guo@HGCNT43:/hgcnt44fs/tcga/data/57cf26b8-b723-40ea-8aa9-a62f4afc2b7f>

samtools flagstat TCGA-10-0931-01A-01R-1564-13\_GRCh37-lite\_rnaseq.bam

337866532 + 32051542 in total (QC-passed reads + QC-failed reads)

221576631 + 15569139 duplicates

305193067 + 17477952 mapped (90.33%:54.53%)

337866532 + 32051542 paired in sequencing

168933266 + 16025771 read1

168933266 + 16025771 read2

277371738 + 12638396 properly paired (82.10%:39.43%)

285759370 + 13022868 with itself and mate mapped

19433697 + 4455084 singletons (5.75%:13.90%)

4138634 + 198536 with mate mapped to a different chr

2357455 + 117357 with mate mapped to a different chr (mapQ>=5)