Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:55:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716442.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_SRR9716442 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716442.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:55:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716442.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	703,797
Mapped reads	596,971 / 84.82%
Unmapped reads	106,826 / 15.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,098 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	13,494 / 1.92%
Duplication rate	1.73%
Clipped reads	598,759 / 85.08%

2.2. ACGT Content

Number/percentage of A's	8,868,654 / 25.83%
Number/percentage of C's	6,574,312 / 19.15%
Number/percentage of T's	10,825,775 / 31.54%
Number/percentage of G's	8,059,490 / 23.48%
Number/percentage of N's	268 / 0%
GC Percentage	42.63%

2.3. Coverage

Mean	0.0111

Standard Deviation	0.1314

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Mismatches and indels

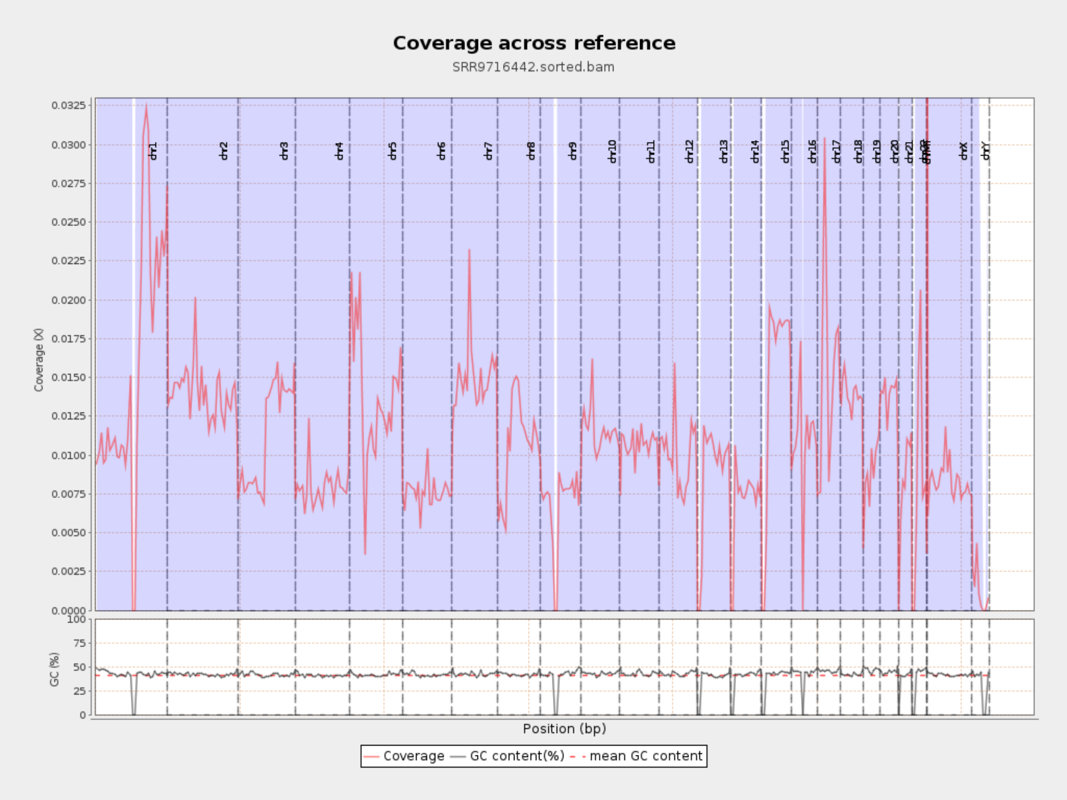
General error rate	0.51%
Mismatches	171,638
Insertions	2,309
Mapped reads with at least one insertion	0.39%
Deletions	5,597
Mapped reads with at least one deletion	0.93%
Homopolymer indels	41.15%

2.6. Chromosome stats

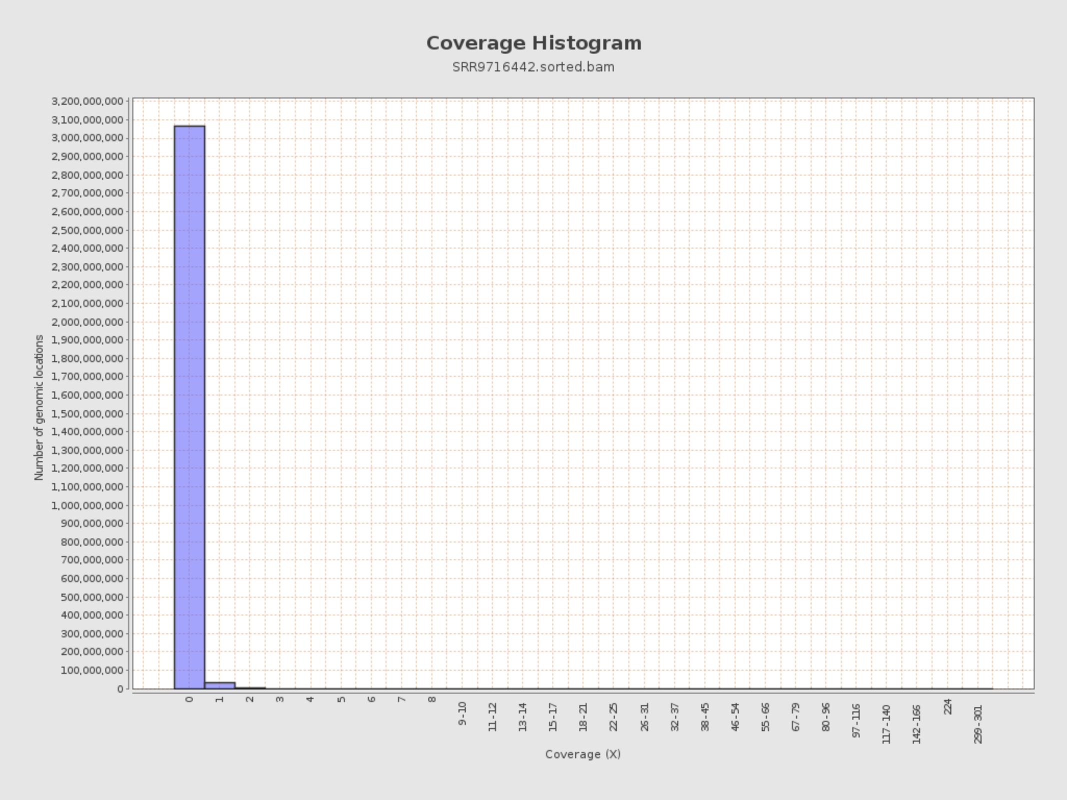
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3838175	0.0154	0.1731
chr2	243199373	3414909	0.014	0.1788
chr3	198022430	2223111	0.0112	0.1103
chr4	191154276	1514253	0.0079	0.0989
chr5	180915260	2504294	0.0138	0.1229
chr6	171115067	1300624	0.0076	0.0953
chr7	159138663	2397132	0.0151	0.1894

chr8	146364022	1584351	0.0108	0.122
chr9	141213431	957332	0.0068	0.1012
chr10	135534747	1582874	0.0117	0.1238
chr11	135006516	1450186	0.0107	0.1327
chr12	133851895	1336491	0.01	0.1044
chr13	115169878	1005809	0.0087	0.0971
chr14	107349540	745304	0.0069	0.089
chr15	102531392	1521592	0.0148	0.1275
chr16	90354753	956870	0.0106	0.1104
chr17	81195210	1279346	0.0158	0.1346
chr18	78077248	1089833	0.014	0.2149
chr19	59128983	536786	0.0091	0.1247
chr20	63025520	874903	0.0139	0.1231
chr21	48129895	395334	0.0082	0.0965
chr22	51304566	450161	0.0088	0.0979
chrMT	16571	3369	0.2033	0.4913
chrX	155270560	1298102	0.0084	0.1031
chrY	59373566	76172	0.0013	0.0448

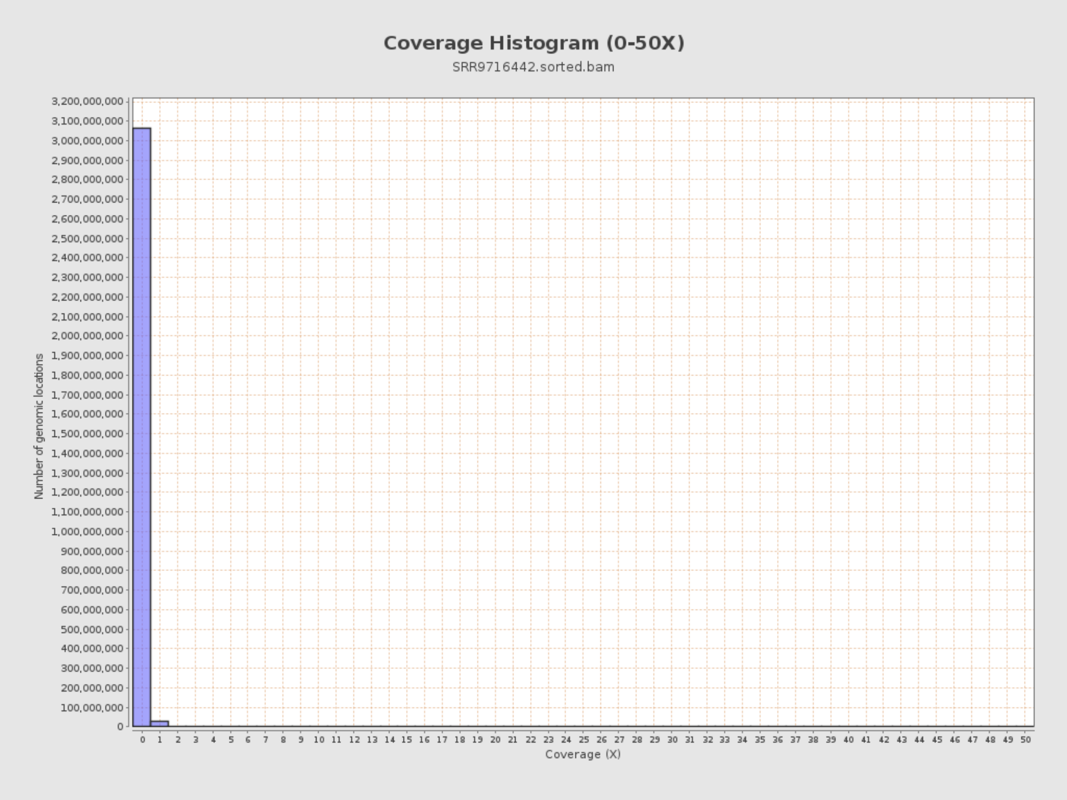
3. Results : Coverage across reference



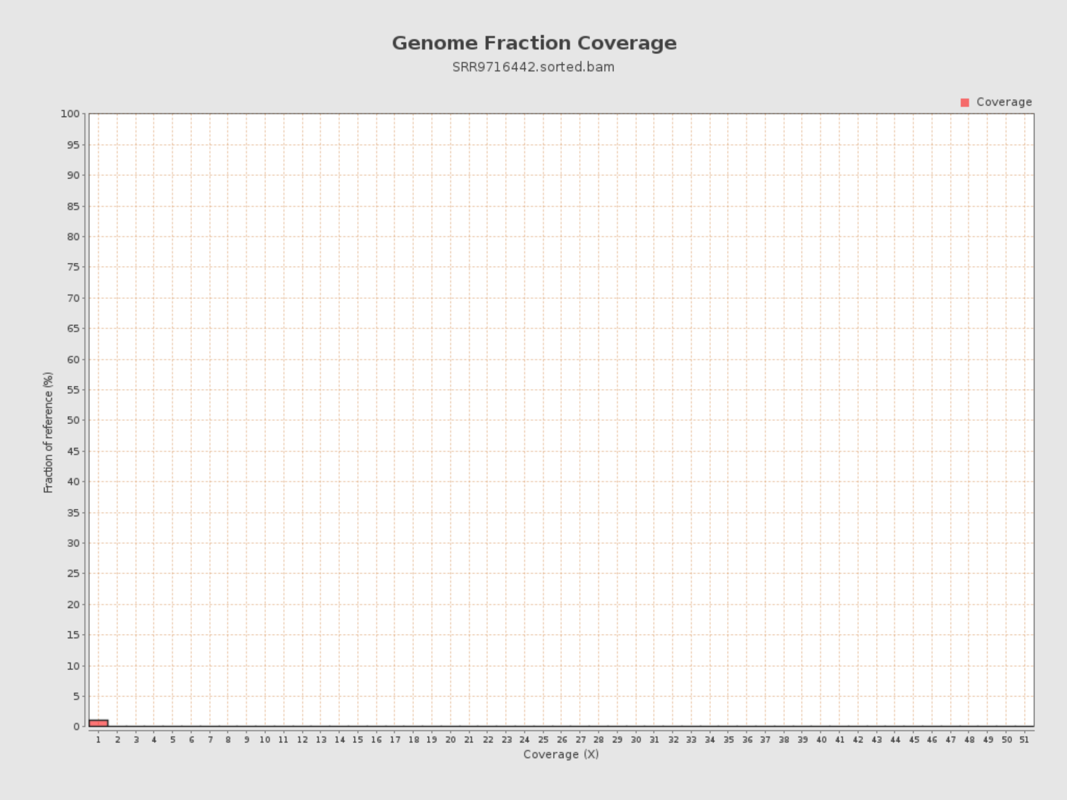
4. Results : Coverage Histogram



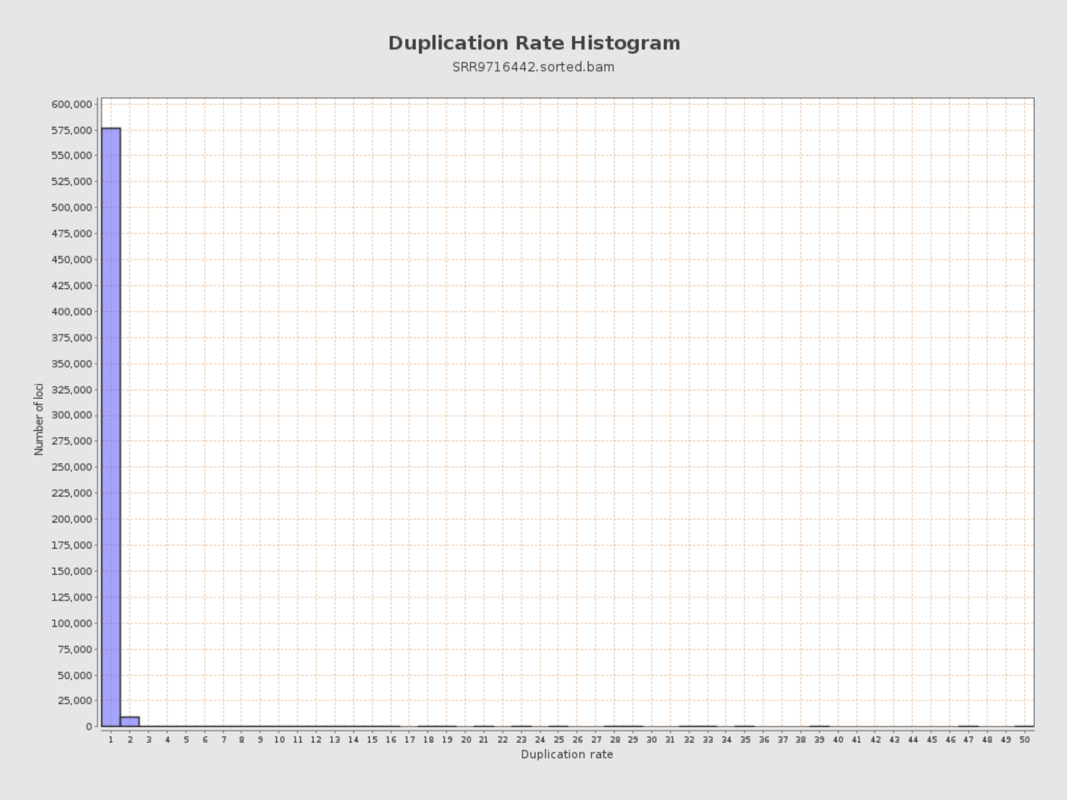
5. Results : Coverage Histogram (0-50X)



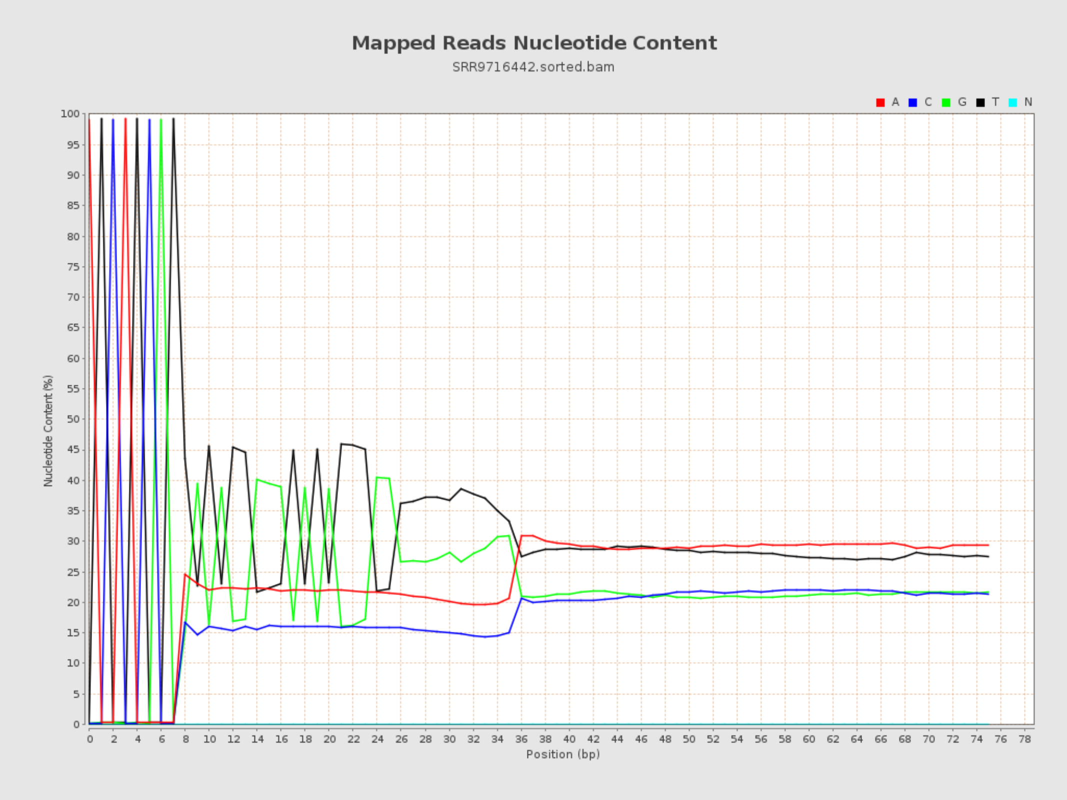
6. Results : Genome Fraction Coverage



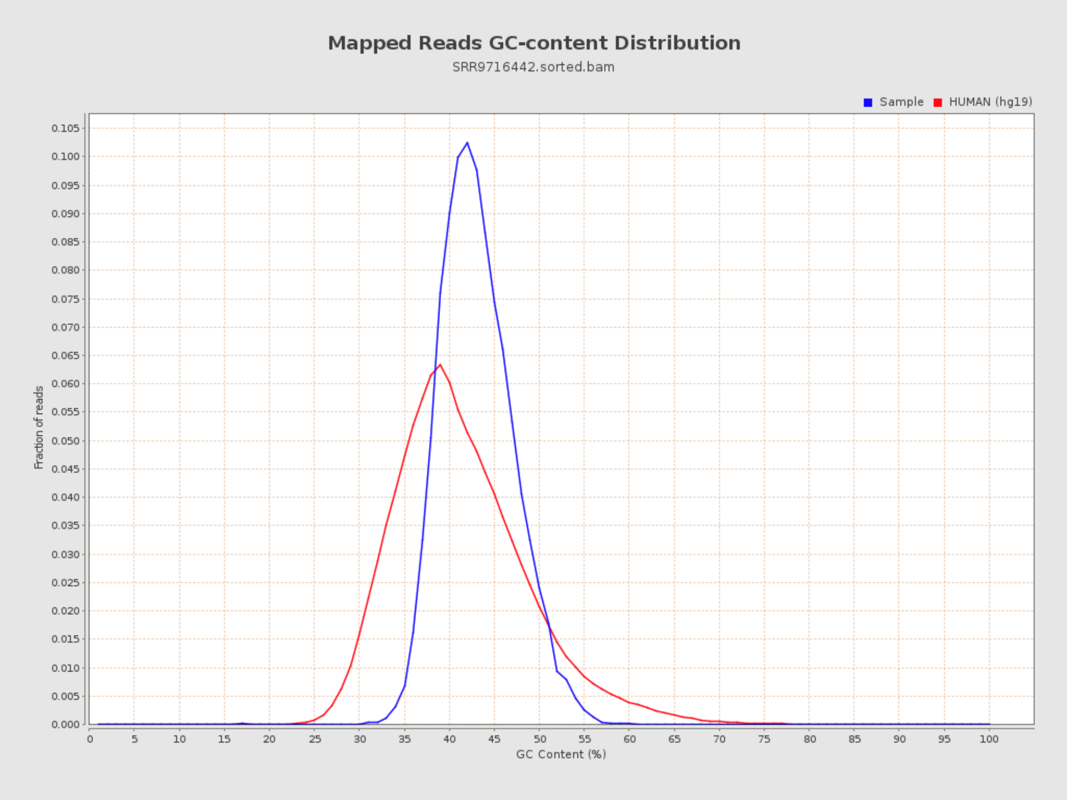
7. Results : Duplication Rate Histogram



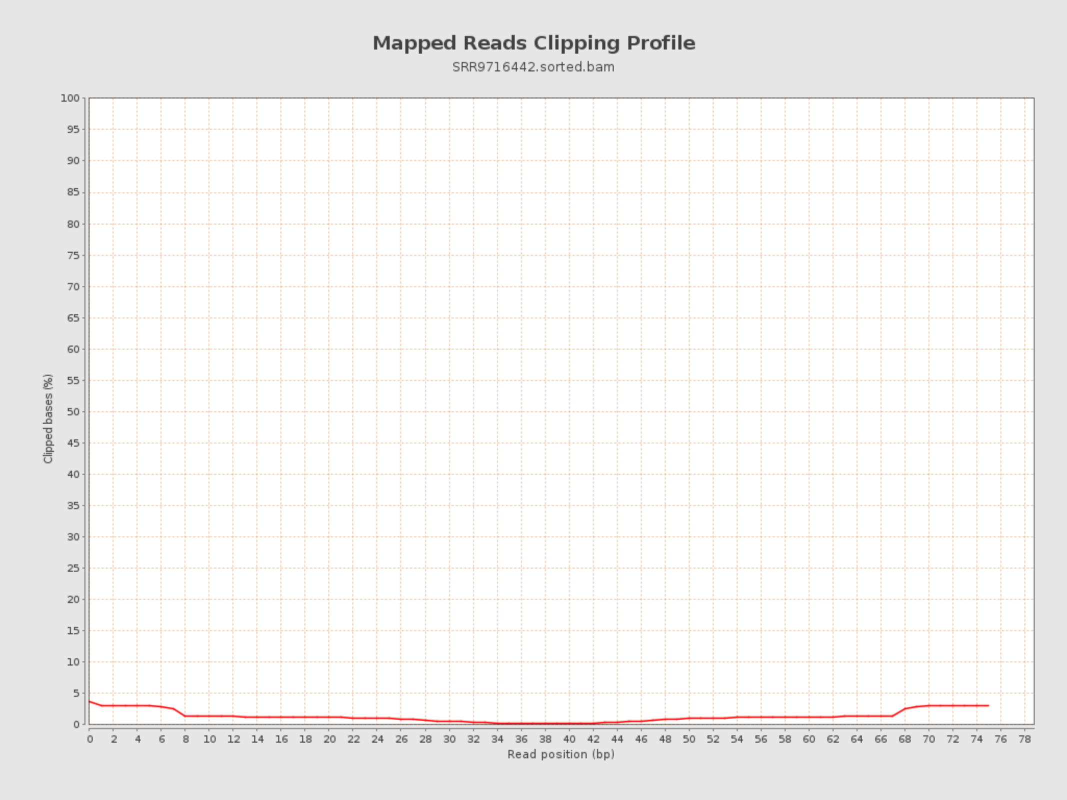
8. Results : Mapped Reads Nucleotide Content



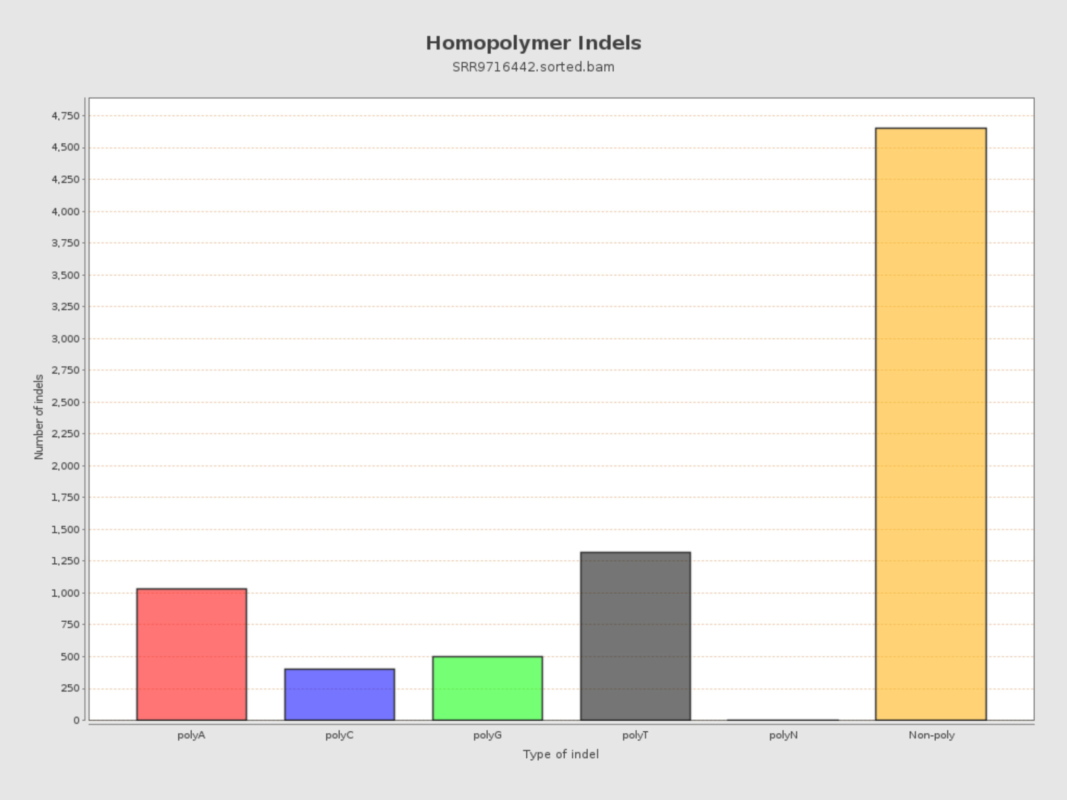
9. Results : Mapped Reads GC-content Distribution



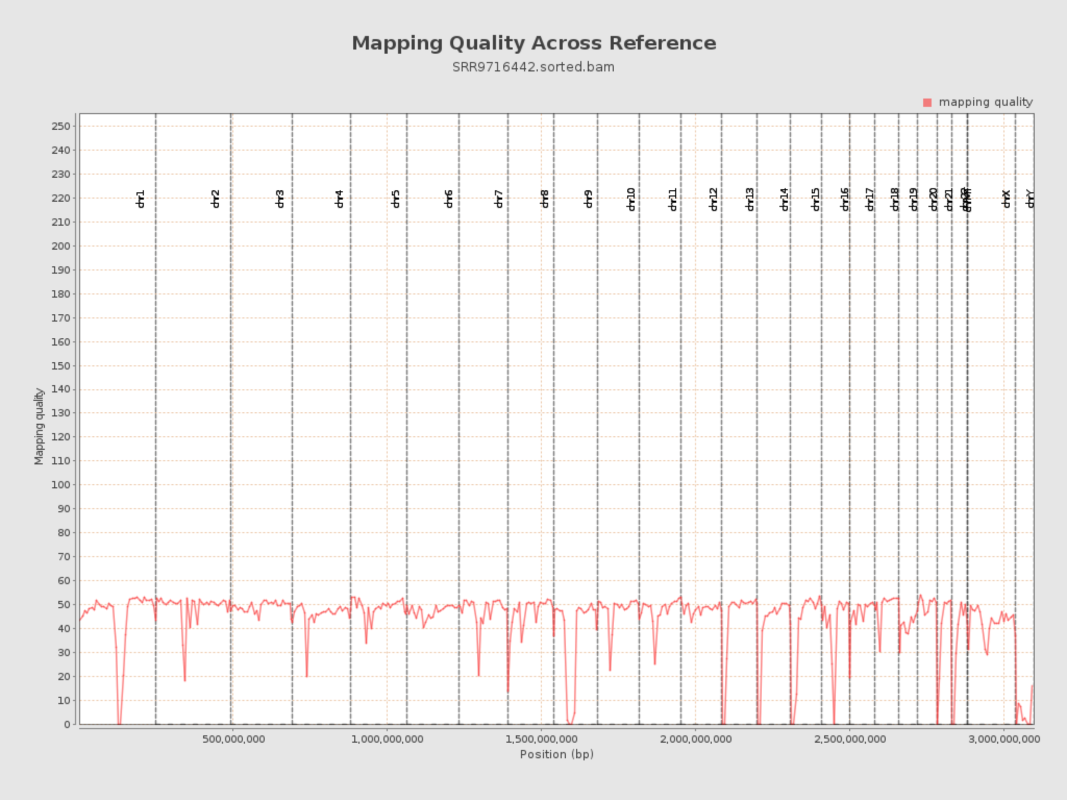
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram