Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:41:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084895.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_SRR3084895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084895.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:41:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,291,871
Mapped reads	2,042,877 / 89.14%
Unmapped reads	248,994 / 10.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,560 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	103,029 / 4.5%
Duplication rate	4.46%
Clipped reads	808,447 / 35.27%

2.2. ACGT Content

Number/percentage of A's	39,348,314 / 28.43%
Number/percentage of C's	24,969,609 / 18.04%
Number/percentage of T's	44,672,347 / 32.28%
Number/percentage of G's	29,379,223 / 21.23%
Number/percentage of N's	21,405 / 0.02%
GC Percentage	39.27%

2.3. Coverage

Mean	0.0447

Standard Deviation	0.3037

2.4. Mapping Quality

Mean Mapping Quality	47.37

2.5. Mismatches and indels

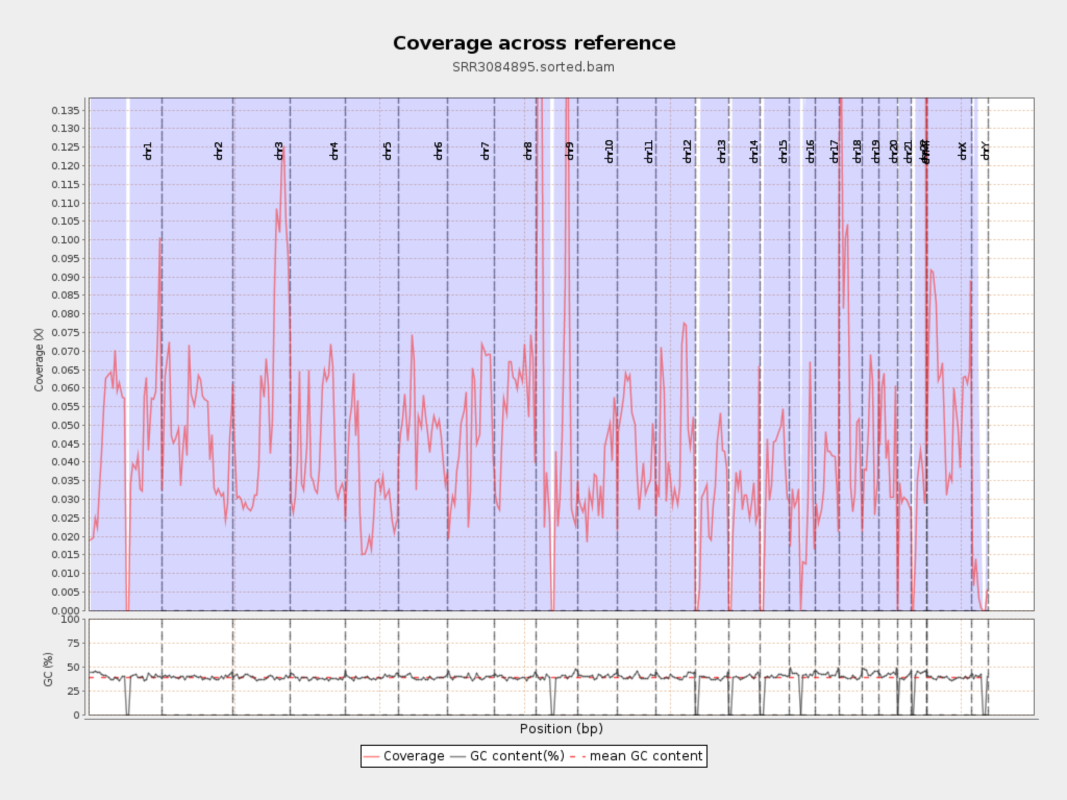
General error rate	0.82%
Mismatches	1,116,231
Insertions	10,359
Mapped reads with at least one insertion	0.5%
Deletions	29,330
Mapped reads with at least one deletion	1.42%
Homopolymer indels	48.81%

2.6. Chromosome stats

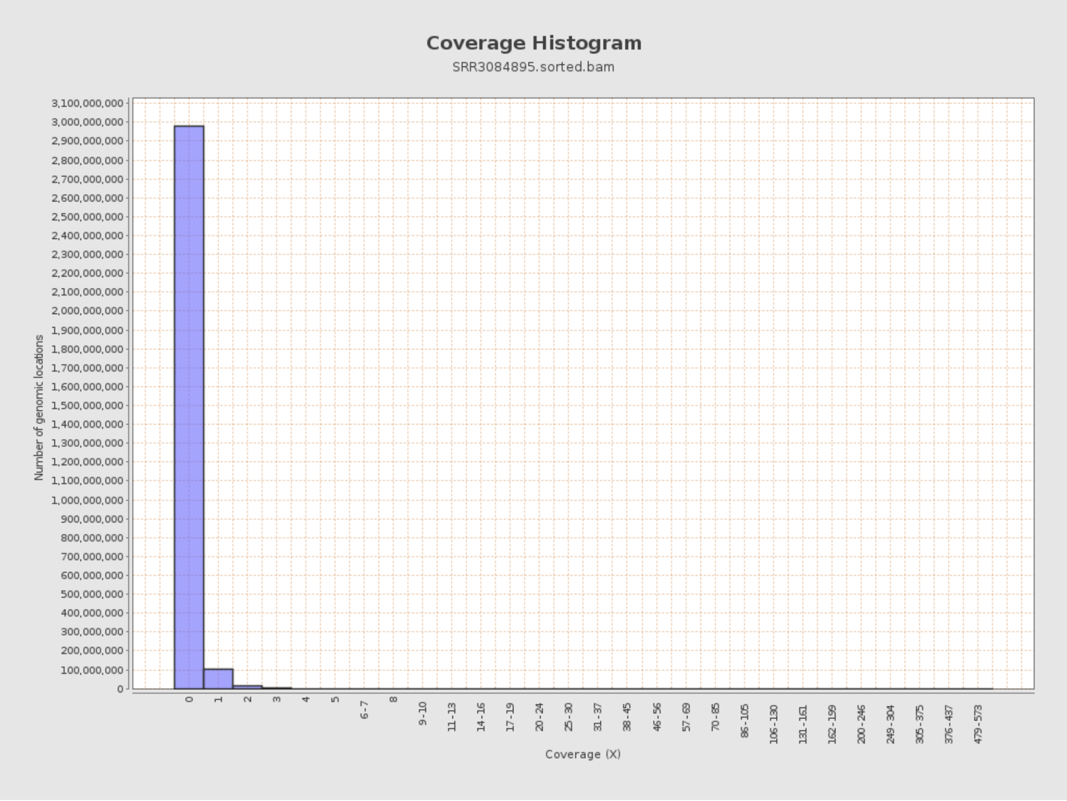
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11687564	0.0469	0.4128
chr2	243199373	11716423	0.0482	0.3539
chr3	198022430	11662688	0.0589	0.2768
chr4	191154276	8370060	0.0438	0.2381
chr5	180915260	5806722	0.0321	0.2068
chr6	171115067	8514395	0.0498	0.2653
chr7	159138663	7765971	0.0488	0.3418

chr8	146364022	8149325	0.0557	0.4634
chr9	141213431	9272038	0.0657	0.378
chr10	135534747	4802058	0.0354	0.2305
chr11	135006516	6135192	0.0454	0.2715
chr12	133851895	6230744	0.0465	0.2475
chr13	115169878	3351037	0.0291	0.1929
chr14	107349540	2830873	0.0264	0.1954
chr15	102531392	3562075	0.0347	0.2111
chr16	90354753	2420411	0.0268	0.2
chr17	81195210	2869719	0.0353	0.2162
chr18	78077248	5455635	0.0699	0.5341
chr19	59128983	2650425	0.0448	0.3273
chr20	63025520	2928215	0.0465	0.2459
chr21	48129895	1310467	0.0272	0.1951
chr22	51304566	1299059	0.0253	0.1768
chrMT	16571	54522	3.2902	2.4038
chrX	155270560	9294641	0.0599	0.2948
chrY	59373566	301963	0.0051	0.1144

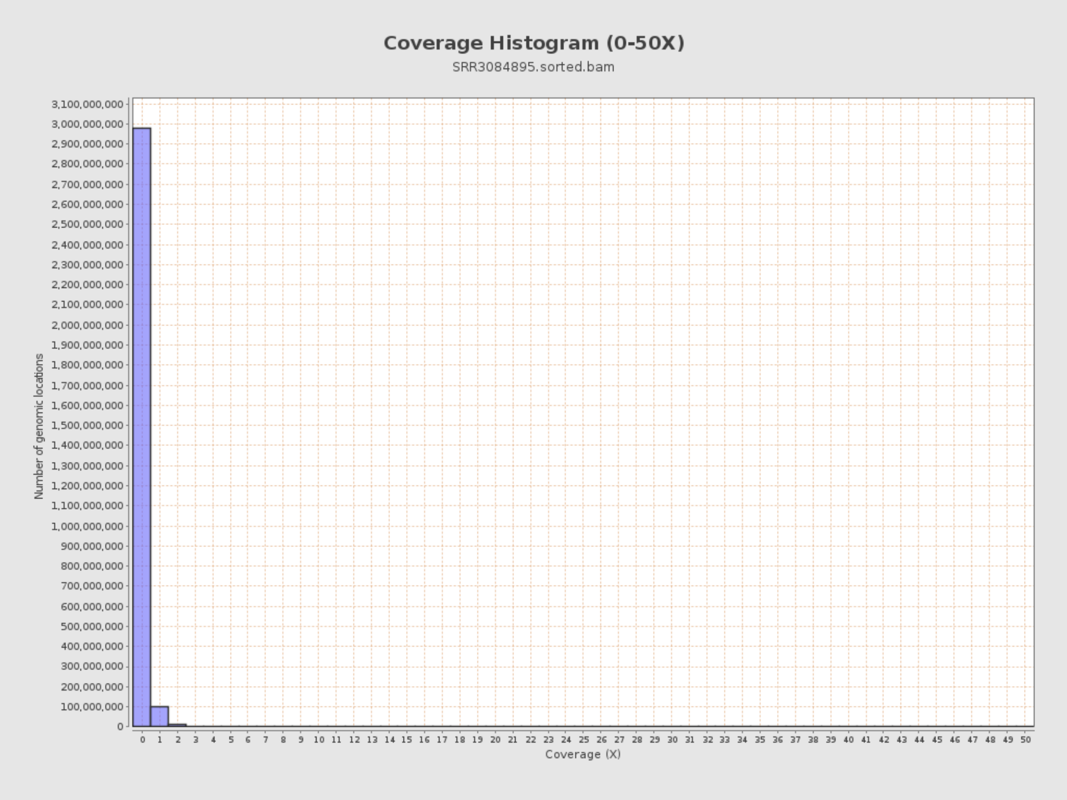
3. Results : Coverage across reference



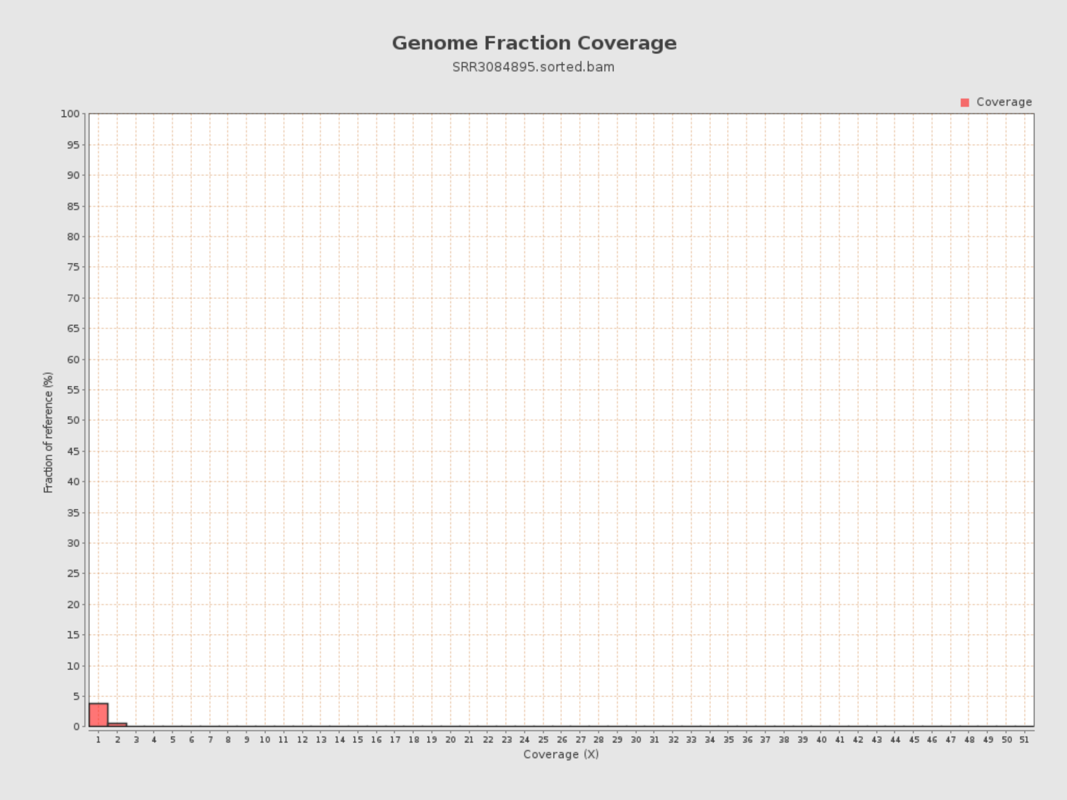
4. Results : Coverage Histogram



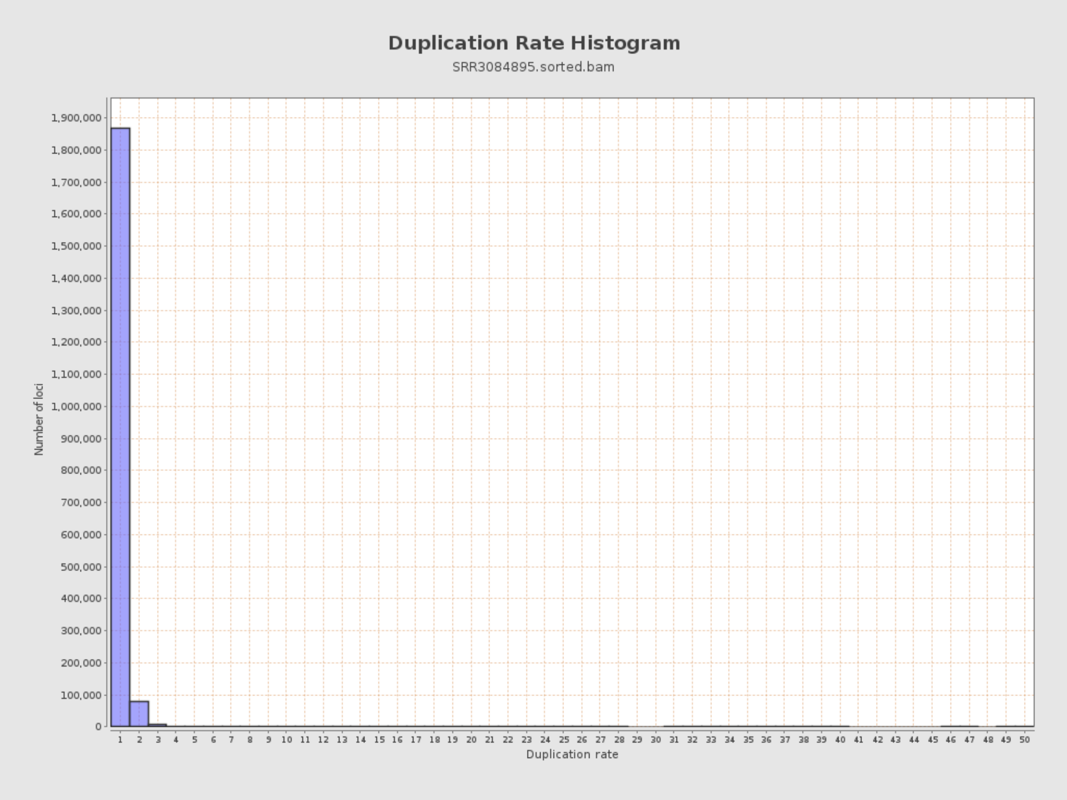
5. Results : Coverage Histogram (0-50X)



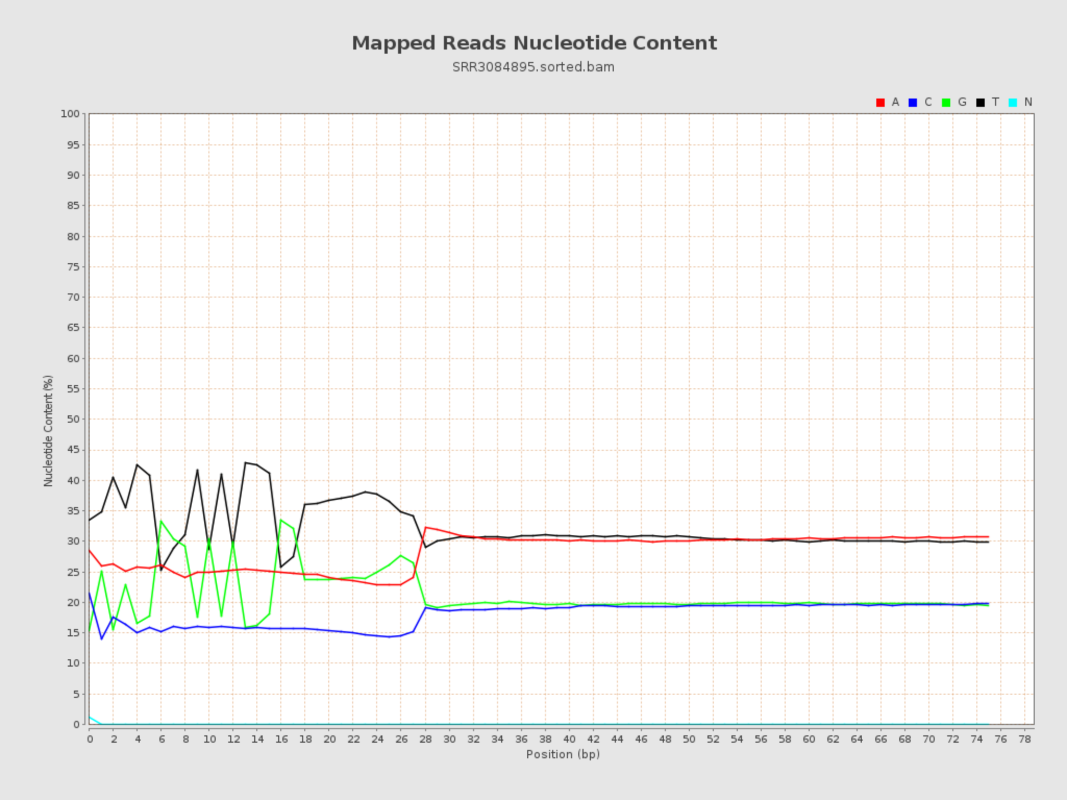
6. Results : Genome Fraction Coverage



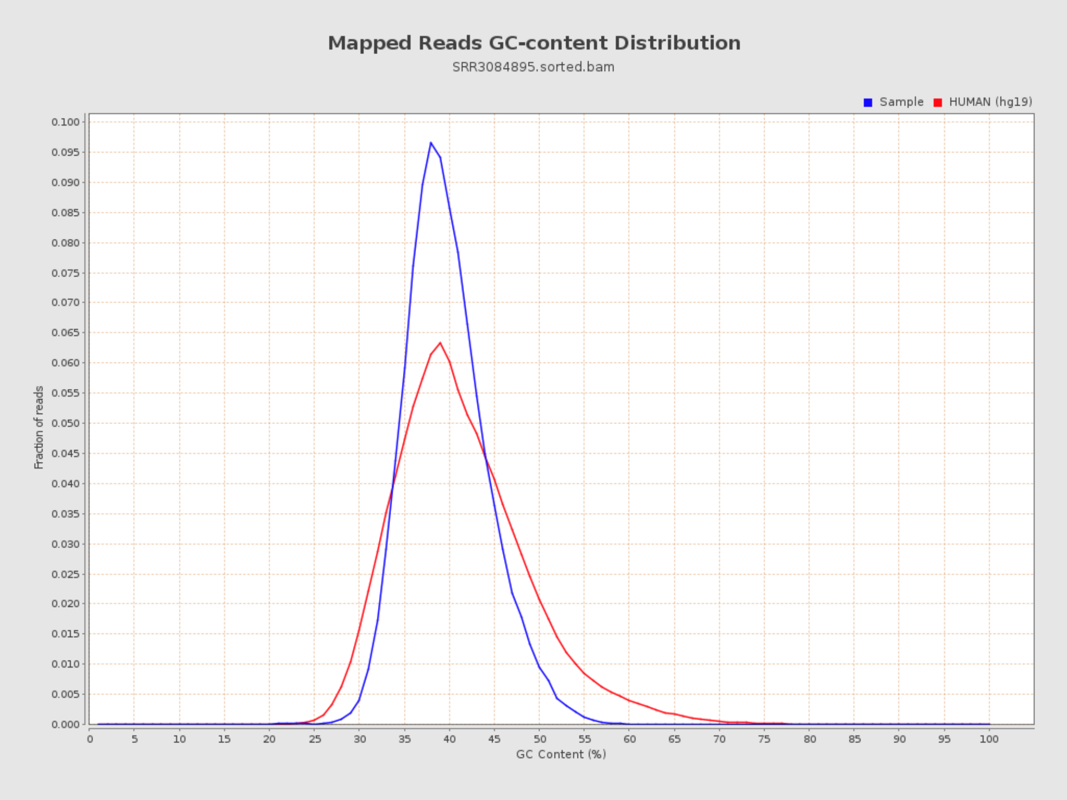
7. Results : Duplication Rate Histogram



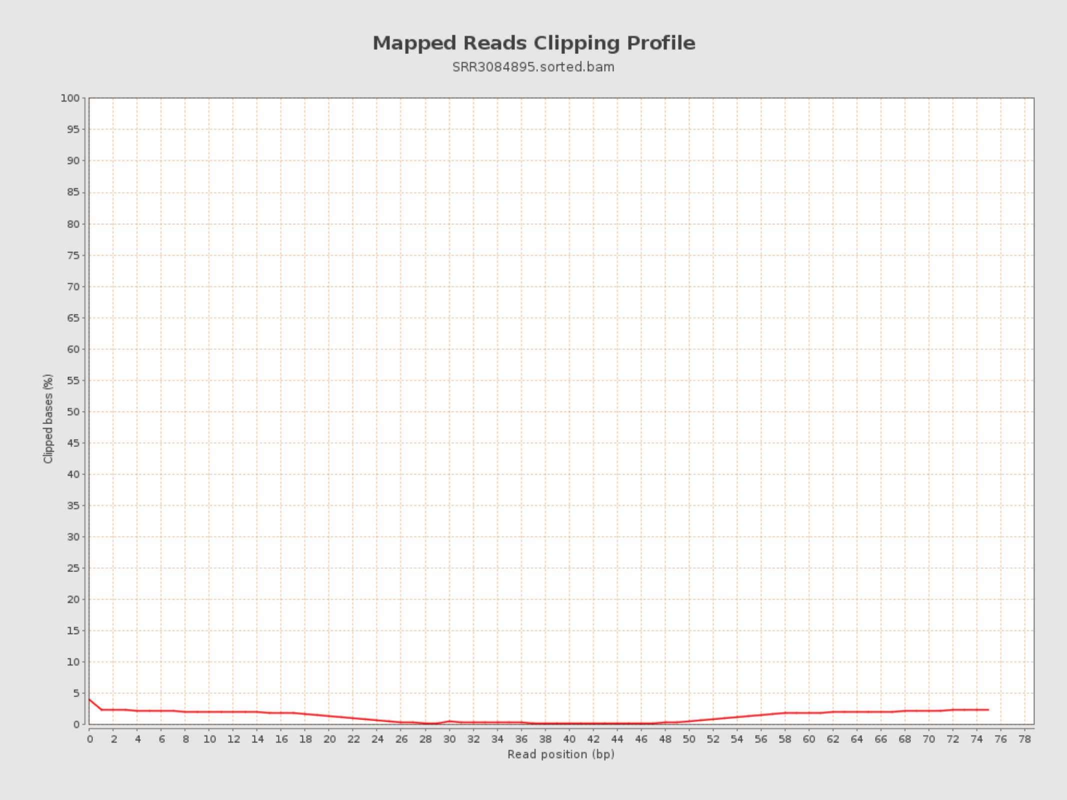
8. Results : Mapped Reads Nucleotide Content



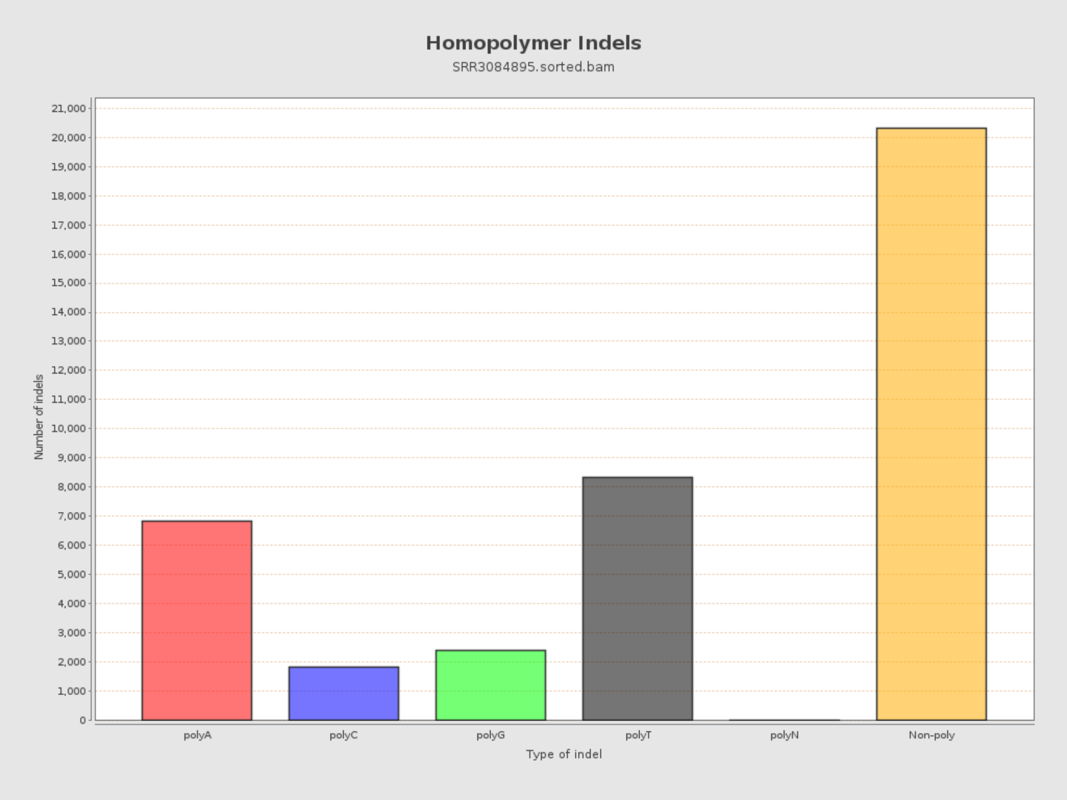
9. Results : Mapped Reads GC-content Distribution



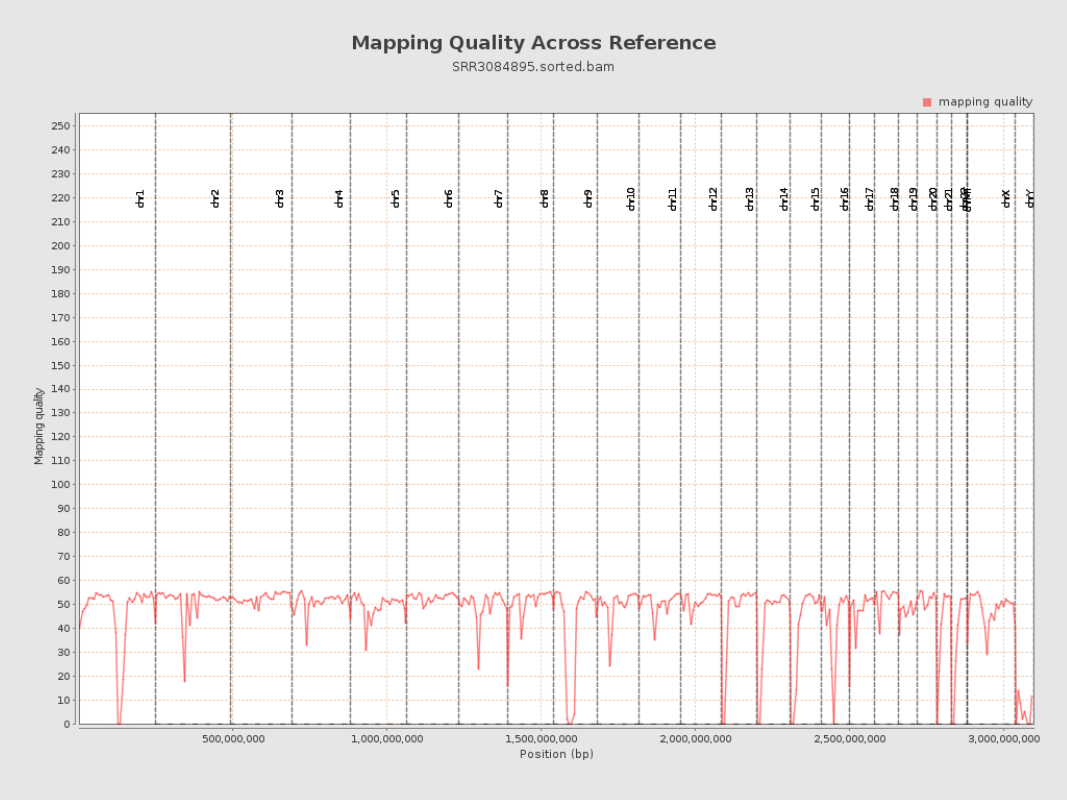
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram