Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:00:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708505.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_SRR1708505 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708505.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:00:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708505.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,953,672
Mapped reads	1,961,451 / 66.41%
Unmapped reads	992,221 / 33.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	378 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	113,164 / 3.83%
Duplication rate	4.34%
Clipped reads	431,965 / 14.62%

2.2. ACGT Content

Number/percentage of A's	26,573,857 / 28.53%
Number/percentage of C's	17,026,449 / 18.28%
Number/percentage of T's	30,104,014 / 32.32%
Number/percentage of G's	19,440,964 / 20.87%
Number/percentage of N's	1,308 / 0%
GC Percentage	39.15%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.3312

2.4. Mapping Quality

Mean Mapping Quality	40.54

2.5. Mismatches and indels

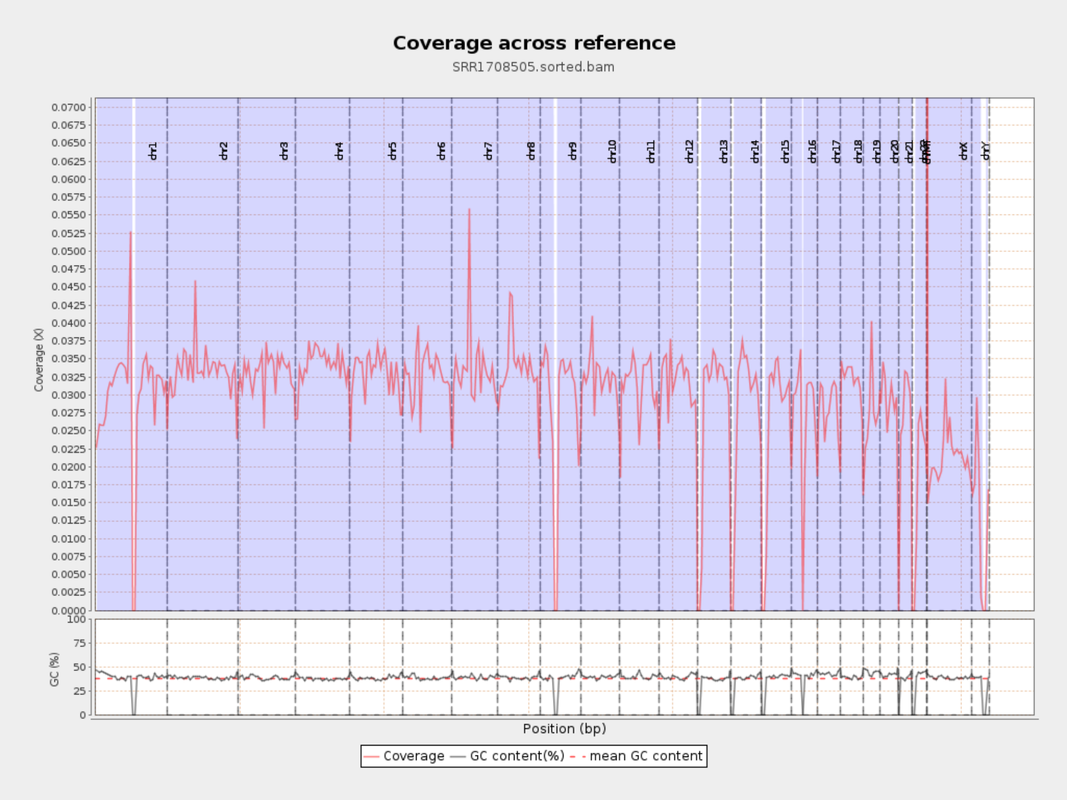
General error rate	0.52%
Mismatches	474,997
Insertions	4,730
Mapped reads with at least one insertion	0.24%
Deletions	13,938
Mapped reads with at least one deletion	0.71%
Homopolymer indels	48.39%

2.6. Chromosome stats

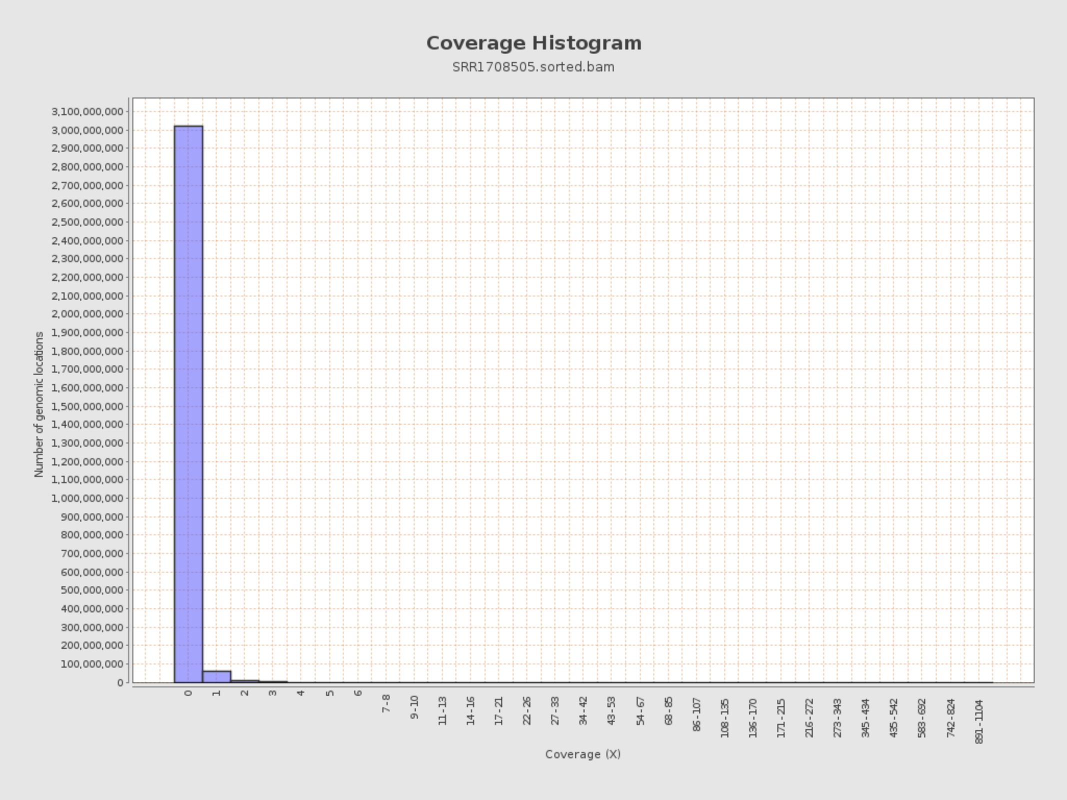
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7411767	0.0297	0.5206
chr2	243199373	8139708	0.0335	0.4822
chr3	198022430	6575253	0.0332	0.2252
chr4	191154276	6518070	0.0341	0.2359
chr5	180915260	6018676	0.0333	0.2226
chr6	171115067	5602967	0.0327	0.2808
chr7	159138663	5340350	0.0336	0.3782

chr8	146364022	4921202	0.0336	0.6326
chr9	141213431	4011078	0.0284	0.2476
chr10	135534747	4383339	0.0323	0.2514
chr11	135006516	4262241	0.0316	0.2878
chr12	133851895	4287510	0.032	0.2204
chr13	115169878	3176117	0.0276	0.2285
chr14	107349540	2912809	0.0271	0.2044
chr15	102531392	2612656	0.0255	0.1953
chr16	90354753	2395251	0.0265	0.202
chr17	81195210	2272280	0.028	0.2481
chr18	78077248	2534985	0.0325	0.37
chr19	59128983	1626307	0.0275	0.3621
chr20	63025520	1835200	0.0291	0.2086
chr21	48129895	1259053	0.0262	0.2133
chr22	51304566	898018	0.0175	0.1655
chrMT	16571	91411	5.5163	3.7297
chrX	155270560	3325499	0.0214	0.1983
chrY	59373566	755688	0.0127	0.1541

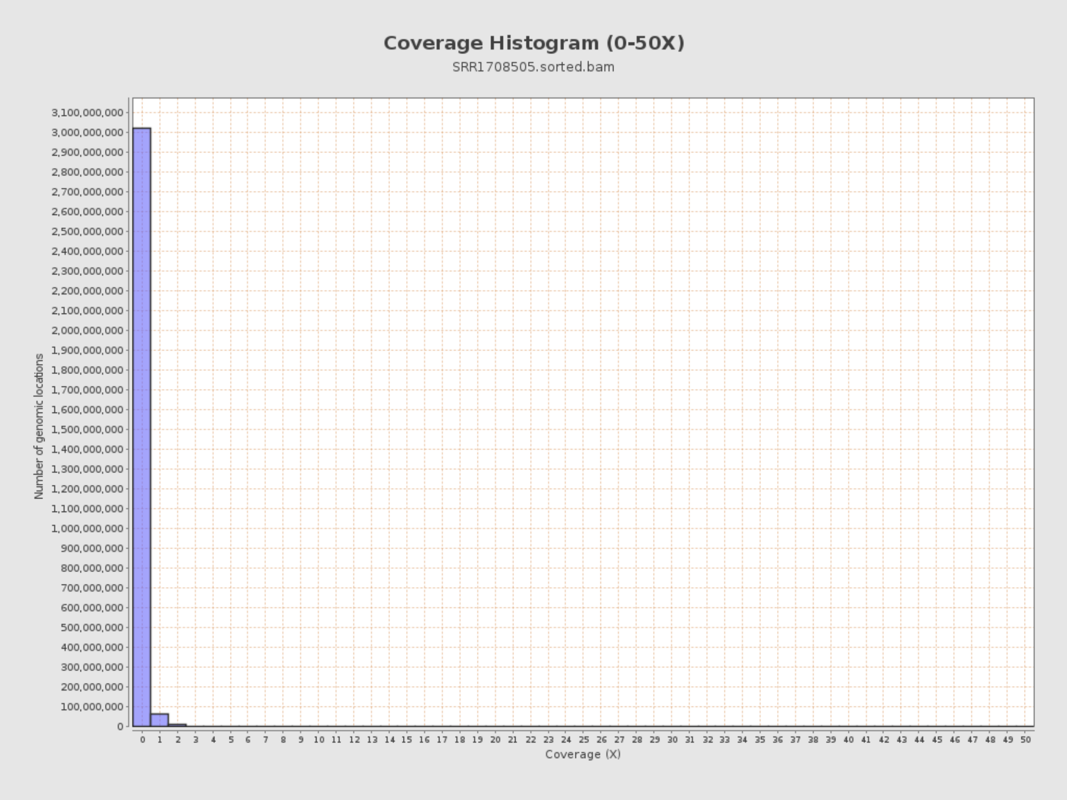
3. Results : Coverage across reference



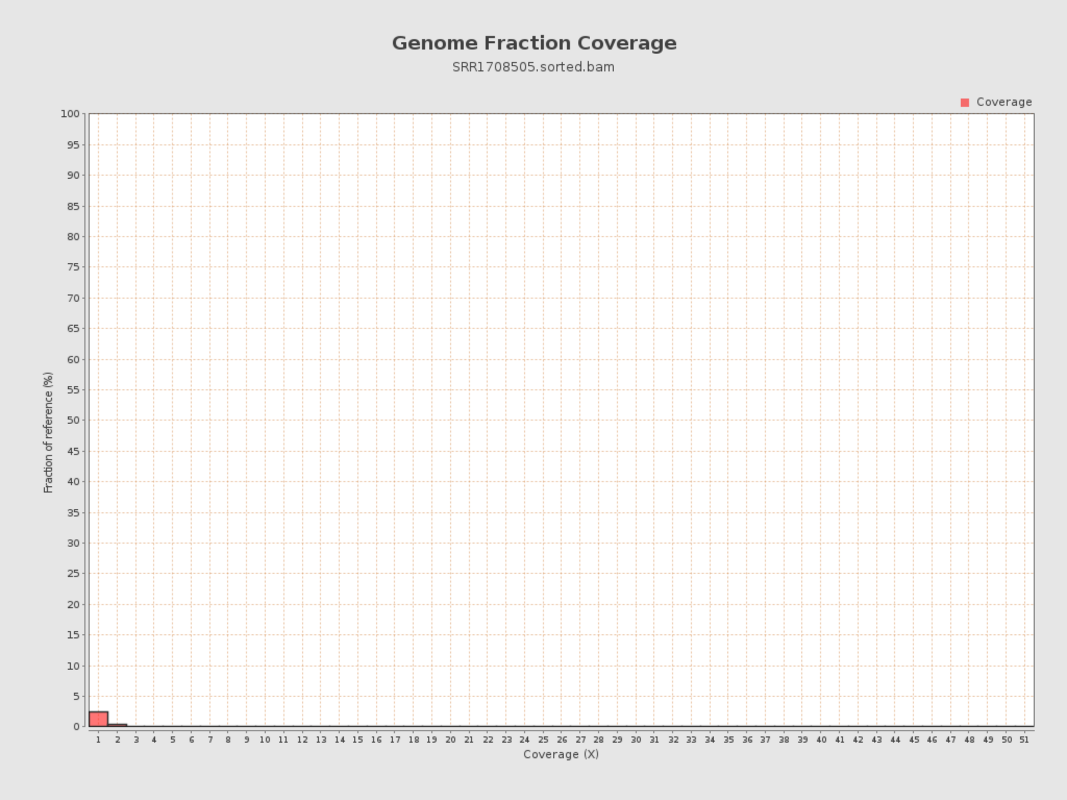
4. Results : Coverage Histogram



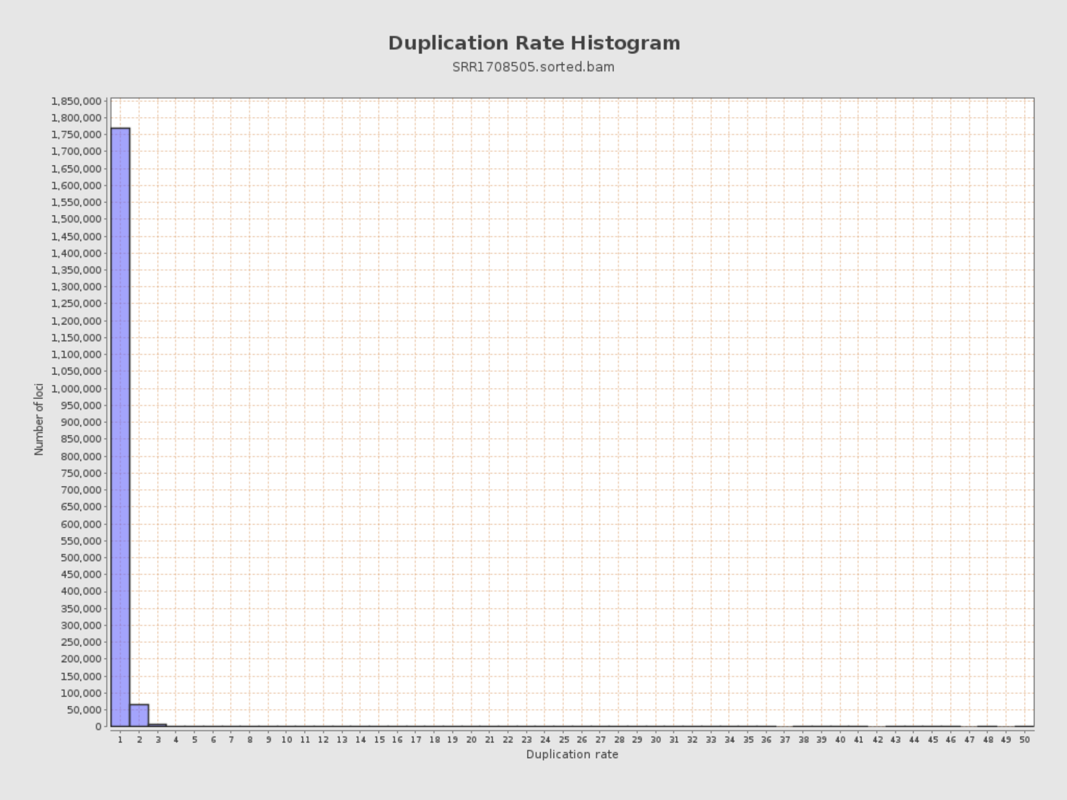
5. Results : Coverage Histogram (0-50X)



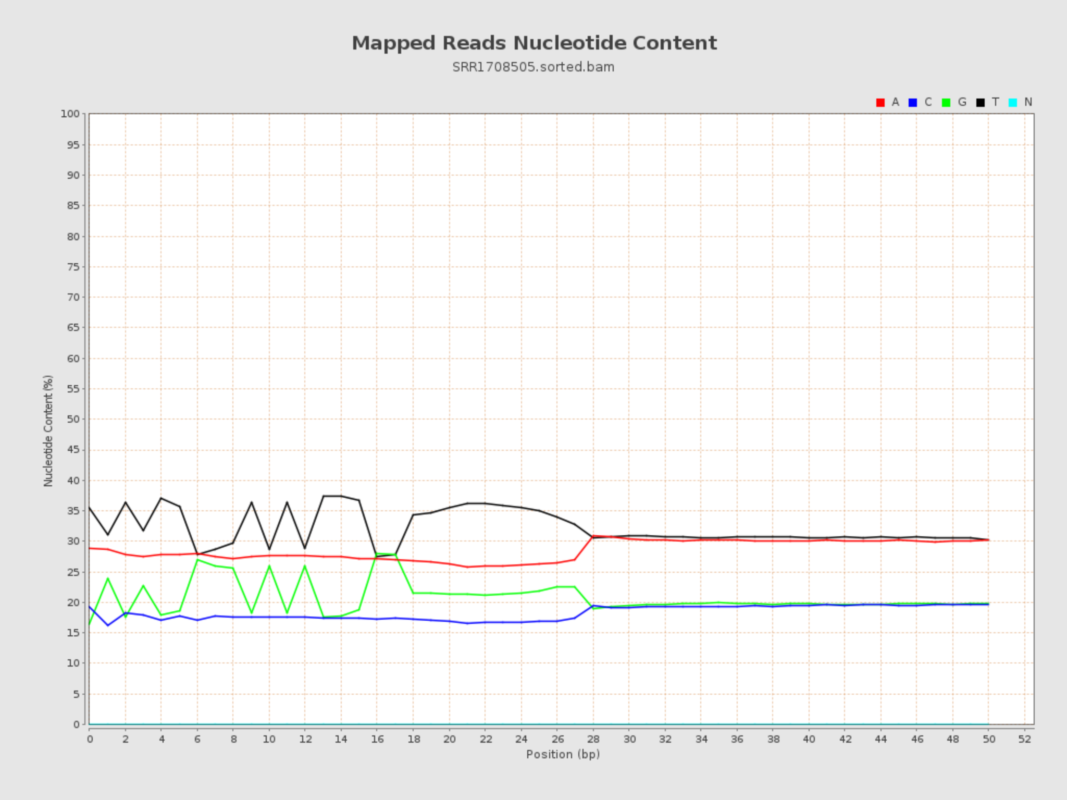
6. Results : Genome Fraction Coverage



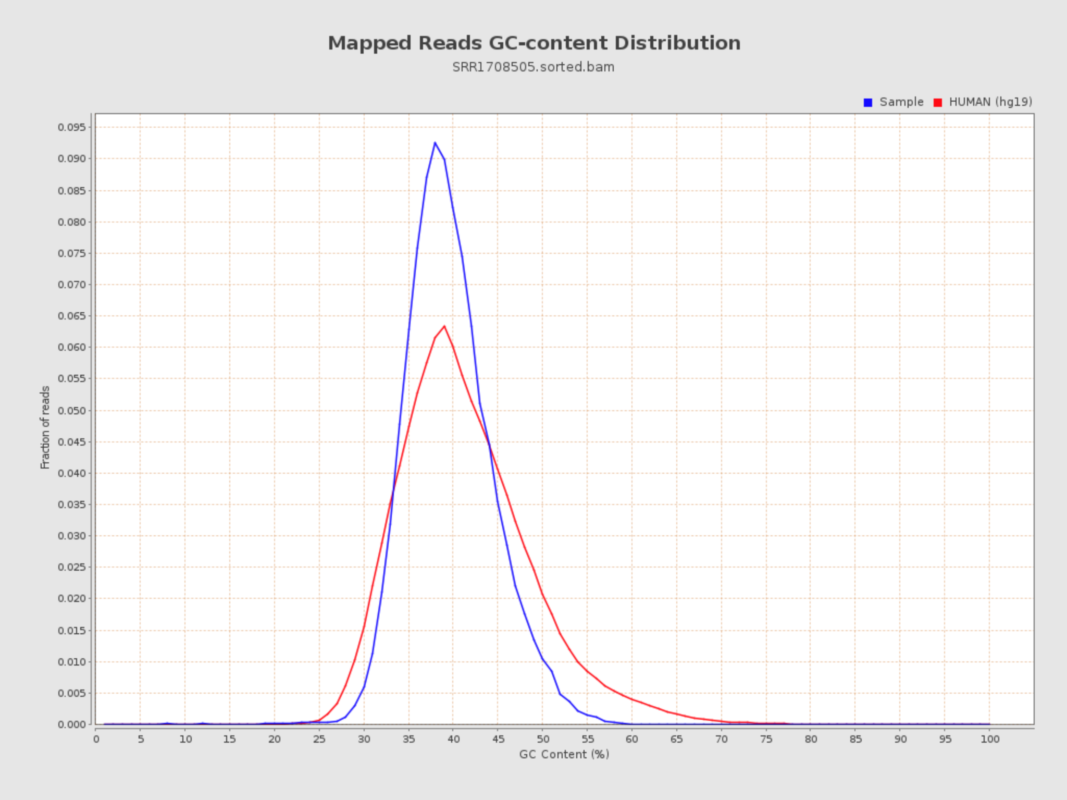
7. Results : Duplication Rate Histogram



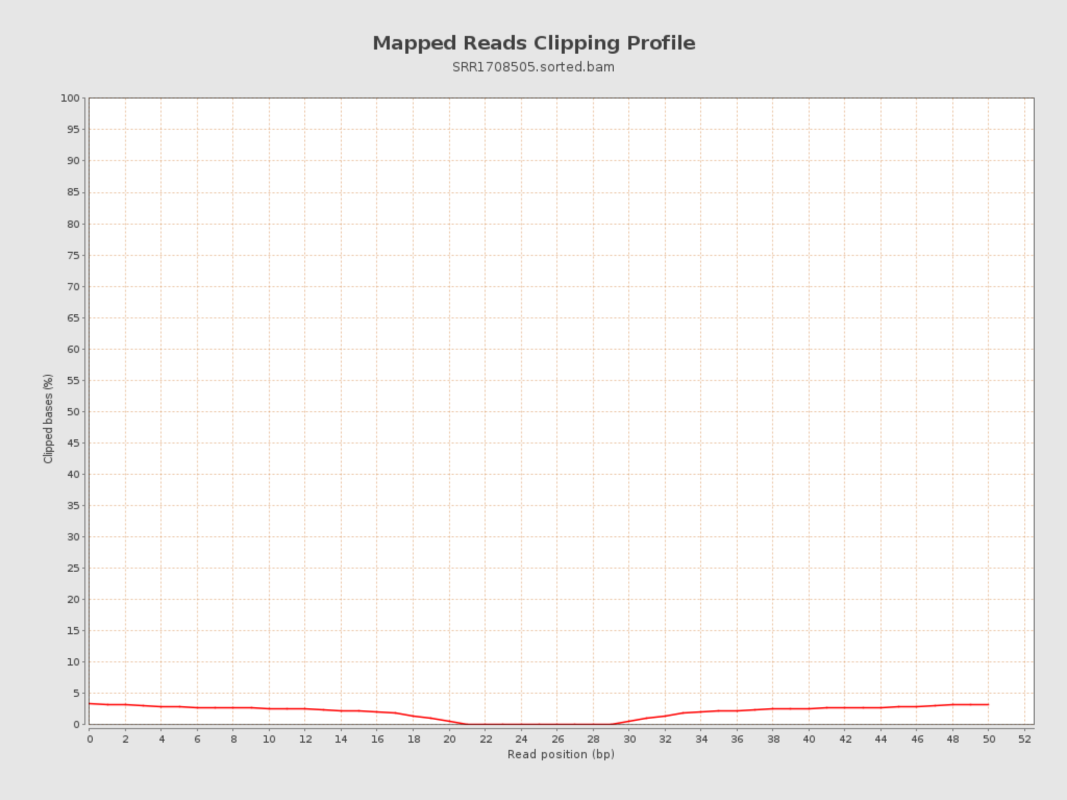
8. Results : Mapped Reads Nucleotide Content



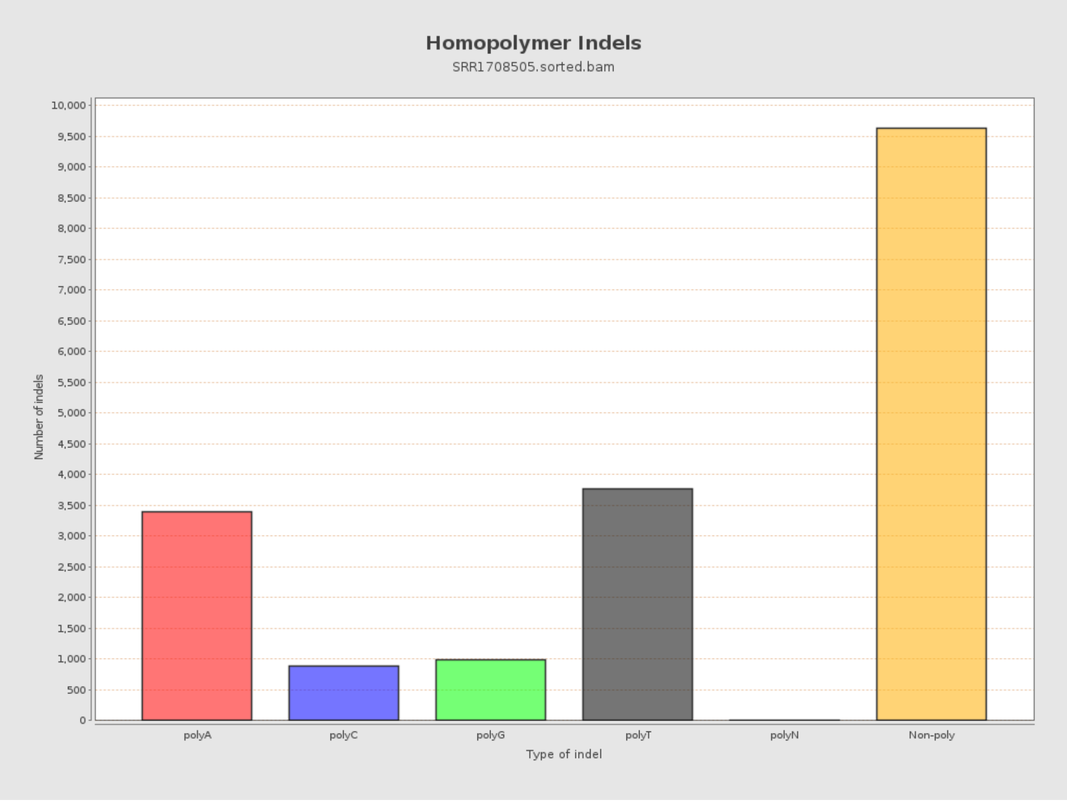
9. Results : Mapped Reads GC-content Distribution



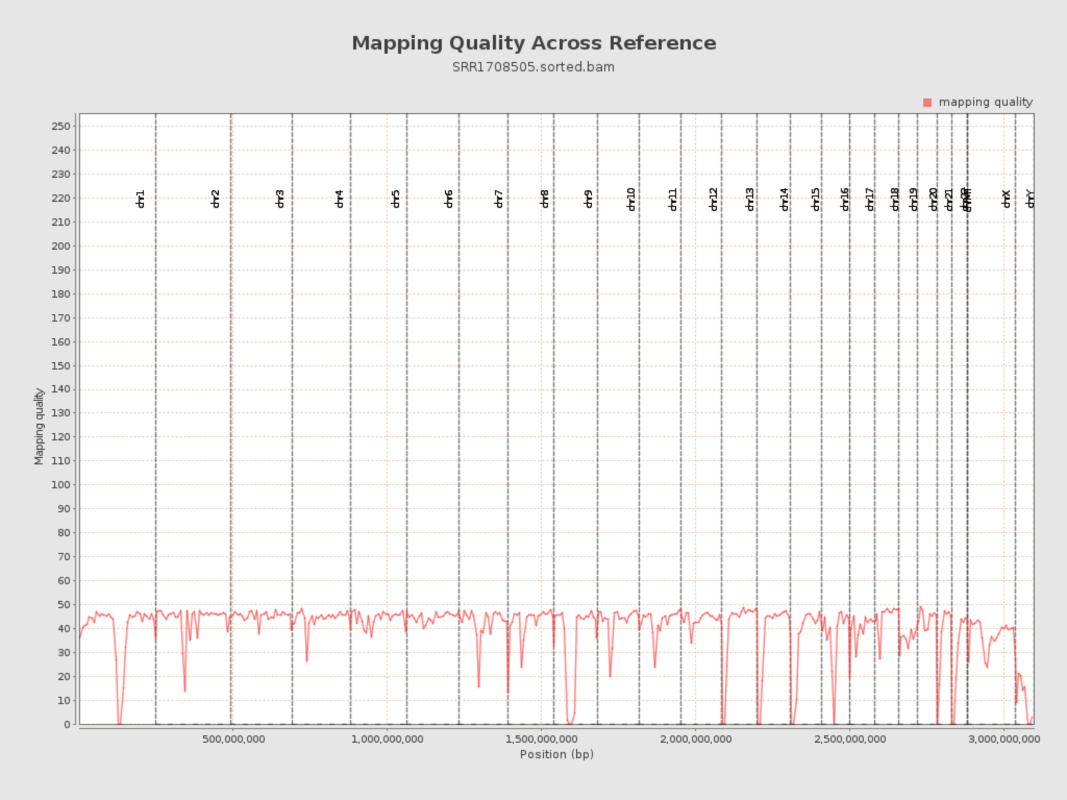
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram