Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:04:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708576.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_SRR1708576 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708576.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:04:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708576.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,836,285
Mapped reads	3,167,555 / 82.57%
Unmapped reads	668,730 / 17.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	83 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	14,695 / 0.38%
Duplication rate	0.46%
Clipped reads	42,975 / 1.12%

2.2. ACGT Content

Number/percentage of A's	48,942,049 / 30.99%
Number/percentage of C's	30,013,464 / 19%
Number/percentage of T's	48,668,645 / 30.81%
Number/percentage of G's	30,320,136 / 19.2%
Number/percentage of N's	7,473 / 0%
GC Percentage	38.2%

2.3. Coverage

Mean	0.051

Standard Deviation	0.2326

2.4. Mapping Quality

Mean Mapping Quality	46.57

2.5. Mismatches and indels

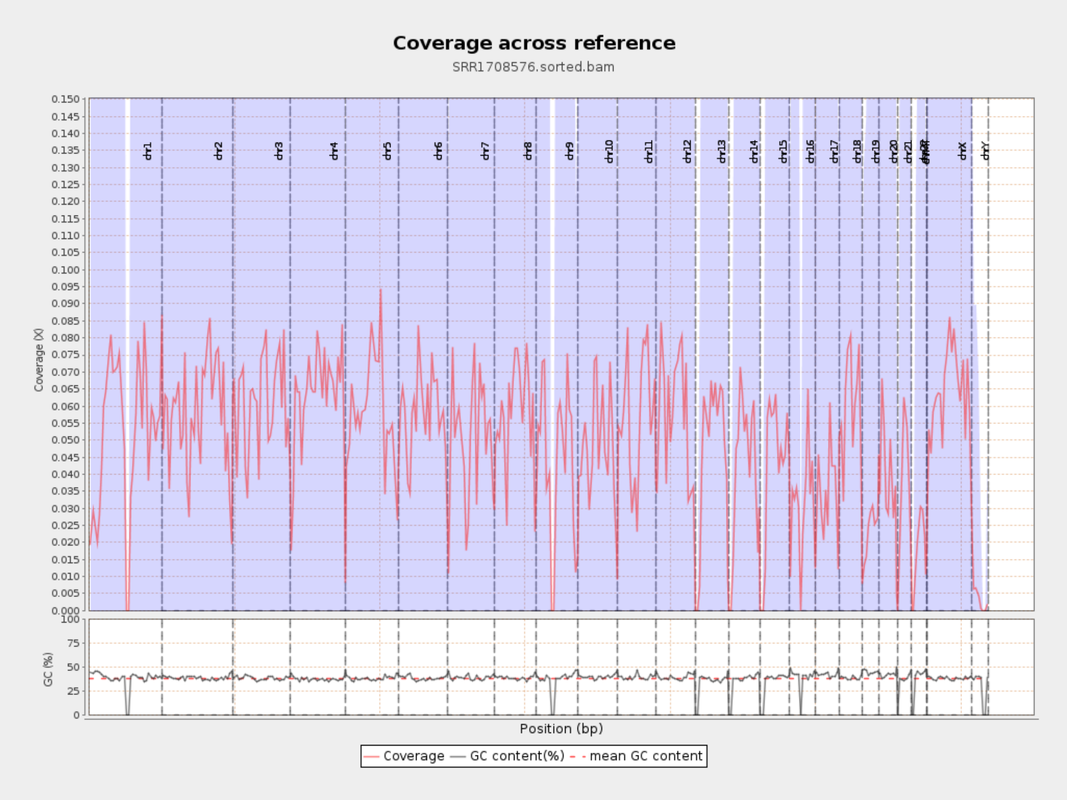
General error rate	0.17%
Mismatches	248,368
Insertions	10,703
Mapped reads with at least one insertion	0.34%
Deletions	8,466
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.1%

2.6. Chromosome stats

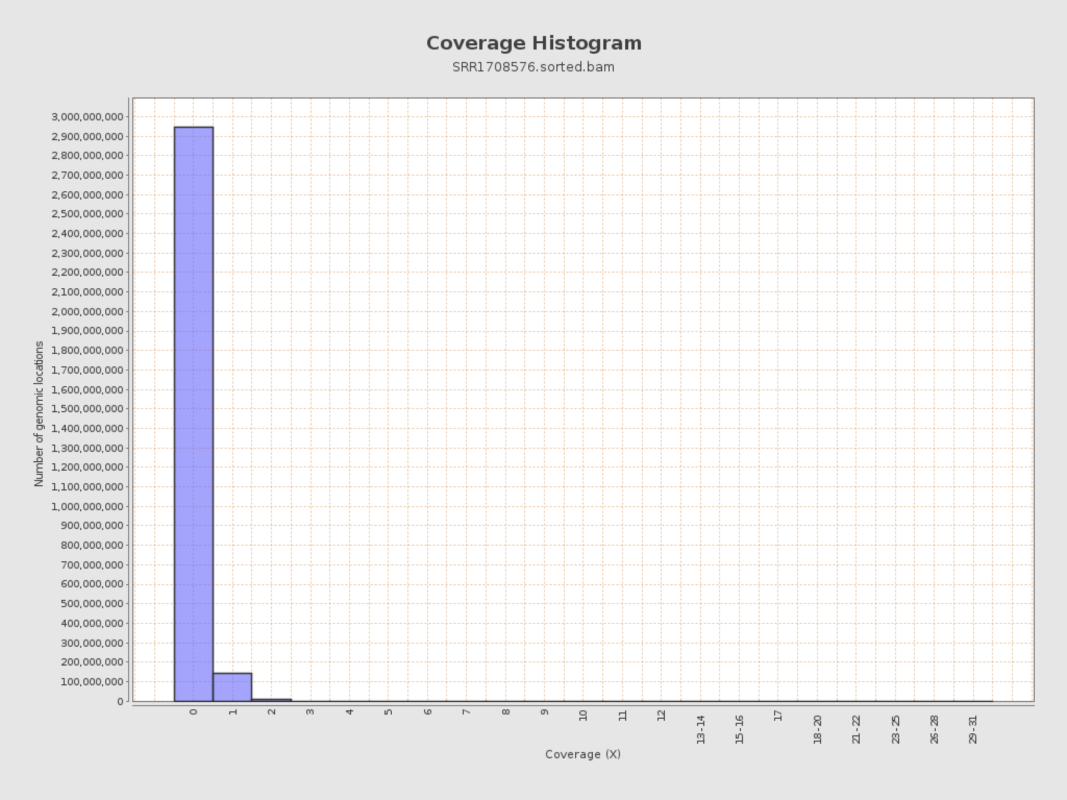
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12866027	0.0516	0.2345
chr2	243199373	14046779	0.0578	0.247
chr3	198022430	12150519	0.0614	0.2543
chr4	191154276	12174614	0.0637	0.2594
chr5	180915260	10726415	0.0593	0.2498
chr6	171115067	9855615	0.0576	0.2463
chr7	159138663	8168203	0.0513	0.2325

chr8	146364022	8583176	0.0586	0.2484
chr9	141213431	6275215	0.0444	0.2173
chr10	135534747	6736585	0.0497	0.2283
chr11	135006516	7691557	0.057	0.2462
chr12	133851895	7674051	0.0573	0.2466
chr13	115169878	5337746	0.0463	0.2219
chr14	107349540	4409665	0.0411	0.2085
chr15	102531392	4339322	0.0423	0.2123
chr16	90354753	2862462	0.0317	0.1824
chr17	81195210	2749429	0.0339	0.1898
chr18	78077248	4726291	0.0605	0.2529
chr19	59128983	1412010	0.0239	0.1581
chr20	63025520	2491827	0.0395	0.2042
chr21	48129895	1716290	0.0357	0.1952
chr22	51304566	894933	0.0174	0.1354
chrMT	16571	300	0.0181	0.1333
chrX	155270560	9841026	0.0634	0.2595
chrY	59373566	236001	0.004	0.0649

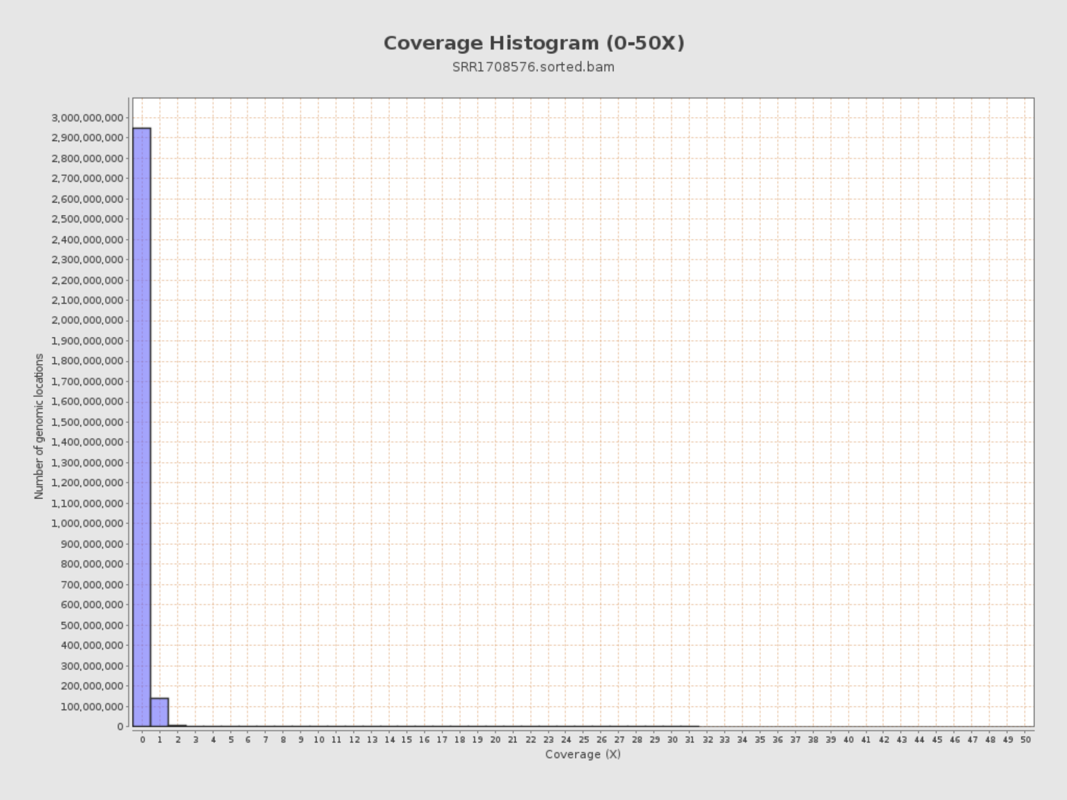
3. Results : Coverage across reference



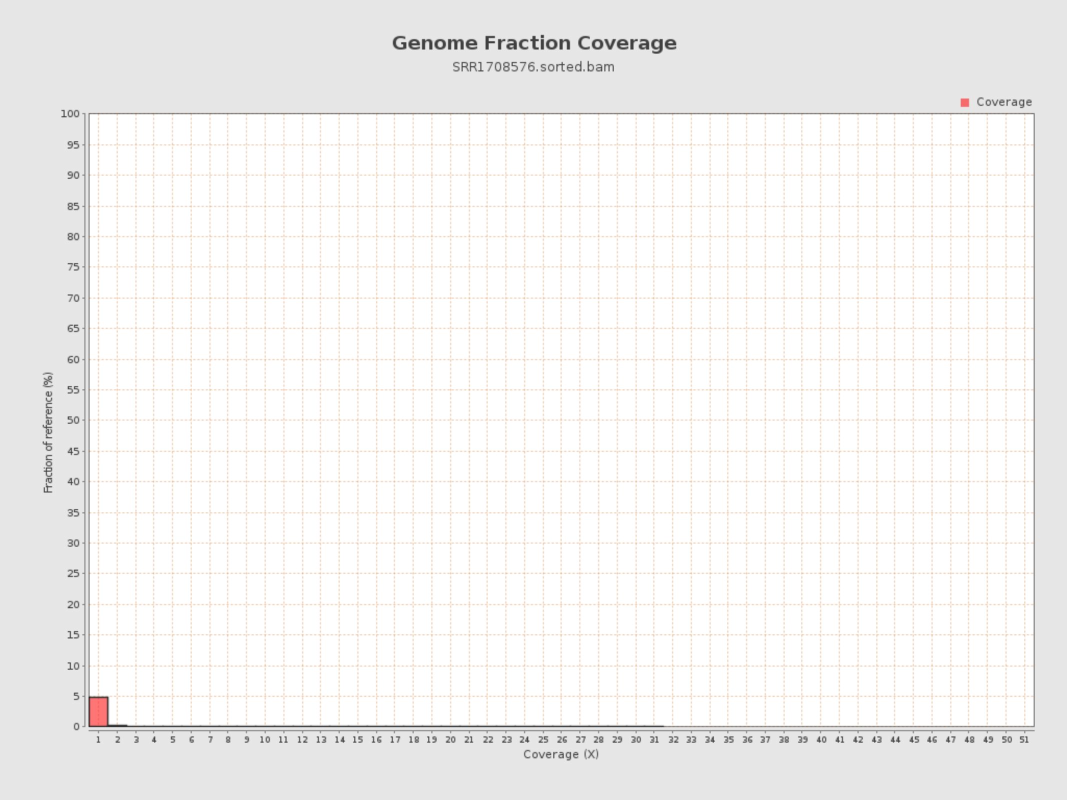
4. Results : Coverage Histogram



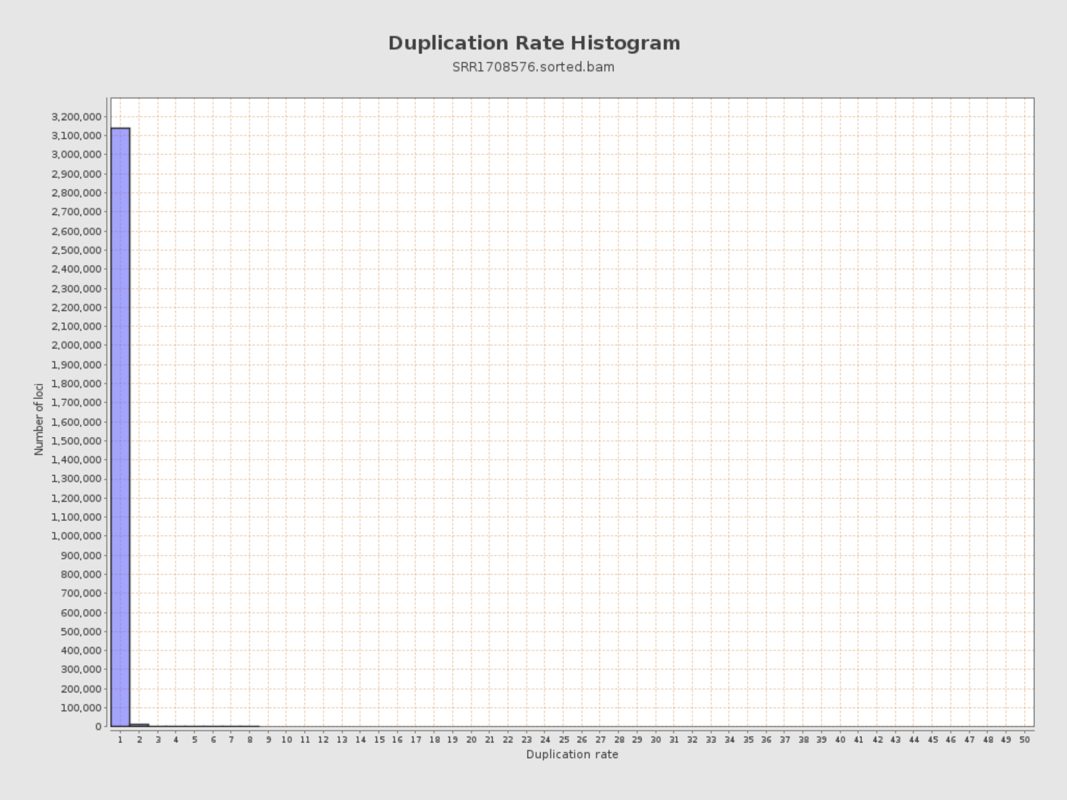
5. Results : Coverage Histogram (0-50X)



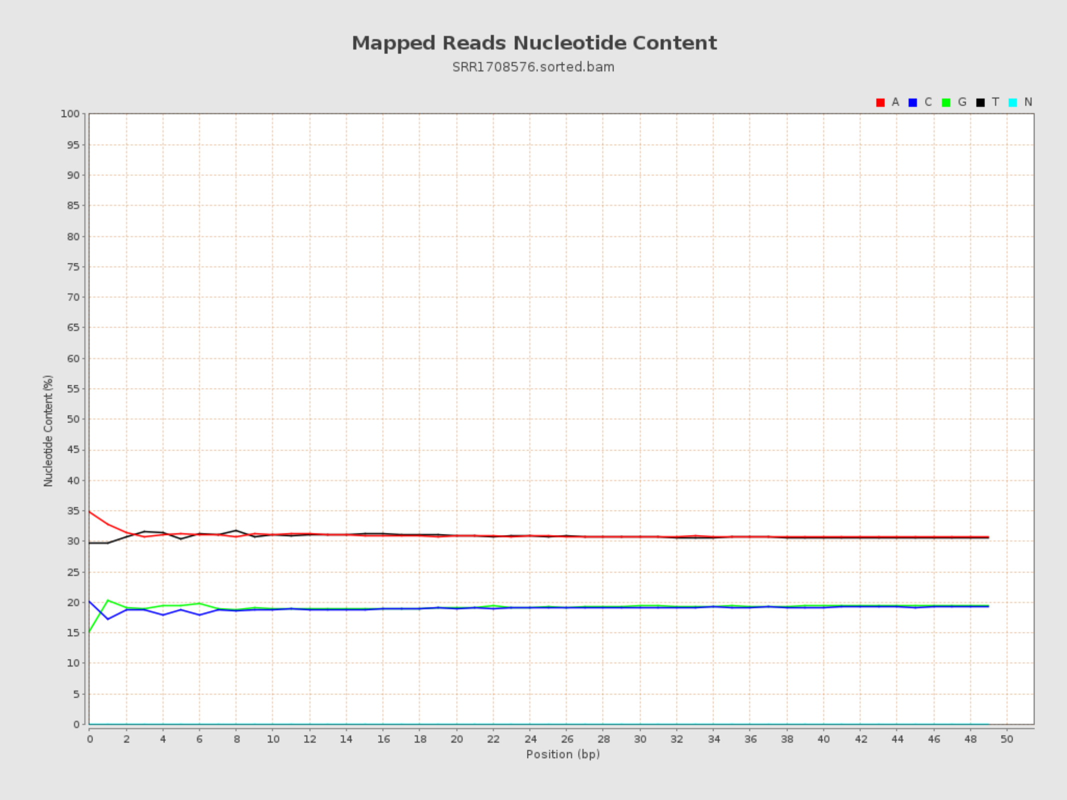
6. Results : Genome Fraction Coverage



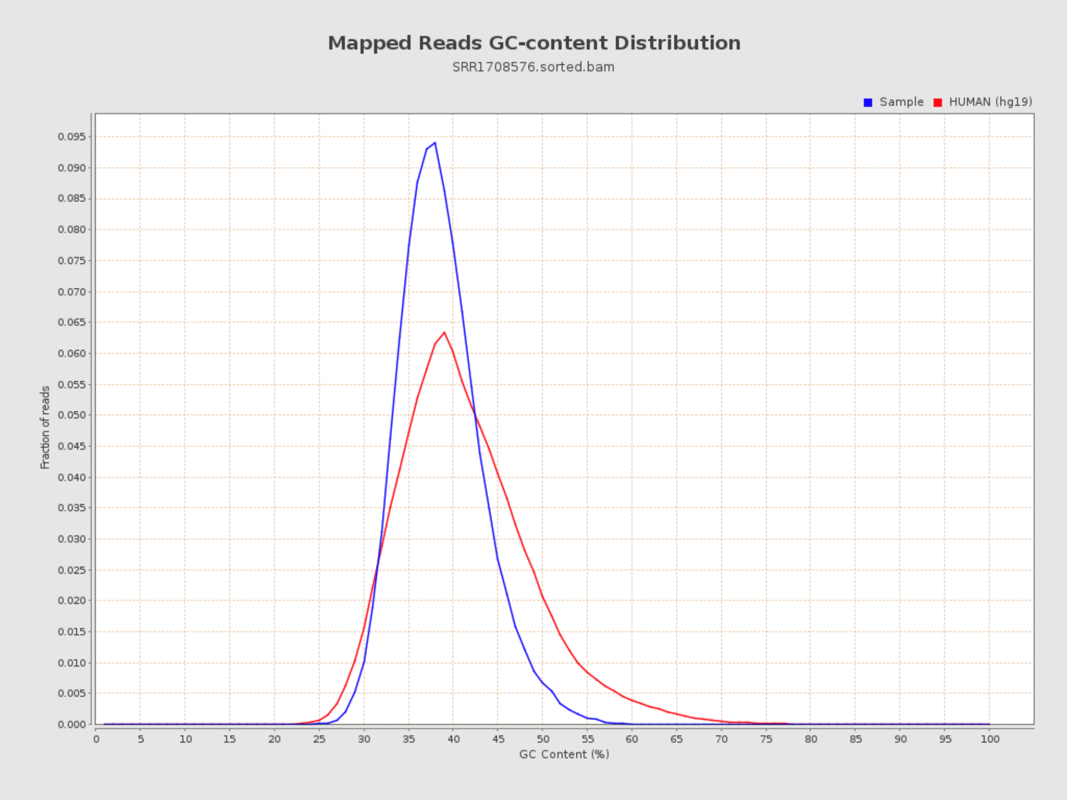
7. Results : Duplication Rate Histogram



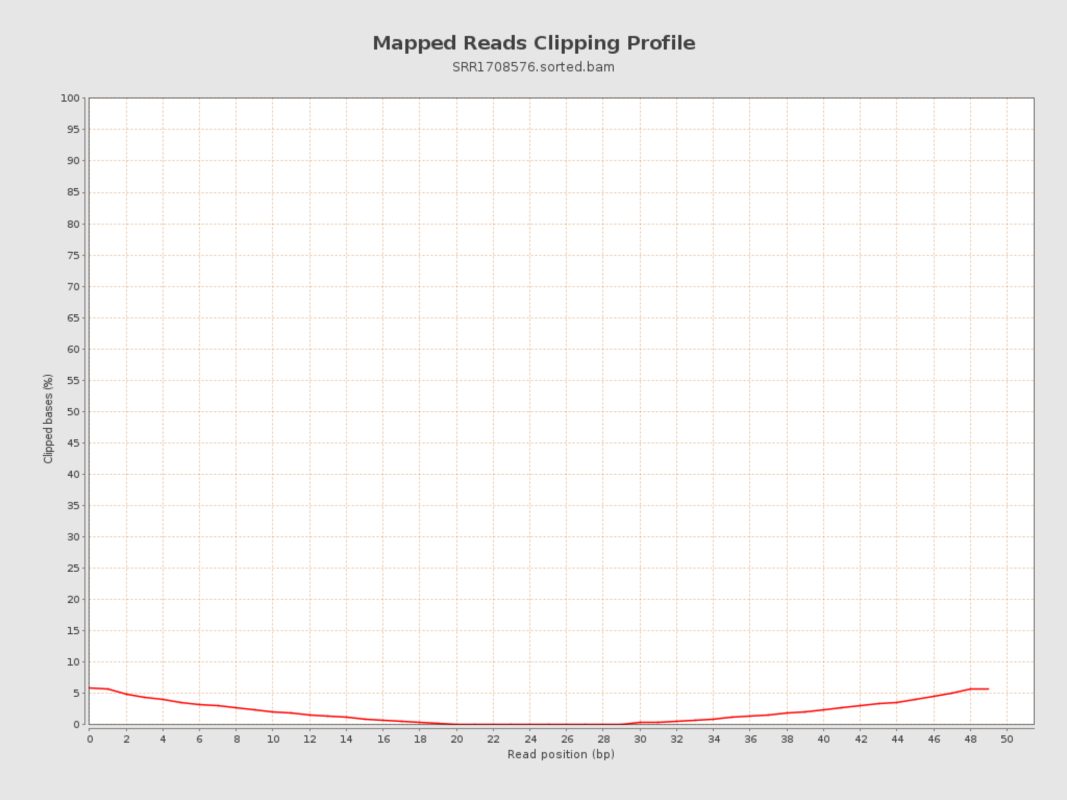
8. Results : Mapped Reads Nucleotide Content



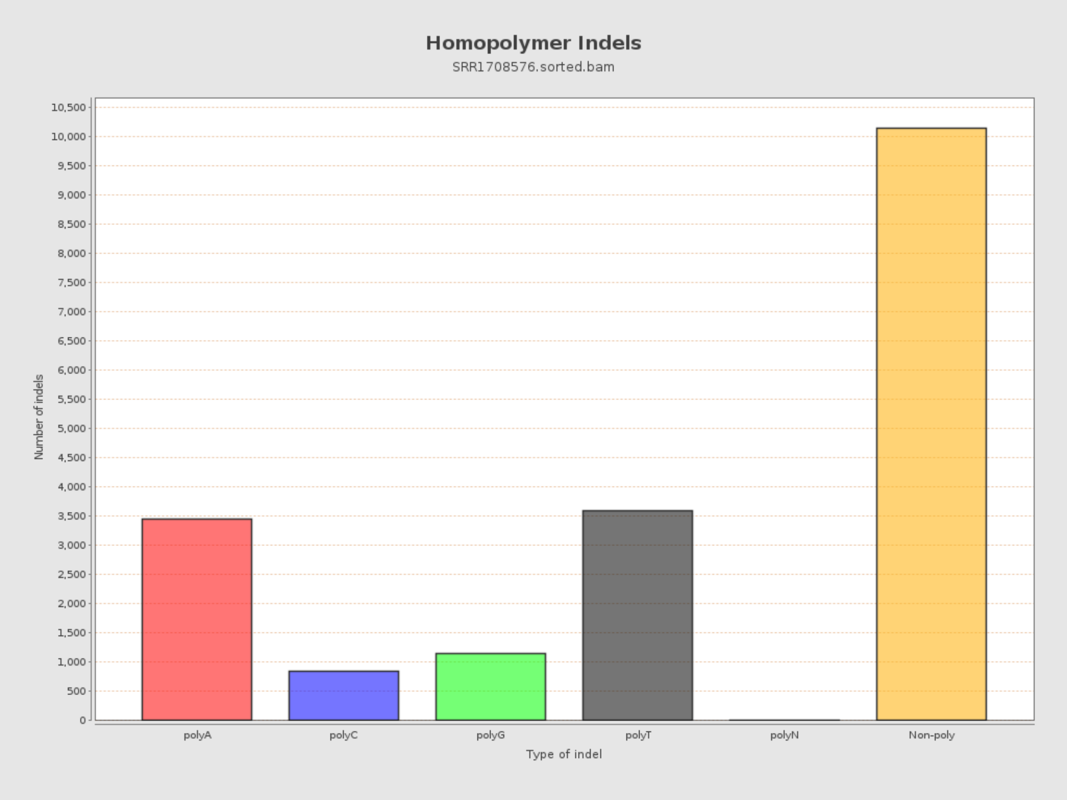
9. Results : Mapped Reads GC-content Distribution



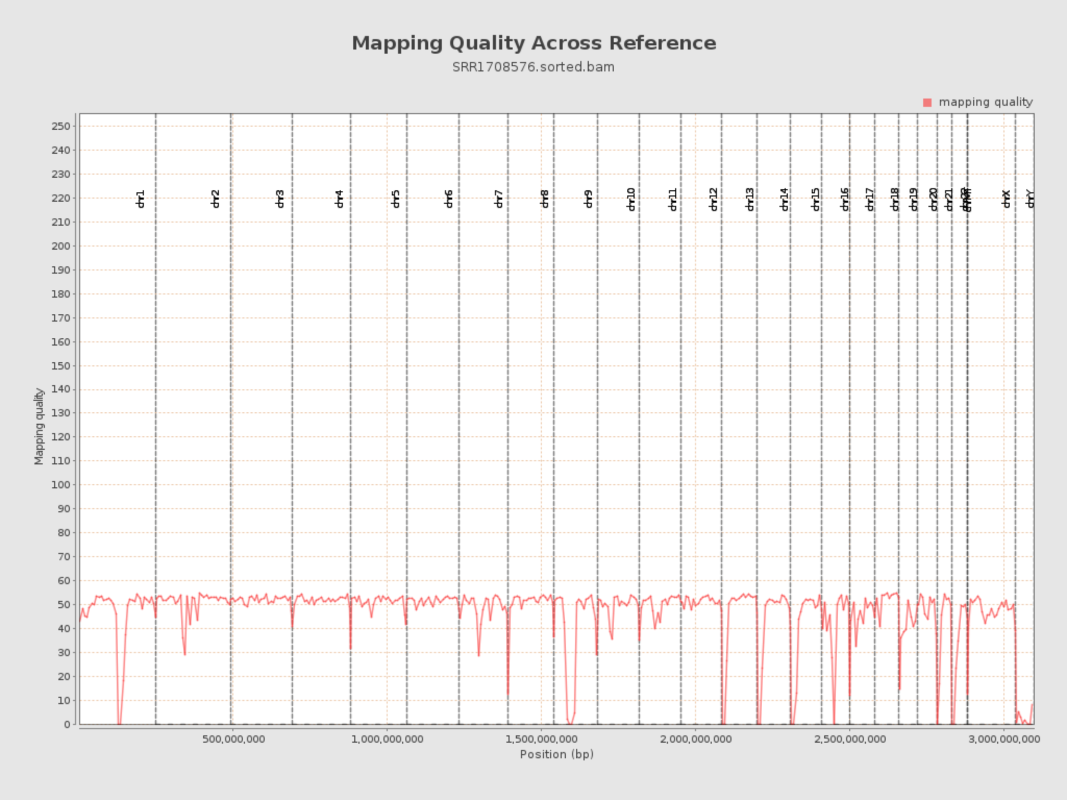
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram