

Synonyms

General Function Checklist

See this page in the users guide: [Personal Synonyms](#)

Chromosome synonyms

Here is an example chromosome synonyms file: [chromosome.txt](#)

```
KlingonChr1 Chr1  
KlingonChr2 Chr2  
KlingonChr3 Chr3  
KlingonChr4 Chr4  
KlingonChr5 Chr5
```

Here is the head of an example bed file, made by taking segments from the A_thaliana_Jun_2009 gene annotations and replacing the chromosome names: [KlingonGenes.bed](#)

```
NovelChrom 3630 5899 AT1G01010.1 0 + 3759 5630 0 6 283,281,120,390,153,461, 0,365,855,1075,1543,1808,  
KlingonChr1 5927 8737 AT1G01020.1 0 - 6914 8666 0 10 336,633,76,67,86,74,46,90,48,167,  
0,509,1229,1456,1636,1834,2014,2308,2489,2643,  
KlingonChr1 6789 8737 AT1G01020.2 0 - 7314 8666 0 8 280,294,86,74,46,90,48,167, 0,367,774,972,1152,1446,1627,1781,  
KlingonChr1 11648 13714 AT1G01030.1 0 - 11863 12940 0 2 1525,380, 0,1686,  
KlingonChr1 23145 31227 AT1G01040.1 0 + 23518 31079 0 20
```

Notice that there is one entry for a chromosome (NovelChrom) that is not in the synonyms file.

1. Navigate to the **Data Sources** tab in **Preferences**.
2. Click ... next to the **Chromosome Synonyms File** field.
3. Add the **chromosome.txt** file.
4. Restart IGB.
5. Open the **A_thaliana_Jun_2009** genome.
6. Load the **KlingonGenes.bed** file from the **Available Data** section.
7. Ensure the **Load Mode** in the **Data Access** tab at the bottom of IGB is set to **Genome**.

Good.

[Species](#)

Arabidopsis thaliana

Genome Version

A_thaliana_Jun_2009

(8) Sequence(s)	Length
Chr1	30427671
Chr2	19698289
Chr3	23459830
Chr4	18585056
Chr5	26975502
ChrC	154478
ChrM	366924
genome	
NovelChrom	5899

Bad.

[Species](#)

Arabidopsis thaliana

Genome Version

A_thaliana_Jun_2009

(13) Sequence...	Length
Chr1	30427671
Chr2	19698289
Chr3	23459830
Chr4	18585056
Chr5	26975502
ChrC	154478
ChrM	366924
genome	
KlingonChr5	632683
NovelChrom	5899
KlingonChr1	145684
KlingonChr2	482086
KlingonChr3	6704226
KlingonChr4	8007510

- The annotations from **KlingonGenes.bed** appear on the same chromosomes as the automatically loaded annotations. (If IGB creates new chromosomes labeled "KlingonChr1" etc, then the link between chromosome "KlingonChr5" and "Chr5" is not functioning.)

- ☐ mac
- ☐ linux
- ☐ windows

Genome version synonyms

Review the user guide page: [Use synonyms.txt to link genome version names to each other.](#)

How to make the test file (These instructions are a work in progress)

You can download the test file I made: [myQL](#)

Unzip that folder, and continue to [How to use the test file.](#)

The following instructions should be viewed as a "fall back".

1. Make an empty folder called "myQL".
2. In the myQL folder, create a plain text file called contents.txt file with this line (it is a tab between 2018 and My; do not include the bullet):
 - A_new_Jun_2018 My new genome as a test
3. In myQL, create a folder called "A_new_Jun_2018"
4. In A_new_Jun_2018, create an annots.xml file with this text:
 - <files>

```
<file name="KlingonGenes.bed" title="new/KlingonGenes" />
```

```
</files>
```

5. In the A_new_Jun_2018 folder, save the KlingonGenes.bed file (see Chromosome synonyms).
6. In the myQL folder, create a folder called "synsFileNotInUse"
7. In the synsFileNotInUse folder, create a text file called synonyms.txt with this text (this is two terms, separated by a tab):

- A_thaliana_Jun_2009 A_new_Jun_2018

The synonyms file will not "work" from this location. This is just its starting position in the test process.

How to use the test file

1. Download the myQL test file here: [myQL](#)
2. Reset preferences to give IGB a clean slate.
3. From the IGB home screen, click the **Species** pull down.

- There is **NO** genome for **A_new** in the **Species** pull down.

- ☐ mac
- ☐ linux
- ☐ windows

1. In the **Data Sources** tab in **Preferences**, add myQL as a Quickload site.
2. From the IGB home screen, click the **Species** pull down.
 - There **IS** a genome for **A_new** in the **Species** pull down.

- ☐ mac
- ☐ linux
- ☐ windows

Open **A_new_Jun_2018**.

- The **myQL** Quickload appears in the **Available Data** section.

- ☐ mac
- ☐ linux
- ☐ windows

1. Add **KlingonGenes** from the **myQL** Quickload.
2. Click **Load Data**.

- The **KlingonGenes** data loaded and Klingon chromosomes are now listed in the panel at the right.

- ☐ mac
- ☐ linux
- ☐ windows

Open **A_thaliana_Jun_2009**.

- There is **NO myQL** Quickload in the **Available Data** section.

- ☐ mac
- ☐ linux
- ☐ windows

In the **Data Sources** tab in **Preferences**, add synonyms.txt file (found in **myQL > synsFileNotInUse**) as a version synonyms file.

- IGB prompted you to restart.

- ☐ mac
- ☐ linux
- ☐ windows

Restart IGB.

- There is **NO** genome for **A_new** in the **Species** pull down.

- ☐ mac
- ☐ linux
- ☐ windows

Open **A_thaliana_Jun_2009**.

- The **myQL** Quickload appears in the **Available Data** section.

- ☐ mac
- ☐ linux
- ☐ windows

1. Add **KlingonGenes** from the **myQL** Quickload.
2. Click **Load Data**.

- The **KlingonGenes** data loaded and Klingon chromosomes are now listed in the panel at the right.

- ☐ mac
- ☐ linux
- ☐ windows

1. Reset preferences to default.
2. In your File Chooser, move the synonyms.txt file from the synsFileNotInUse folder to the myQL folder.
3. Restart IGB.
4. In the **Data Sources** tab in **Preferences**, add myQL as a Quickload site.

- There is **NO** genome for **A_new** in the **Species** pull down.

- ☐ mac
- ☐ linux
- ☐ windows

Open **A_thaliana_Jun_2009**.

- The **myQL** Quickload appears in the **Available Data** section.

- ☐ mac
- ☐ linux
- ☐ windows

1. Add **KlingonGenes** from the **myQL** Quickload.
2. Click **Load Data**.

- The **myQL** Quickload and the KlingonGenes file were loaded without issue with the **A_thaliana_Jun_2009** genome.

- ☐ mac
- ☐ linux
- ☐ windows