```
#!/bin/bash

# location of GenomeAnalysisTK.jar
GATK=/path/to/GenomeAnalysisTK.jar
# commands for BWA and Samtools
BWA=bwa
SAMTOOLS=samtools
# path/command for assemble-multiple.py
ASSEMBLE=/path/to/assemble-multiple.py

# locations of FASTA and GFF reference data -- note that your file
name may vary
FASTA=/path/to/A_nidulans_FGSC_A4_version_sXX-mYY-
rZZ_chromosomes.fasta
FEATURES=/path/to/asp_features_sXX-mYY-rZZ.gff

# index the file

if [ ! -f $FASTA.ann ]; then
    $BWA index -a bwtsw $FASTA
fi

# Assemble each of multiple genomes

for SEQ in $(ls *.txt)
do
    echo "SEQ IS" $SEQ
    # check that it hasn't already been done
    if [ ! -f $SEQ.trim.snps.vcf ];
        then
        PREF=$SAVE_LOCATION/$SEQ.trim
        if [ ! -f $SEQ.trim.sam ] && [ ! -f $PREF.sorted.bam ];
            then
                # cut off adapters
            if [ ! -f $PREF ];
                        then
                        $ASSEMBLE $SEQ 1.2 > $PREF
                fi

        # BWA alignment
        if [ ! -f $PREF.sai ]
            then
             $BWA aln -t 1 -o 5 -O 3 $FASTA $PREF > $PREF.sai
        fi

        $BWA samse -r '@RG\tID:1\tSM:1\tPL:ILLUMINA' $FASTA $PREF.sai
$PREF > $PREF.sam
             rm -rf $PREF
    fi
```

```
    if [ -f $PREF.sam ] && [ ! -f $PREF.sorted.bam ];
         then
        # $SAMTOOLS indexing
        echo "$SAMTOOLS view -bS"
        $SAMTOOLS view -bS $PREF.sam > $PREF.bam
        echo "$SAMTOOLS sort"
        $SAMTOOLS sort $PREF.bam $PREF.sorted
        echo "samtols index"
        $SAMTOOLS index $PREF.sorted.bam
        fi
        if [ ! -f $PREF.realign ];
         then
        # indel realignment
        echo "java -Xmx3g -jar $GATK -I $PREF.sorted.bam -R $FASTA -T
RealignerTargetCreator -o $PREF.intervals"
        java -Xmx3g -jar "$GATK" -I $PREF.sorted.bam -R $FASTA -T
RealignerTargetCreator -o $PREF.intervals -
allowPotentiallyMisencodedQuals
        java -Xmx3g -jar "$GATK" -I $PREF.sorted.bam -R $FASTA -T
IndelRealigner --targetIntervals $PREF.intervals -o $PREF.realign.bam
-allowPotentiallyMisencodedQuals
        fi
        if [ -f $PREF.realign.bam ] && [ ! -f $PREF.sorted.bam ];
         then
        echo "$SAMTOOLS sort"
        $SAMTOOLS sort $PREF.realign.bam $PREF.sorted
        echo "$SAMTOOLS index"
        $SAMTOOLS index $PREF.sorted.bam
        fi
    # Call SNPs
    java -Xmx3g -jar "$GATK" -I $PREF.sorted.bam -R $FASTA -T
UnifiedGenotyper -o $PREF.snps.vcf -stand_call_conf 50.0 -
stand_emit_conf 10.0 -dcov 50 -allowPotentiallyMisencodedQuals

    rm -rf *.trim *.idx *.intervals *.realign* $PREF.bam* *.bam
fi
done
```