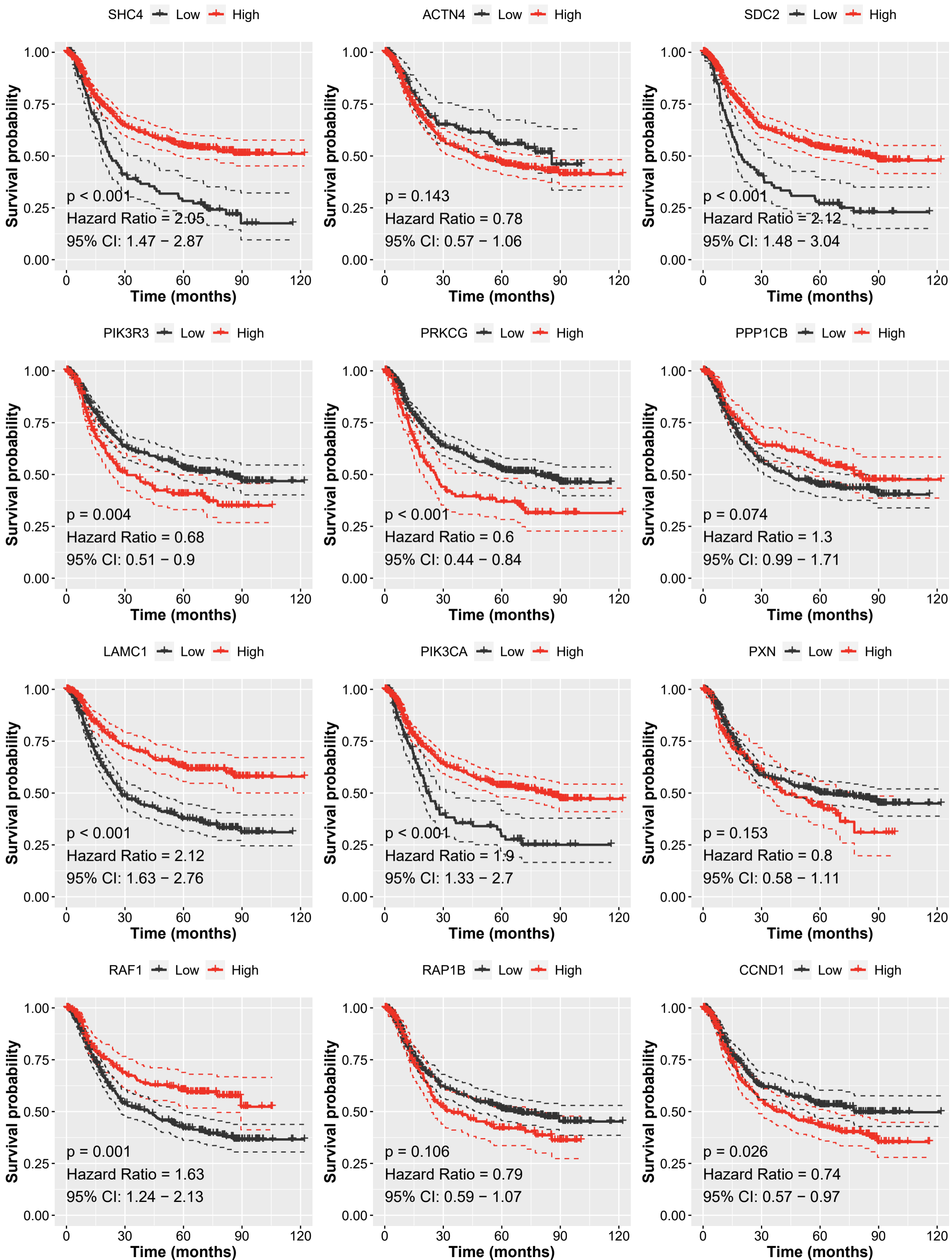
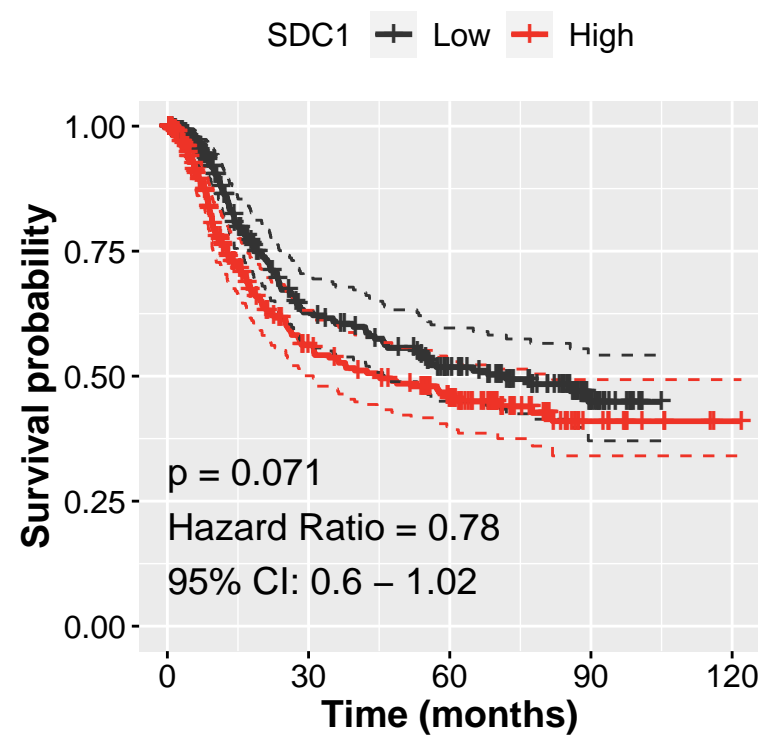
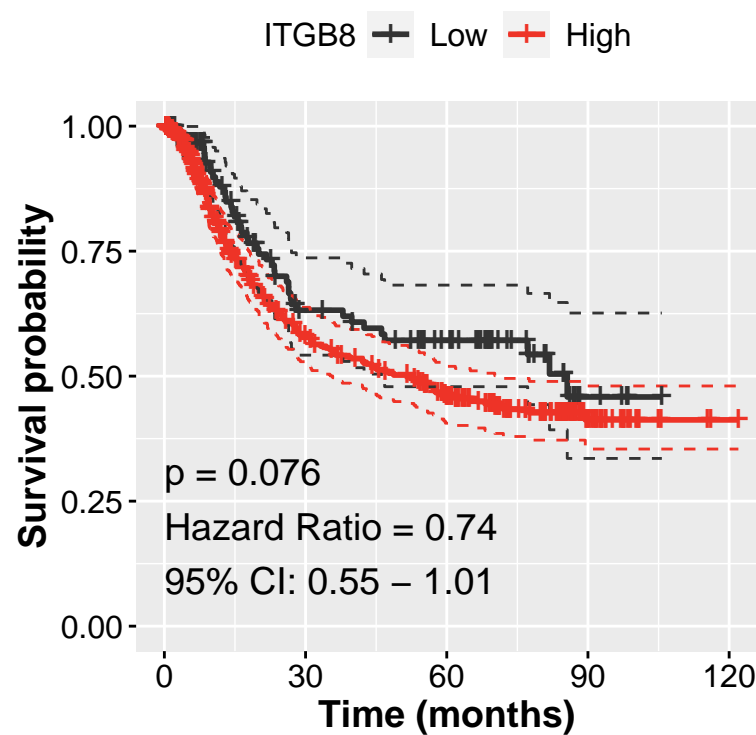
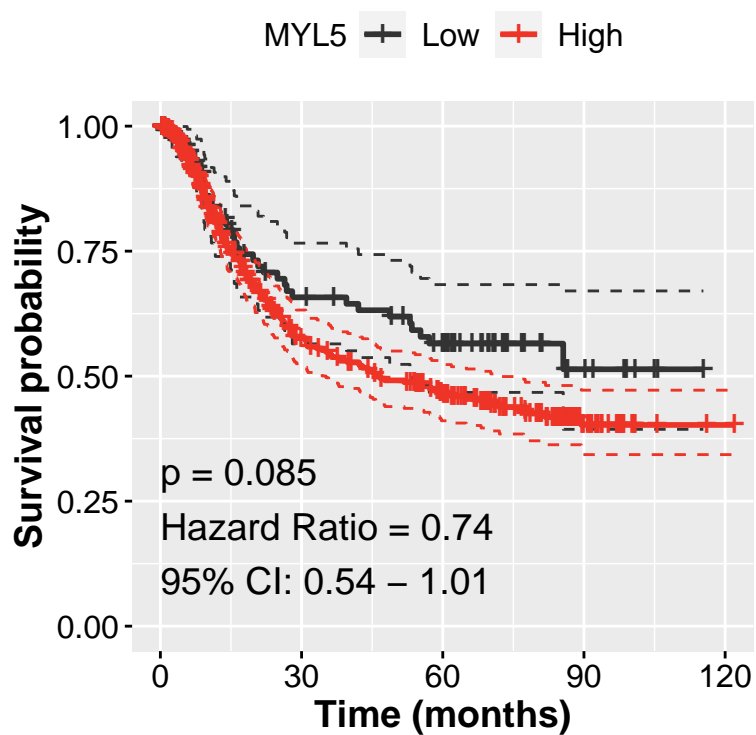
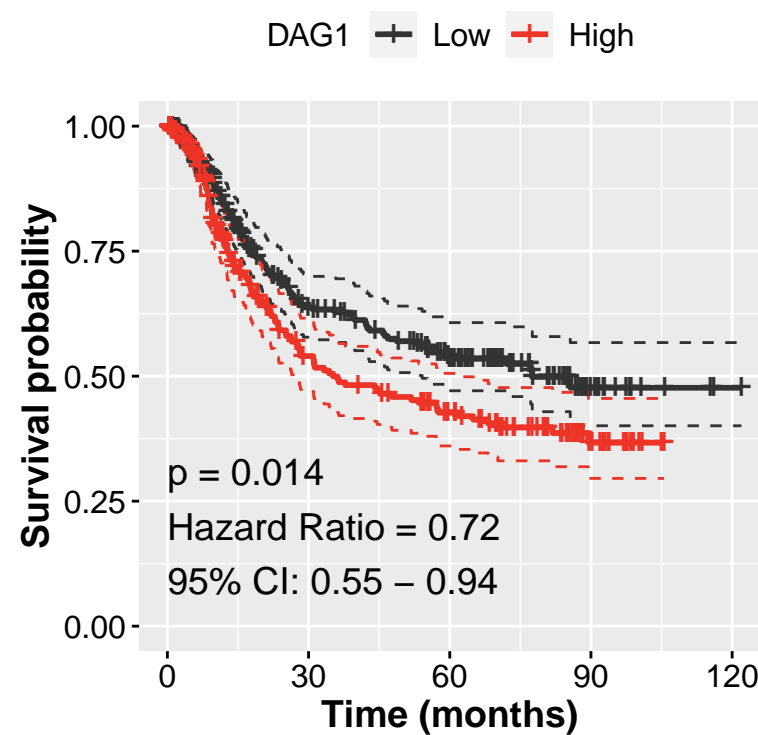
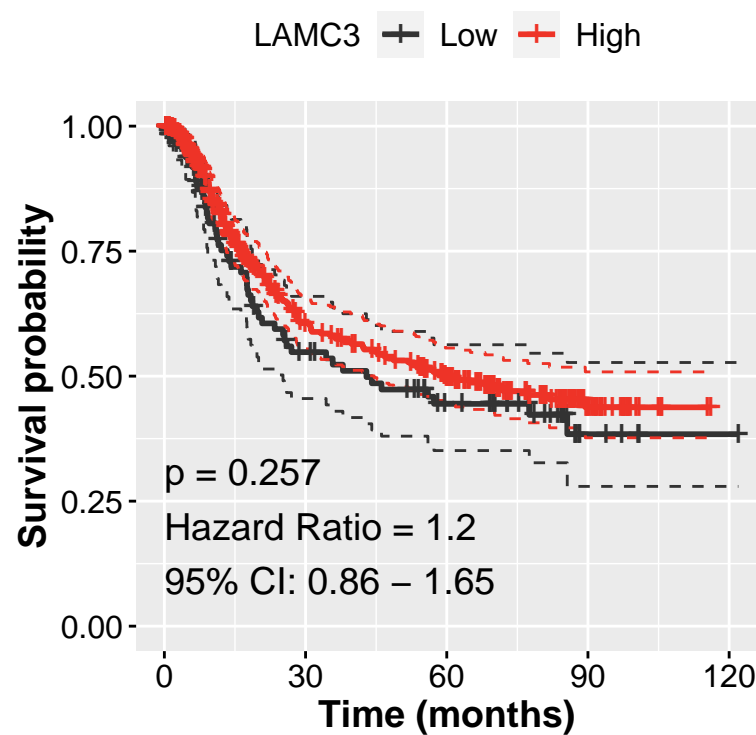
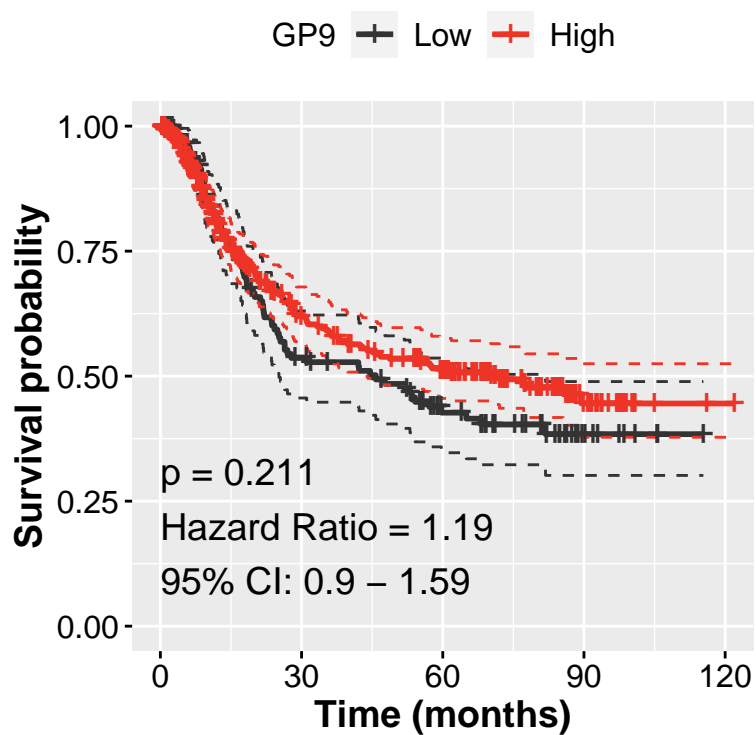
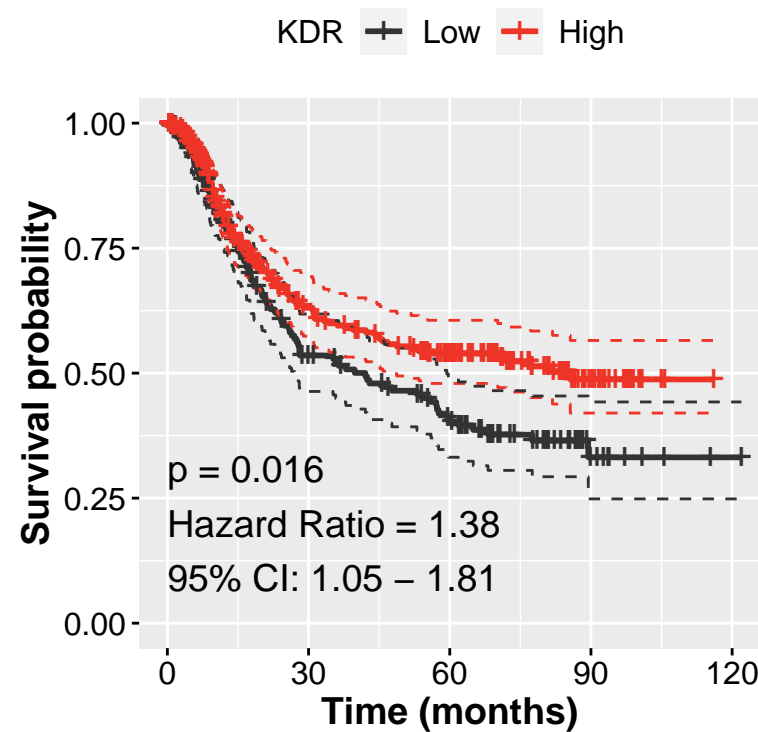
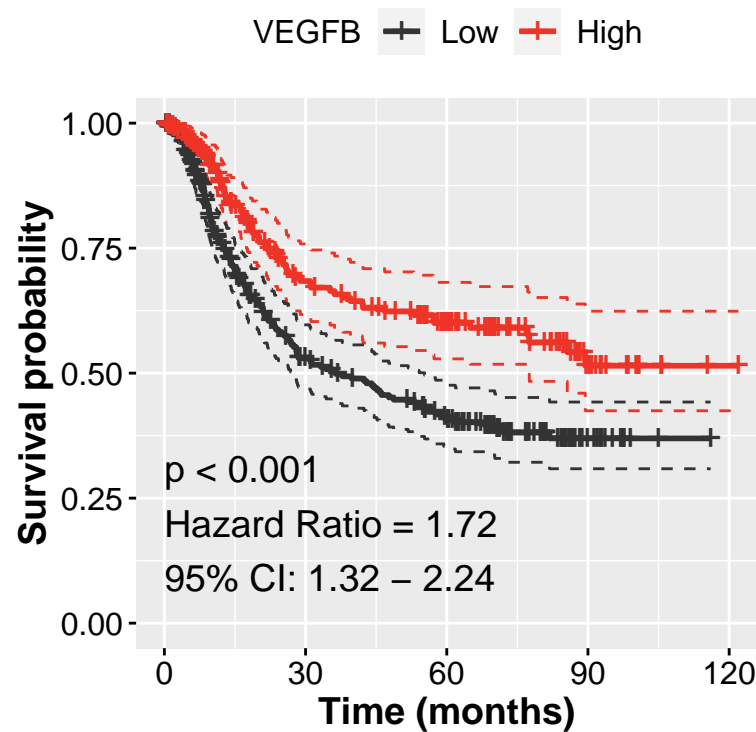
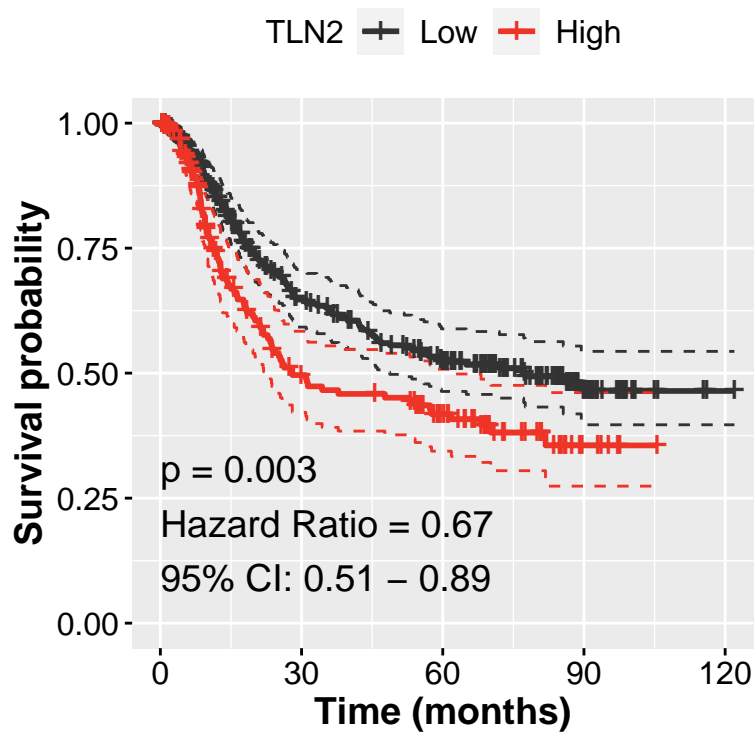
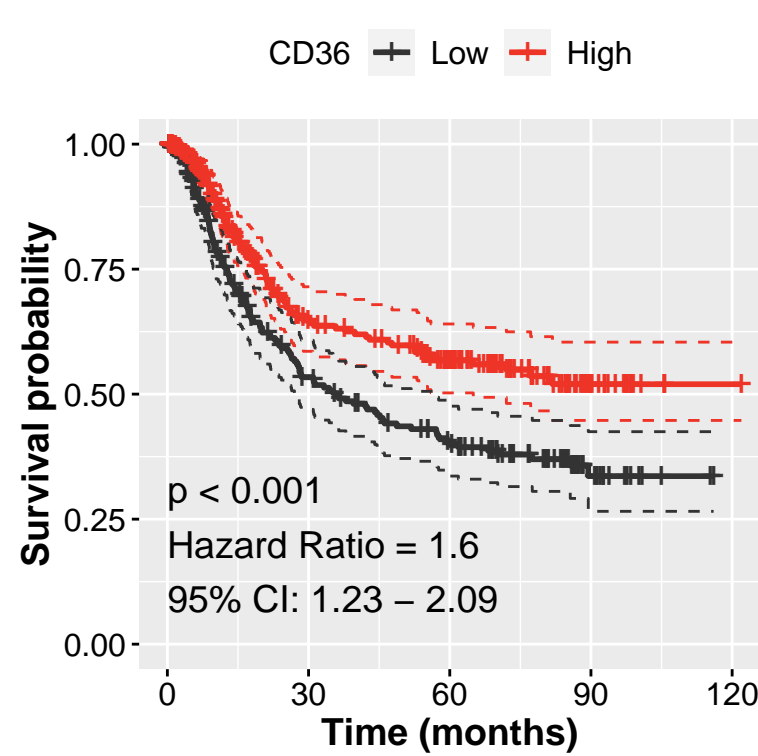
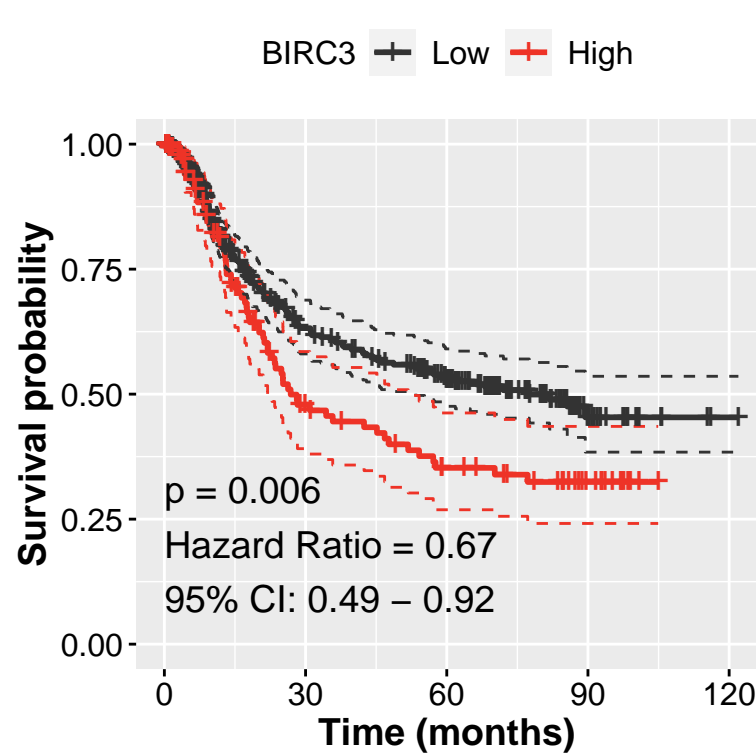
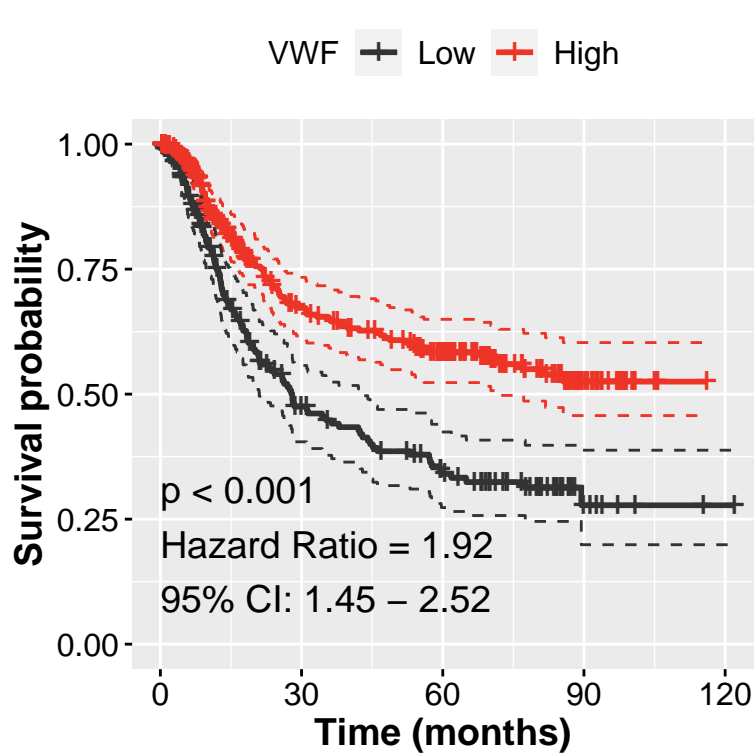
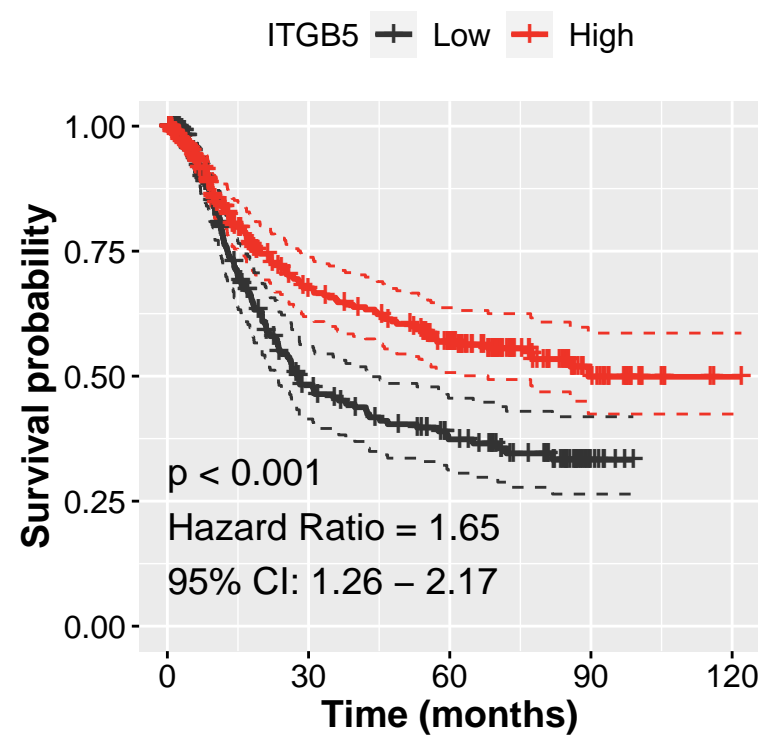
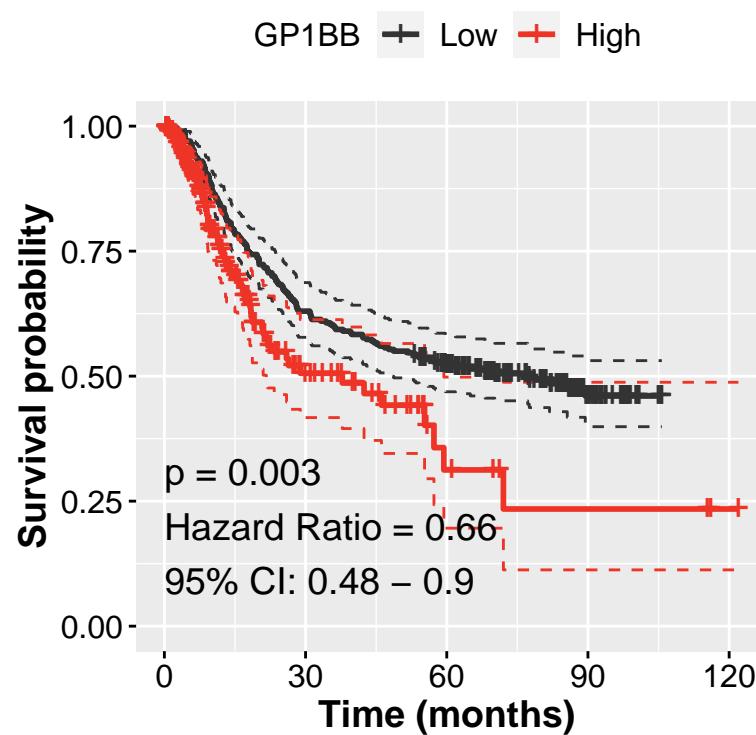
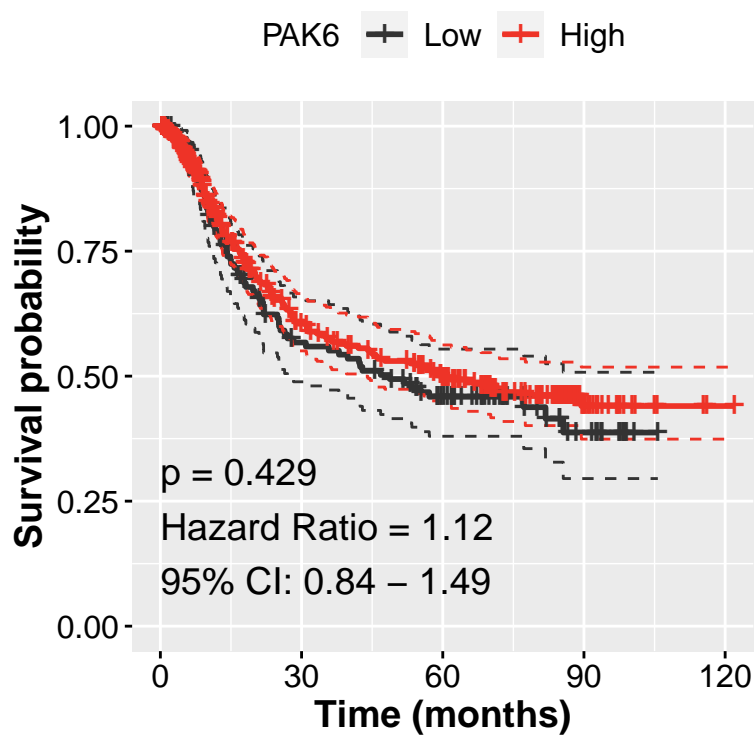
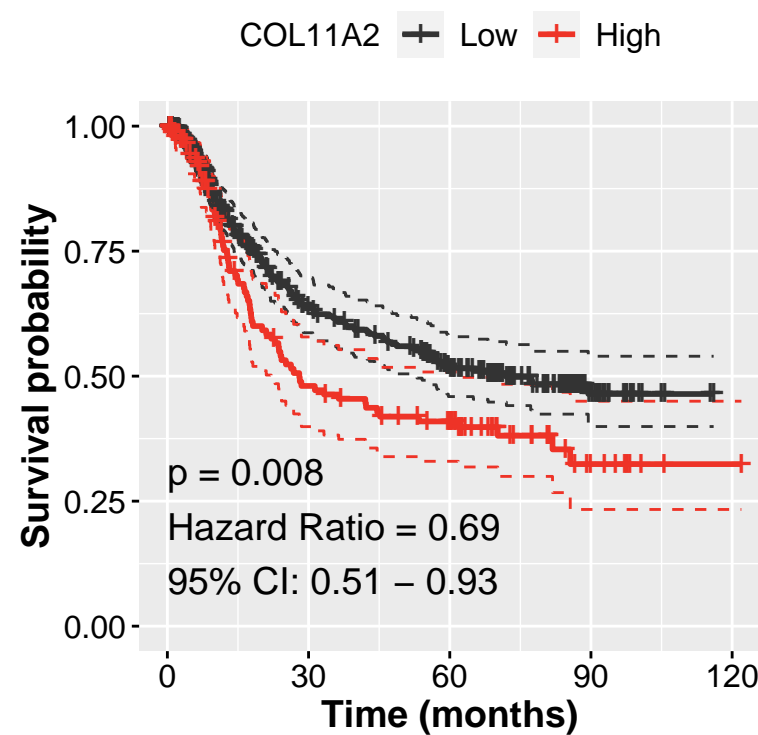
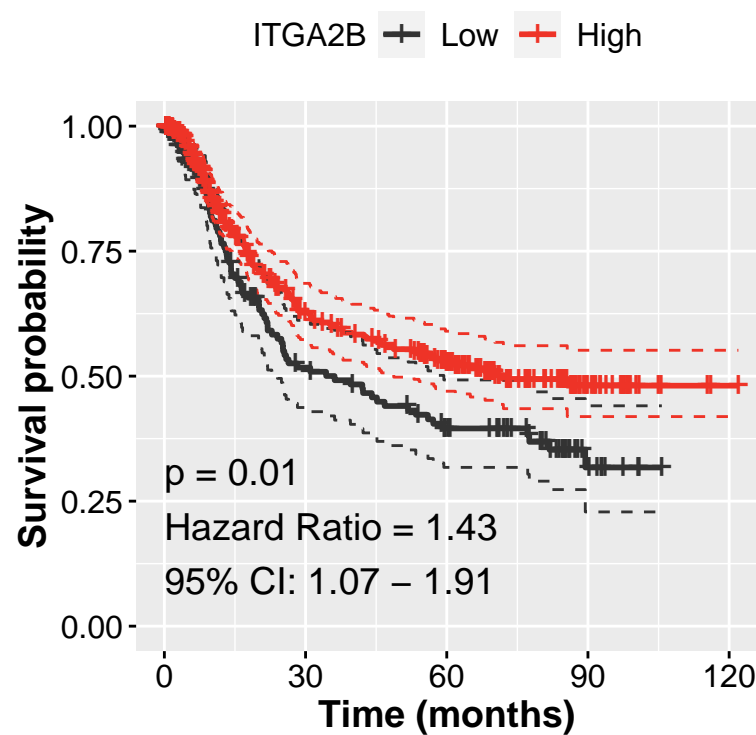
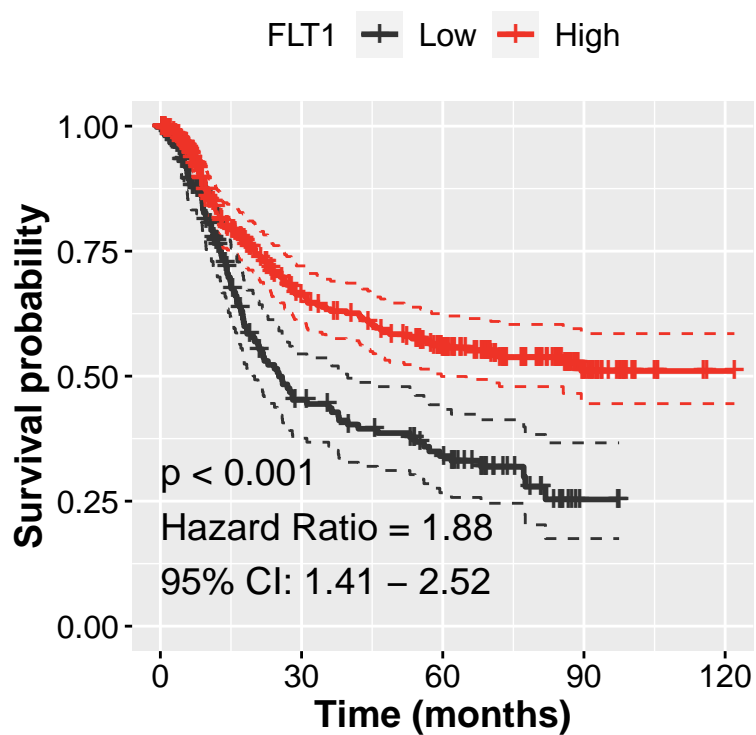
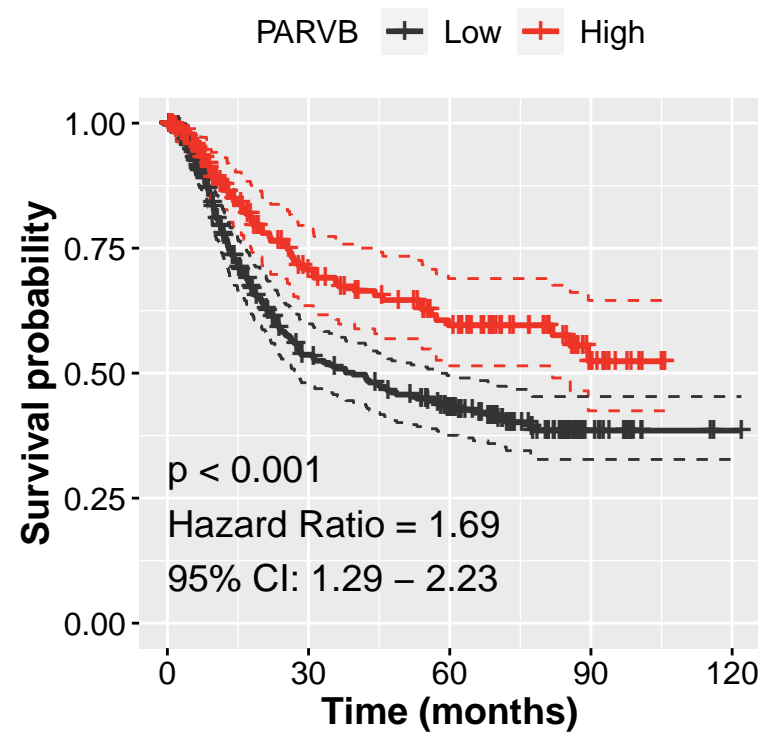
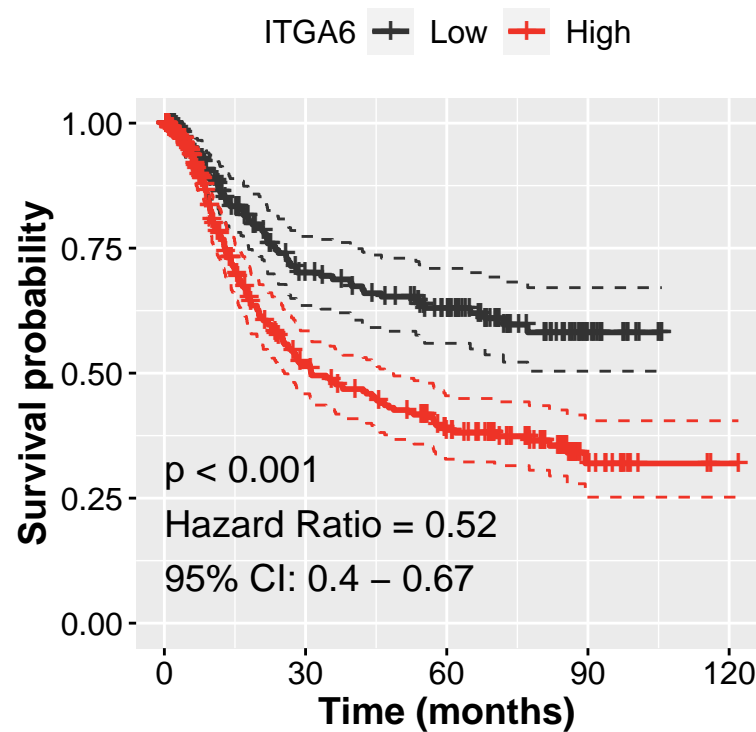
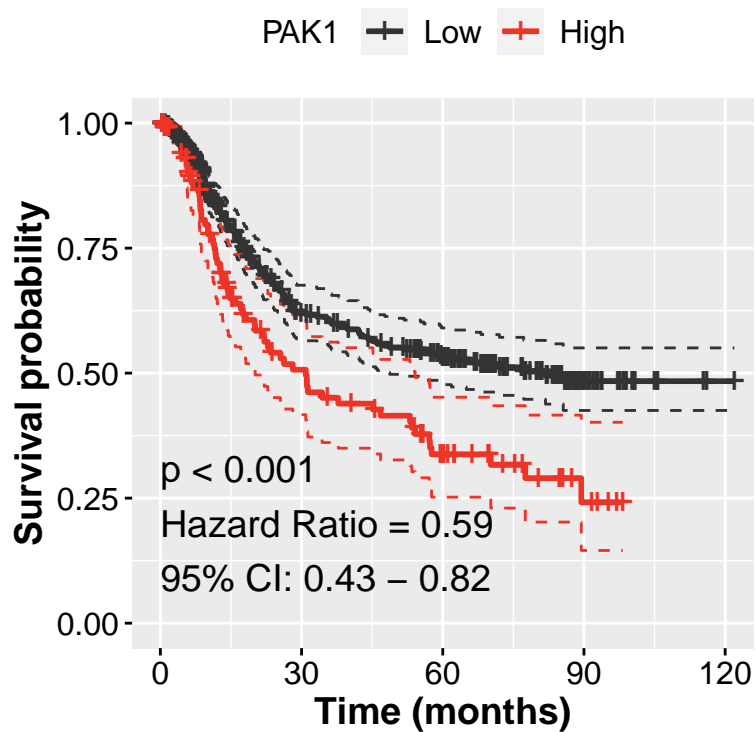
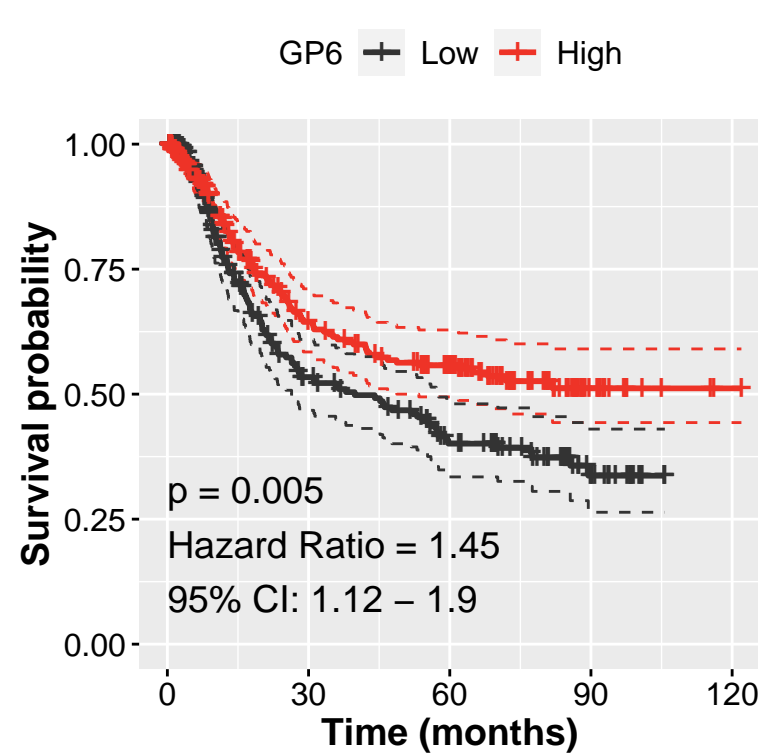
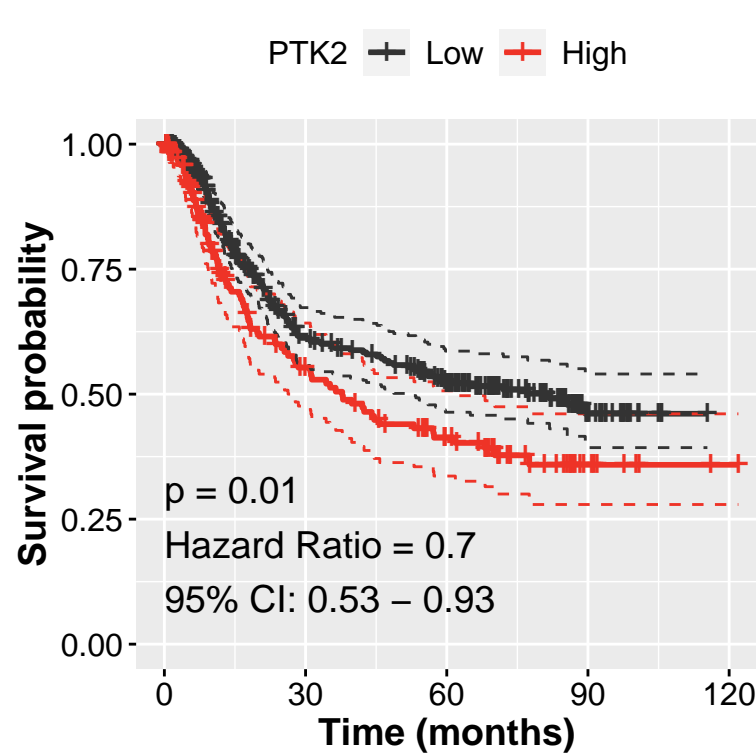
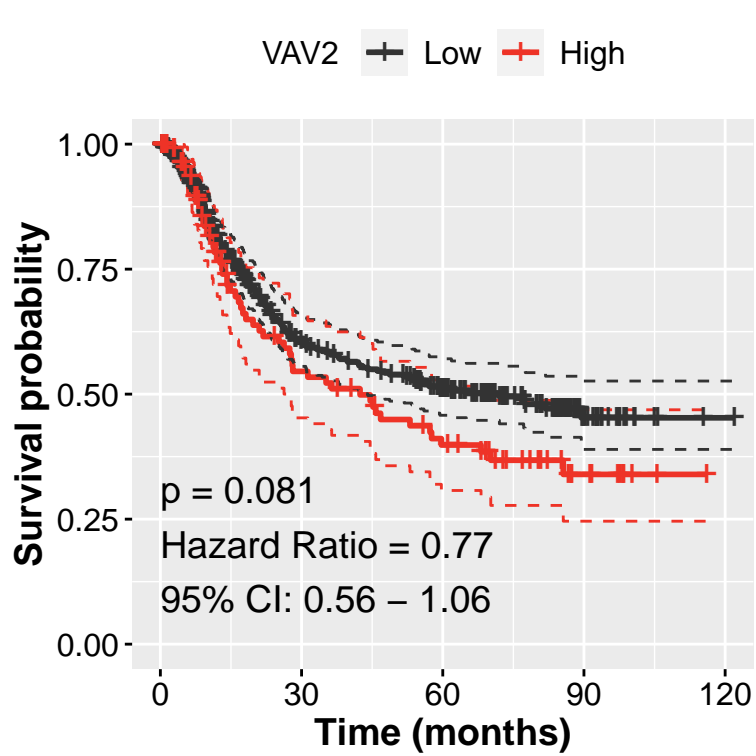


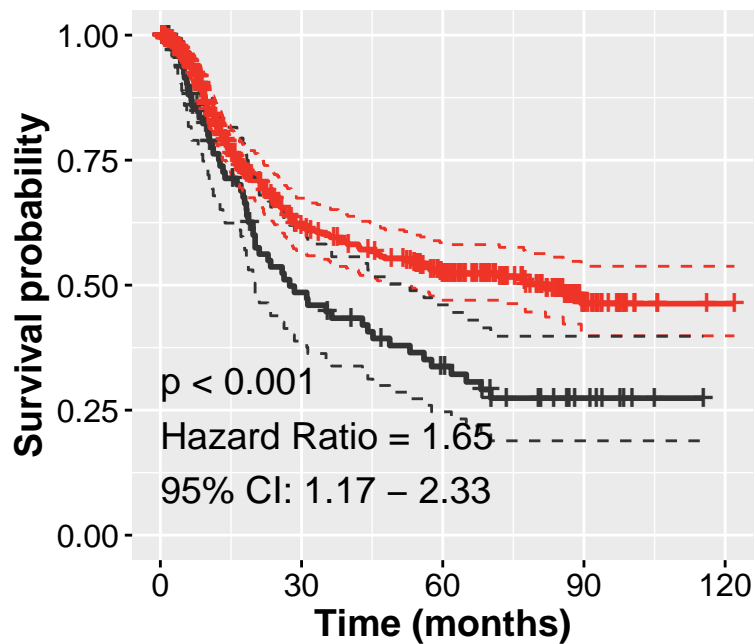
Figure S1. K-M plot showing the prognostic value of 46 selected genes.



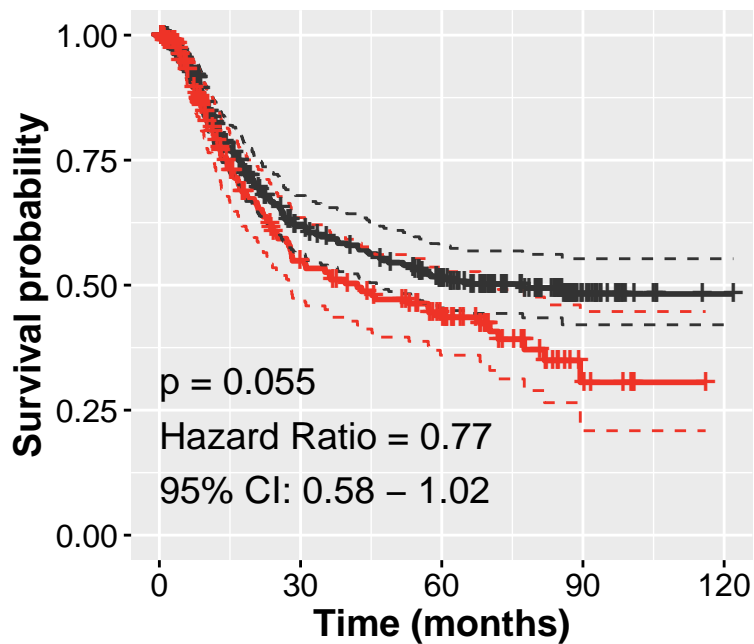




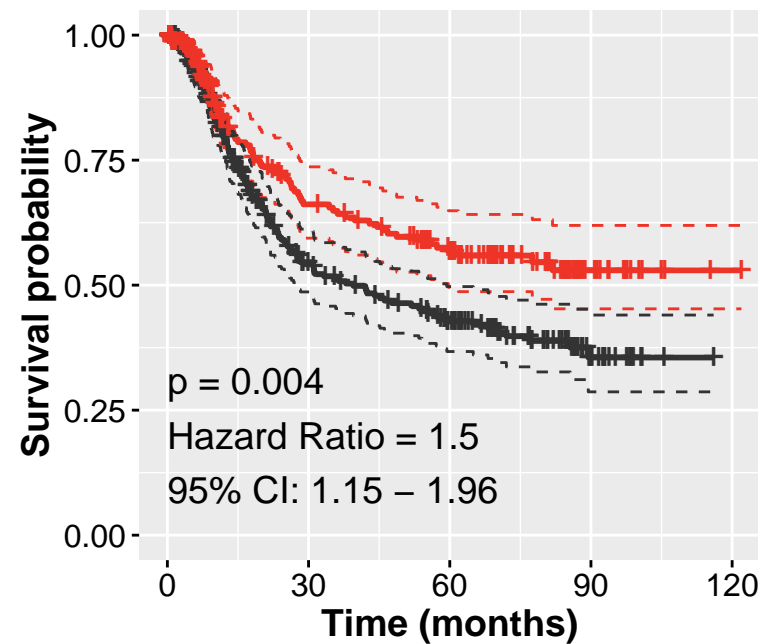
ITGA8 + Low + High



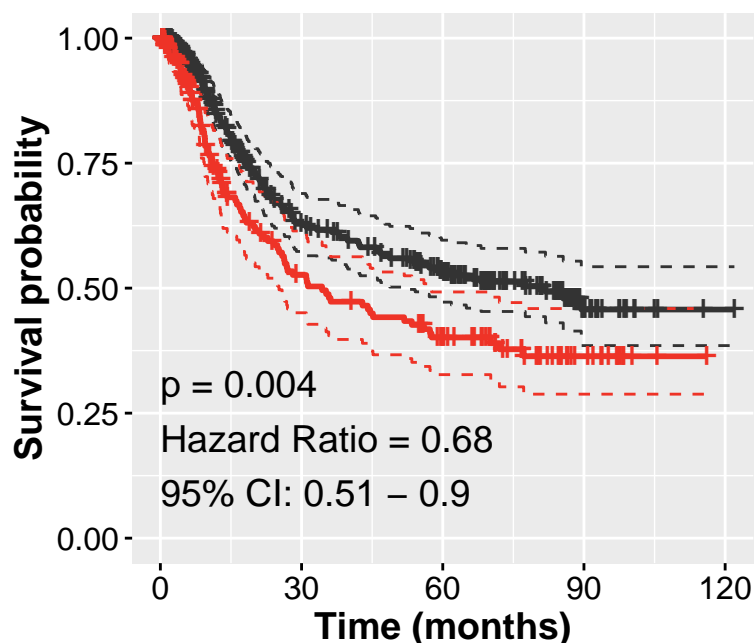
VAV3 + Low + High



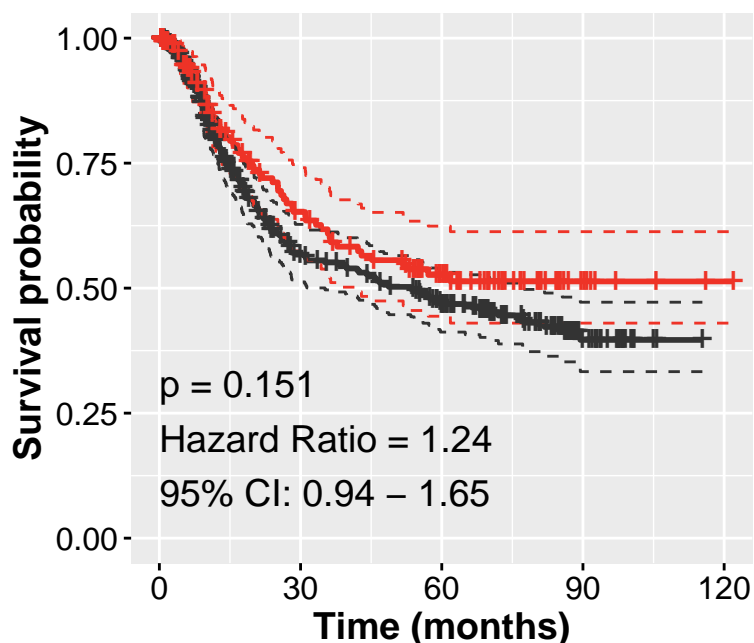
ROCK2 + Low + High



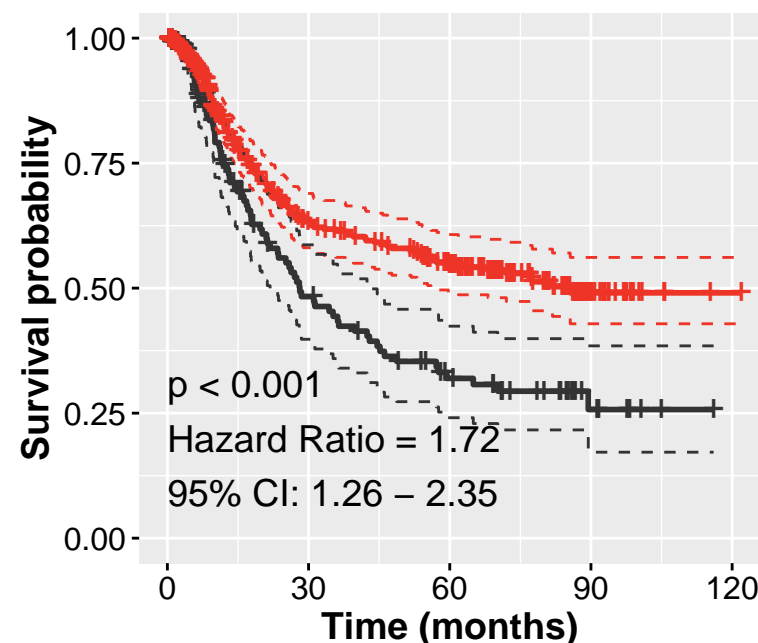
PIK3CB + Low + High



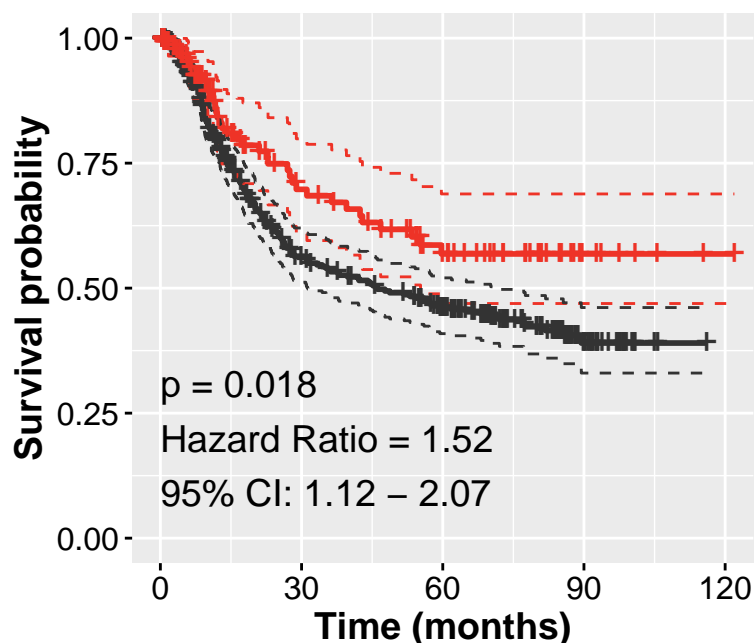
CTNNB1 + Low + High



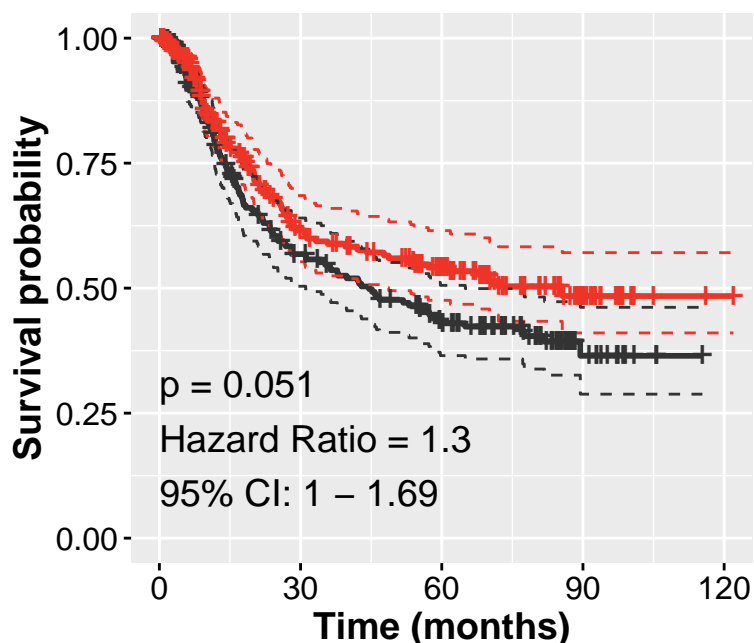
TNN + Low + High



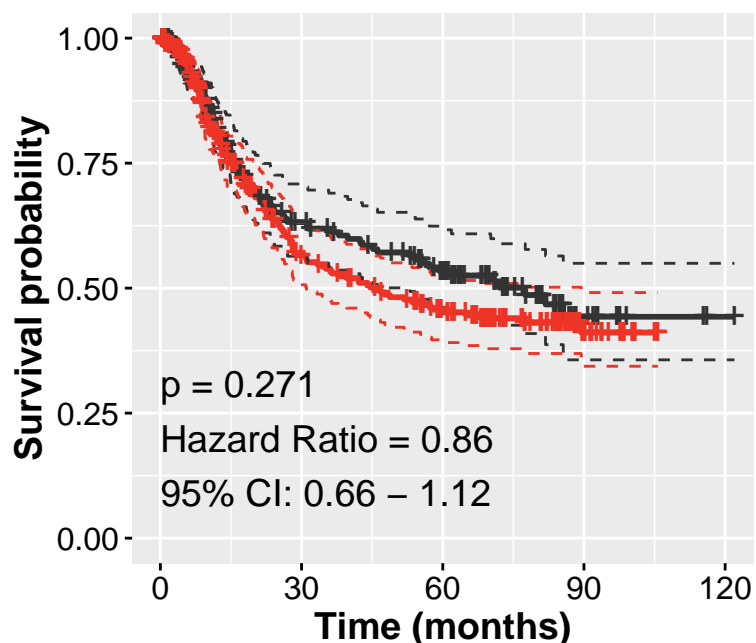
EGF + Low + High



ITGA11 + Low + High



RAPGEF1 + Low + High



SHC3 + Low + High

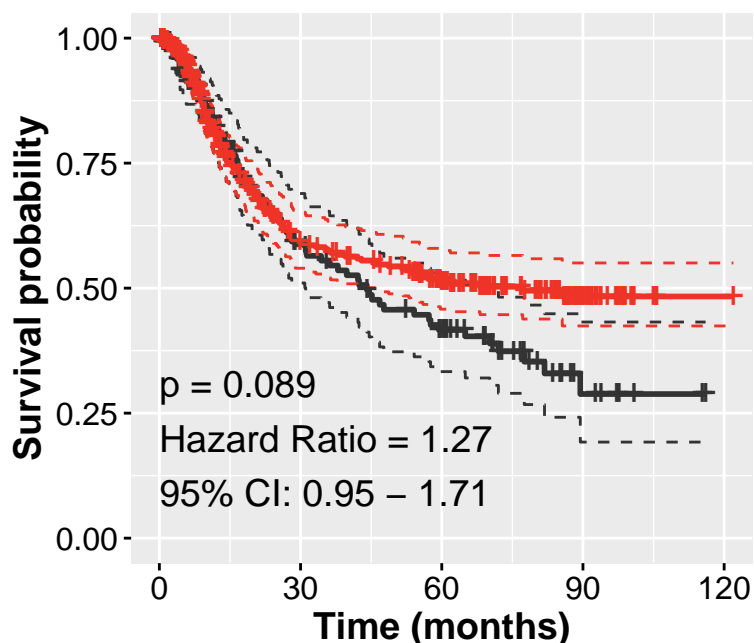


Figure S2. Subgroup analysis by clinical features to assess the prognostic value of the signature.

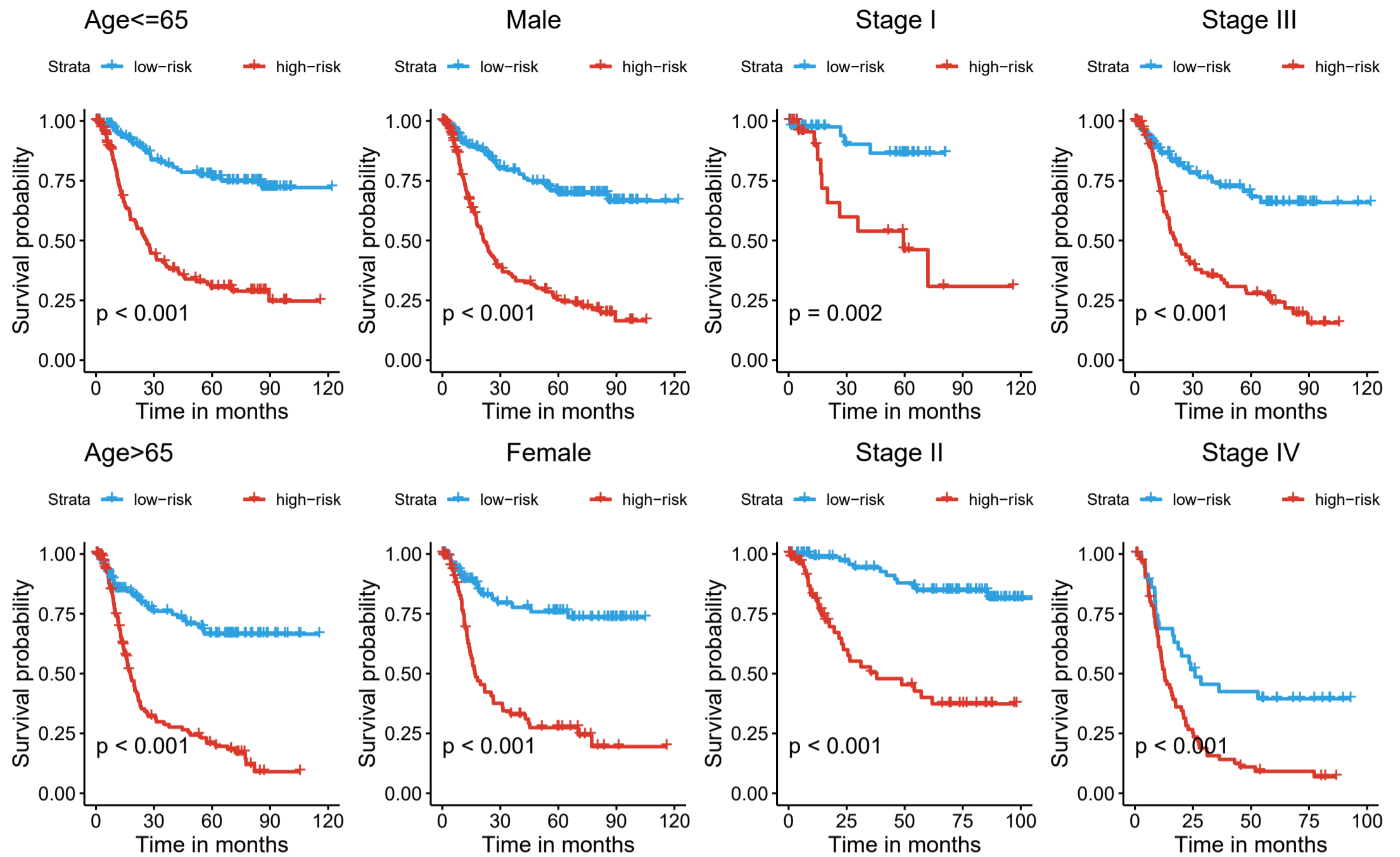


Figure S3. Extracellular matrix pathways positively associated with the infiltration of dendritic cells.

