

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:28:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240037.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_SRR6240037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240037.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:28:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,046,070
Mapped reads	1,652,192 / 80.75%
Unmapped reads	393,878 / 19.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,646 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	115,446 / 5.64%
Duplication rate	5.66%
Clipped reads	1,140,065 / 55.72%

2.2. ACGT Content

Number/percentage of A's	26,528,997 / 26.37%
Number/percentage of C's	16,910,159 / 16.81%
Number/percentage of T's	32,699,573 / 32.5%
Number/percentage of G's	24,403,403 / 24.26%
Number/percentage of N's	63,561 / 0.06%
GC Percentage	41.06%

2.3. Coverage

Mean	0.0325

Standard Deviation	0.3134
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2.4. Mapping Quality

Mean Mapping Quality	44.14
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2.5. Mismatches and indels

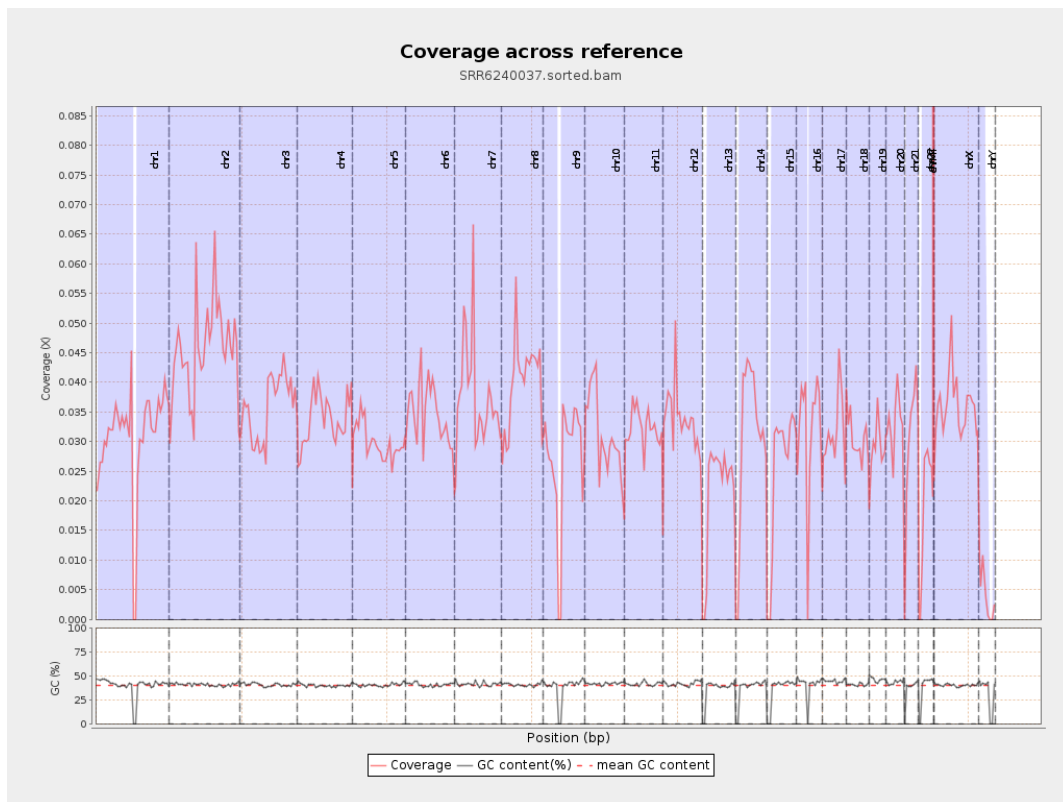
General error rate	1.01%
Mismatches	1,003,797
Insertions	7,347
Mapped reads with at least one insertion	0.44%
Deletions	32,972
Mapped reads with at least one deletion	1.97%
Homopolymer indels	49.8%

2.6. Chromosome stats

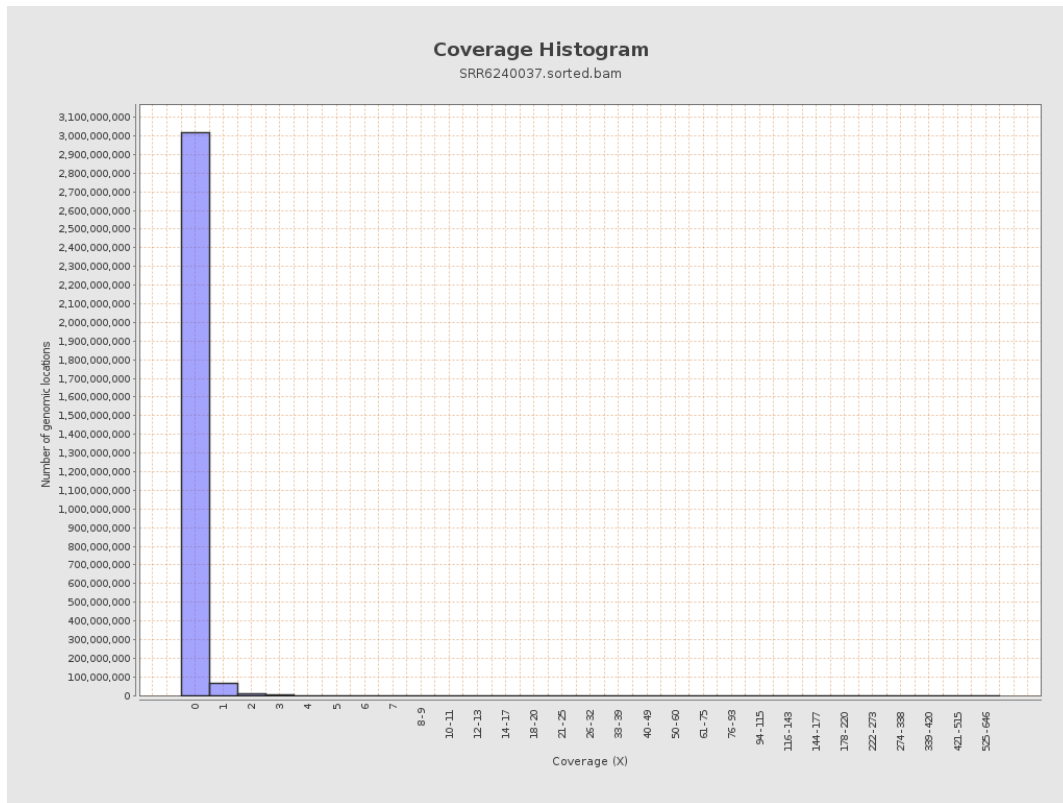
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7699669	0.0309	0.4421
chr2	243199373	11099445	0.0456	0.3923
chr3	198022430	7067218	0.0357	0.2325
chr4	191154276	6466521	0.0338	0.231
chr5	180915260	5400715	0.0299	0.213
chr6	171115067	5908615	0.0345	0.2709
chr7	159138663	6037590	0.0379	0.5908

chr8	146364022	5849063	0.04	0.3711
chr9	141213431	3794990	0.0269	0.2953
chr10	135534747	4250972	0.0314	0.2632
chr11	135006516	4325963	0.032	0.2779
chr12	133851895	4508271	0.0337	0.226
chr13	115169878	2463986	0.0214	0.1764
chr14	107349540	3329924	0.031	0.2301
chr15	102531392	2609736	0.0255	0.2169
chr16	90354753	2874191	0.0318	0.2243
chr17	81195210	2556867	0.0315	0.2301
chr18	78077248	2384515	0.0305	0.427
chr19	59128983	1738688	0.0294	0.3202
chr20	63025520	2043066	0.0324	0.2261
chr21	48129895	1455825	0.0302	0.2205
chr22	51304566	956338	0.0186	0.1618
chrMT	16571	46558	2.8096	3.7284
chrX	155270560	5558698	0.0358	0.2593
chrY	59373566	234539	0.004	0.0856

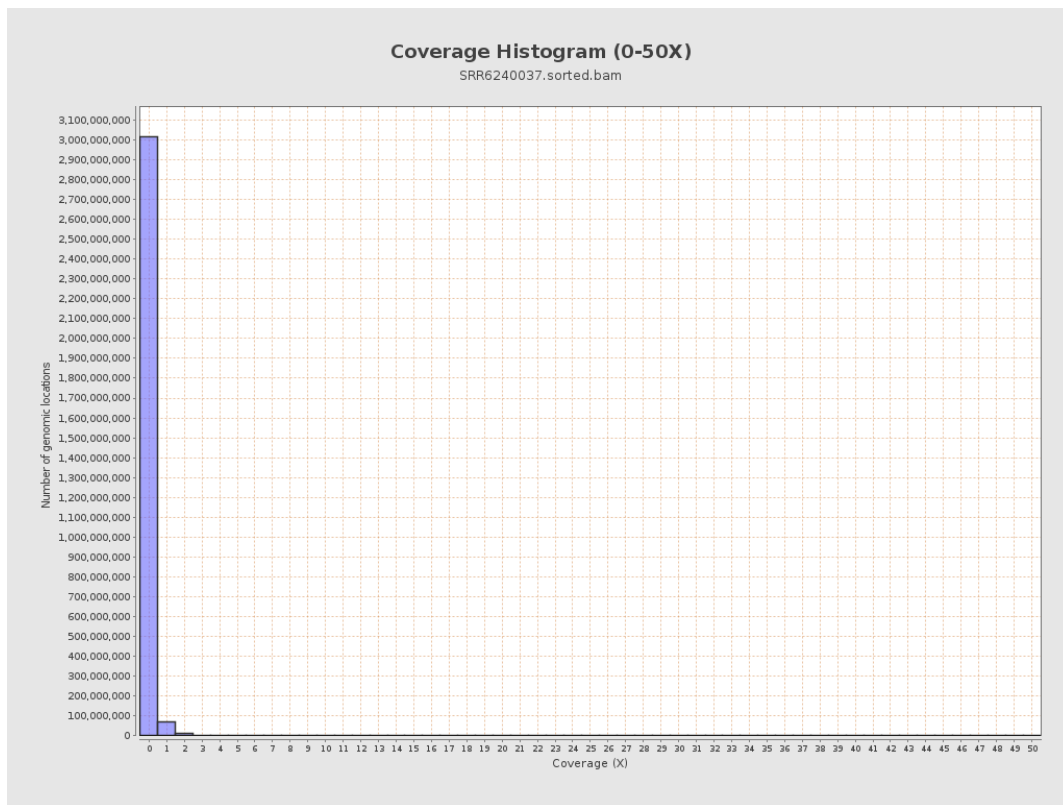
3. Results : Coverage across reference



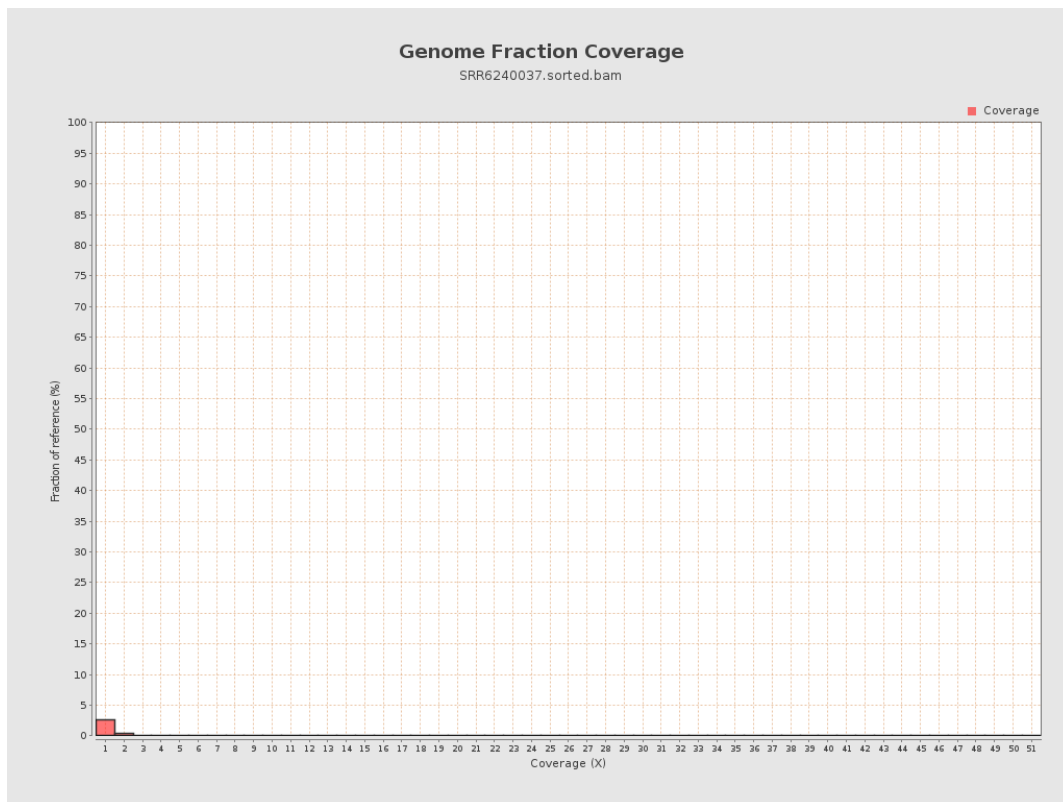
4. Results : Coverage Histogram



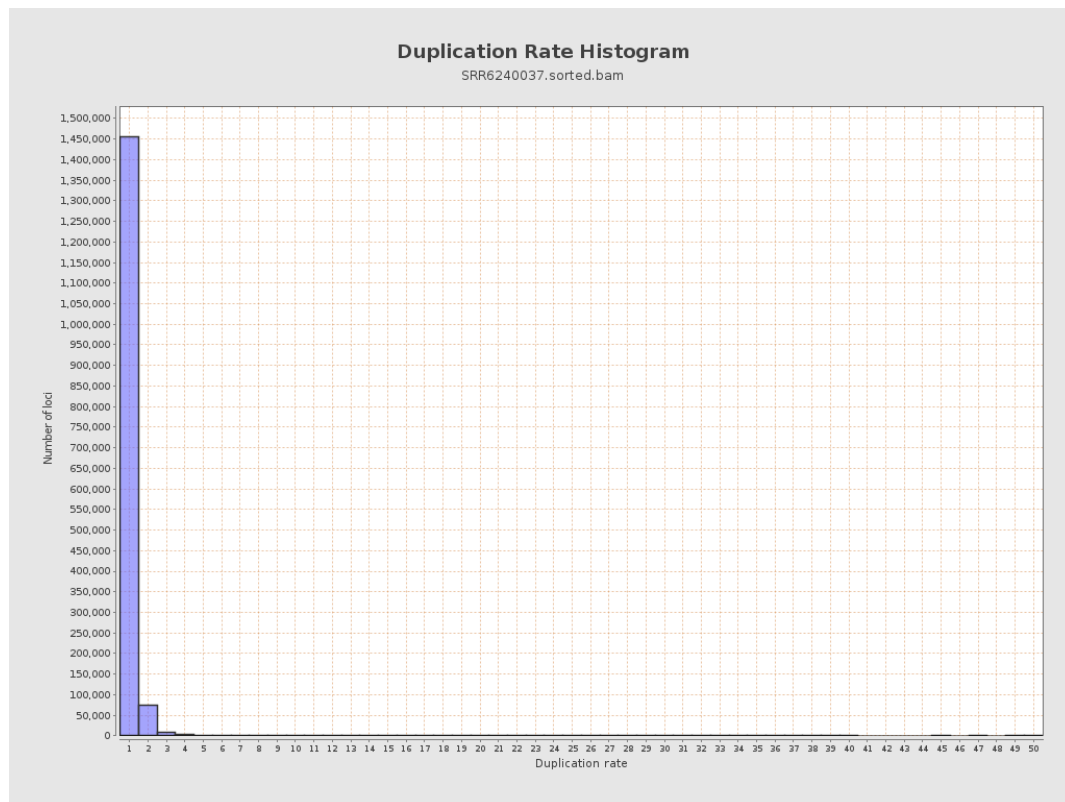
5. Results : Coverage Histogram (0-50X)



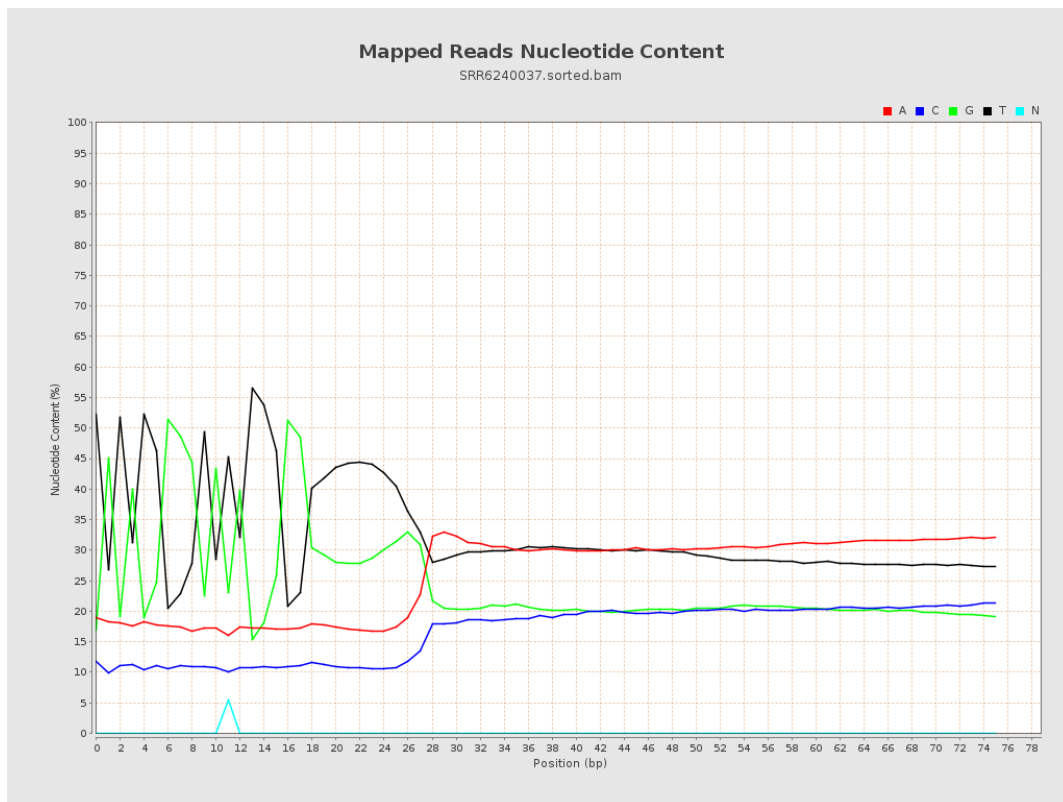
6. Results : Genome Fraction Coverage



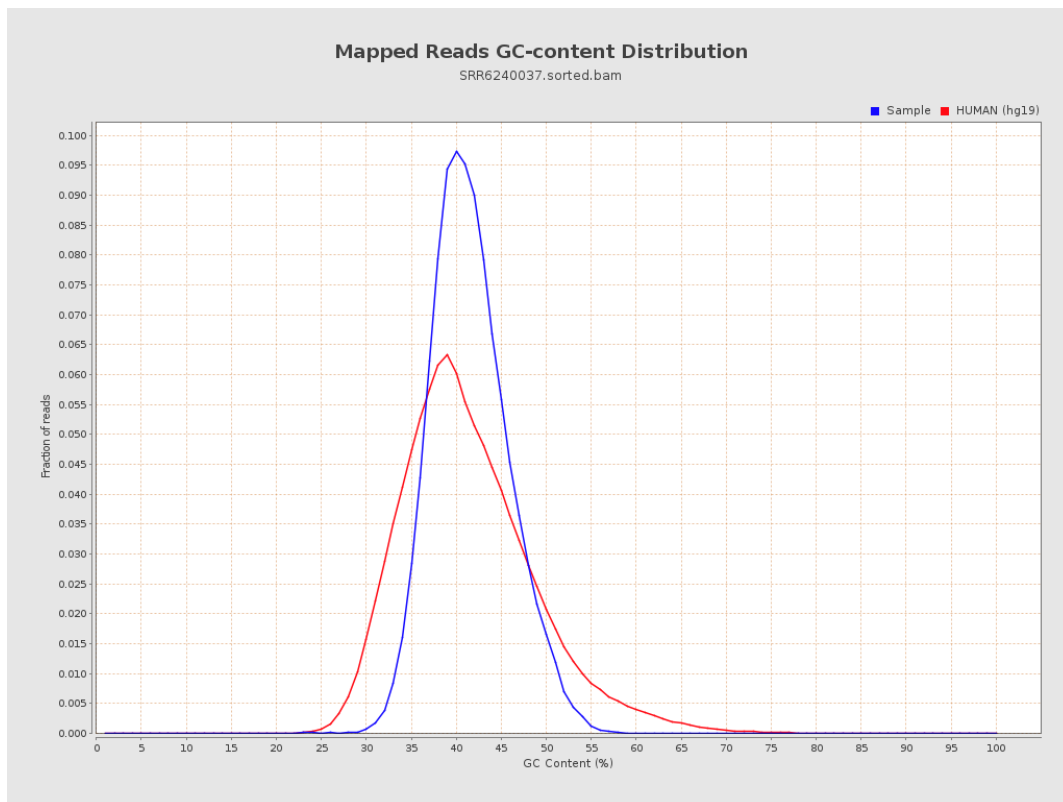
7. Results : Duplication Rate Histogram



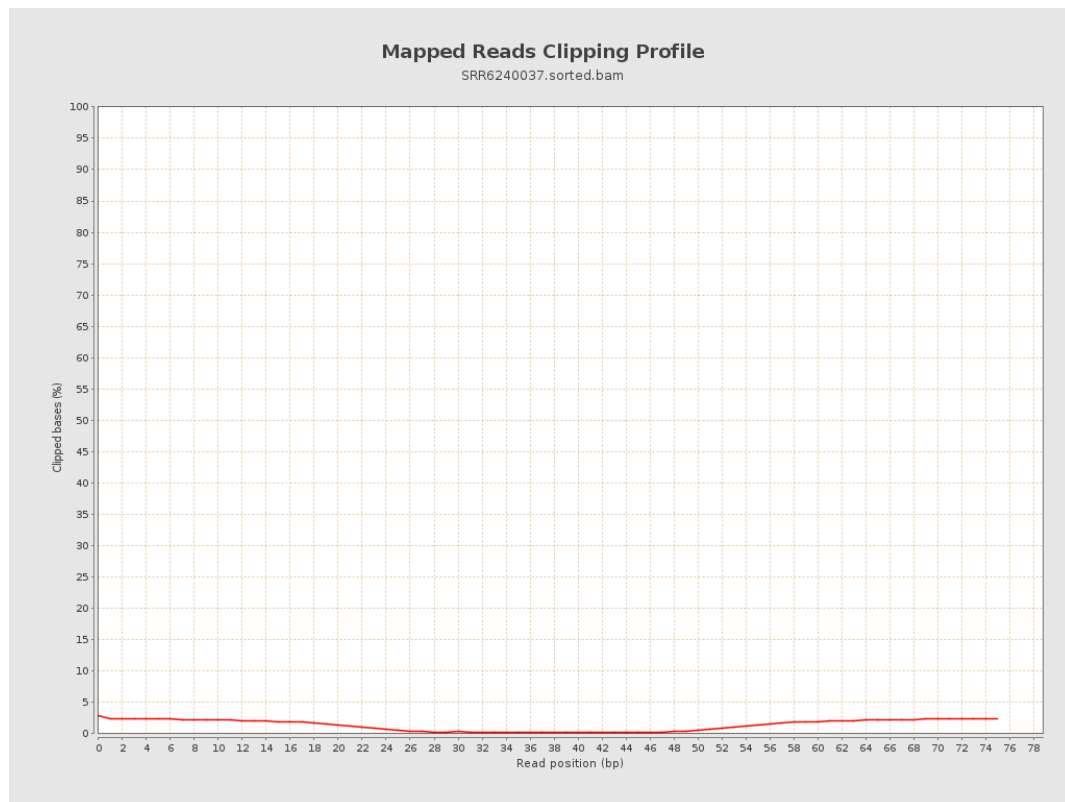
8. Results : Mapped Reads Nucleotide Content



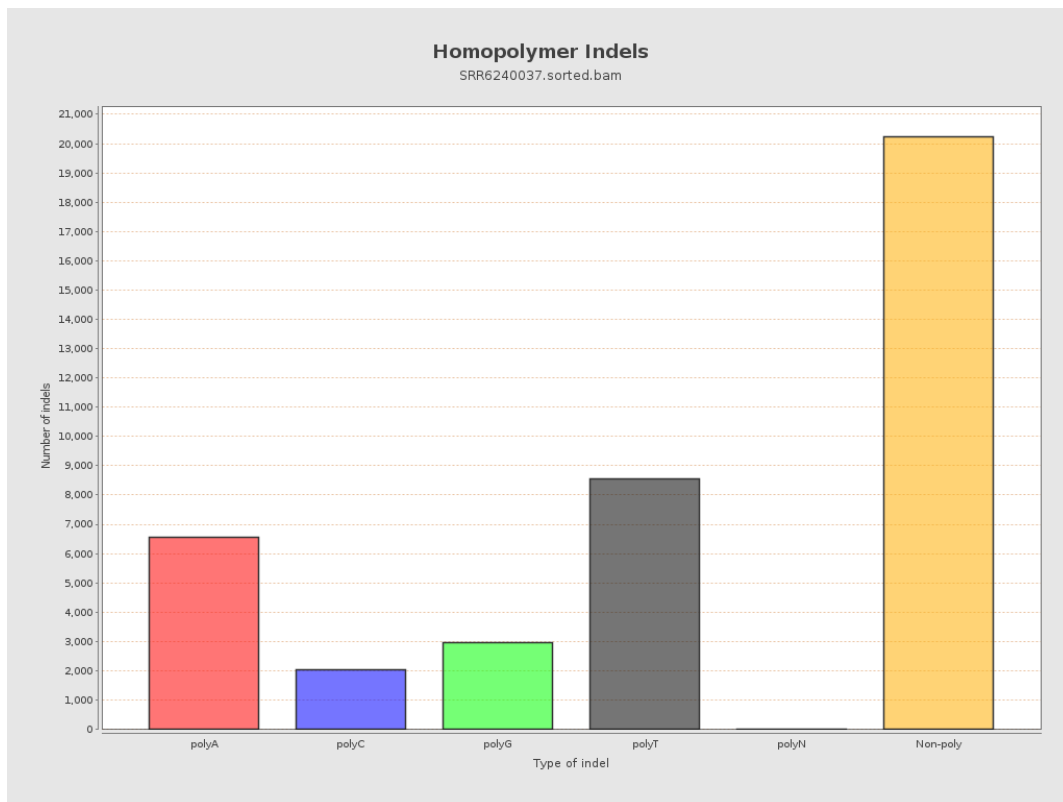
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

