

Visualizing RNA-seq data in the UCSC Genome Browser

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General Overview

RNA-seq is a method to quantify, discover, and characterize RNA from a biological sample. This data can be visualized in the Genome Browser in the following data formats:

Binary indexed

- BAM
- bigBed
- bigWig

Plain text

- BED
- WIG
- bedGraph

Viewing your RNA-seq data

You can visualize your RNA-seq data by creating a **custom track** or a **track hub**.

```
track type=bedGraph name="My RNA-seq data" visibility=full
chr1 207880852 207880879 0.07
chr1 207885427 207885454 0.07
chr1 207885768 207885795 0.07
chr1 207896764 207896791 0.07
chr1 207911349 207911376 0.07
chr1 207911386 207911413 0.07
chr1 207911419 207911477 0.42
```

The same custom track can be repackaged inside of a trackhub for more customization. For large, genome-wide datasets, we recommend converting to a binary-indexed format. These conversion tools can be downloaded from the [utilities directory](#).

```
wigToBigWig rna-seq.wig hg38.chrom.sizes rna-seq.bw
```

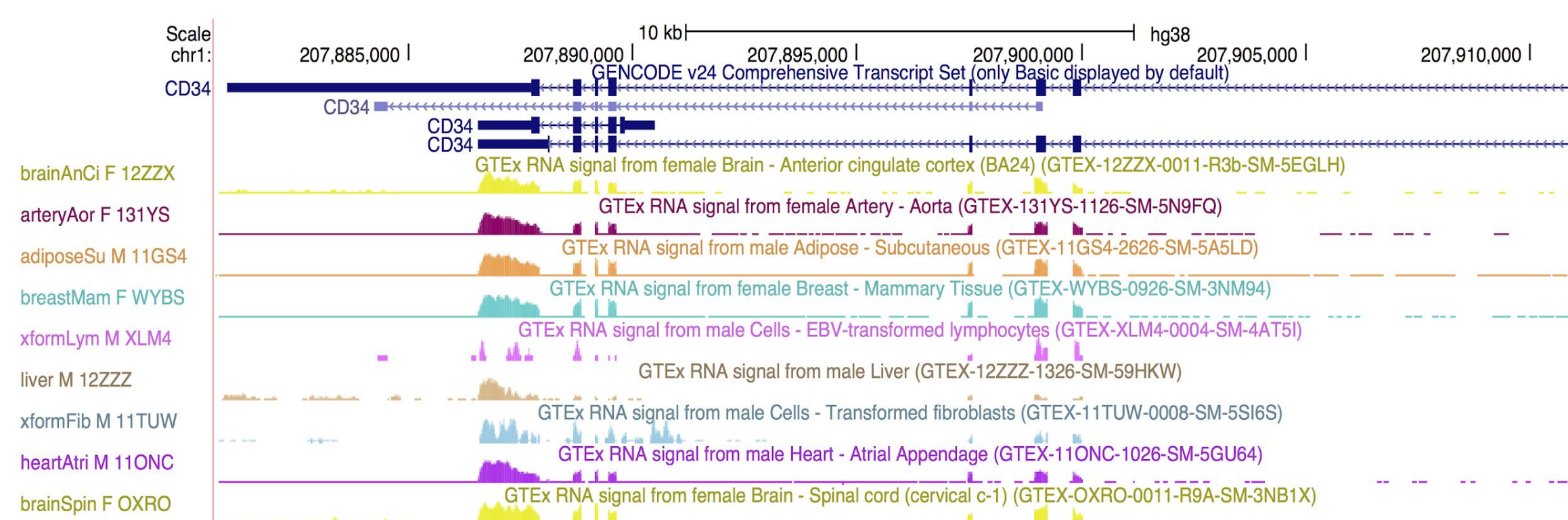
```
track MyRnaSeq_example
shortLabel RNA-seq example
longLabel A longer description of RNA-seq example
bigDataUrl http://yourWebServer/relativePathToFile/rna-seq.bw
type bigWig
autoscale on
color 0,153,76
```

References

[The UCSC Genome Browser database: 2018 update](#): Casper J, Zweig AS, Villarreal C, Tyner C, Speir ML, Rosenbloom KR, Raney BJ, Lee CM, Lee BT, Karolchik D, Hinrichs AS, Haeussler G, Guruvadoo L, Navarro Gonzalez J, Gibson D, Fiddes IT, Eisenhart C, Diekhans M, Clawson H, Barber GP, Armstrong J, Haussler D, Kuhn RM, Kent WJ. *Nucleic Acids Res.* 2018 Jan 4;46(D1):D762-D769. PMID: [29106570](#); PMC: [PMC5753355](#)

Using public hubs

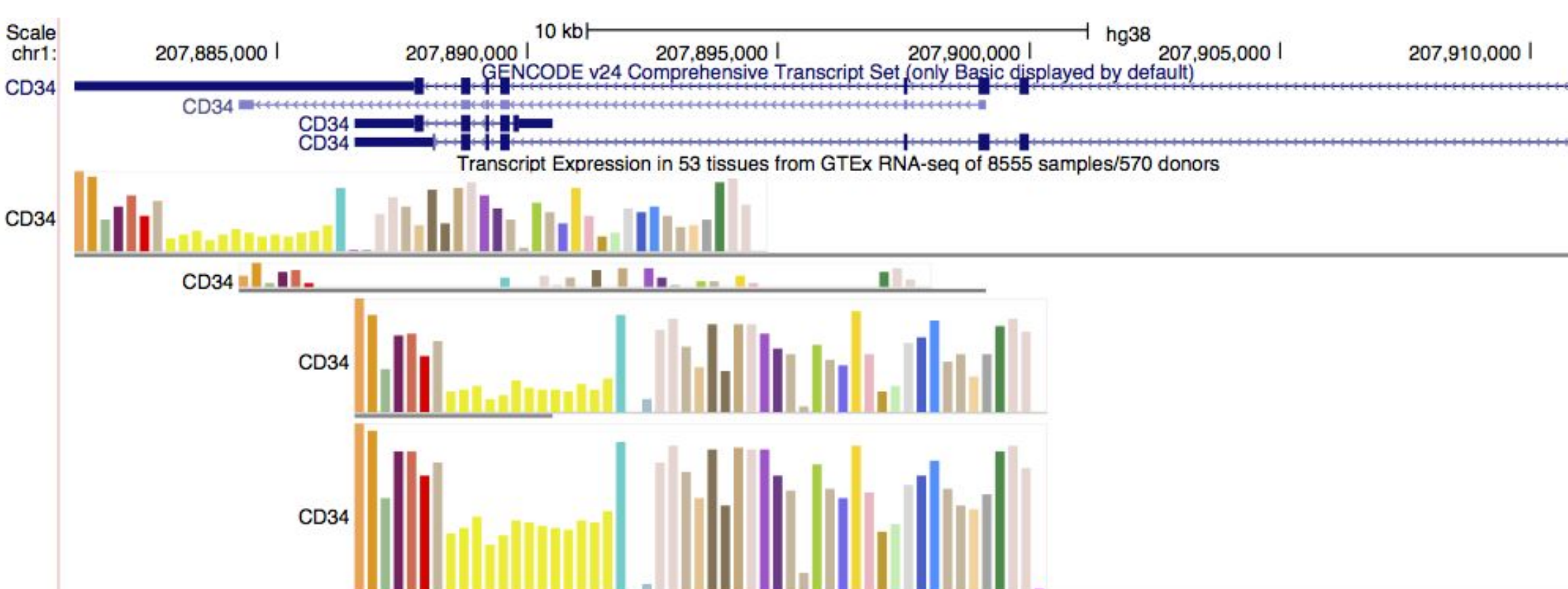
Track hubs are the easiest way to share your data with others. The **GTEx RNA-seq** public hub contains RNA-seq read coverage in 53 tissues from GTEx V6 (7572 samples).



If you require assistance hosting a file, you can learn more about using the free NSF site, Cyverse: <http://www.cyverse.org/>

Condensing RNA-seq Data

barChart track format was created to help visualize tissue expression data. Each bar represents the median transcript expression levels (TPM) in 53 tissues.



Acknowledgements

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More Information

Have questions?
Send us a question on our public mailing list: genome@soe.ucsc.edu

Genome Browser tutorials and videos:
<http://genome.ucsc.edu/training/index.html>

barChart format

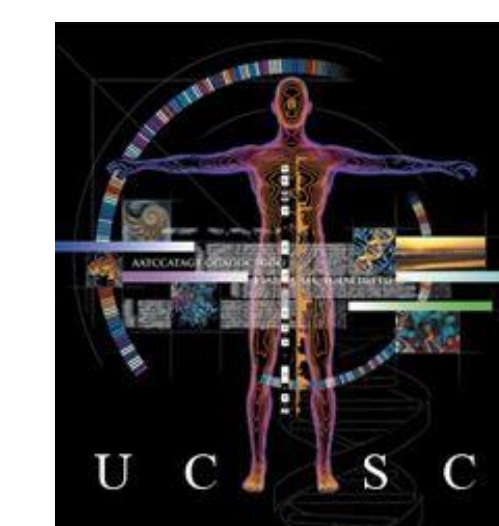
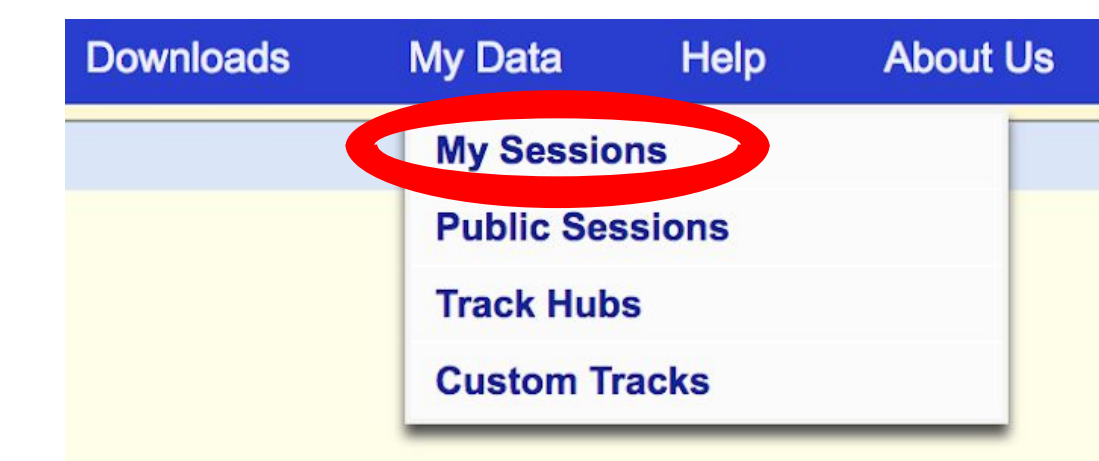
The barChart format is available as a standalone plain text bed6+ format for use with smaller datasets as a custom track, and as a binary indexed format (bigBarChart) suitable for track hubs and large custom tracks.

```
table bigBarChart
"bigBarChart bar graph display"
(
  string chrom;           "Reference sequence chromosome or scaffold"
  uint chromStart;       "Start position in chromosome"
  uint chromEnd;         "End position in chromosome"
  string name;           "Name or ID of item"
  uint score;            "Score (0-1000)"
  char[1] strand;       "'+' or '-' or '.'. Indicates whether the query aligns to the + or - strand on the reference"
  string name2;          "Alternate name of item"
  uint expCount;         "Number of bar graphs in display, must be <= 100"
  float[expCount] expScores; "Comma separated list of category values."
  bigint _dataOffset;    "Offset of sample data in data matrix file, for boxplot on details page, optional only for barChart format"
  int _dataLen;          "Length of sample data row in data matrix file, optional only for barChart format"
)
```

```
track type=barChart name="barChart Example One" description="A barChart file" \
barChartBars="adiposeSubcut breastMamTissue colonTransverse muscleSkeletal wholeBlood" visibility=pack
browser position chr14:95,086,228-95,158,010
chr14 95086227 95158010 ENSG00000100697.10 999 - DICER1 5 10.94,11.60,8.00,6.69,4.89
chr14 95181939 95319906 ENSG00000165959.7 999 - CLMN 5 7.08,9.53,9.32,1.38,1.68
chr14 95417493 95475836 ENSG00000176438.8 999 - SYNE3 5 7.29,3.73,0.74,0.35,1.39
```

Sharing data with others

You can save all of your tracks and browser settings to a snapshot of the Genome Browser called a **session**.



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Digital copy of this poster available at:
http://hgwdev.soe.ucsc.edu/~jairo/posters/ucscPostDoc_2018.pdf