

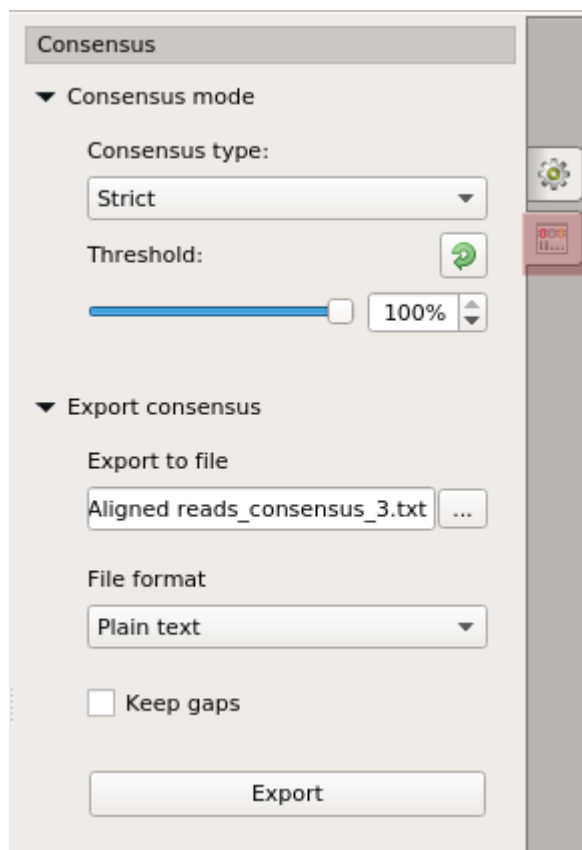
Sanger Reads Consensus

Each base of a consensus sequence is calculated as a function of the corresponding column bases. The *Sanger Reads Editor* allows switching between different consensus modes: Simple extended and Strict.

The Simple extended algorithm selects the best character from the extended DNA alphabet. Only bases with frequencies which are greater than a threshold value are taken into account.

The Strict algorithm returns gap character ('-') if symbol frequency in a column is lower than threshold specified.

To switch the consensus mode go to the *Consensus* tab of the *Options Panel*:



The screenshot shows the 'Consensus' tab of the 'Options Panel' in the Sanger Reads Editor. The panel is divided into two main sections: 'Consensus mode' and 'Export consensus'. In the 'Consensus mode' section, the 'Consensus type' is set to 'Strict' via a dropdown menu. Below it, the 'Threshold' is set to 100%, indicated by a slider and a text box. In the 'Export consensus' section, the 'Export to file' option is selected, with the filename 'Aligned reads_consensus_3.txt' and a file selection button. The 'File format' is set to 'Plain text' via a dropdown menu. There is an unchecked checkbox for 'Keep gaps'. At the bottom of the panel is an 'Export' button. On the right side of the panel, there are two icons: a gear icon for settings and a red button with a white 'X' icon.

- [Export Chromatogram Consensus](#)