

PolyATAC analysis

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Load environment

```
library(Seurat)
library(Signac)
source('E:\\PolyATAC_analysis\\tool\\clone_correlation.R')
```

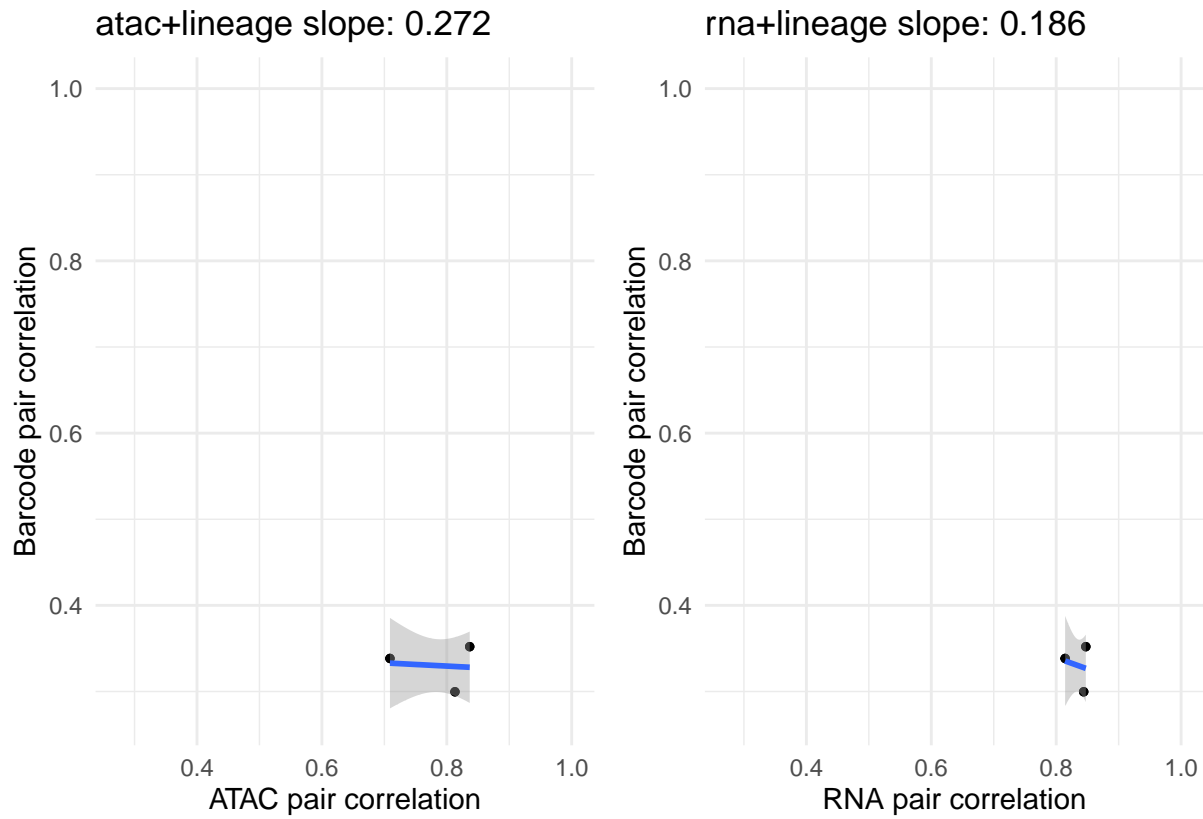
Load data

```
obj = readRDS('E:\\gas_multiomi\\e105\\e105seurat.rds')
```

Modalitties relationships

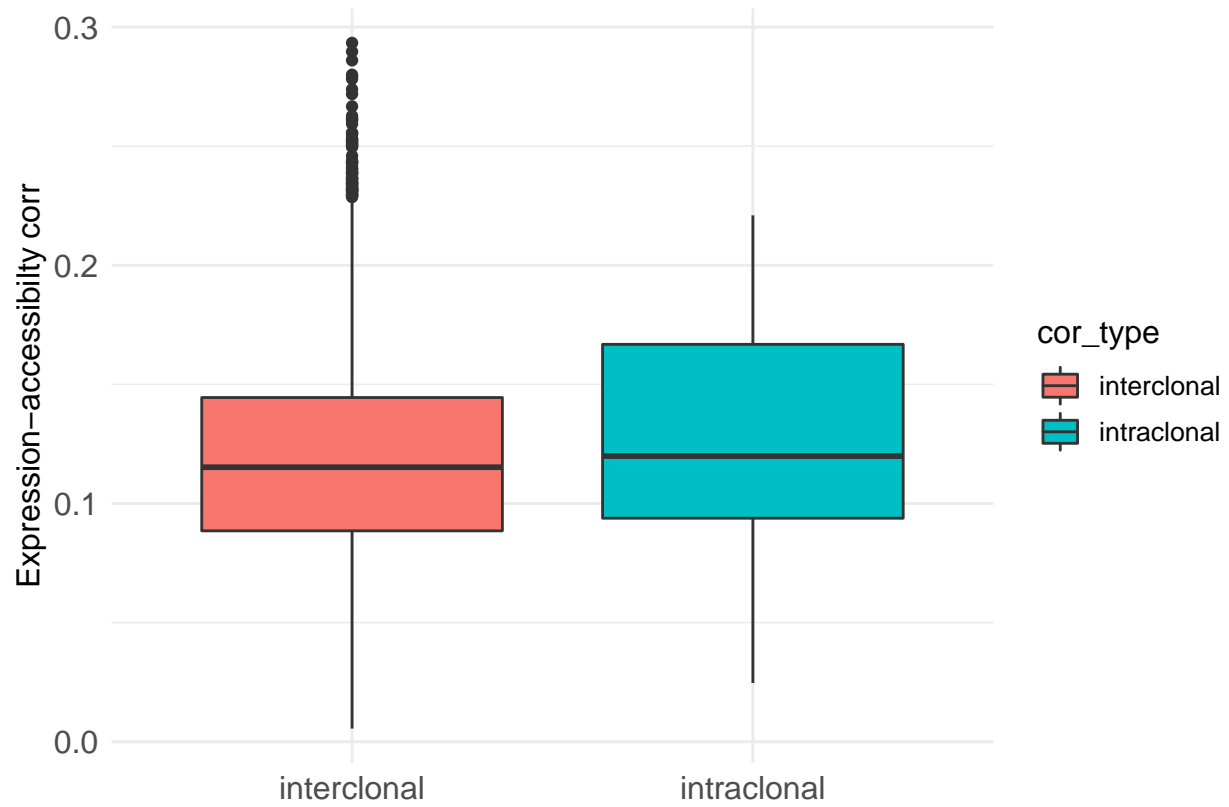
Calculate the correlation between barcode+rna and barcode+atac

```
multi_rel = multi_relationship(obj)
```



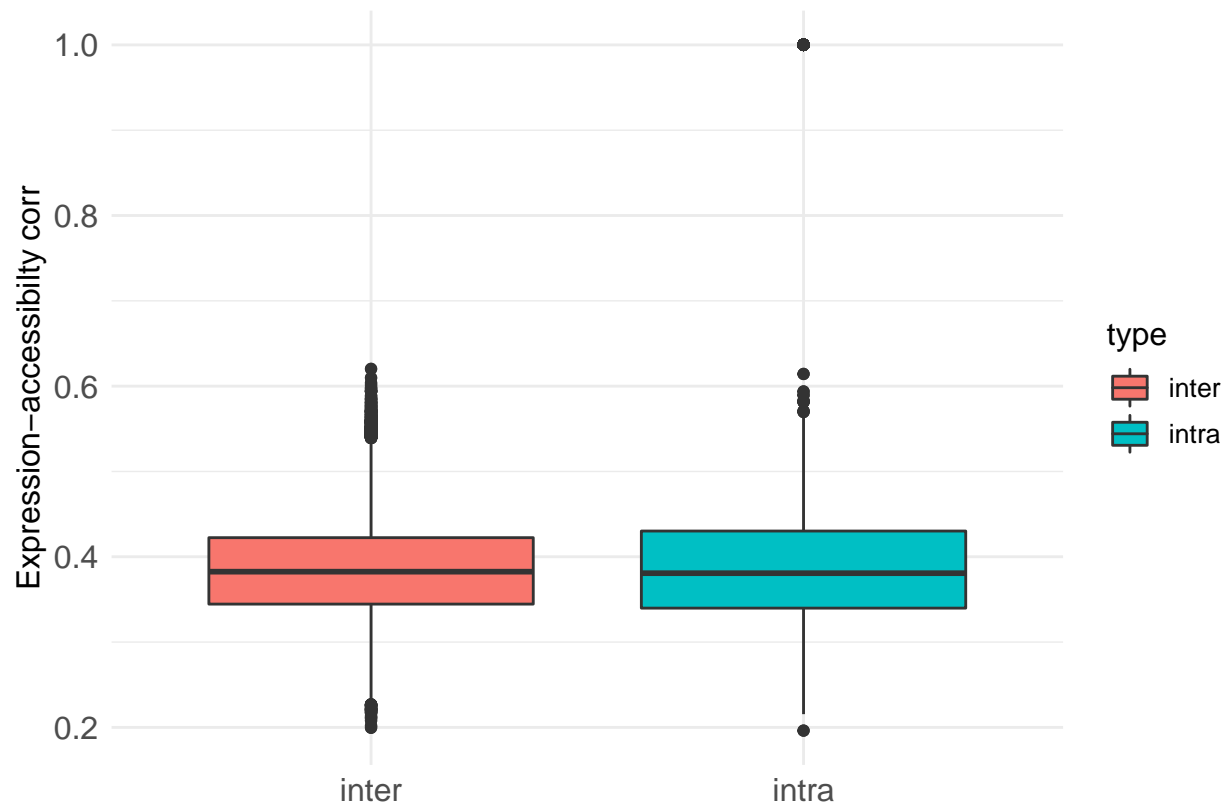
Boxplots comparing intraclonal and interclonal correlation (clone level)

```
rna_atac_relationship(obj)
```



Boxplots comparing single cell rna correlation

```
single_cell_relationship(obj)
```



Boxplots comparing single cell ATAC correlation

```
single_cell_relationship(obj, modality = 'ATAC')
```

