Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:53:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708633.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_SRR1708633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708633.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:53:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,259,773
Mapped reads	2,371,137 / 72.74%
Unmapped reads	888,636 / 27.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	703 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	86,650 / 2.66%
Duplication rate	2.77%
Clipped reads	362,586 / 11.12%

2.2. ACGT Content

Number/percentage of A's	34,102,032 / 29.52%
Number/percentage of C's	21,638,332 / 18.73%
Number/percentage of T's	36,641,825 / 31.72%
Number/percentage of G's	23,124,639 / 20.02%
Number/percentage of N's	10,156 / 0.01%
GC Percentage	38.75%

2.3. Coverage

Mean	0.0373

Standard Deviation	0.3295

2.4. Mapping Quality

Mean Mapping Quality	42.1

2.5. Mismatches and indels

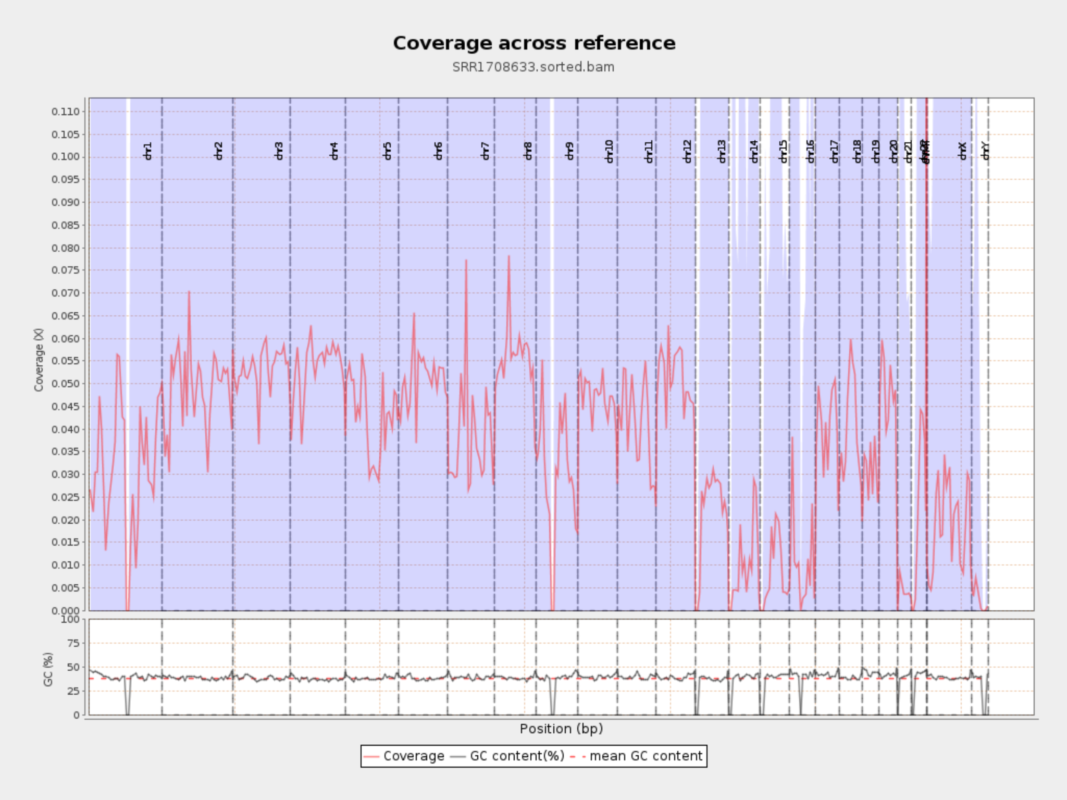
General error rate	0.63%
Mismatches	724,565
Insertions	5,125
Mapped reads with at least one insertion	0.22%
Deletions	13,817
Mapped reads with at least one deletion	0.58%
Homopolymer indels	48.33%

2.6. Chromosome stats

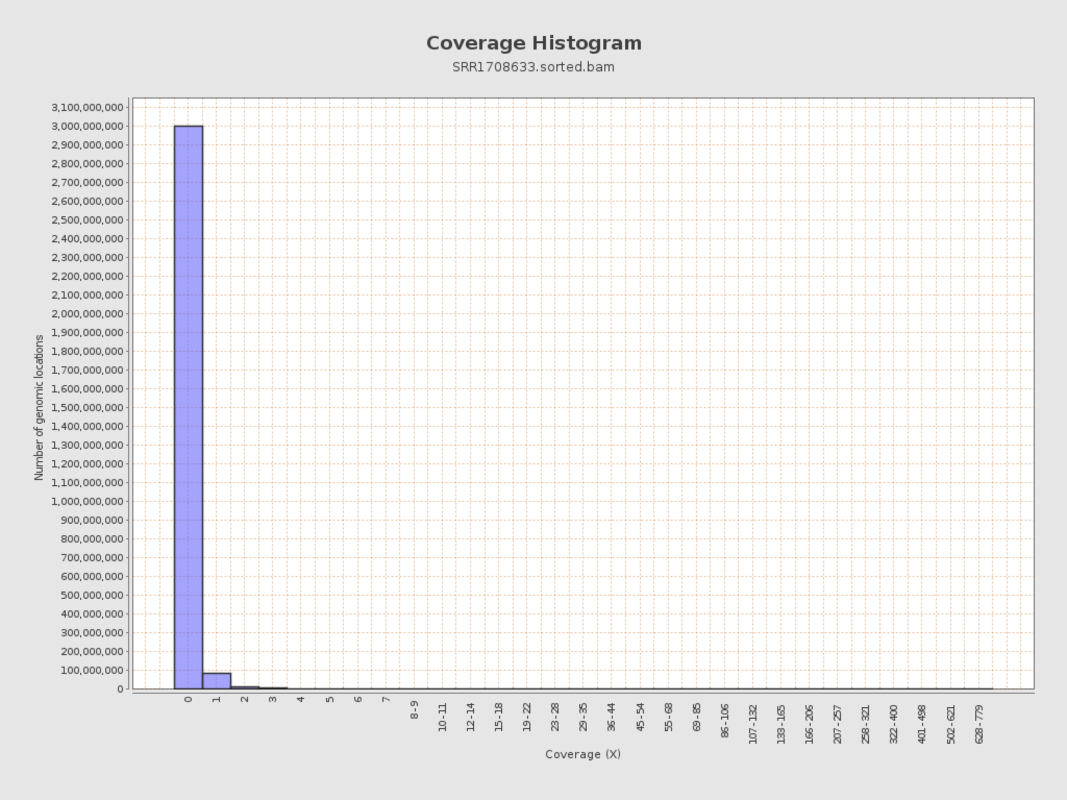
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7802137	0.0313	0.4566
chr2	243199373	11905955	0.049	0.3836
chr3	198022430	10569518	0.0534	0.2705
chr4	191154276	10261814	0.0537	0.2725
chr5	180915260	7723149	0.0427	0.2441
chr6	171115067	8716777	0.0509	0.3178
chr7	159138663	6072883	0.0382	0.581

chr8	146364022	8161062	0.0558	0.5148
chr9	141213431	4222604	0.0299	0.2682
chr10	135534747	6440934	0.0475	0.3316
chr11	135006516	5568387	0.0412	0.3779
chr12	133851895	6866574	0.0513	0.2768
chr13	115169878	2518272	0.0219	0.1731
chr14	107349540	1135407	0.0106	0.1415
chr15	102531392	843402	0.0082	0.107
chr16	90354753	966418	0.0107	0.1261
chr17	81195210	3258910	0.0401	0.3066
chr18	78077248	3170545	0.0406	0.3254
chr19	59128983	1792108	0.0303	0.343
chr20	63025520	3024242	0.048	0.257
chr21	48129895	212796	0.0044	0.1084
chr22	51304566	1167161	0.0227	0.1747
chrMT	16571	4184	0.2525	0.5793
chrX	155270560	2996992	0.0193	0.1993
chrY	59373566	135623	0.0023	0.0628

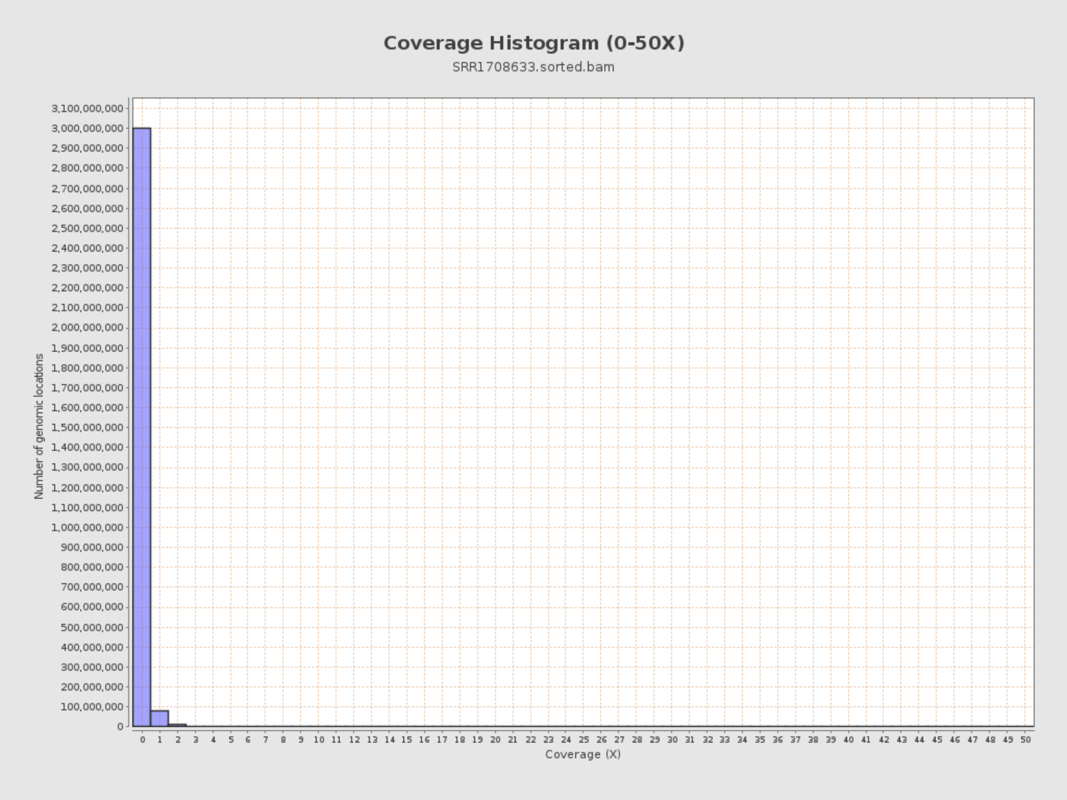
3. Results : Coverage across reference



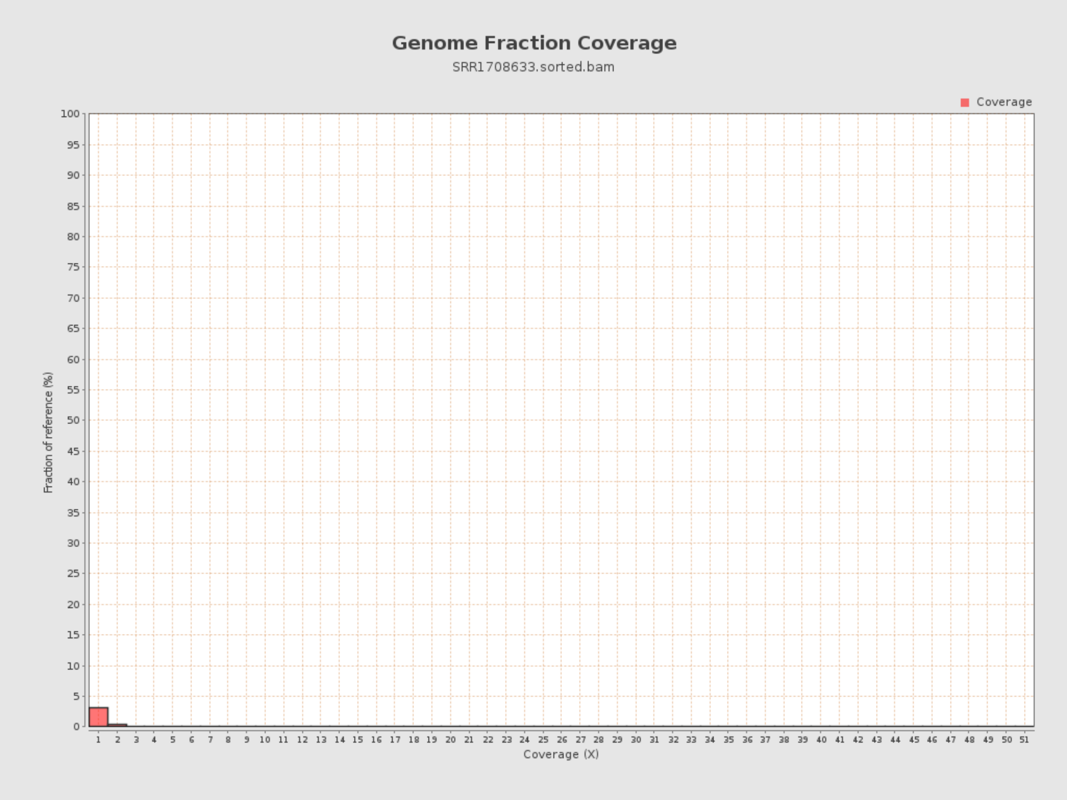
4. Results : Coverage Histogram



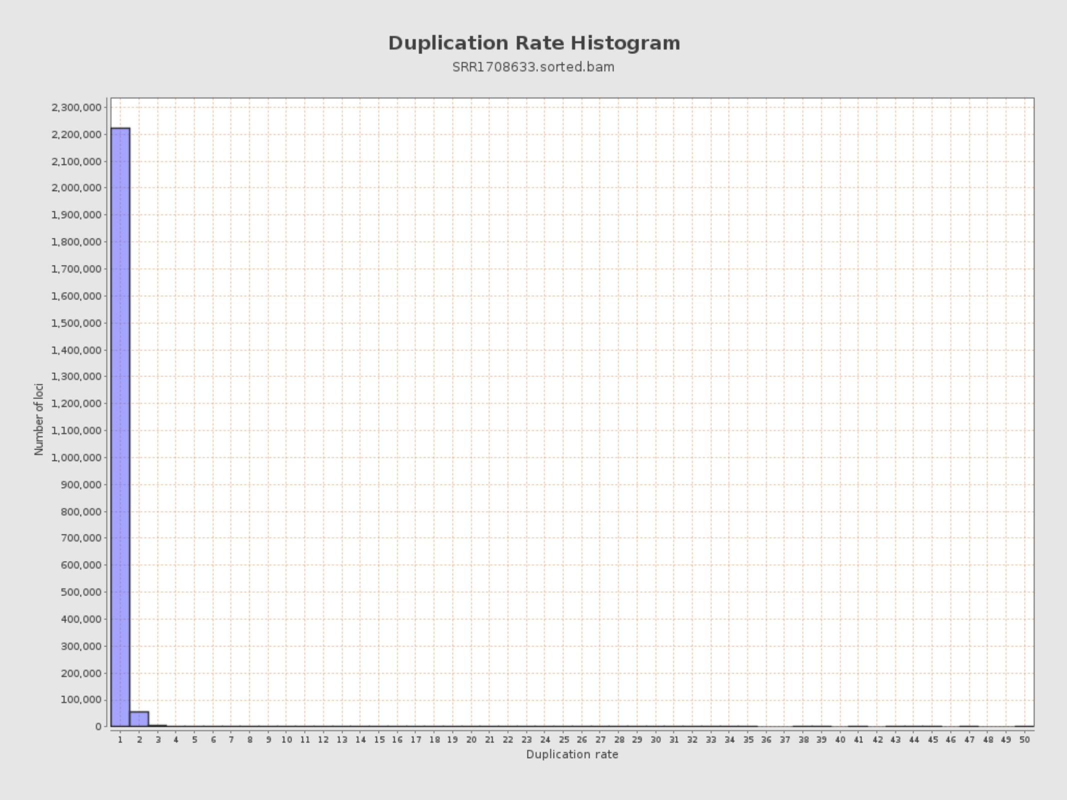
5. Results : Coverage Histogram (0-50X)



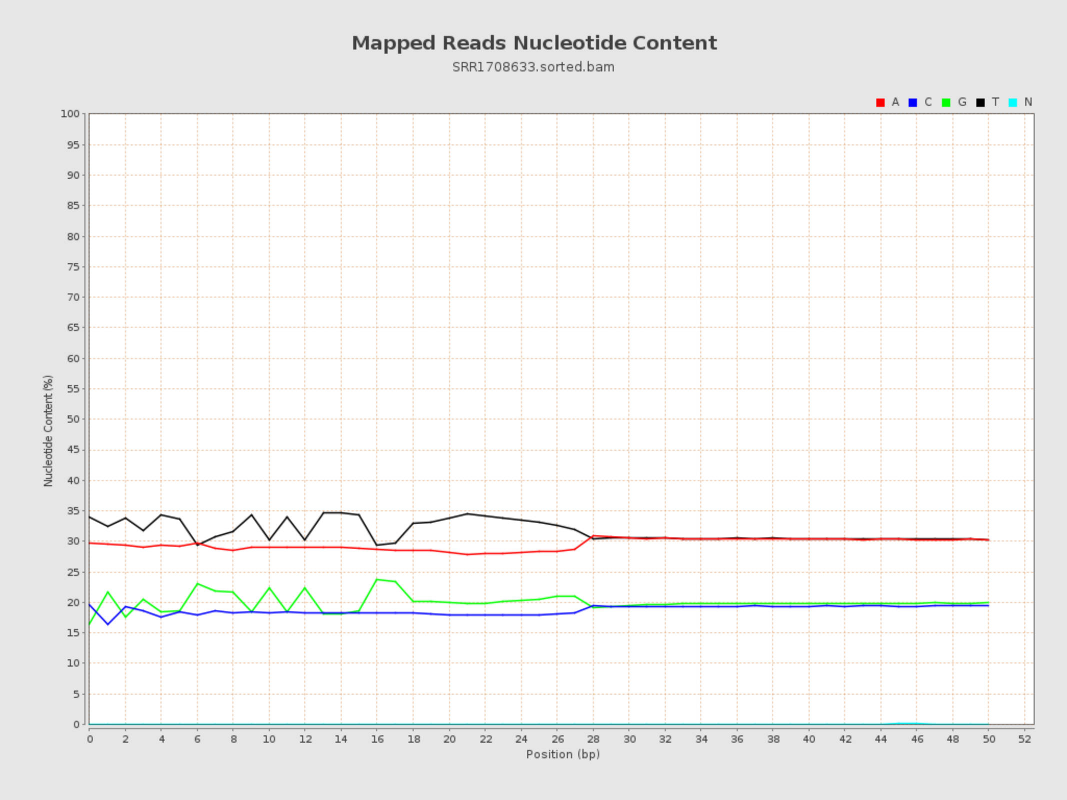
6. Results : Genome Fraction Coverage



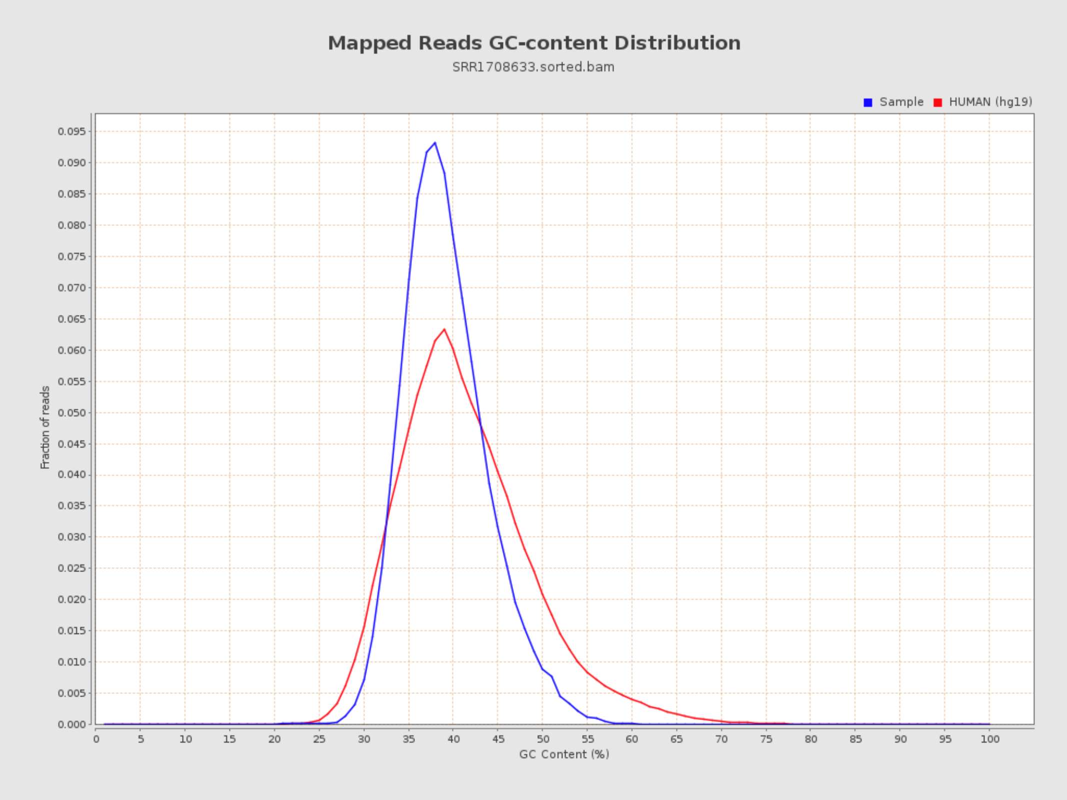
7. Results : Duplication Rate Histogram



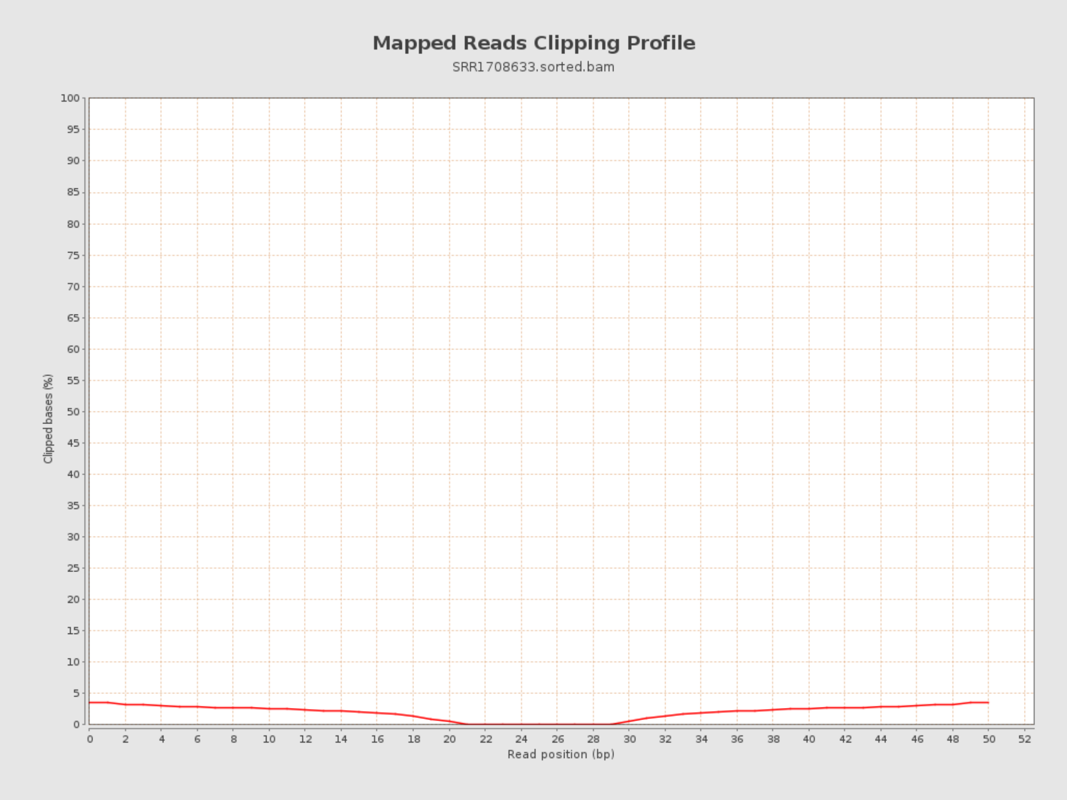
8. Results : Mapped Reads Nucleotide Content



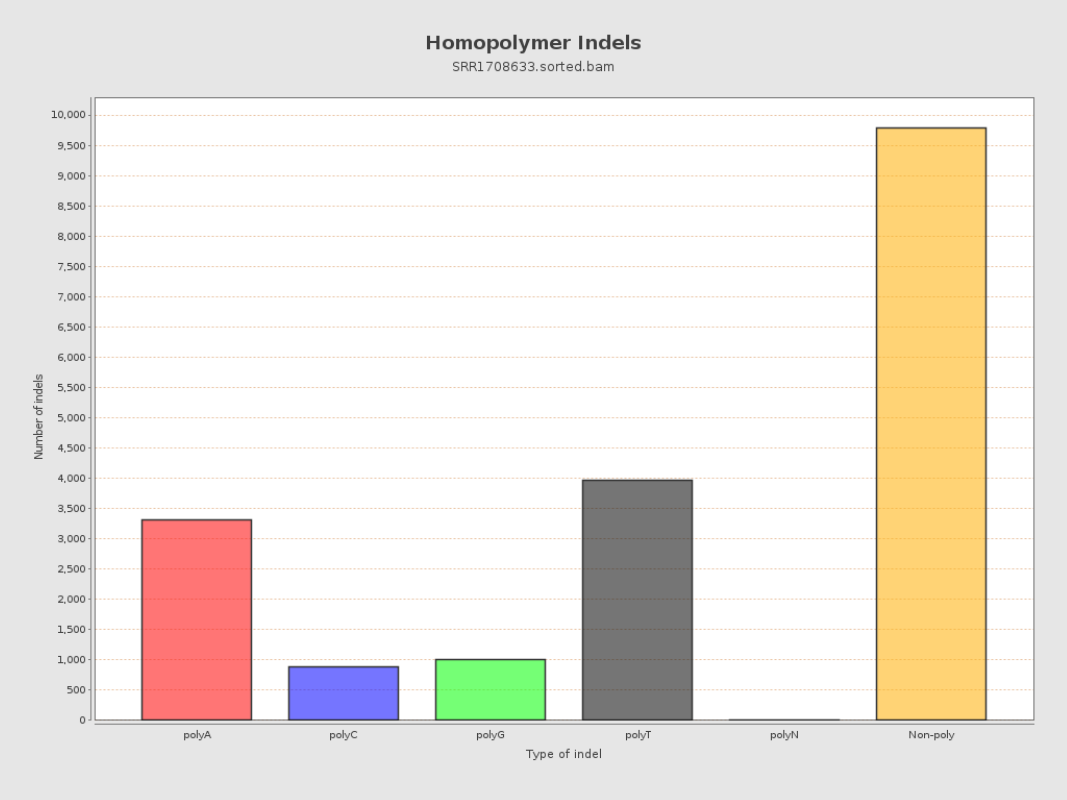
9. Results : Mapped Reads GC-content Distribution



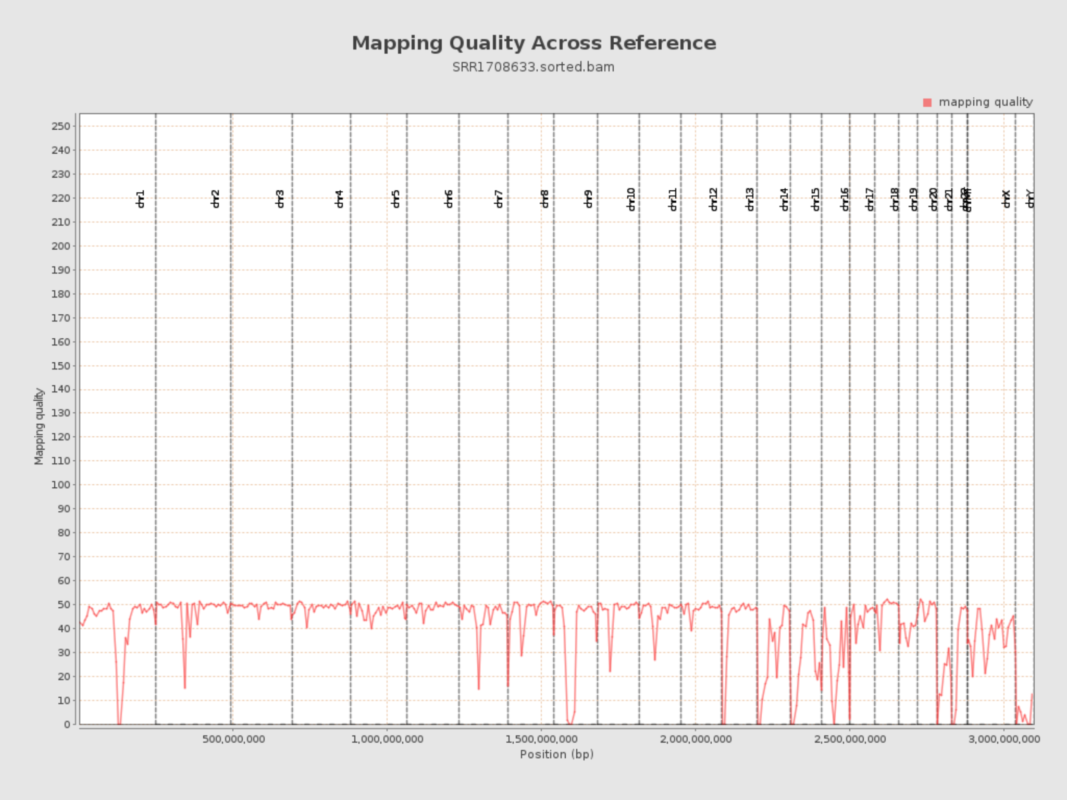
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram