## Map RNA-Seq Reads with TopHat Element

TopHat is a program for mapping RNA-Seq reads to a long reference sequence. It uses Bowtie or Bowtie2 to map the reads and then analyzes the mapping results to identify splice junctions between exons.

Provide URL(s) to FASTA or FASTQ file(s) with NGS RNA-Seq reads to the input port of the element, set up the reference sequence in the parameters. The result is saved to the specified BAM file, URL to the file is passed to the output port. Several UCSC BED tracks are also produced: junctions, insertions, and deletions.

Element type: tophat

## **Parameters**

Parameter	Description	Default value	Parameter in Workflow File	Туре
Reference input type	Select "Sequence" to input a reference genome as a sequence file.  Note that any sequence file format, supported by UGENE, is allowed (FASTA, GenBank, etc.).  The index will be generated automatically in this case.  Select "Index" to input already generated index files, specific for the tool.	Index	reference- input-type	string
Bowtie index folder	The folder with the Bowtie index for the reference sequence.		bowtie-index- dir	string
Bowtie index basename	The basename of the Bowtie index for the reference sequence.		bowtie-index- basename	string
Output folder	The base name of the output folder. It could be modified with a suffix.		out-dir	
Mate inner distance	The expected (mean) inner distance between mate pairs.	50	mate-inner- distance	numeric
Mate standard deviation	The standard deviation for the distribution on inner distances between mate pairs.	20	mate- standard- deviation	numerio
Library type	Specifies RNA-Seq protocol.	fr- unstranded	library-type	numeric
No novel junctions	Only look for reads across junctions indicated in the supplied GFF or junctions file. This parameter is ignored if R aw junctions or Known transcript file is not set.	False	no-novel- junctions	boolean
Raw junctions	The list of raw junctions.		raw- junctions	string
Known transcript file	A set of gene model annotations and/or known transcripts.		known- transcript	string
Max multihits	Instructs TopHat to allow up to this many alignments to the reference for a given read, and suppresses all alignments for reads with more than this many alignments.	20	max- multihits	numerio
Segment length	Each read is cut up into segments, each at least this long. These segments are mapped independently.	25	segment- length	numerio
Fusion search	Turn on fusion mapping.	False	fusion- search	boolean
Transcripto me only	Only align the reads to the transcriptome and report only those mappings as genomic mappings.	False	transcriptom e-only	boolean
Transcripto me max hits	Maximum number of mappings allowed for a read, when aligned to the transcriptome (any reads found with more than this number of mappings will be discarded).	60	transcriptom e-max-hits	numerio
Prefilter multihits	When mapping reads on the transcriptome, some repetitive or low complexity reads that would be discarded in the context of the genome may appear to align to the transcript sequences and thus may end up reported as mapped to those genes only. This option directs TopHat to first align the reads to the whole genome in order to determine and exclude such multi-mapped reads (according to the value of the Max multihits option).	False	prefilter- multihits	boolean
Min anchor length	The anchor length. TopHat will report junctions spanned by reads with at least this many bases on each side of the junction. Note that individual spliced alignments may span a junction with fewer than this many bases on one side. However, every junction involved in spliced alignments is supported by at least one read with this many bases on each side.	8	min-anchor- length	numerio
Splice mismatches	The maximum number of mismatches that may appear in the anchor region of a spliced alignment.	0	splice- mismatches	numeric
Read mismatches	Final read alignments having more than these many mismatches are discarded.	2	read- mismatches	numeric

Segment mismatches	Read segments are mapped independently, allowing up to this many mismatches in each segment alignment.	2	segment- mismatches	numeric
Solexa 1.3 quals	As of the Illumina GA pipeline version 1.3, quality scores are encoded in Phred-scaled base-64. Use this option for FASTQ files from pipeline 1.3 or later.	False	solexa-1-3- quals	boolean
Bowtie version	Specifies which Bowtie version should be used.	Bowtie2	bowtie- version	numeric
Bowtie -n mode	TopHat uses -v in Bowtie for initial read mapping (the default), but with this option, -n is used instead. Read segments are always mapped using -v option.	Use -v mode	bowtie-n- mode	numeric
Bowtie tool path	The path to the Bowtie external tool.	default	bowtie-tool- path	string
SAMtools tool path	The path to the SAMtools tool. Note that the tool is available in the UGENE External Tool Package.	default	samtools- tool-path	string
TopHat tool path	The path to the TopHat external tool in UGENE.	default	path	string
Temporary folder	The directory for temporary files.	default	temp-dir	string
Samples map	The map which divides all input datasets into samples. Every sample has the unique name.			

## Input/Output Ports The element has 1 input port.

Name in GUI: Input reads

Name in Workflow File: in-assembly

Slots:

Slot In GUI	Slot in Workflow File	Туре
Dataset name	dataset	string
Input reads	first.in	assembly
Input reads url	in-url	string
Input paired reads url	paired-url	string
Input paired reads	second.in	assembly

And 1 output port.

Name in GUI: TopHat output

Name in Workflow File: out-assembly

Slots:

Slot In GUI	Slot in Workflow File	Туре
Accepted hits	accepted.hits	assembl y
Accepted hits url	hits-url	string