Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:47:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716385.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_SRR9716385 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716385.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:47:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716385.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,038,290
Mapped reads	940,379 / 90.57%
Unmapped reads	97,911 / 9.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,845 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	23,983 / 2.31%
Duplication rate	1.69%
Clipped reads	940,559 / 90.59%

2.2. ACGT Content

Number/percentage of A's	13,105,032 / 24.55%
Number/percentage of C's	9,834,515 / 18.42%
Number/percentage of T's	17,346,128 / 32.49%
Number/percentage of G's	13,094,668 / 24.53%
Number/percentage of N's	967 / 0%
GC Percentage	42.95%

2.3. Coverage

Mean	0.0172

Standard Deviation	0.1858

2.4. Mapping Quality

Mean Mapping Quality	42.11

2.5. Mismatches and indels

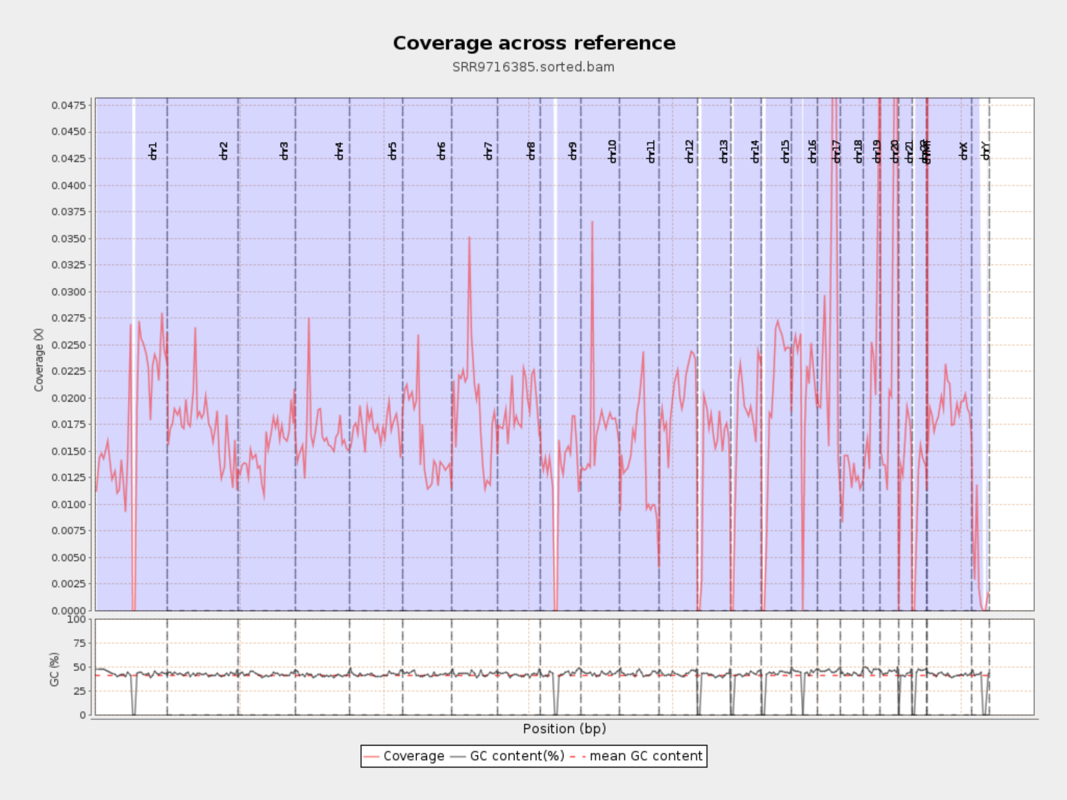
General error rate	0.54%
Mismatches	280,285
Insertions	3,766
Mapped reads with at least one insertion	0.4%
Deletions	10,061
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.21%

2.6. Chromosome stats

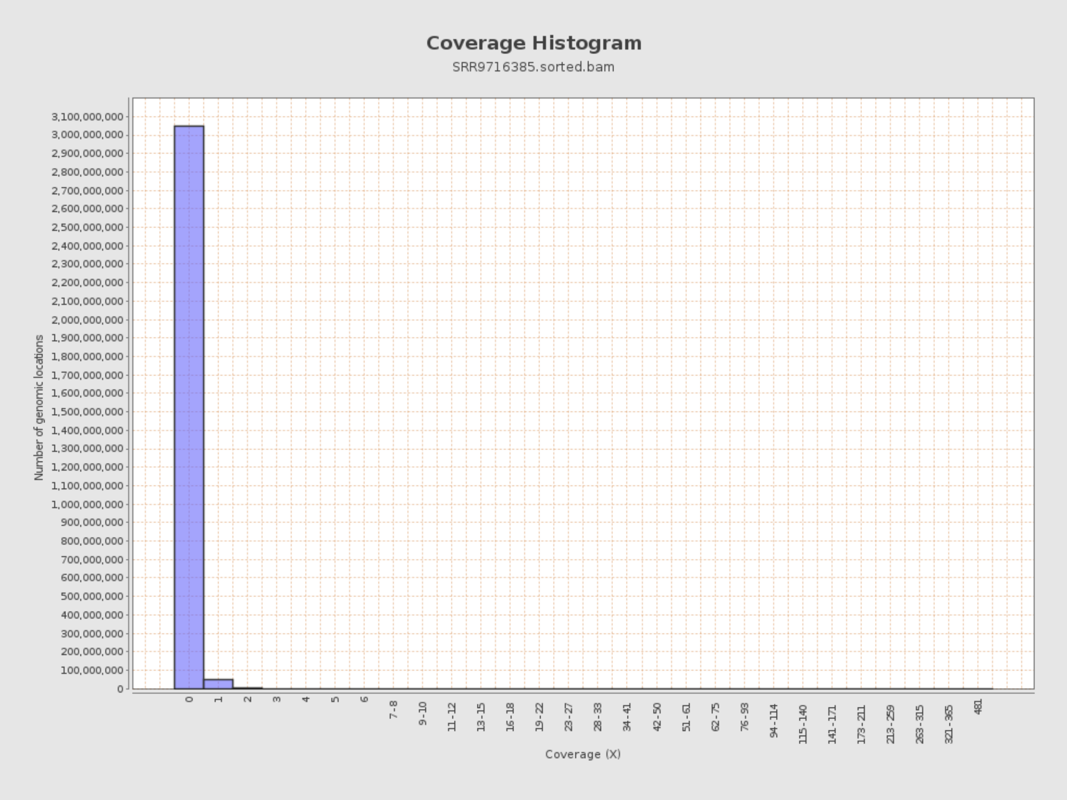
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4332487	0.0174	0.2699
chr2	243199373	4196958	0.0173	0.2478
chr3	198022430	3033366	0.0153	0.1343
chr4	191154276	3155356	0.0165	0.1467
chr5	180915260	3124290	0.0173	0.1391
chr6	171115067	2724094	0.0159	0.1596
chr7	159138663	3098868	0.0195	0.2682

chr8	146364022	2786460	0.019	0.191
chr9	141213431	1824603	0.0129	0.1451
chr10	135534747	2348630	0.0173	0.2046
chr11	135006516	1918529	0.0142	0.1549
chr12	133851895	2693194	0.0201	0.1502
chr13	115169878	1651642	0.0143	0.1266
chr14	107349540	1820048	0.017	0.1397
chr15	102531392	1962443	0.0191	0.1484
chr16	90354753	1879990	0.0208	0.159
chr17	81195210	2404358	0.0296	0.1877
chr18	78077248	964547	0.0124	0.2164
chr19	59128983	1416856	0.024	0.2372
chr20	63025520	1708185	0.0271	0.1779
chr21	48129895	688505	0.0143	0.1368
chr22	51304566	511845	0.01	0.1064
chrMT	16571	11201	0.6759	0.9234
chrX	155270560	2953598	0.019	0.1569
chrY	59373566	187330	0.0032	0.1183

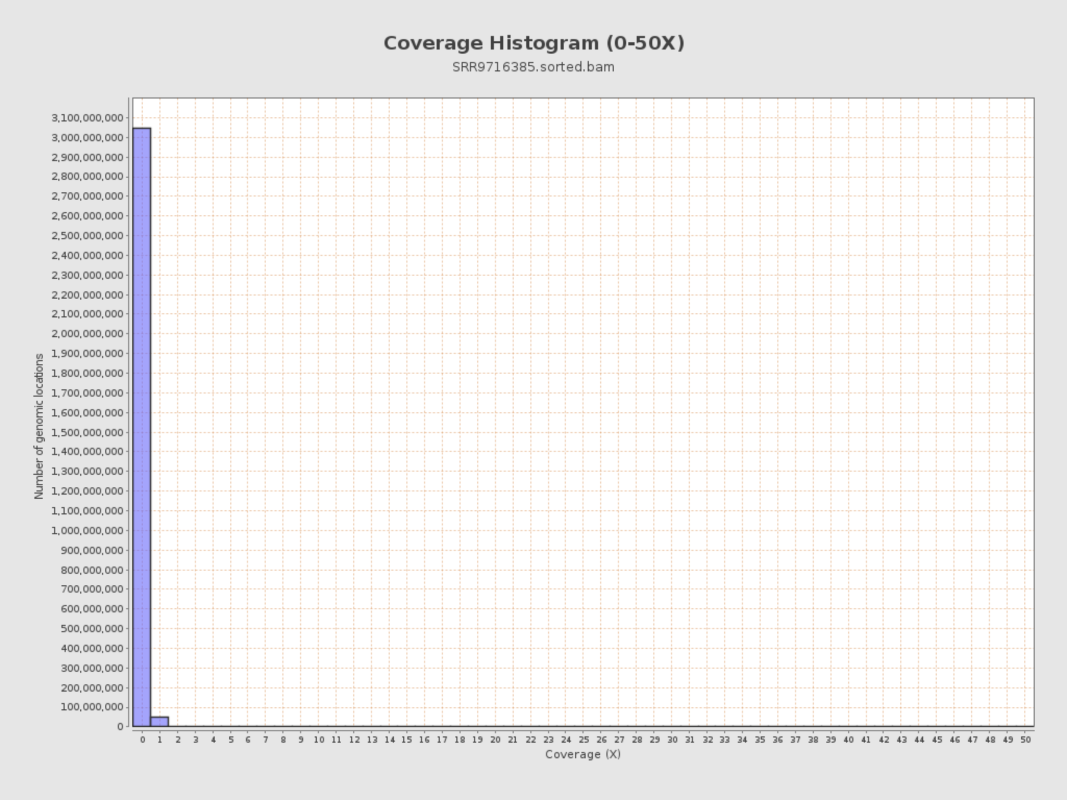
3. Results : Coverage across reference



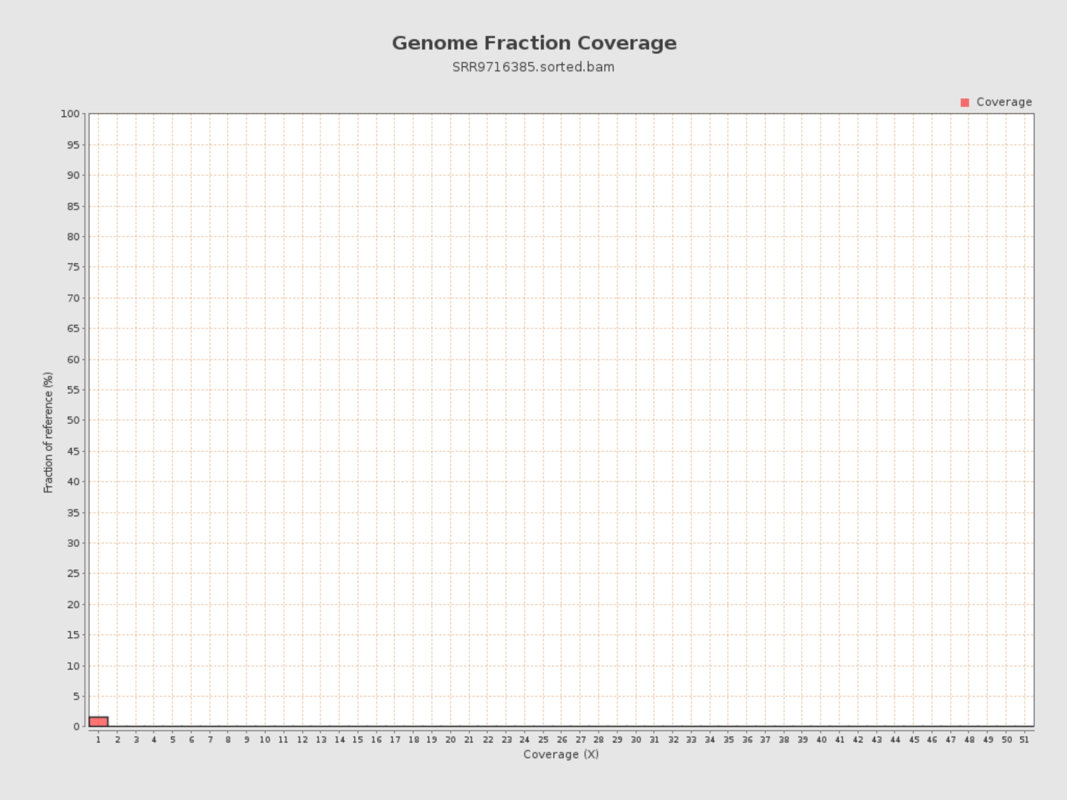
4. Results : Coverage Histogram



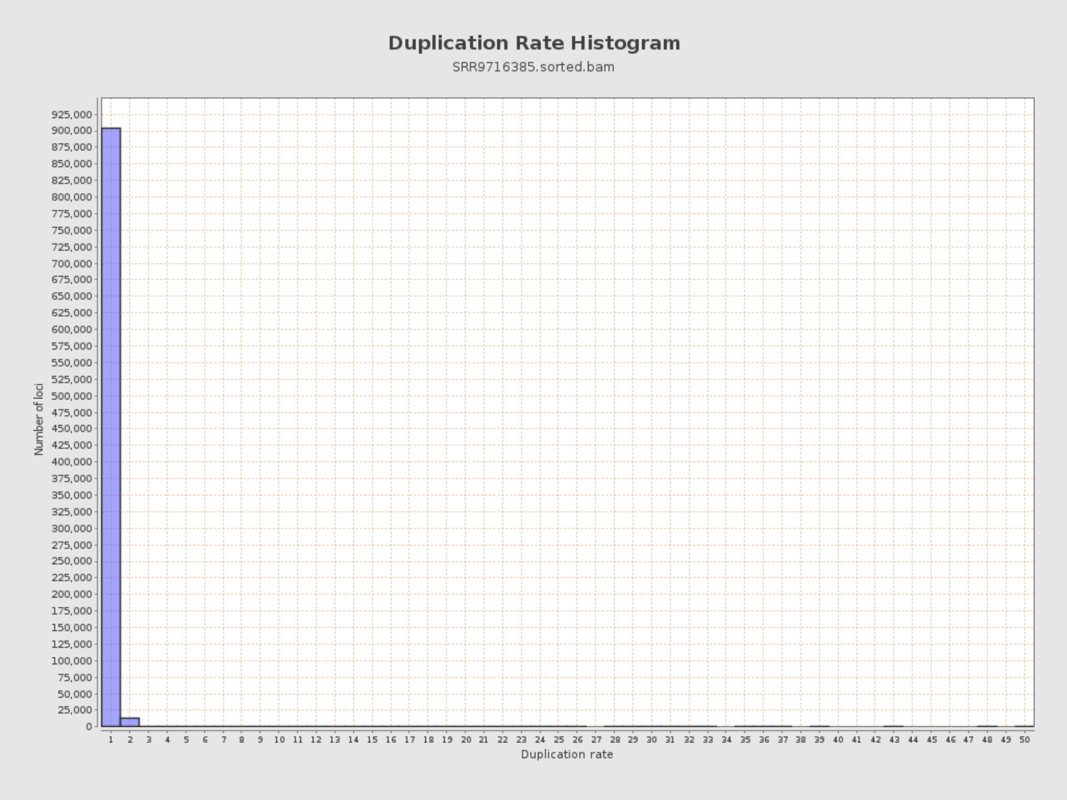
5. Results : Coverage Histogram (0-50X)



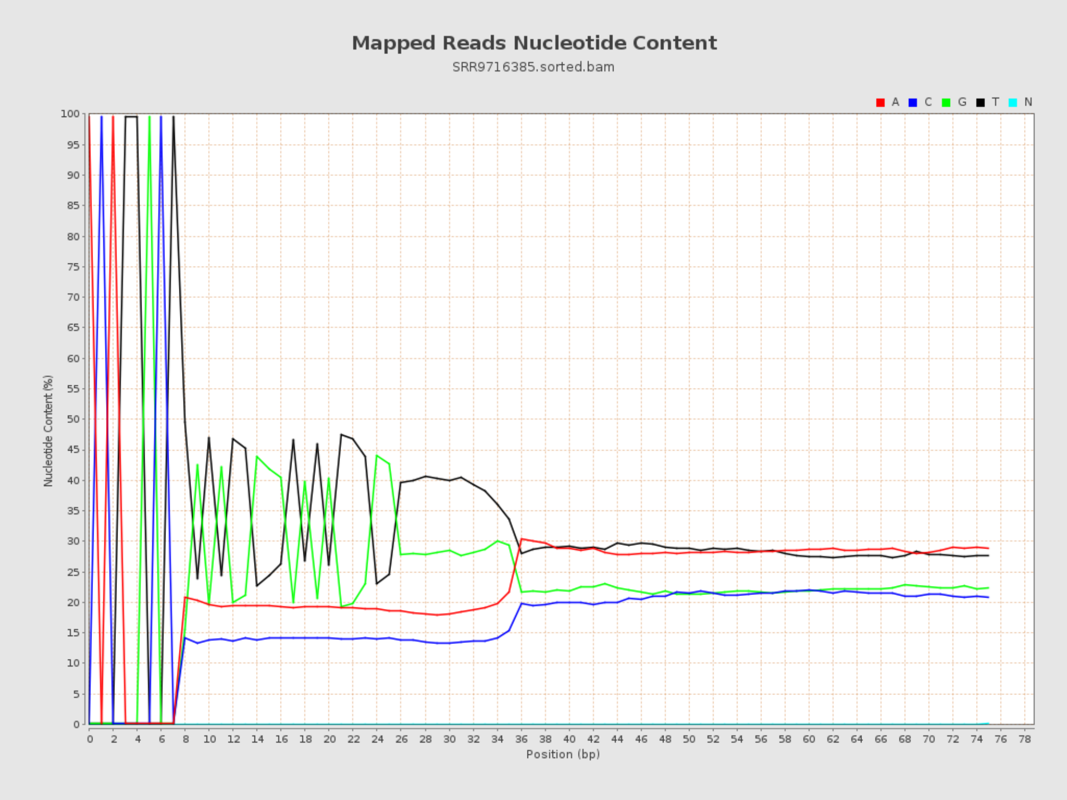
6. Results : Genome Fraction Coverage



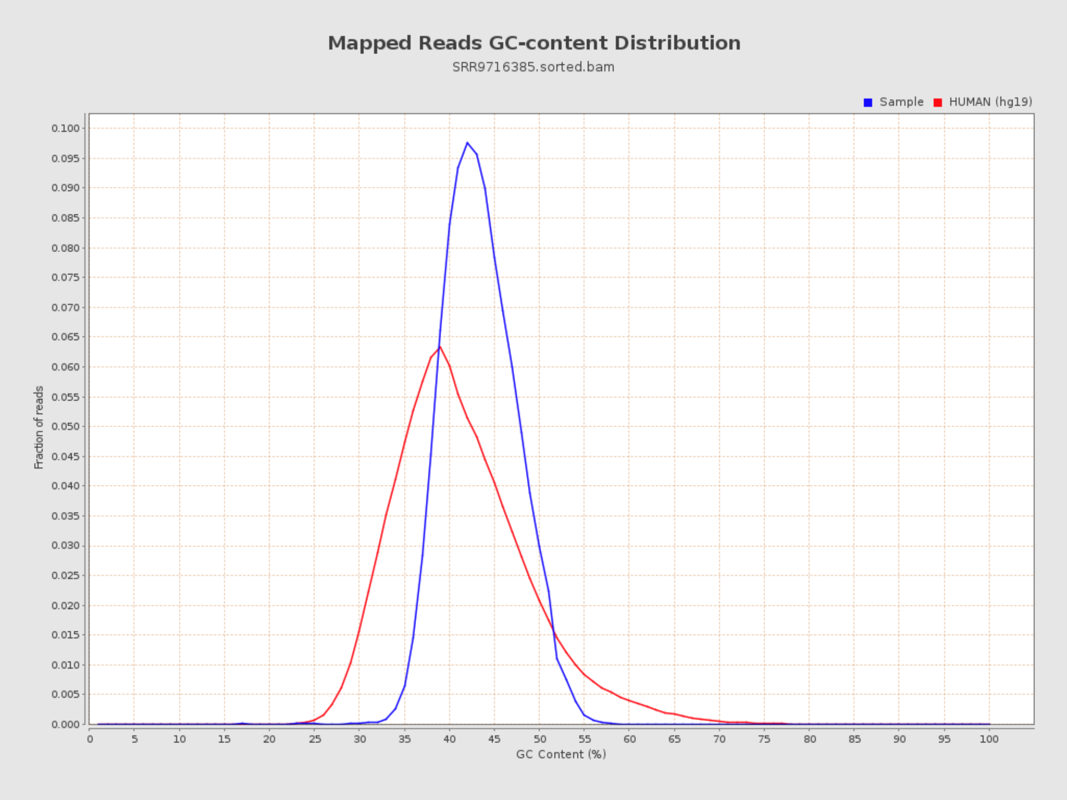
7. Results : Duplication Rate Histogram



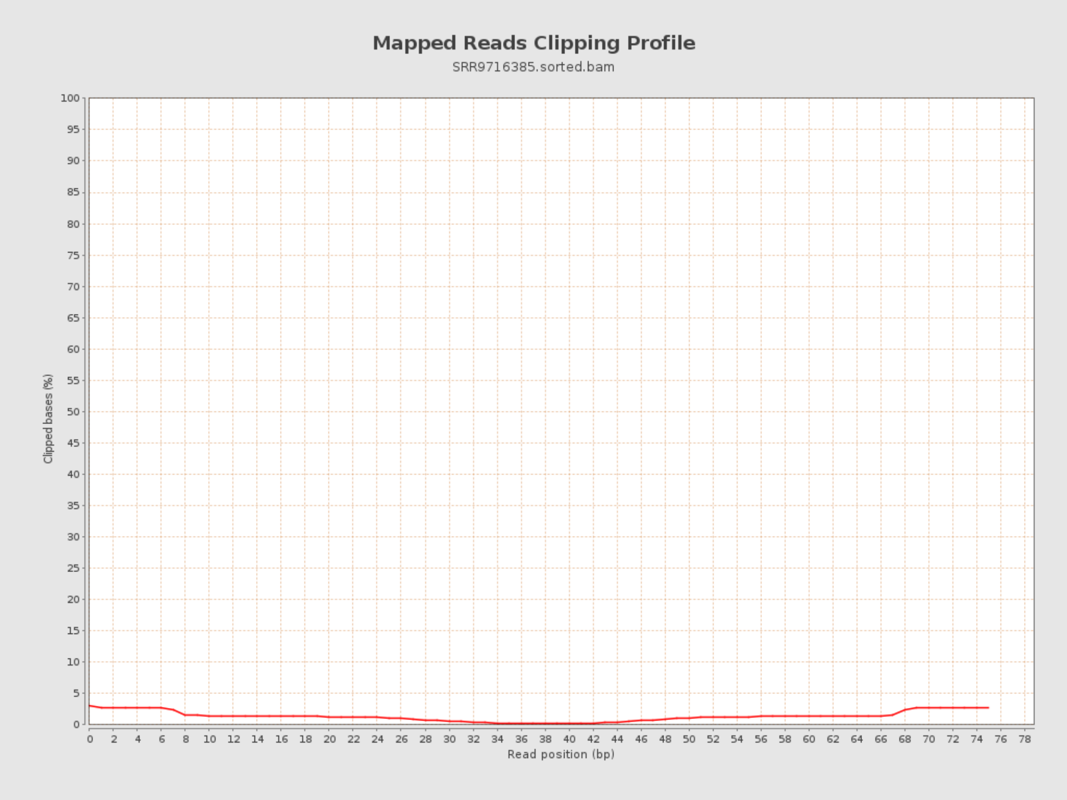
8. Results : Mapped Reads Nucleotide Content



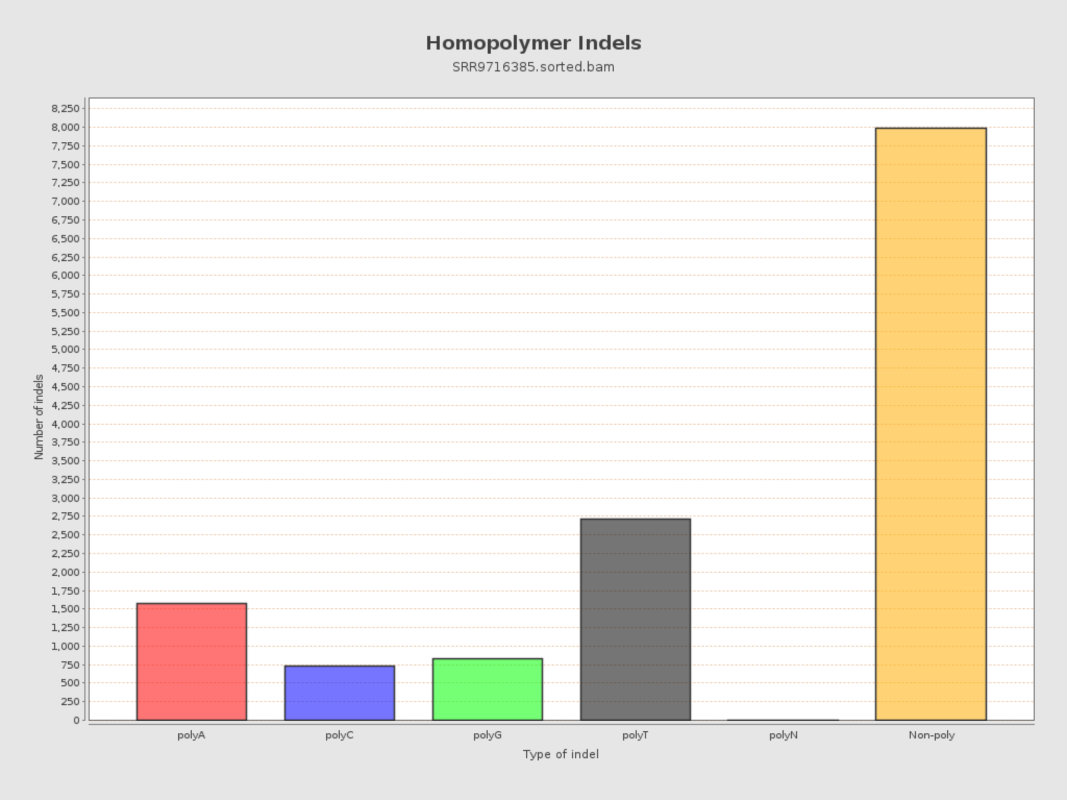
9. Results : Mapped Reads GC-content Distribution



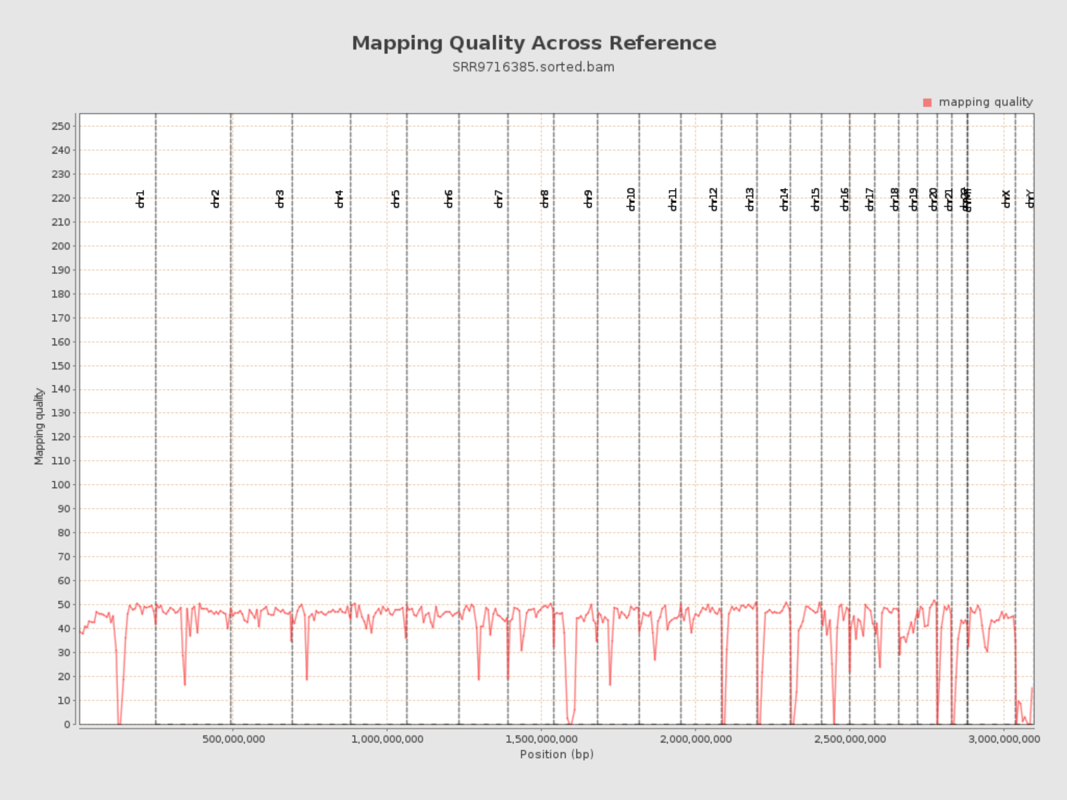
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram