Read sequence; Clustered by base−quality patterns

Base−quality; Clustered by base−quality patterns

Genomic sequence; (diff, c.f. read)

200
150
100
50
0

−20 −10 0 10 20

nucleotide position relative to 3p−trim site

Sequence (X = insertion)

A
C
G
N
T
X

base−call quality

30
20
10