Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:51:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708543.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_SRR1708543 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708543.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:51:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708543.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,888,688
Mapped reads	21,117,546 / 96.48%
Unmapped reads	771,142 / 3.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	497 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	173,234 / 0.79%
Duplication rate	0.81%
Clipped reads	340,008 / 1.55%

2.2. ACGT Content

Number/percentage of A's	324,037,757 / 30.77%
Number/percentage of C's	200,652,462 / 19.05%
Number/percentage of T's	324,232,822 / 30.79%
Number/percentage of G's	203,690,242 / 19.34%
Number/percentage of N's	423,205 / 0.04%
GC Percentage	38.4%

2.3. Coverage

Mean	0.3402

Standard Deviation	0.6446

2.4. Mapping Quality

Mean Mapping Quality	46.39

2.5. Mismatches and indels

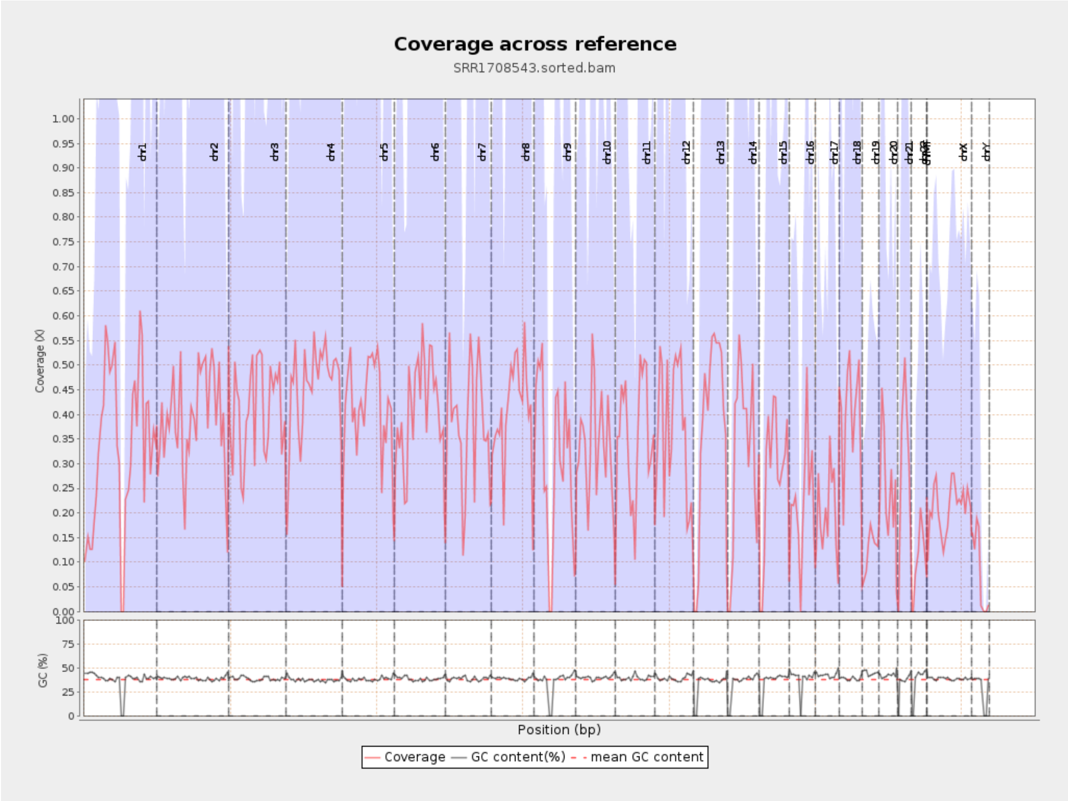
General error rate	0.36%
Mismatches	3,686,899
Insertions	55,826
Mapped reads with at least one insertion	0.26%
Deletions	53,330
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.12%

2.6. Chromosome stats

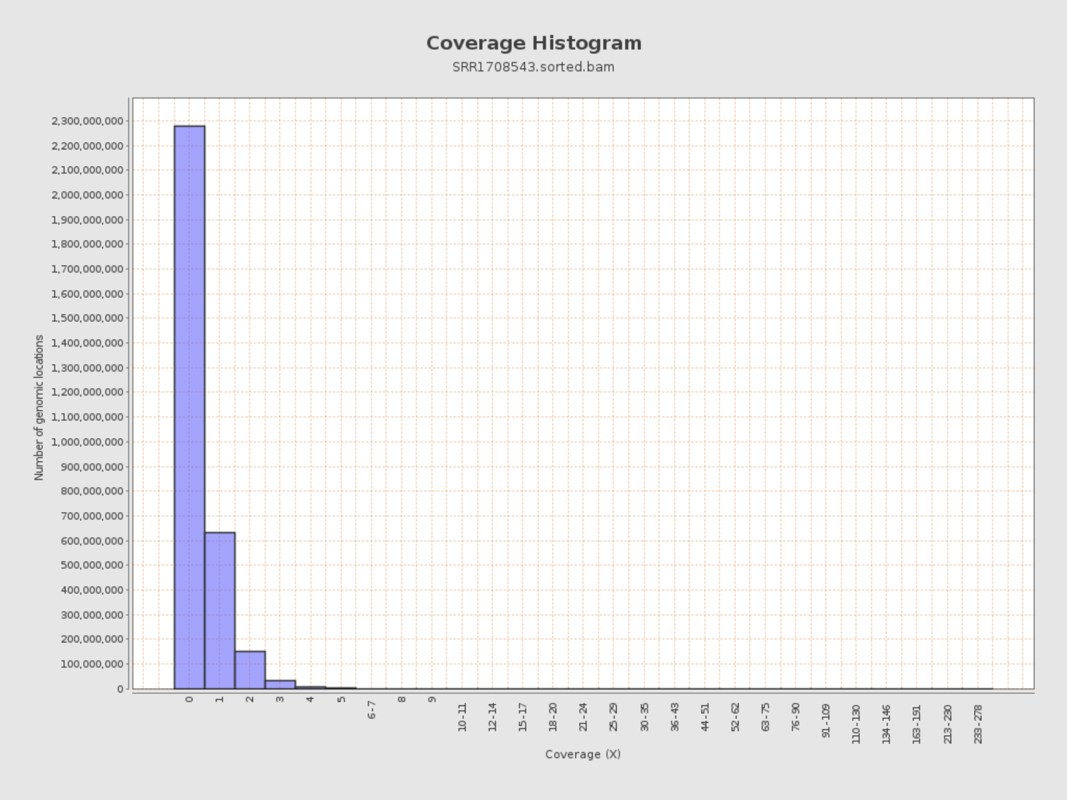
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	82970984	0.3329	0.654
chr2	243199373	95542498	0.3929	0.6788
chr3	198022430	81405254	0.4111	0.6908
chr4	191154276	87367519	0.4571	0.7273
chr5	180915260	74271792	0.4105	0.6906
chr6	171115067	70697423	0.4132	0.6959
chr7	159138663	59844007	0.376	0.6735

chr8	146364022	59643804	0.4075	0.6911
chr9	141213431	43910407	0.311	0.6221
chr10	135534747	46007661	0.3395	0.6321
chr11	135006516	47869153	0.3546	0.6586
chr12	133851895	49013939	0.3662	0.6676
chr13	115169878	44006058	0.3821	0.6843
chr14	107349540	34482199	0.3212	0.6367
chr15	102531392	27959608	0.2727	0.585
chr16	90354753	19657058	0.2176	0.5176
chr17	81195210	16514280	0.2034	0.5009
chr18	78077248	31461099	0.4029	0.6886
chr19	59128983	7381361	0.1248	0.383
chr20	63025520	16187943	0.2568	0.5618
chr21	48129895	13852181	0.2878	0.6213
chr22	51304566	5546397	0.1081	0.3646
chrMT	16571	3849	0.2323	0.4817
chrX	155270560	32724855	0.2108	0.4818
chrY	59373566	4803662	0.0809	0.3173

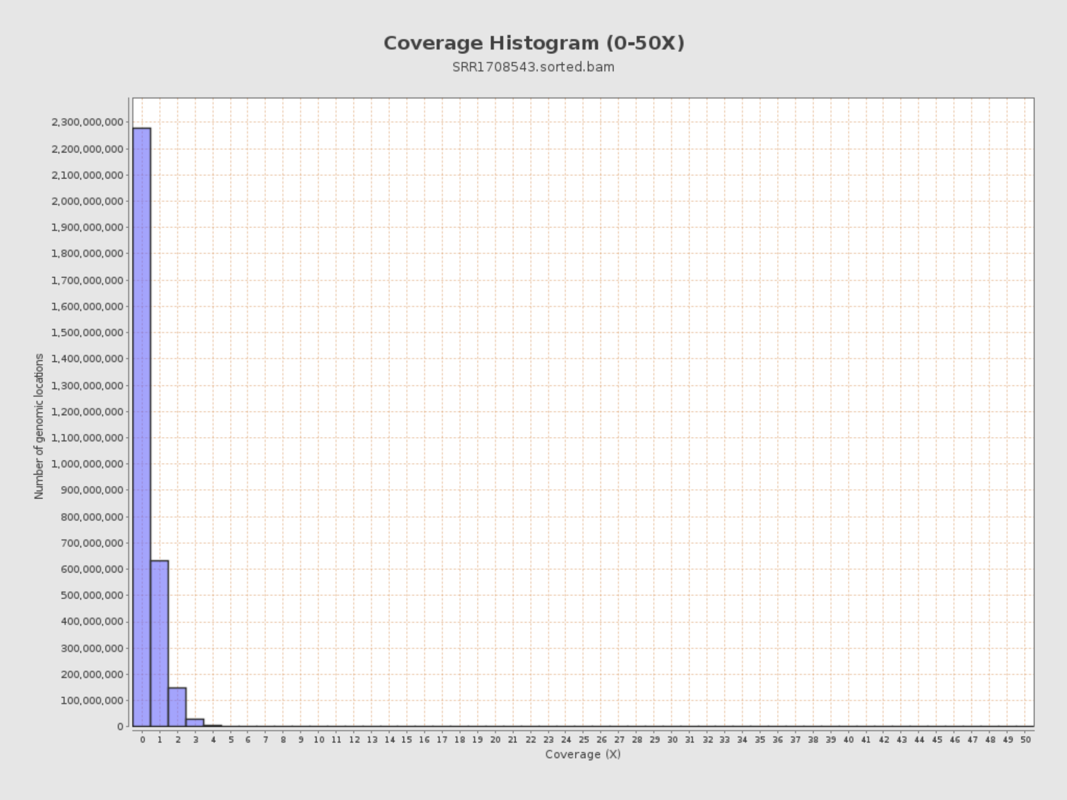
3. Results : Coverage across reference



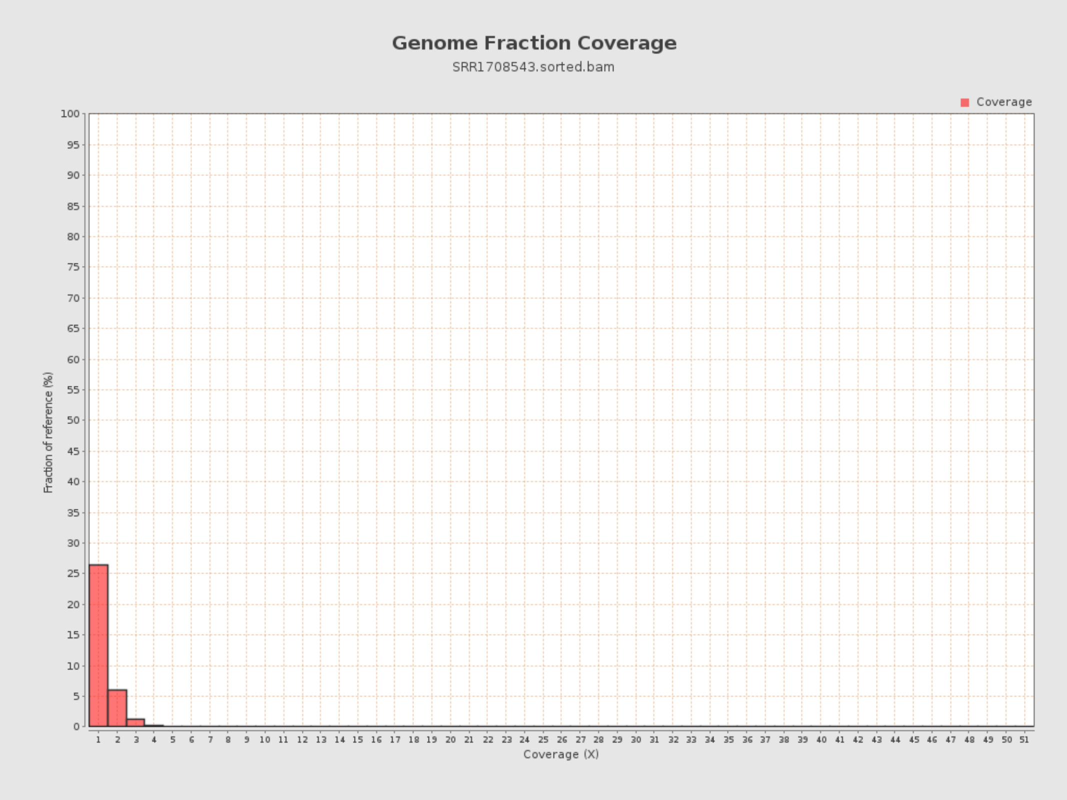
4. Results : Coverage Histogram



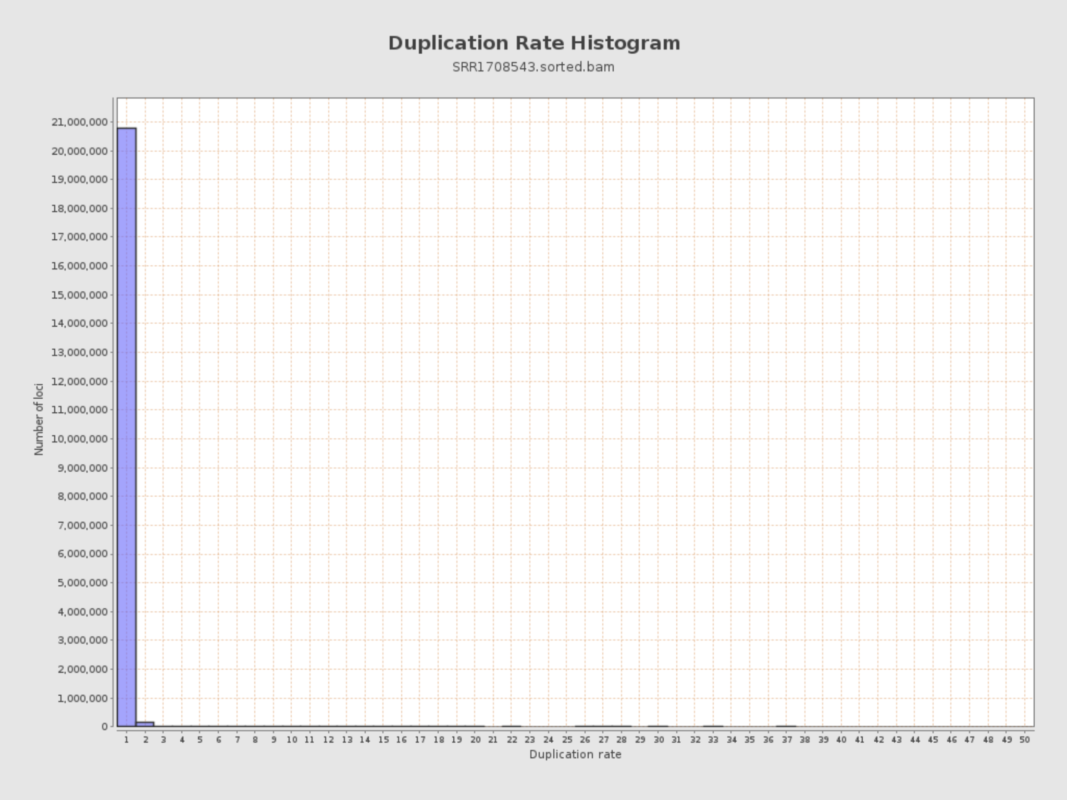
5. Results : Coverage Histogram (0-50X)



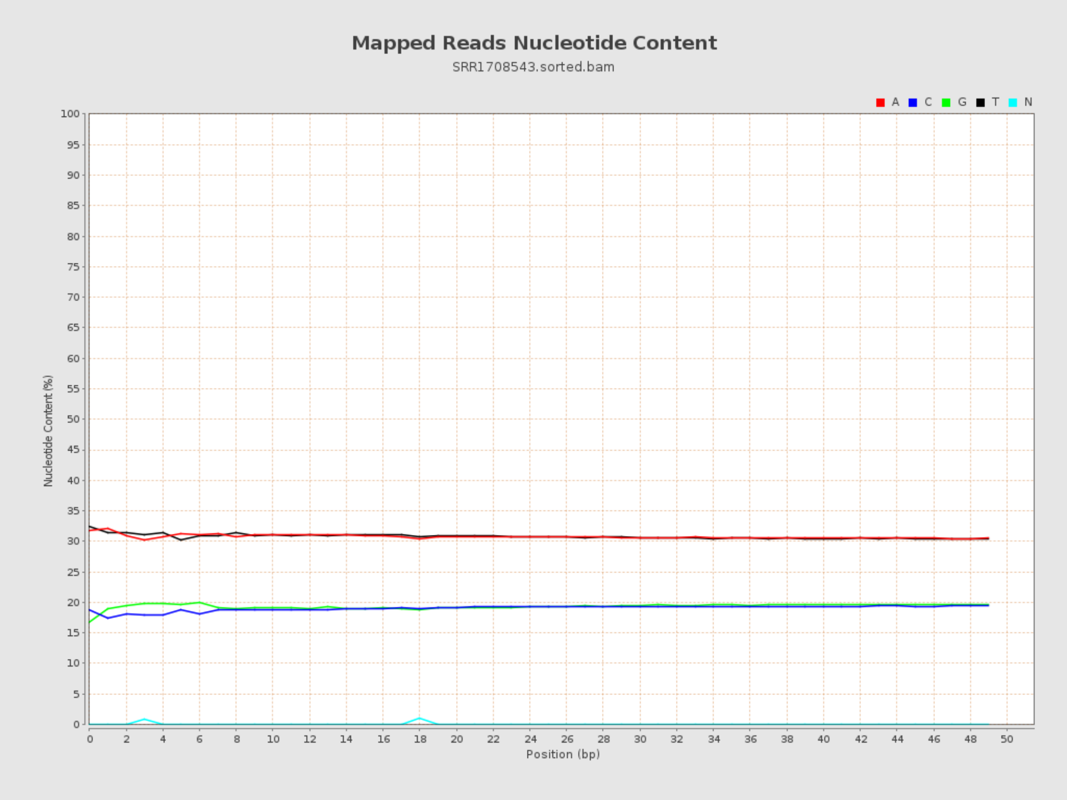
6. Results : Genome Fraction Coverage



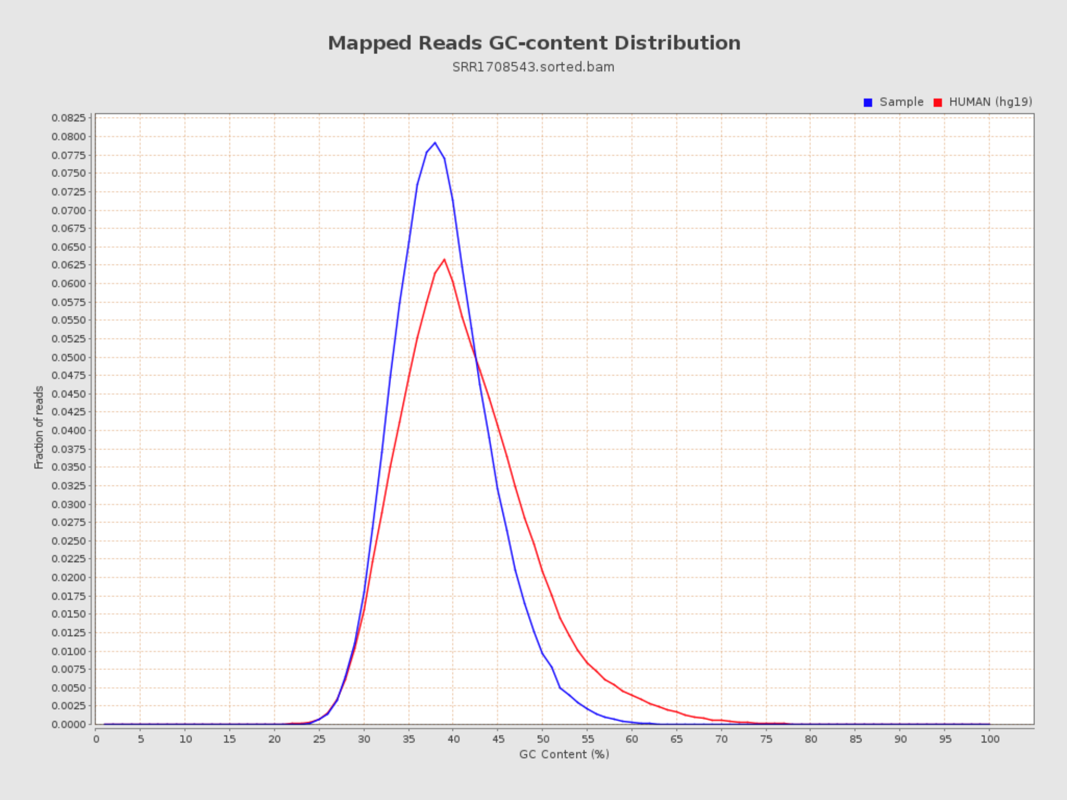
7. Results : Duplication Rate Histogram



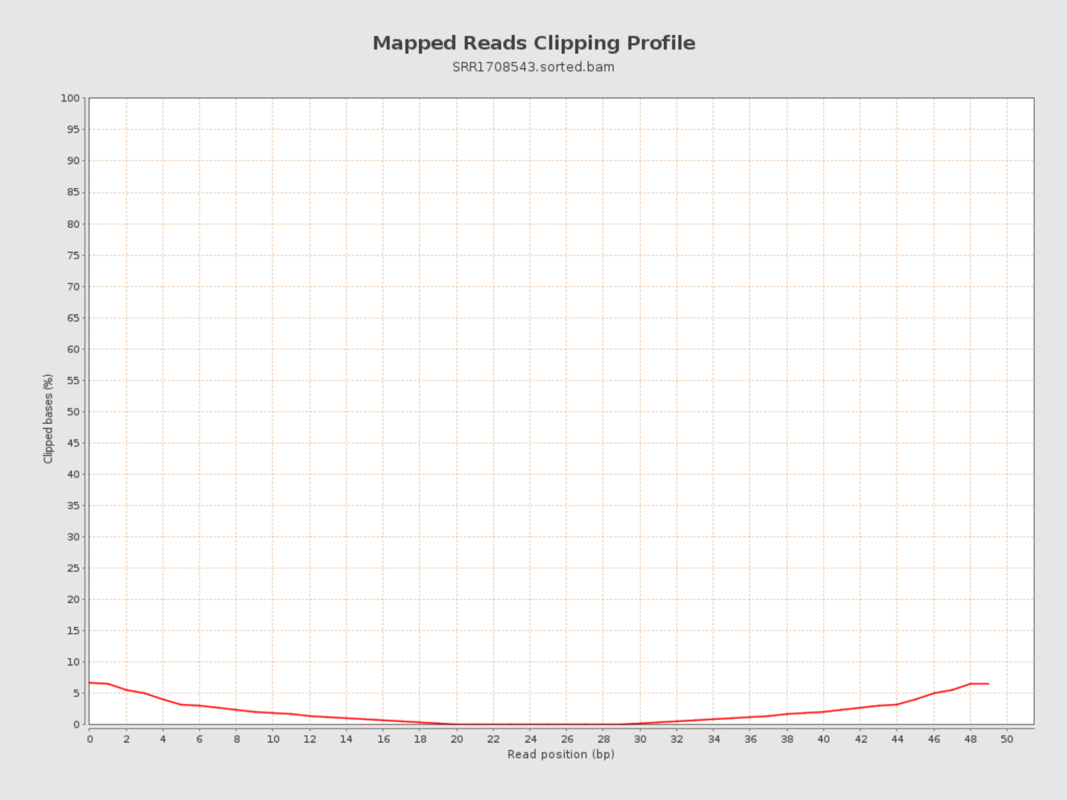
8. Results : Mapped Reads Nucleotide Content



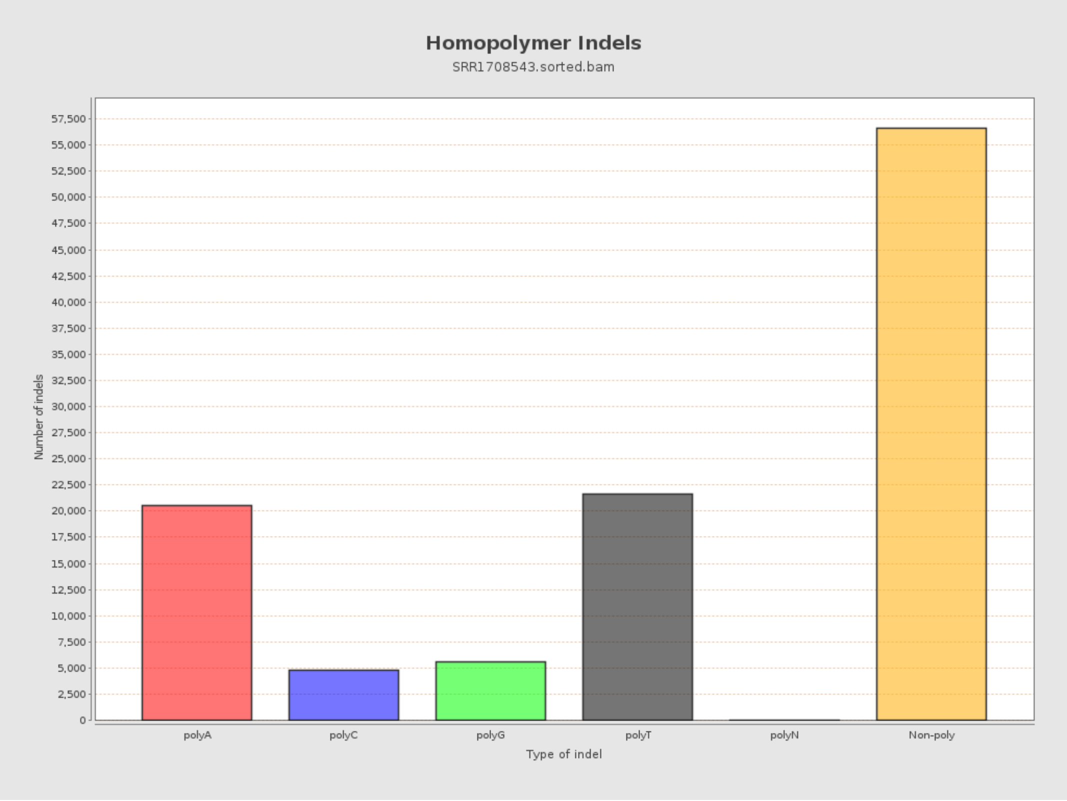
9. Results : Mapped Reads GC-content Distribution



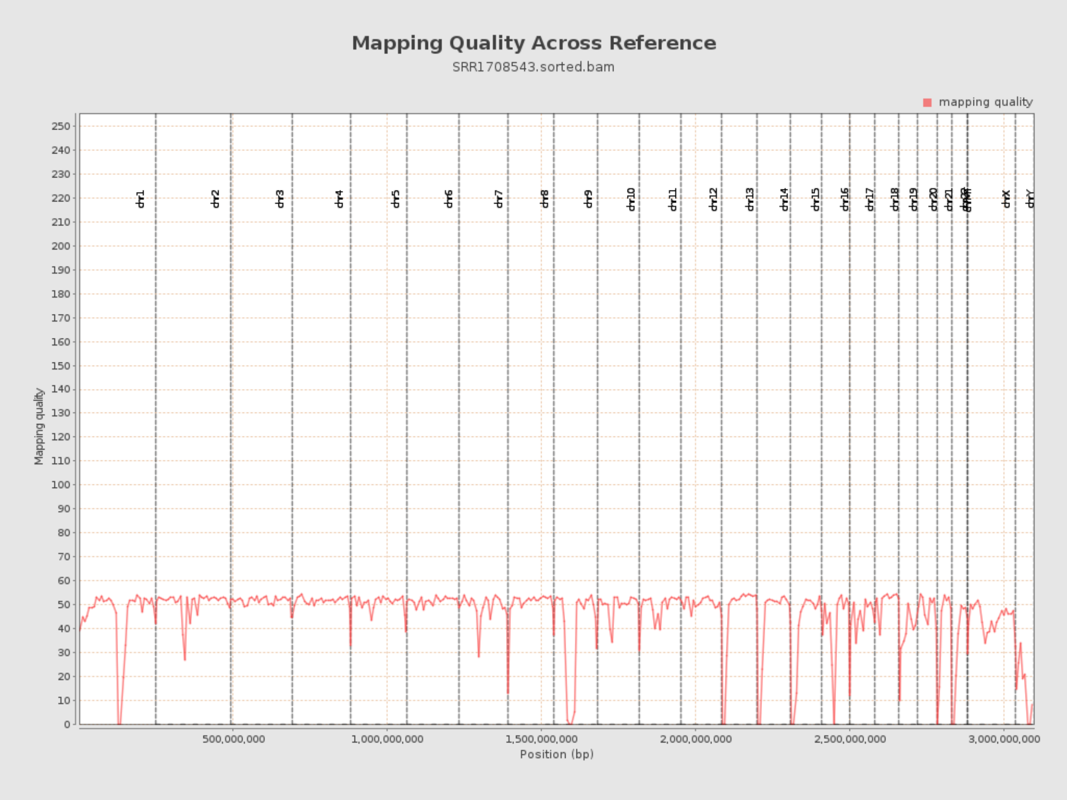
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram