

Alignment: SAM/BAM format

Header

```
@HD VN:1.0      SO:coordinate
@SQ SN:chr1     LN:248956422
@SQ SN:chr10    LN:133797422
@SQ SN:chr11    LN:135086622
...
@PG ID:TopHat  VN:2.0.13  CL:/
data1/igm3/sw/packages/
tophat-2.0.13.Linux_x86_64/
tophat -p 8 -o ...
```

Alignments

```
141217_CIDR4_0073_BHCFG7ADXX:2:1111:3128:29074    345
chr1    10021    0    68M    * ACCCTAA...CCCTAAC    @DC?=2...DDDD@?@
AS:i:0  XN:i:0  XM:i:0      XO:i:0  XG:i:0  NM:i:0      MD:Z:68  YT:Z:UU
NH:i:10    CC:Z:chr10    CP:i:10004    XS:A:-  HI:i:0
. . .
```

SAM format

141217_CIDR4_0073_BHCFG7ADXX:2:1111:3128:29074	Read id
99	FLAG
chr1	Chr
10021	Start
0	Mapping quality
50M	CIGAR (alignment)
=	Mate chr
10151	Mate start
180	Mate dist
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC	Query seq
@DC?=2.FFGE@7>C62>BGABGB9HFBAFIIEHEGFIIIHFAIIGDA<FC	Query base quals
AS:i:0	Alignment score
NM:i:0	Edit distance to reference
NH:i:10	Number of hits
XS:A:-	Strand
HI:i:0	Hit index for this alignment

Tags: [A-Za-z][A-Za-z]:[AifZH]:.*

where A =character; i = integer; f = float; Z=string; H = hex string

(SAMtools) mpileup format

```
#CHR    POS    REF NRDS  BASES                                QUALITIES
17  7574014  A   19      . . . . . . . . . . . . . . . . . . CdA?@C@C6CBCCAB=BBA
# (optional) READPOS
74,72,68,65,61,58,67,55,53,49,48,40,35,34,30,22,32,14,12,8
```

- . match, forward
- , match, reverse
- T mismatch (to T), forward
- t mismatch (toT), reverse
- ^ beginning of read
- \$ end of read
- + [0-9]+[ACGTNacgtn]+ insertion in the reference (e.g., +3ACC)
- [0-9]+[ACGTNacgtn]+ deletion from the reference (e.g., -2GG)
- > reference skip