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. Enter **Optional** details:
    a. Enter Genus name
    b. Enter the Species name
    c. Enter the Variety as appropriate (strain/cultivar/accession)
    d. Choose the Month of the genome release date
    e. Enter the Year in YYYY format.
4. Click **OK** and wait for the genome to load.
5. Open data files as usual. And to view sequence, zoom in and click **Load Sequence**.