Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:44:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708512.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_SRR1708512 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708512.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:44:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708512.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,431,004
Mapped reads	2,385,020 / 69.51%
Unmapped reads	1,045,984 / 30.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	459 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	119,182 / 3.47%
Duplication rate	3.8%
Clipped reads	461,329 / 13.45%

2.2. ACGT Content

Number/percentage of A's	33,273,622 / 29.07%
Number/percentage of C's	21,060,004 / 18.4%
Number/percentage of T's	36,819,197 / 32.17%
Number/percentage of G's	23,288,409 / 20.35%
Number/percentage of N's	1,726 / 0%
GC Percentage	38.75%

2.3. Coverage

Mean	0.037

Standard Deviation	0.403

2.4. Mapping Quality

Mean Mapping Quality	43.14

2.5. Mismatches and indels

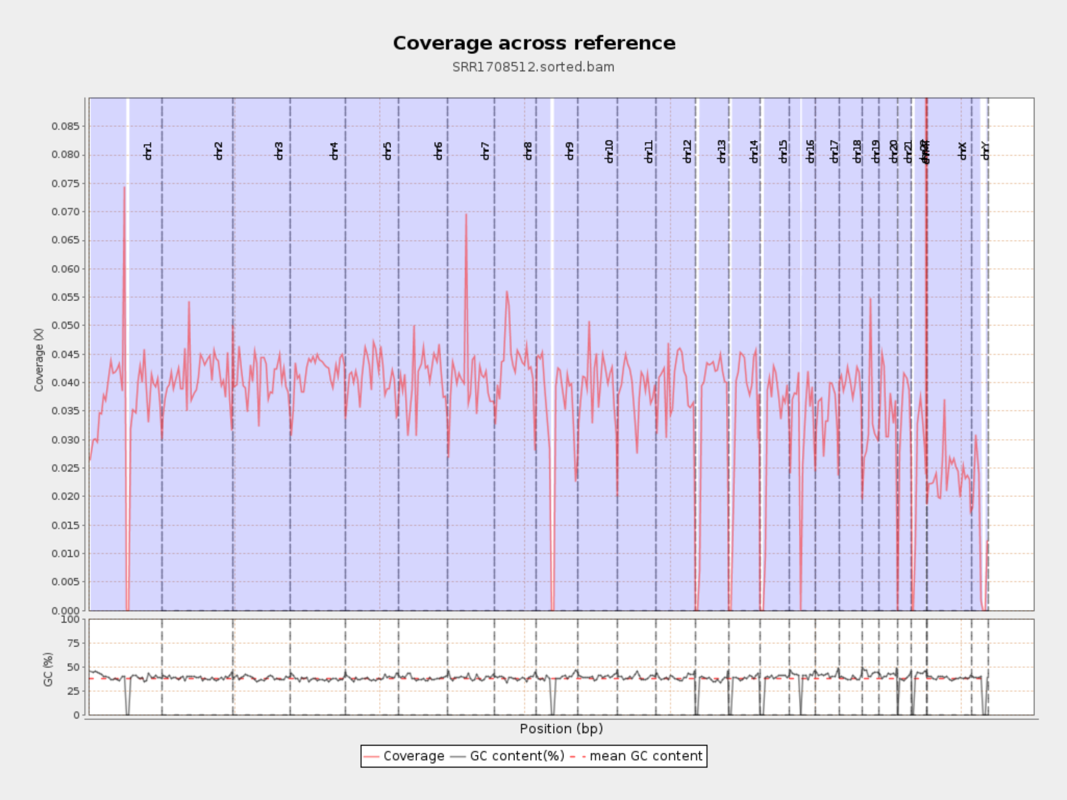
General error rate	0.49%
Mismatches	555,754
Insertions	5,473
Mapped reads with at least one insertion	0.23%
Deletions	13,634
Mapped reads with at least one deletion	0.57%
Homopolymer indels	48.58%

2.6. Chromosome stats

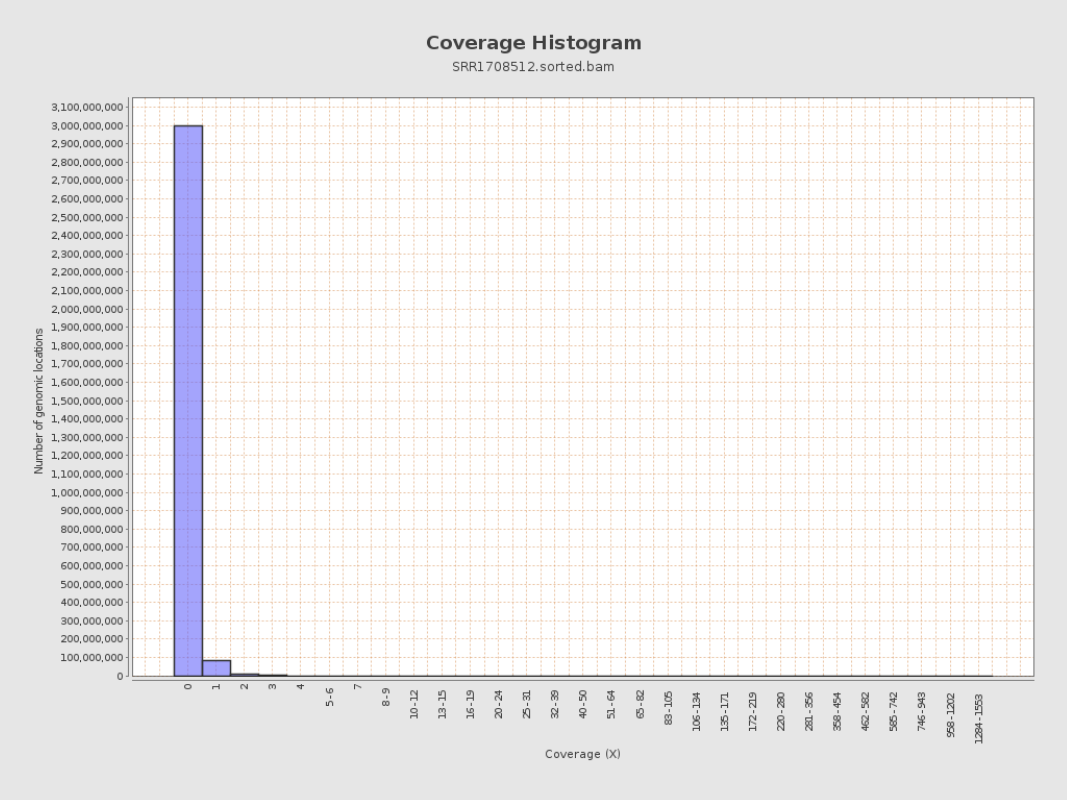
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9093431	0.0365	0.8251
chr2	243199373	9986467	0.0411	0.3274
chr3	198022430	8110160	0.041	0.2349
chr4	191154276	8005977	0.0419	0.2406
chr5	180915260	7435108	0.0411	0.2362
chr6	171115067	6953930	0.0406	0.2852
chr7	159138663	6550879	0.0412	0.4715

chr8	146364022	6283226	0.0429	0.8597
chr9	141213431	4806937	0.034	0.2549
chr10	135534747	5431630	0.0401	0.3003
chr11	135006516	5228667	0.0387	0.3205
chr12	133851895	5260919	0.0393	0.2321
chr13	115169878	4007740	0.0348	0.2194
chr14	107349540	3673966	0.0342	0.2247
chr15	102531392	3158185	0.0308	0.202
chr16	90354753	2937977	0.0325	0.2145
chr17	81195210	2790239	0.0344	0.2774
chr18	78077248	3139216	0.0402	0.4221
chr19	59128983	1933659	0.0327	0.5218
chr20	63025520	2251359	0.0357	0.2201
chr21	48129895	1559151	0.0324	0.2423
chr22	51304566	1158857	0.0226	0.1967
chrMT	16571	211622	12.7706	8.9184
chrX	155270560	3701467	0.0238	0.2023
chrY	59373566	792954	0.0134	0.1408

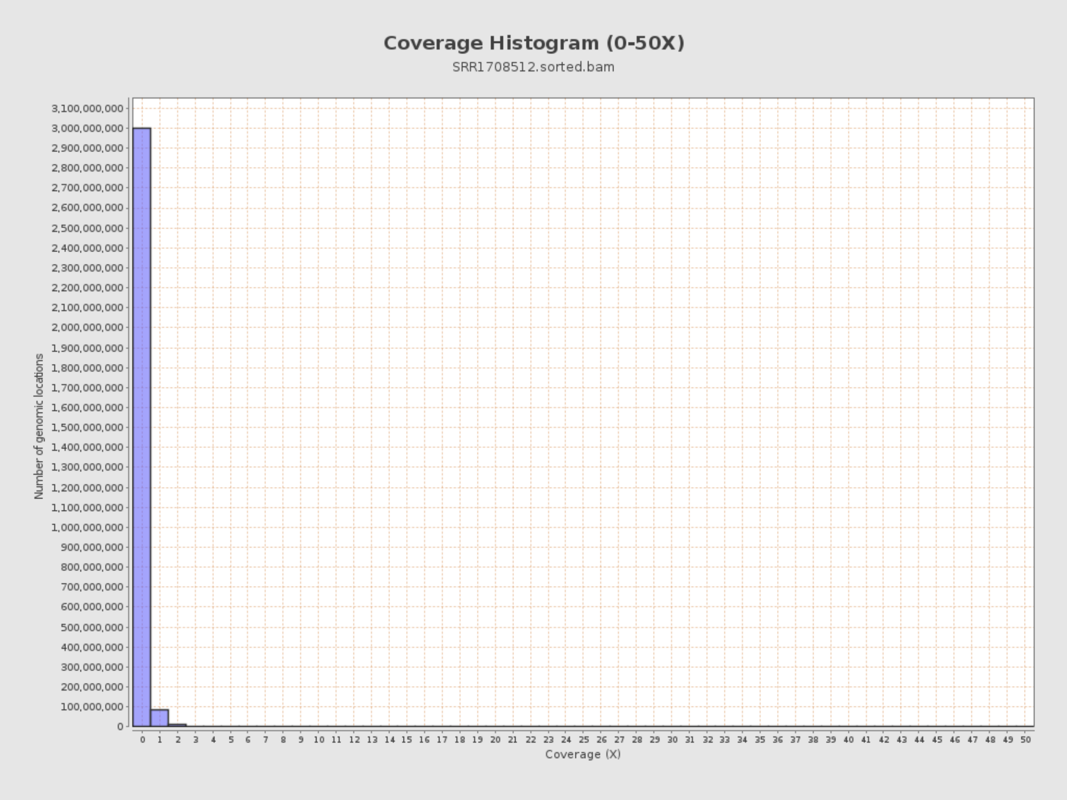
3. Results : Coverage across reference



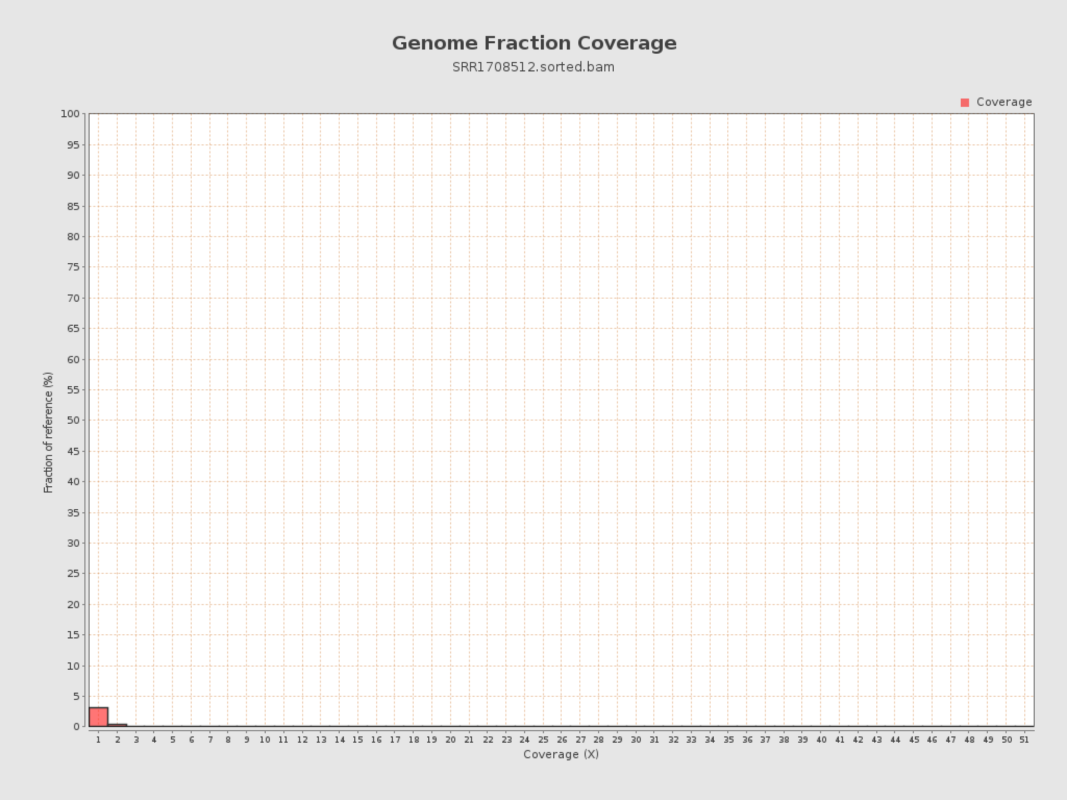
4. Results : Coverage Histogram



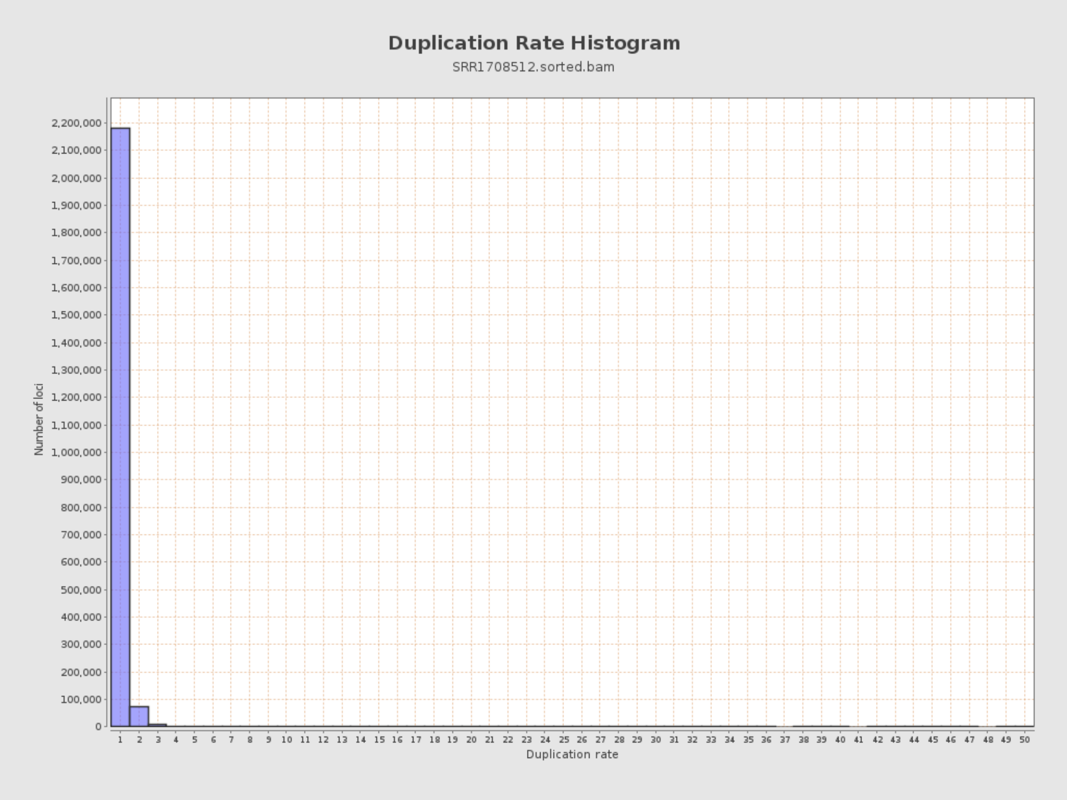
5. Results : Coverage Histogram (0-50X)



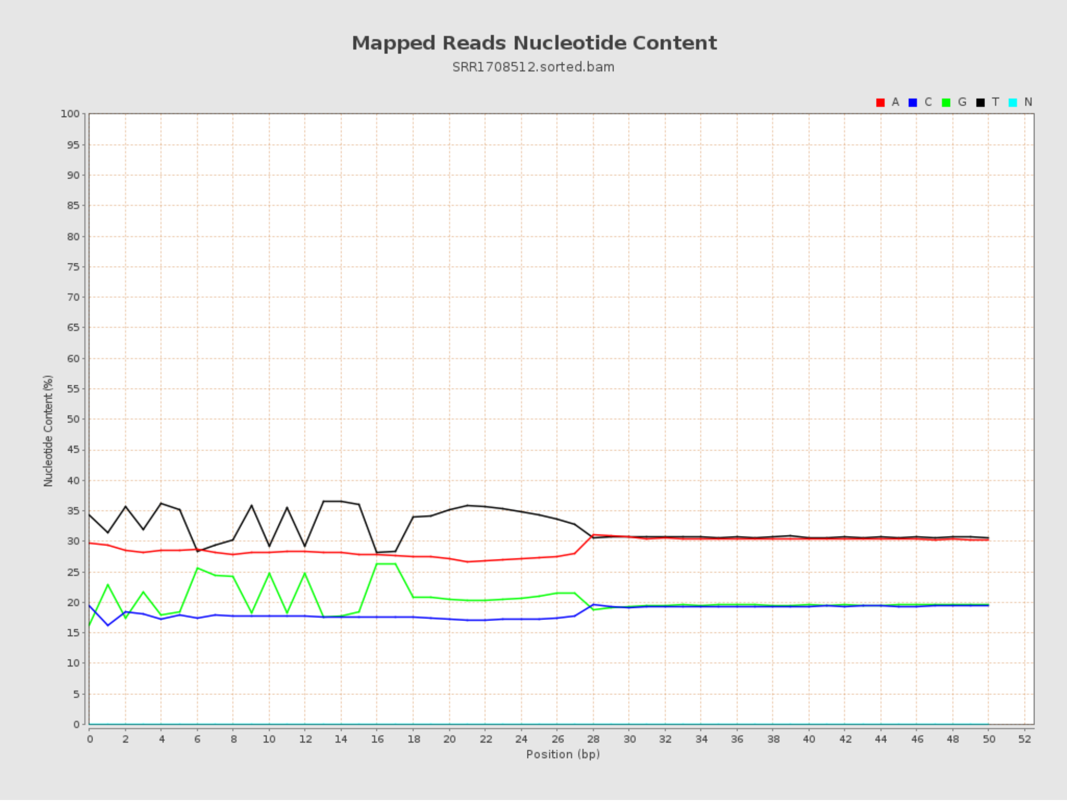
6. Results : Genome Fraction Coverage



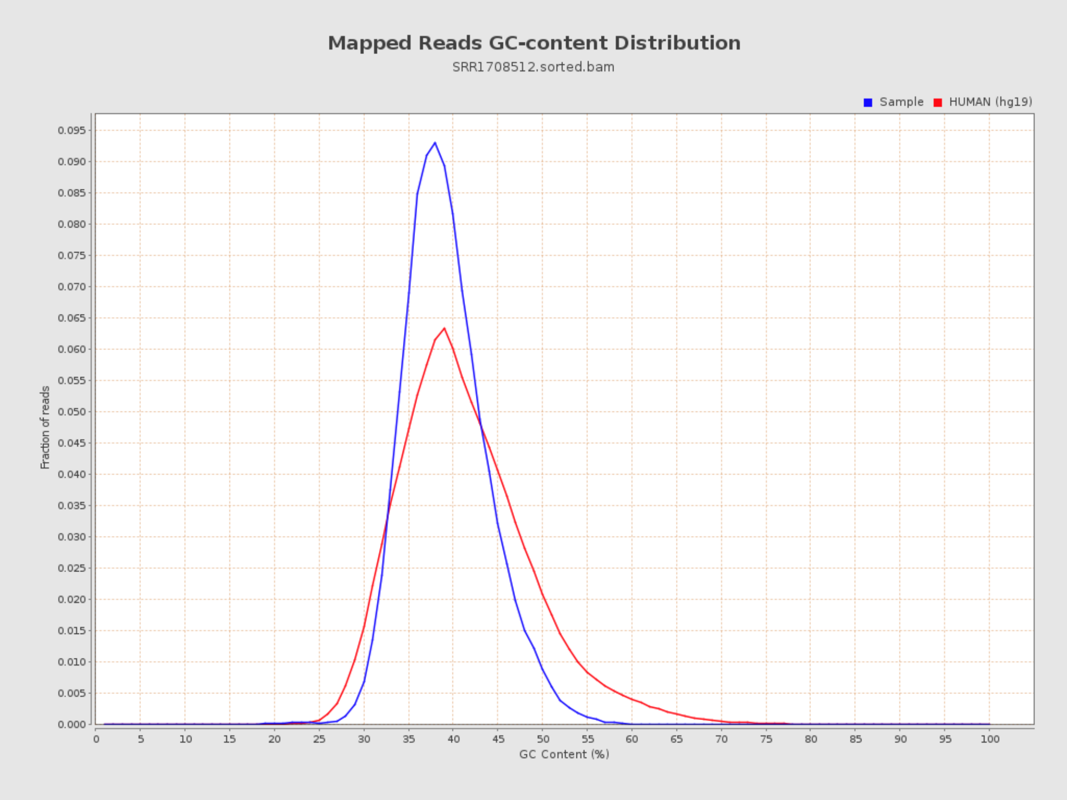
7. Results : Duplication Rate Histogram



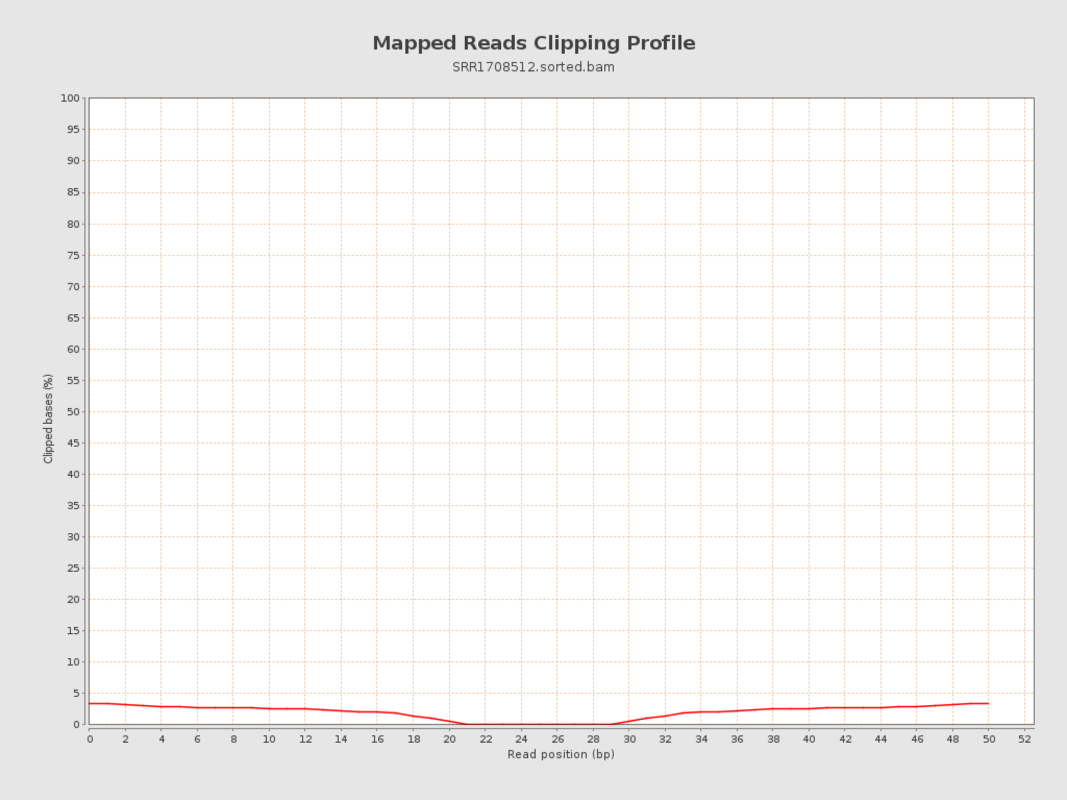
8. Results : Mapped Reads Nucleotide Content



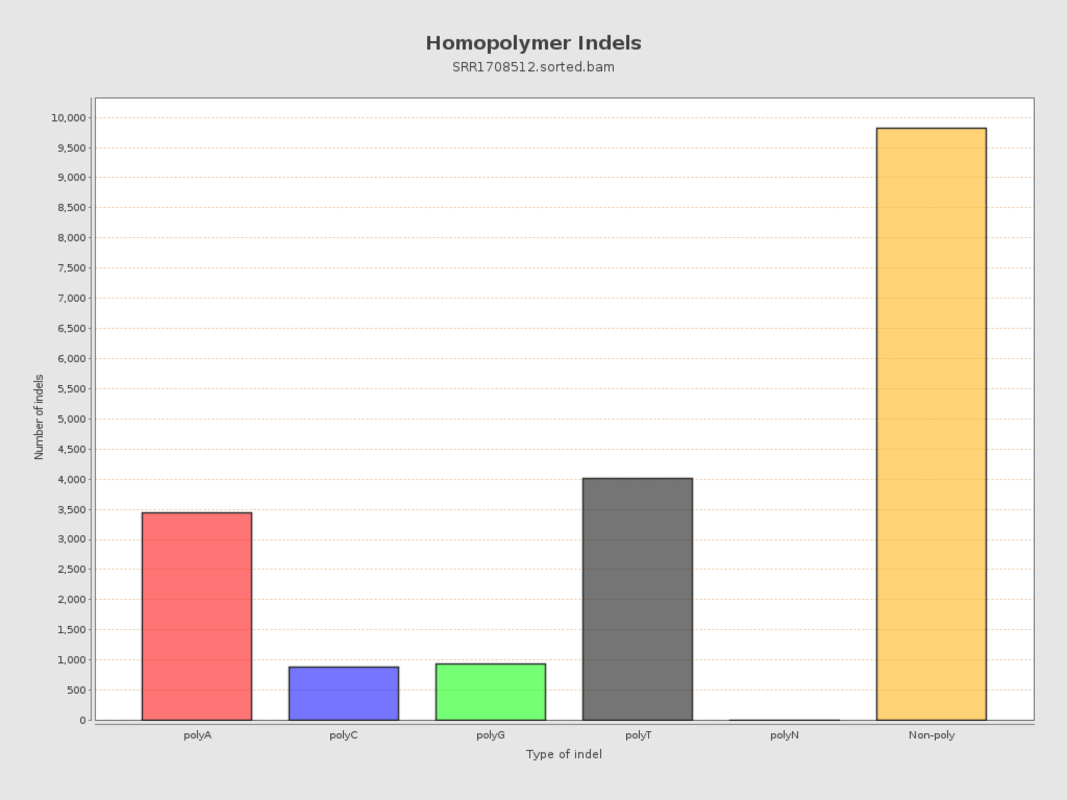
9. Results : Mapped Reads GC-content Distribution



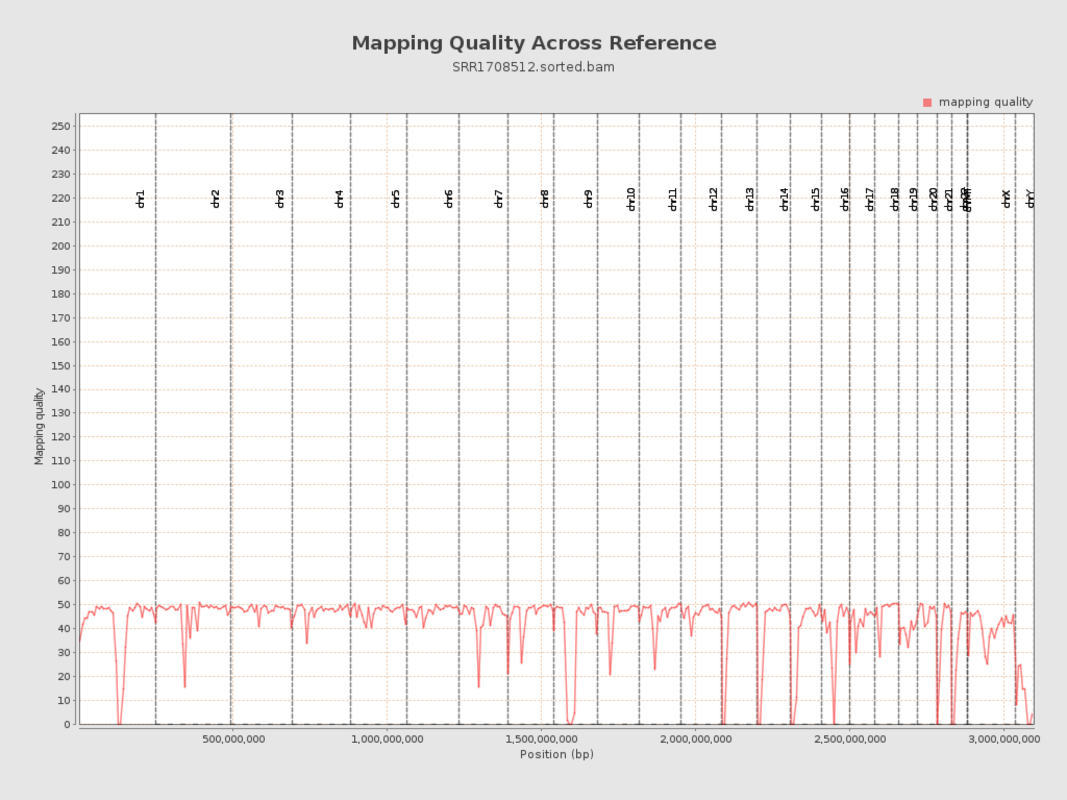
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram