Comparison by treatment: Scott's data

Contents

Intro

I am adapting the previous analysis to old Scott's data. Obviously a lot of the plots are going to be reduced, but in a nutshell will do:

1. Perform contrast of MC-treated vs untreated samples for each cell line.

2. Compare the Wald's t-statistic between the three cell lines.

```r
ratio_of_ratios_deseq <- function(rsem_data,thr = 20)
{
  count_matrix =  rsem_data %>%
    dplyr::select(file,rsem) %>%
    unnest() %>%
    dplyr::select(file,gene_id,expected_count) %>%
    mutate(
      expected_count = floor(expected_count)
      ) %>%
    spread(file,expected_count) %>%
    as_matrix()

  coldata = rsem_data %>%
    dplyr::select(file,cell,treatment) %>%
    mutate(interac = paste(cell,treatment, sep = ".")) %>%
    as.data.frame() %>%
    tibble::remove_rownames() %>%
    tibble::column_to_rownames("file")

  deseq = DESeqDataSetFromMatrix(
    count_matrix,colData = coldata,
    design = ~ cell + treatment + cell:treatment)

  deseq = deseq[ rowSums(assay(deseq) ) > thr,]
  deseq = DESeq(deseq, test = "LRT", reduced =  ~ cell + treatment)

  deseq

}
```
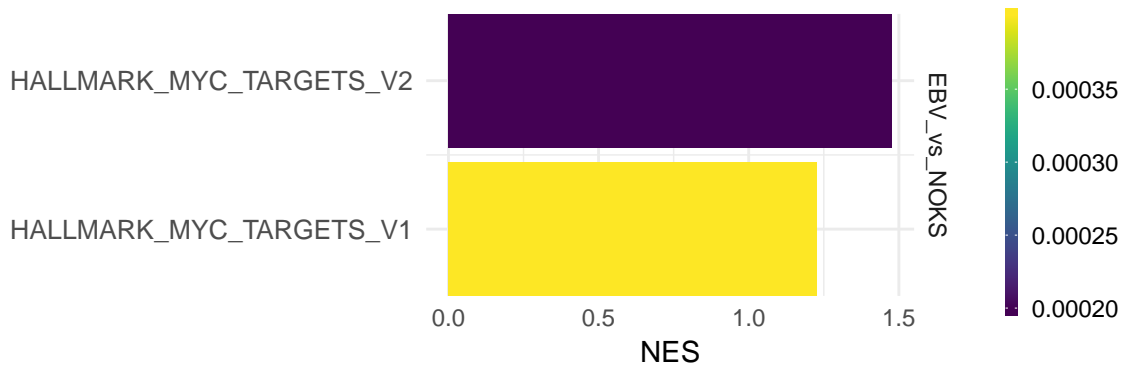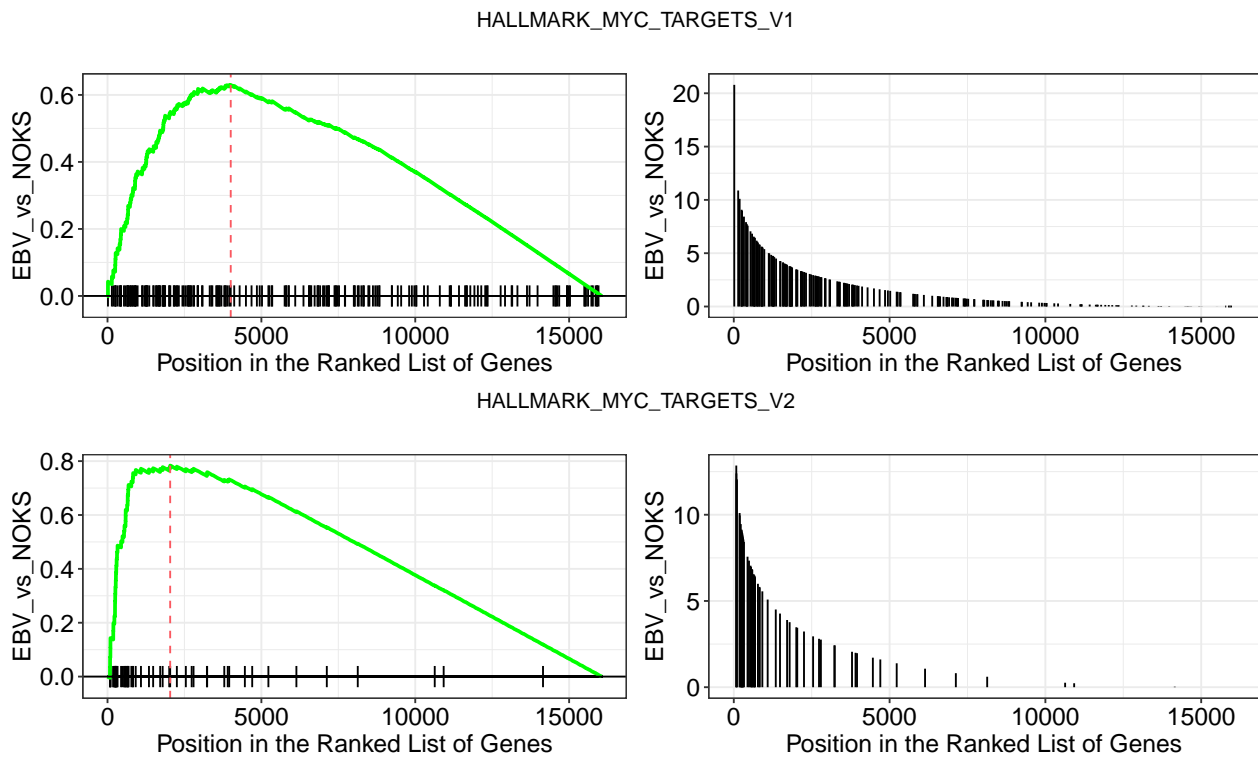
Pathway analysis

This analysis returns a different signal-to-noise metric for each cell line. Hence, we are capable of performing a pathway analysis too.

GSEA plots for `MYC_TARGETS`:

GSEA plot for `DNA_REPAIR`

I picked this pathway because it appear in both of the treated vs untreated pathways of Scott's cell lines, but in none of your data.

HALLMARK_DNA_REPAIR