Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:14:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708510.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_SRR1708510 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708510.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:14:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708510.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,067,162
Mapped reads	2,032,942 / 66.28%
Unmapped reads	1,034,220 / 33.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	381 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	113,481 / 3.7%
Duplication rate	4.19%
Clipped reads	443,865 / 14.47%

2.2. ACGT Content

Number/percentage of A's	27,592,802 / 28.56%
Number/percentage of C's	17,701,383 / 18.32%
Number/percentage of T's	31,160,852 / 32.26%
Number/percentage of G's	20,144,118 / 20.85%
Number/percentage of N's	1,431 / 0%
GC Percentage	39.18%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.3375

2.4. Mapping Quality

Mean Mapping Quality	40.54

2.5. Mismatches and indels

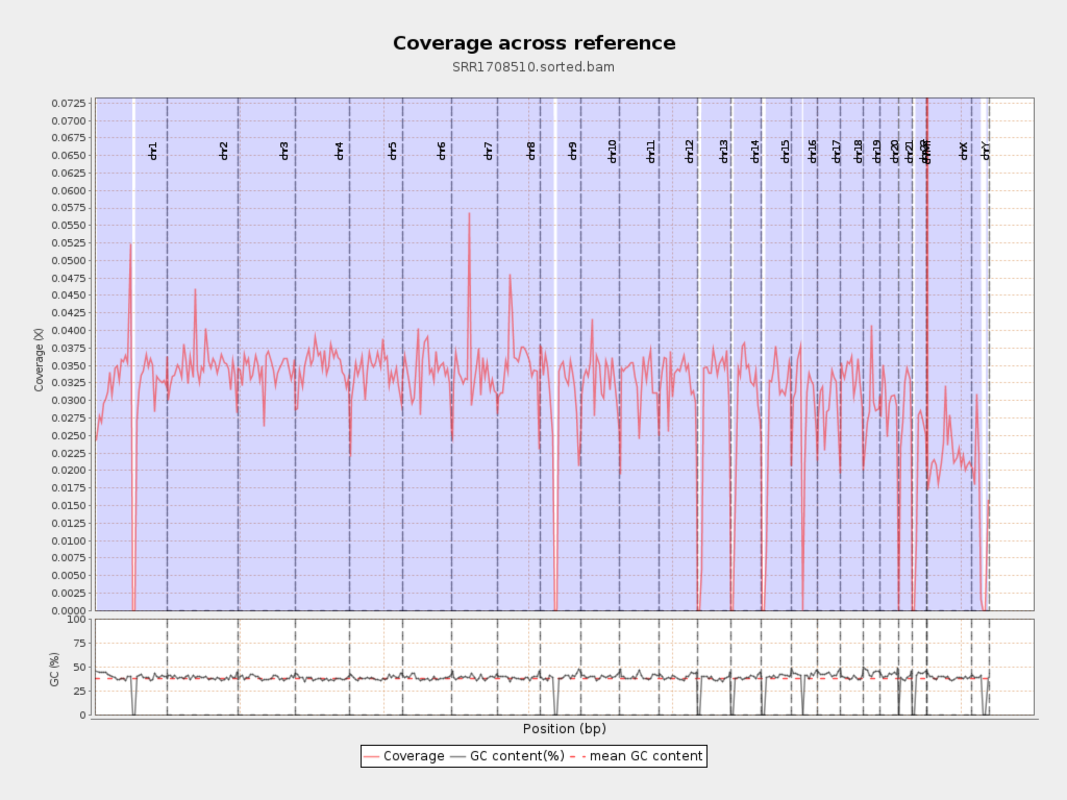
General error rate	0.52%
Mismatches	493,520
Insertions	4,954
Mapped reads with at least one insertion	0.24%
Deletions	14,577
Mapped reads with at least one deletion	0.72%
Homopolymer indels	48.69%

2.6. Chromosome stats

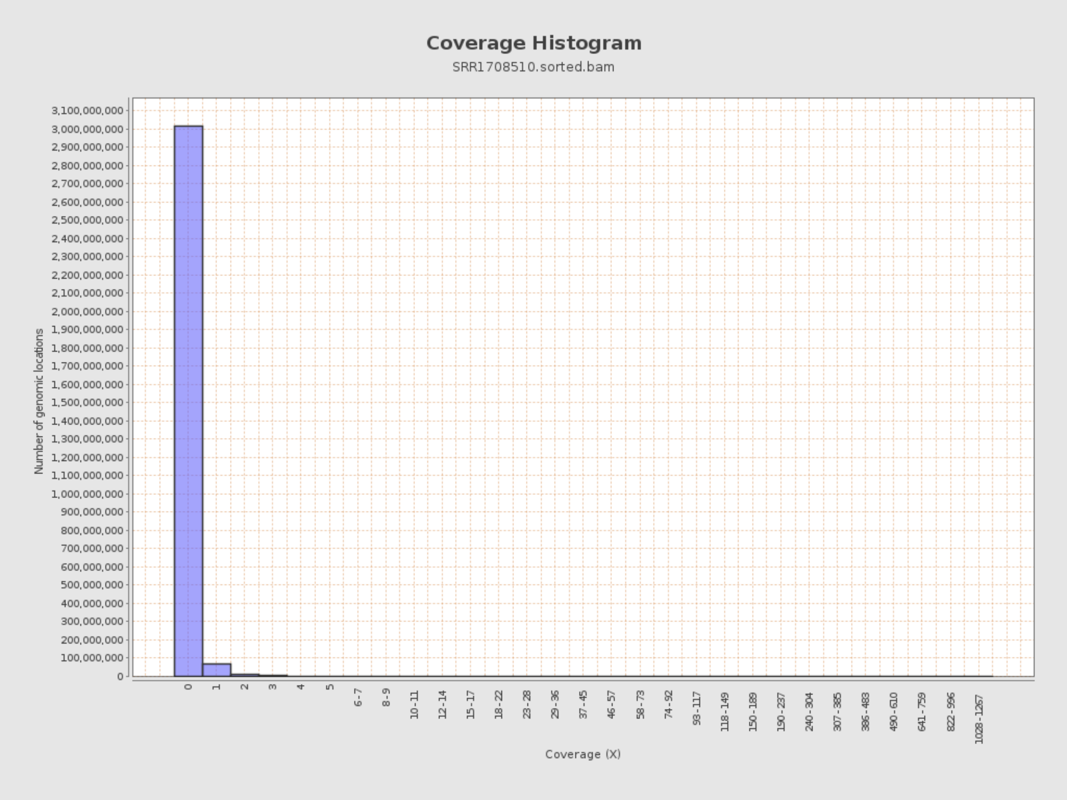
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7753941	0.0311	0.4899
chr2	243199373	8476223	0.0349	0.474
chr3	198022430	6812543	0.0344	0.2264
chr4	191154276	6676777	0.0349	0.2396
chr5	180915260	6177057	0.0341	0.2246
chr6	171115067	5867574	0.0343	0.2936
chr7	159138663	5442806	0.0342	0.4018

chr8	146364022	5176341	0.0354	0.7102
chr9	141213431	4086482	0.0289	0.2535
chr10	135534747	4494843	0.0332	0.254
chr11	135006516	4442581	0.0329	0.2915
chr12	133851895	4430128	0.0331	0.2231
chr13	115169878	3319619	0.0288	0.2291
chr14	107349540	2990396	0.0279	0.2077
chr15	102531392	2752202	0.0268	0.2008
chr16	90354753	2524577	0.0279	0.2075
chr17	81195210	2375888	0.0293	0.2497
chr18	78077248	2634297	0.0337	0.3783
chr19	59128983	1718716	0.0291	0.3404
chr20	63025520	1858769	0.0295	0.2095
chr21	48129895	1293336	0.0269	0.2228
chr22	51304566	959805	0.0187	0.177
chrMT	16571	127499	7.6941	5.0987
chrX	155270560	3438879	0.0221	0.1992
chrY	59373566	791332	0.0133	0.1545

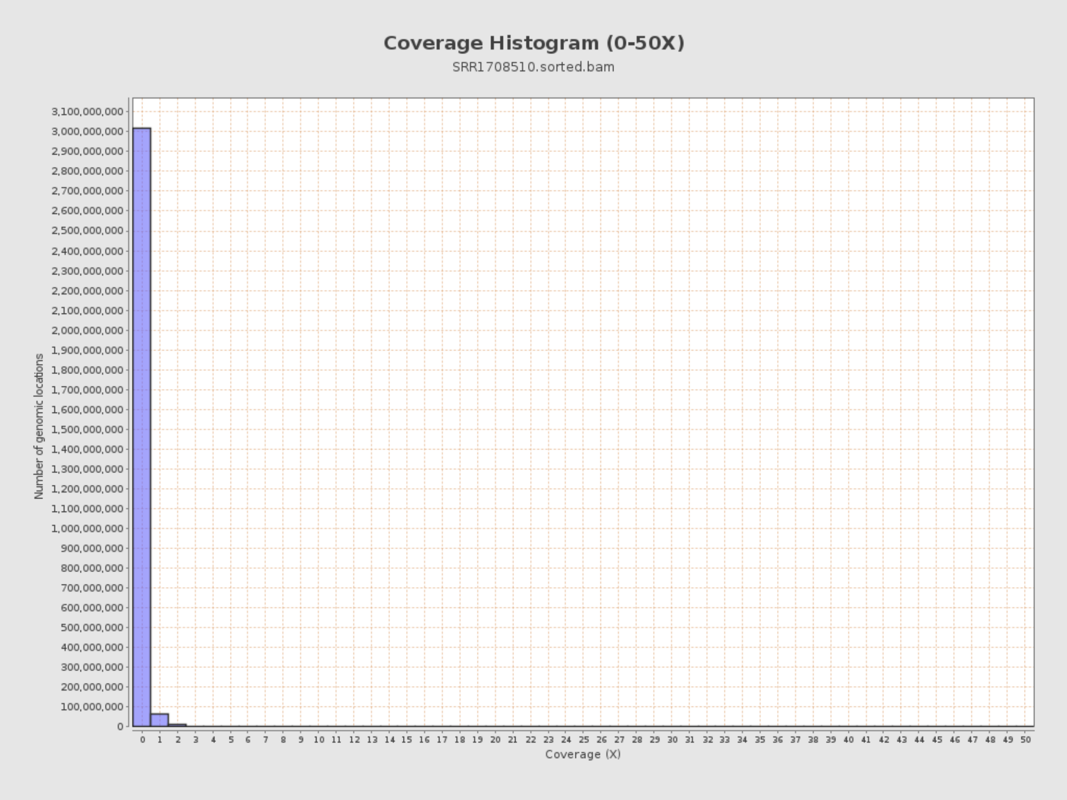
3. Results : Coverage across reference



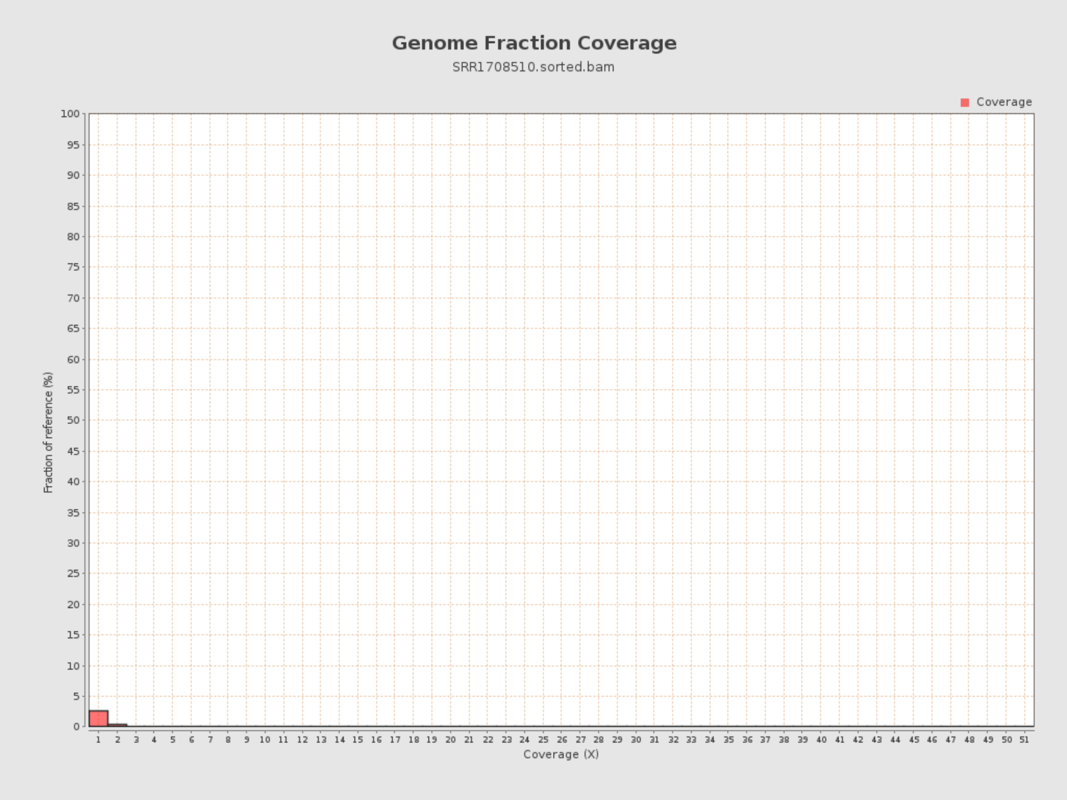
4. Results : Coverage Histogram



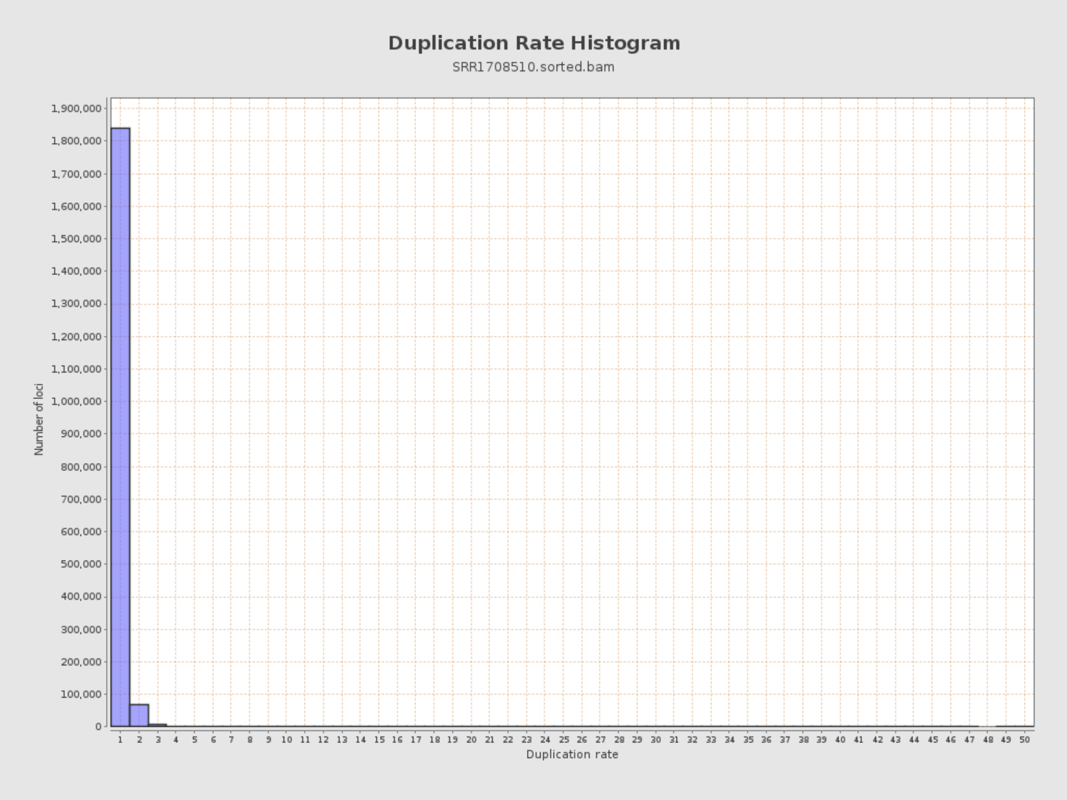
5. Results : Coverage Histogram (0-50X)



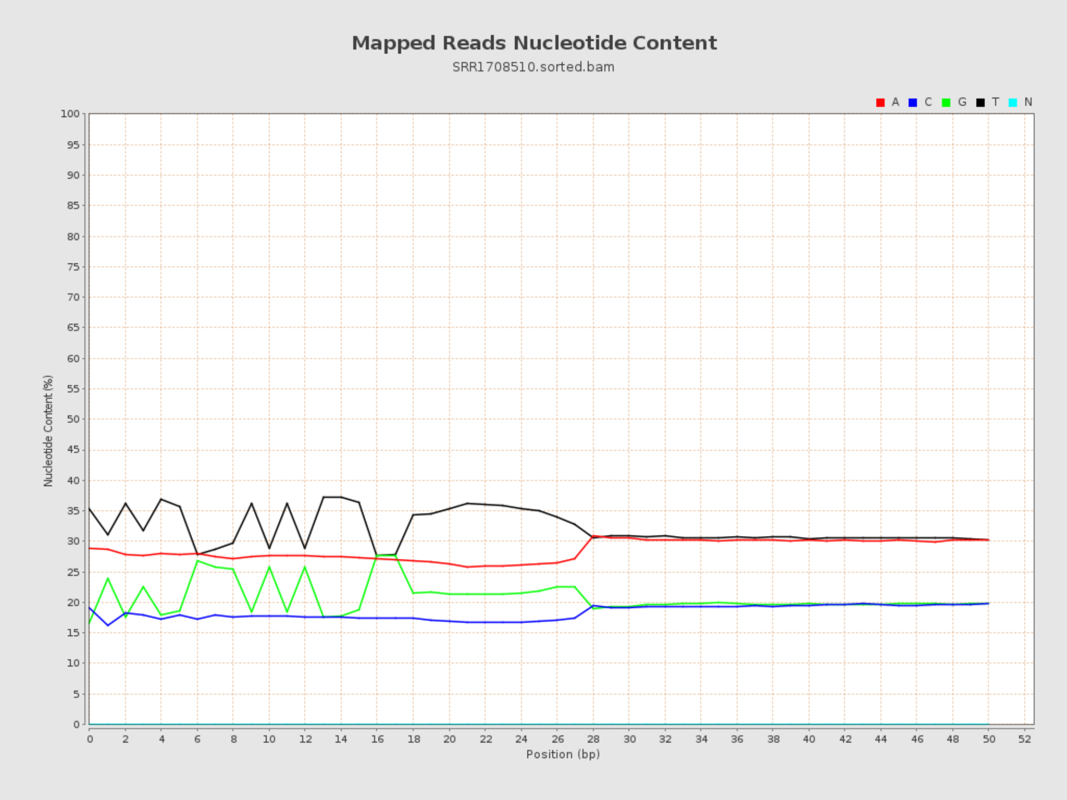
6. Results : Genome Fraction Coverage



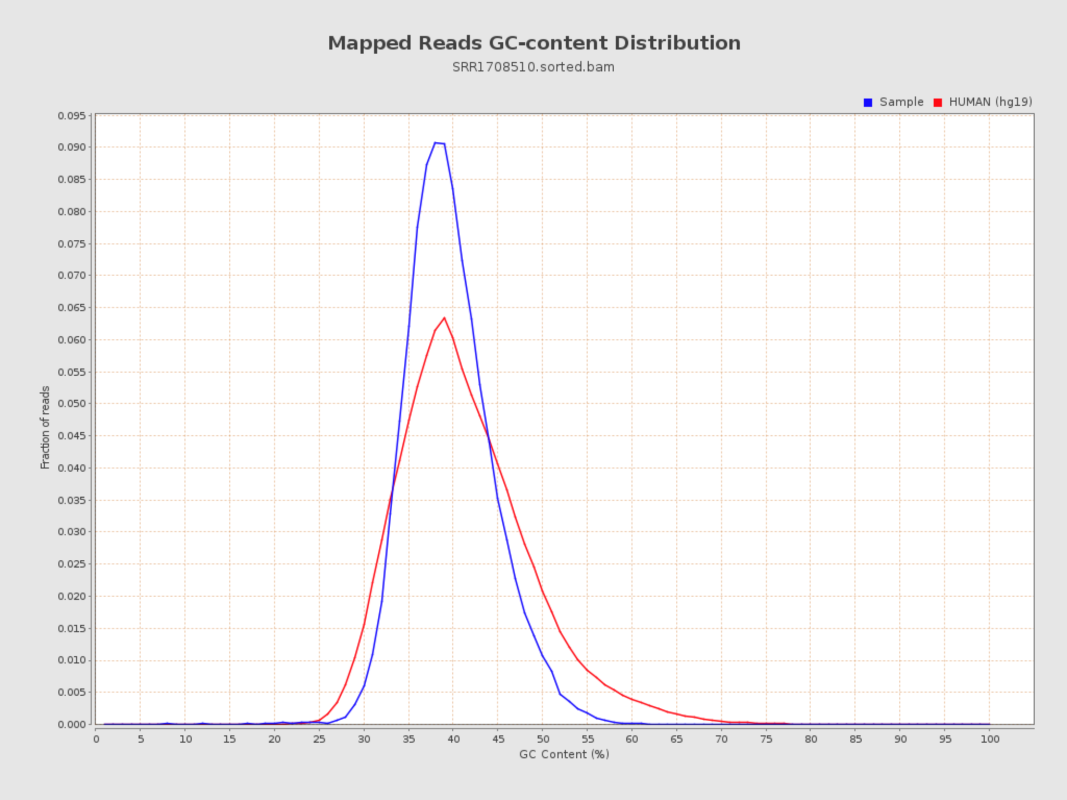
7. Results : Duplication Rate Histogram



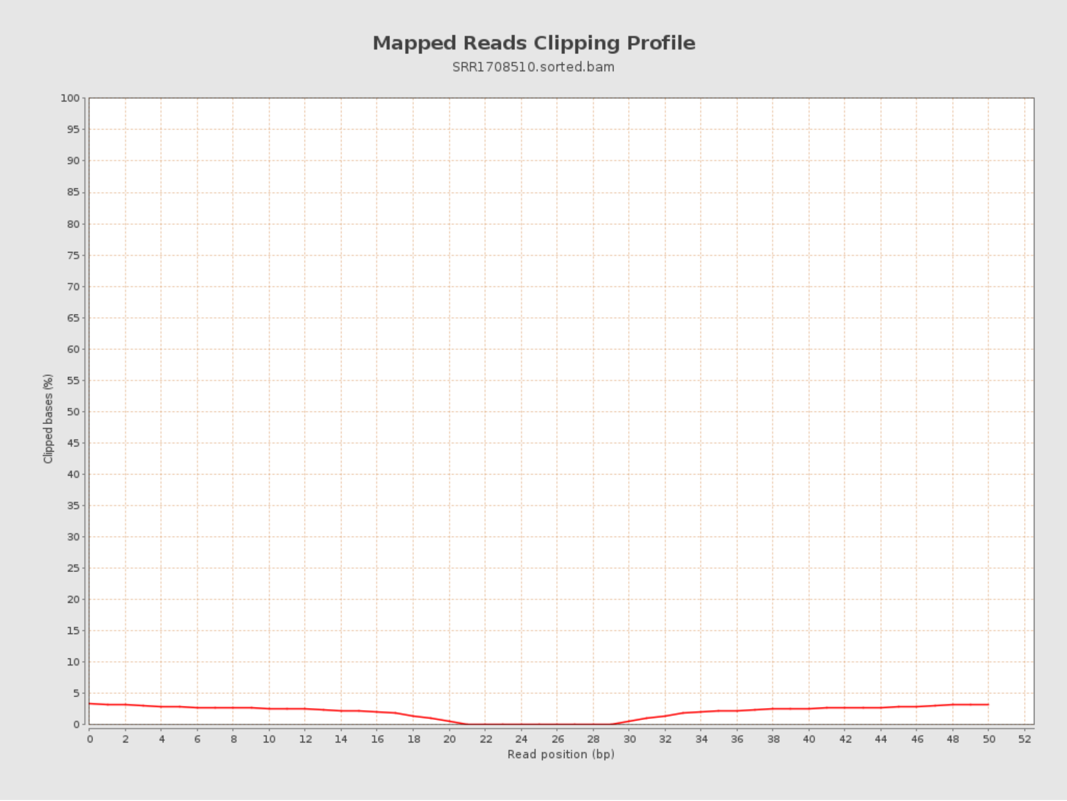
8. Results : Mapped Reads Nucleotide Content



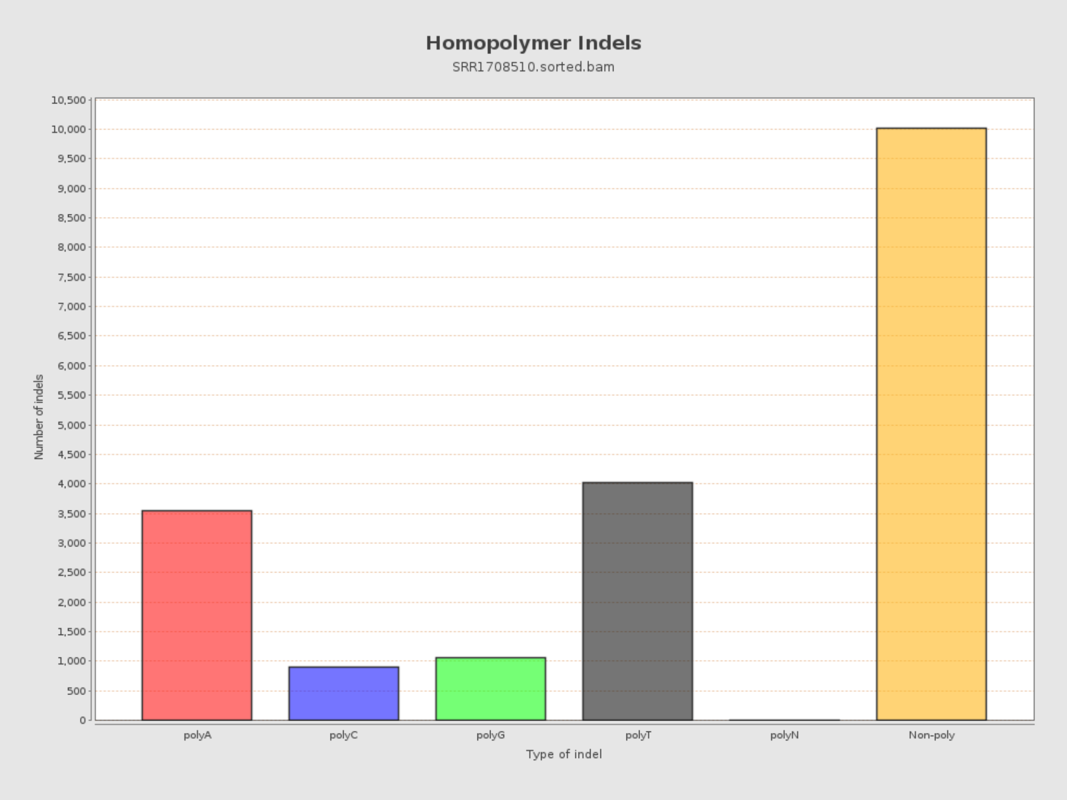
9. Results : Mapped Reads GC-content Distribution



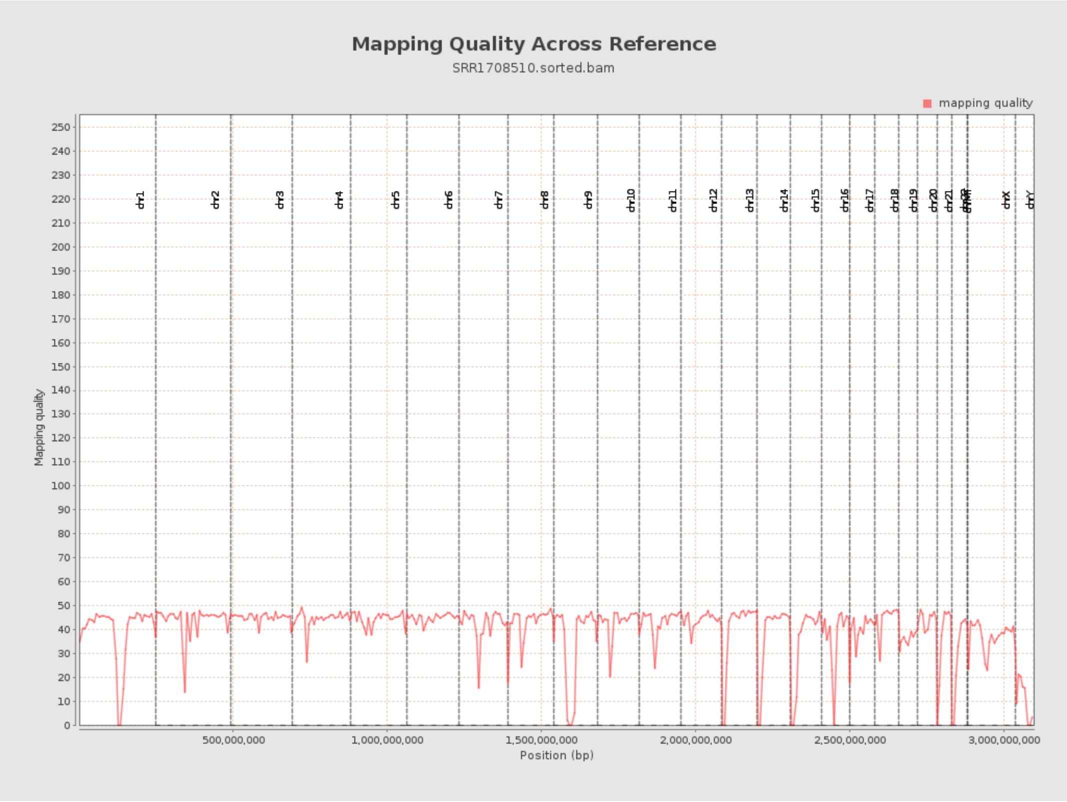
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram