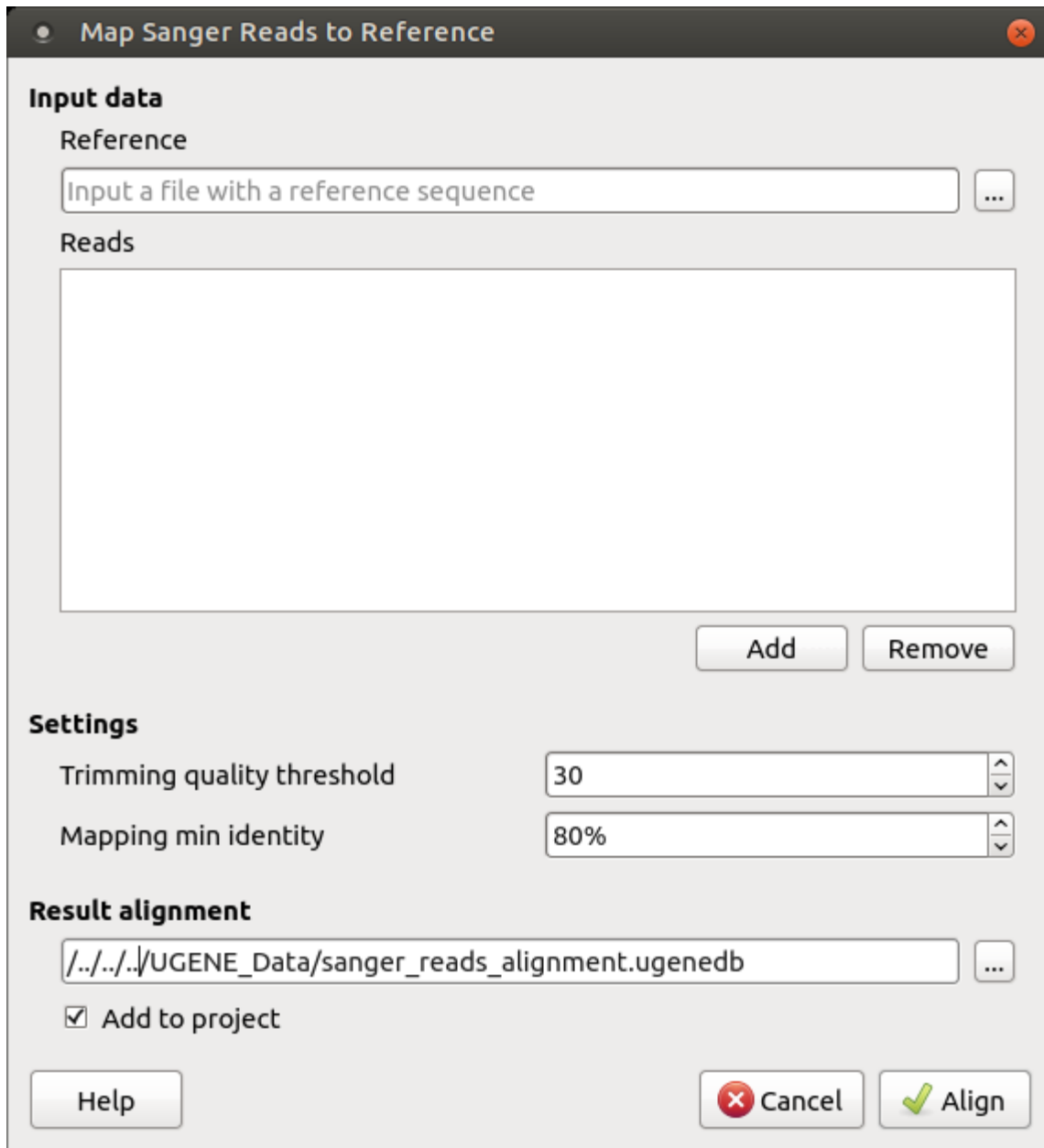


# Mapping Reads to Reference

To map sequence to reference use the *Tools*→ *Sanger data analysis*→ *Map reads to reference* main menu item. The following dialog will appear:



The dialog box is titled "Map Sanger Reads to Reference". It contains several sections: "Input data" with "Reference" and "Reads" subsections; "Settings" with "Trimming quality threshold" and "Mapping min identity" sliders; and "Result alignment" with a file path field and a checkbox. At the bottom are "Help", "Cancel", and "Align" buttons.

**Input data**

**Reference**

Input a file with a reference sequence ...

**Reads**

...

Add Remove

**Settings**

Trimming quality threshold 30

Mapping min identity 80%

**Result alignment**

../../..//UGENE\_Data/sanger\_reads\_alignment.ugenedb ...

☒ Add to project

Help Cancel Align

There are the following parameters:

*Reference sequence* — DNA sequence to align short reads to. This parameter is required.

*Reads* — each added read is a DNA sequence file. At least one read should be added.

You can also configure other parameters.

*Trimming quality threshold* — quality threshold for trimming.

*Mapping min identity* — minimum acceptable read similarity .

Select the required parameters and press the *Align* button.