Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:46:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708631.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_SRR1708631 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708631.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:46:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708631.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,040,064
Mapped reads	2,200,783 / 72.39%
Unmapped reads	839,281 / 27.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	664 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	78,398 / 2.58%
Duplication rate	2.49%
Clipped reads	342,627 / 11.27%

2.2. ACGT Content

Number/percentage of A's	31,829,714 / 29.7%
Number/percentage of C's	20,070,432 / 18.73%
Number/percentage of T's	33,878,858 / 31.61%
Number/percentage of G's	21,396,480 / 19.96%
Number/percentage of N's	9,102 / 0.01%
GC Percentage	38.69%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.3553

2.4. Mapping Quality

Mean Mapping Quality	43.49

2.5. Mismatches and indels

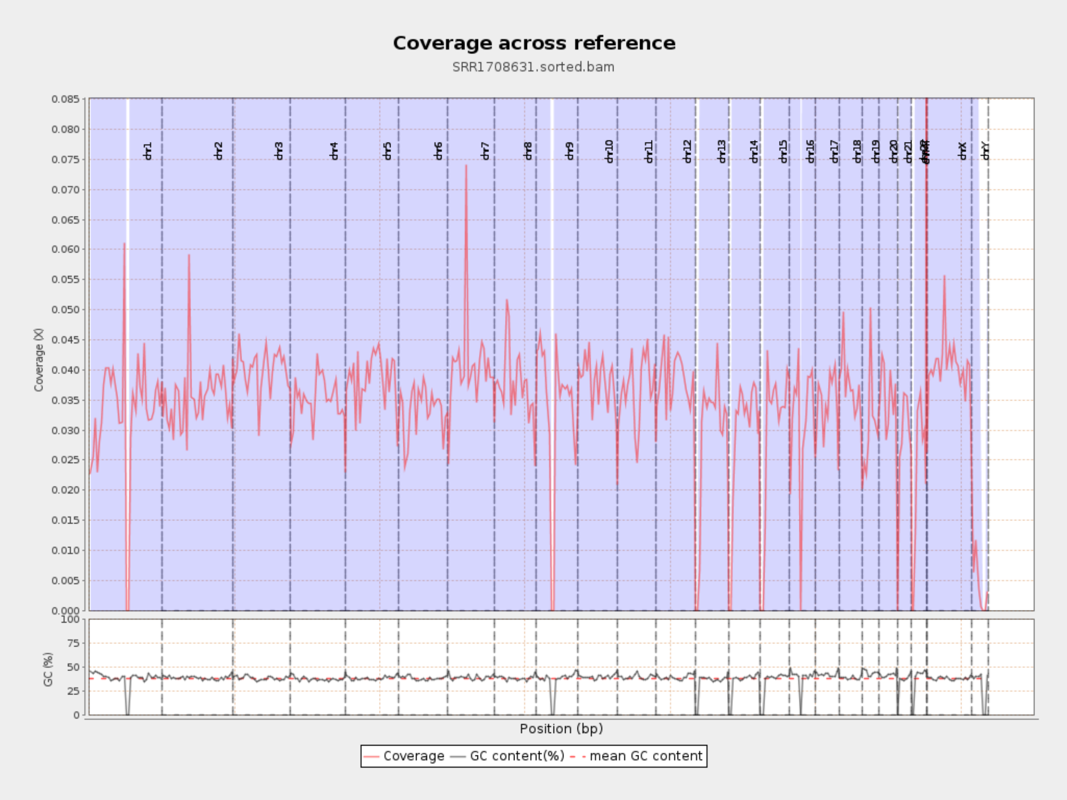
General error rate	0.66%
Mismatches	699,449
Insertions	5,002
Mapped reads with at least one insertion	0.23%
Deletions	13,333
Mapped reads with at least one deletion	0.6%
Homopolymer indels	48.8%

2.6. Chromosome stats

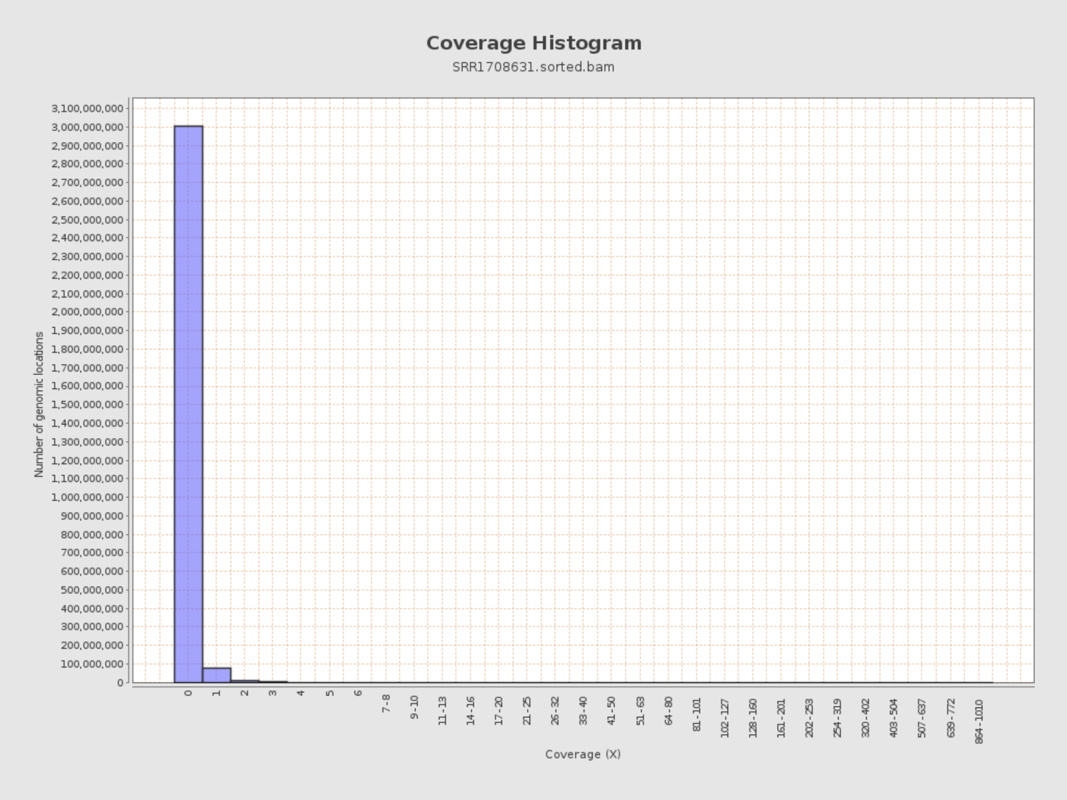
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8202028	0.0329	0.6156
chr2	243199373	8618522	0.0354	0.3549
chr3	198022430	7949696	0.0401	0.2302
chr4	191154276	6696622	0.035	0.2192
chr5	180915260	6983583	0.0386	0.2281
chr6	171115067	5720329	0.0334	0.2474
chr7	159138663	6564296	0.0412	0.4969

chr8	146364022	5475653	0.0374	0.6111
chr9	141213431	4725936	0.0335	0.3094
chr10	135534747	5226879	0.0386	0.2815
chr11	135006516	4931203	0.0365	0.3298
chr12	133851895	5112460	0.0382	0.2305
chr13	115169878	3268545	0.0284	0.1944
chr14	107349540	3094754	0.0288	0.215
chr15	102531392	3010130	0.0294	0.196
chr16	90354753	2843846	0.0315	0.2185
chr17	81195210	2768351	0.0341	0.2508
chr18	78077248	2932157	0.0376	0.6481
chr19	59128983	1821914	0.0308	0.4576
chr20	63025520	2226558	0.0353	0.2232
chr21	48129895	1329655	0.0276	0.2128
chr22	51304566	1131300	0.0221	0.1662
chrMT	16571	3621	0.2185	0.5598
chrX	155270560	6302543	0.0406	0.2644
chrY	59373566	264339	0.0045	0.0962

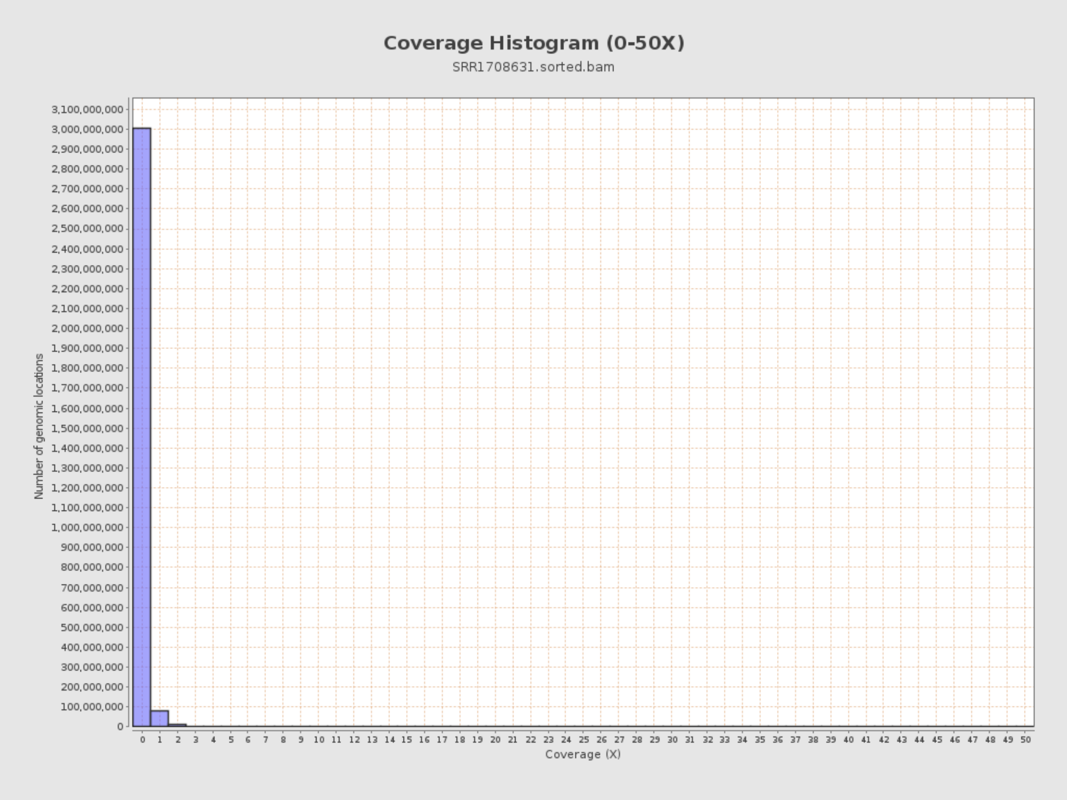
3. Results : Coverage across reference



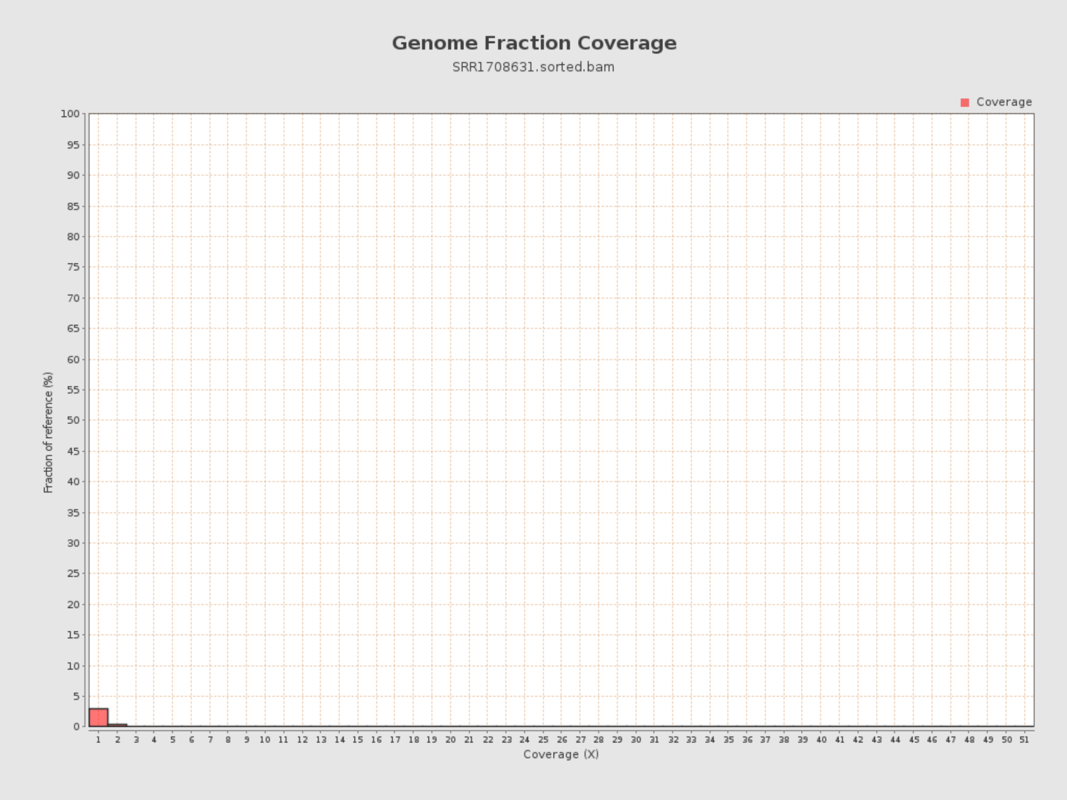
4. Results : Coverage Histogram



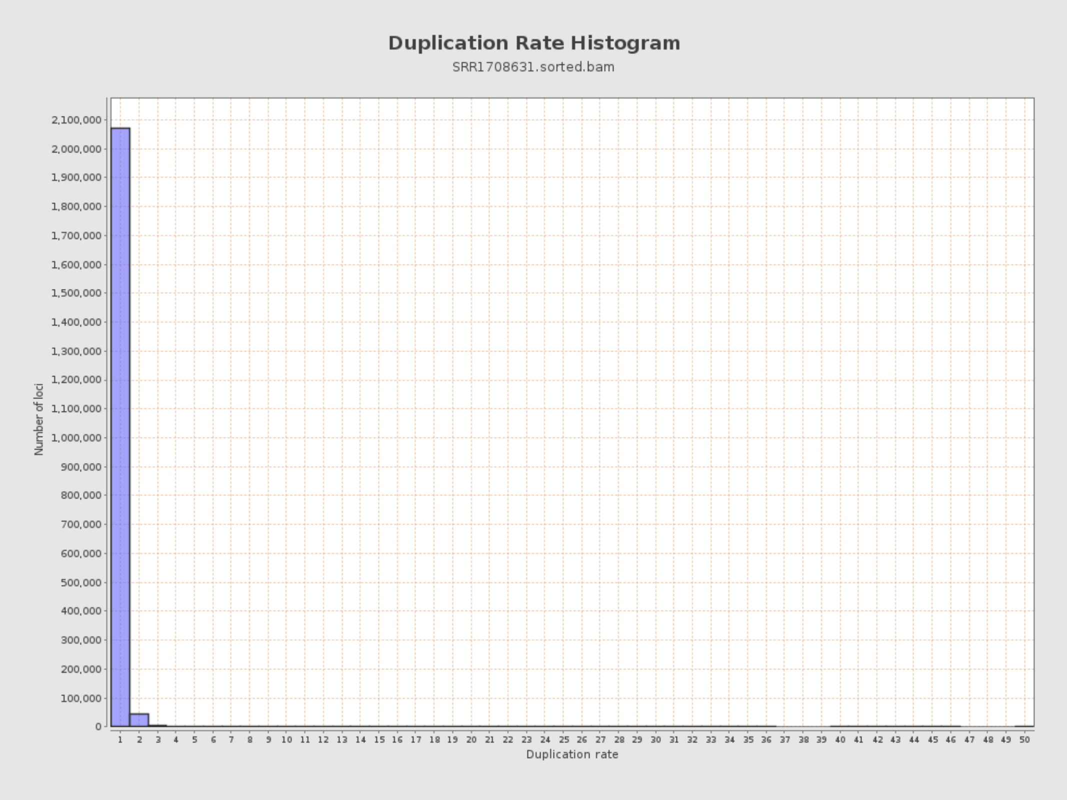
5. Results : Coverage Histogram (0-50X)



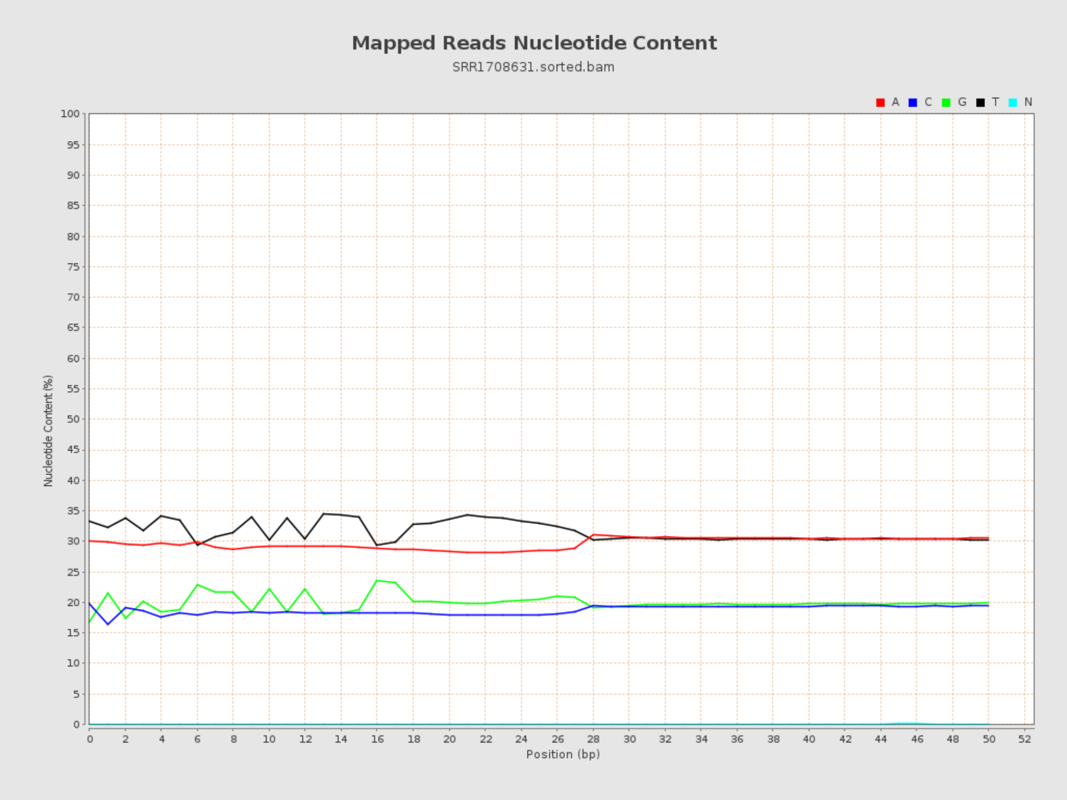
6. Results : Genome Fraction Coverage



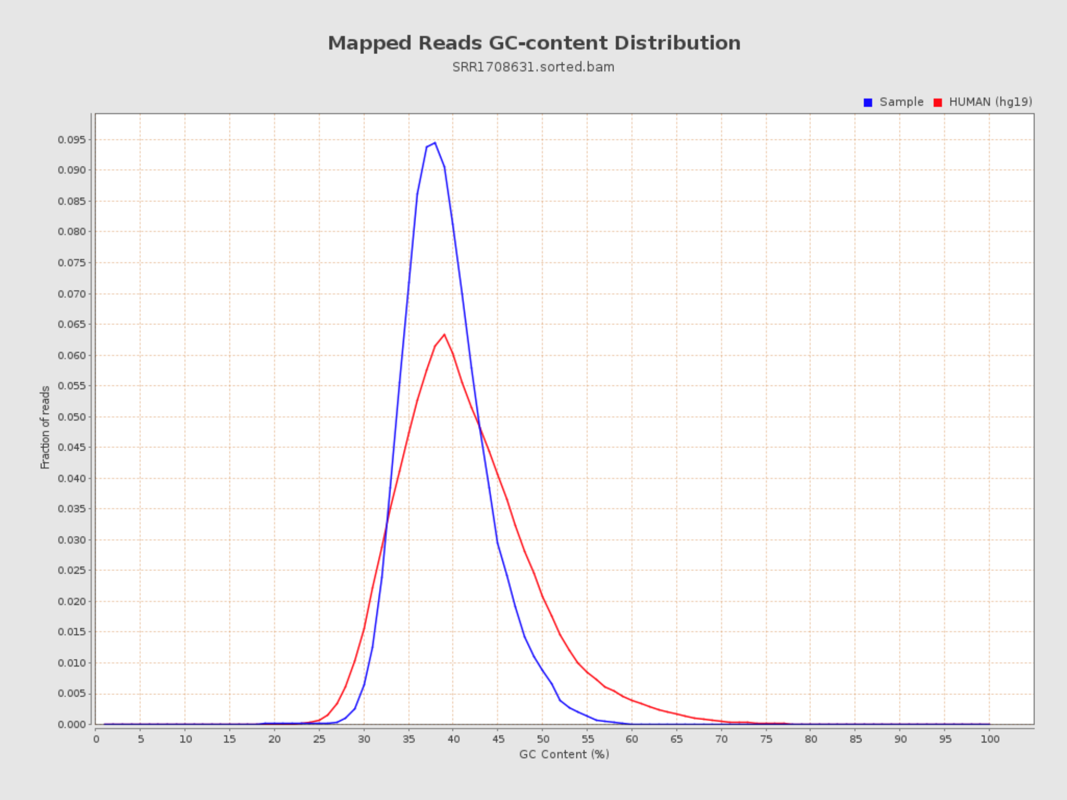
7. Results : Duplication Rate Histogram



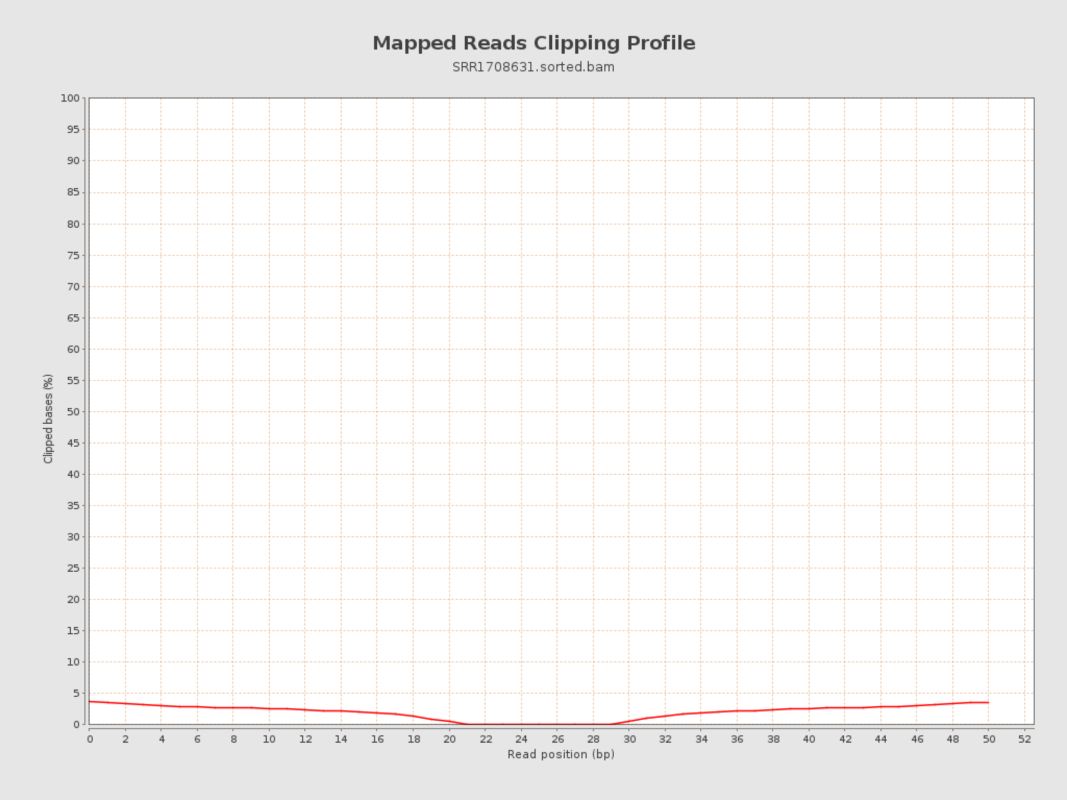
8. Results : Mapped Reads Nucleotide Content



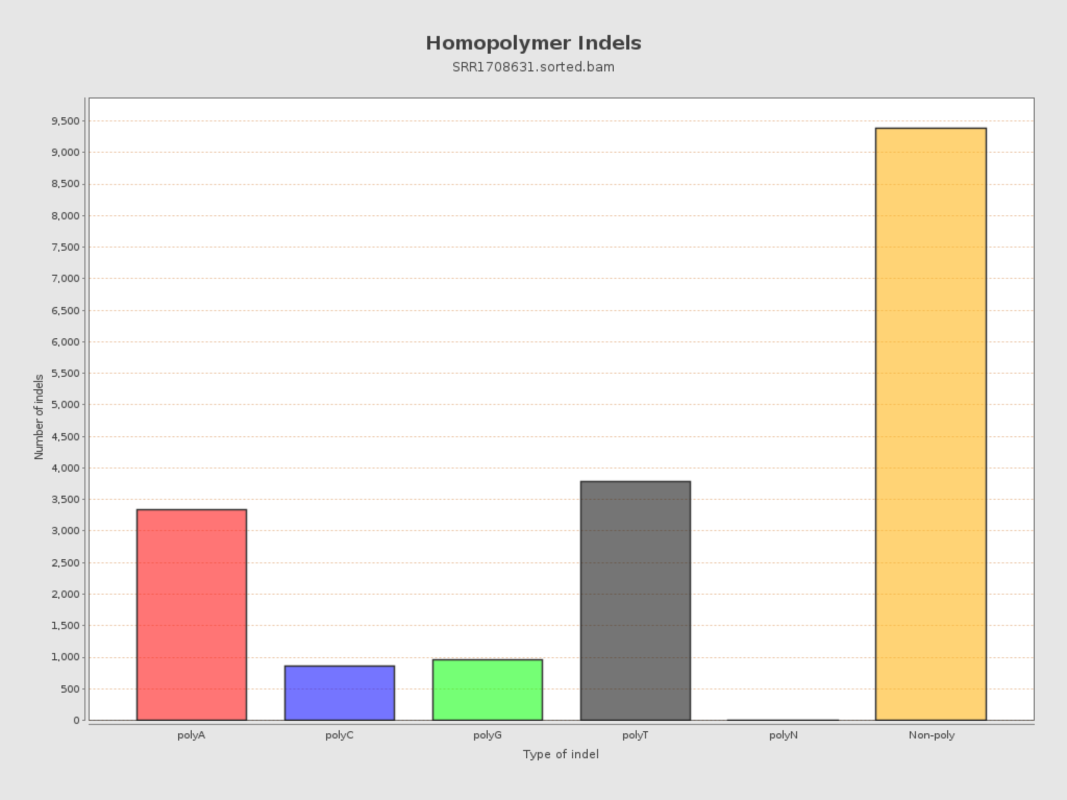
9. Results : Mapped Reads GC-content Distribution



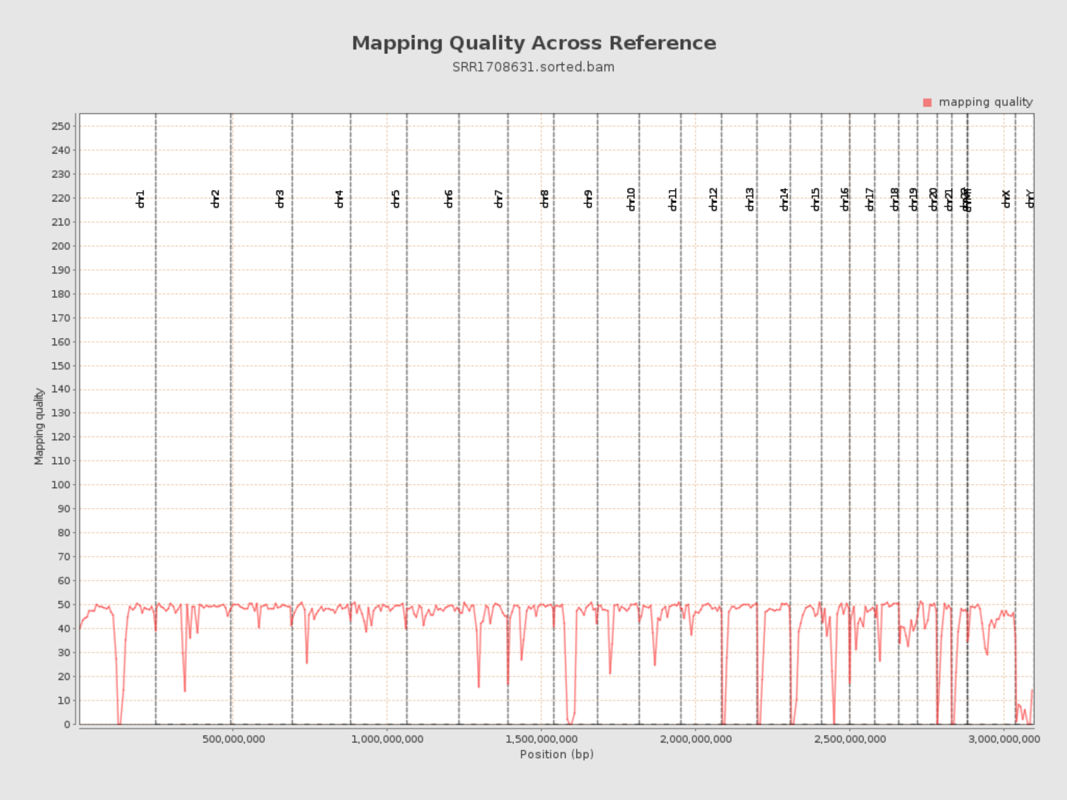
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram