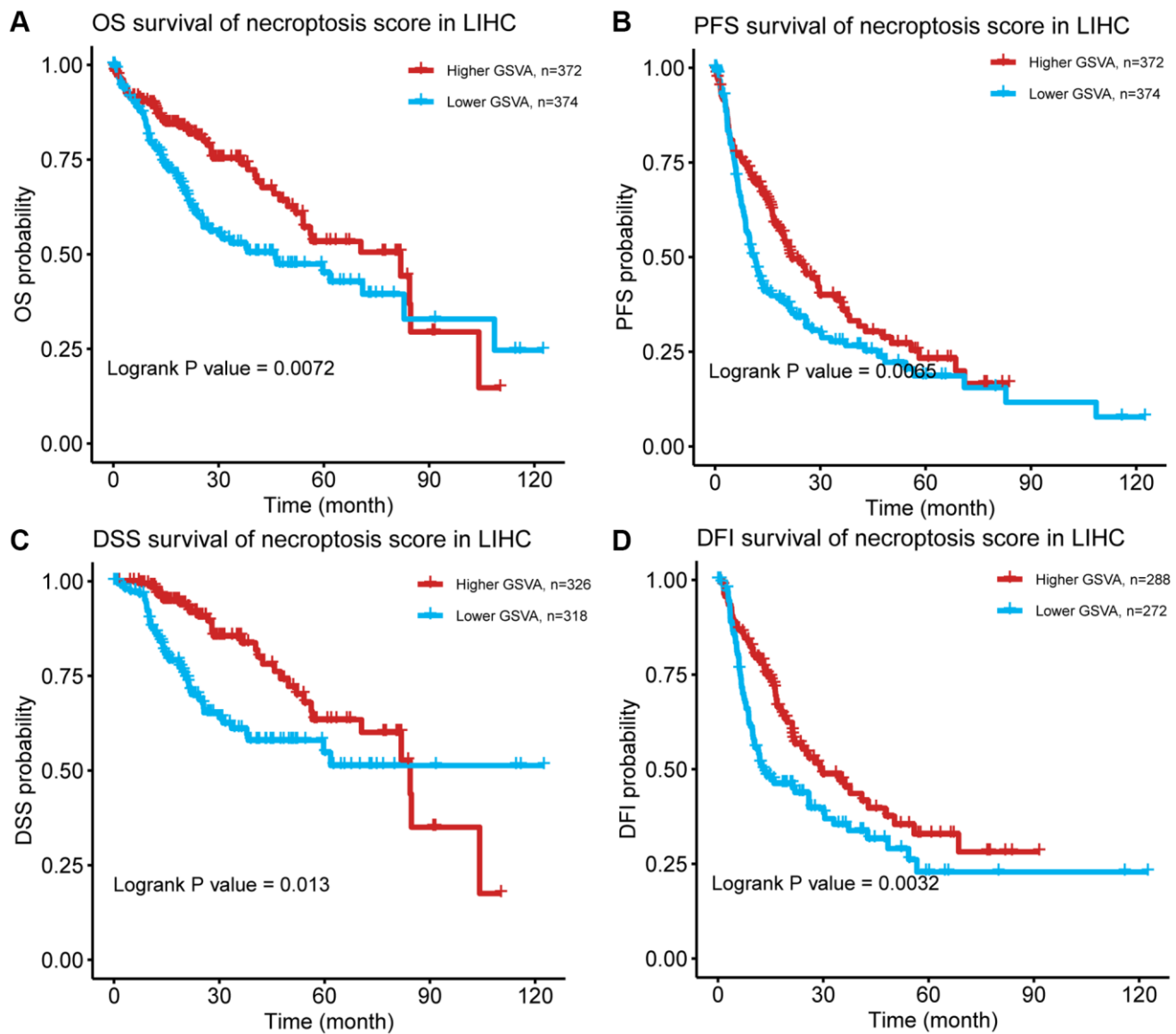
Supplementary Figure 2. SNV summary plot showing the number and types of mutations.



Supplementary Figure 3. (A) CNV type distribution of FAS in GBM and FASLG in LIHC. (B) Homozygous CNV plot showing the percentage of homozygous amplification and deletion of necroptosis-related regulators in different cancers. (C) Scatter plot showing the correlation between FASLG CNV and its mRNA expression in HNSC. (D) Kaplan-Meier curve showing the survival difference between different CNV types and wild type of FASLG in HNSC.



Supplementary Figure 4. (A) Box plot showing the difference of apoptosis pathway activity score between high and low FAS expression groups in KIRP. (B) Box plot showing the difference of apoptosis pathway activity score between high and low FAS expression groups in PAAD. (C) Pathway pie plot showing the global percentage of cancer types in which the specific necroptosis-related regulator has an effect on the specific pathway in pan-cancer.



Supplementary Figure 5. Kaplan-Meier curve showing the survival difference between high and low necroptosis score in LIHC, including OS (A), PFS (B), DSS (C) and DFI (D).