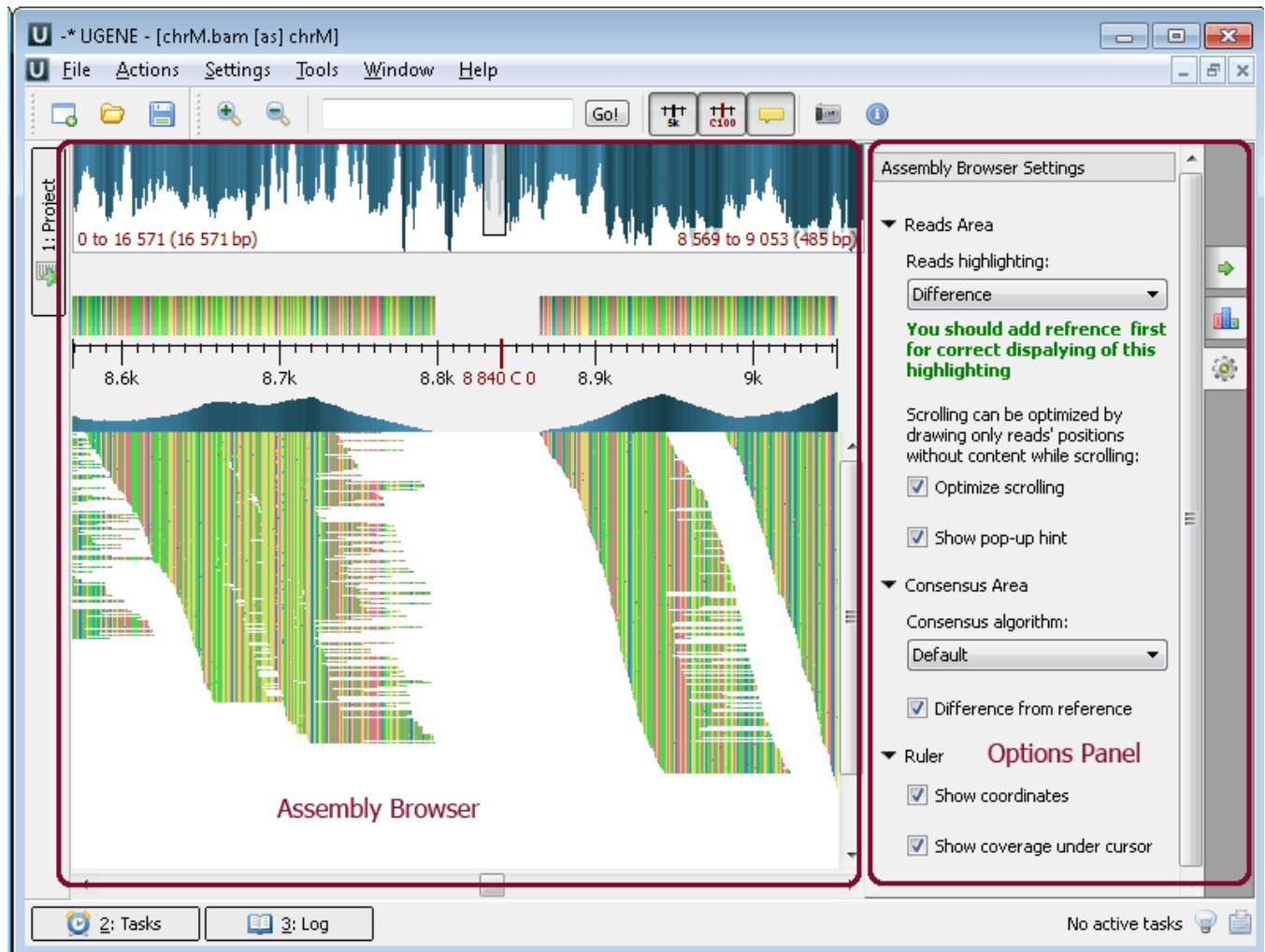


View, align and assemble short reads

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 specification: SAMtools. To activate the *Alignment Editor* open any assembly file. For example you can use the `$ugene/data/samples/Assembly/chrM.bam` file provided with UGENE. After opening the file in UGENE the *Assembly Browser* window appears:



Using the *Assembly Browser* you can: browsing and zooming assembly, getting information about reads, short reads visualization, 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.

U -* UGENE - [chrM.bam [as] chrM]

U File Actions Settings Tools Window Help

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