**Code 1. Hybrid assembly using PacBio and Illumina sequence reads**

cd $project

####### PacBio read overlap

minimap2 -t 30 reads.fasta $project/pacbio/subreads.fasta.gz \

> reads.mappac1.paf

####### Contigs assembly draft

racon -t 30 $project /pacbio/subreads.fasta.gz reads.mappac1.paf reads.fasta \

> racon1.fasta

####### Base error correction 1

minimap2 -t 30 -ax sr racon1.fasta $project/PE450\_bfc\_correct\_trim.fq.gz \

> reads.2.sam

racon -t 30 $project/PE450\_bfc\_correct\_trim.fq.gz reads.2.sam racon1.fasta \

> racon2.fasta

####### Base error correction 2

minimap2 -t 30 -ax sr racon2.fasta $project/PE450\_bfc\_correct\_trim.fq.gz \

> reads.3.paf

racon -t 30 $project/PE450\_bfc\_correct\_trim.fq.gz reads.3.paf racon2.fasta \

> racon3.fasta

###### Contigs merge

cd $project/quickmerge

cut -d ' ' -f1 $project /racon/racon3.fasta > racon3.fasta

cut -d ' ' -f1 $project /minia\_k500/minia\_k500.unitigs.fa \

> minia\_k500.unitigs.fasta

nucmer -t 40 -l 100 -p out \

./racon3.fasta \

./minia\_k500.unitigs.fasta

delta-filter -r -q -l 10000 out.delta > out.rq.delta

quickmerge -d out.rq.delta \

-q ./minia\_k500.unitigs.fasta \

-r ./racon3.fasta \

-hco 5.0 -c 1.5 -l 10000 -ml 5000 -p out