Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:17:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708624.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_SRR1708624 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708624.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:17:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708624.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,299,578
Mapped reads	2,392,799 / 72.52%
Unmapped reads	906,779 / 27.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	789 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	80,764 / 2.45%
Duplication rate	2.33%
Clipped reads	363,431 / 11.01%

2.2. ACGT Content

Number/percentage of A's	34,383,822 / 29.46%
Number/percentage of C's	22,112,019 / 18.95%
Number/percentage of T's	36,706,518 / 31.45%
Number/percentage of G's	23,501,182 / 20.14%
Number/percentage of N's	10,293 / 0.01%
GC Percentage	39.08%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.3719

2.4. Mapping Quality

Mean Mapping Quality	42.59

2.5. Mismatches and indels

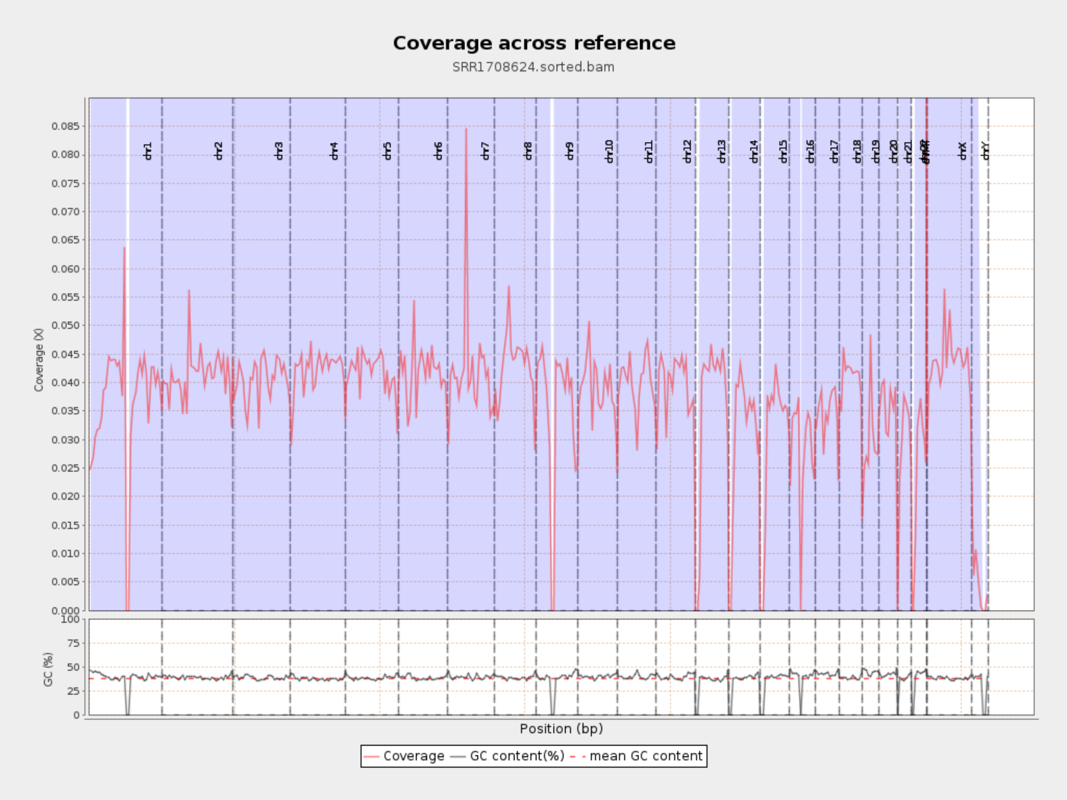
General error rate	0.66%
Mismatches	765,415
Insertions	5,737
Mapped reads with at least one insertion	0.24%
Deletions	15,225
Mapped reads with at least one deletion	0.63%
Homopolymer indels	48.58%

2.6. Chromosome stats

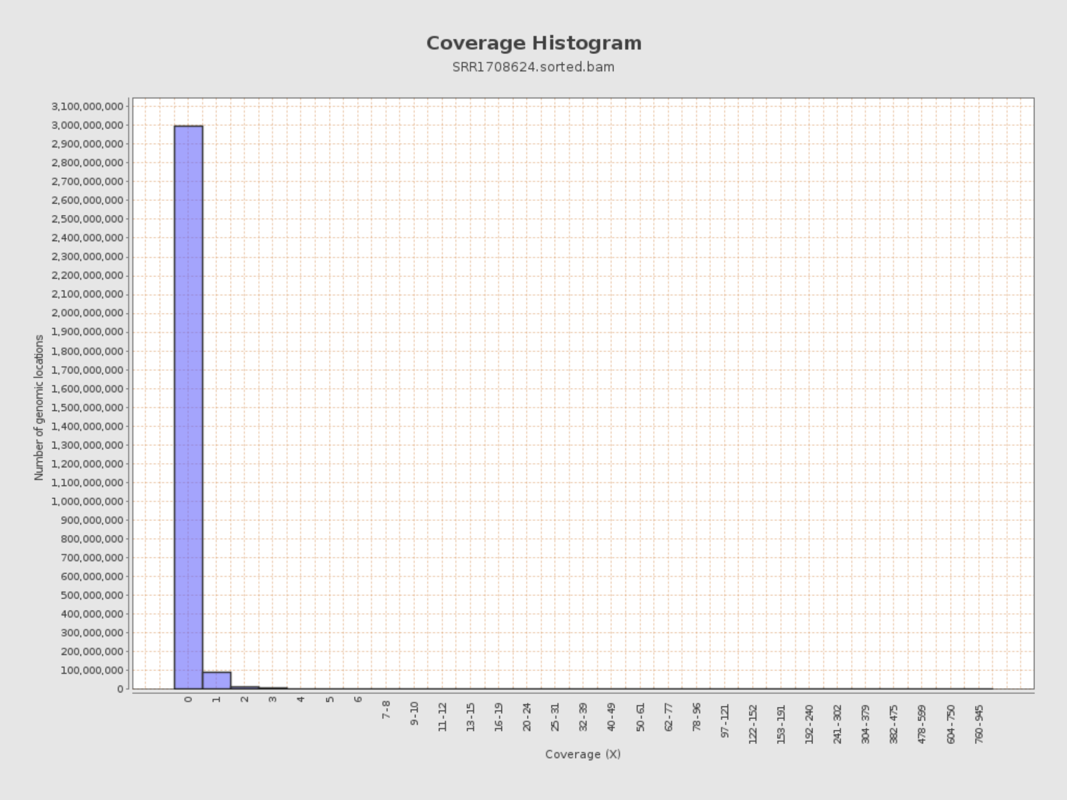
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9191167	0.0369	0.6612
chr2	243199373	10063621	0.0414	0.4022
chr3	198022430	8049782	0.0407	0.2295
chr4	191154276	8075919	0.0422	0.2357
chr5	180915260	7594942	0.042	0.2343
chr6	171115067	7157765	0.0418	0.3189
chr7	159138663	6765788	0.0425	0.6126

chr8	146364022	6291305	0.043	0.5678
chr9	141213431	4974295	0.0352	0.291
chr10	135534747	5348341	0.0395	0.3021
chr11	135006516	5367178	0.0398	0.2923
chr12	133851895	5303854	0.0396	0.2339
chr13	115169878	4062026	0.0353	0.2167
chr14	107349540	3278713	0.0305	0.2181
chr15	102531392	3071513	0.03	0.1954
chr16	90354753	2539772	0.0281	0.2023
chr17	81195210	2791664	0.0344	0.2396
chr18	78077248	3228512	0.0414	0.5719
chr19	59128983	1774569	0.03	0.5063
chr20	63025520	2246079	0.0356	0.2243
chr21	48129895	1364753	0.0284	0.204
chr22	51304566	1160091	0.0226	0.1684
chrMT	16571	1973	0.1191	0.4029
chrX	155270560	6767133	0.0436	0.2633
chrY	59373566	266290	0.0045	0.0835

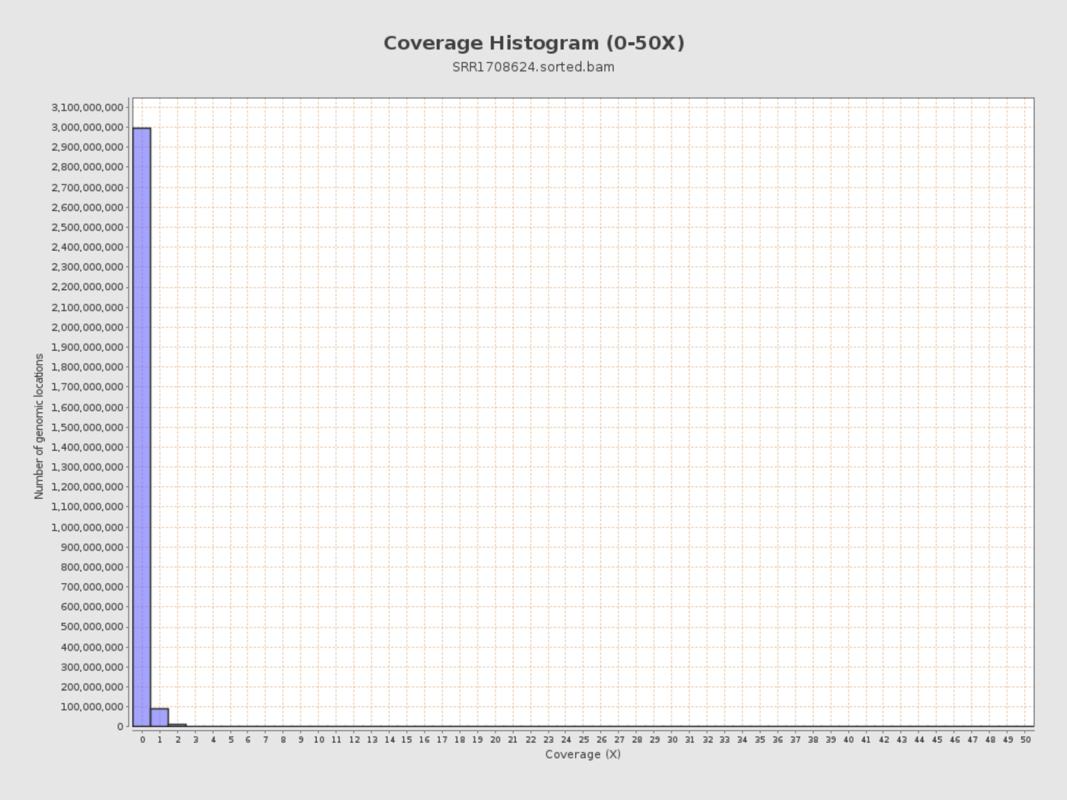
3. Results : Coverage across reference



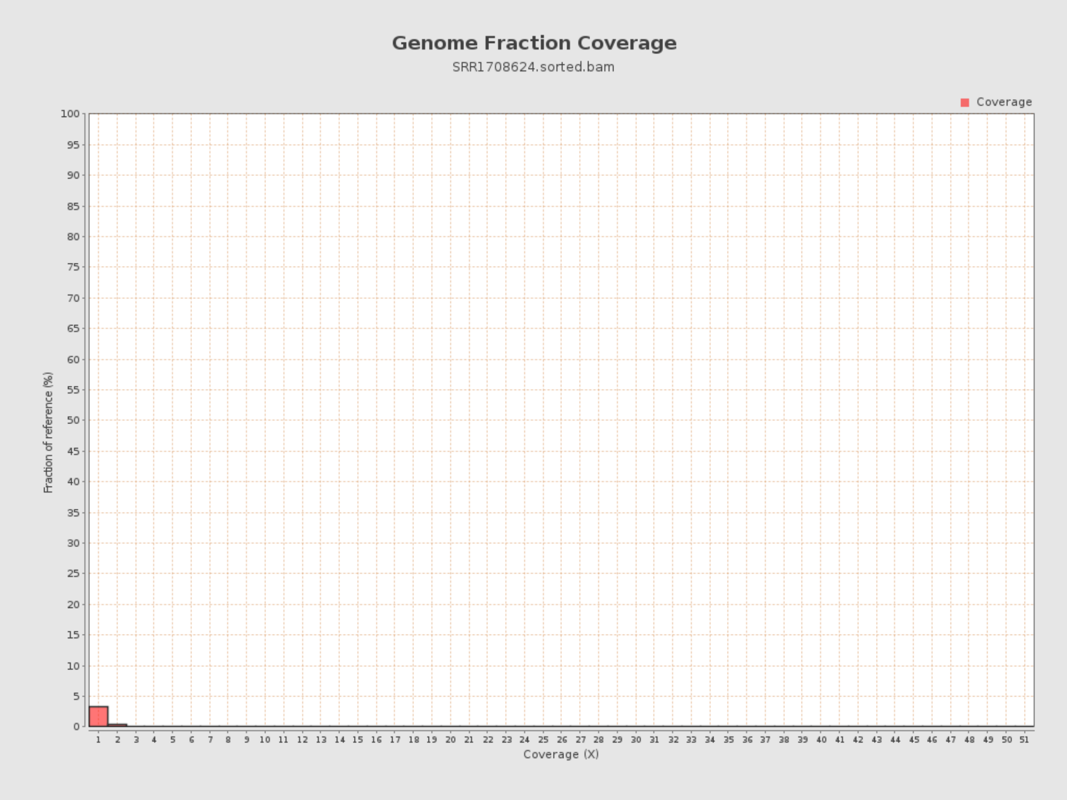
4. Results : Coverage Histogram



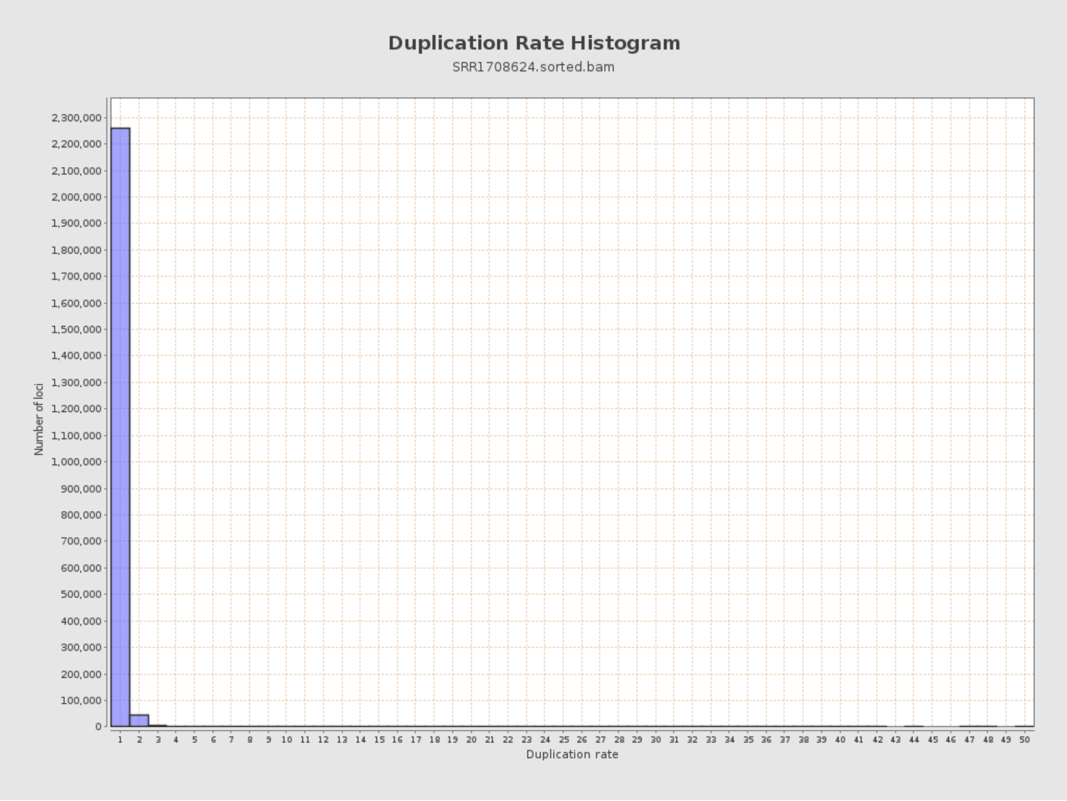
5. Results : Coverage Histogram (0-50X)



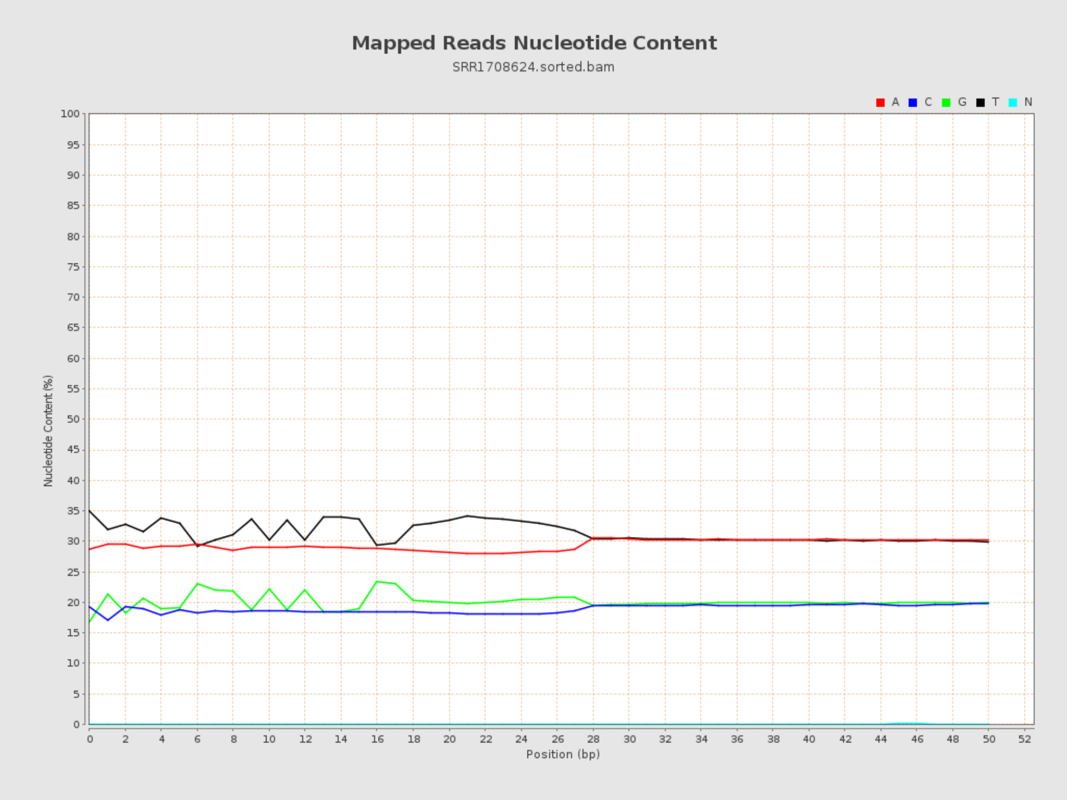
6. Results : Genome Fraction Coverage



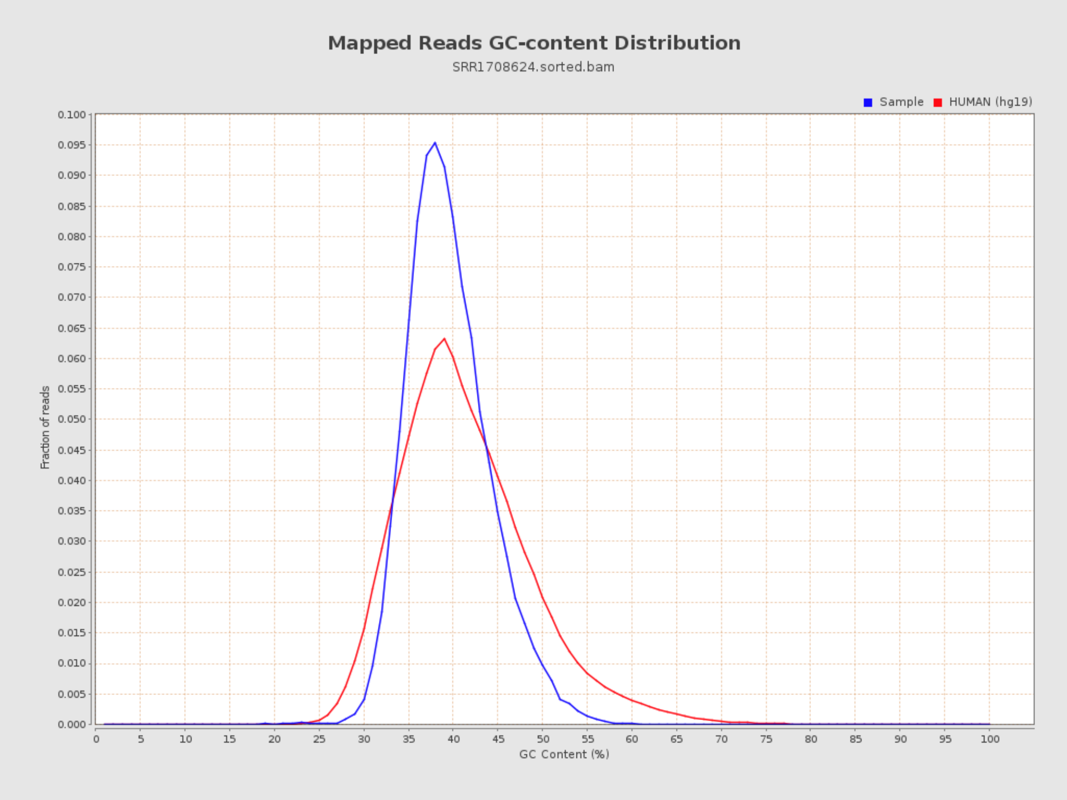
7. Results : Duplication Rate Histogram



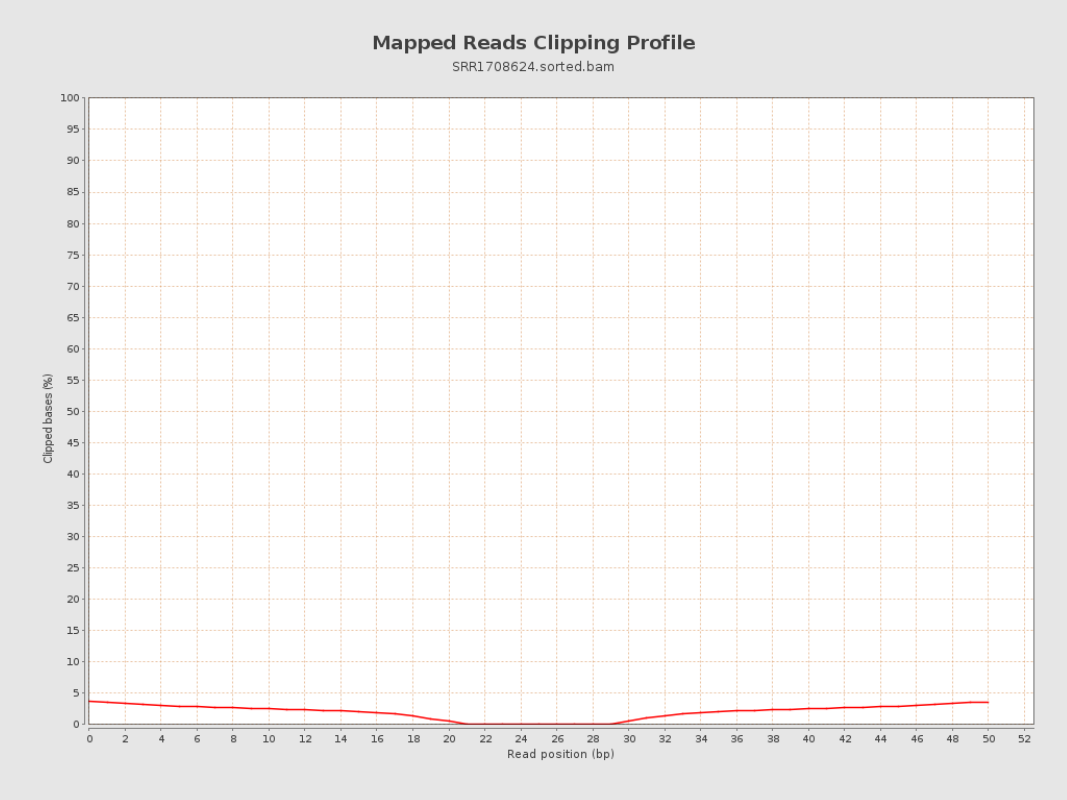
8. Results : Mapped Reads Nucleotide Content



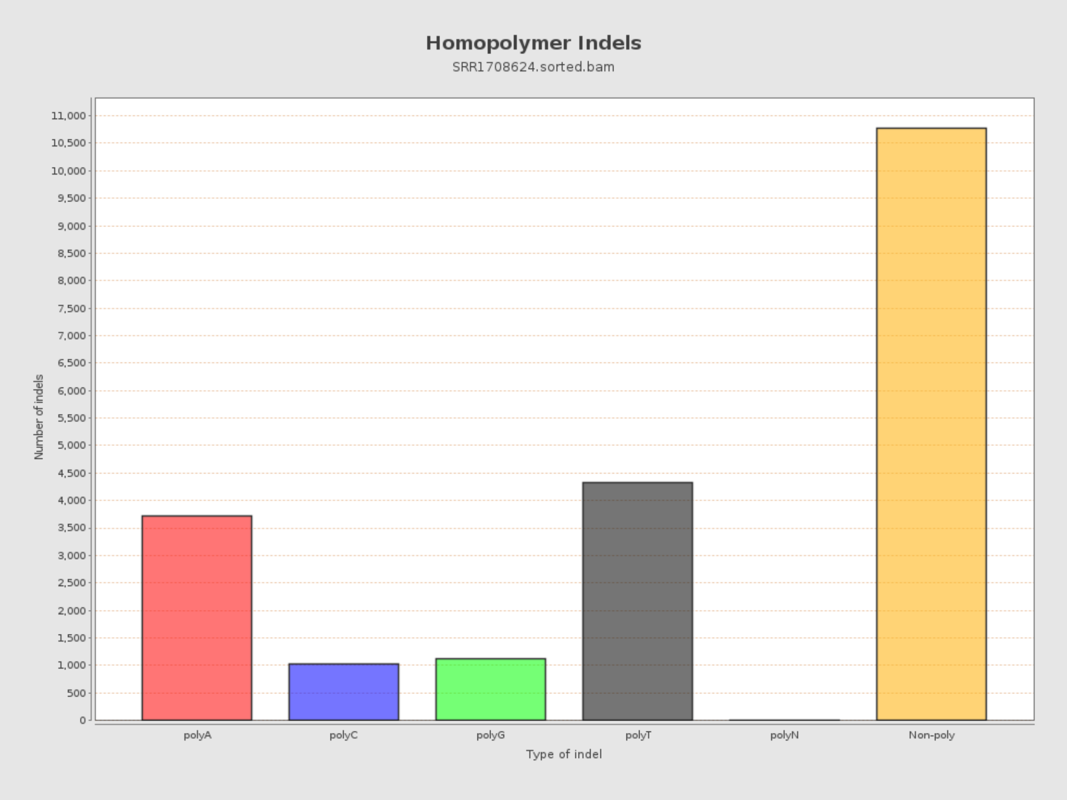
9. Results : Mapped Reads GC-content Distribution



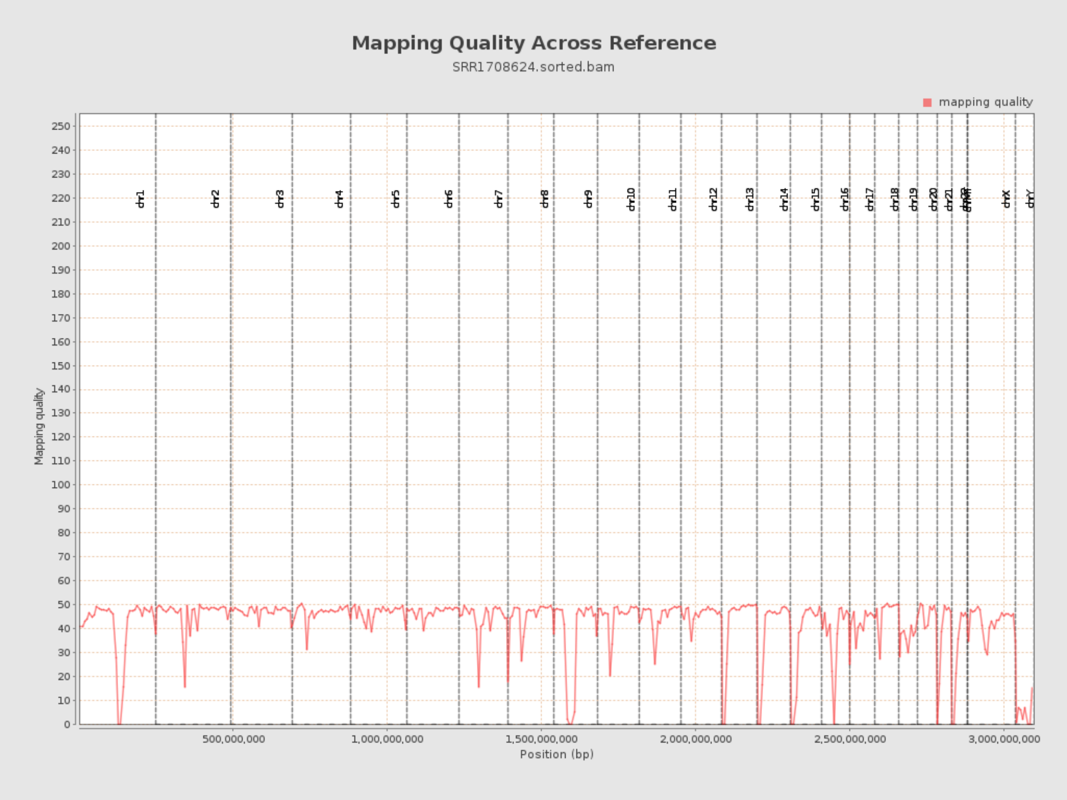
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram