Report_RData

MariyaGolchinpour

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Download the MAF files for the following TCGA projects ACC, SARC, BRCA using the TCGABiolinks package in R.
(a) Save all datasets as RData files in the separate folders and files.
for first part we get all ACC, SARC, BRCA data using the TCGABiolinks and save as RData.

```
library(maftools)
```

(b)Use the maftools package to plot three plots of your choice and save the figures (in PDF and PNG) in a neat folder structure.

for part b : load RData from part a and then plot different maftools plot.

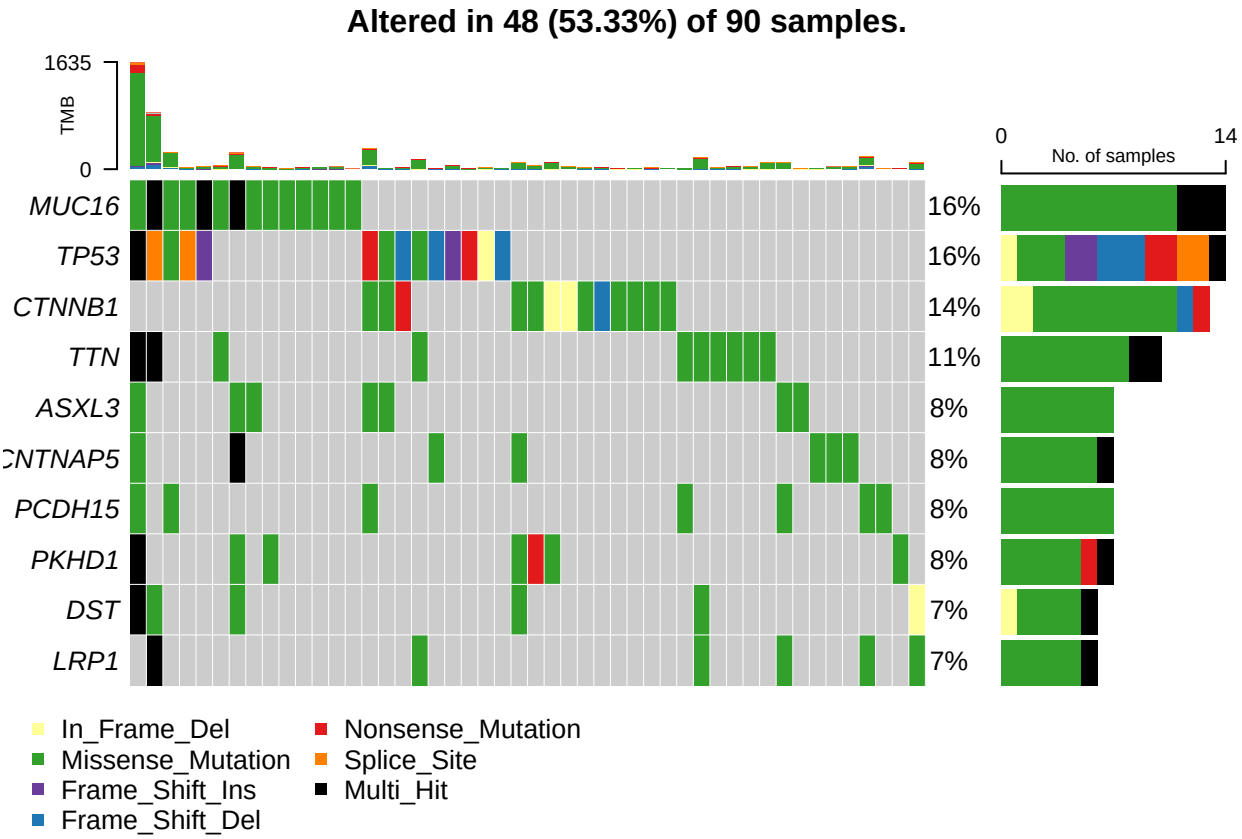
oncoplot

load ACC RData and the plot oncoplot

```
name<- "ACC"
input_name_path=paste0("inputs/maf/",name,"/",name,"_maf.RData")
load(file.path(input_name_path), RData <- new.env() )
laml <- read.maf(maf = RData$maf)
```

```
## -Validating
## -Silent variants: 2118
## -Summarizing
## --Possible FLAGS among top ten genes:
##   MUC16
##   TTN
##   DST
## -Processing clinical data
## --Missing clinical data
## -Finished in 0.553s elapsed (0.974s cpu)
```

```
oncoplot(maf = laml, top = 10)
```



RainfallPlot

load BRCA RData and then plot rainfallPlot

```
name<- "BRCA"
input_name_path=paste0("inputs/maf/",name,"/",name,"_maf.RData")
load(file.path(input_name_path), RData <- new.env() )
laml <- read.maf(maf = RData$maf)
```

```
## -Validating
## -Silent variants: 21938
## -Summarizing
## --Possible FLAGS among top ten genes:
##   TTN
##   MUC16
##   HMCN1
## -Processing clinical data
## --Missing clinical data
## -Finished in 7.461s elapsed (8.210s cpu)
```

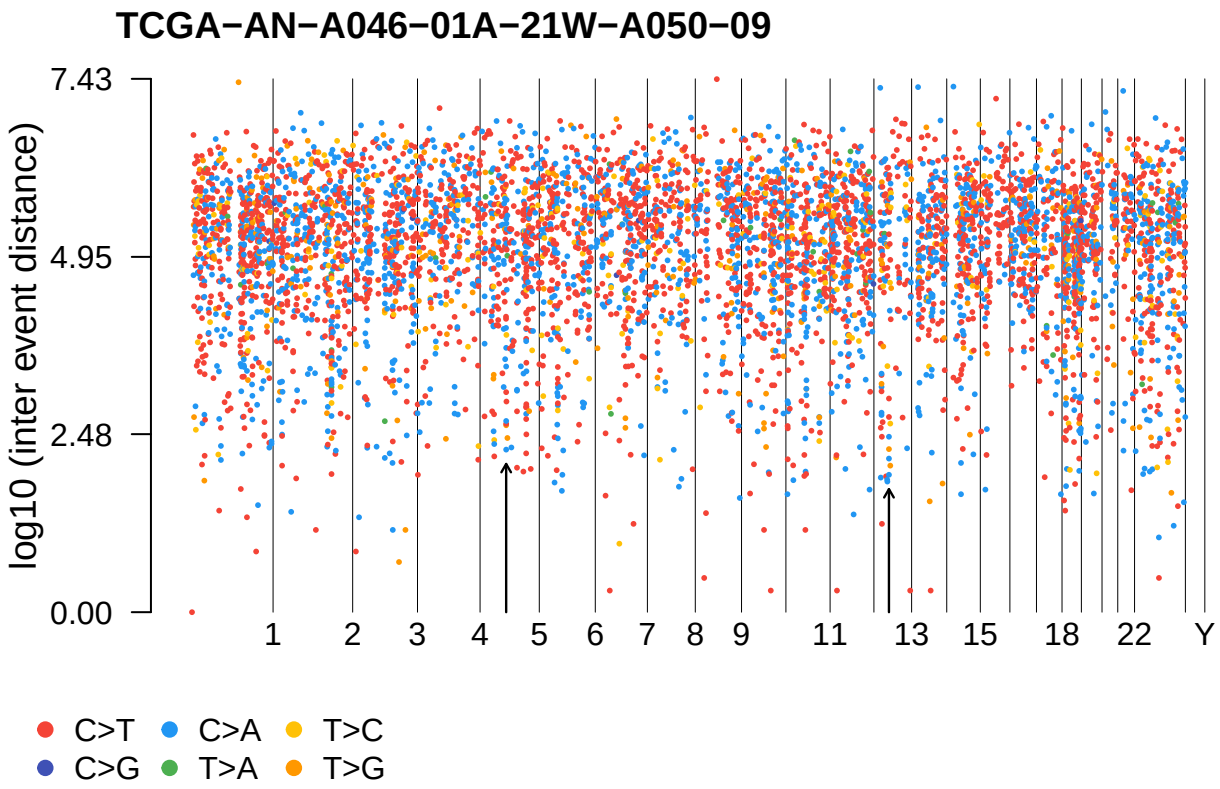
```
rainfallPlot(maf = laml, detectChangePoints = TRUE, pointSize = 0.4)
```

```
## Processing TCGA-AN-A046-01A-21W-A050-09..
```

```
## Kataegis detected at:
```

```
##    Chromosome Start_Position End_Position nMuts Avg_intermutation_dist Size
## 1:          5       79736501     79739125     6               524.8000 2624
## 2:         13       45967816     45969966     7               358.3333 2150
##            Tumor_Sample_Barcode C>A C>T T>G
```

```
## 1: TCGA-AN-A046-01A-21W-A050-09   3   2   1
## 2: TCGA-AN-A046-01A-21W-A050-09   3   3   1
```



SARC plotmafSummary

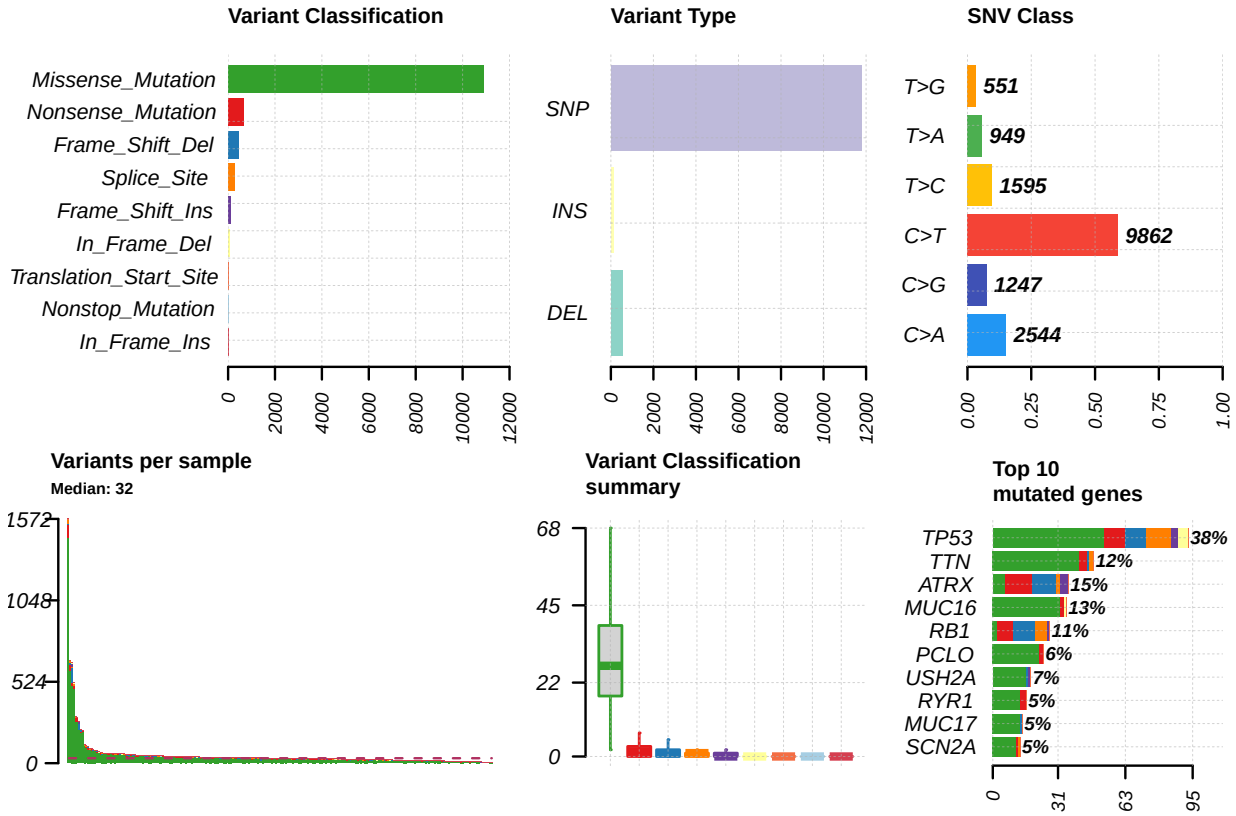
load SARC RData and then plot plotmafSummary

```
name<- "SARC"
input_name_path=paste0("inputs/maf/",name,"/",name,"_maf.RData")
load(file.path(input_name_path), RData <- new.env() )
laml <- read.maf(maf = RData$maf)
```

```
## -Validating
## -Silent variants: 4986
## -Summarizing
## --Possible FLAGS among top ten genes:
##   MUC16
##   TTN
##   USH2A
##   MUC17
## -Processing clinical data
## --Missing clinical data
## -Finished in 0.902s elapsed (1.263s cpu)
```

```
plotmafSummary(maf = laml, rmOutlier = TRUE, addStat = 'median', dashboard = TRUE, titvRaw = FALSE)
```

```
## Warning in titv(maf = maf, useSyn = TRUE, plot = FALSE): Non standard Ti/Tv
## class: 3TRUE
```



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.