

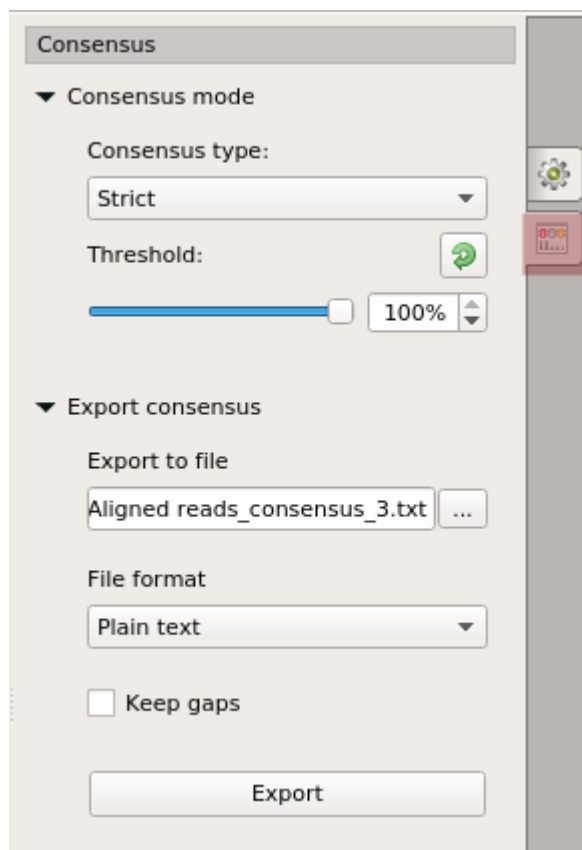
# Sanger Reads Consensus

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 two main sections: "Consensus mode" and "Export consensus".

- Consensus mode:**
  - Consensus type:** A dropdown menu currently set to "Strict".
  - Threshold:** A slider control set to 100%, with a green circular refresh icon to its right.
- Export consensus:**
  - Export to file:** A text field containing "Aligned reads\_consensus\_3.txt" and a file selection button "...".
  - File format:** A dropdown menu currently set to "Plain text".
  - Keep gaps:** An unchecked checkbox.
  - Export:** A large button at the bottom of the section.

On the right side of the panel, there are two icons: a gear icon (settings) and a red button with a white icon (likely a save or apply button).

- [Export Chromatogram Consensus](#)