SAM file format

SAM file contents

@HD VN:1.4 SO:coordinate

```
@SO SN:chr13 LN:114364328
@SO SN:chr17 LN:83257441
@SO SN:chr20 LN:64444167
@RG ID:NOID PG:tmap SM:NOSM
@PG ID:tmap CL:map3 f ref/chr merged.fa -r reseg reads.fastg -i fastg -o 2 -s reseg reads mapped.bam VN:3.4.1
```

16 NM:1:0 A5:1:16 XA:Z:map3-1 X5:1:16 XI:1:1 1XTY1:00427:00223 16 chr13 18193502 50 60518M

JXTYJ:00327:00477 0 chr13 18222266 56 18M385 * 0 0 CCCCACTCTGACCAGCCTCCTGGCCTTCTGTGCTGGTTCCCTCGGTTC 99
92:CBCBBBBA<ABB<BB<=<181:0918<>;A>>>CCDC=B<A?47+*'(((RG:Z:NOID PG:Z:tmapMD:Z:18 NM:i:0 AS:i:18 XA:Z:map3-1 X
5:i:10 XT:i:1</pre>

SAM header

```
@HD VN:1.4 S0:coordinate
@SQ SN:chr13 LN:114364328
@SQ SN:chr17 LN:83257441
@SQ SN:chr20 LN:64444167
@RG ID:NOID PG:tmap SM:NOSM
@PG ID:tmap CL:map3 -f ref/chr merged.fa -r reseq reads.fastq -i fastq -o 2 -s reseq reads mapped.bam VN:3.4.1
```

JXTYJ:09049:09263 0 chrl3 17166350 0 16M1655 * 0 0 ACGCAGCAAACAGAGTGAAATGCCATTITTCTATTTCTGCTTTCCATTTTATATGTGCTT
ATTTTATACATGCCTCAGGGGCATGTTGCTGGTCCCTTTGGGCCAGAAGTTCCAAACCATTCTGCCCTTCAAATAAAGGTCTAGGCCCTTCCAGGAAGT
CTCAGGATGTGG :76;;;;99+:7995:99909;9454444'4555=6;;;666*65-993-27;,;;:655)5;;0;888>>>-98999::+5;44490443-333333
3::(33366884:62:929-3-48:::A;8B@@@\$73889/>@49A;A>>>B<CE9A;99@=?=@377BCCBA8?@??@8 RG:Z:NOID PG:Z:tmap MD:Z:
16 MM1::0 85:i:16 X7::15;:16 XT::15

JXTYJ:00427:00223 16 chrl3 18193502 59 60518M * 0 CTGGGTTGCTTCACTGCAGATATTGAAATACAGAGTGGGCTCTTCTCACTGCAAGC
GGGGAGCTTGGCATTTGCTG AA9AA;CB>8>ACCA???AAAA:A?8>>>@@@>>>BBBBBB<??@BCABAA@A7>>5+::99A<BBBBBAFFBCAA RG:Z:NOID
PG:Z:tmao MD:Z:15A0A0 NM:i:2 A5:i:10 XA:Z:mao3-1 X5:i:-2147483647 XT:i:1

JXTY1:00327:00477 0 chr13 18222266 56 18M385 * 0 0 CCCCACTCTGCACCAGCCTCCTGGCTTCCGTTCTGTGCTGGTTCCCTCGGTTCC 99 92:CBCBBBBA<8B<8B<-(181:0918<>;A>>>CCDC=B<A?47+*'((((RG:Z:NOID PG:Z:tmapMD:Z:18 NM:i:0 AS:i:18 XA:Z:map3-1 X 5:i:10 XT:i:1

SAM body

```
@HD VN:1.4 S0:coordinate
@SO SN:chr13 LN:114364328
@SO_SN:chr17_LN:83257441
@SO SN:chr20 LN:64444167
@RG ID:NOID PG:tmap SM:NOSM
@PG ID:tmap CL:map3 -f ref/chr merged.fa -r reseg reads.fastg -i fastg -o 2 -s reseg reads mapped.bam VN:3.4.1
AAGGCAGTTGGGTAGTGATTACTGCCATTTAGCGTAACTTGCATTTCCTTGTGTTTCTAGTATTTGGC CBD>CDF>BCC=CEE8CCBAA9A=BCCED5AG<CD8A:g:?
>B49844(39:6BABDD596::@A9>@27.----626:=77/5BD9BEGDCC:BA:BBBCB:C=C=A?@BB<ACBA>=>?/919 RG:Z:NOIDPG:Z:tmap MD:Z:1
6 NM:i:0 AS:i:16 XA:Z:map3-1 XS:i:-2147483647 XT:i:1
JXTYJ:00949:00263 0 chr13 17166350 0 16M165S * 0 0 ACGCAGCAAACAGAGTGAAATGCCATTTTTCATATTCTGCTTTCCATTTATATGTGCTT
TATTTATACATGCTCCAGGGGCATGTTTGCTTGGTCCCTTTTGGGCAGTAAGTTCCAAACCTTCTCAATTCTGTCCCTTCAAATAAAGGTCTAGGCCCTTCCTGAGAAAGT
CTCAGGATGTGG :76::@:99+:?995;99909;9454444'4555=6;;;666*65>993<?;<;;:655)5;;0;888>>><9B999::+5;44490443-33333(
3::(33(366884:<6:2:929-3-48:::A:BB@@@65?3889/>@A9A:A>>>B<CE9A:@9@=?=@377BCCBA8?@??@8 RG:Z:NOID PG:Z:tmap MD:Z:
16 NM:i:0 AS:i:16 XA:Z:map3-1 XS:i:16 XT:i:1
JXTYJ:00427:00223 16 chr13 18193502 50 60S18M * 0 0 CTGGGTTGCTTCAGTGCAGATATTGAAATACAGAGTGCGCTCTTCTCTCACTGCAAGC
GGGGAGCTTGGCATTTGCTG AA9AA:CB>8>ACCA???AAAA:A?8>>>@@@o>>>BBBBBB<??@BCABAA@A7>>5+::99A<<B>B@B>FFBCAA RG:Z:NOID
PG:Z:tmap MD:Z:16A0A0 NM:i:2 AS:i:10 XA:Z:map3-1 XS:i:-2147483647 XT:i:1
JXTYJ:00327:00477 0 chr13 18222206 56 18M38S * 0 0 CCCCACTCTGCACCAGCCTCCTGGCCTTCCGCTTCTGTGCTGGTTCCCTCGGTCTC 99
92:CBCBBBBA<ABB<BK=<181:0918<>:A>>>CCDC=B<A?47+*'(((( RG:Z:NOID PG:Z:tmapMD:Z:18 NM:i:0 AS:i:18 XA:Z:map3-1 X
S:i:10 XT:i:1
```

SAM body

| 1XTY1:00949:00263 0 chr13 17166350 0 16M1655 * 0 0 ACGCAGCAAACAGAGTGAAATGCCATTTTTCTATTTCTGCTTTCCATTTATATGTGCTT
TATTTATACATGCCTCCAGGGGCATGTTGCTTGGCTCCTTTGGGCAGTAGTTCCCAAACCCTTCCAAATTCTGTCCCTTCAAATAAAGGTCTAGGCCCTTCCTGAGAAGT
CTCAGGATGTGG :76;;@:99+:7995:99909;9454444'4555-6;;;666*65-993-27;<;;:655)5;;@:888>>>-98999:+5;44490443-33333(
33:(3366884:-62:2929-3-484):481::48:880@06573889/-@49A;A>>>B
 CE9A;09@=?=@377BCCBA8?@?@8 RG:Z:NOID PG:Z:tmap MD:Z:
16 NM1::0 AS::i:16 X3::i:16 XT:i:16 XT:i:16 XT:i:17 XI:18 XI:1

JXTY1:08327:08477 0 chr13 18222266 56 18M38S * 0 0 CCCCACTCTGACCAGCCTCCTGGCTTCTGTGCTGGTTCCTTGGTTCC 99
92:CBCBBBBA<ABB<BB<=<181:0918<>;A>>>CCDC=B<A?47+*'((((RG:Z:NOID PG:Z:tmapMD:Z:18 NM:i:0 AS:i:18 XA:Z:map3-1 X
S:i:10 XT:i:1</pre>

SAM body

From SAM format specification:

| Col | Field | Brief description |
|-----|-------|---------------------------------------|
| 1 | QNAME | Query template NAME |
| 2 | FLAG | bitwise FLAG |
| 3 | RNAME | Reference sequence NAME |
| 4 | POS | 1-based leftmost mapping POSition |
| 5 | MAPQ | MAPping Quality |
| 6 | CIGAR | CIGAR string |
| 7 | RNEXT | Ref. name of the mate/next read |
| 8 | PNEXT | Position of the mate/next read |
| 9 | TLEN | observed Template LENgth |
| 10 | SEQ | segment SEQuence |
| 11 | QUAL | ASCII of Phred-scaled base QUALity+33 |

FLAG field

| Bit | Description | |
|-------|--|--|
| 0×1 | template having multiple segments in sequencing | |
| 0x2 | each segment properly aligned according to the aligner | |
| 0×4 | segment unmapped | |
| 8×0 | next segment in the template unmapped | |
| 0×10 | SEQ being reverse complemented | |
| 0×20 | SEQ of the next segment in the template being reversed | |
| 0×40 | the first segment in the template | |
| 0×80 | the last segment in the template | |
| 0×100 | secondary alignment | |
| 0×200 | not passing quality controls | |
| 0×400 | PCR or optical duplicate | |
| 0×800 | supplementary alignment | |

CIGAR string

| Ор | Description | |
|----|---|--|
| M | alignment match (can be a sequence match or mismatch) | |
| Ι | insertion to the reference | |
| D | deletion from the reference | |
| N | skipped region from the reference | |
| S | soft clipping (clipped sequences present in SEQ) | |
| Н | hard clipping (clipped sequences NOT present in SEQ) | |
| P | padding (silent deletion from padded reference) | |
| = | sequence match | |
| X | sequence mismatch | |