

Download data:

Genome Browser for CHM13:

[https://genome.ucsc.edu/cgi-bin/hgGateway?hgsid=2616392780\\_1mkE6scLsQY434AanEq8sFwaB4ZV](https://genome.ucsc.edu/cgi-bin/hgGateway?hgsid=2616392780_1mkE6scLsQY434AanEq8sFwaB4ZV)

Table browser:

[https://genome.ucsc.edu/cgi-bin/hgTables?hgsid=2616392780\\_1mkE6scLsQY434AanEq8sFwaB4ZV](https://genome.ucsc.edu/cgi-bin/hgTables?hgsid=2616392780_1mkE6scLsQY434AanEq8sFwaB4ZV)

**Assembly accession ID: GCA\_009914755.4** (If you would like to “map” iso-seq data to the genome)

Genes in CHM13 (example only chr1):

**Table Browser**

Use this tool to retrieve and export data from the Genome Browser annotation track database. You can limit retrieval based on data attributes and intersect or merge with data from another track, or retrieve DNA sequence covered by a track. [More...](#)

**Select dataset**

Clade:  Genome:  Assembly:

Group:  Track:

Table:  [Data format description](#)

**Define region of interest**

Region: ☐ Genome ☒ Position  [Lookup](#) [Define regions](#)

Identifiers (names/accessions): [Paste list](#) [Upload list](#)

**Optional: Subset, combine, compare with another track**

Filter: [Create](#)

Intersection: [Create](#)

**Retrieve and display data**

Output format:  Send output to: ☐ Galaxy ☐ GREAT

Output filename:  (add .csv extension if opening in Excel, leave blank to keep output in browser)

Output field separator: ☒ tsv (tab-separated) ☐ csv (for excel)

File type returned: ☒ Plain text ☐ Gzip compressed

[Get output](#) [Summary/Statistics](#)

Sites that are newly introduced in CHM13 (example only chr1):

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Use this tool to retrieve and export data from the Genome Browser annotation track database. You can limit retrieval based on data attributes and intersect or merge with data from another track, or retrieve DNA sequence covered by a track. [More...](#)

**Select dataset**

Clade:  Genome:  Assembly:

Group:  Track:

Table:  [Data format description](#)

**Define region of interest**

Region: ☐ Genome ☒ Position  [Lookup](#) [Define regions](#)

**Optional: Subset, combine, compare with another track**

Filter: [Create](#)

Subtrack merge: [Create](#)

Intersection: [Create](#)

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Long Read RNA (Iso-seq) from CHM13

[https://www.ncbi.nlm.nih.gov/sra/SRX9009501\[accn\]](https://www.ncbi.nlm.nih.gov/sra/SRX9009501[accn])

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