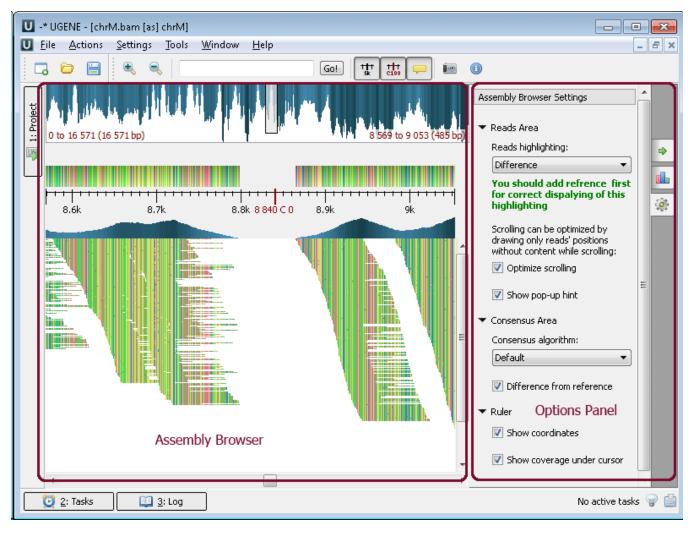
## View, align and assemble short reads

**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.

