Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:02:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708635.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_SRR1708635 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708635.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:02:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708635.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,305,716
Mapped reads	2,330,864 / 70.51%
Unmapped reads	974,852 / 29.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	793 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	76,349 / 2.31%
Duplication rate	2.26%
Clipped reads	375,578 / 11.36%

2.2. ACGT Content

Number/percentage of A's	33,373,415 / 29.46%
Number/percentage of C's	21,305,021 / 18.81%
Number/percentage of T's	35,737,155 / 31.55%
Number/percentage of G's	22,848,129 / 20.17%
Number/percentage of N's	9,768 / 0.01%
GC Percentage	38.98%

2.3. Coverage

Mean	0.0366

Standard Deviation	0.3505

2.4. Mapping Quality

Mean Mapping Quality	42.9

2.5. Mismatches and indels

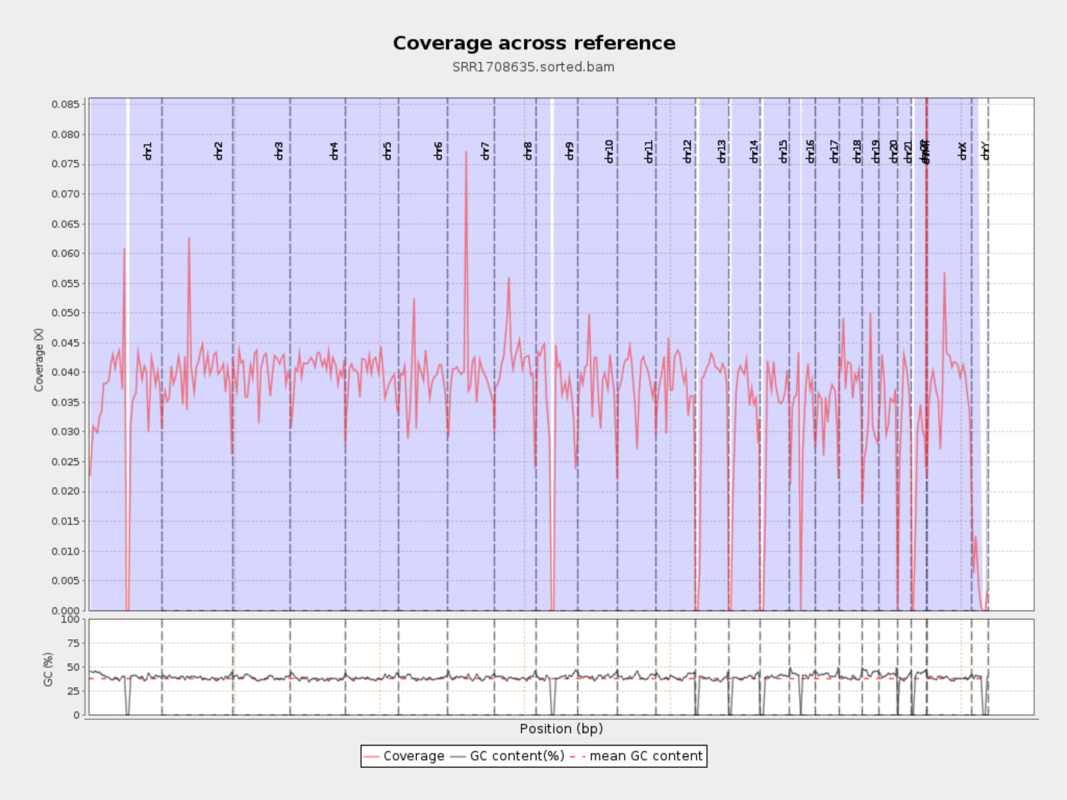
General error rate	0.65%
Mismatches	732,740
Insertions	5,483
Mapped reads with at least one insertion	0.23%
Deletions	14,826
Mapped reads with at least one deletion	0.63%
Homopolymer indels	47.75%

2.6. Chromosome stats

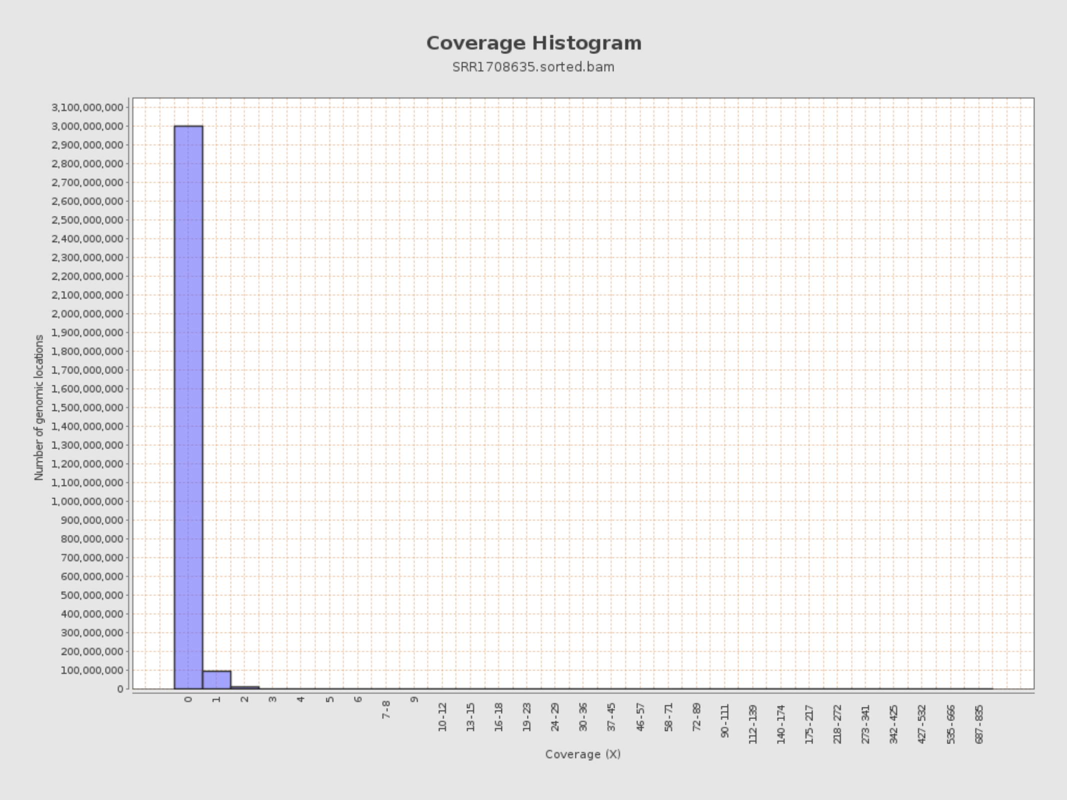
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8885468	0.0356	0.6219
chr2	243199373	9779603	0.0402	0.3799
chr3	198022430	7983488	0.0403	0.2247
chr4	191154276	7782042	0.0407	0.228
chr5	180915260	7163375	0.0396	0.2254
chr6	171115067	6642759	0.0388	0.2882
chr7	159138663	6492521	0.0408	0.5258

chr8	146364022	6111812	0.0418	0.5179
chr9	141213431	4777041	0.0338	0.299
chr10	135534747	5243645	0.0387	0.2866
chr11	135006516	5216983	0.0386	0.2959
chr12	133851895	5132557	0.0383	0.2269
chr13	115169878	3877674	0.0337	0.2043
chr14	107349540	3360676	0.0313	0.2098
chr15	102531392	3167611	0.0309	0.1942
chr16	90354753	2909572	0.0322	0.2144
chr17	81195210	2687857	0.0331	0.231
chr18	78077248	3143087	0.0403	0.6031
chr19	59128983	1851424	0.0313	0.4685
chr20	63025520	2203347	0.035	0.2132
chr21	48129895	1523630	0.0317	0.2153
chr22	51304566	1105062	0.0215	0.1607
chrMT	16571	3926	0.2369	0.5286
chrX	155270560	5977841	0.0385	0.2479
chrY	59373566	272884	0.0046	0.092

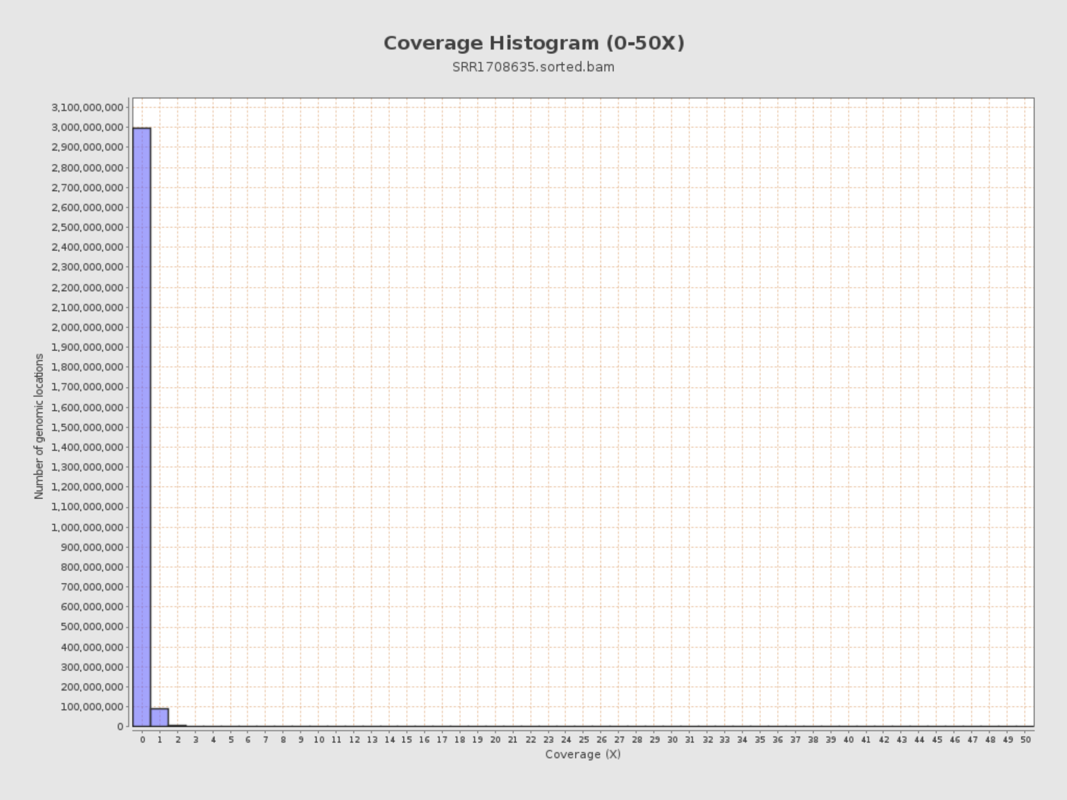
3. Results : Coverage across reference



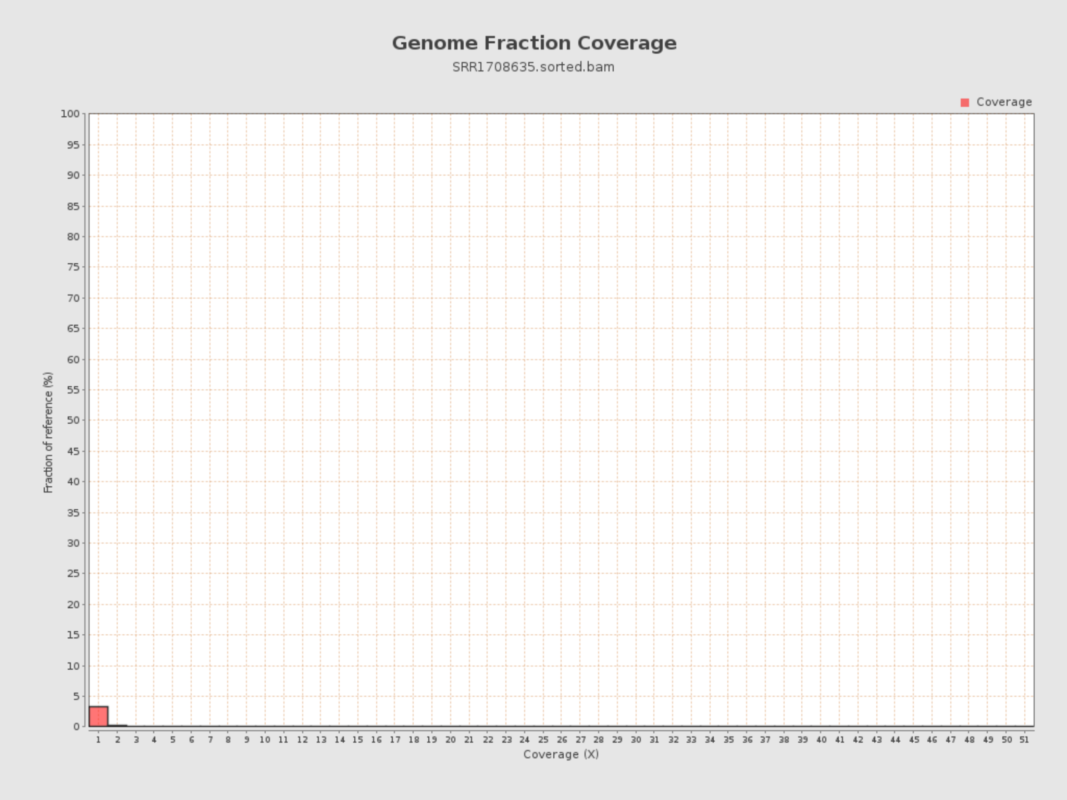
4. Results : Coverage Histogram



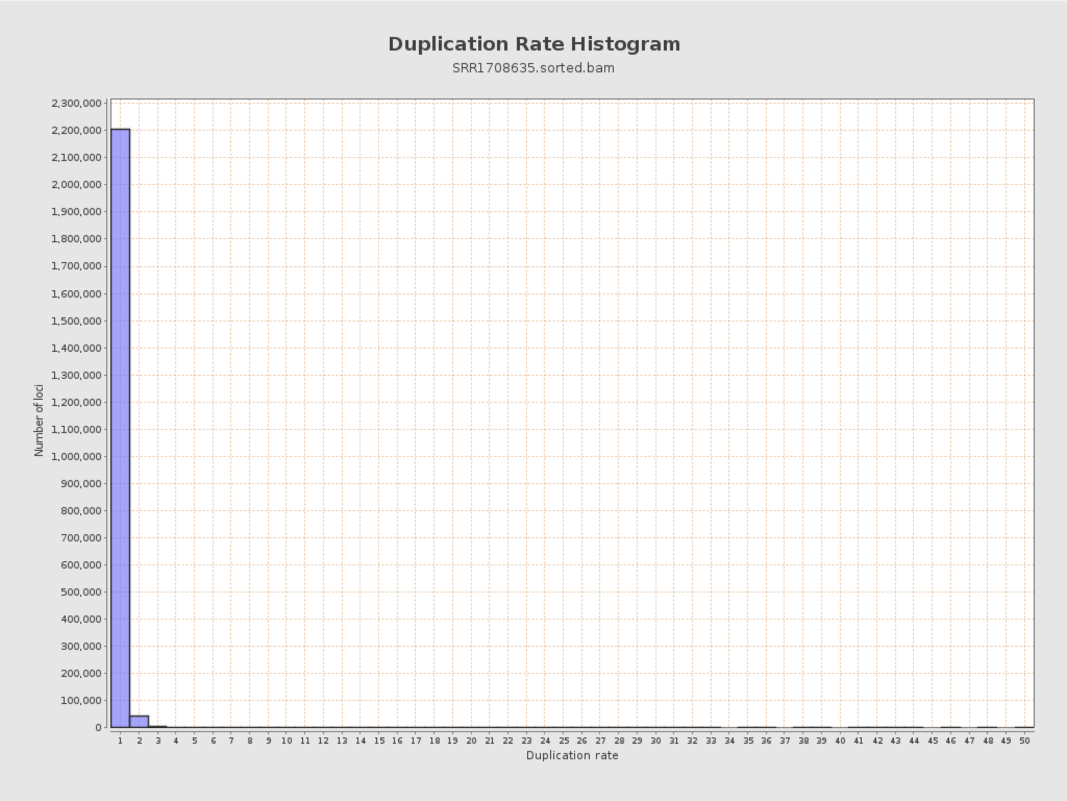
5. Results : Coverage Histogram (0-50X)



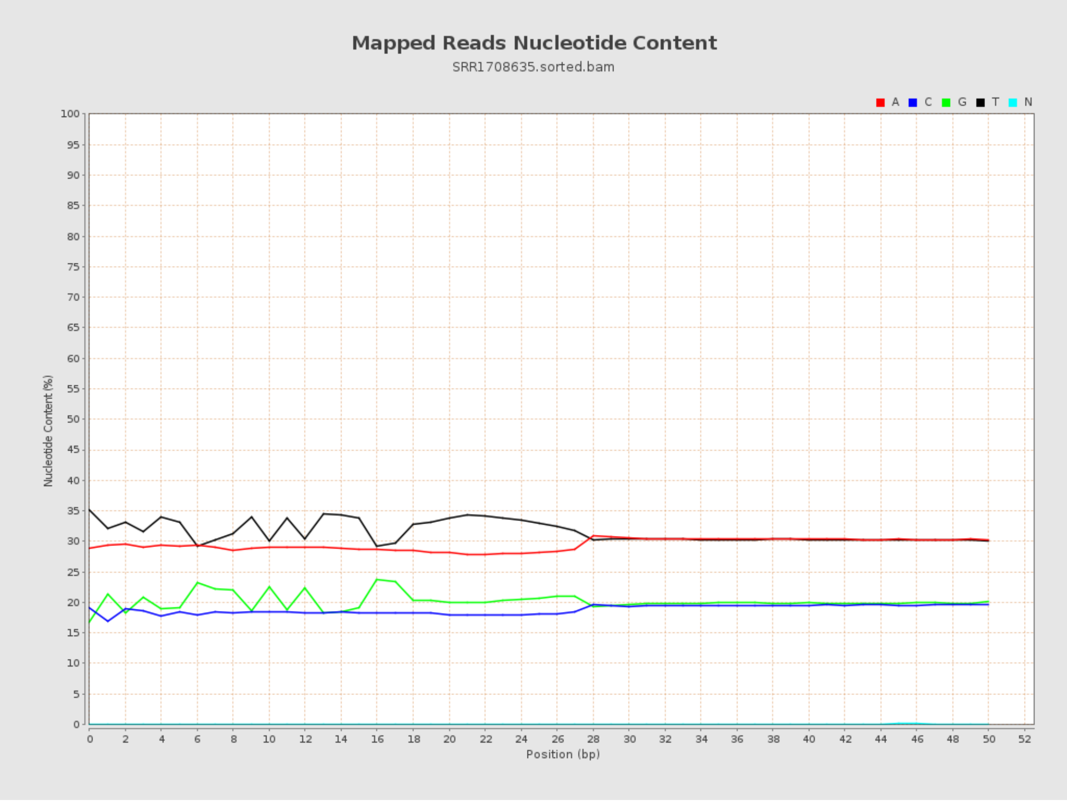
6. Results : Genome Fraction Coverage



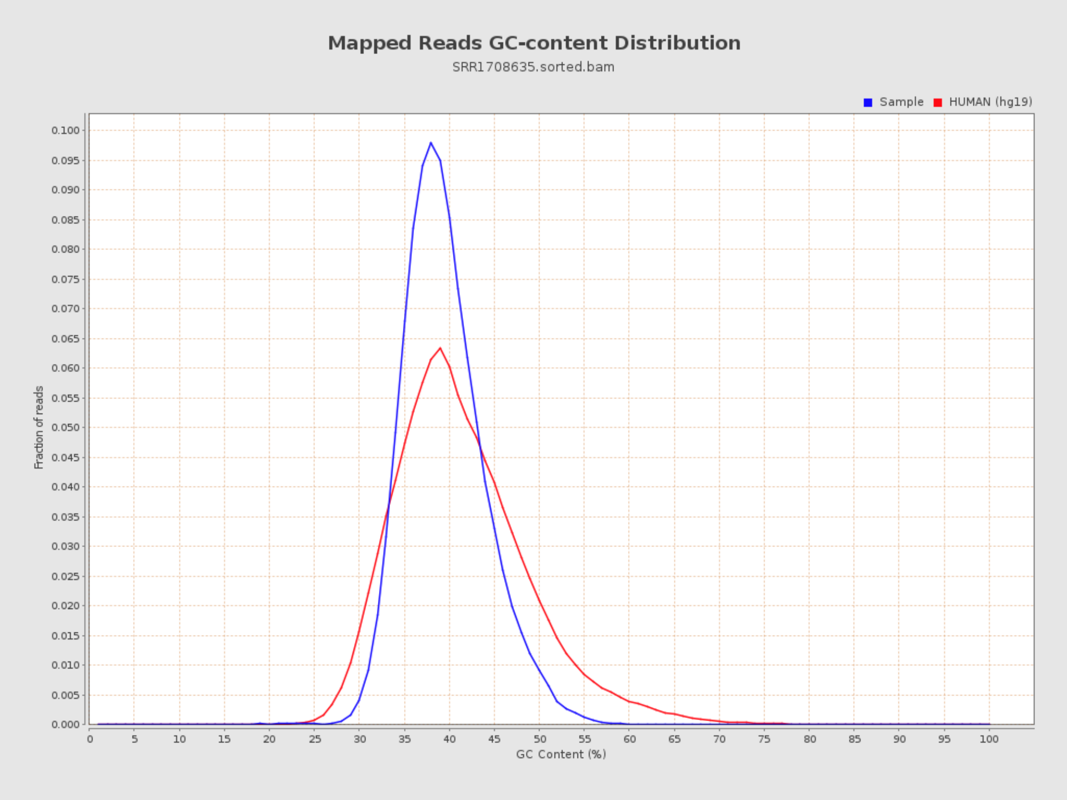
7. Results : Duplication Rate Histogram



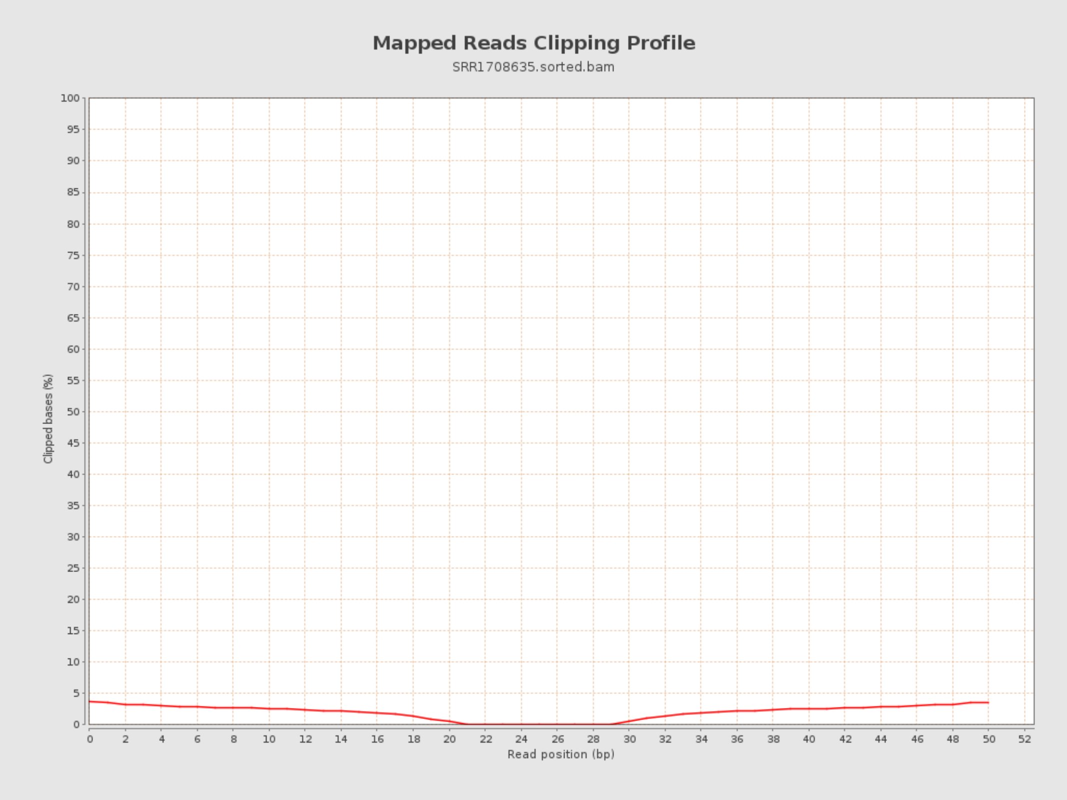
8. Results : Mapped Reads Nucleotide Content



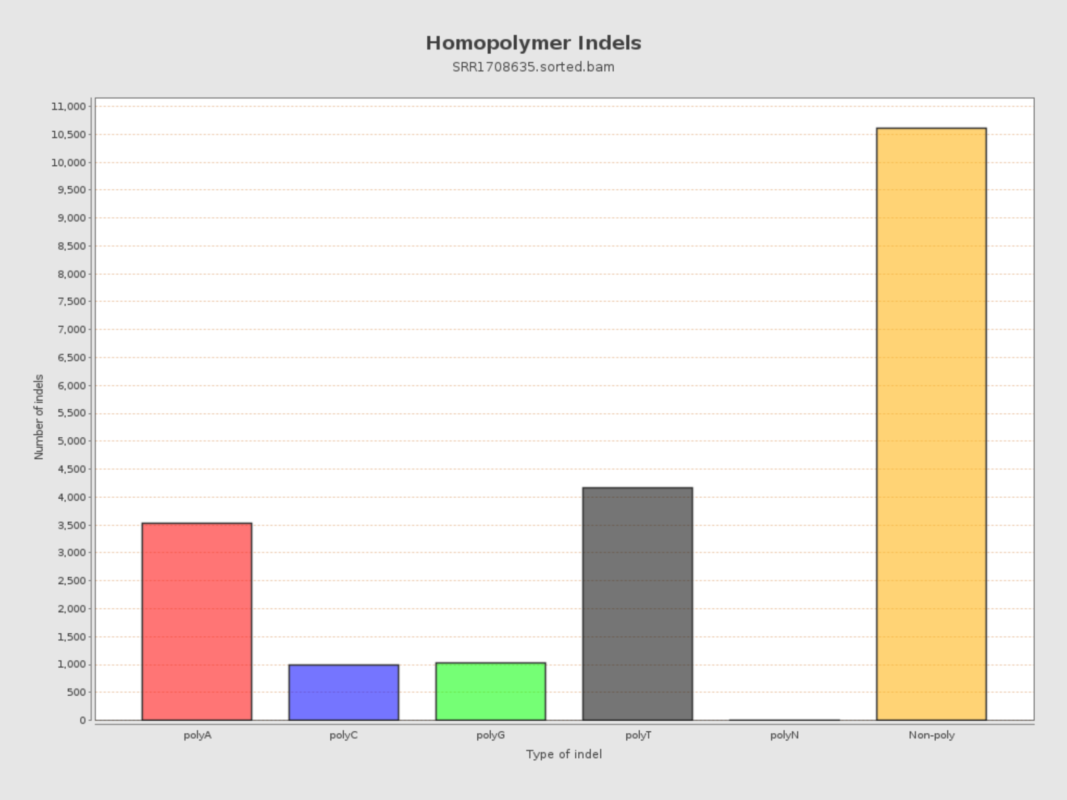
9. Results : Mapped Reads GC-content Distribution



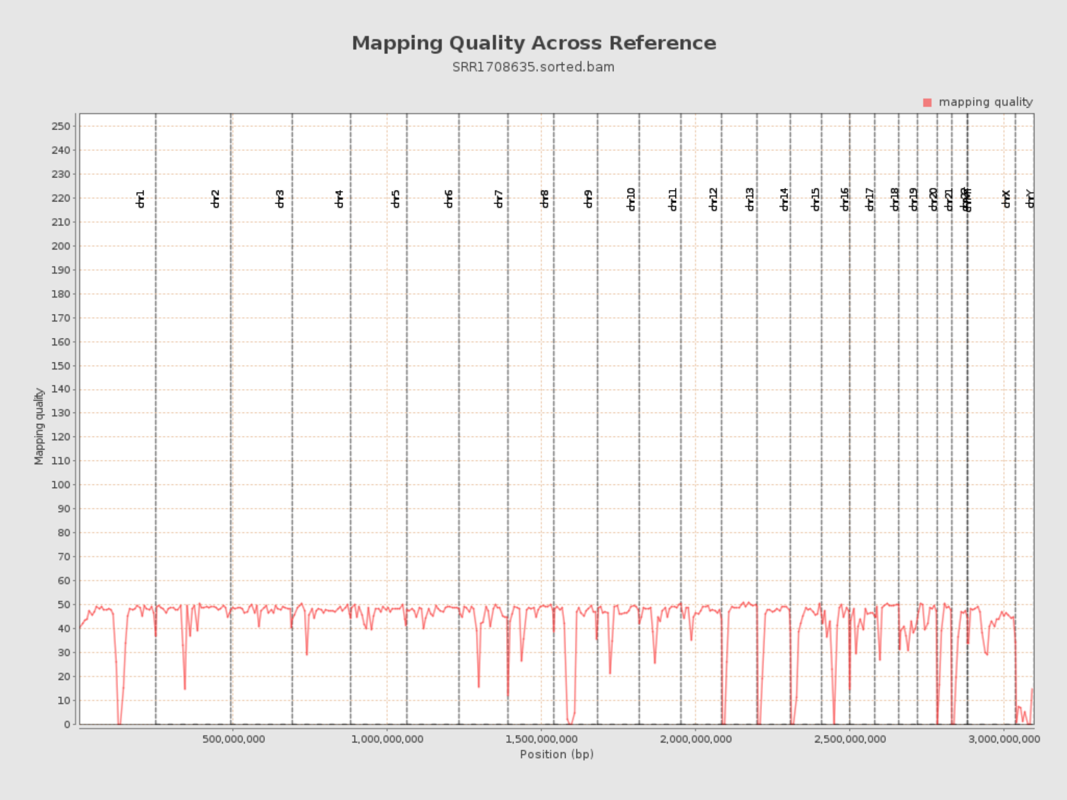
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram