

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:

U Import SAM File

Source URL: Info

Reference: ...

The SAM file does not contain the header. Please, choose the reference sequence.

☐ Import unmapped reads

Destination URL: ...

Import Cancel Help

Select the reference sequence and click *Import* button.

For other assembly files the following dialog appears:

U Import BAM File

Source URL: Info

	Assembly name	Length	URI
1	☒ chrM	16 571	

Select All Deselect All Invert Selection

☐ Import unmapped reads

Destination URL: ...

Import Cancel Help

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.