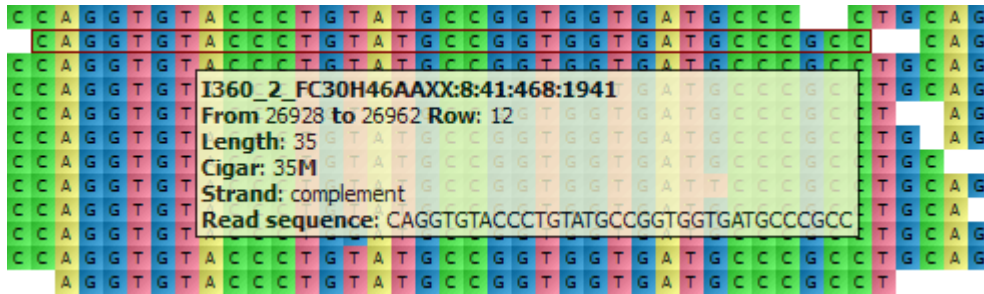


# Getting Information About Read

A read displayed in the *Reads Area* consists of the bases (A, C, G, T). It may also contain the N character that stays for an ambiguous base. Depending on the value of the *Cigar* parameter, the read can be shown partially or gaps can be inserted inside the read (see below).

By default when a read is hovered over in the *Reads Area* a hint appears:



To disable this behaviour click the following button on the toolbar:



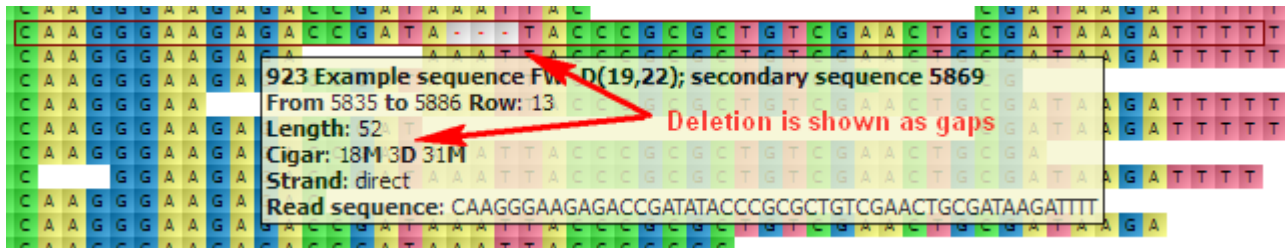
Or uncheck the *Show pop-up hint* check box on the *Assembly Browser Settings* tab of the *Options Panel*.

The hint shows the following information about the read:

- Read name
- Location
- Length
- Cigar
- Strand
- Read sequence

The operations in the *Cigar* parameter are described as follows:

- **M** — Alignment match (can be a sequence match or mismatch).
- **I** — Insertion to the reference. Skipped when the read is aligned to the reference, i.e. it is not shown in the Reads Area, but is present in the read sequence.
- **D** — Deletion from the reference. Gaps are inserted to the read when the read is aligned to the reference. For example:



- **N** — Skipped region from the reference. Behaves as **D**, but has a different biological meaning: for mRNA-to-genome alignment it represents an intron.
- **S** — Soft clipping (clipped sequences are present in the read sequence, i.e. behaves as **I**).
- **H** — Hard clipping (clipped sequences are not present in the read sequence).
- **P** — Padding (silent deletion from padded reference).
- **=** — Exact match to the reference.
- **x** — Reference sequence mismatch.

To copy the information about the read to the clipboard, select the *Copy read information to clipboard* item in the Reads Area context menu. Now you can paste it in any text editor.

To copy the current position of the read select the *Copy current position to clipboard* item in the Reads Area context menu.