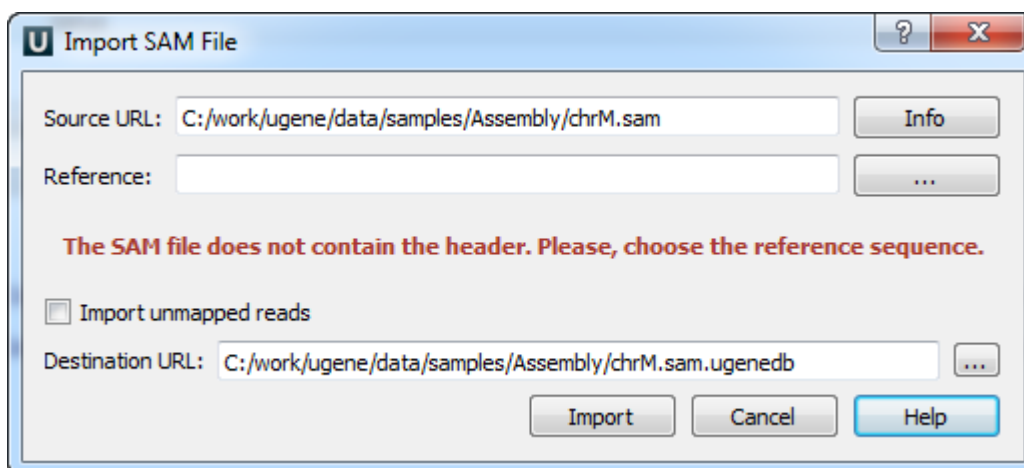


# Import BAM/SAM File

To start working with an assembly import it to the UGENE database file. To do this, [open](#) the assembly file.

For assembly file without header you need to choose a reference sequence:

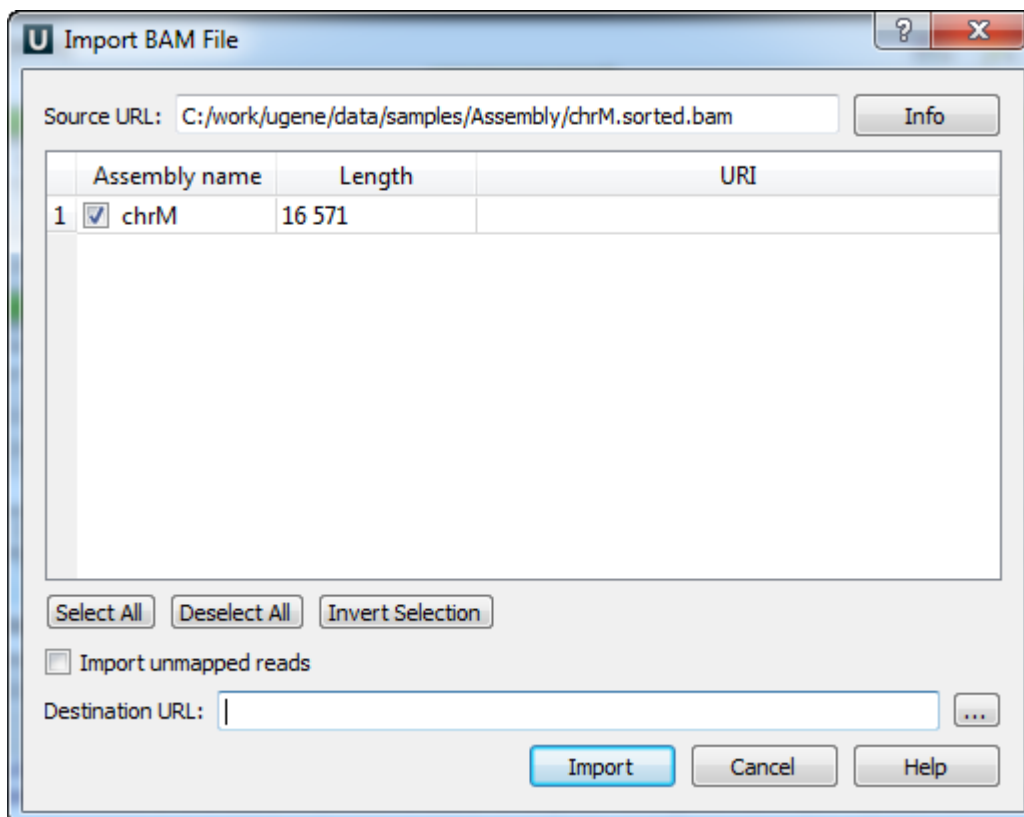


The dialog box titled "Import SAM File" has a blue header bar with a question mark and a close button. It contains the following fields and controls:

- Source URL:** A text field containing "C:/work/ugene/data/samples/Assembly/chrM.sam" and an "Info" button.
- Reference:** An empty text field and a button with three dots.
- Message:** A red text message: "The SAM file does not contain the header. Please, choose the reference sequence."
- Import unmapped reads:** A checkbox that is currently unchecked.
- Destination URL:** A text field containing "C:/work/ugene/data/samples/Assembly/chrM.sam.ugenedb" and a button with three dots.
- Buttons:** "Import", "Cancel", and "Help" buttons at the bottom.

Select the reference sequence and click *Import* button.

For other assembly files the following dialog appears:



The dialog box titled "Import BAM File" has a blue header bar with a question mark and a close button. It contains the following fields and controls:

- Source URL:** A text field containing "C:/work/ugene/data/samples/Assembly/chrM.sorted.bam" and an "Info" button.
- Table:** A table with columns "Assembly name", "Length", and "URI". It contains one row with "chrM" and "16 571". The "chrM" cell has a checked checkbox.
- Buttons:** "Select All", "Deselect All", and "Invert Selection" buttons below the table.
- Import unmapped reads:** A checkbox that is currently unchecked.
- Destination URL:** An empty text field and a button with three dots.
- Buttons:** "Import", "Cancel", and "Help" buttons at the bottom.

The *Source URL* field in the dialog specifies the file to import. The *Info* button nearby can be used to obtain additional information about the file.

There is a list of contigs below the *Source URL*. Check the contigs that you want to import to the database. You can use the *Select All*, *Deselect All* and *Invert Selection* buttons to manage the selection.

The *Destination URL* field specifies the output database file.

If you check the *Import unmapped reads*, then all unmapped reads in the assembly (i.e. read with the unmapped flag or without CIGAR) are imported. Note, however, that they are not visualized in the current UGENE version.

To start the import, click the *Import* button in the dialog. You can see the progress of the import in the [Task View](#). To export a UGENE database file into the SAM format, select the *Actions Export assembly to SAM format* item in the main menu.