Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:38:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708579.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_SRR1708579 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708579.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:38:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708579.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,065,414
Mapped reads	4,956,296 / 97.85%
Unmapped reads	109,118 / 2.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	166 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	49,703 / 0.98%
Duplication rate	1%
Clipped reads	68,363 / 1.35%

2.2. ACGT Content

Number/percentage of A's	76,588,611 / 30.99%
Number/percentage of C's	46,821,921 / 18.94%
Number/percentage of T's	76,285,556 / 30.86%
Number/percentage of G's	47,461,448 / 19.2%
Number/percentage of N's	8,940 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	0.0798

Standard Deviation	0.295

2.4. Mapping Quality

Mean Mapping Quality	46.78

2.5. Mismatches and indels

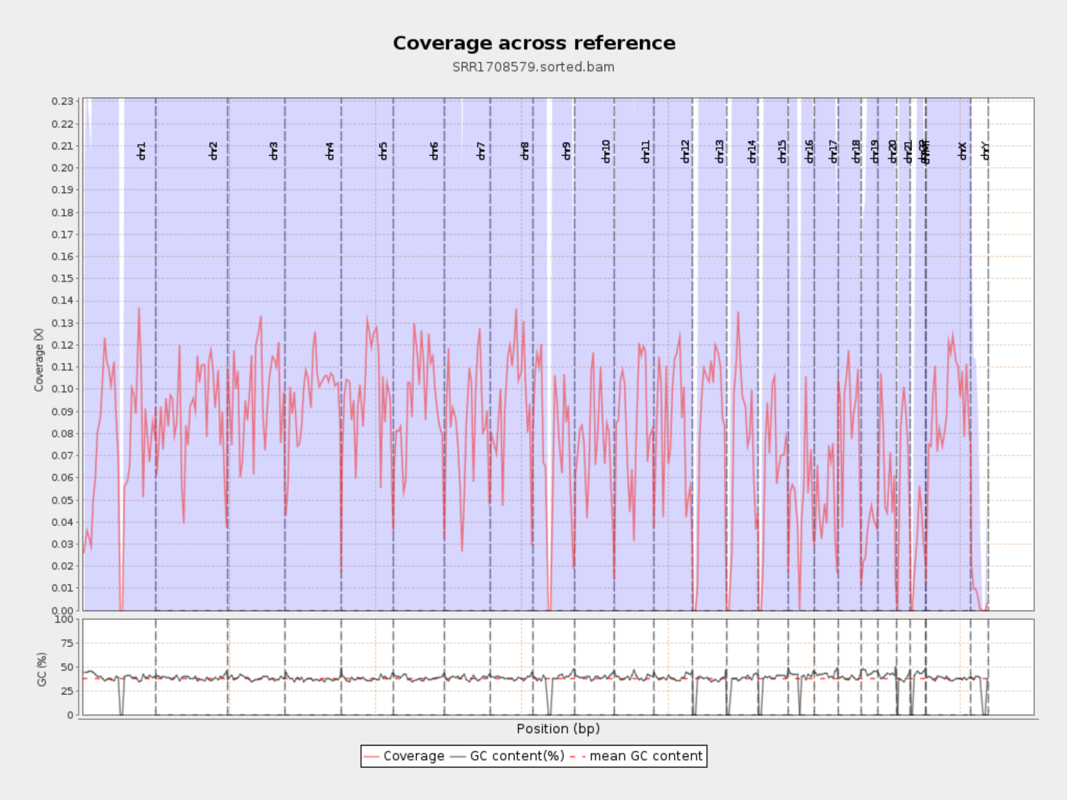
General error rate	0.15%
Mismatches	360,397
Insertions	15,351
Mapped reads with at least one insertion	0.31%
Deletions	12,595
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.41%

2.6. Chromosome stats

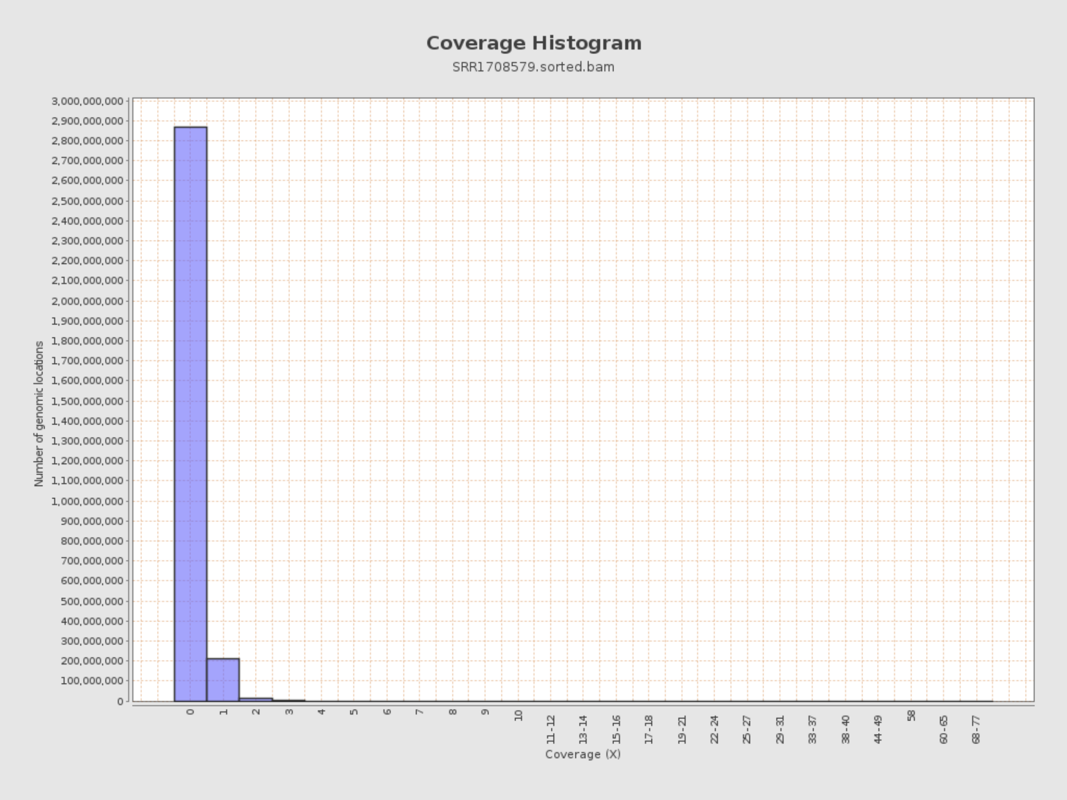
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18644607	0.0748	0.2874
chr2	243199373	21533605	0.0885	0.309
chr3	198022430	19394864	0.0979	0.3255
chr4	191154276	18444285	0.0965	0.3217
chr5	180915260	17385889	0.0961	0.3219
chr6	171115067	16245434	0.0949	0.3202
chr7	159138663	13151405	0.0826	0.2999

chr8	146364022	13927710	0.0952	0.321
chr9	141213431	10437259	0.0739	0.2844
chr10	135534747	10426081	0.0769	0.288
chr11	135006516	11408105	0.0845	0.3038
chr12	133851895	11229645	0.0839	0.302
chr13	115169878	9625301	0.0836	0.3019
chr14	107349540	7948022	0.074	0.2856
chr15	102531392	6514552	0.0635	0.2644
chr16	90354753	4479814	0.0496	0.2318
chr17	81195210	4045998	0.0498	0.2327
chr18	78077248	7020315	0.0899	0.3113
chr19	59128983	2066024	0.0349	0.1933
chr20	63025520	3973396	0.063	0.2625
chr21	48129895	3078564	0.064	0.2662
chr22	51304566	1456487	0.0284	0.1754
chrMT	16571	200	0.0121	0.1092
chrX	155270560	14414968	0.0928	0.3173
chrY	59373566	335299	0.0056	0.0792

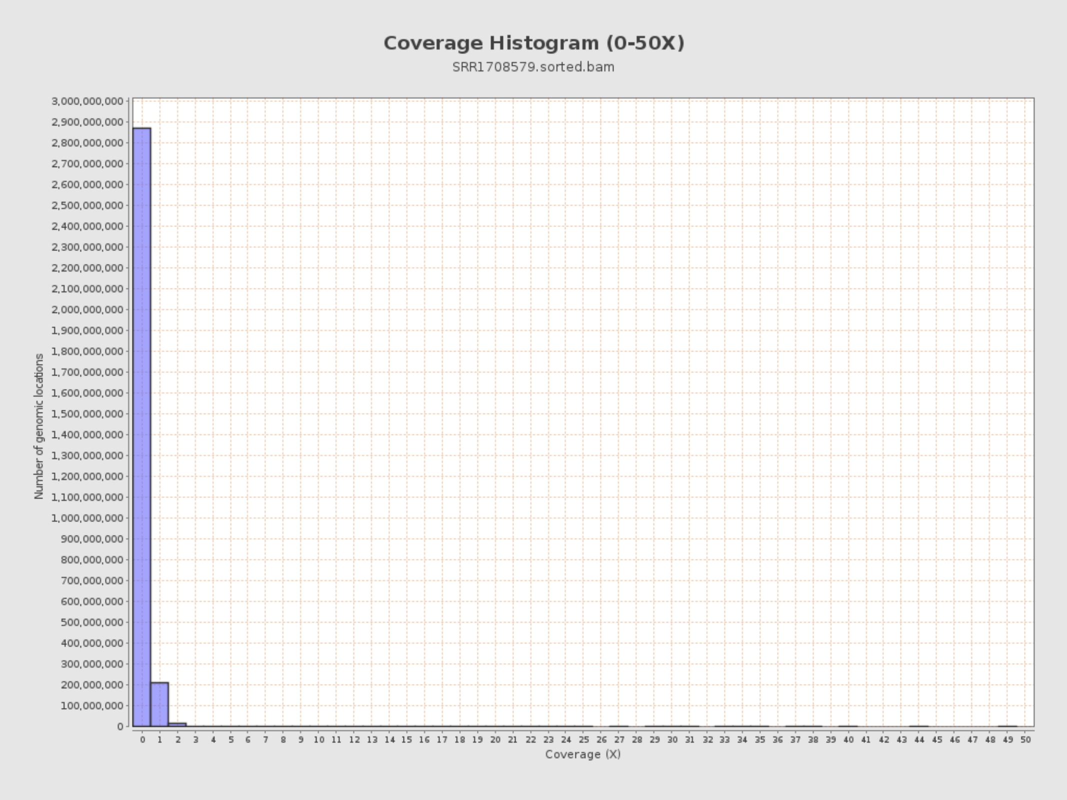
3. Results : Coverage across reference



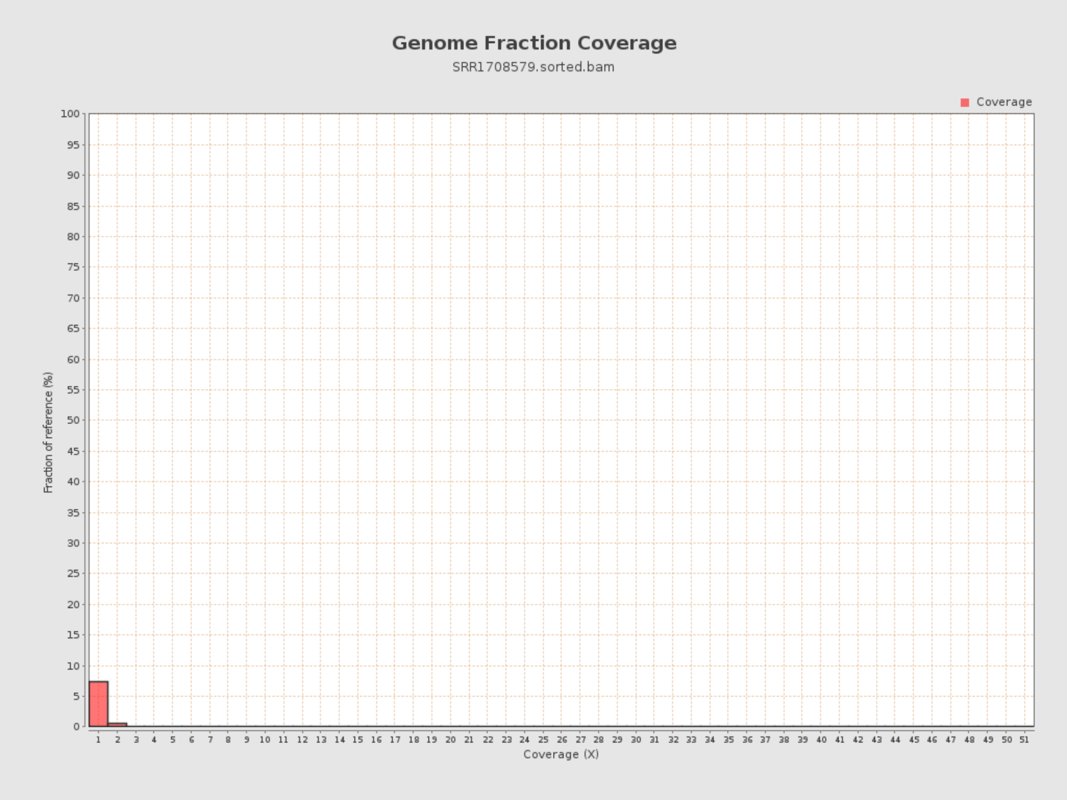
4. Results : Coverage Histogram



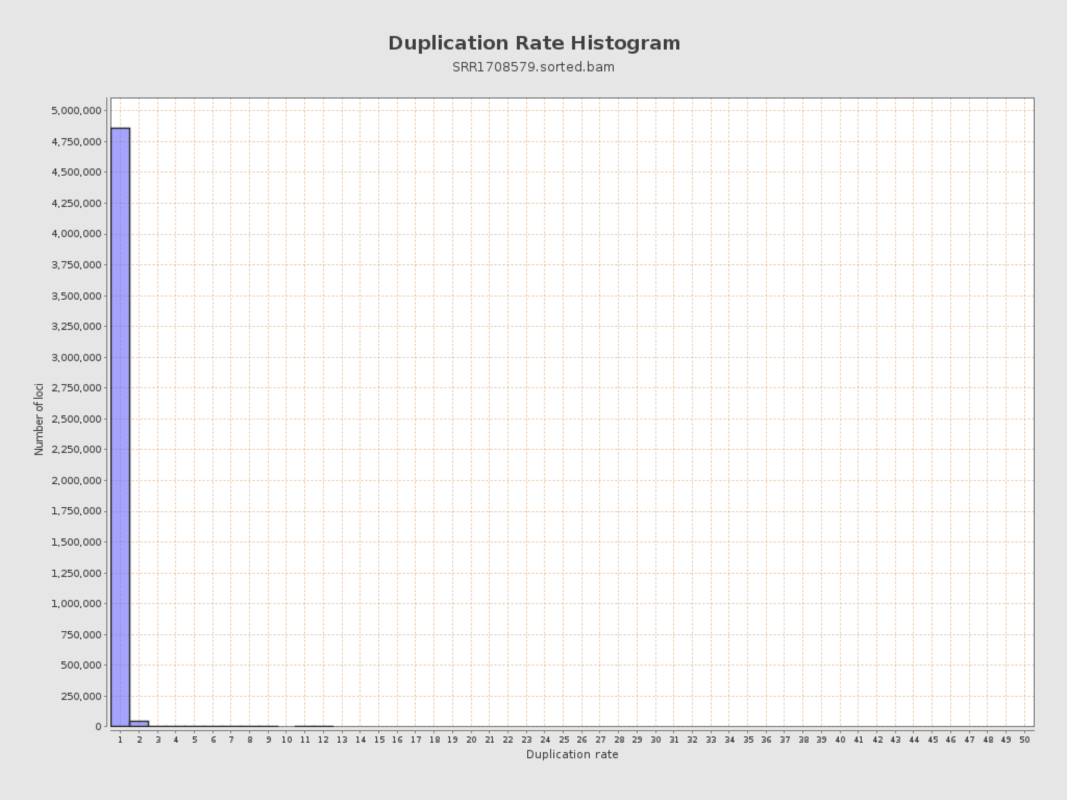
5. Results : Coverage Histogram (0-50X)



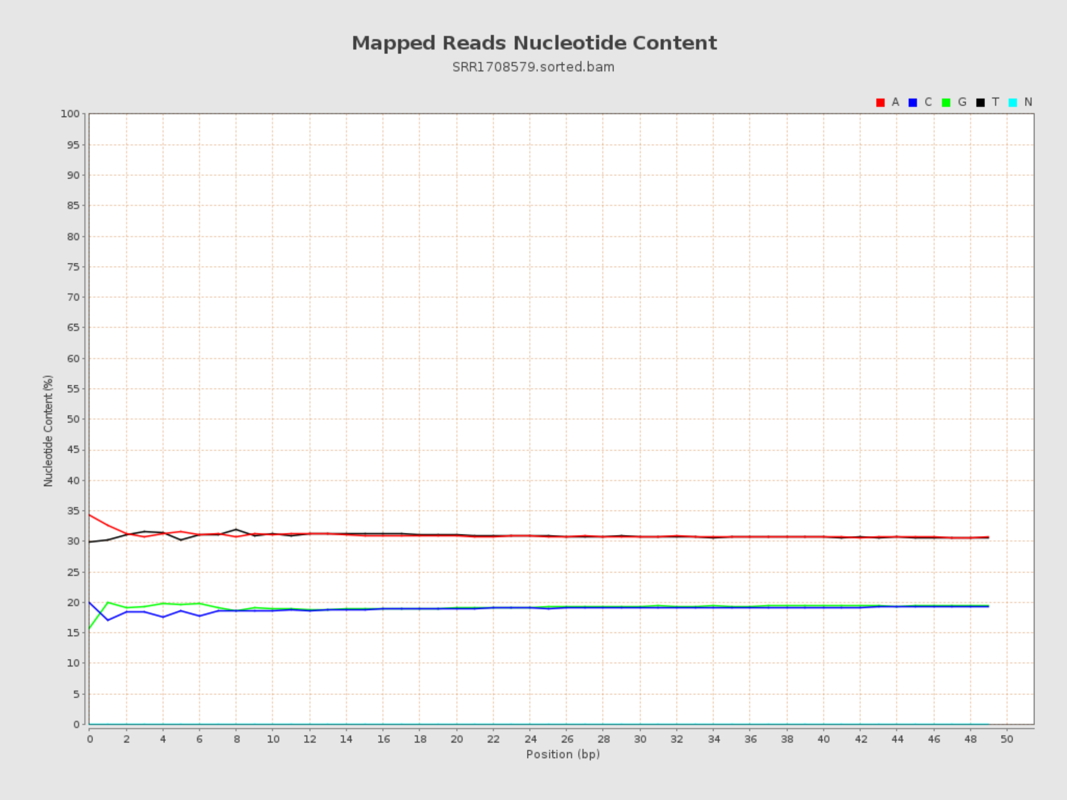
6. Results : Genome Fraction Coverage



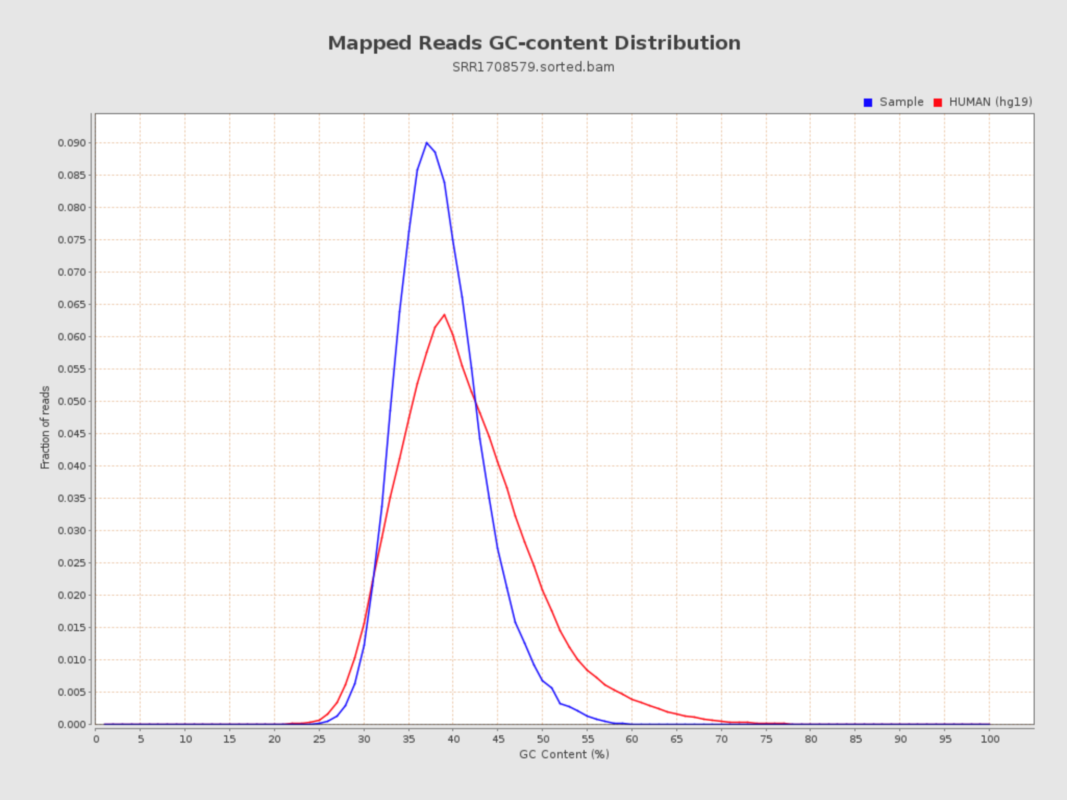
7. Results : Duplication Rate Histogram



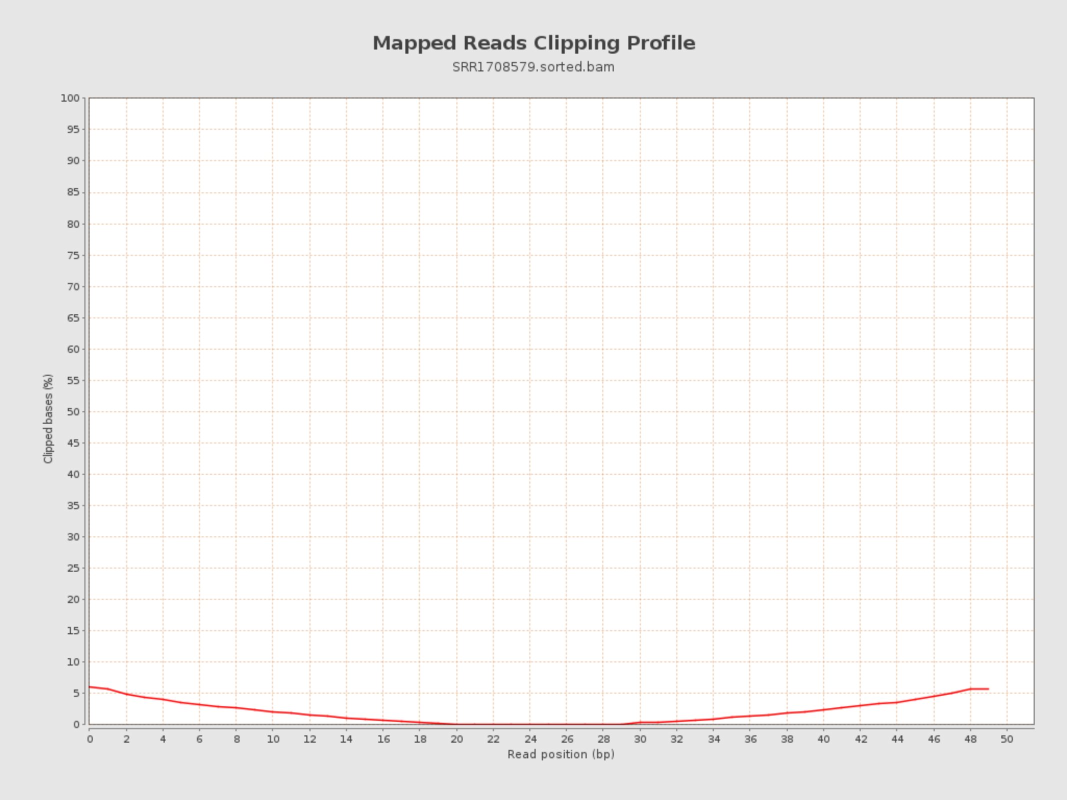
8. Results : Mapped Reads Nucleotide Content



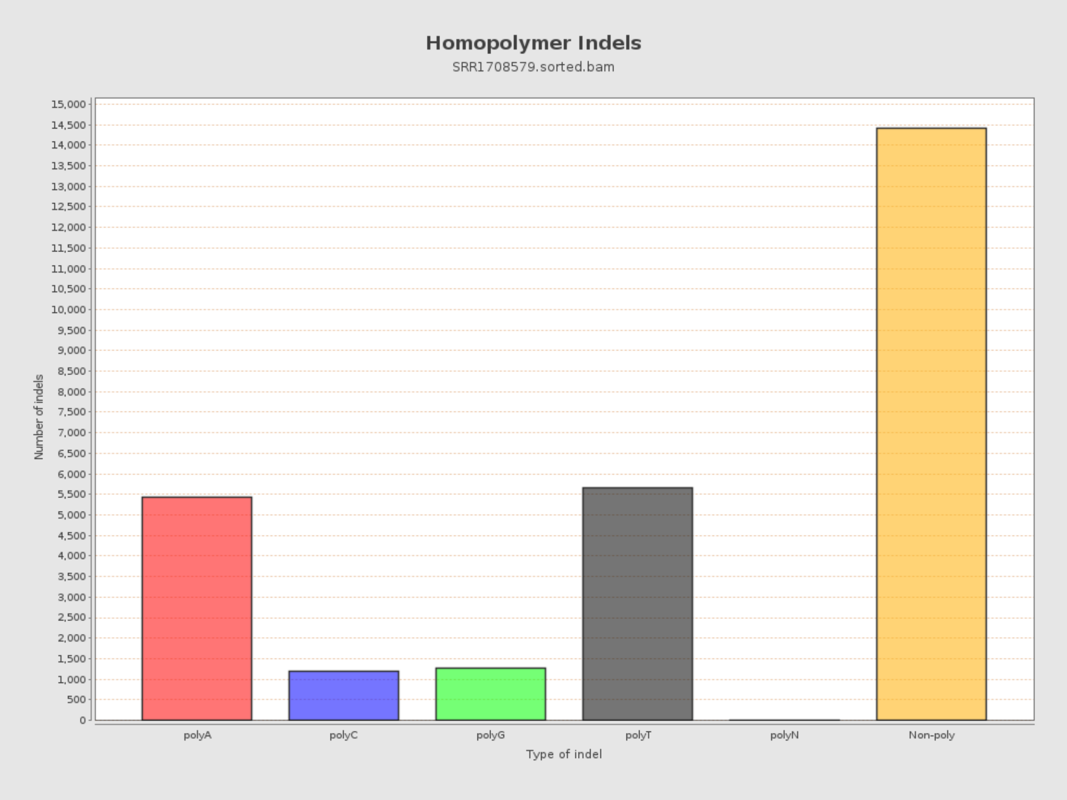
9. Results : Mapped Reads GC-content Distribution



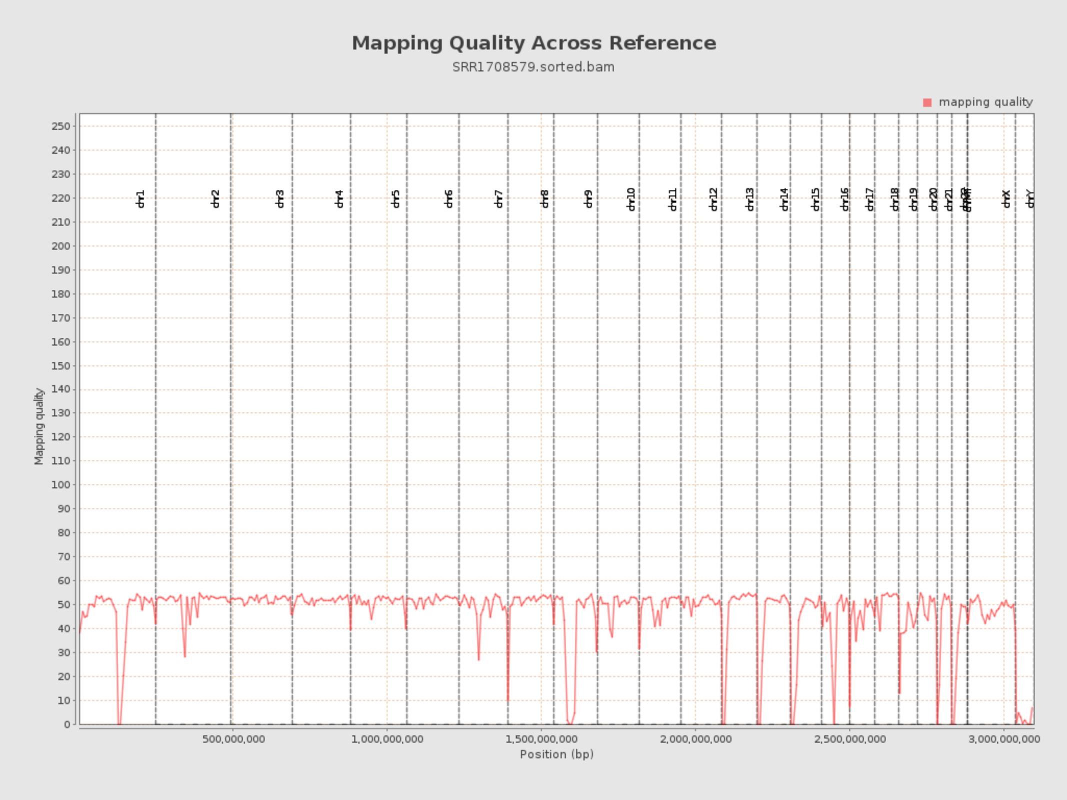
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram