Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:56:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716581.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_SRR9716581 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716581.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:56:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716581.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,605,261
Mapped reads	1,451,122 / 90.4%
Unmapped reads	154,139 / 9.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,280 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	46,124 / 2.87%
Duplication rate	2.22%
Clipped reads	1,453,910 / 90.57%

2.2. ACGT Content

Number/percentage of A's	20,136,813 / 23.92%
Number/percentage of C's	16,724,505 / 19.87%
Number/percentage of T's	27,352,610 / 32.49%
Number/percentage of G's	19,972,344 / 23.72%
Number/percentage of N's	978 / 0%
GC Percentage	43.59%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2652

2.4. Mapping Quality

Mean Mapping Quality	44.24

2.5. Mismatches and indels

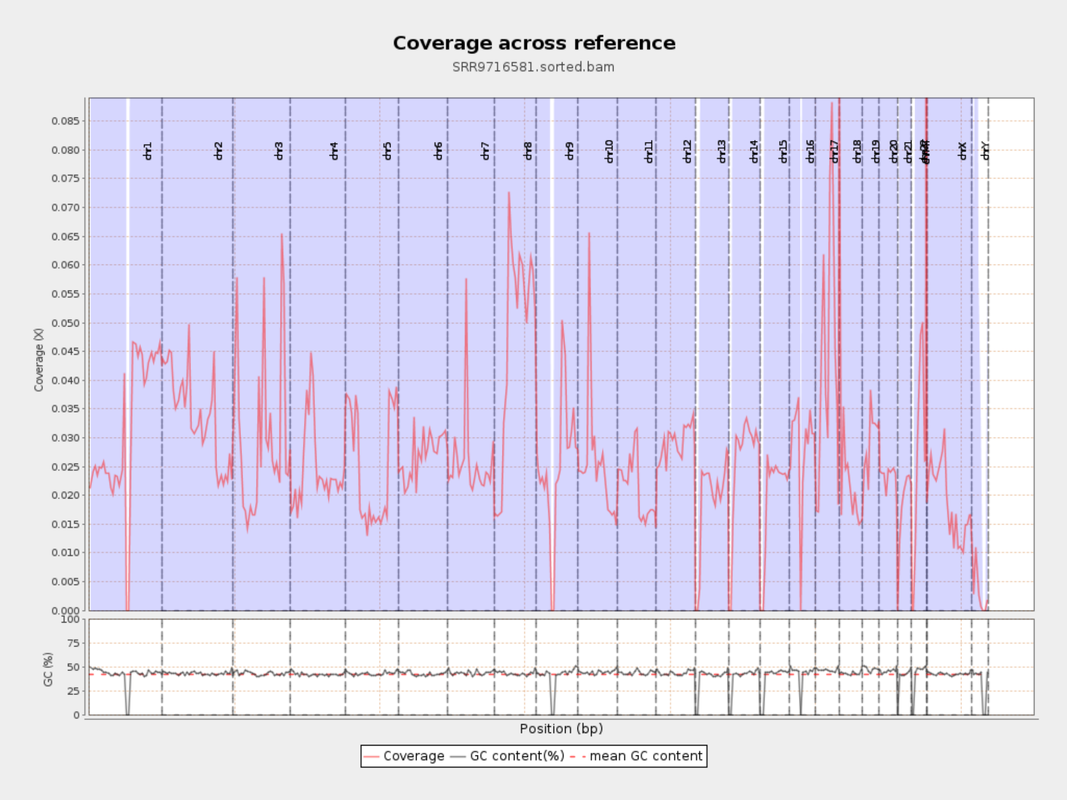
General error rate	0.51%
Mismatches	421,814
Insertions	5,844
Mapped reads with at least one insertion	0.4%
Deletions	16,054
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.74%

2.6. Chromosome stats

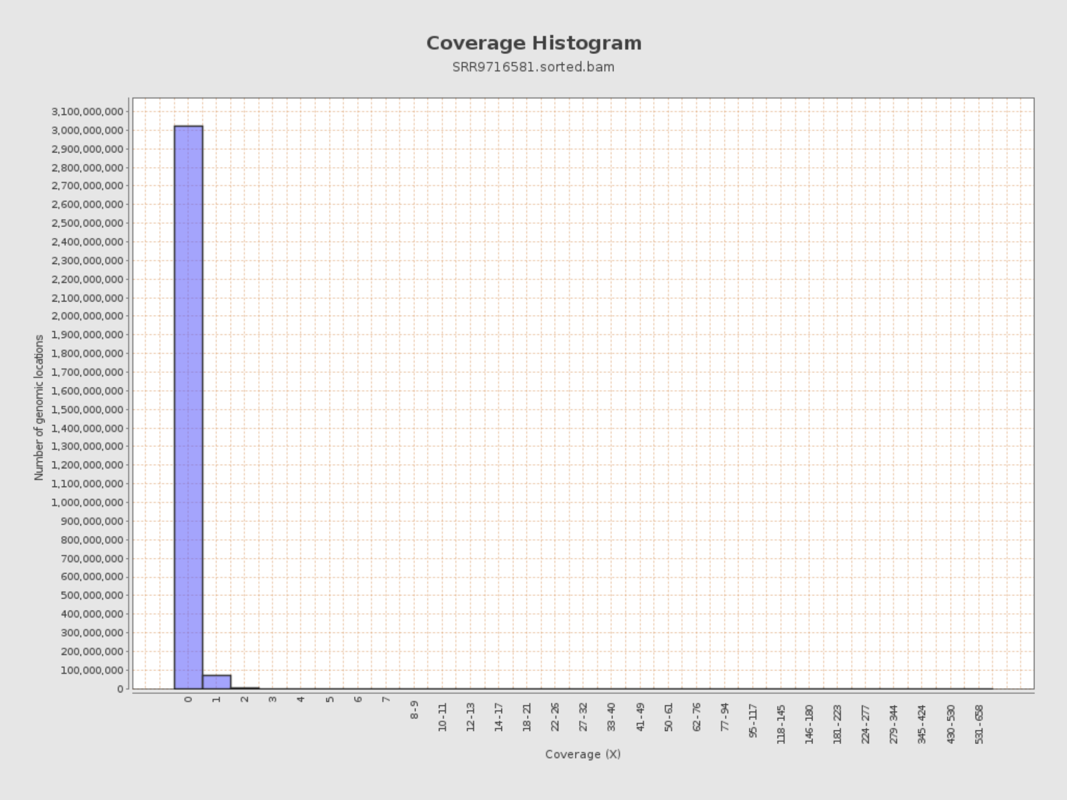
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7751956	0.0311	0.4332
chr2	243199373	8293496	0.0341	0.3394
chr3	198022430	5973453	0.0302	0.1925
chr4	191154276	4716285	0.0247	0.1824
chr5	180915260	4493809	0.0248	0.17
chr6	171115067	4644389	0.0271	0.1943
chr7	159138663	4127268	0.0259	0.4627

chr8	146364022	6947315	0.0475	0.2999
chr9	141213431	3502708	0.0248	0.1971
chr10	135534747	3438001	0.0254	0.3262
chr11	135006516	2867755	0.0212	0.1905
chr12	133851895	3911183	0.0292	0.1978
chr13	115169878	2169664	0.0188	0.149
chr14	107349540	2739162	0.0255	0.1753
chr15	102531392	2022736	0.0197	0.1561
chr16	90354753	2582613	0.0286	0.1916
chr17	81195210	3578630	0.0441	0.2354
chr18	78077248	1899817	0.0243	0.3041
chr19	59128983	1725365	0.0292	0.3524
chr20	63025520	1474120	0.0234	0.1713
chr21	48129895	864470	0.018	0.1517
chr22	51304566	1322520	0.0258	0.1731
chrMT	16571	12076	0.7287	0.9031
chrX	155270560	2959385	0.0191	0.1681
chrY	59373566	194526	0.0033	0.0885

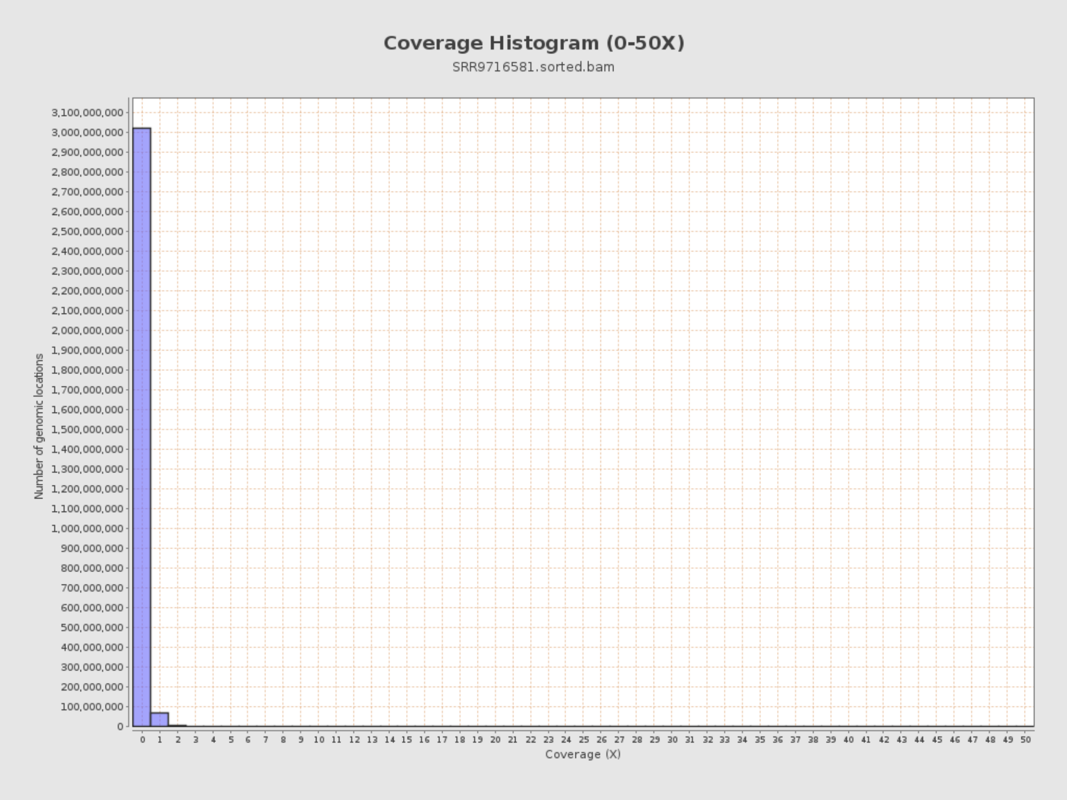
3. Results : Coverage across reference



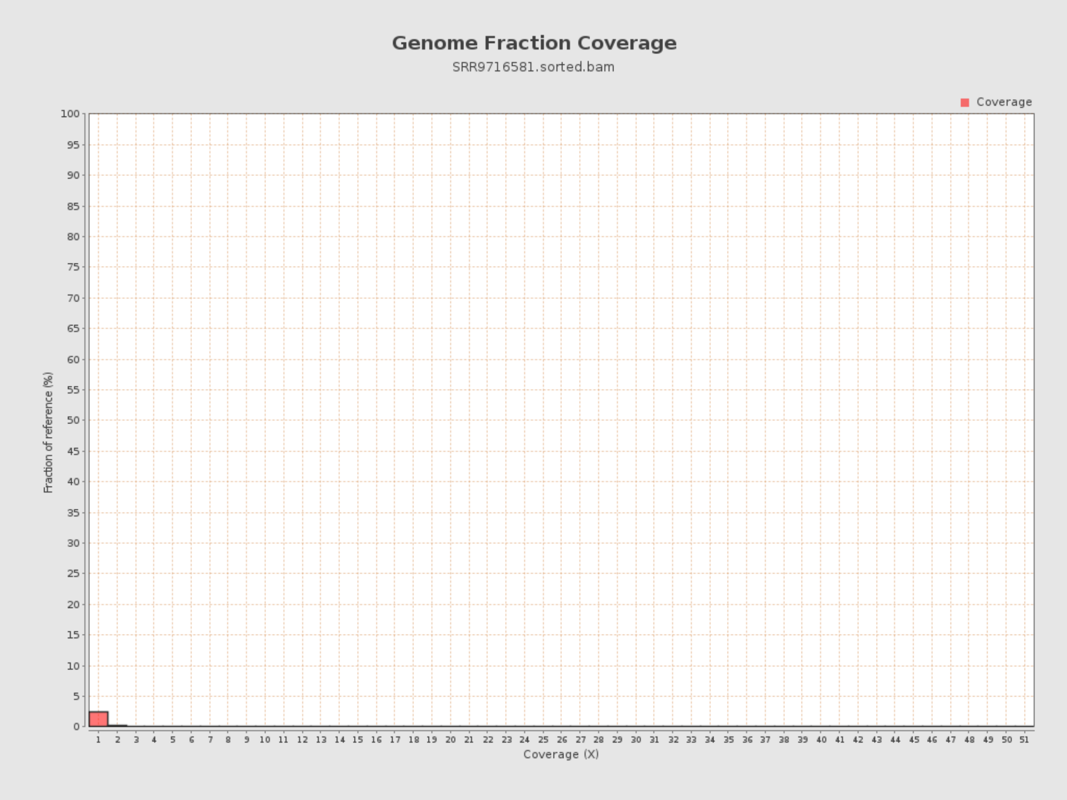
4. Results : Coverage Histogram



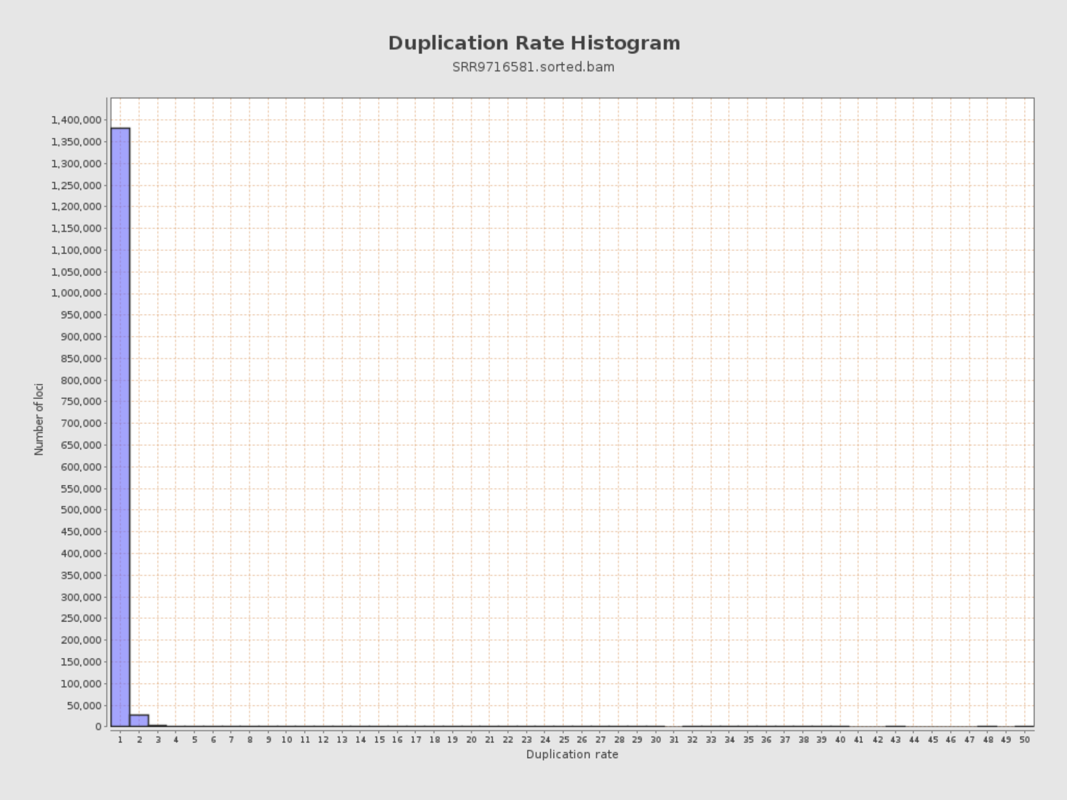
5. Results : Coverage Histogram (0-50X)



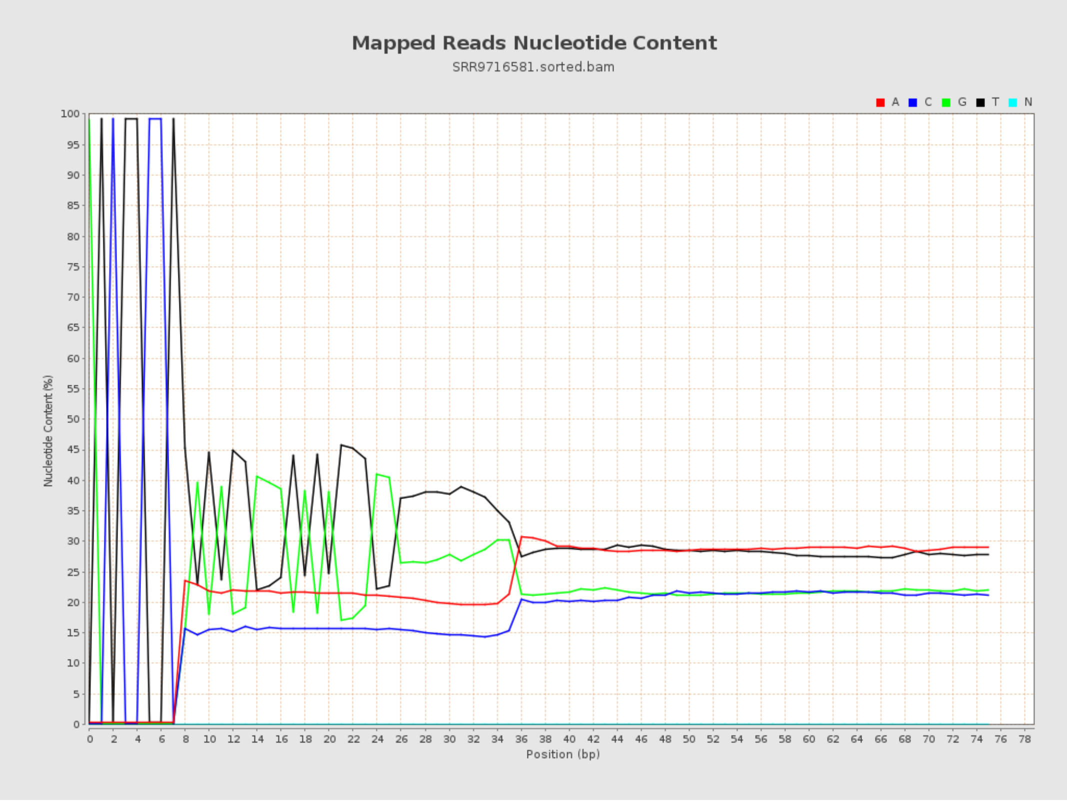
6. Results : Genome Fraction Coverage



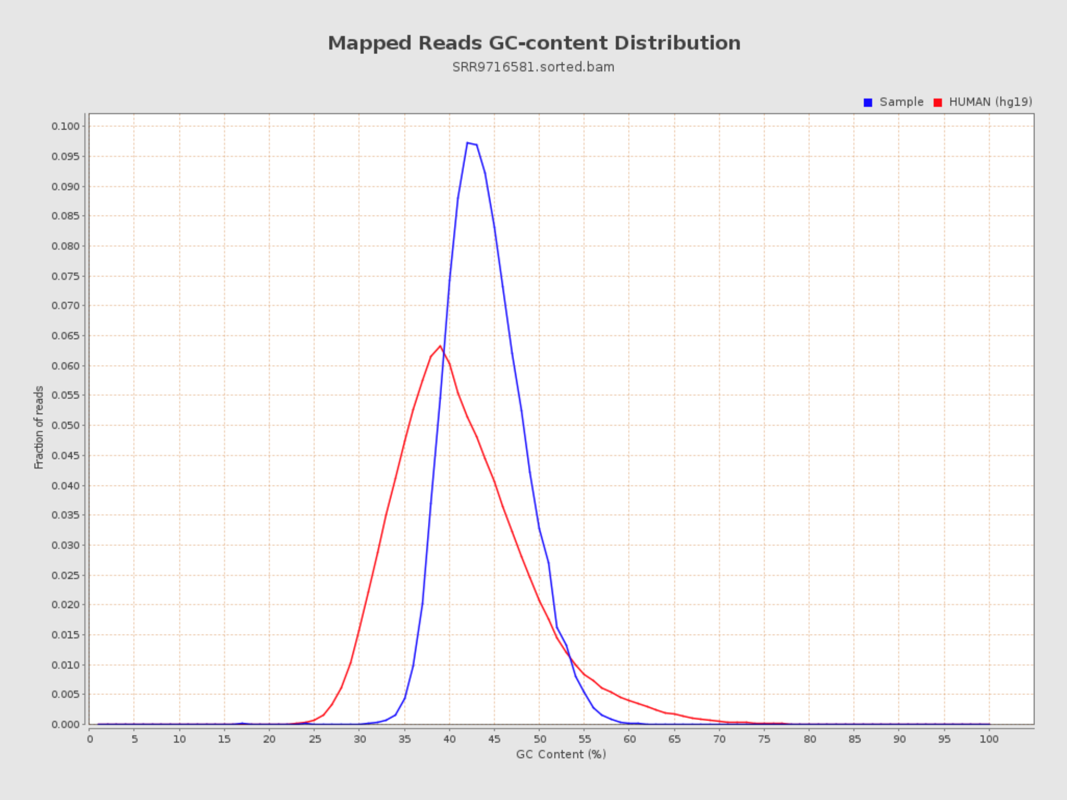
7. Results : Duplication Rate Histogram



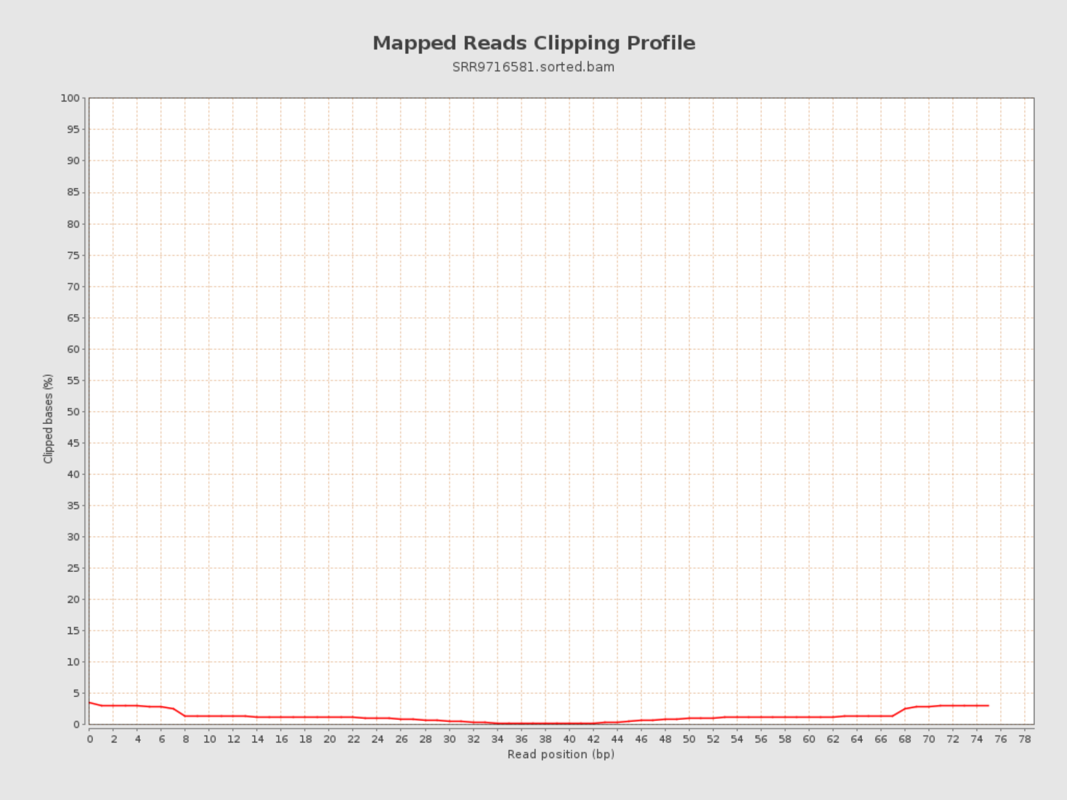
8. Results : Mapped Reads Nucleotide Content



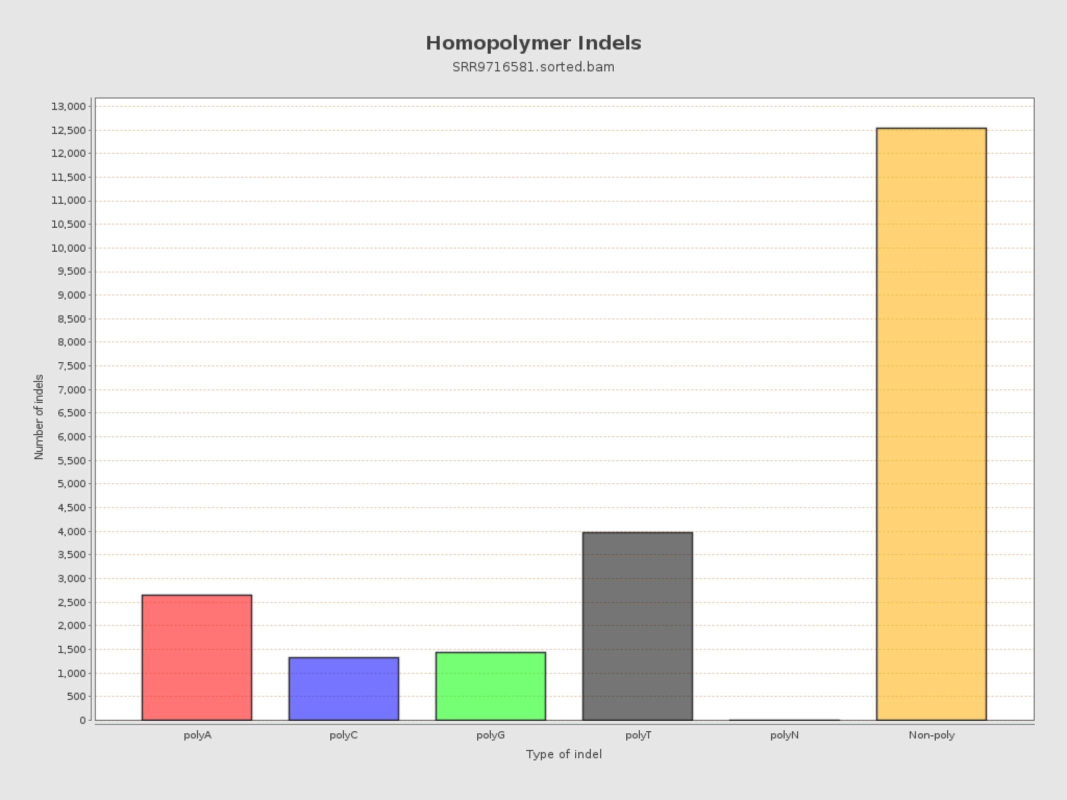
9. Results : Mapped Reads GC-content Distribution



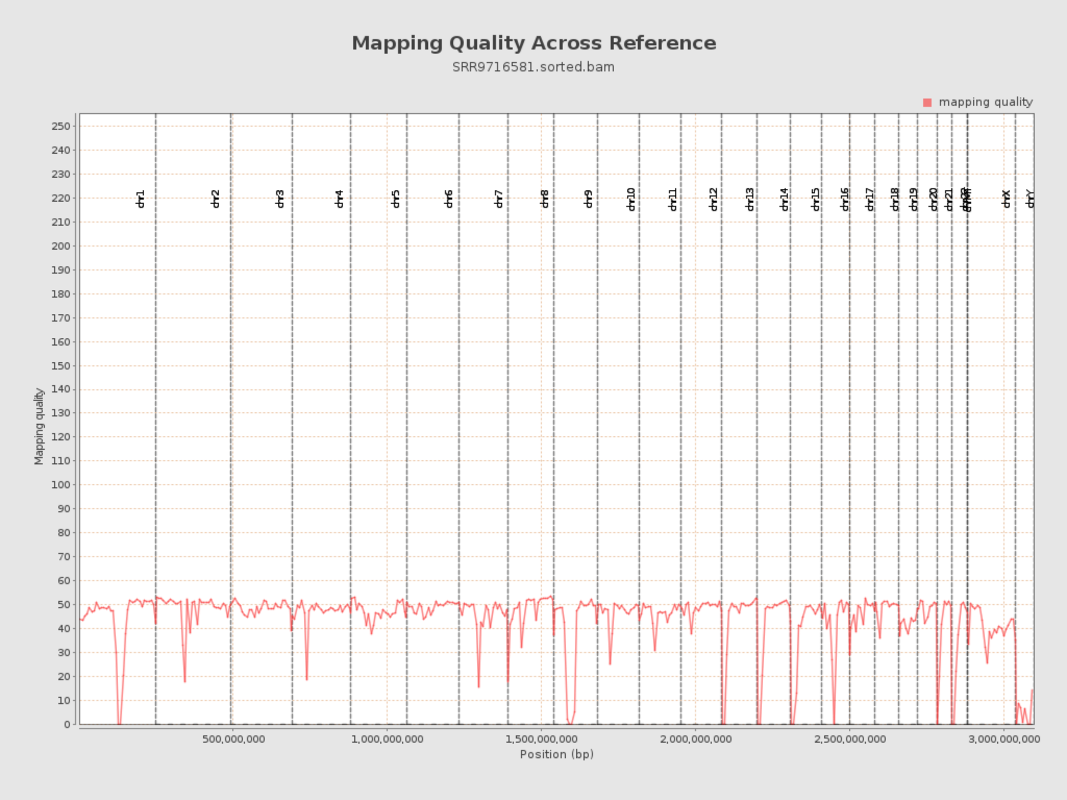
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram