Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:36:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716540.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_SRR9716540 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716540.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:36:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716540.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	597,697
Mapped reads	547,543 / 91.61%
Unmapped reads	50,154 / 8.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,278 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	11,961 / 2%
Duplication rate	1.7%
Clipped reads	548,301 / 91.74%

2.2. ACGT Content

Number/percentage of A's	8,199,757 / 25.81%
Number/percentage of C's	6,206,294 / 19.54%
Number/percentage of T's	9,975,694 / 31.4%
Number/percentage of G's	7,383,887 / 23.24%
Number/percentage of N's	972 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.1256

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

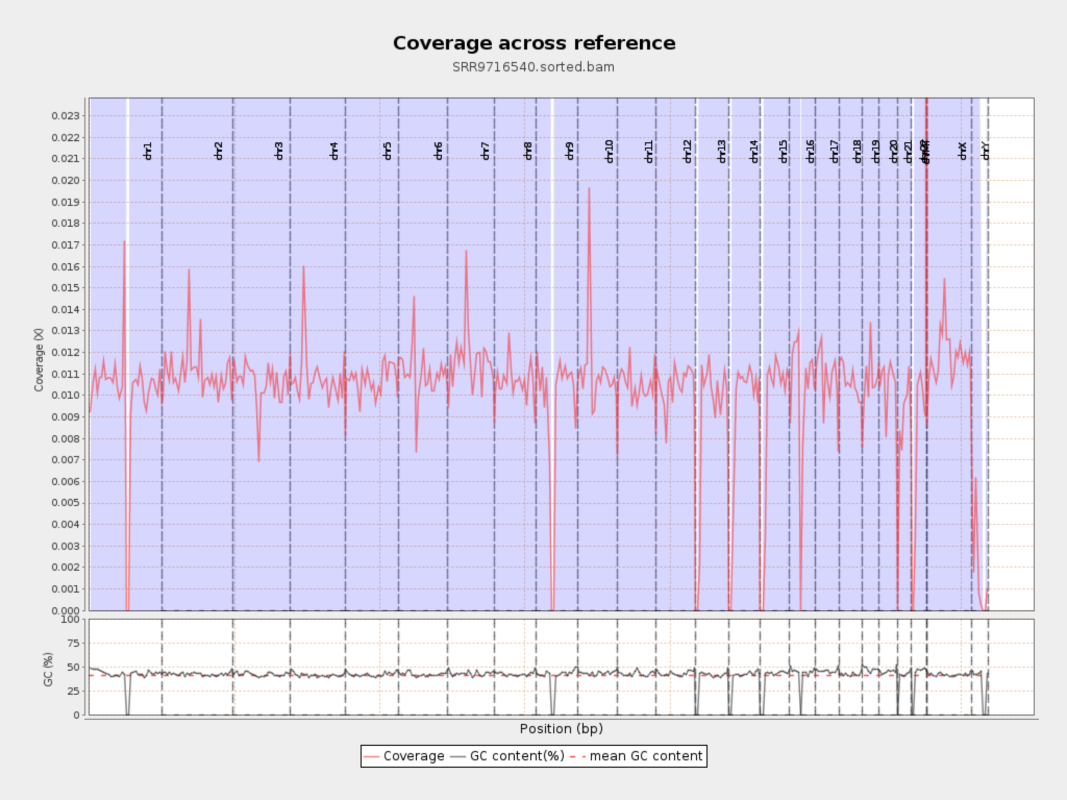
General error rate	0.51%
Mismatches	158,856
Insertions	2,180
Mapped reads with at least one insertion	0.4%
Deletions	5,948
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.26%

2.6. Chromosome stats

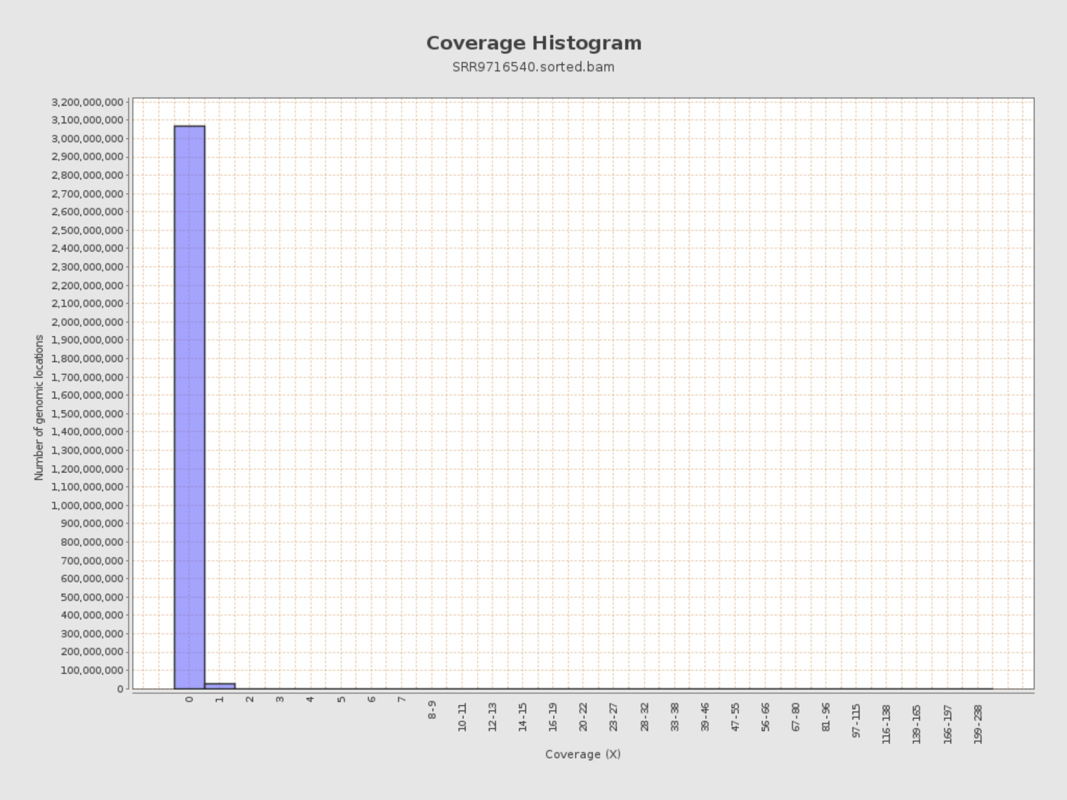
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2510457	0.0101	0.1954
chr2	243199373	2706854	0.0111	0.1431
chr3	198022430	2091510	0.0106	0.1072
chr4	191154276	2067124	0.0108	0.1116
chr5	180915260	1947375	0.0108	0.1079
chr6	171115067	1888931	0.011	0.1168
chr7	159138663	1867920	0.0117	0.1433

chr8	146364022	1562443	0.0107	0.1235
chr9	141213431	1315826	0.0093	0.1124
chr10	135534747	1516561	0.0112	0.1273
chr11	135006516	1414102	0.0105	0.1161
chr12	133851895	1404441	0.0105	0.1074
chr13	115169878	1002771	0.0087	0.0974
chr14	107349540	948049	0.0088	0.0995
chr15	102531392	905782	0.0088	0.0979
chr16	90354753	918427	0.0102	0.1079
chr17	81195210	875381	0.0108	0.1116
chr18	78077248	831338	0.0106	0.1538
chr19	59128983	637070	0.0108	0.1539
chr20	63025520	659463	0.0105	0.1075
chr21	48129895	402553	0.0084	0.1001
chr22	51304566	361723	0.0071	0.0869
chrMT	16571	7933	0.4787	0.7731
chrX	155270560	1833248	0.0118	0.1168
chrY	59373566	98830	0.0017	0.0583

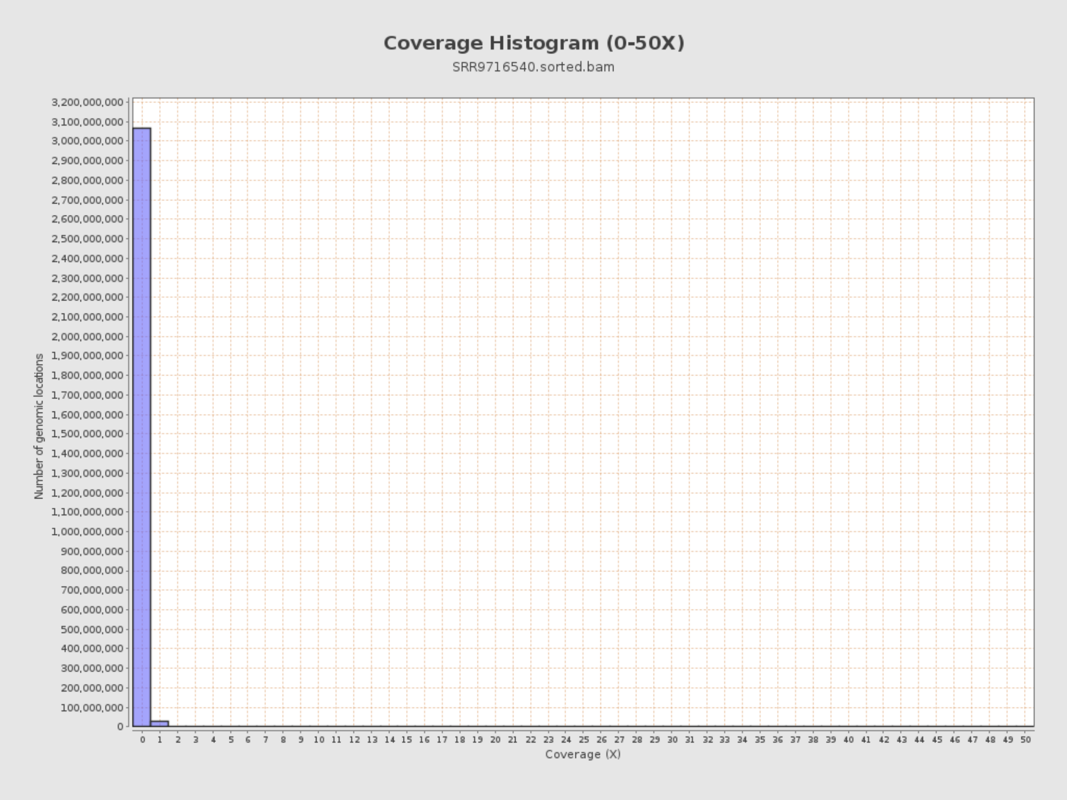
3. Results : Coverage across reference



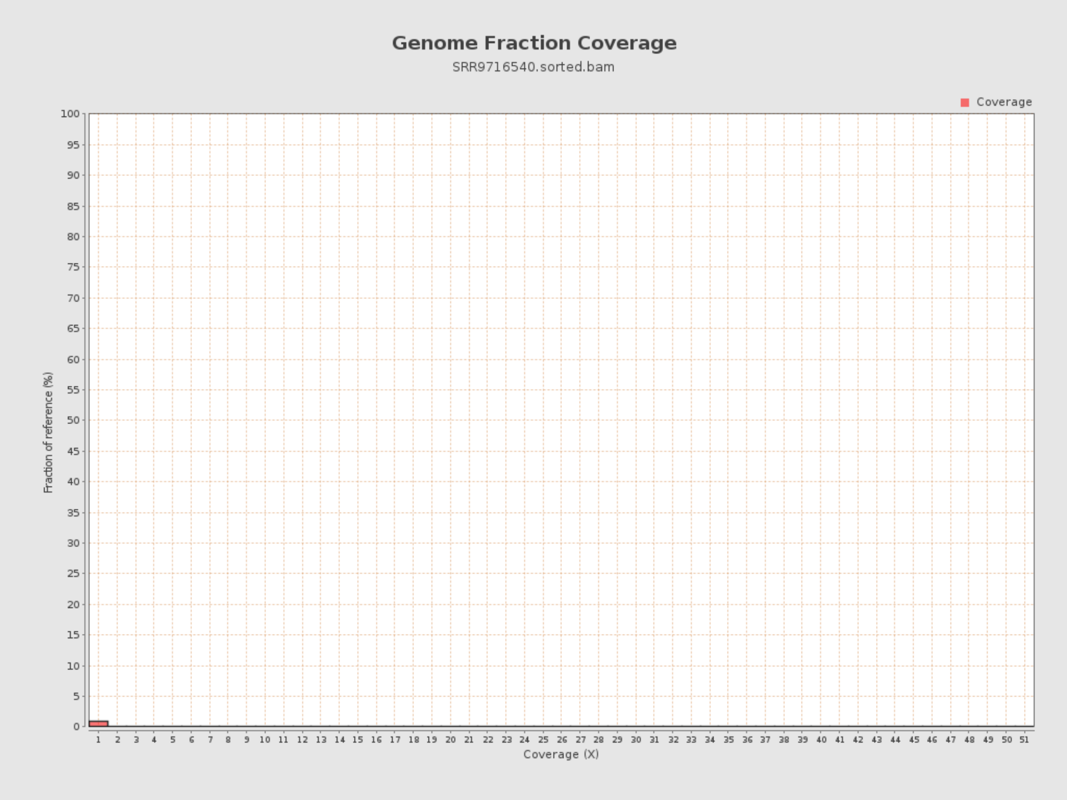
4. Results : Coverage Histogram



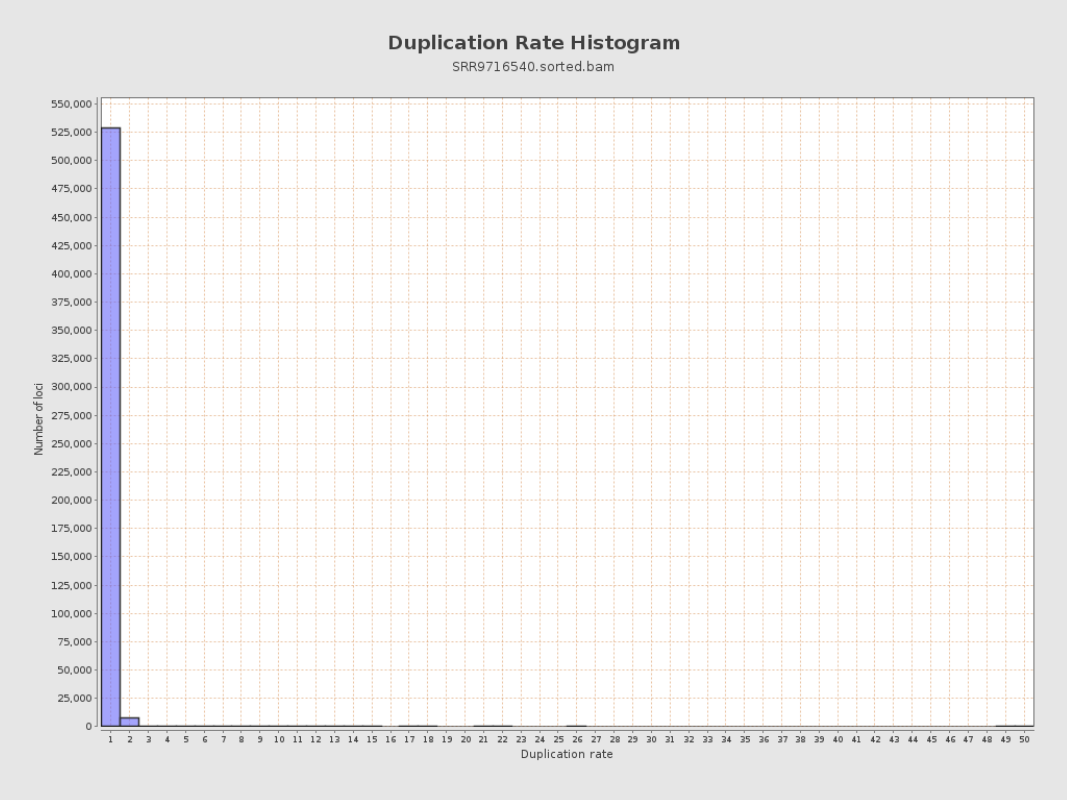
5. Results : Coverage Histogram (0-50X)



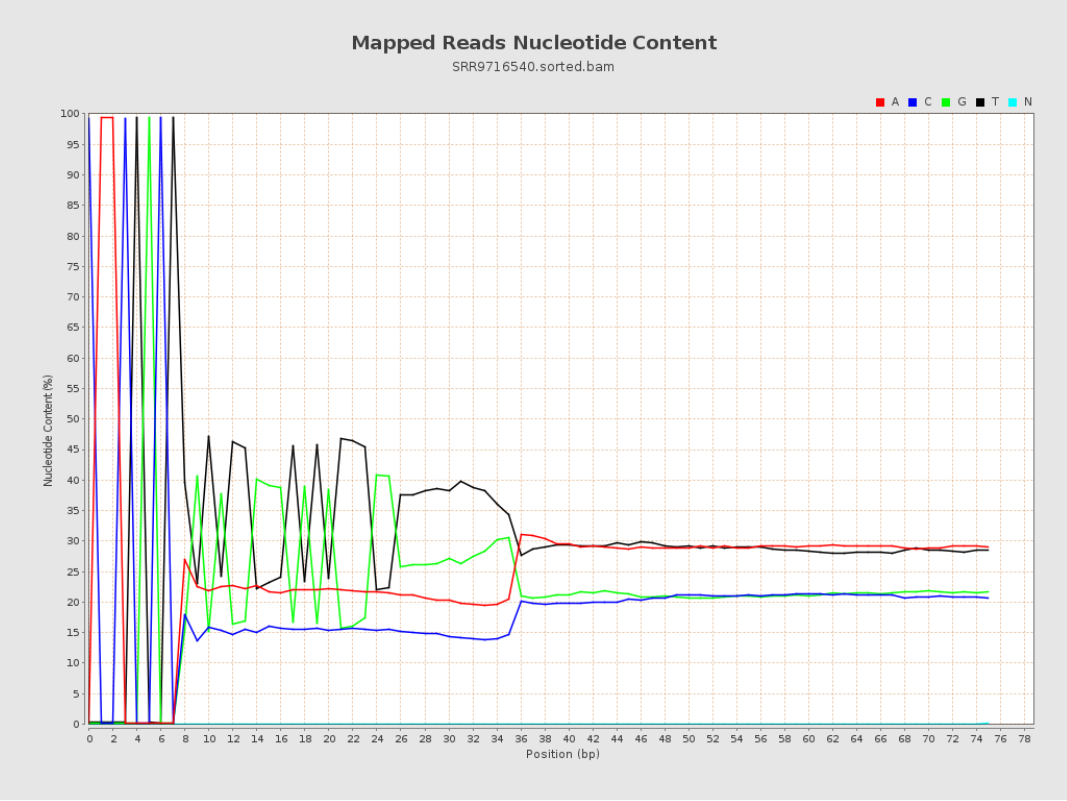
6. Results : Genome Fraction Coverage



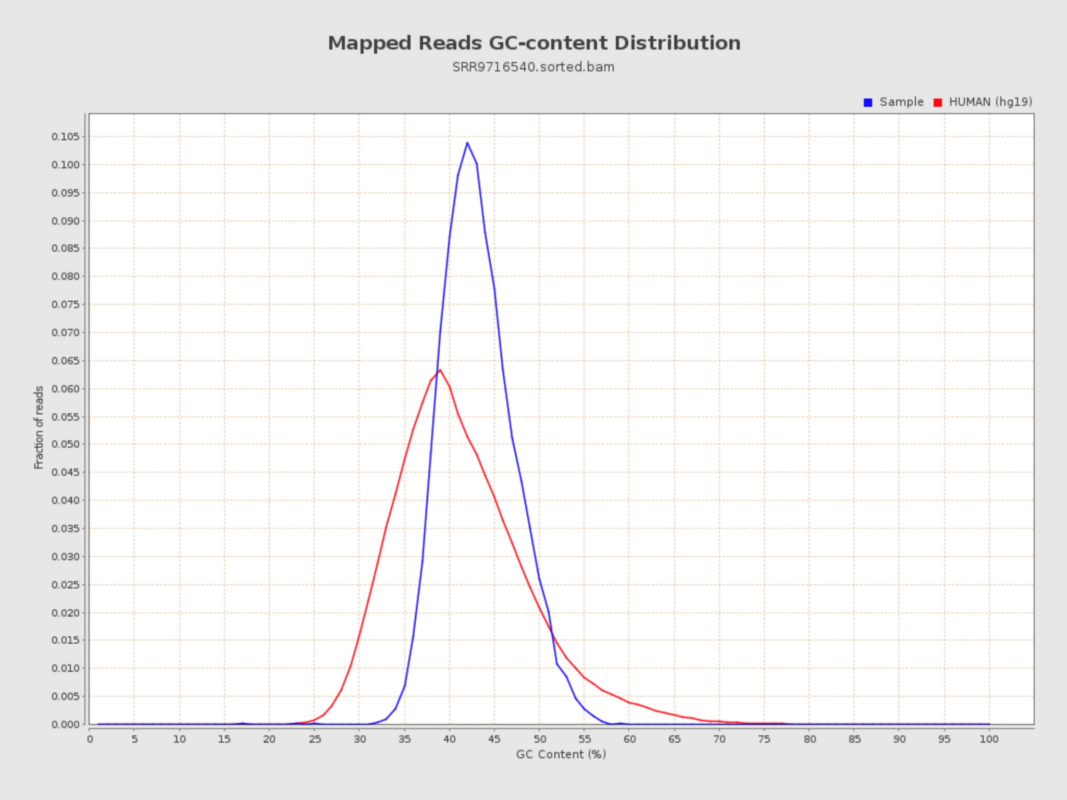
7. Results : Duplication Rate Histogram



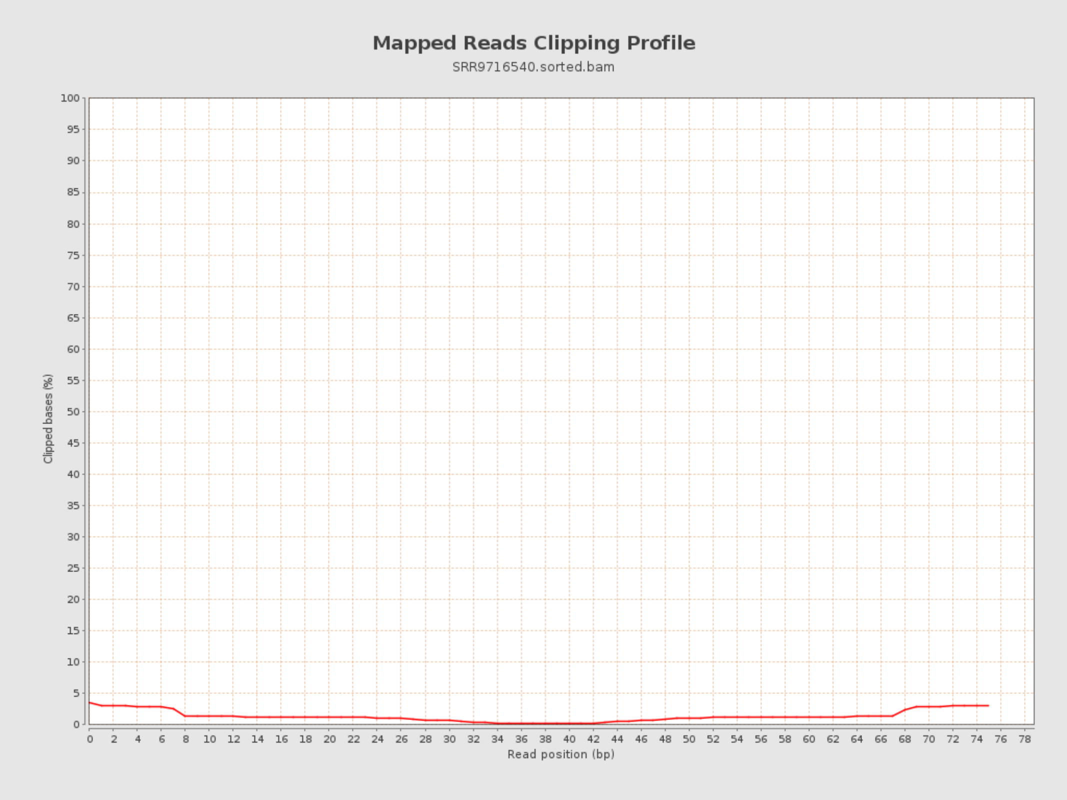
8. Results : Mapped Reads Nucleotide Content



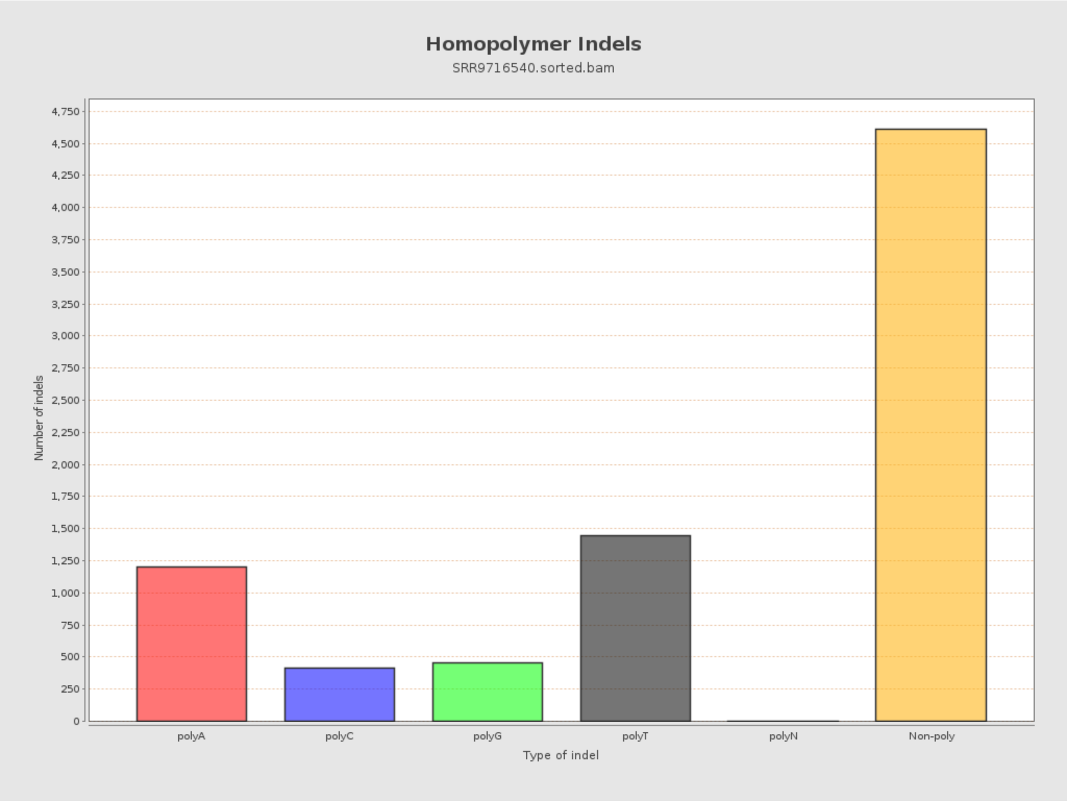
9. Results : Mapped Reads GC-content Distribution



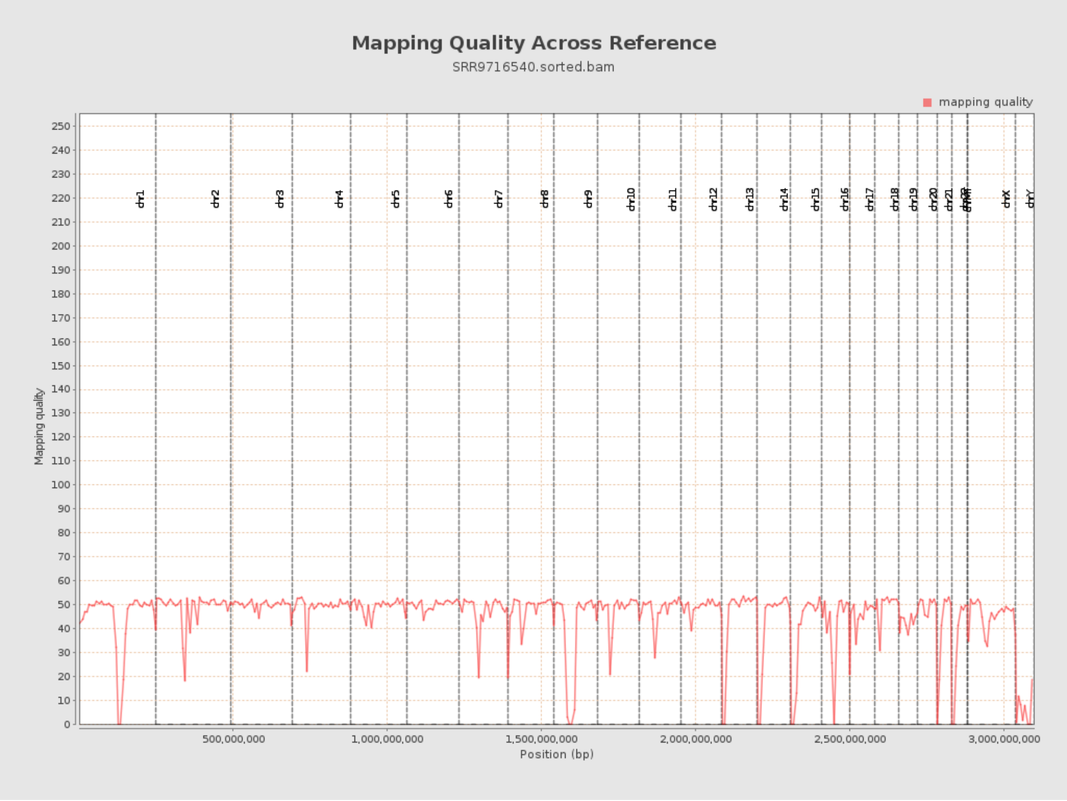
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram