Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:59:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716495.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_SRR9716495 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716495.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:59:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716495.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,446,786
Mapped reads	2,178,516 / 89.04%
Unmapped reads	268,270 / 10.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,666 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	110,452 / 4.51%
Duplication rate	3.8%
Clipped reads	2,182,992 / 89.22%

2.2. ACGT Content

Number/percentage of A's	32,388,796 / 25.7%
Number/percentage of C's	24,578,451 / 19.5%
Number/percentage of T's	39,511,511 / 31.35%
Number/percentage of G's	29,542,651 / 23.44%
Number/percentage of N's	3,647 / 0%
GC Percentage	42.94%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.4059

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

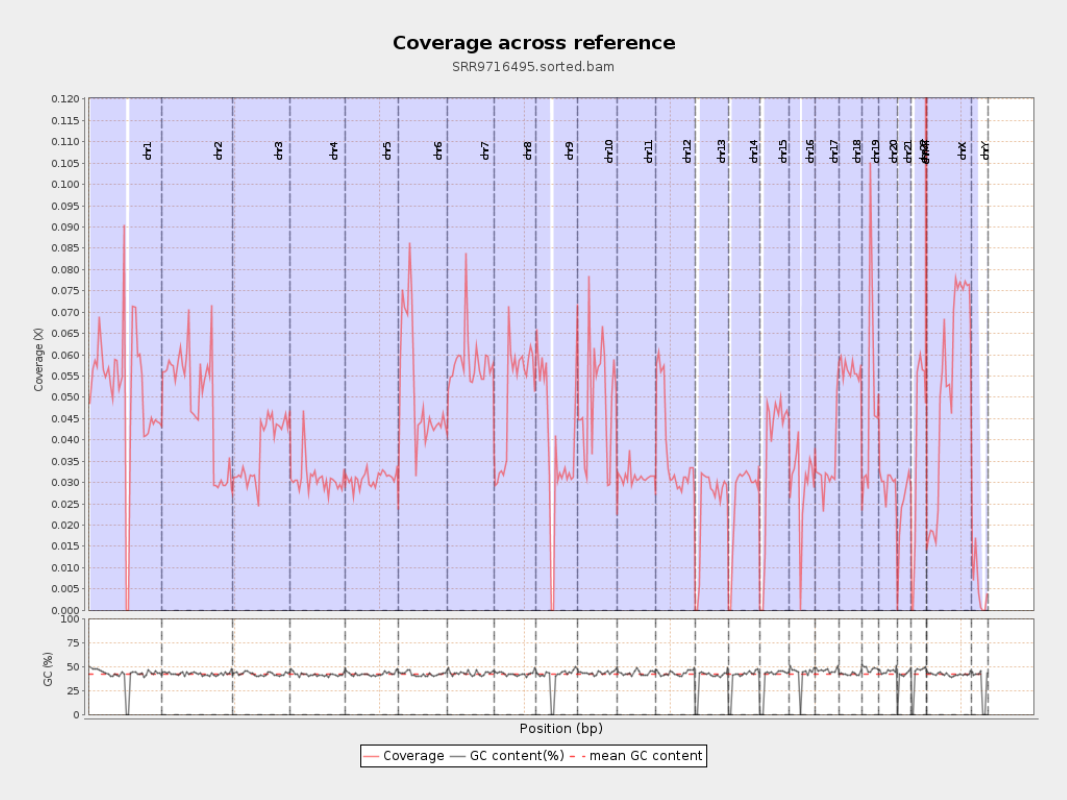
General error rate	0.51%
Mismatches	630,339
Insertions	8,294
Mapped reads with at least one insertion	0.38%
Deletions	23,869
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.9%

2.6. Chromosome stats

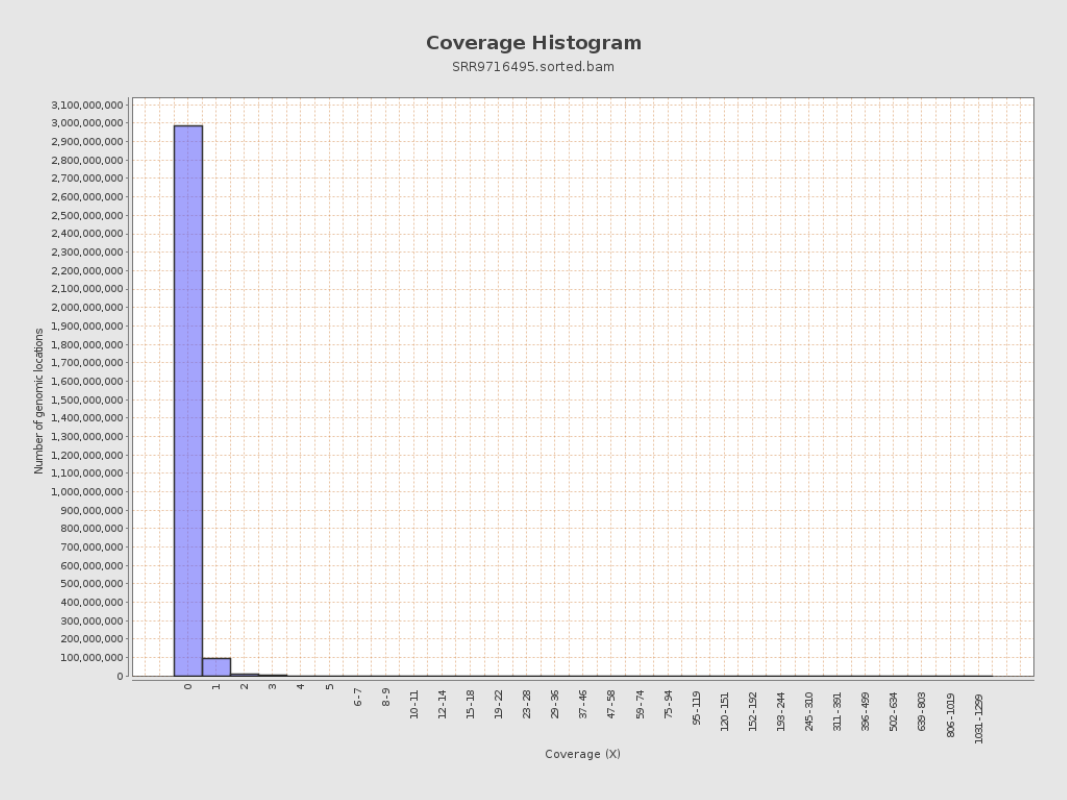
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12795901	0.0513	0.9299
chr2	243199373	11905494	0.049	0.4851
chr3	198022430	7430835	0.0375	0.2217
chr4	191154276	5914086	0.0309	0.2195
chr5	180915260	5590927	0.0309	0.2051
chr6	171115067	8686554	0.0508	0.2945
chr7	159138663	9300346	0.0584	0.5574

chr8	146364022	7359829	0.0503	0.3179
chr9	141213431	5248210	0.0372	0.3097
chr10	135534747	6714622	0.0495	0.348
chr11	135006516	4210537	0.0312	0.2813
chr12	133851895	5019575	0.0375	0.2287
chr13	115169878	2835707	0.0246	0.1788
chr14	107349540	2777319	0.0259	0.2009
chr15	102531392	3799158	0.0371	0.2207
chr16	90354753	2674730	0.0296	0.2163
chr17	81195210	2757215	0.034	0.2196
chr18	78077248	4420217	0.0566	0.5456
chr19	59128983	2974442	0.0503	0.5144
chr20	63025520	1878313	0.0298	0.1979
chr21	48129895	1147987	0.0239	0.1927
chr22	51304566	1989787	0.0388	0.2236
chrMT	16571	124952	7.5404	4.763
chrX	155270560	8193168	0.0528	0.3058
chrY	59373566	313000	0.0053	0.132

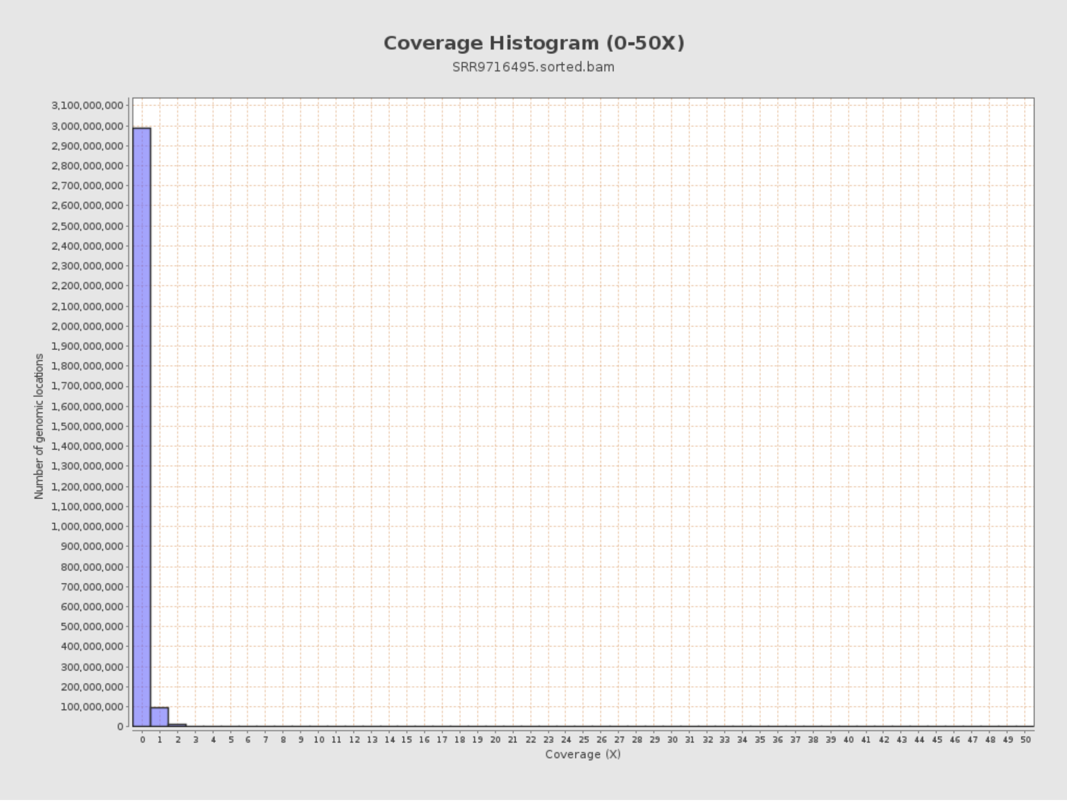
3. Results : Coverage across reference



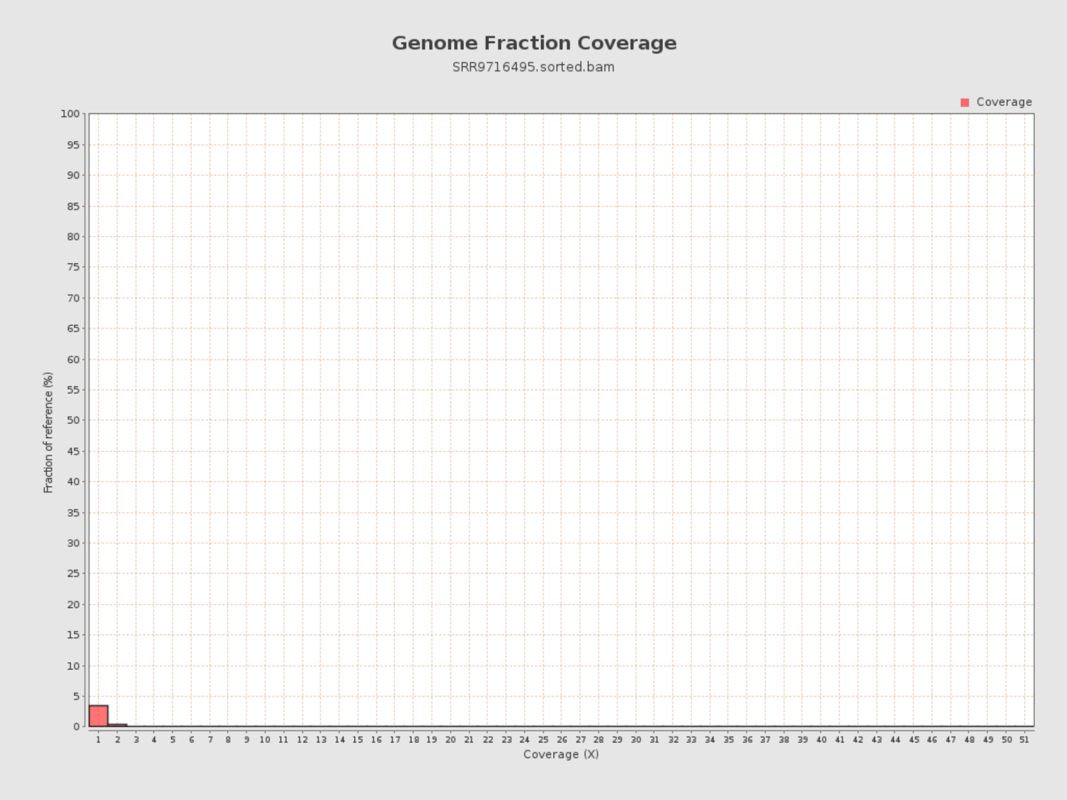
4. Results : Coverage Histogram



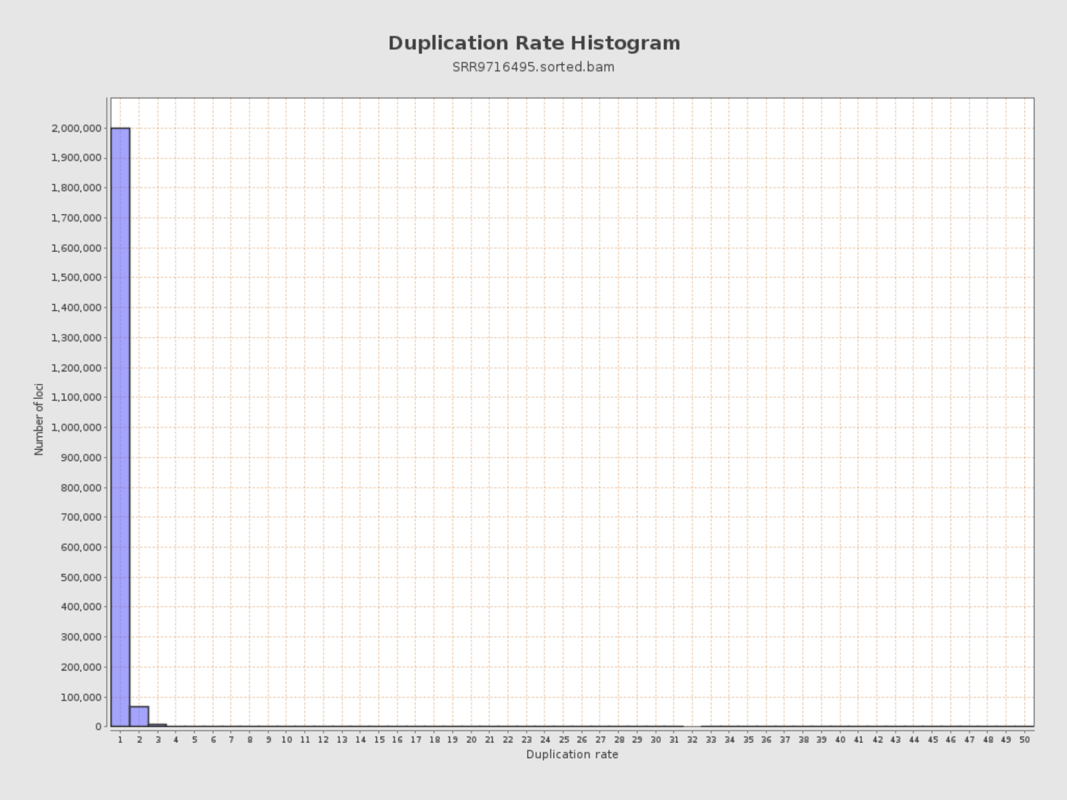
5. Results : Coverage Histogram (0-50X)



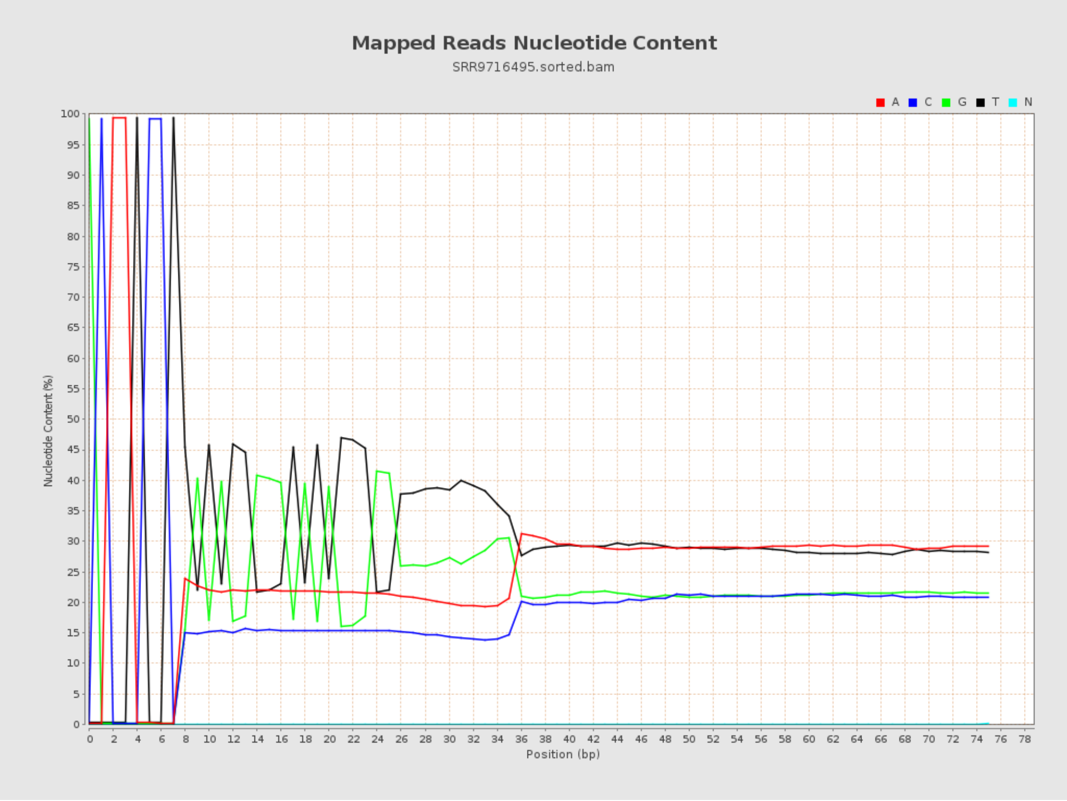
6. Results : Genome Fraction Coverage



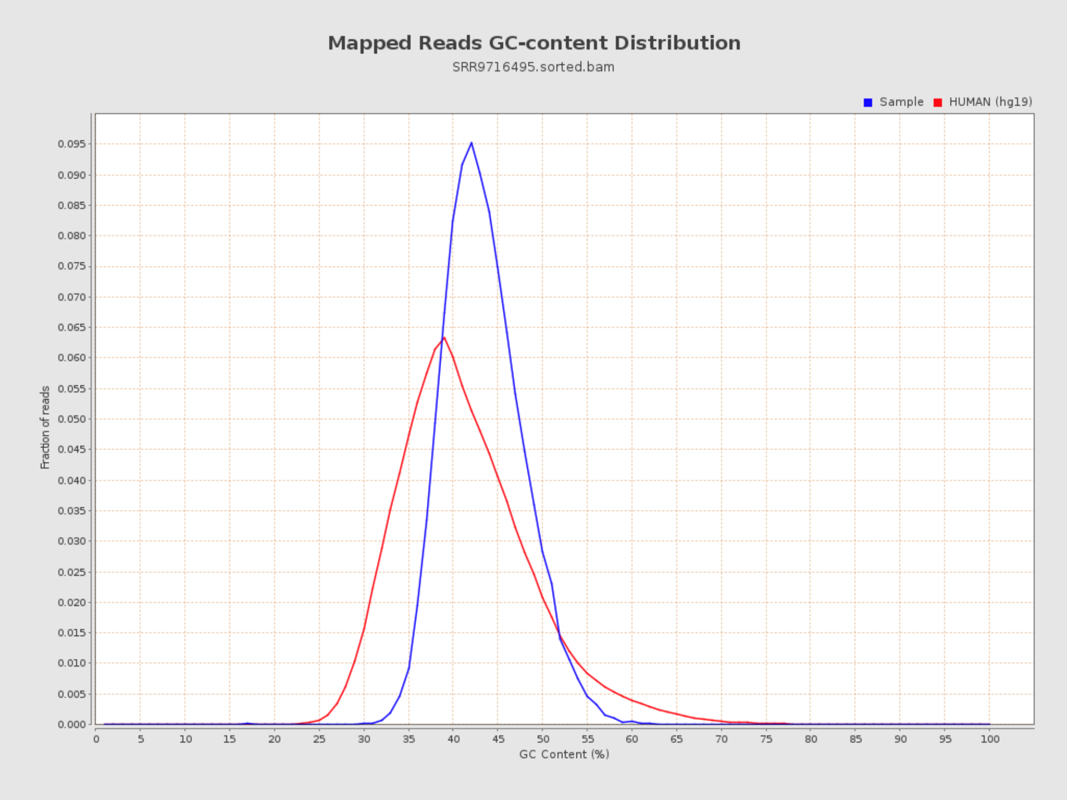
7. Results : Duplication Rate Histogram



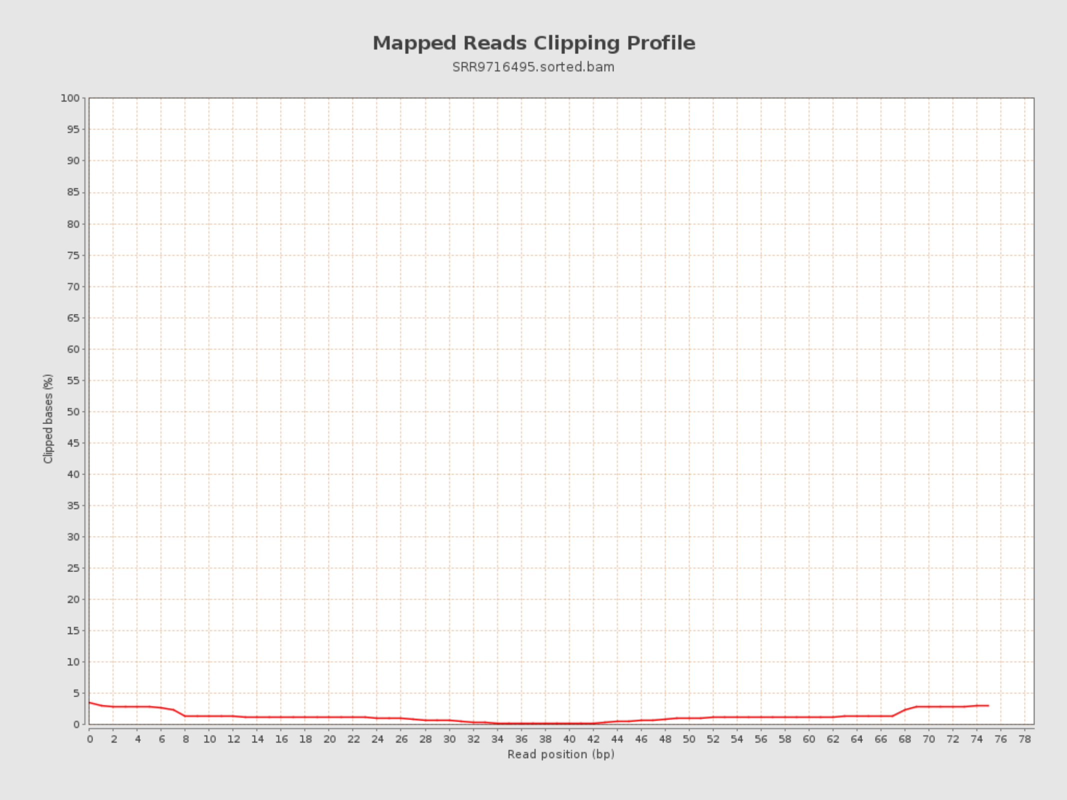
8. Results : Mapped Reads Nucleotide Content



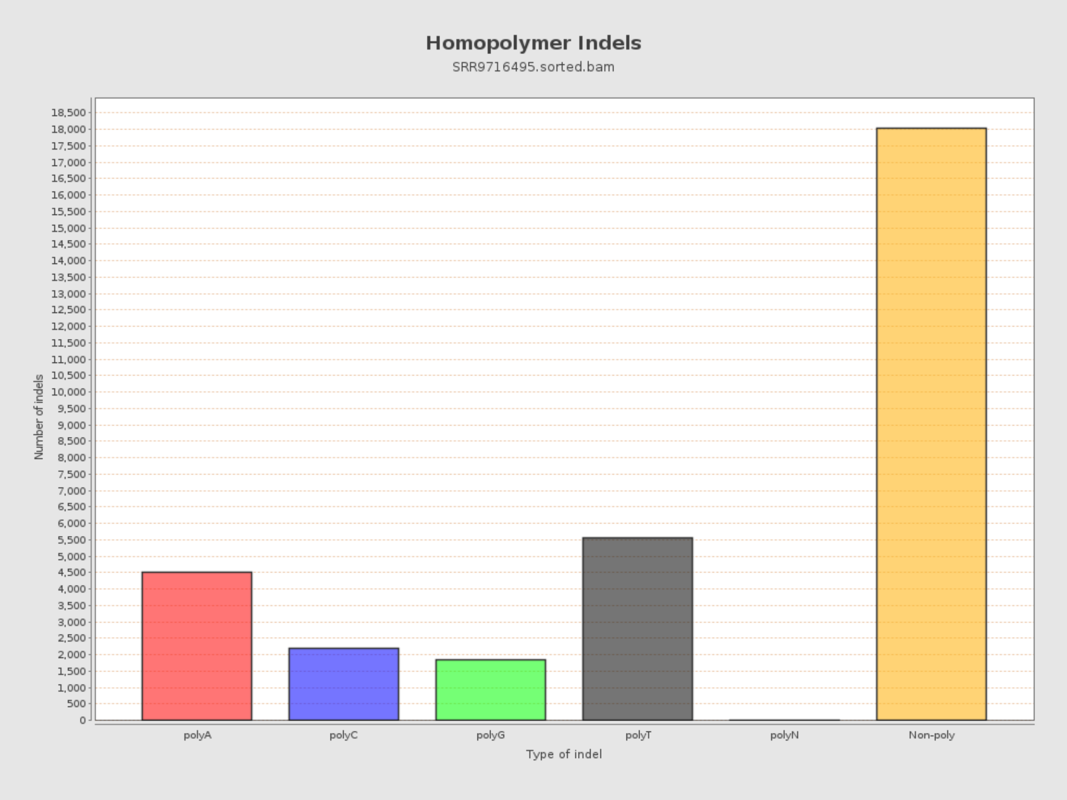
9. Results : Mapped Reads GC-content Distribution



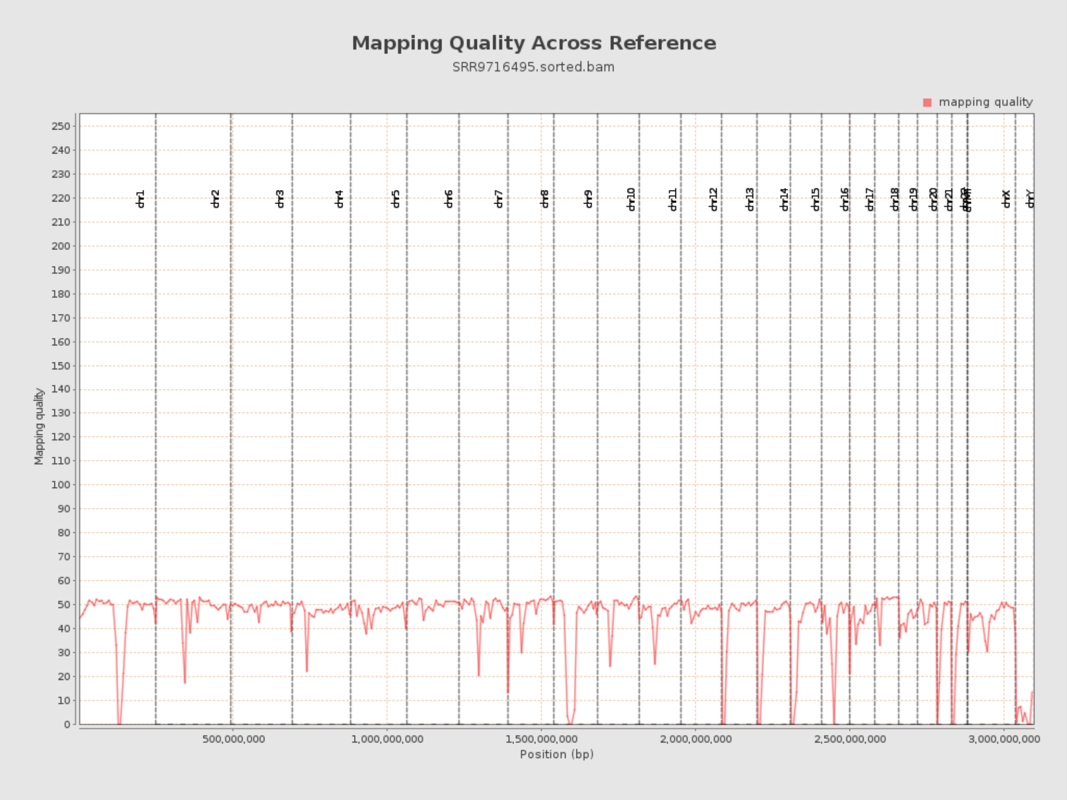
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram