Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:21:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716264.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_SRR9716264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716264.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:21:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,065,908
Mapped reads	843,838 / 79.17%
Unmapped reads	222,070 / 20.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	928 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	64,884 / 6.09%
Duplication rate	6.62%
Clipped reads	844,120 / 79.19%

2.2. ACGT Content

Number/percentage of A's	8,753,972 / 19.69%
Number/percentage of C's	8,631,680 / 19.41%
Number/percentage of T's	14,863,750 / 33.43%
Number/percentage of G's	12,212,899 / 27.47%
Number/percentage of N's	651 / 0%
GC Percentage	46.88%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1538

2.4. Mapping Quality

Mean Mapping Quality	42.99

2.5. Mismatches and indels

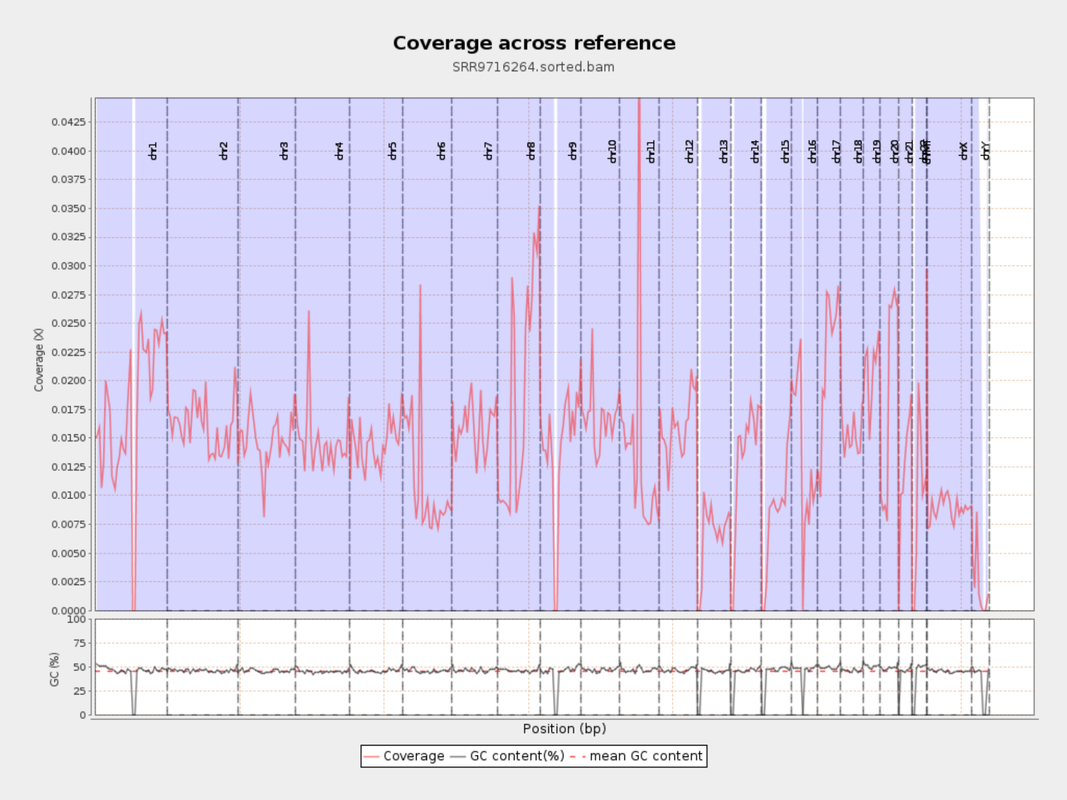
General error rate	0.65%
Mismatches	286,436
Insertions	2,429
Mapped reads with at least one insertion	0.29%
Deletions	6,357
Mapped reads with at least one deletion	0.75%
Homopolymer indels	42.49%

2.6. Chromosome stats

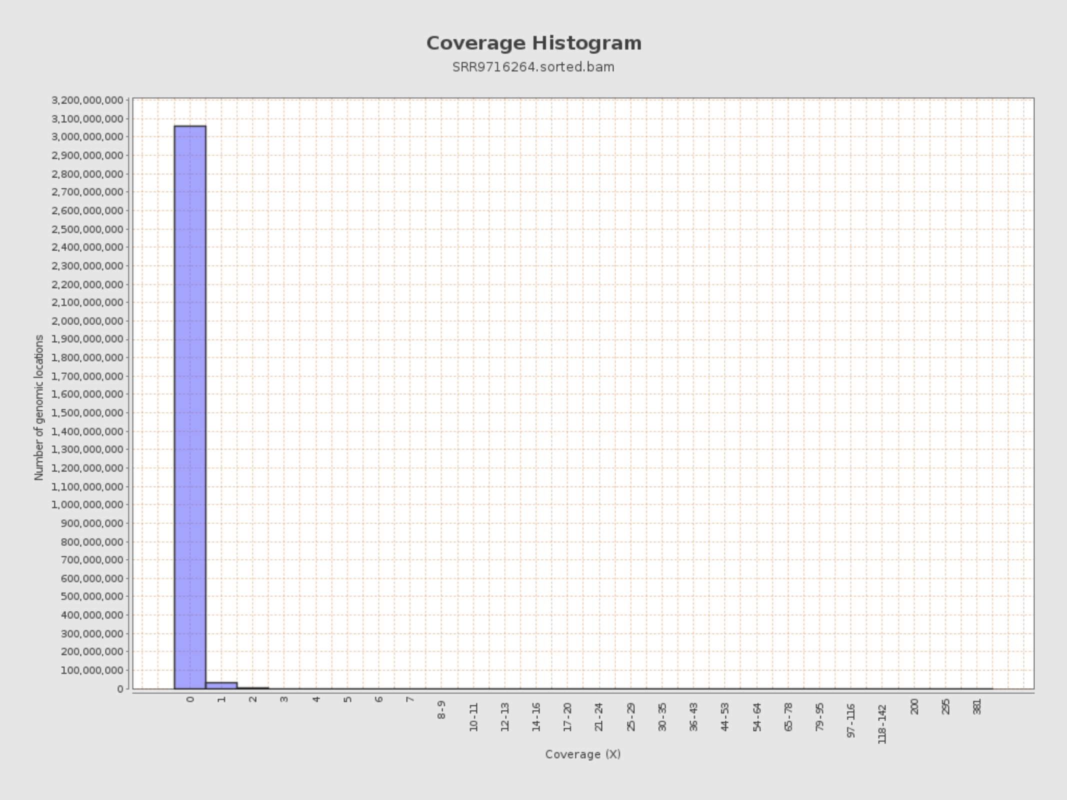
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4383071	0.0176	0.1803
chr2	243199373	3921494	0.0161	0.2195
chr3	198022430	2922330	0.0148	0.1387
chr4	191154276	2844387	0.0149	0.1455
chr5	180915260	2651283	0.0147	0.1381
chr6	171115067	1930708	0.0113	0.1361
chr7	159138663	2551647	0.016	0.1626

chr8	146364022	2744688	0.0188	0.1635
chr9	141213431	1973314	0.014	0.1452
chr10	135534747	2278621	0.0168	0.1701
chr11	135006516	1916026	0.0142	0.1505
chr12	133851895	2146512	0.016	0.1454
chr13	115169878	749862	0.0065	0.0925
chr14	107349540	1408773	0.0131	0.1321
chr15	102531392	872454	0.0085	0.1063
chr16	90354753	1181576	0.0131	0.1402
chr17	81195210	1785647	0.022	0.1757
chr18	78077248	1185882	0.0152	0.1595
chr19	59128983	1229758	0.0208	0.1928
chr20	63025520	1174490	0.0186	0.1637
chr21	48129895	604751	0.0126	0.136
chr22	51304566	503513	0.0098	0.1171
chrMT	16571	492	0.0297	0.1697
chrX	155270560	1380952	0.0089	0.1099
chrY	59373566	131687	0.0022	0.0757

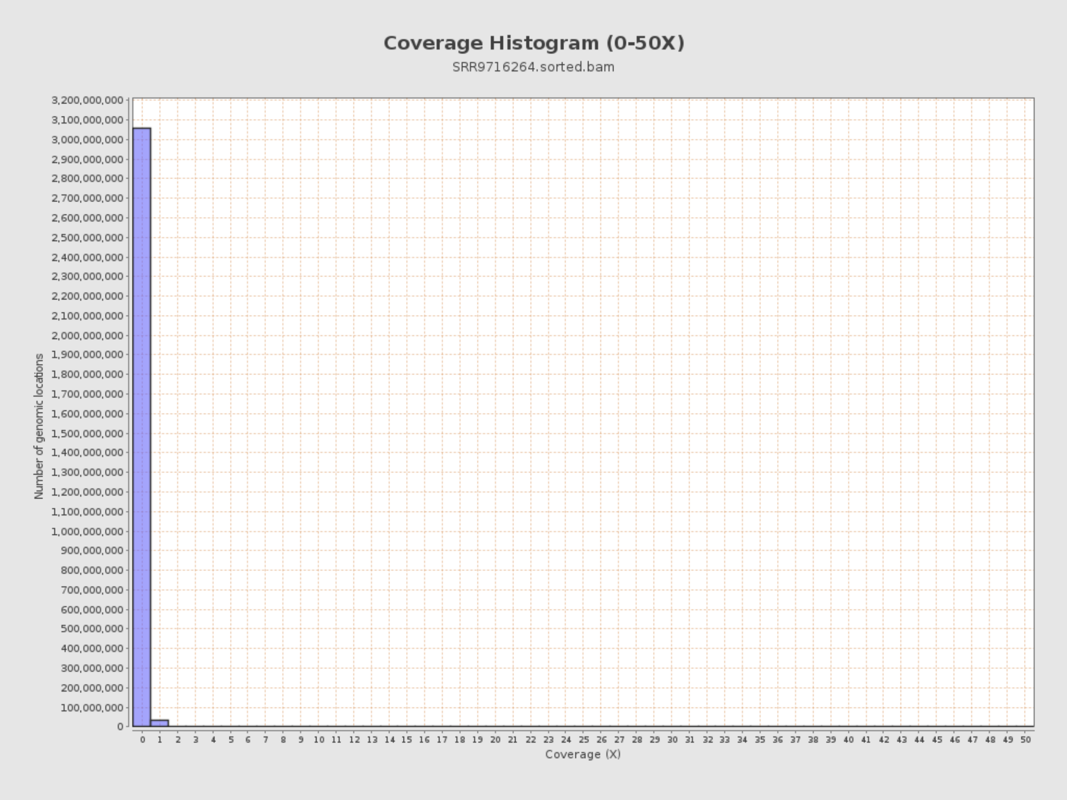
3. Results : Coverage across reference



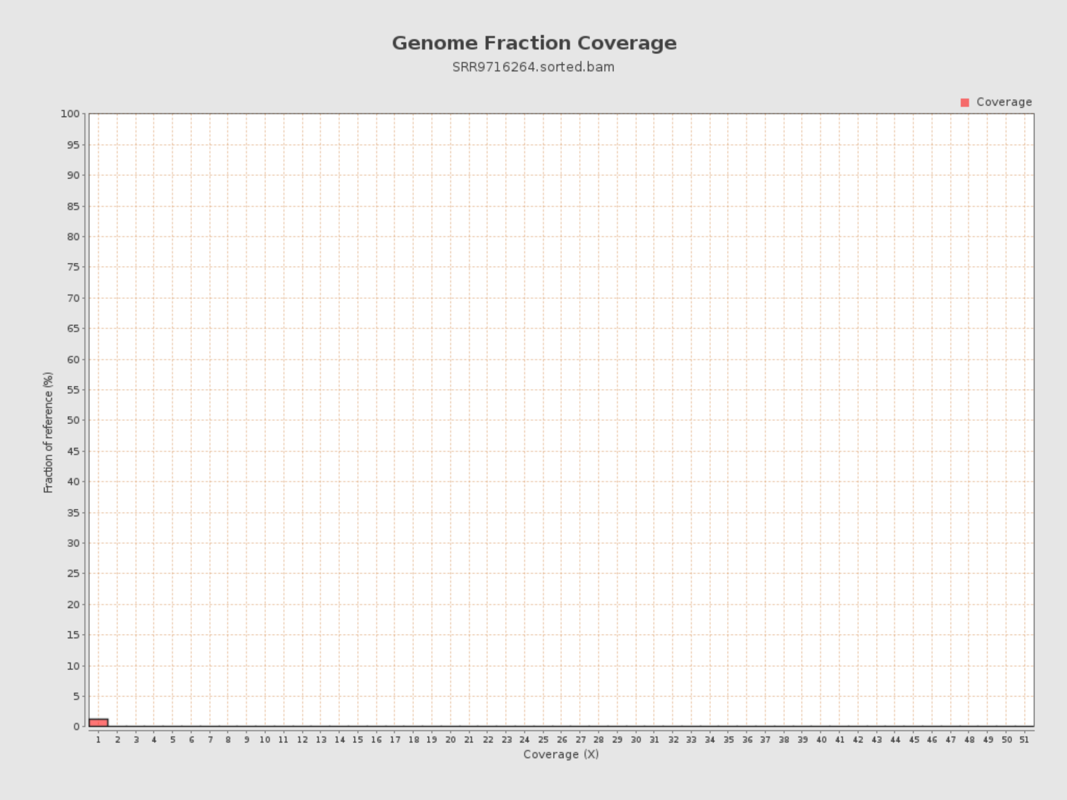
4. Results : Coverage Histogram



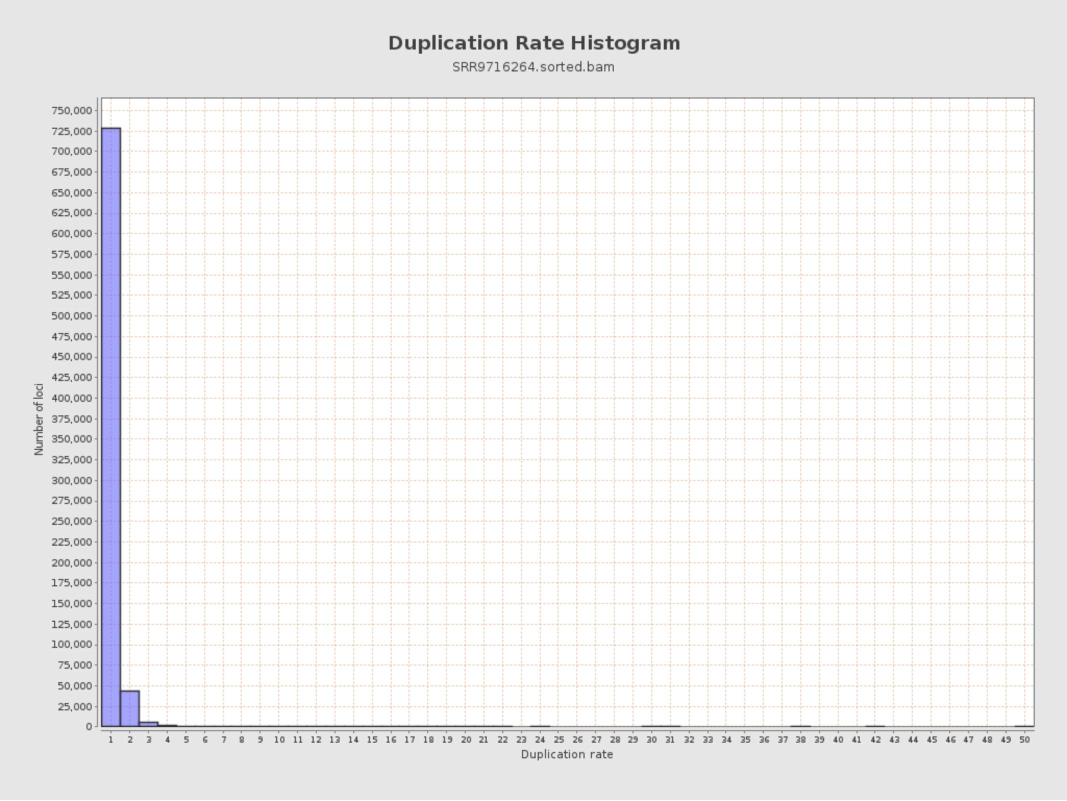
5. Results : Coverage Histogram (0-50X)



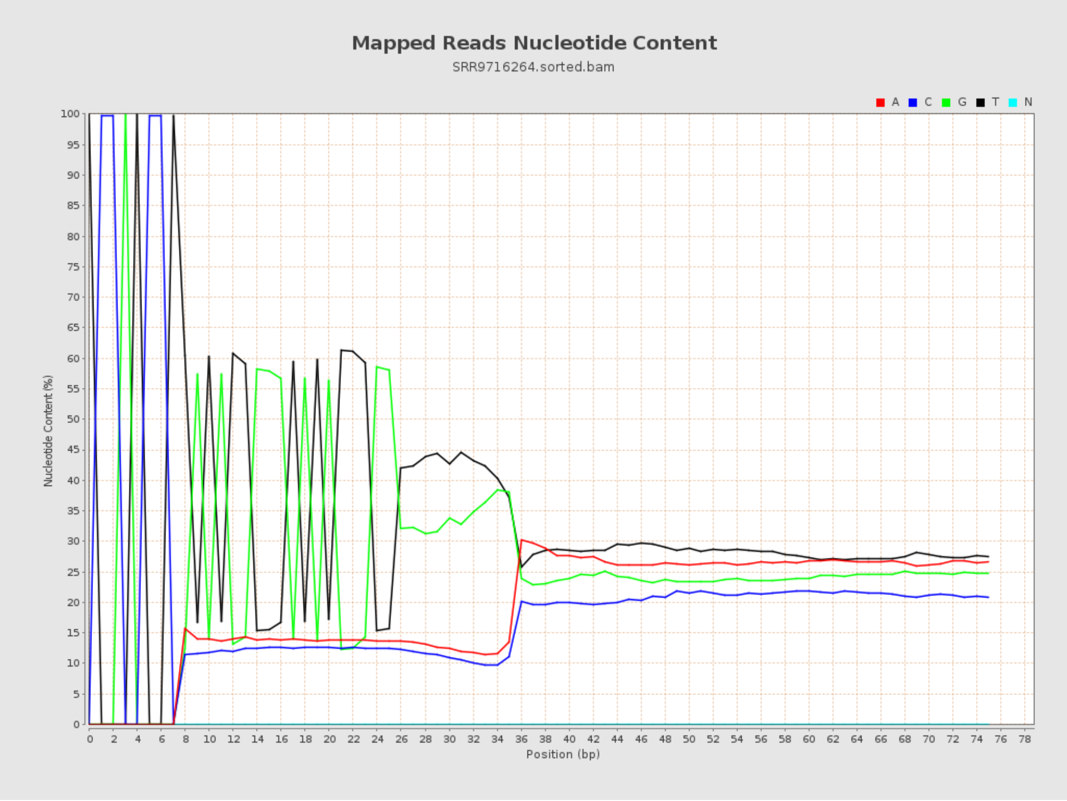
6. Results : Genome Fraction Coverage



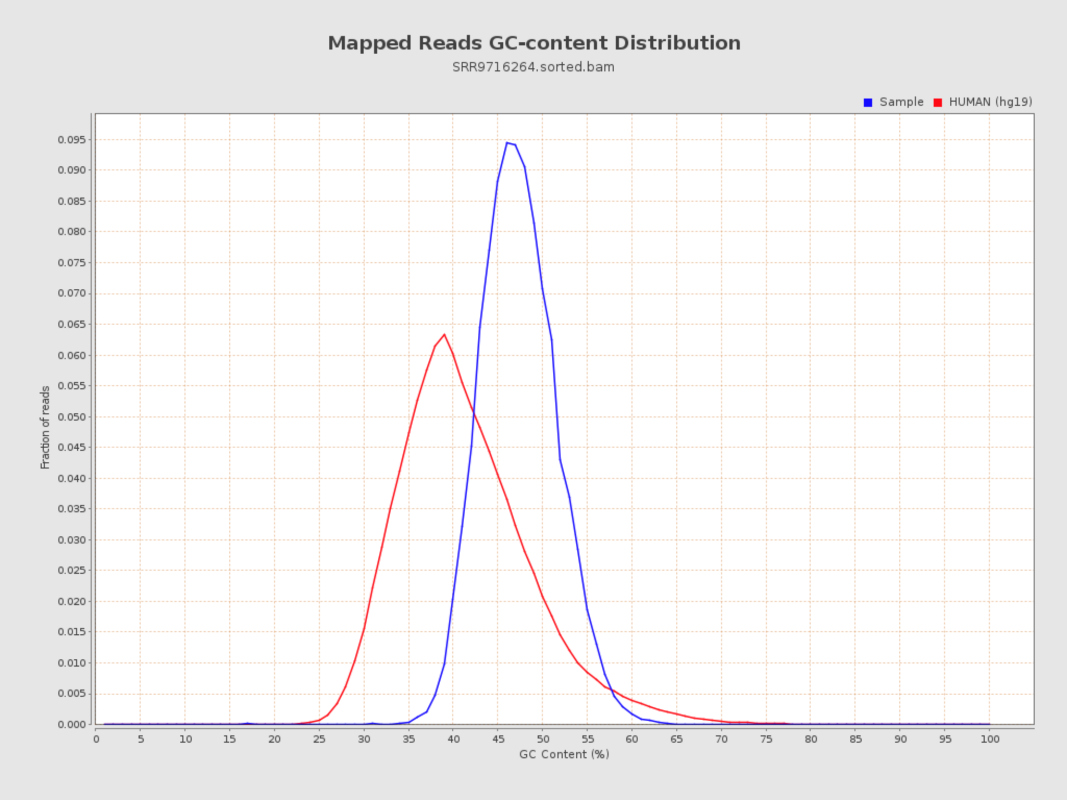
7. Results : Duplication Rate Histogram



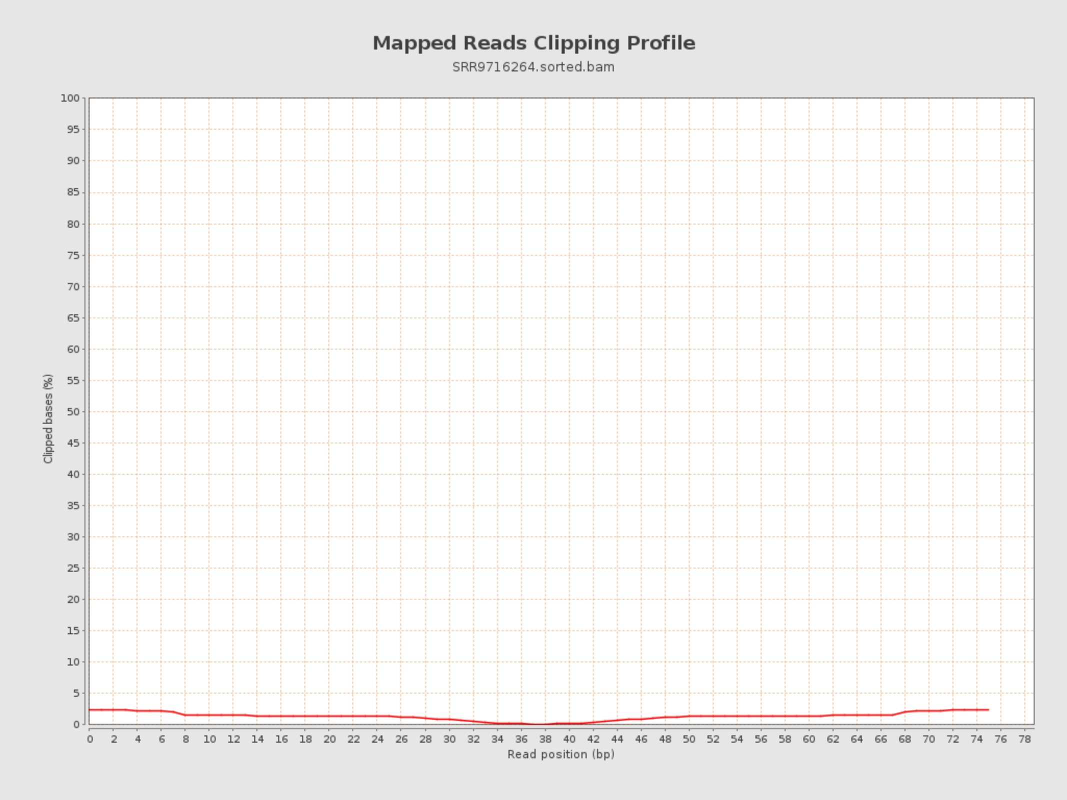
8. Results : Mapped Reads Nucleotide Content



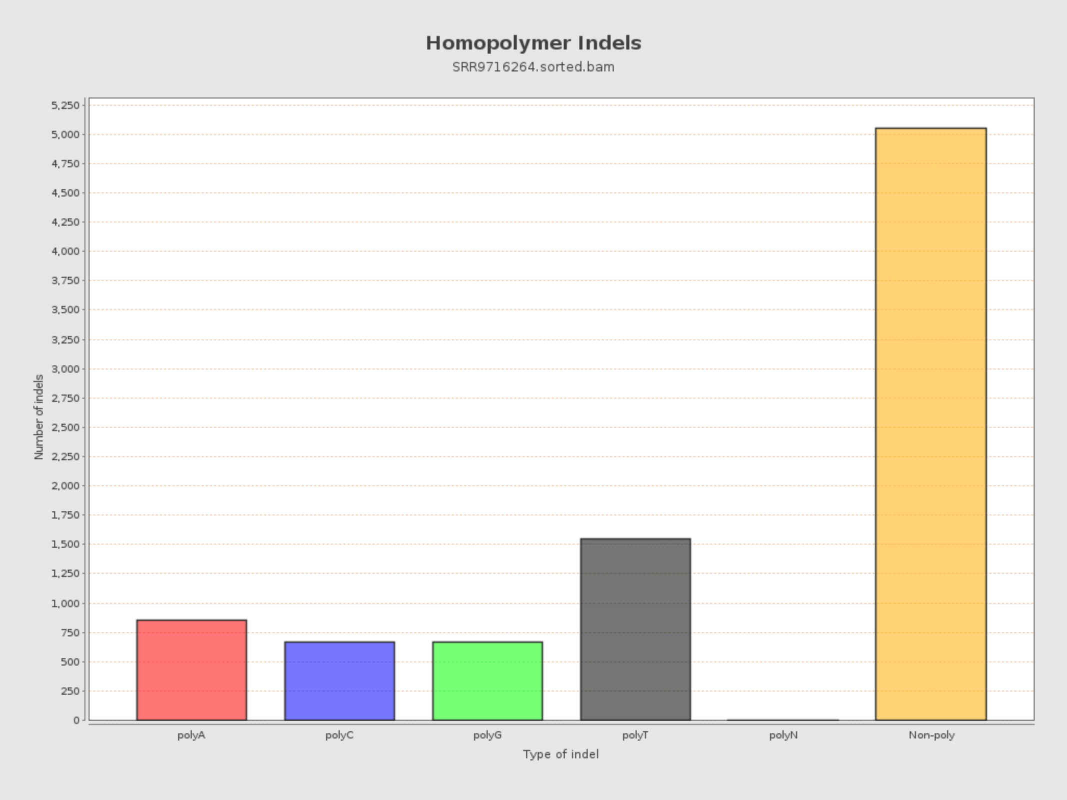
9. Results : Mapped Reads GC-content Distribution



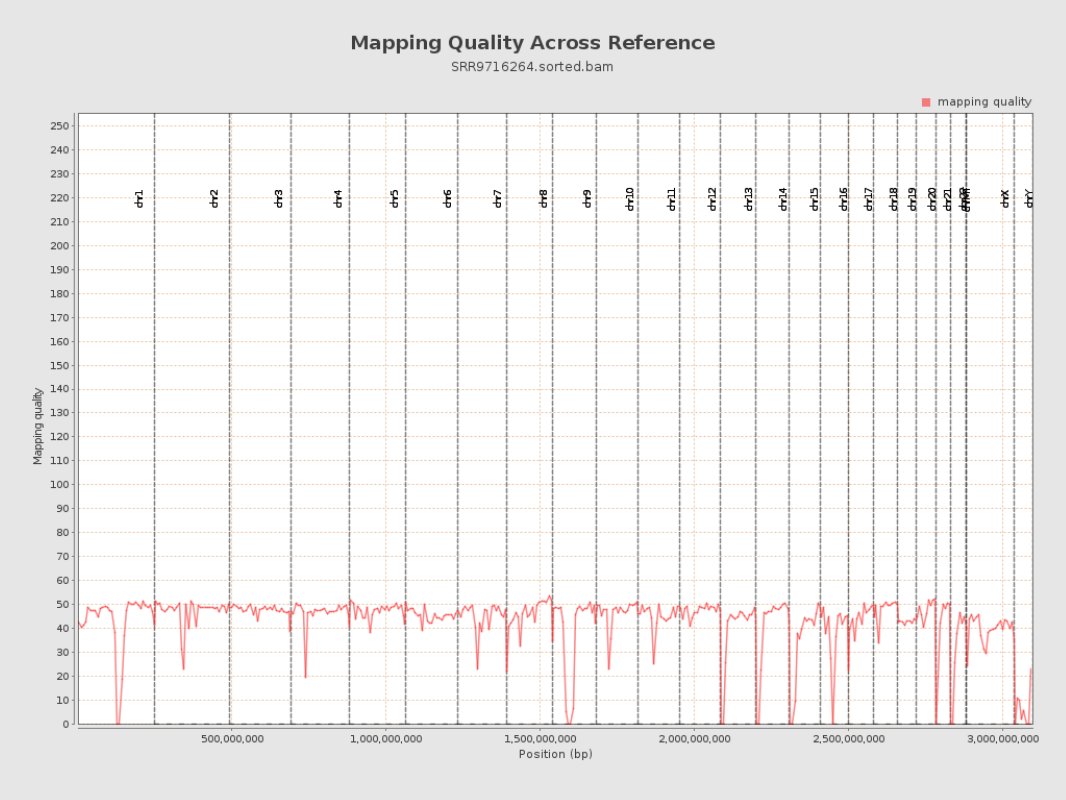
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram