Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:42:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084968.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_SRR3084968 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084968.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:42:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084968.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,747,022
Mapped reads	2,564,213 / 93.35%
Unmapped reads	182,809 / 6.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,254 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	103,108 / 3.75%
Duplication rate	2.73%
Clipped reads	765,088 / 27.85%

2.2. ACGT Content

Number/percentage of A's	54,375,601 / 30.04%
Number/percentage of C's	33,595,197 / 18.56%
Number/percentage of T's	57,446,982 / 31.73%
Number/percentage of G's	35,579,621 / 19.65%
Number/percentage of N's	26,278 / 0.01%
GC Percentage	38.21%

2.3. Coverage

Mean	0.0585

Standard Deviation	0.6825

2.4. Mapping Quality

Mean Mapping Quality	47.4

2.5. Mismatches and indels

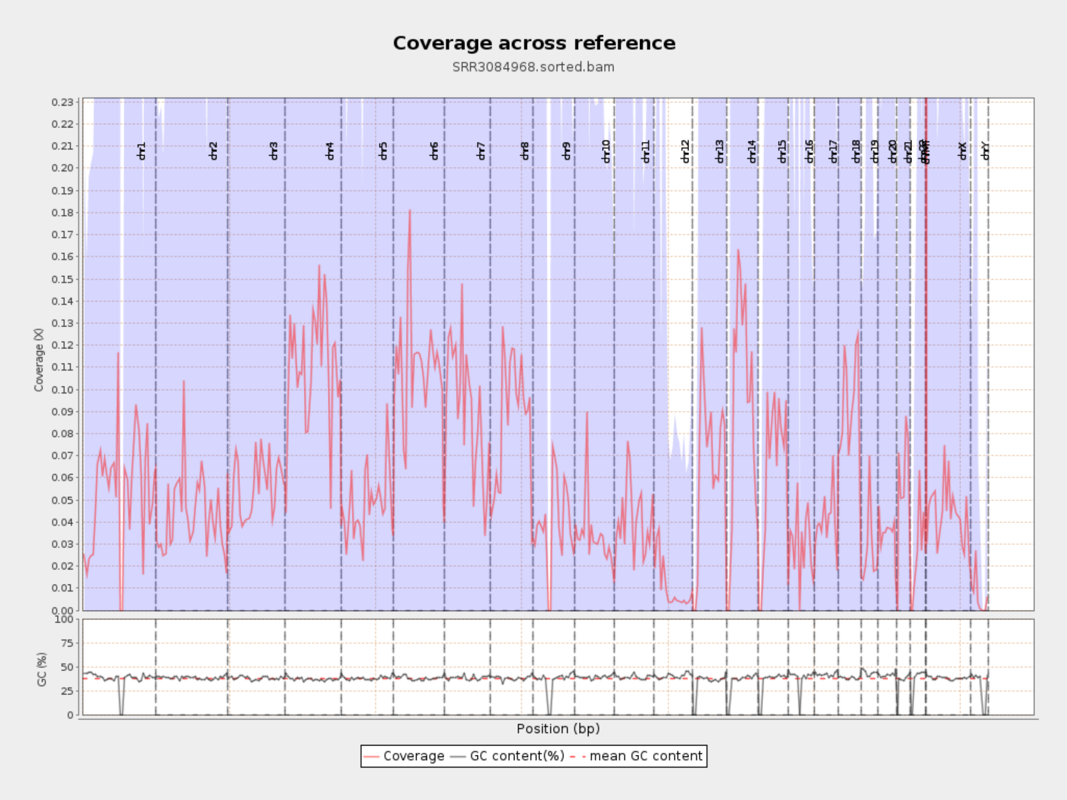
General error rate	0.83%
Mismatches	1,485,078
Insertions	14,670
Mapped reads with at least one insertion	0.57%
Deletions	42,164
Mapped reads with at least one deletion	1.63%
Homopolymer indels	47.83%

2.6. Chromosome stats

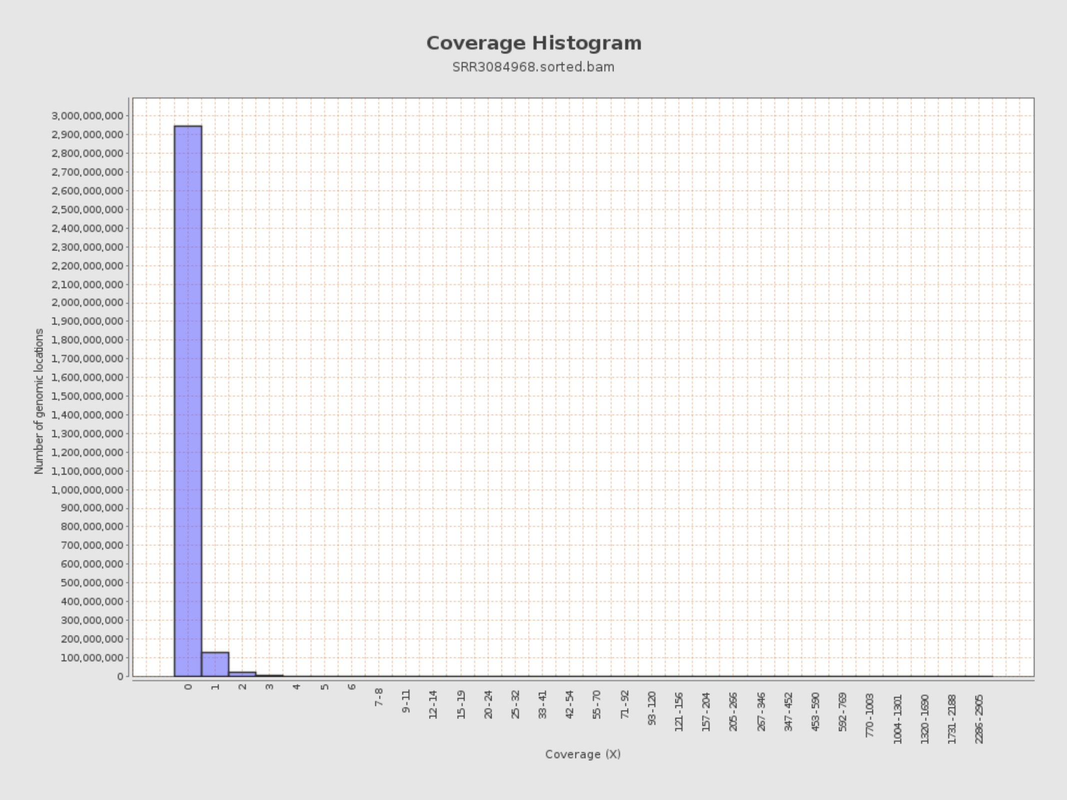
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13222872	0.0531	1.3053
chr2	243199373	10520222	0.0433	0.4751
chr3	198022430	11036126	0.0557	0.28
chr4	191154276	21255423	0.1112	0.3901
chr5	180915260	8713666	0.0482	0.2557
chr6	171115067	19098802	0.1116	0.6051
chr7	159138663	14260065	0.0896	0.6866

chr8	146364022	12738438	0.087	1.8223
chr9	141213431	5675916	0.0402	0.4652
chr10	135534747	4609309	0.034	0.4358
chr11	135006516	5520958	0.0409	0.4587
chr12	133851895	1403919	0.0105	0.1425
chr13	115169878	7820393	0.0679	0.2997
chr14	107349540	10107160	0.0942	0.3806
chr15	102531392	6513595	0.0635	0.2892
chr16	90354753	2592119	0.0287	0.2836
chr17	81195210	3355977	0.0413	0.2793
chr18	78077248	7340159	0.094	1.0012
chr19	59128983	1670063	0.0282	0.8162
chr20	63025520	2252770	0.0357	0.2449
chr21	48129895	2747815	0.0571	0.3012
chr22	51304566	1398739	0.0273	0.1883
chrMT	16571	60928	3.6768	2.8281
chrX	155270560	6762779	0.0436	0.2943
chrY	59373566	414811	0.007	0.2171

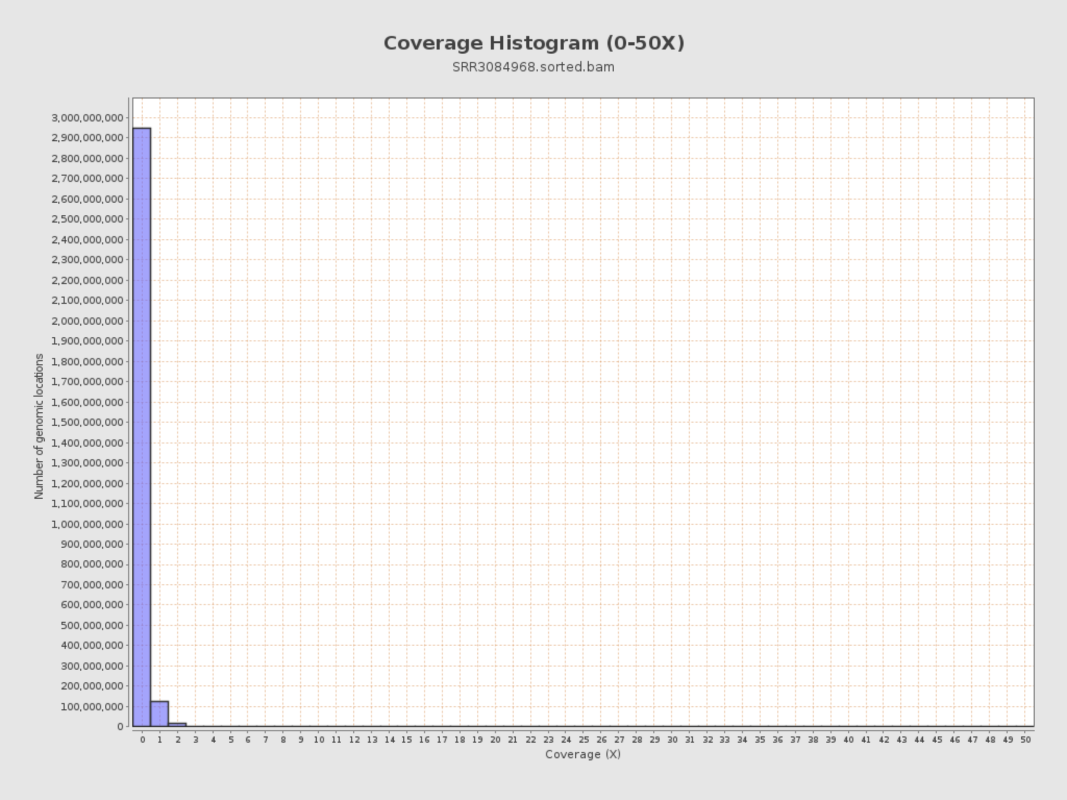
3. Results : Coverage across reference



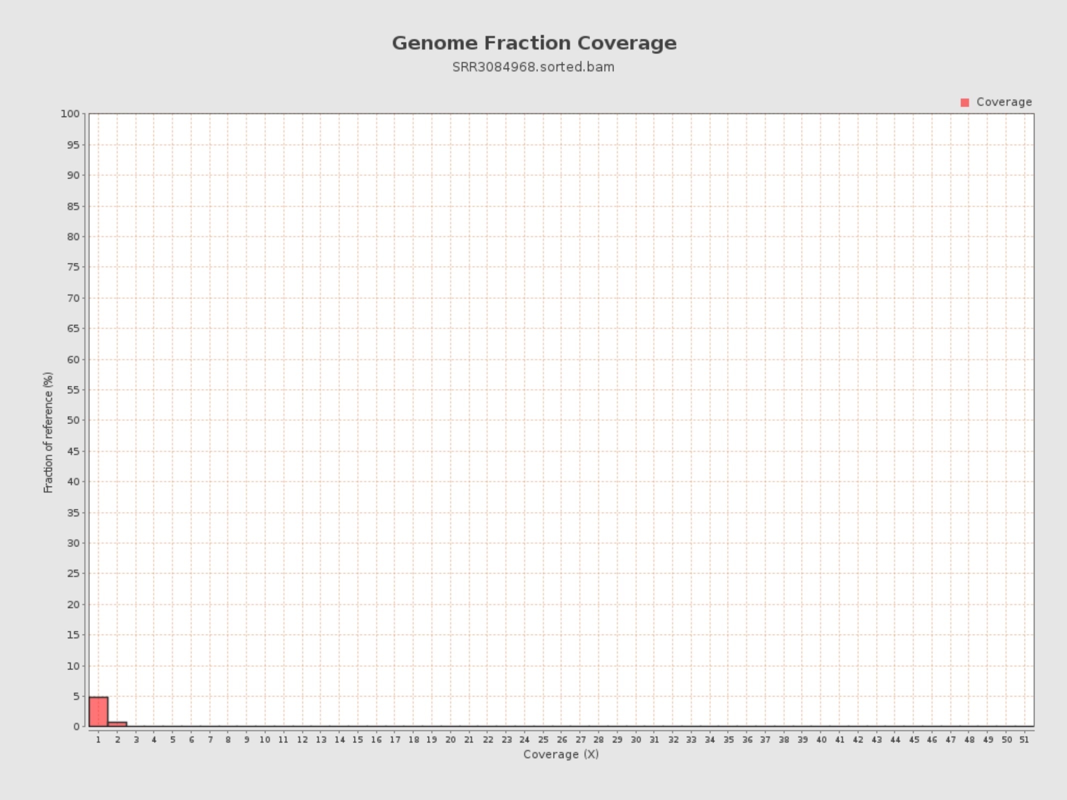
4. Results : Coverage Histogram



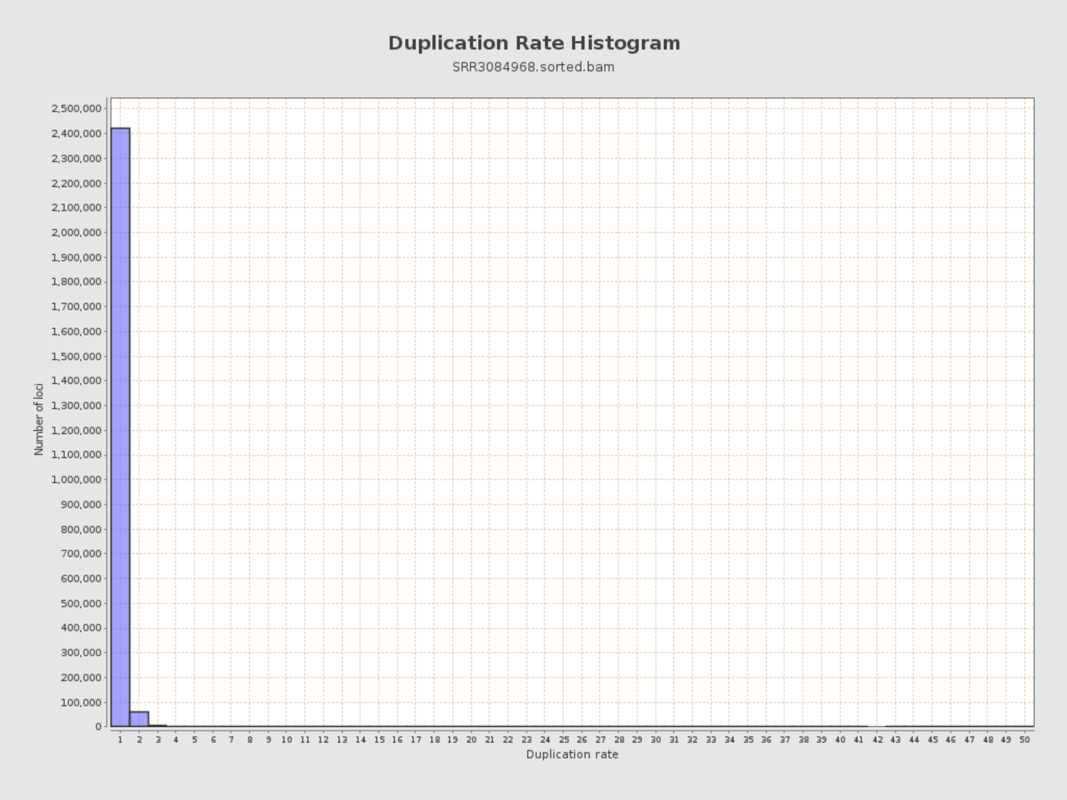
5. Results : Coverage Histogram (0-50X)



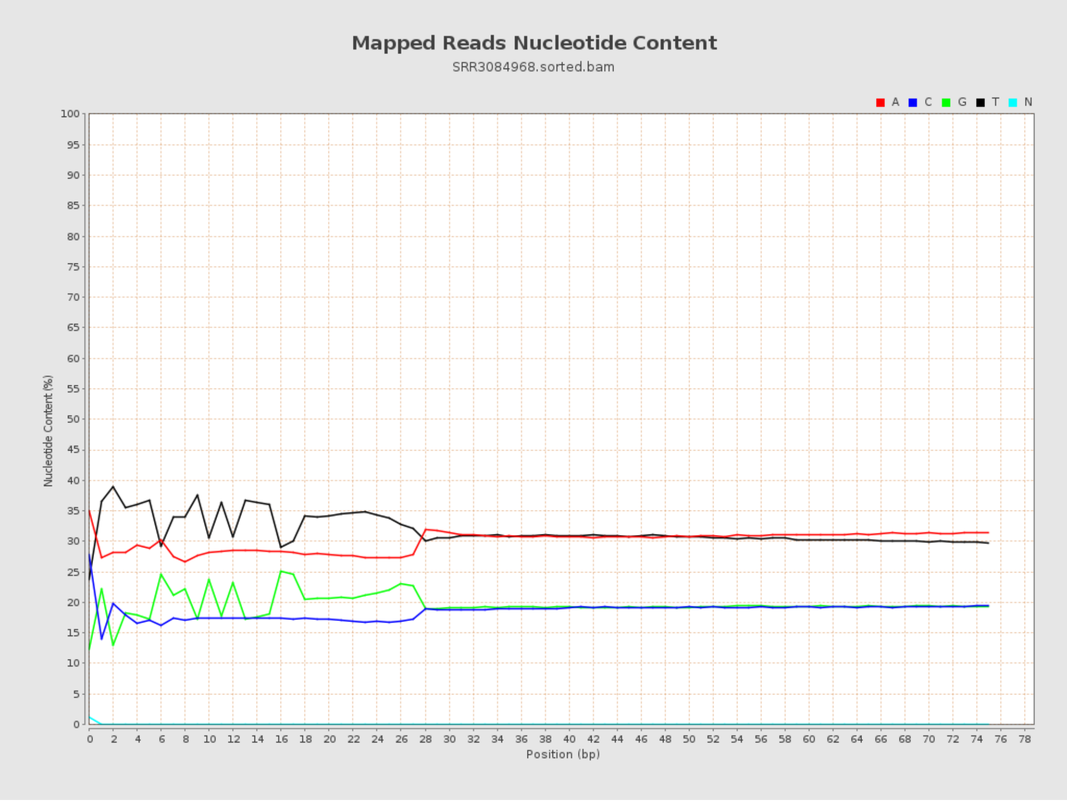
6. Results : Genome Fraction Coverage



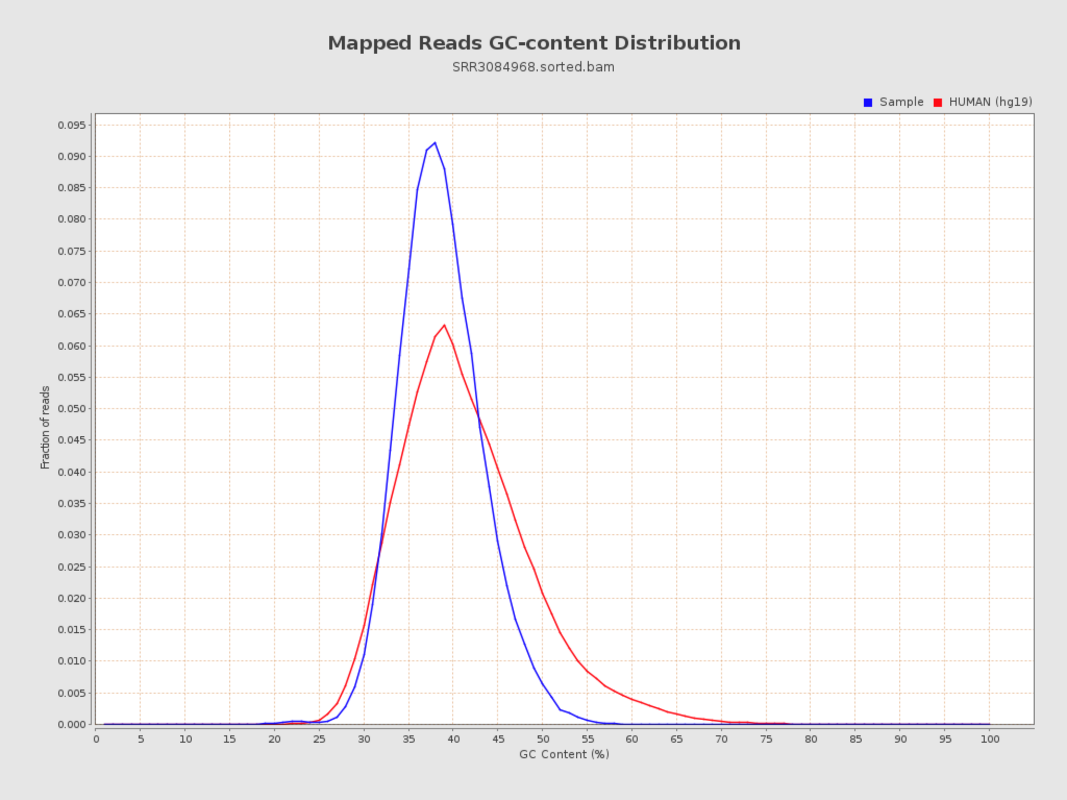
7. Results : Duplication Rate Histogram



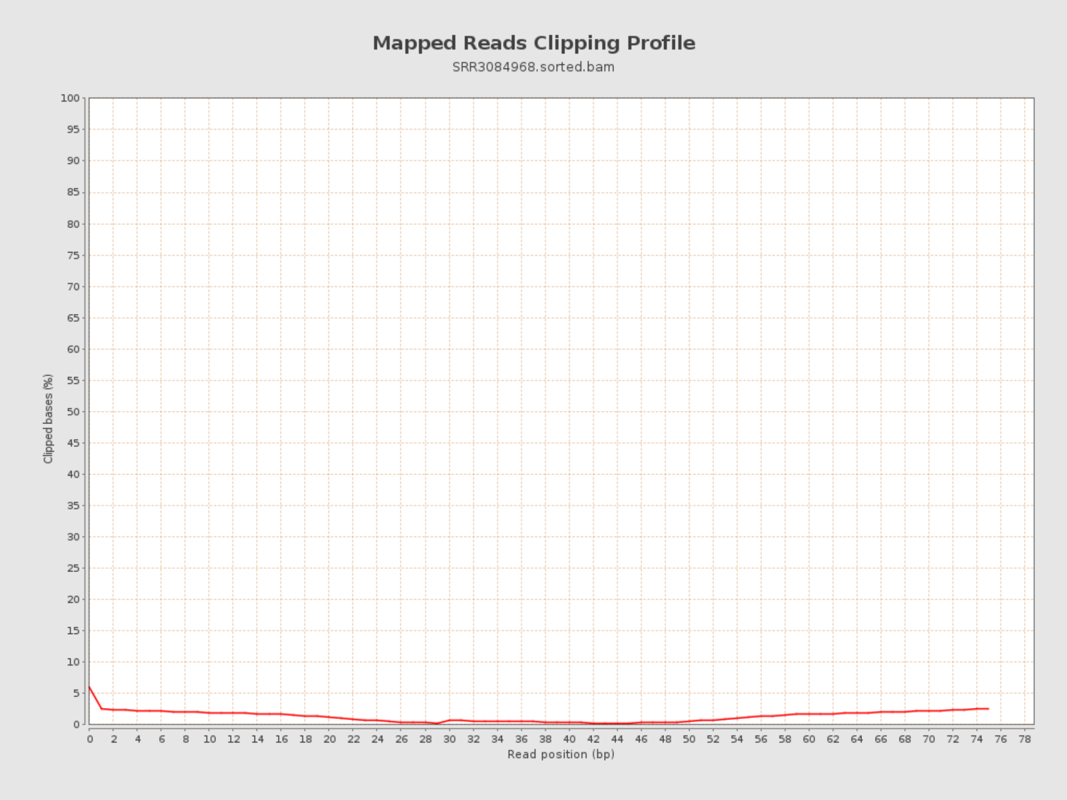
8. Results : Mapped Reads Nucleotide Content



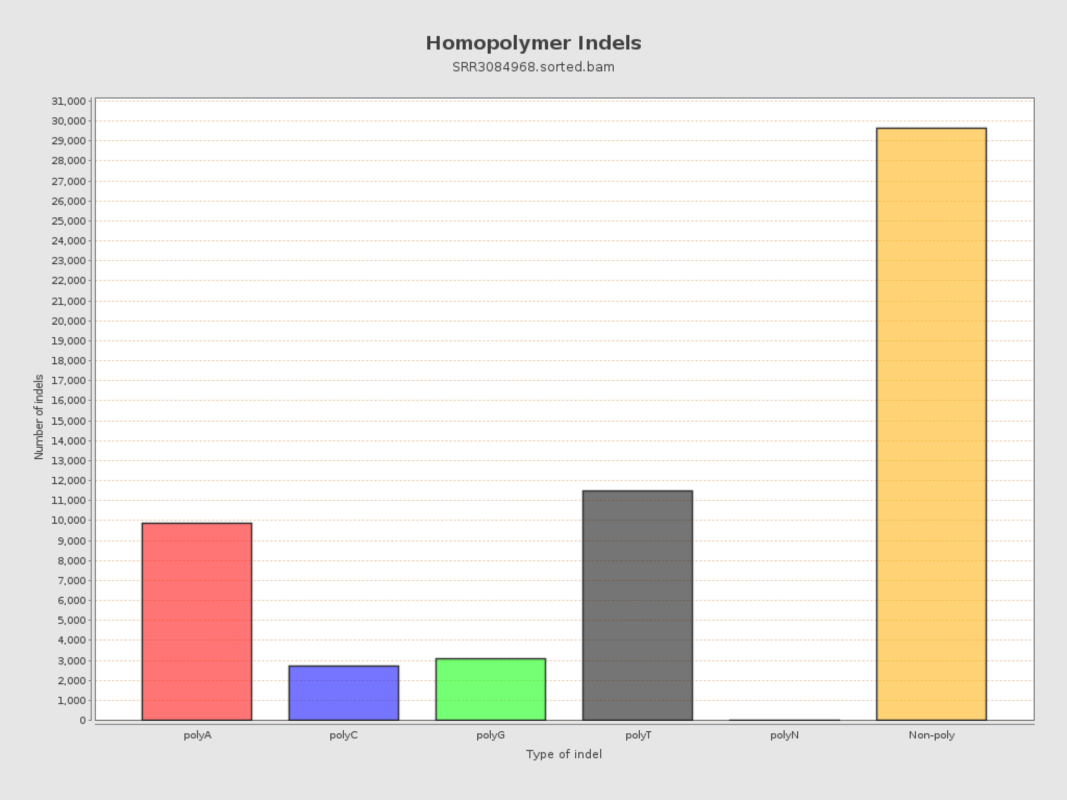
9. Results : Mapped Reads GC-content Distribution



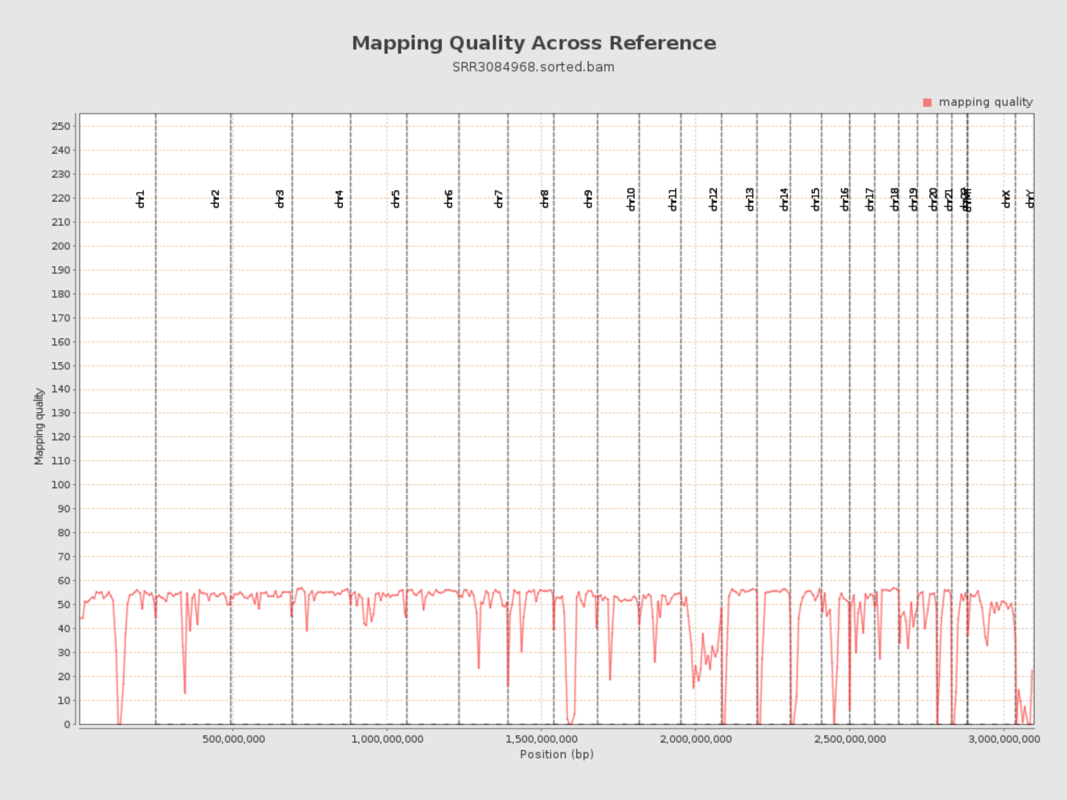
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram