Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:19:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236095.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_SRR6236095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:19:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,111,307
Mapped reads	923,728 / 83.12%
Unmapped reads	187,579 / 16.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,917 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	31,382 / 2.82%
Duplication rate	2.42%
Clipped reads	432,353 / 38.9%

2.2. ACGT Content

Number/percentage of A's	16,920,023 / 27.8%
Number/percentage of C's	10,790,825 / 17.73%
Number/percentage of T's	19,331,161 / 31.76%
Number/percentage of G's	13,781,735 / 22.65%
Number/percentage of N's	33,583 / 0.06%
GC Percentage	40.38%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.2375

2.4. Mapping Quality

Mean Mapping Quality	43.53

2.5. Mismatches and indels

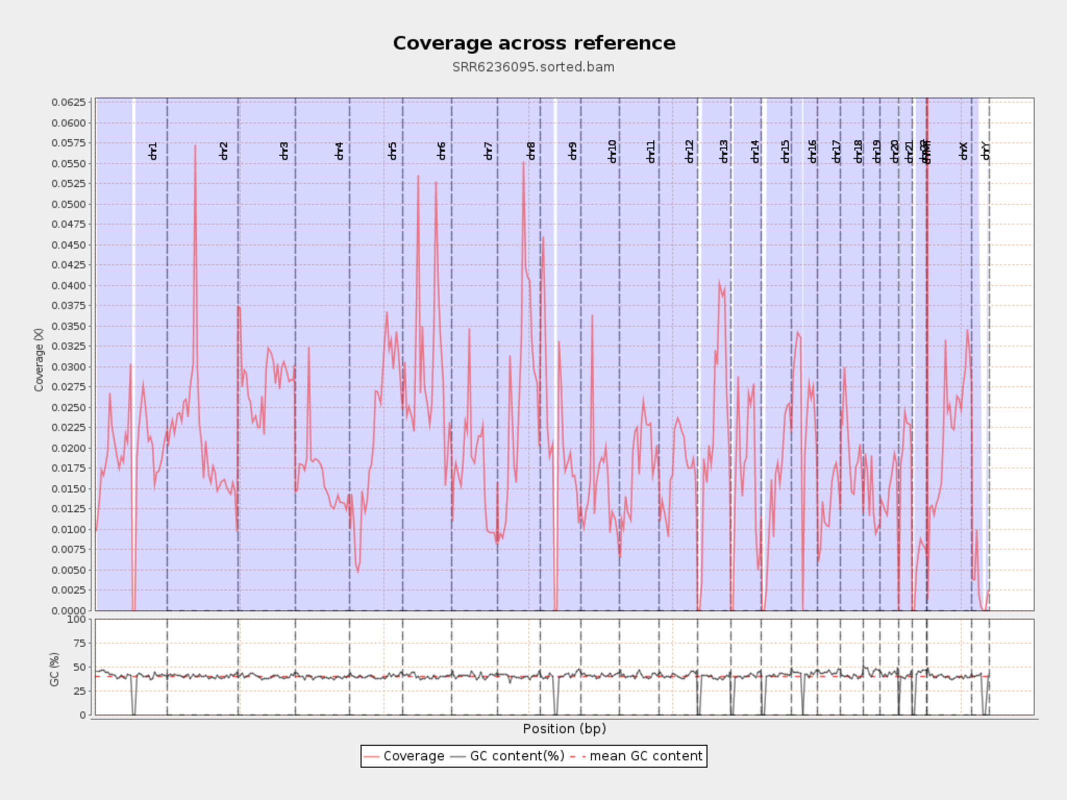
General error rate	0.88%
Mismatches	523,365
Insertions	5,132
Mapped reads with at least one insertion	0.55%
Deletions	16,830
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.76%

2.6. Chromosome stats

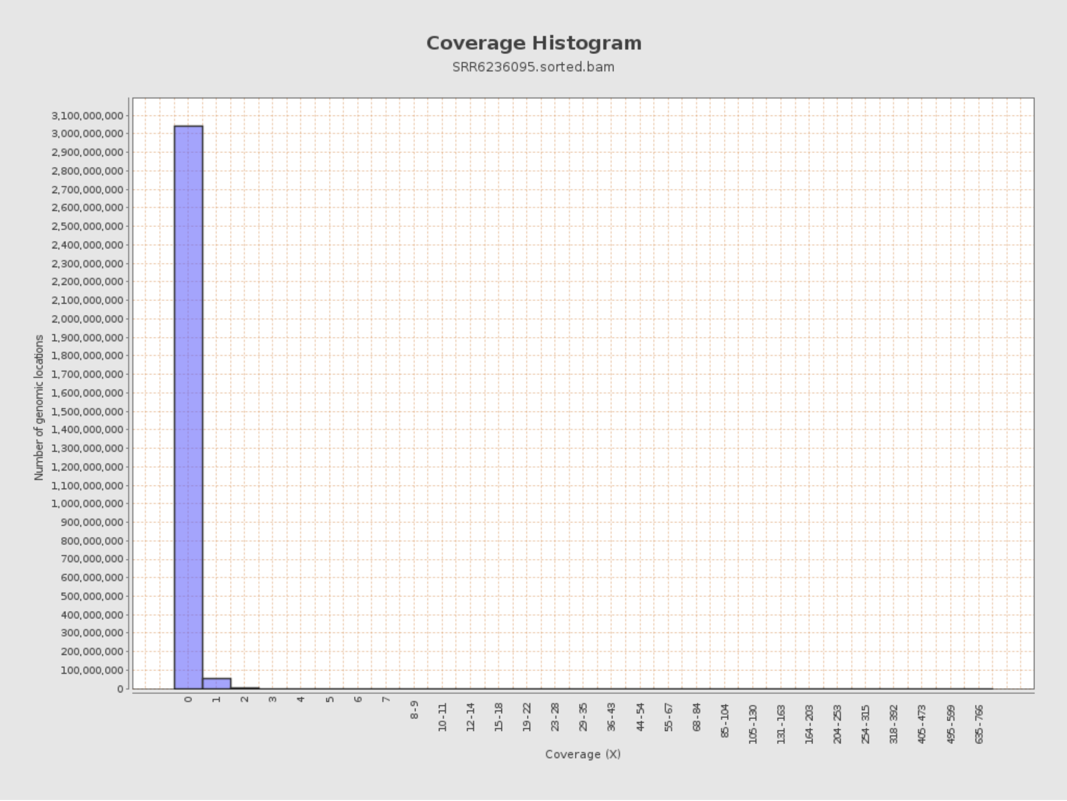
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4698635	0.0189	0.2803
chr2	243199373	5154805	0.0212	0.2802
chr3	198022430	5575023	0.0282	0.178
chr4	191154276	3110416	0.0163	0.1574
chr5	180915260	3989638	0.0221	0.1597
chr6	171115067	5035417	0.0294	0.2535
chr7	159138663	2739068	0.0172	0.2462

chr8	146364022	3766112	0.0257	0.5051
chr9	141213431	2960899	0.021	0.266
chr10	135534747	2046379	0.0151	0.2222
chr11	135006516	2445256	0.0181	0.1961
chr12	133851895	2276819	0.017	0.1456
chr13	115169878	2541398	0.0221	0.1569
chr14	107349540	1666619	0.0155	0.1589
chr15	102531392	1475945	0.0144	0.1328
chr16	90354753	2235604	0.0247	0.1843
chr17	81195210	1027002	0.0126	0.1324
chr18	78077248	1555172	0.0199	0.4203
chr19	59128983	823225	0.0139	0.2401
chr20	63025520	928153	0.0147	0.1358
chr21	48129895	935382	0.0194	0.1787
chr22	51304566	296033	0.0058	0.0791
chrMT	16571	26236	1.5832	1.6504
chrX	155270560	3413364	0.022	0.1756
chrY	59373566	164379	0.0028	0.0969

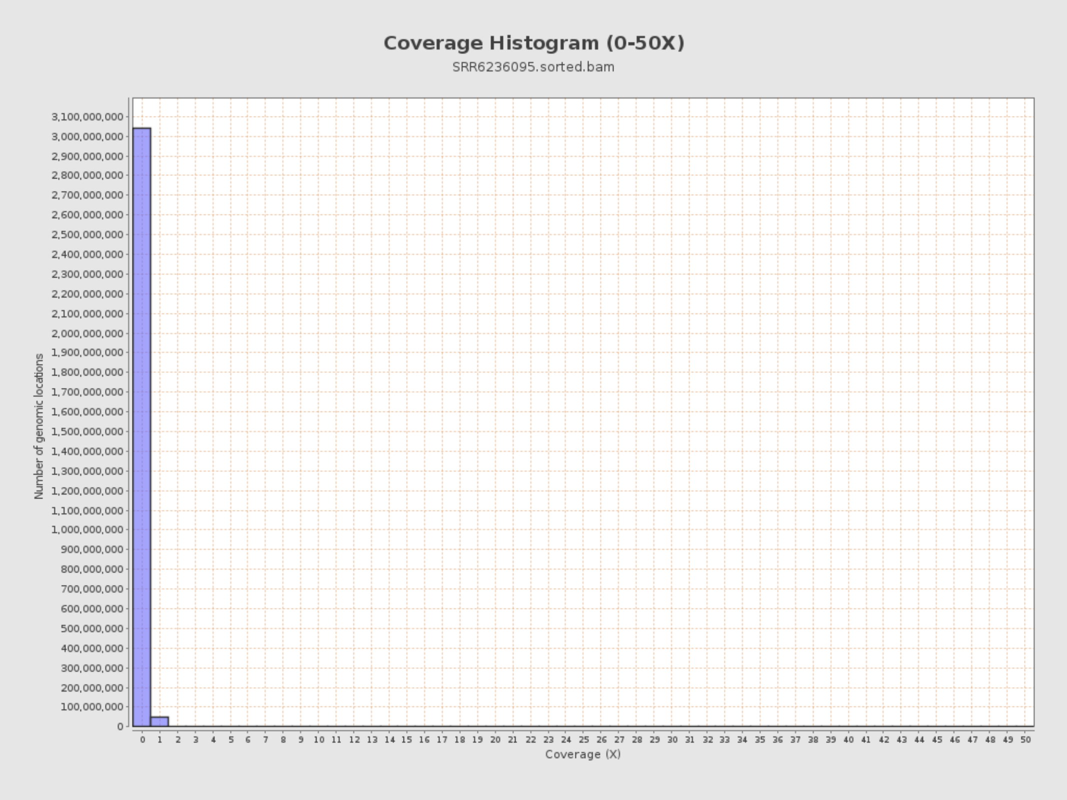
3. Results : Coverage across reference



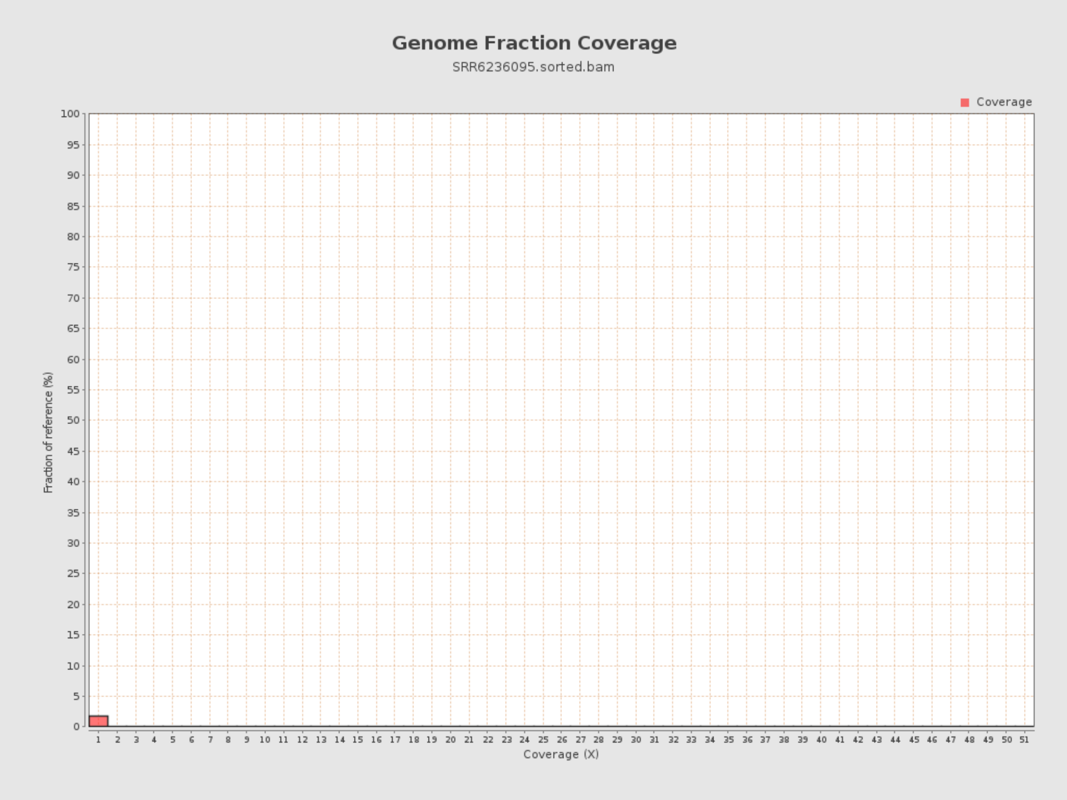
4. Results : Coverage Histogram



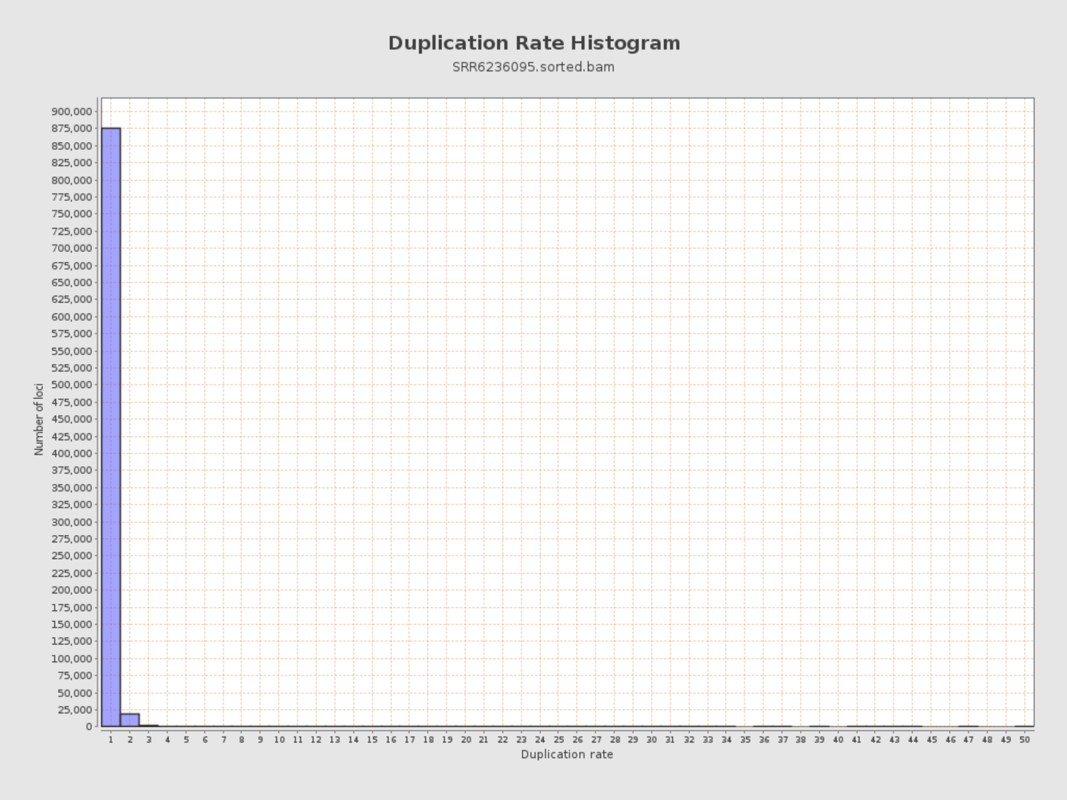
5. Results : Coverage Histogram (0-50X)



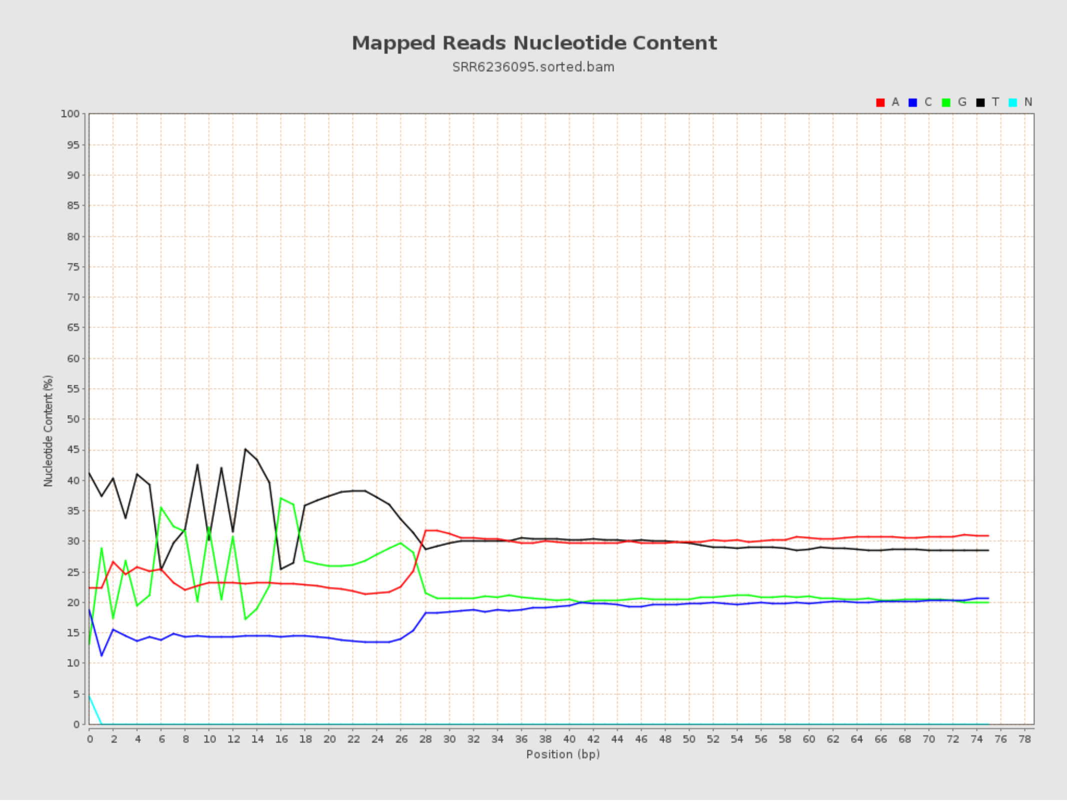
6. Results : Genome Fraction Coverage



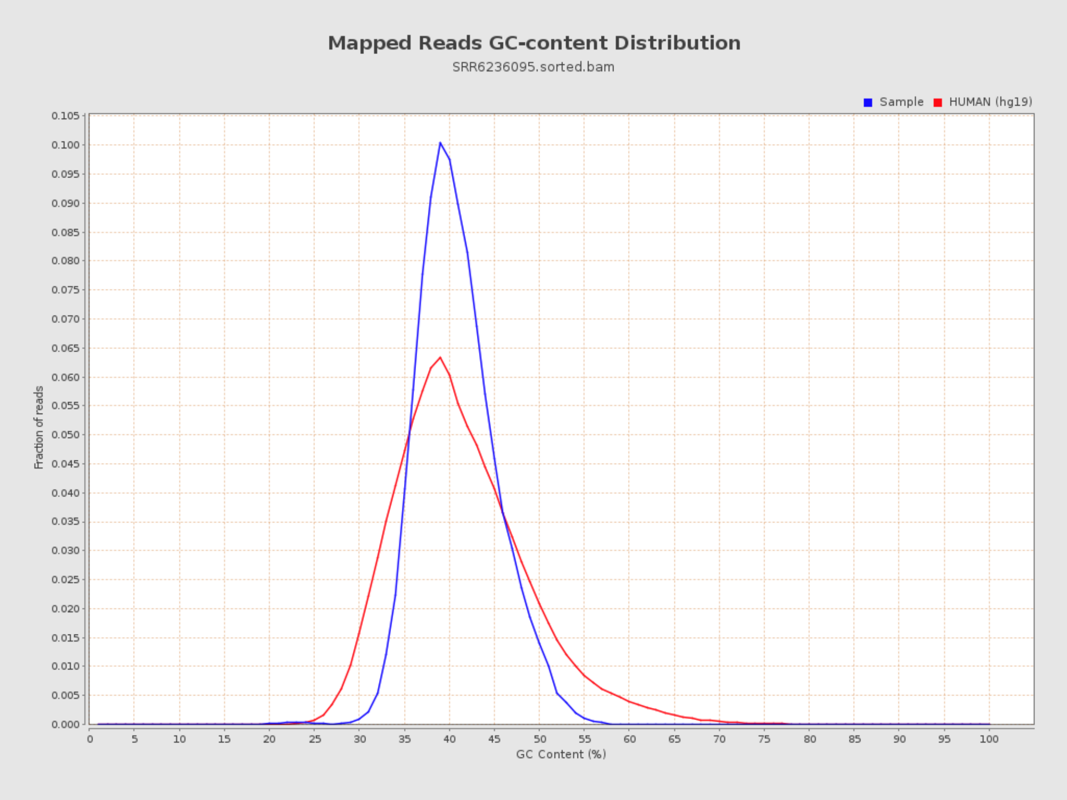
7. Results : Duplication Rate Histogram



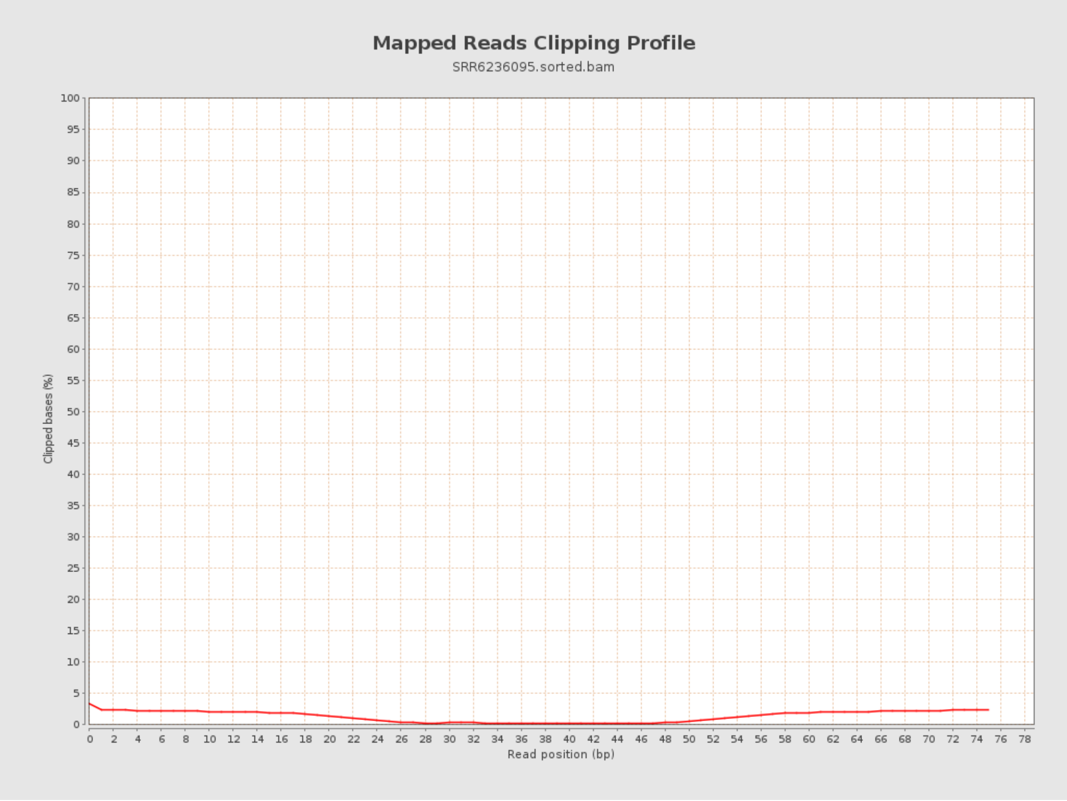
8. Results : Mapped Reads Nucleotide Content



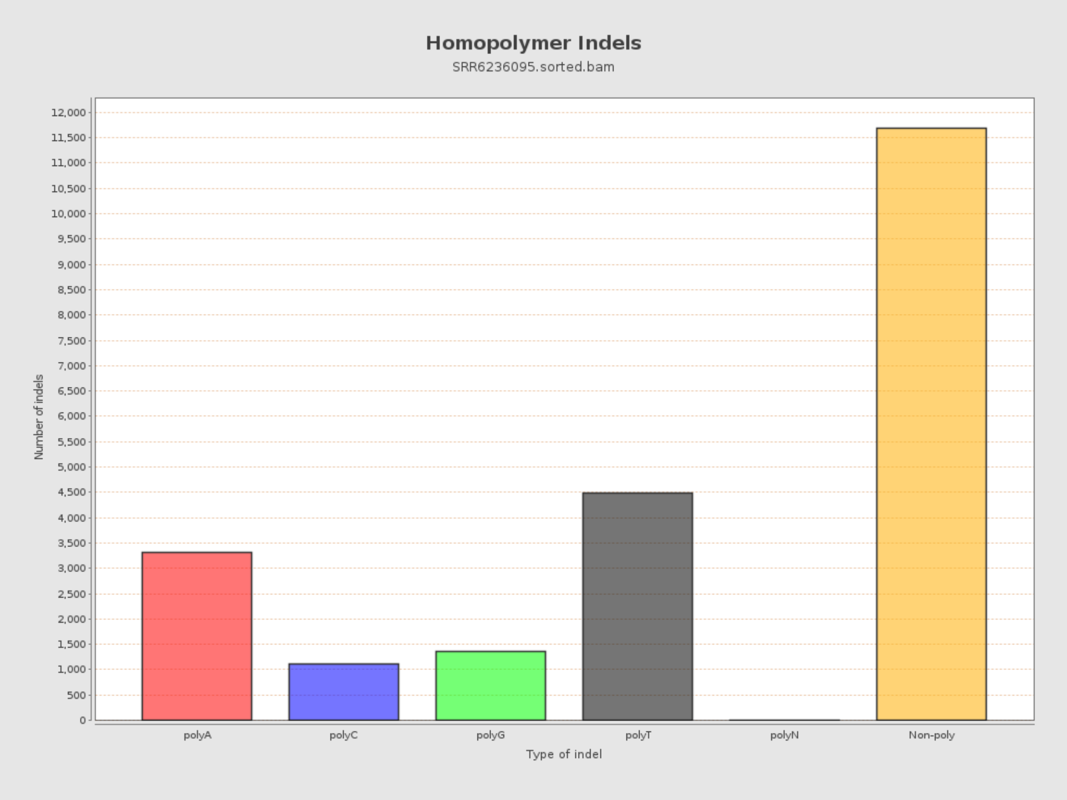
9. Results : Mapped Reads GC-content Distribution



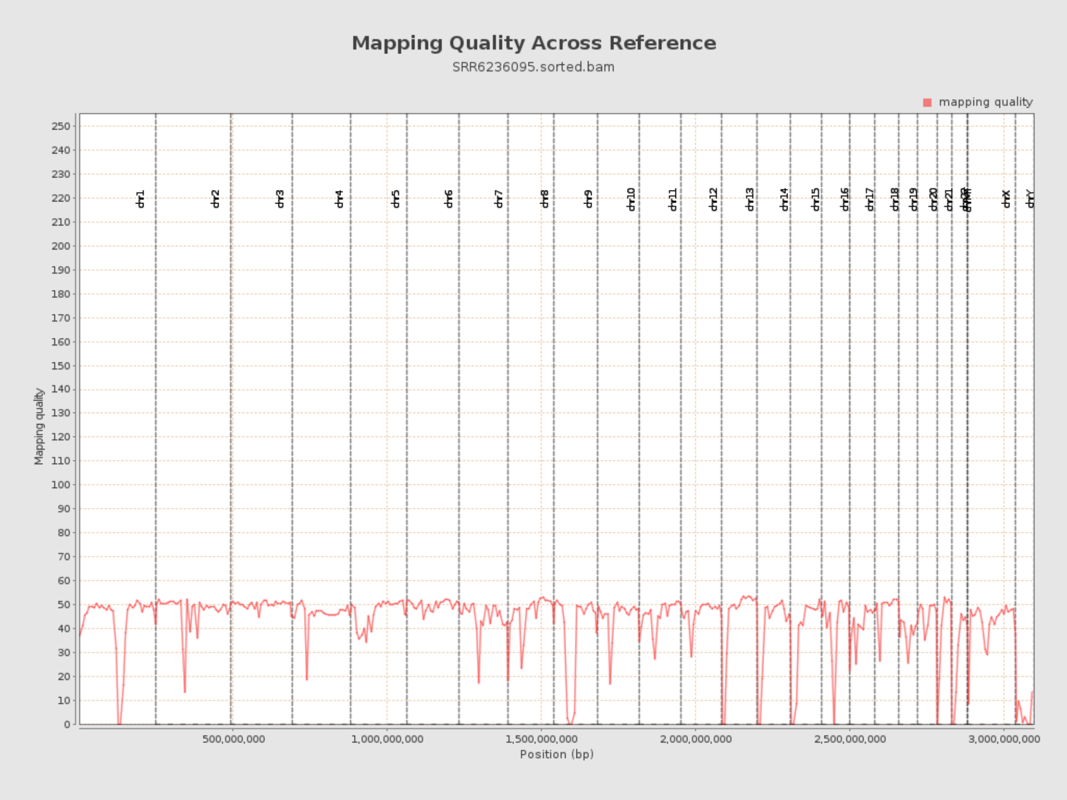
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram