Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:35:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716964.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_SRR9716964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716964.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:35:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	933,986
Mapped reads	872,389 / 93.4%
Unmapped reads	61,597 / 6.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,282 / 2.17%
Read min/max/mean length	30 / 101 / 101.8
Duplicated reads (estimated)	27,918 / 2.99%
Duplication rate	2.42%
Clipped reads	891,041 / 95.4%

2.2. ACGT Content

Number/percentage of A's	17,449,919 / 25.43%
Number/percentage of C's	13,675,824 / 19.93%
Number/percentage of T's	20,208,578 / 29.45%
Number/percentage of G's	17,282,440 / 25.19%
Number/percentage of N's	2,576 / 0%
GC Percentage	45.12%

2.3. Coverage

Mean	0.0222

Standard Deviation	0.2056

2.4. Mapping Quality

Mean Mapping Quality	47.11

2.5. Mismatches and indels

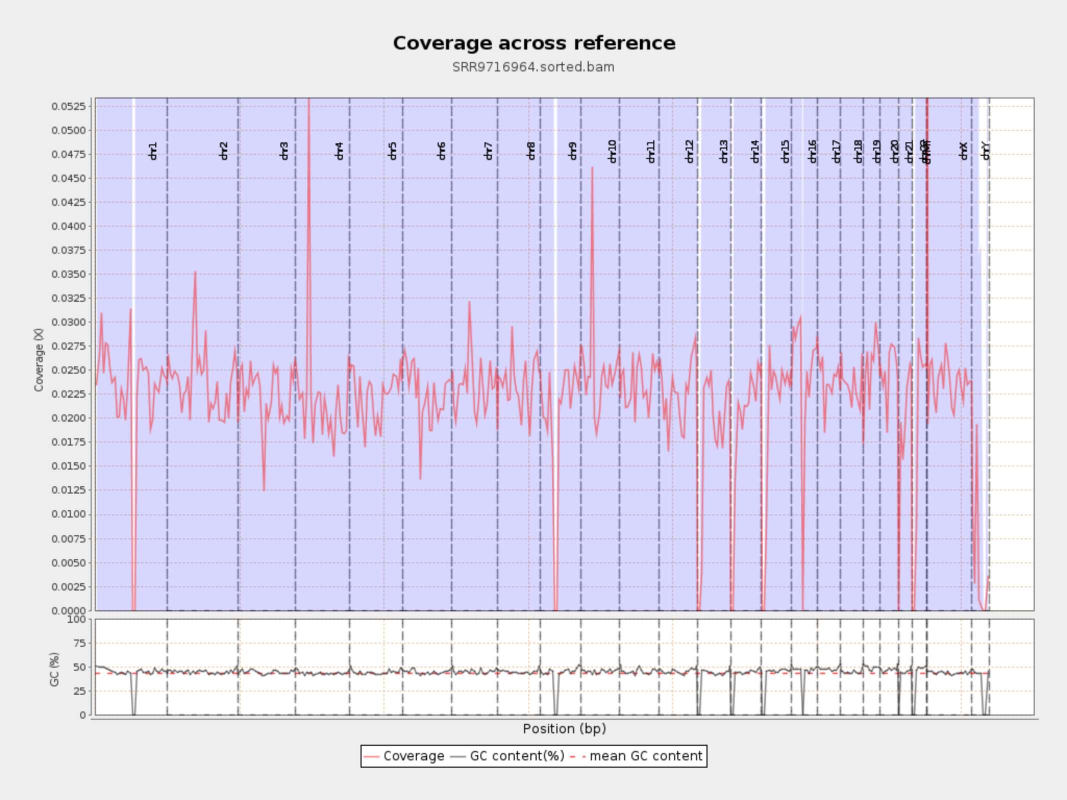
General error rate	0.67%
Mismatches	441,884
Insertions	6,561
Mapped reads with at least one insertion	0.74%
Deletions	13,233
Mapped reads with at least one deletion	1.49%
Homopolymer indels	38.2%

2.6. Chromosome stats

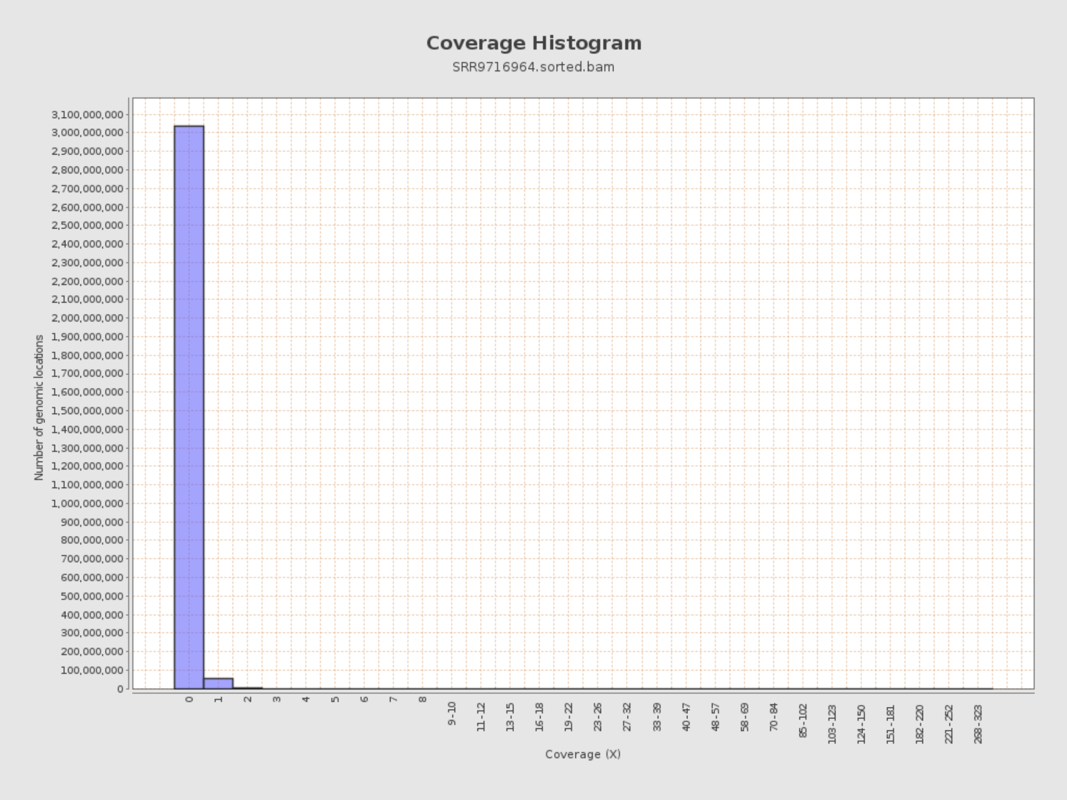
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5658829	0.0227	0.2866
chr2	243199373	5806589	0.0239	0.2214
chr3	198022430	4419811	0.0223	0.161
chr4	191154276	4256045	0.0223	0.2245
chr5	180915260	4052689	0.0224	0.1619
chr6	171115067	3860443	0.0226	0.1669
chr7	159138663	3753752	0.0236	0.2478

chr8	146364022	3463746	0.0237	0.1998
chr9	141213431	2805723	0.0199	0.1818
chr10	135534747	3404621	0.0251	0.277
chr11	135006516	3200436	0.0237	0.2138
chr12	133851895	3032804	0.0227	0.1647
chr13	115169878	2058391	0.0179	0.1451
chr14	107349540	2031364	0.0189	0.1615
chr15	102531392	2007885	0.0196	0.1521
chr16	90354753	2167048	0.024	0.178
chr17	81195210	1946426	0.024	0.182
chr18	78077248	1820887	0.0233	0.2607
chr19	59128983	1506822	0.0255	0.2226
chr20	63025520	1571006	0.0249	0.1808
chr21	48129895	922747	0.0192	0.1904
chr22	51304566	936374	0.0183	0.1481
chrMT	16571	7599	0.4586	0.7915
chrX	155270560	3688971	0.0238	0.1738
chrY	59373566	266366	0.0045	0.2097

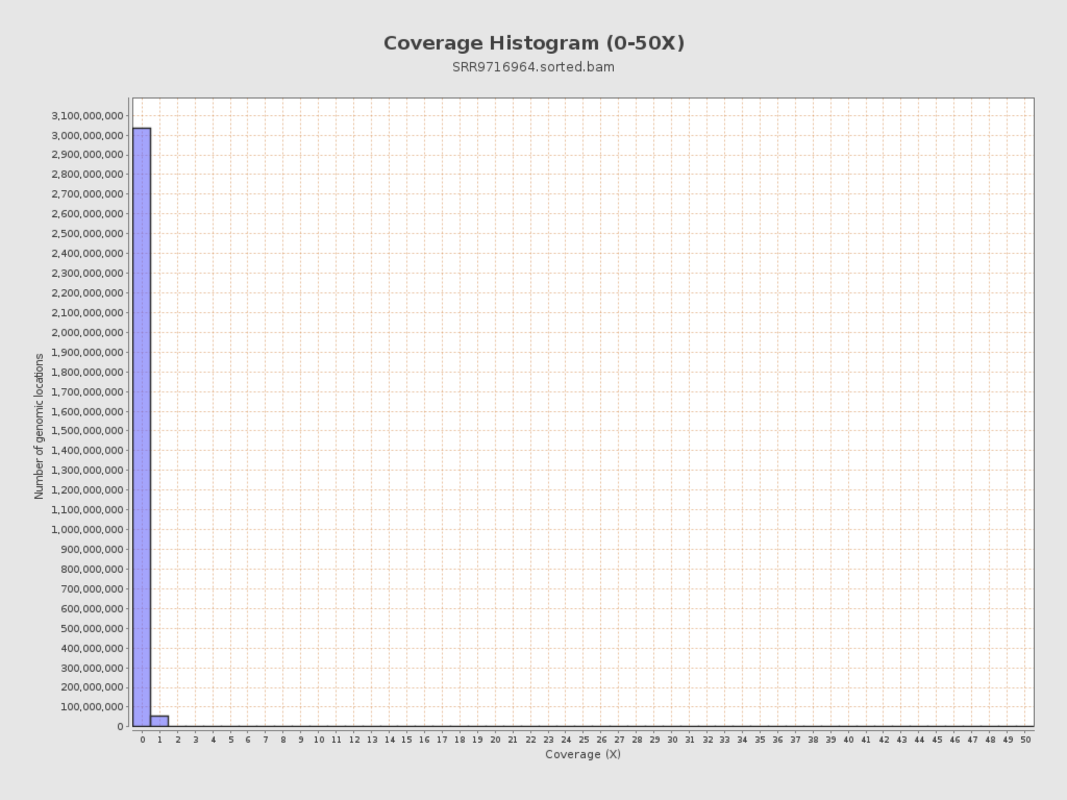
3. Results : Coverage across reference



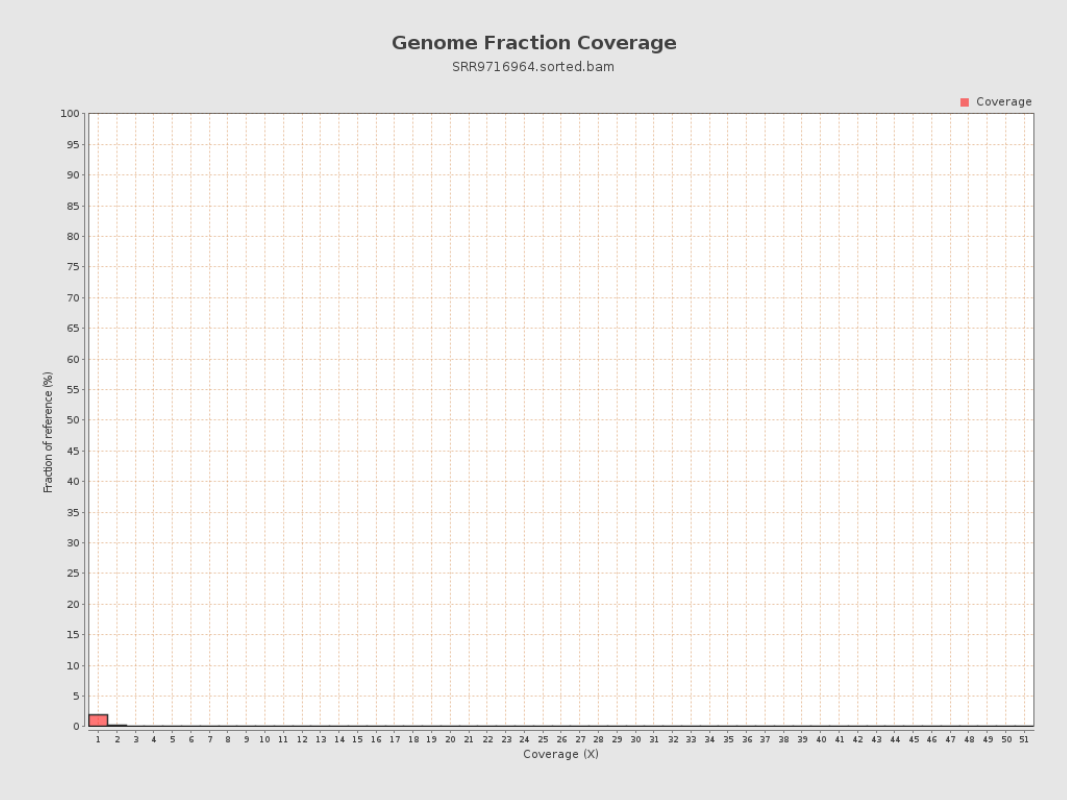
4. Results : Coverage Histogram



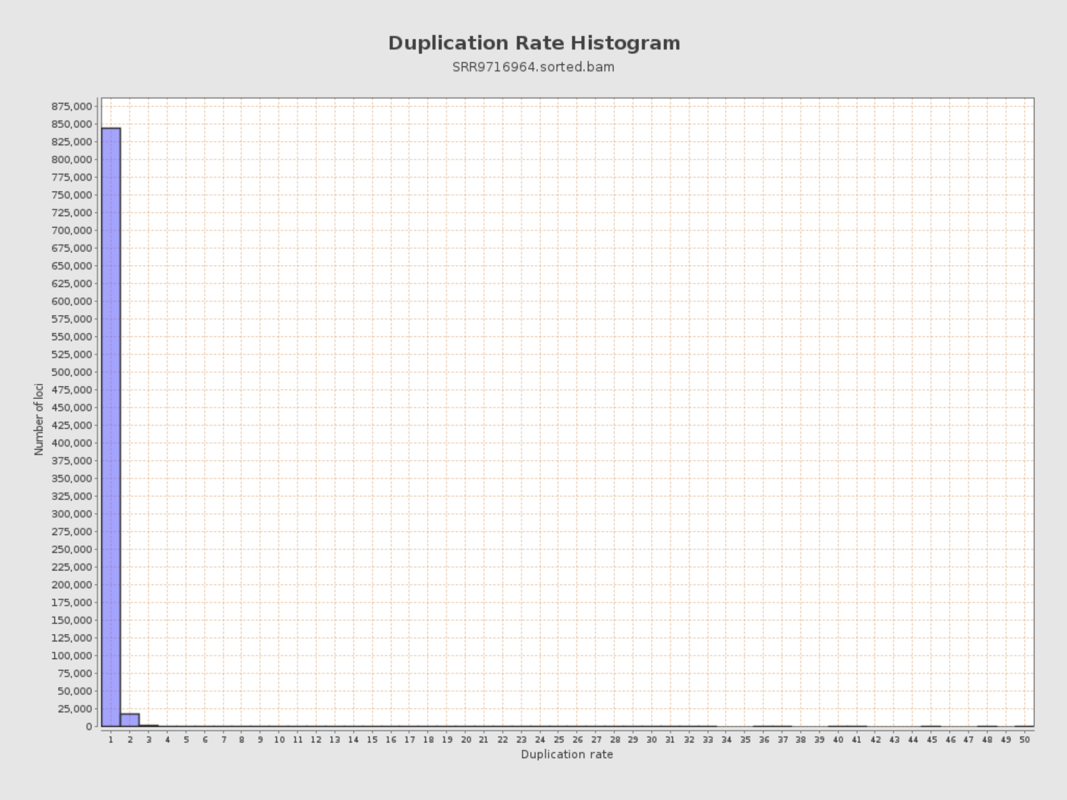
5. Results : Coverage Histogram (0-50X)



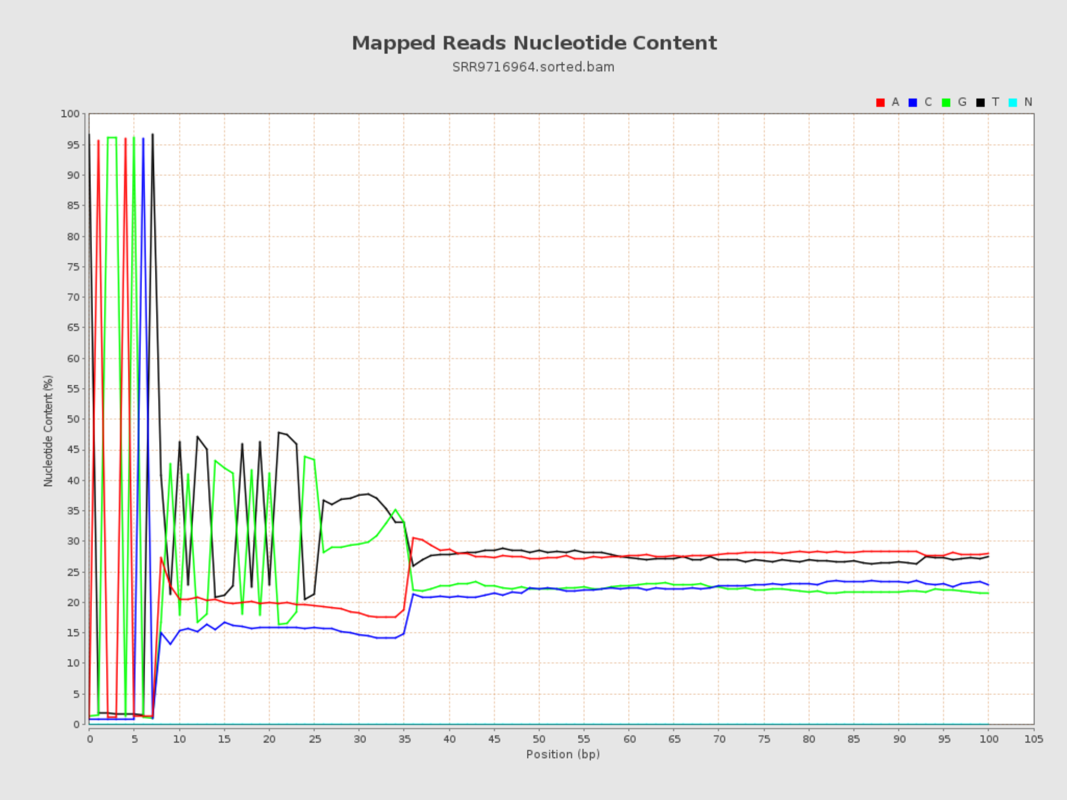
6. Results : Genome Fraction Coverage



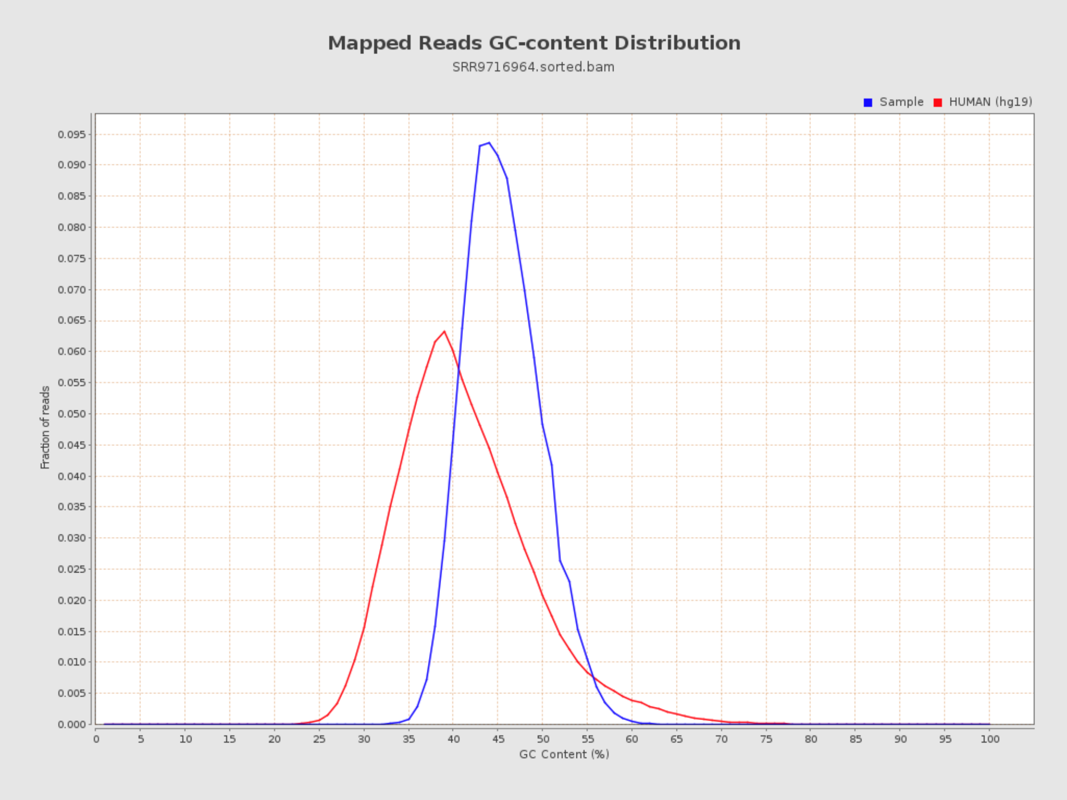
7. Results : Duplication Rate Histogram



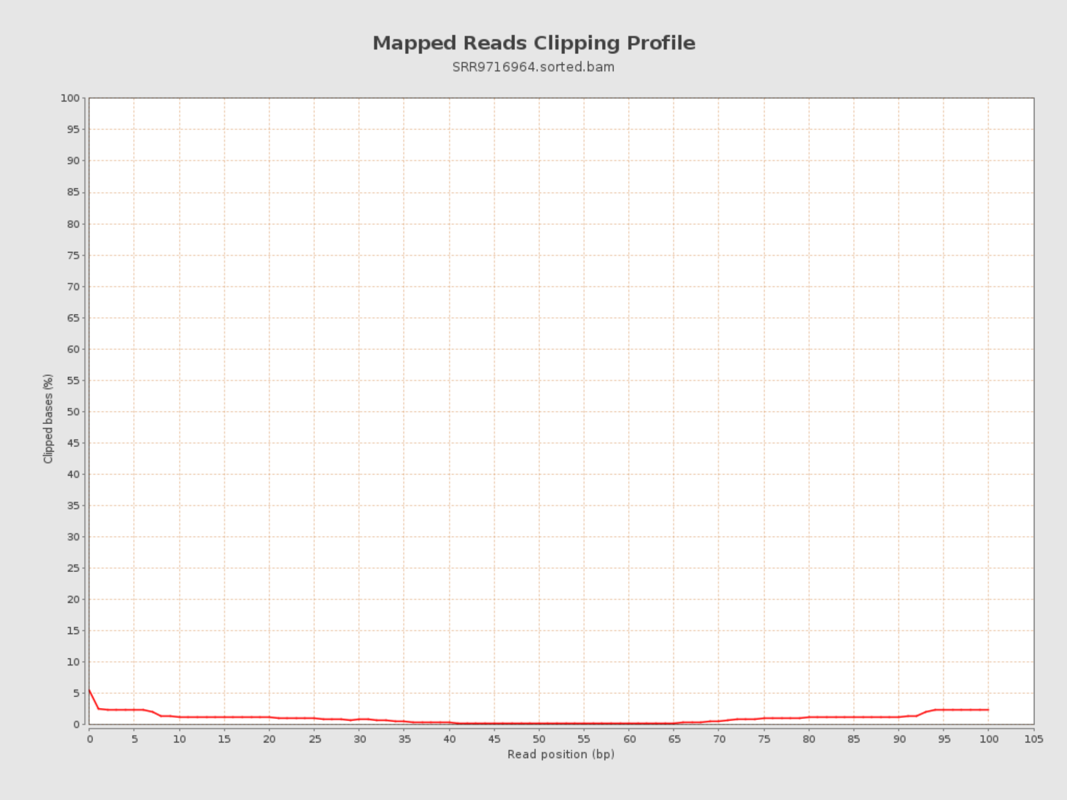
8. Results : Mapped Reads Nucleotide Content



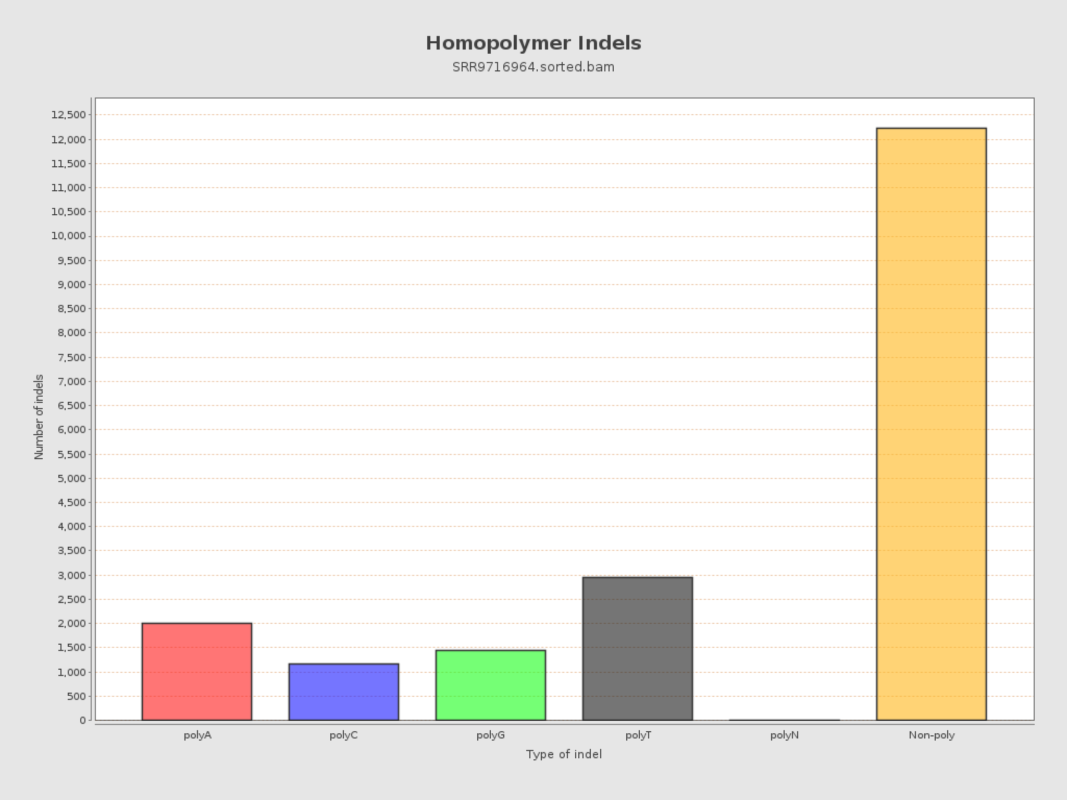
9. Results : Mapped Reads GC-content Distribution



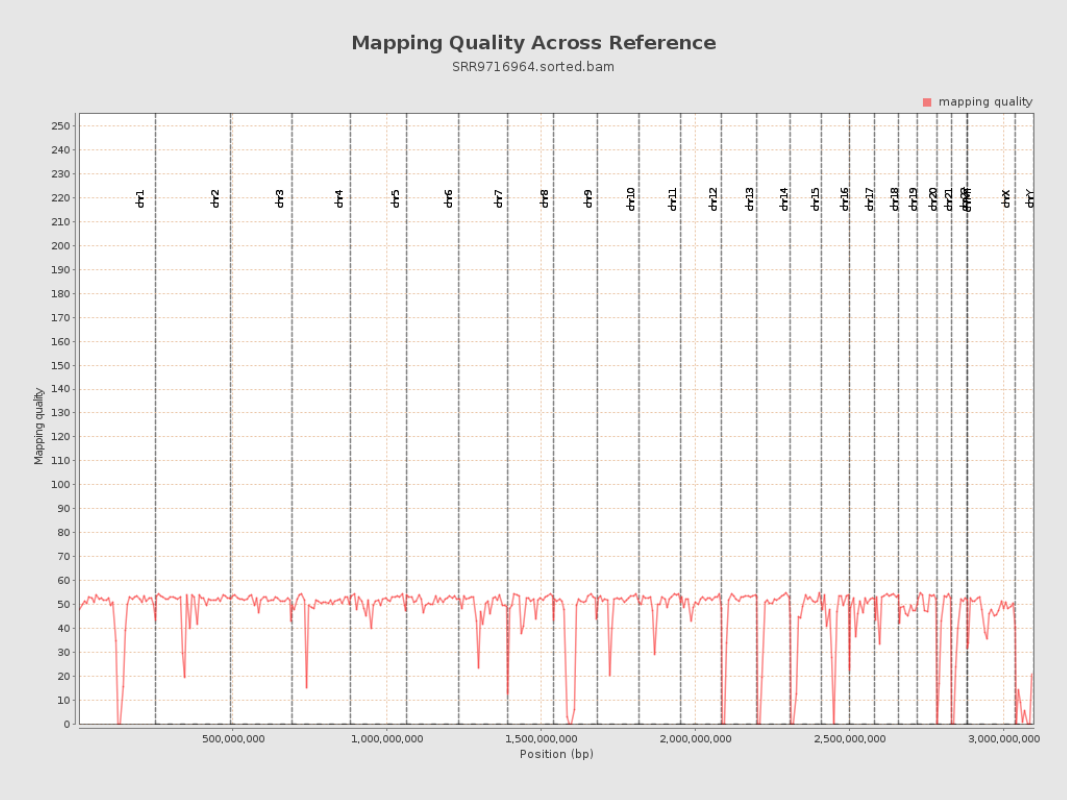
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram