Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:31:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236079.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_SRR6236079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:31:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,403,393
Mapped reads	1,207,104 / 86.01%
Unmapped reads	196,289 / 13.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,630 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	63,823 / 4.55%
Duplication rate	4.49%
Clipped reads	747,399 / 53.26%

2.2. ACGT Content

Number/percentage of A's	21,220,353 / 28.1%
Number/percentage of C's	13,930,329 / 18.45%
Number/percentage of T's	23,893,287 / 31.64%
Number/percentage of G's	16,421,855 / 21.75%
Number/percentage of N's	40,025 / 0.05%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2309

2.4. Mapping Quality

Mean Mapping Quality	41.4

2.5. Mismatches and indels

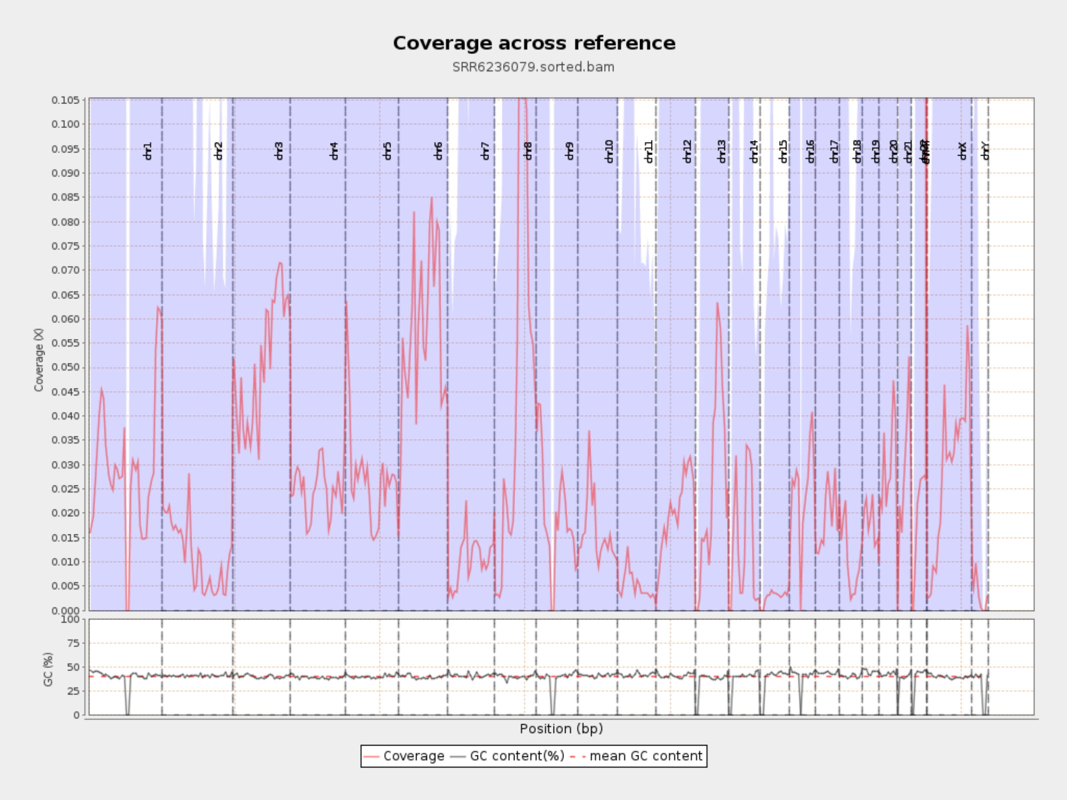
General error rate	1%
Mismatches	742,221
Insertions	5,676
Mapped reads with at least one insertion	0.47%
Deletions	21,727
Mapped reads with at least one deletion	1.78%
Homopolymer indels	44.87%

2.6. Chromosome stats

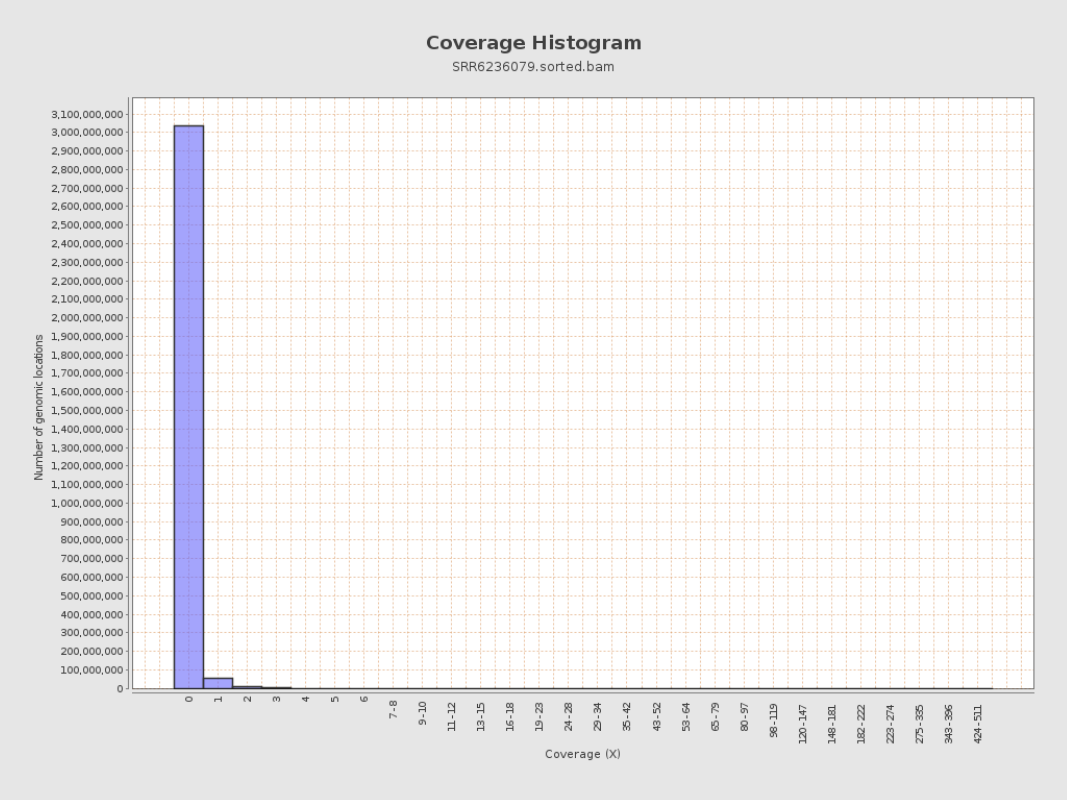
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7245910	0.0291	0.3134
chr2	243199373	2770810	0.0114	0.2277
chr3	198022430	10110120	0.0511	0.2677
chr4	191154276	4747669	0.0248	0.1897
chr5	180915260	4964806	0.0274	0.1955
chr6	171115067	9765374	0.0571	0.3326
chr7	159138663	1612371	0.0101	0.1945

chr8	146364022	6641579	0.0454	0.404
chr9	141213431	2764655	0.0196	0.1863
chr10	135534747	2197974	0.0162	0.1999
chr11	135006516	718123	0.0053	0.1096
chr12	133851895	2764547	0.0207	0.1709
chr13	115169878	2966870	0.0258	0.195
chr14	107349540	1387175	0.0129	0.1392
chr15	102531392	293401	0.0029	0.0719
chr16	90354753	2268130	0.0251	0.1917
chr17	81195210	1545522	0.019	0.1658
chr18	78077248	839819	0.0108	0.2595
chr19	59128983	1078604	0.0182	0.2435
chr20	63025520	1897110	0.0301	0.2054
chr21	48129895	1339209	0.0278	0.1988
chr22	51304566	943130	0.0184	0.1567
chrMT	16571	66116	3.9899	3.3845
chrX	155270560	4422882	0.0285	0.2088
chrY	59373566	191417	0.0032	0.0753

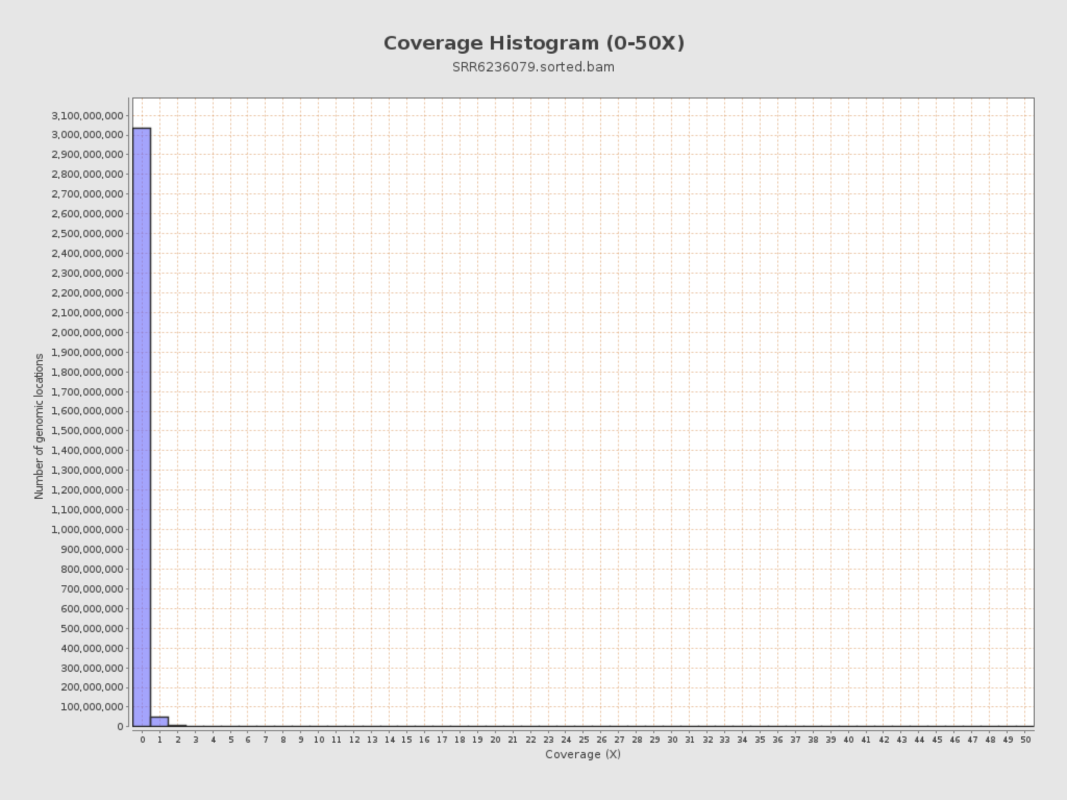
3. Results : Coverage across reference



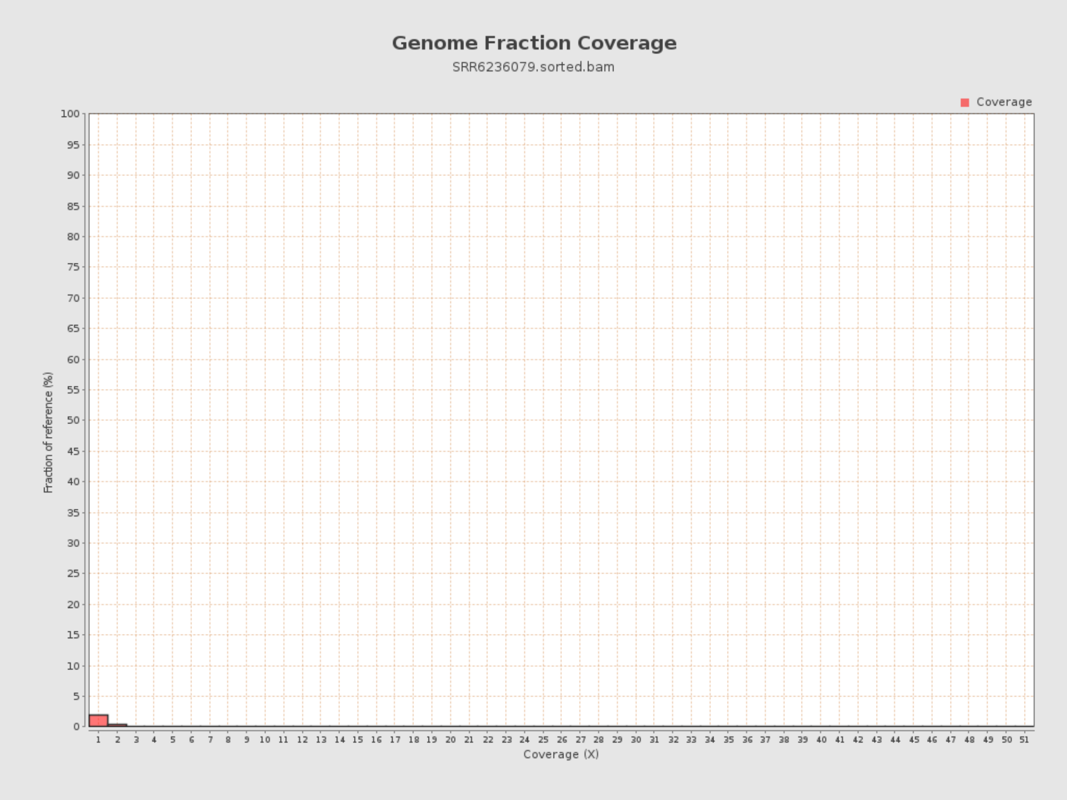
4. Results : Coverage Histogram



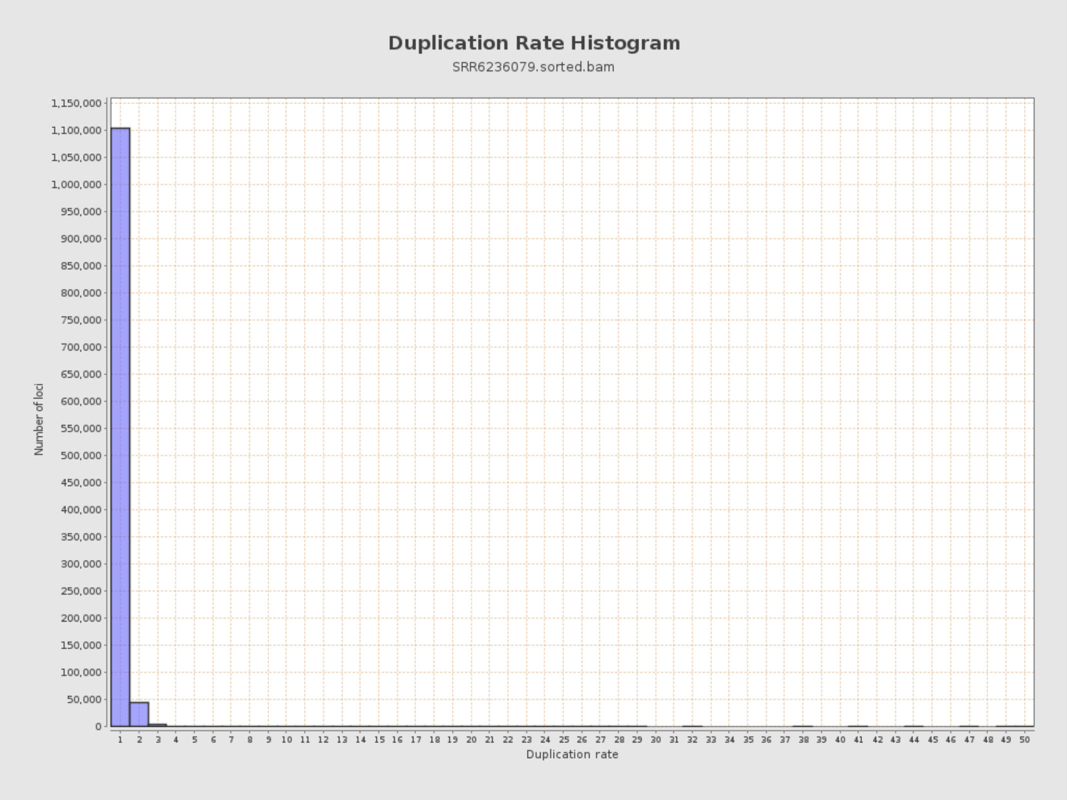
5. Results : Coverage Histogram (0-50X)



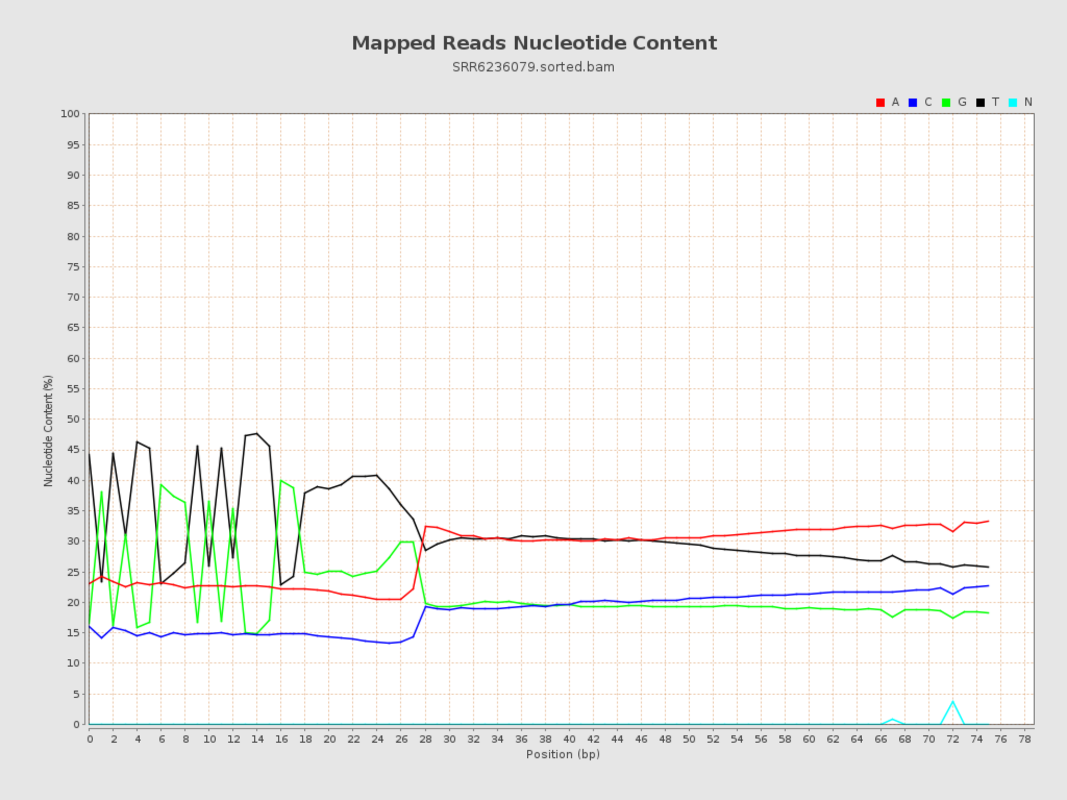
6. Results : Genome Fraction Coverage



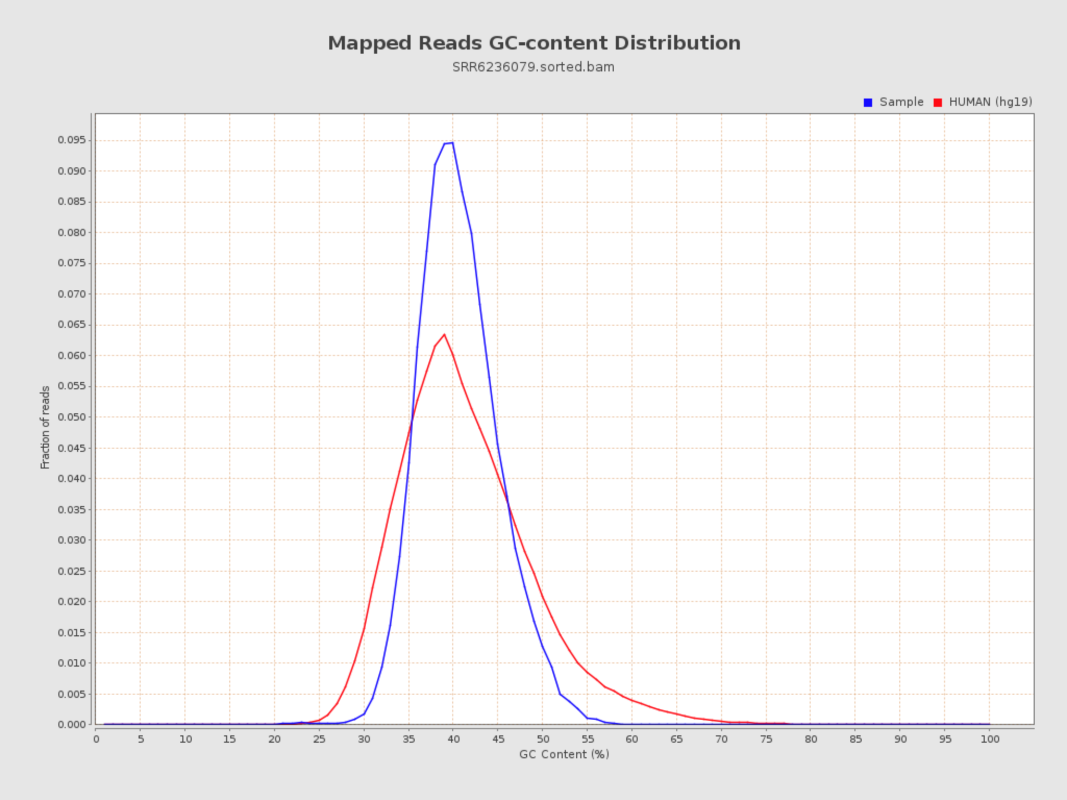
7. Results : Duplication Rate Histogram



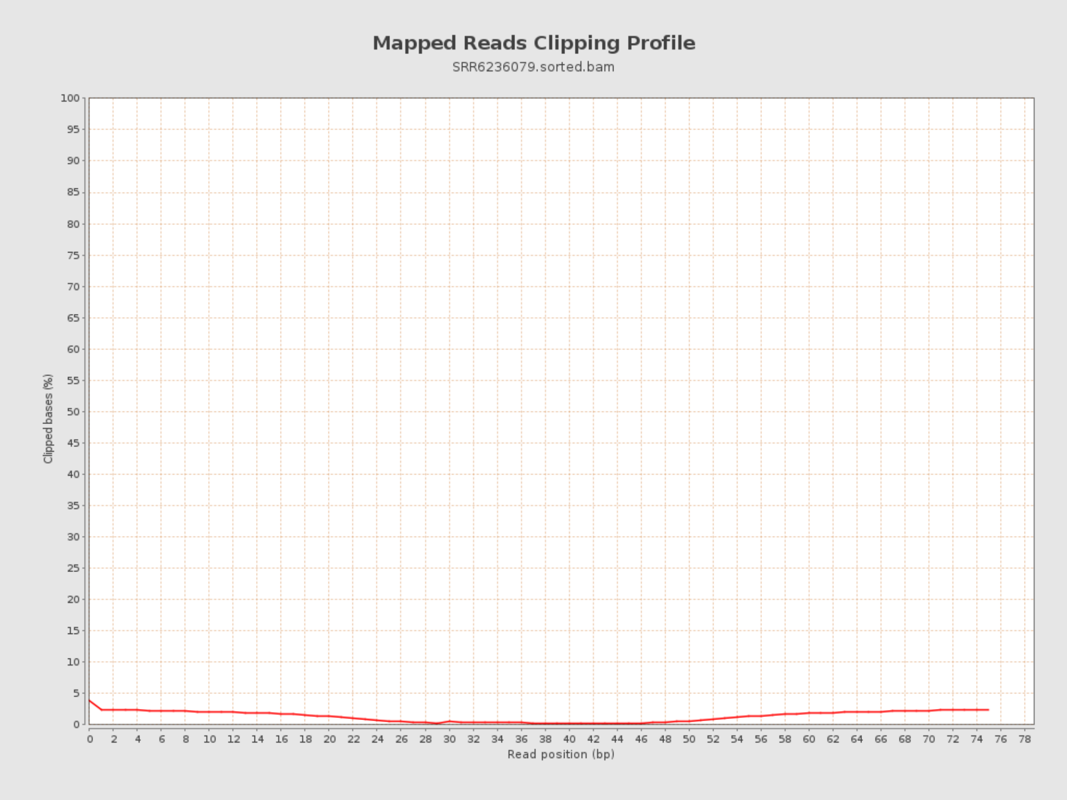
8. Results : Mapped Reads Nucleotide Content



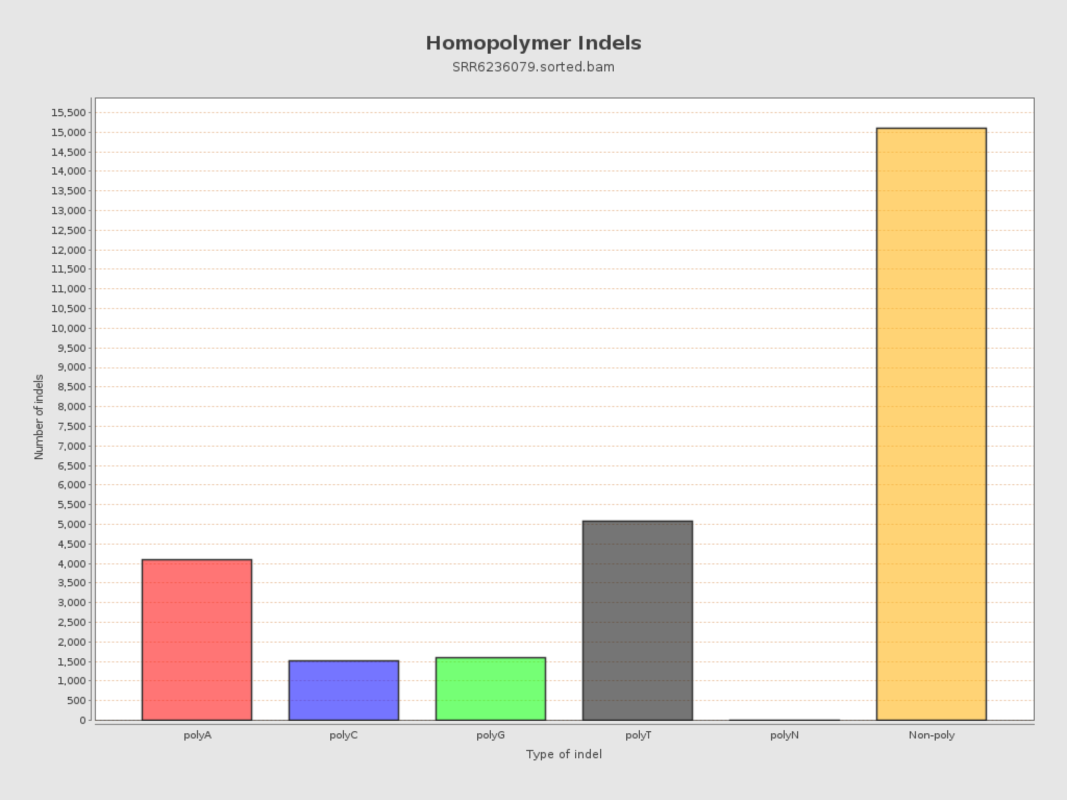
9. Results : Mapped Reads GC-content Distribution



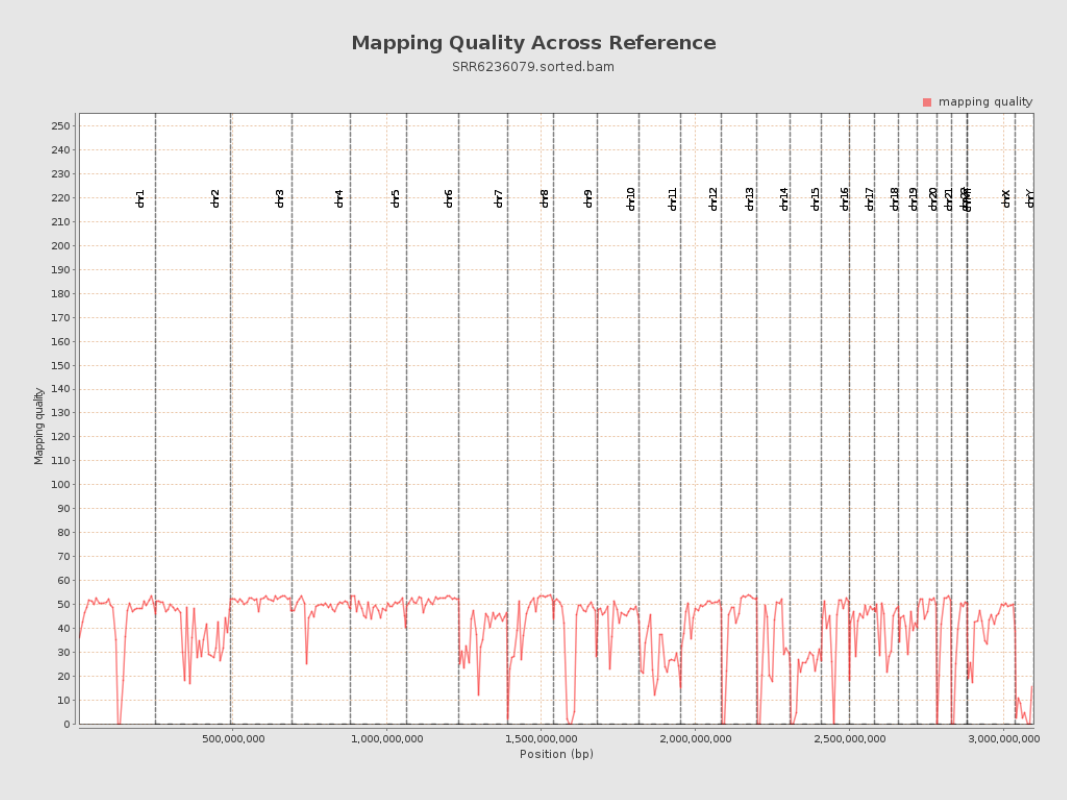
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram