R Project

```
library(readr)
res<- read.csv("res.csv", row.names = 1)
head(res)
```

GeneSymbol <fctr>	baseMean <dbl>	log2FoldChange <dbl>	lfcSE <dbl>	stat <dbl>	pvalue <dbl>	padj <dbl>
1 DDX11L1	0	NA	NA	NA	NA	NA
2 WASH7P	0	NA	NA	NA	NA	NA
3 MIR6859-3	0	NA	NA	NA	NA	NA
4 MIR6859-2	0	NA	NA	NA	NA	NA
5 MIR6859-1	0	NA	NA	NA	NA	NA
6 MIR6859-4	0	NA	NA	NA	NA	NA

6 rows

```
final <- as.data.frame(res)
head(final)
```

| GeneSymbol <fctr>	baseMean <dbl>	log2FoldChange <dbl>	lfcSE <dbl>	stat <dbl>	pvalue <dbl>	padj <dbl>
1 DDX11L1	0	NA	NA	NA	NA	NA
2 WASH7P	0	NA	NA	NA	NA	NA
3 MIR6859-3	0	NA	NA	NA	NA	NA
4 MIR6859-2	0	NA	NA	NA	NA	NA
5 MIR6859-1	0	NA	NA	NA	NA	NA
6 MIR6859-4	0	NA	NA	NA	NA	NA

6 rows

```
library(ggplot2)
ggplot(final, aes(x=baseMean, y=log2FoldChange)) +
   geom_point(aes(colour = padj<0.1), size=1)
```
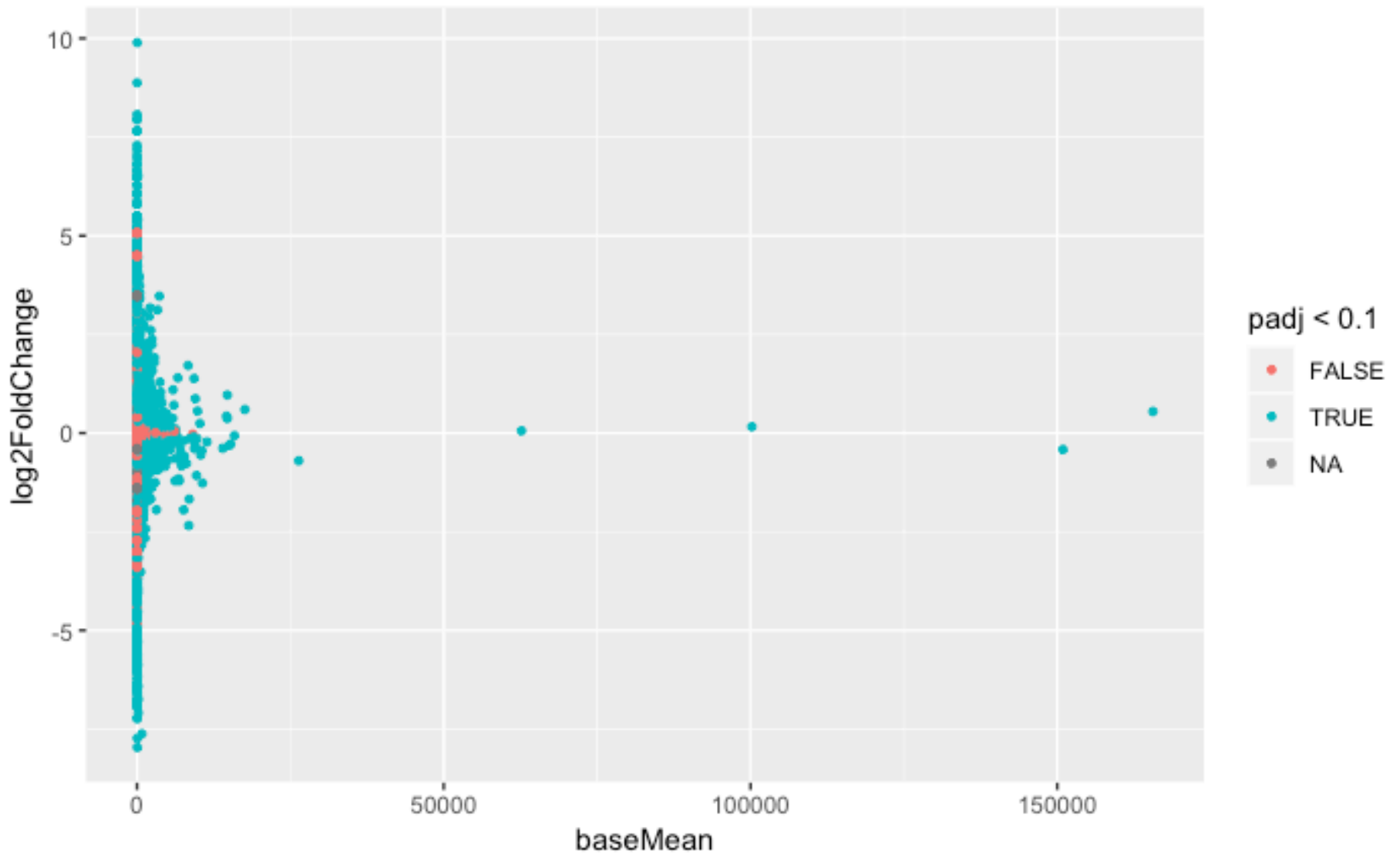
```
ggplot(final, aes(x=baseMean, y=log2FoldChange)) +
   geom_point(aes(colour = padj<0.1), size=1)+
   geom_hline(aes(yintercept =0), colour ="blue", size =1.2)+
   scale_x_continuous(trans = "log10", limits = c(0.1, 300000))
```
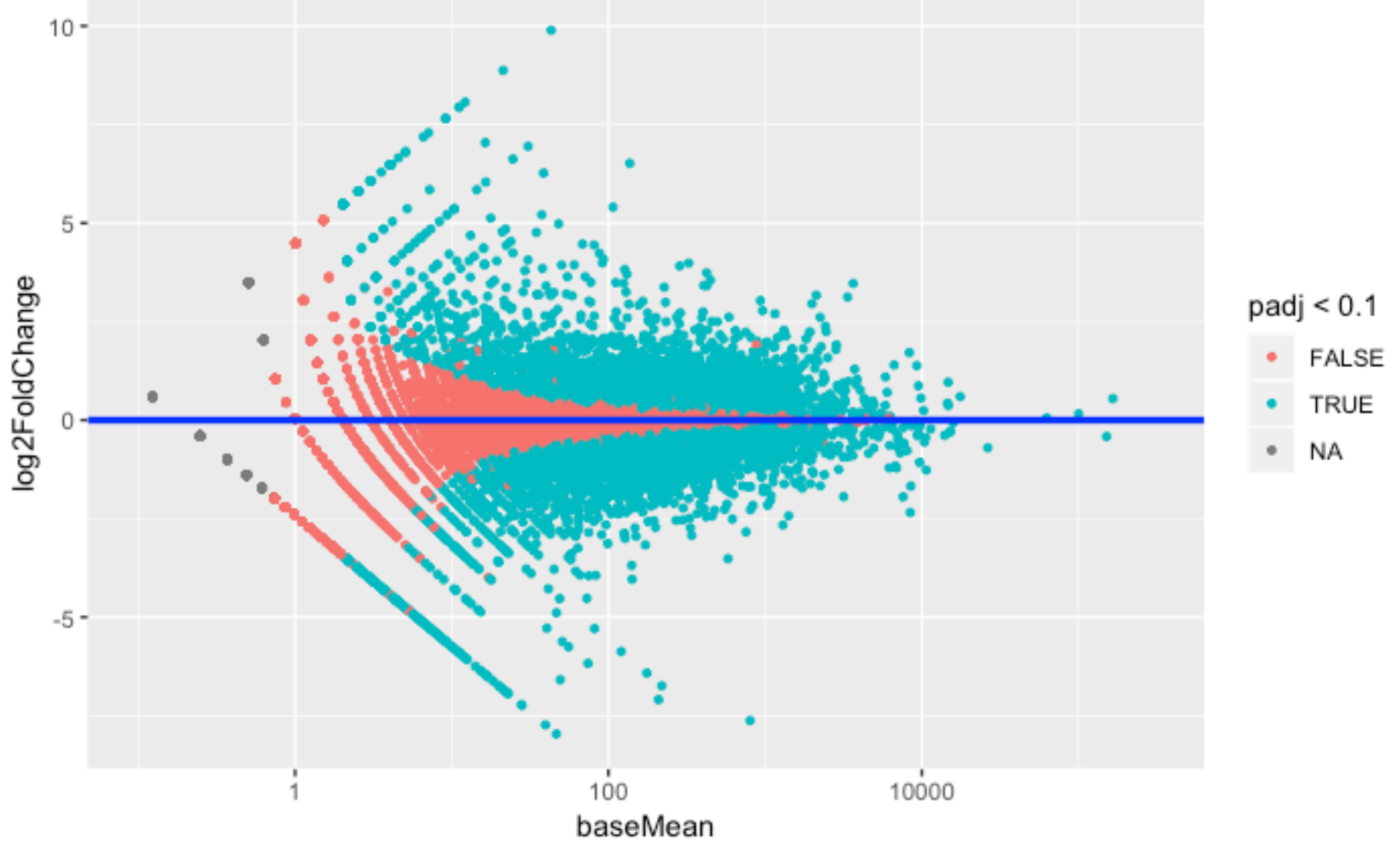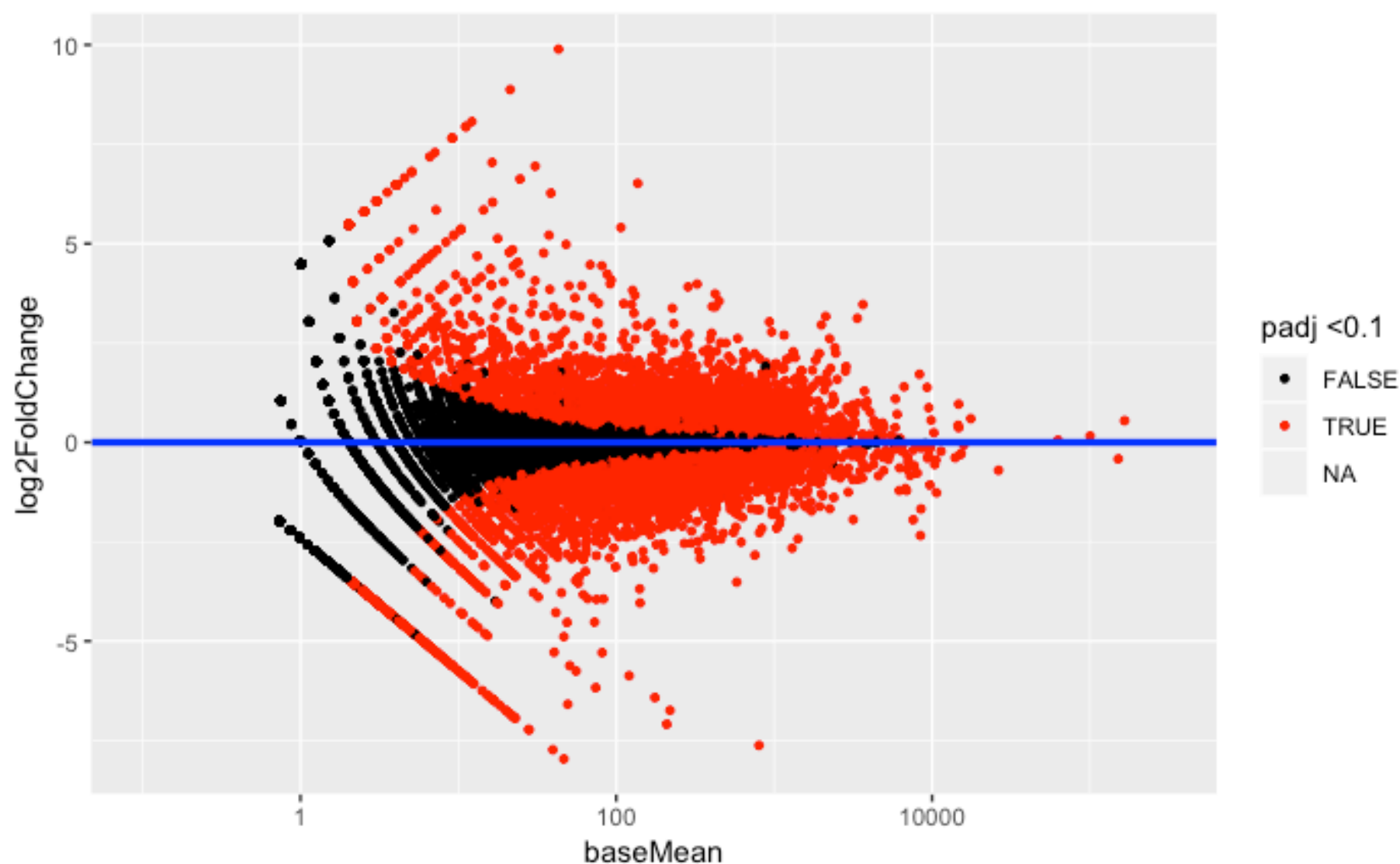
```
ggplot(final, aes(x=baseMean, y=log2FoldChange)) +
  geom_point(aes(colour = padj<0.1), size=1)+
  geom_hline(aes(yintercept =0), colour ="blue", size =1.2)+
  scale_color_manual(name='padj <0.1', values = setNames(c('red', 'black'), c(T,F)))+
  scale_x_continuous(trans = "log10", limits = c(0.1, 300000))
```

```
theme_1 <- theme_bw() +
  theme(axis.title = element_text(size = 12),
        axis.text = element_text(size = 8))
ggplot(final, aes(x=baseMean, y=log2FoldChange)) +
  geom_point(aes(colour = padj<0.1), size=1)+
  geom_hline(aes(yintercept =0), colour ="blue", size =1)+
  scale_color_manual(name='padj <0.1', values = setNames(c('red', 'black'), c(T,F)))+
  scale_x_continuous(trans = "log10", limits = c(0.1, 300000))+
  theme_1
```
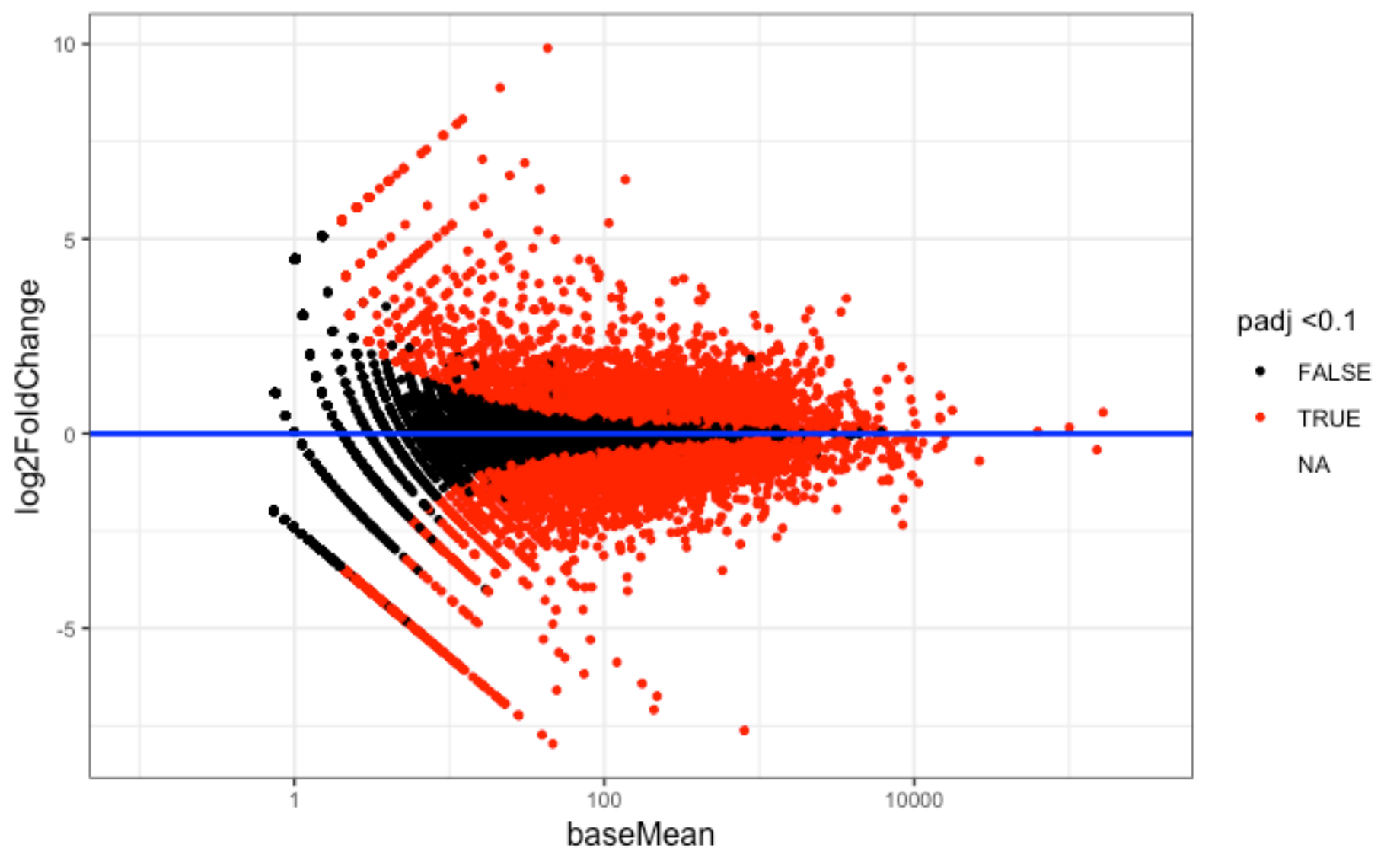
```
ggplot(final, aes(x=baseMean, y=log2FoldChange)) +
    geom_point(aes(colour = padj<0.1), size=1)+
    geom_hline(aes(yintercept =0), colour ="blue", size =1)+
    scale_color_manual(name='padj <0.1', values = setNames(c('red', 'black'), c(T,F))
)+
    scale_x_continuous(trans = "log10", limits = c(0.1, 300000))+
  geom_text(aes(label=GeneSymbol),
            color = 'gray20',
            data = final %>%
              filter(GeneSymbol %in% padj < 0.1))
```

Legend:
padj <0.1
- FALSE (black)
- TRUE (red)
- NA

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```
order <- final[order(final$padj),]
topR <- rbind( order[ order[,'log2FoldChange'] > 0, ][1:n,],
               order[ order[,'log2FoldChange'] < 0, ][n:1,] )
top20 <-topR[1:20,]
top20
```

	GeneSym…	baseMean	log2FoldChange	lfcSE	stat	pvalue	
	<fctr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	
37	ISG15	932.3712	3.0334576	0.08004379	37.89748	0.000000e+00	0.0
159	ERRFI1	1831.0891	2.0643043	0.05299500	38.95282	0.000000e+00	0.0
3414	SCD	2829.6049	1.7920463	0.04309464	41.58397	0.000000e+00	0.0
5182	HSPA8	2275.2478	1.8642108	0.04748086	39.26236	0.000000e+00	0.0
7246	RPPH1	165600.4365	0.5467732	0.00953963	57.31598	0.000000e+00	0.0
8273	GREM1	2120.1368	3.1703884	0.05797584	54.68464	0.000000e+00	0.0
9665	MT2A	2451.8712	2.2471130	0.04756282	47.24516	0.000000e+00	0.0
13196	FTL	14733.3347	0.9636975	0.02151414	44.79367	0.000000e+00	0.0

| 14255 TMSB10 | 8320.9946 | 1.7122875 | 0.02759413 | 62.05260 | 0.000000e+00 | 0.0 |
| 19358 MSMO1 | 1989.8795 | 2.9555778 | 0.05665227 | 52.17051 | 0.000000e+00 | 0.0 |

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```
ggplot(final, aes(x=baseMean, y=log2FoldChange)) +
  geom_point(aes(colour = padj<0.1), size=1)+
  geom_hline(aes(yintercept =0), colour ="blue", size =1)+
  scale_color_manual(name='padj <0.1', values = setNames(c('red', 'black'), c(T,F)))+
  scale_x_continuous(trans = "log10", limits = c(0.1, 300000))+
  geom_text(aes(label=GeneSymbol),
            color = 'gray20',
            data = final %>%
                filter(GeneSymbol %in% top20))
```