y quality

out the first few lines of the
`ty.fasta`

efers to gene 1 and i1 refers
e. This can become
ology assessment or

. An easy way to do this is to
ach correspond to a

`y.fasta`

ou can do this with the
hort job.

d and select

`Trinity.fasta`

editor (hint: `nano` works

`.job`
ou will see scores like contig

scriptome analyses. They are
d can be influenced by the
fter we do transcript
be more informative. Aside
re useful information about
these methods next.

at we used in the assembler
how well paired end reads
timate of how well our

t that is included in Trinity.

ill fill it out yourself. Leave
s and load the

```
target trinity_out_dir.Trinity.fasta \ --seqType fq \ --left data/wt_SRR1582651_1.fastq \ --right data/wt_SRR1582651_2.fastq \ --aligner bowtie --
```

en submit it.

ost of the output to the
files generated with

eads mapped. We will
bly with the script
l .

we will load the Trinity

```
bowtie_out/bowtie_out.
```

k at the log file. It should look

```
```

ned properly to the
ere 'improperly aligned'. This
ed up on different contigs.
gemented. In this case, this is
or this workshop. If we were
kely be much higher. A
ds properly mapped to the
t is possible that you should

nscripts

ased on the number of fully
is to BLAST the transcripts
use a reduced version of

CPUs and the default

```
fasta \
blastx.outfmt6 \
SLOTS -max_target_seqs
```

job and submit it.

outfmt6 . We will use the
script to generate a table
ipts that contain full length

the command line:

```
blastx.outfmt6 trinit
t.pep | column -t
```

```
elow
```

90 and 100% length, 17
mn is a cumulative number,
equence length.