

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 divided into several sections:

- Project Panel:** Located on the left, it shows a list of reads: SZYD_Cas9_CR53, SZYD_Cas9_CR54, SZYD_Cas9_CR55, and SZYD_Cas9_CR56, each with a green arrow pointing to its alignment.
- Reference and Consensus:** At the top of the main workspace, the reference sequence is shown as 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. Below it, 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' are highlighted in pink and red, respectively.
- Chromatogram Area:** This section shows two chromatograms. The top one is for read SZYD_Cas9_CR53, and the bottom one is for SZYD_Cas9_CR54. The chromatograms show peaks for each base, with a prominent peak for 'C' at position 4025 in the second read.
- Options Panel:** Located on the right, it contains settings for the consensus area, such as Consensus mode (Simple extended), Consensus type (Simple extended), and Threshold (100%). It also includes an Export consensus section with options for Export to file (Aligned reads_consensus_3.txt), File format (Plain text), and a checkbox for Keep gaps. An Export button is at the bottom of this panel.
- Overview:** At the bottom of the main workspace, an overview track shows the alignment of reads across a genomic region from 0 to 11k11878. Green arrows represent reads SZYD_Cas9_CR53, CR54, and CR55, while blue arrows represent SZYD_Cas9_CR56.

The interface also includes a status bar at the bottom with task and log windows, and a Help button in the bottom right corner.