# PDAC gene expression analysis

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### Setup

load required libraries

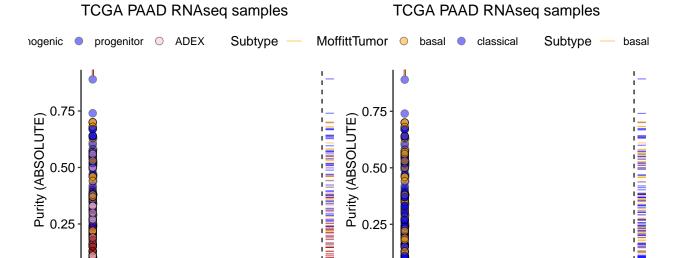
Select data set

Calculate signature scores and  $\operatorname{SSC}$ 

#### Results

Tumor classifier and ABSOLUTE

```
## 'geom_smooth()' using formula 'y ~ x'
## 'geom_smooth()' using formula 'y ~ x'
```



0.5

0.1

0.0

0.2

0.3

Tumor classifier

0.4

0.5

0.2

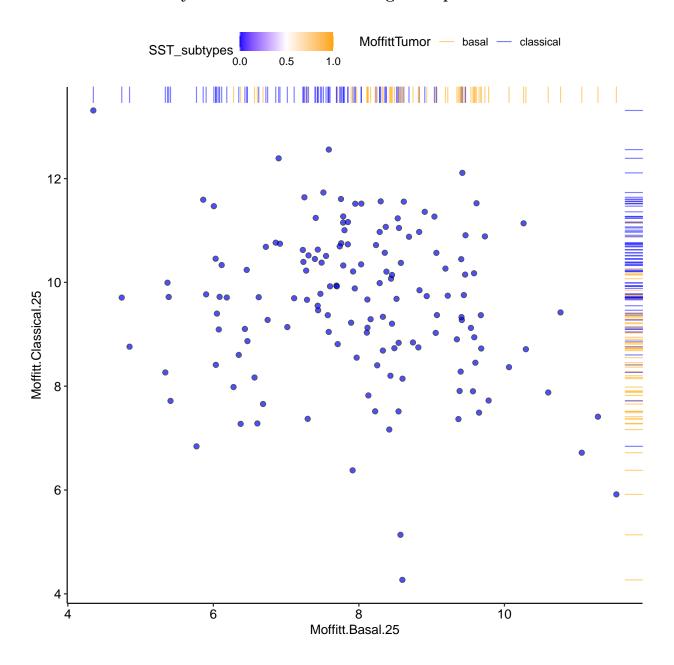
Tumor classifier

0.3

0.4

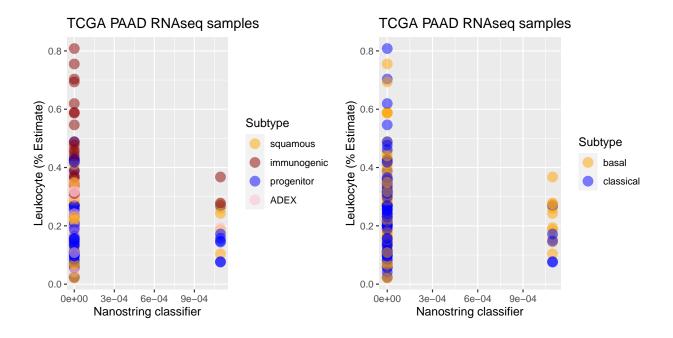
0.1

Classifier consistency with basal and classical gene top  $25~\mathrm{scores}$ 



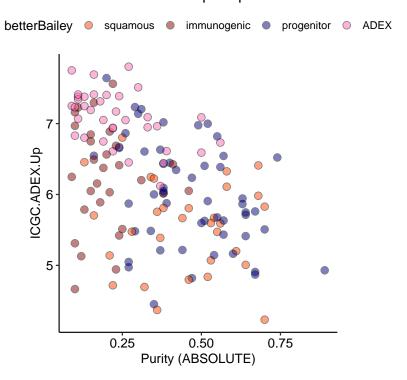
#### Tumor classifier and leukocyte percent

```
## 'geom_smooth()' using formula 'y ~ x'
## 'geom_smooth()' using formula 'y ~ x'
```



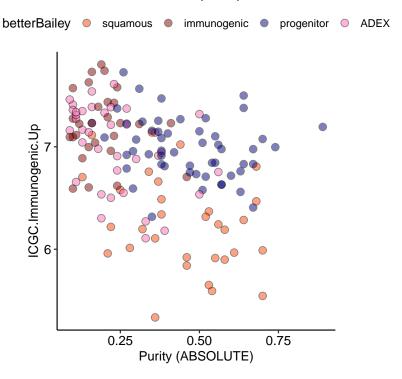
#### Gene expression signatures and ABSOLUTE

### TCGA PAAD RNAseq samples

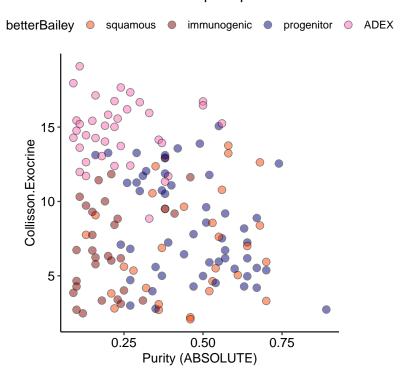


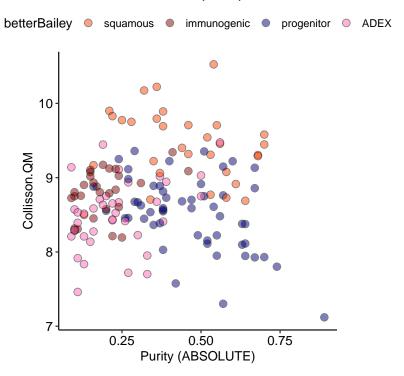
## [1] -0.4653

## [1] 0



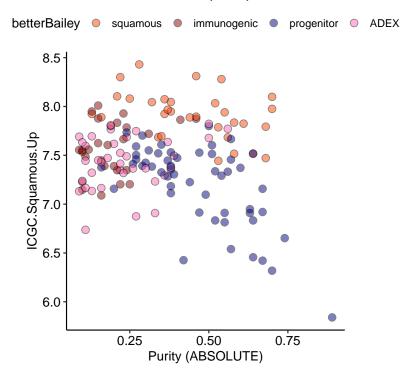
## [1] -0.39961 ## [1] 4.4e-07



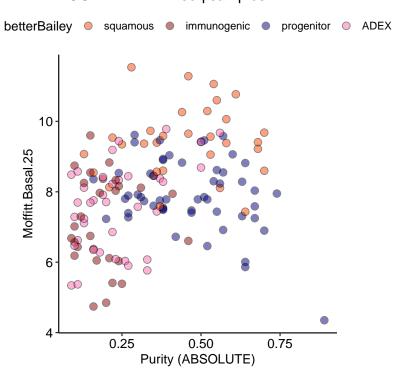


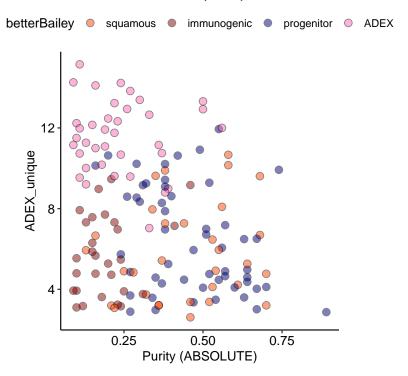
## [1] 0.02214

## [1] 0.7887321

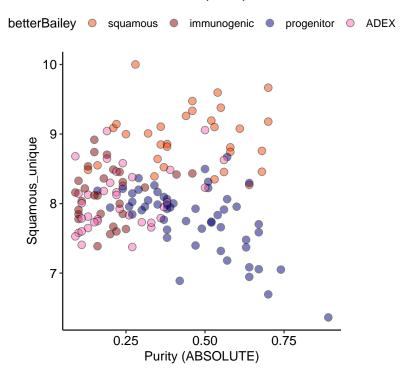


## [1] -0.23559 ## [1] 0.00382416

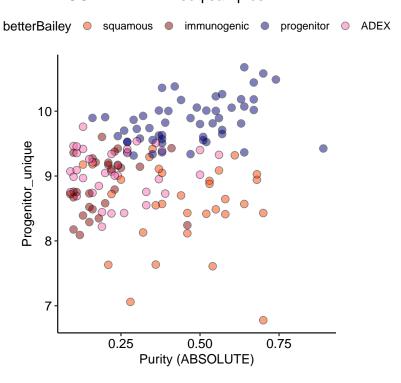


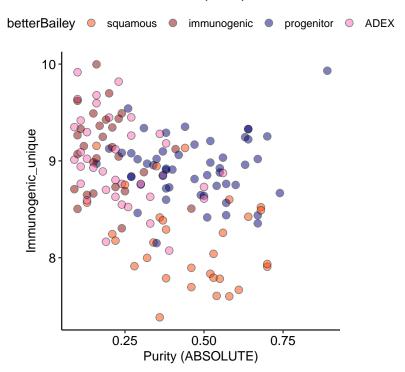


- ## [1] -0.28683
- ## [1] 0.00039027

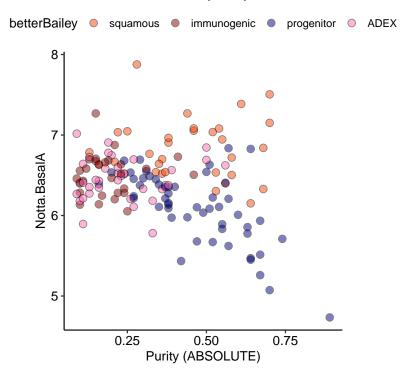


## [1] -0.04365 ## [1] 0.5971286

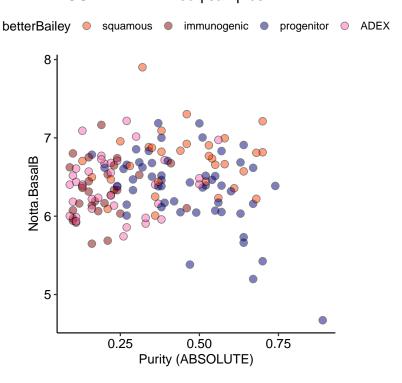




- ## [1] -0.33341
- ## [1] 3.253e-05

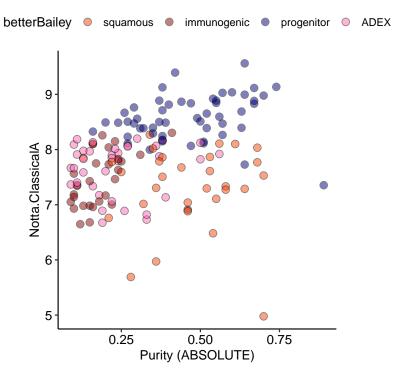


## [1] -0.28578 ## [1] 0.00041095

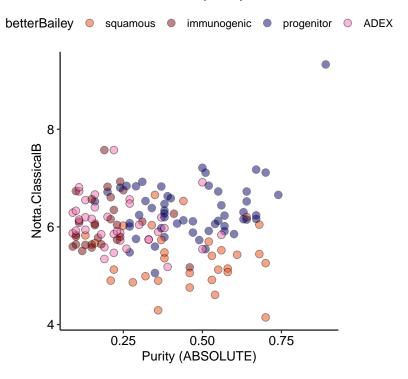


## [1] -0.0334 ## [1] 0.6859157

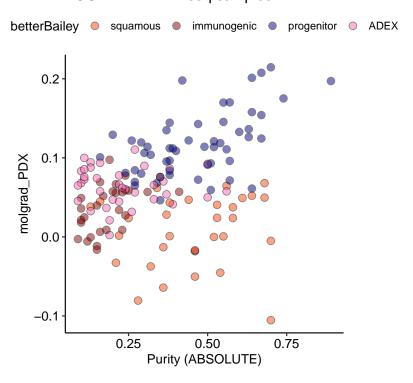
#### TCGA PAAD RNAseq samples



## [1] 0.31296 ## [1] 0.00010186

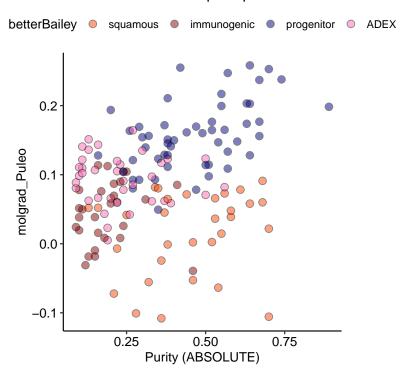


## [1] 0.01946 ## [1] 0.8138013

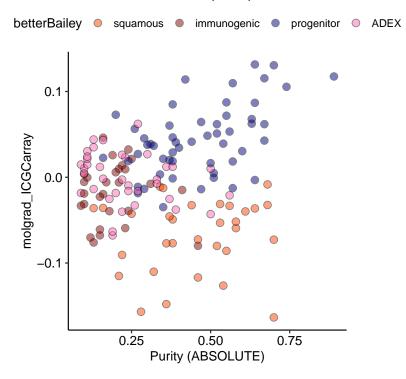


## [1] 0.32931 ## [1] 4.116e-05

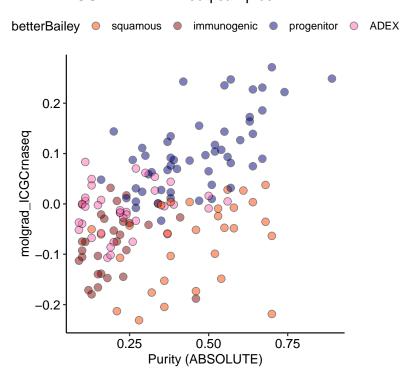
#### TCGA PAAD RNAseq samples



## [1] 0.30058 ## [1] 0.00019559

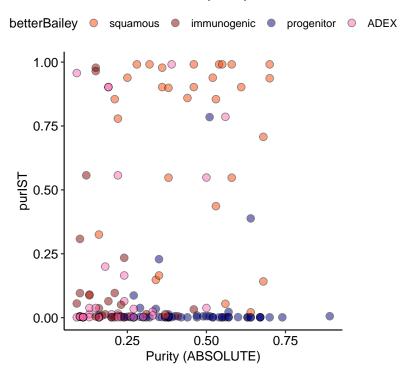


## [1] 0.18857 ## [1] 0.02127291

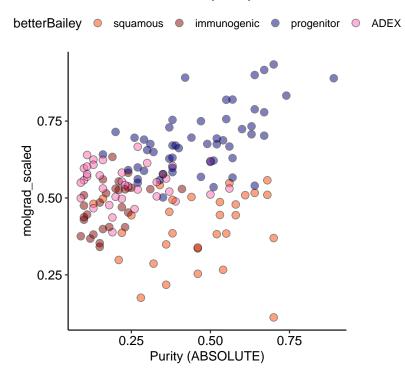


## [1] 0.48297 ## [1] 0

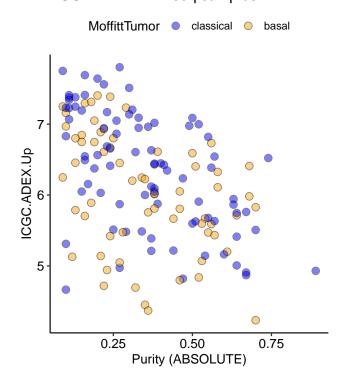
#### TCGA PAAD RNAseq samples



## [1] 0.12816 ## [1] 0.1193119

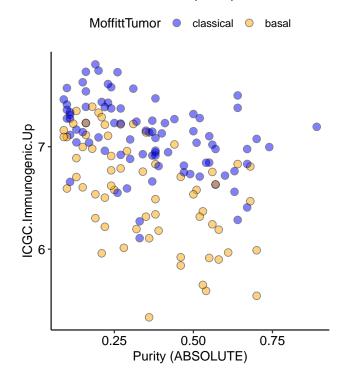


## [1] 0.32931 ## [1] 4.116e-05

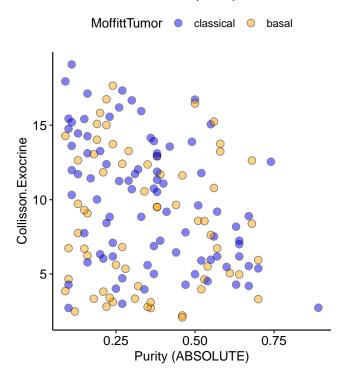


## [1] -0.4653 ## [1] 0

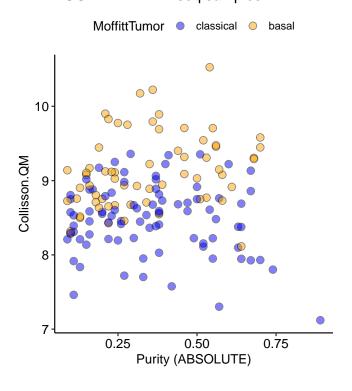
#### TCGA PAAD RNAseq samples

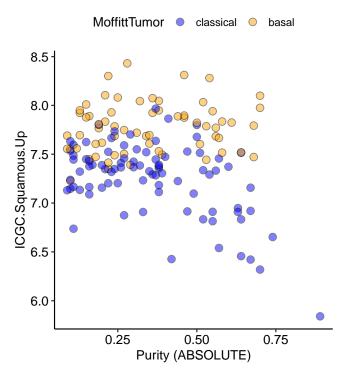


## [1] -0.39961 ## [1] 4.4e-07

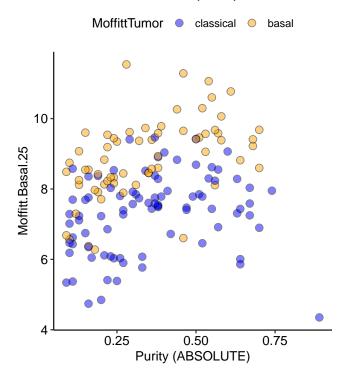


## [1] -0.24672 ## [1] 0.00241885

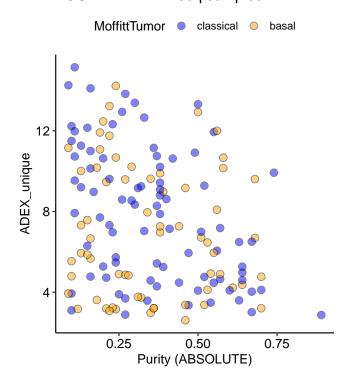




- ## [1] -0.23559
- ## [1] 0.00382416

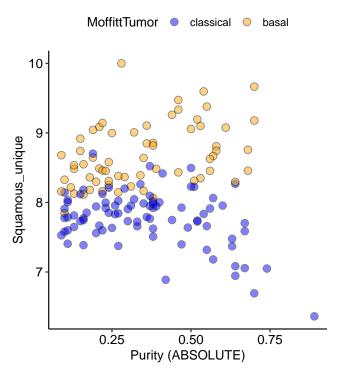


## [1] 0.26279 ## [1] 0.00120413

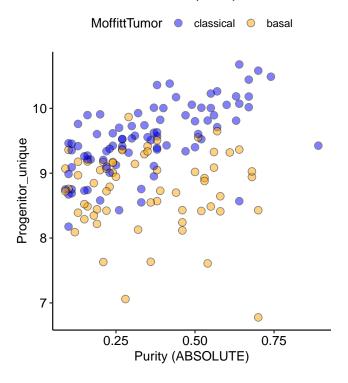


## [1] -0.28683 ## [1] 0.00039027

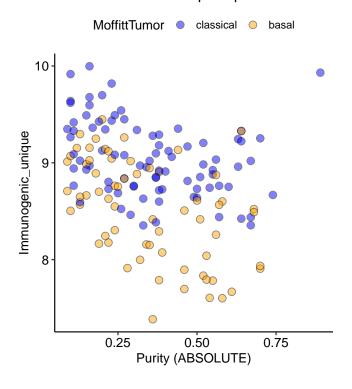
#### TCGA PAAD RNAseq samples



## [1] -0.04365 ## [1] 0.5971286

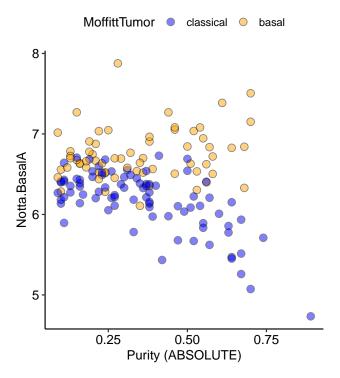


## [1] 0.28355 ## [1] 0.00045791

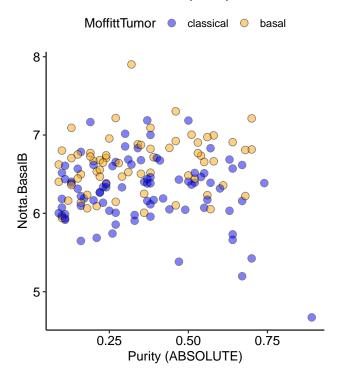


## [1] -0.33341 ## [1] 3.253e-05

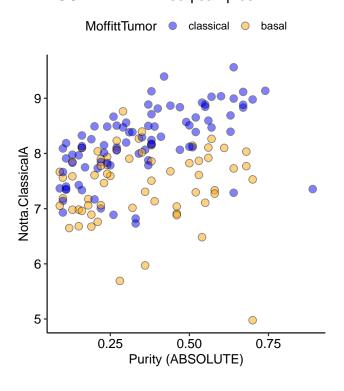
## TCGA PAAD RNAseq samples



## [1] -0.28578 ## [1] 0.00041095

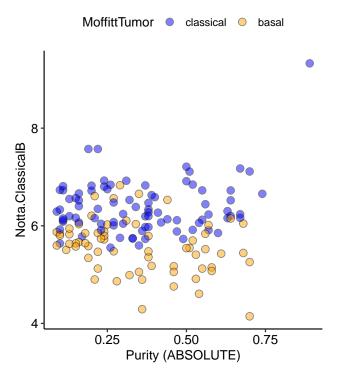


## [1] -0.0334 ## [1] 0.6859157

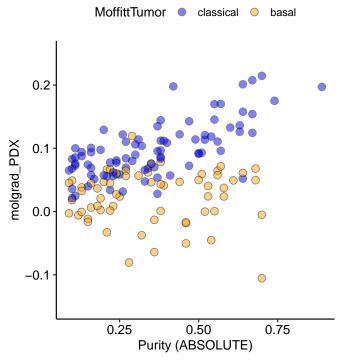


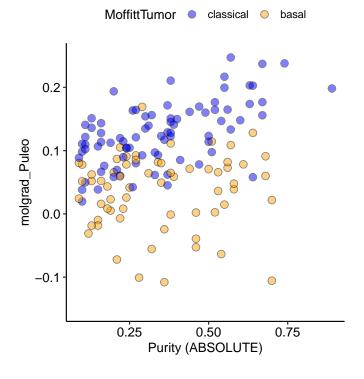
## [1] 0.31296 ## [1] 0.00010186

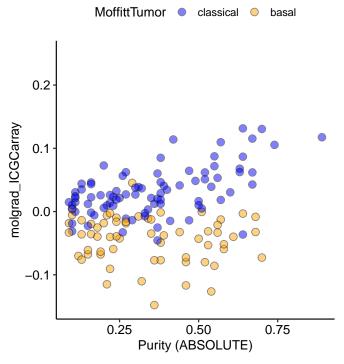
## TCGA PAAD RNAseq samples

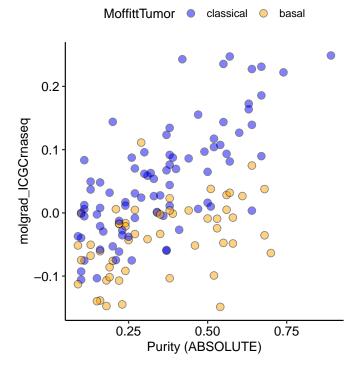


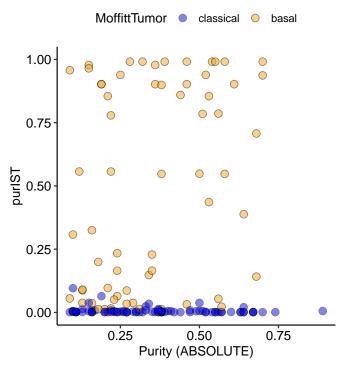
## [1] 0.01946 ## [1] 0.8138013

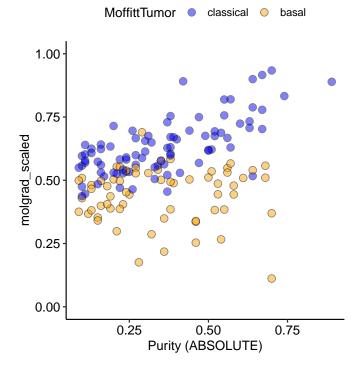












## PDL1 expression

