Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:57:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708591.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_SRR1708591 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708591.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:57:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708591.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,874,348
Mapped reads	2,810,739 / 97.79%
Unmapped reads	63,609 / 2.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	89 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	26,588 / 0.93%
Duplication rate	0.95%
Clipped reads	38,102 / 1.33%

2.2. ACGT Content

Number/percentage of A's	43,445,918 / 30.99%
Number/percentage of C's	26,547,584 / 18.94%
Number/percentage of T's	43,244,615 / 30.85%
Number/percentage of G's	26,937,523 / 19.22%
Number/percentage of N's	4,803 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	0.0453

Standard Deviation	0.2188

2.4. Mapping Quality

Mean Mapping Quality	46.71

2.5. Mismatches and indels

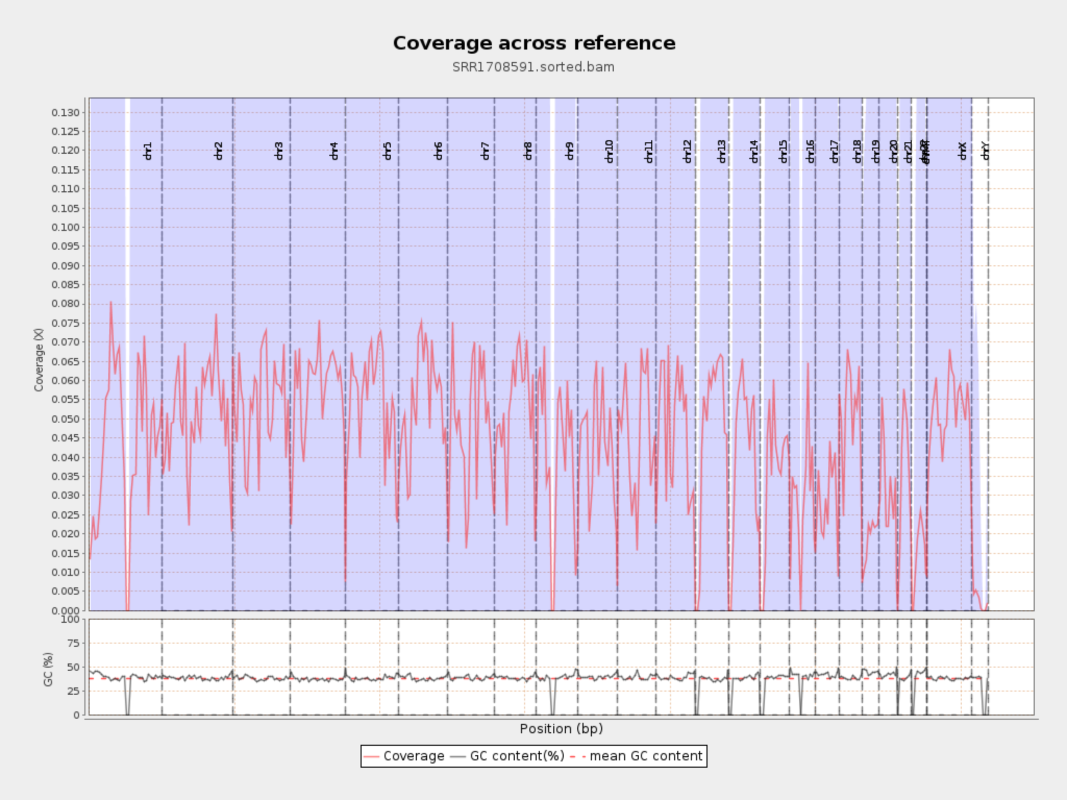
General error rate	0.16%
Mismatches	206,940
Insertions	8,877
Mapped reads with at least one insertion	0.32%
Deletions	7,213
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.07%

2.6. Chromosome stats

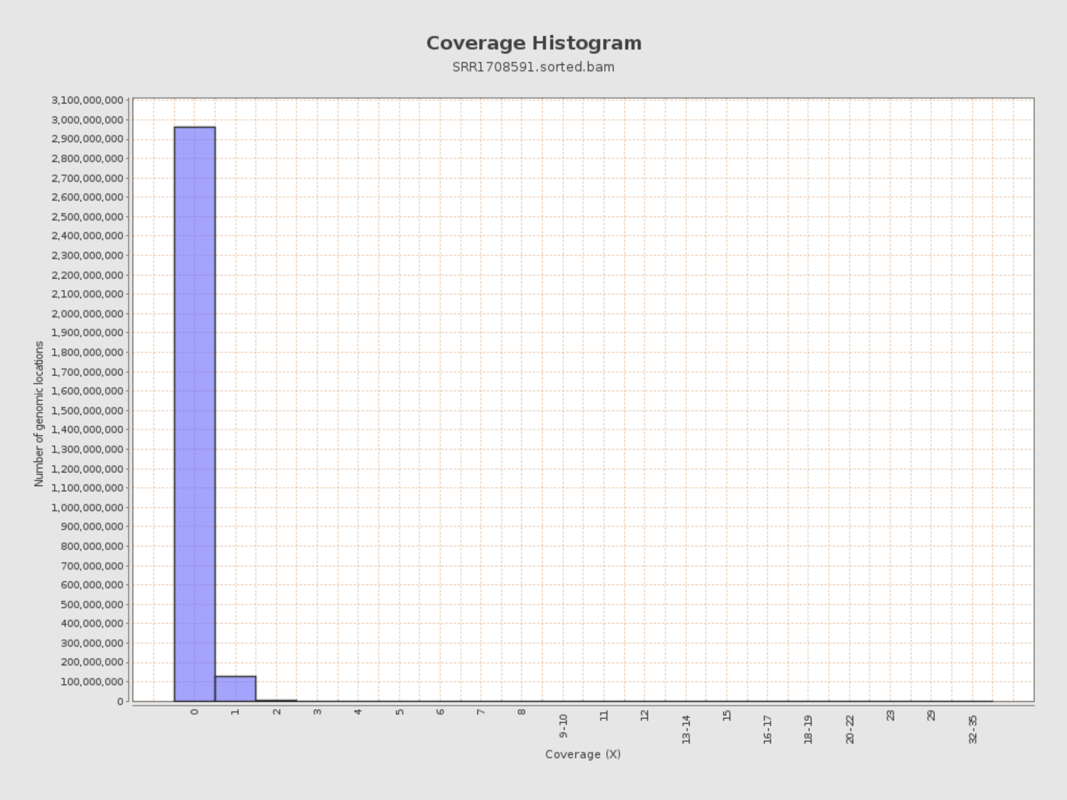
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10886869	0.0437	0.2156
chr2	243199373	12506403	0.0514	0.2325
chr3	198022430	10746127	0.0543	0.2387
chr4	191154276	11106198	0.0581	0.2471
chr5	180915260	9943734	0.055	0.2401
chr6	171115067	9274871	0.0542	0.2386
chr7	159138663	7772021	0.0488	0.2271

chr8	146364022	7738496	0.0529	0.2357
chr9	141213431	5759641	0.0408	0.2079
chr10	135534747	5995671	0.0442	0.2157
chr11	135006516	6195451	0.0459	0.2204
chr12	133851895	6293082	0.047	0.2225
chr13	115169878	5331196	0.0463	0.221
chr14	107349540	4336750	0.0404	0.2069
chr15	102531392	3650786	0.0356	0.1946
chr16	90354753	2666710	0.0295	0.1767
chr17	81195210	2264467	0.0279	0.1715
chr18	78077248	4029645	0.0516	0.233
chr19	59128983	1118432	0.0189	0.1407
chr20	63025520	2025595	0.0321	0.1841
chr21	48129895	1640156	0.0341	0.1907
chr22	51304566	745614	0.0145	0.1235
chrMT	16571	150	0.0091	0.0947
chrX	155270560	7983282	0.0514	0.2327
chrY	59373566	181313	0.0031	0.0565

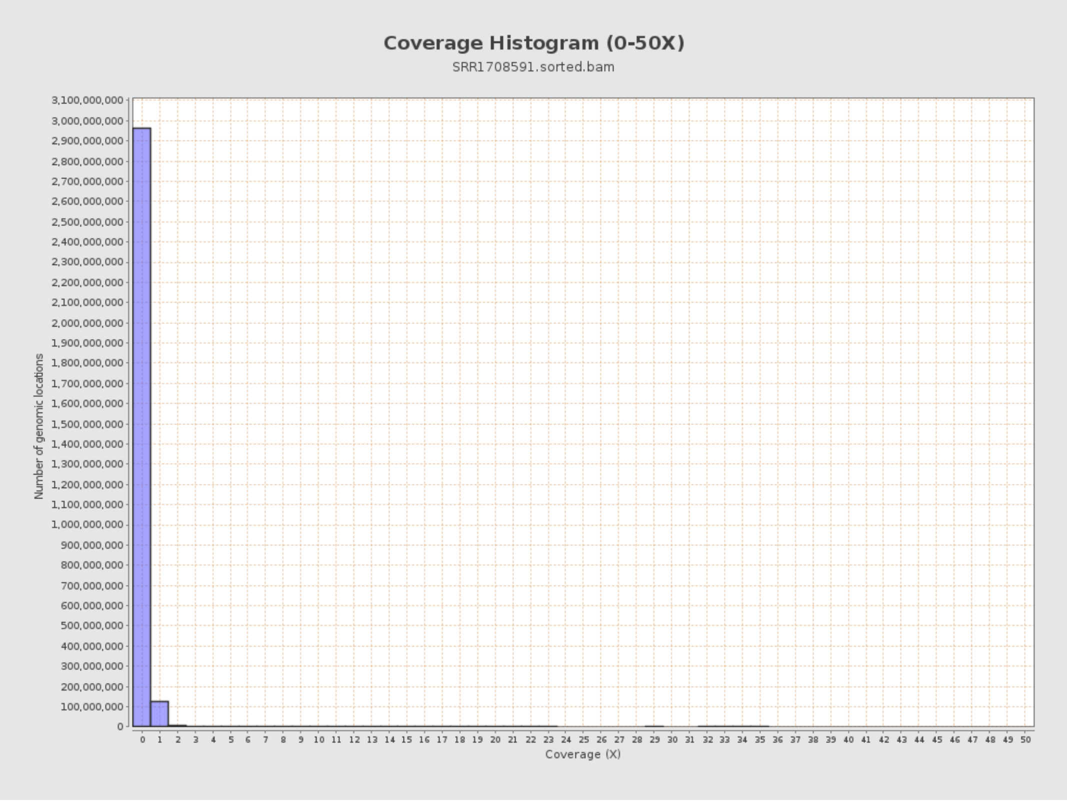
3. Results : Coverage across reference



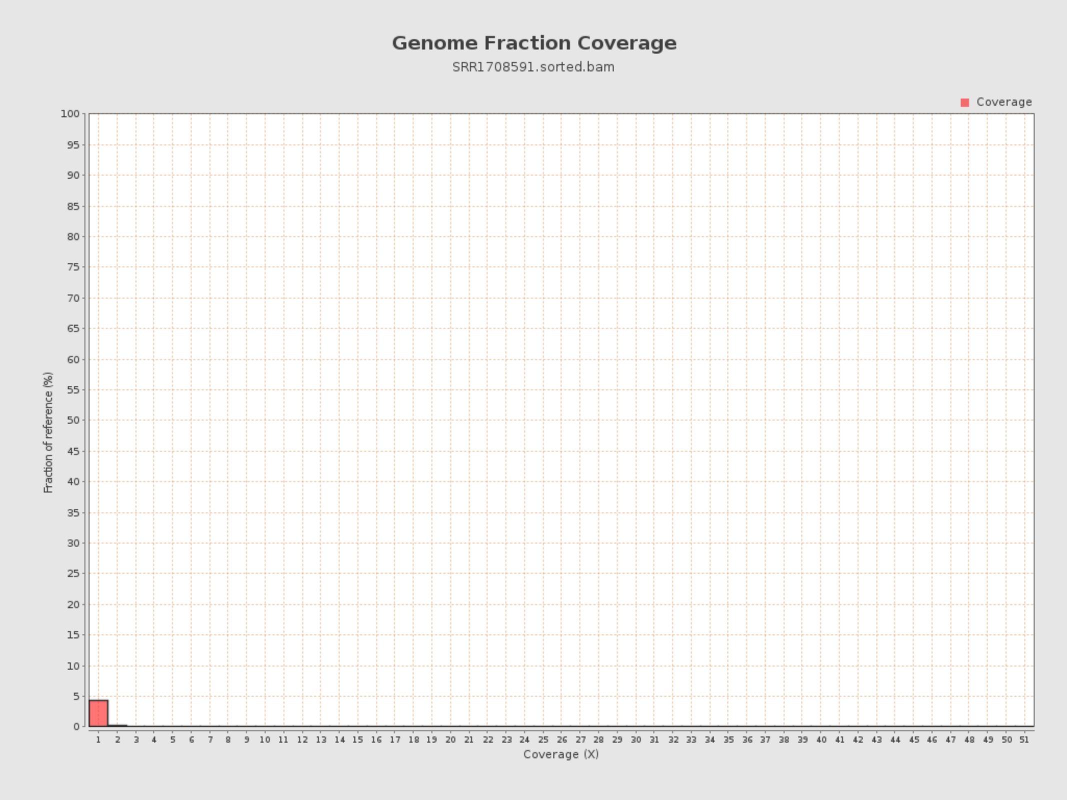
4. Results : Coverage Histogram



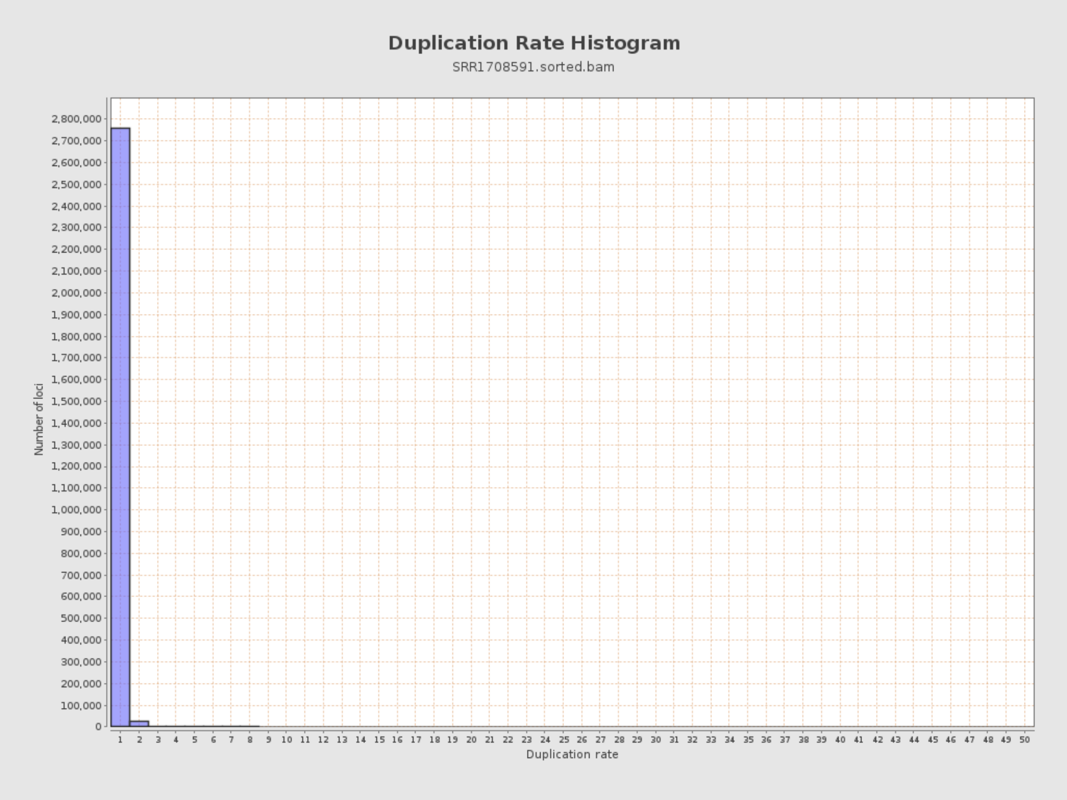
5. Results : Coverage Histogram (0-50X)



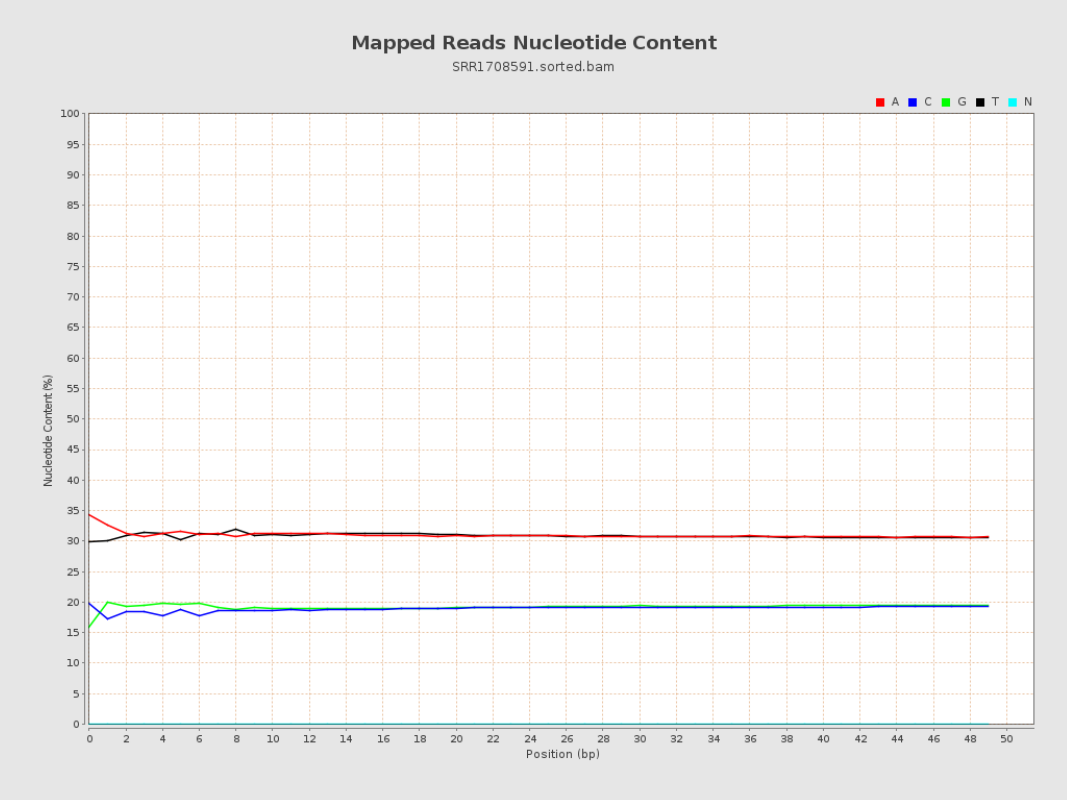
6. Results : Genome Fraction Coverage



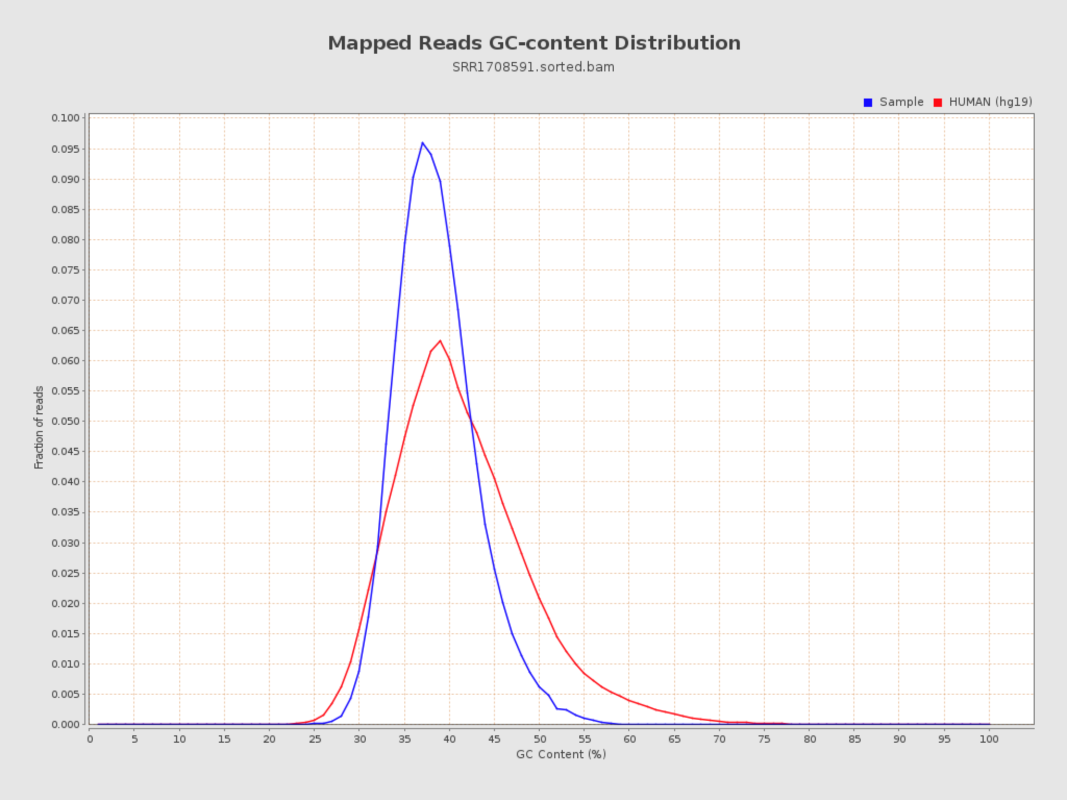
7. Results : Duplication Rate Histogram



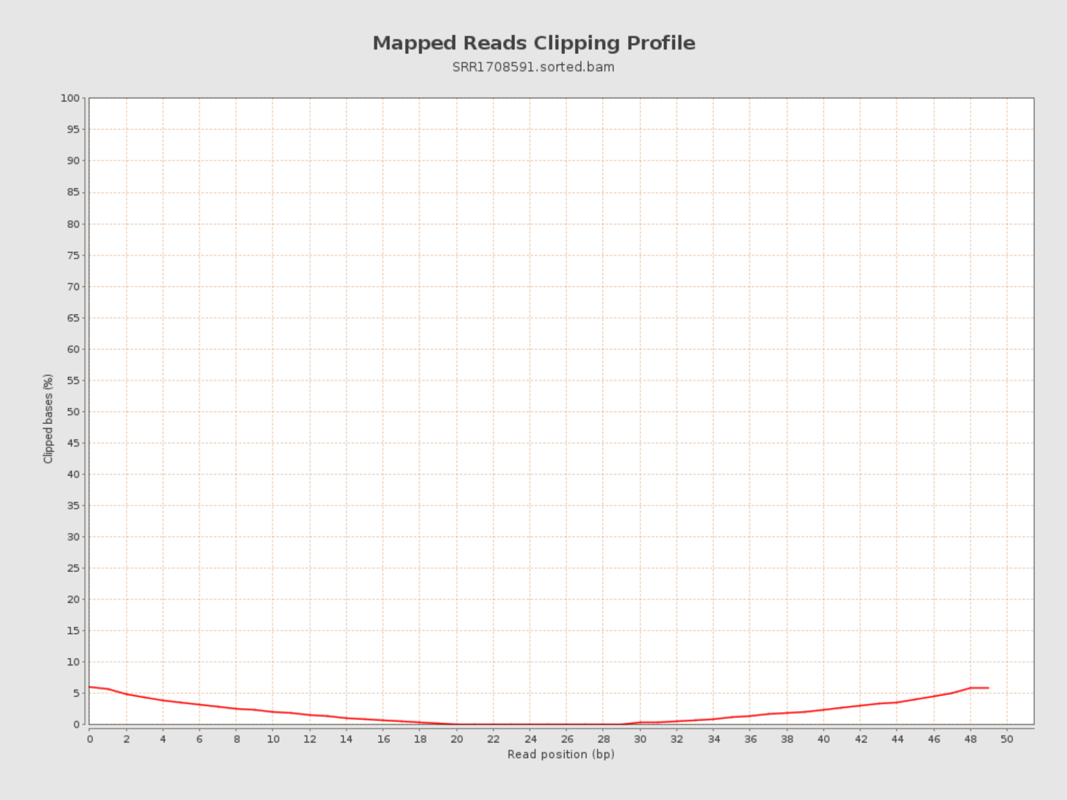
8. Results : Mapped Reads Nucleotide Content



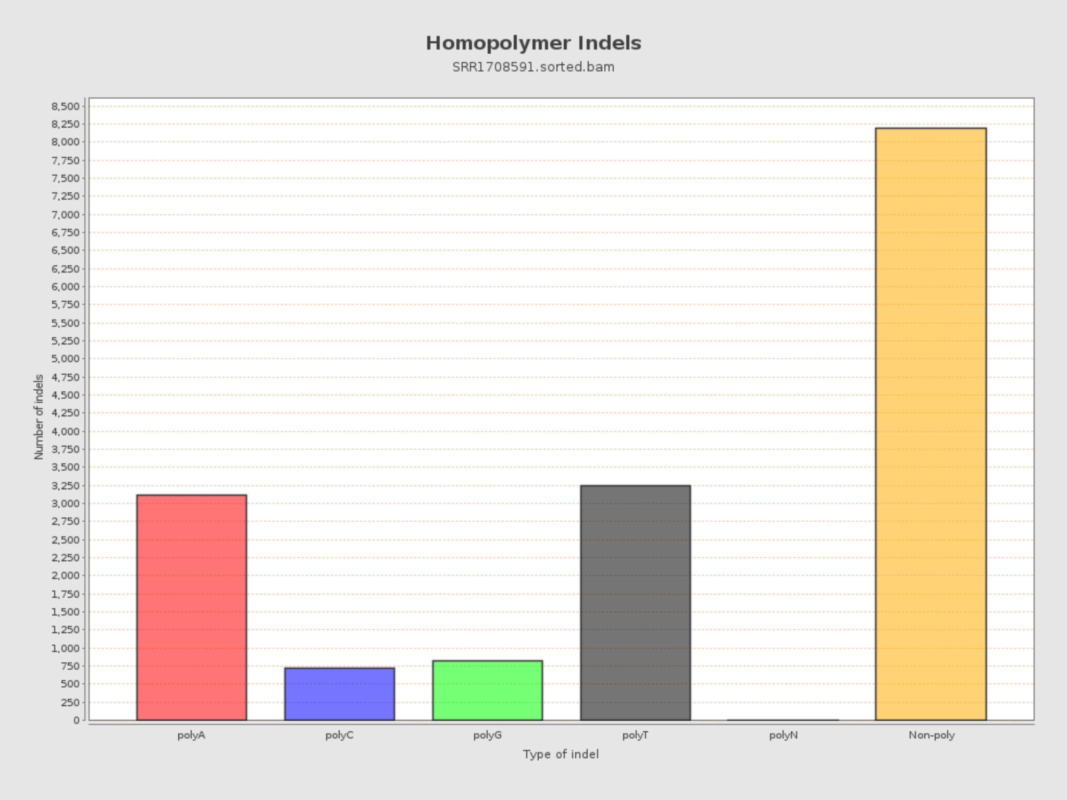
9. Results : Mapped Reads GC-content Distribution



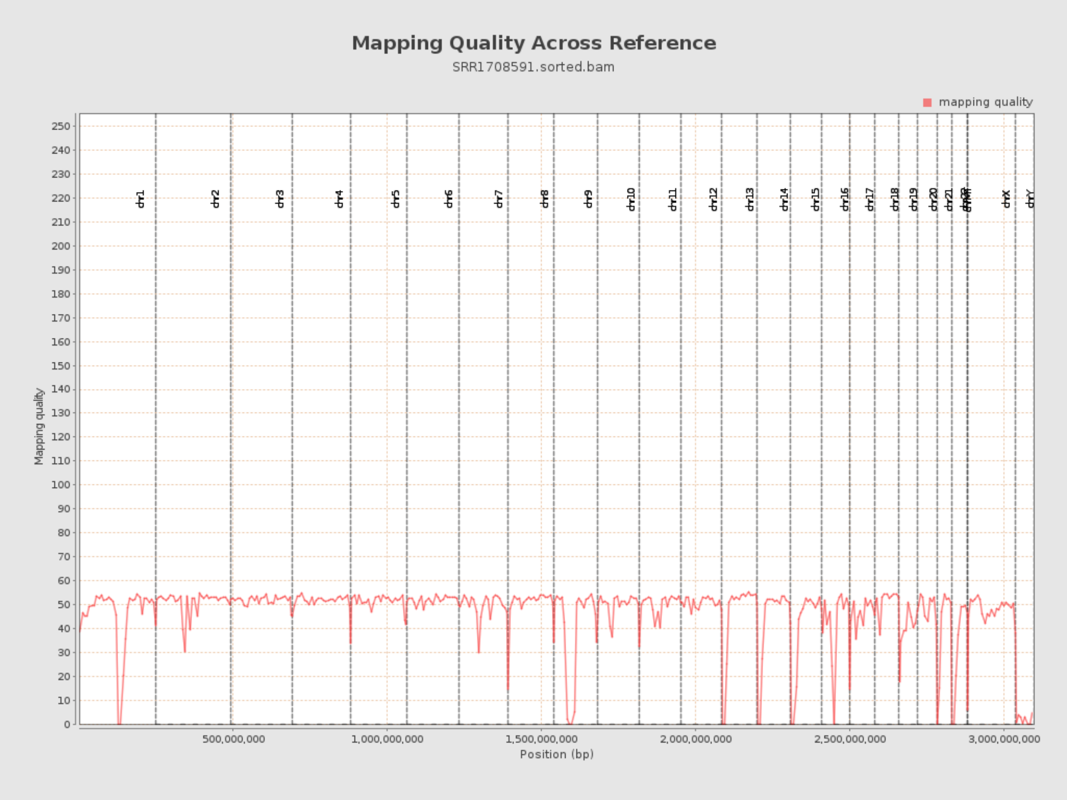
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram