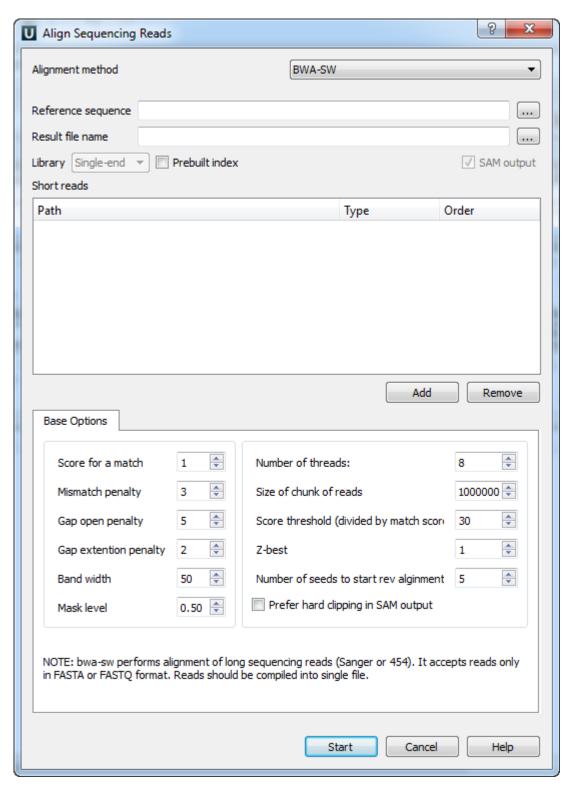# Aligning Short Reads with BWA-SW

When you select the *Tools Align to reference Align short reads* item in the main menu, the *Align Sequencing Reads* dialog appears. Set value of the *Align short reads method* parameter to *BWA-SW*. The dialog looks as follows:

There are the following parameters:

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

    Result file name — file in SAM format to write the result of the alignment into. This parameter is required.

Prebuilt index — check this box to use an index file instead of a source reference sequence. Also you can *build it manually*.

SAM output — always save the output file in the SAM format (the option is disabled for *BWA*).

Short reads — each added short read is a small DNA sequence file. At least one read should be added.

You can also configure other parameters.

Score for a match (-a) — score of a match.

Mismatch penalty (-b) — mismatch penalty.

Gap open penalty (-q) — gap open penalty.

Gap extention penalty (-r) — Gap extension penalty. The penalty for a contiguous gap of size k is q+k*r.

Band width (-w) - Band width in the banded alignment.

Mask level (-c) - Coefficient for threshold adjustment according to query length. Given an l-long query, the threshold for a hit to be retained is a*max{T,c*log(l)}.

Number of threads (-t) - Number of threads in the multi-threading mode.

Size of chunk of reads (-s) - Maximum SA interval size for initiating a seed. Higher -s increases accuracy at the cost of speed.

Score threshold (divided by much score) (-T) - minimum score threshold.

Z-best (-z) - Z-best heuristics. Higher -z increases accuracy at the cost of speed.

Number of seeds to start rev alignment (-N) - Minimum number of seeds supporting the resultant alignment to skip reverse alignment.

Prefer hard clipping in SAM output (-H) - use hard clipping in the SAM output. This option may dramatically reduce the redundancy of output when mapping long contig or BAC sequences.

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