Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:21:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708556.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_SRR1708556 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708556.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:21:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708556.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,175,563
Mapped reads	3,444,562 / 82.49%
Unmapped reads	731,001 / 17.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	96 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	16,097 / 0.39%
Duplication rate	0.46%
Clipped reads	47,201 / 1.13%

2.2. ACGT Content

Number/percentage of A's	53,209,609 / 30.98%
Number/percentage of C's	32,616,381 / 18.99%
Number/percentage of T's	53,023,648 / 30.87%
Number/percentage of G's	32,900,601 / 19.16%
Number/percentage of N's	7,281 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	0.0555

Standard Deviation	0.2421

2.4. Mapping Quality

Mean Mapping Quality	46.52

2.5. Mismatches and indels

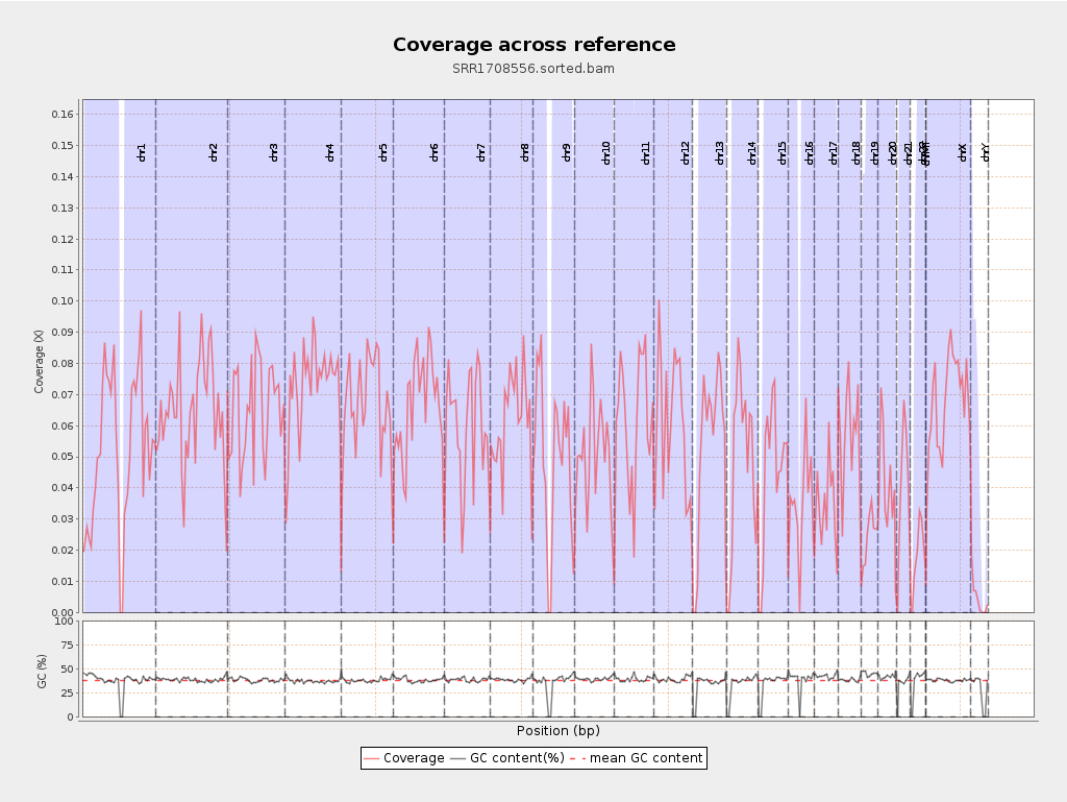
General error rate	0.17%
Mismatches	270,099
Insertions	11,428
Mapped reads with at least one insertion	0.33%
Deletions	9,178
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.61%

2.6. Chromosome stats

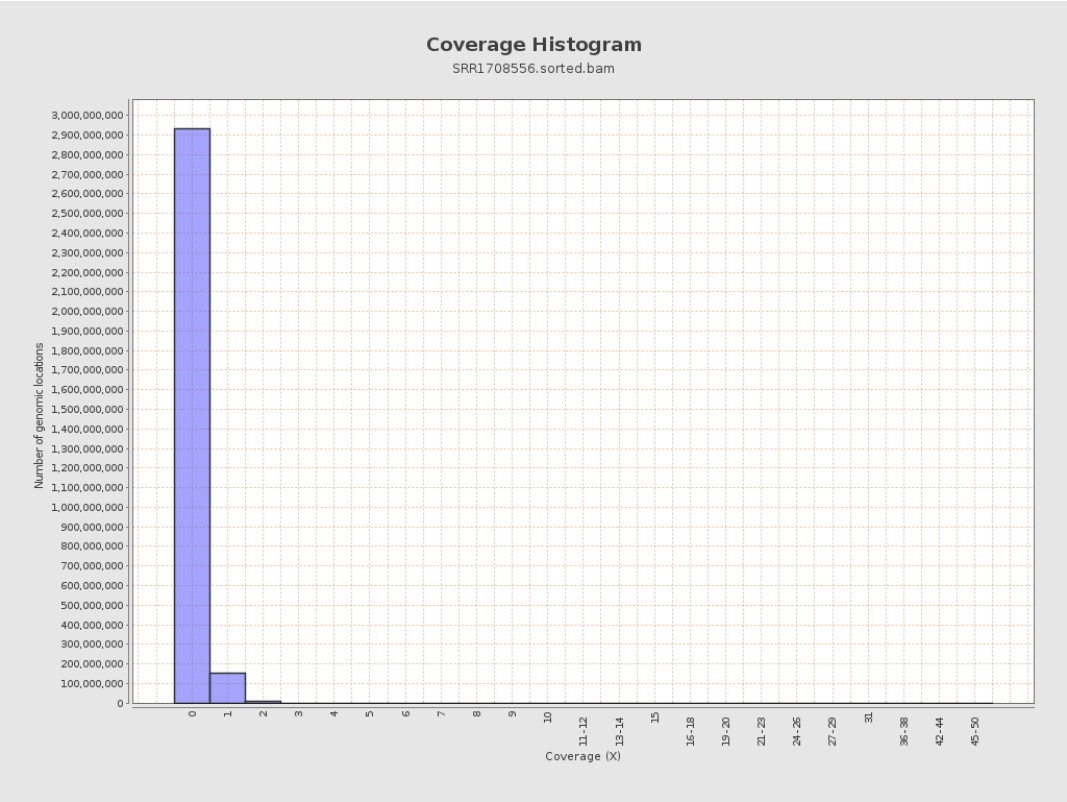
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12931659	0.0519	0.2352
chr2	243199373	15656210	0.0644	0.26
chr3	198022430	12900918	0.0651	0.2613
chr4	191154276	13952316	0.073	0.2761
chr5	180915260	11951778	0.0661	0.263
chr6	171115067	11457393	0.067	0.2649
chr7	159138663	9335279	0.0587	0.2487

chr8	146364022	9103742	0.0622	0.2552
chr9	141213431	7048932	0.0499	0.2298
chr10	135534747	6913176	0.051	0.2311
chr11	135006516	8324157	0.0617	0.256
chr12	133851895	8034427	0.06	0.2515
chr13	115169878	6172195	0.0536	0.2378
chr14	107349540	5254945	0.049	0.228
chr15	102531392	4564086	0.0445	0.2175
chr16	90354753	3085838	0.0342	0.1897
chr17	81195210	2857840	0.0352	0.1926
chr18	78077248	4467313	0.0572	0.245
chr19	59128983	1454089	0.0246	0.1604
chr20	63025520	2640038	0.0419	0.2101
chr21	48129895	1859902	0.0386	0.203
chr22	51304566	927904	0.0181	0.1379
chrMT	16571	143	0.0086	0.0925
chrX	155270560	10624009	0.0684	0.2686
chrY	59373566	254904	0.0043	0.068

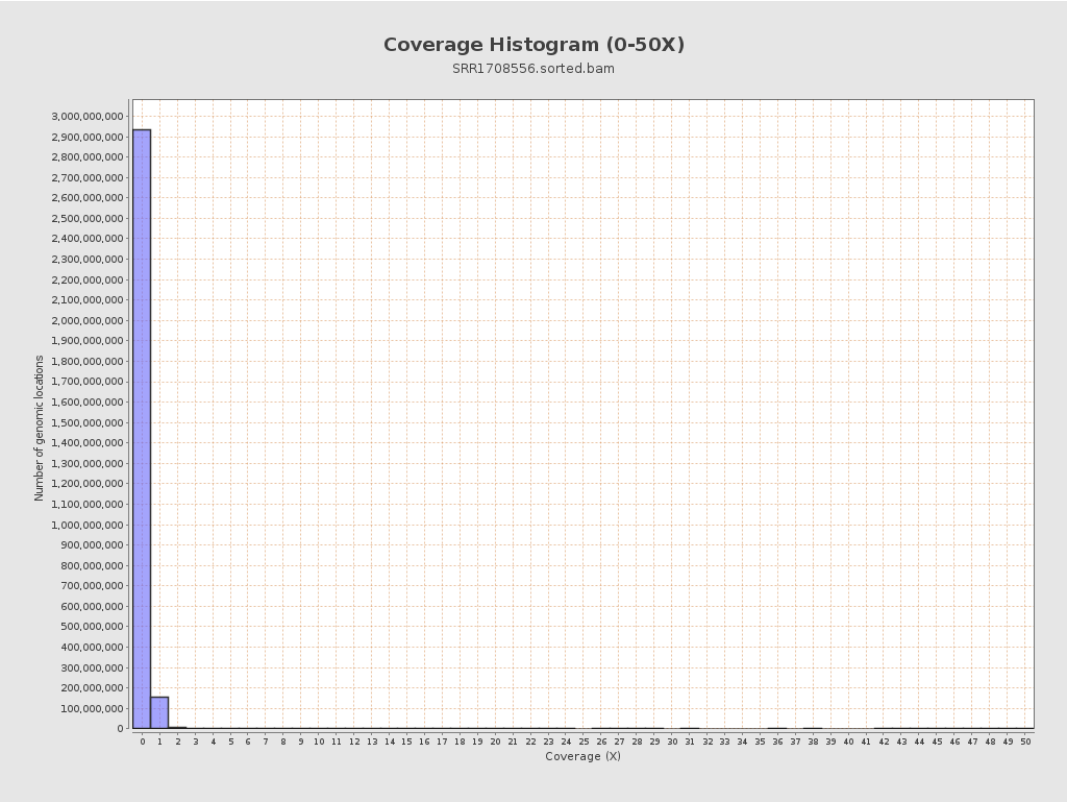
3. Results : Coverage across reference



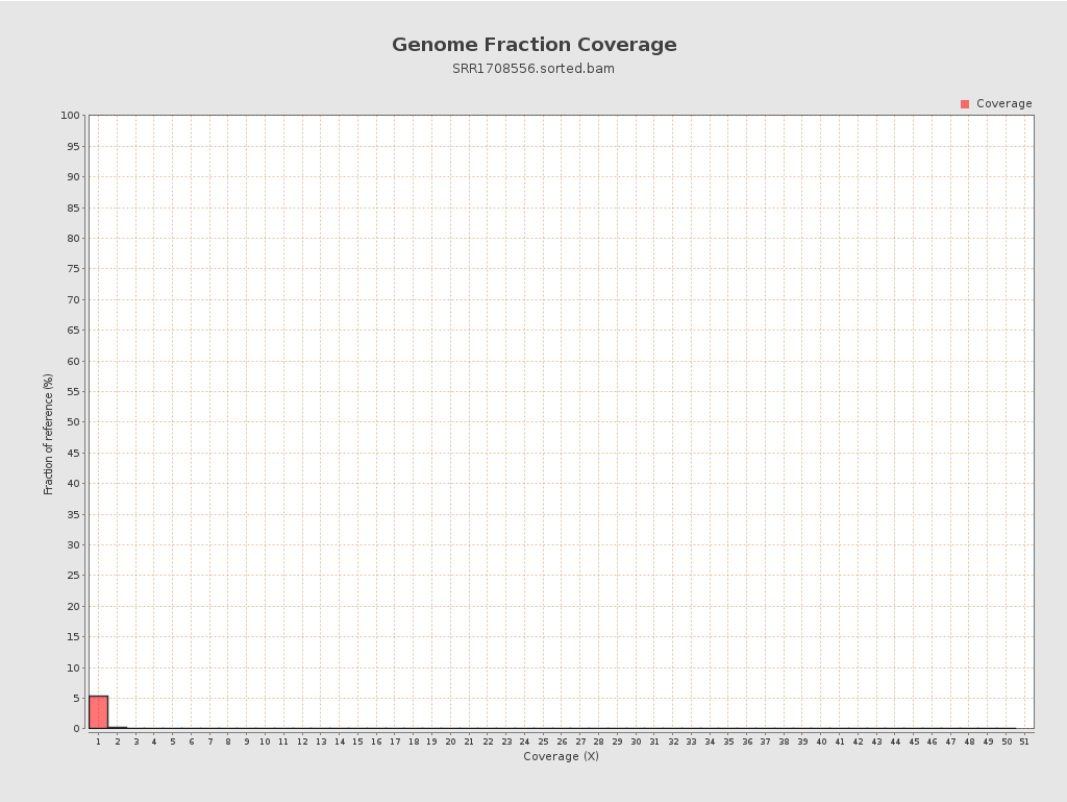
4. Results : Coverage Histogram



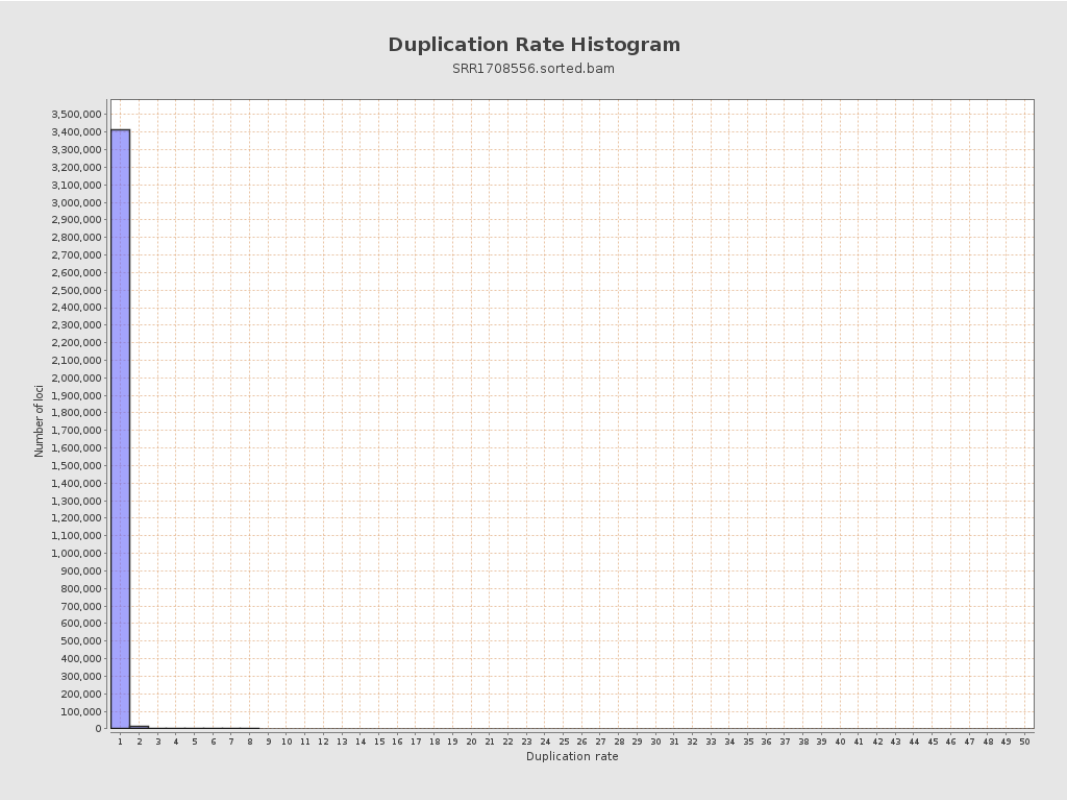
5. Results : Coverage Histogram (0-50X)



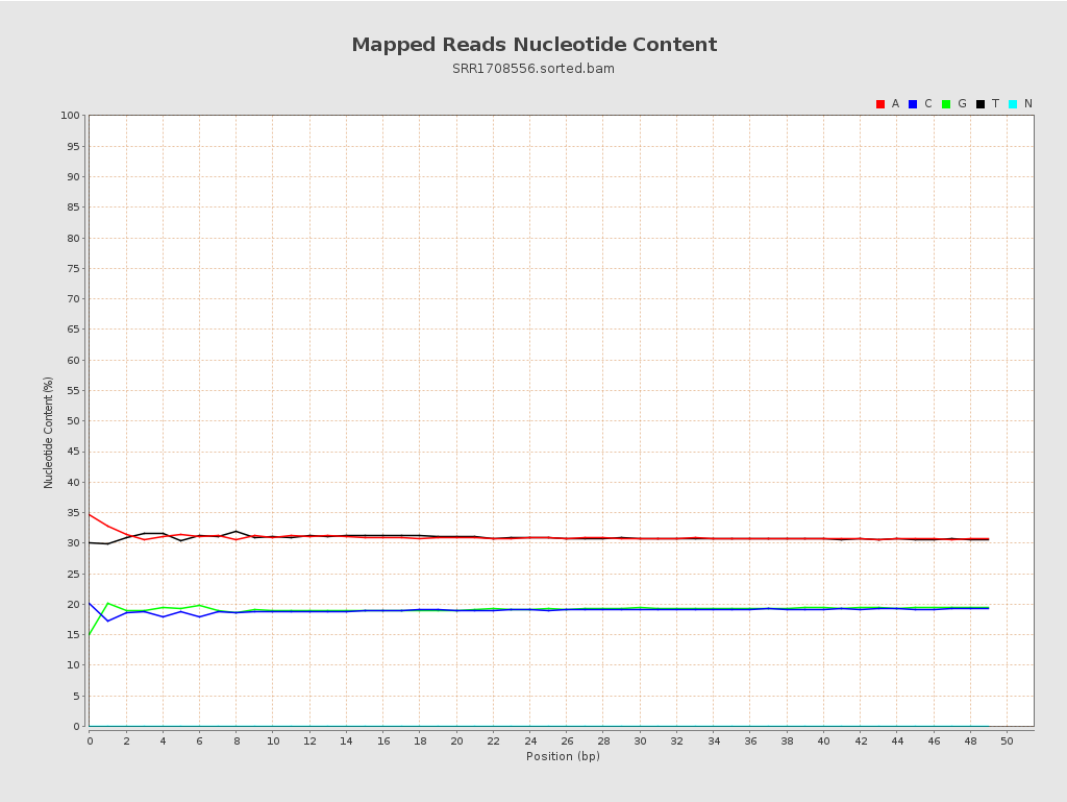
6. Results : Genome Fraction Coverage



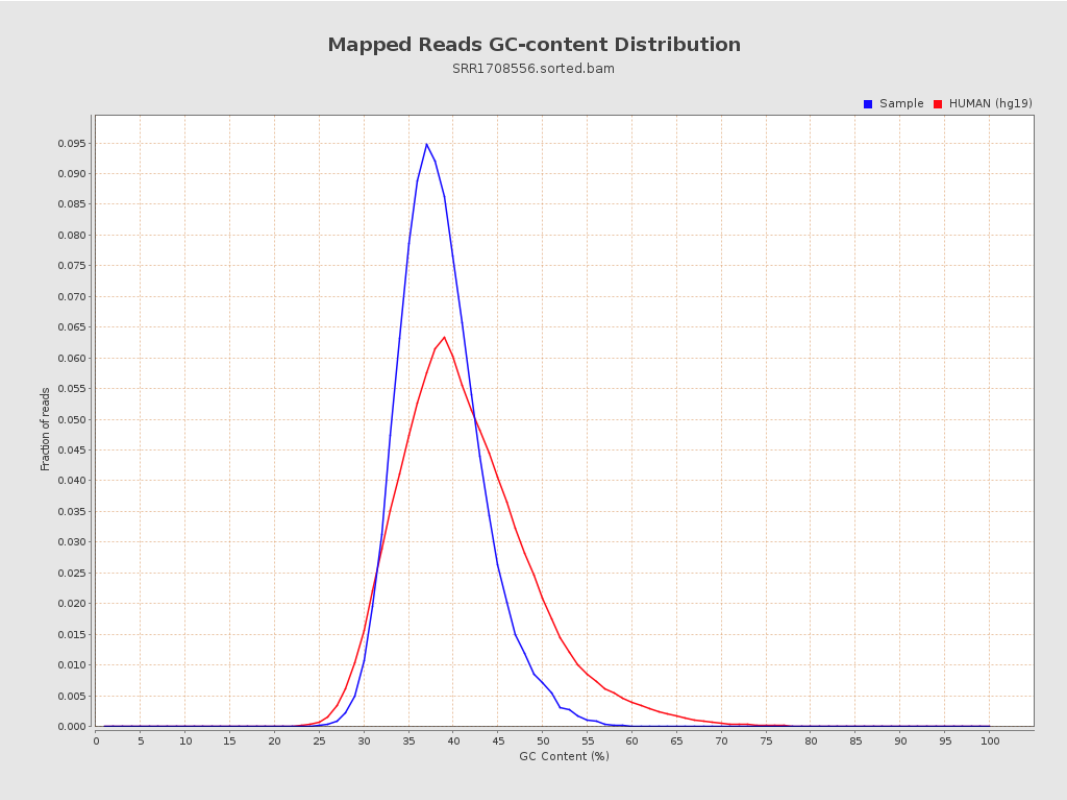
7. Results : Duplication Rate Histogram



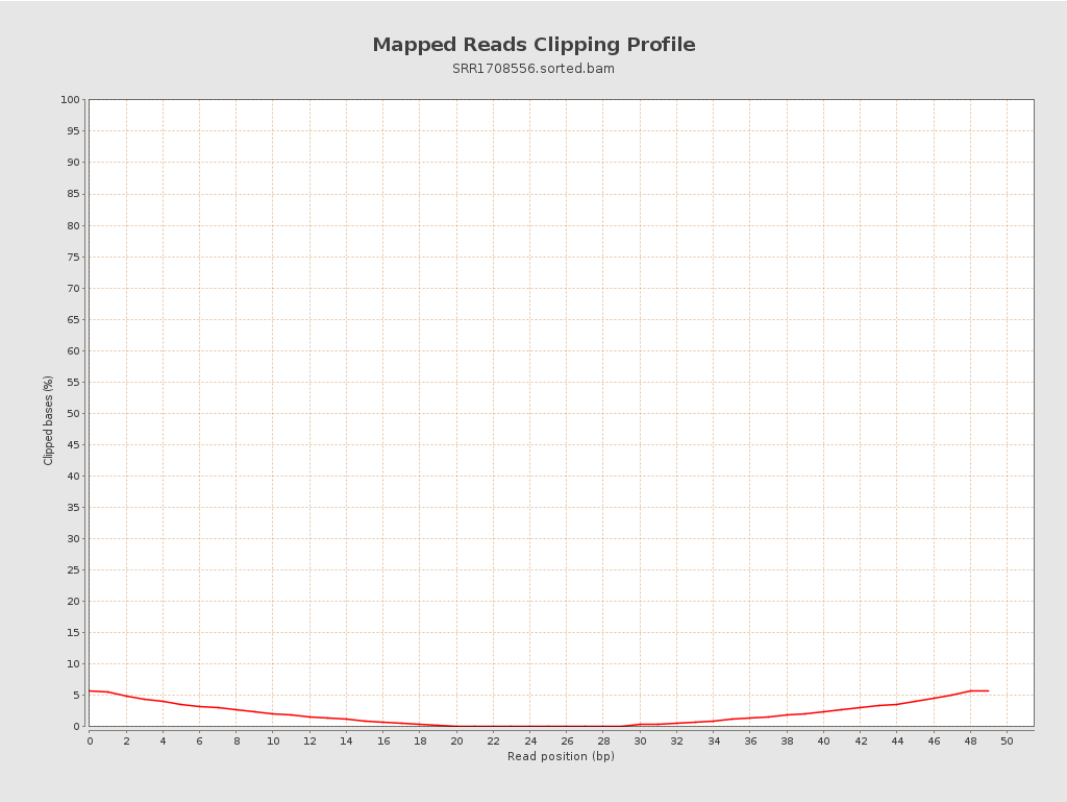
8. Results : Mapped Reads Nucleotide Content



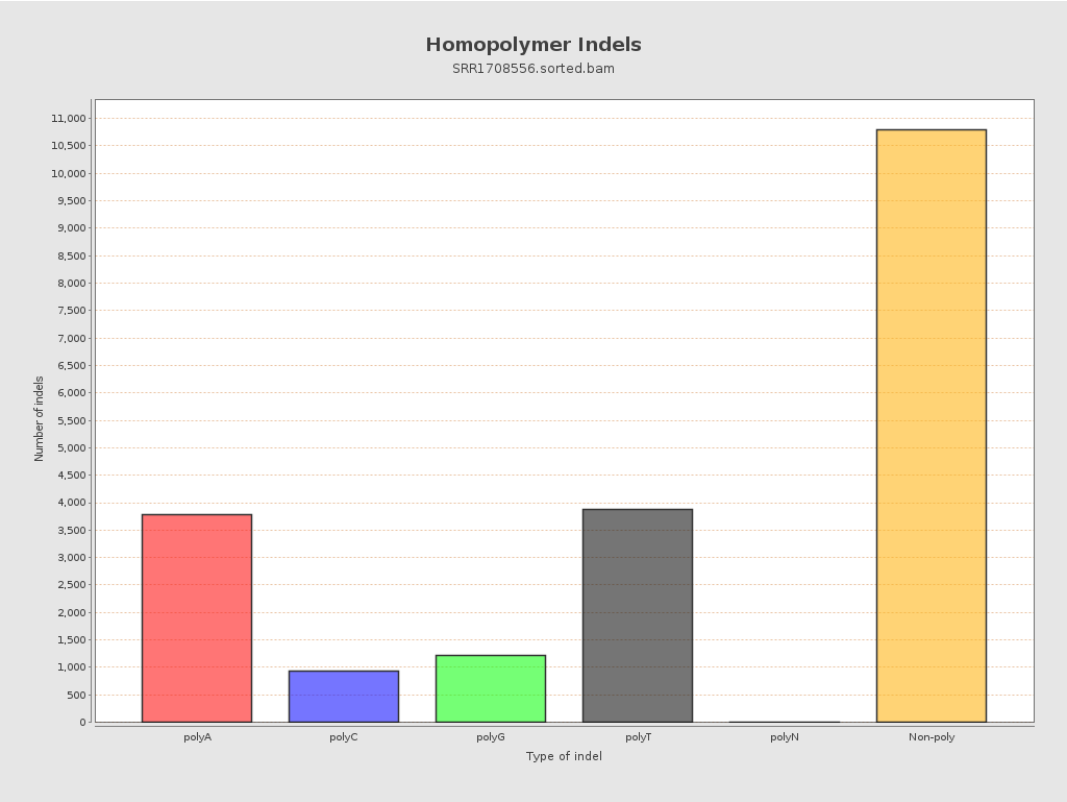
9. Results : Mapped Reads GC-content Distribution



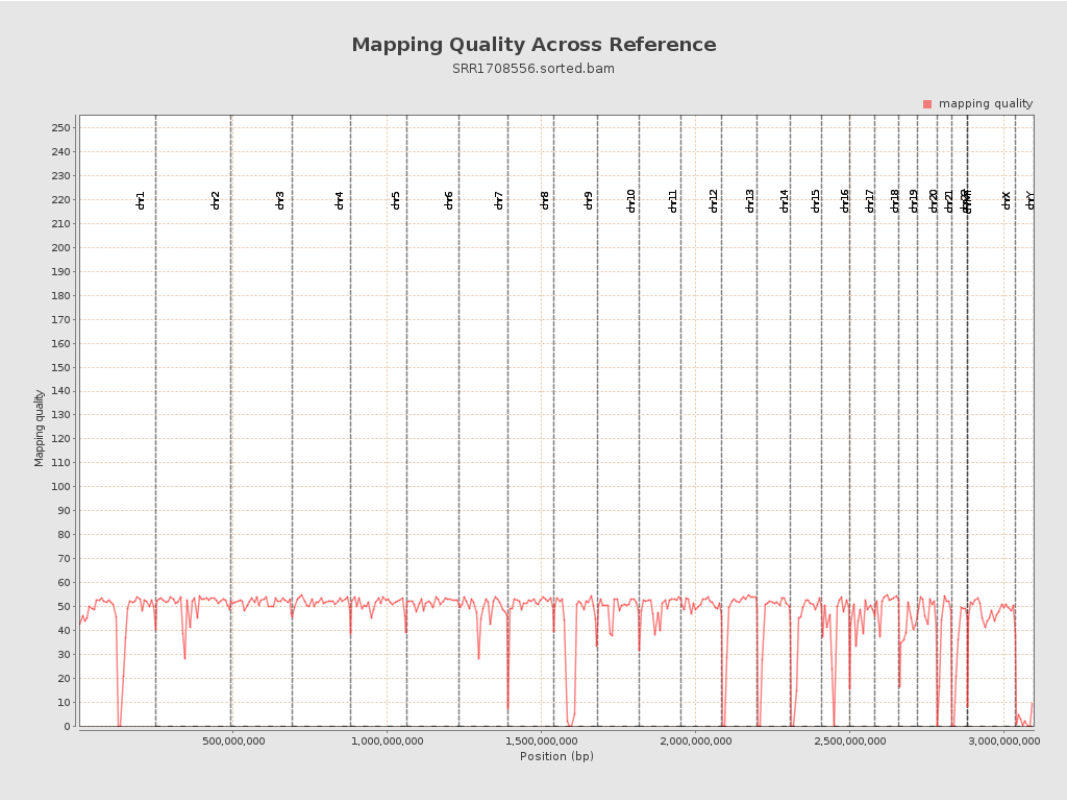
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram