

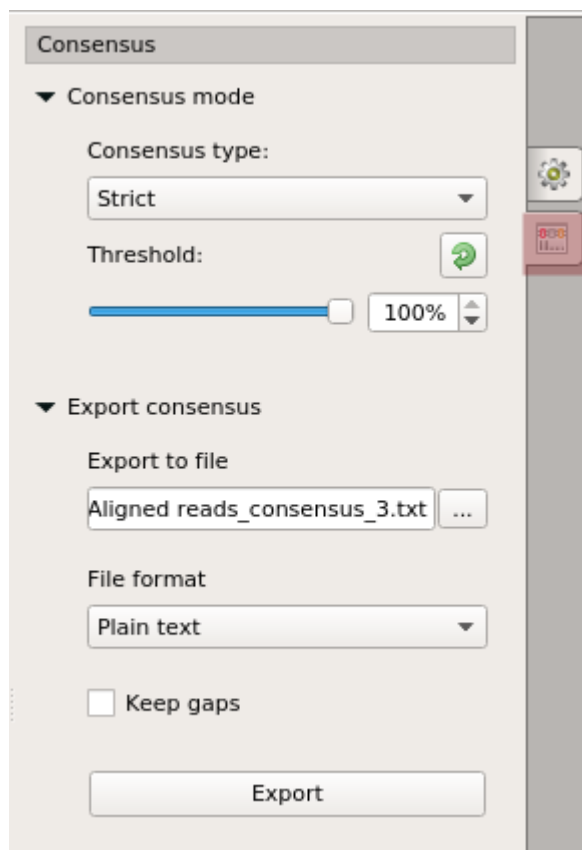
# Sanger Reads Consensus

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 shown with a slider bar and a numeric input field set to '100%'. The 'Export consensus' section is also expanded, showing 'Export to file' with a text field containing 'Aligned reads\_consensus\_3.txt' and a file selection button. Below that, 'File format' is set to 'Plain text' in a dropdown menu. There is an unchecked checkbox for 'Keep gaps'. At the bottom is a large 'Export' button. The sidebar on the right contains a gear icon and a red button with a white icon.

- [Export Chromatogram Consensus](#)