.sam to circos-compatible .tsv (almost)

```
awk -F "\t" '{if($2=="0" || $2=="16") print $3,$4,$16}' infile.sam| grep -F "SA:Z:" | awk -F' |,'
'BEGIN{OFS="\t";} {print $1, $2, $2, $3, $4, $4}' | sed 's/NC_00000/chr/g ; s/NC_0000/chr/g ; s/SA:Z://g ;
s/\.9//g ; s/\.10//g ; s/\.11//g ; s/\.12//g ; s/\.14//g' | sort | uniq -c | awk 'BEGIN{OFS="\t";} {print
$2,$3,$4,$5,$6,$7,$1}' > infile.sam.Circos.tsv
```

- awk identifies tab "/t" as the separator and selects any lines with column 2 having 0 or 16 values and pipes that to:
- grep which keeps only lines with an "SA:Z:" that are chimeric and pipes that to:
- awk again which recognized either space or comma as a separator and prints columns 1,2,2,3,4,4 and those lines are piped to:

  (the duplicate columns are for circos start and end values for links)
- sed, which stream edits the data to replace NC_00000 with chr, remove SA:Z:, and removes specific things after decimals on chromosome numbers in a global manner and then pipes that to:
- sort to put all lines in alphanumeric order which are piped to:
- uniq which eliminated duplicates while counting them and them pipes that to:
- awk which uses tab "\t" as an output formatting element to print columns 2-7, and 1 to produce:
- Chrom_left   start   end   Chrom_right   start   end   count