Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:55:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716253.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_SRR9716253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716253.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:55:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,192,555
Mapped reads	2,046,258 / 93.33%
Unmapped reads	146,297 / 6.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,182 / 1.83%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	115,751 / 5.28%
Duplication rate	4.4%
Clipped reads	2,081,603 / 94.94%

2.2. ACGT Content

Number/percentage of A's	40,640,103 / 25.58%
Number/percentage of C's	32,325,923 / 20.35%
Number/percentage of T's	46,144,466 / 29.04%
Number/percentage of G's	39,757,135 / 25.02%
Number/percentage of N's	5,987 / 0%
GC Percentage	45.37%

2.3. Coverage

Mean	0.0513

Standard Deviation	0.4142

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

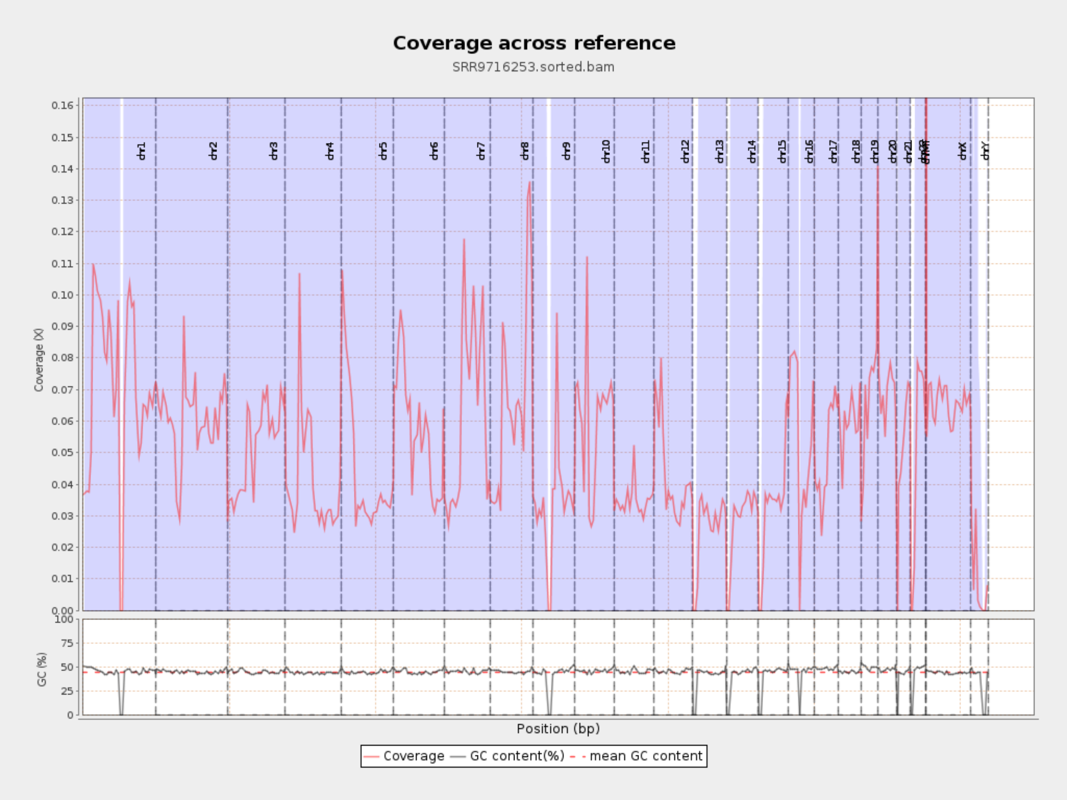
General error rate	0.68%
Mismatches	1,037,644
Insertions	14,617
Mapped reads with at least one insertion	0.7%
Deletions	28,950
Mapped reads with at least one deletion	1.39%
Homopolymer indels	38.77%

2.6. Chromosome stats

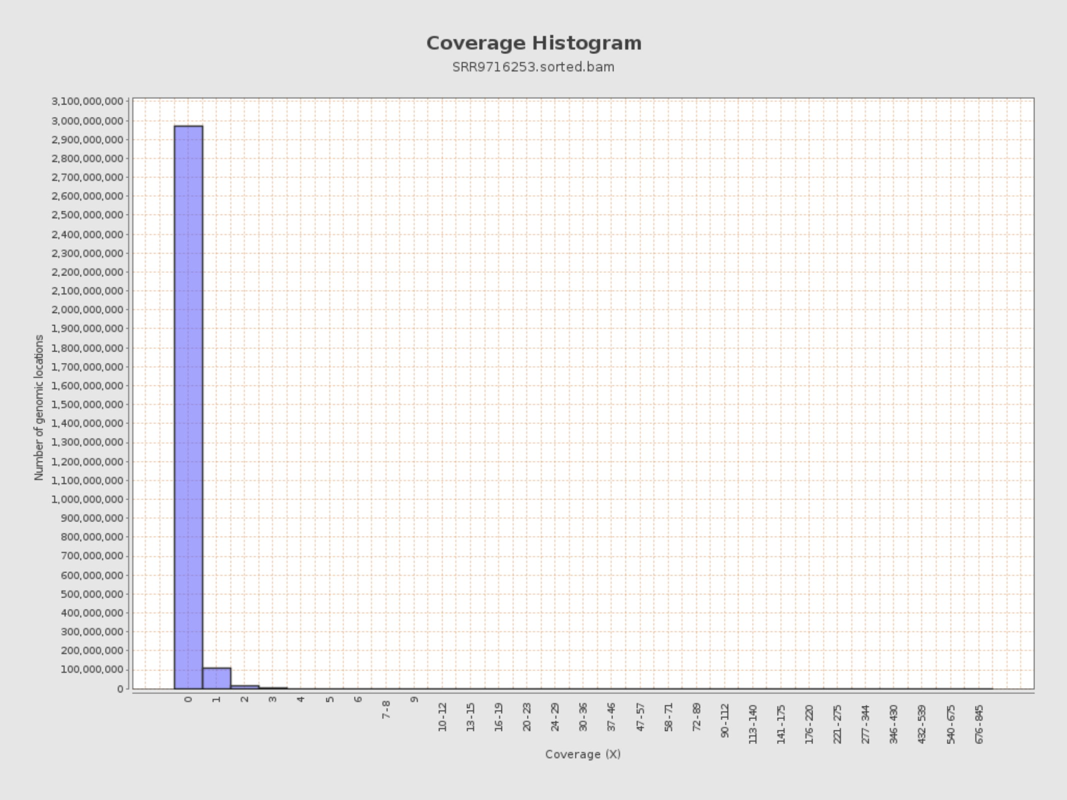
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17707663	0.071	0.7957
chr2	243199373	14828488	0.061	0.45
chr3	198022430	10232607	0.0517	0.2741
chr4	191154276	7749038	0.0405	0.3579
chr5	180915260	8158506	0.0451	0.2573
chr6	171115067	9721606	0.0568	0.31
chr7	159138663	10024884	0.063	0.5345

chr8	146364022	9867388	0.0674	0.4464
chr9	141213431	4815945	0.0341	0.2976
chr10	135534747	8157795	0.0602	0.5591
chr11	135006516	4708852	0.0349	0.2986
chr12	133851895	5851983	0.0437	0.2518
chr13	115169878	2982675	0.0259	0.19
chr14	107349540	3058775	0.0285	0.2237
chr15	102531392	3272441	0.0319	0.2127
chr16	90354753	4891383	0.0541	0.3045
chr17	81195210	4023823	0.0496	0.2977
chr18	78077248	4637679	0.0594	0.4359
chr19	59128983	4054688	0.0686	0.604
chr20	63025520	4350675	0.069	0.3406
chr21	48129895	2485066	0.0516	0.3409
chr22	51304566	2570214	0.0501	0.2803
chrMT	16571	58752	3.5455	3.3552
chrX	155270560	10183843	0.0656	0.3298
chrY	59373566	539220	0.0091	0.2967

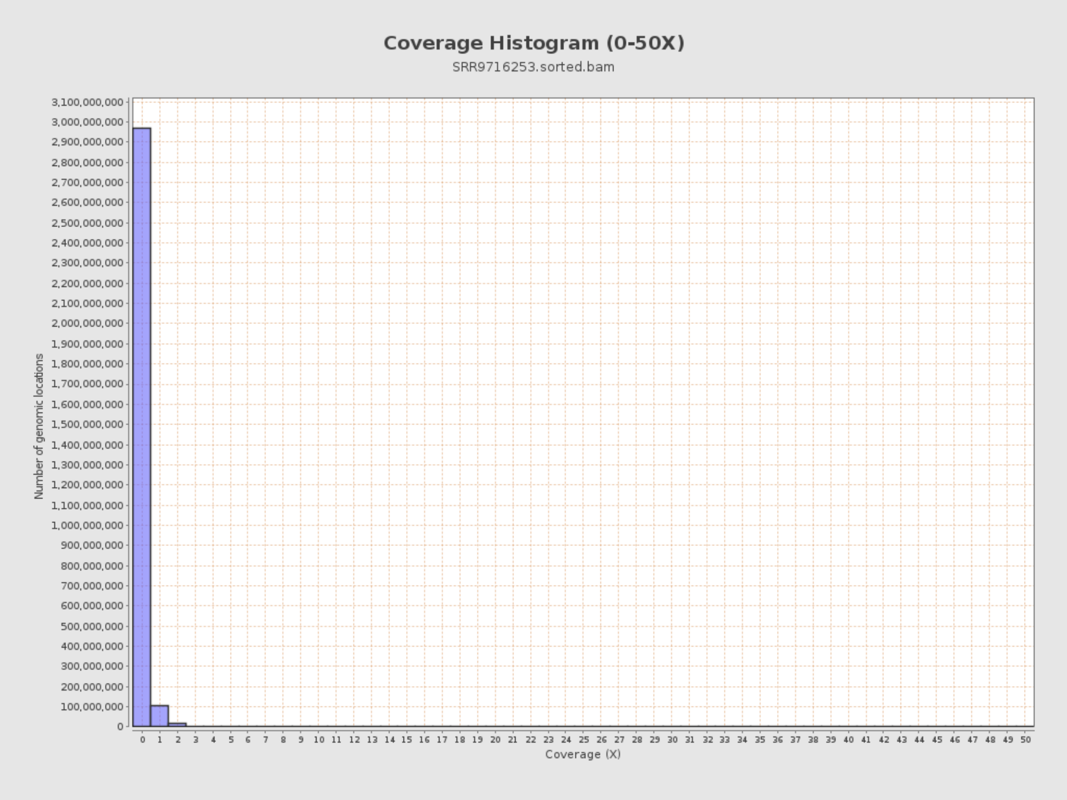
3. Results : Coverage across reference



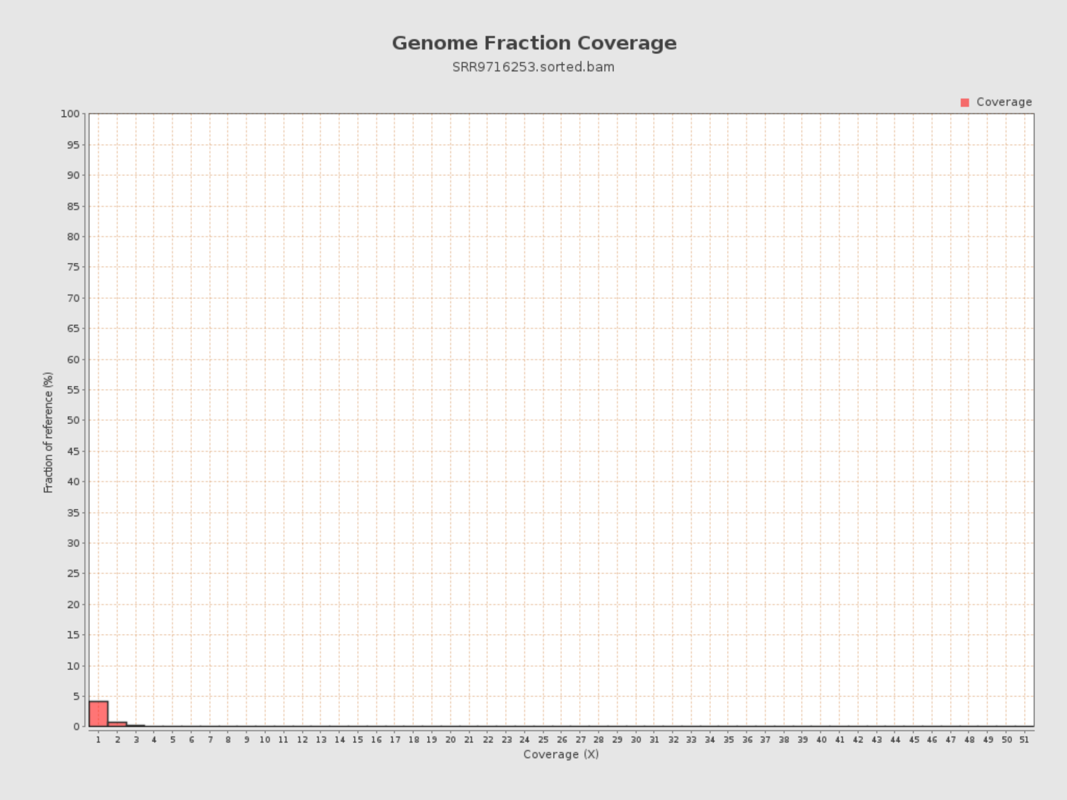
4. Results : Coverage Histogram



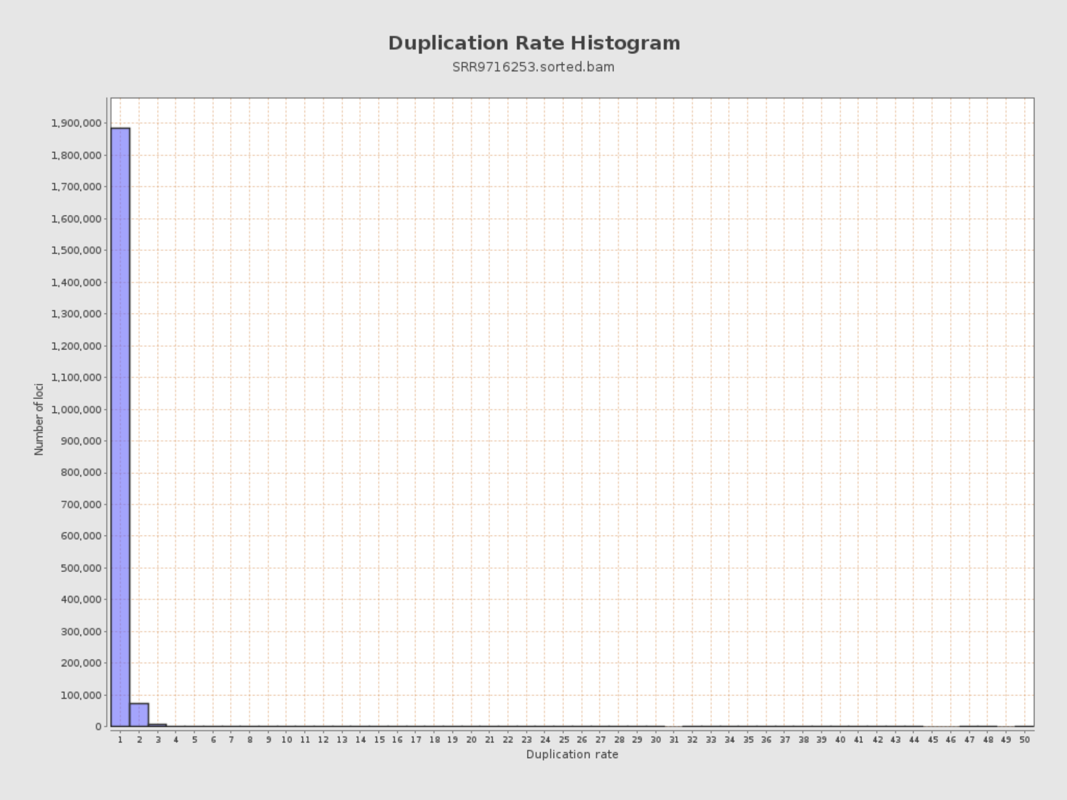
5. Results : Coverage Histogram (0-50X)



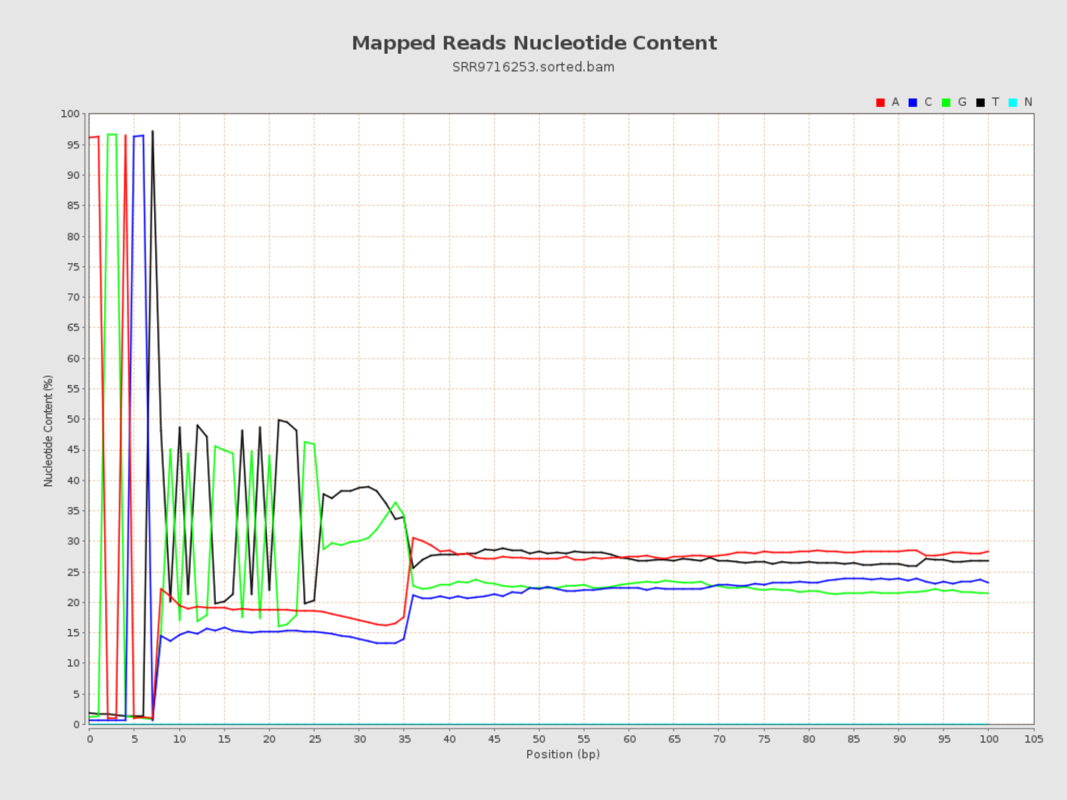
6. Results : Genome Fraction Coverage



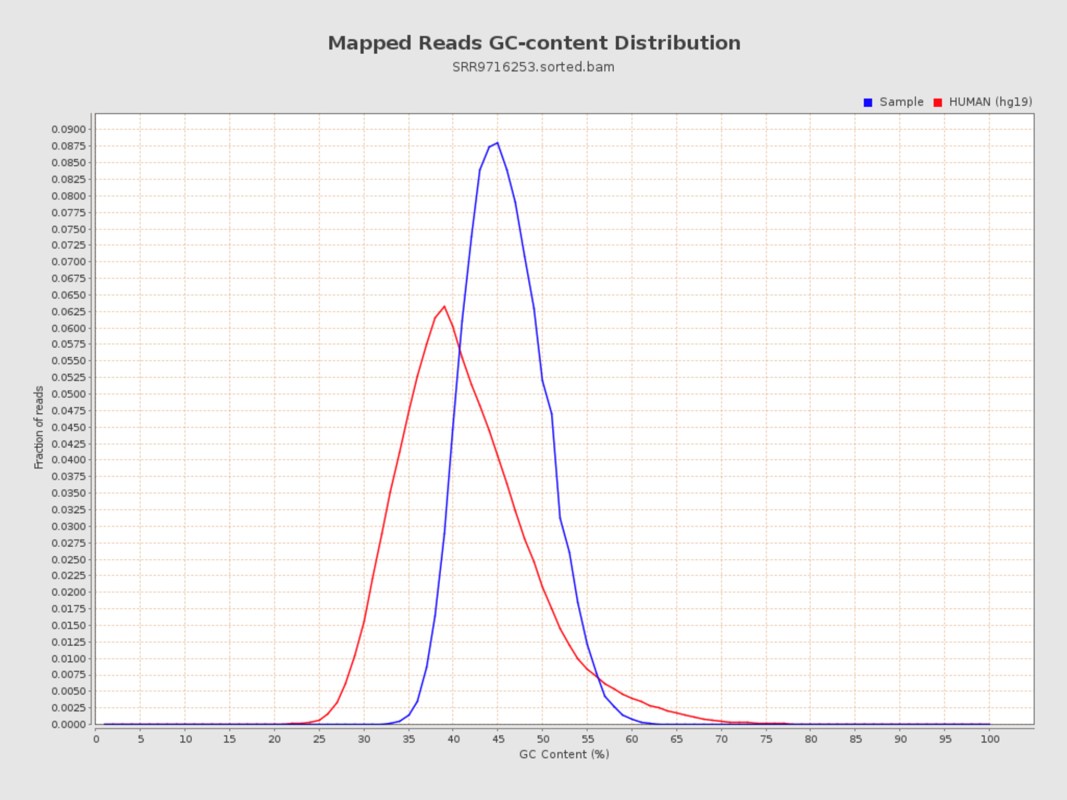
7. Results : Duplication Rate Histogram



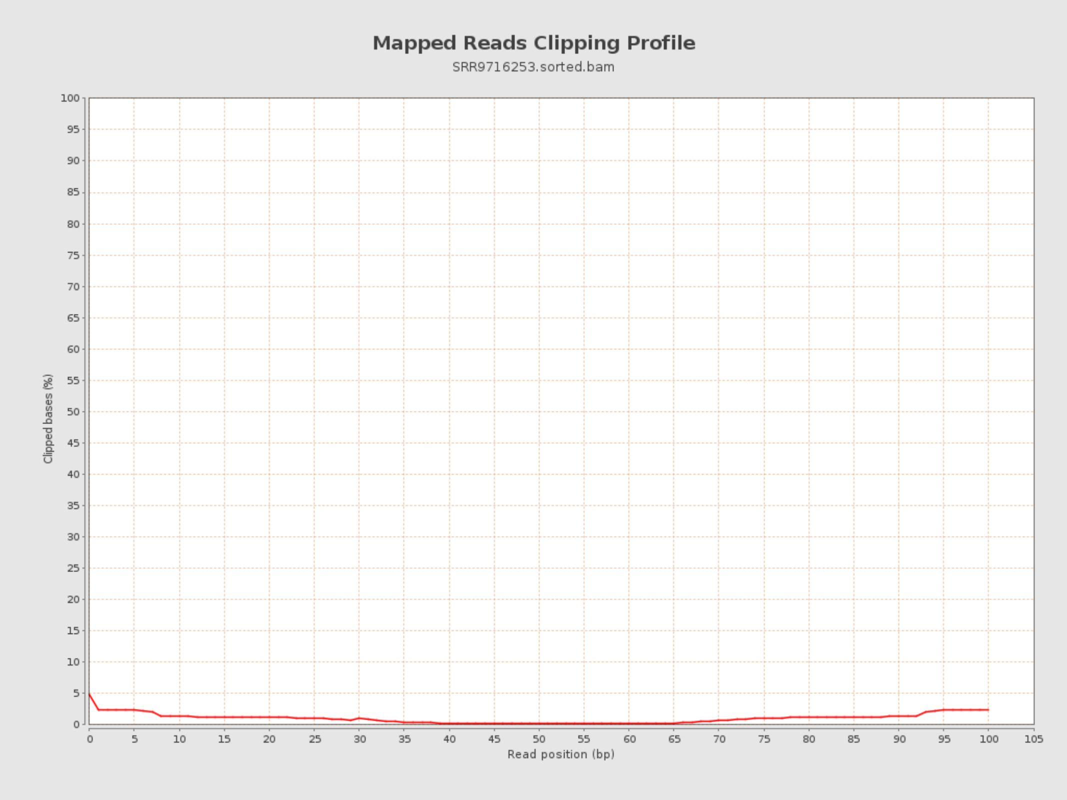
8. Results : Mapped Reads Nucleotide Content



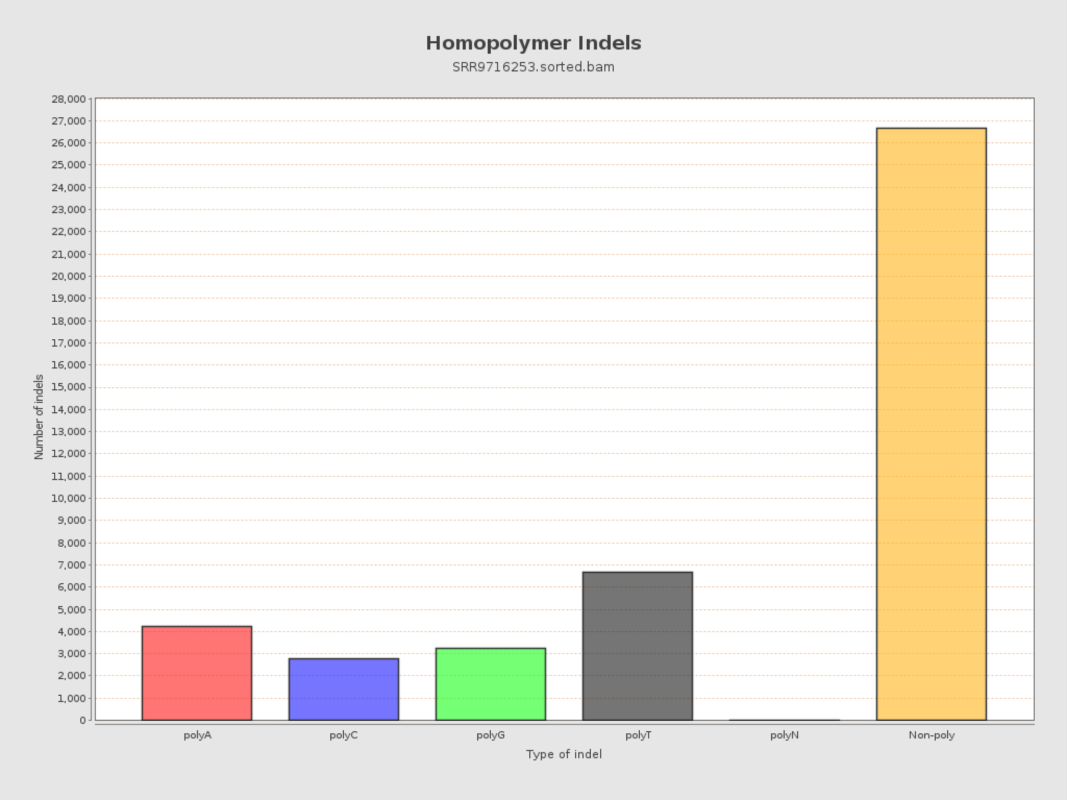
9. Results : Mapped Reads GC-content Distribution



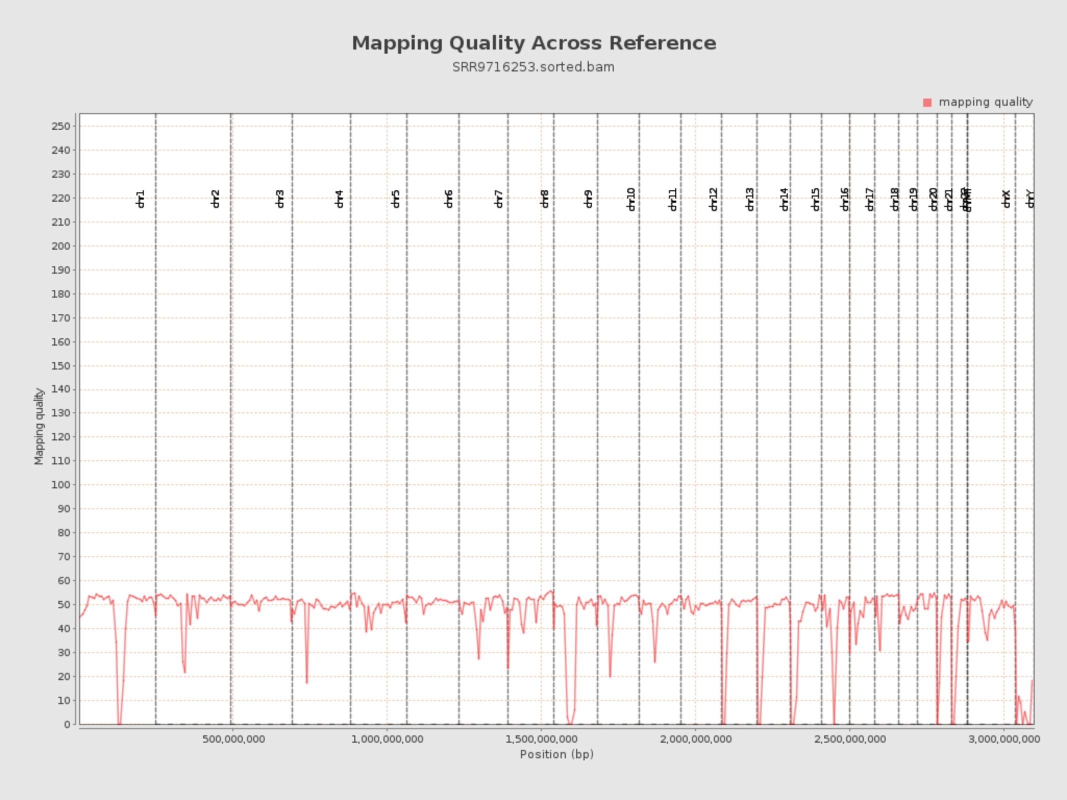
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram