Zea Mays SNP Calling

We sequenced three lines of *zea mays*, using paired-end sequencing. This sequencing was done by our sequencing core and we received the data on 2013-05-10. Each variety should have **two** sequences files, with suffixes `_R1.fastq` and `_R2.fastq`, indicating which member of the pair it is.

Sequencing Files

All raw FASTQ sequences are in `data/seqs/`:

```
$ find data/seqs -name "*.fastq"
data/seqs/zmaysA_R1.fastq
data/seqs/zmaysA_R2.fastq
data/seqs/zmaysB_R1.fastq
data/seqs/zmaysB_R2.fastq
data/seqs/zmaysC_R1.fastq
data/seqs/zmaysC_R2.fastq
```

Quality Control Steps

After the sequencing data was received, our first stage of analysis was to ensure the sequences were high quality. We ran each of the three lines' two paired-end FASTQ files through a quality diagnostic and control pipeline. Our planned pipeline is:

1. Create base quality diagnostic graphs.
2. Check reads for adapter sequences.
3. Trim adapter sequences.
4. Trim poor quality bases.

Recommended trimming programs:

- Trimmomatic
- Scythe