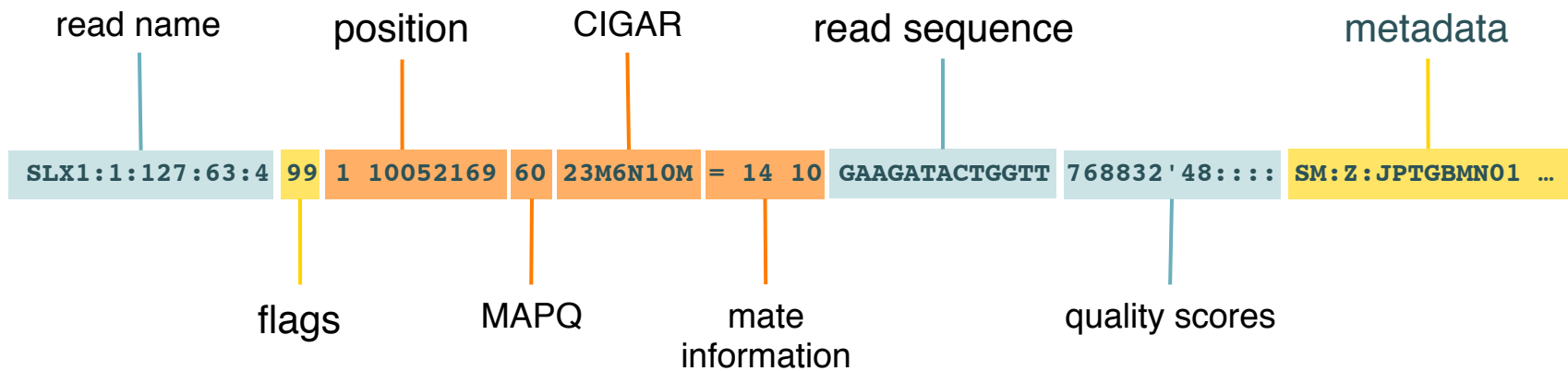


Output format: Sequence/Binary Alignment Map (SAM/BAM)

HEADER containing metadata (sequence dictionary, read group definitions etc)

RECORDS containing structured read information (1 line per read record)



- Added mapping info summarizes **position**, **quality**, and **structure** for each **read**
- A BAM file can contain data from a single or from several samples

Data Pre-processing

