

Figures and Tables for PCA Genomics Signatures Paper

Sehyun Oh

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Contents

1	Benchmark CRC paper	2
1.1	CRC_top10_validated_ind.tsv	2
1.2	CRC subtyping	2
1.3	CRC binary clinical variables	6
2	Benchmark multiPLIER	10
2.1	sle_neutrophil.rds	10
2.2	nares_neutrophil.rds	12

1 Benchmark CRC paper

1.1 CRC_top10_validated_ind.tsv

A data frame of top 10 validated indexes from 18 CRC datasets. This table was created in CRC/repeat_Fig4A.Rmd

```
x <- read.table("CRC/outputs/CRC_top10_validated_ind.tsv")
head(x)
```

	val_ind_1	val_ind_2	val_ind_3	val_ind_4	val_ind_5
#> GSE12225.GPL3676_eset	312	21	468	684	119
#> GSE12945_eset	312	981	832	684	758
#> GSE13067_eset	188	833	324	220	192
#> GSE13294_eset	1575	833	192	58	188
#> GSE14095_eset	2	1032	338	1387	725
#> GSE14333_eset	832	188	834	1575	833

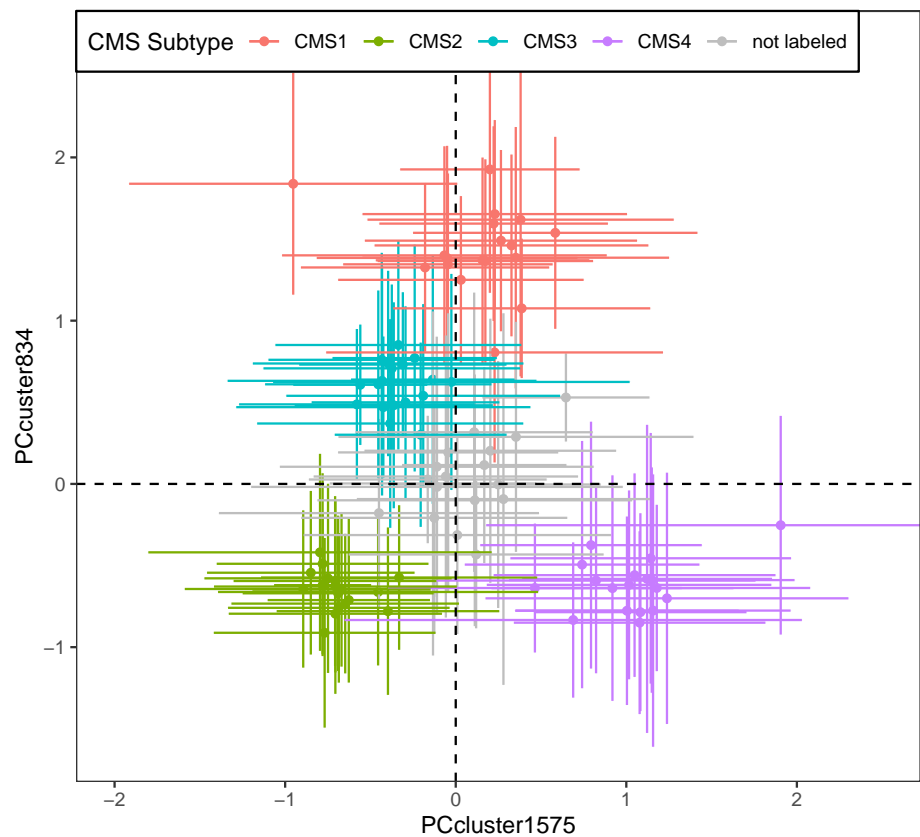
	val_ind_6	val_ind_7	val_ind_8	val_ind_9	val_ind_10
#> GSE12225.GPL3676_eset	758	504	153	1016	27
#> GSE12945_eset	119	468	21	516	504
#> GSE13067_eset	1575	1166	438	868	1467
#> GSE13294_eset	187	832	1008	2538	1166
#> GSE14095_eset	1726	188	1843	1575	189
#> GSE14333_eset	220	192	61	579	595

1.2 CRC subtyping

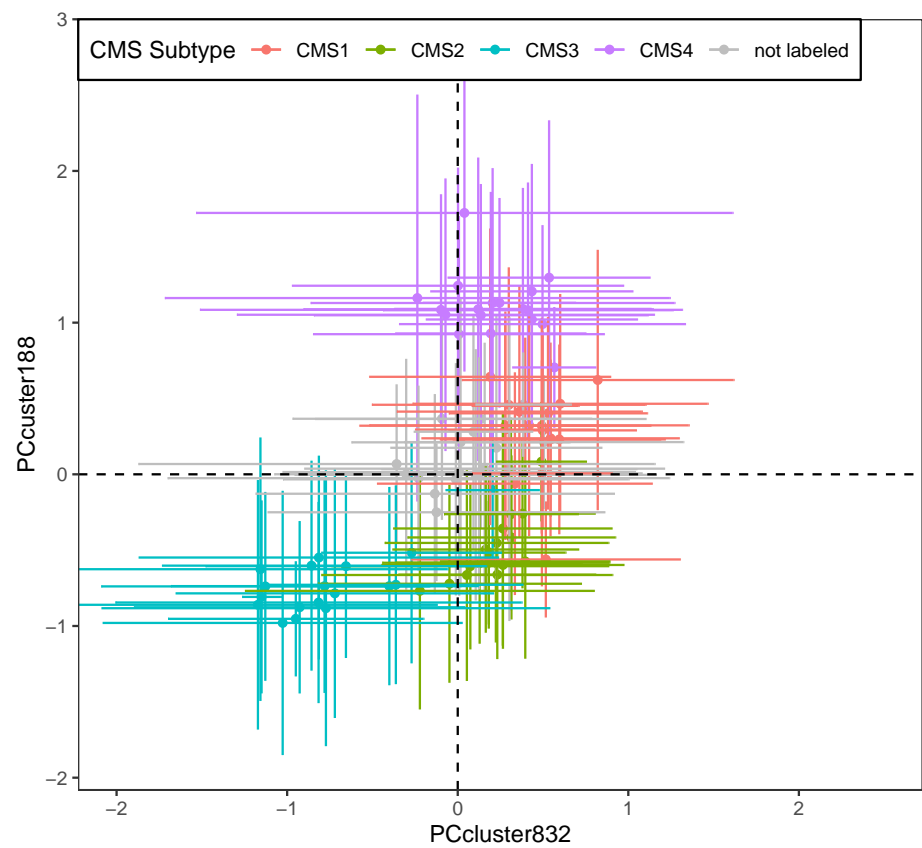
Scatter plots showing how different signatures perform with CRC subtyping. These plots were created in CRC/repeat_Fig4A.Rmd

```
all <- list.files("CRC/outputs")
scatterplots <- all[grep("scatter_", all)]

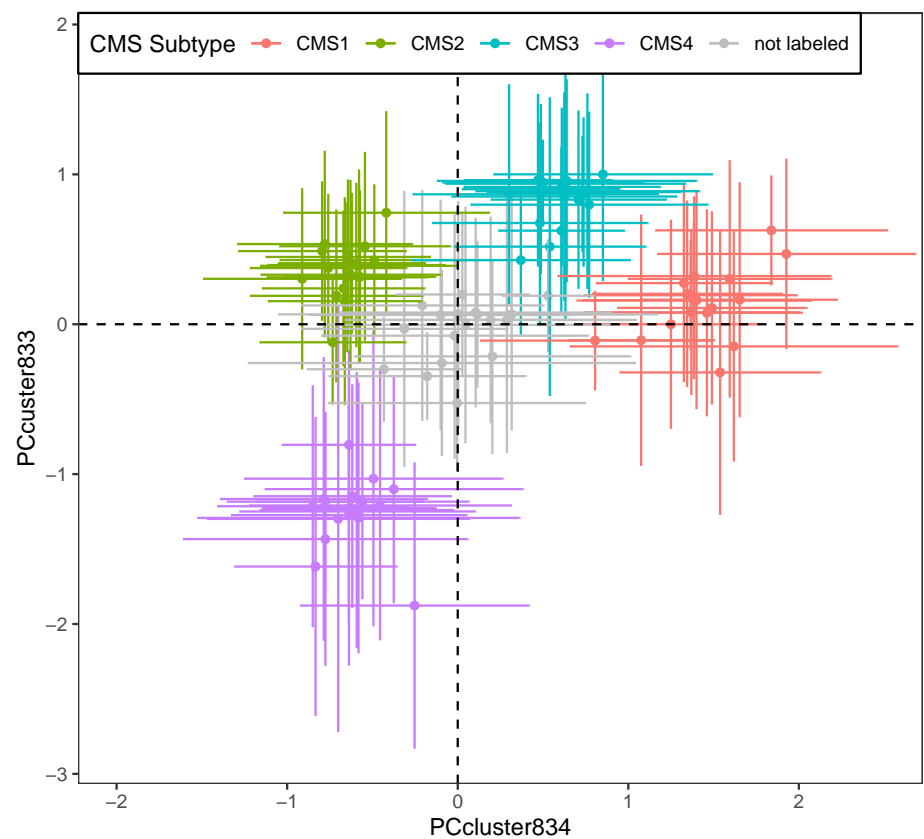
for (plot in scatterplots) {
  x <- readRDS(file.path("CRC/outputs", plot))
  print(x)
}
#> $value
```



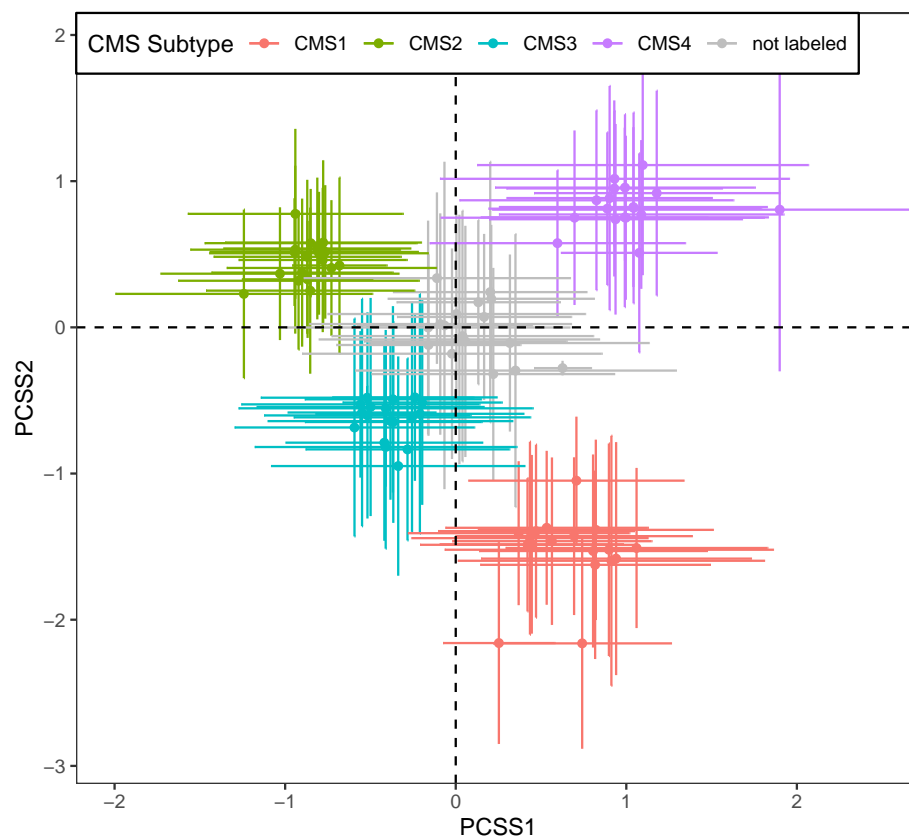
```
#>  
#> $visible  
#> [1] FALSE  
#>  
#> $value
```



```
#>  
#> $visible  
#> [1] FALSE  
#>  
#> $value
```



```
#>  
#> $visible  
#> [1] FALSE
```

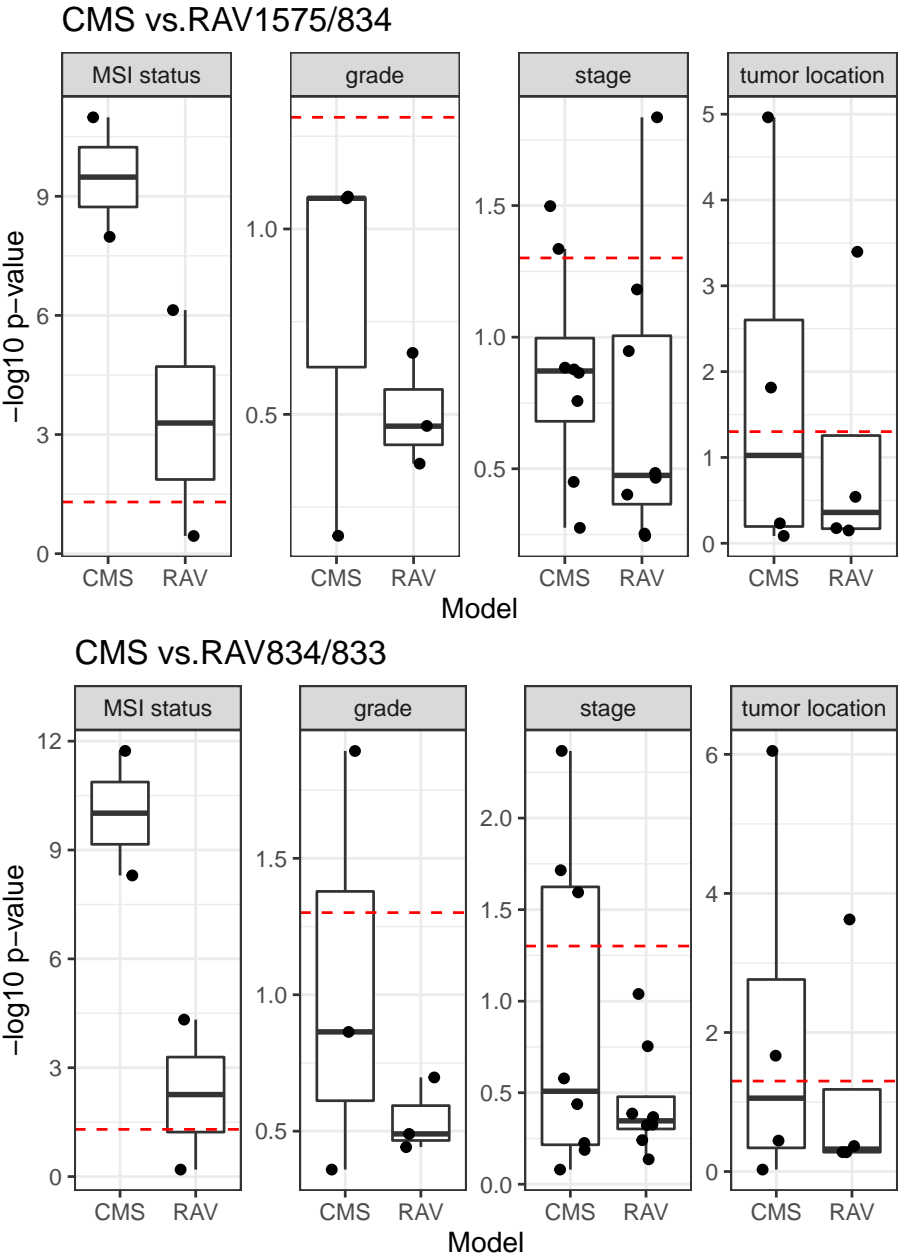


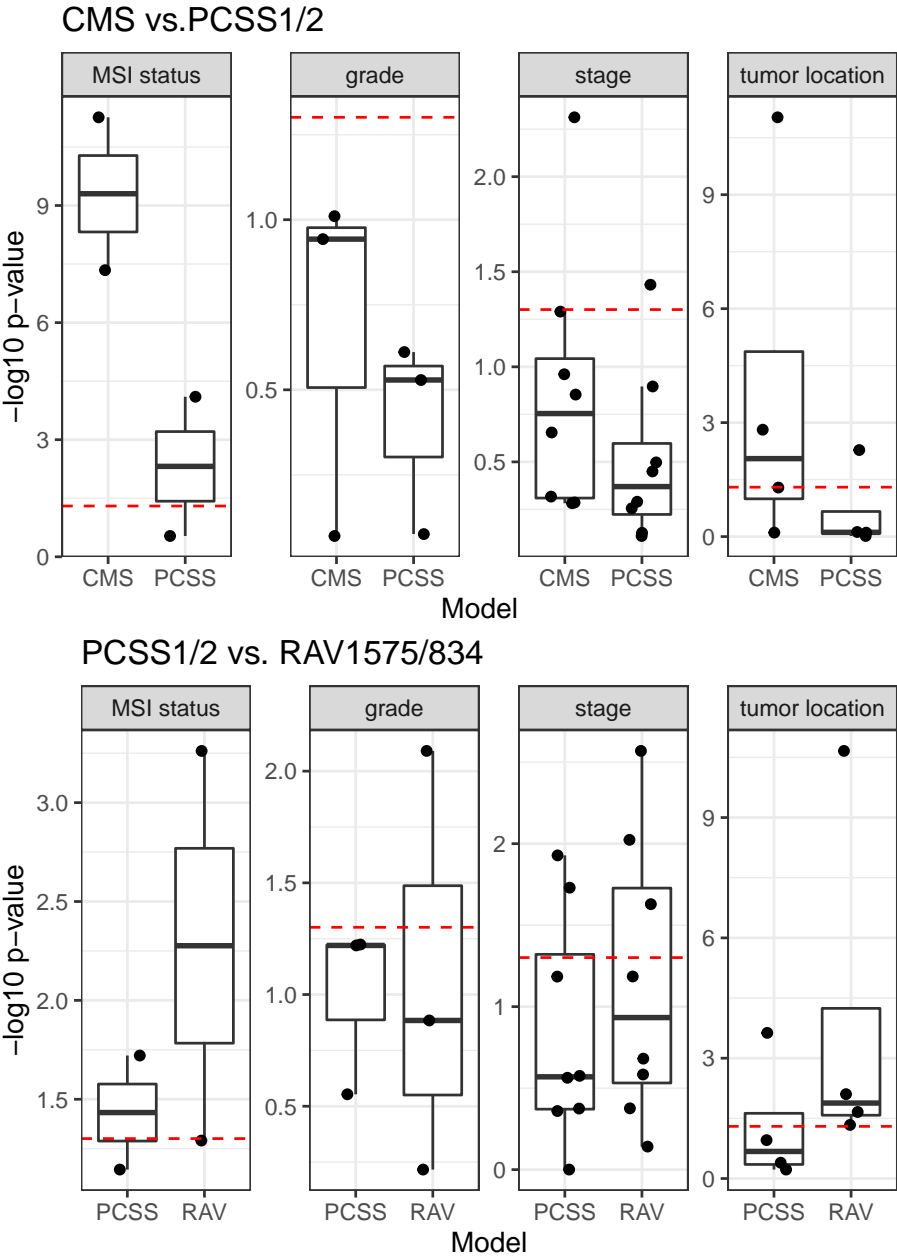
1.3 CRC binary clinical variables

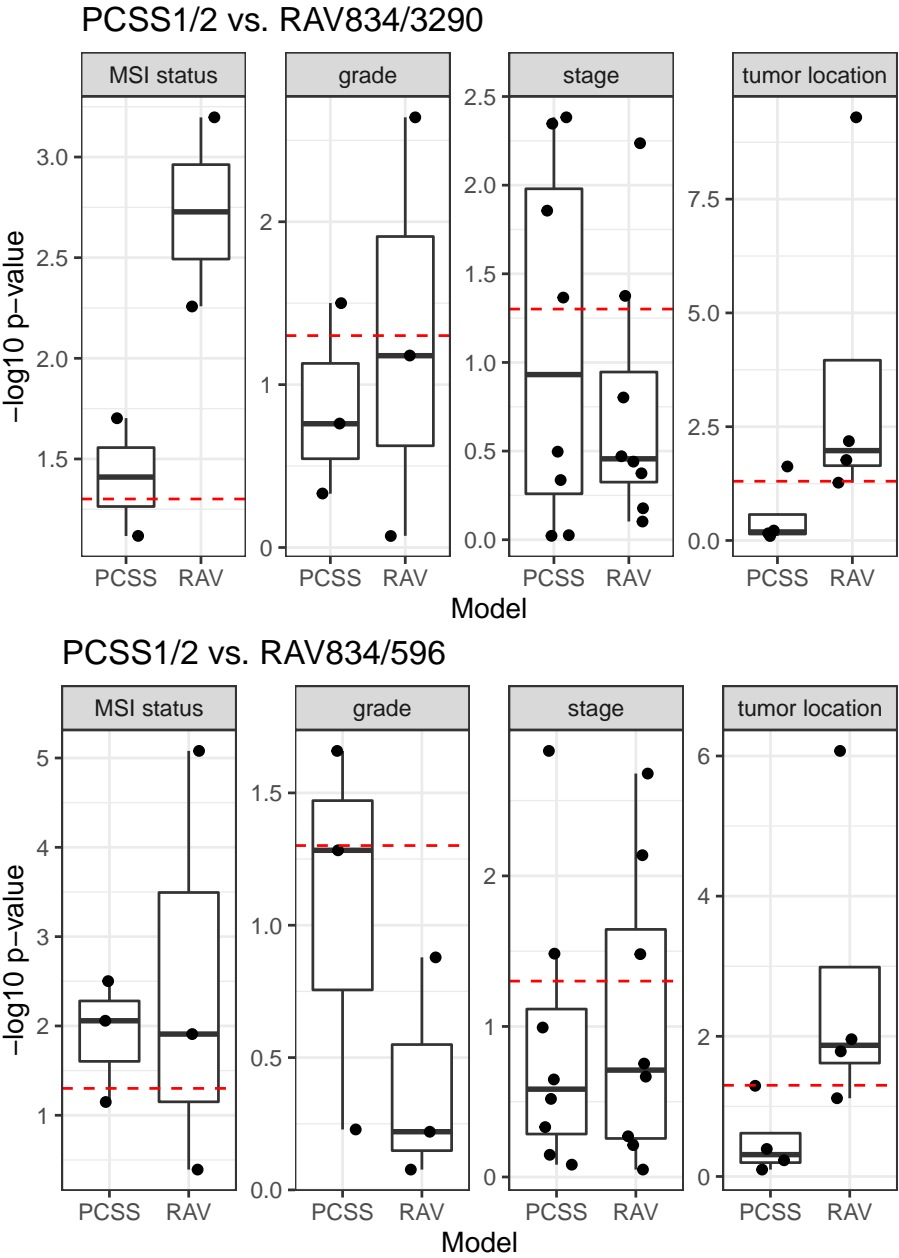
Bar plots comparing different models in differentiating CRC binary clinical variables. These plots were created in `CRC/repeat_Fig4C.Rmd`

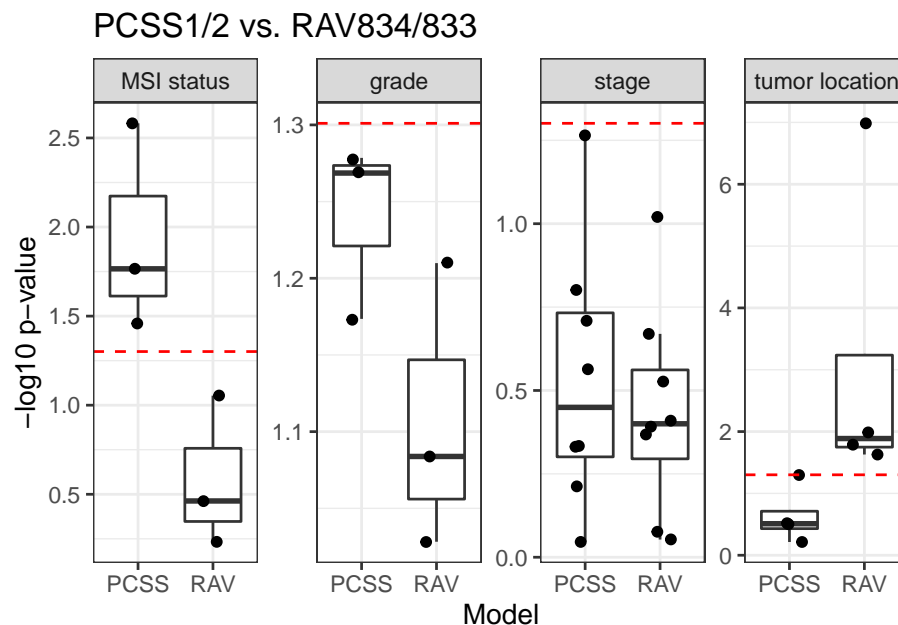
```
all <- list.files("CRC/outputs")
barplots <- all[grep("boxplot_", all)]

for (plot in barplots) {
  x <- readRDS(file.path("CRC/outputs", plot))
  print(x$value)
}
```







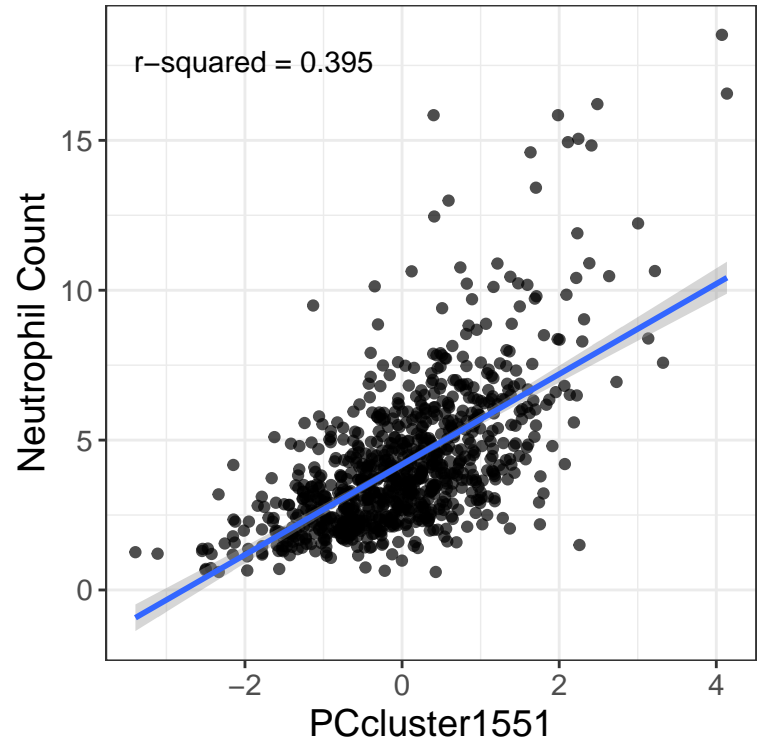


2 Benchmark multiPLIER

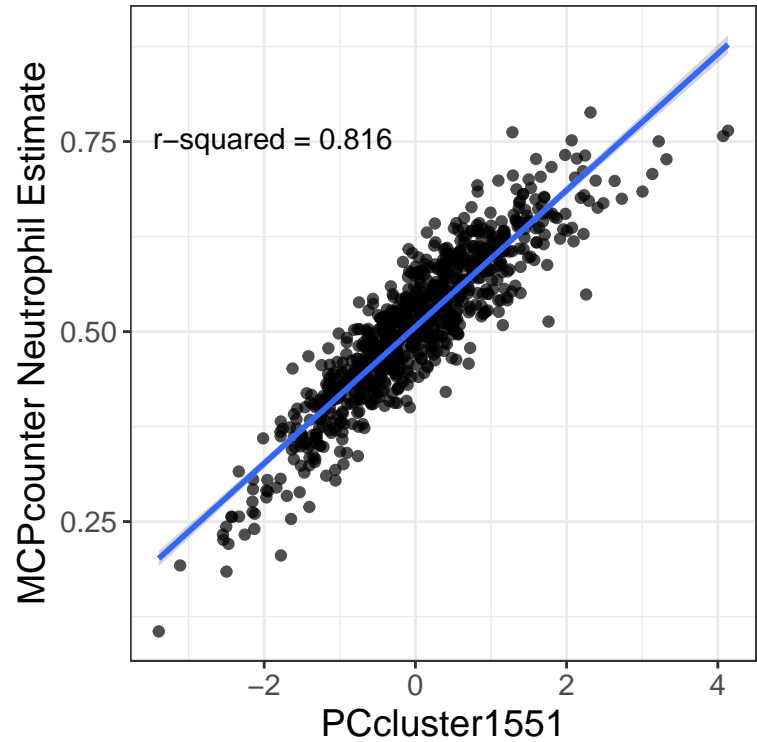
2.1 sle_neutrophil.rds

Two scatter plots of PCcluster1551 x Neutrophil count/estimate of SLE-WB dataset. This plot was created in SLE-WB/repeat_Fig3_SLE-WB.Rmd

```
x <- readRDS("SLE-WB/sle_neutrophil.rds")
x
#> [[1]]
```



```
#>  
#> [[2]]
```



2.2 nares_neutrophil.rds

A scatter plot of PCcluster1551 x Neutrophil estimate of NARES dataset. This plot was created in NARES/repeat_Fig3_NARES.Rmd

```
x <- readRDS("NARES/nares_neutrophil.rds")  
x
```

