Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:31:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716266.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_SRR9716266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716266.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:31:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,590,429
Mapped reads	883,274 / 55.54%
Unmapped reads	707,155 / 44.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	932 / 0.06%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	29,499 / 1.85%
Duplication rate	2.58%
Clipped reads	883,313 / 55.54%

2.2. ACGT Content

Number/percentage of A's	8,817,243 / 20.42%
Number/percentage of C's	6,136,962 / 14.21%
Number/percentage of T's	14,948,025 / 34.62%
Number/percentage of G's	13,273,893 / 30.74%
Number/percentage of N's	667 / 0%
GC Percentage	44.96%

2.3. Coverage

Mean	0.014

Standard Deviation	0.156

2.4. Mapping Quality

Mean Mapping Quality	39.77

2.5. Mismatches and indels

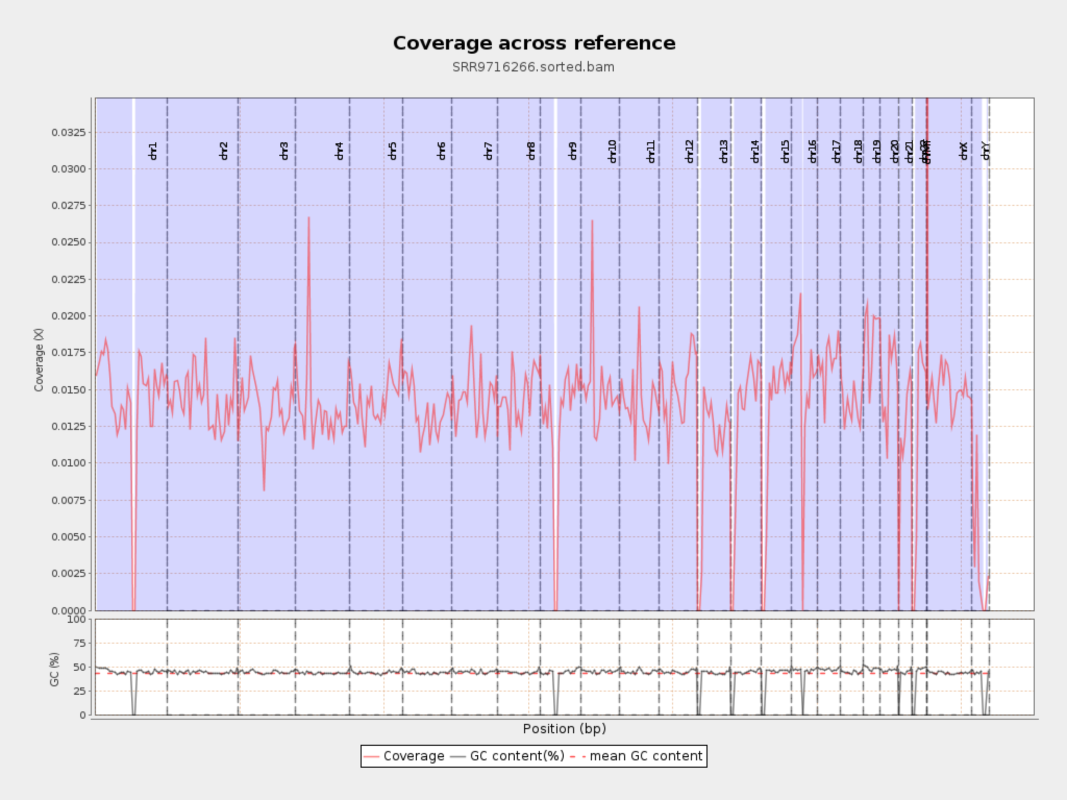
General error rate	0.82%
Mismatches	347,799
Insertions	2,552
Mapped reads with at least one insertion	0.29%
Deletions	6,032
Mapped reads with at least one deletion	0.68%
Homopolymer indels	39.96%

2.6. Chromosome stats

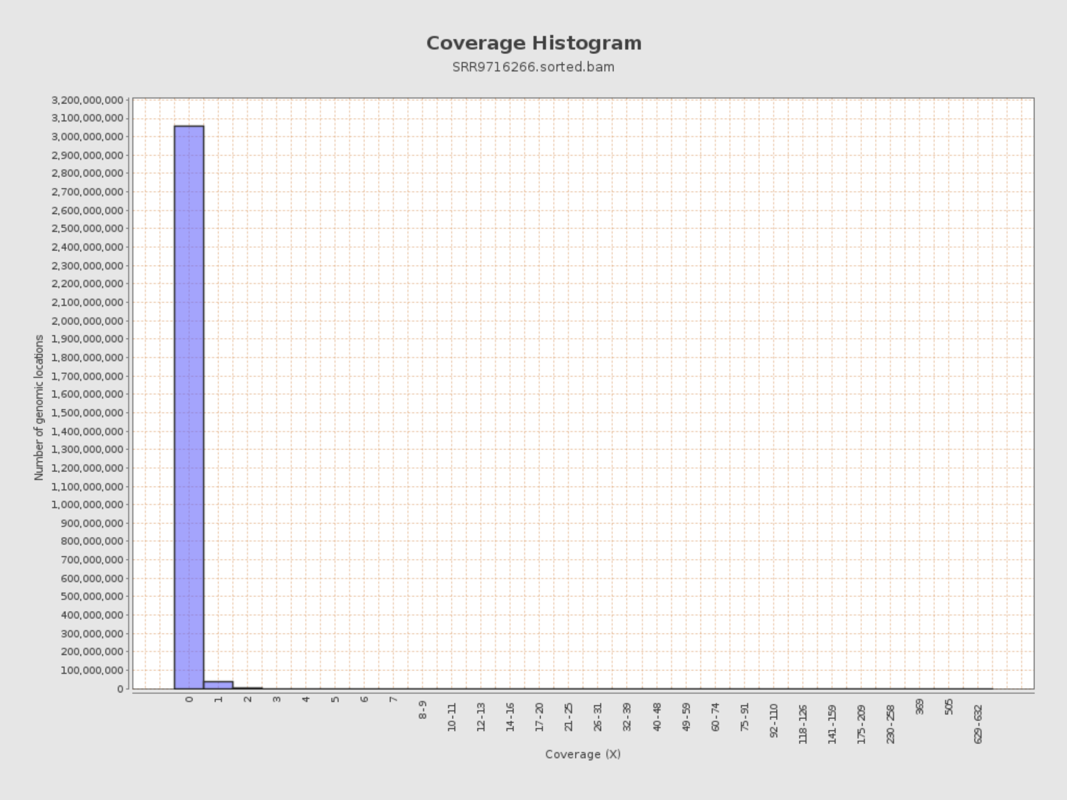
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3537517	0.0142	0.1431
chr2	243199373	3498599	0.0144	0.2904
chr3	198022430	2748771	0.0139	0.1265
chr4	191154276	2667545	0.014	0.141
chr5	180915260	2608232	0.0144	0.1279
chr6	171115067	2330207	0.0136	0.1721
chr7	159138663	2323639	0.0146	0.1441

chr8	146364022	2131874	0.0146	0.1336
chr9	141213431	1790048	0.0127	0.1318
chr10	135534747	2045573	0.0151	0.1617
chr11	135006516	1927669	0.0143	0.1388
chr12	133851895	2027008	0.0151	0.1324
chr13	115169878	1230005	0.0107	0.1143
chr14	107349540	1372790	0.0128	0.1226
chr15	102531392	1291678	0.0126	0.1224
chr16	90354753	1377806	0.0152	0.1453
chr17	81195210	1373974	0.0169	0.1405
chr18	78077248	1087148	0.0139	0.1485
chr19	59128983	1100648	0.0186	0.159
chr20	63025520	977061	0.0155	0.1356
chr21	48129895	577989	0.012	0.1277
chr22	51304566	598446	0.0117	0.1156
chrMT	16571	53058	3.2019	3.172
chrX	155270560	2312867	0.0149	0.1363
chrY	59373566	196307	0.0033	0.1017

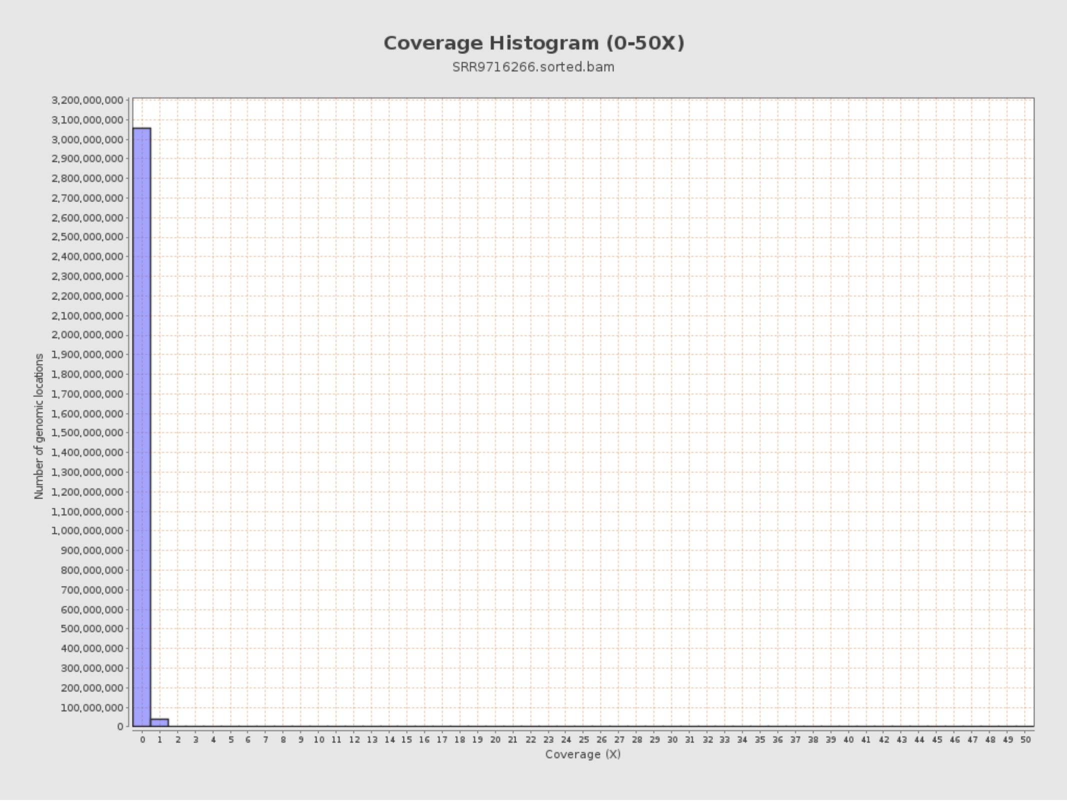
3. Results : Coverage across reference



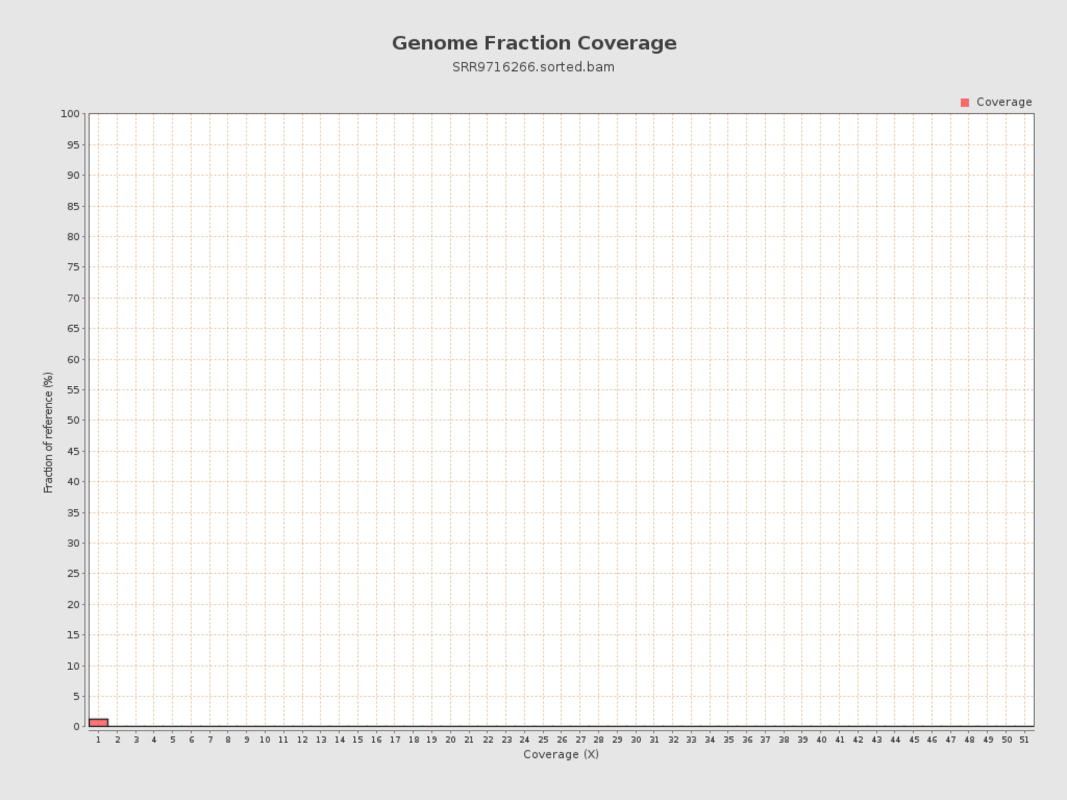
4. Results : Coverage Histogram



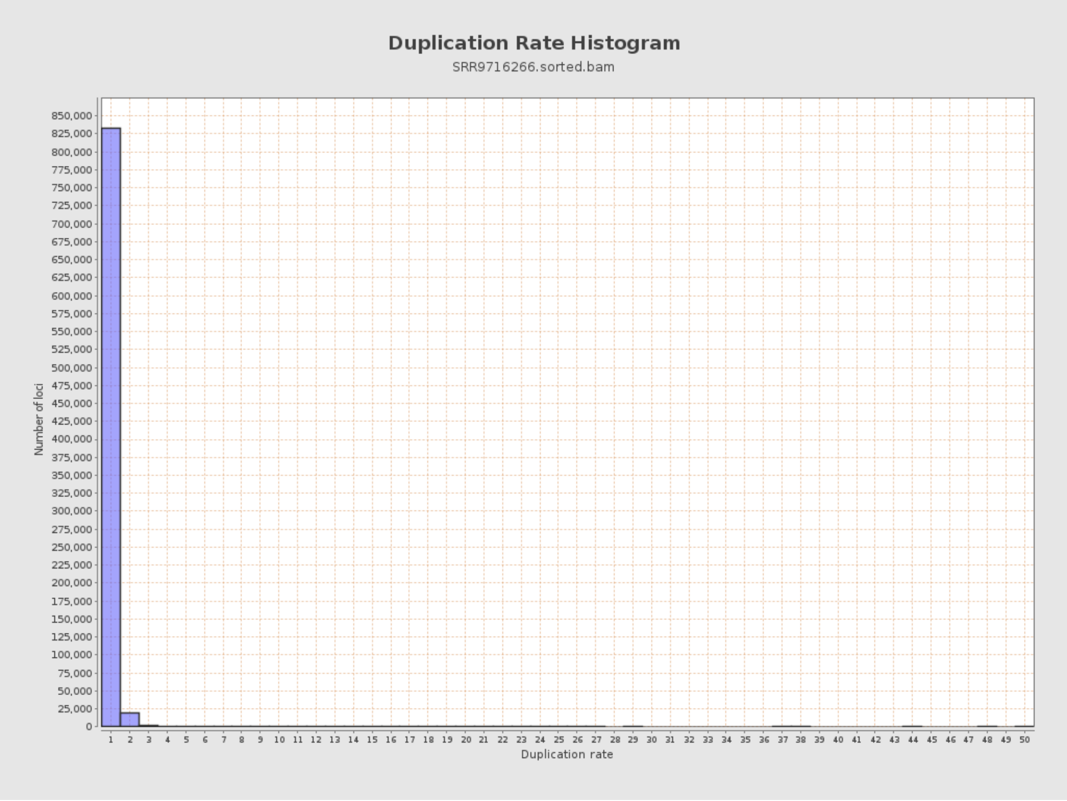
5. Results : Coverage Histogram (0-50X)



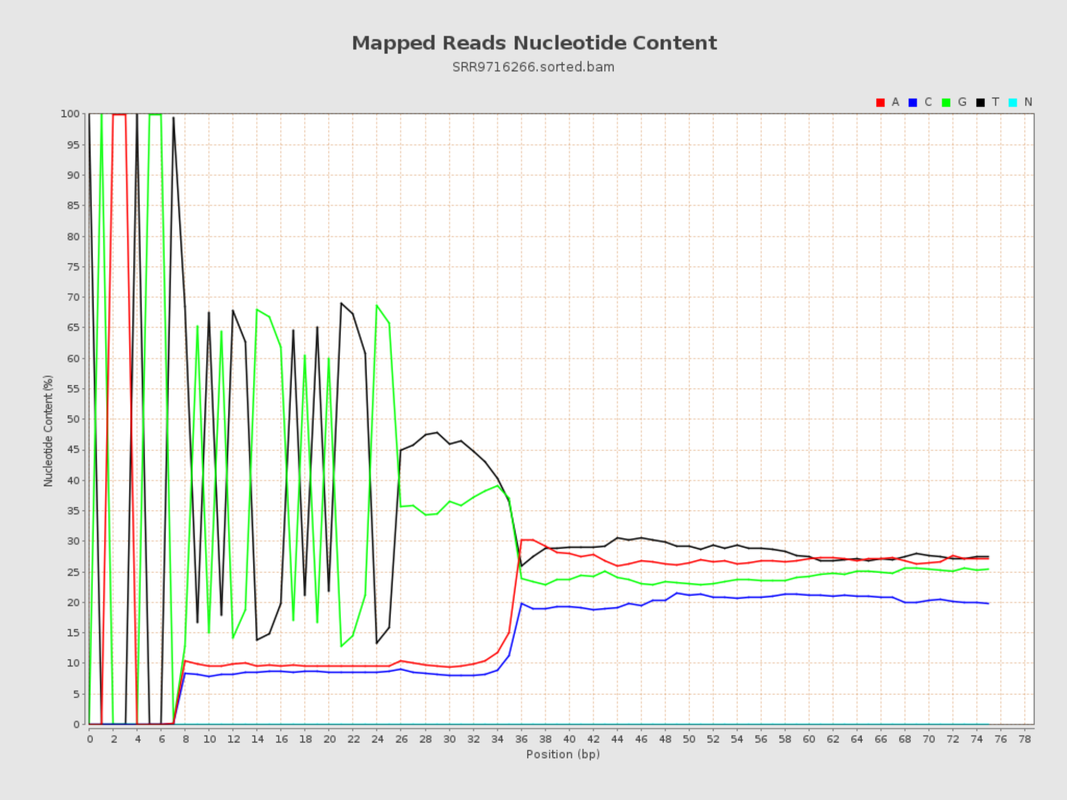
6. Results : Genome Fraction Coverage



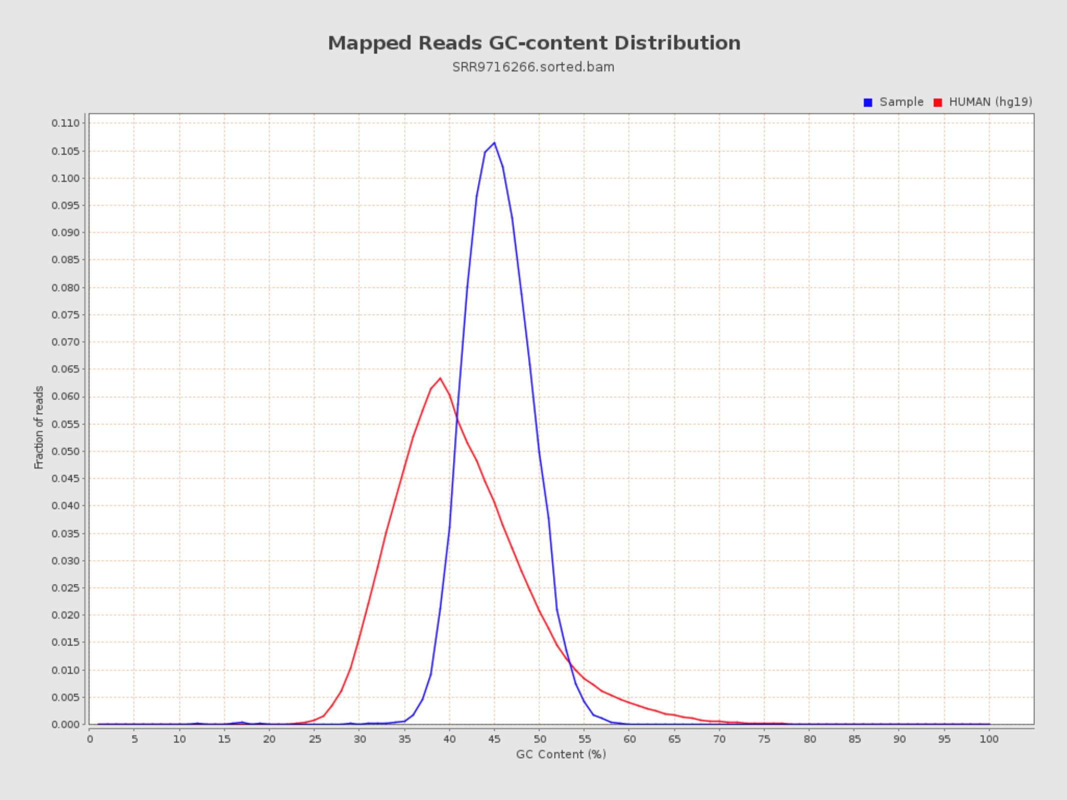
7. Results : Duplication Rate Histogram



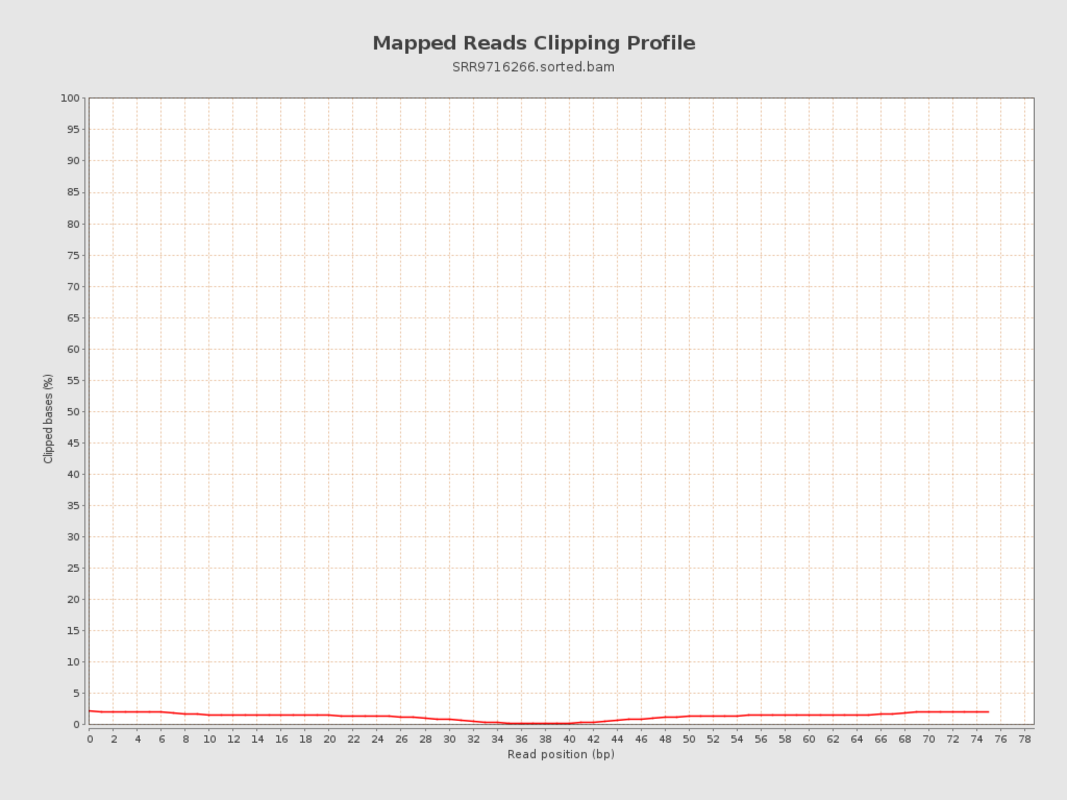
8. Results : Mapped Reads Nucleotide Content



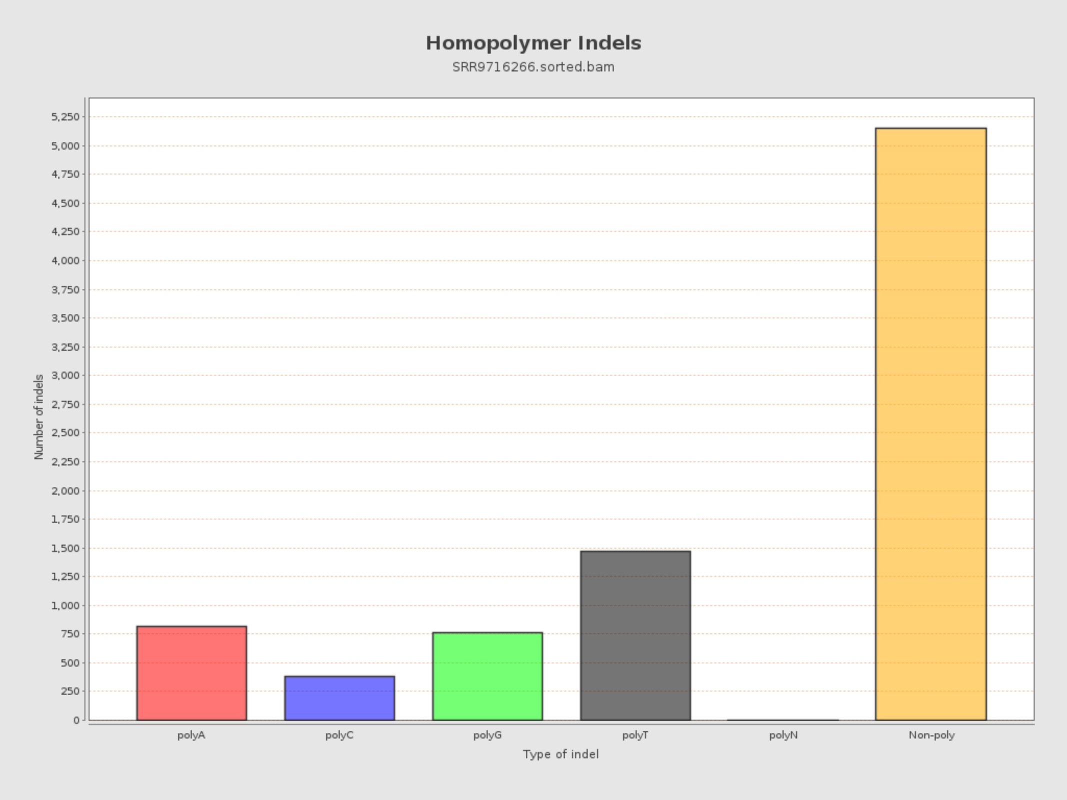
9. Results : Mapped Reads GC-content Distribution



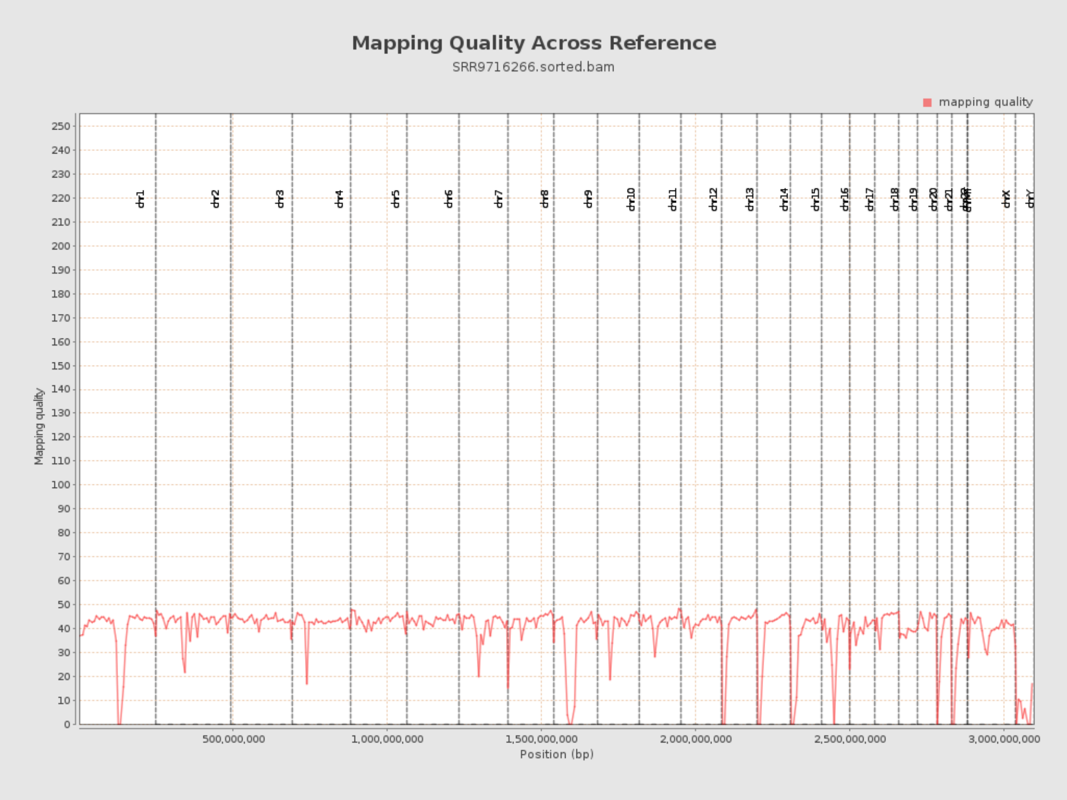
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram