Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:43:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708516.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_SRR1708516 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708516.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:43:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708516.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,377,568
Mapped reads	2,225,177 / 65.88%
Unmapped reads	1,152,391 / 34.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	959 / 0.03%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	95,265 / 2.82%
Duplication rate	3.05%
Clipped reads	531,457 / 15.73%

2.2. ACGT Content

Number/percentage of A's	29,706,209 / 28.2%
Number/percentage of C's	19,733,620 / 18.73%
Number/percentage of T's	33,472,030 / 31.77%
Number/percentage of G's	22,431,356 / 21.29%
Number/percentage of N's	1,461 / 0%
GC Percentage	40.03%

2.3. Coverage

Mean	0.034

Standard Deviation	0.3262

2.4. Mapping Quality

Mean Mapping Quality	39.24

2.5. Mismatches and indels

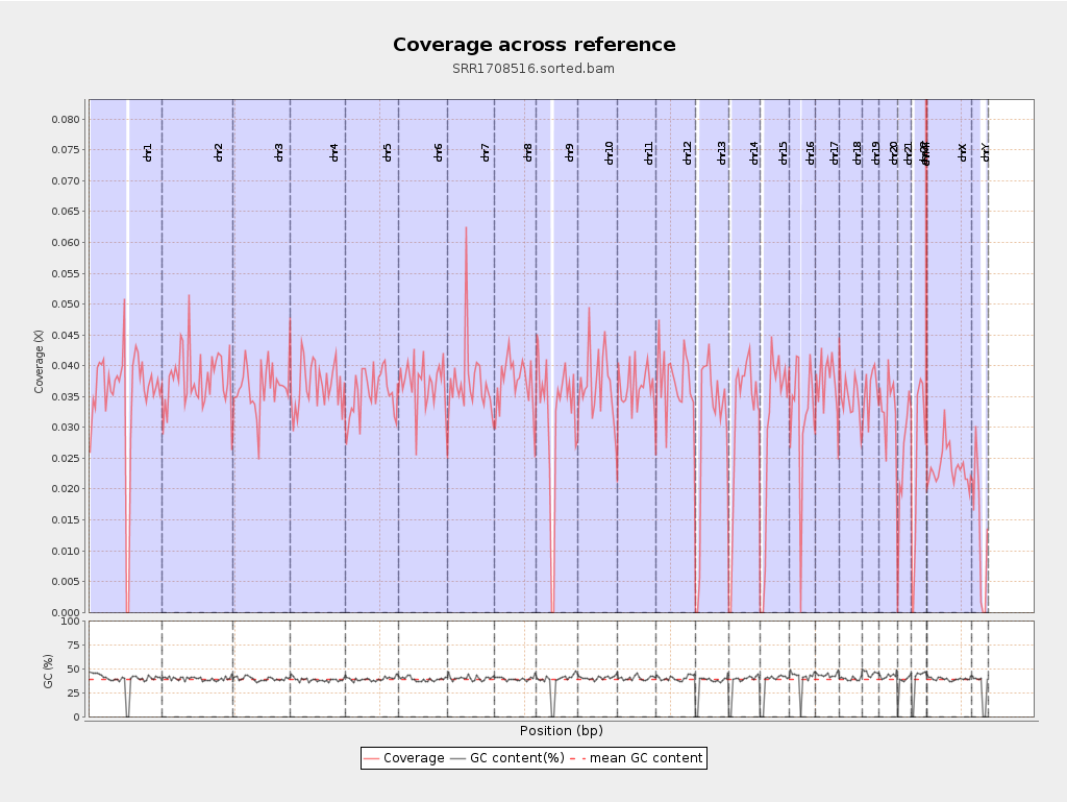
General error rate	0.54%
Mismatches	556,749
Insertions	6,223
Mapped reads with at least one insertion	0.28%
Deletions	17,017
Mapped reads with at least one deletion	0.76%
Homopolymer indels	46.88%

2.6. Chromosome stats

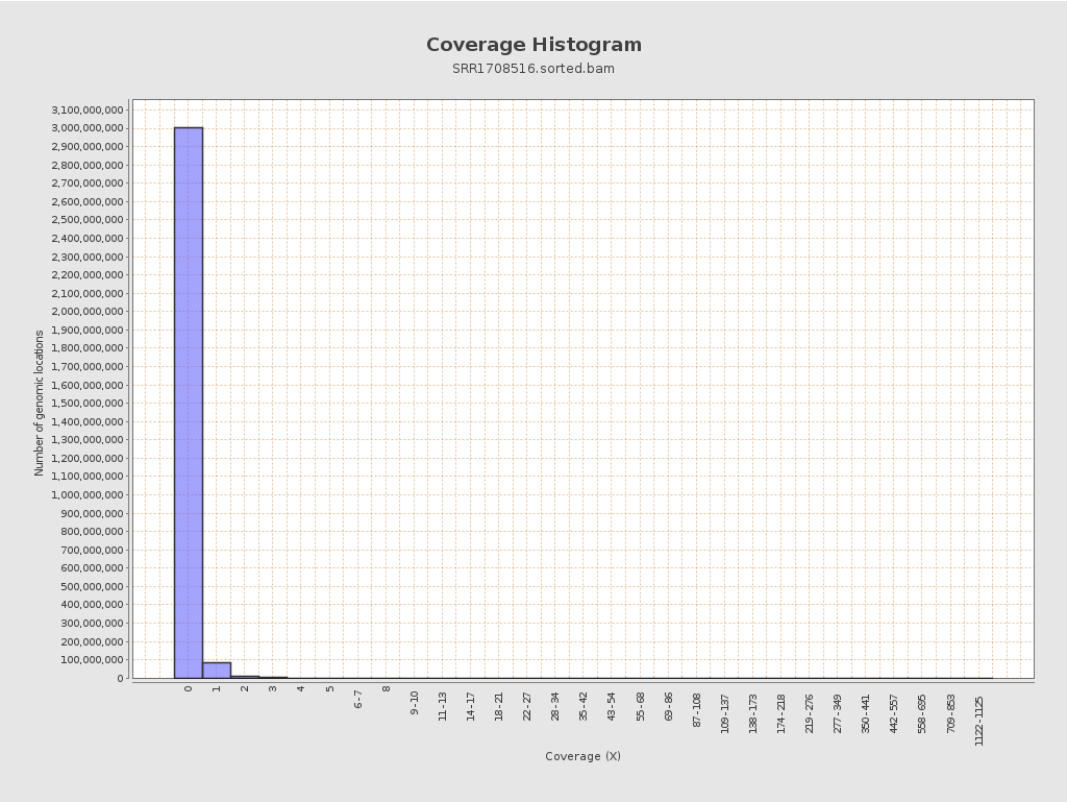
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8761960	0.0352	0.4672
chr2	243199373	9207782	0.0379	0.5294
chr3	198022430	7196410	0.0363	0.2287
chr4	191154276	7021045	0.0367	0.2303
chr5	180915260	6420402	0.0355	0.2182
chr6	171115067	6345585	0.0371	0.3432
chr7	159138663	5954531	0.0374	0.4085

chr8	146364022	5428554	0.0371	0.463
chr9	141213431	4446075	0.0315	0.263
chr10	135534747	5004194	0.0369	0.269
chr11	135006516	4895476	0.0363	0.2886
chr12	133851895	5033495	0.0376	0.232
chr13	115169878	3441243	0.0299	0.2805
chr14	107349540	3339358	0.0311	0.2131
chr15	102531392	3069774	0.0299	0.2123
chr16	90354753	2890598	0.032	0.2168
chr17	81195210	3018314	0.0372	0.2537
chr18	78077248	2734139	0.035	0.36
chr19	59128983	2122738	0.0359	0.3569
chr20	63025520	2095725	0.0333	0.2179
chr21	48129895	1204852	0.025	0.202
chr22	51304566	1232711	0.024	0.1932
chrMT	16571	115040	6.9422	4.6923
chrX	155270560	3648088	0.0235	0.2049
chrY	59373566	742416	0.0125	0.1456

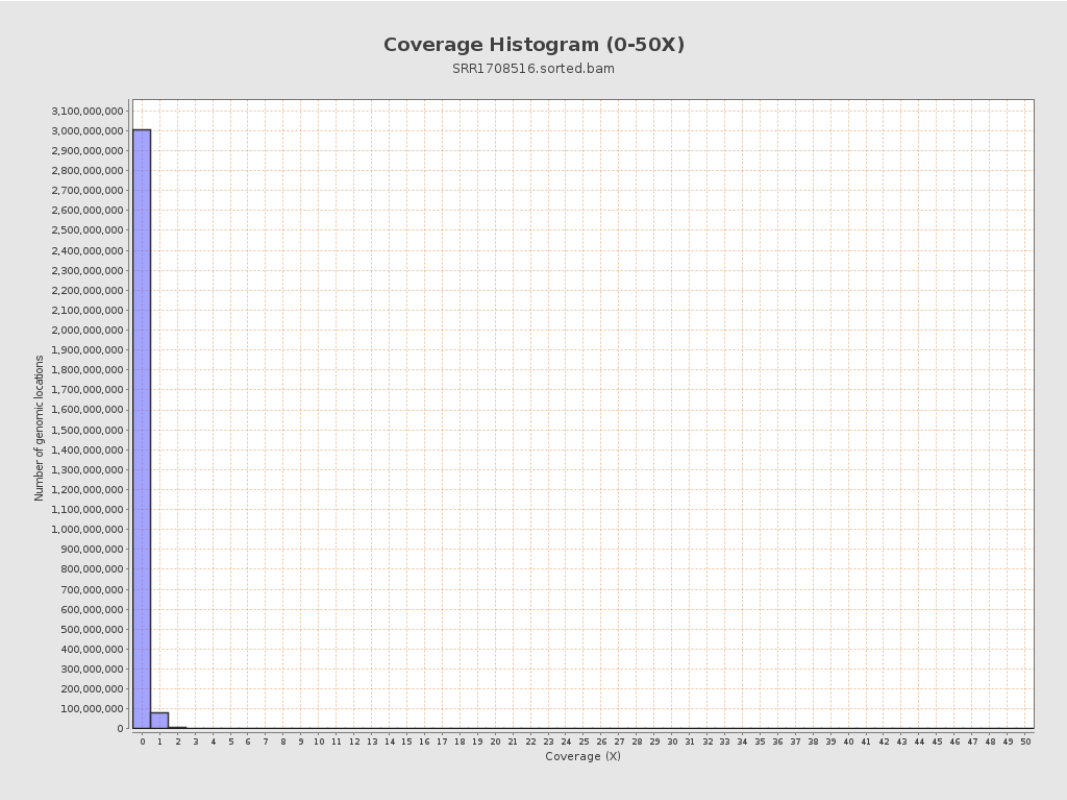
3. Results : Coverage across reference



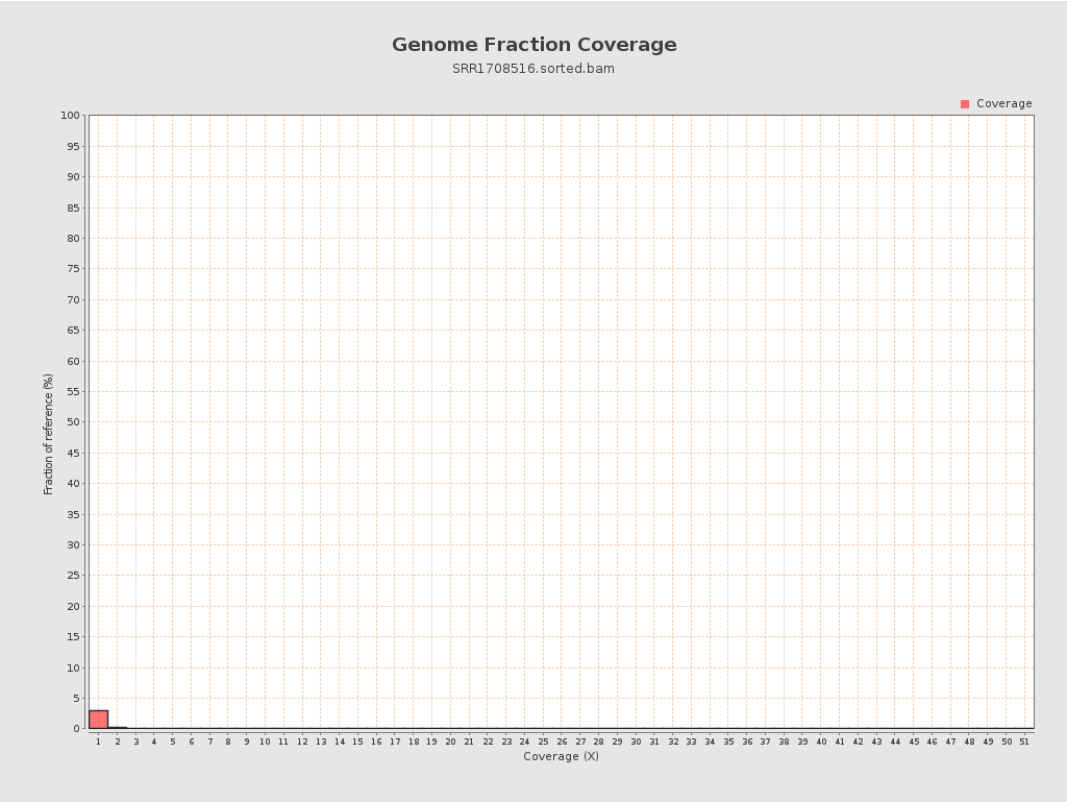
4. Results : Coverage Histogram



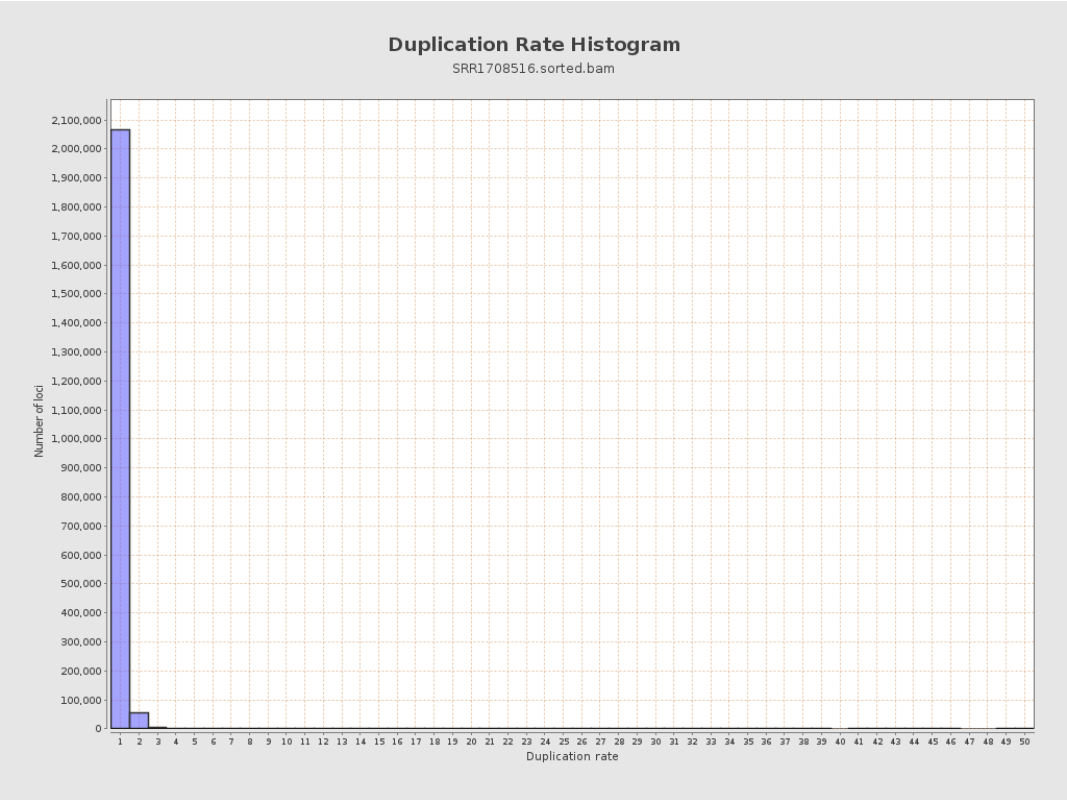
5. Results : Coverage Histogram (0-50X)



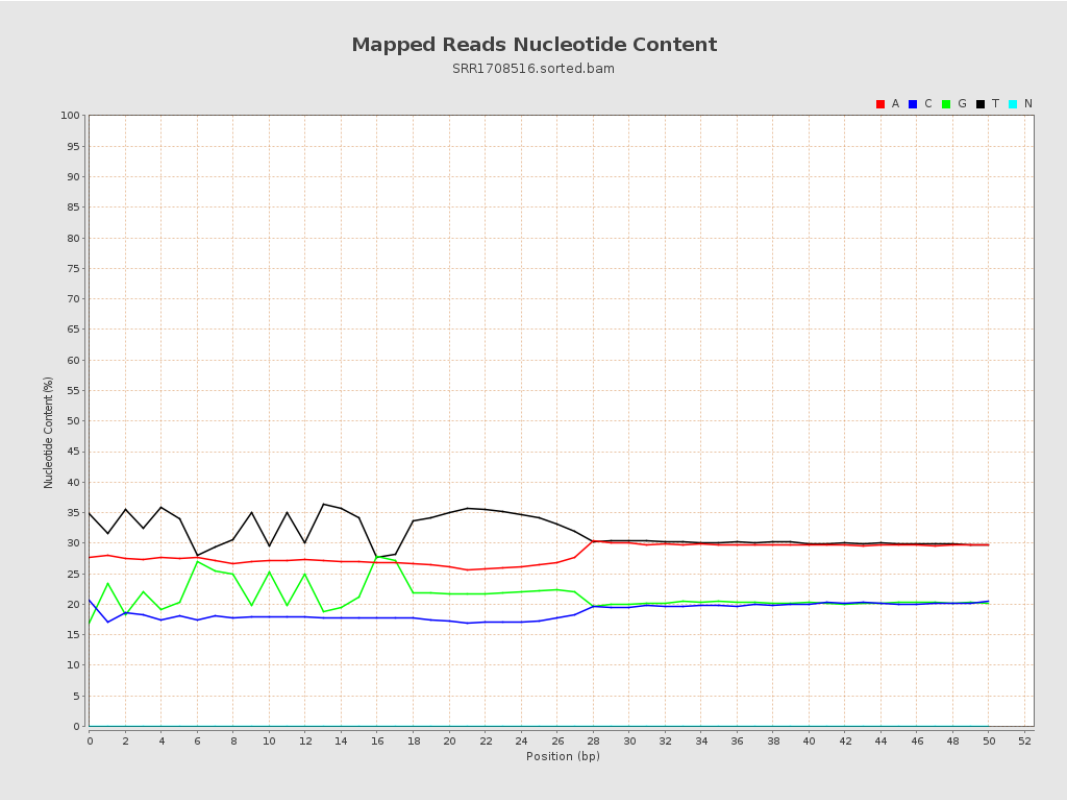
6. Results : Genome Fraction Coverage



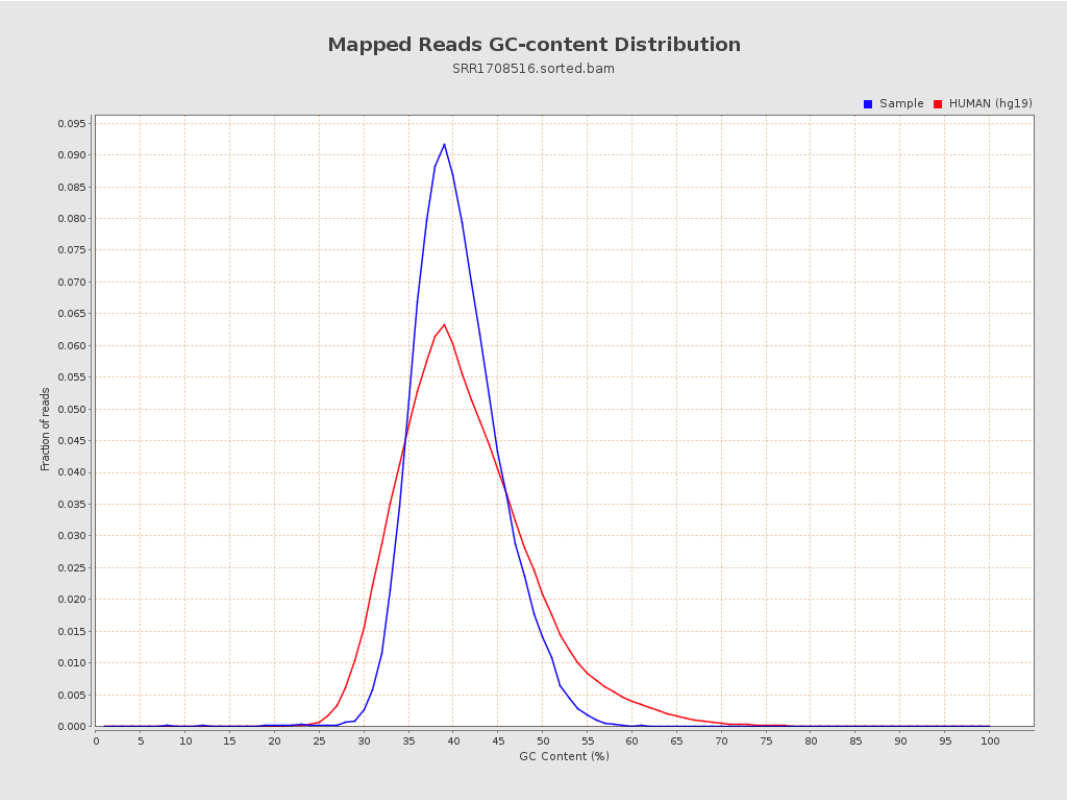
7. Results : Duplication Rate Histogram



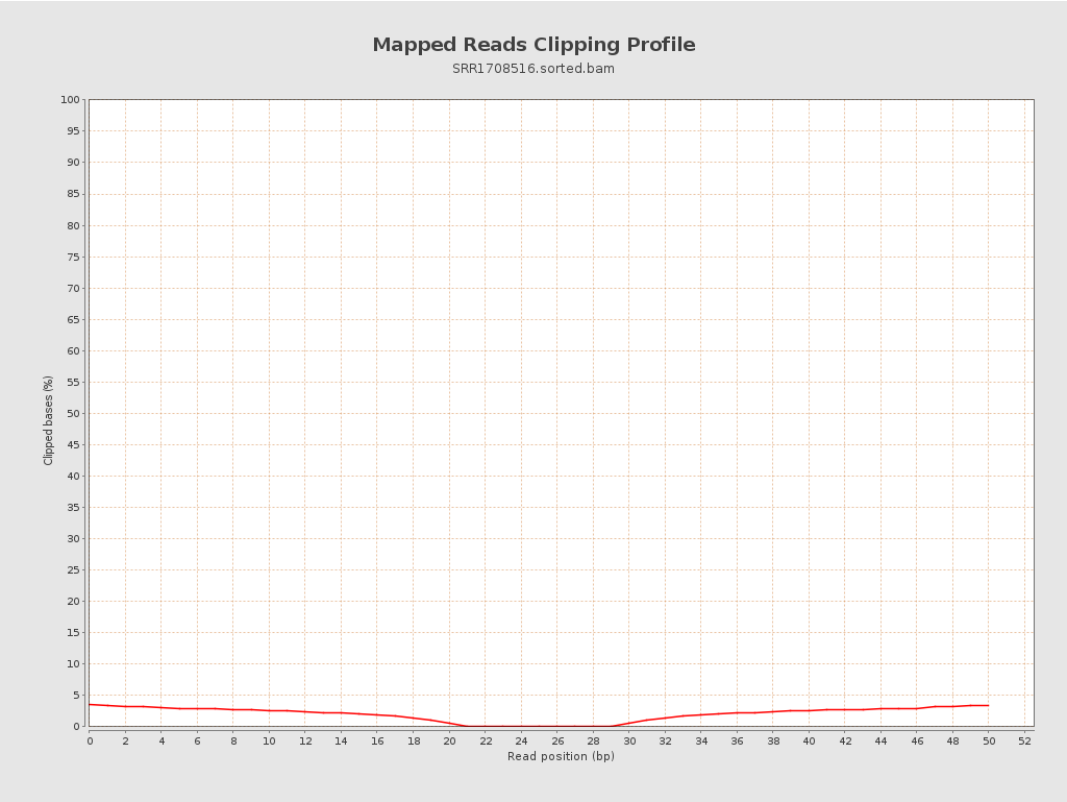
8. Results : Mapped Reads Nucleotide Content



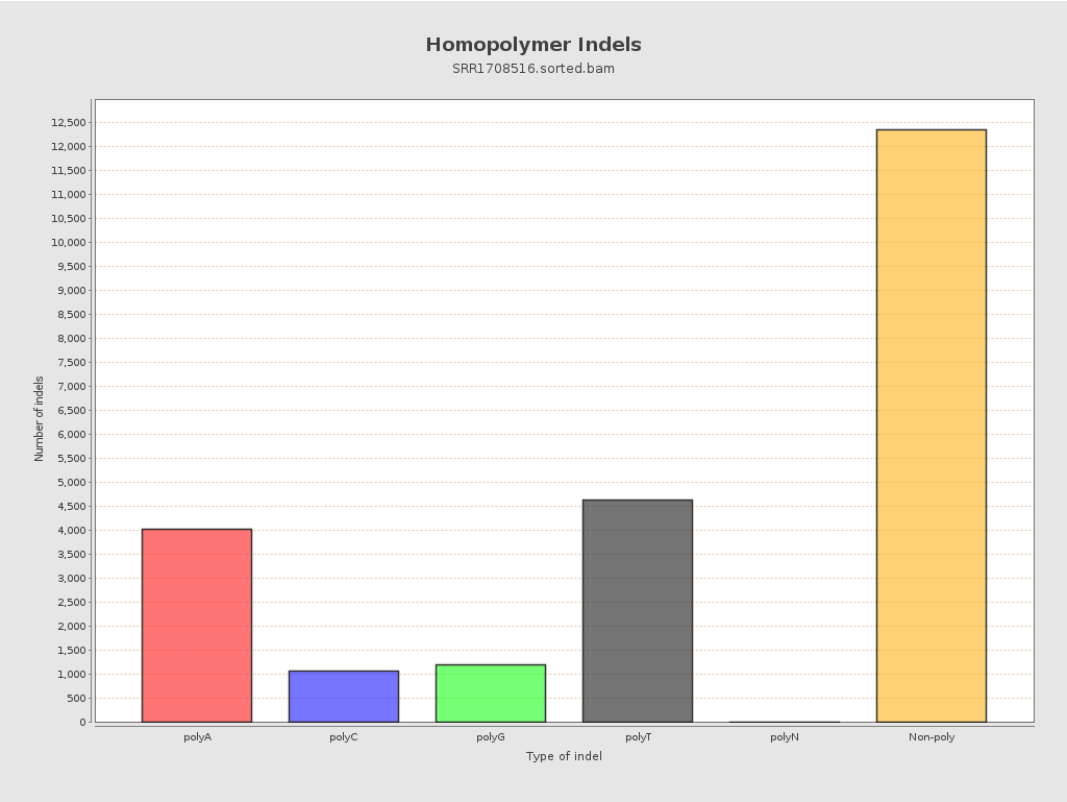
9. Results : Mapped Reads GC-content Distribution



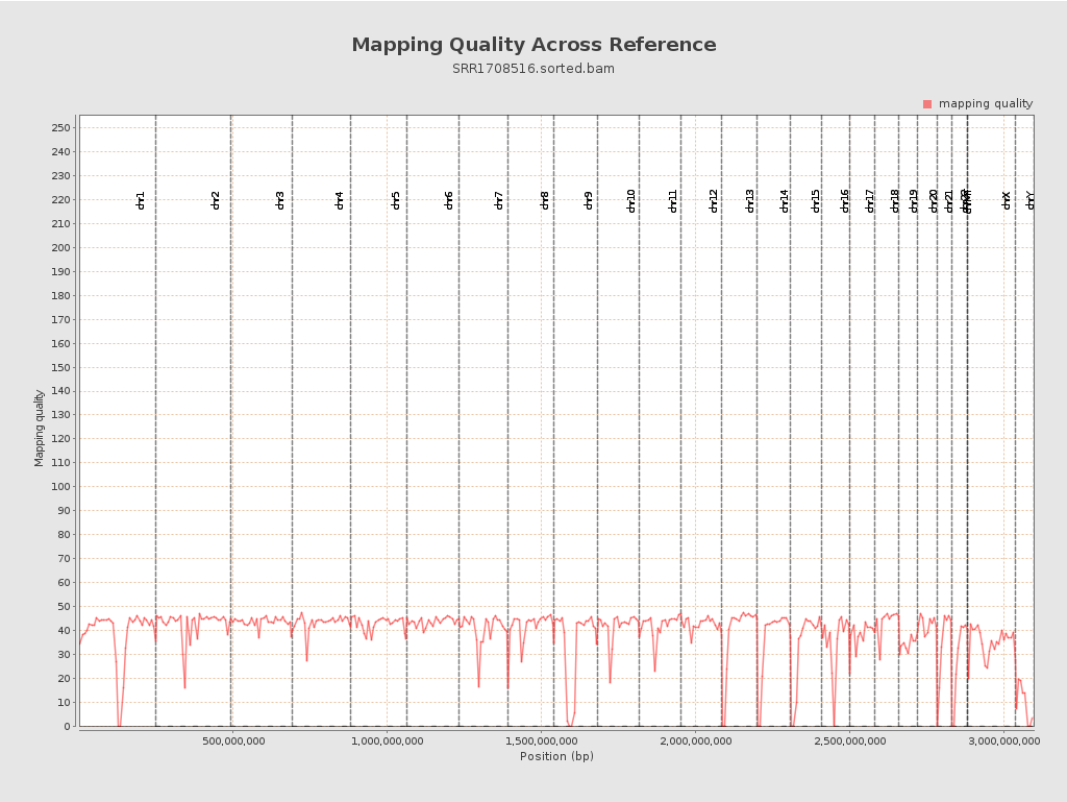
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram