Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:38:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716574.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_SRR9716574 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716574.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:38:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716574.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	798,782
Mapped reads	751,415 / 94.07%
Unmapped reads	47,367 / 5.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,454 / 2.19%
Read min/max/mean length	30 / 101 / 101.8
Duplicated reads (estimated)	21,127 / 2.64%
Duplication rate	2.08%
Clipped reads	767,304 / 96.06%

2.2. ACGT Content

Number/percentage of A's	14,886,024 / 25.47%
Number/percentage of C's	12,170,036 / 20.83%
Number/percentage of T's	16,747,108 / 28.66%
Number/percentage of G's	14,631,856 / 25.04%
Number/percentage of N's	2,355 / 0%
GC Percentage	45.86%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.187

2.4. Mapping Quality

Mean Mapping Quality	46.57

2.5. Mismatches and indels

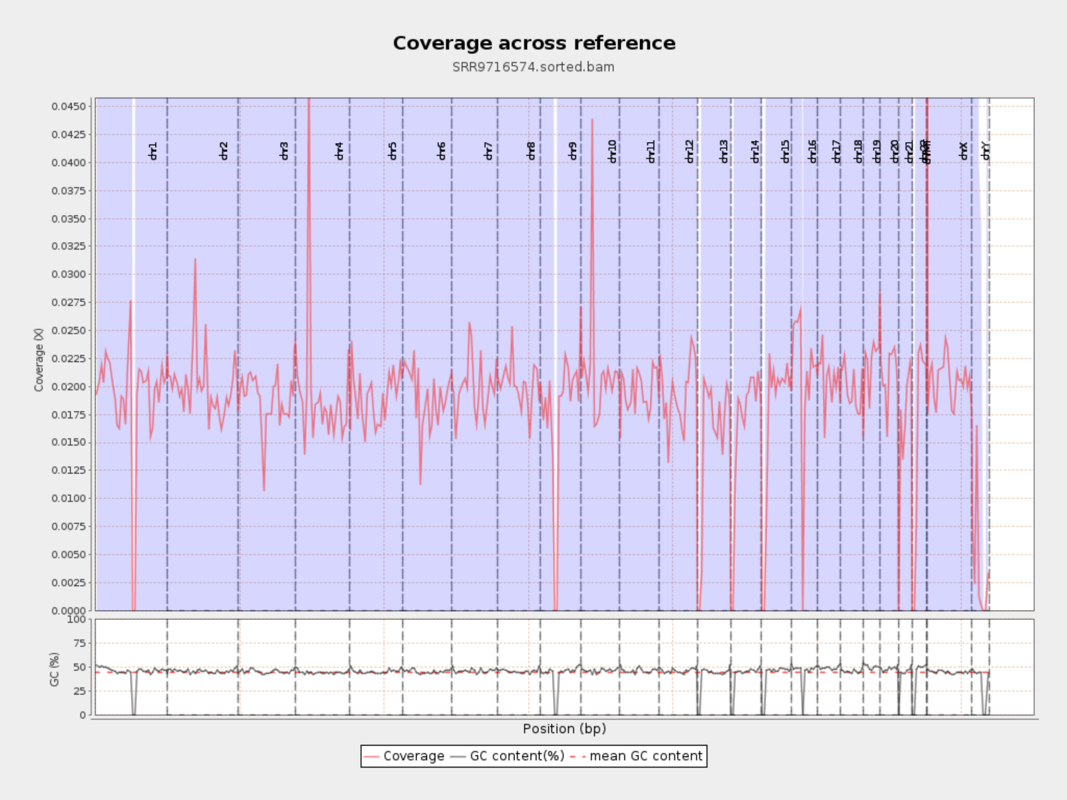
General error rate	0.67%
Mismatches	373,221
Insertions	5,709
Mapped reads with at least one insertion	0.75%
Deletions	10,659
Mapped reads with at least one deletion	1.39%
Homopolymer indels	37.96%

2.6. Chromosome stats

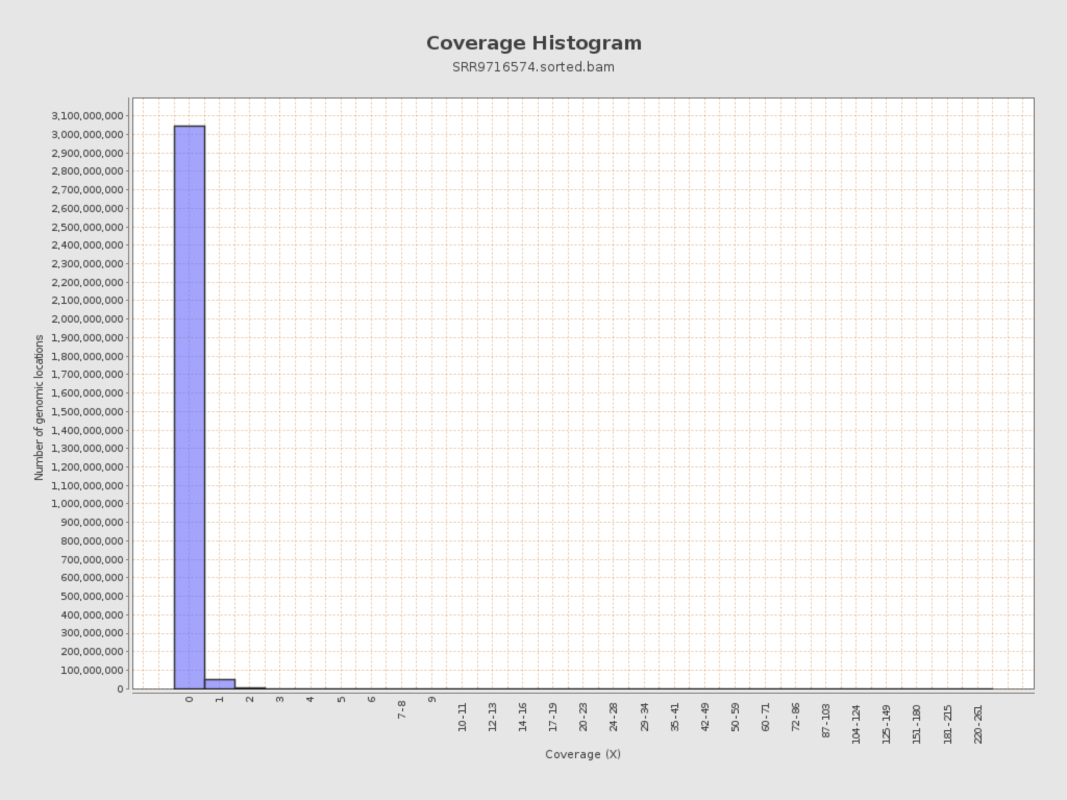
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4715100	0.0189	0.237
chr2	243199373	4884670	0.0201	0.2085
chr3	198022430	3720298	0.0188	0.1465
chr4	191154276	3713251	0.0194	0.2072
chr5	180915260	3473736	0.0192	0.1497
chr6	171115067	3257110	0.019	0.1536
chr7	159138663	3167082	0.0199	0.208

chr8	146364022	2947272	0.0201	0.187
chr9	141213431	2435571	0.0172	0.1697
chr10	135534747	2919370	0.0215	0.2819
chr11	135006516	2668487	0.0198	0.1869
chr12	133851895	2589562	0.0193	0.1509
chr13	115169878	1739715	0.0151	0.1319
chr14	107349540	1738474	0.0162	0.1455
chr15	102531392	1729305	0.0169	0.1401
chr16	90354753	1876965	0.0208	0.1642
chr17	81195210	1682960	0.0207	0.1678
chr18	78077248	1540199	0.0197	0.2482
chr19	59128983	1318139	0.0223	0.2077
chr20	63025520	1321839	0.021	0.1644
chr21	48129895	798672	0.0166	0.178
chr22	51304566	801792	0.0156	0.1381
chrMT	16571	2395	0.1445	0.4216
chrX	155270560	3193567	0.0206	0.162
chrY	59373566	224458	0.0038	0.1789

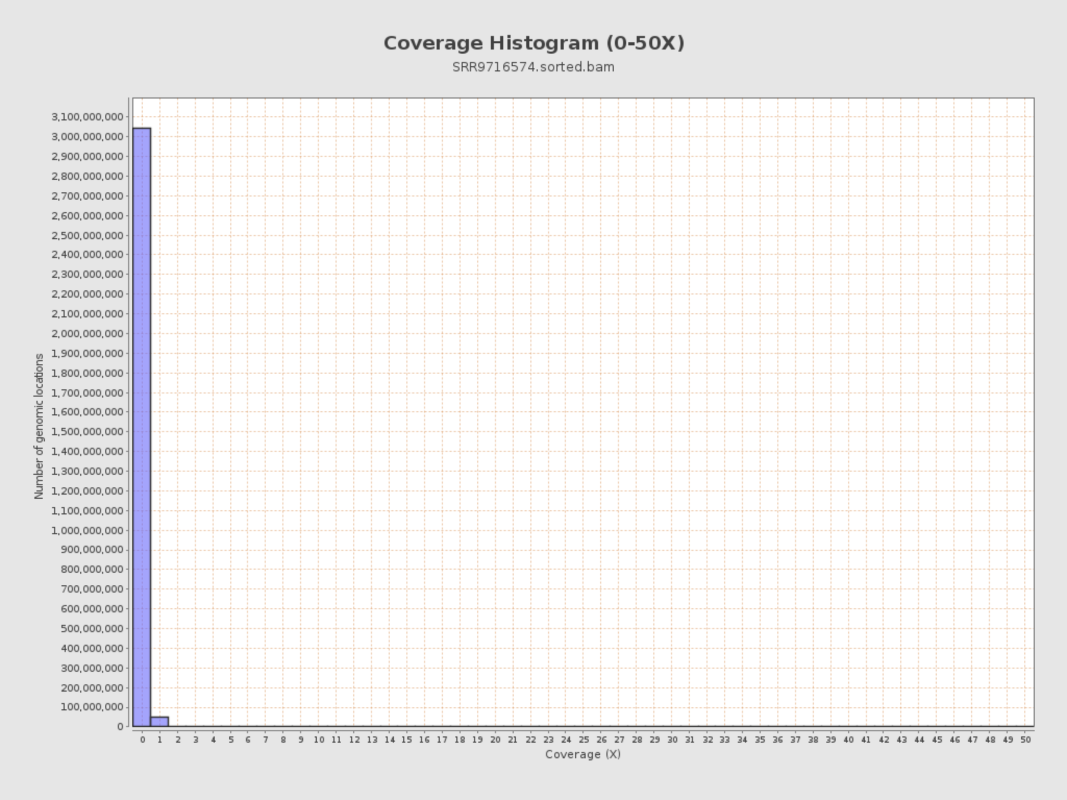
3. Results : Coverage across reference



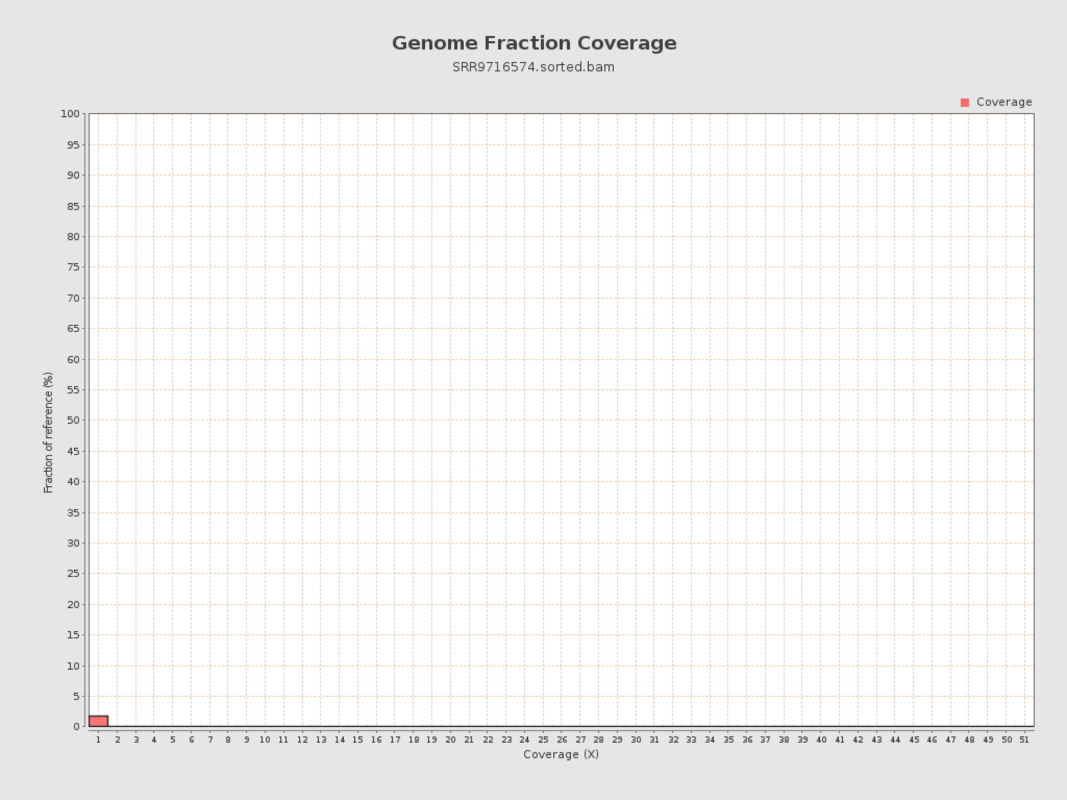
4. Results : Coverage Histogram



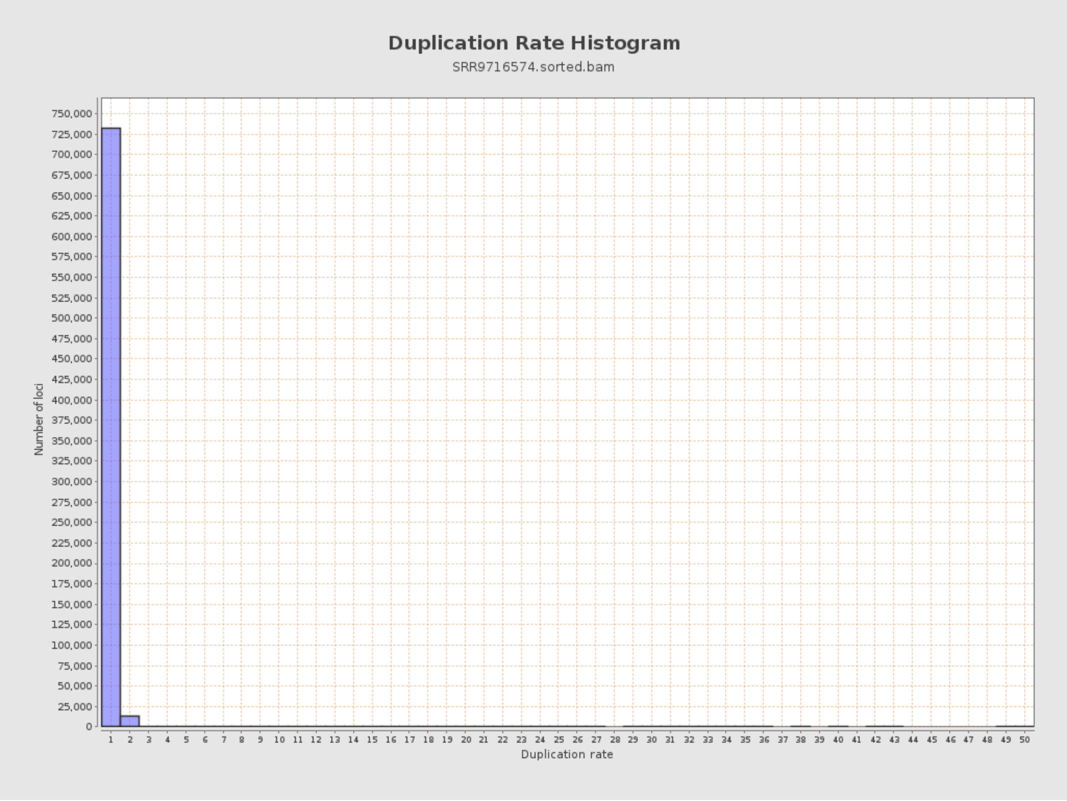
5. Results : Coverage Histogram (0-50X)



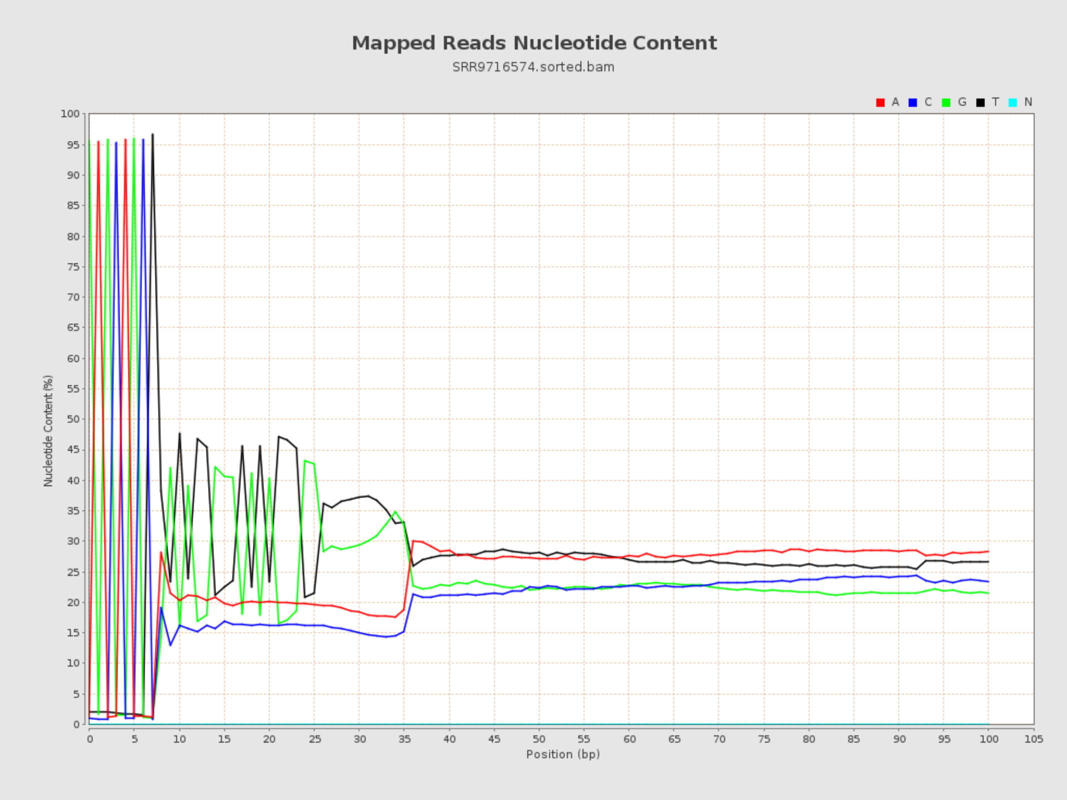
6. Results : Genome Fraction Coverage



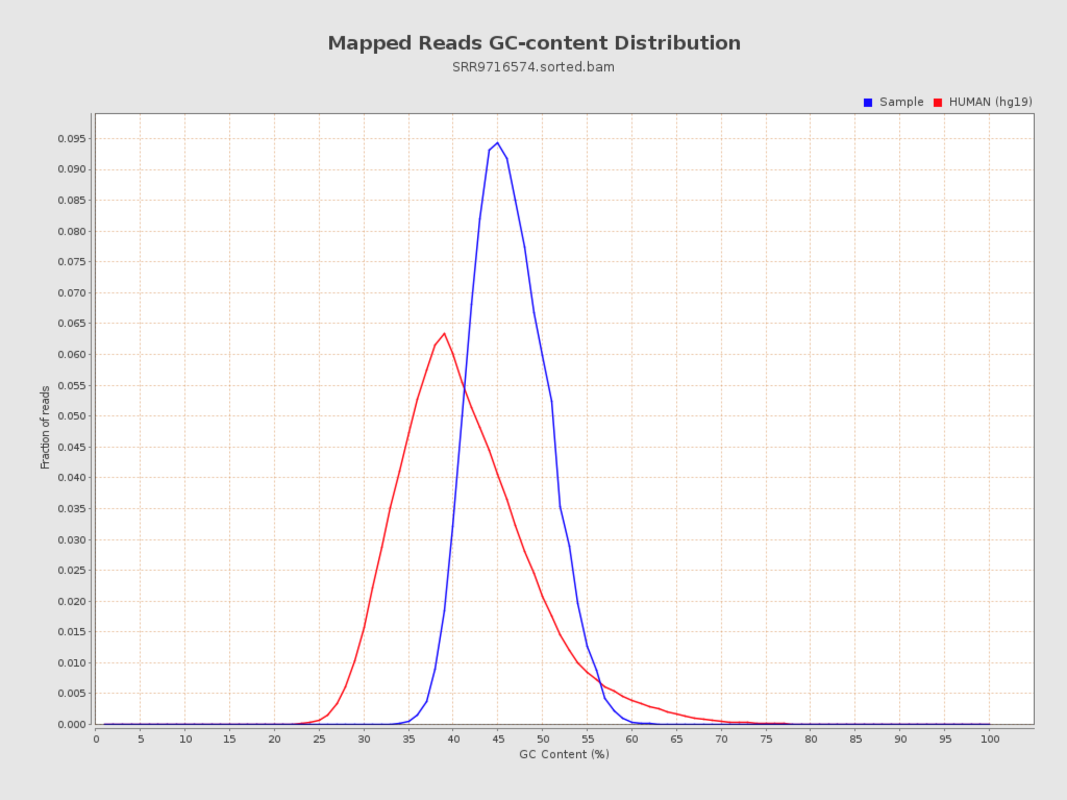
7. Results : Duplication Rate Histogram



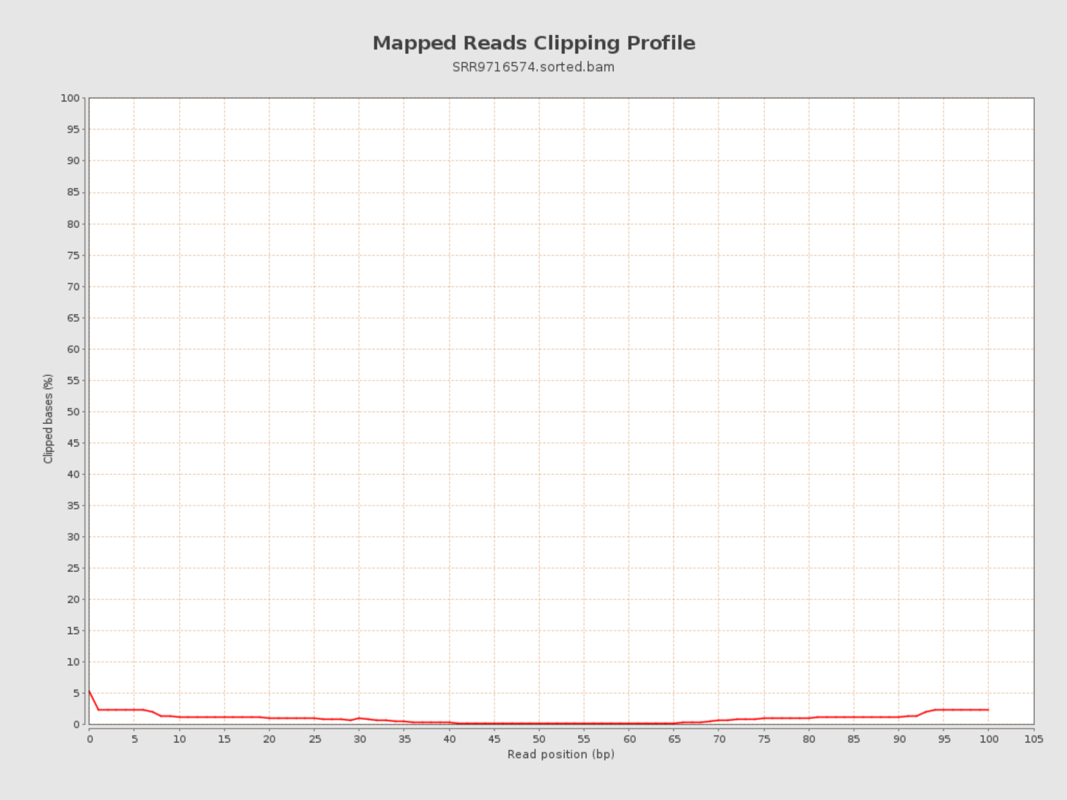
8. Results : Mapped Reads Nucleotide Content



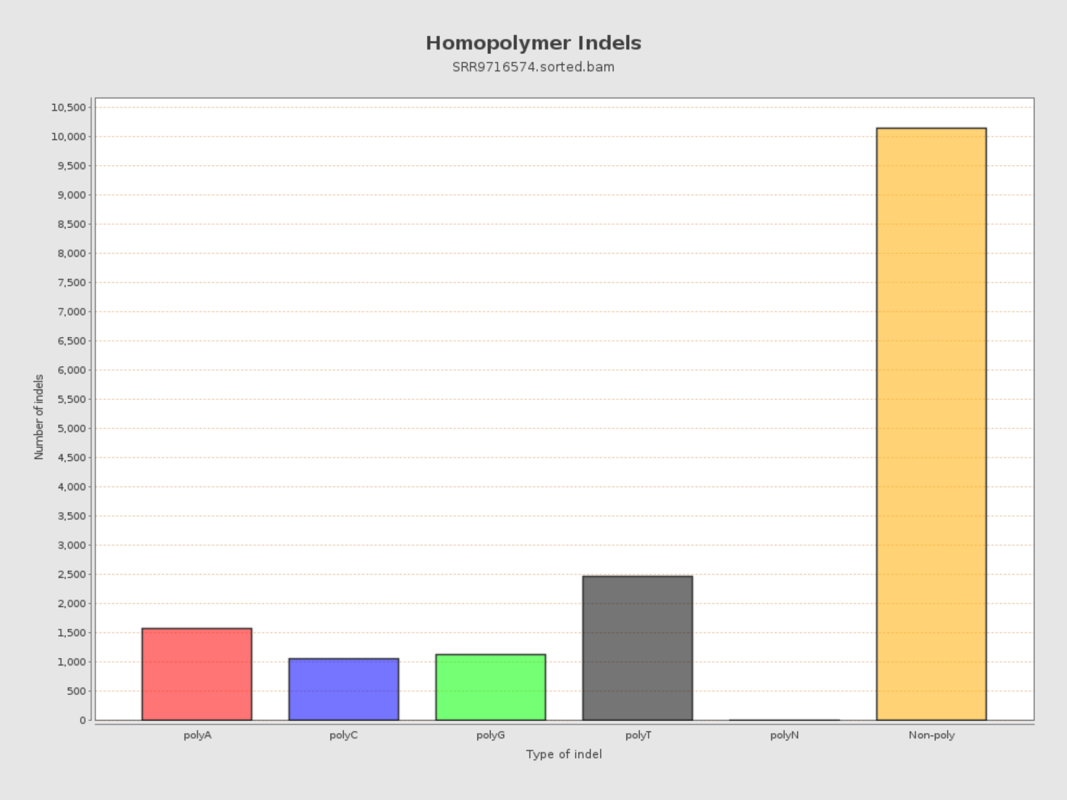
9. Results : Mapped Reads GC-content Distribution



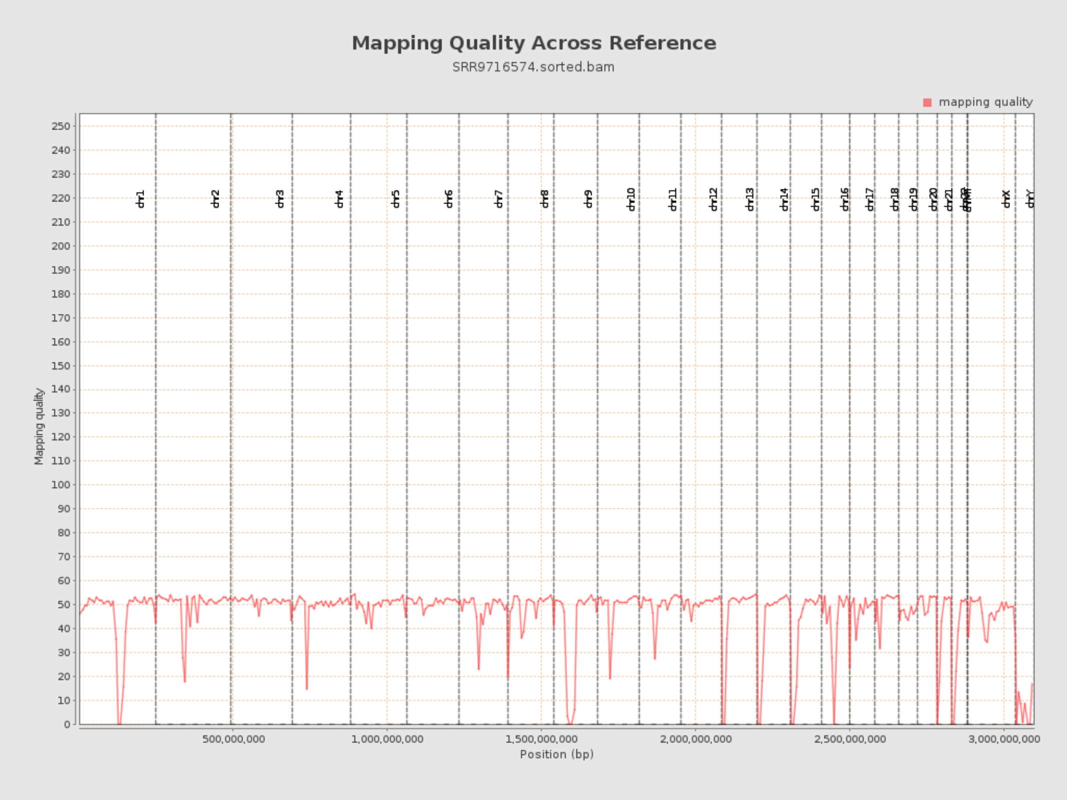
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram