Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:04:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708563.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_SRR1708563 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708563.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:04:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708563.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,240,877
Mapped reads	3,502,636 / 82.59%
Unmapped reads	738,241 / 17.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	115 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	125,786 / 2.97%
Duplication rate	3.51%
Clipped reads	53,124 / 1.25%

2.2. ACGT Content

Number/percentage of A's	53,918,380 / 30.88%
Number/percentage of C's	33,368,163 / 19.11%
Number/percentage of T's	53,517,948 / 30.65%
Number/percentage of G's	33,785,894 / 19.35%
Number/percentage of N's	7,067 / 0%
GC Percentage	38.46%

2.3. Coverage

Mean	0.0564

Standard Deviation	0.4875

2.4. Mapping Quality

Mean Mapping Quality	41.75

2.5. Mismatches and indels

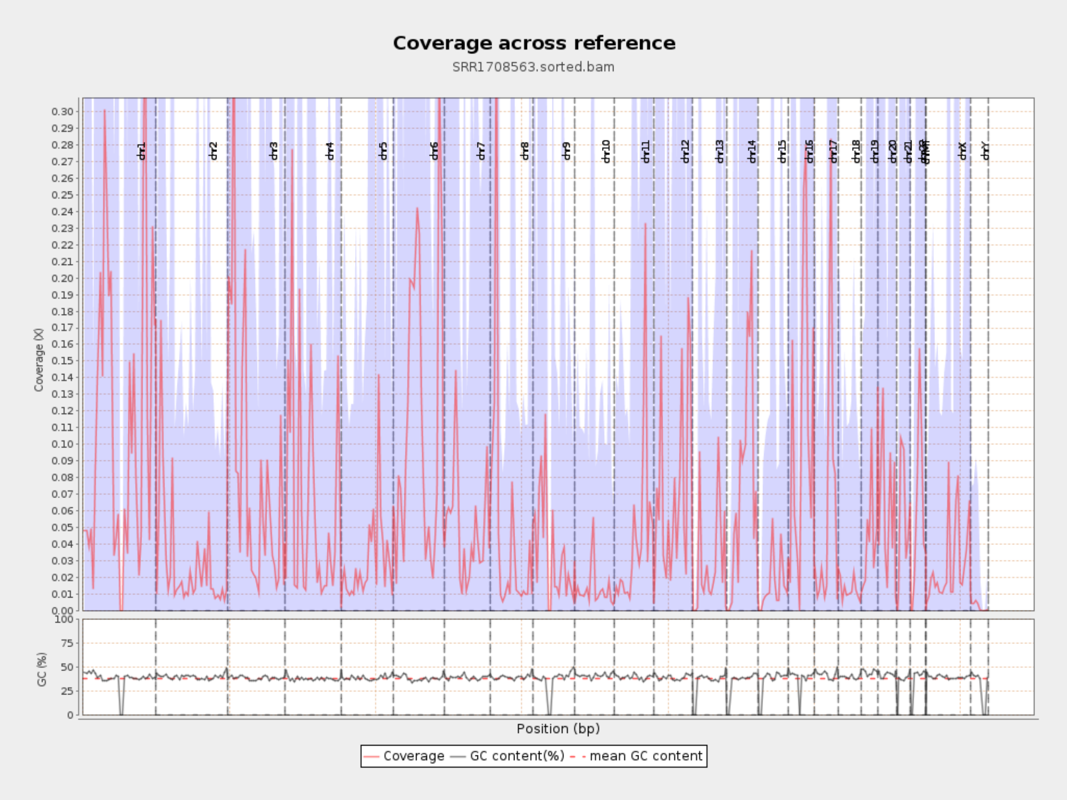
General error rate	0.17%
Mismatches	278,920
Insertions	13,052
Mapped reads with at least one insertion	0.37%
Deletions	9,157
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.35%

2.6. Chromosome stats

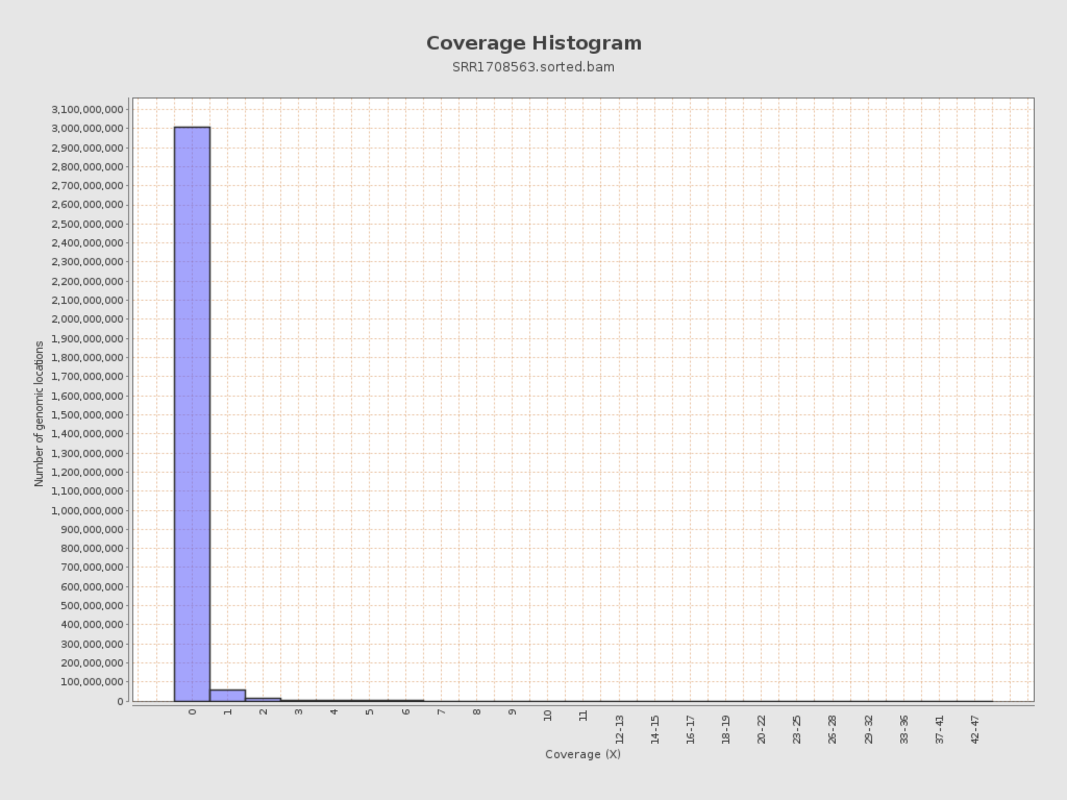
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28820909	0.1156	0.7548
chr2	243199373	6864802	0.0282	0.3302
chr3	198022430	16417160	0.0829	0.5419
chr4	191154276	12702157	0.0664	0.5448
chr5	180915260	5523055	0.0305	0.276
chr6	171115067	19533744	0.1142	0.7722
chr7	159138663	7926662	0.0498	0.4059

chr8	146364022	7085531	0.0484	0.5187
chr9	141213431	4929634	0.0349	0.2693
chr10	135534747	1834108	0.0135	0.1549
chr11	135006516	6070287	0.045	0.4373
chr12	133851895	9768863	0.073	0.5327
chr13	115169878	3482244	0.0302	0.3249
chr14	107349540	8479600	0.079	0.5798
chr15	102531392	1546634	0.0151	0.2106
chr16	90354753	10067397	0.1114	0.6701
chr17	81195210	5498238	0.0677	0.6291
chr18	78077248	1012132	0.013	0.1288
chr19	59128983	2738681	0.0463	0.3255
chr20	63025520	4085354	0.0648	0.4867
chr21	48129895	2532895	0.0526	0.5408
chr22	51304566	3220050	0.0628	0.4594
chrMT	16571	0	0	0
chrX	155270560	4332892	0.0279	0.3315
chrY	59373566	139931	0.0024	0.0532

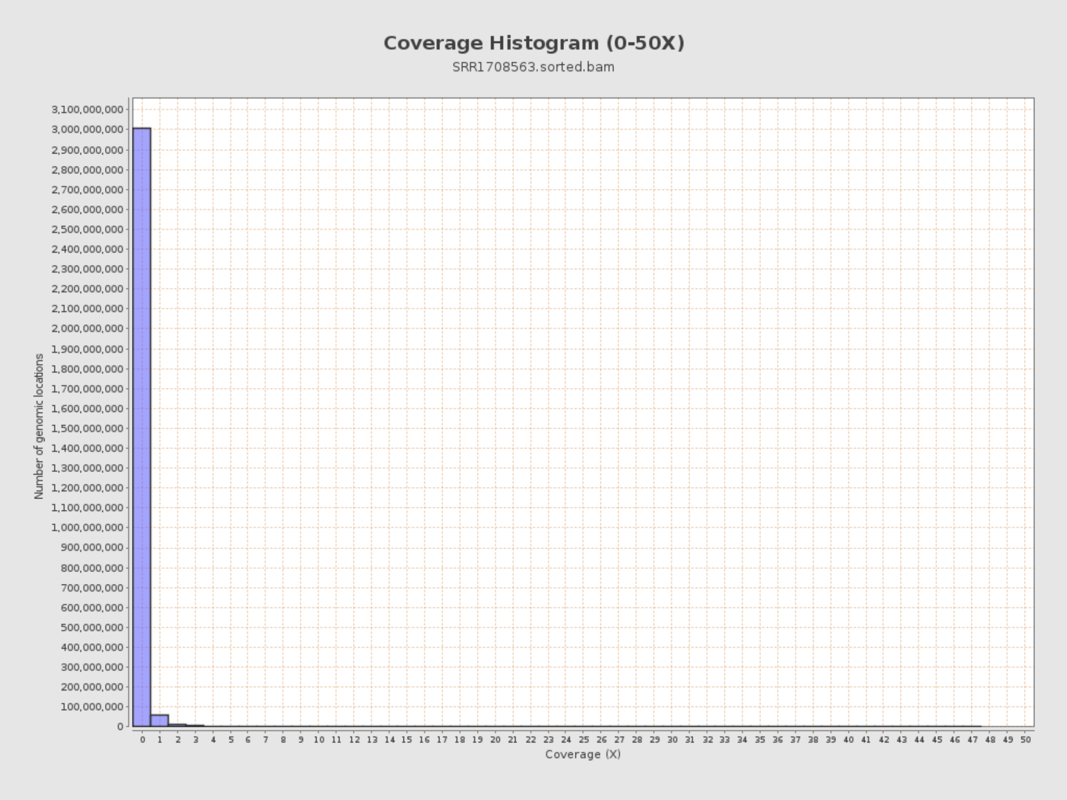
3. Results : Coverage across reference



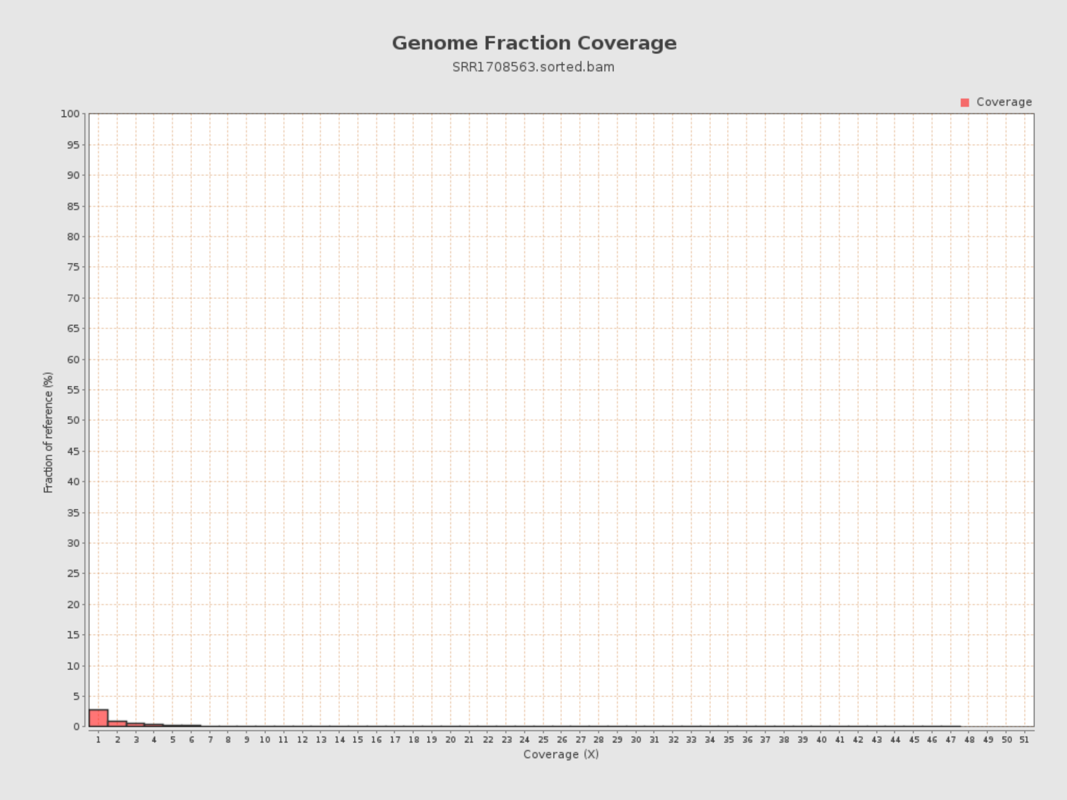
4. Results : Coverage Histogram



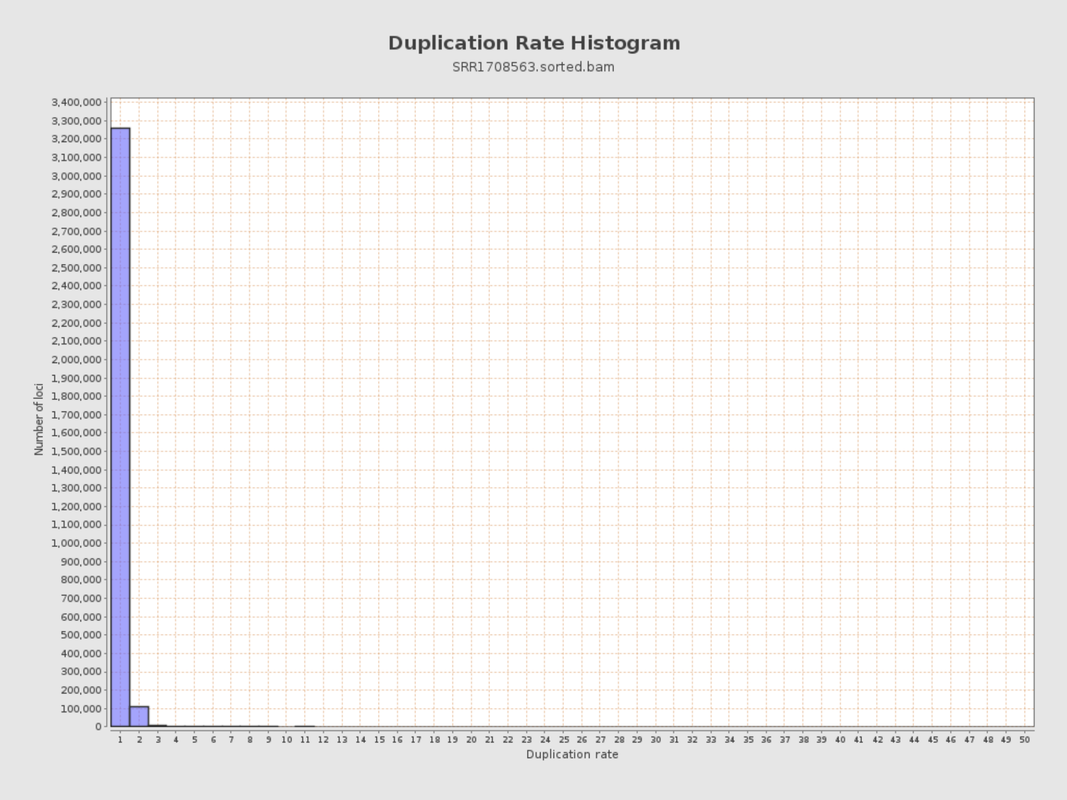
5. Results : Coverage Histogram (0-50X)



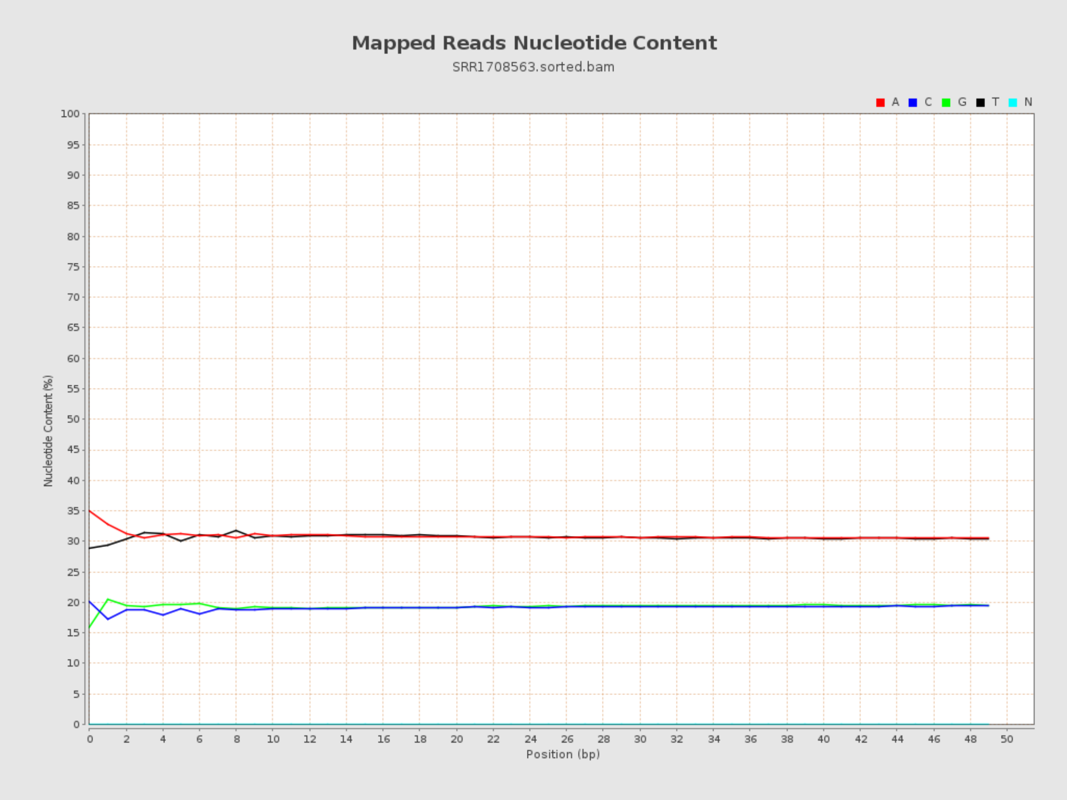
6. Results : Genome Fraction Coverage



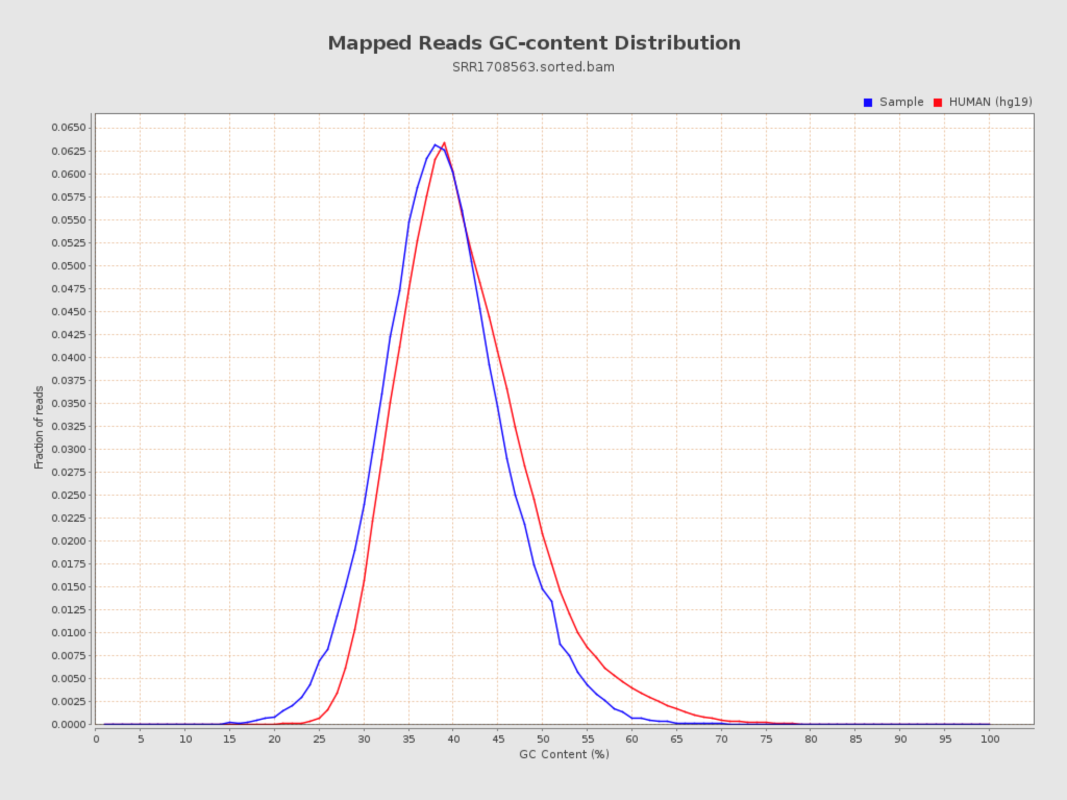
7. Results : Duplication Rate Histogram



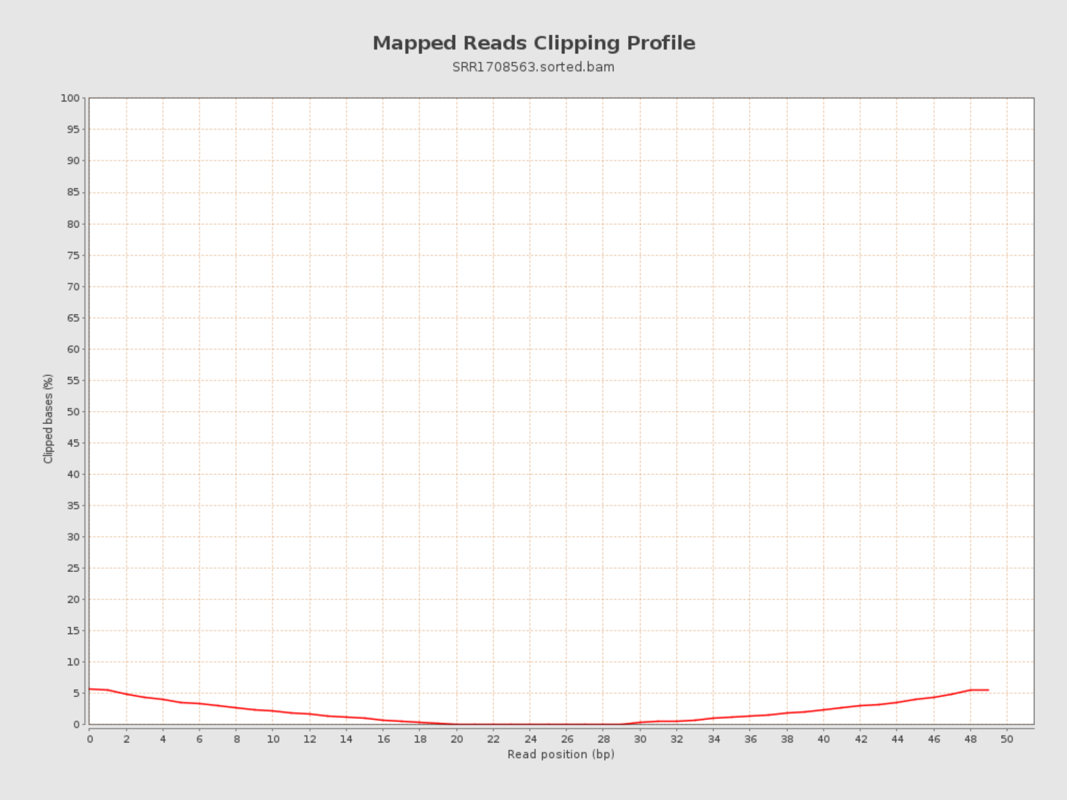
8. Results : Mapped Reads Nucleotide Content



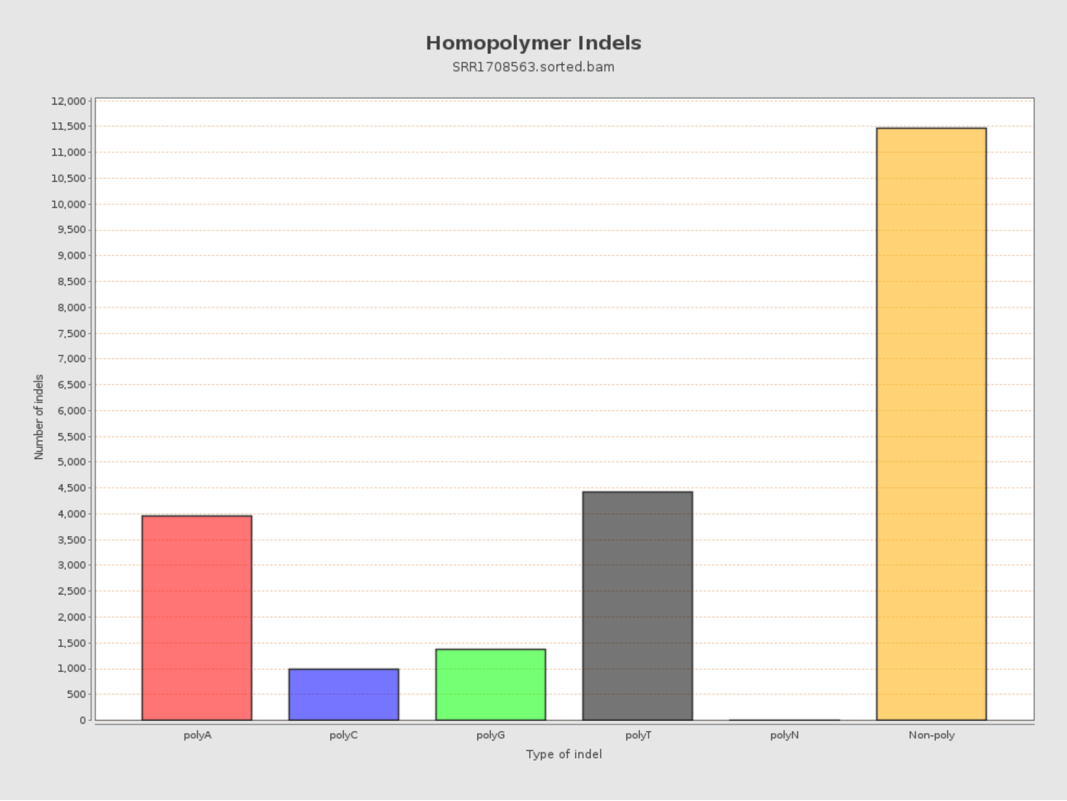
9. Results : Mapped Reads GC-content Distribution



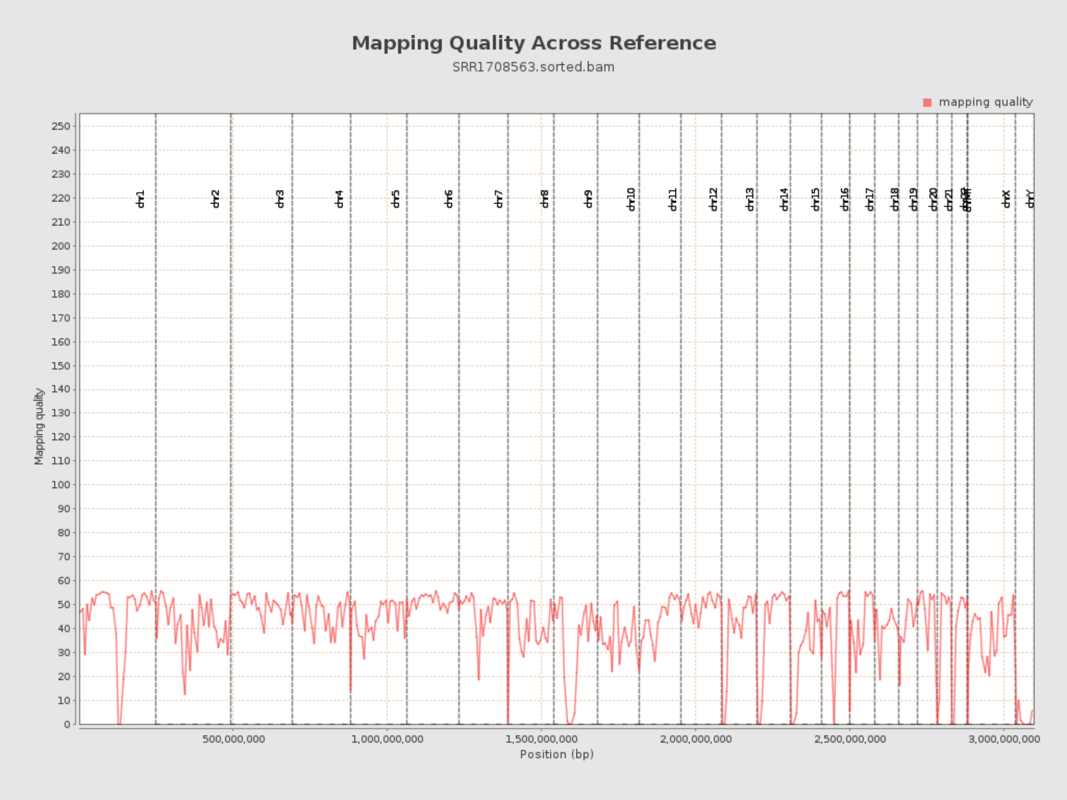
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram