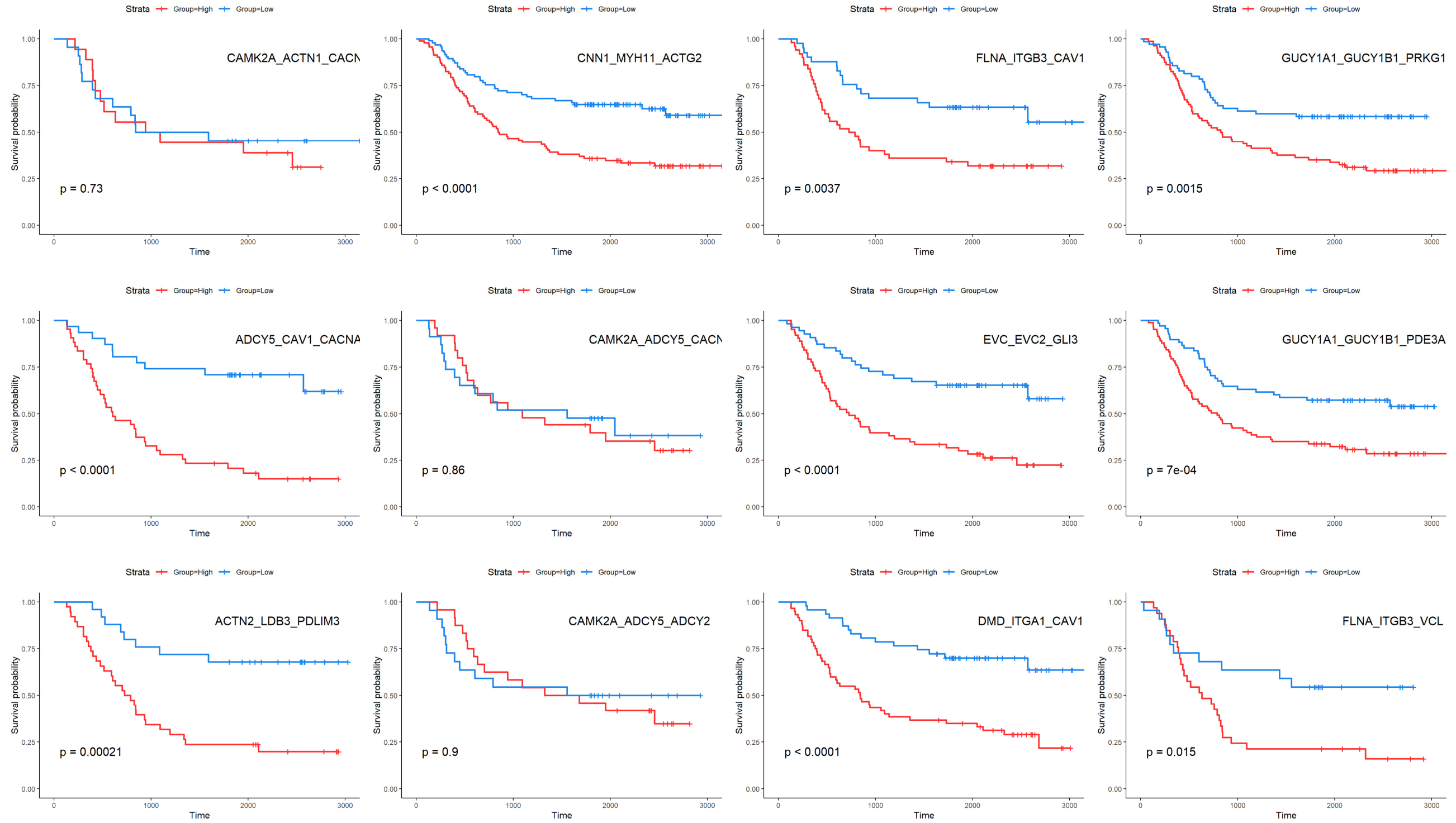
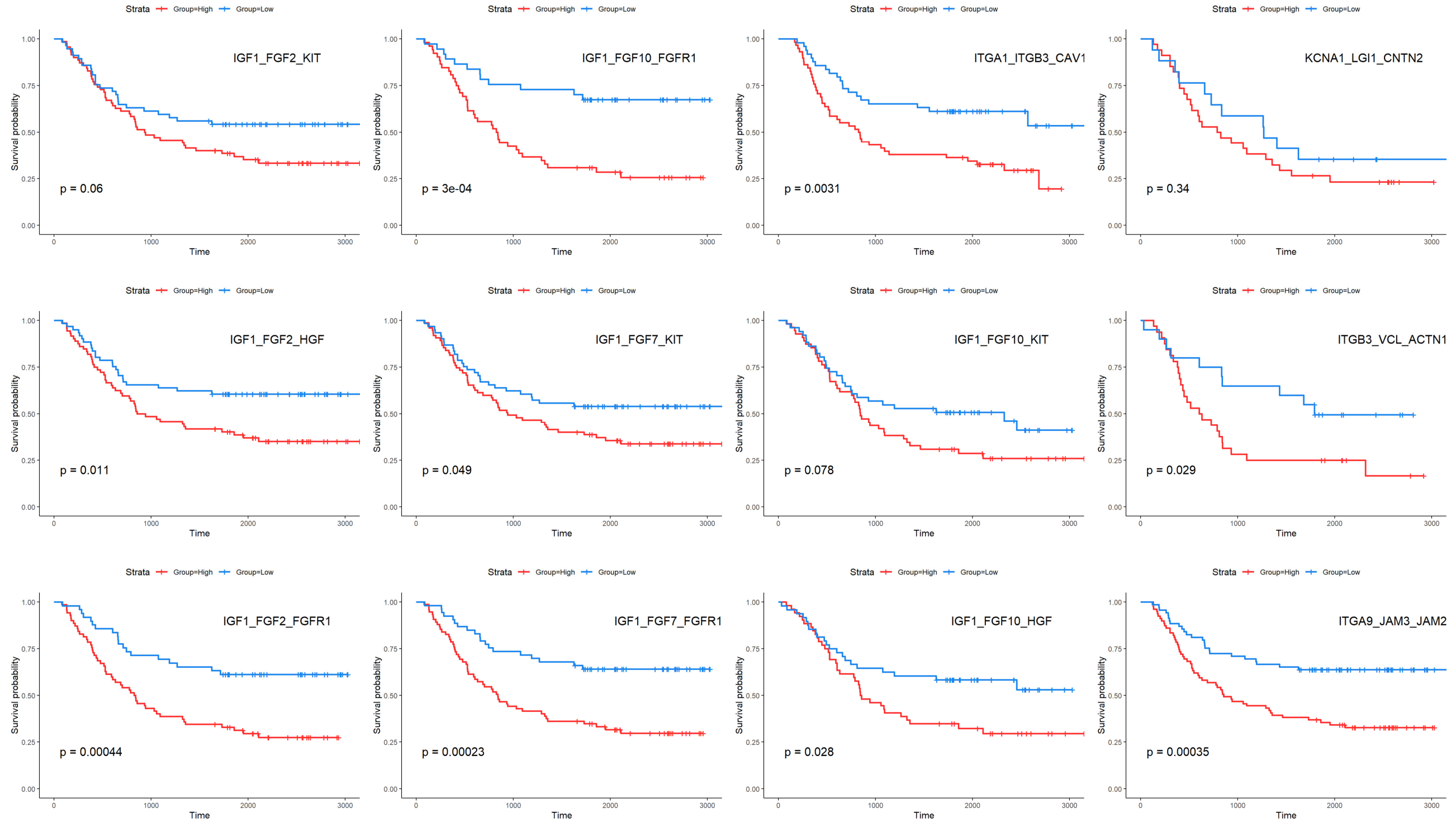
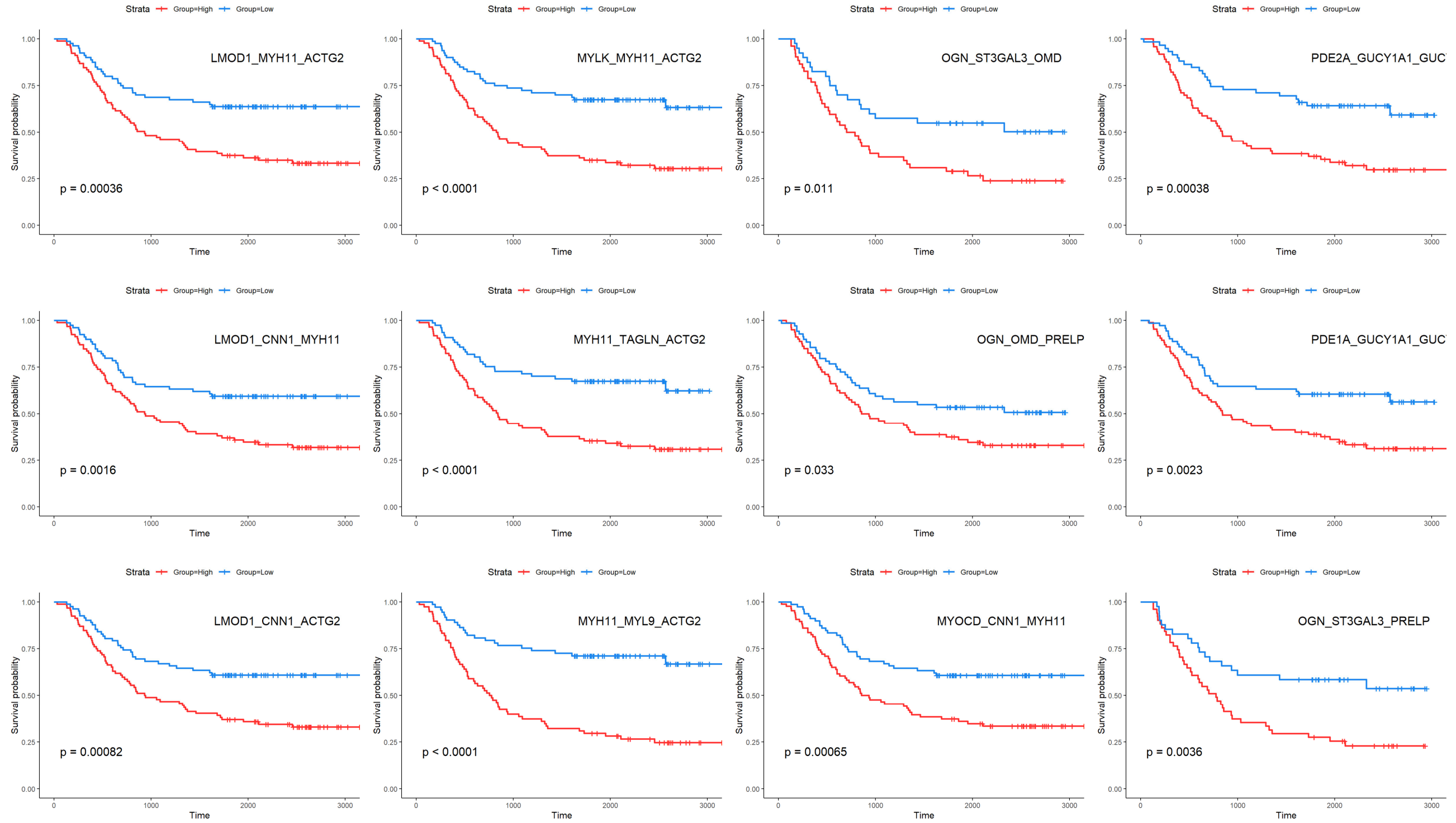


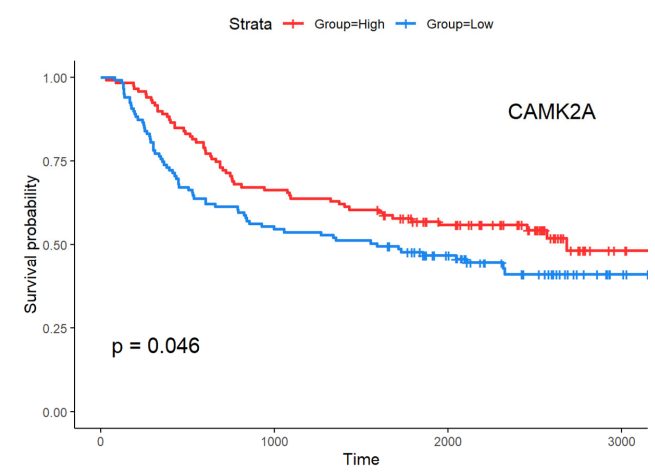
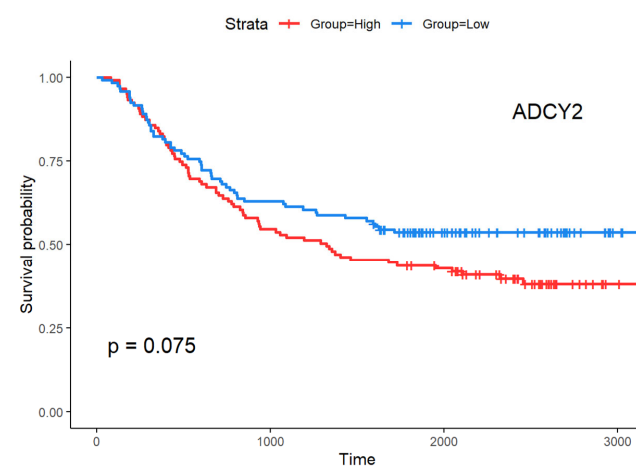
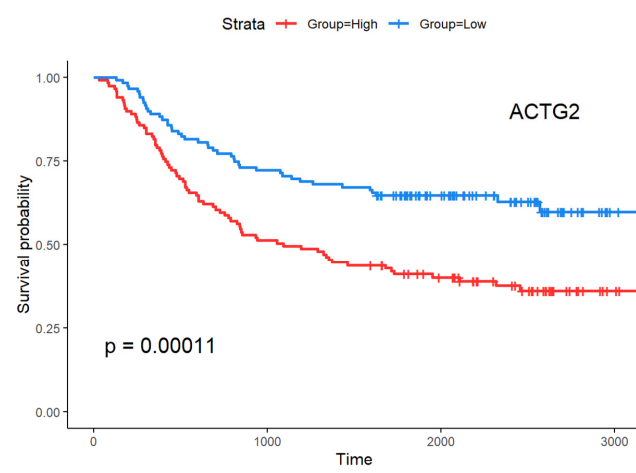
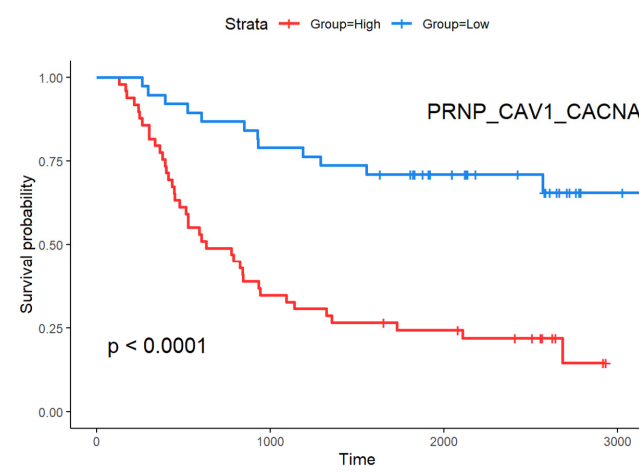
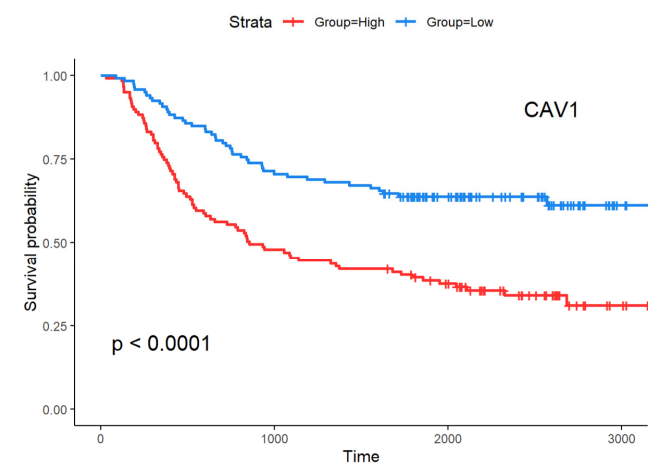
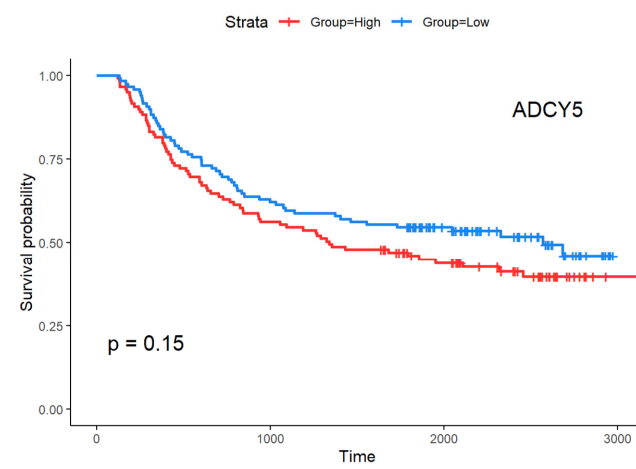
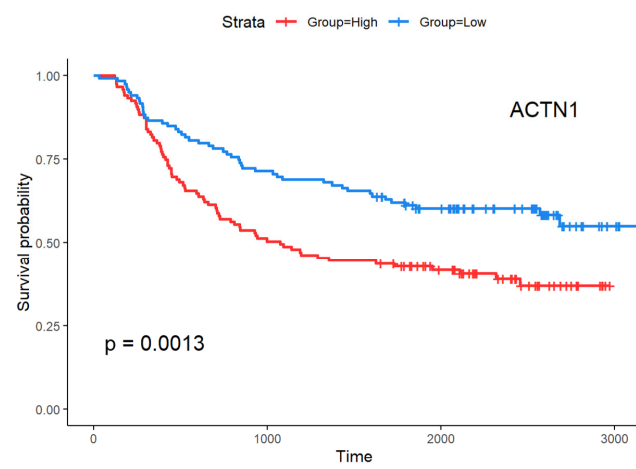
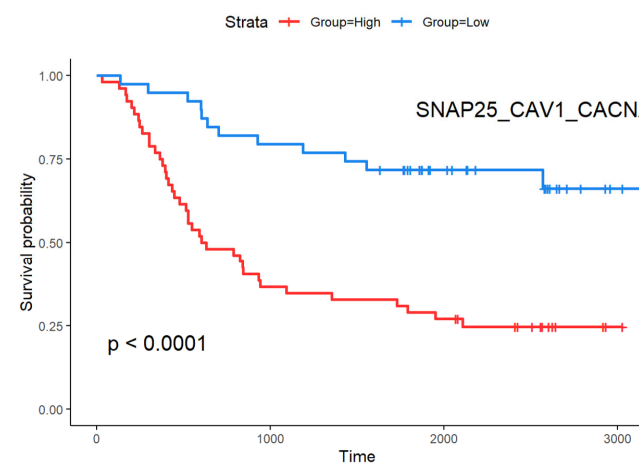
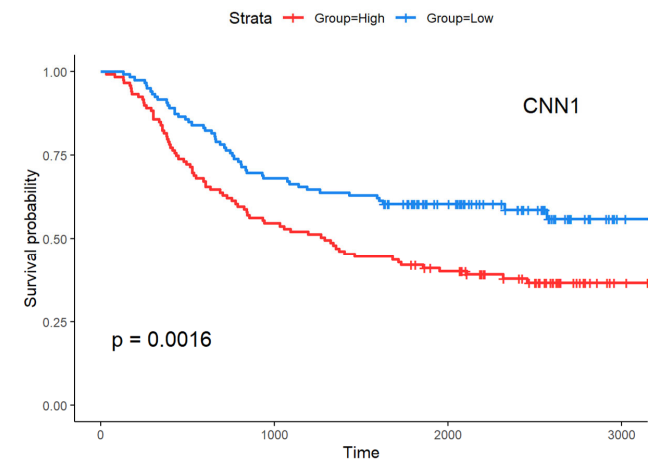
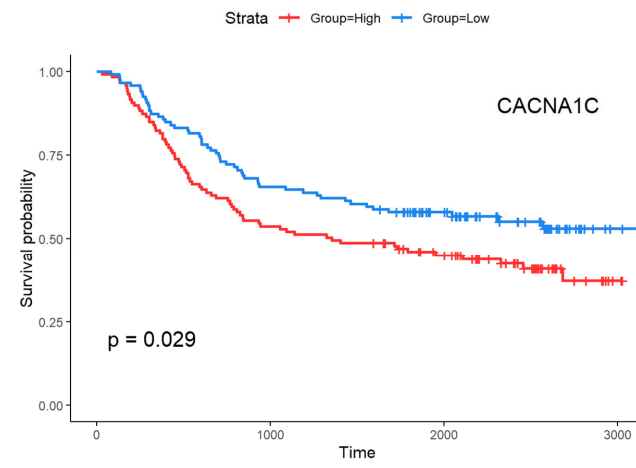
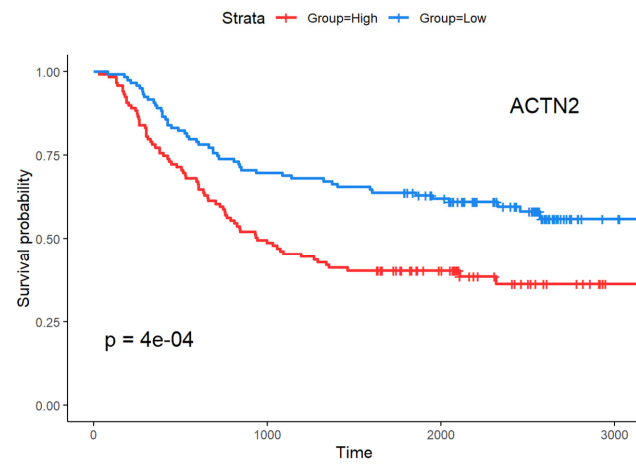
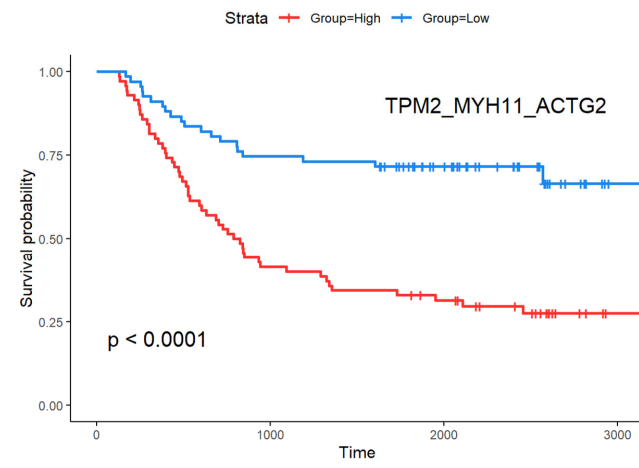
**Supplementary Figure S4 Kaplan-Meier survival curves of TCGA cohort for all of the top-scoring three-membered motifs as well as each member of the motifs in isolation.** For motif members, the 'High' and 'Low' groups represent the top and bottom 40% of the samples in terms of the expression of the respective genes. For the whole motifs, the intersection of the samples among the top 40% of samples and the bottom 40% of samples based on the expression of each of the three members of the respective motifs was used to form 'High' and 'low' groups

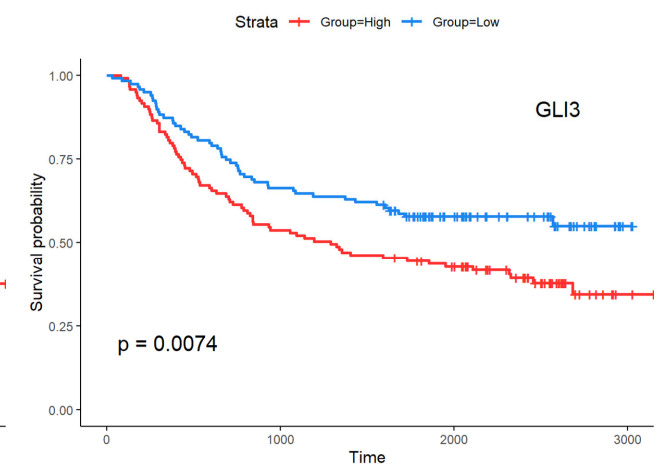
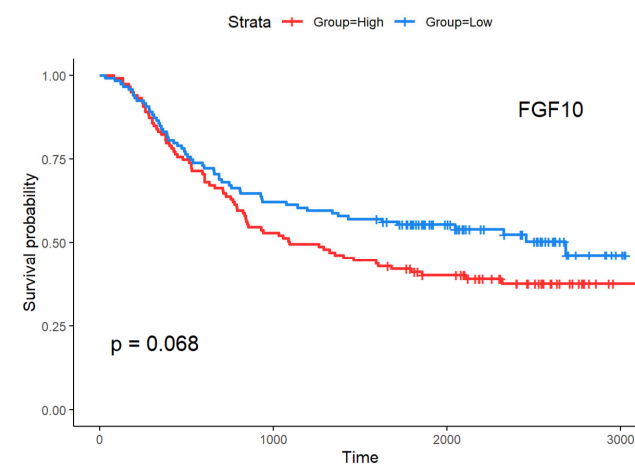
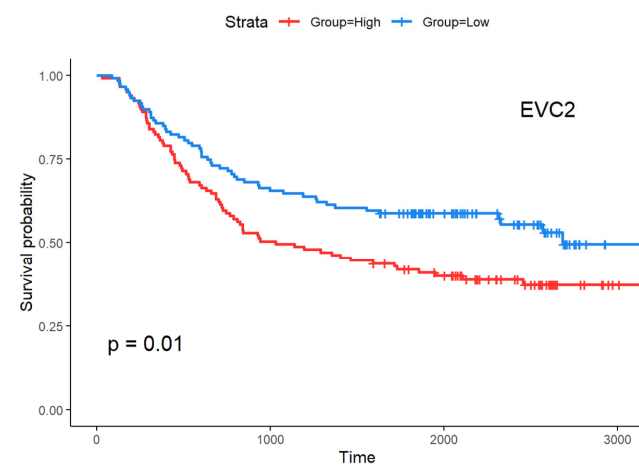
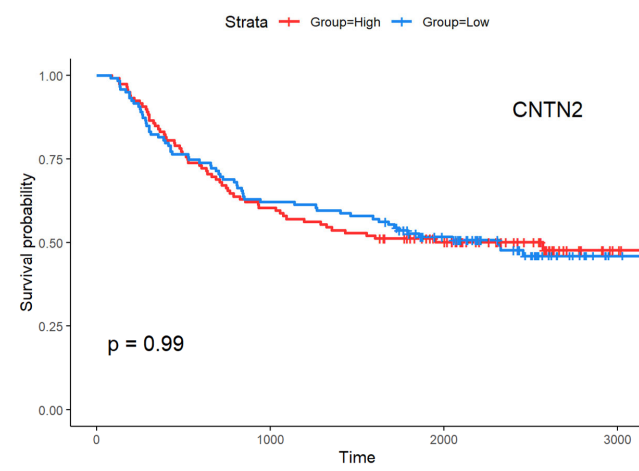
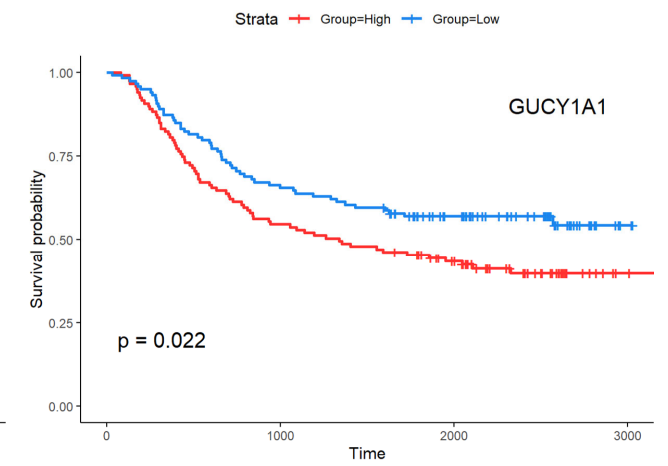
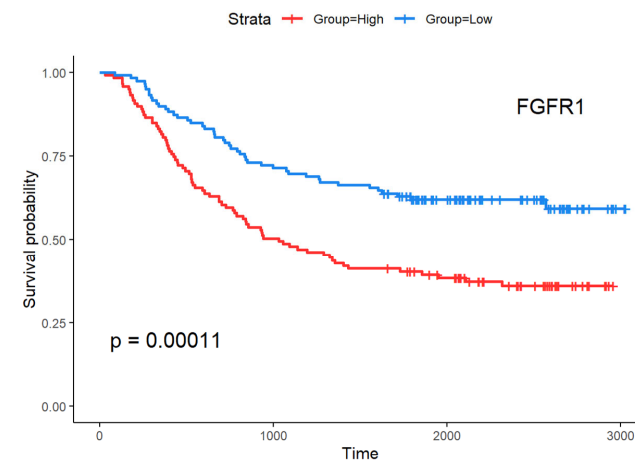
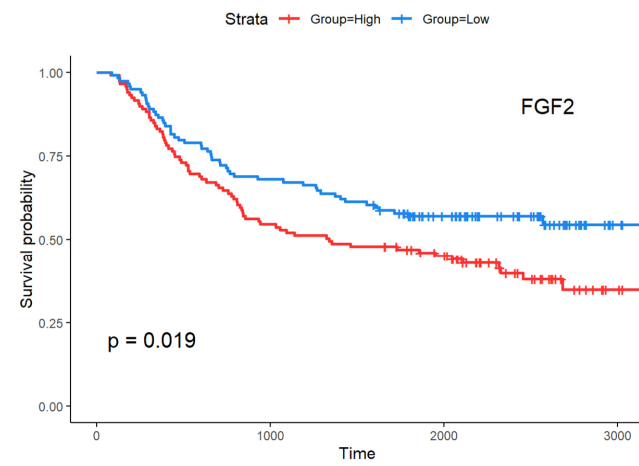
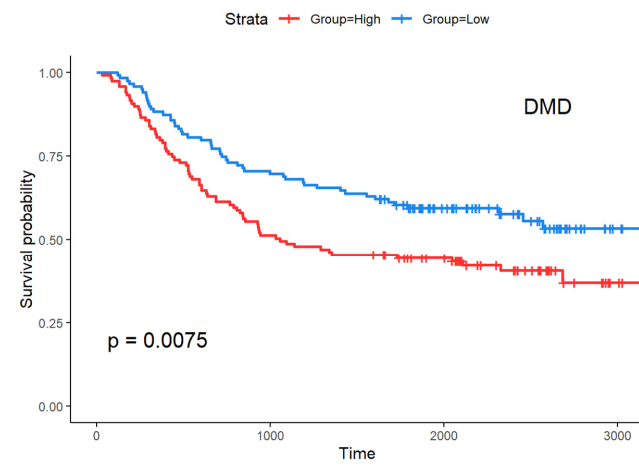
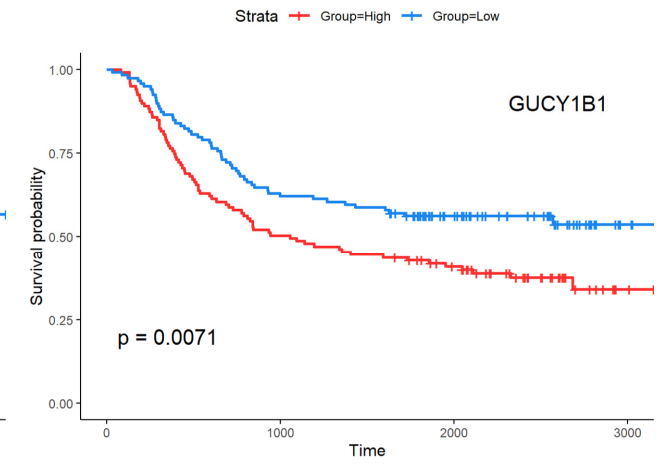
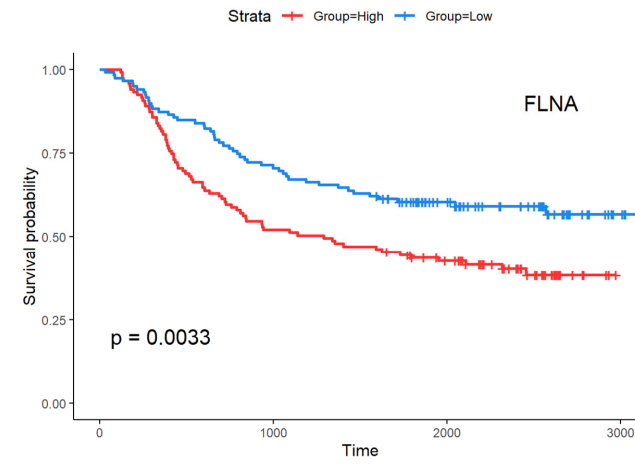
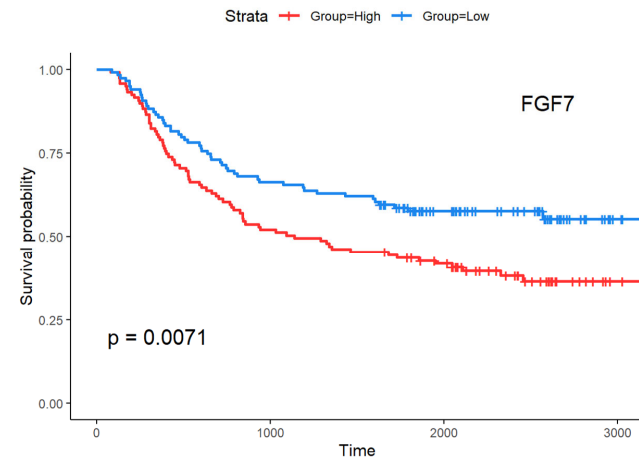
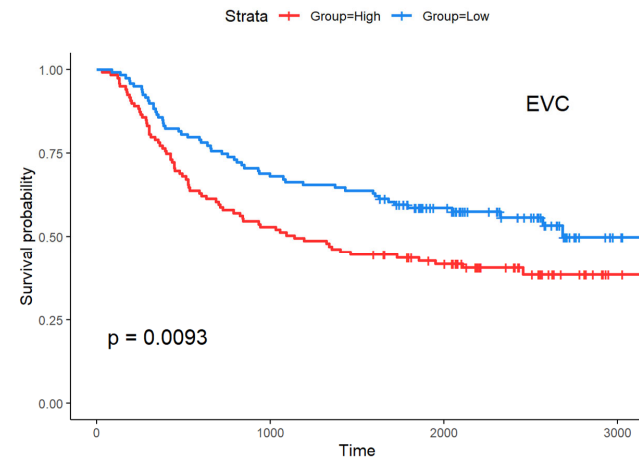


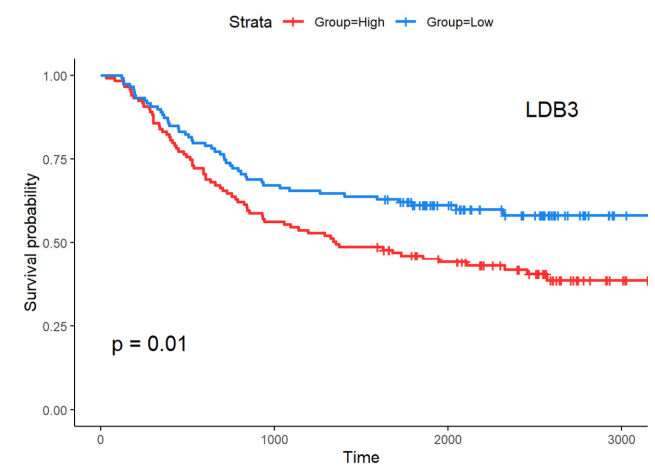
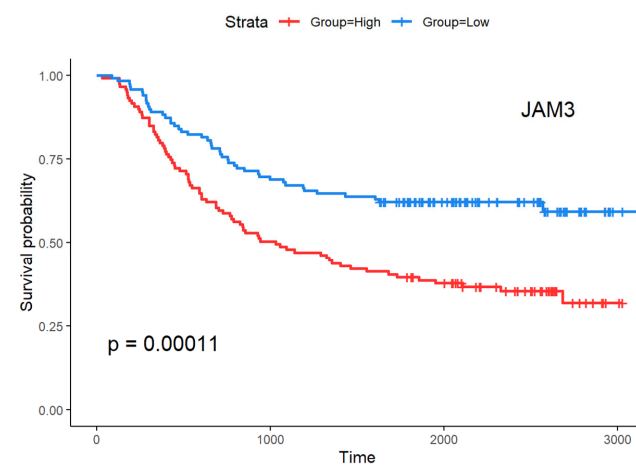
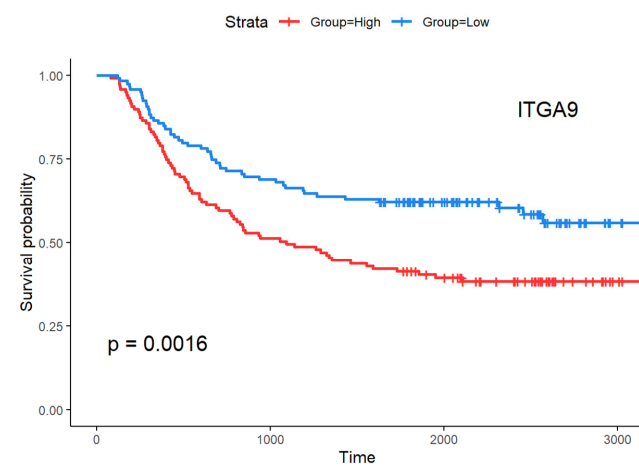
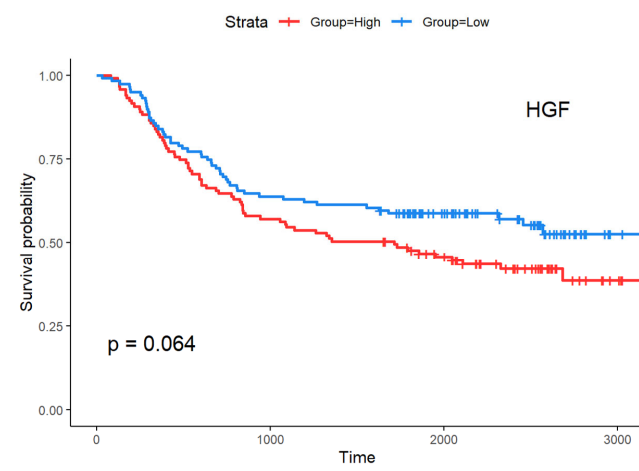
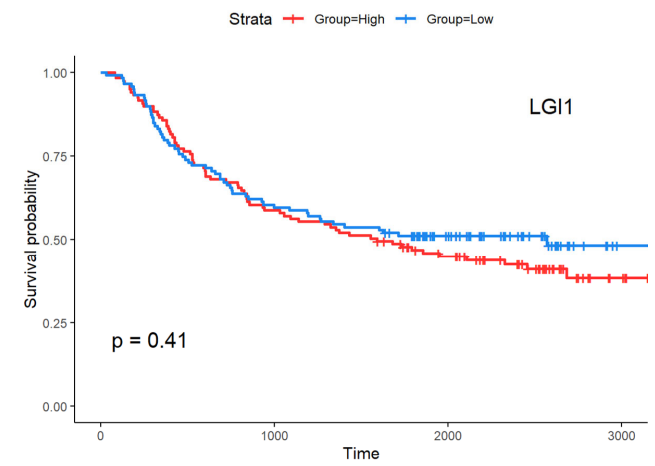
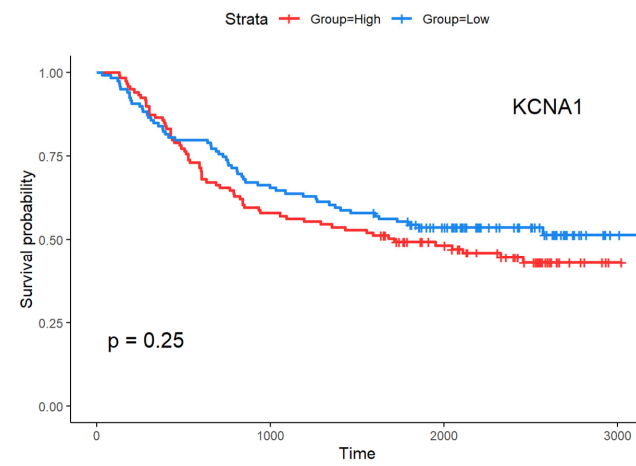
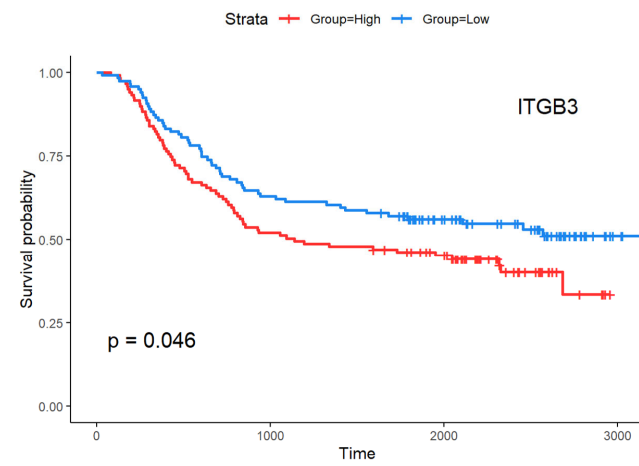
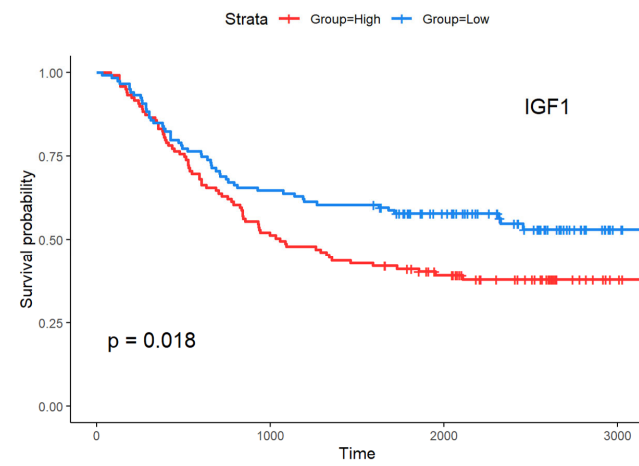
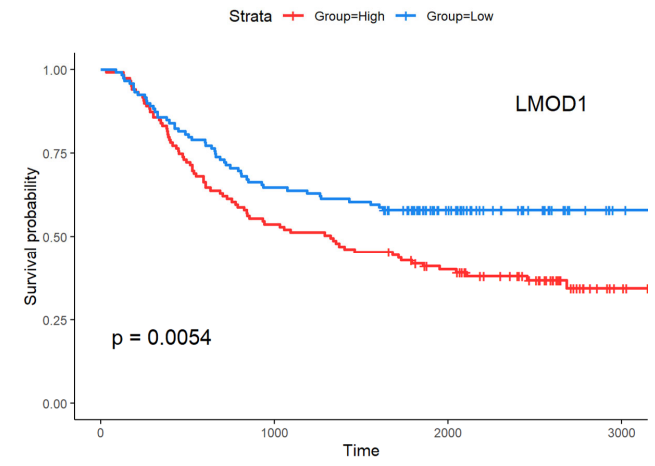
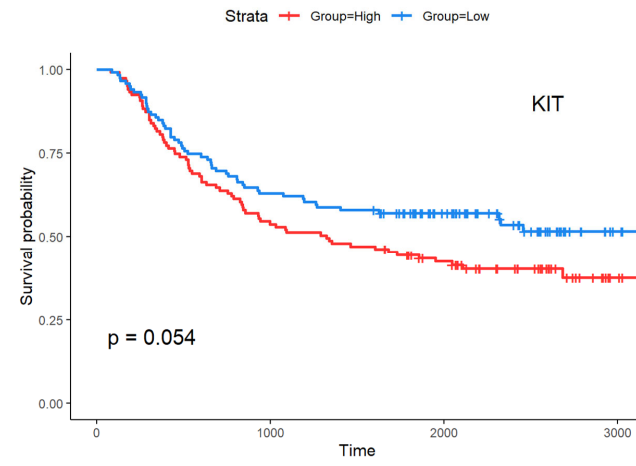
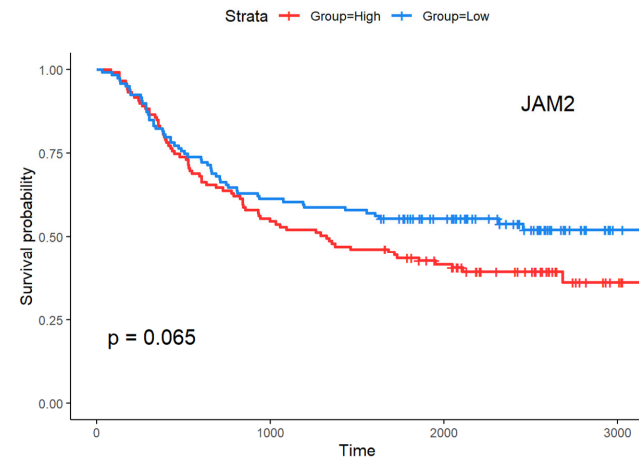
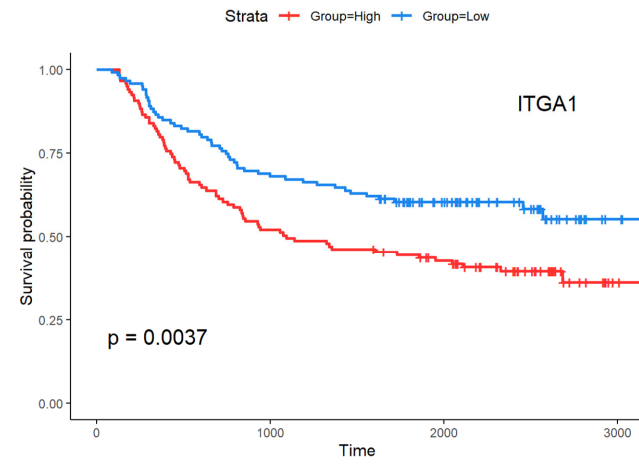


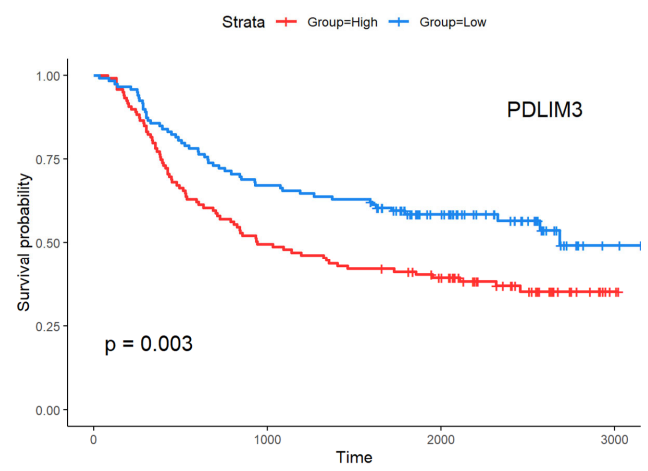
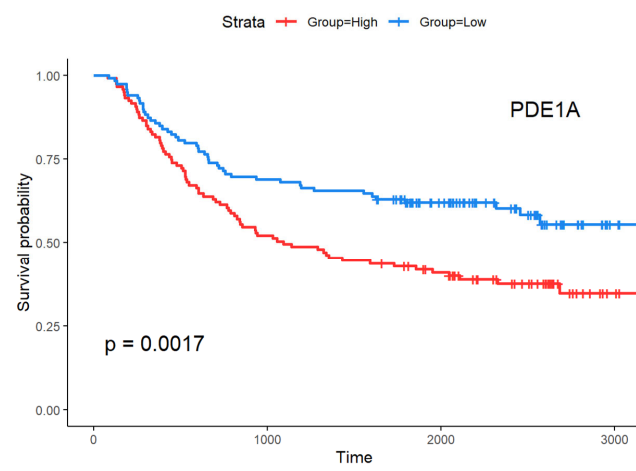
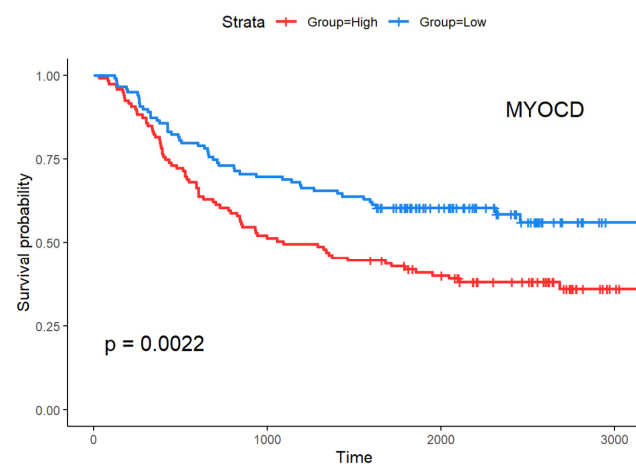
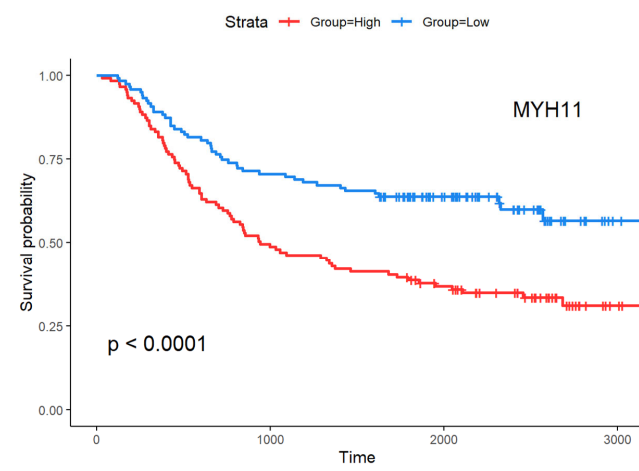
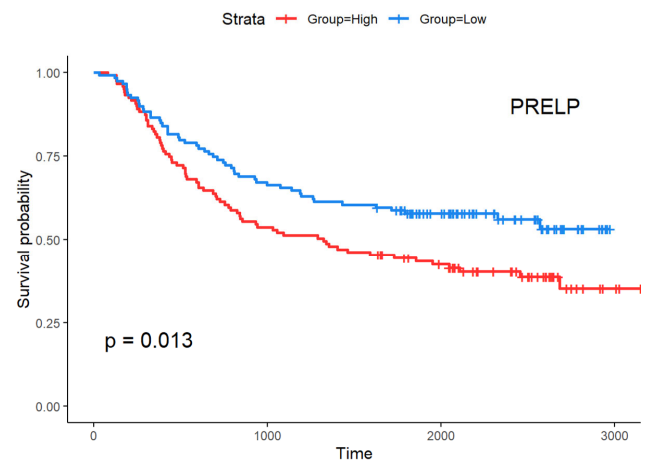
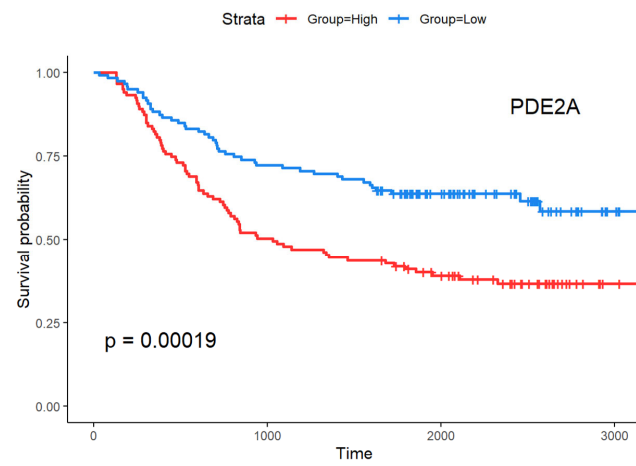
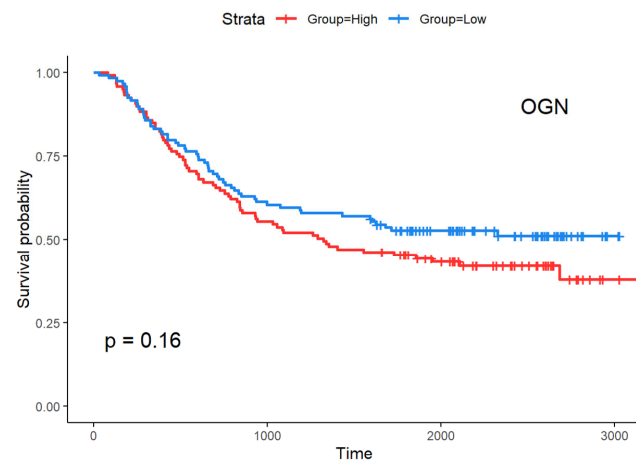
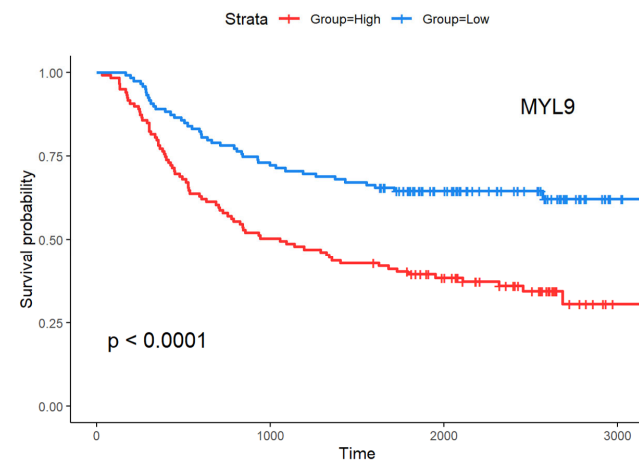
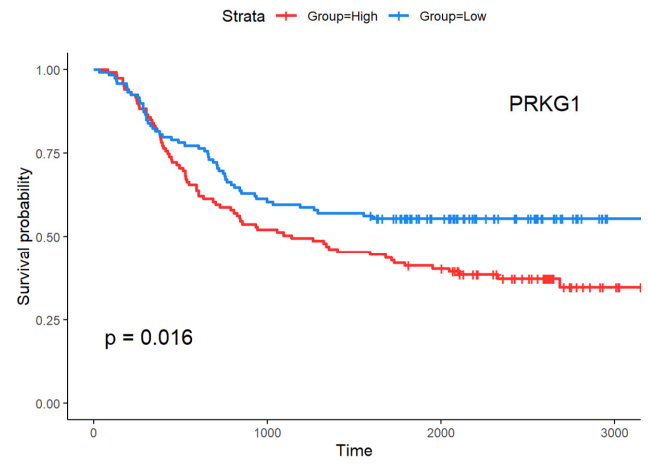
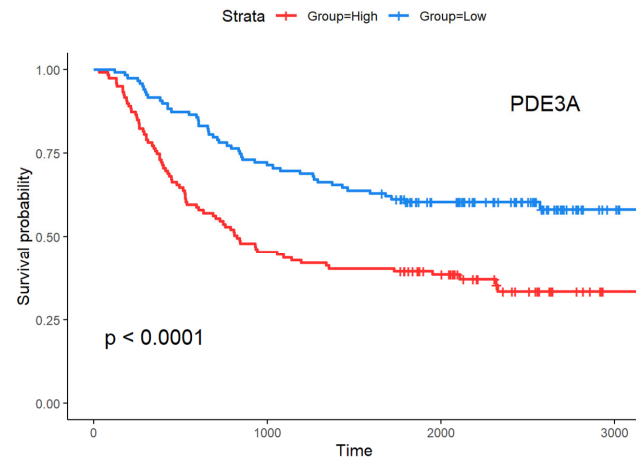
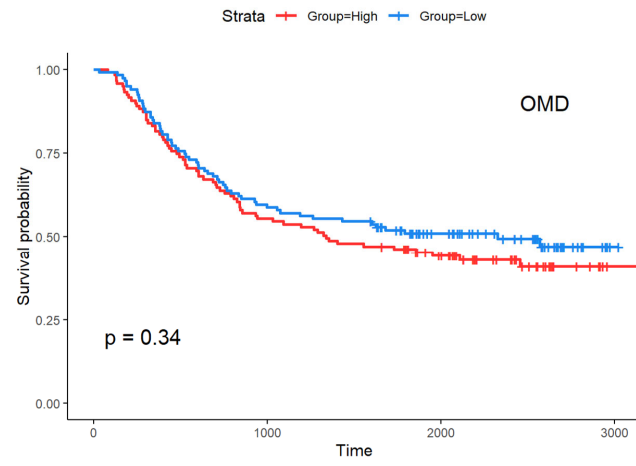
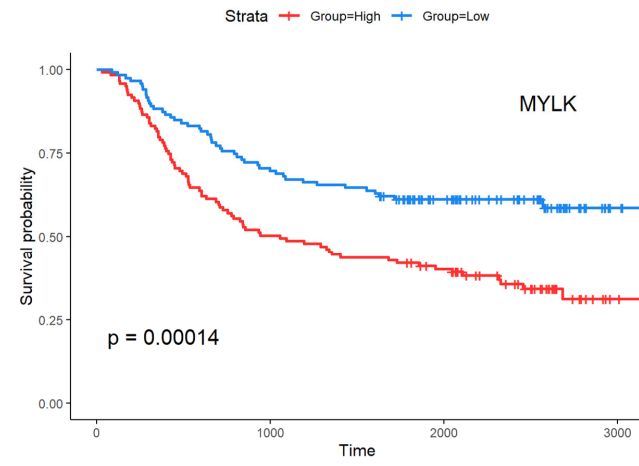


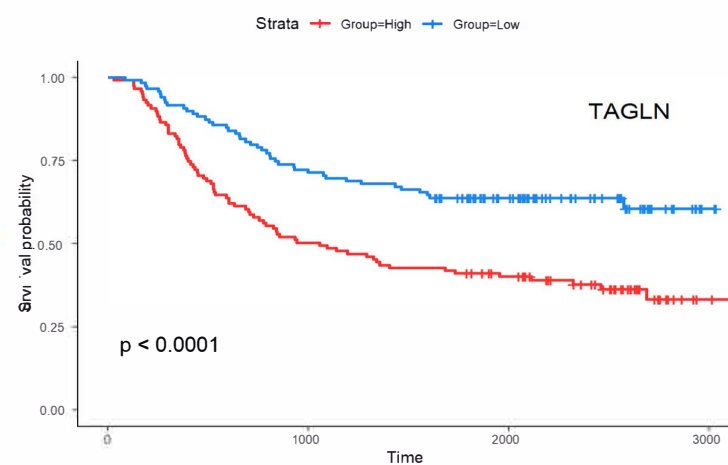
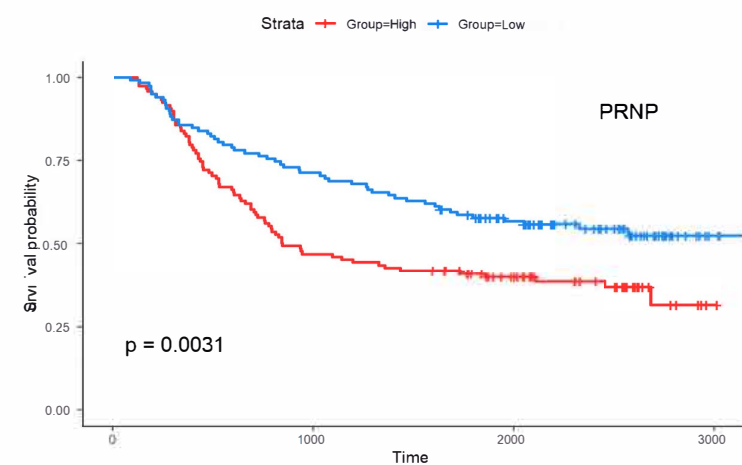
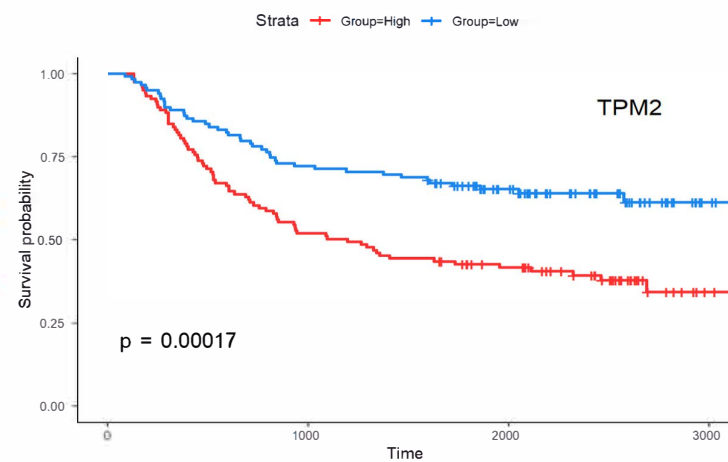
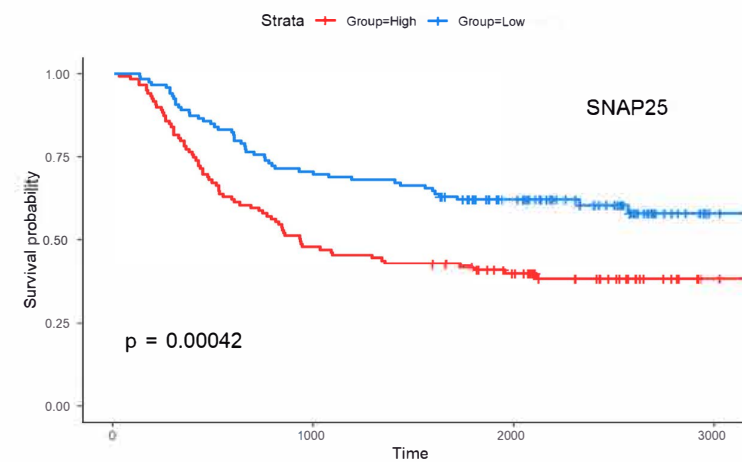
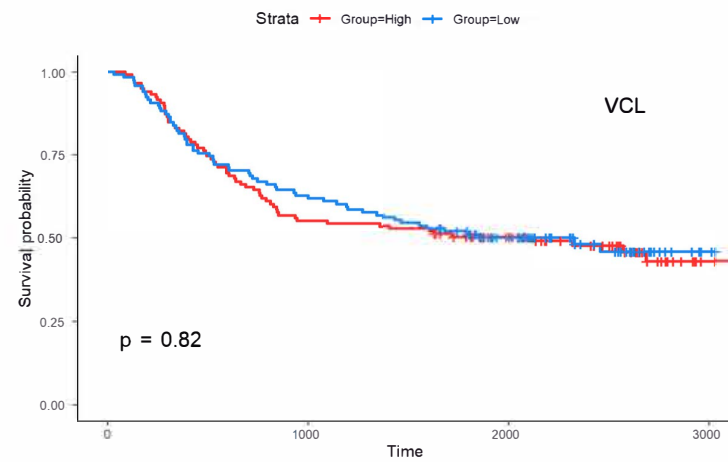
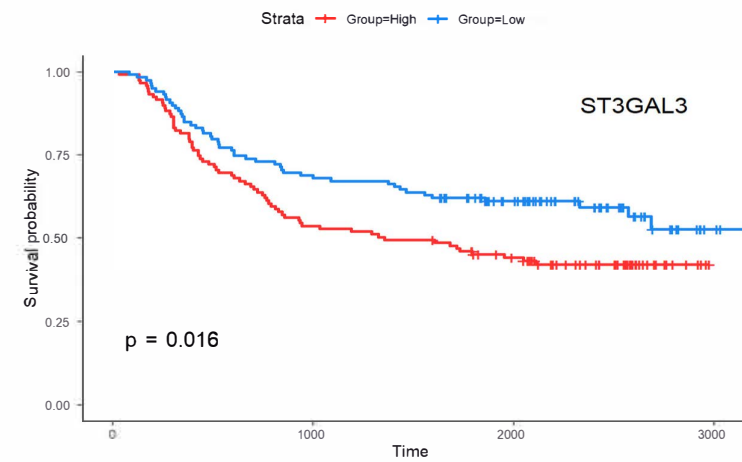






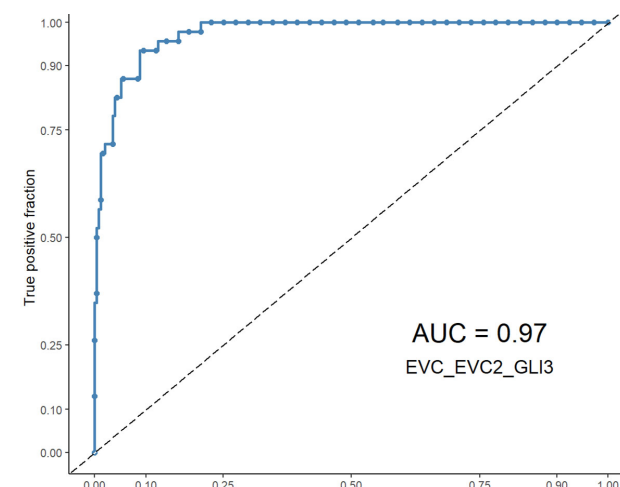
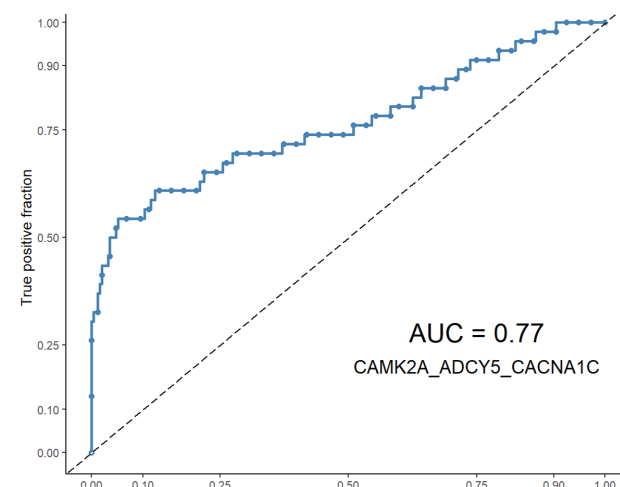
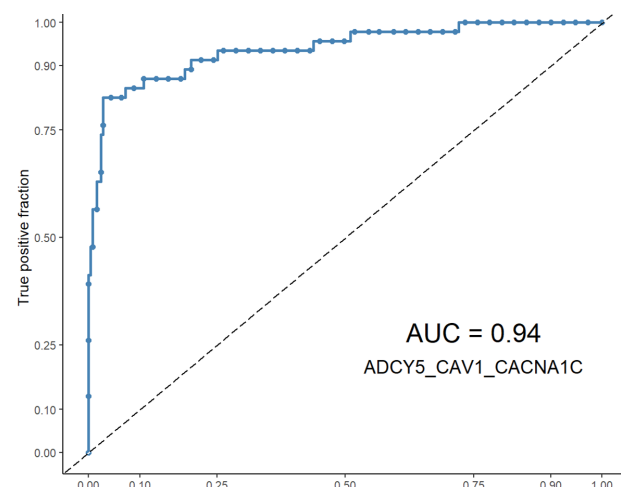
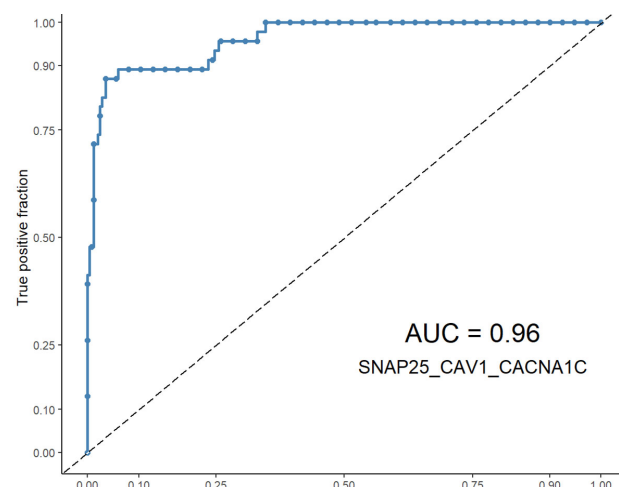
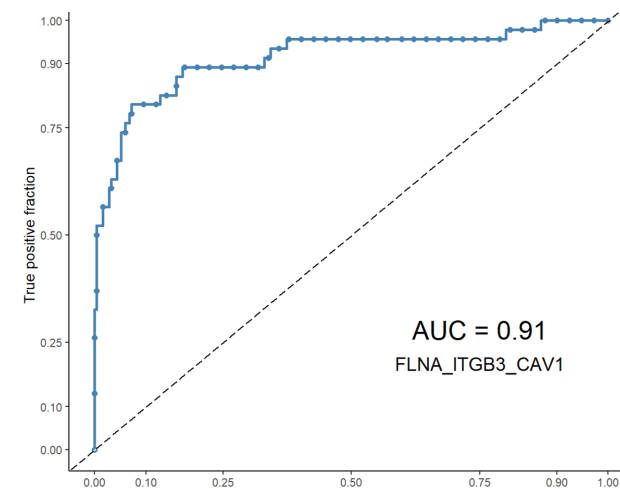
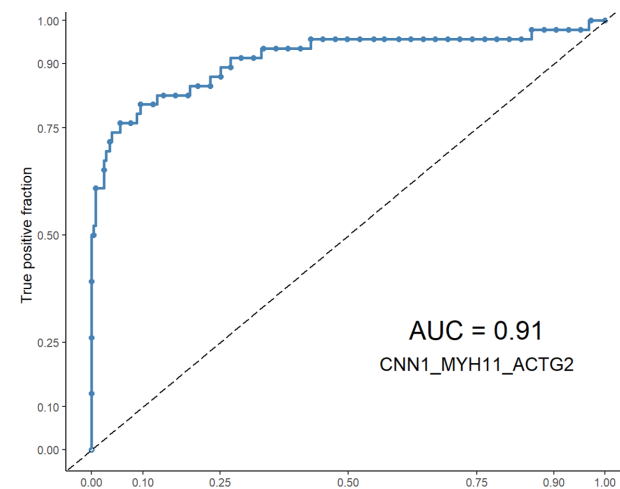
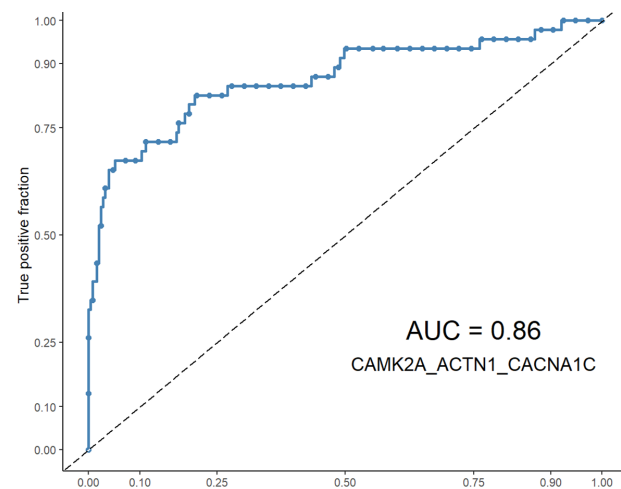
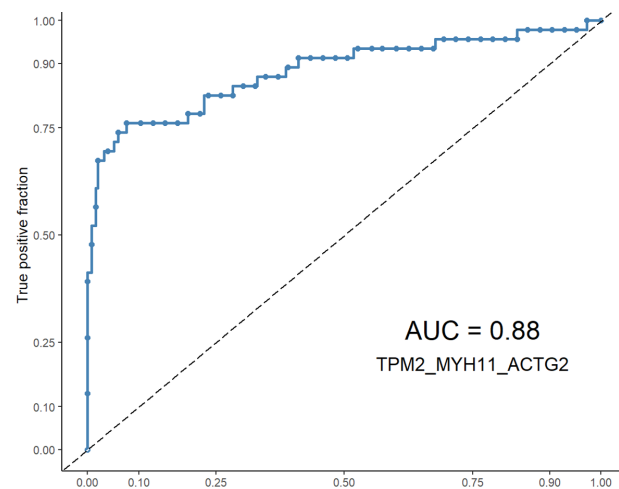
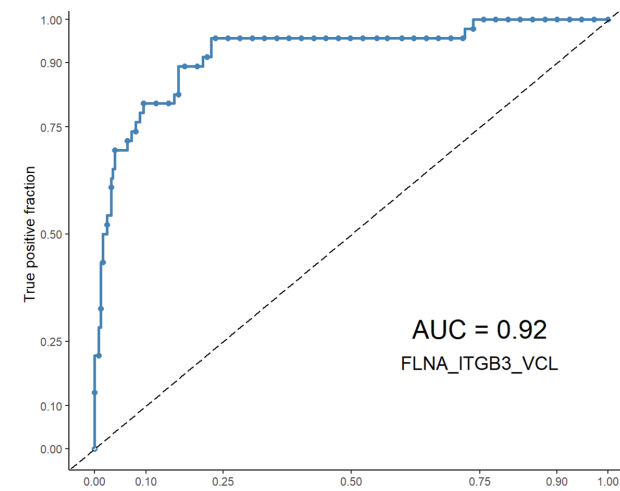
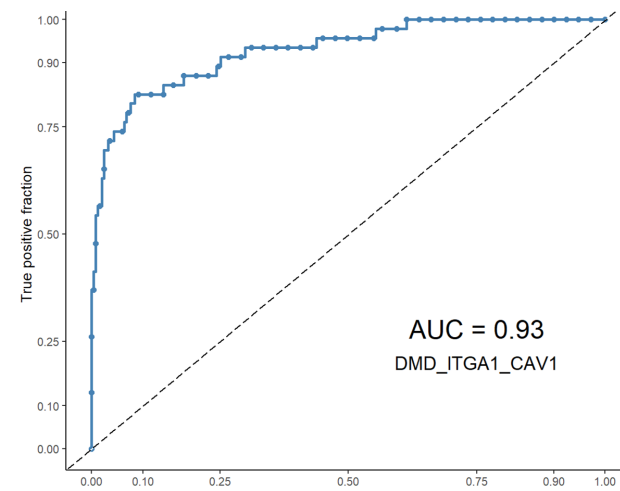
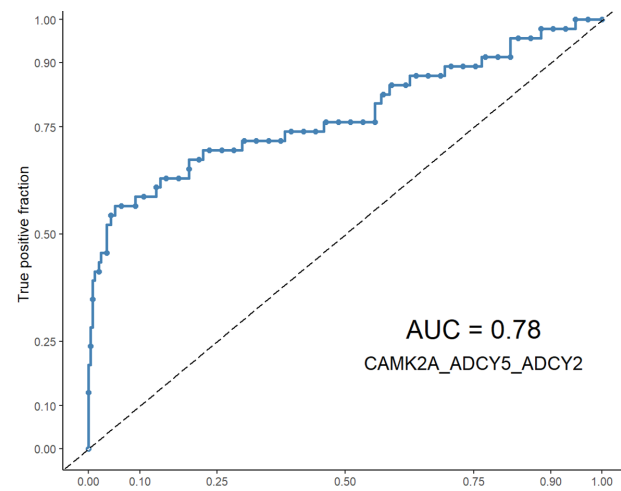
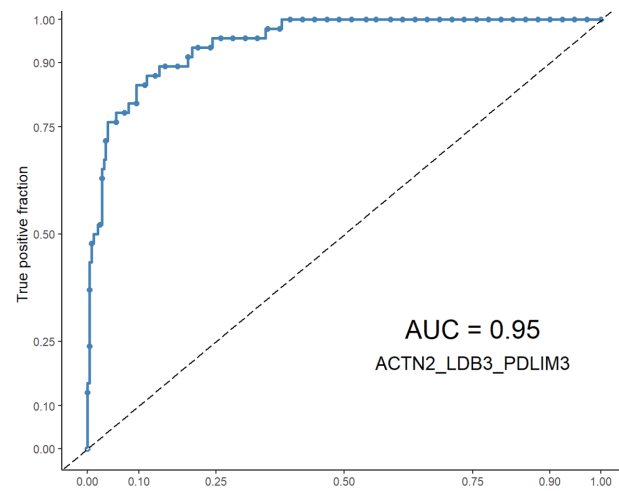


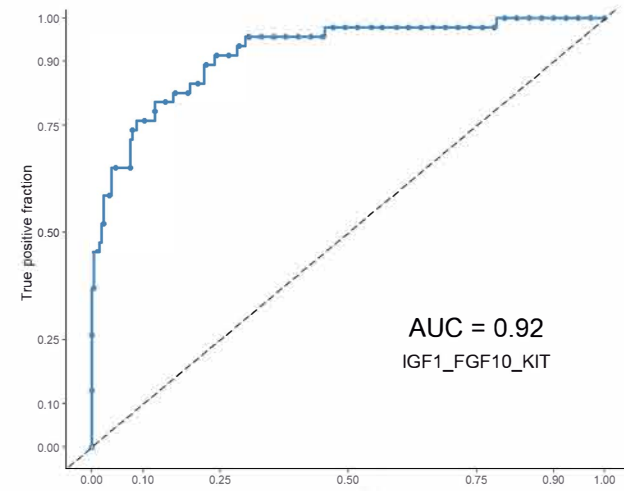
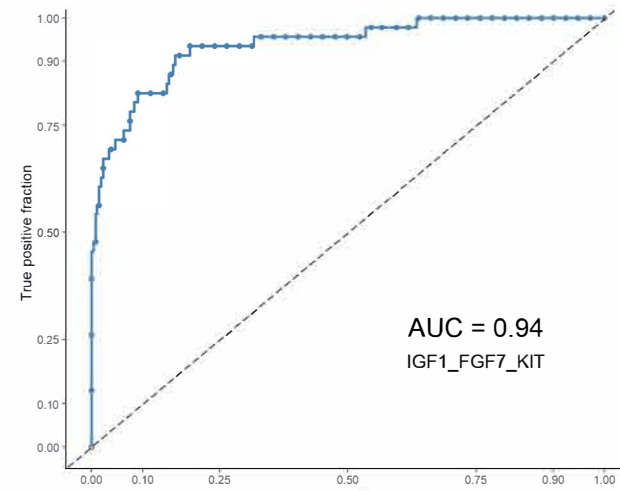
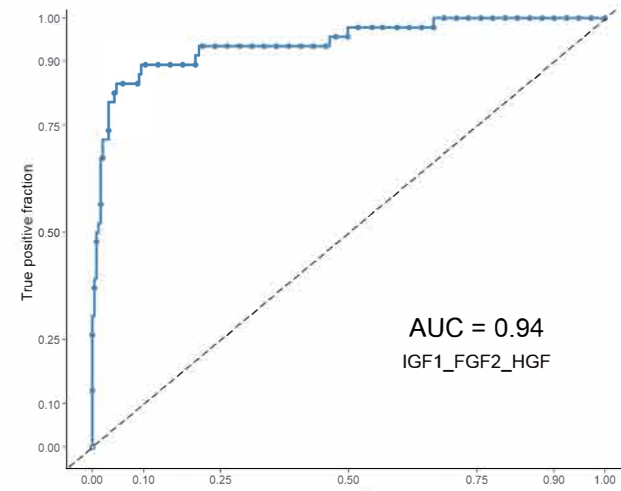
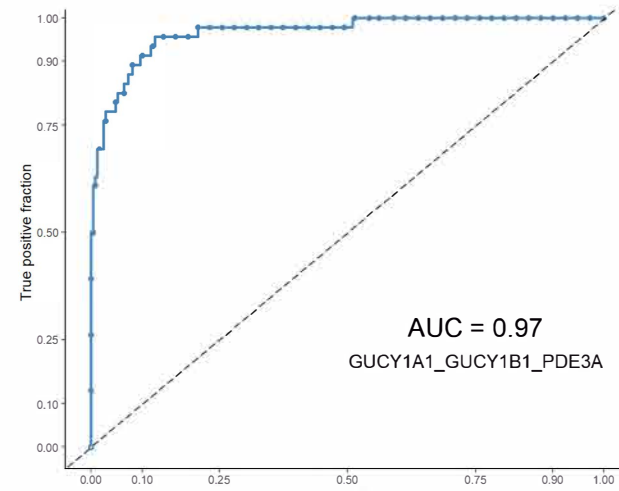
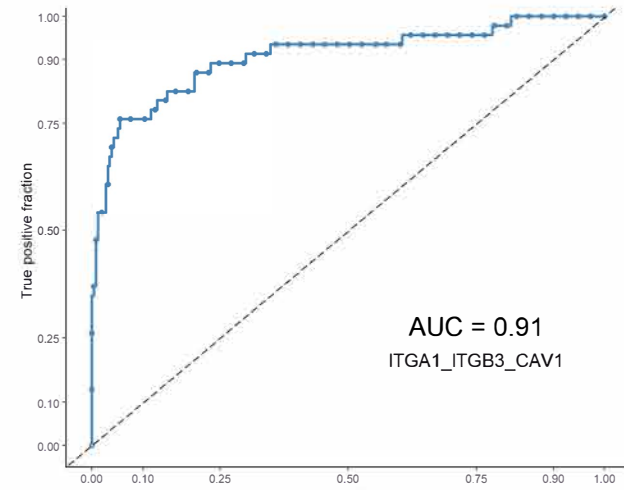
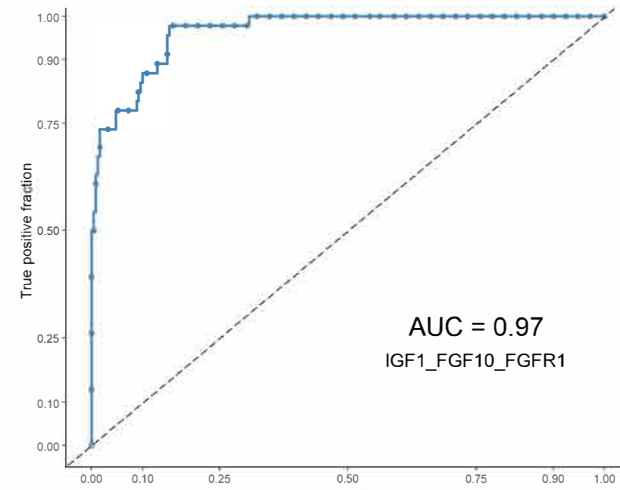
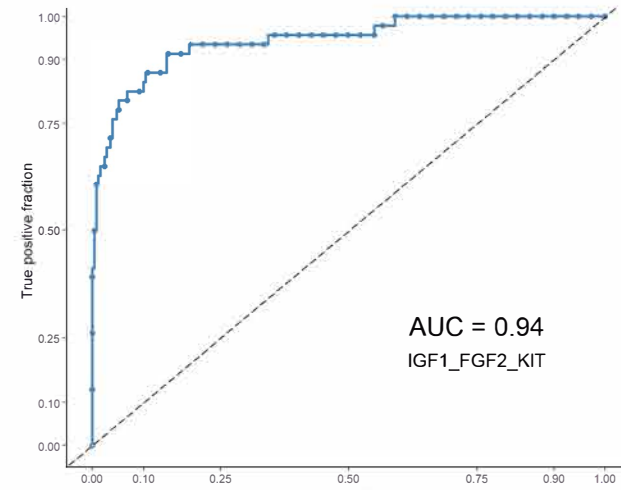
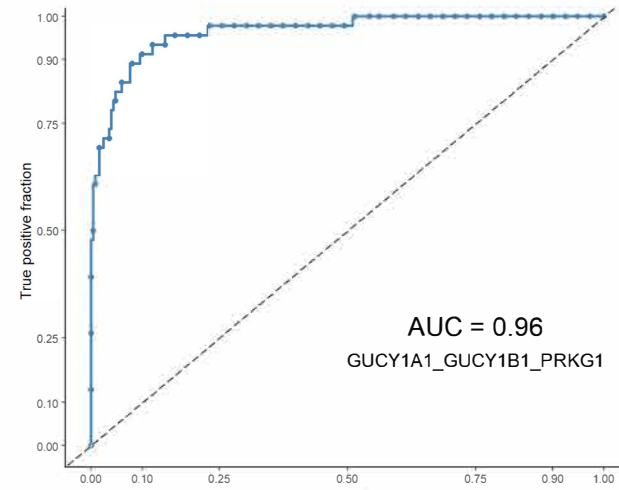
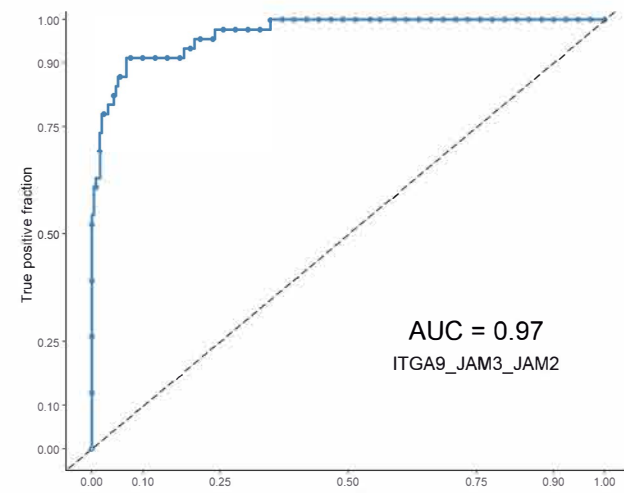
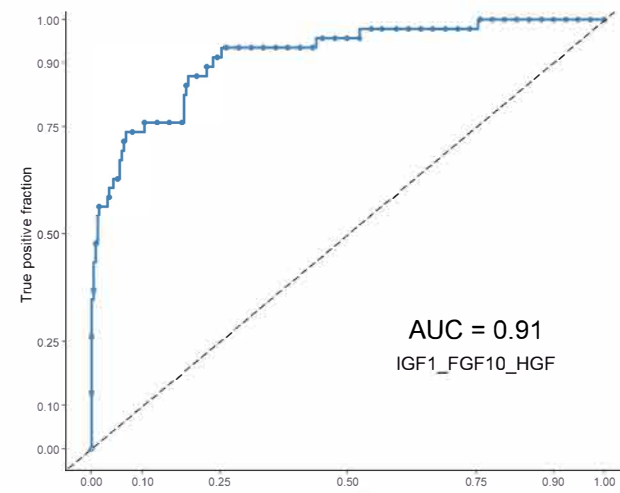
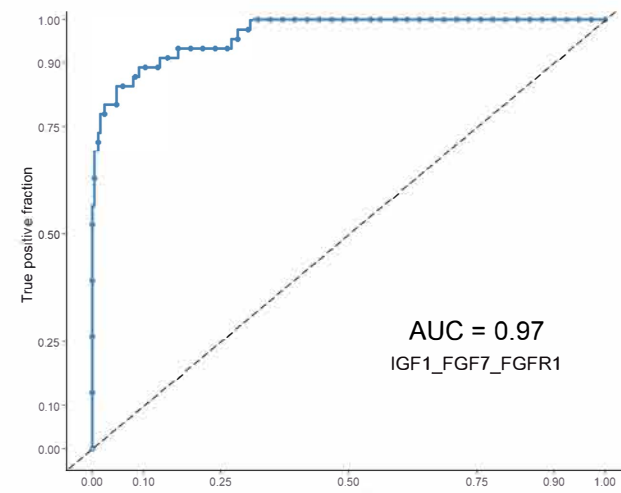
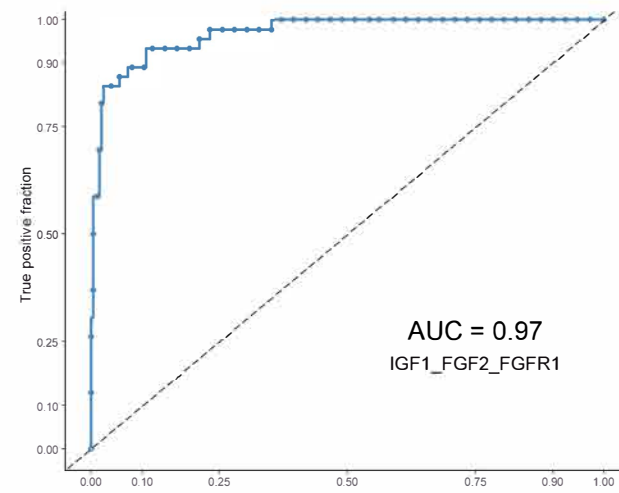


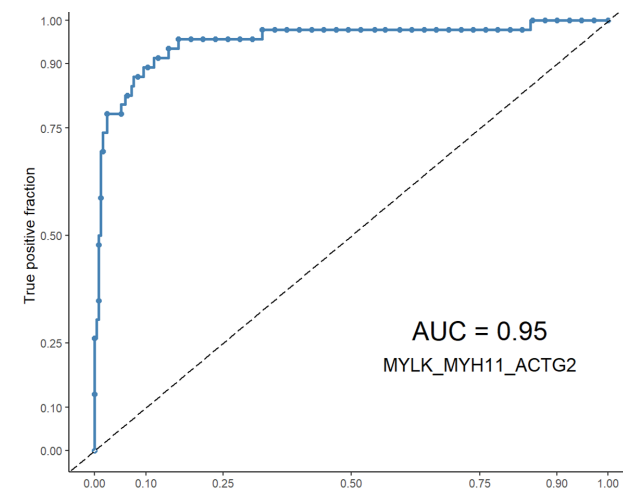
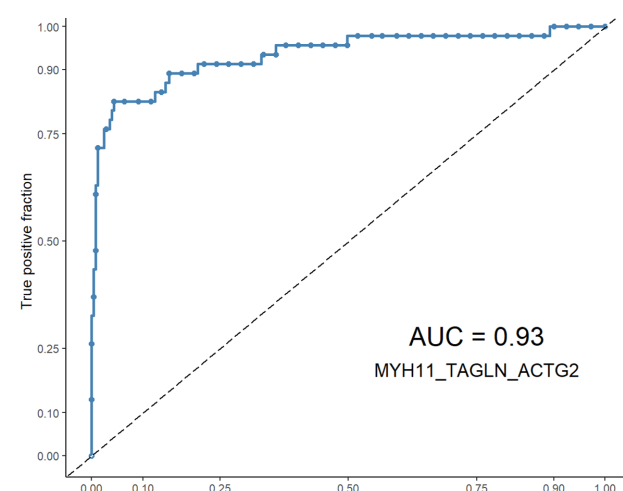
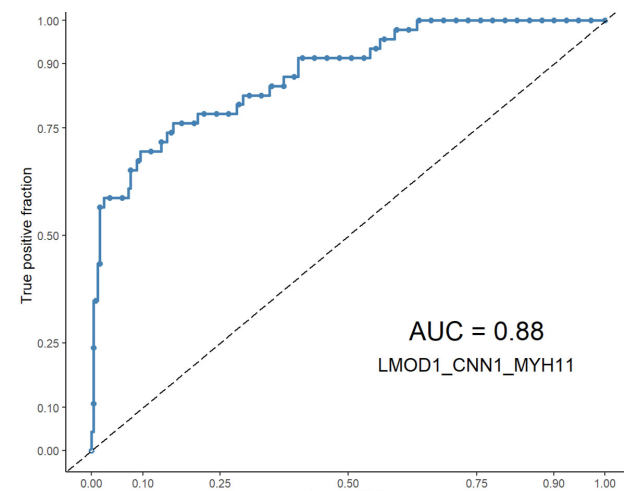
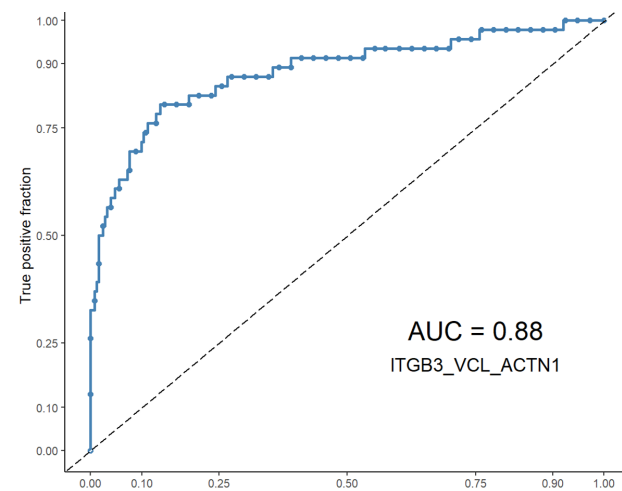
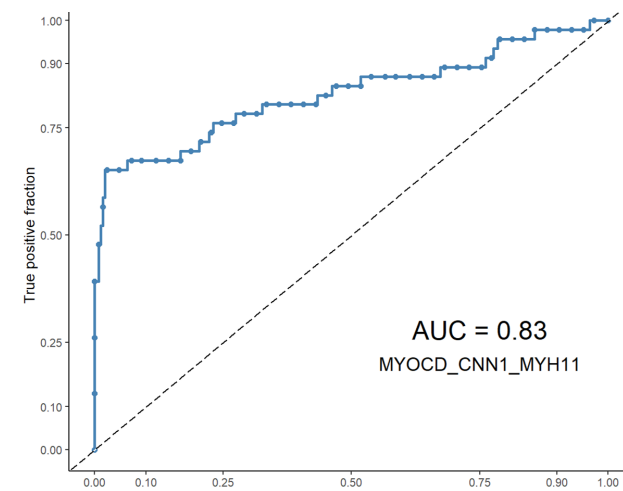
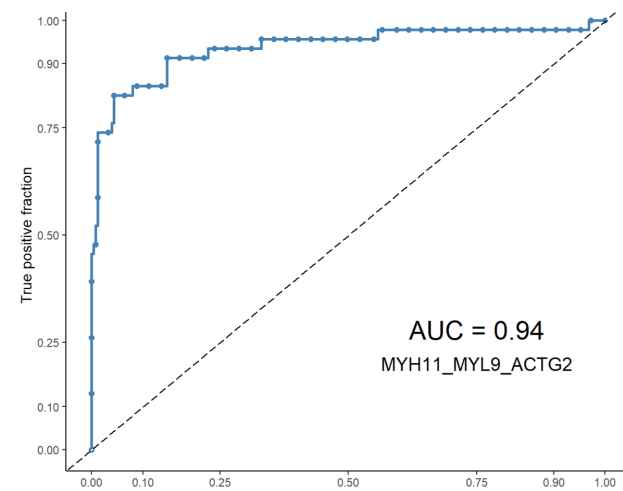
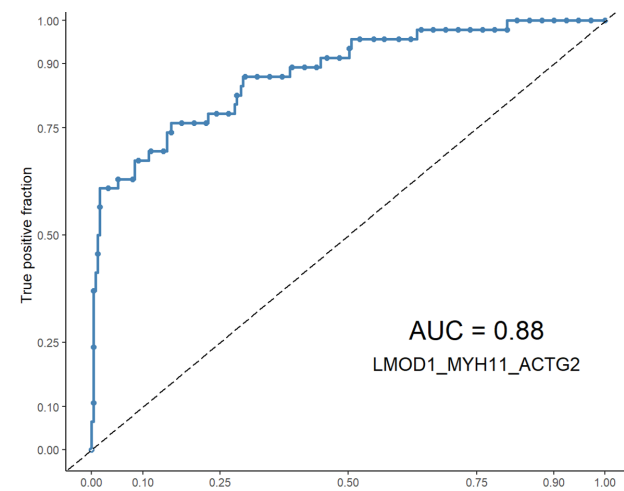
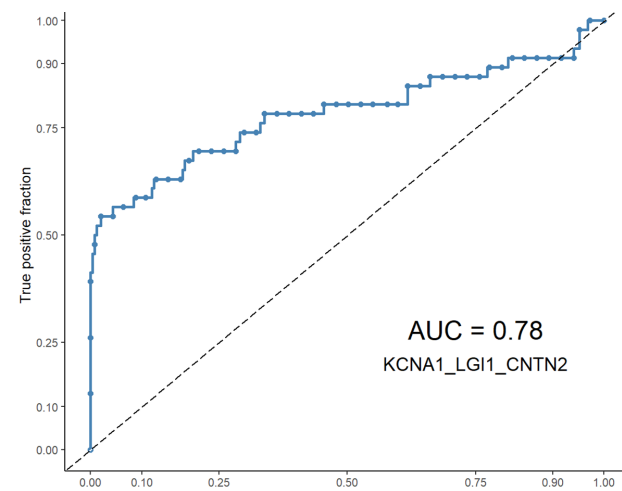
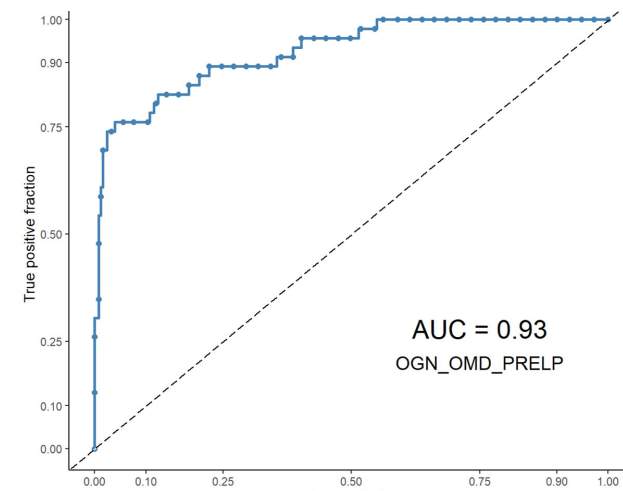
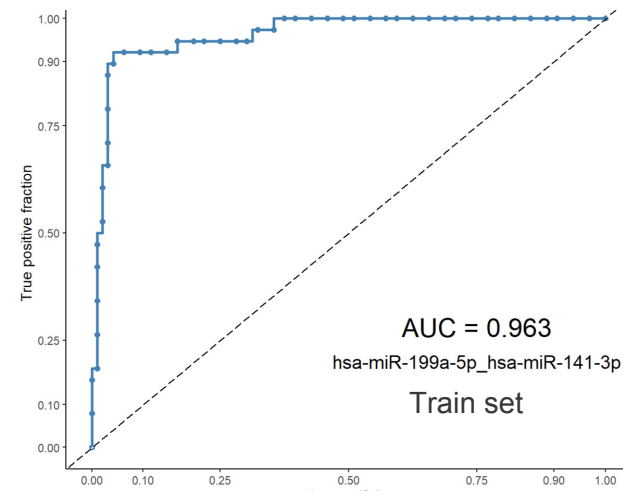
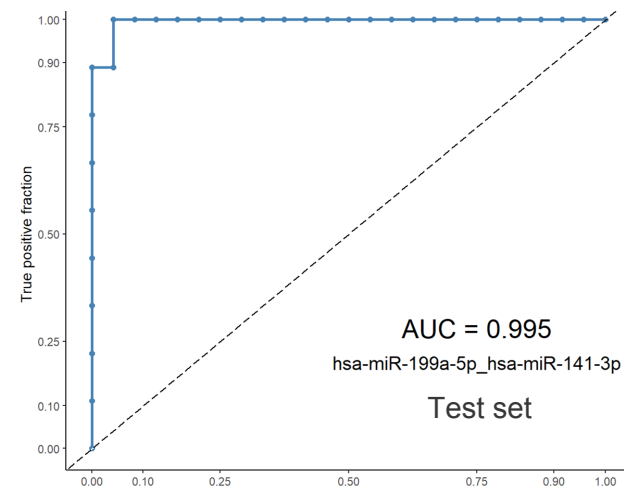
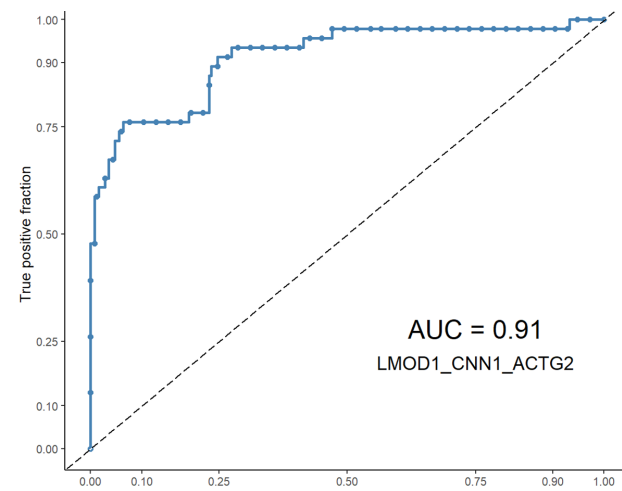


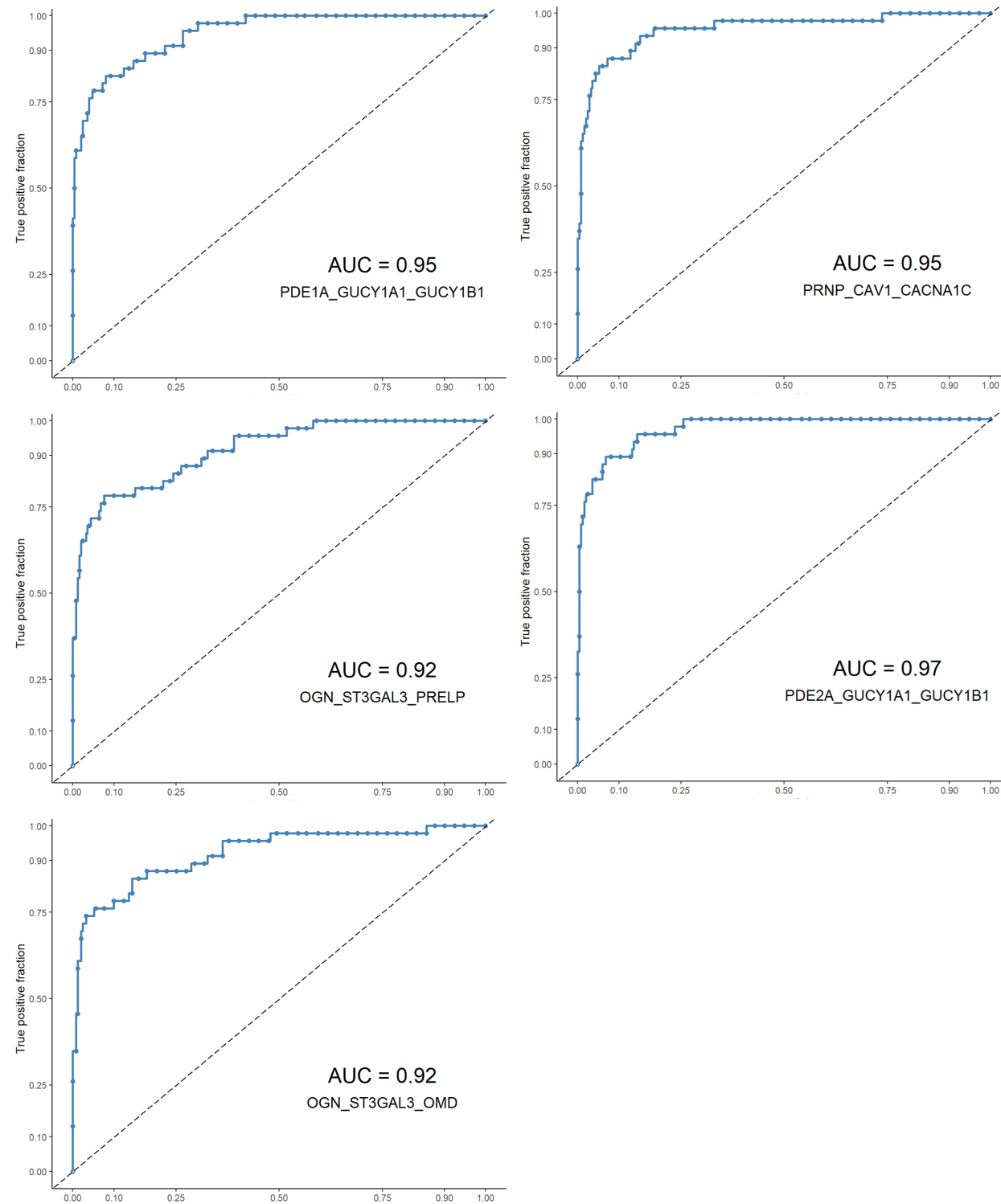
**Supplementary Figure S5 Kaplan-Meier survival curves of the ACRG cohort for all of the top-scoring three-membered motifs as well as each member of the motifs in isolation.** For motif members, the 'High' and 'Low' groups represent the top and bottom 40% of the samples in terms of the expression of the respective genes. For the whole motifs, the intersection of the samples among the top 40% of samples and the bottom 40% of samples based on the expression of each of the three members of the respective motifs was used to form 'High' and 'Low' groups











**Supplementary Figure S6 The receiver operating characteristic (ROC) curves of the diagnostic performance of the models trained on TCGA cohort data in the validation cohort.** The ACRG cohort was used for validation of the diagnostic performance of the mRNA motifs. In addition, the diagnostic performance of the miRNA-based discriminating model in both training (80% of TCGA samples) and test (the remaining TCGA samples) sets is also shown