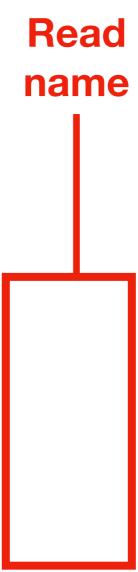
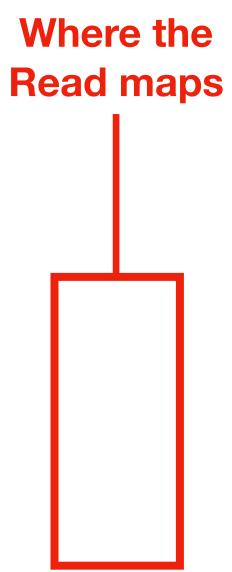
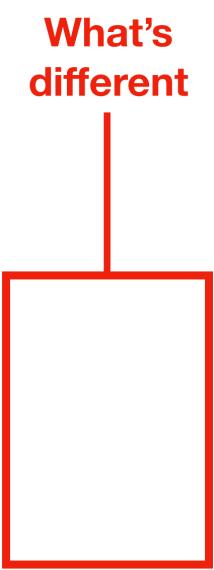


Coor	12345678901234 5678901234567890123456789012345
ref	AGCATGTTAGATAA**GATAGCTGTGCTAGTAGGCAGTCAGCGCCAT
+r001/1	TTAGATAAAGGATA*CTG
+r002	aaaAGATAA*GGATA
+r003	gcctaAGCTAA
+r004	ATAGCTTCAGC
-r003	ttagctTAGGC
-r001/2	CAGCGGCAT
1	

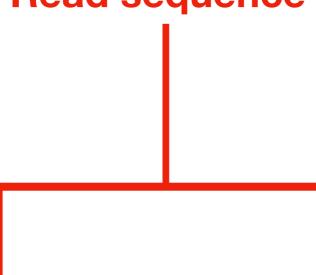
```
QHD VN:1.6 SO:coordinate
QSQ SN:ref LN:45
r001
                                                                  99 ref 7 30 8M2I4M1D3M = 37 39 TTAGATAAAGGATACTG *
r002
                                                         0 \text{ ref } 9 \text{ } 30 \text{ } 3\text{S}6\text{M}1\text{P}1\text{I}4\text{M} * 0 0 \text{ } 
                                                                                                                                                                                                                                                                                                 * 0
r003
                                                        0 ref 9 30 5S6M
                                                                                                                                                                                                                                                                                                                                                               O GCCTAAGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * SA:Z:ref,29,-,6H5M,17,0;
r004
                                                                 0 ref 16 30 6M14N5M
                                                                                                                                                                                                                                                                                                 * 0
                                                                                                                                                                                                                                                                                                                                                                O ATAGCTTCAGC
r003 2064 ref 29 17 6H5M
                                                                                                                                                                                                                                                                                                                                                                  O TAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * SA:Z:ref,9,+,5S6M,30,1;
                                                                                                                                                                                                                                                                                                  * 0
                                              147 ref 37 30 9M
                                                                                                                                                                                                                                                                                                = 7 -39 CAGCGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NM:i:1
r001
```







The original Read sequence



Additional metadata

Example alignment

```
12345678901234
         Coor
                                    5678901234567890123456789012345
                   AGCATGTTAGATAA**GATAGCTGTGCTAGTAGGCAGTCAGCGCCAT
         ref
         +r001/1
                         TTAGATAAAGGATA*CTG
         +r002
                         aaaAGATAA*GGATA
         +r003
                      gcctaAGCTAA
                                      ATAGCT....TCAGC
         +r004
          -r003
                                             ttagctTAGGC
          -r001/2
                                                            CAGCGGCAT
                                       The original
                                                              Additional
                    What's
       Where the
                                                               metadata
                   different
                                      Read sequence
      Read maps
QHD VN:1.6 SO:coordinate
OSD SN:ref LN:45
      99 ref
r001
              7 30 8M2I4M1D3M = 37
                                   39 TTAGATAAAGGATACTG *
              9 30 3S6M1P1I4M *
                                   O AAAAGATAAGGATA
r002
       0 ref
              9 30 5S6M
                                   O GCCTAAGCTAA
r003
                                                      * SA:Z:ref,29,-,6H5M,17,0;
       0 ref
       0 ref 16 30 6M14N5M
                                   O ATAGCTTCAGC
r004
r003 2064 ref 29 17 6H5M
                                   O TAGGC
                                                      * SA:Z:ref,9,+,5S6M,30,1;
r001 147 ref 37 30 9M
                                  -39 CAGCGGCAT
                                                      * NM:i:1
```

Key features of SAM

Widely adopted. Nearly every read aligner uses it, many analysis tools accept it as input

"Lossless" - SAM files include all the information in the raw reads (even those that don't map to the genome)

Can be stored in a binary format and heavily compressed

Can be indexed for fast lookup. You can easily extract all the alignments for a specific locus.