Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:39:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716490.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_SRR9716490 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716490.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:39:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716490.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,269,823
Mapped reads	1,044,411 / 82.25%
Unmapped reads	225,412 / 17.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,157 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	23,381 / 1.84%
Duplication rate	1.54%
Clipped reads	1,045,719 / 82.35%

2.2. ACGT Content

Number/percentage of A's	14,094,179 / 23.94%
Number/percentage of C's	10,671,210 / 18.13%
Number/percentage of T's	19,254,885 / 32.71%
Number/percentage of G's	14,848,770 / 25.22%
Number/percentage of N's	785 / 0%
GC Percentage	43.35%

2.3. Coverage

Mean	0.019

Standard Deviation	0.1919

2.4. Mapping Quality

Mean Mapping Quality	42.35

2.5. Mismatches and indels

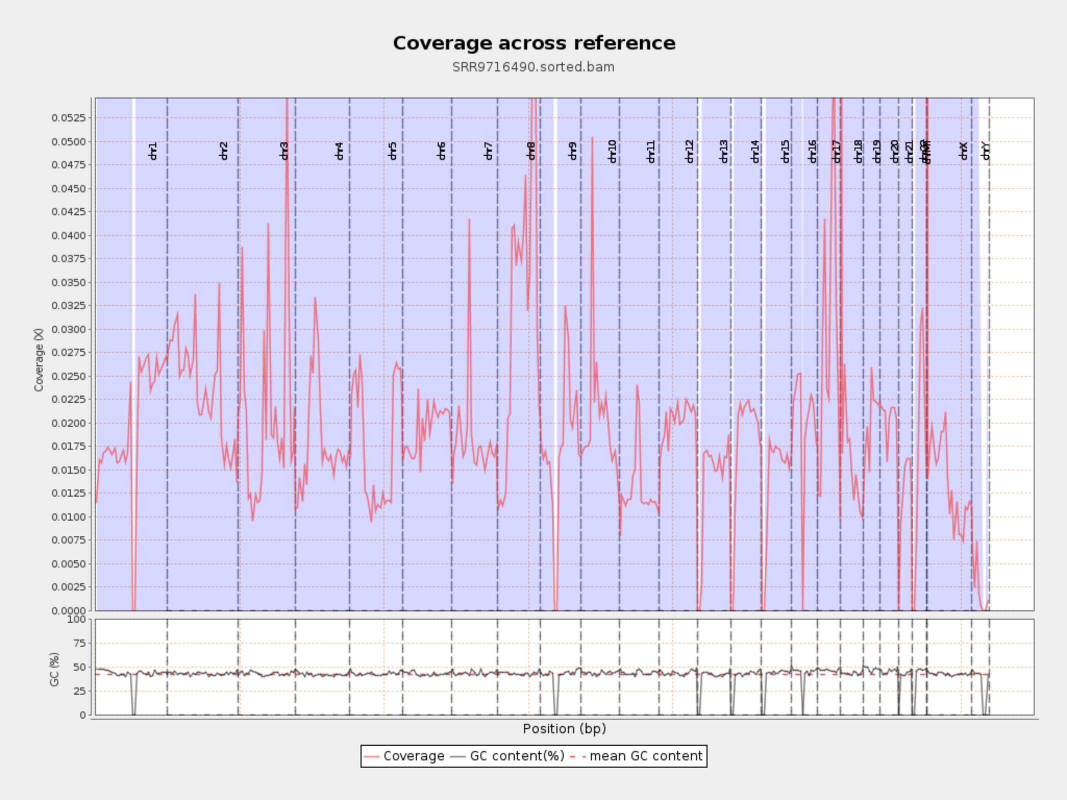
General error rate	0.54%
Mismatches	312,257
Insertions	4,282
Mapped reads with at least one insertion	0.41%
Deletions	11,709
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.42%

2.6. Chromosome stats

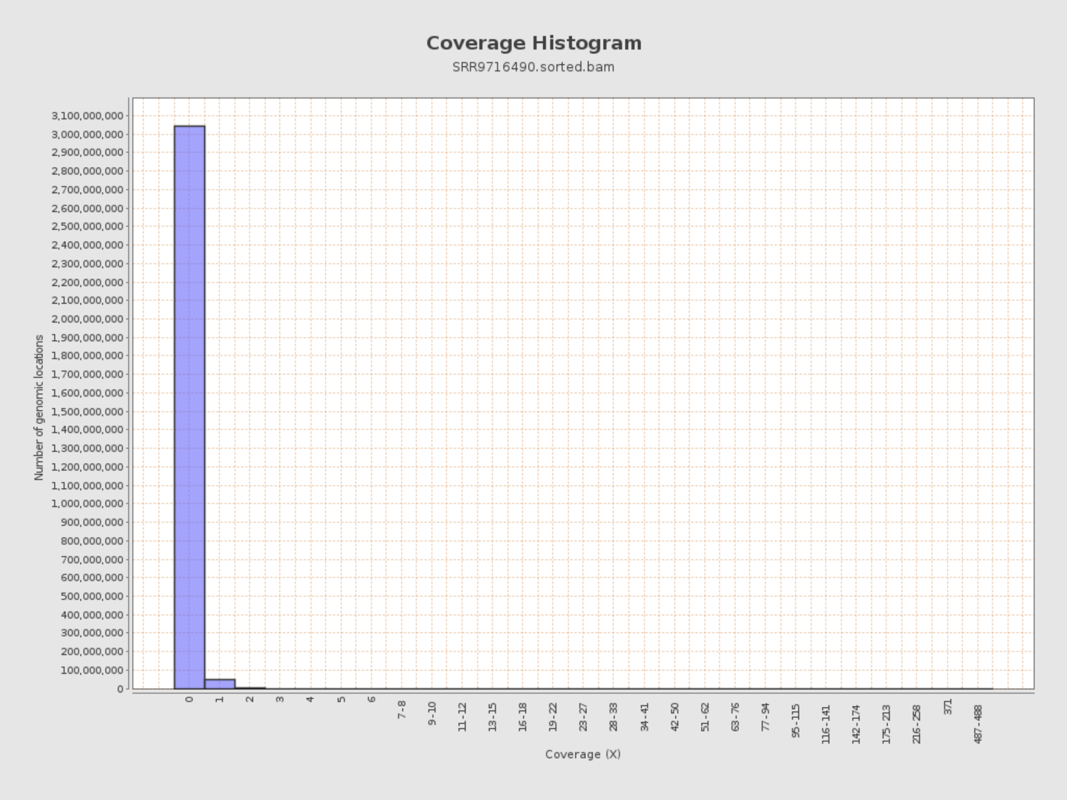
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4844457	0.0194	0.2392
chr2	243199373	5769359	0.0237	0.2655
chr3	198022430	4185211	0.0211	0.1598
chr4	191154276	3423052	0.0179	0.1479
chr5	180915260	3166909	0.0175	0.1394
chr6	171115067	3316460	0.0194	0.16
chr7	159138663	2933068	0.0184	0.322

chr8	146364022	4898080	0.0335	0.2183
chr9	141213431	2420907	0.0171	0.1547
chr10	135534747	2817575	0.0208	0.253
chr11	135006516	1781802	0.0132	0.1402
chr12	133851895	2705689	0.0202	0.1577
chr13	115169878	1553977	0.0135	0.123
chr14	107349540	1893263	0.0176	0.1429
chr15	102531392	1391704	0.0136	0.1257
chr16	90354753	1783740	0.0197	0.1564
chr17	81195210	2413685	0.0297	0.1888
chr18	78077248	1410652	0.0181	0.2179
chr19	59128983	1194709	0.0202	0.2283
chr20	63025520	1271410	0.0202	0.1544
chr21	48129895	605544	0.0126	0.1211
chr22	51304566	844534	0.0165	0.1363
chrMT	16571	8411	0.5076	0.7707
chrX	155270560	2117156	0.0136	0.1394
chrY	59373566	136856	0.0023	0.0689

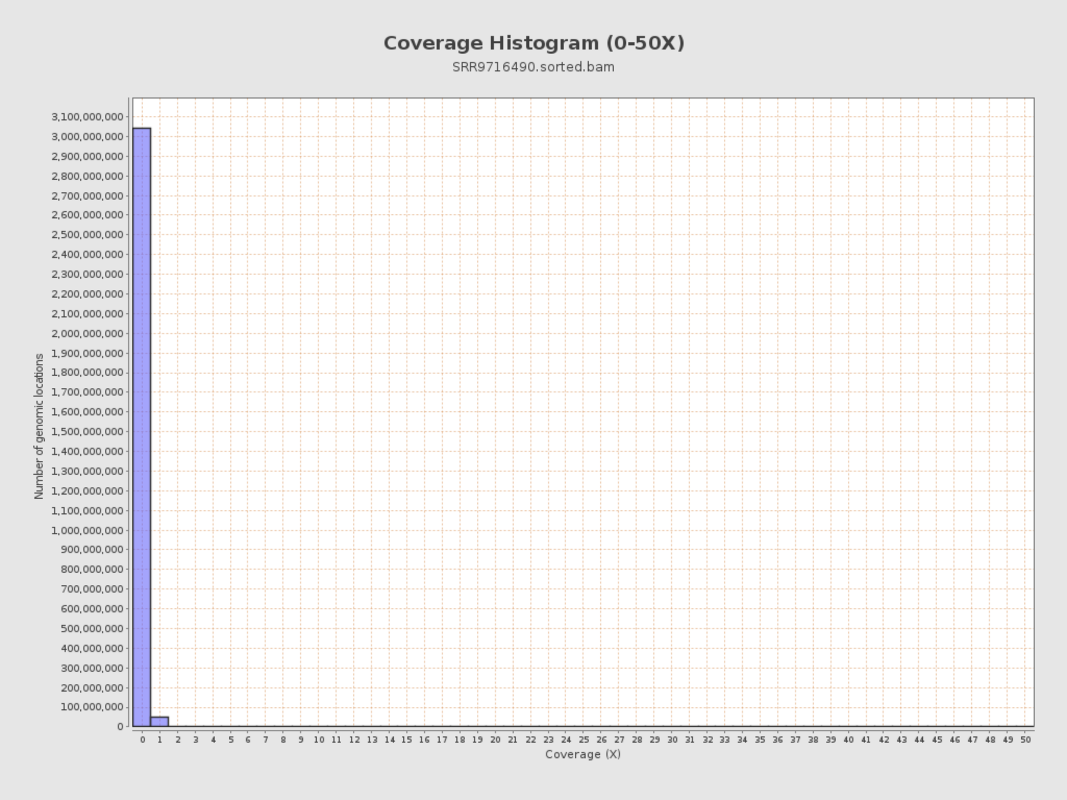
3. Results : Coverage across reference



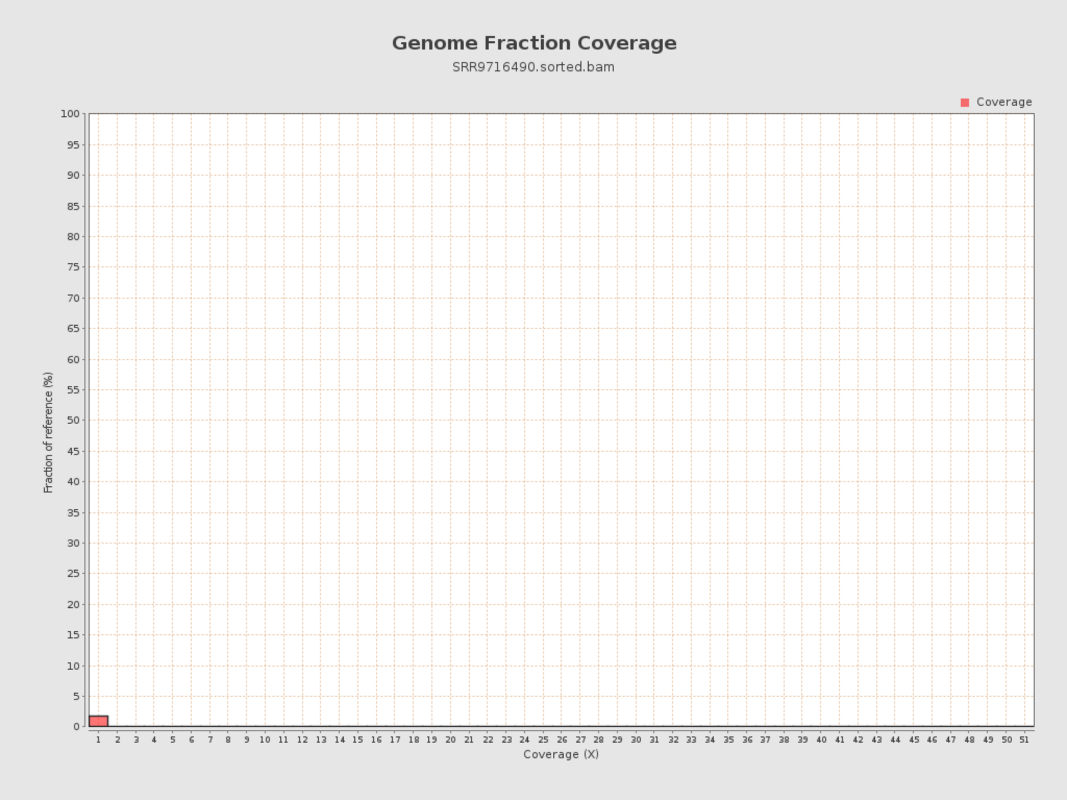
4. Results : Coverage Histogram



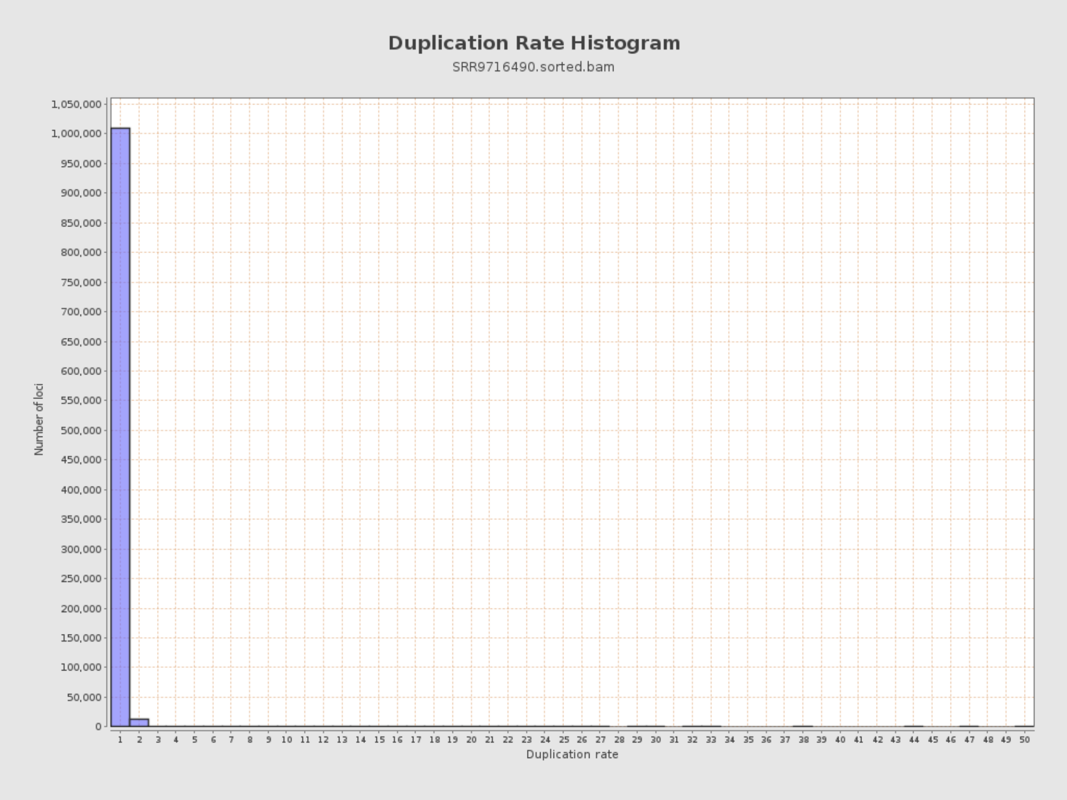
5. Results : Coverage Histogram (0-50X)



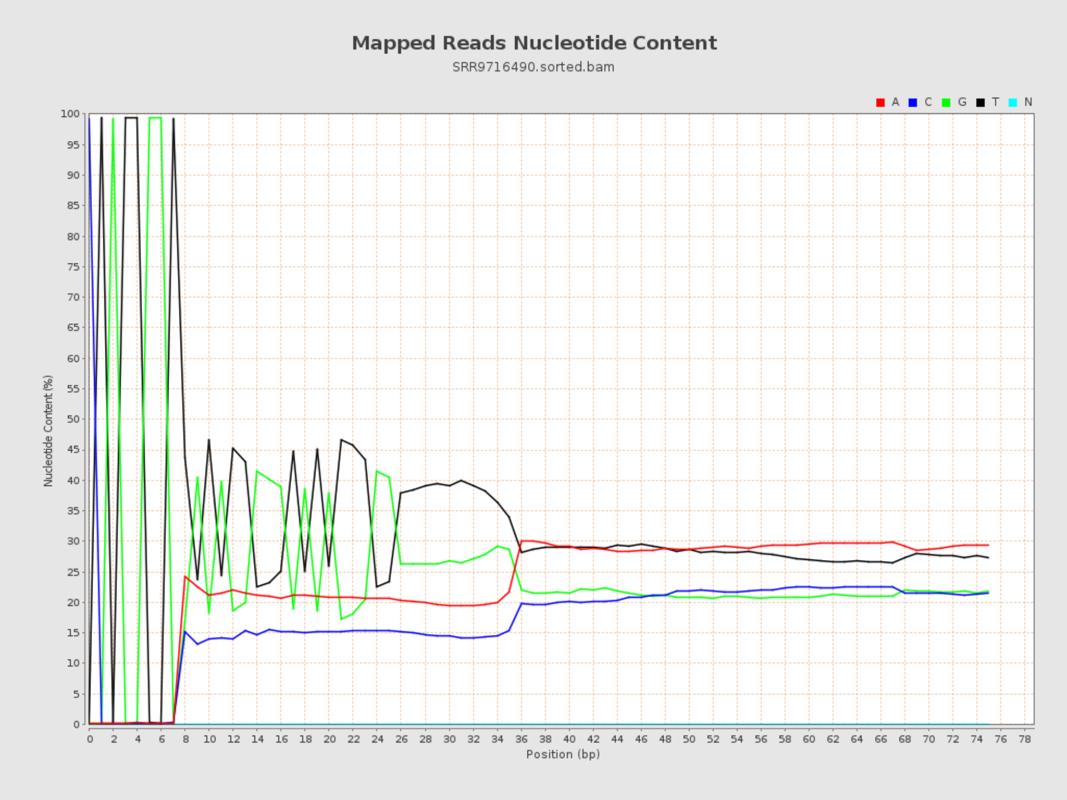
6. Results : Genome Fraction Coverage



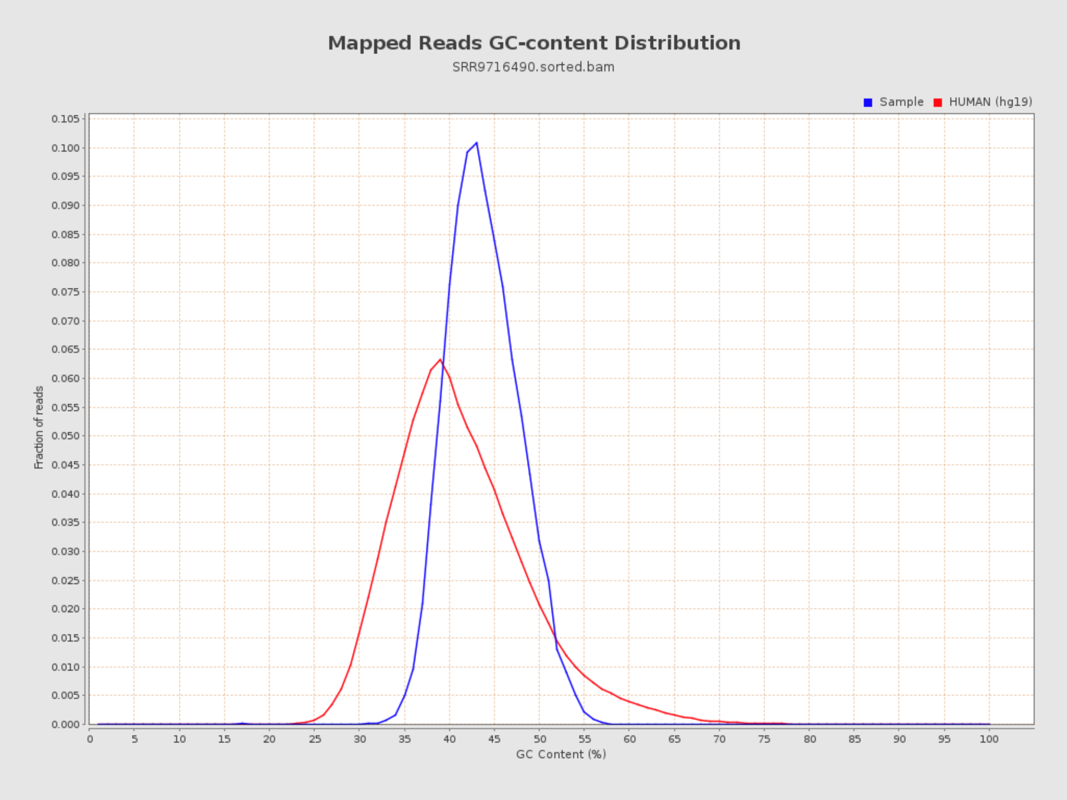
7. Results : Duplication Rate Histogram



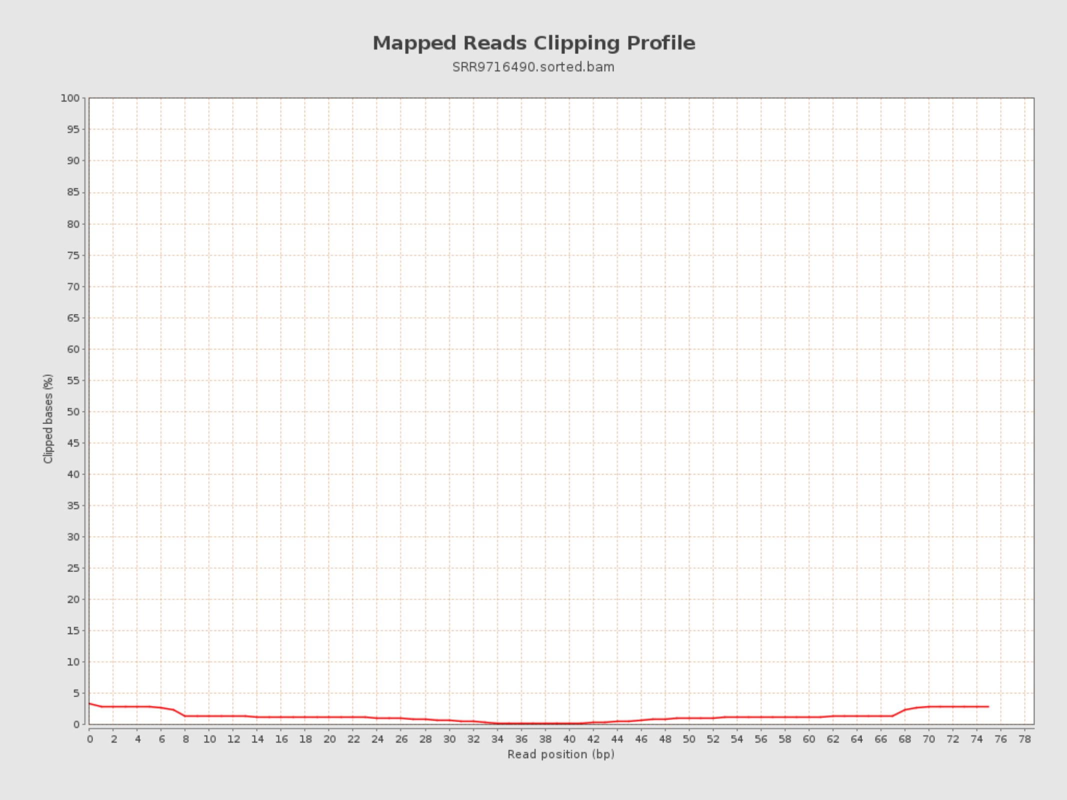
8. Results : Mapped Reads Nucleotide Content



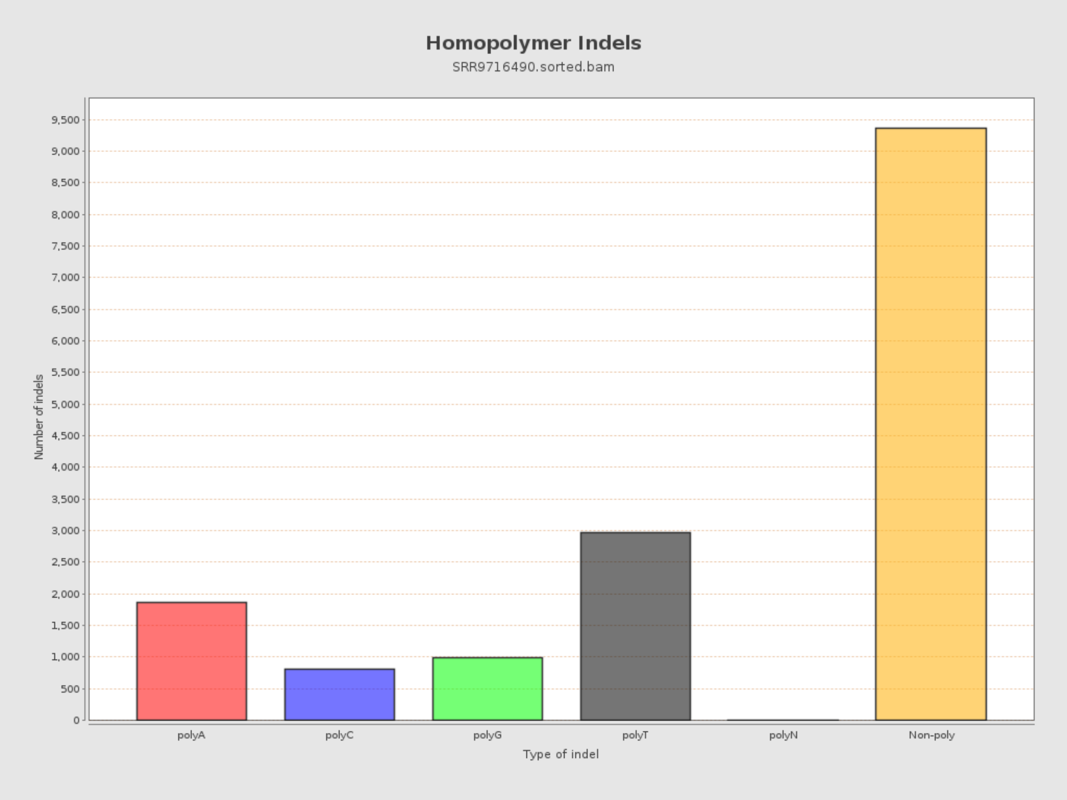
9. Results : Mapped Reads GC-content Distribution



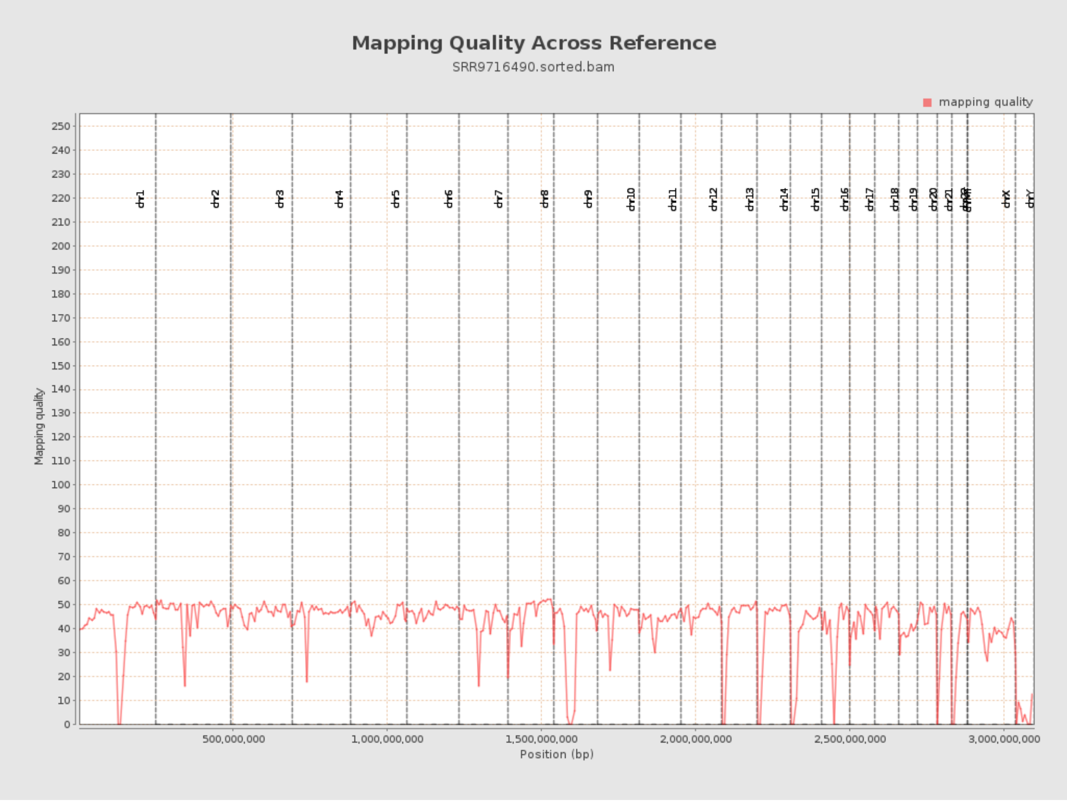
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram