

```
#!/bin/bash
```

```
rgline="ID:${sample}\tPU:${sample}\tSM:${sample}\tPL:ILLUMINA\tLB:${sample}"
```

```
STAR \
  --runThreadN 12 \
  --genomeDir $index_path \
  --readFilesIn $fq_files \
  --outSAMtype BAM Unsorted \
  --outSAMunmapped Within \
  --outSAMattrRGline \${rgline} \
  --outSAMattributes NH HI AS nM NM \
  --quantMode GeneCounts
```