genotyping with mpileup

Now that we have our reads aligned to a reference we can call genotypes for our samples

mpileup is an easy to use method for genotyping included in the samtools package

**Run mpileup on our read alignments (sorted bam files):**

```
run mpileup

#start and idev session if you haven't
idev

#copy over the exercise directory
cds
cd rad_intro/
cp -r
/work/02260/grovesd/lonestar/intro_to_rad_2017/genotyping/ddRAD_mpileup .
cd ddRAD_mpileup/

#index the reference for samtools
module load samtools
samtools faidx stickleback_chrom3.fasta

#make a list of the bam files
ls *.bam > my_bamfiles.txt

#run mpileup
samtools mpileup -f stickleback_chrom3.fasta -t DP,AD,ADF,ADR,SP -u -b
my_bamfiles.txt > mpileup_results.bcf

#now call genotypes from the mpileup results
bcftools call -vmO v -o raw_calls.vcf mpileup_results.bcf
```

Quality filter the variant calls:
quality filter variants

# use vcftools to get information about our variant set
vcftools --vcf raw_calls.vcf

# returns this:
  VCFtools - 0.1.15
  (C) Adam Auton and Anthony Marcketta 2009

  Parameters as interpreted:
  --vcf raw_calls.vcf

  After filtering, kept 3 out of 3 Individuals
  After filtering, kept 14117 out of a possible 14117 Sites

# now quality filter the raw calls
bcftools filter --exclude 'QUAL < 30' raw_calls.vcf | bcftools view > qced_calls.vcf

# check the new quality checked vcf
vcftools --vcf qced_calls.vcf