Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:58:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236087.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_SRR6236087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:58:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,632,969
Mapped reads	1,419,582 / 86.93%
Unmapped reads	213,387 / 13.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,359 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	68,940 / 4.22%
Duplication rate	3.78%
Clipped reads	638,321 / 39.09%

2.2. ACGT Content

Number/percentage of A's	26,165,004 / 27.8%
Number/percentage of C's	16,839,214 / 17.89%
Number/percentage of T's	30,409,925 / 32.31%
Number/percentage of G's	20,674,952 / 21.96%
Number/percentage of N's	38,938 / 0.04%
GC Percentage	39.85%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.327

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

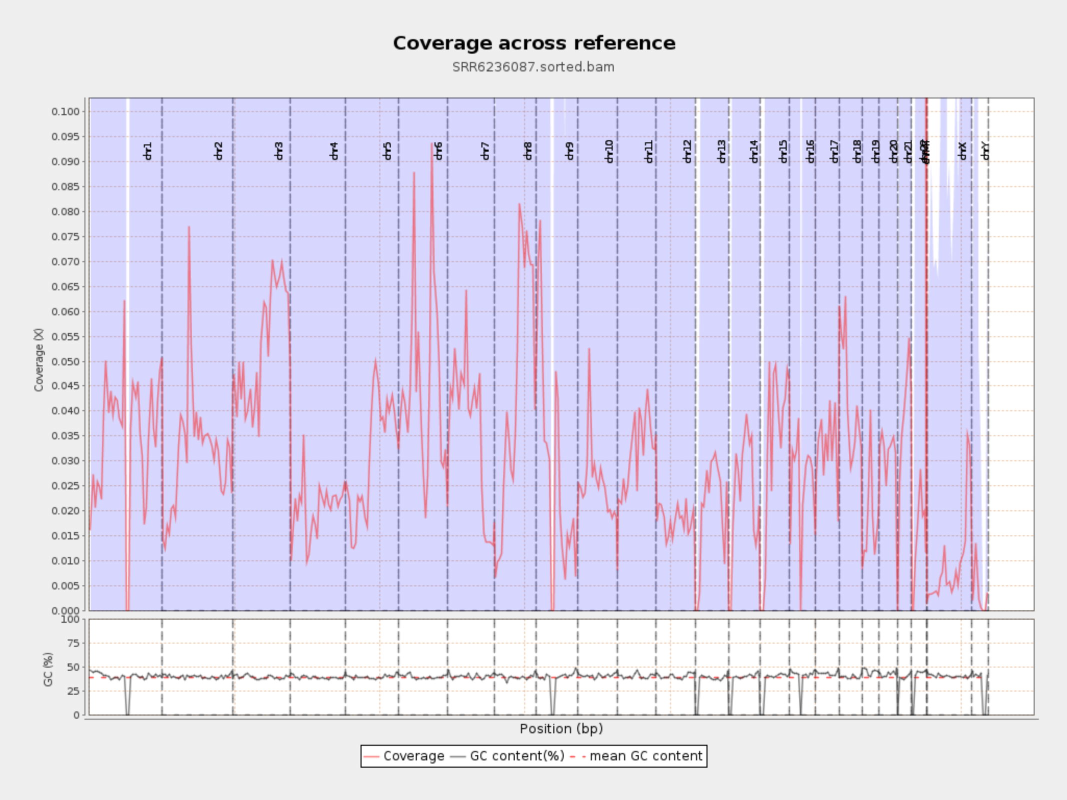
General error rate	0.83%
Mismatches	769,644
Insertions	7,045
Mapped reads with at least one insertion	0.49%
Deletions	27,913
Mapped reads with at least one deletion	1.94%
Homopolymer indels	46.26%

2.6. Chromosome stats

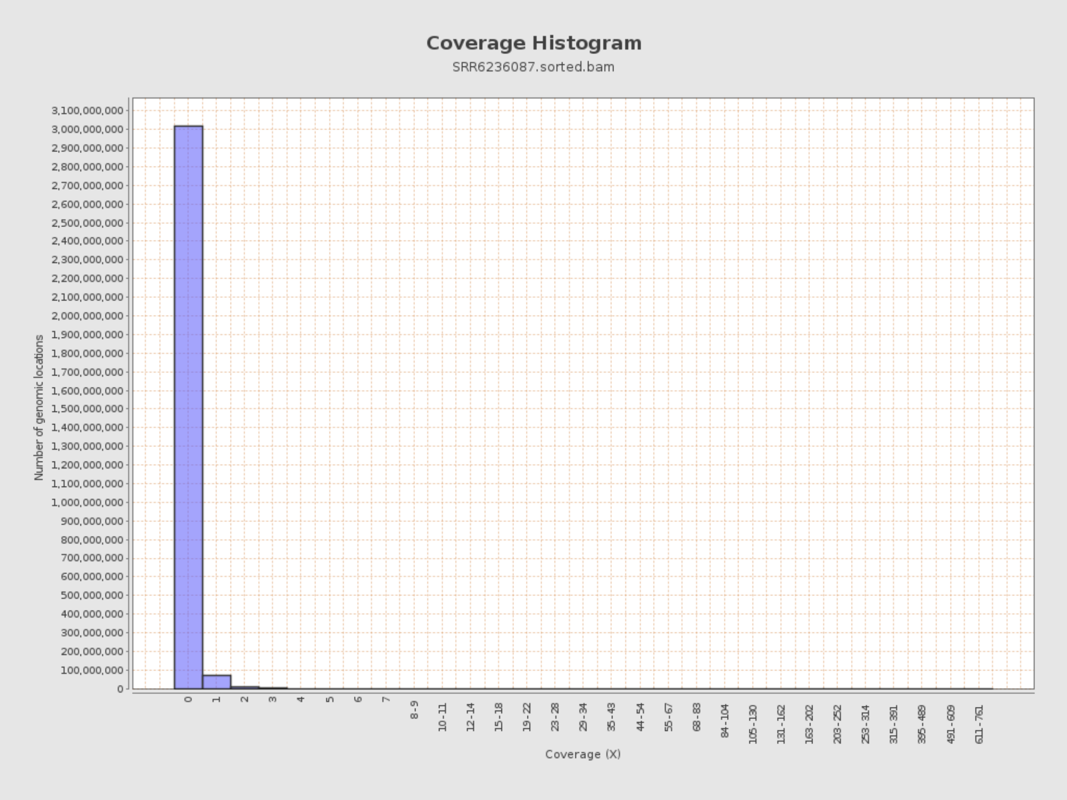
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8506191	0.0341	0.5761
chr2	243199373	7685820	0.0316	0.3713
chr3	198022430	10545108	0.0533	0.2615
chr4	191154276	3882600	0.0203	0.1822
chr5	180915260	5628013	0.0311	0.2022
chr6	171115067	7760514	0.0454	0.3641
chr7	159138663	5823130	0.0366	0.3705

chr8	146364022	6416740	0.0438	0.5521
chr9	141213431	3930146	0.0278	0.3254
chr10	135534747	3497808	0.0258	0.2841
chr11	135006516	4232857	0.0314	0.2588
chr12	133851895	2409116	0.018	0.1643
chr13	115169878	2331224	0.0202	0.1601
chr14	107349540	2488571	0.0232	0.1878
chr15	102531392	3318276	0.0324	0.2054
chr16	90354753	2348097	0.026	0.2001
chr17	81195210	2633330	0.0324	0.2434
chr18	78077248	3333640	0.0427	0.516
chr19	59128983	1114269	0.0188	0.379
chr20	63025520	1980102	0.0314	0.2039
chr21	48129895	1789831	0.0372	0.2415
chr22	51304566	753239	0.0147	0.1344
chrMT	16571	89365	5.3929	3.931
chrX	155270560	1481424	0.0095	0.1354
chrY	59373566	197150	0.0033	0.1113

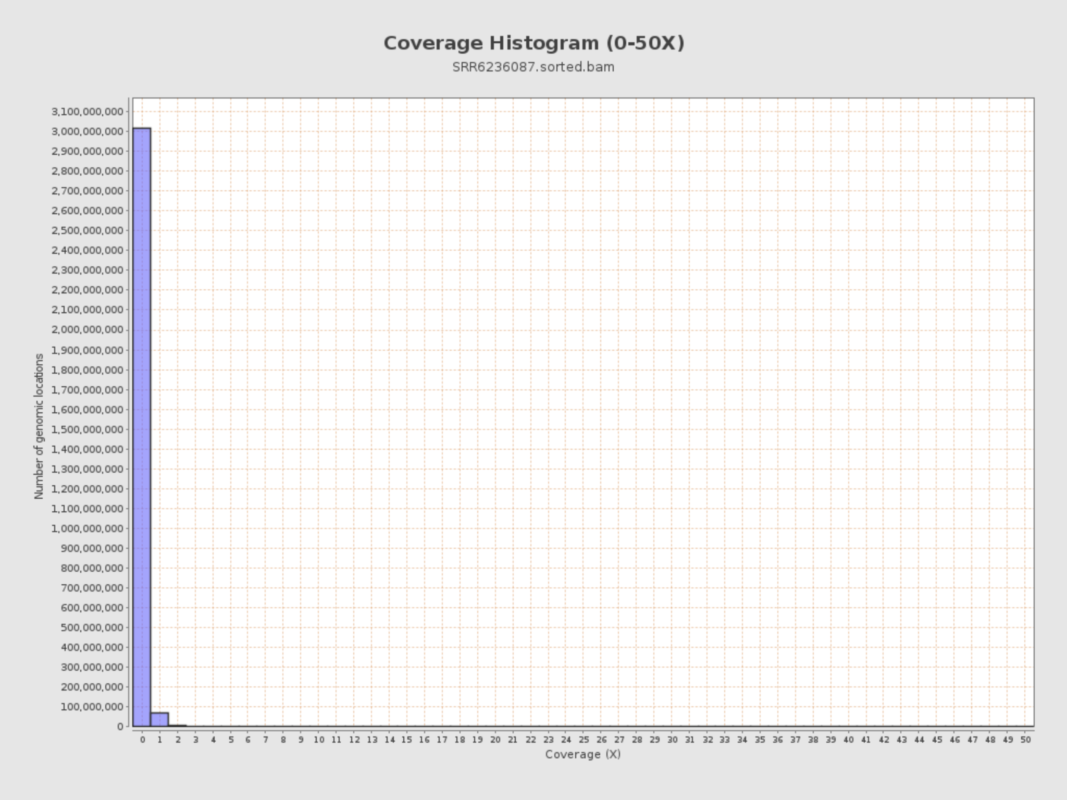
3. Results : Coverage across reference



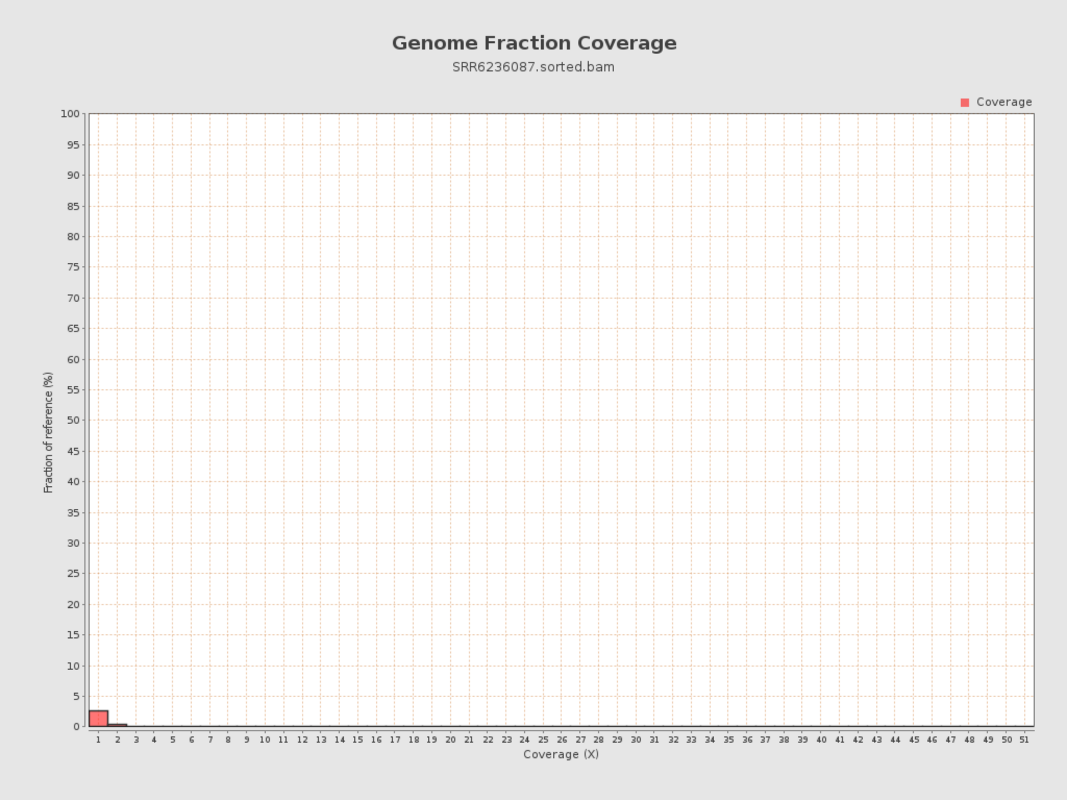
4. Results : Coverage Histogram



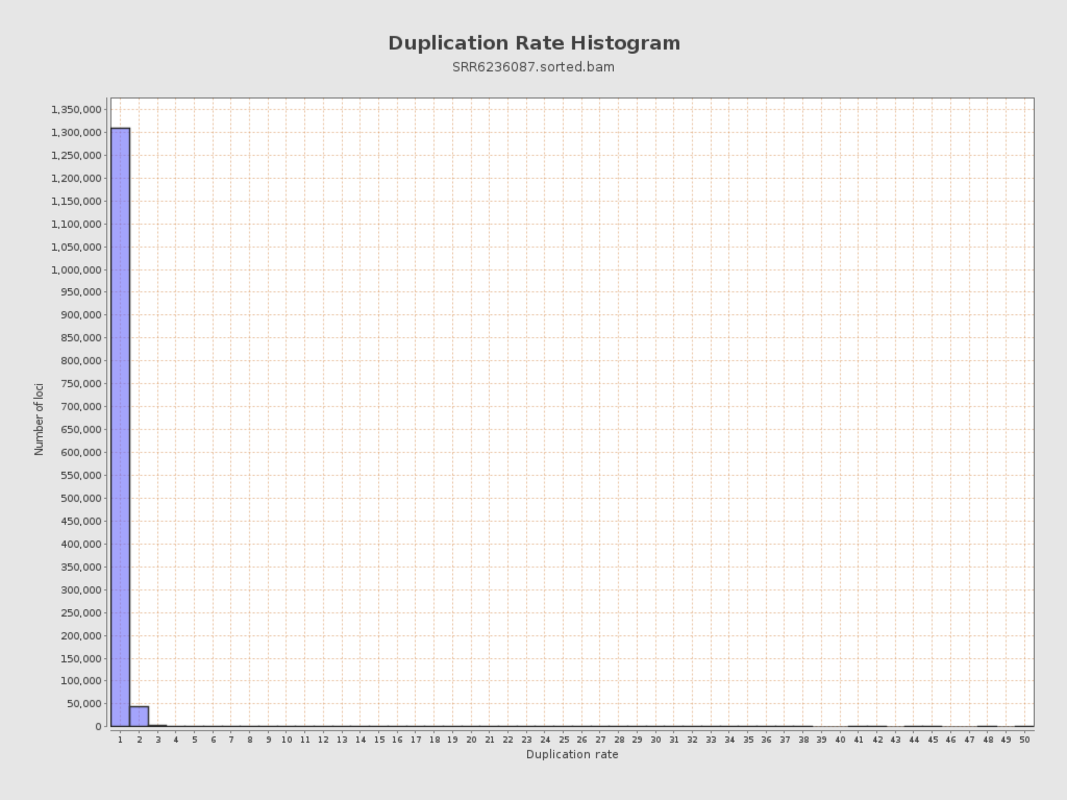
5. Results : Coverage Histogram (0-50X)



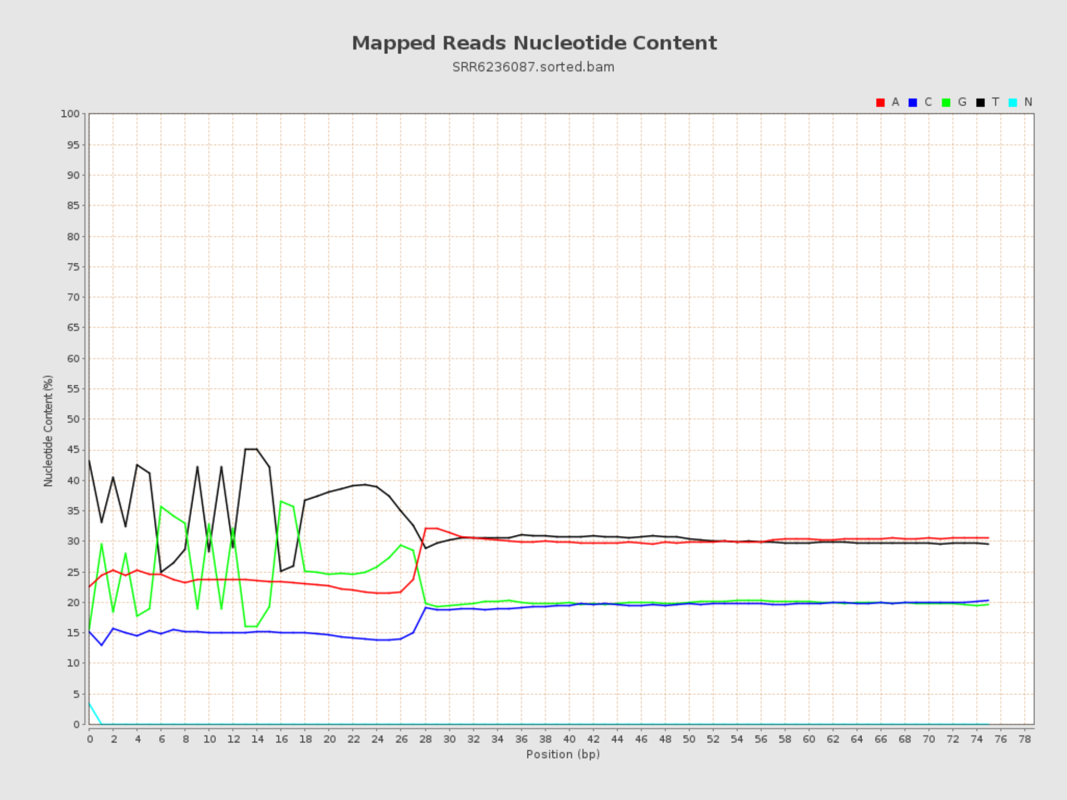
6. Results : Genome Fraction Coverage



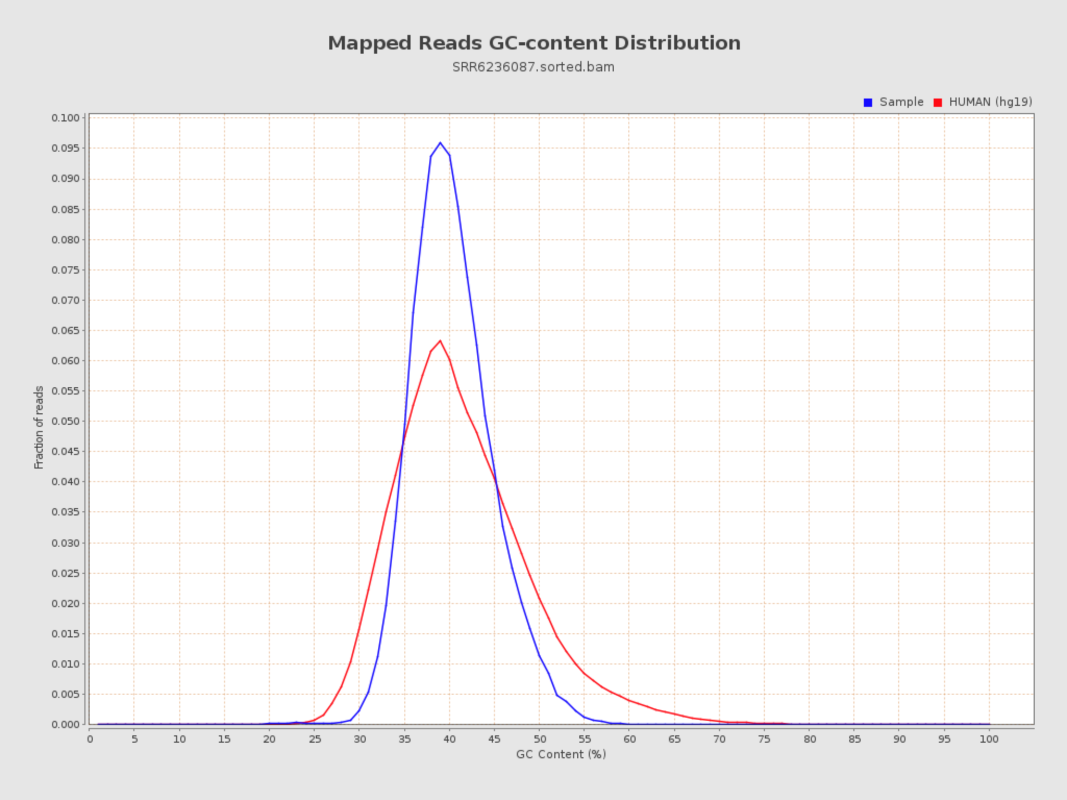
7. Results : Duplication Rate Histogram



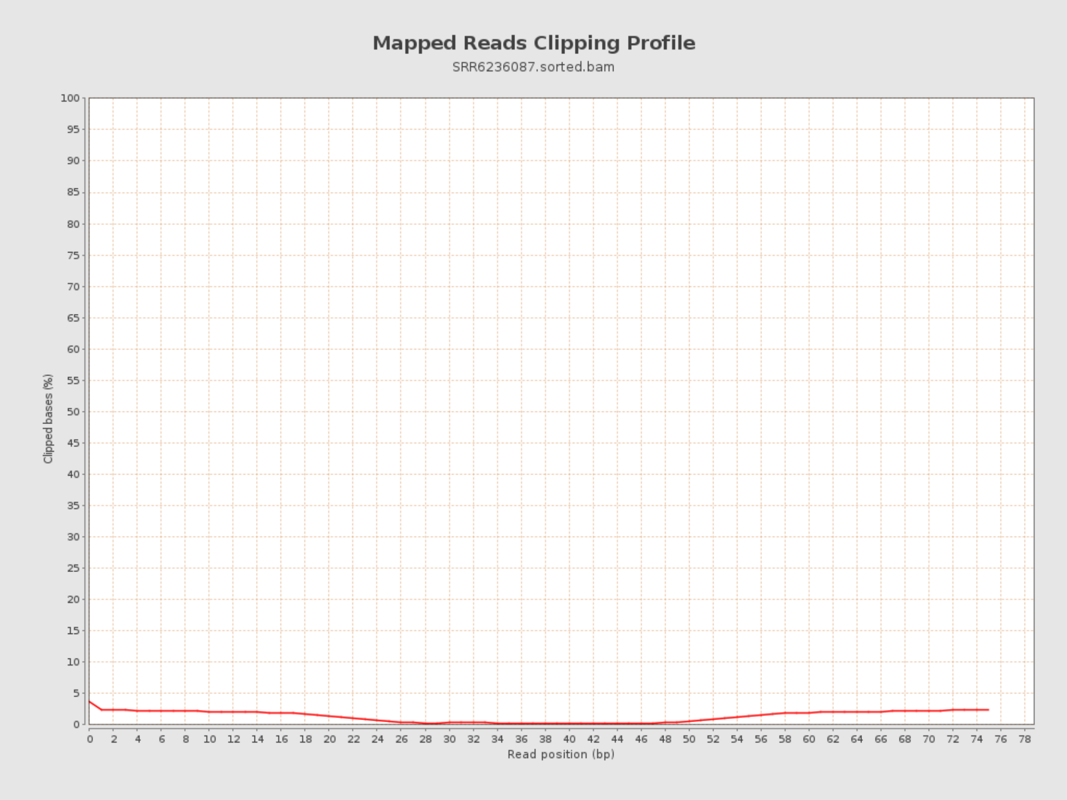
8. Results : Mapped Reads Nucleotide Content



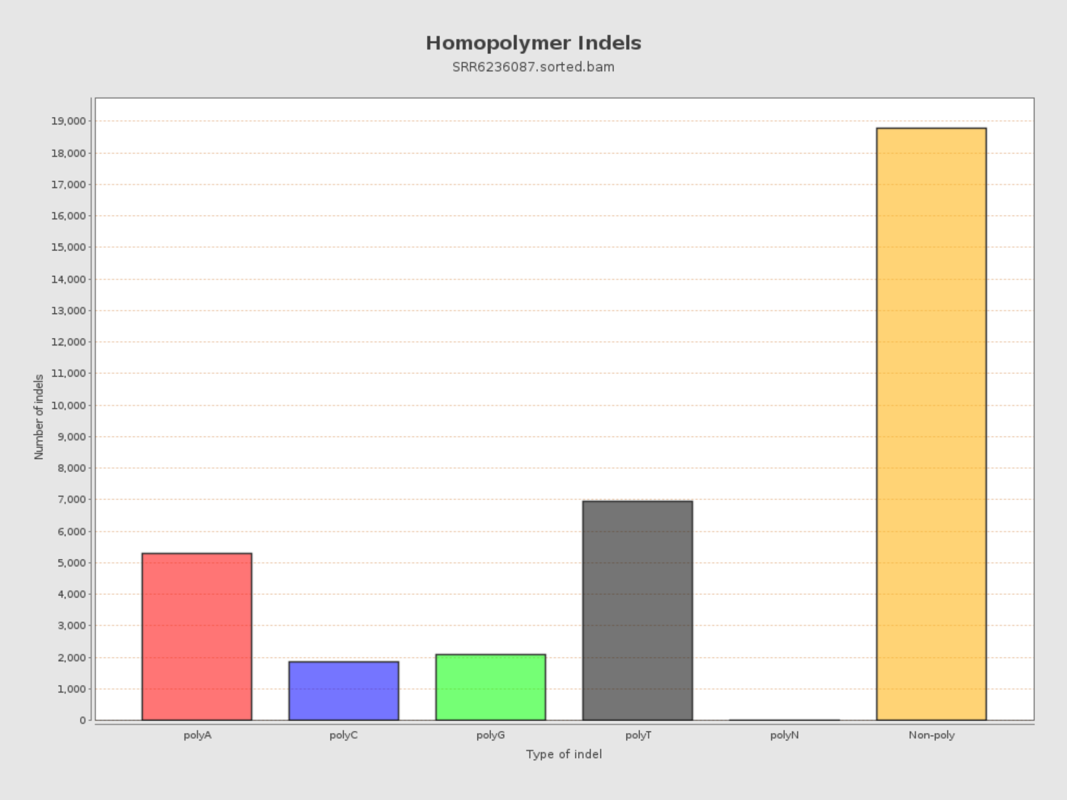
9. Results : Mapped Reads GC-content Distribution



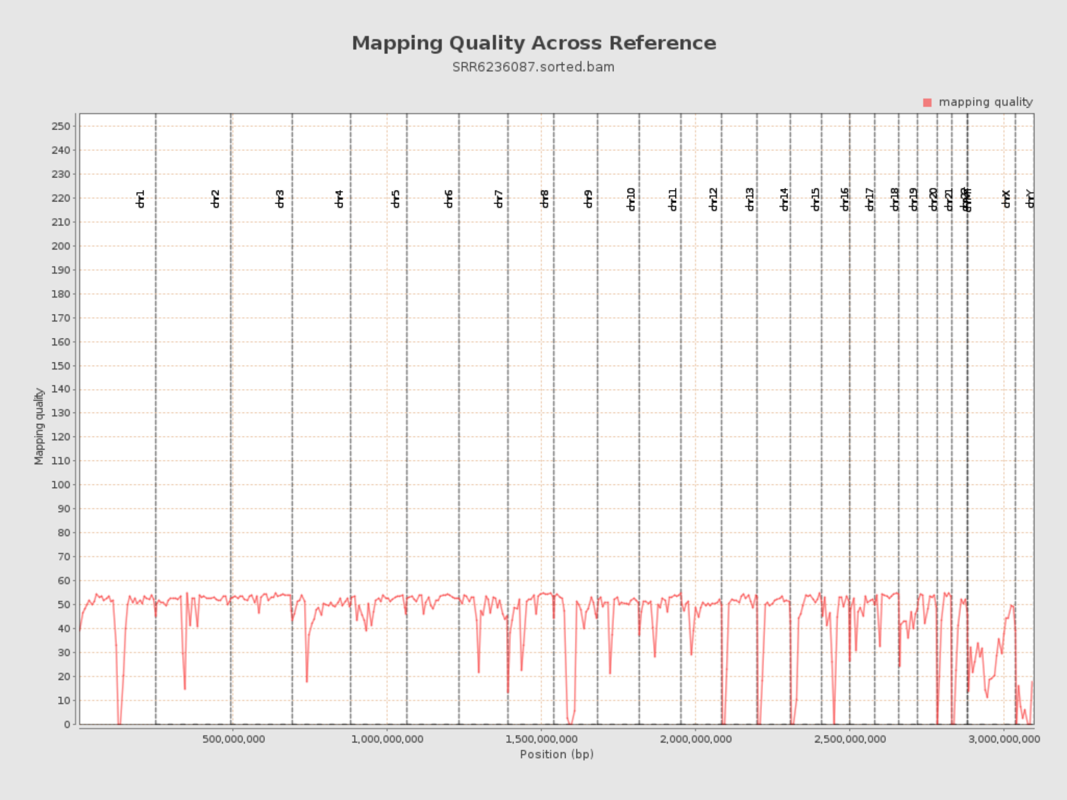
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram