cardiac aging

run fastQC for general quality control

trimming adaptor sequence
> most RNA-Seq do not need this step, small RNA-Seq or ATAC-Seq will need this one

mapping: tophat

for all samples, the mappability is around or larger than 90%

read counts for each gene: bam file sorting and htseq-count

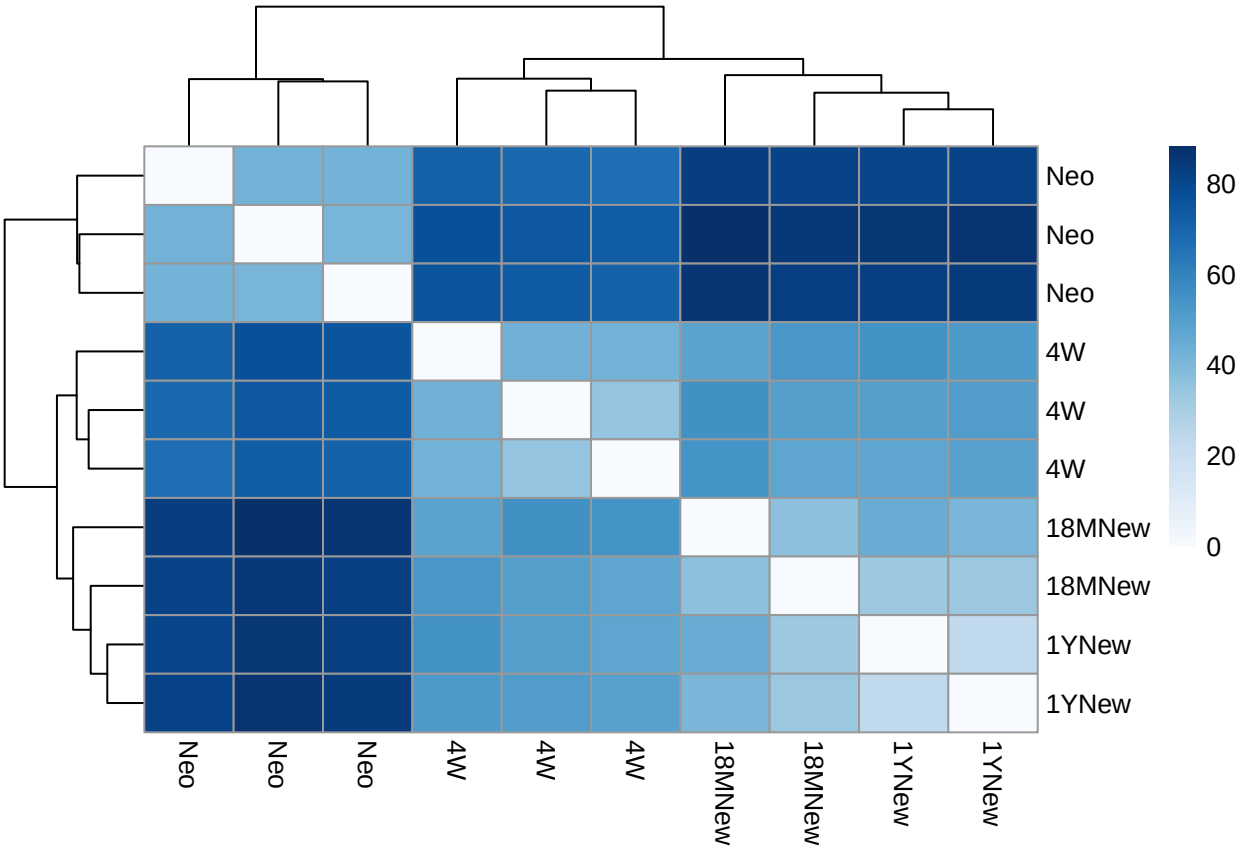
Sample: Read count in genes (alignment not unique)
Neo-1: 72M (38M)
Neo-2: 63M (39M)
Neo-3: 63M (33M)
4W-1: 75M (19M)
4W-2: 75M (19M)
4W-3: 74M (28M)
14W-1: 81M (26M)
14W-2: 62M (32M)
14M-3: 72M (42M)
1Y-1: 77M (33M)
1Y-2: 77M (36M)
1Y-3: 10M (21M)
18M-1: 41M (65M)
18M-2: 40M (66M)
18M-3: 23M (12M)

Gene quantification: readcount2TPM

Creating DESeqDataSet

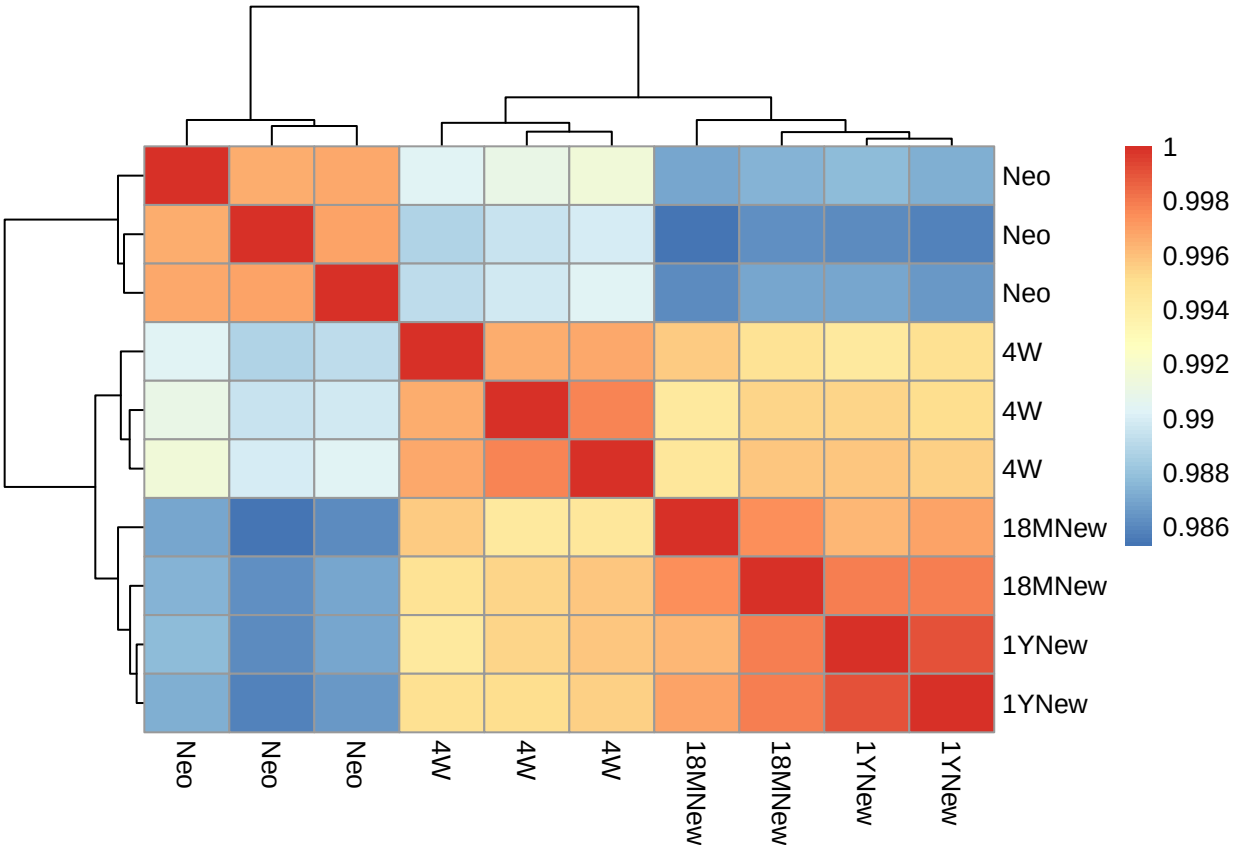
Pre-filtering and Log transformation

Quality control: clustering of sample distances

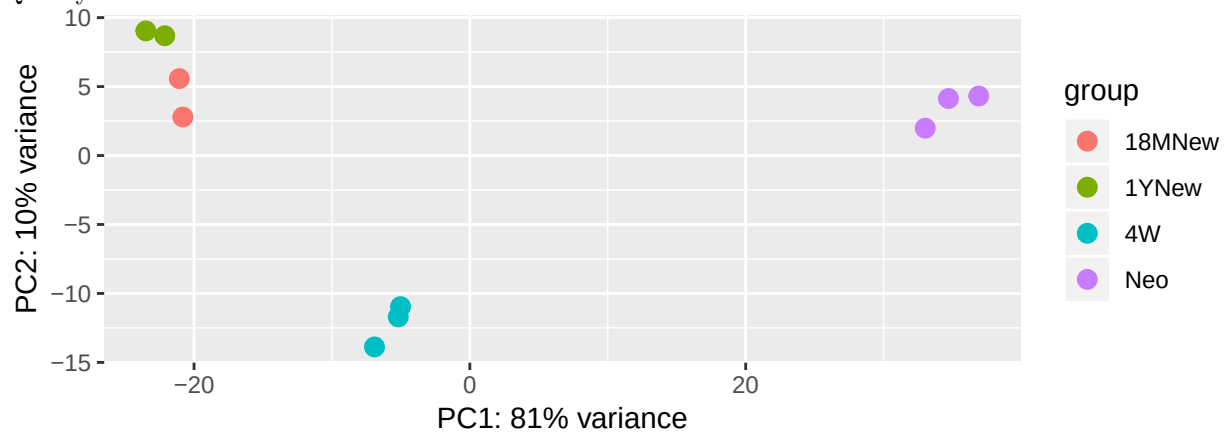


Quality control: clustering of sample correlations

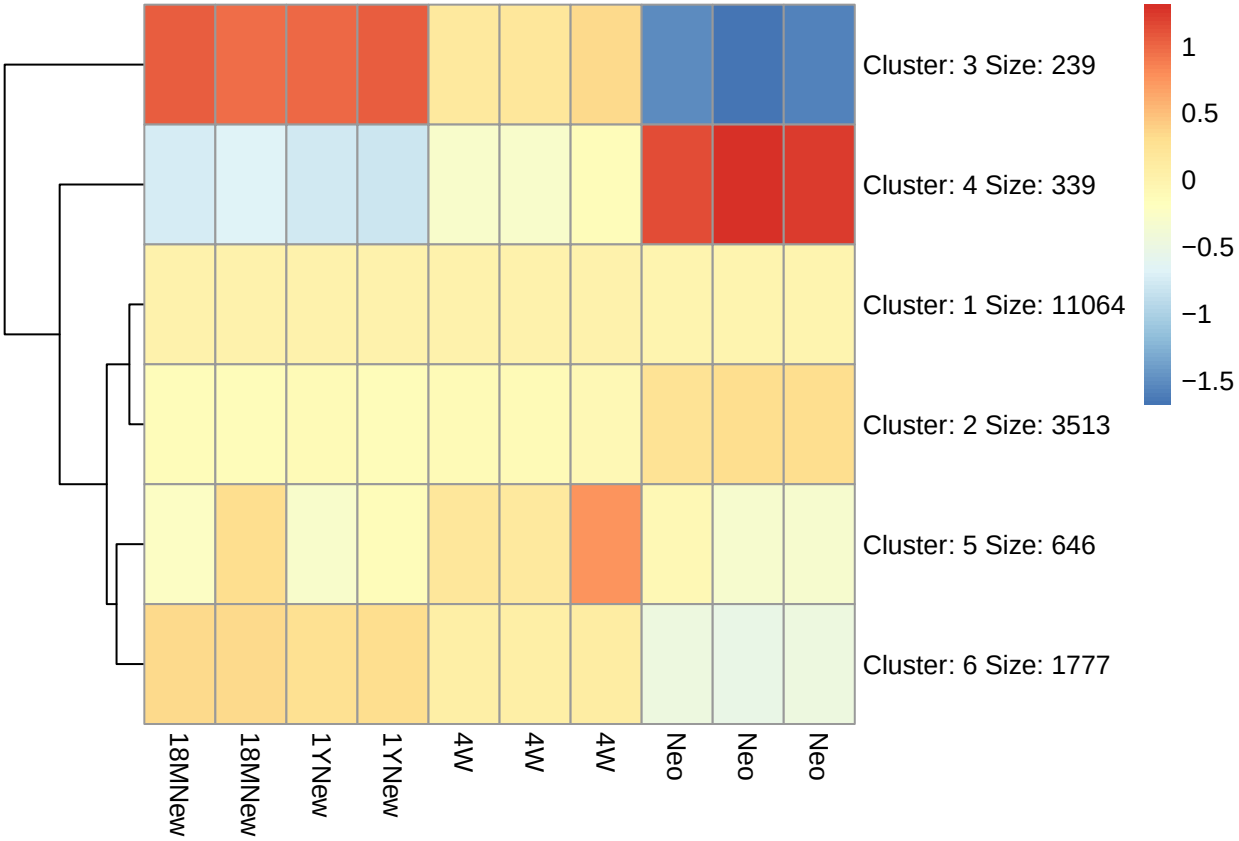
```
## corrplot 0.84 loaded
```



Quality control: PCA



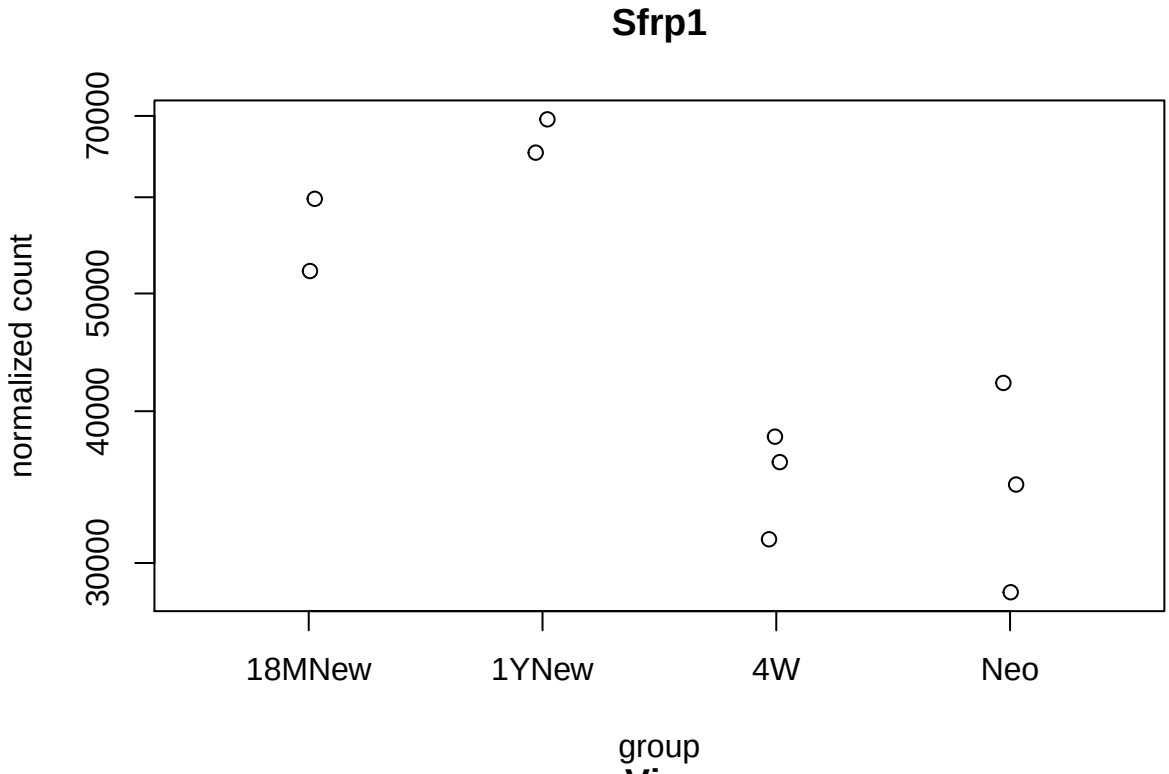
K-means clustering of all genes for all samples

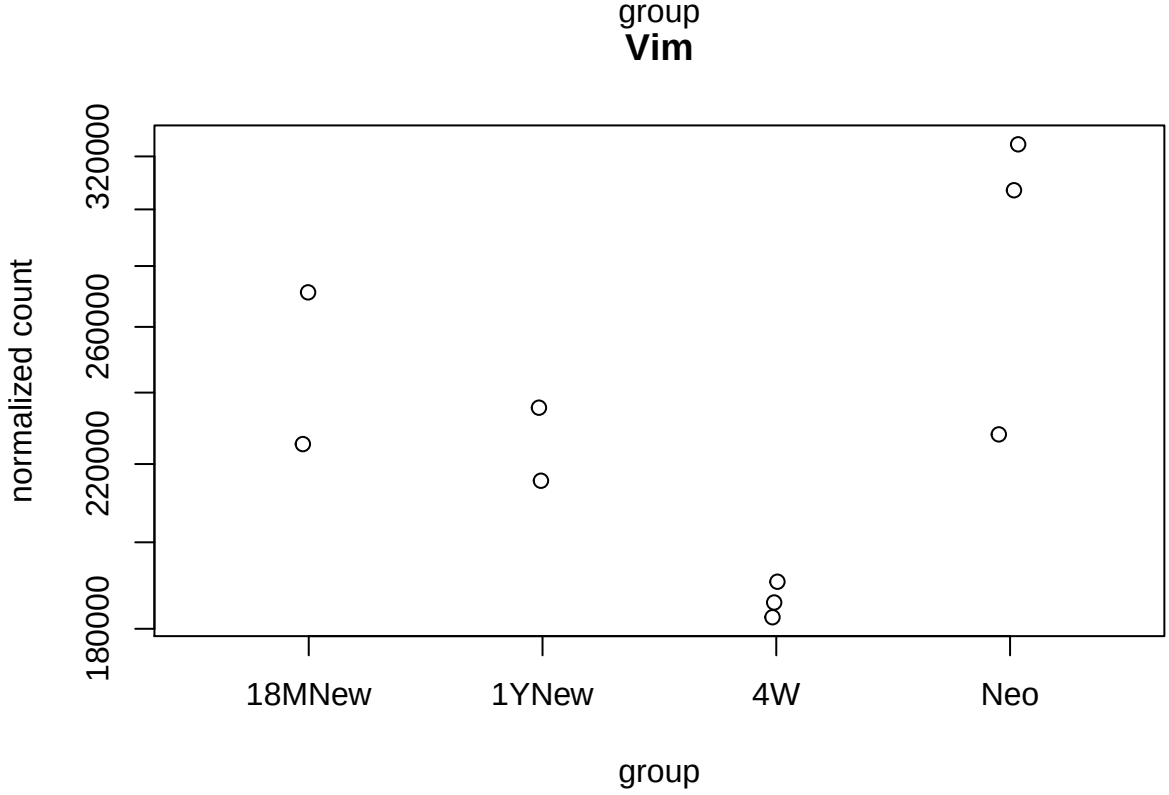


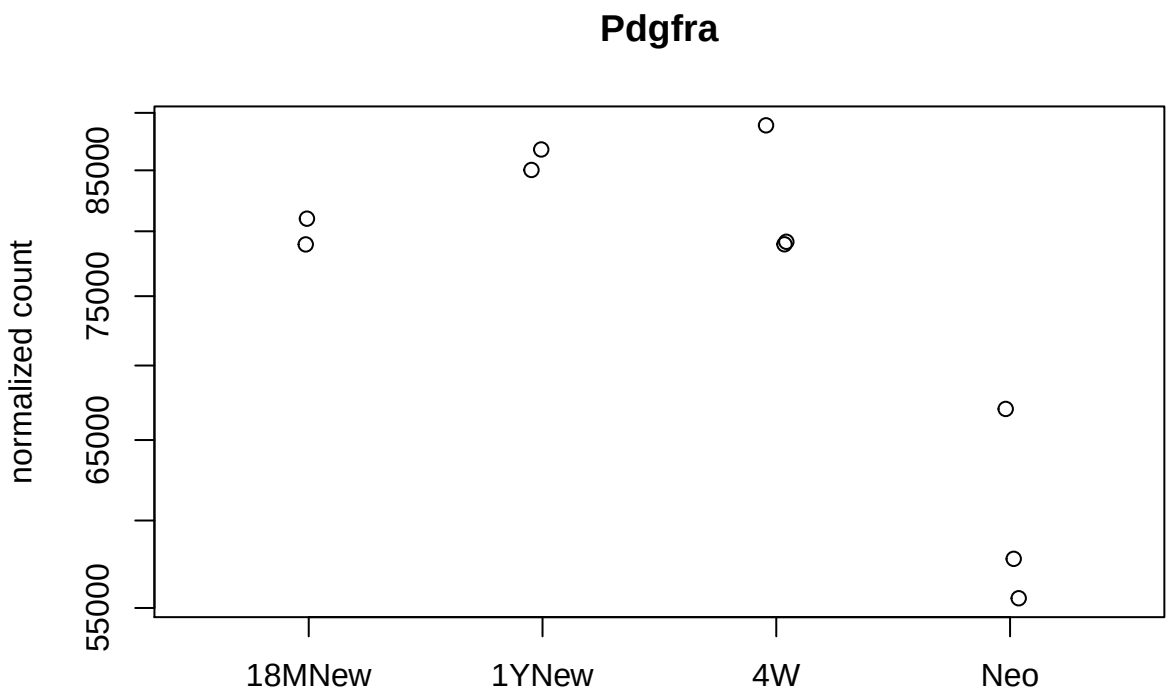
Normalize gene counts

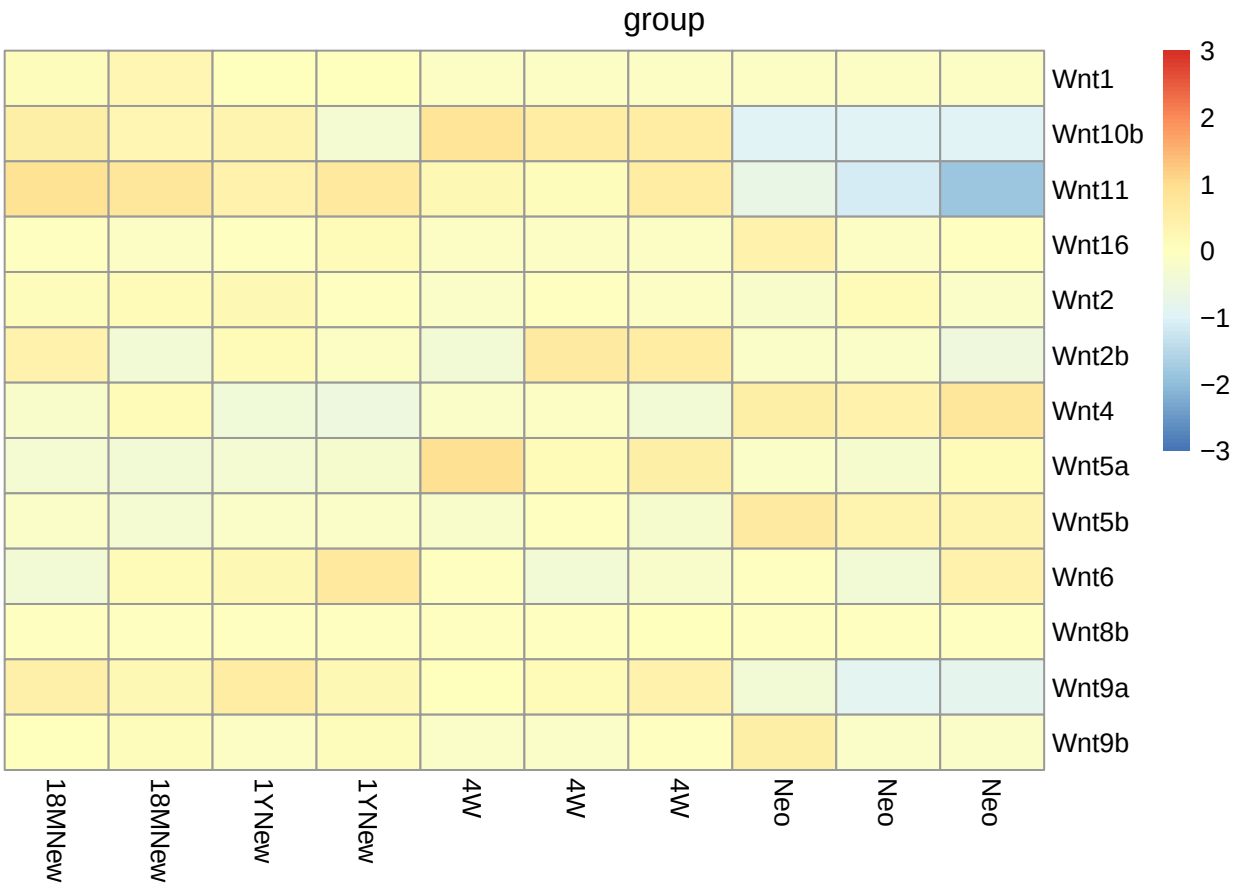
Plot specific gene expression values

```
##
## Attaching package: 'gplots'

## The following object is masked from 'package:IRanges':
##
##     space

## The following object is masked from 'package:S4Vectors':
##
##     space

## The following object is masked from 'package:stats':
##
##     lowess
```


Sfrp1
normalized count
70000
50000
40000
30000
18MNew
1YNew
4W
Neo
group


Vim
normalized count
320000
260000
220000
180000
18MNew
1YNew
4W
Neo
group





MAplot of DEGs