

CTCF QTLd

Evelin Aasna

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Kõik kromatiini avatuse külmud

```
caQTL = read.table("/gpfs/rocket/home/a72094/projects/chromatin_to_splicing/tabix/cqn_permutations_10000")
```

```
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 külmud, mis on seotud CTCF QTLga

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

```
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 külmud, mis on seotud CTCF QTLga

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

```
tabel109["featureCounts", ] = tabel1_rida("featureCounts", r)
tabel109["upstream", ] = tabel1_rida("upstream", r)
tabel109["contained", ] = tabel1_rida("contained", r)
tabel109["downstream", ] = tabel1_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 ülesindatud?

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

H1: RNA tunnusega seotud kühmude hulgas on CTCF QTLd ülesindatud

```
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 QTLdega

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

```
test_tabel(tabel08)
```

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

```
test_tabel(tabel09)
```

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