SAM/BAM Formats

SAM (Sequence Alignment/Map) Format

```
Header: @HD VN:1.6 SO:coordinate
@SQ SN:chr1 LN:248956422
Alignment: READ1 99 chr1 10001 60 76M = 10052 127 ACGT... IIII...
```

SAM (Text)

• Human-readable
• Tab-delimited
• Large file size
• 11 mandatory fields

BAM (Binary)

• Compressed SAM
• ~3-5x smaller
• Faster to process
• Requires indexing (.bai)

Key SAM Fields

• QNAME - Read name

• FLAG - Bitwise flag (paired, mapped, reverse, etc.)

• RNAME - Reference sequence name (chromosome)

• POS - Alignment position

• MAPQ - Mapping quality score

- CIGAR - Alignment string (M=match, I=insertion, D=deletion)