

# SAM format: FLAG

0x1	multiple segments (mates)
0x2	each segment properly aligned
0x4	segment unmapped
0x8	next segment unmapped
0x10	SEQ is reverse complemented in the alignment
0x20	SEQ of next segment is reverse complemented
0x40	first segment (mate)
0x80	last segment (mate)
0x100	secondary alignment
0x200	not passing quality checks
0x400	PCR or optical duplicate
0x800	supplementary alignment

**Example:**  $99_{10} = 6 \cdot 16 + 3 = 63_{16} = 0000\ 0110\ 0011_2$

**0011** Paired, Proper pair, Mapped, Mate mapped,

**0110** Forward, Mate reverse, First in pair, Not second (last) in pair,

**0000** Passed quality check, Not PCR duplicate, Not a suppl. alignment

# SAM format: CIGAR

M match (sequence match or substitution)  
I insertion to the reference  
D deletion from the reference  
N skipped region (intron)  
S soft clipping (sequence start or end not aligned;  
seq appears in SEQ)  
H hard clipping (seq not in SEQ)  
P padding first segment (mate)  
= sequence match  
X sequence mismatch

## Examples:

Reference: C C A T A C T G A A C T G A C T A A C  
Read: A C T A G A A T G G C T 3M1I3M1D5M

Reference: A T A C T G T . . . A G G A A C T G  
Read: A C T 1000 G A A C T 3M1000N5M