Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:43:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716543.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_SRR9716543 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716543.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:43:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716543.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,545,157
Mapped reads	1,274,153 / 82.46%
Unmapped reads	271,004 / 17.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,325 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	47,633 / 3.08%
Duplication rate	2.93%
Clipped reads	1,277,209 / 82.66%

2.2. ACGT Content

Number/percentage of A's	18,667,772 / 25.47%
Number/percentage of C's	13,587,553 / 18.54%
Number/percentage of T's	23,713,157 / 32.35%
Number/percentage of G's	17,333,652 / 23.65%
Number/percentage of N's	2,036 / 0%
GC Percentage	42.18%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.226

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

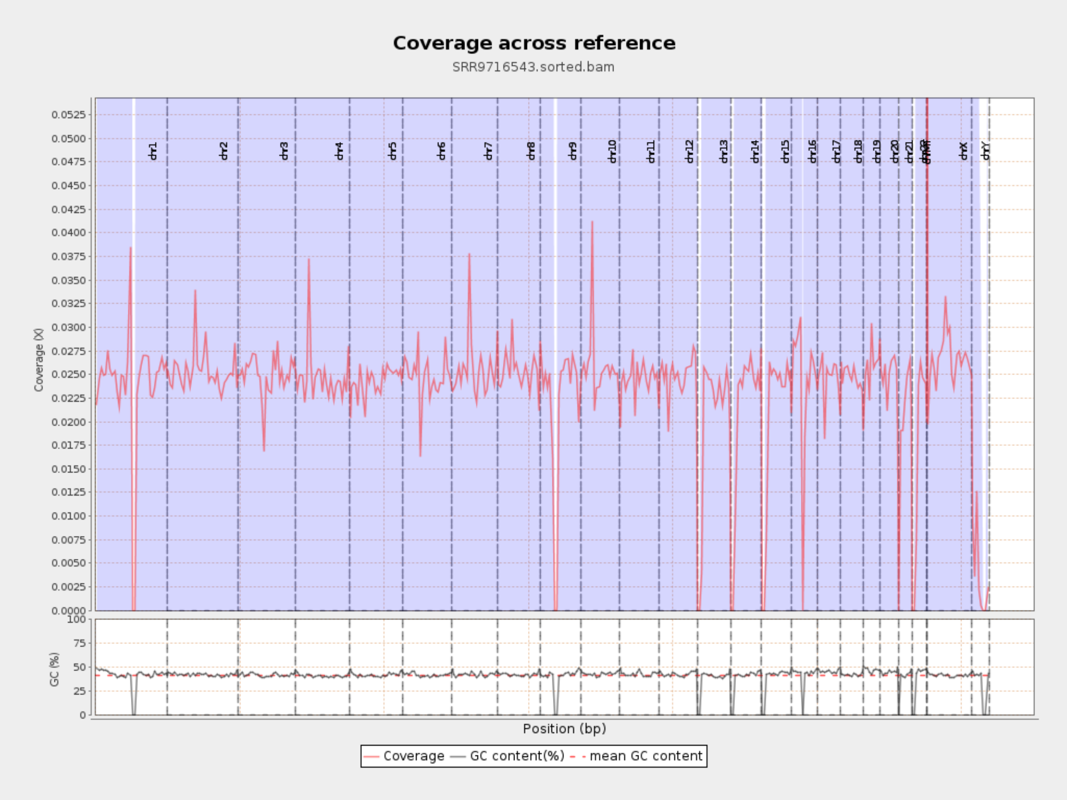
General error rate	0.51%
Mismatches	365,805
Insertions	5,584
Mapped reads with at least one insertion	0.44%
Deletions	13,192
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.18%

2.6. Chromosome stats

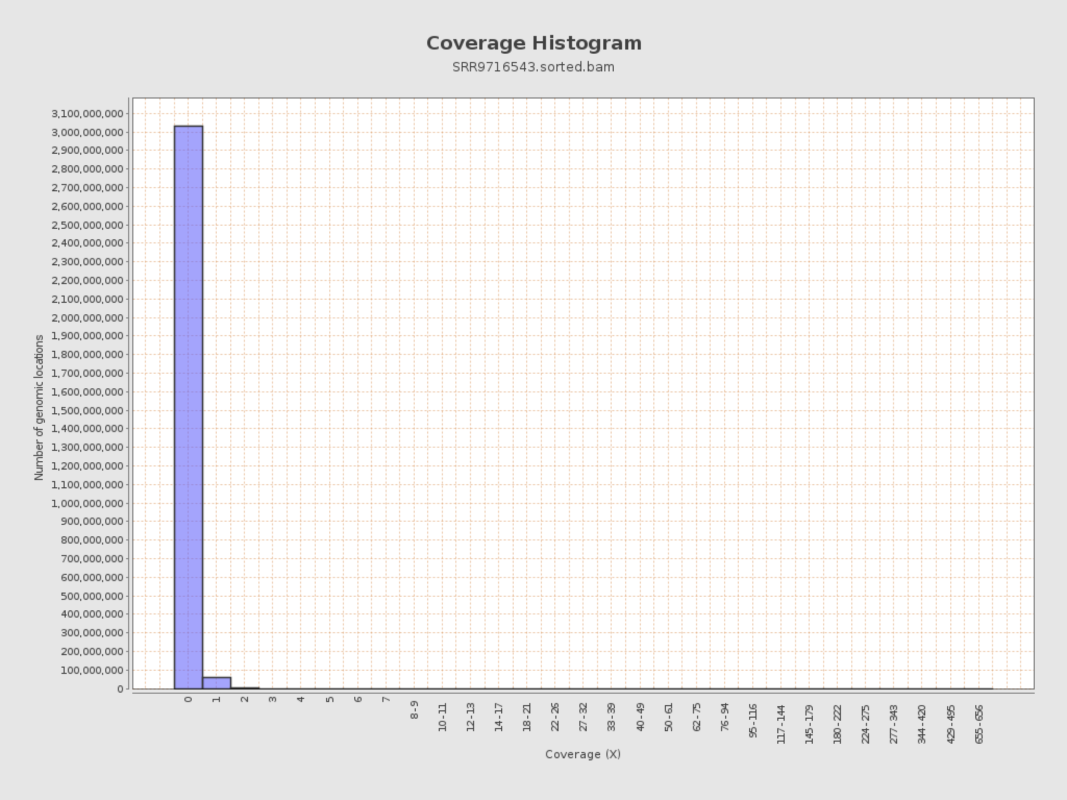
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5923553	0.0238	0.3774
chr2	243199373	6164719	0.0253	0.3161
chr3	198022430	4944594	0.025	0.172
chr4	191154276	4731881	0.0248	0.1833
chr5	180915260	4415964	0.0244	0.1703
chr6	171115067	4225956	0.0247	0.1932
chr7	159138663	4058212	0.0255	0.259

chr8	146364022	3702802	0.0253	0.2136
chr9	141213431	3067198	0.0217	0.1897
chr10	135534747	3510559	0.0259	0.2245
chr11	135006516	3324097	0.0246	0.1993
chr12	133851895	3340510	0.025	0.1749
chr13	115169878	2282558	0.0198	0.1549
chr14	107349540	2205274	0.0205	0.1591
chr15	102531392	2070109	0.0202	0.1572
chr16	90354753	2136575	0.0236	0.178
chr17	81195210	1994306	0.0246	0.1761
chr18	78077248	1933933	0.0248	0.2975
chr19	59128983	1531312	0.0259	0.2849
chr20	63025520	1565705	0.0248	0.1742
chr21	48129895	972789	0.0202	0.1663
chr22	51304566	864343	0.0168	0.1404
chrMT	16571	4304	0.2597	0.5799
chrX	155270560	4137563	0.0266	0.1919
chrY	59373566	216295	0.0036	0.1003

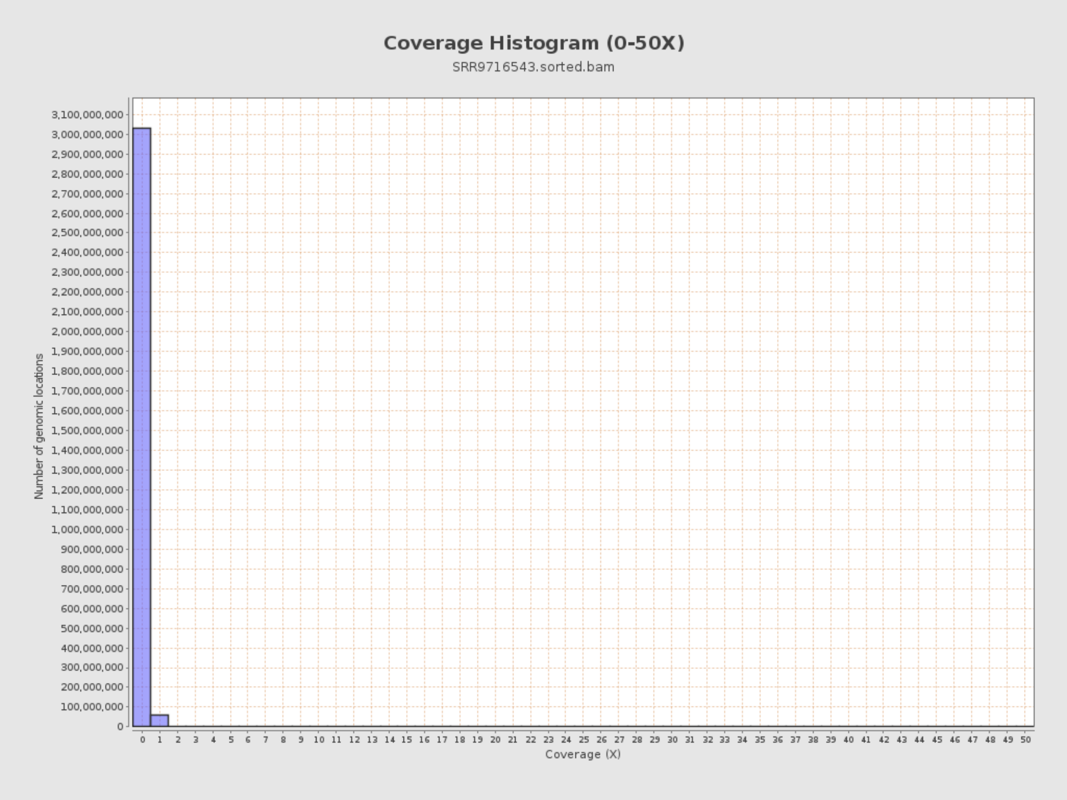
3. Results : Coverage across reference



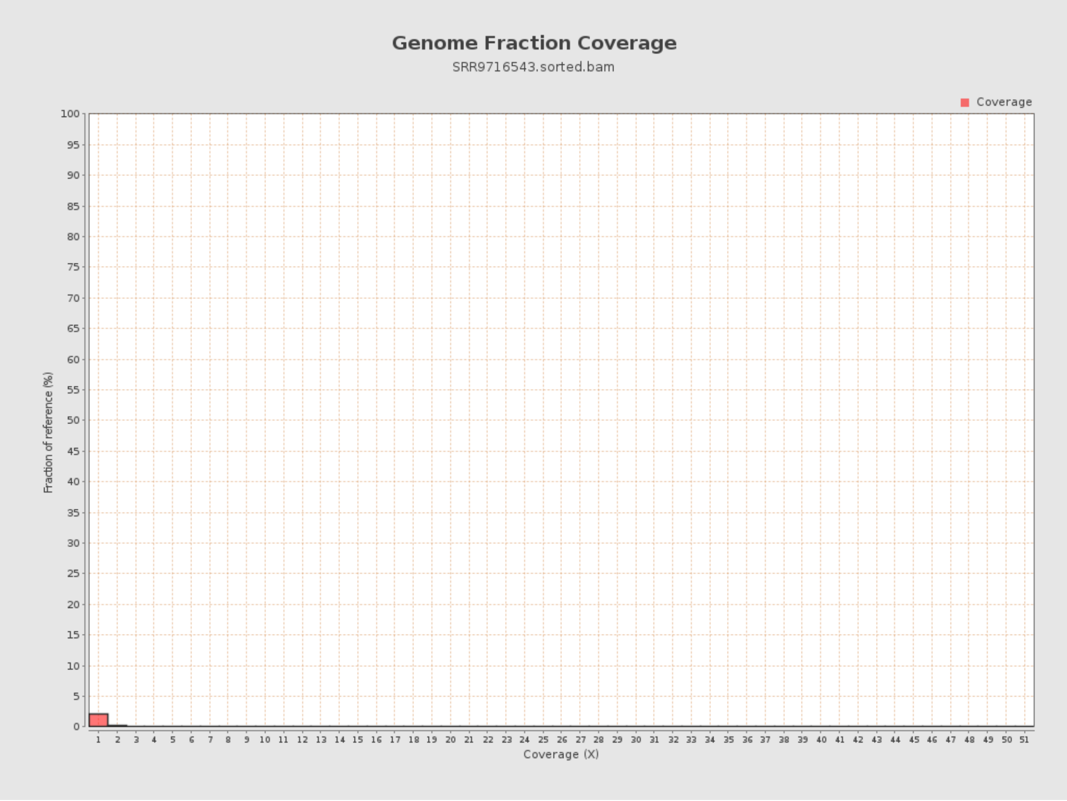
4. Results : Coverage Histogram



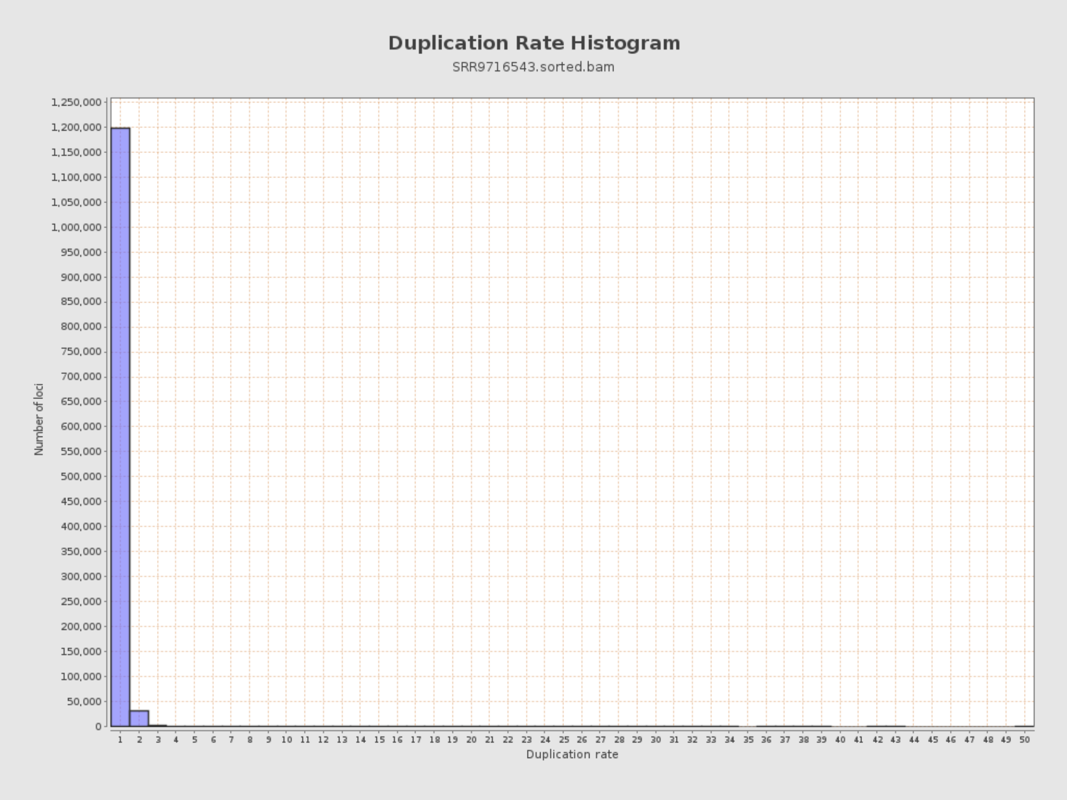
5. Results : Coverage Histogram (0-50X)



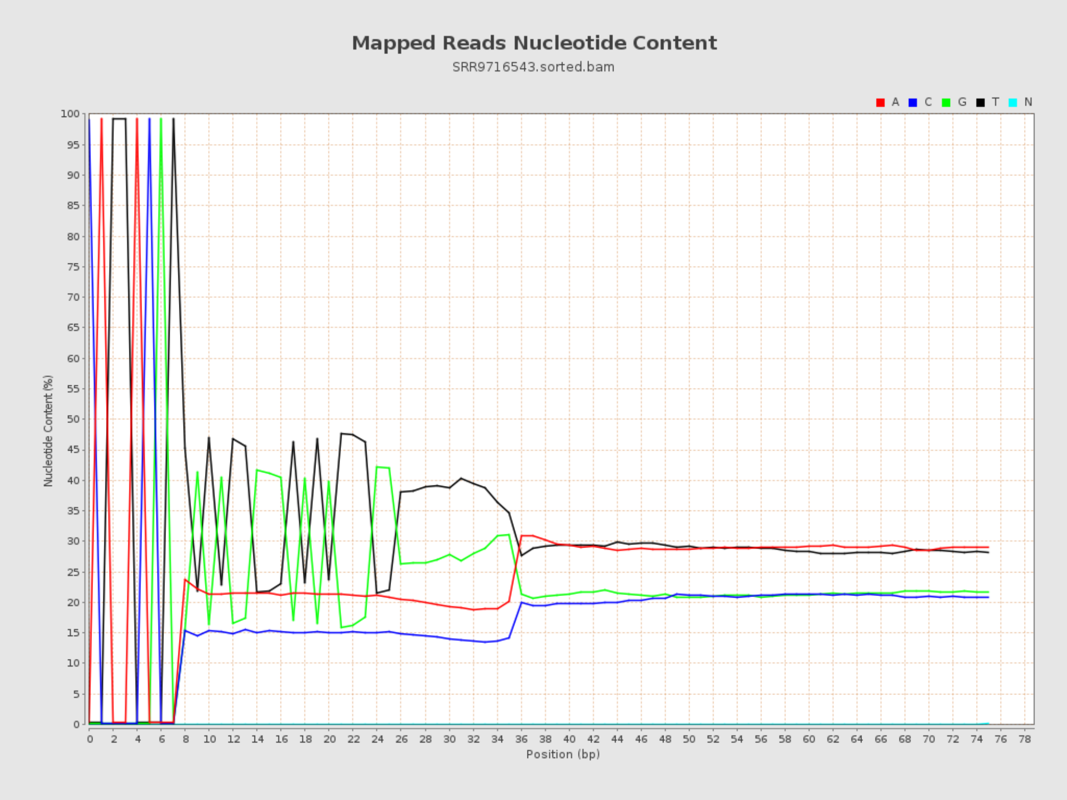
6. Results : Genome Fraction Coverage



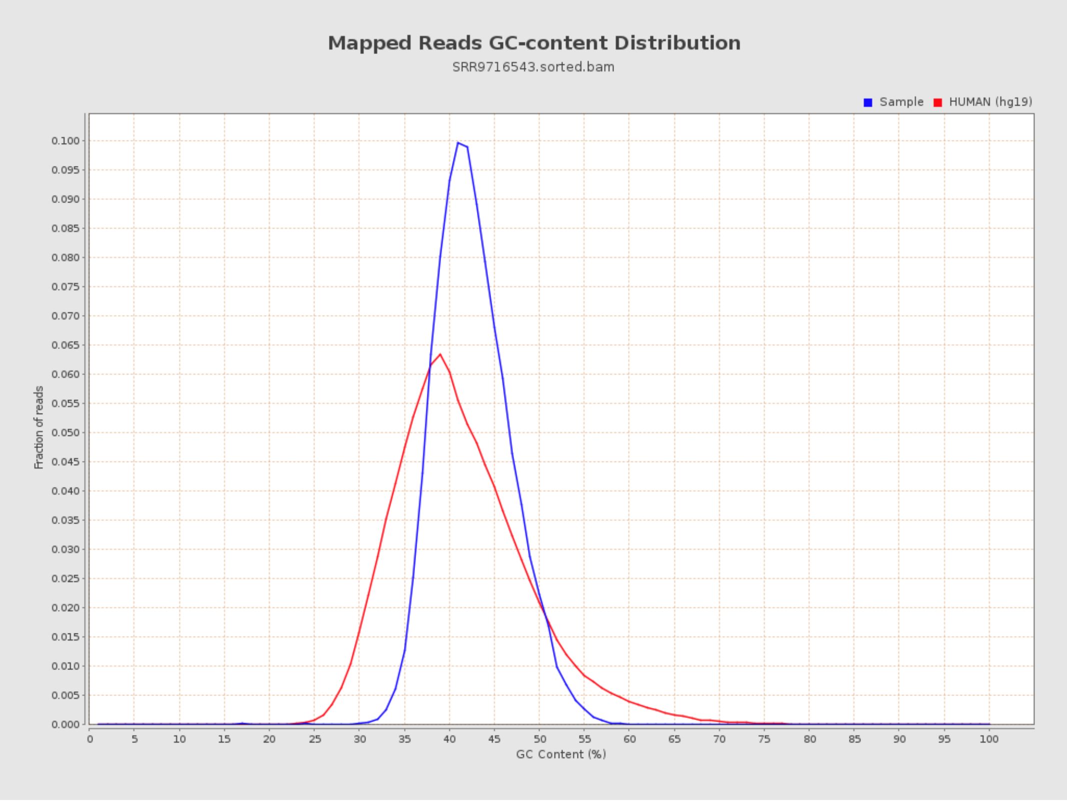
7. Results : Duplication Rate Histogram



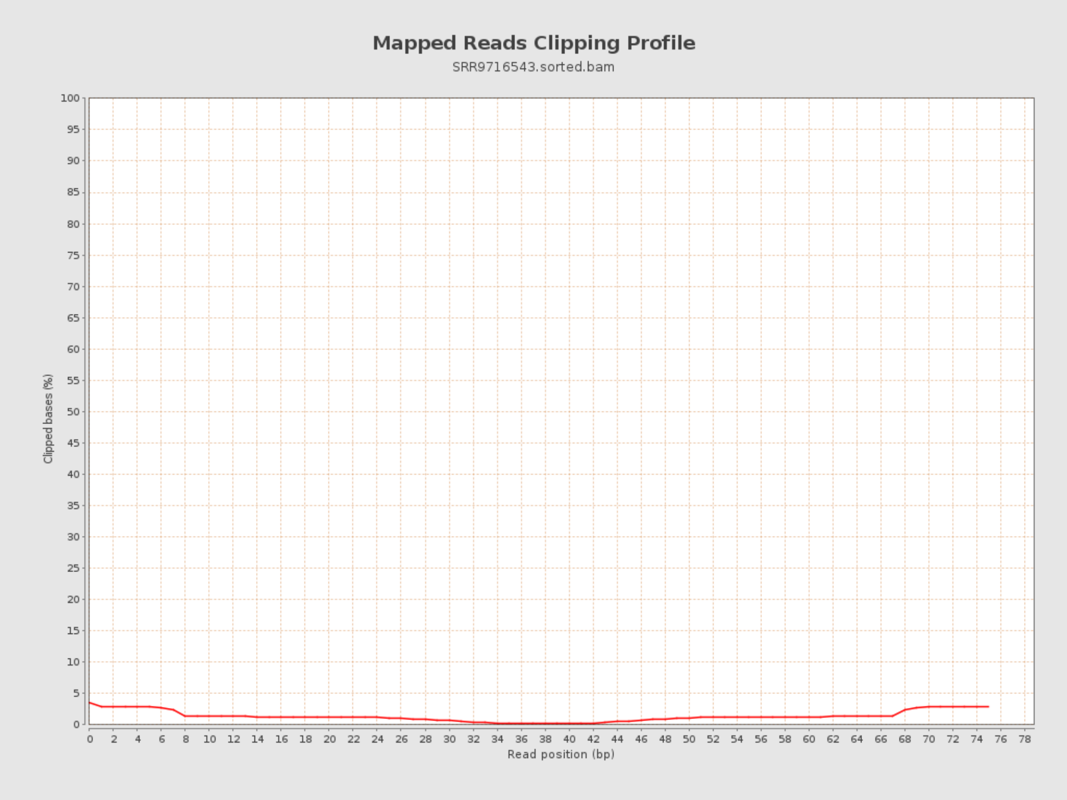
8. Results : Mapped Reads Nucleotide Content



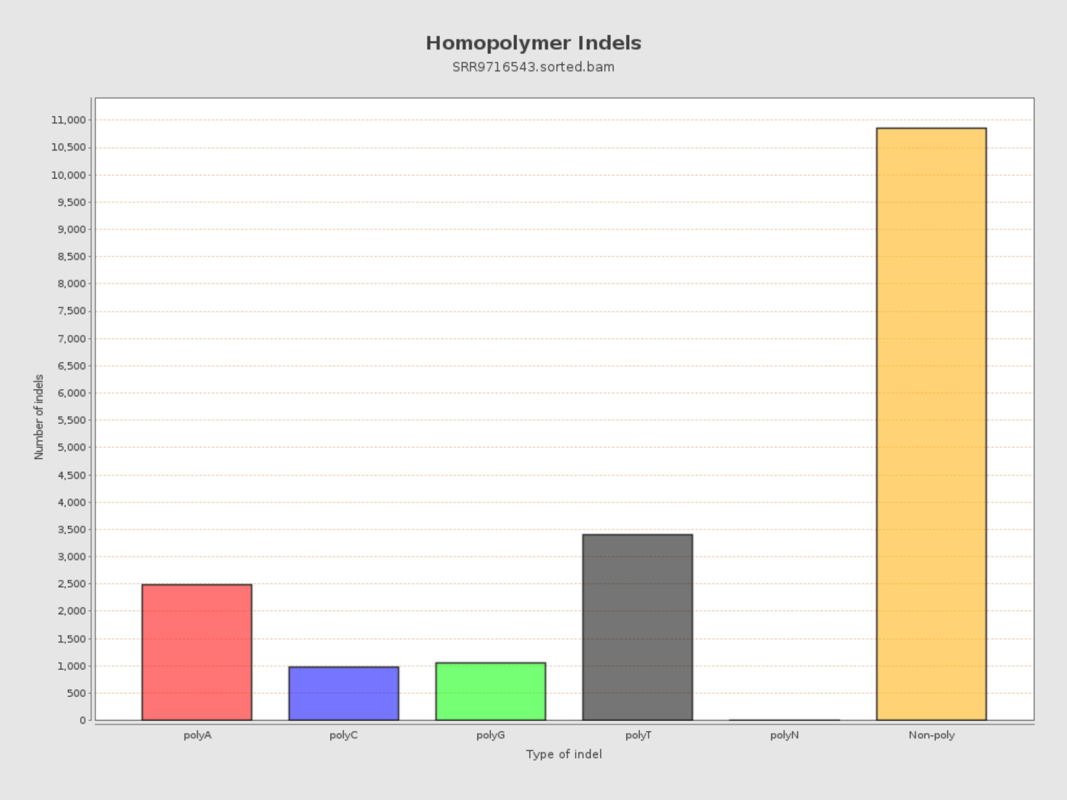
9. Results : Mapped Reads GC-content Distribution



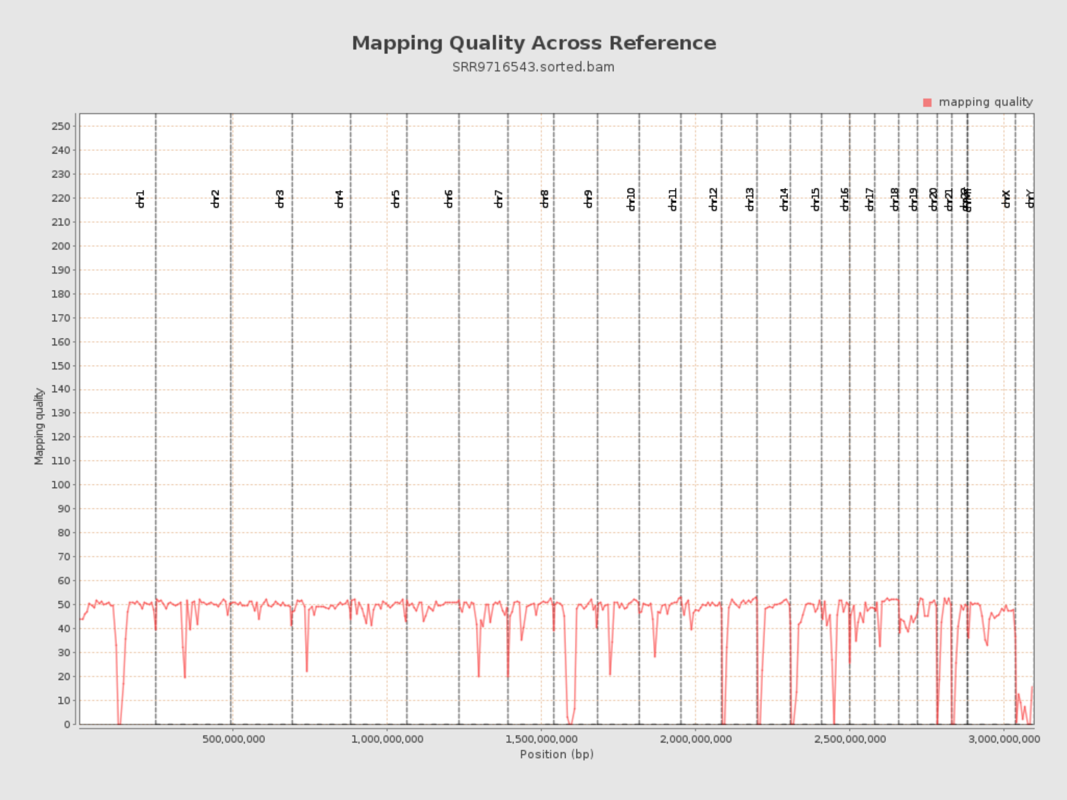
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram