

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:49:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236064.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_SRR6236064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:49:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,942,488
Mapped reads	1,608,102 / 82.79%
Unmapped reads	334,386 / 17.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,718 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	114,805 / 5.91%
Duplication rate	5.65%
Clipped reads	789,759 / 40.66%

2.2. ACGT Content

Number/percentage of A's	29,137,871 / 27.74%
Number/percentage of C's	18,211,219 / 17.34%
Number/percentage of T's	34,607,087 / 32.94%
Number/percentage of G's	23,048,702 / 21.94%
Number/percentage of N's	46,413 / 0.04%
GC Percentage	39.28%

2.3. Coverage

Mean	0.034

Standard Deviation	0.4237
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2.4. Mapping Quality

Mean Mapping Quality	45.09
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2.5. Mismatches and indels

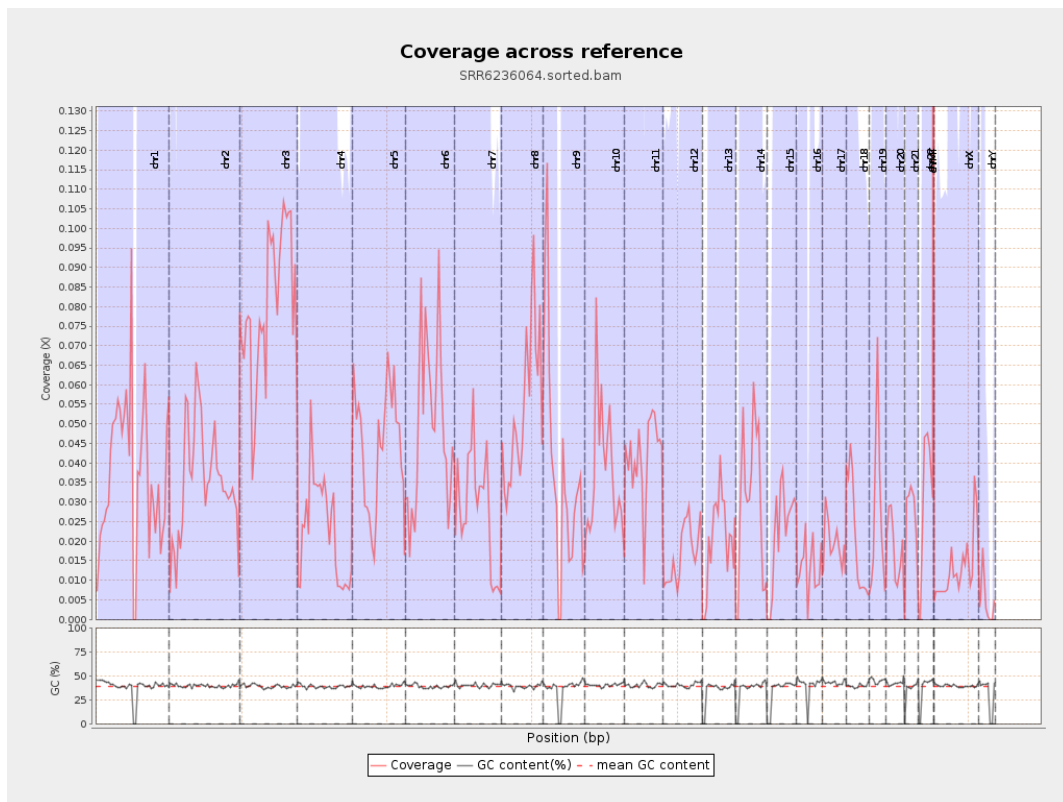
General error rate	0.88%
Mismatches	912,416
Insertions	7,920
Mapped reads with at least one insertion	0.49%
Deletions	34,360
Mapped reads with at least one deletion	2.11%
Homopolymer indels	45.46%

2.6. Chromosome stats

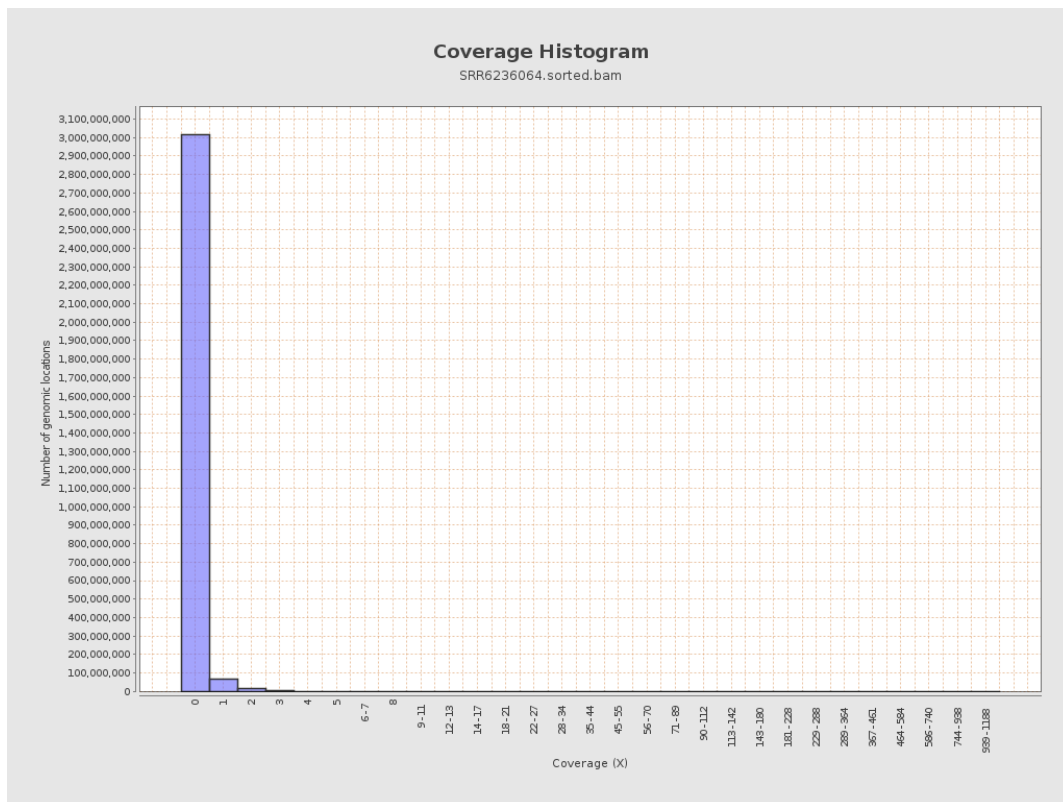
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9173872	0.0368	0.9204
chr2	243199373	8521567	0.035	0.3787
chr3	198022430	16036805	0.081	0.3565
chr4	191154276	4362837	0.0228	0.2267
chr5	180915260	8050616	0.0445	0.2646
chr6	171115067	8394785	0.0491	0.3987
chr7	159138663	4464672	0.0281	0.3372

chr8	146364022	7902431	0.054	0.7659
chr9	141213431	5214257	0.0369	0.3373
chr10	135534747	5102506	0.0376	0.3929
chr11	135006516	5550163	0.0411	0.3545
chr12	133851895	2248845	0.0168	0.1712
chr13	115169878	2340030	0.0203	0.1745
chr14	107349540	3198841	0.0298	0.224
chr15	102531392	2290104	0.0223	0.1862
chr16	90354753	1177421	0.013	0.1697
chr17	81195210	1562099	0.0192	0.191
chr18	78077248	1612444	0.0207	0.6043
chr19	59128983	1638106	0.0277	0.4785
chr20	63025520	1177151	0.0187	0.1747
chr21	48129895	1194118	0.0248	0.2167
chr22	51304566	1572952	0.0307	0.2131
chrMT	16571	17345	1.0467	1.3514
chrX	155270560	2043387	0.0132	0.1635
chrY	59373566	263512	0.0044	0.1445

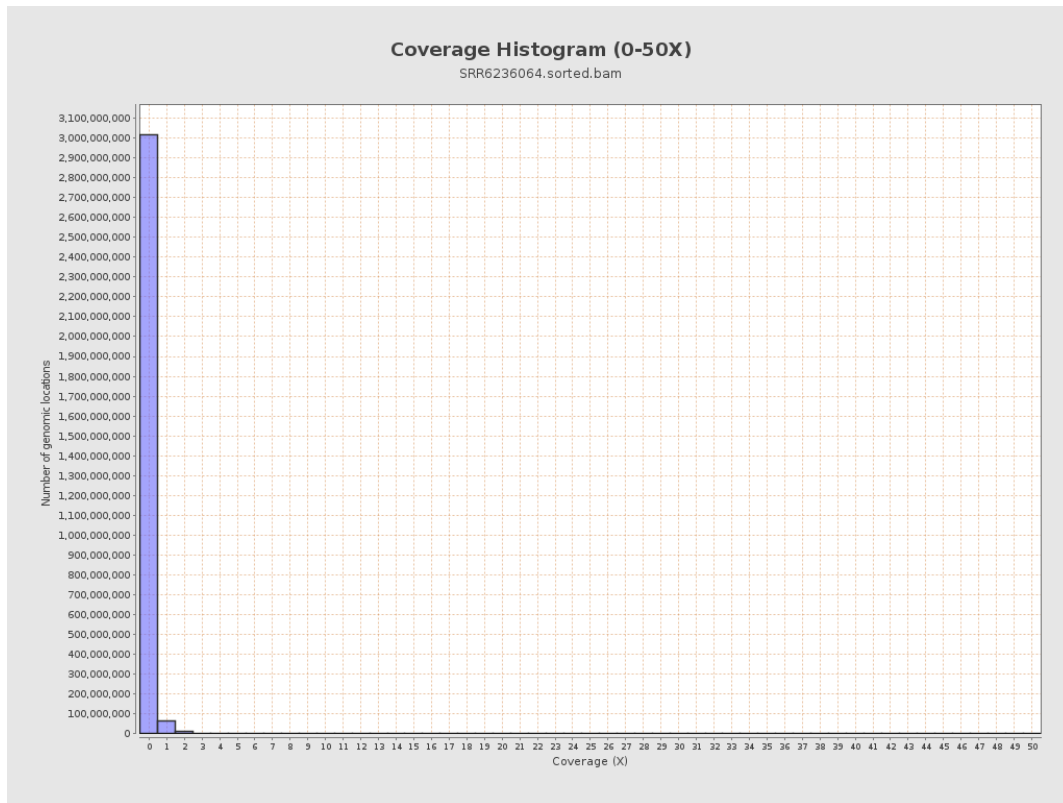
3. Results : Coverage across reference



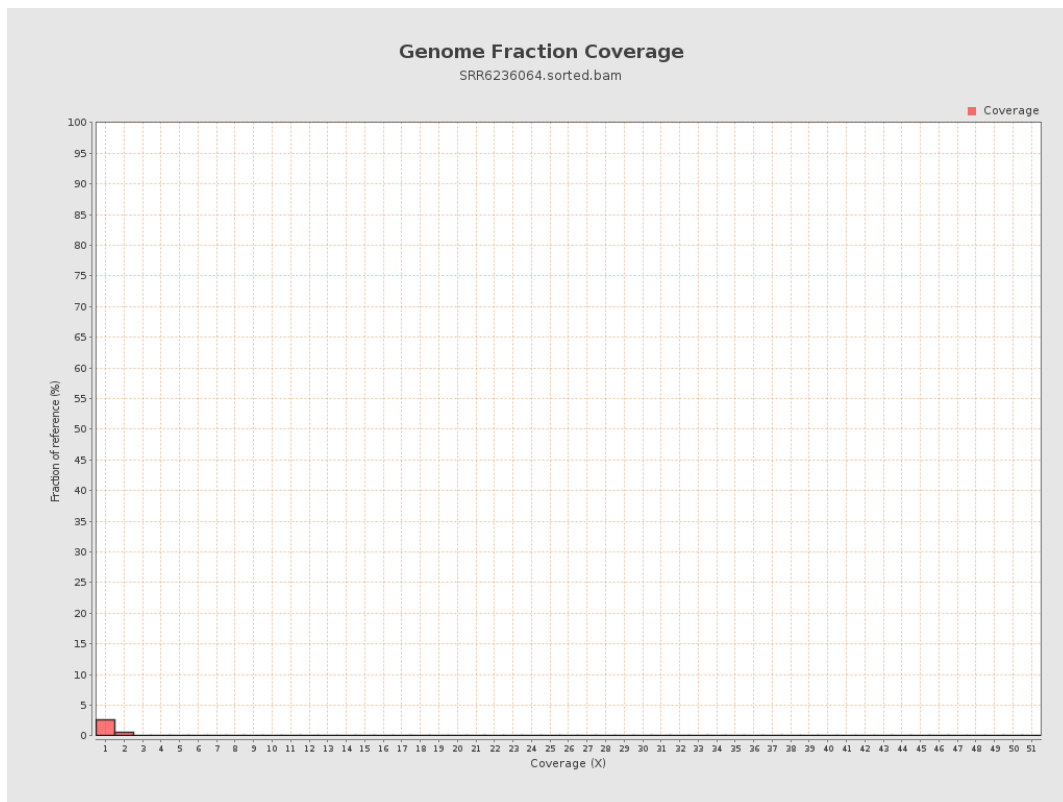
4. Results : Coverage Histogram



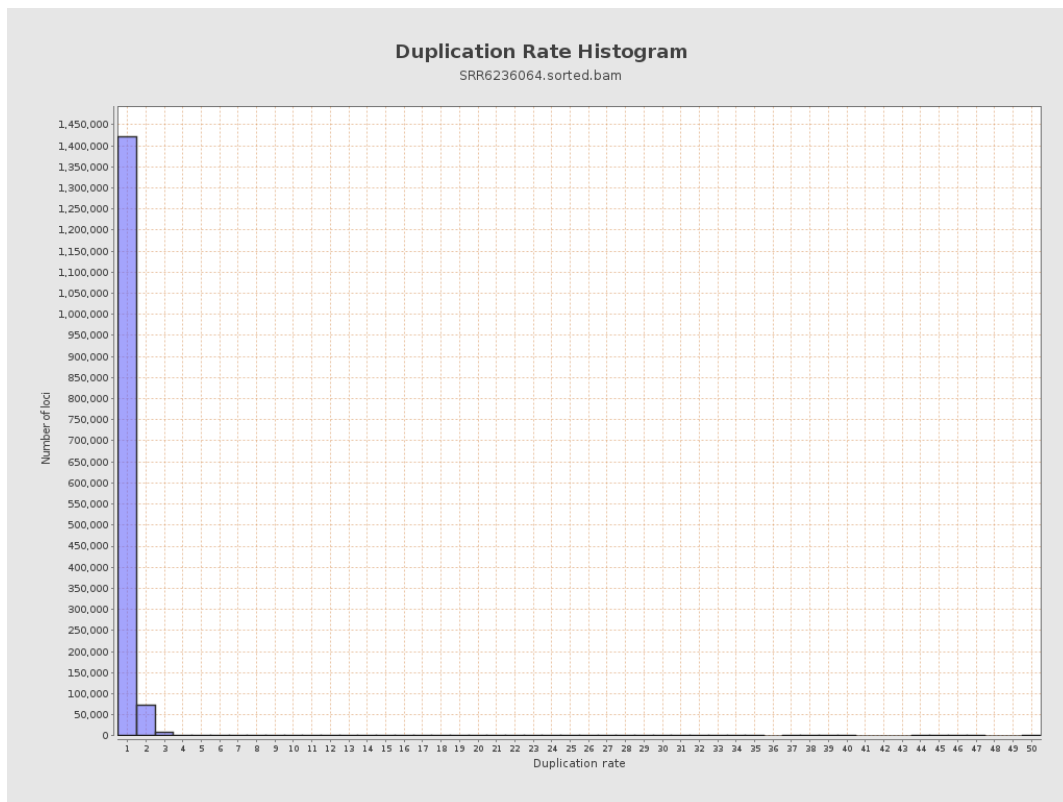
5. Results : Coverage Histogram (0-50X)



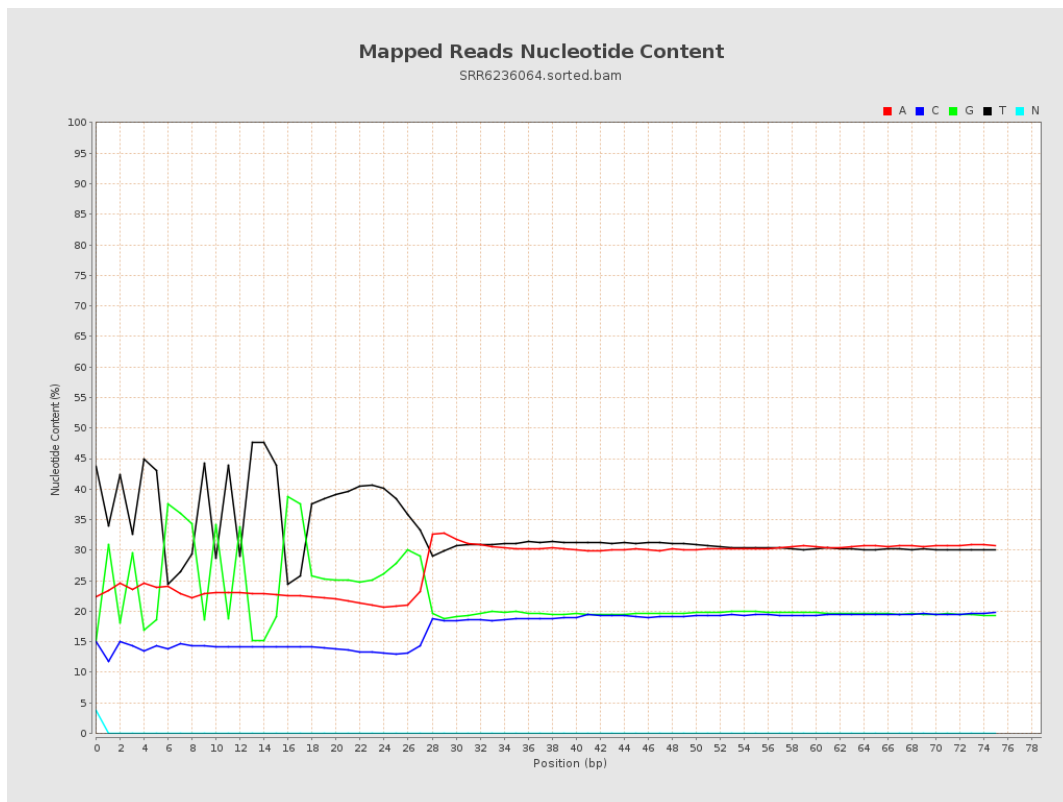
6. Results : Genome Fraction Coverage



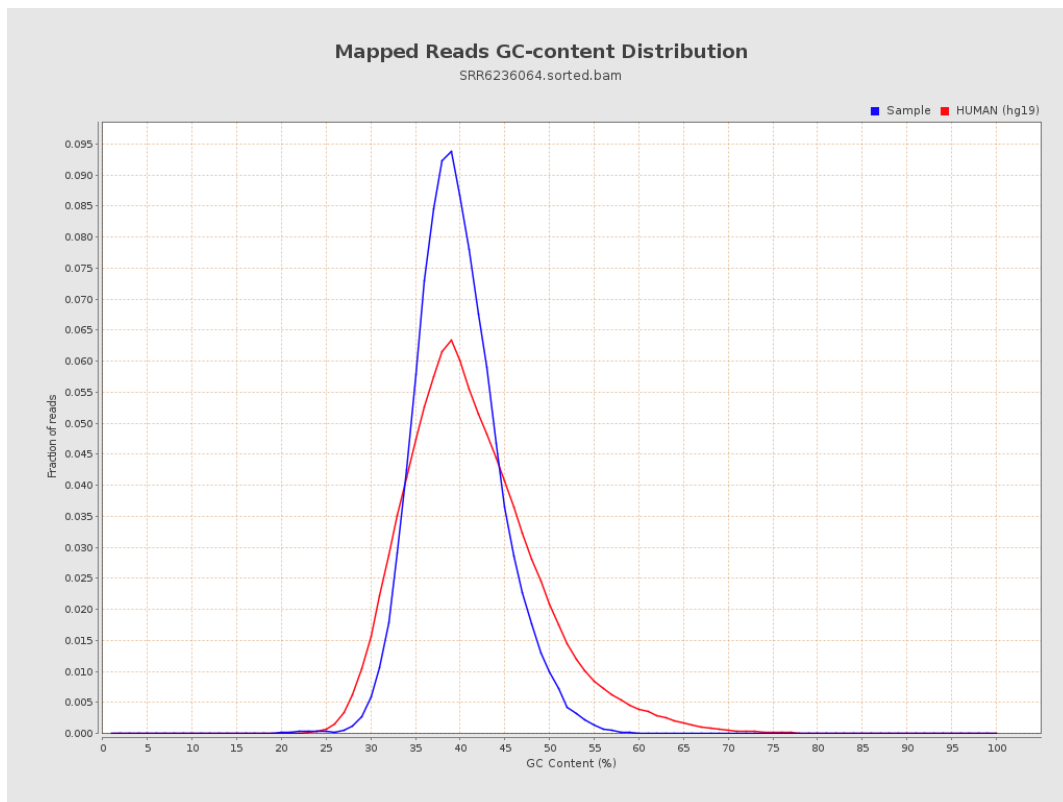
7. Results : Duplication Rate Histogram



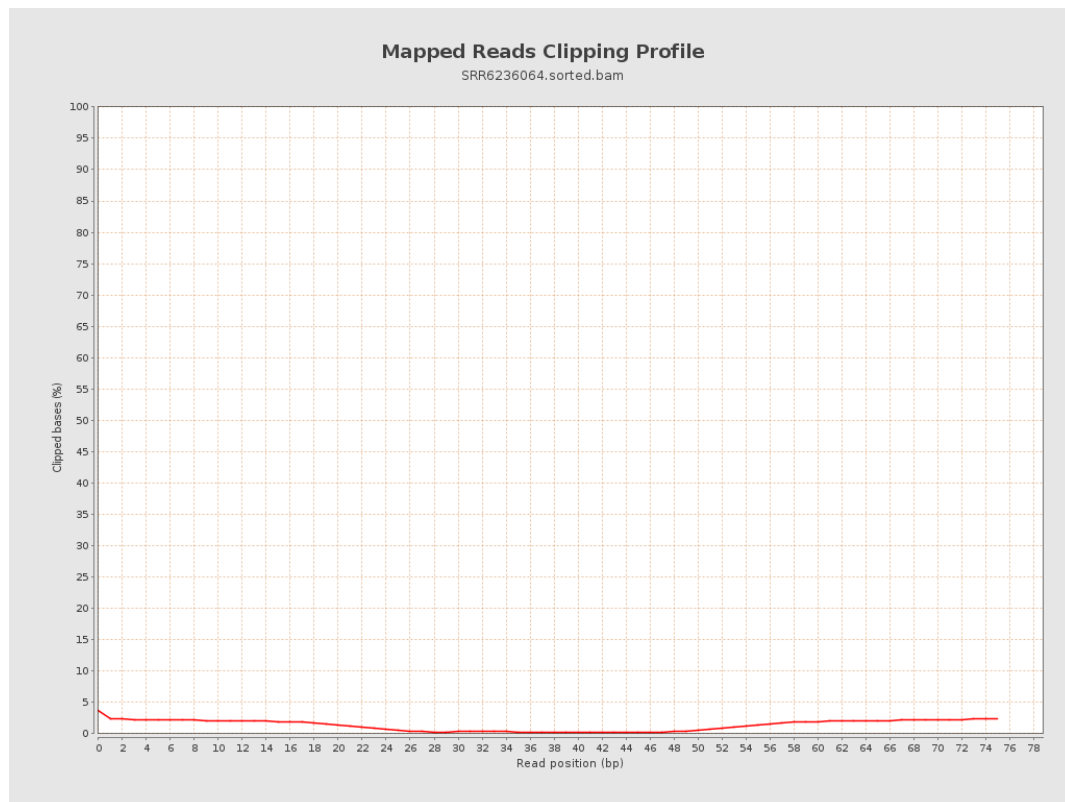
8. Results : Mapped Reads Nucleotide Content



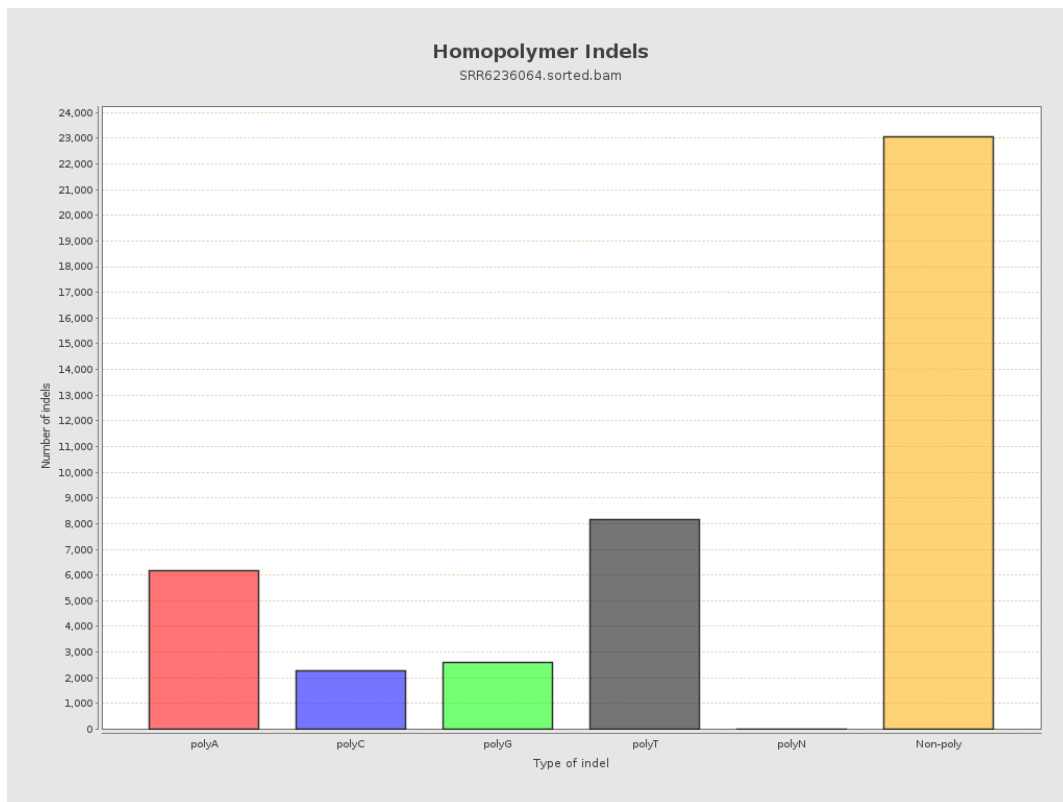
9. Results : Mapped Reads GC-content Distribution



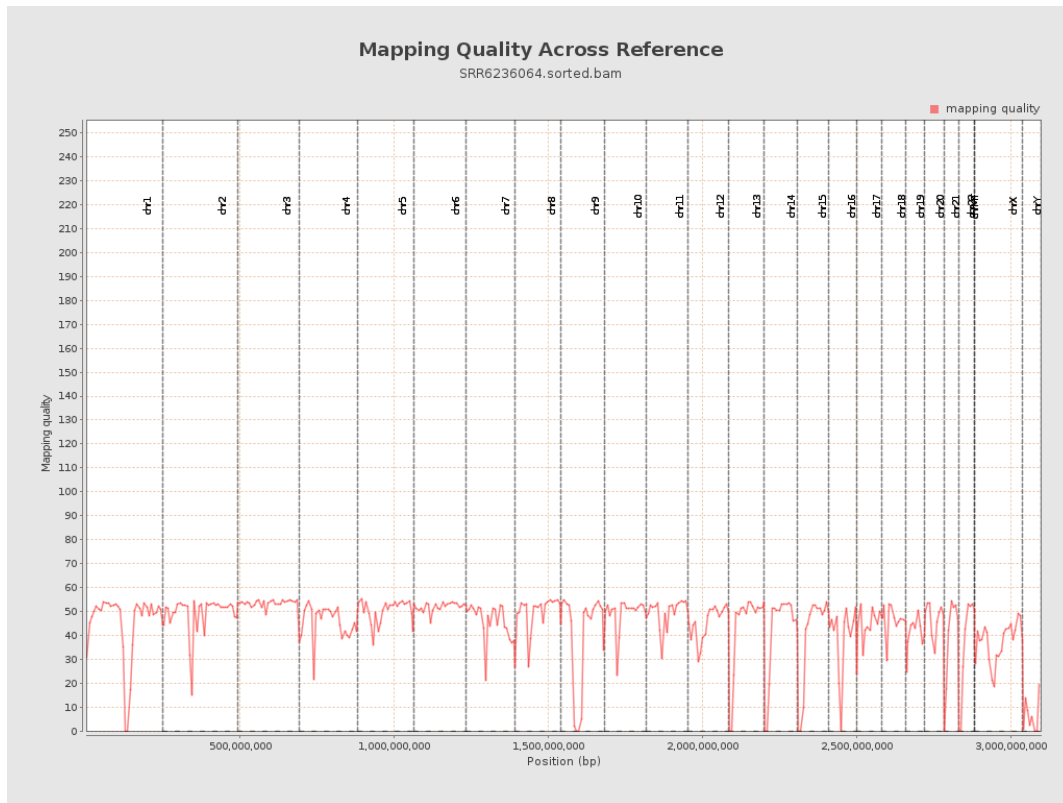
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

