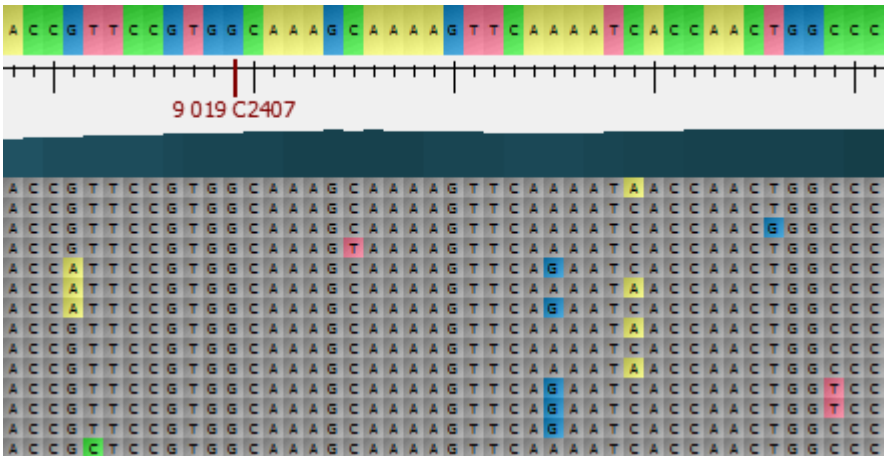
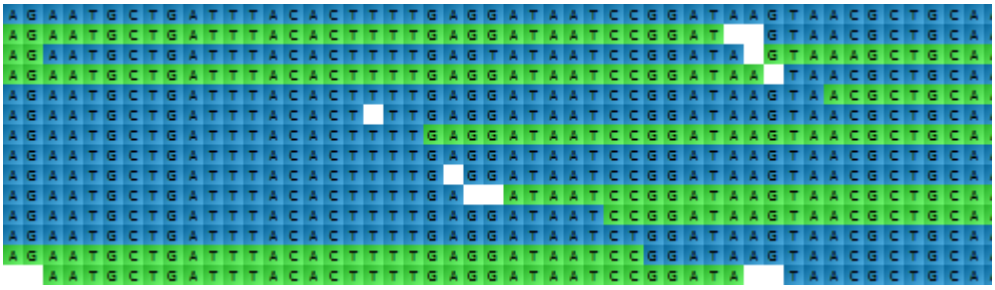
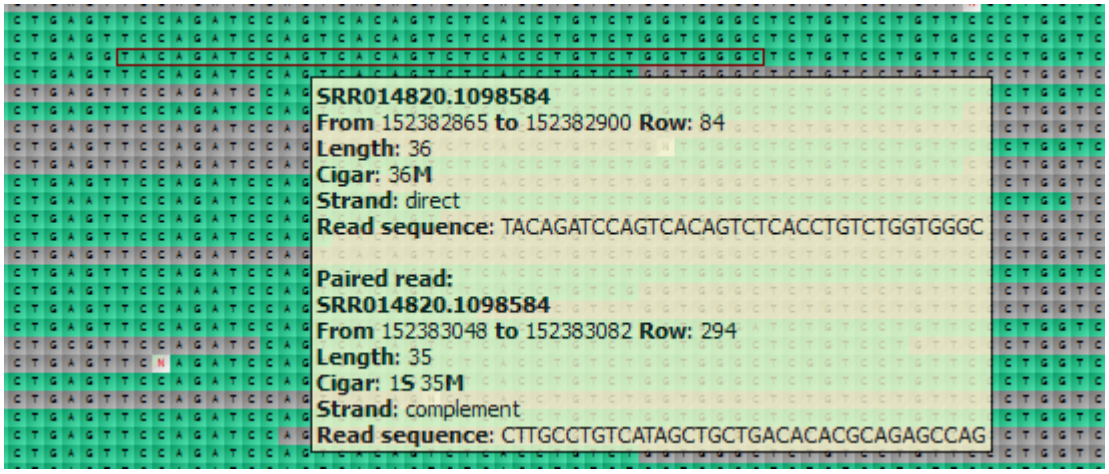
Reads Highlighting

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.