

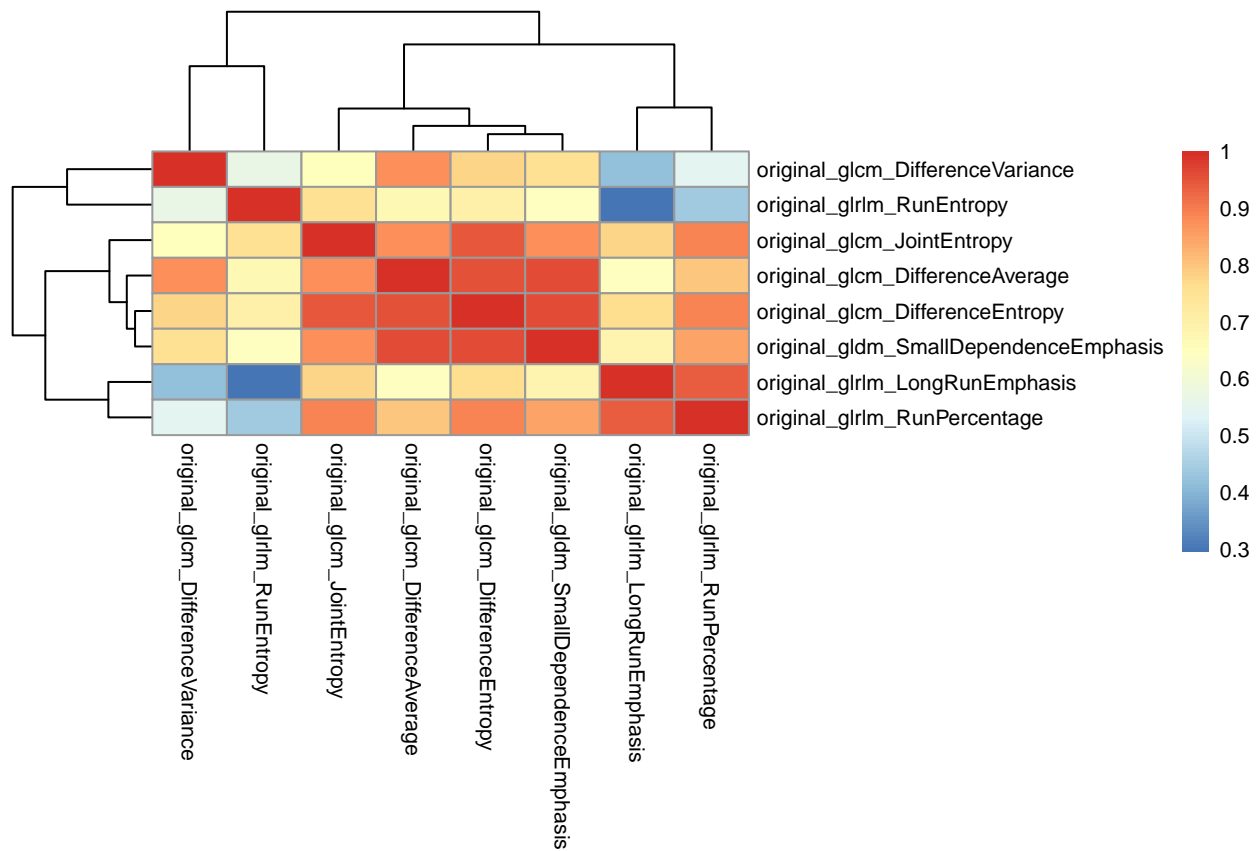
Radiomics

Loading Everything

Project Plan

What features to take?

- Not sure to take Zone Entropy or not
- Run Entropy and Zone Entropy do not follow the same patten on biplot



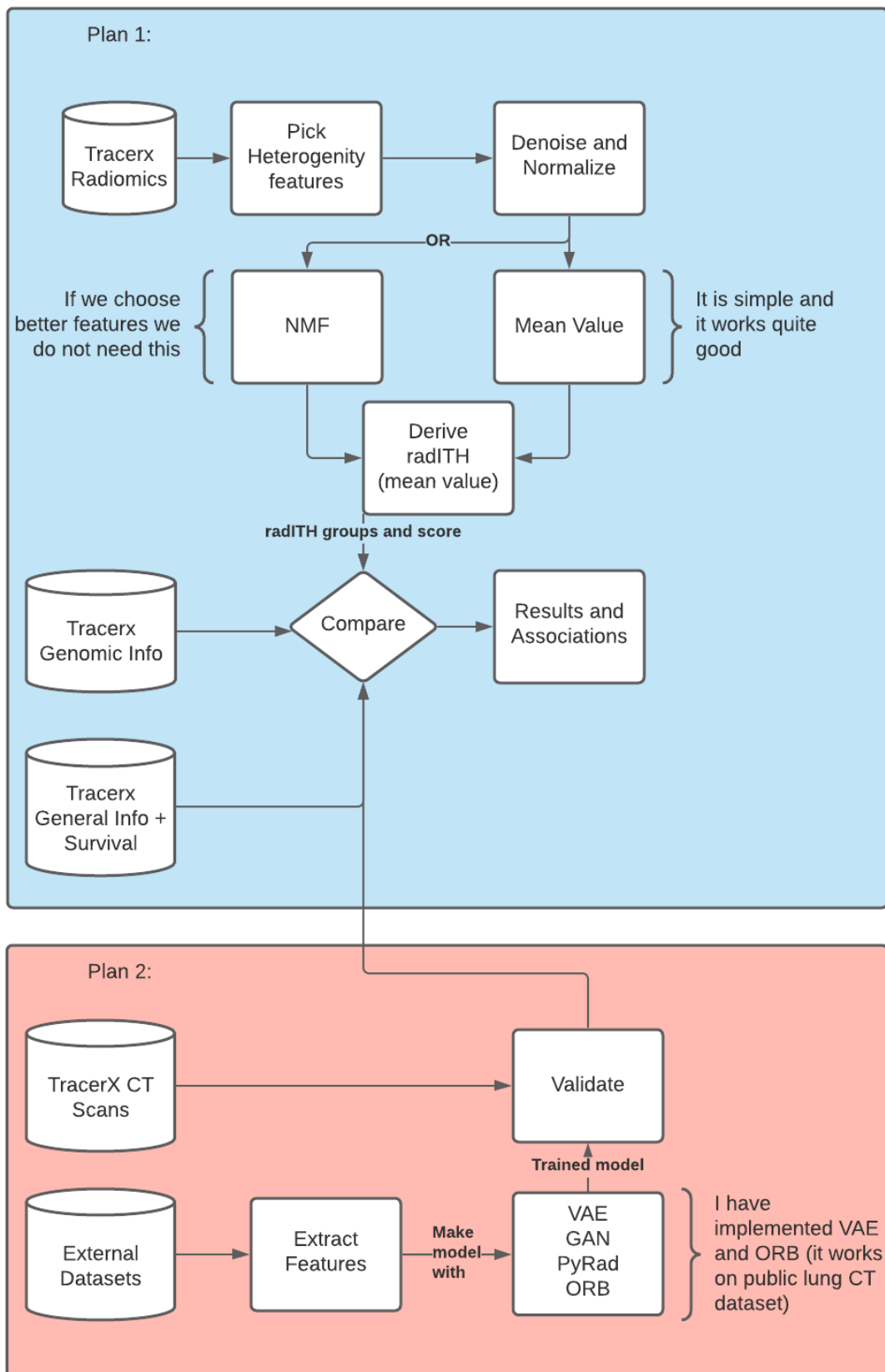
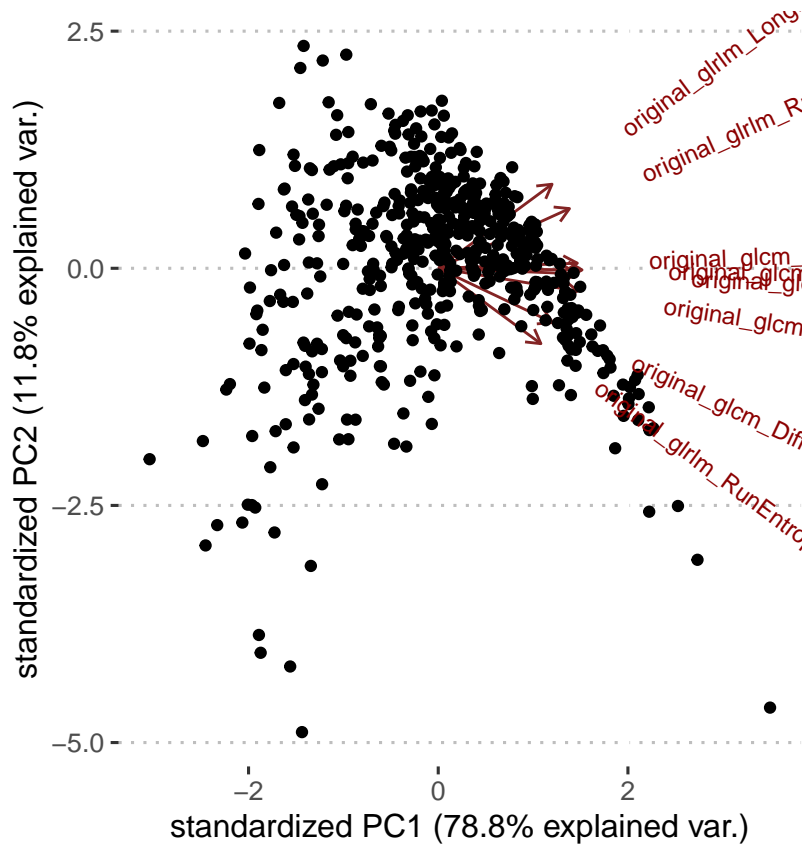


Figure 1: Project Plan



Important measures to check

- We will compare diameter to volume to ITH

```
pyrad$volume = as.numeric(pyrad$original_shape_MeshVolume)
pyrad$volume_from_pyrad = as.numeric(pyrad$original_shape_MeshVolume)
pyrad$diameter = as.numeric(pyrad$original_shape_Maximum2DDiameterSlice)
```

how to define radITH

- Do we need to normalize something by volume?
- Numbers were a bit wierd when divided by volume therefore I did not divide anything with volume

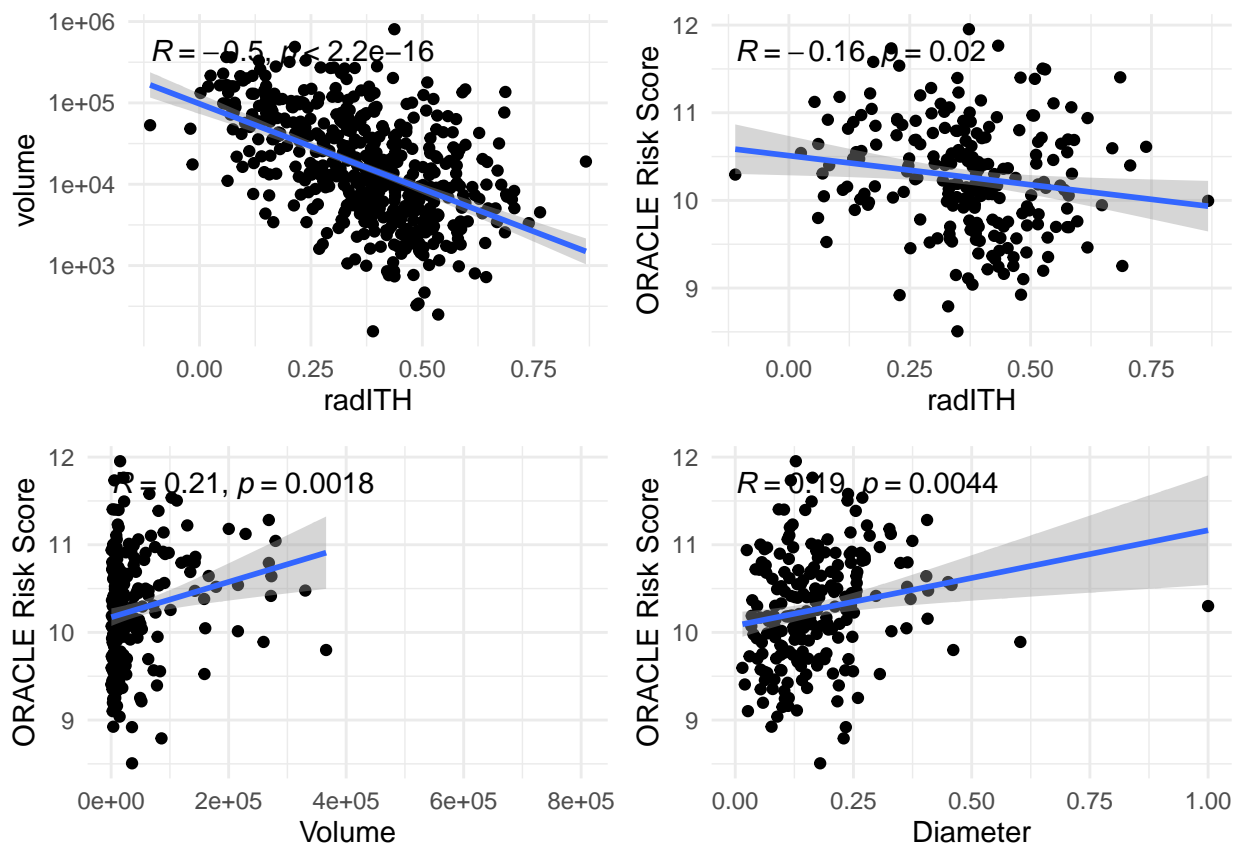
```
# weighted mean
# w = 1-abs(cor(pyrad[,features_of_interest], pyrad[, "volume"]))
# pyrad$radITH = apply(pyrad[,features_of_interest],1, function(x){
#   weighted.mean(x[features_of_interest], w = w)
# })
```

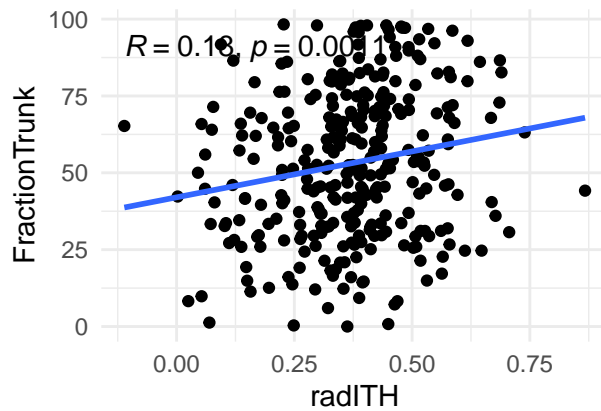
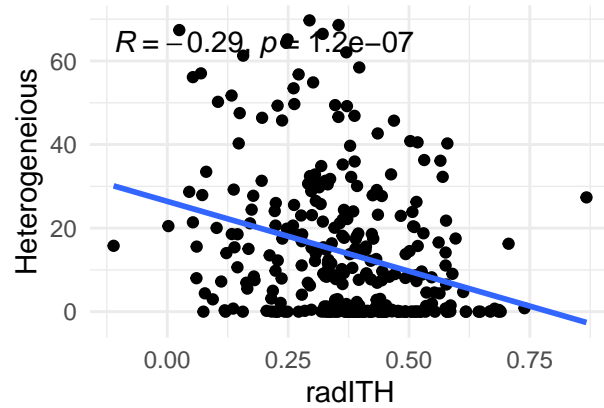
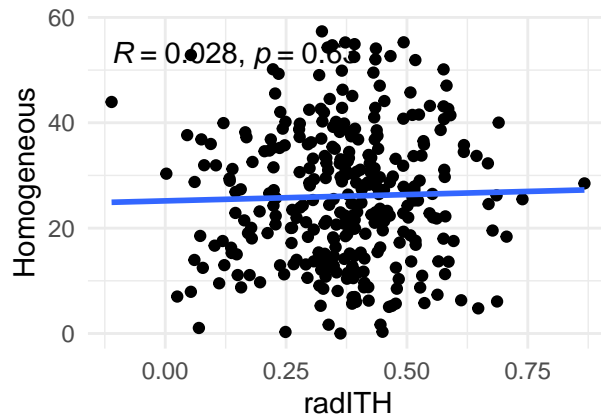
```
pyrad$radITH = rowMeans(pyrad[,features_of_interest], na.rm = T)
Q = 3

pyrad$volume_group = gtools::quantcut(pyrad$volume, q=Q, na.rm=TRUE)
pyrad$diameter_group = gtools::quantcut(pyrad$diameter, q=Q, na.rm=TRUE)
pyrad$radITH_group = gtools::quantcut(pyrad$radITH, q=Q, na.rm=TRUE)
```

Expected correlations

- Negative cor radITH to volume





Mutations

Let's group DRIVER mutations by Sanchez Vega def

Let's test Sanchez Vega Muts vs radITH groups (q =3)

```
## [1] "Adeno fisher test results"

## [1] "nrf2"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.03115
## alternative hypothesis: two.sided
##
## [1] "pi3k"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.01356
```

```

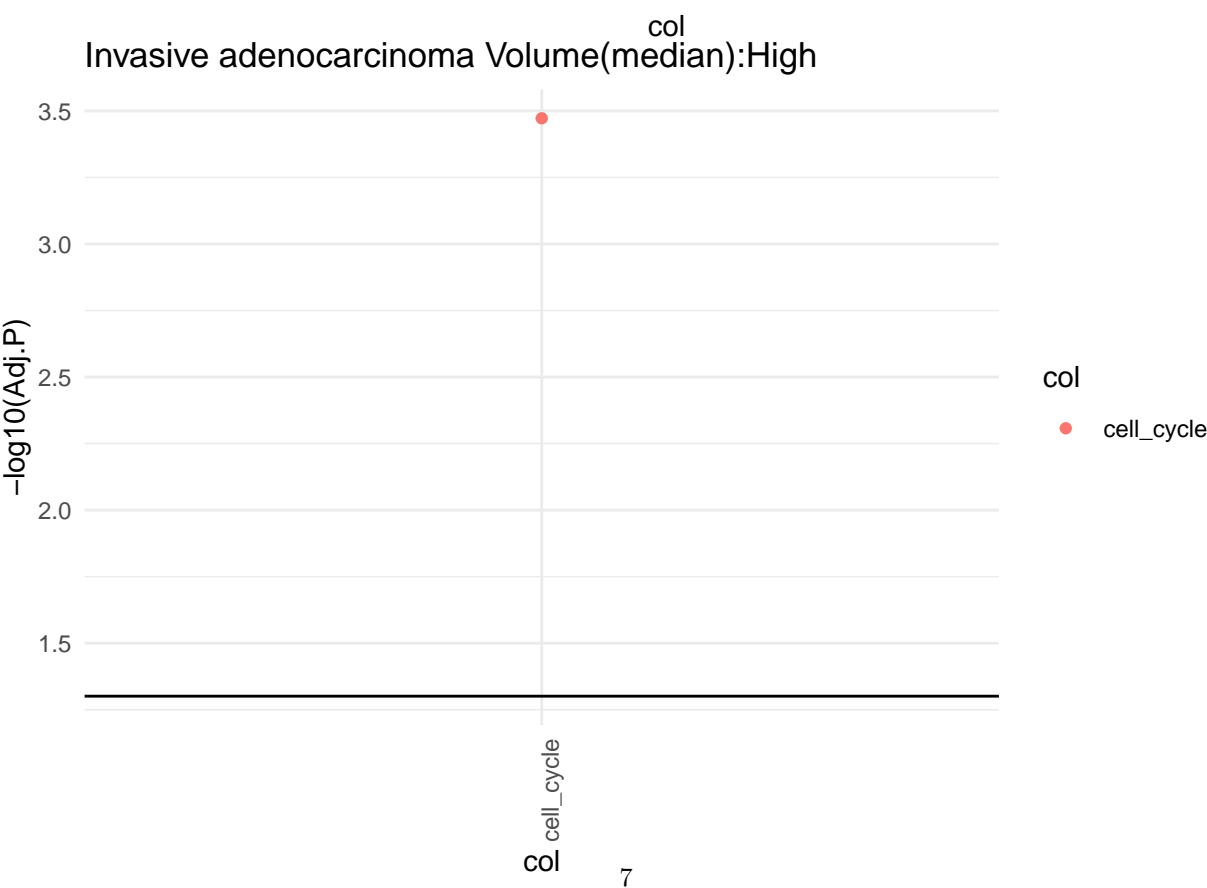
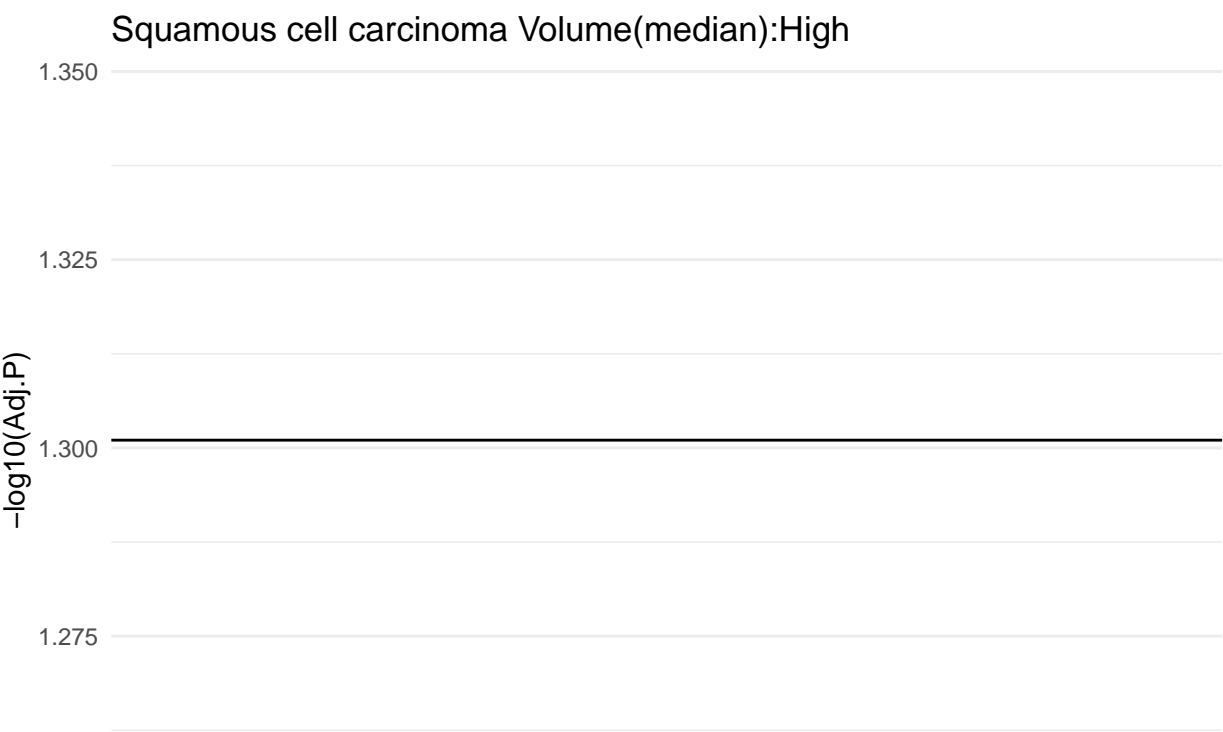
## alternative hypothesis: two.sided
##
## [1] "cell_cycle"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.000566
## alternative hypothesis: two.sided

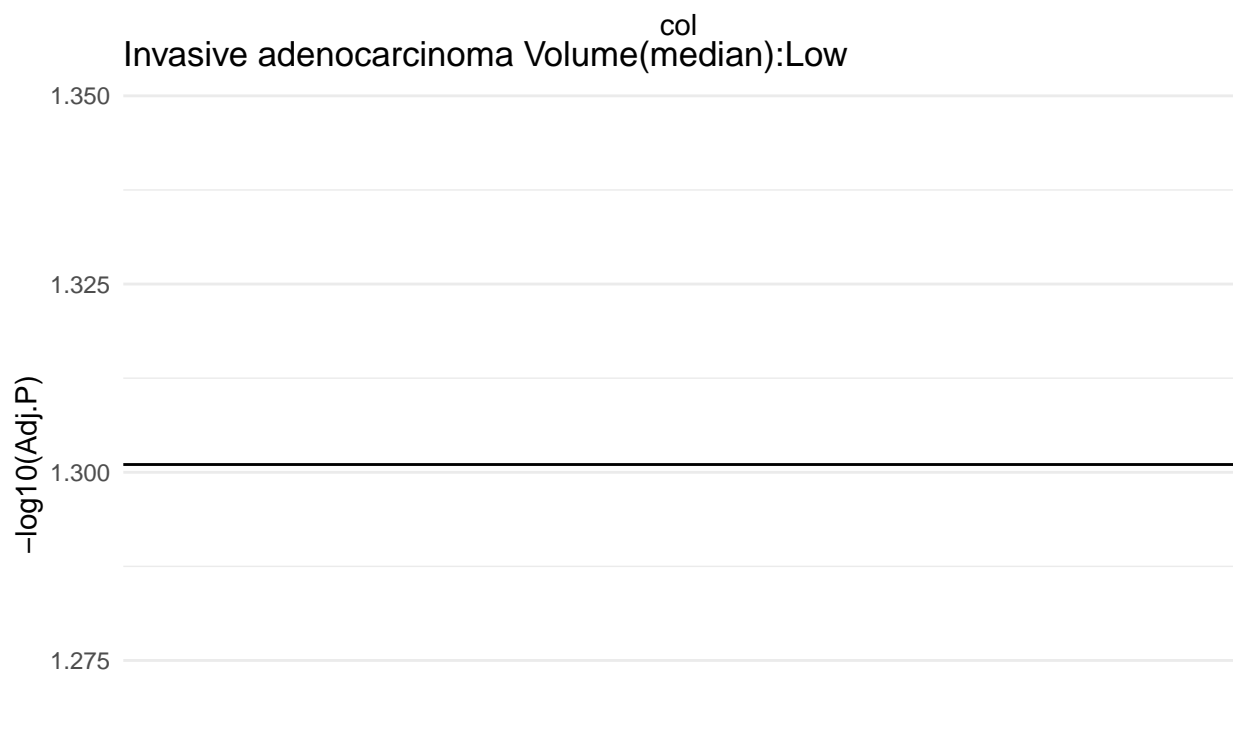
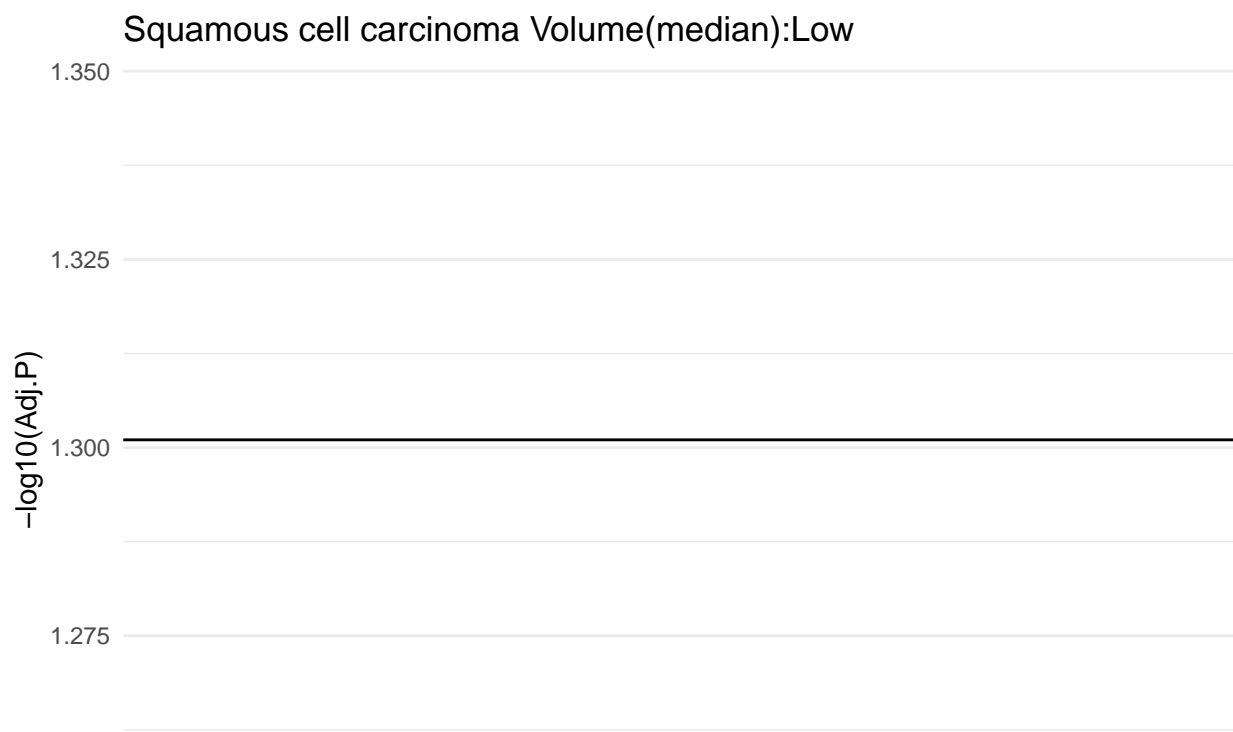
## [1] "Squamous fisher test results"

## [1] "rtk_kras"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.02937
## alternative hypothesis: two.sided
##
## [1] "pi3k"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.04171
## alternative hypothesis: two.sided

```

SanchezVega vs radITH groups (q = 3) vs pathology vs volume (Median)





col

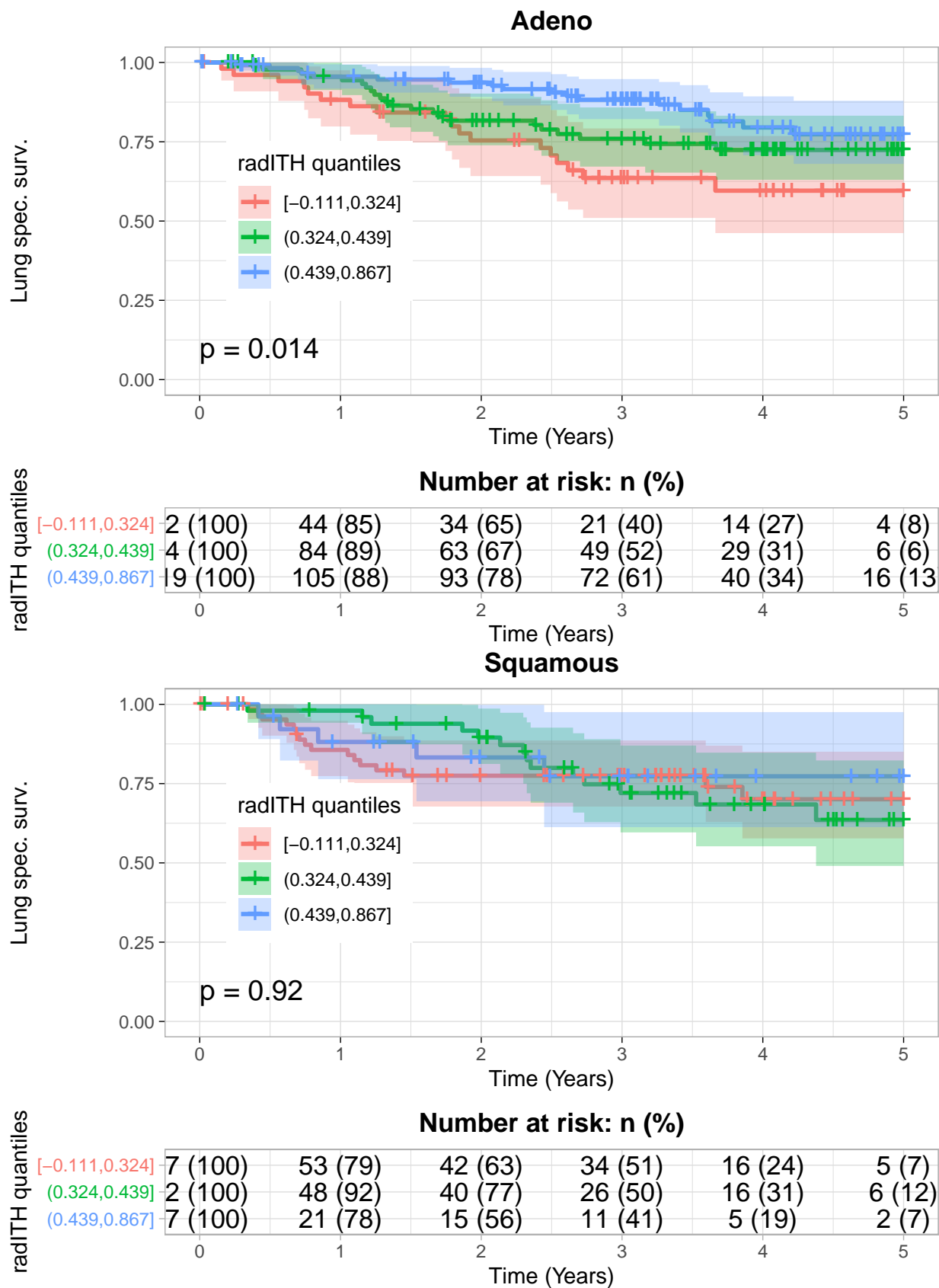
Does Volume or diameter predict biology?

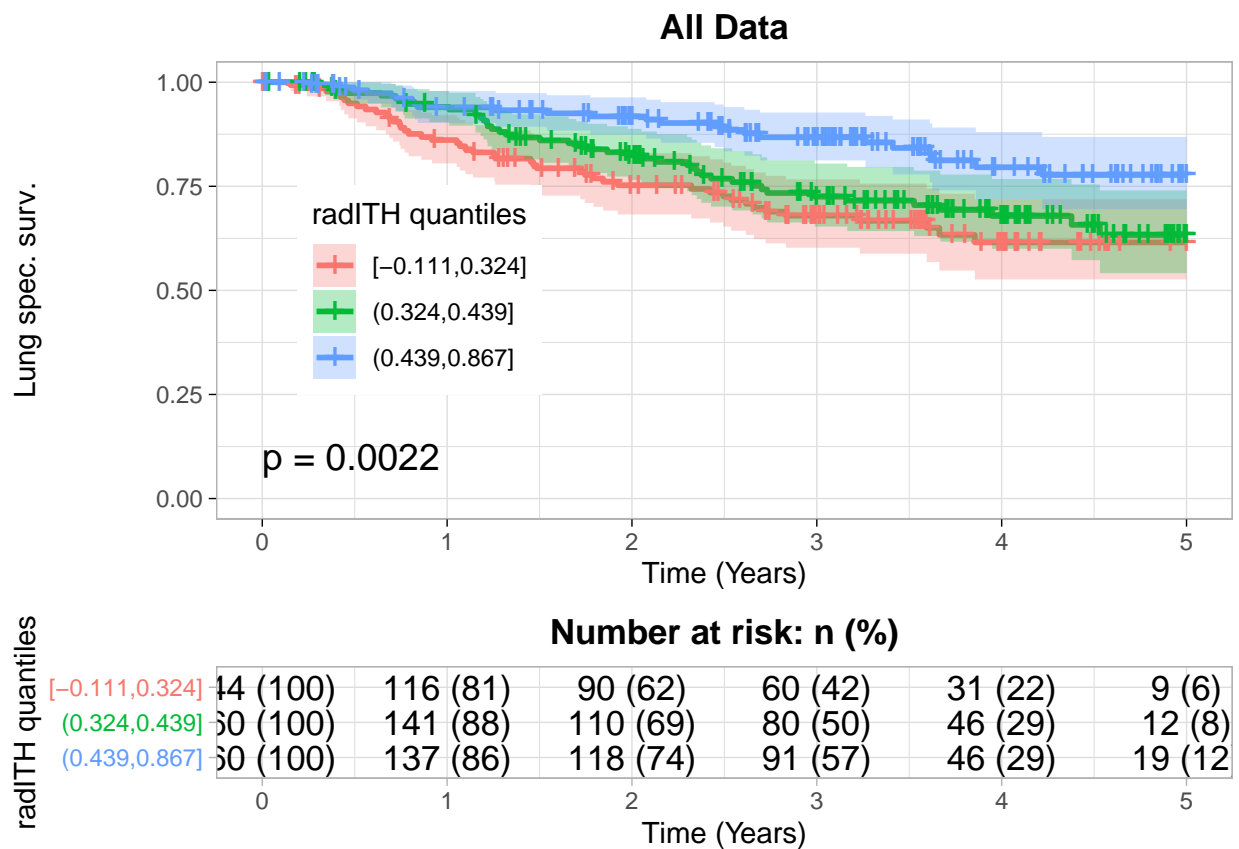
- Diameter is not associated at all
- Volume is associated with HIPPO

```
## [1] "Adeno fisher test results"
```

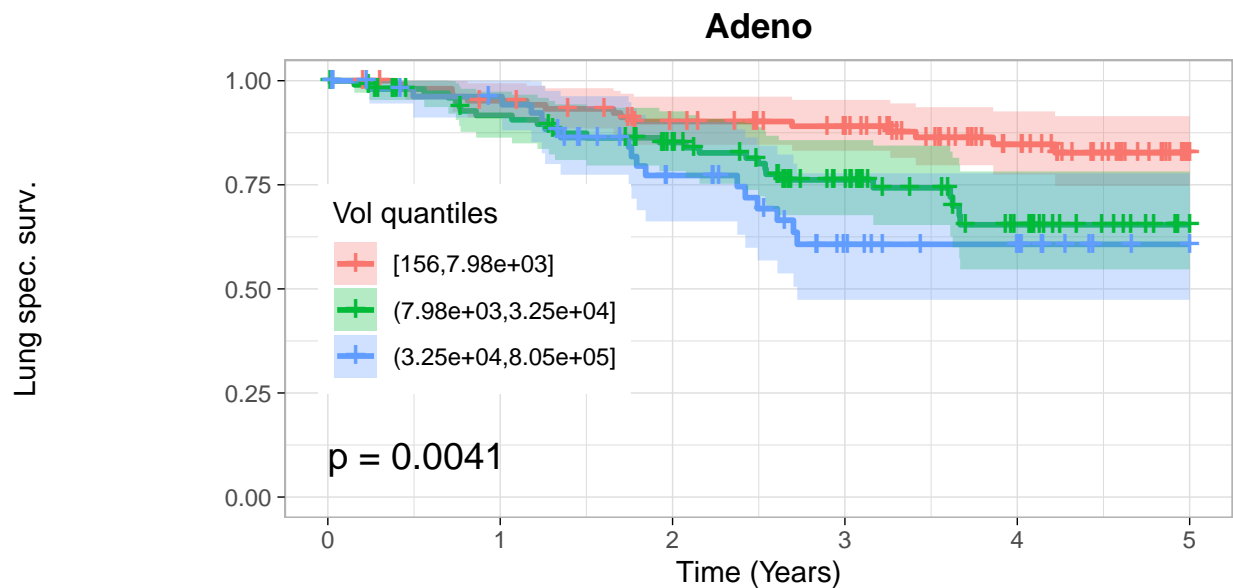
```
## [1] "Squamous fisher test results"
```

How does radITH associate with survival?





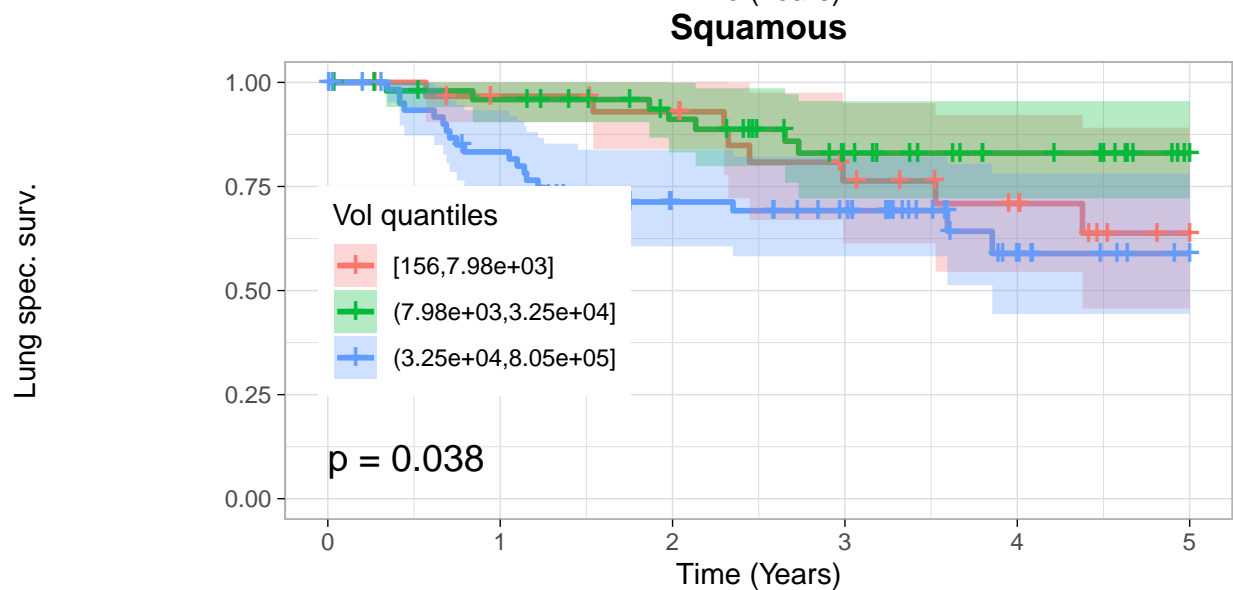
How does volume (diameter) associate to survival?



Number at risk: n (%)

| | | | | | | |
|---------------------|----------|---------|---------|---------|---------|---------|
| Vol quantiles | 0 | 1 | 2 | 3 | 4 | 5 |
| [156,7.98e+03] | 96 (100) | 98 (92) | 86 (81) | 76 (72) | 47 (44) | 17 (16) |
| (7.98e+03,3.25e+04] | 93 (100) | 86 (83) | 72 (70) | 49 (48) | 25 (24) | 6 (6) |
| (3.25e+04,8.05e+05] | 96 (100) | 49 (88) | 32 (57) | 17 (30) | 11 (20) | 3 (5) |

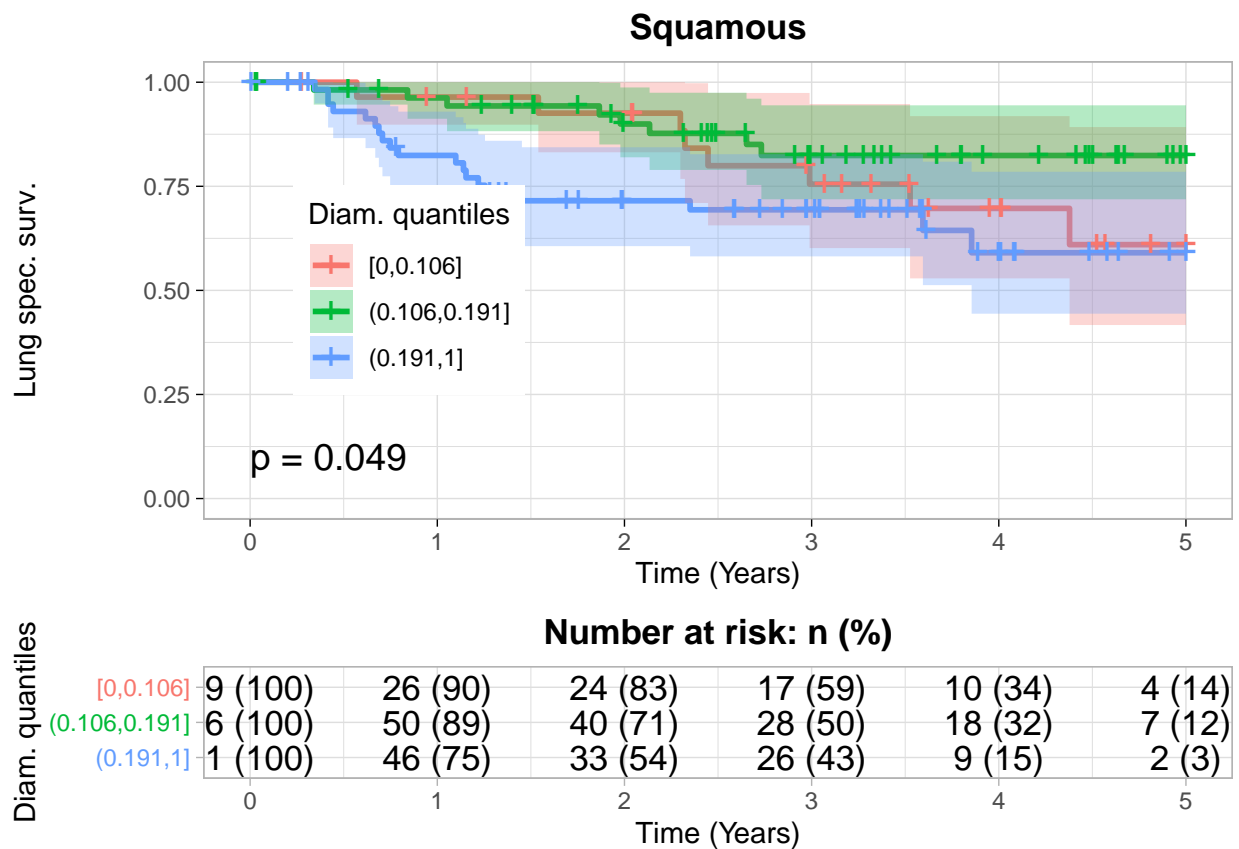
Time (Years)



Number at risk: n (%)

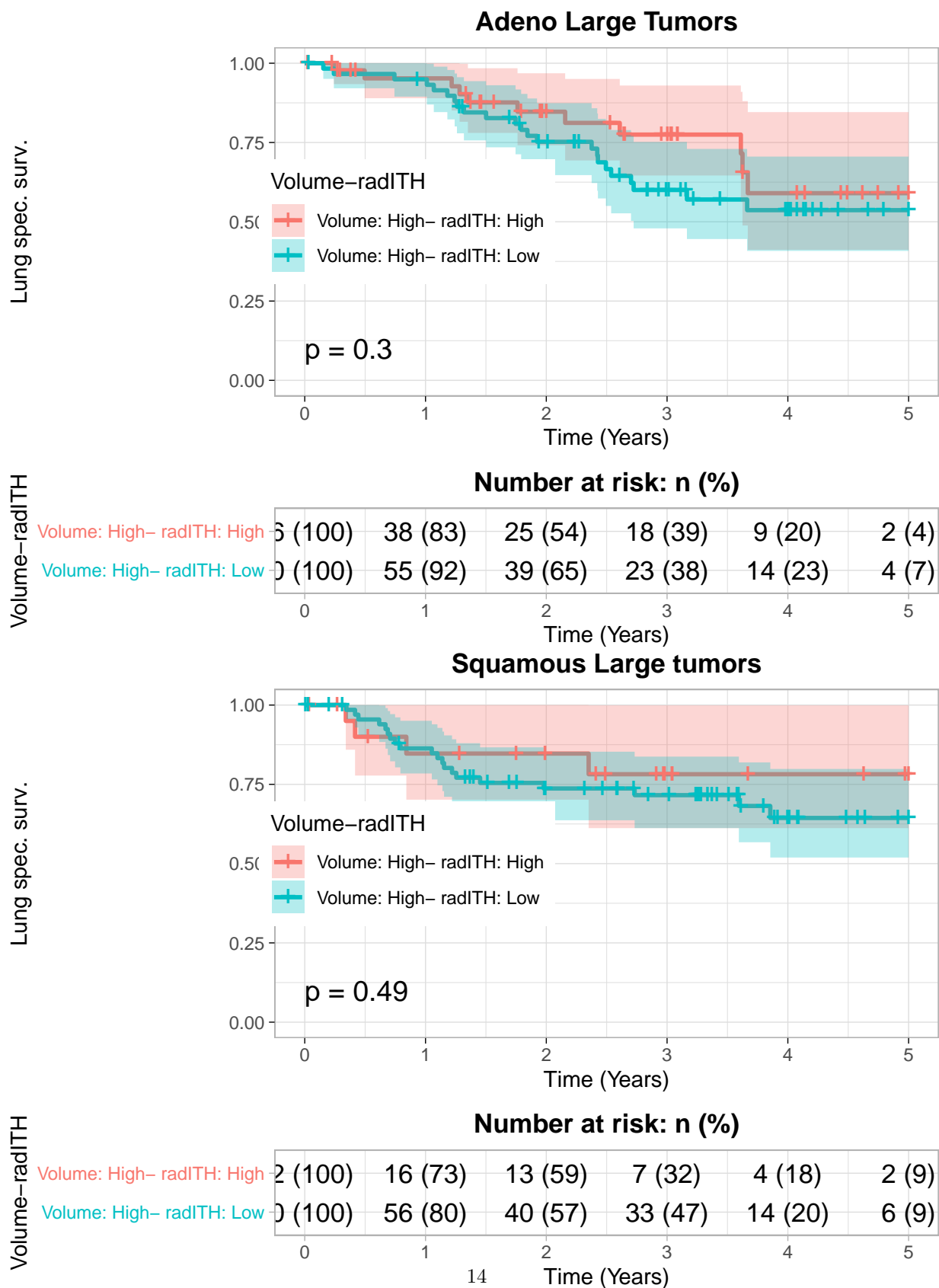
| | | | | | | |
|---------------------|---------|---------|---------|---------|---------|--------|
| Vol quantiles | 0 | 1 | 2 | 3 | 4 | 5 |
| [156,7.98e+03] | 1 (100) | 27 (87) | 25 (81) | 17 (55) | 12 (39) | 5 (16) |
| (7.98e+03,3.25e+04] | 1 (100) | 46 (90) | 38 (75) | 26 (51) | 17 (33) | 7 (14) |
| (3.25e+04,8.05e+05] | 4 (100) | 49 (77) | 34 (53) | 28 (44) | 8 (12) | 1 (2) |

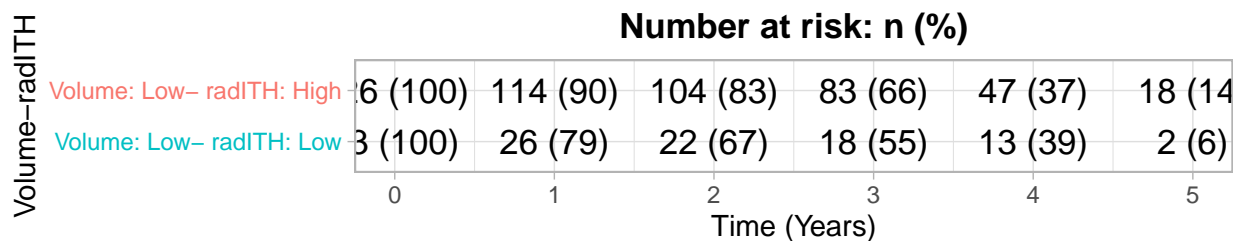
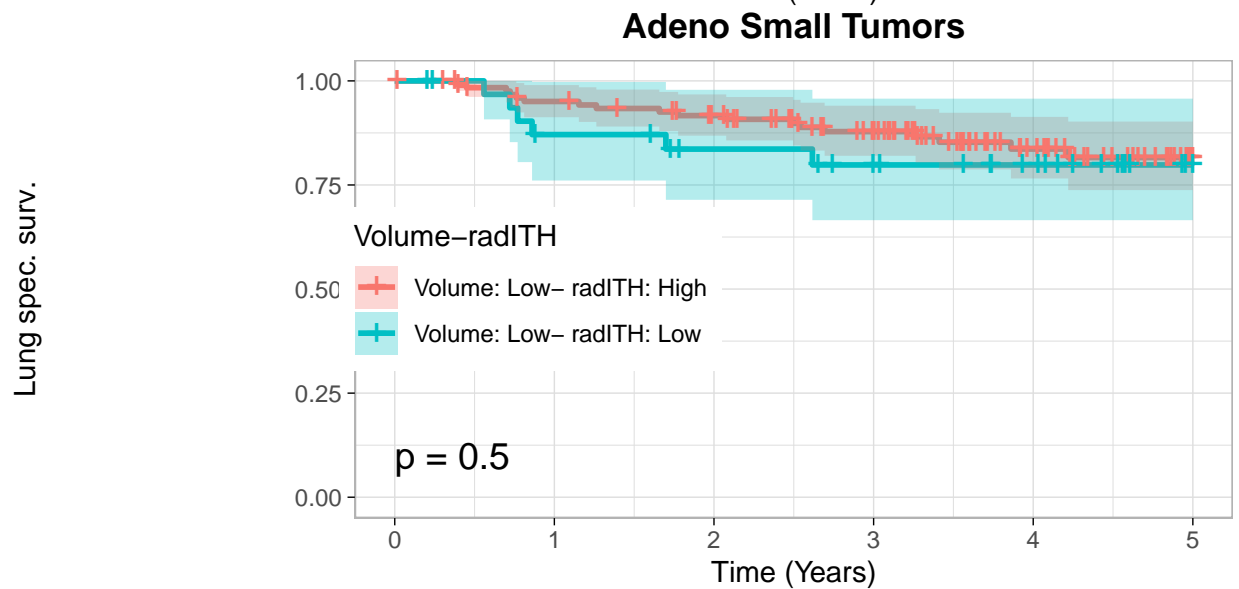
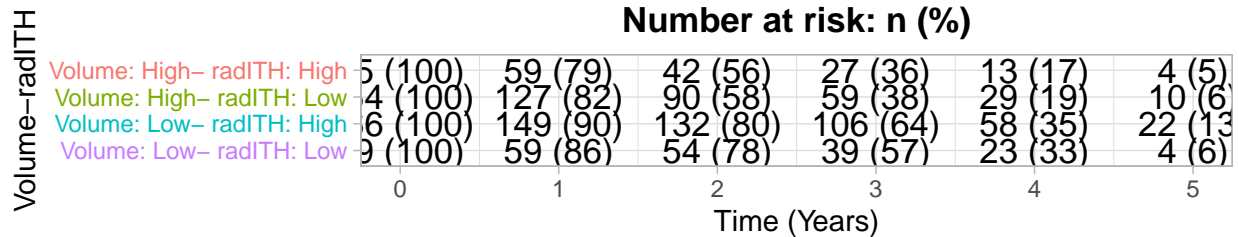
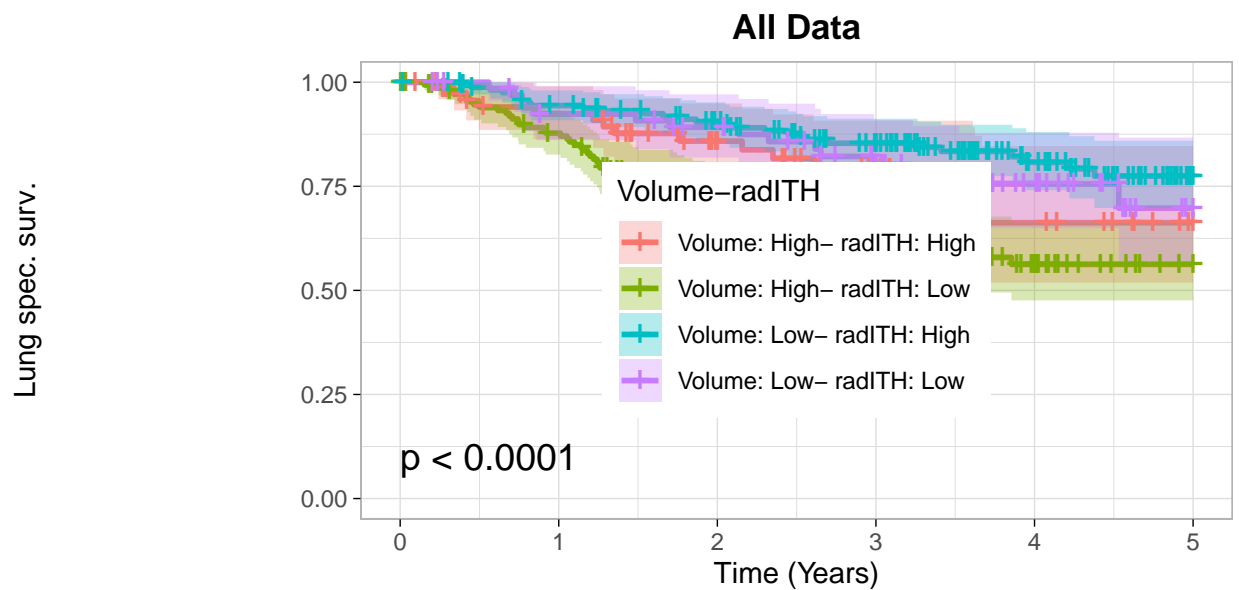
Time (Years)

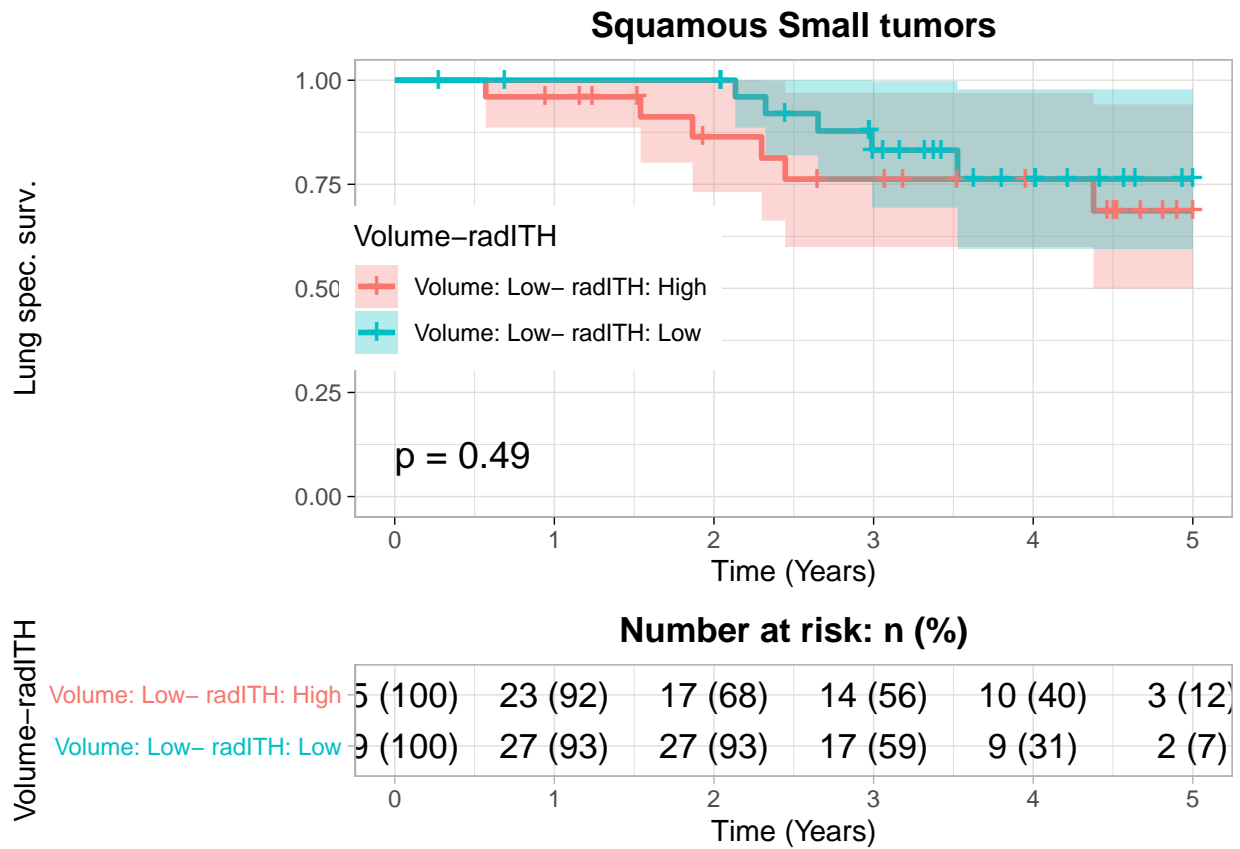


Can we overlap radITH and Volume groups and check survival?

In order to increase group sizes, all measures will be split by median (Q=2)

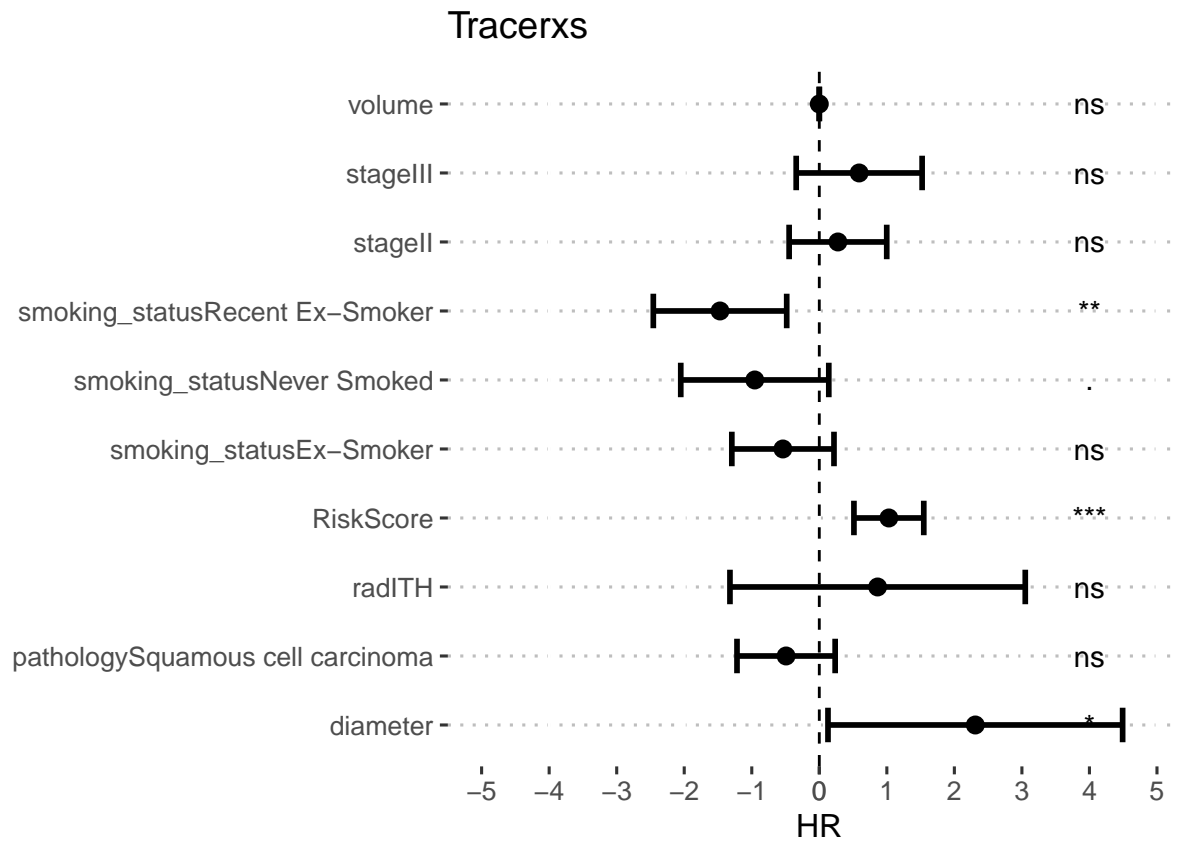






Coxph Model

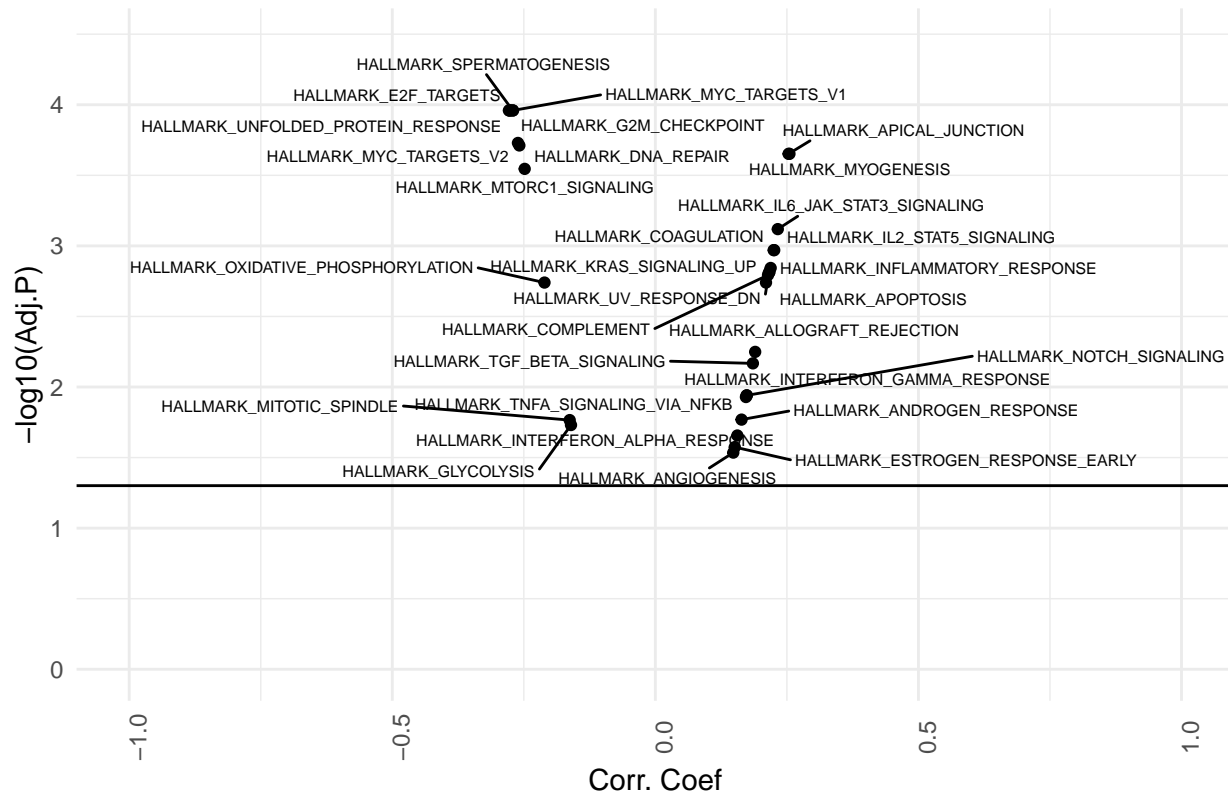
- radlTH does not help improve cox ph model



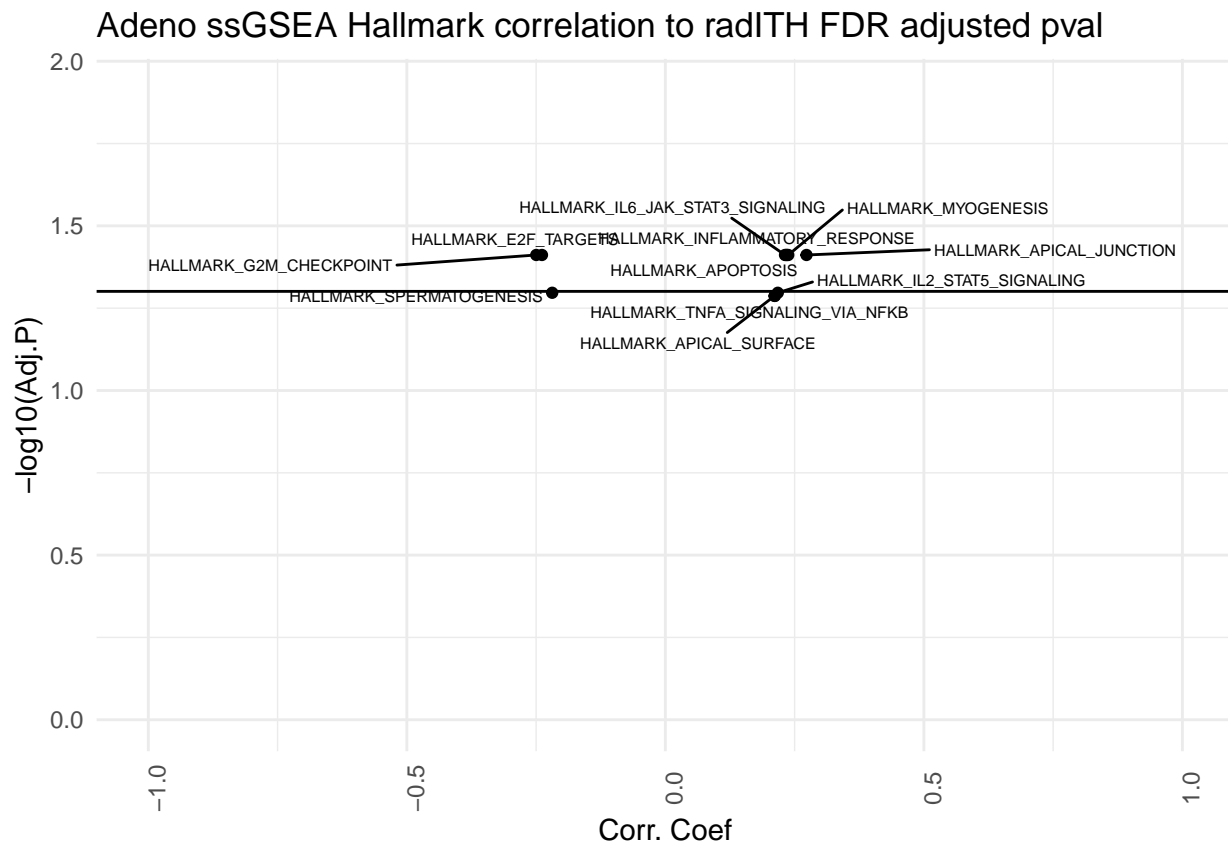
Hallmarks all samples

- Association (cor) of radITH with hallmarks
- Hallmarks computed with SS-GSEA
- P values are adjusted using FDR

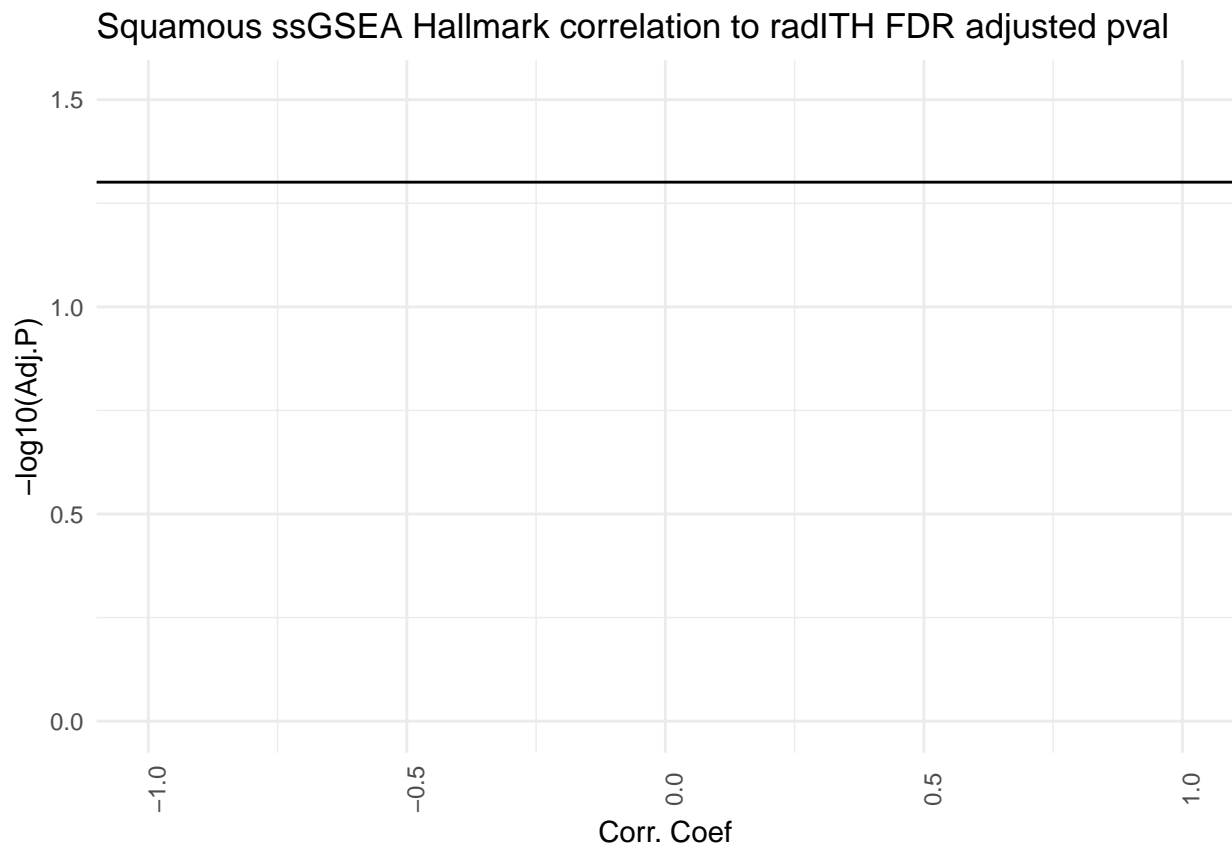
All samples ssGSEA Hallmark correlation to radlTH FDR adjusted pval



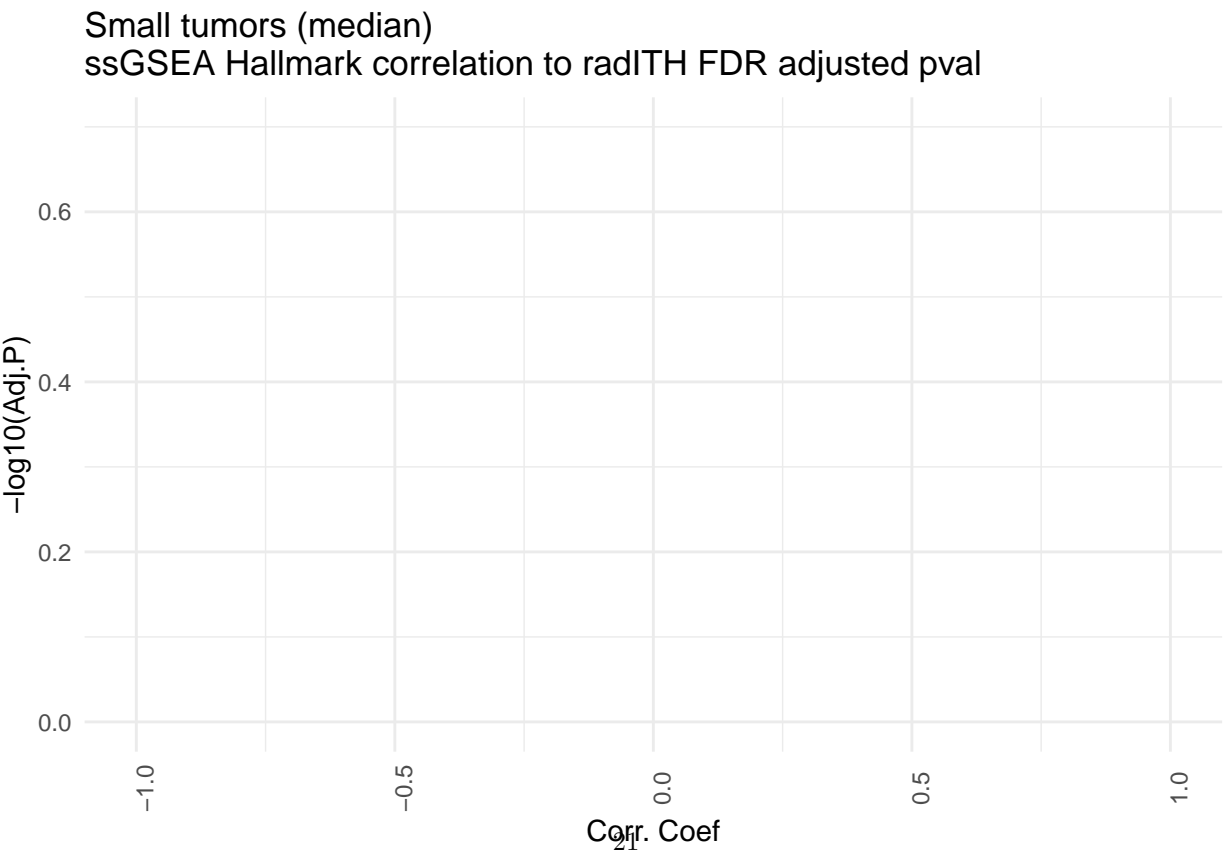
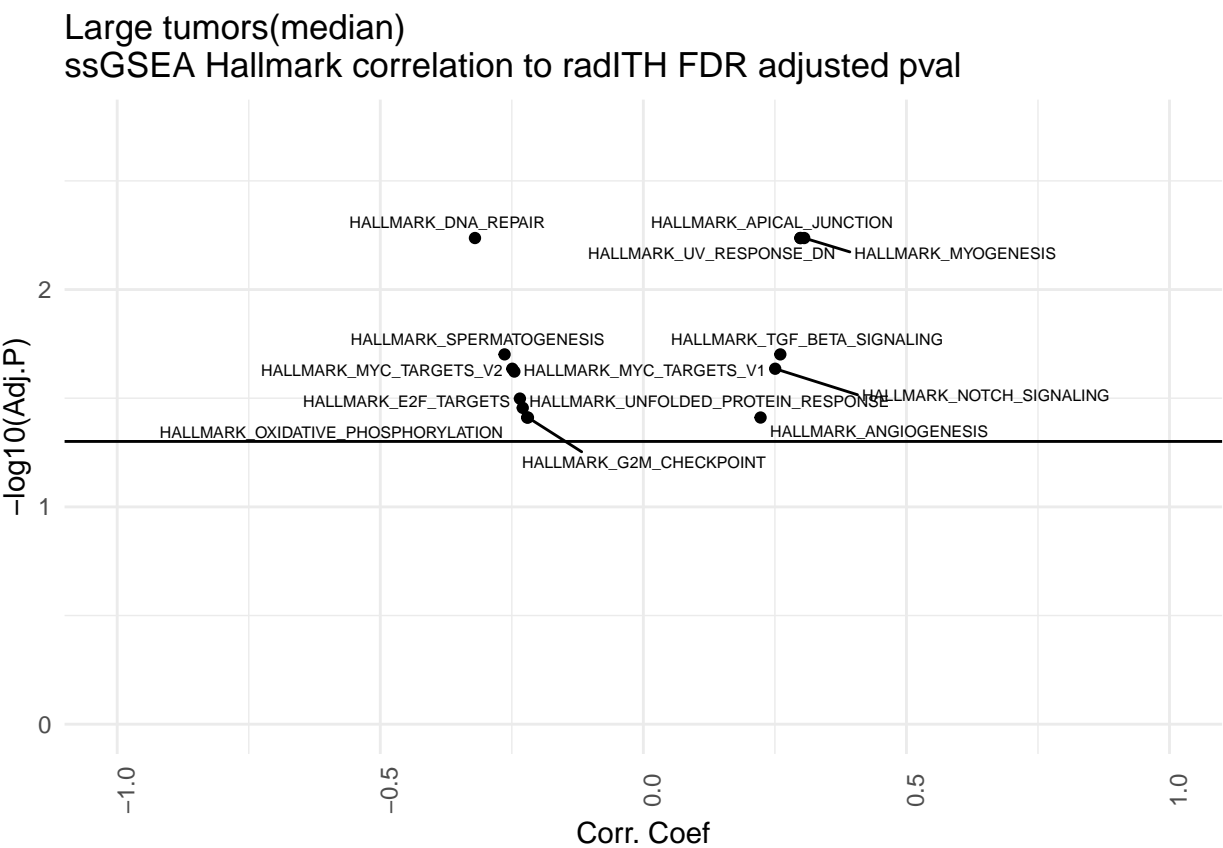
Hallmarks Adeno



Hallmarks Squamous

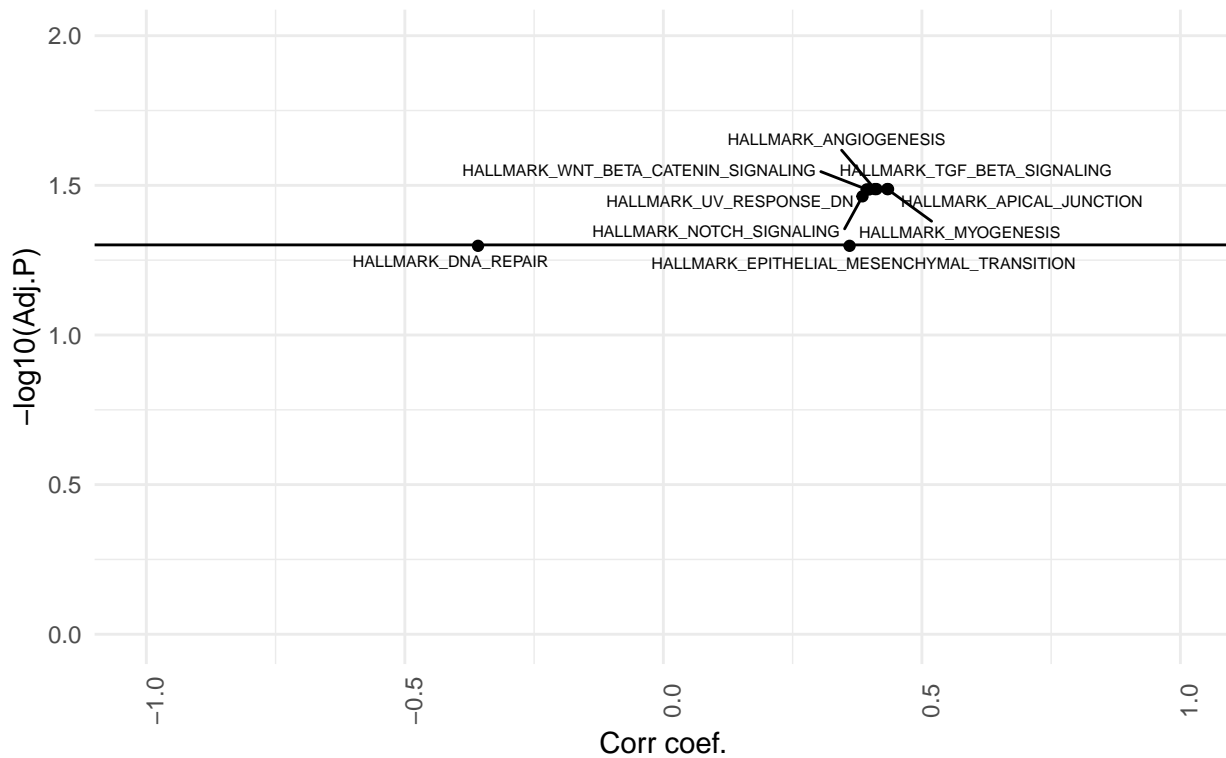


Hallmark expression-radITH Correlation in Large vs Small tumors (all samples)

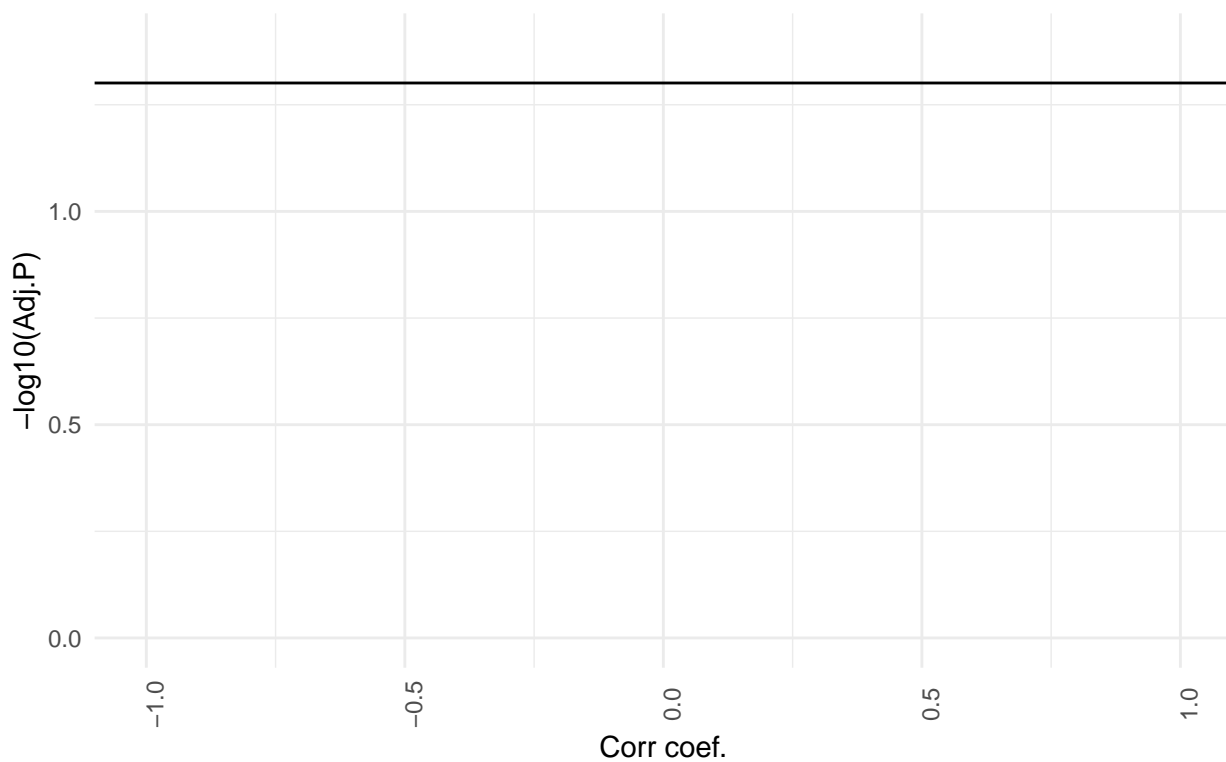


Let's split by Size and Pathology and repeat

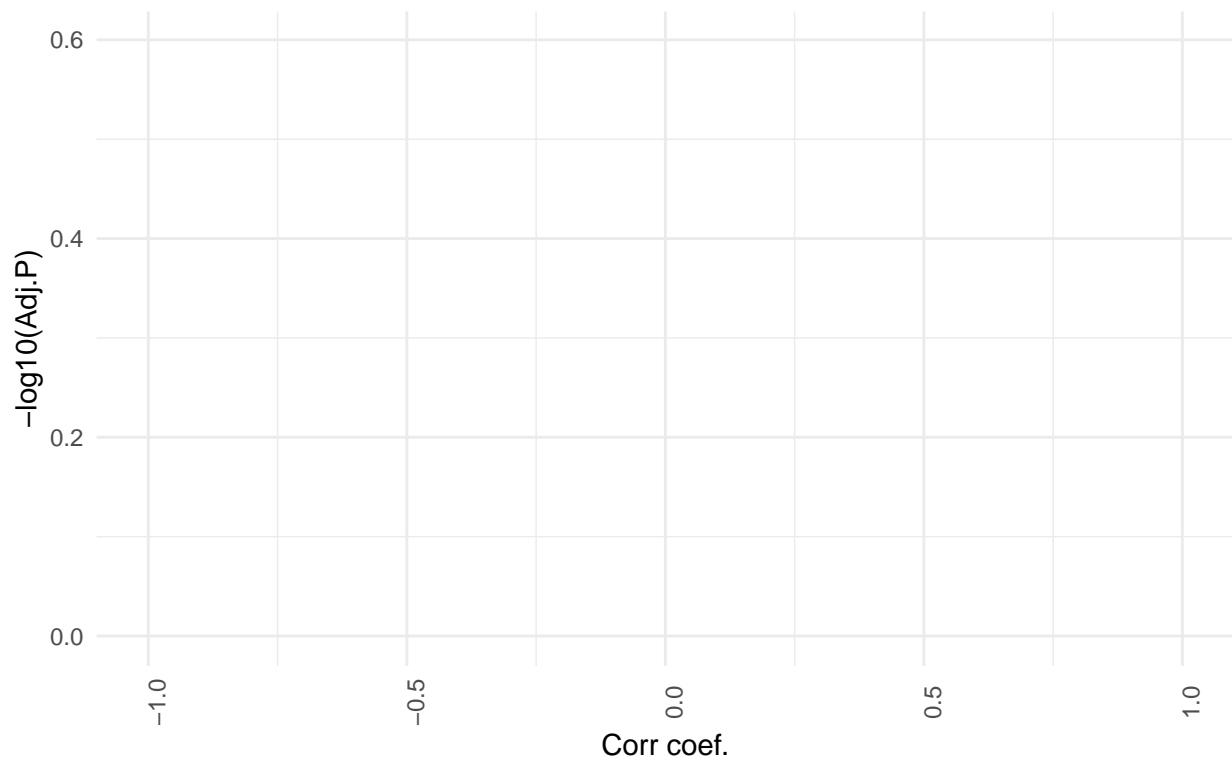
Squamous cell carcinoma Volume(median): High
ssGSEA Hallmark correlation to radITH FDR adjusted pval



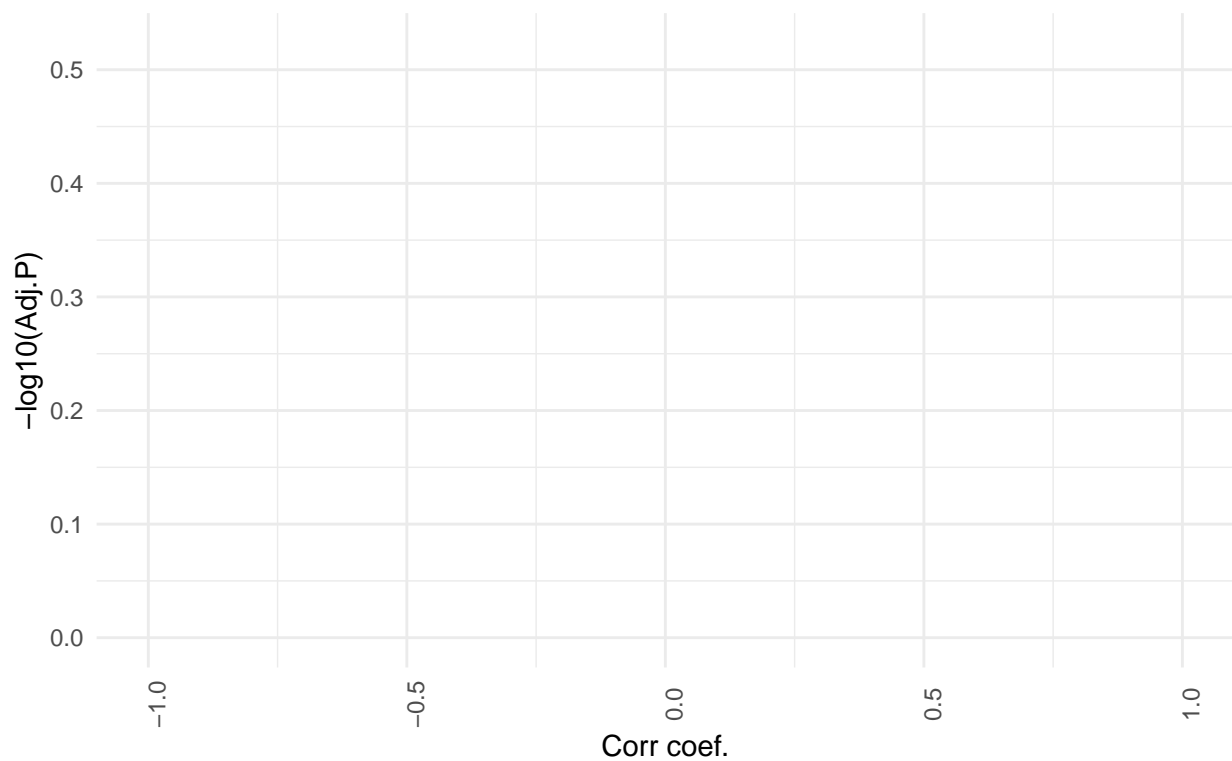
Invasive adenocarcinoma Volume(median): High
ssGSEA Hallmark correlation to radITH FDR adjusted pval



Squamous cell carcinoma Volume(median): Low
ssGSEA Hallmark correlation to radlTH FDR adjusted pval

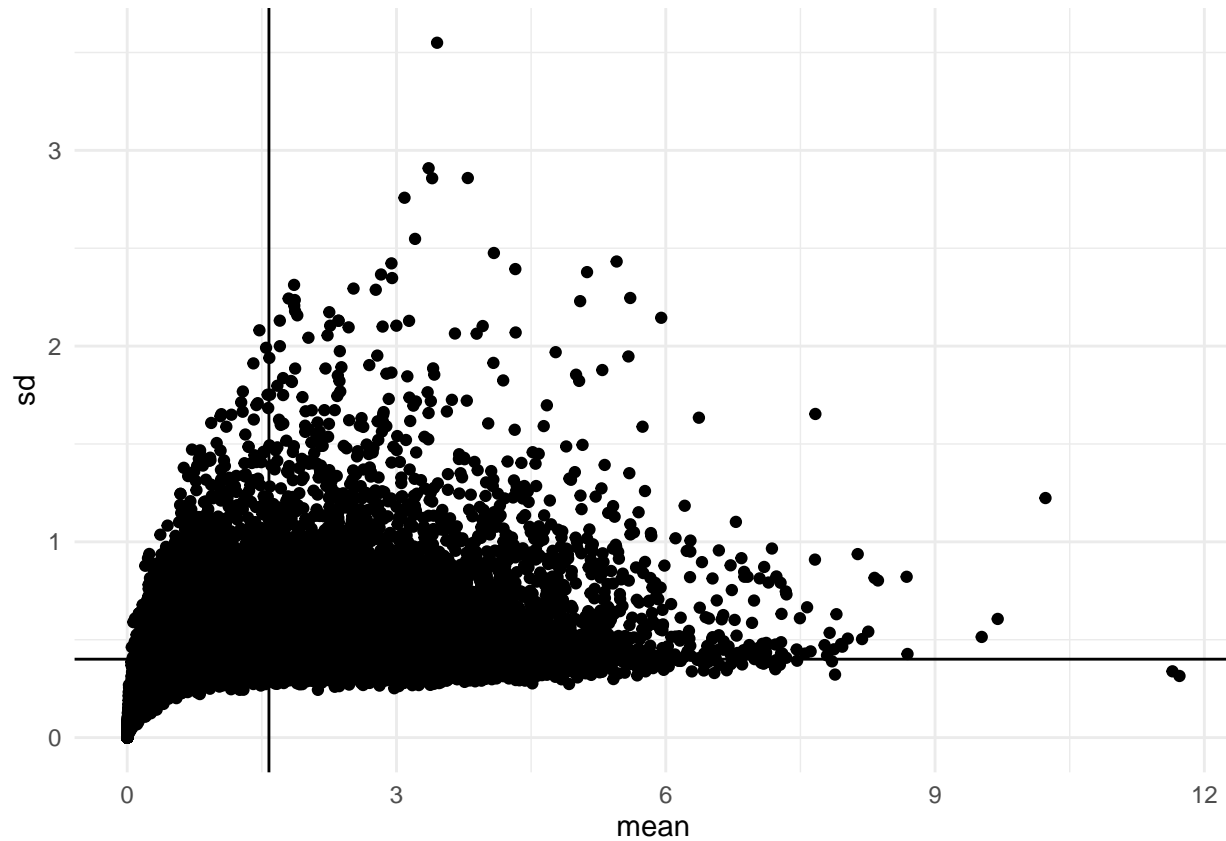


Invasive adenocarcinoma Volume(median): Low
ssGSEA Hallmark correlation to radlTH FDR adjusted pval



Picking genes for Gene Expression Analysis

- Mean and SD value based on entire cohort



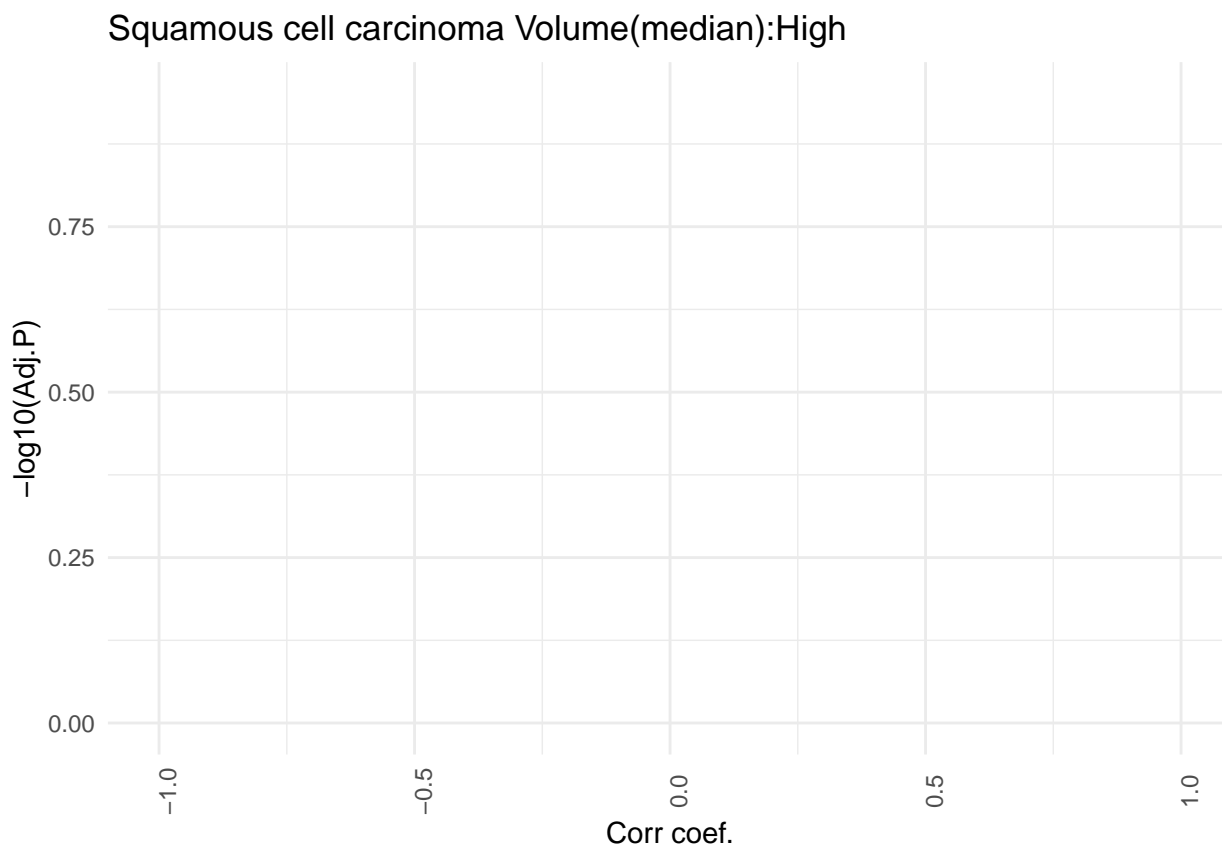
Number of Genes after cutoff: 10332

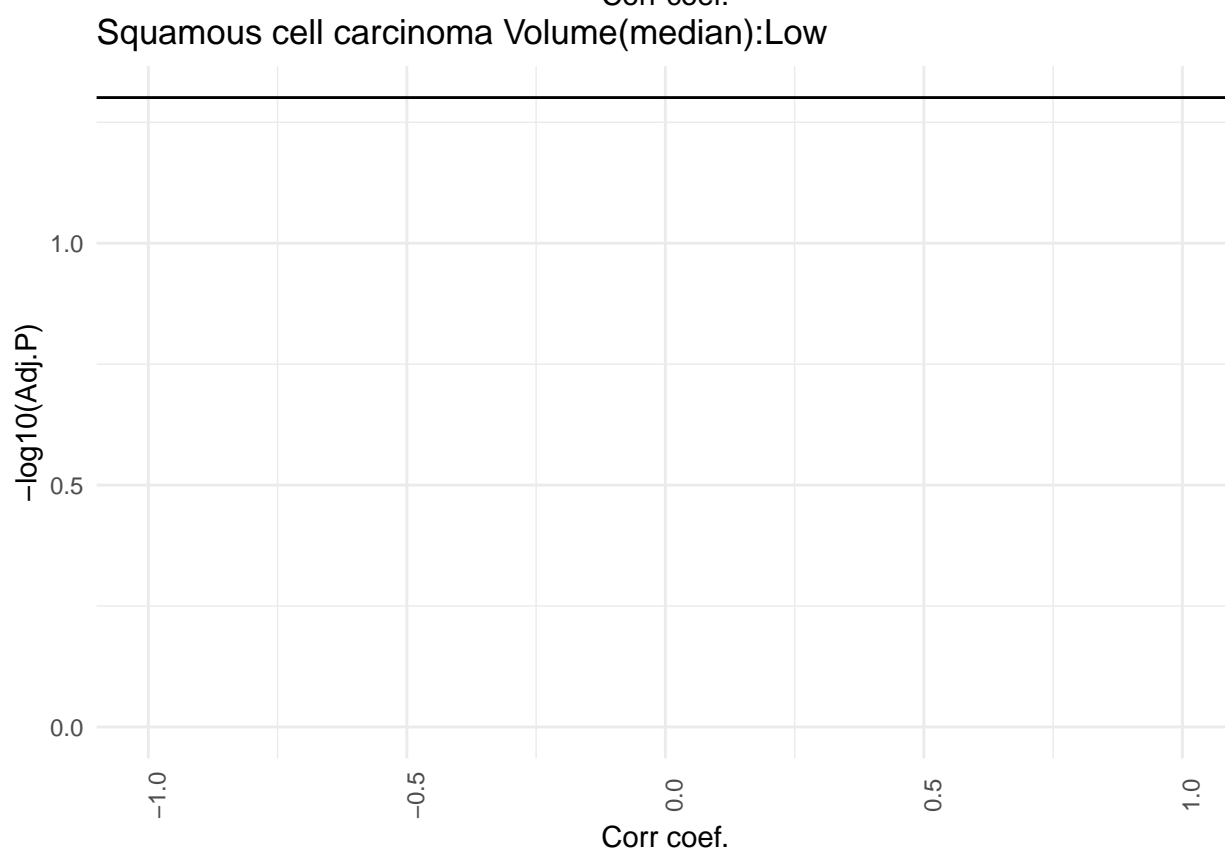
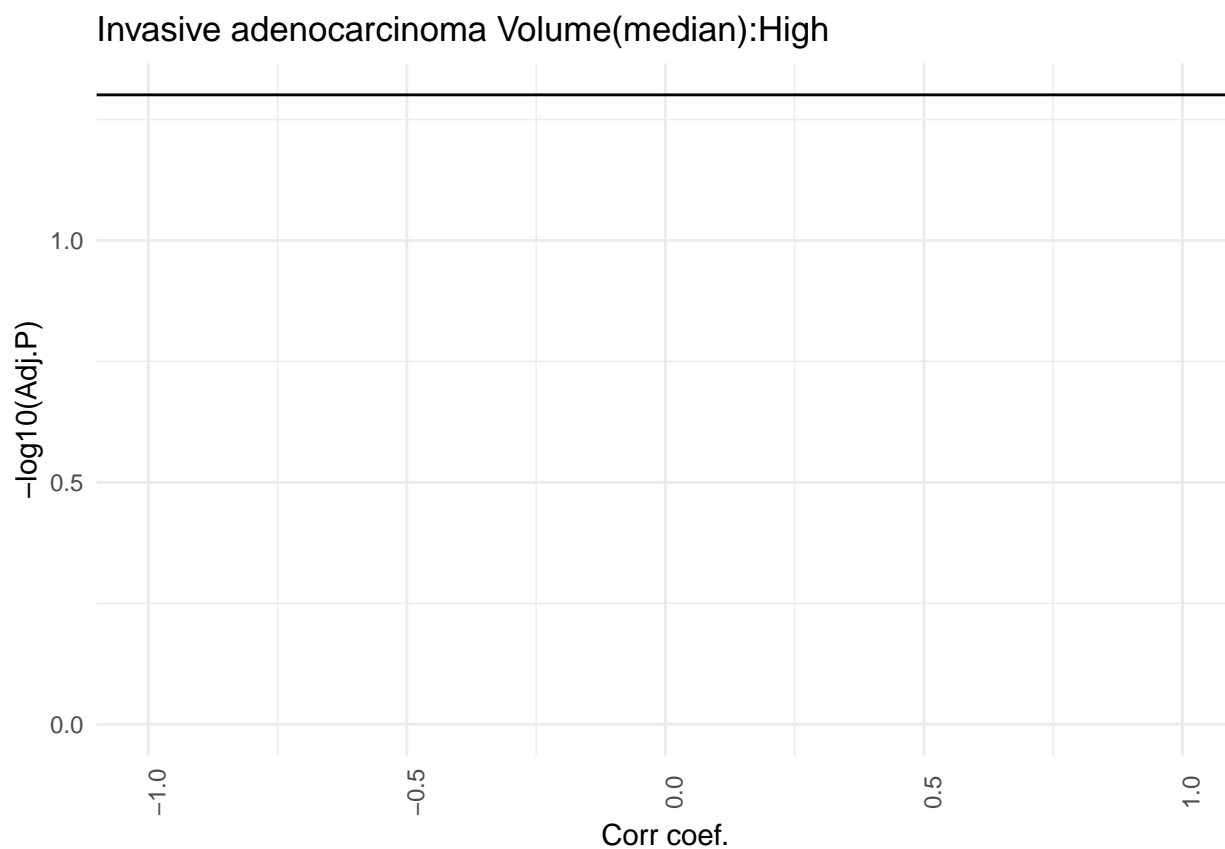
Gene Expression Analysis without volume

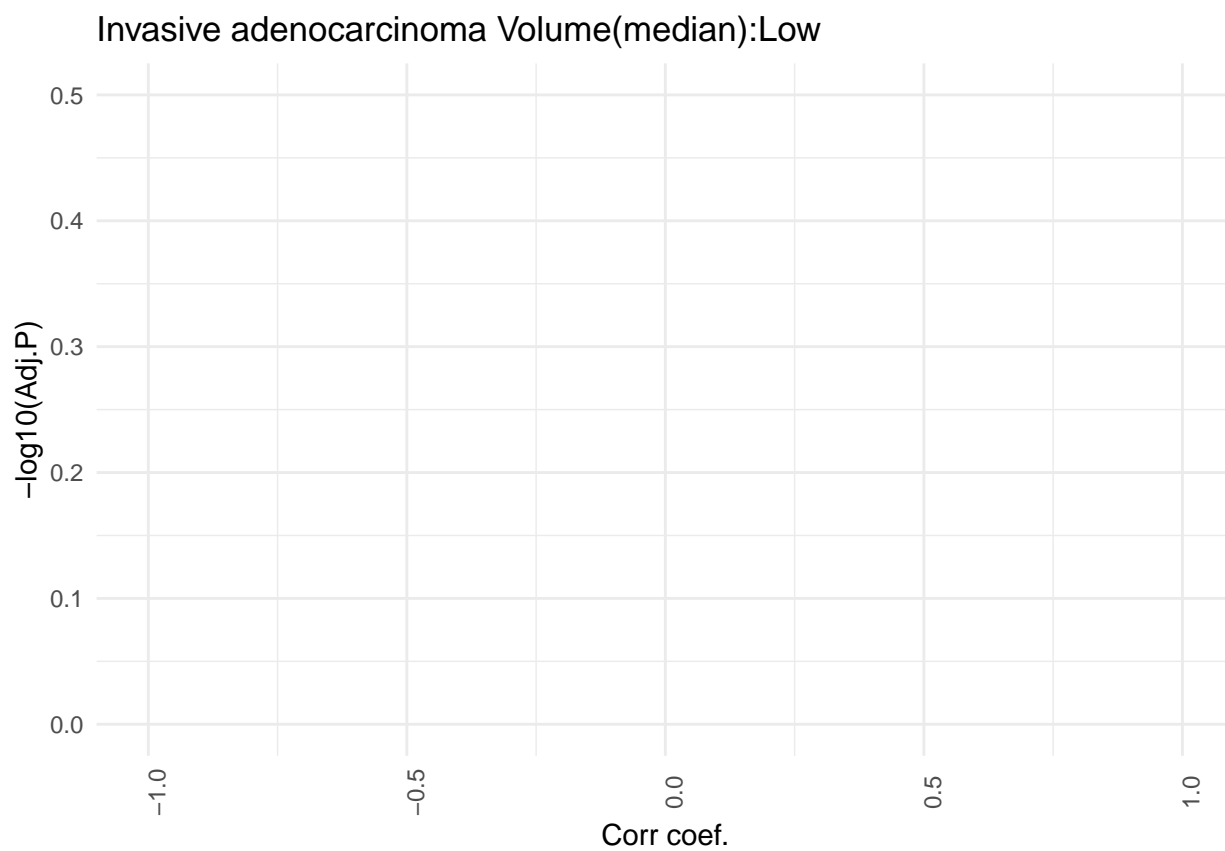
- Genes that were picked for analysis were based on mean and SD (entire cohort)

Gene Expression Analysis by volume group and cancer type

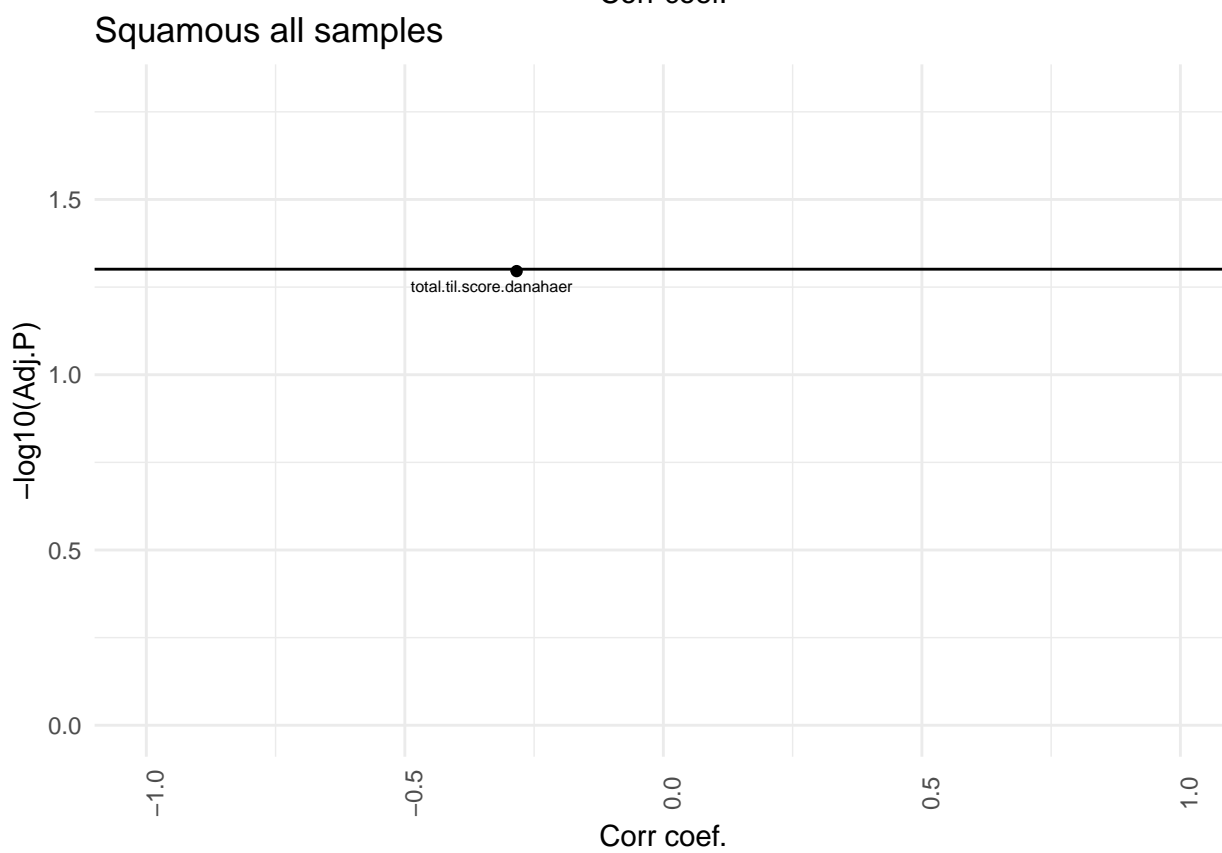
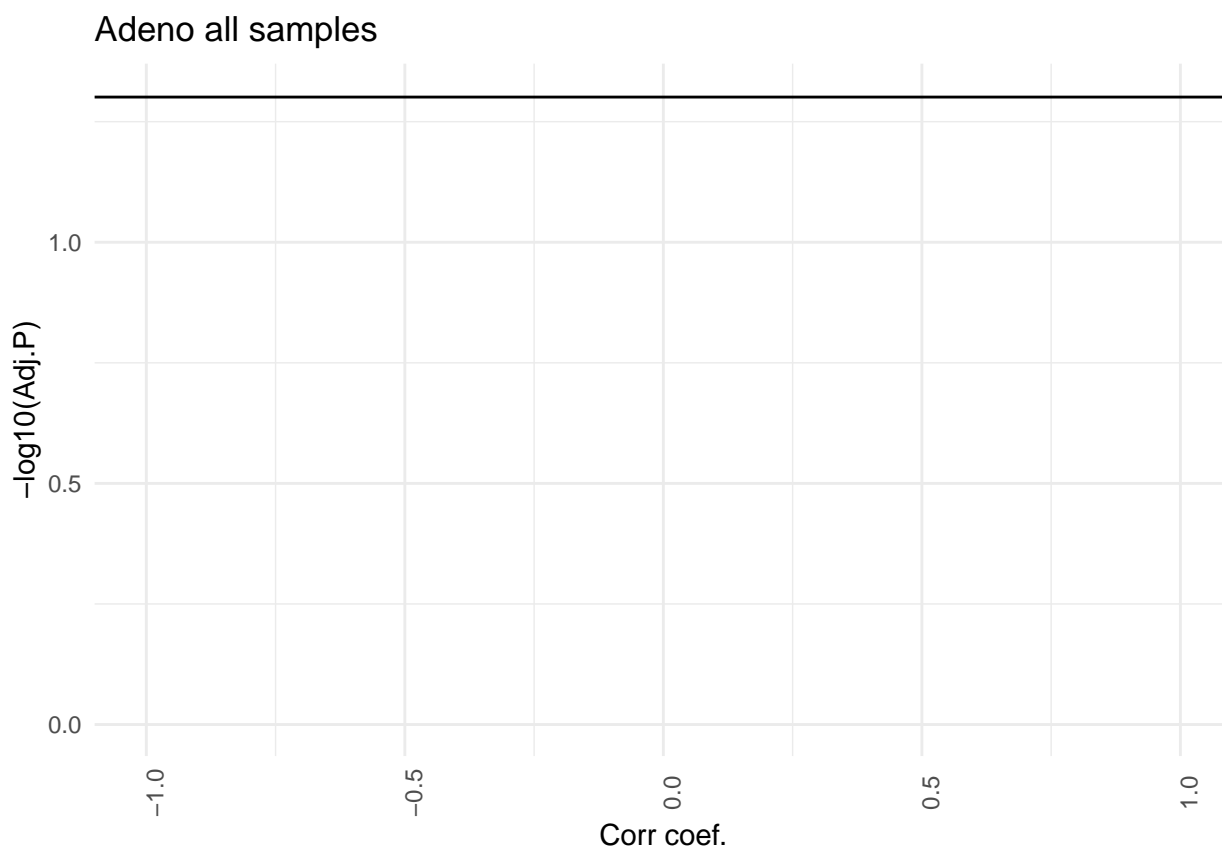
- Genes that were picked for analysis were based on mean and SD (entire cohort)



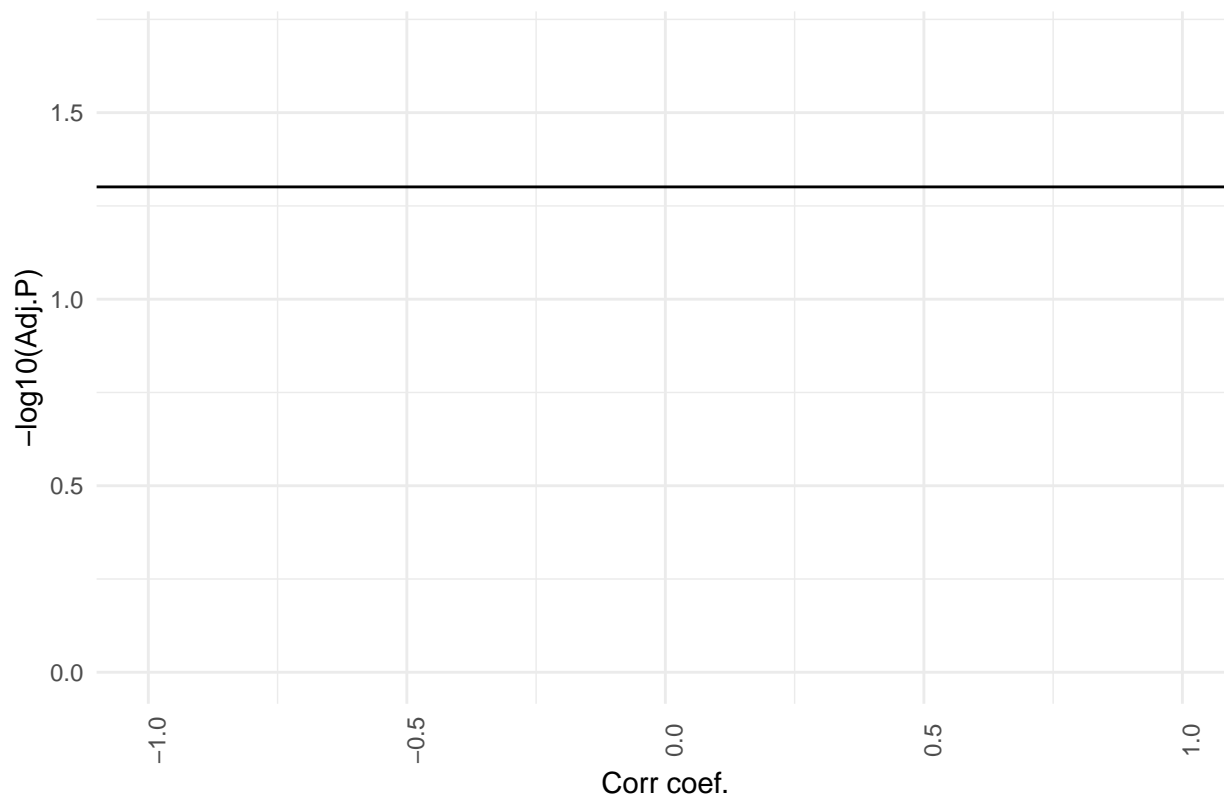




Chr Instability and TIL



Squamous cell carcinoma Volume(median):High



Invasive adenocarcinoma Volume(median):High

