Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:51:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716579.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_SRR9716579 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716579.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:51:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716579.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,567,868
Mapped reads	1,441,498 / 91.94%
Unmapped reads	126,370 / 8.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,565 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	41,973 / 2.68%
Duplication rate	1.95%
Clipped reads	1,448,235 / 92.37%

2.2. ACGT Content

Number/percentage of A's	20,245,659 / 24.05%
Number/percentage of C's	16,195,807 / 19.24%
Number/percentage of T's	26,549,026 / 31.53%
Number/percentage of G's	21,201,532 / 25.18%
Number/percentage of N's	1,055 / 0%
GC Percentage	44.42%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2728

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

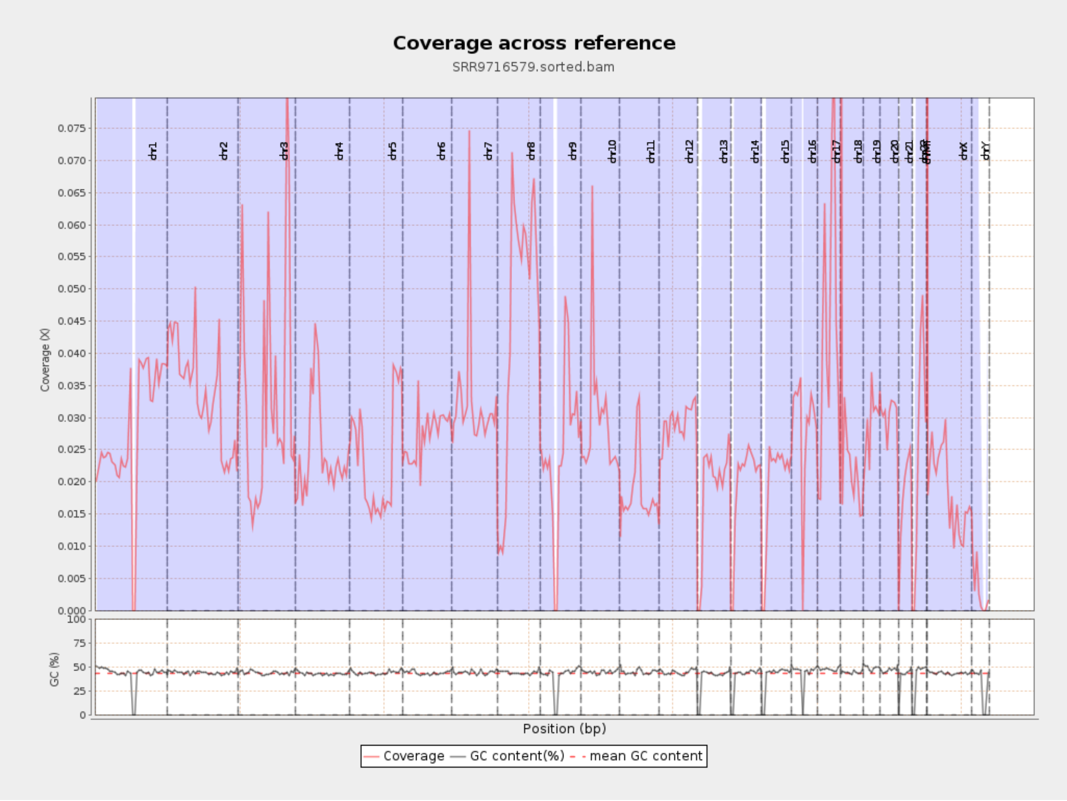
General error rate	0.51%
Mismatches	417,946
Insertions	4,469
Mapped reads with at least one insertion	0.31%
Deletions	15,507
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.68%

2.6. Chromosome stats

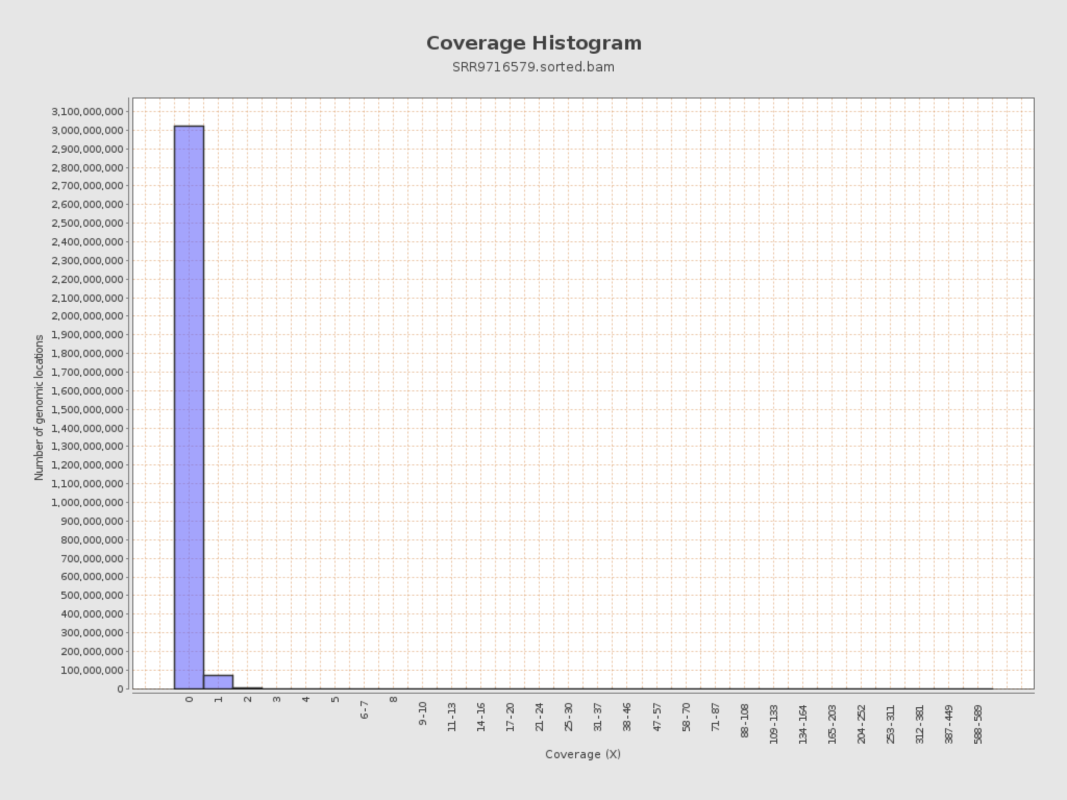
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6930999	0.0278	0.368
chr2	243199373	8219665	0.0338	0.3195
chr3	198022430	6545544	0.0331	0.2056
chr4	191154276	4668701	0.0244	0.1769
chr5	180915260	4201398	0.0232	0.1632
chr6	171115067	4663011	0.0273	0.1946
chr7	159138663	5172733	0.0325	0.6333

chr8	146364022	6742355	0.0461	0.2952
chr9	141213431	3496150	0.0248	0.2002
chr10	135534747	3964895	0.0293	0.3381
chr11	135006516	2496110	0.0185	0.1807
chr12	133851895	3883959	0.029	0.2008
chr13	115169878	2158013	0.0187	0.1459
chr14	107349540	2100738	0.0196	0.1549
chr15	102531392	1958911	0.0191	0.1522
chr16	90354753	2541813	0.0281	0.1887
chr17	81195210	3566976	0.0439	0.2339
chr18	78077248	1977879	0.0253	0.2923
chr19	59128983	1718718	0.0291	0.34
chr20	63025520	1907268	0.0303	0.1963
chr21	48129895	861732	0.0179	0.1481
chr22	51304566	1305317	0.0254	0.1717
chrMT	16571	56639	3.418	2.7252
chrX	155270560	2896449	0.0187	0.1647
chrY	59373566	181731	0.0031	0.0797

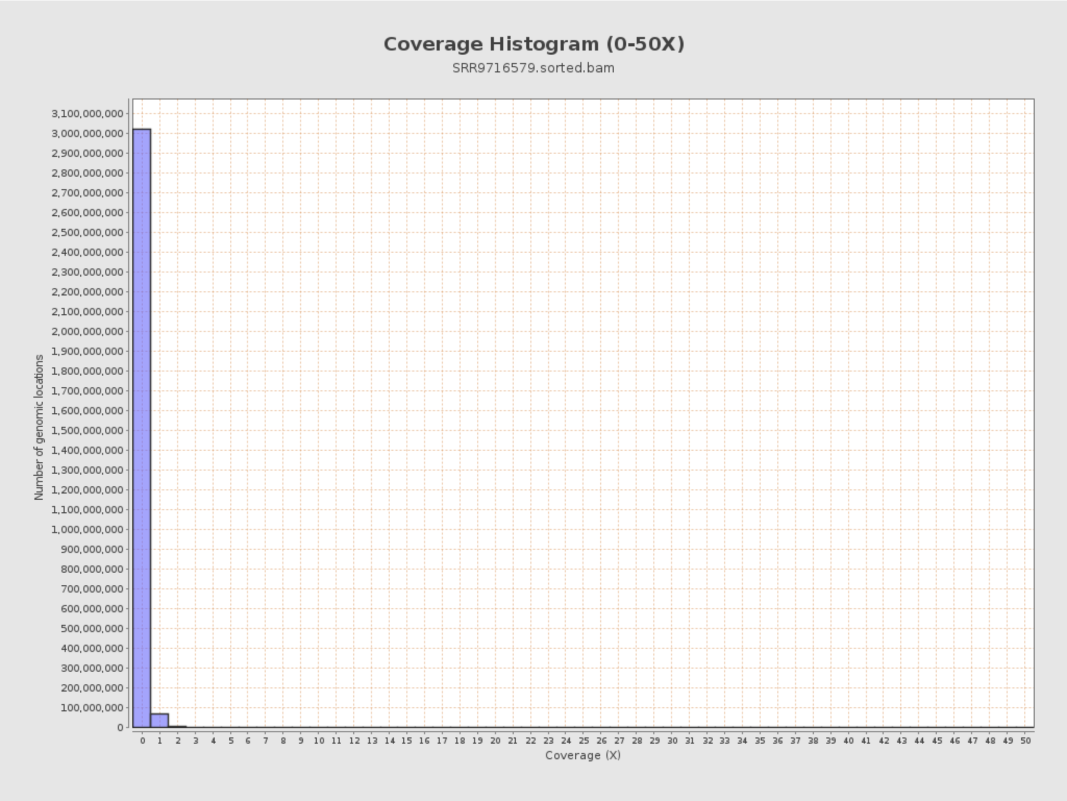
3. Results : Coverage across reference



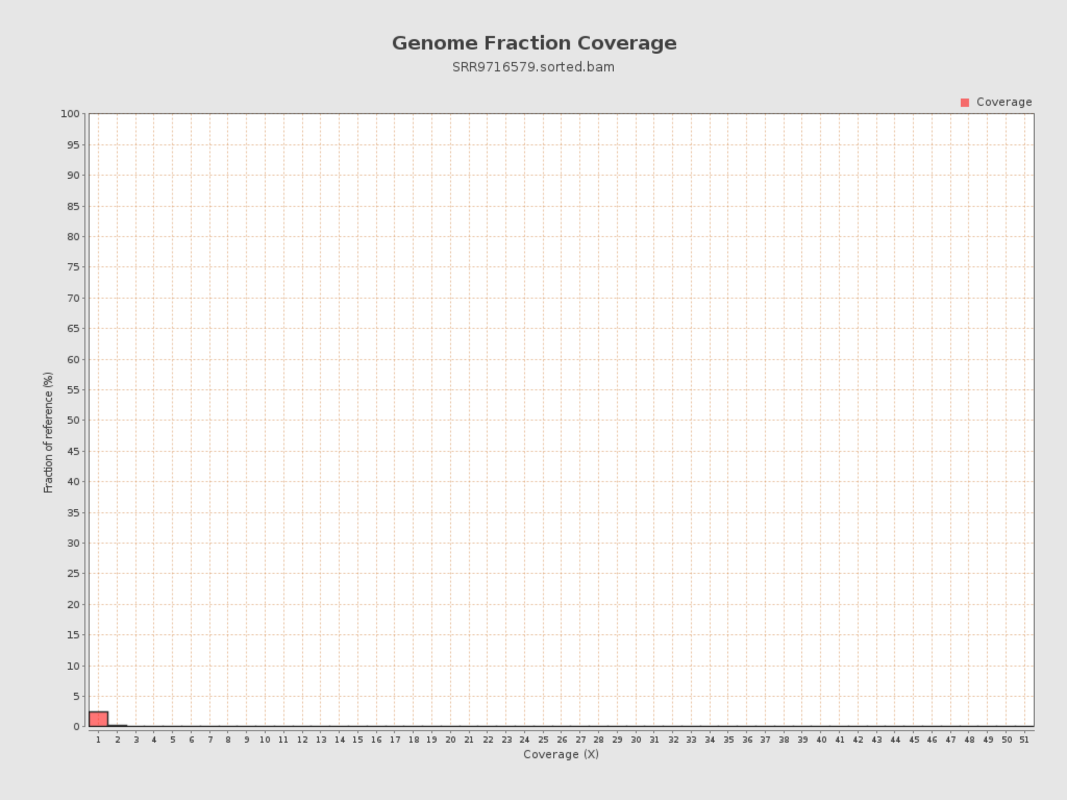
4. Results : Coverage Histogram



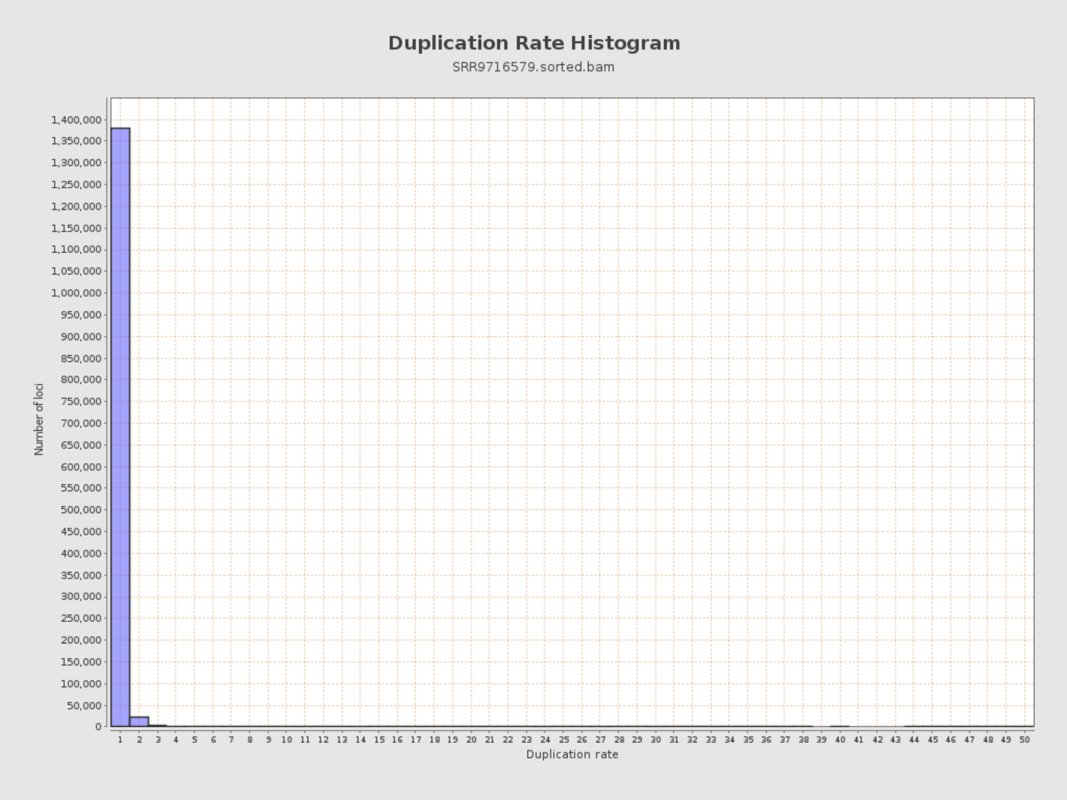
5. Results : Coverage Histogram (0-50X)



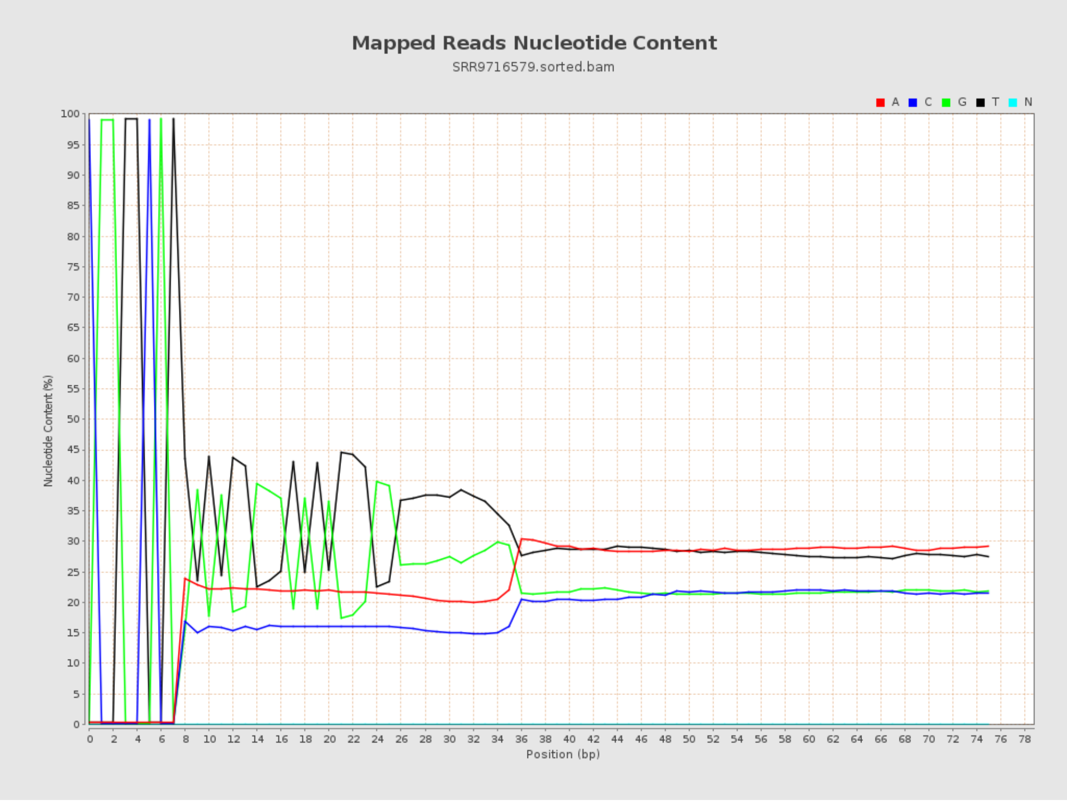
6. Results : Genome Fraction Coverage



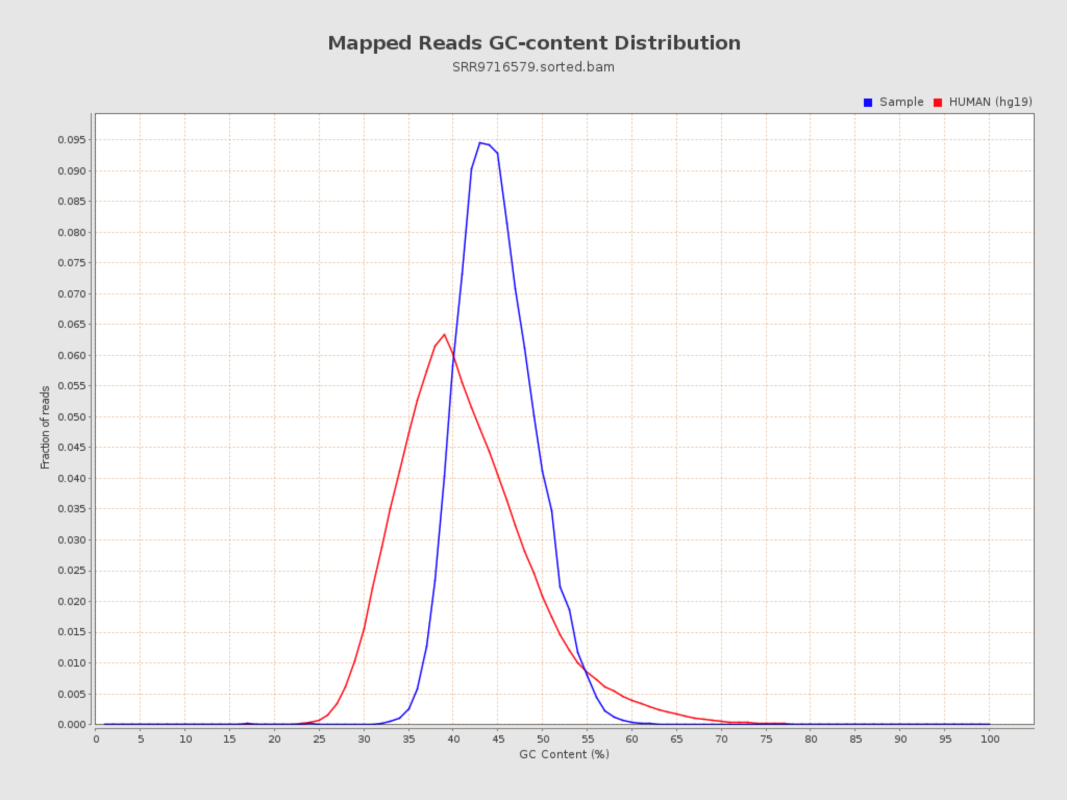
7. Results : Duplication Rate Histogram



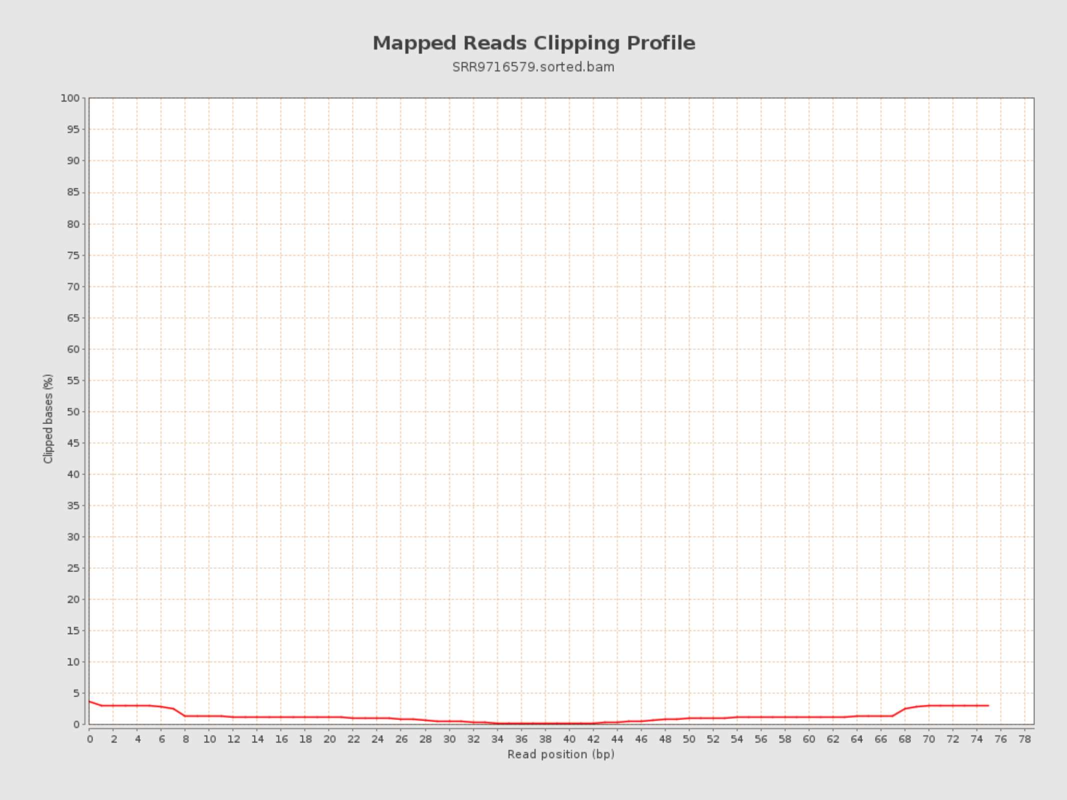
8. Results : Mapped Reads Nucleotide Content



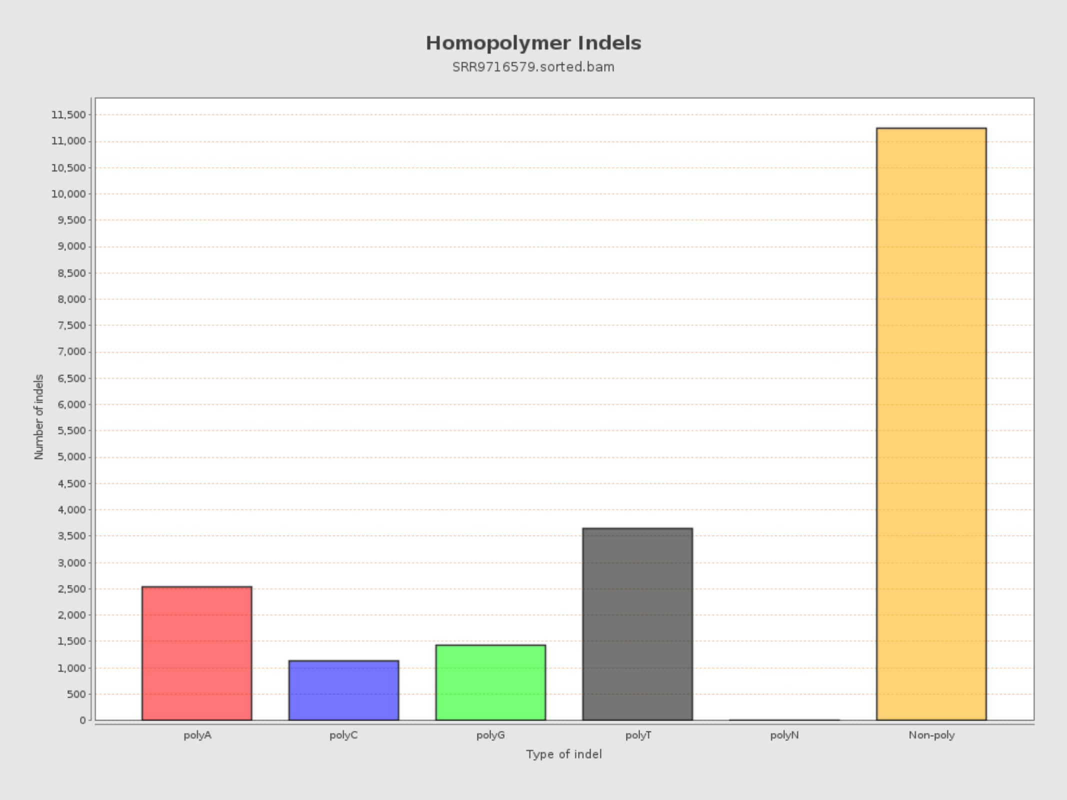
9. Results : Mapped Reads GC-content Distribution



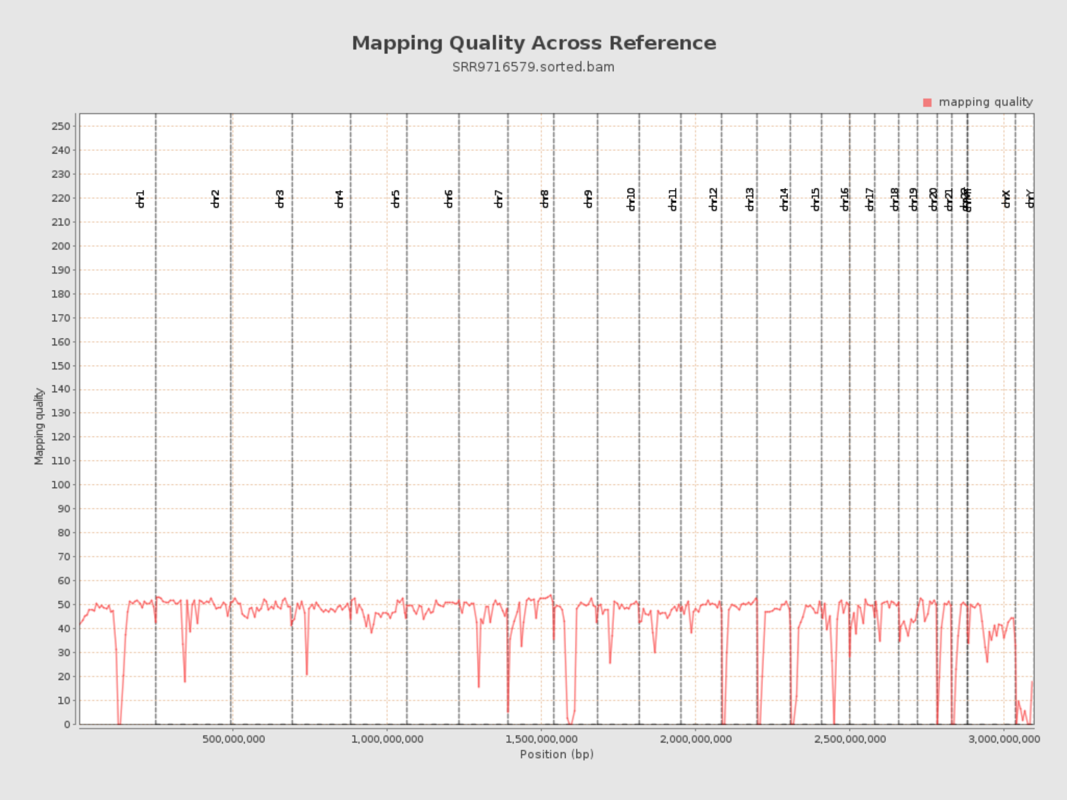
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram