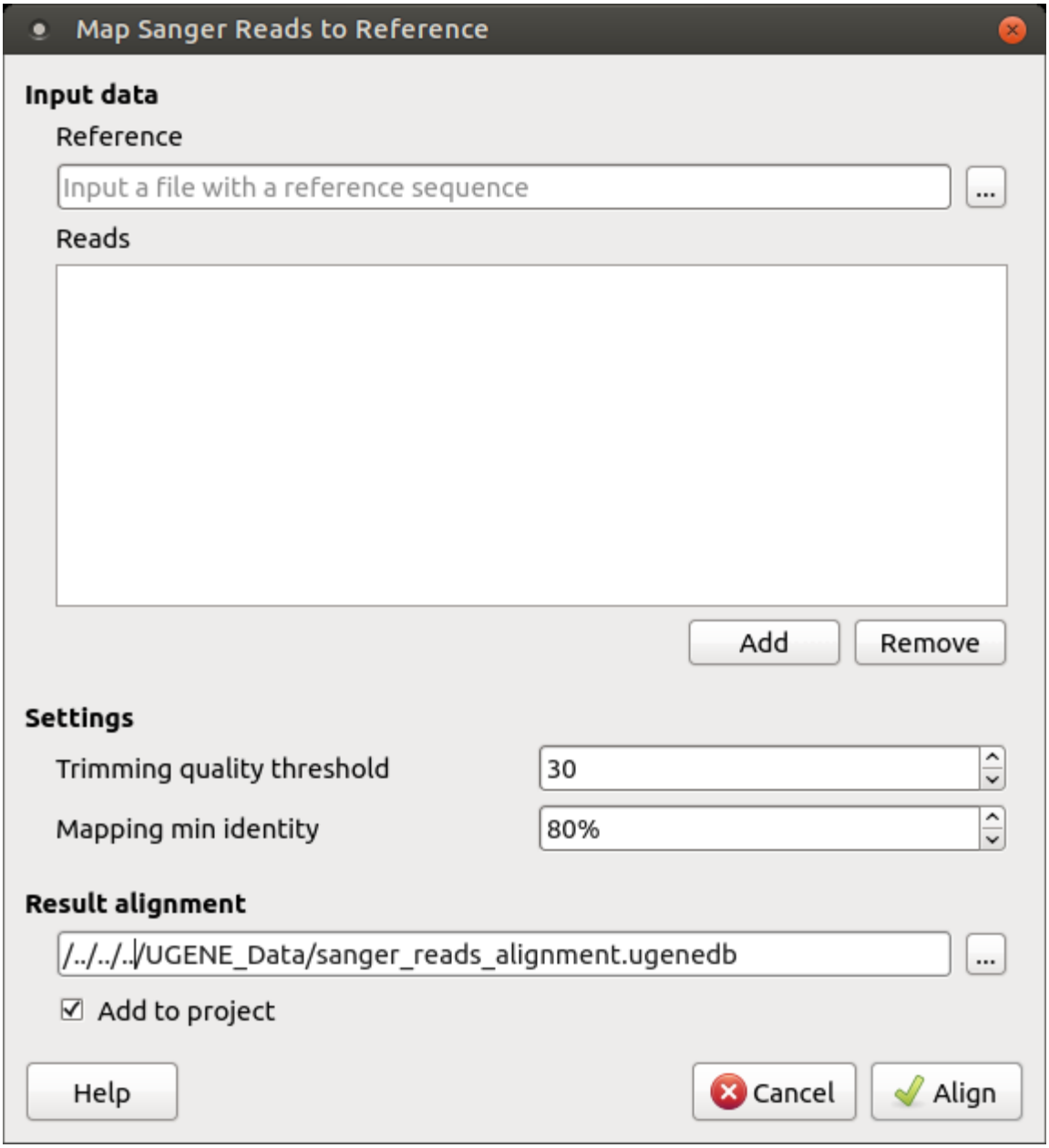
Mapping Reads to Reference

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



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.