**PAGIT Notes**

Must type before running:

source $HOME/appl\_taito/pagit/PAGIT/sourceme.pagit

**ABACAS**

Ref: *S. albulus* NK660 (CP007574.1)

(Removed plasmid from reference sequence first, manually)

perl $HOME/appl\_taito/pagit/PAGIT/ABACAS/abacas.pl

-r GCF\_000695235.1\_ASM69523v1\_genomic.fasta

-q ATCC\_31615.final.scaffolds.fasta

-p nucmer

-m

-b

-o ATCC\_31615

Combine (concatenate) mapped and unmapped reads for IMAGE

cat ATCC\_31615.fasta ATCC\_31615.contigsInbin.fas > mappedAndUnmapped.fasta

**IMAGE**

De-interleave ec reads first:

./deinterleave\_fastq.sh < *name*.fastq pairedReadsPart\_1.fastq pairedReadsPart\_2.fastq

(source: gist.github.com/nathanhaigh/3521724)

\* Files names must be as above!

Check each file has the same length (also interleaved file is x2):

expr $(cat name.fastq | wc -l) / 4

Run (as batch job):

perl $HOME/appl\_taito/pagit/PAGIT/IMAGE/image.pl

-scaffolds mappedAndUnmapped.fasta

-prefix pairedReadsPart

-iteration 1

-all\_iteration 3

-dir\_prefix ite

-kmer 91

Re-run with different kmers (separate batch jobs):

perl $HOME/appl\_taito/pagit/PAGIT/IMAGE/restartIMAGE.pl

ite3 71 3 partitioned

perl $HOME/appl\_taito/pagit/PAGIT/IMAGE/restartIMAGE.pl

ite6 51 3 partitioned

perl $HOME/appl\_taito/pagit/PAGIT/IMAGE/restartIMAGE.pl

ite9 31 3 partitioned

Re-scaffold (in ite12 folder):

perl $HOME/appl\_taito/pagit/PAGIT/IMAGE/contigs2scaffolds.pl

new.fa new.read.placed 300 0 scaffolds