Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:28:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082893.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_SRR3082893 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082893.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:28:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082893.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,060,544
Mapped reads	3,353,221 / 82.58%
Unmapped reads	707,323 / 17.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,916 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	162,705 / 4.01%
Duplication rate	3.74%
Clipped reads	1,385,349 / 34.12%

2.2. ACGT Content

Number/percentage of A's	64,312,374 / 28.32%
Number/percentage of C's	41,359,356 / 18.21%
Number/percentage of T's	73,317,070 / 32.28%
Number/percentage of G's	48,125,794 / 21.19%
Number/percentage of N's	12,016 / 0.01%
GC Percentage	39.4%

2.3. Coverage

Mean	0.0734

Standard Deviation	0.6014

2.4. Mapping Quality

Mean Mapping Quality	46.38

2.5. Mismatches and indels

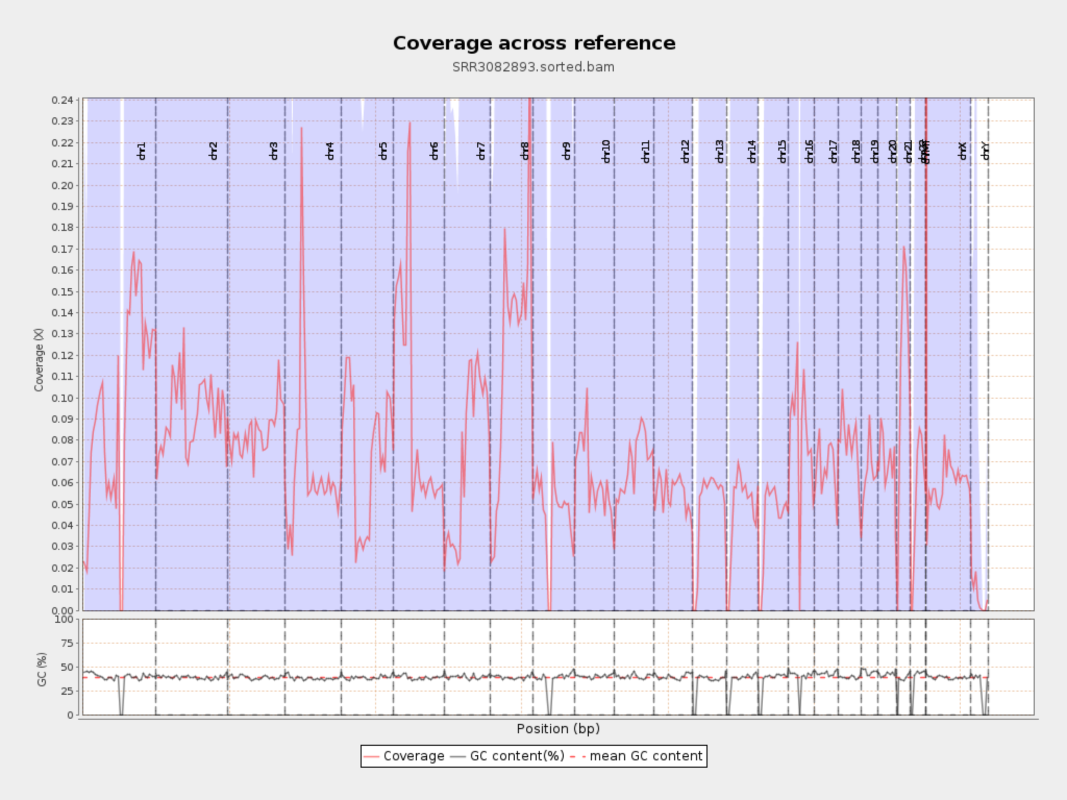
General error rate	0.91%
Mismatches	2,026,436
Insertions	18,970
Mapped reads with at least one insertion	0.56%
Deletions	48,619
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.54%

2.6. Chromosome stats

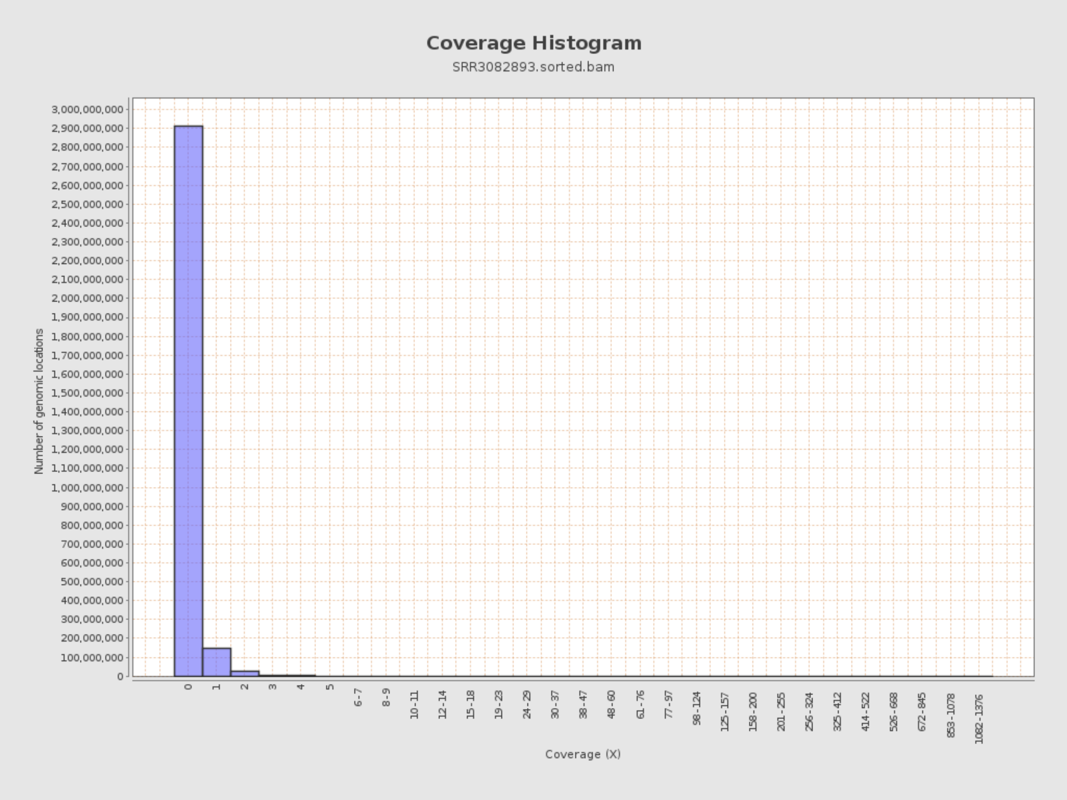
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23737718	0.0952	1.2635
chr2	243199373	22533021	0.0927	0.6479
chr3	198022430	16643482	0.084	0.3462
chr4	191154276	13152568	0.0688	0.3291
chr5	180915260	13235139	0.0732	0.3251
chr6	171115067	16270934	0.0951	0.5802
chr7	159138663	11701848	0.0735	0.5663

chr8	146364022	18056298	0.1234	0.8787
chr9	141213431	6576825	0.0466	0.5109
chr10	135534747	8511304	0.0628	0.4735
chr11	135006516	9305012	0.0689	0.4429
chr12	133851895	7400049	0.0553	0.2926
chr13	115169878	5542807	0.0481	0.2589
chr14	107349540	5050108	0.047	0.3022
chr15	102531392	4297346	0.0419	0.2421
chr16	90354753	7233065	0.0801	0.4021
chr17	81195210	5515799	0.0679	0.411
chr18	78077248	6216562	0.0796	1.1279
chr19	59128983	3853985	0.0652	0.7737
chr20	63025520	4449439	0.0706	0.3388
chr21	48129895	5351509	0.1112	0.4167
chr22	51304566	2739443	0.0534	0.2717
chrMT	16571	147984	8.9303	5.9655
chrX	155270560	9294699	0.0599	0.3482
chrY	59373566	392605	0.0066	0.1381

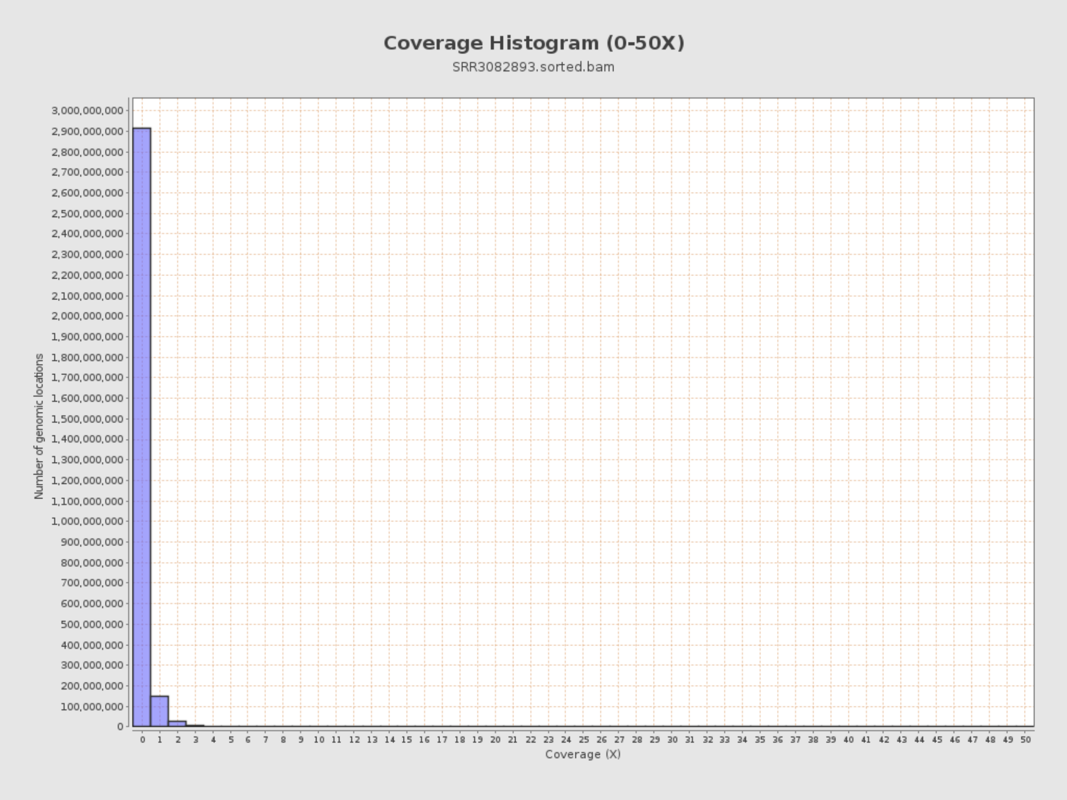
3. Results : Coverage across reference



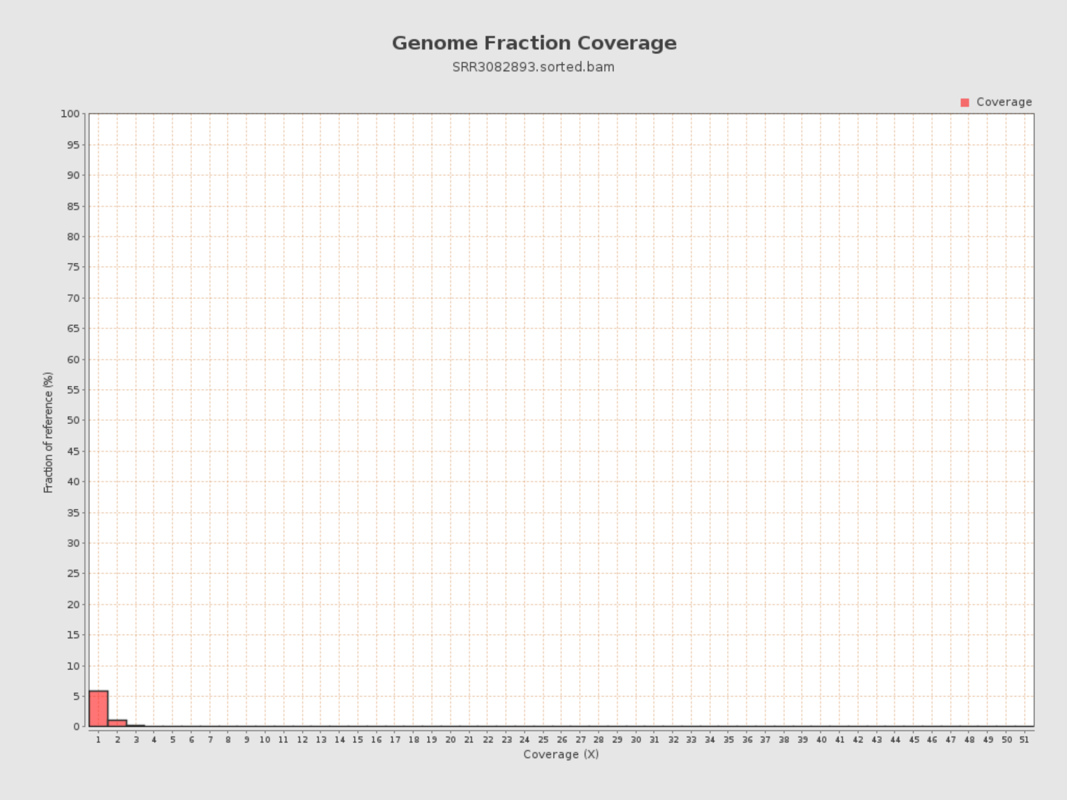
4. Results : Coverage Histogram



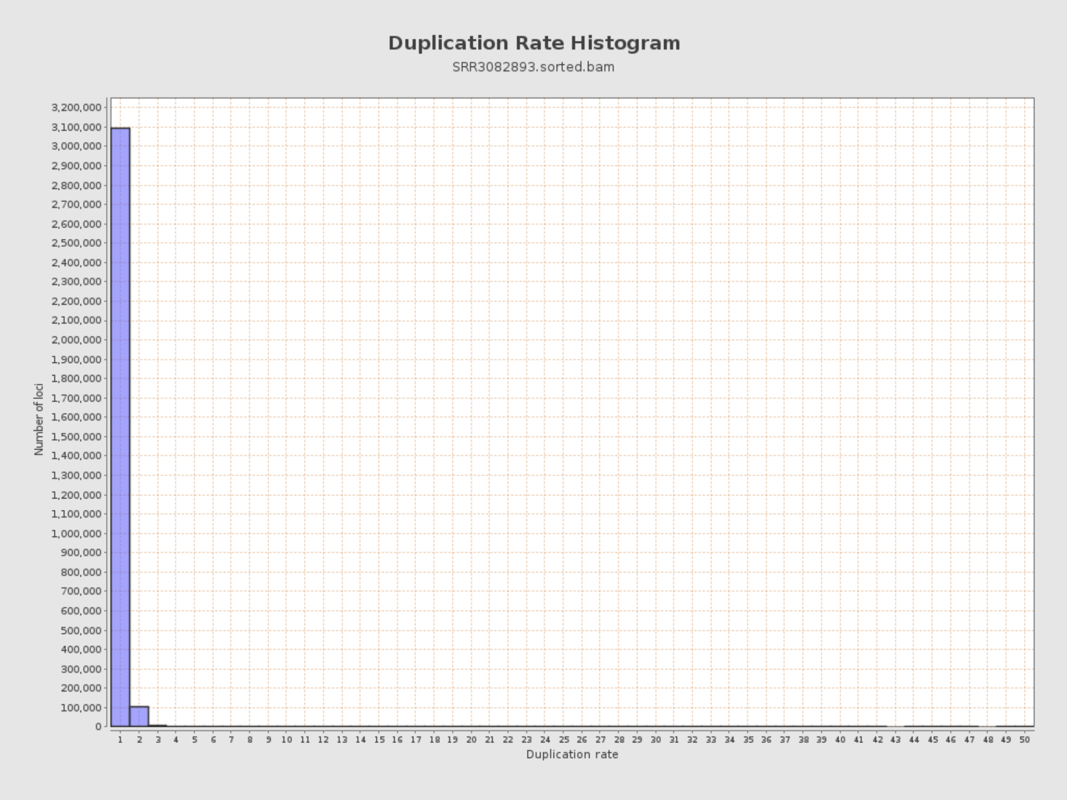
5. Results : Coverage Histogram (0-50X)



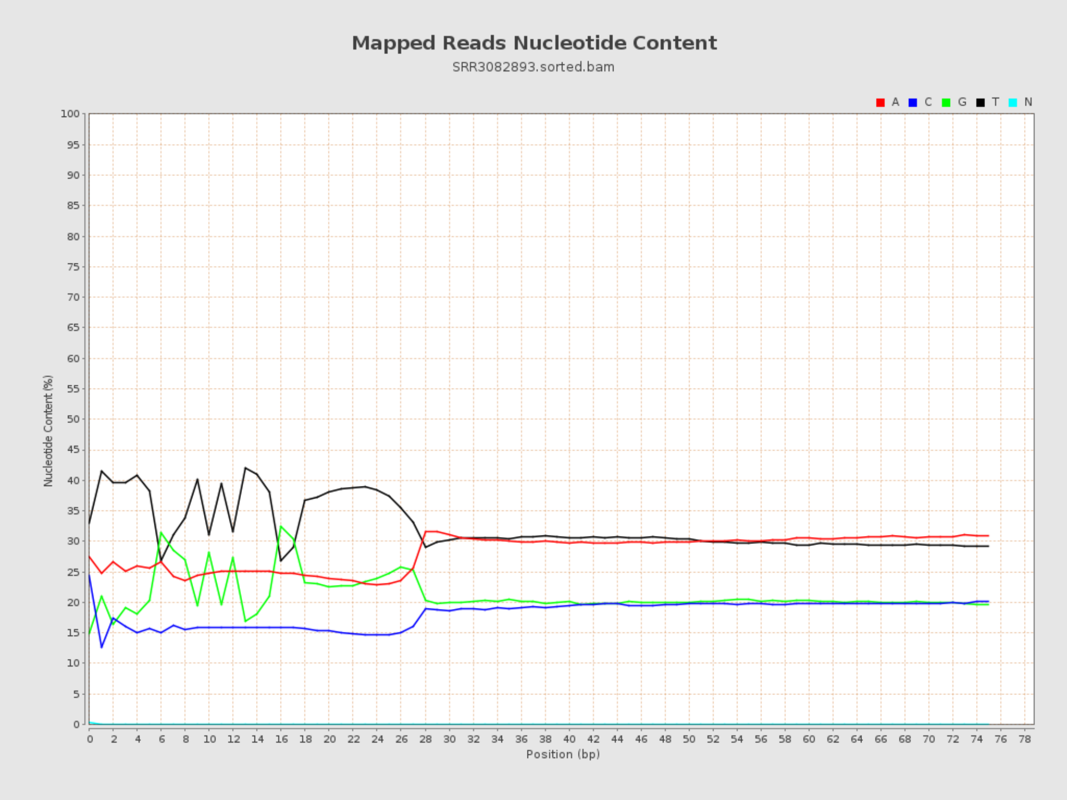
6. Results : Genome Fraction Coverage



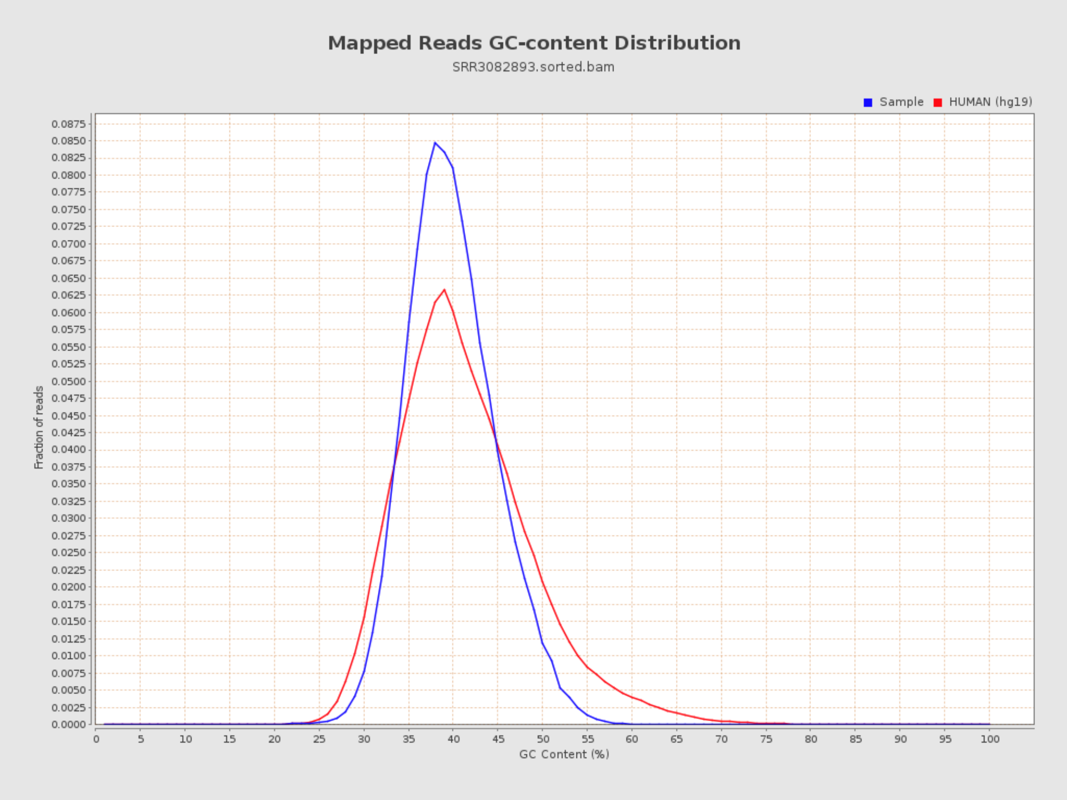
7. Results : Duplication Rate Histogram



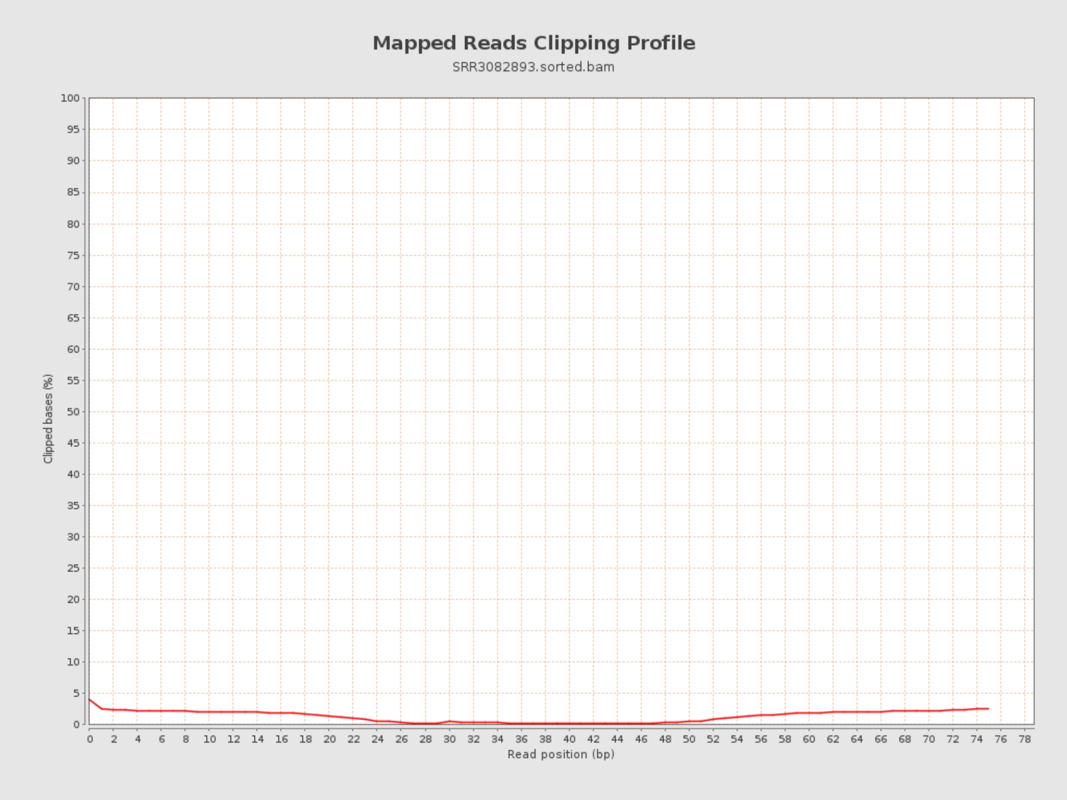
8. Results : Mapped Reads Nucleotide Content



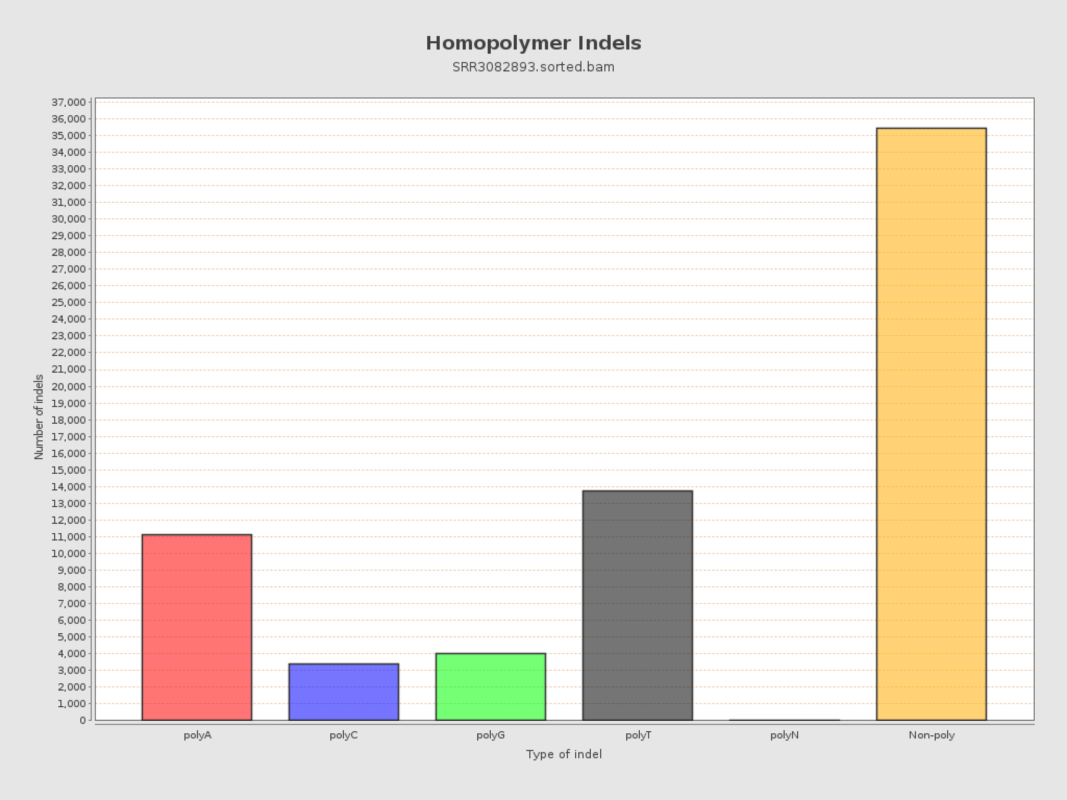
9. Results : Mapped Reads GC-content Distribution



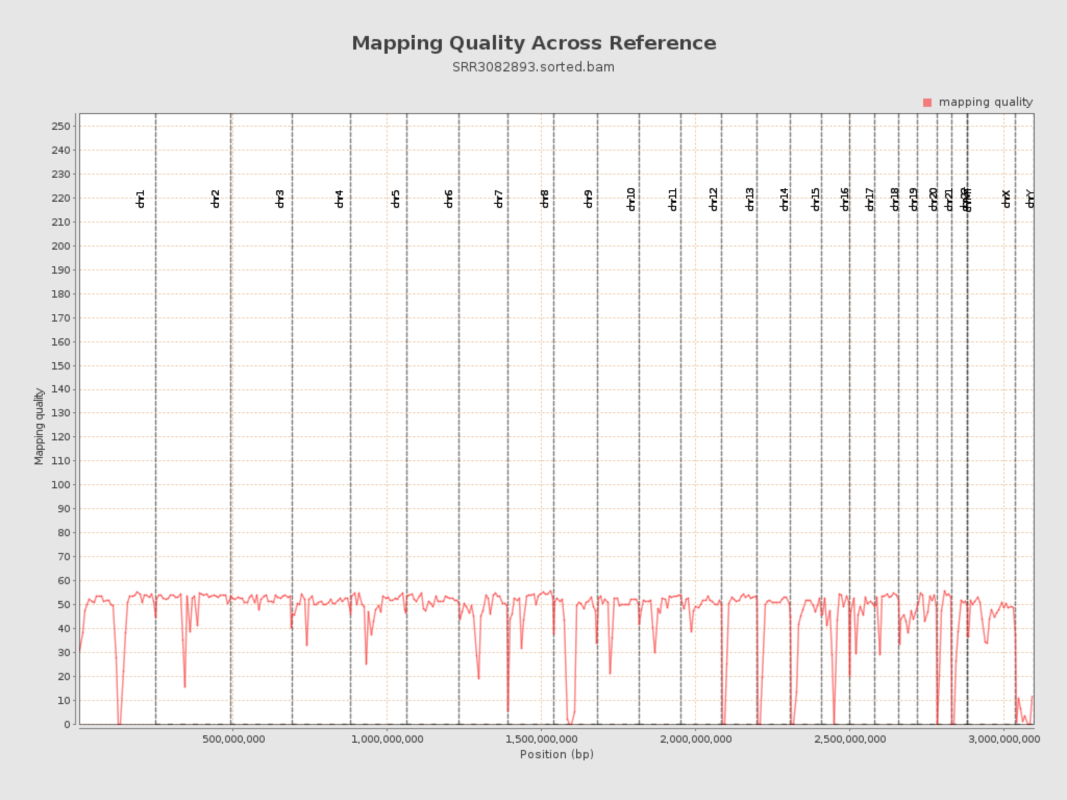
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram