Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:30:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084965.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_SRR3084965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084965.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:30:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,058,631
Mapped reads	2,751,750 / 89.97%
Unmapped reads	306,881 / 10.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,296 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	128,362 / 4.2%
Duplication rate	3.34%
Clipped reads	1,300,450 / 42.52%

2.2. ACGT Content

Number/percentage of A's	51,952,424 / 28.43%
Number/percentage of C's	33,709,979 / 18.45%
Number/percentage of T's	57,274,564 / 31.34%
Number/percentage of G's	39,790,277 / 21.77%
Number/percentage of N's	24,222 / 0.01%
GC Percentage	40.22%

2.3. Coverage

Mean	0.0591

Standard Deviation	0.5887

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

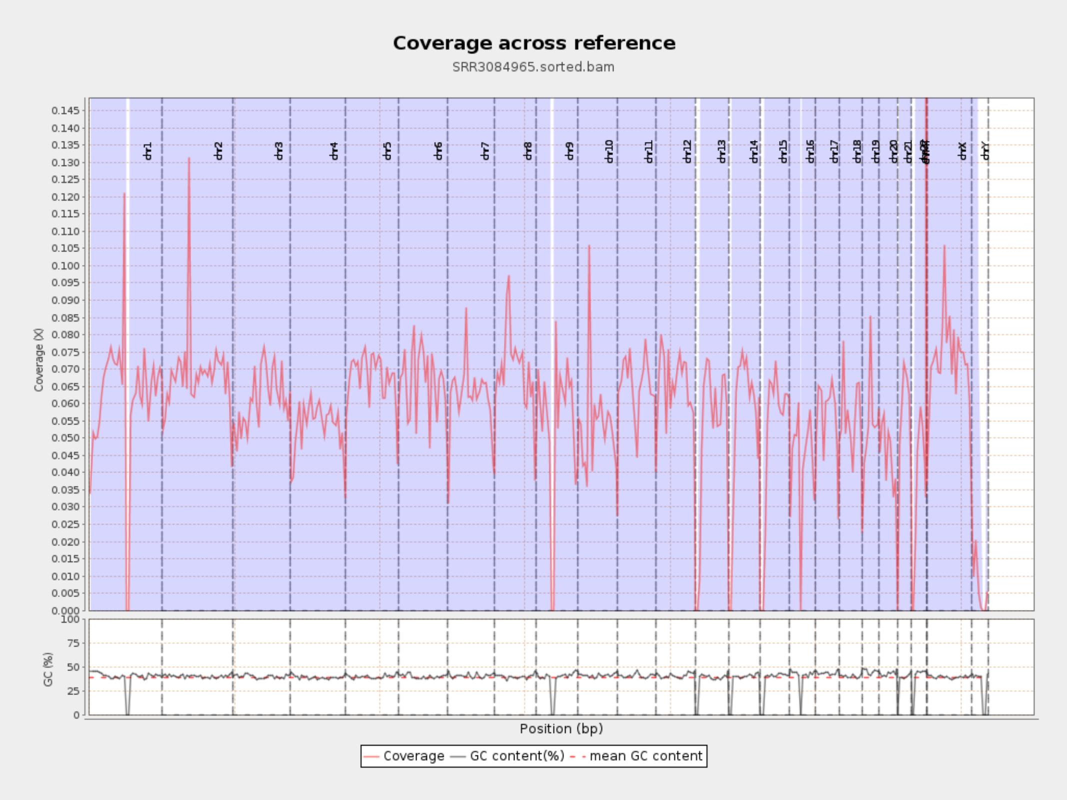
General error rate	0.87%
Mismatches	1,566,198
Insertions	14,406
Mapped reads with at least one insertion	0.52%
Deletions	42,156
Mapped reads with at least one deletion	1.52%
Homopolymer indels	46.53%

2.6. Chromosome stats

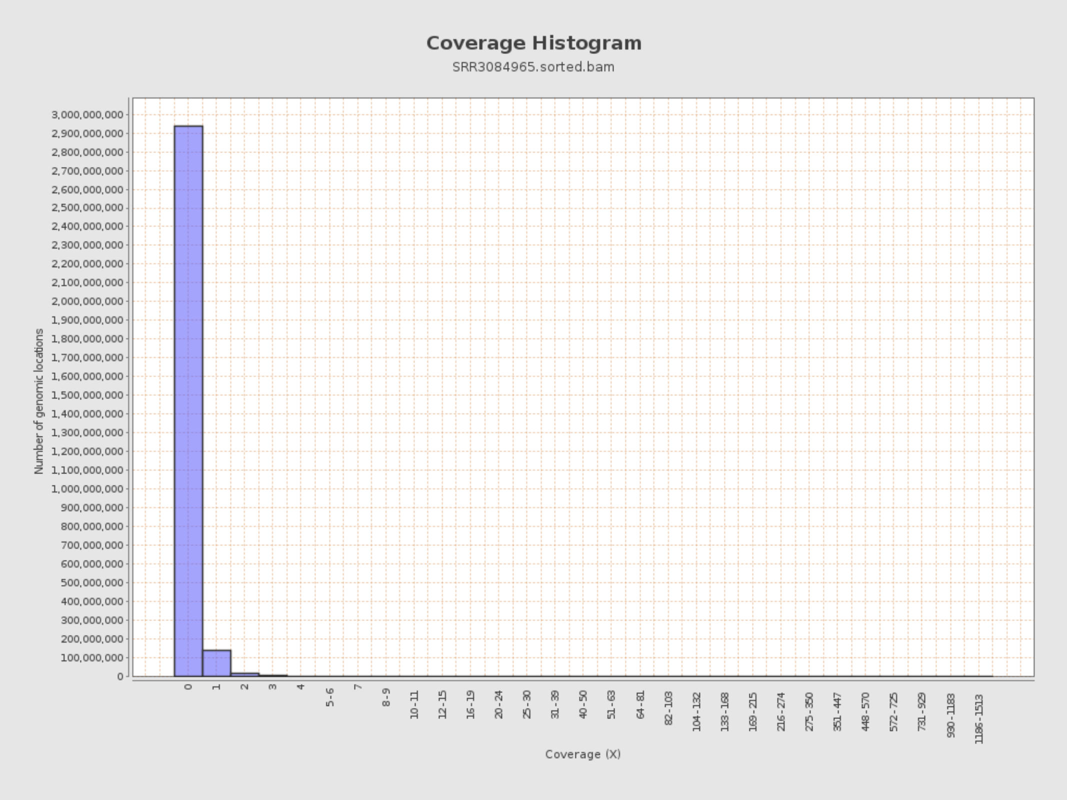
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15415544	0.0618	1.2167
chr2	243199373	16764569	0.0689	0.6552
chr3	198022430	12117168	0.0612	0.288
chr4	191154276	10247658	0.0536	0.2696
chr5	180915260	12295539	0.068	0.2981
chr6	171115067	11377582	0.0665	0.3669
chr7	159138663	9999543	0.0628	0.4829

chr8	146364022	10214031	0.0698	0.9555
chr9	141213431	7682264	0.0544	0.5404
chr10	135534747	7344386	0.0542	0.5951
chr11	135006516	8793180	0.0651	0.515
chr12	133851895	8787889	0.0657	0.2988
chr13	115169878	5862270	0.0509	0.2495
chr14	107349540	5817042	0.0542	0.3172
chr15	102531392	5151077	0.0502	0.261
chr16	90354753	3903356	0.0432	0.3128
chr17	81195210	4579334	0.0564	0.3097
chr18	78077248	4418014	0.0566	1.1567
chr19	59128983	3208277	0.0543	0.8291
chr20	63025520	2807985	0.0446	0.26
chr21	48129895	2589803	0.0538	0.288
chr22	51304566	1776732	0.0346	0.2064
chrMT	16571	34043	2.0544	1.7363
chrX	155270560	11214500	0.0722	0.3905
chrY	59373566	417472	0.007	0.1328

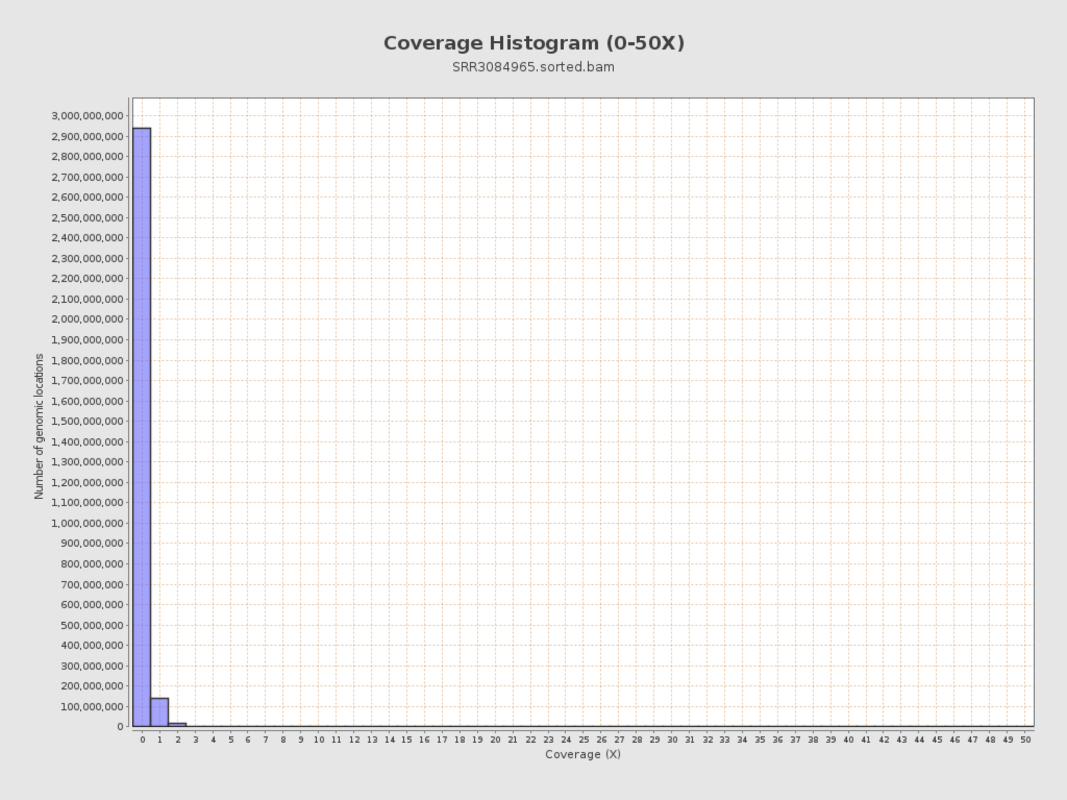
3. Results : Coverage across reference



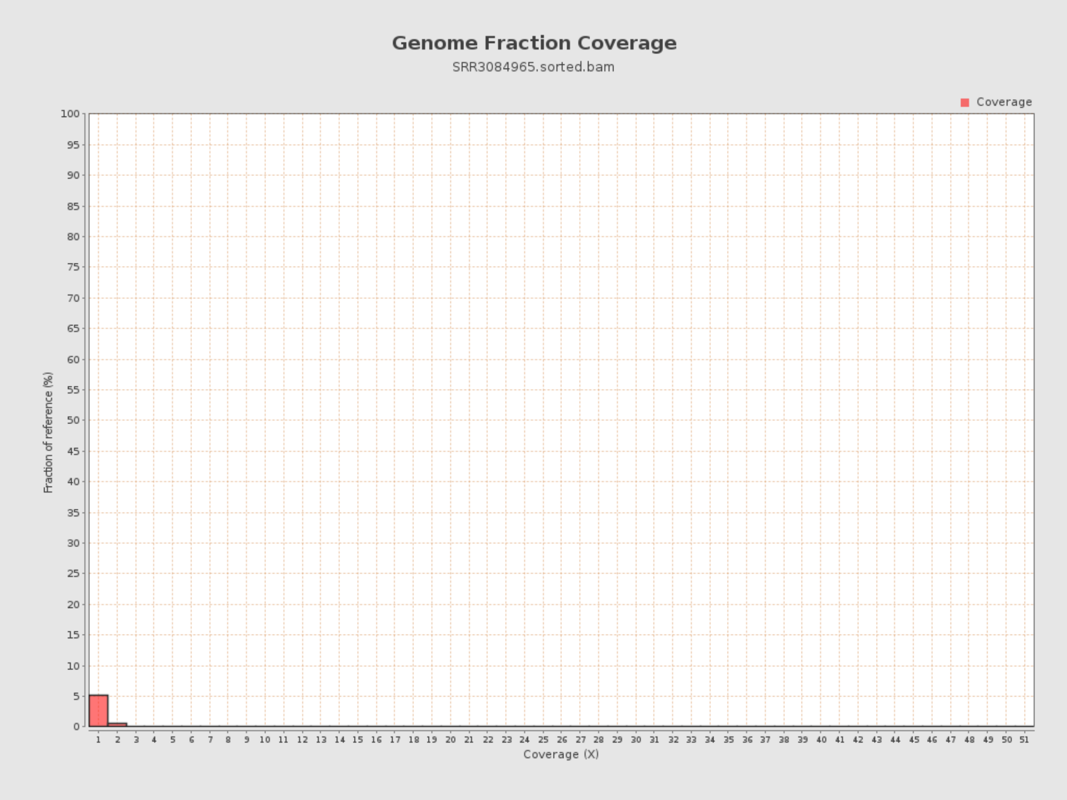
4. Results : Coverage Histogram



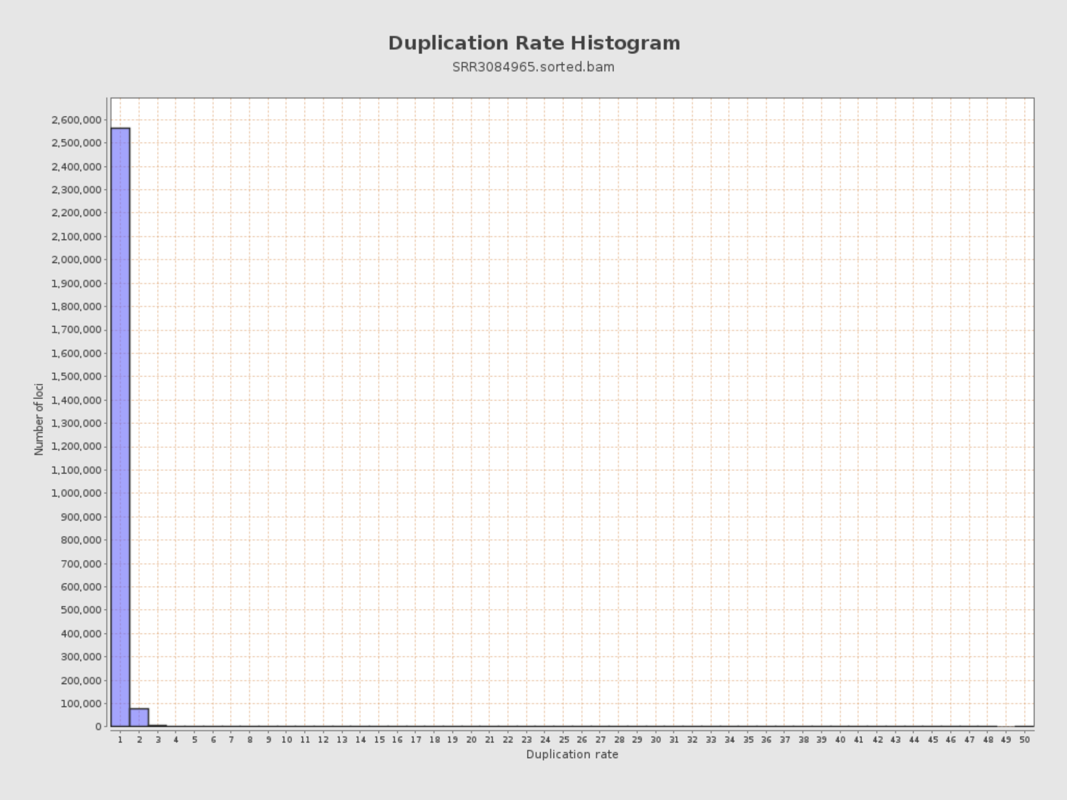
5. Results : Coverage Histogram (0-50X)



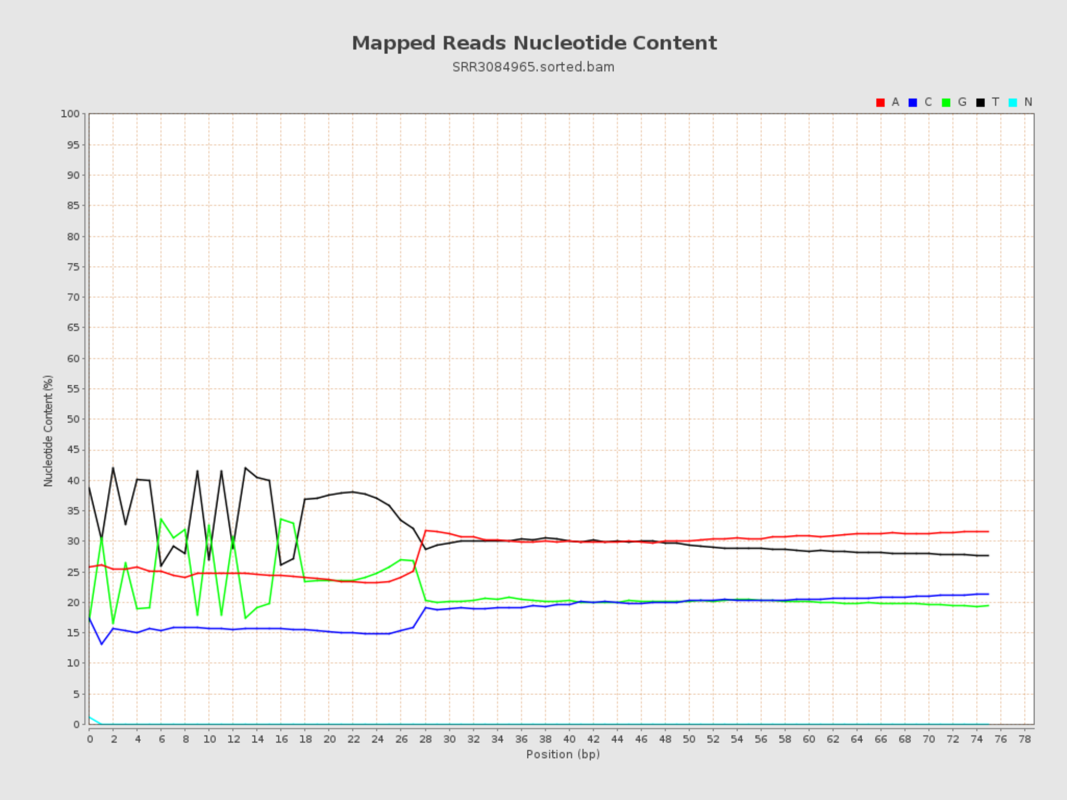
6. Results : Genome Fraction Coverage



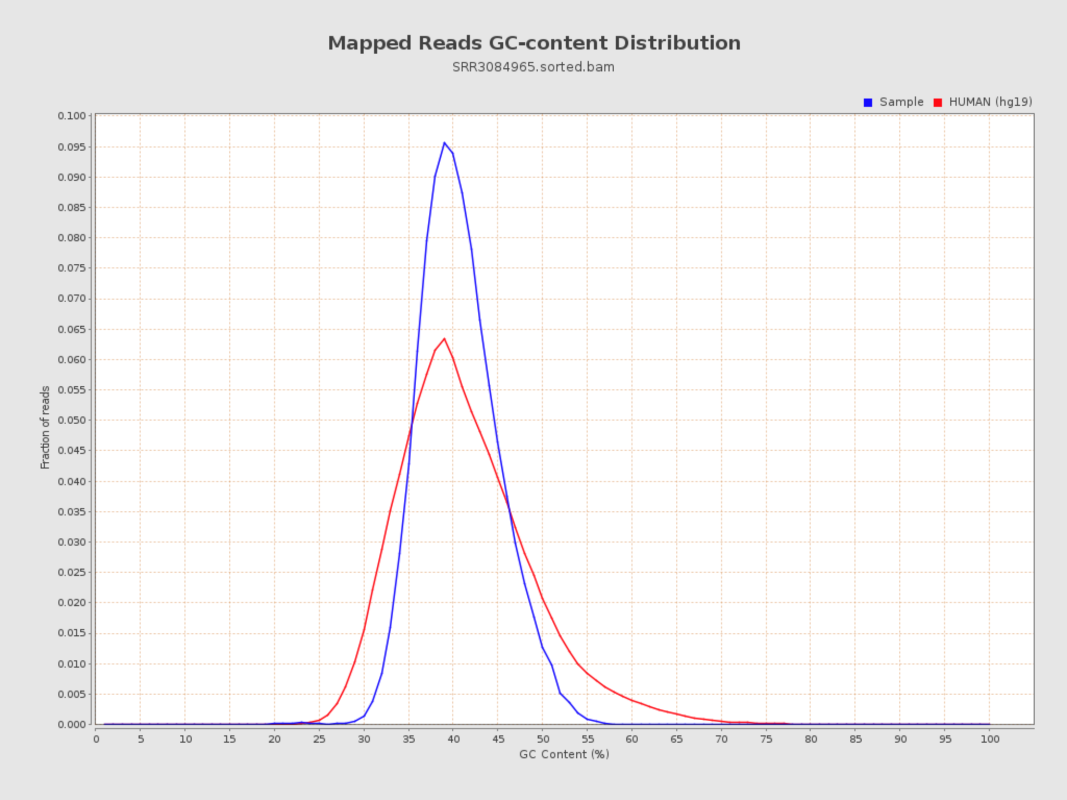
7. Results : Duplication Rate Histogram



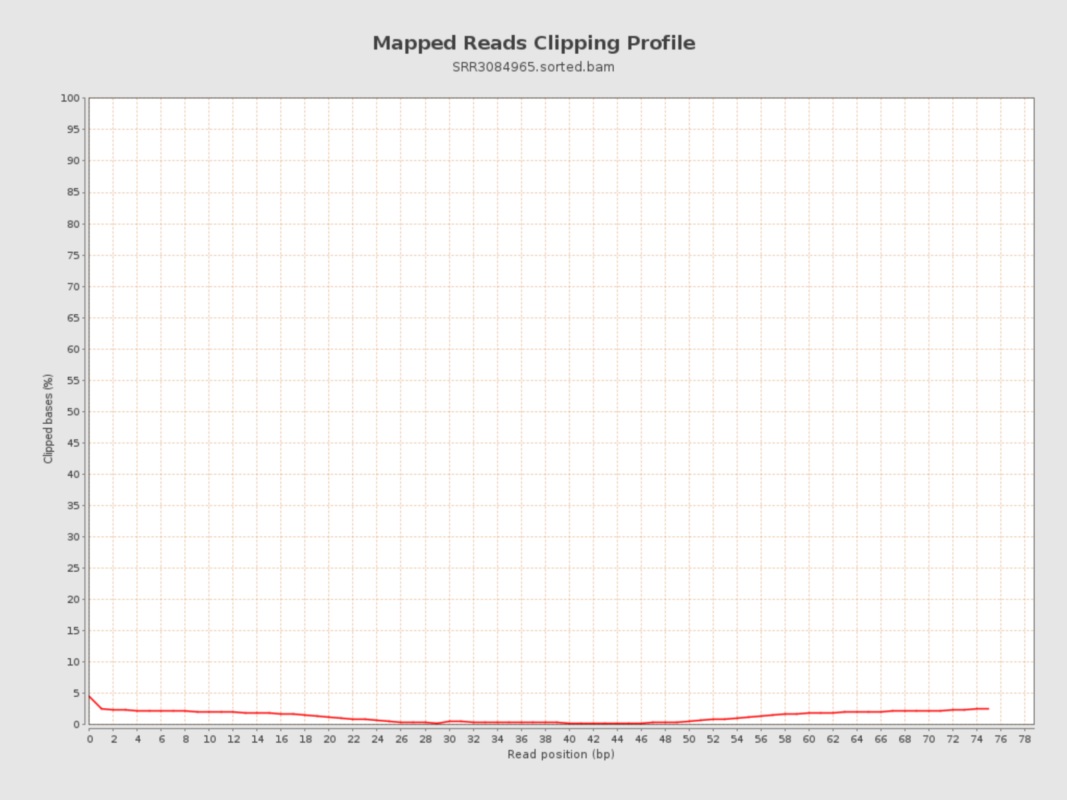
8. Results : Mapped Reads Nucleotide Content



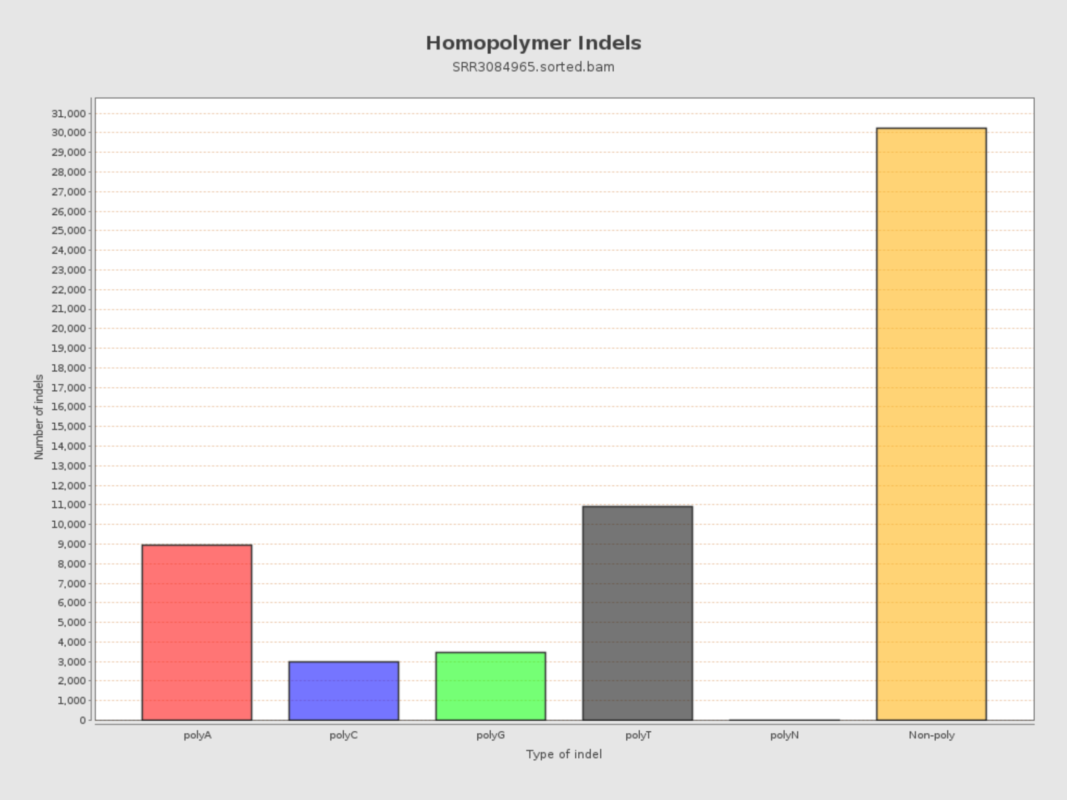
9. Results : Mapped Reads GC-content Distribution



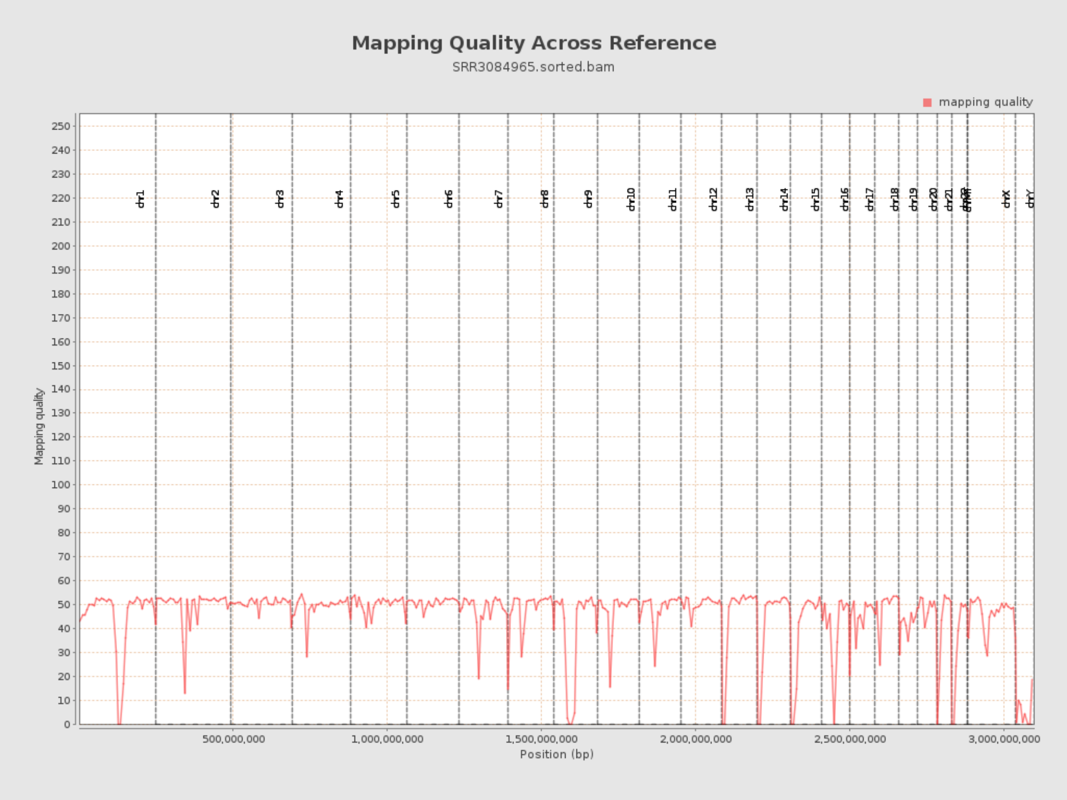
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram