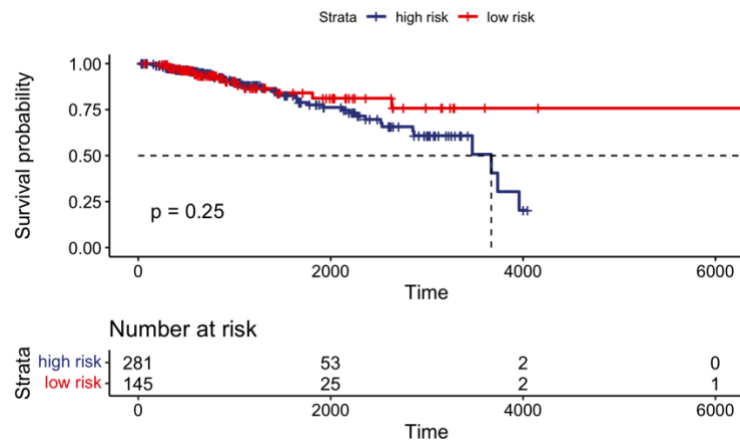Since we change the legends of figures to present in the final report, we re-run all the codes of survival analysis again and might got different results, that is mainly due to the uncertainty brought by the clustering algorithms, but the overall results are unchanged. The results shown in the final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


Breast train set for RNAseq of 2 groups: Euclidean distance measurement and Complete linkage method for the Hierarchical Clustering algorithm
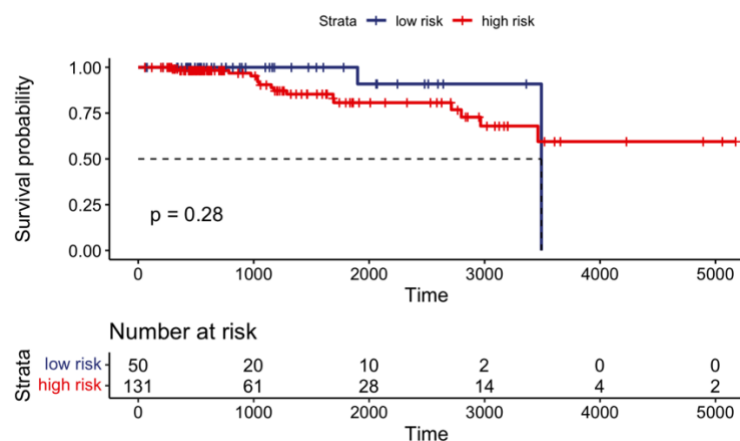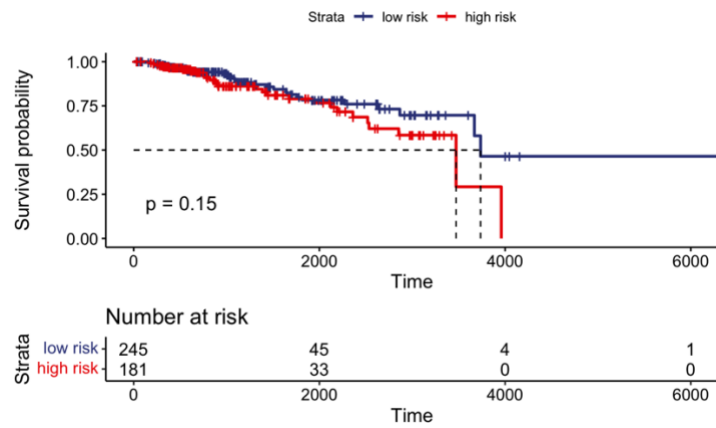

Breast test set for RNAseq of 2 groups: Euclidean distance measurement and Complete linkage method for the Hierarchical Clustering algorithm
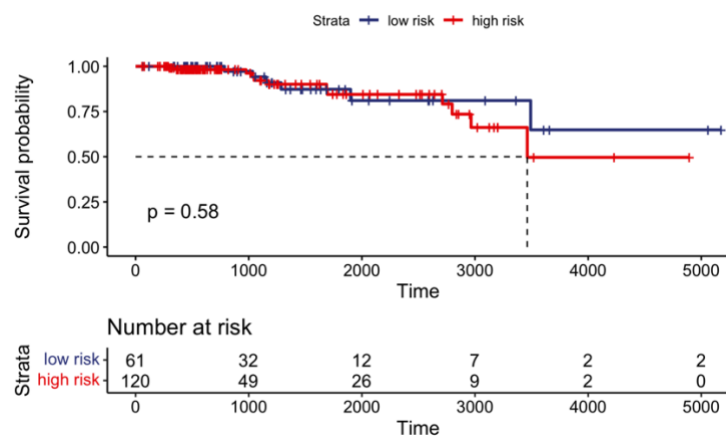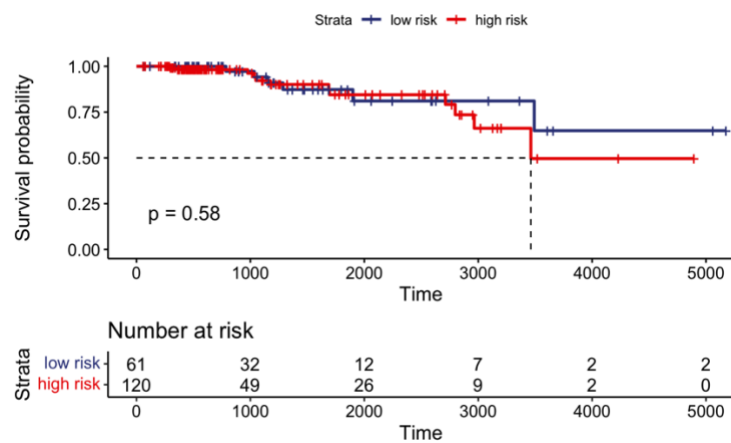

Breast train set for SCNV of 2 groups: Canberra distance measurement and Ward linkage method for the Hierarchical Clustering
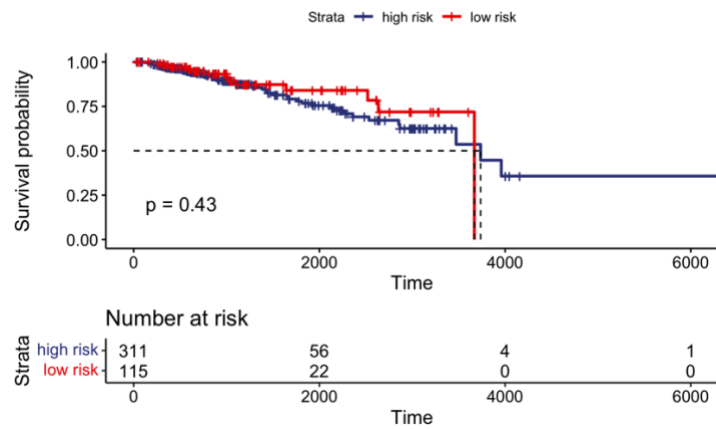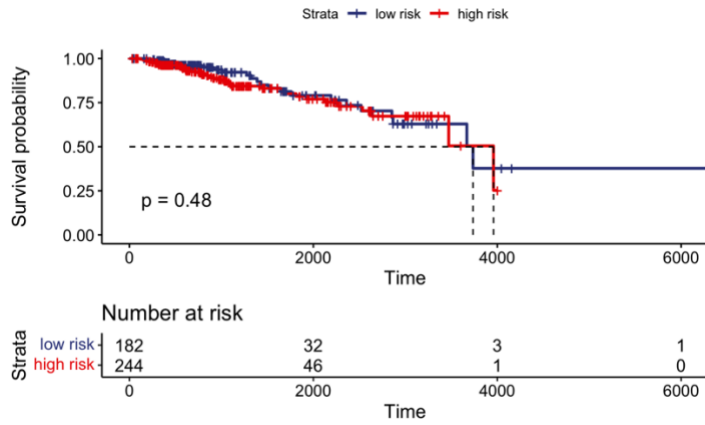
Breast test set for SCNV of 2 groups: Manhattan distance measurement and Ward linkage method for the Hierarchical Clustering
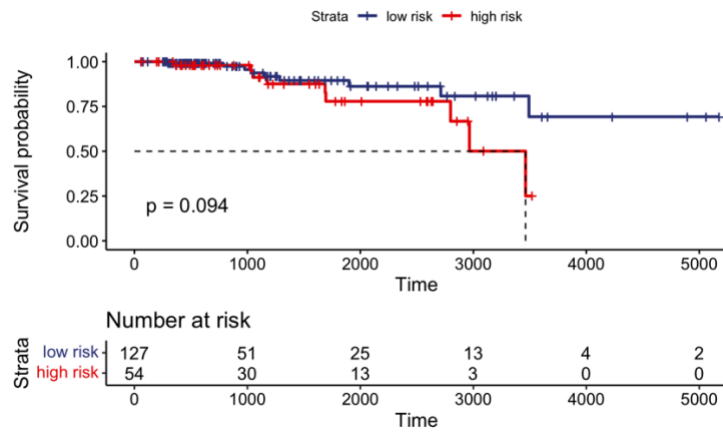

Breast train set for miRNA of 2 groups: Canberra distance measurement and Average linkage method for the Hierarchical Clustering

Breast test set for miRNA of 2 groups: Manhattan distance measurement and Ward linkage method for the Hierarchical Clustering

Breast train set for Methylation of 2 groups: combination of Canberra distance measurement and Ward linkage method for the Hierarchical Clustering

Breast test set for Methylation of 2 groups: Manhattan distance measurement and Ward linkage method for the Hierarchical Clustering