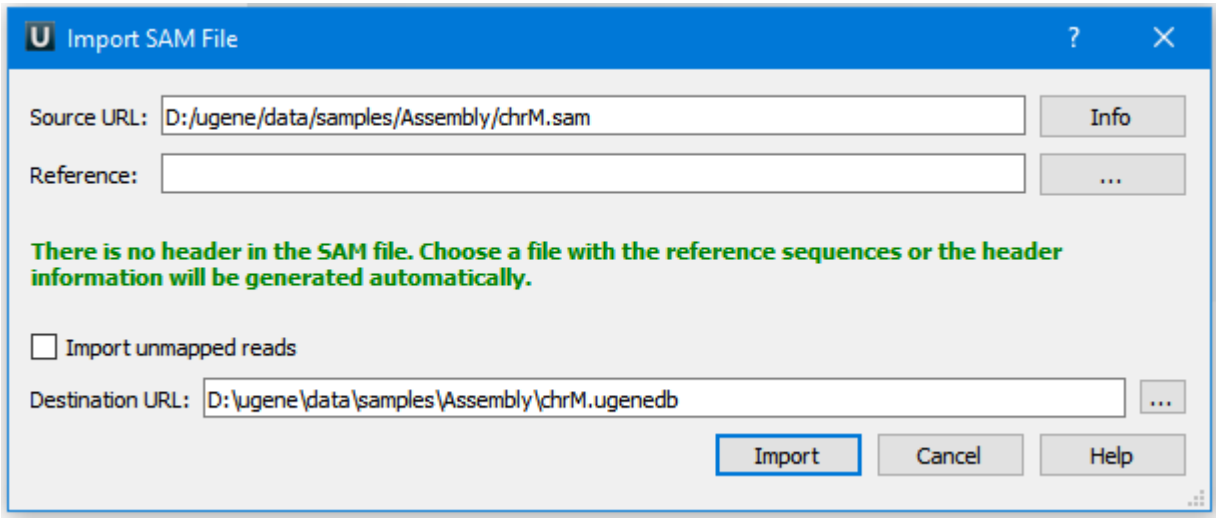
Import BAM and SAM Files

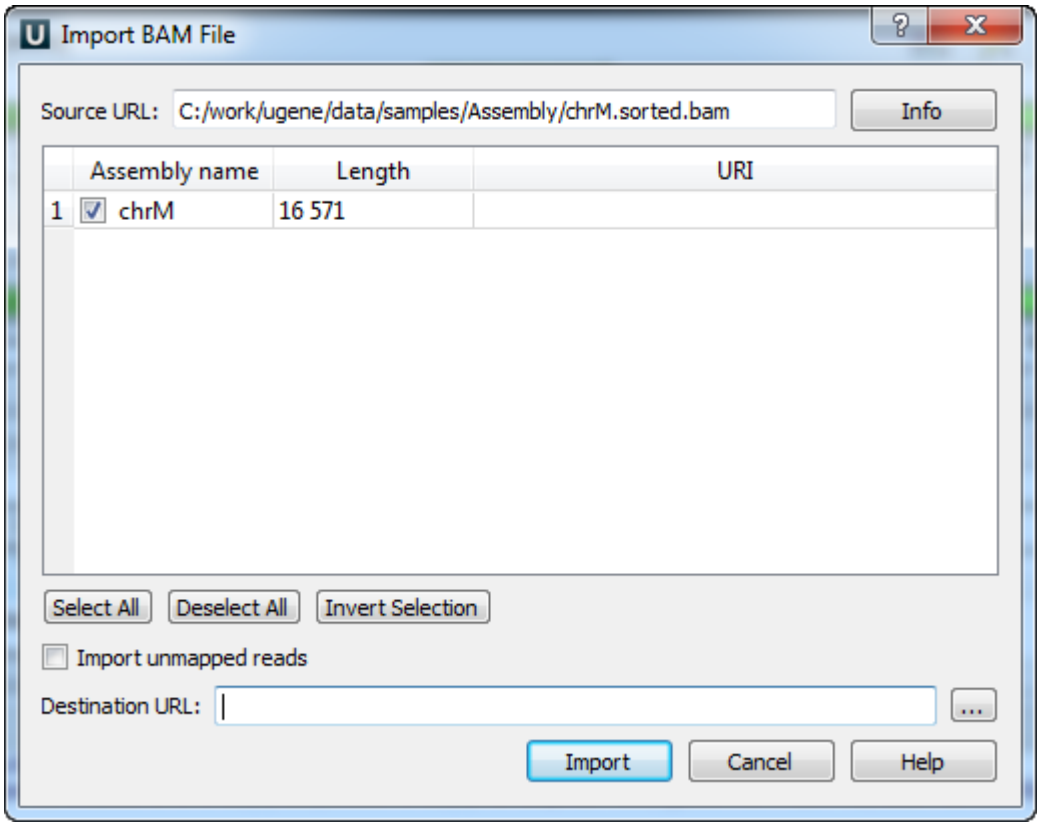
To start working with an assembly import it to the UGENE database file. To do this, *open* the assembly file.

For assembly file without header you can select the file with the reference sequence, otherwise the header information will be generated automatically.



Select if you want the referense sequence and click *Import* button.

For other assembly files the following dialog appears:



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 vizualized 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.