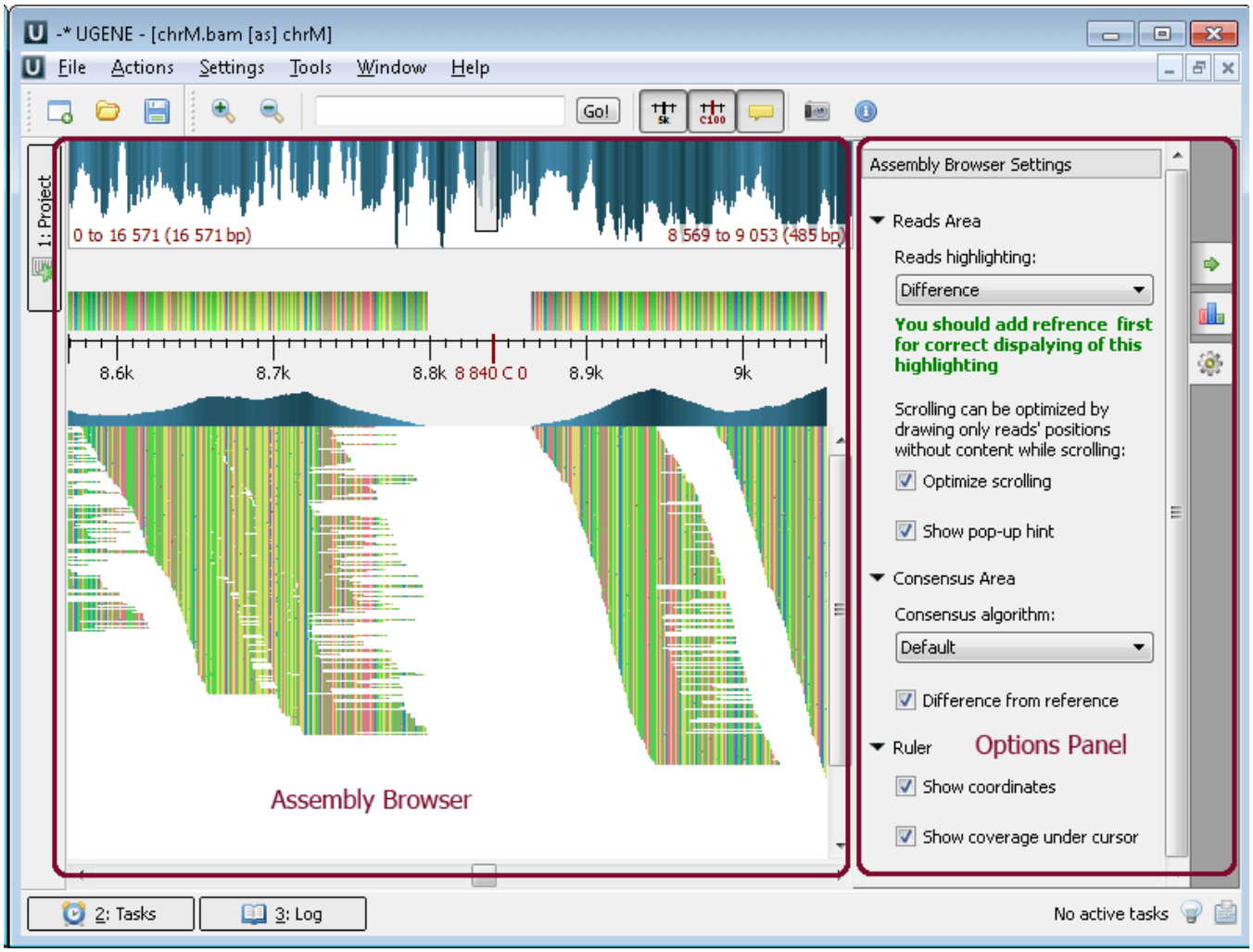
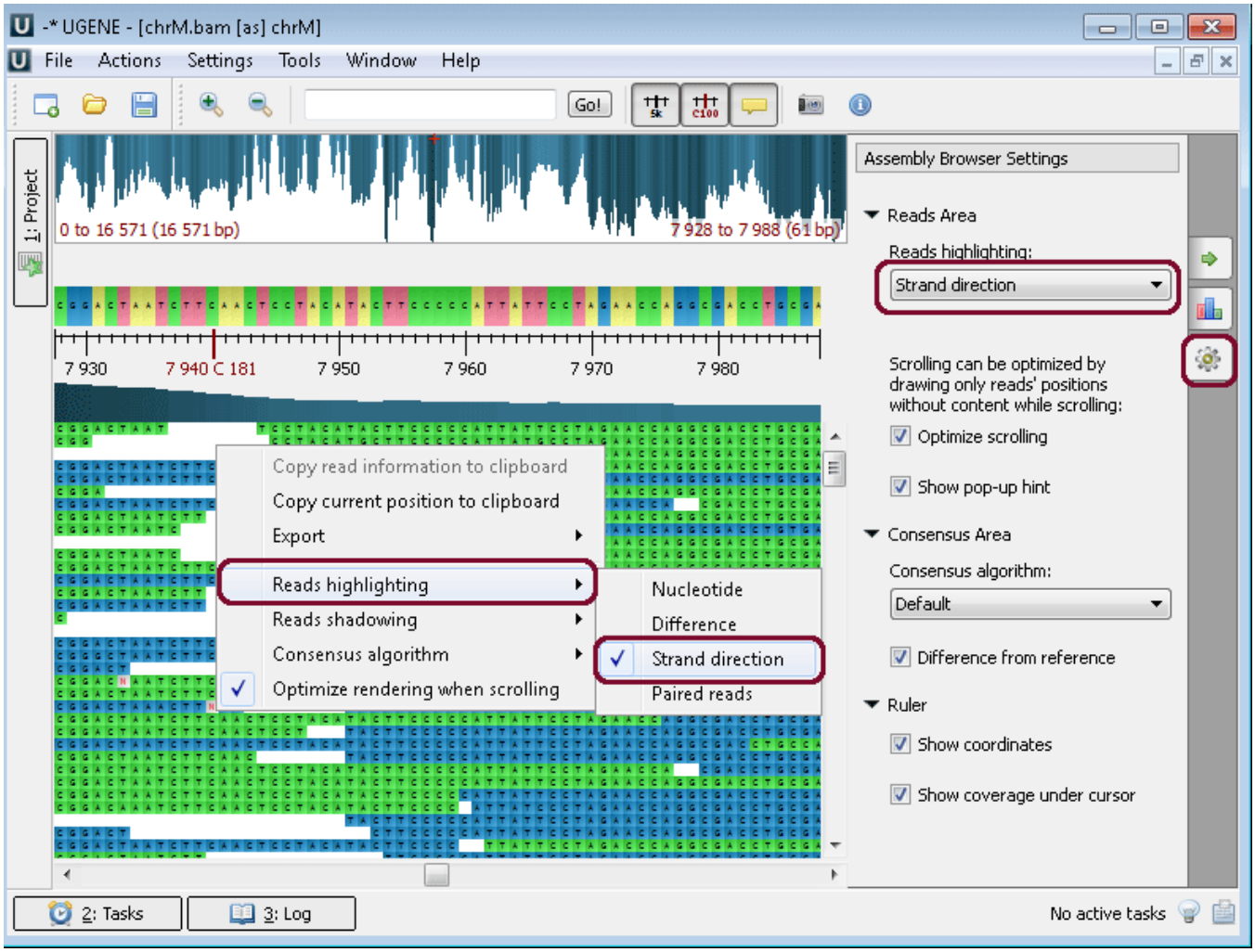
View, align and assemble short reads

SAM/BAM files (*Assembly Browser*). *Assembly Browser* is used to visualize and efficiently browse large next generation sequence assemblies. Currently supported formats are SAM (Sequence Alignment/Map) and BAM, which is a binary version of the SAM format. Both formats are produced by SAMtools and described in the following specication: SAMtools. To activate the *Alignment Editor* open any assembly le. For example you can use the $*ugene/data/samples/Assembly/chrM.bam* le provided with UGENE. After opening the le in UGENE the *Assembly Browser* window appears:



Using the *Assembly Browser* you can: browsing and zooming assembly, getting information about reads, short reads vizualization, associating reference sequence, consensus sequence, exporting.

Example 3: Highlighting the strand of reads. You can do this using the context menu or the Options Panel.


-* UGENE - [chrM.bam [as] chrM]
File
Actions
Settings
Tools
Window
Help
Go!
1: Project
0 to 16 571 (16 571 bp)
7 928 to 7 988 (61 bp)
7 930
7 940 C 181
7 950
7 960
7 970
7 980
Copy read information to clipboard
Copy current position to clipboard
Export
Reads highlighting
Reads shadowing
Consensus algorithm
Optimize rendering when scrolling
Nucleotide
Difference
Strand direction
Paired reads
Assembly Browser Settings
Reads Area
Reads highlighting:
Strand direction
Scrolling can be optimized by drawing only reads' positions without content while scrolling:
Optimize scrolling
Show pop-up hint
Consensus Area
Consensus algorithm:
Default
Difference from reference
Ruler
Show coordinates
Show coverage under cursor
2: Tasks
3: Log
No active tasks