

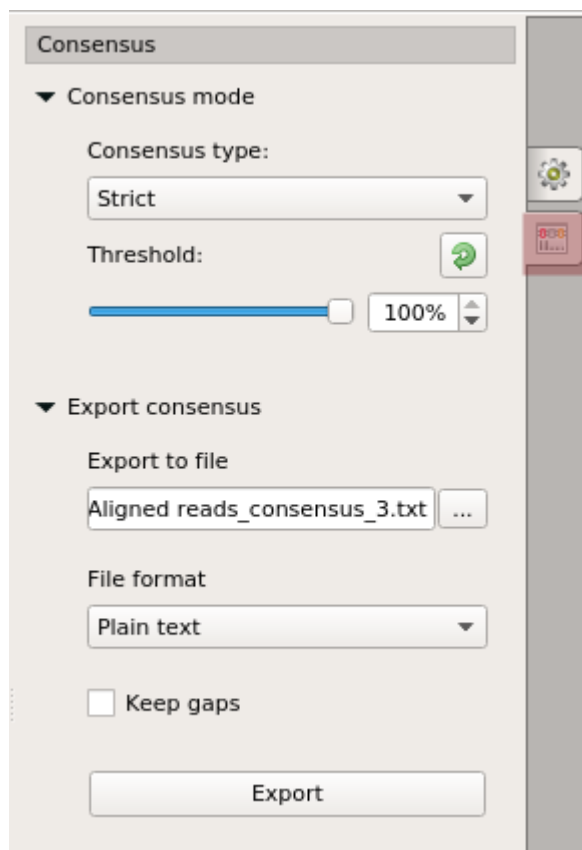
# Sanger Reads Consensus

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 titled "Consensus" with the following settings:

- Consensus mode**
  - Consensus type: Strict (dropdown menu)
  - Threshold: 100% (slider and input field)
- Export consensus**
  - Export to file: Aligned reads\_consensus\_3.txt (text input with browse button)
  - File format: Plain text (dropdown menu)
  - Keep gaps
  - Export button

- [Export Chromatogram Consensus](#)