Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:17:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004096.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_SRR6004096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004096.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:17:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,426,248
Mapped reads	2,090,156 / 86.15%
Unmapped reads	336,092 / 13.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,264 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	97,050 / 4%
Duplication rate	3.6%
Clipped reads	1,271,761 / 52.42%

2.2. ACGT Content

Number/percentage of A's	36,037,227 / 27.35%
Number/percentage of C's	24,140,372 / 18.32%
Number/percentage of T's	41,183,304 / 31.25%
Number/percentage of G's	30,392,963 / 23.06%
Number/percentage of N's	17,784 / 0.01%
GC Percentage	41.38%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.379

2.4. Mapping Quality

Mean Mapping Quality	43.4

2.5. Mismatches and indels

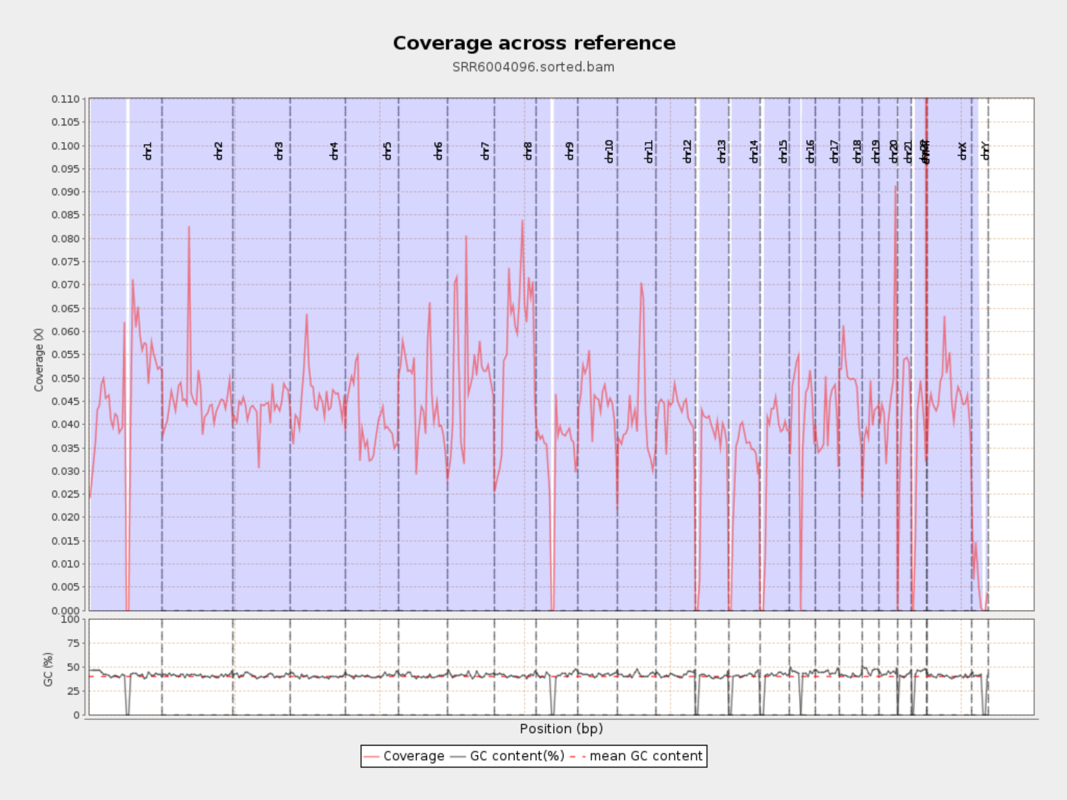
General error rate	1.02%
Mismatches	1,321,885
Insertions	11,565
Mapped reads with at least one insertion	0.55%
Deletions	48,517
Mapped reads with at least one deletion	2.29%
Homopolymer indels	47.34%

2.6. Chromosome stats

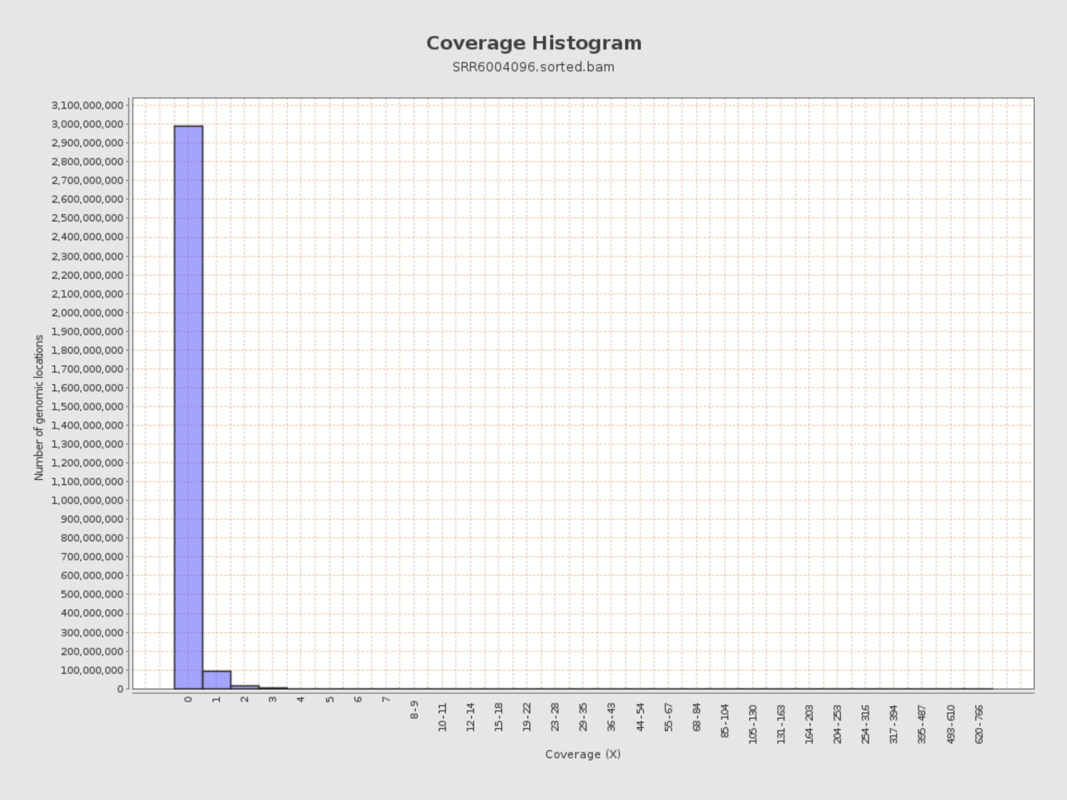
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11402639	0.0457	0.518
chr2	243199373	11108714	0.0457	0.5305
chr3	198022430	8651438	0.0437	0.247
chr4	191154276	8686534	0.0454	0.264
chr5	180915260	7313966	0.0404	0.2401
chr6	171115067	7907454	0.0462	0.2969
chr7	159138663	8085347	0.0508	0.6715

chr8	146364022	8361320	0.0571	0.43
chr9	141213431	4639397	0.0329	0.3561
chr10	135534747	6236626	0.046	0.3105
chr11	135006516	5679594	0.0421	0.3996
chr12	133851895	5743860	0.0429	0.2507
chr13	115169878	3770791	0.0327	0.216
chr14	107349540	3235557	0.0301	0.2428
chr15	102531392	3389437	0.0331	0.233
chr16	90354753	3822768	0.0423	0.2652
chr17	81195210	3281067	0.0404	0.2691
chr18	78077248	3877496	0.0497	0.6488
chr19	59128983	2403791	0.0407	0.4167
chr20	63025520	3068892	0.0487	0.2712
chr21	48129895	2001115	0.0416	0.256
chr22	51304566	1535866	0.0299	0.2043
chrMT	16571	121806	7.3506	6.6632
chrX	155270560	7200532	0.0464	0.2956
chrY	59373566	323614	0.0055	0.1091

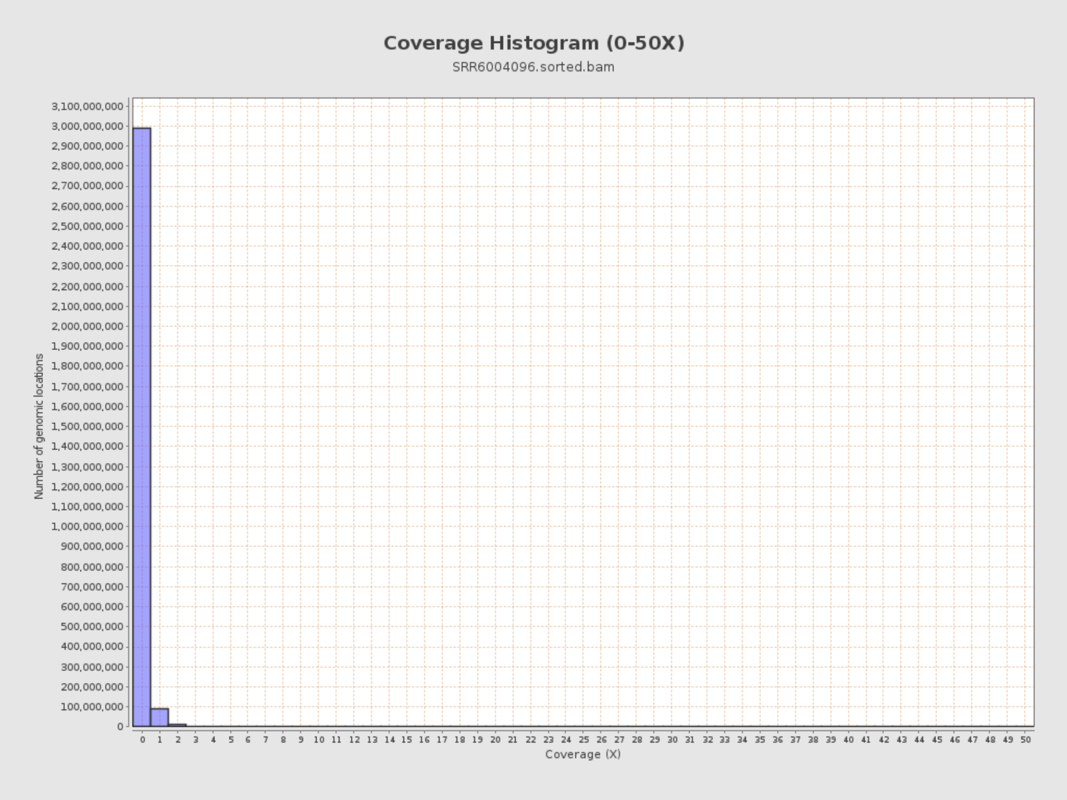
3. Results : Coverage across reference



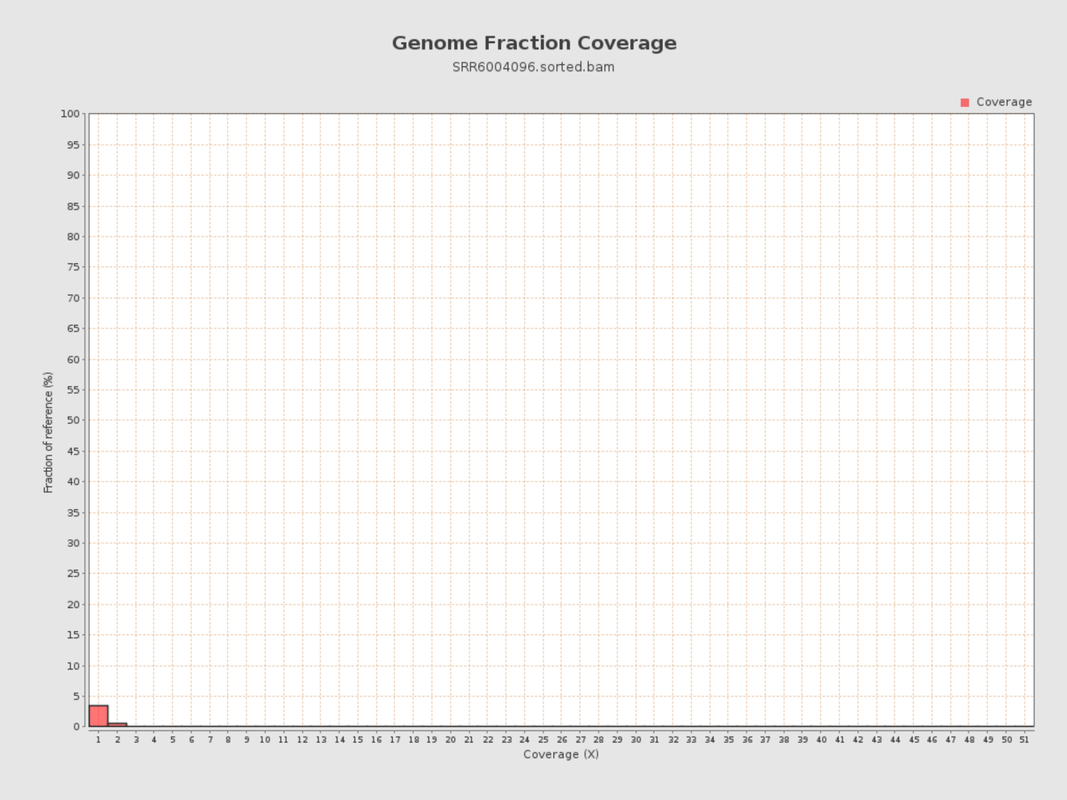
4. Results : Coverage Histogram



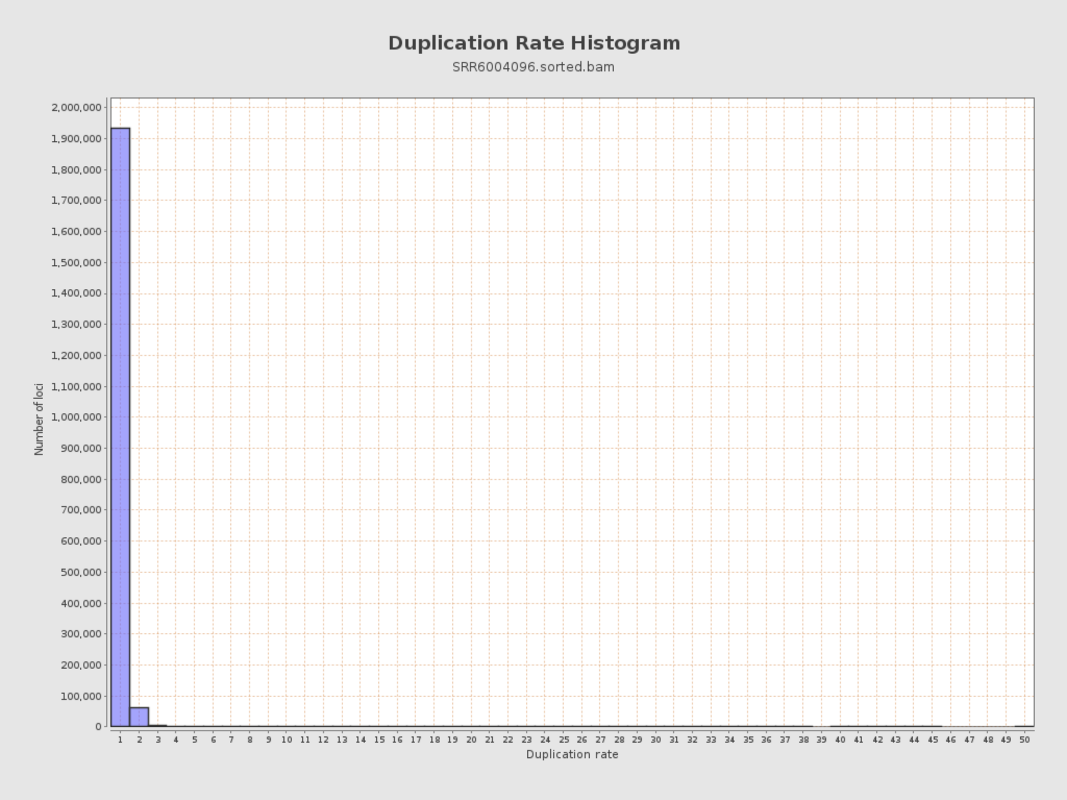
5. Results : Coverage Histogram (0-50X)



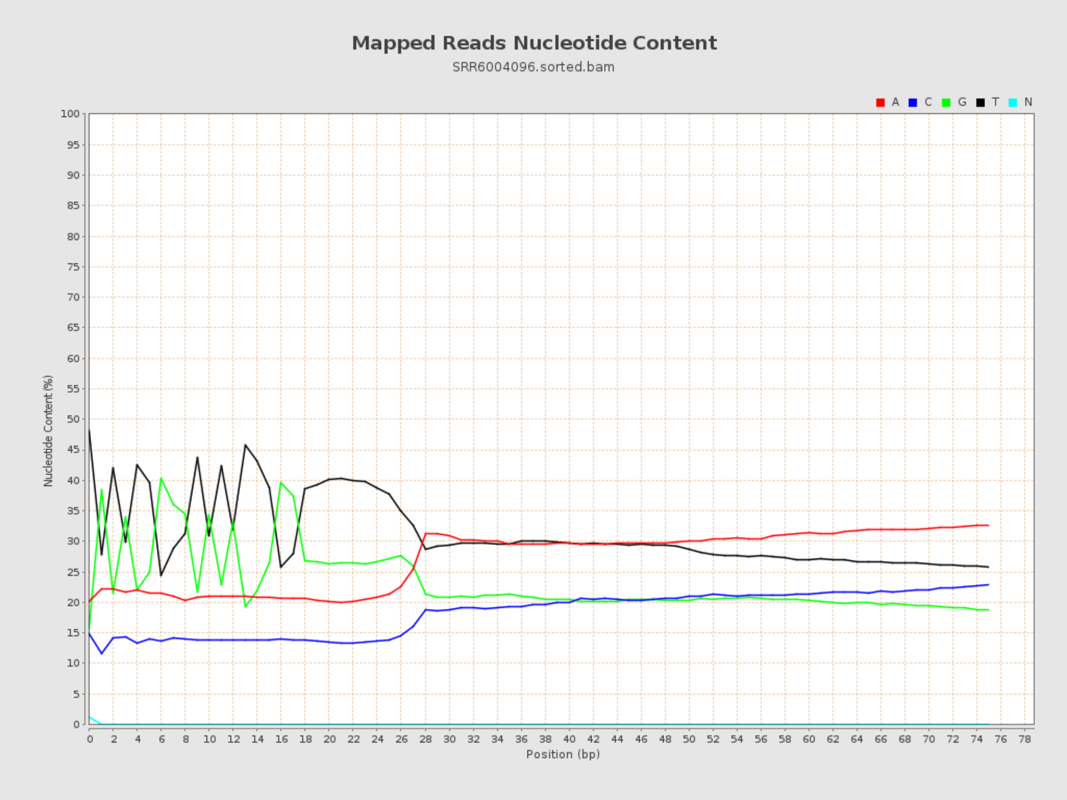
6. Results : Genome Fraction Coverage



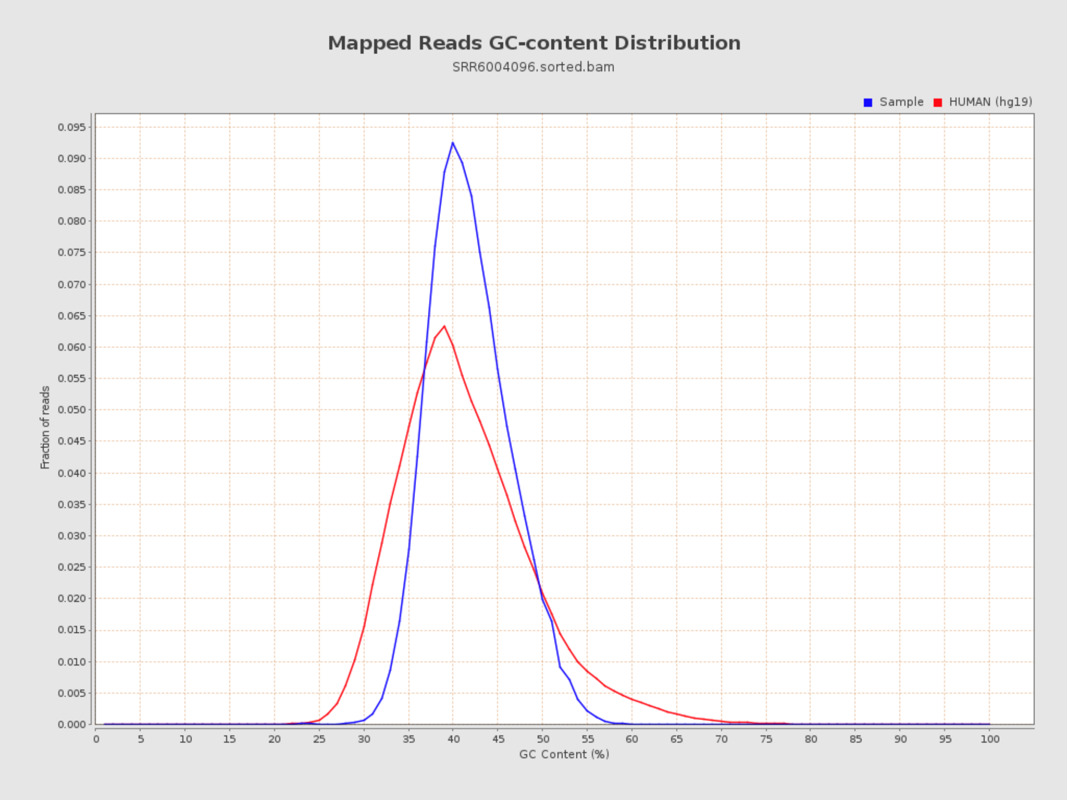
7. Results : Duplication Rate Histogram



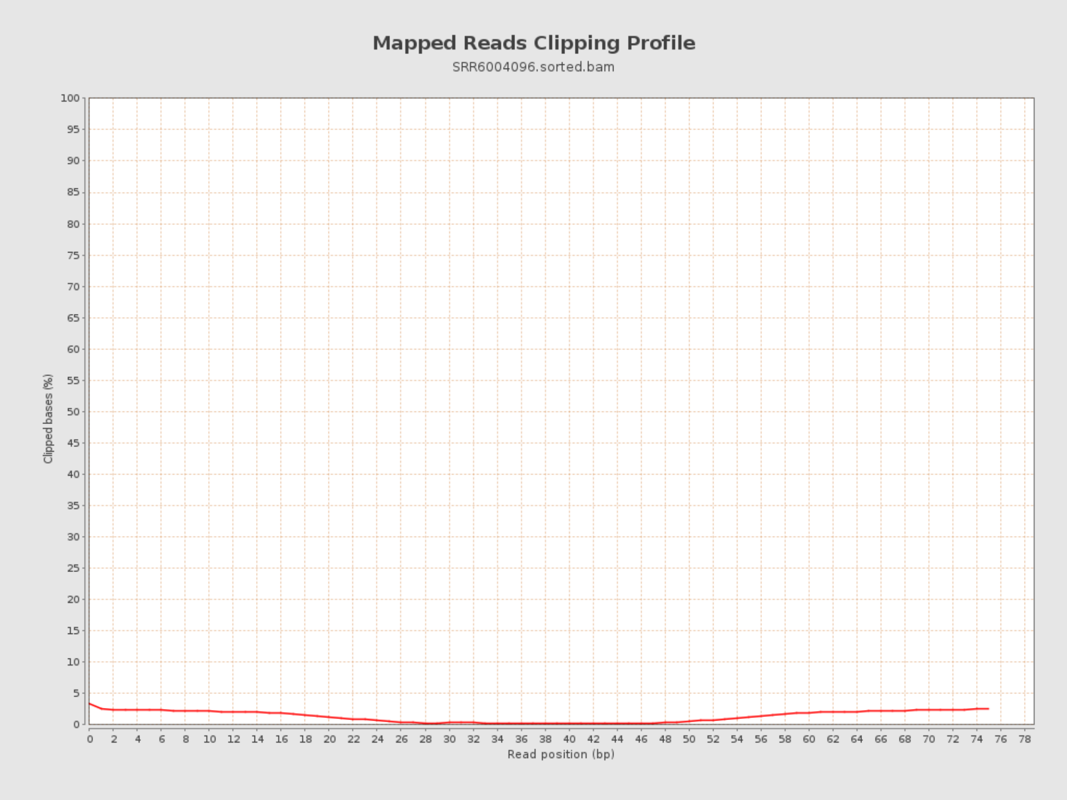
8. Results : Mapped Reads Nucleotide Content



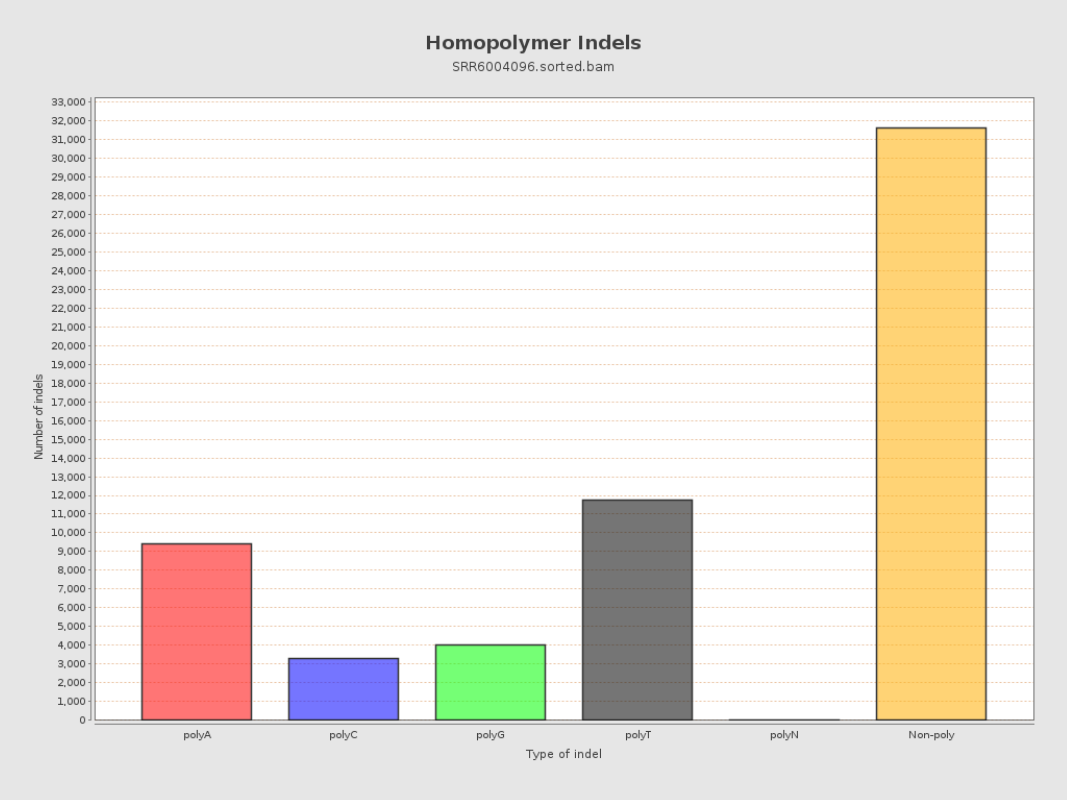
9. Results : Mapped Reads GC-content Distribution



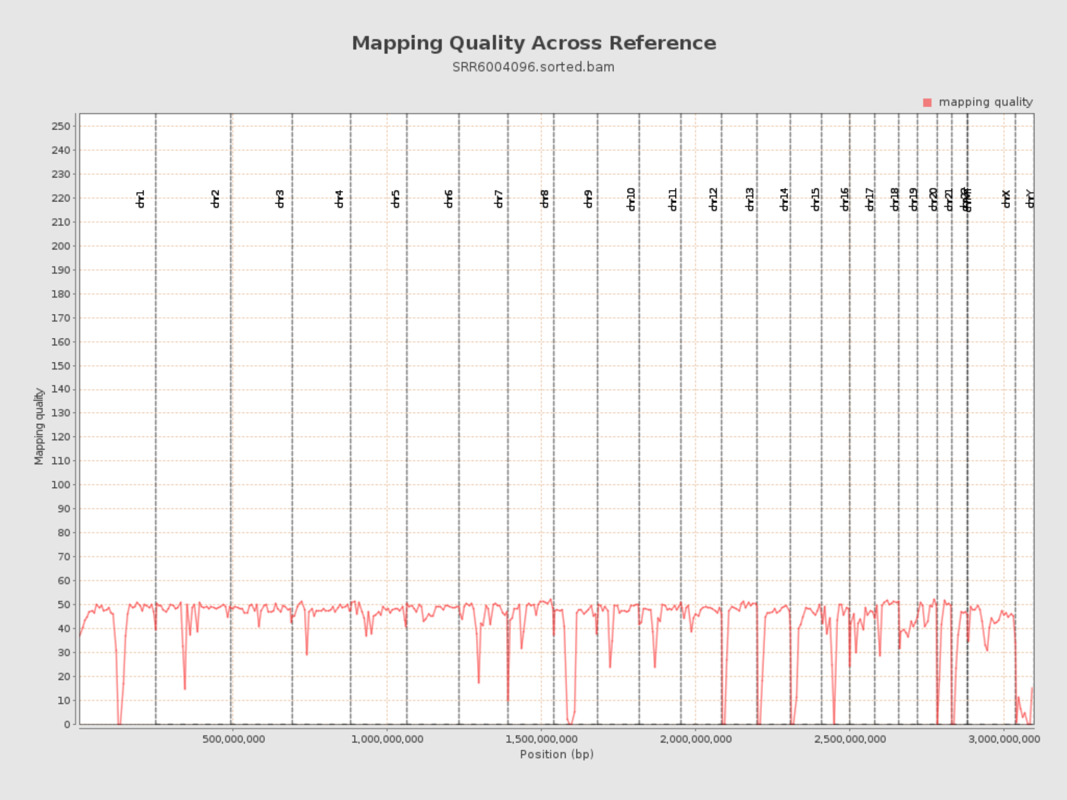
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram