Assemblies with newbler
and Illumina or Ion Torrent data

Using IonTorrent data with newbler

- IonTorrent data comes in sff file format
- shotgun sff files can be added the same way as 454 sff files
- mate pair data cannot be added as sff files, as newbler does not recognize the linker sequence
- I have prepared the mate pair files so that newbler understand them
- you will need a fasta file and a corresponding qual file. You only need to tell newbler the name of the fasta file, it will look for a qual file *in the same folder* and *with the same name* but ending in .qual
- have a look into these files, pay attention to the sequence headers
- see http://contig.wordpress.com/2011/01/21/newbler-input-ii-sequencing-reads-from-other-platforms/ for background information
- add these mate pair files before any shotgun or paired end files, and add the -p flag before the filename (forcing these to be treated as mate pairs):

```
runAssembly -o asm_name \
    -p path/to/matepair_read1.fasta \
    -p path/to/matepair_read2.fasta \
    path/to/other/file
```

Using Illumina data with newbler
- paired end fastq data can be read automatically by newbler, so you can just add those:

```
runAssembly -o asm_name \
    -p path/to/read1.fastq \
    -p path/to/read2.fastq
```

- mate pair data cannot be added as fastq files, but needs to be specially prepared
- I have prepared the mate pair files so that newbler understand them

- you will need a fasta file and a corresponding qual file. You only need to tell newbler the name of the fasta file, it will look for a qual file *in the same folder* and *with the same name* but ending in .qual
- have a look into these files, pay attention to the sequence headers
- see http://contig.wordpress.com/2011/01/21/newbler-input-ii-sequencing-reads-from-other-platforms/ for background information
- add these mate pair files before any shotgun or paired end files, and add the -p flag before the filename (forcing these to be treated as mate pairs):

```
runAssembly -o asm_name \
    -p path/to/matepair_read1.fasta \
    -p path/to/matepair_read2.fasta \
    path/to/other/file
```