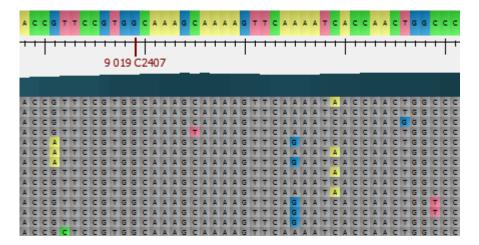
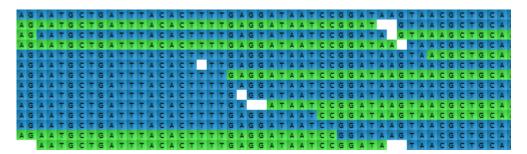
## **Reads Highlighting**

To apply a reads highlighting mode, select it in the Reads highlighting menu of the Reads Area context menu or on the Assembly Browser Settings tab of the Options Panel. The following modes are available:

- Nucleotide shows all nucleotides in different colors. It is used by default.
- Difference highlights gaps and nucleotides that differ from the reference sequence. You should add a reference first for correct displaying of this highlighting.



• Strand direction — highlights reads located on the direct strand in blue and reads on the complement strand in green.



· Paired reads — highlights all paired reads in green. Note that the information about the pair is shown in the hint.

