

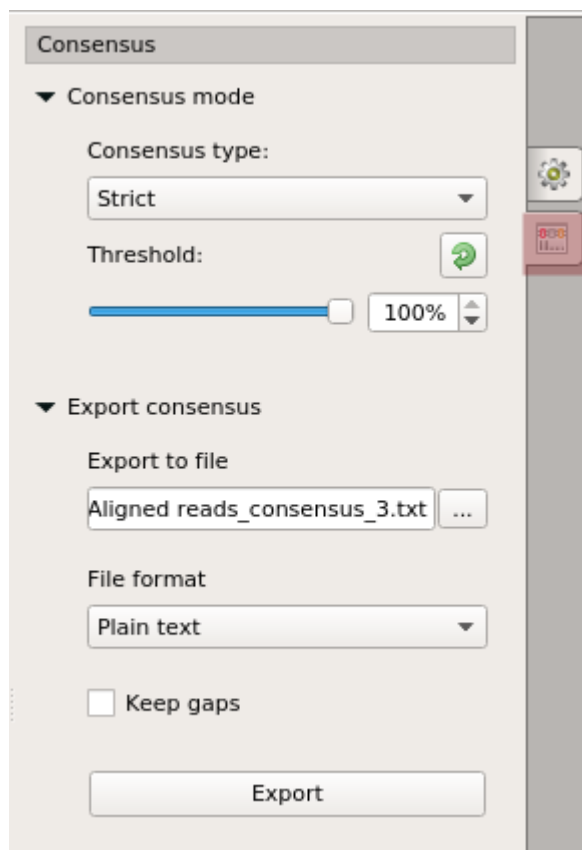
# Sanger Reads Consensus

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 window titled "Consensus". It contains two main sections: "Consensus mode" and "Export consensus".

**Consensus mode section:**

- Consensus type:** A dropdown menu currently set to "Strict".
- Threshold:** A slider control with a blue bar and a white knob, currently positioned at 100%. To the right of the slider is a "100%" label and a small up/down arrow button.

**Export consensus section:**

- Export to file:** A text input field containing "Aligned reads\_consensus\_3.txt" followed by a three-dot menu 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 window, there is a vertical toolbar with two icons: a gear icon (settings) and a red button with a white icon (likely a save or apply button).

- [Export Chromatogram Consensus](#)