**Permanent files:**

**Step1.1 Quality Statistics generation and bad read filtering**

* \*\_stat
* \*.html,
* 6 plots for each fastq file\*\_avgQual.png, \*\_baseCompostion.png, \*\_QualRangePerBase.png, \*\_ gcDistribution.png, \*\_ qualDistribution.png, \*\_ QualRangePerBase.png,
* \*\_summary.png (summary plot)

**Step 1.2 Quality based trimming of filtered files**

* read1.fastq\_filtered\_trimmed
* read2.fastq\_filtered\_trimmed

**Step3.1: Picard SortSam.jar**

* aln.bam
* aln.bai

**Step3.5: Base Quality Recalibration Print Reads**

* realigned\_BQSR.bam
* realigned\_BQSR.bai

**Step 3.6: Picard CollectAlignmentSummaryMetrics**

* Metricsfile.txt

**Step4.1: SNP detection**

* SNP.vcf

**Step4.2: Adding dbSNP ID**

* output.vcf
* output.vcf.idx

**Step5: Calling Indels from paired Tumor and Normal samples**

* indels.vcf
* indels.vcf.idx