

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:35:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251054.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10251054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:35:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,395,790
Mapped reads	3,263,184 / 96.09%
Unmapped reads	132,606 / 3.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,203 / 0.89%
Read min/max/mean length	30 / 80 / 80.32
Duplicated reads (estimated)	789,591 / 23.25%
Duplication rate	21.43%
Clipped reads	444,120 / 13.08%

2.2. ACGT Content

Number/percentage of A's	75,008,918 / 29.56%
Number/percentage of C's	50,149,443 / 19.76%
Number/percentage of T's	75,660,598 / 29.82%
Number/percentage of G's	52,911,754 / 20.85%
Number/percentage of N's	19,710 / 0.01%
GC Percentage	40.62%

2.3. Coverage

Mean	0.082

Standard Deviation	0.9163
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2.4. Mapping Quality

Mean Mapping Quality	48.21
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2.5. Mismatches and indels

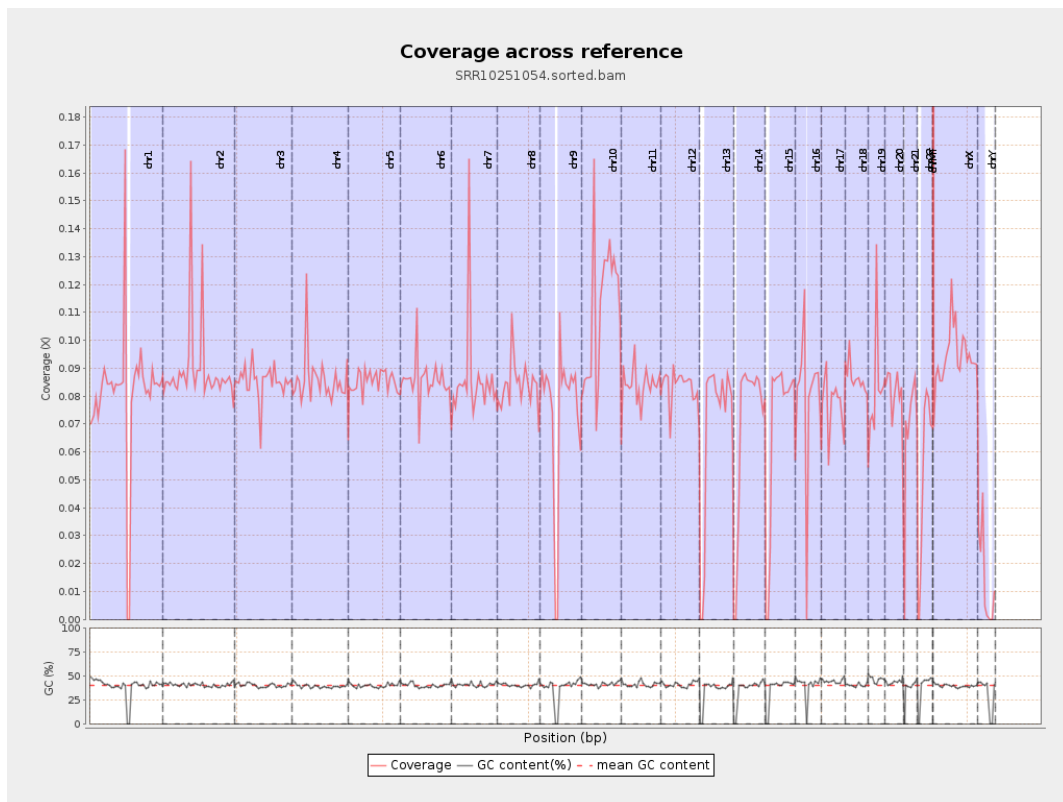
General error rate	0.62%
Mismatches	1,517,236
Insertions	32,187
Mapped reads with at least one insertion	0.97%
Deletions	89,574
Mapped reads with at least one deletion	2.7%
Homopolymer indels	45.56%

2.6. Chromosome stats

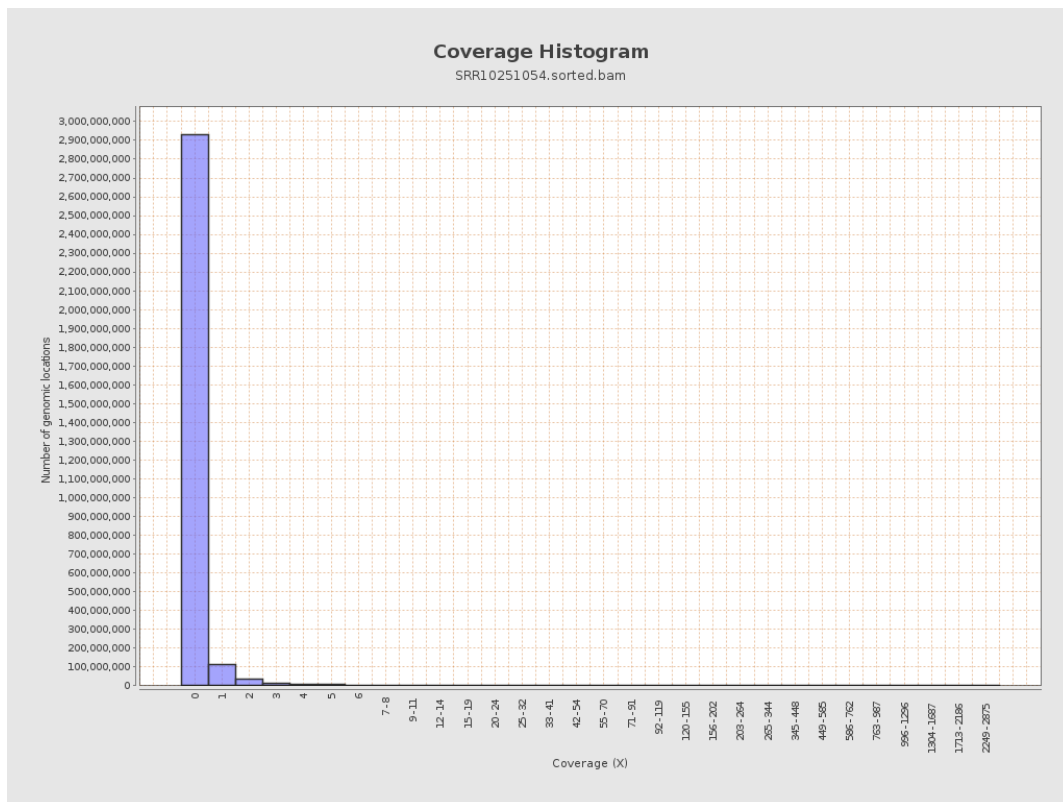
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20178966	0.081	1.9689
chr2	243199373	21786414	0.0896	1.0219
chr3	198022430	16883755	0.0853	0.4193
chr4	191154276	16456135	0.0861	0.4887
chr5	180915260	15430436	0.0853	0.4289
chr6	171115067	14649106	0.0856	0.5286
chr7	159138663	13678027	0.086	1.3412

chr8	146364022	12293644	0.084	0.639
chr9	141213431	10565075	0.0748	0.9494
chr10	135534747	14958501	0.1104	0.936
chr11	135006516	11325796	0.0839	0.5849
chr12	133851895	11189423	0.0836	0.4253
chr13	115169878	7949941	0.069	0.3698
chr14	107349540	7583658	0.0706	0.6237
chr15	102531392	7007680	0.0683	0.3672
chr16	90354753	7085116	0.0784	0.6731
chr17	81195210	6318343	0.0778	0.5097
chr18	78077248	6754850	0.0865	1.1174
chr19	59128983	4930372	0.0834	1.9122
chr20	63025520	5121073	0.0813	0.4551
chr21	48129895	3299919	0.0686	0.423
chr22	51304566	2715354	0.0529	0.3365
chrMT	16571	278656	16.8159	9.1823
chrX	155270560	14638683	0.0943	0.5098
chrY	59373566	830812	0.014	0.7525

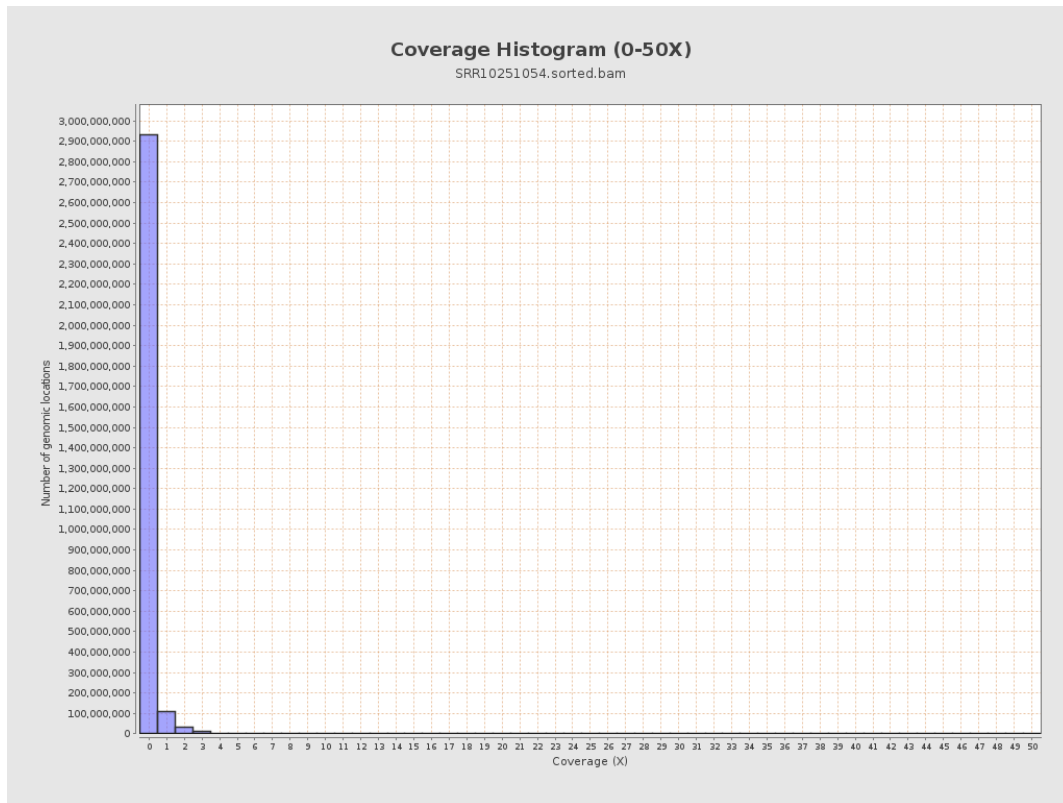
3. Results : Coverage across reference



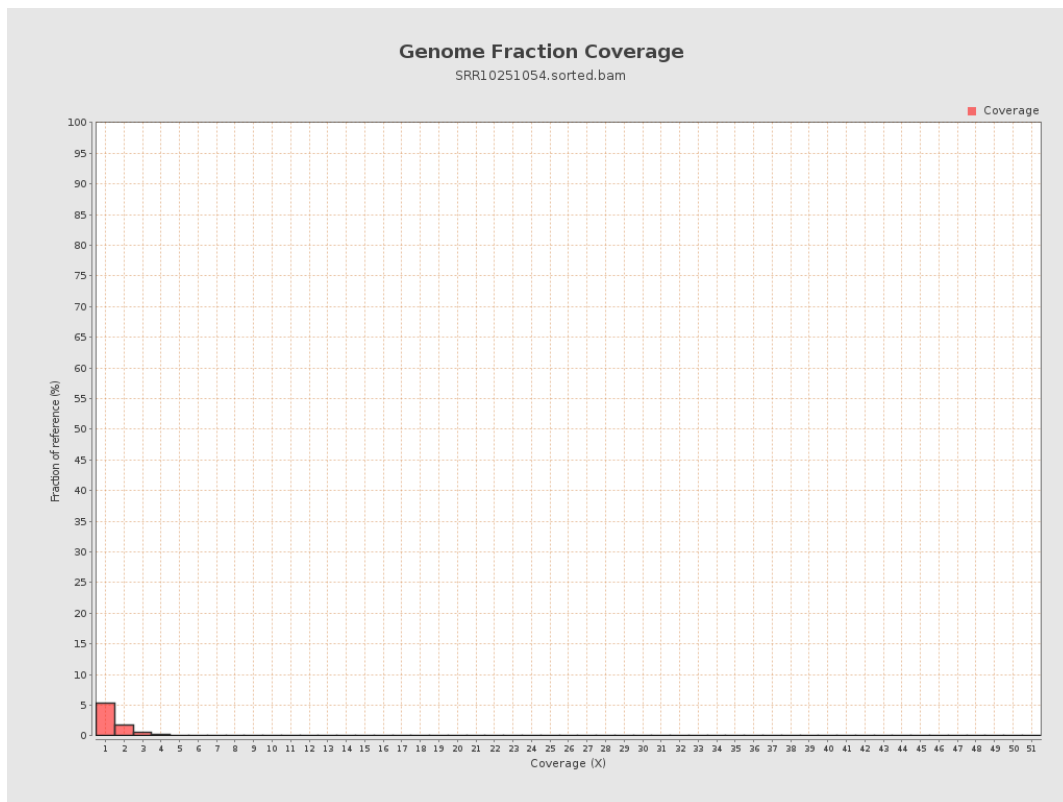
4. Results : Coverage Histogram



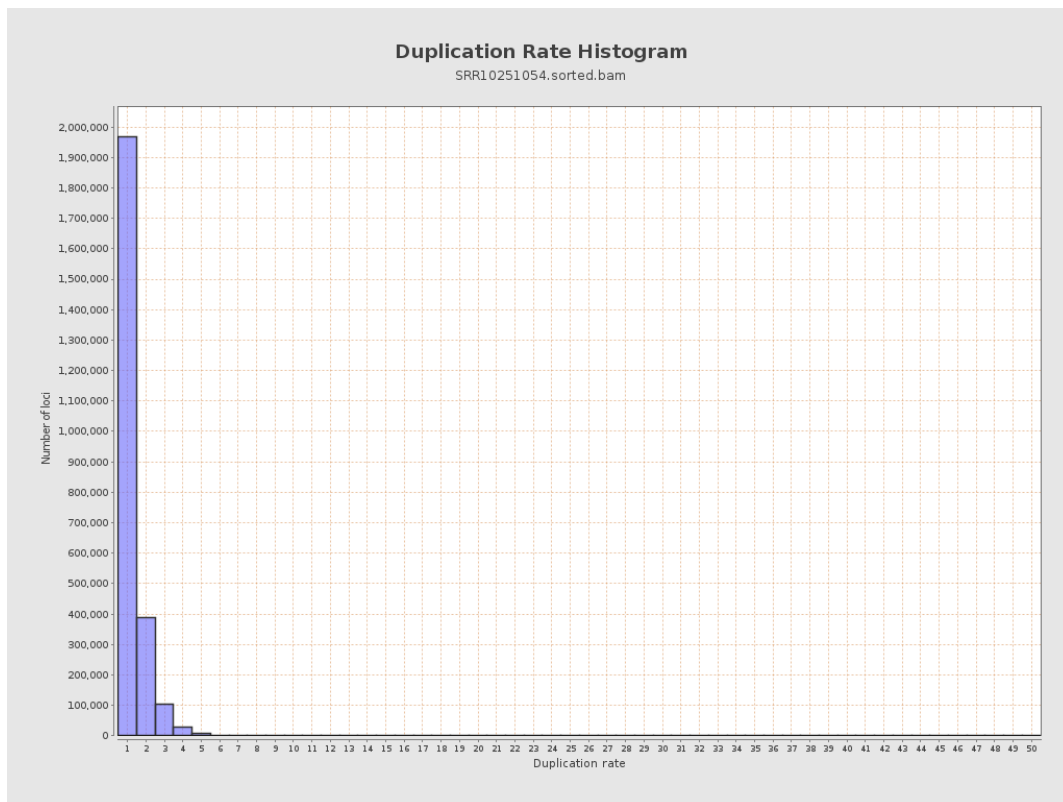
5. Results : Coverage Histogram (0-50X)



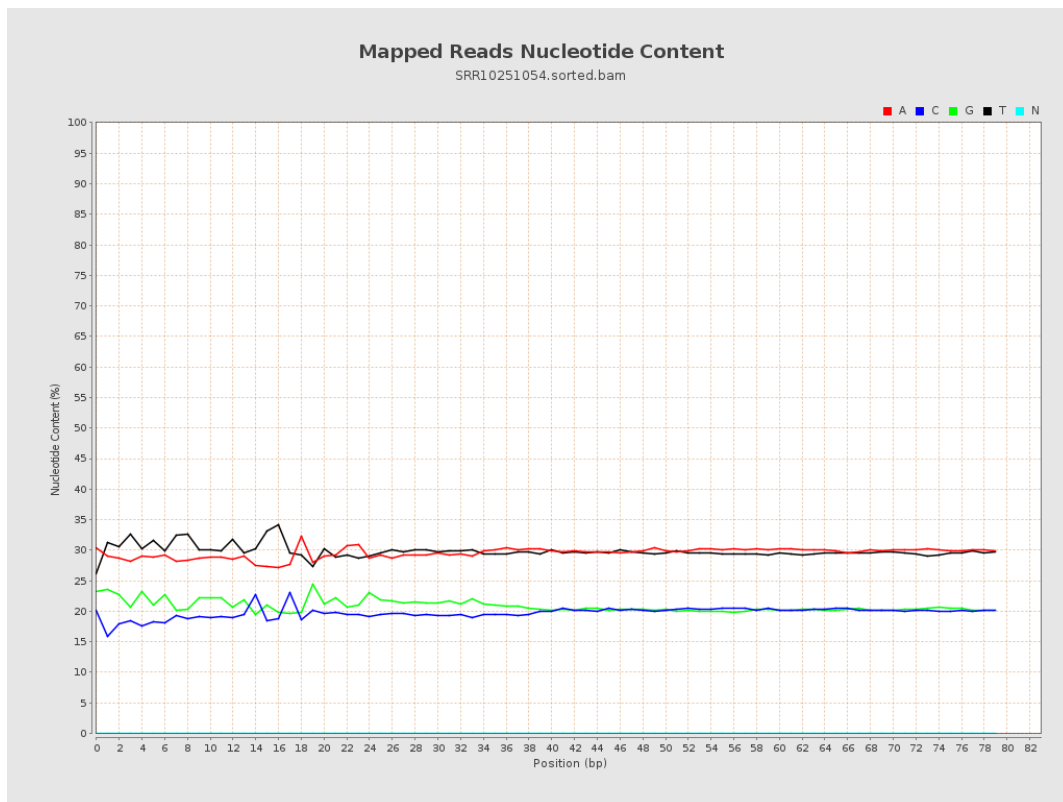
6. Results : Genome Fraction Coverage



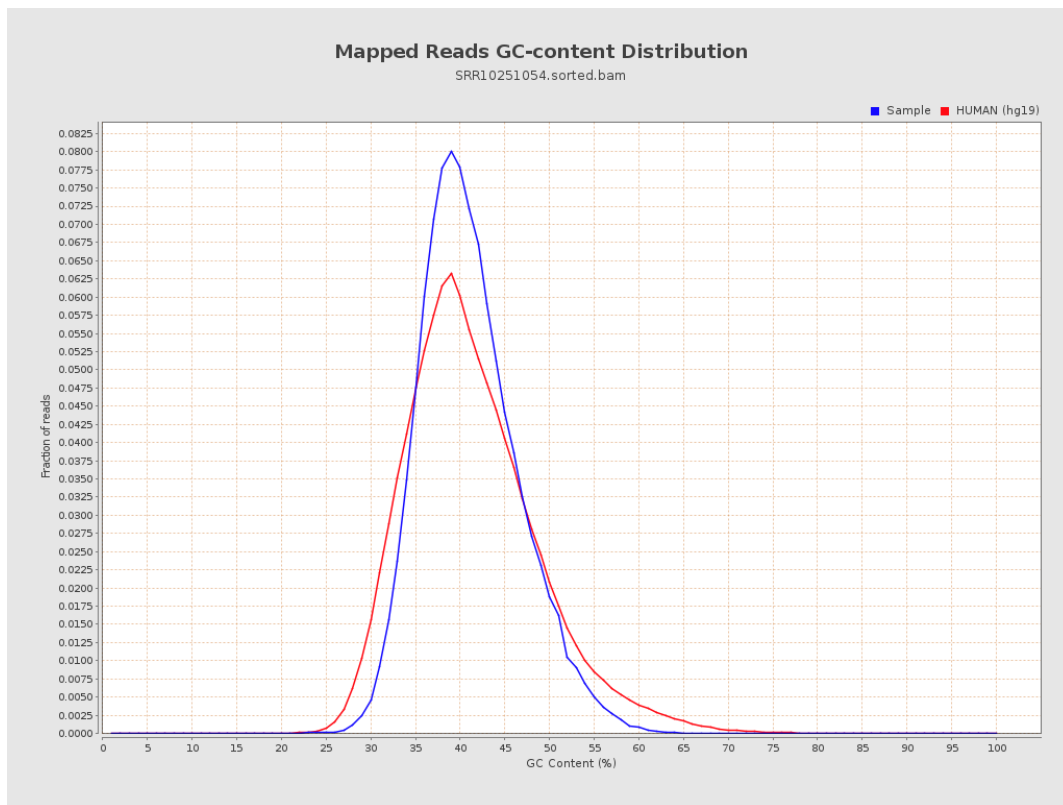
7. Results : Duplication Rate Histogram



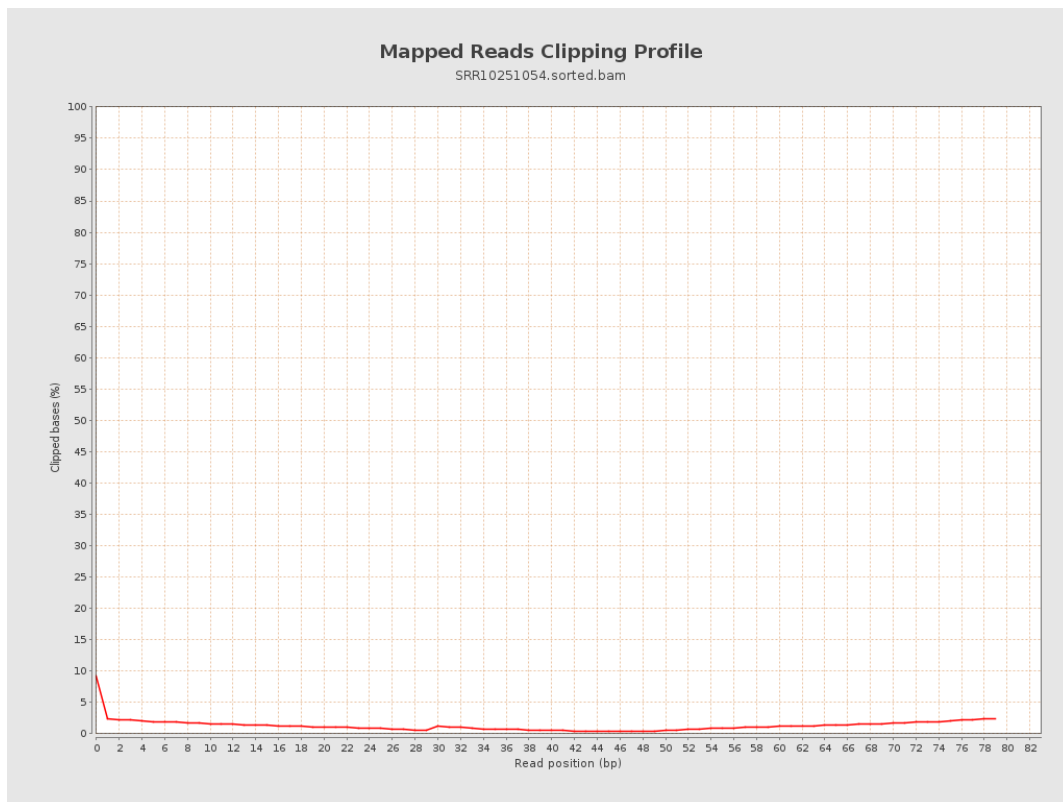
8. Results : Mapped Reads Nucleotide Content



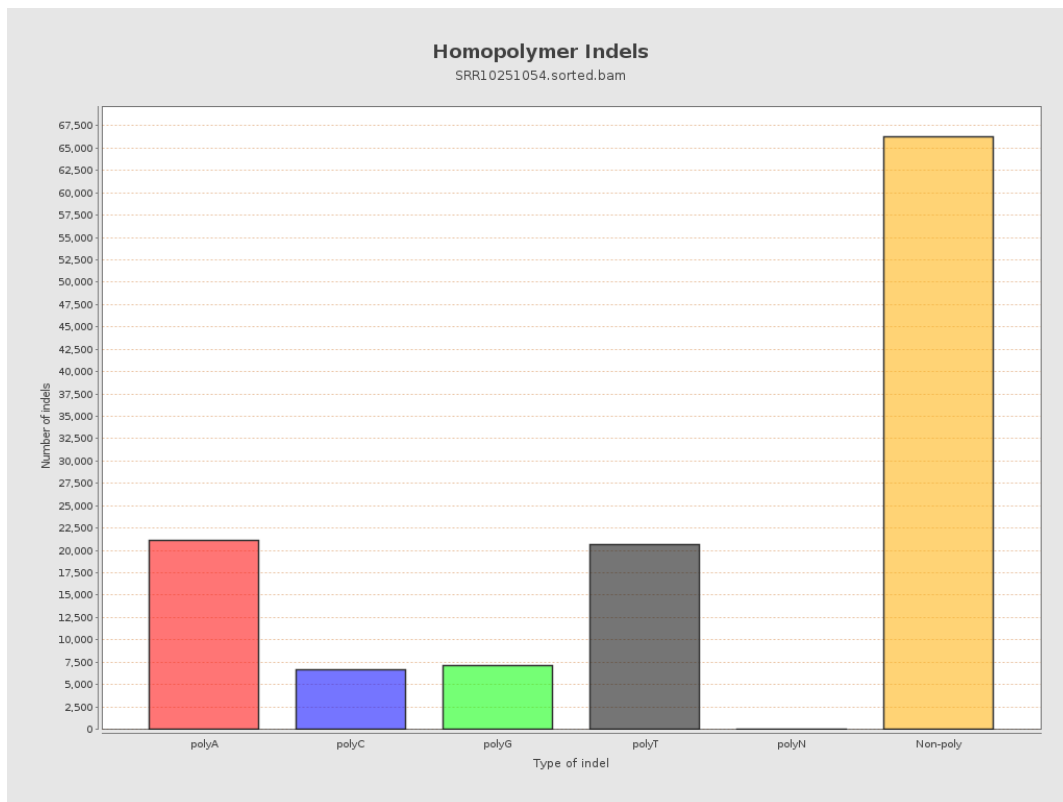
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

