

Single Ended alignment of read length 50	
Ref: CAGTGCTCTAGTCGATCGTTATCAGCTAGTCGATGCGTATGGCTAGCTAC Read: TTGTGCTCTCGTCTCGTTATCAGCTAGACGATGCGAATATGGATAGCGGG CIGAR: 2S11M2D22M2I10M3S MD: 7A3^G^A14T12C4 NH tag: 3 SAM format Flag: 256	Relevant information for each alignment is collected. NH tag holds the number of time a read is aligned to the reference.
Expand the CIGAR and the MD String	
CIGAR: MMMMMMMMMMMDDMMMMMMMMMMMMMMMMMMMMMMMIIMMMMMMMMMM MD: MMMMMMMXMMDDMMMMMMMMMMMMMMMMXMMMMMMMIIMMMMMXMMMM	Both CIGAR and MD string is expanded to determine the nucleotides that are mismatches or are insertion/deletions
Overlay the reference and the read to determine indel and mismatched nucleotides	
CIGAR: MMMMMMMMMMMDDMMMMMMMMMMMMMMMMMMMMMMMIIMMMMMMMMMM MD: MMMMMMMXMMDDMMMMMMMMMMMMMMMMXMMMMMMMIIMMMMMXMMMM Ref: CAGTGCTCTAGTCGATCGTTATCAGCTAGTCGATGCG TATGGCTAGCTAC Read: TTGTGCTCTCGTC TCGTTATCAGCTAGACGATGCGAATATGGATAGCGGG MD(modified): MMMMMM)MMDDMMMMMMMMMMMMMM&MMMMMM!!MMMM&MMMM	The reference sequence is adjusted to accommodate insertion nucleotides and the read sequence is adjusted to accommodate deletion nucleotides. Mismatches and insert nucleotides are represented by different characters.
Construct the Integrated CIGAR	
Integrated CIGAR: TT7M)3M2D14M&7M!!5M&4MGGG	Integrated CIGAR is constructed by including the soft-clips
Construct the final Integrated CIGAR (No quality scores stored)	
NH tag: 3 SAM format Flag: 256 Integrated CIGAR: TT7M)3M2D14M&7M!!5M&4MGGG3 Integrated CIGAR: TT7B)3B2D14B&7B!!5B&4BGGG3	The final Integrated CIGAR is constructed by replacing the matching character with a letter to represent the SAM format flag. The value of the NH tag is appended.
Construct the final Integrated CIGAR (With quality scores)	
NH tag: 3 SAM format Flag: 256 Integrated CIGAR: TT7M)3M2D14M&7M!!5M&4MGGG3 Integrated CIGAR: TQ ₁ TQ ₂ 7B)Q ₃ 3B2D14B&Q ₄ 7B!Q ₅ !Q ₆ 5B&Q ₇ 4BGQ ₈ GQ ₉ GQ ₁₀ 3	If quality scores are requested to be stored, then the quality scores for only the nucleotides that are mismatched to the reference or inserts are stored.
Append MAPQ and AS tag Values	
AS tag: 50 MAPQ: 255 Integrated CIGAR: TT7M)3M2D14M&7M!!5M&4MGGG3~50~255 Integrated CIGAR: TQ ₁ TQ ₂ 7B)Q ₃ 3B2D14B&Q ₄ 7B!Q ₅ !Q ₆ 5B&Q ₇ 4BGQ ₈ GQ ₉ GQ ₁₀ 3~50~255	If alignment scores are requested to be stored, then the value of the AS tag along with the MAPQ values are retained within the Integrated CIGAR.
Add number of repetitions of the same read	
Integrated CIGAR: TT7M)3M2D14M&7M!!5M&4MGGG3~50~255-4 Integrated CIGAR: TQ ₁ TQ ₂ 7B)Q ₃ 3B2D14B&Q ₄ 7B!Q ₅ !Q ₆ 5B&Q ₇ 4BGQ ₈ GQ ₉ GQ ₁₀ 3~50~255-4	Due to several rounds of PCR, multiple reads could be sequenced from the same nucleotide position of the reference. ABRIDGE will store a single representation and record the number of repetitions of the read.
Exact same mapping of adjoining sequence with different SAM format Flag	
Integrated CIGAR1: TT7B)3B2D14B&7B!!5B&4BGGG3~50~255-4 Integrated CIGAR2: TT7C)3C2D14C&7C!!5C&4CGGG3~43~250-2 Final CIGAR2: C~43~250-2	If adjoining alignments have the same integrated CIGARR with only a different SAM Format Flag, then the representation is reduced to only the SAM Format Flag and the alignment scores with the repetition of reads