

SAM/BAM Quick Reference

A practical guide to alignment files, core fields and a basic samtools workflow.

SAM and BAM at a glance

Format	SAM	BAM
Representation	Human-readable text	Binary compressed form of SAM
Typical size	Larger	Smaller
Inspection	Open with text tools	Use samtools
Indexable	Not typically	Yes, after coordinate sorting
Common downstream use	Debugging / interchange	Routine alignment storage and analysis

Essential SAM fields

Field	Meaning
QNAME	Read/query name
FLAG	Bitwise alignment flag
RNAME	Reference sequence / chromosome
POS	1-based leftmost alignment position
MAPQ	Mapping quality
CIGAR	Alignment operations
RNEXT / PNEXT	Mate reference and position
SEQ / QUAL	Read sequence and base quality

Common samtools workflow

```
samtools view -bS alignments.sam > alignments.bam
samtools sort alignments.bam -o alignments.sorted.bam
samtools index alignments.sorted.bam
samtools flagstat alignments.sorted.bam
```