Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:30:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708612.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_SRR1708612 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708612.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:30:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708612.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,650,536
Mapped reads	1,606,687 / 60.62%
Unmapped reads	1,043,849 / 39.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	413 / 0.02%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	69,179 / 2.61%
Duplication rate	3.49%
Clipped reads	299,136 / 11.29%

2.2. ACGT Content

Number/percentage of A's	22,358,170 / 28.91%
Number/percentage of C's	14,729,897 / 19.05%
Number/percentage of T's	24,209,479 / 31.3%
Number/percentage of G's	16,032,372 / 20.73%
Number/percentage of N's	6,675 / 0.01%
GC Percentage	39.78%

2.3. Coverage

Mean	0.025

Standard Deviation	0.2451

2.4. Mapping Quality

Mean Mapping Quality	41.59

2.5. Mismatches and indels

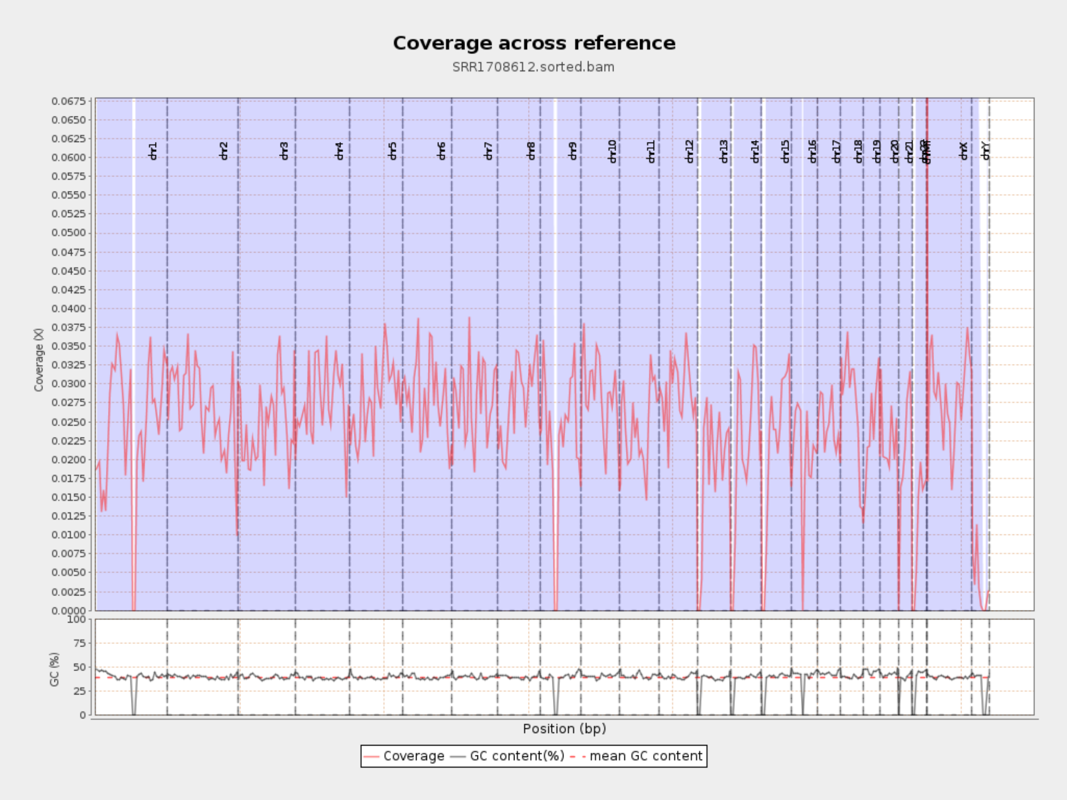
General error rate	0.69%
Mismatches	524,632
Insertions	3,927
Mapped reads with at least one insertion	0.24%
Deletions	13,044
Mapped reads with at least one deletion	0.81%
Homopolymer indels	49%

2.6. Chromosome stats

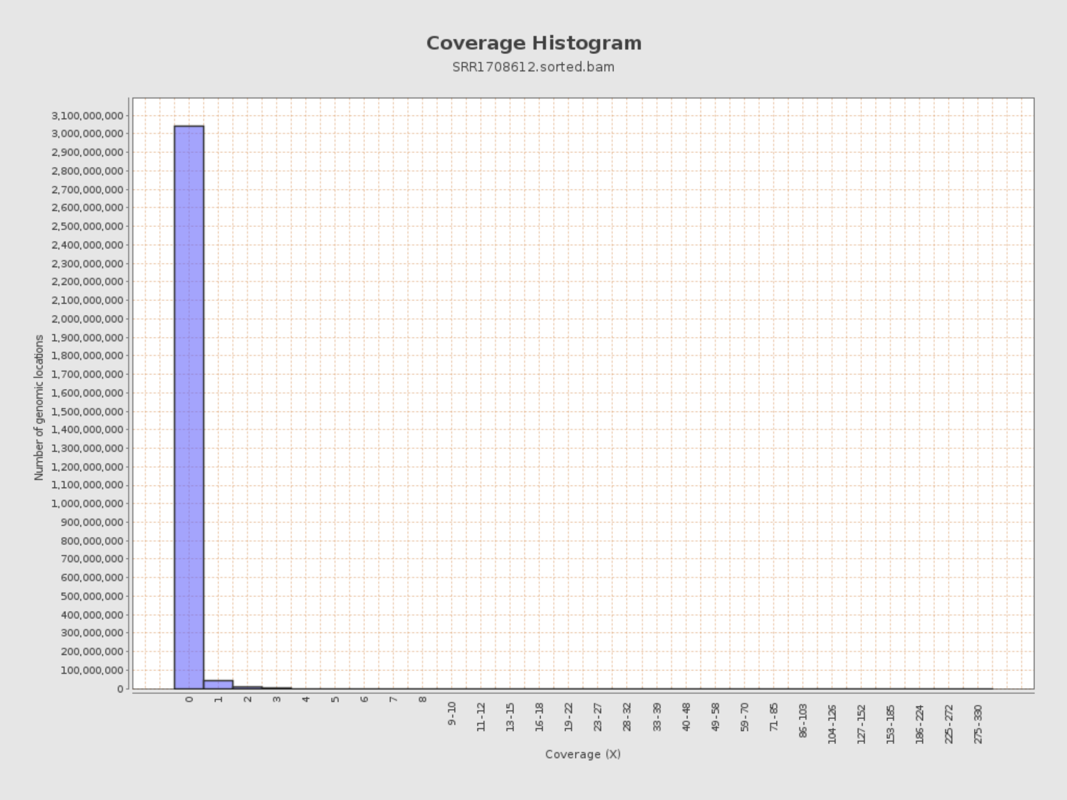
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6077106	0.0244	0.3024
chr2	243199373	6565481	0.027	0.2793
chr3	198022430	4848557	0.0245	0.2102
chr4	191154276	5302032	0.0277	0.2302
chr5	180915260	5097145	0.0282	0.2269
chr6	171115067	4859788	0.0284	0.2576
chr7	159138663	4500834	0.0283	0.3061

chr8	146364022	4083976	0.0279	0.2617
chr9	141213431	3229544	0.0229	0.2341
chr10	135534747	3877517	0.0286	0.2447
chr11	135006516	3333243	0.0247	0.2477
chr12	133851895	3883699	0.029	0.2328
chr13	115169878	2137629	0.0186	0.1851
chr14	107349540	2297515	0.0214	0.2016
chr15	102531392	2230659	0.0218	0.1986
chr16	90354753	1830533	0.0203	0.1916
chr17	81195210	1998423	0.0246	0.224
chr18	78077248	2164117	0.0277	0.3369
chr19	59128983	1408464	0.0238	0.2941
chr20	63025520	1416144	0.0225	0.2062
chr21	48129895	1018026	0.0212	0.2
chr22	51304566	604603	0.0118	0.1412
chrMT	16571	2803	0.1692	0.4833
chrX	155270560	4386859	0.0283	0.2341
chrY	59373566	202174	0.0034	0.0876

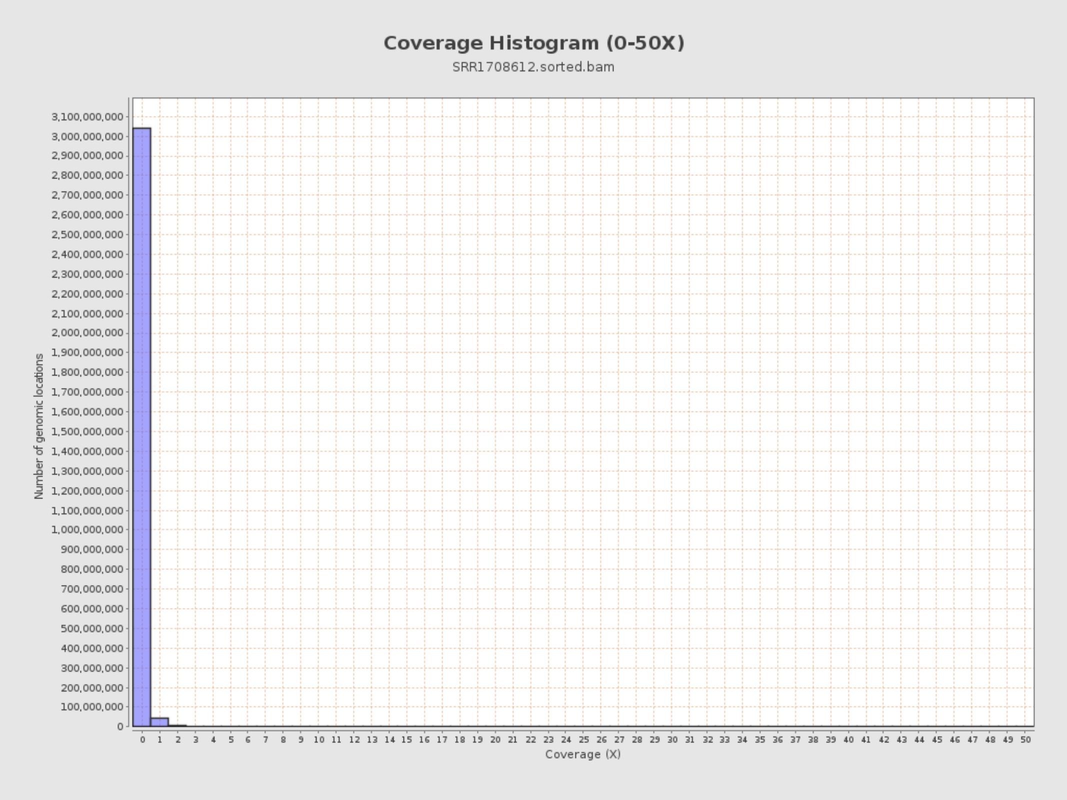
3. Results : Coverage across reference



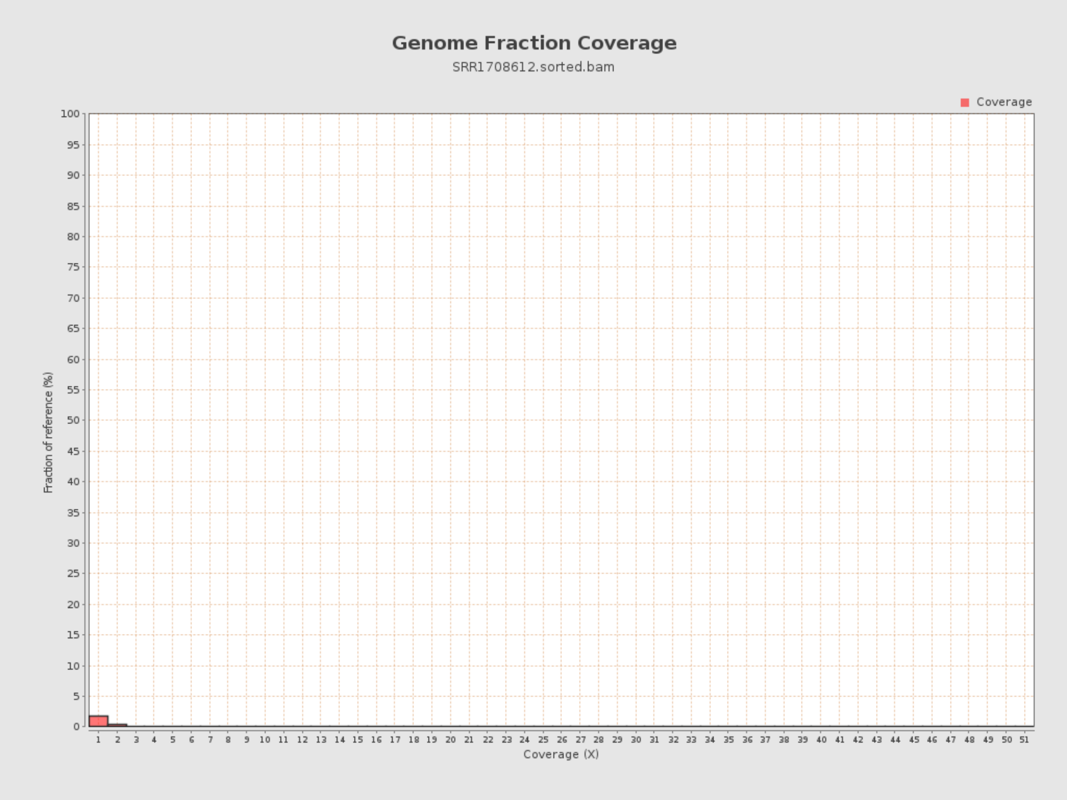
4. Results : Coverage Histogram



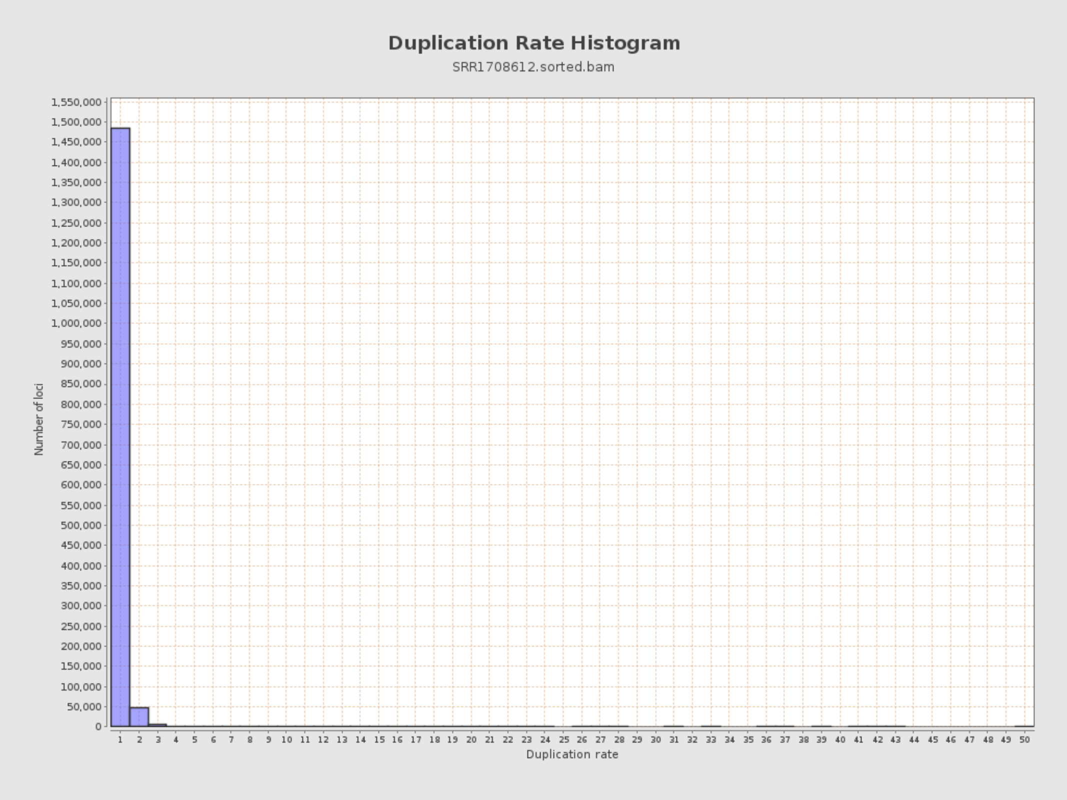
5. Results : Coverage Histogram (0-50X)



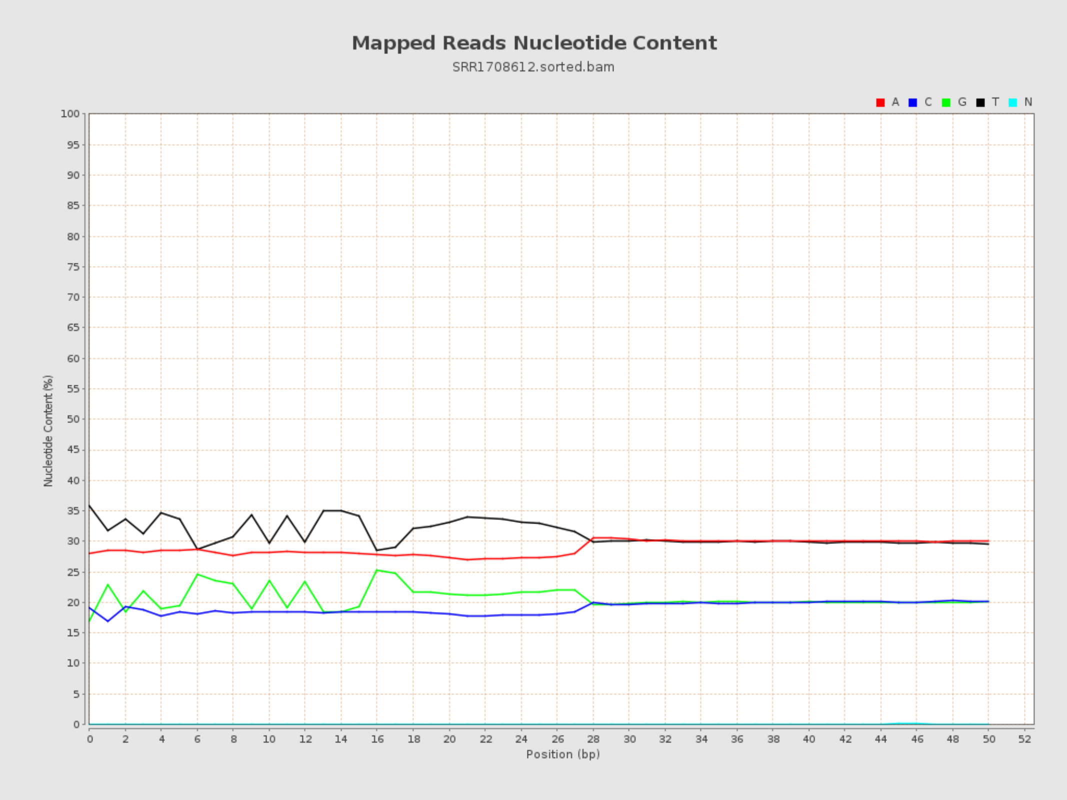
6. Results : Genome Fraction Coverage



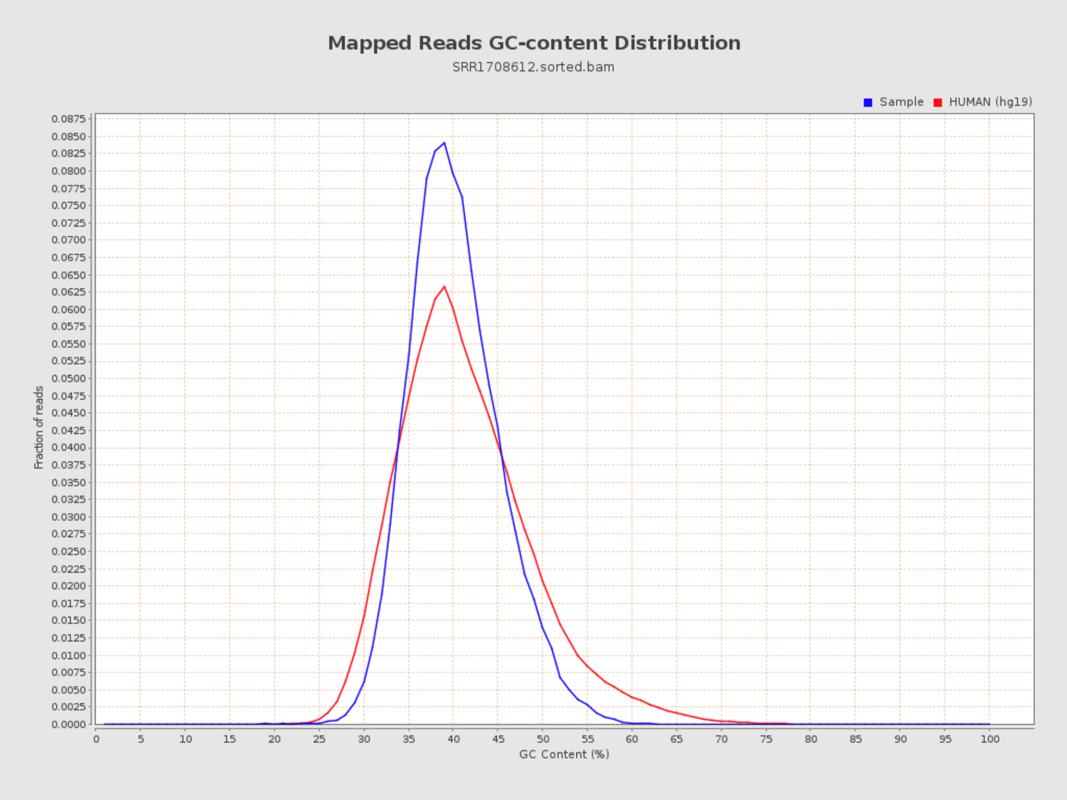
7. Results : Duplication Rate Histogram



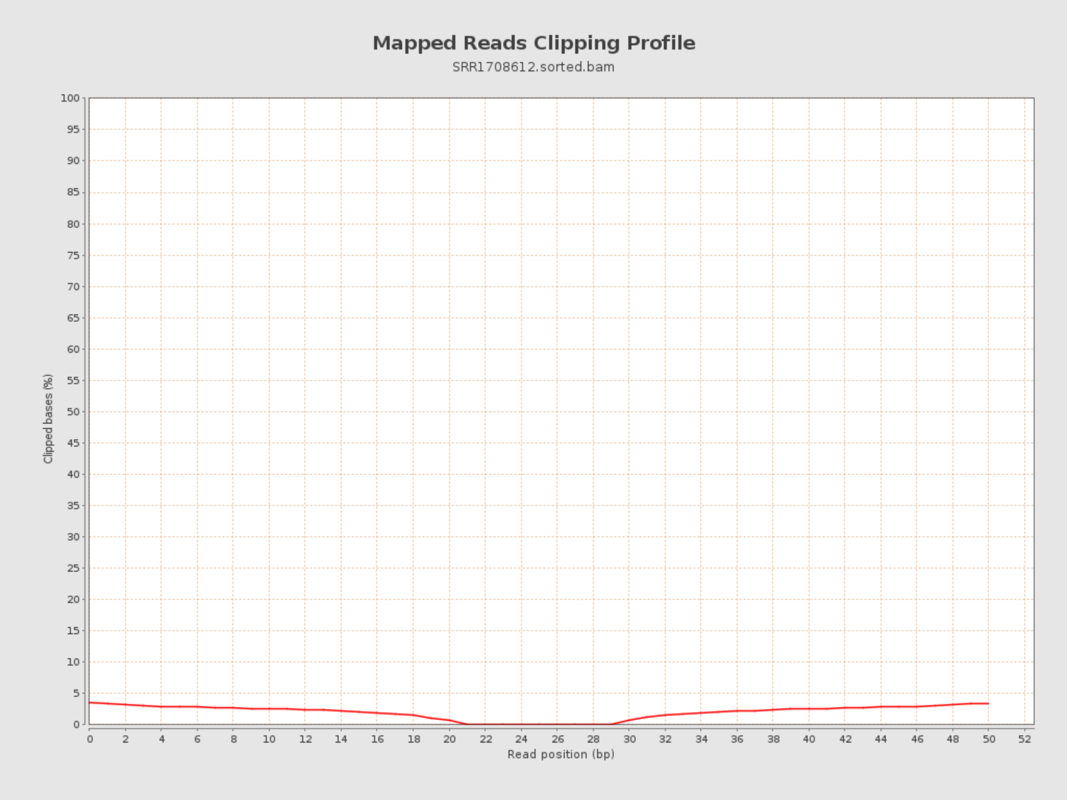
8. Results : Mapped Reads Nucleotide Content



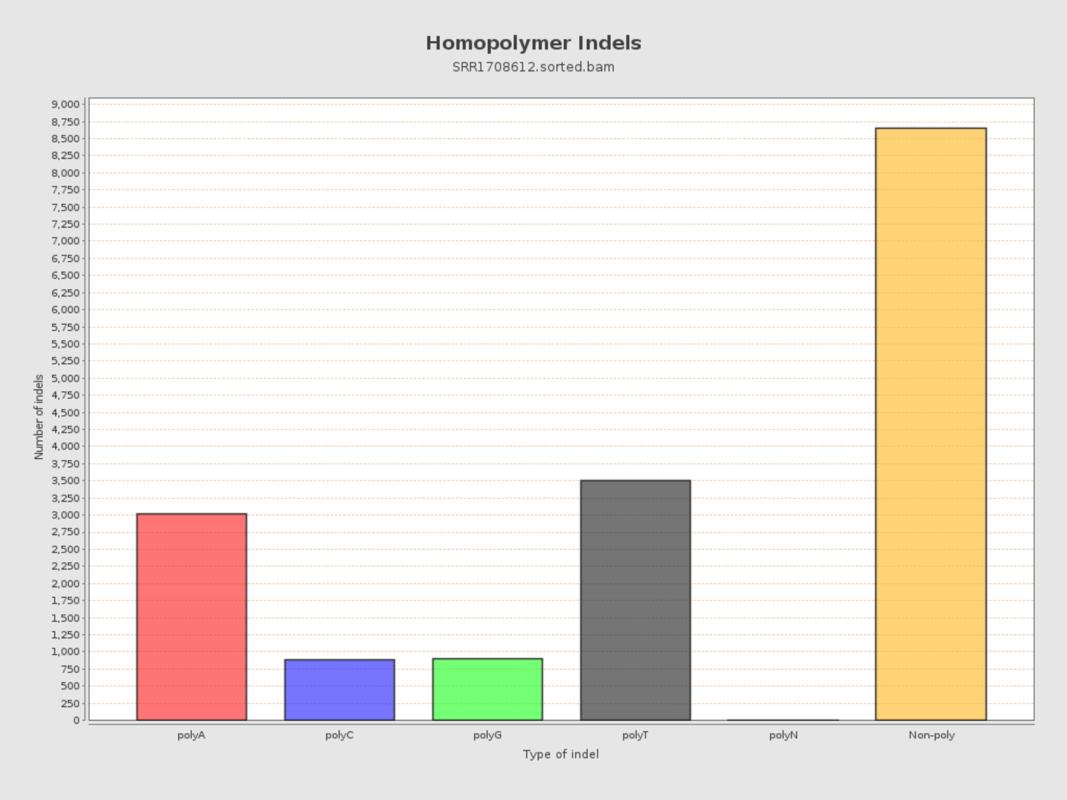
9. Results : Mapped Reads GC-content Distribution



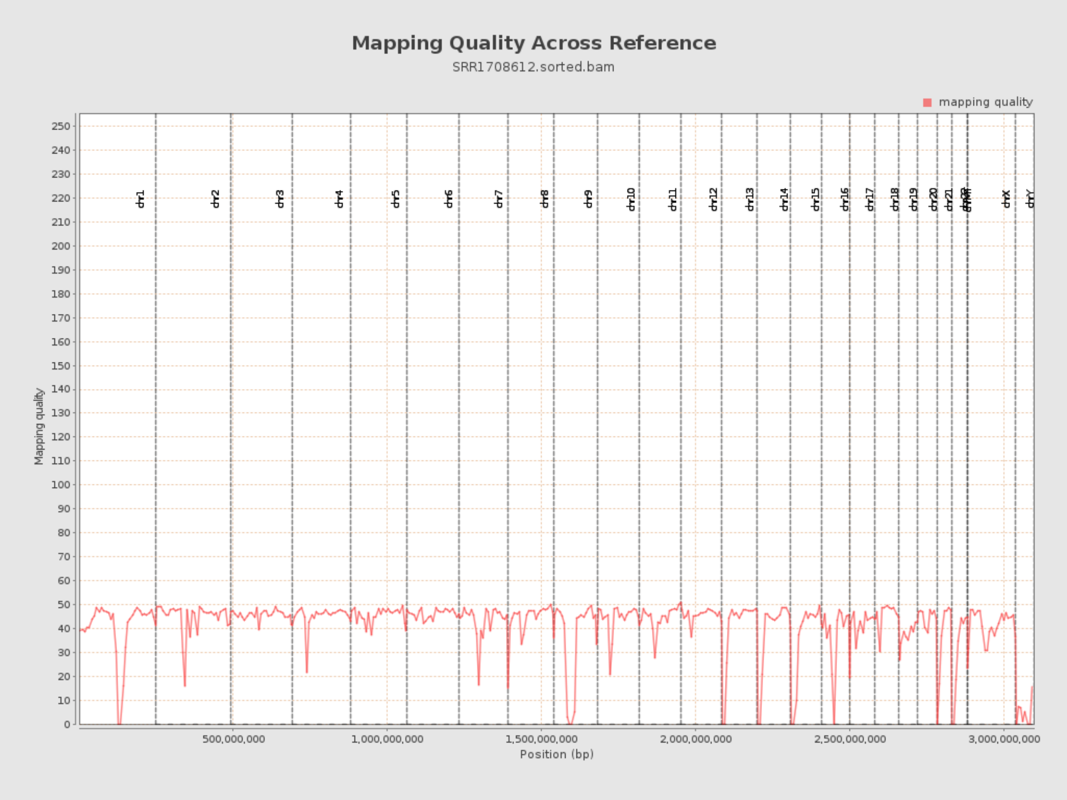
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram