

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:51:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240194.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_SRR6240194 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240194.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:51:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240194.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,519,363
Mapped reads	1,975,883 / 78.43%
Unmapped reads	543,480 / 21.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,472 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	210,350 / 8.35%
Duplication rate	8.84%
Clipped reads	1,353,783 / 53.74%

2.2. ACGT Content

Number/percentage of A's	31,883,920 / 26.58%
Number/percentage of C's	20,777,023 / 17.32%
Number/percentage of T's	39,370,582 / 32.82%
Number/percentage of G's	27,912,808 / 23.27%
Number/percentage of N's	26,996 / 0.02%
GC Percentage	40.58%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3701
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2.4. Mapping Quality

Mean Mapping Quality	44.89
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2.5. Mismatches and indels

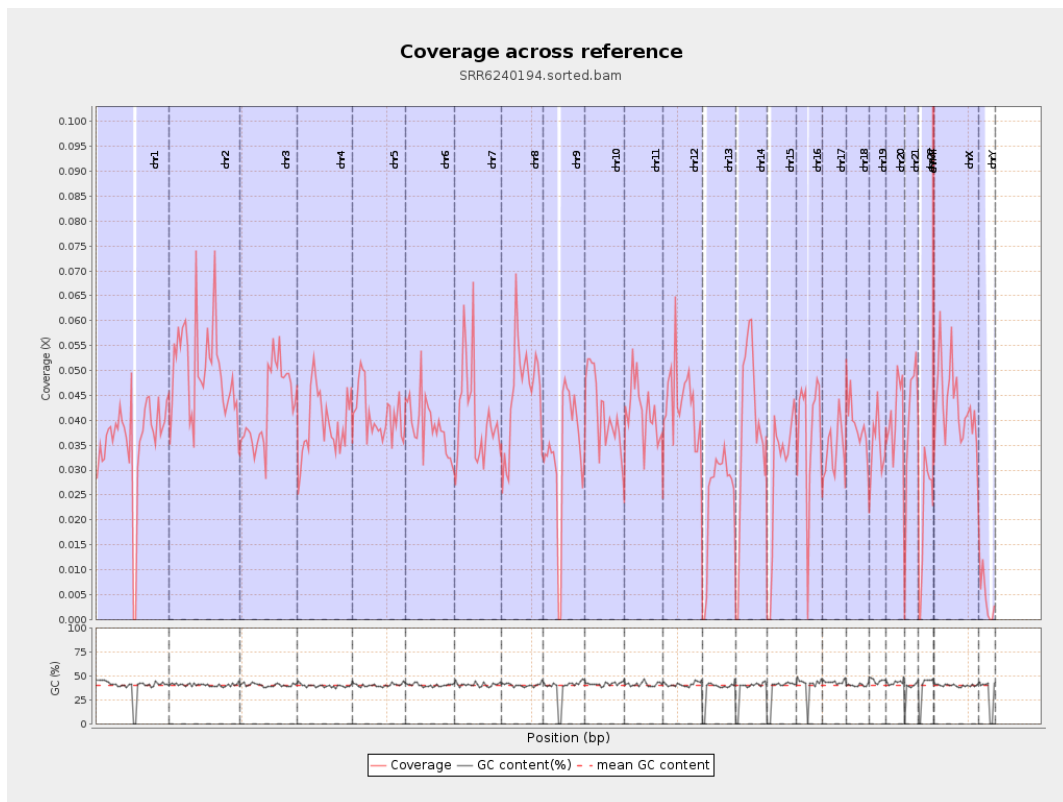
General error rate	0.95%
Mismatches	1,126,617
Insertions	8,347
Mapped reads with at least one insertion	0.42%
Deletions	38,283
Mapped reads with at least one deletion	1.91%
Homopolymer indels	48.04%

2.6. Chromosome stats

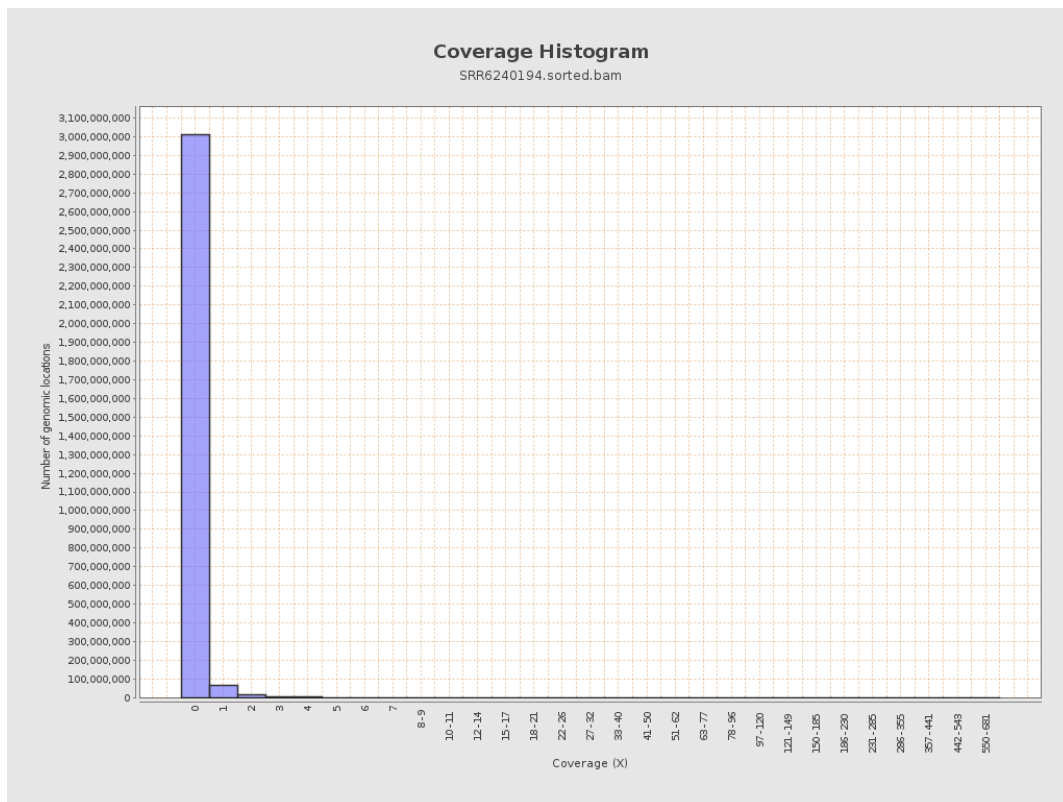
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8938912	0.0359	0.5326
chr2	243199373	12148589	0.05	0.4939
chr3	198022430	8484979	0.0428	0.273
chr4	191154276	7505243	0.0393	0.2736
chr5	180915260	7432463	0.0411	0.2713
chr6	171115067	6634786	0.0388	0.3234
chr7	159138663	6537305	0.0411	0.593

chr8	146364022	6646158	0.0454	0.435
chr9	141213431	4765859	0.0337	0.352
chr10	135534747	5678918	0.0419	0.3135
chr11	135006516	5594216	0.0414	0.3737
chr12	133851895	5837595	0.0436	0.2797
chr13	115169878	2834045	0.0246	0.2053
chr14	107349540	4130996	0.0385	0.2747
chr15	102531392	3057706	0.0298	0.2603
chr16	90354753	3423041	0.0379	0.2639
chr17	81195210	2739310	0.0337	0.2689
chr18	78077248	3068059	0.0393	0.5515
chr19	59128983	2085854	0.0353	0.3884
chr20	63025520	2564682	0.0407	0.2695
chr21	48129895	1919466	0.0399	0.2757
chr22	51304566	1069311	0.0208	0.1847
chrMT	16571	36617	2.2097	2.5203
chrX	155270560	6639423	0.0428	0.3048
chrY	59373566	263198	0.0044	0.0923

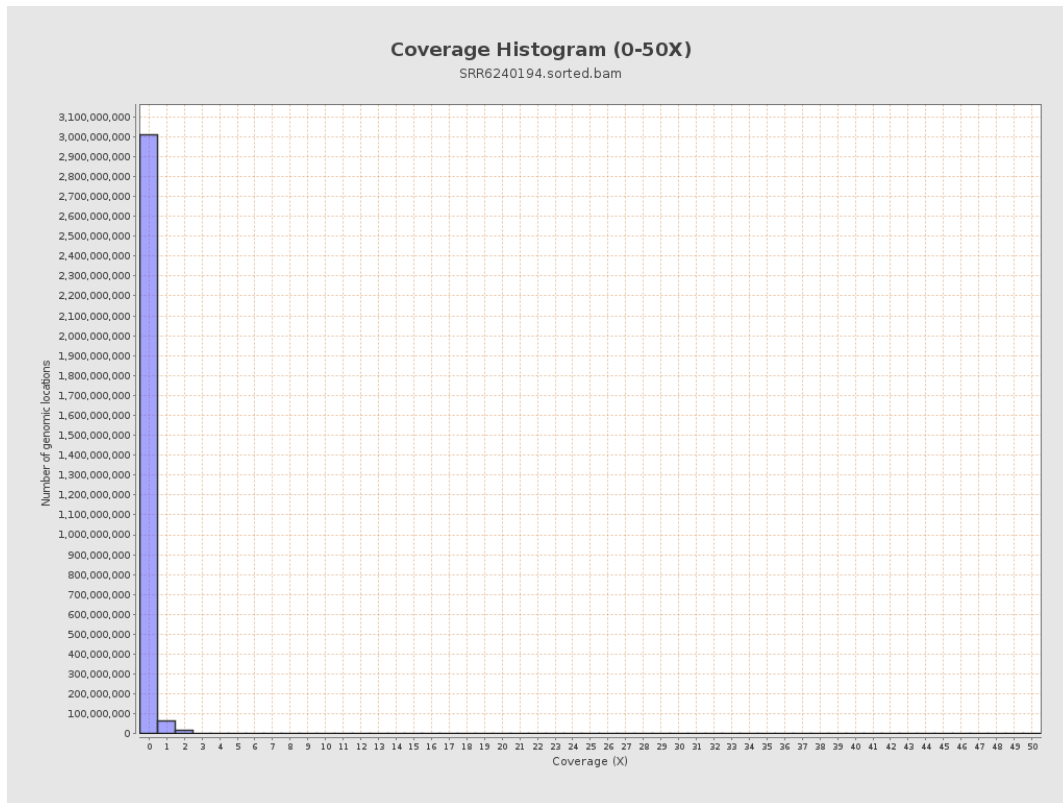
3. Results : Coverage across reference



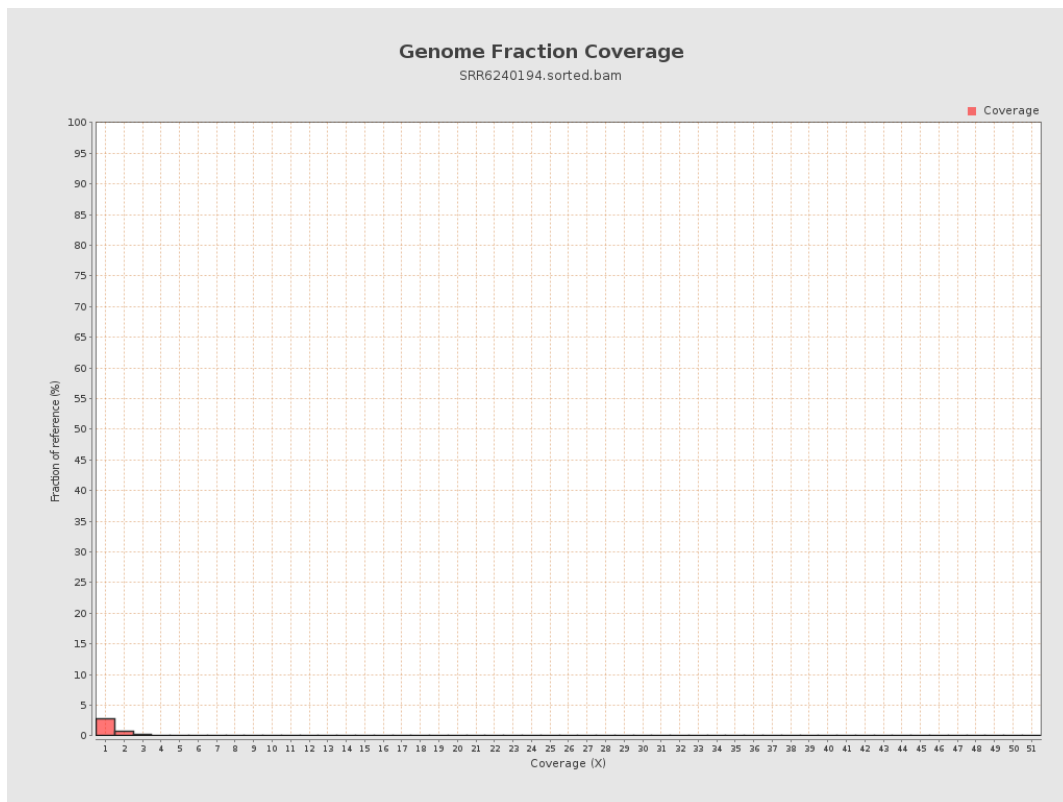
4. Results : Coverage Histogram



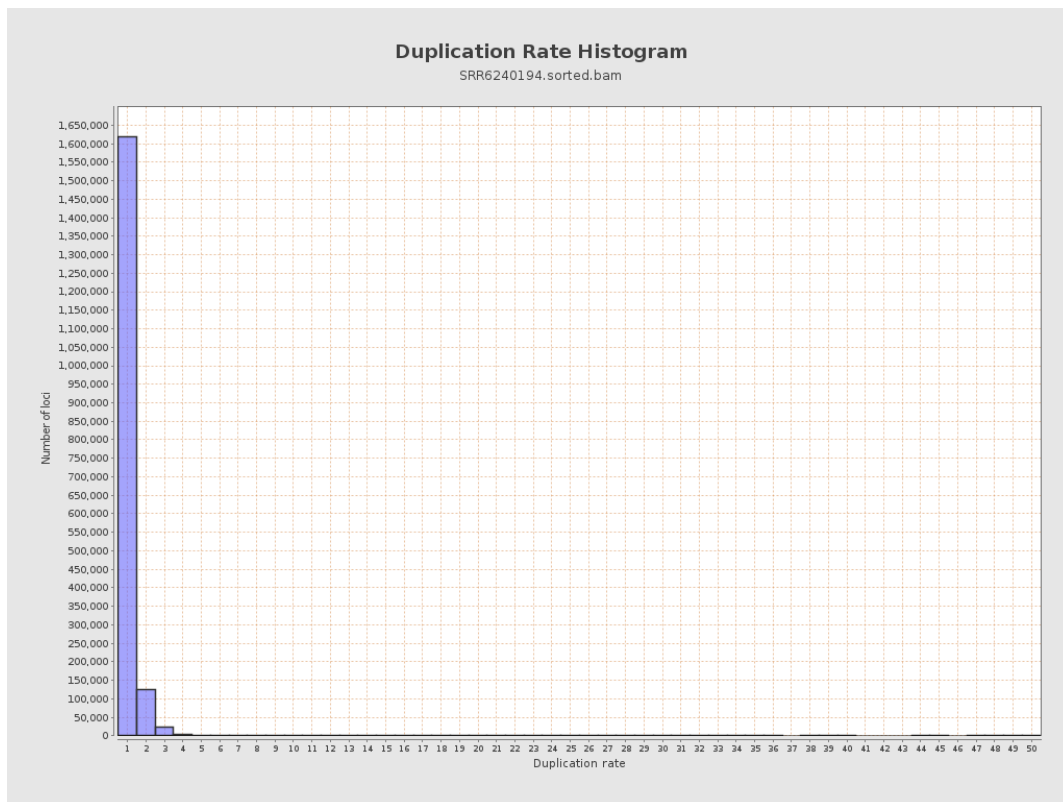
5. Results : Coverage Histogram (0-50X)



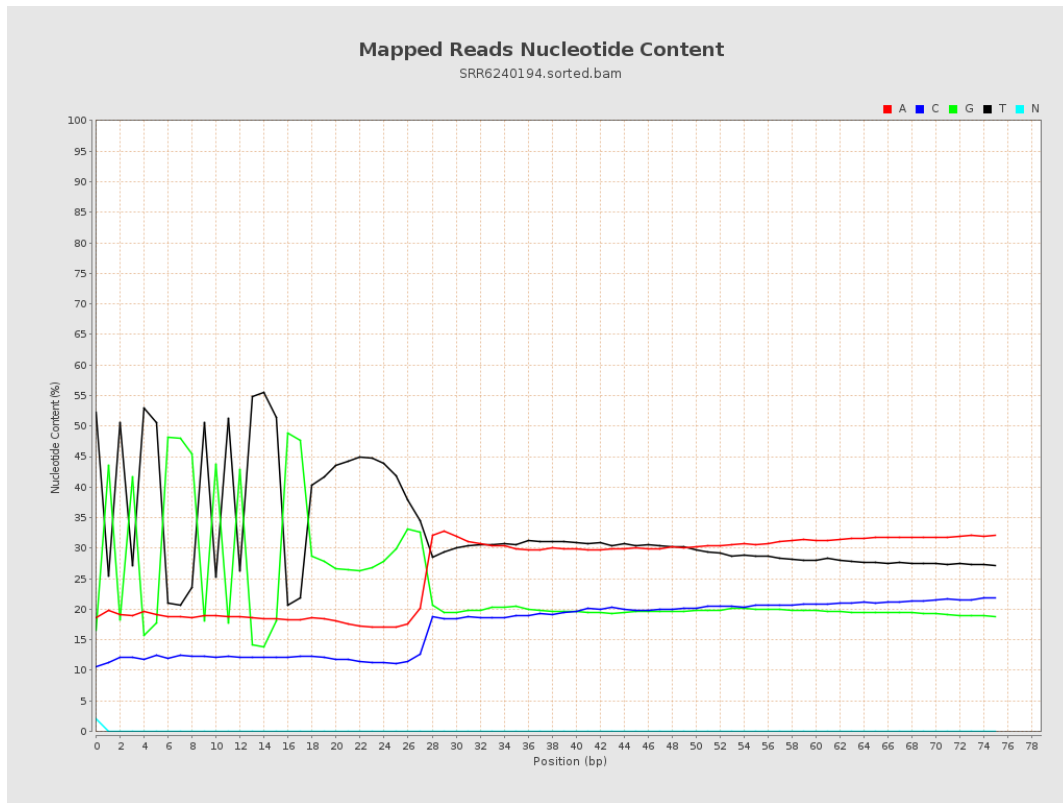
6. Results : Genome Fraction Coverage



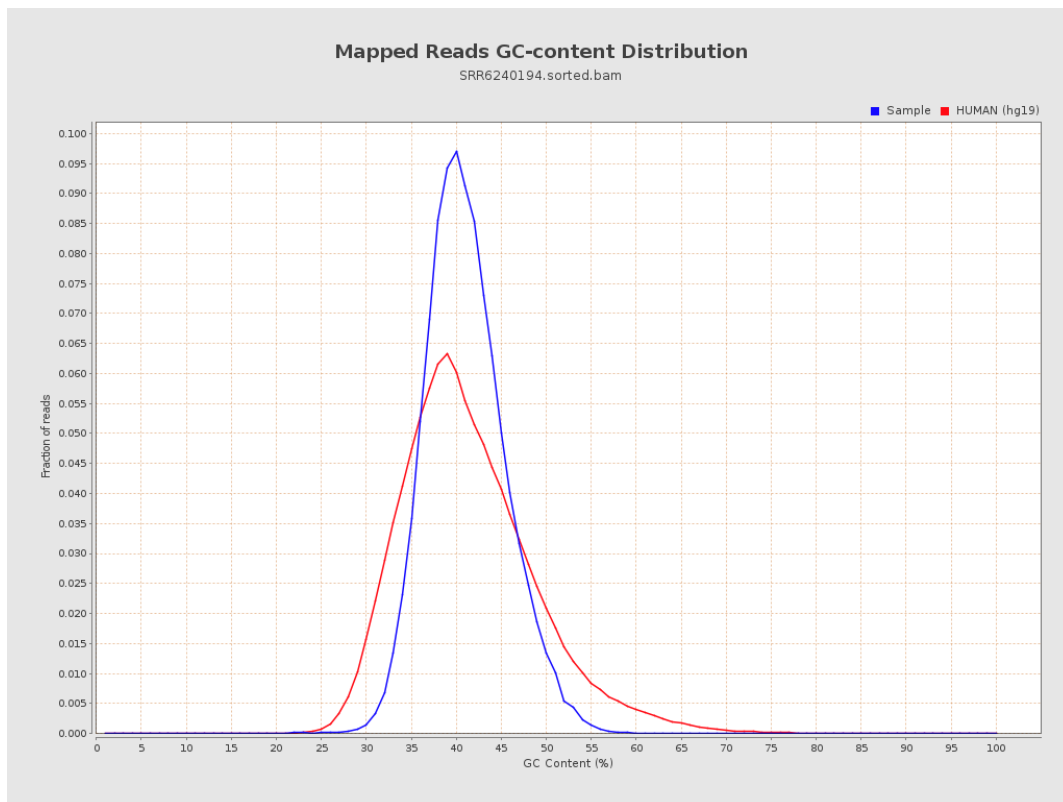
7. Results : Duplication Rate Histogram



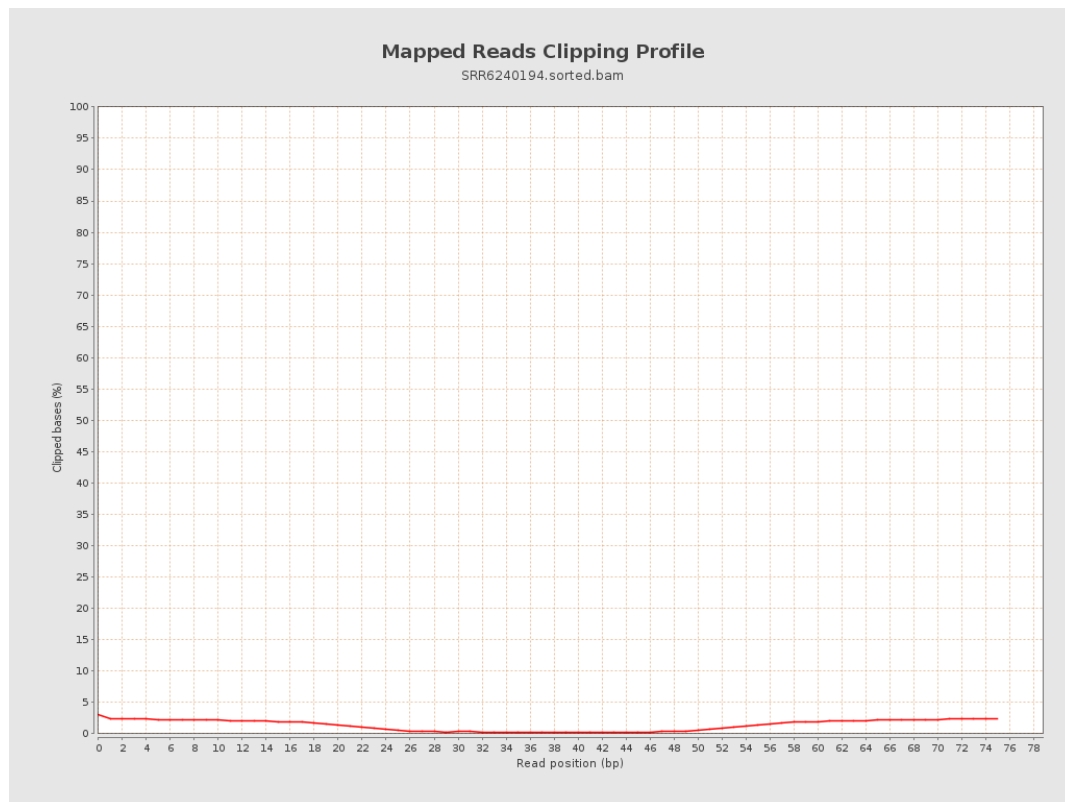
8. Results : Mapped Reads Nucleotide Content



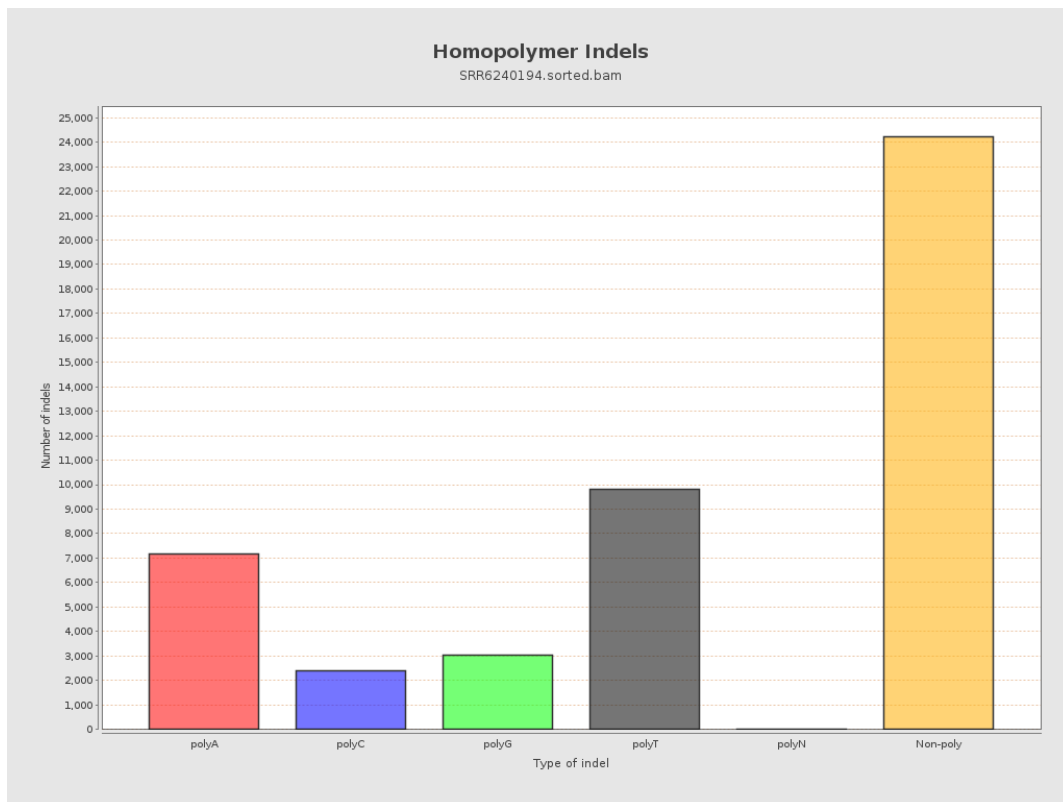
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

