

CIGAR summarizes alignment structure

CIGAR = Concise Idiosyncratic Gapped Alignment Report

```
read1 99 ref 2 30 3M1D2M1I1M = 14 20 CATCTAG *
```

RefPos: 1 2 3 4 5 6 7 8 9
Reference: C C A T A C T - G A
Read: C A T - C T A G
POS: 2
CIGAR: 3M1D2M1I1M

See also:

- SAM format spec: <http://samtools.github.io/hts-specs/SAMv1.pdf>
- Explain SAM flags: <http://broadinstitute.github.io/picard/explain-flags.html>

Data Pre-processing

