

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)

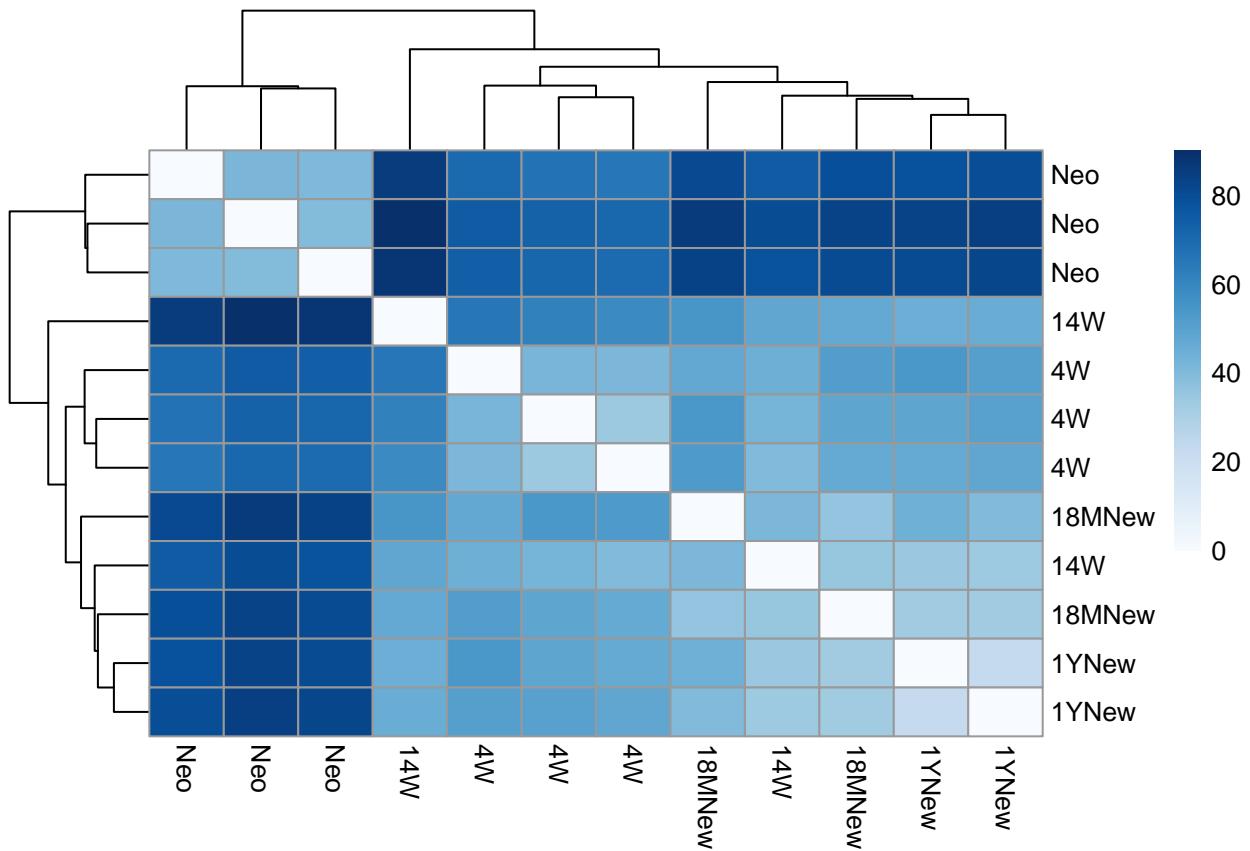
1YNew-1: 79M (26M) 1YNew-2: 64M (27M) 18MNew-1: 68M (25M) 18MNew-2: 69M (39M)

Gene quantification: readcount2TPM

Creating DESeqDataSet

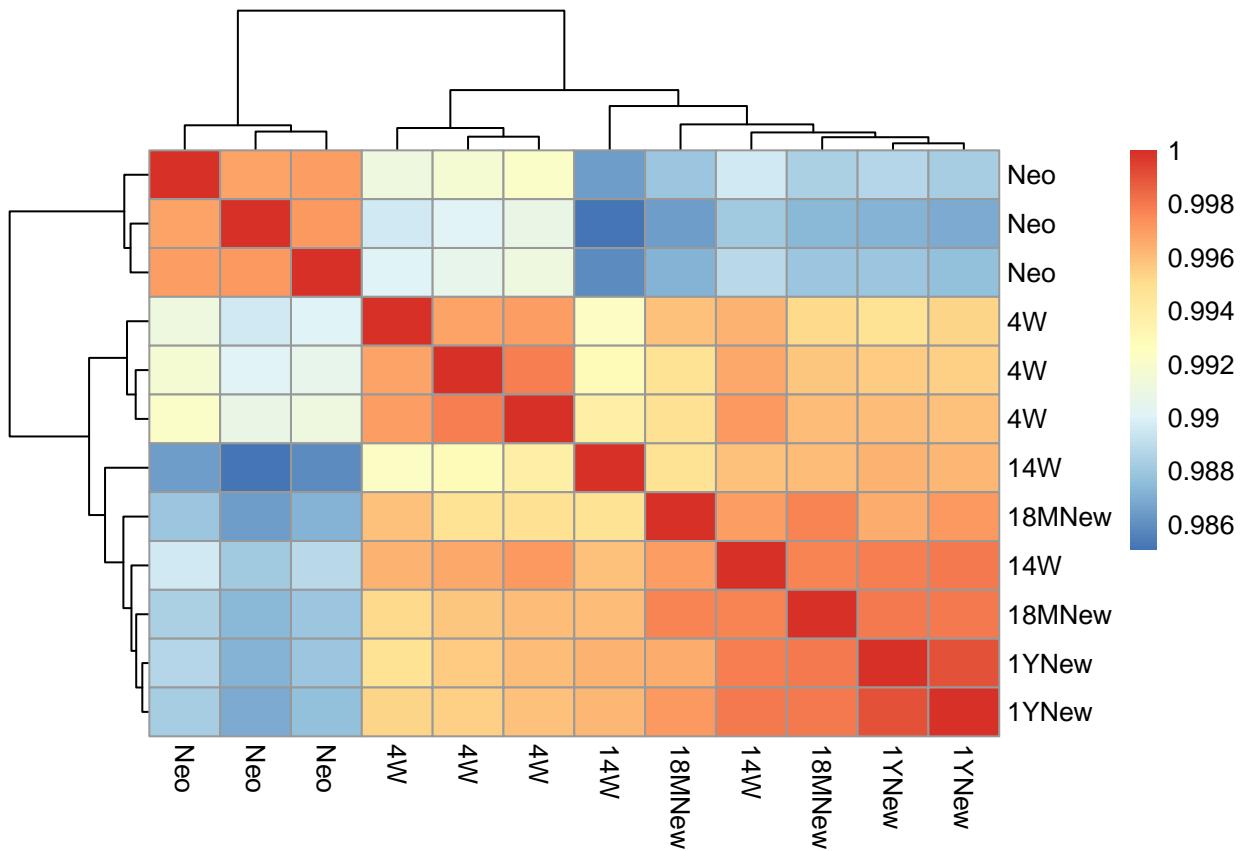
Pre-filtering and Log transformation

Quality control: clustering of sample distances

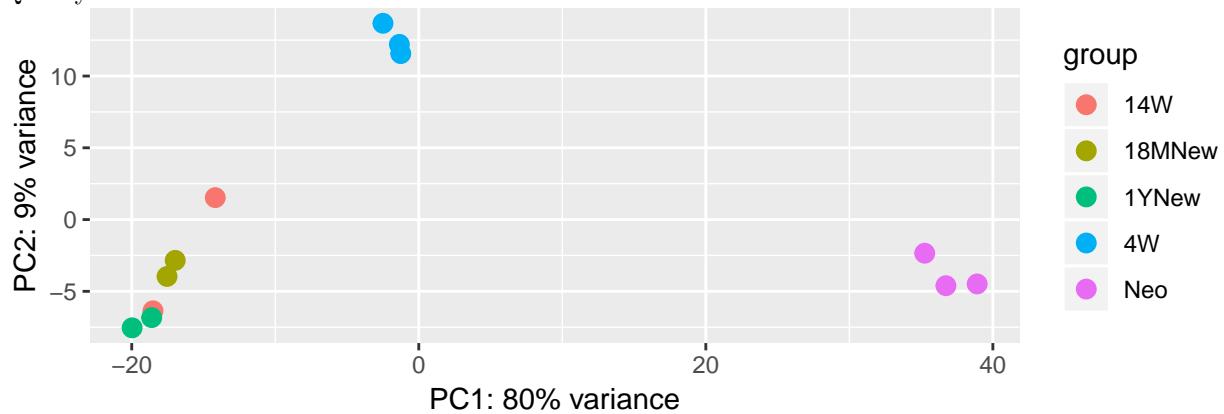


Quality control: clustering of sample correlations

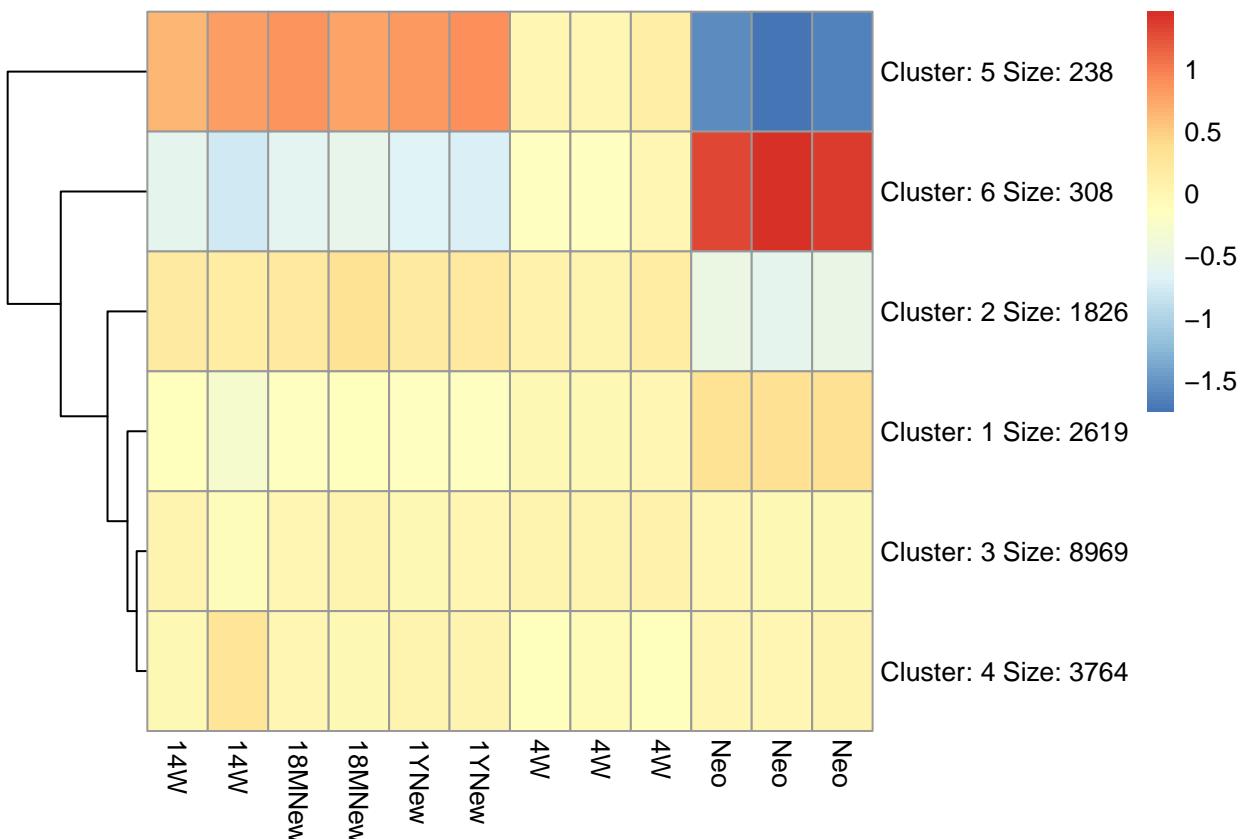
```
## corrplot 0.84 loaded
```



Quality control: PCA



K-means clustering of all genes for all samples

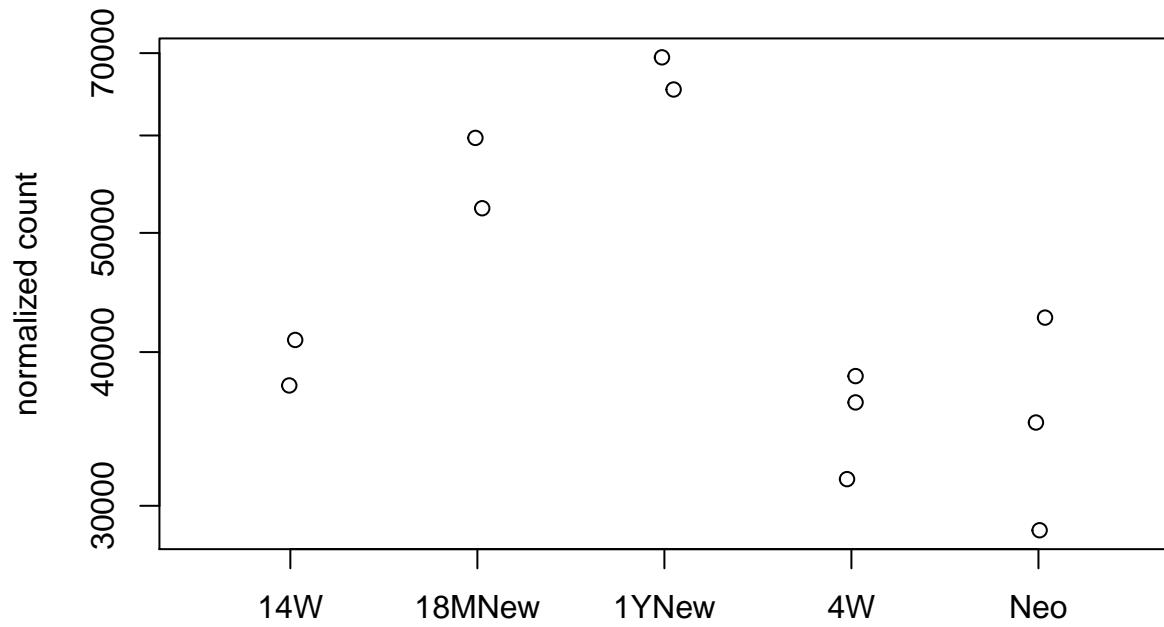


Normalize gene counts

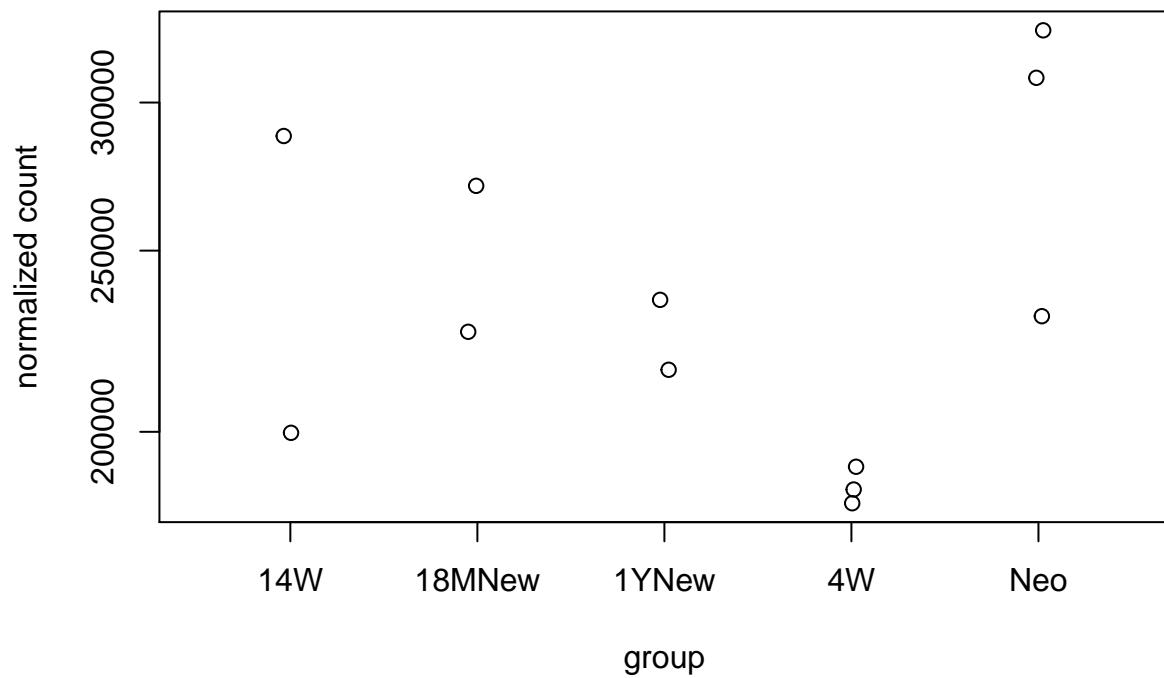
Plot specific gene expression values

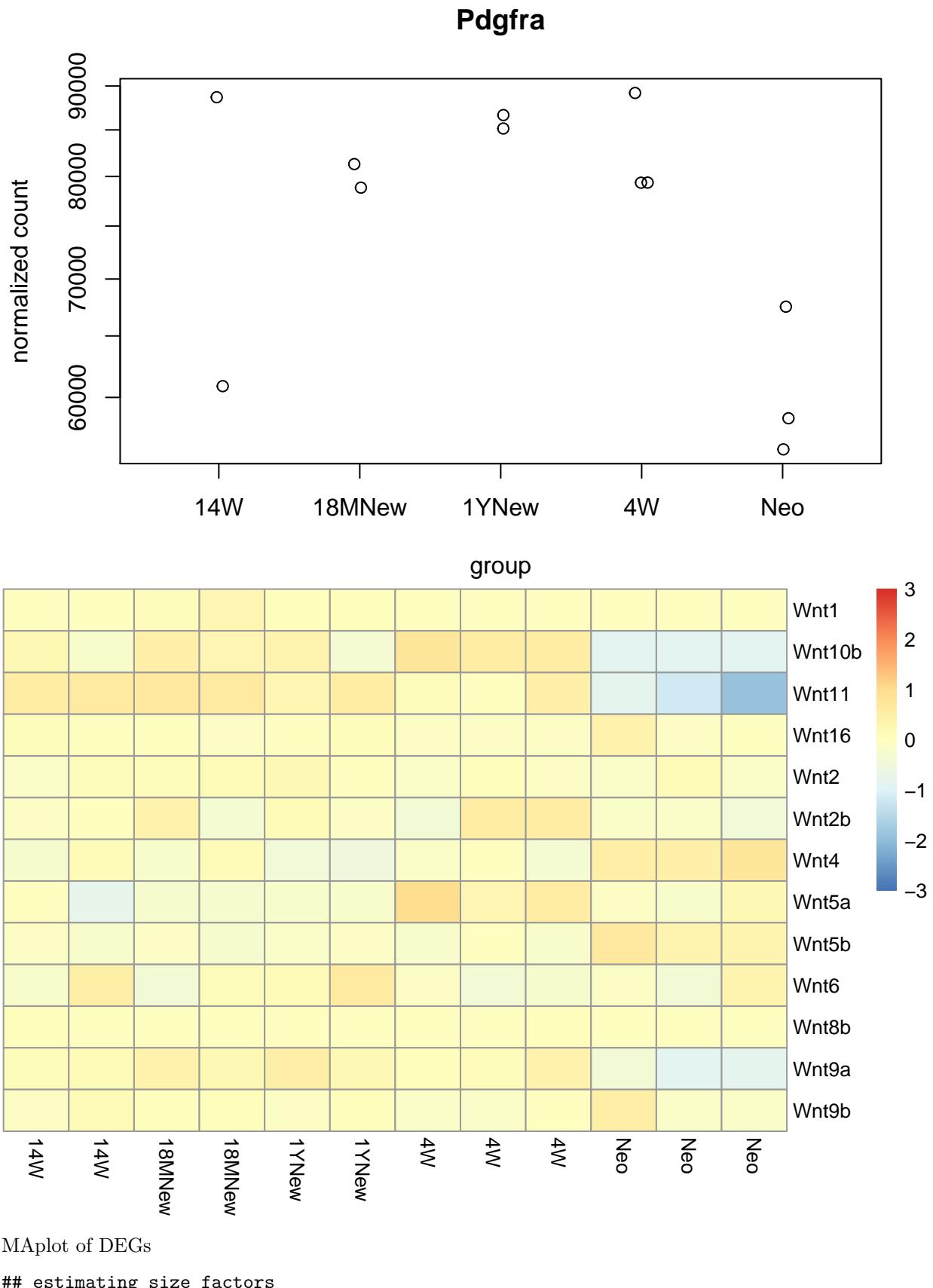
```
##
## Attaching package: 'gplots'
##
## The following object is masked from 'package:IRanges':
##      space
##
## The following object is masked from 'package:S4Vectors':
##      space
##
## The following object is masked from 'package:stats':
##      lowess
```

Sfrp1



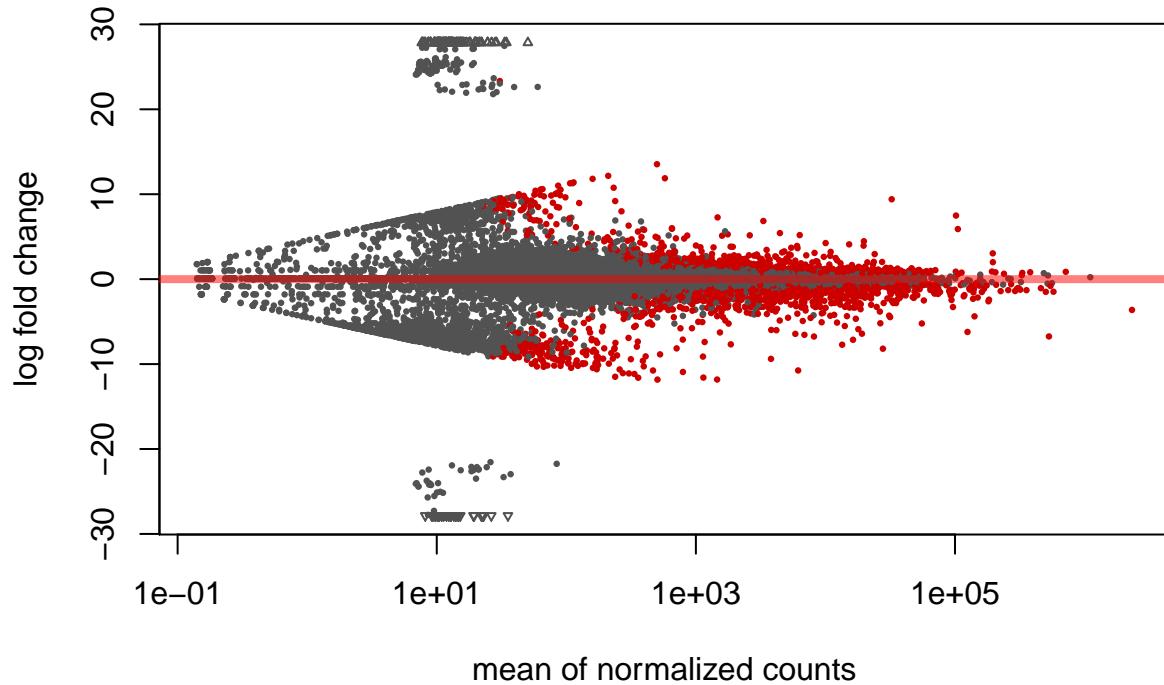
group Vim





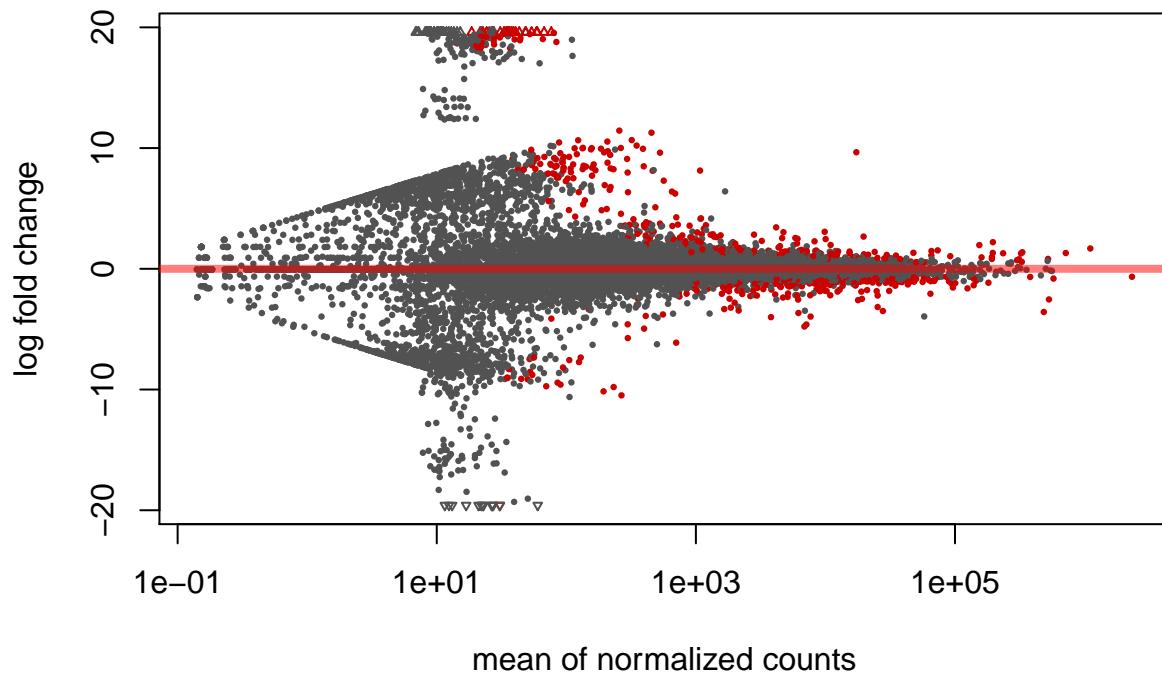
```
## estimating dispersions  
## gene-wise dispersion estimates  
## mean-dispersion relationship  
## final dispersion estimates  
## fitting model and testing
```

Neo VS 4W



```
## Loading required package: AnnotationDbi  
##  
## 'select()' returned 1:many mapping between keys and columns  
## 'select()' returned 1:many mapping between keys and columns
```

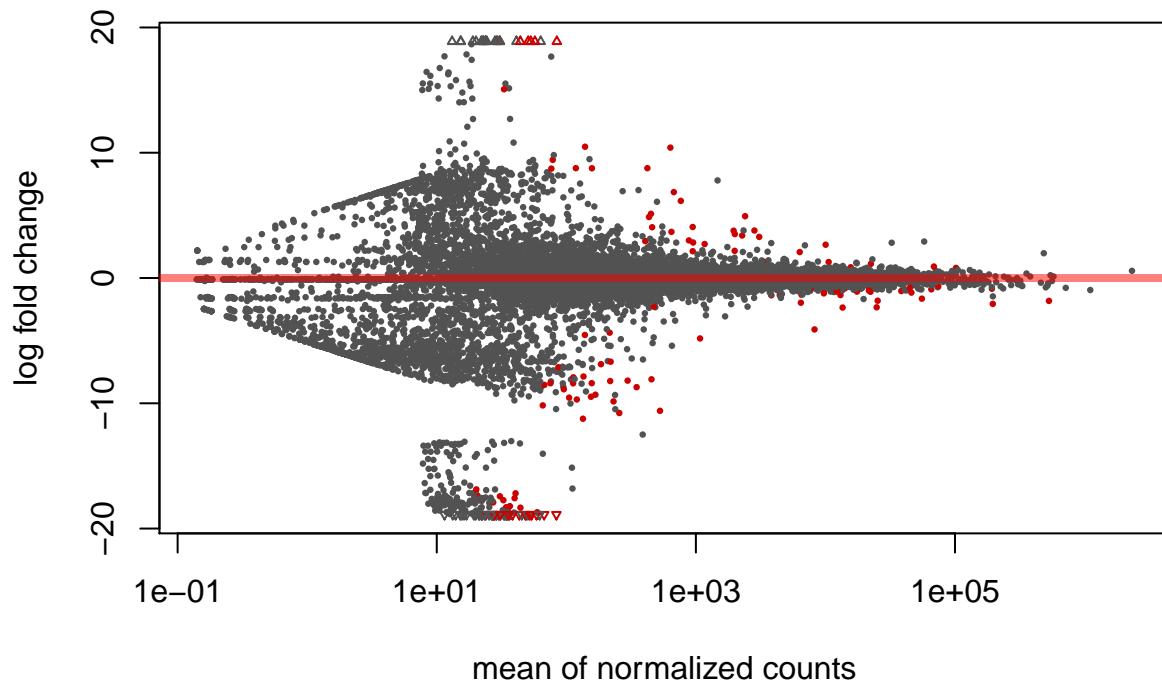
4W VS 14W



mean of normalized counts

```
## 'select()' returned 1:many mapping between keys and columns  
## 'select()' returned 1:many mapping between keys and columns
```

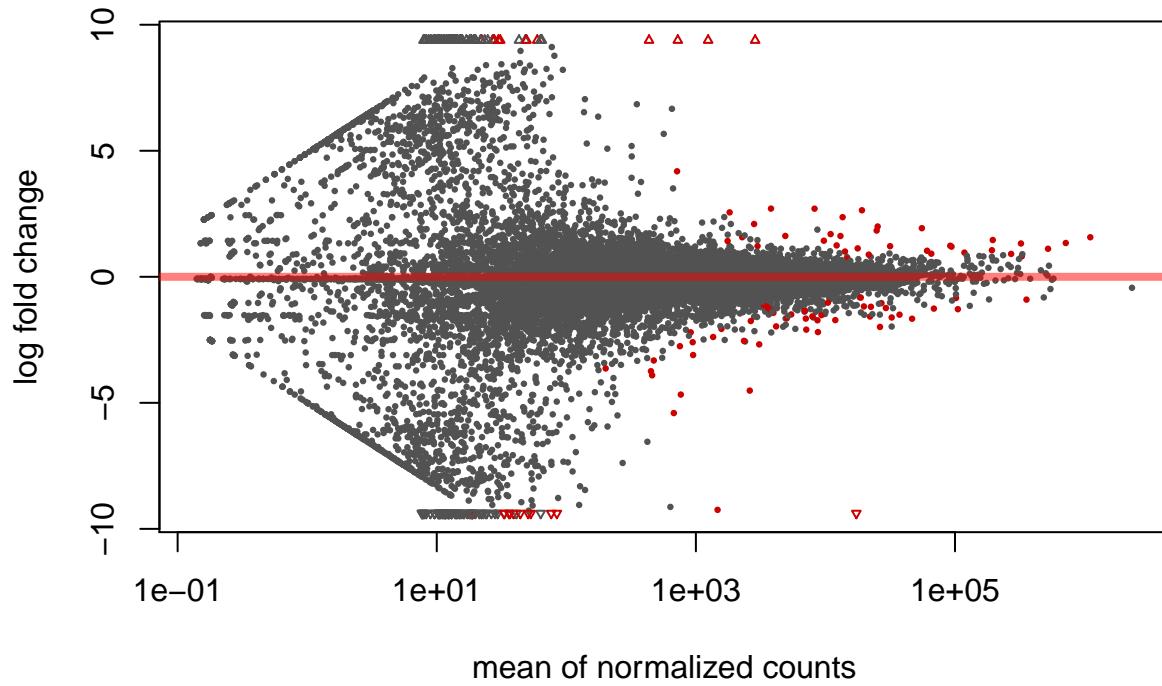
14W VS 1Y



mean of normalized counts

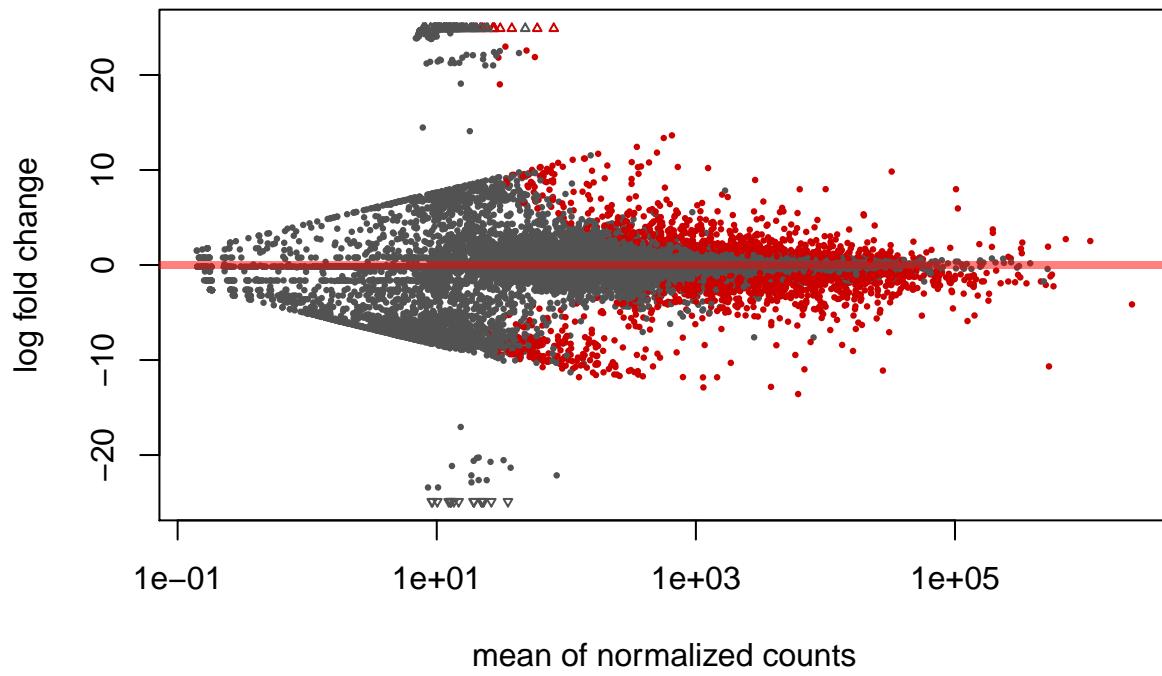
```
## 'select()' returned 1:many mapping between keys and columns  
## 'select()' returned 1:many mapping between keys and columns
```

1Y VS 18M



```
## 'select()' returned 1:many mapping between keys and columns  
## 'select()' returned 1:many mapping between keys and columns
```

Neo VS 18M



```
## 'select()' returned 1:many mapping between keys and columns  
## 'select()' returned 1:many mapping between keys and columns
```