Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:50:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708632.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_SRR1708632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708632.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:50:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,695,197
Mapped reads	1,916,021 / 71.09%
Unmapped reads	779,176 / 28.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	570 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	61,883 / 2.3%
Duplication rate	2.3%
Clipped reads	304,008 / 11.28%

2.2. ACGT Content

Number/percentage of A's	27,464,889 / 29.48%
Number/percentage of C's	17,445,218 / 18.73%
Number/percentage of T's	29,463,699 / 31.63%
Number/percentage of G's	18,779,832 / 20.16%
Number/percentage of N's	8,263 / 0.01%
GC Percentage	38.88%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.3059

2.4. Mapping Quality

Mean Mapping Quality	43.3

2.5. Mismatches and indels

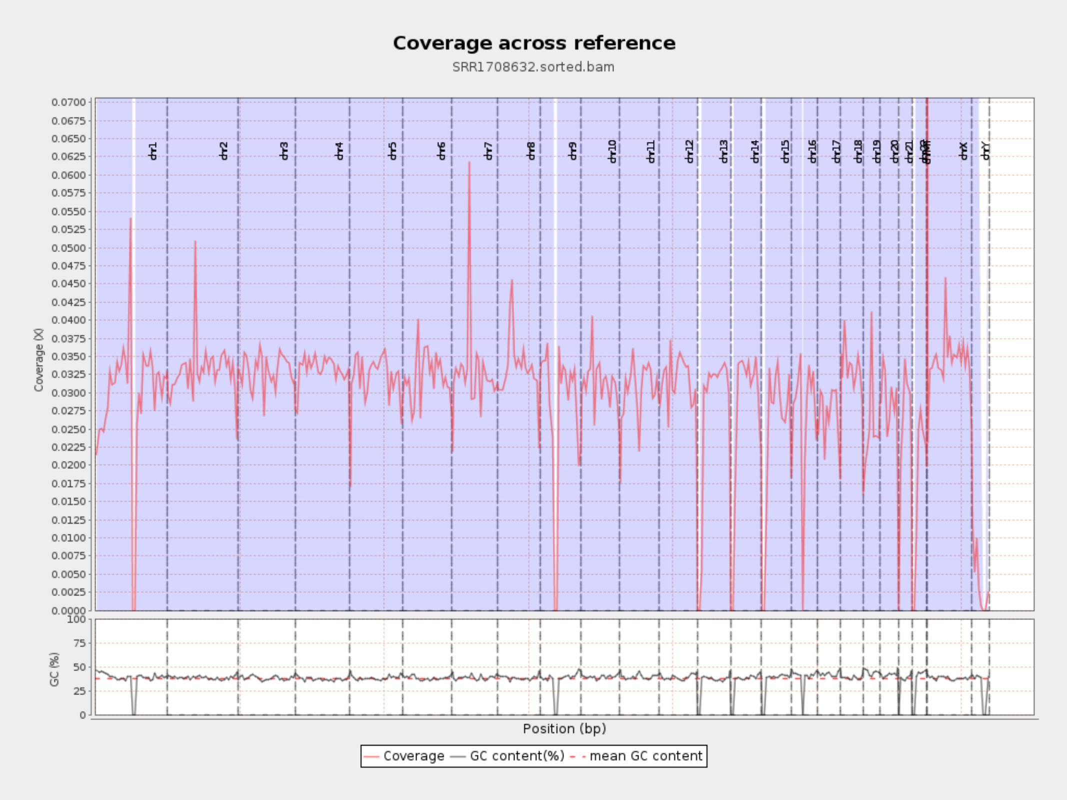
General error rate	0.65%
Mismatches	595,975
Insertions	4,252
Mapped reads with at least one insertion	0.22%
Deletions	11,713
Mapped reads with at least one deletion	0.61%
Homopolymer indels	48.01%

2.6. Chromosome stats

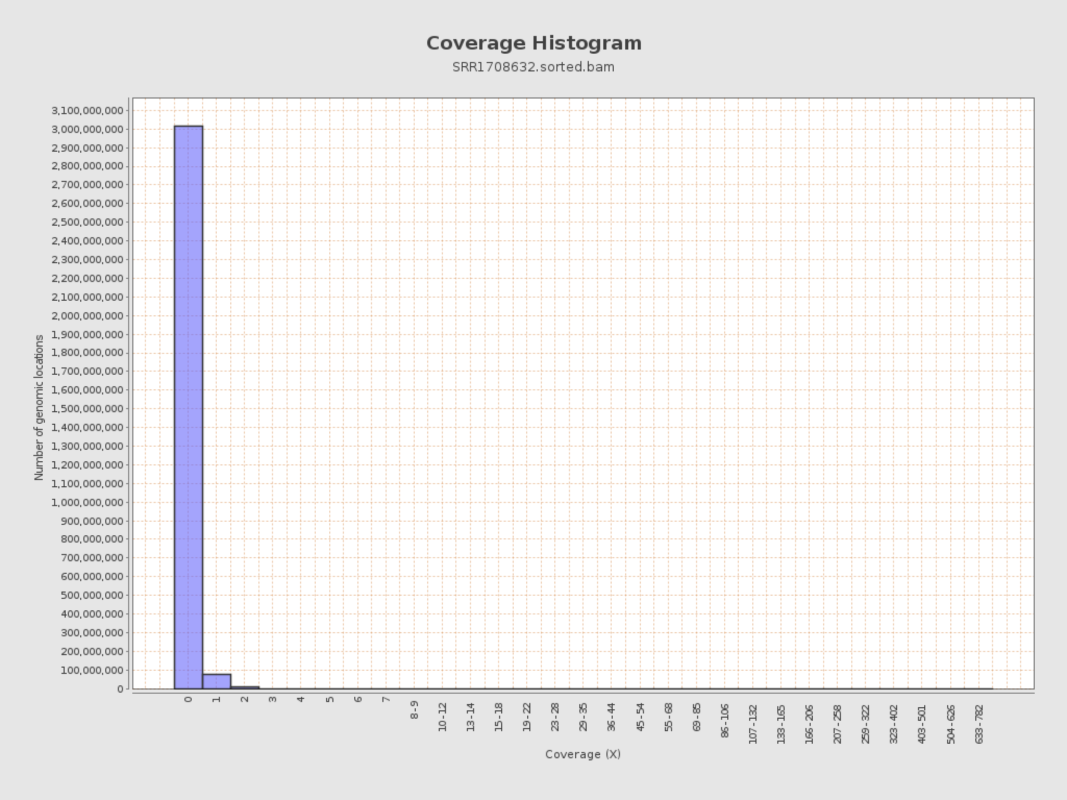
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7361188	0.0295	0.5457
chr2	243199373	8076942	0.0332	0.3221
chr3	198022430	6558284	0.0331	0.2018
chr4	191154276	6348455	0.0332	0.2048
chr5	180915260	5890524	0.0326	0.2026
chr6	171115067	5527803	0.0323	0.2447
chr7	159138663	5276654	0.0332	0.4336

chr8	146364022	4916548	0.0336	0.4839
chr9	141213431	3922465	0.0278	0.2541
chr10	135534747	4246827	0.0313	0.2509
chr11	135006516	4107694	0.0304	0.2563
chr12	133851895	4243298	0.0317	0.2025
chr13	115169878	3078849	0.0267	0.1819
chr14	107349540	2903591	0.027	0.1932
chr15	102531392	2494848	0.0243	0.1714
chr16	90354753	2386800	0.0264	0.1884
chr17	81195210	2187846	0.0269	0.2077
chr18	78077248	2615370	0.0335	0.5125
chr19	59128983	1500781	0.0254	0.3804
chr20	63025520	1822410	0.0289	0.1925
chr21	48129895	1214141	0.0252	0.1864
chr22	51304566	893292	0.0174	0.1432
chrMT	16571	6275	0.3787	0.682
chrX	155270560	5372589	0.0346	0.2296
chrY	59373566	226169	0.0038	0.0801

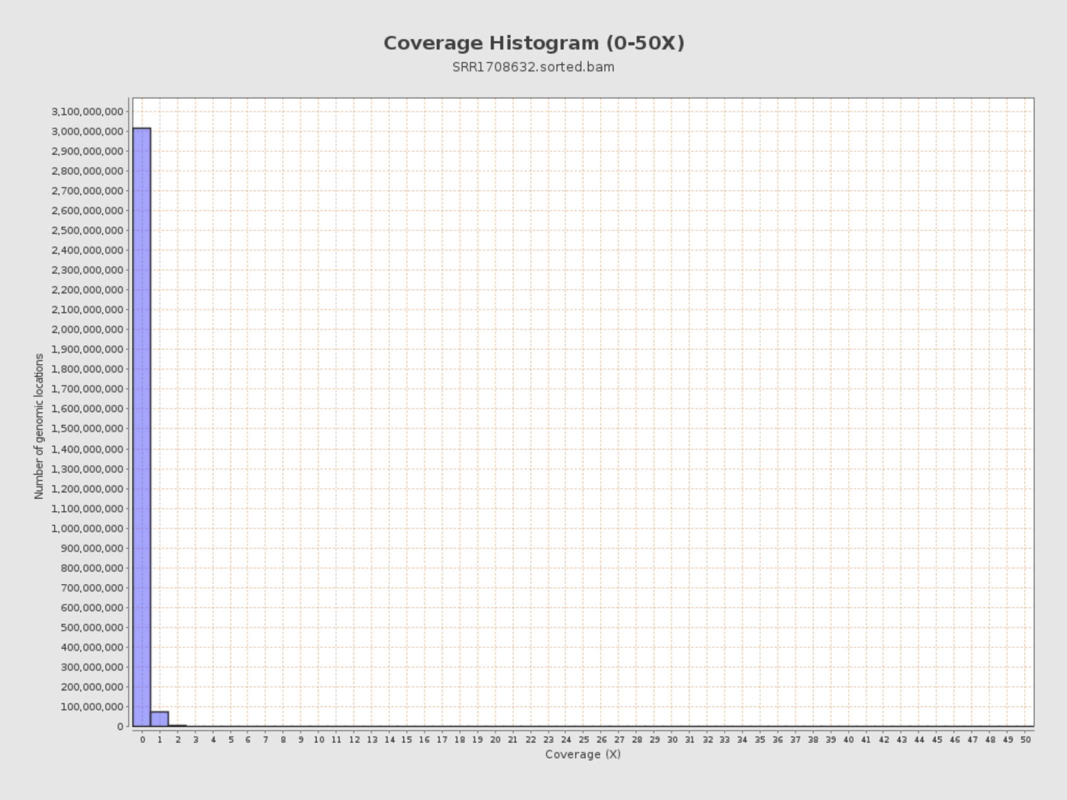
3. Results : Coverage across reference



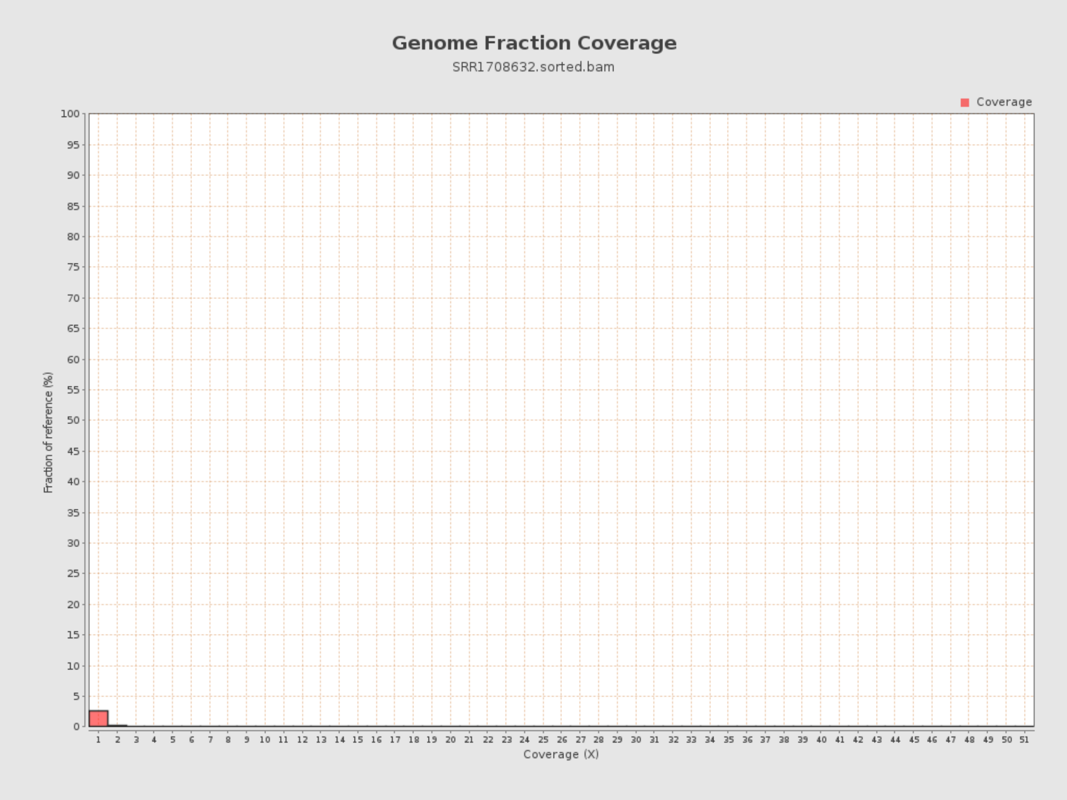
4. Results : Coverage Histogram



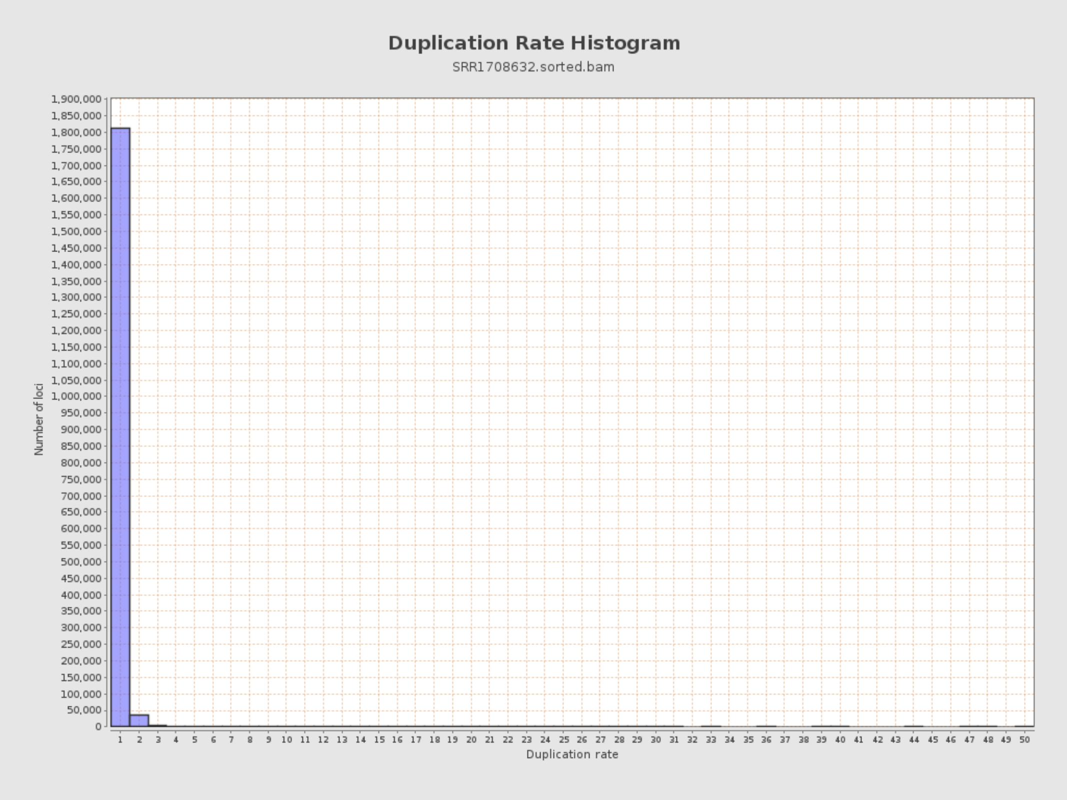
5. Results : Coverage Histogram (0-50X)



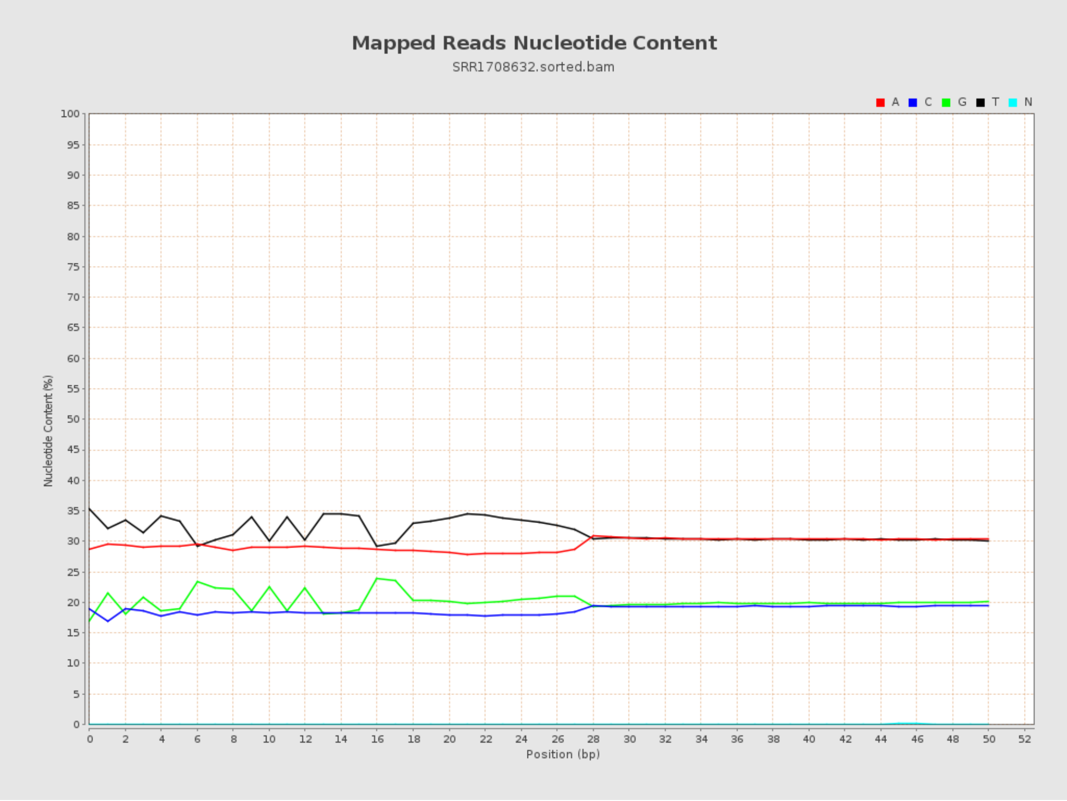
6. Results : Genome Fraction Coverage



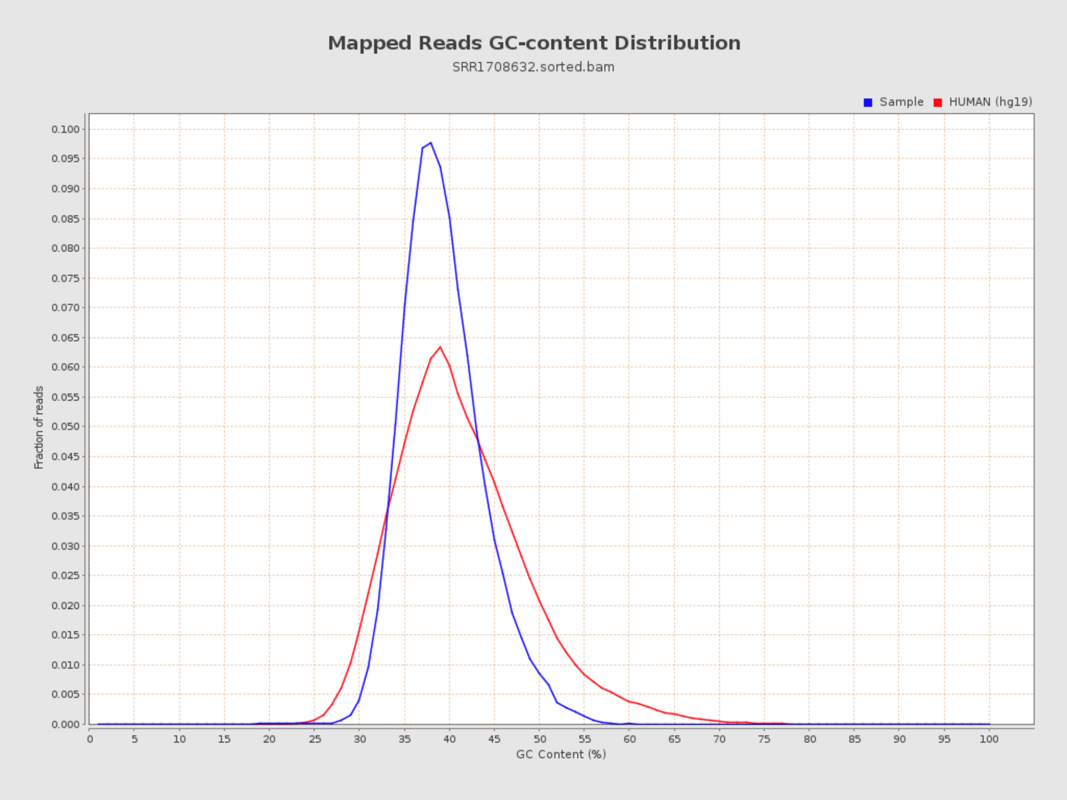
7. Results : Duplication Rate Histogram



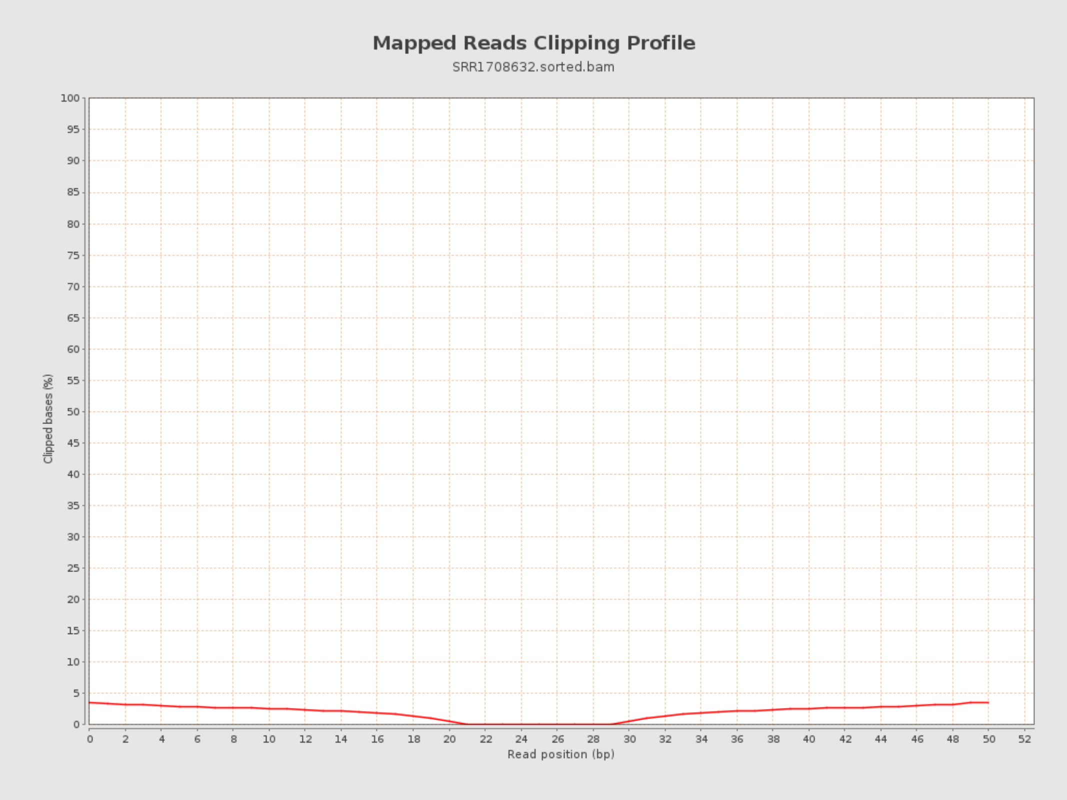
8. Results : Mapped Reads Nucleotide Content



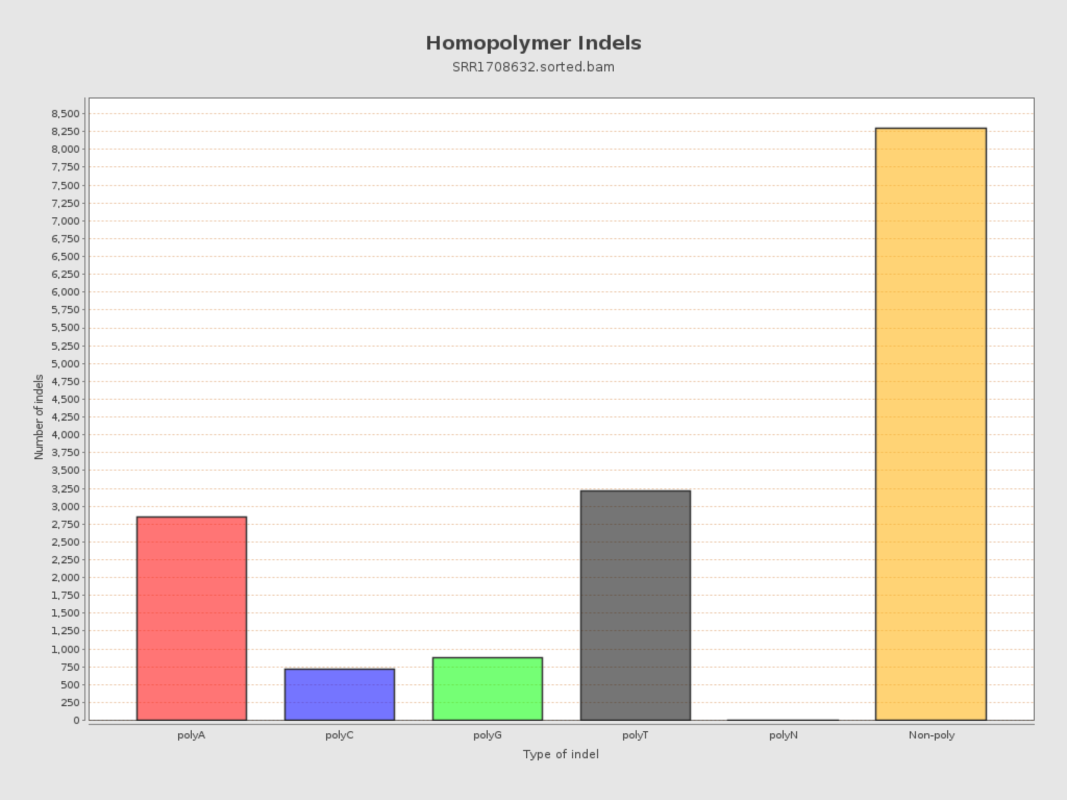
9. Results : Mapped Reads GC-content Distribution



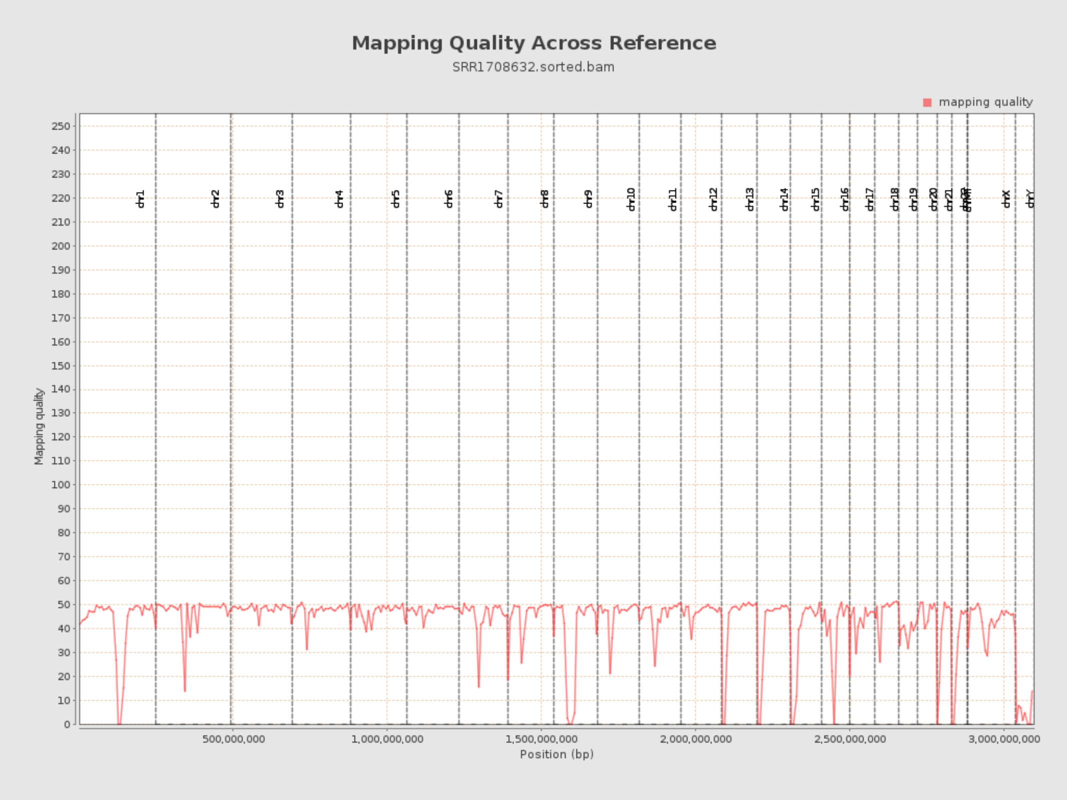
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram