Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:26:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708530.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_SRR1708530 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708530.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:26:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708530.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,202,887
Mapped reads	2,194,173 / 68.51%
Unmapped reads	1,008,714 / 31.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,289 / 0.04%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	85,224 / 2.66%
Duplication rate	2.67%
Clipped reads	539,913 / 16.86%

2.2. ACGT Content

Number/percentage of A's	29,735,809 / 28.63%
Number/percentage of C's	19,054,106 / 18.35%
Number/percentage of T's	33,332,835 / 32.09%
Number/percentage of G's	21,739,012 / 20.93%
Number/percentage of N's	1,435 / 0%
GC Percentage	39.28%

2.3. Coverage

Mean	0.0336

Standard Deviation	0.4011

2.4. Mapping Quality

Mean Mapping Quality	41.45

2.5. Mismatches and indels

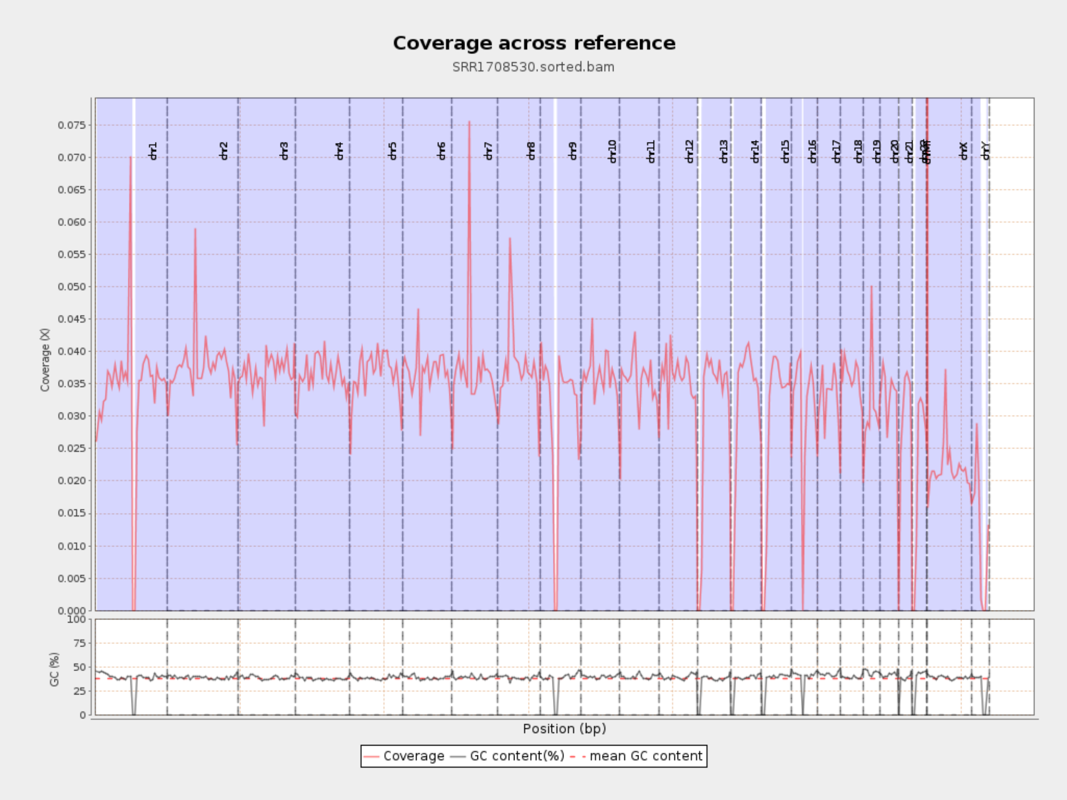
General error rate	0.53%
Mismatches	537,935
Insertions	5,872
Mapped reads with at least one insertion	0.27%
Deletions	13,400
Mapped reads with at least one deletion	0.61%
Homopolymer indels	46.31%

2.6. Chromosome stats

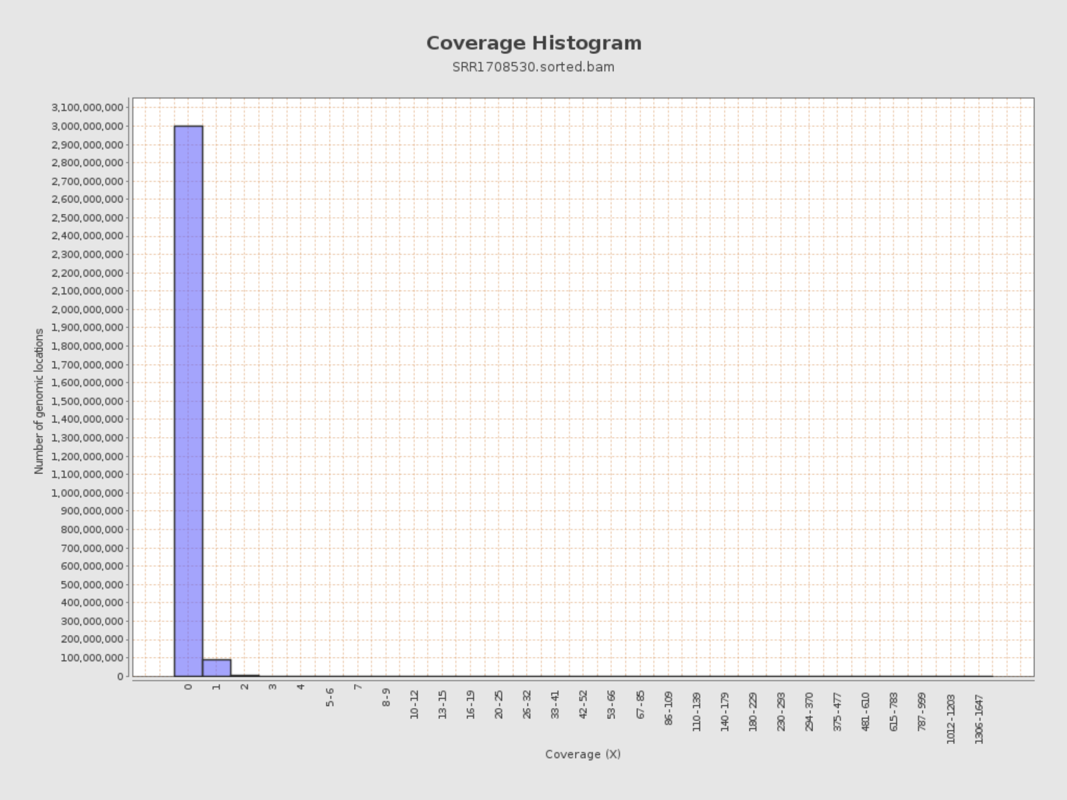
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8436127	0.0338	0.7992
chr2	243199373	9157470	0.0377	0.326
chr3	198022430	7307283	0.0369	0.2086
chr4	191154276	6938233	0.0363	0.2125
chr5	180915260	6650300	0.0368	0.2095
chr6	171115067	6316544	0.0369	0.2581
chr7	159138663	5976398	0.0376	0.506

chr8	146364022	5499429	0.0376	0.9115
chr9	141213431	4348072	0.0308	0.2504
chr10	135534747	4897369	0.0361	0.2835
chr11	135006516	4789360	0.0355	0.3735
chr12	133851895	4806787	0.0359	0.2104
chr13	115169878	3489778	0.0303	0.1885
chr14	107349540	3289332	0.0306	0.1997
chr15	102531392	2979821	0.0291	0.1834
chr16	90354753	2757142	0.0305	0.1982
chr17	81195210	2659348	0.0328	0.2882
chr18	78077248	2824709	0.0362	0.4314
chr19	59128983	1869504	0.0316	0.5189
chr20	63025520	2085596	0.0331	0.1966
chr21	48129895	1394372	0.029	0.2299
chr22	51304566	1095423	0.0214	0.1795
chrMT	16571	169610	10.2354	7.8554
chrX	155270560	3425556	0.0221	0.2036
chrY	59373566	720081	0.0121	0.1369

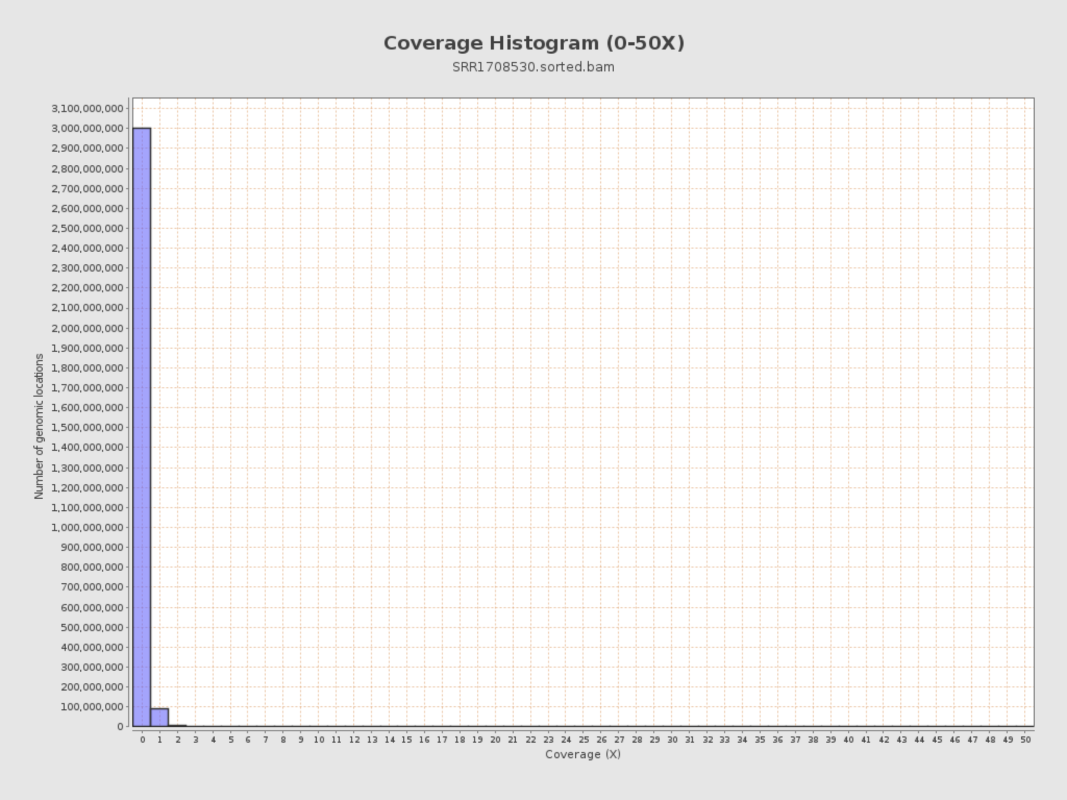
3. Results : Coverage across reference



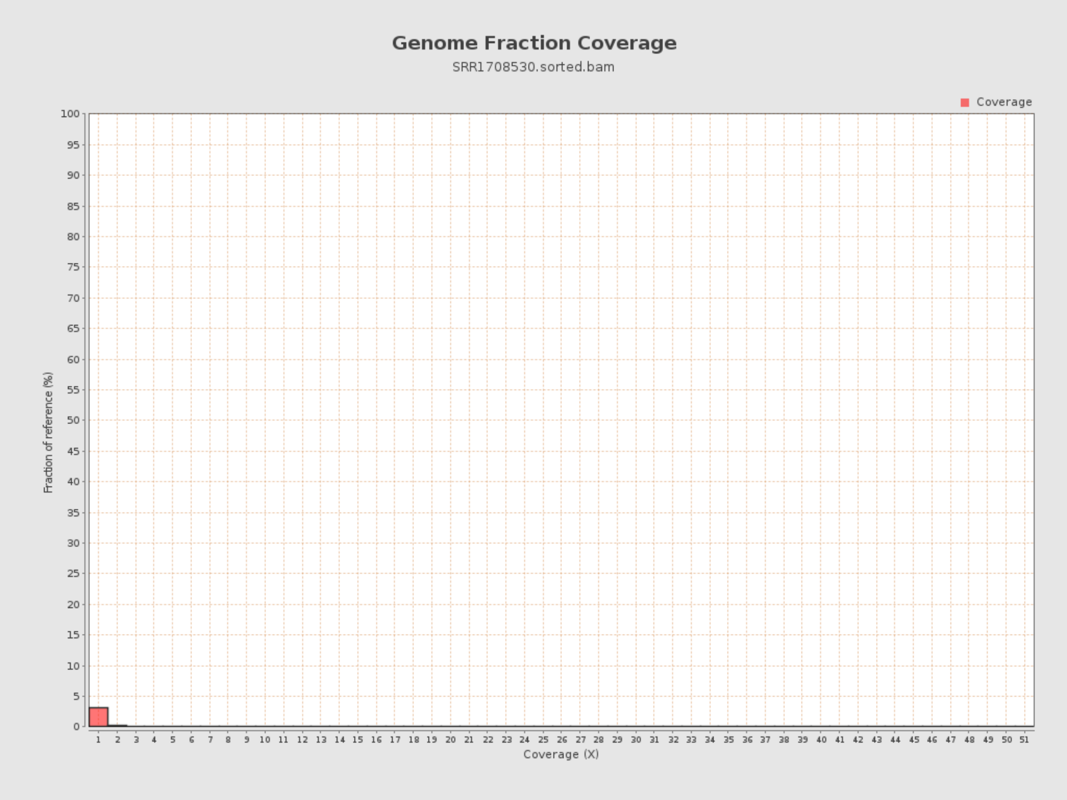
4. Results : Coverage Histogram



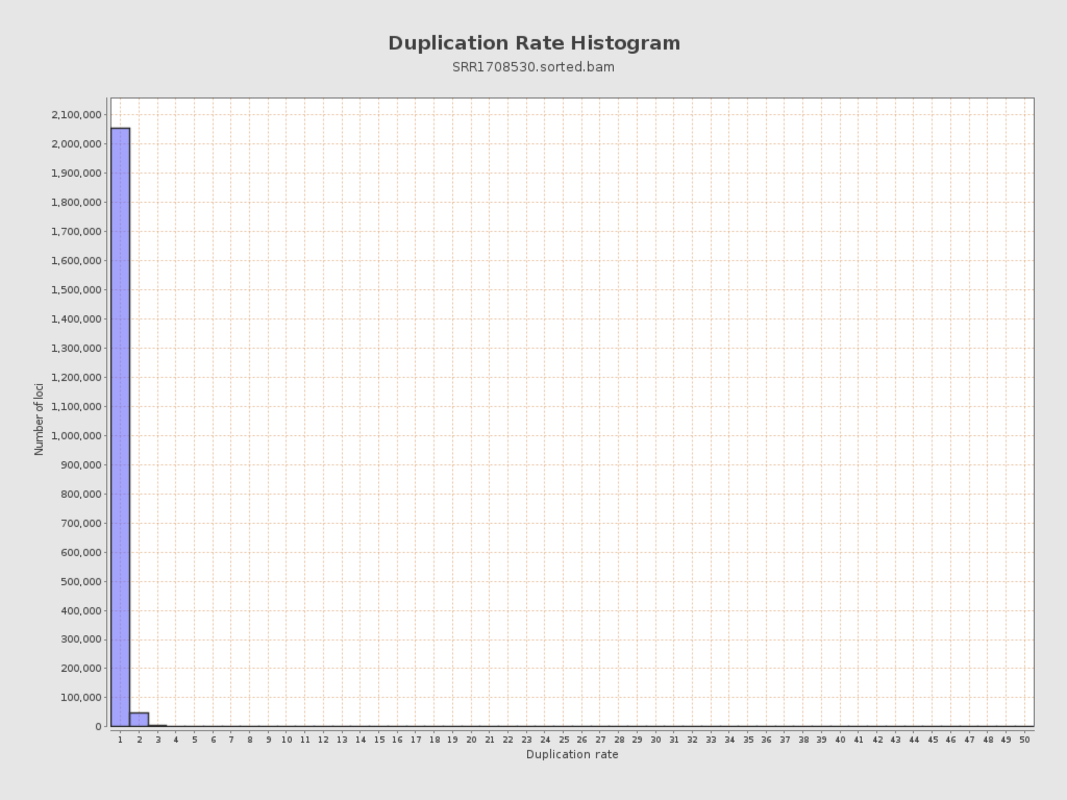
5. Results : Coverage Histogram (0-50X)



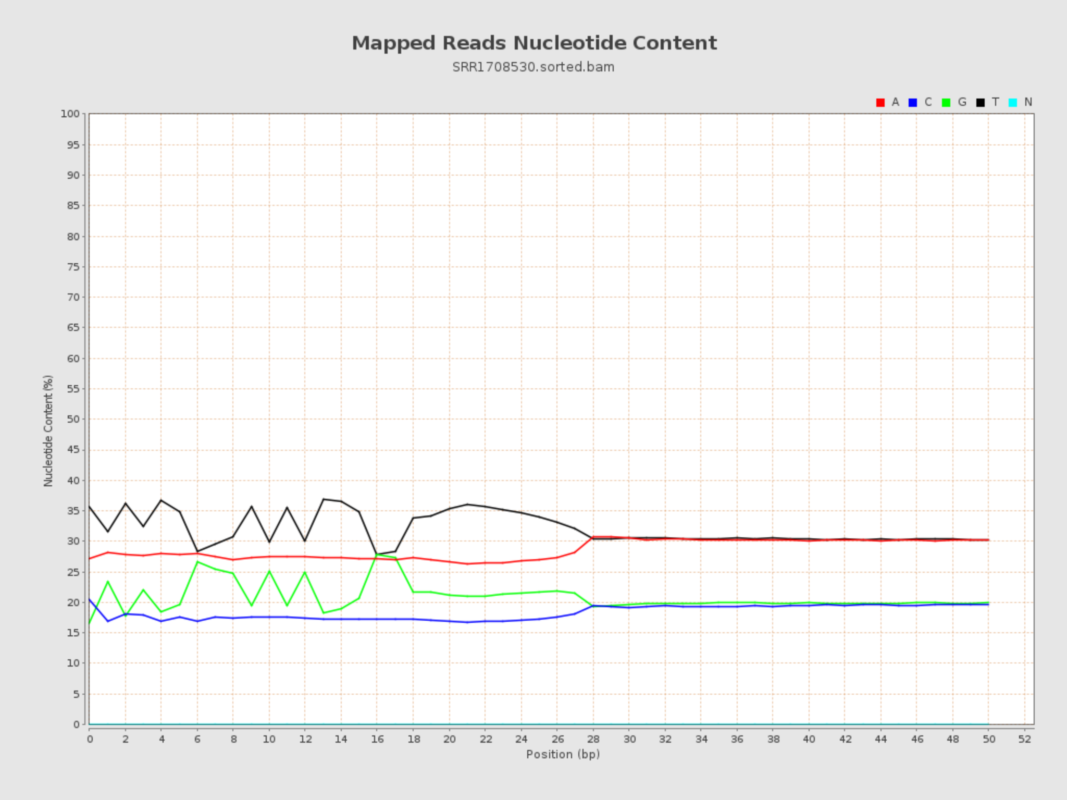
6. Results : Genome Fraction Coverage



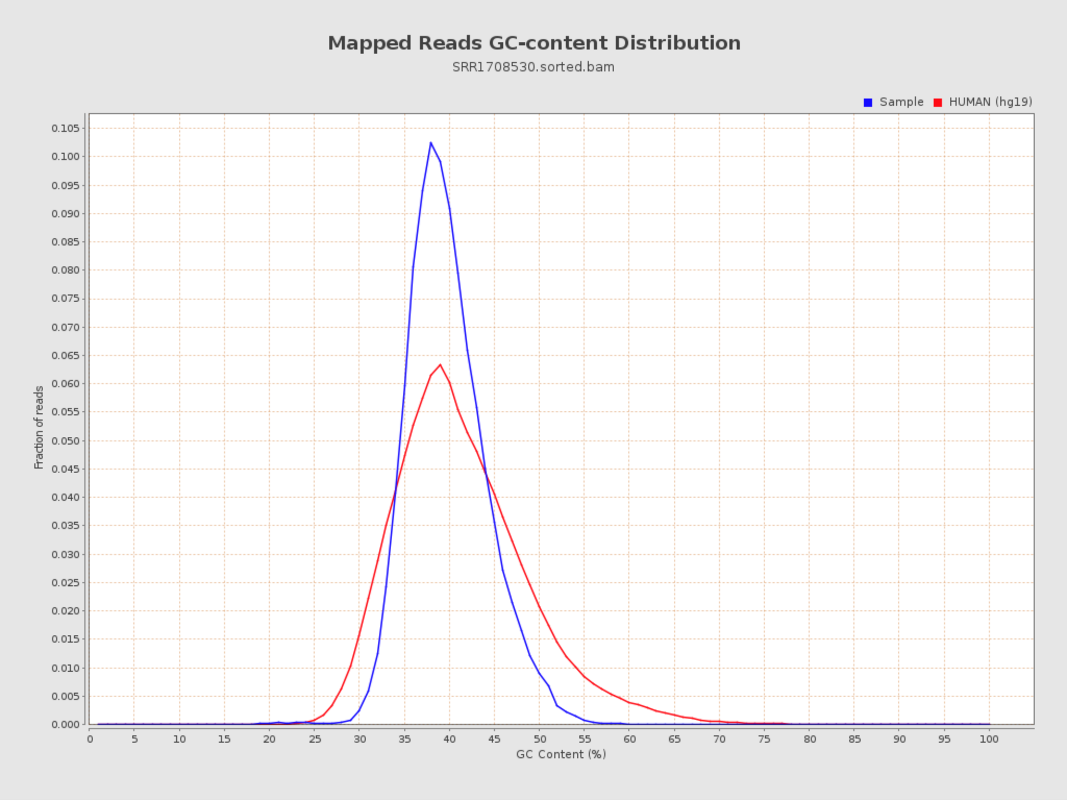
7. Results : Duplication Rate Histogram



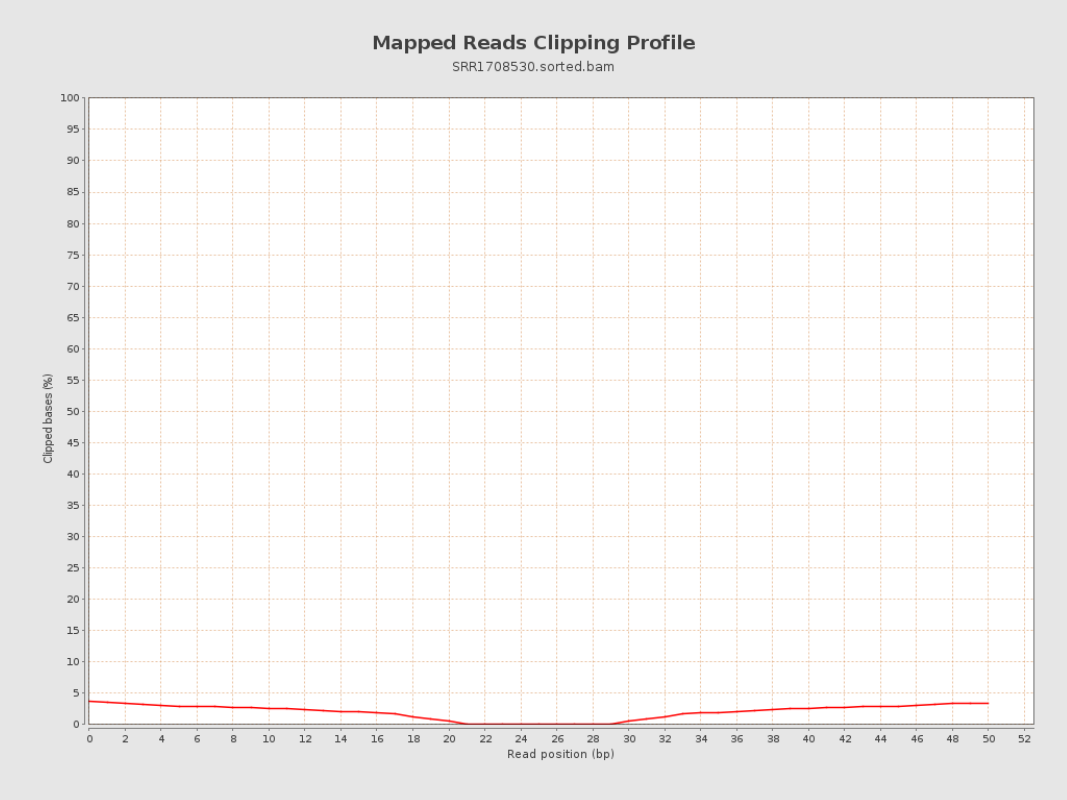
8. Results : Mapped Reads Nucleotide Content



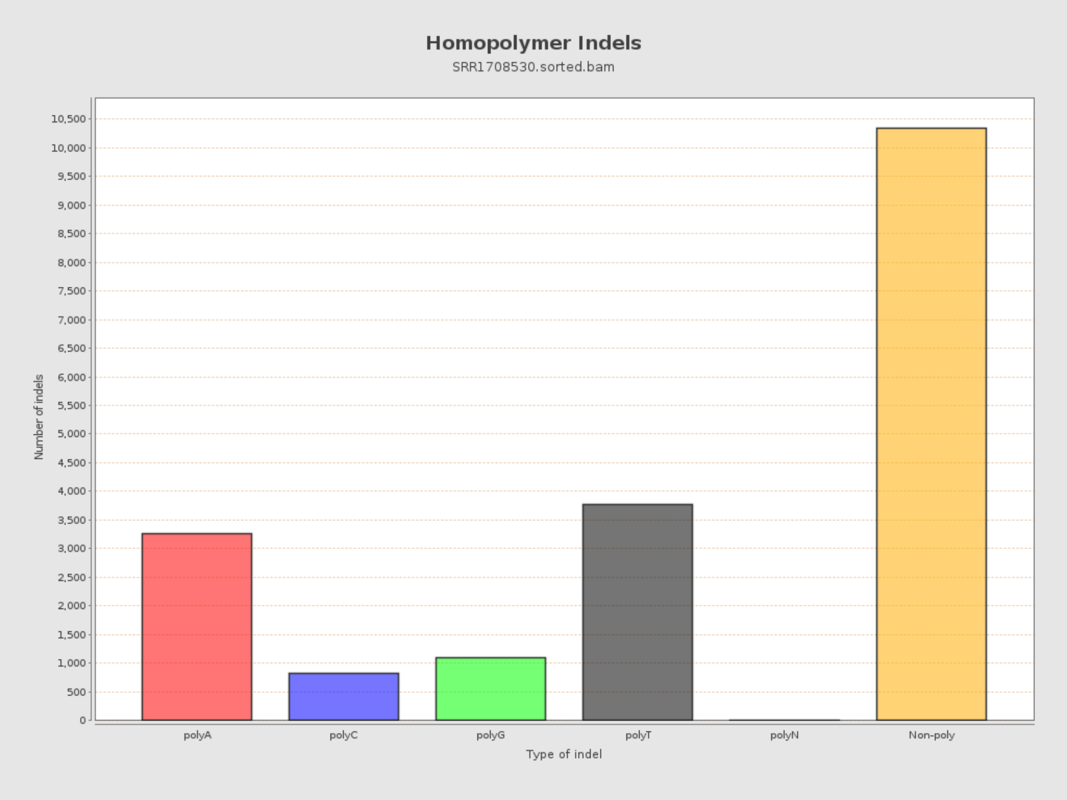
9. Results : Mapped Reads GC-content Distribution



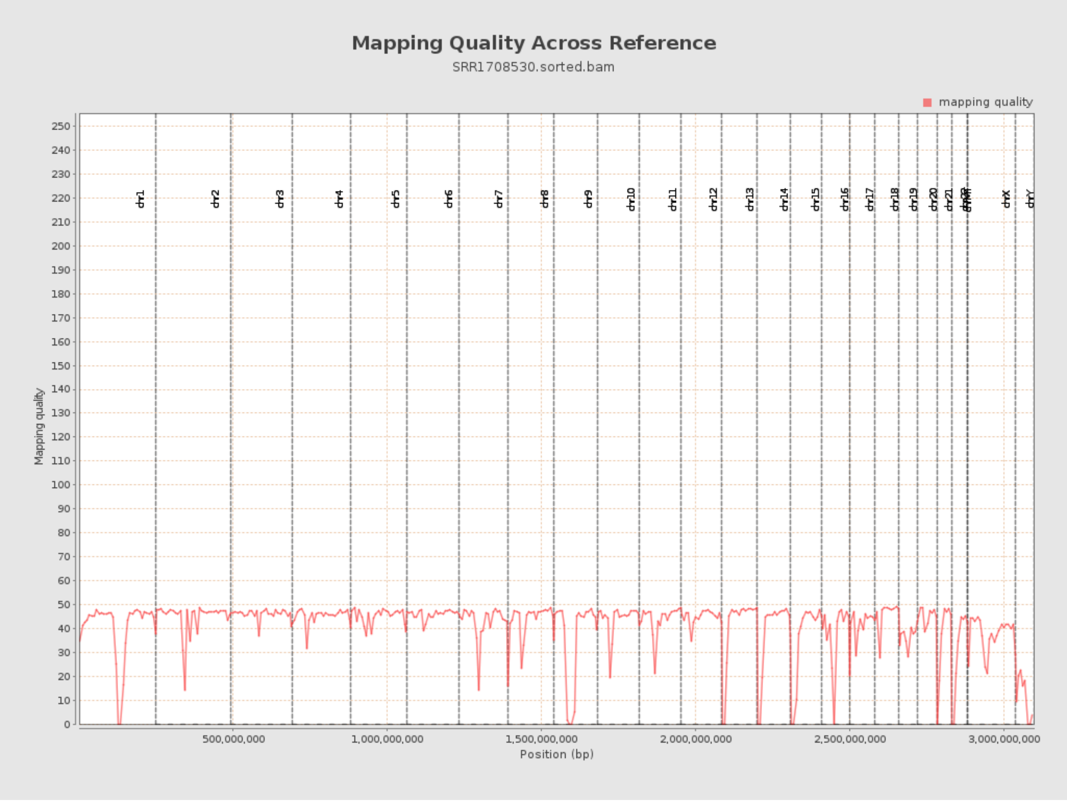
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram