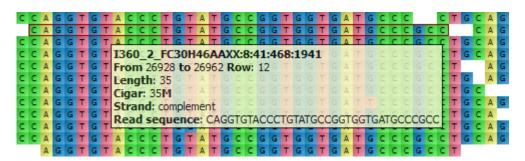
Getting Information About Read

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 ambigous 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:



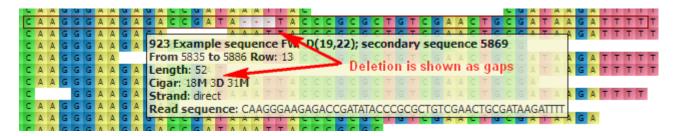
Or uncheck the Show pop-up hint check box on the Assembly Browser Settings tab of the Options Panel.

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.