

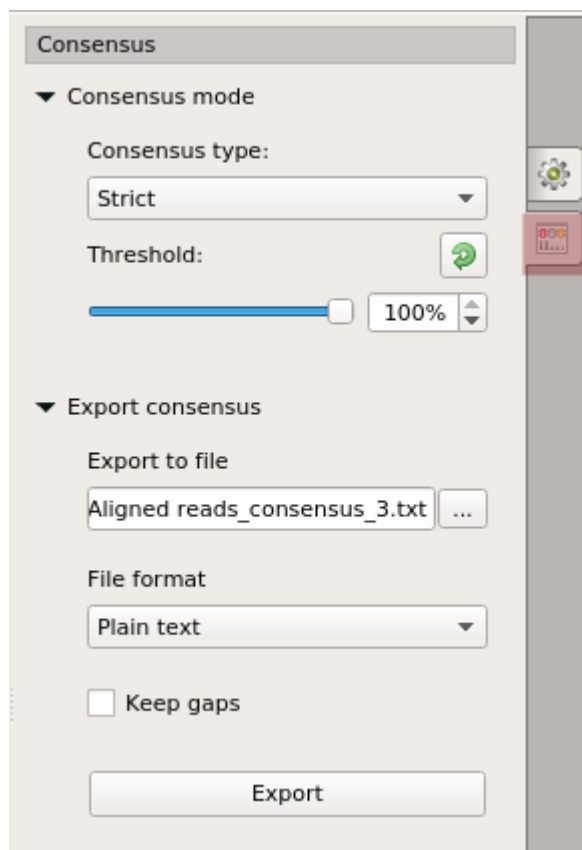
# Sanger Reads Consensus

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 has a light beige background and a grey sidebar on the right. The 'Consensus mode' section is expanded, showing 'Consensus type:' with a dropdown menu set to 'Strict'. Below it, 'Threshold:' is set to 100% with a slider and a refresh button. The 'Export consensus' section is also expanded, showing 'Export to file' with a text box containing 'Aligned reads\_consensus\_3.txt' and a file selection button. Below that, 'File format' is set to 'Plain text' with a dropdown menu. There is an unchecked checkbox for 'Keep gaps' and an 'Export' button at the bottom.

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](#)