

Sanger Reads Editor Components

Here is the default layout of the editor:

The screenshot displays the UGENE Sanger Reads Editor interface. At the top, the menu bar includes File, Actions, Settings, Tools, Window, and Help. Below the menu is the Editor Toolbar. The main workspace is titled "reference_sanger_reads_alignment_8 [mc] Aligned reads" and "Consensus Area".

The workspace shows a reference sequence (KM099231) and a consensus sequence. The reference sequence is: G C T T G T G C C G G C C C A T C A C T T T C A C G A G C T. The consensus sequence is: G C T T G T G C C N S C C C A T C A C T T T C A C G A G C T. The N and S characters indicate mismatches. Below the sequences, a chromatogram area shows the signal for each base. The chromatogram area is labeled "Chromatogram Area".

On the right side, there is an Options Panel for the Consensus. It includes a "Consensus mode" section with a "Consensus type" dropdown set to "Simple extended" and a "Threshold" slider set to 100%. Below this is an "Export consensus" section with an "Export to file" button, a file name field "Aligned reads_consensus_3.txt", a "File format" dropdown set to "Plain text", a "Keep gaps" checkbox, and an "Export" button.

At the bottom of the workspace, there is an "Overview" section showing a genomic map with a scale from 0 to 11k 878. The map shows several reads aligned to the reference sequence. The "Overview" section is labeled "Overview".

The status bar at the bottom shows "2: Tasks", "3: Log", and "No active tasks".