Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:49:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716545.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_SRR9716545 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716545.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:49:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716545.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	982,939
Mapped reads	932,845 / 94.9%
Unmapped reads	50,094 / 5.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,940 / 2.03%
Read min/max/mean length	30 / 101 / 101.75
Duplicated reads (estimated)	31,822 / 3.24%
Duplication rate	2.64%
Clipped reads	951,121 / 96.76%

2.2. ACGT Content

Number/percentage of A's	18,682,976 / 25.62%
Number/percentage of C's	15,421,276 / 21.15%
Number/percentage of T's	21,323,609 / 29.24%
Number/percentage of G's	17,494,925 / 23.99%
Number/percentage of N's	2,676 / 0%
GC Percentage	45.14%

2.3. Coverage

Mean	0.0236

Standard Deviation	0.2325

2.4. Mapping Quality

Mean Mapping Quality	46.44

2.5. Mismatches and indels

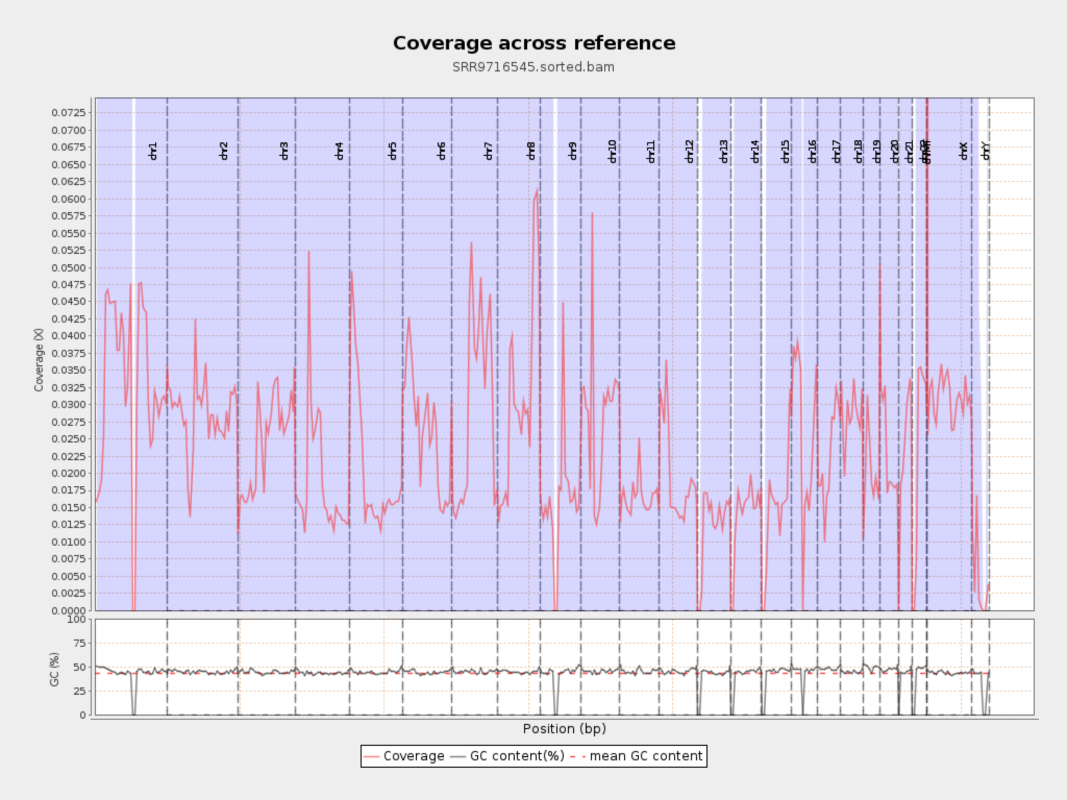
General error rate	0.65%
Mismatches	456,140
Insertions	6,644
Mapped reads with at least one insertion	0.7%
Deletions	13,034
Mapped reads with at least one deletion	1.37%
Homopolymer indels	36.54%

2.6. Chromosome stats

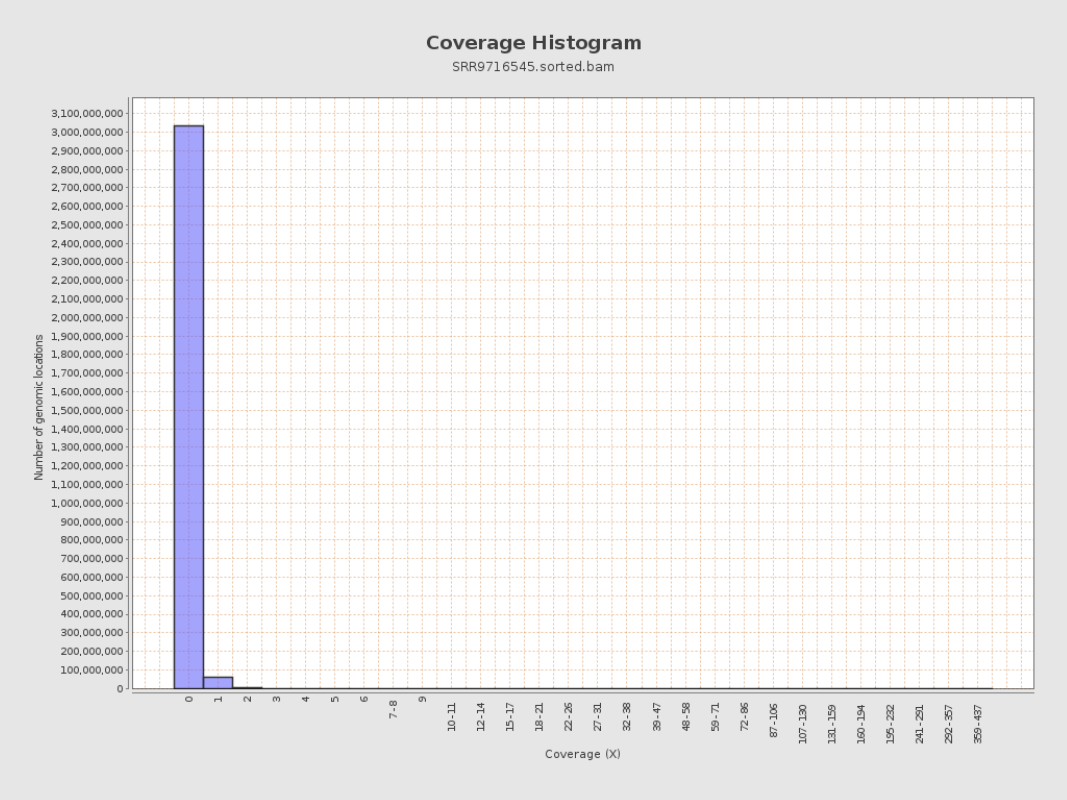
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8201231	0.0329	0.4212
chr2	243199373	6993456	0.0288	0.2379
chr3	198022430	4872490	0.0246	0.1749
chr4	191154276	3558483	0.0186	0.2004
chr5	180915260	3772321	0.0209	0.1593
chr6	171115067	4483717	0.0262	0.1862
chr7	159138663	4698790	0.0295	0.301

chr8	146364022	4530287	0.031	0.2534
chr9	141213431	2236475	0.0158	0.1634
chr10	135534747	3872549	0.0286	0.3282
chr11	135006516	2251975	0.0167	0.1818
chr12	133851895	2686584	0.0201	0.1561
chr13	115169878	1402571	0.0122	0.1204
chr14	107349540	1472922	0.0137	0.1362
chr15	102531392	1464598	0.0143	0.1302
chr16	90354753	2290152	0.0253	0.1864
chr17	81195210	1811146	0.0223	0.1778
chr18	78077248	2227948	0.0285	0.2575
chr19	59128983	1273870	0.0215	0.3044
chr20	63025520	1430274	0.0227	0.1727
chr21	48129895	1142874	0.0237	0.1962
chr22	51304566	1184027	0.0231	0.1717
chrMT	16571	27078	1.6341	1.6849
chrX	155270560	4813239	0.031	0.2026
chrY	59373566	254016	0.0043	0.1636

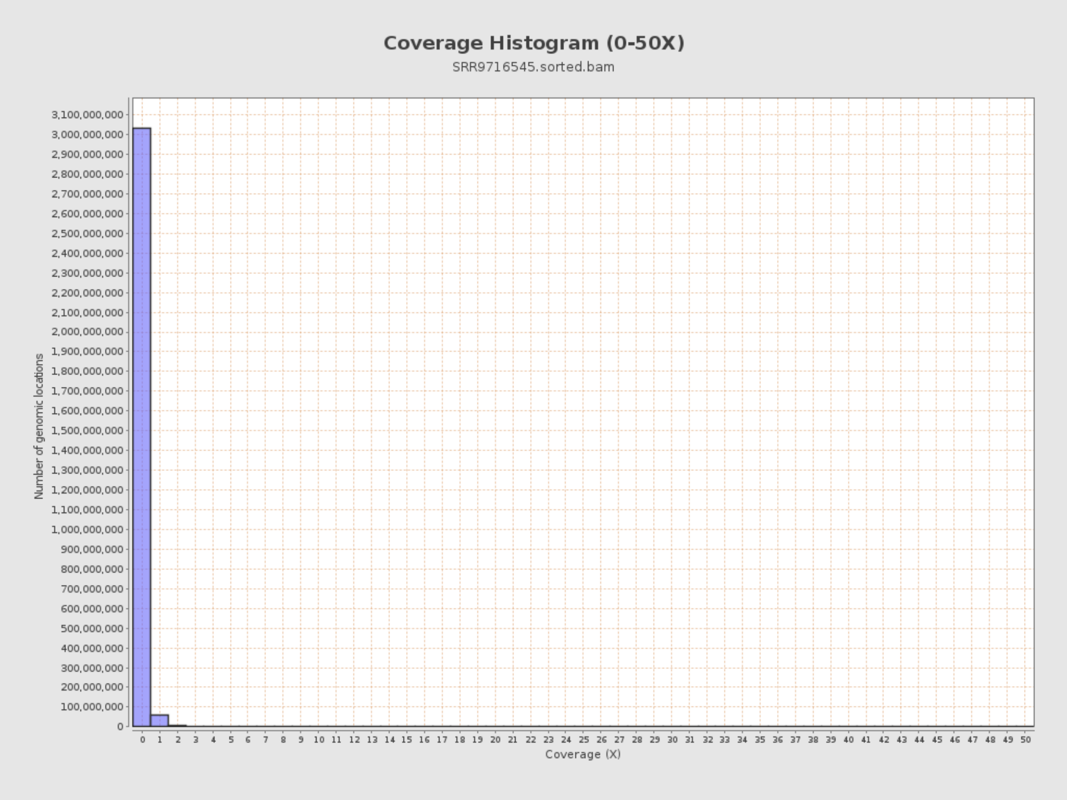
3. Results : Coverage across reference



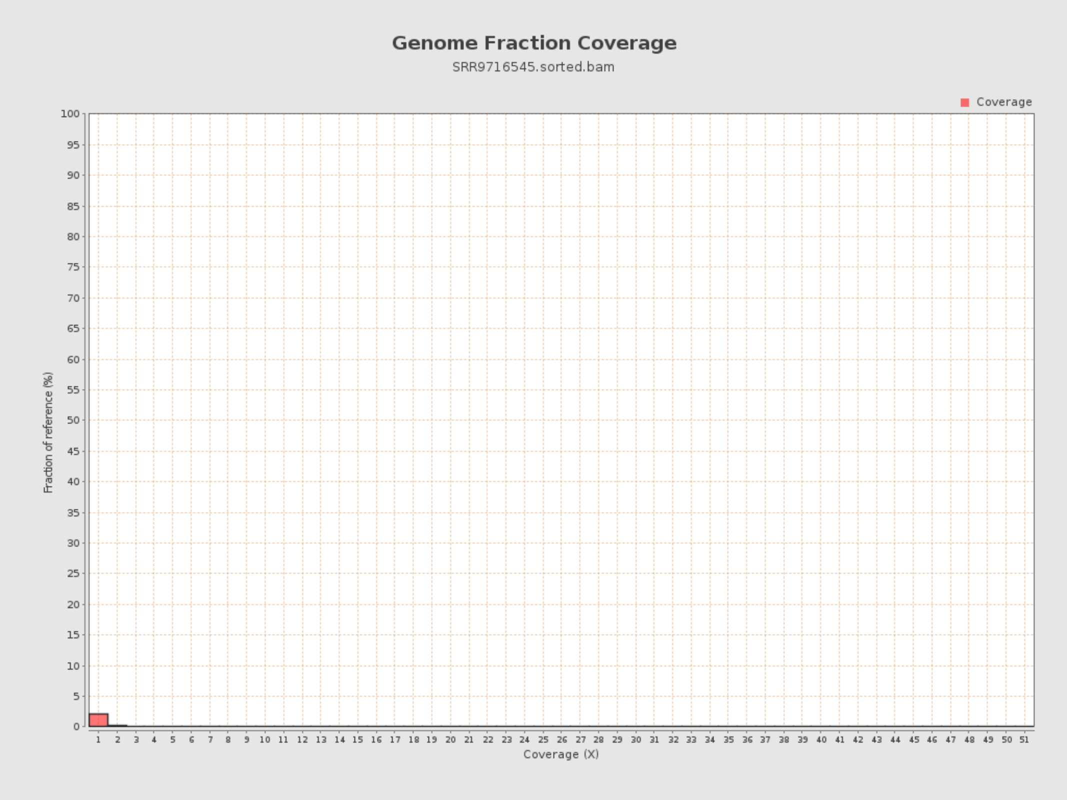
4. Results : Coverage Histogram



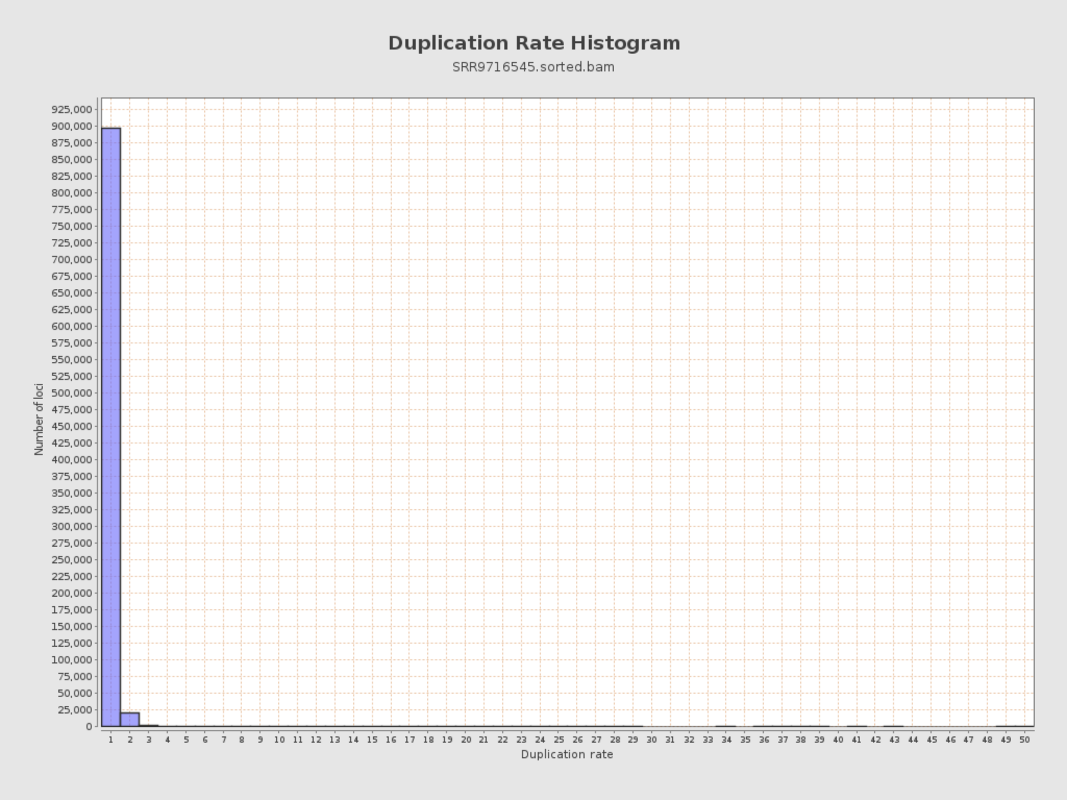
5. Results : Coverage Histogram (0-50X)



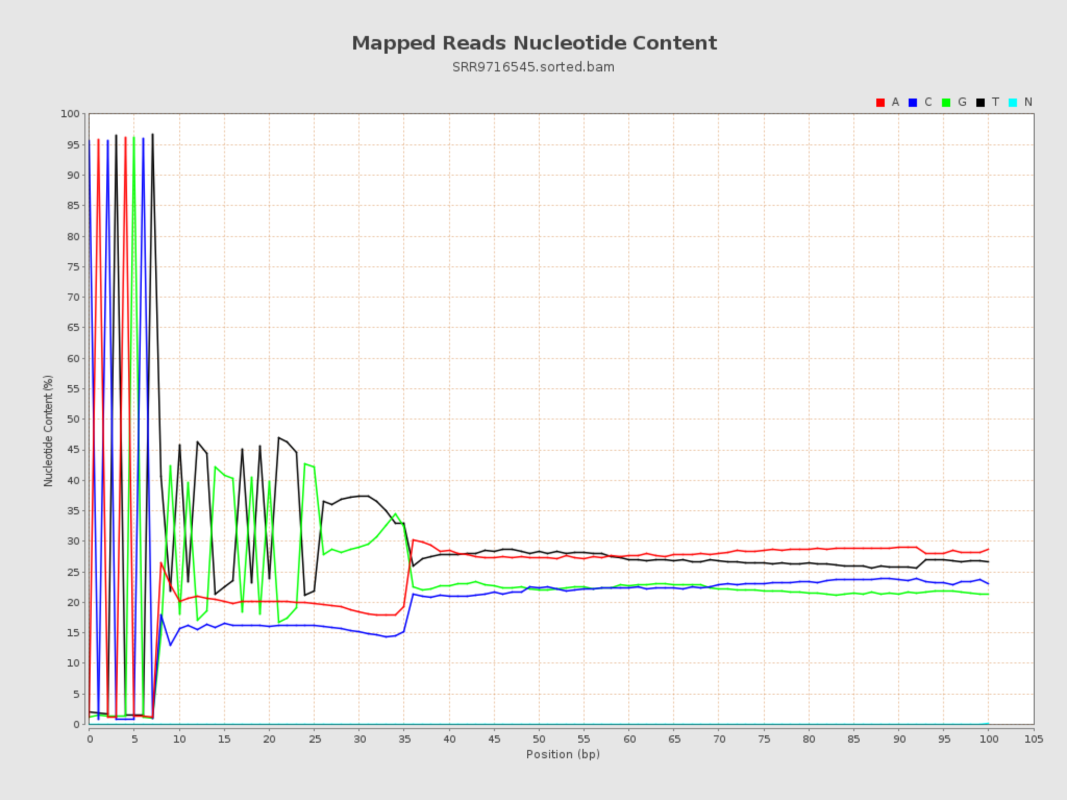
6. Results : Genome Fraction Coverage



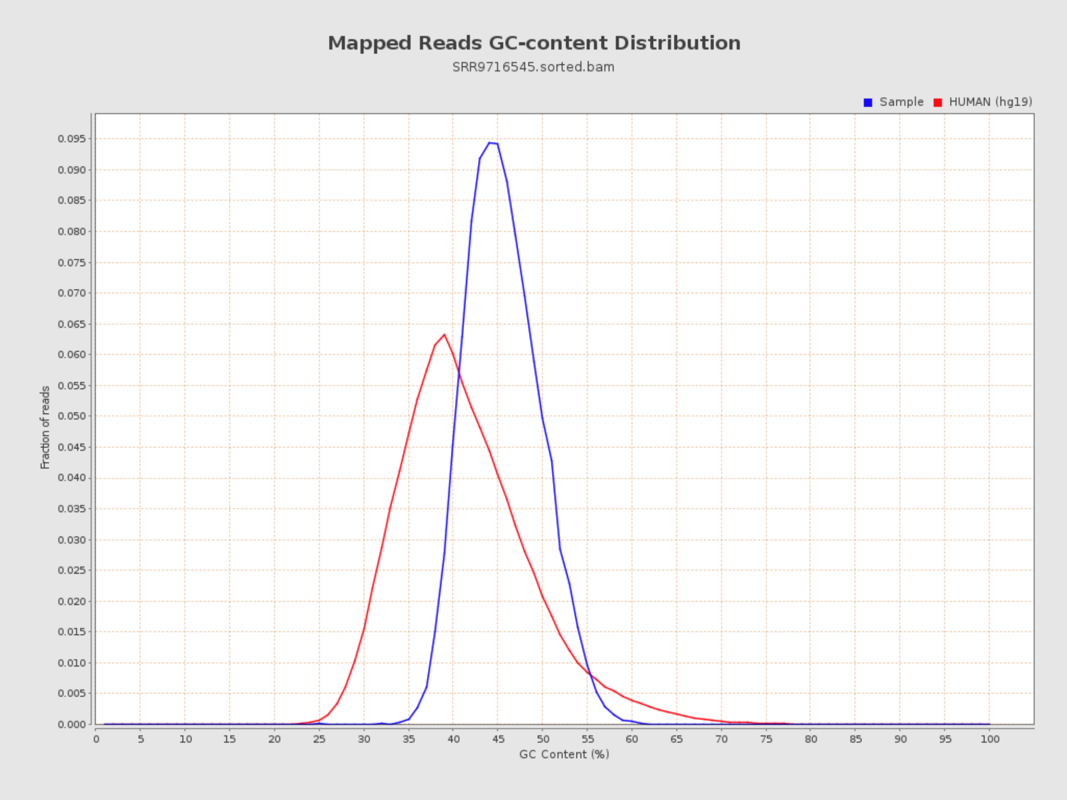
7. Results : Duplication Rate Histogram



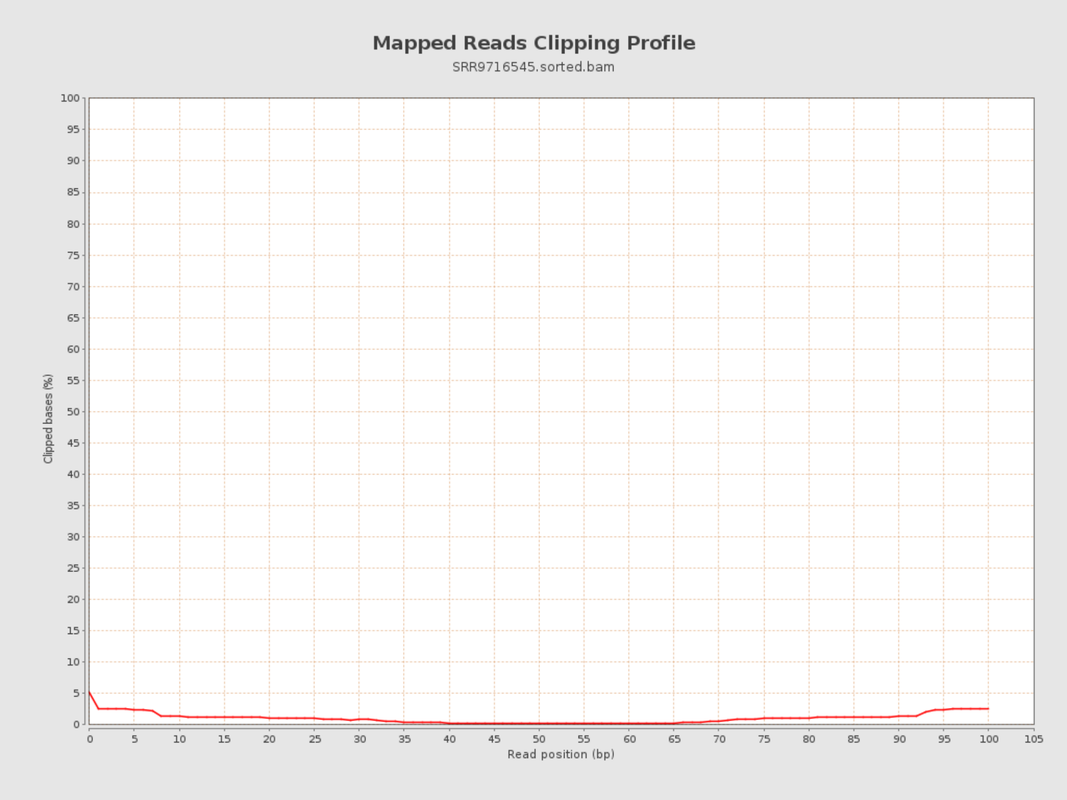
8. Results : Mapped Reads Nucleotide Content



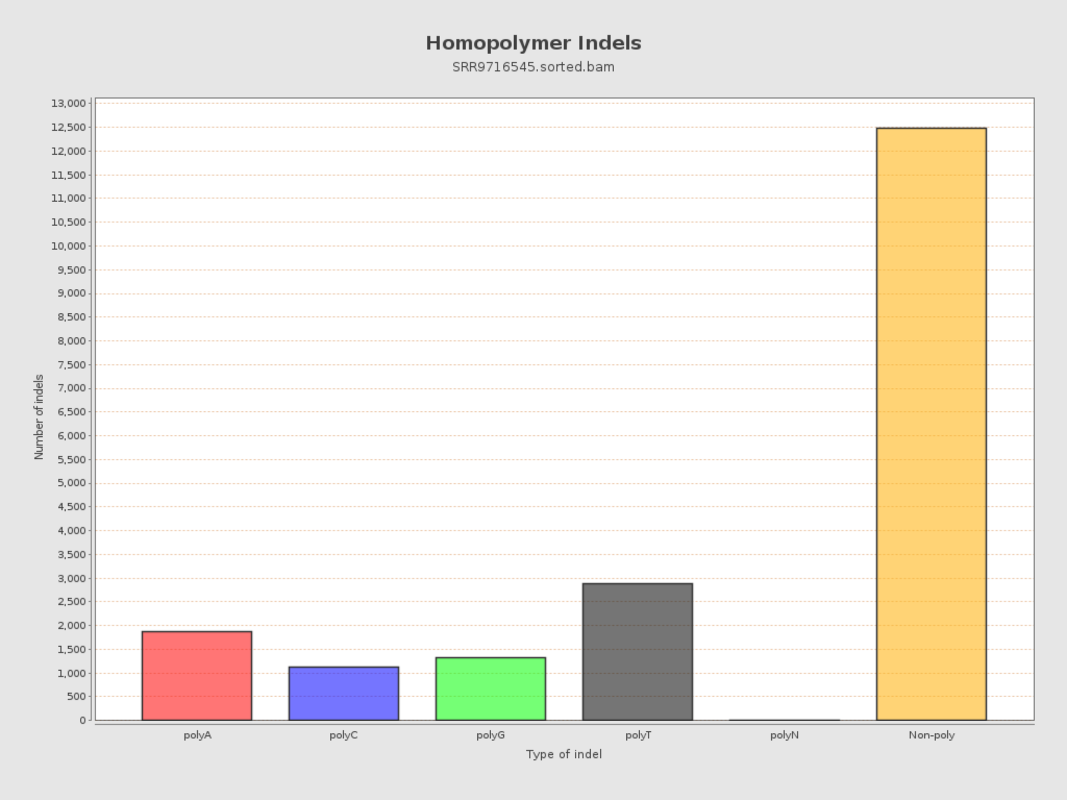
9. Results : Mapped Reads GC-content Distribution



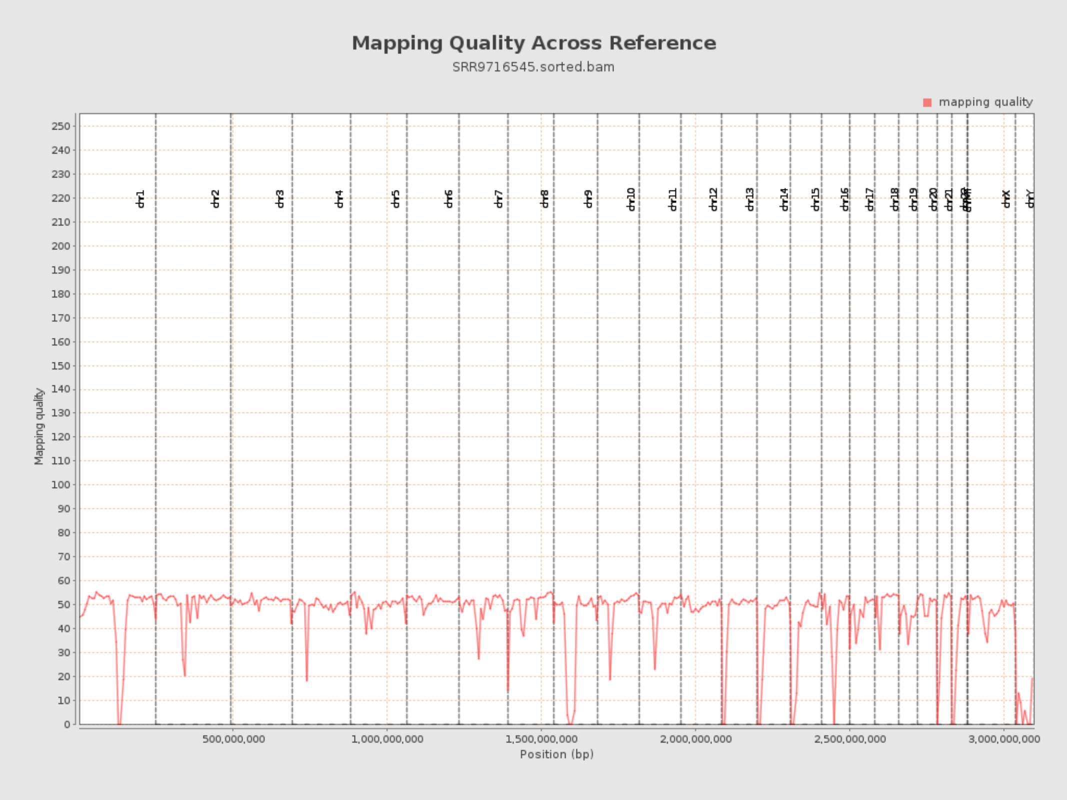
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram