software	purpose	command
picard	regenerate fastq files from BAM file aligned to hg18	`java -d64 -Xmx4g -jar SamToFastq.jar I=$pfx.bam F=$pfx.1.fastq F2=$pfx.2.fastq 2>&1`
bwa	align fastq files to hg19	`bwa aln -q 30 -t 8 $hgReference $fastq > $fastq.aln.sai`
bwa, samtools	convert aligned fastq files into new BAM file	`bwa sampe -a 600 -P -r "$RG" $hgReference $fastq1.aln.sai $fastq2.aln.sai $fastq1 $fastq2 | samtools view -bSh -o $outprefix.bam -`
samtools	sort and index new BAM file	`samtools sort -@ 16 $outprefix.bam $outprefix.sorted 2, samtools index $outprefix.sorted.bam 2`
samtools	remove duplicate reads from BAM files	`samtools rmdup ../$tumorpfx/$tumorpfx.out.sorted.bam $tumorpfx.dedup.bam`
GATK	indel realignment	`java -d64 -jar $gatkJar -R $hgReference -T IndelRealigner -rf BadCigar -I $tumorpfx.dedup.bam -known $G1000.Mills -known $G1000.Phase1.Indels -targetIntervals $tumorpfx.intervals -o $tumorpfx.realn.bam`
GATK	base recalibration	`java -d64 -jar $gatkJar -nct 8 -T BaseRecalibrator -rf BadCigar -I $tumorpfx.realn.bam -R $hgReference -knownSites $dbSNP -o $tumorpfx.recal.grp`
samtools	index recalibrated BAM file	`samtools index $tumorpfx.realn.recal.bam`
SomaticSniper	call somatic mutations, generate VCF	`bam-somaticsniper -q 40 -Q 40 -J -s 0.001 -F vcf -f $hgReference $tumorbam $normalbam $tumorpfx.SS.vcf`