Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:48:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081967.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_SRR3081967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081967.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:48:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,131,519
Mapped reads	2,874,647 / 91.8%
Unmapped reads	256,872 / 8.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,777 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	130,066 / 4.15%
Duplication rate	3.4%
Clipped reads	1,058,568 / 33.8%

2.2. ACGT Content

Number/percentage of A's	56,623,068 / 28.76%
Number/percentage of C's	36,415,200 / 18.49%
Number/percentage of T's	61,879,548 / 31.43%
Number/percentage of G's	41,958,160 / 21.31%
Number/percentage of N's	25,341 / 0.01%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0636

Standard Deviation	0.556

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

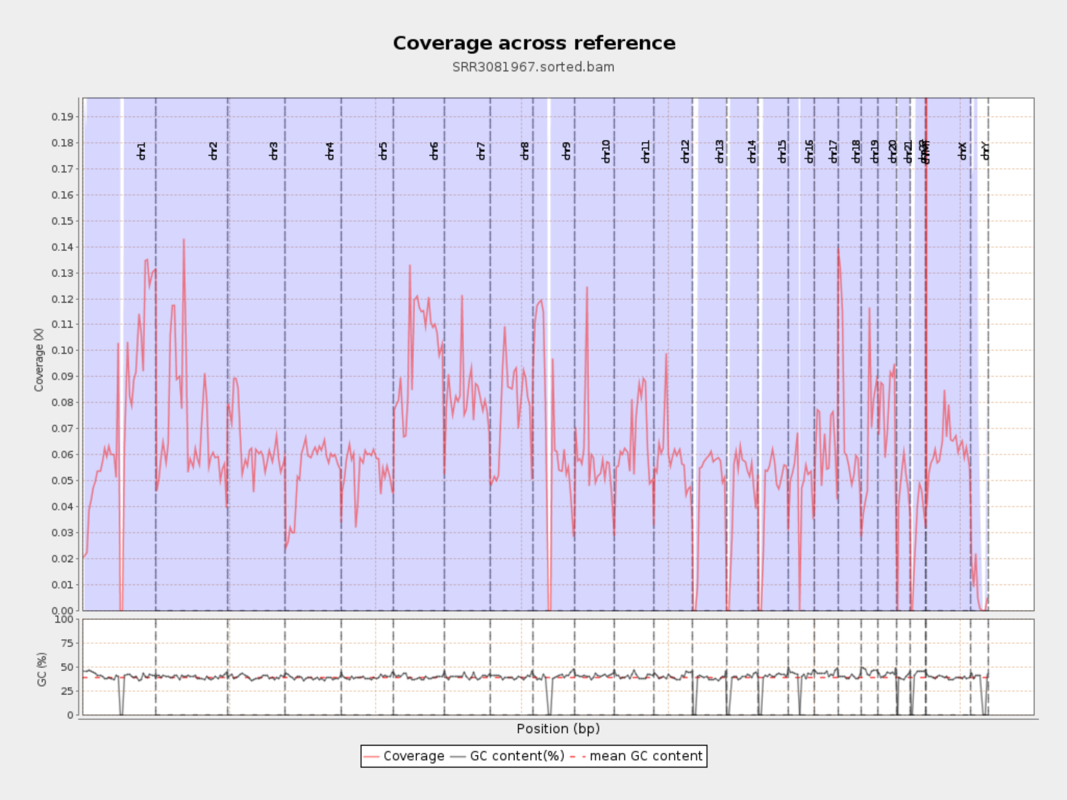
General error rate	0.79%
Mismatches	1,523,351
Insertions	14,145
Mapped reads with at least one insertion	0.49%
Deletions	41,624
Mapped reads with at least one deletion	1.43%
Homopolymer indels	48.13%

2.6. Chromosome stats

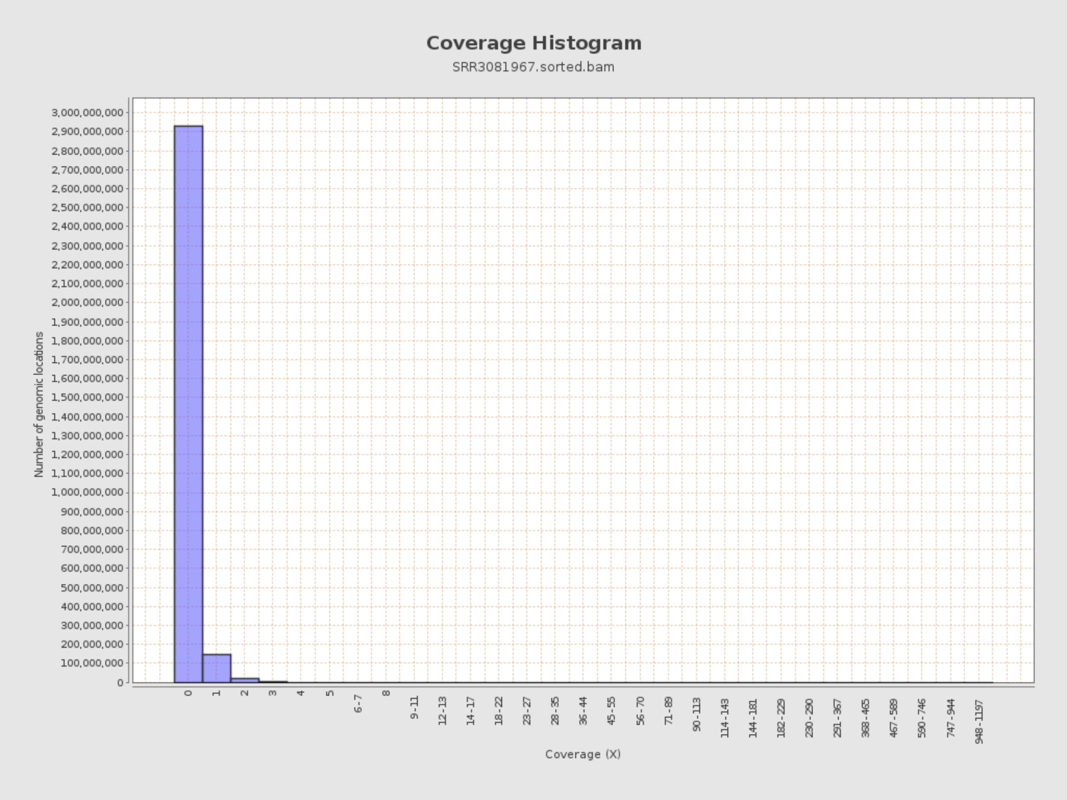
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18192860	0.073	1.0706
chr2	243199373	17364703	0.0714	0.6819
chr3	198022430	12629015	0.0638	0.2899
chr4	191154276	10253442	0.0536	0.2819
chr5	180915260	9801594	0.0542	0.2666
chr6	171115067	17221876	0.1006	0.4732
chr7	159138663	13085690	0.0822	0.7462

chr8	146364022	11323848	0.0774	0.8296
chr9	141213431	9661888	0.0684	0.5362
chr10	135534747	8011330	0.0591	0.5793
chr11	135006516	8818899	0.0653	0.3841
chr12	133851895	7843671	0.0586	0.2878
chr13	115169878	5391146	0.0468	0.244
chr14	107349540	4897846	0.0456	0.2736
chr15	102531392	4493852	0.0438	0.2396
chr16	90354753	4205382	0.0465	0.3093
chr17	81195210	5207625	0.0641	0.3138
chr18	78077248	5683158	0.0728	0.9058
chr19	59128983	3993206	0.0675	0.7565
chr20	63025520	5005009	0.0794	0.3258
chr21	48129895	2122495	0.0441	0.2745
chr22	51304566	1546139	0.0301	0.1923
chrMT	16571	127938	7.7206	4.6386
chrX	155270560	9671493	0.0623	0.3353
chrY	59373566	420439	0.0071	0.1612

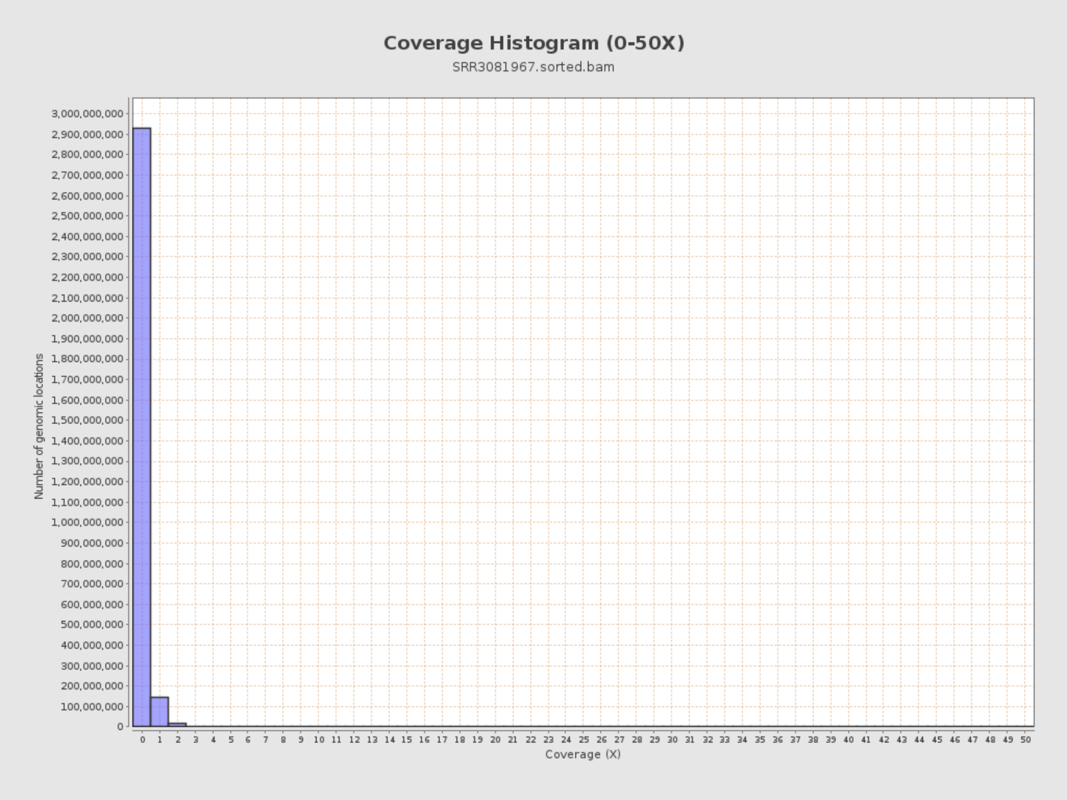
3. Results : Coverage across reference



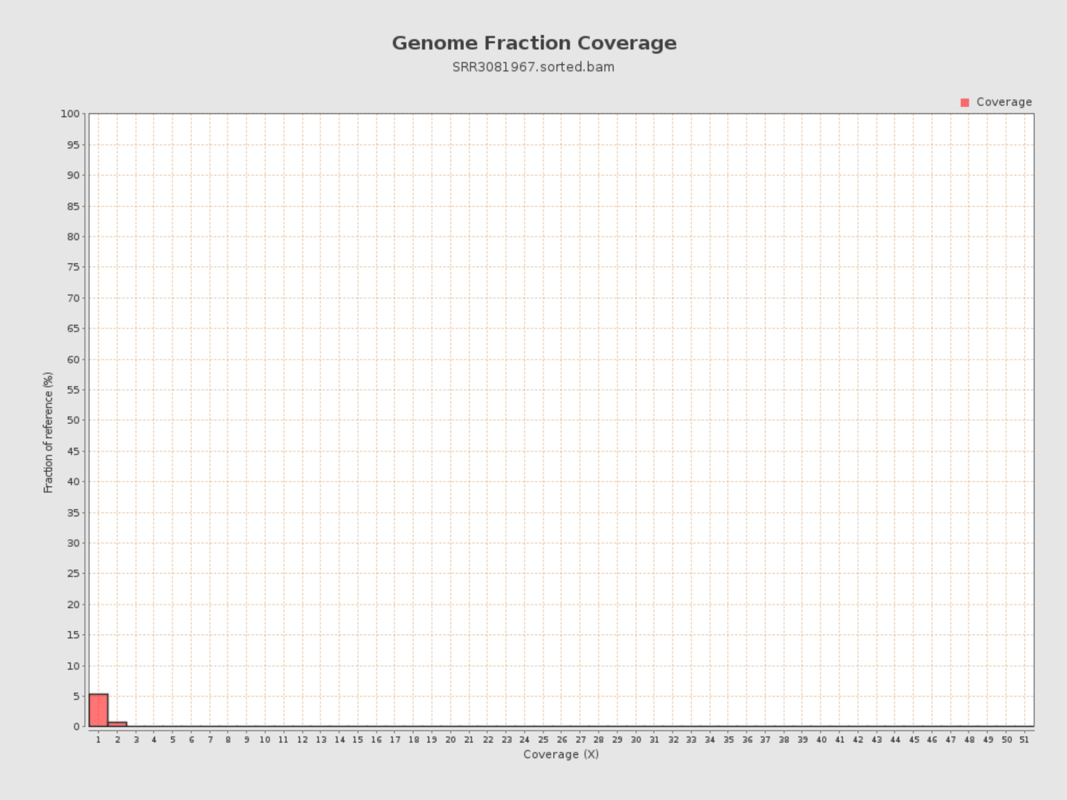
4. Results : Coverage Histogram



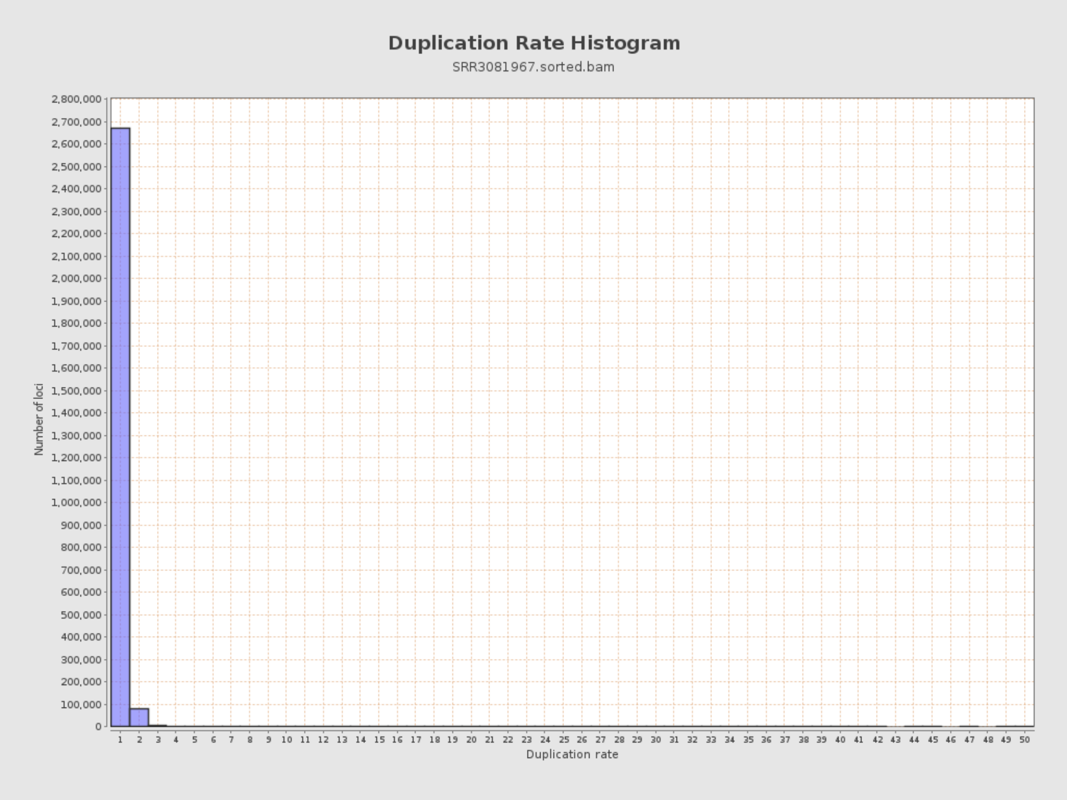
5. Results : Coverage Histogram (0-50X)



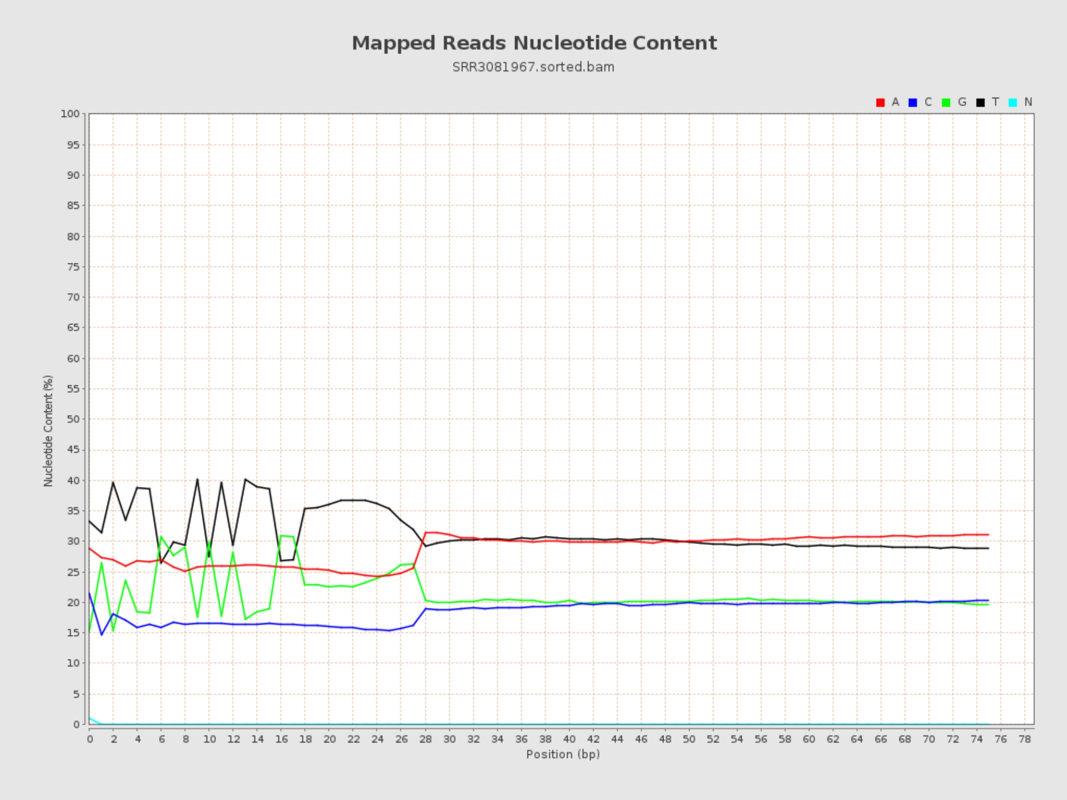
6. Results : Genome Fraction Coverage



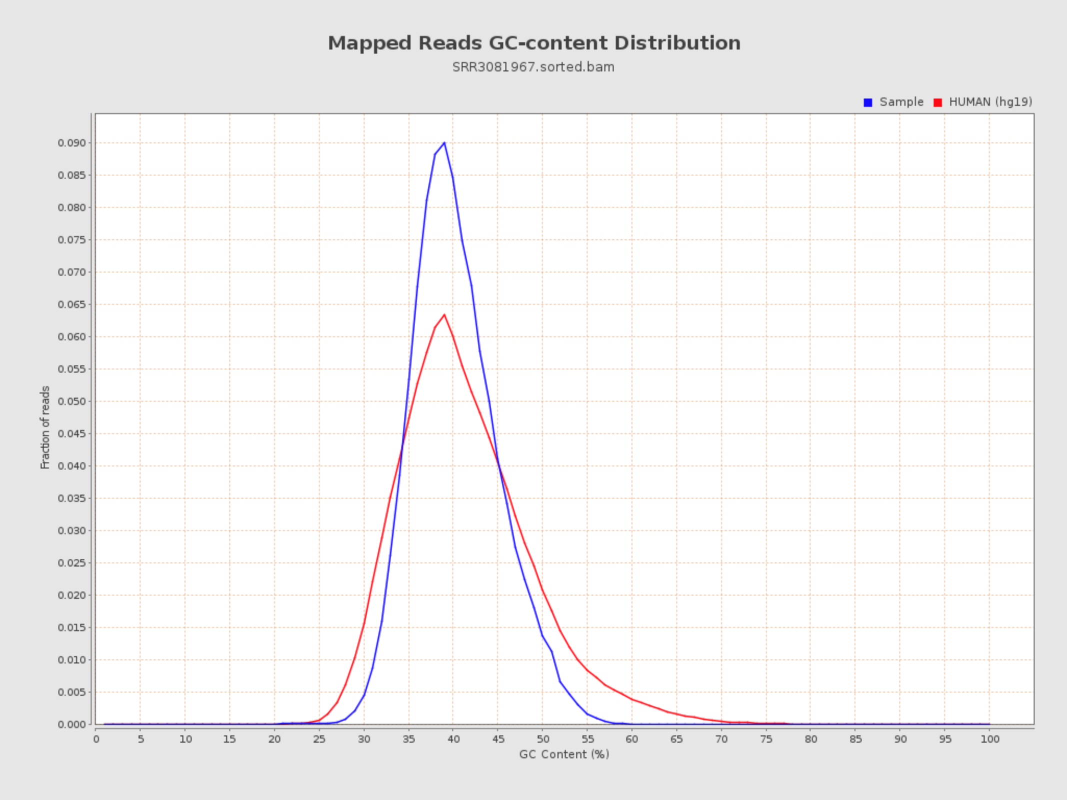
7. Results : Duplication Rate Histogram



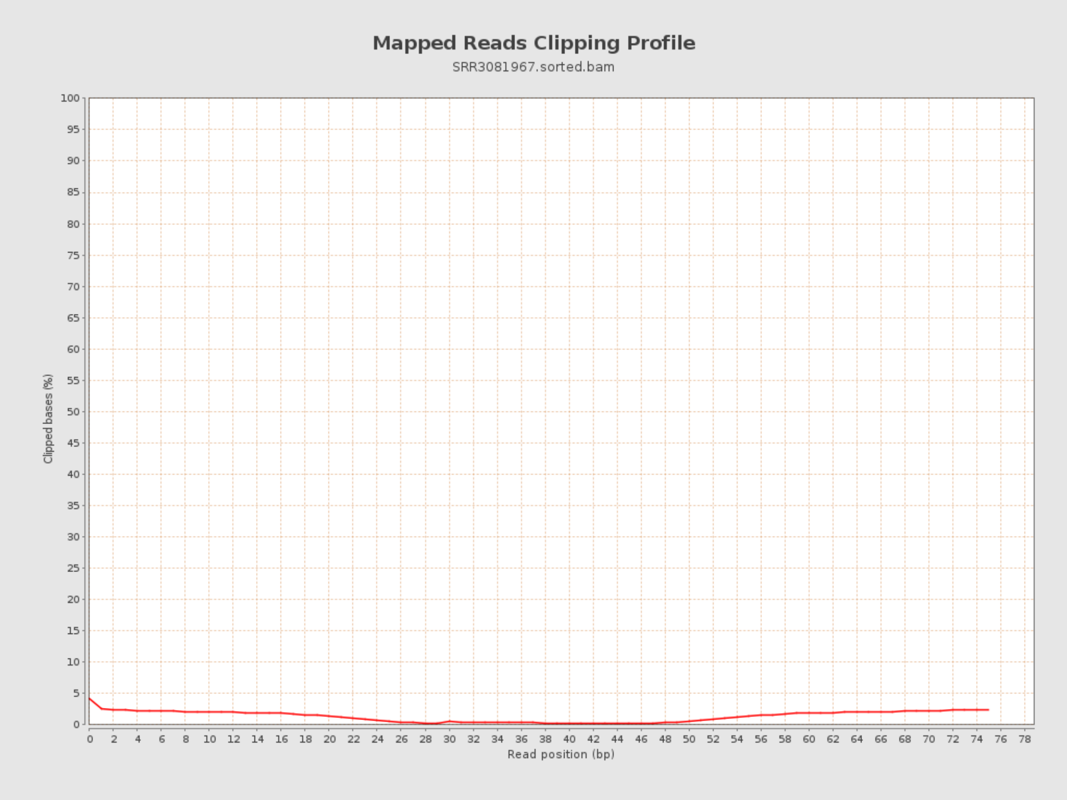
8. Results : Mapped Reads Nucleotide Content



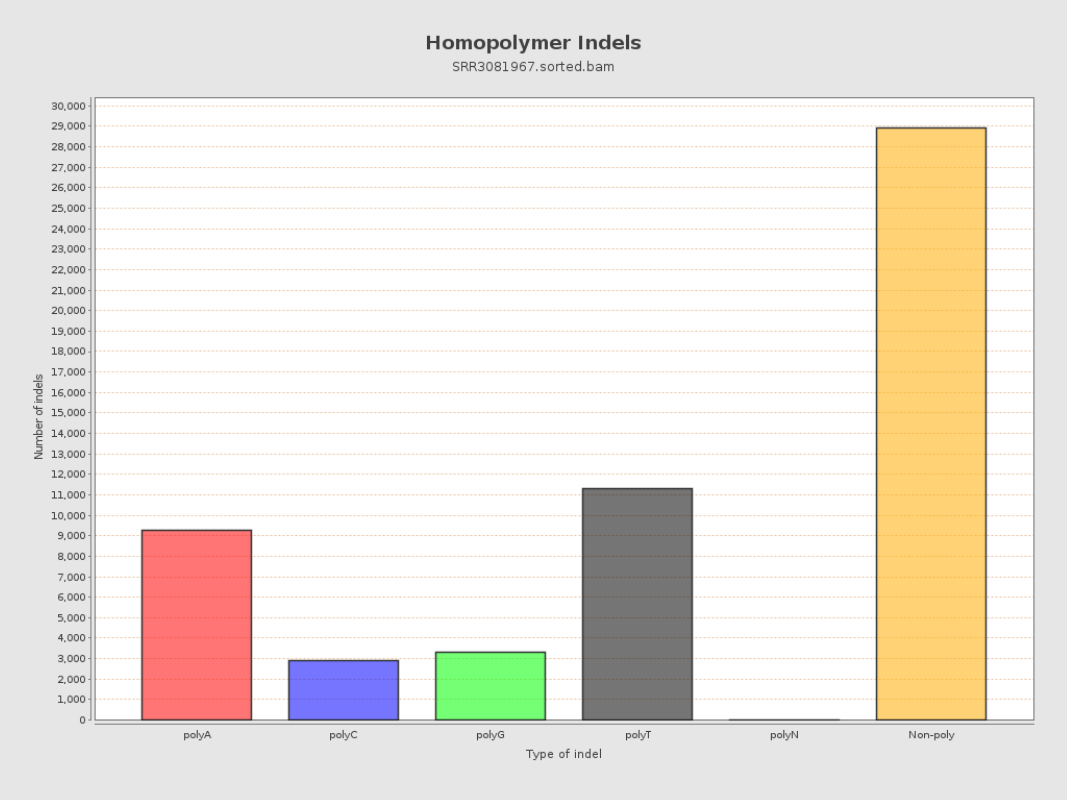
9. Results : Mapped Reads GC-content Distribution



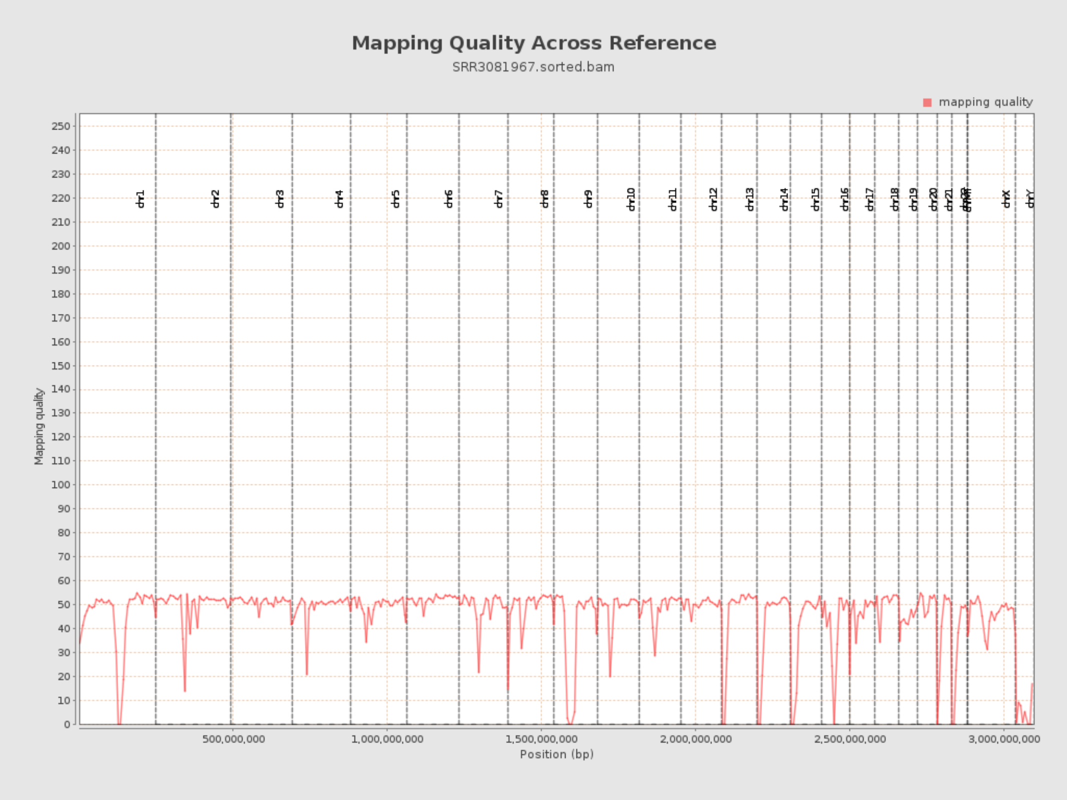
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram