

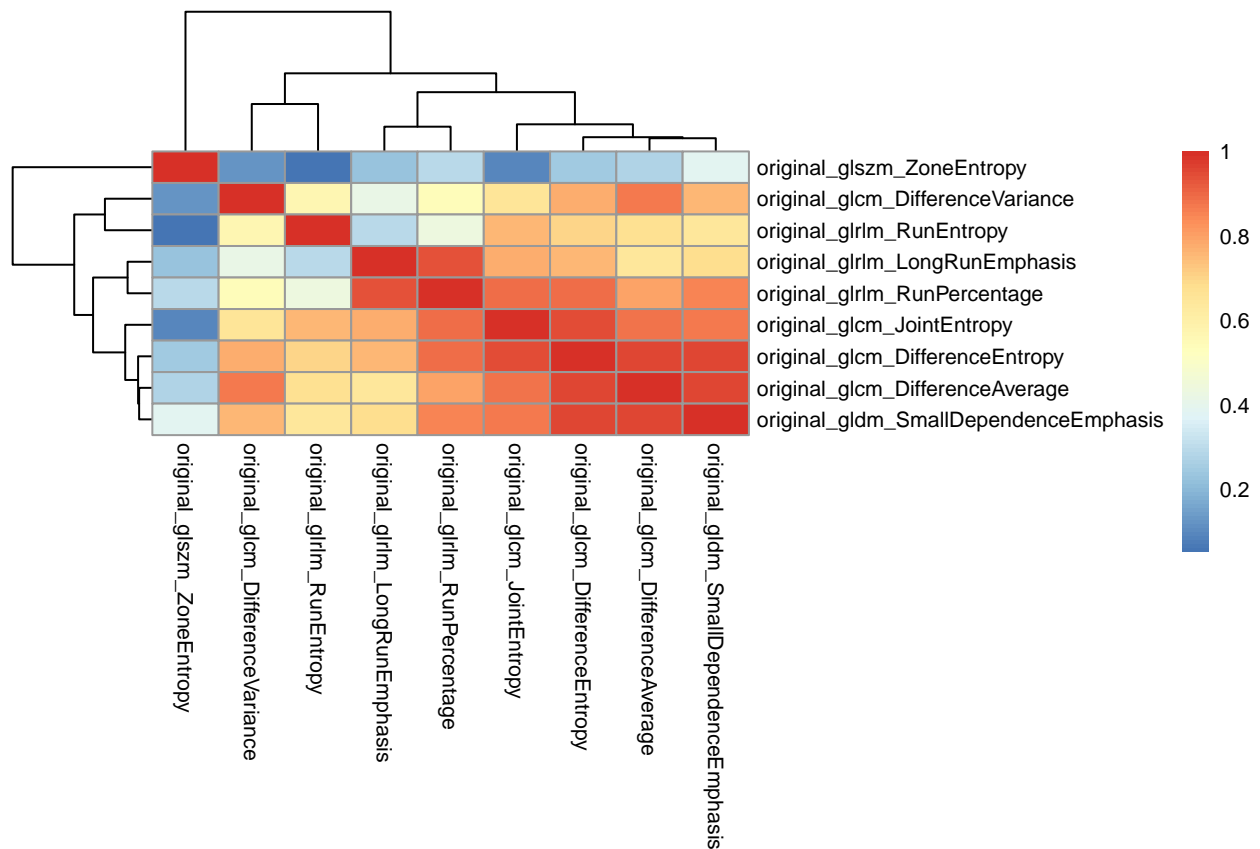
Radiomics

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



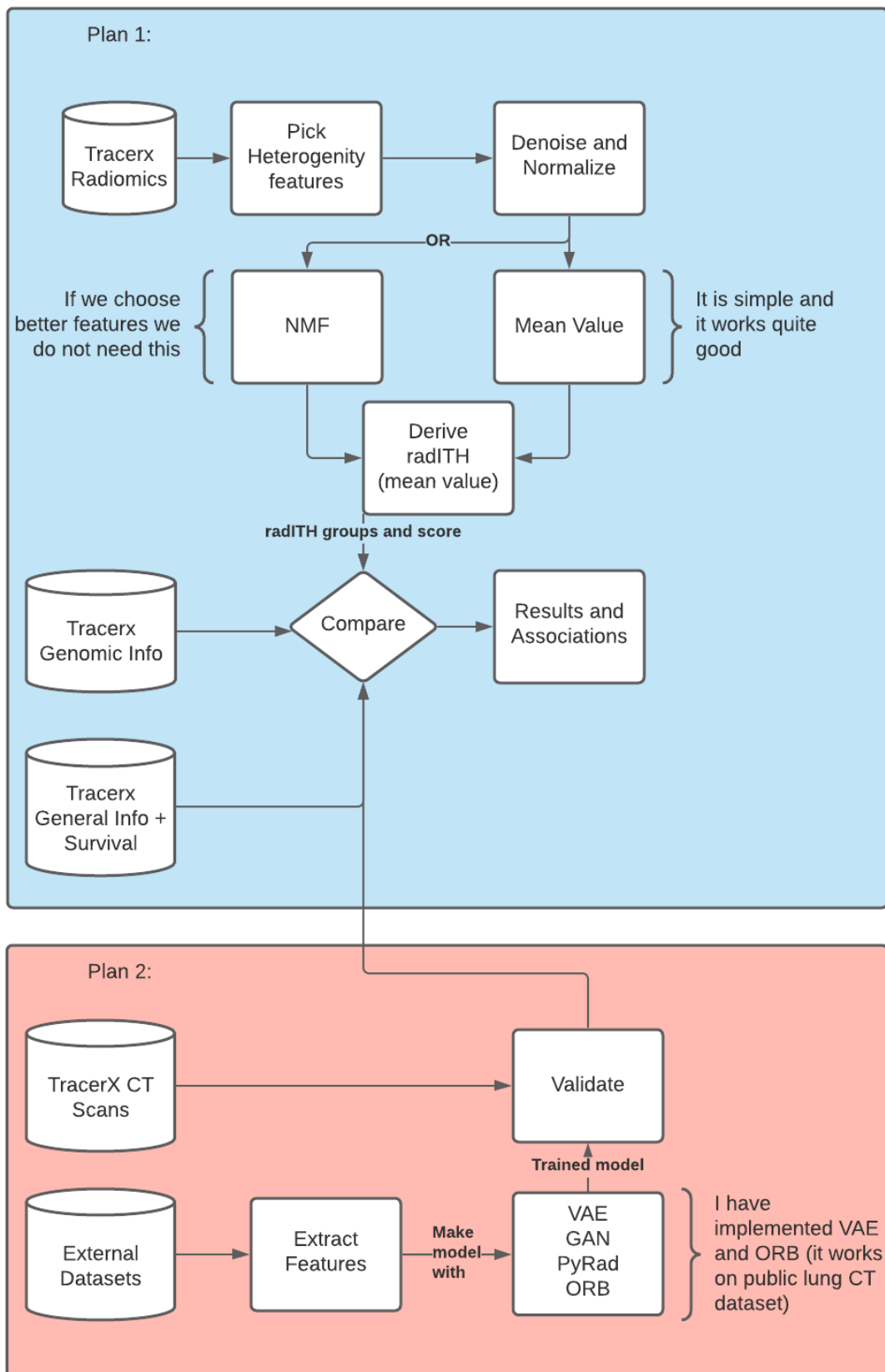
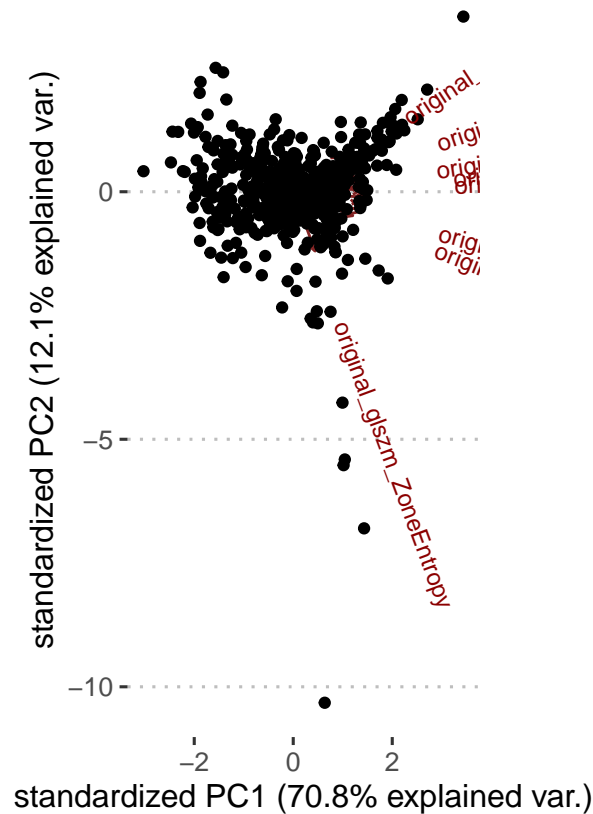


Figure 1: Project Plan



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)
})

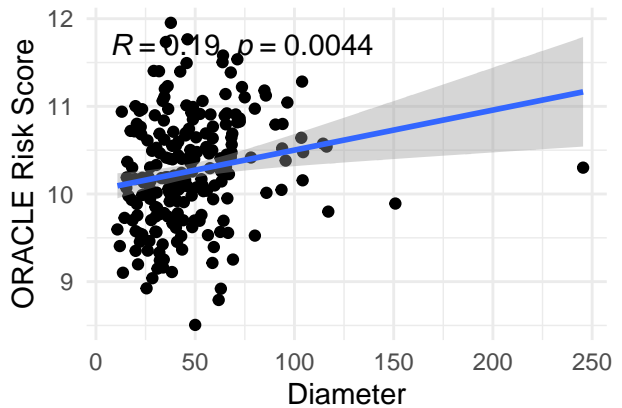
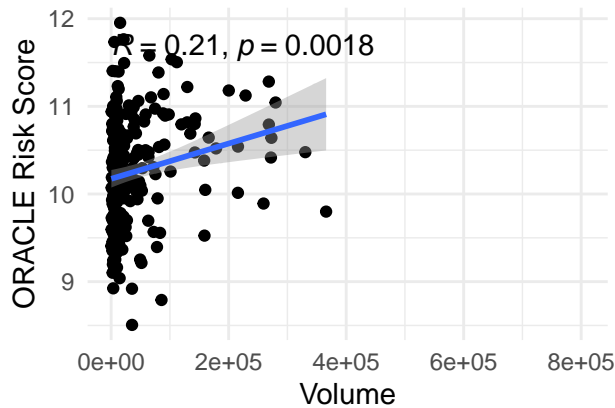
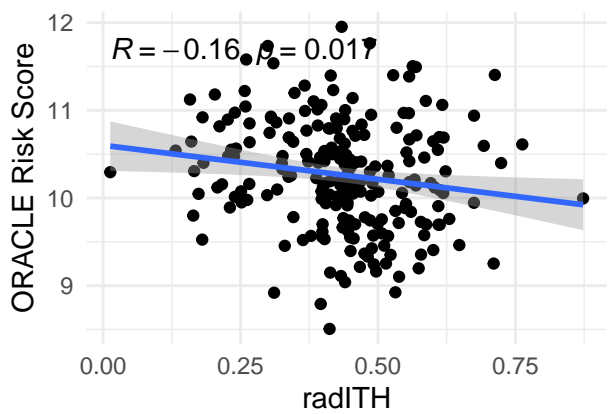
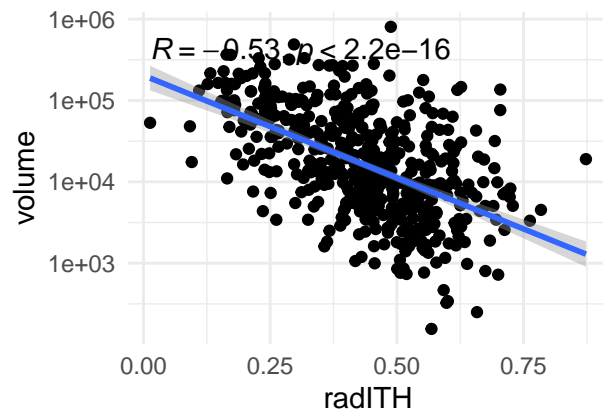
#pyrad$radITH = rowMeans(pyrad[,features_of_interest], na.rm = T)
```

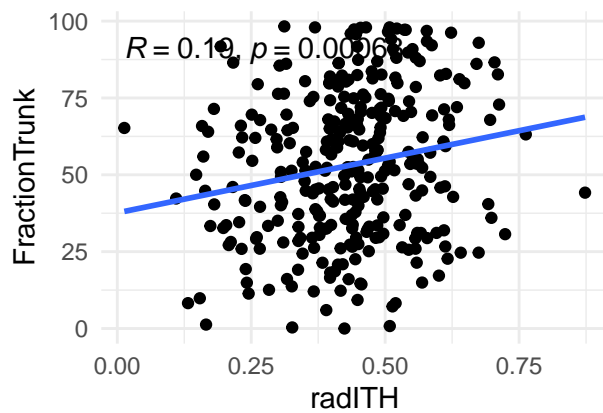
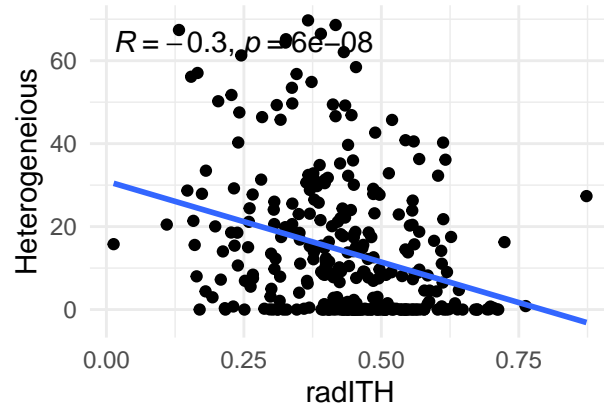
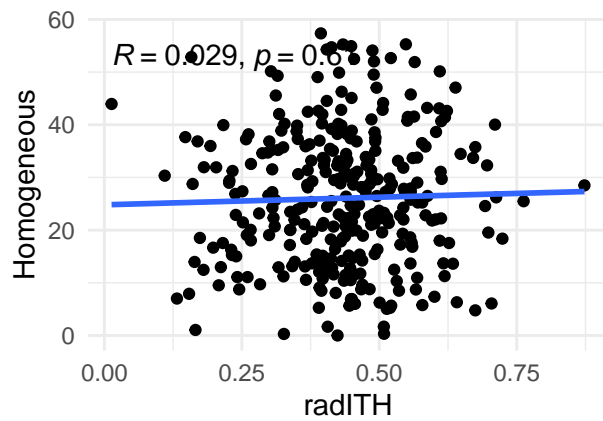
Q = 3

```
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$radlTH_group = gtools::quantcut(pyrad$radlTH, q=Q, na.rm=TRUE)
```

Expected correlations

- Negative cor radlTH 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$radITH_group, tmp[, col])
## p-value = 0.03559
## alternative hypothesis: two.sided
##
## [1] "pi3k"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.0346
```

```

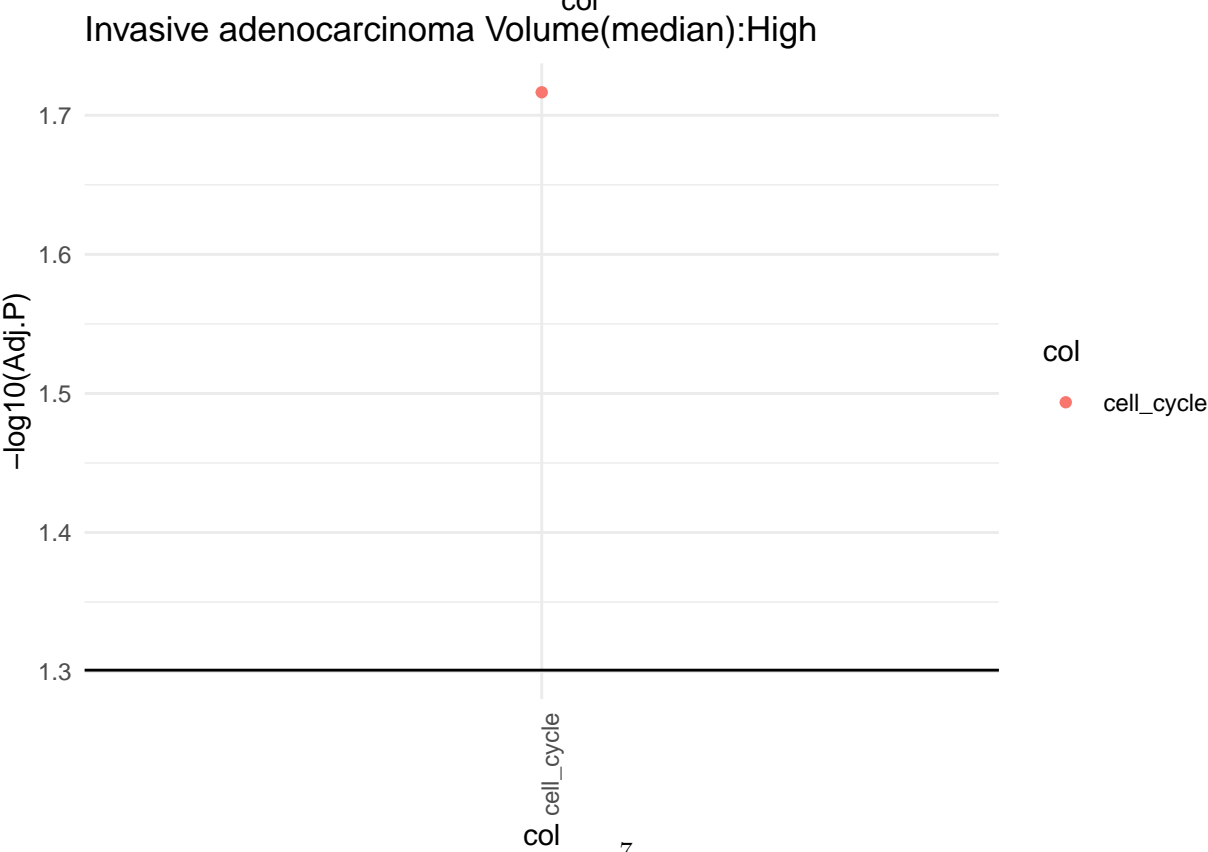
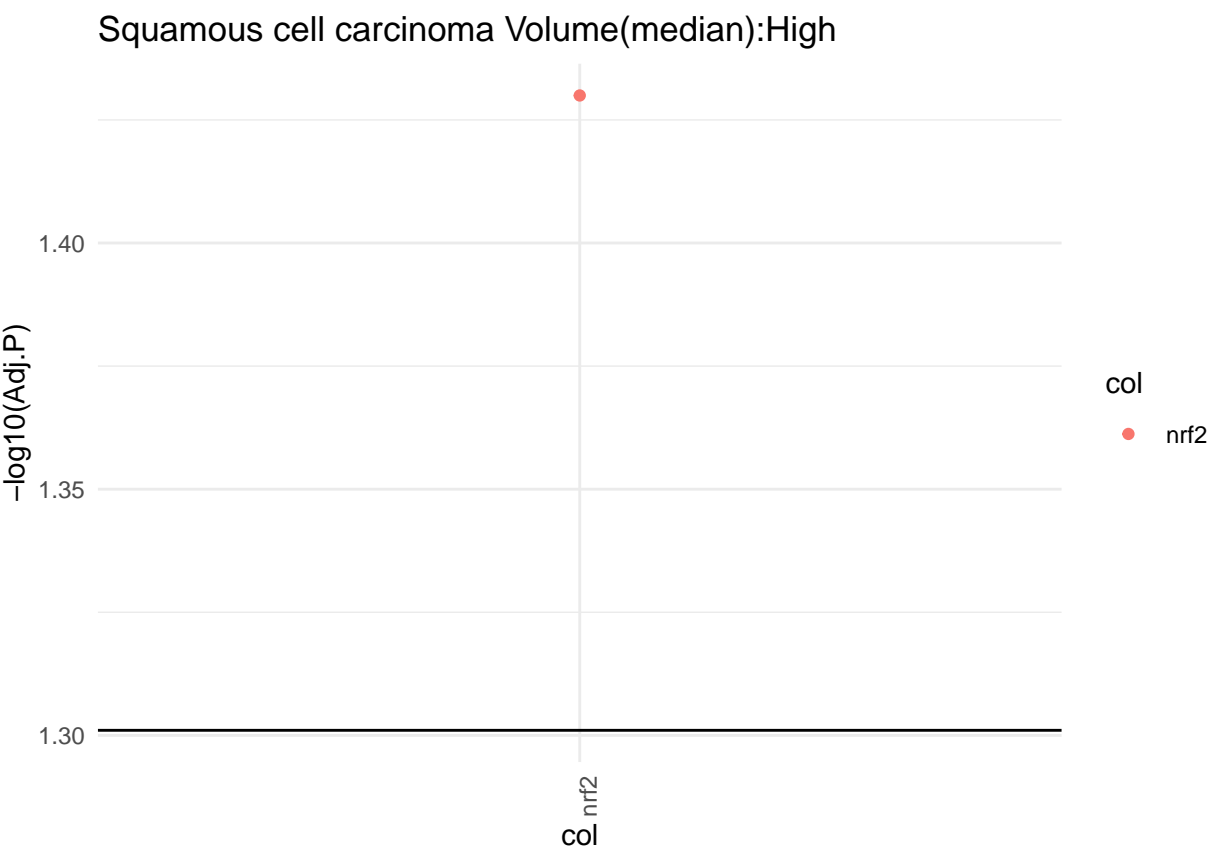
## alternative hypothesis: two.sided
##
## [1] "cell_cycle"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.007461
## alternative hypothesis: two.sided

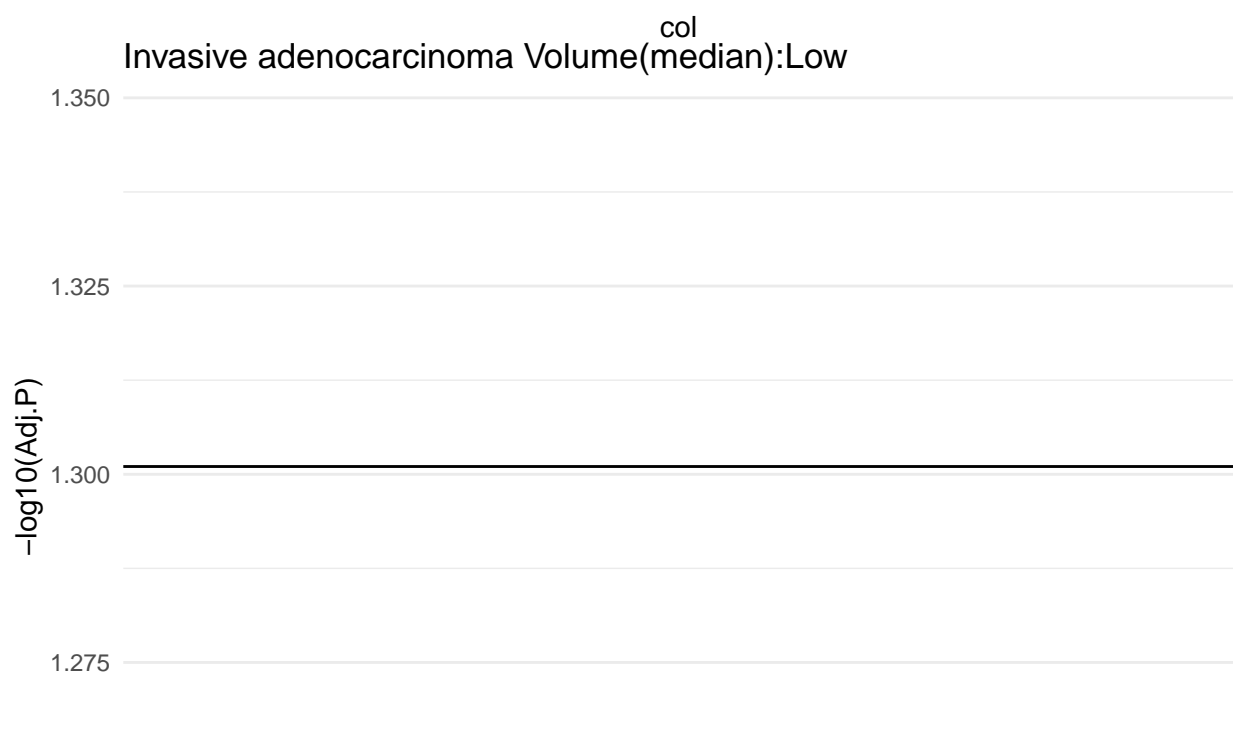
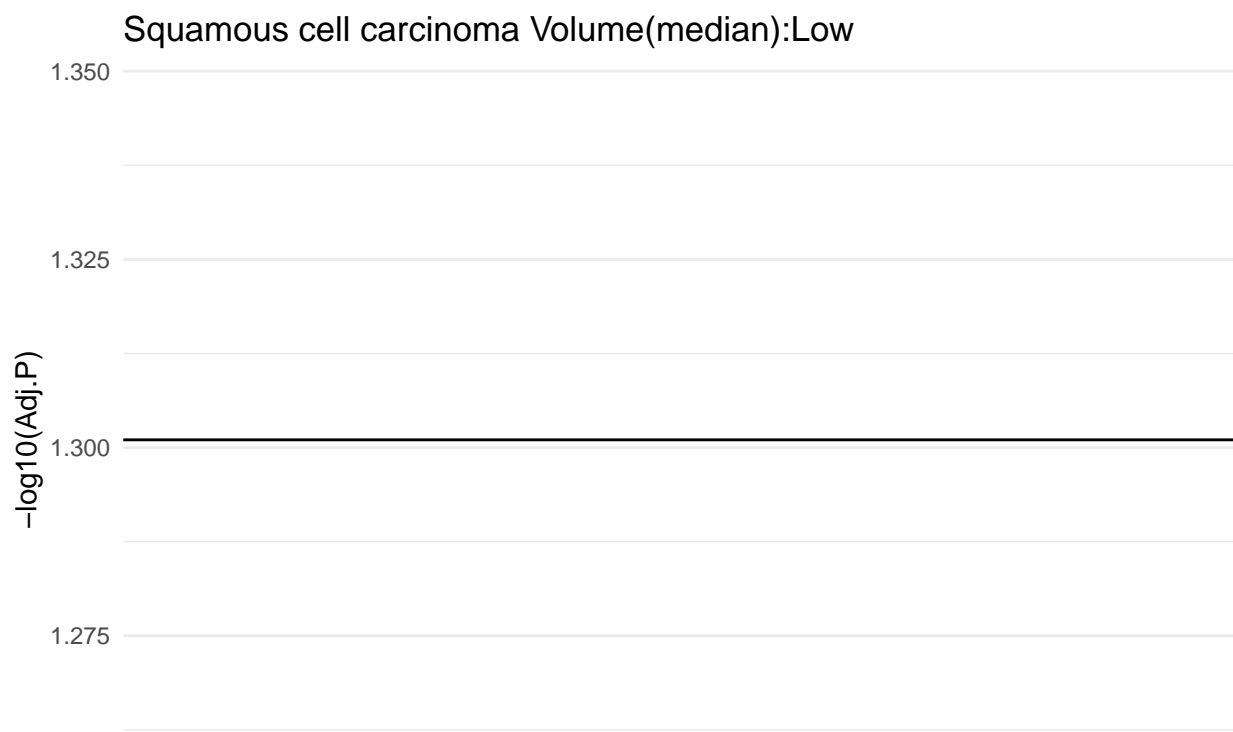
## [1] "Squamous fisher test results"

## [1] "rtk_kras"
##
## Fisher's Exact Test for Count Data
##
## data:  table(tmp$radITH_group, tmp[, col])
## p-value = 0.007555
## alternative hypothesis: two.sided

```

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





col

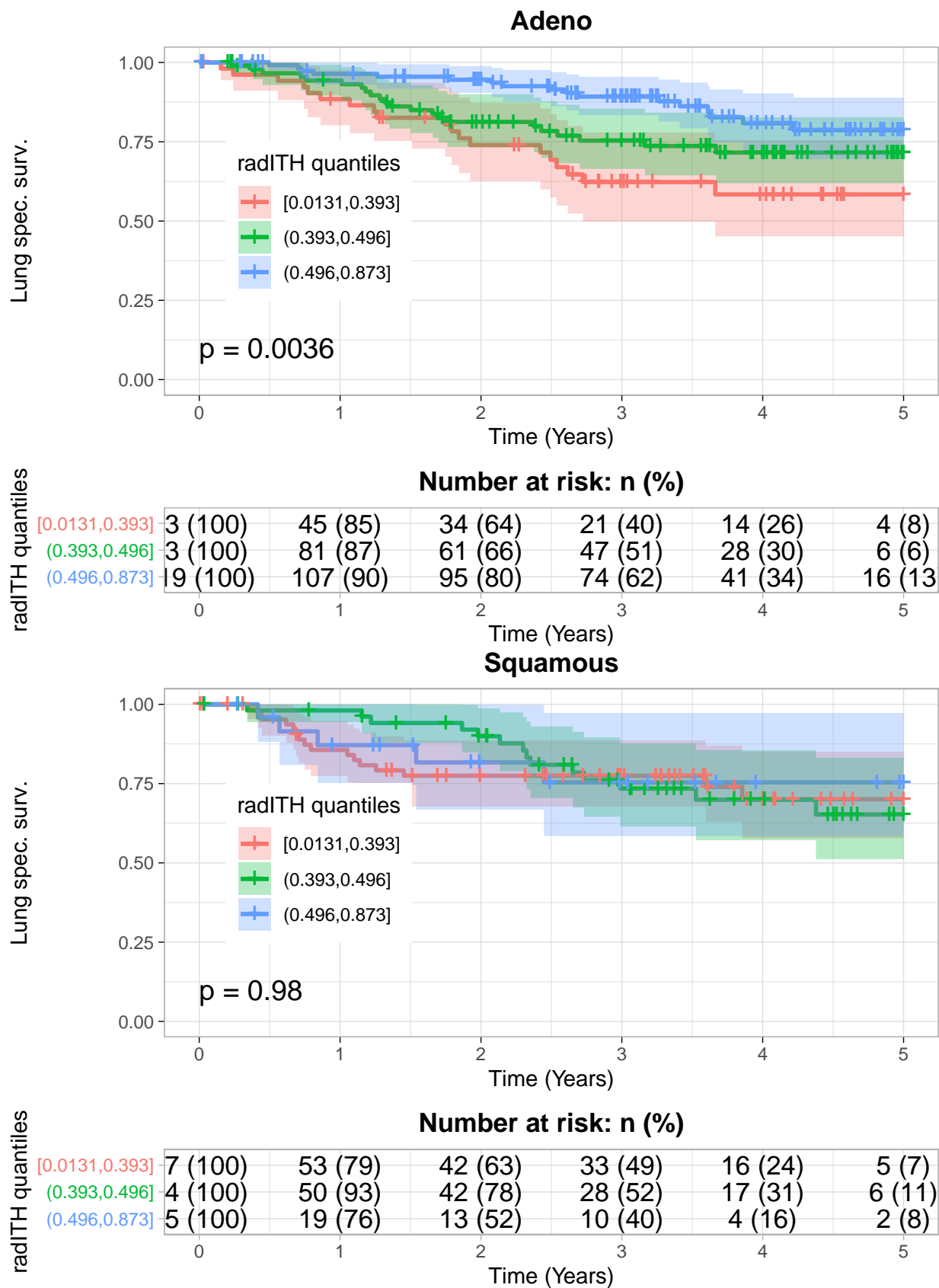
Does Volume or diameter predict biology?

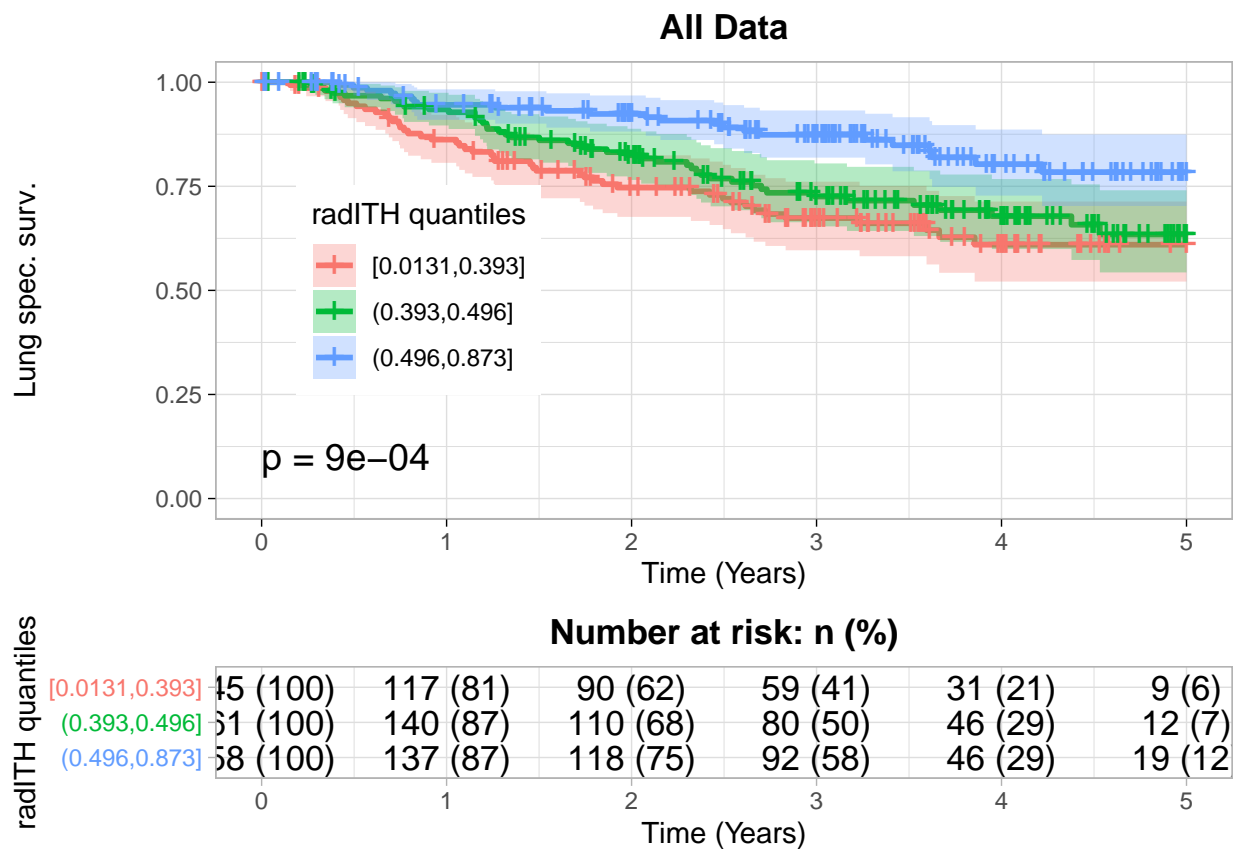
- Diameter is not associated at all
- Volume is associated with HIPPO

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

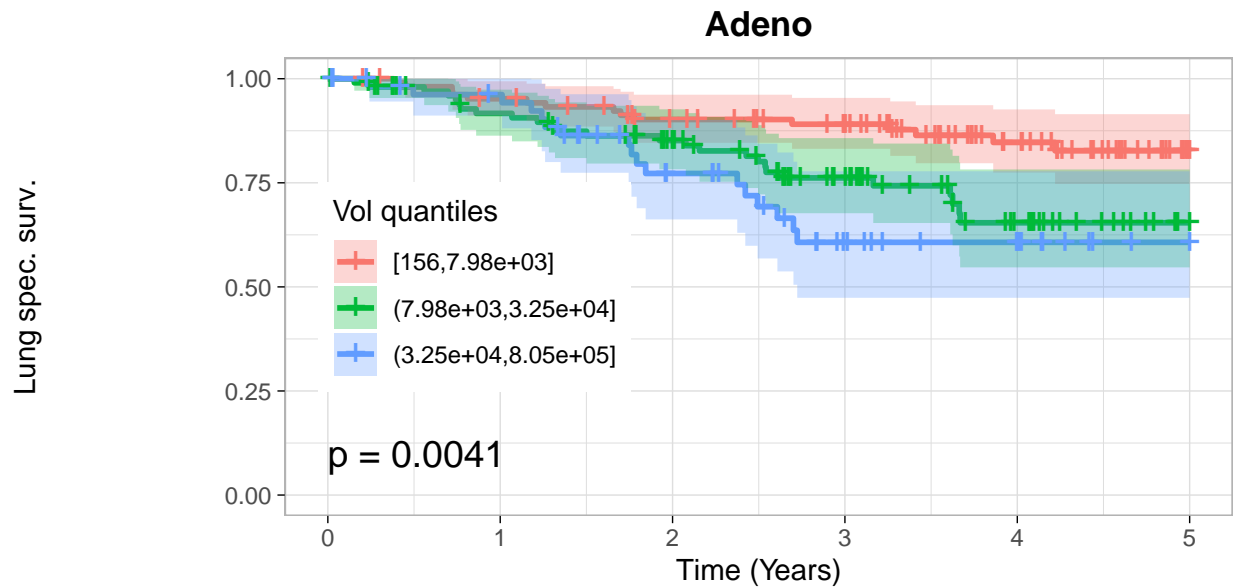
```
## [1] "Squamous fisher test results"
```

How does radITH associate with survival?





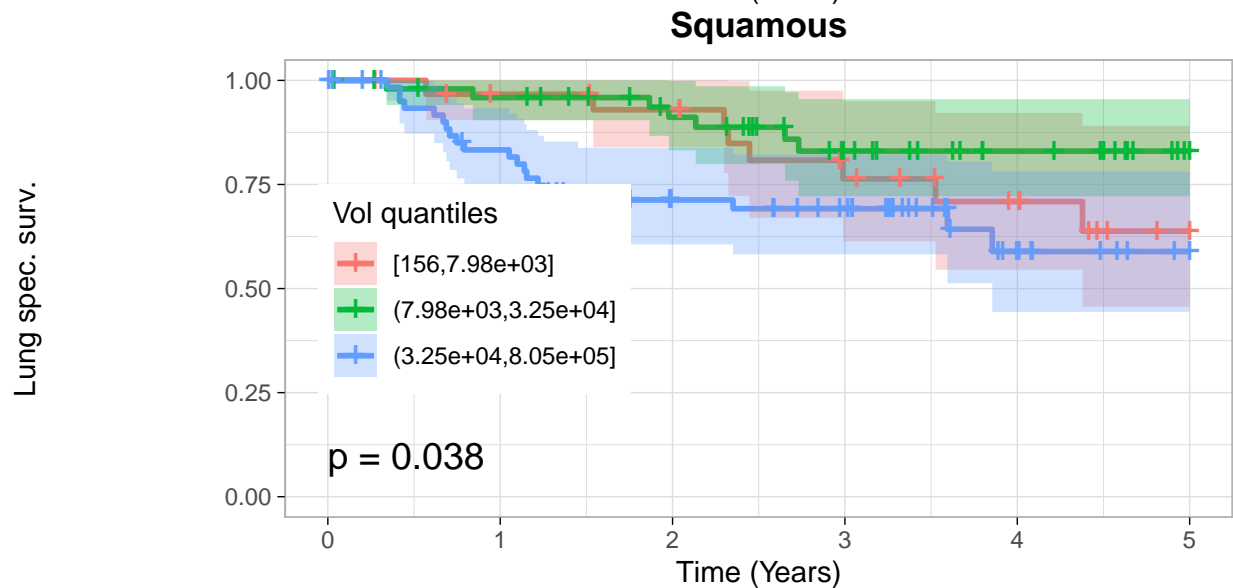
How does volume (diameter) associate to survival?



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)

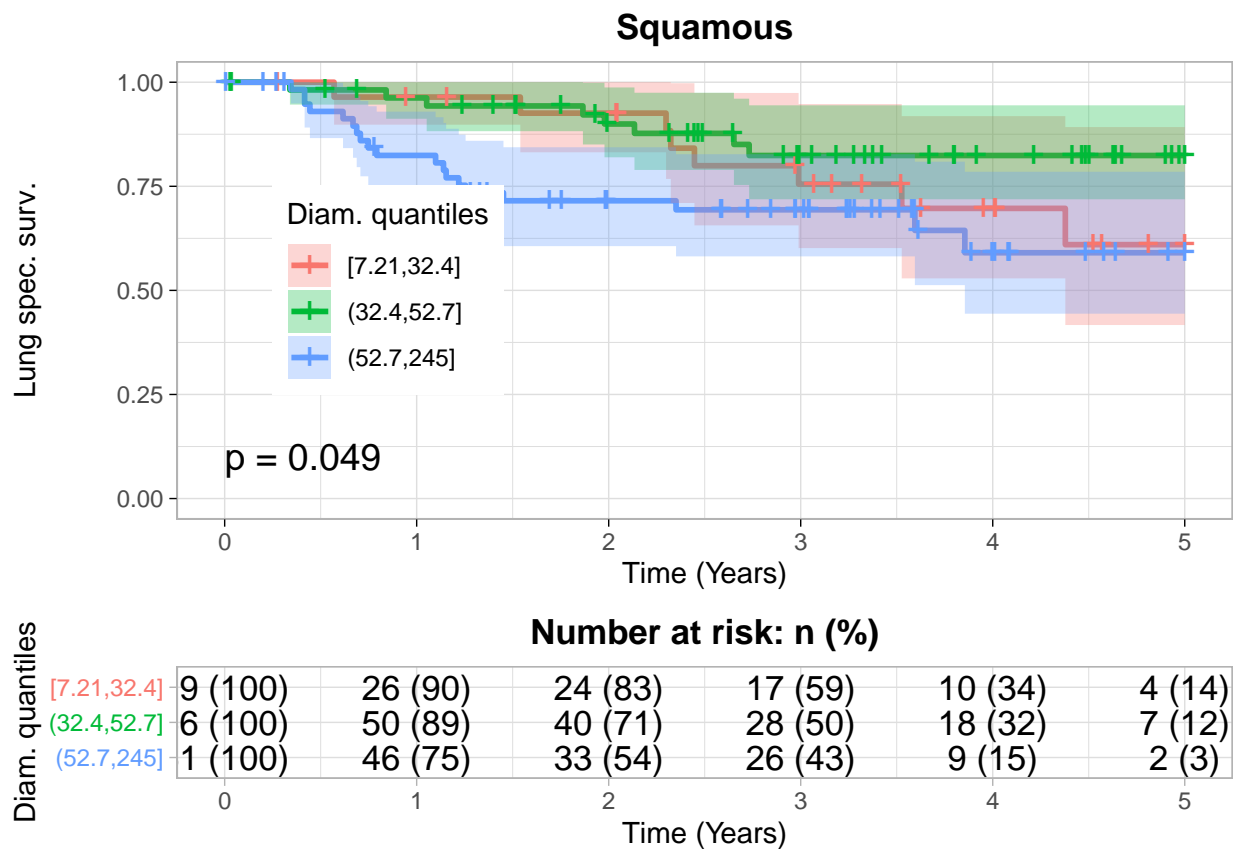
Time (Years)



Number at risk: n (%)

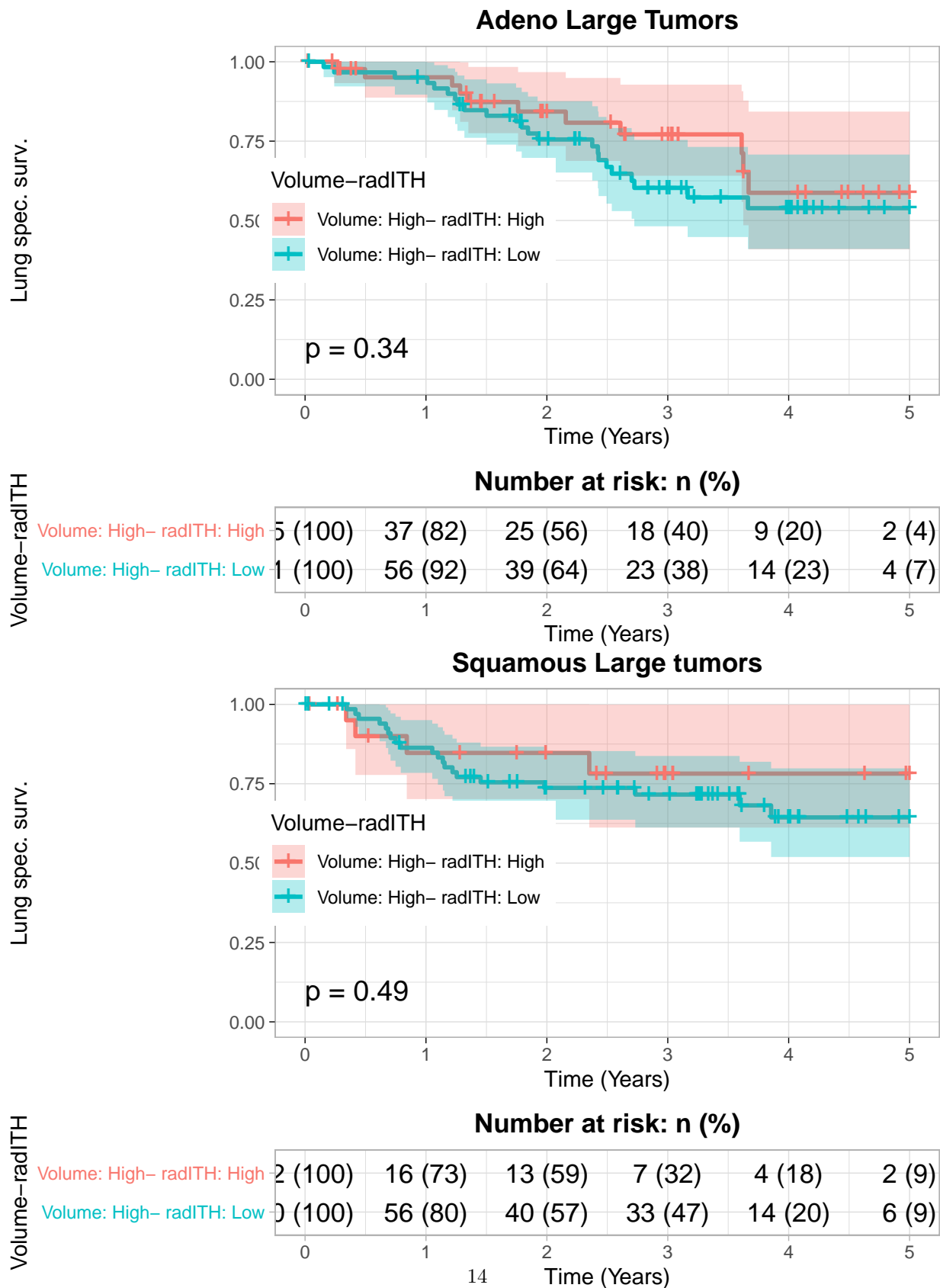
Vol quantiles	0	1	2	3	4	5
[156,7.98e+03]	1 (100)	27 (87)	25 (81)	17 (55)	12 (39)	5 (16)
(7.98e+03,3.25e+04]	1 (100)	46 (90)	38 (75)	26 (51)	17 (33)	7 (14)
(3.25e+04,8.05e+05]	4 (100)	49 (77)	34 (53)	28 (44)	8 (12)	1 (2)

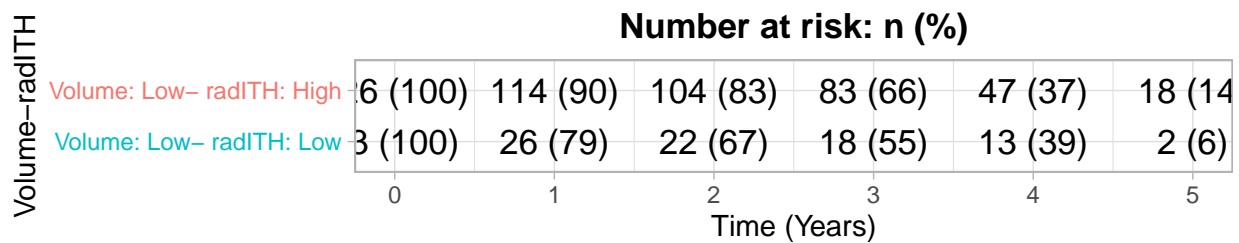
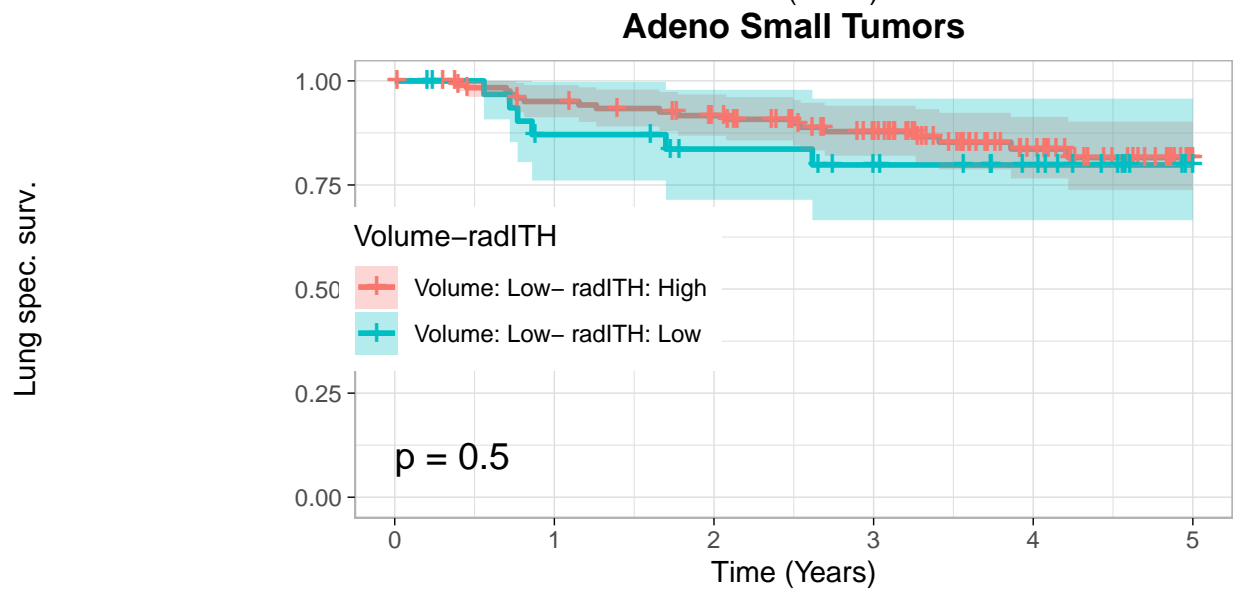
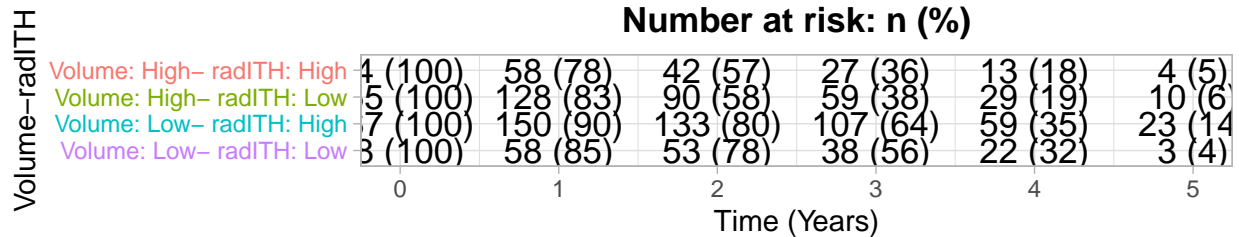
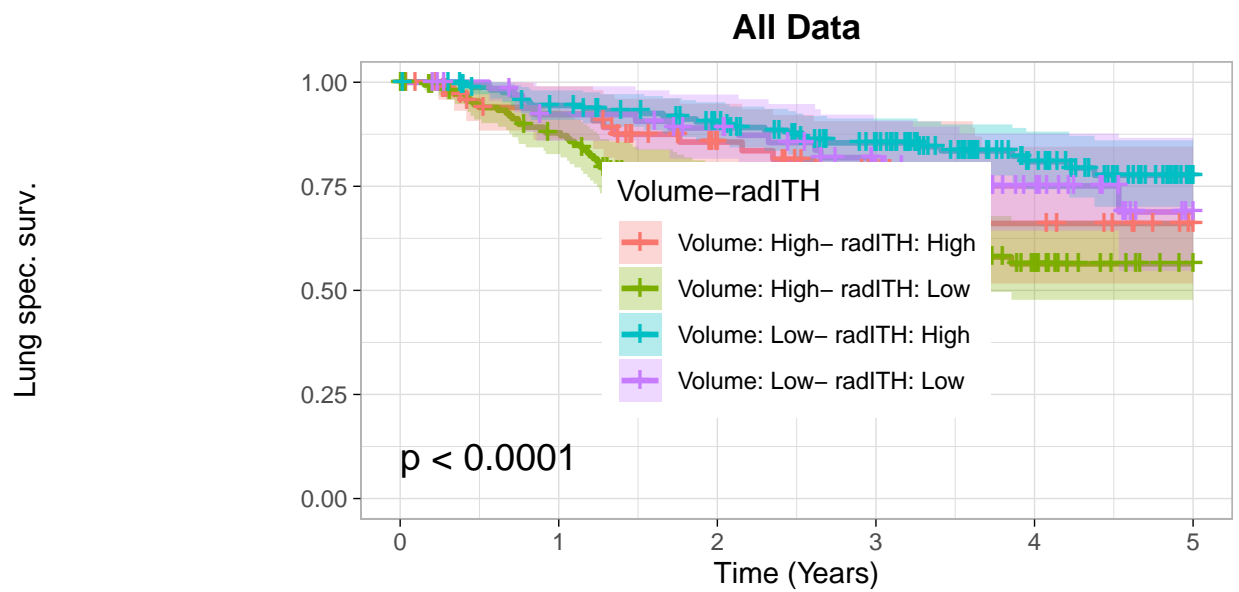
Time (Years)

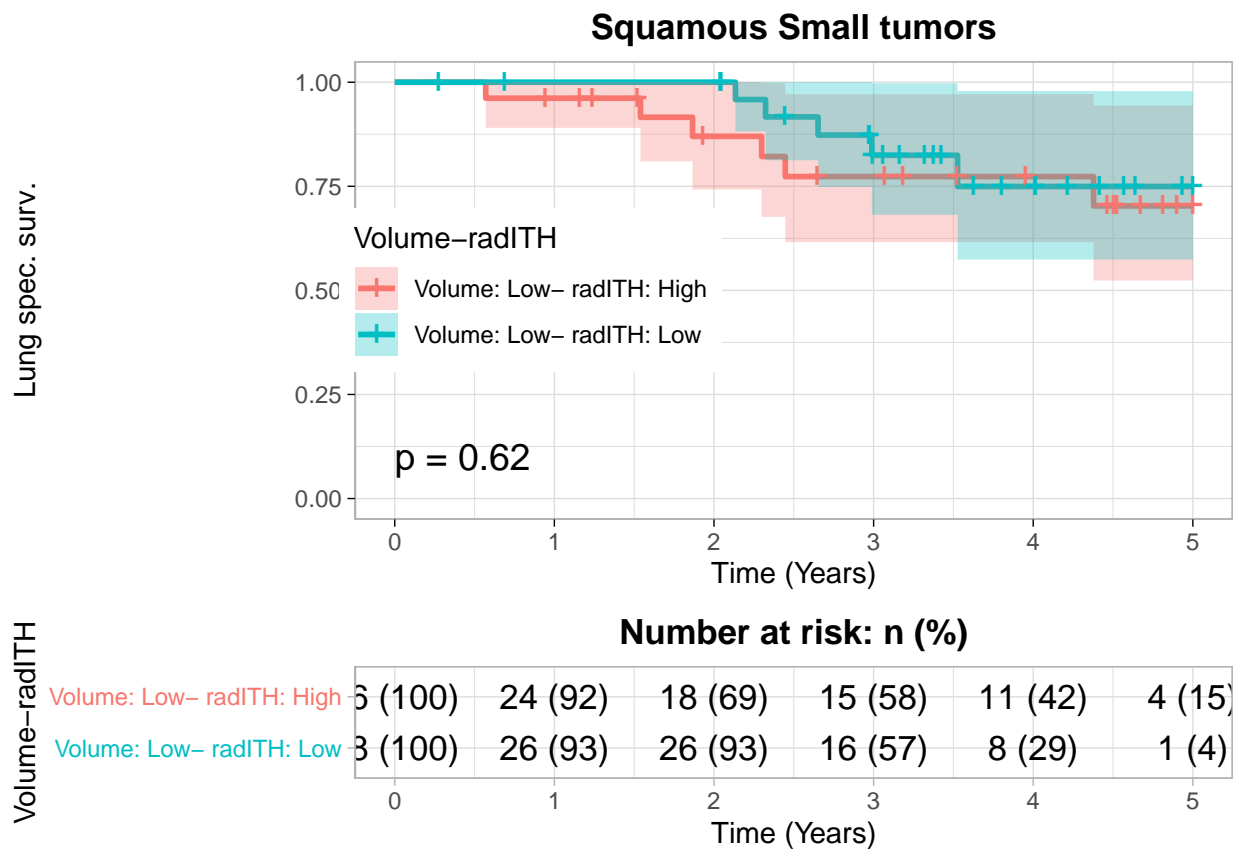


Can we overlap radITH and Volume groups and check survival?

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

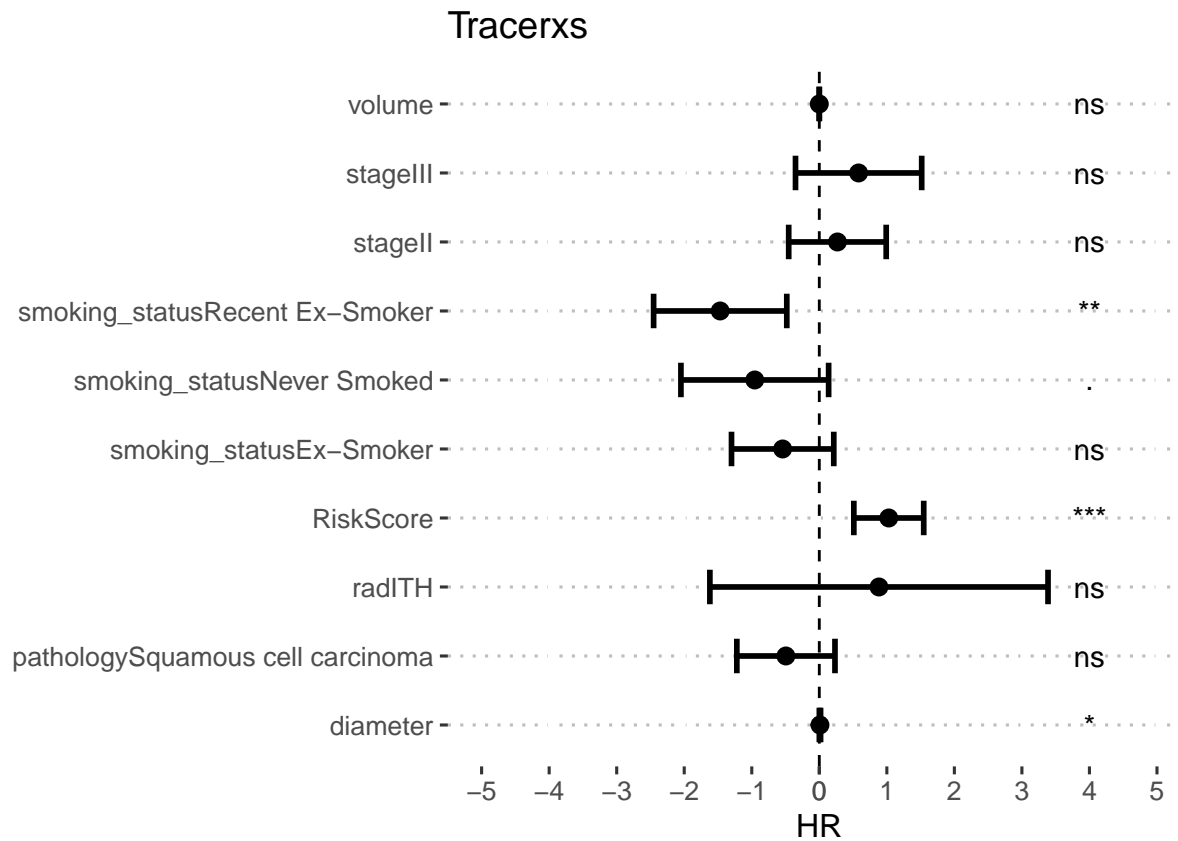






Coxph Model

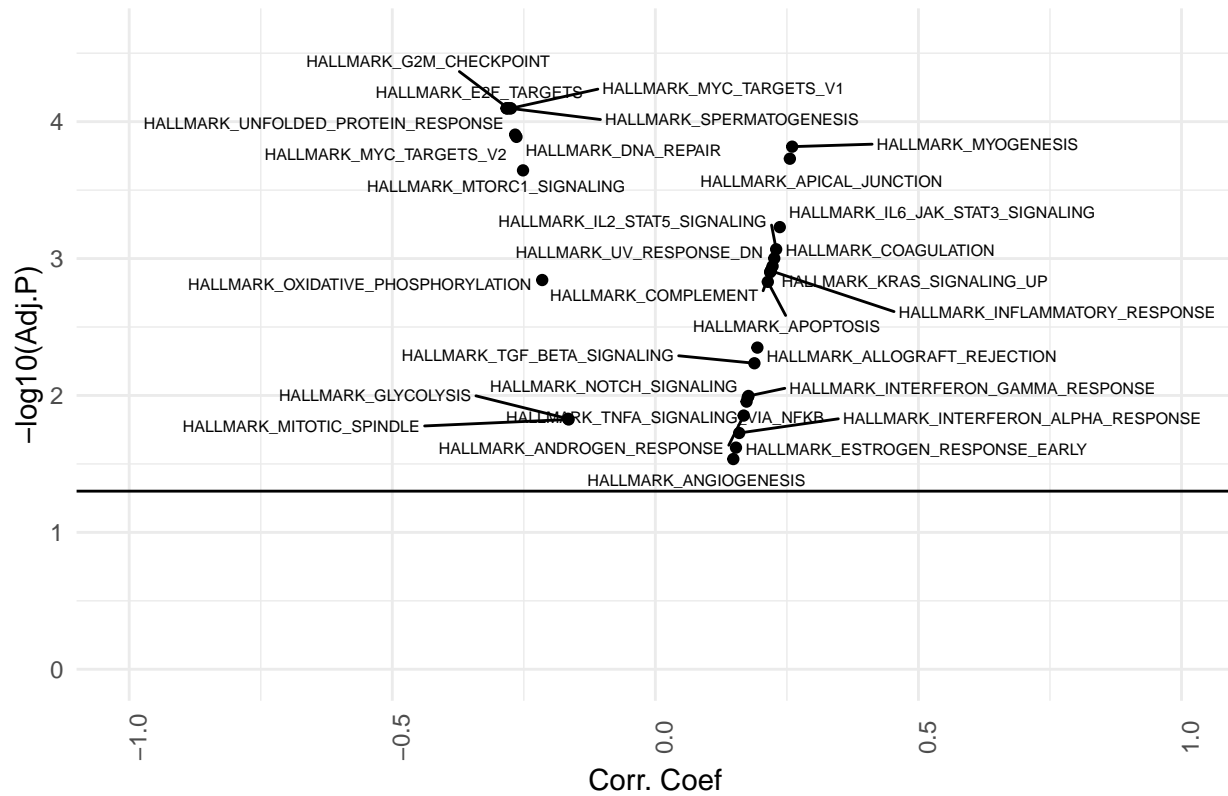
- radlTH does not help improve cox ph model



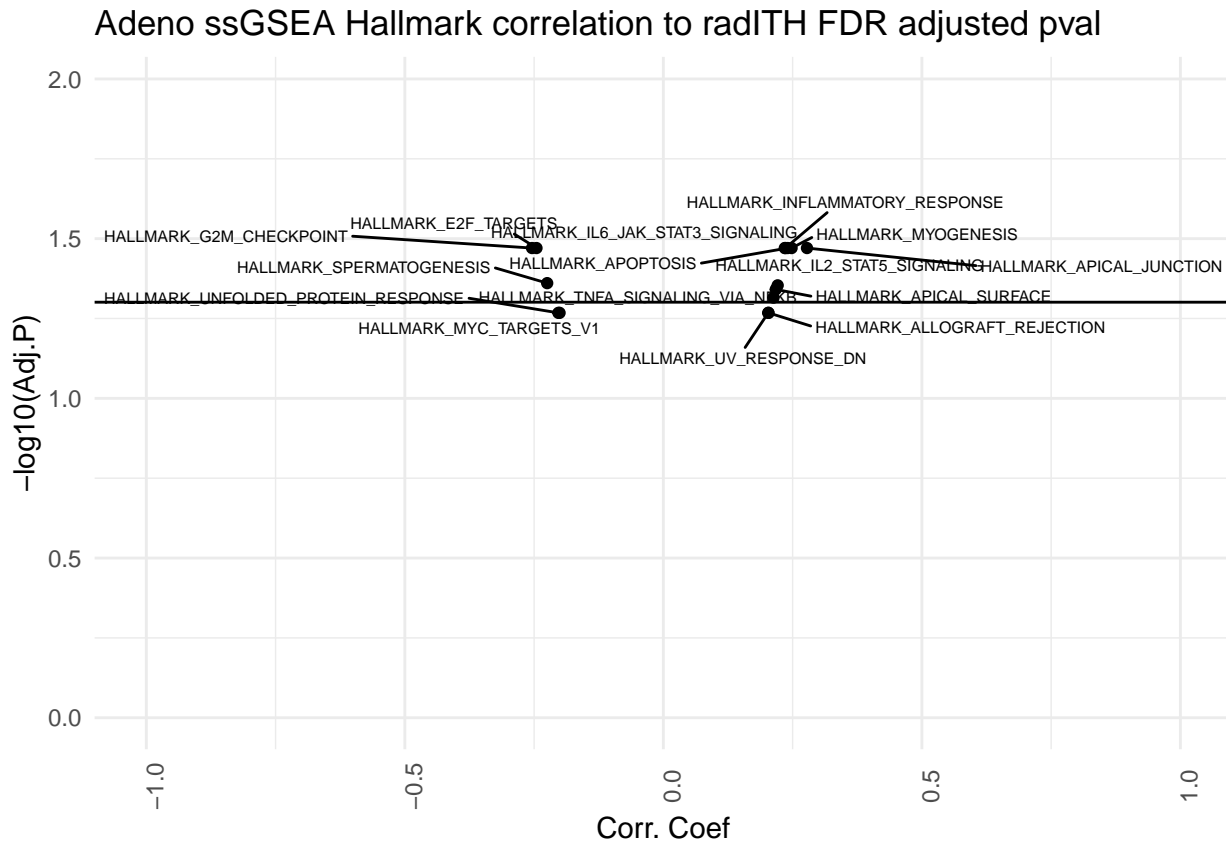
Hallmarks all samples

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

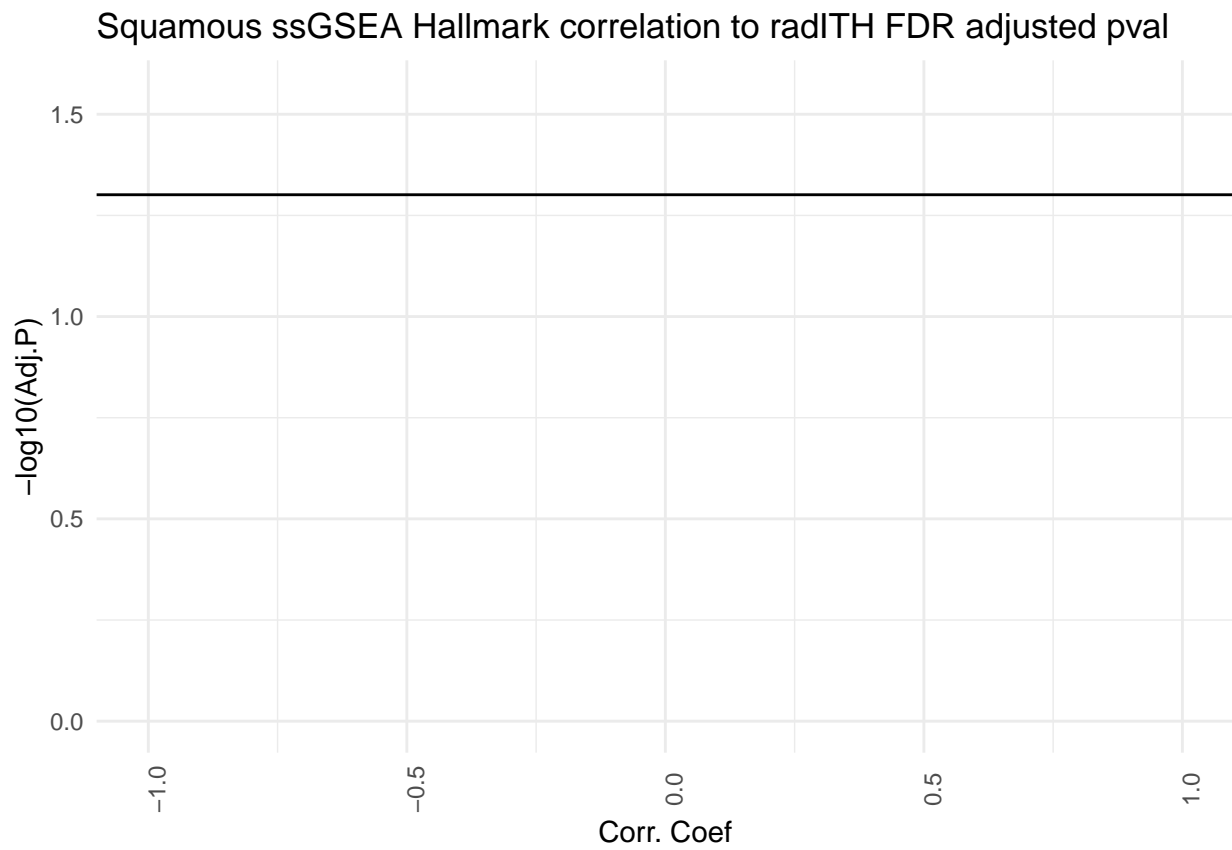
All samples ssGSEA Hallmark correlation to radlTH FDR adjusted pval



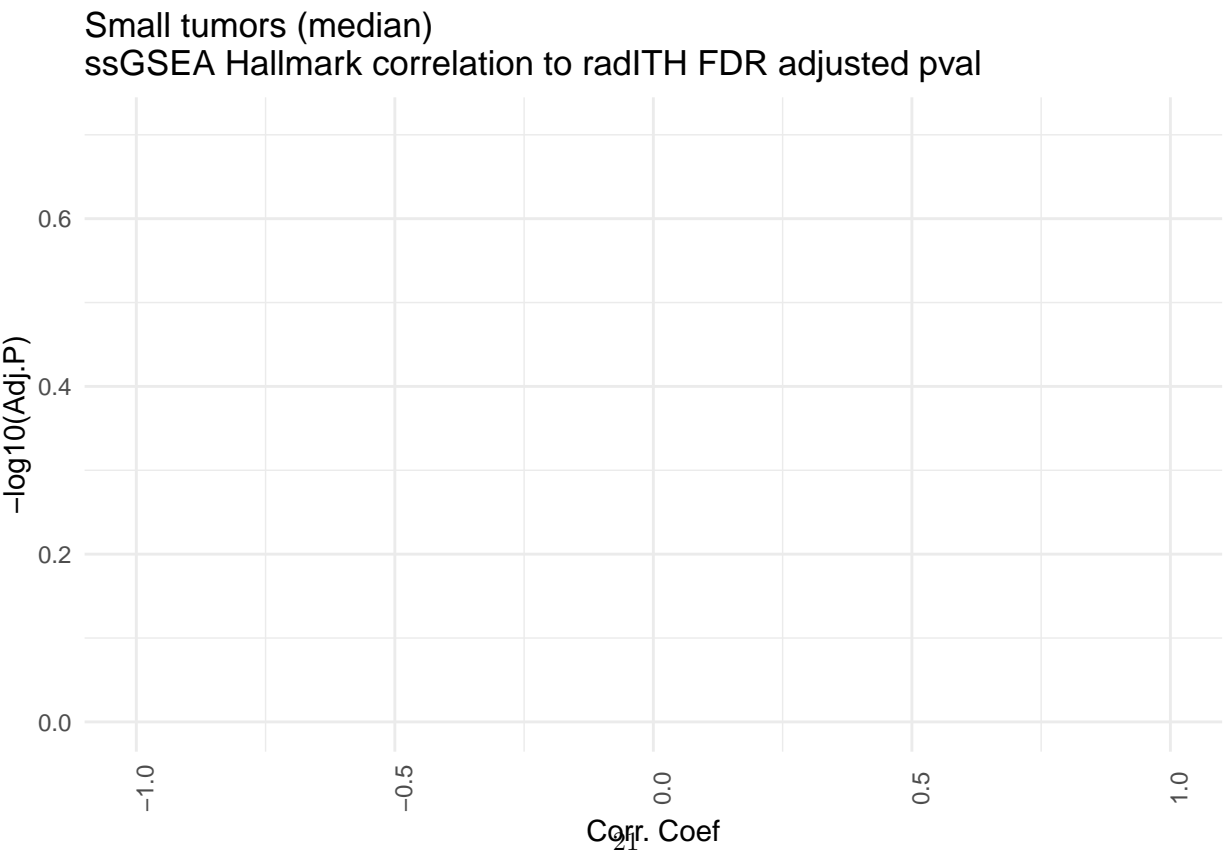
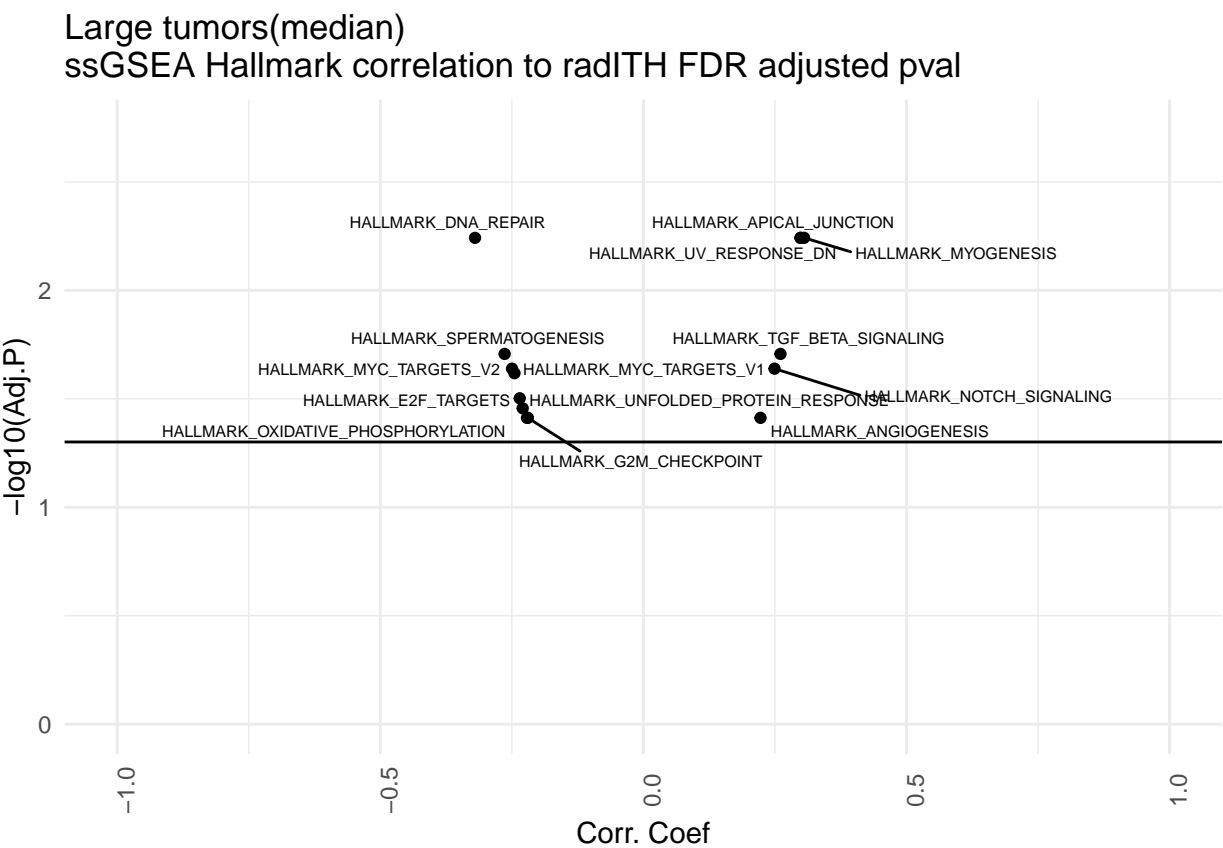
Hallmarks Adeno



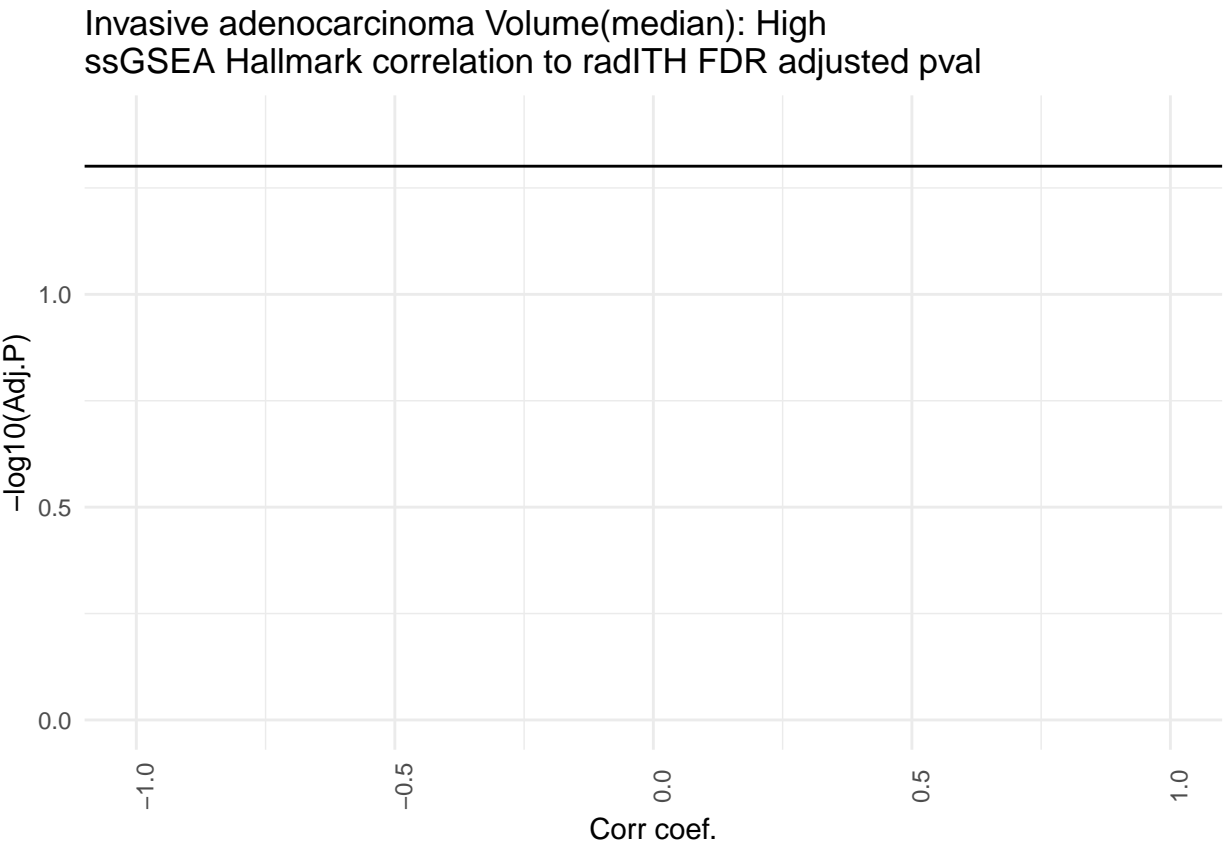
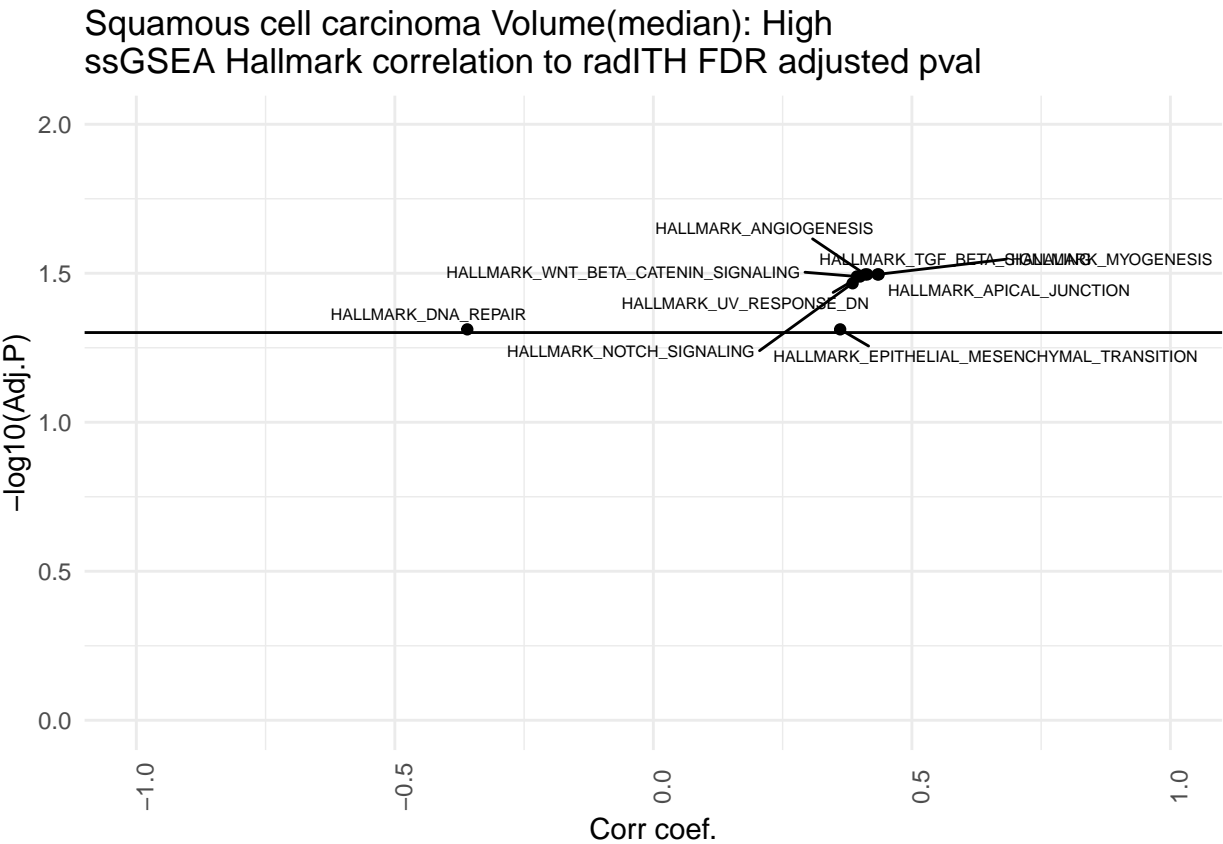
Hallmarks Squamous



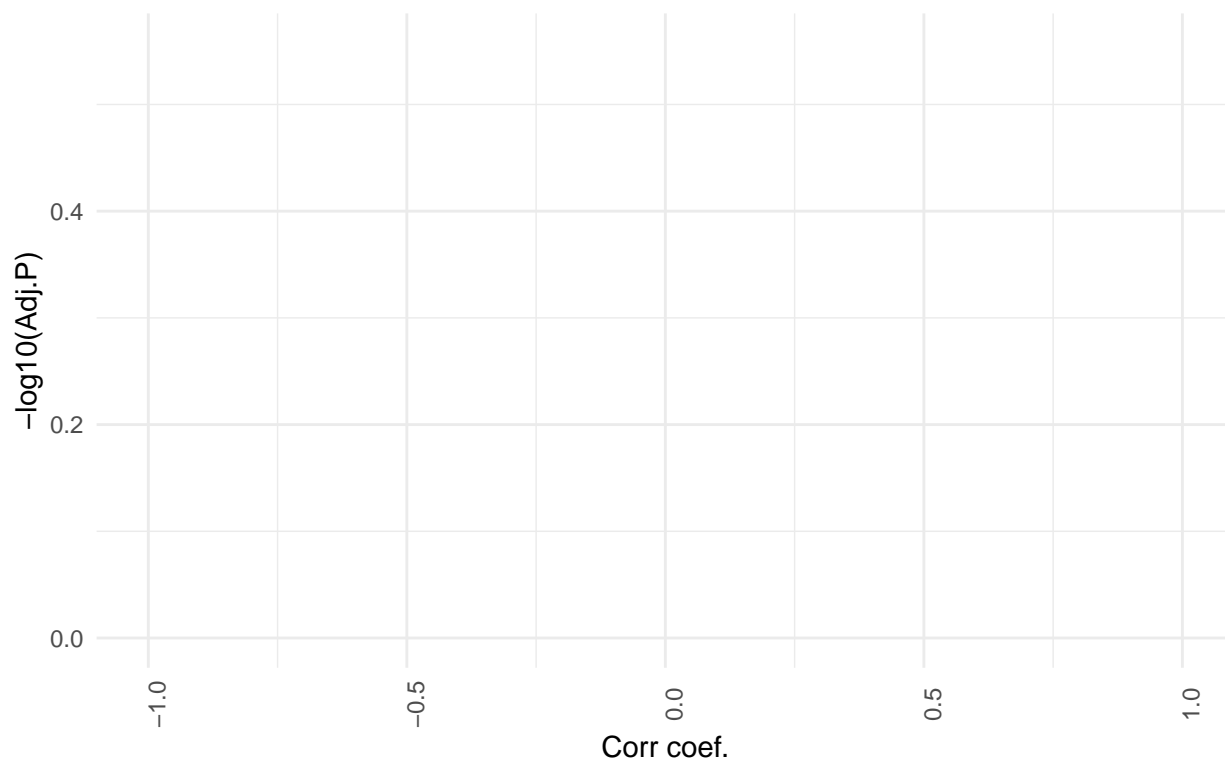
Hallmark expression-radITH Correlation in Large vs Small tumors (all samples)



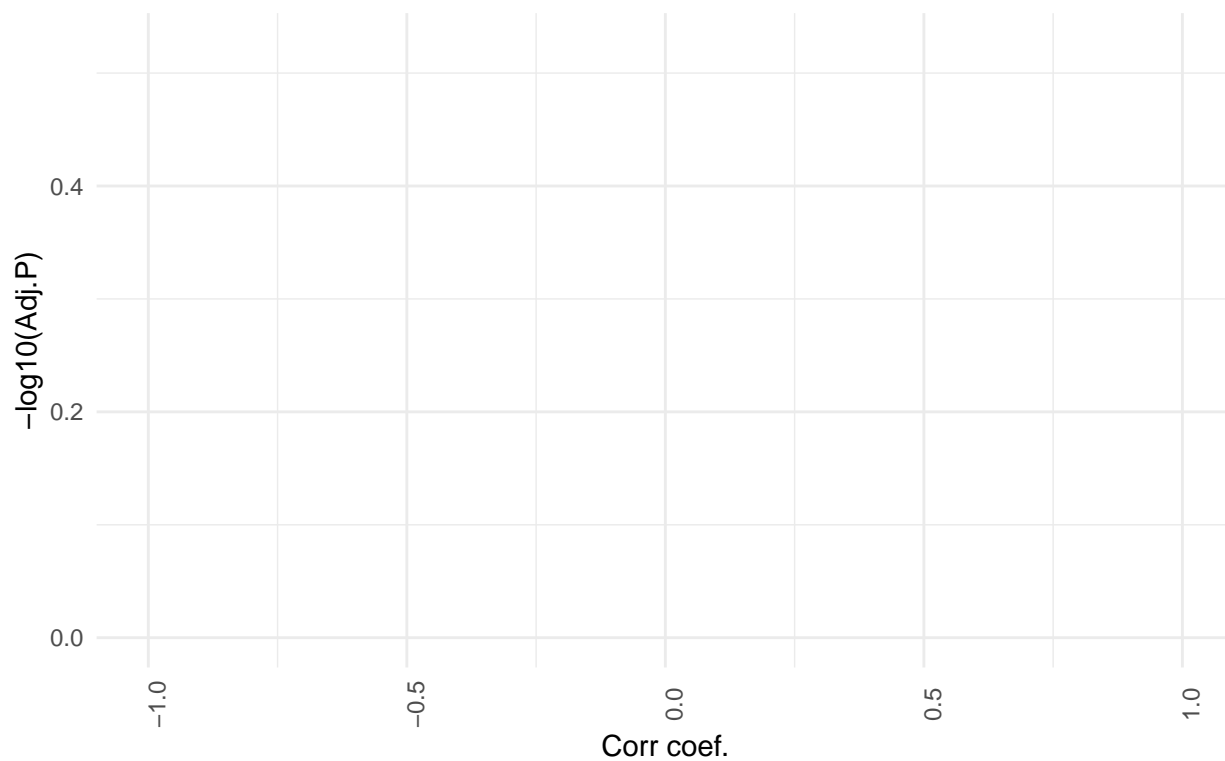
Let's split by Size and Pathology and repeat



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

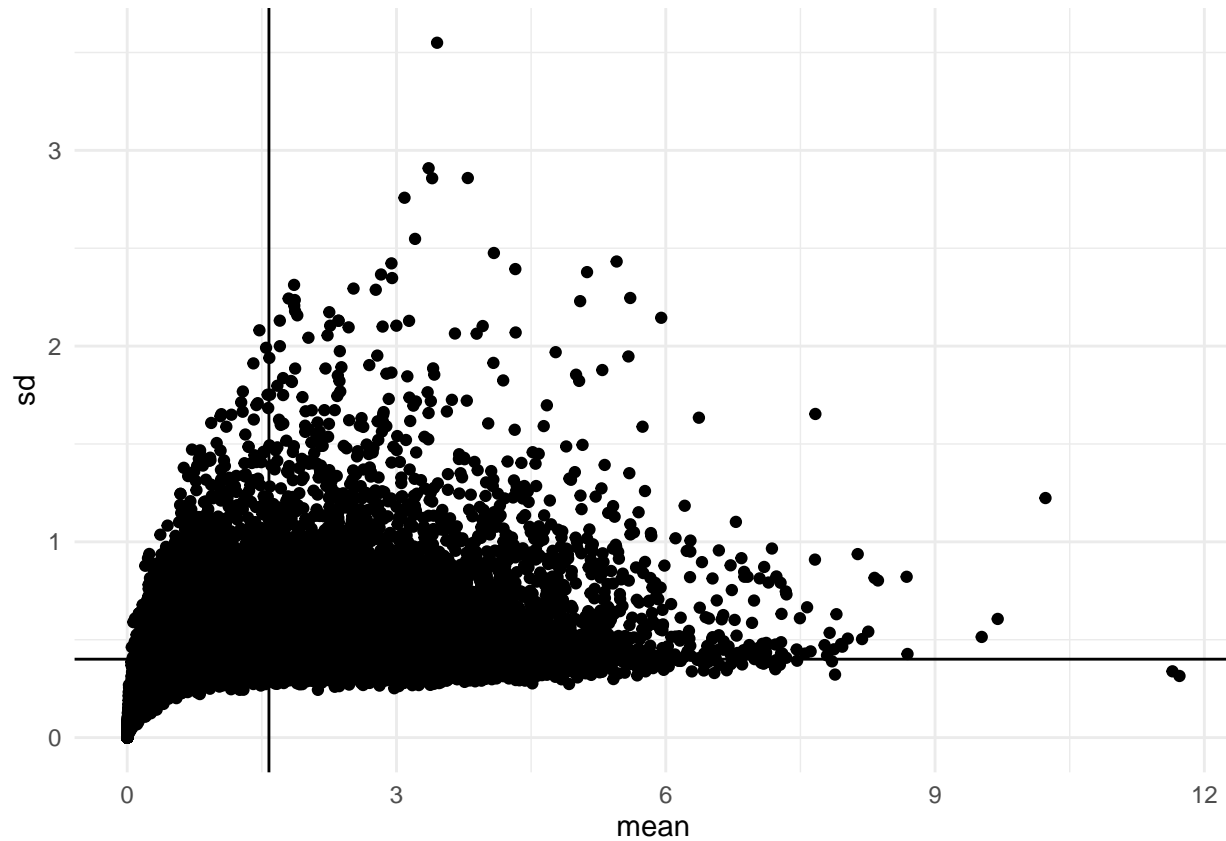


Invasive adenocarcinoma Volume(median): Low
ssGSEA Hallmark correlation to radlTH FDR adjusted pval



Picking genes for Gene Expression Analysis

- Mean and SD value based on entire cohort



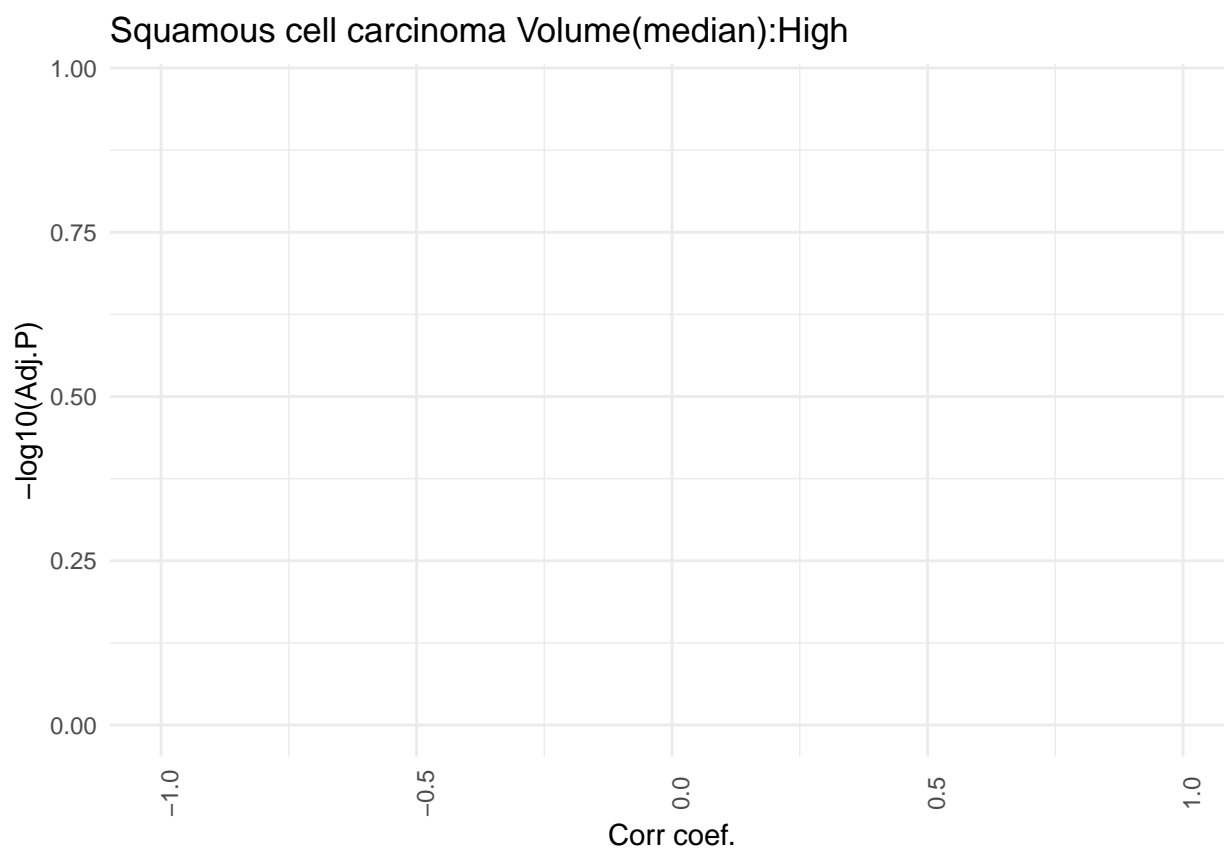
Number of Genes after cutoff: 10332

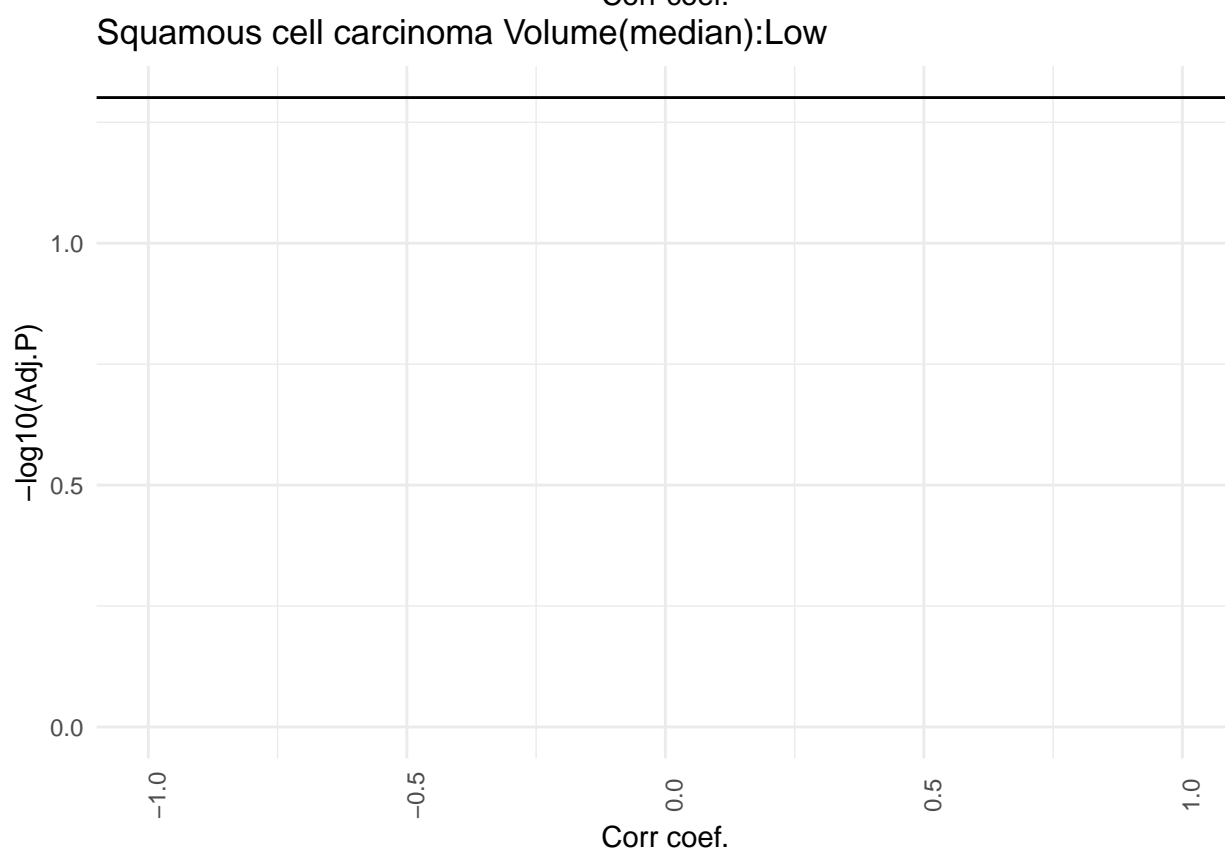
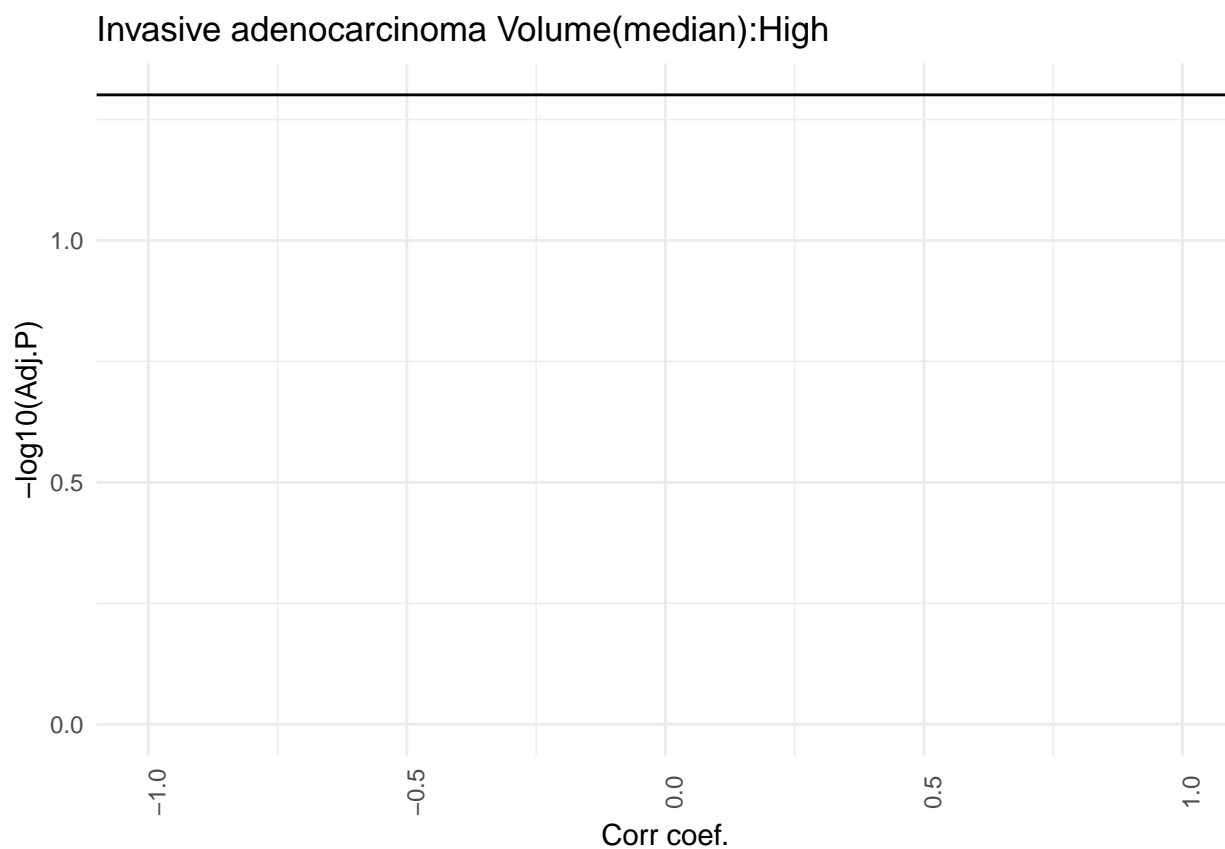
Gene Expression Analysis without volume

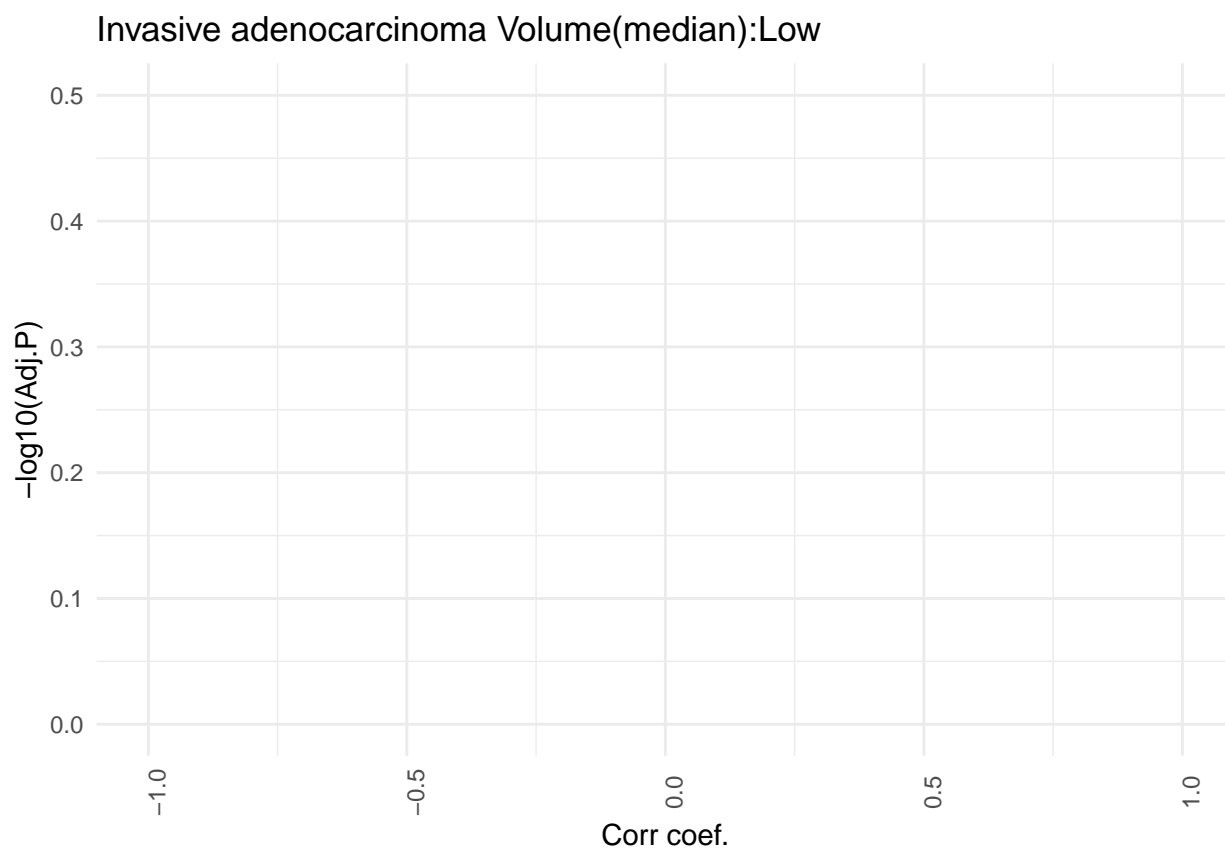
- Genes that were picked for analysis were based on mean and SD (entire cohort)

Gene Expression Analysis by volume group and cancer type

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

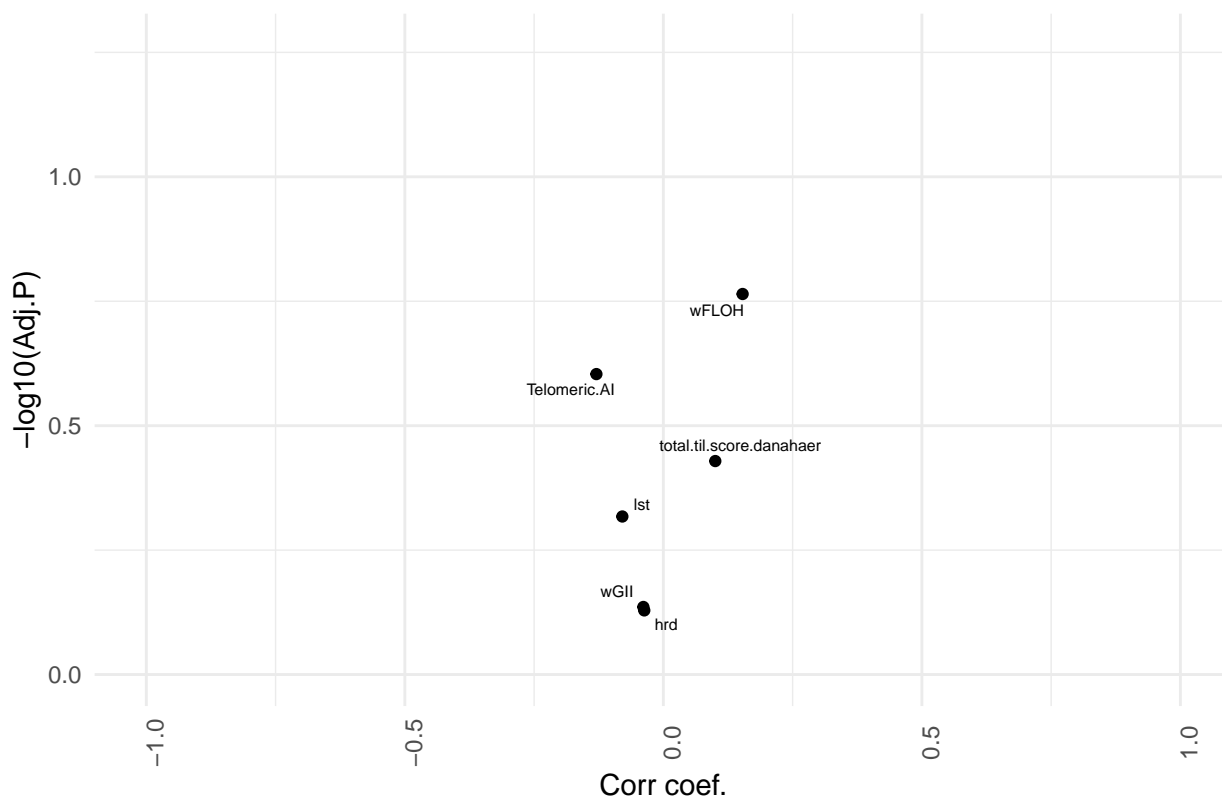




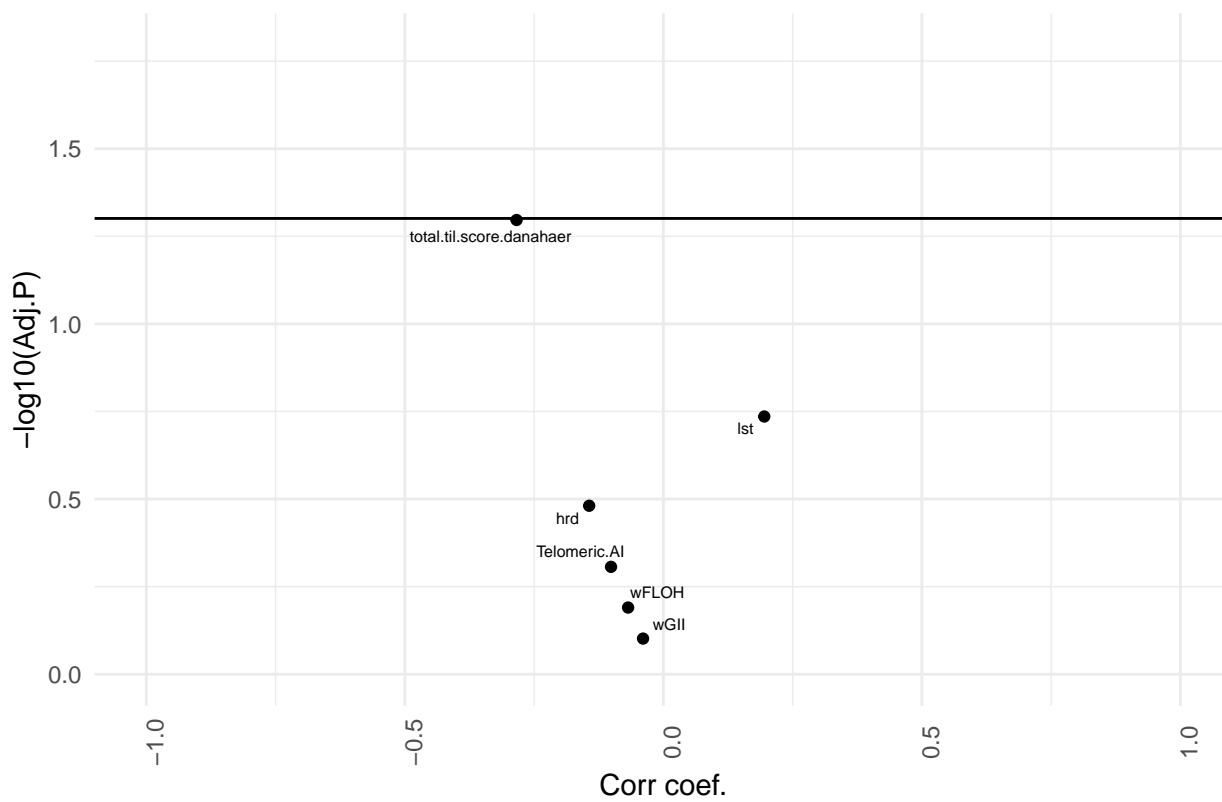


Chr Instability and TIL

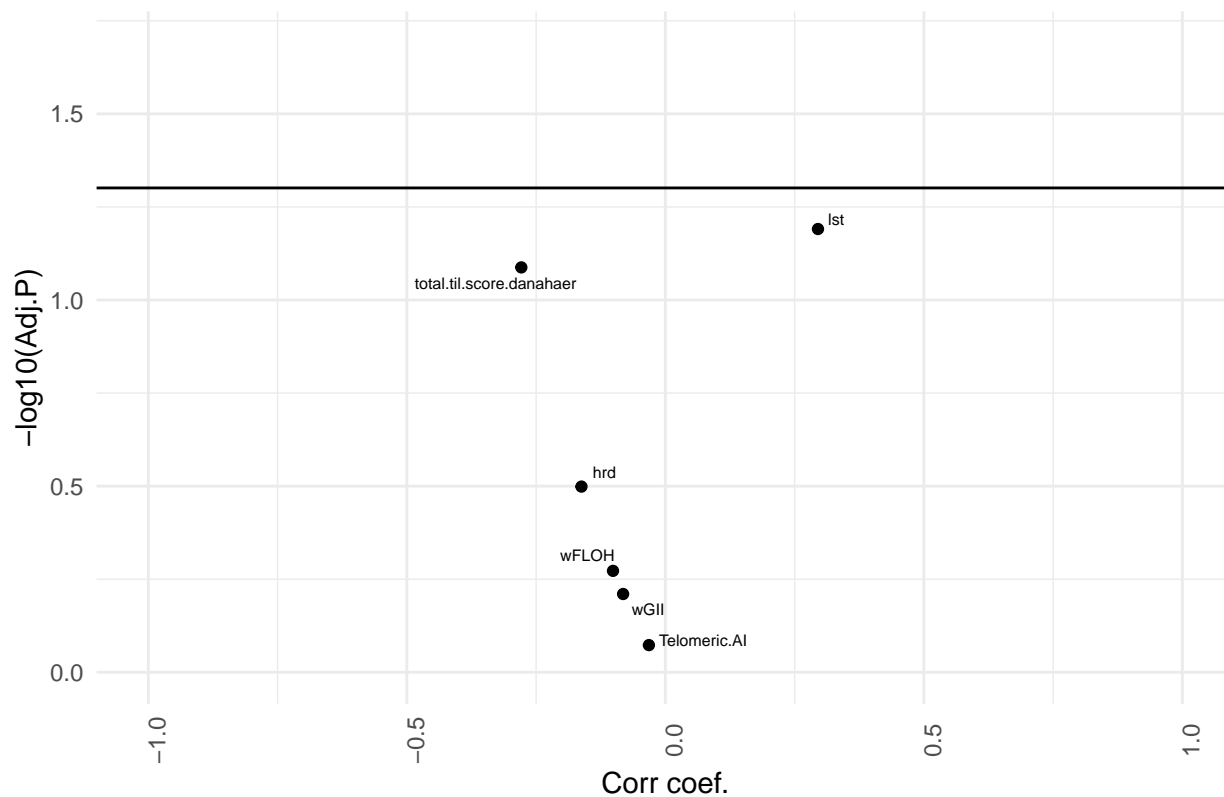
Adeno all samples



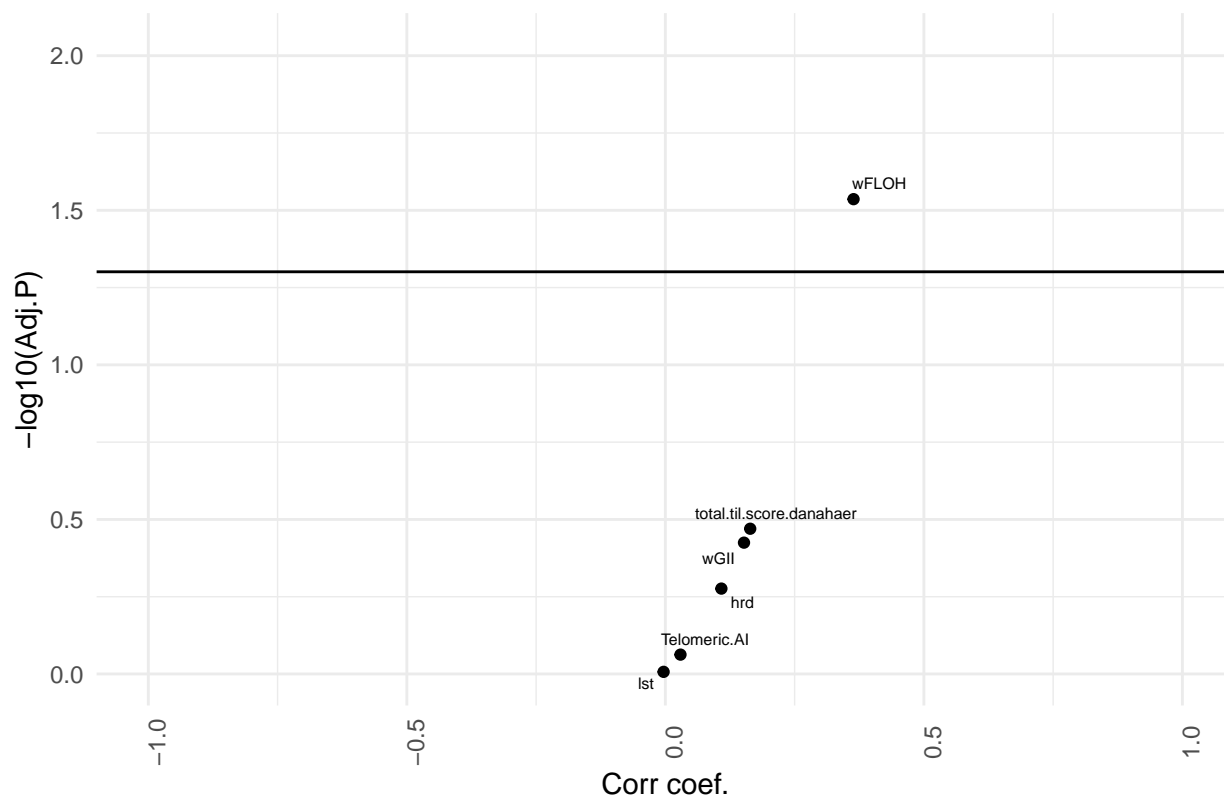
Squamous all samples



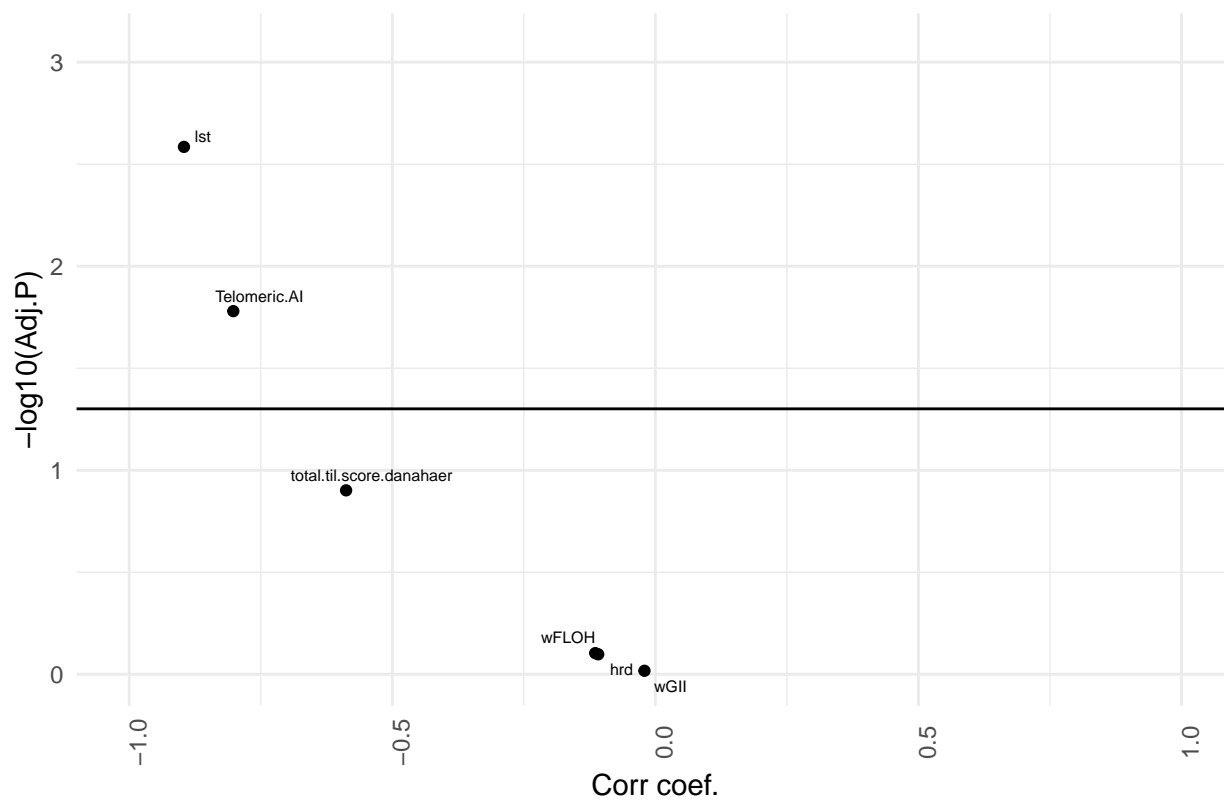
Squamous cell carcinoma Volume(median):High



Invasive adenocarcinoma Volume(median):High



Squamous cell carcinoma Volume(median):Low



Invasive adenocarcinoma Volume(median):Low

