Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:53:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716512.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_SRR9716512 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716512.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:53:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716512.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	833,424
Mapped reads	770,765 / 92.48%
Unmapped reads	62,659 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,247 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	16,202 / 1.94%
Duplication rate	1.49%
Clipped reads	771,814 / 92.61%

2.2. ACGT Content

Number/percentage of A's	11,962,091 / 26.15%
Number/percentage of C's	9,299,559 / 20.33%
Number/percentage of T's	13,933,290 / 30.45%
Number/percentage of G's	10,555,134 / 23.07%
Number/percentage of N's	619 / 0%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1633

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

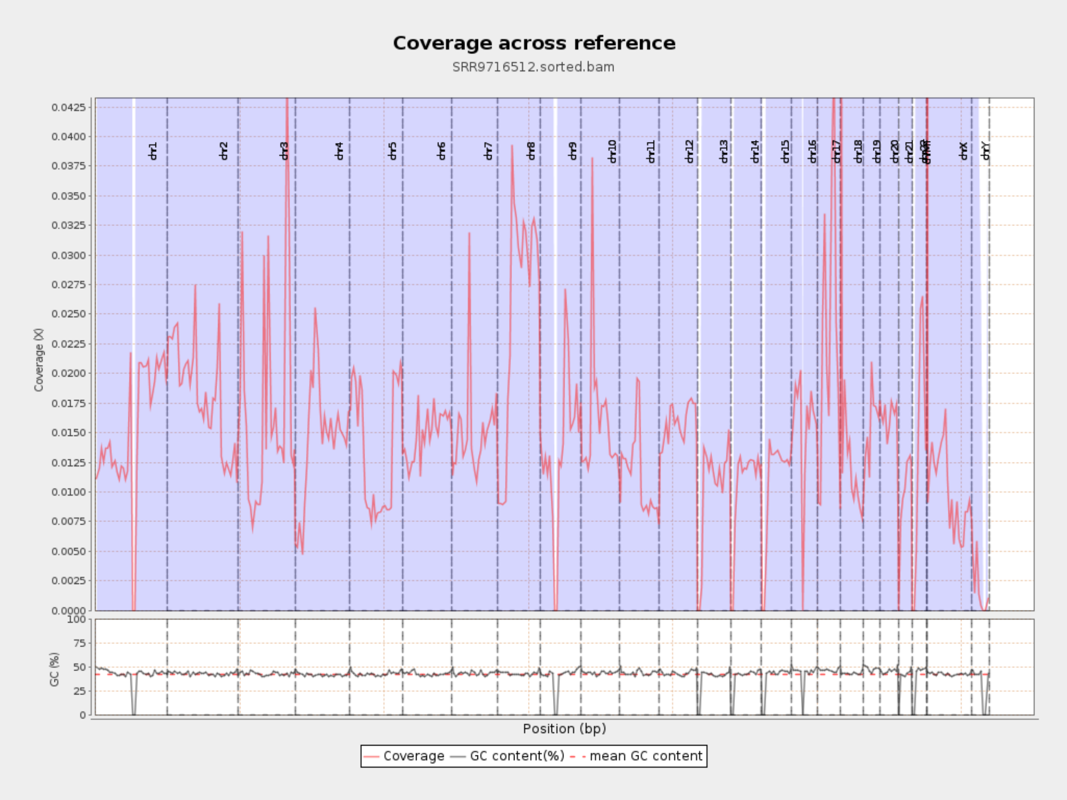
General error rate	0.5%
Mismatches	222,563
Insertions	3,811
Mapped reads with at least one insertion	0.49%
Deletions	8,488
Mapped reads with at least one deletion	1.09%
Homopolymer indels	40.25%

2.6. Chromosome stats

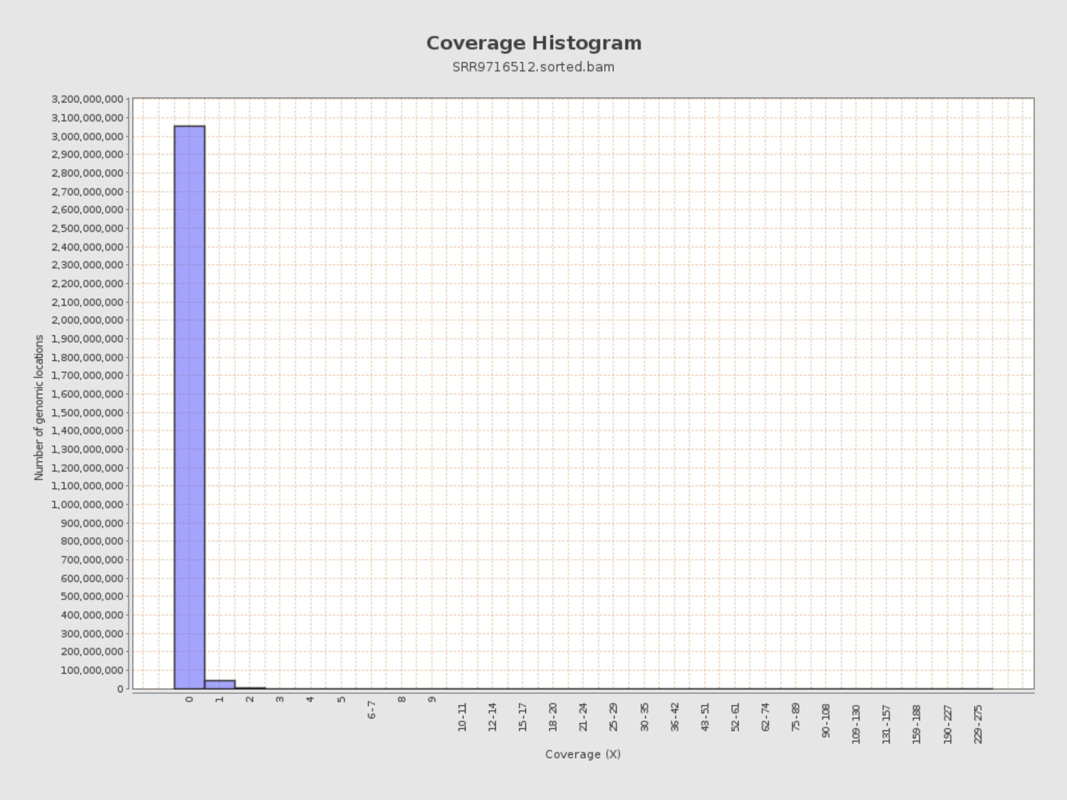
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3774328	0.0151	0.2368
chr2	243199373	4438477	0.0183	0.191
chr3	198022430	3370402	0.017	0.1401
chr4	191154276	2779038	0.0145	0.1341
chr5	180915260	2416427	0.0134	0.1203
chr6	171115067	2543842	0.0149	0.1321
chr7	159138663	2411212	0.0152	0.2466

chr8	146364022	3758934	0.0257	0.2025
chr9	141213431	1895824	0.0134	0.1303
chr10	135534747	2172770	0.016	0.2165
chr11	135006516	1574643	0.0117	0.1257
chr12	133851895	2117006	0.0158	0.14
chr13	115169878	1178574	0.0102	0.1051
chr14	107349540	1114946	0.0104	0.1069
chr15	102531392	1088726	0.0106	0.1087
chr16	90354753	1379154	0.0153	0.1326
chr17	81195210	1898135	0.0234	0.1637
chr18	78077248	1060163	0.0136	0.1834
chr19	59128983	920148	0.0156	0.2114
chr20	63025520	1018700	0.0162	0.1393
chr21	48129895	470987	0.0098	0.1081
chr22	51304566	694587	0.0135	0.1215
chrMT	16571	8555	0.5163	0.7883
chrX	155270560	1574191	0.0101	0.1137
chrY	59373566	104263	0.0018	0.0563

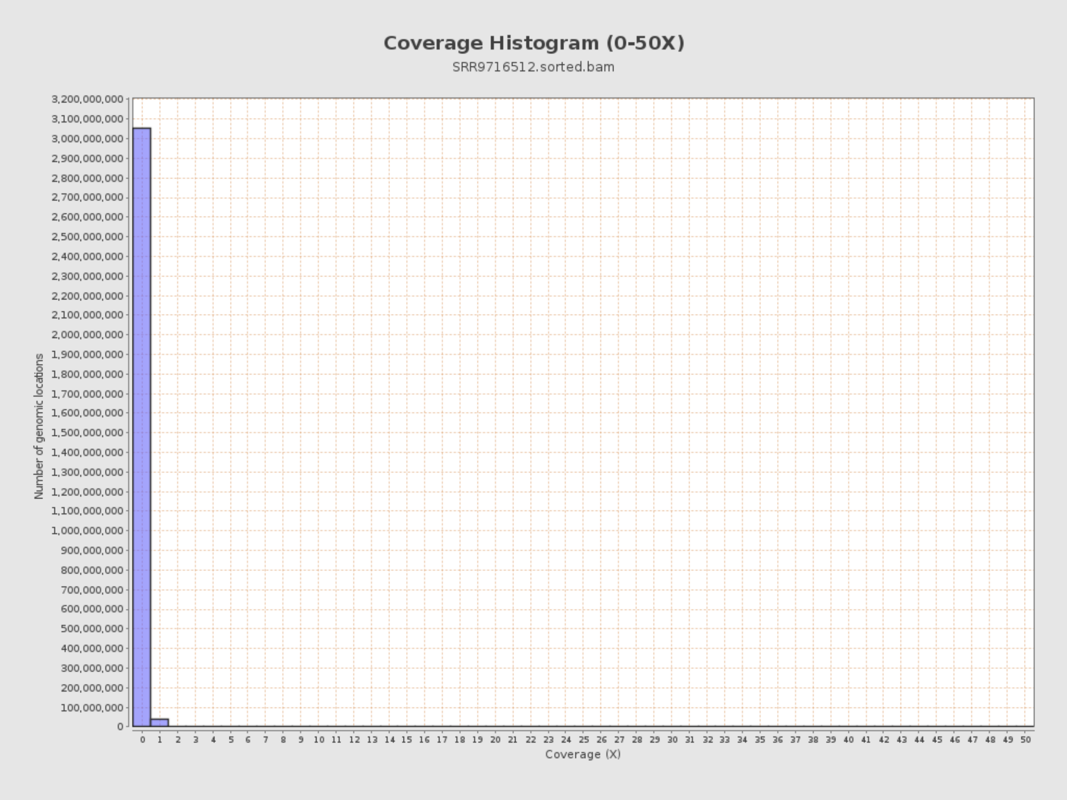
3. Results : Coverage across reference



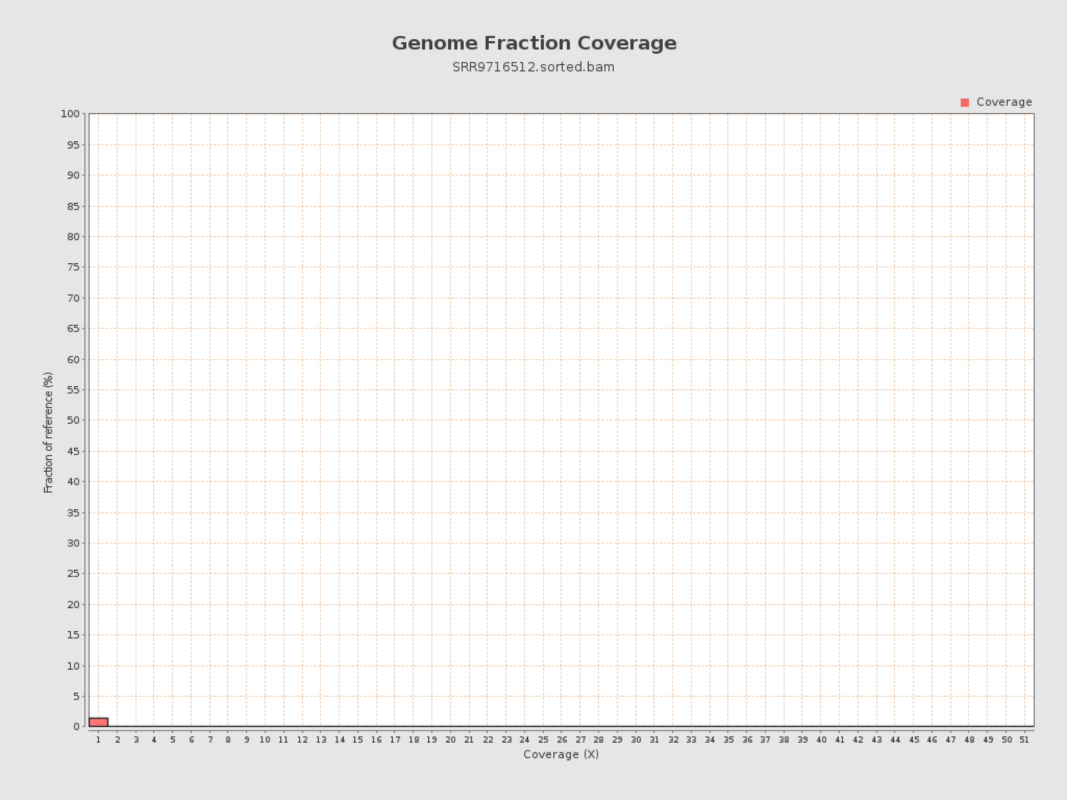
4. Results : Coverage Histogram



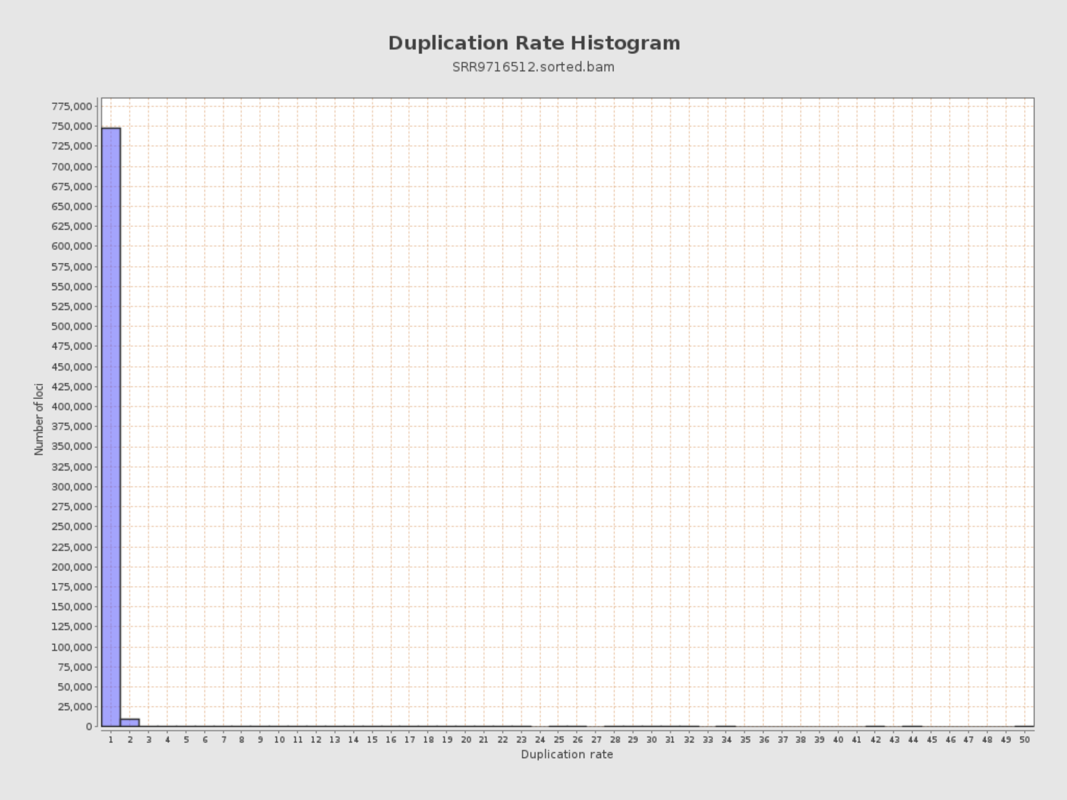
5. Results : Coverage Histogram (0-50X)



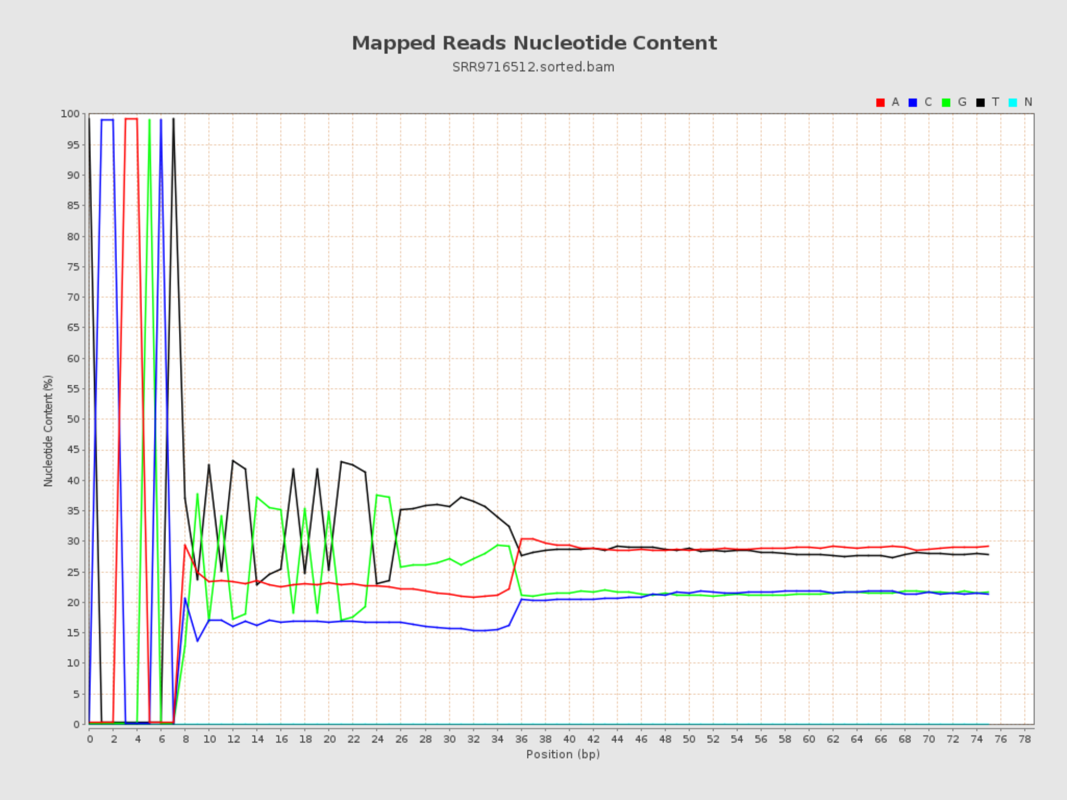
6. Results : Genome Fraction Coverage



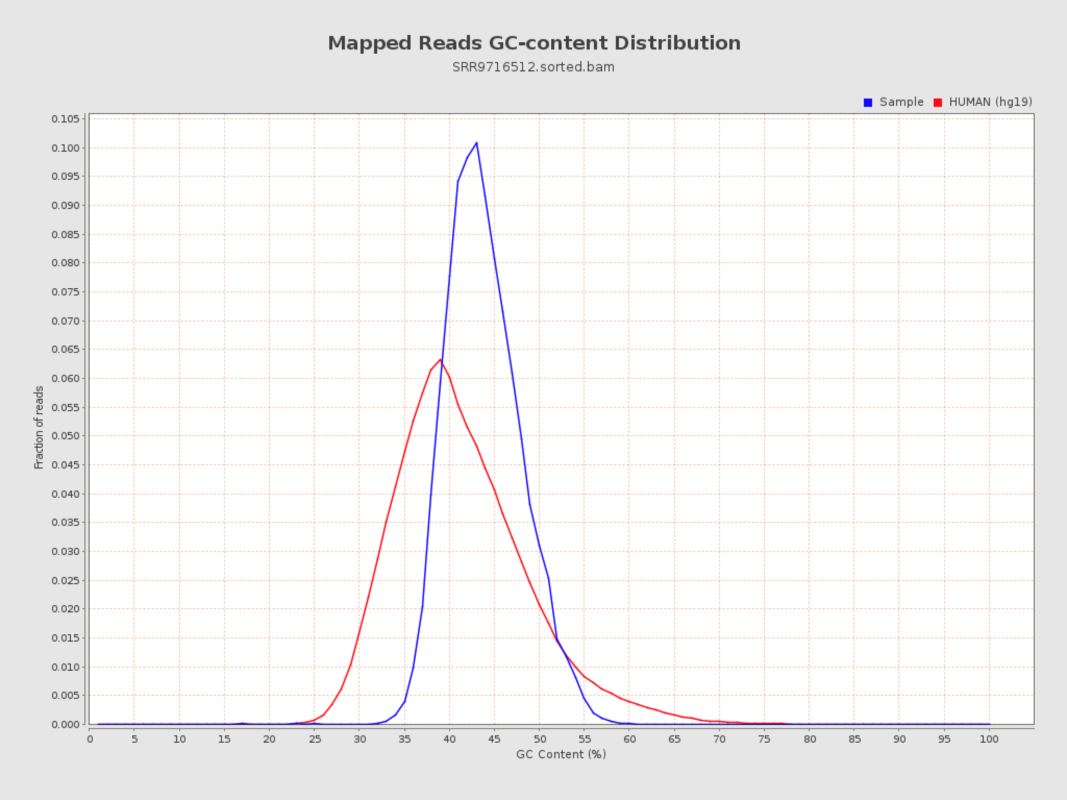
7. Results : Duplication Rate Histogram



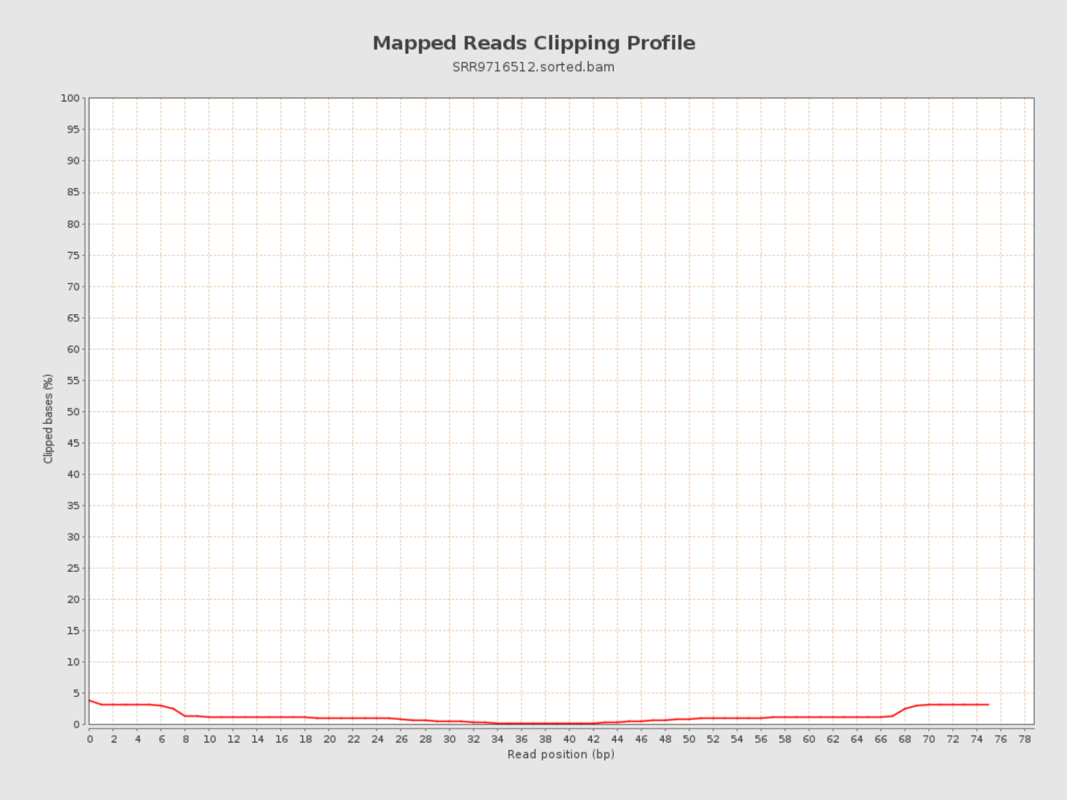
8. Results : Mapped Reads Nucleotide Content



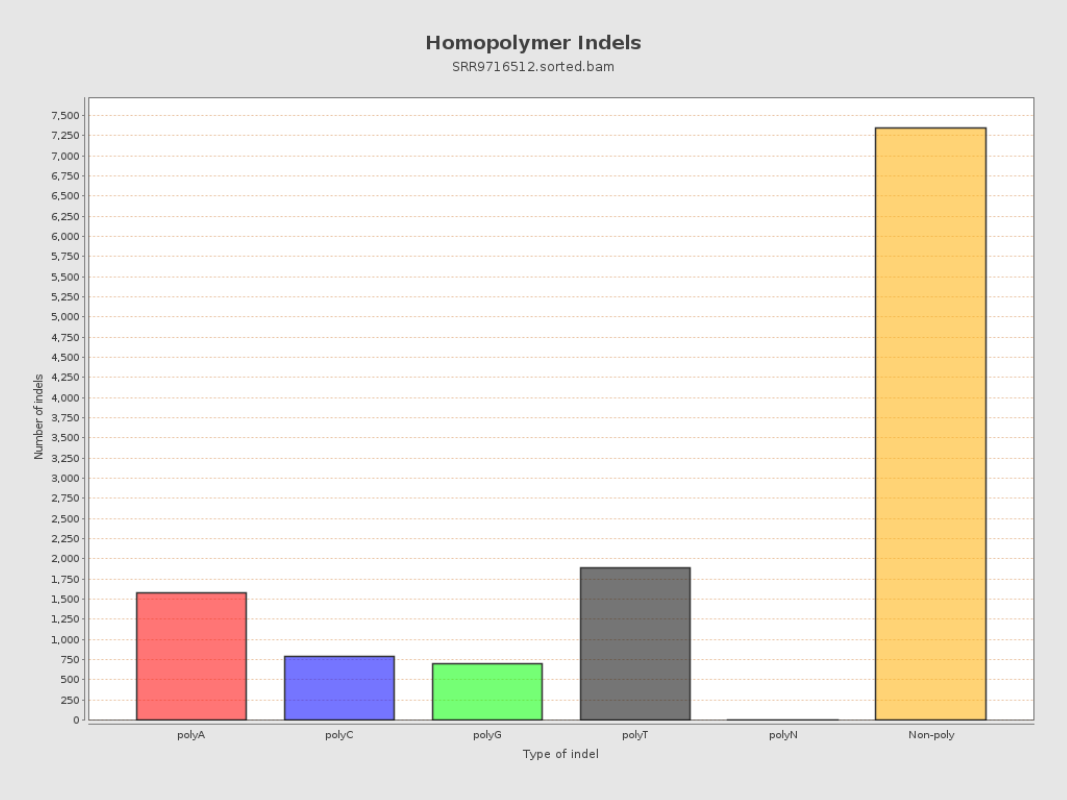
9. Results : Mapped Reads GC-content Distribution



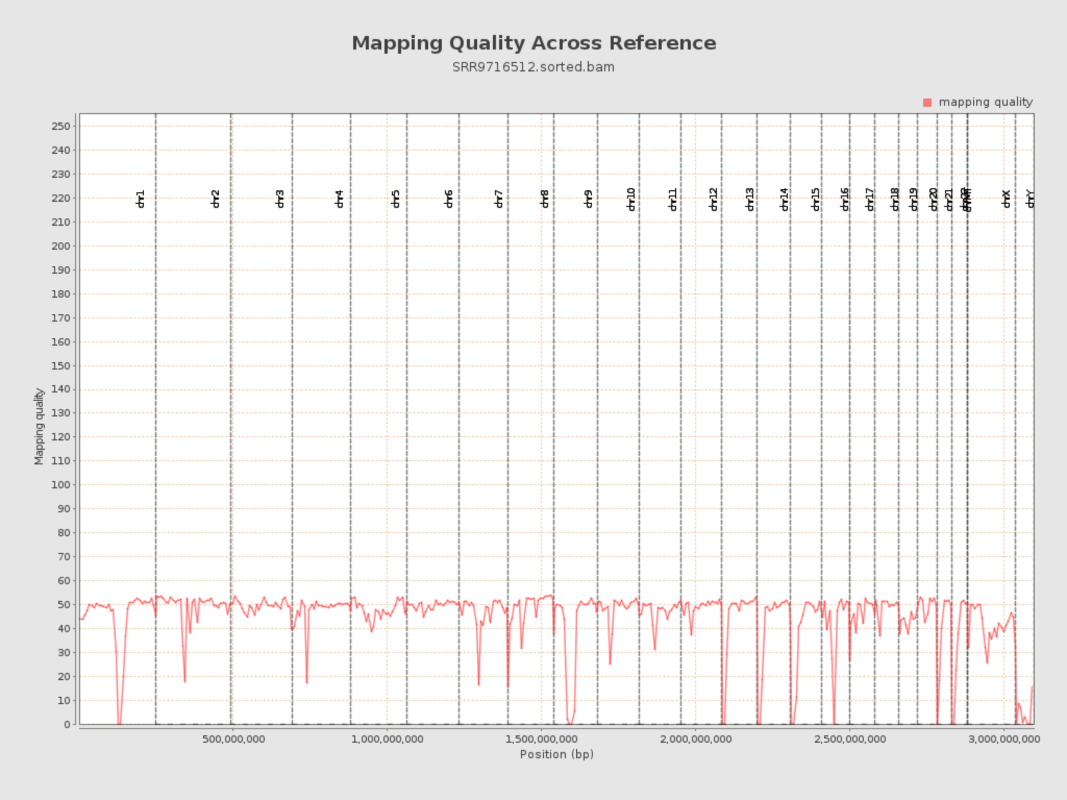
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram