Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:55:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716236.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_SRR9716236 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716236.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:55:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716236.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,026,388
Mapped reads	1,825,737 / 90.1%
Unmapped reads	200,651 / 9.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,828 / 1.37%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	89,967 / 4.44%
Duplication rate	3.1%
Clipped reads	1,849,791 / 91.29%

2.2. ACGT Content

Number/percentage of A's	35,300,183 / 24.7%
Number/percentage of C's	28,637,038 / 20.03%
Number/percentage of T's	45,252,016 / 31.66%
Number/percentage of G's	33,739,869 / 23.6%
Number/percentage of N's	8,305 / 0.01%
GC Percentage	43.64%

2.3. Coverage

Mean	0.0462

Standard Deviation	0.5243

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

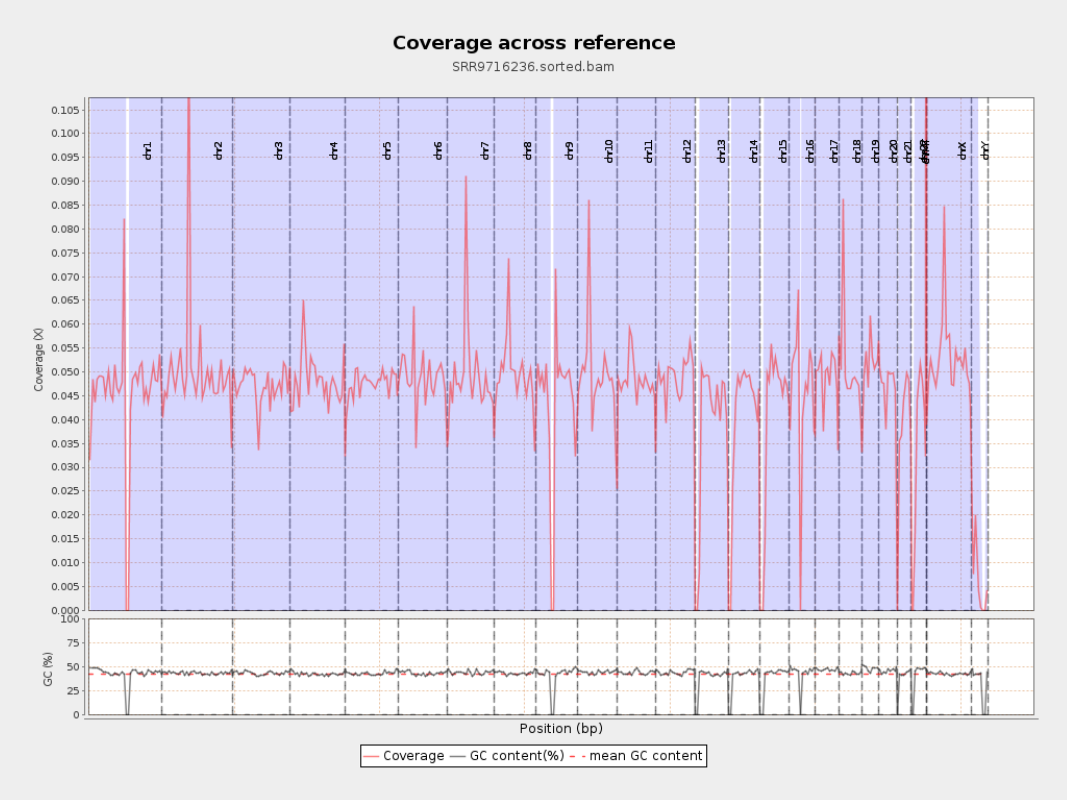
General error rate	0.89%
Mismatches	1,248,863
Insertions	12,916
Mapped reads with at least one insertion	0.7%
Deletions	36,382
Mapped reads with at least one deletion	1.96%
Homopolymer indels	44.29%

2.6. Chromosome stats

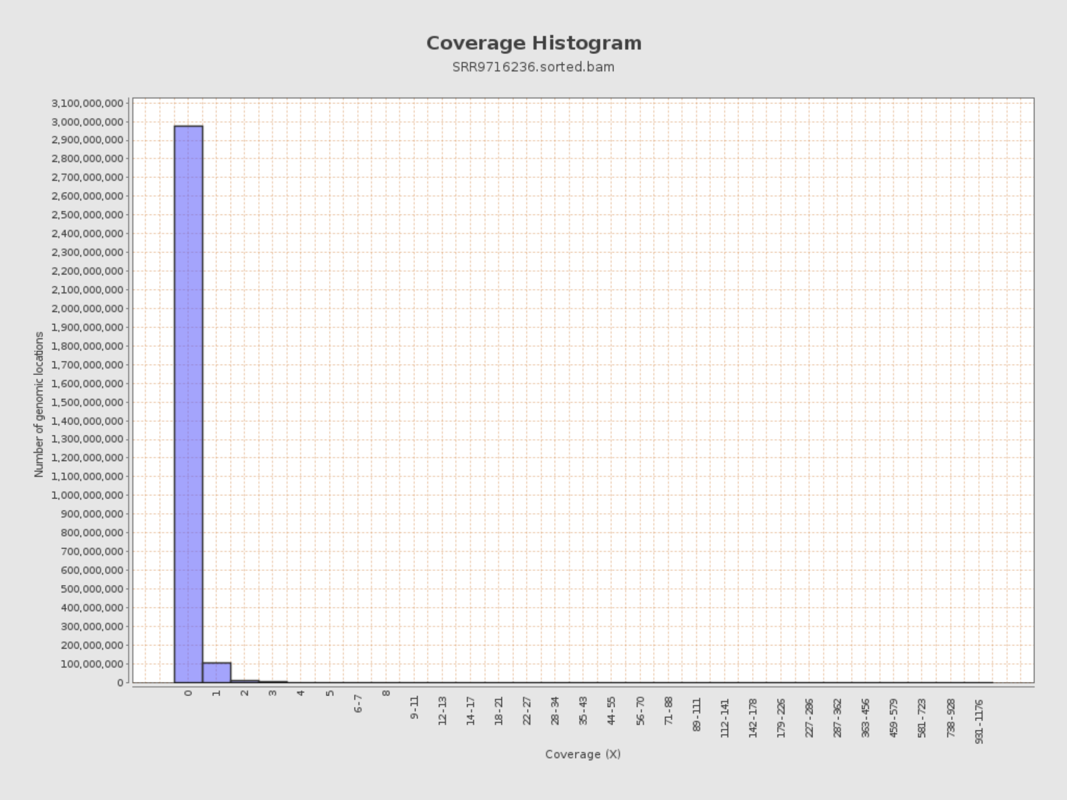
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11322480	0.0454	0.7905
chr2	243199373	12316452	0.0506	0.8198
chr3	198022430	9316032	0.047	0.25
chr4	191154276	9232881	0.0483	0.2791
chr5	180915260	8617996	0.0476	0.259
chr6	171115067	8353401	0.0488	0.3311
chr7	159138663	7932168	0.0498	0.6917

chr8	146364022	7267182	0.0497	0.7265
chr9	141213431	6080112	0.0431	0.5922
chr10	135534747	6728155	0.0496	0.4727
chr11	135006516	6481145	0.048	0.5196
chr12	133851895	6534411	0.0488	0.262
chr13	115169878	4373089	0.038	0.2199
chr14	107349540	4225344	0.0394	0.3311
chr15	102531392	4071189	0.0397	0.2317
chr16	90354753	4112805	0.0455	0.2894
chr17	81195210	3937002	0.0485	0.2943
chr18	78077248	4044420	0.0518	1.1206
chr19	59128983	3063307	0.0518	0.6174
chr20	63025520	2915283	0.0463	0.2759
chr21	48129895	1834632	0.0381	0.251
chr22	51304566	1630488	0.0318	0.2049
chrMT	16571	9751	0.5884	0.8886
chrX	155270560	8227097	0.053	0.4013
chrY	59373566	372940	0.0063	0.1676

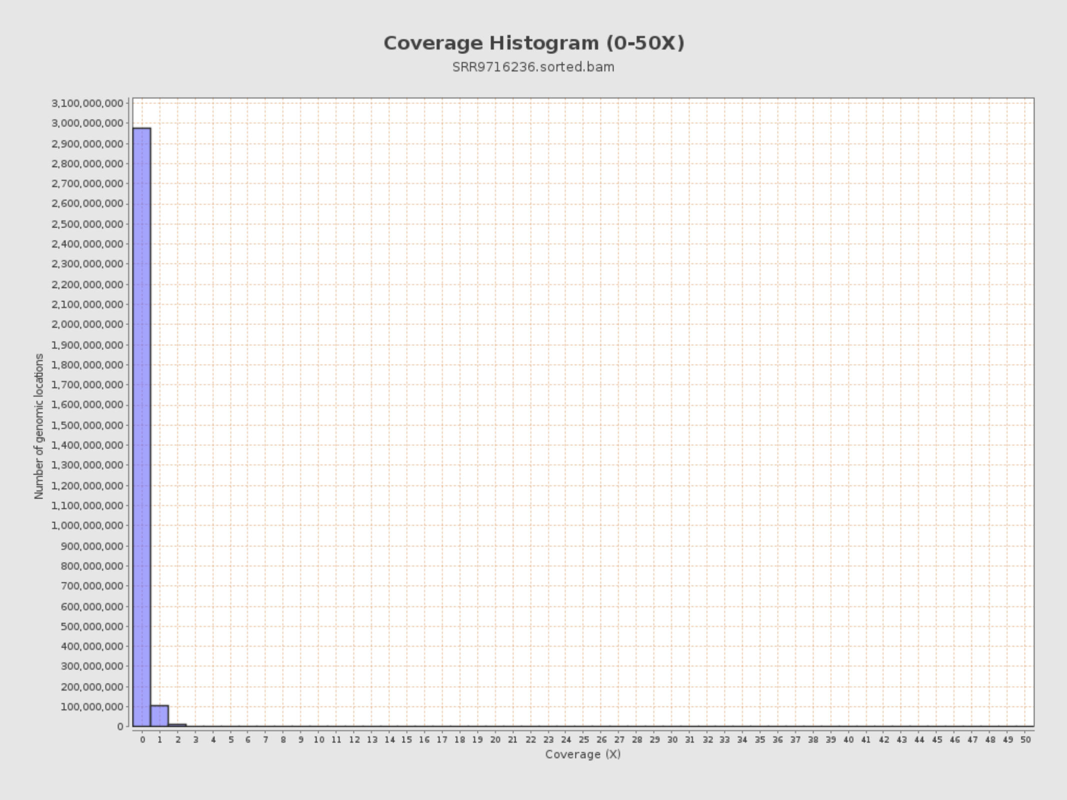
3. Results : Coverage across reference



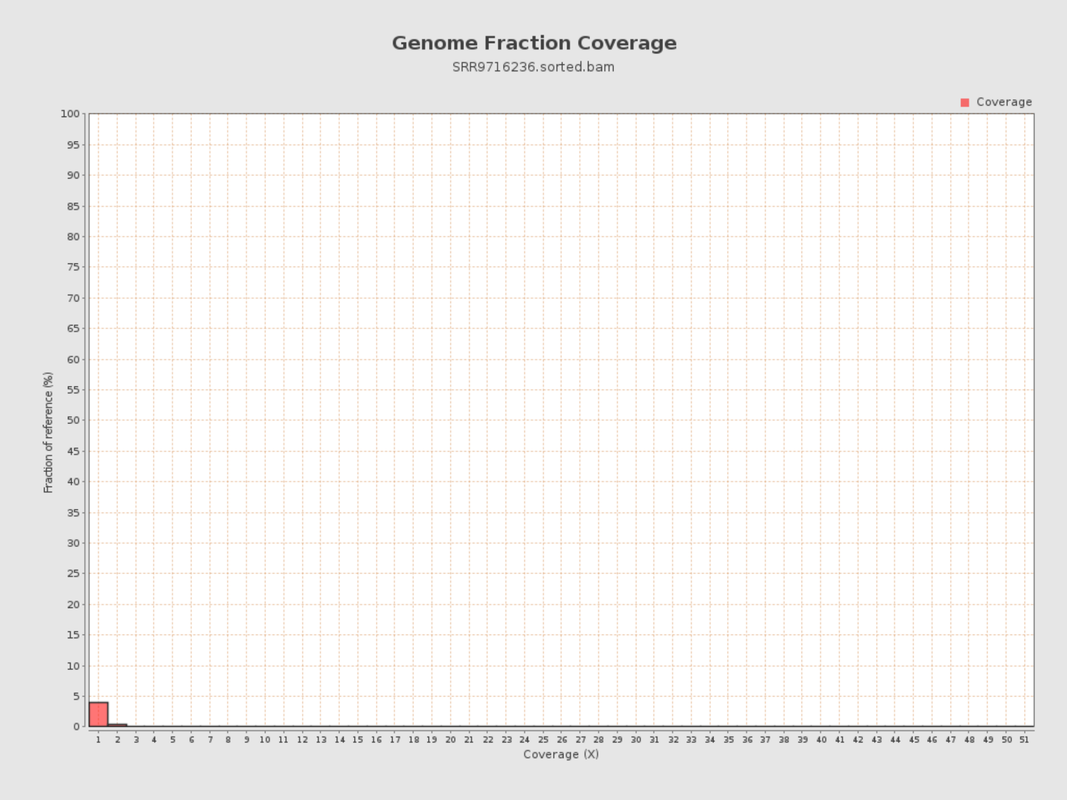
4. Results : Coverage Histogram



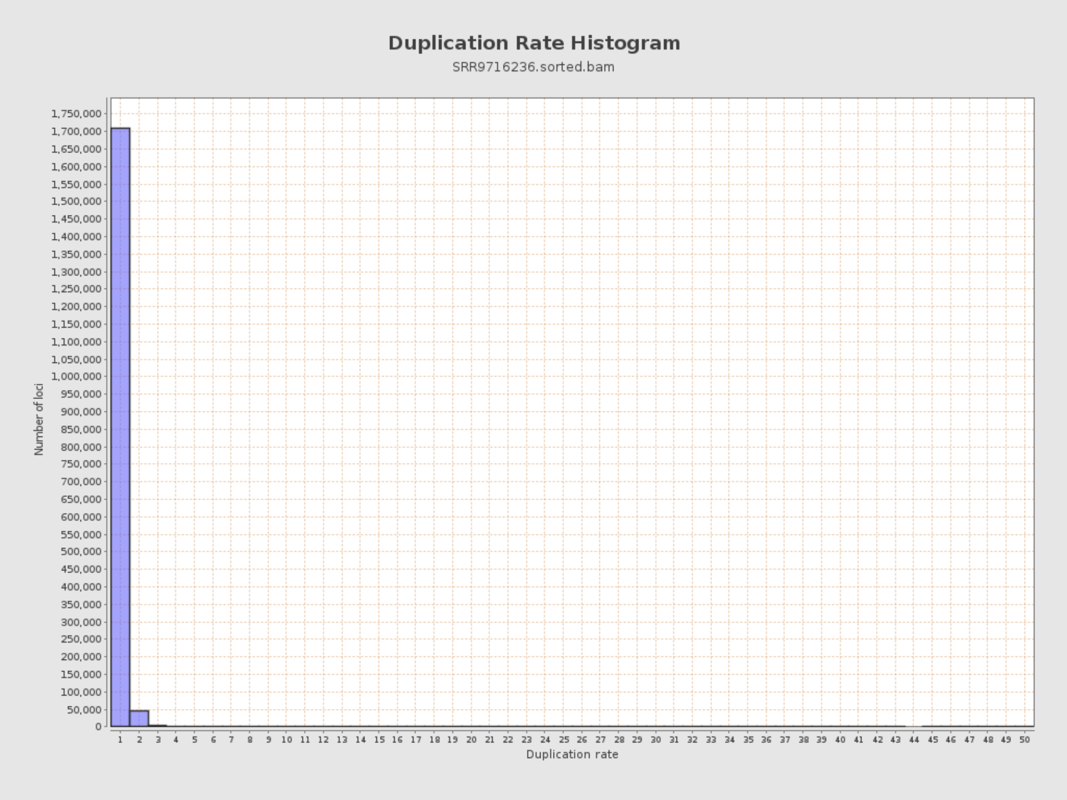
5. Results : Coverage Histogram (0-50X)



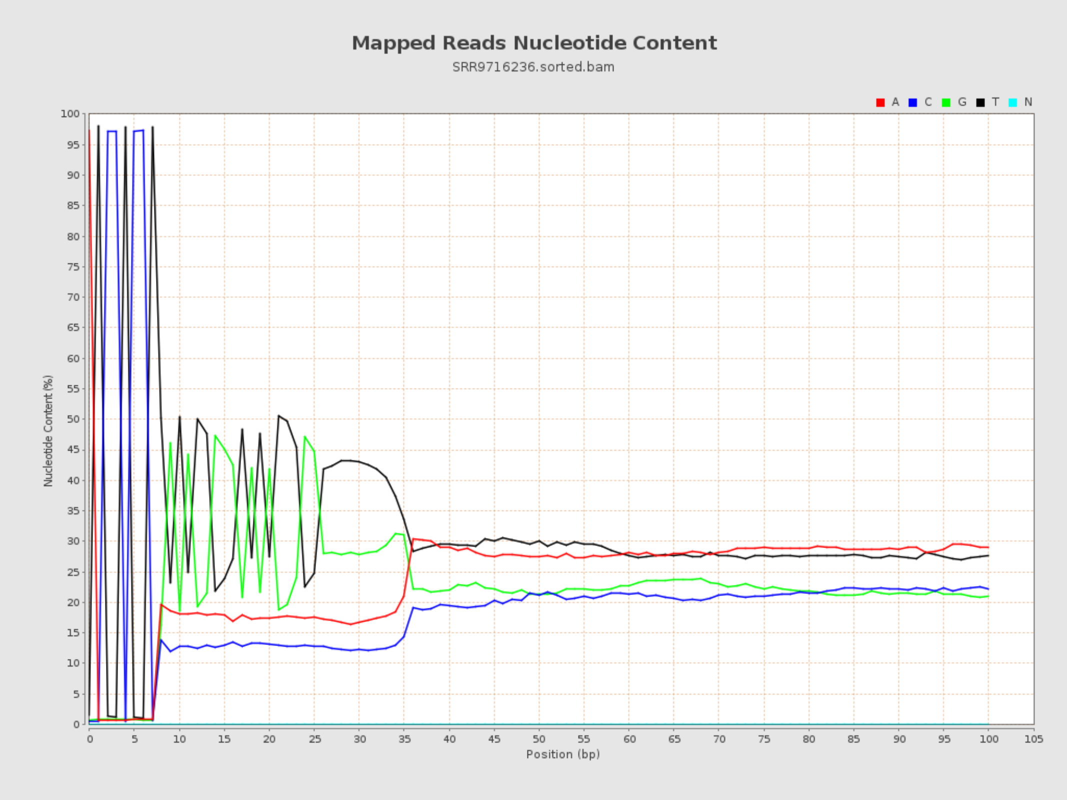
6. Results : Genome Fraction Coverage



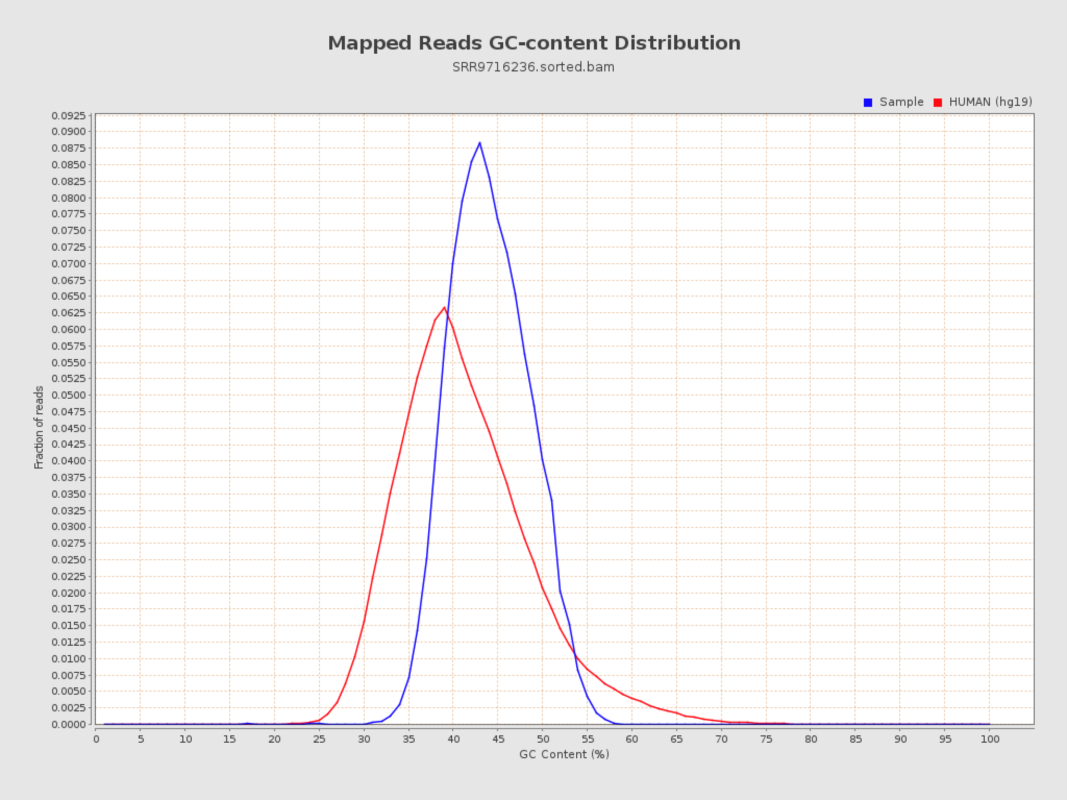
7. Results : Duplication Rate Histogram



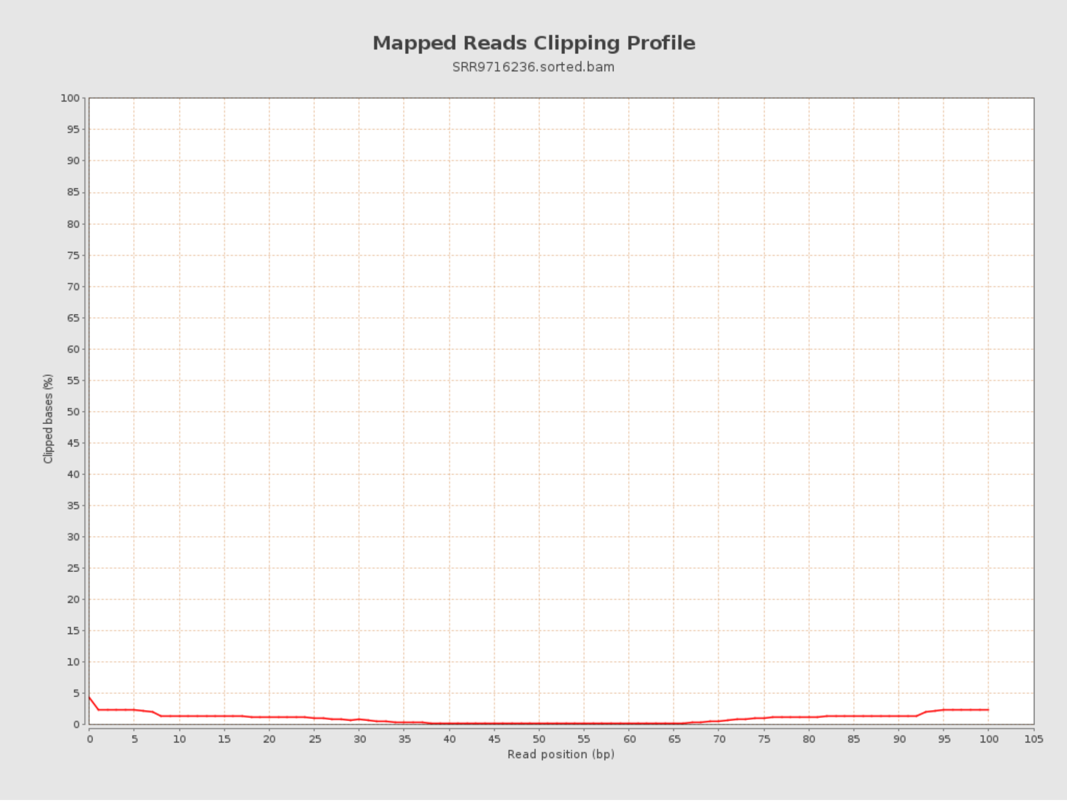
8. Results : Mapped Reads Nucleotide Content



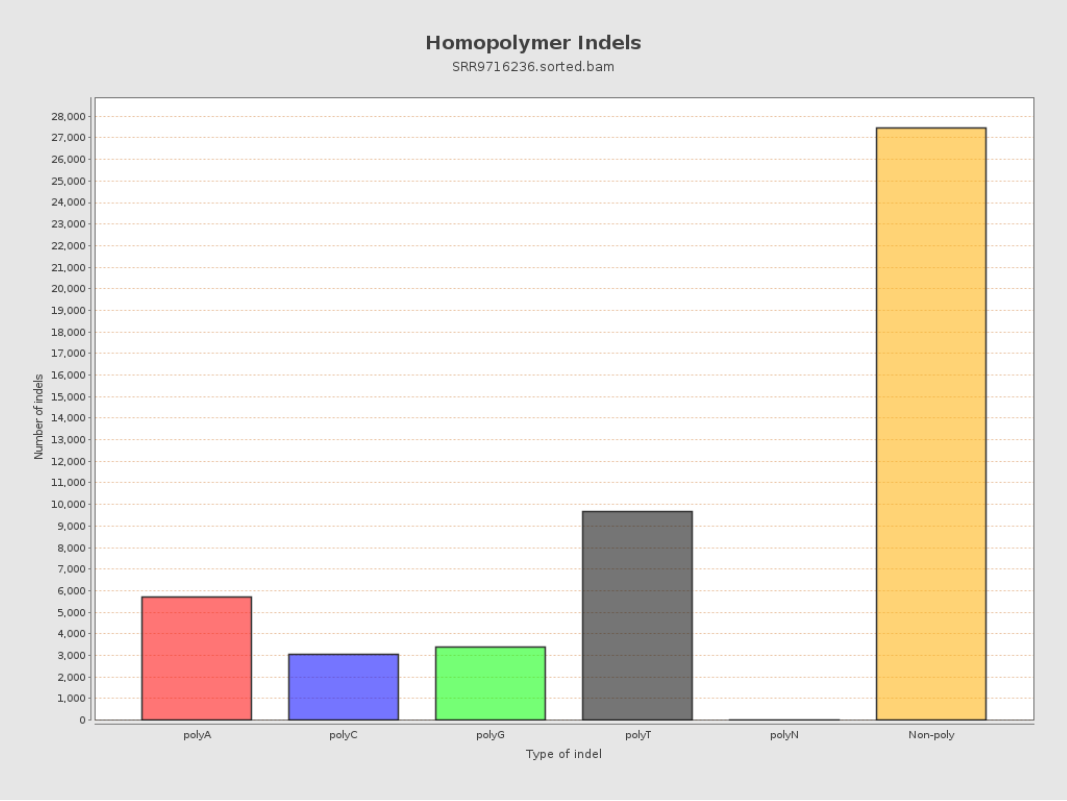
9. Results : Mapped Reads GC-content Distribution



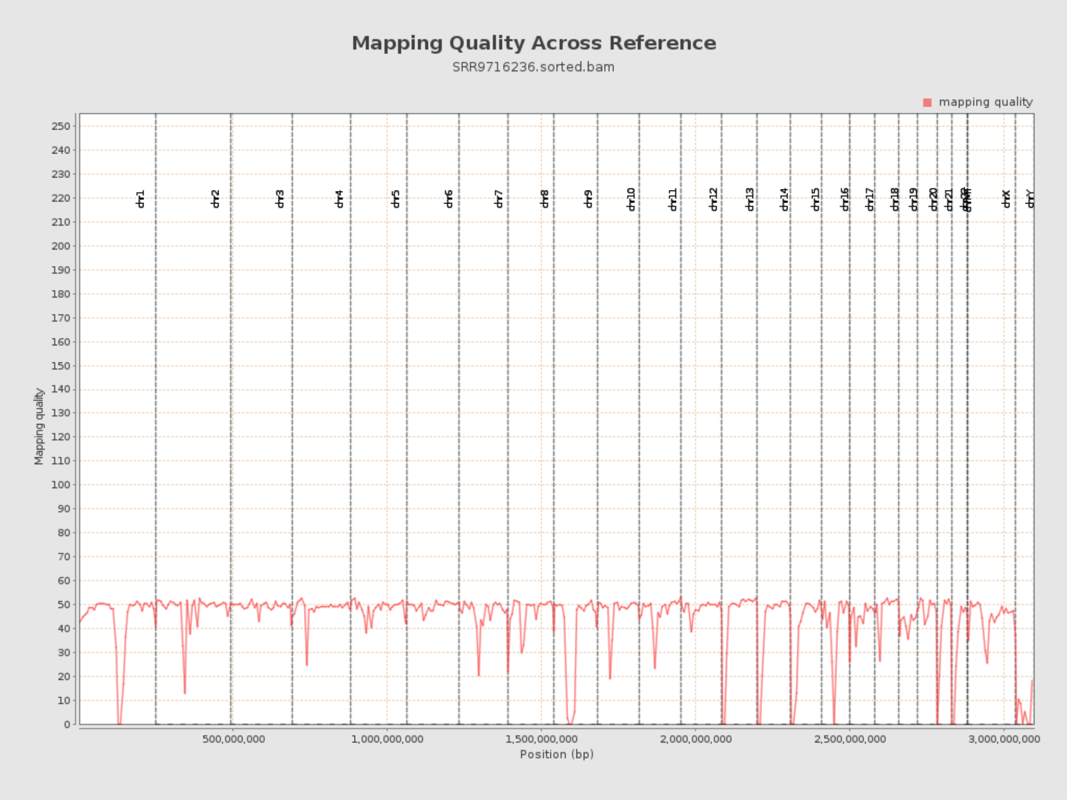
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram