## 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 referenece sequence:

U Import SAM File						
Source URL:	C:/work/ugene/data/samples/Assembly/chrM.sam Info					
Reference:						
The SAM file does not contain the header. Please, choose the reference sequence.						
Import unmapped reads						
Destination U	RL: C:/work/ugene/data/samples/Assembly/chrM.sam.ugenedb					
	Import Cancel Help					

Select the referense sequence and click Import button.

For other assembly files the following dialog appears:

U Import BAM File						
Source URL:	Info					
Assembly	y name	Length	URI			
1 🔽 chrM		16 571				
Select All Deselect All Invert Selection						
Import unmapped reads						
Destination UR	L:					
			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 Inv ert 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.