Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:29:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716246.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_SRR9716246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716246.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:29:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,124,866
Mapped reads	1,896,164 / 89.24%
Unmapped reads	228,702 / 10.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,125 / 1.28%
Read min/max/mean length	30 / 101 / 101.47
Duplicated reads (estimated)	97,685 / 4.6%
Duplication rate	3.43%
Clipped reads	1,920,537 / 90.38%

2.2. ACGT Content

Number/percentage of A's	36,890,999 / 25.07%
Number/percentage of C's	27,401,944 / 18.62%
Number/percentage of T's	47,065,368 / 31.98%
Number/percentage of G's	35,785,580 / 24.32%
Number/percentage of N's	7,752 / 0.01%
GC Percentage	42.94%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.5043

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

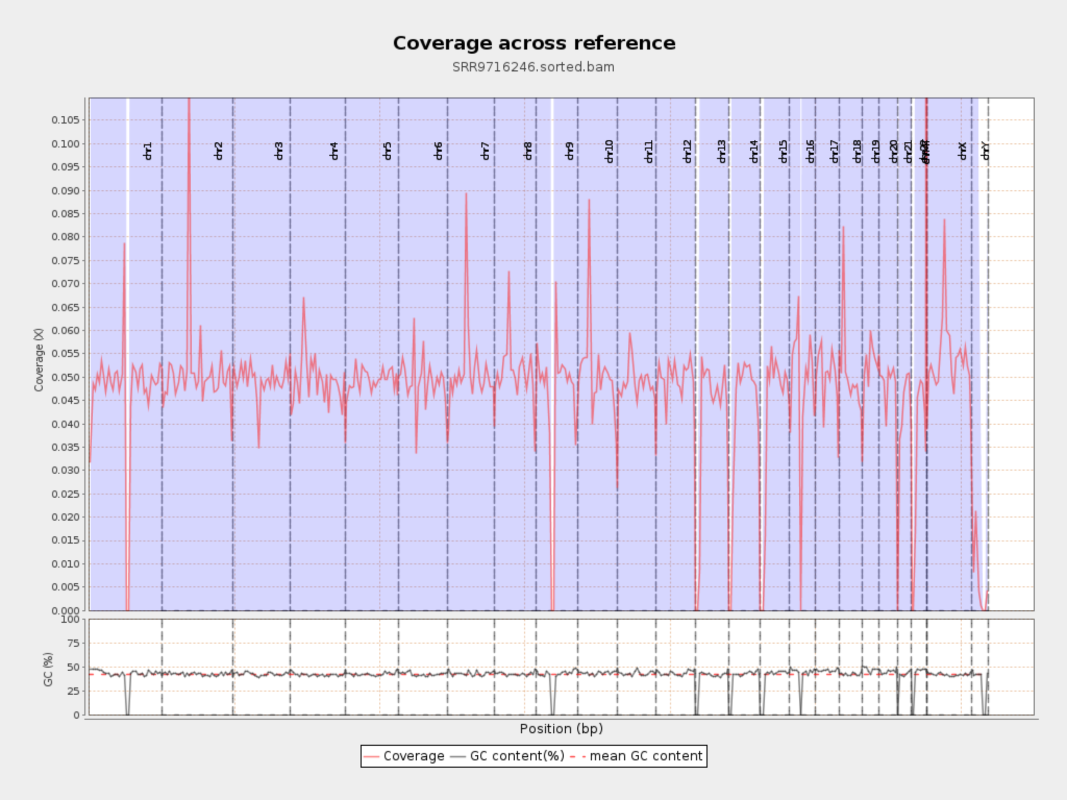
General error rate	0.91%
Mismatches	1,316,163
Insertions	13,835
Mapped reads with at least one insertion	0.72%
Deletions	37,490
Mapped reads with at least one deletion	1.95%
Homopolymer indels	43.7%

2.6. Chromosome stats

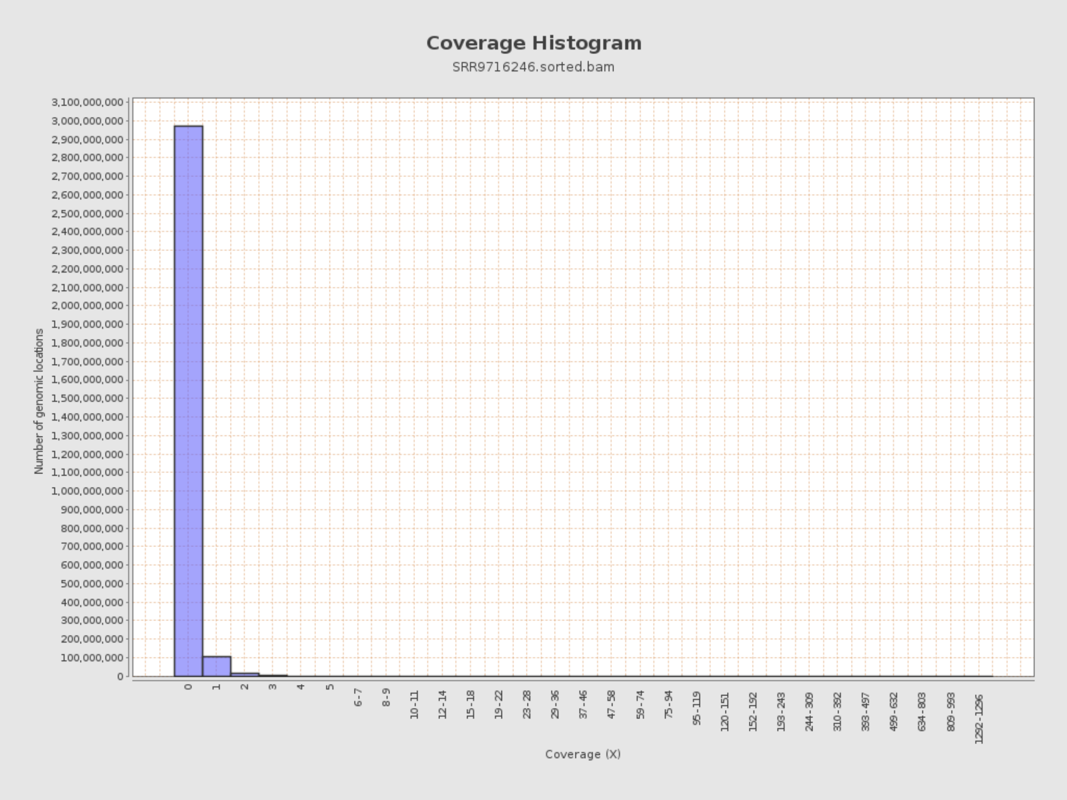
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11631347	0.0467	0.7409
chr2	243199373	12598598	0.0518	0.8205
chr3	198022430	9769313	0.0493	0.2574
chr4	191154276	9423673	0.0493	0.2899
chr5	180915260	8937611	0.0494	0.2661
chr6	171115067	8405052	0.0491	0.3272
chr7	159138663	8250540	0.0518	0.6581

chr8	146364022	7492907	0.0512	0.6789
chr9	141213431	6305219	0.0447	0.5505
chr10	135534747	6970904	0.0514	0.4548
chr11	135006516	6564522	0.0486	0.5176
chr12	133851895	6660715	0.0498	0.2646
chr13	115169878	4632445	0.0402	0.2313
chr14	107349540	4445620	0.0414	0.3105
chr15	102531392	4177819	0.0407	0.2422
chr16	90354753	4342714	0.0481	0.2985
chr17	81195210	4043675	0.0498	0.2946
chr18	78077248	4032006	0.0516	1.0192
chr19	59128983	3113859	0.0527	0.5686
chr20	63025520	3016972	0.0479	0.289
chr21	48129895	1929358	0.0401	0.2578
chr22	51304566	1636274	0.0319	0.2056
chrMT	16571	15390	0.9287	1.2456
chrX	155270560	8429302	0.0543	0.3861
chrY	59373566	390162	0.0066	0.1779

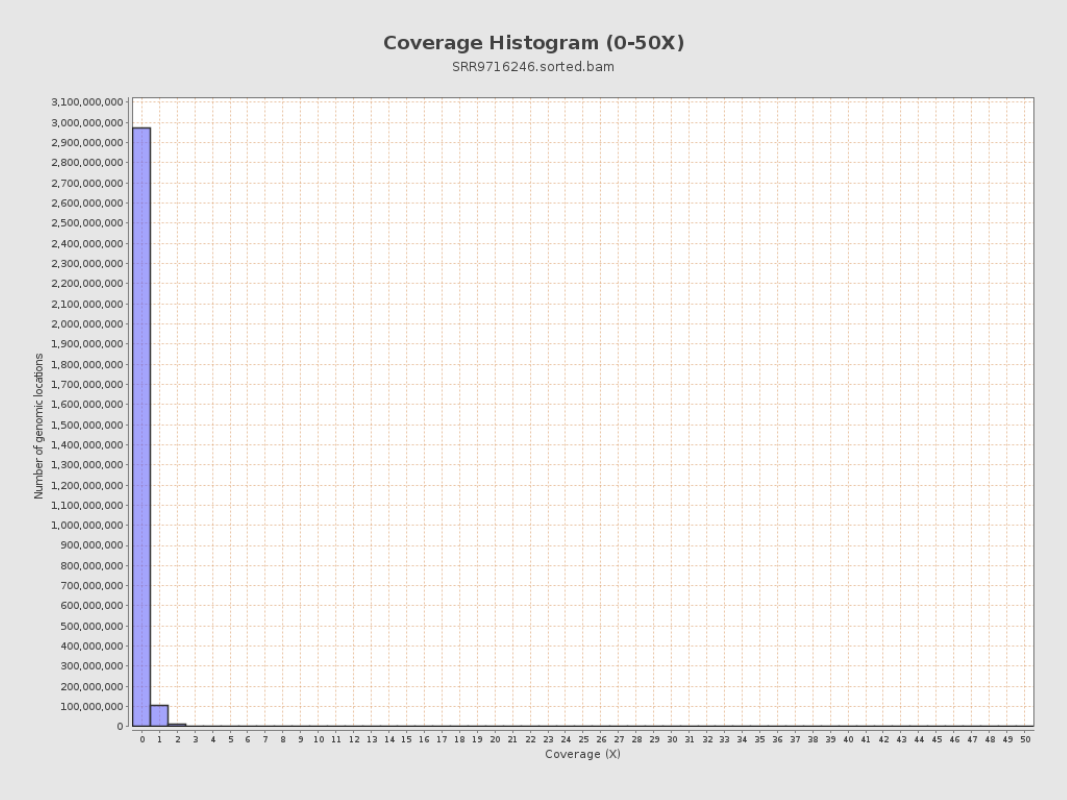
3. Results : Coverage across reference



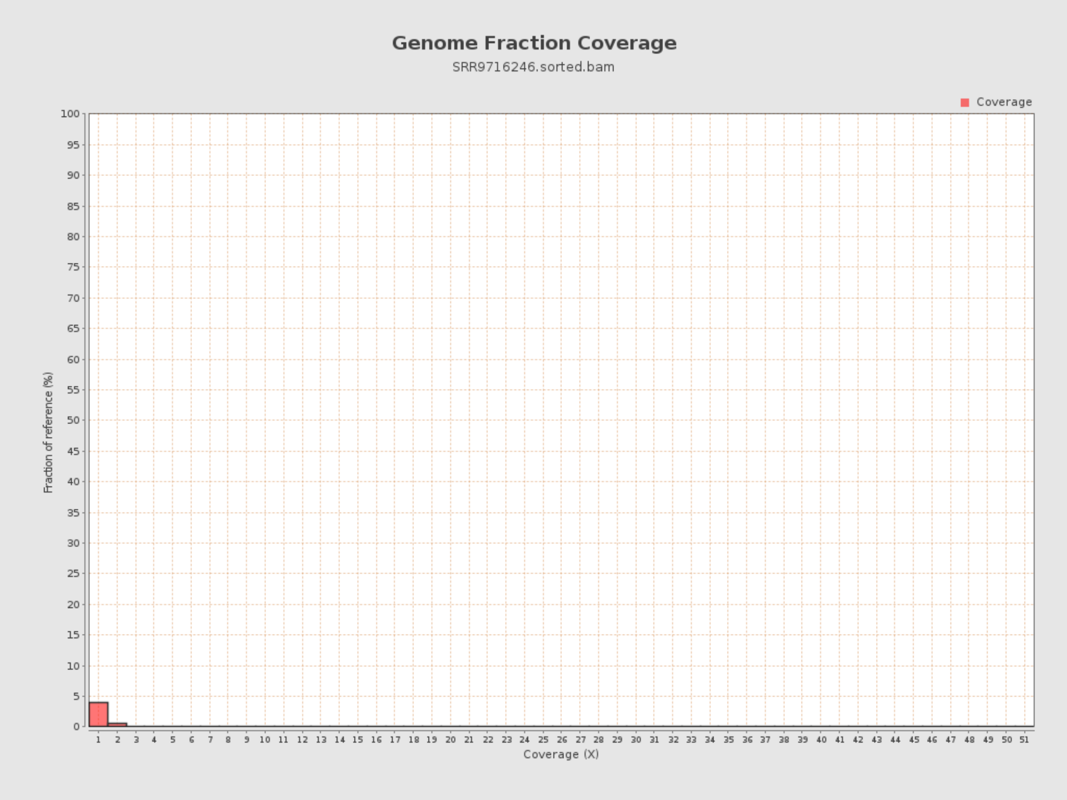
4. Results : Coverage Histogram



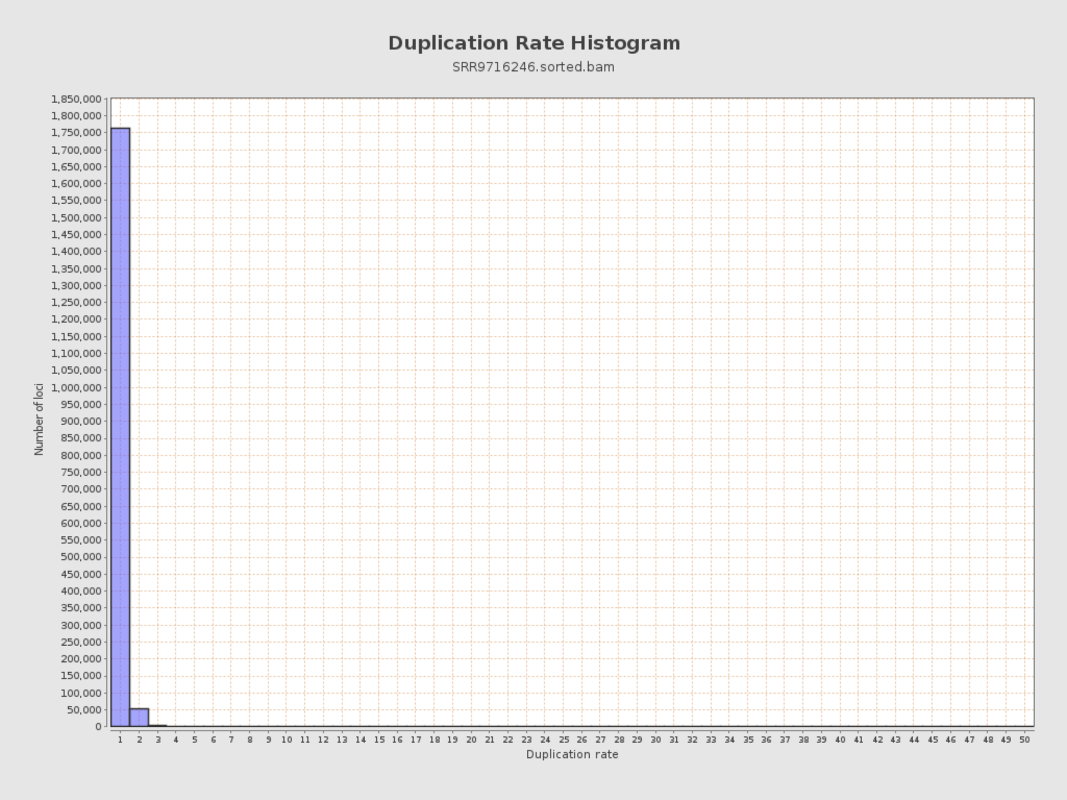
5. Results : Coverage Histogram (0-50X)



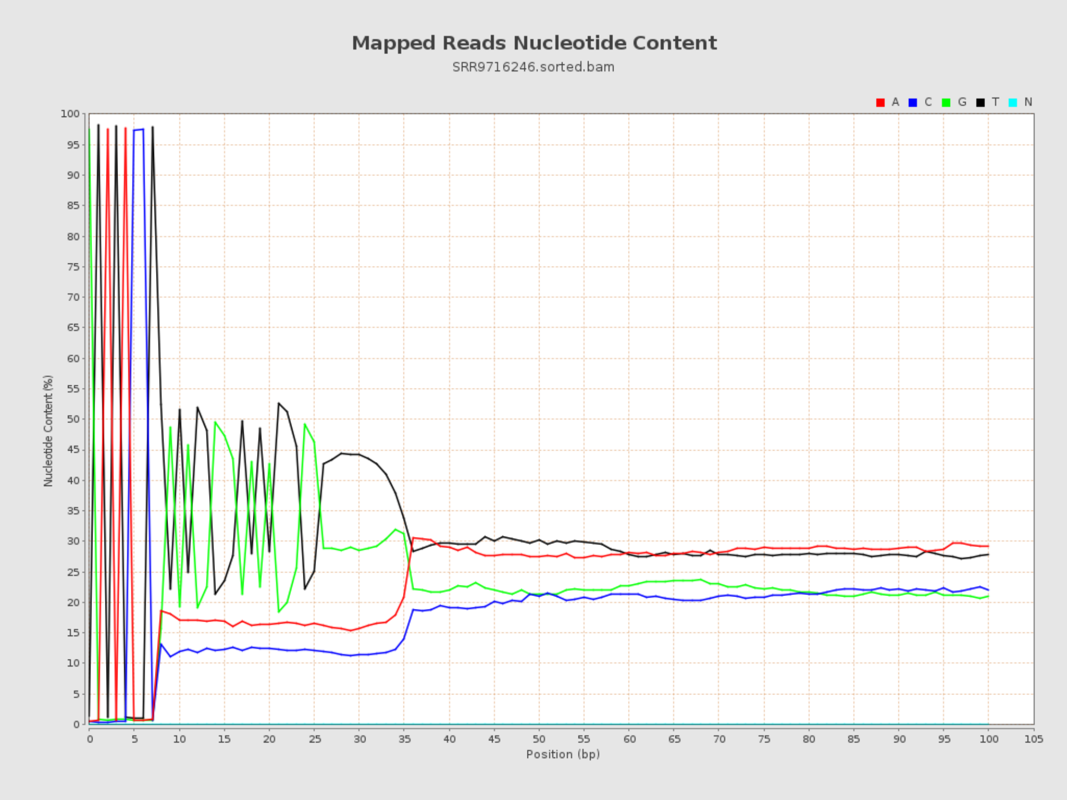
6. Results : Genome Fraction Coverage



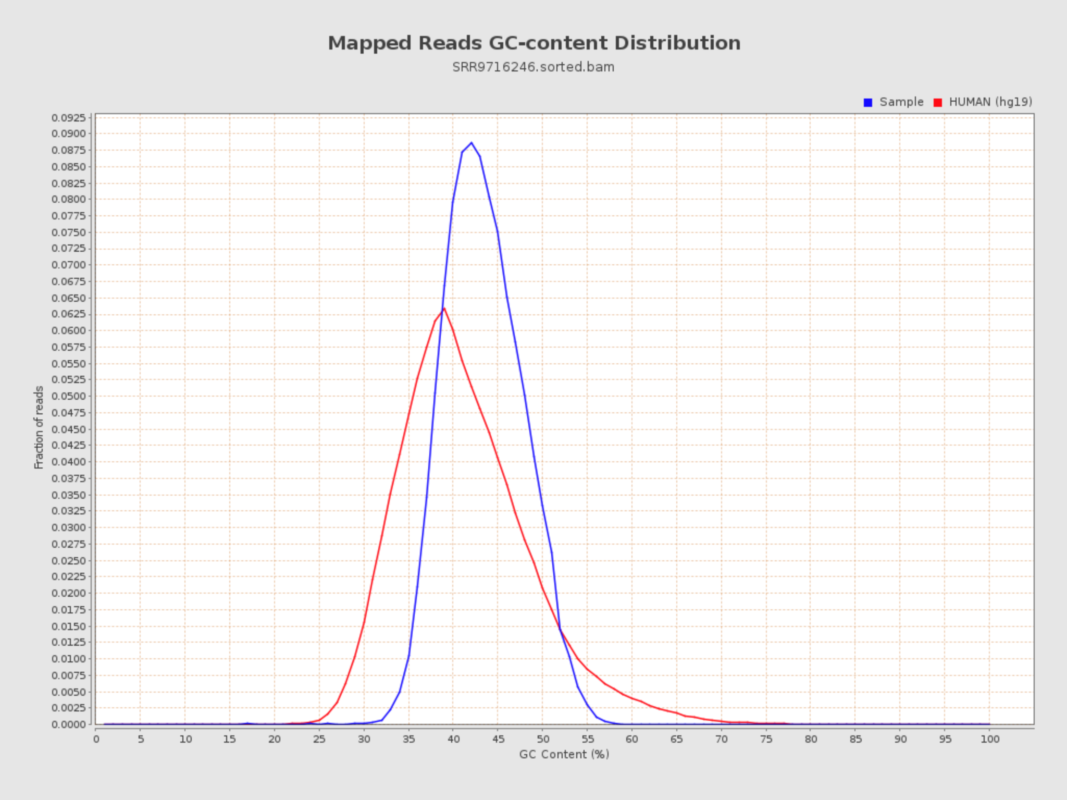
7. Results : Duplication Rate Histogram



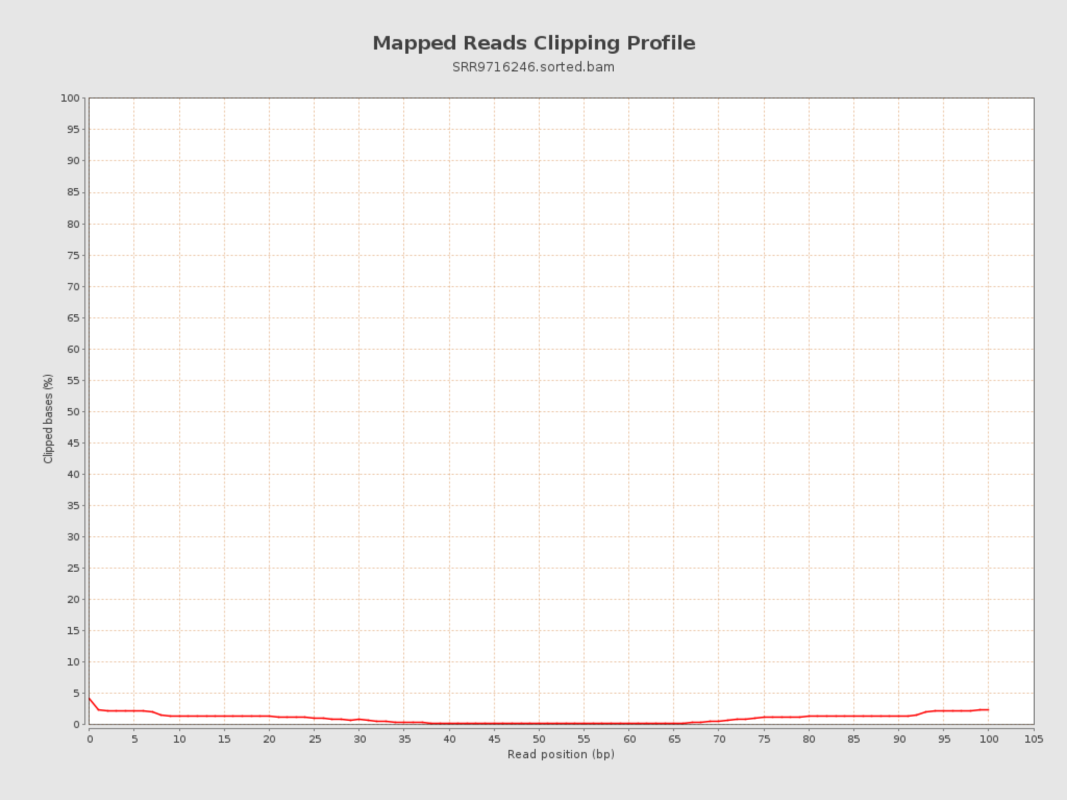
8. Results : Mapped Reads Nucleotide Content



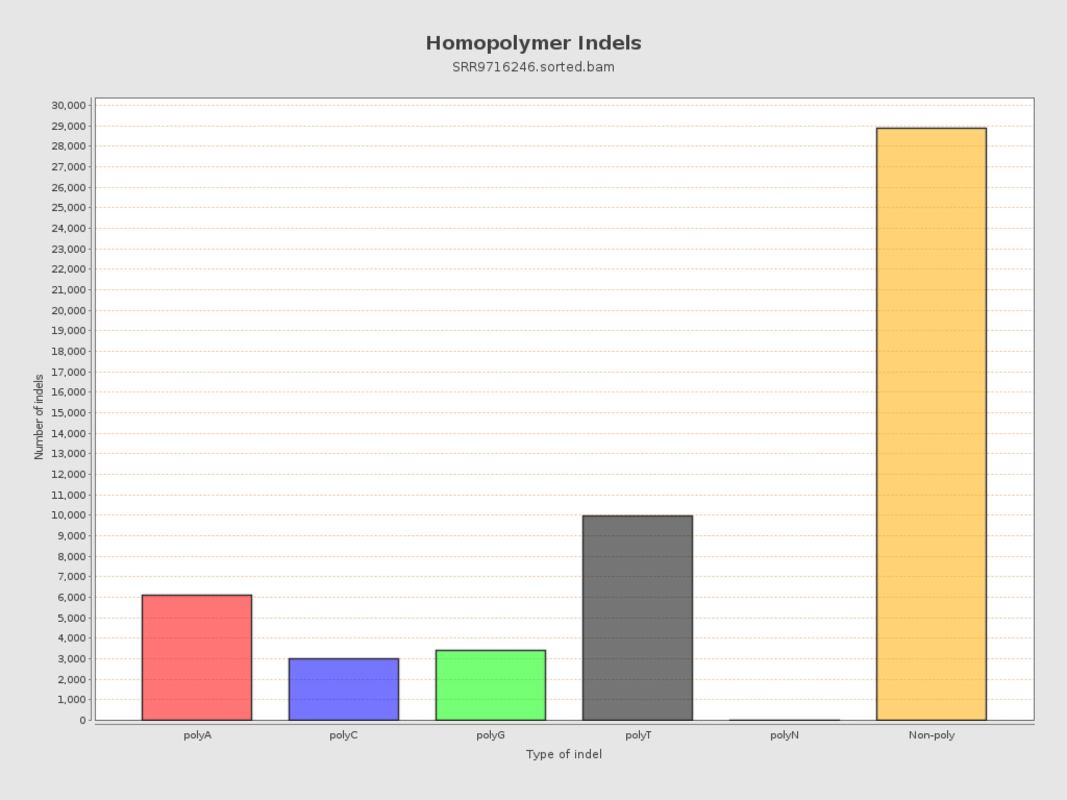
9. Results : Mapped Reads GC-content Distribution



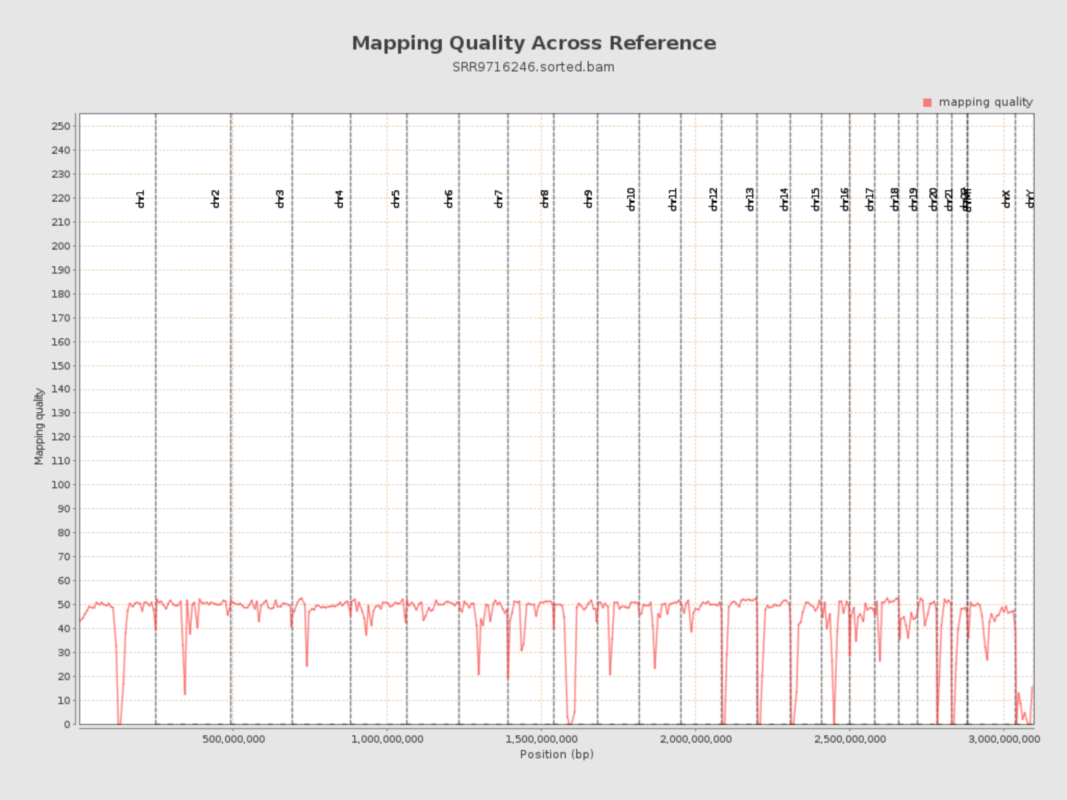
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram