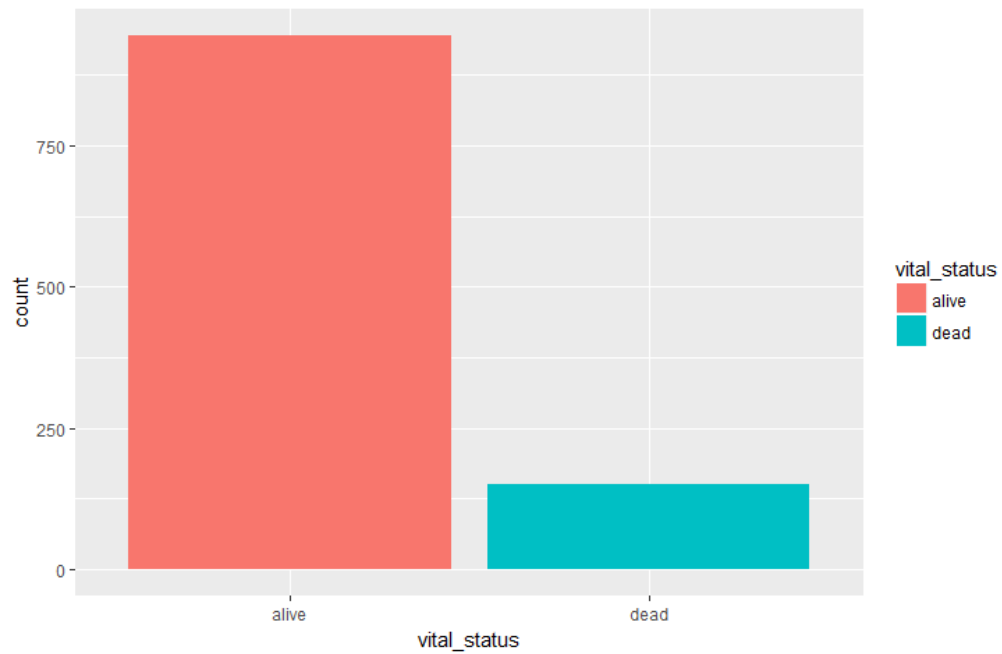
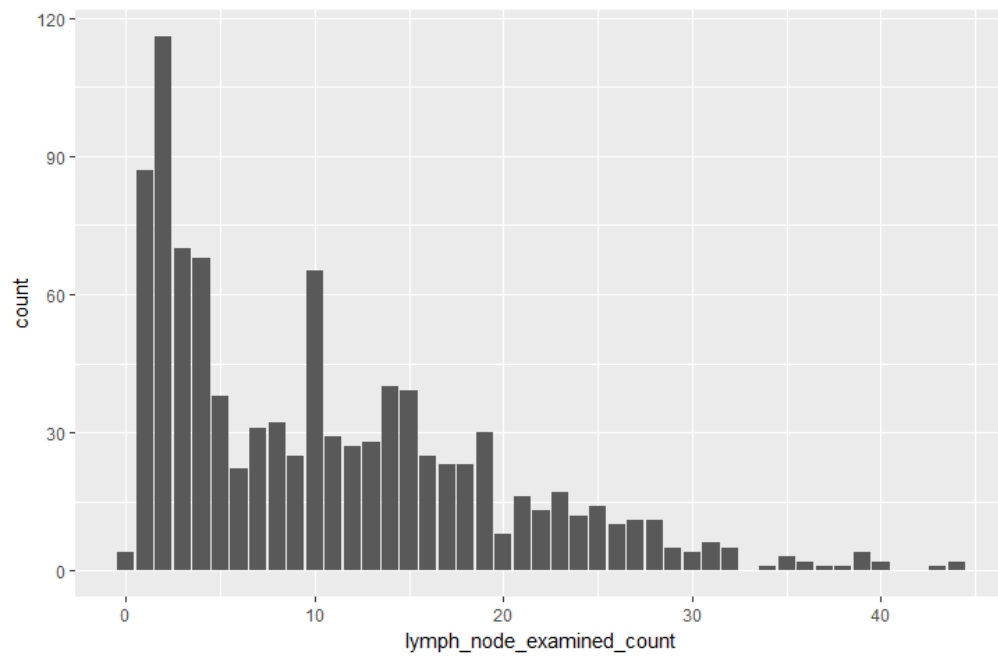
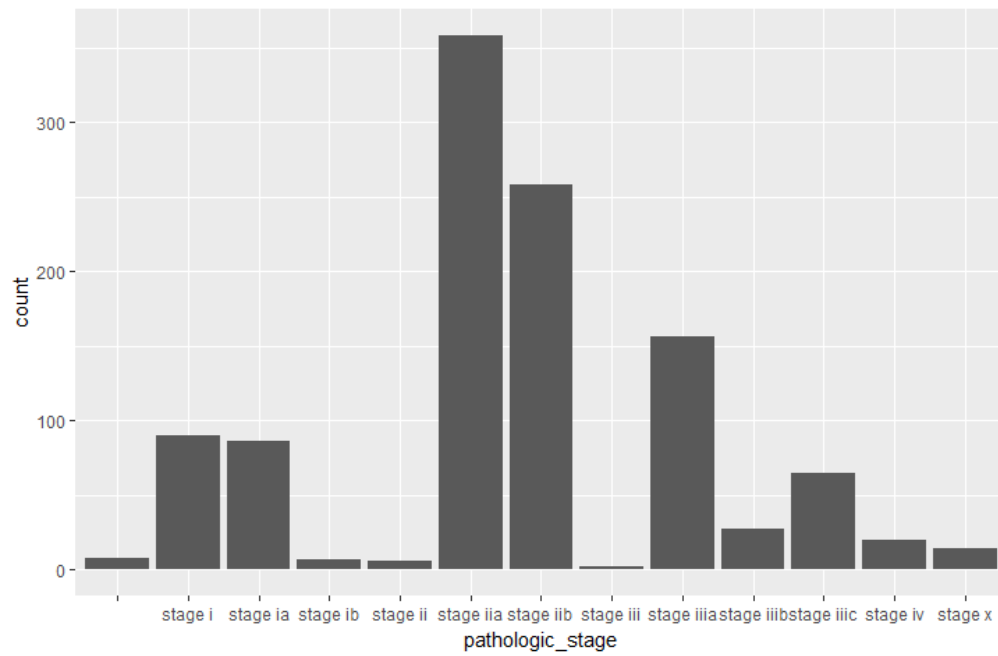


APPENDIX

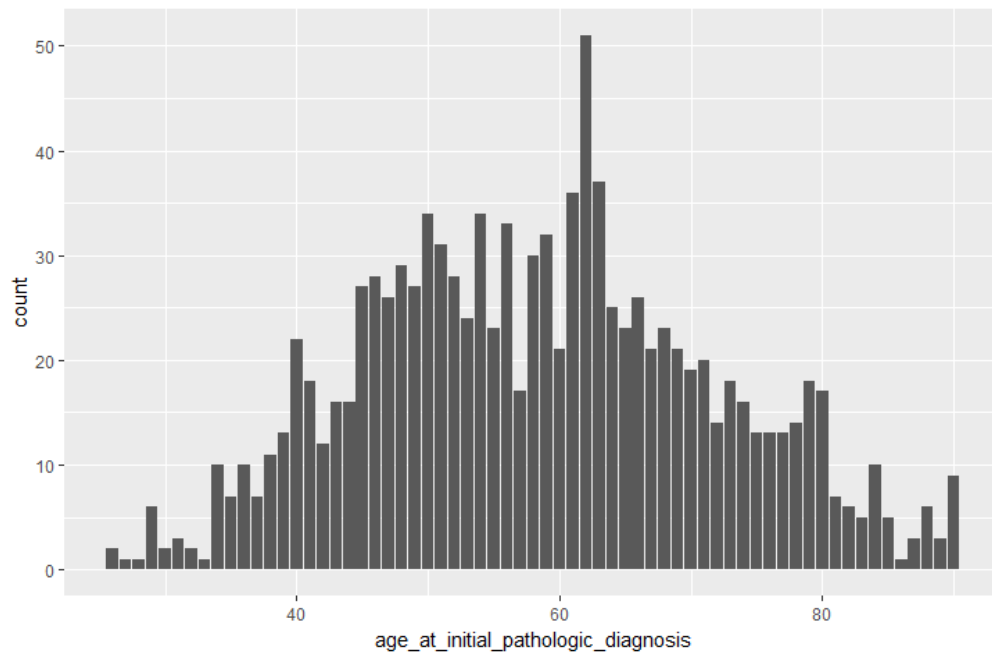
Distributions of these variables are as below. Maximum number of patients were alive at the time when I have downloaded the dataset. Very less records with dead as viatal_status.



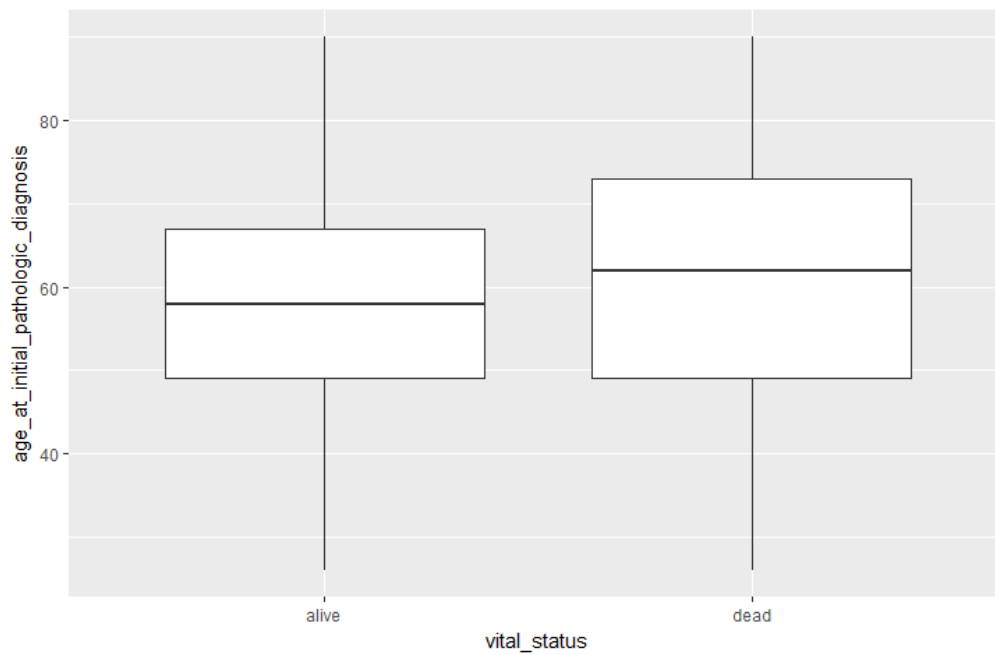
Patients with Stage iia and stage iib are highest. This variable has some of the data. 8 records don't have stage details in the dataset.



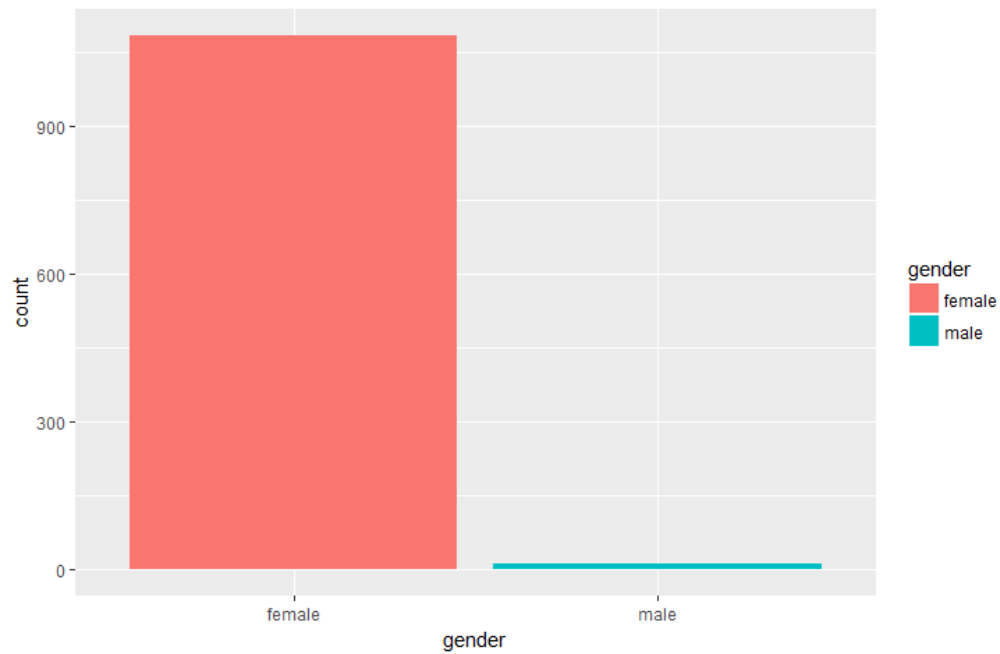
Records with 2 examined lymph-nodes are highest and 126 records don't have details about this variable.



Maximum patients were at age of 62 at the time of initial pathologic diagnosis. Less cases with diagnosis at early stage of the life.

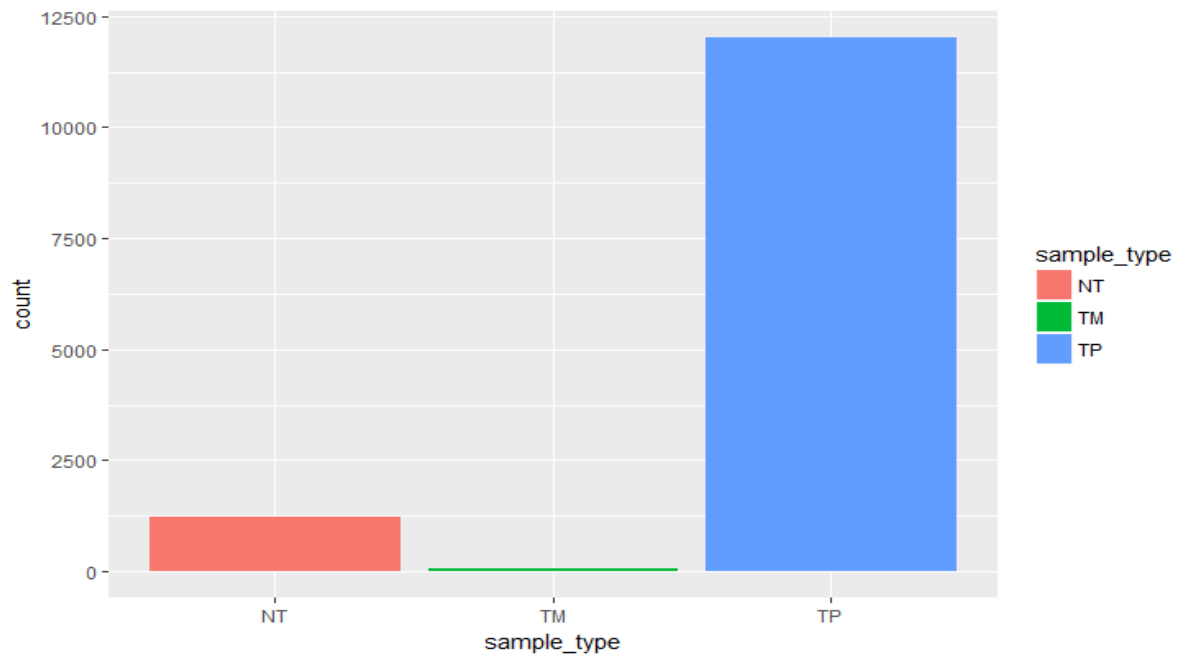


Records with dead as vital_status are more variable than alive. Median for dead is little bit higher than the median of alive.

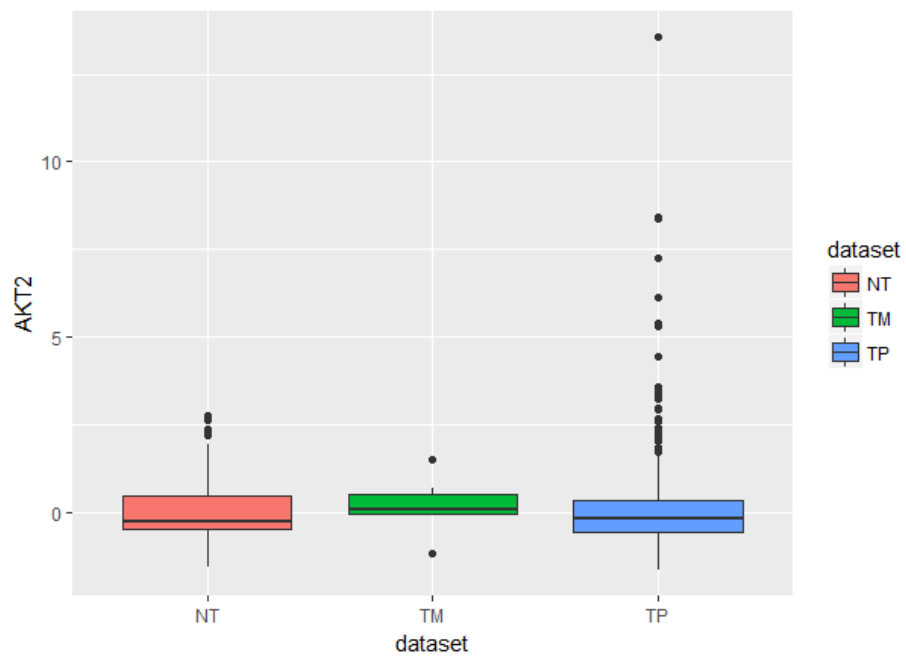
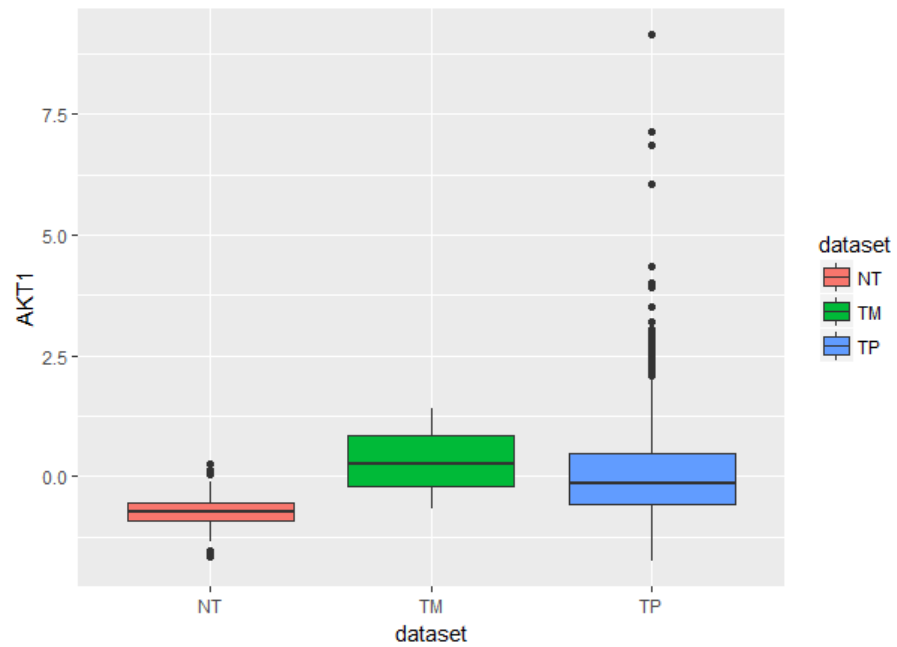


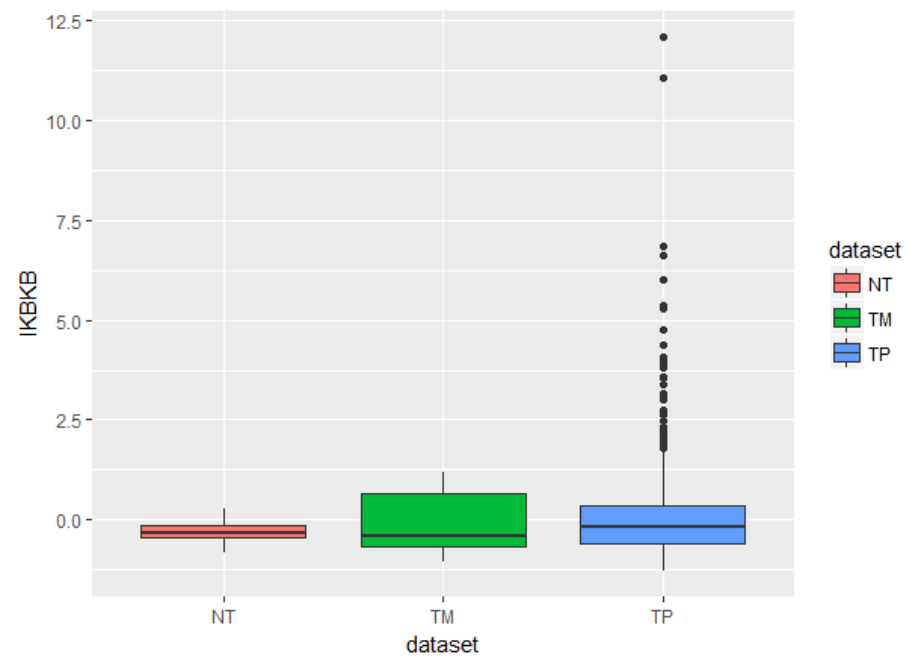
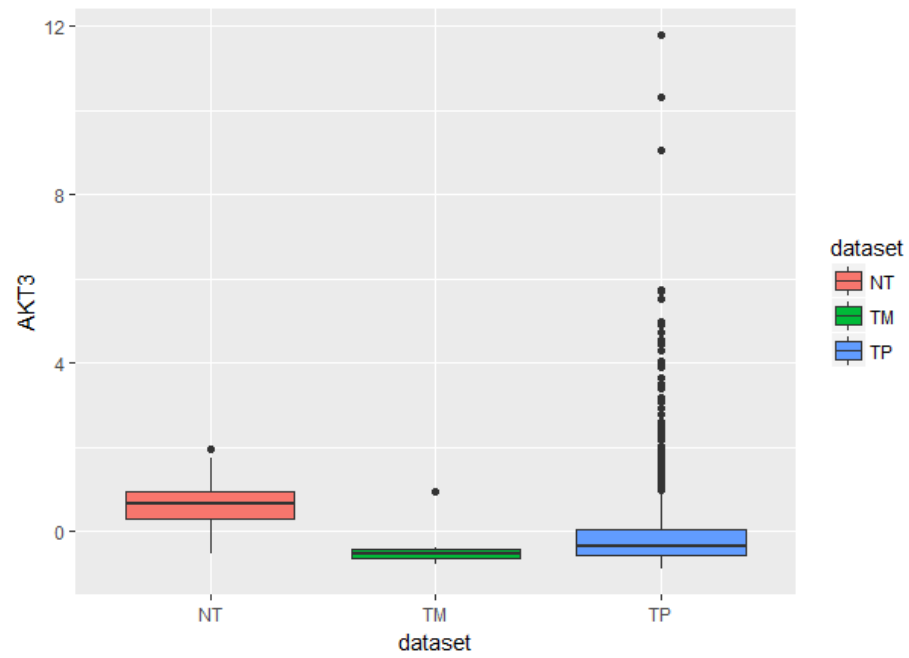
There are 12 male records with breast cancer and 1085 female records.

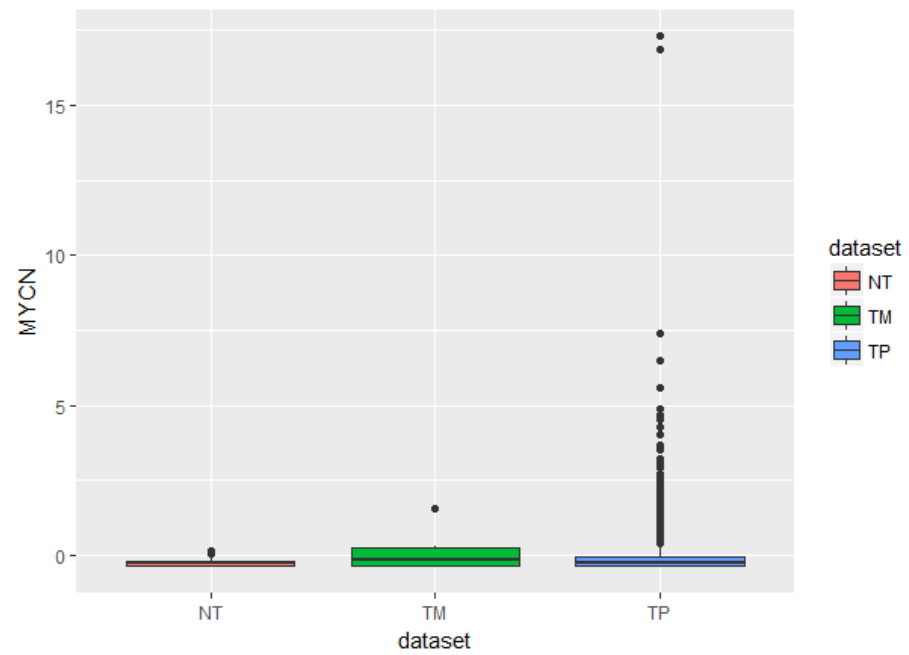
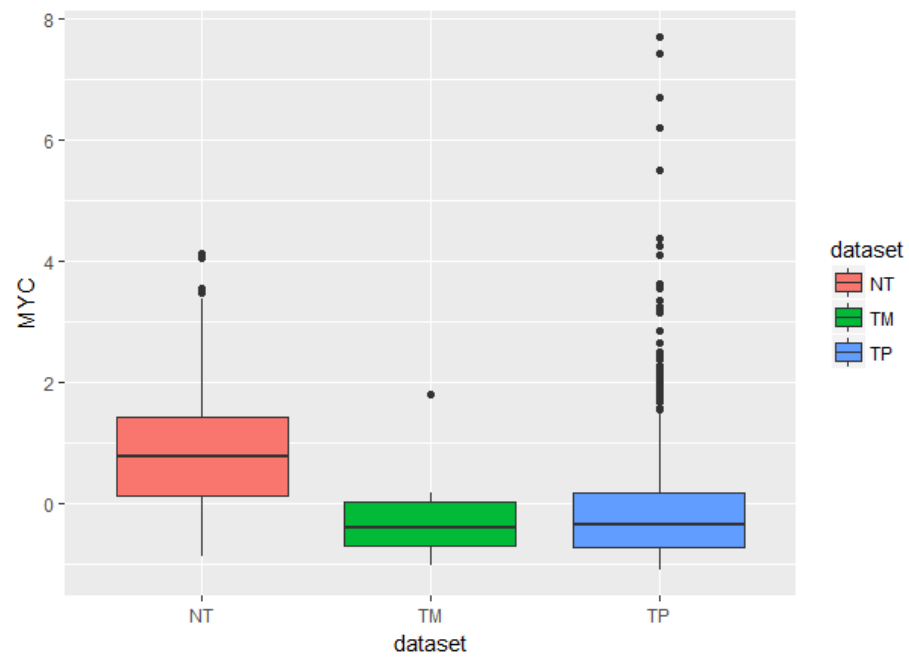
To download mRNA expression and Z.SCORE for my selected gene of interest, I have used Barcode present in the clinical dataset identical for each record and downloaded expression of selected genes using Firebrowse web API for R. There wasn't any record in mRNA expression for 4 barcodes and I have excluded the. Resulting mRNA expression dataset contains 13332 records for three (NT, TP and TM) sample types.

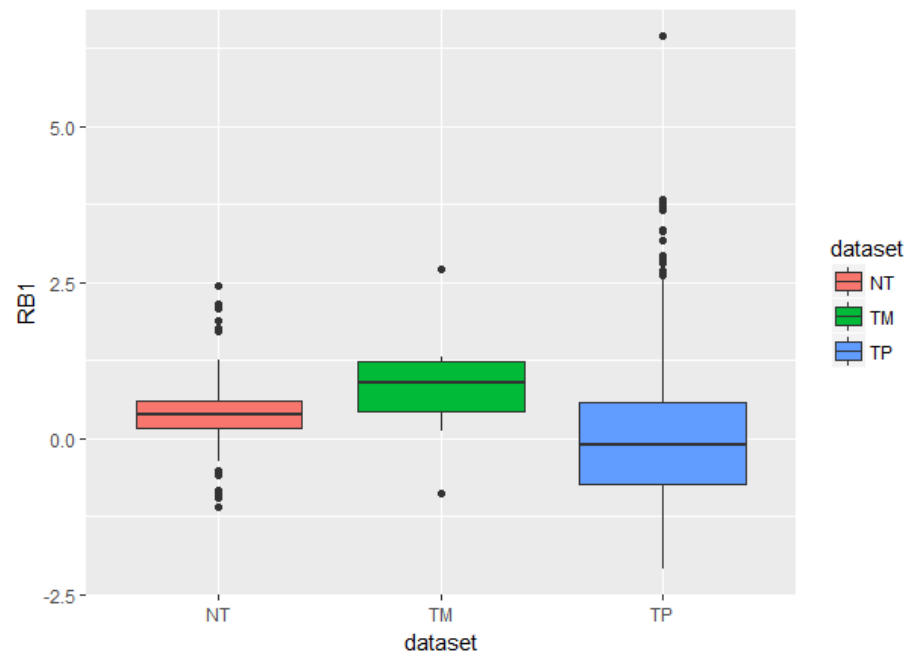
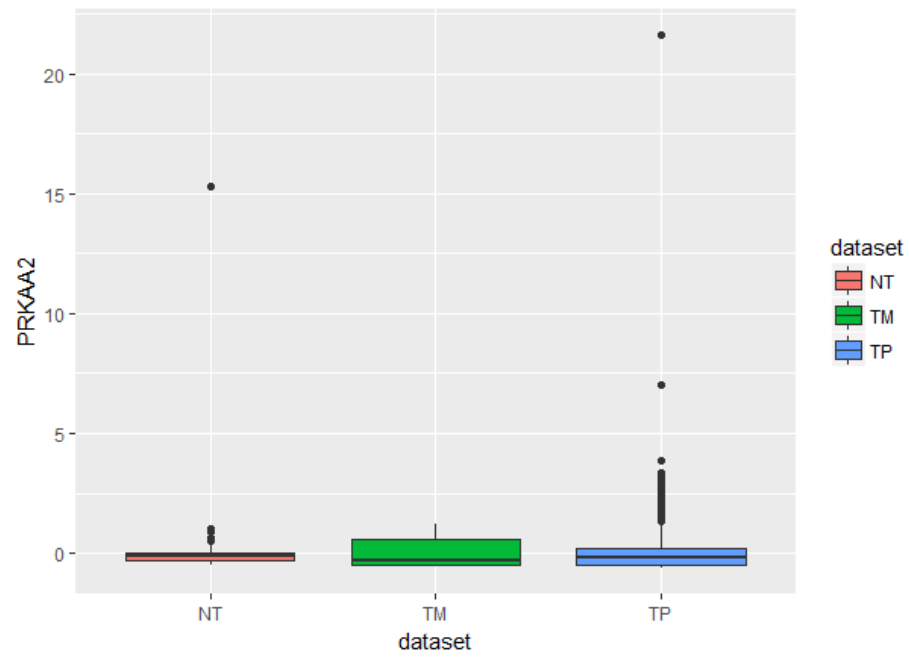


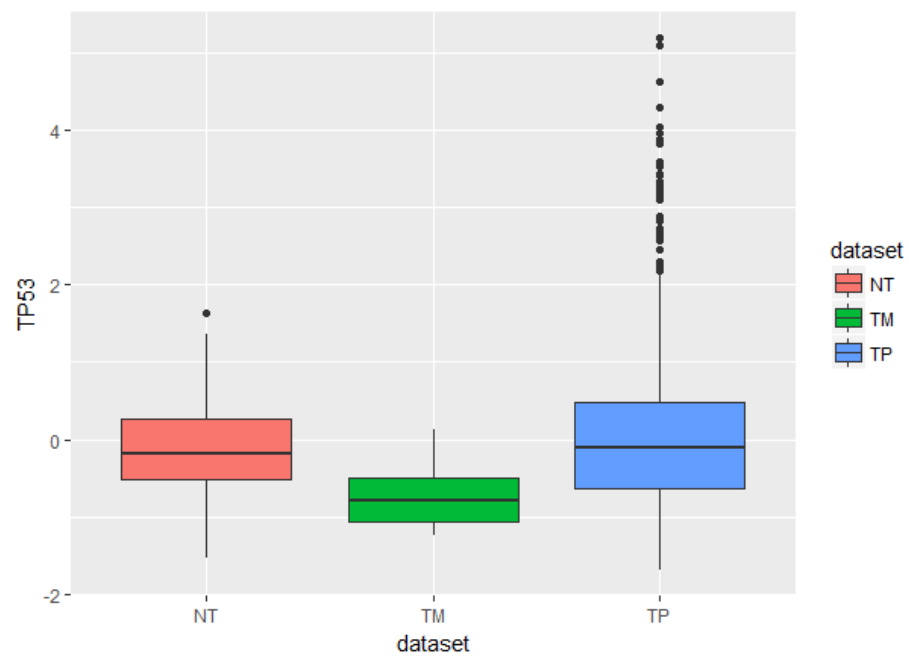
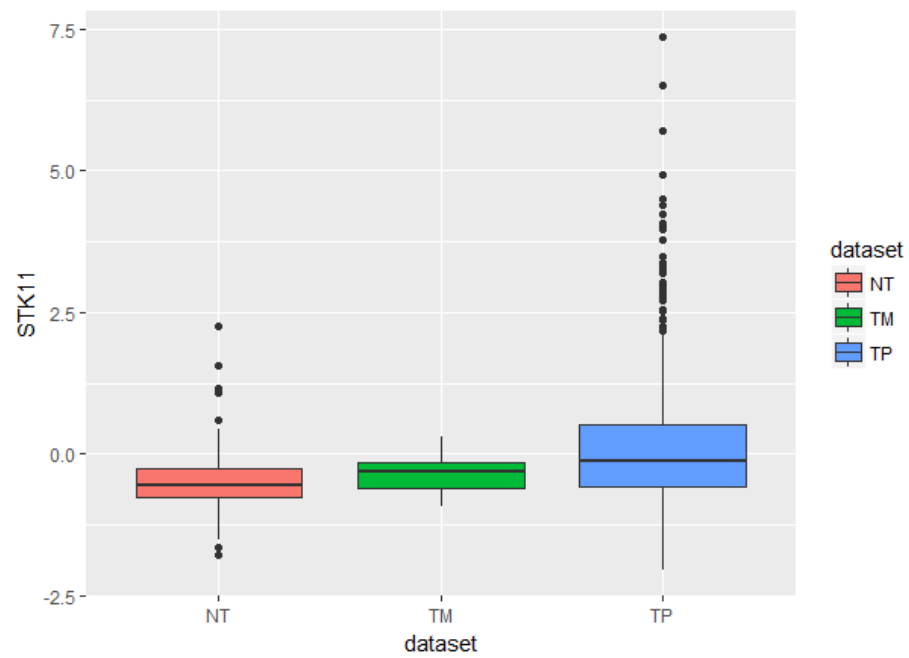
I have rearranged mRNA expression dataset and merged z_score and expression of each of the gene to respective barcode of clinical dataset. I have plotted zscore and expression distribution for each of the gene across three sample types using box plot and they are as below.



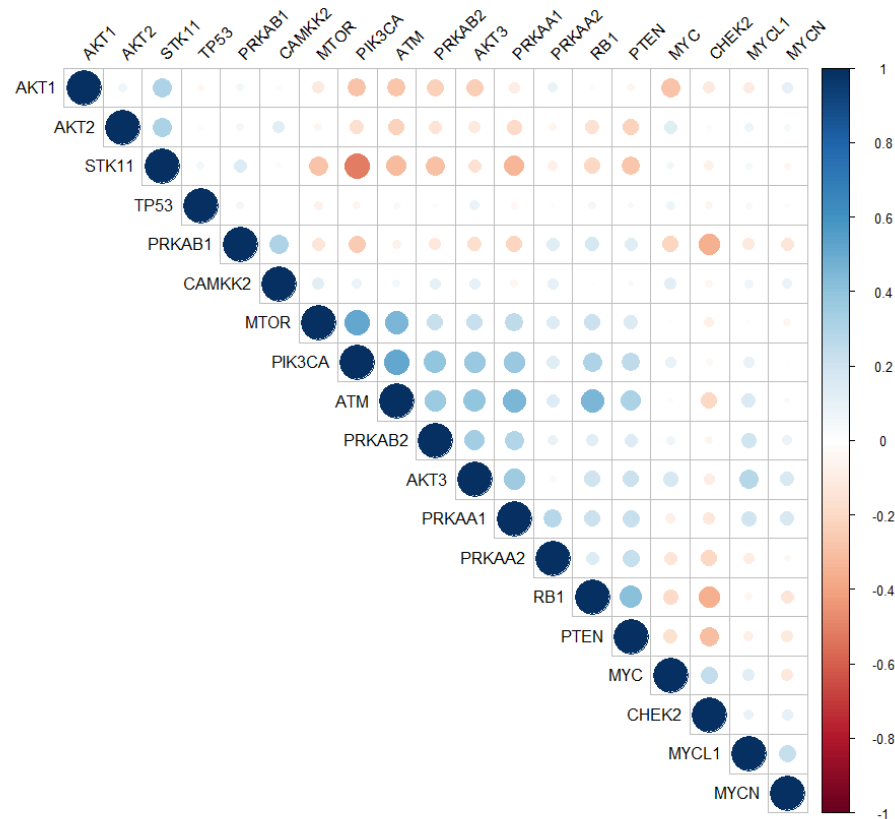




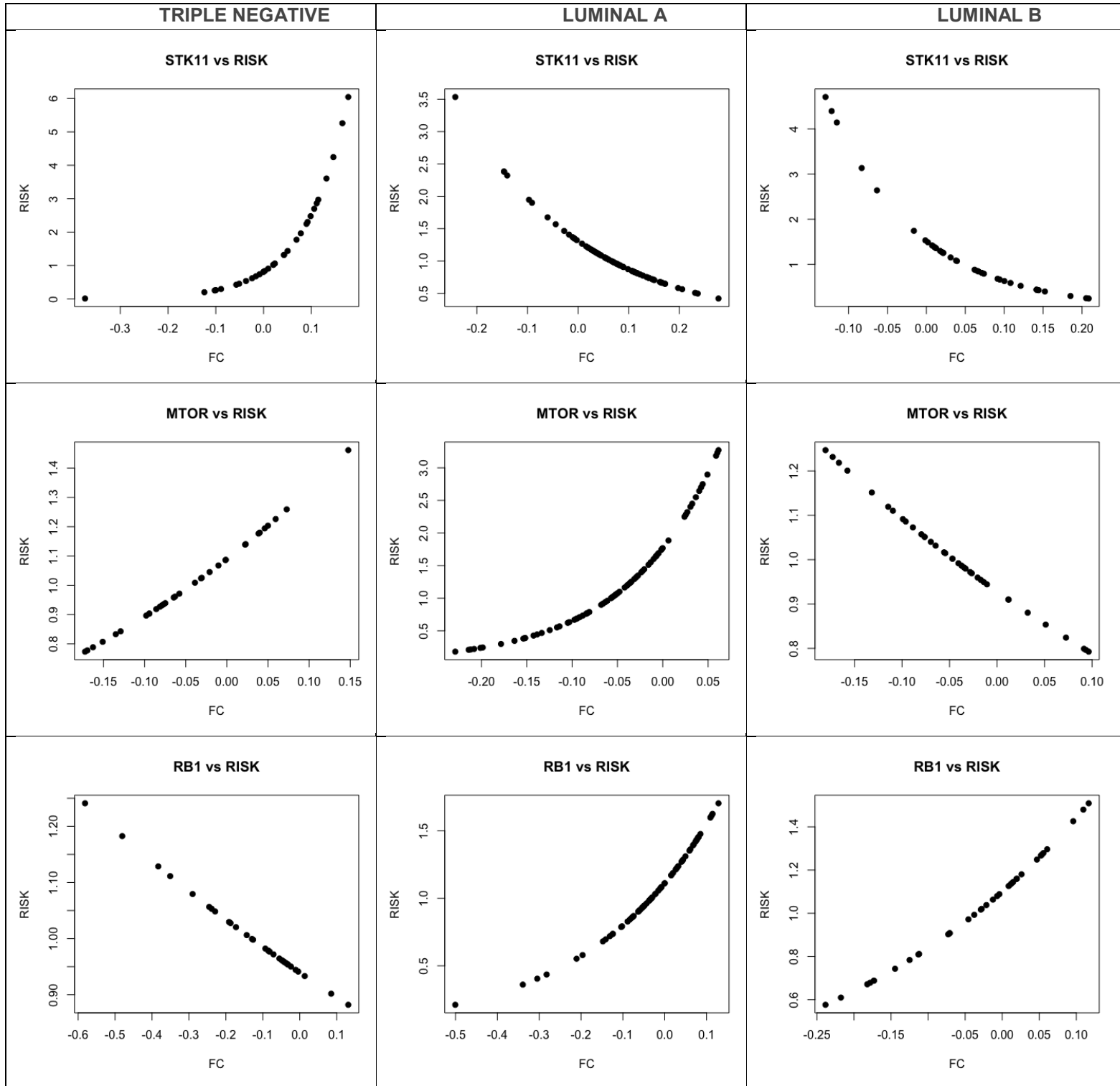


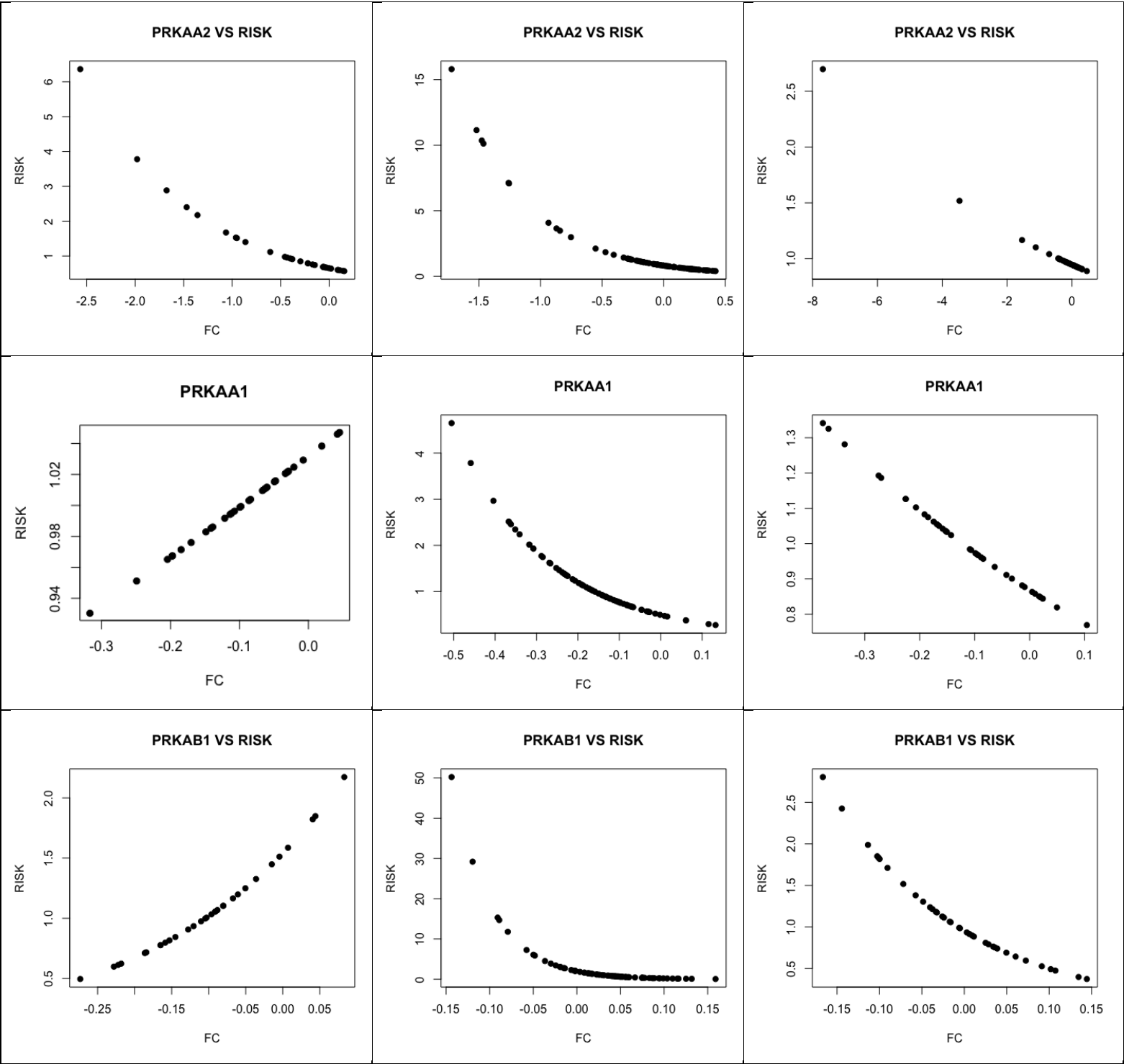


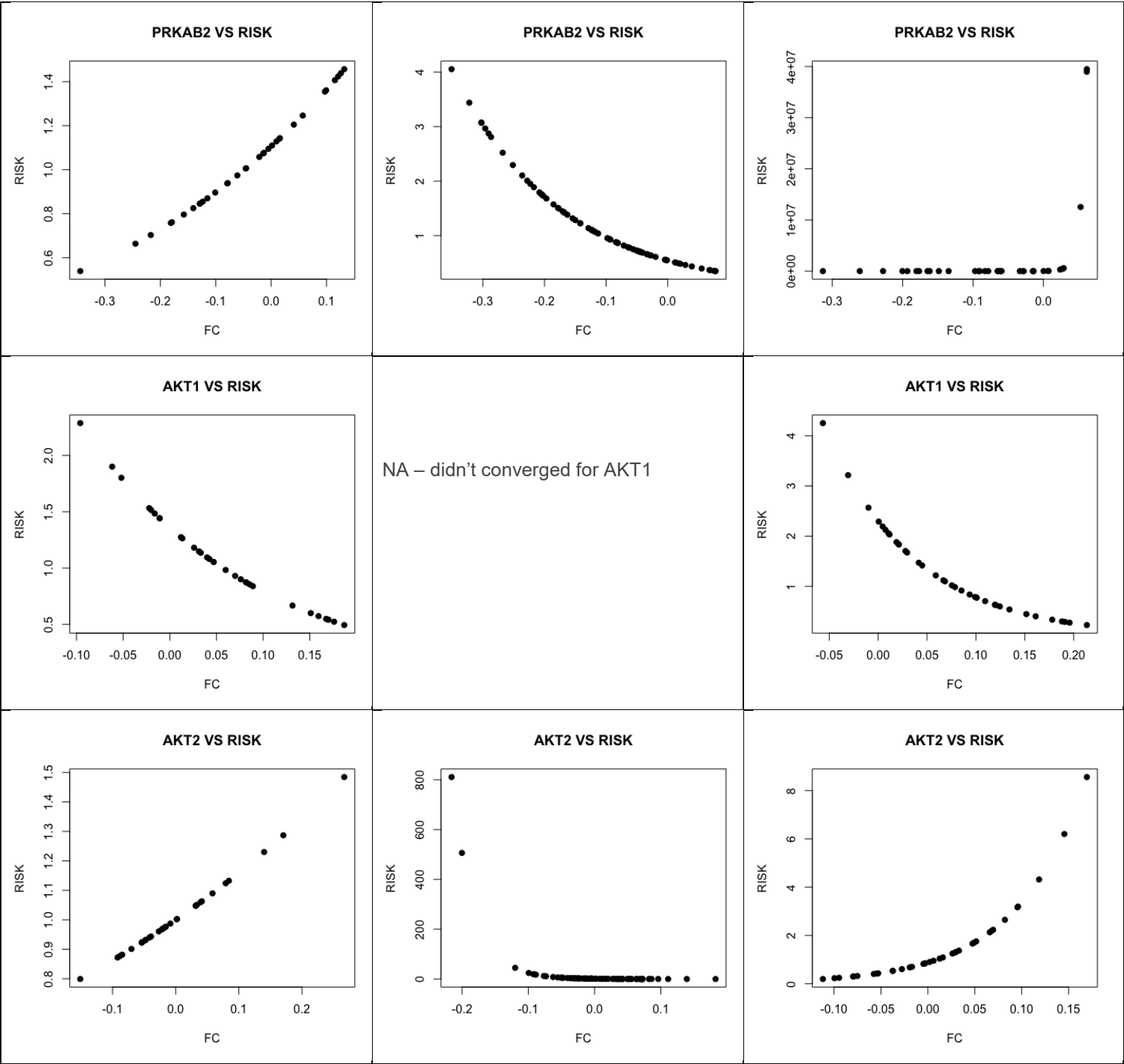
Correlation plot across gene using expression is as below.

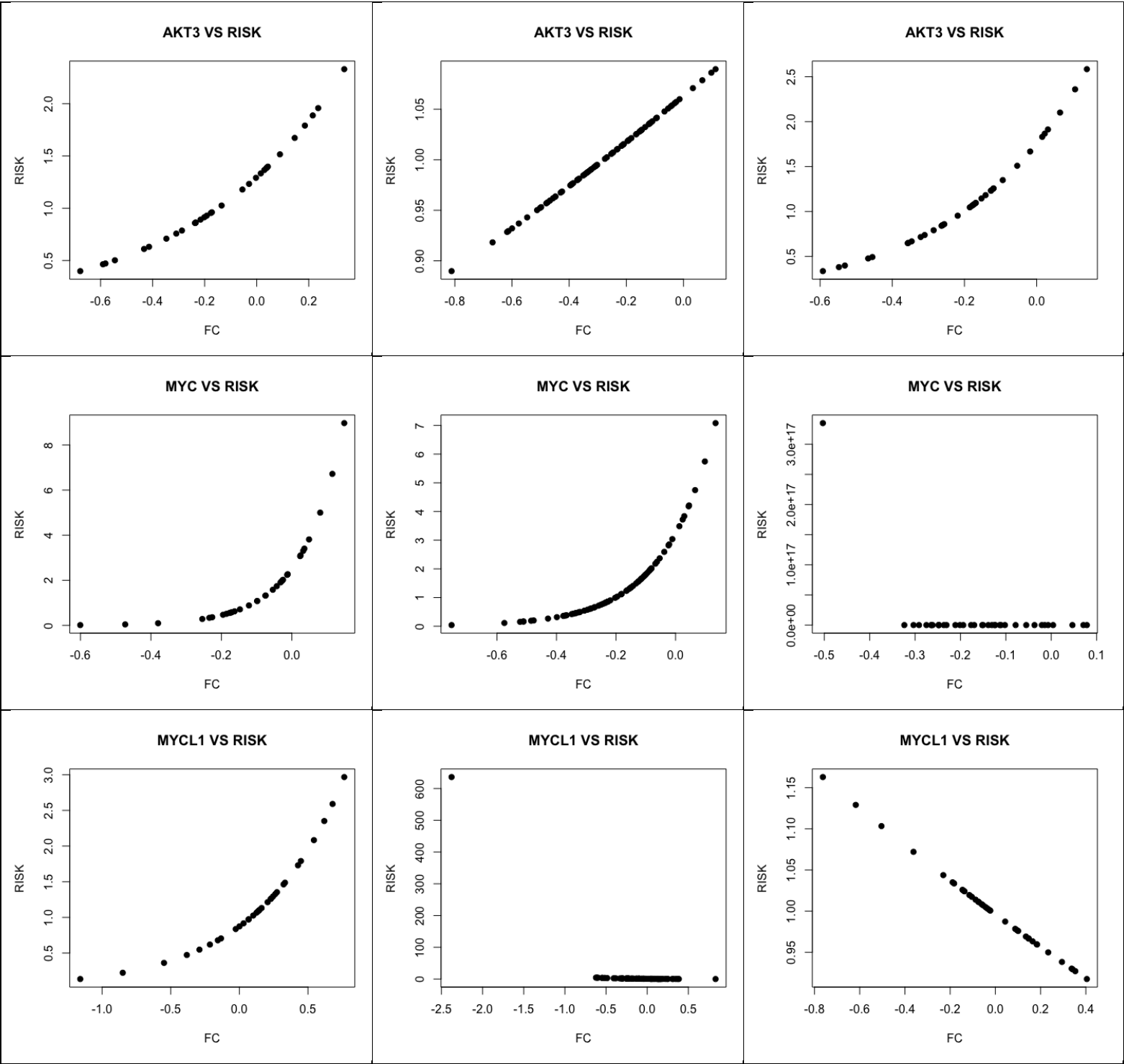


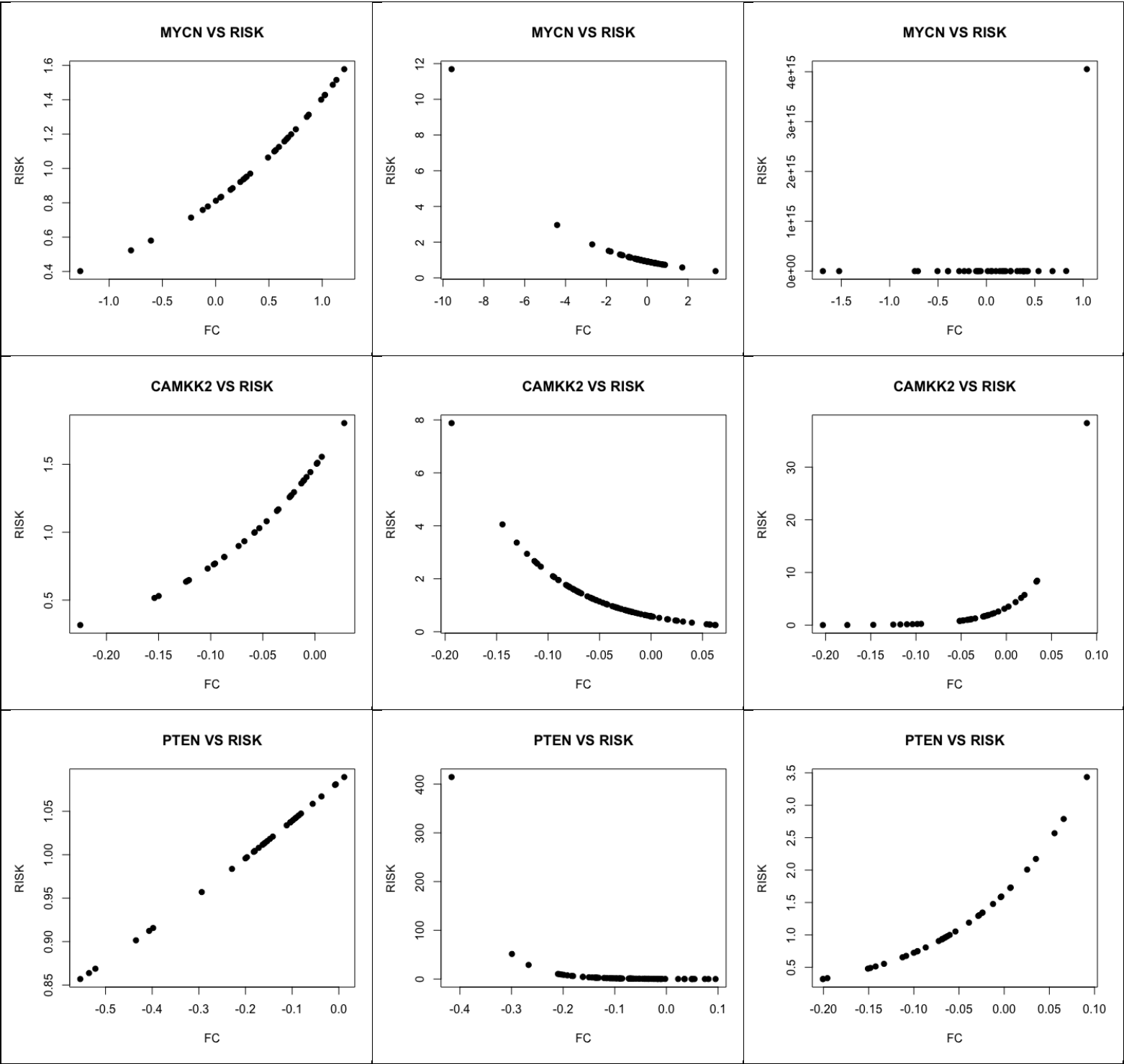
RISK PLOTS

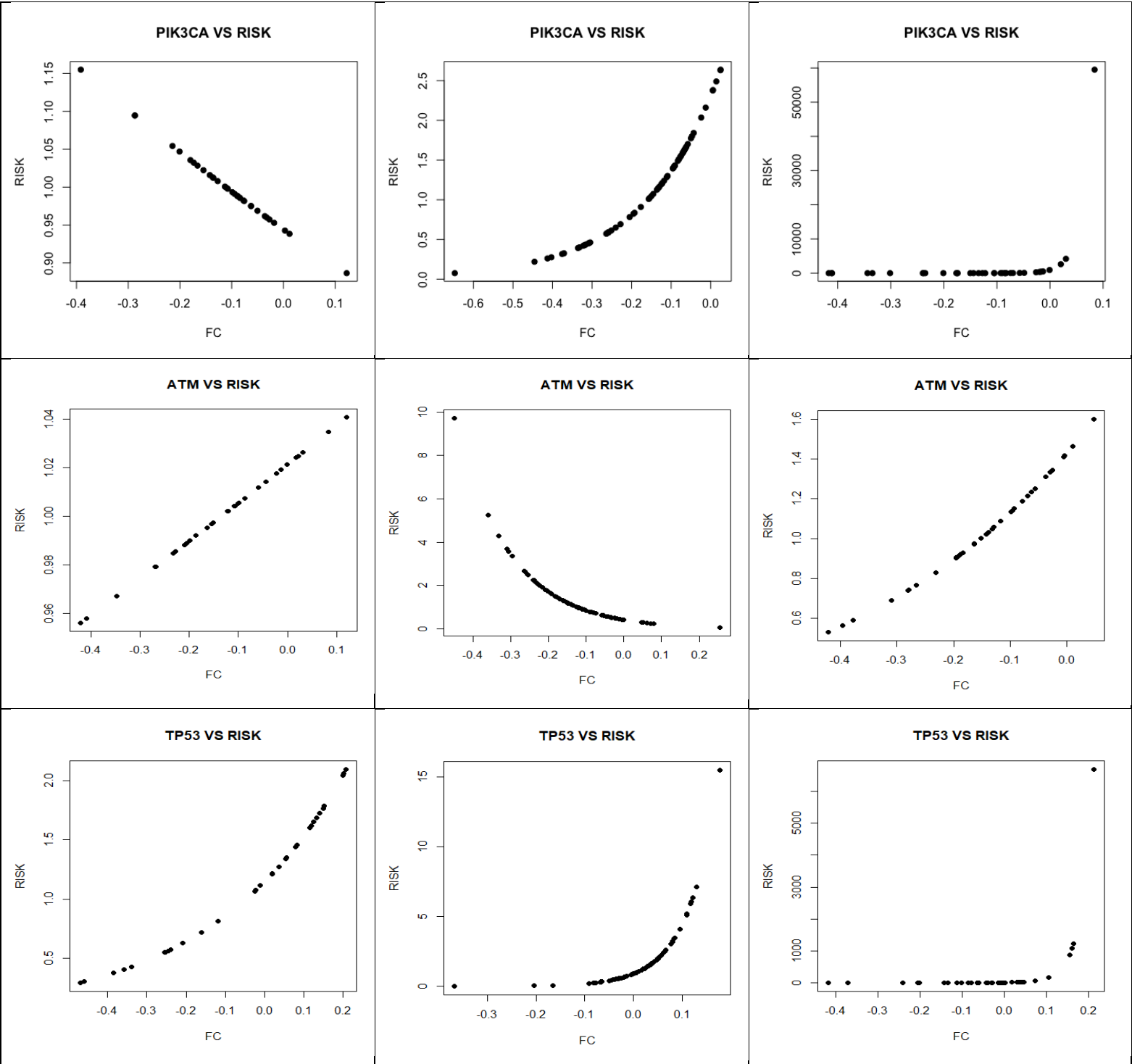












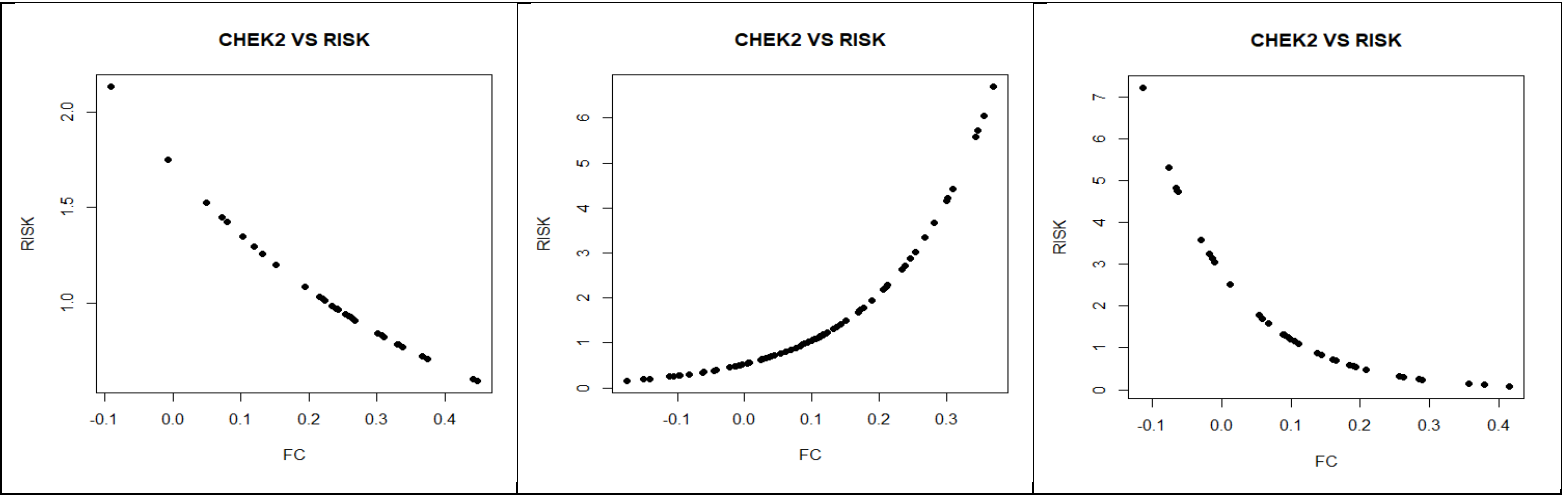


TABLE 1

SURVIVAL PLOTS

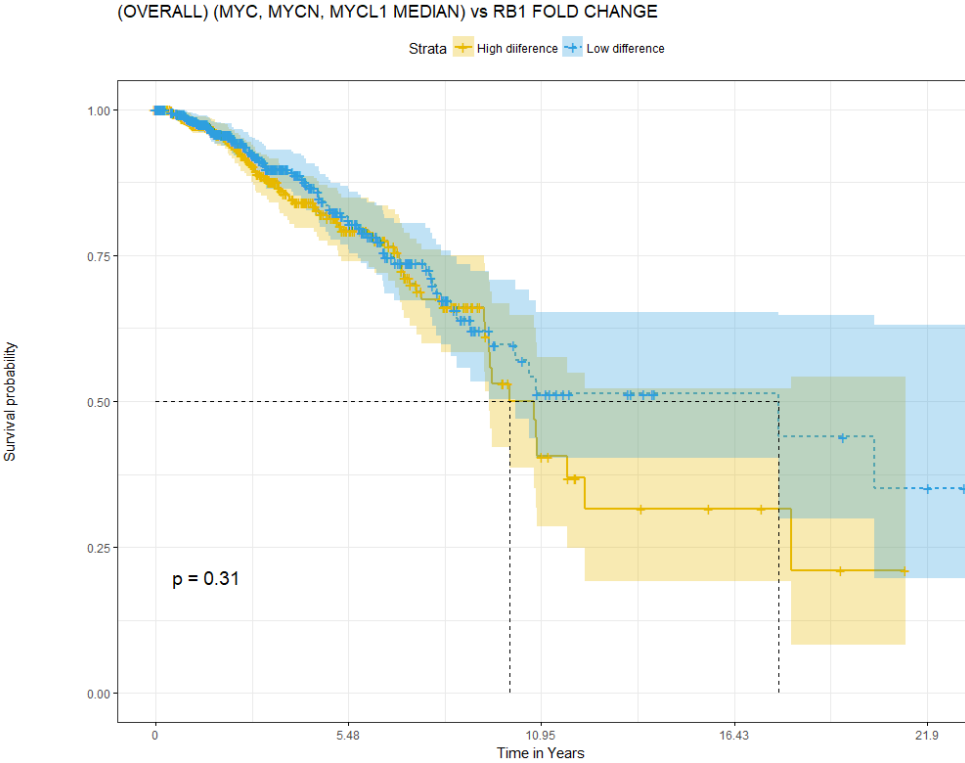


Figure 5

(TRIPLE NEGATIVE) - (MYC, MYCN, MYCL1 MEDIAN) vs RB1 FOLD CHANGE

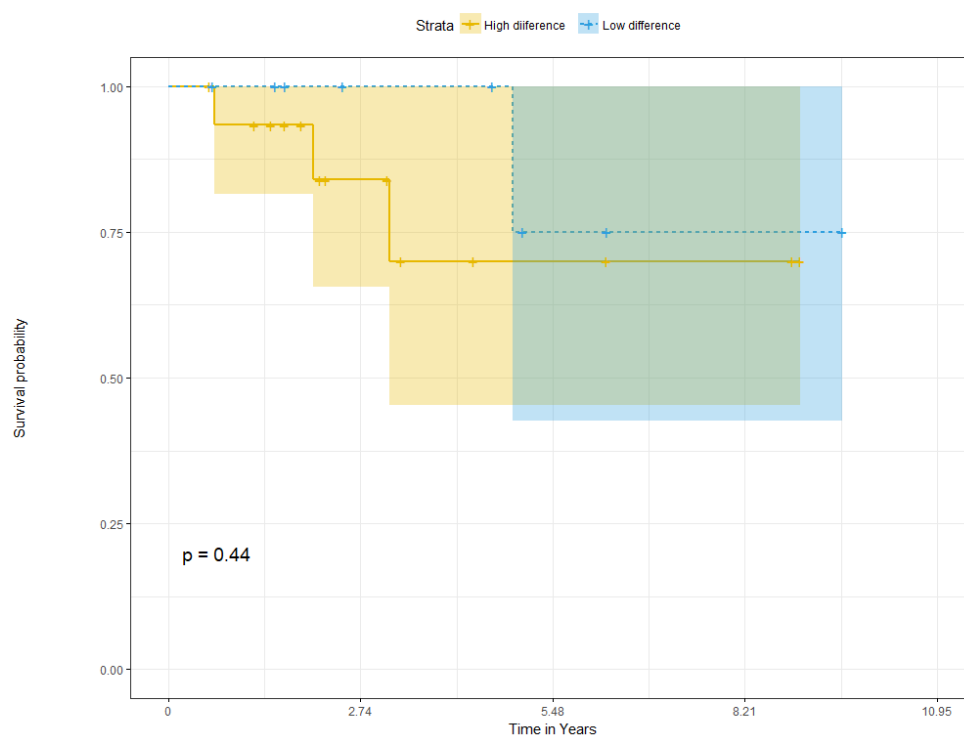


Figure 6

(LUMINAL) - (MYC, MYCN, MYCL1 MEDIAN) vs RB1 FOLD CHANGE

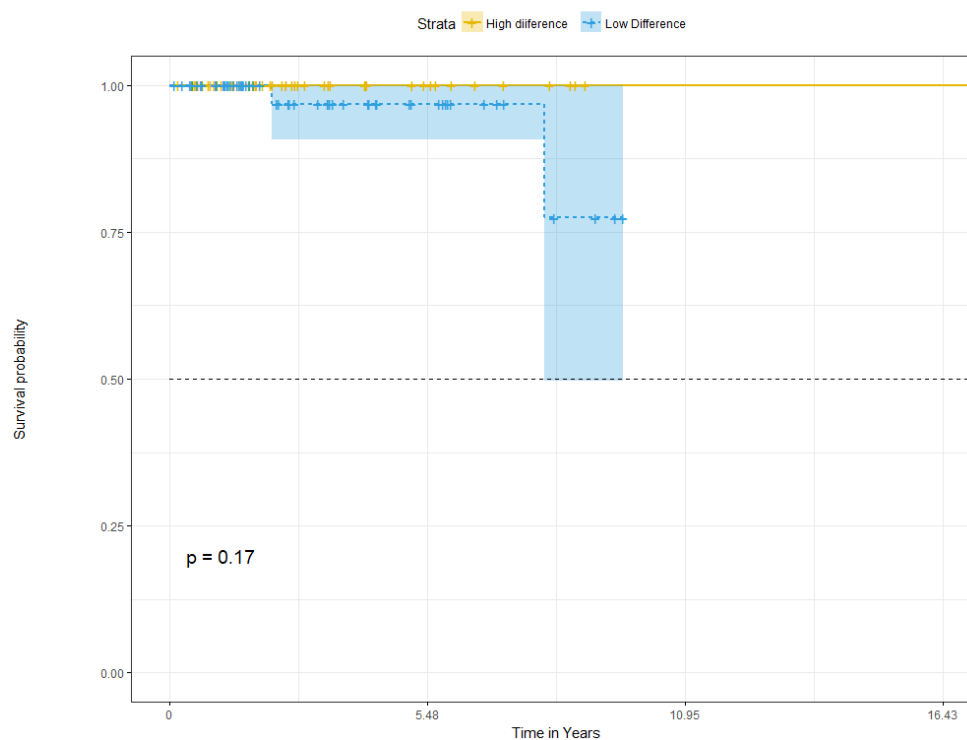


Figure 7

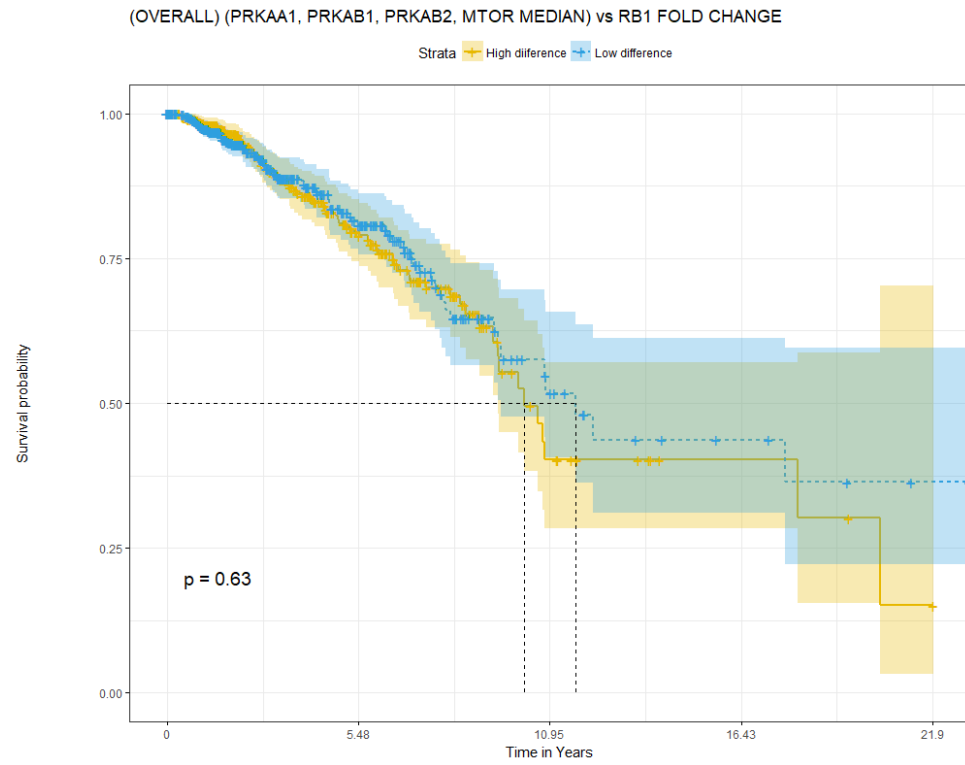


Figure 8

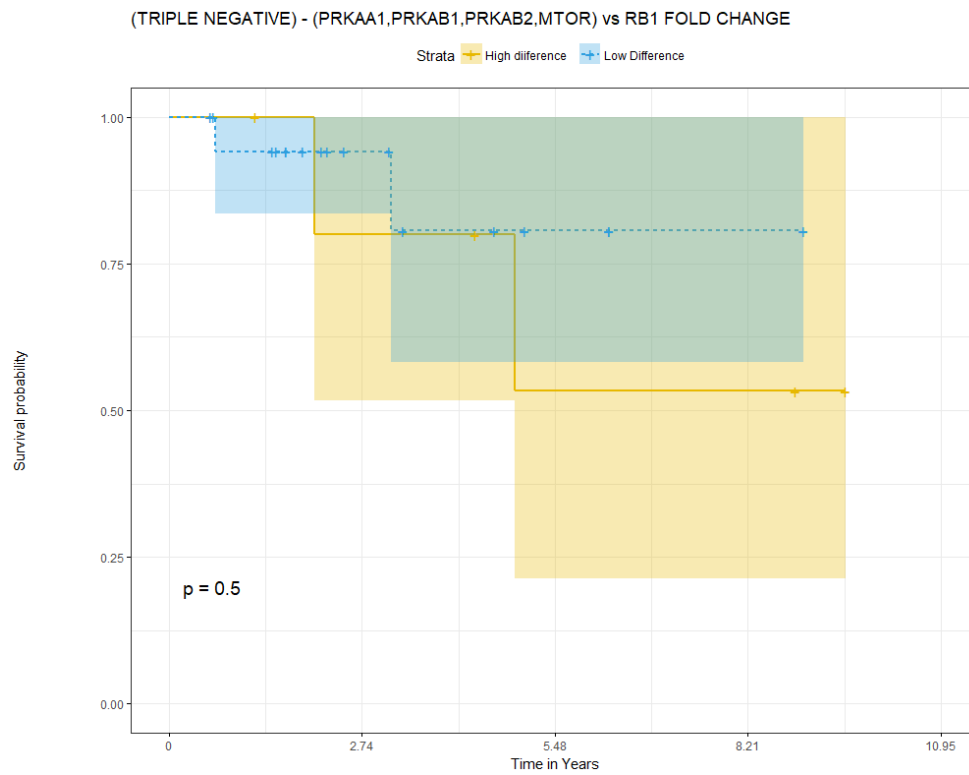


Figure 9

(OVERALL) (PRKAA1, PRKAB1, PRKAB2, MTOR, STK11 MEDIAN) vs RB1 FOLD CHANGE

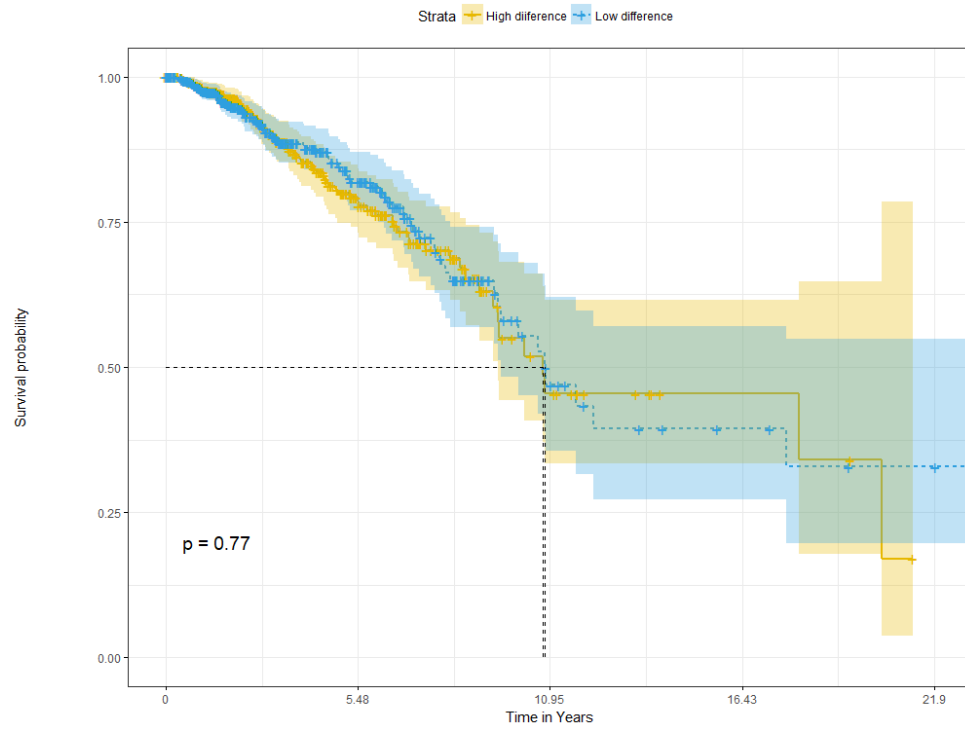


Figure 10

(TRIPLE NEGATIVE) - (PRKAA1,PRKAA2,PRKAB1,PRKAB2,MTOR, STK11 MEDIAN) vs RB1 FOLD CHANG

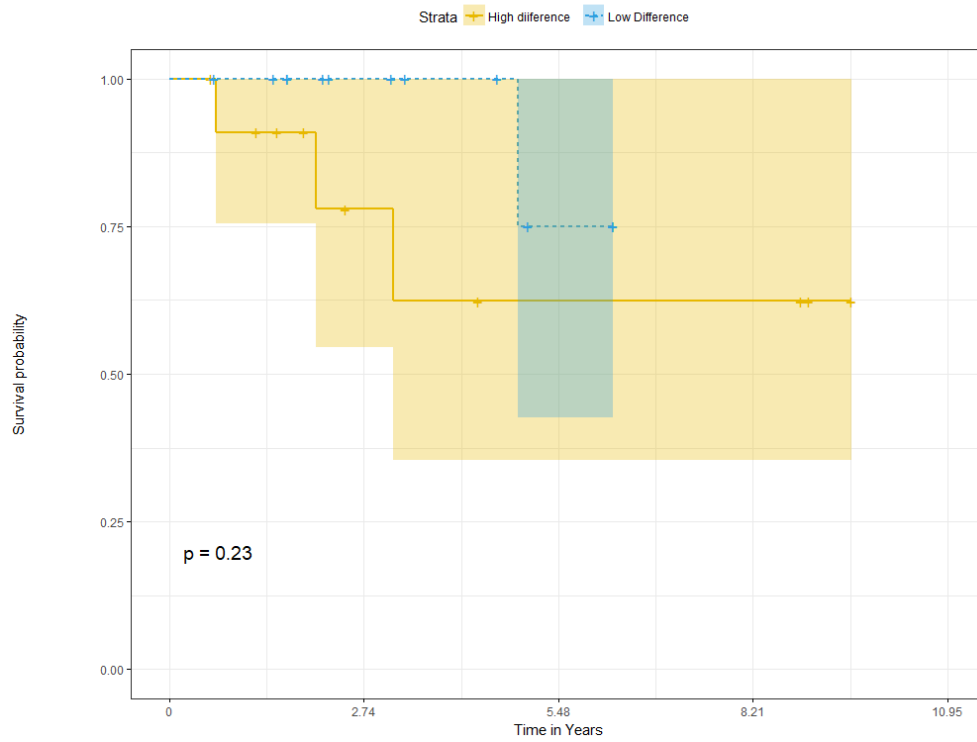


Figure 11

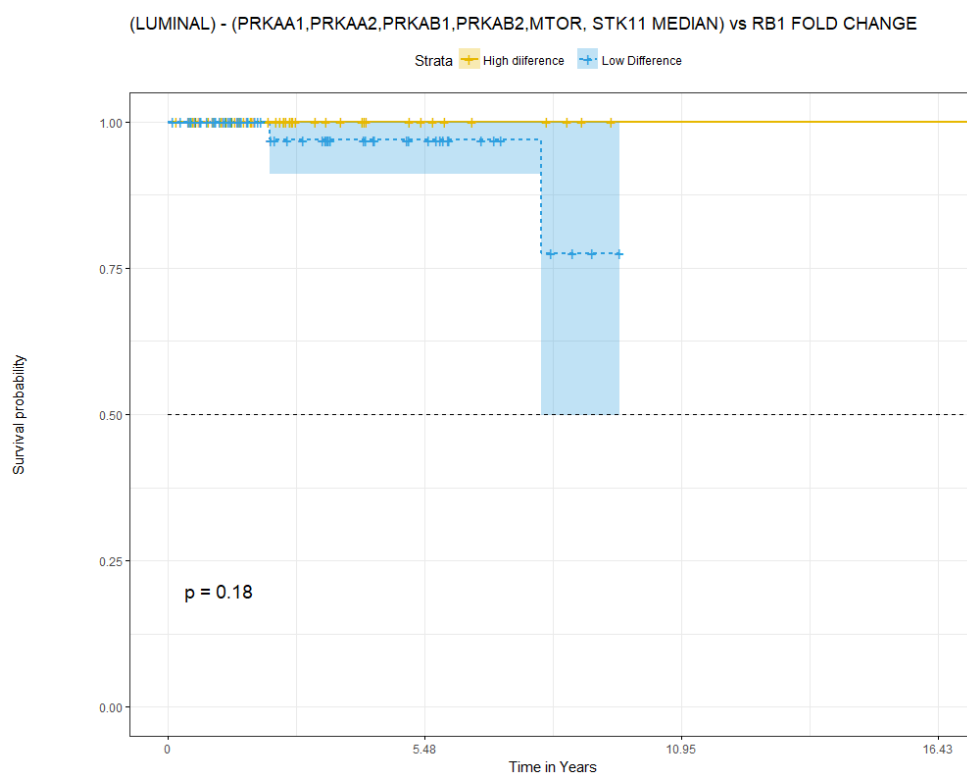


Figure 12