Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:27:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231769.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_SRR6231769 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231769.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:27:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231769.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,673,127
Mapped reads	1,062,642 / 63.51%
Unmapped reads	610,485 / 36.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,346 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	32,369 / 1.93%
Duplication rate	2.41%
Clipped reads	626,641 / 37.45%

2.2. ACGT Content

Number/percentage of A's	18,719,885 / 28.04%
Number/percentage of C's	10,764,063 / 16.12%
Number/percentage of T's	21,448,032 / 32.12%
Number/percentage of G's	15,835,950 / 23.72%
Number/percentage of N's	2,420 / 0%
GC Percentage	39.84%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2108

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

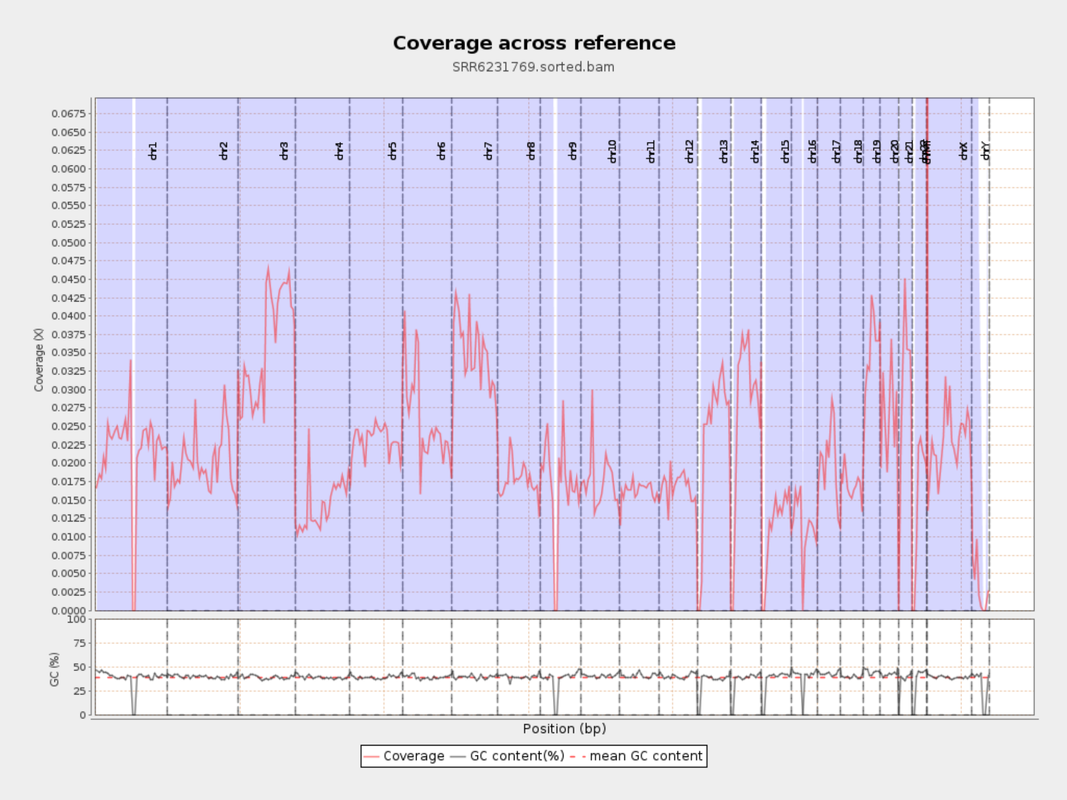
General error rate	0.97%
Mismatches	637,273
Insertions	5,110
Mapped reads with at least one insertion	0.48%
Deletions	16,687
Mapped reads with at least one deletion	1.55%
Homopolymer indels	45.95%

2.6. Chromosome stats

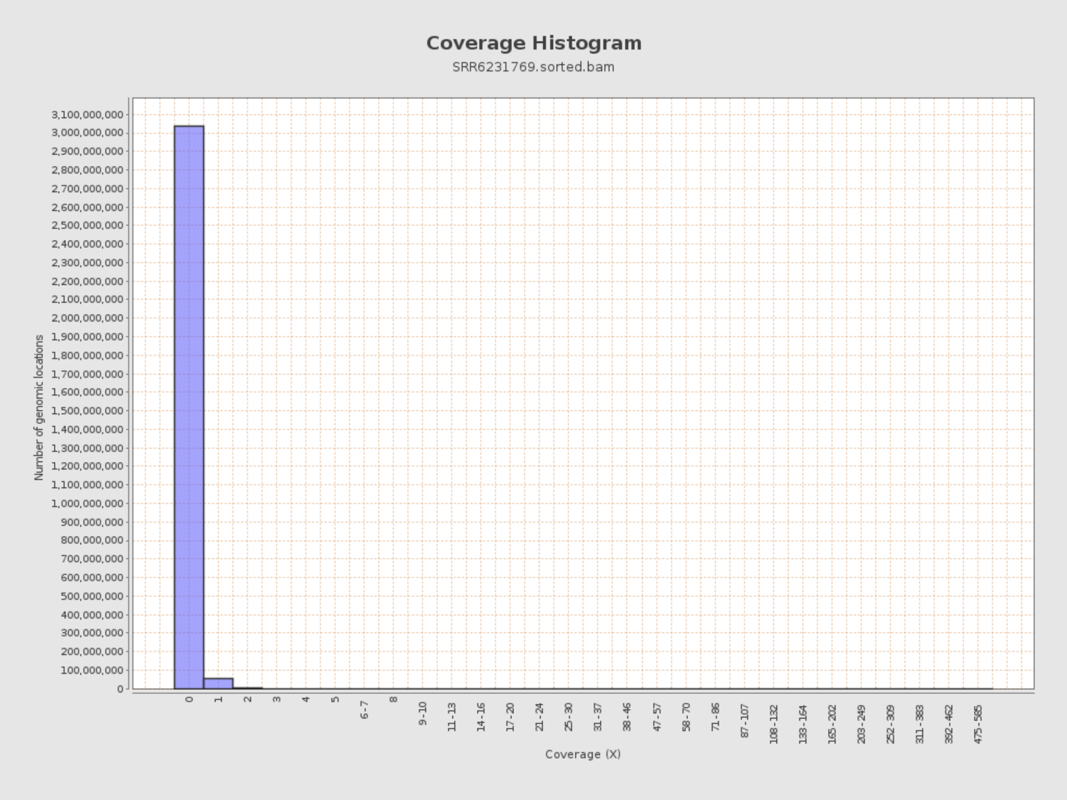
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5352996	0.0215	0.3274
chr2	243199373	4848676	0.0199	0.2036
chr3	198022430	7184421	0.0363	0.2045
chr4	191154276	2750745	0.0144	0.1347
chr5	180915260	4208494	0.0233	0.1633
chr6	171115067	4461883	0.0261	0.1901
chr7	159138663	5561277	0.0349	0.2952

chr8	146364022	2599878	0.0178	0.3798
chr9	141213431	2396566	0.017	0.1567
chr10	135534747	2390514	0.0176	0.1767
chr11	135006516	2203927	0.0163	0.154
chr12	133851895	2245322	0.0168	0.1388
chr13	115169878	2719494	0.0236	0.1642
chr14	107349540	2910082	0.0271	0.1804
chr15	102531392	1155143	0.0113	0.1137
chr16	90354753	1017620	0.0113	0.1242
chr17	81195210	1624751	0.02	0.1572
chr18	78077248	1331156	0.017	0.2532
chr19	59128983	2091798	0.0354	0.2327
chr20	63025520	1658333	0.0263	0.1752
chr21	48129895	1469550	0.0305	0.1912
chr22	51304566	778559	0.0152	0.1321
chrMT	16571	74443	4.4924	3.6778
chrX	155270560	3578324	0.023	0.1685
chrY	59373566	185601	0.0031	0.0743

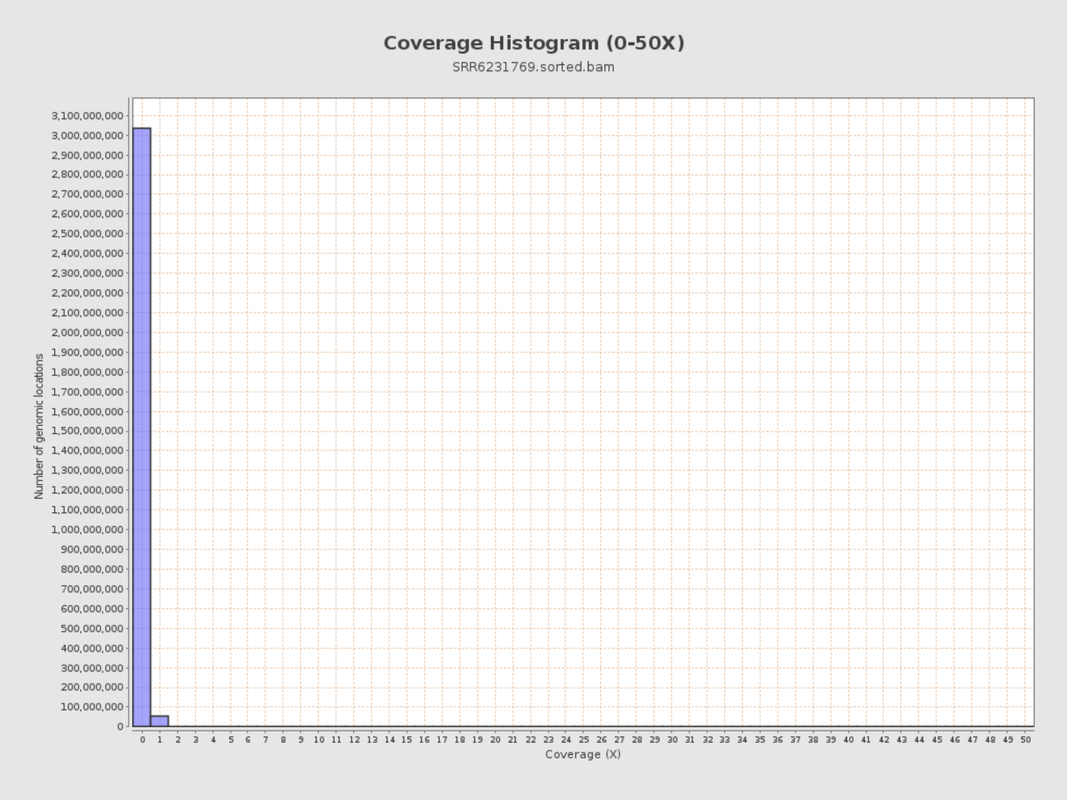
3. Results : Coverage across reference



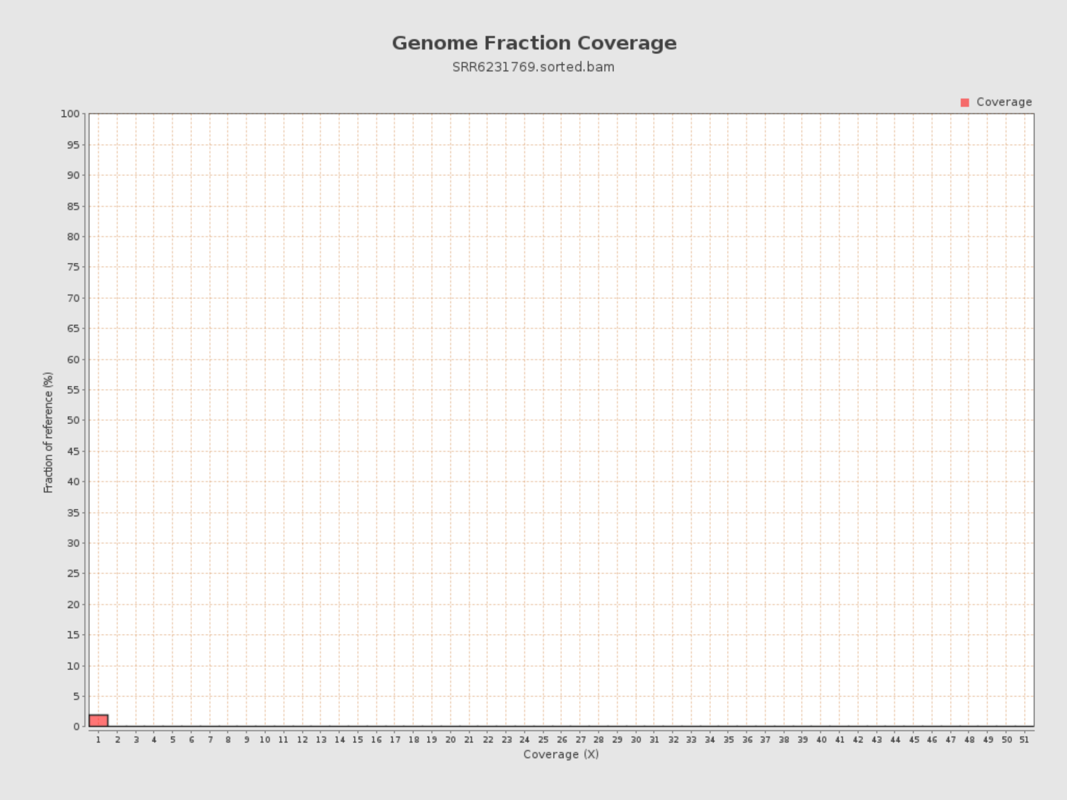
4. Results : Coverage Histogram



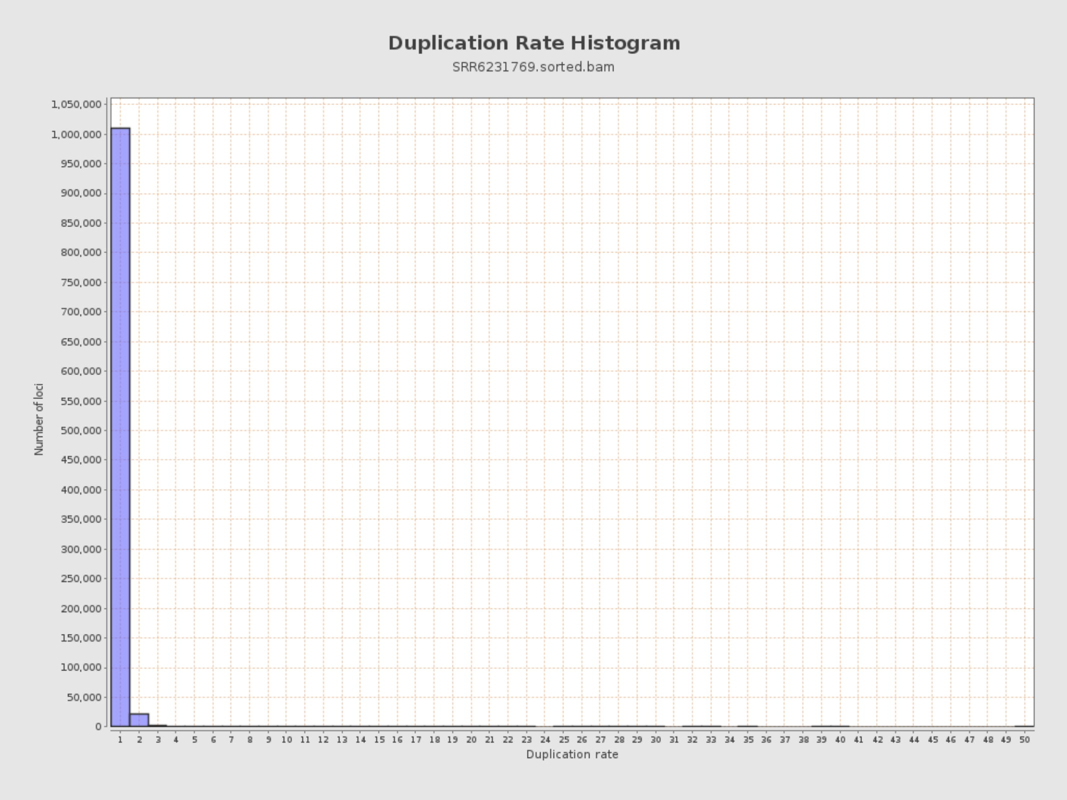
5. Results : Coverage Histogram (0-50X)



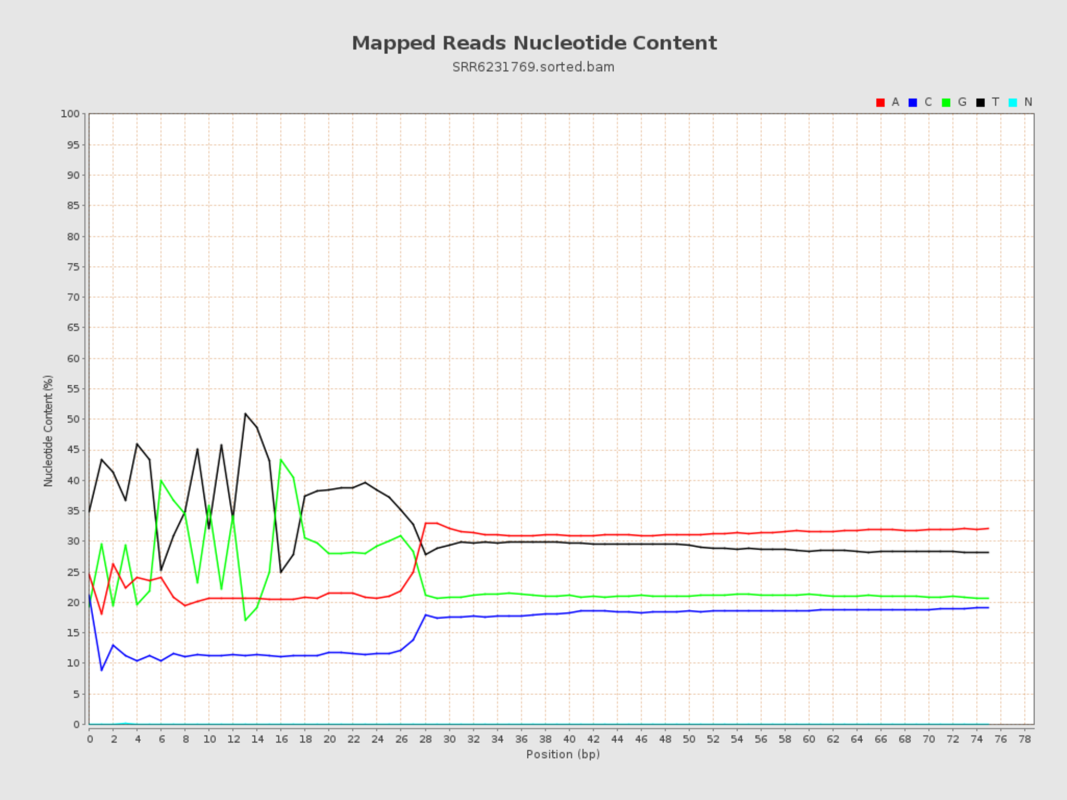
6. Results : Genome Fraction Coverage



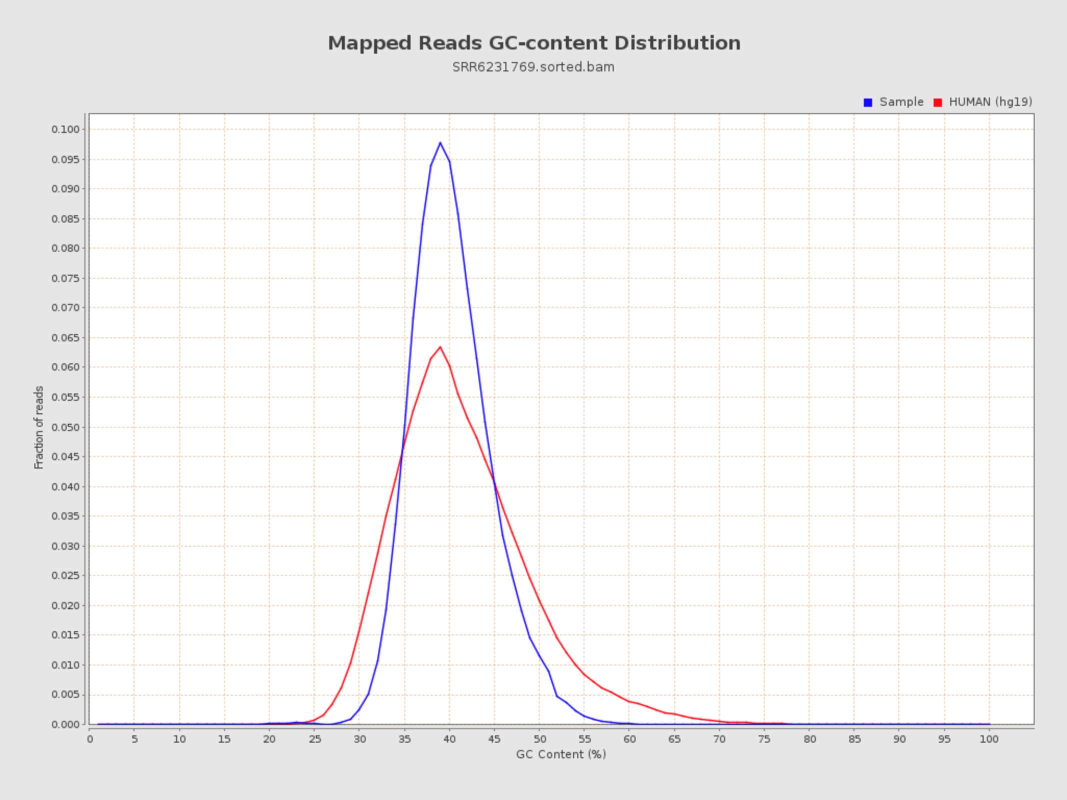
7. Results : Duplication Rate Histogram



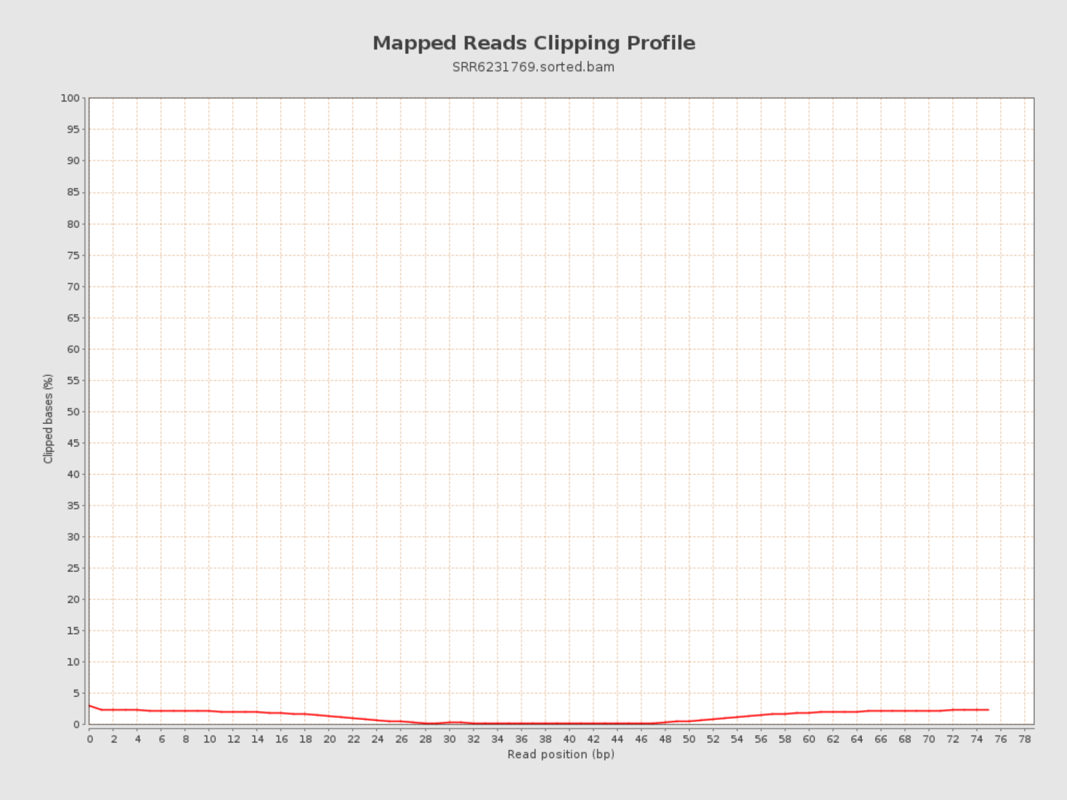
8. Results : Mapped Reads Nucleotide Content



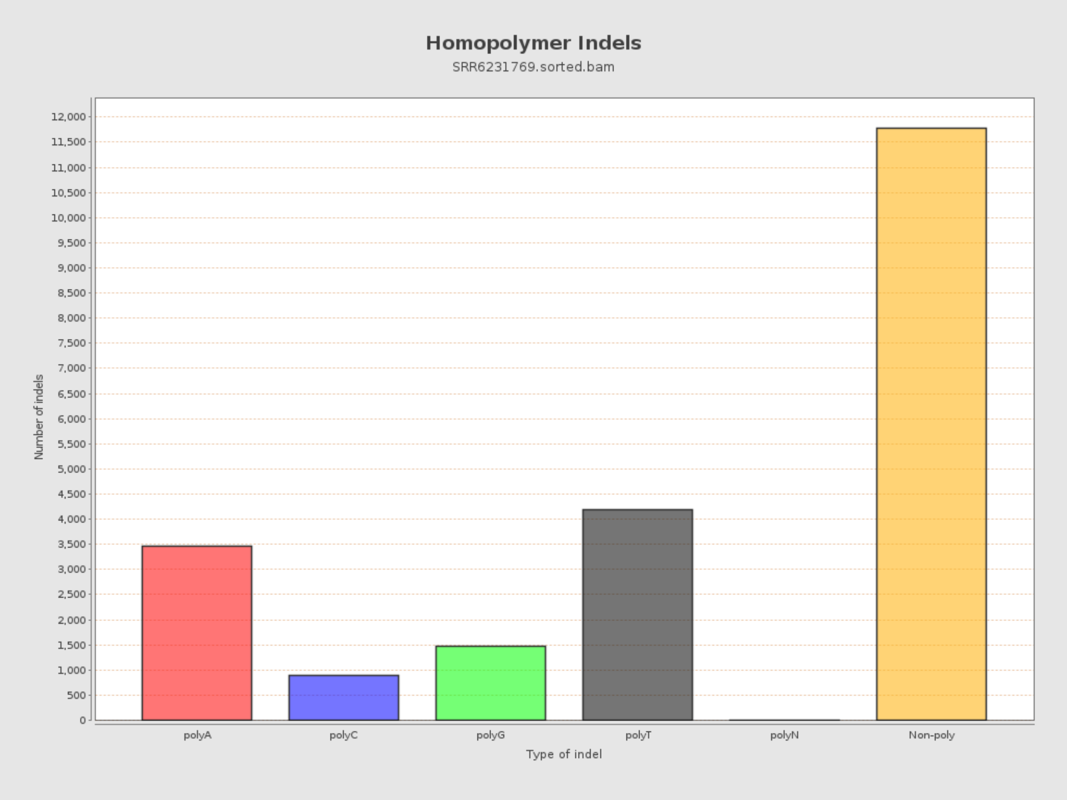
9. Results : Mapped Reads GC-content Distribution



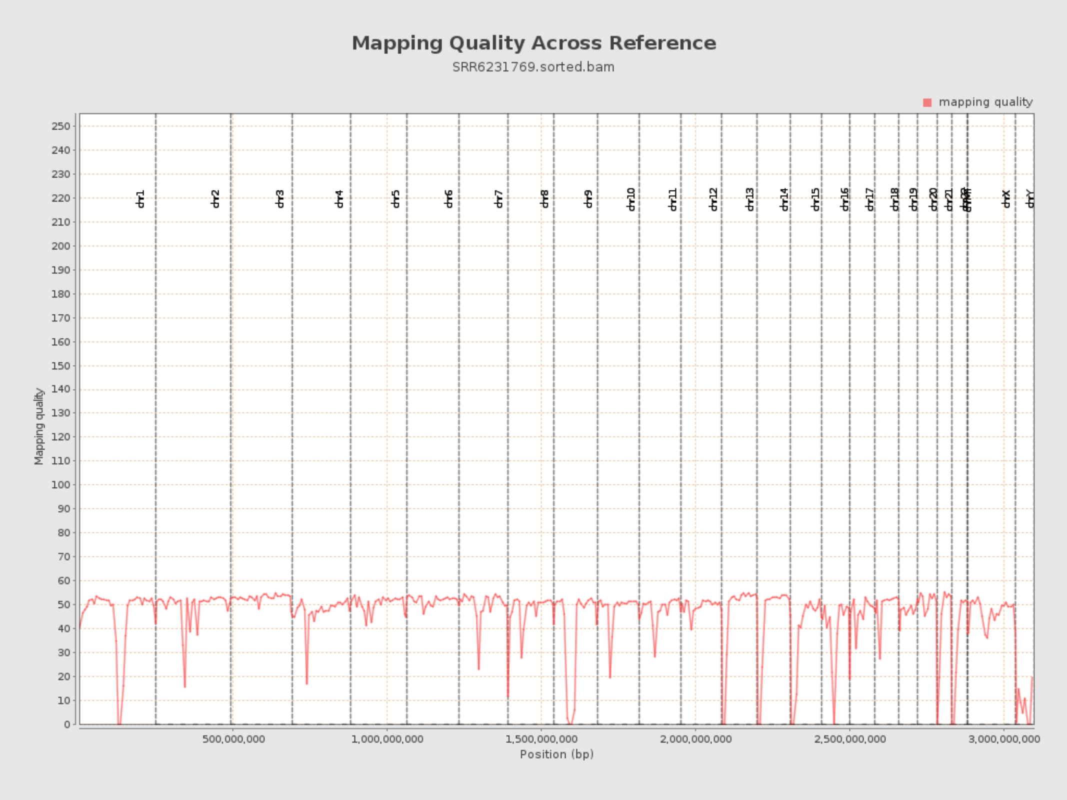
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram