STAR alignment parameters

```
##### Final user re-defined parameters-----------------:
runThreadN                        4
readFilesCommand                  zcat
outSAMtype                        BAM   SortedByCoordinate
outSAMattributes                  NH   HI   AS   NM   MD
outSAMunmapped                    Within
outFilterType                     BySJout
quantMode                         TranscriptomeSAM   GeneCounts
twopassMode                       Basic
```