

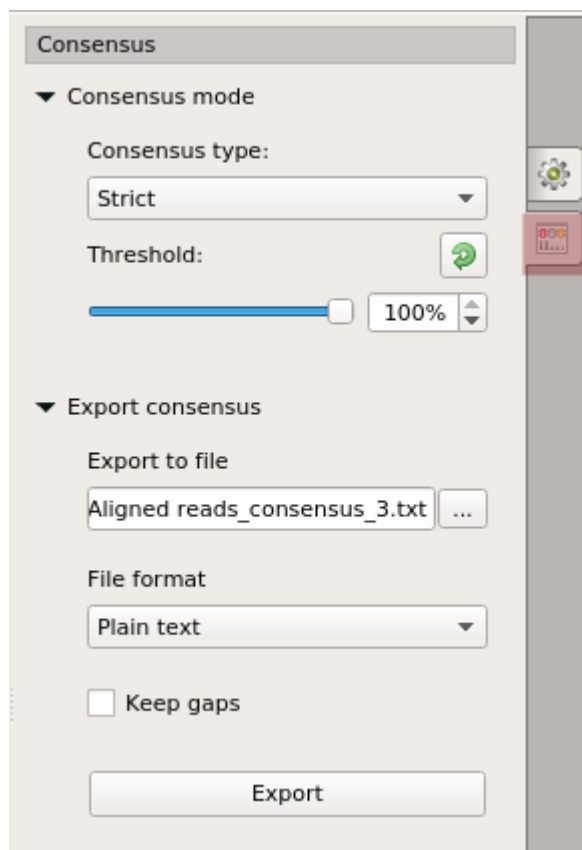
Sanger Reads Consensus

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 image shows a software interface for the 'Consensus' tab. It features a 'Consensus mode' section with a 'Consensus type' dropdown set to 'Strict' and a 'Threshold' slider set to 100%. Below this is an 'Export consensus' section with an 'Export to file' text box containing 'Aligned reads_consensus_3.txt', a 'File format' dropdown set to 'Plain text', and a 'Keep gaps' checkbox. An 'Export' button is at the bottom. On the right side of the panel, there are two icons: a gear icon and a red icon with a white 'X'.

Consensus

▼ Consensus mode

Consensus type:

Strict

Threshold:

100%

▼ Export consensus

Export to file

Aligned reads_consensus_3.txt ...

File format

Plain text

☐ Keep gaps

Export

- [Export Chromatogram Consensus](#)