

```

HWI-ST375_61:5:1:8083:2647      97      3L      3061297 37      100M      =      3069973 8776
GAGTGCGAGAGGGTCGGCCTGCTTATGCTGCGGTTGCGCCCGCCCTCGCTCCCCCTCGCACTCTTTCCATGTTTTCAAGGCGCATAATGCAAGAGC
GCC      EEEEEEECEEEGGEGEF AFDGAGGDFBFFGEEFBEBEEEEFEBC-A>>-@ABA#####
#####      XD:Z:42AGT1AC1A4AC1C1CTAAACC2CACGCC2T1AA1AA2C2CGG1C1CTCAA1      SM:i:37 AS:i:0

```

<Sequence Name> <Hexadecimal Flag> <Reference Sequence Chromosome Name> <Position>
 <Mapping Quality Score> <CIGAR String> <Mate Reference Sequence Chromosome Name> <Mate Position>
 <Insert Size> <Sequence> <Sequence Confidence String> <Mismatch Tag> <Single Read Tag> <Pair Read Tag>

The Boolean operators are:

- == equal
- != not equal
- > greater than
- < less than
- >= greater than or equal to
- <= less than or equal to

awk '{if(\$9 > 1000 || \$9 < -1000){print \$0}}' filein.sam > fileout.sam

This will print each line where column 9 is greater than 1000 or less than -1000.

awk '{if(\$7 == "="){print \$0}}' filein.sam > fileout.sam

This will print all lines where column 7 is an equals sign to the new file.

awk '{if(\$2 == 83 || \$2 == 147 || \$2 == 99 || \$2 == 163){print \$0}}' filein.sam > fileout.sam

This will print all lines where column 2 is equal to 83, 147, 99, or 163