

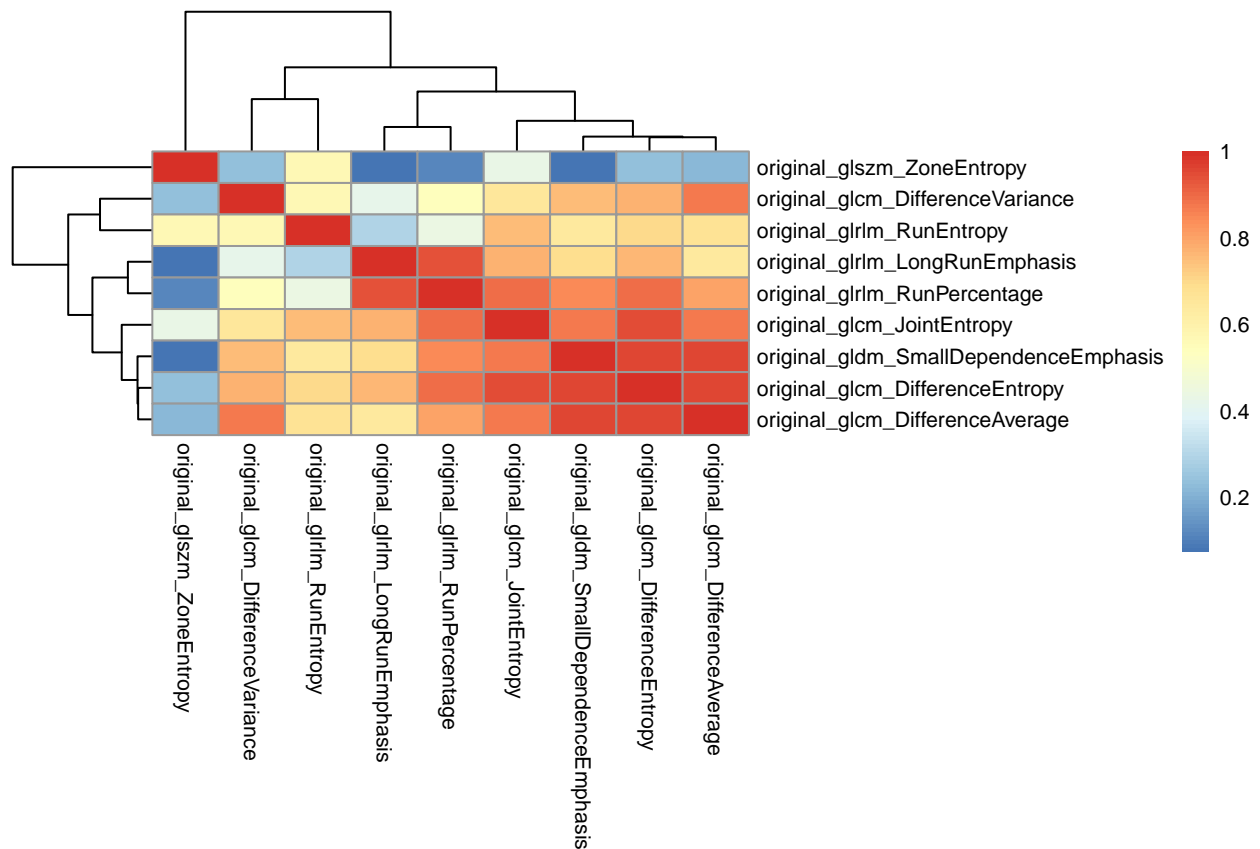
# Radiomics

## 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



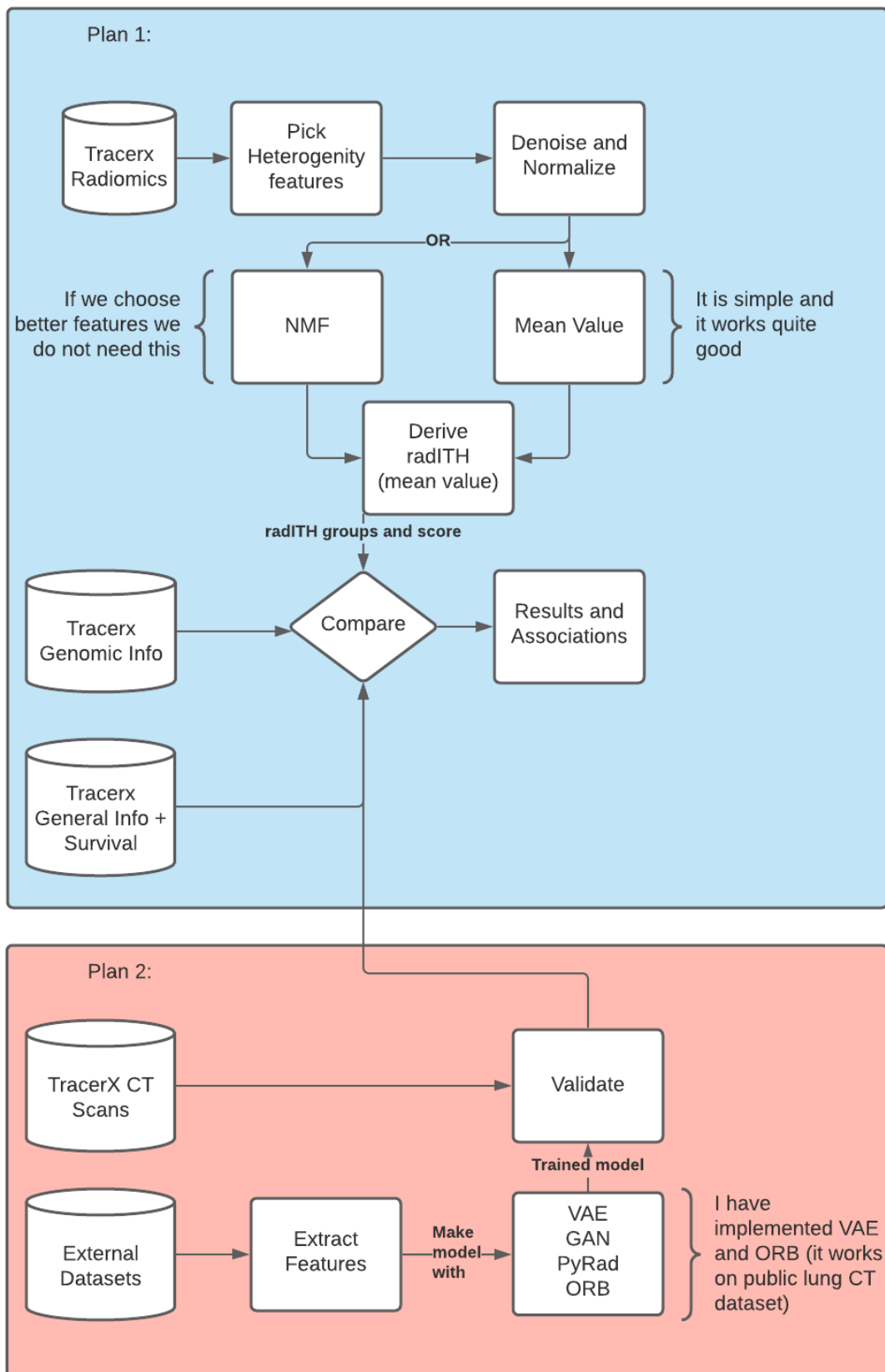
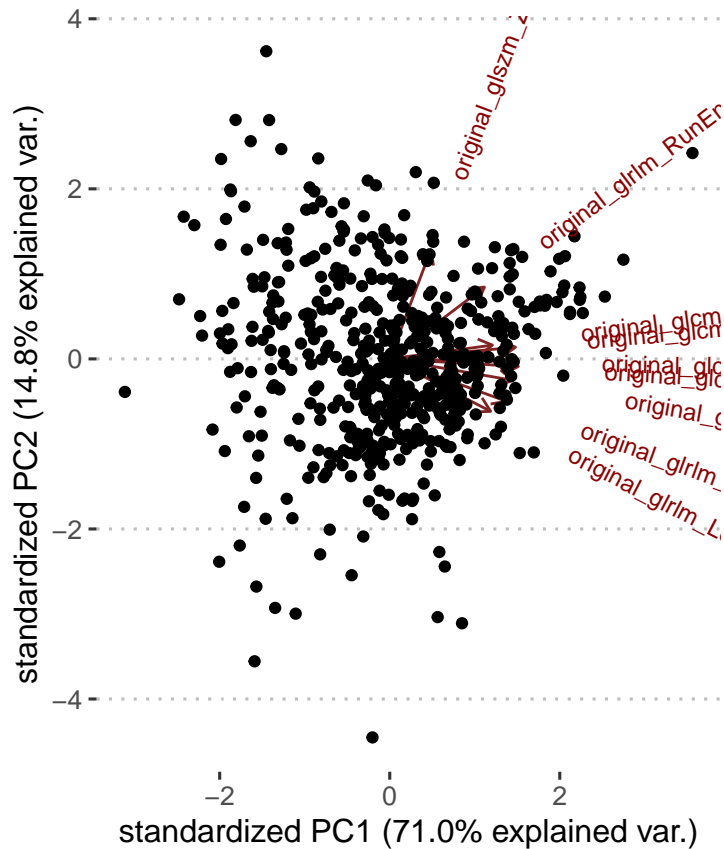


Figure 1: Project Plan



## 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

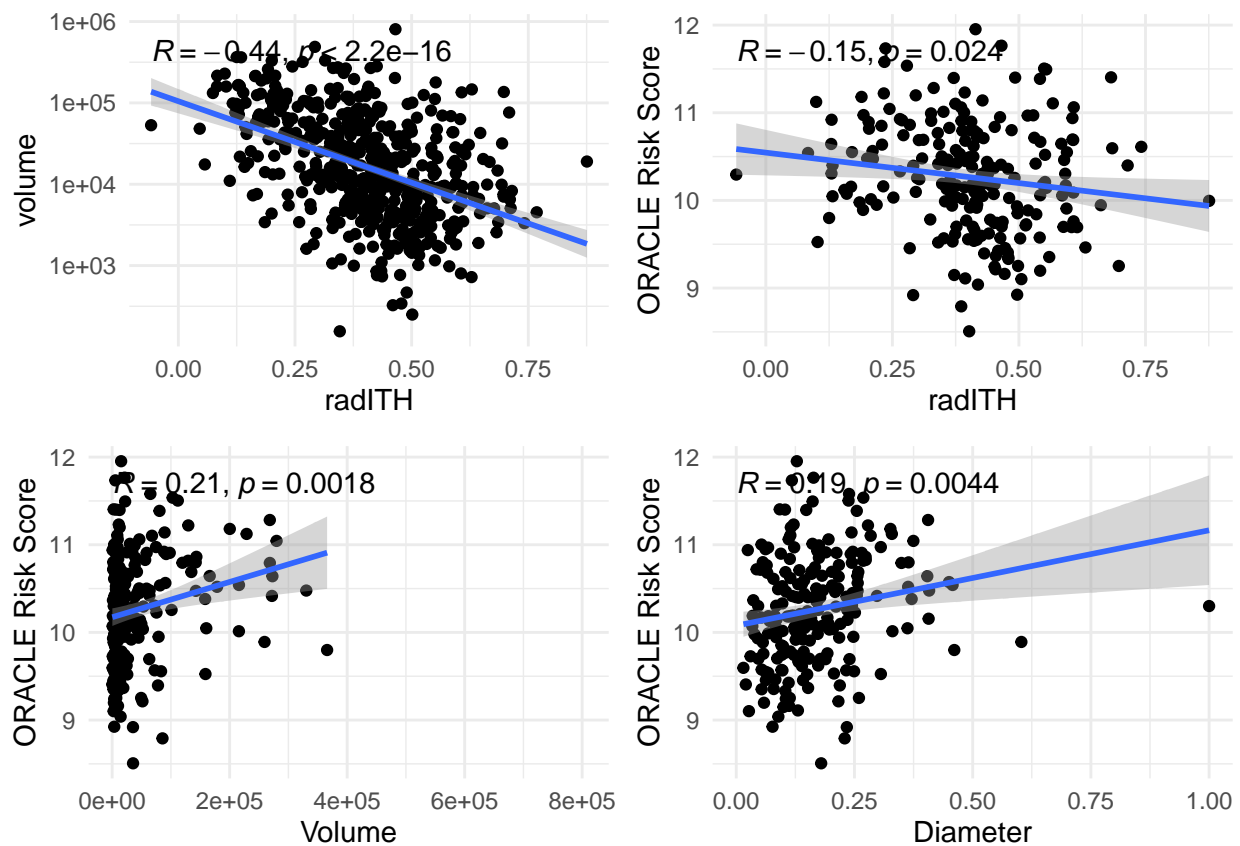
```
# weighted mean
# w = 1-abs(cor(pyrad[,features_of_interest], pyrad[, "volume"]))
# pyrad$radITH = apply(pyrad[,features_of_interest],1, function(x){
#   weighted.mean(x[features_of_interest], w = w)
# })
```

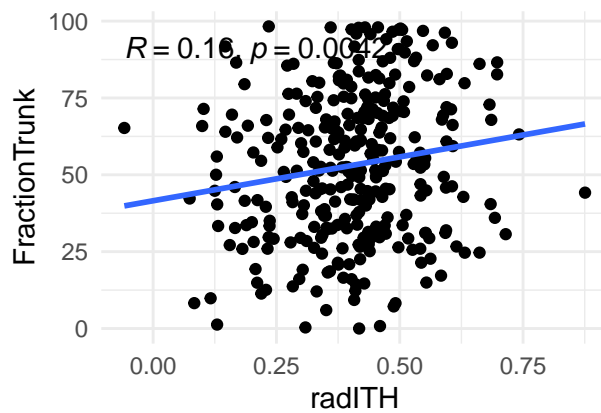
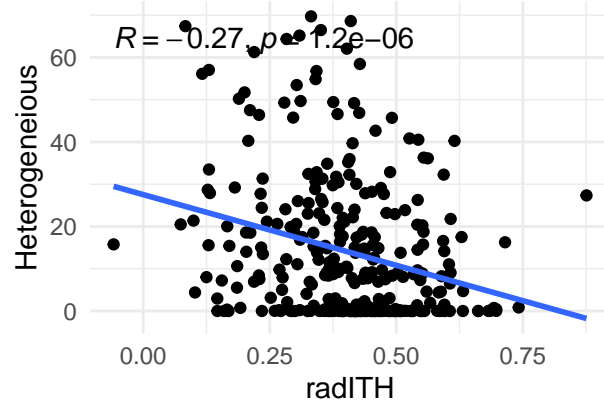
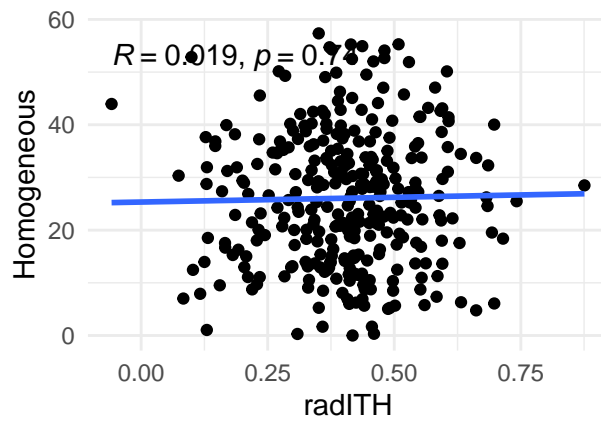
```
pyrad$radITH = rowMeans(pyrad[,features_of_interest], na.rm = T)
Q = 3

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$radITH_group, tmp[, col])
## p-value = 0.02679
## alternative hypothesis: two.sided
##
## [1] "pi3k"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.003382
```

```

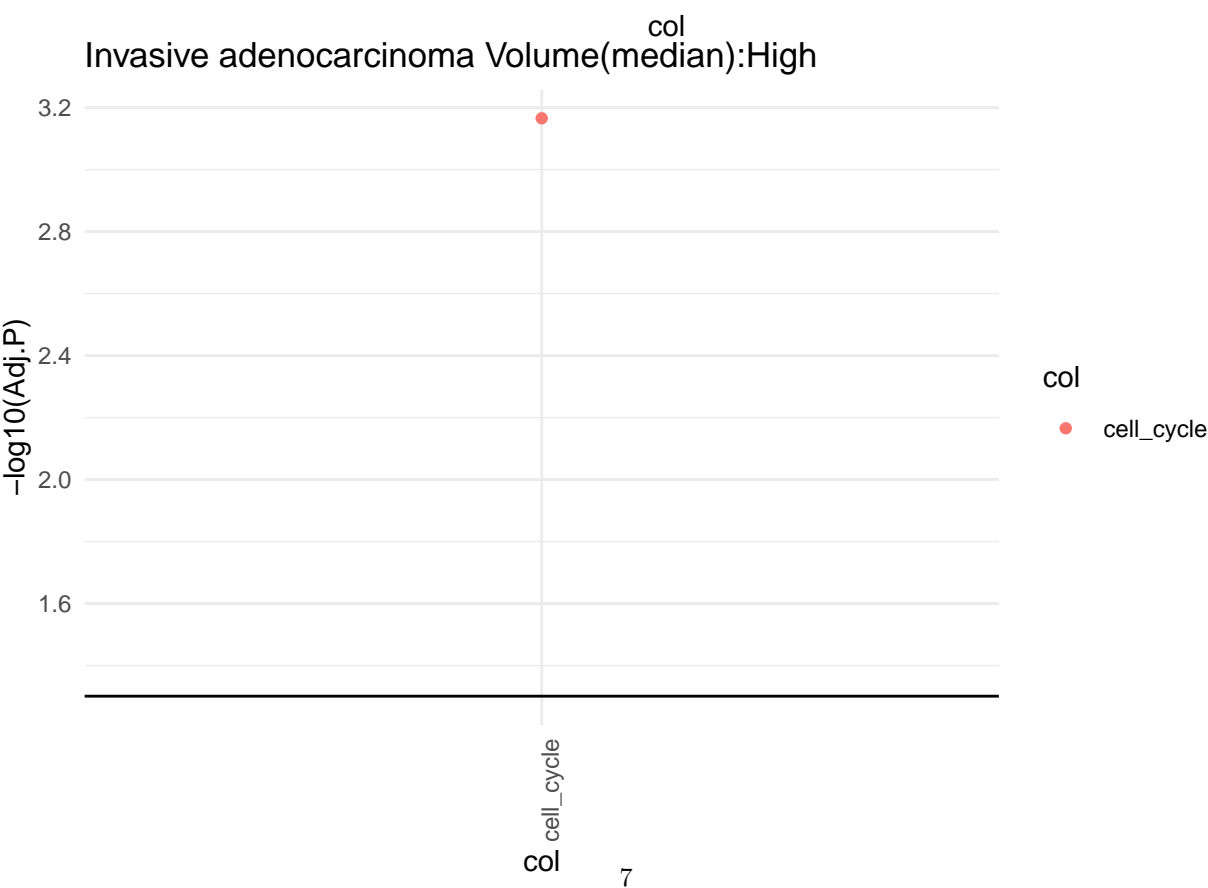
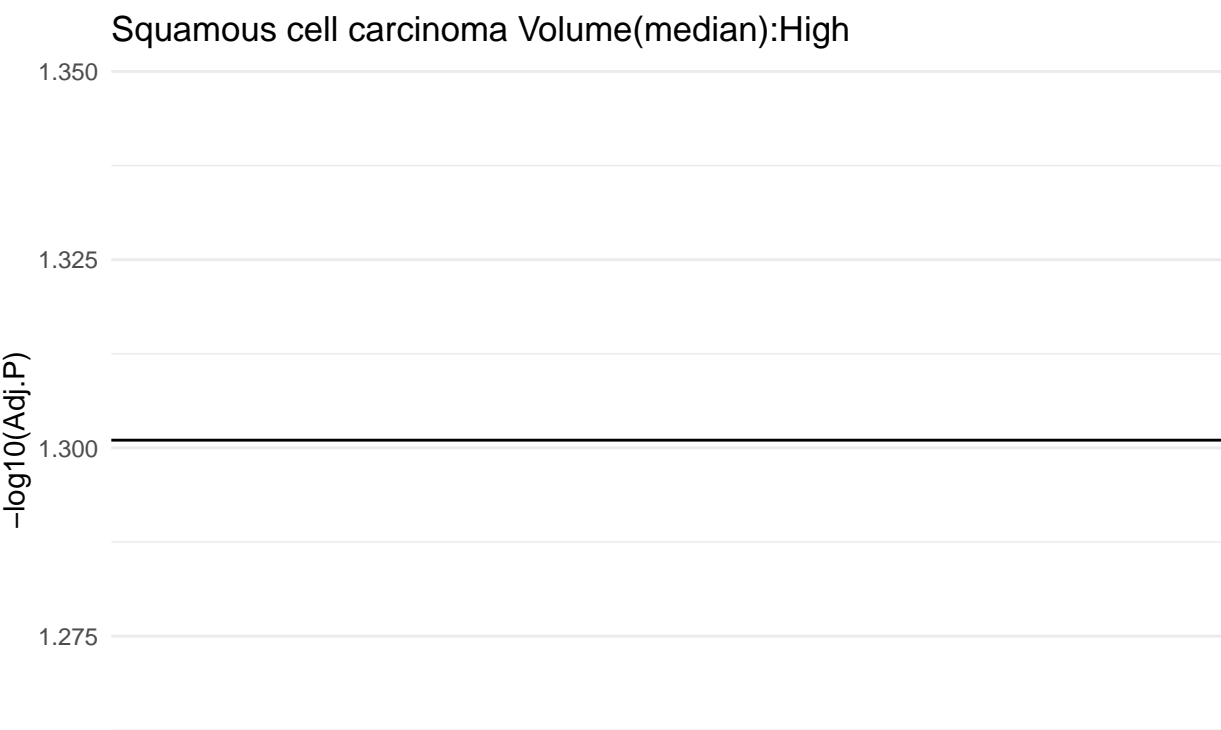
## alternative hypothesis: two.sided
##
## [1] "cell_cycle"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.0003902
## alternative hypothesis: two.sided
##
## [1] "wnt"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.04017
## alternative hypothesis: two.sided

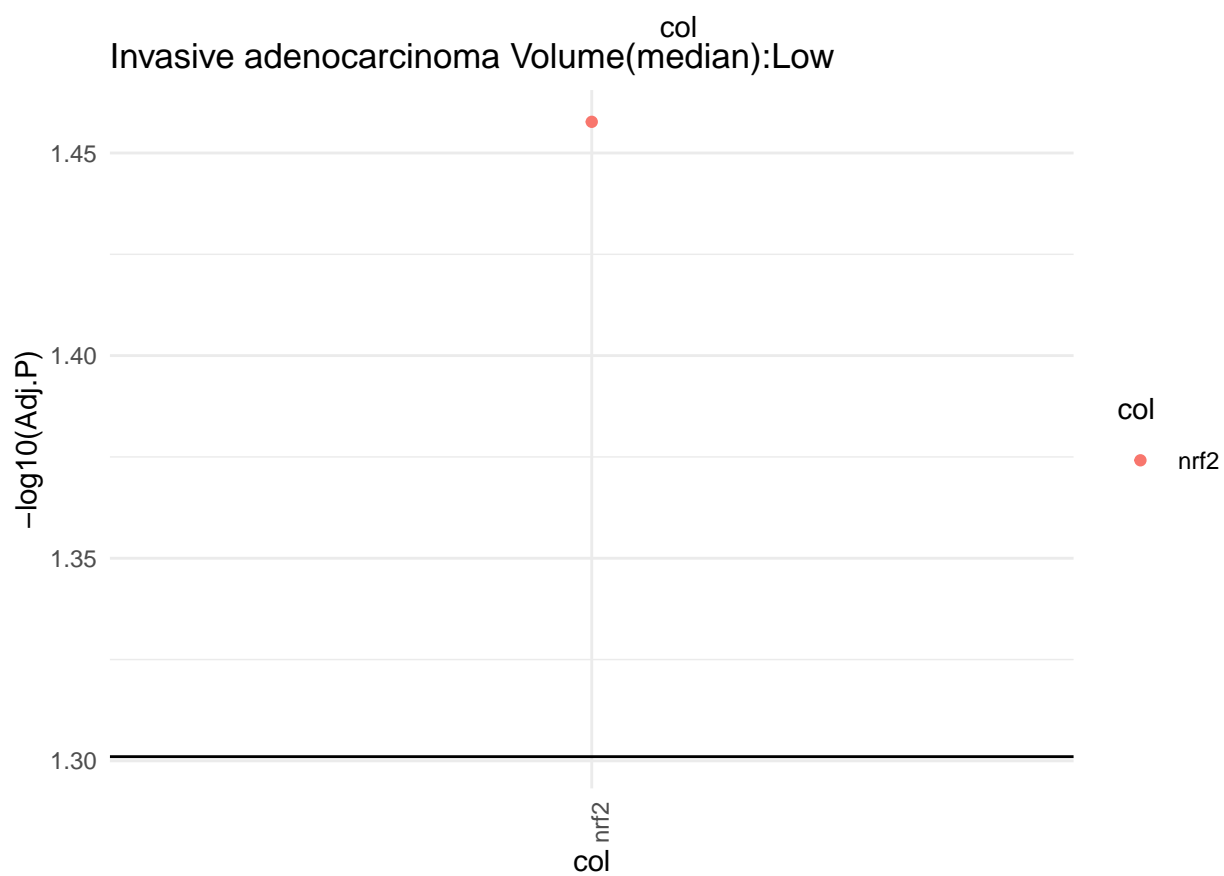
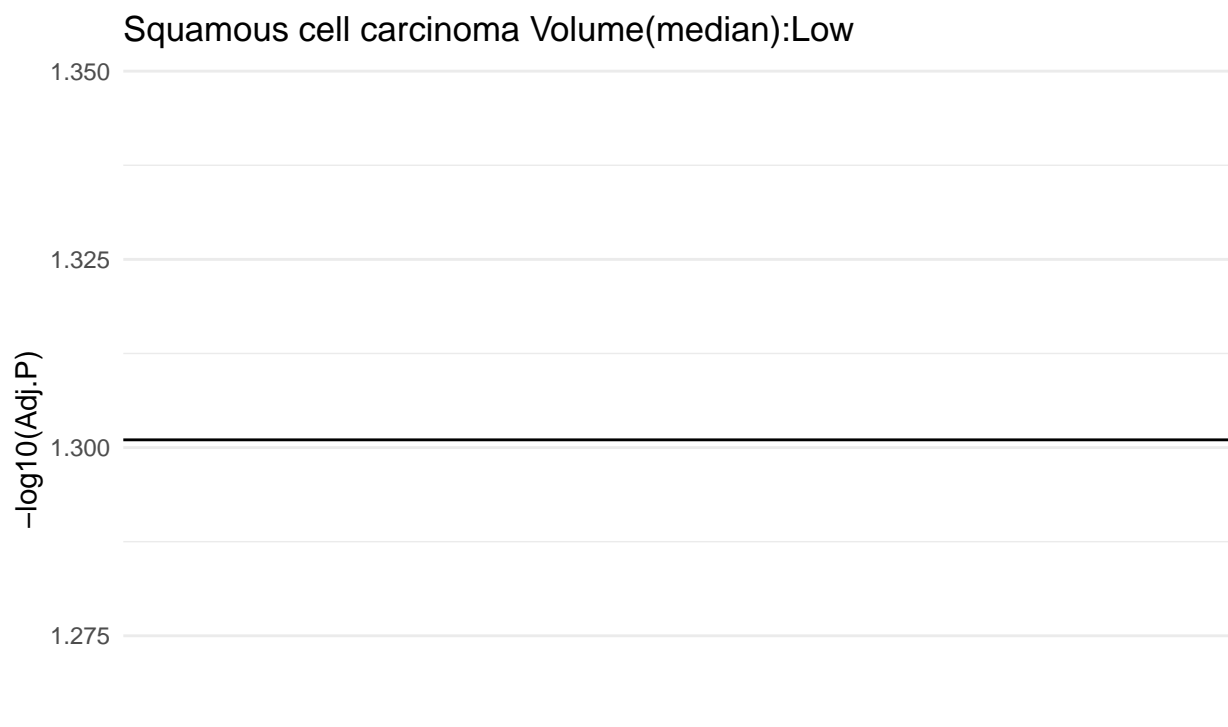
## [1] "Squamous fisher test results"

## [1] "rtk_kras"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.01748
## alternative hypothesis: two.sided
##
## [1] "pi3k"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.007167
## alternative hypothesis: two.sided

```

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







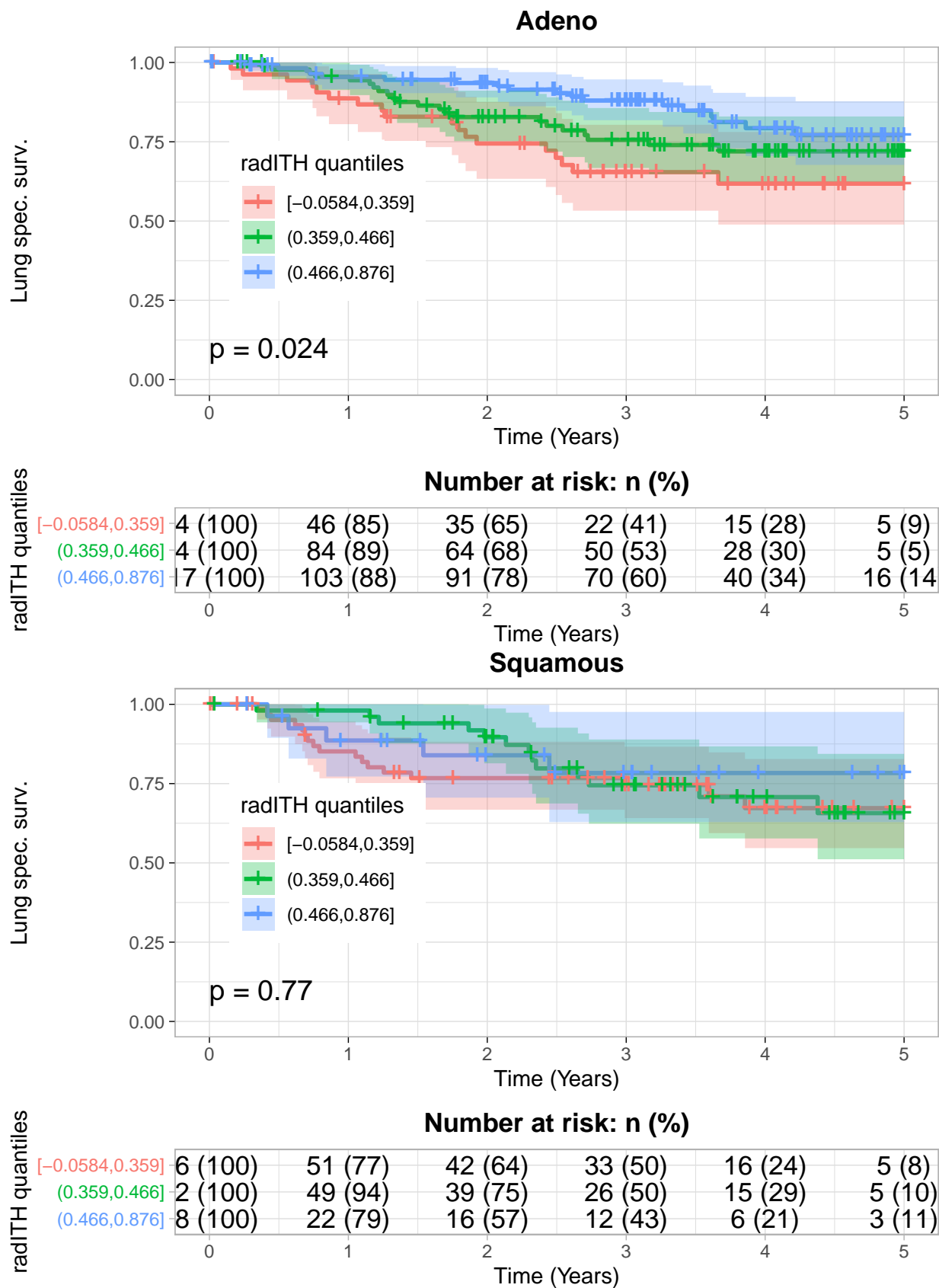
## Does Volume or diameter predict biology?

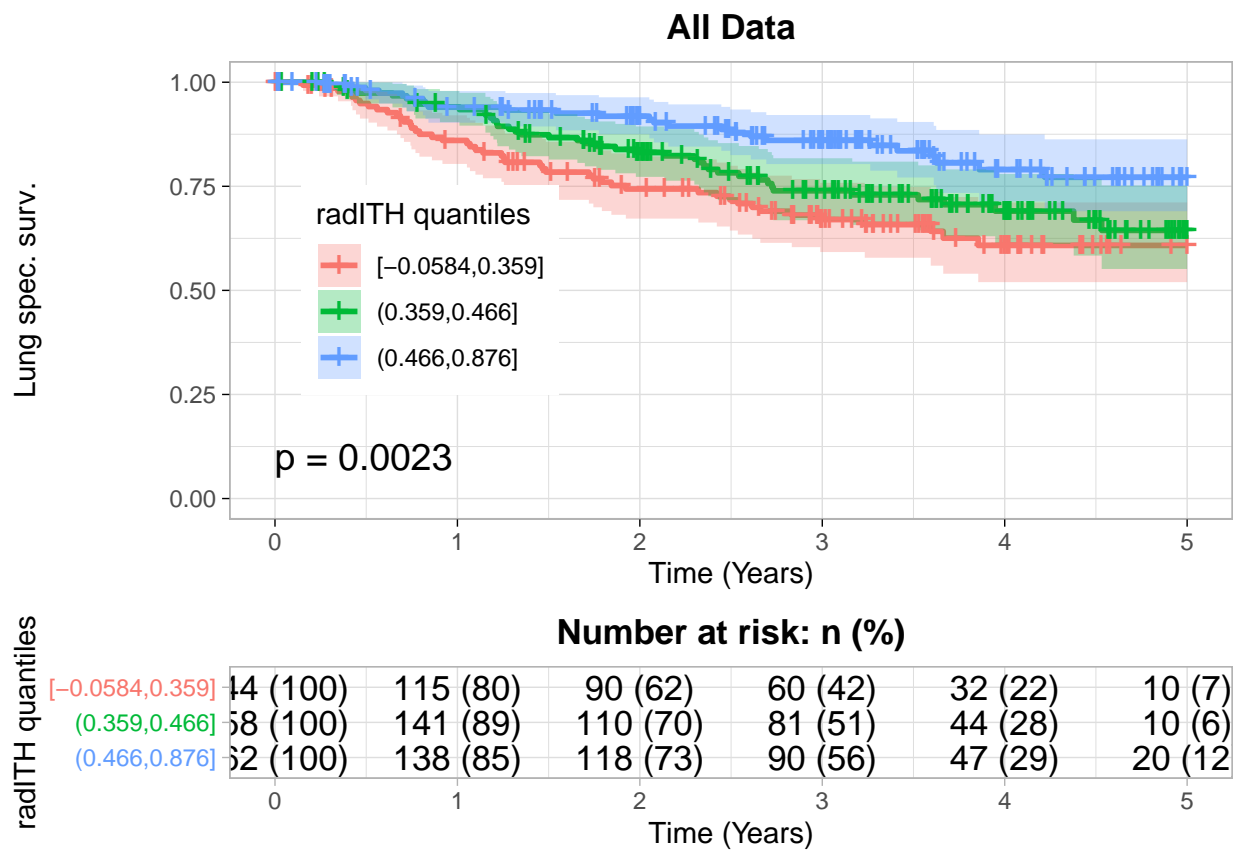
- Diameter is not associated at all
- Volume is associated with HIPPO

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

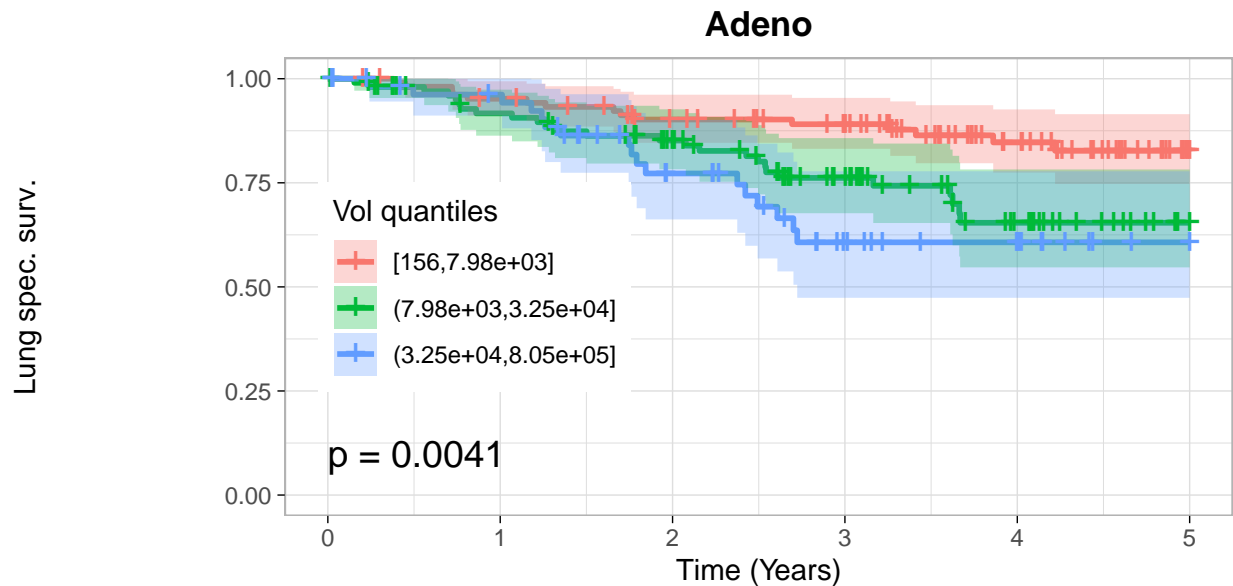
```
## [1] "Squamous fisher test results"
```

How does radITH associate with survival?





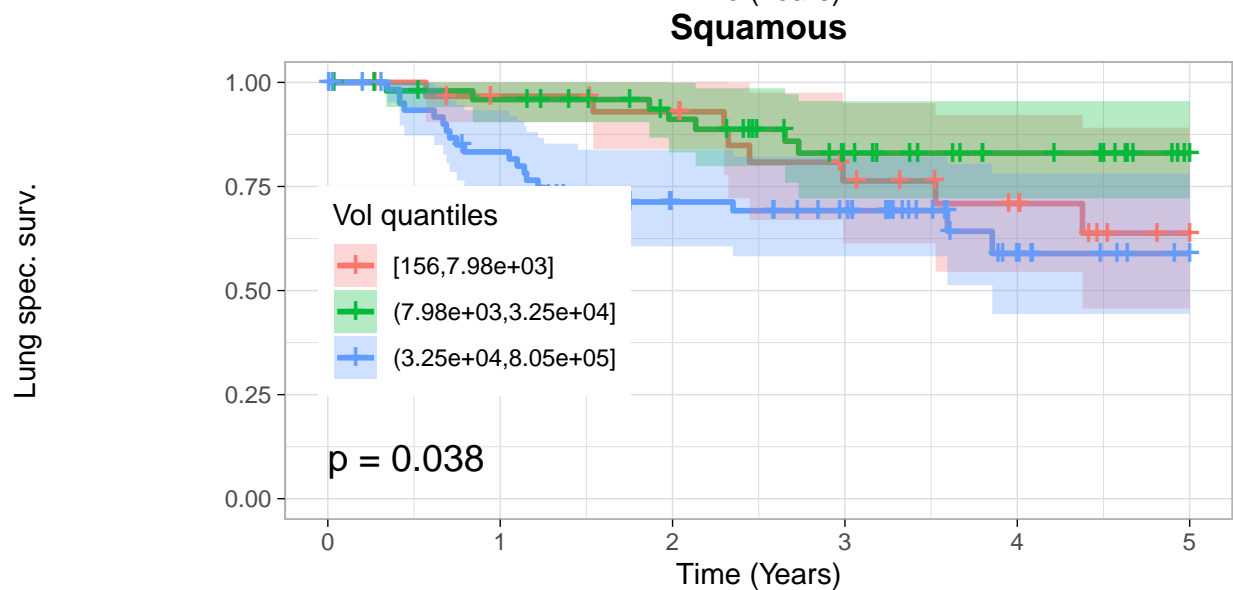
How does volume (diameter) associate to survival?



**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)

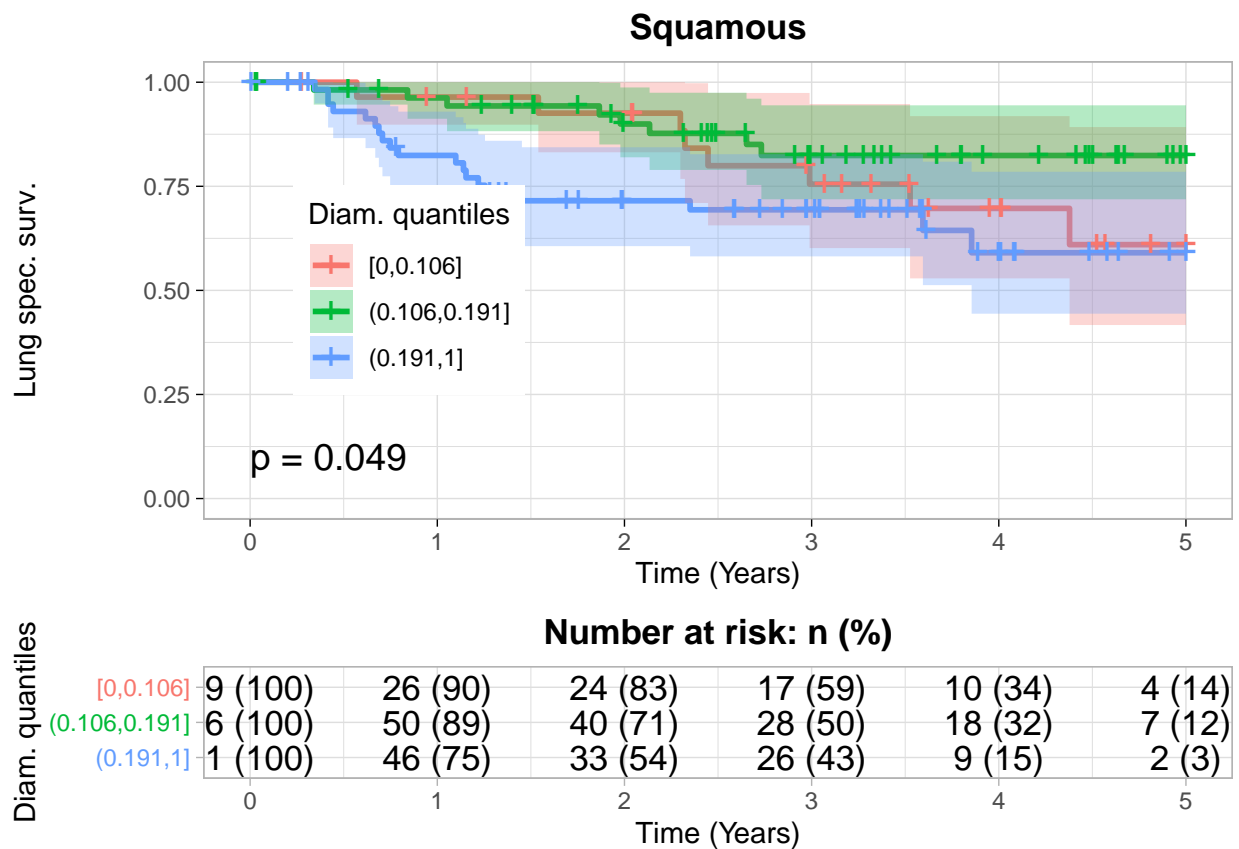
Time (Years)



**Number at risk: n (%)**

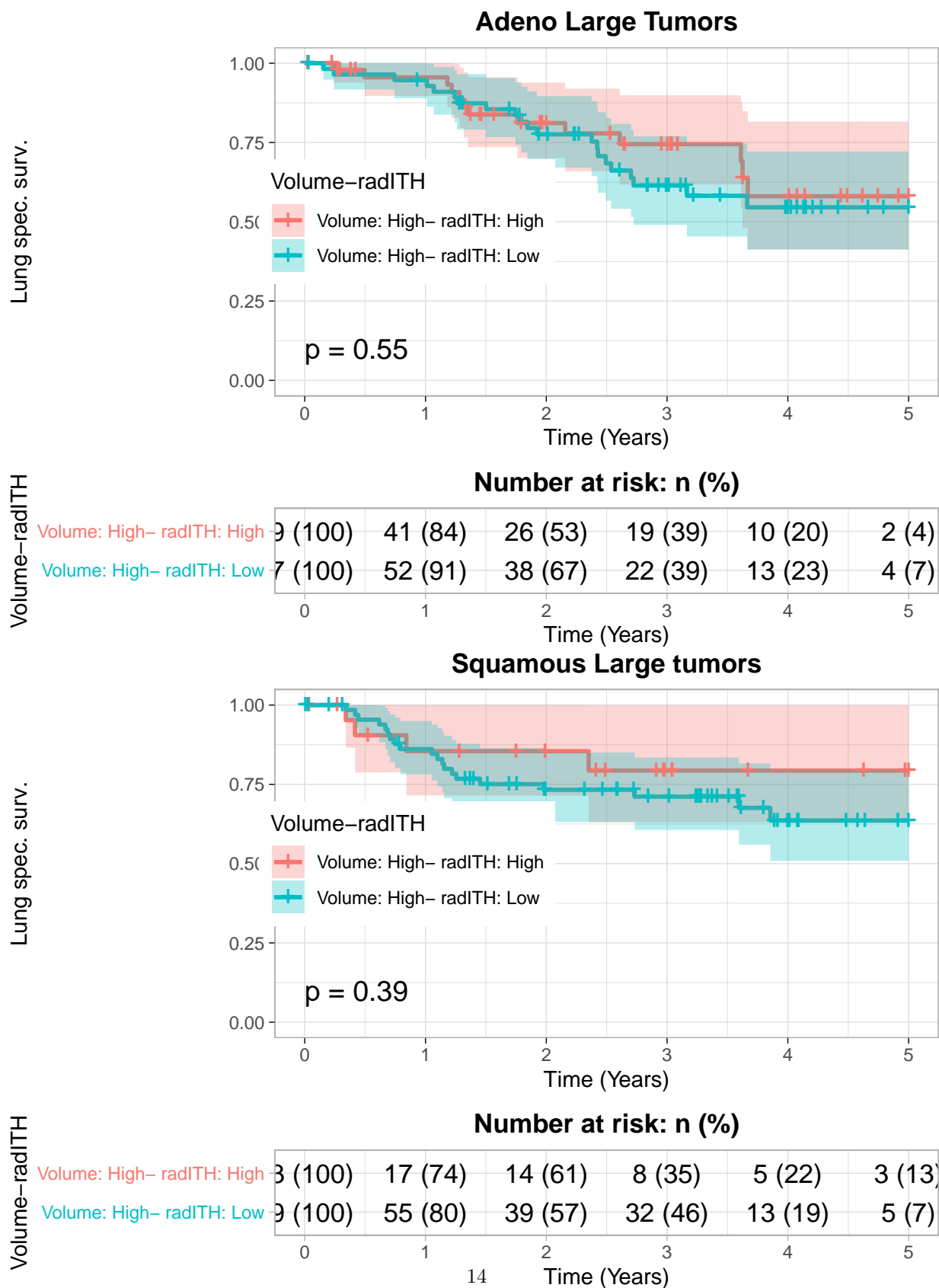
Vol quantiles	0	1	2	3	4	5
[156,7.98e+03]	1 (100)	27 (87)	25 (81)	17 (55)	12 (39)	5 (16)
(7.98e+03,3.25e+04]	1 (100)	46 (90)	38 (75)	26 (51)	17 (33)	7 (14)
(3.25e+04,8.05e+05]	4 (100)	49 (77)	34 (53)	28 (44)	8 (12)	1 (2)

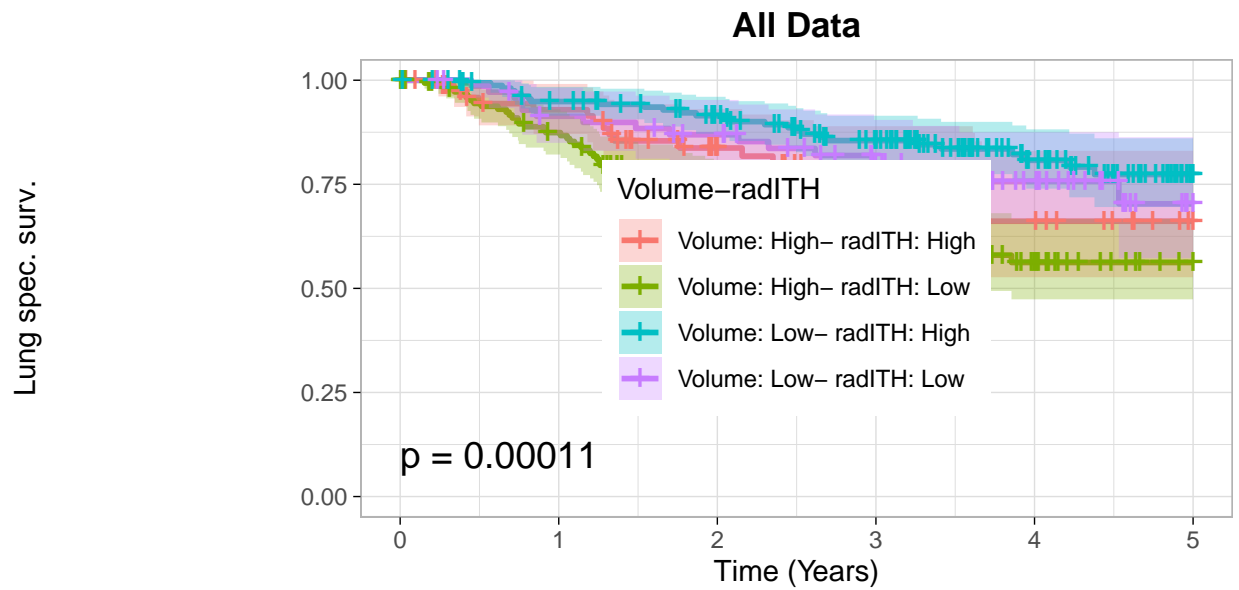
Time (Years)



# Can we overlap radITH and Volume groups and check survival?

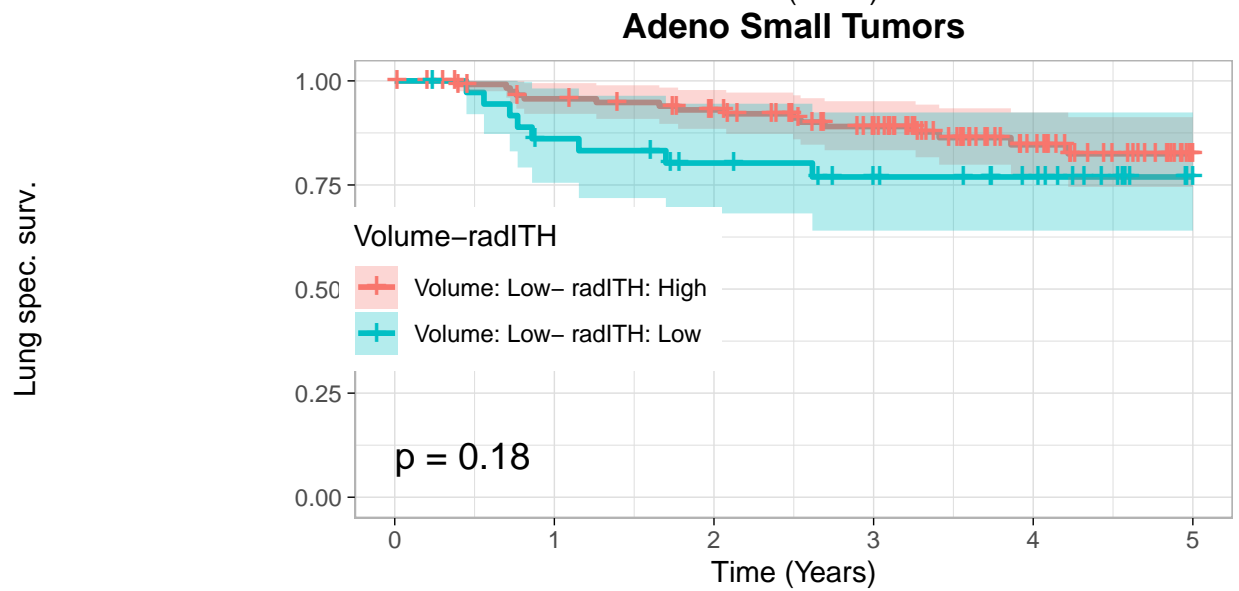
In order to increase group sizes, all measures will be split by median (Q=2)





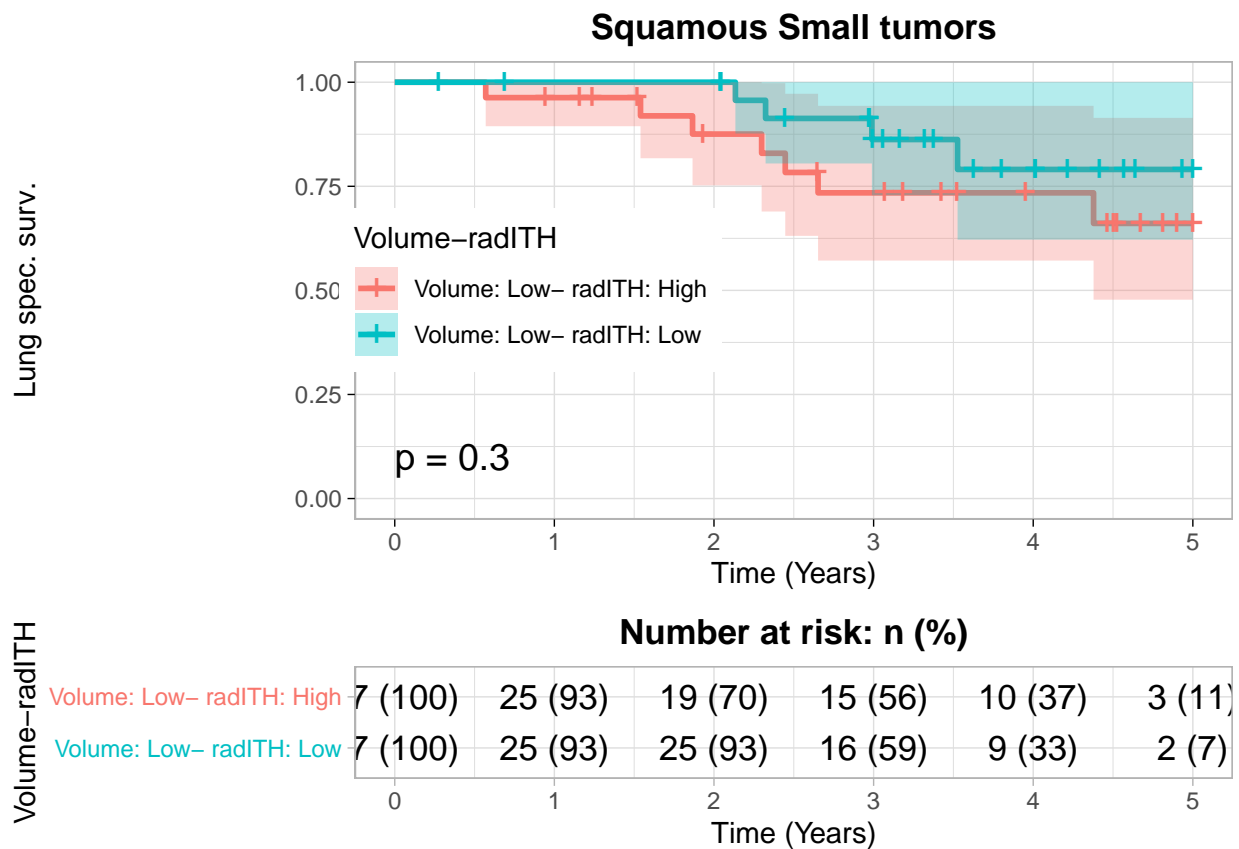
**Number at risk: n (%)**

	0	1	2	3	4	5
Volume: High- radlTH: High	9 (100)	63 (80)	44 (56)	29 (37)	15 (19)	5 (6)
Volume: High- radlTH: Low	0 (100)	123 (82)	88 (59)	57 (38)	27 (18)	9 (6)
Volume: Low- radlTH: High	3 (100)	146 (90)	130 (80)	104 (64)	56 (34)	21 (13)
Volume: Low- radlTH: Low	2 (100)	62 (86)	56 (78)	41 (57)	25 (35)	5 (7)



**Number at risk: n (%)**

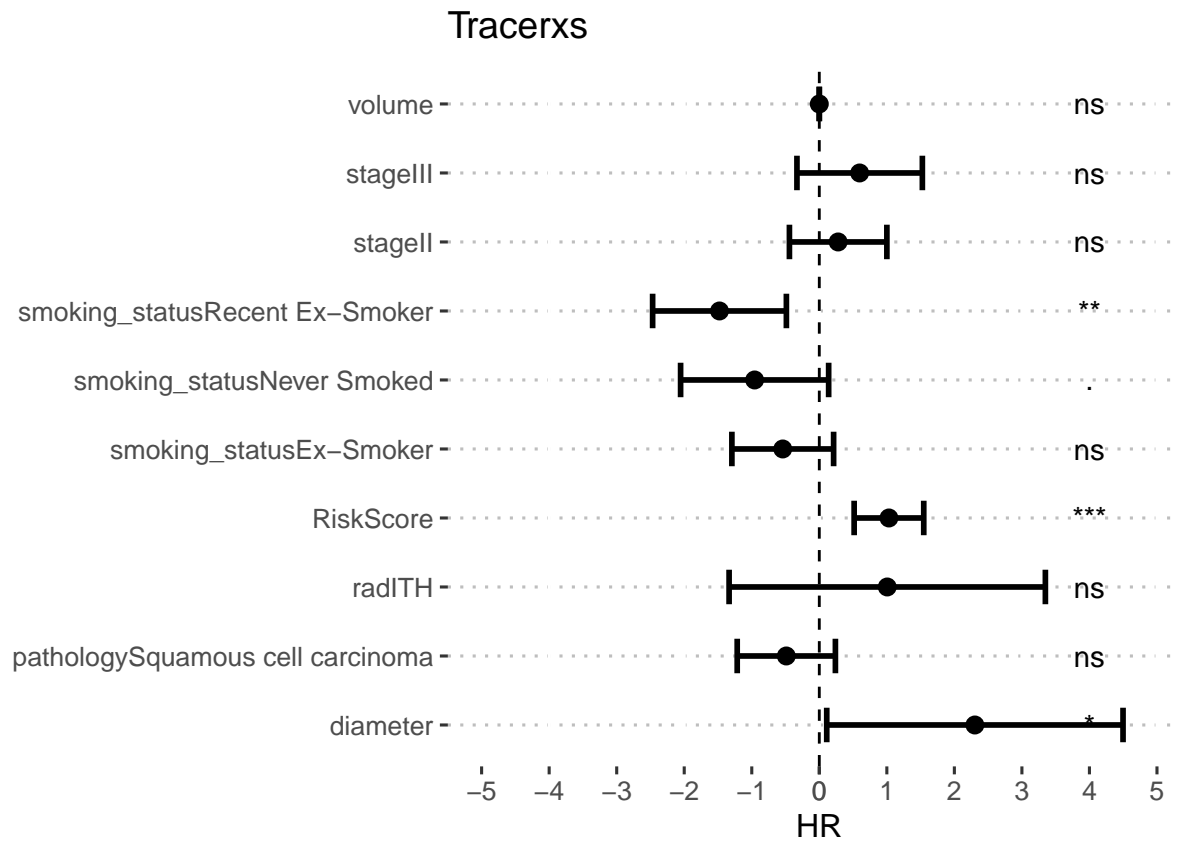
	0	1	2	3	4	5
Volume: Low- radlTH: High	2 (100)	110 (90)	101 (83)	81 (66)	45 (37)	17 (14)
Volume: Low- radlTH: Low	7 (100)	30 (81)	25 (68)	20 (54)	15 (41)	3 (8)



## Coxph Model

- radlTH does not help improve cox ph model

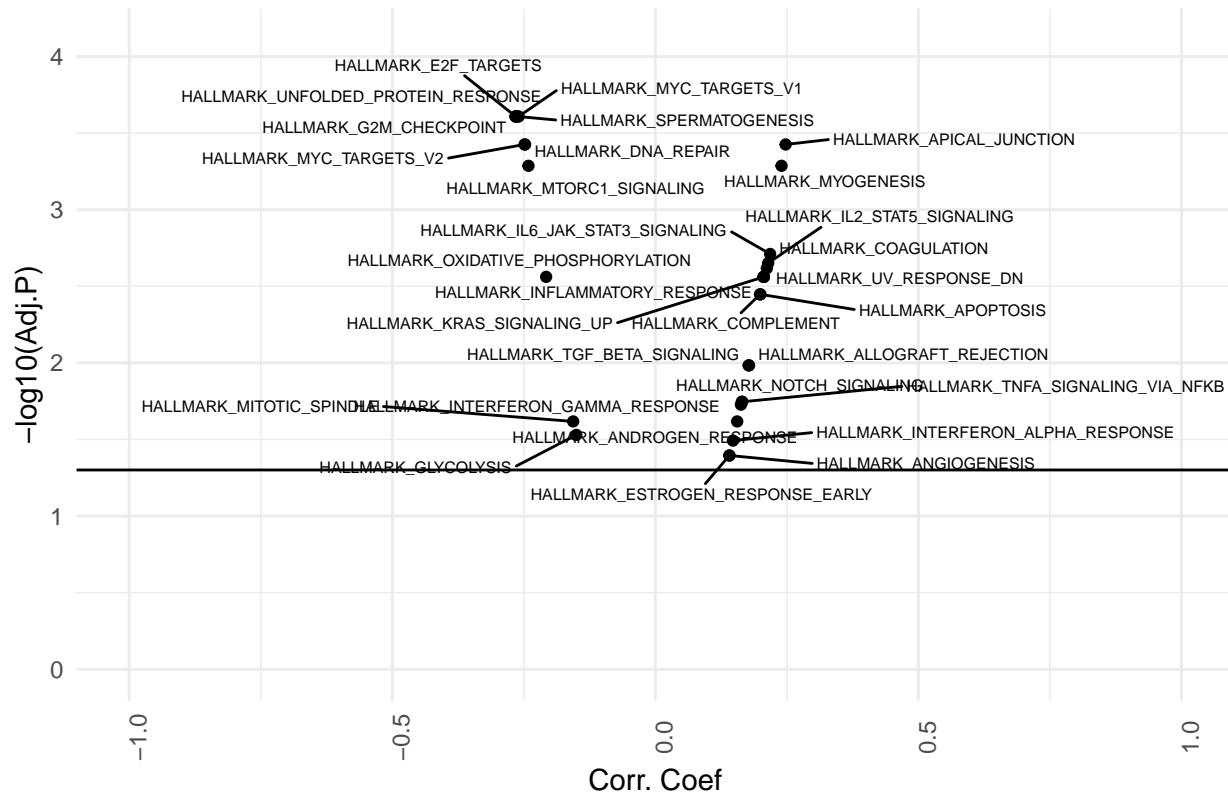




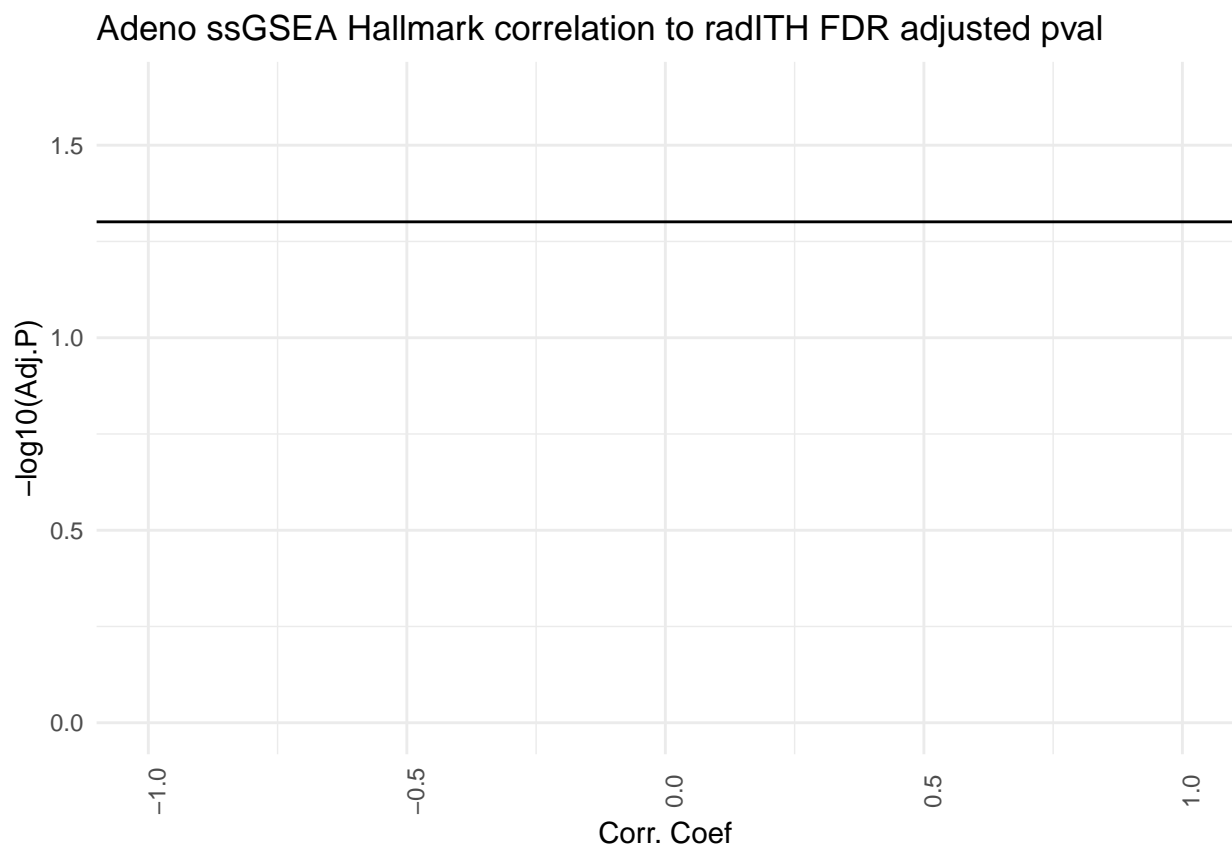
## Hallmarks all samples

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

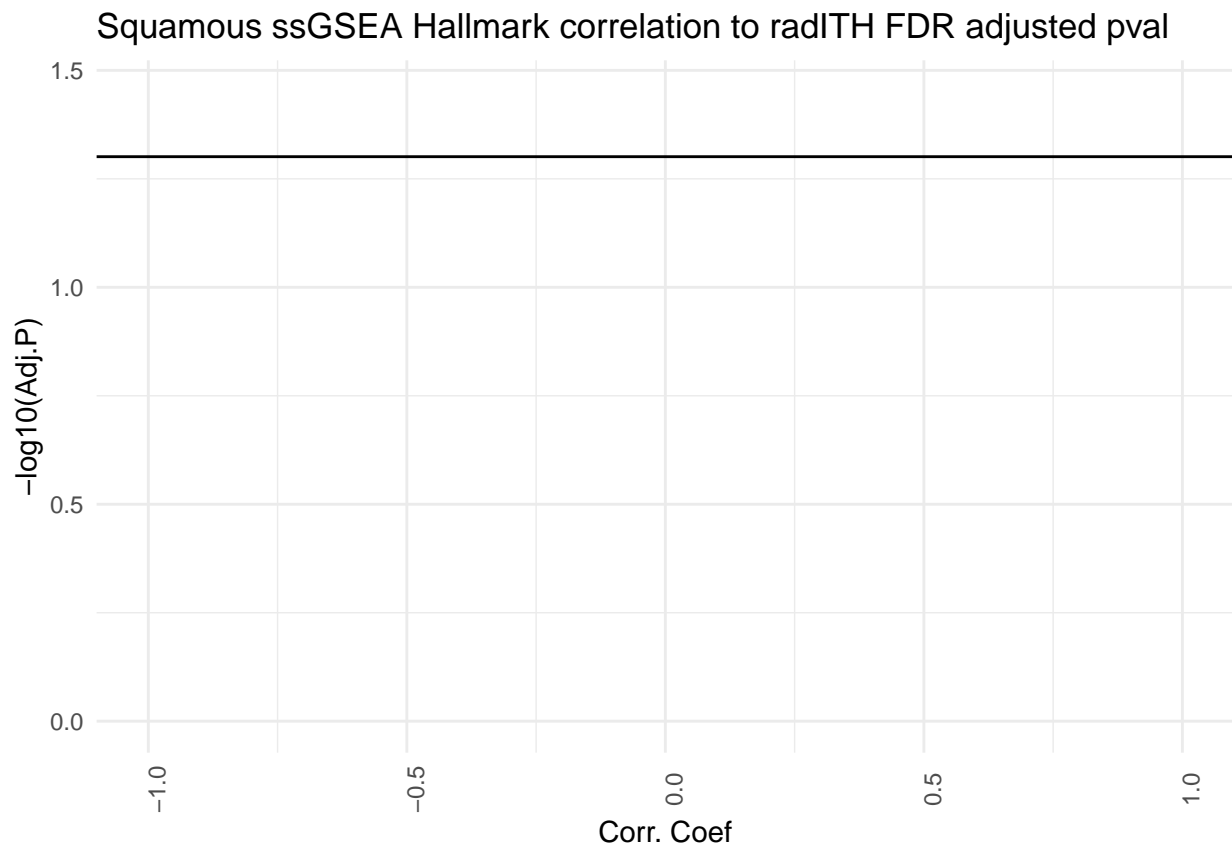
# All samples ssGSEA Hallmark correlation to radlTH FDR adjusted pval



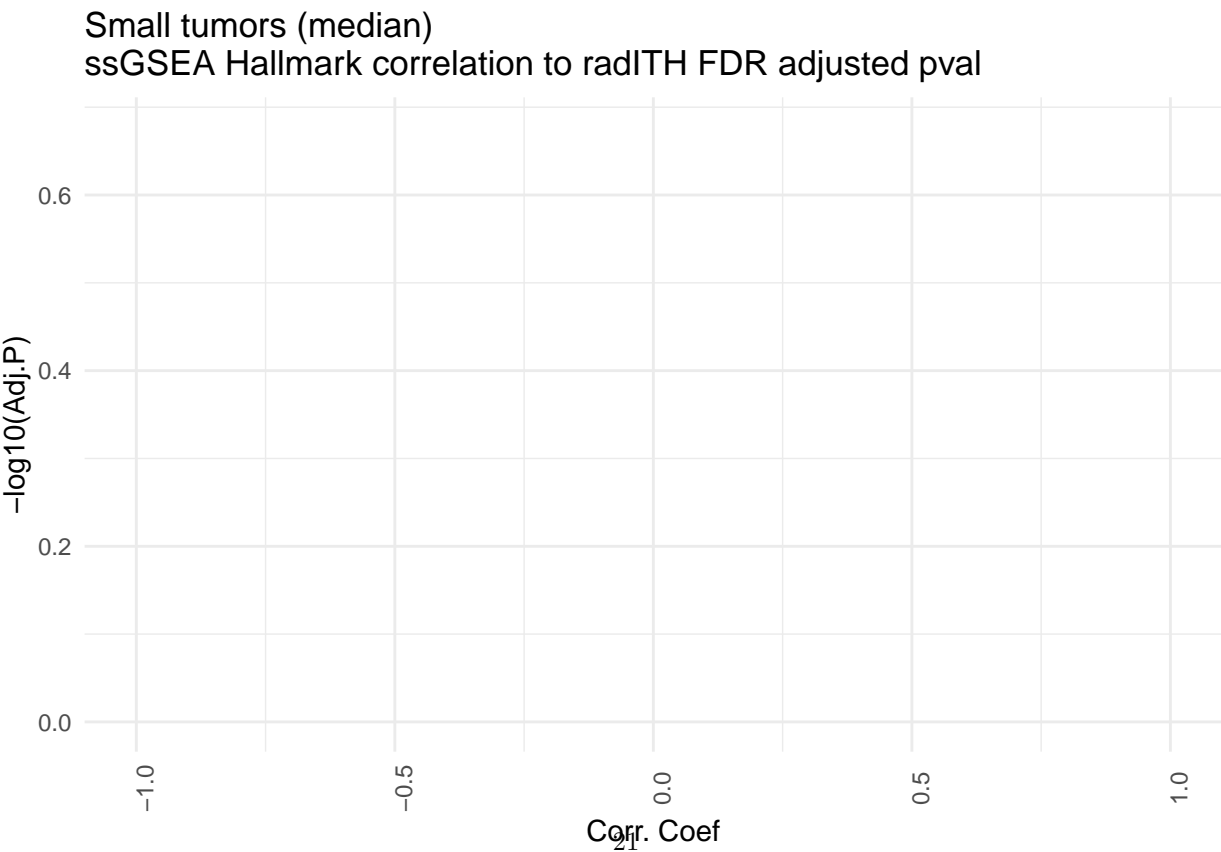
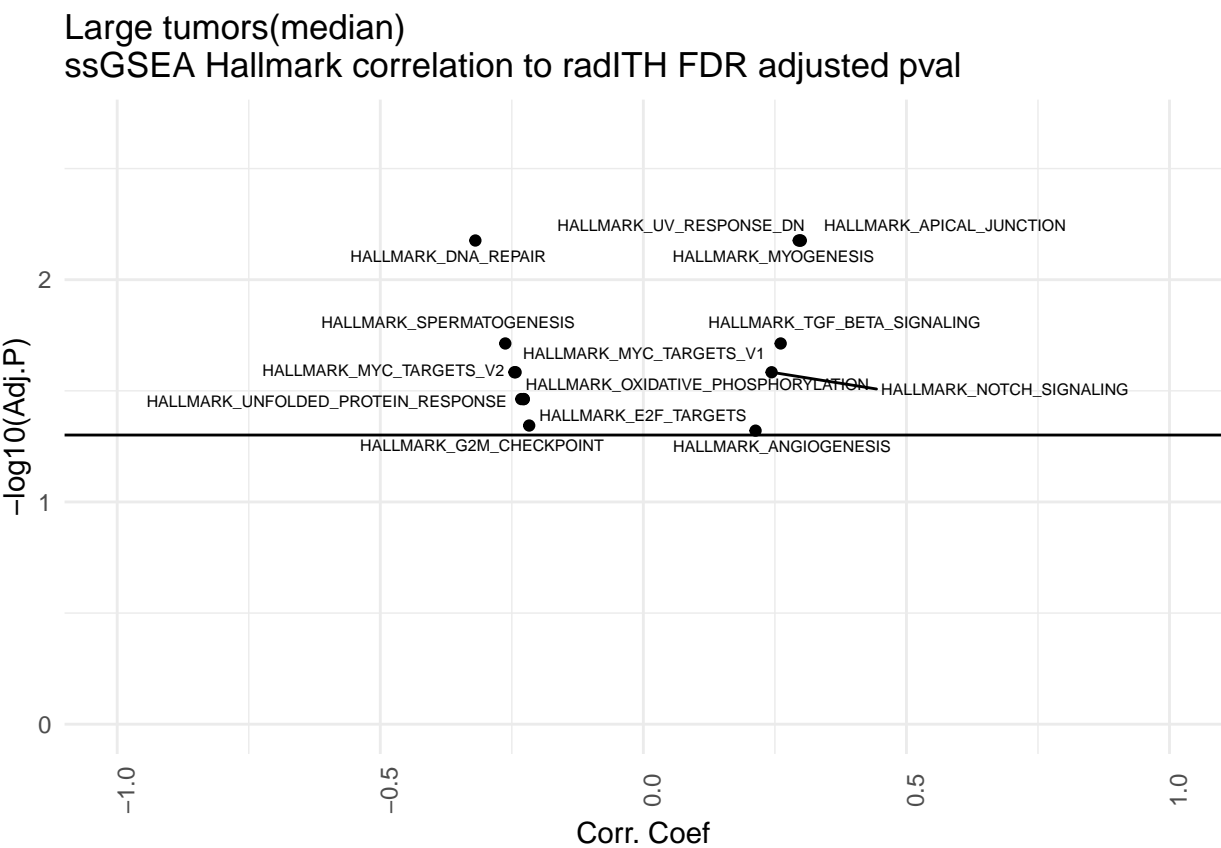
## Hallmarks Adeno



## Hallmarks Squamous

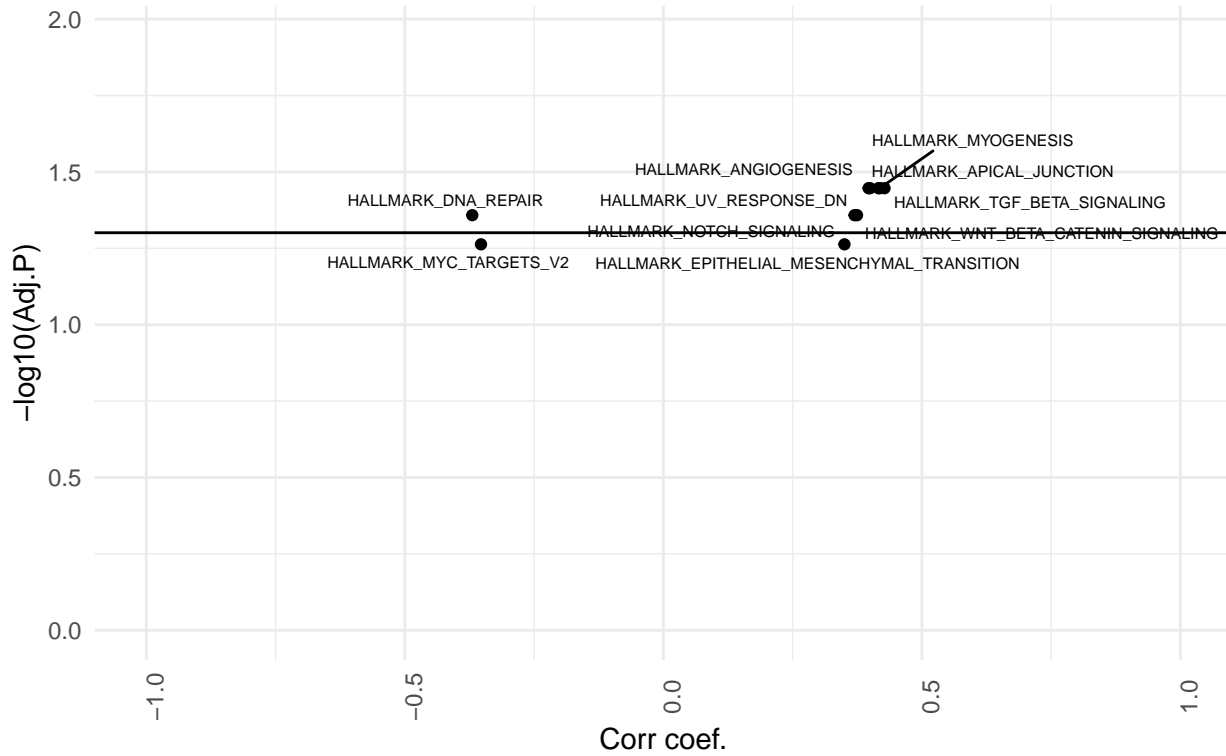


# Hallmark expression-radITH Correlation in Large vs Small tumors (all samples)

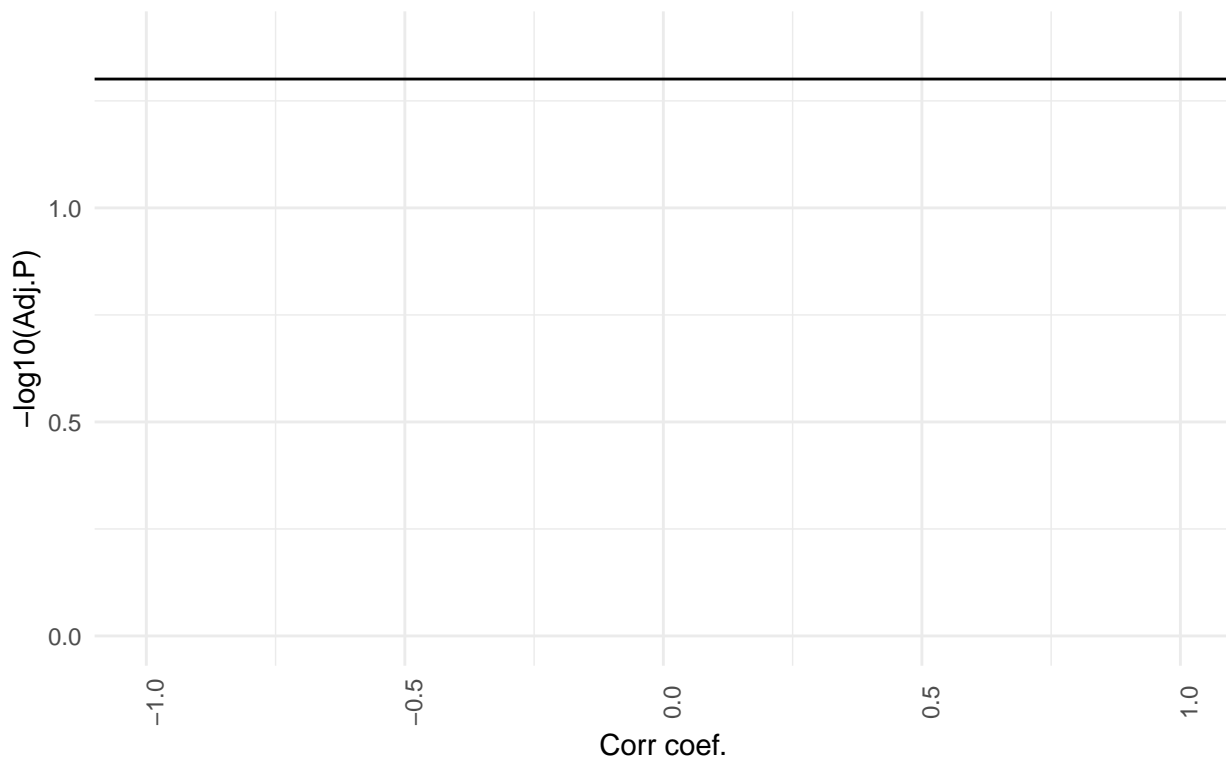


Let's split by Size and Pathology and repeat

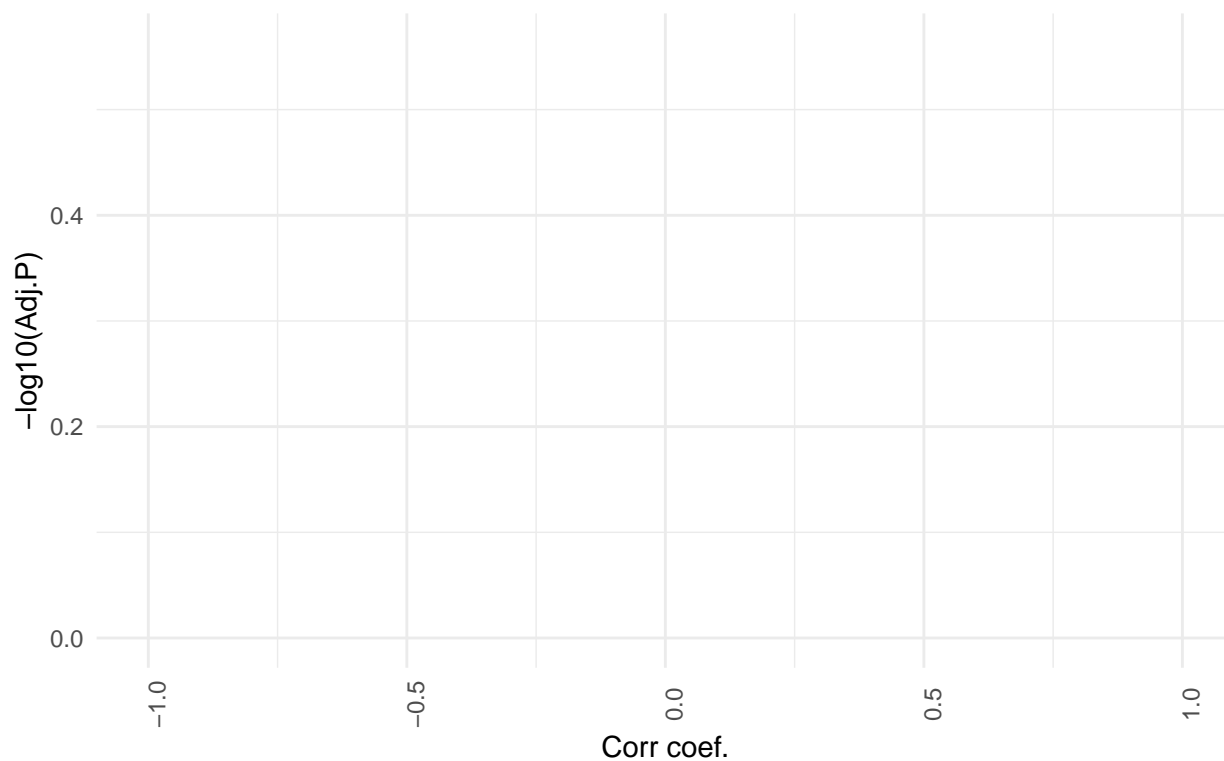
Squamous cell carcinoma Volume(median): High  
ssGSEA Hallmark correlation to radITH FDR adjusted pval



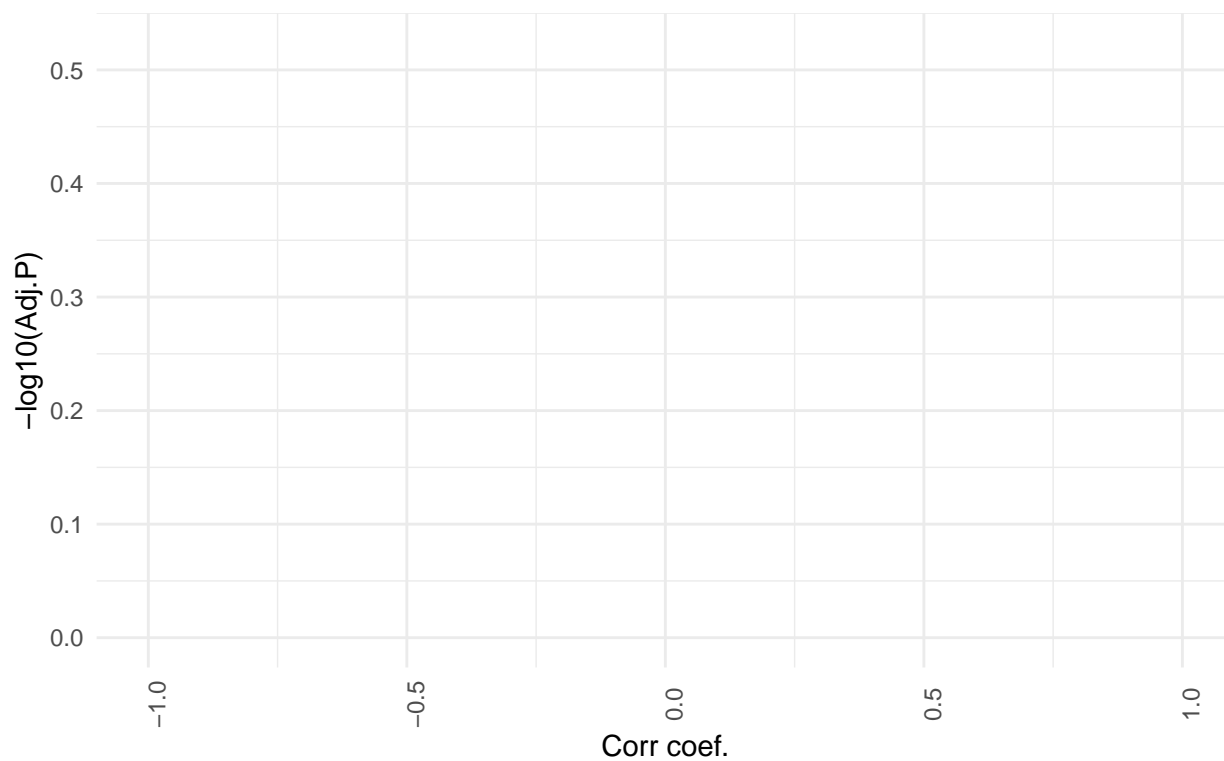
Invasive adenocarcinoma Volume(median): High  
ssGSEA Hallmark correlation to radITH FDR adjusted pval



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

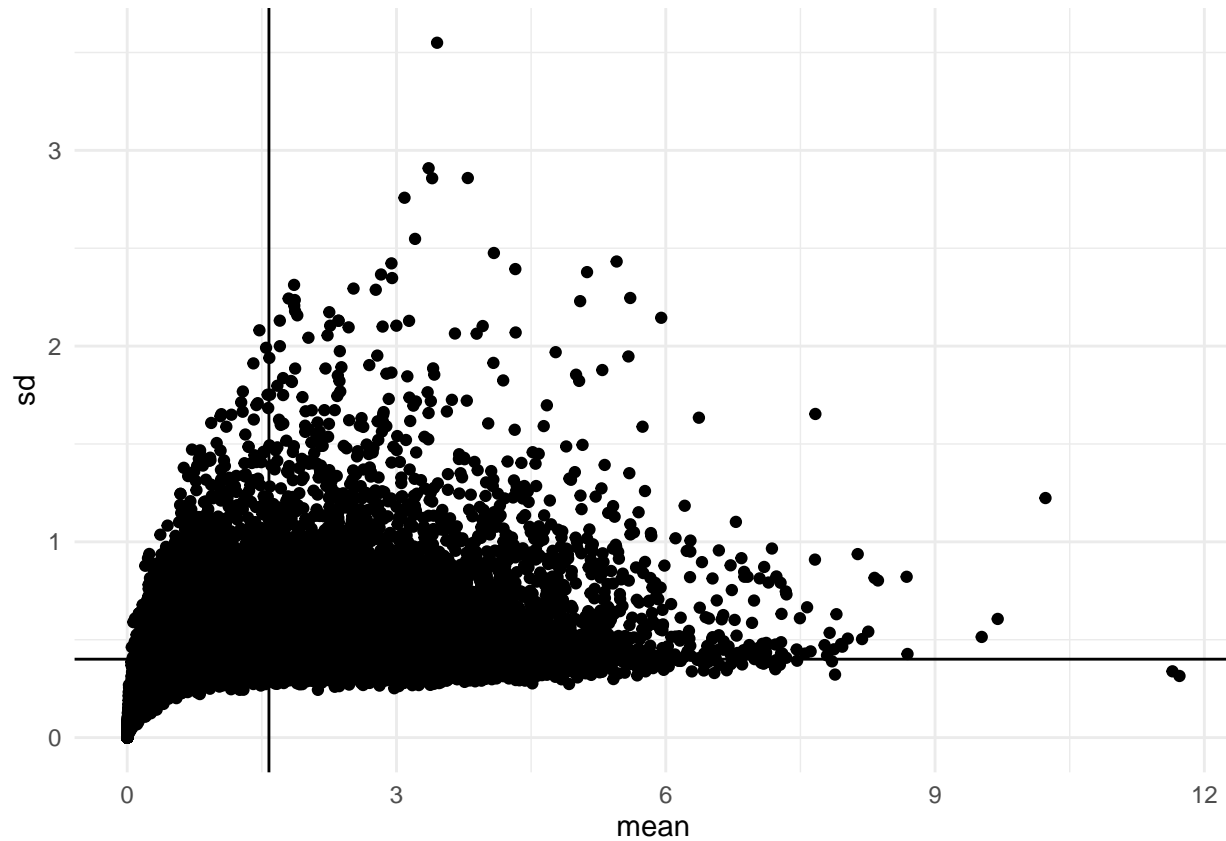


Invasive adenocarcinoma Volume(median): Low  
ssGSEA Hallmark correlation to radlTH FDR adjusted pval



## Picking genes for Gene Expression Analysis

- Mean and SD value based on entire cohort

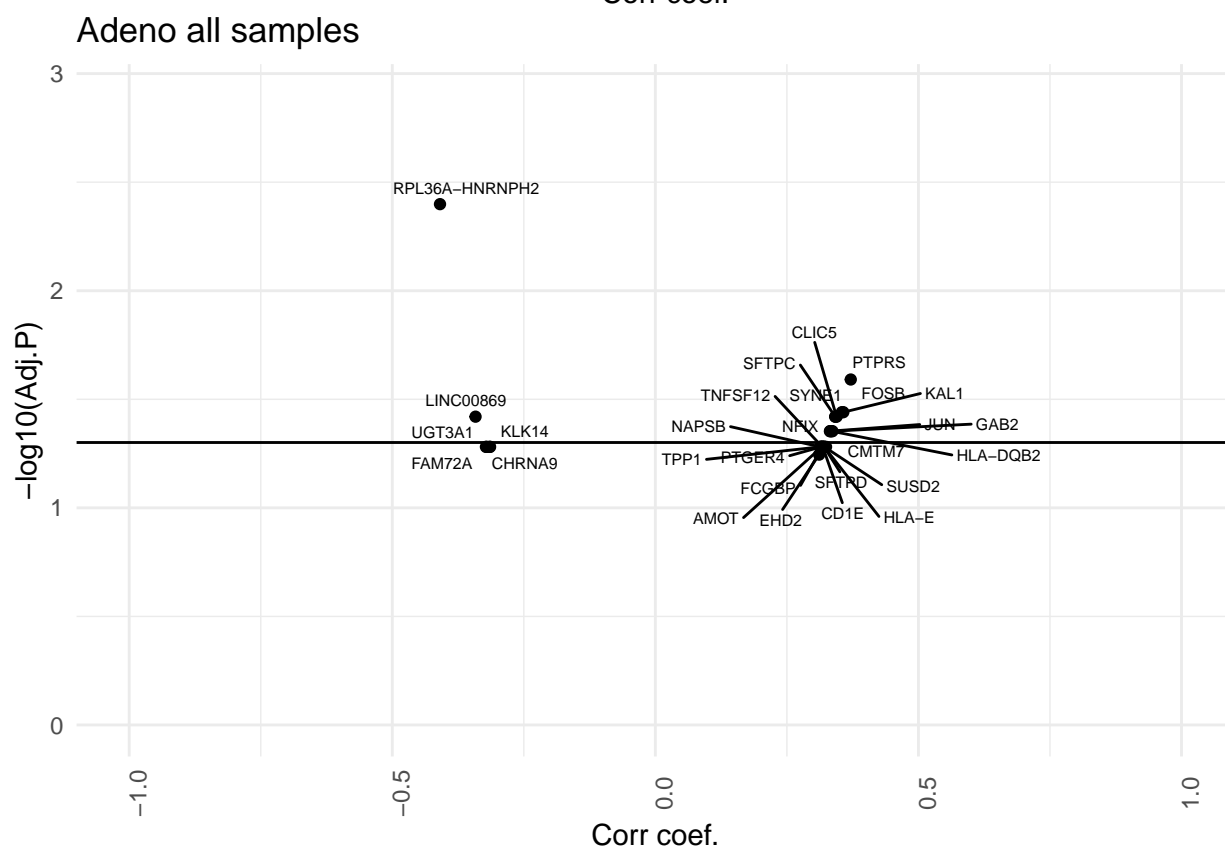
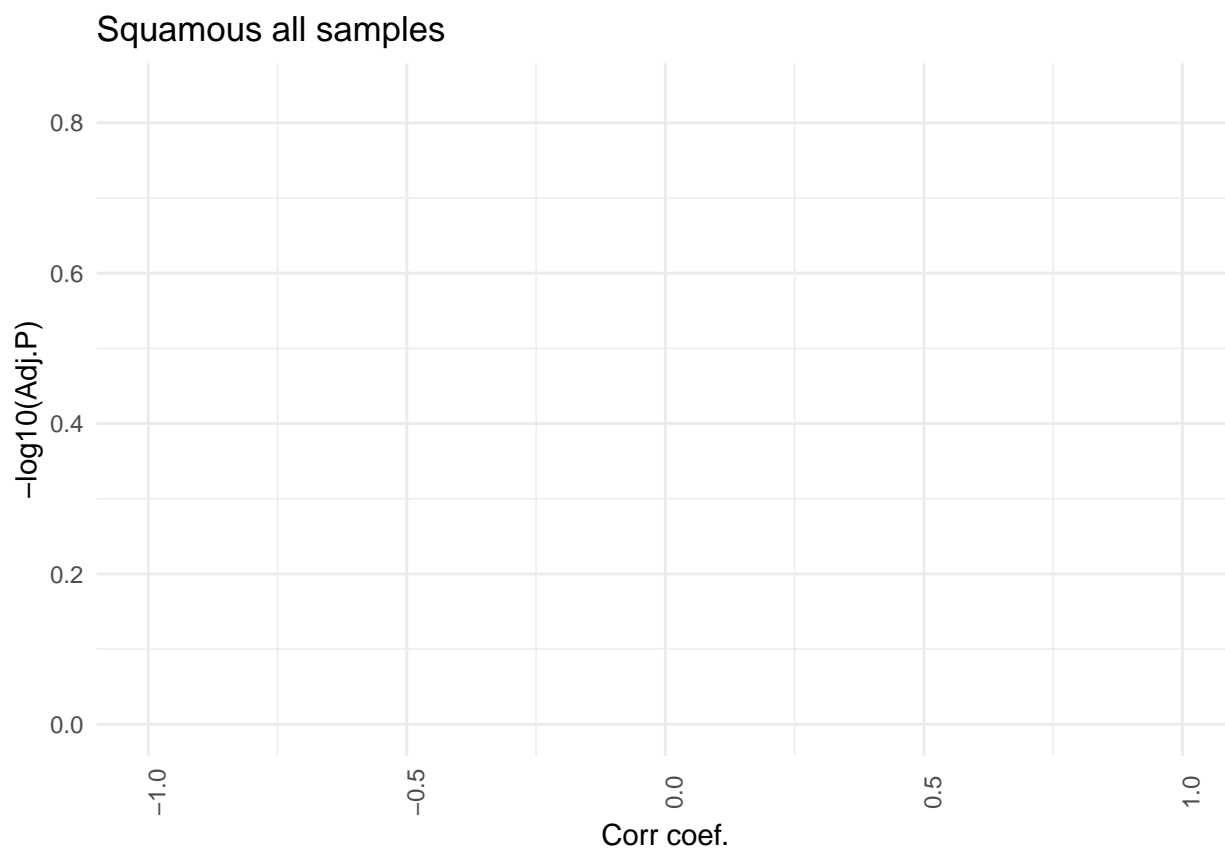


## Number of Genes after cutoff: 10332

## Gene Expression Analysis without volume

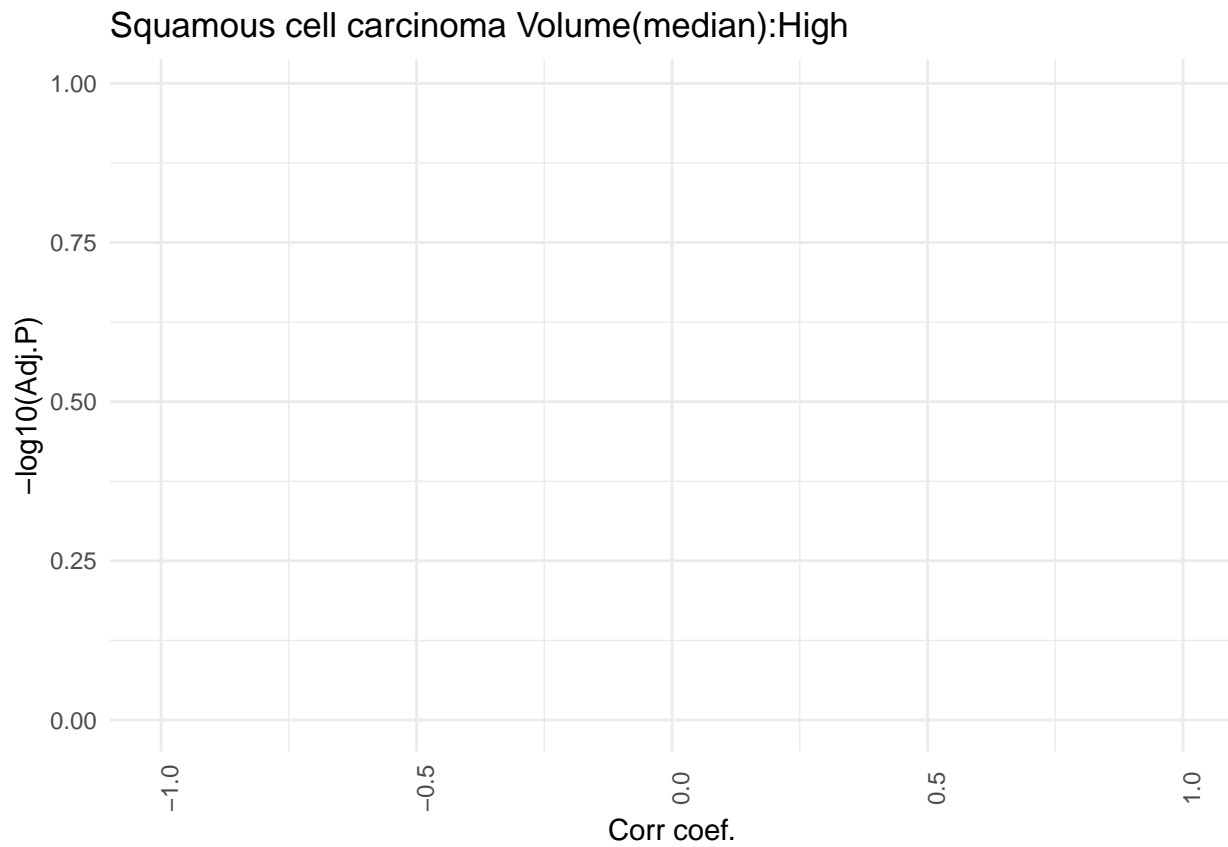
- Genes that were picked for analysis were based on mean and SD (entire cohort)

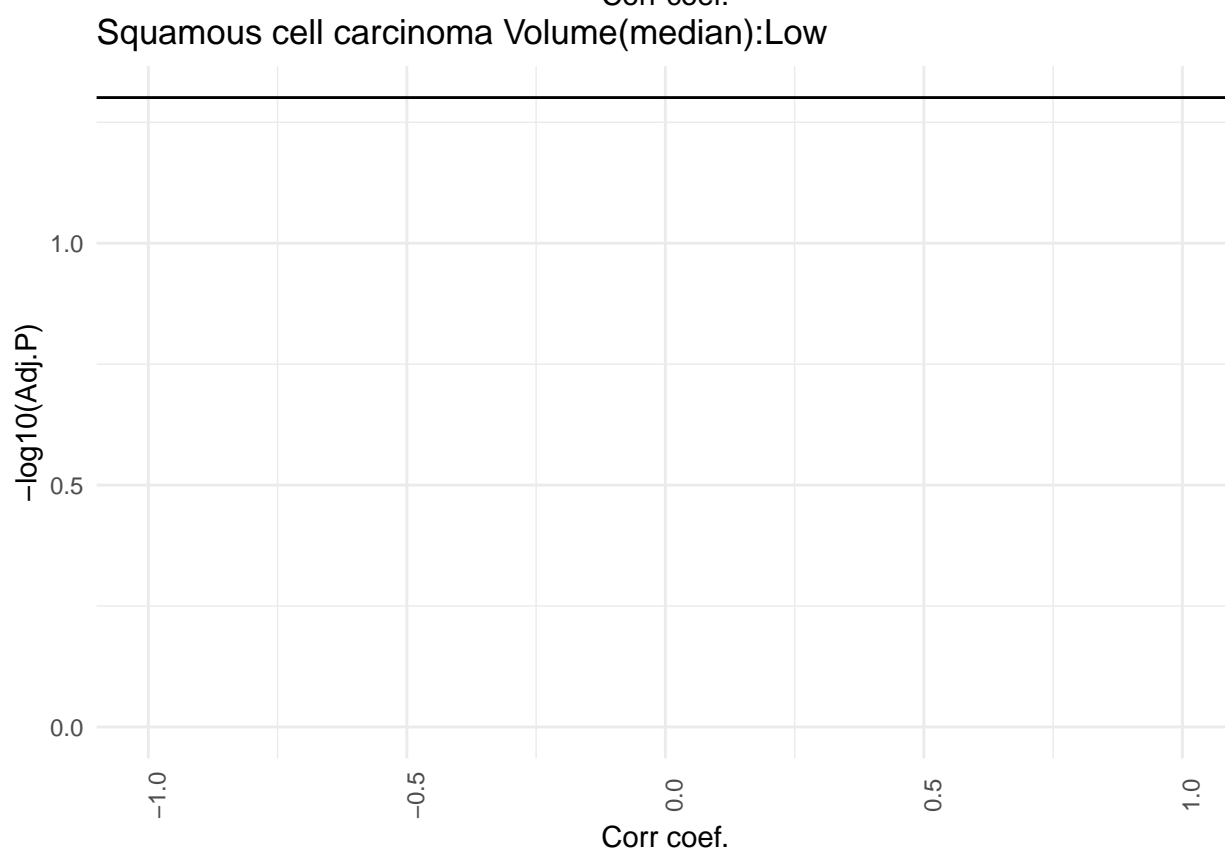
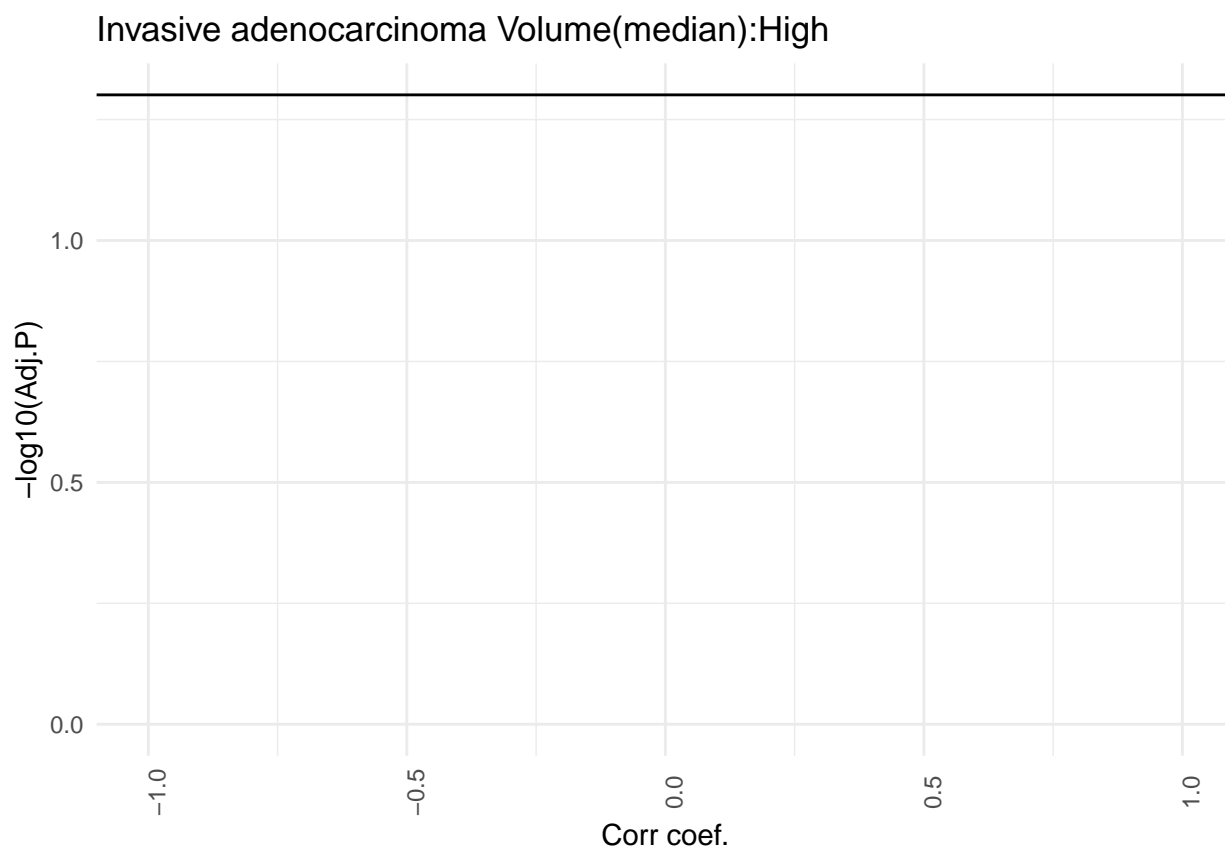


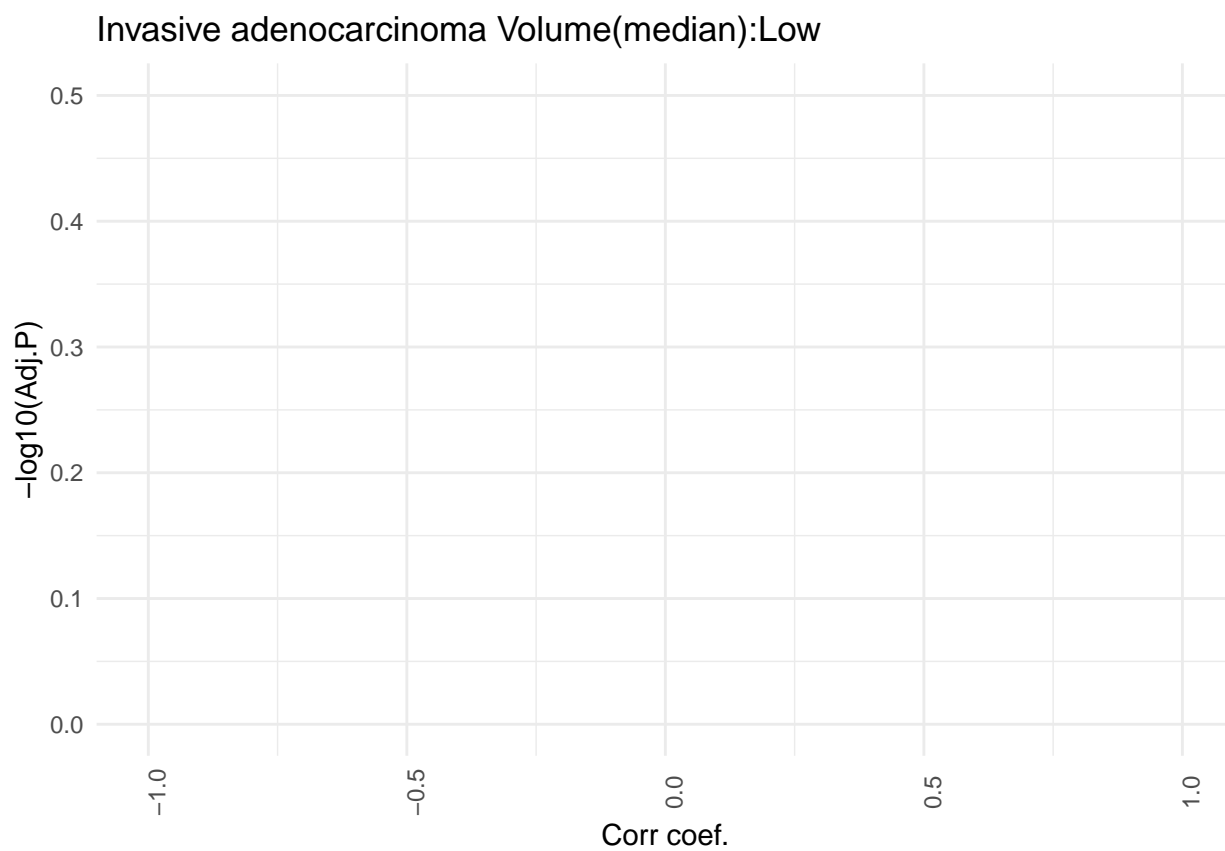


## Gene Expression Analysis by volume group and cancer type

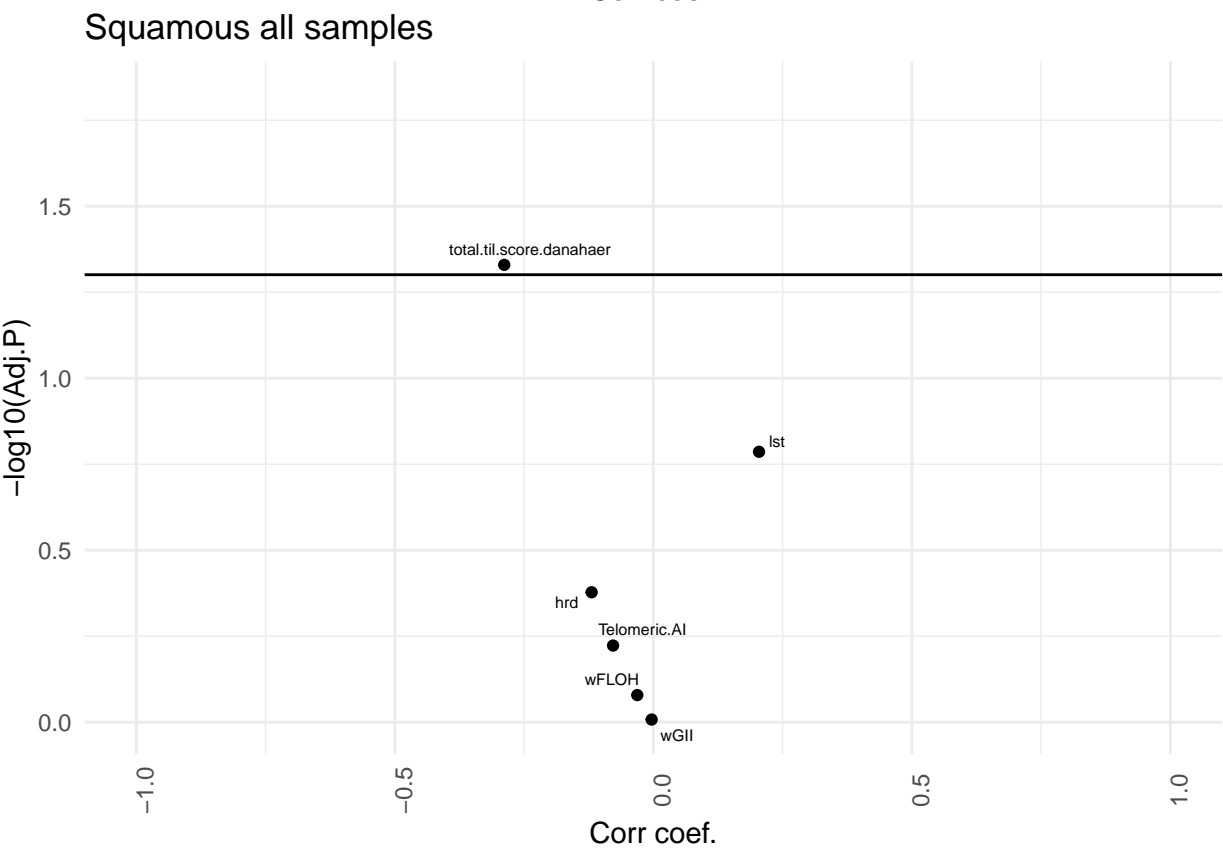
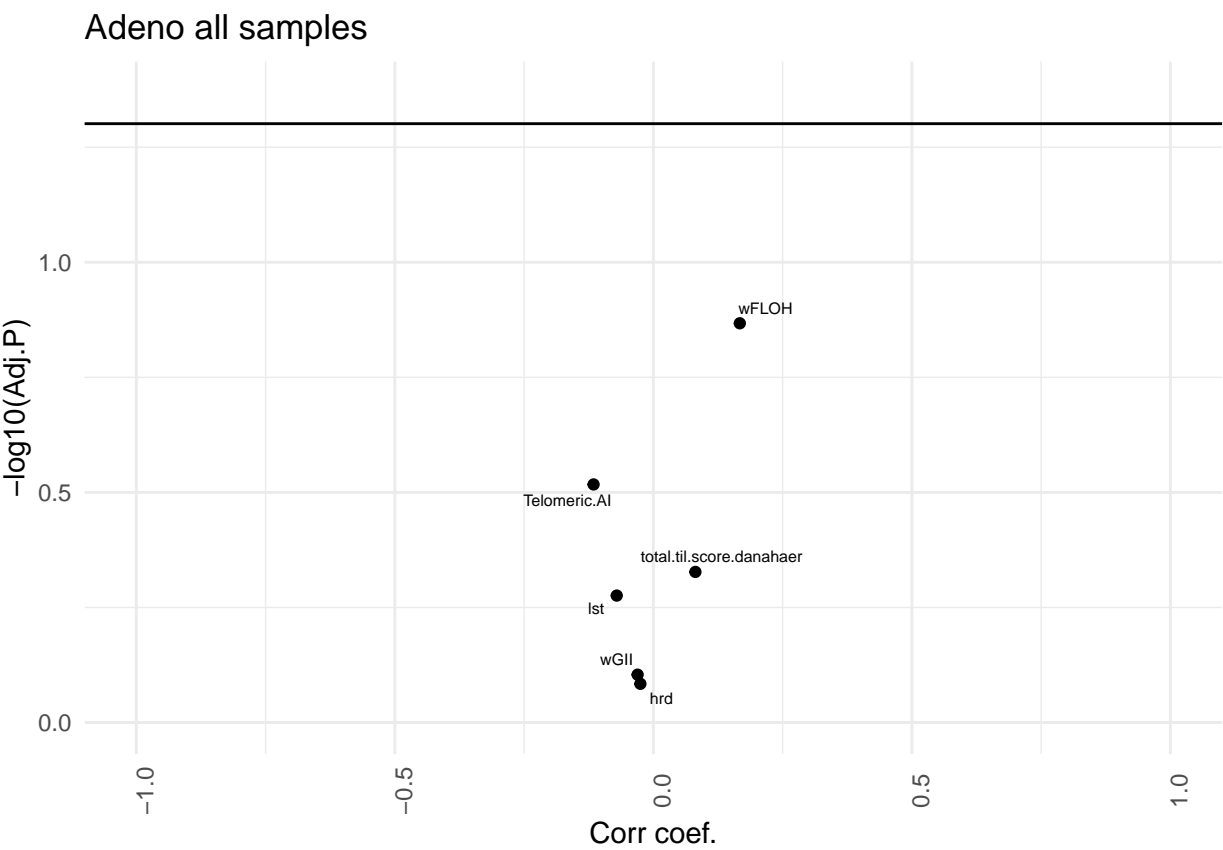
- Genes that were picked for analysis were based on mean and SD (entire cohort)



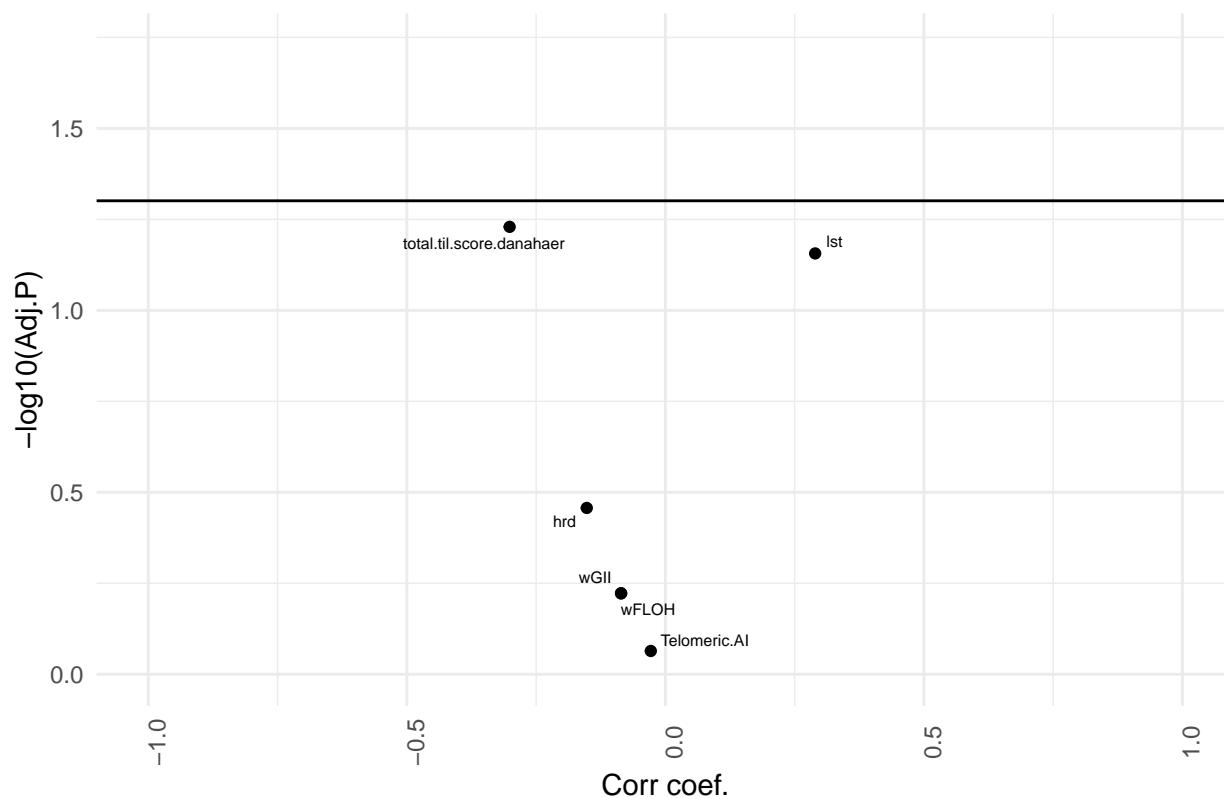




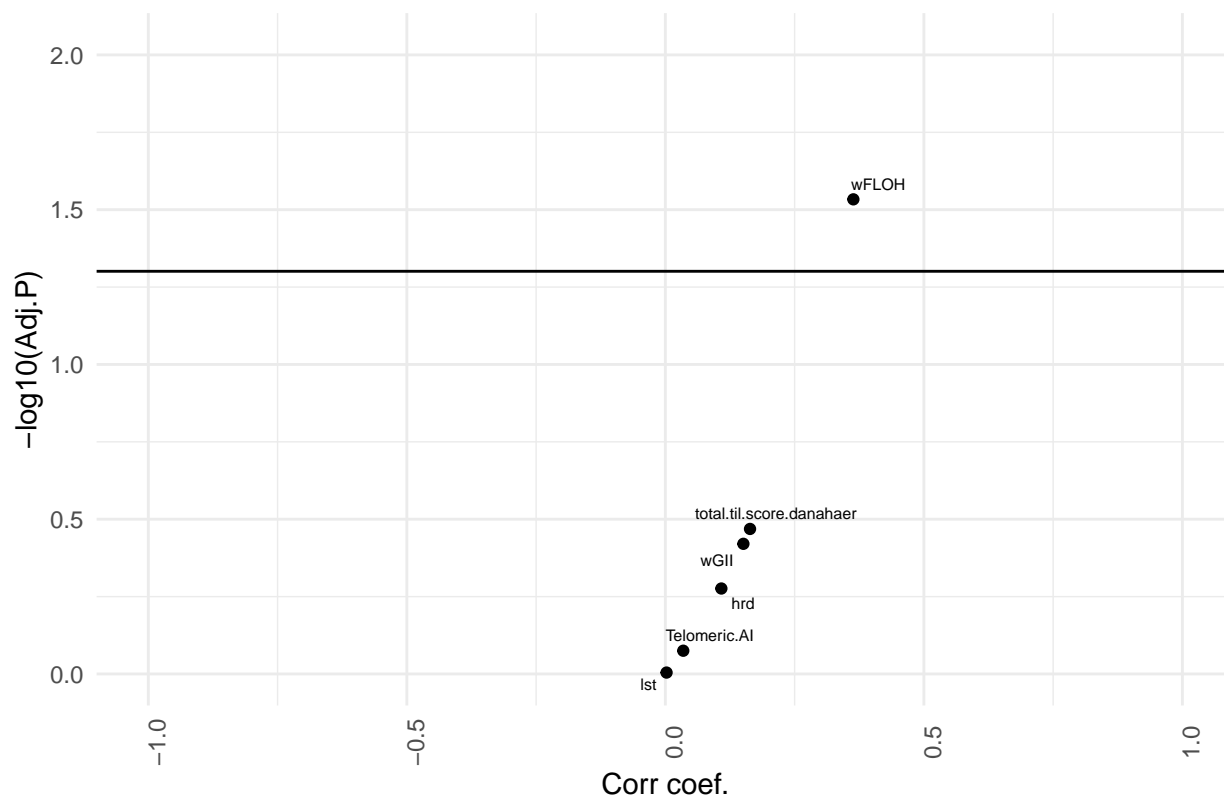
# Chr Instability and TIL



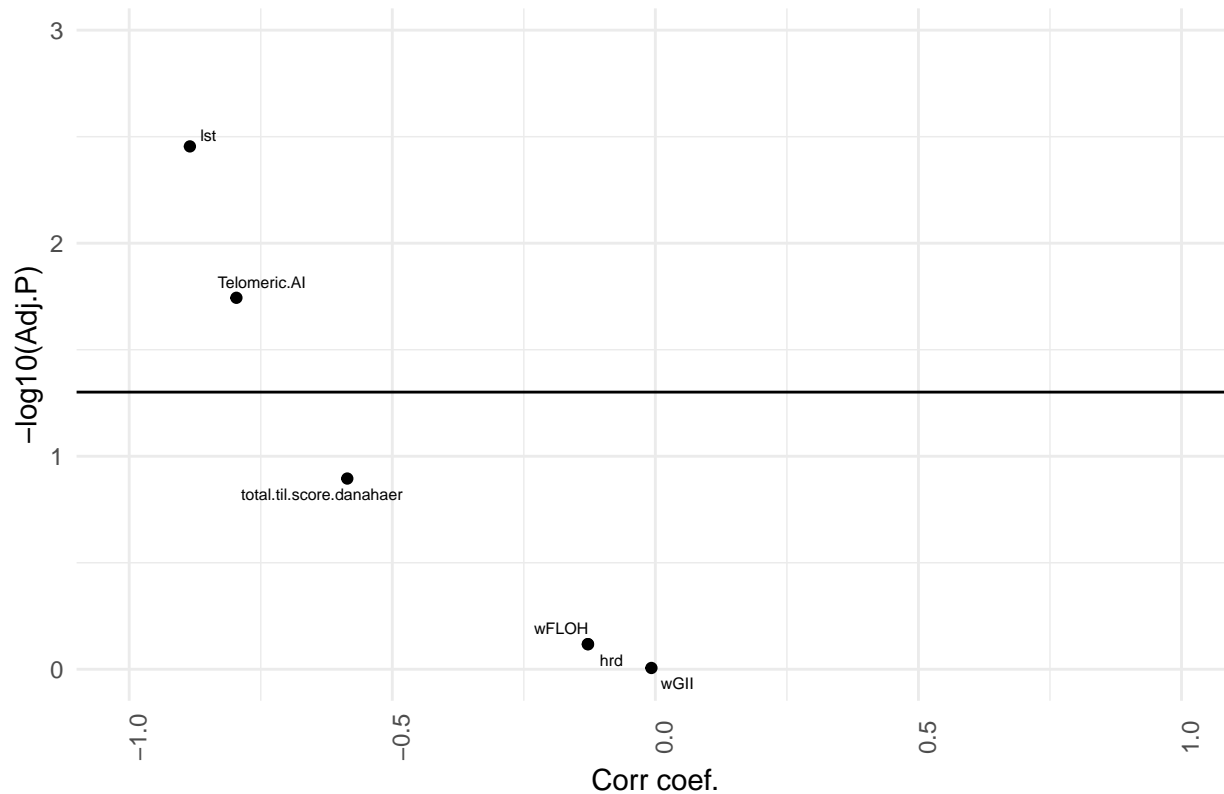
### Squamous cell carcinoma Volume(median):High



### Invasive adenocarcinoma Volume(median):High



### Squamous cell carcinoma Volume(median):Low



### Invasive adenocarcinoma Volume(median):Low

