

Custom Genomes (Genomes not in IGB)

IGB supports many species and genome versions, not just the species shown on the start screen. To check whether a genome is available in IGB, click the **Current Sequence** tab and use the **Species** and **Genome Version** menus to look for your genome of interest.

However, if your genome is not available, you can still use IGB. Here's how:

How to open a custom genome

1. Select **File > Open Genome from File...** (or click the DNA icon in the **Toolbar**.)
2. Select a sequence file to use as the reference genome (fasta or 2bit format).
3. **Optional:** Enter an IGB-friendly genome version name (optional)
4. **Optional:** Enter the species name, including genus, species and variety as appropriate (optional)
5. Click **OK** and wait for the genome to load.
6. Open data files as usual. And to view sequence, zoom in and click **Load Sequence**.

1. choose reference sequence (2bit is best; fasta is fine.)

2. enter IGB-friendly genome version name (optional)

3. enter genus, species, variety (optional)

4. click OK

IGB-friendly genome version names look like:

G_species_MMM_YYYY
or
G_species_variety*_MMM_YYYY

- **G** - first letter of genus
- **species** - species name
- **variety*** - zero or more strain, cultivar, or accession names (optional)
- **MMM** - 3-letter abbreviation of month when the genome version was released
- **YYYY** - year of release

For examples, see the **Genome Version** menu in the **Current Genome** tab.