TBX20 RNA-Seq data subset

Daniel Bindreither

October 19, 2016

1 Introduction

The TBX20 data set [4] provides ChIP-Seq and RNA-Seq data. In here only the RNA-Seq part of the data is utilized. The raw data where downloaded from Gene Expression Omnibus (GEO) [1], accession number GSM767225-GSM767230. TBX20 (T-box 20) in general is a transcriptional regulator essential for cardiac development and maintenance of mouse heart tissue. In this study TXB20 was knocked-out by using a Tamoxifen mediated conditional knock-out system. Transcriptional changes caused by the ablation of the second exon of TBX20 result in rapid onset of heart failures and the subsequent death of the mice. TBX20 knock-out adult heart tissue was compared to wild type adult heart tissue. This package provides a subset of the RNA-Seq data (chromosome 19) for demonstrating the capabilities of the SpliceGraph package. The vignette describes how to access the phenotypic data and the raw reads aligned with Bowtie [3] to the mm9 assembly of Mus musculus from UCSC Genome Browser [2].

Accessing the experimental design ...

```r
> library("TBX20BamSubset")
> fn <- system.file("extdata", "phenoData.txt", +
    package="TBX20BamSubset")
> pd <- read.table(fn, header=TRUE, +
    stringsAsFactors=FALSE)
```

Accessing the raw reads ...

```r
> library("Rsamtools")
> fls <- getBamFileList()
> bfs <- BamFileList(fls)
```
<table>
<thead>
<tr>
<th></th>
<th>SRX</th>
<th>SRR</th>
<th>GSM</th>
<th>condition</th>
<th>replicate</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>SRX085099</td>
<td>SRR316184</td>
<td>GSM767225</td>
<td>normal</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>SRX085100</td>
<td>SRR316185</td>
<td>GSM767226</td>
<td>normal</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>SRX085101</td>
<td>SRR316186</td>
<td>GSM767227</td>
<td>normal</td>
<td>3</td>
</tr>
<tr>
<td>4</td>
<td>SRX085102</td>
<td>SRR316187</td>
<td>GSM767228</td>
<td>Tbx20 knockout</td>
<td>1</td>
</tr>
<tr>
<td>5</td>
<td>SRX085103</td>
<td>SRR316188</td>
<td>GSM767229</td>
<td>Tbx20 knockout</td>
<td>2</td>
</tr>
<tr>
<td>6</td>
<td>SRX085104</td>
<td>SRR316189</td>
<td>GSM767230</td>
<td>Tbx20 knockout</td>
<td>3</td>
</tr>
</tbody>
</table>

Table 1: Design of the TBX20 experiment

References


2 Session Information

R version 3.3.1 (2016-06-21)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.1 LTS

locale:
[1] LC_CTYPE=en_US.UTF-8   LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8     LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8 LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8    LC_NAME=C
[9] LC_ADDRESS=C            LC_TELEPHONE=C

attached base packages:
[1] stats4 parallel stats graphics grDevices utils datasets
[8] methods base

other attached packages:
[1] xtable_1.8-2 TBX20BamSubset_1.10.0 Rsamtools_1.26.0
[4] Biostrings_2.42.0 XVector_0.14.0 GenomicRanges_1.26.0
[7] GenomeInfoDb_1.10.0 iRanges_2.8.0 S4Vectors_0.12.0
[10] BiocGenerics_0.20.0

loaded via a namespace (and not attached):
[1] zlibbioc_1.20.0 tools_3.3.1 BiocParallel_1.8.0 bitops_1.0-6