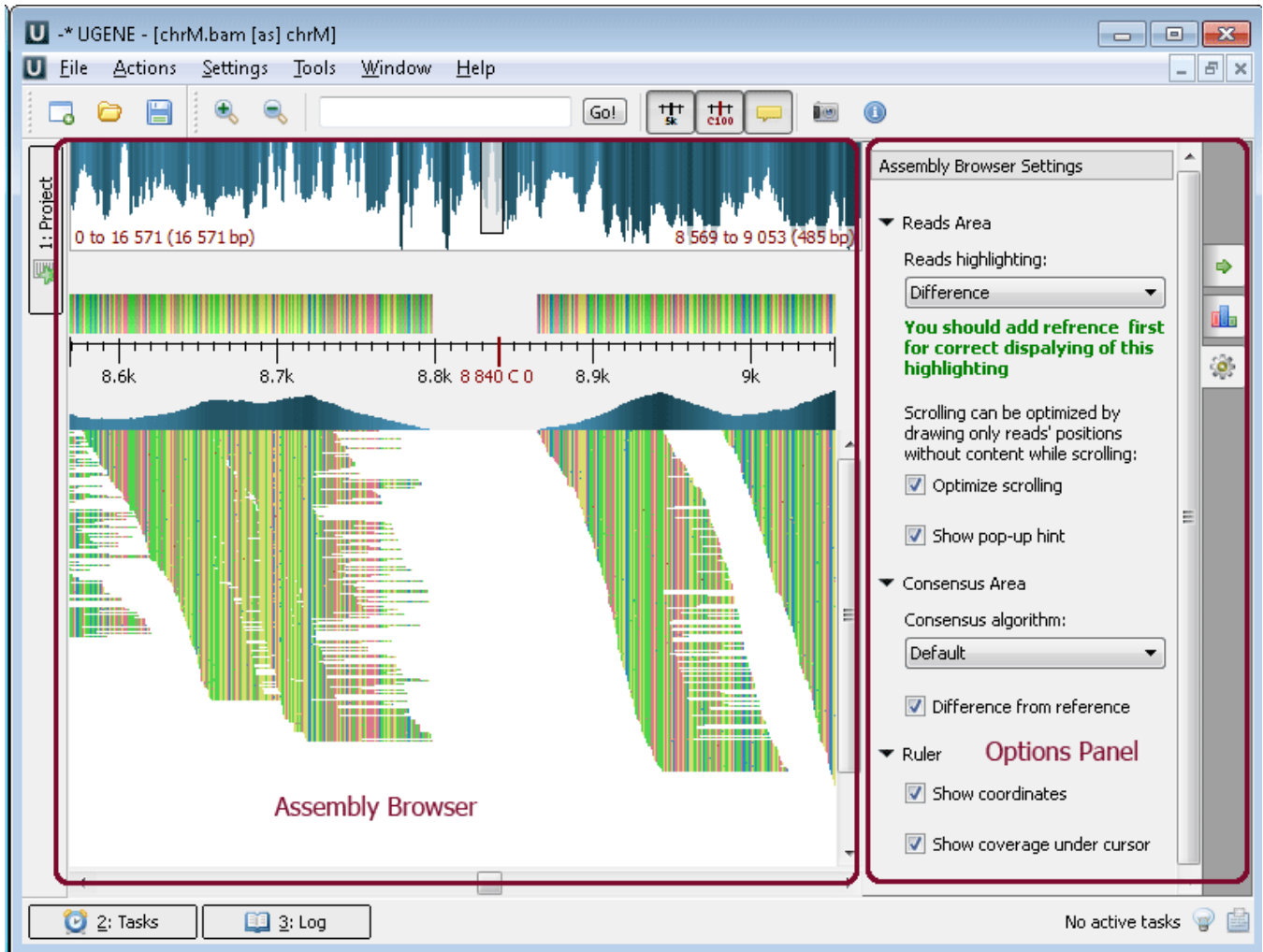


# View, align and assemble short reads

**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)

CGGACTAATCTTCCTCAACTCCTACATACTTCCCCCATTATTCCTAGAACCCAGGCCGACCTGCCG

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