

# Bowtie Aligning Short Reads

When you select the *Tools* > *DNA Assembly* > *Align short reads* item in the main menu, the *Align Short Reads* dialog appears. Set value of the *Align short reads method* parameter to *Bowtie*. The dialog looks as follows:

**U Map NGS Reads to Reference** ? X

Mapping tool: Bowtie

Reference sequence:  ...

Result file name:  ...

Library: Single-end ☒ SAM output

Short reads

Path	Type	Order
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Add Remove

**Parameters**

Mode: -n mode 2

☐ Maq error (--maqerr) 70

☐ Seed length (--seedlen) 28

☐ Maximum of backtracks (--maxbts) 800

☐ Descriptors memory usage (--chunkmbs) 64

☐ Seed (--seed) 0

**Flags**

☐ No Maq rounding (--nomaqround)

☐ No forward orientation (--nofw)

☐ No reverse-complement orientation (--norc)

☐ Try as hard (--tryhard)

☐ Best alignments (--best)

☐ All alignments (--all)

Start Cancel Help

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.

*Library* - single-end or paired-end reads.

*Prebuilt index* — check this box to use an index file instead of a source reference sequence. The index is a set of 6 files with suffixes .1.ebwt, .2.ebwt, .3.ebwt, .4.ebwt, .rev.1.ebwt, and .rev.2.ebwt. The index is created during the alignment. Also you can [build it manually](#).

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

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



Short reads length for *Bowtie* can't be more than 1024.

You can also configure other parameters. They are the same as in the original *Bowtie* (you can read detailed description of the parameters on the [Bowtie manual page](#)).

Select one of the following alignment modes:

The *-n* alignment mode:

When the *-n mode* is selected, *Bowtie* determines which alignments are valid according to the following policy. Alignments may have no more than N mismatches (where N is a number 0-3) in the first L bases (where L is a number 5 or greater, set with *Seed length*) on the high-quality (left) end of the read. The sum of the Phred quality values at all mismatched positions (not just in the seed) may not exceed E (set with *Maq error*). Where qualities are unavailable (e.g. if the reads are from a FASTA file), the Phred quality defaults to 40.

The *-v* alignment mode:

In *-v mode*, alignments may have no more than V mismatches, where V may be a number from 0 through 3. Quality values are ignored. The *-v mode* is mutually exclusive with the *-n mode*.

The following parameters are available:

*Maq error* (*-maqerr*) — maximum permitted total of quality values at all mismatched read positions throughout the entire alignment, not just in the “seed”. The default is 70. By default, *Bowtie* rounds quality values to the nearest 10 and saturates at 30. Note that the rounding can be disabled with *No Maq rounding*.

*Seed Length* (*-seedlen*) — the number of bases on the high-quality end of the read to which the *-n* applies. The lowest permitted setting is 5 and the default is 28.

*Maximum of backtracks* (*-maxbts*) — the maximum number of backtracks (default: 125 without *Best*, 800 with *Best*). A “backtrack” is the introduction of a speculative substitution into the alignment.

*Descriptors memory usage* (*-chunkmbs*) — the number of megabytes of memory a given thread is given to store path descriptors in the *Best* flag. Default: 64. This parameter is available if the *Best* flag is checked.

*Seed* (*-seed*) — pseudo-random number generator.

The following flags are available:

*No Maq rounding* (*-nomaground*) — Maq (Mapping and Assembly with Quality) accepts quality values in the Phred quality scale, but internally rounds values to the nearest 10, with a maximum of 30. By default, *Bowtie* also rounds this way. *No Maq rounding* prevents this rounding in *Bowtie*.

*No forward orientation* (*-nofw*) — do not attempt to align against the forward reference strand.

*No reverse-complement orientation* (*-norc*) — do not attempt to align against the reverse-complement reference strand.

*Try as hard* (*-tryhard*) — try as hard as possible to find valid alignments when they exist, including paired-end alignments.

*Best alignments* (*-best*) — make *Bowtie* guarantee that reported singleton alignments are “best” in terms of stratum (i.e. number of mismatches, or mismatches in the seed for the case of *-n mode*) and in terms of the quality values at the mismatched position(s).

*All alignments* (*-all*) — report all valid alignments per read or pair. Validity of alignments is determined by the alignment policy (combined effects of *-n mode*, *-v mode*, *Seed length*, and *Maq error*).

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