

TEST SAM FILE



Not aligned (should not be loaded but counted as not aligned)

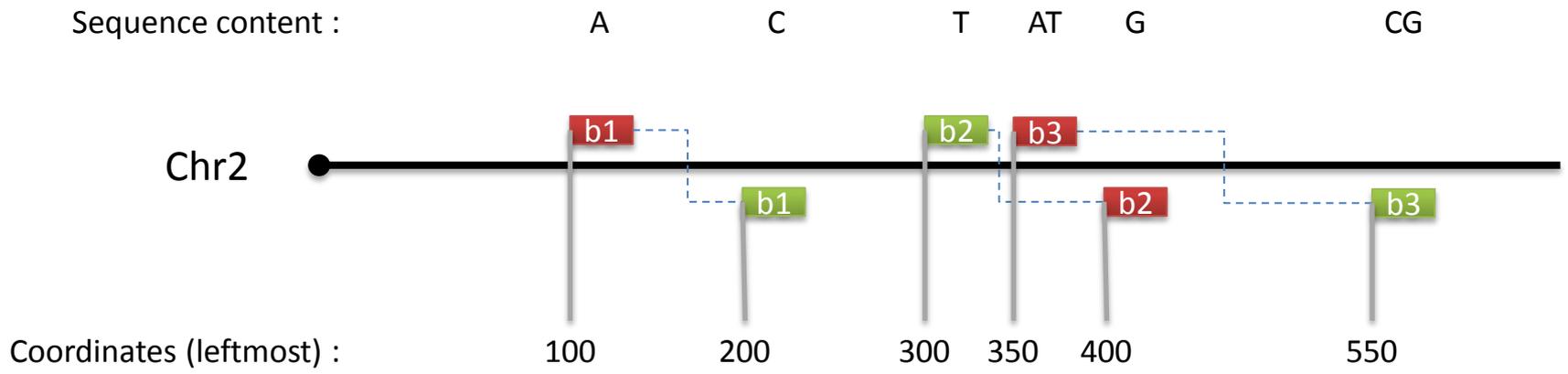


First in pair

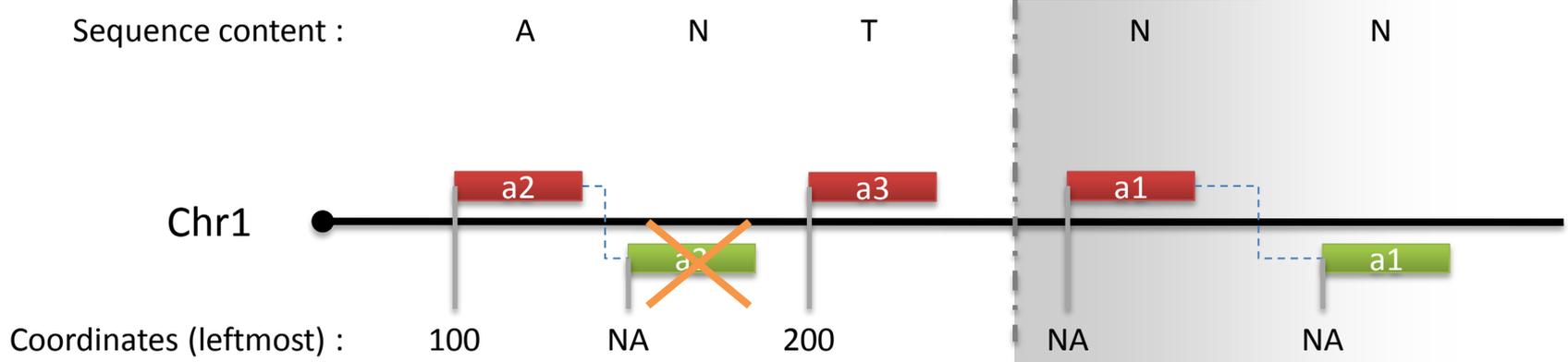


Second in pair

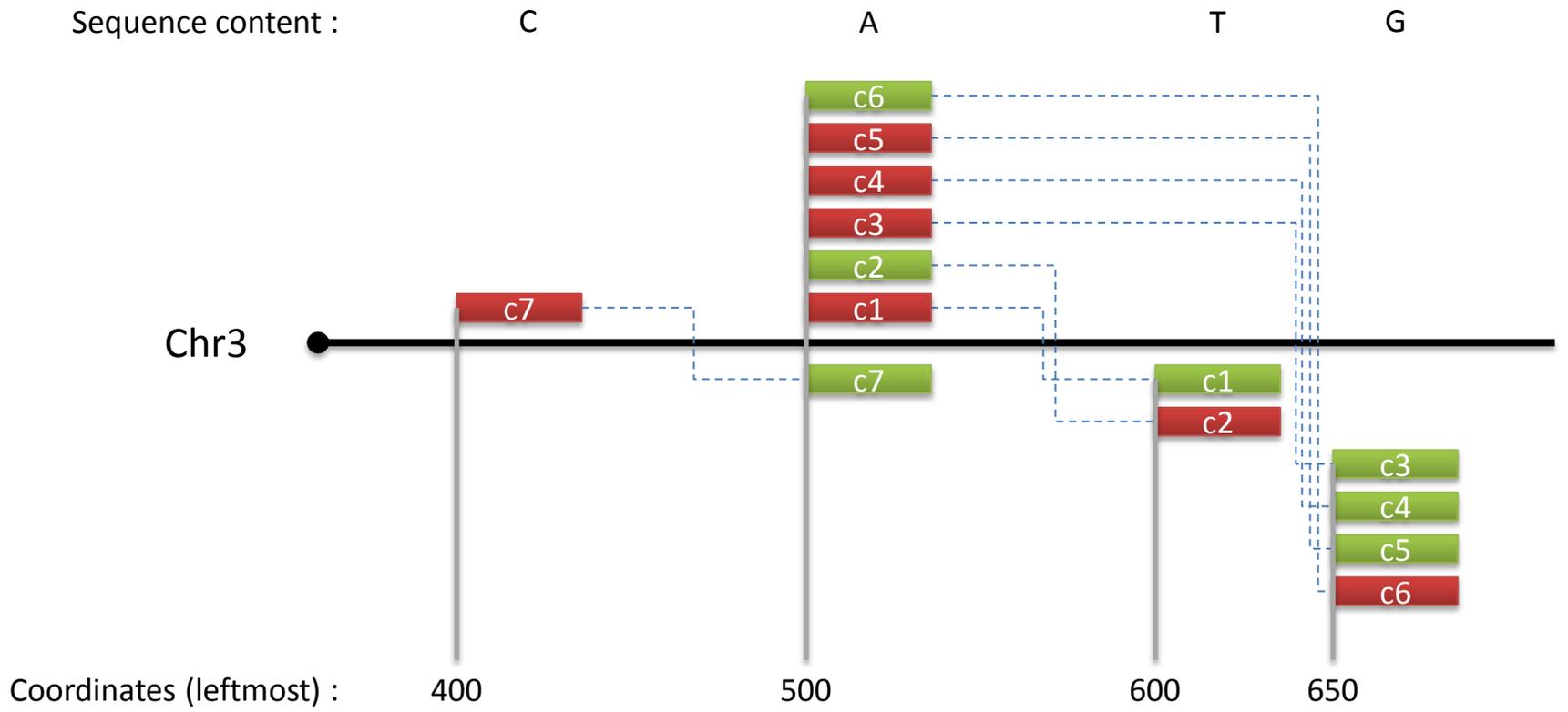
Typical reads for pileup (pairs b1 to b3)



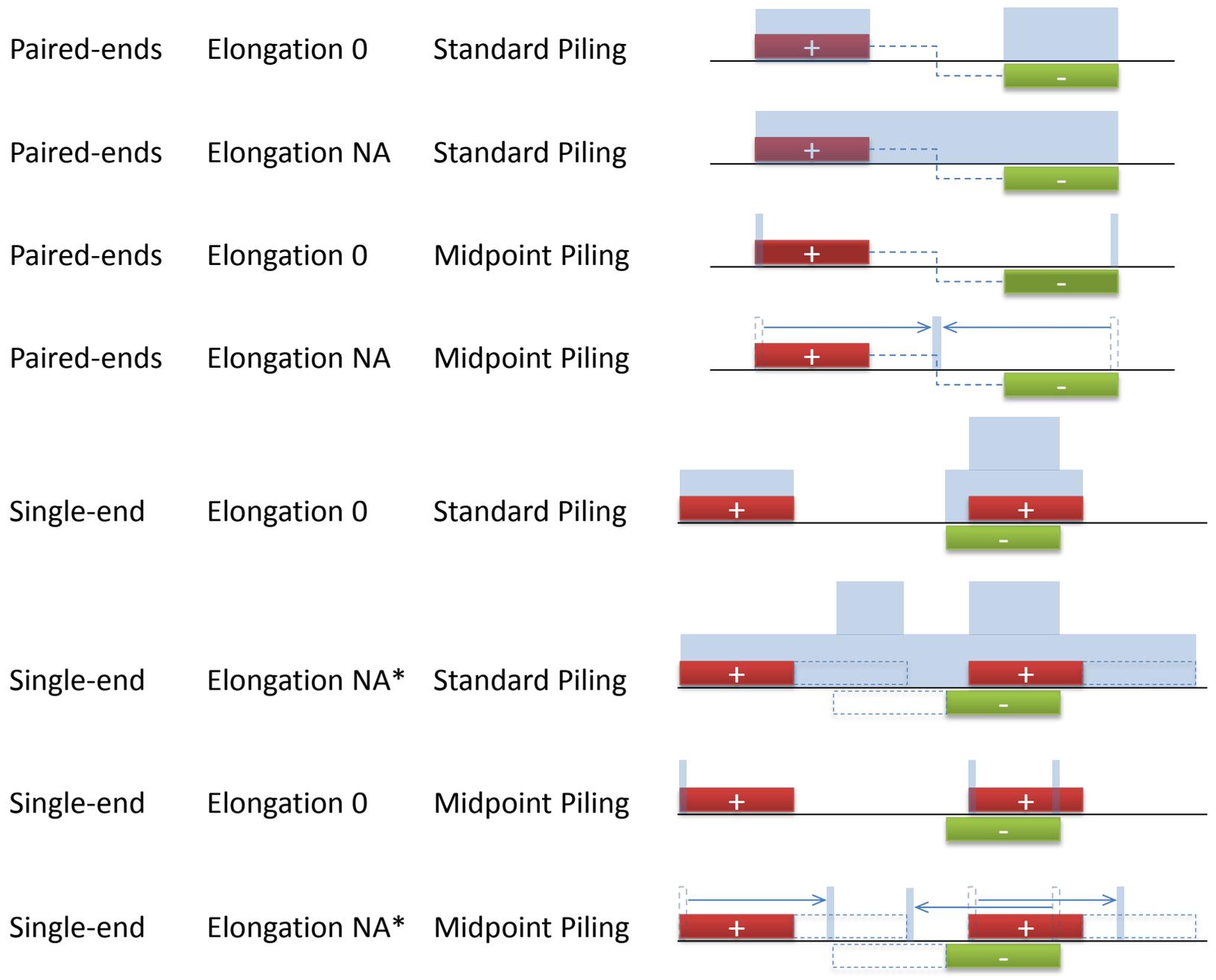
Not aligned , orphan loading, or mix-mode (IDs a1 to a3)



Artefacts : pairs c1 to c7 (for thresholds 0 and 2)

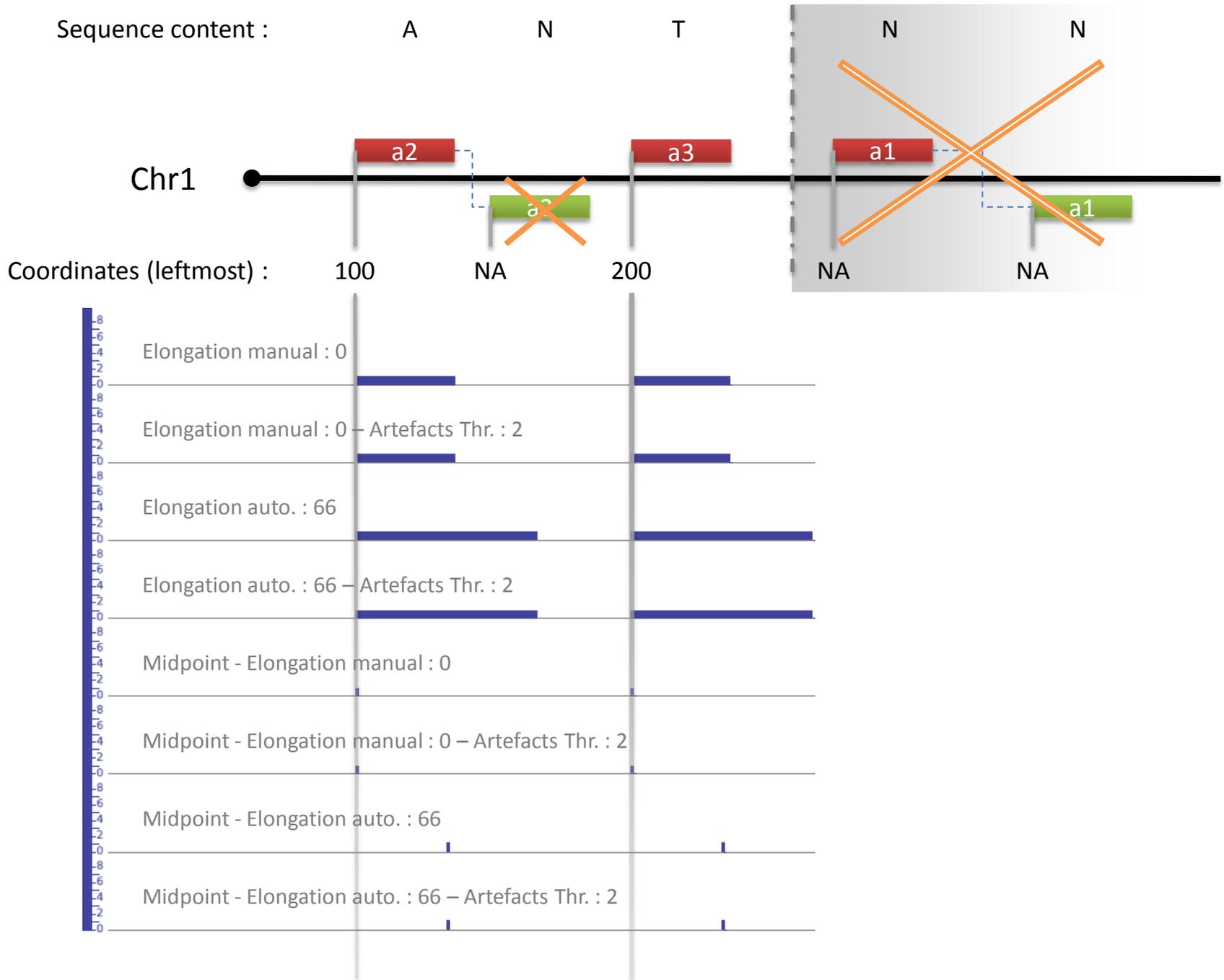


Piling strategies

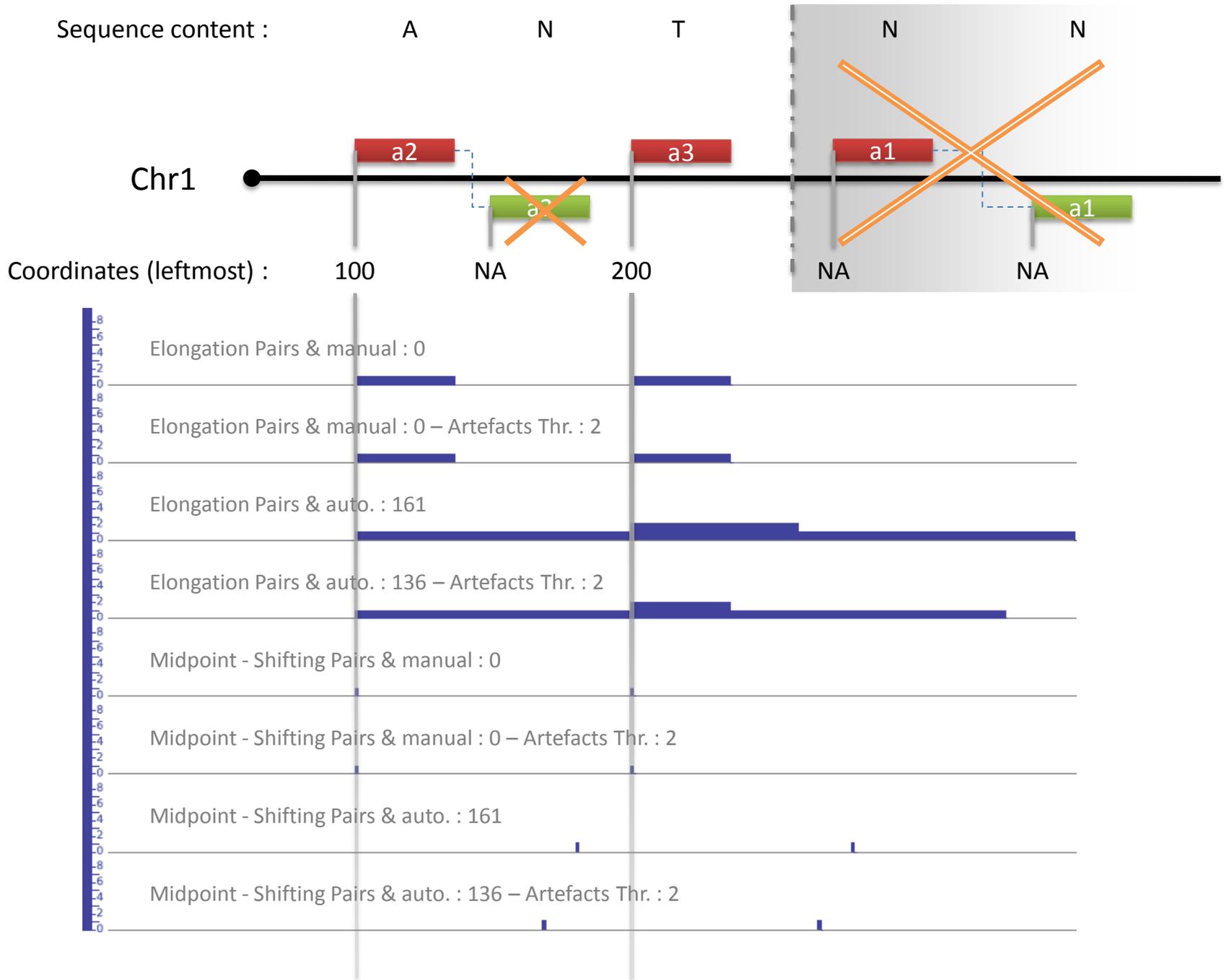


* NA for automatic estimation or manual specification

Not aligned , orphan loading, or mix-mode (IDs a1 to a3) Validation Single-End



Not aligned , orphan loading, or mix-mode (IDs a1 to a3) Validation Paired-Ends

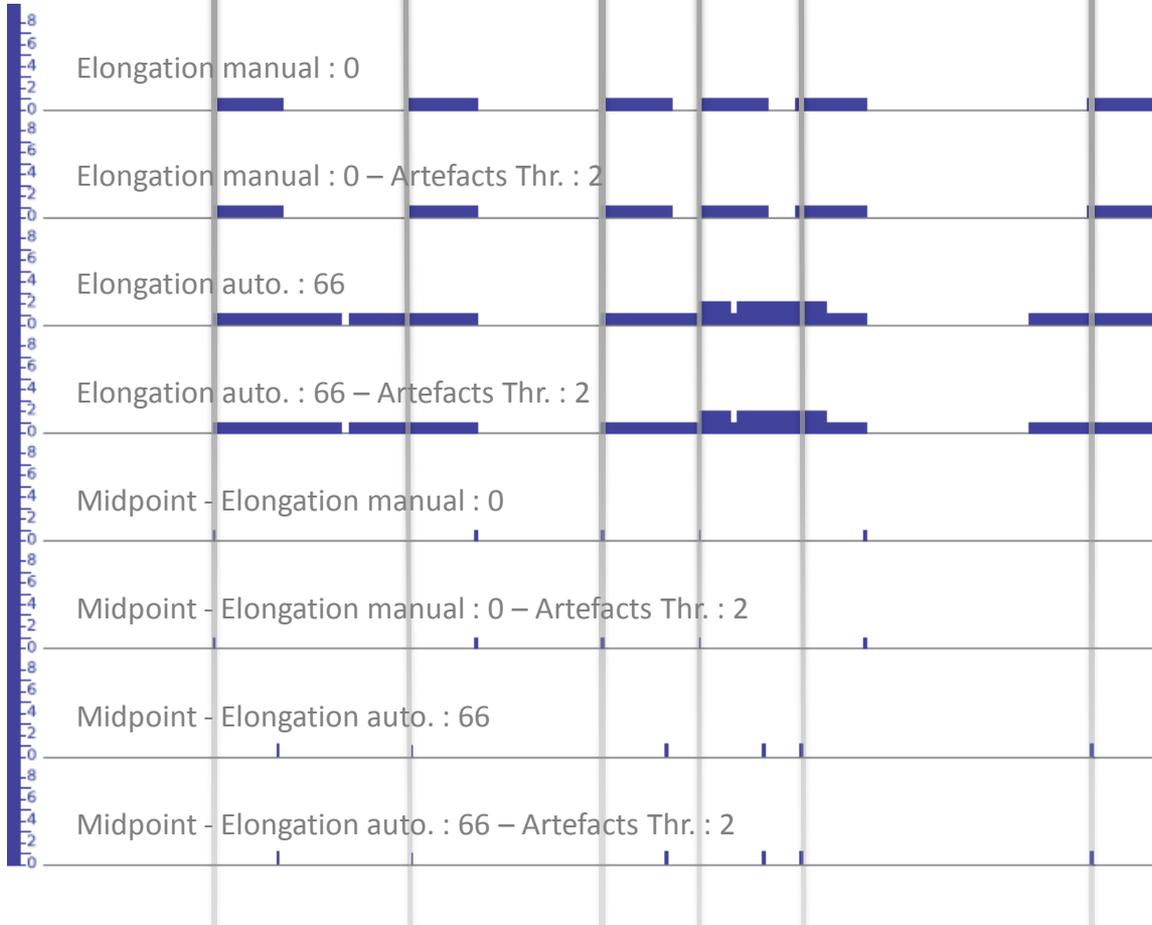


Typical reads for pileup (pairs b1 to b3) Validation Single-End

Sequence content : A C T AT G CG



Coordinates (leftmost) : 100 200 300 350 400 550



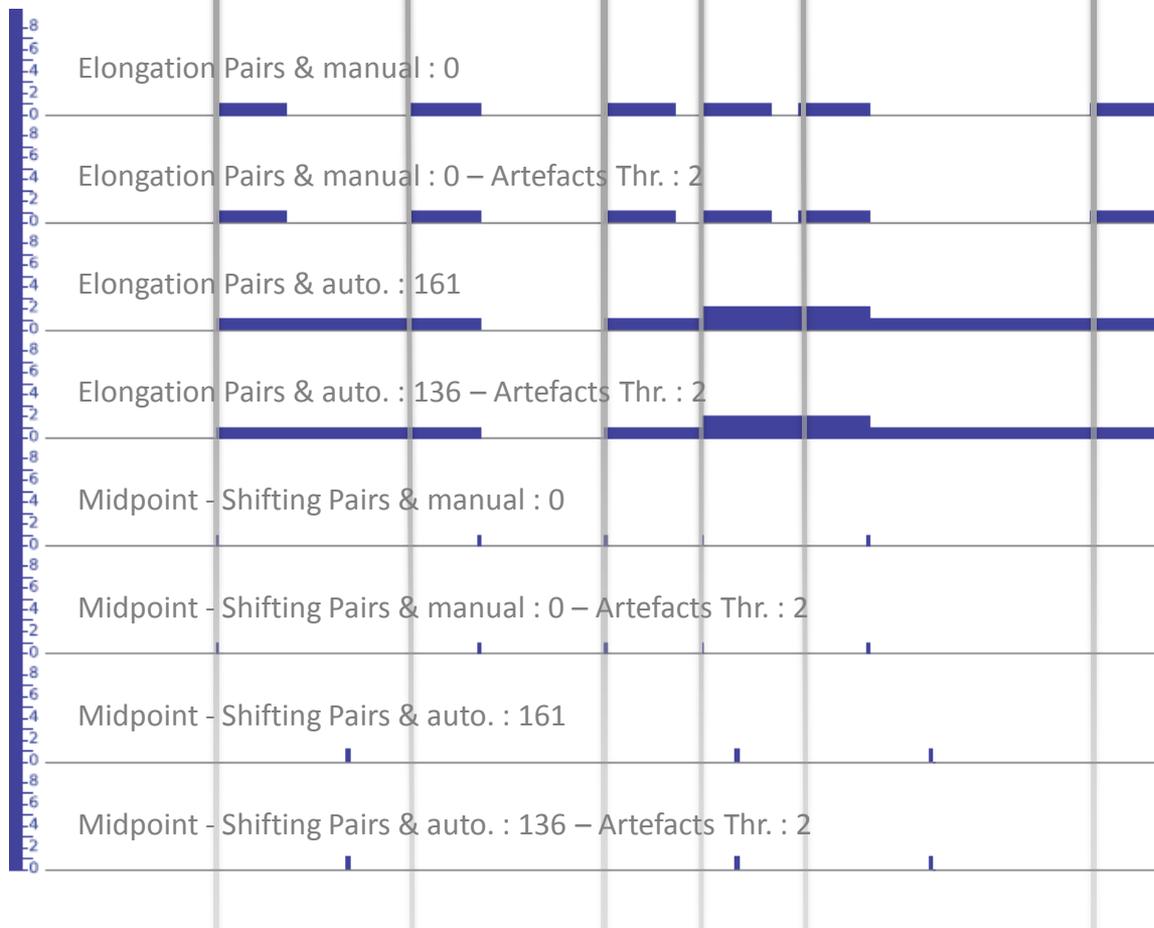
Typical reads for pileup (pairs b1 to b3)

Validation Paired-Ends

Sequence content : A C T AT G CG



Coordinates (leftmost) : 100 200 300 350 400 550



Artefacts : pairs c1 to c7 (for thresholds 0 and 2)

Validation Single-End

Sequence content :

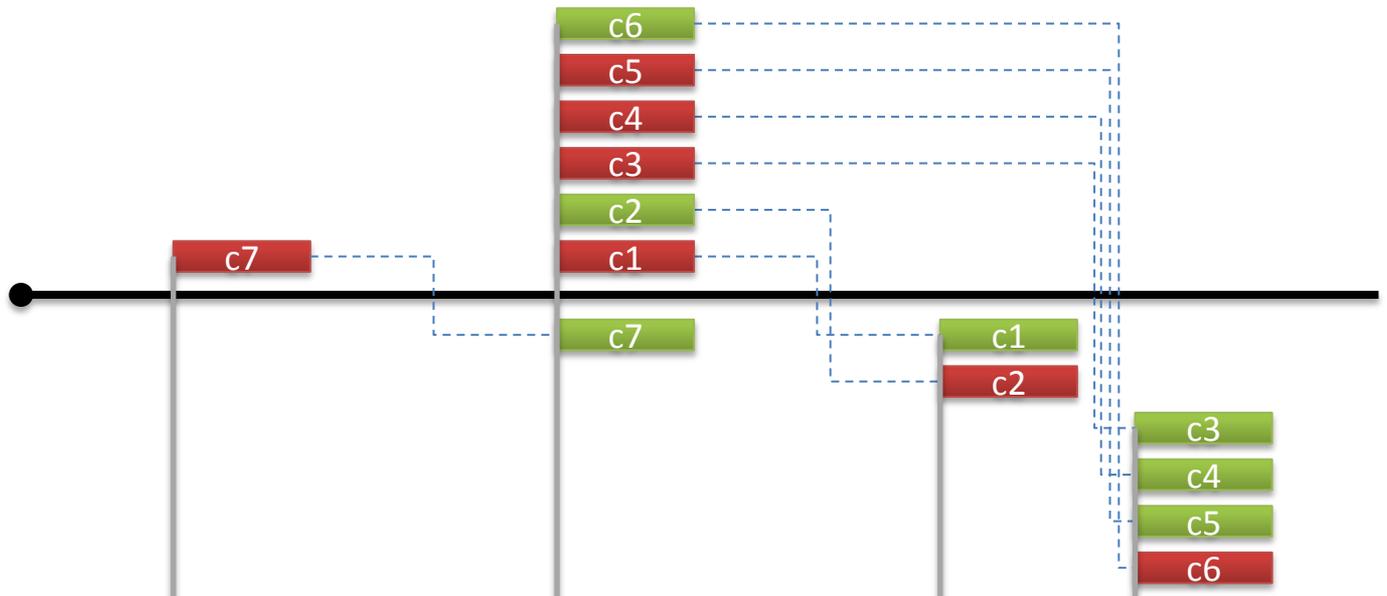
C

A

T

G

Chr3



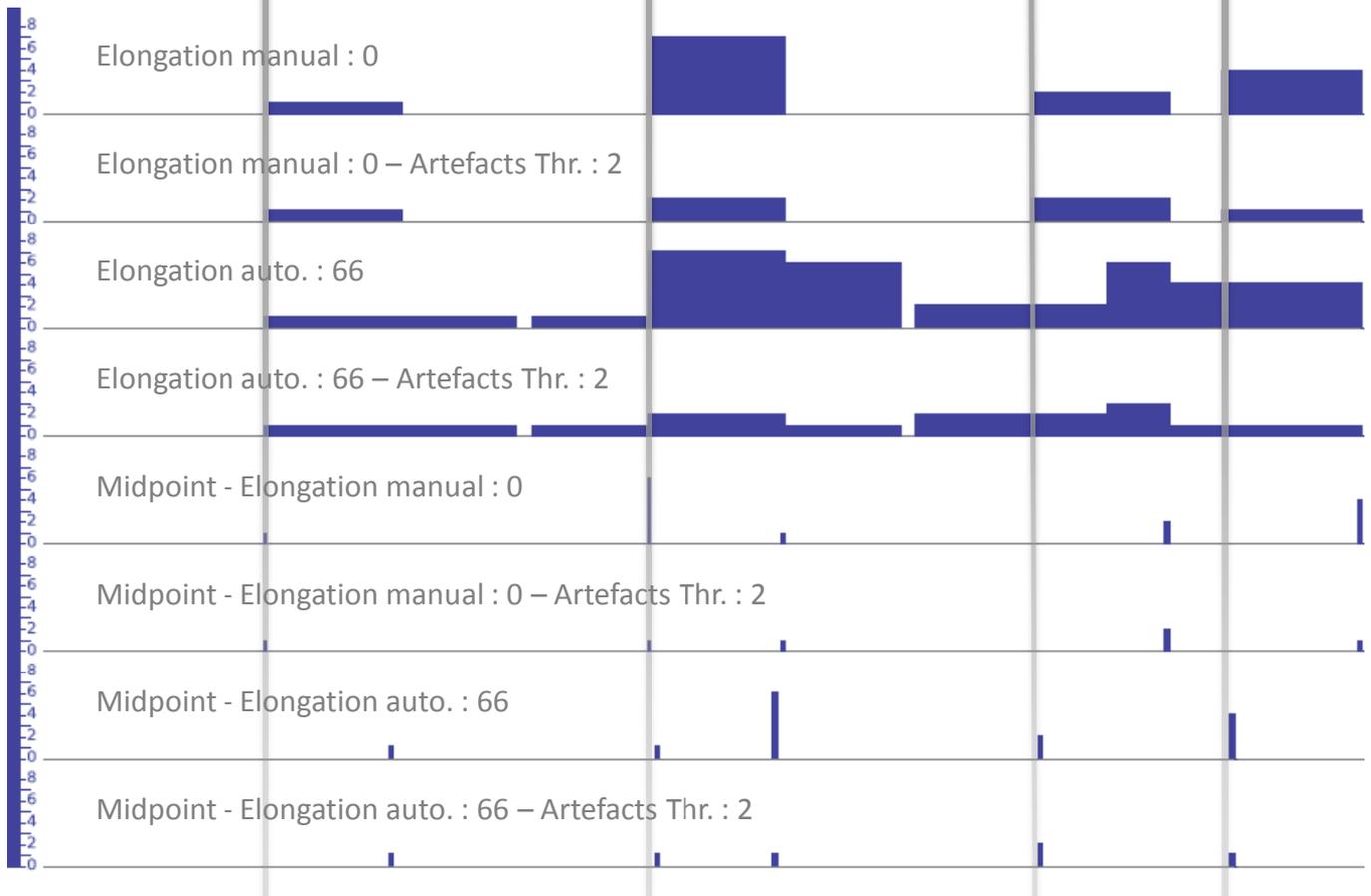
Coordinates (leftmost) :

400

500

600

650



Artefacts : pairs c1 to c7 (for thresholds 0 and 2)

Validation Paired-Ends

Sequence content :

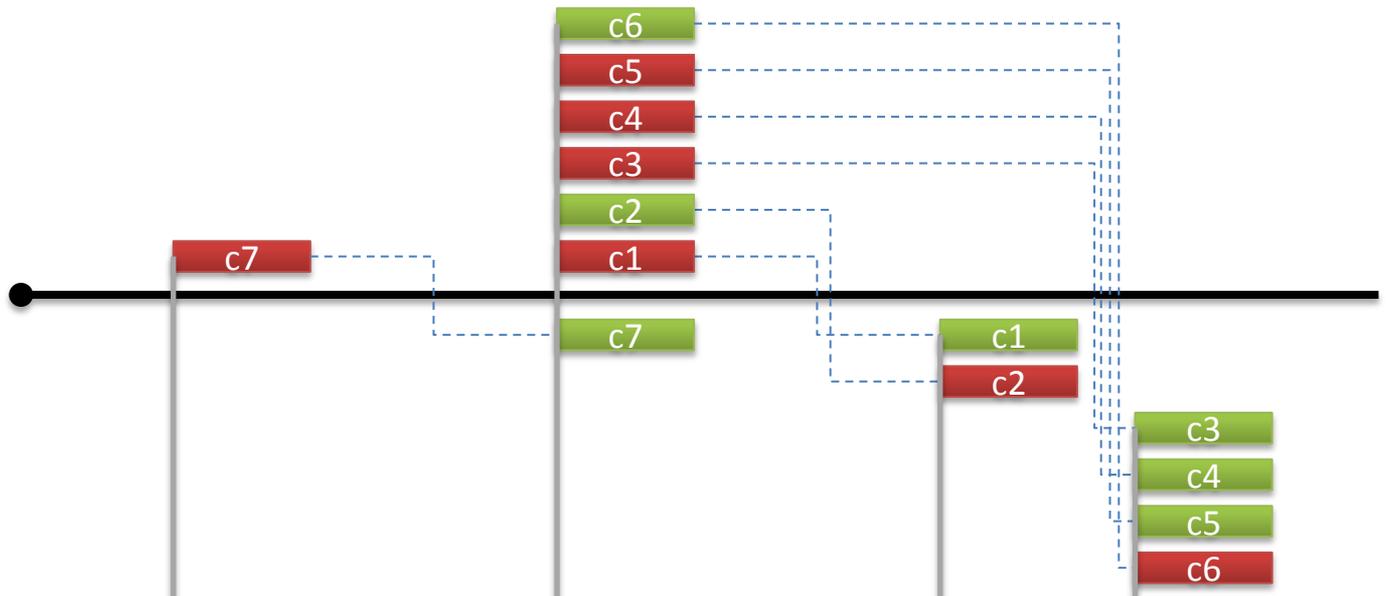
C

A

T

G

Chr3



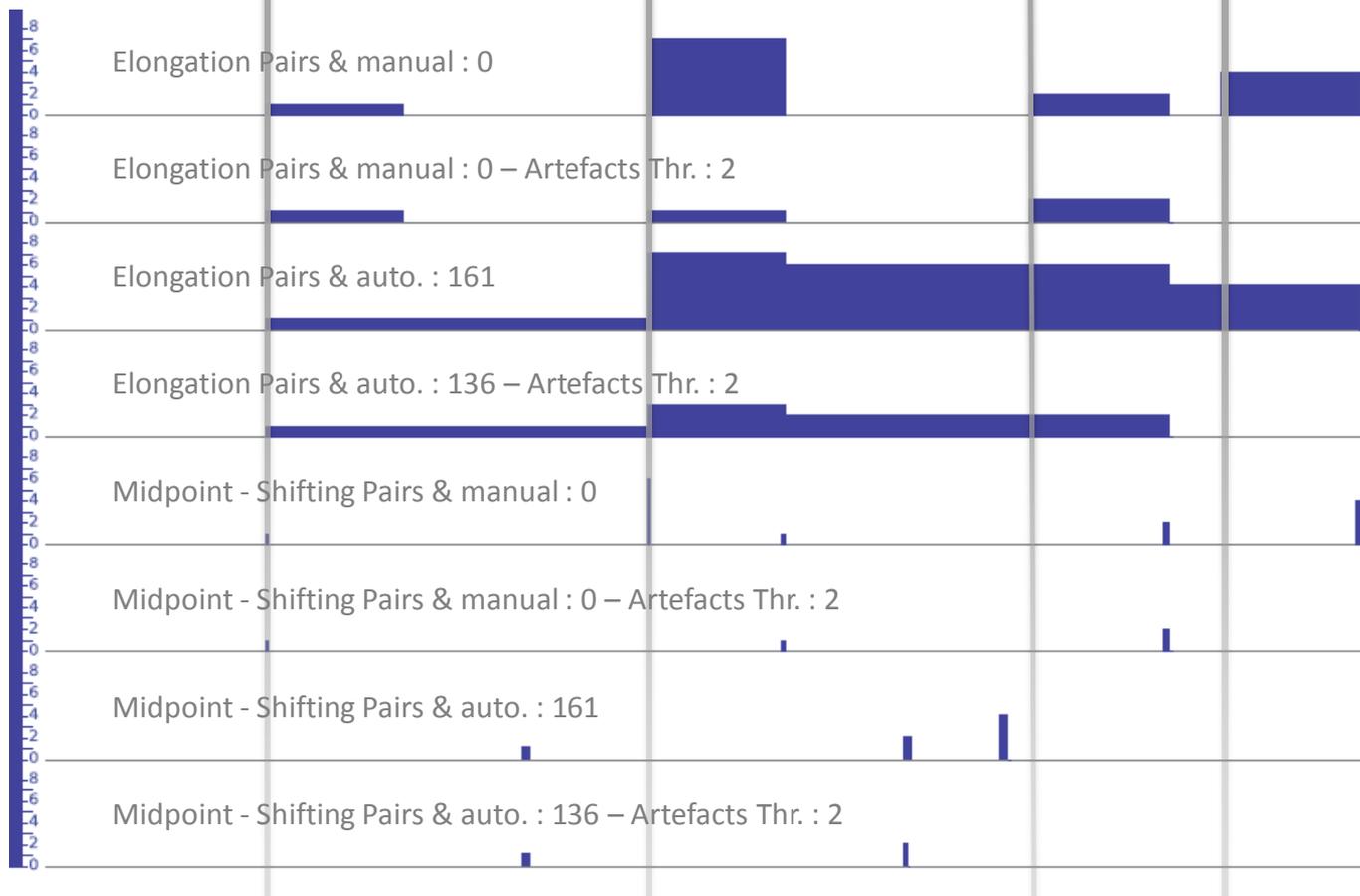
Coordinates (leftmost) :

400

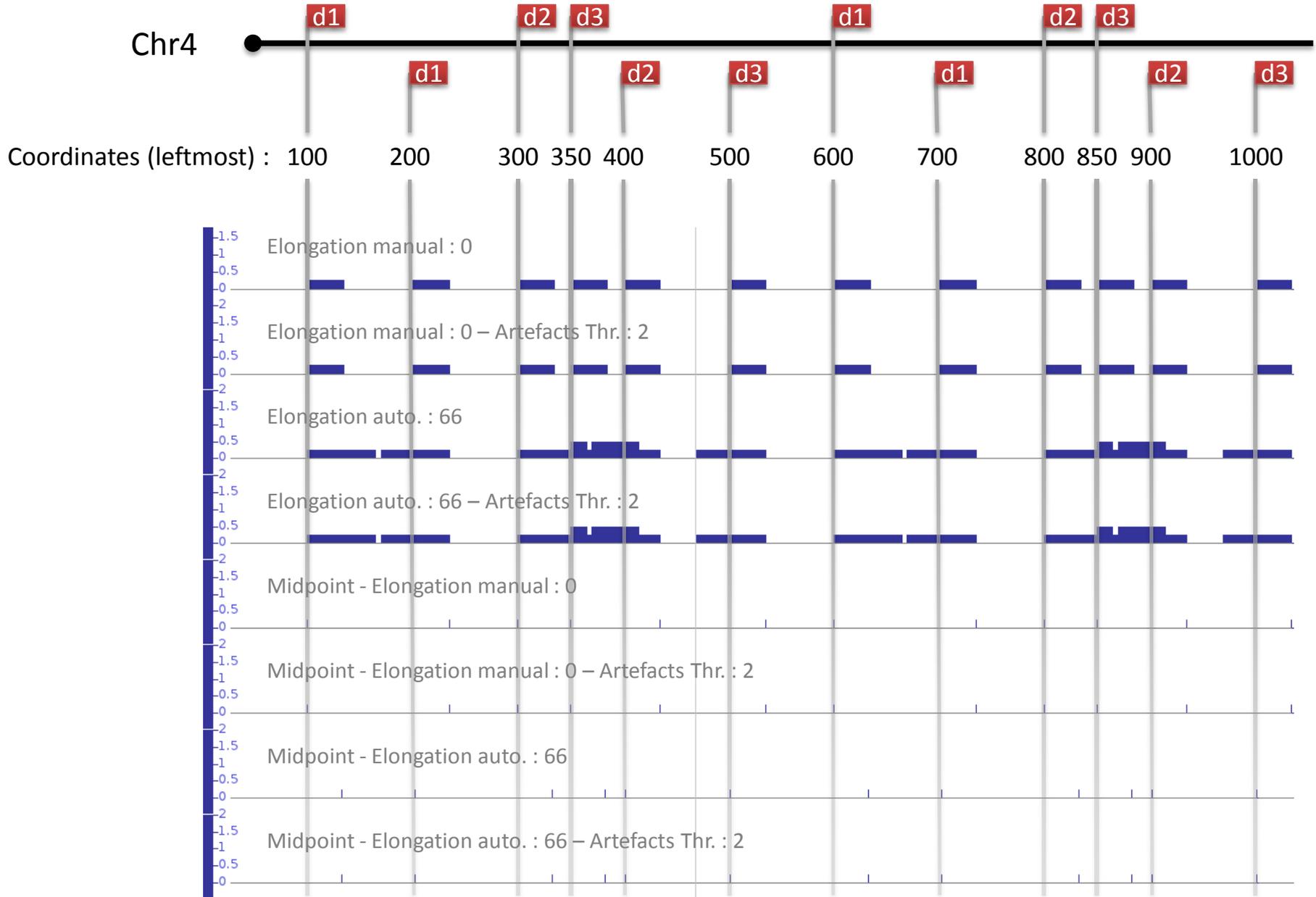
500

600

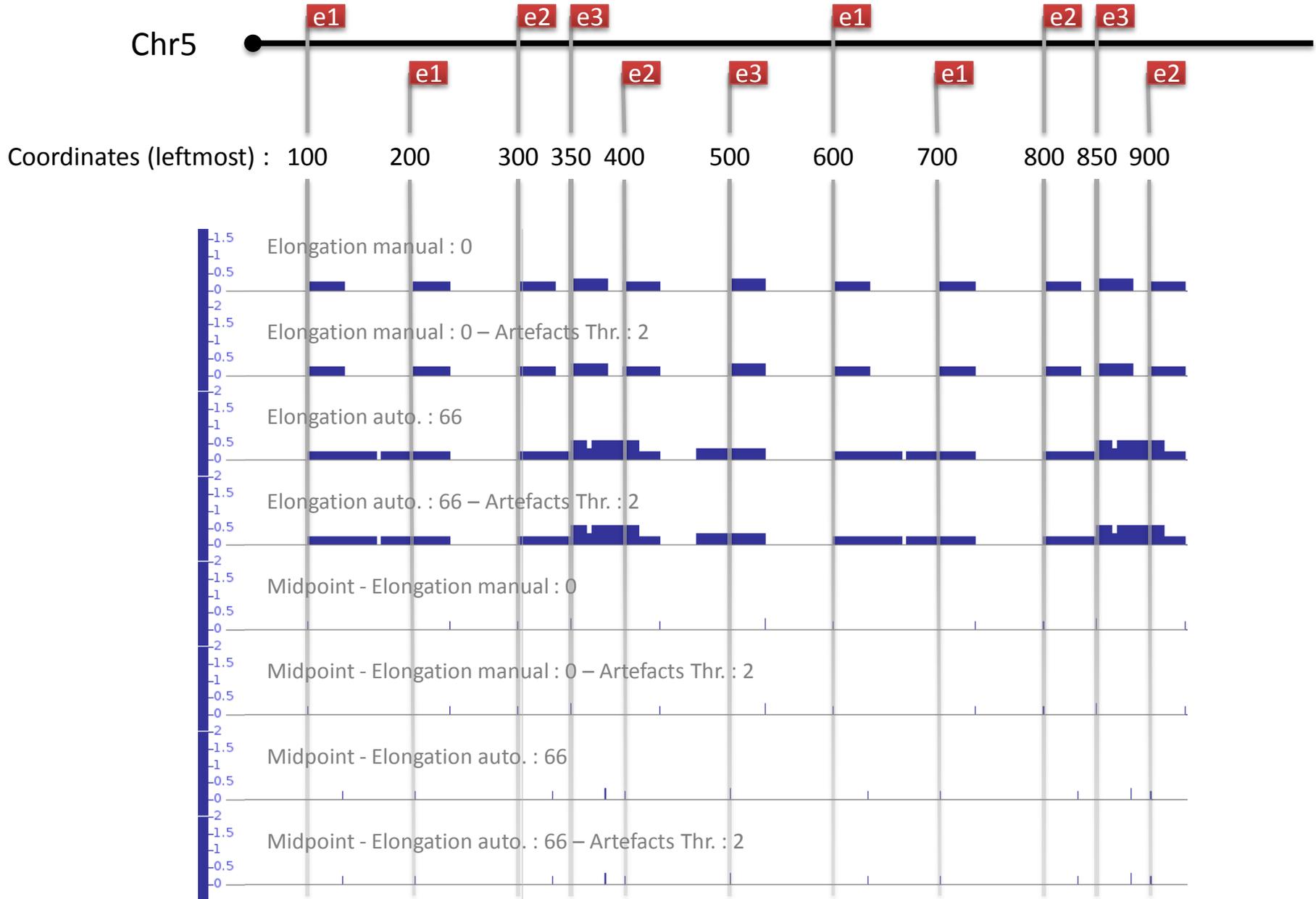
650



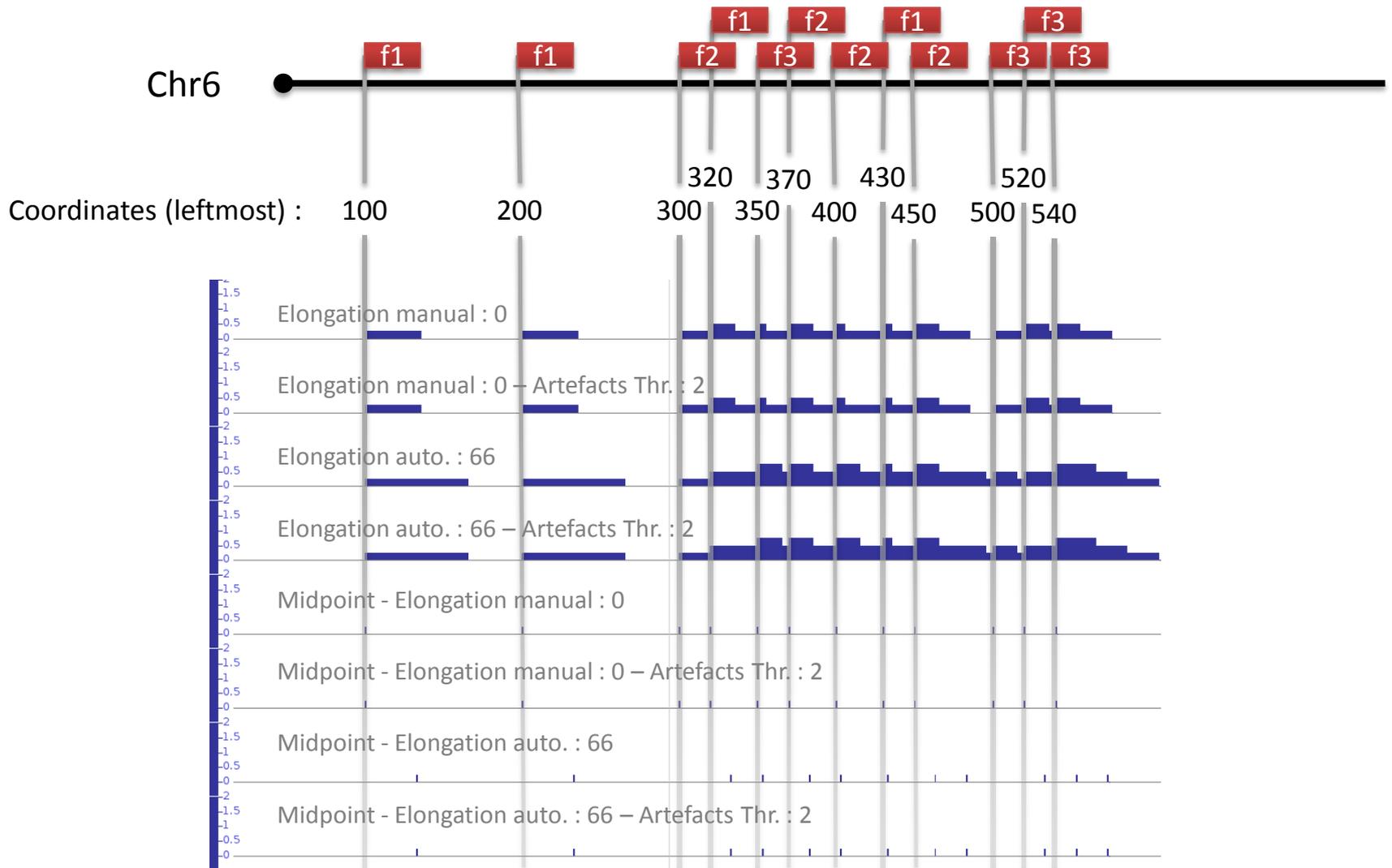
Multiread for pileup test 1
3 tags repeated 4 time each, no overlap
Validation Single-End



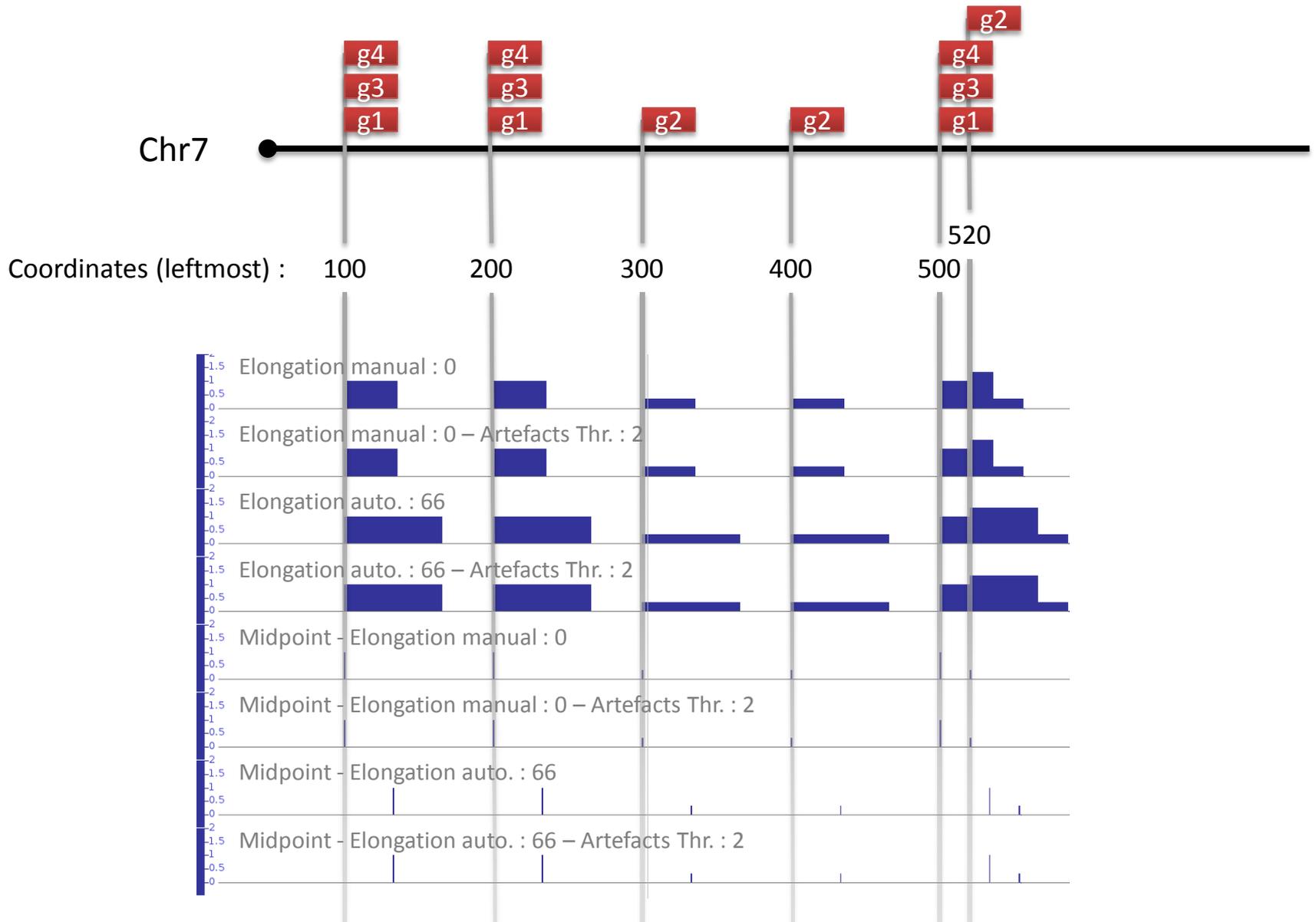
Multiread for pileup test 2
2 tags repeated 4 time each, 1 tag repeated 3 times, no overlap
Validation Single-End



Multiread for pileup test 3
3 tags repeated 4 time each with overlap
Validation Single-End



Multiread for pileup test 4
4 tags repeated 3 time each with artefact
Validation Single-End



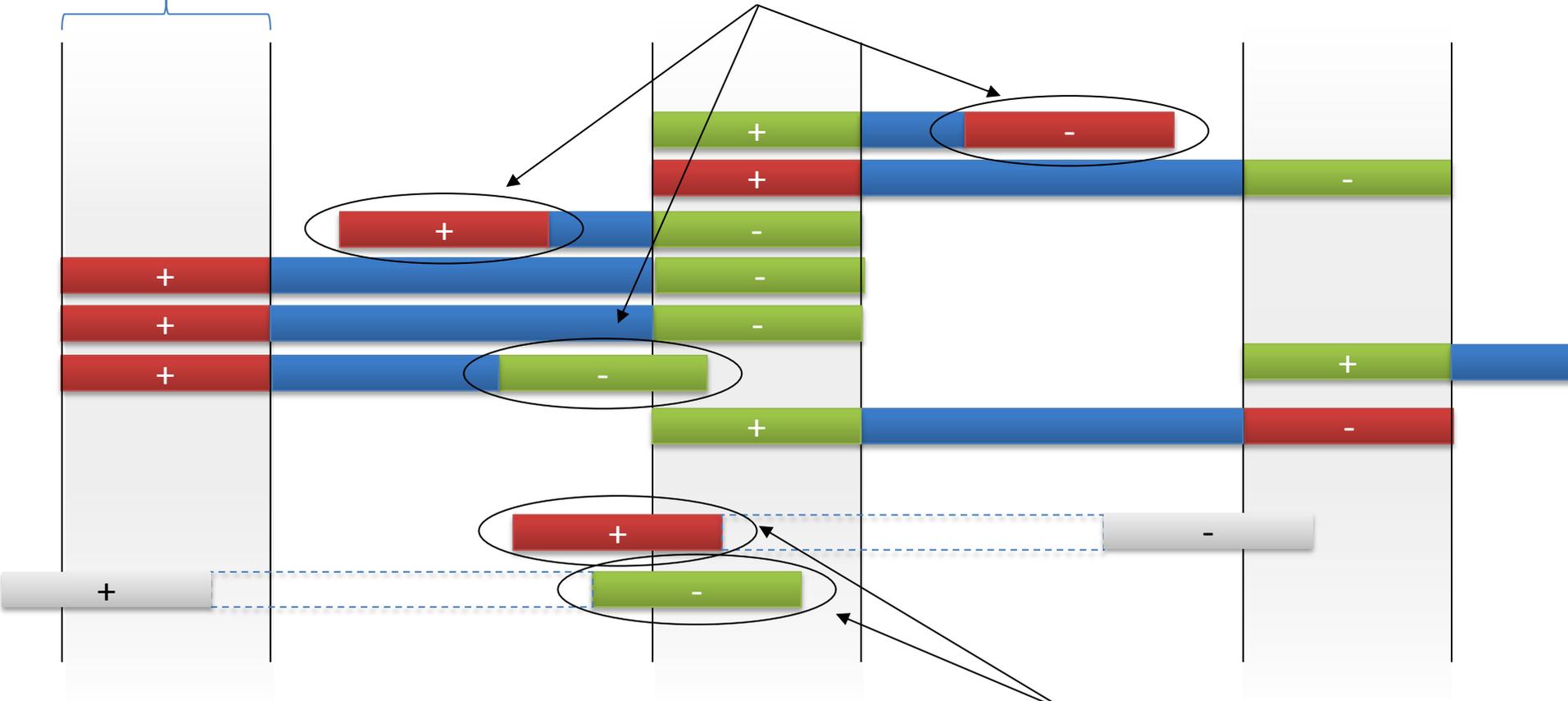


First In Pair
Second In Pair
Insert Core
Not Aligned

Orphans (Paired-ends)

Artefact region

Orphan mates from artefact removal



Orphan mates