

Gene Combined pvalues

Noor Pratap Singh

12/31/2021

```
suppressPackageStartupMessages(source("run_limma.R"))
dirSal <- "/fs/cbcb-lab/rob/students/noor/shoal_proj/swim/sal_best/vbprior=1e0"
load("/fs/cbcb-lab/rob/students/noor/Uncertainty/mikelove-swimdown-216aldd/simulate/data/simulate.rda")
```

Doing differential analysis on old shoal

Weight 0.00001

```
dirShoal <- "/fs/cbcb-lab/rob/students/noor/shoal_proj/swim/shoal_best/vbprior=1e0/c=1e-05"
runDE(dirSal, dirShoal)
```

```
## importing quantifications
```

```
## reading in files with read_tsv
```

```
## 1 2 3 4 5 6 7 8 9 10 11 12
```

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```

```
## found matching transcriptome:
## [ GENCODE - Homo sapiens - release 28 ]
```

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```
## loading existing TxDb created: 2021-12-23 21:26:44
## Loading required package: GenomicFeatures
## Loading required package: AnnotationDbi
```

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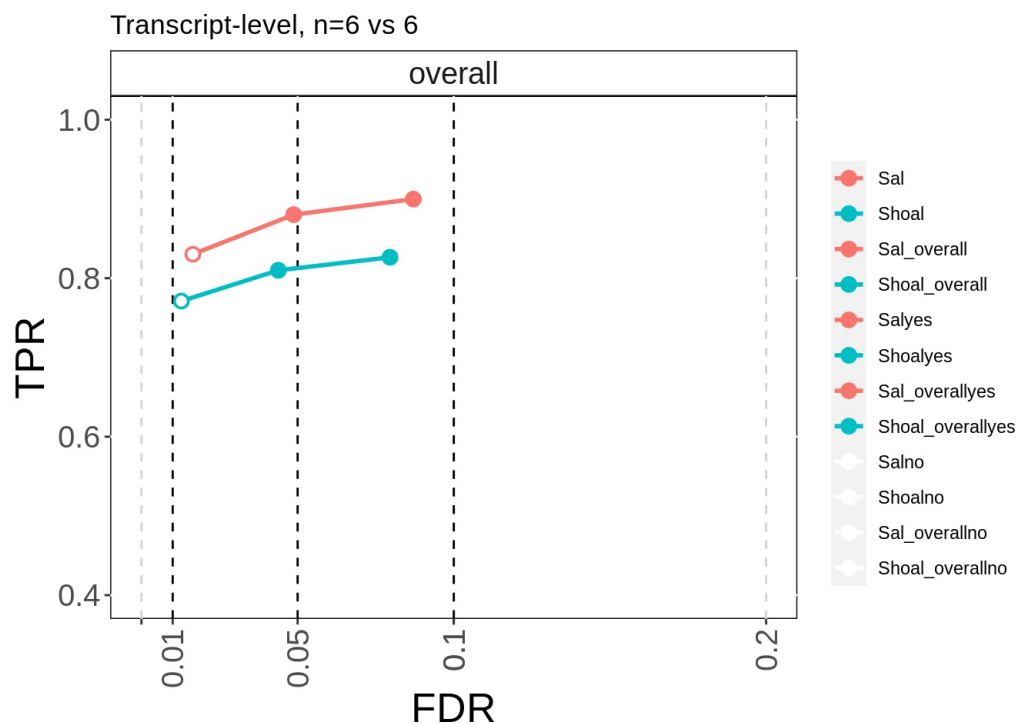
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Weight 100 aka optimal

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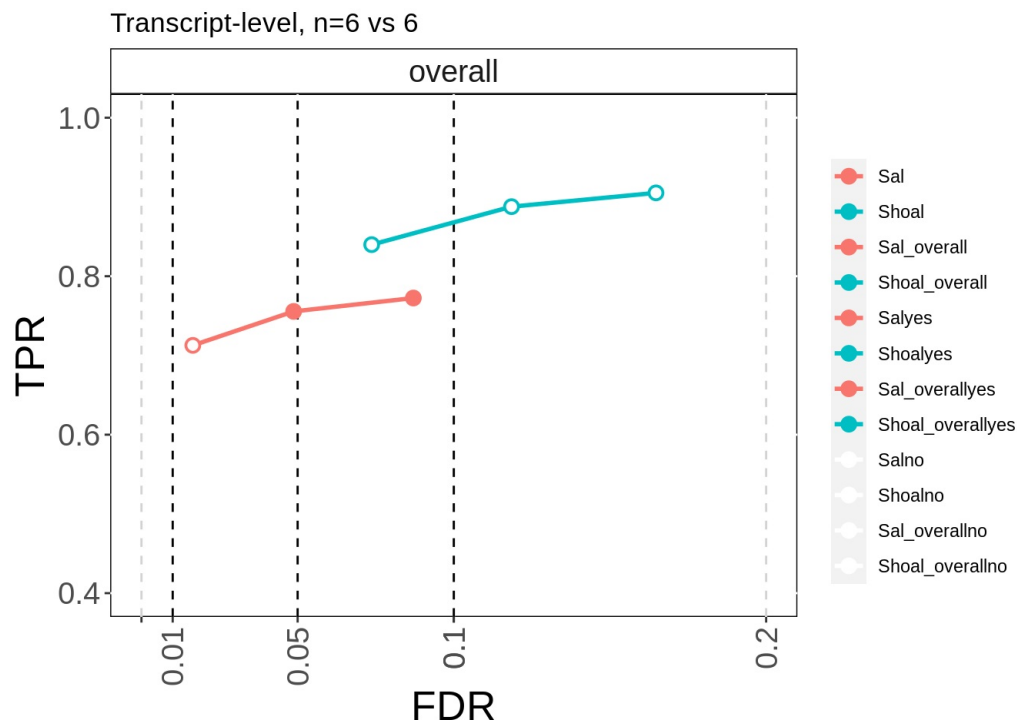
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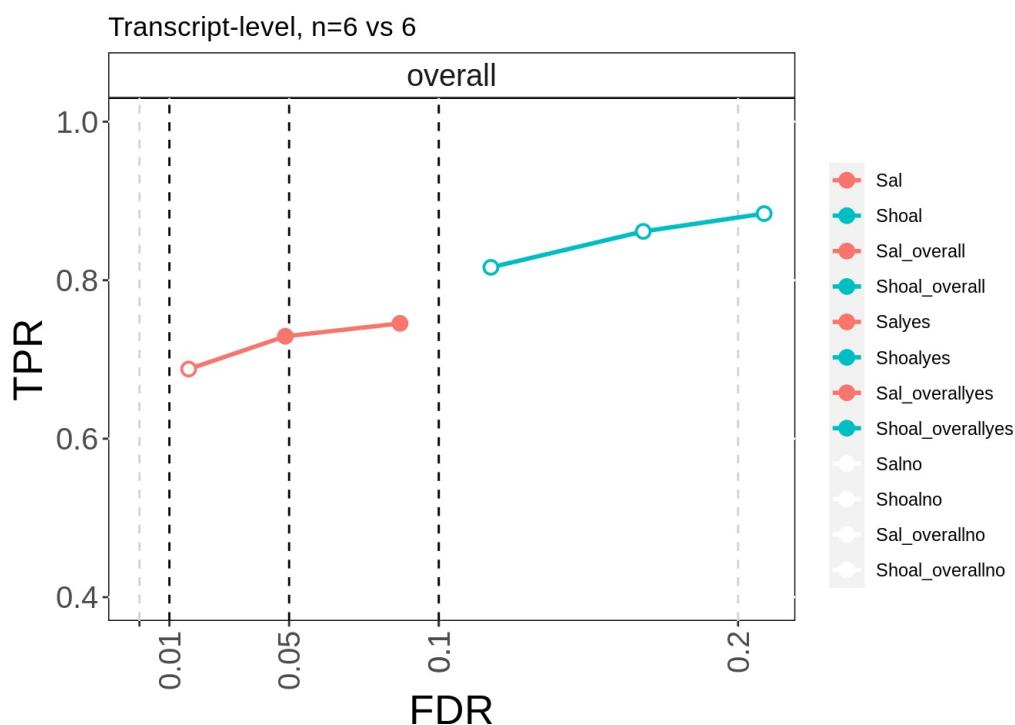
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Doing differential analysis on shoal with fixed prior

Weight 0.00001

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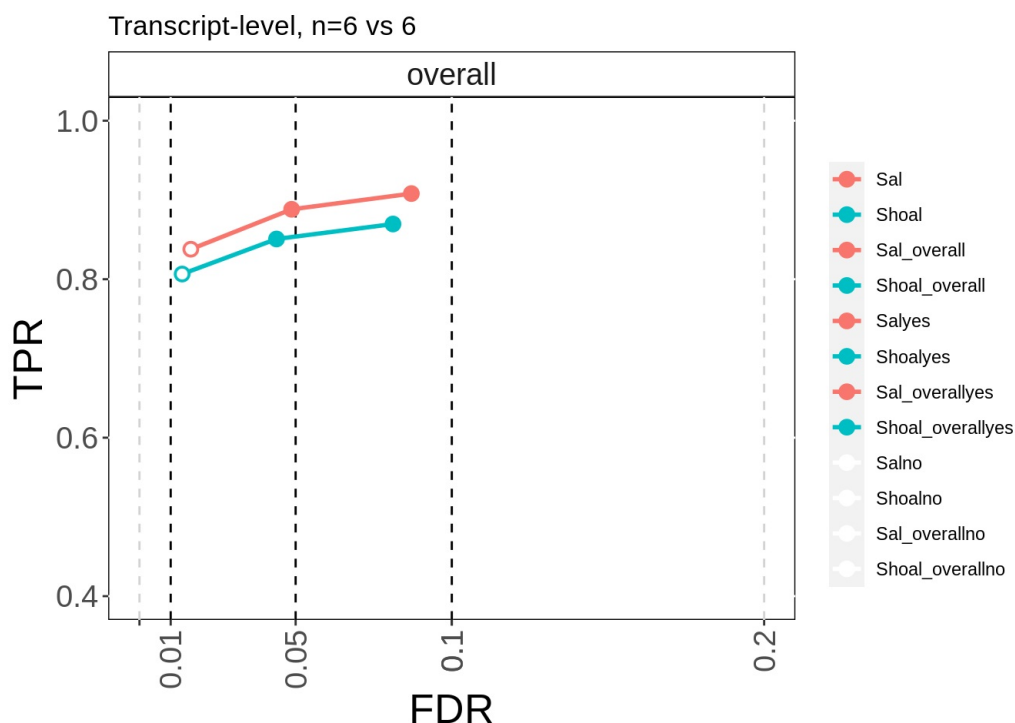
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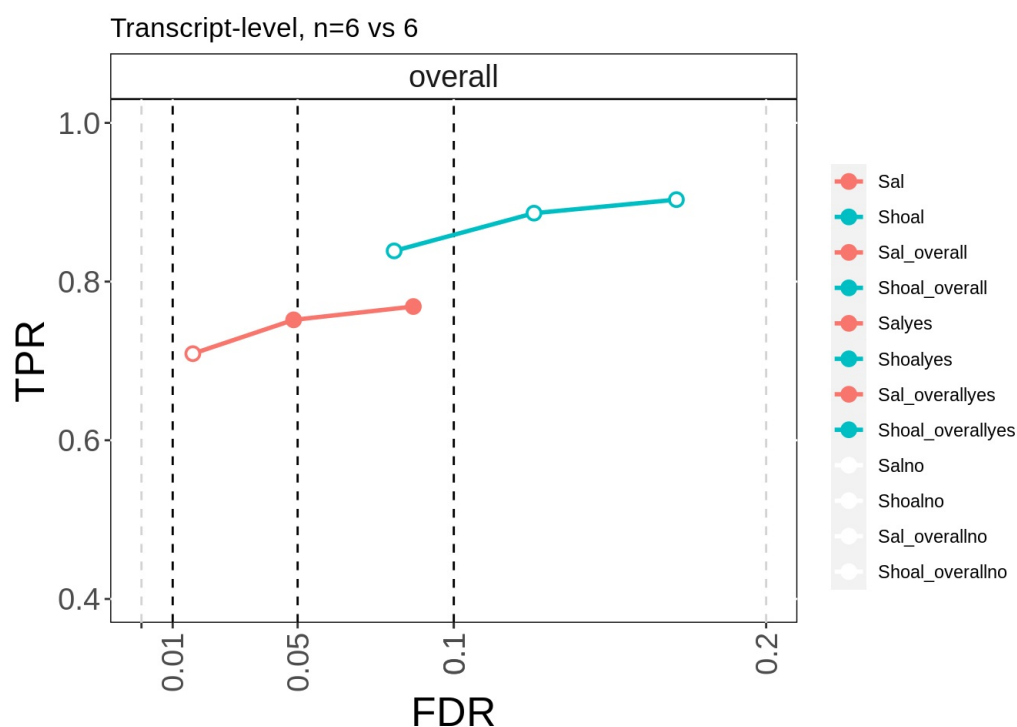
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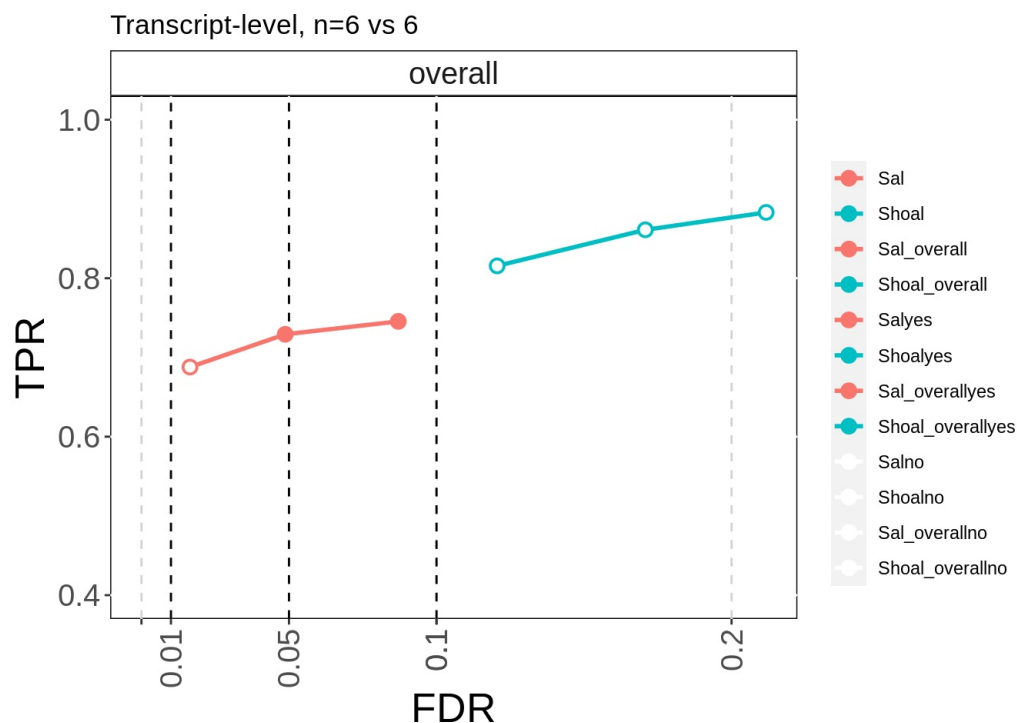
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Doing differential analysis on updated shoal

Weight 0.00001

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dirShoal <- "/fs/cbcb-lab/rob/students/noor/shoal_proj/swim/shoal_best_updated/vbprior=1e0/c=1e-05"
runDE(dirSal, dirShoal)
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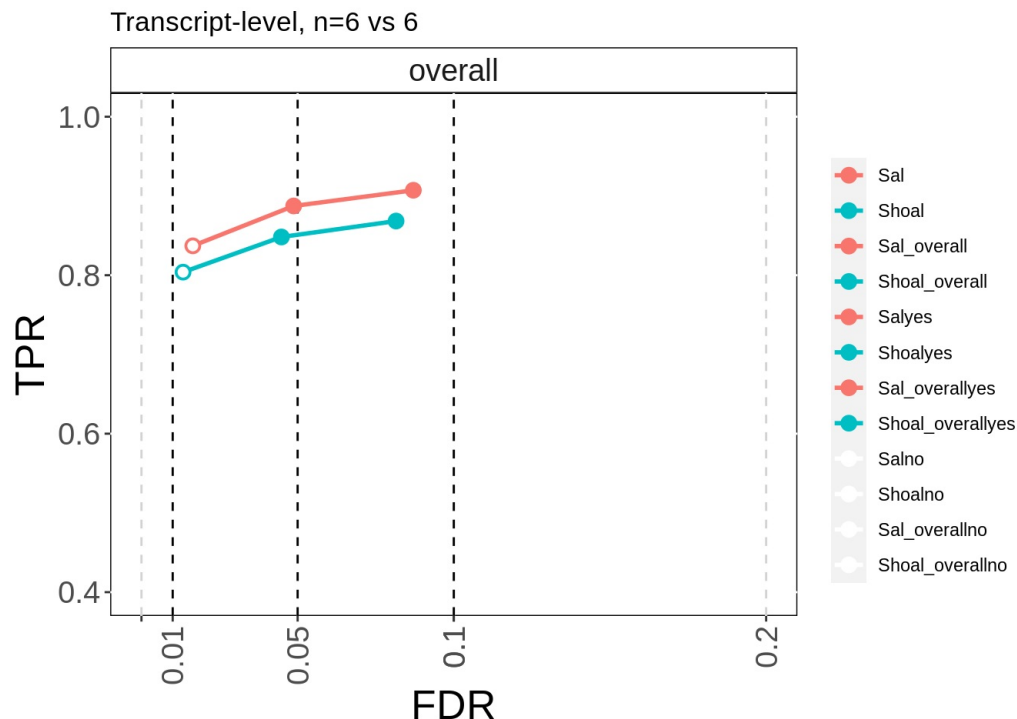


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Weight 0.1

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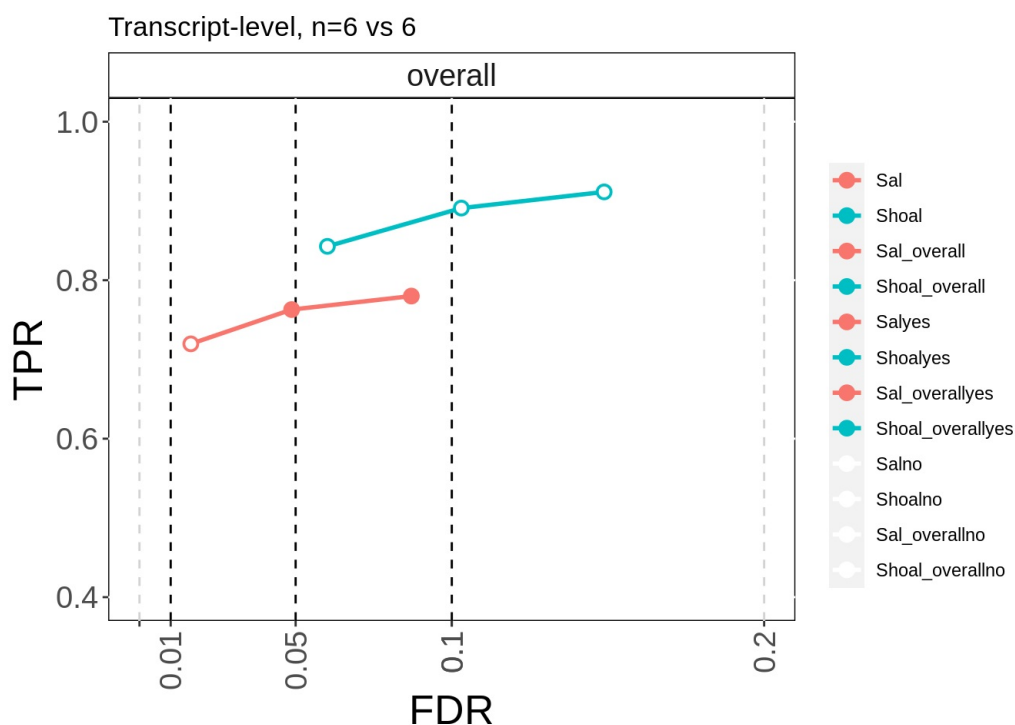
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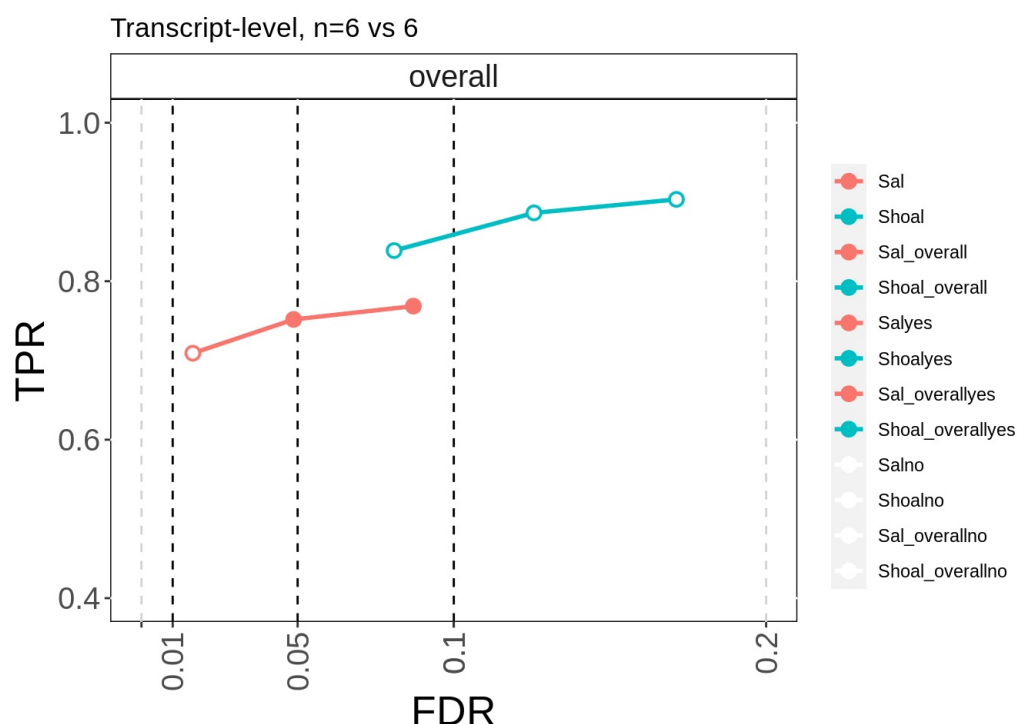
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## See https://www.bioconductor.org/packages/devel/bioc/vignettes/BiocFileCache/inst/doc/BiocFileCache.html#default-caching-location-update
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```
## Warning: It is deprecated to specify `guide = FALSE` to remove a guide. Please
## use `guide = "none"` instead.
```

