filter_steps_single

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Load the data

```
single<-readRDS("data/single.rds")
test_line<-readRDS("data/geuvadis_quantile.rds")
cancer<-readRDS("data/cancer_annot.rds")
potential_single_cell<-readRDS("data/potential_single_cell.rds")

seq_mean=seq(0,4.6,by=0.1)
```

Starting numbers

```
#Total number of single-end samples:
nrow(single)
```

```
## [1] 105048
```

Filter #1:

Filter based on single cell

```
# number of samples removed in this step
scRNA<-which(single$external_id %in% potential_single_cell)
length(scRNA)
```

```
## [1] 1119
```

```
single<-single[-scRNA,]
```

Filter #2:

Filter based on total read count for 75% of SNPs in each sample

```
quantile(single$read75, na.rm=T)
```

```
##      0%     25%     50%     75%    100%
##     9.0    23.0    31.0    40.0 10468.5
```

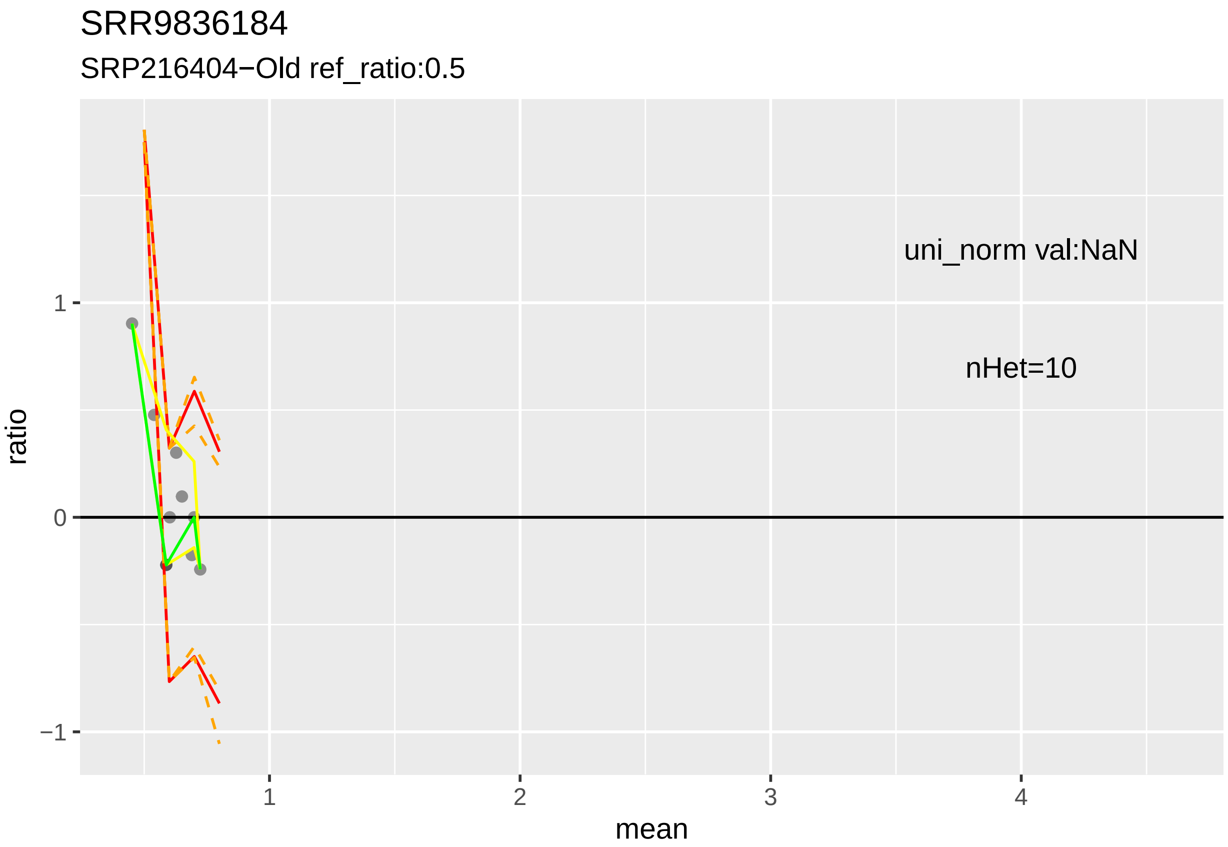
```
low_count<-single %>% filter(read75>10)

# number of samples removed in this step
nrow(single)- nrow(low_count)
```

```
## [1] 14517
```

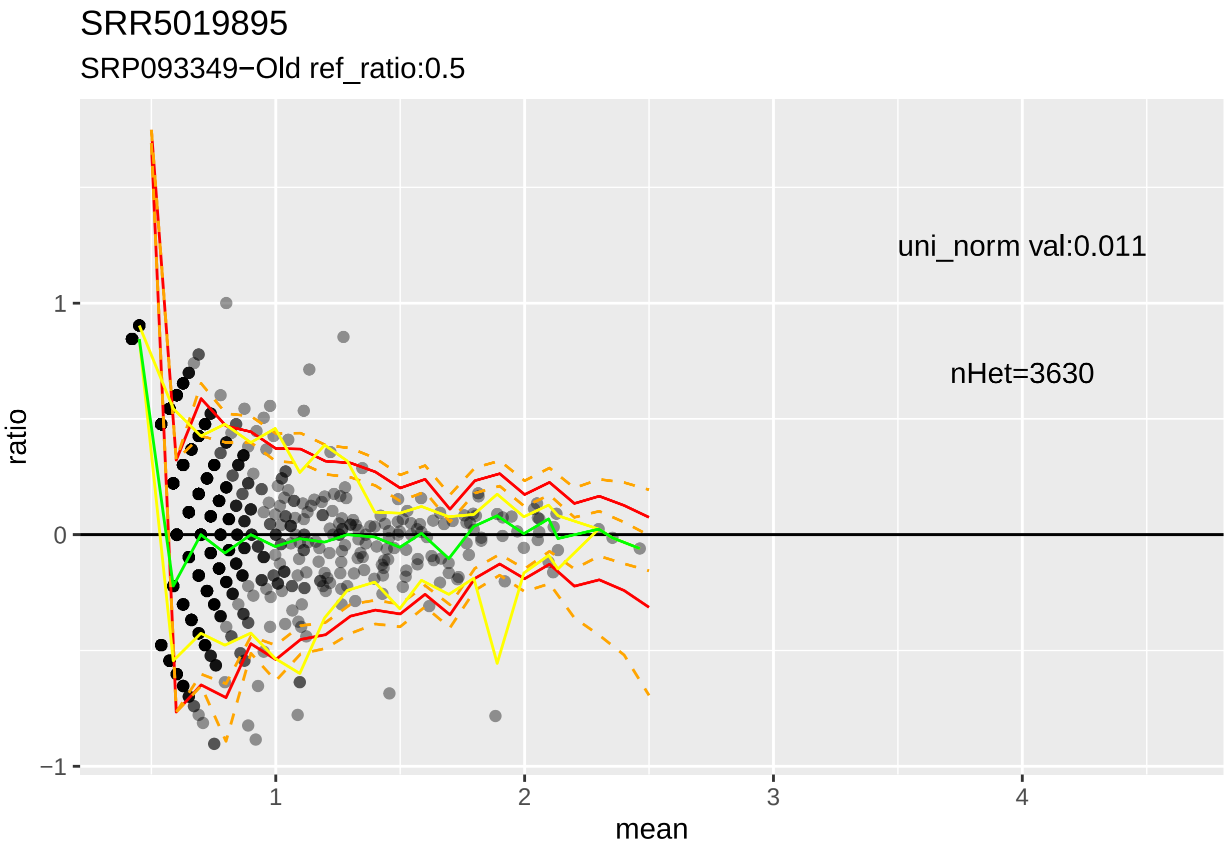
Plot filter 2

```
plot_df<-single %>% filter(read75<=10)


data_samp<-plot_df[sample(nrow(plot_df), 4),]

make_plot(data_samp)
```

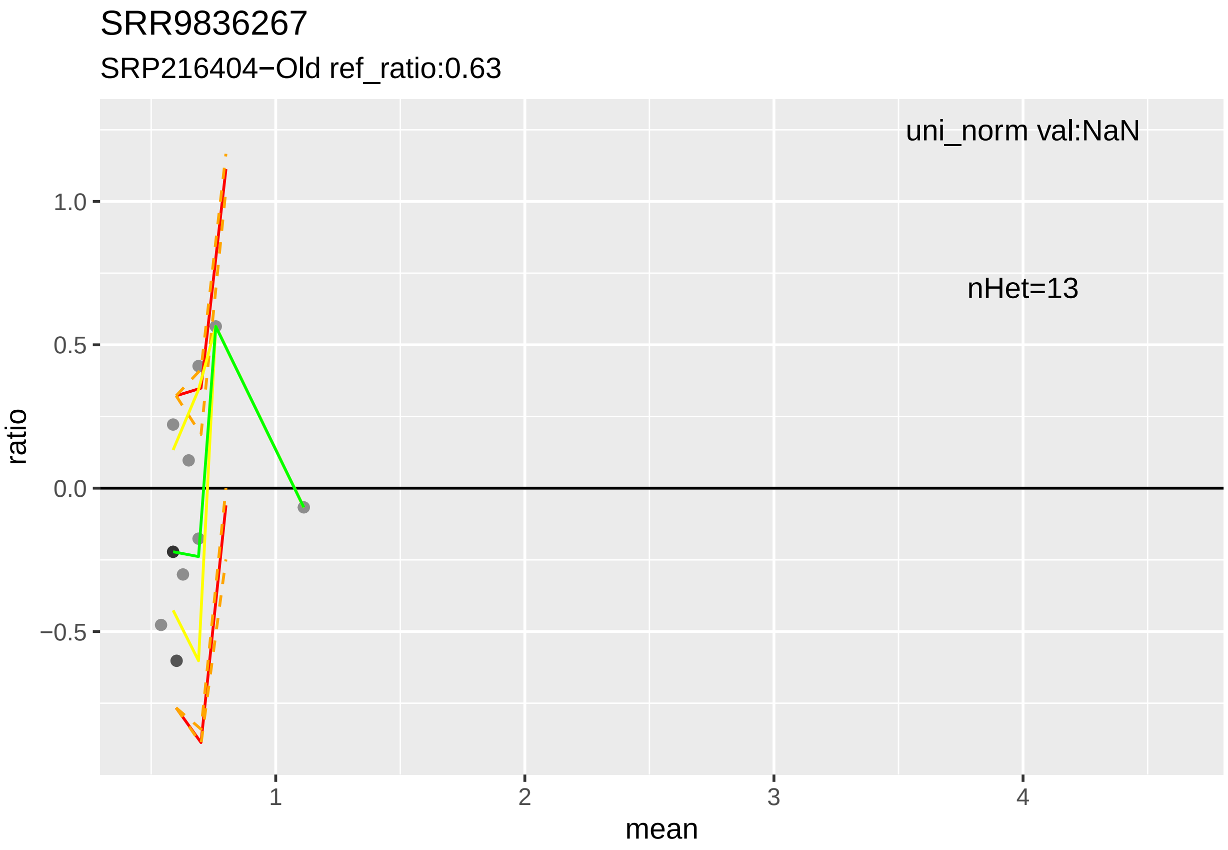
```
## [1] 1
## [1] "ase found"
```



```
## [1] 2
## [1] "ase found"
```



```
## [1] 3
## [1] "ase found"
```



```
## [1] 4
## [1] "ase found"
```

```
## null device
##           1
```

Filter #3:

Filter based on low number of heterozygous

```
quantile(low_count$nHet, na.rm=T)
```

```
##     0%    25%    50%    75%   100%
##      5   1377   4261   8236 247526
```

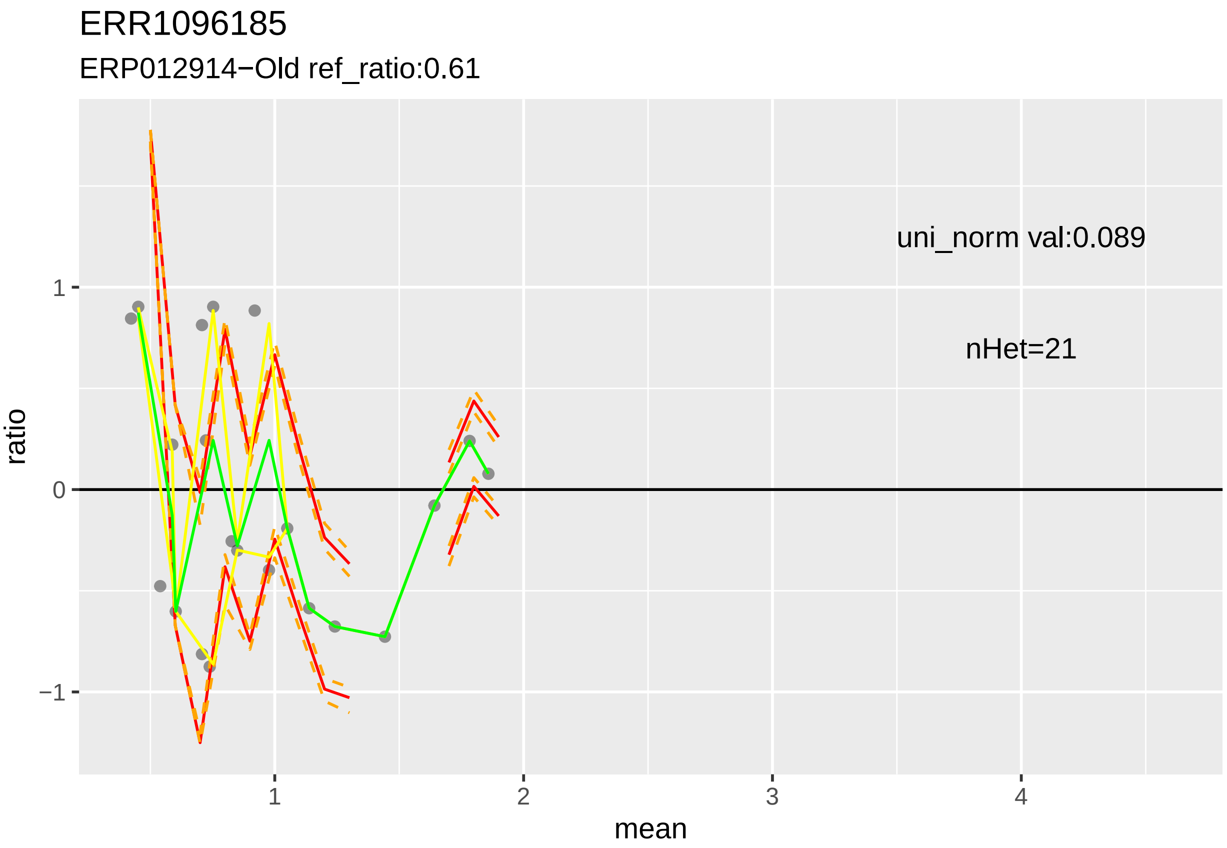
```
nhet<- low_count %>% filter(nHet>500)

# number of samples removed in this step
nrow(low_count)- nrow(nhet)
```

```
## [1] 11947
```

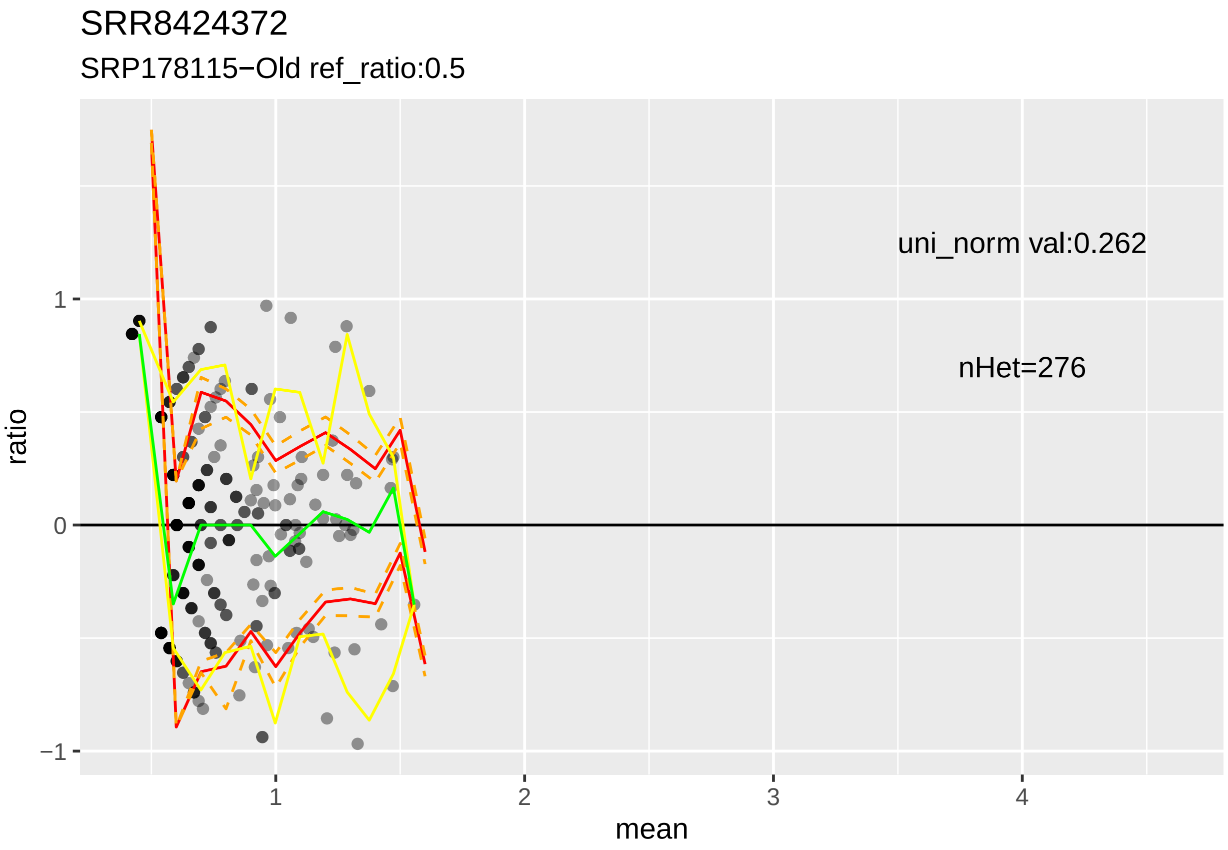
Plot filter 3

```
plot_df<-low_count %>% filter(nHet<=1000)


data_samp<-plot_df[sample(nrow(plot_df), 4),]

make_plot(data_samp)
```

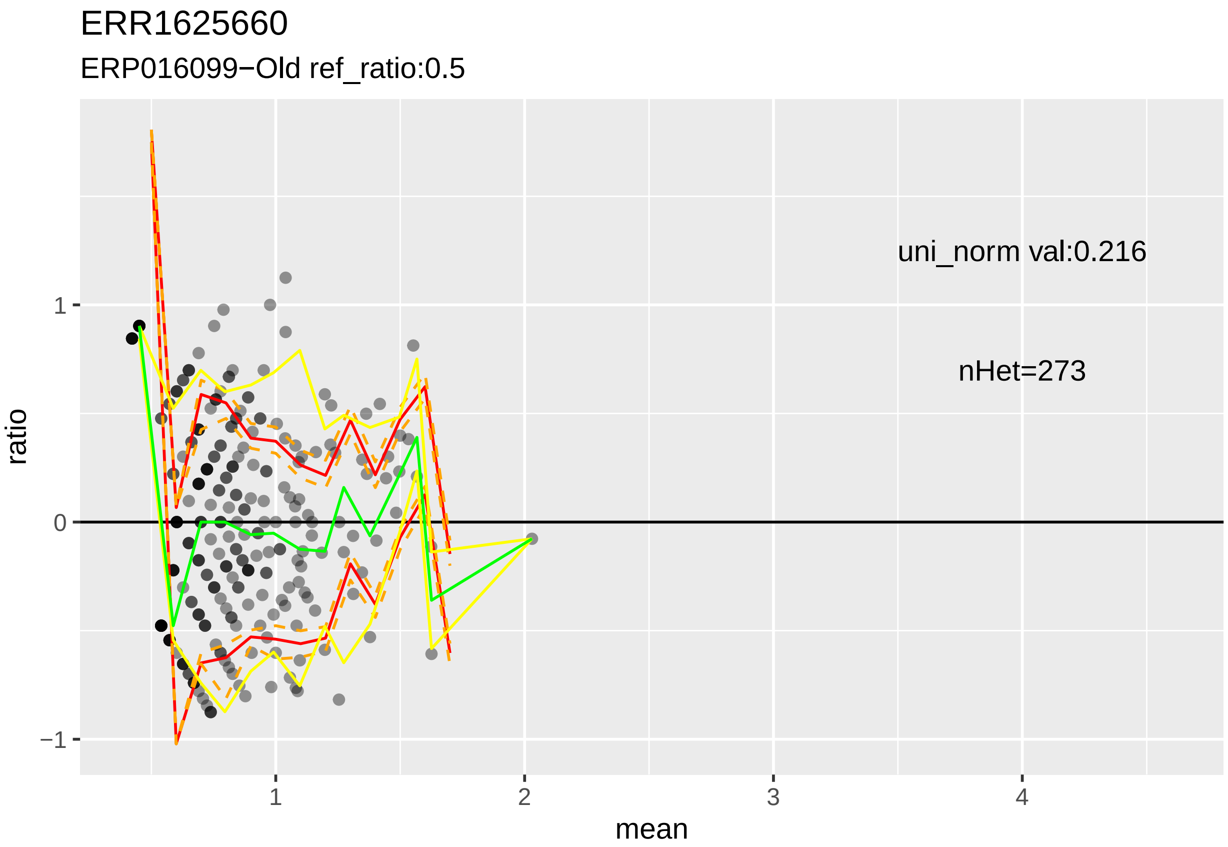
```
## [1] 1
## [1] "ase found"
```



```
## [1] 2
## [1] "ase found"
```



```
## [1] 3
## [1] "ase found"
```



```
## [1] 4
## [1] "ase found"
```

```
## null device
##           1
```

Filter #4:

Filter cancer samples

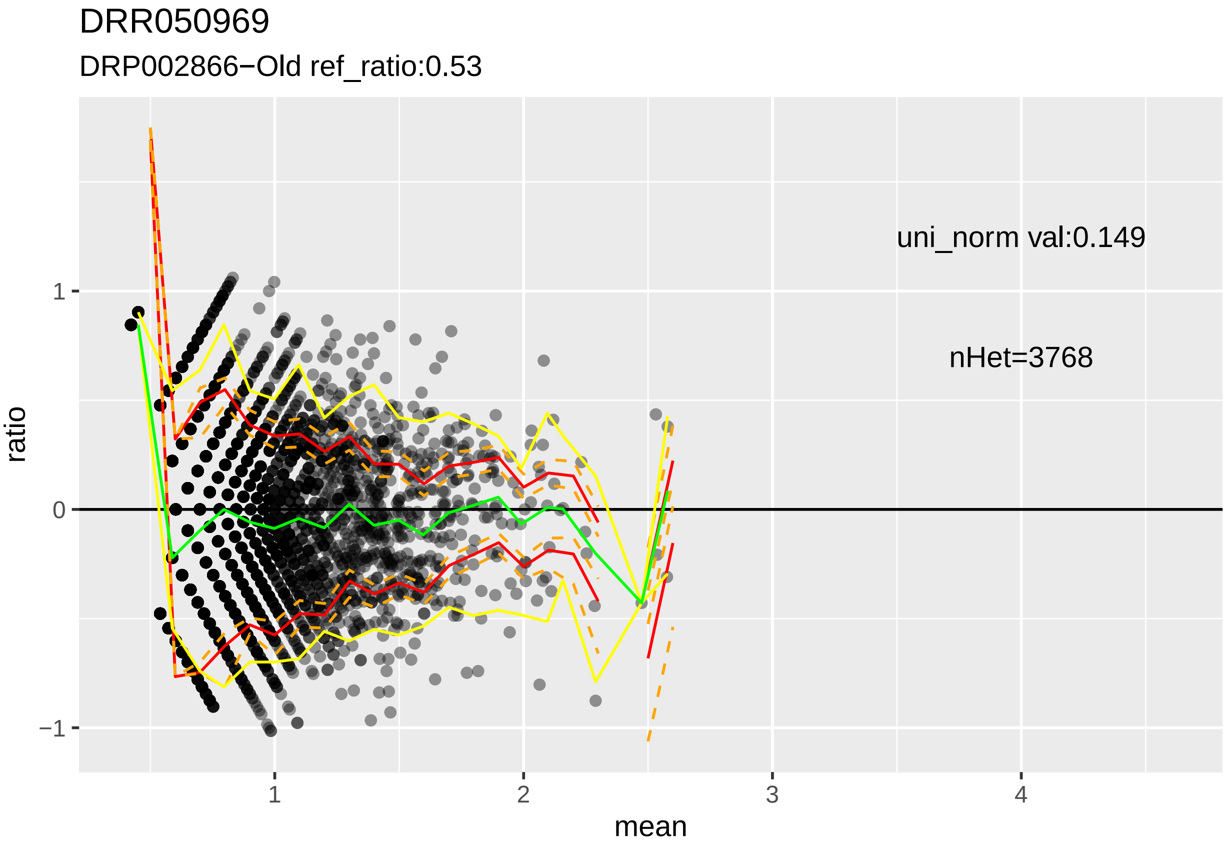
```
single_noncancer<-nhet[-which(nhet$sample_acc %in% cancer[,1]),]

# number of samples removed in this step
nrow(nhet)- nrow(single_noncancer)
```

```
## [1] 12920
```

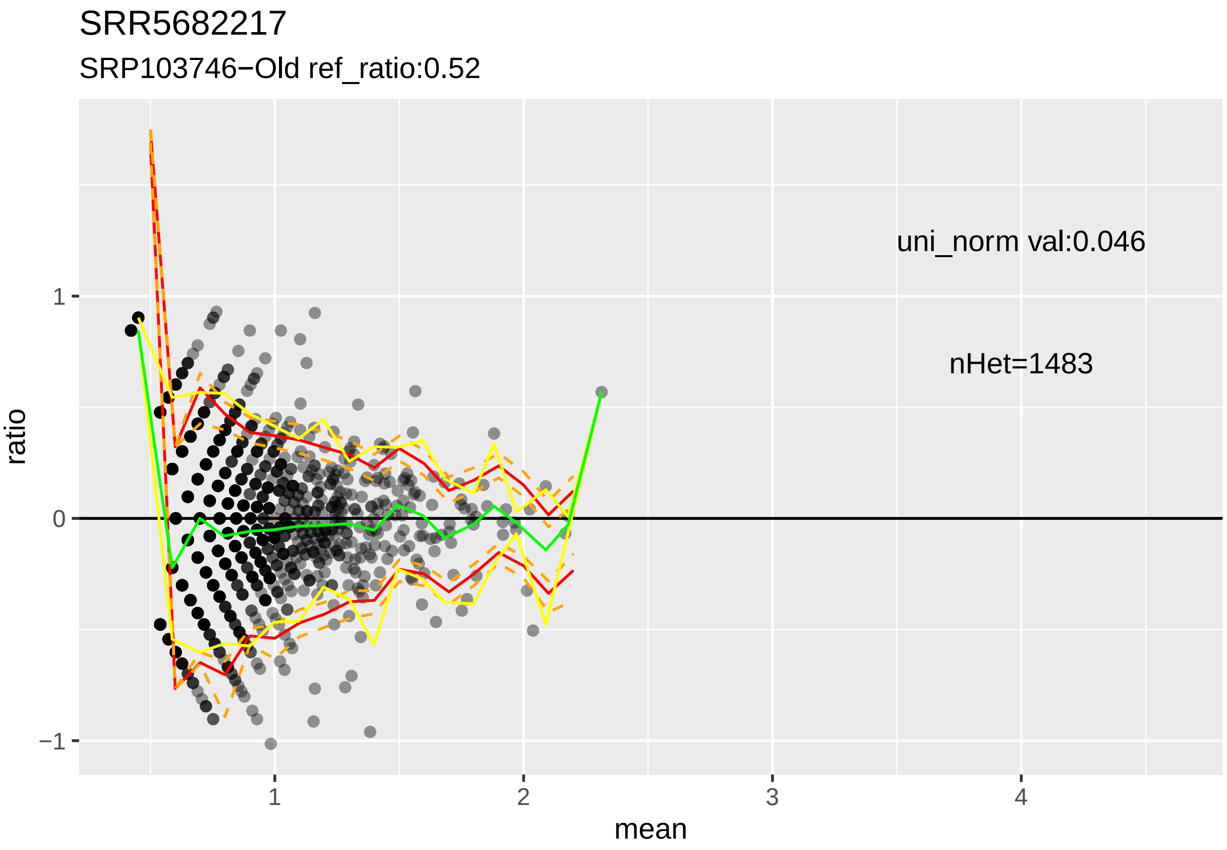
Plot filter 4

```r
plot_df<-nhet[which(nhet$sample_acc %in% cancer[,1]),]


data_samp<-plot_df[sample(nrow(plot_df), 4),]

make_plot(data_samp)
```

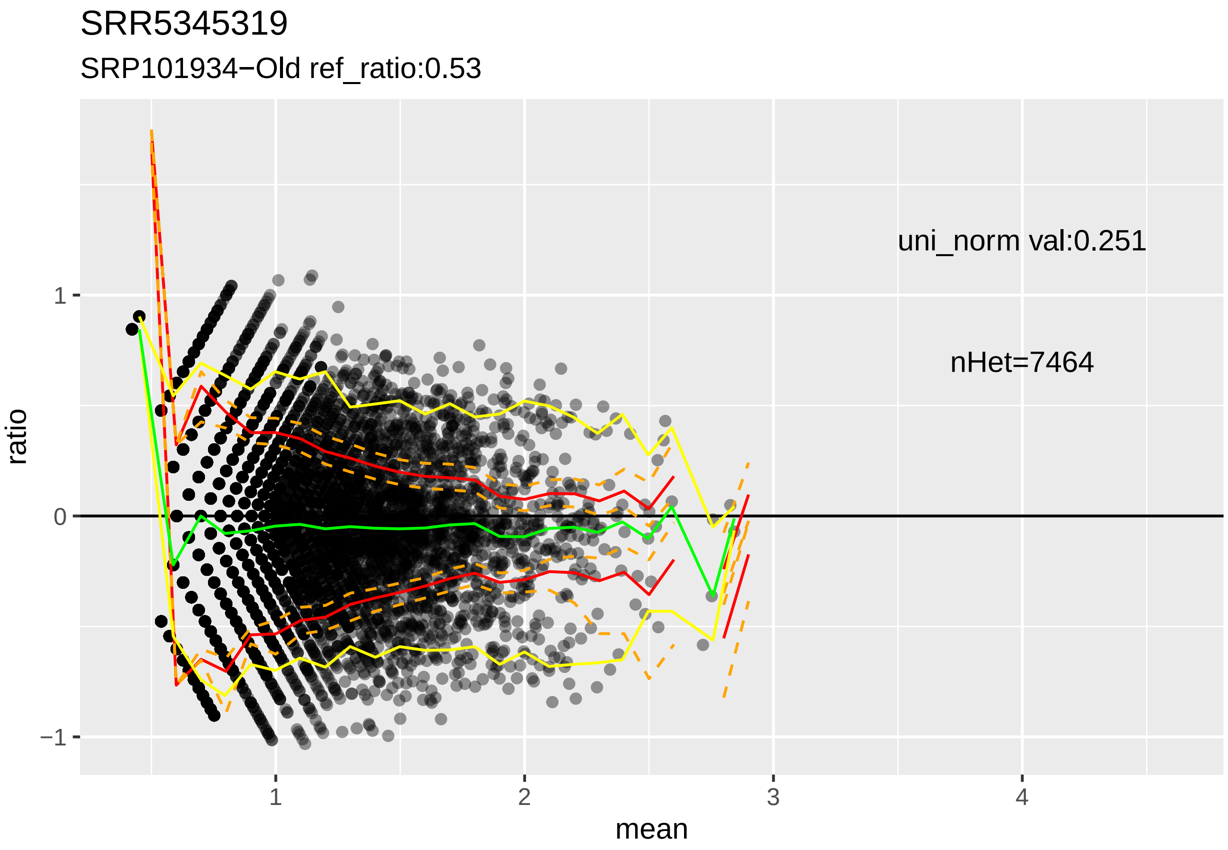
```
## [1] 1
## [1] "ase found"
```



```
## [1] 2
## [1] "ase found"
```



```
## [1] 3
## [1] "ase found"
```



```
## [1] 4
## [1] "ase found"
```

```
## null device
##           1
```

Filter #5:

Filter based on extreme median ref-ratio

```
quantile(single_noncancer$ref_ratio, na.rm=T)
```

```
##        0%       25%       50%       75%      100%
## 0.1764706 0.5147787 0.5263158 0.5333333 0.8034759
```

```
fold_c<- single_noncancer %>% filter(ref_ratio>0.4, ref_ratio<0.6 )

# number of samples removed in this step
nrow(single_noncancer)- nrow(fold_c)
```

```
## [1] 2359
```

Filter #6:

Filter based on uni_norm value

```
quantile(single$uni_norm, na.rm=T)
```

```
##           0%          25%          50%          75%         100% 
## 4.677412e-06 5.642309e-02 1.258057e-01 2.112597e-01 1.349228e+00
```

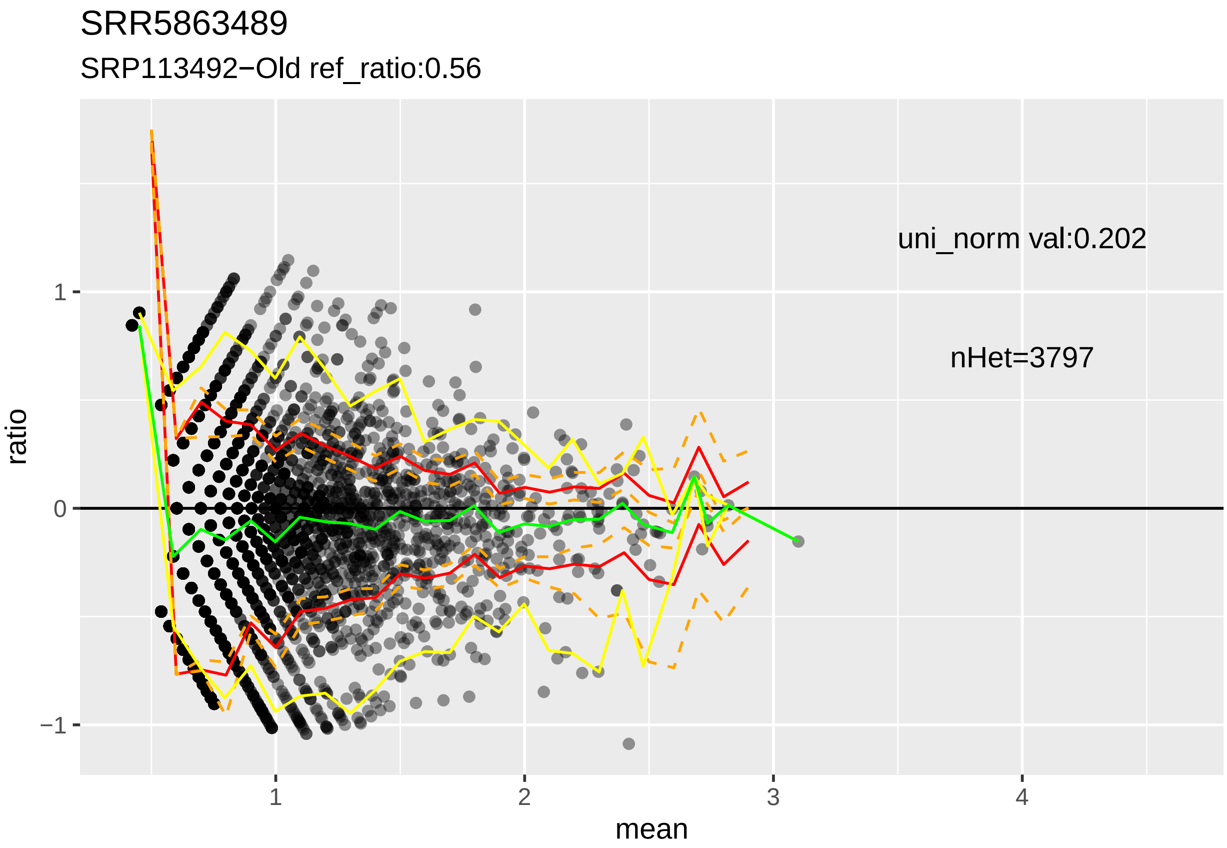
```
good<- fold_c %>%  filter(uni_norm<0.185)

# number of samples removed in this step
nrow(fold_c)- nrow(good)
```

```
## [1] 24659
```

Plot filter 6

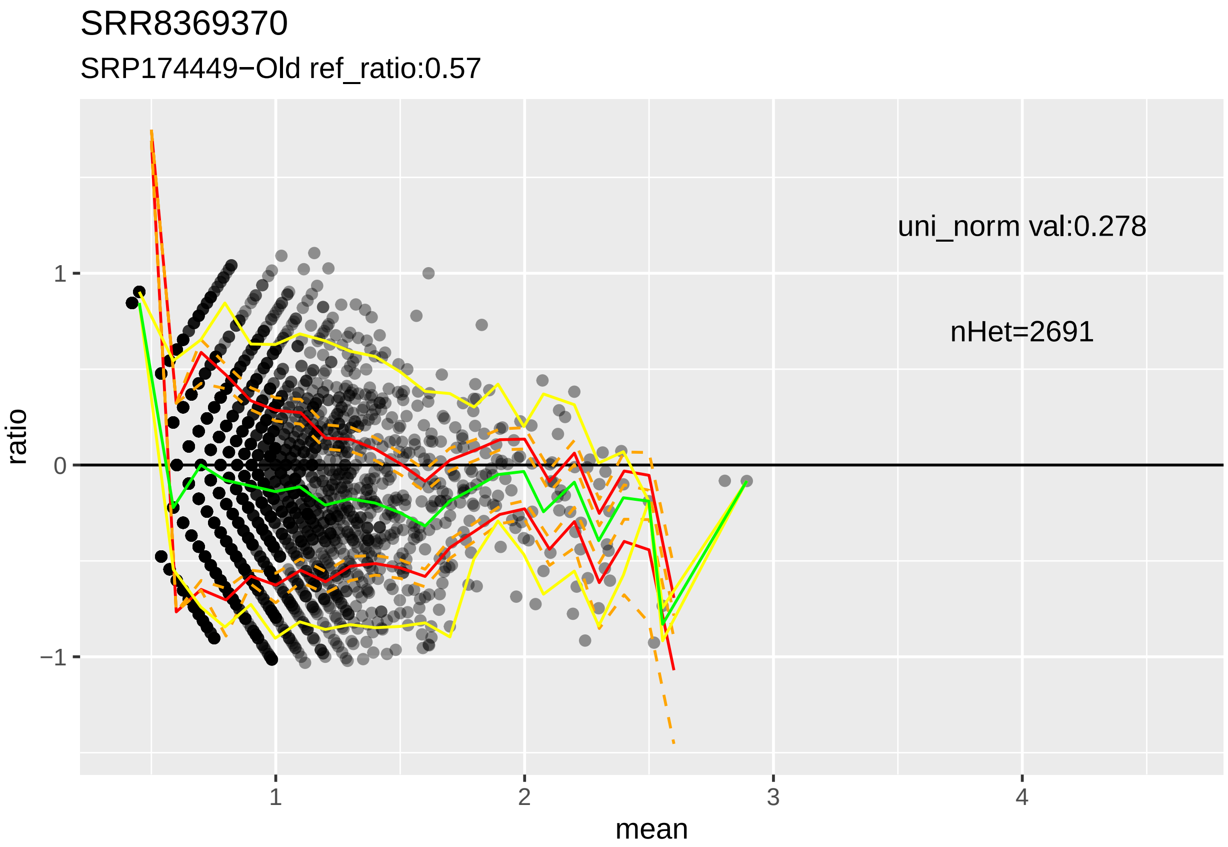
```
plot_df<-fold_c %>%  filter(uni_norm>0.185)


data_samp<-plot_df[sample(nrow(plot_df), 4),]

make_plot(data_samp)
```

```
## [1] 1
## [1] "ase found"
```

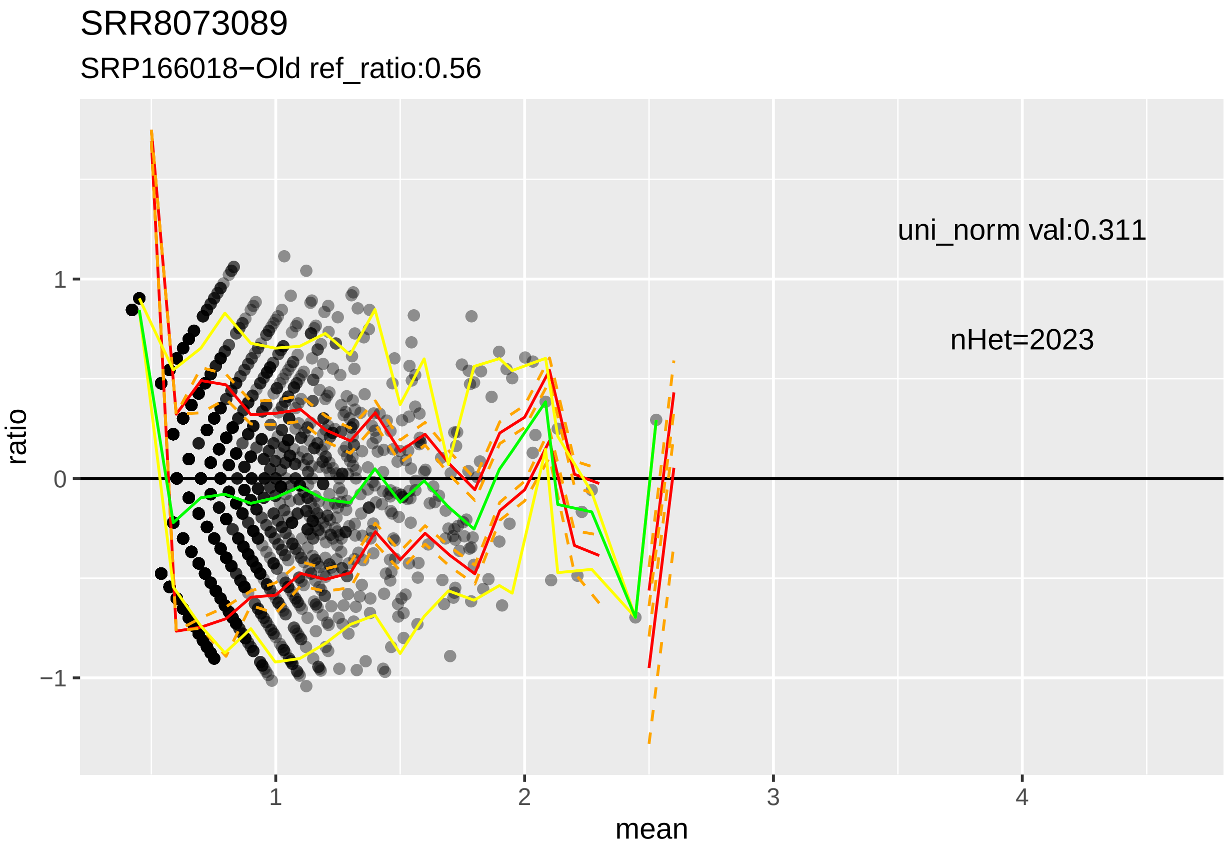

SRR5863489

SRP113492−Old ref_ratio:0.56

```
## [1] 2
## [1] "ase found"
```



```
## [1] 3
## [1] "ase found"
```



```
## [1] 4
## [1] "ase found"
```

```
## null device
##           1
```

Final number of samples:

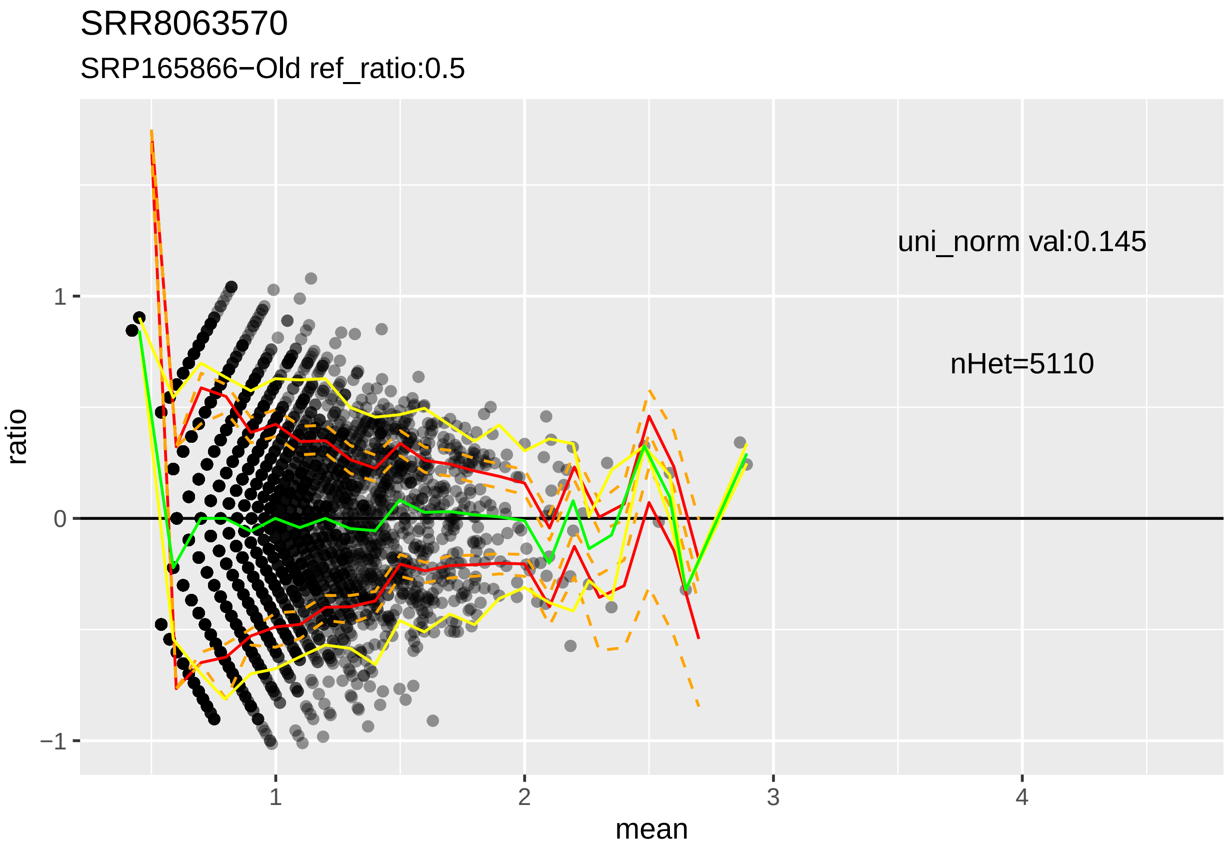
```
nrow(good)
```

```
## [1] 37527
```

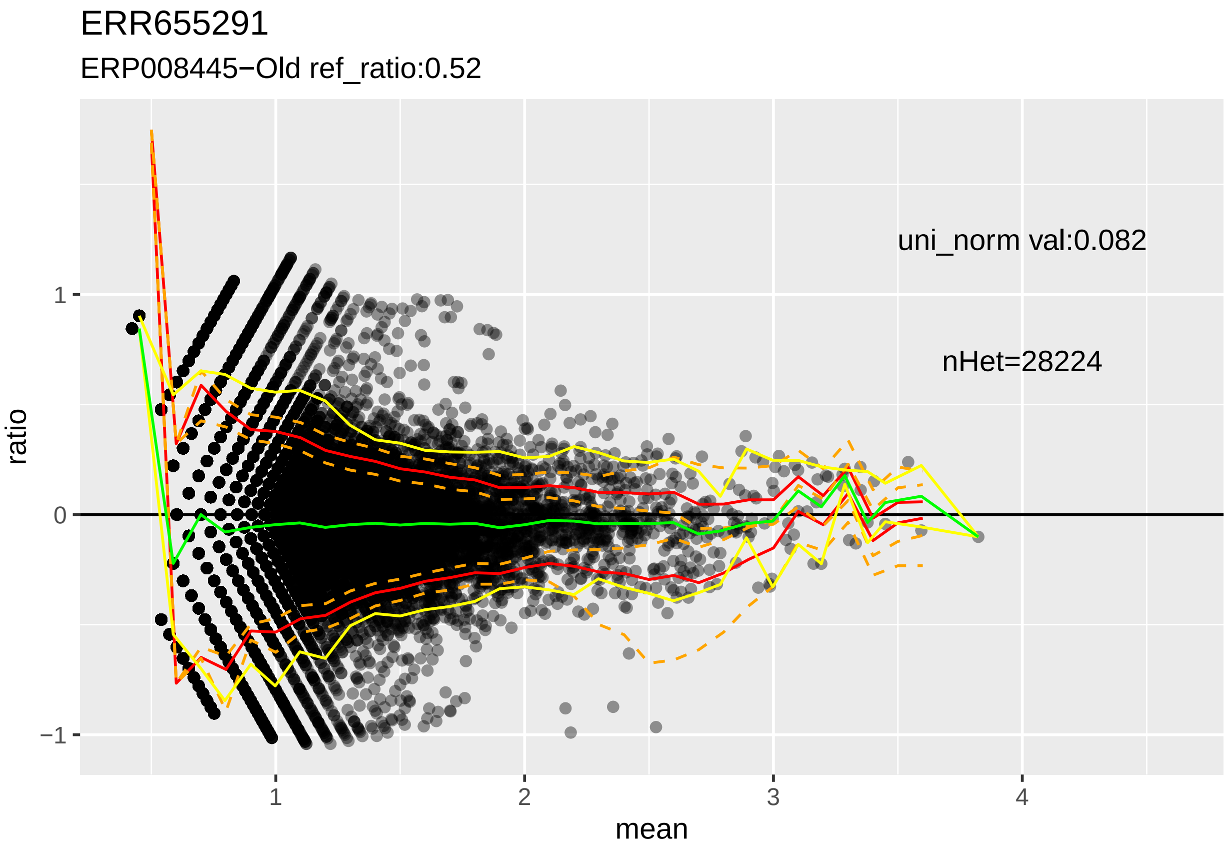
Plot Good samples

```
data_samp<-good[sample(nrow(good), 4),]

make_plot(data_samp)
```

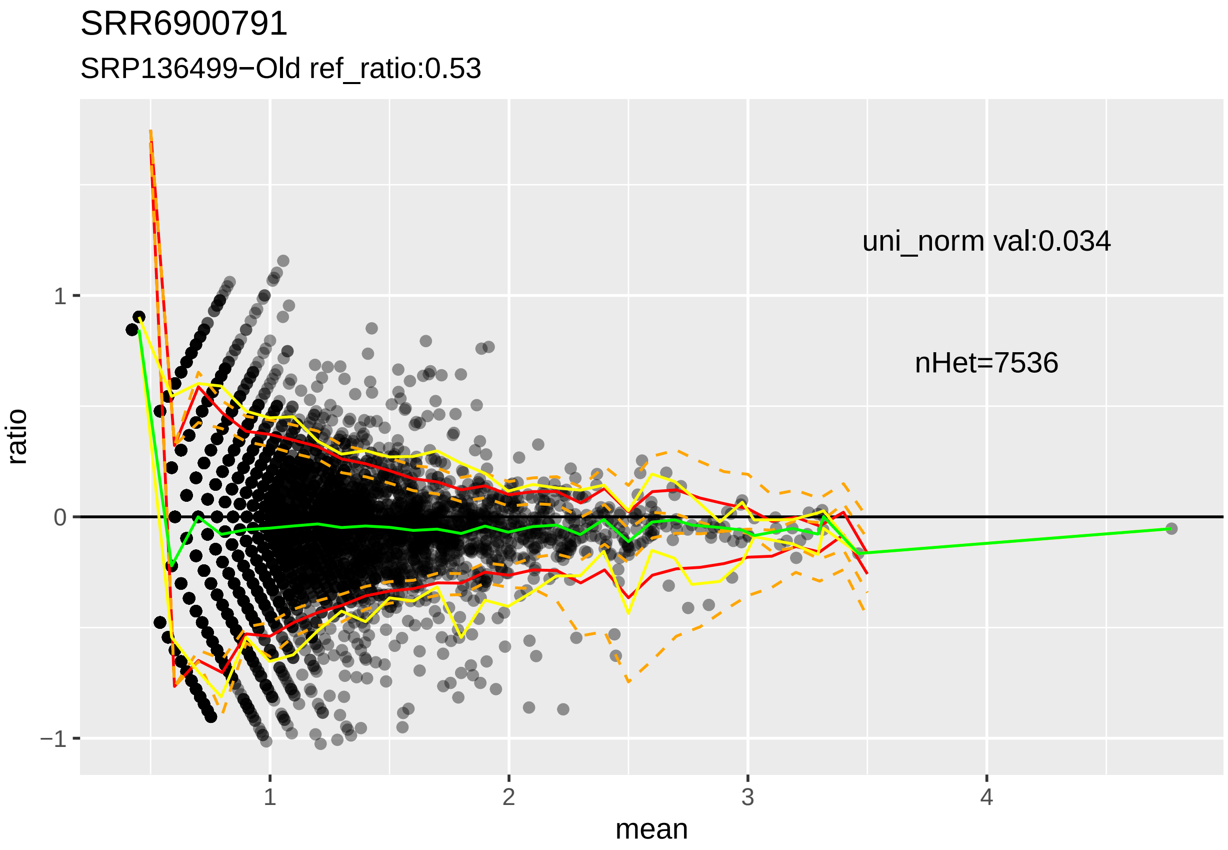
```
## [1] 1
## [1] "ase found"
```



```
## [1] 2
## [1] "ase found"
```



```
## [1] 3
## [1] "ase found"
```



```
## [1] 4
## [1] "ase found"
```

```
## null device
##           1
```