Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:41:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708531.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_SRR1708531 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708531.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:41:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708531.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,824,949
Mapped reads	1,984,175 / 70.24%
Unmapped reads	840,774 / 29.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,388 / 0.05%
Read min/max/mean length	30 / 51 / 51.02
Duplicated reads (estimated)	71,256 / 2.52%
Duplication rate	2.49%
Clipped reads	463,469 / 16.41%

2.2. ACGT Content

Number/percentage of A's	27,232,327 / 28.83%
Number/percentage of C's	17,563,380 / 18.59%
Number/percentage of T's	30,072,165 / 31.84%
Number/percentage of G's	19,587,819 / 20.74%
Number/percentage of N's	1,242 / 0%
GC Percentage	39.33%

2.3. Coverage

Mean	0.0305

Standard Deviation	0.3485

2.4. Mapping Quality

Mean Mapping Quality	41.35

2.5. Mismatches and indels

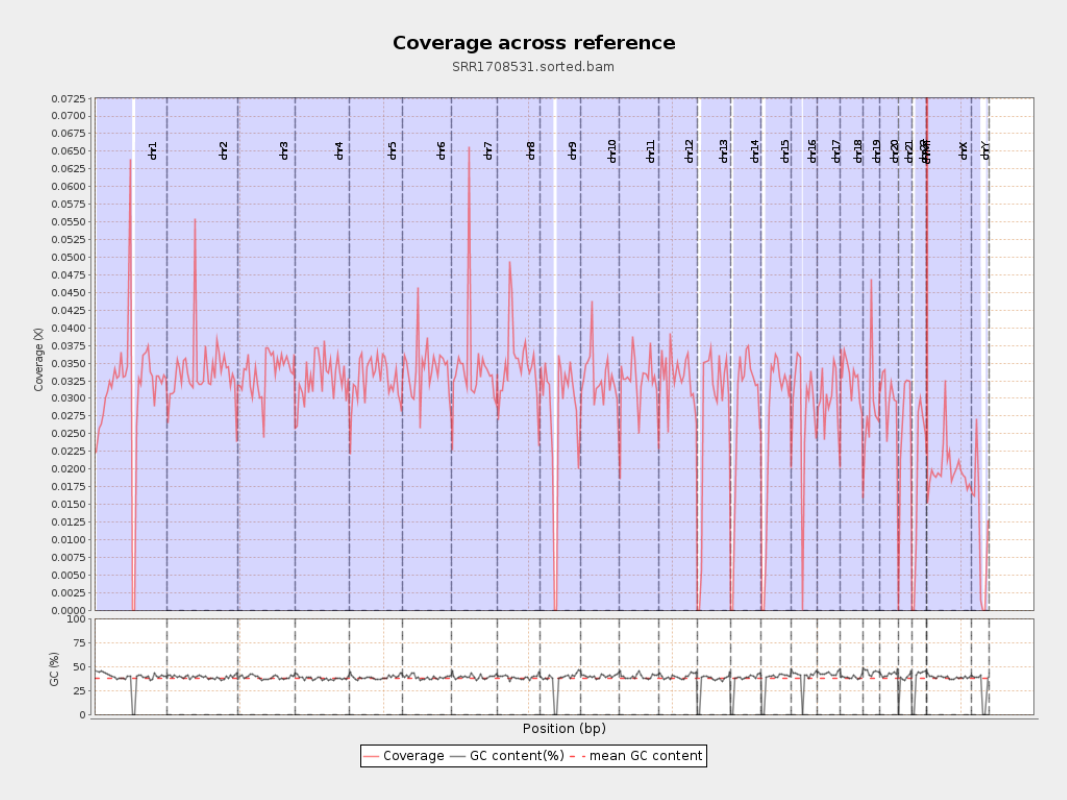
General error rate	0.53%
Mismatches	489,767
Insertions	5,637
Mapped reads with at least one insertion	0.28%
Deletions	12,475
Mapped reads with at least one deletion	0.63%
Homopolymer indels	46.11%

2.6. Chromosome stats

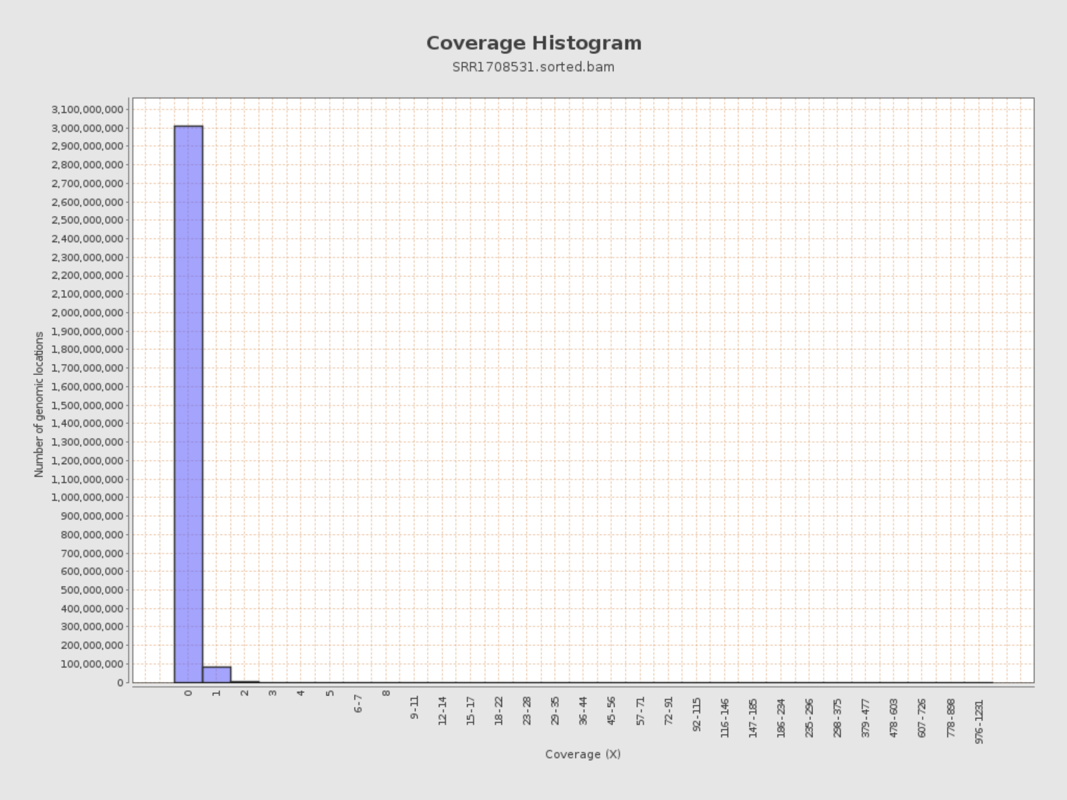
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7713585	0.0309	0.6975
chr2	243199373	8232849	0.0339	0.3029
chr3	198022430	6654949	0.0336	0.1969
chr4	191154276	6266755	0.0328	0.197
chr5	180915260	5945715	0.0329	0.1954
chr6	171115067	5831151	0.0341	0.2547
chr7	159138663	5477413	0.0344	0.428

chr8	146364022	5100854	0.0349	0.7035
chr9	141213431	3910822	0.0277	0.2388
chr10	135534747	4434728	0.0327	0.263
chr11	135006516	4417103	0.0327	0.3102
chr12	133851895	4407984	0.0329	0.2004
chr13	115169878	3187393	0.0277	0.1807
chr14	107349540	2956042	0.0275	0.186
chr15	102531392	2707086	0.0264	0.1732
chr16	90354753	2507222	0.0277	0.1916
chr17	81195210	2415572	0.0298	0.2534
chr18	78077248	2570745	0.0329	0.4251
chr19	59128983	1712902	0.029	0.5054
chr20	63025520	1877356	0.0298	0.1866
chr21	48129895	1242823	0.0258	0.2105
chr22	51304566	974616	0.019	0.165
chrMT	16571	143469	8.6578	6.6358
chrX	155270560	3118614	0.0201	0.1787
chrY	59373566	668208	0.0113	0.1291

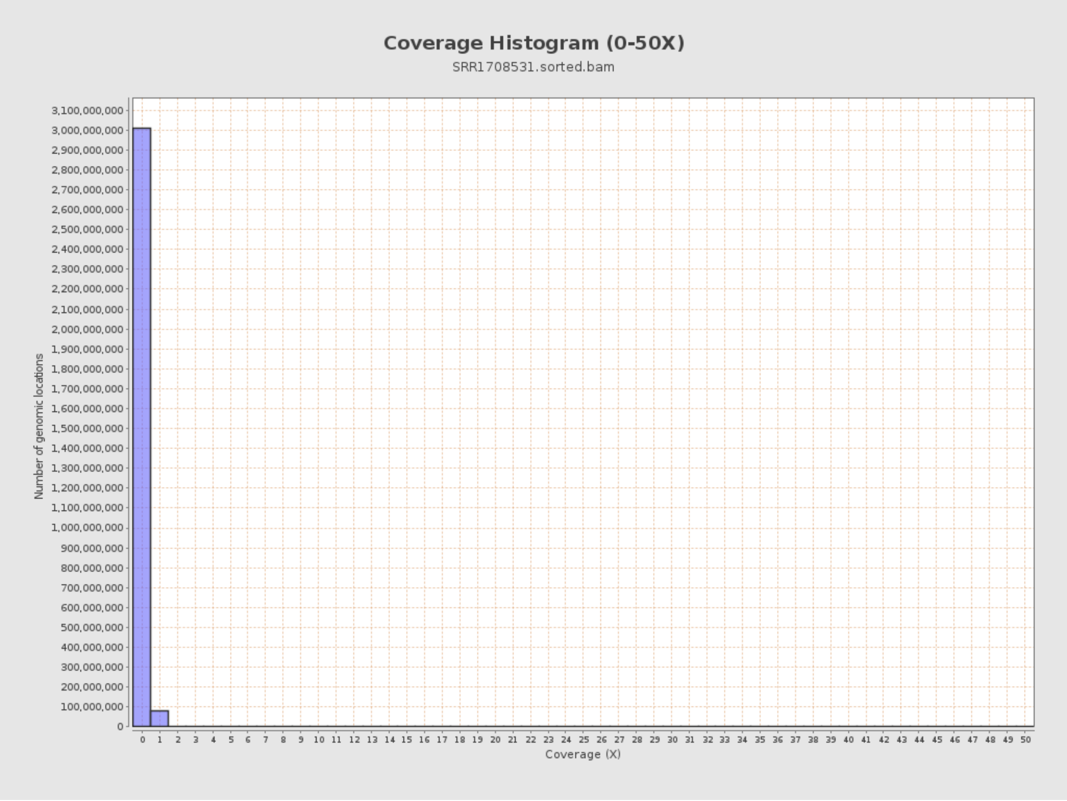
3. Results : Coverage across reference



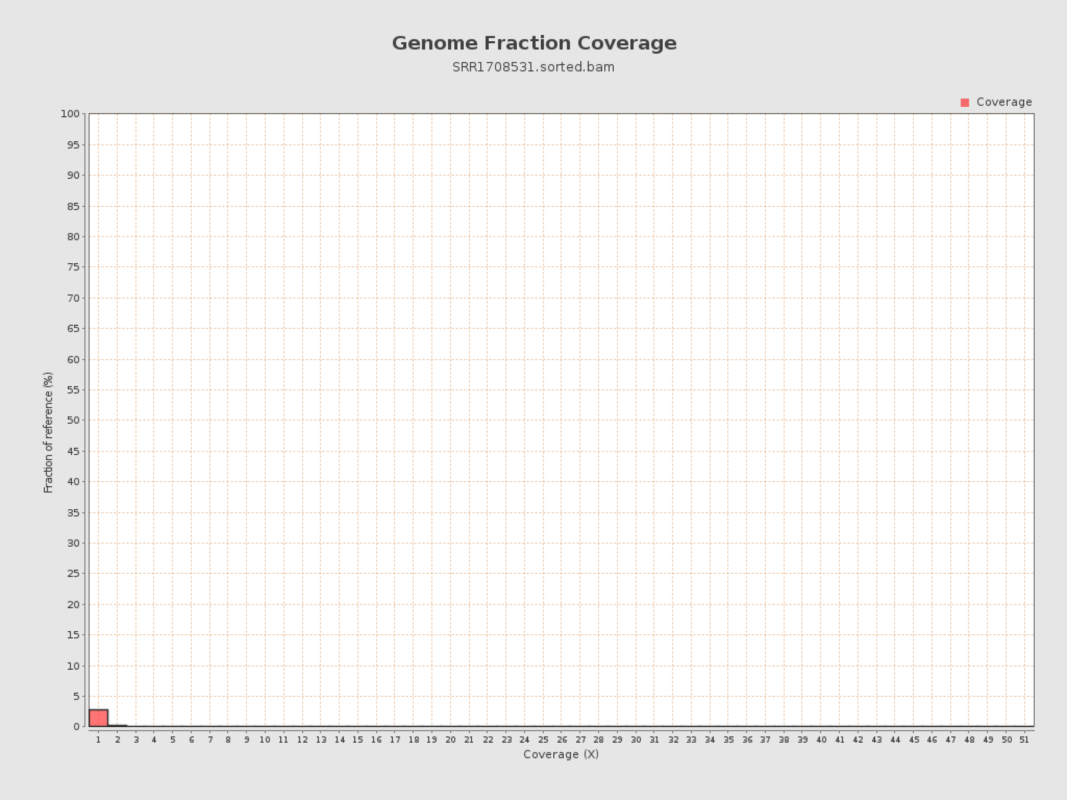
4. Results : Coverage Histogram



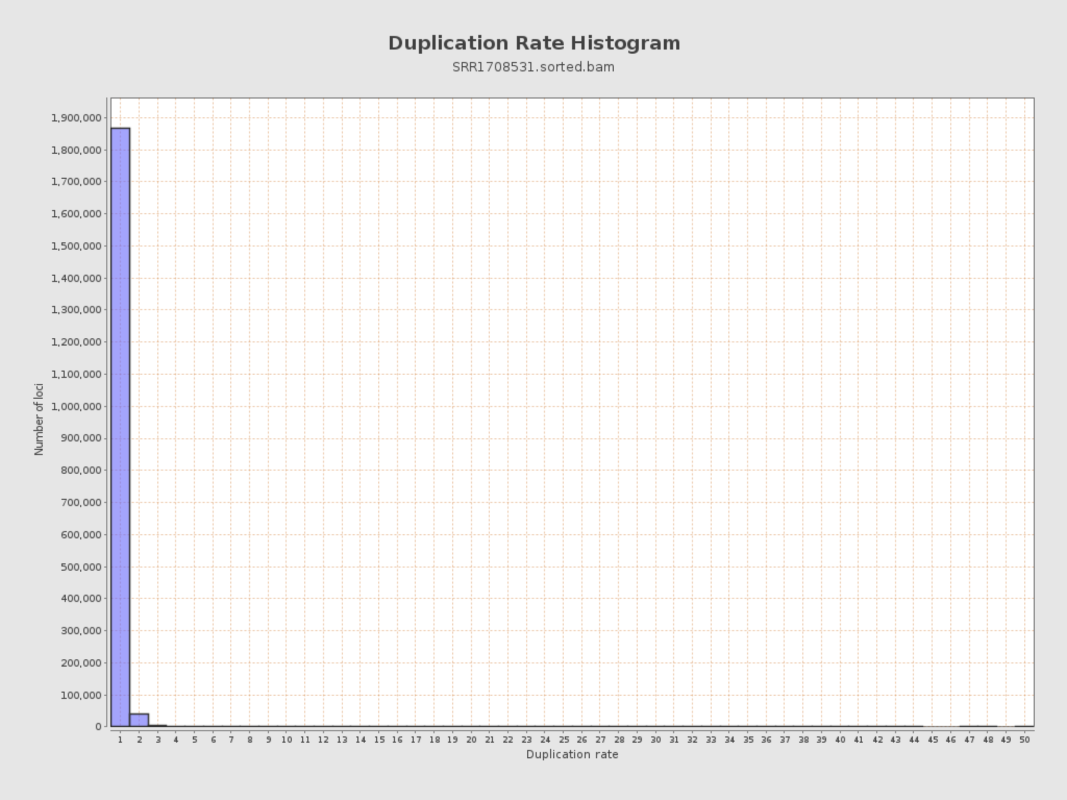
5. Results : Coverage Histogram (0-50X)



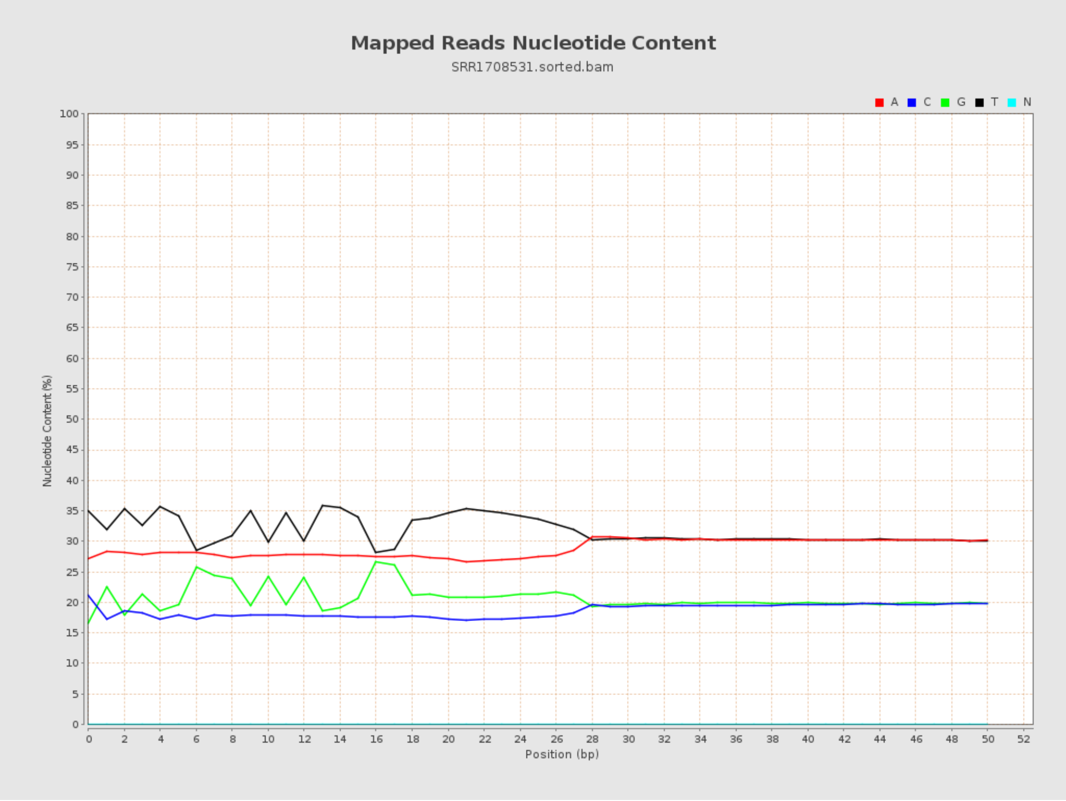
6. Results : Genome Fraction Coverage



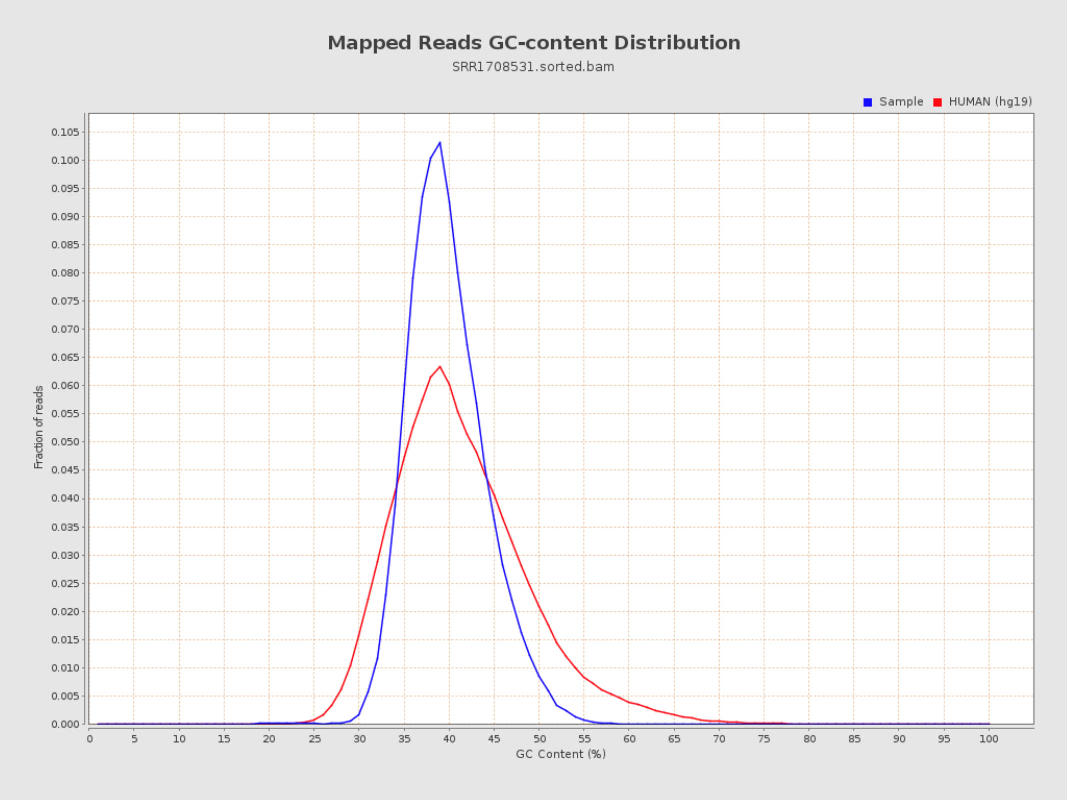
7. Results : Duplication Rate Histogram



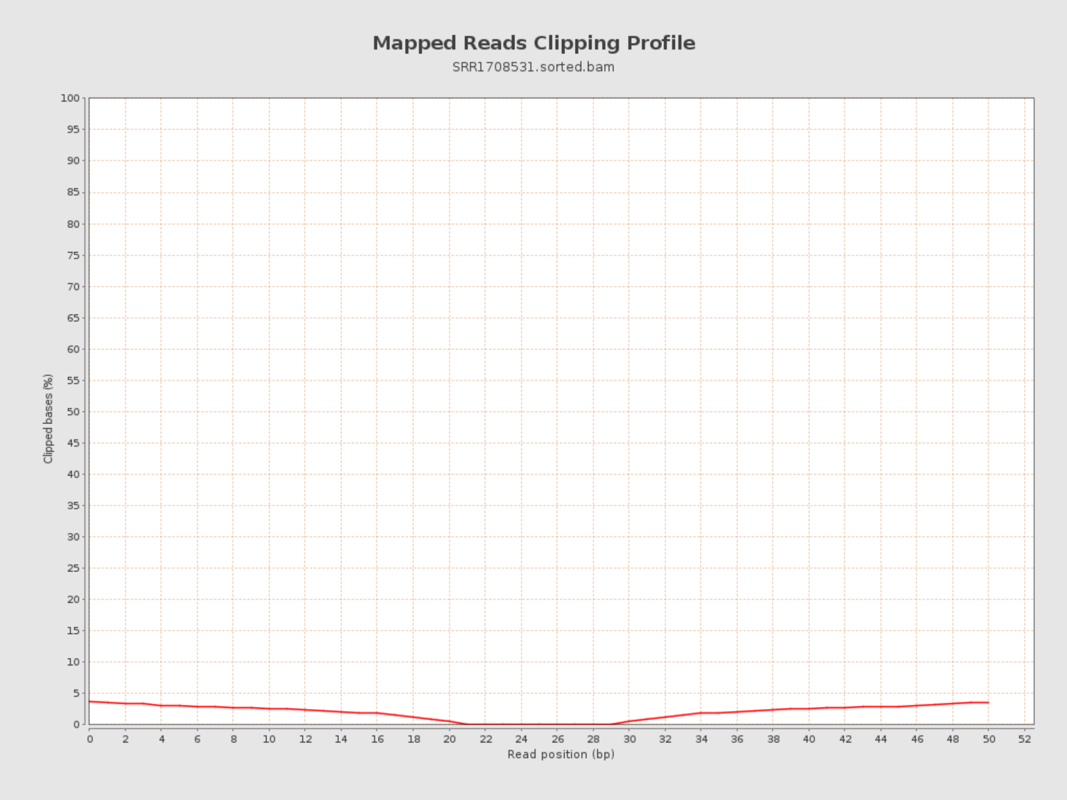
8. Results : Mapped Reads Nucleotide Content



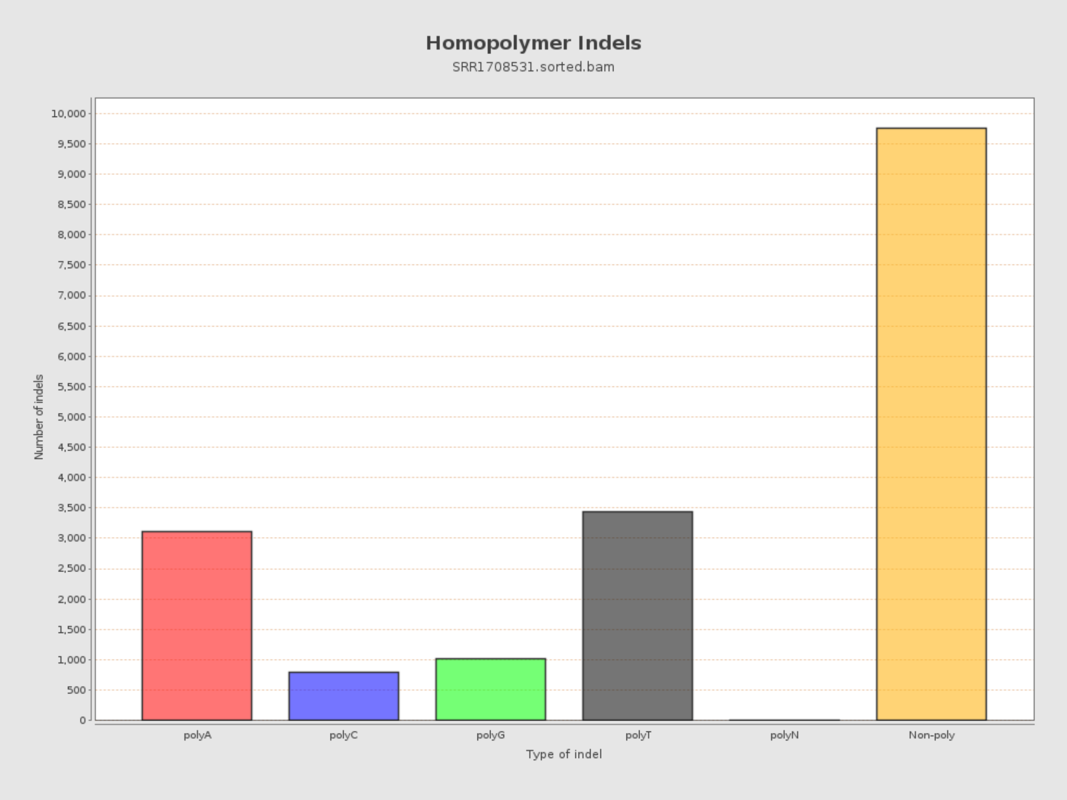
9. Results : Mapped Reads GC-content Distribution



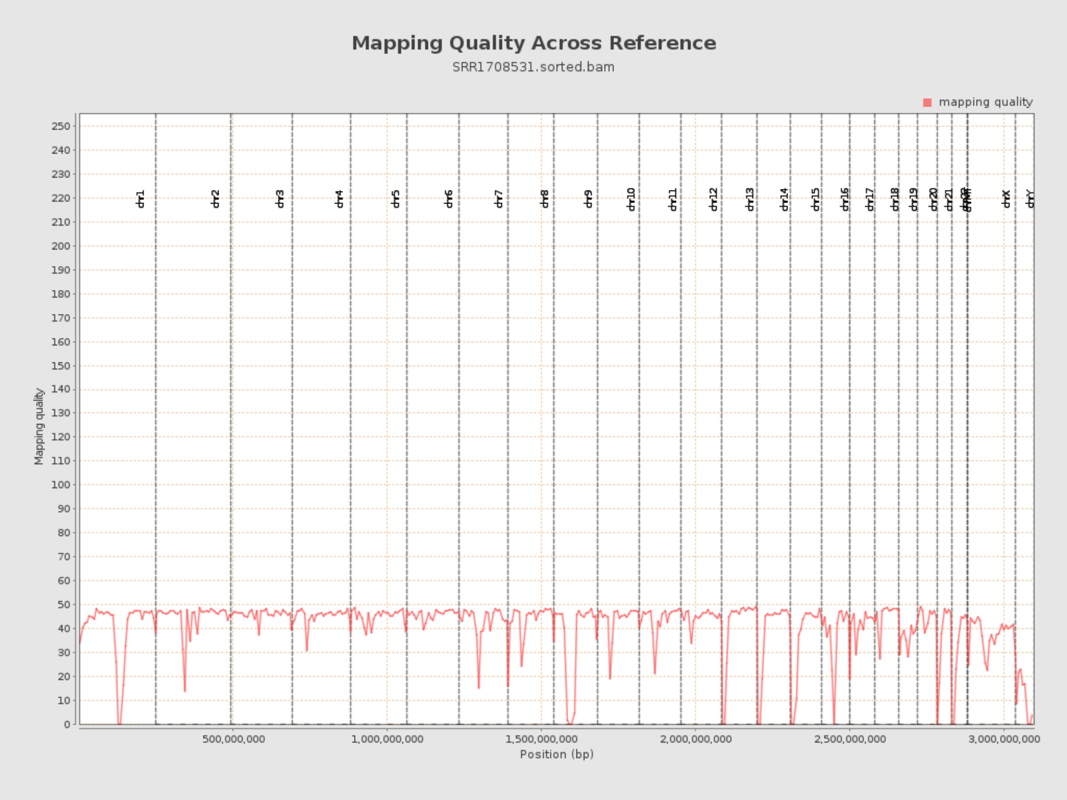
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram