CTCF QTLd

Evelin Aasna

3/5/2019

Kõik kromatiini avatuse kühmud

```
caQTL = read.table("/gpfs/rocket/home/a72094/projects/chromatin_to_splicing/tabix/cqn_permutations_1000

path = "/gpfs/rocket/home/a72094/projects/chromatin_to_splicing/results"
```

Leian üle kõigi RNA tunnuste kühmude arvu, millel

1. leidub seos RNA tunnusega ja CTCFga <- RNA_CTCF
2. leidub seos RNA tunnusega aga mitte CTCFga <- RNA_no_CTCF
3. ei leidu seos RNA tunnusega aga leidub CTCFga <- no_RNA_CTCF
4. ei leidu seos RNA tunnusega ega CTCFga <- no_RNA_no_CTCF

lisaks: seotud RNA tunnusega(vb CTCF) <- RNA

Leian seose CTCF QTLdega üle kõigi RNA tunnuste kokku

```
r = "08"
```

Kromatiini avatuse kühmud, mis on seotud CTCF QTLga

```
ATAC_CTCF = read.table(paste("/gpfs/rocket/home/a72094/projects/chromatin_to_splicing/results/ctcf/cqn_

tabel08["featureCounts", ] = tabeli_rida("featureCounts", r)
tabel08["upstream", ] = tabeli_rida("upstream", r)
tabel08["contained", ] = tabeli_rida("contained", r)
tabel08["downstream", ] = tabeli_rida("downstream", r)
tabel08["kokku", ] = kokku_rida(r)
tabel08
```

```
##                RNA_CTCF RNA_CTCF% RNA_no_CTCF RNA_no_CTCF% no_RNA_CTCF
## featureCounts       108     22.78        1321         5.20         366
## upstream             21      4.43         280         1.10         453
## contained            27      5.70         426         1.68         447
## downstream           31      6.54         310         1.22         443
## kokku               127     26.79        1808         7.12         347
##                no_RNA_no_CTCF
## featureCounts           24077
## upstream                25118
## contained               24972
## downstream              25088
## kokku                   23590
```

```
r = "09"
```

Kromatiini avatuse kühmud, mis on seotud CTCF QTLga

```
ATAC_CTCF = read.table(paste("/gpfs/rocket/home/a72094/projects/chromatin_to_splicing/results/ctcf/cqn_

tabel09["featureCounts", ] = tabeli_rida("featureCounts", r)
tabel09["upstream", ] = tabeli_rida("upstream", r)
tabel09["contained", ] = tabeli_rida("contained", r)
tabel09["downstream", ] = tabeli_rida("downstream", r)
```

```
tabel09["kokku", ] = kokku_rida(r)
tabel09
```

```
##                RNA_CTCF RNA_CTCF% RNA_no_CTCF RNA_no_CTCF% no_RNA_CTCF
## featureCounts       49     16.01         907         3.55         257
## upstream             7      2.29         167         0.65         299
## contained           14      4.58         258         1.01         292
## downstream           7      2.29         192         0.75         299
## kokku               62     20.26        1218         4.76         244
##                no_RNA_no_CTCF
## featureCounts           24659
## upstream                25399
## contained               25308
## downstream              25374
## kokku                   24348
```

Kas kokku **25872** kromatiini kühmu? (Mittelõikuvad hulgad)

```
as.symbol(rowSums(within(tabel08, rm("RNA_CTCF%", "RNA_no_CTCF%"))) == 25872 & rowSums(within(tabel09, :
```

`TRUE`

Kontroll, kas madalama r2 taseme juures olen leidnud rohkem seotud RNA tunnuseid

```
as.symbol(tabel08[,"RNA_CTCF"]>tabel09[,"RNA_CTCF"] & tabel08[,"RNA_no_CTCF"]>tabel09[,"RNA_no_CTCF"])
```

`TRUE`

Kas teatud RNA taseme tunnusega seotud kühmude hulgas on CTCF QTLd üleesindatud?

H0: CTCF seondumine ei ole põhiline transkriptsiooni kontrollimehhanism. CTCF QTLga seostumine ei väljendu fenotüübis

H1: RNA tunnusega seotud kühmude hulgas on CTCF QTLd üleesindatud

```
p_tabel
```

```
##                         0.8          0.9
## featureCounts 1.692958e-37 4.175081e-18
## upstream      2.048844e-07 4.792580e-03
## contained     9.842165e-08 5.036724e-06
## downstream    2.831457e-13 9.732330e-03
## kokku         3.852088e-38 1.286451e-21
```


Kas CTCF QTLga seotud caQTL mõjutab suurema tõenäosusega näiteks splaissimist kui geeniekspressiooni?

H0: mõlemat tüüpi RNA taseme tunnusega seotud kühmude hulgas leidub võrdne osakaal ülekatet CTCF QLTdega

H1: Veerus oleva RNA tunnuse puhul on CTCF QTLdega seotud kühmude osakaal suurem

```
test_tabel(tabel08)
```

```
##               featureCounts  upstream contained downstream
## featureCounts            NA 0.4182175 0.1478965  0.8545547
## upstream          0.6741890        NA 0.3392301  0.8698721
## contained         0.8966689 0.7630340        NA  0.9647290
## downstream        0.2005428 0.2022238 0.0623374         NA
```

```
test_tabel(tabel09)
```

```
##              featureCounts  upstream contained downstream
## featureCounts            NA 0.3473592 0.5773416  0.2222141
## upstream         0.7858212        NA 0.7787877  0.5043544
## contained        0.5459921 0.3812181        NA  0.2702713
## downstream       0.8763842 0.7023161 0.8586751         NA
```