

# ICGC PACA-CA clustering

Ryan Kawalerski

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## Setup for PACA\_CA

Load required libraries

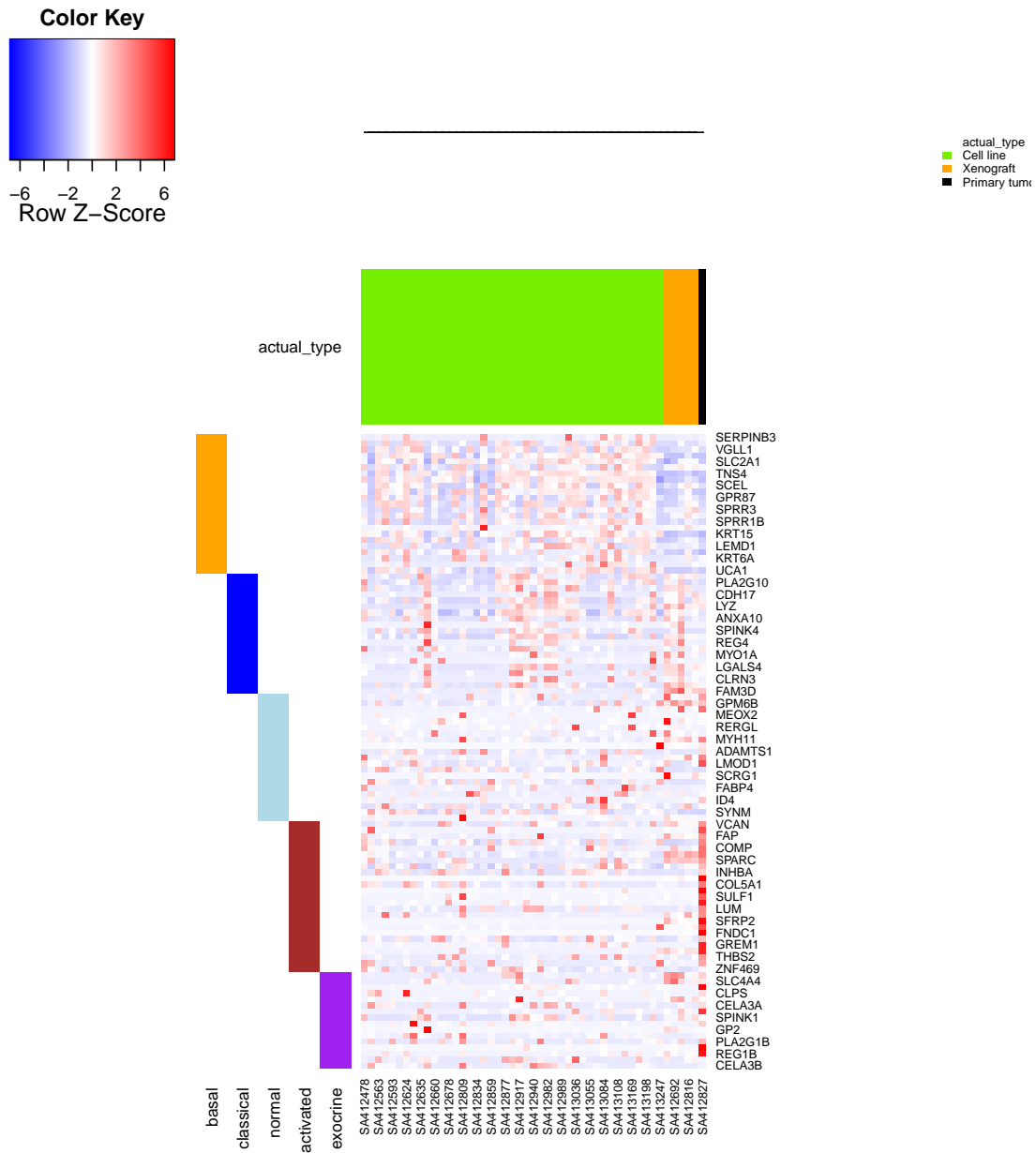
Select dataset and remove unwanted genes

Calculate signature scores and SSC

Append TSP scores to expression data frames

# Results

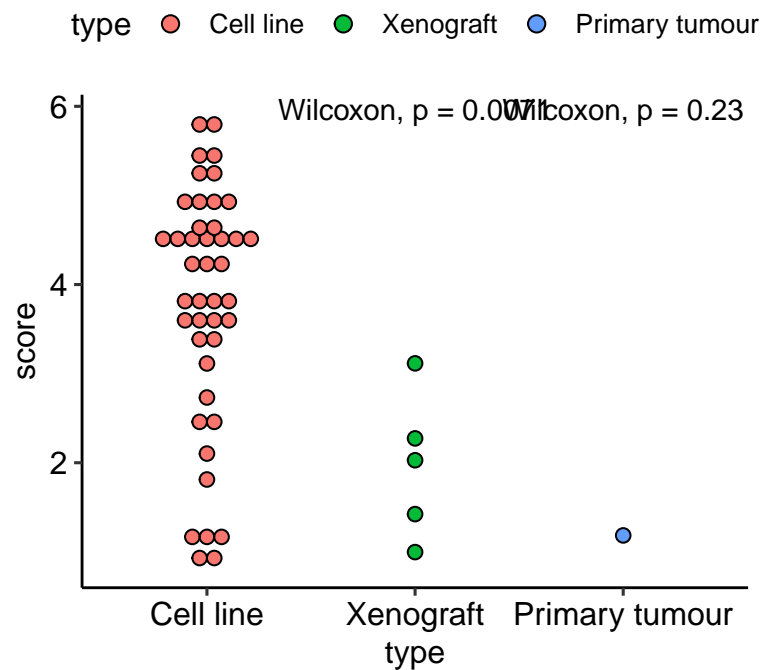
## Heat maps



## Boxplots to show gene expression in the above heatmap

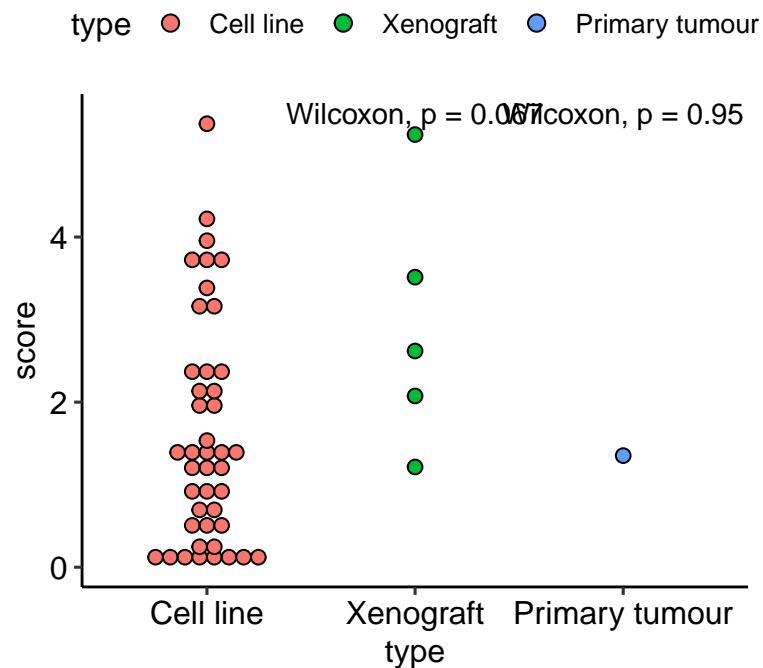
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.Basal.25 score



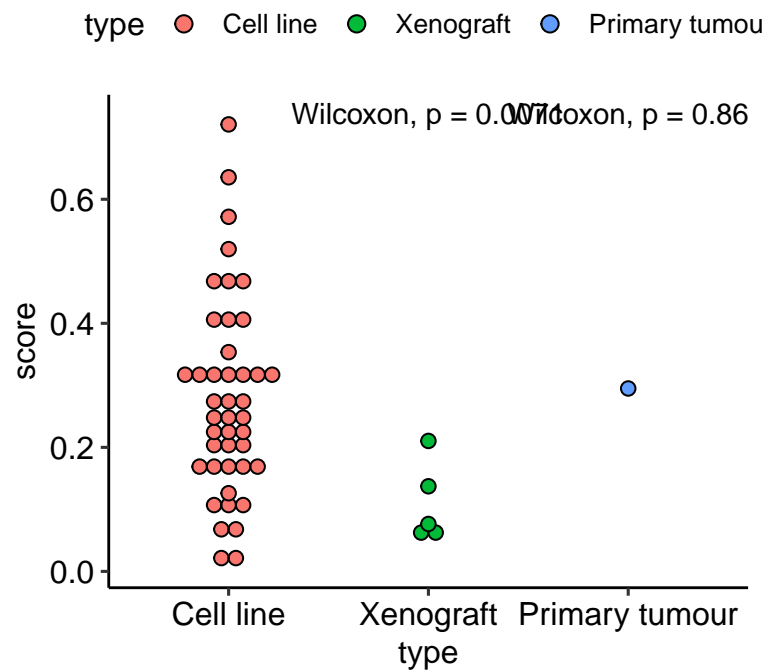
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.Classical.25 score



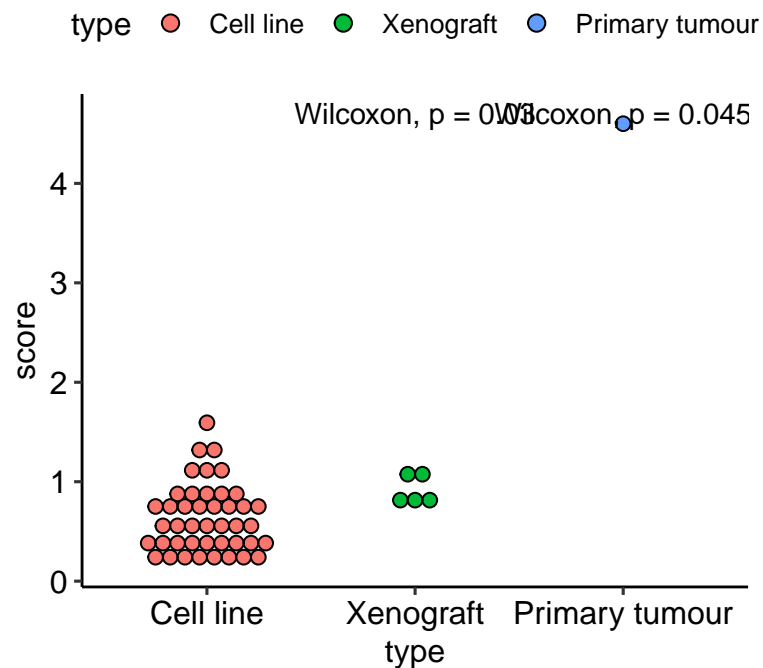
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.Normal.25 score



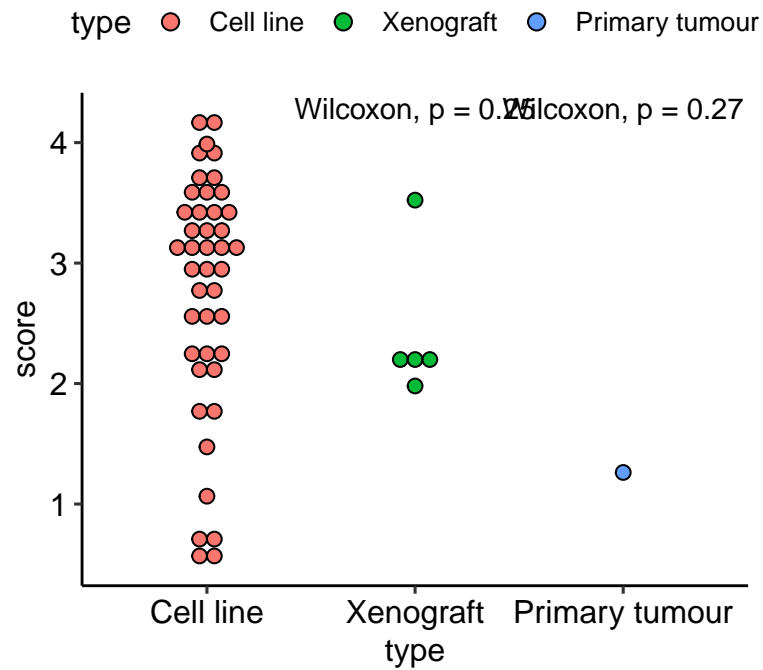
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.Activated.25 score



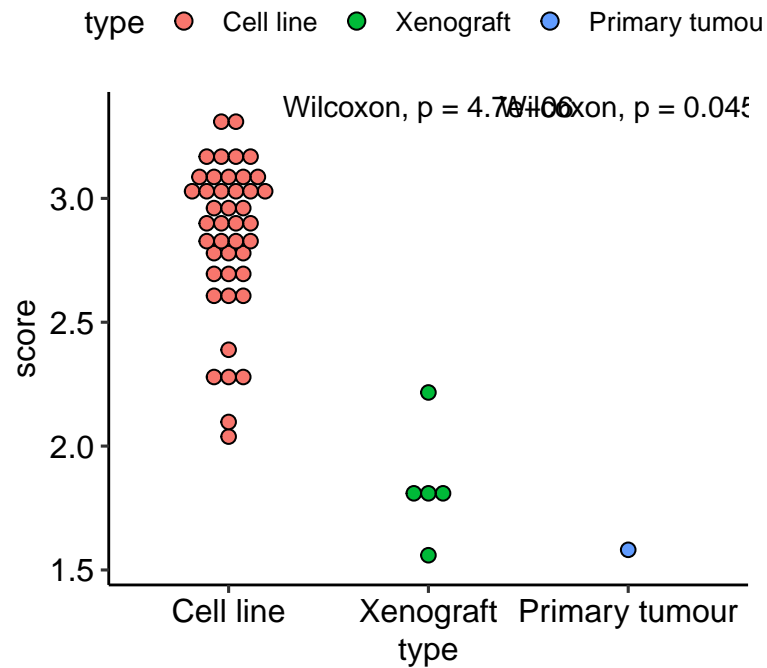
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.Tumor score



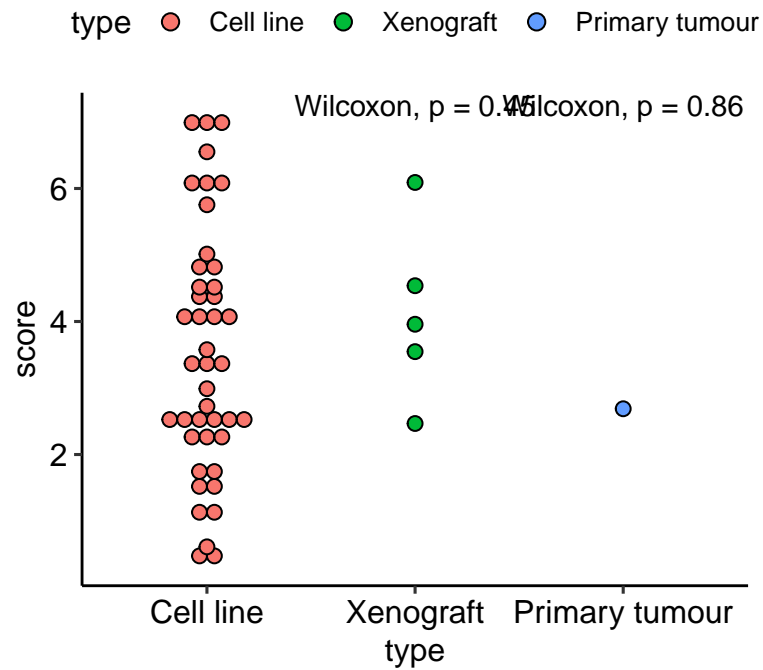
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

### Puleo.Centroids score



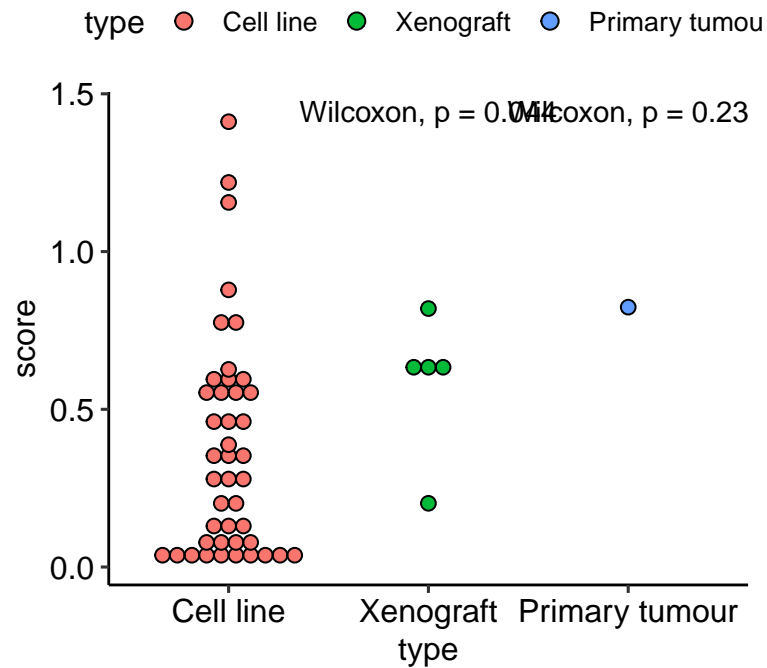
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

## Collisson.Classical score



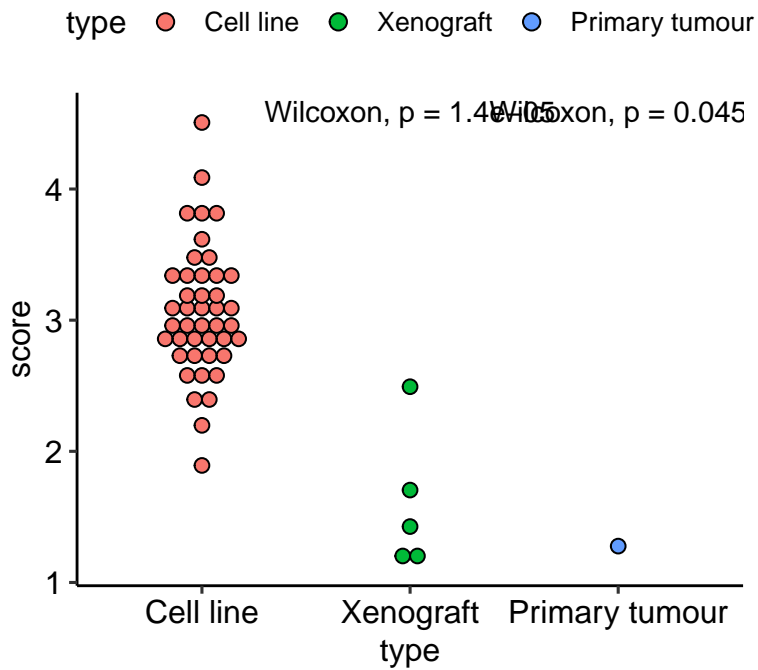
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Collisson.Exocrine score



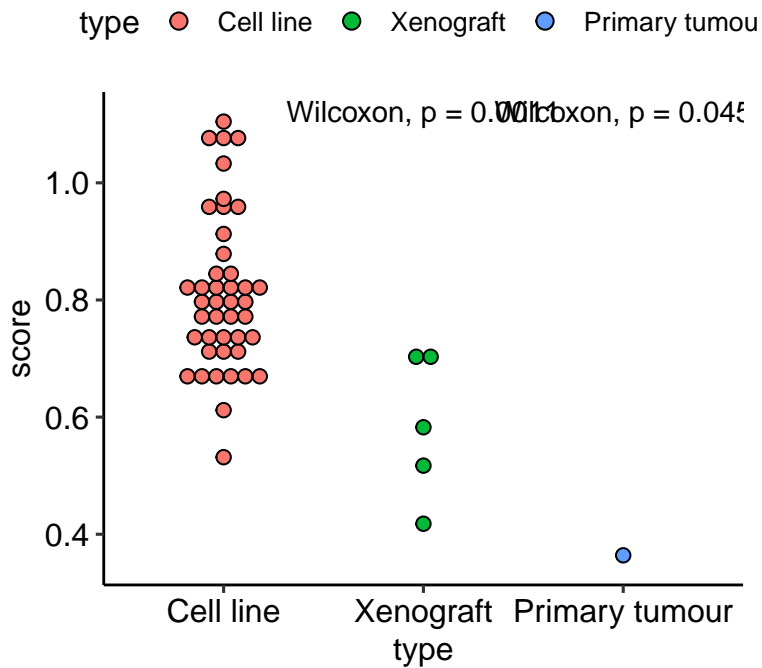
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Collisson.QM score



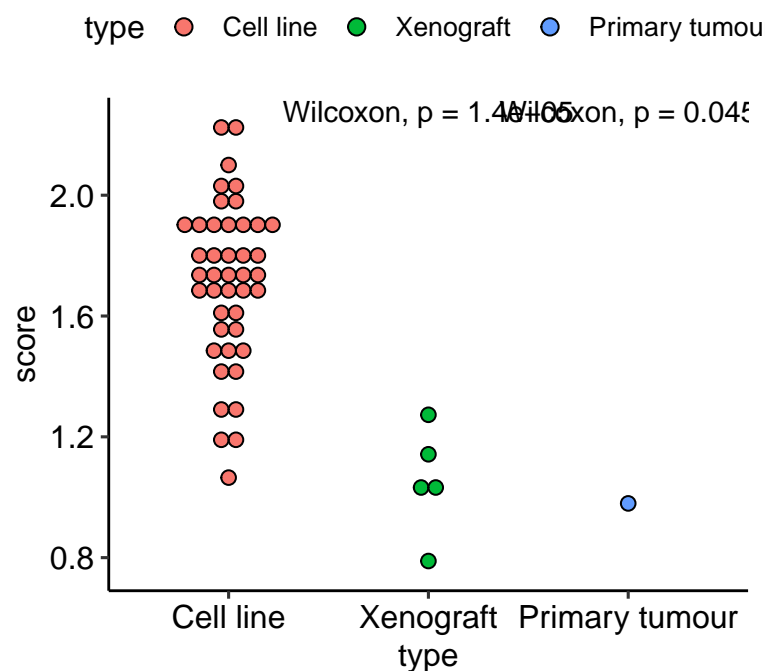
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## ICGC.ADEX.Up score



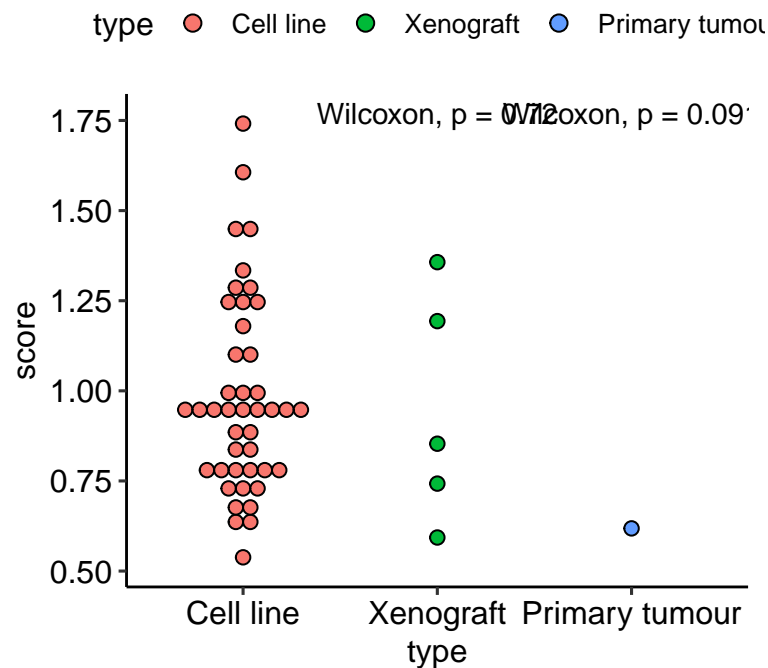
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## ICGC.ADEX.Down score



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

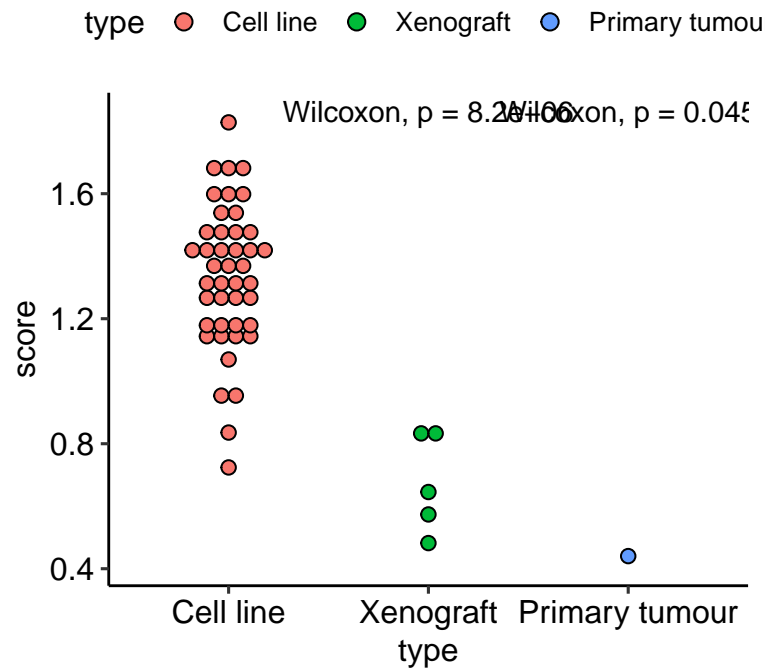
## ICGC.Immunogenic.Up score



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

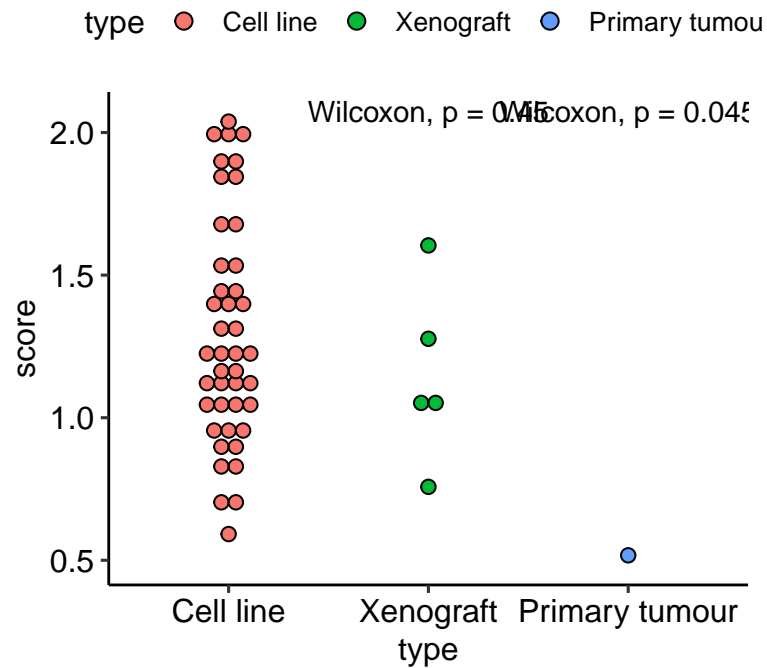


## ICGC.Immunogenic.Down score



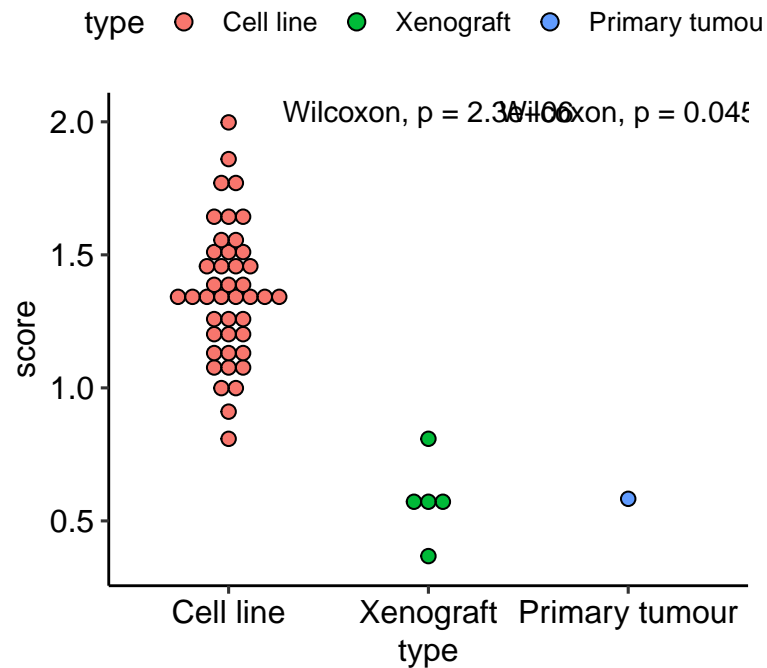
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## ICGC.Progenitor.Up score



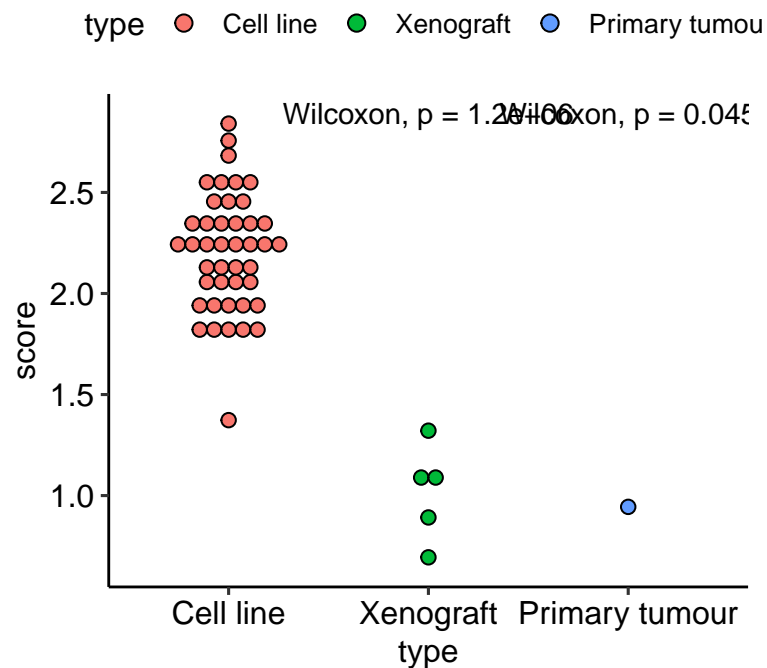
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## ICGC.Progenitor.Down score



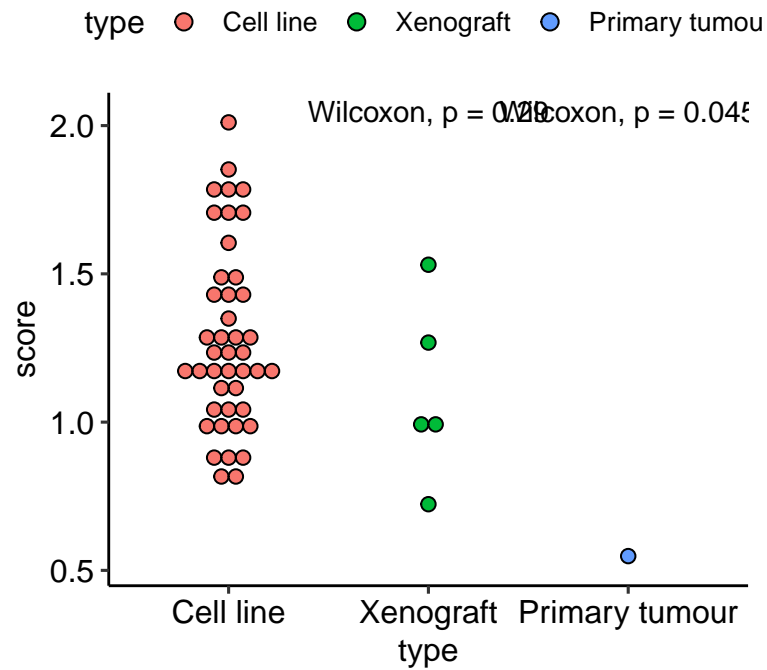
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

## ICGC.Squamous.Up score



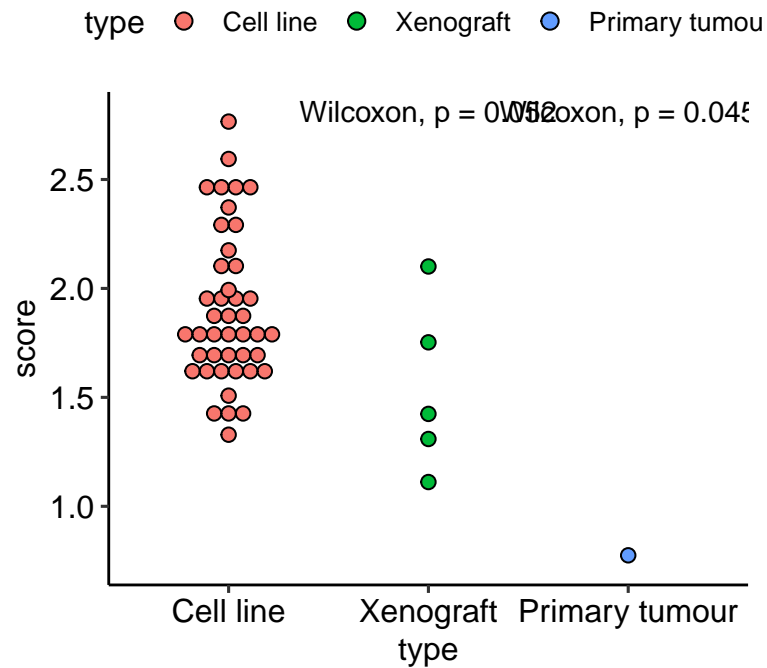
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

## ICGC.Squamous.Down score



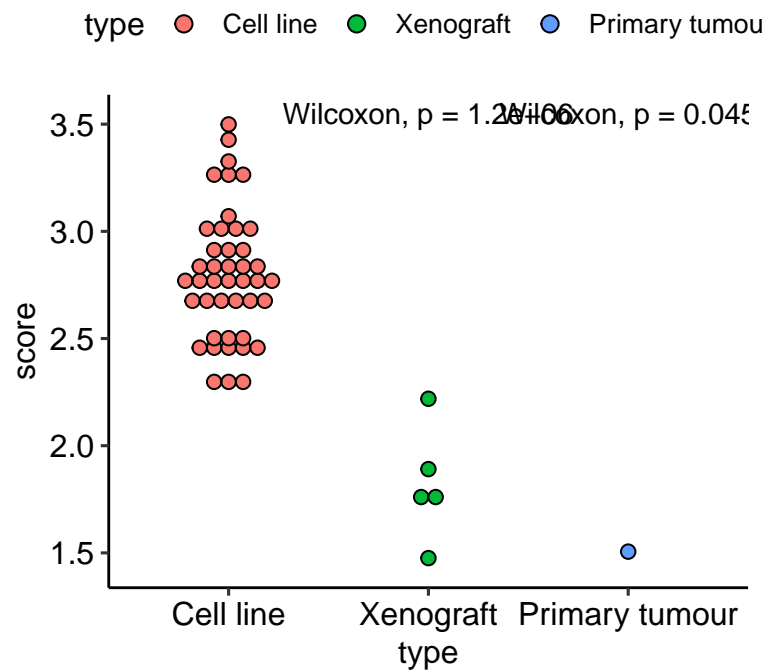
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## ICGC.SAM score



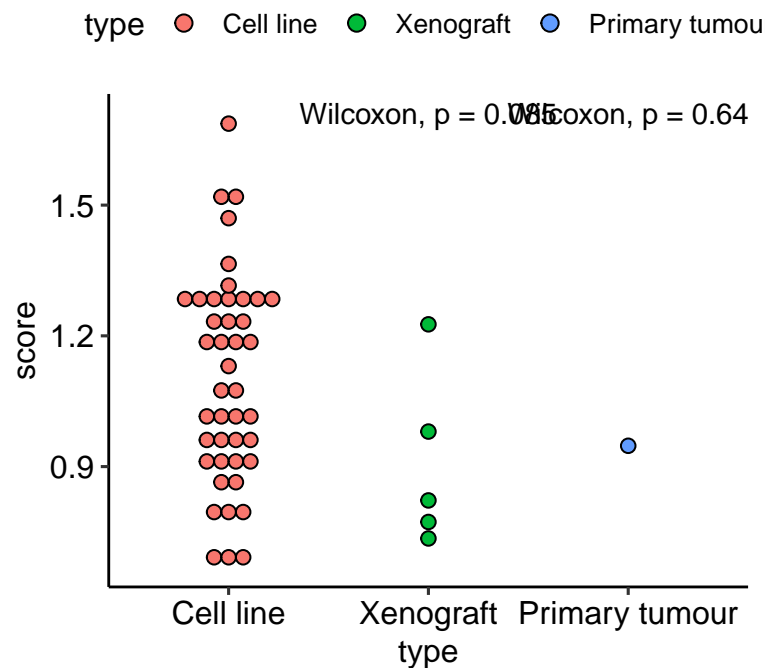
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Scarpa\_PanNET score



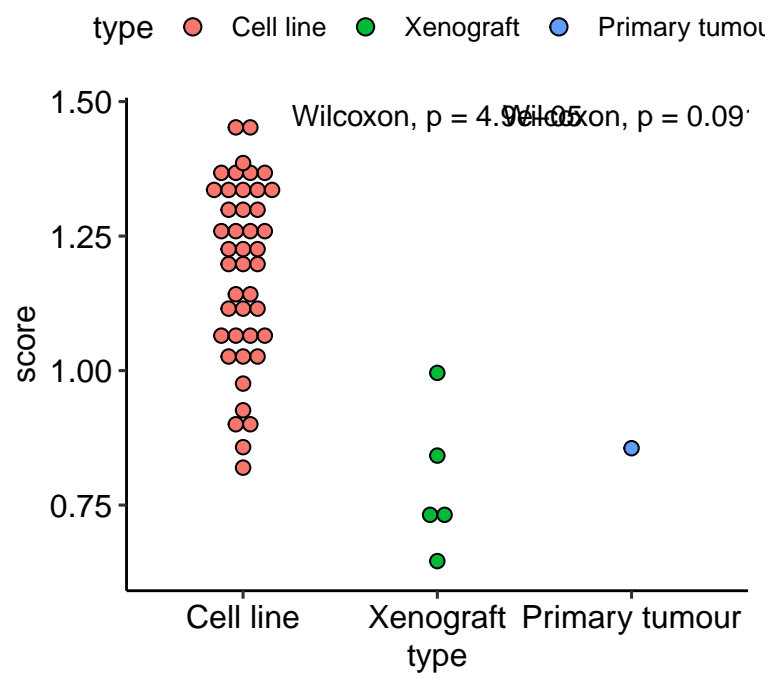
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

## Moffitt.Top5s score



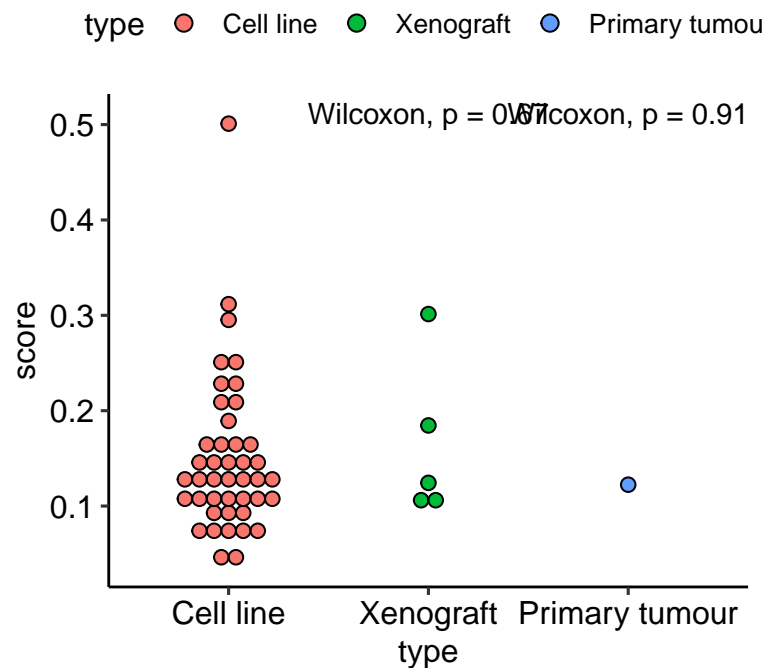
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

### Moffitt.Top25s score



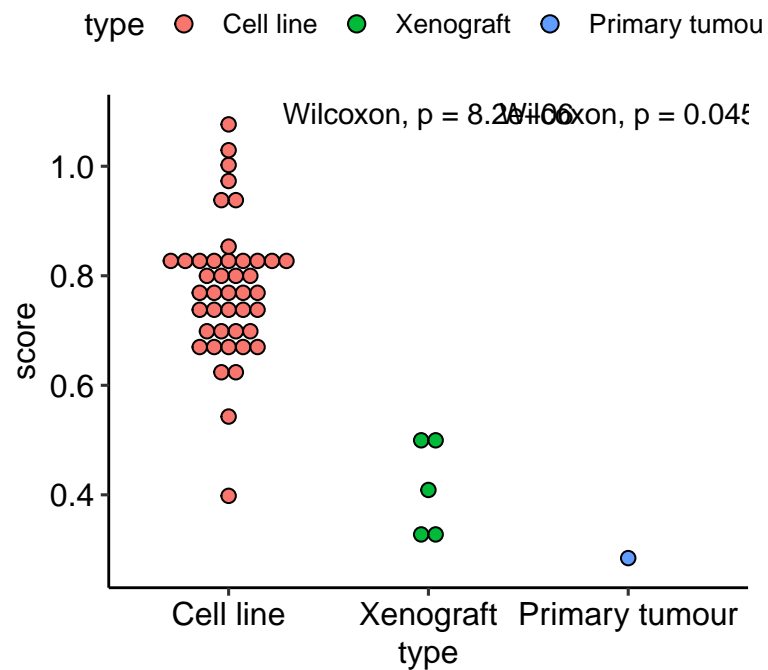
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F1\_Liver.top25 score



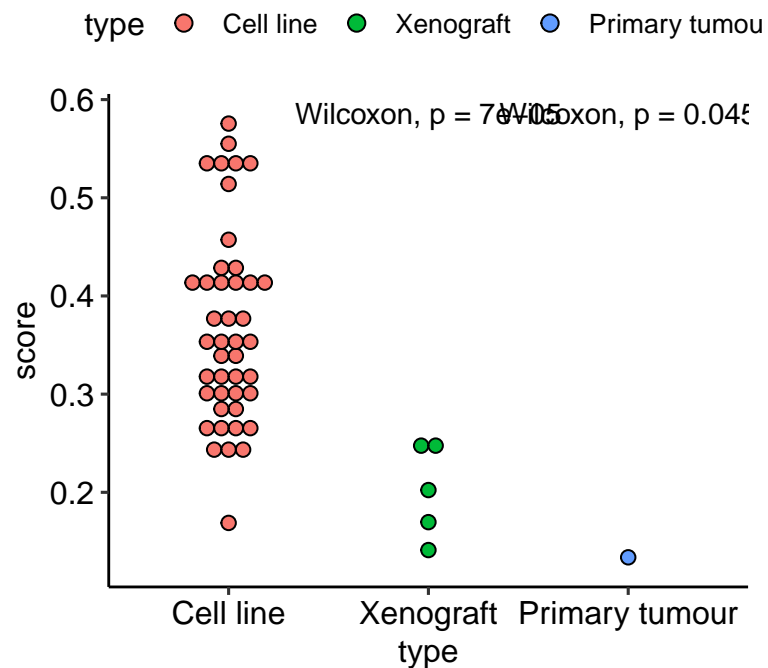
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F1\_Liver.top250 score



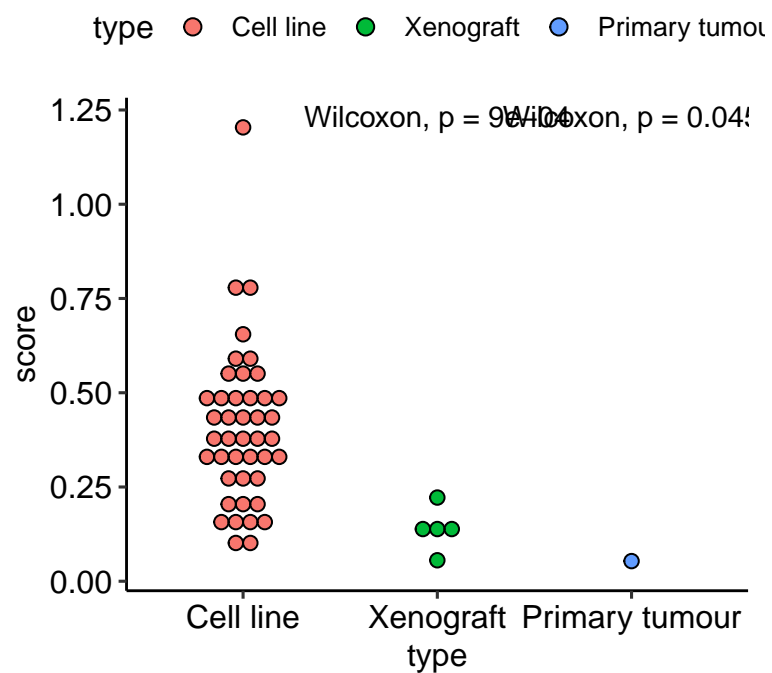
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F1\_Liver.top100 score



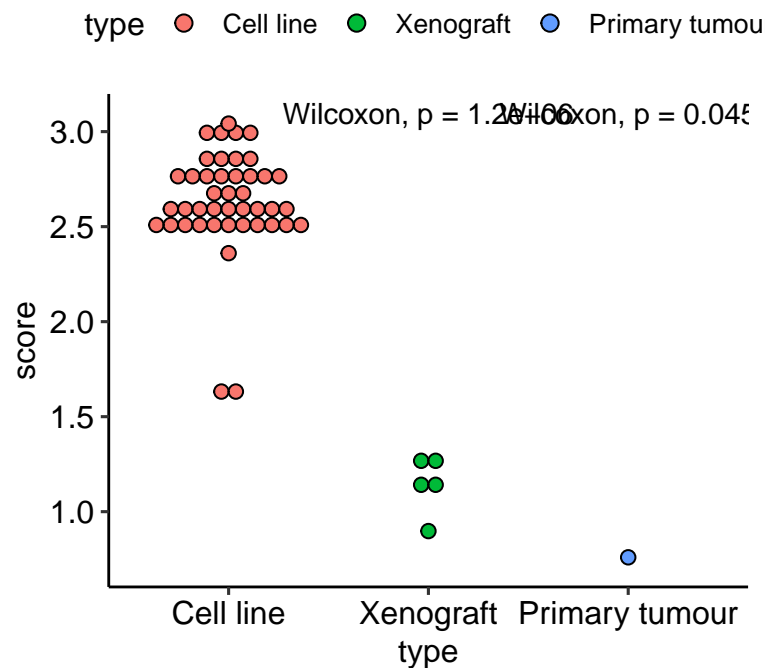
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F2.top25 score



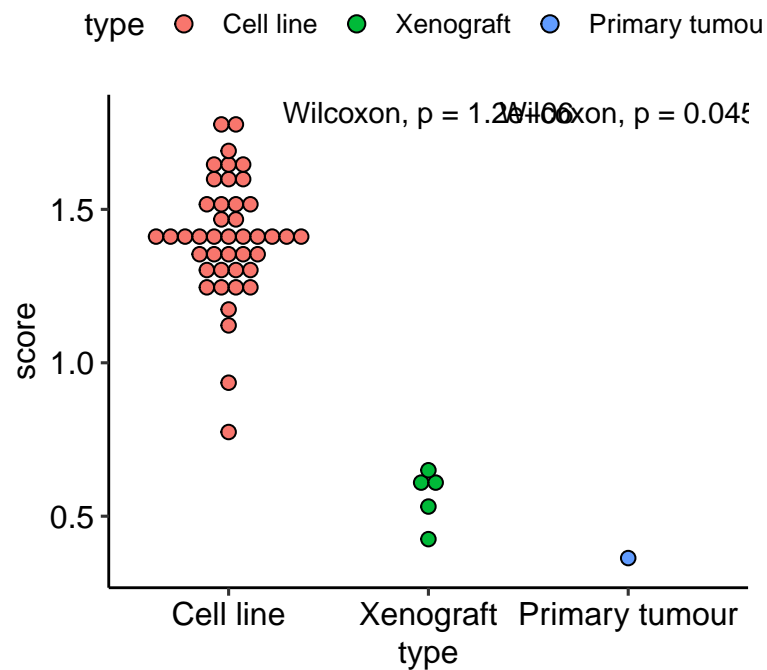
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F2.top250 score



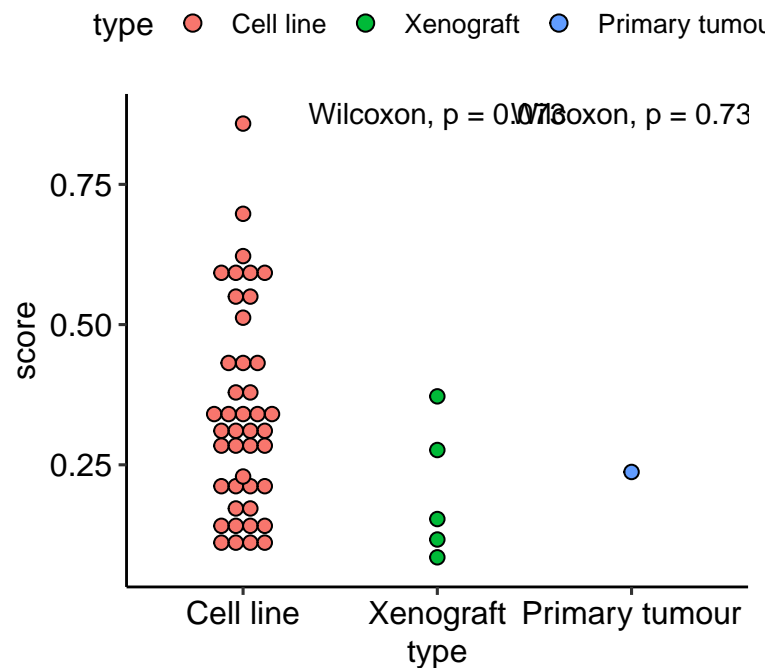
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F2.top100 score



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

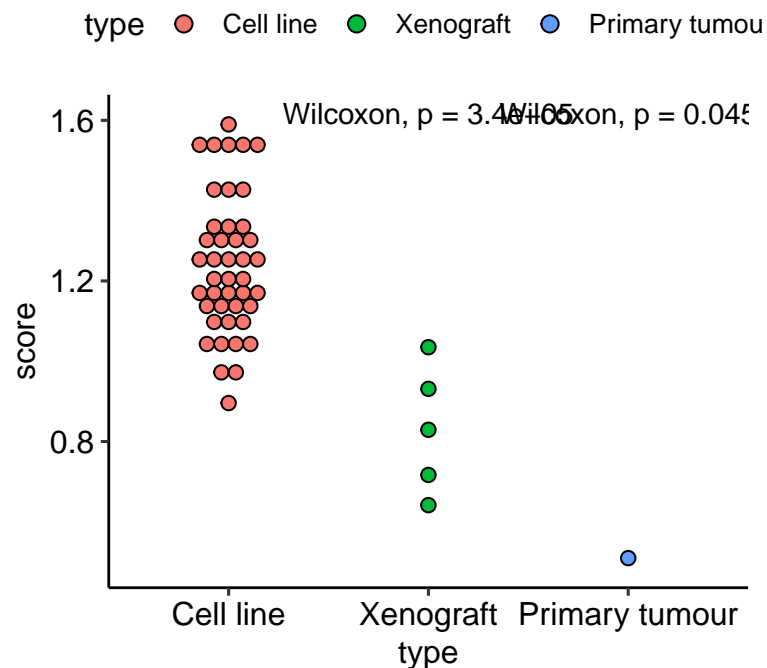
### Moffitt.F3\_Exocrine.top25 score



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

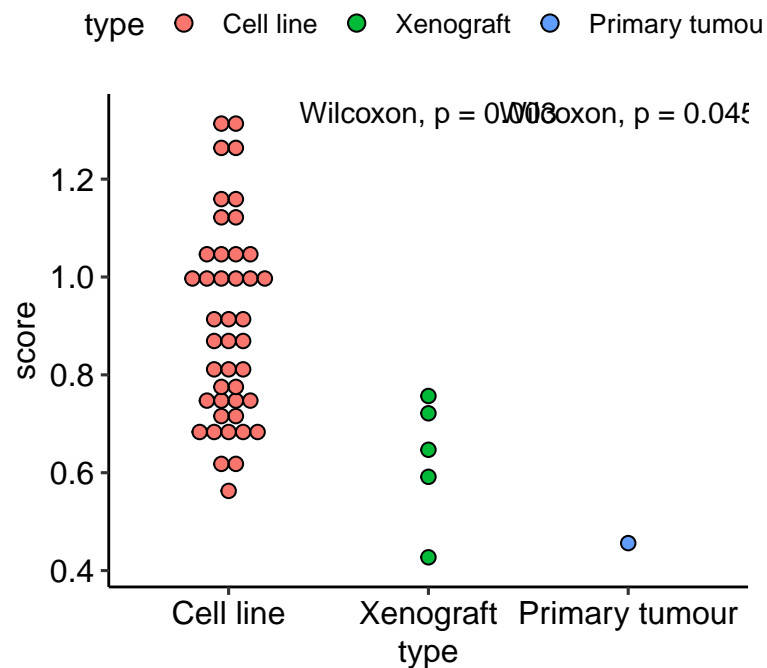


### Moffitt.F3\_Exocrine.top250 score



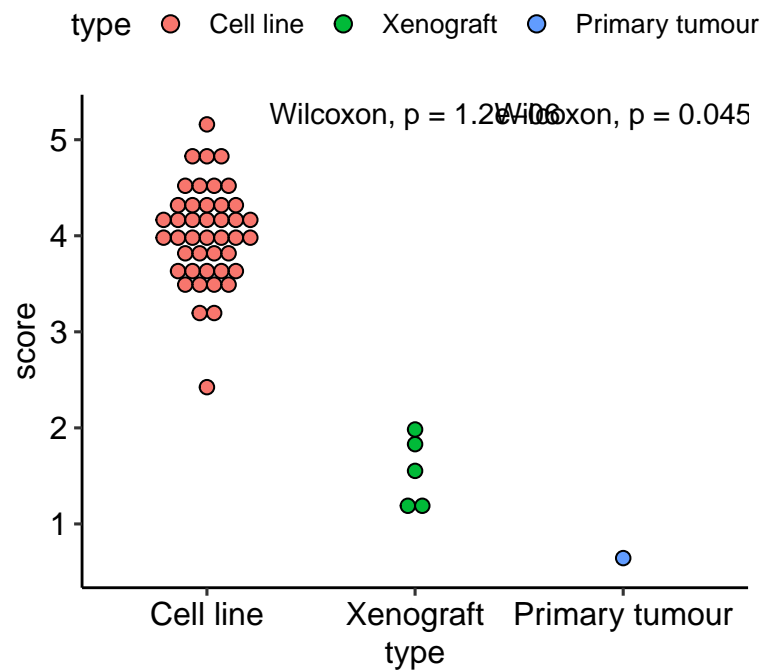
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F3\_Exocrine.top100 score



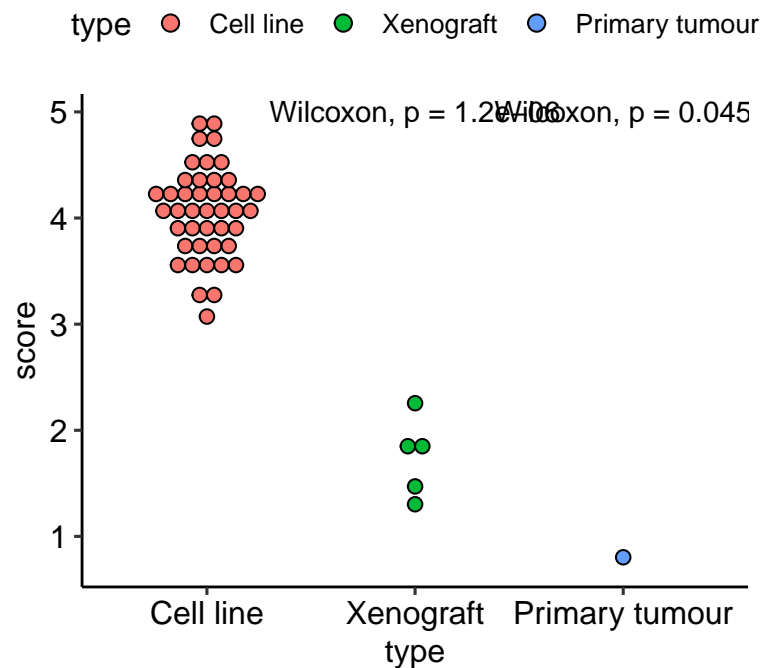
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F4\_CellCycle.top25 score



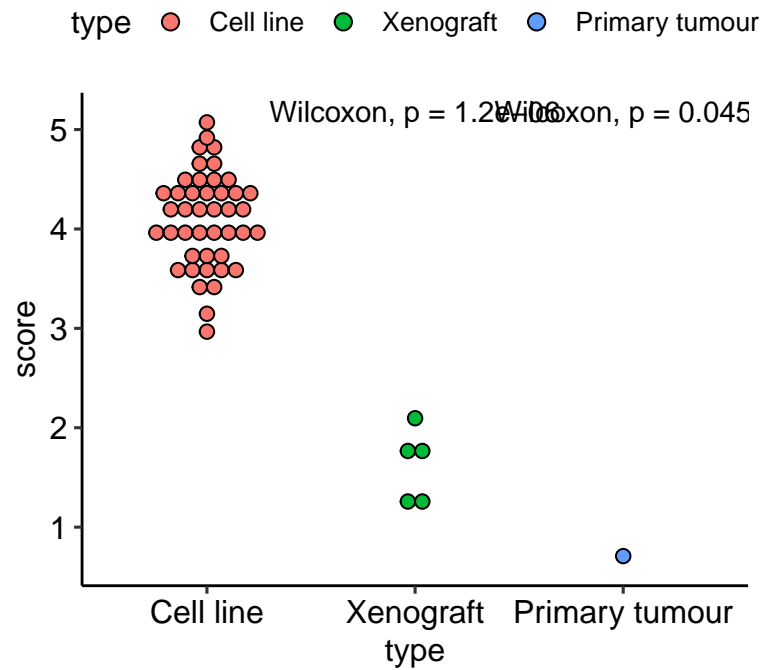
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F4\_CellCycle.top250 score



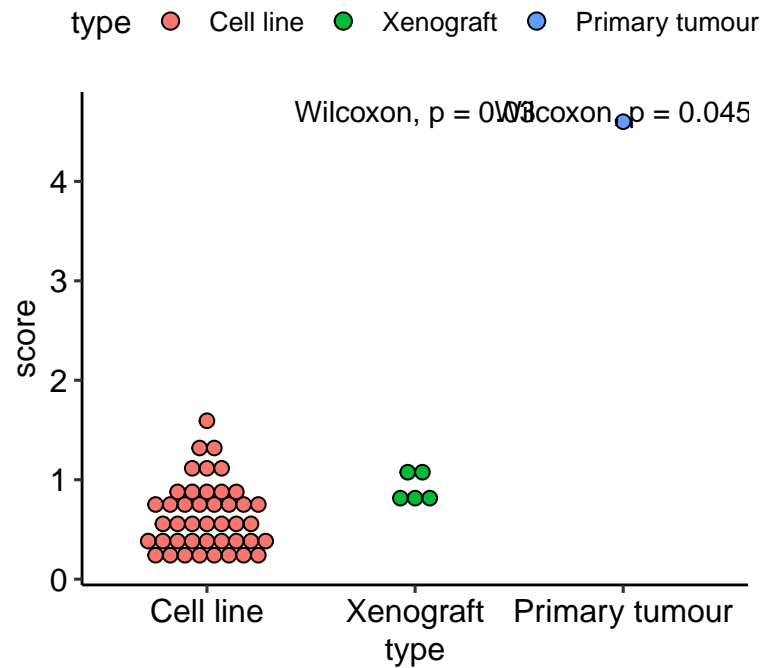
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F4\_CellCycle.top100 score



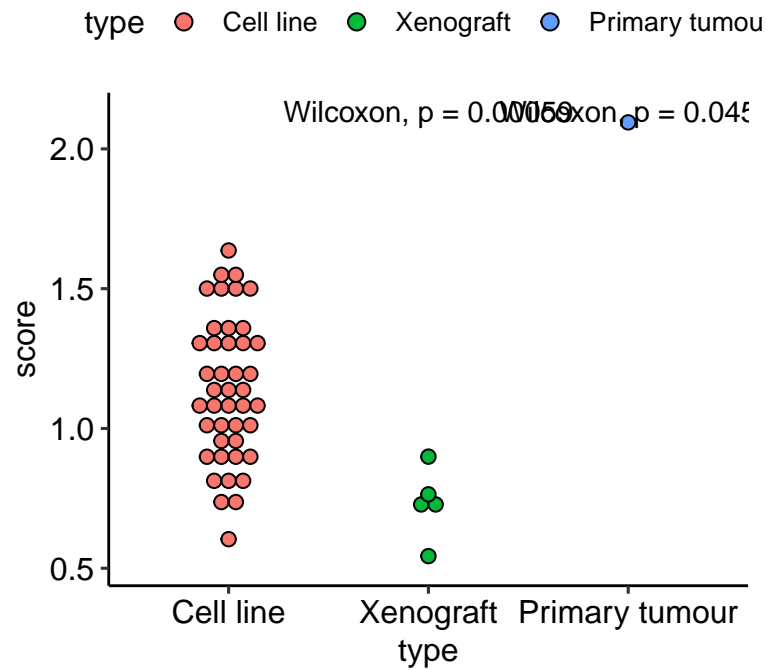
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F5\_ActivatedStroma.top25 score



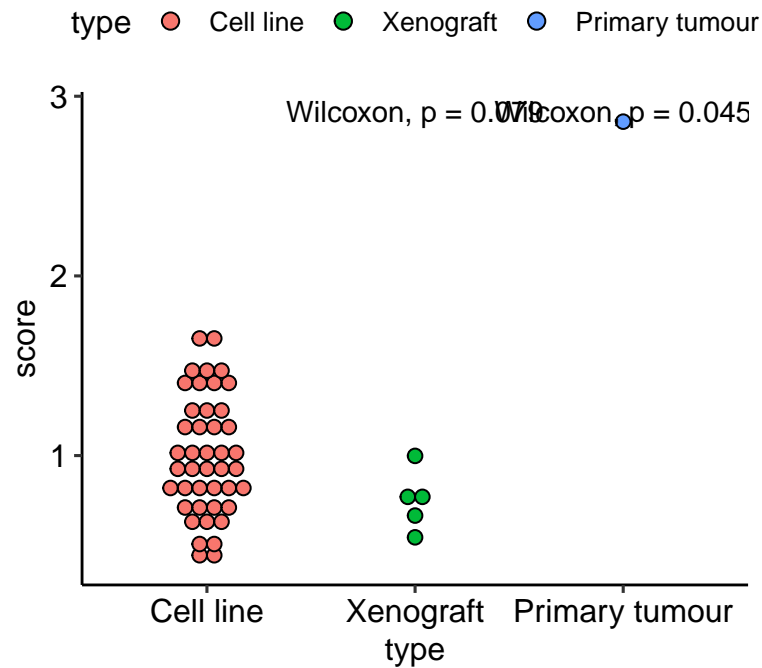
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F5\_ActivatedStroma.top250 score



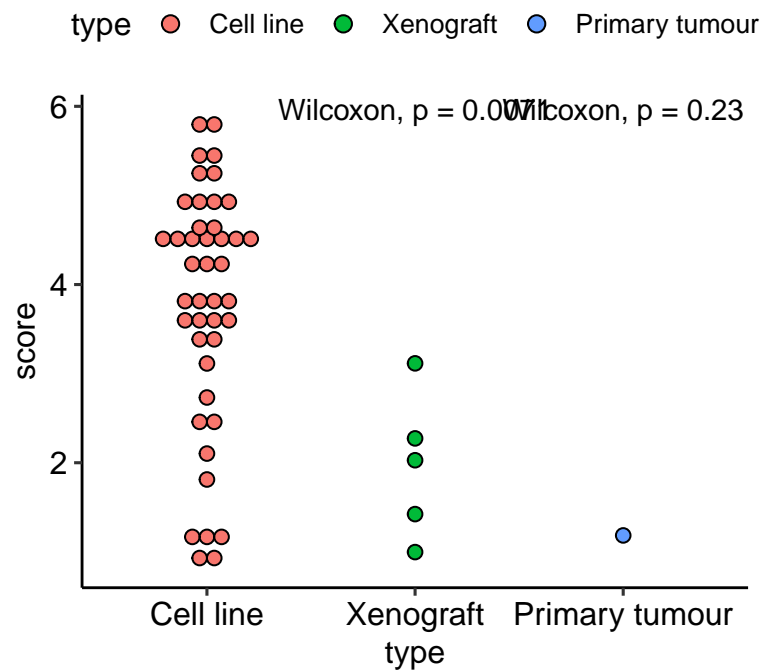
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F5\_ActivatedStroma.top100 score



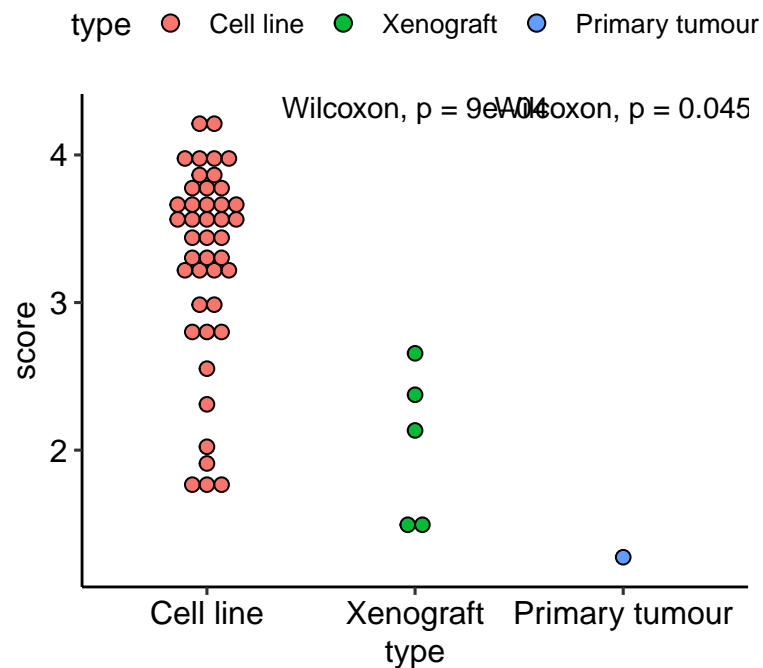
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F6\_BasalLike.top25 score



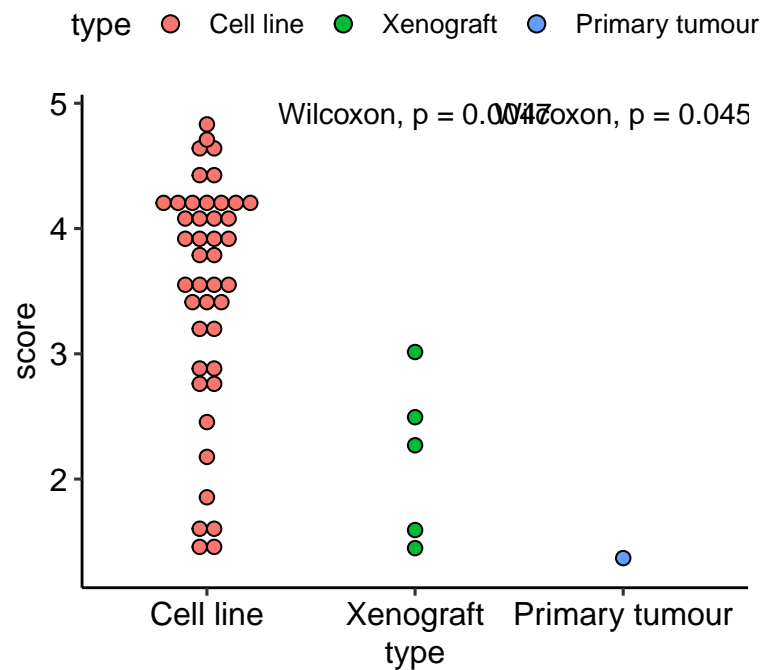
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F6\_BasalLike.top250 score



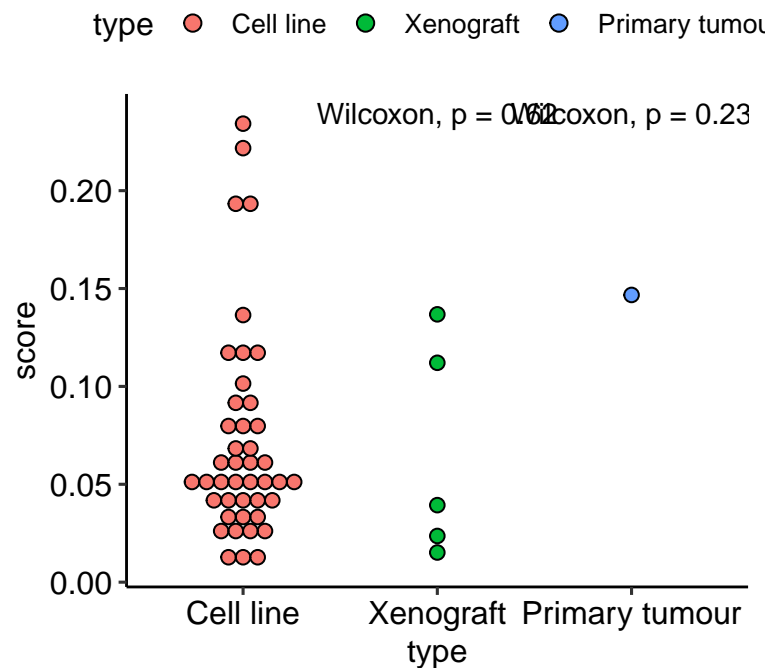
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F6\_BasalLike.top100 score



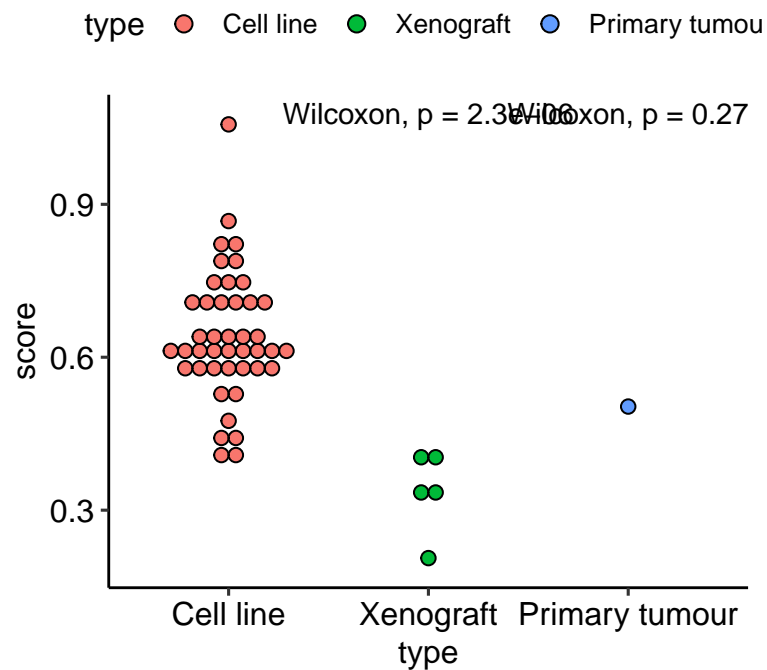
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F7\_Immune.top25 score



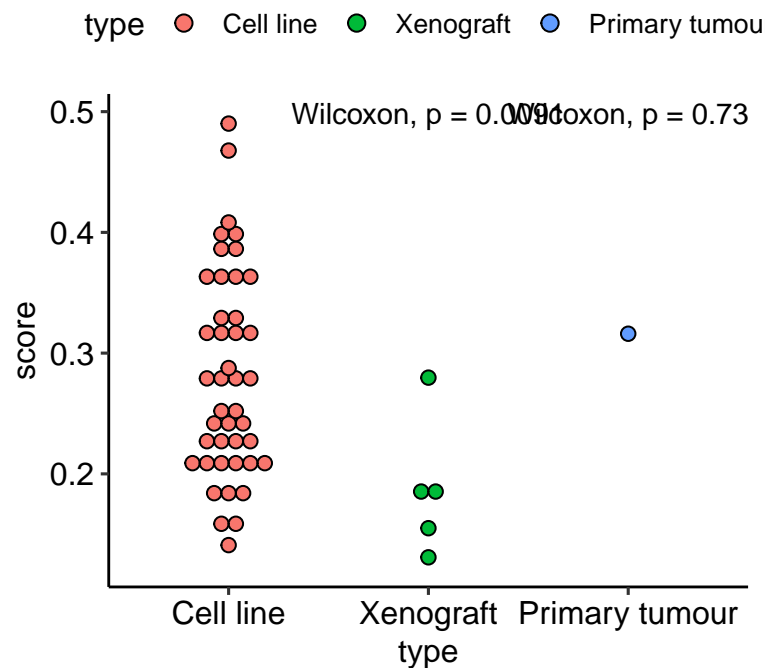
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F7\_Immune.top250 score



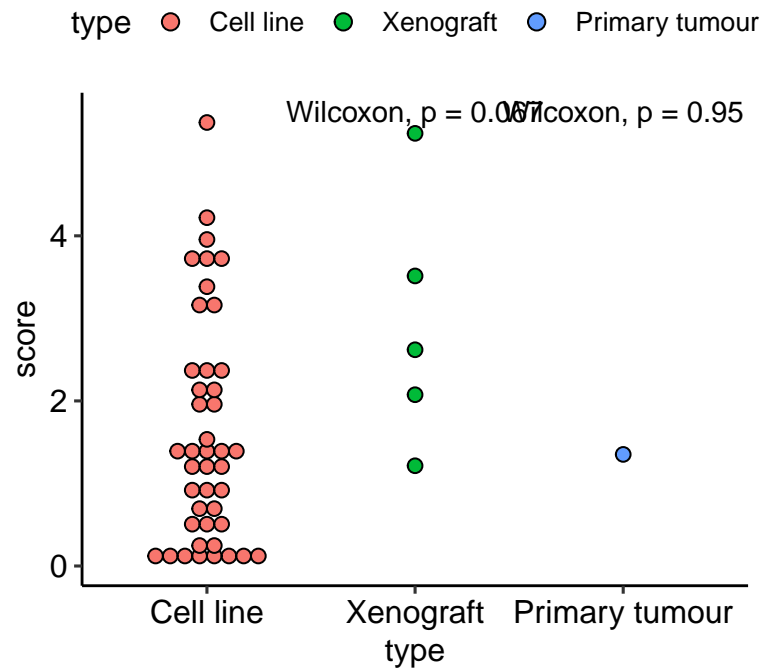
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F7\_Immune.top100 score



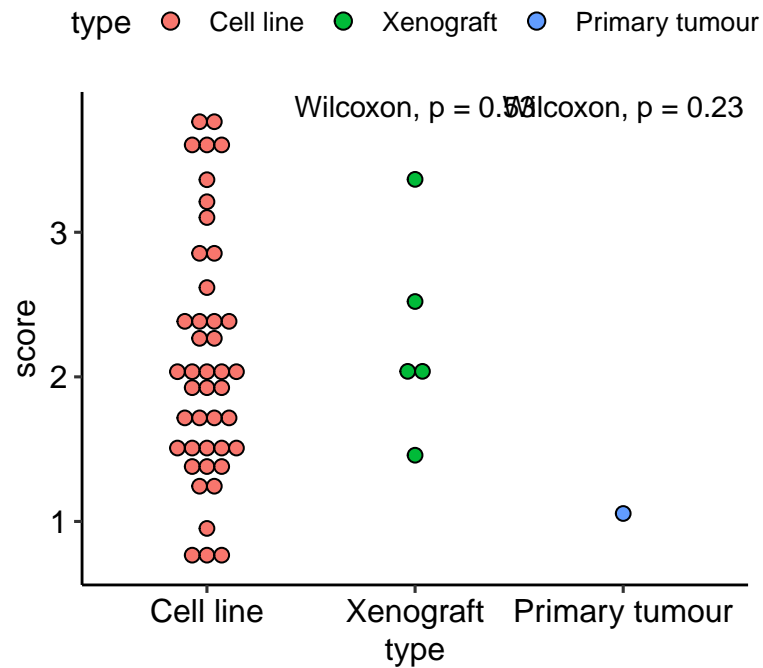
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F8\_Classical.top25 score



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F8\_Classical.top250 score

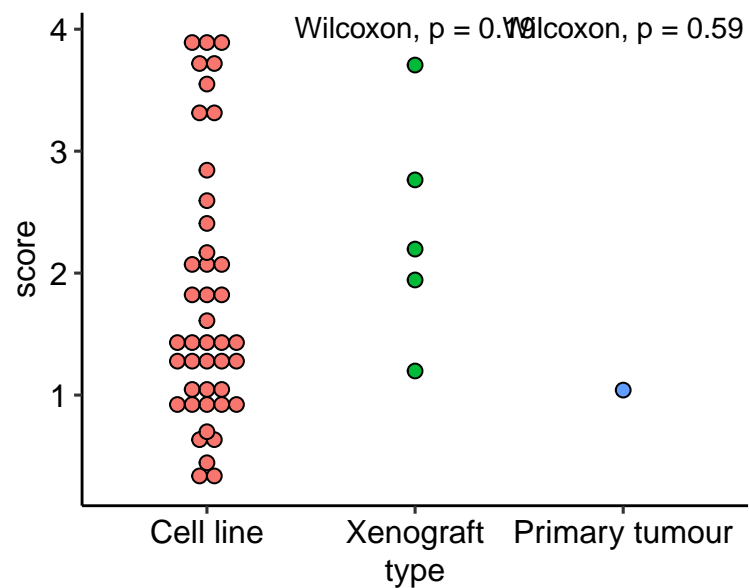


## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.



## Moffitt.F8\_Classical.top100 score

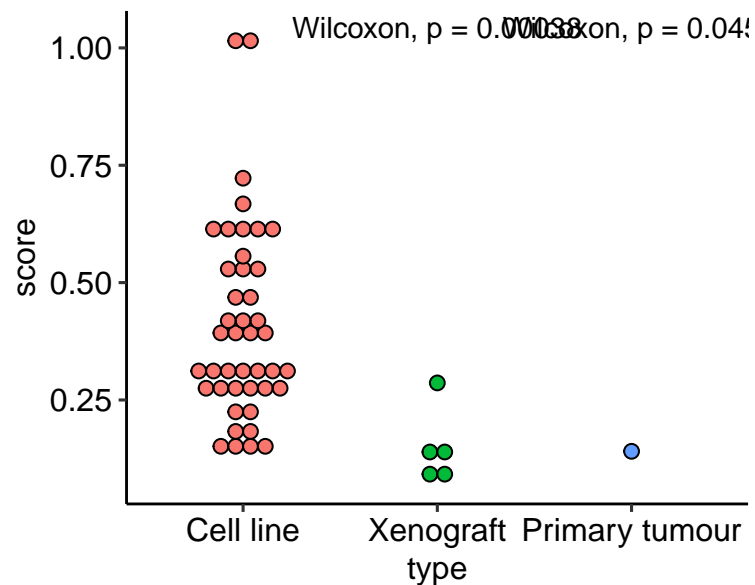
type   ● Cell line   ● Xenograft   ● Primary tumour



```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

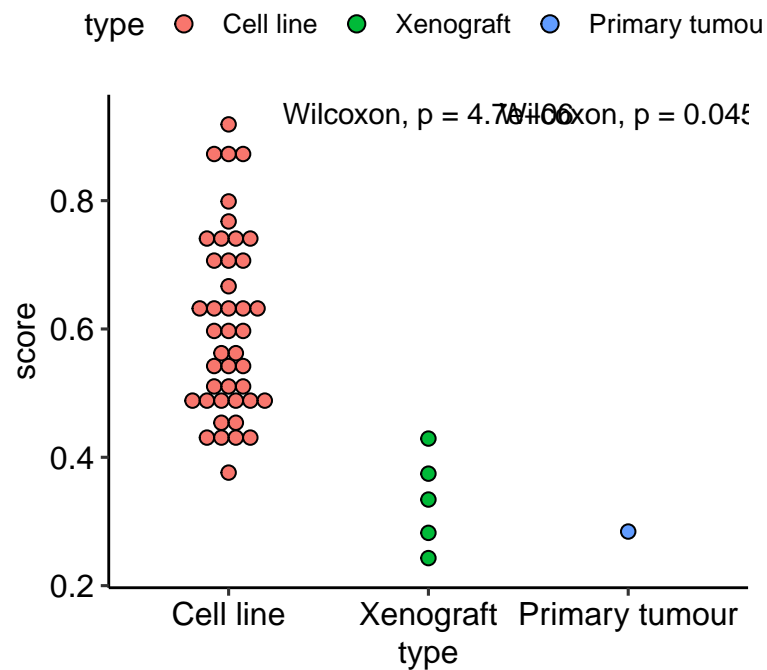
## Moffitt.F9\_Lung.top25 score

type   ● Cell line   ● Xenograft   ● Primary tumour



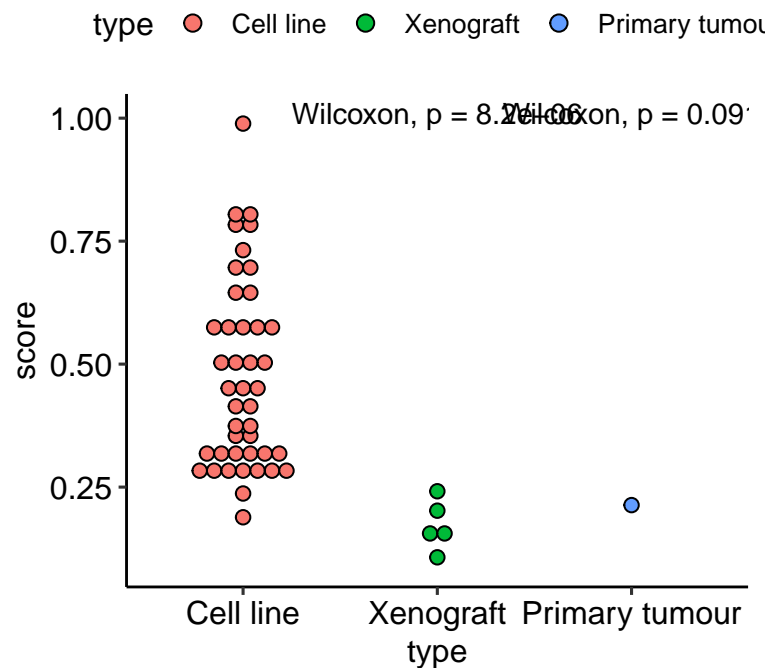
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

### Moffitt.F9\_Lung.top250 score



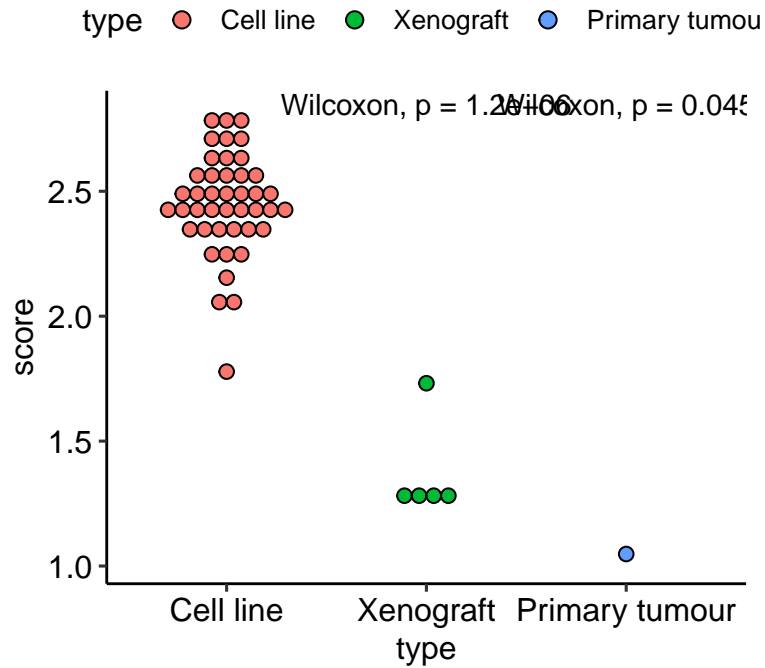
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F9\_Lung.top100 score



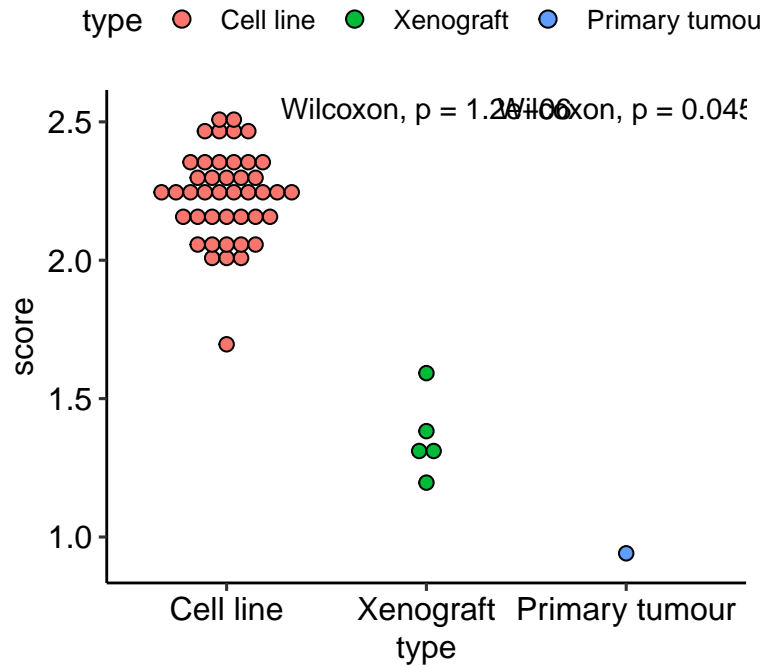
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F10.top25 score



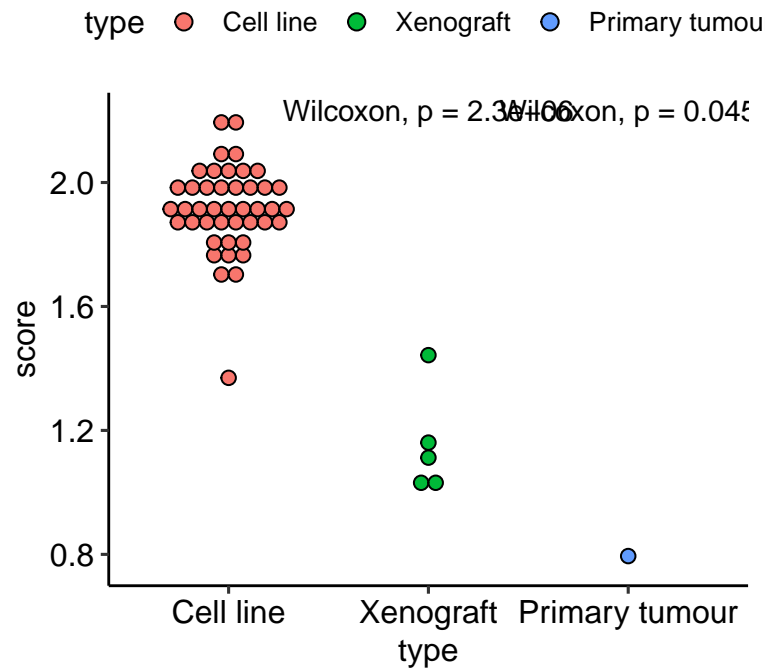
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

## Moffitt.F10.top250 score



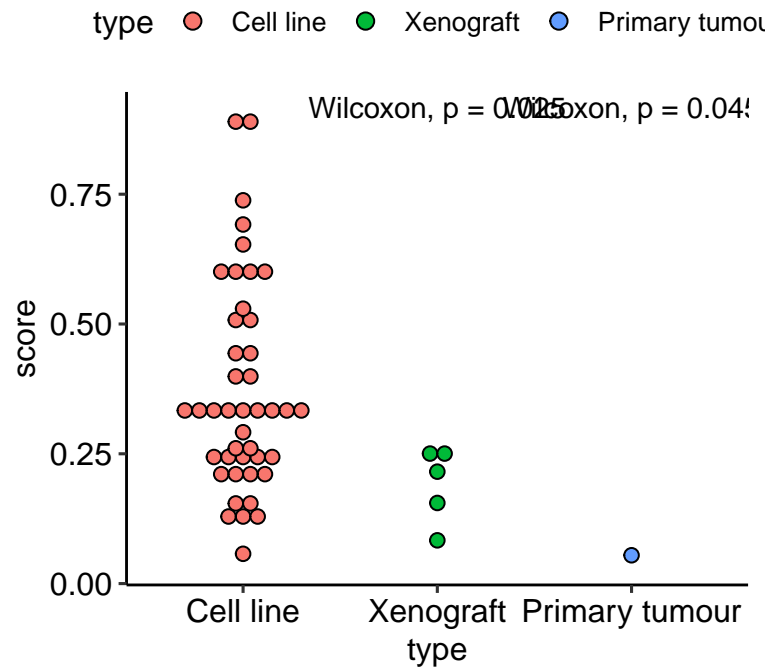
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

## Moffitt.F10.top100 score



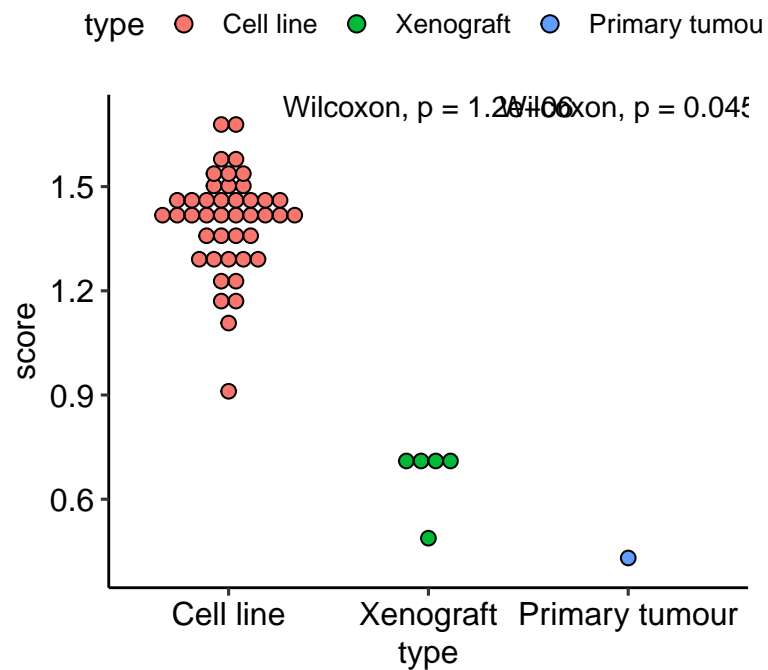
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

## Moffitt.F11\_Muscle.top25 score



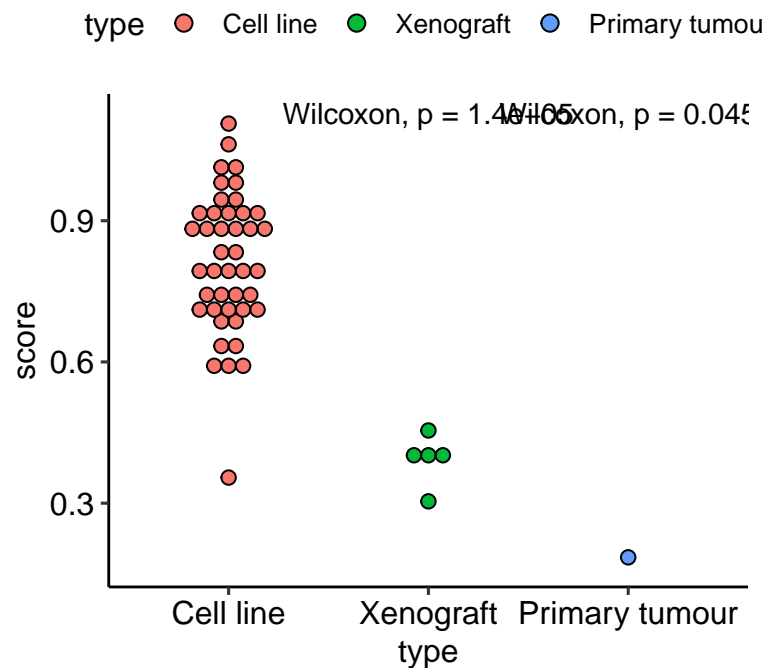
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

### Moffitt.F11\_Muscle.top250 score



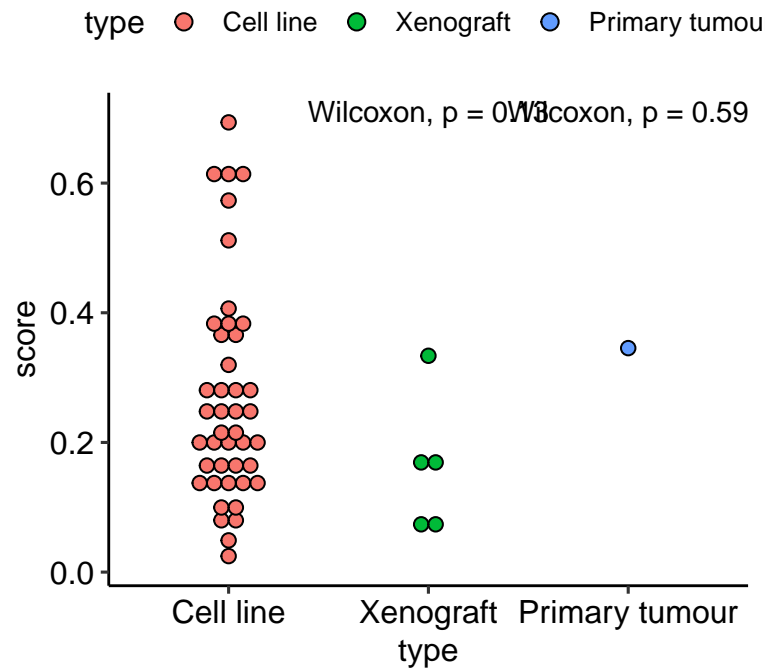
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F11\_Muscle.top100 score



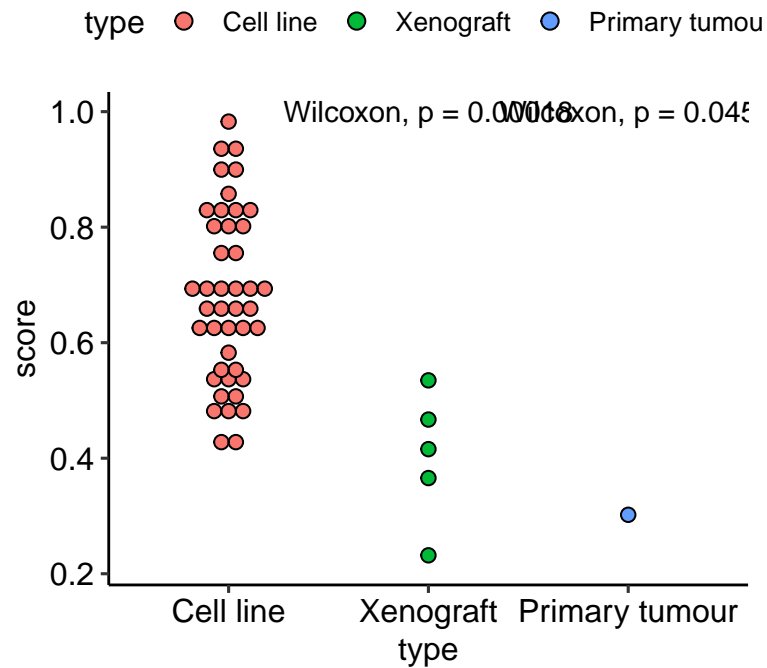
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F12\_Endocrine.top25 score



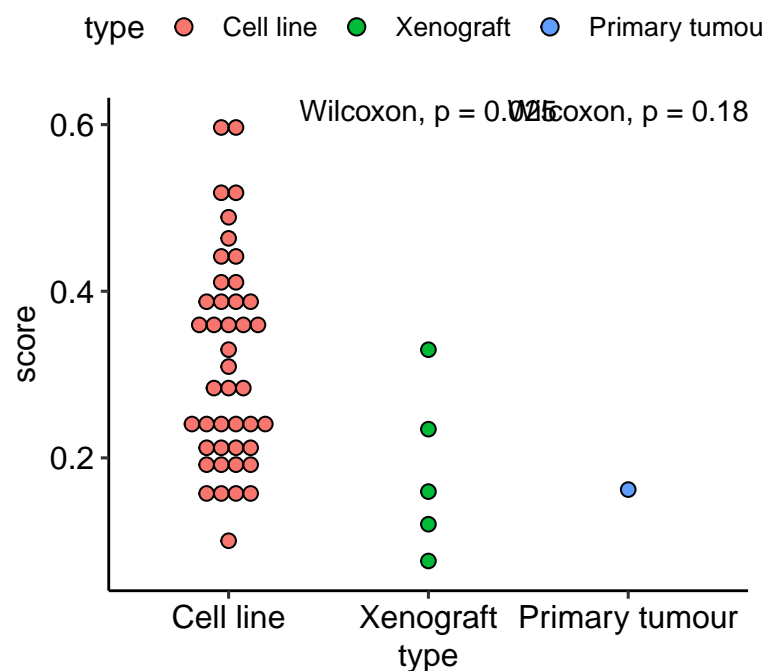
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F12\_Endocrine.top250 score



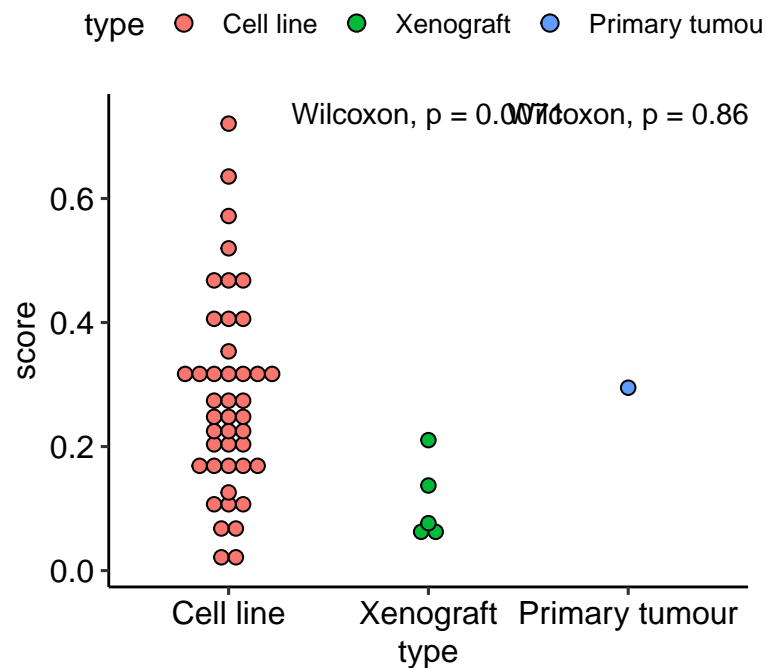
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F12\_Endocrine.top100 score

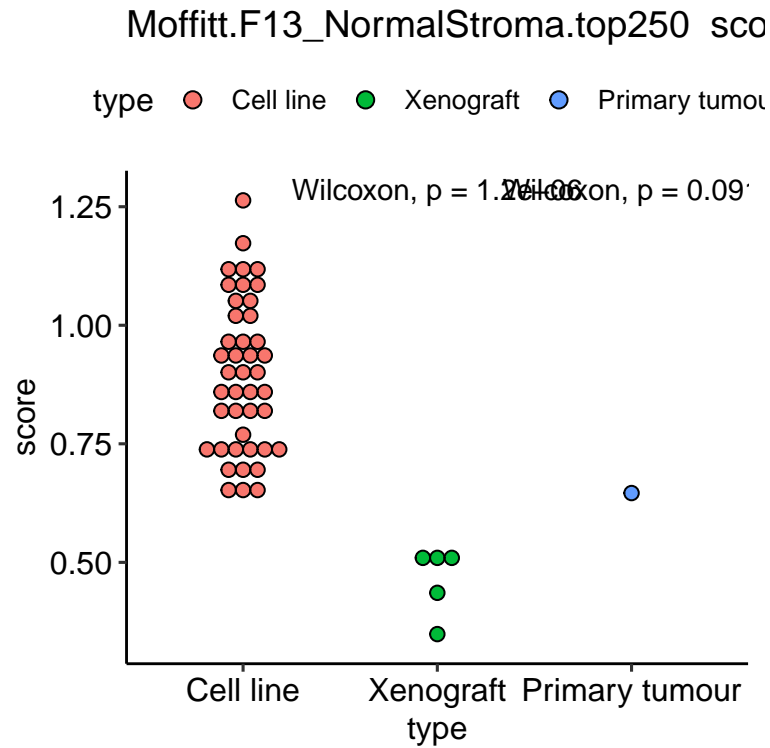


## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

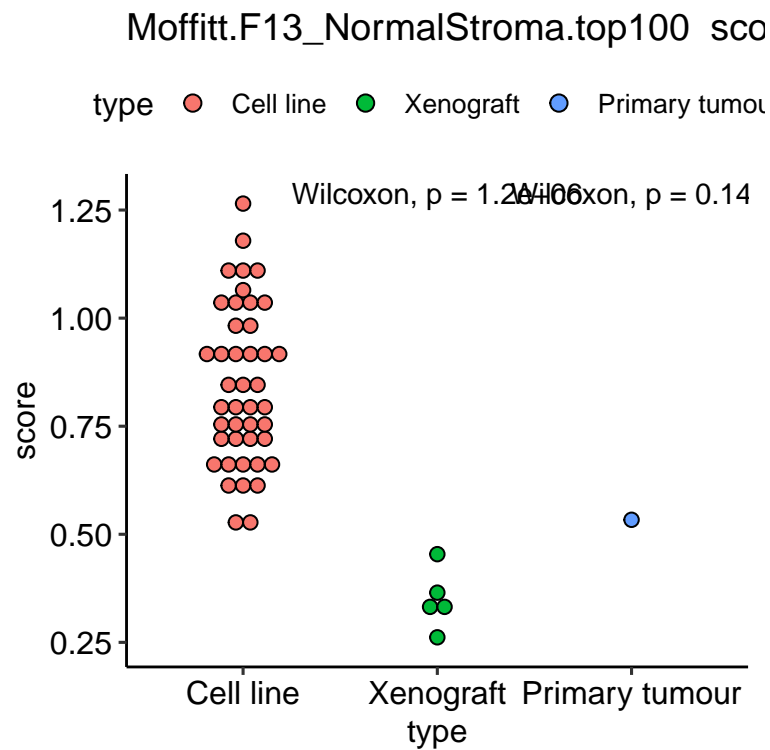
### Moffitt.F13\_NormalStroma.top25 score



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.



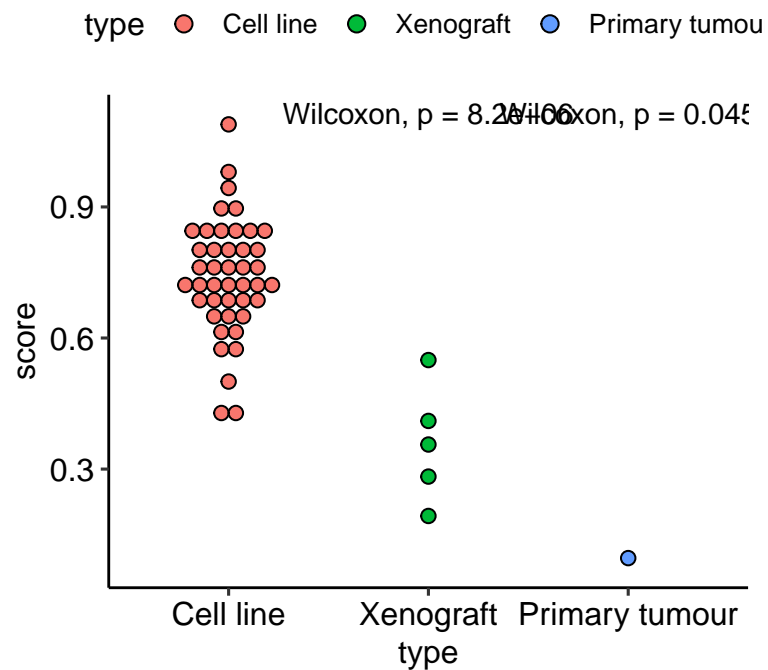
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

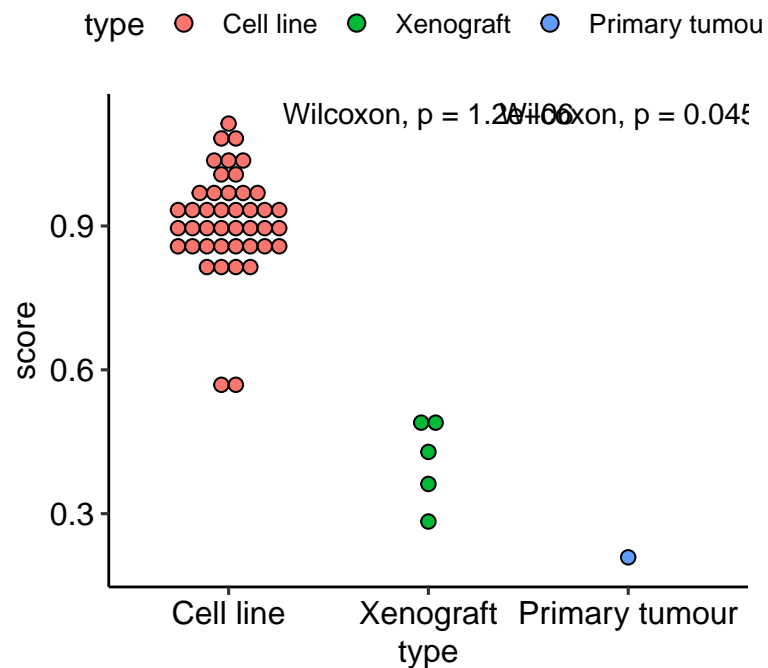


## Moffitt.F14.top25 score



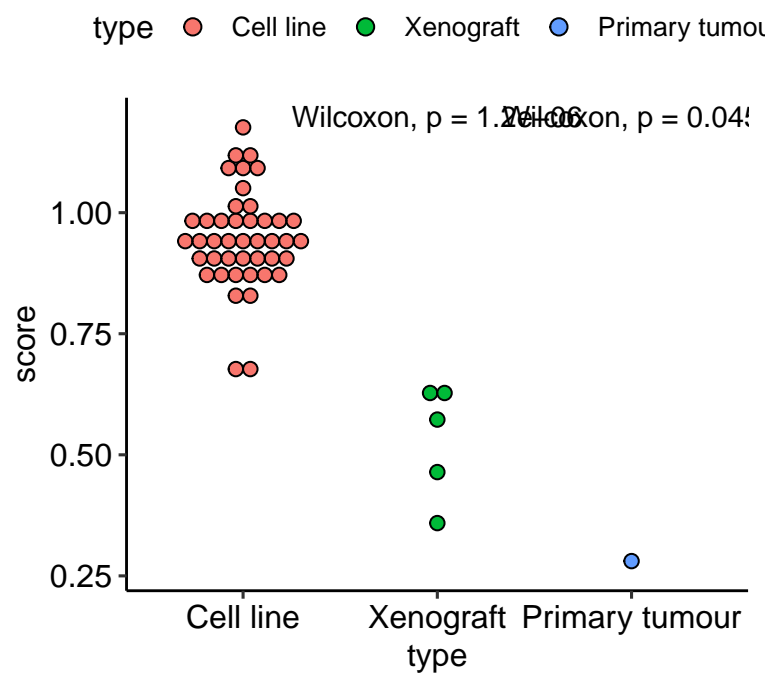
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Moffitt.F14.top250 score



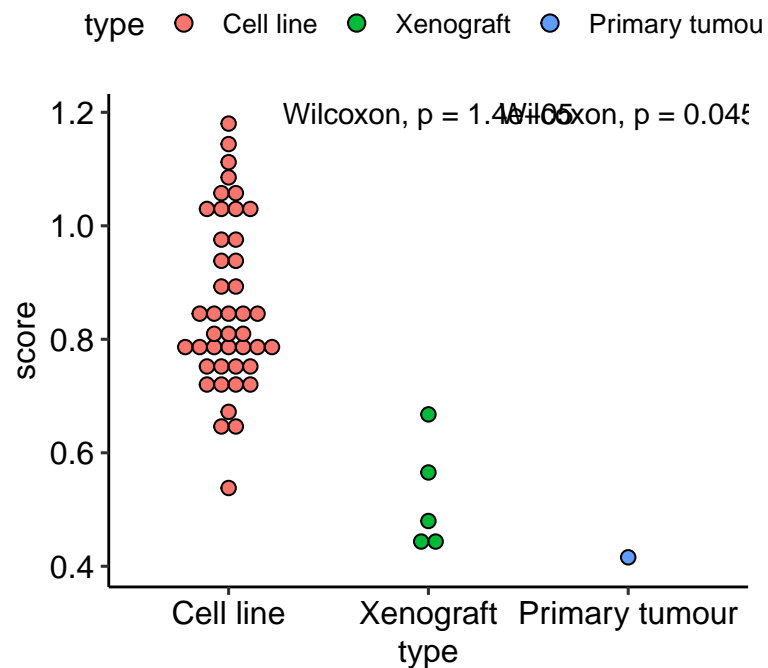
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### Moffitt.F14.top100 score



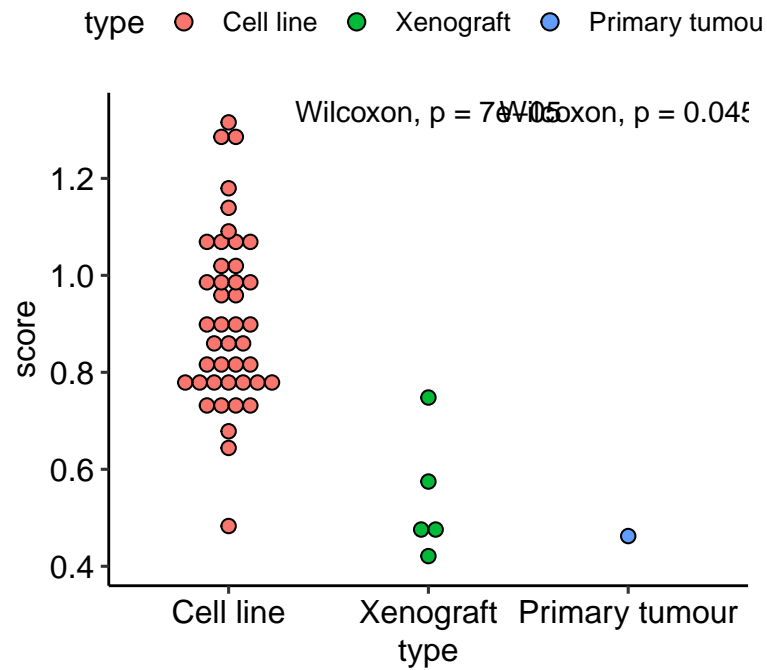
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### CIBERSORT.B.cells.naive score



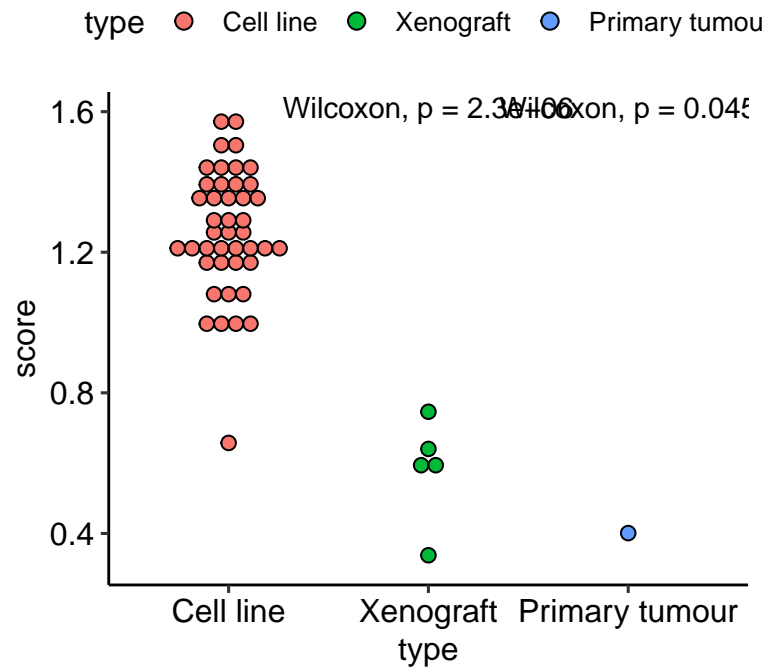
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## CIBERSORT.B.cells.memory score



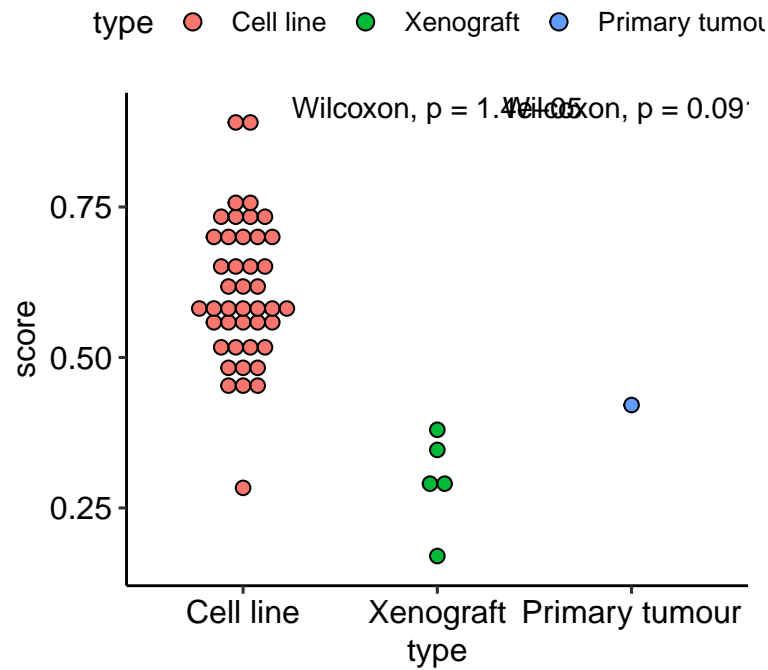
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## CIBERSORT.Plasma.cells score



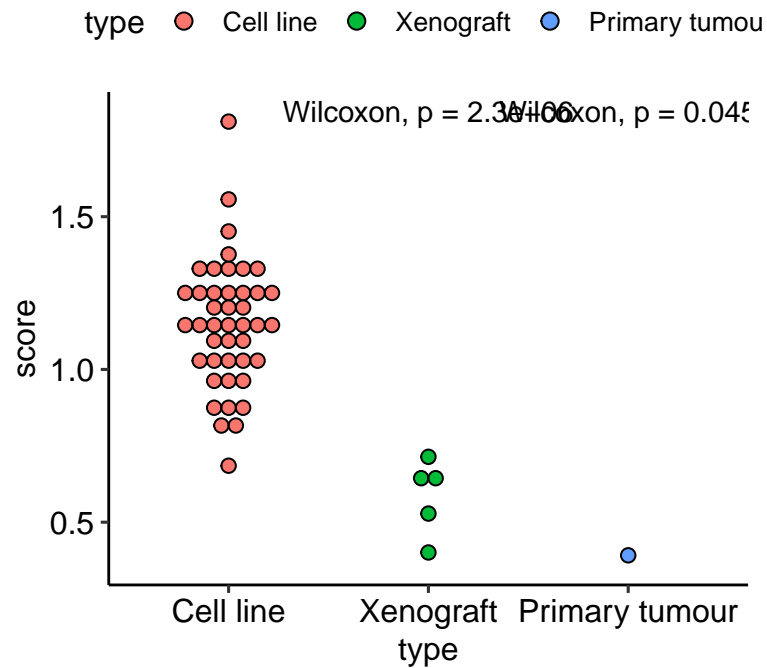
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### CIBERSORT.T.cells.CD8 score



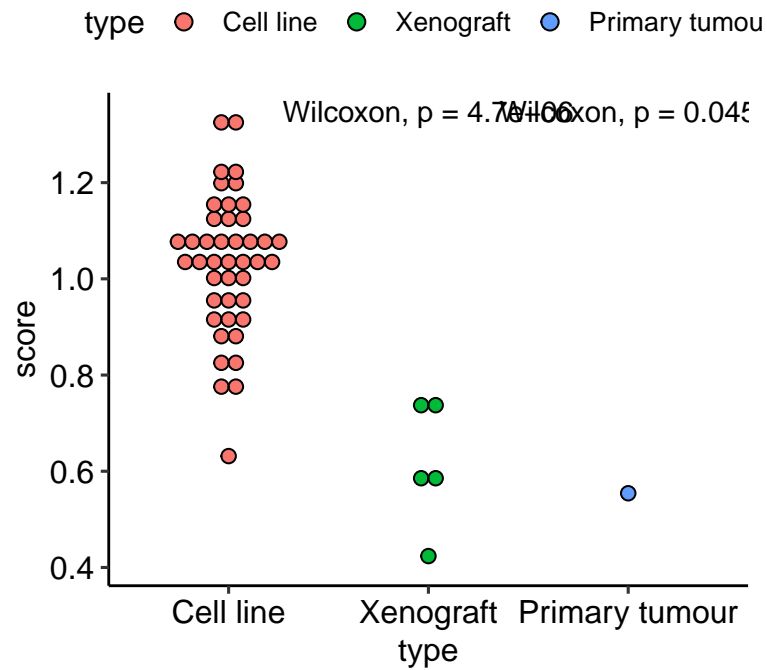
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### CIBERSORT.T.cells.CD4.naive score



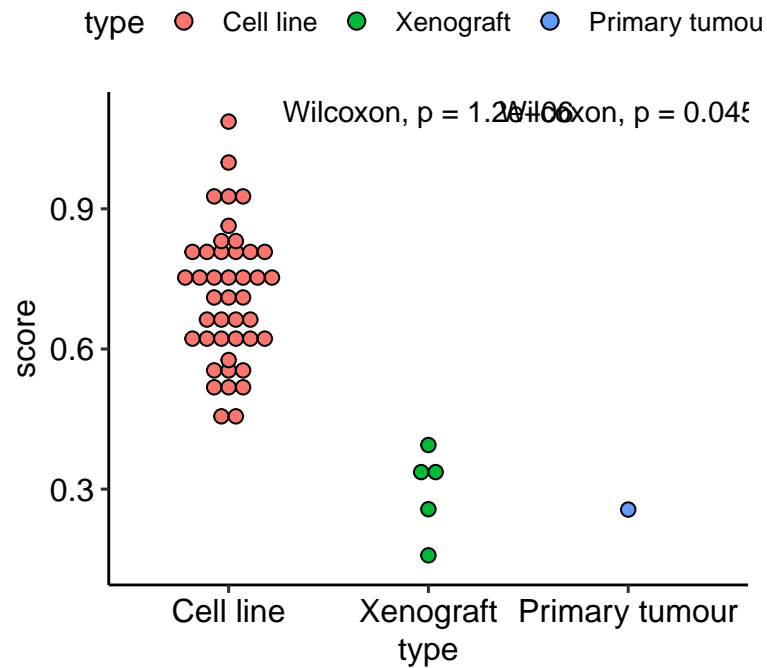
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## CIBERSORT.T.cells.CD4.memory.restin



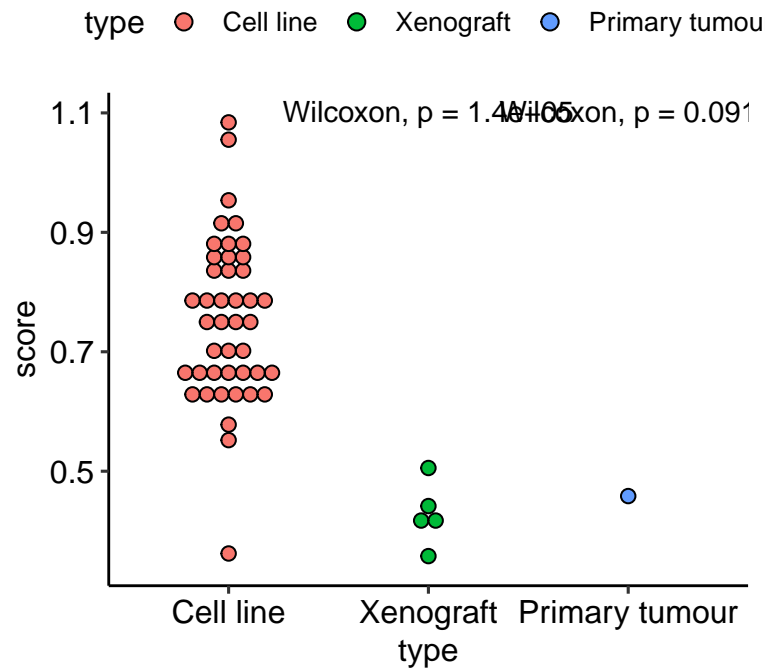
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## CIBERSORT.T.cells.CD4.memory.active



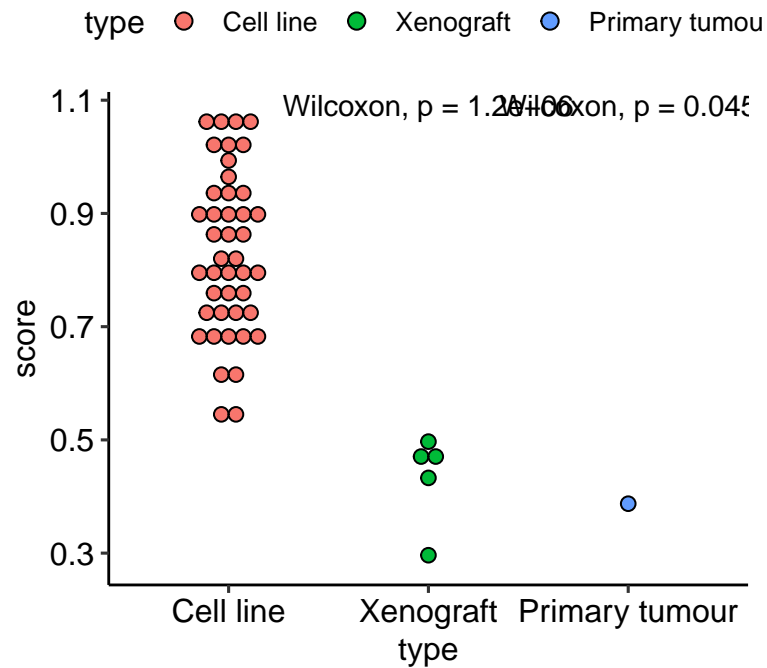
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### CIBERSORT.T.cells.follicular.helper scc



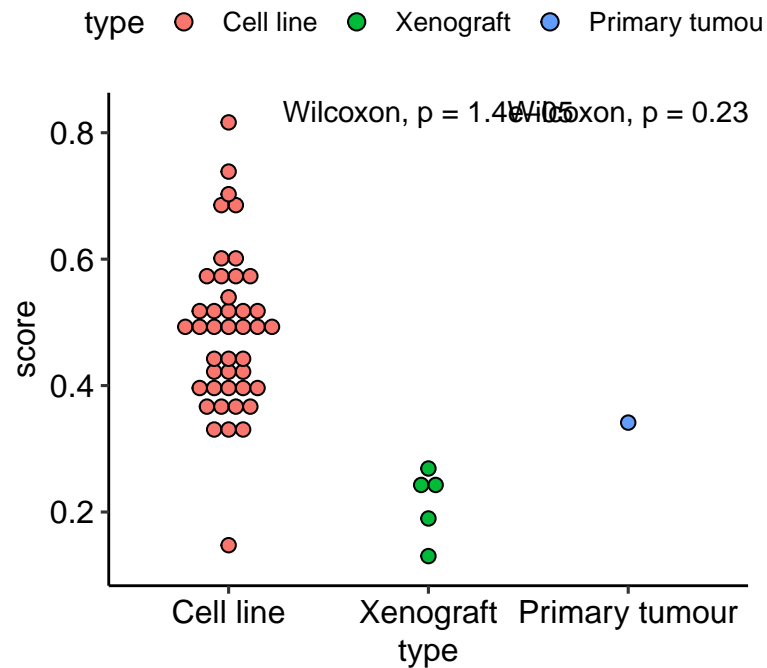
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### CIBERSORT.T.cells.regulatory..Tregs. s



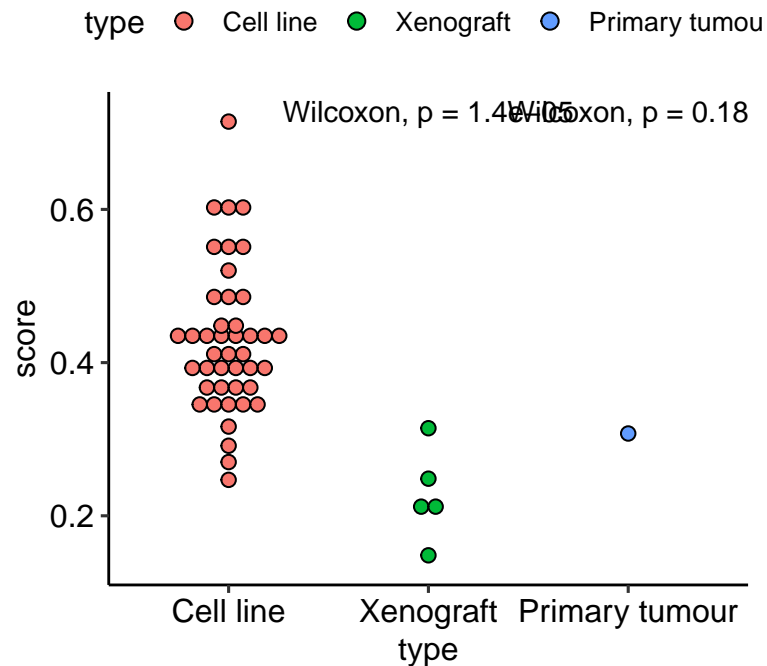
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## CIBERSORT.T.cells.gamma.delta score



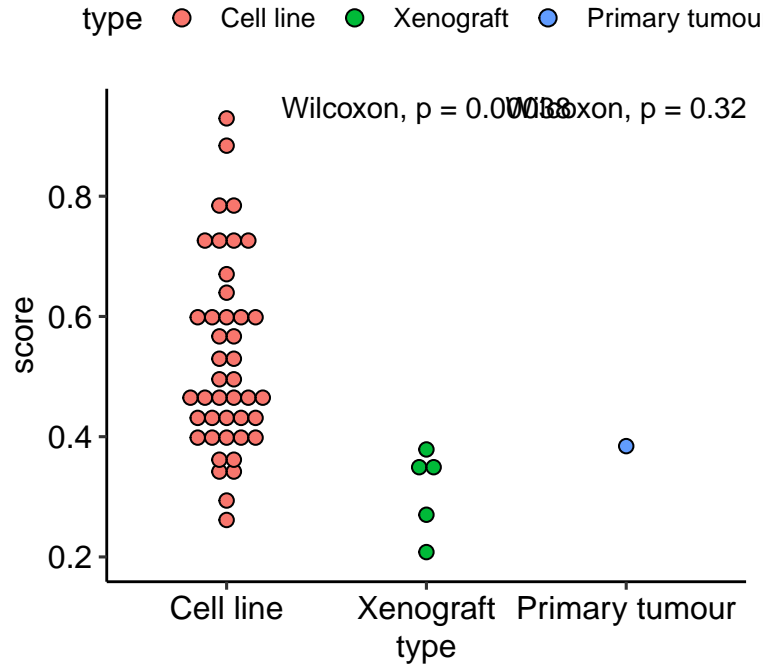
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## CIBERSORT.NK.cells.resting score



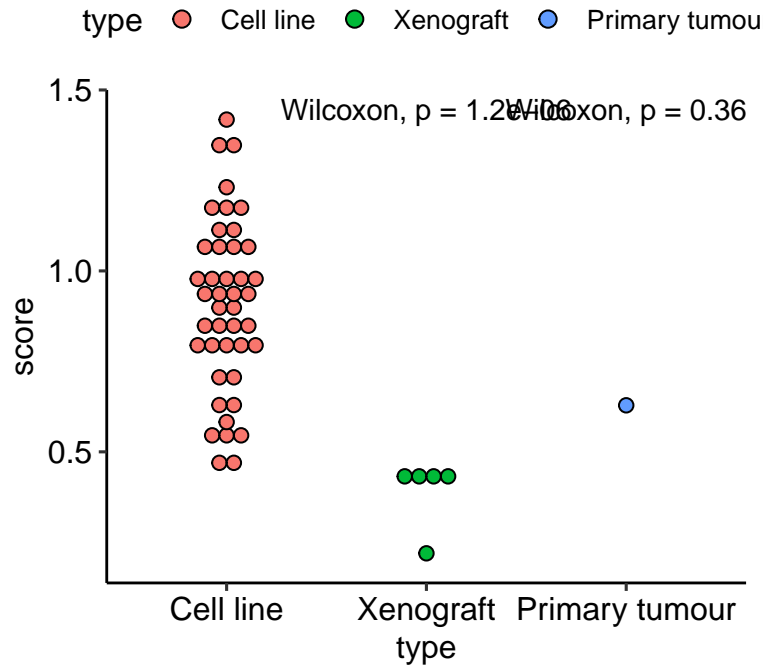
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## CIBERSORT.NK.cells.activated score



```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

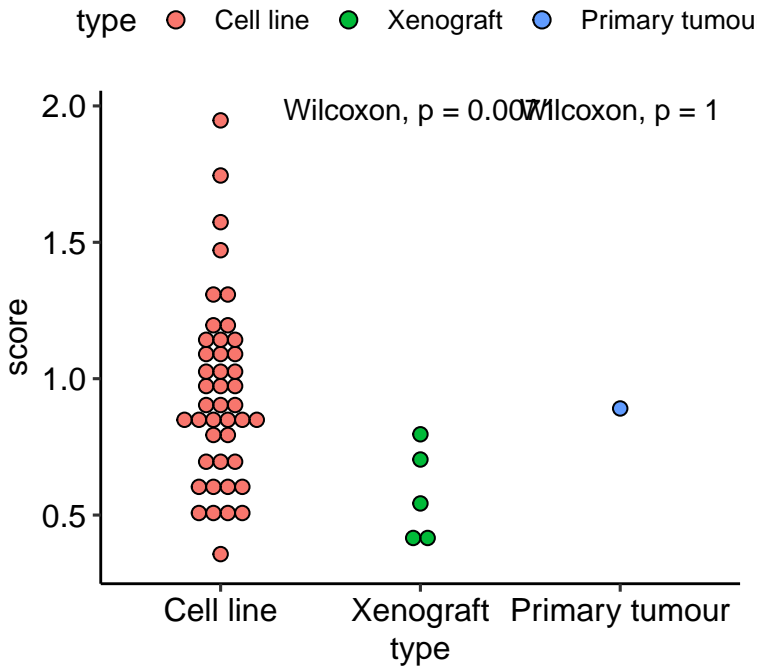
## CIBERSORT.Monocytes score



```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

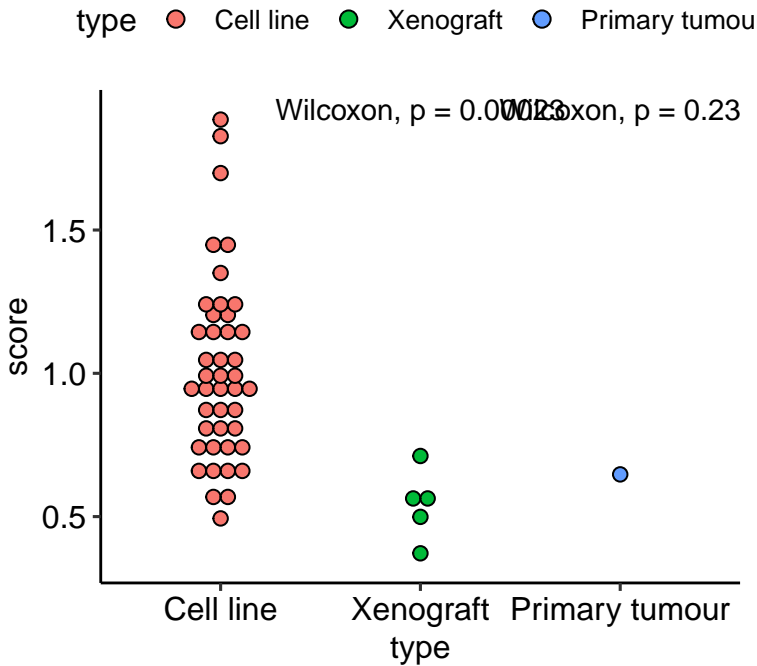


## CIBERSORT.Macrophages.M0 score



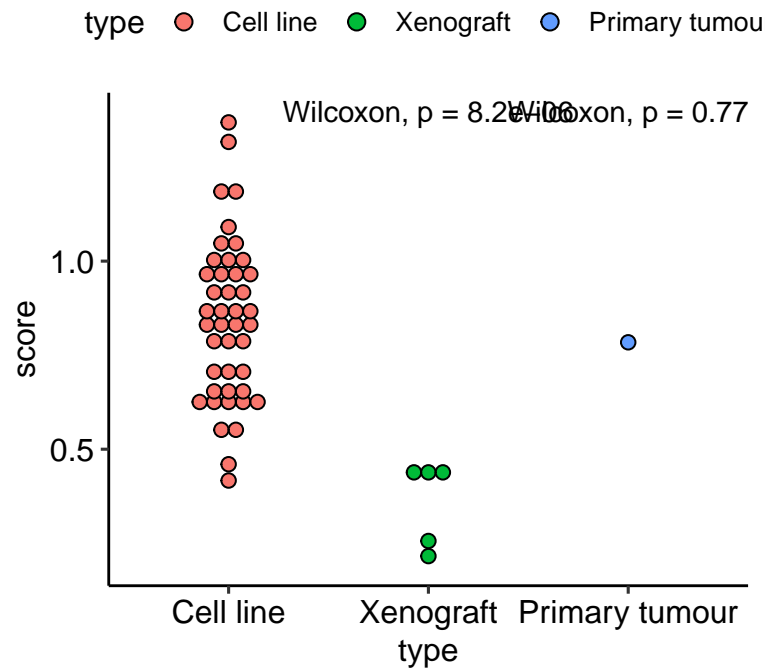
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

## CIBERSORT.Macrophages.M1 score



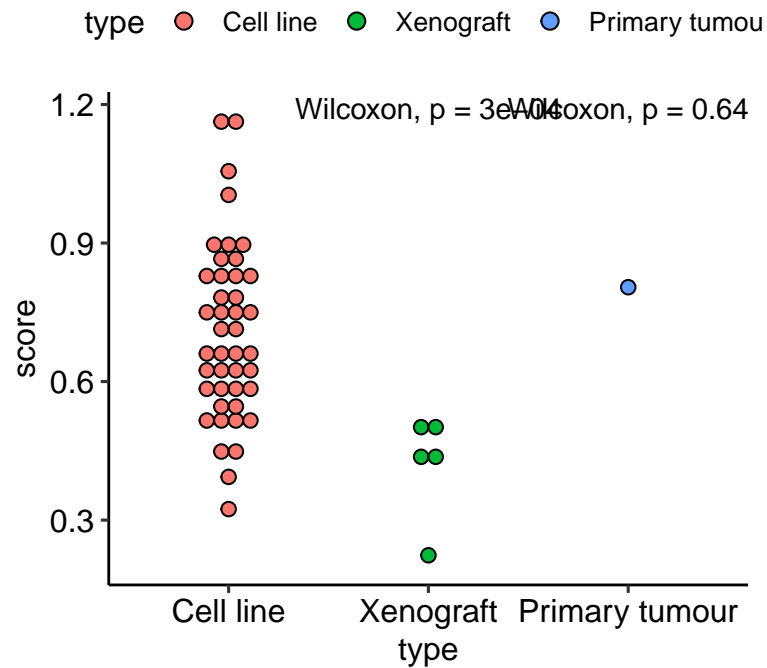
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

## CIBERSORT.Macrophages.M2 score



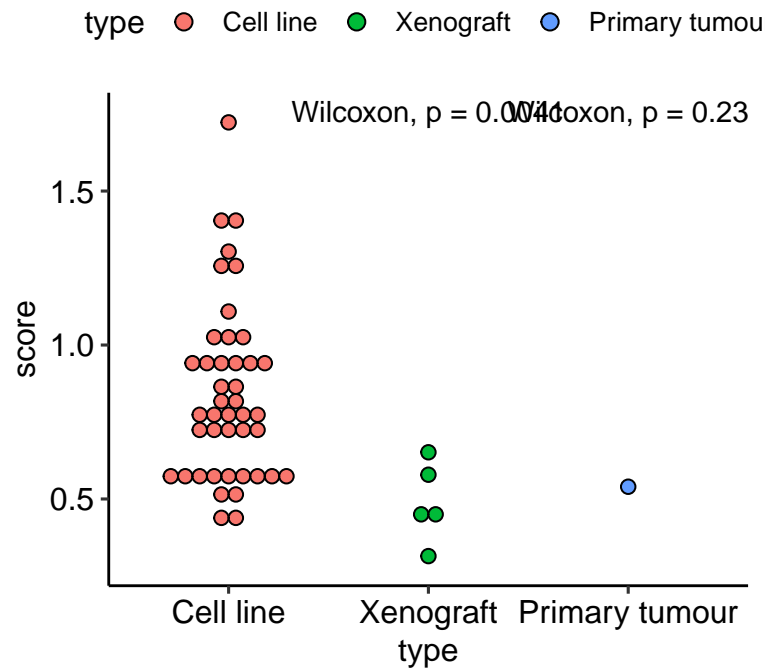
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## CIBERSORT.Dendritic.cells.resting sco



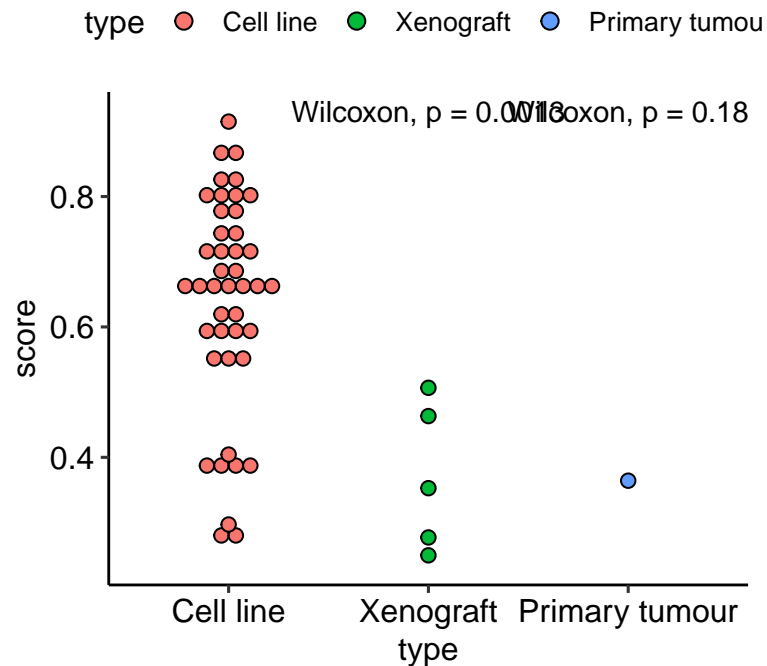
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### CIBERSORT.Dendritic.cells.activated score



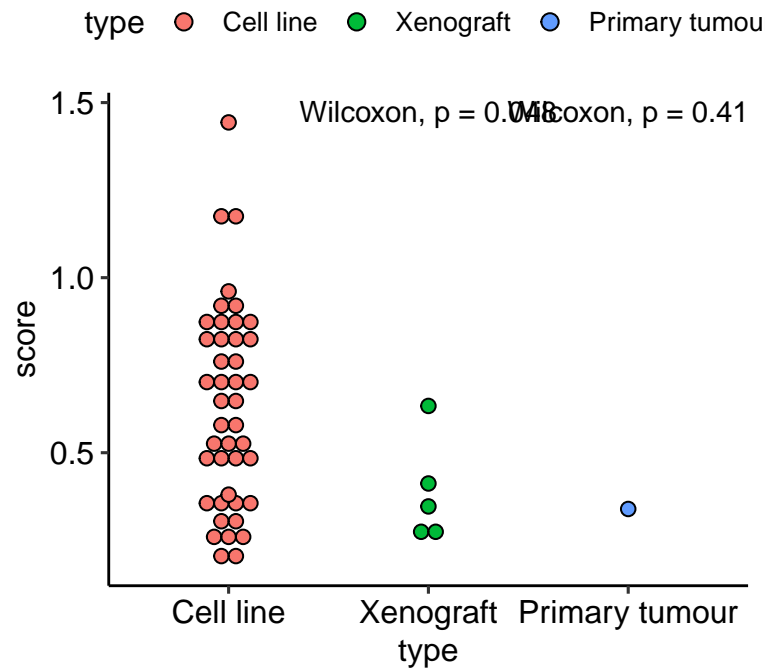
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### CIBERSORT.Mast.cells.resting score



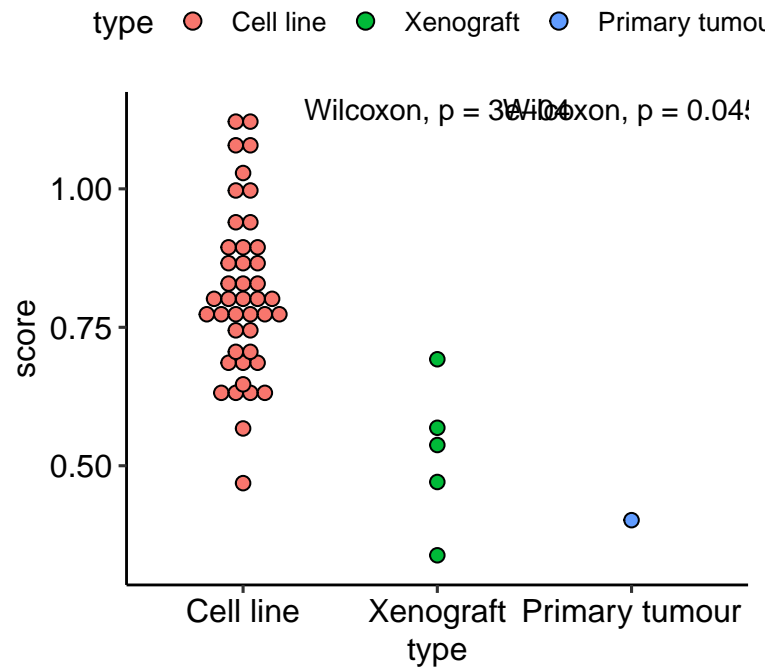
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### CIBERSORT.Mast.cells.activated score



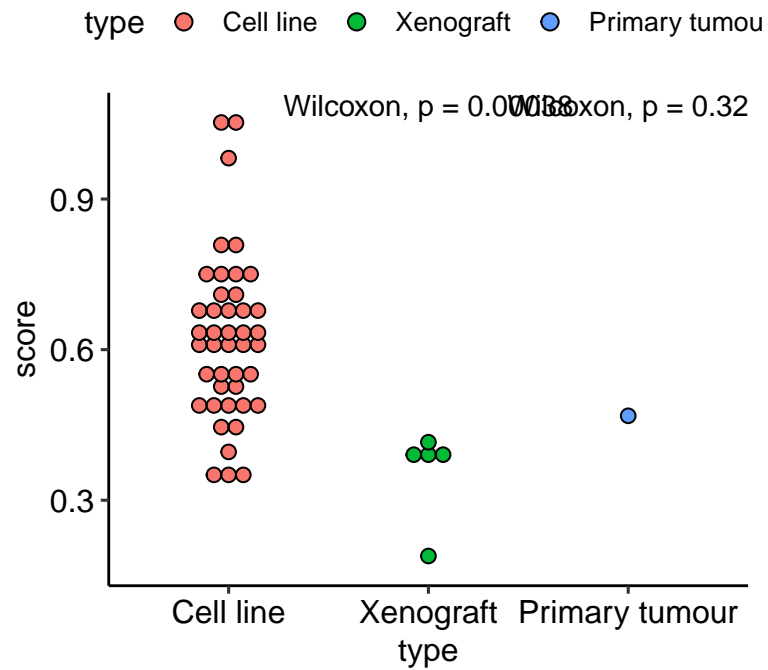
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

### CIBERSORT.Eosinophils score



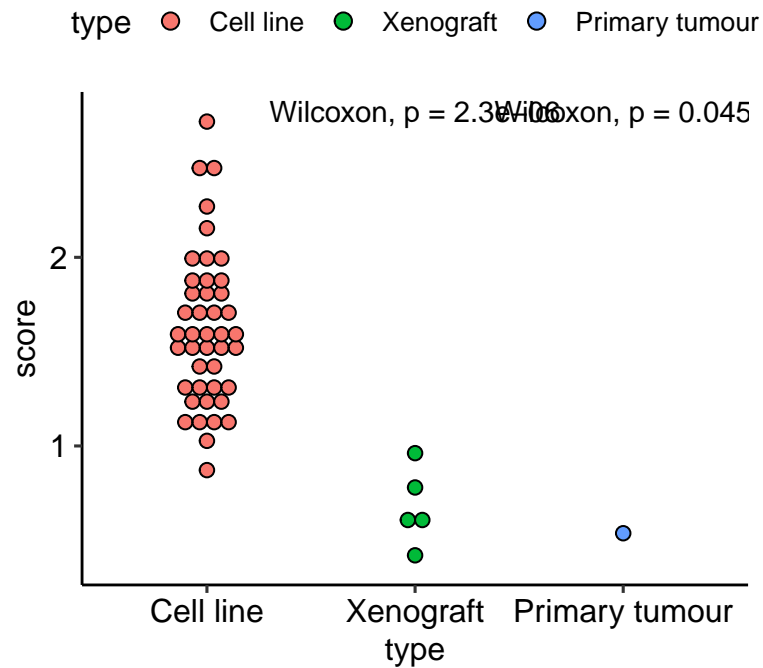
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## CIBERSORT.Neutrophils score



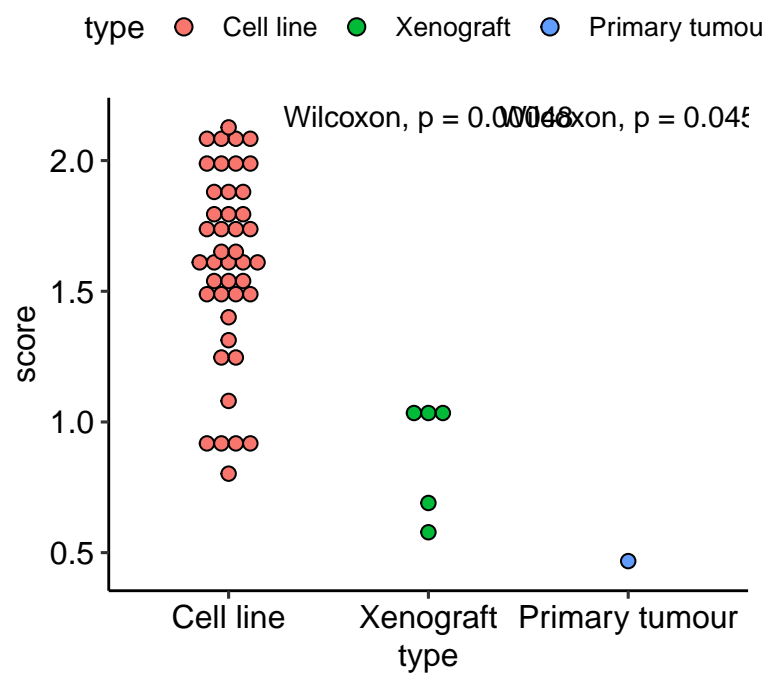
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Notta.BasalA score



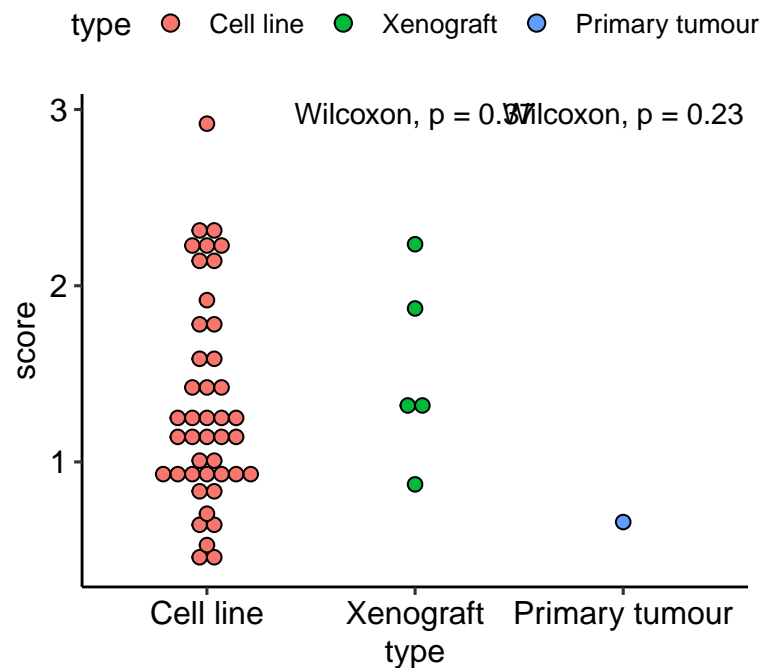
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Notta.BasalB score



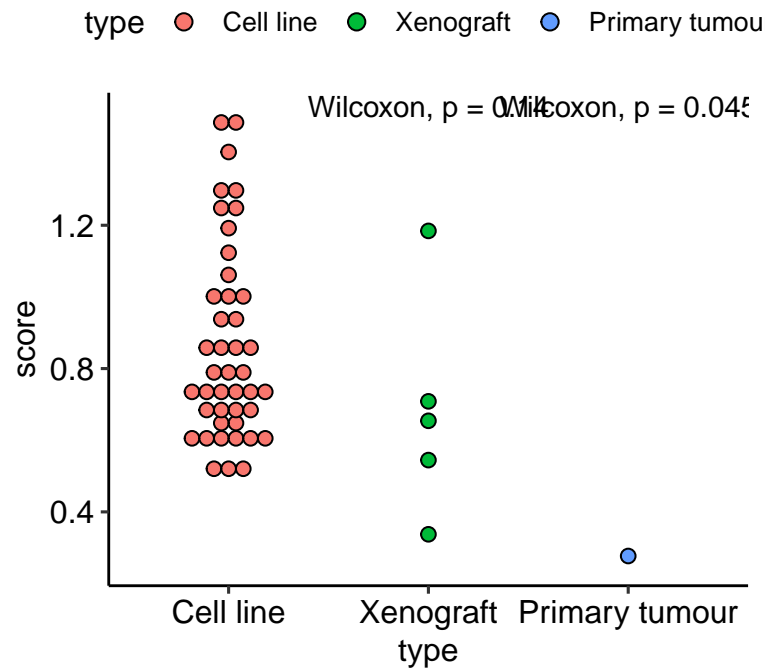
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Notta.ClassicalA score



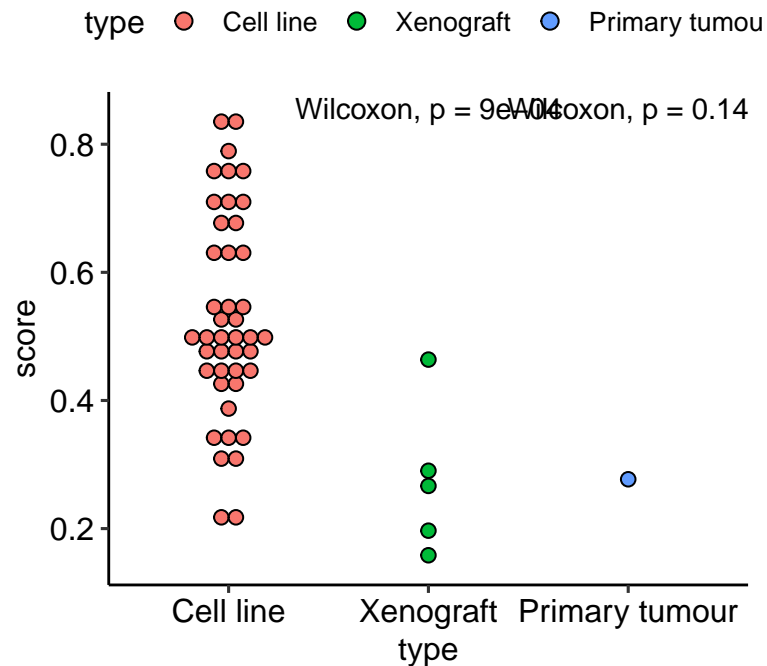
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Notta.ClassicalB score



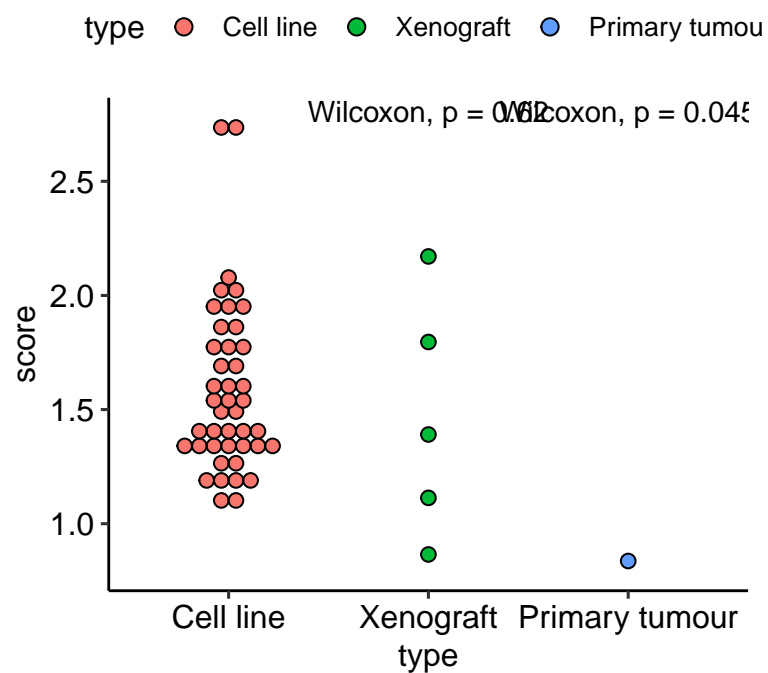
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## ADEX\_unique score



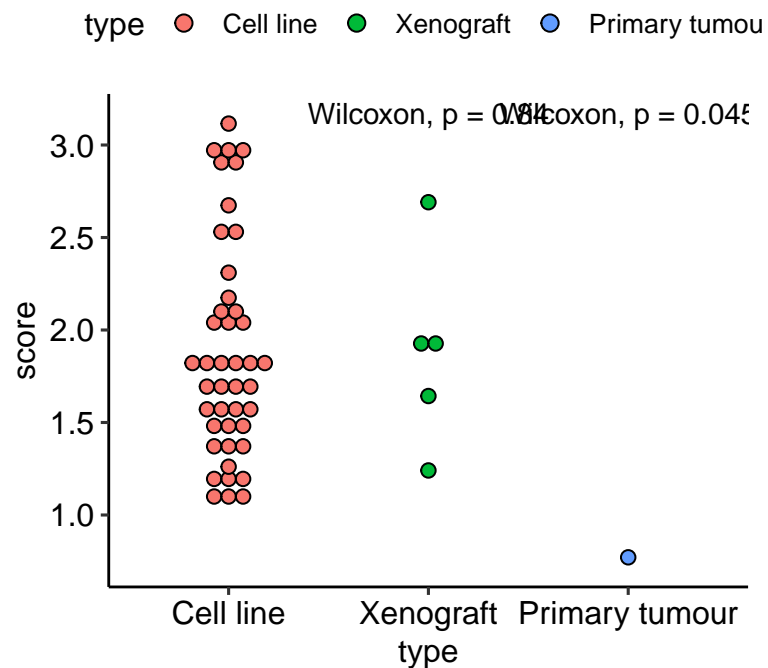
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

## Immunogenic\_unique score



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

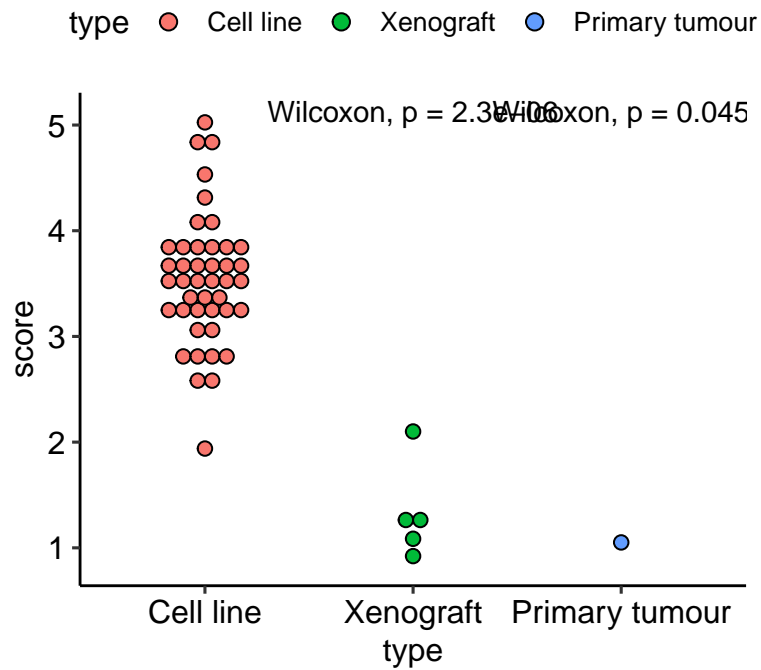
## Progenitor\_unique score



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.

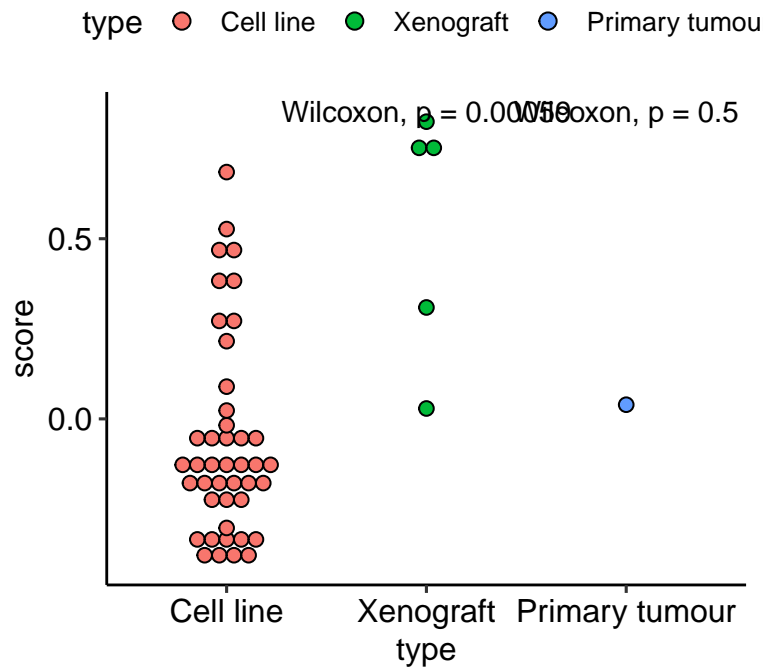


Squamous\_unique score

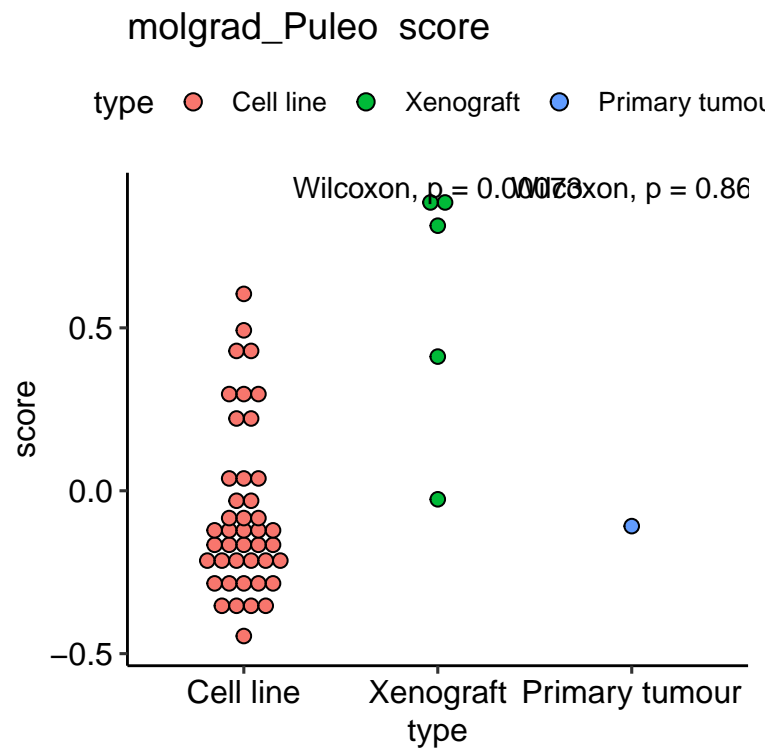


```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```

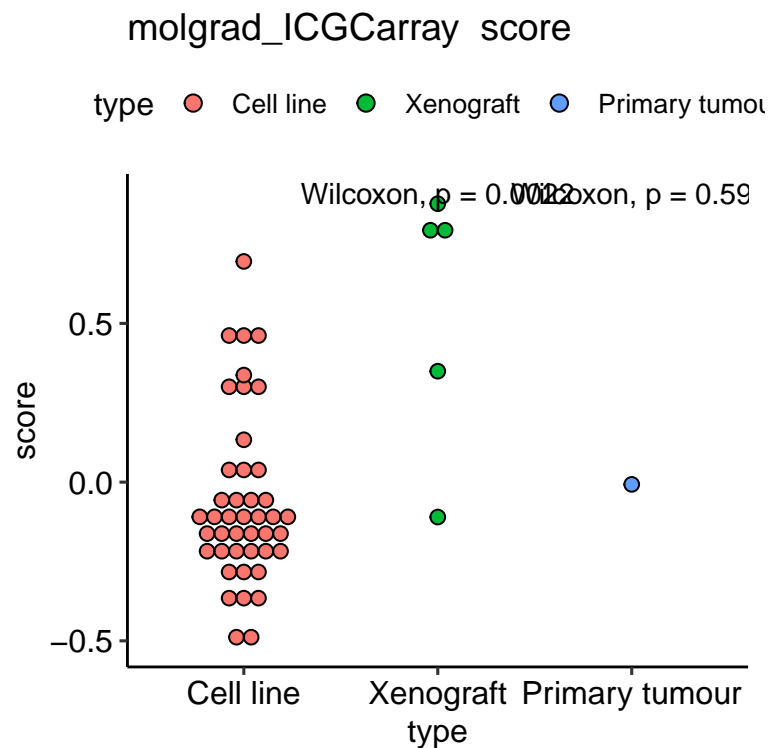
## molgrad\_PDX score



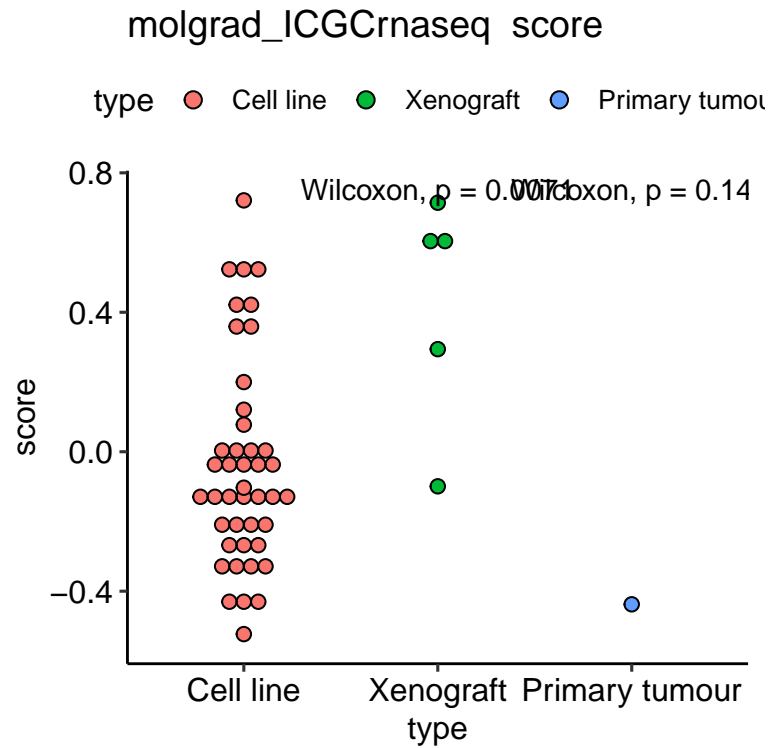
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.
```



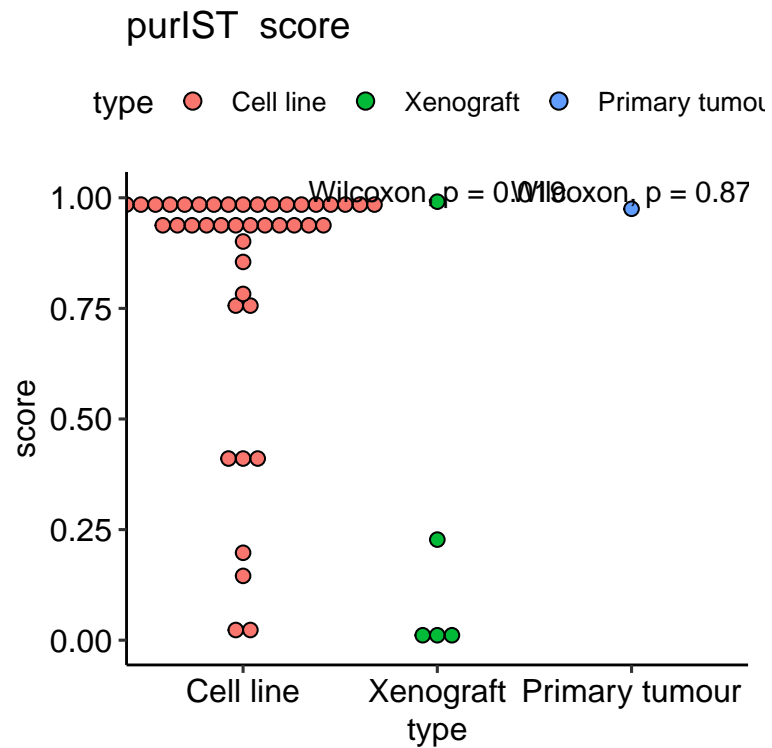
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.



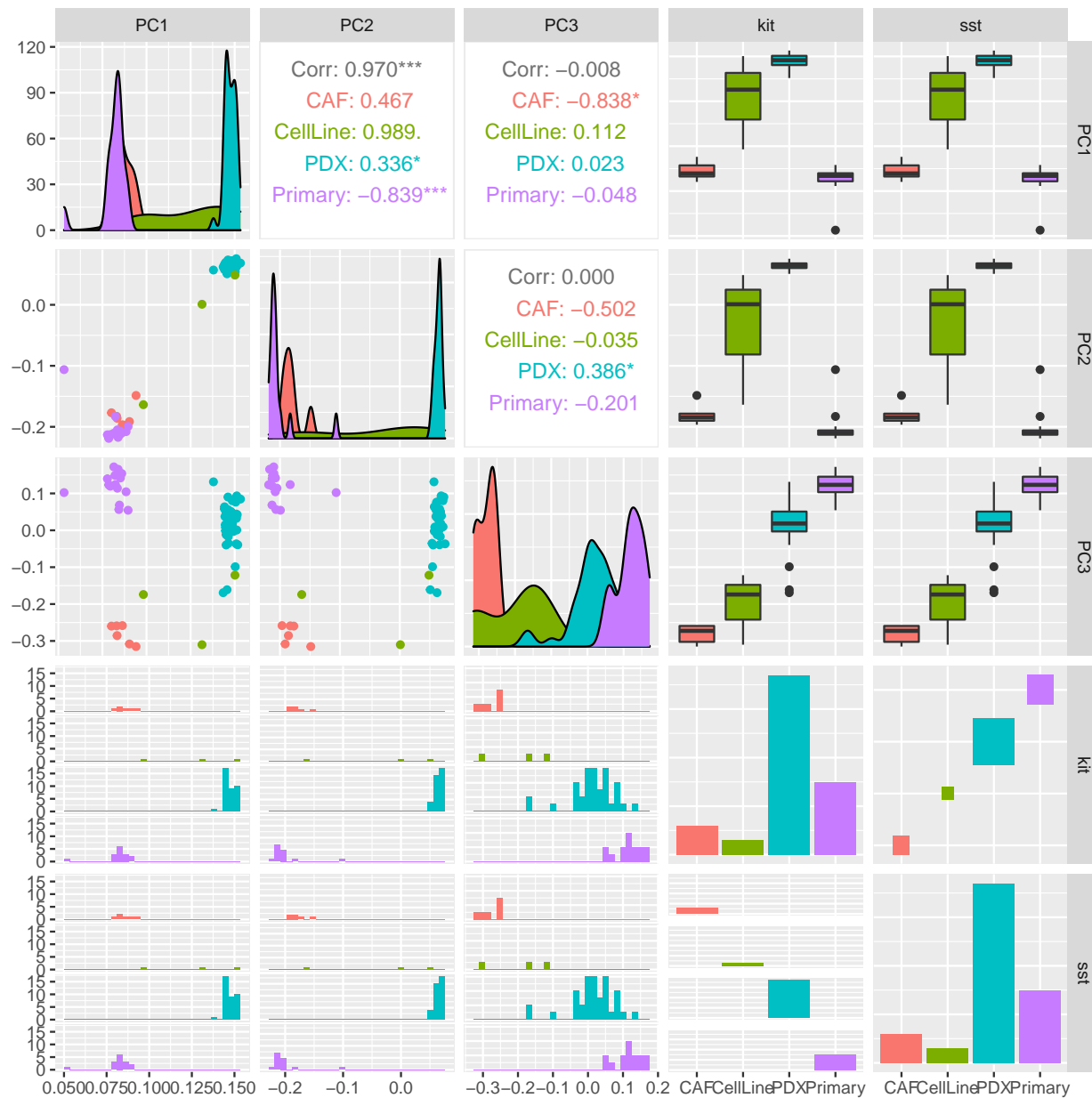
## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.



## Bin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'.



## Generate PCA plots

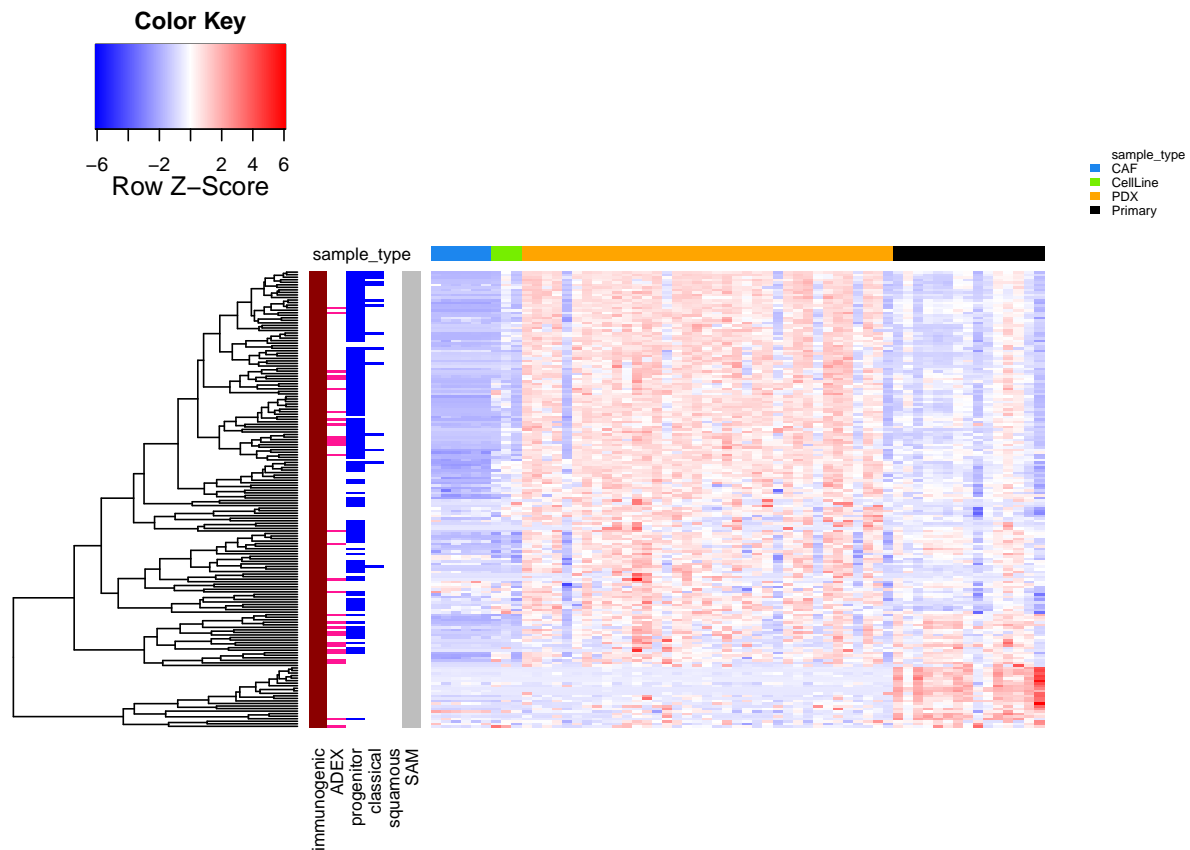


### Calculate signature scores and SSC

## Append TSP scores to expression data frames

## Results

## Heat maps

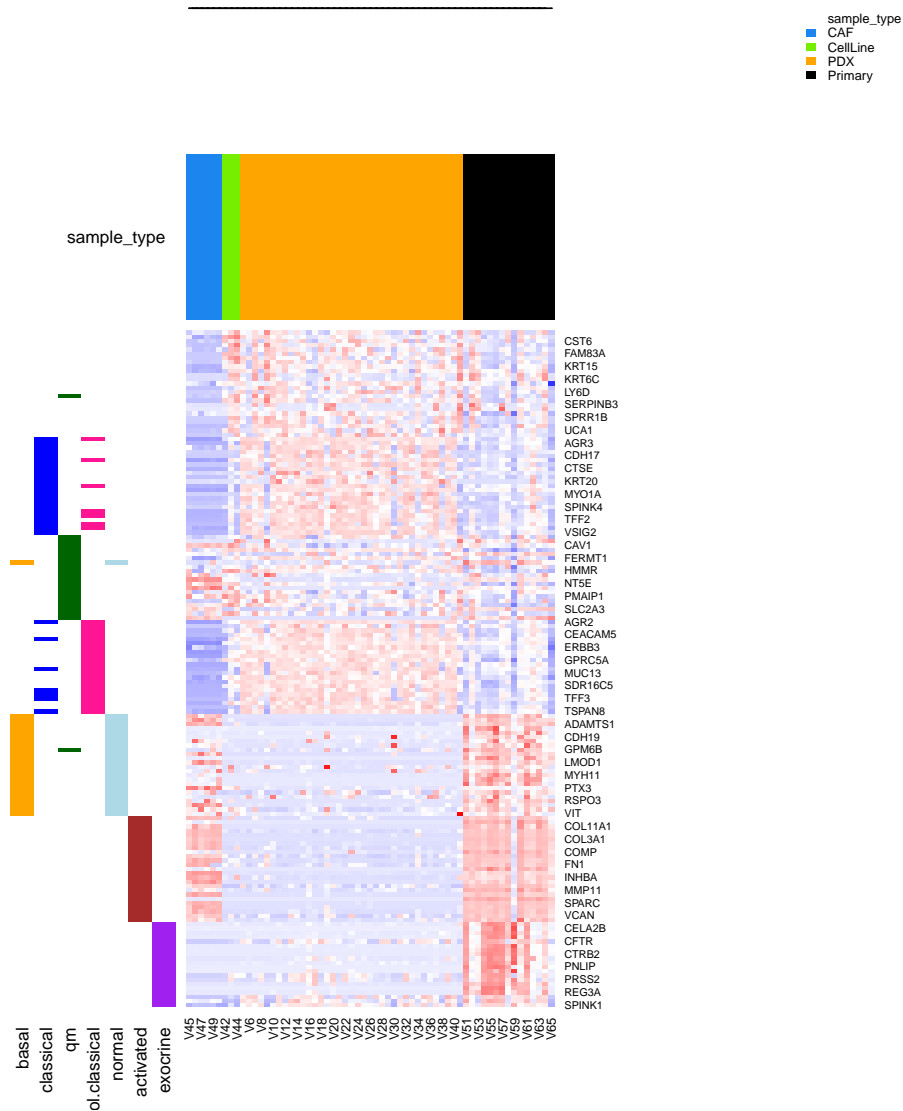
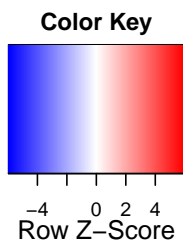


```
## [1] "% of progenitor overlap with immunogenic"
```

```
## [1] 0.2592593
```

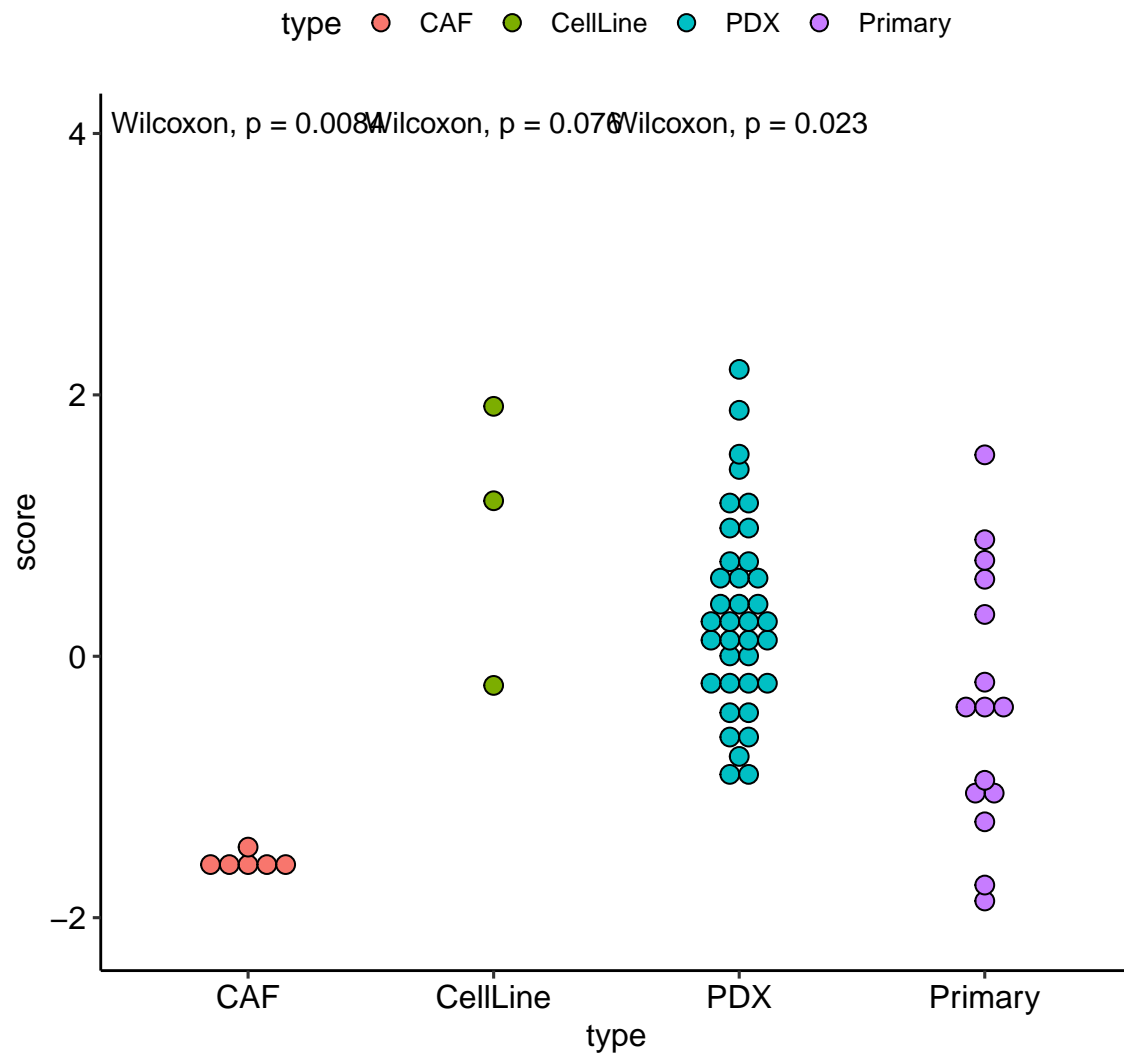
```
## [1] "% of ADEX overlap with immunogenic"
```

```
## [1] 0.09064327
```

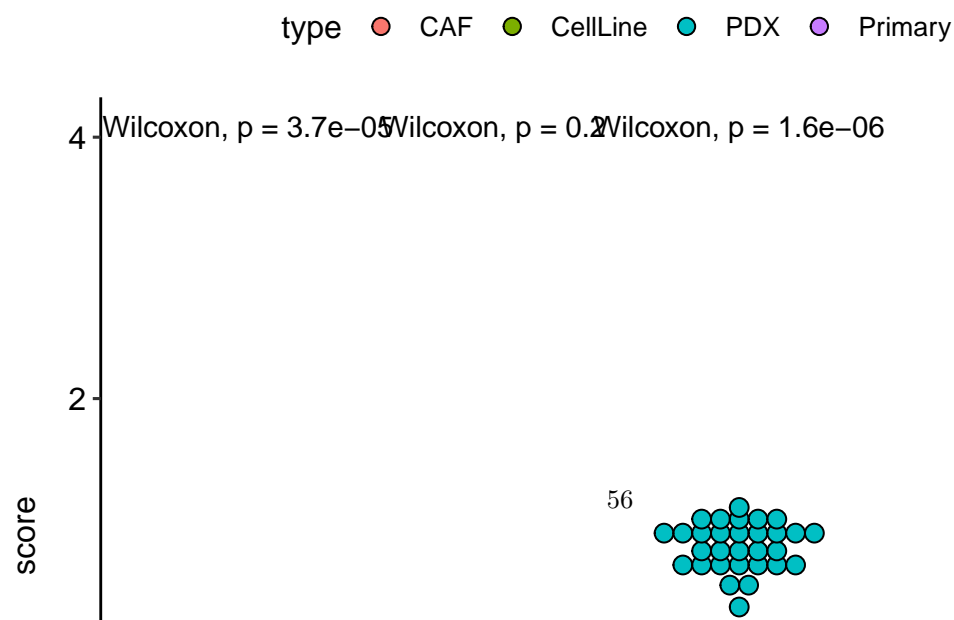


### Boxplots to show gene expression in the above heatmap

## Moffitt.Basal.25 score

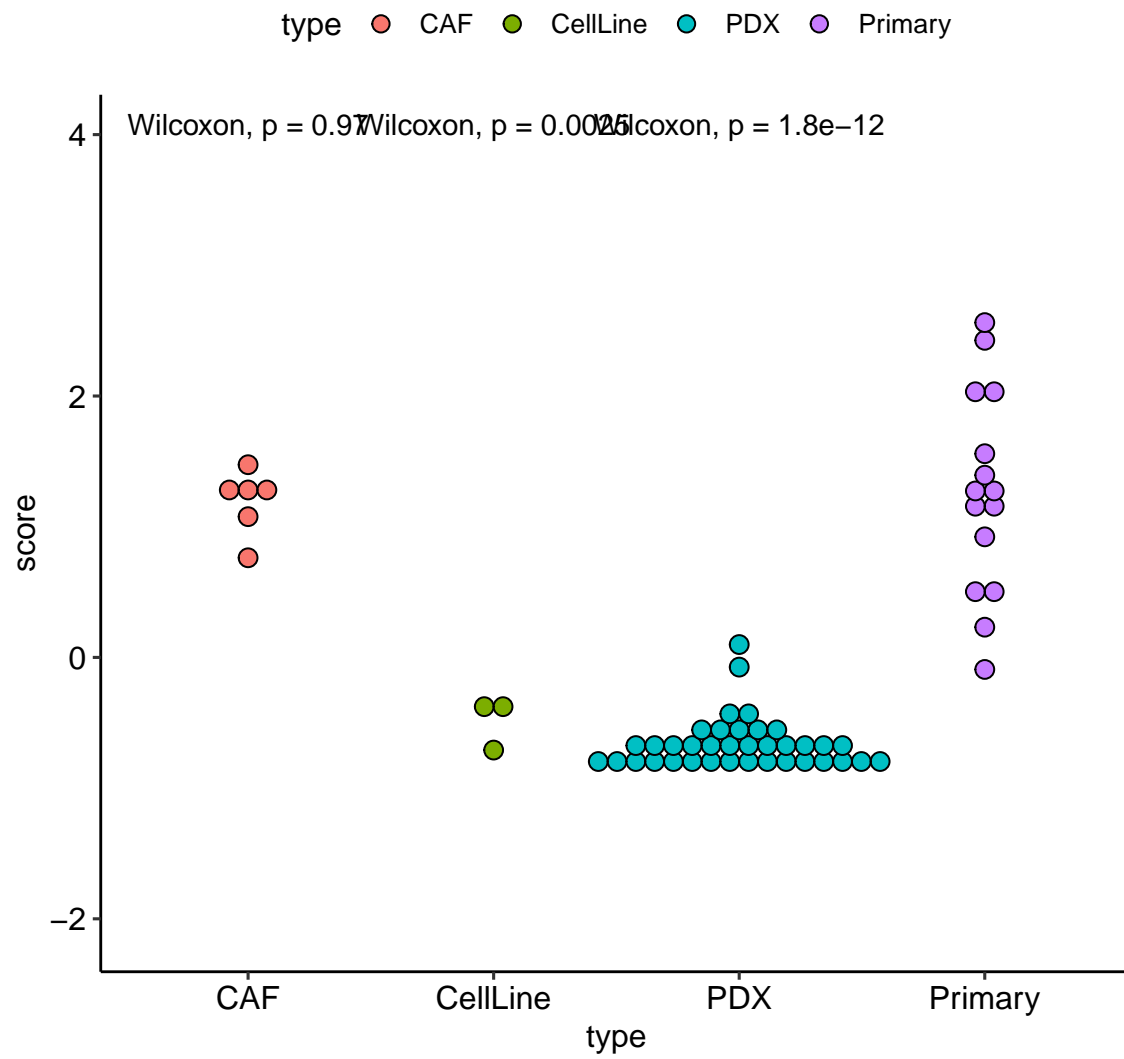


## Moffitt.Classical.25 score

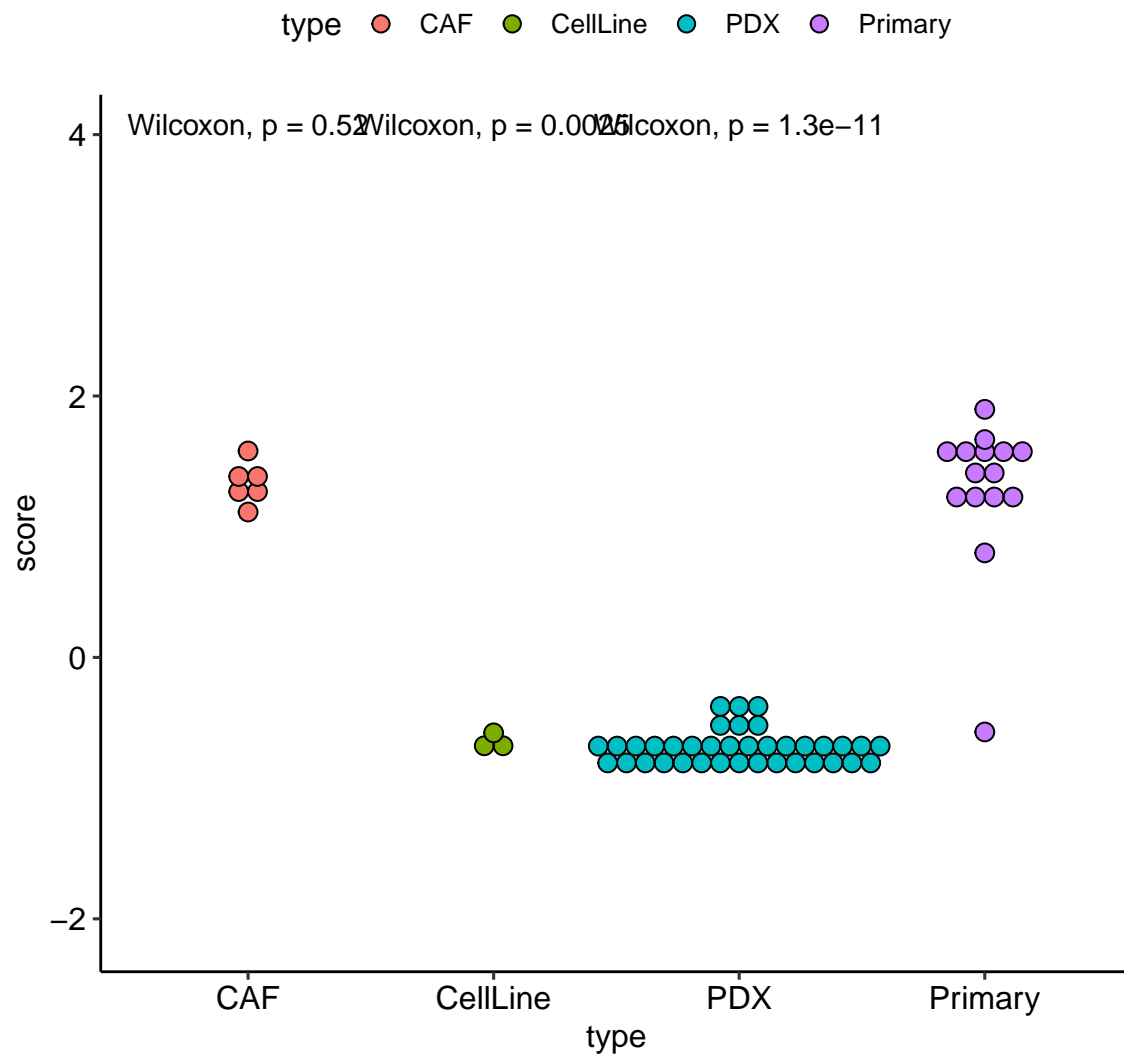




## Moffitt.Normal.25 score



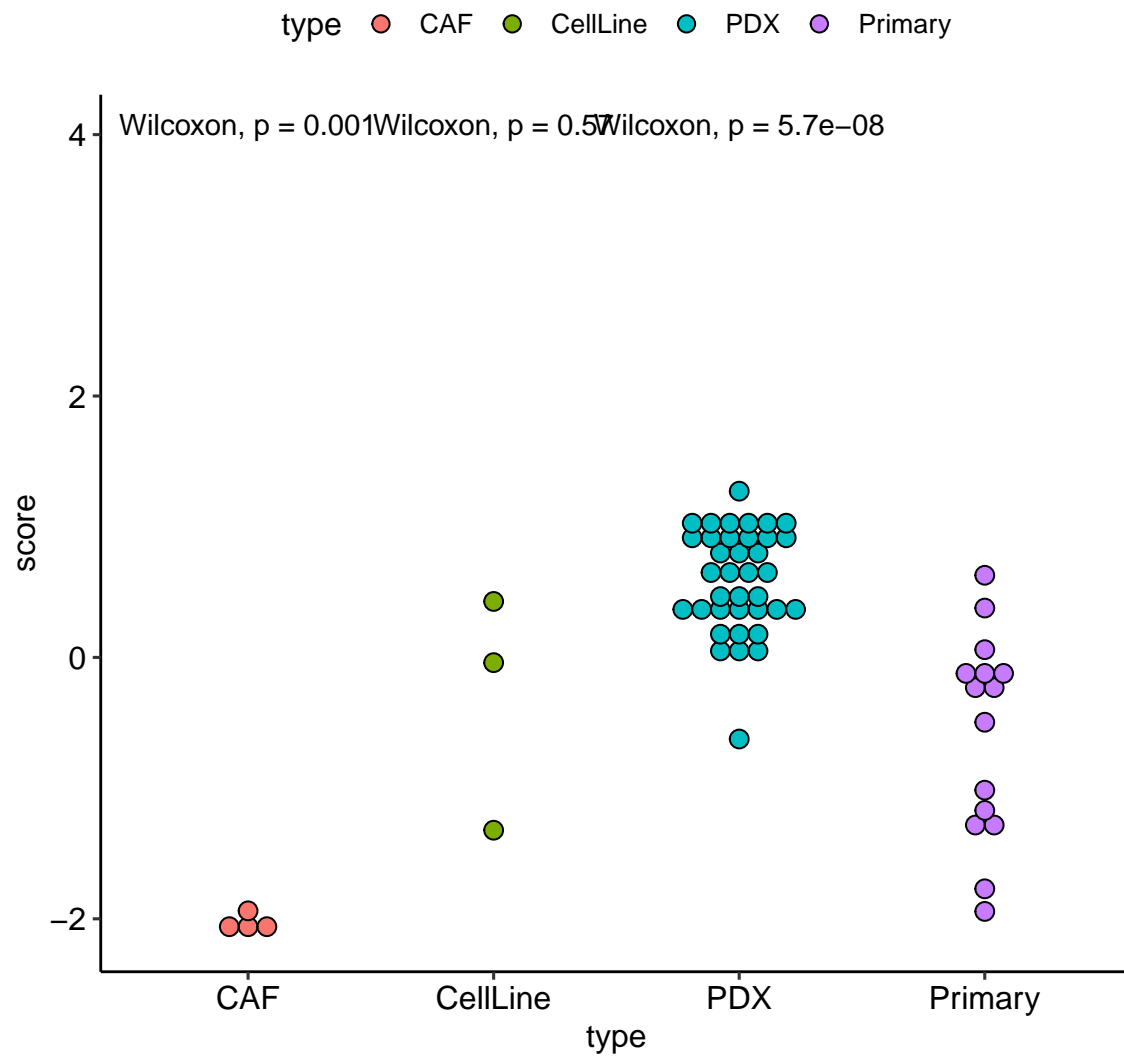
## Moffitt.Activated.25 score



## Warning: Removed 2 rows containing non-finite values (stat\_bindot).

## Warning: Removed 2 rows containing non-finite values (stat\_compare\_means).

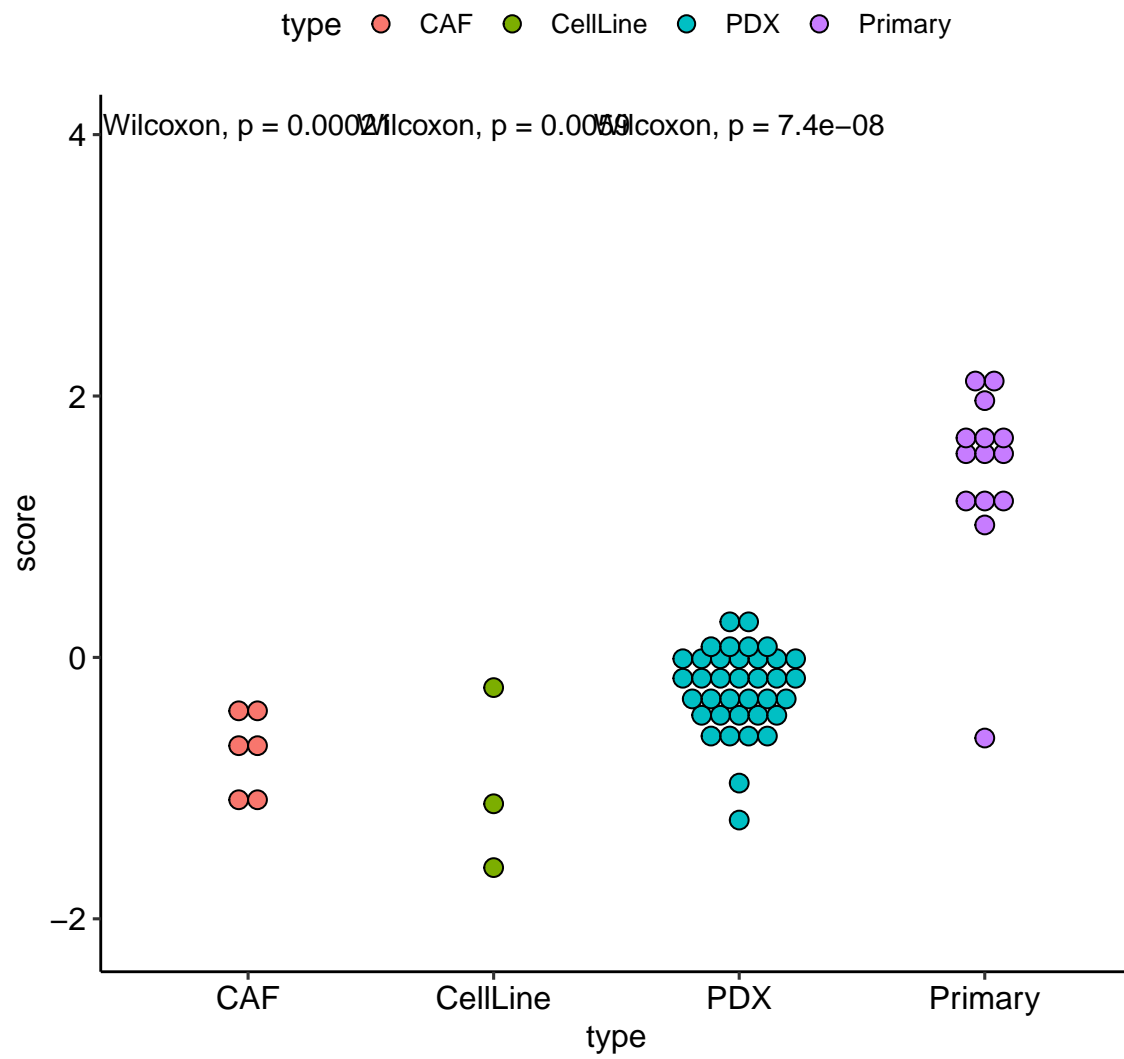
## Moffitt.Tumor score



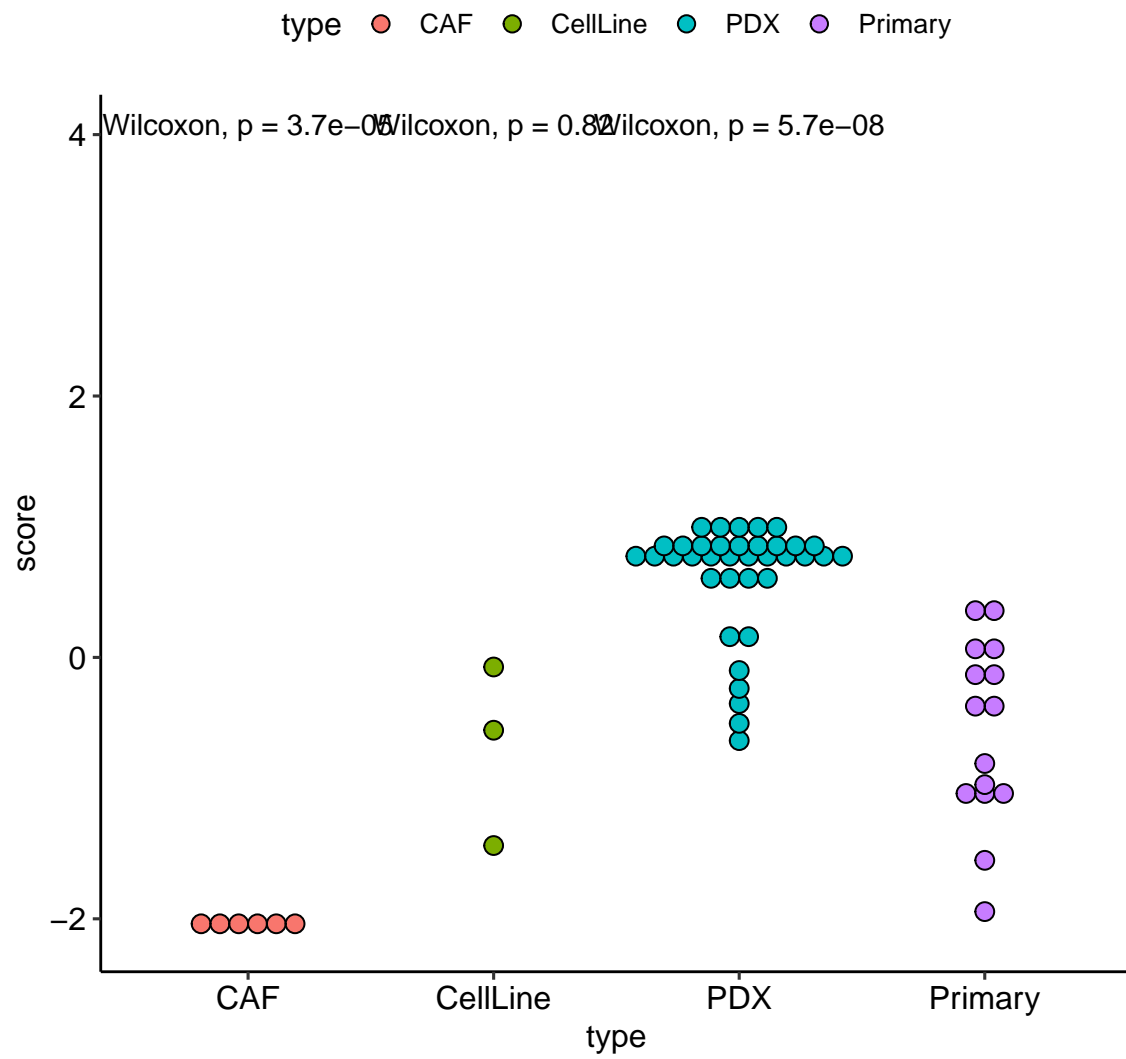
## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

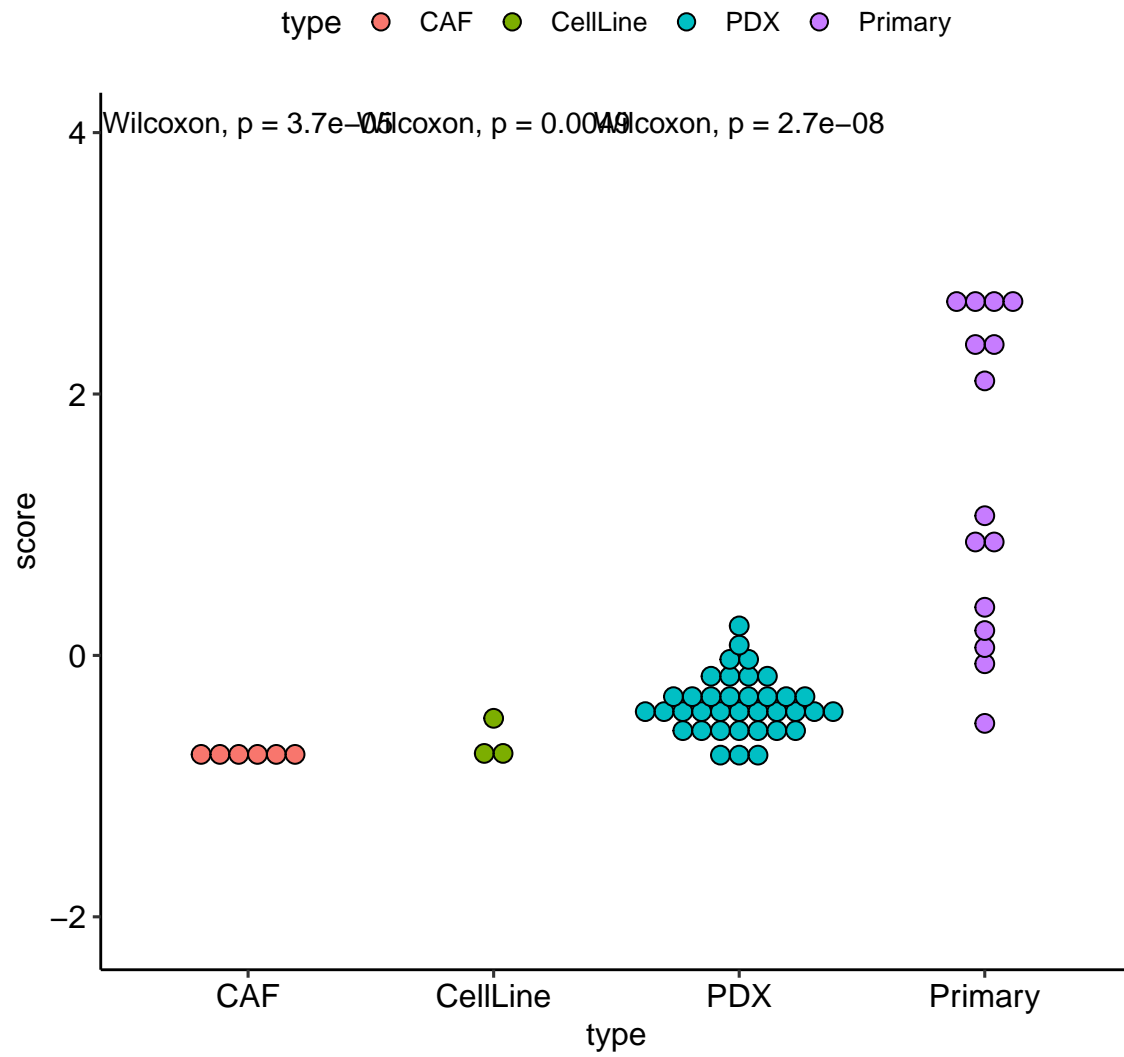
## Puleo.Centroids score



## Collisson.Classical score



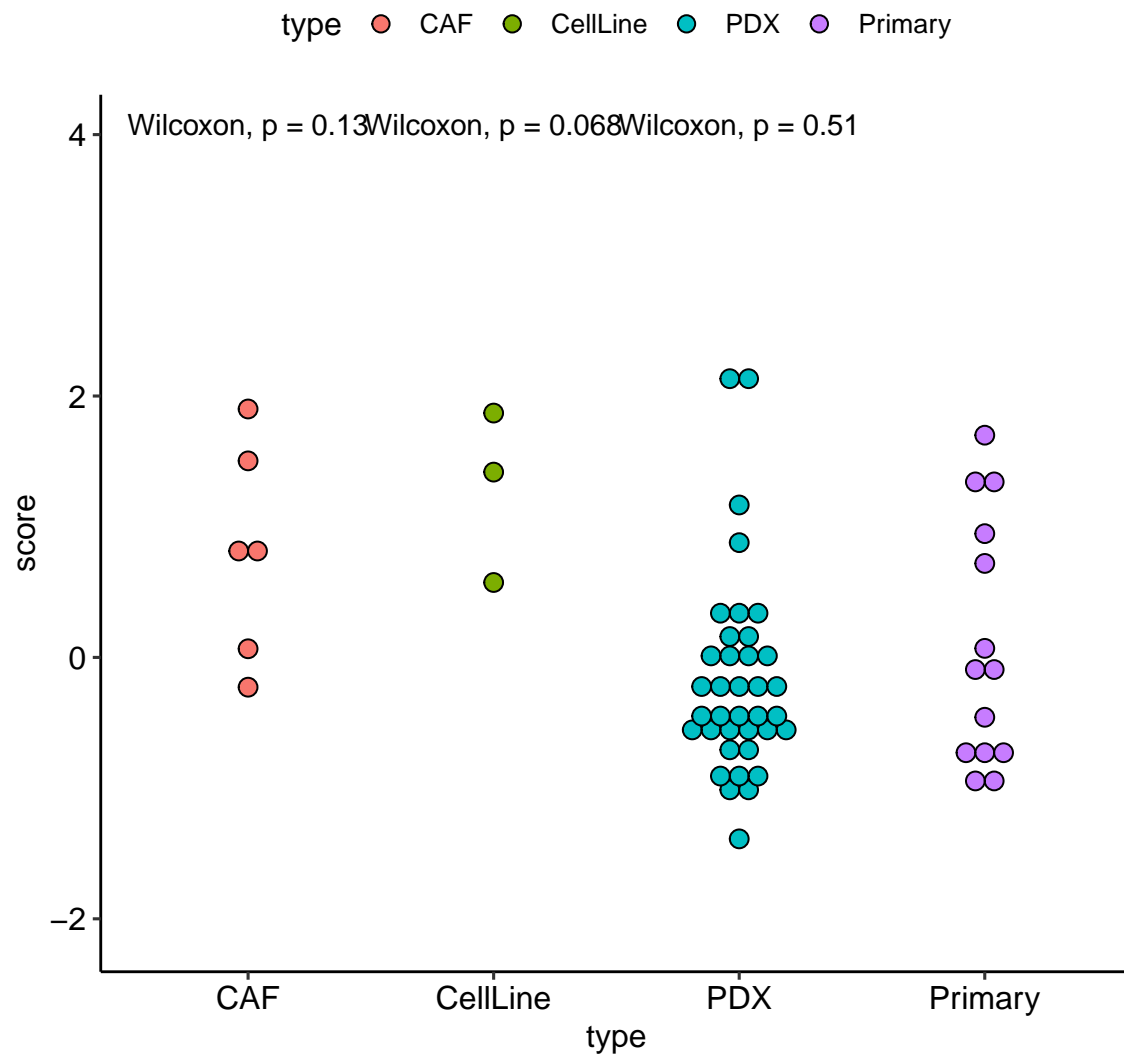
## Collisson.Exocrine score



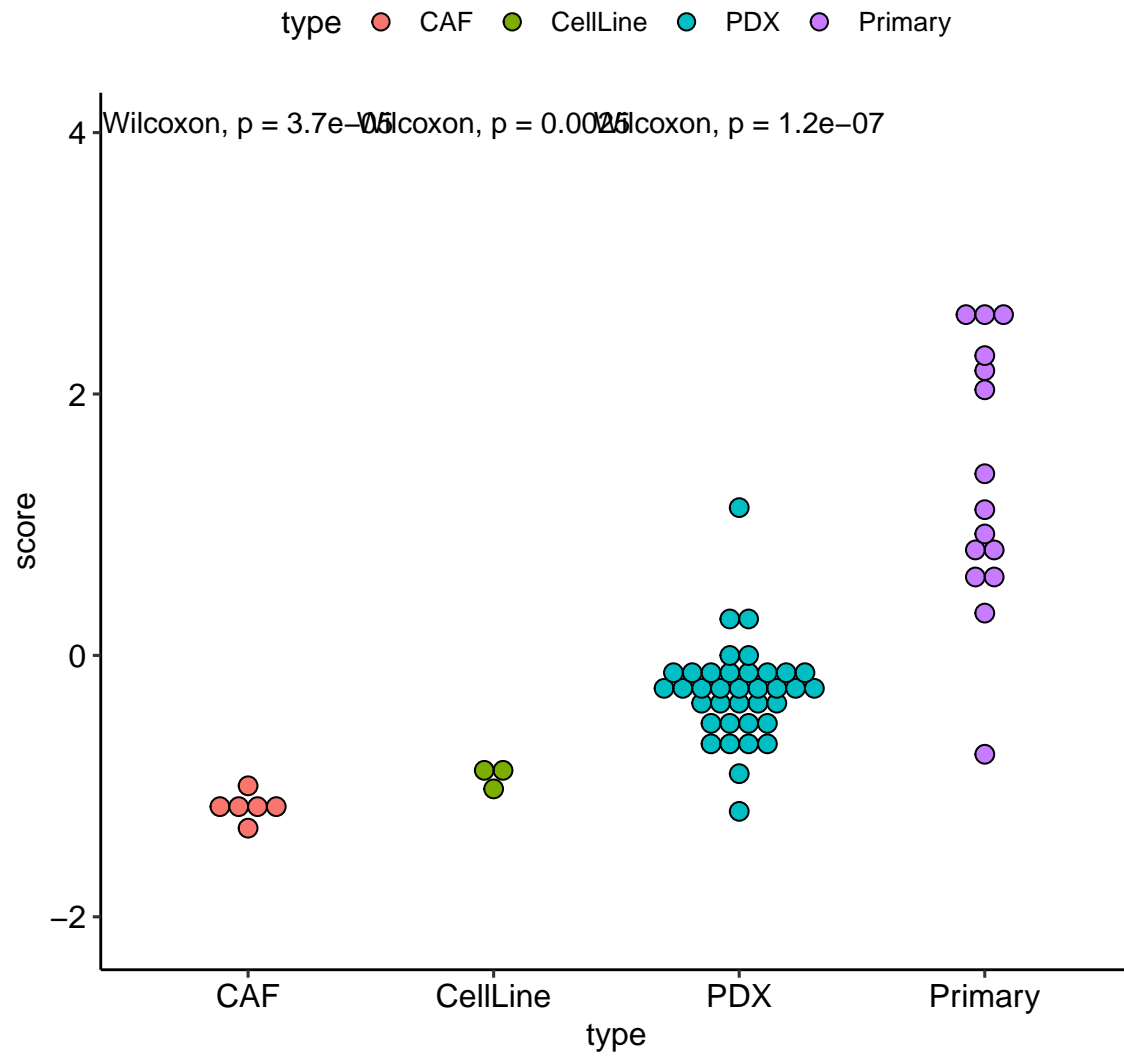
## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

## Collisson.QM score



## ICGC.ADEX.Up score

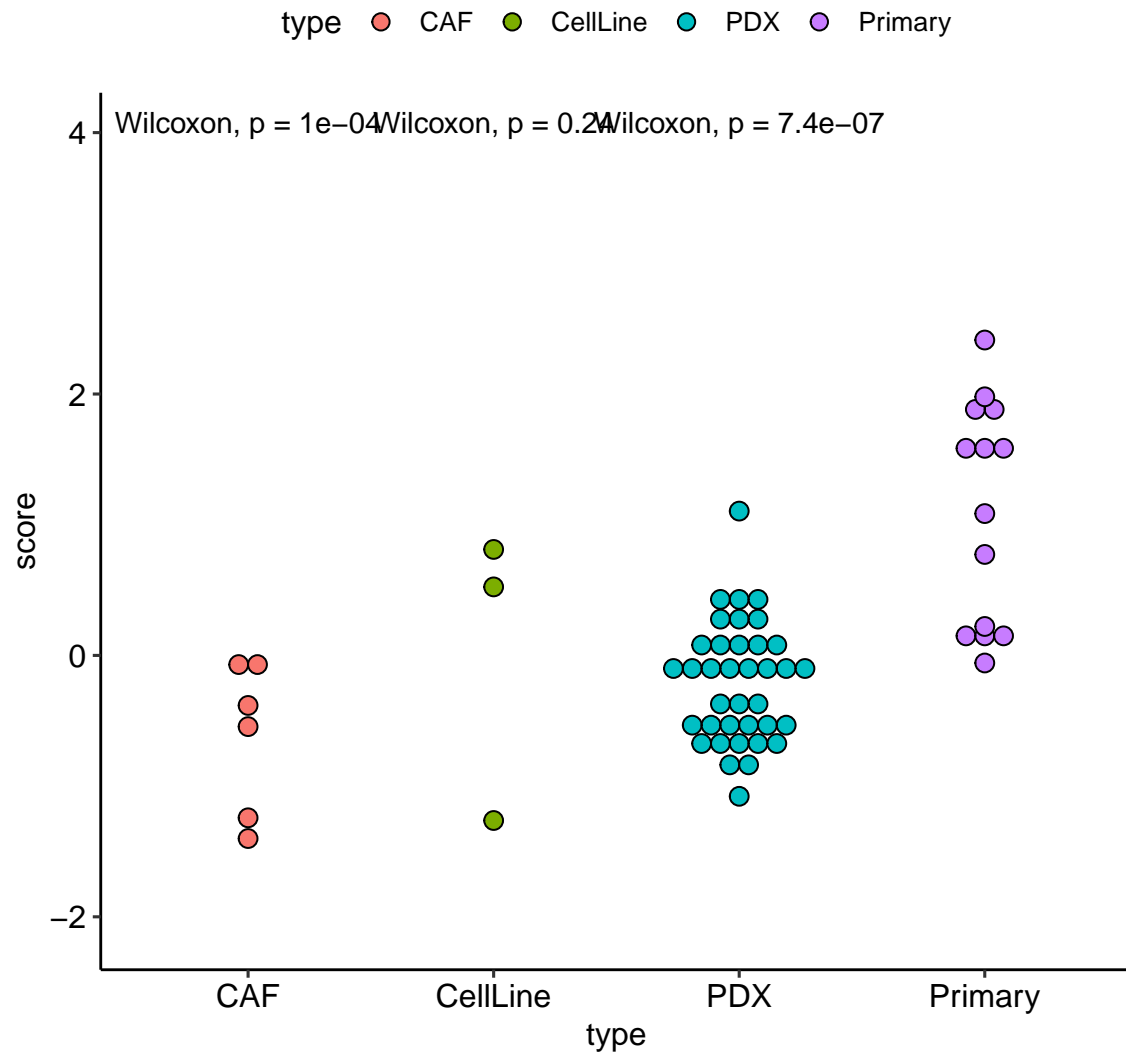


## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

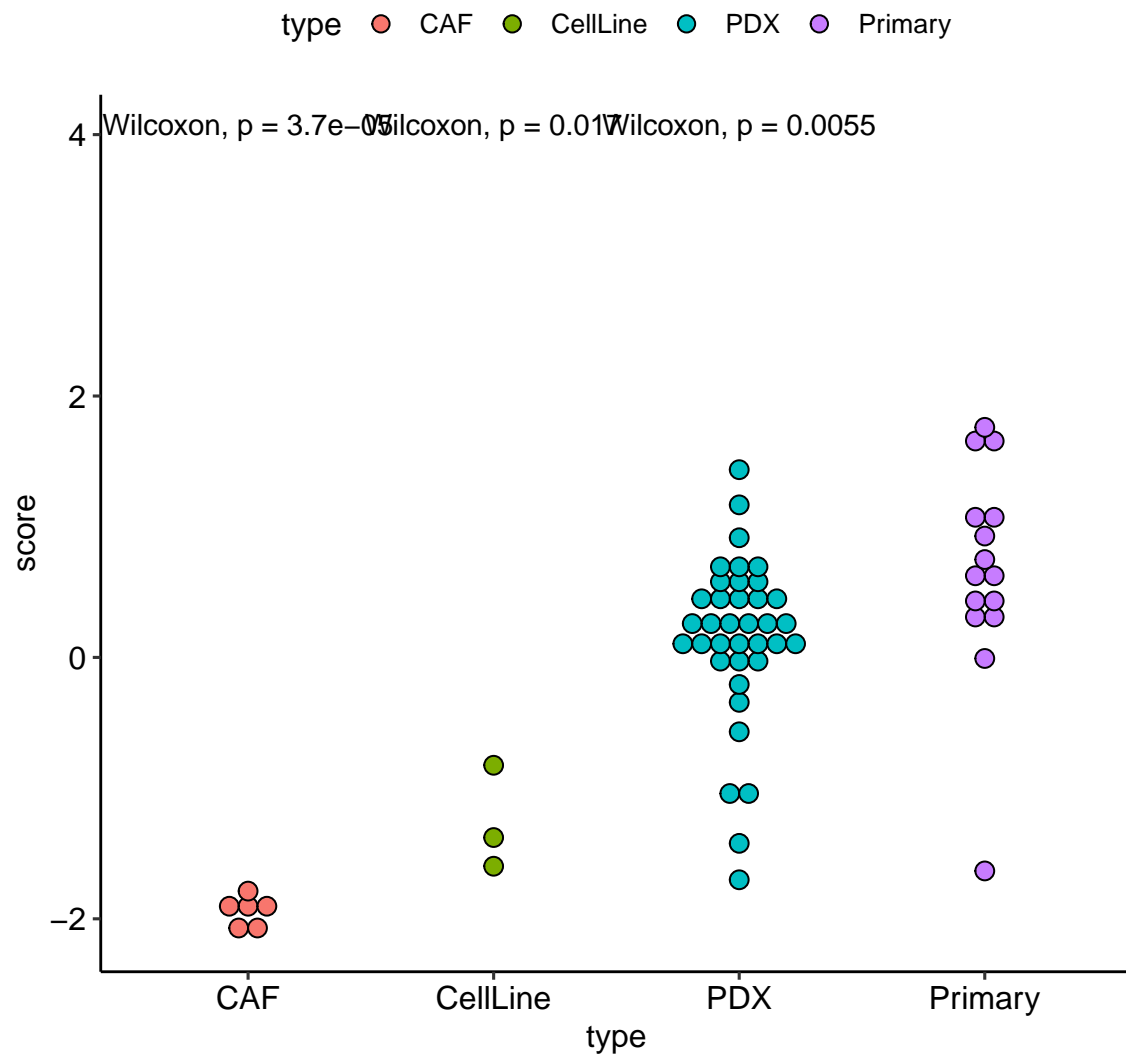
## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).



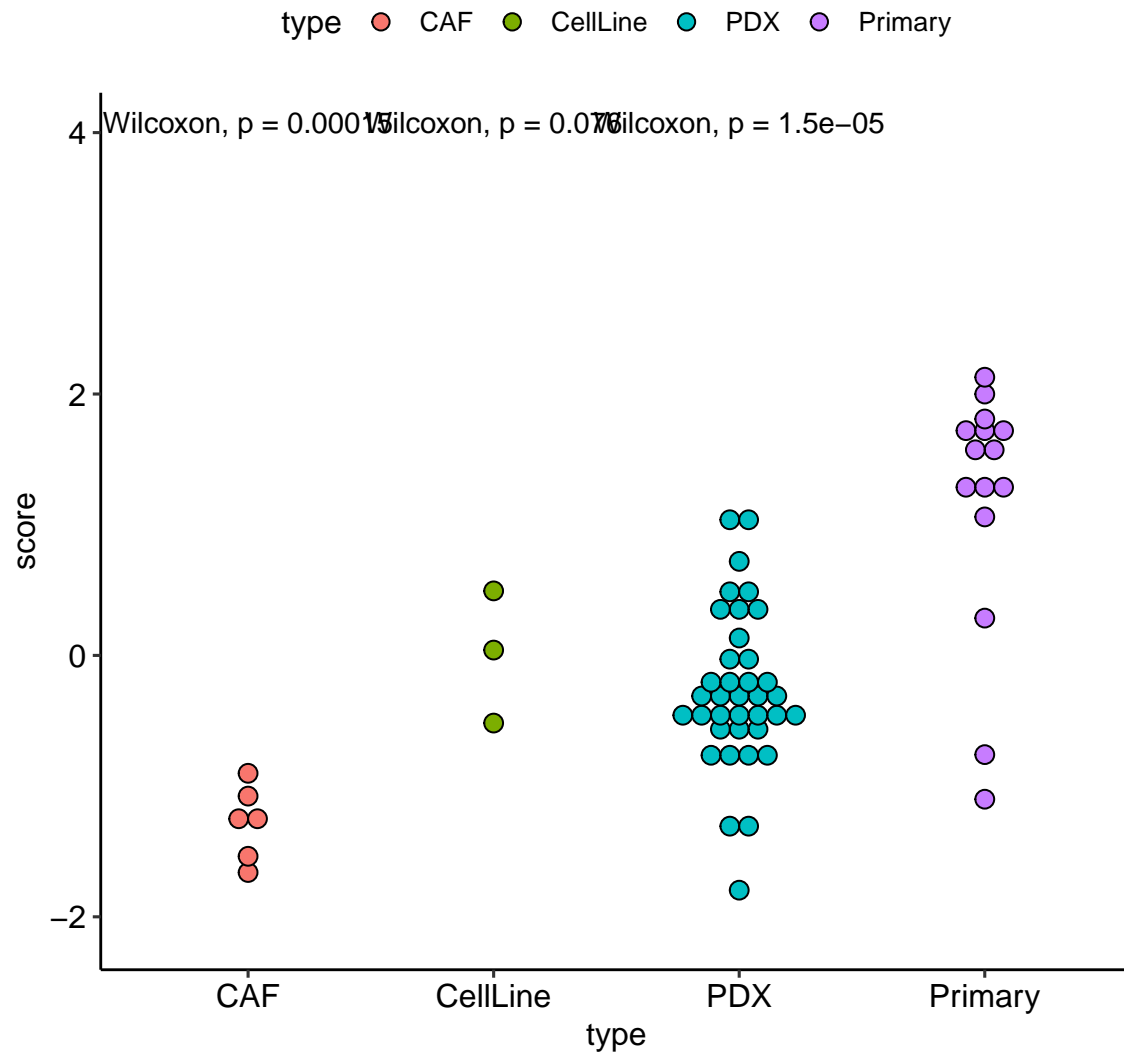
# ICGC.ADEX.Down score



# ICGC.Immunogenic.Up score



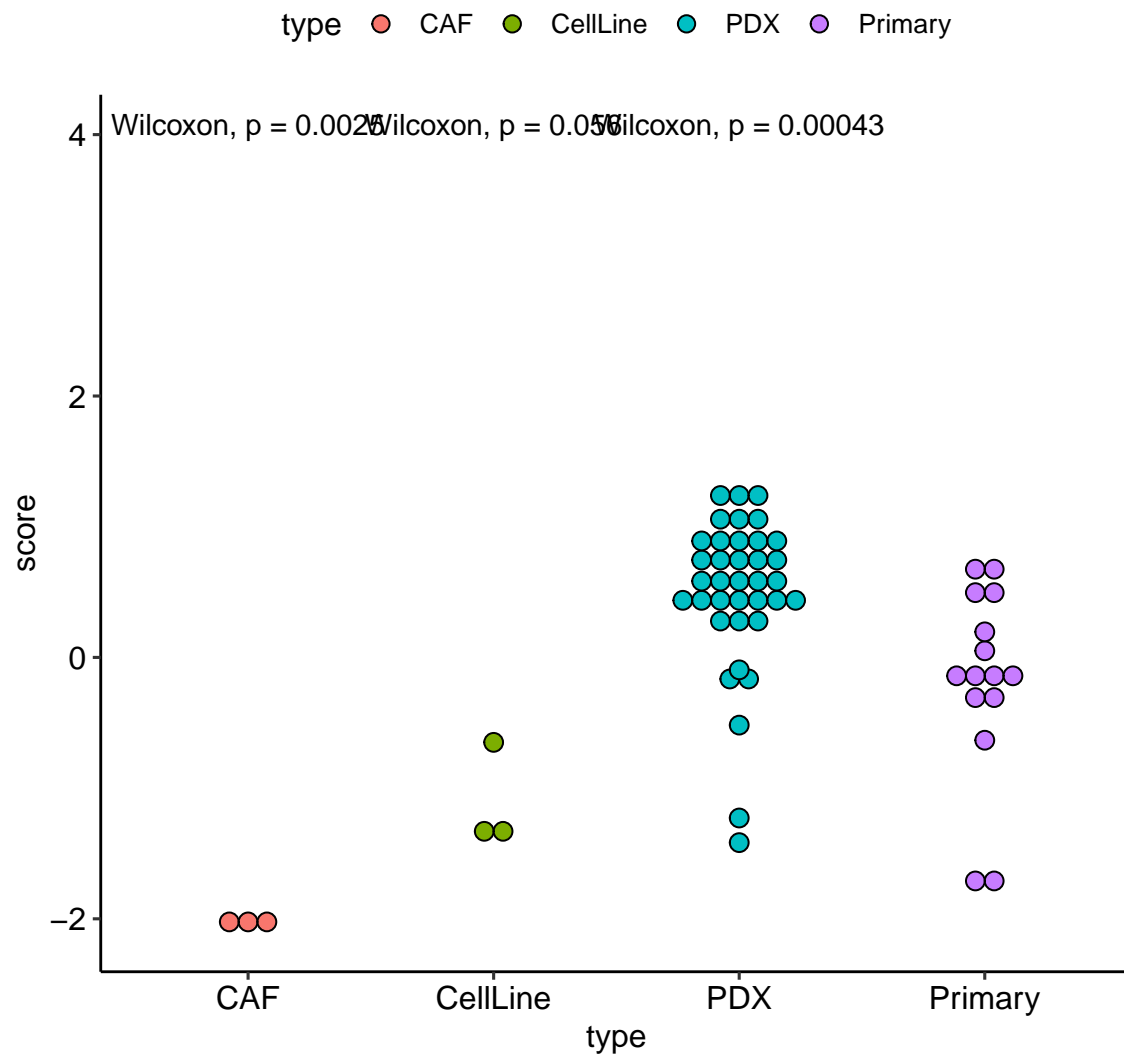
## ICGC.Immunogenic.Down score



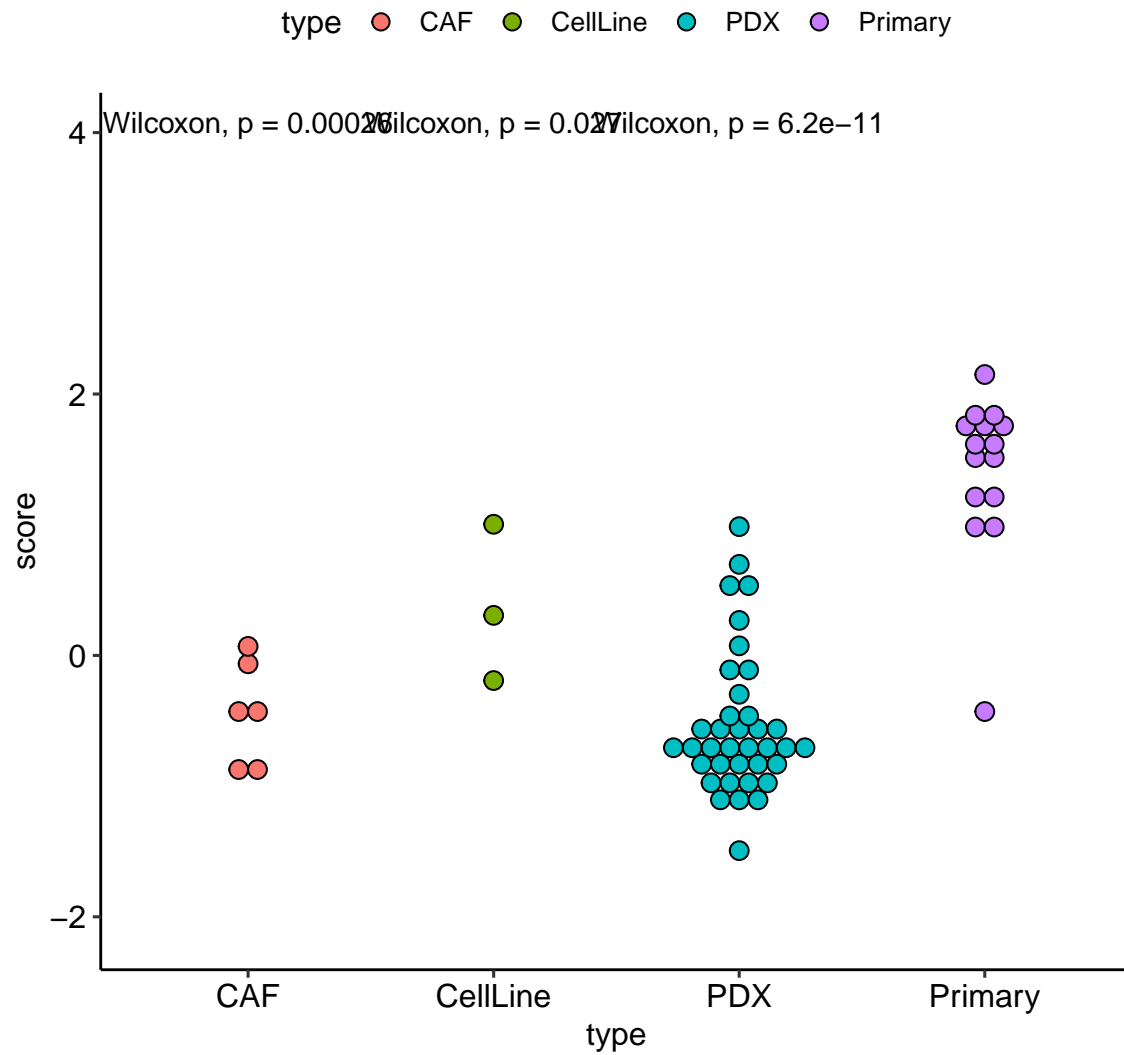
## Warning: Removed 3 rows containing non-finite values (stat\_bindot).

## Warning: Removed 3 rows containing non-finite values (stat\_compare\_means).

## ICGC.Progenitor.Up score



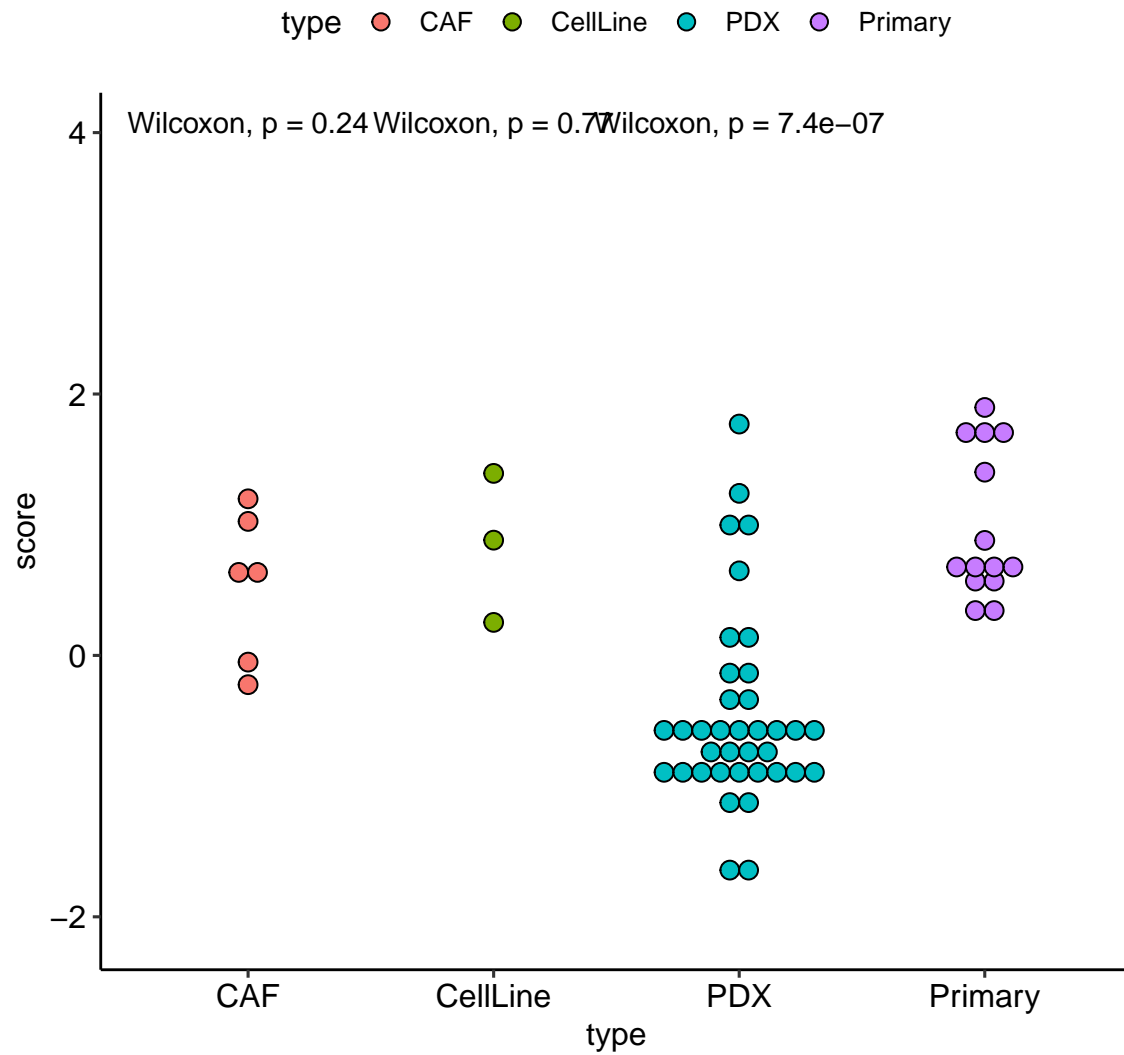
## ICGC.Progenitor.Down score



```
## Warning: Removed 1 rows containing non-finite values (stat_bindot).
```

```
## Warning: Removed 1 rows containing non-finite values (stat_compare_means).
```

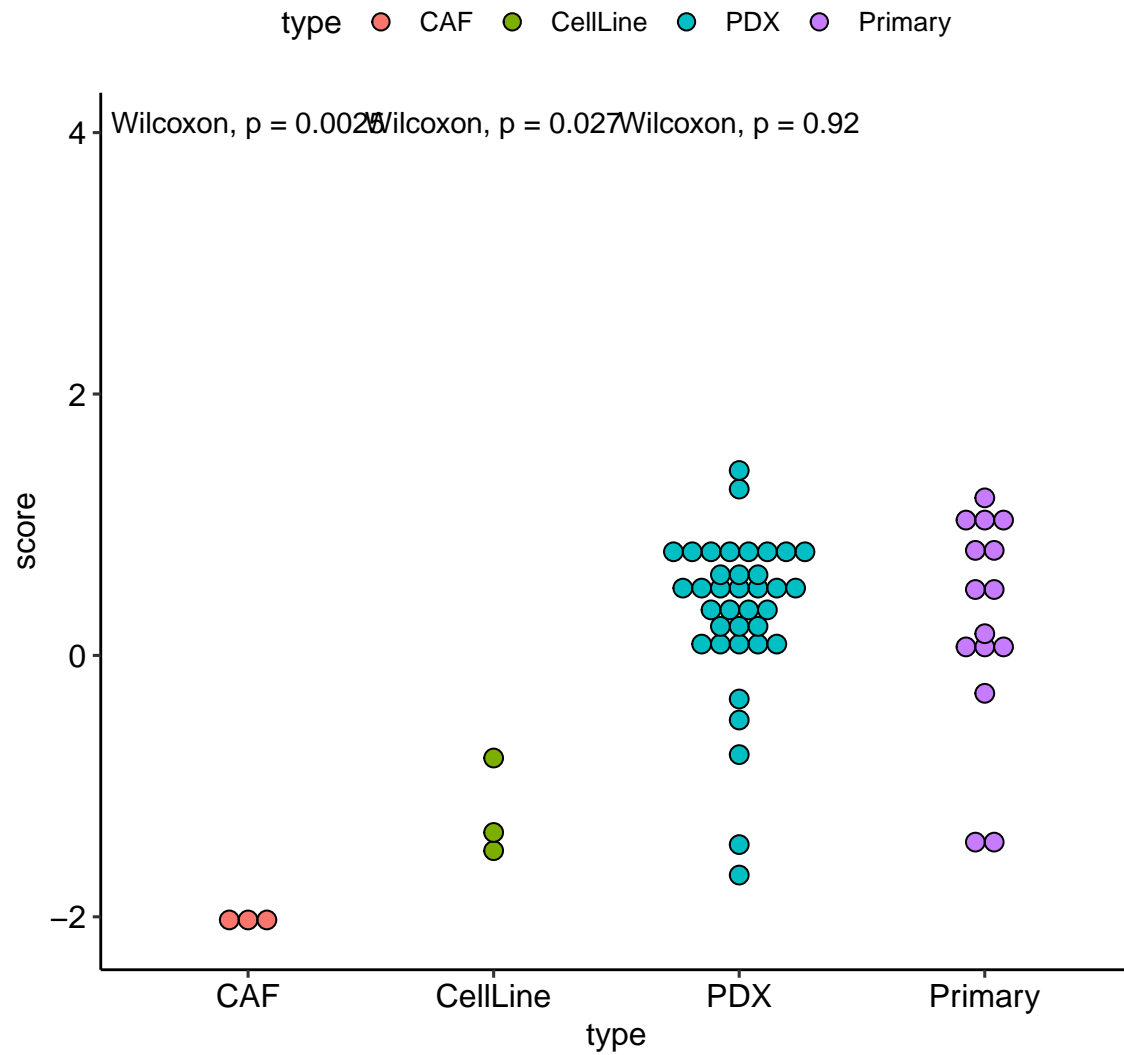
## ICGC.Squamous.Up score



```
## Warning: Removed 3 rows containing non-finite values (stat_bindot).
```

```
## Warning: Removed 3 rows containing non-finite values (stat_compare_means).
```

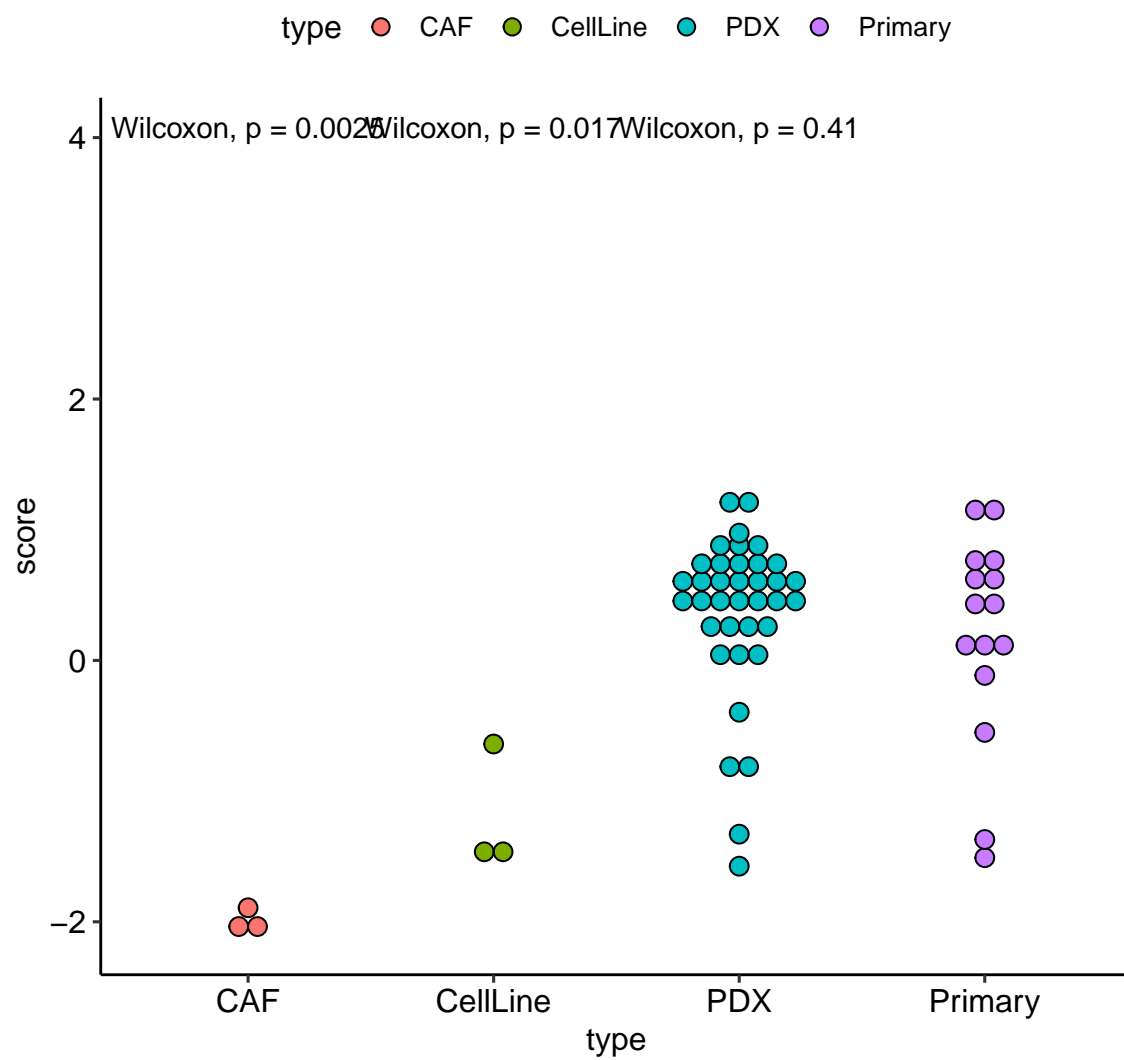
## ICGC.Squamous.Down score



## Warning: Removed 3 rows containing non-finite values (stat\_bindot).

## Warning: Removed 3 rows containing non-finite values (stat\_compare\_means).

## ICGC.SAM score

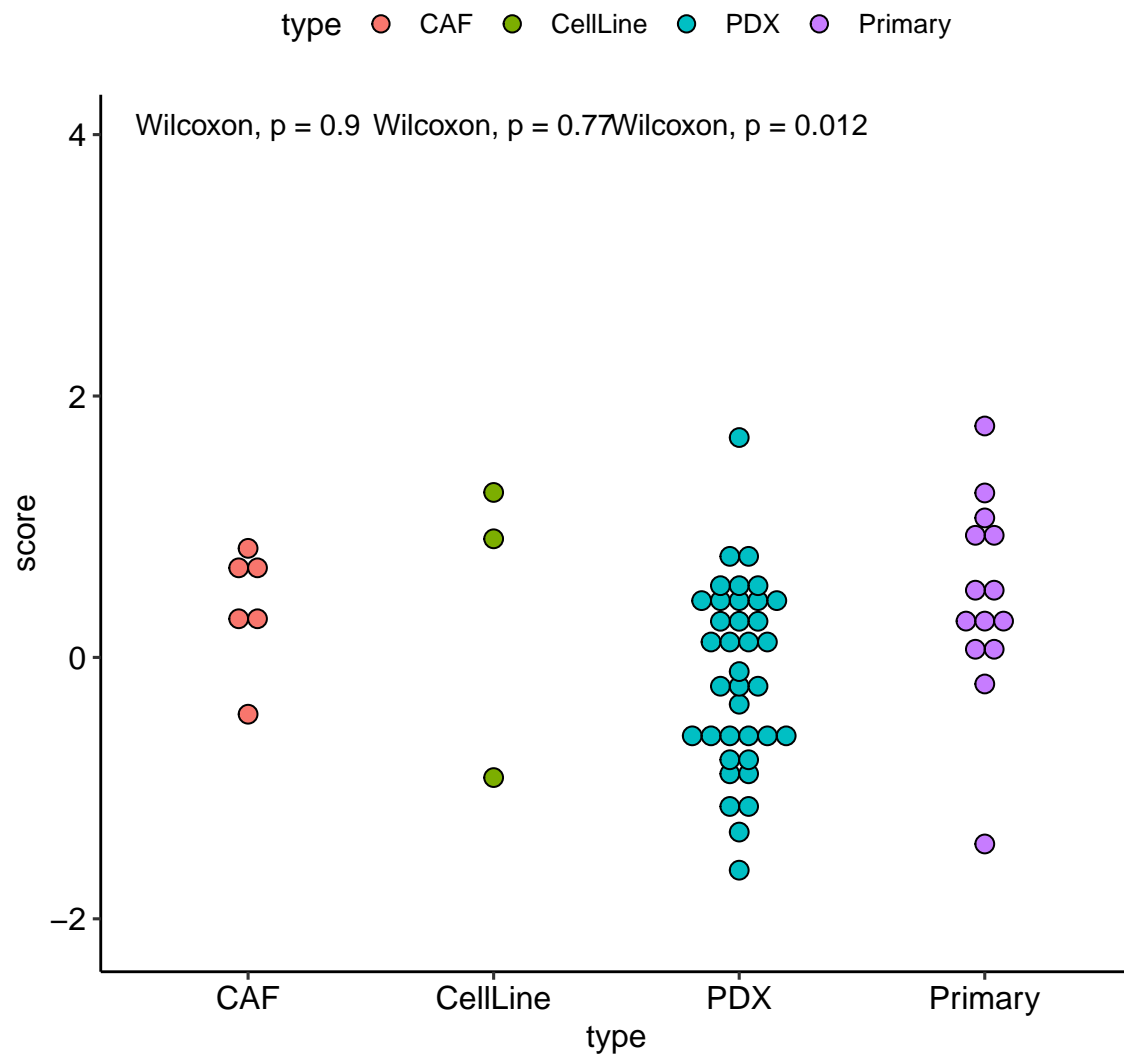


## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

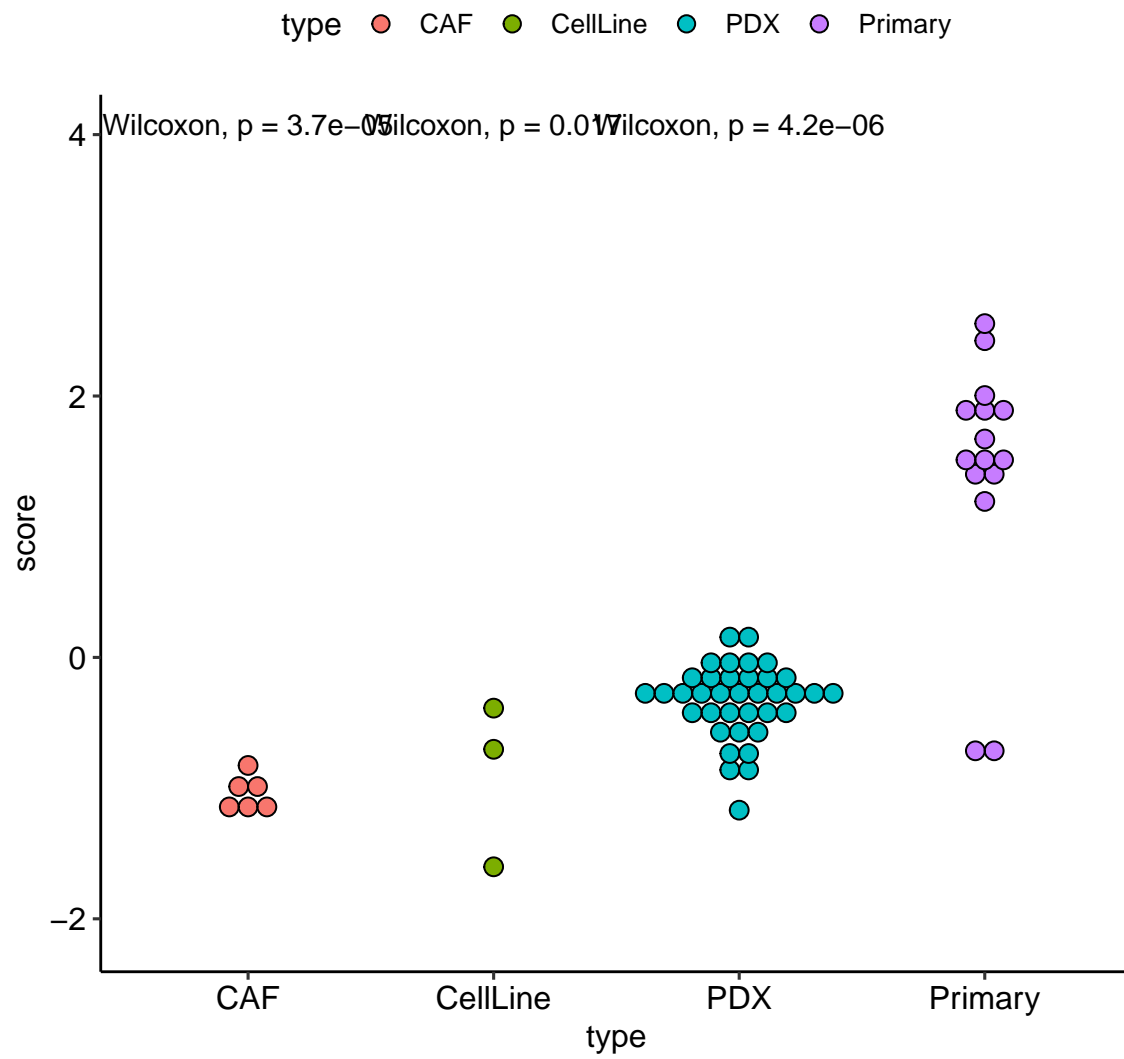
## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).



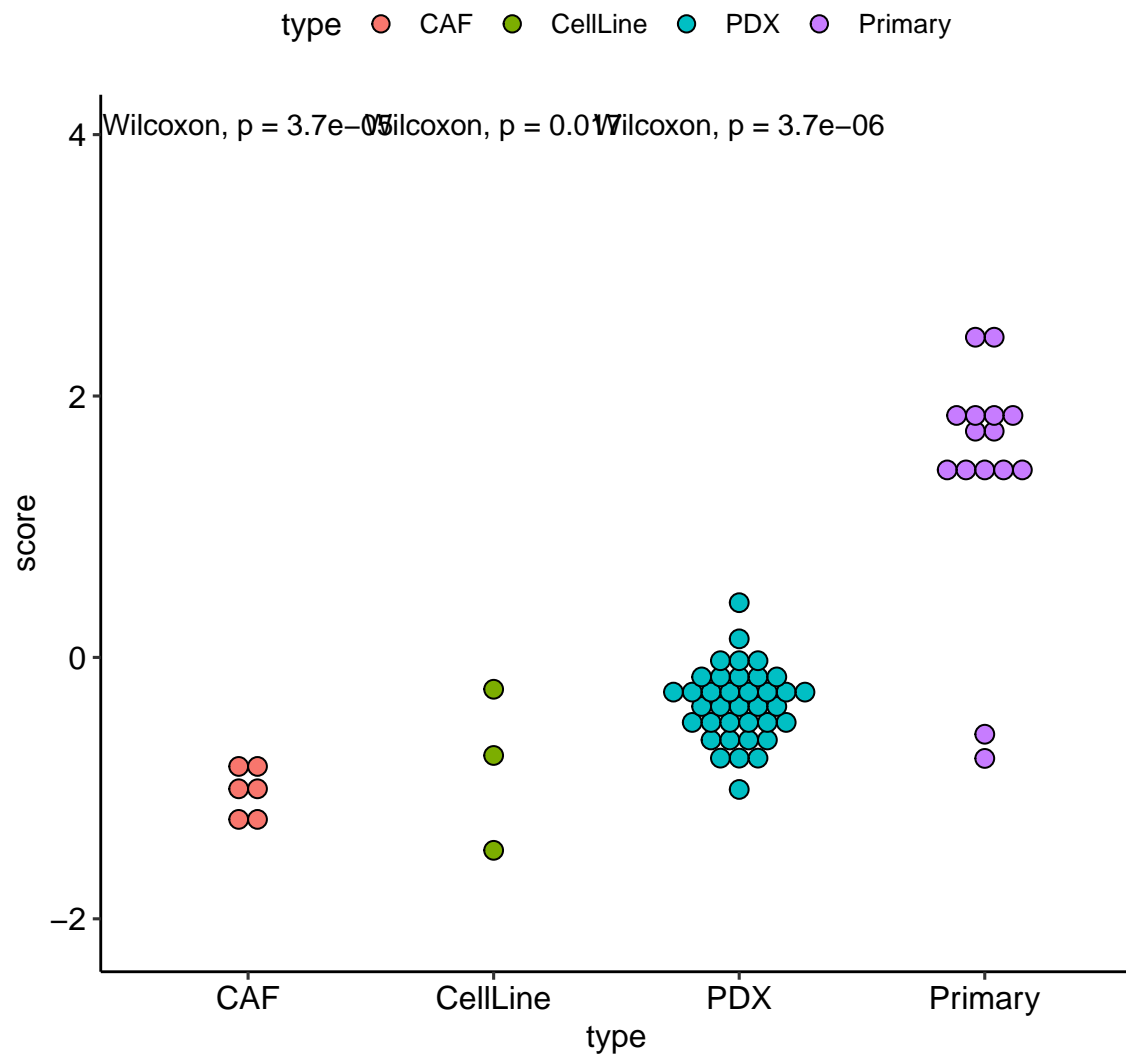
## Scarpa\_PanNET score



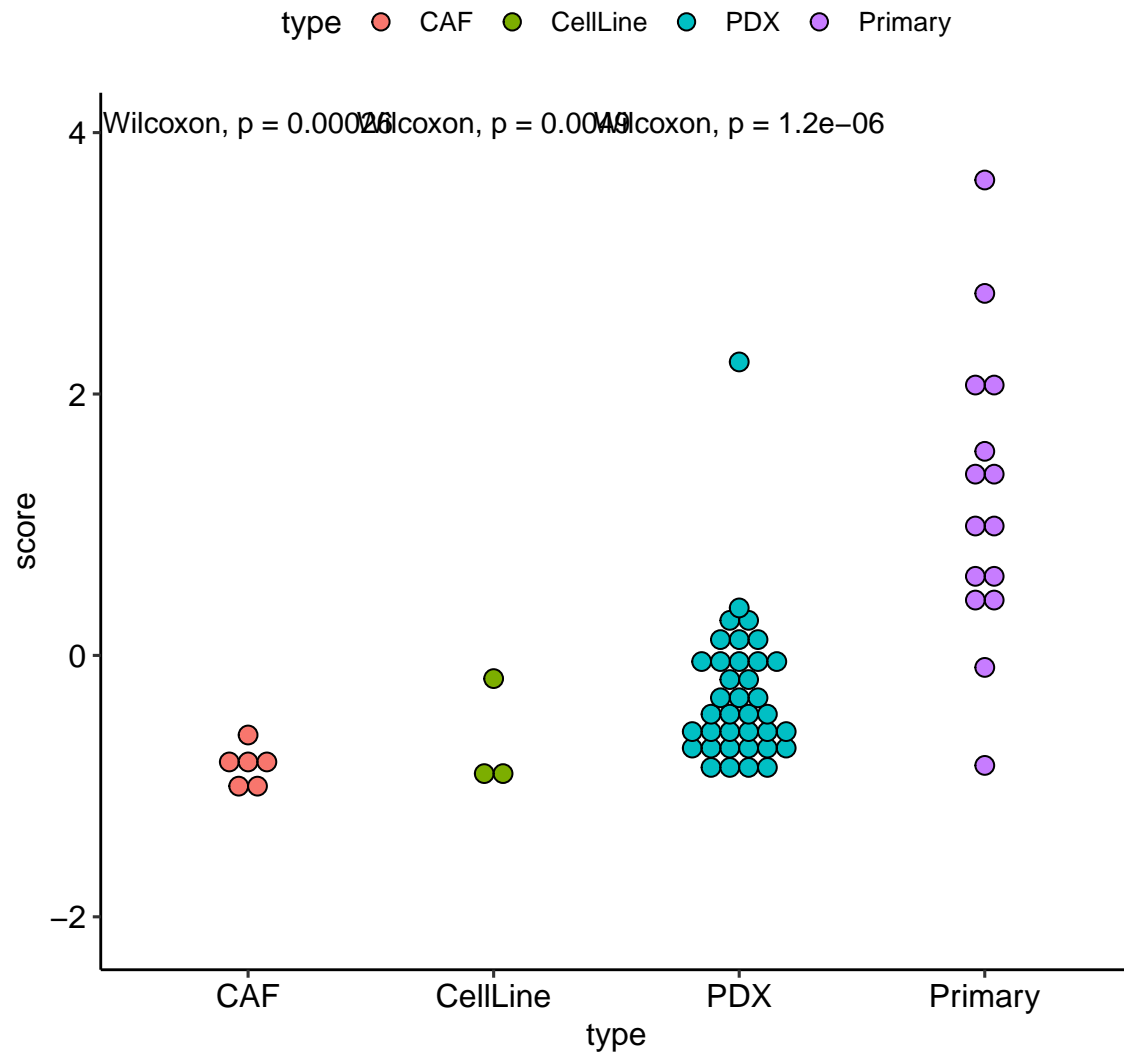
## Moffitt.Top5s score



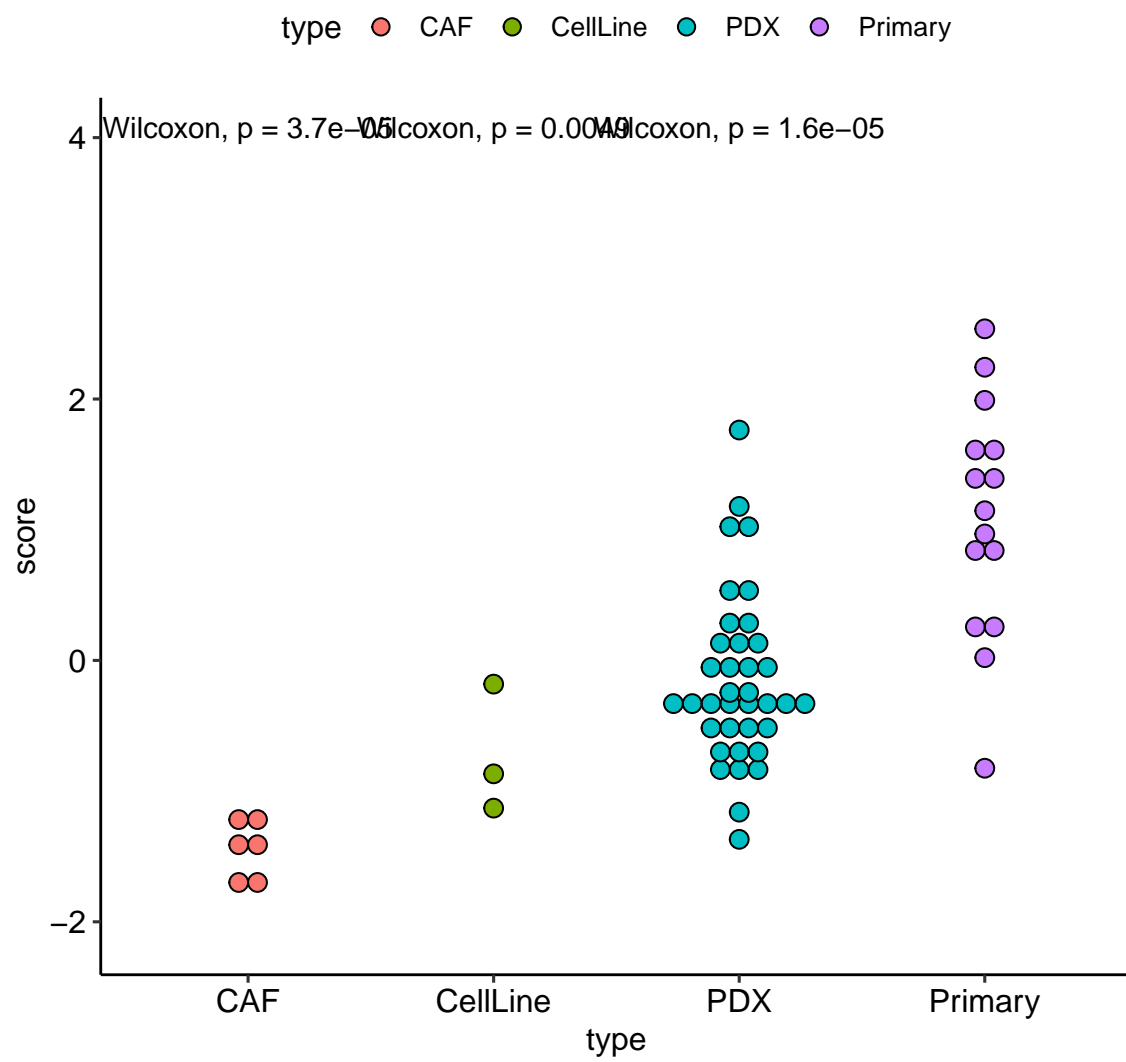
# Moffitt.Top25s score



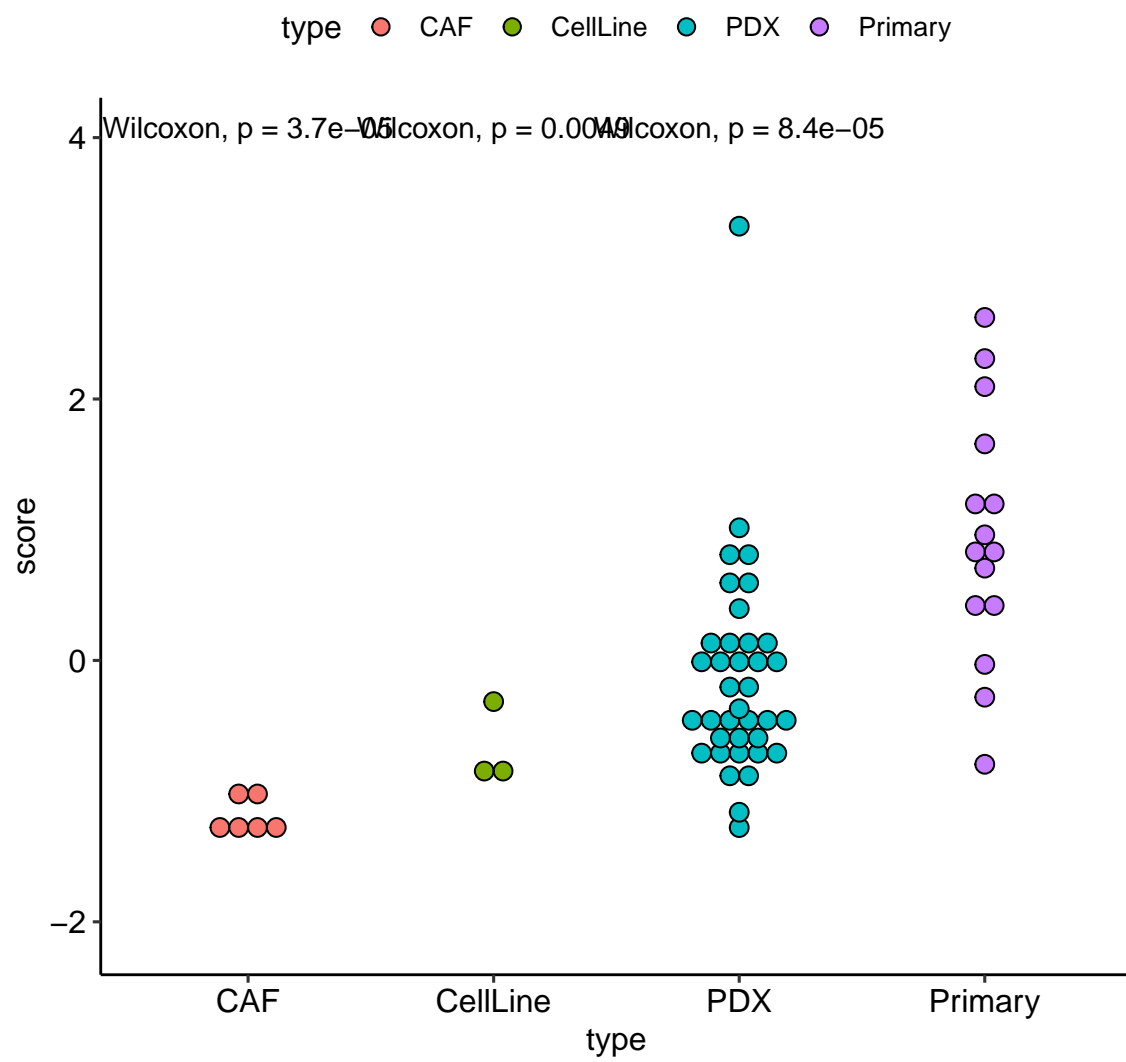
## Moffitt.F1\_Liver.top25 score



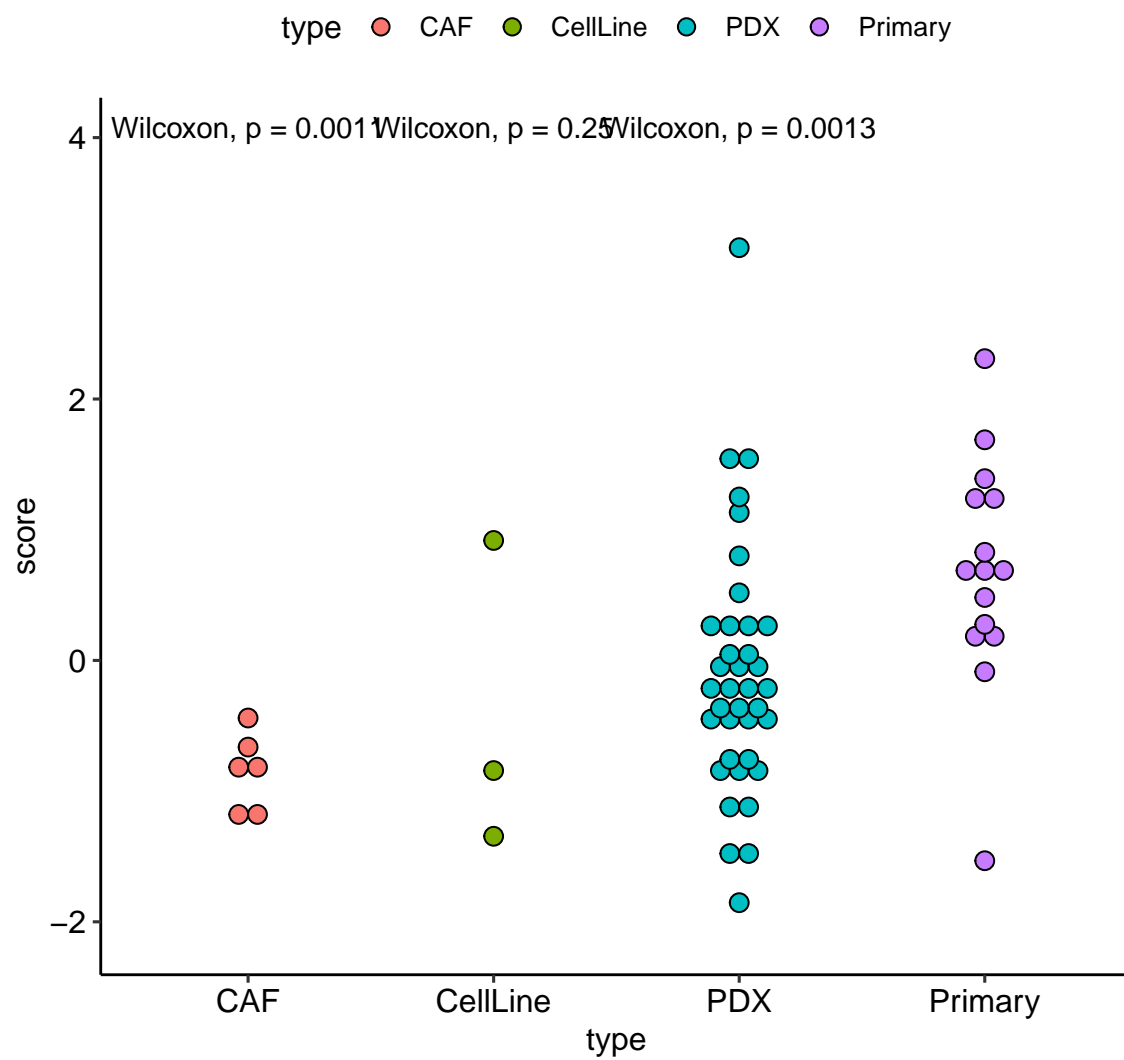
# Moffitt.F1\_Liver.top250 score



# Moffitt.F1\_Liver.top100 score



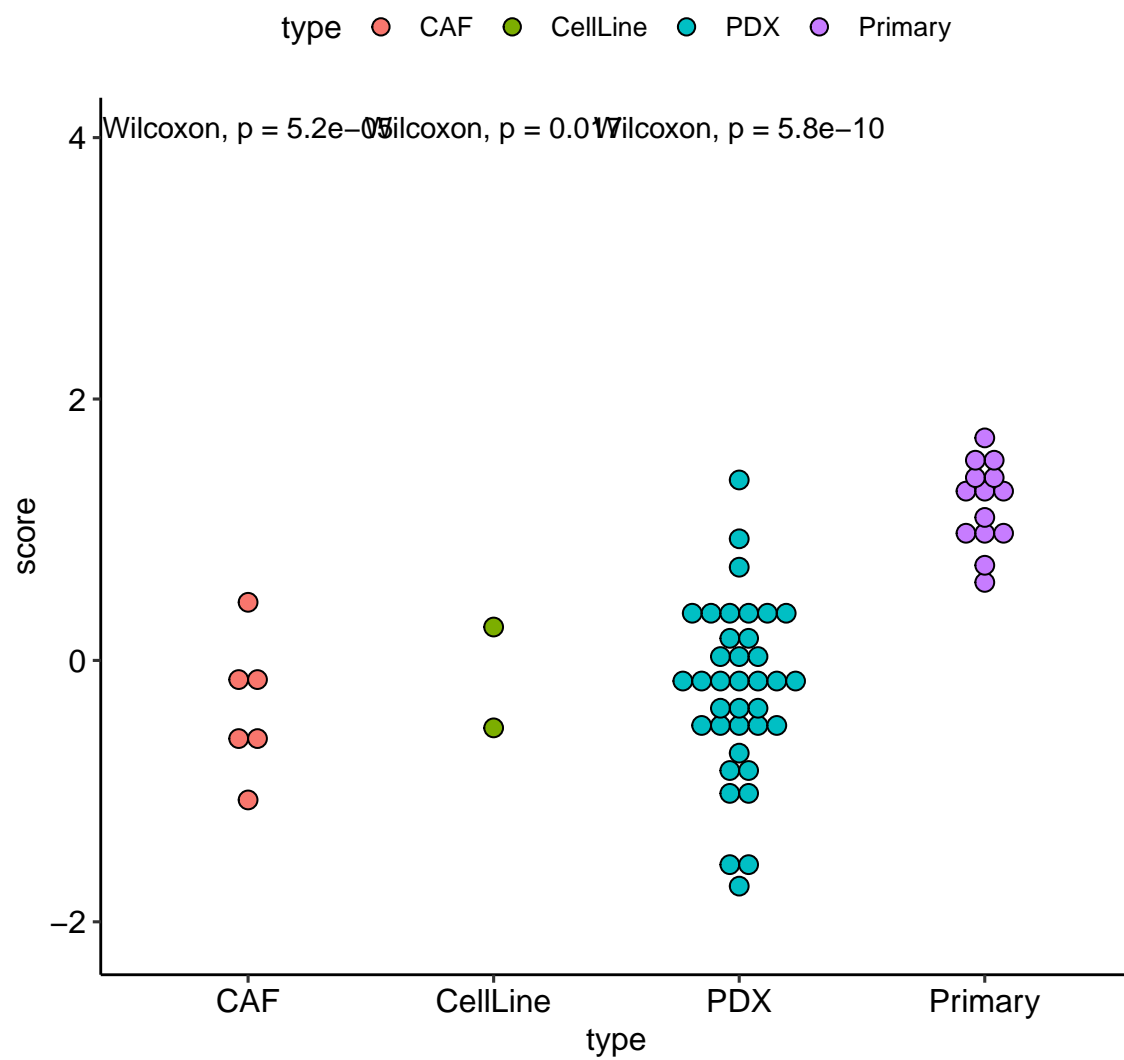
## Moffitt.F2.top25 score



## Warning: Removed 2 rows containing non-finite values (stat\_bindot).

## Warning: Removed 2 rows containing non-finite values (stat\_compare\_means).

## Moffitt.F2.top250 score

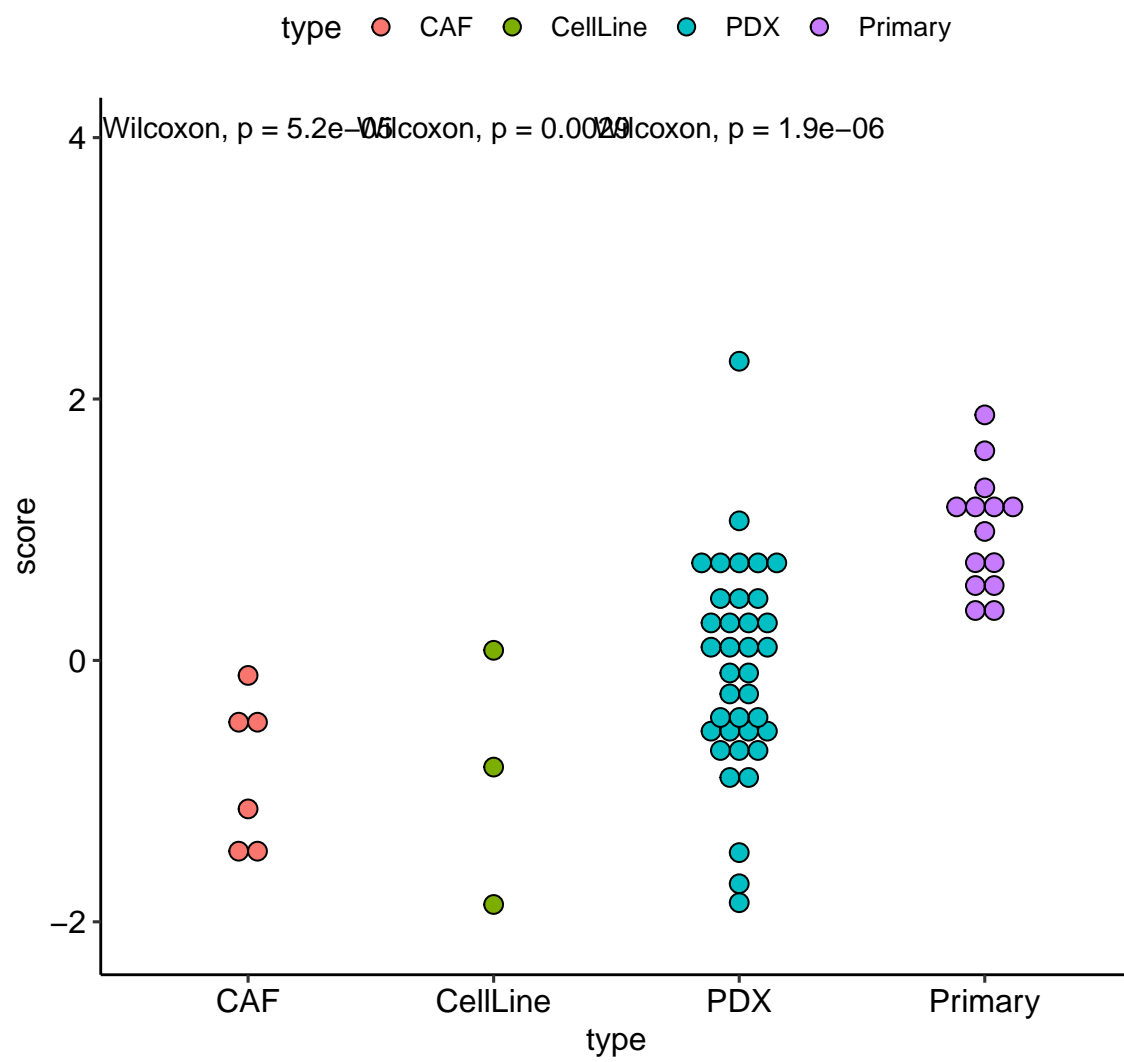


## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

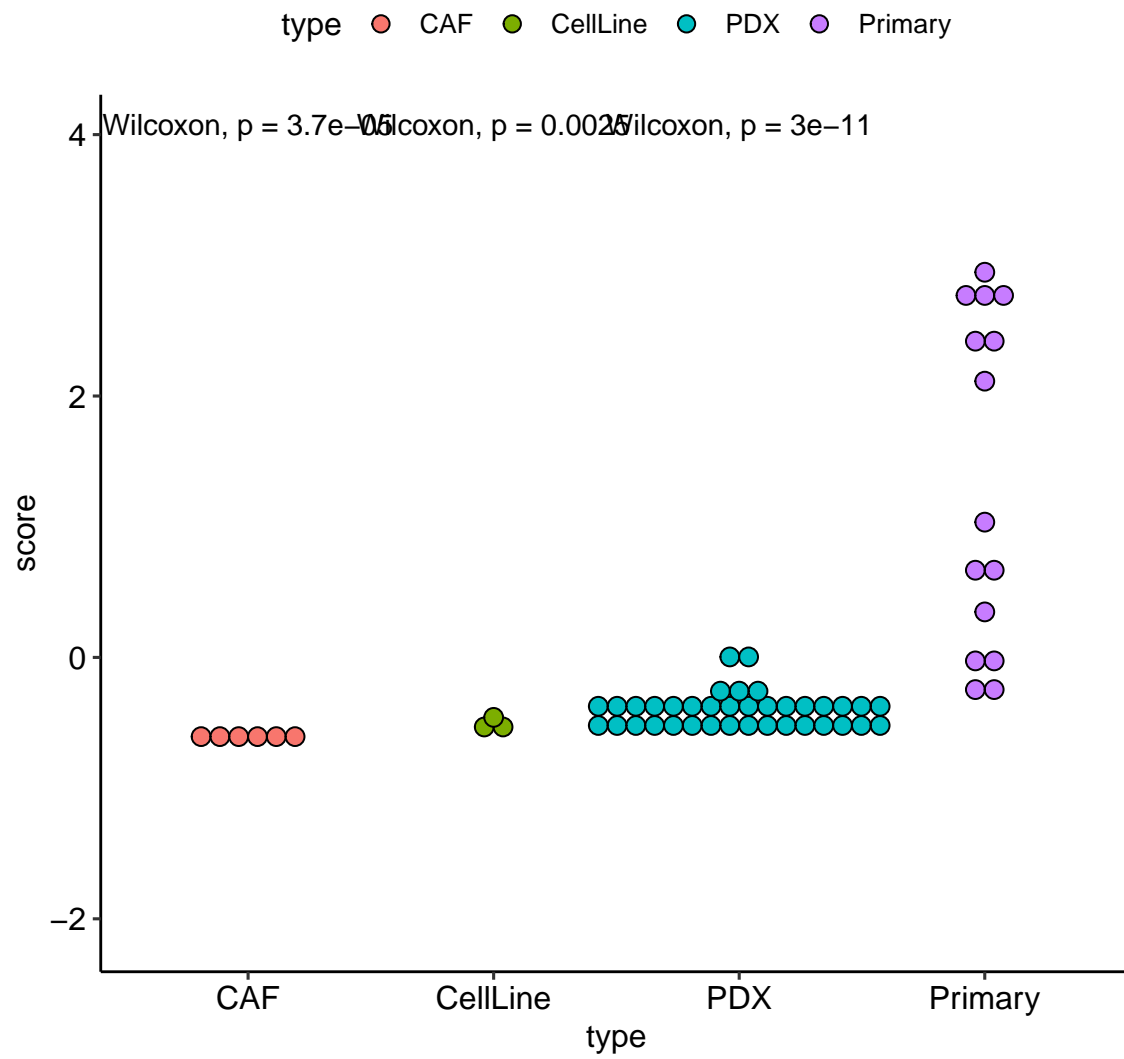
## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).



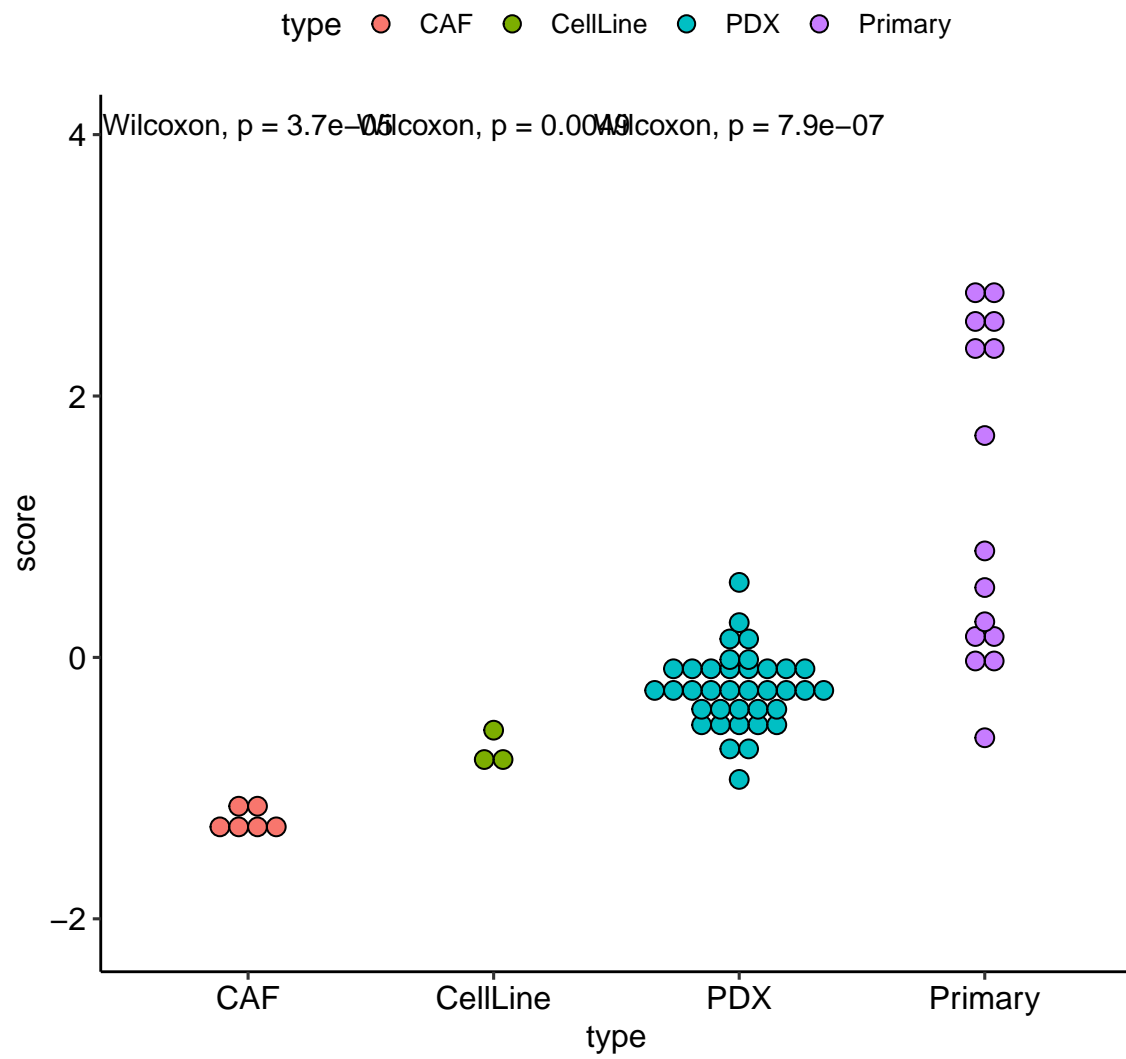
## Moffitt.F2.top100 score



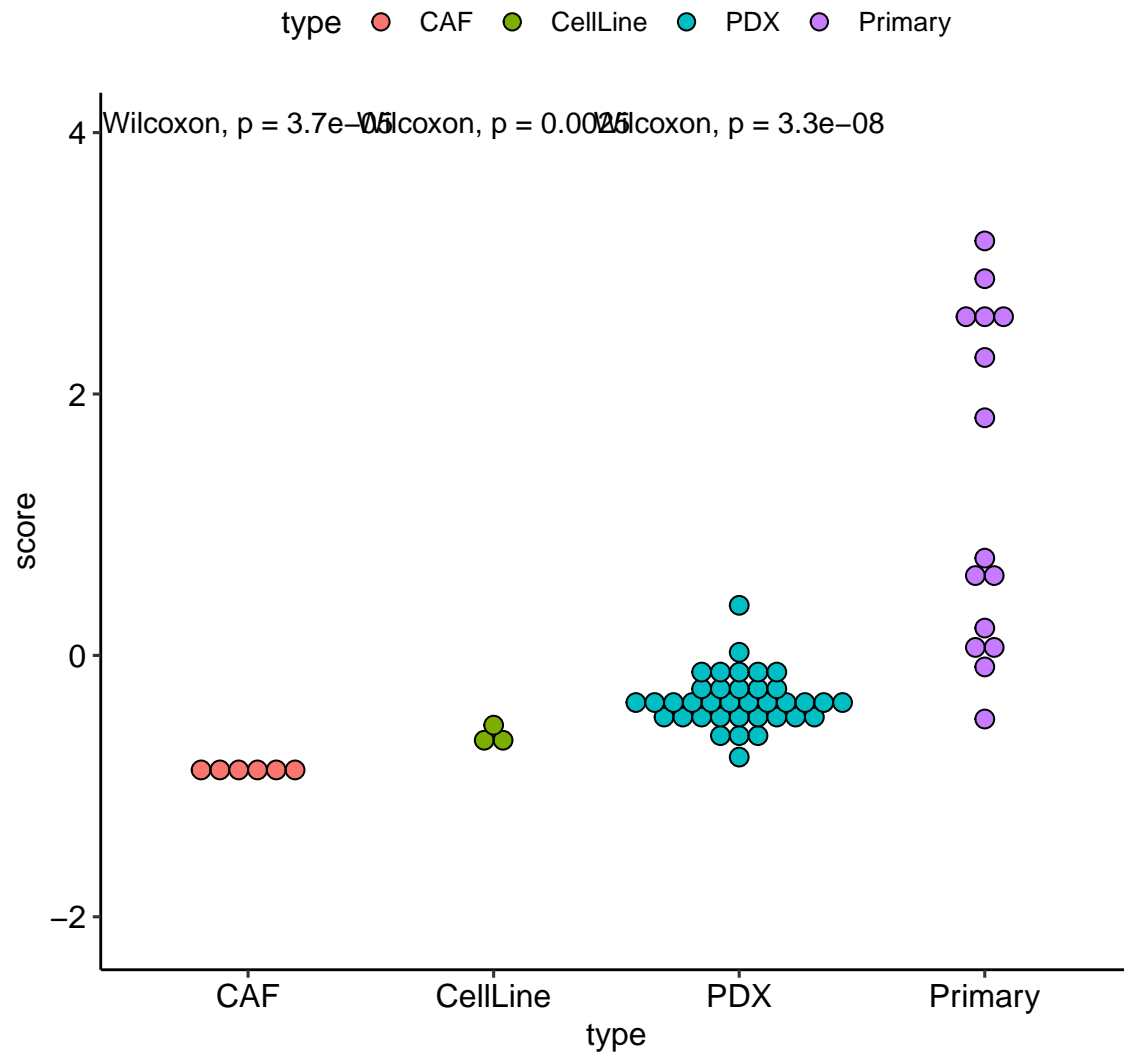
## Moffitt.F3\_Exocrine.top25 score



# Moffitt.F3\_Exocrine.top250 score



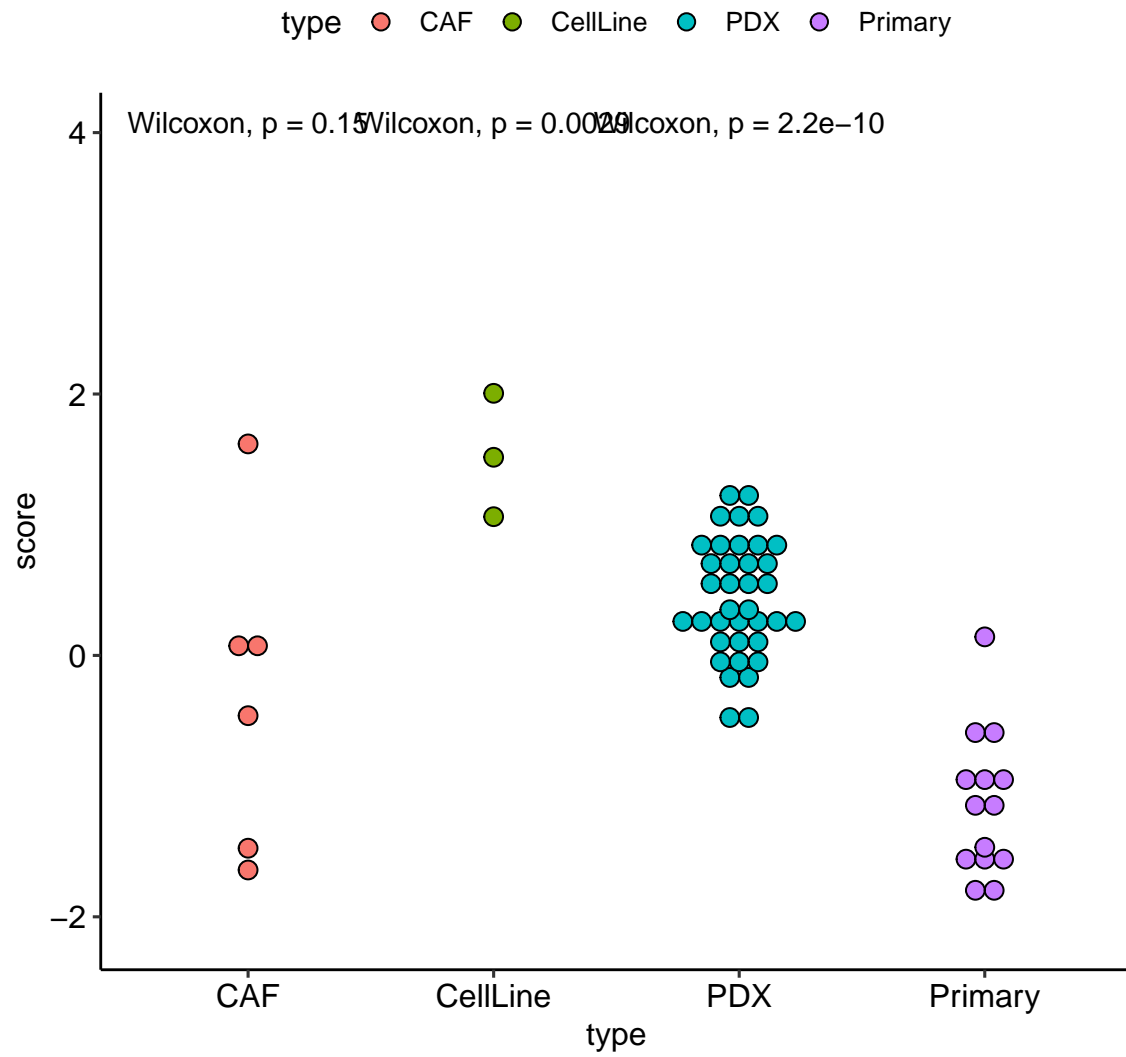
# Moffitt.F3\_Exocrine.top100 score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

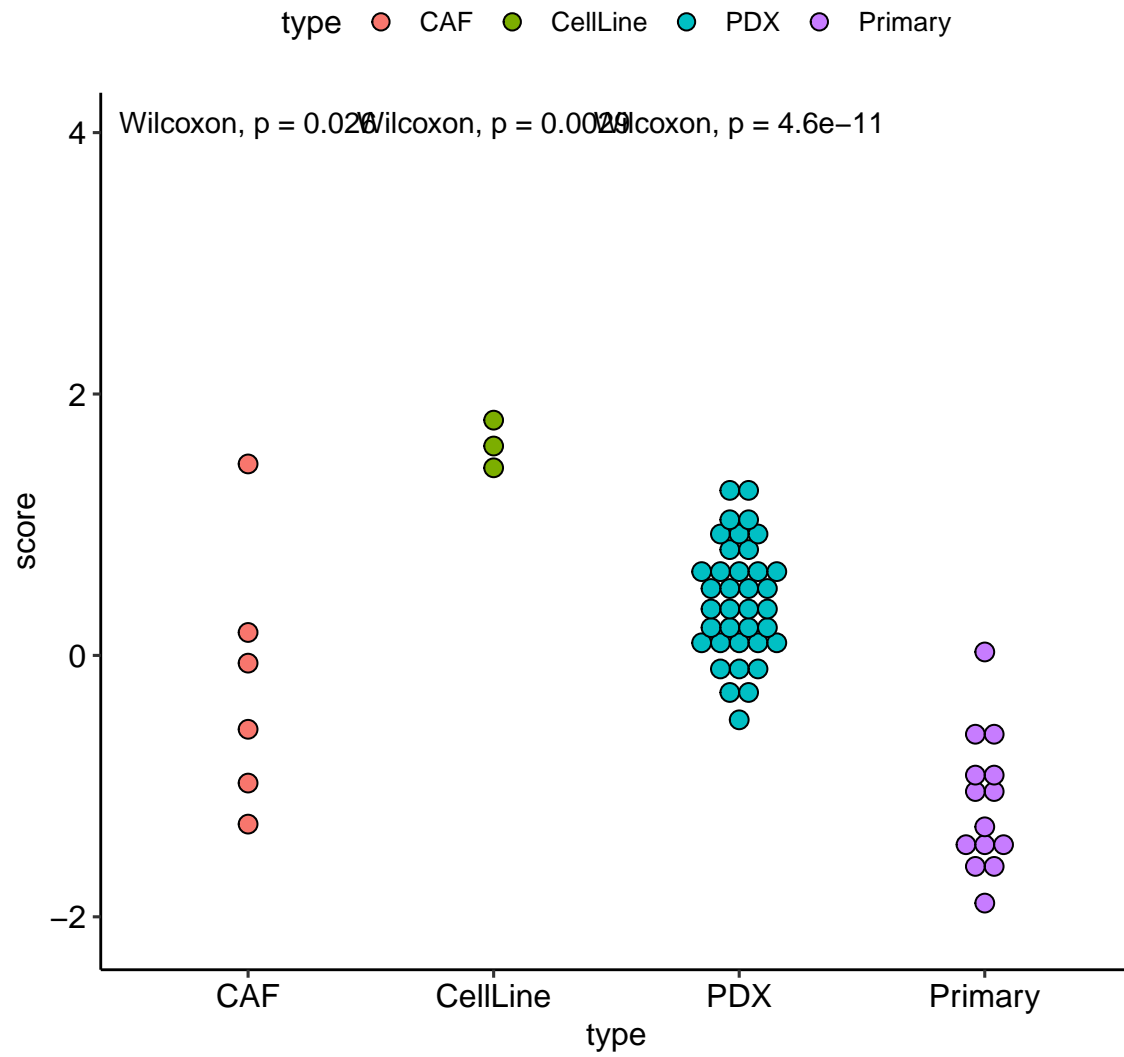
# Moffitt.F4\_CellCycle.top25 score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

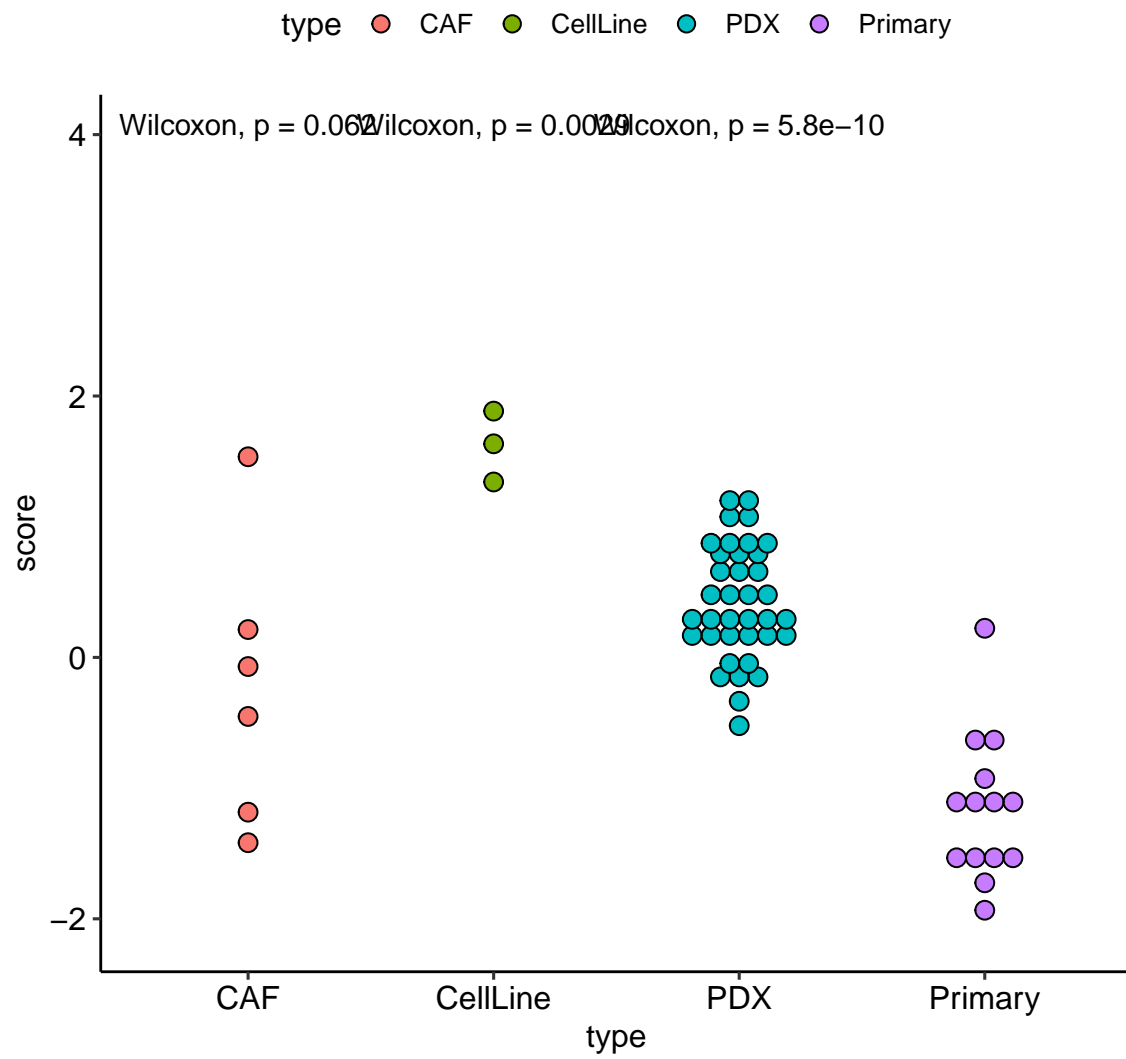
## Moffitt.F4\_CellCycle.top250 score



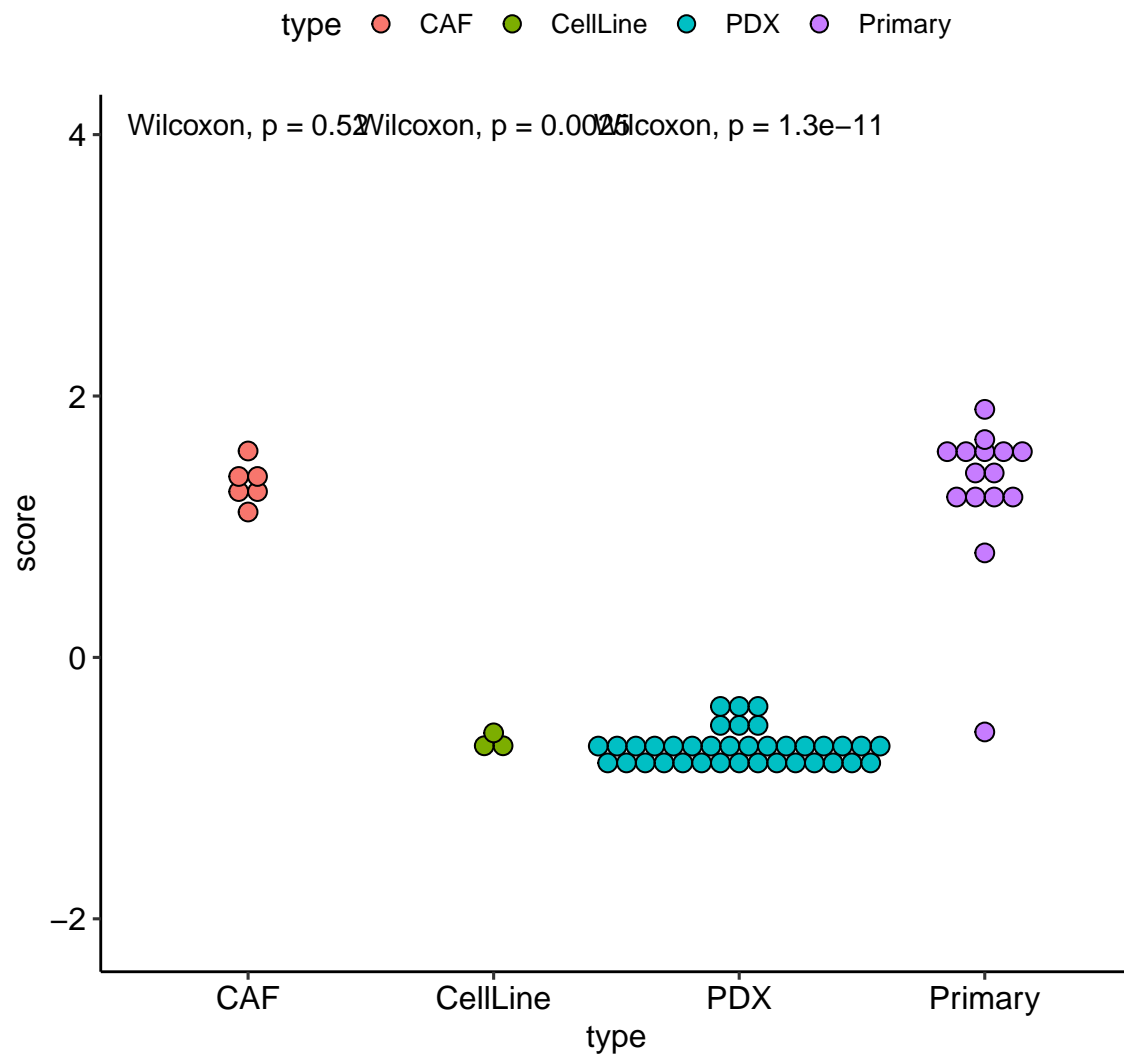
## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

# Moffitt.F4\_CellCycle.top100 score

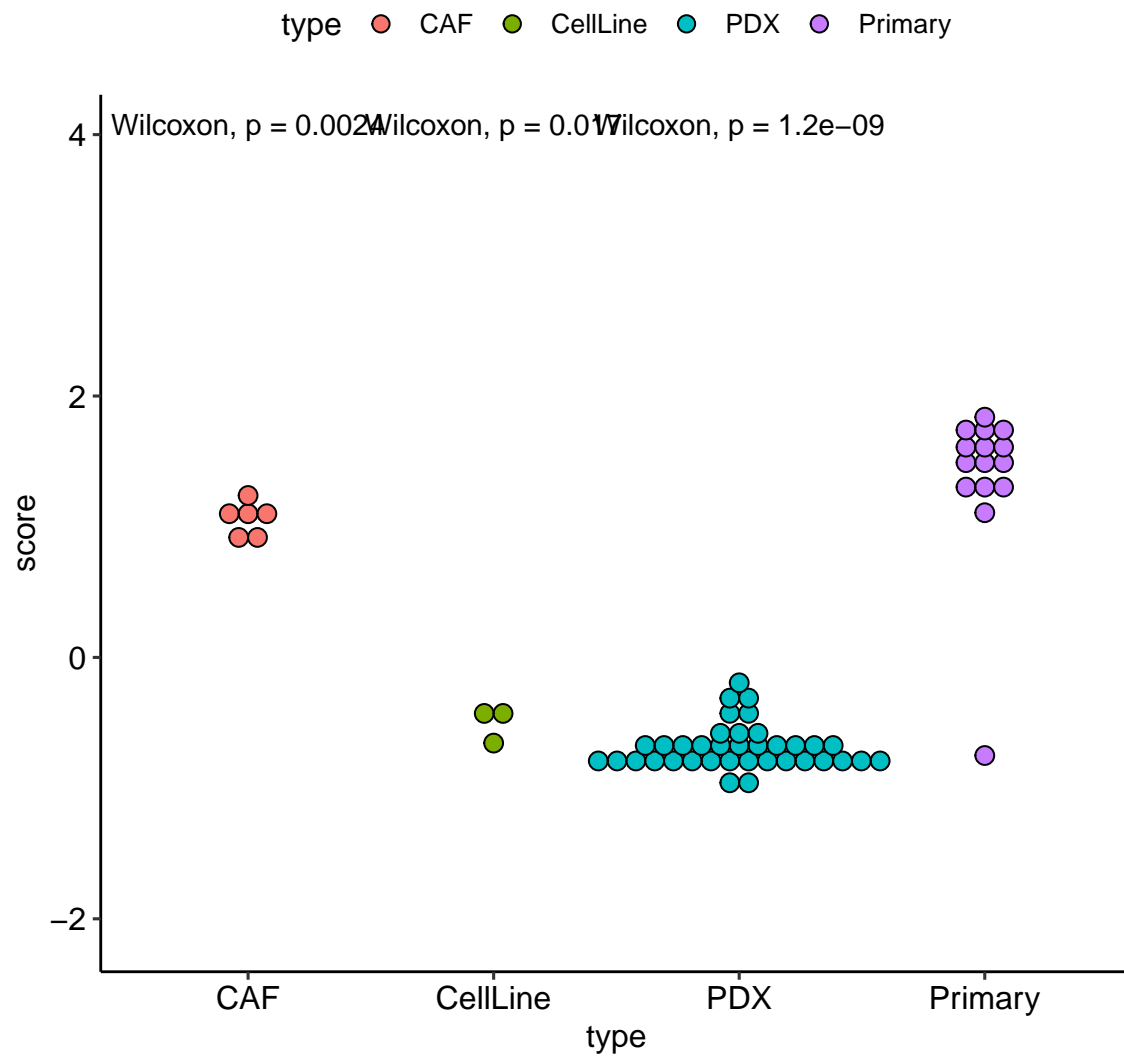


## Moffitt.F5\_ActivatedStroma.top25 score

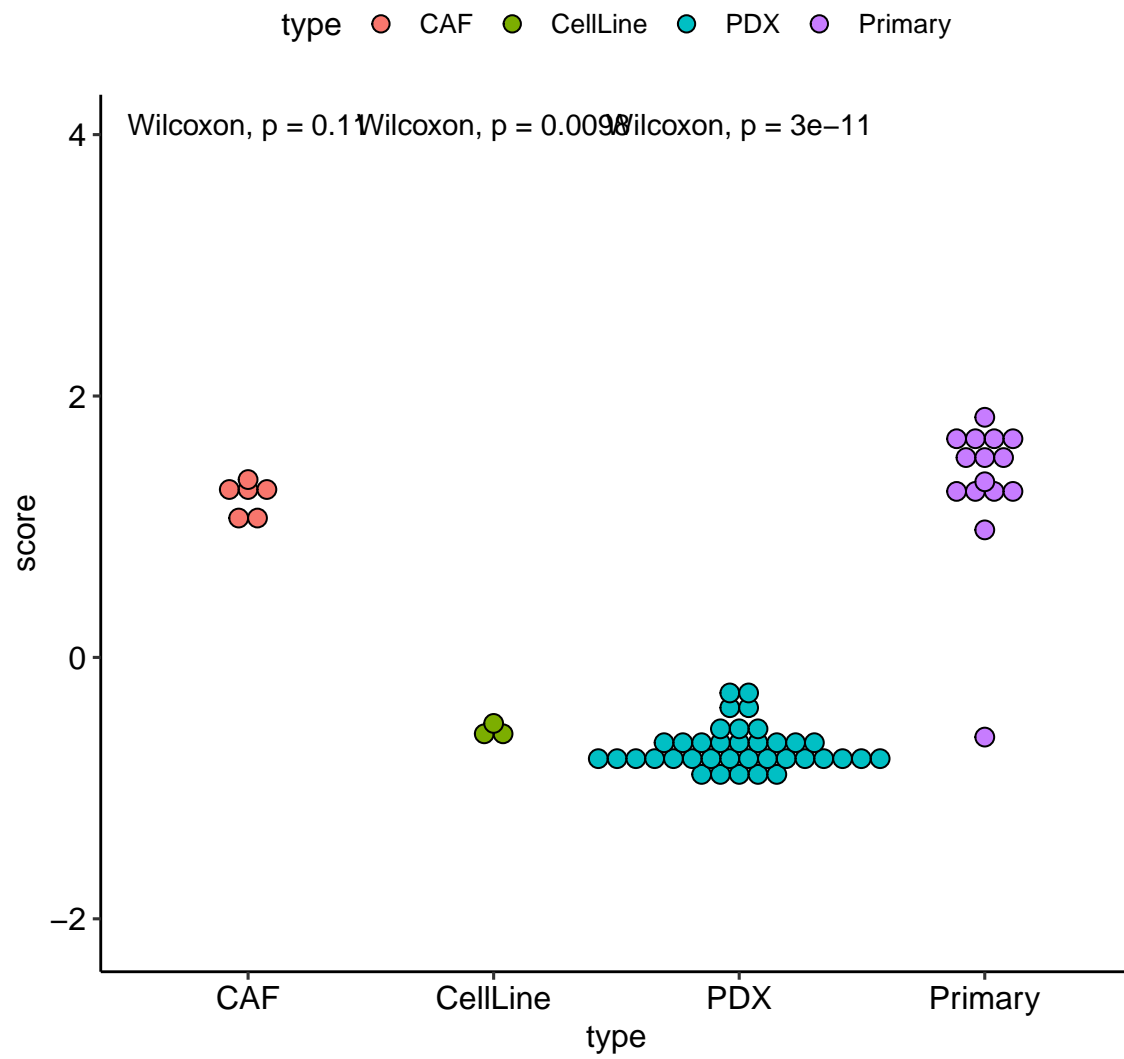




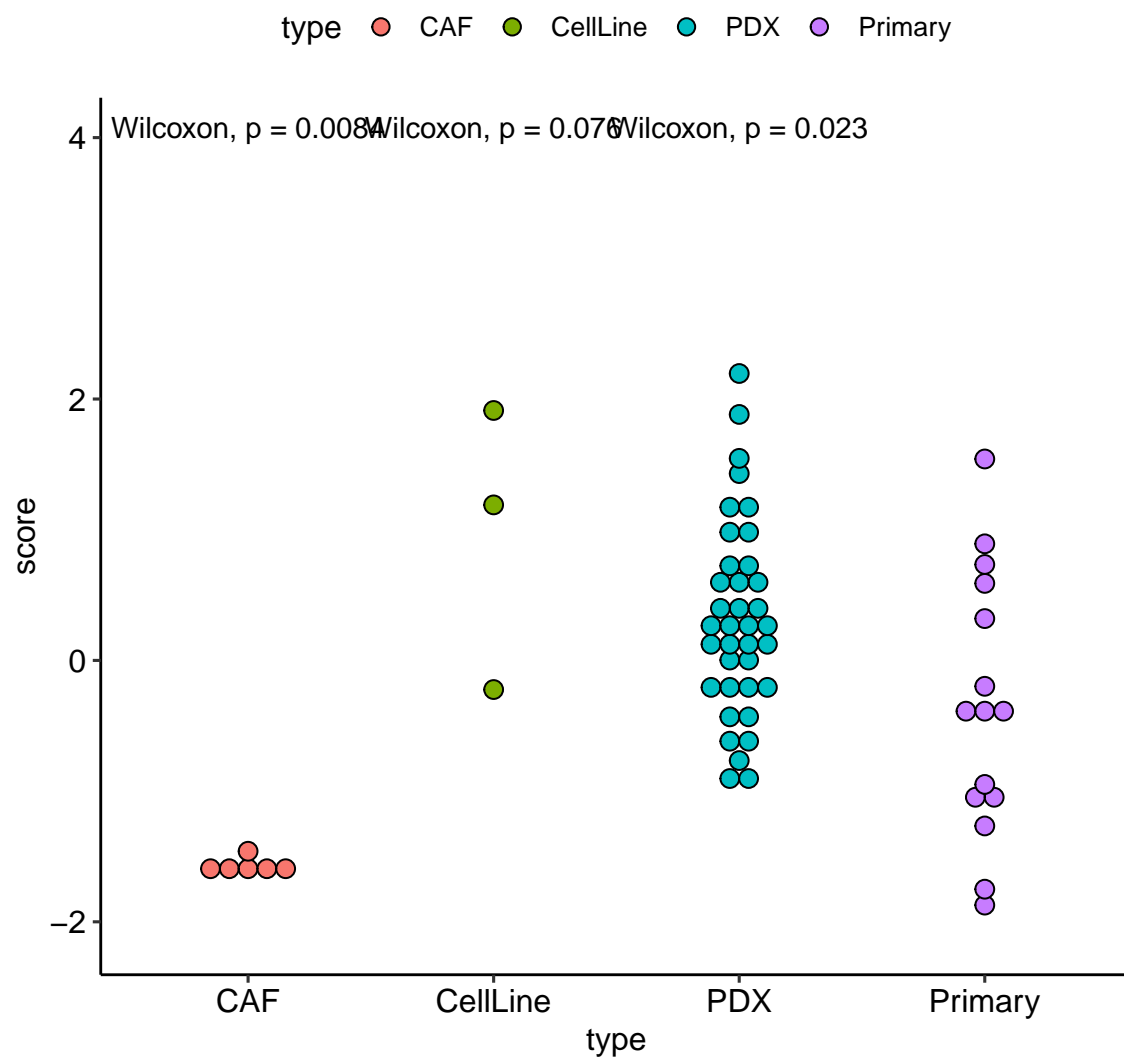
## Moffitt.F5\_ActivatedStroma.top250 score



## Moffitt.F5\_ActivatedStroma.top100 score



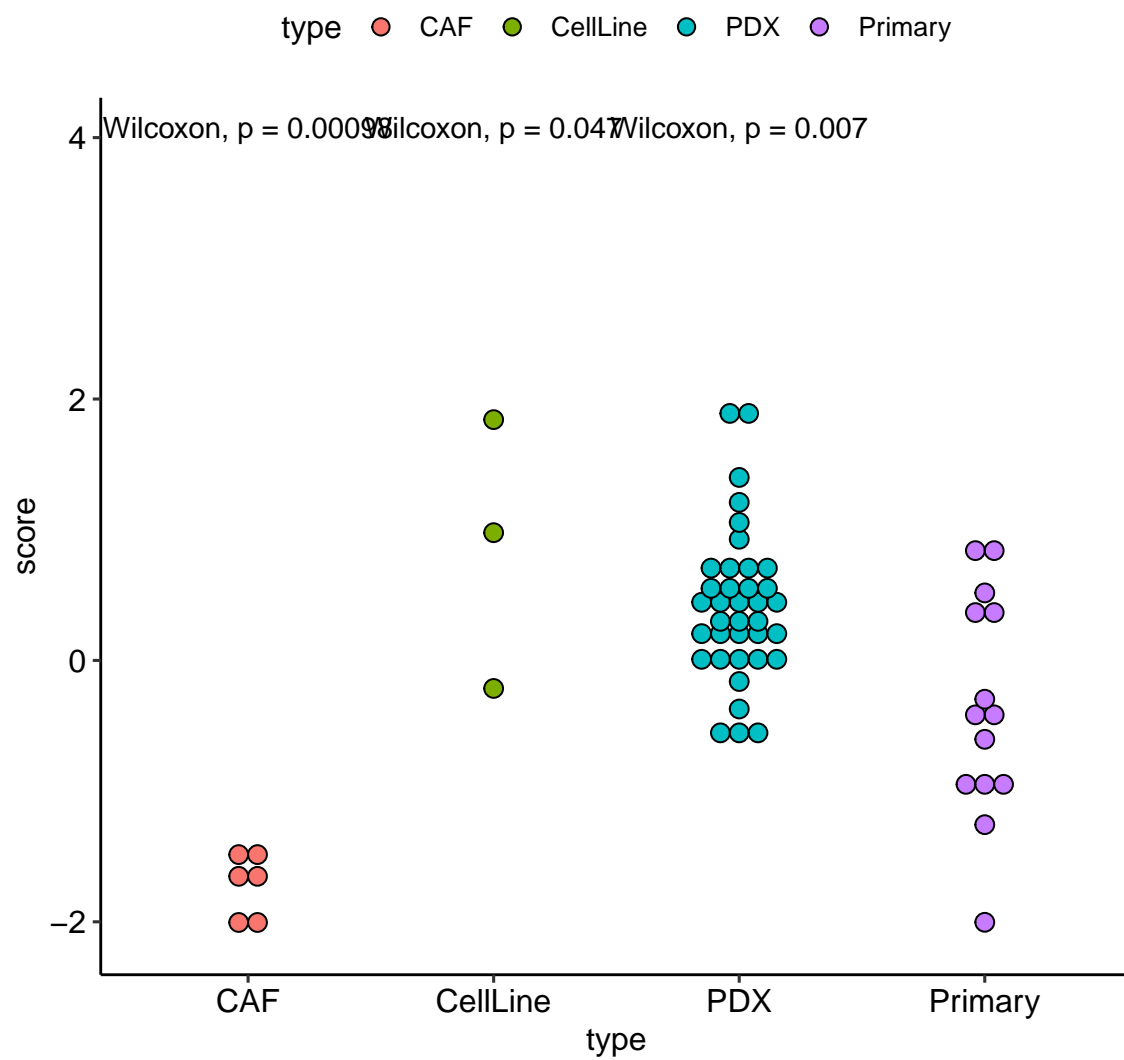
## Moffitt.F6\_BasalLike.top25 score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

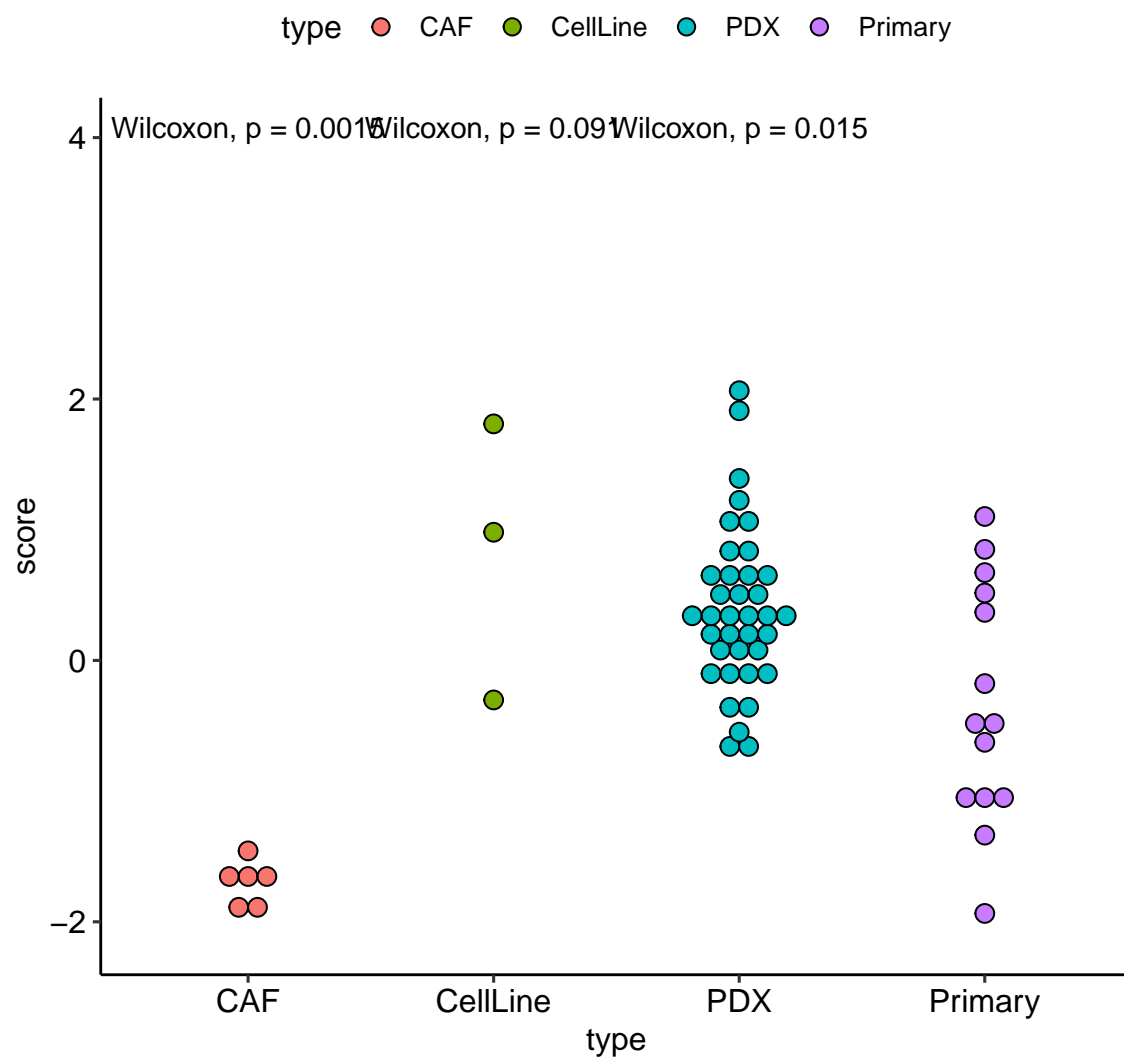
## Moffitt.F6\_BasalLike.top250 score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

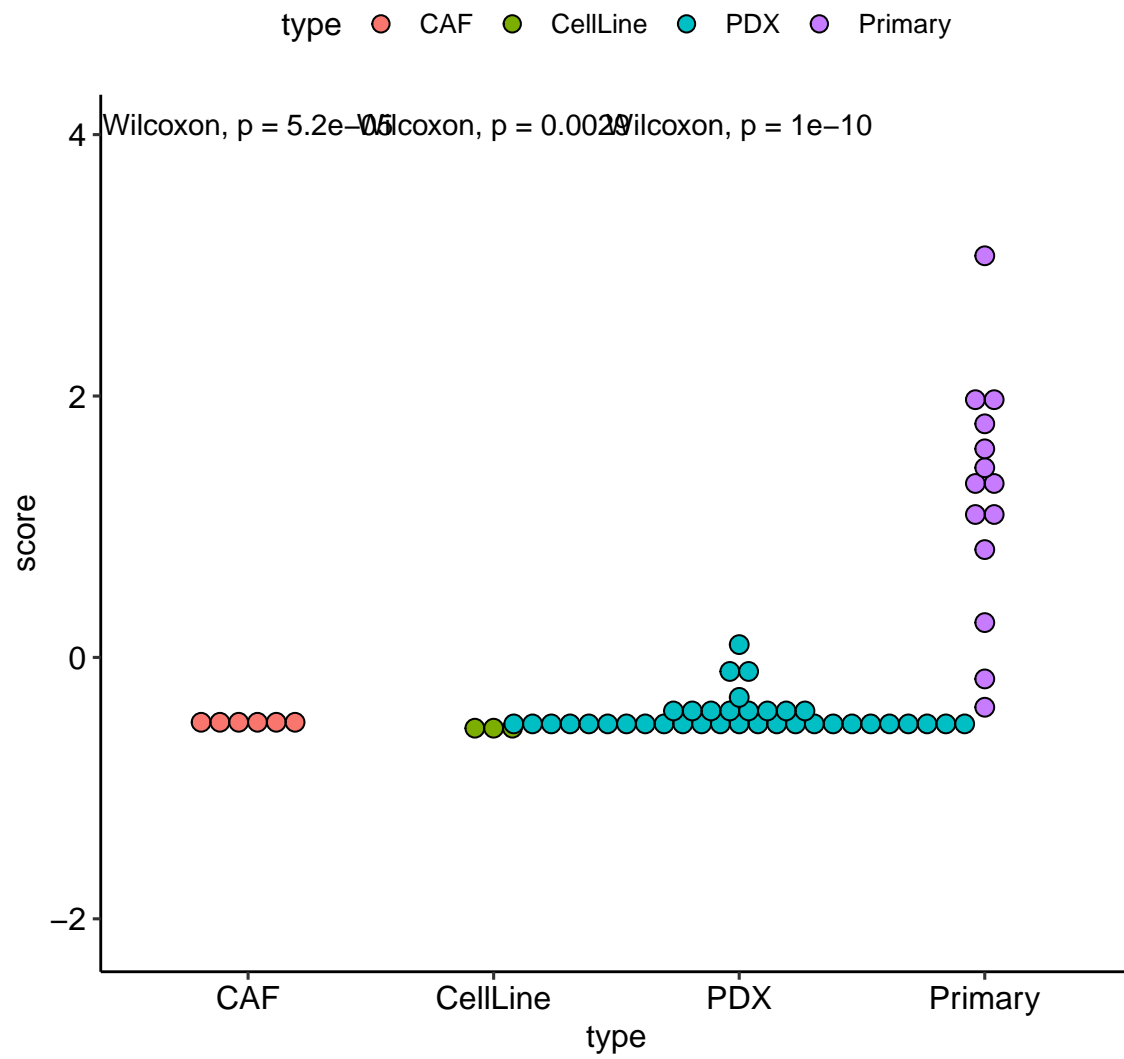
## Moffitt.F6\_BasalLike.top100 score



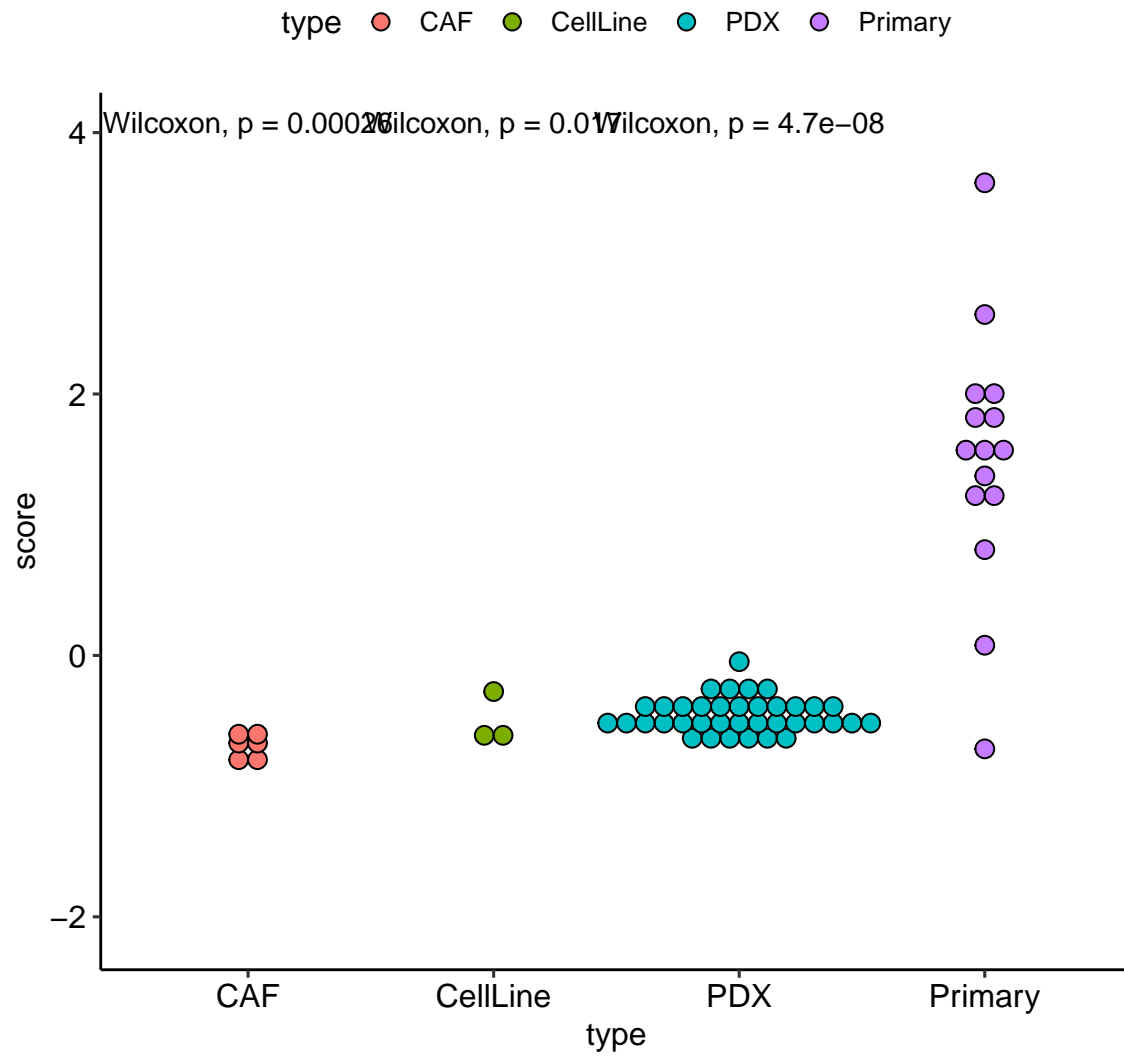
## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

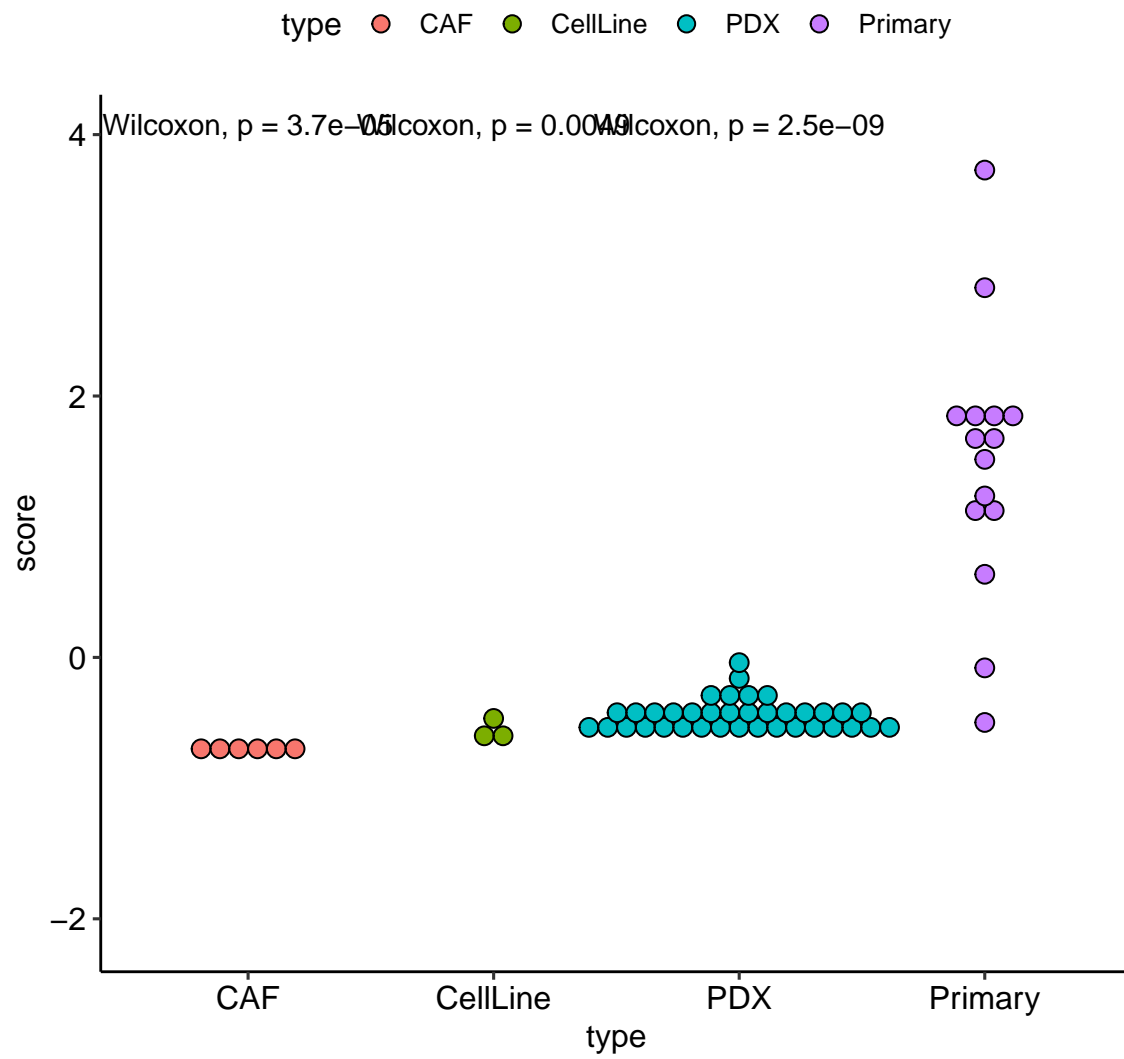
## Moffitt.F7\_Immune.top25 score



## Moffitt.F7\_Immune.top250 score

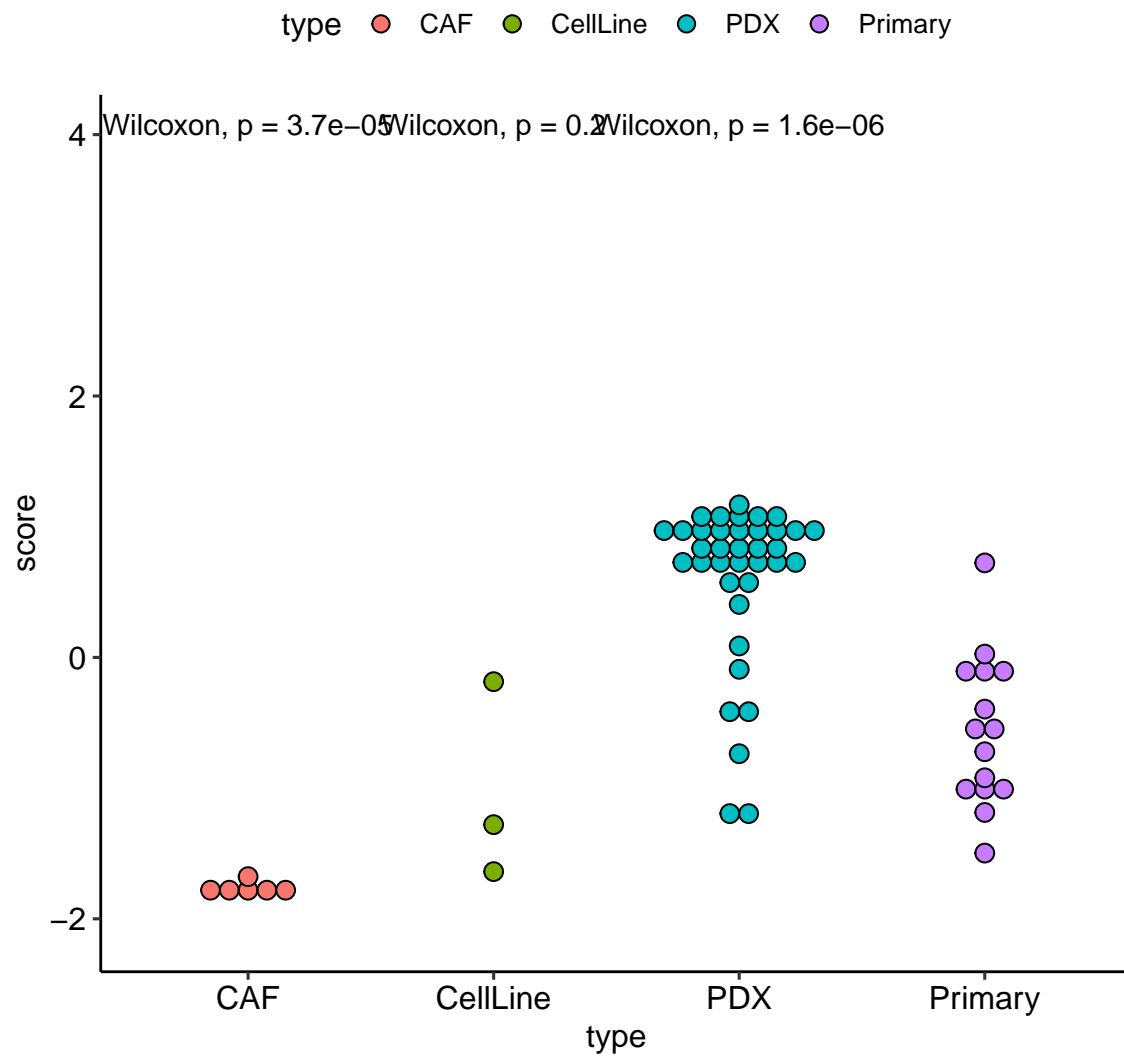


## Moffitt.F7\_Immune.top100 score

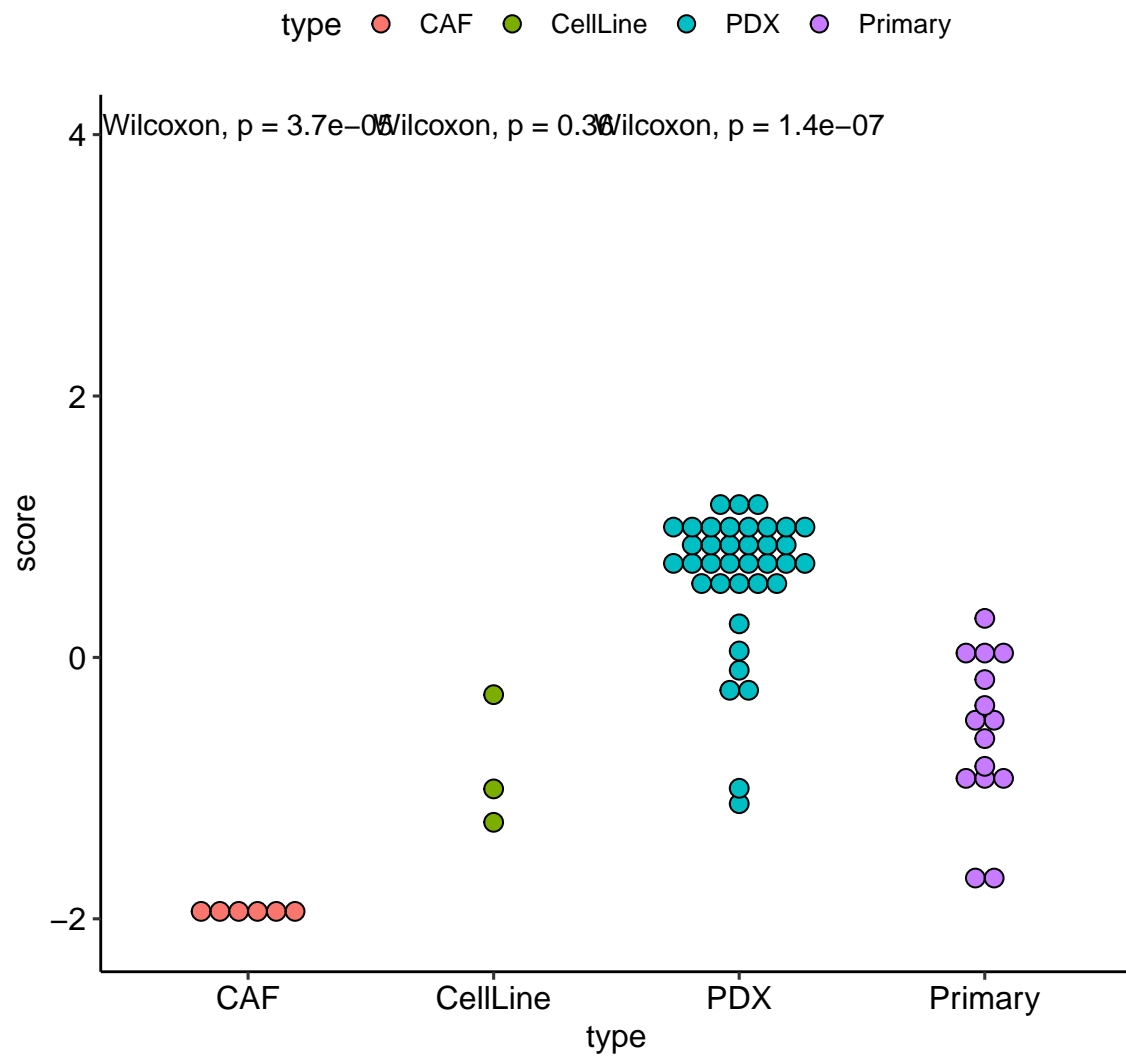




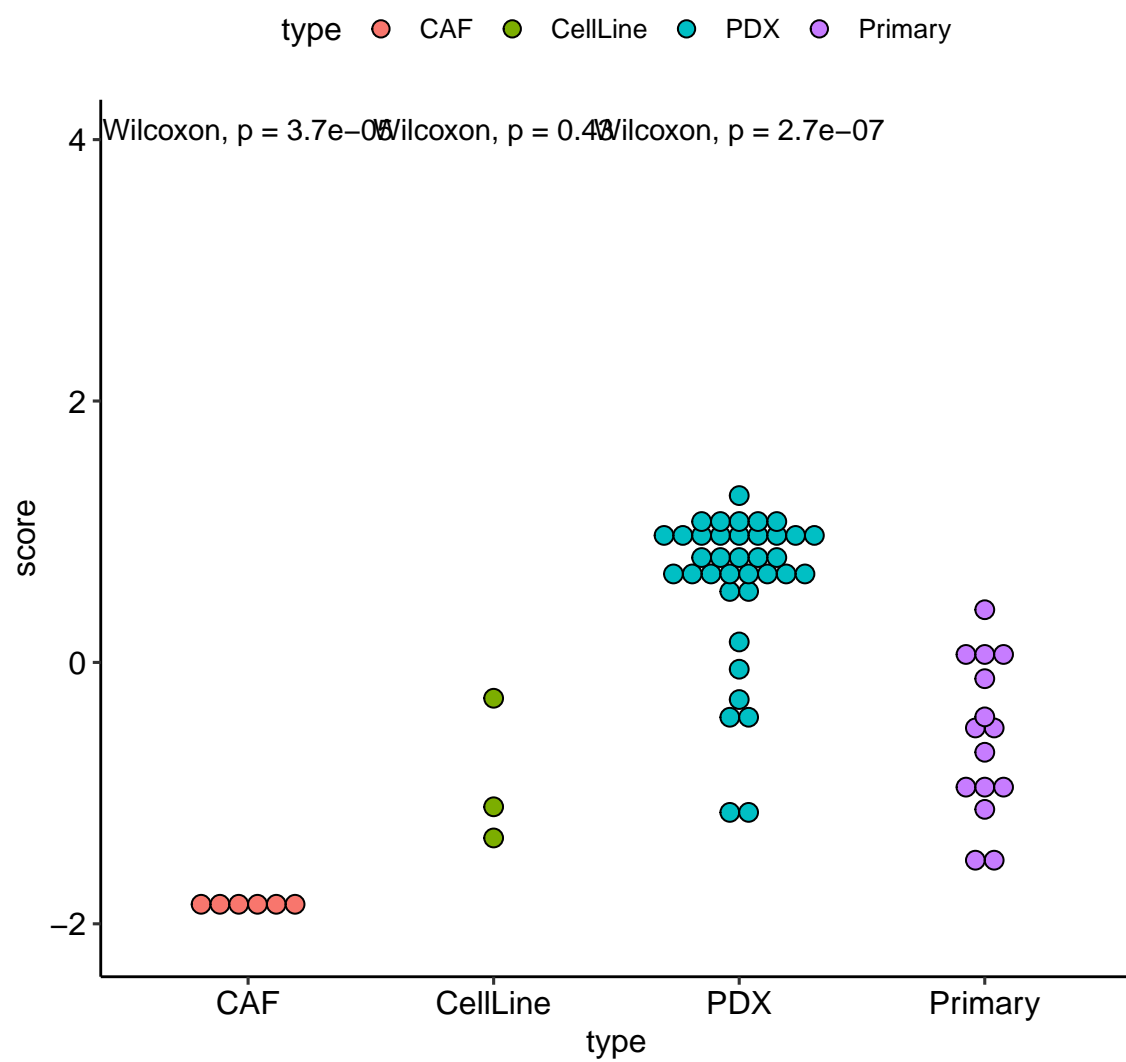
## Moffitt.F8\_Classical.top25 score



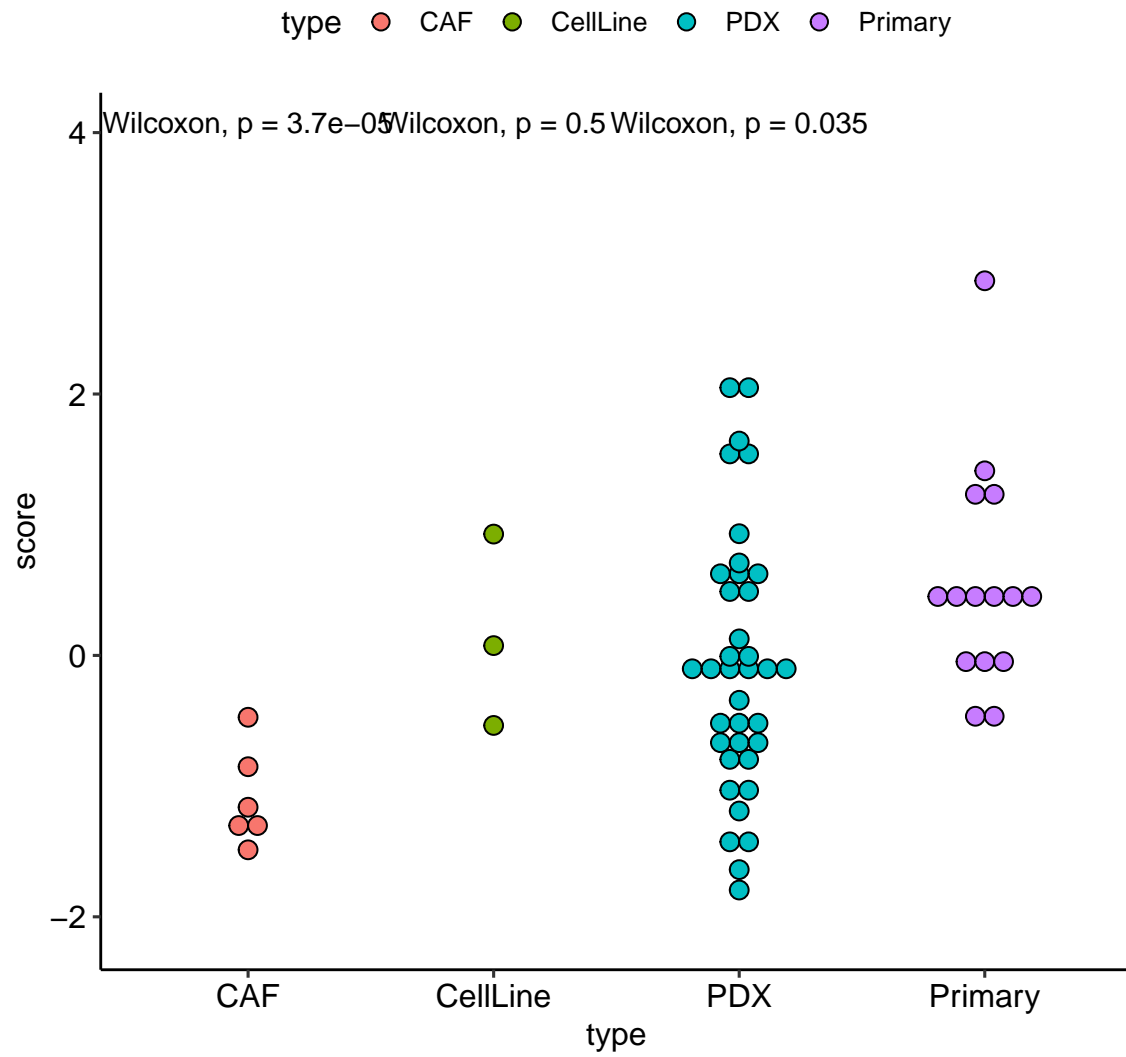
# Moffitt.F8\_Classical.top250 score



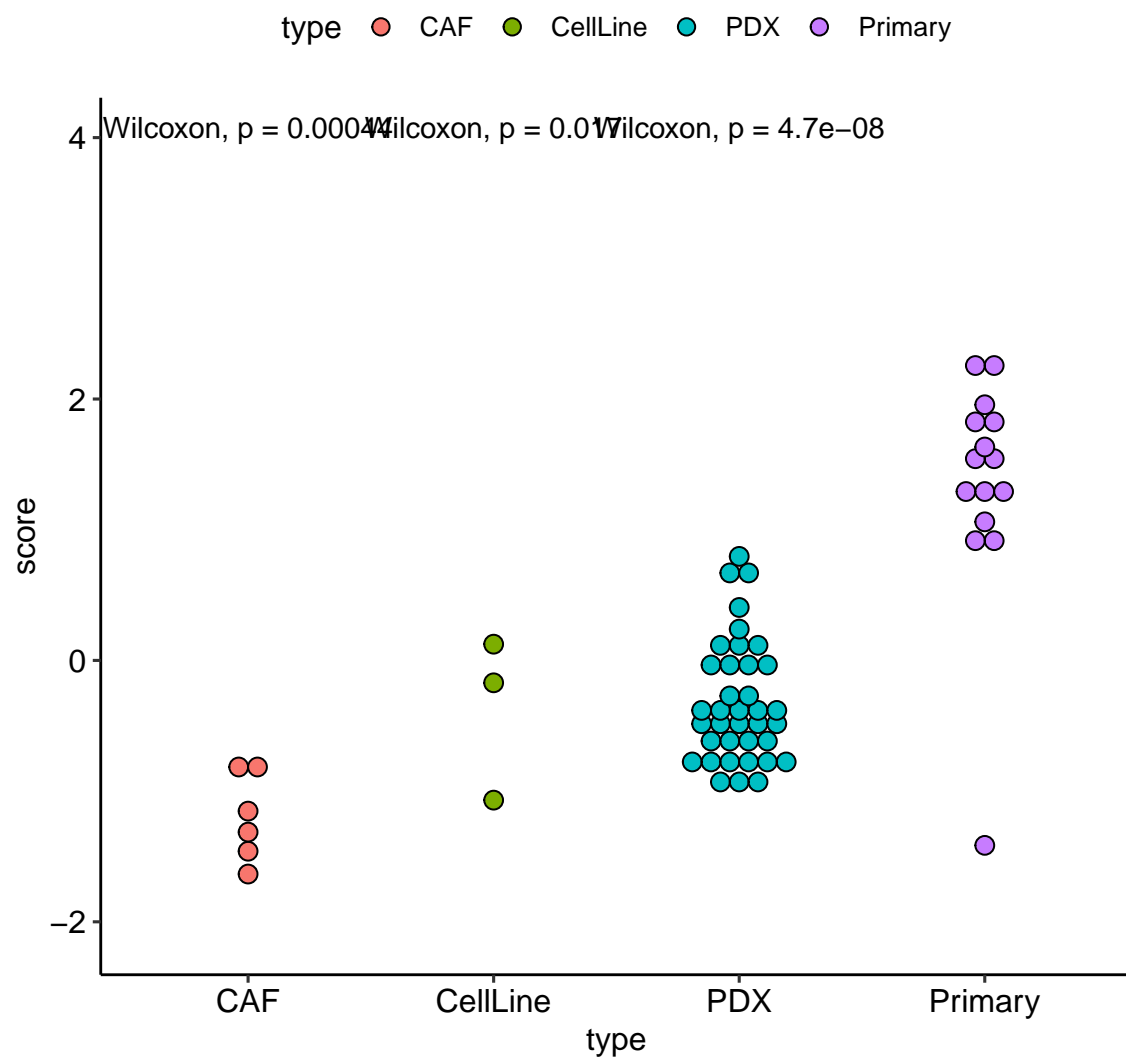
# Moffitt.F8\_Classical.top100 score



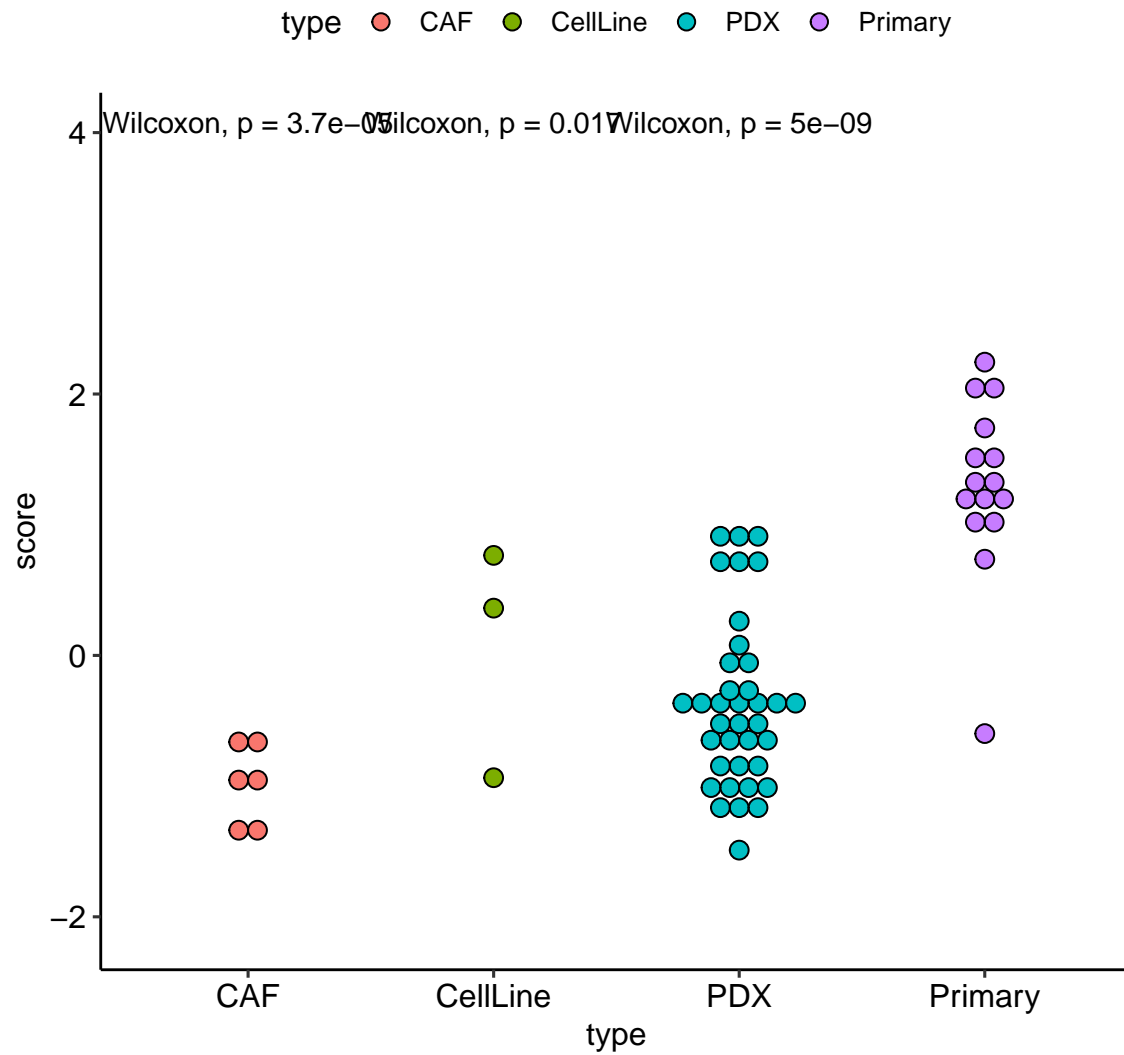
# Moffitt.F9\_Lung.top25 score



# Moffitt.F9\_Lung.top250 score



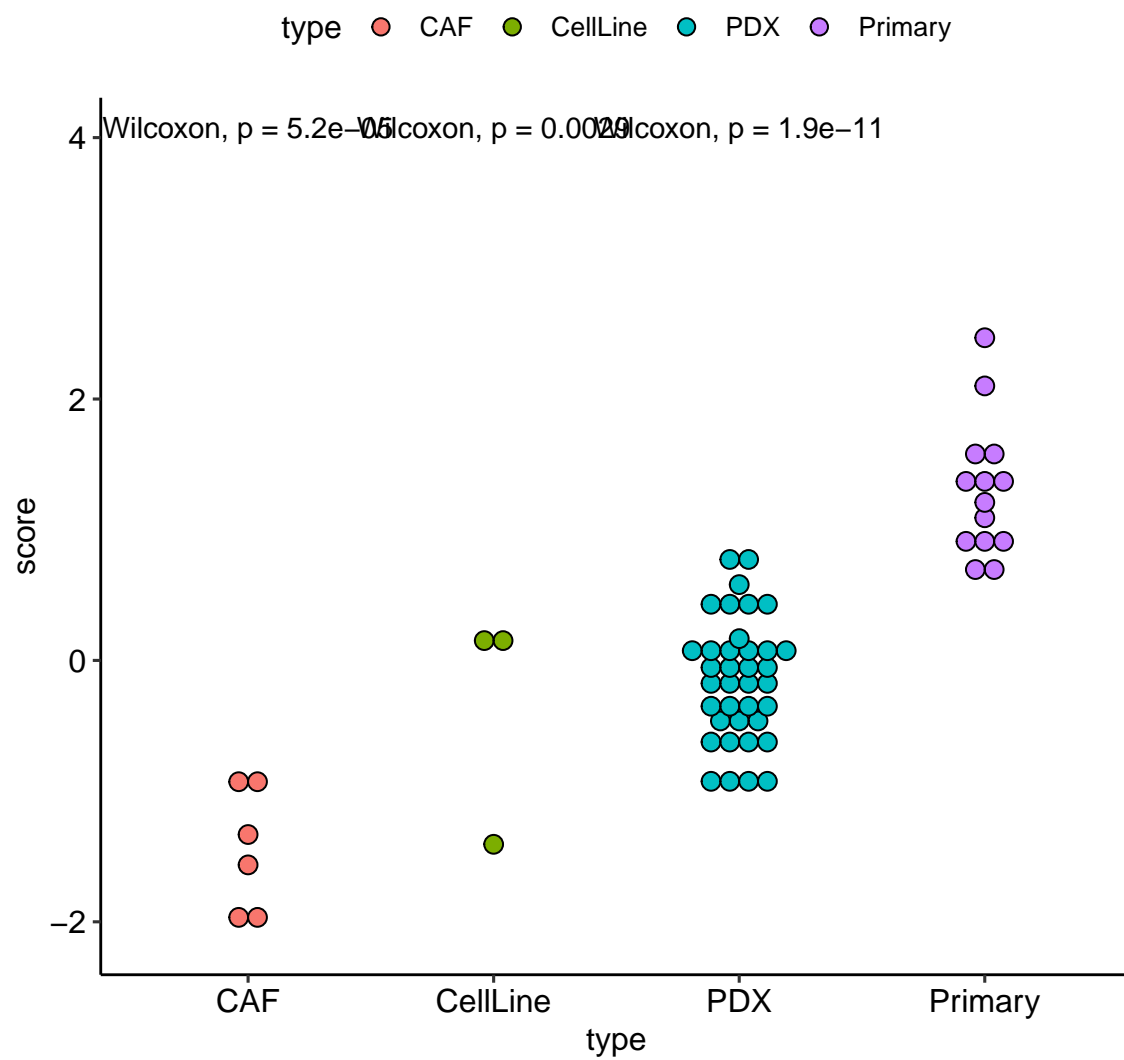
# Moffitt.F9\_Lung.top100 score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

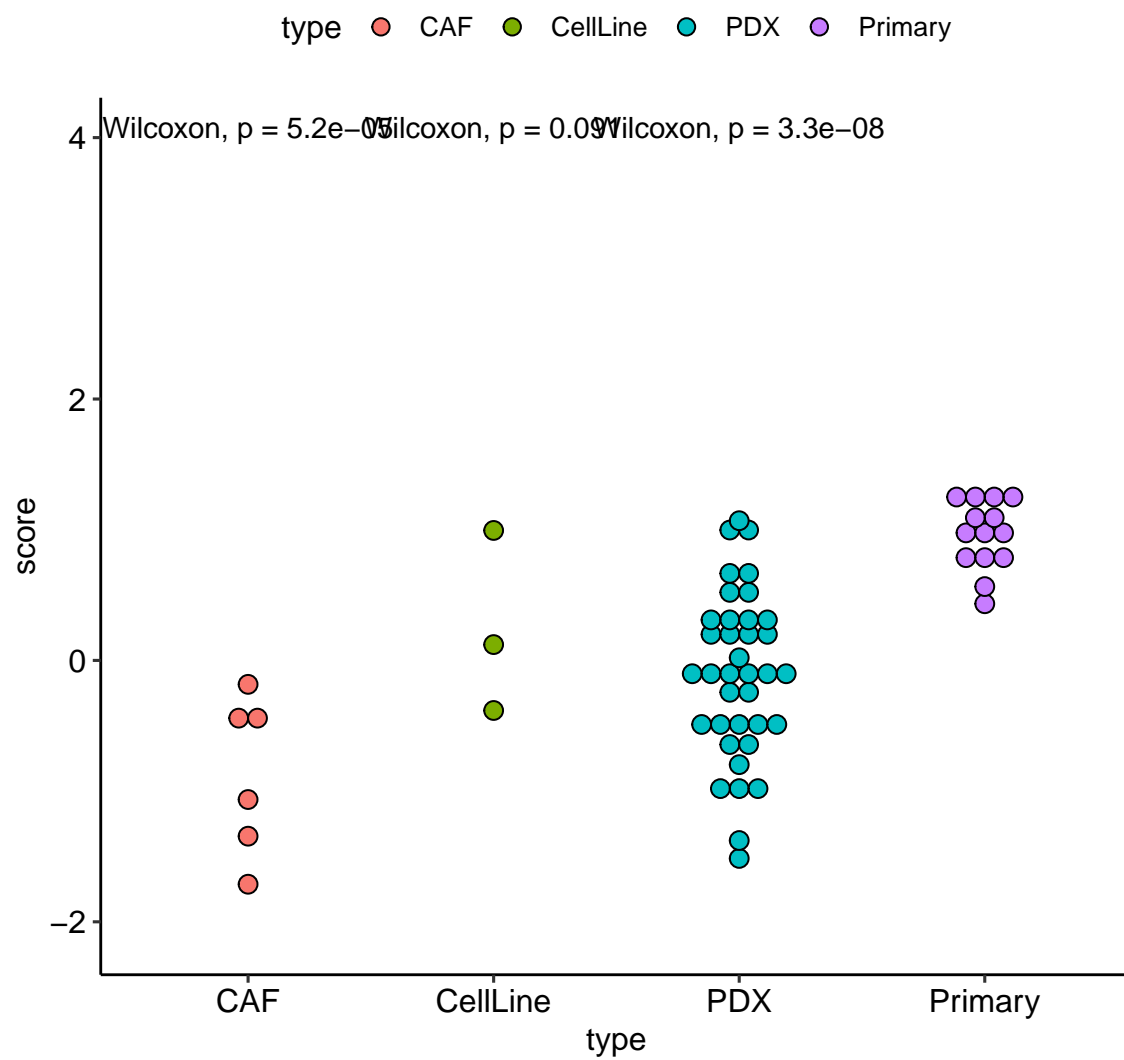
# Moffitt.F10.top25 score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

## Moffitt.F10.top250 score

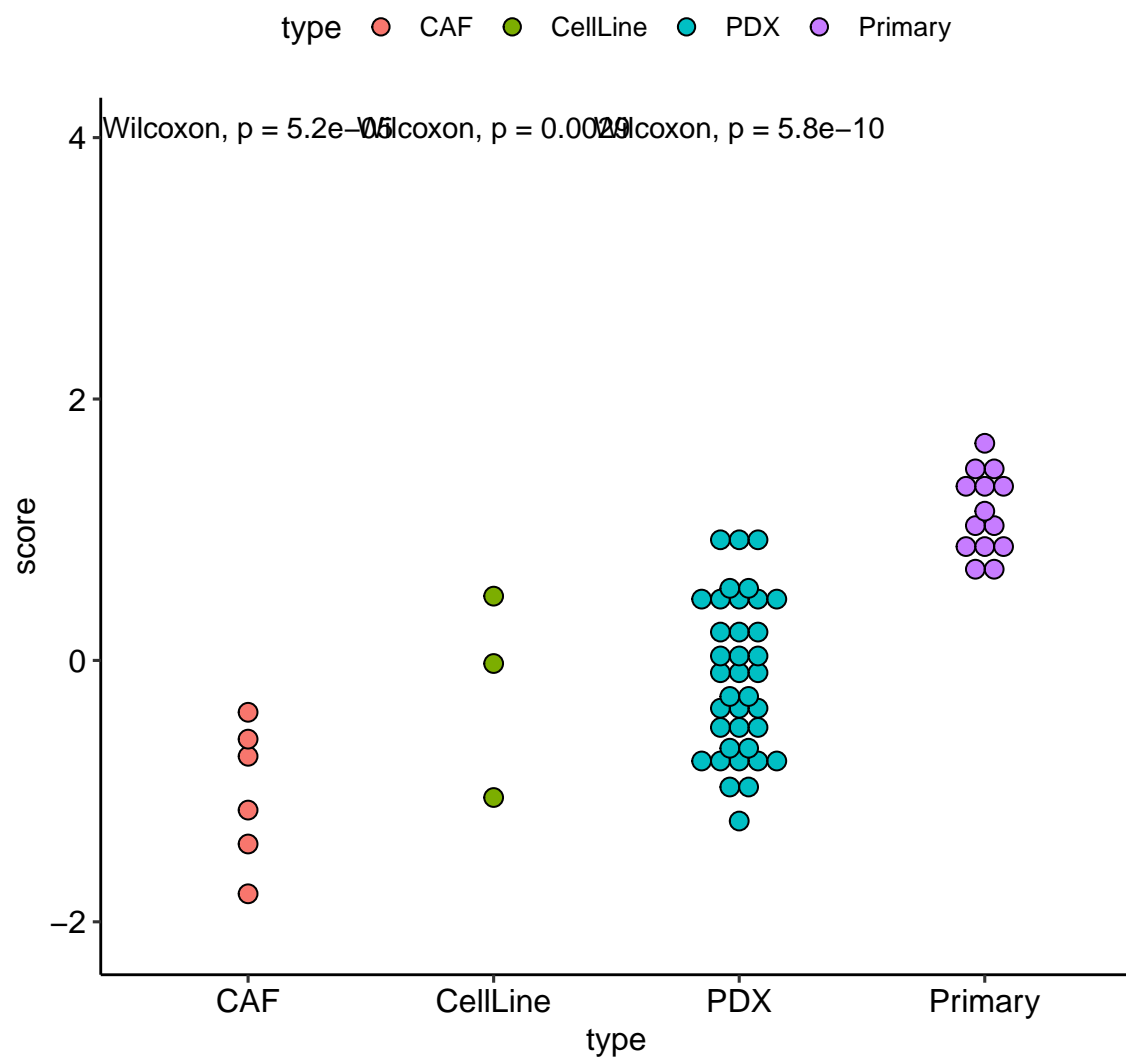


## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

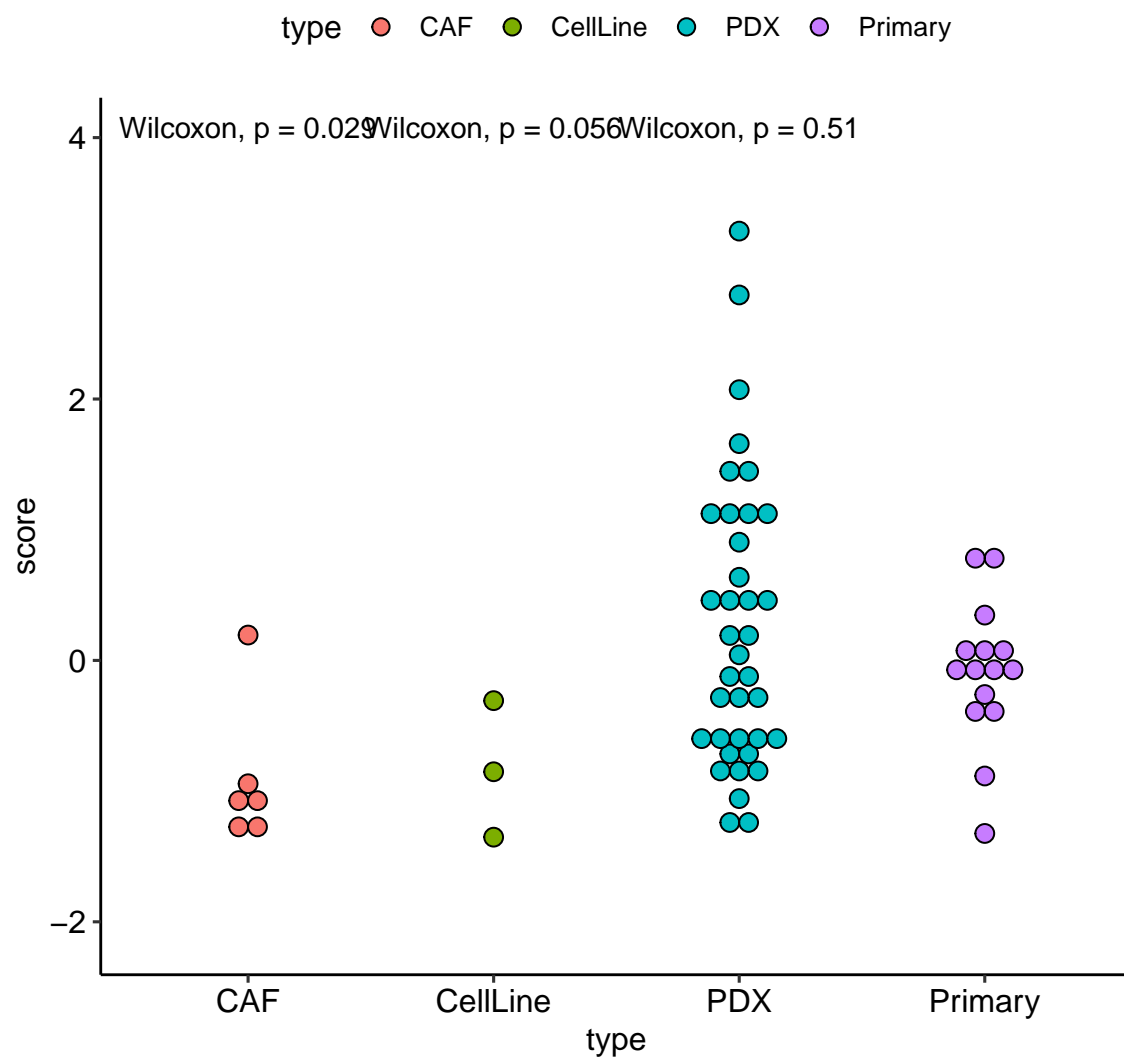
## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).



# Moffitt.F10.top100 score



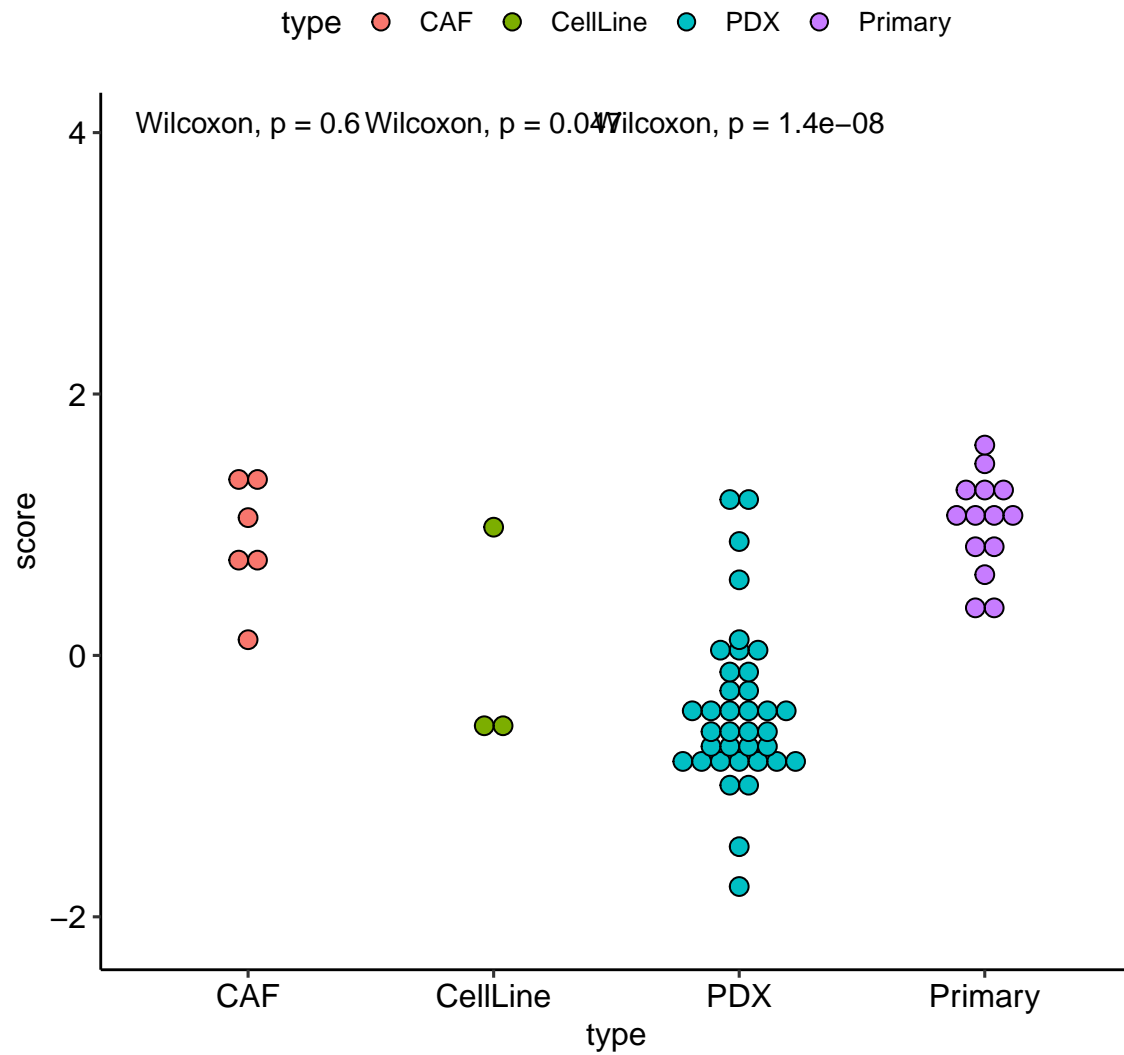
# Moffitt.F11\_Muscle.top25 score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

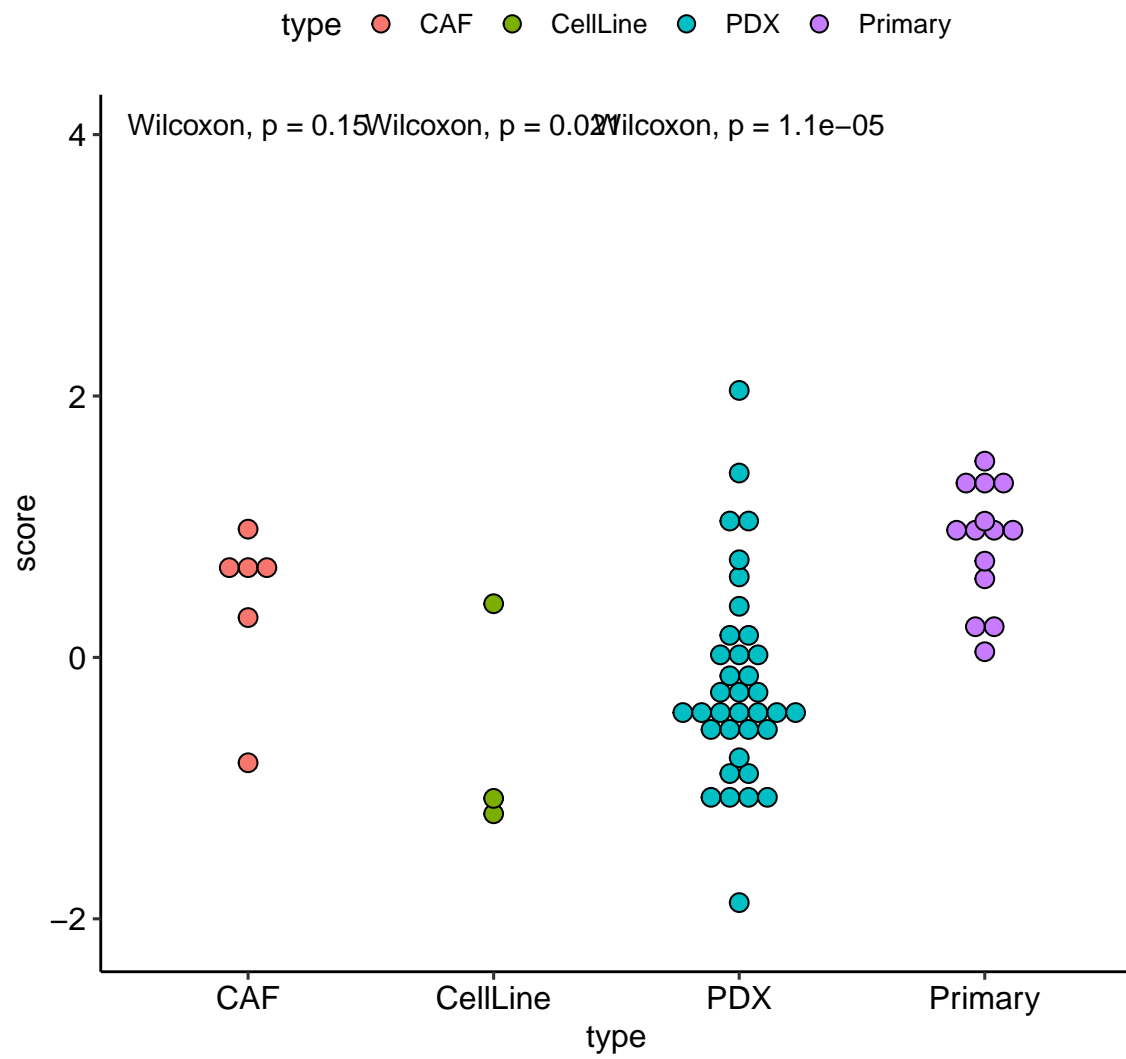
## Moffitt.F11\_Muscle.top250 score



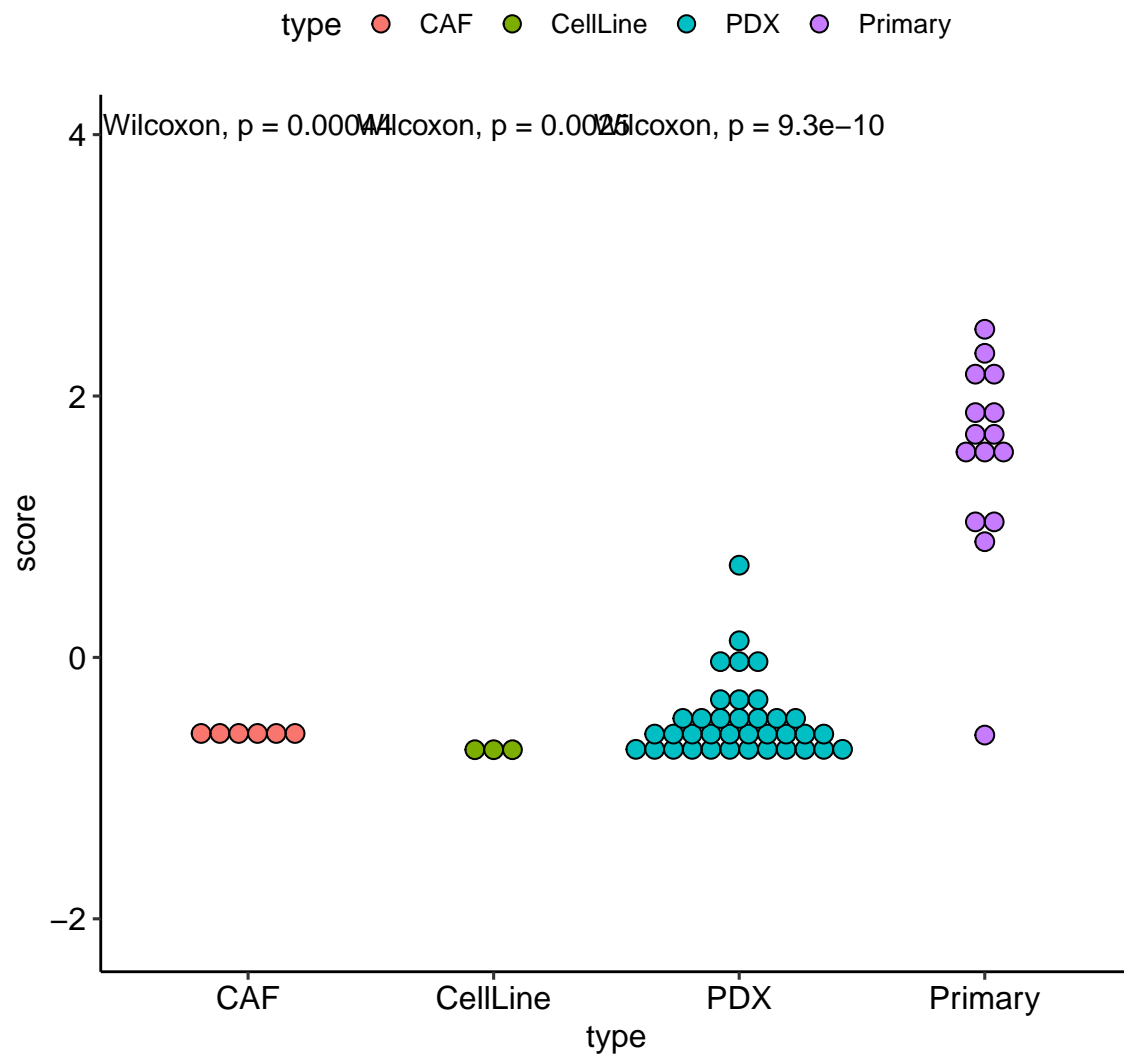
```
## Warning: Removed 2 rows containing non-finite values (stat_bindot).
```

```
## Warning: Removed 2 rows containing non-finite values (stat_compare_means).
```

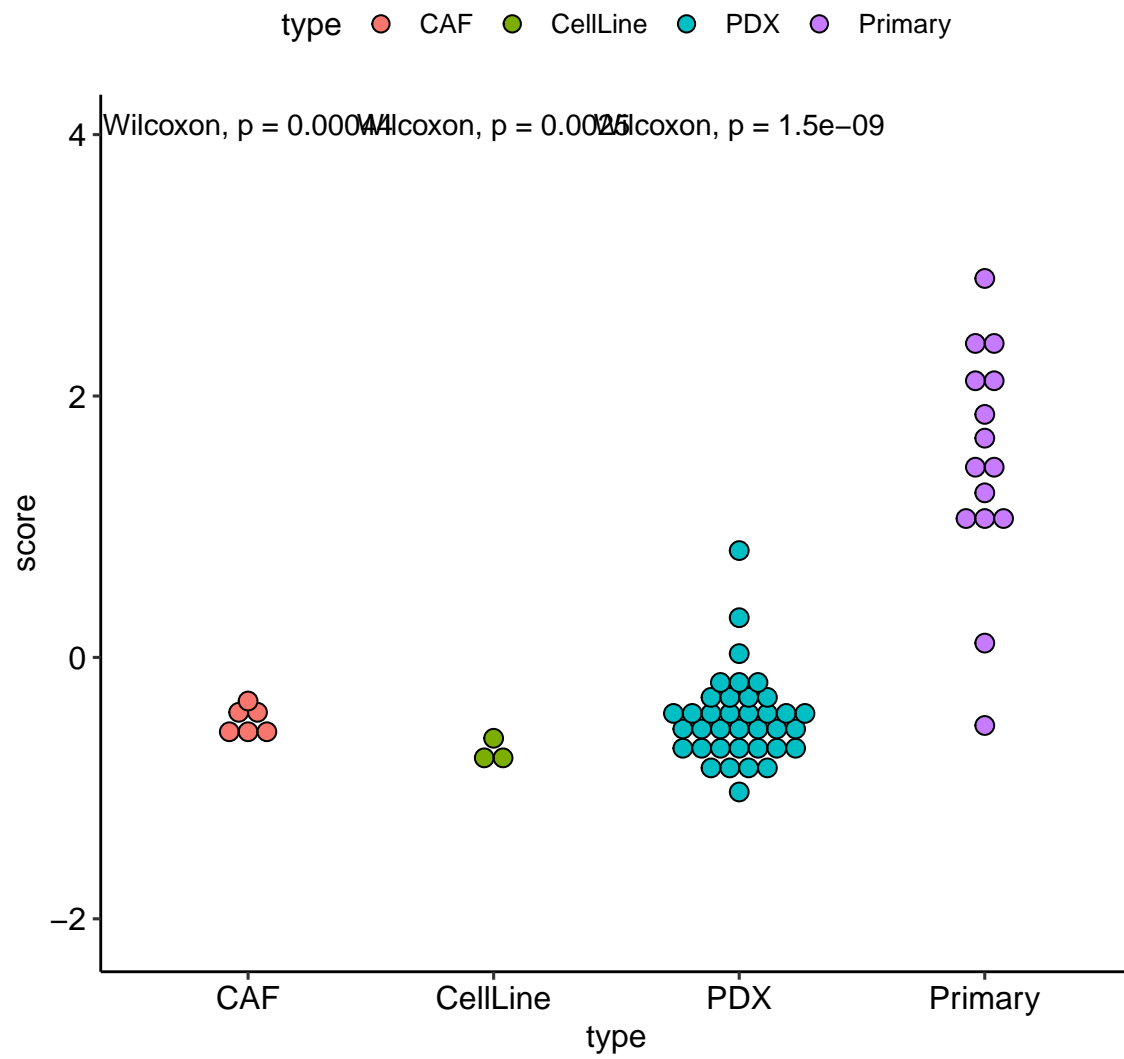
# Moffitt.F11\_Muscle.top100 score



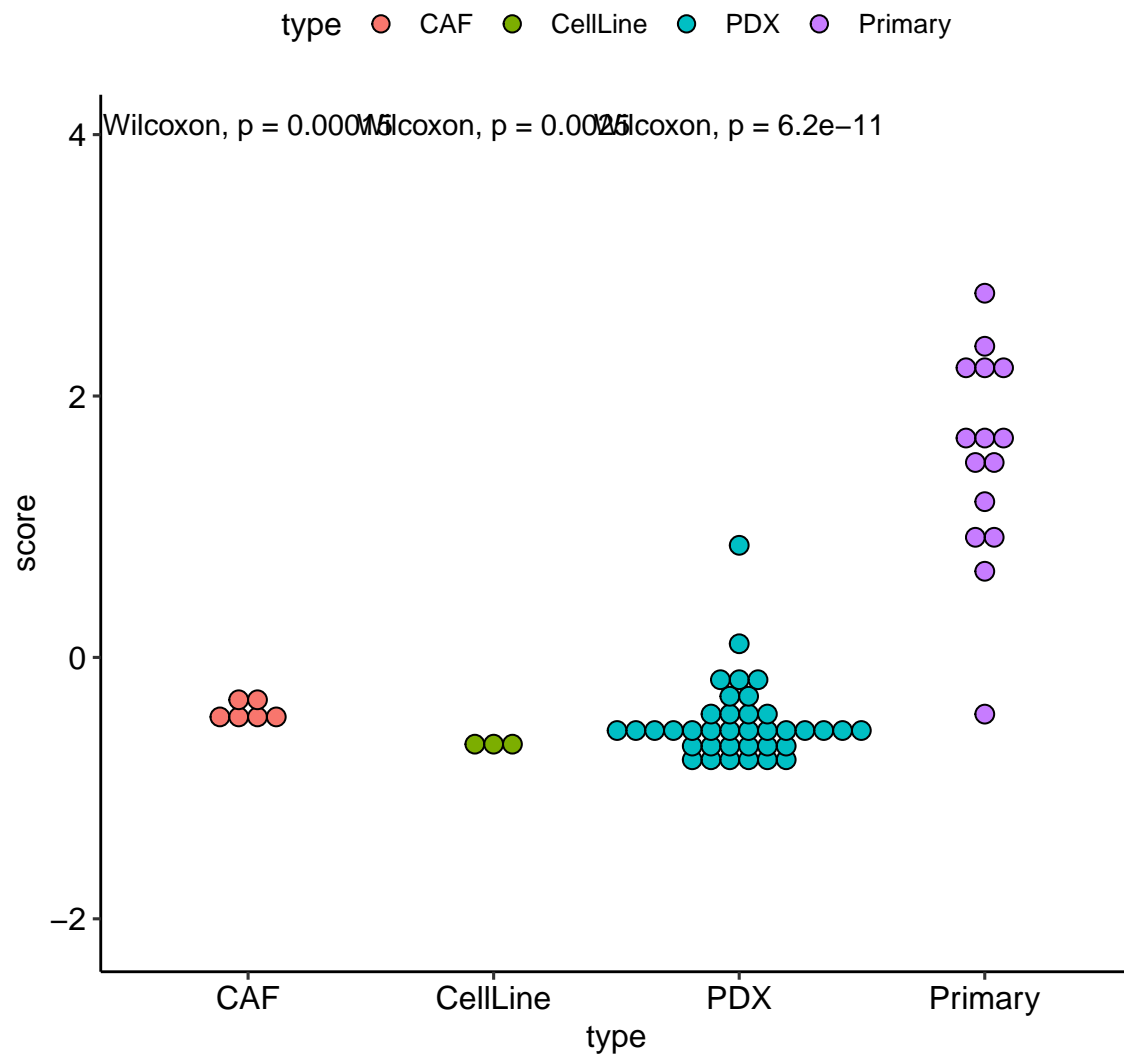
## Moffitt.F12\_Endocrine.top25 score



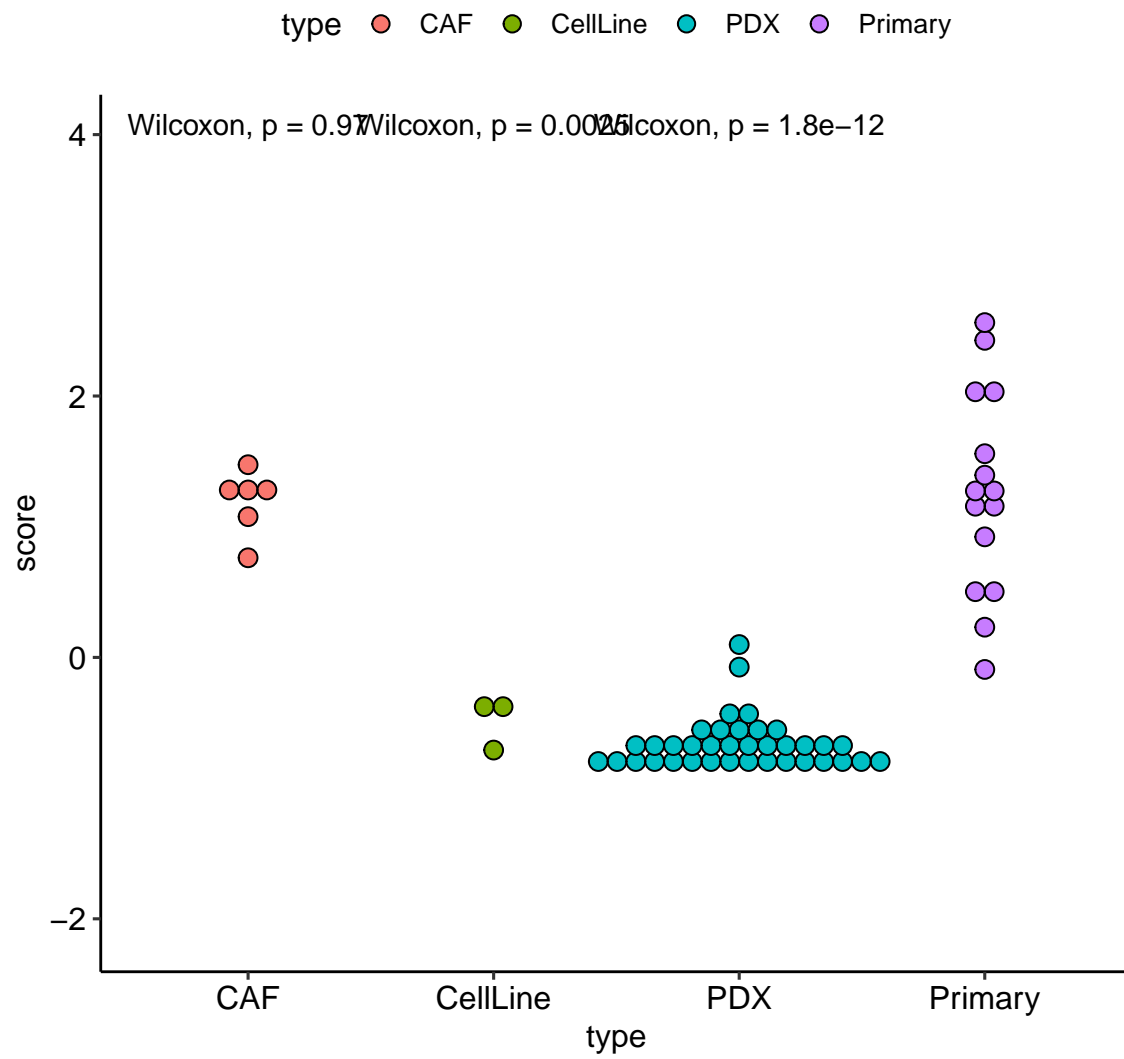
## Moffitt.F12\_Endocrine.top250 score



## Moffitt.F12\_Endocrine.top100 score

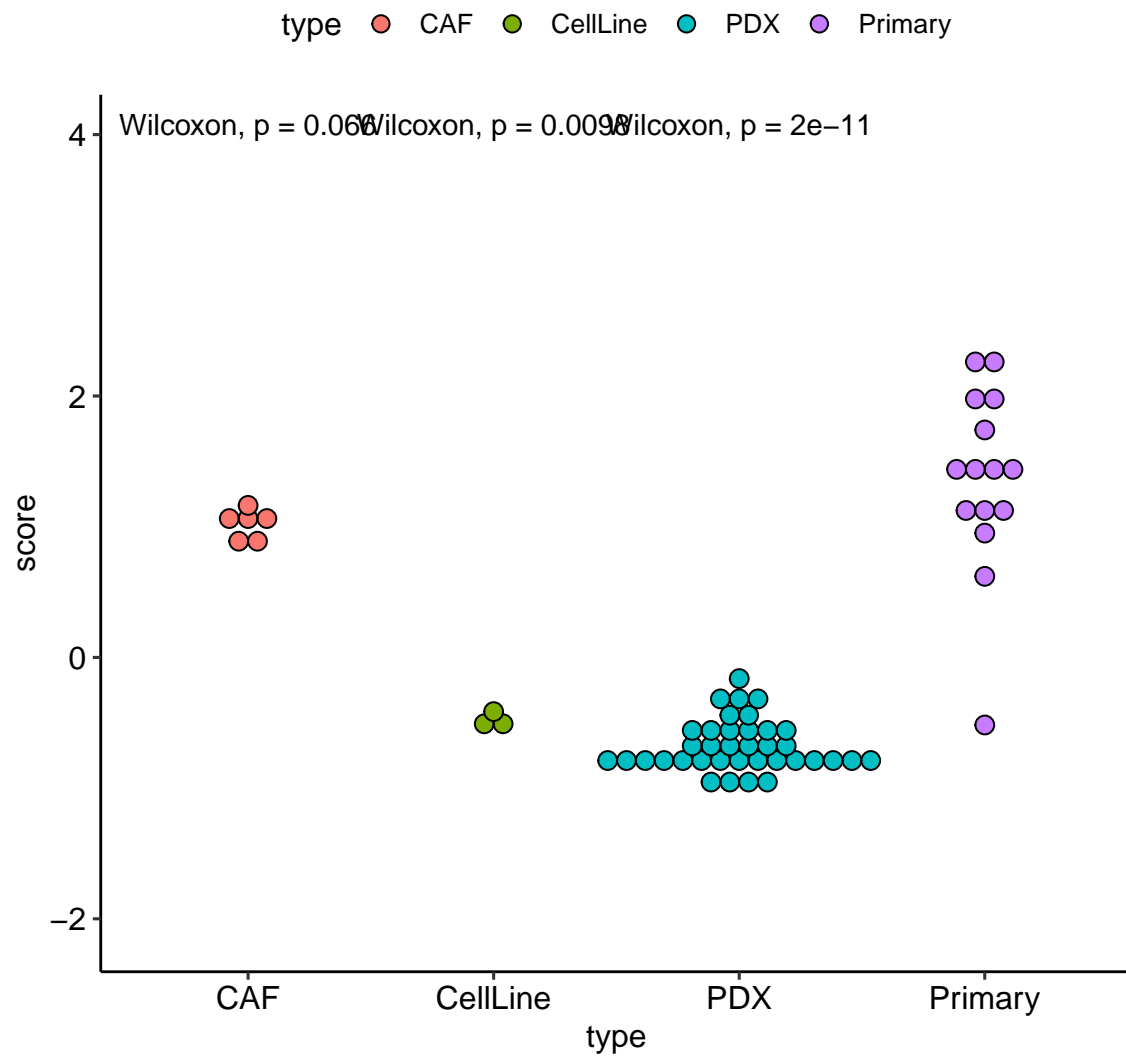


## Moffitt.F13\_NormalStroma.top25 score

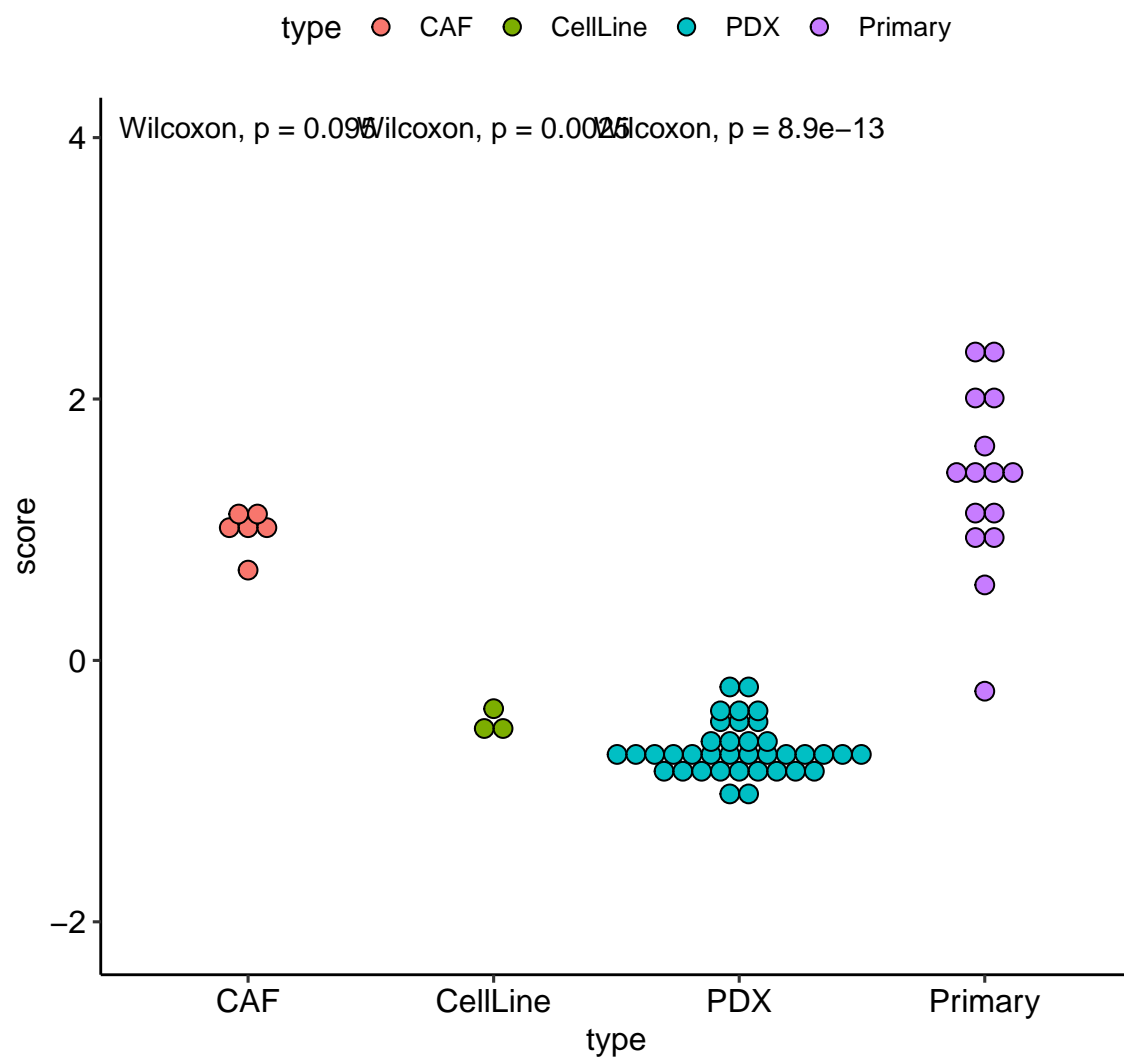




# Moffitt.F13\_NormalStroma.top250 score



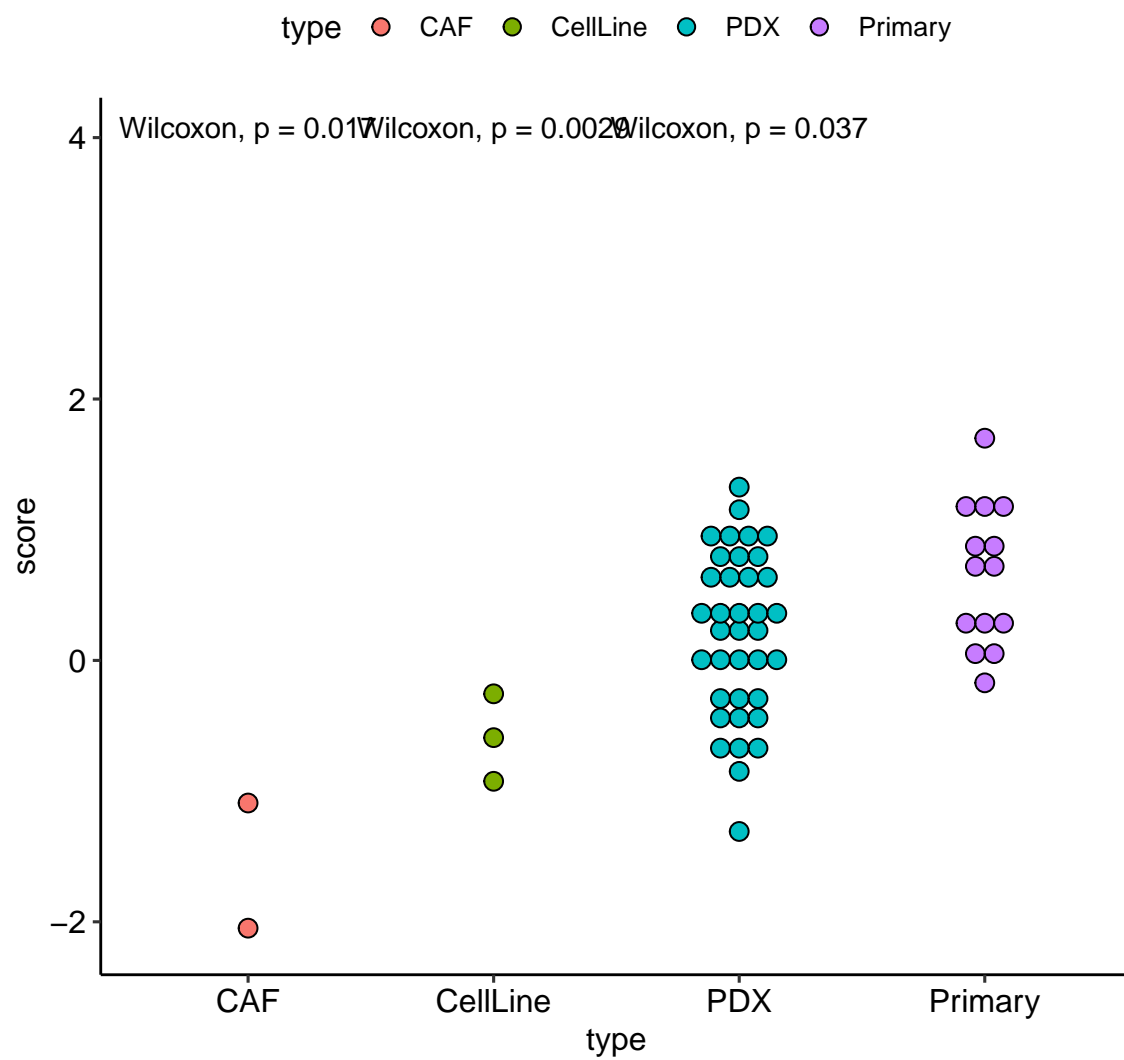
# Moffitt.F13\_NormalStroma.top100 score



## Warning: Removed 5 rows containing non-finite values (stat\_bindot).

## Warning: Removed 5 rows containing non-finite values (stat\_compare\_means).

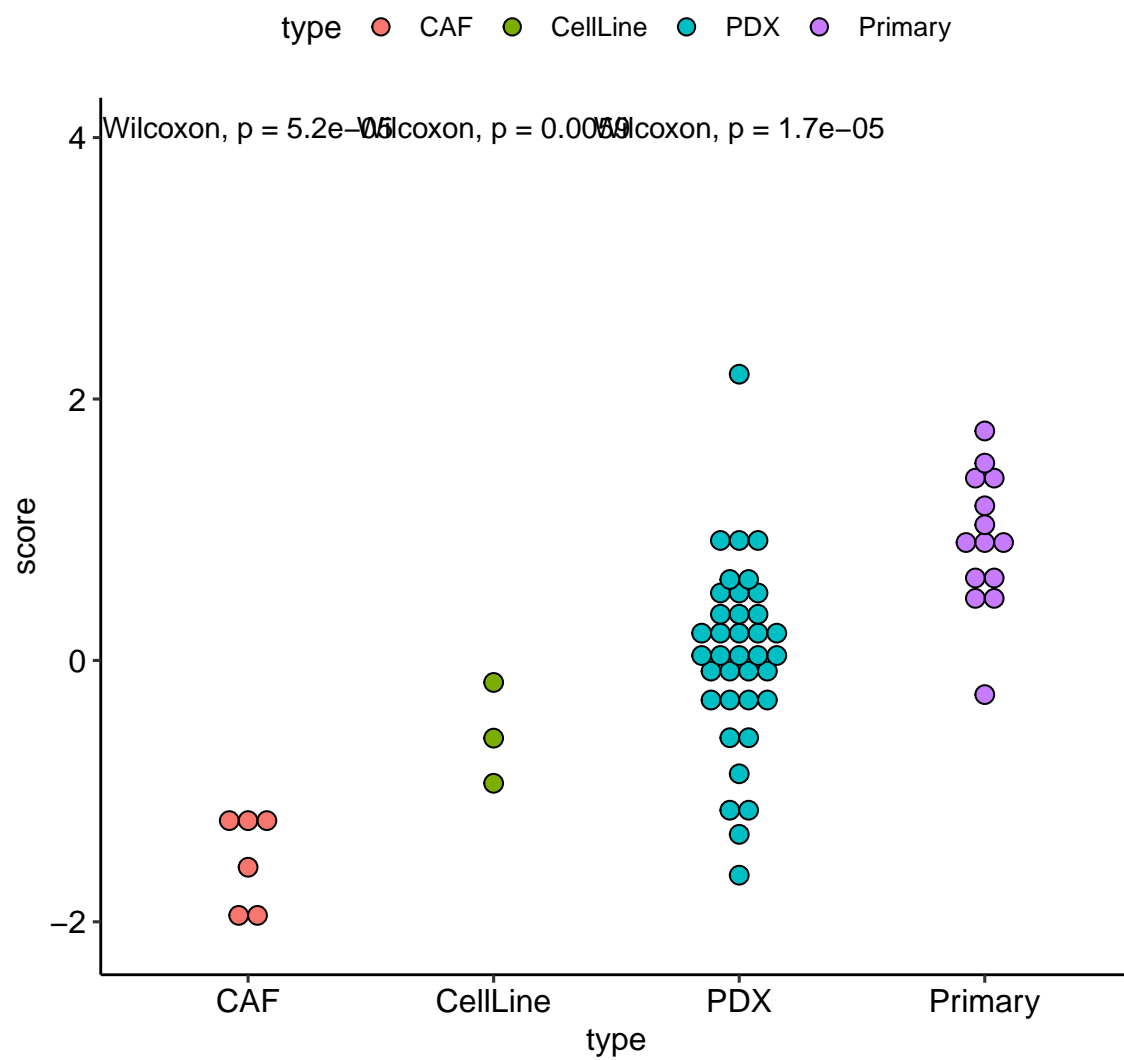
## Moffitt.F14.top25 score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

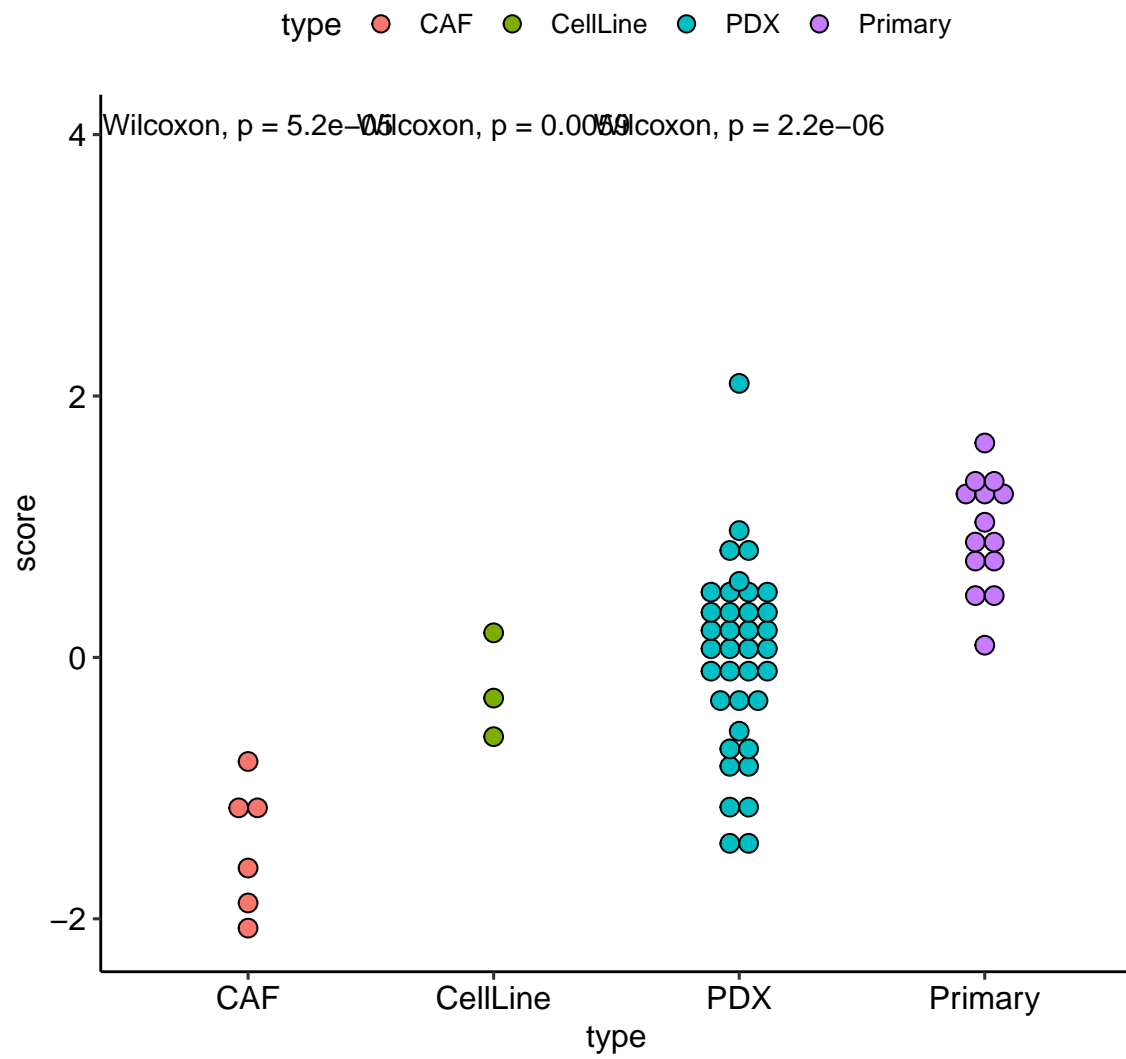
## Moffitt.F14.top250 score



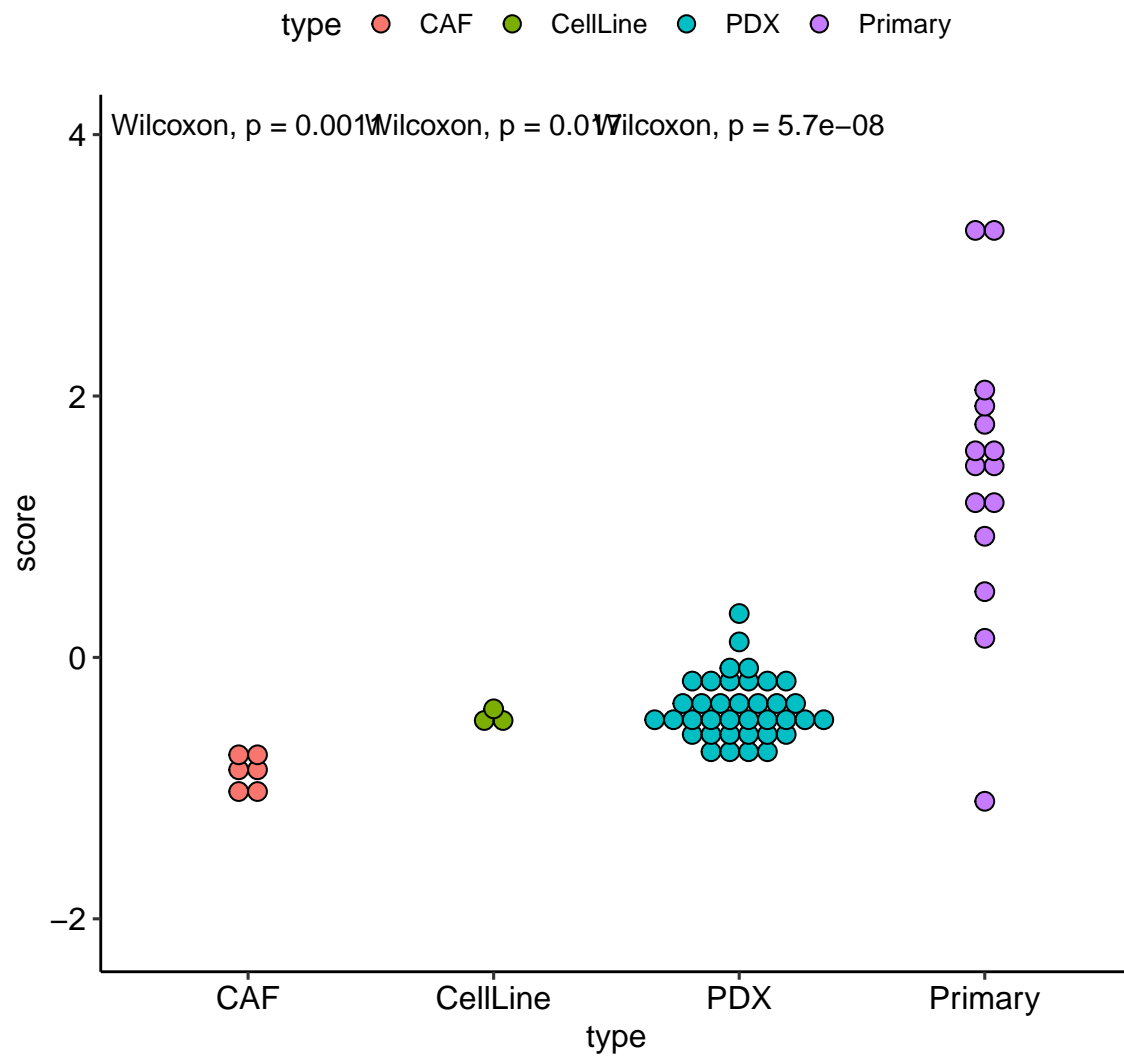
## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

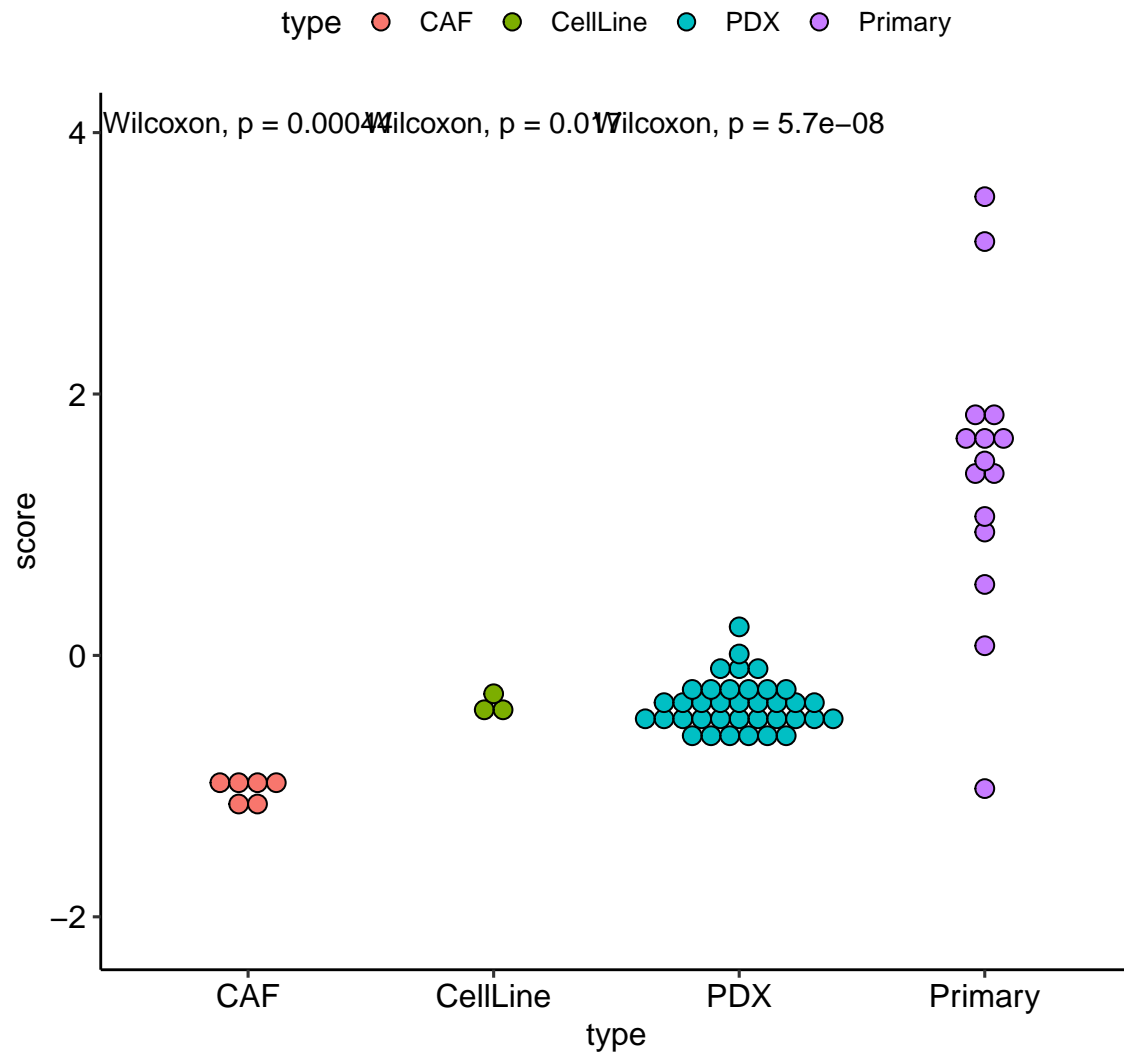
# Moffitt.F14.top100 score



CIBERSORT.B.cells.naive score



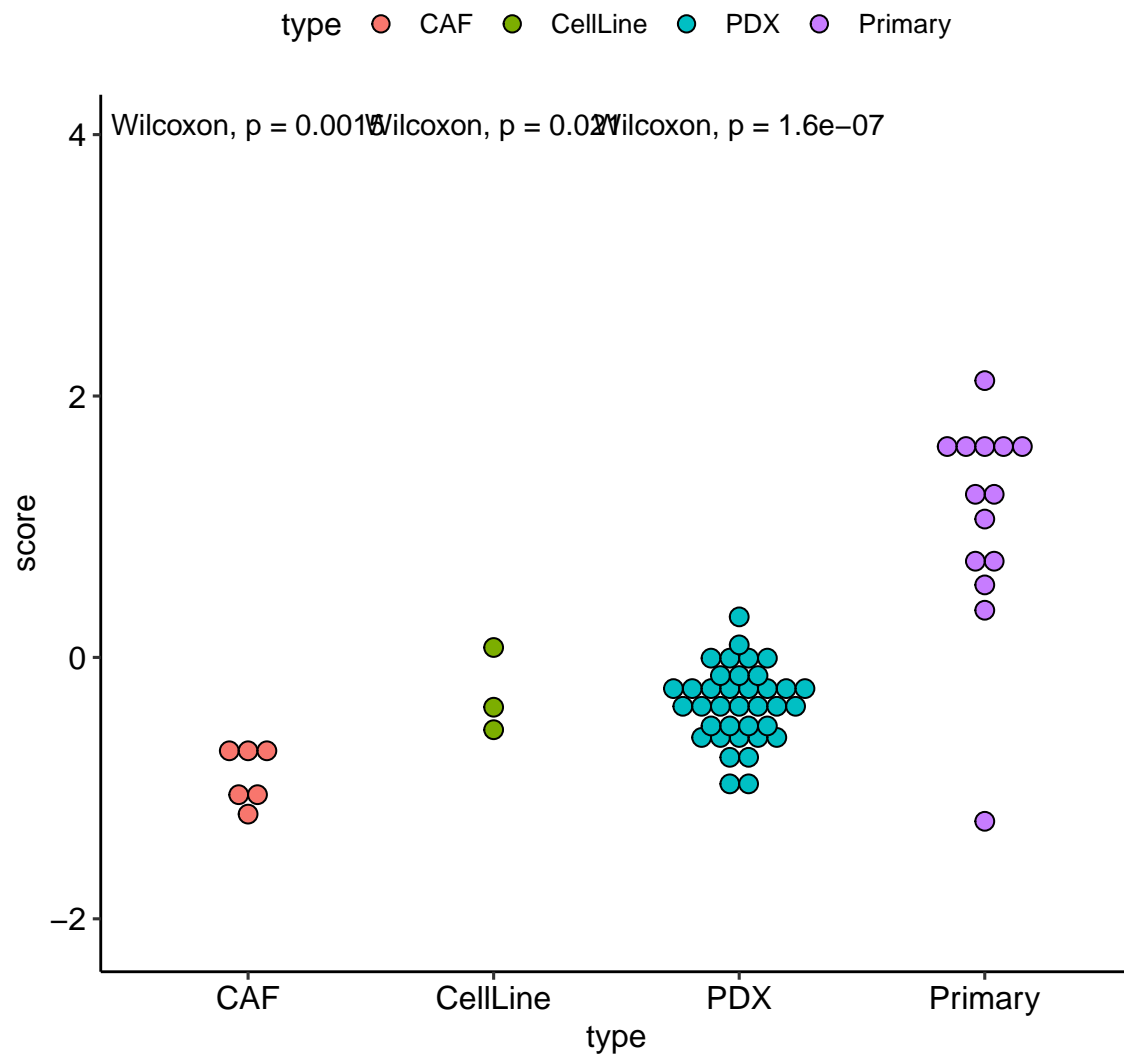
# CIBERSORT.B.cells.memory score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

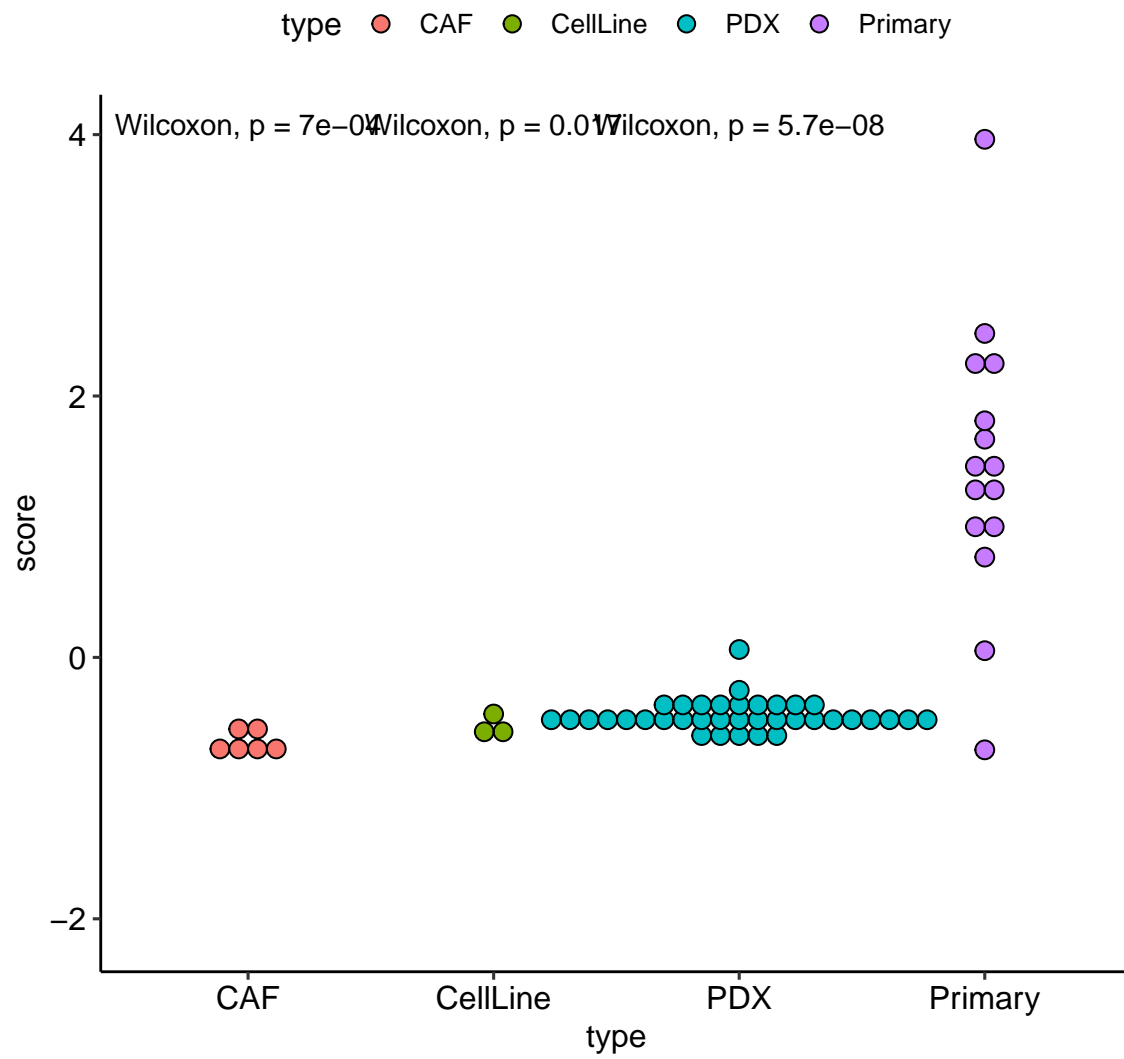
## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

CIBERSORT.Plasma.cells score

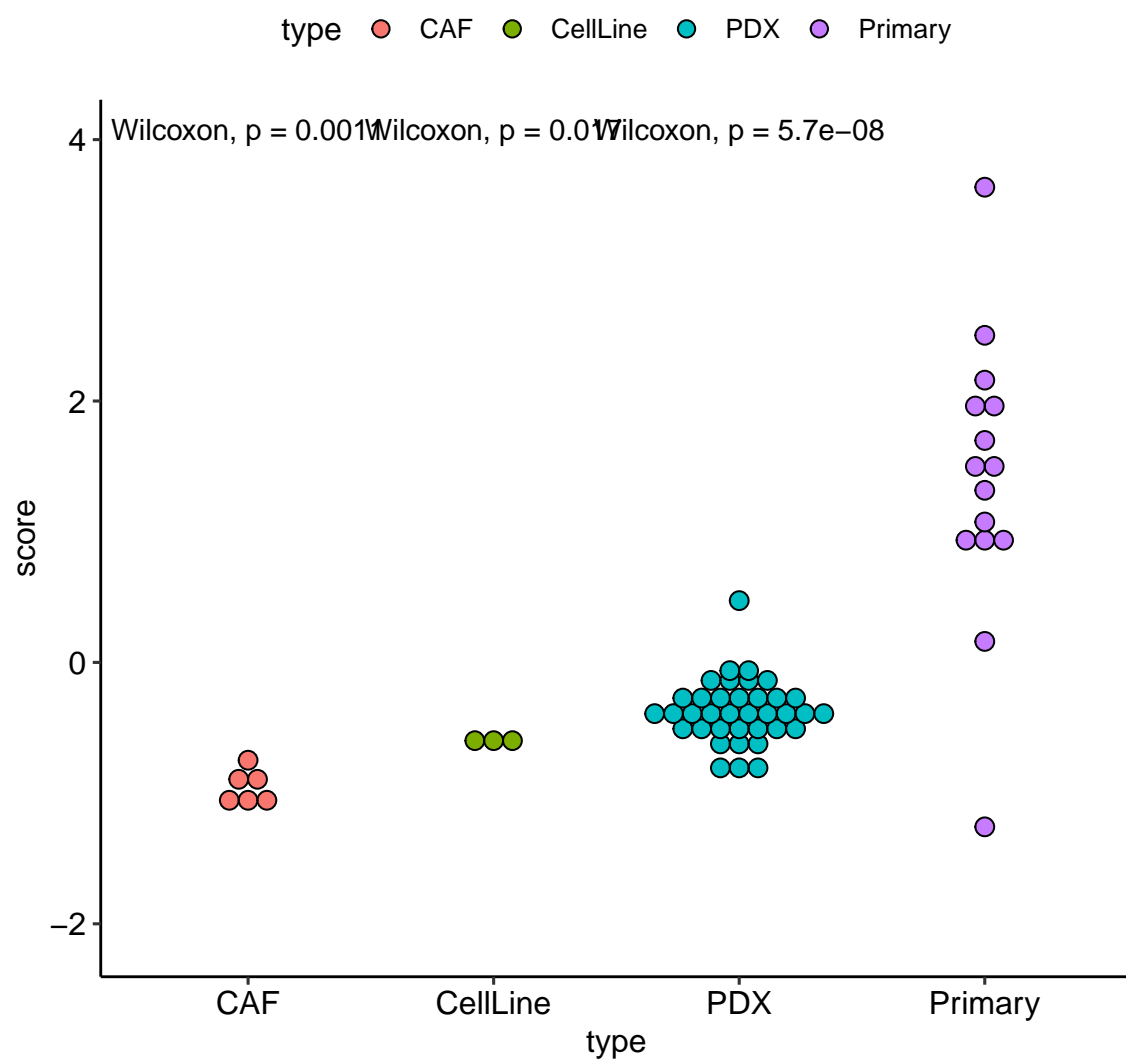




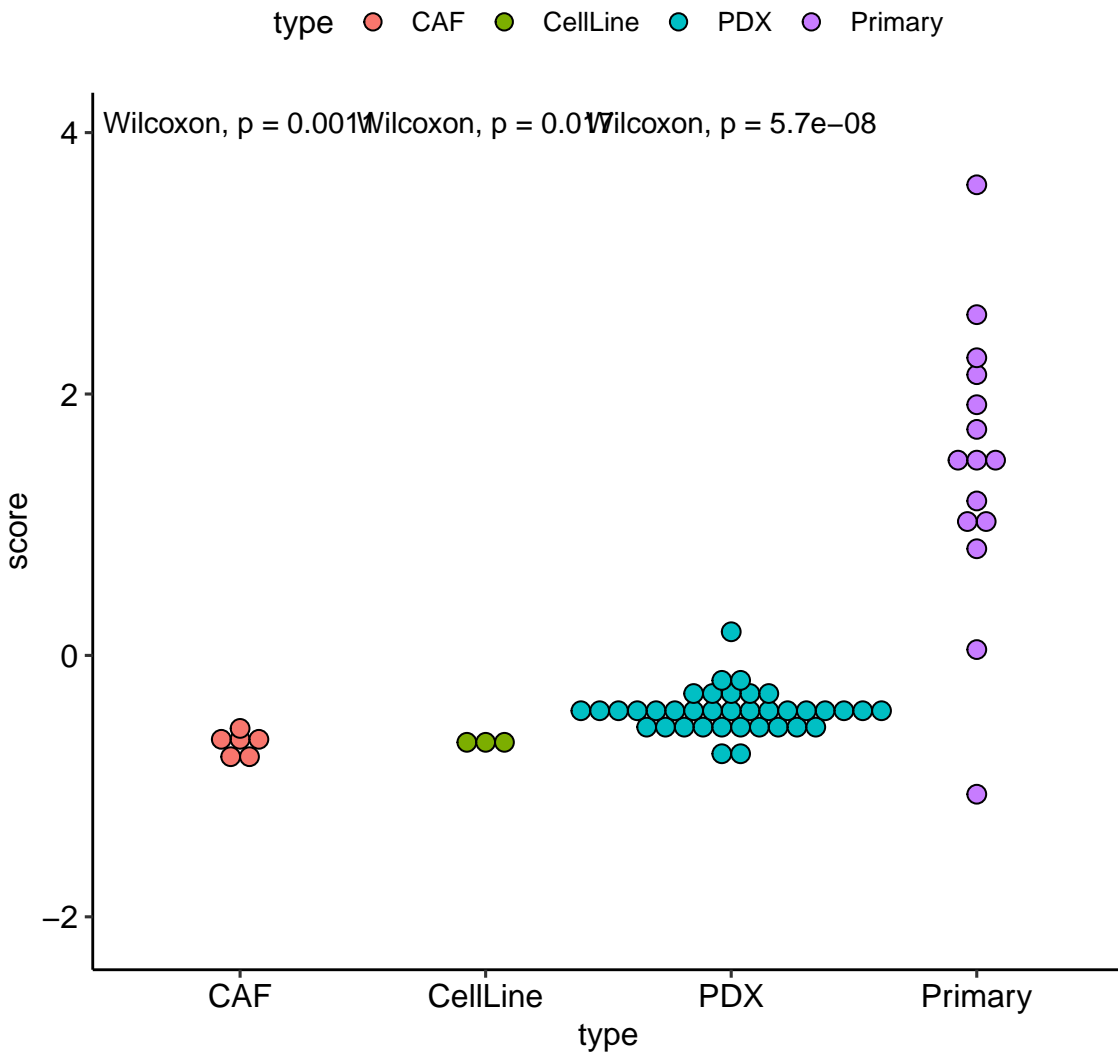
CIBERSORT.T.cells.CD8 score



# CIBERSORT.T.cells.CD4.naive score



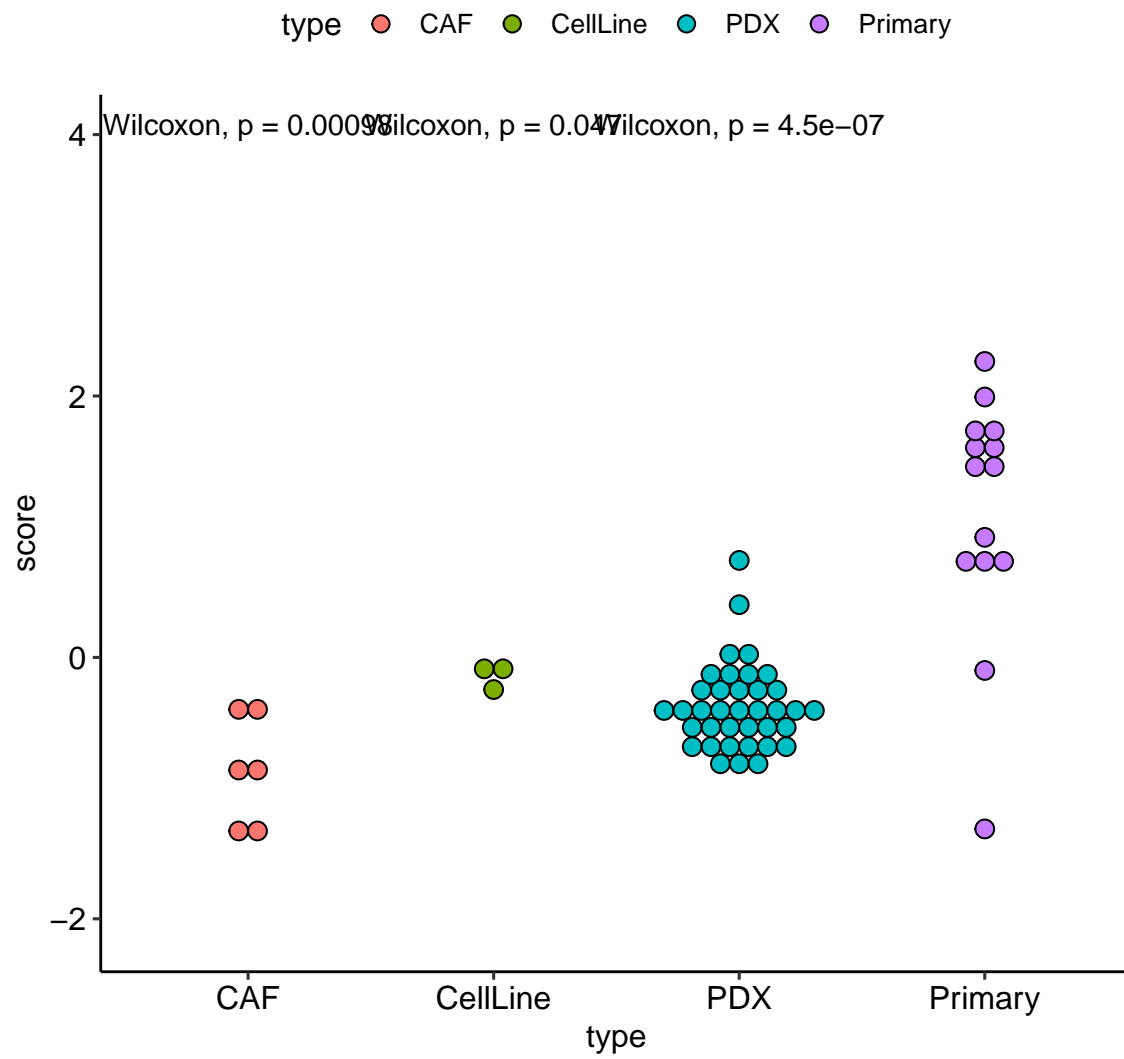
# CIBERSORT.T.cells.CD4.memory.resting score



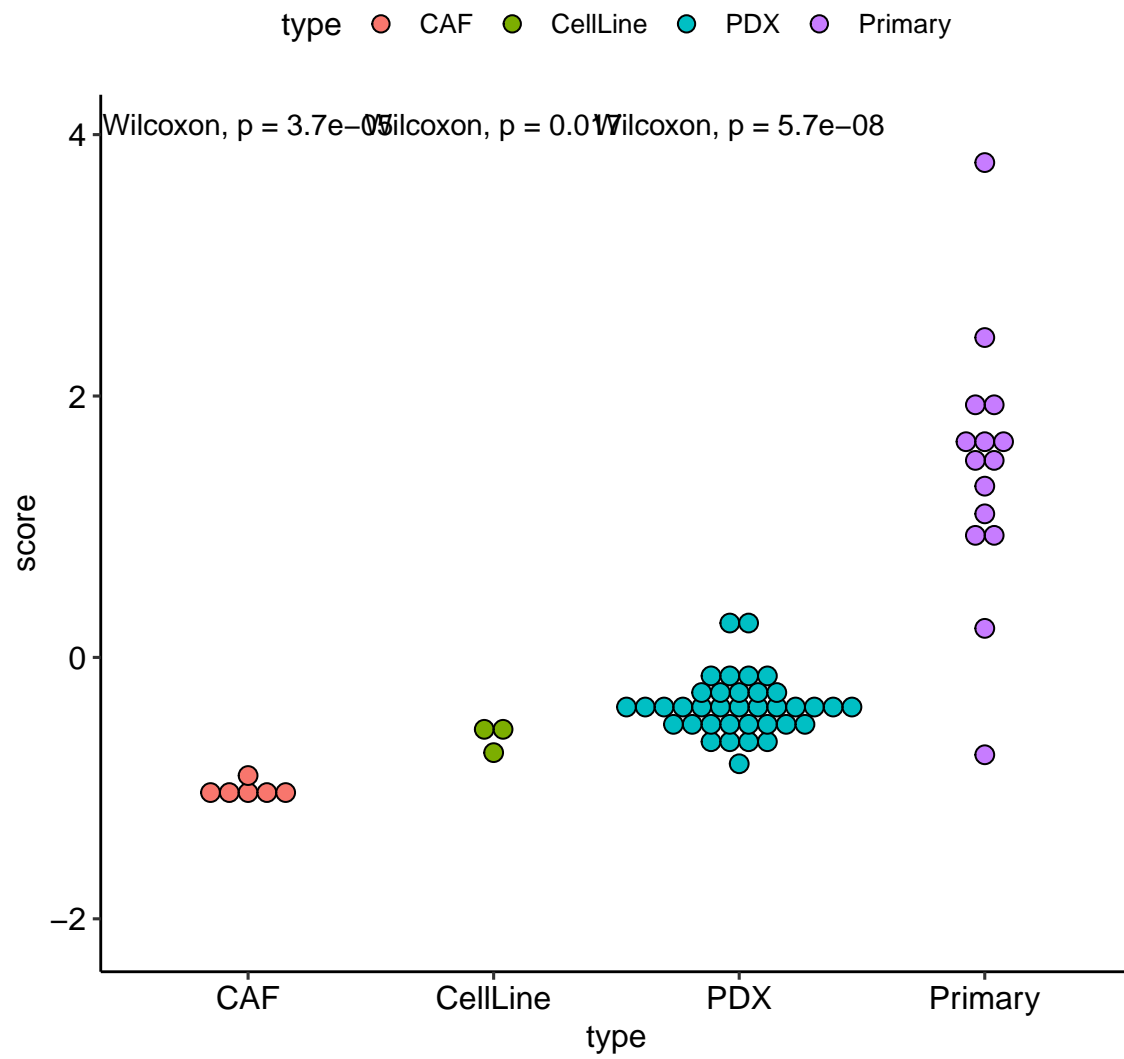
## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

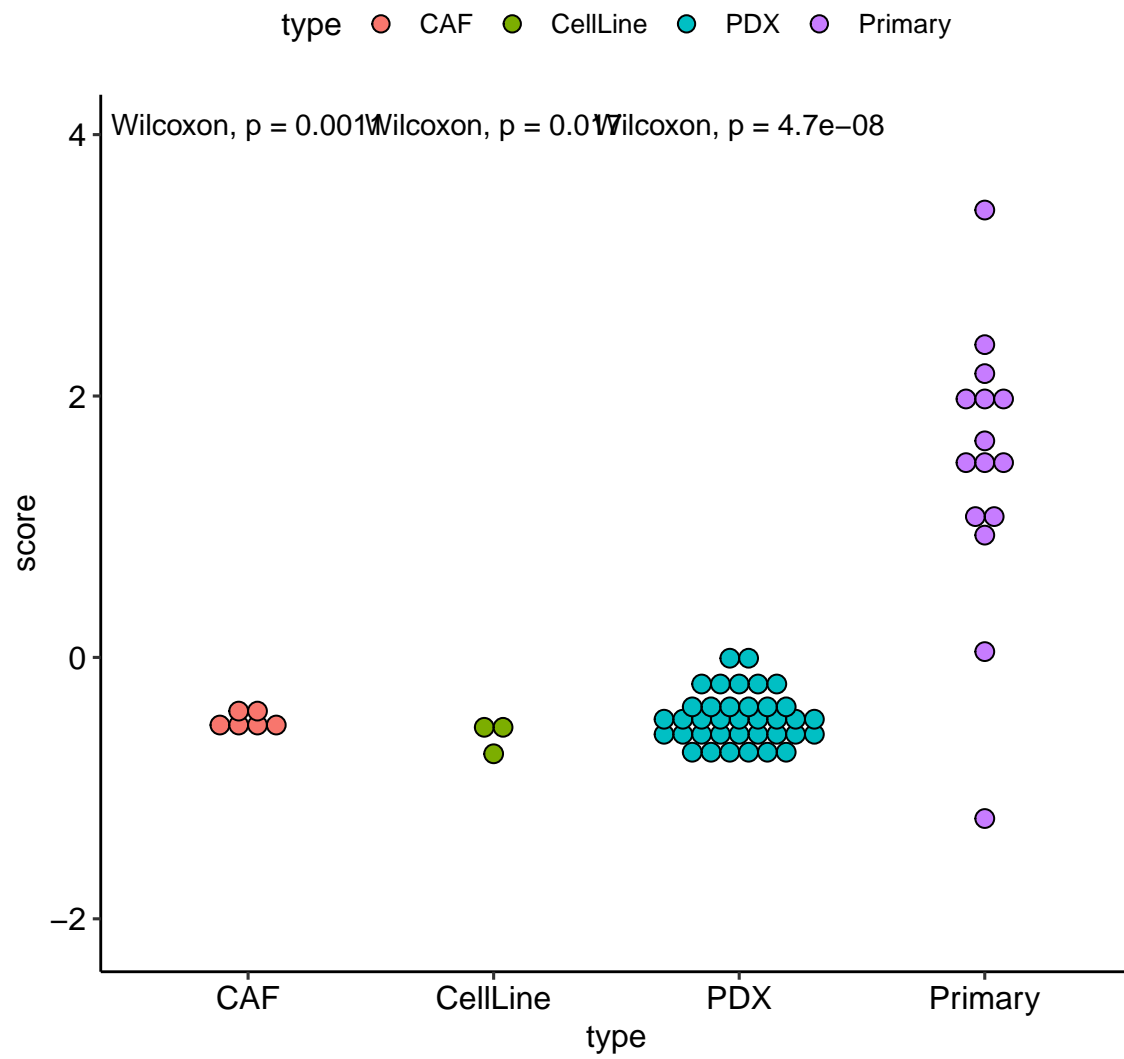
CIBERSORT.T.cells.CD4.memory.activated score



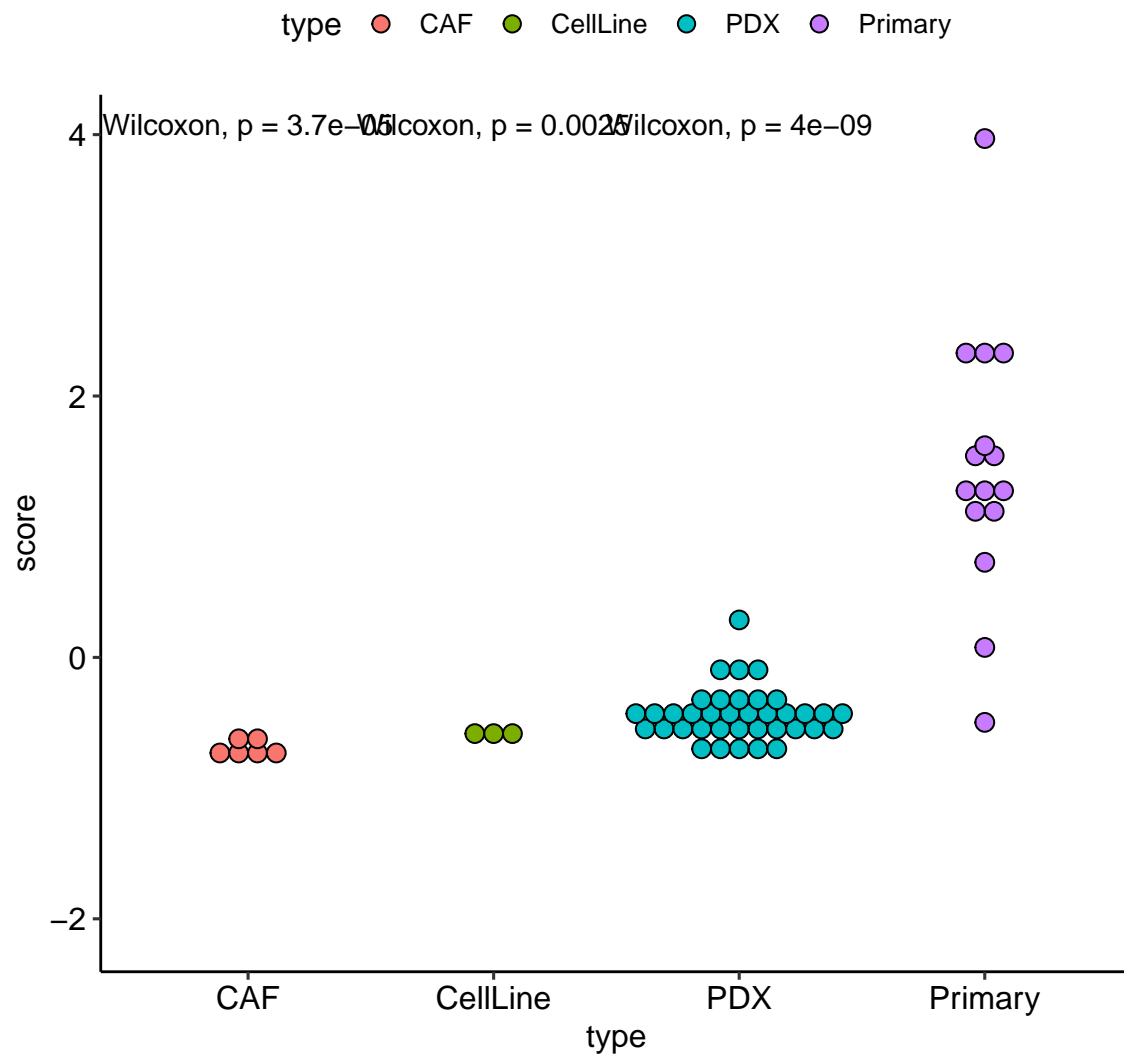
CIBERSORT.T.cells.follicular.helper score



CIBERSORT.T.cells.regulatory..Tregs. score



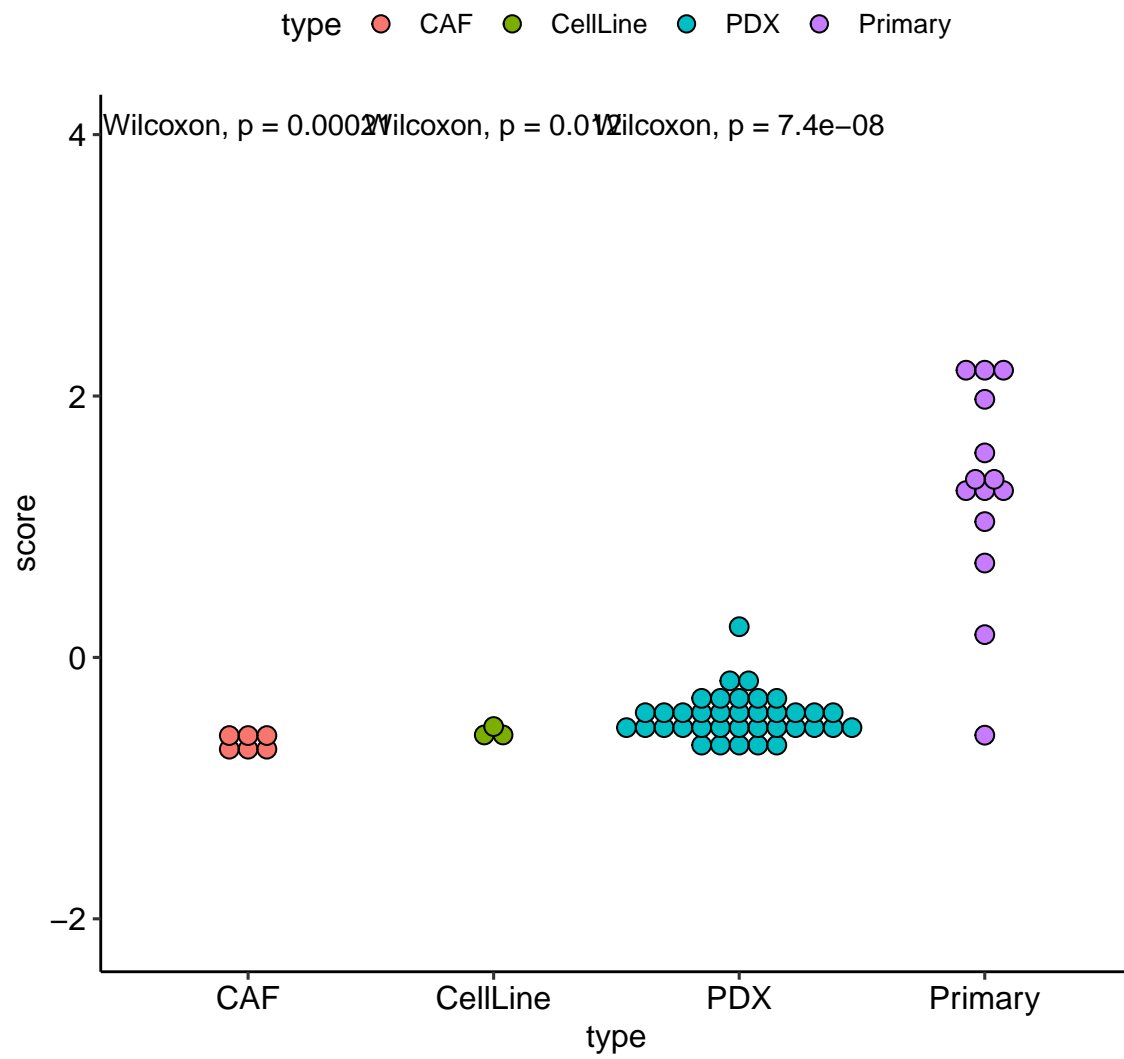
# CIBERSORT.T.cells.gamma.delta score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

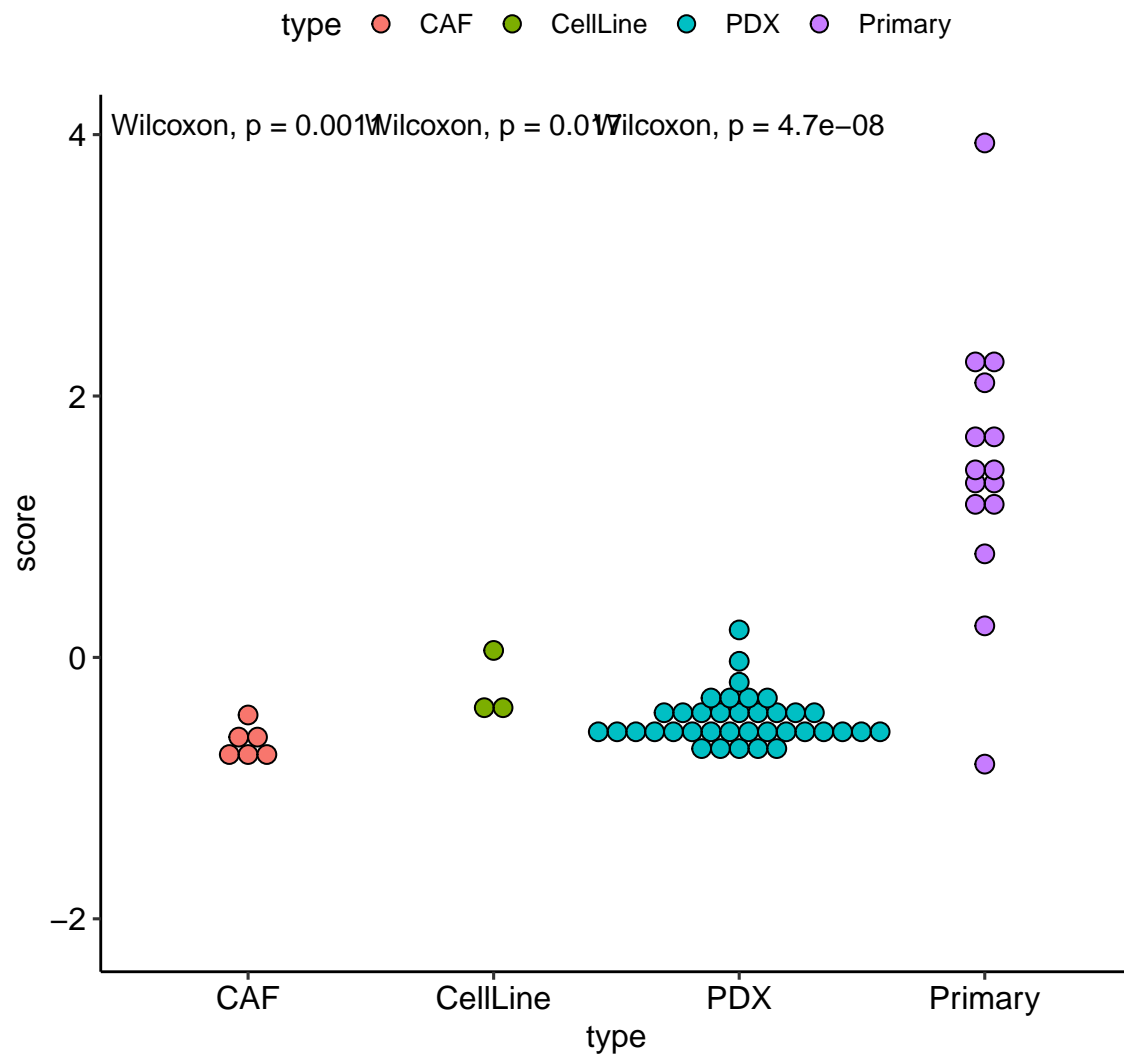
## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

CIBERSORT.NK.cells.resting score

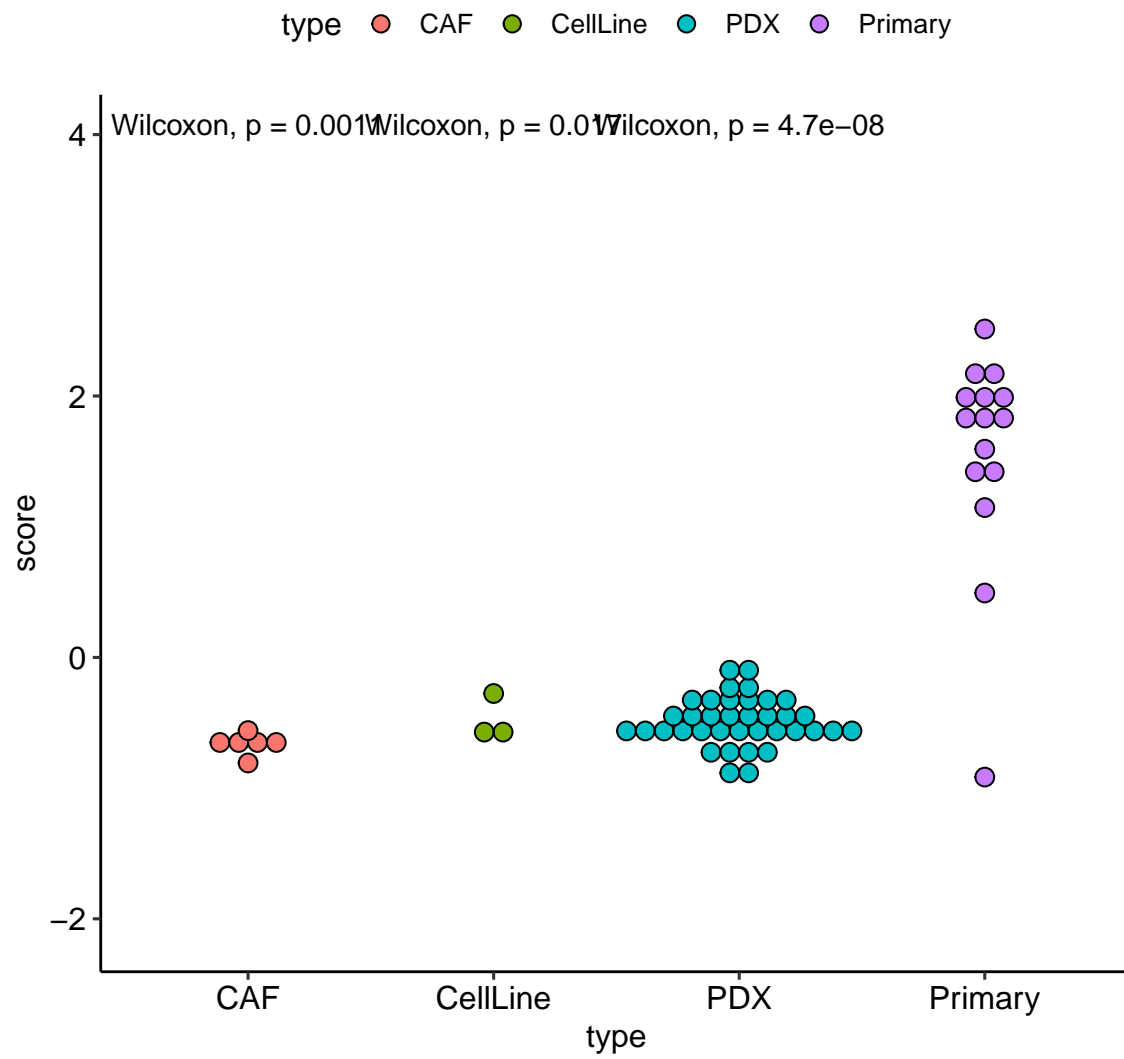




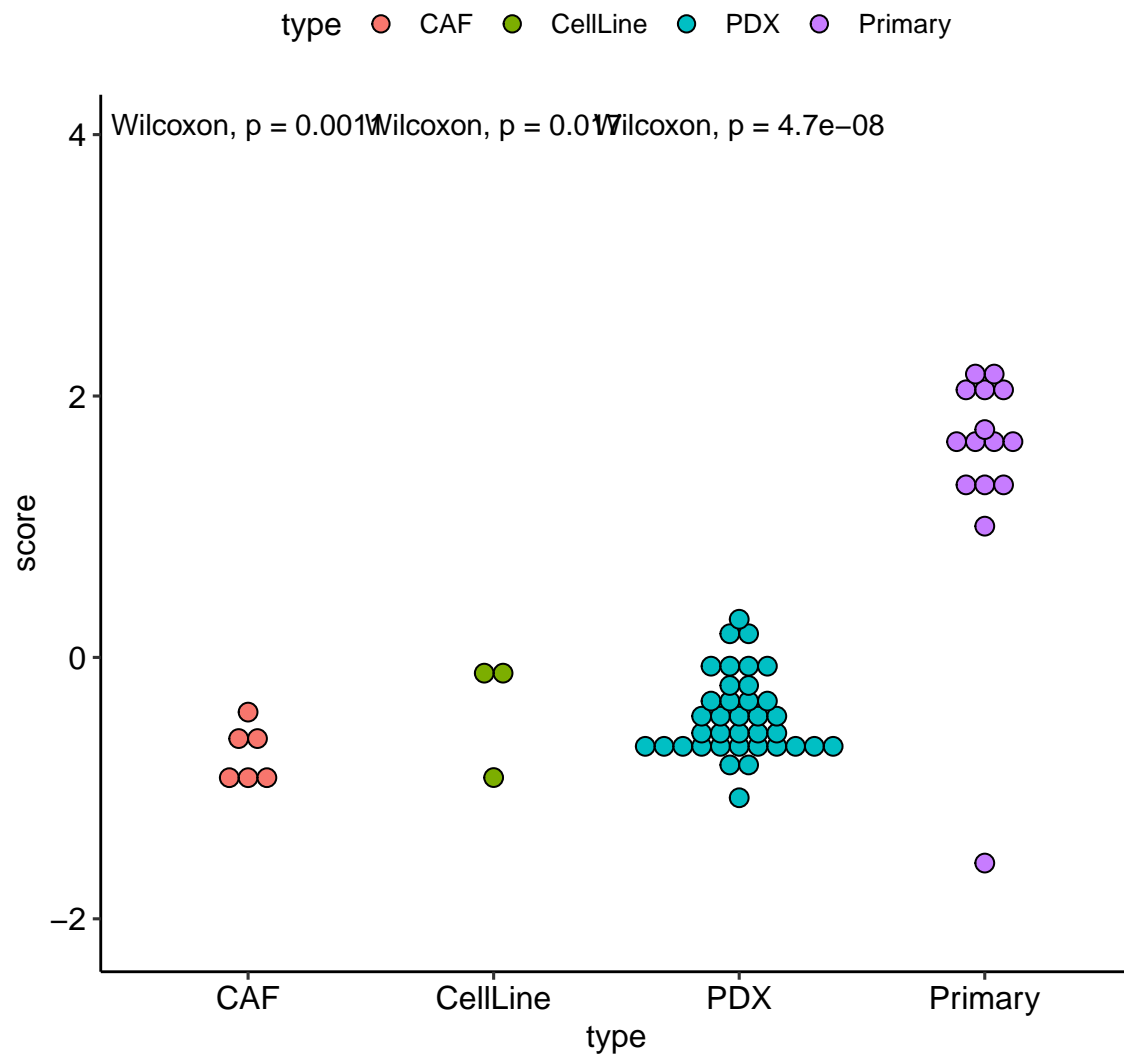
CIBERSORT.NK.cells.activated score



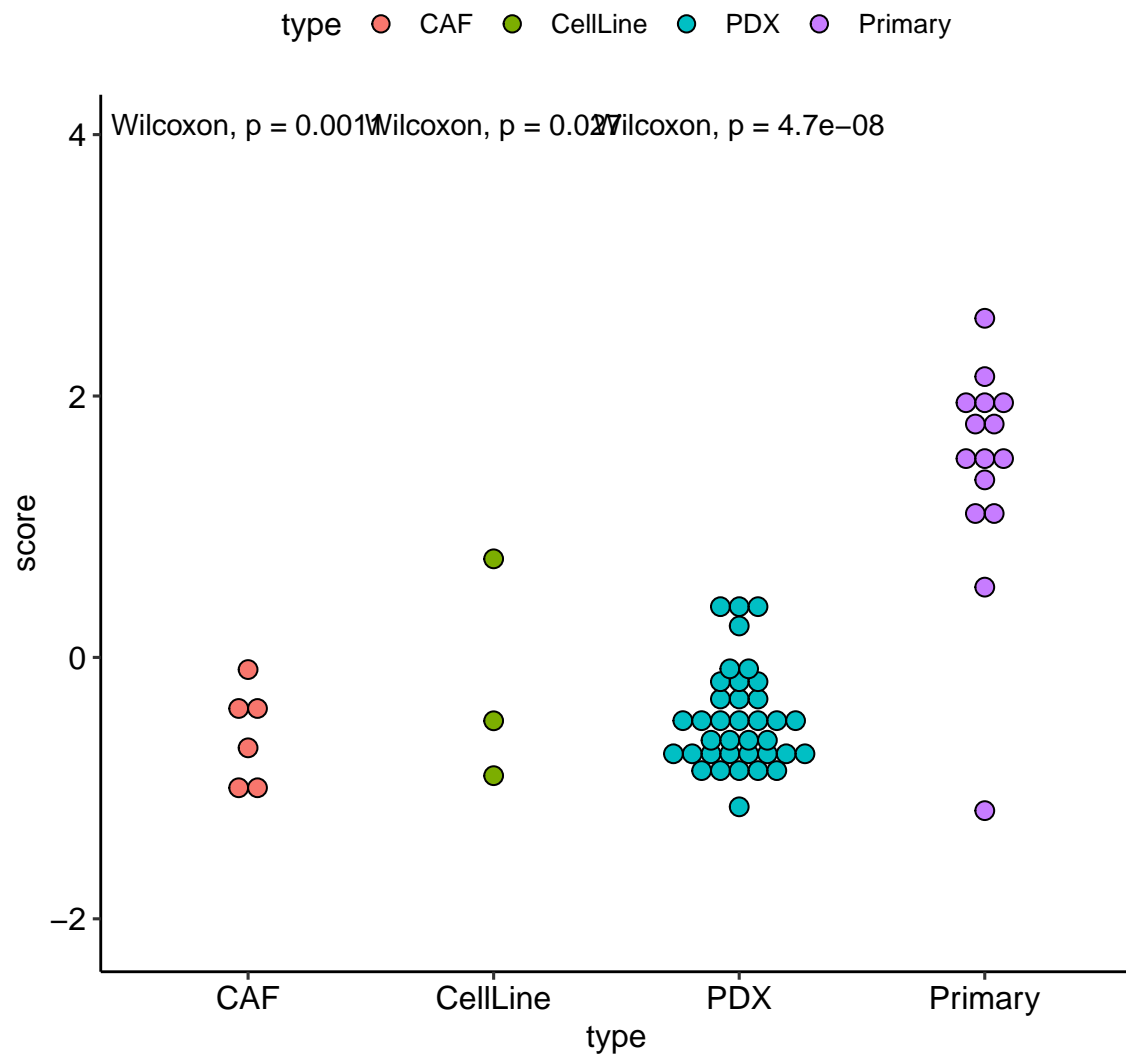
CIBERSORT.Monocytes score



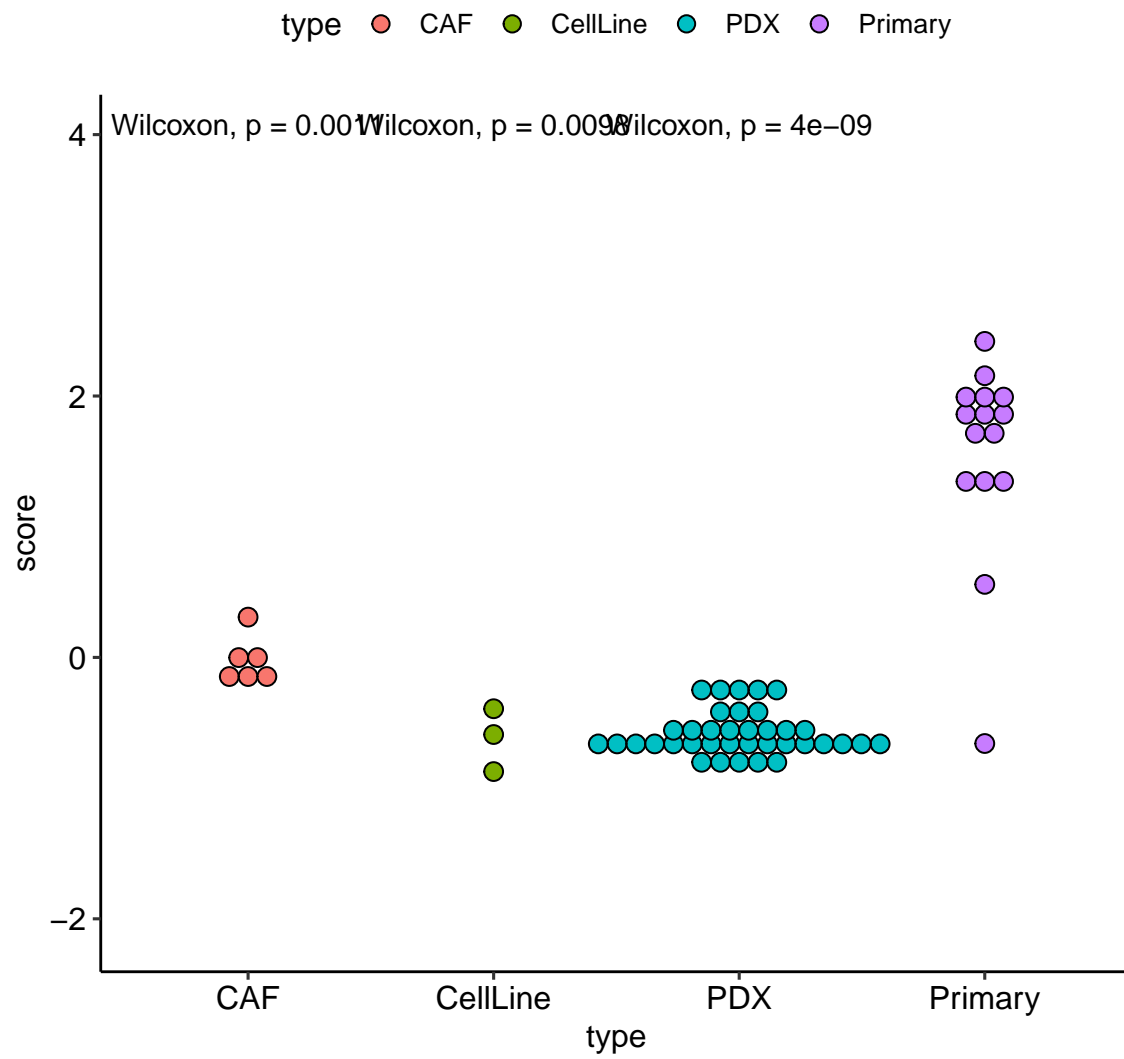
CIBERSORT.Macrophages.M0 score



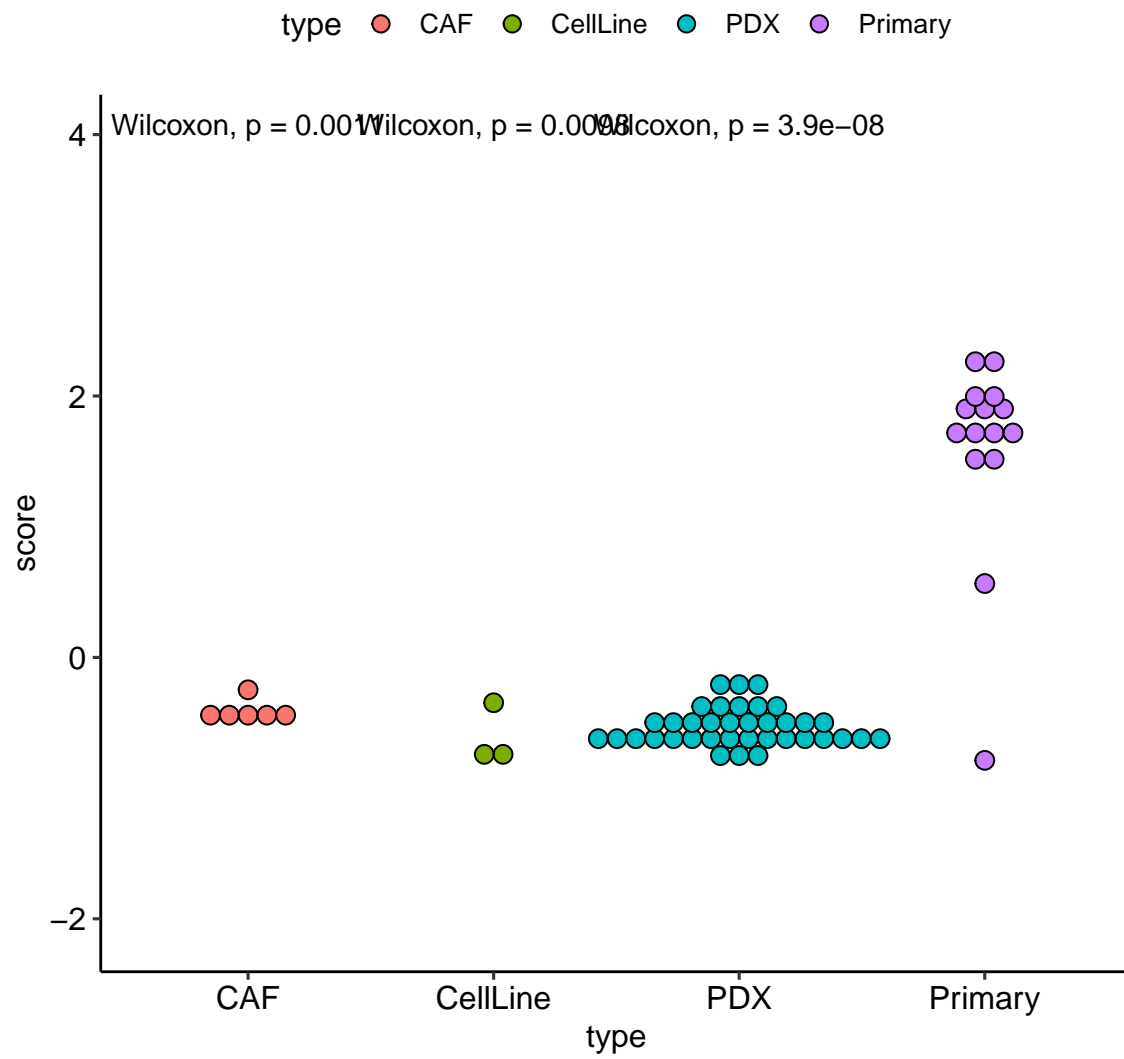
# CIBERSORT.Macrophages.M1 score



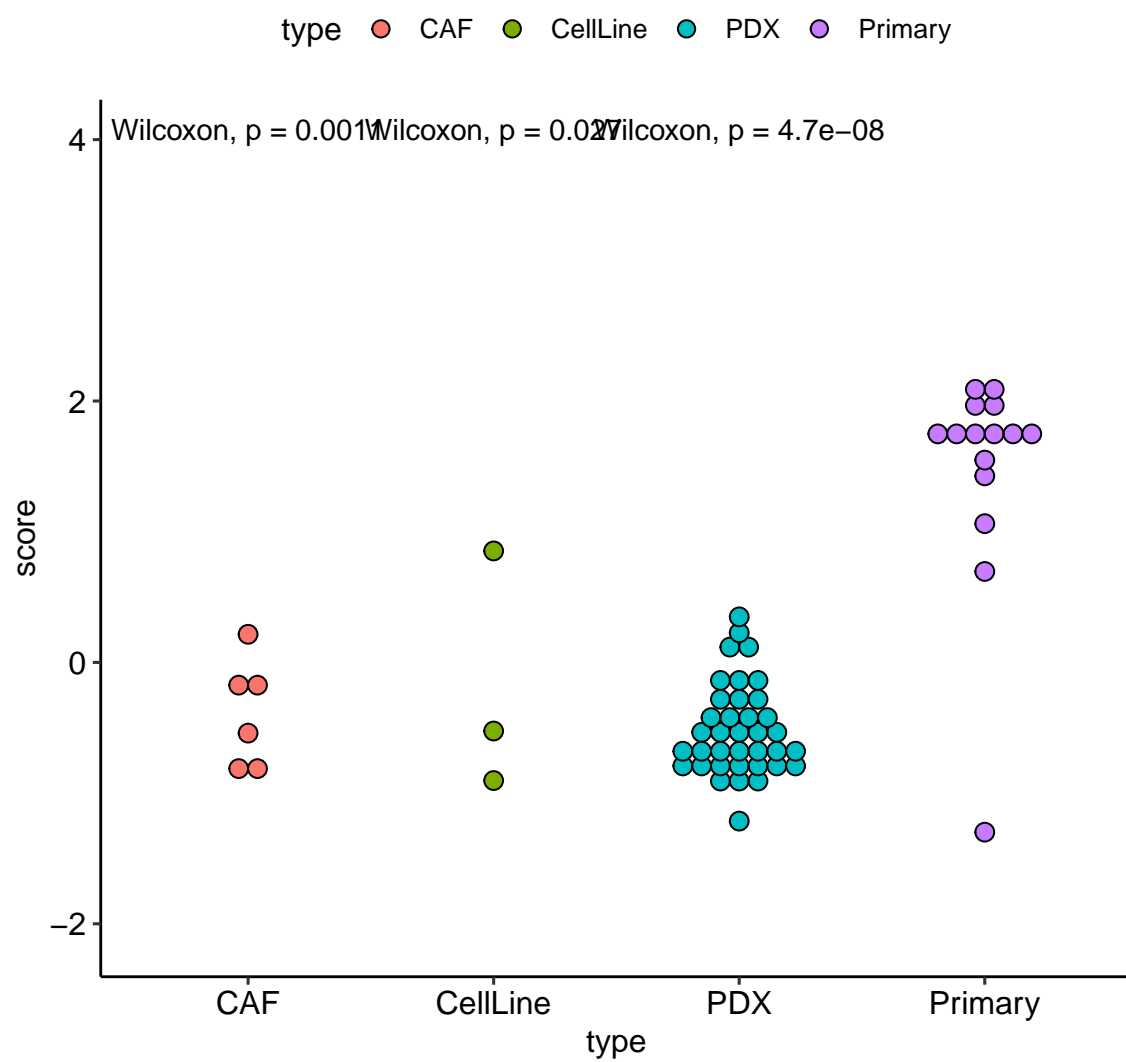
CIBERSORT.Macrophages.M2 score



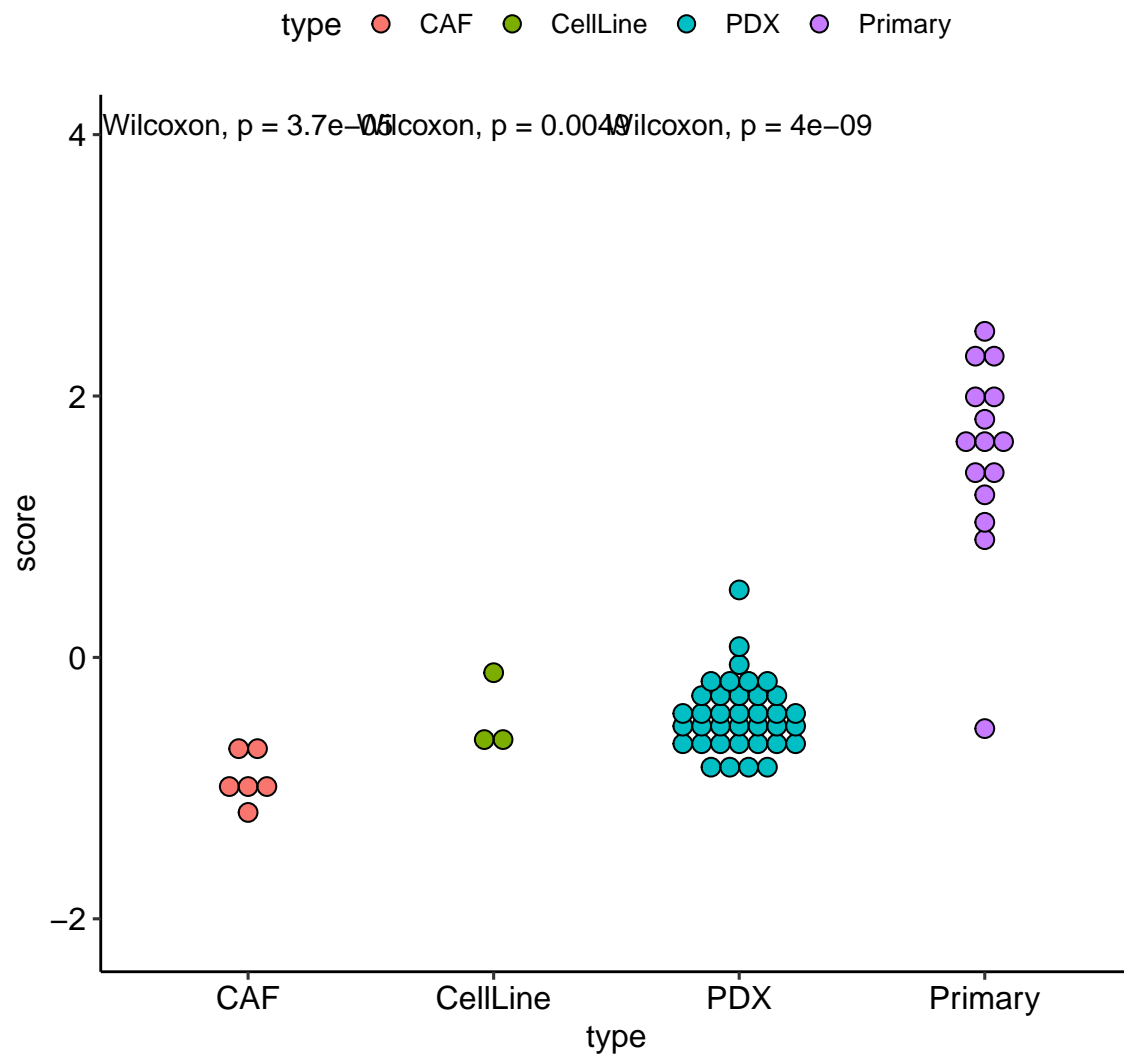
CIBERSORT.Dendritic.cells.resting score



# CIBERSORT.Dendritic.cells.activated score

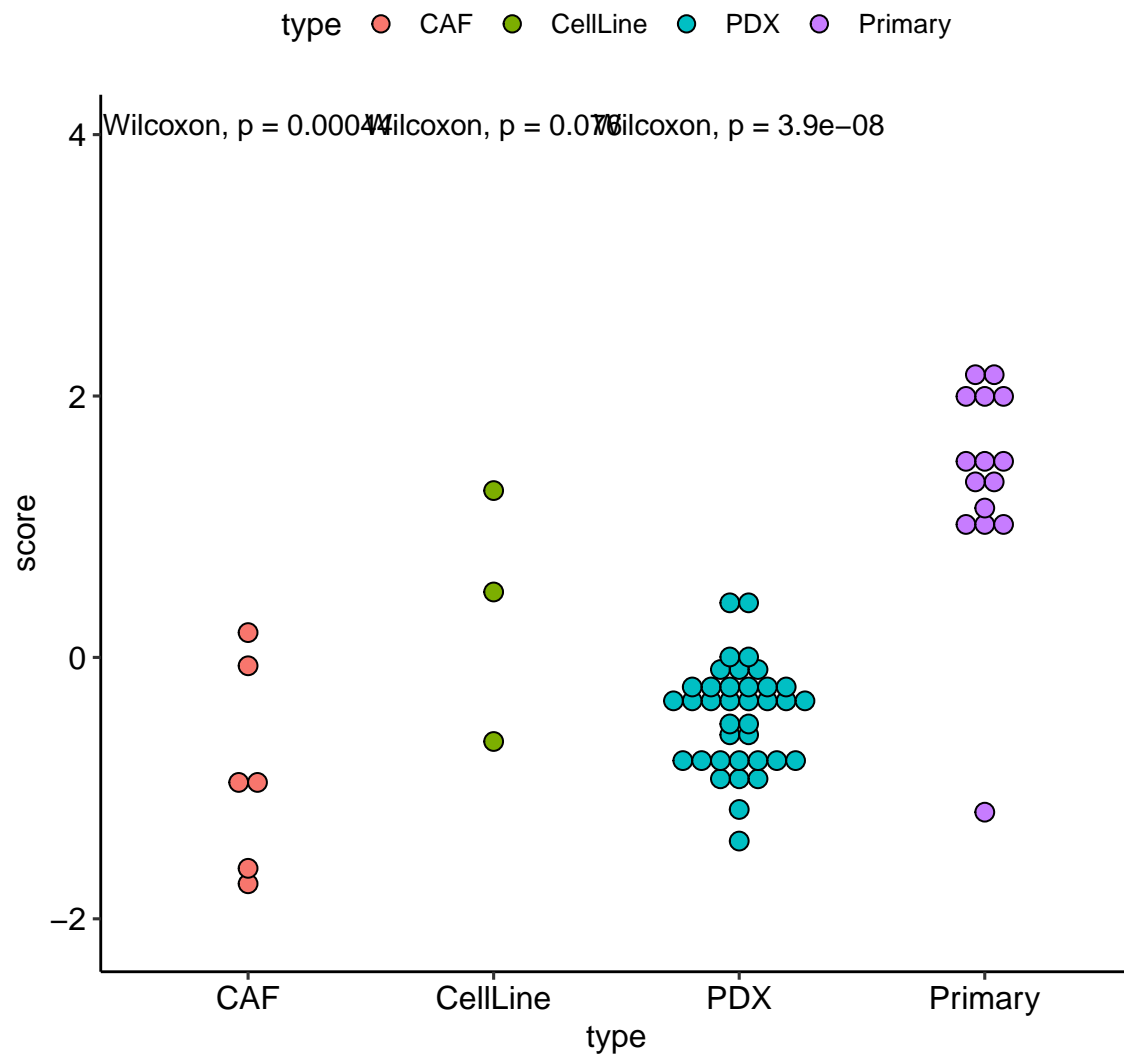


CIBERSORT.Mast.cells.resting score

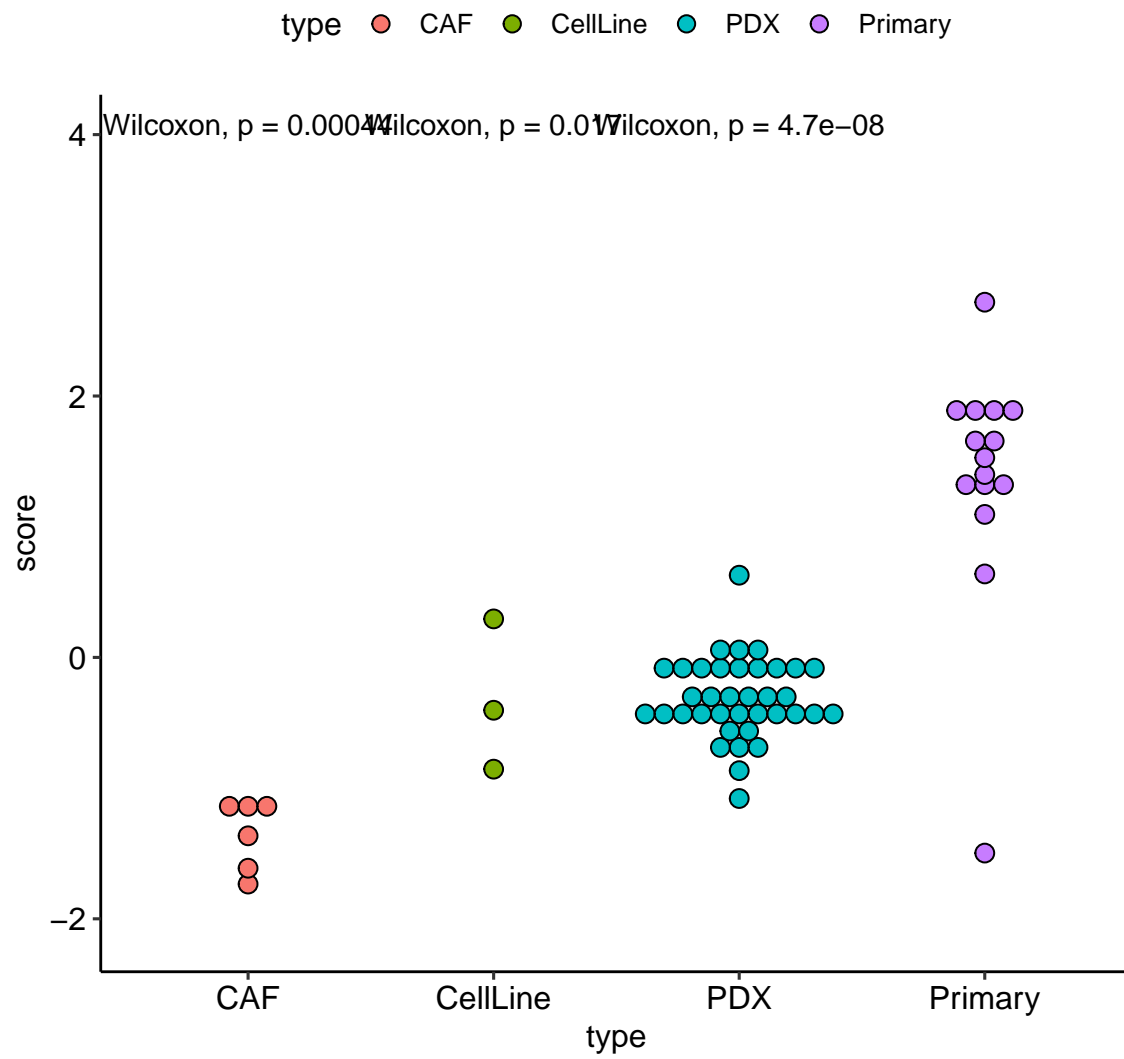




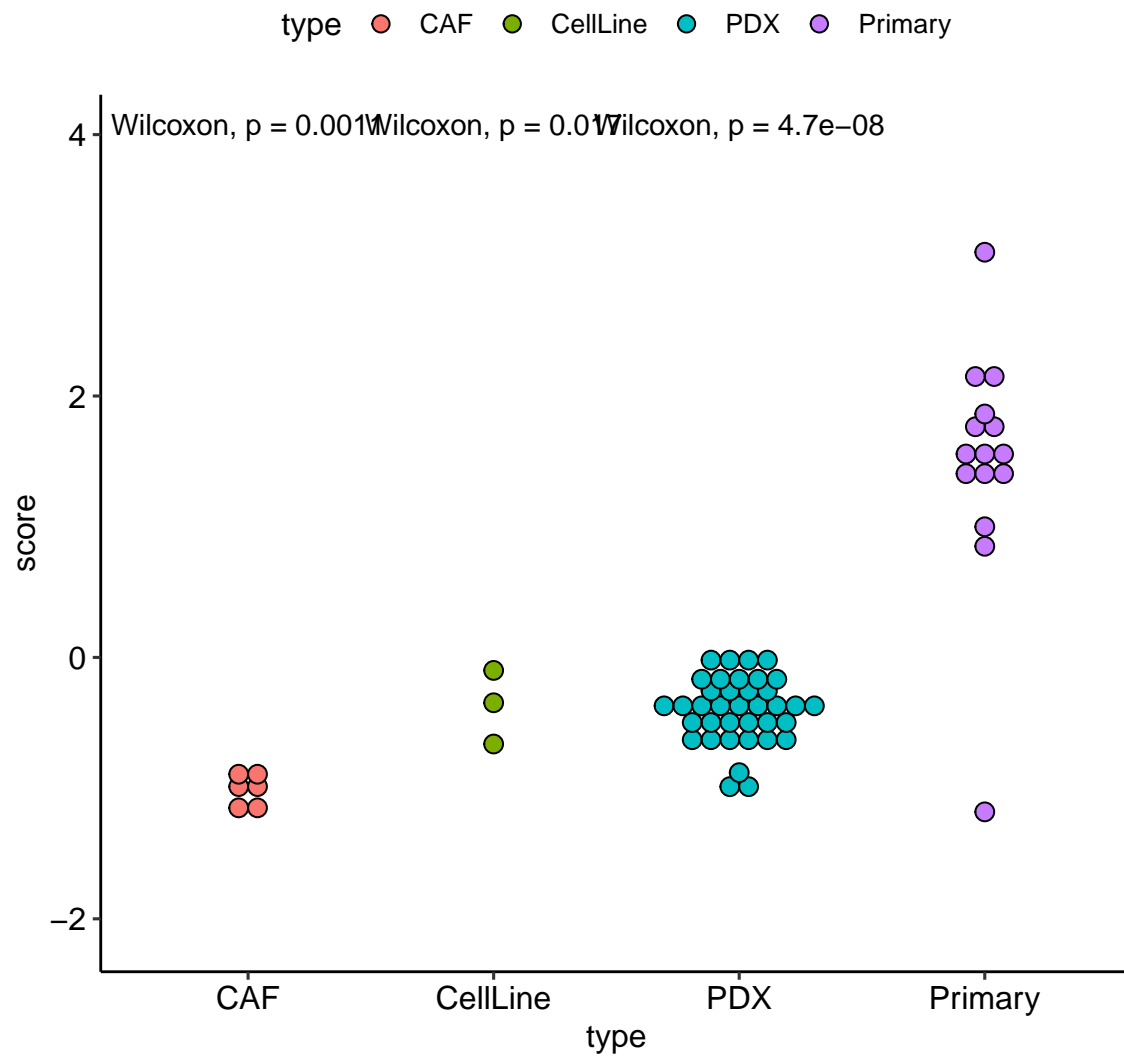
CIBERSORT.Mast.cells.activated score



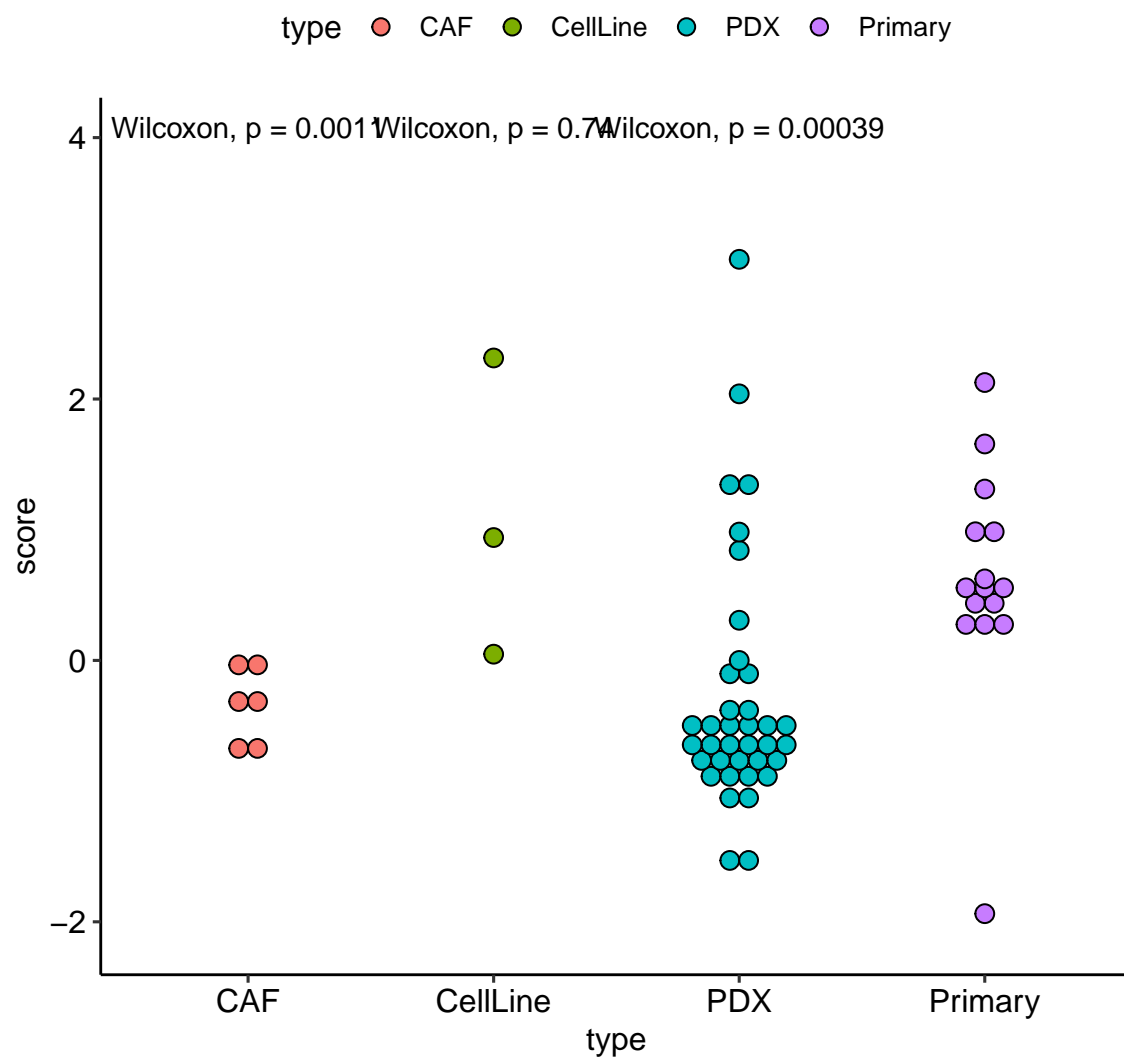
CIBERSORT.Eosinophils score



### CIBERSORT.Neutrophils score



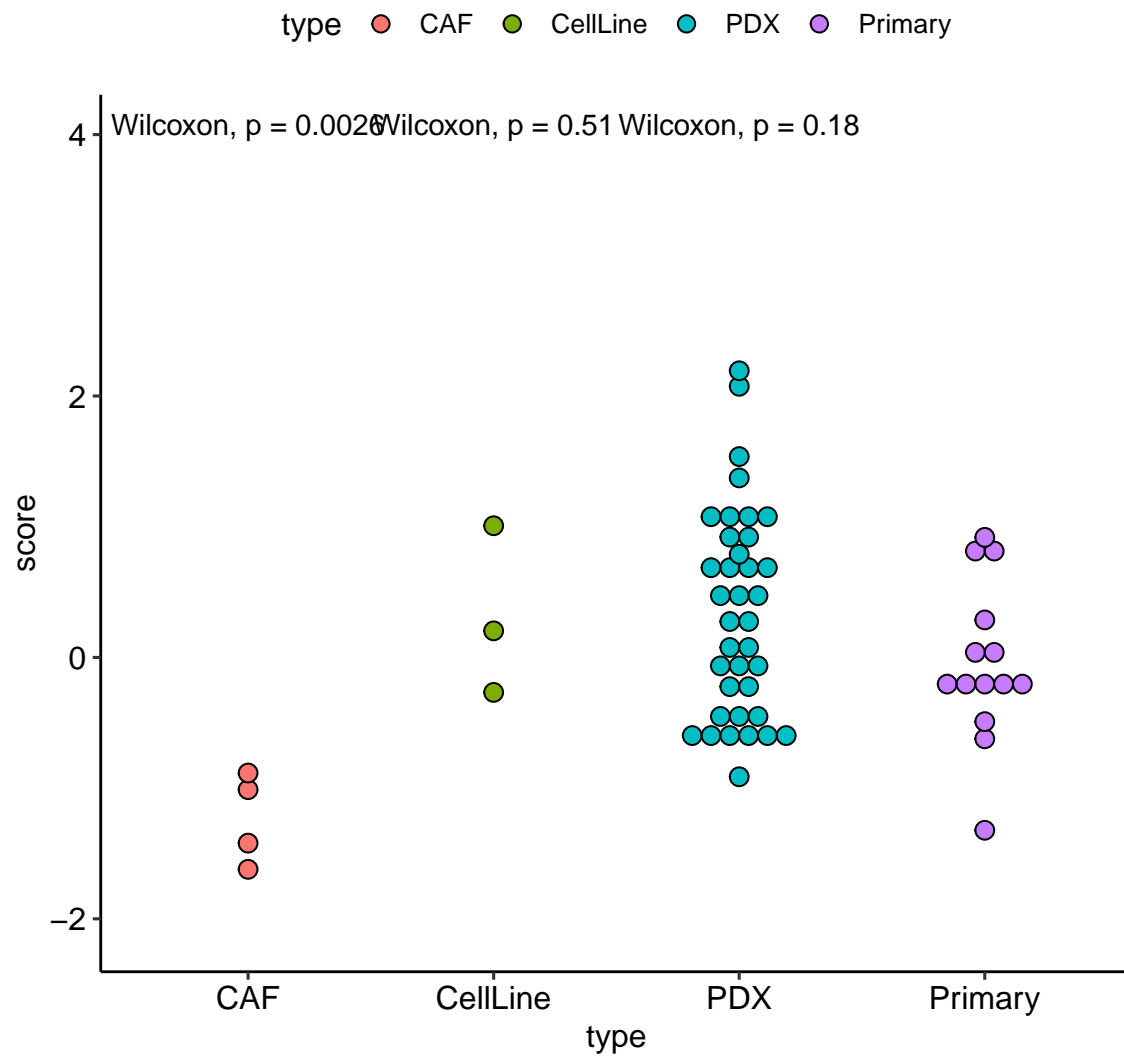
## Notta.BasalA score



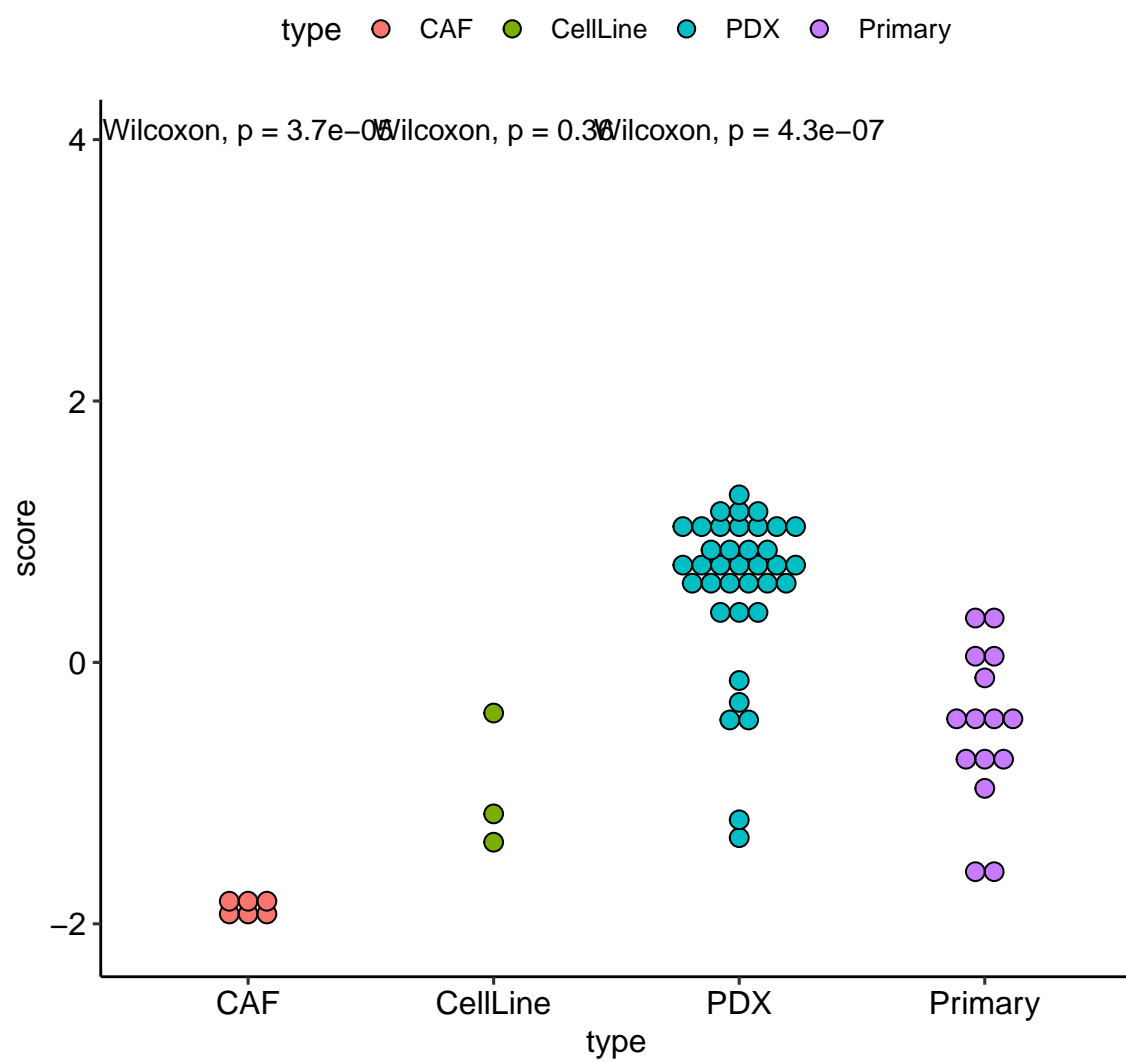
## Warning: Removed 3 rows containing non-finite values (stat\_bindot).

## Warning: Removed 3 rows containing non-finite values (stat\_compare\_means).

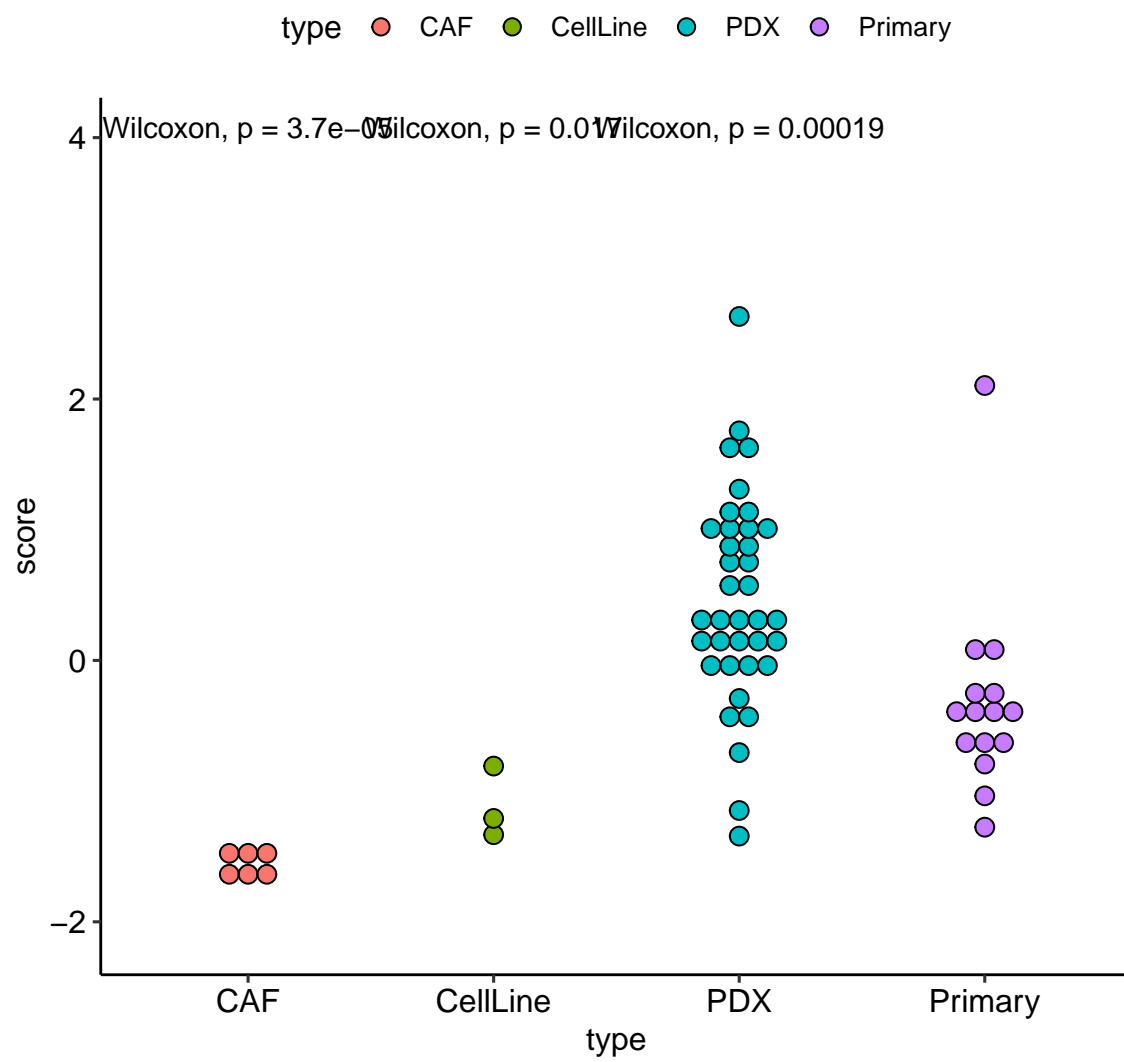
## Notta.BasalB score



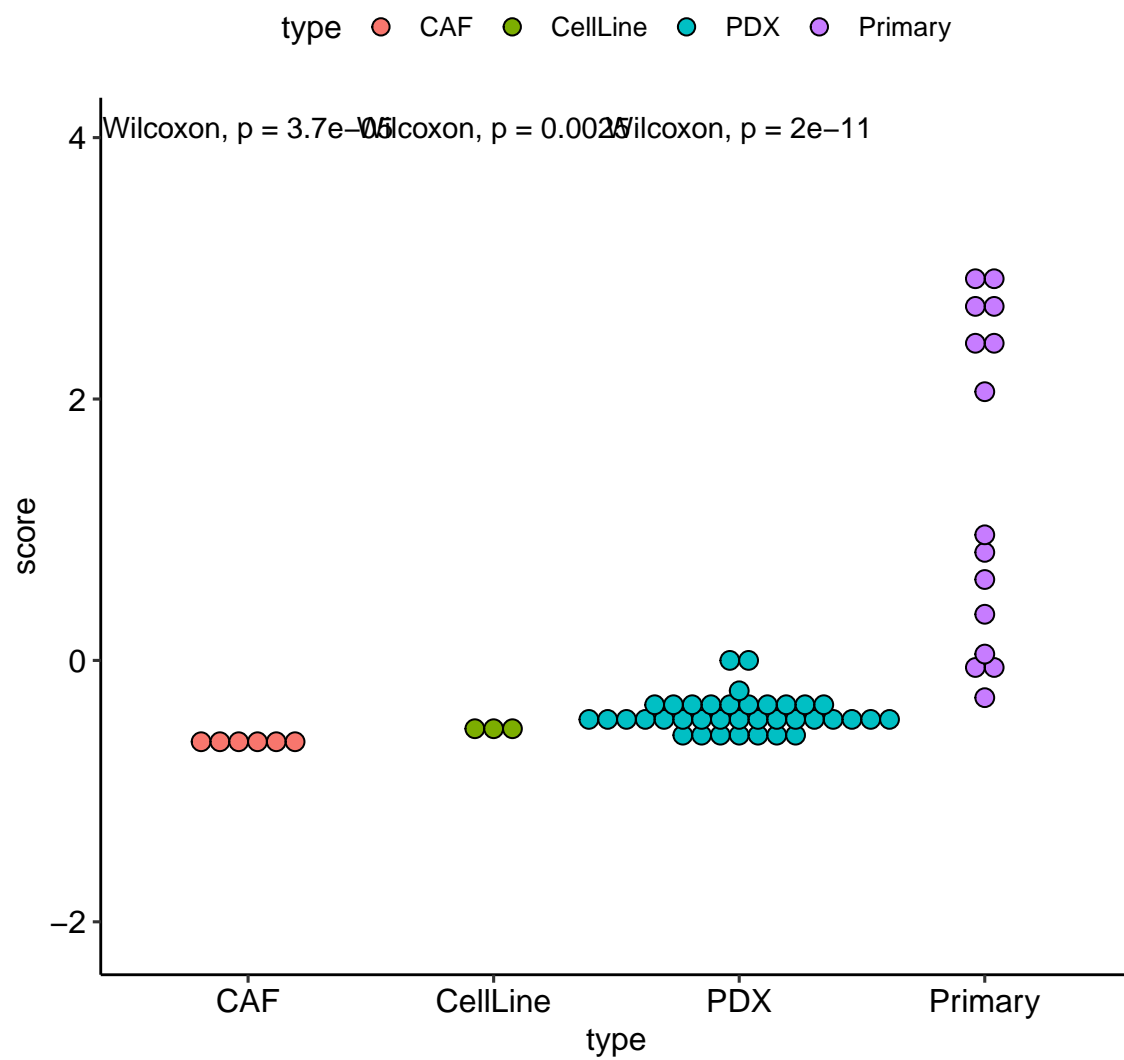
# Notta.ClassicalA score



Notta.ClassicalB score

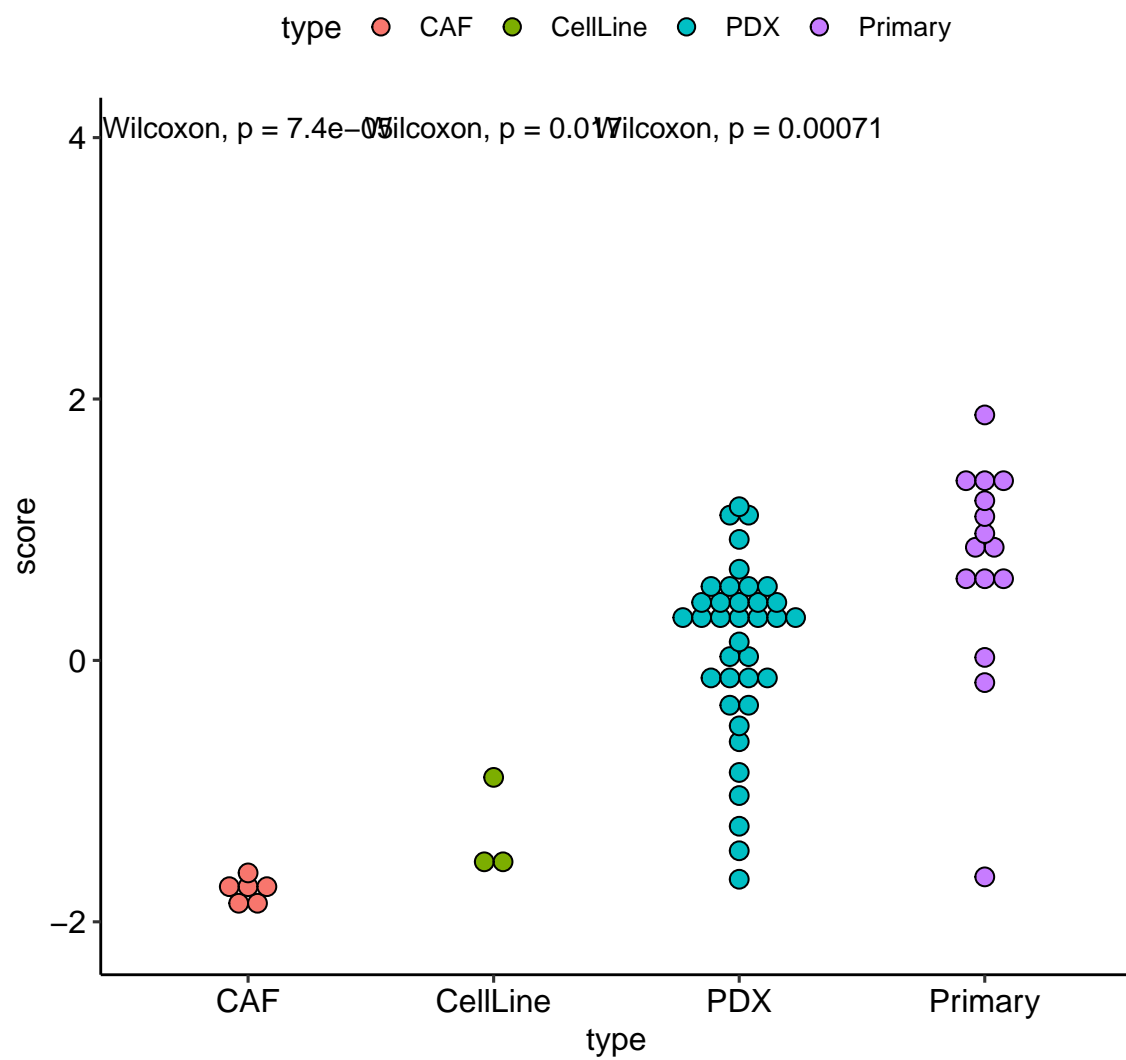


ADEX\_unique score

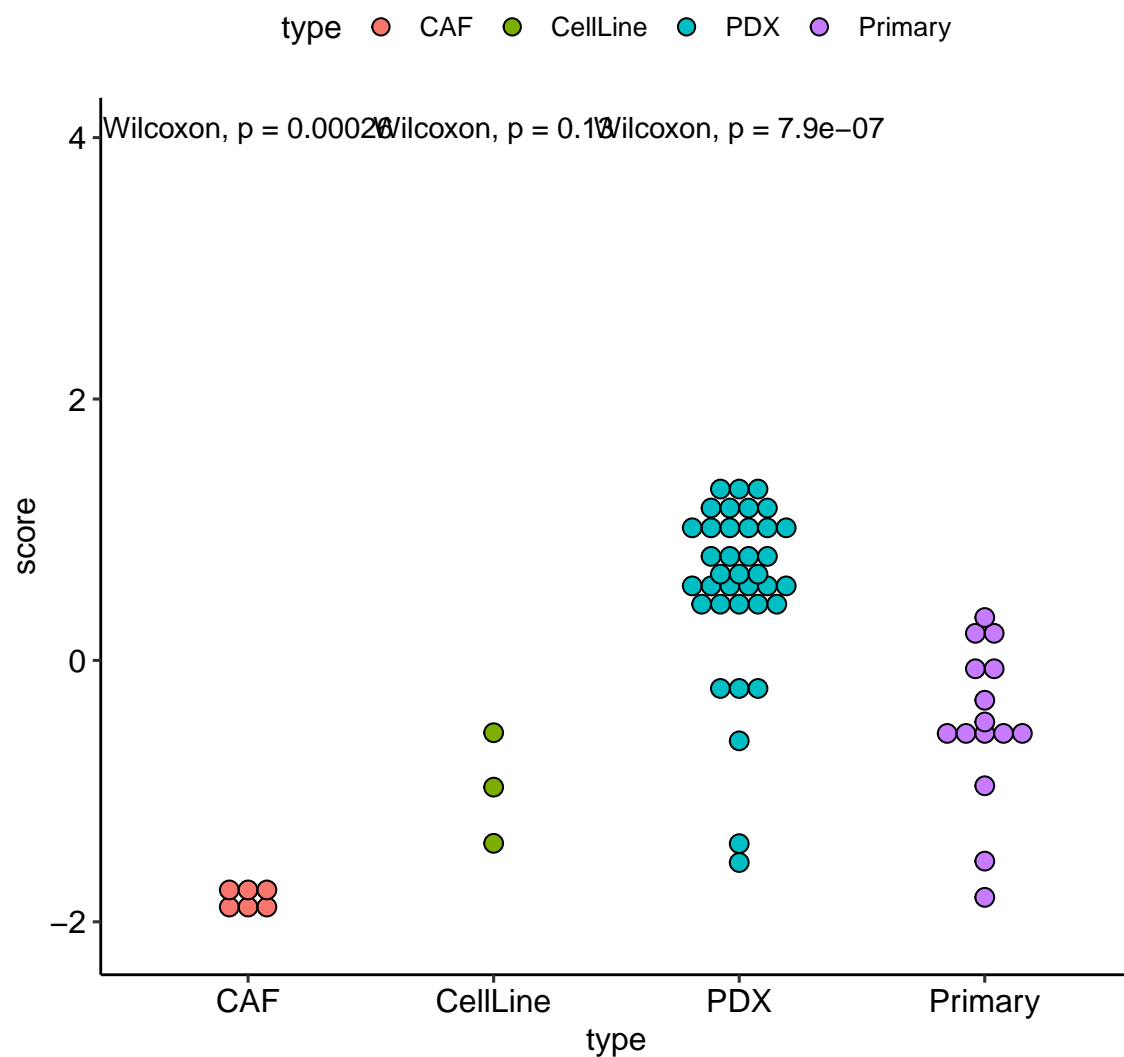




# Immunogenic\_unique score



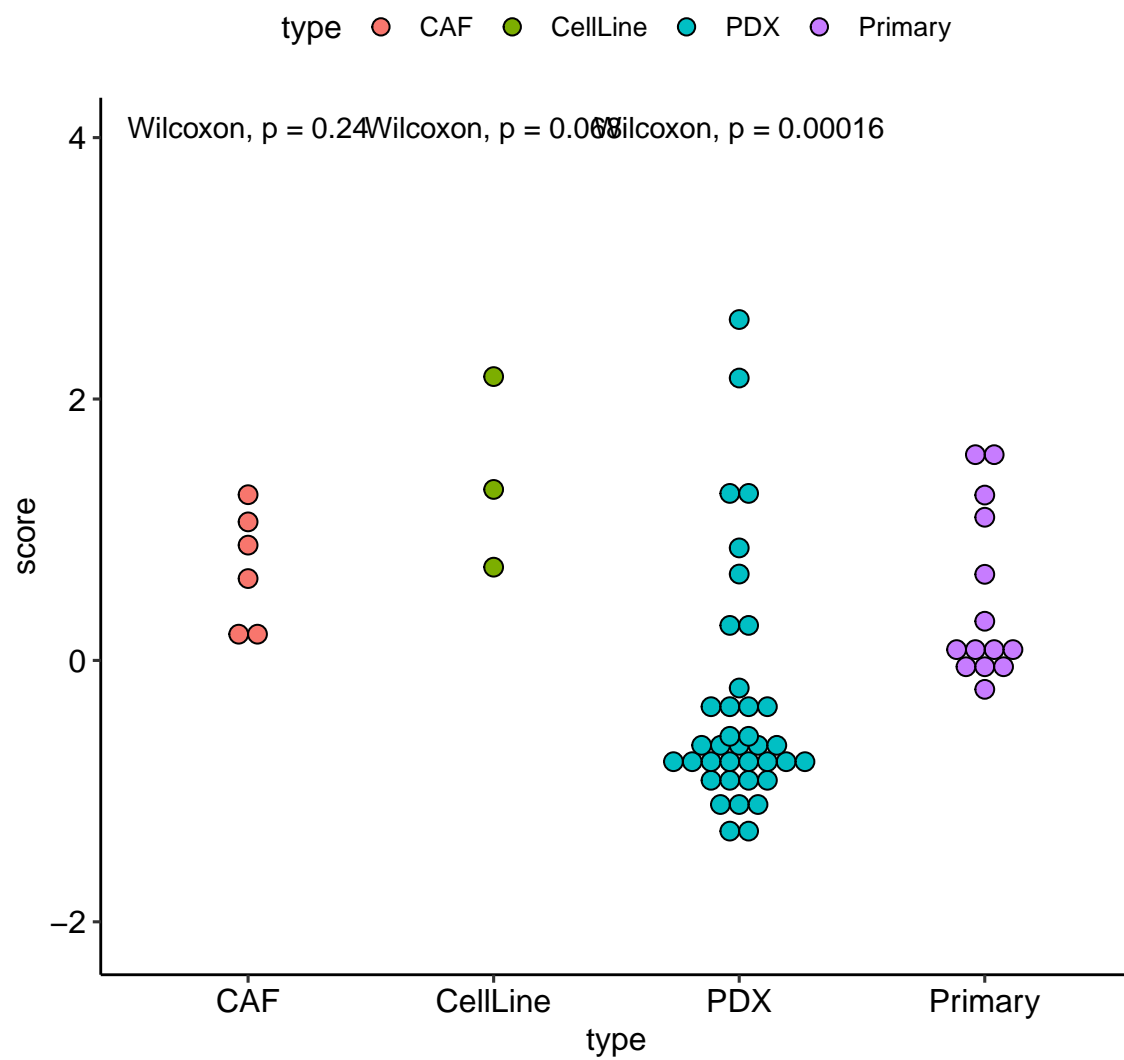
## Progenitor\_unique score



## Warning: Removed 1 rows containing non-finite values (stat\_bindot).

## Warning: Removed 1 rows containing non-finite values (stat\_compare\_means).

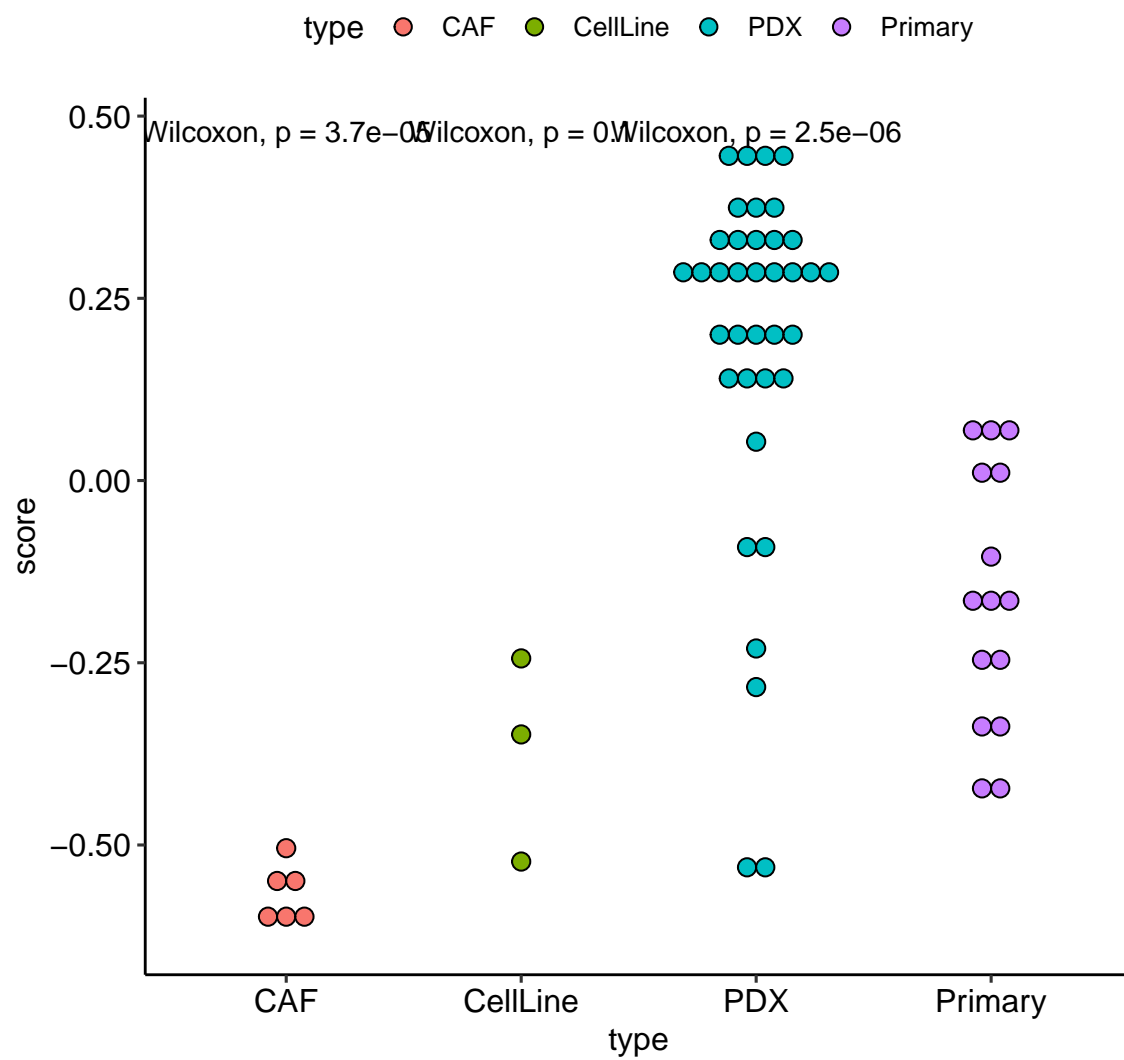
Squamous\_unique score







## molgrad\_ICGCarry score



## molgrad\_ICGCrnaseq score

