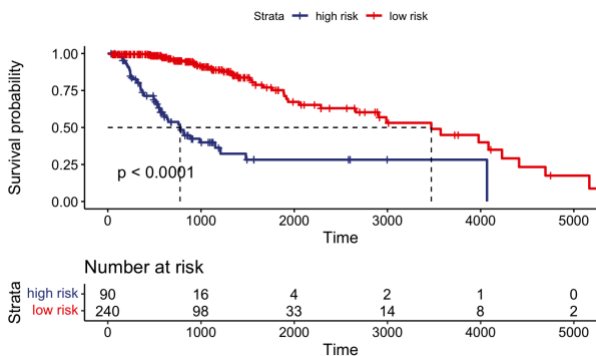
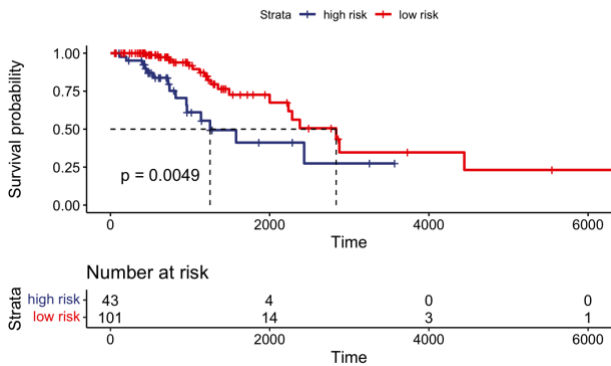


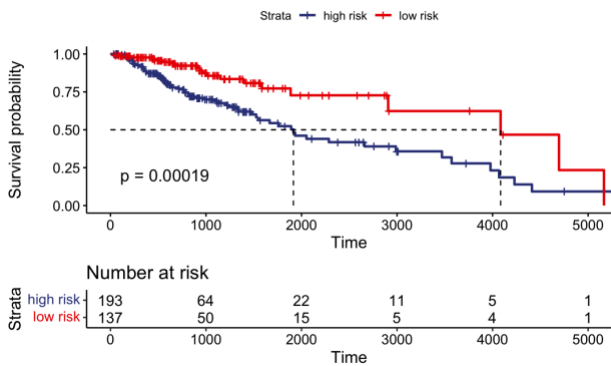
Since we change the legends of figures to present in the final report, we re-run all the codes of survival analysis again and might got different results, that is mainly due to the uncertainty brought by the clustering algorithms, but the overall results are unchanged. The results shown in the final reports are listed below:



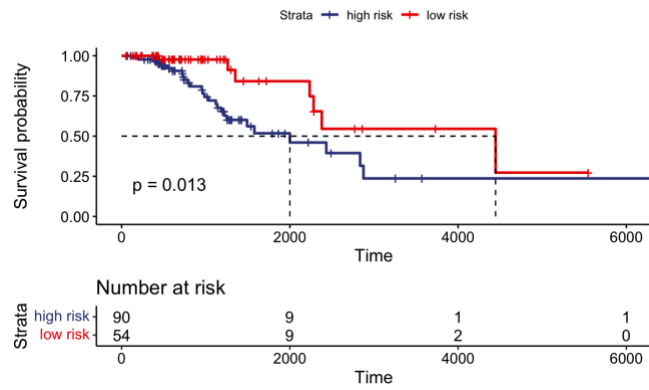
Glioma train set for SCNV of 2 groups: Manhattan distance measurement and Median linkage method for the Hierarchical Clustering



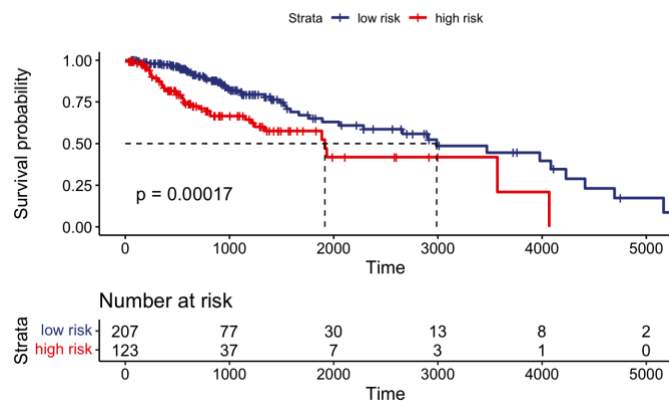
Glioma test set for SCNV of 2 groups: Canberra distance measurement and Mcquitty linkage method for the Hierarchical Clustering



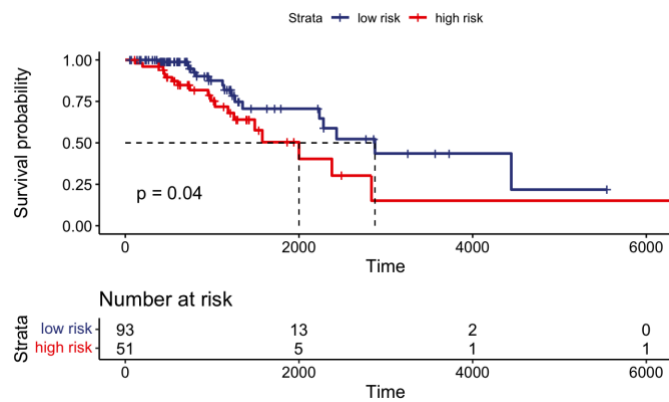
Glioma train set for RNAseq of 2 groups: Euclidean distance measurement and Ward linkage method for the Hierarchical Clustering



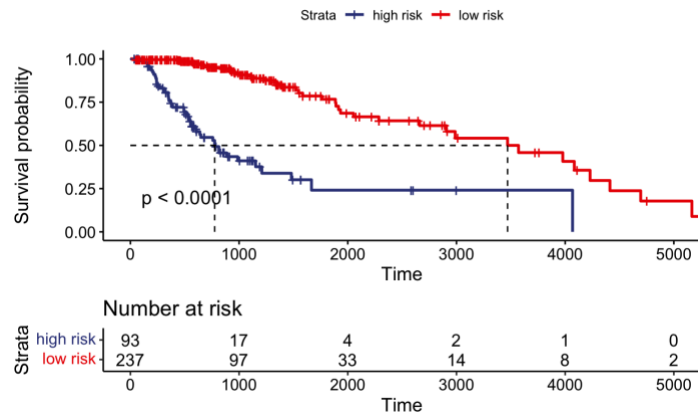
Glioma test set for RNAseq of 2 groups: Euclidean distance measurement and Ward linkage method for the Hierarchical Clustering



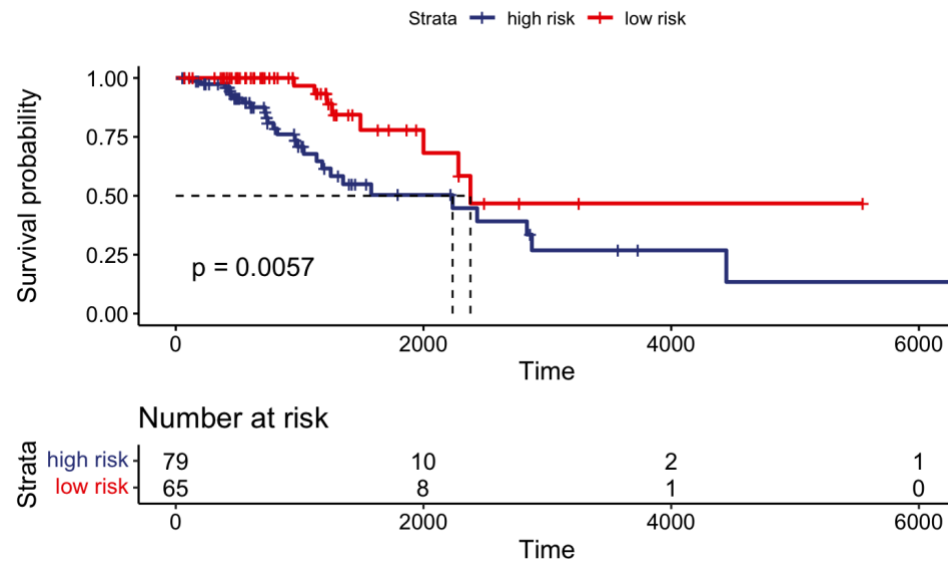
Glioma train set for miRNA of 2 groups: Canberra distance measurement and Mcquitty linkage method for the Hierarchical Clustering algorithm



Glioma test set for miRNA of 2 groups: Canberra distance measurement and Mcquitty linkage method for the Hierarchical Clustering algorithm



Glioma train set for Methylation of 2 groups: Euclidean distance measurement and Centroid linkage method for the Hierarchical Clustering



Glioma test set for Methylation of 2 groups: Canberra distance measurement and Average linkage for the Hierarchical Clustering