Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:08:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716448.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_SRR9716448 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716448.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:08:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716448.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,077,139
Mapped reads	978,585 / 90.85%
Unmapped reads	98,554 / 9.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,969 / 1.85%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	34,827 / 3.23%
Duplication rate	2.07%
Clipped reads	997,321 / 92.59%

2.2. ACGT Content

Number/percentage of A's	19,338,155 / 25.22%
Number/percentage of C's	14,765,510 / 19.26%
Number/percentage of T's	23,908,246 / 31.18%
Number/percentage of G's	18,666,417 / 24.34%
Number/percentage of N's	4,549 / 0.01%
GC Percentage	43.6%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.316

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Mismatches and indels

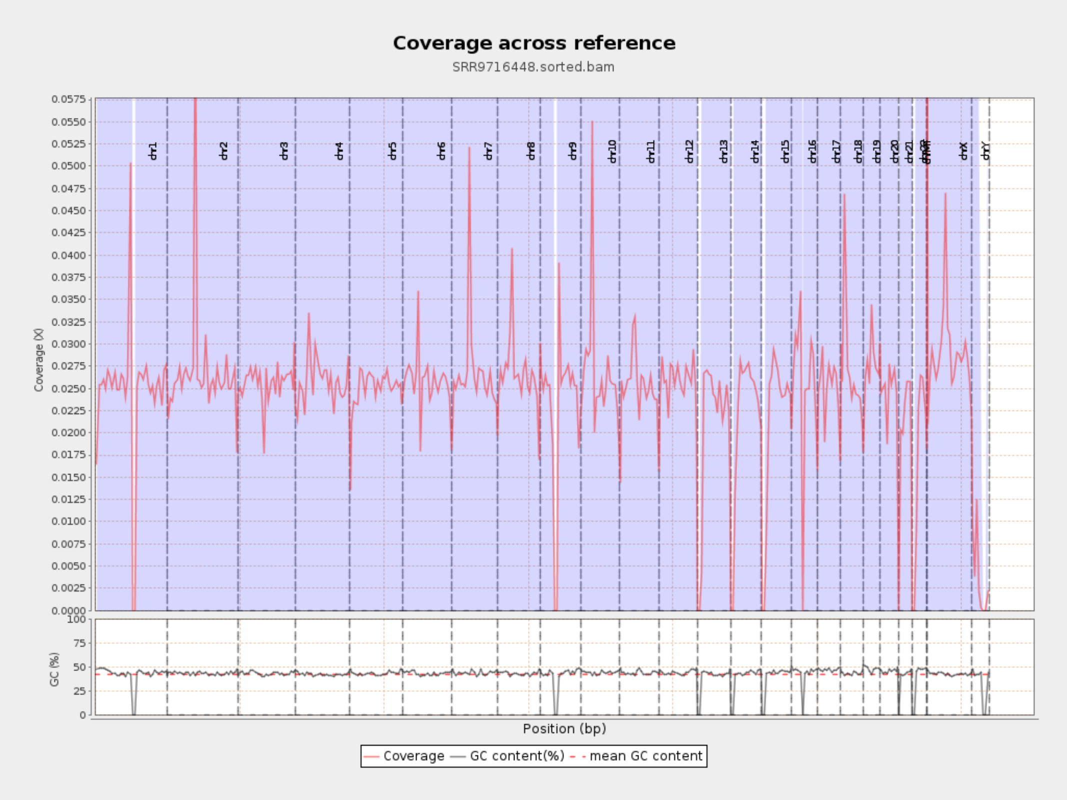
General error rate	0.82%
Mismatches	615,789
Insertions	7,203
Mapped reads with at least one insertion	0.73%
Deletions	18,916
Mapped reads with at least one deletion	1.9%
Homopolymer indels	43.05%

2.6. Chromosome stats

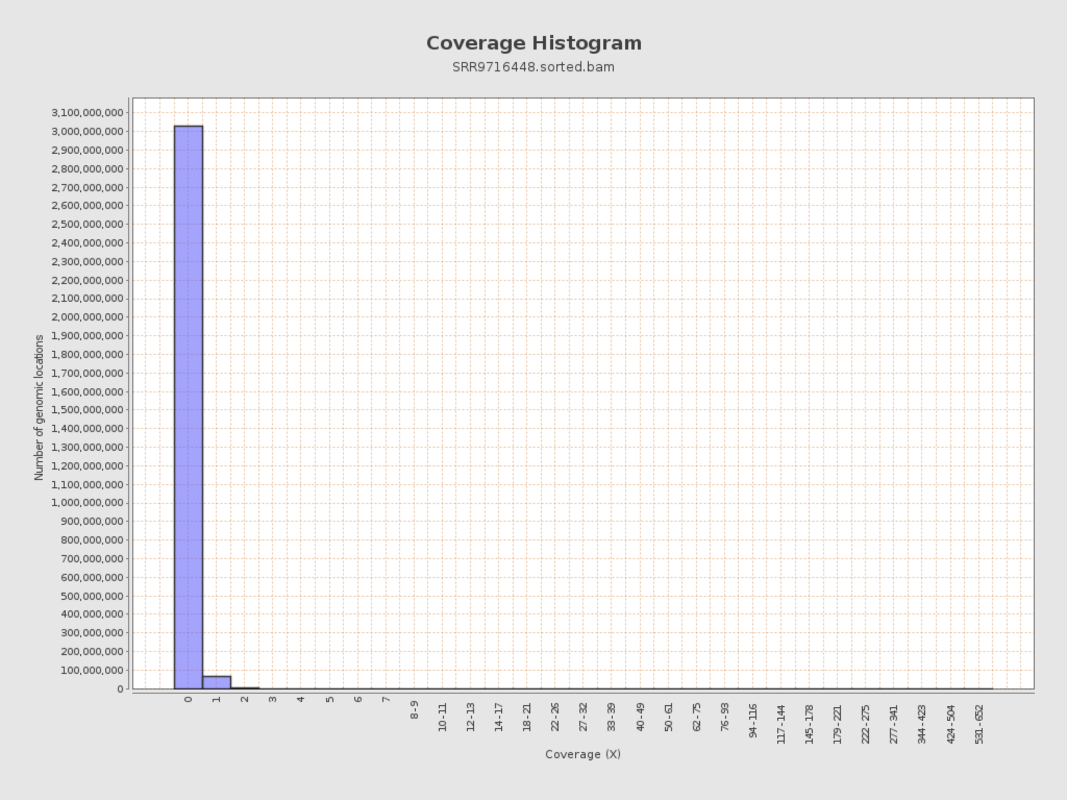
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6130984	0.0246	0.5418
chr2	243199373	6589600	0.0271	0.4374
chr3	198022430	5062482	0.0256	0.1751
chr4	191154276	4938121	0.0258	0.186
chr5	180915260	4566394	0.0252	0.1748
chr6	171115067	4413406	0.0258	0.2084
chr7	159138663	4287391	0.0269	0.4091

chr8	146364022	3913802	0.0267	0.3834
chr9	141213431	3252139	0.023	0.3304
chr10	135534747	3654730	0.027	0.3127
chr11	135006516	3449576	0.0256	0.3077
chr12	133851895	3476511	0.026	0.1766
chr13	115169878	2351005	0.0204	0.152
chr14	107349540	2311297	0.0215	0.1955
chr15	102531392	2148418	0.021	0.1584
chr16	90354753	2252182	0.0249	0.2007
chr17	81195210	2036720	0.0251	0.1906
chr18	78077248	2128316	0.0273	0.6219
chr19	59128983	1641101	0.0278	0.396
chr20	63025520	1530201	0.0243	0.1772
chr21	48129895	981808	0.0204	0.1647
chr22	51304566	858950	0.0167	0.1391
chrMT	16571	2787	0.1682	0.5253
chrX	155270560	4524455	0.0291	0.2495
chrY	59373566	213207	0.0036	0.1062

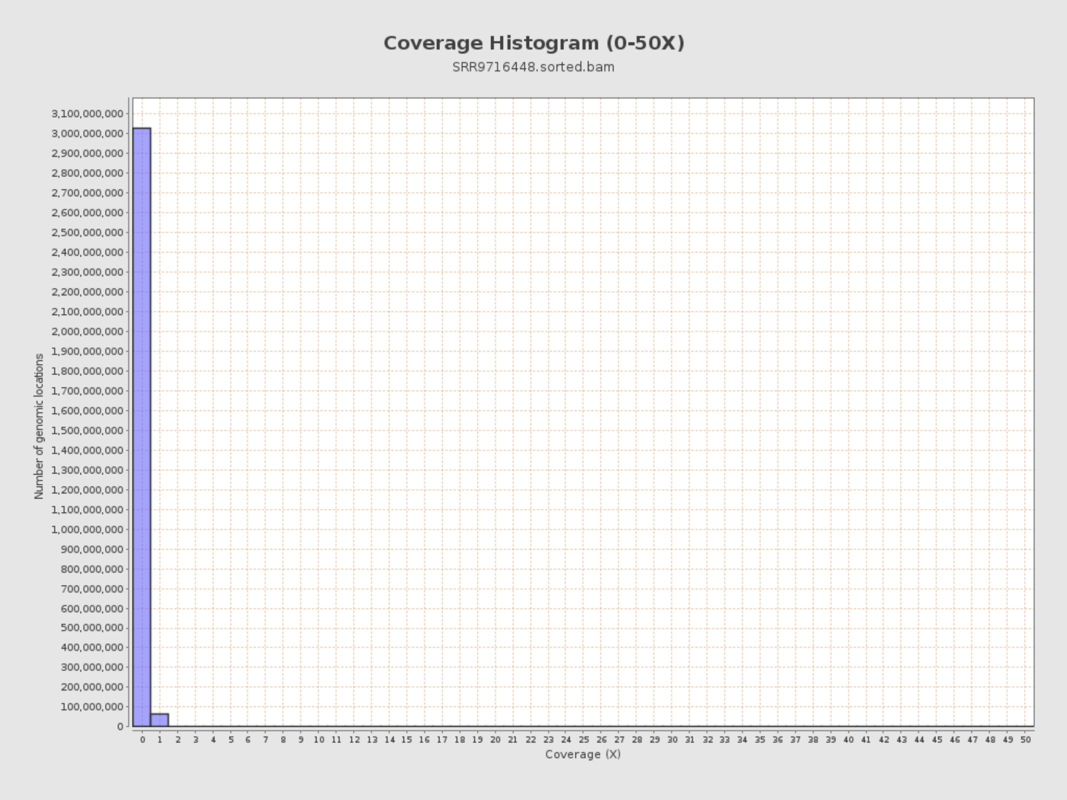
3. Results : Coverage across reference



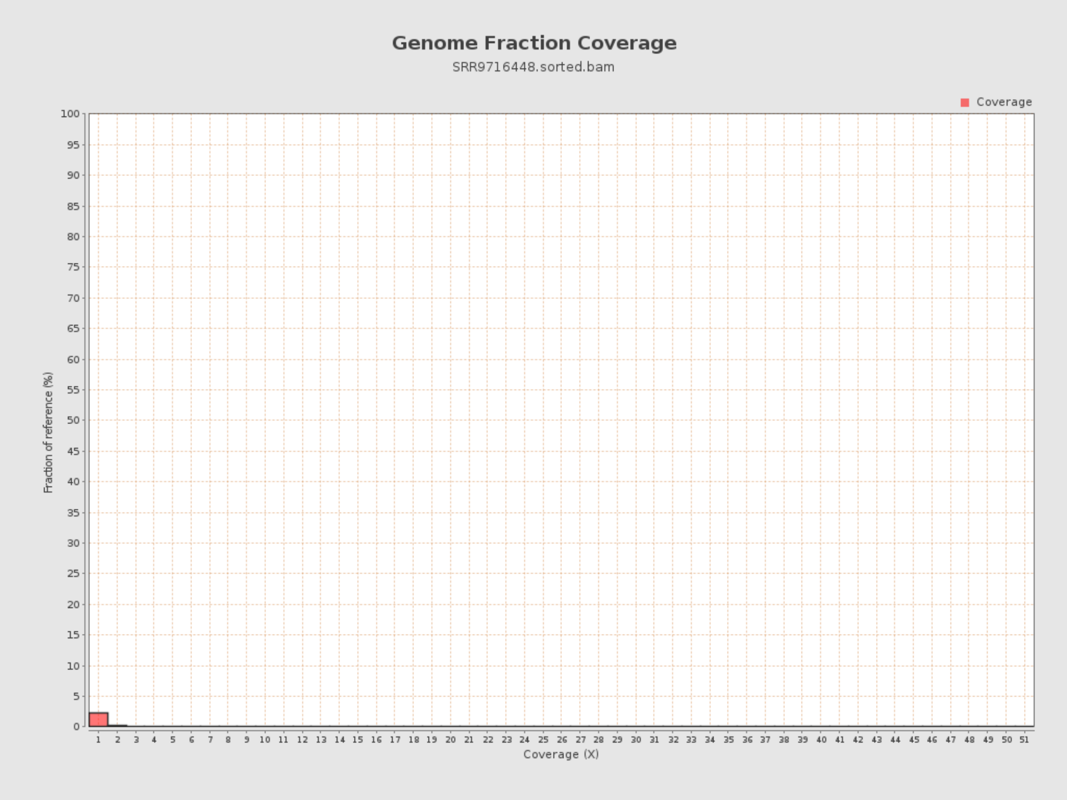
4. Results : Coverage Histogram



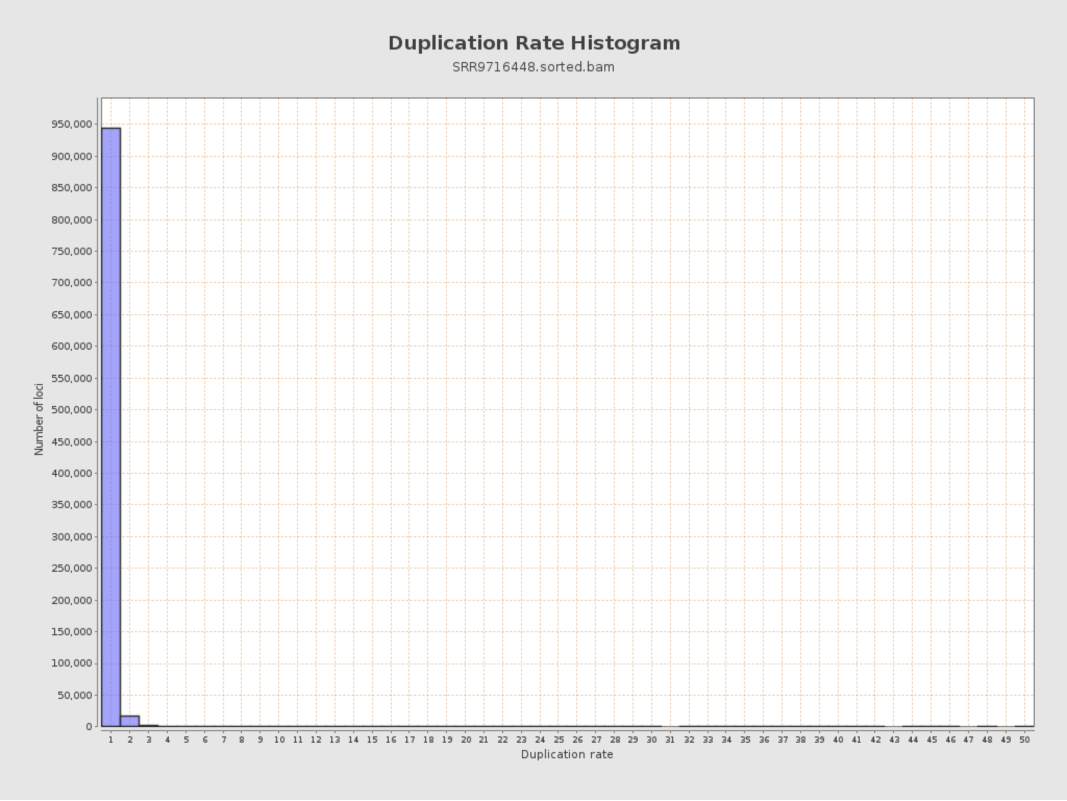
5. Results : Coverage Histogram (0-50X)



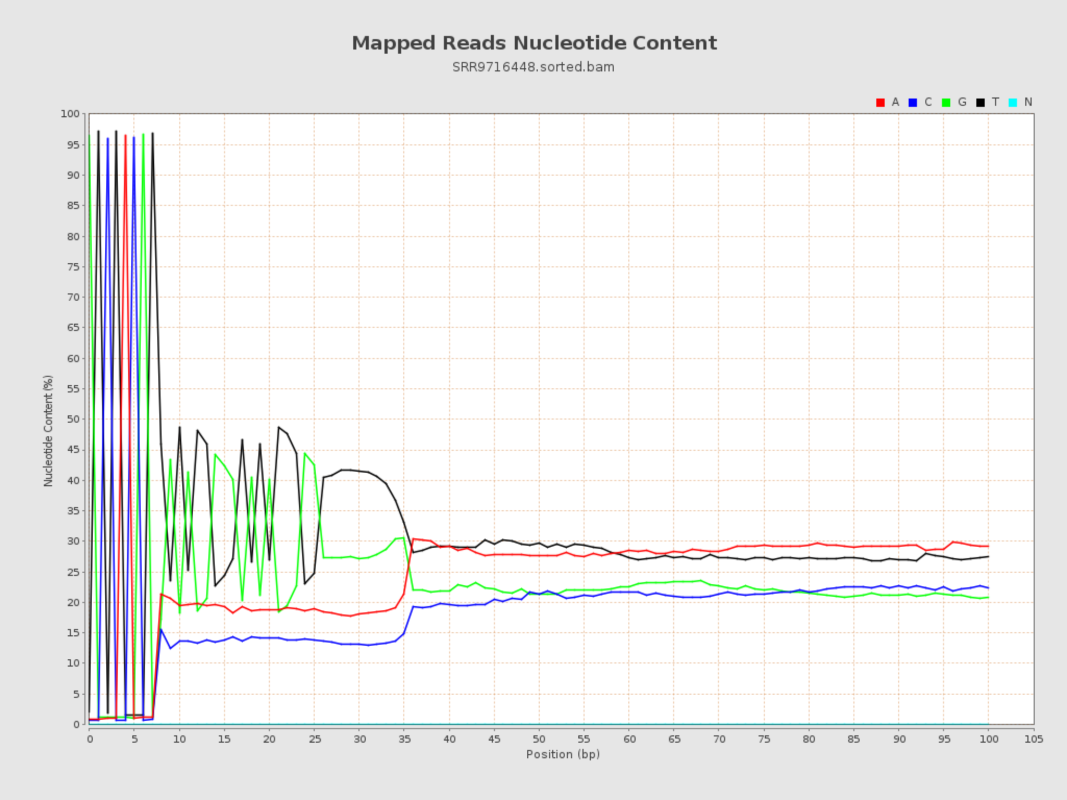
6. Results : Genome Fraction Coverage



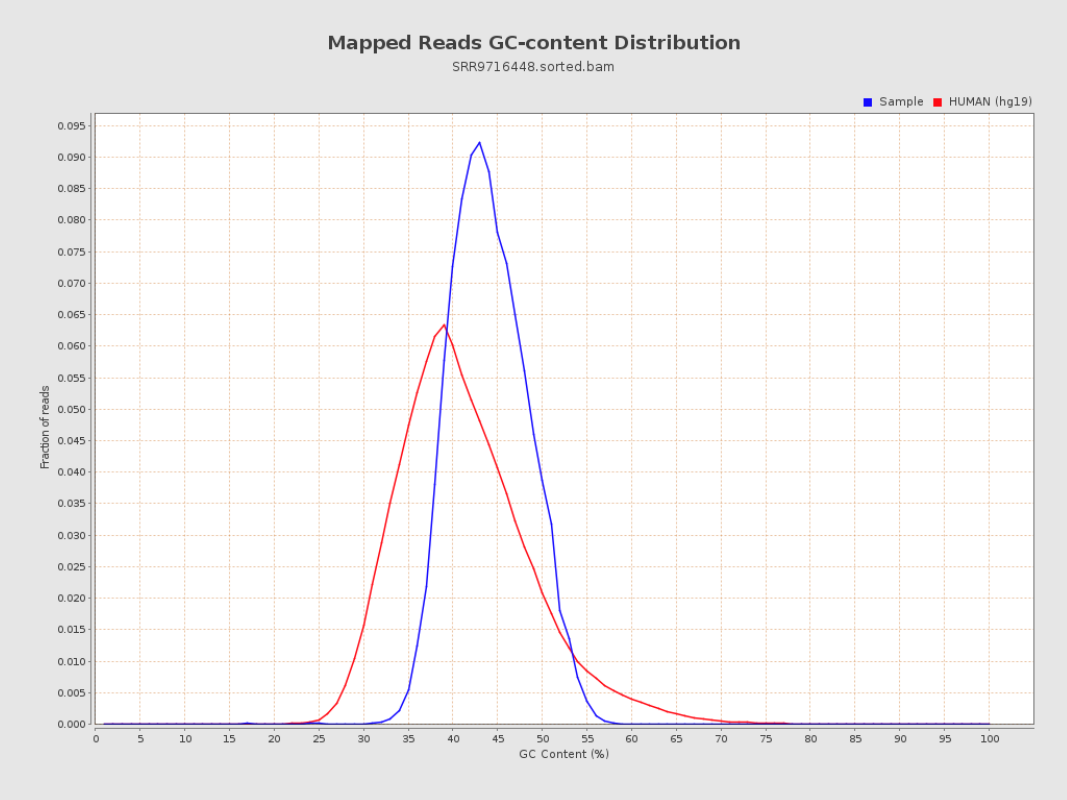
7. Results : Duplication Rate Histogram



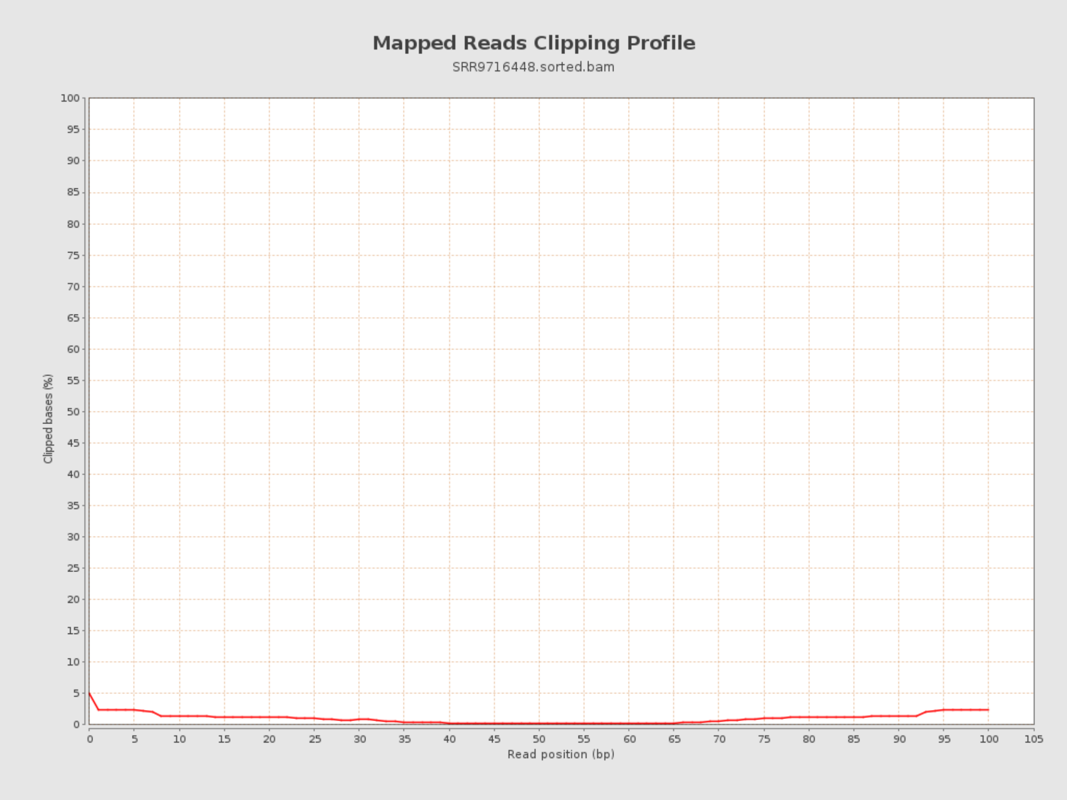
8. Results : Mapped Reads Nucleotide Content



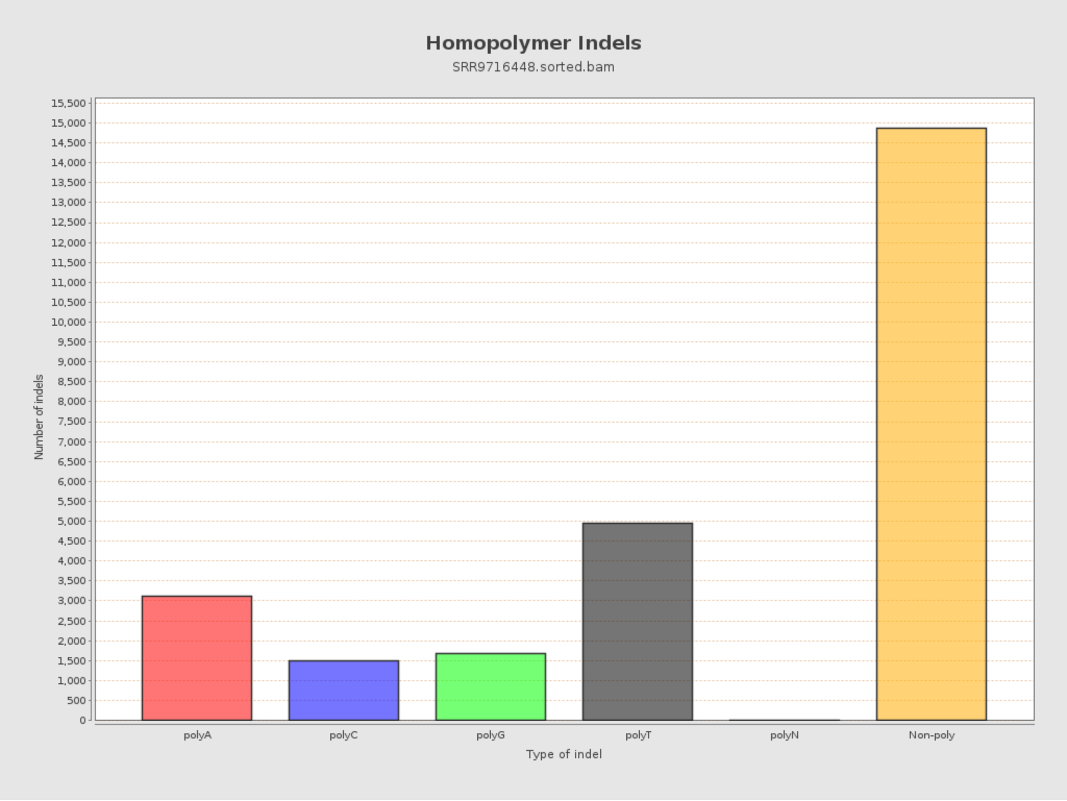
9. Results : Mapped Reads GC-content Distribution



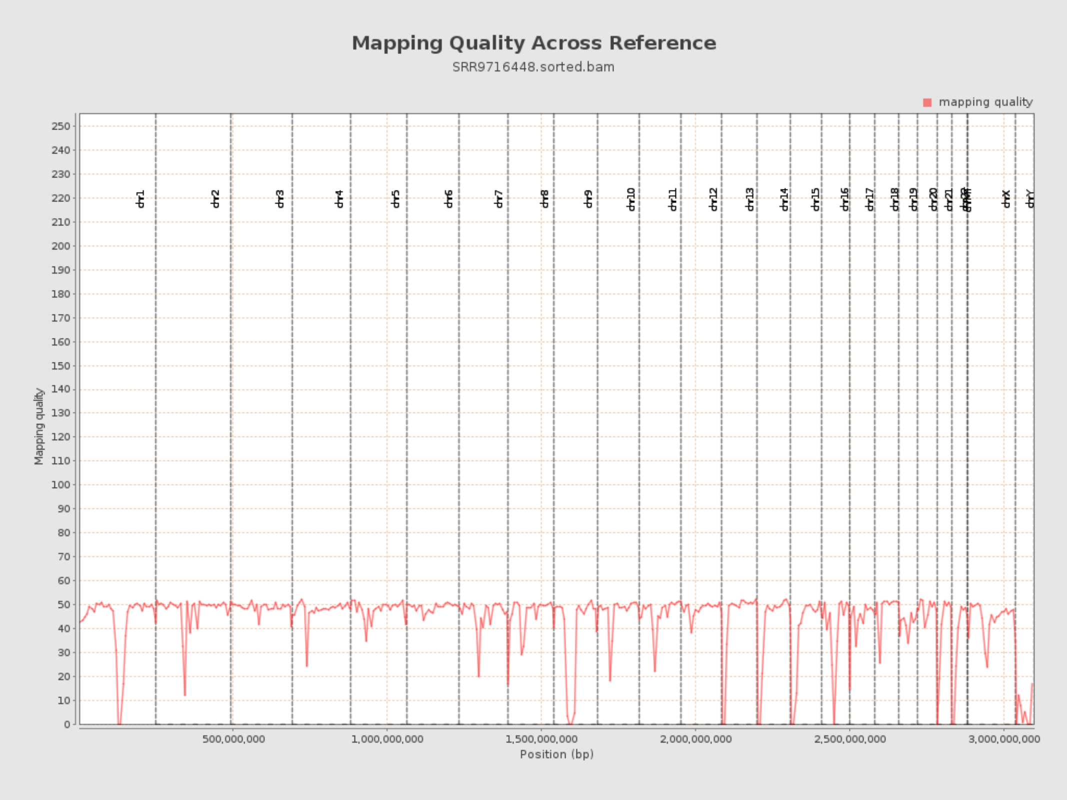
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram