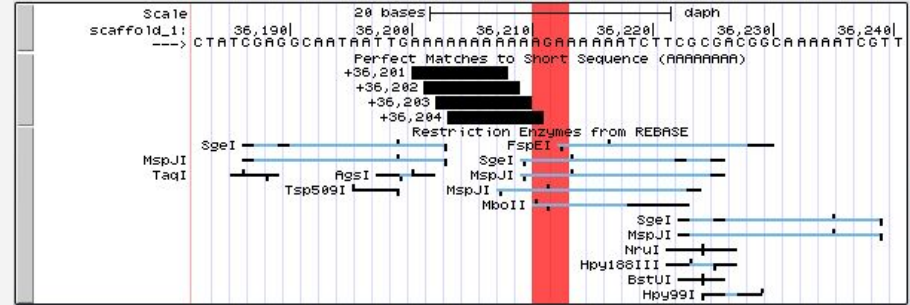


UCSC Browser Assembly Hubs To Visualize and Analyze New Genomes

```
>scaffold_1
GTTGTAATACTCTATTCTACAATAAACCAA
TCATAGGTTGAATTGGCGTTGAAGTAAACAAA
...
>scaffold_2
AGTTATGACAACTATAAAAAGTCGGTAGAGACAAAAG
TCGTTCTGGGACGAAGCGACCAAACTGAGCACAAGAT
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATT
TAGAAAATTTCCAGGAAGTTTGAAGTTGCTA
...
```

```
hubDirectory
|__hub.txt
|__genomes.txt
|__hg19
|__trackDb.txt
```



Assembly Hubs

Examples of Existing Assembly Hubs and Analyzing Variants

Sharing hubs via Public Hubs and Public Sessions

Binary Indexed Files used for Visualizing Data in Hubs

bigDataUrl for “big” files

Text Files used to define Track Hubs

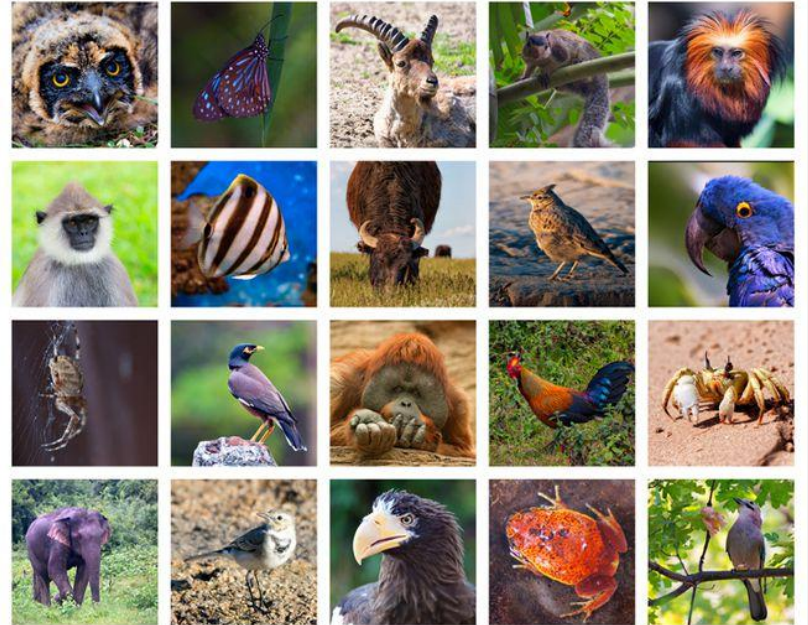
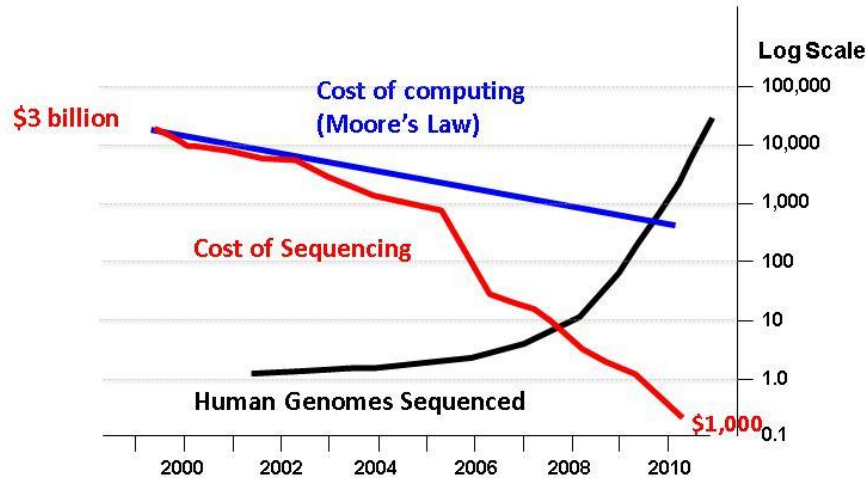
hub.txt -> genomes.txt -> trackDb.txt

Building an Assembly Hub for a FASTA file from Cucumber

UCSC Browser Assembly Hubs Increased Availability of New Assemblies

Adapted from
The Economist

The Sequencing Explosion



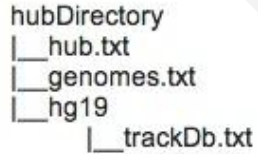
Examples of Hubs and Resources

Genbank Assembly Hubs

<http://genome-test.gi.ucsc.edu/gbdb/hubs/genbank/>

Ensembl Track Hub Registry

<https://trackhubregistry.org/>



```
hubDirectory  
|__hub.txt  
|__genomes.txt  
|__hg19  
|__trackDb.txt
```

UCSC Public Hubs

<http://genome.ucsc.edu/cgi-bin/hgHubConnect>

G-OnRamp

<http://gonramp.wustl.edu/>

CyVerse Discovery Environment byte-range supported data hosting

<https://de.cyverse.org/de/>

Public Track Hubs

UCSC Public Hubs *moderated collection of track hubs*

<http://genome.ucsc.edu/cgi-bin/hgGateway>



Browse/Select Species

POPULAR SPECIES



Human



Mouse



Rat



Fruitfly



Worm



Yeast

duck

Assembly Hub: CESAR Gene Mappings

hub.anaPla1

Assembly Hub: Croc and Bird Hub

anaPla1

Mouse strain assemblies (16)

Human

Search term

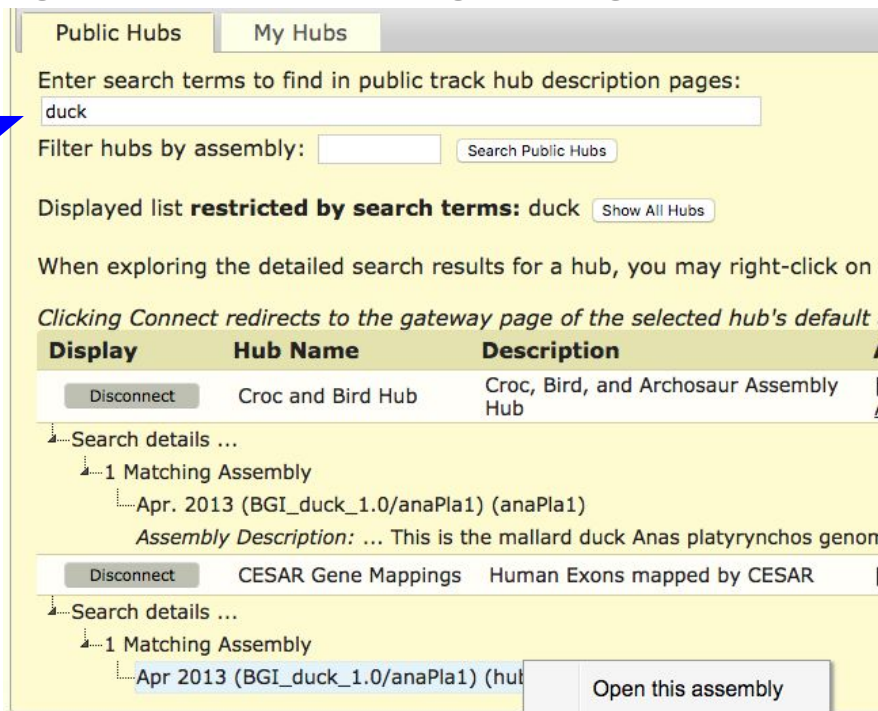


Public Track Hubs

UCSC Public Hubs *moderated collection of track hubs*

<http://genome.ucsc.edu/cgi-bin/hgHubConnect>

Search term



Public Hubs My Hubs

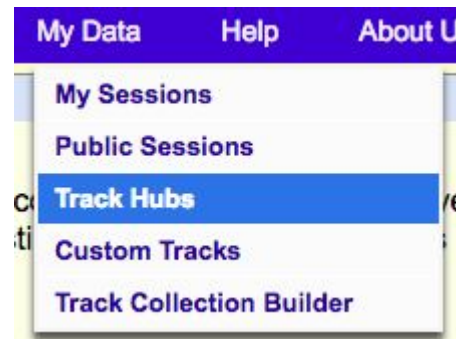
Enter search terms to find in public track hub description pages:
duck

Filter hubs by assembly: Search Public Hubs

Displayed list **restricted by search terms:** duck Show All Hubs

When exploring the detailed search results for a hub, you may right-click on a
Clicking Connect redirects to the gateway page of the selected hub's default assembly

Display	Hub Name	Description	Assembly
Disconnect	Croc and Bird Hub	Croc, Bird, and Archosaur Assembly Hub	[A]
Search details ...			
1 Matching Assembly			
Apr. 2013 (BGI_duck_1.0/anaPla1) (anaPla1)			
Assembly Description: ... This is the mallard duck <i>Anas platyrhynchos</i> genome			
Disconnect	CESAR Gene Mappings	Human Exons mapped by CESAR	[A]
Search details ...			
1 Matching Assembly			
Apr 2013 (BGI_duck_1.0/anaPla1) (hub)			
Open this assembly			



My Data Help About U

- My Sessions
- Public Sessions
- Track Hubs**
- Custom Tracks
- Track Collection Builder

Assembly Hubs via Sessions

Public Sessions *community contributed views of the Browser*

<http://genome.ucsc.edu/cgi-bin/hgPublicSessions>

Public Sessions

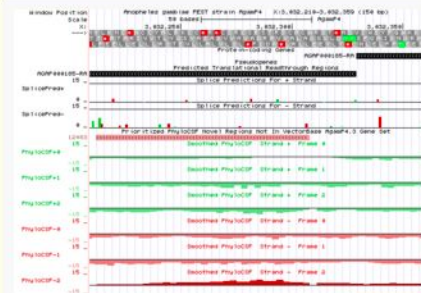
Sessions allow users to save snapshots of the Genome Browser and its current configuration, including displayed tracks, position, and custom track data. The Public Sessions tool allows users to easily share those sessions that they deem interesting with the rest of the world's researchers. You can add your own sessions to this list by checking the appropriate box on the [Session Management](#) page.

See the [Sessions User's Guide](#) for more information.

Sort by: Creation (oldest first)

Show entries

Search:

Screenshot	Session Properties
	<p>Description: This is an assembly hub for the AgamP4 assembly of <i>Anopheles gambiae</i> PEST strain. It includes the assembly; the coding genes and pseudogenes from vectorbase version 4.3; predicted stop codon readthrough regions; PhyloCSF tracks showing evolutionary protein-coding potential; splice-prediction tracks using the maximum-entropy splice-prediction algorithm; and novel coding and pseudogene predictions using PhyloCSF, excluding regions already annotated in vectorbase version 4.3</p> <p>Author: iljung Session Name: AgamP4 Genome Assembly: hub_102577_AgamP4 Creation Date: 2016-08-09 Views: 366</p> <p>Description: We sequenced the hermaphroditic freshwater snail, <i>Biomphalaria glabrata</i> (strain BB02), the host for the medically</p>

My Data Help About

- My Sessions
- Public Sessions**
- Track Hubs
- Custom Tracks

hub_

Assembly Hubs via Sessions

Public Sessions *community contributed views of the Browser*

1) Search *snail*

Search:

Session Properties

Description: We sequenced the hermaphroditic freshwater snail, *Biomphalaria glabrata* (strain BB02), the host for the

My Data Help About

- My Sessions
- Public Sessions**
- Track Hubs
- Custom Tracks

2) Click image under screenshot to load the session

3) Click the “*base*” zoom-in button

base

UCSC Genome Browser on Snail *Biomphalaria glabrata* Assembly (bioGla0)

move <<< << < > >> >>> zoom in 1.5x 3x 10x **base** zoom out 1.5x 3x 10x 100x

LGUN_random_Scaffold6274:11,486-11,678 193 bp. go

Scale 50 bases | bioGla0

LGUN_random_Scaf: 11,500 11,510 11,520 11,530 11,540 11,550 11,560 11,570 11,580 11,590 11,600 11,610 11,620 11,630

AGCAATGTACACAGGTTTACTTTTATCCGTGCATAAATAGCAAAAAACACATTTTATACATCCCAAGGTCATACATTGAAAACTCCCTTAAATAAAGTATAGCAGAGACATCTGGTGGATCCCTTAGATGATTTTAA

Vectorbase Genes

BGLB012233-RA 44 I Y V P K V K I L

NM_001311308 44 I Y V P K V K I L

RefSeq Genes

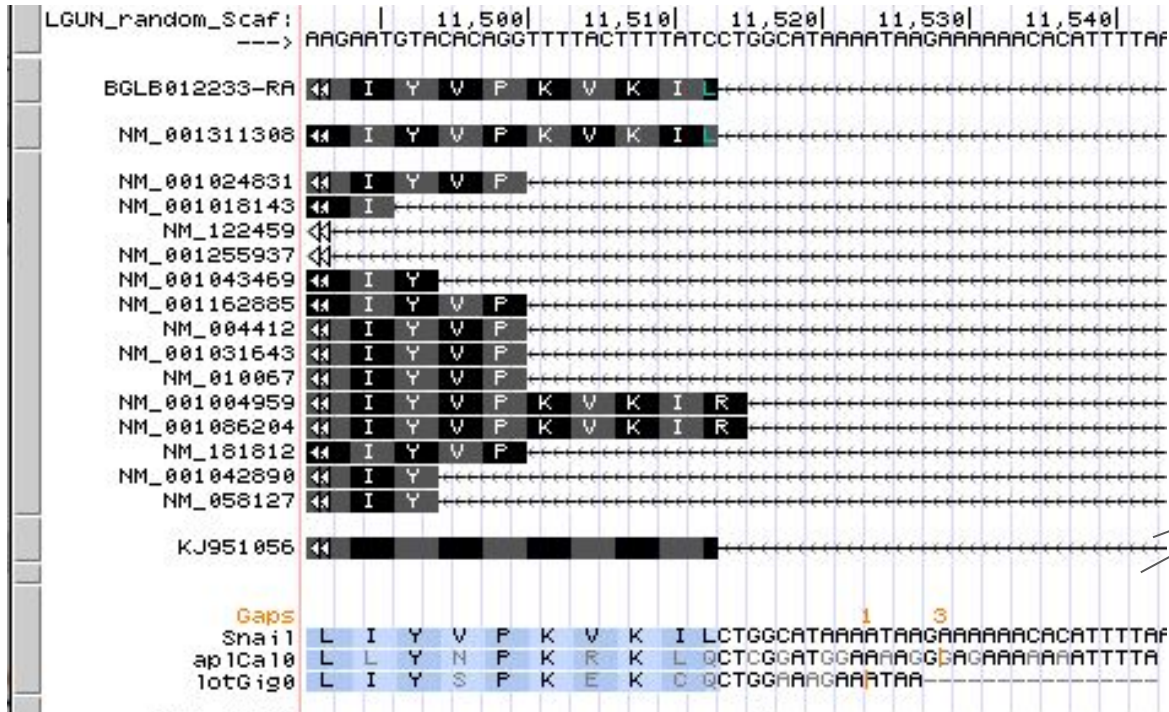
NM_001024831 44 I Y V P

NM_001018143 44 I

Other RefSeq Genes

Analyzing a variant on an assembly hub

Variant Annotation Integrator (VAI) *process SNPs on provided prediction tracks*



Collection of many Gene PredictionTracks (file type **bigGenePred**). Files allows display of AA codons based on reference assembly sequence.

A genomic alignment track (file type **bigPSL**). mRNAs from GenBank aligned to reference.

A Multiple Alignment Track (file type **bigMaf**). Allows display of other genomes aligned to this reference.

Analyzing a variant on an assembly hub

Variant Annotation Integrator (VAI) *process SNPs on provided prediction tracks*

*Add a Custom
Track*

My Data	View	Help
My Sessions		ss
Public Sessions		ps
Track Hubs		th
Custom Tracks		ct
Track Collection Builder		tc

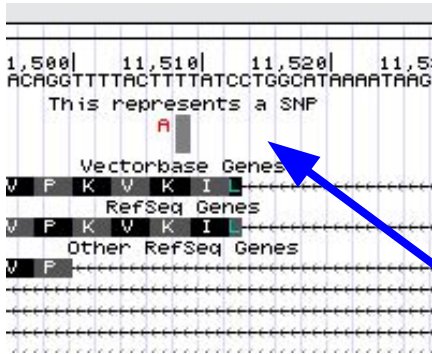
```
track type=pgSnp name=myData visibility=pack description="This represents a SNP"  
LGUN_random_Scaffold6274 11508 11509 A 1 0 0
```

Paste URLs or data: Or upload: No file chosen

```
track type=pgSnp name=myData visibility=pack description="This represents a SNP"  
LGUN_random_Scaffold6274 11508 11509 A 1 0 0
```

Analyzing a variant on an assembly hub

Variant Annotation Integrator (VAI) *process SNPs on provided prediction tracks*



Custom Track

Variant Annotation Integrator

Select Genome Assembly and Region
clade genome assembly
Snail Assembly Snail Biomphalaria glabrata
region to annotate
genome

Select Variants
variants: This represents a SNP
maximum number of variants to be processed
manage custom tracks track hubs To reset all user c

Select Genes
The gene predictions selected here will be used to
etc.
Vectorbase Genes

Define Filters
+ Functional role

Configure Output
output format: Variant Effect Predictor (HTML)

Analyzing a variant on an assembly hub


Variant Annotation Integrator (VAI) *process SNPs on provided prediction tracks*

UCSC Genome Bioinformatics

Annotated Variants in VEP/HTML format

Variants: This represents a SNP (customTrash.t1_genome_25c4_7da4a0)
Transcripts: Vectorbase Genes (http://ilya.unm.edu/Bg_hub/vecBaseGenes.bb)

Uploaded Variation	Location	Allele	Gene	Feature	Feature type	Consequence	Position in cDNA	Position in CDS	Position in protein	Amino acid change	Codon change	Co-located Variation	Extra
LGUN_random_Scaffold6274_11509_A	LGUN_random_Scaffold6274:11509	A	BGLB012233	BGLB012233-RA	Transcript	stop_gained	163	163	55	K/*	Aaa/Taa	-	EXON=2/6

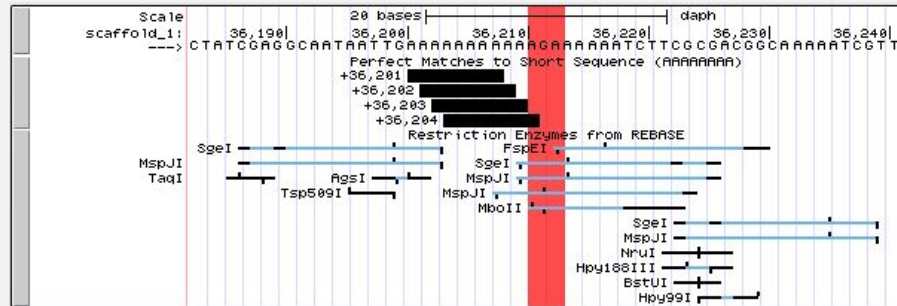


Consequence	Position in cDNA	Position in CDS	Position in protein	Amino acid change
stop_gained	163	163	55	K/*

Building a 2bit file: binary indexed FASTA

```
>scaffold_1
GTTGTAAATACTCTATTCTACAATAAAACCAA
TCATAGGTTGAATTGGCGTTGAAGTAAACAAA
...
>scaffold_2
AGTTATGACAACTATAAAAAGTCGGTAGAGACAAAAG
TCGTTCTGGGACGAAGCGACCAAACTGAGCACAAGAT
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATT
TAGAAAATTTCCAGGAAGTTTGAAGTTGCTAT
...
```

```
hubDirectory
|__hub.txt
|__genomes.txt
|__hg19
|__trackDb.txt
```



A 2bit file is a binary indexed version of a FASTA file
(stores sequence ACGT as 00 01 11 10)

`faToTwoBit` `input.fasta` `output.2bit`




```
>scaffold_1
GTTGTAAATACTCTATTCTACAATAAAACCAAAGATAACTCTTTATCAG
TCATAGGTTGAATTGGCGTTGAAGTAAACAAAAAATACTGCTCAAAGG
...
>scaffold_2
AGTTATGACAAACTATAAAAAGTCGGTAGAGACAAAAGCGAAAAGGATCT
TCGTTTCGTGGACGAAGCGACCAAACCTGAGCACAAGATAAATCCCGAATA
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATTTTAGAAAAATGGTTCA
TAGAAAAATTTCCAGGAAGTTTGAAGTTGCTATAATGATTATTTCTCTTG
...
>scaffold_4
ATACTGCCCATGCCTCATCTACTCCCTTCTTAACCTTTTCATCAACAAC
TGCTTAAGTTGGTCATCACTGACTGAGTGAGCCCAAACCTGGAATAGCTGT
...
```

The resulting binary file **output.2bit** can have data more easily extracted and can also be viewed in Genome Browsers.

Extracting a specific window location of data from a BAM and 2bit file


samtools view http://location_of/file.bam "chr1:1499900-1500055" > output.sam



```
PRESLEY_0030:6:5:16900:3432#0/2 65 chr1 10047 254 67M9S * 0 0 CCTAACCTAACCTAACCTAACCC
fa]hfafe]a_cfaddfcaffW_edfabfcdfc^cace^c\d\aaWaJYZZ\K^VZTaBBB888888
PRESLEY_0030:6:26:1717:9490#0/2 65 chr1 10053 254 61M15S * 0 0 CCTAACCTAACCTAACCTAACCC
f_fcdefhfhaecffdf]ffdcf]ffcff]cb`bb[d]db*W`^^^_Y^BBBB8888888888888888
PRESLEY_0030:5:69:17883:15567#0/2 65 chr1 10060 255 2573M1S * 0 0 AACTAACCTAACCTAA
hgfgghhhfhhhhhhhhghghhhhhghghhhhhhhghghhhchghfchfhhadbhhea]_cfca[
PRESLEY_0030:5:75:7248:15014#0/2 65 chr1 10060 255 2573M1S * 0 0 AACTAACCTAACCTAA
hfhfgghghfhhhhffghghdghcagfhhhhfchhfhc fhgcedfaff_hdfeeehaacc[Rchhh]egbd[bb
PRESLEY_0030:5:101:10596:3305#0/2 65 chr1 10060 255 2573M1S * 0 0 AACTAACCTAACCTAA
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhghghghhhhhhhghghd_dnhgceded^a^
.....
```

twoBitToFa -seq=chr1 -start=1499900 -end=1500055

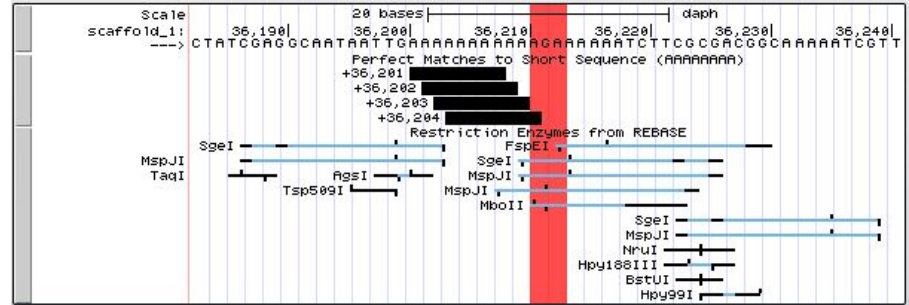
twoBitPath <http://yourGenome/your.2bit> output.fa



```
>chr1:1499900-1500055
GCTACCATCACCCAAAAAGCTGAGGAGTTTGAATTCCTTCAGCACAACT
ATCATTAAATTAATTTTTGAACCTCTGAGCCTGGAAGAGAAAAACAGGTTTG
GTTCAACATGAAGAATACTGTGATTTGACCCGTGACAGAGCTTTCTGTTA
```

Assembly Track Hubs

bigDataUrl http://location_of/file.bam



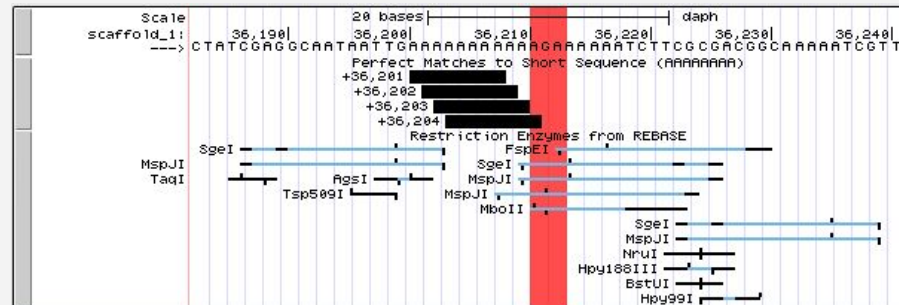
twoBitPath <http://yourGenome/your.2bit>



Building the Hub Text (.txt) Files

```
>scaffold_1
GTTGTAATACTCTATTCTACAATAAACCAA
TCATAGGTTGAATTGGCGTTGAAGTAAACAAA
...
>scaffold_2
AGTTATGACAACTATAAAAAGTCGGTAGAGACAAAAG
TCGTTCTGGGACGAAGCGACCAAACTGAGCACAAGAT
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATT
TAGAAAATTTCCAGGAAGTTTGAAGTTGCTA
...
```

hubDirectory
|__hub.txt
|__genomes.txt
|__hg19
|__trackDb.txt



Track Hubs

Track Hubs are text files (**hub.txt**, **genomes.txt**, **trackDb.txt**) that describe and point to the location of binary indexed data files (**twoBitPath**, **bigDataUrl**)

hubDirectory

|

|_hub.txt

|_genomes.txt

|_genomeDirectory1

|_trackDb.txt

Informs location of genome 2bit file(s): **twoBitPath**

Informs location of track data file(s): **bigDataUrl**

Track Hubs

Track Hubs are text files (**hub.txt**, **genomes.txt**, **trackDb.txt**) that describe and point to the location of binary indexed data files (**twoBitPath**, **bigDataUrl**)

hub.txt

hub *MyHubsNameWithoutSpaces*
shortLabel *My Hub's Name*
longLabel *Longer label about my hub.*
email *myEmail@address*
genomesFile *http://location_of/genomes.txt*



genomes.txt

genome *yourGenome*
trackDb *http://location_of/trackDb.txt*
twoBitPath *http://location_of/output.2bit*
...

trackDb.txt

track *cytoBandIdeo*
type *bigBed*
longLabel *Chromosome ideogram with cytogenetic bands*
shortLabel *cytoBandIdeo*
bigDataUrl *http://location_of/yourCytoBandIdeo.bigBed*

track *bam1*
type *bam*
shortLabel *BAM example*
longLabel *A BAM file for my genome data*
visibility *dense*
bigDataUrl *http://location_of/file.bam*

...

Each new track gets a new stanza

bigDataUrl lines point to location of binary indexed data
More trackDb parameters can be defined too (color, ect.)

Track Hubs

Track Hubs are text files (**hub.txt**, **genomes.txt**, **trackDb.txt**) that describe and point to the location of binary indexed data files (**twoBitPath**, **bigDataUrl**)

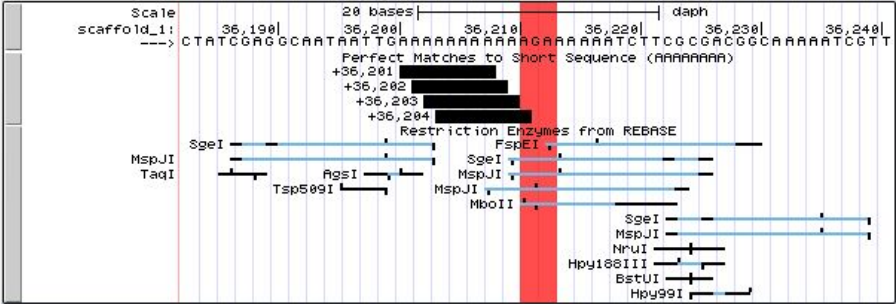
The screenshot displays a web-based genomic track interface. It features three main track groups, each with a dark blue header bar containing a minus sign icon on the left and a 'refresh' button on the right. The first group is titled 'Mapping' and includes sub-tracks for 'Base Position' (set to 'dense'), 'Assembly' (set to 'hide'), 'Gap' (set to 'hide'), 'Restr Enzymes' (set to 'full'), and 'Short Match' (set to 'squish'). The second group is titled 'Genes' and includes a sub-track for 'Genscan Genes' (set to 'hide'). The third group is titled 'Variation'. The sub-tracks within each group are displayed on a light gray background.

The groups.txt file in **genomes.txt** defines the blue bars grouping tracks in assembly hubs.

Building an Assembly Hub for Cucumber

```
>scaffold_1
GTTGTAATACTCTATTCTACAATAAAACCAA
TCATAGGTTGAATTGGCGTTGAAGTAAACAAA
...
>scaffold_2
AGTTATGACAACTATAAAAAGTCGGTAGAGACAAAAG
TCGTTCTGGGACGAAGCGACCAAACTGAGCACAAGATA
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATT
TAGAAAATTTCCAGGAAGTTTGAAGTTGCTAT
...
```

- hubDirectory
- |__hub.txt
- |__genomes.txt
- |__hg19
- |__trackDb.txt



Build the 2bit for Cucumber

Navigate to NCBI and find the latest Cucumber Genome:

<https://www.ncbi.nlm.nih.gov/assembly/?term=Cucumber>



Select 2017 B10v2 and click the “Download the GenBank assembly” link

Full Report ▾

B10v2

Organism name: [Cucumis sativus \(cucumber\)](#)

Infraspecific name: Cultivar: Borszczagowski

Isolate: B10

Send to: ▾

Access the data

Download the GenBank assembly

BLAST search the assembly

Download the full sequence

See [Genome Information for Cucumis sativus](#)

Build the 2bit for Cucumber

Obtain the link for the full Fasta file
(GCA_001483825.2_B10v2_genomic.fna.gz):

```
wget  
ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/001/483/825/GCA_001483825.2_B10v2/  
GCA_001483825.2_B10v2_genomic.fna.gz
```

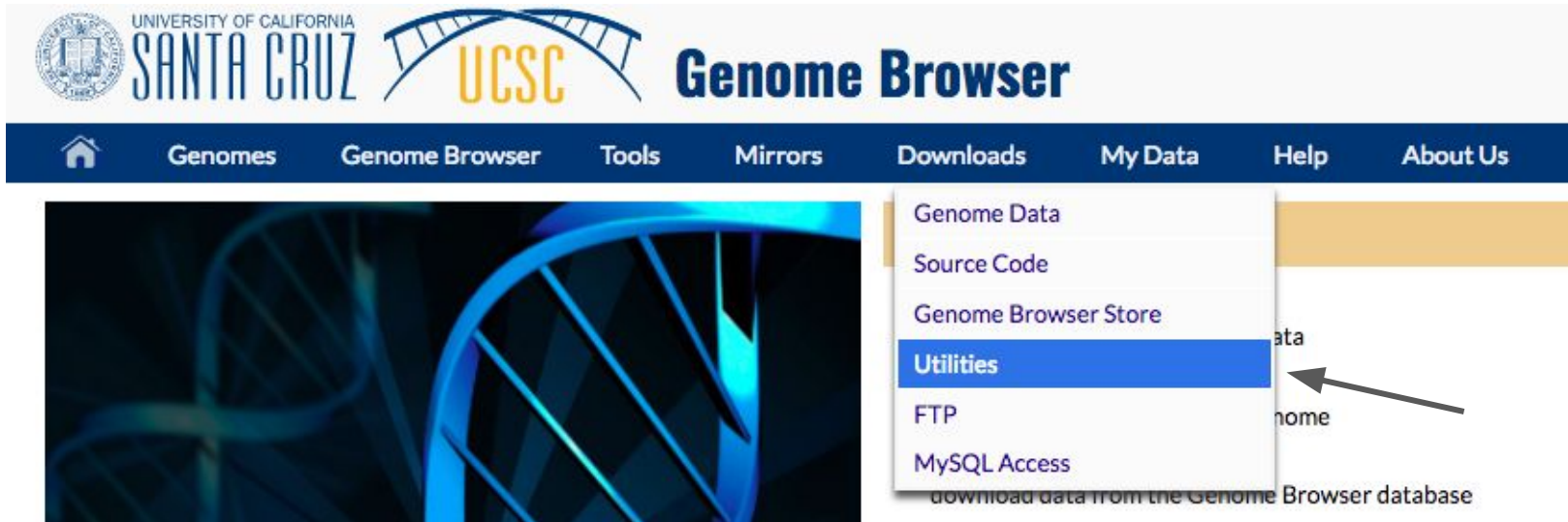
Unzip the fasta file:

```
gzip -d GCA_001483825.2_B10v2_genomic.fna.gz
```

Build the 2bit for Cucumber

Obtain utilities from the UCSC Genome Browser

`faToTwoBit` and other standalone command-line **Utilities** are downloadable tools available on Linux and UNIX platforms.



The image shows the UCSC Genome Browser website header and navigation menu. The header includes the University of California Santa Cruz logo, the UCSC logo, and the text "Genome Browser". The navigation menu includes "Genomes", "Genome Browser", "Tools", "Mirrors", "Downloads", "My Data", "Help", and "About Us". A dropdown menu is open under "Downloads", listing "Genome Data", "Source Code", "Genome Browser Store", "Utilities", "FTP", and "MySQL Access". The "Utilities" option is highlighted in blue, and an arrow points to it from the right. Below the menu, there is a partial view of a page with the text "data" and "home" visible, and a line of text at the bottom: "download data from the Genome Browser database".

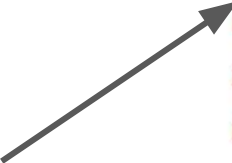
Build the 2bit for Cucumber

Obtain utilities from the UCSC Genome Browser

`faToTwoBit` and other standalone command-line **Utilities** are downloadable tools available on Linux and UNIX platforms.

Utilities

The [utilities directory](#) offers downloads of pre-compiled standalone binaries for:

- [LiftOver](#) (which may also be accessed via the [web version](#)). The over.chain lift
 - Other command-line utilities
 - [Blat](#) ▶
- 

Build the 2bit for Cucumber

Obtain utilities from the UCSC Genome Browser

`faToTwoBit` and other standalone command-line **Utilities** are downloadable tools available on Linux and UNIX platforms.

faCount	09-Jan-2018	15:55	4.1M
faFilter	09-Jan-2018	15:55	4.1M
faFilterN	09-Jan-2018	15:55	4.3M
faFrag	09-Jan-2018	15:55	4.1M
faNoise	09-Jan-2018	15:55	4.1M
faOneRecord	09-Jan-2018	15:55	4.1M
faPolyASizes	09-Jan-2018	15:55	4.1M
faRandomize	09-Jan-2018	15:55	4.1M
faRc	09-Jan-2018	15:55	4.1M
faSize	09-Jan-2018	15:55	4.1M
faSomeRecords	09-Jan-2018	15:55	4.1M
faSplit	09-Jan-2018	15:55	4.1M
faToFastq	09-Jan-2018	15:56	4.1M
faToTab	09-Jan-2018	15:56	4.1M
faToTwoBit	09-Jan-2018	15:56	4.2M
faTrans	09-Jan-2018	15:56	4.1M
fastqStatsAndSubsample	09-Jan-2018	15:55	4.2M
fastqToFa	09-Jan-2018	15:55	4.2M
featureBits	09-Jan-2018	15:57	16M
fetchChromSizes	09-Jan-2018	16:01	2.7K
findMotif	09-Jan-2018	15:56	4.2M
...



Build the 2bit for Cucumber

Obtain utilities from the UCSC Genome Browser

```
wget http://hgdownload.soe.ucsc.edu/admin/exe/linux.x86_64/faToTwoBit
```

```
wget http://hgdownload.soe.ucsc.edu/admin/exe/linux.x86_64/twoBitInfo
```

```
wget http://hgdownload.soe.ucsc.edu/admin/exe/linux.x86_64/bedToBigBed
```

Build the 2bit for Cucumber

Use `faToTwoBit`:

`faToTwoBit GCA_001483825.2_B10v2_genomic.fna cucumber.2bit`



```
>scaffold_1
GTTGTAAACTCTATTCTACAATAAAACAAAAGATAACTCTTTATCAG
TCATAGGTTGAATTGGCGTTGAAGTAAAACAAAAAATACTGCTCAAAAGG
...
>scaffold_2
AGTTATGACAAACTATAAAAAAGTCGGTAGAGACAAAAGCGAAAAGGATCT
TCGTTTCGTGGACGAAGCGACCAAACTGAGCACAAAGATAAATCCCGAATA
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATTTTAGAAAAATGGTTCA
TAGAAAAATTTCCAGGAAGTTTGAAGTTGCTATAATGATTATTTCTCTTG
...
>scaffold_4
ATACTGCCCATGCCTCATCTACTCCCTTCTTAACCTTTTCATCAACAACT
TGCTTAAGTTGGTCATCACTGACTGAGTGAGCCCAAACCTGGAATAGCTGT
...
```

The resulting binary file **cucumber.2bit** will be referenced in **twoBitPath** in the genomes.txt file

Build a Cytoband Track from the Cucumber 2bit

Extract the size of the chromosomes in cucumber for building indexes

`twoBitInfo cucumber.2bit cucumber.chrom.sizes`



LKUO02000001.1	12661638
LKUO02000002.1	16711
LKUO02000003.1	11978
LKUO02000004.1	5190334
LKUO02000005.1	16581
LKUO02000006.1	25283
LKUO02000007.1	27846
LKUO02000008.1	17515
LKUO02000009.1	19313
LKUO02000010.1	273978

Build a Cytoband Track from the Cucumber 2bit

From the `chrom.sizes` create a BED file that will represent chromosomes

```
cat cucumber.chrom.sizes | awk '{print $1,0,$2,$1,"gneg"}' >  
yourCytobandIdeo.bed
```



LKUO02000001.1	12661638
LKUO02000002.1	16711
LKUO02000003.1	11978
LKUO02000004.1	5190334
LKUO02000005.1	16581
LKUO02000006.1	25283
LKUO02000007.1	27846
LKUO02000008.1	17515
LKUO02000009.1	19313
LKUO02000010.1	273978




LKUO02000001.1	0	12661638	LKUO02000001.1	gneg
LKUO02000002.1	0	16711	LKUO02000002.1	gneg
LKUO02000003.1	0	11978	LKUO02000003.1	gneg
LKUO02000004.1	0	5190334	LKUO02000004.1	gneg
LKUO02000005.1	0	16581	LKUO02000005.1	gneg
LKUO02000006.1	0	25283	LKUO02000006.1	gneg

Build a Cytoband Track from the Cucumber 2bit

Use `bedToBigBed` to wrap text data into a binary indexed version

```
bedToBigBed -type=bed4 yourCytoBandIdeo.bed -as=cytoBand.as cucumber.chrom.sizes  
yourCytoBandIdeo.bigBed
```



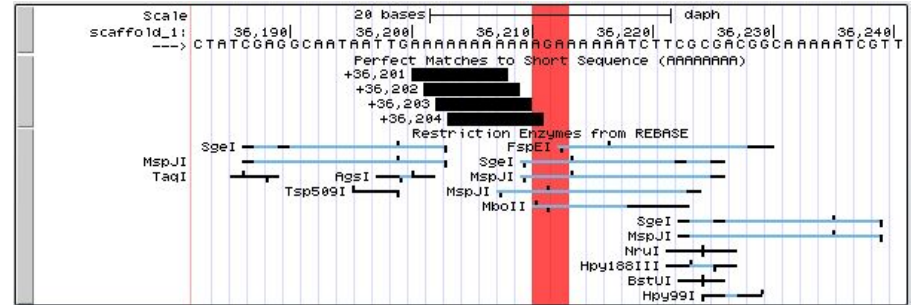
```
LKUO02000001.1 0 12661638 LKUO02000001.1 gneg  
LKUO02000002.1 0 16711 LKUO02000002.1 gneg  
LKUO02000003.1 0 11978 LKUO02000003.1 gneg  
LKUO02000004.1 0 5190334 LKUO02000004.1 gneg  
LKUO02000005.1 0 16581 LKUO02000005.1 gneg  
LKUO02000006.1 0 25283 LKUO02000006.1 gneg
```

```
table cytoBandIdeo  
"cytoBandIdeo describes...."  
(  
  string chrom;      "Reference.... "  
  uint  chromStart; "Start..."  
  uint  chromEnd;   "End..."  
  string name;      "Name of item"  
  string gieStain;  "Giemsa stain..".  
)
```

Turned
**yourCytoBandIdeo.
bed** text file into a
binary indexed
version:
**yourCytoBandIdeo.
bigBed**

Build the hub.txt, genomes.txt, trackDb.txt

bigDataUrl http://location_of/yourCytoBandIdeo.bigBed



twoBitPath <http://yourGenome/cucumber.2bit>

Build the hub.txt, genomes.txt, trackDb.txt

Obtain example files from a simple assembly hub:

```
wget http://hgwdev.gi.ucsc.edu/~brianlee/examples/trackHub/simple/hub.txt
```

```
wget http://hgwdev.gi.ucsc.edu/~brianlee/examples/trackHub/simple/genomes.txt
```

```
wget http://hgwdev.gi.ucsc.edu/~brianlee/examples/trackHub/simple/trackDb.txt
```

```
wget http://hgwdev.gi.ucsc.edu/~brianlee/examples/trackHub/simple/groups.txt
```

Build the hub.txt, genomes.txt, trackDb.txt

Edit the hub.txt, **genomes.txt** and **trackDb.txt** to use correct locations and correct cucumber chromosome names

hub.txt

```
hub c01
shortLabel cucumber
longLabel This is displaying B10v2 cucumber genome from GenBank
email myEmail@address
genomesFile genomes.txt
```



genomes.txt

```
genome cucSat1
trackDb trackDb.txt
scientificName Cucumis sativus
description 2017/05/19 GCA_001483825.2
organism Cucumber
defaultPos LKU002000001.1:1000000-2000000
groups groups.txt
htmlPath https://www.ncbi.nlm.nih.gov/assembly/GCA_001483825.2
twoBitPath cucumber.2bit
```

trackDb.txt

```
track cytoBandIdeo
type bigBed
longLabel Chromosome ideogram with cytogenetic bands
shortLabel cytoBandIdeo
bigDataUrl yourCytoBandIdeo.bigBed
```



Build the hub.txt, genomes.txt, trackDb.txt

Edit the **genomes.txt** to include blat servers

<http://path.lab.edu/to/>

Location of 2bit

|_genomes.txt

|_cucumber.2bit

genomes.txt

genome cucSat1

...

blat hgwdev.gi.ucsc.edu 166669

transBlat hgwdev.gi.ucsc.edu 166666

(trans is short for "translated" AA search)

gfServer start localhost 166666 -trans -mask **cucumber.2bit** &

gfServer start localhost 166669 -stepSize=5 **cucumber.2bit** &

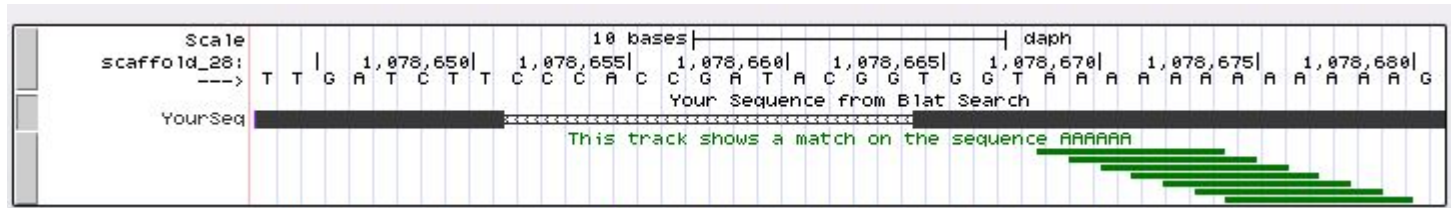
Additional Tools Available on Assembly Hubs

- BLAT search sequence or amino-acid matched

BLAT Search Genome

Genome: Assembly: Query type: Sort output: Output type:

```
TACGTCTGACCGCACTTTAGTTAGATACCATCGCCAAGCTGACTTTTTTT
TTTTTACAAAAGATCAAGGCGGATGAAAGAAGCCTTTTGTTAATGCACT
TTTCTTCATCCAG
```



Summary of Assembly Track Hubs

Remotely Hosted Data

Binary indexed files: `twoBitPath`,
`bigDataUrl`

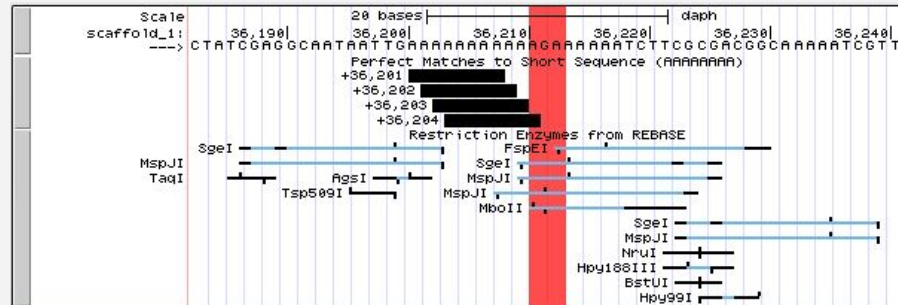
`twoBitPath`,
`bigDataUrl`

```
>scaffold_1
GTTGTAATACTCTATTCTACAATAAAACCAA
TCATAGGTTGAATTGGCGTTGAAGTAAAACAAA
...
>scaffold_2
AGTTATGACAACTATAAAAAAGTCGGTAGAGACAAAAG
TCGTTTCGTGGACGAAGCGACCAAACTGAGCACAAGATA
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATT
TAGAAAATTTCCAGGAAGTTTGAAGTTGCTA
...
```

Text files: `hub.txt`,
`genomes.txt`,
`trackDb.txt`

```
hubDirectory
|__hub.txt
|__genomes.txt
|__hg19
|__trackDb.txt
```

Visualizable at UCSC



live demo:

[http:// genome.ucsc.edu](http://genome.ucsc.edu)

bit.ly/UCSC_UO