Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:08:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236112.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_SRR6236112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:08:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,667,044
Mapped reads	1,491,065 / 89.44%
Unmapped reads	175,979 / 10.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,299 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	62,880 / 3.77%
Duplication rate	3.12%
Clipped reads	589,639 / 35.37%

2.2. ACGT Content

Number/percentage of A's	28,433,230 / 28.23%
Number/percentage of C's	18,149,180 / 18.02%
Number/percentage of T's	32,374,791 / 32.15%
Number/percentage of G's	21,687,114 / 21.53%
Number/percentage of N's	63,278 / 0.06%
GC Percentage	39.56%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.3658

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

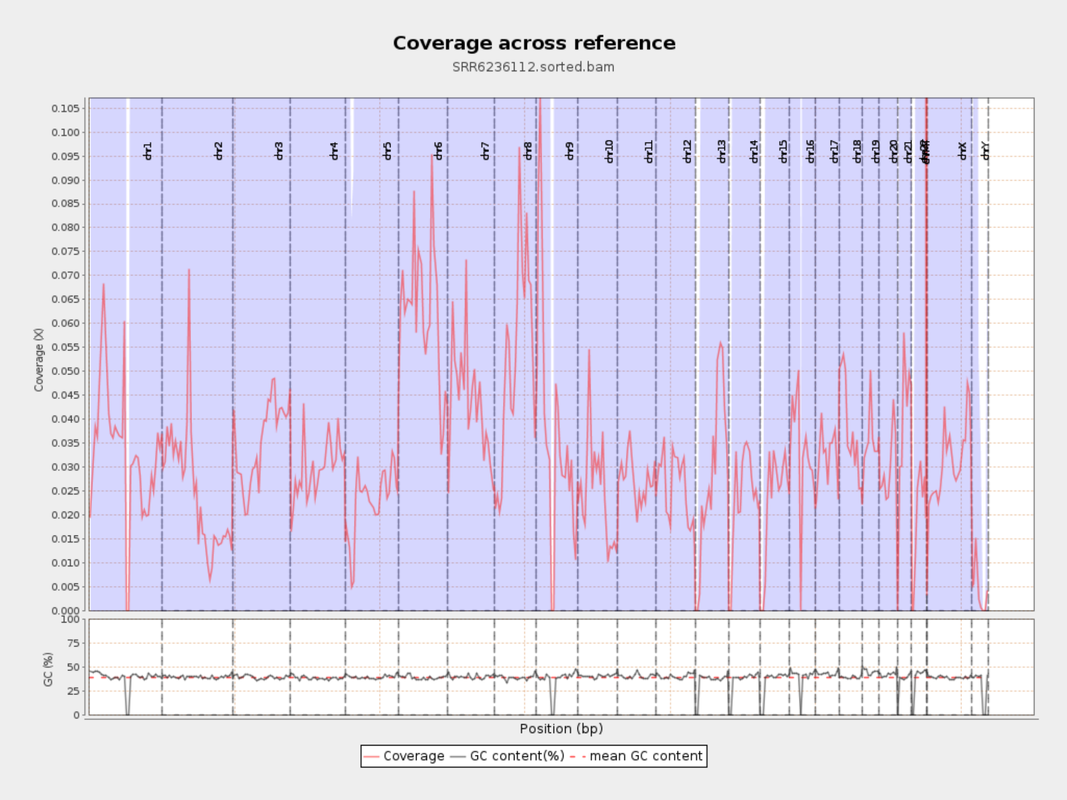
General error rate	0.87%
Mismatches	860,874
Insertions	7,840
Mapped reads with at least one insertion	0.52%
Deletions	32,579
Mapped reads with at least one deletion	2.16%
Homopolymer indels	46.38%

2.6. Chromosome stats

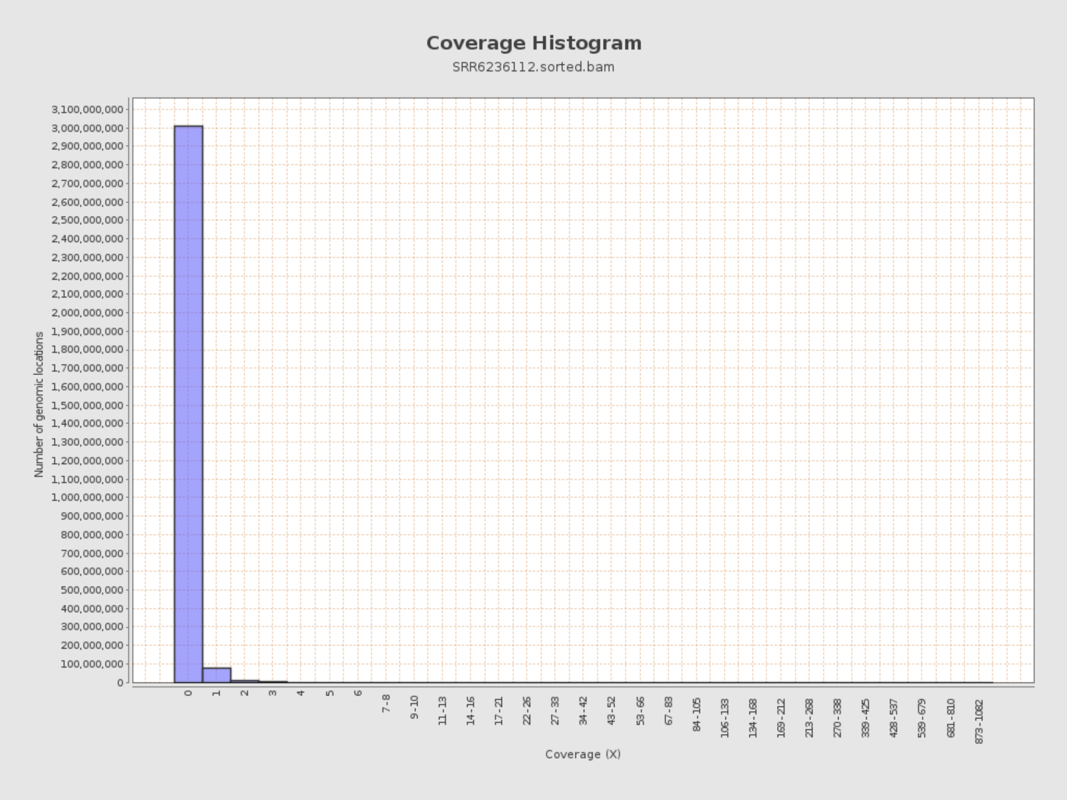
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8334029	0.0334	0.629
chr2	243199373	6039624	0.0248	0.3286
chr3	198022430	6994768	0.0353	0.2106
chr4	191154276	5664207	0.0296	0.218
chr5	180915260	4167591	0.023	0.1763
chr6	171115067	10581376	0.0618	0.3826
chr7	159138663	6999791	0.044	0.5266

chr8	146364022	7607570	0.052	0.7315
chr9	141213431	5277380	0.0374	0.3479
chr10	135534747	3398247	0.0251	0.2895
chr11	135006516	3653855	0.0271	0.2583
chr12	133851895	3475333	0.026	0.1898
chr13	115169878	3284522	0.0285	0.1888
chr14	107349540	2506790	0.0234	0.1895
chr15	102531392	2334003	0.0228	0.1696
chr16	90354753	2995056	0.0331	0.2379
chr17	81195210	2591522	0.0319	0.2282
chr18	78077248	3022662	0.0387	0.5982
chr19	59128983	2100331	0.0355	0.4517
chr20	63025520	1852556	0.0294	0.1981
chr21	48129895	1859020	0.0386	0.2481
chr22	51304566	965723	0.0188	0.1514
chrMT	16571	90357	5.4527	3.8998
chrX	155270560	4728320	0.0305	0.2162
chrY	59373566	240443	0.004	0.1239

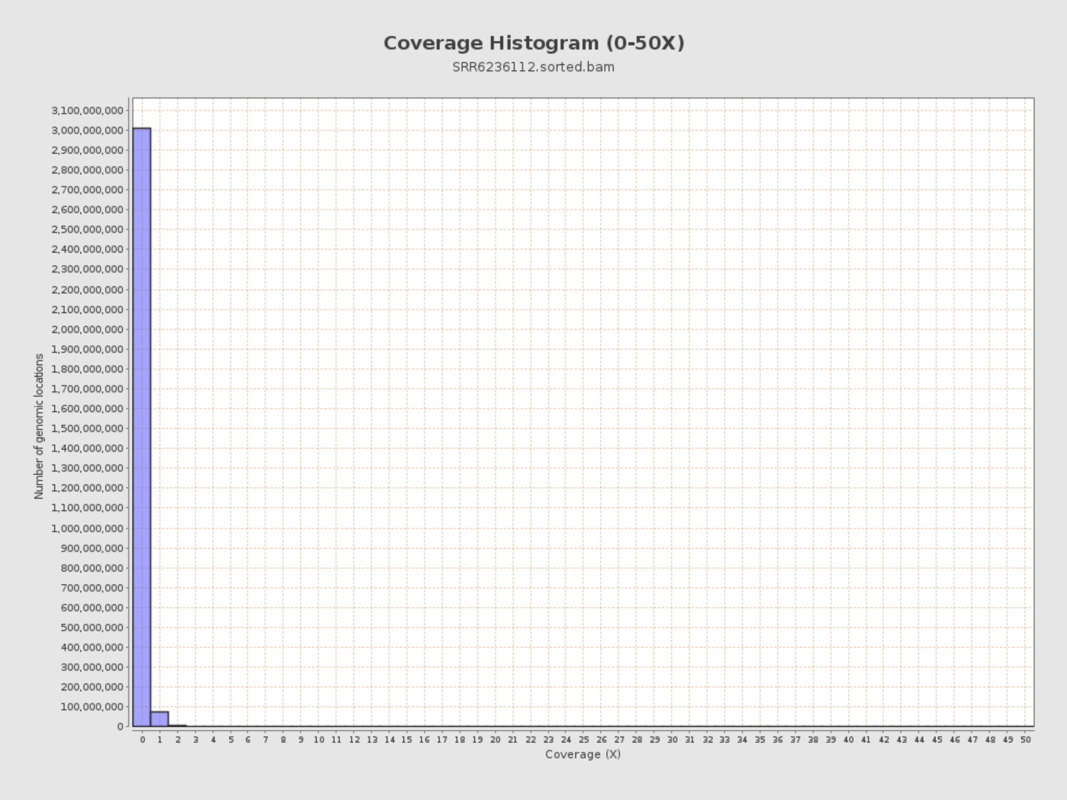
3. Results : Coverage across reference



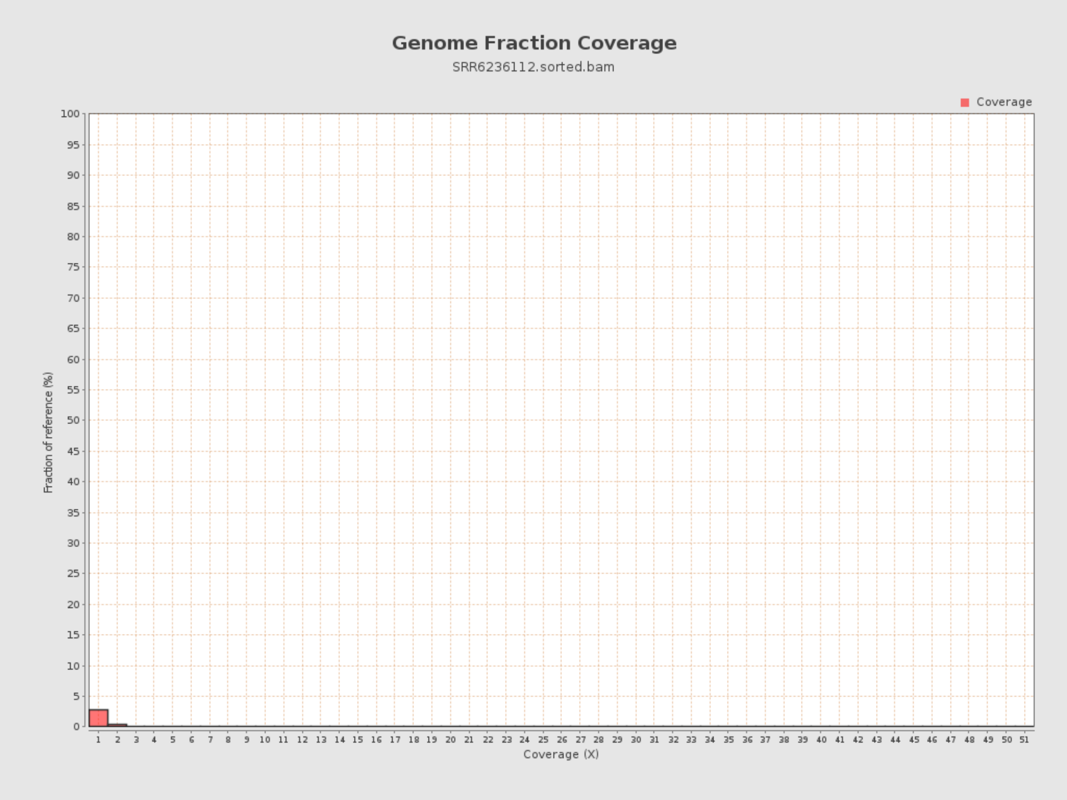
4. Results : Coverage Histogram



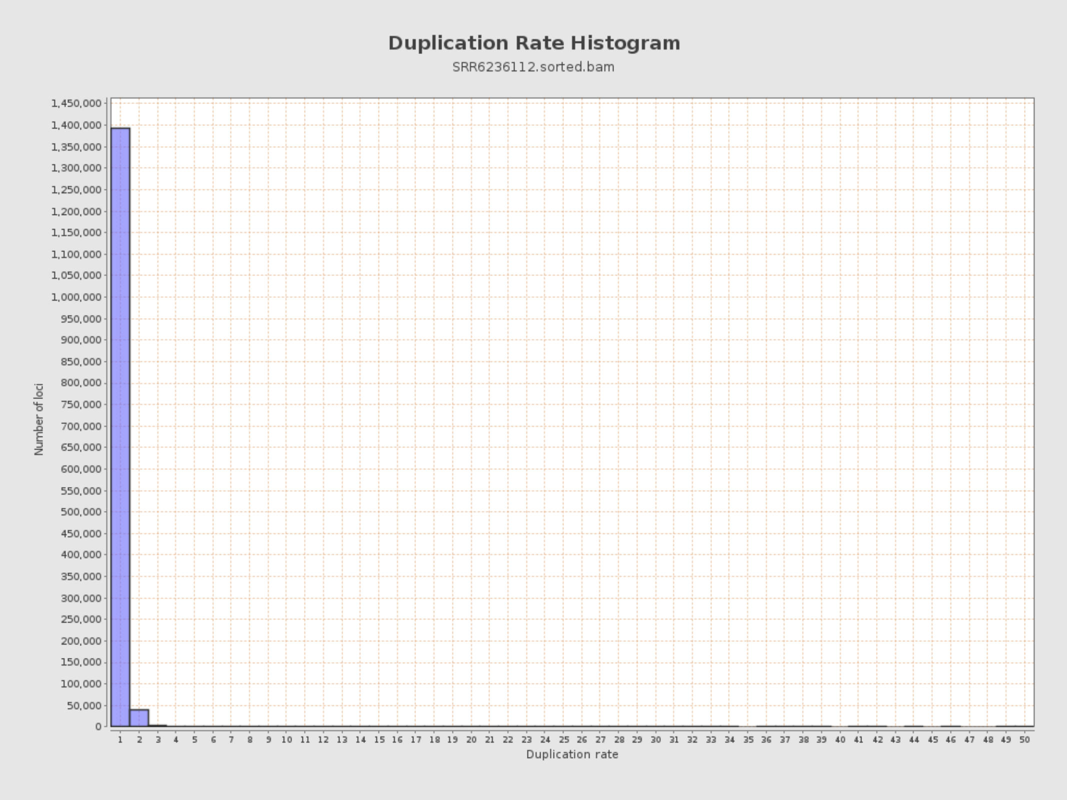
5. Results : Coverage Histogram (0-50X)



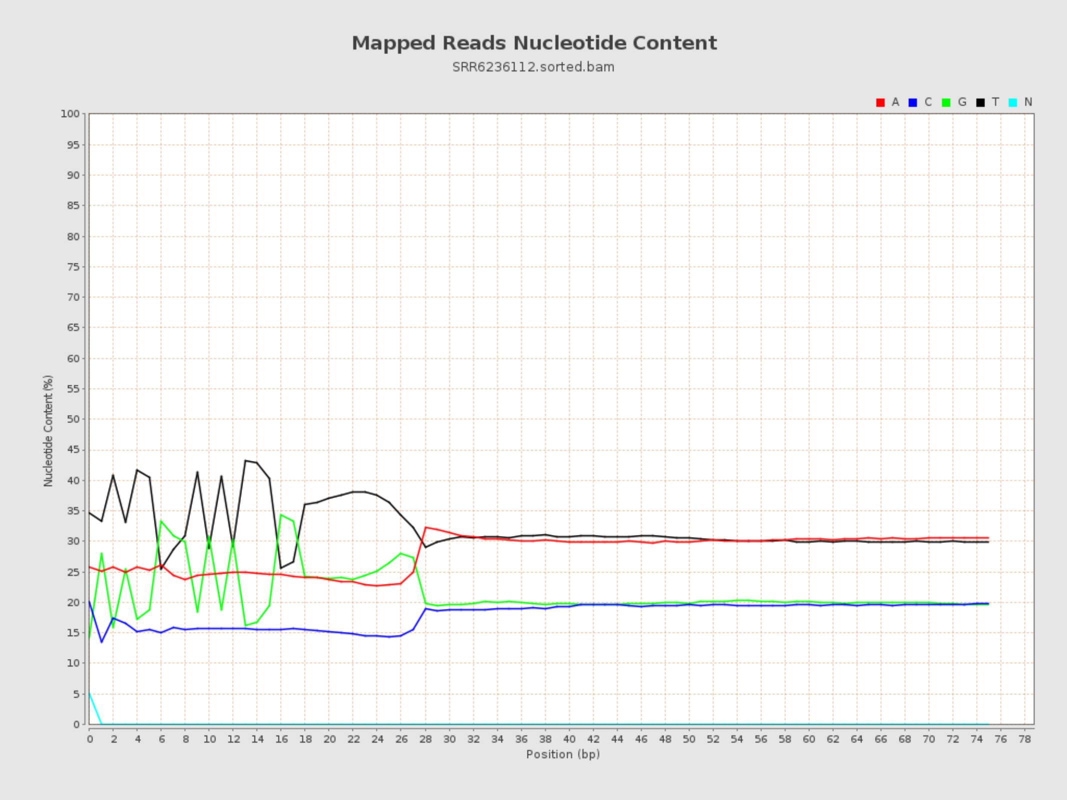
6. Results : Genome Fraction Coverage



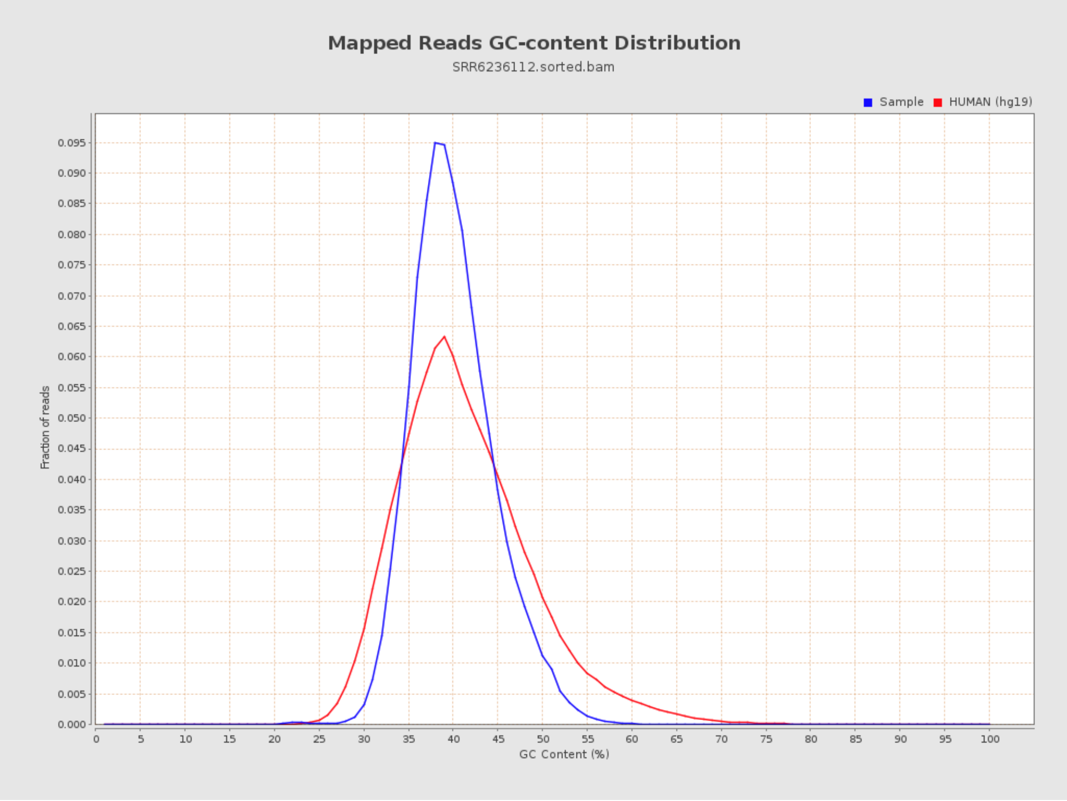
7. Results : Duplication Rate Histogram



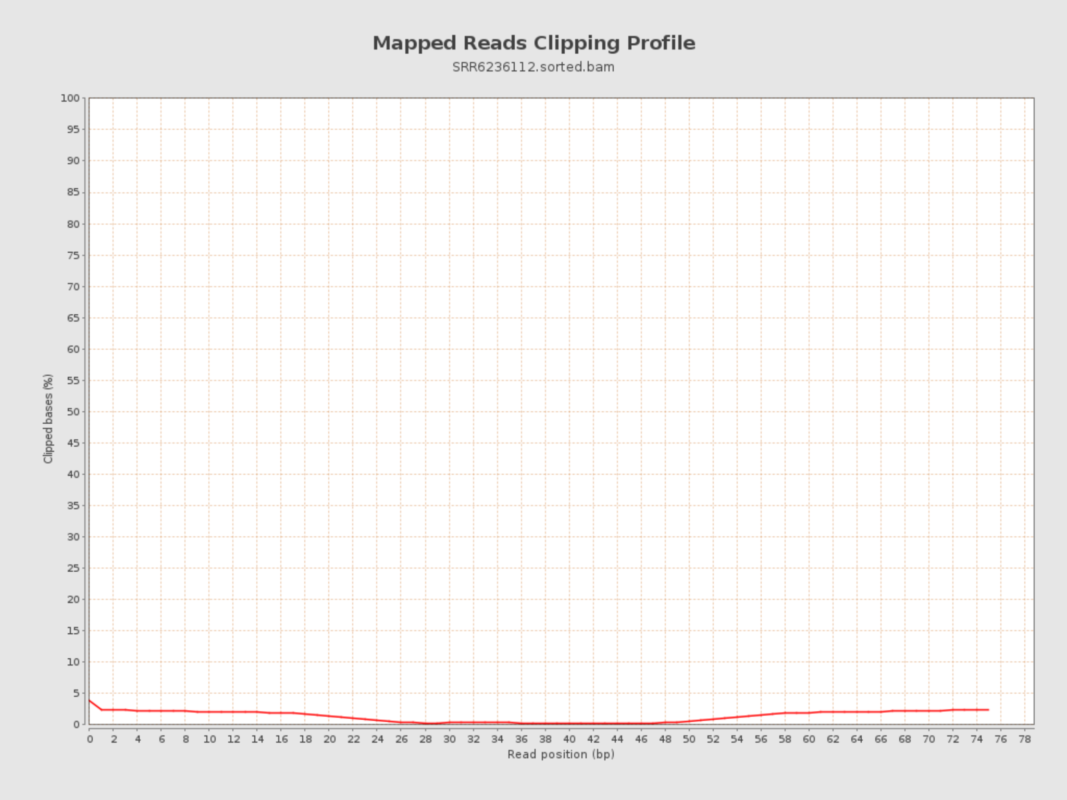
8. Results : Mapped Reads Nucleotide Content



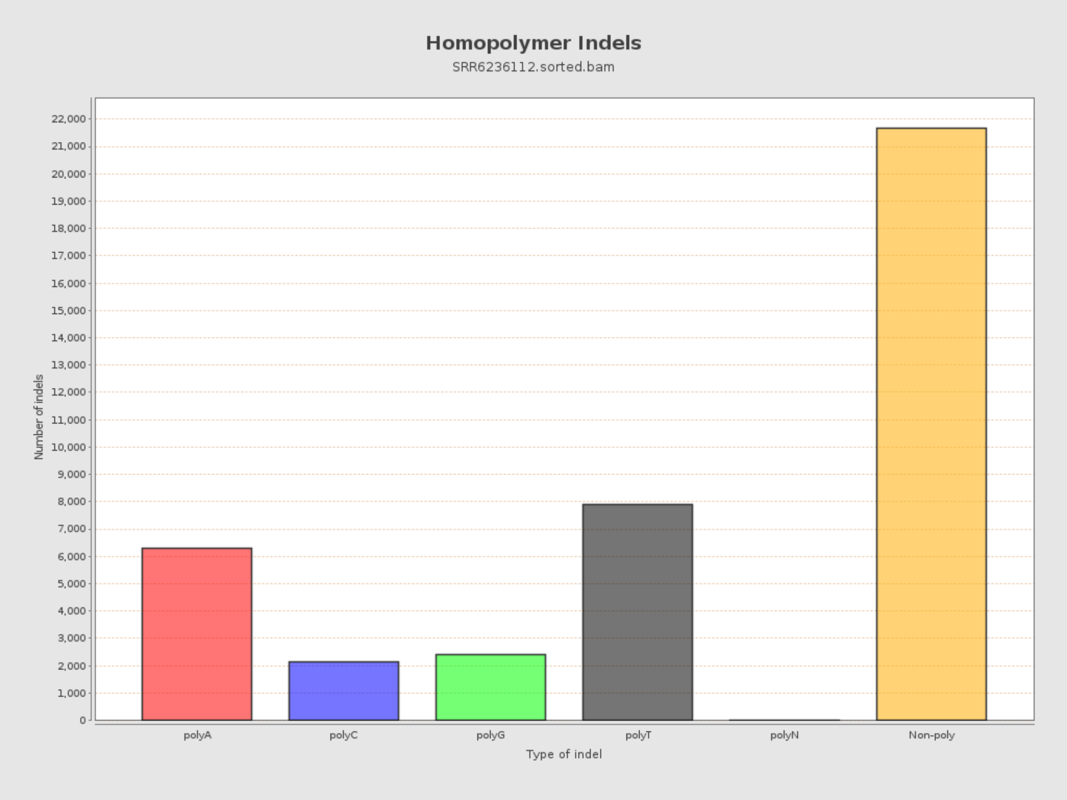
9. Results : Mapped Reads GC-content Distribution



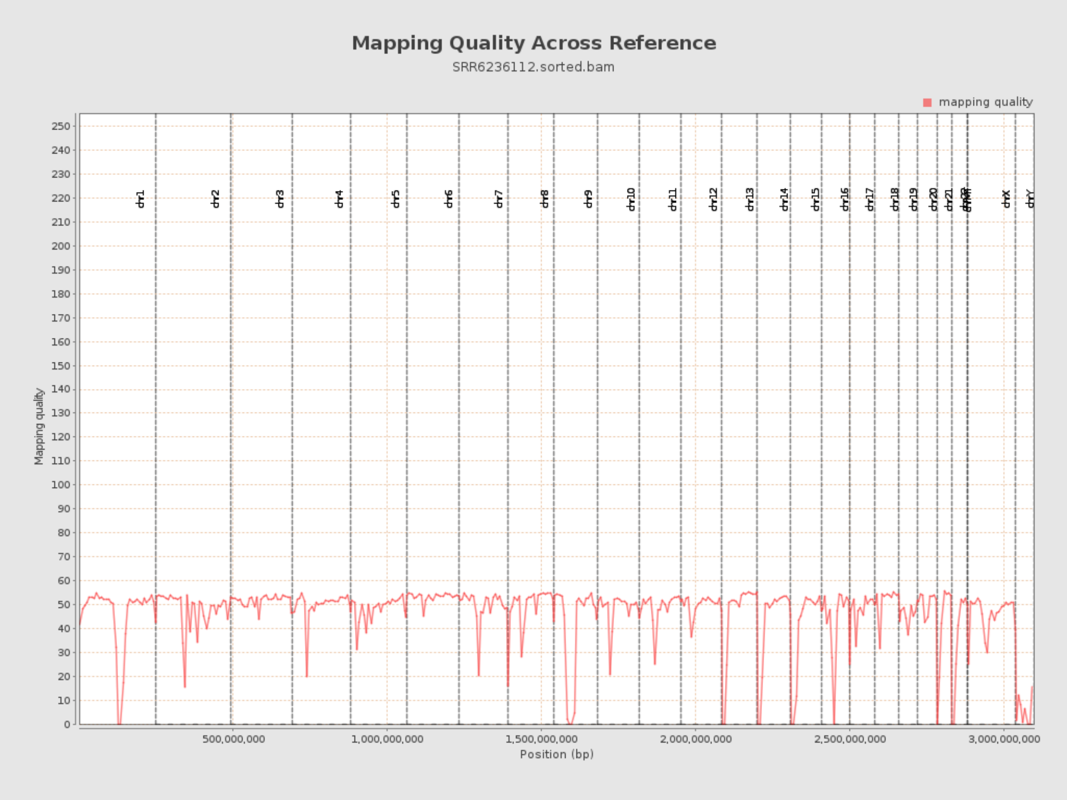
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram