**fastqc**

fastqc file1.fq

**fastx**

fastx\_quality\_stats -Q 33 -i file1.fq -o file1.xls

**trimmomatic**

trimmomatic PE 1.fq 2.fq p\_1.fq u\_1.fq p\_2.fq u\_2.fq ILLUMINACLIP:ADP.txt:2:30:10:8:TRUE SLIDINGWINDOW:4:15

**bwa**

bwa mem -t 9 Genome.fa p\_1.fq p\_2.fq | samtools view -b -o p.bam

bwa mem -t 9 Genome.fa u.fq | samtools view -b -o u.bam

**picard**

picard MergeSamFiles I=file\_p.bam I=file\_u.bam O=file.bam

picard SortSam I=file.bam O=file\_sorted.bam SO=coordinate

picard MarkDuplicates I=file\_sorted.bam O=file\_dedup.bam M=/metrics.txt

**mpileup**

bcftools mpileup -f Genome.fa file1.bam file2.bam file3.bam file4.bam | bcftools call -c -v --skip-variants indels -o file.vcf

**pcangsd**

pcangsd.py -plink file\_plink -kinship -threads 10 -e 1 -o file\_out

**FST**

vcftools --vcf file.vcf -—weir-fst-pop pop\_1.txt --weir-fst-pop pop\_2.txt --out out.txt

**smartpca**

smartpca -p P2\_pca.par

**fastsimcoal**

fsc26 -t file.tpl -n 500000 N 250000 -m -e file.est -M 0.001 -l 10 -L 100

**make a STRUCTURE file**

vcftools --vcf file.vcf --plink --out /file\_plink

plink -file file\_plink --allow-extra-chr --allow-no-sex --indep-pairwise 100 5 .5 --out file\_plink

plink -file file\_plink --allow-extra-chr --allow-no-sex --extract file.prune.in --make-bed --out file\_plink

plink -file file\_plink --allow-extra-chr --allow-no-sex --extract /file.prune.in --recode structure --out file.str

**vcfutils**

bcftools mpileup -f \_Genome.fa file.bam | bcftools call -c | vcfutils.pl vcf2fq -d 10 -D 100 | gzip > file.fq.gz

**fq2psmcfa**

fq2psmcfa -q20 file.fq.gz > file.psmcfa

**psmc**

psmc -N25 -t15 -r5 -p "4+25\*2+4+6" -o file.psmc file.psmcfa