Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:06:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716240.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_SRR9716240 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716240.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:06:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716240.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,240,650
Mapped reads	1,968,427 / 87.85%
Unmapped reads	272,223 / 12.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,332 / 1.31%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	96,981 / 4.33%
Duplication rate	3.15%
Clipped reads	1,993,737 / 88.98%

2.2. ACGT Content

Number/percentage of A's	39,410,600 / 25.44%
Number/percentage of C's	27,542,240 / 17.78%
Number/percentage of T's	48,976,399 / 31.61%
Number/percentage of G's	38,994,105 / 25.17%
Number/percentage of N's	8,962 / 0.01%
GC Percentage	42.95%

2.3. Coverage

Mean	0.0501

Standard Deviation	0.5445

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

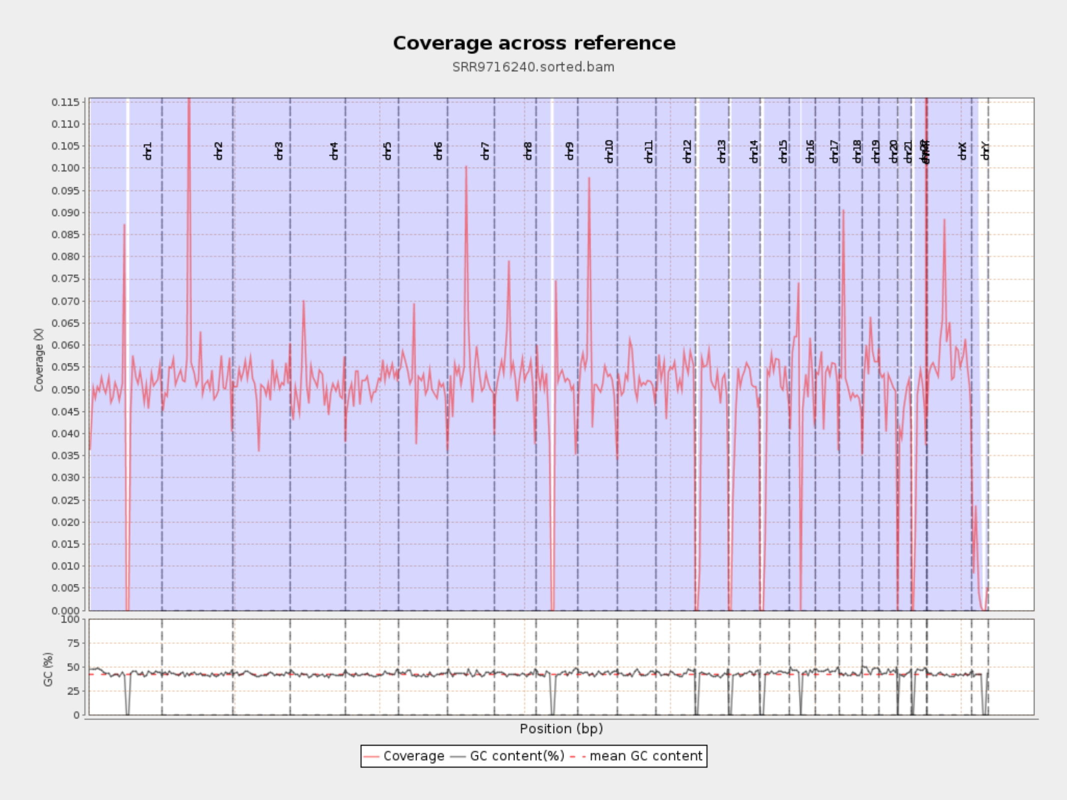
General error rate	0.86%
Mismatches	1,305,595
Insertions	14,671
Mapped reads with at least one insertion	0.73%
Deletions	38,038
Mapped reads with at least one deletion	1.91%
Homopolymer indels	44.12%

2.6. Chromosome stats

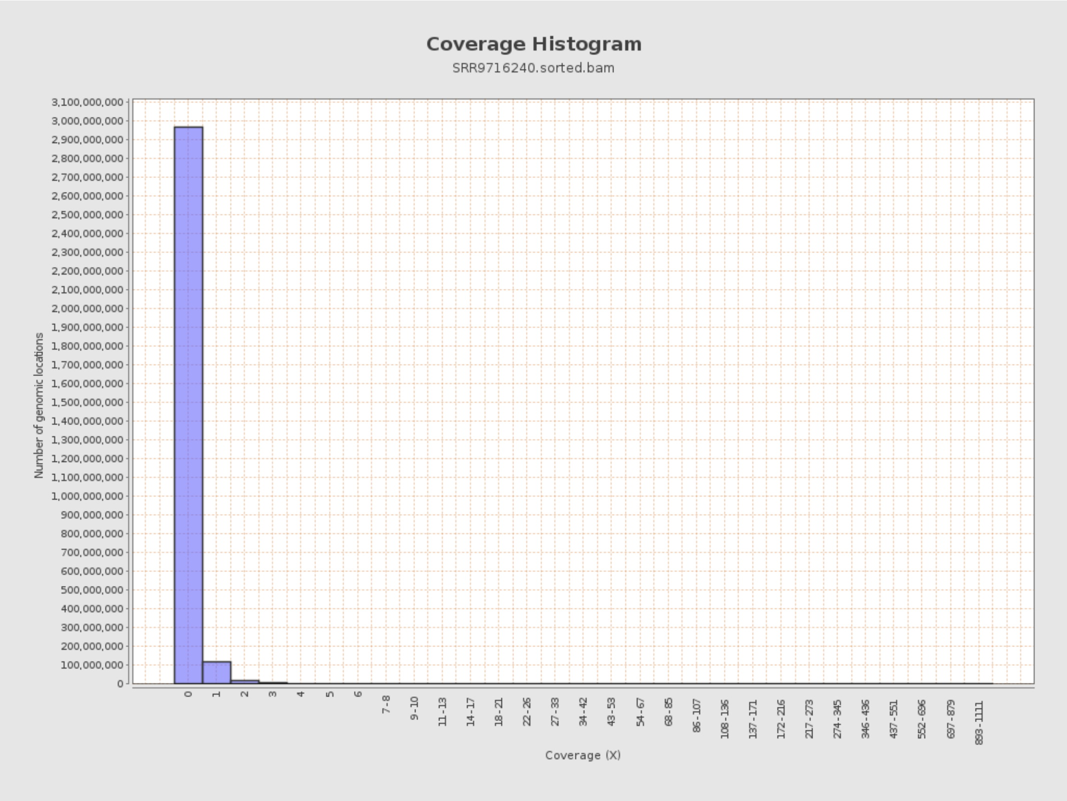
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12025543	0.0482	0.8648
chr2	243199373	13354730	0.0549	0.8153
chr3	198022430	10204688	0.0515	0.2637
chr4	191154276	9711154	0.0508	0.2917
chr5	180915260	9305648	0.0514	0.2717
chr6	171115067	8897798	0.052	0.3408
chr7	159138663	8743466	0.0549	0.7438

chr8	146364022	7949945	0.0543	0.7303
chr9	141213431	6499354	0.046	0.5778
chr10	135534747	7342595	0.0542	0.523
chr11	135006516	6968287	0.0516	0.5197
chr12	133851895	7150337	0.0534	0.2753
chr13	115169878	5051620	0.0439	0.2399
chr14	107349540	4646106	0.0433	0.3295
chr15	102531392	4431637	0.0432	0.2475
chr16	90354753	4566047	0.0505	0.3167
chr17	81195210	4252666	0.0524	0.3088
chr18	78077248	4193726	0.0537	1.1676
chr19	59128983	3357174	0.0568	0.6441
chr20	63025520	3135051	0.0497	0.2858
chr21	48129895	1976093	0.0411	0.2639
chr22	51304566	1755957	0.0342	0.2105
chrMT	16571	32337	1.9514	2.029
chrX	155270560	9014650	0.0581	0.3917
chrY	59373566	431681	0.0073	0.2018

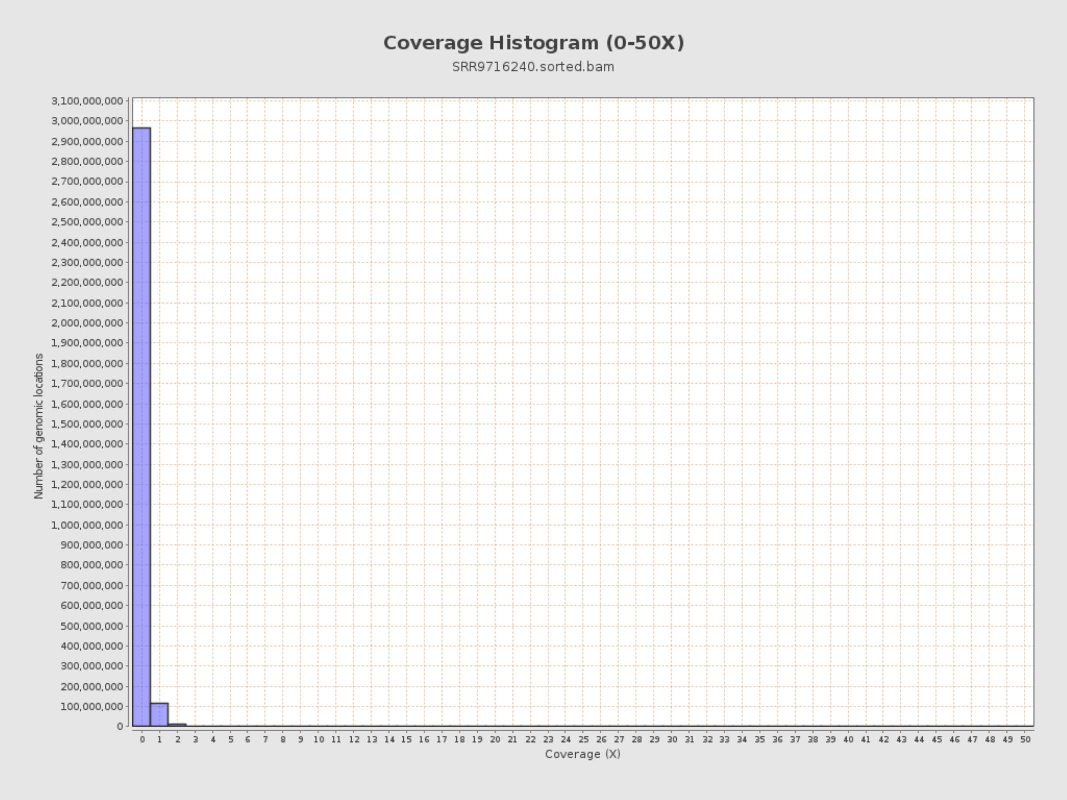
3. Results : Coverage across reference



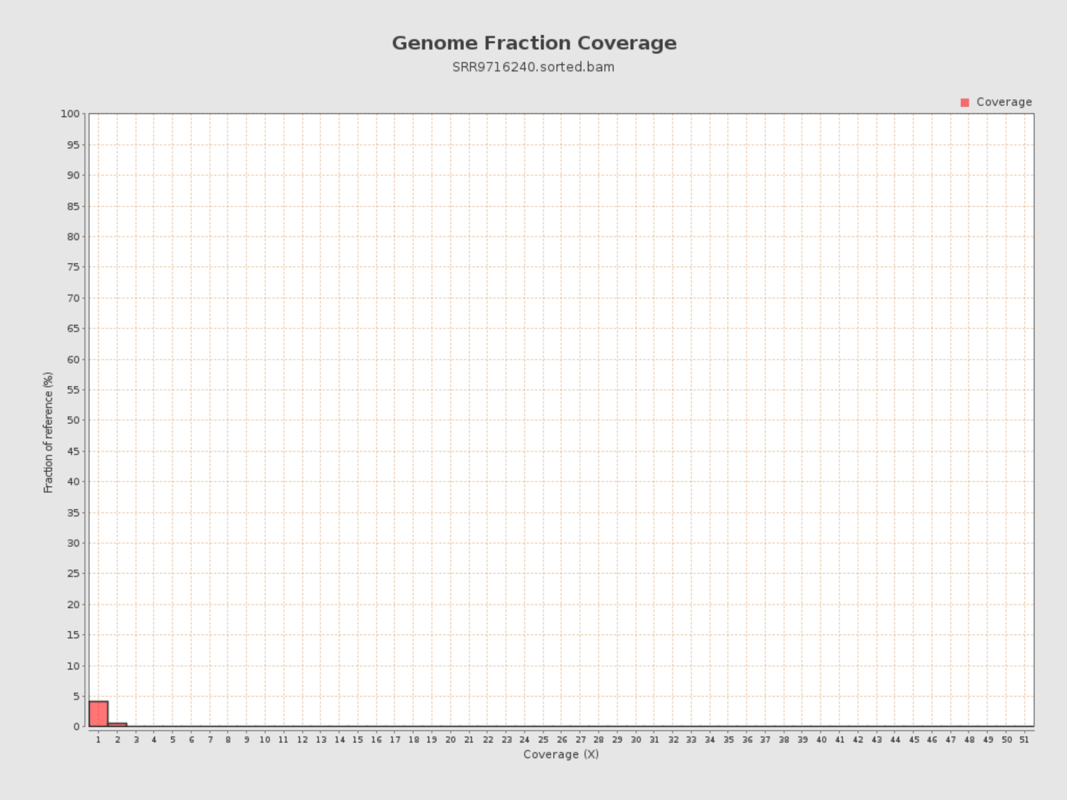
4. Results : Coverage Histogram



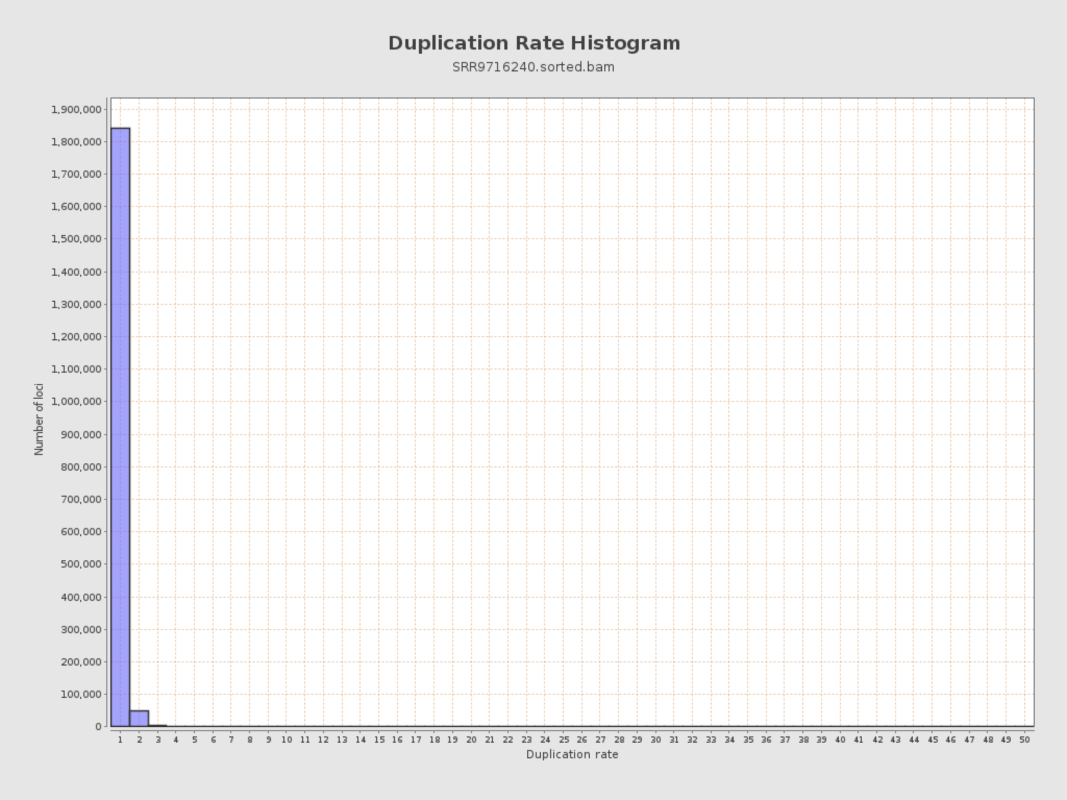
5. Results : Coverage Histogram (0-50X)



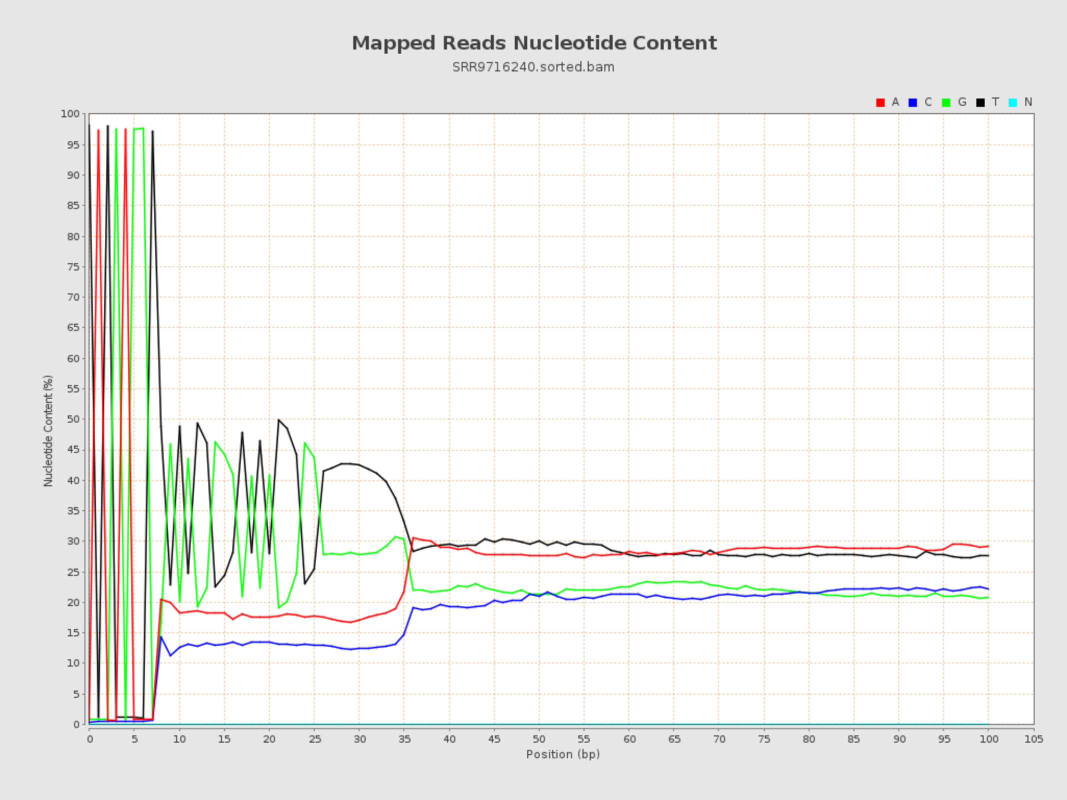
6. Results : Genome Fraction Coverage



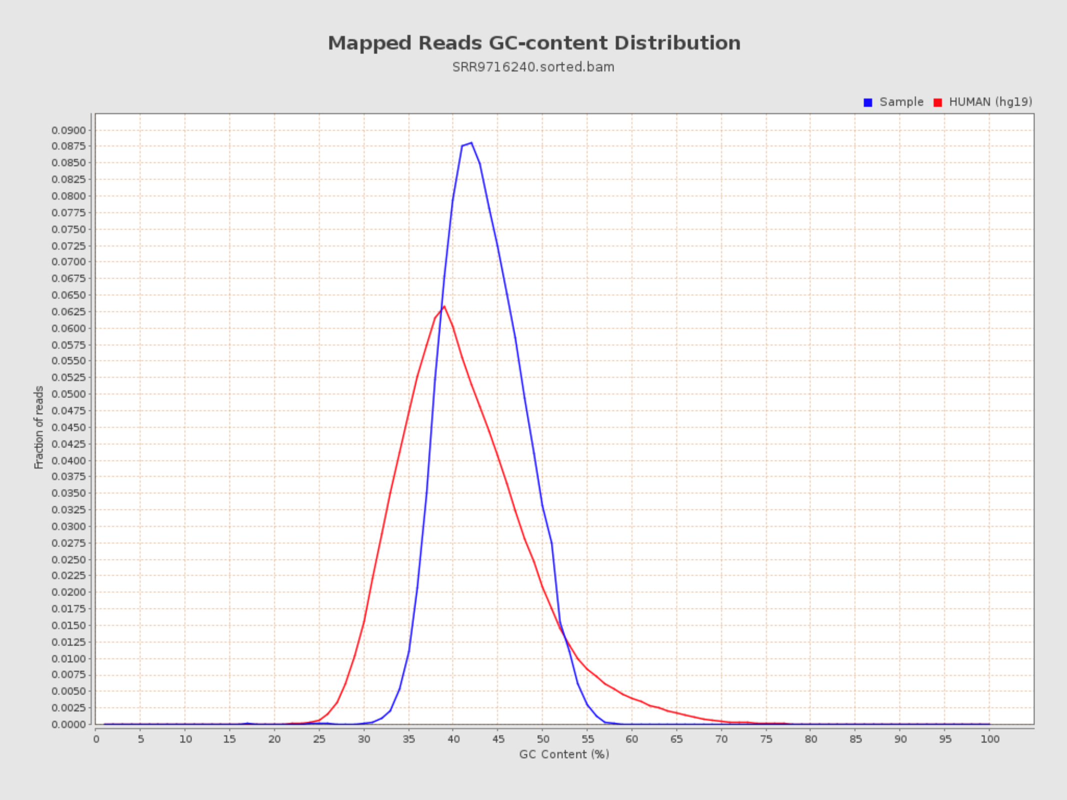
7. Results : Duplication Rate Histogram



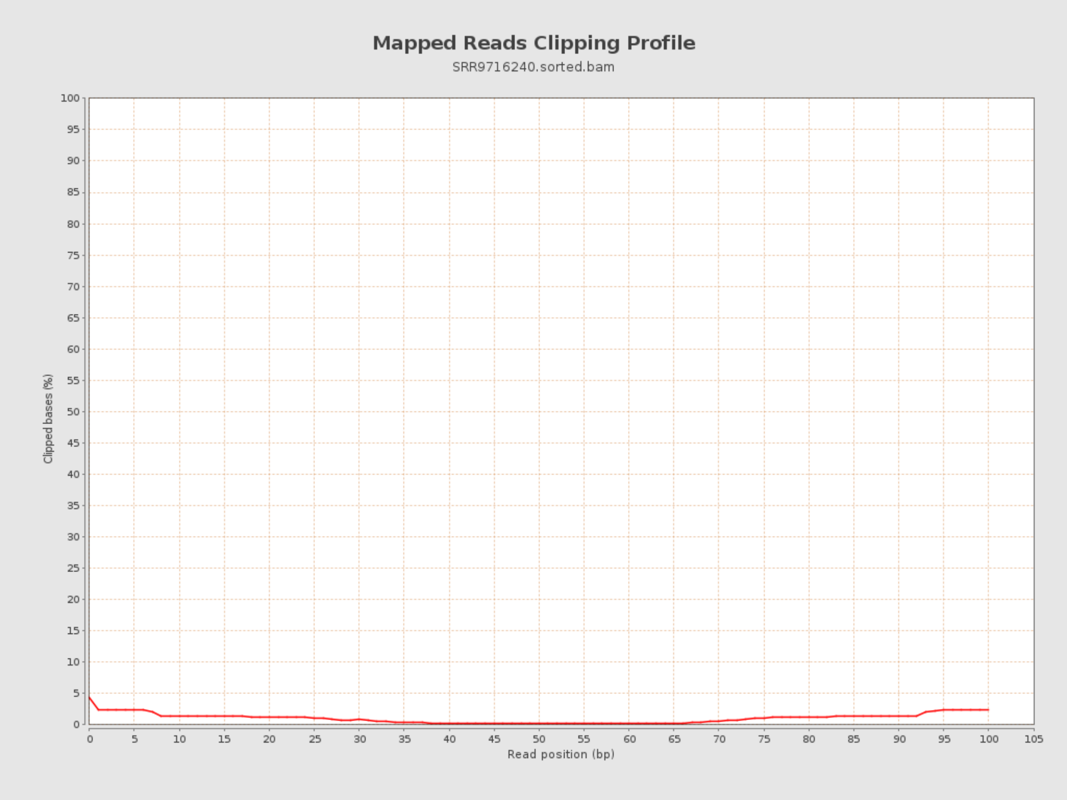
8. Results : Mapped Reads Nucleotide Content



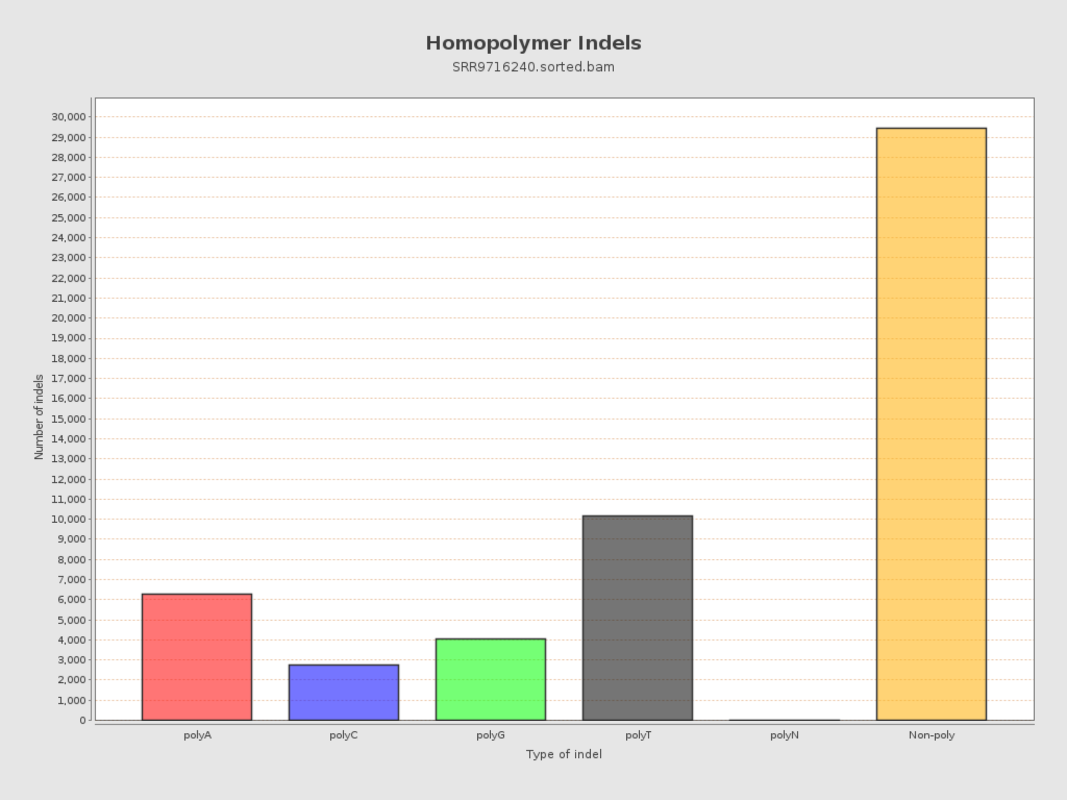
9. Results : Mapped Reads GC-content Distribution



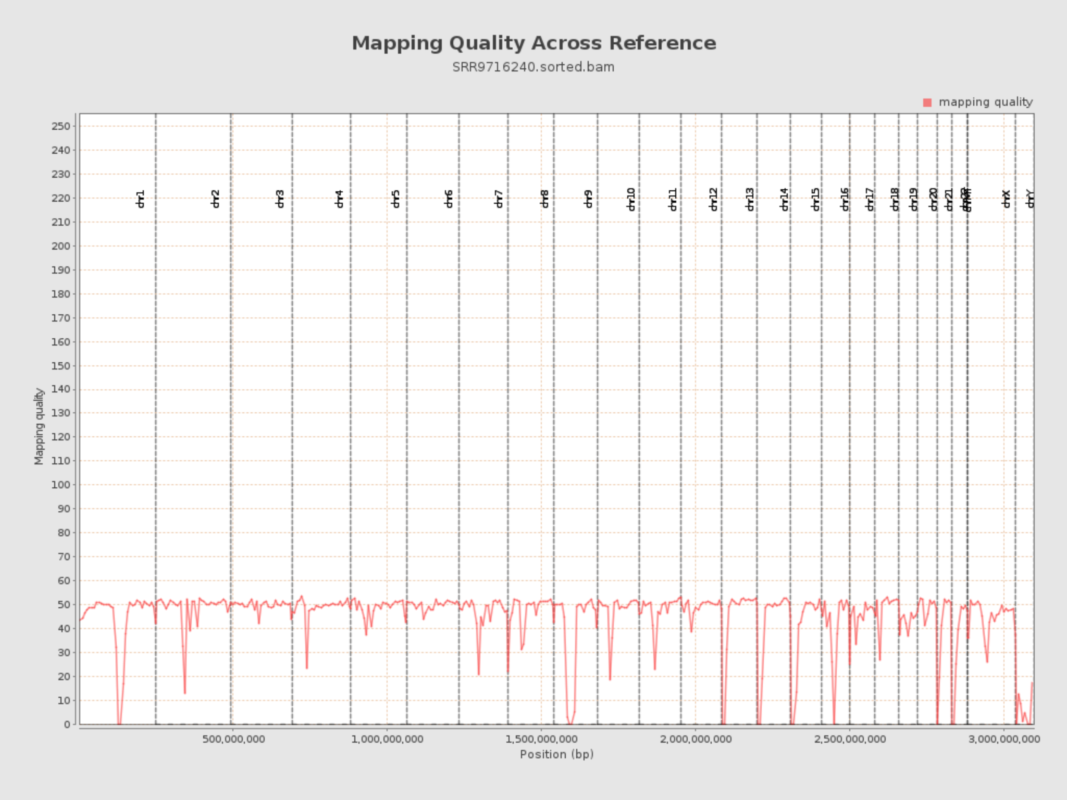
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram