```
STAR_INDEX=/net/gs/vol4/shared/trapnelllab/genome569A/scRNAseq-pipeline/worm-genome/STAR-index

STAR --genomeDir $STAR_INDEX \
     --readFilesIn small_reads.fastq \
     --outFileNamePrefix example/ \
     --outSAMtype BAM Unsorted \
     --outSAMstrandField intronMotif
```

Sample problem 1

Download "small_reads.fastq"

Use STAR to map these reads to the worm genome

```
STAR_INDEX=/net/gs/vol4/shared/trapnelllab/genome569A/scRNAseq-pipeline/worm-genome/STAR-index

STAR --genomeDir $STAR_INDEX \
     --readFilesIn small_reads.fastq \
     --outFileNamePrefix example/ \
     --outSAMtype BAM Unsorted \
     --outSAMstrandField intronMotif
```

SAM