

Additional File S5: Pipeline commands

Pre-Processing

Indel Realignment:

```
${JAVADIR}java -Xmx3g -jar ${GATK}GenomeAnalysisTK.jar \  
-T RealignerTargetCreator \  
-R ${reference} \  
-I ${temp}${region}.bam \  
-known ${dbSNP_work} \  
-o ${temp}${region}.RTCintervals.list \  
-L ${region} \  
-l INFO \  
-log ${log}${region}.RealignerTargetCreator.log
```

```
${JAVADIR}java -Xmx3g -jar ${GATK}GenomeAnalysisTK.jar \  
-T IndelRealigner \  
-R ${reference} \  
-I ${temp}${region}.bam \  
-targetIntervals ${temp}${region}.RTCintervals.list \  
-known ${dbSNP_work} \  
-L ${region} \  
--consensusDeterminationModel USE_SW \  
-o ${temp}${region}.realigned.bam \  
-l INFO \  
-log ${log}${region}.IndelRealigner.log
```

Base Quality Score Recalibration:

```
{JAVADIR}java -Xmx3g -jar {GATK}GenomeAnalysisTK.jar \  
-T BaseRecalibrator \  
-R {reference} \  
-L {region} \  
-I {temp}{region}.realigned.bam \  
-knownSites {dbSNP_work} \  
-o {temp}{region}.realigned.grp \  
-l INFO
```

```
{JAVADIR}java -Xmx3g -jar {GATK}GenomeAnalysisTK.jar \  
-T BaseRecalibrator \  
-R {reference} \  
-L {region} \  
-I {temp}{region}.realigned.bam \  
-BQSR {temp}{region}.realigned.grp \  
-knownSites {dbSNP_work} \  
-o {temp}{region}.realigned.recal.grp \  
-l INFO
```

```
{JAVADIR}java -Xmx3g -jar {GATK}GenomeAnalysisTK.jar \  
-T PrintReads \  
-R {reference} \  
-L {region} \  
-I {temp}{region}.realigned.bam \  
-BQSR {temp}{region}.realigned.grp \  
-o {temp}{region}.realigned.recal.bam \  
-l INFO \  
-log {log}{region}.realigned.recal.bam.log
```

Variant Calling

Unified Genotyper:

```
{JAVADIR}java -Xmx3g -jar {GATK}GenomeAnalysisTK.jar \  
-T UnifiedGenotyper \  
-R {reference} \  
-L {region} \  
-I {temp}{region}.bam \  
-o {results}{region}.UG.raw.vcf \  
--dbsnp dbSNP_work \  
-out_mode EMIT_VARIANTS_ONLY \  
-stand_call_conf 30.0 \  
-stand_emit_conf 30.0 \  
--genotype_likelihoods_model BOTH \  
-l INFO \  
-log {log}{region}.UnifiedGenotyper.log
```

Haplotype Caller:

```
{JAVADIR}java -Xmx3g -jar {GATK}GenomeAnalysisTK.jar \  
-T HaplotypeCaller \  
-R {reference} \  
-L {region} \  
-I {temp}{region}.bam \  
--dbsnp dbSNP_work \  
-stand_call_conf 30.0 \  
-stand_emit_conf 30.0 \  
-o {results}{region}.HC.raw.vcf \  
-l INFO \  
-log {log}{region}.HaplotypeCaller.log
```

Samtools:

```
{SAMTOOLS}samtools mpileup -f {reference} -r {region} -A -C50 -E -D -S -u {temp}{region}.bam | \  
{BCFTOOLS}bcftools view -cvgb - > {temp}{region}.raw.bcf 2> {temp}{region}.raw.bcf.log  
{BCFTOOLS}bcftools view {temp}{region}.raw.bcf | {vcfutils} varFilter -D800 - > {results}{region}.flt.vcf
```

Platypus:

```
python ${platypus}Platypus.py callVariants --refFile=${reference} --bamFiles=${temp}${region}.bam --output=${results}${region}.platypus.vcf
```