Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:30:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708511.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_SRR1708511 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708511.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:30:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708511.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,241,806
Mapped reads	2,157,656 / 66.56%
Unmapped reads	1,084,150 / 33.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	651 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	96,076 / 2.96%
Duplication rate	3.11%
Clipped reads	506,034 / 15.61%

2.2. ACGT Content

Number/percentage of A's	29,157,846 / 28.52%
Number/percentage of C's	18,779,214 / 18.37%
Number/percentage of T's	32,838,365 / 32.12%
Number/percentage of G's	21,451,998 / 20.98%
Number/percentage of N's	1,374 / 0%
GC Percentage	39.35%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3586

2.4. Mapping Quality

Mean Mapping Quality	39.56

2.5. Mismatches and indels

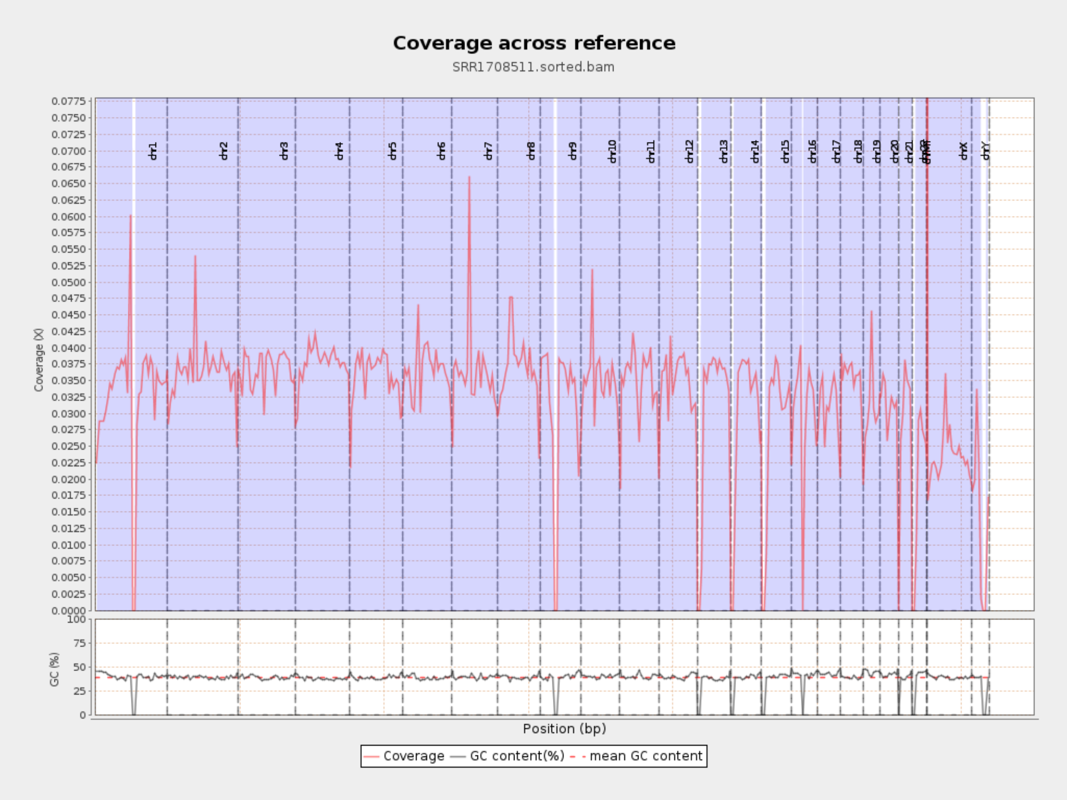
General error rate	0.54%
Mismatches	544,102
Insertions	5,683
Mapped reads with at least one insertion	0.26%
Deletions	16,021
Mapped reads with at least one deletion	0.74%
Homopolymer indels	47.72%

2.6. Chromosome stats

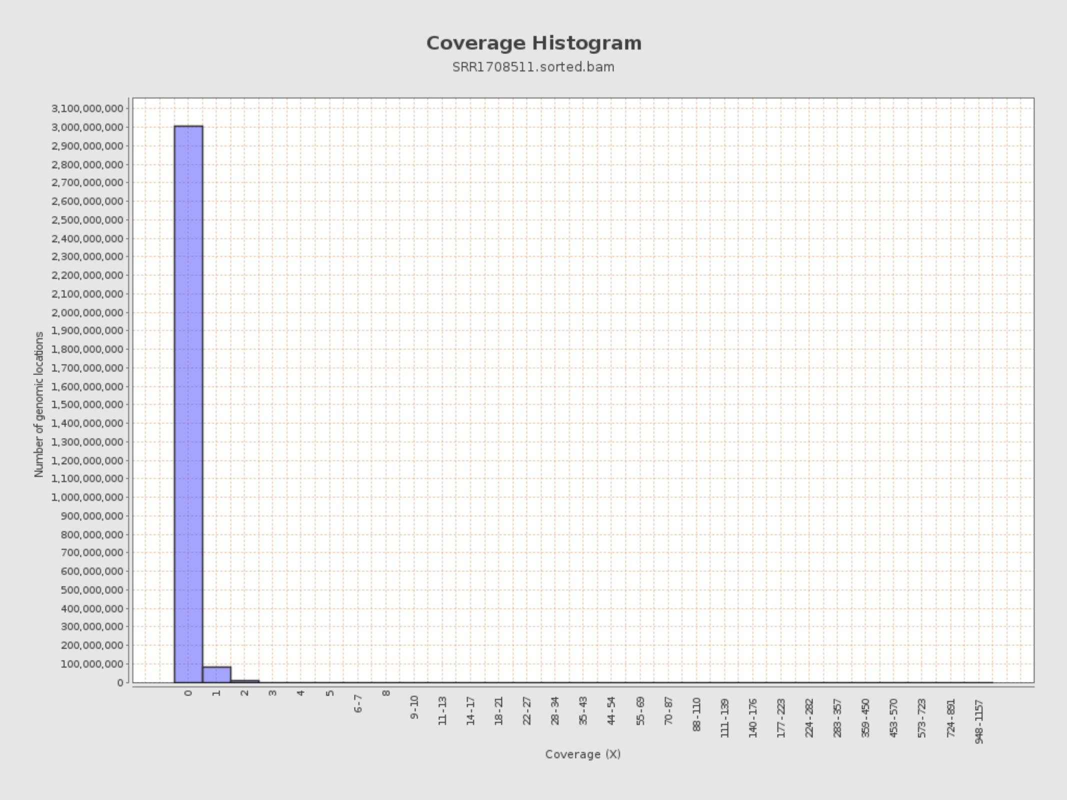
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8142734	0.0327	0.6079
chr2	243199373	8883121	0.0365	0.509
chr3	198022430	7274235	0.0367	0.2263
chr4	191154276	7186618	0.0376	0.2321
chr5	180915260	6534345	0.0361	0.2192
chr6	171115067	6246744	0.0365	0.3033
chr7	159138663	5842191	0.0367	0.4271

chr8	146364022	5423215	0.0371	0.6603
chr9	141213431	4355425	0.0308	0.2687
chr10	135534747	4759702	0.0351	0.2783
chr11	135006516	4759559	0.0353	0.3145
chr12	133851895	4701776	0.0351	0.2209
chr13	115169878	3496407	0.0304	0.2354
chr14	107349540	3148697	0.0293	0.2072
chr15	102531392	2804389	0.0274	0.1978
chr16	90354753	2660620	0.0294	0.2077
chr17	81195210	2507754	0.0309	0.2608
chr18	78077248	2792244	0.0358	0.4259
chr19	59128983	1837685	0.0311	0.4266
chr20	63025520	1952178	0.031	0.2034
chr21	48129895	1379196	0.0287	0.2176
chr22	51304566	997330	0.0194	0.1734
chrMT	16571	61689	3.7227	2.8138
chrX	155270560	3672423	0.0237	0.2111
chrY	59373566	832634	0.014	0.1586

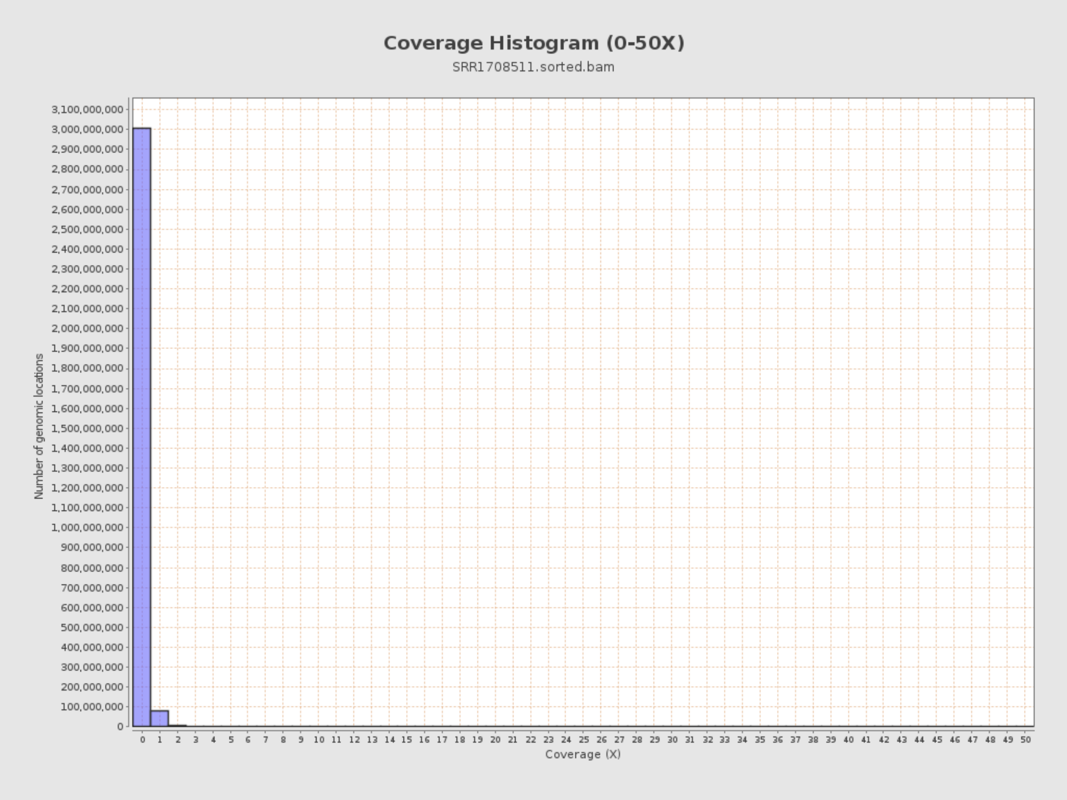
3. Results : Coverage across reference



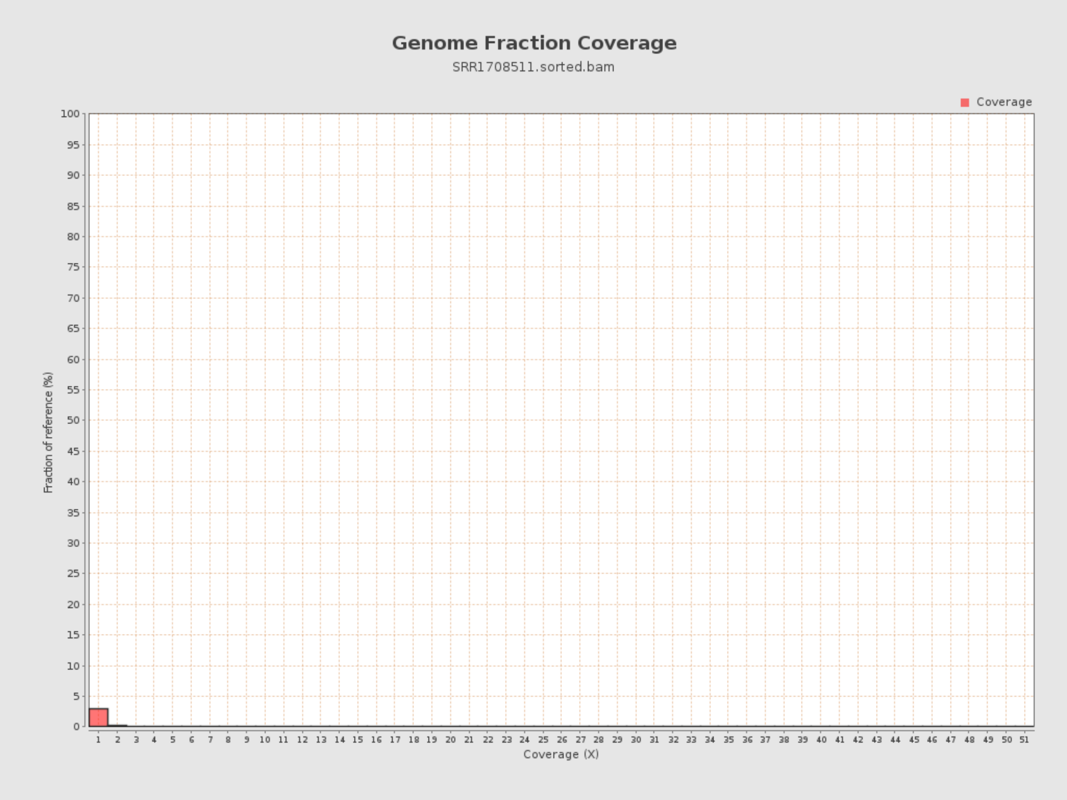
4. Results : Coverage Histogram



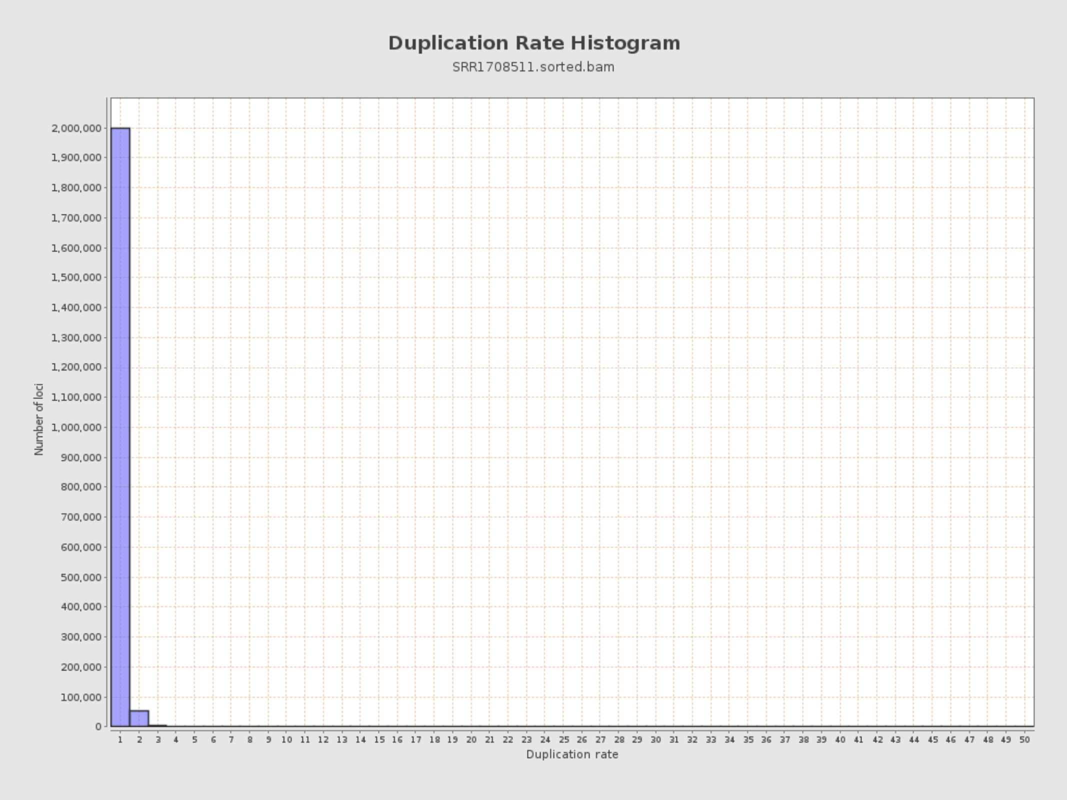
5. Results : Coverage Histogram (0-50X)



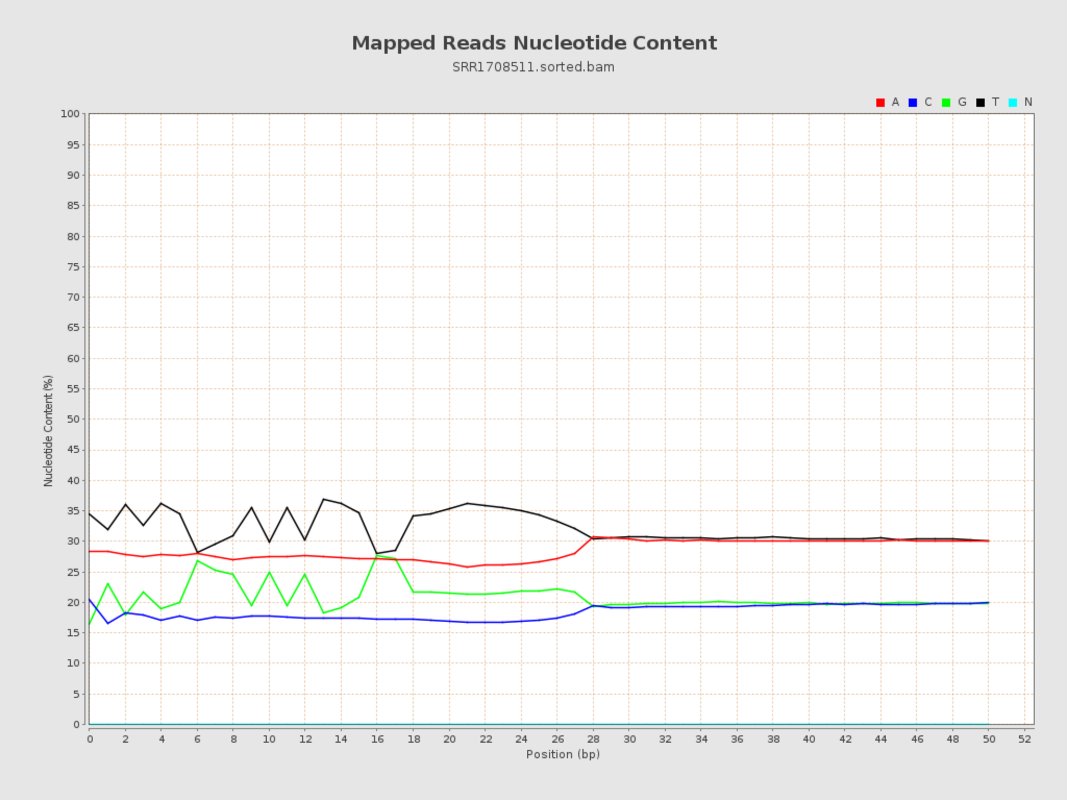
6. Results : Genome Fraction Coverage



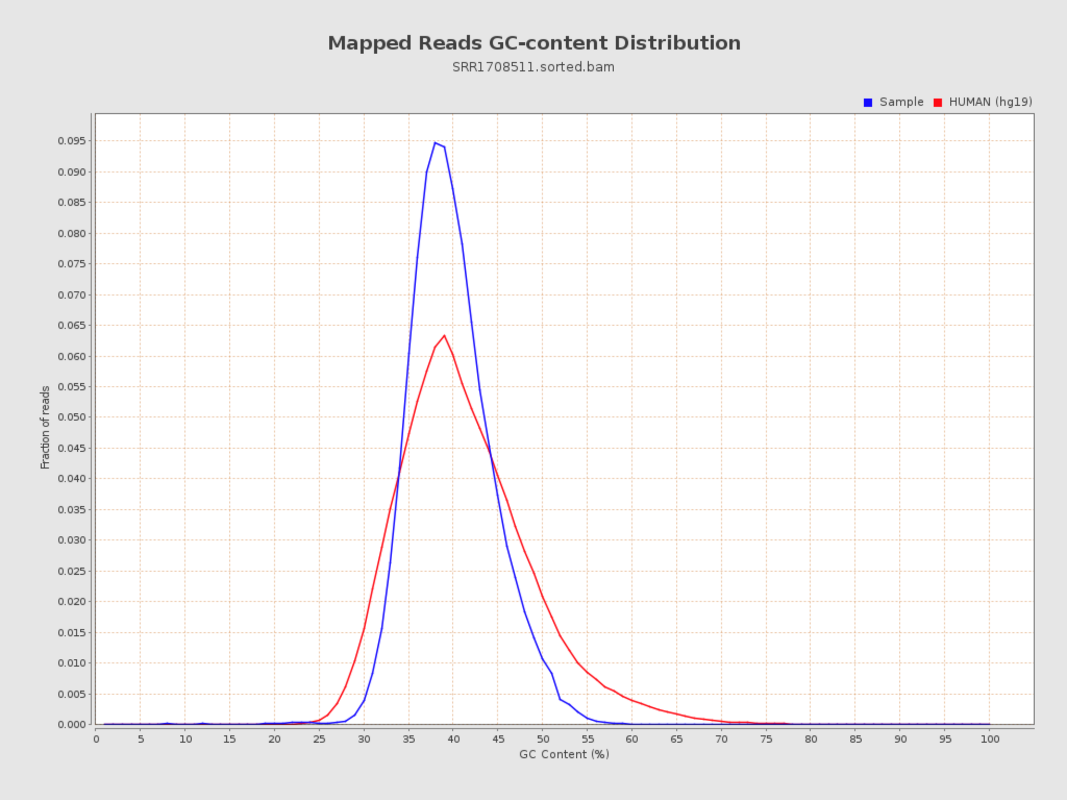
7. Results : Duplication Rate Histogram



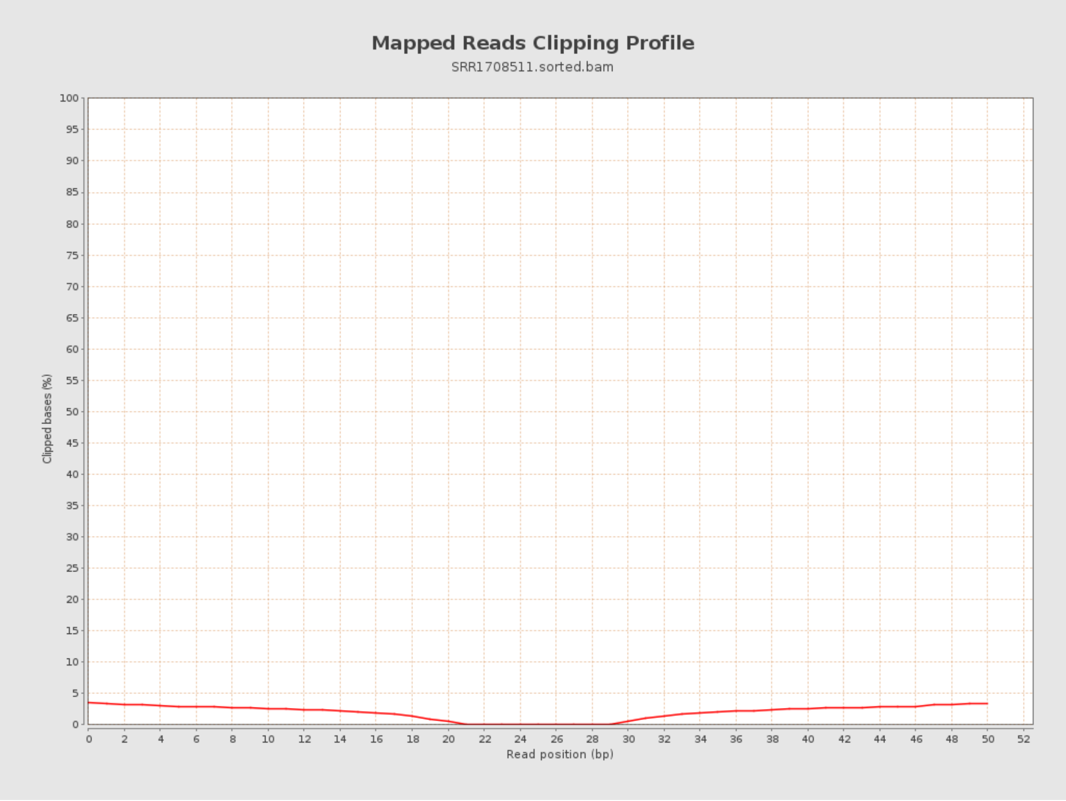
8. Results : Mapped Reads Nucleotide Content



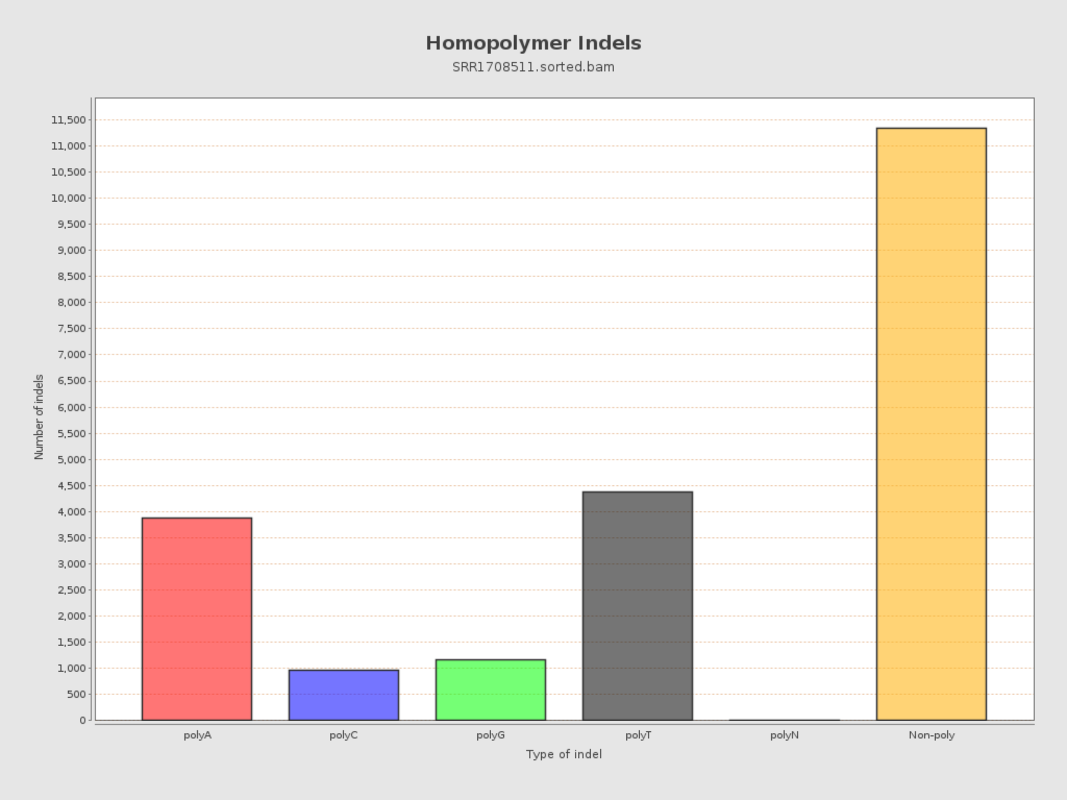
9. Results : Mapped Reads GC-content Distribution



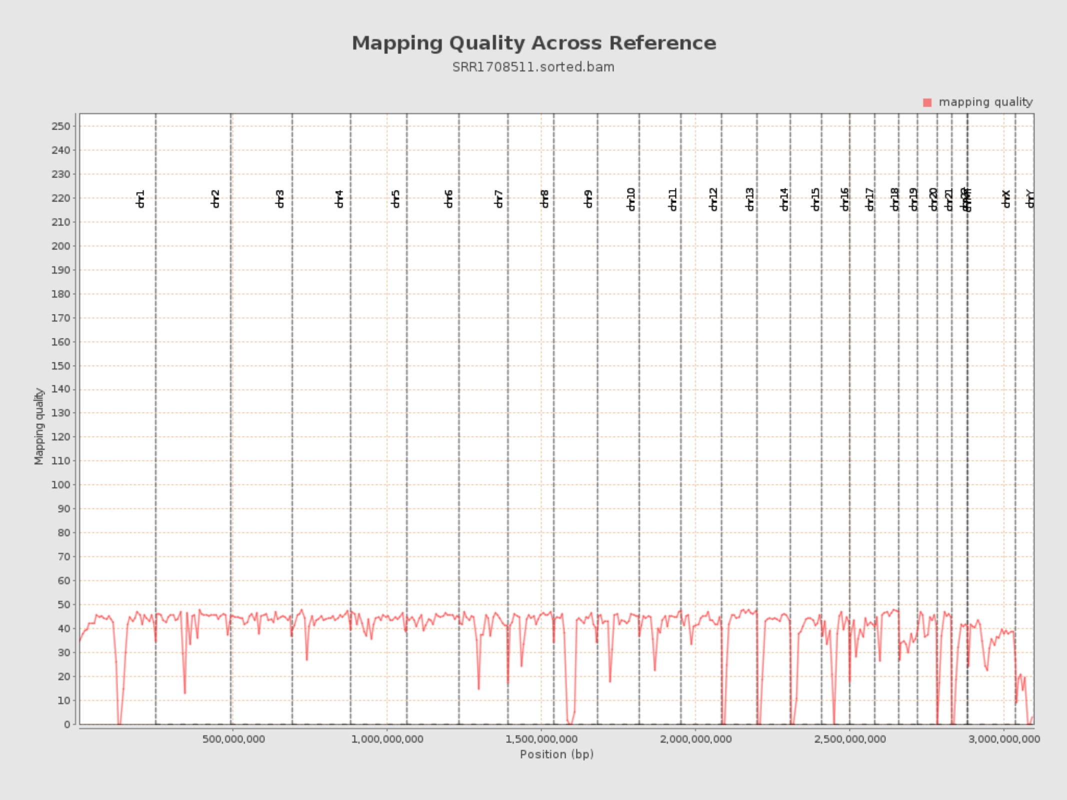
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram