Group 02 - Skin Cancer

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# **Preparations**

## 1.Loading following packages:

library(ggplot2)  
library(relaimpo)  
library(factoextra)  
library(gridExtra)  
library(reshape2)  
library(data.table)  
library(cluster)  
library(rstudioapi)  
library(pheatmap)  
library(caret)  
library(tidyverse)  
library(dendextend)  
library(factoextra)  
library(devtools)  
library(ggfortify)  
library(rstudioapi)   
library(data.table)   
library(ggplot2)   
library(scales)   
library(stats)  
library(caTools)

## (2. Setting the sys-path and loading the data)

The sys-path was used in R, but markdown could not knit it so the data was loaded as explained in step 3.

root.dir = dirname(rstudioapi::getSourceEditorContext()$path)  
data = readRDS(paste0(root.dir, "/DepMap19Q1\_allData.RDS"))

## 3. Loading the data set:

data = readRDS("C:/Users/Isip/Documents/Project 2/DepMap19Q1\_allData.RDS")

# **Part 1: Data Cleanup**

## **1.1 Extracting and splitting our data**

Defining a new matrix only containing the mutation data which is structured differently from the other matrices.

mut <- data$mutation

Additionally to the mutation matrix another matrix is needed containing all matrices except the mutation data.

'%!in%' <- function(x,y)!('%in%'(x,y)) # defining an operator that will only pick the data that is NOT defined in the list; so the data that needs to be excluded  
dt\_new <- lapply(which(names(data) %!in% "mutation"), function(a) data[[a]]) # extracting the non-mutation data   
names(dt\_new) <- names(data)[which(names(data) %!in% "mutation")] # renaming the data with the original names

Defining which samples will be taken out of the original dataset

sample\_case = c("Skin Cancer")

Looking at the annotation matrix and searching only for the primary diseases matching the previous defined sample\_case. A vector containing all the cell lines with skin cancer as the primary disease is obtained.

samples = data$annotation$DepMap\_ID[which(data$annotation$Primary.Disease == sample\_case)]

34 cell lines have the primary disease skin cancer.

Extracting all cell lines defined in the previous step out of the data (except the mutation matrix).

processed\_data <- lapply(1:length(dt\_new), function(a) { # picking the data for our sample   
 dat\_picker <- dt\_new[[a]] # picking one file at each iteration   
 if(names(dt\_new[a])== "annotation"){ # treating the annotations differnetly because the cell line names are in a colum and are not the columnames like in the other matrices  
 output <- dat\_picker[which(dat\_picker[,1] %in% samples),]  
 } else {  
 output <- dat\_picker[,which(colnames(dat\_picker) %in% samples)]# only taking the skin cancer cell lines   
 output <- output[complete.cases(output),] # only taking rows without NAs   
 output <- output[order(rownames(output)),] # reordering the genes according to their name  
 }  
 return(output)  
})  
names(processed\_data) <- names(dt\_new) # renameing the objects according to the original data  
rm(dt\_new,sample\_case) # removing objects which are not need anymore

Extracting the previously defined cell lines from the mutation data.

ids = which(names(mut) %in% samples)   
allDepMap\_mutation\_SkinCancer = lapply(ids, function(a) {  
 mut[[a]]})  
rm(mut, ids, data) #tidying

Losing the mutations which are not deleterious meaning not interesting to us.

allDepMap\_mutation\_SkinCancer = lapply(1:34, function(a) {  
 allDepMap\_mutation\_SkinCancer[[a]][which(allDepMap\_mutation\_SkinCancer[[a]][,"isDeleterious"]== TRUE), ]  
 })  
names(allDepMap\_mutation\_SkinCancer) <- samples

Losing all genes which are not in every data frame. First, all gene names have to be picked out of the data.

Genenames <- unique(c(rownames(processed\_data[[1]]),rownames(processed\_data[[2]]),rownames(processed\_data[[3]]),rownames(processed\_data[[4]])))

Then picking these genes which are in all 4 data frames which are needed for further analysis.

i <- 1  
out <- vector("character", length(seq\_along(1:16970)))# length of the matrix   
for (x in seq\_along(Genenames)) {  
 if(Genenames[x] %in% rownames(processed\_data$expression) & Genenames[x] %in% rownames(processed\_data$copynumber) & Genenames[x] %in% rownames(processed\_data$kd.ceres) & Genenames[x] %in% rownames(processed\_data$kd.prob))  
 {out[i] <- Genenames[x]  
 i <- i+1  
 }   
}  
  
allDepMap\_annotation\_SkinCancer <- processed\_data$annotation # saving the annotation object in a seperate dataframe  
# because it doesnt contain any information about the genes   
  
processed\_data <- lapply(processed\_data[1:4], function(a) {  
 a <- a[which(rownames(a) %in% out),]  
 return(a)  
})  
  
processed\_data$mutation <- allDepMap\_mutation\_SkinCancer  
processed\_data$annotation <- allDepMap\_annotation\_SkinCancer  
rm(i,out, Genenames,x, allDepMap\_annotation\_SkinCancer, samples, allDepMap\_mutation\_SkinCancer)

Looking at the processed data

lapply(processed\_data, head)

## $expression  
## ACH-000014 ACH-000274 ACH-000304 ACH-000322 ACH-000348 ACH-000401  
## A1BG 6.08661395 0.79908731 5.21179100 5.24716800 5.67694436 4.62468581  
## A1CF 0.05658353 0.08406426 0.01435529 0.04264434 0.00000000 0.00000000  
## A2M 6.14425036 7.95006009 6.83605000 6.00360224 4.62993941 4.14241344  
## A2ML1 0.23878686 0.01435529 0.00000000 0.00000000 0.01435529 0.01435529  
## A4GALT 0.97819563 0.02856915 0.12432810 0.98550043 3.09592442 0.05658353  
## A4GNT 0.07038933 0.11103131 0.00000000 0.04264434 0.09761080 0.15055968  
## ACH-000404 ACH-000425 ACH-000450 ACH-000458 ACH-000477 ACH-000550  
## A1BG 4.35543920 5.6088092 4.90352037 2.91073266 5.21878117 3.00000000  
## A1CF 0.01435529 0.0000000 0.01435529 0.02856915 0.00000000 0.01435529  
## A2M 4.23649262 4.1160320 0.87184365 0.15055968 7.50000529 0.50589093  
## A2ML1 0.05658353 0.0000000 0.00000000 0.11103131 0.08406426 0.00000000  
## A4GALT 1.93357264 0.7136958 0.04264434 3.53605290 3.23266076 2.01792191  
## A4GNT 0.21412481 0.2265085 0.09761080 0.02856915 0.01435529 0.26303441  
## ACH-000579 ACH-000580 ACH-000614 ACH-000632 ACH-000661 ACH-000765  
## A1BG 4.99819550 4.21955577 5.95559179 5.14159628 5.07553300 5.12598200  
## A1CF 0.00000000 0.01435529 0.00000000 0.00000000 0.00000000 0.00000000  
## A2M 3.86294725 7.10737402 1.58496250 2.87970577 4.27052900 2.11769500  
## A2ML1 0.00000000 0.01435529 0.04264434 0.09761080 0.00000000 0.00000000  
## A4GALT 0.00000000 0.01435529 0.11103131 3.64385619 1.30451100 0.05658353  
## A4GNT 0.04264434 0.11103131 0.16349873 0.07038933 0.07038933 0.00000000  
## ACH-000788 ACH-000799 ACH-000805 ACH-000810 ACH-000822 ACH-000827  
## A1BG 4.71149491 4.47638169 5.49185310 4.93310047 5.87184365 4.63865300  
## A1CF 0.01435529 0.01435529 0.00000000 0.00000000 0.08406426 0.01435529  
## A2M 1.67807191 6.75207953 7.33252893 7.46229777 8.12236212 3.24944500  
## A2ML1 0.01435529 0.01435529 0.04264434 0.00000000 0.01435529 0.00000000  
## A4GALT 0.33342373 0.48542683 0.44360665 0.04264434 0.13750352 0.59454850  
## A4GNT 0.01435529 0.13750352 0.01435529 0.00000000 0.09761080 0.32192810  
## ACH-000881 ACH-000882 ACH-000884 ACH-000915 ACH-000968 ACH-001239  
## A1BG 4.74092756 5.0518071 5.2720232 5.62877360 4.37016428 5.43596200  
## A1CF 0.01435529 0.0000000 0.0000000 0.00000000 0.00000000 0.08406426  
## A2M 0.67807191 3.4633609 0.1890338 1.40053793 1.38956681 3.80838500  
## A2ML1 0.00000000 0.0000000 0.0000000 0.01435529 0.04264434 0.00000000  
## A4GALT 0.01435529 0.8559897 0.0000000 0.08406426 0.05658353 0.16349870  
## A4GNT 0.07038933 0.1763228 0.2509616 0.07038933 0.00000000 0.00000000  
## ACH-001328 ACH-001523 ACH-001550 ACH-001552  
## A1BG 0.88752530 1.45943200 3.45943200 1.13750400  
## A1CF 0.00000000 0.00000000 0.00000000 0.01435529  
## A2M 0.20163390 0.42223300 0.53605290 6.43912400  
## A2ML1 0.07038933 1.64154600 0.00000000 0.00000000  
## A4GALT 2.88362100 4.73552200 3.73552200 2.25398900  
## A4GNT 0.00000000 0.02856915 0.07038933 0.12432810  
##   
## $copynumber  
## ACH-000014 ACH-000274 ACH-000304 ACH-000322 ACH-000348 ACH-000401  
## A1BG 0.0989 -0.097469 0.0184 0.0536 0.2243 -0.3384  
## A1CF -0.3120 0.005770 -0.9286 -0.3620 -0.2004 -0.3723  
## A2M 0.1110 0.014809 0.0080 0.0876 -0.1028 -0.1540  
## A2ML1 0.1110 0.014809 0.0080 0.1893 -0.1028 -0.1540  
## A4GALT 0.0580 -0.011931 0.0359 0.2368 -0.1255 0.2199  
## A4GNT 0.0961 -0.001092 0.0207 0.4689 0.2784 0.4726  
## ACH-000404 ACH-000425 ACH-000450 ACH-000458 ACH-000477 ACH-000550  
## A1BG -0.022307 0.0764 -0.1396 -0.4496 -0.027449 0.1501  
## A1CF -0.903048 -0.6957 -0.5844 0.0539 -0.295058 0.1532  
## A2M 0.039112 0.1406 -0.0922 0.1233 0.118007 0.4619  
## A2ML1 0.039112 0.1688 -0.0922 0.1233 0.118007 0.4619  
## A4GALT -0.020720 0.2226 0.5669 -0.4813 0.132716 0.2868  
## A4GNT 0.061321 0.8102 0.3392 0.4795 0.263405 0.2049  
## ACH-000579 ACH-000580 ACH-000614 ACH-000632 ACH-000661 ACH-000765  
## A1BG 0.0386 -0.0773 -0.0416 0.1545 -0.216485 -0.245591  
## A1CF -0.7448 -1.0253 -0.4873 -0.3467 -0.235150 -0.244737  
## A2M 0.0618 -0.0295 0.1386 -0.3945 0.157620 -0.248476  
## A2ML1 0.1621 -0.0295 0.1386 -0.3945 0.157620 -0.248476  
## A4GALT 0.1265 0.5558 0.7224 0.1664 0.388845 0.409699  
## A4GNT 0.2391 -0.0724 0.0038 0.0868 0.182210 0.336595  
## ACH-000788 ACH-000799 ACH-000805 ACH-000810 ACH-000822 ACH-000827  
## A1BG -0.1277 0.280709 -0.049072 -0.4531 0.0243 -0.091521  
## A1CF -0.1013 -1.211382 0.011745 0.0201 -0.9432 -0.072792  
## A2M -0.0707 -0.248236 0.564218 0.2046 0.3548 -0.074585  
## A2ML1 -0.0707 -0.248236 0.564218 0.2046 0.0190 -0.074585  
## A4GALT -0.0341 0.261440 0.533162 0.0759 0.0076 -0.060605  
## A4GNT -0.1225 0.318668 0.031600 0.3615 0.0261 -0.071187  
## ACH-000881 ACH-000882 ACH-000884 ACH-000915 ACH-000968 ACH-001239  
## A1BG -0.0981 -0.0752 -0.252723 -0.0420 -0.1993 0.0861  
## A1CF -0.0993 -0.5115 -0.283120 0.0787 0.1848 -0.1950  
## A2M -0.0978 0.2883 0.287264 0.2824 0.0162 -0.6115  
## A2ML1 -0.0978 0.2883 0.287264 0.2973 0.0907 -0.6115  
## A4GALT -0.0633 0.6046 0.658183 0.3209 0.4929 0.1784  
## A4GNT 0.3708 -0.0615 0.680377 0.2324 0.1863 0.1741  
## ACH-001328 ACH-001523 ACH-001550 ACH-001552  
## A1BG 0.237953 -0.010866 0.589809 -0.236371  
## A1CF 0.205969 0.333912 -0.005699 -0.238685  
## A2M 0.086664 0.319005 0.018019 0.358375  
## A2ML1 0.086664 0.319005 0.018019 0.358375  
## A4GALT 0.520720 -0.245144 0.029083 -0.201801  
## A4GNT 0.795922 0.573875 -0.022959 -0.251651  
##   
## $kd.ceres  
## ACH-000014 ACH-000274 ACH-000304 ACH-000322 ACH-000348  
## A1BG 0.11297899 0.09000078 0.123999117 0.17552003 0.05979116  
## A1CF -0.03533250 0.13896177 0.274438862 0.08205882 0.07506780  
## A2M 0.02880611 -0.07116082 -0.201401893 0.01866713 -0.05790399  
## A2ML1 0.16933390 0.10695957 0.291635816 0.20971252 0.09614451  
## A4GALT -0.08469817 -0.11183837 -0.164706825 0.07185597 -0.05414073  
## A4GNT -0.11754729 0.03983944 -0.005448509 -0.01545300 0.07601372  
## ACH-000401 ACH-000404 ACH-000425 ACH-000450 ACH-000458  
## A1BG 0.01571426 0.15256591 0.10555947 0.25129888 -0.10417050  
## A1CF 0.13868584 -0.05875901 -0.06461427 0.15003282 -0.02252161  
## A2M -0.17537252 0.05636695 0.02333974 0.14438356 -0.04081274  
## A2ML1 0.17156352 0.40394912 0.14116950 0.13541851 0.22712718  
## A4GALT 0.07607467 0.18406217 -0.11092708 -0.03212903 0.03671359  
## A4GNT 0.30488592 -0.08651345 0.07087229 0.12781440 -0.03223494  
## ACH-000477 ACH-000550 ACH-000579 ACH-000580 ACH-000614  
## A1BG 0.289795251 0.064205553 -0.065927430 0.03900611 0.14787728  
## A1CF 0.214437533 0.023580779 0.018053764 0.21690115 0.05171624  
## A2M -0.079851905 0.070822818 -0.003640272 0.03293732 0.01588641  
## A2ML1 -0.002144861 0.159409641 0.176745631 0.19270165 0.21205031  
## A4GALT -0.017404291 -0.072617685 -0.052971926 0.13070161 -0.02915081  
## A4GNT 0.129863168 -0.002612098 0.021171447 0.25699461 0.09435134  
## ACH-000632 ACH-000661 ACH-000765 ACH-000788 ACH-000799  
## A1BG 0.07342843 0.11854019 0.13019056 0.075362954 0.16021122  
## A1CF 0.06146017 0.19061023 0.16687445 0.009515992 0.06723195  
## A2M -0.05419496 -0.22653119 -0.06098627 -0.013598704 0.08540012  
## A2ML1 0.02936908 0.18428373 0.13123895 0.116638897 0.26393918  
## A4GALT 0.08274937 0.01155620 -0.11906126 -0.015256143 0.26058108  
## A4GNT 0.05657774 0.03895288 0.14439266 0.009148800 -0.08060116  
## ACH-000805 ACH-000810 ACH-000822 ACH-000827 ACH-000881  
## A1BG 0.084490523 -0.04293609 0.05076328 0.06990686 0.090286180  
## A1CF 0.034492430 0.27697291 0.06875785 0.03013687 0.130647356  
## A2M -0.053101940 0.16541854 0.05971664 0.02994108 0.047257009  
## A2ML1 0.203319334 0.13568434 0.16224922 0.19716850 0.222404888  
## A4GALT -0.077855787 0.35519130 -0.01871676 -0.02874038 0.001594528  
## A4GNT 0.009138719 -0.02462126 0.15301507 0.02080483 0.111101876  
## ACH-000882 ACH-000884 ACH-000915 ACH-000968 ACH-001239  
## A1BG 0.091655310 0.124539609 0.097316192 0.057175999 0.10082827  
## A1CF 0.049074699 -0.006389477 0.100542286 0.042134343 0.02929016  
## A2M 0.028052767 -0.102855586 0.008481948 0.004705052 -0.08792387  
## A2ML1 0.127508109 0.221749333 0.222150837 0.116615510 0.17664700  
## A4GALT 0.003775685 -0.184789775 0.076660517 -0.093583597 -0.14796202  
## A4GNT -0.016035666 0.020713244 -0.013231889 0.117817465 0.13577597  
## ACH-001328 ACH-001523 ACH-001550 ACH-001552  
## A1BG 0.06235456 0.047442518 0.09430238 0.11018942  
## A1CF 0.06190935 0.068521854 -0.01647004 0.04904597  
## A2M -0.04807576 -0.183453865 -0.06984297 -0.23064847  
## A2ML1 -0.01919207 0.169044086 0.13405833 0.28542924  
## A4GALT -0.04499389 -0.004494762 -0.02043337 0.14849100  
## A4GNT 0.10498836 0.001322608 0.03114364 0.10368129  
##   
## $kd.prob  
## ACH-000014 ACH-000274 ACH-000304 ACH-000322 ACH-000348  
## A1BG 0.002774072 0.004409101 0.002713543 0.0009701586 0.006625887  
## A1CF 0.023529328 0.002004631 0.000372957 0.0042621316 0.005132902  
## A2M 0.009873198 0.039221771 0.103075053 0.0104720660 0.037397252  
## A2ML1 0.001095265 0.003375634 0.000306326 0.0005420935 0.003550176  
## A4GALT 0.042860321 0.061256566 0.075245128 0.0049555556 0.035654746  
## A4GNT 0.061754873 0.009330674 0.014367402 0.0163943897 0.005049978  
## ACH-000401 ACH-000404 ACH-000425 ACH-000450 ACH-000458  
## A1BG 0.0117352429 0.003135382 0.002901371 0.0004100476 0.0464558466  
## A1CF 0.0021811675 0.025875878 0.035766409 0.0019507213 0.0168004926  
## A2M 0.0963755135 0.008272532 0.010890342 0.0021181433 0.0214251016  
## A2ML1 0.0013745352 0.000262358 0.001531532 0.0024096666 0.0002294311  
## A4GALT 0.0052394664 0.002308675 0.060966941 0.0214618827 0.0071673051  
## A4GNT 0.0002388802 0.033578458 0.005185378 0.0026843227 0.0191412094  
## ACH-000477 ACH-000550 ACH-000579 ACH-000580 ACH-000614  
## A1BG 0.0002224852 0.005801467 0.033045243 0.0095084541 0.0021462149  
## A1CF 0.0008443796 0.010724591 0.012078956 0.0005820796 0.0091992210  
## A2M 0.0524759450 0.005232583 0.015870331 0.0103358077 0.0149334347  
## A2ML1 0.0210323317 0.001140321 0.001325248 0.0008796355 0.0007153432  
## A4GALT 0.0254666787 0.038088623 0.028538781 0.0024275918 0.0263544134  
## A4GNT 0.0033117352 0.015569959 0.011615808 0.0002860357 0.0049529692  
## ACH-000632 ACH-000661 ACH-000765 ACH-000788 ACH-000799  
## A1BG 0.005151548 0.0031137157 0.0015961600 0.005910396 0.0014461984  
## A1CF 0.006222339 0.0008783533 0.0008507932 0.016381712 0.0061736308  
## A2M 0.031209180 0.1900070432 0.0261359974 0.022648853 0.0047245563  
## A2ML1 0.010096251 0.0009843391 0.0015693337 0.002909376 0.0002163243  
## A4GALT 0.004443711 0.0156043317 0.0514260243 0.023146039 0.0002314125  
## A4GNT 0.006709058 0.0106412772 0.0012565590 0.016468639 0.0403699454  
## ACH-000805 ACH-000810 ACH-000822 ACH-000827 ACH-000881  
## A1BG 0.0037992033 0.0248907969 0.010574261 0.0057660593 0.0043388543  
## A1CF 0.0081254560 0.0006141604 0.008059043 0.0104787149 0.0021815590  
## A2M 0.0268238520 0.0025531353 0.009249661 0.0105085179 0.0086177116  
## A2ML1 0.0005122671 0.0036198519 0.001667088 0.0006179602 0.0003972486  
## A4GALT 0.0363164080 0.0001924957 0.027583280 0.0233890287 0.0168383553  
## A4GNT 0.0116854998 0.0206953521 0.001969579 0.0119760173 0.0030582151  
## ACH-000882 ACH-000884 ACH-000915 ACH-000968 ACH-001239  
## A1BG 0.004183716 0.0021058063 0.004140484 0.007199169 0.003678157  
## A1CF 0.008248605 0.0155411448 0.003931522 0.009016403 0.011343510  
## A2M 0.011323740 0.0520569202 0.015111621 0.015328238 0.052237636  
## A2ML1 0.002278859 0.0004013114 0.000491419 0.002812611 0.000963672  
## A4GALT 0.016068235 0.1200383051 0.005693294 0.052245657 0.098162530  
## A4GNT 0.021115046 0.0105867006 0.020154265 0.002760348 0.002025516  
## ACH-001328 ACH-001523 ACH-001550 ACH-001552  
## A1BG 0.004772867 0.0054803799 0.006028054 0.0023994436  
## A1CF 0.004807247 0.0039041575 0.025789567 0.0060316862  
## A2M 0.023198464 0.0993526535 0.047495451 0.1389002562  
## A2ML1 0.015813331 0.0006472537 0.003382596 0.0001068761  
## A4GALT 0.022259553 0.0119590984 0.027047780 0.0012949414  
## A4GNT 0.002385176 0.0109876250 0.014230393 0.0026577123  
##   
## $mutation  
## $mutation$`ACH-000014`  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome  
## 1: 4090 AL669831.1 0 37 1  
## 2: 4101 COL16A1 1307 37 1  
## 3: 4109 ZFP69B 65243 37 1  
## 4: 4110 KLF17 128209 37 1  
## 5: 4115 LPPR5 0 37 1  
## 6: 4116 COL11A1 1301 37 1  
## 7: 4117 KIAA1324 57535 37 1  
## 8: 4130 FMO4 2329 37 1  
## 9: 4142 CD46 4179 37 1  
## 10: 4147 AC138393.1 0 37 1  
## 11: 4162 TSPAN15 23555 37 10  
## 12: 4169 WAPAL 23063 37 10  
## 13: 4171 CYP2C8 1558 37 10  
## 14: 4174 VWA2 340706 37 10  
## 15: 4187 ZBED5 58486 37 11  
## 16: 4193 ARFGAP2 84364 37 11  
## 17: 4204 SLC22A25 387601 37 11  
## 18: 4213 TRPC6 7225 37 11  
## 19: 4220 SORL1 6653 37 11  
## 20: 4221 C11orf63 79864 37 11  
## 21: 4227 VWF 7450 37 12  
## 22: 4230 ZNF384 171017 37 12  
## 23: 4243 GLS2 27165 37 12  
## 24: 4252 TMTC2 160335 37 12  
## 25: 4254 CCDC38 120935 37 12  
## 26: 4266 VPS33A 65082 37 12  
## 27: 4267 HIP1R 9026 37 12  
## 28: 4299 SERPINA9 327657 37 14  
## 29: 4338 CLEC16A 23274 37 16  
## 30: 4349 WWOX 51741 37 16  
## 31: 4354 SERPINF2 5345 37 17  
## 32: 4374 FLOT2 2319 37 17  
## 33: 4377 C17orf75 64149 37 17  
## 34: 4378 MYO1D 4642 37 17  
## 35: 4383 KRT25 147183 37 17  
## 36: 4387 FKBP10 60681 37 17  
## 37: 4411 DSC2 1824 37 18  
## 38: 4468 SBK3 100130827 37 19  
## 39: 4473 ZNF805 390980 37 19  
## 40: 4485 SIX3 6496 37 2  
## 41: 4509 TTN 7273 37 2  
## 42: 4510 TTN 7273 37 2  
## 43: 4517 TRAK2 66008 37 2  
## 44: 4537 NCOA6 23054 37 20  
## 45: 4551 PEX26 55670 37 22  
## 46: 4559 PHF21B 112885 37 22  
## 47: 4569 KIF15 56992 37 3  
## 48: 4572 RBM6 10180 37 3  
## 49: 4573 RBM5 10181 37 3  
## 50: 4574 NPRL2 10641 37 3  
## 51: 4599 ATP13A5 344905 37 3  
## 52: 4603 NMU 10874 37 4  
## 53: 4619 MYO10 4651 37 5  
## 54: 4634 TIGD6 81789 37 5  
## 55: 4657 HLA-DQB2 3120 37 6  
## 56: 4662 C6orf222 389384 37 6  
## 57: 4666 ZNF451 26036 37 6  
## 58: 4672 BCKDHB 594 37 6  
## 59: 4679 IL22RA2 116379 37 6  
## 60: 4681 ADGB 79747 37 6  
## 61: 4682 RAET1G 353091 37 6  
## 62: 4702 REPIN1 29803 37 7  
## 63: 4704 TMEM176B 28959 37 7  
## 64: 4711 RP11-1102P16.1 0 37 8  
## 65: 4714 MTERFD1 0 37 8  
## 66: 4732 NOL6 65083 37 9  
## 67: 4737 ZCCHC6 79670 37 9  
## 68: 4746 KIAA0368 23392 37 9  
## 69: 4754 C9orf114 51490 37 9  
## 70: 4786 LRCH2 57631 37 X  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome  
## Start\_position End\_position Strand Variant\_Classification  
## 1: 739121 739121 + Splice\_Site  
## 2: 32136240 32136240 + Frame\_Shift\_Del  
## 3: 40923072 40923072 + Frame\_Shift\_Del  
## 4: 44584524 44584524 + De\_novo\_Start\_OutOfFrame  
## 5: 99380380 99380380 + Nonsense\_Mutation  
## 6: 103488540 103488540 + Nonsense\_Mutation  
## 7: 109715178 109715178 + Nonsense\_Mutation  
## 8: 171301990 171301990 + Frame\_Shift\_Del  
## 9: 207934766 207934766 + Nonsense\_Mutation  
## 10: 224216349 224216349 + Splice\_Site  
## 11: 71243446 71243446 + Splice\_Site  
## 12: 88259565 88259565 + Frame\_Shift\_Del  
## 13: 96826964 96826964 + Splice\_Site  
## 14: 116013409 116013409 + Splice\_Site  
## 15: 10875435 10875436 + Frame\_Shift\_Ins  
## 16: 47196853 47196853 + Frame\_Shift\_Del  
## 17: 62984786 62984786 + Splice\_Site  
## 18: 101375333 101375334 + Frame\_Shift\_Ins  
## 19: 121460883 121460883 + Splice\_Site  
## 20: 122828161 122828162 + Frame\_Shift\_Ins  
## 21: 6121252 6121252 + Splice\_Site  
## 22: 6777167 6777167 + Nonsense\_Mutation  
## 23: 56865271 56865271 + Nonstop\_Mutation  
## 24: 83080749 83080754 + De\_novo\_Start\_OutOfFrame  
## 25: 96284709 96284709 + Splice\_Site  
## 26: 122724475 122724476 + Frame\_Shift\_Ins  
## 27: 123339931 123339932 + Frame\_Shift\_Ins  
## 28: 94931079 94931079 + Nonsense\_Mutation  
## 29: 11141159 11141159 + Frame\_Shift\_Del  
## 30: 78142384 78142384 + Splice\_Site  
## 31: 1651891 1651891 + Splice\_Site  
## 32: 27209255 27209353 + Splice\_Site  
## 33: 30662462 30662462 + Splice\_Site  
## 34: 31087623 31087624 + Frame\_Shift\_Ins  
## 35: 38911514 38911514 + Nonsense\_Mutation  
## 36: 39978475 39978475 + Splice\_Site  
## 37: 28662232 28662233 + Frame\_Shift\_Ins  
## 38: 56056864 56056864 + Splice\_Site  
## 39: 57766038 57766038 + Nonsense\_Mutation  
## 40: 45169865 45169865 + Nonsense\_Mutation  
## 41: 179438935 179438944 + Frame\_Shift\_Del  
## 42: 179579150 179579150 + Nonsense\_Mutation  
## 43: 202260166 202260166 + Splice\_Site  
## 44: 33380317 33380317 + De\_novo\_Start\_OutOfFrame  
## 45: 18562758 18562758 + Frame\_Shift\_Del  
## 46: 45281743 45281743 + Splice\_Site  
## 47: 44879831 44879832 + Frame\_Shift\_Ins  
## 48: 50099527 50099528 + Frame\_Shift\_Del  
## 49: 50154570 50154570 + Frame\_Shift\_Del  
## 50: 50388225 50388225 + De\_novo\_Start\_OutOfFrame  
## 51: 193081963 193081963 + Nonsense\_Mutation  
## 52: 56466701 56466701 + Nonsense\_Mutation  
## 53: 16670968 16670969 + Frame\_Shift\_Ins  
## 54: 149379973 149379973 + De\_novo\_Start\_OutOfFrame  
## 55: 32729506 32729507 + Frame\_Shift\_Ins  
## 56: 36287353 36287354 + Frame\_Shift\_Ins  
## 57: 57012217 57012218 + Frame\_Shift\_Ins  
## 58: 80910707 80910707 + Nonsense\_Mutation  
## 59: 137468926 137468926 + Frame\_Shift\_Del  
## 60: 147122318 147122318 + Splice\_Site  
## 61: 150240413 150240413 + Nonsense\_Mutation  
## 62: 150065912 150065912 + De\_novo\_Start\_OutOfFrame  
## 63: 150493784 150493784 + De\_novo\_Start\_OutOfFrame  
## 64: 72448078 72448079 + De\_novo\_Start\_OutOfFrame  
## 65: 97263175 97263176 + Frame\_Shift\_Ins  
## 66: 33466944 33466944 + Frame\_Shift\_Del  
## 67: 88925724 88925724 + Splice\_Site  
## 68: 114145501 114145501 + Nonsense\_Mutation  
## 69: 131586173 131586173 + Splice\_Site  
## 70: 114419006 114419006 + Nonsense\_Mutation  
## Start\_position End\_position Strand Variant\_Classification  
## Variant\_Type  
## 1: SNP  
## 2: DEL  
## 3: DEL  
## 4: SNP  
## 5: SNP  
## 6: SNP  
## 7: SNP  
## 8: DEL  
## 9: SNP  
## 10: SNP  
## 11: SNP  
## 12: DEL  
## 13: SNP  
## 14: SNP  
## 15: INS  
## 16: DEL  
## 17: SNP  
## 18: INS  
## 19: SNP  
## 20: INS  
## 21: SNP  
## 22: SNP  
## 23: SNP  
## 24: DEL  
## 25: SNP  
## 26: INS  
## 27: INS  
## 28: SNP  
## 29: DEL  
## 30: SNP  
## 31: SNP  
## 32: DEL  
## 33: SNP  
## 34: INS  
## 35: SNP  
## 36: SNP  
## 37: INS  
## 38: SNP  
## 39: SNP  
## 40: SNP  
## 41: DEL  
## 42: SNP  
## 43: SNP  
## 44: DEL  
## 45: DEL  
## 46: SNP  
## 47: INS  
## 48: DEL  
## 49: DEL  
## 50: SNP  
## 51: SNP  
## 52: SNP  
## 53: INS  
## 54: SNP  
## 55: INS  
## 56: INS  
## 57: INS  
## 58: SNP  
## 59: DEL  
## 60: SNP  
## 61: SNP  
## 62: SNP  
## 63: SNP  
## 64: INS  
## 65: INS  
## 66: DEL  
## 67: SNP  
## 68: SNP  
## 69: SNP  
## 70: SNP  
## Variant\_Type  
## Reference\_Allele  
## 1: A  
## 2: G  
## 3: T  
## 4: C  
## 5: G  
## 6: C  
## 7: G  
## 8: A  
## 9: G  
## 10: A  
## 11: G  
## 12: T  
## 13: C  
## 14: G  
## 15: -  
## 16: A  
## 17: C  
## 18: -  
## 19: G  
## 20: -  
## 21: C  
## 22: G  
## 23: T  
## 24: GCTGGG  
## 25: C  
## 26: -  
## 27: -  
## 28: C  
## 29: T  
## 30: G  
## 31: G  
## 32: CCTGGGGACAAAAGGGGCAGAAGGGGAAGGTGAGTGAGTAGAGGTCCTGAGTCATCATGGTCCCATCACCCCTGAGCTTCCCATCCTTGAACCCACATA  
## 33: C  
## 34: -  
## 35: G  
## 36: T  
## 37: -  
## 38: C  
## 39: C  
## 40: C  
## 41: TTGGCCTTCA  
## 42: C  
## 43: A  
## 44: T  
## 45: C  
## 46: C  
## 47: -  
## 48: AG  
## 49: C  
## 50: C  
## 51: C  
## 52: A  
## 53: -  
## 54: G  
## 55: -  
## 56: -  
## 57: -  
## 58: C  
## 59: T  
## 60: G  
## 61: C  
## 62: G  
## 63: C  
## 64: -  
## 65: -  
## 66: C  
## 67: C  
## 68: G  
## 69: C  
## 70: C  
## Reference\_Allele  
## Tumor\_Seq\_Allele1 dbSNP\_RS  
## 1: G <NA>  
## 2: - <NA>  
## 3: -   
## 4: A <NA>  
## 5: A <NA>  
## 6: A <NA>  
## 7: A   
## 8: - <NA>  
## 9: A <NA>  
## 10: G <NA>  
## 11: A   
## 12: -   
## 13: T   
## 14: C   
## 15: T <NA>  
## 16: -   
## 17: T <NA>  
## 18: GT rs201176913  
## 19: A <NA>  
## 20: A <NA>  
## 21: A   
## 22: A <NA>  
## 23: G   
## 24: - rs56311034  
## 25: T <NA>  
## 26: A <NA>  
## 27: C <NA>  
## 28: A   
## 29: -   
## 30: C <NA>  
## 31: A   
## 32: - rs373765414|rs34442762|rs369574598|rs201809072  
## 33: T <NA>  
## 34: A <NA>  
## 35: A rs528755553  
## 36: C <NA>  
## 37: T rs397517390  
## 38: A <NA>  
## 39: G <NA>  
## 40: T   
## 41: - <NA>  
## 42: T <NA>  
## 43: G   
## 44: - <NA>  
## 45: -   
## 46: A   
## 47: A <NA>  
## 48: -   
## 49: - <NA>  
## 50: A <NA>  
## 51: T <NA>  
## 52: C   
## 53: G <NA>  
## 54: A rs142265676  
## 55: T <NA>  
## 56: A   
## 57: A <NA>  
## 58: T rs398124594  
## 59: -   
## 60: C <NA>  
## 61: A   
## 62: A <NA>  
## 63: T <NA>  
## 64: A <NA>  
## 65: T <NA>  
## 66: -   
## 67: T   
## 68: A <NA>  
## 69: T   
## 70: A   
## Tumor\_Seq\_Allele1 dbSNP\_RS  
## dbSNP\_Val\_Status  
## 1: <NA>  
## 2: <NA>  
## 3:   
## 4: <NA>  
## 5: <NA>  
## 6: <NA>  
## 7:   
## 8: <NA>  
## 9: <NA>  
## 10: <NA>  
## 11:   
## 12:   
## 13:   
## 14:   
## 15: <NA>  
## 16:   
## 17: <NA>  
## 18:   
## 19: <NA>  
## 20: <NA>  
## 21:   
## 22: <NA>  
## 23:   
## 24: byFrequency  
## 25: <NA>  
## 26: <NA>  
## 27: <NA>  
## 28:   
## 29:   
## 30: <NA>  
## 31:   
## 32: byFrequency  
## 33: <NA>  
## 34: <NA>  
## 35: <NA>  
## 36: <NA>  
## 37:   
## 38: <NA>  
## 39: <NA>  
## 40:   
## 41: <NA>  
## 42: <NA>  
## 43:   
## 44: <NA>  
## 45:   
## 46:   
## 47: <NA>  
## 48:   
## 49: <NA>  
## 50: <NA>  
## 51: <NA>  
## 52:   
## 53: <NA>  
## 54: byFrequency  
## 55: <NA>  
## 56:   
## 57: <NA>  
## 58: <NA>  
## 59:   
## 60: <NA>  
## 61:   
## 62: <NA>  
## 63: <NA>  
## 64: <NA>  
## 65: <NA>  
## 66:   
## 67:   
## 68: <NA>  
## 69:   
## 70:   
## dbSNP\_Val\_Status  
## Genome\_Change  
## 1: g.chr1:739121A>G  
## 2: g.chr1:32136240delG  
## 3: g.chr1:40923072delT  
## 4: g.chr1:44584524C>A  
## 5: g.chr1:99380380G>A  
## 6: g.chr1:103488540C>A  
## 7: g.chr1:109715178G>A  
## 8: g.chr1:171301990delA  
## 9: g.chr1:207934766G>A  
## 10: g.chr1:224216349A>G  
## 11: g.chr10:71243446G>A  
## 12: g.chr10:88259565delT  
## 13: g.chr10:96826964C>T  
## 14: g.chr10:116013409G>C  
## 15: g.chr11:10875435\_10875436insT  
## 16: g.chr11:47196853delA  
## 17: g.chr11:62984786C>T  
## 18: g.chr11:101375333\_101375334insGT  
## 19: g.chr11:121460883G>A  
## 20: g.chr11:122828161\_122828162insA  
## 21: g.chr12:6121252C>A  
## 22: g.chr12:6777167G>A  
## 23: g.chr12:56865271T>G  
## 24: g.chr12:83080749\_83080754delGCTGGG  
## 25: g.chr12:96284709C>T  
## 26: g.chr12:122724475\_122724476insA  
## 27: g.chr12:123339931\_123339932insC  
## 28: g.chr14:94931079C>A  
## 29: g.chr16:11141159delT  
## 30: g.chr16:78142384G>C  
## 31: g.chr17:1651891G>A  
## 32: g.chr17:27209255\_27209353delCCTGGGGACAAAAGGGGCAGAAGGGGAAGGTGAGTGAGTAGAGGTCCTGAGTCATCATGGTCCCATCACCCCTGAGCTTCCCATCCTTGAACCCACATA  
## 33: g.chr17:30662462C>T  
## 34: g.chr17:31087623\_31087624insA  
## 35: g.chr17:38911514G>A  
## 36: g.chr17:39978475T>C  
## 37: g.chr18:28662232\_28662233insT  
## 38: g.chr19:56056864C>A  
## 39: g.chr19:57766038C>G  
## 40: g.chr2:45169865C>T  
## 41: g.chr2:179438935\_179438944delTTGGCCTTCA  
## 42: g.chr2:179579150C>T  
## 43: g.chr2:202260166A>G  
## 44: g.chr20:33380317delT  
## 45: g.chr22:18562758delC  
## 46: g.chr22:45281743C>A  
## 47: g.chr3:44879831\_44879832insA  
## 48: g.chr3:50099527\_50099528delAG  
## 49: g.chr3:50154570delC  
## 50: g.chr3:50388225C>A  
## 51: g.chr3:193081963C>T  
## 52: g.chr4:56466701A>C  
## 53: g.chr5:16670968\_16670969insG  
## 54: g.chr5:149379973G>A  
## 55: g.chr6:32729506\_32729507insT  
## 56: g.chr6:36287353\_36287354insA  
## 57: g.chr6:57012217\_57012218insA  
## 58: g.chr6:80910707C>T  
## 59: g.chr6:137468926delT  
## 60: g.chr6:147122318G>C  
## 61: g.chr6:150240413C>A  
## 62: g.chr7:150065912G>A  
## 63: g.chr7:150493784C>T  
## 64: g.chr8:72448078\_72448079insA  
## 65: g.chr8:97263175\_97263176insT  
## 66: g.chr9:33466944delC  
## 67: g.chr9:88925724C>T  
## 68: g.chr9:114145501G>A  
## 69: g.chr9:131586173C>T  
## 70: g.chrX:114419006C>A  
## Genome\_Change  
## Annotation\_Transcript Tumor\_Sample\_Barcode  
## 1: ENST00000599533.1 ACH-000014  
## 2: ENST00000373672.3 ACH-000014  
## 3: ENST00000411995.2 ACH-000014  
## 4: ENST00000372299.3 ACH-000014  
## 5: ENST00000263177.4 ACH-000014  
## 6: ENST00000370096.3 ACH-000014  
## 7: ENST00000369939.3 ACH-000014  
## 8: ENST00000367749.3 ACH-000014  
## 9: ENST00000358170.2 ACH-000014  
## 10: ENST00000600307.1 ACH-000014  
## 11: ENST00000373290.2 ACH-000014  
## 12: ENST00000298767.5 ACH-000014  
## 13: ENST00000371270.3 ACH-000014  
## 14: ENST00000392982.3 ACH-000014  
## 15: ENST00000432999.2 ACH-000014  
## 16: ENST00000524782.1 ACH-000014  
## 17: ENST00000306494.6 ACH-000014  
## 18: ENST00000344327.3 ACH-000014  
## 19: ENST00000260197.7 ACH-000014  
## 20: ENST00000531316.1 ACH-000014  
## 21: ENST00000261405.5 ACH-000014  
## 22: ENST00000396801.3 ACH-000014  
## 23: ENST00000311966.4 ACH-000014  
## 24: ENST00000321196.3 ACH-000014  
## 25: ENST00000344280.3 ACH-000014  
## 26: ENST00000267199.4 ACH-000014  
## 27: ENST00000253083.4 ACH-000014  
## 28: ENST00000380365.3 ACH-000014  
## 29: ENST00000409790.1 ACH-000014  
## 30: ENST00000566780.1 ACH-000014  
## 31: ENST00000324015.3 ACH-000014  
## 32: ENST00000394908.4 ACH-000014  
## 33: ENST00000577809.1 ACH-000014  
## 34: ENST00000318217.5 ACH-000014  
## 35: ENST00000312150.4 ACH-000014  
## 36: ENST00000321562.4 ACH-000014  
## 37: ENST00000280904.6 ACH-000014  
## 38: ENST00000420723.3 ACH-000014  
## 39: ENST00000414468.2 ACH-000014  
## 40: ENST00000260653.3 ACH-000014  
## 41: ENST00000591111.1 ACH-000014  
## 42: ENST00000591111.1 ACH-000014  
## 43: ENST00000332624.3 ACH-000014  
## 44: ENST00000374796.2 ACH-000014  
## 45: ENST00000329627.7 ACH-000014  
## 46: ENST00000313237.5 ACH-000014  
## 47: ENST00000326047.4 ACH-000014  
## 48: ENST00000266022.4 ACH-000014  
## 49: ENST00000347869.3 ACH-000014  
## 50: ENST00000232501.3 ACH-000014  
## 51: ENST00000342358.4 ACH-000014  
## 52: ENST00000264218.3 ACH-000014  
## 53: ENST00000513610.1 ACH-000014  
## 54: ENST00000515406.2 ACH-000014  
## 55: ENST00000437316.2 ACH-000014  
## 56: ENST00000437635.2 ACH-000014  
## 57: ENST00000370706.4 ACH-000014  
## 58: ENST00000320393.6 ACH-000014  
## 59: ENST00000296980.2 ACH-000014  
## 60: ENST00000397944.3 ACH-000014  
## 61: ENST00000367360.2 ACH-000014  
## 62: ENST00000397281.2 ACH-000014  
## 63: ENST00000429904.2 ACH-000014  
## 64: ENST00000523987.1 ACH-000014  
## 65: ENST00000287025.3 ACH-000014  
## 66: ENST00000379471.2 ACH-000014  
## 67: ENST00000375963.3 ACH-000014  
## 68: ENST00000338205.5 ACH-000014  
## 69: ENST00000361256.5 ACH-000014  
## 70: ENST00000317135.8 ACH-000014  
## Annotation\_Transcript Tumor\_Sample\_Barcode  
## cDNA\_Change  
## 1: c.17T>C  
## 2: c.3158delC  
## 3: c.397delT  
## 4: <NA>  
## 5: c.895C>T  
## 6: c.1003G>T  
## 7: c.684G>A  
## 8: c.770delA  
## 9: c.648G>A  
## 10: c.23T>C  
## 11:   
## 12: c.1435delA  
## 13:   
## 14:   
## 15: c.1057\_1058insA  
## 16: c.276delT  
## 17: c.830G>A  
## 18: c.366\_367insAC  
## 19: c.4213G>A  
## 20: c.2101\_2102insA  
## 21:   
## 22: c.1447C>T  
## 23: c.1809A>C  
## 24: <NA>  
## 25: <NA>  
## 26: c.1113\_1114insT  
## 27: c.972\_973insC  
## 28: c.1015G>T  
## 29: c.1826delT  
## 30: c.172G>C  
## 31:   
## 32: c.580delTATGTGGGTTCAAGGATGGGAAGCTCAGGGGTGATGGGACCATGATGACTCAGGACCTCTACTCACTCACCTTCCCCTTCTGCCCCTTTTGTCCCCAGG  
## 33: <NA>  
## 34: c.1057\_1058insT  
## 35: c.10C>T  
## 36: c.1564T>C  
## 37: c.1234\_1235insA  
## 38: <NA>  
## 39: c.1851C>G  
## 40: c.622C>T  
## 41: c.66992\_67001delTGAAGGCCAA  
## 42: c.25400G>A  
## 43: c.771T>C  
## 44: <NA>  
## 45: c.349delC  
## 46: c.1273G>T  
## 47: c.3236\_3237insA  
## 48: c.2572\_2573delAG  
## 49: c.2158delC  
## 50: <NA>  
## 51: c.170G>A  
## 52: c.477T>G  
## 53: c.5549\_5550insC  
## 54: <NA>  
## 55: c.294\_295insA  
## 56: c.1702\_1703insT  
## 57: c.1334\_1335insA  
## 58: c.799C>T  
## 59: c.575delA  
## 60: <NA>  
## 61: c.397G>T  
## 62: <NA>  
## 63: <NA>  
## 64: <NA>  
## 65: c.635\_636insA  
## 66: c.1916delG  
## 67: c.3275G>A  
## 68: c.3793C>T  
## 69: c.915G>A  
## 70: c.589G>T  
## cDNA\_Change  
## Codon\_Change Protein\_Change isDeleterious  
## 1: c.(16-18)aTa>aCa p.I6T TRUE  
## 2: c.(3157-3159)ccafs p.P1053fs TRUE  
## 3: c.(397-399)tggfs p.W133fs TRUE  
## 4: <NA> <NA> TRUE  
## 5: c.(895-897)Cga>Tga p.R299\* TRUE  
## 6: c.(1003-1005)Gaa>Taa p.E335\* TRUE  
## 7: c.(682-684)tgG>tgA p.W228\* TRUE  
## 8: c.(769-771)gaafs p.E257fs TRUE  
## 9: c.(646-648)tgG>tgA p.W216\* TRUE  
## 10: c.(22-24)aTa>aCa p.I8T TRUE  
## 11: c.e2-1 TRUE  
## 12: c.(1435-1437)agafs p.R479fs TRUE  
## 13: c.e3+1 TRUE  
## 14: c.e3-1 TRUE  
## 15: c.(1057-1059)attfs p.I353fs TRUE  
## 16: c.(274-276)tttfs p.F92fs TRUE  
## 17: c.(829-831)aGg>aAg p.R277K TRUE  
## 18: c.(364-369)cactcafs p.S123fs TRUE  
## 19: c.(4213-4215)Gat>Aat p.D1405N TRUE  
## 20: c.(2101-2103)gaafs p.E701fs TRUE  
## 21: c.e33+1 TRUE  
## 22: c.(1447-1449)Cag>Tag p.Q483\* TRUE  
## 23: c.(1807-1809)tgA>tgC p.\*603C TRUE  
## 24: <NA> <NA> TRUE  
## 25: c.e9-1 <NA> TRUE  
## 26: c.(1111-1116)tttgatfs p.D372fs TRUE  
## 27: c.(973-975)cccfs p.P325fs TRUE  
## 28: c.(1015-1017)Gga>Tga p.G339\* TRUE  
## 29: c.(1825-1827)attfs p.I609fs TRUE  
## 30: c.(172-174)Gat>Cat p.D58H TRUE  
## 31: c.e8-1 TRUE  
## 32: c.(580-582)tat>at p.Y194del TRUE  
## 33: c.e6-1 <NA> TRUE  
## 34: c.(1057-1059)tgtfs p.C353fs TRUE  
## 35: c.(10-12)Cga>Tga p.R4\* TRUE  
## 36: c.(1564-1566)Ttc>Ctc p.F522L TRUE  
## 37: c.(1234-1236)accfs p.T412fs TRUE  
## 38: c.e1+1 <NA> TRUE  
## 39: c.(1849-1851)taC>taG p.Y617\* TRUE  
## 40: c.(622-624)Cag>Tag p.Q208\* TRUE  
## 41: c.(66991-67002)ctgaaggccaacfs p.LKAN22331fs TRUE  
## 42: c.(25399-25401)tGg>tAg p.W8467\* TRUE  
## 43: c.(769-771)cgT>cgC p.R257R TRUE  
## 44: <NA> <NA> TRUE  
## 45: c.(349-351)cccfs p.P118fs TRUE  
## 46: c.(1273-1275)Gtc>Ttc p.V425F TRUE  
## 47: c.(3235-3240)tcaaaafs p.SK1079fs TRUE  
## 48: c.(2572-2574)agafs p.R858fs TRUE  
## 49: c.(2158-2160)cccfs p.P720fs TRUE  
## 50: <NA> <NA> TRUE  
## 51: c.(169-171)tGg>tAg p.W57\* TRUE  
## 52: c.(475-477)taT>taG p.Y159\* TRUE  
## 53: c.(5548-5550)cctfs p.P1850fs TRUE  
## 54: <NA> <NA> TRUE  
## 55: c.(292-297)gagcggfs p.R99fs TRUE  
## 56: c.(1702-1704)tacfs p.Y568fs TRUE  
## 57: c.(1333-1338)ccaaaafs p.PK445fs TRUE  
## 58: c.(799-801)Cag>Tag p.Q267\* TRUE  
## 59: c.(574-576)aatfs p.N192fs TRUE  
## 60: c.e34-1 <NA> TRUE  
## 61: c.(397-399)Gga>Tga p.G133\* TRUE  
## 62: <NA> <NA> TRUE  
## 63: <NA> <NA> TRUE  
## 64: <NA> <NA> TRUE  
## 65: c.(634-636)aatfs p.N212fs TRUE  
## 66: c.(1915-1917)ggcfs p.G639fs TRUE  
## 67: c.(3274-3276)gGt>gAt p.G1092D TRUE  
## 68: c.(3793-3795)Cga>Tga p.R1265\* TRUE  
## 69: c.(913-915)agG>agA p.R305R TRUE  
## 70: c.(589-591)Gaa>Taa p.E197\* TRUE  
## Codon\_Change Protein\_Change isDeleterious  
## isTCGAhotspot TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF  
## 1: FALSE 0 FALSE 0 NA  
## 2: FALSE 0 FALSE 0 NA  
## 3: FALSE 0 FALSE 0 NA  
## 4: FALSE 0 FALSE 0 NA  
## 5: FALSE 0 FALSE 0 8.237e-06  
## 6: FALSE 0 FALSE 0 8.238e-06  
## 7: FALSE 0 FALSE NA NA  
## 8: FALSE 0 FALSE 0 8.237e-06  
## 9: FALSE 0 FALSE 0 NA  
## 10: FALSE 0 FALSE 0 NA  
## 11: FALSE 0 FALSE 0 NA  
## 12: TRUE 4 FALSE 0 NA  
## 13: FALSE 0 FALSE 0 NA  
## 14: FALSE 0 FALSE 0 NA  
## 15: FALSE 0 FALSE 0 NA  
## 16: FALSE 0 FALSE 0 8.236e-06  
## 17: FALSE 0 FALSE 0 NA  
## 18: FALSE 0 FALSE 0 NA  
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## 20: FALSE 0 FALSE 0 NA  
## 21: FALSE 0 FALSE 0 NA  
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## 29: FALSE 0 FALSE NA NA  
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## 34: FALSE 0 FALSE 0 NA  
## 35: FALSE 0 FALSE 0 8.246e-06  
## 36: FALSE 0 FALSE 0 NA  
## 37: FALSE 0 FALSE 0 NA  
## 38: FALSE 0 FALSE 0 NA  
## 39: FALSE 0 FALSE 0 1.648e-05  
## 40: FALSE 0 FALSE 0 NA  
## 41: FALSE 0 FALSE 0 NA  
## 42: FALSE 0 FALSE 0 NA  
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## 50: FALSE 0 FALSE 0 NA  
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## 52: FALSE 0 FALSE 0 NA  
## 53: FALSE 0 FALSE 0 8.270e-06  
## 54: FALSE 0 FALSE 0 NA  
## 55: FALSE 0 FALSE 0 NA  
## 56: TRUE 3 FALSE 0 3.295e-05  
## 57: FALSE 0 FALSE 0 NA  
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## 65: FALSE 0 FALSE 0 4.942e-05  
## 66: TRUE 4 FALSE 0 NA  
## 67: FALSE 0 FALSE 0 NA  
## 68: FALSE 0 FALSE 0 NA  
## 69: FALSE 0 FALSE 0 NA  
## 70: FALSE 0 FALSE 0 NA  
## isTCGAhotspot TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF  
## VA\_WES\_AC CGA\_WES\_AC SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC  
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## 2: <NA> <NA> <NA> <NA> <NA> <NA>  
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## 5: <NA> <NA> <NA> <NA> 37:13 <NA>  
## 6: <NA> <NA> <NA> <NA> <NA> <NA>  
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## 9: <NA> <NA> <NA> <NA> <NA> <NA>  
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## 18: <NA> <NA> <NA> <NA> <NA> <NA>  
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## 20: <NA> <NA> <NA> <NA> 5:9 <NA>  
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## 22: <NA> <NA> <NA> <NA> 106:257 <NA>  
## 23: <NA> <NA> <NA> <NA> <NA> <NA>  
## 24: <NA> <NA> <NA> <NA> 9:7 <NA>  
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## 26: <NA> <NA> <NA> <NA> 14:81 <NA>  
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## 32: <NA> <NA> <NA> <NA> 278:0 <NA>  
## 33: <NA> <NA> <NA> <NA> 2:2 <NA>  
## 34: <NA> <NA> <NA> <NA> 7:38 <NA>  
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## 54: <NA> <NA> <NA> <NA> 17:0 <NA>  
## 55: <NA> <NA> <NA> <NA> 10:0 <NA>  
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## 57: <NA> <NA> <NA> <NA> 9:44 <NA>  
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## VA\_WES\_AC CGA\_WES\_AC SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC  
## RD\_AC WGS\_AC Variant\_annotation DepMap\_ID  
## 1: <NA> 5:19 damaging ACH-000014  
## 2: <NA> 8:35 damaging ACH-000014  
## 3: <NA> 12:31 damaging ACH-000014  
## 4: <NA> 5:22 damaging ACH-000014  
## 5: <NA> 18:11 damaging ACH-000014  
## 6: <NA> 8:22 damaging ACH-000014  
## 7: <NA> 5:35 damaging ACH-000014  
## 8: <NA> 20:18 damaging ACH-000014  
## 9: <NA> 9:30 damaging ACH-000014  
## 10: <NA> 8:9 damaging ACH-000014  
## 11: <NA> 6:34 damaging ACH-000014  
## 12: <NA> 6:16 damaging ACH-000014  
## 13: <NA> 5:23 damaging ACH-000014  
## 14: <NA> 5:23 damaging ACH-000014  
## 15: <NA> 5:32 damaging ACH-000014  
## 16: <NA> 5:31 damaging ACH-000014  
## 17: <NA> 12:23 damaging ACH-000014  
## 18: <NA> 5:24 damaging ACH-000014  
## 19: <NA> 7:24 damaging ACH-000014  
## 20: <NA> <NA> damaging ACH-000014  
## 21: <NA> 5:38 damaging ACH-000014  
## 22: <NA> 9:28 damaging ACH-000014  
## 23: <NA> 6:38 other non-conserving ACH-000014  
## 24: <NA> <NA> damaging ACH-000014  
## 25: <NA> 5:29 damaging ACH-000014  
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## 28: <NA> 6:37 damaging ACH-000014  
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## 30: <NA> 15:15 damaging ACH-000014  
## 31: <NA> 5:38 damaging ACH-000014  
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## 33: <NA> 19:20 damaging ACH-000014  
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## 35: <NA> 27:19 damaging ACH-000014  
## 36: <NA> 7:28 damaging ACH-000014  
## 37: <NA> 4:30 damaging ACH-000014  
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## 59: <NA> 5:25 damaging ACH-000014  
## 60: <NA> 4:26 damaging ACH-000014  
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## 64: <NA> 4:26 damaging ACH-000014  
## 65: <NA> <NA> damaging ACH-000014  
## 66: <NA> 5:32 damaging ACH-000014  
## 67: <NA> 4:24 damaging ACH-000014  
## 68: <NA> 23:13 damaging ACH-000014  
## 69: <NA> 4:29 damaging ACH-000014  
## 70: <NA> 4:32 damaging ACH-000014  
## RD\_AC WGS\_AC Variant\_annotation DepMap\_ID  
##   
## $mutation$`ACH-000274`  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## 1: 86621 HSPG2 3339 37 1 22150695  
## 2: 86623 LUZP1 7798 37 1 23420084  
## 3: 86625 TMEM57 55219 37 1 25785185  
## 4: 86634 WNT2B 7482 37 1 113058881  
## 5: 86639 BCL9 607 37 1 147076669  
## 6: 86647 HMCN1 83872 37 1 186024781  
## 7: 86648 ZBTB41 360023 37 1 197145702  
## 8: 86653 USP54 159195 37 10 75290099  
## 9: 86654 ADK 132 37 10 75960521  
## 10: 86659 CCDC147 0 37 10 106207507  
## 11: 86667 FAM111A 63901 37 11 58919775  
## 12: 86688 NACA 4666 37 12 57111533  
## 13: 86694 FBXO21 23014 37 12 117615411  
## 14: 86717 FBN1 2200 37 15 48773870  
## 15: 86728 PHKG2 5261 37 16 30764880  
## 16: 86742 ABCA8 10351 37 17 66928543  
## 17: 86746 SLC16A3 9123 37 17 80194747  
## 18: 86759 C19orf60 55049 37 19 18699803  
## 19: 86773 GPR113 165082 37 2 26537420  
## 20: 86797 GART 2618 37 21 34911478  
## 21: 86802 KREMEN1 83999 37 22 29490379  
## 22: 86805 RABL2B 11158 37 22 51207956  
## 23: 86808 IRAK2 3656 37 3 10283873  
## 24: 86817 ATP2C1 27032 37 3 130613154  
## 25: 86824 STIM2 57620 37 4 27010053  
## 26: 86825 TBC1D1 23216 37 4 38097713  
## 27: 86832 CENPE 1062 37 4 104117084  
## 28: 86851 DOCK2 1794 37 5 169127065  
## 29: 86854 HLA-G 3135 37 6 29795950  
## 30: 86859 LMBRD1 55788 37 6 70411439  
## 31: 86862 FILIP1 27145 37 6 76023702  
## 32: 86873 FIGNL1 63979 37 7 50514613  
## 33: 86894 VPS13B 157680 37 8 100847965  
## 34: 86905 FBXW5 54461 37 9 139837149  
## 35: 86909 ZNF630 57232 37 X 47918004  
## 36: 86910 BTK 695 37 X 100608908  
## 37: 86912 CCDC160 347475 37 X 133378874  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## End\_position Strand Variant\_Classification Variant\_Type  
## 1: 22150795 + Splice\_Site DEL  
## 2: 23420085 + Frame\_Shift\_Ins INS  
## 3: 25785186 + Frame\_Shift\_Ins INS  
## 4: 113058881 + Nonsense\_Mutation SNP  
## 5: 147076669 + De\_novo\_Start\_OutOfFrame SNP  
## 6: 186024782 + Frame\_Shift\_Ins INS  
## 7: 197145703 + Frame\_Shift\_Ins INS  
## 8: 75290100 + Frame\_Shift\_Ins INS  
## 9: 75960521 + Splice\_Site SNP  
## 10: 106207507 + Nonsense\_Mutation SNP  
## 11: 58919776 + Frame\_Shift\_Del DEL  
## 12: 57111534 + Frame\_Shift\_Ins INS  
## 13: 117615412 + Frame\_Shift\_Ins INS  
## 14: 48773871 + Frame\_Shift\_Ins INS  
## 15: 30764881 + Splice\_Site INS  
## 16: 66928544 + Frame\_Shift\_Ins INS  
## 17: 80194747 + Splice\_Site SNP  
## 18: 18699803 + Splice\_Site SNP  
## 19: 26537420 + Nonsense\_Mutation SNP  
## 20: 34911478 + Splice\_Site SNP  
## 21: 29490379 + Frame\_Shift\_Del DEL  
## 22: 51207957 + Frame\_Shift\_Ins INS  
## 23: 10283874 + Frame\_Shift\_Del DEL  
## 24: 130613154 + De\_novo\_Start\_OutOfFrame SNP  
## 25: 27010054 + Frame\_Shift\_Ins INS  
## 26: 38097713 + Splice\_Site DEL  
## 27: 104117085 + Frame\_Shift\_Ins INS  
## 28: 169127065 + Frame\_Shift\_Del DEL  
## 29: 29795951 + Frame\_Shift\_Ins INS  
## 30: 70411440 + Splice\_Site INS  
## 31: 76023702 + Nonsense\_Mutation SNP  
## 32: 50514614 + Frame\_Shift\_Ins INS  
## 33: 100847965 + Splice\_Site SNP  
## 34: 139837149 + Splice\_Site SNP  
## 35: 47918005 + Frame\_Shift\_Ins INS  
## 36: 100608909 + Frame\_Shift\_Ins INS  
## 37: 133378875 + Frame\_Shift\_Ins INS  
## End\_position Strand Variant\_Classification Variant\_Type  
## Reference\_Allele  
## 1: TACCTGCAGTCATCCAGGCCCAAGAAGTATGAGCTGGGGCAGGACCGGGGGGTGGGGTGCTGGGACCAGGGAAGGGAGAGGAAGGGCCAGGTGCCAGGACC  
## 2: -  
## 3: -  
## 4: C  
## 5: G  
## 6: -  
## 7: -  
## 8: -  
## 9: G  
## 10: G  
## 11: TG  
## 12: -  
## 13: -  
## 14: -  
## 15: -  
## 16: -  
## 17: G  
## 18: A  
## 19: T  
## 20: G  
## 21: G  
## 22: -  
## 23: AG  
## 24: C  
## 25: -  
## 26: T  
## 27: -  
## 28: C  
## 29: -  
## 30: -  
## 31: G  
## 32: -  
## 33: A  
## 34: T  
## 35: -  
## 36: -  
## 37: -  
## Reference\_Allele  
## Tumor\_Seq\_Allele1  
## 1: -  
## 2: T  
## 3: A  
## 4: T  
## 5: A  
## 6: A  
## 7: T  
## 8: T  
## 9: T  
## 10: T  
## 11: -  
## 12: G  
## 13: T  
## 14: T  
## 15: GA  
## 16: A  
## 17: A  
## 18: G  
## 19: A  
## 20: T  
## 21: -  
## 22: T  
## 23: -  
## 24: A  
## 25: A  
## 26: -  
## 27: T  
## 28: -  
## 29: GA  
## 30: A  
## 31: A  
## 32: T  
## 33: G  
## 34: C  
## 35: A  
## 36: C  
## 37: T  
## Tumor\_Seq\_Allele1  
## dbSNP\_RS  
## 1: rs117182812|rs80040276|rs561983449|rs369215923|rs559484140|rs543798581|rs535694981|rs528829386|rs372638570|rs78845480  
## 2: <NA>  
## 3: <NA>  
## 4:   
## 5: <NA>  
## 6:   
## 7: <NA>  
## 8: rs557300029  
## 9:   
## 10:   
## 11:   
## 12: <NA>  
## 13: rs34443379  
## 14: <NA>  
## 15:   
## 16: <NA>  
## 17:   
## 18: <NA>  
## 19:   
## 20: rs141635320  
## 21:   
## 22: <NA>  
## 23:   
## 24: <NA>  
## 25: <NA>  
## 26: <NA>  
## 27: <NA>  
## 28:   
## 29: <NA>  
## 30: rs202207965  
## 31:   
## 32: <NA>  
## 33: rs558911841  
## 34:   
## 35: <NA>  
## 36: <NA>  
## 37: <NA>  
## dbSNP\_RS  
## dbSNP\_Val\_Status  
## 1: byFrequency  
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## 3: <NA>  
## 4:   
## 5: <NA>  
## 6:   
## 7: <NA>  
## 8:   
## 9:   
## 10:   
## 11:   
## 12: <NA>  
## 13: <NA>  
## 14: <NA>  
## 15:   
## 16: <NA>  
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## 20:   
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## 26: <NA>  
## 27: <NA>  
## 28:   
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## 30: byFrequency  
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## 32: <NA>  
## 33:   
## 34:   
## 35: <NA>  
## 36: <NA>  
## 37: <NA>  
## dbSNP\_Val\_Status  
## Genome\_Change  
## 1: g.chr1:22150695\_22150795delTACCTGCAGTCATCCAGGCCCAAGAAGTATGAGCTGGGGCAGGACCGGGGGGTGGGGTGCTGGGACCAGGGAAGGGAGAGGAAGGGCCAGGTGCCAGGACC  
## 2: g.chr1:23420084\_23420085insT  
## 3: g.chr1:25785185\_25785186insA  
## 4: g.chr1:113058881C>T  
## 5: g.chr1:147076669G>A  
## 6: g.chr1:186024781\_186024782insA  
## 7: g.chr1:197145702\_197145703insT  
## 8: g.chr10:75290099\_75290100insT  
## 9: g.chr10:75960521G>T  
## 10: g.chr10:106207507G>T  
## 11: g.chr11:58919775\_58919776delTG  
## 12: g.chr12:57111533\_57111534insG  
## 13: g.chr12:117615411\_117615412insT  
## 14: g.chr15:48773870\_48773871insT  
## 15: g.chr16:30764880\_30764881insGA  
## 16: g.chr17:66928543\_66928544insA  
## 17: g.chr17:80194747G>A  
## 18: g.chr19:18699803A>G  
## 19: g.chr2:26537420T>A  
## 20: g.chr21:34911478G>T  
## 21: g.chr22:29490379delG  
## 22: g.chr22:51207956\_51207957insT  
## 23: g.chr3:10283873\_10283874delAG  
## 24: g.chr3:130613154C>A  
## 25: g.chr4:27010053\_27010054insA  
## 26: g.chr4:38097713delT  
## 27: g.chr4:104117084\_104117085insT  
## 28: g.chr5:169127065delC  
## 29: g.chr6:29795950\_29795951insGA  
## 30: g.chr6:70411439\_70411440insA  
## 31: g.chr6:76023702G>A  
## 32: g.chr7:50514613\_50514614insT  
## 33: g.chr8:100847965A>G  
## 34: g.chr9:139837149T>C  
## 35: g.chrX:47918004\_47918005insA  
## 36: g.chrX:100608908\_100608909insC  
## 37: g.chrX:133378874\_133378875insT  
## Genome\_Change  
## Annotation\_Transcript Tumor\_Sample\_Barcode  
## 1: ENST00000374695.3 ACH-000274  
## 2: ENST00000302291.4 ACH-000274  
## 3: ENST00000374343.4 ACH-000274  
## 4: ENST00000369684.4 ACH-000274  
## 5: ENST00000234739.3 ACH-000274  
## 6: ENST00000271588.4 ACH-000274  
## 7: ENST00000367405.4 ACH-000274  
## 8: ENST00000339859.4 ACH-000274  
## 9: ENST00000286621.2 ACH-000274  
## 10: ENST00000369704.3 ACH-000274  
## 11: ENST00000528737.1 ACH-000274  
## 12: ENST00000454682.1 ACH-000274  
## 13: ENST00000330622.5 ACH-000274  
## 14: ENST00000316623.5 ACH-000274  
## 15: ENST00000563588.1 ACH-000274  
## 16: ENST00000269080.2 ACH-000274  
## 17: ENST00000581287.1 ACH-000274  
## 18: ENST00000358607.6 ACH-000274  
## 19: ENST00000311519.1 ACH-000274  
## 20: ENST00000381831.3 ACH-000274  
## 21: ENST00000407188.1 ACH-000274  
## 22: ENST00000395598.3 ACH-000274  
## 23: ENST00000256458.4 ACH-000274  
## 24: ENST00000508532.1 ACH-000274  
## 25: ENST00000467011.1 ACH-000274  
## 26: ENST00000261439.4 ACH-000274  
## 27: ENST00000265148.3 ACH-000274  
## 28: ENST00000256935.8 ACH-000274  
## 29: ENST00000360323.6 ACH-000274  
## 30: ENST00000370577.3 ACH-000274  
## 31: ENST00000237172.7 ACH-000274  
## 32: ENST00000419119.1 ACH-000274  
## 33: ENST00000358544.2 ACH-000274  
## 34: ENST00000325285.3 ACH-000274  
## 35: ENST00000409324.3 ACH-000274  
## 36: ENST00000308731.7 ACH-000274  
## 37: ENST00000517294.1 ACH-000274  
## Annotation\_Transcript Tumor\_Sample\_Barcode  
## cDNA\_Change  
## 1: c.12816\_12818delGGTCCTGGCACCTGGCCCTTCCTCTCCCTTCCCTGGTCCCAGCACCCCACCCCCCGGTCCTGCCCCAGCTCATACTTCTTGGGCCTGGATGACTGCAGGTA  
## 2: c.670\_671insA  
## 3: c.956\_957insA  
## 4: c.523C>T  
## 5: <NA>  
## 6: c.7119\_7120insA  
## 7: c.1870\_1871insA  
## 8: c.1629\_1630insA  
## 9:   
## 10: c.2308G>T  
## 11: c.634\_635delTG  
## 12: c.3780\_3781insC  
## 13: c.505\_506insA  
## 14: c.3945\_3946insA  
## 15:   
## 16: c.682\_683insT  
## 17: c.366G>A  
## 18: <NA>  
## 19: c.994A>T  
## 20: c.144C>A  
## 21: c.225delG  
## 22: c.430\_431insA  
## 23: c.1839\_1840delAG  
## 24: <NA>  
## 25: c.1153\_1154insA  
## 26: <NA>  
## 27: c.349\_350insA  
## 28: c.1180delC  
## 29: c.200\_201insGA  
## 30:   
## 31: c.1846C>T  
## 32: c.372\_373insA  
## 33: c.10016A>G  
## 34:   
## 35: c.1826\_1827insT  
## 36: c.1699\_1700insG  
## 37: c.44\_45insT  
## cDNA\_Change  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## 1: c.(12814-12819)agggtc>agc p.RV4272fs TRUE FALSE  
## 2: c.(670-672)atgfs p.M224fs TRUE FALSE  
## 3: c.(955-960)tcaaaafs p.SK319fs TRUE FALSE  
## 4: c.(523-525)Cga>Tga p.R175\* TRUE FALSE  
## 5: <NA> <NA> TRUE FALSE  
## 6: c.(7120-7122)aaafs p.K2374fs TRUE FALSE  
## 7: c.(1870-1872)atafs p.I624fs TRUE FALSE  
## 8: c.(1627-1632)aaacctfs p.P544fs TRUE FALSE  
## 9: c.e2-1 TRUE FALSE  
## 10: c.(2308-2310)Gga>Tga p.G770\* TRUE FALSE  
## 11: c.(634-636)tgtfs p.C212fs TRUE FALSE  
## 12: c.(3778-3783)cccaaafs p.K1261fs TRUE FALSE  
## 13: c.(505-507)attfs p.I169fs TRUE FALSE  
## 14: c.(3943-3948)aaaggafs p.G1316fs TRUE FALSE  
## 15: c.e6+2 TRUE FALSE  
## 16: c.(682-684)tccfs p.S228fs TRUE FALSE  
## 17: c.(364-366)acG>acA p.T122T TRUE FALSE  
## 18: c.e2-1 <NA> TRUE FALSE  
## 19: c.(994-996)Aag>Tag p.K332\* TRUE FALSE  
## 20: c.(142-144)acC>acA p.T48T TRUE FALSE  
## 21: c.(223-225)gagfs p.E75fs TRUE FALSE  
## 22: c.(430-432)agcfs p.S144fs TRUE FALSE  
## 23: c.(1837-1842)aaagagfs p.E615fs TRUE FALSE  
## 24: <NA> <NA> TRUE FALSE  
## 25: c.(1153-1155)gaafs p.E385fs TRUE FALSE  
## 26: c.e14+2 <NA> TRUE FALSE  
## 27: c.(349-351)attfs p.I117fs TRUE FALSE  
## 28: c.(1180-1182)cgcfs p.R394fs TRUE TRUE  
## 29: c.(199-204)ccgaggfs p.PR67fs TRUE FALSE  
## 30: c.e11-2 TRUE FALSE  
## 31: c.(1846-1848)Cga>Tga p.R616\* TRUE FALSE  
## 32: c.(370-375)aaattcfs p.F125fs TRUE FALSE  
## 33: c.(10015-10017)cAg>cGg p.Q3339R TRUE FALSE  
## 34: c.e5-2 TRUE FALSE  
## 35: c.(1825-1827)ttcfs p.F609fs TRUE FALSE  
## 36: c.(1699-1701)gaafs p.E567fs TRUE FALSE  
## 37: c.(43-48)ccttttfs p.PF15fs TRUE FALSE  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## 1: 0 FALSE 0 NA <NA> <NA>  
## 2: 0 FALSE 0 NA <NA> <NA>  
## 3: 0 FALSE 0 NA <NA> <NA>  
## 4: 0 FALSE 0 NA 31:41 31:41  
## 5: 0 FALSE 0 NA <NA> <NA>  
## 6: 0 FALSE 0 NA <NA> <NA>  
## 7: 0 FALSE 0 NA <NA> <NA>  
## 8: 0 FALSE 0 NA <NA> <NA>  
## 9: 0 FALSE 0 NA 5:13 5:13  
## 10: 0 FALSE 0 NA 24:22 24:22  
## 11: 0 FALSE 0 2.471e-05 78:2 80:2  
## 12: 0 FALSE 0 NA <NA> <NA>  
## 13: 0 FALSE 0 NA <NA> <NA>  
## 14: 0 FALSE 0 NA <NA> <NA>  
## 15: NA FALSE 0 NA <NA> 30:32  
## 16: 0 FALSE 0 NA <NA> <NA>  
## 17: 0 FALSE 0 NA 34:34 34:34  
## 18: 0 FALSE 0 NA <NA> <NA>  
## 19: 0 FALSE 0 NA 21:24 21:24  
## 20: 0 FALSE 0 NA 19:49 19:49  
## 21: 0 FALSE 0 2.483e-05 14:21 14:24  
## 22: 0 FALSE 0 NA <NA> <NA>  
## 23: 0 FALSE 0 NA 34:42 41:43  
## 24: 0 FALSE 0 NA <NA> <NA>  
## 25: 0 FALSE 0 NA <NA> <NA>  
## 26: 0 FALSE 0 NA <NA> <NA>  
## 27: 0 FALSE 0 NA <NA> <NA>  
## 28: 5 FALSE 0 NA 94:3 97:2  
## 29: 0 FALSE 1 NA <NA> <NA>  
## 30: NA FALSE 0 NA 7:9 6:8  
## 31: 0 FALSE NA NA 94:100 94:100  
## 32: 0 FALSE 0 NA <NA> <NA>  
## 33: 0 FALSE 0 1.647e-05 10:21 10:21  
## 34: 0 FALSE 0 8.264e-06 5:6 5:6  
## 35: 0 FALSE 0 NA <NA> <NA>  
## 36: 0 FALSE 0 NA <NA> <NA>  
## 37: 0 FALSE 0 NA <NA> <NA>  
## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## 1: <NA> <NA> 308:15 <NA> <NA> <NA>  
## 2: <NA> <NA> 16:41 <NA> <NA> <NA>  
## 3: <NA> <NA> 10:60 <NA> <NA> <NA>  
## 4: <NA> <NA> <NA> <NA> <NA> <NA>  
## 5: <NA> <NA> 55:32 <NA> <NA> <NA>  
## 6: <NA> <NA> 10:39 <NA> <NA> <NA>  
## 7: <NA> <NA> 5:18 <NA> <NA> <NA>  
## 8: <NA> <NA> 9:53 <NA> <NA> <NA>  
## 9: <NA> <NA> <NA> 67:79 <NA> <NA>  
## 10: <NA> <NA> <NA> <NA> <NA> <NA>  
## 11: <NA> <NA> 154:0 <NA> <NA> <NA>  
## 12: <NA> <NA> <NA> 7:17 <NA> <NA>  
## 13: <NA> <NA> 18:55 <NA> <NA> <NA>  
## 14: <NA> <NA> 5:20 <NA> <NA> <NA>  
## 15: <NA> <NA> <NA> <NA> <NA> <NA>  
## 16: <NA> <NA> 8:39 <NA> <NA> <NA>  
## 17: <NA> <NA> 41:119 <NA> <NA> <NA>  
## 18: <NA> <NA> 144:30 <NA> <NA> <NA>  
## 19: <NA> <NA> <NA> <NA> <NA> <NA>  
## 20: <NA> <NA> 125:178 <NA> <NA> <NA>  
## 21: <NA> <NA> 92:157 <NA> <NA> <NA>  
## 22: <NA> <NA> 11:54 <NA> <NA> <NA>  
## 23: <NA> <NA> 13:0 134:147 <NA> <NA>  
## 24: <NA> <NA> 38:42 <NA> <NA> <NA>  
## 25: <NA> <NA> 10:43 <NA> <NA> <NA>  
## 26: <NA> <NA> 6:5 <NA> <NA> <NA>  
## 27: <NA> <NA> 7:26 <NA> <NA> <NA>  
## 28: <NA> <NA> 3:1 <NA> <NA> <NA>  
## 29: <NA> <NA> 16:0 <NA> <NA> <NA>  
## 30: <NA> <NA> <NA> <NA> <NA> <NA>  
## 31: <NA> <NA> <NA> <NA> <NA> <NA>  
## 32: <NA> <NA> 17:112 <NA> <NA> <NA>  
## 33: <NA> <NA> 19:13 19:16 <NA> <NA>  
## 34: <NA> <NA> 118:65 <NA> <NA> <NA>  
## 35: <NA> <NA> 5:9 <NA> <NA> <NA>  
## 36: <NA> <NA> <NA> 20:179 <NA> <NA>  
## 37: <NA> <NA> 6:21 <NA> <NA> <NA>  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## Variant\_annotation DepMap\_ID  
## 1: damaging ACH-000274  
## 2: damaging ACH-000274  
## 3: damaging ACH-000274  
## 4: damaging ACH-000274  
## 5: damaging ACH-000274  
## 6: damaging ACH-000274  
## 7: damaging ACH-000274  
## 8: damaging ACH-000274  
## 9: damaging ACH-000274  
## 10: damaging ACH-000274  
## 11: damaging ACH-000274  
## 12: damaging ACH-000274  
## 13: damaging ACH-000274  
## 14: damaging ACH-000274  
## 15: damaging ACH-000274  
## 16: damaging ACH-000274  
## 17: damaging ACH-000274  
## 18: damaging ACH-000274  
## 19: damaging ACH-000274  
## 20: damaging ACH-000274  
## 21: damaging ACH-000274  
## 22: damaging ACH-000274  
## 23: damaging ACH-000274  
## 24: damaging ACH-000274  
## 25: damaging ACH-000274  
## 26: damaging ACH-000274  
## 27: damaging ACH-000274  
## 28: damaging ACH-000274  
## 29: damaging ACH-000274  
## 30: damaging ACH-000274  
## 31: damaging ACH-000274  
## 32: damaging ACH-000274  
## 33: damaging ACH-000274  
## 34: damaging ACH-000274  
## 35: damaging ACH-000274  
## 36: damaging ACH-000274  
## 37: damaging ACH-000274  
## Variant\_annotation DepMap\_ID  
##   
## $mutation$`ACH-000304`  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## 1: 96460 COL11A1 1301 37 1 103461597  
## 2: 96475 RASAL2 9462 37 1 178412040  
## 3: 96476 HMCN1 83872 37 1 186024781  
## 4: 96477 BRINP3 339479 37 1 190423785  
## 5: 96485 IARS2 55699 37 1 220307803  
## 6: 96498 ECD 11319 37 10 74899185  
## 7: 96505 DCLRE1A 9937 37 10 115609831  
## 8: 96544 HDAC7 51564 37 12 48185370  
## 9: 96561 MAP1LC3B2 643246 37 12 117014124  
## 10: 96566 PIWIL1 9271 37 12 130830979  
## 11: 96601 NARG2 0 37 15 60768365  
## 12: 96608 CRAMP1L 57585 37 16 1676070  
## 13: 96610 PKD1 5310 37 16 2140883  
## 14: 96643 AURKB 9212 37 17 8108191  
## 15: 96652 FLCN 201163 37 17 17122331  
## 16: 96653 SLC5A10 125206 37 17 18872655  
## 17: 96654 SLC5A10 125206 37 17 18872655  
## 18: 96655 SLC5A10 125206 37 17 18872656  
## 19: 96672 BPTF 2186 37 17 65907571  
## 20: 96675 ZBTB14 7541 37 18 5293319  
## 21: 96699 RFXANK 8625 37 19 19304837  
## 22: 96718 ZNF155 7711 37 19 44500454  
## 23: 96724 ZNF28 7576 37 19 53302859  
## 24: 96739 AAK1 22848 37 2 69746310  
## 25: 96744 ANKRD36 375248 37 2 97856900  
## 26: 96748 RABL2A 11159 37 2 114398947  
## 27: 96749 MAP3K2 10746 37 2 128096510  
## 28: 96760 FSIP2 401024 37 2 186656175  
## 29: 96782 LTN1 26046 37 21 30332020  
## 30: 96799 TCF20 6942 37 22 42608252  
## 31: 96815 ACOX2 8309 37 3 58508255  
## 32: 96825 ATR 545 37 3 142261554  
## 33: 96841 RASSF6 166824 37 4 74464358  
## 34: 96844 BMP3 651 37 4 81967149  
## 35: 96855 PIK3R1 5295 37 5 67592108  
## 36: 96866 DOCK2 1794 37 5 169482359  
## 37: 96869 SLC22A23 63027 37 6 3273365  
## 38: 96875 HLA-DQB2 3120 37 6 32729506  
## 39: 96877 SLC26A8 116369 37 6 35930398  
## 40: 96887 ASCC3 10973 37 6 101246699  
## 41: 96891 SLC2A12 154091 37 6 134350764  
## 42: 96894 PDGFA 5154 37 7 540842  
## 43: 96906 AC006014.1 0 37 7 74999924  
## 44: 96918 ZNF800 168850 37 7 127013548  
## 45: 96927 CSMD1 64478 37 8 3076806  
## 46: 96953 MPDZ 8777 37 9 13125320  
## 47: 96957 UNC13B 10497 37 9 35404028  
## 48: 96959 ZNF658 26149 37 9 40773330  
## 49: 96982 CTPS2 56474 37 X 16711322  
## 50: 96983 MAP3K15 389840 37 X 19389141  
## 51: 96984 CXorf23 256643 37 X 19984223  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## End\_position Strand Variant\_Classification Variant\_Type  
## 1: 103461597 + Splice\_Site SNP  
## 2: 178412041 + Frame\_Shift\_Ins INS  
## 3: 186024782 + Frame\_Shift\_Ins INS  
## 4: 190423785 + Splice\_Site SNP  
## 5: 220307803 + Nonsense\_Mutation SNP  
## 6: 74899186 + Frame\_Shift\_Ins INS  
## 7: 115609832 + Frame\_Shift\_Ins INS  
## 8: 48185370 + Splice\_Site SNP  
## 9: 117014124 + Stop\_Codon\_Del DEL  
## 10: 130830979 + Nonsense\_Mutation SNP  
## 11: 60768365 + Splice\_Site SNP  
## 12: 1676070 + Frame\_Shift\_Del DEL  
## 13: 2140883 + Splice\_Site SNP  
## 14: 8108191 + Nonstop\_Mutation SNP  
## 15: 17122331 + Splice\_Site SNP  
## 16: 18872655 + Splice\_Site SNP  
## 17: 18872656 + Splice\_Site DNP  
## 18: 18872656 + Splice\_Site SNP  
## 19: 65907571 + Nonsense\_Mutation SNP  
## 20: 5293319 + De\_novo\_Start\_OutOfFrame SNP  
## 21: 19304837 + Frame\_Shift\_Del DEL  
## 22: 44500454 + Nonsense\_Mutation SNP  
## 23: 53302942 + Stop\_Codon\_Del DEL  
## 24: 69746311 + Frame\_Shift\_Ins INS  
## 25: 97856900 + Nonsense\_Mutation SNP  
## 26: 114398948 + Frame\_Shift\_Ins INS  
## 27: 128096511 + Frame\_Shift\_Ins INS  
## 28: 186656175 + Nonsense\_Mutation SNP  
## 29: 30332020 + Splice\_Site SNP  
## 30: 42608252 + Frame\_Shift\_Del DEL  
## 31: 58508255 + Nonsense\_Mutation SNP  
## 32: 142261555 + Frame\_Shift\_Ins INS  
## 33: 74464358 + Splice\_Site SNP  
## 34: 81967149 + Nonsense\_Mutation SNP  
## 35: 67592108 + Nonsense\_Mutation SNP  
## 36: 169482365 + Frame\_Shift\_Del DEL  
## 37: 3273365 + Nonsense\_Mutation SNP  
## 38: 32729507 + Frame\_Shift\_Ins INS  
## 39: 35930398 + Splice\_Site SNP  
## 40: 101246699 + Nonsense\_Mutation SNP  
## 41: 134350764 + Nonsense\_Mutation SNP  
## 42: 540842 + Frame\_Shift\_Del DEL  
## 43: 74999925 + Splice\_Site INS  
## 44: 127013549 + Frame\_Shift\_Ins INS  
## 45: 3076806 + Frame\_Shift\_Del DEL  
## 46: 13125320 + Nonsense\_Mutation SNP  
## 47: 35404028 + Nonstop\_Mutation SNP  
## 48: 40773330 + Nonsense\_Mutation SNP  
## 49: 16711323 + Frame\_Shift\_Ins INS  
## 50: 19389141 + Nonsense\_Mutation SNP  
## 51: 19984223 + Nonsense\_Mutation SNP  
## End\_position Strand Variant\_Classification Variant\_Type  
## Reference\_Allele  
## 1: C  
## 2: -  
## 3: -  
## 4: C  
## 5: C  
## 6: -  
## 7: -  
## 8: T  
## 9: A  
## 10: G  
## 11: C  
## 12: C  
## 13: A  
## 14: A  
## 15: A  
## 16: G  
## 17: GG  
## 18: G  
## 19: G  
## 20: C  
## 21: G  
## 22: C  
## 23: AAGGTTTCTCTCCACTATGAAGTCTATGATGGTATACAAGGTTTGACATCTGACTGAAGGTCTTGCCACACTCATTACACTTTC  
## 24: -  
## 25: G  
## 26: -  
## 27: -  
## 28: G  
## 29: C  
## 30: A  
## 31: G  
## 32: -  
## 33: T  
## 34: C  
## 35: C  
## 36: AAGAATA  
## 37: G  
## 38: -  
## 39: C  
## 40: C  
## 41: G  
## 42: A  
## 43: -  
## 44: -  
## 45: C  
## 46: G  
## 47: T  
## 48: G  
## 49: -  
## 50: C  
## 51: C  
## Reference\_Allele  
## Tumor\_Seq\_Allele1  
## 1: T  
## 2: A  
## 3: A  
## 4: G  
## 5: T  
## 6: T  
## 7: A  
## 8: C  
## 9: -  
## 10: A  
## 11: A  
## 12: -  
## 13: G  
## 14: G  
## 15: G  
## 16: A  
## 17: AA  
## 18: A  
## 19: T  
## 20: T  
## 21: -  
## 22: T  
## 23: -  
## 24: G  
## 25: T  
## 26: A  
## 27: T  
## 28: T  
## 29: A  
## 30: -  
## 31: A  
## 32: A  
## 33: C  
## 34: T  
## 35: T  
## 36: -  
## 37: T  
## 38: T  
## 39: T  
## 40: A  
## 41: A  
## 42: -  
## 43: A  
## 44: T  
## 45: -  
## 46: A  
## 47: G  
## 48: A  
## 49: T  
## 50: T  
## 51: A  
## Tumor\_Seq\_Allele1  
## dbSNP\_RS  
## 1: <NA>  
## 2: <NA>  
## 3:   
## 4: <NA>  
## 5: <NA>  
## 6: <NA>  
## 7: <NA>  
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## 9: <NA>  
## 10: <NA>  
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## 16: <NA>  
## 17: <NA>  
## 18: <NA>  
## 19: <NA>  
## 20: rs373698889  
## 21: rs559367724  
## 22: <NA>  
## 23: rs371999424|rs574153174|rs563827798|rs9917046|rs9917044|rs549512525  
## 24: <NA>  
## 25: <NA>  
## 26:   
## 27: <NA>  
## 28: <NA>  
## 29: <NA>  
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## 37: rs372807040  
## 38: <NA>  
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## 40: <NA>  
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## 44: <NA>  
## 45: <NA>  
## 46: <NA>  
## 47: <NA>  
## 48: rs367816856  
## 49: <NA>  
## 50: <NA>  
## 51: <NA>  
## dbSNP\_RS  
## dbSNP\_Val\_Status  
## 1: <NA>  
## 2: <NA>  
## 3:   
## 4: <NA>  
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## 6: <NA>  
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## 8: <NA>  
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## 22: <NA>  
## 23: byFrequency  
## 24: <NA>  
## 25: <NA>  
## 26:   
## 27: <NA>  
## 28: <NA>  
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## 46: <NA>  
## 47: <NA>  
## 48: <NA>  
## 49: <NA>  
## 50: <NA>  
## 51: <NA>  
## dbSNP\_Val\_Status  
## Genome\_Change  
## 1: g.chr1:103461597C>T  
## 2: g.chr1:178412040\_178412041insA  
## 3: g.chr1:186024781\_186024782insA  
## 4: g.chr1:190423785C>G  
## 5: g.chr1:220307803C>T  
## 6: g.chr10:74899185\_74899186insT  
## 7: g.chr10:115609831\_115609832insA  
## 8: g.chr12:48185370T>C  
## 9: g.chr12:117014124delA  
## 10: g.chr12:130830979G>A  
## 11: g.chr15:60768365C>A  
## 12: g.chr16:1676070delC  
## 13: g.chr16:2140883A>G  
## 14: g.chr17:8108191A>G  
## 15: g.chr17:17122331A>G  
## 16: g.chr17:18872655G>A  
## 17: g.chr17:18872655\_18872656GG>AA  
## 18: g.chr17:18872656G>A  
## 19: g.chr17:65907571G>T  
## 20: g.chr18:5293319C>T  
## 21: g.chr19:19304837delG  
## 22: g.chr19:44500454C>T  
## 23: g.chr19:53302859\_53302942delAAGGTTTCTCTCCACTATGAAGTCTATGATGGTATACAAGGTTTGACATCTGACTGAAGGTCTTGCCACACTCATTACACTTTC  
## 24: g.chr2:69746310\_69746311insG  
## 25: g.chr2:97856900G>T  
## 26: g.chr2:114398947\_114398948insA  
## 27: g.chr2:128096510\_128096511insT  
## 28: g.chr2:186656175G>T  
## 29: g.chr21:30332020C>A  
## 30: g.chr22:42608252delA  
## 31: g.chr3:58508255G>A  
## 32: g.chr3:142261554\_142261555insA  
## 33: g.chr4:74464358T>C  
## 34: g.chr4:81967149C>T  
## 35: g.chr5:67592108C>T  
## 36: g.chr5:169482359\_169482365delAAGAATA  
## 37: g.chr6:3273365G>T  
## 38: g.chr6:32729506\_32729507insT  
## 39: g.chr6:35930398C>T  
## 40: g.chr6:101246699C>A  
## 41: g.chr6:134350764G>A  
## 42: g.chr7:540842delA  
## 43: g.chr7:74999924\_74999925insA  
## 44: g.chr7:127013548\_127013549insT  
## 45: g.chr8:3076806delC  
## 46: g.chr9:13125320G>A  
## 47: g.chr9:35404028T>G  
## 48: g.chr9:40773330G>A  
## 49: g.chrX:16711322\_16711323insT  
## 50: g.chrX:19389141C>T  
## 51: g.chrX:19984223C>A  
## Genome\_Change  
## Annotation\_Transcript Tumor\_Sample\_Barcode cDNA\_Change  
## 1: ENST00000370096.3 ACH-000304 c.2243G>A  
## 2: ENST00000462775.1 ACH-000304 c.714\_715insA  
## 3: ENST00000271588.4 ACH-000304 c.7119\_7120insA  
## 4: ENST00000367462.3 ACH-000304 c.236G>C  
## 5: ENST00000302637.5 ACH-000304 c.1897C>T  
## 6: ENST00000372979.4 ACH-000304 c.1302\_1303insA  
## 7: ENST00000361384.2 ACH-000304 c.1032\_1033insT  
## 8: ENST00000427332.2 ACH-000304 c.1815A>G  
## 9: ENST00000556529.1 ACH-000304 <NA>  
## 10: ENST00000245255.3 ACH-000304 c.381G>A  
## 11: ENST00000261520.4 ACH-000304 c.43G>T  
## 12: ENST00000397412.3 ACH-000304 c.443delC  
## 13: ENST00000262304.4 ACH-000304 <NA>  
## 14: ENST00000585124.1 ACH-000304 c.1033T>C  
## 15: ENST00000285071.4 ACH-000304 <NA>  
## 16: ENST00000395645.3 ACH-000304 c.560G>A  
## 17: ENST00000395645.3 ACH-000304 c.560\_561GG>AA  
## 18: ENST00000395645.3 ACH-000304 c.561G>A  
## 19: ENST00000321892.4 ACH-000304 c.3949G>T  
## 20: ENST00000357006.4 ACH-000304 <NA>  
## 21: ENST00000303088.4 ACH-000304 c.82delG  
## 22: ENST00000270014.2 ACH-000304 c.445C>T  
## 23: ENST00000457749.2 ACH-000304 <NA>  
## 24: ENST00000409085.4 ACH-000304 c.1272\_1273insC  
## 25: ENST00000461153.2 ACH-000304 c.2329G>T  
## 26: ENST00000393167.3 ACH-000304 c.424\_425insA  
## 27: ENST00000409947.1 ACH-000304 c.120\_121insA  
## 28: ENST00000424728.1 ACH-000304 c.4312G>T  
## 29: ENST00000361371.5 ACH-000304 <NA>  
## 30: ENST00000359486.3 ACH-000304 c.3060delT  
## 31: ENST00000302819.5 ACH-000304 c.1600C>T  
## 32: ENST00000350721.4 ACH-000304 c.3402\_3403insT  
## 33: ENST00000342081.3 ACH-000304 c.239A>G  
## 34: ENST00000282701.2 ACH-000304 c.574C>T  
## 35: ENST00000521381.1 ACH-000304 c.1924C>T  
## 36: ENST00000256935.8 ACH-000304 c.4264\_4270delAAGAATA  
## 37: ENST00000406686.3 ACH-000304 c.1985C>A  
## 38: ENST00000437316.2 ACH-000304 c.294\_295insA  
## 39: ENST00000490799.1 ACH-000304 c.1366G>A  
## 40: ENST00000369162.2 ACH-000304 c.1285G>T  
## 41: ENST00000275230.5 ACH-000304 c.199C>T  
## 42: ENST00000354513.5 ACH-000304 c.491delT  
## 43: ENST00000594196.1 ACH-000304 <NA>  
## 44: ENST00000393313.1 ACH-000304 c.1841\_1842insA  
## 45: ENST00000520002.1 ACH-000304 c.4646delG  
## 46: ENST00000319217.7 ACH-000304 c.4702C>T  
## 47: ENST00000378495.3 ACH-000304 c.4774T>G  
## 48: ENST00000602553.1 ACH-000304 c.1945C>T  
## 49: ENST00000443824.1 ACH-000304 c.580\_581insA  
## 50: ENST00000338883.4 ACH-000304 c.3336G>A  
## 51: ENST00000379682.4 ACH-000304 c.586G>T  
## Annotation\_Transcript Tumor\_Sample\_Barcode cDNA\_Change  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## 1: c.(2242-2244)gGt>gAt p.G748D TRUE FALSE  
## 2: c.(715-717)aaafs p.K239fs TRUE FALSE  
## 3: c.(7120-7122)aaafs p.K2374fs TRUE FALSE  
## 4: c.(235-237)aGg>aCg p.R79T TRUE FALSE  
## 5: c.(1897-1899)Cag>Tag p.Q633\* TRUE FALSE  
## 6: c.(1300-1305)aaagaafs p.E435fs TRUE FALSE  
## 7: c.(1030-1035)tttaaafs p.K345fs TRUE TRUE  
## 8: c.(1813-1815)gcA>gcG p.A605A TRUE FALSE  
## 9: <NA> <NA> TRUE FALSE  
## 10: c.(379-381)tgG>tgA p.W127\* TRUE FALSE  
## 11: c.(43-45)Gat>Tat p.D15Y TRUE FALSE  
## 12: c.(442-444)tctfs p.S149fs TRUE FALSE  
## 13: c.e43+1 <NA> TRUE FALSE  
## 14: c.(1033-1035)Tga>Cga p.\*345R TRUE FALSE  
## 15: c.e9+1 <NA> TRUE FALSE  
## 16: c.(559-561)gGg>gAg p.G187E TRUE FALSE  
## 17: c.(559-561)gGG>gAA p.G187E TRUE FALSE  
## 18: c.(559-561)ggG>ggA p.G187G TRUE FALSE  
## 19: c.(3949-3951)Gaa>Taa p.E1317\* TRUE FALSE  
## 20: <NA> <NA> TRUE FALSE  
## 21: c.(82-84)ggafs p.G28fs TRUE FALSE  
## 22: c.(445-447)Cag>Tag p.Q149\* TRUE FALSE  
## 23: <NA> <NA> TRUE FALSE  
## 24: c.(1270-1275)cccagcfs p.S425fs TRUE FALSE  
## 25: c.(2329-2331)Gga>Tga p.G777\* TRUE FALSE  
## 26: c.(424-426)caafs p.Q142fs TRUE FALSE  
## 27: c.(118-123)aaacagfs p.Q41fs TRUE FALSE  
## 28: c.(4312-4314)Gaa>Taa p.E1438\* TRUE FALSE  
## 29: c.e13-1 <NA> TRUE FALSE  
## 30: c.(3058-3060)cctfs p.P1020fs TRUE FALSE  
## 31: c.(1600-1602)Cag>Tag p.Q534\* TRUE FALSE  
## 32: c.(3400-3405)tttaacfs p.N1135fs TRUE FALSE  
## 33: c.(238-240)gAg>gGg p.E80G TRUE FALSE  
## 34: c.(574-576)Cga>Tga p.R192\* TRUE FALSE  
## 35: c.(1924-1926)Cga>Tga p.R642\* TRUE TRUE  
## 36: c.(4264-4272)aagaataagfs p.KNK1422fs TRUE FALSE  
## 37: c.(1984-1986)tCg>tAg p.S662\* TRUE FALSE  
## 38: c.(292-297)gagcggfs p.R99fs TRUE FALSE  
## 39: c.(1366-1368)Gct>Act p.A456T TRUE FALSE  
## 40: c.(1285-1287)Gga>Tga p.G429\* TRUE FALSE  
## 41: c.(199-201)Cag>Tag p.Q67\* TRUE FALSE  
## 42: c.(490-492)ttafs p.L164fs TRUE FALSE  
## 43: c.e3-2 <NA> TRUE FALSE  
## 44: c.(1840-1842)aacfs p.N614fs TRUE FALSE  
## 45: c.(4645-4647)ggcfs p.G1549fs TRUE FALSE  
## 46: c.(4702-4704)Cag>Tag p.Q1568\* TRUE FALSE  
## 47: c.(4774-4776)Tga>Gga p.\*1592G TRUE FALSE  
## 48: c.(1945-1947)Caa>Taa p.Q649\* TRUE FALSE  
## 49: c.(580-582)accfs p.T194fs TRUE FALSE  
## 50: c.(3334-3336)tgG>tgA p.W1112\* TRUE FALSE  
## 51: c.(586-588)Gag>Tag p.E196\* TRUE FALSE  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## 1: 0 FALSE 0 NA <NA> <NA>  
## 2: 0 FALSE 0 8.237e-06 <NA> <NA>  
## 3: 0 FALSE 0 NA <NA> <NA>  
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## 6: 0 FALSE 0 NA <NA> <NA>  
## 7: 3 FALSE 0 1.647e-05 <NA> <NA>  
## 8: 0 FALSE 0 NA <NA> <NA>  
## 9: 0 FALSE 0 NA <NA> <NA>  
## 10: 0 FALSE 0 NA <NA> <NA>  
## 11: 0 FALSE 0 NA <NA> <NA>  
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## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## 1: 29:0 30:0 <NA> <NA> <NA> <NA>  
## 2: <NA> <NA> 6:13 <NA> <NA> <NA>  
## 3: <NA> <NA> 29:176 <NA> <NA> <NA>  
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## 8: 7:0 <NA> 70:0 <NA> <NA> <NA>  
## 9: <NA> <NA> 4:5 <NA> <NA> <NA>  
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## 12: <NA> <NA> 25:46 <NA> <NA> <NA>  
## 13: 8:3 8:3 16:4 <NA> <NA> <NA>  
## 14: 34:39 34:39 201:87 <NA> <NA> <NA>  
## 15: 13:28 13:28 23:4 5:7 <NA> <NA>  
## 16: 22:17 <NA> 21:21 <NA> <NA> <NA>  
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## 19: 24:31 23:32 35:77 <NA> <NA> <NA>  
## 20: 10:10 11:10 13:32 <NA> <NA> <NA>  
## 21: 89:39 129:169 123:198 <NA> <NA> <NA>  
## 22: 64:66 61:64 <NA> <NA> <NA> <NA>  
## 23: <NA> <NA> 58:11 <NA> <NA> <NA>  
## 24: <NA> 7:30 <NA> <NA> <NA> <NA>  
## 25: 117:171 108:160 4:5 <NA> <NA> <NA>  
## 26: <NA> <NA> 8:31 <NA> <NA> <NA>  
## 27: <NA> <NA> 7:35 <NA> <NA> <NA>  
## 28: 37:62 37:63 <NA> <NA> <NA> <NA>  
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## 30: <NA> 14:36 14:16 <NA> <NA> <NA>  
## 31: 23:25 21:27 <NA> <NA> <NA> <NA>  
## 32: <NA> <NA> 7:30 <NA> <NA> <NA>  
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## 34: 108:124 107:121 <NA> <NA> <NA> <NA>  
## 35: 95:0 95:0 103:1 64:1 <NA> <NA>  
## 36: 7:0 11:44 <NA> <NA> <NA> <NA>  
## 37: 34:66 33:65 10:28 <NA> <NA> <NA>  
## 38: <NA> <NA> 22:0 <NA> <NA> <NA>  
## 39: 77:30 77:30 <NA> <NA> <NA> <NA>  
## 40: 36:39 <NA> 28:44 <NA> <NA> <NA>  
## 41: 45:38 45:38 <NA> <NA> <NA> <NA>  
## 42: 96:35 134:537 85:277 89:325 <NA> <NA>  
## 43: <NA> <NA> 8:24 <NA> <NA> <NA>  
## 44: <NA> <NA> 12:59 <NA> <NA> <NA>  
## 45: 17:3 21:44 <NA> <NA> <NA> <NA>  
## 46: 50:0 50:0 26:0 <NA> <NA> <NA>  
## 47: 17:23 16:23 <NA> <NA> <NA> <NA>  
## 48: 195:248 188:247 <NA> <NA> <NA> <NA>  
## 49: <NA> <NA> 9:39 <NA> <NA> <NA>  
## 50: 44:0 46:0 <NA> <NA> <NA> <NA>  
## 51: 52:4 49:3 <NA> <NA> <NA> <NA>  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## Variant\_annotation DepMap\_ID  
## 1: damaging ACH-000304  
## 2: damaging ACH-000304  
## 3: damaging ACH-000304  
## 4: damaging ACH-000304  
## 5: damaging ACH-000304  
## 6: damaging ACH-000304  
## 7: damaging ACH-000304  
## 8: damaging ACH-000304  
## 9: other non-conserving ACH-000304  
## 10: damaging ACH-000304  
## 11: damaging ACH-000304  
## 12: damaging ACH-000304  
## 13: damaging ACH-000304  
## 14: other non-conserving ACH-000304  
## 15: damaging ACH-000304  
## 16: damaging ACH-000304  
## 17: damaging ACH-000304  
## 18: damaging ACH-000304  
## 19: damaging ACH-000304  
## 20: damaging ACH-000304  
## 21: damaging ACH-000304  
## 22: damaging ACH-000304  
## 23: other non-conserving ACH-000304  
## 24: damaging ACH-000304  
## 25: damaging ACH-000304  
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## 28: damaging ACH-000304  
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## 34: damaging ACH-000304  
## 35: damaging ACH-000304  
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## 38: damaging ACH-000304  
## 39: damaging ACH-000304  
## 40: damaging ACH-000304  
## 41: damaging ACH-000304  
## 42: damaging ACH-000304  
## 43: damaging ACH-000304  
## 44: damaging ACH-000304  
## 45: damaging ACH-000304  
## 46: damaging ACH-000304  
## 47: other non-conserving ACH-000304  
## 48: damaging ACH-000304  
## 49: damaging ACH-000304  
## 50: damaging ACH-000304  
## 51: damaging ACH-000304  
## Variant\_annotation DepMap\_ID  
##   
## $mutation$`ACH-000322`  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## 1: 104320 LPAR3 23566 37 1 85279793  
## 2: 104325 EPS8L3 79574 37 1 110301694  
## 3: 104327 ATP1A1 476 37 1 116936319  
## 4: 104333 HMCN1 83872 37 1 186024781  
## 5: 104334 C1orf106 55765 37 1 200881242  
## 6: 104335 TMEM81 388730 37 1 205052948  
## 7: 104340 ESRRG 2104 37 1 216978426  
## 8: 104342 IARS2 55699 37 1 220310228  
## 9: 104357 MUC6 4588 37 11 1031907  
## 10: 104367 GLYATL2 219970 37 11 58611906  
## 11: 104377 ATM 472 37 11 108216585  
## 12: 104378 ATM 472 37 11 108216585  
## 13: 104379 ATM 472 37 11 108216586  
## 14: 104389 GPRC5D 55507 37 12 13102516  
## 15: 104399 TMTC2 160335 37 12 83080749  
## 16: 104400 ANO4 121601 37 12 101413904  
## 17: 104412 LRRC9 341883 37 14 60498714  
## 18: 104414 SYNE2 23224 37 14 64469996  
## 19: 104416 SIPA1L1 26037 37 14 72128103  
## 20: 104418 BTBD7 55727 37 14 93709220  
## 21: 104430 HYKK 123688 37 15 78805550  
## 22: 104437 CREBBP 1387 37 16 3795356  
## 23: 104441 ZKSCAN2 342357 37 16 25251357  
## 24: 104461 MYO1D 4642 37 17 31087623  
## 25: 104469 TMEM100 55273 37 17 53798135  
## 26: 104520 TRIP12 9320 37 2 230724210  
## 27: 104533 LAMA5 3911 37 20 60892834  
## 28: 104536 NCAM2 4685 37 21 22906970  
## 29: 104537 BRWD1 54014 37 21 40665735  
## 30: 104542 CECR2 27443 37 22 18031826  
## 31: 104544 RASL10A 10633 37 22 29711522  
## 32: 104545 ISX 91464 37 22 35463310  
## 33: 104550 IL17RE 132014 37 3 9945781  
## 34: 104556 CCR3 1232 37 3 46307076  
## 35: 104558 PXK 54899 37 3 58368270  
## 36: 104572 PALLD 23022 37 4 169845406  
## 37: 104580 VCAN 1462 37 5 82837081  
## 38: 104589 LCP2 3937 37 5 169694012  
## 39: 104591 ELOVL2 54898 37 6 10984133  
## 40: 104624 KEL 3792 37 7 142658447  
## 41: 104629 ATAD2 29028 37 8 124335211  
## 42: 104638 KCNV2 169522 37 9 2718181  
## 43: 104641 ELAVL2 1993 37 9 23701461  
## 44: 104642 KIAA1045 23349 37 9 34977551  
## 45: 104643 NPR2 4882 37 9 35792155  
## 46: 104657 NKAP 79576 37 X 119070384  
## 47: 104658 ACTRT1 139741 37 X 127185836  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## End\_position Strand Variant\_Classification Variant\_Type  
## 1: 85279793 + Nonsense\_Mutation SNP  
## 2: 110301695 + Frame\_Shift\_Ins INS  
## 3: 116936320 + Frame\_Shift\_Ins INS  
## 4: 186024782 + Frame\_Shift\_Ins INS  
## 5: 200881242 + Nonsense\_Mutation SNP  
## 6: 205052949 + Frame\_Shift\_Ins INS  
## 7: 216978426 + De\_novo\_Start\_OutOfFrame SNP  
## 8: 220310229 + Frame\_Shift\_Ins INS  
## 9: 1031907 + Nonsense\_Mutation SNP  
## 10: 58611906 + Splice\_Site SNP  
## 11: 108216585 + Nonsense\_Mutation SNP  
## 12: 108216586 + Nonsense\_Mutation DNP  
## 13: 108216586 + Nonsense\_Mutation SNP  
## 14: 13102516 + Nonsense\_Mutation SNP  
## 15: 83080754 + De\_novo\_Start\_OutOfFrame DEL  
## 16: 101413905 + Frame\_Shift\_Ins INS  
## 17: 60498714 + Splice\_Site SNP  
## 18: 64469996 + Nonsense\_Mutation SNP  
## 19: 72128104 + Frame\_Shift\_Ins INS  
## 20: 93709221 + Frame\_Shift\_Ins INS  
## 21: 78805551 + Frame\_Shift\_Ins INS  
## 22: 3795356 + Splice\_Site SNP  
## 23: 25251358 + Frame\_Shift\_Ins INS  
## 24: 31087624 + Frame\_Shift\_Ins INS  
## 25: 53798136 + Frame\_Shift\_Ins INS  
## 26: 230724211 + Frame\_Shift\_Ins INS  
## 27: 60892834 + Splice\_Site SNP  
## 28: 22906970 + Nonsense\_Mutation SNP  
## 29: 40665735 + Splice\_Site SNP  
## 30: 18031826 + Splice\_Site SNP  
## 31: 29711522 + De\_novo\_Start\_OutOfFrame SNP  
## 32: 35463310 + Splice\_Site SNP  
## 33: 9945781 + Nonsense\_Mutation SNP  
## 34: 46307076 + Nonsense\_Mutation SNP  
## 35: 58368271 + Frame\_Shift\_Ins INS  
## 36: 169845406 + Splice\_Site SNP  
## 37: 82837082 + Frame\_Shift\_Ins INS  
## 38: 169694012 + Splice\_Site SNP  
## 39: 10984133 + Nonsense\_Mutation SNP  
## 40: 142658447 + Splice\_Site SNP  
## 41: 124335212 + Frame\_Shift\_Ins INS  
## 42: 2718181 + Nonsense\_Mutation SNP  
## 43: 23701462 + Frame\_Shift\_Ins INS  
## 44: 34977552 + Frame\_Shift\_Ins INS  
## 45: 35792155 + De\_novo\_Start\_OutOfFrame SNP  
## 46: 119070385 + Frame\_Shift\_Ins INS  
## 47: 127185837 + Frame\_Shift\_Ins INS  
## End\_position Strand Variant\_Classification Variant\_Type  
## Reference\_Allele Tumor\_Seq\_Allele1 dbSNP\_RS  
## 1: G T <NA>  
## 2: - CT rs201335250  
## 3: - G <NA>  
## 4: - A   
## 5: C T <NA>  
## 6: - T <NA>  
## 7: C T <NA>  
## 8: - T <NA>  
## 9: G A   
## 10: C T rs117831599  
## 11: G A <NA>  
## 12: GG AA <NA>  
## 13: G A <NA>  
## 14: G T <NA>  
## 15: GCTGGG - rs56311034  
## 16: - A <NA>  
## 17: A G <NA>  
## 18: C T <NA>  
## 19: - A rs79690878|rs369992908  
## 20: - T <NA>  
## 21: - C <NA>  
## 22: C A <NA>  
## 23: - T <NA>  
## 24: - A <NA>  
## 25: - A   
## 26: - T <NA>  
## 27: G T rs565333663  
## 28: G T <NA>  
## 29: A G <NA>  
## 30: A G <NA>  
## 31: C T <NA>  
## 32: G A rs577009157  
## 33: C T rs144881083  
## 34: C T <NA>  
## 35: - A <NA>  
## 36: C G <NA>  
## 37: - A <NA>  
## 38: C T <NA>  
## 39: G A rs191521211  
## 40: G A rs537228922  
## 41: - G <NA>  
## 42: G T rs140256288  
## 43: - T <NA>  
## 44: - TGTGG rs552529109|rs532446577  
## 45: C A rs375985640  
## 46: - T <NA>  
## 47: - C <NA>  
## Reference\_Allele Tumor\_Seq\_Allele1 dbSNP\_RS  
## dbSNP\_Val\_Status Genome\_Change  
## 1: <NA> g.chr1:85279793G>T  
## 2: <NA> g.chr1:110301694\_110301695insCT  
## 3: <NA> g.chr1:116936319\_116936320insG  
## 4: g.chr1:186024781\_186024782insA  
## 5: <NA> g.chr1:200881242C>T  
## 6: <NA> g.chr1:205052948\_205052949insT  
## 7: <NA> g.chr1:216978426C>T  
## 8: <NA> g.chr1:220310228\_220310229insT  
## 9: g.chr11:1031907G>A  
## 10: byFrequency g.chr11:58611906C>T  
## 11: <NA> g.chr11:108216585G>A  
## 12: <NA> g.chr11:108216585\_108216586GG>AA  
## 13: <NA> g.chr11:108216586G>A  
## 14: <NA> g.chr12:13102516G>T  
## 15: byFrequency g.chr12:83080749\_83080754delGCTGGG  
## 16: <NA> g.chr12:101413904\_101413905insA  
## 17: <NA> g.chr14:60498714A>G  
## 18: <NA> g.chr14:64469996C>T  
## 19: <NA> g.chr14:72128103\_72128104insA  
## 20: <NA> g.chr14:93709220\_93709221insT  
## 21: <NA> g.chr15:78805550\_78805551insC  
## 22: <NA> g.chr16:3795356C>A  
## 23: <NA> g.chr16:25251357\_25251358insT  
## 24: <NA> g.chr17:31087623\_31087624insA  
## 25: g.chr17:53798135\_53798136insA  
## 26: <NA> g.chr2:230724210\_230724211insT  
## 27: <NA> g.chr20:60892834G>T  
## 28: <NA> g.chr21:22906970G>T  
## 29: <NA> g.chr21:40665735A>G  
## 30: <NA> g.chr22:18031826A>G  
## 31: <NA> g.chr22:29711522C>T  
## 32: <NA> g.chr22:35463310G>A  
## 33: <NA> g.chr3:9945781C>T  
## 34: <NA> g.chr3:46307076C>T  
## 35: <NA> g.chr3:58368270\_58368271insA  
## 36: <NA> g.chr4:169845406C>G  
## 37: <NA> g.chr5:82837081\_82837082insA  
## 38: <NA> g.chr5:169694012C>T  
## 39: <NA> g.chr6:10984133G>A  
## 40: <NA> g.chr7:142658447G>A  
## 41: <NA> g.chr8:124335211\_124335212insG  
## 42: <NA> g.chr9:2718181G>T  
## 43: <NA> g.chr9:23701461\_23701462insT  
## 44: <NA> g.chr9:34977551\_34977552insTGTGG  
## 45: <NA> g.chr9:35792155C>A  
## 46: <NA> g.chrX:119070384\_119070385insT  
## 47: <NA> g.chrX:127185836\_127185837insC  
## dbSNP\_Val\_Status Genome\_Change  
## Annotation\_Transcript Tumor\_Sample\_Barcode cDNA\_Change  
## 1: ENST00000440886.1 ACH-000322 c.798C>A  
## 2: ENST00000361965.4 ACH-000322 c.450\_451insAG  
## 3: ENST00000295598.5 ACH-000322 c.1634\_1635insG  
## 4: ENST00000271588.4 ACH-000322 c.7119\_7120insA  
## 5: ENST00000367342.4 ACH-000322 c.1876C>T  
## 6: ENST00000367167.3 ACH-000322 c.500\_501insA  
## 7: ENST00000360012.3 ACH-000322 <NA>  
## 8: ENST00000302637.5 ACH-000322 c.2024\_2025insT  
## 9: ENST00000421673.2 ACH-000322 c.262C>T  
## 10: ENST00000287275.1 ACH-000322 <NA>  
## 11: ENST00000452508.2 ACH-000322 c.8534G>A  
## 12: ENST00000452508.2 ACH-000322 c.8534\_8535GG>AA  
## 13: ENST00000452508.2 ACH-000322 c.8535G>A  
## 14: ENST00000228887.1 ACH-000322 c.803C>A  
## 15: ENST00000321196.3 ACH-000322 <NA>  
## 16: ENST00000392977.3 ACH-000322 c.827\_828insA  
## 17: ENST00000445360.1 ACH-000322 c.3923A>G  
## 18: ENST00000344113.4 ACH-000322 c.4345C>T  
## 19: ENST00000555818.1 ACH-000322 c.2174\_2175insA  
## 20: ENST00000334746.5 ACH-000322 c.2797\_2798insA  
## 21: ENST00000569878.1 ACH-000322 c.120\_121insC  
## 22: ENST00000262367.5 ACH-000322 <NA>  
## 23: ENST00000328086.7 ACH-000322 c.2683\_2684insA  
## 24: ENST00000318217.5 ACH-000322 c.1057\_1058insT  
## 25: ENST00000575734.1 ACH-000322 c.296\_297insT  
## 26: ENST00000283943.5 ACH-000322 c.178\_179insA  
## 27: ENST00000252999.3 ACH-000322 c.7240C>A  
## 28: ENST00000400546.1 ACH-000322 c.2395G>T  
## 29: ENST00000333229.2 ACH-000322 <NA>  
## 30: ENST00000400585.2 ACH-000322 c.3896A>G  
## 31: ENST00000216101.6 ACH-000322 <NA>  
## 32: ENST00000308700.6 ACH-000322 <NA>  
## 33: ENST00000383814.3 ACH-000322 c.214C>T  
## 34: ENST00000357422.2 ACH-000322 c.427C>T  
## 35: ENST00000356151.2 ACH-000322 c.231\_232insA  
## 36: ENST00000505667.1 ACH-000322 c.3059C>G  
## 37: ENST00000265077.3 ACH-000322 c.8259\_8260insA  
## 38: ENST00000046794.5 ACH-000322 <NA>  
## 39: ENST00000354666.3 ACH-000322 c.772C>T  
## 40: ENST00000355265.2 ACH-000322 c.223C>T  
## 41: ENST00000287394.5 ACH-000322 c.4097\_4098insC  
## 42: ENST00000382082.3 ACH-000322 c.442G>T  
## 43: ENST00000397312.2 ACH-000322 c.628\_629insA  
## 44: ENST00000242315.3 ACH-000322 c.1019\_1020insTGTGG  
## 45: ENST00000342694.2 ACH-000322 <NA>  
## 46: ENST00000371410.3 ACH-000322 c.548\_549insA  
## 47: ENST00000371124.3 ACH-000322 c.349\_350insG  
## Annotation\_Transcript Tumor\_Sample\_Barcode cDNA\_Change  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## 1: c.(796-798)tgC>tgA p.C266\* TRUE FALSE  
## 2: c.(448-453)gagctgfs p.L151fs TRUE FALSE  
## 3: c.(1633-1638)ctggggfs p.LG545fs TRUE FALSE  
## 4: c.(7120-7122)aaafs p.K2374fs TRUE FALSE  
## 5: c.(1876-1878)Cga>Tga p.R626\* TRUE FALSE  
## 6: c.(499-501)aacfs p.N167fs TRUE FALSE  
## 7: <NA> <NA> TRUE FALSE  
## 8: c.(2023-2028)cctgatfs p.D676fs TRUE FALSE  
## 9: c.(262-264)Cga>Tga p.R88\* TRUE FALSE  
## 10: c.e1+1 <NA> TRUE FALSE  
## 11: c.(8533-8535)tGg>tAg p.W2845\* TRUE FALSE  
## 12: c.(8533-8535)tGG>tAA p.W2845\* TRUE FALSE  
## 13: c.(8533-8535)tgG>tgA p.W2845\* TRUE FALSE  
## 14: c.(802-804)tCg>tAg p.S268\* TRUE FALSE  
## 15: <NA> <NA> TRUE FALSE  
## 16: c.(826-831)ggaaaafs p.GK276fs TRUE FALSE  
## 17: c.(3922-3924)gAt>gGt p.D1308G TRUE FALSE  
## 18: c.(4345-4347)Caa>Taa p.Q1449\* TRUE FALSE  
## 19: c.(2173-2178)ccaaaafs p.PK725fs TRUE FALSE  
## 20: c.(2797-2799)acafs p.T933fs TRUE FALSE  
## 21: c.(121-123)cctfs p.P41fs TRUE FALSE  
## 22: c.e22-1 <NA> TRUE FALSE  
## 23: c.(2683-2685)agtfs p.S895fs TRUE FALSE  
## 24: c.(1057-1059)tgtfs p.C353fs TRUE FALSE  
## 25: c.(295-297)ttafs p.L99fs TRUE TRUE  
## 26: c.(178-180)acgfs p.T60fs TRUE FALSE  
## 27: c.(7240-7242)Caa>Aaa p.Q2414K TRUE FALSE  
## 28: c.(2395-2397)Gaa>Taa p.E799\* TRUE FALSE  
## 29: c.e8+1 <NA> TRUE FALSE  
## 30: c.(3895-3897)cAg>cGg p.Q1299R TRUE FALSE  
## 31: <NA> <NA> TRUE FALSE  
## 32: c.e1+1 <NA> TRUE FALSE  
## 33: c.(214-216)Cga>Tga p.R72\* TRUE FALSE  
## 34: c.(427-429)Cga>Tga p.R143\* TRUE TRUE  
## 35: c.(232-234)aaafs p.K78fs TRUE FALSE  
## 36: c.(3058-3060)gCt>gGt p.A1020G TRUE FALSE  
## 37: c.(8260-8262)aaafs p.K2754fs TRUE FALSE  
## 38: c.e9+1 <NA> TRUE FALSE  
## 39: c.(772-774)Cga>Tga p.R258\* TRUE FALSE  
## 40: c.(223-225)Cgc>Tgc p.R75C TRUE FALSE  
## 41: c.(4096-4098)catfs p.H1366fs TRUE FALSE  
## 42: c.(442-444)Gaa>Taa p.E148\* TRUE FALSE  
## 43: c.(628-630)accfs p.T210fs TRUE TRUE  
## 44: c.(1018-1023)catgtgfs p.-341fs TRUE FALSE  
## 45: <NA> <NA> TRUE FALSE  
## 46: c.(547-549)aagfs p.K183fs TRUE FALSE  
## 47: c.(349-351)gaafs p.E117fs TRUE FALSE  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## 1: 0 FALSE 0 NA <NA> <NA>  
## 2: 0 FALSE 0 NA <NA> <NA>  
## 3: 0 FALSE 0 NA <NA> <NA>  
## 4: 0 FALSE 0 NA <NA> <NA>  
## 5: 0 FALSE 0 NA <NA> <NA>  
## 6: 0 FALSE 0 NA <NA> <NA>  
## 7: 0 FALSE 0 NA <NA> <NA>  
## 8: 0 FALSE 0 NA <NA> <NA>  
## 9: 0 FALSE 0 3.304e-05 <NA> <NA>  
## 10: 0 FALSE 0 NA <NA> <NA>  
## 11: 0 FALSE 1 NA <NA> <NA>  
## 12: 0 FALSE 1 NA <NA> <NA>  
## 13: 0 FALSE 1 NA <NA> <NA>  
## 14: 0 FALSE 0 NA <NA> <NA>  
## 15: 0 FALSE 0 NA <NA> <NA>  
## 16: 0 FALSE 0 NA <NA> <NA>  
## 17: 0 FALSE 0 NA <NA> <NA>  
## 18: 0 FALSE 0 NA <NA> <NA>  
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## 21: 0 FALSE 0 2.480e-05 <NA> <NA>  
## 22: 0 FALSE 0 NA <NA> <NA>  
## 23: 0 FALSE 0 NA <NA> <NA>  
## 24: 0 FALSE 0 NA <NA> <NA>  
## 25: 4 FALSE 0 NA <NA> <NA>  
## 26: 0 FALSE 0 NA <NA> <NA>  
## 27: 0 FALSE 0 NA <NA> <NA>  
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## 33: 0 FALSE 0 4.942e-05 <NA> <NA>  
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## 46: 0 FALSE 0 NA <NA> <NA>  
## 47: 0 FALSE 0 NA <NA> <NA>  
## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## 1: 9:54 9:49 15:85 <NA> <NA> 6:22  
## 2: <NA> <NA> <NA> <NA> <NA> 5:15  
## 3: <NA> 14:30 <NA> <NA> <NA> 17:27  
## 4: <NA> <NA> 31:210 <NA> <NA> <NA>  
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## 6: <NA> <NA> 5:18 <NA> <NA> <NA>  
## 7: <NA> <NA> <NA> <NA> <NA> 4:30  
## 8: <NA> 22:46 <NA> <NA> <NA> 10:26  
## 9: 15:14 15:14 <NA> <NA> <NA> 21:12  
## 10: <NA> <NA> <NA> <NA> <NA> 5:38  
## 11: 180:2 <NA> 42:0 <NA> <NA> 23:0  
## 12: <NA> 171:2 <NA> 64:0 <NA> <NA>  
## 13: 178:2 <NA> 42:0 <NA> <NA> 23:0  
## 14: 29:116 28:112 <NA> <NA> <NA> <NA>  
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## 17: <NA> <NA> <NA> <NA> <NA> 7:27  
## 18: <NA> <NA> <NA> <NA> <NA> 5:26  
## 19: <NA> <NA> 9:32 <NA> <NA> <NA>  
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## 21: 29:33 62:71 13:11 <NA> <NA> 23:20  
## 22: <NA> <NA> <NA> 14:77 <NA> 17:73  
## 23: <NA> <NA> 5:19 <NA> <NA> <NA>  
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## 29: 22:11 22:12 <NA> <NA> <NA> 25:10  
## 30: 27:101 25:99 <NA> <NA> <NA> 10:38  
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## 34: 22:60 22:59 <NA> <NA> <NA> 6:30  
## 35: <NA> <NA> 9:43 <NA> <NA> <NA>  
## 36: 31:16 30:17 86:64 <NA> <NA> 17:20  
## 37: <NA> <NA> 13:84 <NA> <NA> <NA>  
## 38: 37:118 36:117 <NA> <NA> <NA> 5:27  
## 39: 40:82 35:76 24:34 <NA> <NA> 11:28  
## 40: 34:20 31:20 <NA> <NA> <NA> 31:16  
## 41: <NA> <NA> 23:157 <NA> <NA> <NA>  
## 42: 10:2 10:2 <NA> <NA> <NA> 32:0  
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## 45: <NA> <NA> <NA> <NA> <NA> 16:0  
## 46: <NA> <NA> 11:75 <NA> <NA> <NA>  
## 47: 75:54 130:41 <NA> <NA> <NA> 15:4  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## Variant\_annotation DepMap\_ID  
## 1: damaging ACH-000322  
## 2: damaging ACH-000322  
## 3: damaging ACH-000322  
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## 16: damaging ACH-000322  
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## 19: damaging ACH-000322  
## 20: damaging ACH-000322  
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## 22: damaging ACH-000322  
## 23: damaging ACH-000322  
## 24: damaging ACH-000322  
## 25: damaging ACH-000322  
## 26: damaging ACH-000322  
## 27: damaging ACH-000322  
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## 29: damaging ACH-000322  
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## Variant\_annotation DepMap\_ID  
##   
## $mutation$`ACH-000348`  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## 1: 113224 HMGCL 3155 37 1 24129053  
## 2: 113227 CSMD2 114784 37 1 34498294  
## 3: 113230 GPBP1L1 60313 37 1 46151246  
## 4: 113231 GPBP1L1 60313 37 1 46151247  
## 5: 113236 COL11A1 1301 37 1 103379194  
## 6: 113249 TOR1AIP2 163590 37 1 179846458  
## 7: 113263 DNMBP 23268 37 10 101646158  
## 8: 113274 SLC22A9 114571 37 11 63137624  
## 9: 113283 DYRK4 8798 37 12 4722866  
## 10: 113284 NCAPD2 9918 37 12 6626664  
## 11: 113287 CAPRIN2 65981 37 12 30884312  
## 12: 113322 UNC13C 440279 37 15 54308080  
## 13: 113353 TP53 7157 37 17 7578433  
## 14: 113355 ARHGAP44 9912 37 17 12844372  
## 15: 113365 BRIP1 83990 37 17 59886117  
## 16: 113368 DCXR 51181 37 17 79994736  
## 17: 113379 NFATC1 4772 37 18 77211024  
## 18: 113382 HMG20B 10362 37 19 3575556  
## 19: 113389 PKN1 5585 37 19 14578451  
## 20: 113394 ZNF99 7652 37 19 22939546  
## 21: 113409 KLK8 11202 37 19 51503306  
## 22: 113417 ZNF606 80095 37 19 58514235  
## 23: 113425 CNTNAP5 129684 37 2 125530564  
## 24: 113431 TTN 7273 37 2 179411203  
## 25: 113439 HDAC4 9759 37 2 240085586  
## 26: 113445 SCAF4 57466 37 21 33074654  
## 27: 113450 SUMO3 6612 37 21 46238029  
## 28: 113454 SLC16A8 23539 37 22 38478668  
## 29: 113463 KLHL40 131377 37 3 42727954  
## 30: 113475 ZBTB20 26137 37 3 114477912  
## 31: 113476 NCK1 4690 37 3 136664926  
## 32: 113486 BOD1L1 259282 37 4 13598773  
## 33: 113494 ARSK 153642 37 5 94922345  
## 34: 113504 KIAA0319 9856 37 6 24580087  
## 35: 113510 BAG6 7917 37 6 31607004  
## 36: 113511 GPR111 222611 37 6 47649921  
## 37: 113514 CDC40 51362 37 6 110551333  
## 38: 113516 L3MBTL3 84456 37 6 130374070  
## 39: 113531 PCLO 27445 37 7 82580168  
## 40: 113568 MT-ND2 4536 37 M 4811  
## 41: 113571 MT-CO1 4512 37 M 6146  
## 42: 113584 CXorf23 256643 37 X 19947906  
## 43: 113586 ARMCX1 51309 37 X 100808906  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## End\_position Strand Variant\_Classification Variant\_Type  
## 1: 24129053 + Splice\_Site SNP  
## 2: 34498294 + Nonsense\_Mutation SNP  
## 3: 46151246 + Splice\_Site SNP  
## 4: 46151247 + Splice\_Site SNP  
## 5: 103379194 + Splice\_Site SNP  
## 6: 179846458 + De\_novo\_Start\_OutOfFrame SNP  
## 7: 101646158 + Nonsense\_Mutation SNP  
## 8: 63137624 + Nonsense\_Mutation SNP  
## 9: 4722866 + Nonsense\_Mutation SNP  
## 10: 6626759 + Splice\_Site DEL  
## 11: 30884313 + Frame\_Shift\_Ins INS  
## 12: 54308080 + Nonsense\_Mutation SNP  
## 13: 7578433 + Nonsense\_Mutation SNP  
## 14: 12844372 + Splice\_Site SNP  
## 15: 59886117 + Splice\_Site SNP  
## 16: 79994736 + Splice\_Site SNP  
## 17: 77211025 + Frame\_Shift\_Ins INS  
## 18: 3575557 + Frame\_Shift\_Ins INS  
## 19: 14578526 + Splice\_Site DEL  
## 20: 22939547 + IGR INS  
## 21: 51503306 + Nonsense\_Mutation SNP  
## 22: 58514235 + De\_novo\_Start\_OutOfFrame SNP  
## 23: 125530564 + Nonsense\_Mutation SNP  
## 24: 179411203 + Nonsense\_Mutation SNP  
## 25: 240085586 + Nonsense\_Mutation SNP  
## 26: 33074655 + Frame\_Shift\_Ins INS  
## 27: 46238029 + De\_novo\_Start\_OutOfFrame SNP  
## 28: 38478668 + Splice\_Site SNP  
## 29: 42727954 + Nonsense\_Mutation SNP  
## 30: 114477912 + De\_novo\_Start\_OutOfFrame SNP  
## 31: 136664927 + Frame\_Shift\_Ins INS  
## 32: 13598774 + Frame\_Shift\_Ins INS  
## 33: 94922346 + Frame\_Shift\_Ins INS  
## 34: 24580087 + Splice\_Site SNP  
## 35: 31607004 + Splice\_Site SNP  
## 36: 47649927 + Frame\_Shift\_Del DEL  
## 37: 110551333 + Nonstop\_Mutation SNP  
## 38: 130374071 + Frame\_Shift\_Ins INS  
## 39: 82580168 + Nonsense\_Mutation SNP  
## 40: 4811 + Nonstop\_Mutation SNP  
## 41: 6146 + Nonstop\_Mutation SNP  
## 42: 19947907 + Frame\_Shift\_Ins INS  
## 43: 100808907 + Frame\_Shift\_Ins INS  
## End\_position Strand Variant\_Classification Variant\_Type  
## Reference\_Allele  
## 1: C  
## 2: G  
## 3: A  
## 4: C  
## 5: G  
## 6: T  
## 7: G  
## 8: C  
## 9: C  
## 10: AGGTAAGTAGACTTGGTCCACCAAAAGAGAAGGAATTAAATGGAAACAGGGATGAAATTATGTCATTTACTGACCCTGCTATTCATTTTACCTGAT  
## 11: -  
## 12: G  
## 13: G  
## 14: G  
## 15: G  
## 16: T  
## 17: -  
## 18: -  
## 19: CAGGTGACACCACTCCCTGGCCCCCTGTCCACCACCCCTGCCCGCTGTCCTTGTTCTCACCAGTGGCCTCTCTCCA  
## 20: -  
## 21: G  
## 22: C  
## 23: C  
## 24: G  
## 25: A  
## 26: -  
## 27: C  
## 28: C  
## 29: G  
## 30: G  
## 31: -  
## 32: -  
## 33: -  
## 34: G  
## 35: C  
## 36: TATCCTC  
## 37: A  
## 38: -  
## 39: G  
## 40: A  
## 41: A  
## 42: -  
## 43: -  
## Reference\_Allele  
## Tumor\_Seq\_Allele1  
## 1: T  
## 2: A  
## 3: T  
## 4: A  
## 5: A  
## 6: A  
## 7: A  
## 8: A  
## 9: T  
## 10: -  
## 11: T  
## 12: T  
## 13: T  
## 14: A  
## 15: T  
## 16: C  
## 17: A  
## 18: AA  
## 19: -  
## 20: G  
## 21: A  
## 22: T  
## 23: T  
## 24: A  
## 25: C  
## 26: T  
## 27: T  
## 28: T  
## 29: T  
## 30: C  
## 31: A  
## 32: A  
## 33: A  
## 34: A  
## 35: A  
## 36: -  
## 37: C  
## 38: A  
## 39: A  
## 40: G  
## 41: G  
## 42: T  
## 43: T  
## Tumor\_Seq\_Allele1  
## dbSNP\_RS  
## 1: <NA>  
## 2: <NA>  
## 3: <NA>  
## 4: <NA>  
## 5: rs528959090  
## 6: rs141378981  
## 7: <NA>  
## 8: <NA>  
## 9: <NA>  
## 10: rs370592792|rs71584849  
## 11: <NA>  
## 12: <NA>  
## 13: <NA>  
## 14: <NA>  
## 15: rs140097800  
## 16: <NA>  
## 17: <NA>  
## 18: <NA>  
## 19: rs200041057|rs367991508|rs374721792|rs367996849|rs375220133|rs370933714  
## 20: <NA>  
## 21: <NA>  
## 22: <NA>  
## 23: <NA>  
## 24: <NA>  
## 25: <NA>  
## 26: <NA>  
## 27: <NA>  
## 28: rs550353622  
## 29: <NA>  
## 30: <NA>  
## 31: <NA>  
## 32: <NA>  
## 33: <NA>  
## 34: <NA>  
## 35: <NA>  
## 36: <NA>  
## 37: <NA>  
## 38: <NA>  
## 39: <NA>  
## 40: <NA>  
## 41: <NA>  
## 42: <NA>  
## 43: <NA>  
## dbSNP\_RS  
## dbSNP\_Val\_Status  
## 1: <NA>  
## 2: <NA>  
## 3: <NA>  
## 4: <NA>  
## 5: <NA>  
## 6: byFrequency  
## 7: <NA>  
## 8: <NA>  
## 9: <NA>  
## 10: <NA>  
## 11: <NA>  
## 12: <NA>  
## 13: <NA>  
## 14: <NA>  
## 15: <NA>  
## 16: <NA>  
## 17: <NA>  
## 18: <NA>  
## 19: <NA>  
## 20: <NA>  
## 21: <NA>  
## 22: <NA>  
## 23: <NA>  
## 24: <NA>  
## 25: <NA>  
## 26: <NA>  
## 27: <NA>  
## 28: <NA>  
## 29: <NA>  
## 30: <NA>  
## 31: <NA>  
## 32: <NA>  
## 33: <NA>  
## 34: <NA>  
## 35: <NA>  
## 36: <NA>  
## 37: <NA>  
## 38: <NA>  
## 39: <NA>  
## 40: <NA>  
## 41: <NA>  
## 42: <NA>  
## 43: <NA>  
## dbSNP\_Val\_Status  
## Genome\_Change  
## 1: g.chr1:24129053C>T  
## 2: g.chr1:34498294G>A  
## 3: g.chr1:46151246A>T  
## 4: g.chr1:46151247C>A  
## 5: g.chr1:103379194G>A  
## 6: g.chr1:179846458T>A  
## 7: g.chr10:101646158G>A  
## 8: g.chr11:63137624C>A  
## 9: g.chr12:4722866C>T  
## 10: g.chr12:6626664\_6626759delAGGTAAGTAGACTTGGTCCACCAAAAGAGAAGGAATTAAATGGAAACAGGGATGAAATTATGTCATTTACTGACCCTGCTATTCATTTTACCTGAT  
## 11: g.chr12:30884312\_30884313insT  
## 12: g.chr15:54308080G>T  
## 13: g.chr17:7578433G>T  
## 14: g.chr17:12844372G>A  
## 15: g.chr17:59886117G>T  
## 16: g.chr17:79994736T>C  
## 17: g.chr18:77211024\_77211025insA  
## 18: g.chr19:3575556\_3575557insAA  
## 19: g.chr19:14578451\_14578526delCAGGTGACACCACTCCCTGGCCCCCTGTCCACCACCCCTGCCCGCTGTCCTTGTTCTCACCAGTGGCCTCTCTCCA  
## 20: g.chr19:22939546\_22939547insG  
## 21: g.chr19:51503306G>A  
## 22: g.chr19:58514235C>T  
## 23: g.chr2:125530564C>T  
## 24: g.chr2:179411203G>A  
## 25: g.chr2:240085586A>C  
## 26: g.chr21:33074654\_33074655insT  
## 27: g.chr21:46238029C>T  
## 28: g.chr22:38478668C>T  
## 29: g.chr3:42727954G>T  
## 30: g.chr3:114477912G>C  
## 31: g.chr3:136664926\_136664927insA  
## 32: g.chr4:13598773\_13598774insA  
## 33: g.chr5:94922345\_94922346insA  
## 34: g.chr6:24580087G>A  
## 35: g.chr6:31607004C>A  
## 36: g.chr6:47649921\_47649927delTATCCTC  
## 37: g.chr6:110551333A>C  
## 38: g.chr6:130374070\_130374071insA  
## 39: g.chr7:82580168G>A  
## 40: g.chrM:4811A>G  
## 41: g.chrM:6146A>G  
## 42: g.chrX:19947906\_19947907insT  
## 43: g.chrX:100808906\_100808907insT  
## Genome\_Change  
## Annotation\_Transcript Tumor\_Sample\_Barcode  
## 1: ENST00000374490.3 ACH-000348  
## 2: ENST00000373381.4 ACH-000348  
## 3: ENST00000355105.3 ACH-000348  
## 4: ENST00000355105.3 ACH-000348  
## 5: ENST00000370096.3 ACH-000348  
## 6: ENST00000367612.3 ACH-000348  
## 7: ENST00000324109.4 ACH-000348  
## 8: ENST00000279178.3 ACH-000348  
## 9: ENST00000540757.2 ACH-000348  
## 10: ENST00000315579.5 ACH-000348  
## 11: ENST00000395805.2 ACH-000348  
## 12: ENST00000260323.11 ACH-000348  
## 13: ENST00000269305.4 ACH-000348  
## 14: ENST00000379672.5 ACH-000348  
## 15: ENST00000259008.2 ACH-000348  
## 16: ENST00000306869.2 ACH-000348  
## 17: ENST00000427363.2 ACH-000348  
## 18: ENST00000333651.6 ACH-000348  
## 19: ENST00000242783.6 ACH-000348  
## 20: ENST00000596209.1 ACH-000348  
## 21: ENST00000600767.1 ACH-000348  
## 22: ENST00000341164.4 ACH-000348  
## 23: ENST00000431078.1 ACH-000348  
## 24: ENST00000591111.1 ACH-000348  
## 25: ENST00000345617.3 ACH-000348  
## 26: ENST00000286835.7 ACH-000348  
## 27: ENST00000332859.6 ACH-000348  
## 28: ENST00000320521.5 ACH-000348  
## 29: ENST00000287777.4 ACH-000348  
## 30: ENST00000471418.1 ACH-000348  
## 31: ENST00000481752.1 ACH-000348  
## 32: ENST00000040738.5 ACH-000348  
## 33: ENST00000380009.4 ACH-000348  
## 34: ENST00000378214.3 ACH-000348  
## 35: ENST00000375964.6 ACH-000348  
## 36: ENST00000296862.1 ACH-000348  
## 37: ENST00000368932.1 ACH-000348  
## 38: ENST00000529410.1 ACH-000348  
## 39: ENST00000333891.9 ACH-000348  
## 40: ENST00000361453.3 ACH-000348  
## 41: ENST00000361624.2 ACH-000348  
## 42: ENST00000379682.4 ACH-000348  
## 43: ENST00000372829.3 ACH-000348  
## Annotation\_Transcript Tumor\_Sample\_Barcode  
## cDNA\_Change  
## 1: c.878G>A  
## 2: c.418C>T  
## 3: <NA>  
## 4: <NA>  
## 5: c.4031C>T  
## 6: <NA>  
## 7: c.3517C>T  
## 8: c.96C>A  
## 9: c.1510C>T  
## 10: c.1319\_1320delAGGTAAGTAGACTTGGTCCACCAAAAGAGAAGGAATTAAATGGAAACAGGGATGAAATTATGTCATTTACTGACCCTGCTATTCATTTTACCTGAT  
## 11: c.1024\_1025insA  
## 12: c.2980G>T  
## 13: c.497C>A  
## 14: <NA>  
## 15: c.629C>A  
## 16: c.304A>G  
## 17: c.1660\_1661insA  
## 18: c.370\_371insAA  
## 19: c.1806\_1808delCAGGTGACACCACTCCCTGGCCCCCTGTCCACCACCCCTGCCCGCTGTCCTTGTTCTCACCAGTGGCCTCTCTCCA  
## 20: <NA>  
## 21: c.439C>T  
## 22: <NA>  
## 23: c.2719C>T  
## 24: c.89932C>T  
## 25: c.524T>G  
## 26: c.359\_360insA  
## 27: <NA>  
## 28: c.213G>A  
## 29: c.844G>T  
## 30: <NA>  
## 31: c.728\_729insA  
## 32: c.7973\_7974insT  
## 33: c.779\_780insA  
## 34: c.1371C>T  
## 35: <NA>  
## 36: c.1626\_1632delTATCCTC  
## 37: c.1739A>C  
## 38: c.516\_517insA  
## 39: c.9736C>T  
## 40: c.342A>G  
## 41: c.243A>G  
## 42: c.2102\_2103insA  
## 43: c.993\_994insT  
## cDNA\_Change  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## 1: c.(877-879)gGt>gAt p.G293D TRUE FALSE  
## 2: c.(418-420)Cag>Tag p.Q140\* TRUE FALSE  
## 3: c.e2+1 <NA> TRUE FALSE  
## 4: c.e2+1 <NA> TRUE FALSE  
## 5: c.(4030-4032)cCg>cTg p.P1344L TRUE FALSE  
## 6: <NA> <NA> TRUE FALSE  
## 7: c.(3517-3519)Cag>Tag p.Q1173\* TRUE FALSE  
## 8: c.(94-96)taC>taA p.Y32\* TRUE FALSE  
## 9: c.(1510-1512)Cag>Tag p.Q504\* TRUE FALSE  
## 10: c.(1318-1320)aag>a p.K440del TRUE FALSE  
## 11: c.(1024-1026)acafs p.T342fs TRUE FALSE  
## 12: c.(2980-2982)Gga>Tga p.G994\* TRUE FALSE  
## 13: c.(496-498)tCa>tAa p.S166\* TRUE TRUE  
## 14: c.e8-1 <NA> TRUE FALSE  
## 15: c.(628-630)cCc>cAc p.P210H TRUE FALSE  
## 16: c.(304-306)Aga>Gga p.R102G TRUE FALSE  
## 17: c.(1660-1662)gggfs p.G554fs TRUE FALSE  
## 18: c.(370-372)gagfs p.E124fs TRUE FALSE  
## 19: c.(1804-1809)tgcagg>tgg p.CR602fs TRUE FALSE  
## 20: <NA> <NA> TRUE FALSE  
## 21: c.(439-441)Cag>Tag p.Q147\* TRUE FALSE  
## 22: <NA> <NA> TRUE FALSE  
## 23: c.(2719-2721)Cga>Tga p.R907\* TRUE TRUE  
## 24: c.(89932-89934)Cga>Tga p.R29978\* TRUE FALSE  
## 25: c.(523-525)tTa>tGa p.L175\* TRUE FALSE  
## 26: c.(358-360)aatfs p.N120fs TRUE FALSE  
## 27: <NA> <NA> TRUE FALSE  
## 28: c.(211-213)acG>acA p.T71T TRUE FALSE  
## 29: c.(844-846)Gag>Tag p.E282\* TRUE FALSE  
## 30: <NA> <NA> TRUE FALSE  
## 31: c.(727-732)ccaaaafs p.PK243fs TRUE FALSE  
## 32: c.(7972-7974)ttgfs p.L2658fs TRUE FALSE  
## 33: c.(778-783)acaaaafs p.TK260fs TRUE FALSE  
## 34: c.(1369-1371)agC>agT p.S457S TRUE FALSE  
## 35: c.e25-1 <NA> TRUE FALSE  
## 36: c.(1624-1632)cttatcctcfs p.LIL542fs TRUE FALSE  
## 37: c.(1738-1740)tAa>tCa p.\*580S TRUE FALSE  
## 38: c.(517-519)aaafs p.K173fs TRUE FALSE  
## 39: c.(9736-9738)Cga>Tga p.R3246\* TRUE TRUE  
## 40: c.(340-342)tgA>tgG p.\*114W TRUE FALSE  
## 41: c.(241-243)tgA>tgG p.\*81W TRUE FALSE  
## 42: c.(2101-2103)aagfs p.K701fs TRUE FALSE  
## 43: c.(994-996)tttfs p.F332fs TRUE FALSE  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## 1: 0 FALSE 0 NA <NA> <NA>  
## 2: 0 FALSE 0 NA <NA> <NA>  
## 3: 0 FALSE 0 NA <NA> <NA>  
## 4: 0 FALSE 0 NA <NA> <NA>  
## 5: 0 FALSE 0 3.295e-05 <NA> <NA>  
## 6: 0 FALSE 0 NA <NA> <NA>  
## 7: 0 FALSE 0 NA <NA> <NA>  
## 8: 0 FALSE 0 8.236e-06 <NA> <NA>  
## 9: 0 FALSE 0 NA <NA> <NA>  
## 10: 0 FALSE 0 NA <NA> <NA>  
## 11: 0 FALSE 0 NA <NA> <NA>  
## 12: 0 FALSE 0 NA <NA> <NA>  
## 13: 5 TRUE 47 NA <NA> <NA>  
## 14: 0 FALSE 0 NA <NA> <NA>  
## 15: 0 FALSE 0 1.647e-05 <NA> <NA>  
## 16: 0 FALSE 0 NA <NA> <NA>  
## 17: 0 FALSE 0 NA <NA> <NA>  
## 18: 0 FALSE 0 NA <NA> <NA>  
## 19: 0 FALSE 0 NA <NA> <NA>  
## 20: 0 FALSE 0 NA <NA> <NA>  
## 21: 0 FALSE 0 NA <NA> <NA>  
## 22: 0 FALSE 0 NA <NA> <NA>  
## 23: 5 FALSE 0 8.273e-06 <NA> <NA>  
## 24: 0 FALSE 0 NA <NA> <NA>  
## 25: 0 FALSE 0 NA <NA> <NA>  
## 26: 0 FALSE 0 NA <NA> <NA>  
## 27: 0 FALSE 0 NA <NA> <NA>  
## 28: 0 FALSE 0 NA <NA> <NA>  
## 29: 0 FALSE 0 NA <NA> <NA>  
## 30: 0 FALSE 0 NA <NA> <NA>  
## 31: 0 FALSE 0 NA <NA> <NA>  
## 32: 0 FALSE 0 NA <NA> <NA>  
## 33: 0 FALSE 0 NA <NA> <NA>  
## 34: 0 FALSE 0 NA <NA> <NA>  
## 35: 0 FALSE 0 NA <NA> <NA>  
## 36: 0 FALSE 0 2.482e-05 <NA> <NA>  
## 37: 0 FALSE 0 NA <NA> <NA>  
## 38: 0 FALSE 0 NA <NA> <NA>  
## 39: 3 FALSE 0 8.279e-06 <NA> <NA>  
## 40: 0 FALSE 0 NA <NA> <NA>  
## 41: 0 FALSE 0 NA <NA> <NA>  
## 42: 0 FALSE 0 NA <NA> <NA>  
## 43: 0 FALSE 0 NA <NA> <NA>  
## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## 1: 42:4 41:4 197:37 <NA> <NA> 26:9  
## 2: 8:1 8:1 15:1 <NA> <NA> 23:5  
## 3: <NA> <NA> <NA> <NA> <NA> 4:26  
## 4: <NA> <NA> <NA> <NA> <NA> 5:26  
## 5: <NA> <NA> <NA> <NA> <NA> 5:26  
## 6: <NA> <NA> 163:3 <NA> <NA> <NA>  
## 7: 80:2 78:2 53:1 <NA> <NA> 32:0  
## 8: 66:90 65:89 <NA> <NA> <NA> 9:25  
## 9: 30:38 30:37 87:82 105:144 <NA> 16:15  
## 10: <NA> <NA> 268:4 <NA> <NA> <NA>  
## 11: <NA> <NA> 15:94 <NA> <NA> <NA>  
## 12: 12:11 12:9 <NA> 87:59 <NA> 26:17  
## 13: 25:0 24:0 42:0 143:0 <NA> 30:0  
## 14: 166:4 161:4 <NA> <NA> <NA> 34:0  
## 15: <NA> 29:36 <NA> 117:122 <NA> 8:8  
## 16: 12:9 11:9 185:184 <NA> <NA> 25:14  
## 17: <NA> 42:73 11:1 4:5 <NA> 13:17  
## 18: <NA> <NA> 35:280 <NA> <NA> 7:22  
## 19: <NA> <NA> 275:18 <NA> <NA> <NA>  
## 20: <NA> <NA> <NA> <NA> <NA> 10:25  
## 21: 16:18 16:18 <NA> <NA> <NA> 15:16  
## 22: <NA> <NA> <NA> <NA> <NA> 22:22  
## 23: 36:87 36:85 <NA> <NA> <NA> 10:22  
## 24: 161:99 153:93 <NA> 180:93 <NA> 23:14  
## 25: 52:38 50:39 11:18 59:22 <NA> 28:17  
## 26: <NA> <NA> 13:40 <NA> <NA> <NA>  
## 27: <NA> <NA> <NA> <NA> <NA> 9:5  
## 28: <NA> <NA> <NA> <NA> <NA> 20:16  
## 29: 61:36 57:35 <NA> <NA> <NA> 24:17  
## 30: <NA> <NA> <NA> <NA> <NA> 14:22  
## 31: <NA> <NA> 26:176 <NA> <NA> <NA>  
## 32: <NA> 13:33 21:69 <NA> <NA> 6:26  
## 33: <NA> <NA> 6:26 <NA> <NA> <NA>  
## 34: 6:8 6:9 <NA> <NA> <NA> 17:10  
## 35: 11:13 13:13 25:1 <NA> <NA> 14:17  
## 36: 16:0 17:20 <NA> <NA> <NA> 19:23  
## 37: 24:23 21:22 47:30 <NA> <NA> 23:12  
## 38: <NA> <NA> 8:13 <NA> <NA> <NA>  
## 39: 104:136 101:130 <NA> <NA> <NA> <NA>  
## 40: <NA> <NA> <NA> <NA> <NA> 952:0  
## 41: <NA> 29:1 <NA> <NA> <NA> 950:1  
## 42: <NA> <NA> 5:20 <NA> <NA> <NA>  
## 43: <NA> <NA> 19:124 <NA> <NA> <NA>  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## Variant\_annotation DepMap\_ID  
## 1: damaging ACH-000348  
## 2: damaging ACH-000348  
## 3: damaging ACH-000348  
## 4: damaging ACH-000348  
## 5: damaging ACH-000348  
## 6: damaging ACH-000348  
## 7: damaging ACH-000348  
## 8: damaging ACH-000348  
## 9: damaging ACH-000348  
## 10: damaging ACH-000348  
## 11: damaging ACH-000348  
## 12: damaging ACH-000348  
## 13: damaging ACH-000348  
## 14: damaging ACH-000348  
## 15: damaging ACH-000348  
## 16: damaging ACH-000348  
## 17: damaging ACH-000348  
## 18: damaging ACH-000348  
## 19: damaging ACH-000348  
## 20: other conserving ACH-000348  
## 21: damaging ACH-000348  
## 22: damaging ACH-000348  
## 23: damaging ACH-000348  
## 24: damaging ACH-000348  
## 25: damaging ACH-000348  
## 26: damaging ACH-000348  
## 27: damaging ACH-000348  
## 28: damaging ACH-000348  
## 29: damaging ACH-000348  
## 30: damaging ACH-000348  
## 31: damaging ACH-000348  
## 32: damaging ACH-000348  
## 33: damaging ACH-000348  
## 34: damaging ACH-000348  
## 35: damaging ACH-000348  
## 36: damaging ACH-000348  
## 37: other non-conserving ACH-000348  
## 38: damaging ACH-000348  
## 39: damaging ACH-000348  
## 40: other non-conserving ACH-000348  
## 41: other non-conserving ACH-000348  
## 42: damaging ACH-000348  
## 43: damaging ACH-000348  
## Variant\_annotation DepMap\_ID  
##   
## $mutation$`ACH-000401`  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## 1: 133859 KAZN 23254 37 1 14925642  
## 2: 133865 LUZP1 7798 37 1 23420084  
## 3: 133869 KLF17 128209 37 1 44595414  
## 4: 133876 LRRC7 57554 37 1 70225930  
## 5: 133877 DNAJB4 11080 37 1 78481819  
## 6: 133898 CACNA1S 779 37 1 201081318  
## 7: 133900 CR1 1378 37 1 207739225  
## 8: 133914 ARMC4 55130 37 10 28233229  
## 9: 133919 RTKN2 219790 37 10 63957747  
## 10: 133923 NUTM2D 728130 37 10 89126037  
## 11: 133928 ERLIN1 10613 37 10 101927130  
## 12: 133936 HIPK3 10114 37 11 33370832  
## 13: 133938 CKAP5 9793 37 11 46829682  
## 14: 133943 PLEKHB1 58473 37 11 73360130  
## 15: 133946 TMEM133 83935 37 11 100863194  
## 16: 133952 SLC38A1 81539 37 12 46600938  
## 17: 133953 PFKM 5213 37 12 48535611  
## 18: 133957 SPRYD3 84926 37 12 53471044  
## 19: 133971 TMTC3 160418 37 12 88588948  
## 20: 133972 GAS2L3 283431 37 12 101017619  
## 21: 133975 SELPLG 6404 37 12 109017351  
## 22: 133980 UBC 7316 37 12 125397972  
## 23: 133991 ACIN1 22985 37 14 23528665  
## 24: 134008 CSPG4 1464 37 15 75980260  
## 25: 134042 KRT17 3872 37 17 39780376  
## 26: 134050 INTS2 57508 37 17 59945338  
## 27: 134094 MLTK 0 37 2 174128624  
## 28: 134107 NFS1 9054 37 20 34278488  
## 29: 134131 SMARCC1 6599 37 3 47676722  
## 30: 134147 MRPS22 56945 37 3 139074554  
## 31: 134150 SPATA16 83893 37 3 172643165  
## 32: 134156 PIGZ 80235 37 3 196674030  
## 33: 134177 PTCD2 79810 37 5 71631622  
## 34: 134182 SLC22A5 6584 37 5 131728180  
## 35: 134196 ATXN1 6310 37 6 16307054  
## 36: 134222 PLG 5340 37 6 161132107  
## 37: 134223 DACT2 168002 37 6 168708899  
## 38: 134241 ZNF800 168850 37 7 127013548  
## 39: 134255 MTMR9 66036 37 8 11163803  
## 40: 134257 C8orf58 541565 37 8 22460797  
## 41: 134270 FAM83A 84985 37 8 124195514  
## 42: 134283 FAM129B 64855 37 9 130294051  
## 43: 134287 OLFM1 10439 37 9 138011820  
## 44: 134289 MT-CO3 4514 37 M 9983  
## V1 Hugo\_Symbol Entrez\_Gene\_Id NCBI\_Build Chromosome Start\_position  
## End\_position Strand Variant\_Classification Variant\_Type  
## 1: 14925643 + Frame\_Shift\_Ins INS  
## 2: 23420085 + Frame\_Shift\_Ins INS  
## 3: 44595415 + Frame\_Shift\_Ins INS  
## 4: 70225930 + Nonsense\_Mutation SNP  
## 5: 78481820 + Frame\_Shift\_Ins INS  
## 6: 201081318 + Nonsense\_Mutation SNP  
## 7: 207739226 + Frame\_Shift\_Ins INS  
## 8: 28233230 + Frame\_Shift\_Ins INS  
## 9: 63957748 + Frame\_Shift\_Ins INS  
## 10: 89126037 + Nonsense\_Mutation SNP  
## 11: 101927131 + Frame\_Shift\_Ins INS  
## 12: 33370832 + Splice\_Site SNP  
## 13: 46829683 + Frame\_Shift\_Ins INS  
## 14: 73360133 + Splice\_Site DEL  
## 15: 100863195 + Frame\_Shift\_Ins INS  
## 16: 46600938 + Splice\_Site SNP  
## 17: 48535611 + Splice\_Site SNP  
## 18: 53471044 + Splice\_Site SNP  
## 19: 88588949 + Frame\_Shift\_Ins INS  
## 20: 101017619 + Nonsense\_Mutation SNP  
## 21: 109017351 + Nonsense\_Mutation SNP  
## 22: 125397972 + Nonsense\_Mutation SNP  
## 23: 23528665 + Nonsense\_Mutation SNP  
## 24: 75980261 + Frame\_Shift\_Del DEL  
## 25: 39780377 + Frame\_Shift\_Ins INS  
## 26: 59945339 + Frame\_Shift\_Ins INS  
## 27: 174128625 + Splice\_Site INS  
## 28: 34278488 + Splice\_Site SNP  
## 29: 47676723 + Frame\_Shift\_Ins INS  
## 30: 139074555 + Frame\_Shift\_Ins INS  
## 31: 172643166 + Frame\_Shift\_Ins INS  
## 32: 196674031 + Stop\_Codon\_Ins INS  
## 33: 71631622 + Splice\_Site SNP  
## 34: 131728181 + Frame\_Shift\_Ins INS  
## 35: 16307055 + Frame\_Shift\_Ins INS  
## 36: 161132107 + Splice\_Site SNP  
## 37: 168708900 + Frame\_Shift\_Ins INS  
## 38: 127013549 + Frame\_Shift\_Ins INS  
## 39: 11163803 + Nonsense\_Mutation SNP  
## 40: 22460798 + Frame\_Shift\_Ins INS  
## 41: 124195514 + Nonsense\_Mutation SNP  
## 42: 130294052 + Frame\_Shift\_Ins INS  
## 43: 138011820 + Nonsense\_Mutation SNP  
## 44: 9983 + Nonstop\_Mutation SNP  
## End\_position Strand Variant\_Classification Variant\_Type  
## Reference\_Allele Tumor\_Seq\_Allele1 dbSNP\_RS  
## 1: - G <NA>  
## 2: - T <NA>  
## 3: - C <NA>  
## 4: C T   
## 5: - A <NA>  
## 6: C T   
## 7: - G <NA>  
## 8: - G <NA>  
## 9: - T <NA>  
## 10: C T <NA>  
## 11: - T <NA>  
## 12: A G   
## 13: - T <NA>  
## 14: AGAG -   
## 15: - T <NA>  
## 16: G A rs201587500  
## 17: G A   
## 18: A C <NA>  
## 19: - A <NA>  
## 20: C T   
## 21: G A   
## 22: G A <NA>  
## 23: C A <NA>  
## 24: GA - rs531178999  
## 25: - G rs564768263|rs374327168  
## 26: - A <NA>  
## 27: - T   
## 28: C G <NA>  
## 29: - G rs142615890  
## 30: - T   
## 31: - T <NA>  
## 32: - G <NA>  
## 33: T G <NA>  
## 34: - G rs267607053|rs369179457  
## 35: - A <NA>  
## 36: A G   
## 37: - G <NA>  
## 38: - T <NA>  
## 39: C A <NA>  
## 40: - A <NA>  
## 41: C T <NA>  
## 42: - T <NA>  
## 43: C A   
## 44: A G <NA>  
## Reference\_Allele Tumor\_Seq\_Allele1 dbSNP\_RS  
## dbSNP\_Val\_Status Genome\_Change  
## 1: <NA> g.chr1:14925642\_14925643insG  
## 2: <NA> g.chr1:23420084\_23420085insT  
## 3: <NA> g.chr1:44595414\_44595415insC  
## 4: g.chr1:70225930C>T  
## 5: <NA> g.chr1:78481819\_78481820insA  
## 6: g.chr1:201081318C>T  
## 7: <NA> g.chr1:207739225\_207739226insG  
## 8: <NA> g.chr10:28233229\_28233230insG  
## 9: <NA> g.chr10:63957747\_63957748insT  
## 10: <NA> g.chr10:89126037C>T  
## 11: <NA> g.chr10:101927130\_101927131insT  
## 12: g.chr11:33370832A>G  
## 13: <NA> g.chr11:46829682\_46829683insT  
## 14: g.chr11:73360130\_73360133delAGAG  
## 15: <NA> g.chr11:100863194\_100863195insT  
## 16: g.chr12:46600938G>A  
## 17: g.chr12:48535611G>A  
## 18: <NA> g.chr12:53471044A>C  
## 19: <NA> g.chr12:88588948\_88588949insA  
## 20: g.chr12:101017619C>T  
## 21: g.chr12:109017351G>A  
## 22: <NA> g.chr12:125397972G>A  
## 23: <NA> g.chr14:23528665C>A  
## 24: byFrequency g.chr15:75980260\_75980261delGA  
## 25: <NA> g.chr17:39780376\_39780377insG  
## 26: <NA> g.chr17:59945338\_59945339insA  
## 27: g.chr2:174128624\_174128625insT  
## 28: <NA> g.chr20:34278488C>G  
## 29: <NA> g.chr3:47676722\_47676723insG  
## 30: g.chr3:139074554\_139074555insT  
## 31: <NA> g.chr3:172643165\_172643166insT  
## 32: <NA> g.chr3:196674030\_196674031insG  
## 33: <NA> g.chr5:71631622T>G  
## 34: <NA> g.chr5:131728180\_131728181insG  
## 35: <NA> g.chr6:16307054\_16307055insA  
## 36: g.chr6:161132107A>G  
## 37: <NA> g.chr6:168708899\_168708900insG  
## 38: <NA> g.chr7:127013548\_127013549insT  
## 39: <NA> g.chr8:11163803C>A  
## 40: <NA> g.chr8:22460797\_22460798insA  
## 41: <NA> g.chr8:124195514C>T  
## 42: <NA> g.chr9:130294051\_130294052insT  
## 43: g.chr9:138011820C>A  
## 44: <NA> g.chrM:9983A>G  
## dbSNP\_Val\_Status Genome\_Change  
## Annotation\_Transcript Tumor\_Sample\_Barcode cDNA\_Change  
## 1: ENST00000376030.2 ACH-000401 c.149\_150insG  
## 2: ENST00000302291.4 ACH-000401 c.670\_671insA  
## 3: ENST00000372299.3 ACH-000401 c.471\_472insC  
## 4: ENST00000035383.5 ACH-000401 c.43C>T  
## 5: ENST00000370763.5 ACH-000401 c.902\_903insA  
## 6: ENST00000362061.3 ACH-000401 c.150G>A  
## 7: ENST00000367049.4 ACH-000401 c.3909\_3910insG  
## 8: ENST00000305242.5 ACH-000401 c.1664\_1665insC  
## 9: ENST00000373789.3 ACH-000401 c.1749\_1750insA  
## 10: ENST00000381697.2 ACH-000401 c.1777C>T  
## 11: ENST00000421367.2 ACH-000401 c.537\_538insA  
## 12: ENST00000303296.4 ACH-000401 c.2806A>G  
## 13: ENST00000529230.1 ACH-000401 c.876\_877insA  
## 14: ENST00000354190.5 ACH-000401 c.92\_94delAGAG  
## 15: ENST00000303130.2 ACH-000401 c.155\_156insT  
## 16: ENST00000398637.5 ACH-000401 c.563C>T  
## 17: ENST00000312352.7 ACH-000401   
## 18: ENST00000301463.4 ACH-000401 c.25T>G  
## 19: ENST00000266712.6 ACH-000401 c.2267\_2268insA  
## 20: ENST00000539410.1 ACH-000401 c.1036C>T  
## 21: ENST00000550948.1 ACH-000401 c.733C>T  
## 22: ENST00000538617.1 ACH-000401 c.346C>T  
## 23: ENST00000262710.1 ACH-000401 c.3718G>T  
## 24: ENST00000308508.5 ACH-000401 c.3145\_3146delTC  
## 25: ENST00000311208.8 ACH-000401 c.385\_386insC  
## 26: ENST00000444766.3 ACH-000401 c.3300\_3301insT  
## 27: ENST00000375213.3 ACH-000401   
## 28: ENST00000374092.4 ACH-000401 <NA>  
## 29: ENST00000254480.5 ACH-000401 c.2603\_2604insC  
## 30: ENST00000495075.1 ACH-000401 c.909\_910insT  
## 31: ENST00000351008.3 ACH-000401 c.1198\_1199insA  
## 32: ENST00000412723.1 ACH-000401 <NA>  
## 33: ENST00000380639.5 ACH-000401 c.549T>G  
## 34: ENST00000245407.3 ACH-000401 c.1323\_1324insG  
## 35: ENST00000244769.4 ACH-000401 c.1953\_1954insT  
## 36: ENST00000308192.9 ACH-000401   
## 37: ENST00000366795.3 ACH-000401 c.1537\_1538insC  
## 38: ENST00000393313.1 ACH-000401 c.1841\_1842insA  
## 39: ENST00000221086.3 ACH-000401 c.696C>A  
## 40: ENST00000289989.5 ACH-000401 c.1076\_1077insA  
## 41: ENST00000518448.1 ACH-000401 c.418C>T  
## 42: ENST00000373312.3 ACH-000401 c.61\_62insA  
## 43: ENST00000371793.3 ACH-000401 c.1254C>A  
## 44: ENST00000362079.2 ACH-000401 c.777A>G  
## Annotation\_Transcript Tumor\_Sample\_Barcode cDNA\_Change  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## 1: c.(148-153)ccgggafs p.PG50fs TRUE FALSE  
## 2: c.(670-672)atgfs p.M224fs TRUE FALSE  
## 3: c.(472-474)ctgfs p.L158fs TRUE FALSE  
## 4: c.(43-45)Cga>Tga p.R15\* TRUE FALSE  
## 5: c.(901-906)ccaaaafs p.PK301fs TRUE FALSE  
## 6: c.(148-150)tgG>tgA p.W50\* TRUE FALSE  
## 7: c.(3910-3912)ggafs p.G1304fs TRUE FALSE  
## 8: c.(1663-1665)gcafs p.A555fs TRUE FALSE  
## 9: c.(1747-1752)gaagccfs p.A584fs TRUE FALSE  
## 10: c.(1777-1779)Caa>Taa p.Q593\* TRUE FALSE  
## 11: c.(535-540)gaagccfs p.A180fs TRUE FALSE  
## 12: c.(2806-2808)Agt>Ggt p.S936G TRUE FALSE  
## 13: c.(874-879)aaatggfs p.W293fs TRUE FALSE  
## 14: c.(91-96)cagagg>cgg p.Q31fs TRUE FALSE  
## 15: c.(154-159)ccttttfs p.PF52fs TRUE FALSE  
## 16: c.(562-564)tCa>tTa p.S188L TRUE FALSE  
## 17: c.e16+1 TRUE FALSE  
## 18: c.(25-27)Ttt>Gtt p.F9V TRUE FALSE  
## 19: c.(2266-2271)gcaaaafs p.AK756fs TRUE TRUE  
## 20: c.(1036-1038)Cag>Tag p.Q346\* TRUE FALSE  
## 21: c.(733-735)Caa>Taa p.Q245\* TRUE FALSE  
## 22: c.(346-348)Cag>Tag p.Q116\* TRUE FALSE  
## 23: c.(3718-3720)Gag>Tag p.E1240\* TRUE FALSE  
## 24: c.(3145-3147)tcgfs p.S1049fs TRUE FALSE  
## 25: c.(385-387)cgtfs p.R129fs TRUE FALSE  
## 26: c.(3298-3303)tttatgfs p.M1101fs TRUE FALSE  
## 27: c.e19+1 TRUE FALSE  
## 28: c.e5-1 <NA> TRUE FALSE  
## 29: c.(2602-2604)acafs p.T868fs TRUE FALSE  
## 30: c.(910-912)tatfs p.Y304fs TRUE FALSE  
## 31: c.(1198-1200)atafs p.I400fs TRUE TRUE  
## 32: <NA> <NA> TRUE FALSE  
## 33: c.(547-549)agT>agG p.S183R TRUE FALSE  
## 34: c.(1324-1326)gccfs p.A442fs TRUE FALSE  
## 35: c.(1951-1956)tttgtgfs p.V652fs TRUE FALSE  
## 36: c.e4-1 TRUE FALSE  
## 37: c.(1537-1539)cagfs p.Q513fs TRUE FALSE  
## 38: c.(1840-1842)aacfs p.N614fs TRUE FALSE  
## 39: c.(694-696)taC>taA p.Y232\* TRUE FALSE  
## 40: c.(1075-1080)gcaaaafs p.AK359fs TRUE FALSE  
## 41: c.(418-420)Cag>Tag p.Q140\* TRUE FALSE  
## 42: c.(61-63)accfs p.T21fs TRUE FALSE  
## 43: c.(1252-1254)taC>taA p.Y418\* TRUE FALSE  
## 44: c.(775-777)tgA>tgG p.\*259W TRUE FALSE  
## Codon\_Change Protein\_Change isDeleterious isTCGAhotspot  
## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## 1: 0 FALSE 0 NA <NA> <NA>  
## 2: 0 FALSE 0 NA <NA> <NA>  
## 3: 0 FALSE 0 NA <NA> <NA>  
## 4: 0 FALSE 0 NA <NA> <NA>  
## 5: 0 FALSE 0 NA <NA> <NA>  
## 6: 0 FALSE 0 NA <NA> <NA>  
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## 8: 0 FALSE 0 NA <NA> <NA>  
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## 11: 0 FALSE 0 NA <NA> <NA>  
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## 13: 0 FALSE 0 NA <NA> <NA>  
## 14: 0 FALSE 0 NA <NA> <NA>  
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## 17: 0 FALSE 0 2.471e-05 <NA> <NA>  
## 18: 0 FALSE 0 NA <NA> <NA>  
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## 42: 0 FALSE 0 NA <NA> <NA>  
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## TCGAhsCnt isCOSMIChotspot COSMIChsCnt ExAC\_AF VA\_WES\_AC CGA\_WES\_AC  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## 1: <NA> 4:9 <NA> <NA> <NA> <NA>  
## 2: <NA> <NA> 14:77 <NA> <NA> <NA>  
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## 6: 16:27 15:25 <NA> <NA> <NA> <NA>  
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## 9: <NA> 7:43 <NA> <NA> <NA> <NA>  
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## 12: 44:4 43:4 34:1 <NA> <NA> <NA>  
## 13: <NA> <NA> 27:137 <NA> <NA> <NA>  
## 14: <NA> 4:6 <NA> <NA> <NA> <NA>  
## 15: <NA> <NA> 11:41 <NA> <NA> <NA>  
## 16: 17:29 15:28 15:28 <NA> <NA> <NA>  
## 17: 38:42 42:46 9:4 <NA> <NA> <NA>  
## 18: <NA> 10:20 <NA> <NA> <NA> <NA>  
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## 20: 38:50 40:49 112:93 <NA> <NA> <NA>  
## 21: 10:7 10:14 3:4 <NA> <NA> <NA>  
## 22: 85:104 81:98 <NA> <NA> <NA> <NA>  
## 23: 5:26 5:29 <NA> <NA> <NA> <NA>  
## 24: 9:3 13:30 27:240 <NA> <NA> <NA>  
## 25: <NA> 10:60 <NA> <NA> <NA> <NA>  
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## 30: 22:18 40:42 136:175 <NA> <NA> <NA>  
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## 41: 11:28 16:33 <NA> <NA> <NA> <NA>  
## 42: <NA> <NA> 12:14 <NA> <NA> <NA>  
## 43: <NA> 7:23 <NA> <NA> <NA> <NA>  
## 44: <NA> 31:0 766:5 <NA> <NA> <NA>  
## SangerWES\_AC SangerRecalibWES\_AC RNAseq\_AC HC\_AC RD\_AC WGS\_AC  
## Variant\_annotation DepMap\_ID  
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## 3: damaging ACH-000401  
## 4: damaging ACH-000401  
## 5: damaging ACH-000401  
## 6: damaging ACH-000401  
## 7: damaging ACH-000401  
## 8: damaging ACH-000401  
## 9: damaging ACH-000401  
## 10: damaging ACH-000401  
## 11: damaging ACH-000401  
## 12: damaging ACH-000401  
## 13: damaging ACH-000401  
## 14: damaging ACH-000401  
## 15: damaging ACH-000401  
## 16: damaging ACH-000401  
## 17: damaging ACH-000401  
## 18: damaging ACH-000401  
## 19: damaging ACH-000401  
## 20: damaging ACH-000401  
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## 22: damaging ACH-000401  
## 23: damaging ACH-000401  
## 24: damaging ACH-000401  
## 25: damaging ACH-000401  
## 26: damaging ACH-000401  
## 27: damaging ACH-000401  
## 28: damaging ACH-000401  
## 29: damaging ACH-000401  
## 30: damaging ACH-000401  
## 31: damaging ACH-000401  
## 32: other non-conserving ACH-000401  
## 33: damaging ACH-000401  
## 34: damaging ACH-000401  
## 35: damaging ACH-000401  
## 36: damaging ACH-000401  
## 37: damaging ACH-000401  
## 38: damaging ACH-000401  
## 39: damaging ACH-000401  
## 40: damaging ACH-000401  
## 41: damaging ACH-000401  
## 42: damaging ACH-000401  
## 43: damaging ACH-000401  
## 44: other non-conserving ACH-000401  
## Variant\_annotation DepMap\_ID  
##   
##   
## $annotation  
## DepMap\_ID CCLE\_Name Aliases Primary.Disease  
## 13 ACH-000014 HS294T\_SKIN Hs 294T;A101D;Hs 294.T Skin Cancer  
## 269 ACH-000274 HS852T\_SKIN Hs 852.T Skin Cancer  
## 299 ACH-000304 WM115\_SKIN WM-115 Skin Cancer  
## 317 ACH-000322 HT144\_SKIN HT-144 Skin Cancer  
## 343 ACH-000348 RPMI7951\_SKIN RPMI-7951 Skin Cancer  
## 393 ACH-000401 COLO800\_SKIN COLO-800 Skin Cancer  
## Subtype.Disease Gender Source  
## 13 Melanoma Male ATCC  
## 269 Melanoma ATCC  
## 299 Melanoma Female ATCC  
## 317 Melanoma Male ATCC  
## 343 Melanoma Female ATCC  
## 393 Melanoma Male ATCC

# **Part 2: Data vizualisation**

## **2.1 Preparing our data for plotting**

### **2.1.1 Extracting our data for plotting**

Not all the data is needed for plotting so the data is prepared for the following plots.

generalPlottingData <- lapply(1:(length(processed\_data)-2), function(a) { # the annotation matrix is not needed  
 dtPicker <- processed\_data[[a]]  
 out <- melt(dtPicker) # binding the data togehter that it has samples and values as columns  
 out$Gene <- rep(rownames(dtPicker), ncol(dtPicker)) # adding the genes; probably this might be useful in a later stage  
 out$Case <- names(processed\_data)[1:(length(processed\_data)-1)][a]# adding a labelling column  
 colnames(out) <- c("Sample", "Value", "Gene", "Case") # renameing the columns  
 return(out)  
})

## No id variables; using all as measure variables  
## No id variables; using all as measure variables  
## No id variables; using all as measure variables  
## No id variables; using all as measure variables

names(generalPlottingData) <- names(processed\_data)[1:(length(processed\_data)-2)] # renameing the data

### **2.1.2 Plotting Data - Driver Mutations**

Producing a vector encompasing every gene which at least mutated once.

singleGenes <- as.vector(unique(as.data.frame(rbindlist(lapply(seq\_along(processed\_data$mutation), function(a) {  
 out <- as.data.frame(as.vector(unique(processed\_data$mutation[[a]]$Hugo\_Symbol)))}))))[,1])

Creating a data frame containing the mutation rate of every gene.

geneCounts <- sapply(seq\_along(singleGenes), function(a) {  
 genePicker <- singleGenes[a] # picking one gene  
 sumGene <- lapply(seq\_along(processed\_data$mutation), function(b) {  
 mutPicker <- processed\_data$mutation[[b]] # picking one of the 34 mutation lists  
 out <- as.data.frame(length(which(mutPicker$Hugo\_Symbol == genePicker))) # looking how often an entry is in the mutation list  
 return(out)  
 })  
 geneCount <- colSums(as.data.frame(rbindlist(sumGene))) # summing it up to get the total count for each gene  
 return(geneCount)  
})  
names(geneCounts) <- singleGenes # renameing   
geneCounts <- as.data.frame(geneCounts) # creating a nice data frame  
colnames(geneCounts) <- c("Value")  
geneCounts <- geneCounts[order(-geneCounts$Value), , drop = FALSE] # sorting the data frame  
head(geneCounts)

## Value  
## TTN 13  
## TP53 9  
## HMCN1 8  
## TMTC2 7  
## RYR2 7  
## CACNA1I 7

Extacting the data for the top 10 which will be our driver mutations in the further investigation.

dataTopDriverGenes <- lapply(1:(length(processed\_data)-2), function(a) { # picking the data for our sample   
 dat\_picker <- processed\_data[[a]] # picking one file at each iteration   
 output <- dat\_picker[which(rownames(dat\_picker) %in% rownames(geneCounts)[1:10]),] # comparing the rownames of the picked data with the names of the 10 most mutated genes  
 return(output)  
})  
names(dataTopDriverGenes) <- names(processed\_data)[1:4]  
  
rm(singleGenes)

### **2.1.3 Extracting the drivermutations for every Celline**

Putting all mutation data in one matrix.

oneMatrix <- data.frame()  
for (i in c(1:34)) { # 34 are the cell lines of interest  
 oneMatrix <- rbind(oneMatrix,processed\_data$mutation[[i]][,Hugo\_Symbol:DepMap\_ID])  
}

Extracting just the column of the gene name and the cell line.

celllinesMutations <- oneMatrix[which(oneMatrix$Hugo\_Symbol %in% rownames(geneCounts)[1:10] ),]  
celllinesMutations <- cbind(celllinesMutations$Hugo\_Symbol, celllinesMutations$DepMap\_ID)

Extracting the drivermuations for every cell line out of the data frame and putting it into another data frame so it can be used for plotting.

Genes <- c("COL11A1,TMTC2,TTN", " HMCN1", "COL11A1,HMCN1,SLC510", "HMCN1,TMTC2", "COL11A1,TP53,TTN","none","ZNF292","RYR2","HMCN" ,"none2","none3", "TP53, TTN","HMCN1", "TTN,ZNF292","TMTC2,TP53,NEB","TP53", "TMTC2,NEB","none4","TMTC2,TTN,ZNF292", "none5","CACNA1I","HMCN1,TP53,ZNF292","none6","none7","HMCN1,TMTC2,ZNF292","RYR2,TMTC2,NEB","RYR2,NEB,TTN,CACNA1I","HMCM1,TP53","TTN","COL11A1,SLC5A10","COL11A1,CACNA1I","TTN,CACNA1I","RYR2,CACNA1I,ZNF292","TP53,TTN,CACNA1I" )  
celllines <- c(colnames(processed\_data$expression))  
cellinesMutations <- as.data.frame(cbind(celllines, Genes))  
  
rm(oneMatrix, Genes, celllinesMutations, celllines,i)

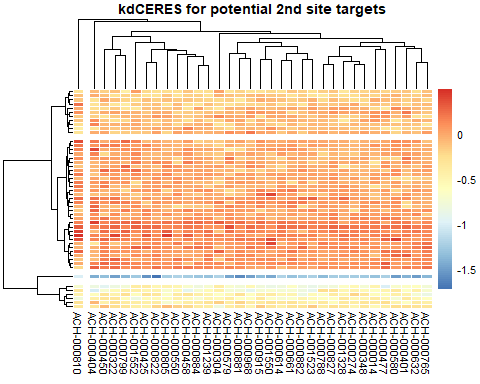
The explanation for the previous extraction will be outlined in the following visualization part.

## **2.2 Visualizing our data**

### **2.2.1 Heatmap with the knock down data**

Starting with a heatmap of the knock down data (the kd.ceres matrix). This matrix consists of gene knockdown scores. The impact of the knocked out gene on the cell survival is reflected by that score. The impact can be a reduction or an increase in proliferation. It could also mean that there is no change in cell proliferation at all. Smaller values refer to higher importance. Useing only the first 50 genes because otherwise the computer was overchallenged and could sometimes not produce the heatmap.

pheatmap(as.matrix(processed\_data$kd.ceres[1:50,]), clustering\_method = "ward.D2",border\_color = "white", fontsize = 8,   
 main = paste0("kdCERES for potential 2nd site targets"),  
 show\_rownames = F, show\_colnames = T,  
 cutree\_rows = 4,  
 cutree\_cols = 2,   
 fontsize\_row=10)

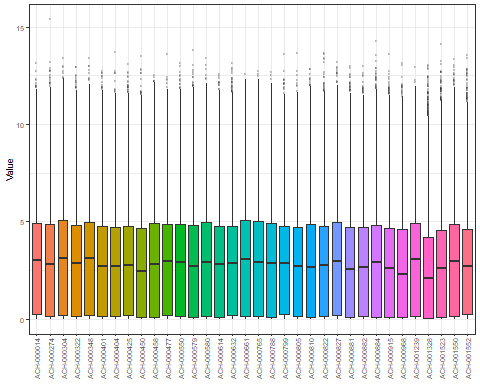


* *We can see that there are clear differences between the knockdown data depending on the knocked out gene in a specific cell.*
* *The cell lines behave differently when the same gene is knocked out.*

### **2.2.2 Distribution of the expression values between the different cell lines**

Creating a boxplot with the expression matrix to see how the expression of the genes is distributed over the different cell lines.

ggplot(data = generalPlottingData$expression, aes(x=Sample, y=Value)) +  
 geom\_boxplot(aes(fill = Sample), outlier.size = 0.1, outlier.alpha = 0.2) + # reconstructing the outliers a bit (reduce them in size; because we are interested in the boxplots and not the outliers)  
 theme\_bw(base\_size = 7) + # formating the size of the theme nicely  
 theme(legend.position= "none", # defining the legend position (here no leghend will be needed)  
 legend.direction="horizontal", #define the legend direction if one is there  
 plot.title = element\_text(hjust = 0.5), # making the title of the plot into the middle  
 axis.text.x = element\_text(angle = 90, vjust = 0.5, hjust=1), # defining the orientation of the text on the x-axis  
 legend.title= element\_blank(), # no title of the legend should be plotted  
 axis.title.x = element\_blank(), # no title of the x-axis is relevant; because that would be samples and that is cleare due to the naming  
 strip.text.y = element\_text(angle = 90)) # defining the orientation of the text of the y-axis

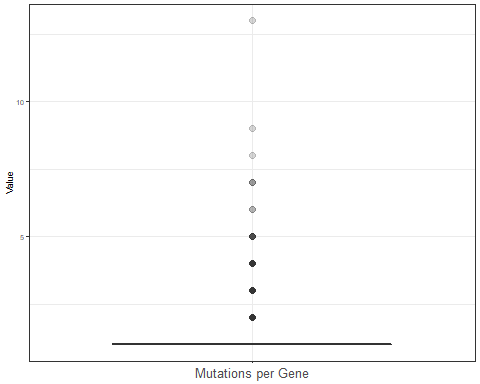


* *Many genes are distributed between the 25 and 75 quantile. But there are also some outliers which are of special interest for us in the following data analysis.*
* *For now we can say that the data is differnetly distributed between the celllines based on different mutations in the different cell lines.*

### **2.2.3 Plotting how often a gene is mutated over all cell line**

A second boxplot using the mutation matrix should show generally how often genes are mutated.

geneCounts <- cbind(geneCounts, "Mutations per Gene")  
  
ggplot(data = geneCounts, aes(x="Mutations per Gene", y=Value)) +  
 geom\_boxplot(aes(fill = "Mutations per Gene"), outlier.size = 2, outlier.alpha = 0.2) + # reconstructing the outliers a bit (so reduce them in size; because we are interested in the boxplots and not the outliers)  
 theme\_bw(base\_size = 7) + # formating the size of the theme nicely  
 theme(legend.position= "none", # defining the legend position (here no leghend will be needed)  
 legend.direction="horizontal", # defining the legend direction if one is there  
 plot.title = element\_text(hjust = 0.5), # making the title of the plot into the middle  
 axis.text.x = element\_text(angle = 0, vjust = 0.5, hjust= 0.5, size = 10), # defining the orientation of the text on the x-axis  
 legend.title= element\_blank(), # no title of the legend should be plotted  
 axis.title.x = element\_blank(), # no title of the x-axis is relevant; because that would be samples and that is cleare due to the naming  
 strip.text.y = element\_text(angle = 90)) # defining the orientation of the text of the y-axis

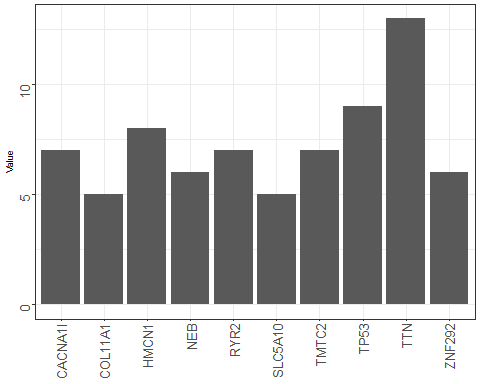


* + As it can bee seen in the boxplot, there are genes which significantly mutated more often than others.\*
* *We have a different number of mutations per gene. Following this it shoud be possible to identify the genes which mutated most.*

### **2.2.4 Top 10 mutated genes**

Now we want to see which mutations are the top 10 mutated genes.

plotData <- geneCounts[1:10, ,drop = FALSE]  
  
plotData$Gene <- rownames(plotData)  
  
ggplot(data = plotData) +  
 (geom\_bar(mapping = aes(x = Gene, y = Value), stat = "identity")) +  
 theme\_bw(base\_size = 7) + # formating the size of the theme nicely  
 theme(legend.position= "none", # defining the legend position (here no legend will be needed)  
 legend.direction="horizontal", # defining the legend direction if one is there  
 plot.title = element\_text(hjust = 0.5), # making the title of the plot into the middle  
 axis.text.x = element\_text(angle = 90, vjust = 0.5, hjust=1, size = 10), # defining the orientation of the text on the x-axis  
 axis.text.y = element\_text(angle = 90, vjust = 0.5, hjust=1, size = 10), # defining the orientation of the text on the x-axis  
 legend.title= element\_blank(), # no title of the legend should be plotted  
 axis.title.x = element\_blank(), # no title of the x-axis is relevant; because that would be samples and that is cleare due to the naming  
 strip.text.y = element\_text(angle = 90)) # defining the orientation of the text of the y-axis



rm(plotData)

* *These 10 Genes are our driver genes of which we want to identify interactions with other genes.*

# **3. Dimensionality reduction**

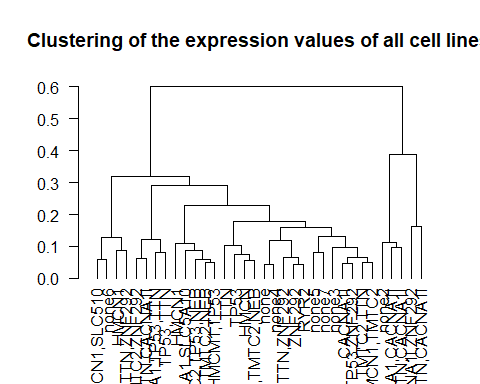
General questions:

* Can we group the different driver mutations together so that we can see in which other genes the cell lines with a specific driver mutation differentiate?
* With Dimnsionality reduction we could gain insight which other genes are our secound targets.

## **3.1 Hierachical clustering**

Creating a hierachical cluster with our driver mutations.

drivergene <- 3   
# determines which of the driver mutations will be seen in the cluster at the x axis  
dataset <- processed\_data$expression # determines which dataset we use  
  
colnames(dataset)[which(colnames(dataset) %in% unique(cellinesMutations[which(cellinesMutations[,1] == rownames(geneCounts)[drivergene]),2]))] <- rownames(geneCounts)[drivergene]  
colnames(dataset) <- cellinesMutations$Genes  
  
cor.mat = cor(dataset[1:50,], method = "spearman")  
cor.dist = as.dist(1 - cor.mat)  
cor.hc = hclust(cor.dist, method = "ward.D2")  
cor.hc = as.dendrogram(cor.hc)  
plot(cor.hc, las = 2, cex.lab = 2, main = "Clustering of the expression values of all cell lines")



rm(drivergene, realcelllinenames, dataset, cor.hc, cor.mat, cor.dist)

## Warning in rm(drivergene, realcelllinenames, dataset, cor.hc, cor.mat,  
## cor.dist): Objekt 'realcelllinenames' nicht gefunden

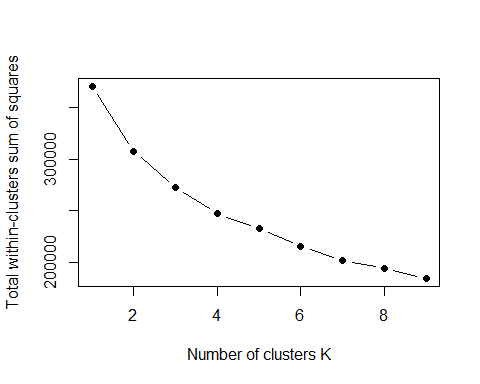
## **3.2 K-means**

Performing a k-means.

dataset <- t(processed\_data$expression[-which(rownames(processed\_data$expression) %in% rownames(geneCounts)[1:10]),])   
# determining which dataset we use  
# trying to cluster the cell lines with the same driver mutations in the same cluster according to the   
# expression data without the expression of the driver mutations  
# Searching for the cause of the diffences between the cell lines besides the expression of the driver mutations   
  
rownames(dataset) <- cellinesMutations$Genes  
  
dataset <- dataset[,-which(apply(dataset, 2, function(x) {  
 var(x)  
}) == 0)]

For choosing the best number centers for the clusters the kink method was used.

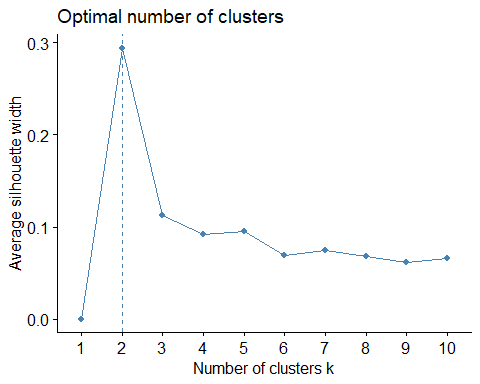
wss = sapply(1:9, function(k) {  
 kmeans(x = dataset, centers = k)$tot.withinss  
})  
plot(1:9, wss, type = "b", pch = 19, xlab = "Number of clusters K", ylab = "Total within-clusters sum of squares")



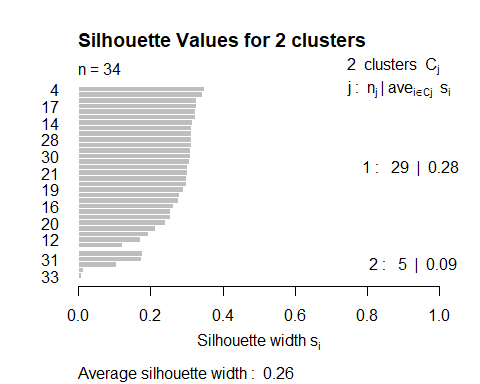
* *But theres no kink in this curve so we need to use other methods to tell us how much centers would be best to choose.*

Now we try the silouette method.

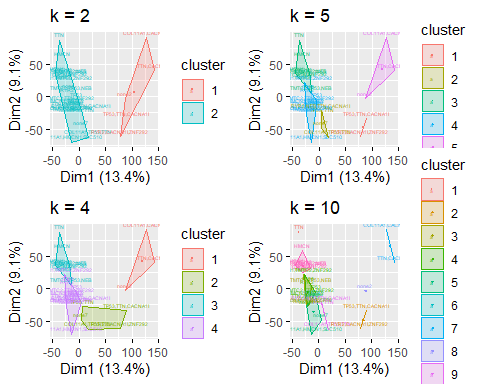
fviz\_nbclust(dataset, kmeans, method = "silhouette")



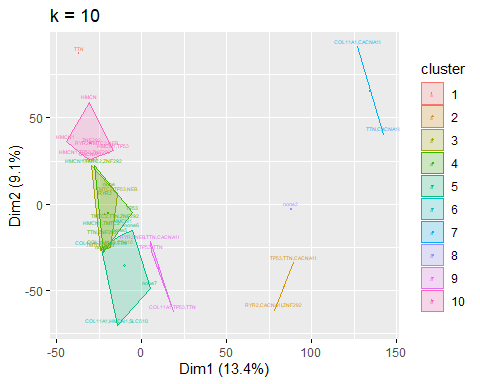
# according to the silhouette method the clustering with two centers seems to be the best one  
  
# taking a look at the clustering with different centers (2, 4, 5, 10)   
km = kmeans(x =dataset, centers = 2, nstart = 100)  
plot(silhouette(km$cluster,dist(dataset)), main = "Silhouette Values for 2 clusters")



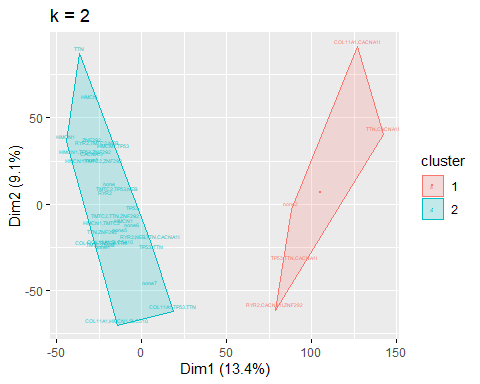
km2 <- kmeans(dataset, centers = 2, nstart = 100)  
km3 <- kmeans(dataset, centers = 5, nstart = 100)  
km4 <- kmeans(dataset, centers = 4, nstart = 100)  
km5 <- kmeans(dataset, centers = 10, nstart = 100)  
  
p1 <- fviz\_cluster(km2,geom = "text", labelsize = 4, data = dataset) + ggtitle("k = 2")  
p2 <- fviz\_cluster(km3, geom = "text", labelsize = 4, data = dataset) + ggtitle("k = 5")  
p3 <- fviz\_cluster(km4, geom = "text", labelsize = 4, data = dataset) + ggtitle("k = 4")  
p4 <- fviz\_cluster(km5, geom = "text", labelsize = 4, data = dataset) + ggtitle("k = 10")  
  
grid.arrange(p1, p2, p3, p4, nrow = 2)



plot(p4) # clustering with 10 centers does not conclude in clusters with the same driver mutations



# having more than one driver mutation in most cell lines may cause this  
  
plot(p1)



rm(km,km2,km3,km4,km5,p1,p2,p3,p4, dataset,wss)

* *The clustering with two centers seems to be the best one.*
* *Our next step in the pca will be to see which of the genes drive the differentation of the celllines in this plot because they will be the most variable and thus most interesting ones.*

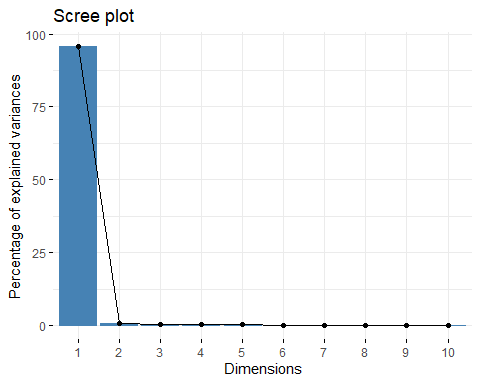
# **3.3 PCA**

Investigating with a principal component analysis why the data clusters together the way it does. Looking at the first two principal components because they are the most interesting.

#drivergene <- 4 # determining which of the driver mutations will be seen in the cluster at the x axis  
dataset <- processed\_data$expression # determining which dataset will be used  
  
  
#colnames(dataset)[which(colnames(dataset) %in% unique(ZelllinesMutations[which(ZelllinesMutations[,1] == topDriverGenes[drivergene]),2]))] <- topDriverGenes[drivergene]  
colnames(dataset)<- cellinesMutations$Genes  
  
pca = prcomp(t(dataset), center = F, scale. = F)  
summary(pca)

## Importance of components:  
## PC1 PC2 PC3 PC4 PC5  
## Standard deviation 495.3869 46.27533 35.11722 26.07913 24.64502  
## Proportion of Variance 0.9573 0.00835 0.00481 0.00265 0.00237  
## Cumulative Proportion 0.9573 0.96567 0.97048 0.97313 0.97550  
## PC6 PC7 PC8 PC9 PC10  
## Standard deviation 21.01126 20.73196 19.77350 19.31929 17.76823  
## Proportion of Variance 0.00172 0.00168 0.00153 0.00146 0.00123  
## Cumulative Proportion 0.97723 0.97890 0.98043 0.98188 0.98312  
## PC11 PC12 PC13 PC14 PC15  
## Standard deviation 17.71421 16.8245 16.18356 15.71160 15.43367  
## Proportion of Variance 0.00122 0.0011 0.00102 0.00096 0.00093  
## Cumulative Proportion 0.98434 0.9854 0.98647 0.98743 0.98836  
## PC16 PC17 PC18 PC19 PC20  
## Standard deviation 15.26658 14.96113 14.46341 13.90066 13.62804  
## Proportion of Variance 0.00091 0.00087 0.00082 0.00075 0.00072  
## Cumulative Proportion 0.98927 0.99014 0.99096 0.99171 0.99243  
## PC21 PC22 PC23 PC24 PC25  
## Standard deviation 13.48726 13.20117 13.08648 12.66417 12.34321  
## Proportion of Variance 0.00071 0.00068 0.00067 0.00063 0.00059  
## Cumulative Proportion 0.99314 0.99382 0.99449 0.99512 0.99571  
## PC26 PC27 PC28 PC29 PC30  
## Standard deviation 11.96792 11.74491 11.66818 11.40272 11.21416  
## Proportion of Variance 0.00056 0.00054 0.00053 0.00051 0.00049  
## Cumulative Proportion 0.99627 0.99681 0.99734 0.99785 0.99834  
## PC31 PC32 PC33 PC34  
## Standard deviation 10.83176 10.65546 10.26134 9.49512  
## Proportion of Variance 0.00046 0.00044 0.00041 0.00035  
## Cumulative Proportion 0.99879 0.99924 0.99965 1.00000

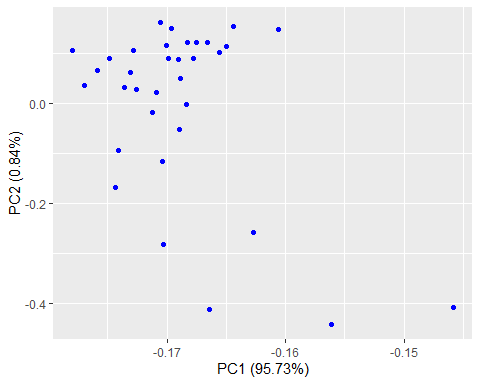
# showing labels (cell lines)  
  
  
fviz\_eig(pca)



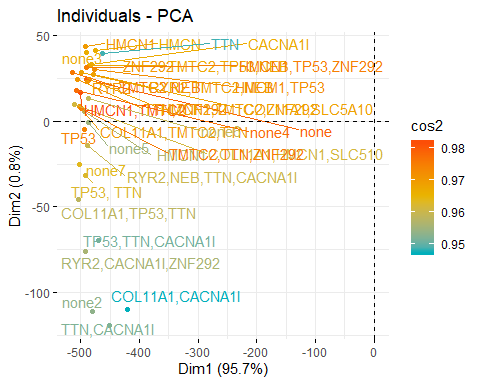
str(pca)

## List of 5  
## $ sdev : num [1:34] 495.4 46.3 35.1 26.1 24.6 ...  
## $ rotation: num [1:16970, 1:34] -9.20e-03 -3.19e-05 -7.79e-03 -1.45e-04 -2.30e-03 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:16970] "A1BG" "A1CF" "A2M" "A2ML1" ...  
## .. ..$ : chr [1:34] "PC1" "PC2" "PC3" "PC4" ...  
## $ center : logi FALSE  
## $ scale : logi FALSE  
## $ x : num [1:34, 1:34] -502 -494 -511 -500 -504 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:34] "COL11A1,TMTC2,TTN" " HMCN1" "COL11A1,HMCN1,SLC510" "HMCN1,TMTC2" ...  
## .. ..$ : chr [1:34] "PC1" "PC2" "PC3" "PC4" ...  
## - attr(\*, "class")= chr "prcomp"

autoplot(pca, colour = 'blue')



fviz\_pca\_ind(pca,  
 col.ind = "cos2", # color by the quality of representation  
 gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),  
 repel = TRUE, # Avoid text overlapping  
)

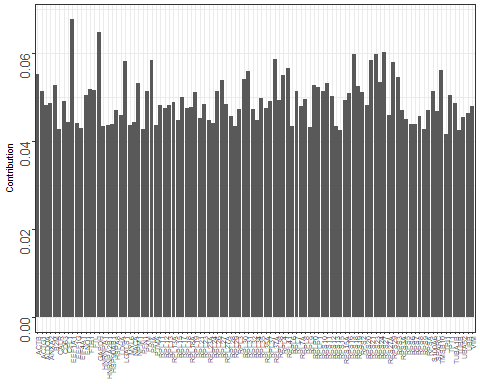


* *Again we see two clusters.*
* *The first principal component contains the most information about the data.*

var\_coord\_func <- function(loadings, comp.sdev){  
 loadings\*comp.sdev  
}  
  
loadings <- pca$rotation  
sdev <- pca$sdev  
var.coord <- t(apply(loadings, 1, var\_coord\_func, sdev))   
  
var.cos2 <- var.coord^2  
comp.cos2 <- apply(var.cos2, 2, sum)  
contrib <- function(var.cos2, comp.cos2){var.cos2\*100/comp.cos2}  
  
var.contrib <- t(apply(var.cos2,1, contrib, comp.cos2))  
head(var.contrib[, 1:4])

## PC1 PC2 PC3 PC4  
## A1BG 8.458140e-03 4.042140e-02 2.820464e-03 1.626858e-03  
## A1CF 1.017925e-07 9.118405e-08 6.046034e-06 1.241073e-05  
## A2M 6.063349e-03 4.405875e-02 8.758703e-02 1.918378e-02  
## A2ML1 2.113426e-06 8.293155e-04 5.108695e-04 6.804066e-04  
## A4GALT 5.277506e-04 5.244157e-02 2.770271e-03 6.278979e-03  
## A4GNT 3.632784e-06 1.020123e-08 5.599425e-05 1.554282e-05

top100var.contrib <- var.contrib[,1]  
top100var.contrib <- as.data.frame(top100var.contrib[order(-top100var.contrib)])  
top100var.contrib$Genes <- rownames(top100var.contrib)  
top100var.contrib <- top100var.contrib[1:100,]  
colnames(top100var.contrib)[1] <- "Contribution"  
  
  
ggplot(data = top100var.contrib) +  
 (geom\_bar(mapping = aes(x = Genes, y = Contribution), stat = "identity")) +  
 theme\_bw(base\_size = 7) + # formating the size of the theme nicely  
 theme(legend.position= "none", # defining the legend position (here no leghend will be needed)  
 legend.direction="horizontal", # defining the legend direction if one is there  
 plot.title = element\_text(hjust = 0.5), # making the title of the plot into the middle  
 axis.text.x = element\_text(angle = 90, vjust = 0.5, hjust=1, size = 5), # defining the orientation of the text on the x-axis  
 axis.text.y = element\_text(angle = 90, vjust = 0.5, hjust=1, size = 10), # defining the orientation of the text on the y-axis  
 legend.title= element\_blank(), # no title of the legend should be plotted  
 axis.title.x = element\_blank(), # no title of the x-axis is relevant; because that would be samples and that is cleare due to the naming  
 strip.text.y = element\_text(angle = 90)) # defining the orientation of the text of the y-axis



* *These are the components which are contributing the most to our variation in the data. Maybe we will find some of these in our result of the p-test.*

rm(drivergene, realcelllinenames, dataset, loadings, pca, realcelllinenames, var.contrib, var.coord, var.cos2, comp.cos2, sdev)

## Warning in rm(drivergene, realcelllinenames, dataset, loadings, pca,  
## realcelllinenames, : Objekt 'drivergene' nicht gefunden

## Warning in rm(drivergene, realcelllinenames, dataset, loadings, pca,  
## realcelllinenames, : Objekt 'realcelllinenames' nicht gefunden  
  
## Warning in rm(drivergene, realcelllinenames, dataset, loadings, pca,  
## realcelllinenames, : Objekt 'realcelllinenames' nicht gefunden

# **4. Statistical test**

We want to perform a p-test and compare the p-values.

driverGenes <- rownames(geneCounts)[1:10] # only using the TOP 10 driver genes  
ttestgenes <- rownames(processed\_data$kd.ceres)  
  
potSecondSites <- lapply(seq\_along(driverGenes), function(a) {  
 genePicker <- driverGenes[a] # picking one driver gene  
 print(paste0("I am doing driver mut: ", a))  
 output <- sapply(seq\_along(rownames(processed\_data$kd.ceres)), function(b) { #the kdCERES matrix is of interest take its' rownames as refrence  
 secondSitePicker <- rownames(processed\_data$kd.ceres)[b] # picking a potetnial 2nd site target  
 if (secondSitePicker != genePicker) {  
 drMUT <- processed\_data$kd.ceres[which(rownames(processed\_data$kd.ceres) == genePicker),] # picking the driver mut data  
 sndMUT <- as.vector(processed\_data$kd.ceres[which(rownames(processed\_data$kd.ceres) == secondSitePicker),]) # picking the 2nd site data  
 cor.val <- cor.test(unlist(drMUT, use.names=FALSE) , unlist(sndMUT, use.names=FALSE), method = "spearman") # making a spearman correlation  
 return(cor.val$p.value) # returning the p-values  
 } else {  
 return(1)  
 }  
 })  
 names(output) <- rownames(processed\_data$kd.ceres) # renaming all  
 output <- as.data.frame(output) # getting a nice data frame  
 return(output)  
})

## [1] "I am doing driver mut: 1"  
## [1] "I am doing driver mut: 2"  
## [1] "I am doing driver mut: 3"  
## [1] "I am doing driver mut: 4"  
## [1] "I am doing driver mut: 5"  
## [1] "I am doing driver mut: 6"  
## [1] "I am doing driver mut: 7"  
## [1] "I am doing driver mut: 8"  
## [1] "I am doing driver mut: 9"  
## [1] "I am doing driver mut: 10"

names(potSecondSites) <- driverGenes # renaming the list of lists  
lapply(potSecondSites, head) # looking at the nice data

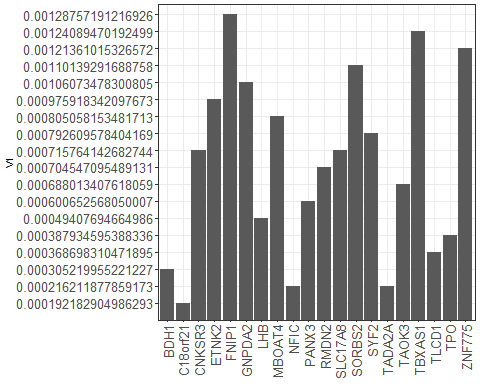
## $TTN  
## output  
## A1BG 0.70023480  
## A1CF 0.39115670  
## A2M 0.34286907  
## A2ML1 0.11397865  
## A4GALT 0.19132453  
## A4GNT 0.01504808  
##   
## $TP53  
## output  
## A1BG 0.28160340  
## A1CF 0.70023480  
## A2M 0.39697321  
## A2ML1 0.64097590  
## A4GALT 0.09015868  
## A4GNT 0.60183071  
##   
## $HMCN1  
## output  
## A1BG 0.4227534  
## A1CF 0.8657359  
## A2M 0.6534159  
## A2ML1 0.7917565  
## A4GALT 0.8725280  
## A4GNT 0.3437615  
##   
## $TMTC2  
## output  
## A1BG 0.45154526  
## A1CF 0.43701759  
## A2M 0.95872743  
## A2ML1 0.75867863  
## A4GALT 0.01716129  
## A4GNT 0.62127398  
##   
## $RYR2  
## output  
## A1BG 0.879329218  
## A1CF 0.669727445  
## A2M 0.002884766  
## A2ML1 0.213302043  
## A4GALT 0.088108676  
## A4GNT 0.304196025  
##   
## $CACNA1I  
## output  
## A1BG 0.93400823  
## A1CF 0.09259686  
## A2M 0.14278128  
## A2ML1 0.61030460  
## A4GALT 0.10401228  
## A4GNT 0.53711418  
##   
## $ZNF292  
## output  
## A1BG 0.27458108  
## A1CF 0.75736391  
## A2M 0.57435603  
## A2ML1 0.07565286  
## A4GALT 0.38922902  
## A4GNT 0.08058396  
##   
## $NEB  
## output  
## A1BG 0.42275339  
## A1CF 0.07595393  
## A2M 0.36190890  
## A2ML1 0.33314716  
## A4GALT 0.04869324  
## A4GNT 0.05084604  
##   
## $COL11A1  
## output  
## A1BG 0.07535272  
## A1CF 0.49777121  
## A2M 0.80910520  
## A2ML1 0.26539892  
## A4GALT 0.18653536  
## A4GNT 0.68237842  
##   
## $SLC5A10  
## output  
## A1BG 0.991742072  
## A1CF 0.467398656  
## A2M 0.834622511  
## A2ML1 0.453641927  
## A4GALT 0.916192275  
## A4GNT 0.007613915

Now that we got all those p-values we want to order the data according to their p-values. So we can see the smallest ones which are the most important ones.

potSecondSites <- lapply(potSecondSites, function(a){  
 a <- as.data.frame(cbind(a$output, rownames(a)))  
 a <- a[order(a[1]), ]  
})

Selecting the 20 genes out of every DriverGene List with the lowest p score.

potSecondSitestop20 <- lapply(seq\_along(potSecondSites), function (a){  
 output <- potSecondSites[[a]][1:20,]  
 return(output)  
})  
names(potSecondSitestop20) <- driverGenes  
  
ggplot(data = potSecondSitestop20$TTN) +  
 (geom\_bar(mapping = aes(x = V2, y = V1), stat = "identity")) +  
 theme\_bw(base\_size = 7) + # formating the size of the theme nicely  
 theme(legend.position= "none", # defining the legend position (here no legend will be needed)  
 legend.direction="horizontal", # defining the legend direction if one is there  
 plot.title = element\_text(hjust = 0.5), # making the title of the plot into the middle  
 axis.text.x = element\_text(angle = 90, vjust = 0.5, hjust=1, size = 10), # defining the orientation of the text on the x-axis  
 axis.text.y = element\_text(angle = 0, vjust = 0.5, hjust=1, size = 10), # defining the orientation of the text on the y-axis  
 legend.title= element\_blank(), # no title of the legend should be plotted  
 axis.title.x = element\_blank(), # no title of the x-axis is relevant; because that would be samples and that is cleare due to the naming  
 strip.text.y = element\_text(angle = 90)) # defining the orientation of the text of the y-axis



rm(potSecondSites, ttestgenes)

# **5. Multiple linear regression analysis**

## **5.1 Predicting the expression of our driver genes with all the data**

Creating a data frame for the multiple linear regression. In this data frame all the columns are the data frames and the rows represent the genes in every cell line.

With this data frame the linear regression is performed. After that the predicted values are compared with the real values of the data\_set by a spearman correlation. Performing this with every driver gene.

a <- generalPlottingData$expression[,1:3]  
a <-a[,c(1,3,2)]  
copynumber <- generalPlottingData$copynumber[,2]  
kd.ceres <- generalPlottingData$kd.ceres[,2]  
kd.prob <- generalPlottingData$kd.prob[,2]  
  
RegData <- cbind(a,copynumber,kd.ceres,kd.prob)  
  
# doing the multiple linear regression   
# comparing the predicted values of our model with the real values of the test\_data by spearman correlaton  
# doing this for every driver gene  
  
Regressionanalysis <-lapply(1:10, function(x){  
 RegData <- cbind(a,copynumber,kd.ceres,kd.prob)  
 Driverexpression <- c()  
 for (i in 1:34) { # 34 = te skin cancer cell lines  
 a <- 16970\*i # 16970 = number of genes  
 c <- (16970\* (i-1))+1  
 b <- colnames(processed\_data$expression)[i]  
 Driverexpression[c:a] <- processed\_data$expression[rownames(geneCounts)[x],b]  
 }  
 print(paste0("I am doing driver mut: ", rownames(geneCounts)[x]))  
 RegData <- cbind(RegData,Driverexpression)  
 RegData <-as.data.frame(RegData)  
 colnames(RegData) <- as.vector(colnames(RegData))  
 set.seed(123) # initializing the random numbers  
 split = sample.split(RegData, SplitRatio = 0.8) # splitting the dataset into 4/5 Training and 1/5 Testing dataset  
 training\_set = subset(RegData, split == TRUE) # using the labels to get the training data  
 test\_set = subset(RegData, split == FALSE)   
 rm(RegData)  
 # fitting the multiple linear regression to the Training set  
 regressor = lm(Driverexpression ~ Value + copynumber + kd.ceres + kd.prob , data = training\_set) # predicting profit based on ALL (=.) the input variables for one company   
 # predicting the test set results  
 y\_pred = predict(regressor, newdata = test\_set, se.fit = TRUE) # predicting the expression based on the testing data   
 test\_set$Prediction = y\_pred$fit # adding the predictions to the dataset  
 # comparing the predictions (last column) with the real values of the startups (2nd last column)  
 Results <- cor.test(test\_set$Driverexpression, test\_set$Prediction, method = "spearman", exact=FALSE)  
 return(Results)  
})

## [1] "I am doing driver mut: TTN"  
## [1] "I am doing driver mut: TP53"  
## [1] "I am doing driver mut: HMCN1"  
## [1] "I am doing driver mut: TMTC2"  
## [1] "I am doing driver mut: RYR2"  
## [1] "I am doing driver mut: CACNA1I"  
## [1] "I am doing driver mut: ZNF292"  
## [1] "I am doing driver mut: NEB"  
## [1] "I am doing driver mut: COL11A1"  
## [1] "I am doing driver mut: SLC5A10"

names(Regressionanalysis) <- rownames(geneCounts)[1:10]  
Regressionanalysis <- as.vector(Regressionanalysis)  
rm(RegData,kd.ceres,kd.prob,copynumber,a)  
  
  
ResultsRegression <- melt(lapply(1:length(Regressionanalysis), function(x){  
 return(Regressionanalysis[[x]][3])  
}))  
ResultsRegression <- cbind(ResultsRegression,melt(lapply(1:length(Regressionanalysis), function(x){  
 return(Regressionanalysis[[x]][1])  
})))  
  
ResultsRegression$L2 <- rownames(geneCounts)[1:10]  
ResultsRegression <- ResultsRegression [,c(2,1,4)]  
colnames(ResultsRegression) <- c("DriverGene", "pvalue", "Svalue" )  
  
print(ResultsRegression)

## DriverGene pvalue Svalue  
## 1 TTN 5.509211e-16 7.317806e+14  
## 2 TP53 4.997652e-09 7.359220e+14  
## 3 HMCN1 5.739113e-37 7.233205e+14  
## 4 TMTC2 1.486016e-36 7.234577e+14  
## 5 RYR2 1.671884e-30 7.255677e+14  
## 6 CACNA1I 7.949257e-20 7.299161e+14  
## 7 ZNF292 9.481412e-12 7.341441e+14  
## 8 NEB 5.286592e-14 7.328378e+14  
## 9 COL11A1 1.548789e-77 7.124150e+14  
## 10 SLC5A10 4.727922e-25 7.276653e+14

# with these low p-values we can say with confidence that our Model is able to reproduce and predict   
# the Expressionvalues of our drivergenes   
  
# using just our top 20 out of the statistical testing we hoped to see that the p values would not increase that much   
# this would verify our these that these genes are the essential components which drive the differnet expression of the Driver Gene   
# as you can see below this ist not the case and the p values are very much increased

* + so with this result we can not define confidently the secound targets.\*

# **6. RESULTS**

Resultspresentation <- lapply(1:length(potSecondSitestop20), function(x){  
 return(potSecondSitestop20[[x]][2])  
})  
  
names(Resultspresentation) <- rownames(geneCounts)[1:10]  
print(Resultspresentation)

## $TTN  
## V2  
## 1619 C18orf21  
## 9311 NFIC  
## 14283 TADA2A  
## 1308 BDH1  
## 14708 TLCD1  
## 15183 TPO  
## 7750 LHB  
## 10332 PANX3  
## 14321 TAOK3  
## 12208 RMDN2  
## 2967 CNKSR3  
## 13171 SLC17A8  
## 14213 SYF2  
## 8296 MBOAT4  
## 4571 ETNK2  
## 5693 GNPDA2  
## 13698 SORBS2  
## 16853 ZNF775  
## 14435 TBXAS1  
## 5161 FNIP1  
##   
## $TP53  
## V2  
## 2499 CDKN1A  
## 11816 RAD50  
## 14298 TAF4  
## 14764 TMCC1  
## 4371 ELP5  
## 2900 CLNS1A  
## 3317 CSNK1E  
## 15153 TP53BP1  
## 1038 ATE1  
## 5012 FEM1B  
## 10303 PAGR1  
## 12378 RPL23  
## 16904 ZNF862  
## 11548 PSME3  
## 11231 PPP1R42  
## 4149 DYNLT1  
## 11199 PPP1R12A  
## 9363 NIPBL  
## 16084 WDR83  
## 14889 TMEM207  
##   
## $HMCN1  
## V2  
## 3855 DLEC1  
## 7868 LPA  
## 14241 SYT1  
## 2696 CHI3L2  
## 1086 ATP13A4  
## 15195 TPRX1  
## 3970 DNM1  
## 997 ASGR1  
## 5454 GCKR  
## 321 ADO  
## 2893 CLMN  
## 564 AMTN  
## 12134 RHBDD2  
## 14043 STBD1  
## 5219 FPGT  
## 8695 MRGPRX1  
## 289 ADCY2  
## 11622 PTPN13  
## 16185 XPO4  
## 6637 IFNW1  
##   
## $TMTC2  
## V2  
## 6823 INPP1  
## 6415 HPCAL4  
## 6838 INSL4  
## 10807 PIM1  
## 1630 C19orf44  
## 13439 SLC6A5  
## 12357 RPF2  
## 13018 SHBG  
## 14524 TENM4  
## 9418 NME1  
## 12112 RGS13  
## 11239 PPP2R2A  
## 13478 SLCO2A1  
## 12557 RWDD3  
## 4841 FAM78A  
## 15160 TP53RK  
## 7610 LAMC1  
## 14552 TEX33  
## 5893 GRIK4  
## 16316 ZC3H7A  
##   
## $RYR2  
## V2  
## 5170 FOS  
## 10974 PLSCR1  
## 4126 DUSP7  
## 13270 SLC26A8  
## 4693 FAM118B  
## 13662 SNX21  
## 12493 RRP8  
## 6148 HERC4  
## 2600 CEP57L1  
## 15432 TSPO  
## 13161 SLC16A7  
## 6609 IFITM2  
## 10984 PLXNA2  
## 4233 EFCAB14  
## 8288 MBIP  
## 16664 ZNF501  
## 12256 RNF14  
## 13123 SLC10A1  
## 4750 FAM177A1  
## 173 ACSF3  
##   
## $CACNA1I  
## V2  
## 13544 SMDT1  
## 8832 MSX2  
## 7726 LGALS12  
## 9657 NUCB1  
## 7536 KRTAP21-3  
## 4033 DPRX  
## 3564 DAOA  
## 10200 OSBPL3  
## 10618 PENK  
## 4608 EXOC3L4  
## 11025 PNPLA5  
## 12802 SEH1L  
## 760 APOBEC3F  
## 9013 MYO1H  
## 15604 UBA52  
## 12857 SERHL2  
## 1598 C16orf97  
## 3660 DDR1  
## 39 ABCA7  
## 15108 TNRC6B  
##   
## $ZNF292  
## V2  
## 7630 LARP4B  
## 10984 PLXNA2  
## 13213 SLC24A1  
## 13373 SLC39A9  
## 10203 OSBPL7  
## 15231 TRAPPC10  
## 12266 RNF152  
## 1824 C6orf99  
## 5586 GLB1  
## 8021 LSM5  
## 10214 OSMR  
## 14875 TMEM190  
## 15768 UNC93A  
## 10717 PHF5A  
## 3094 COPA  
## 11354 PRKCSH  
## 16138 WNT5A  
## 8275 MAX  
## 2703 CHL1  
## 4649 F2RL2  
##   
## $NEB  
## V2  
## 3318 CSNK1G1  
## 3931 DNAJC10  
## 7082 KCNAB3  
## 12359 RPGRIP1L  
## 2675 CHCHD5  
## 15311 TRIM61  
## 9390 NKX6-1  
## 11828 RAD9B  
## 16674 ZNF514  
## 3429 CWC25  
## 2332 CD22  
## 13376 SLC40A1  
## 8895 MTRNR2L2  
## 4583 EVA1A  
## 5809 GPR183  
## 14900 TMEM219  
## 1213 BAALC  
## 11643 PTPRH  
## 15120 TOM1L2  
## 8621 MOCOS  
##   
## $COL11A1  
## V2  
## 3713 DEFB108B  
## 5233 FRK  
## 10256 OXT  
## 16705 ZNF560  
## 2882 CLIC6  
## 9029 MYOM1  
## 14943 TMEM37  
## 930 ARMS2  
## 11982 RBP1  
## 1922 CACNG7  
## 7372 KLHL36  
## 4932 FBXO11  
## 15437 TSPYL6  
## 1078 ATP10D  
## 8008 LRTOMT  
## 14339 TAS2R13  
## 1898 CACHD1  
## 5332 GABBR2  
## 15616 UBASH3B  
## 11202 PPP1R13B  
##   
## $SLC5A10  
## V2  
## 8177 MAP2K4  
## 13850 SPNS2  
## 16525 ZNF256  
## 6648 IFT52  
## 13815 SPEM1  
## 7249 KIAA1324L  
## 4226 EEF2K  
## 8987 MYL4  
## 10888 PLAC8L1  
## 14539 TEX10  
## 16738 ZNF593  
## 15072 TNFSF12  
## 13018 SHBG  
## 3795 DHRS11  
## 11358 PRKD3  
## 11415 PRPSAP2  
## 10410 PCBP4  
## 13153 SLC16A11  
## 14303 TAF6L  
## 4107 DUSP10

print(top100var.contrib[1:20,2])

## [1] "EEF1A1" "GAPDH" "RPS27" "RPS23" "RPS18" "RPL37A" "PPIA"   
## [8] "RPS21" "LGALS1" "RPS29" "RPL41" "TMSB10" "RPL31" "ACTB"   
## [15] "RPL4" "RPS3" "RPL30" "RPL27" "RPS24" "RPS11"

which(top100var.contrib[1:20,2] %in% as.character(melt(Resultspresentation)[,1]))

## Using V2 as id variables  
## Using V2 as id variables  
## Using V2 as id variables  
## Using V2 as id variables  
## Using V2 as id variables  
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## Using V2 as id variables  
## Using V2 as id variables  
## Using V2 as id variables  
## Using V2 as id variables

## integer(0)

* *Our ten driver mutations are : TTN, TP53, HMCN1, TMTC2, RYR2, CACNA1I, ZNF292, NEB, COL11A1, SLC5A10. We defined them with a barplot at the beginning.*
* *Our goal was to find possible second side targets interacting with these driver mutations more often than other mutations and which are of a greater importance than other interactin genes.*
* *We tried to define these targets with a PCA and a p-test.But the 2nd targets from the pca and the regression are not overlapping. This could be due to the data or mistakes we made in the skript. Also the kmeans and the PCA do not reproduce the same second side targets.*
* *However we decided to present the targets we defined with the p-test. As shown above we have listed the top 20 second side targets from the p-test for each gene.*
* *The regression model shows a really low p-value at which leads us to the conclucion that the above listed genes could be taken in account as targets for drug development in skin cancer.*

Predicting the expression of the driver mutations with the expression of the other genes

# we also wanted to do another Regression model on just the expression data with the so that the coeffizients of the   
# analysis would tell us how improtant each gene is for the model, but this regression does not work and we doesnt know why   
# maybe you can take a look and help us   
#dataset <- t(processed\_data$expression)  
  
#dataset <- as.data.frame(dataset)  
  
  
  
#set.seed(123) #initialize the random numbers  
#split = sample.split(dataset, SplitRatio = 0.5) #split the dataset into 4/5 Training and 1/5 Testing dataset  
#training\_set = subset(dataset, split == TRUE) #use the labels to get the training data  
#test\_set = subset(dataset, split == FALSE)   
#rm(dataset)  
  
  
# Fitting Multiple Linear Regression to the Training set  
# regressor = lm(TP53 ~ ., data = training\_set) #predict profit based on ALL (=.) the input variables for one company   
  
# Predicting the Test set results  
# y\_pred = predict(regressor, newdata = test\_set, se.fit = TRUE) #predict the expression based on your testing data   
# test\_set$Prediction = y\_pred$fit #add your predictions to the dataset  
#Now compare the Predictions (last column) with the real values of the startups (2nd last column)  
# Results <- cor.test(test\_set$Driverexpression, test\_set$Prediction, method = "spearman", exact=FALSE)  
  
  
  
  
  
  
  
sessionInfo()

## R version 3.6.0 (2019-04-26)  
## Platform: x86\_64-w64-mingw32/x64 (64-bit)  
## Running under: Windows 10 x64 (build 17134)  
##   
## Matrix products: default  
##   
## locale:  
## [1] LC\_COLLATE=German\_Germany.1252 LC\_CTYPE=German\_Germany.1252   
## [3] LC\_MONETARY=German\_Germany.1252 LC\_NUMERIC=C   
## [5] LC\_TIME=German\_Germany.1252   
##   
## attached base packages:  
## [1] grid stats graphics grDevices utils datasets methods   
## [8] base   
##   
## other attached packages:  
## [1] caTools\_1.17.1.2 scales\_1.0.0 ggfortify\_0.4.7   
## [4] usethis\_1.5.0 devtools\_2.0.2 dendextend\_1.12.0  
## [7] forcats\_0.4.0 stringr\_1.4.0 dplyr\_0.8.1   
## [10] purrr\_0.3.2 readr\_1.3.1 tidyr\_0.8.3   
## [13] tibble\_2.1.3 tidyverse\_1.2.1 caret\_6.0-84   
## [16] lattice\_0.20-38 pheatmap\_1.0.12 rstudioapi\_0.10   
## [19] cluster\_2.1.0 data.table\_1.12.2 reshape2\_1.4.3   
## [22] gridExtra\_2.3 factoextra\_1.0.5 relaimpo\_2.2-3   
## [25] mitools\_2.4 survey\_3.36 survival\_2.44-1.1  
## [28] Matrix\_1.2-17 boot\_1.3-22 MASS\_7.3-51.4   
## [31] ggplot2\_3.2.0   
##   
## loaded via a namespace (and not attached):  
## [1] nlme\_3.1-139 bitops\_1.0-6 fs\_1.3.1   
## [4] lubridate\_1.7.4 RColorBrewer\_1.1-2 httr\_1.4.0   
## [7] rprojroot\_1.3-2 tools\_3.6.0 backports\_1.1.4   
## [10] R6\_2.4.0 rpart\_4.1-15 DBI\_1.0.0   
## [13] lazyeval\_0.2.2 colorspace\_1.4-1 nnet\_7.3-12   
## [16] withr\_2.1.2 prettyunits\_1.0.2 tidyselect\_0.2.5   
## [19] processx\_3.3.1 compiler\_3.6.0 cli\_1.1.0   
## [22] rvest\_0.3.4 xml2\_1.2.0 desc\_1.2.0   
## [25] labeling\_0.3 callr\_3.2.0 digest\_0.6.19   
## [28] rmarkdown\_1.13 pkgconfig\_2.0.2 htmltools\_0.3.6   
## [31] sessioninfo\_1.1.1 rlang\_0.3.4 readxl\_1.3.1   
## [34] generics\_0.0.2 jsonlite\_1.6 ModelMetrics\_1.2.2  
## [37] magrittr\_1.5 Rcpp\_1.0.1 munsell\_0.5.0   
## [40] viridis\_0.5.1 stringi\_1.4.3 yaml\_2.2.0   
## [43] pkgbuild\_1.0.3 plyr\_1.8.4 recipes\_0.1.5   
## [46] ggrepel\_0.8.1 crayon\_1.3.4 haven\_2.1.0   
## [49] splines\_3.6.0 hms\_0.4.2 knitr\_1.23   
## [52] ps\_1.3.0 pillar\_1.4.1 ggpubr\_0.2.1   
## [55] ggsignif\_0.5.0 corpcor\_1.6.9 pkgload\_1.0.2   
## [58] codetools\_0.2-16 stats4\_3.6.0 glue\_1.3.1   
## [61] evaluate\_0.14 remotes\_2.1.0 modelr\_0.1.4   
## [64] foreach\_1.4.4 cellranger\_1.1.0 gtable\_0.3.0   
## [67] assertthat\_0.2.1 xfun\_0.7 gower\_0.2.1   
## [70] prodlim\_2018.04.18 broom\_0.5.2 class\_7.3-15   
## [73] viridisLite\_0.3.0 timeDate\_3043.102 iterators\_1.0.10   
## [76] memoise\_1.1.0 lava\_1.6.5 ipred\_0.9-9

# **finally done at least for now :)**