Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:14:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716242.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_SRR9716242 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716242.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:14:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716242.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,893,732
Mapped reads	1,738,596 / 91.81%
Unmapped reads	155,136 / 8.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,759 / 1.57%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	82,623 / 4.36%
Duplication rate	2.95%
Clipped reads	1,765,416 / 93.22%

2.2. ACGT Content

Number/percentage of A's	34,810,911 / 25.55%
Number/percentage of C's	26,455,684 / 19.42%
Number/percentage of T's	42,446,551 / 31.15%
Number/percentage of G's	32,531,891 / 23.88%
Number/percentage of N's	8,213 / 0.01%
GC Percentage	43.29%

2.3. Coverage

Mean	0.044

Standard Deviation	0.509

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

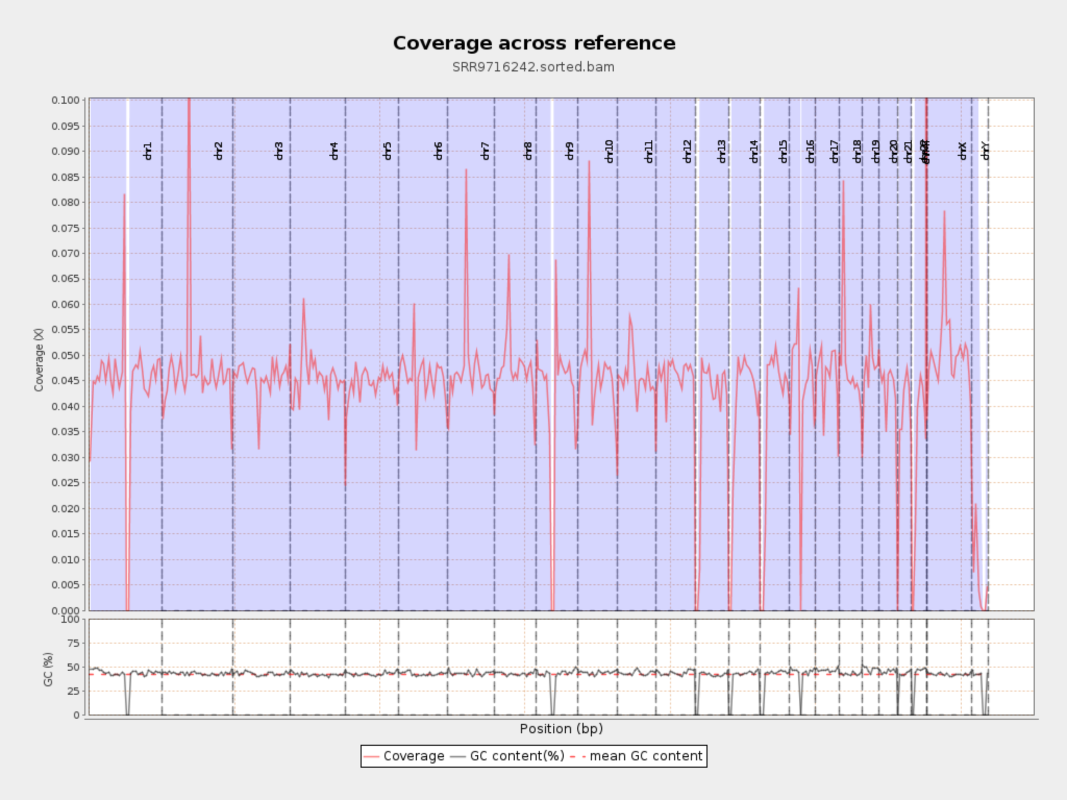
General error rate	0.85%
Mismatches	1,131,748
Insertions	13,147
Mapped reads with at least one insertion	0.75%
Deletions	34,910
Mapped reads with at least one deletion	1.98%
Homopolymer indels	43.37%

2.6. Chromosome stats

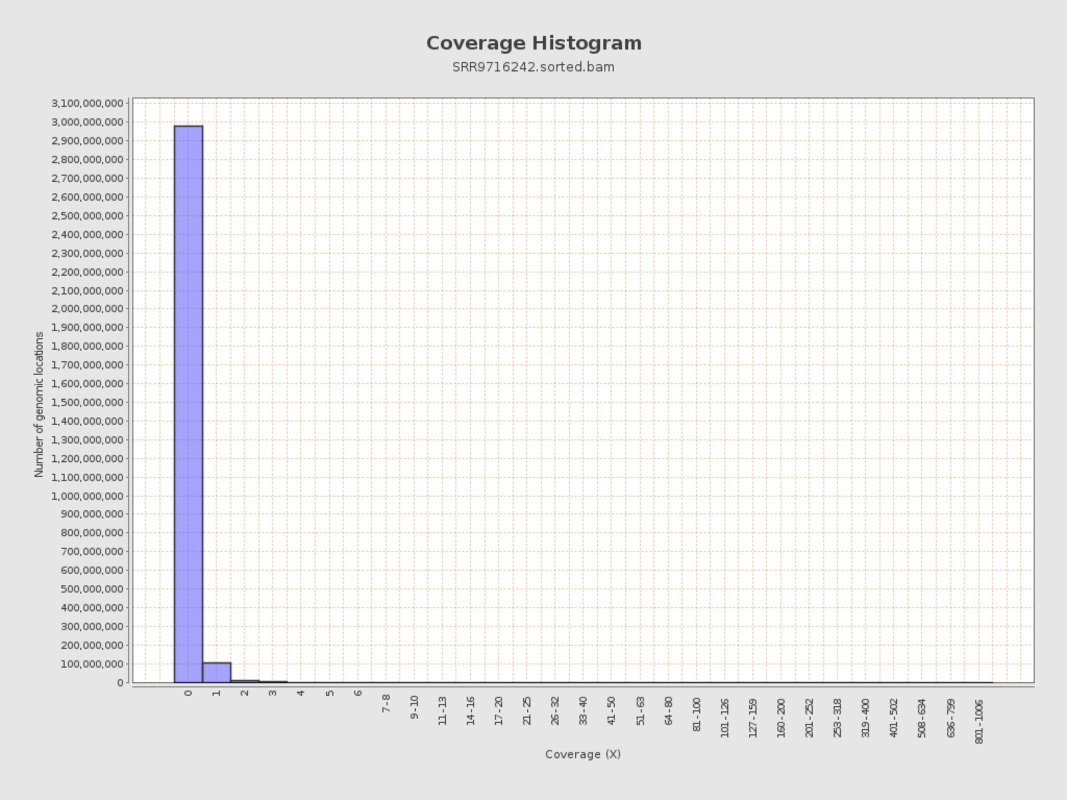
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10936780	0.0439	0.844
chr2	243199373	11644175	0.0479	0.7499
chr3	198022430	9046849	0.0457	0.2437
chr4	191154276	8742541	0.0457	0.2659
chr5	180915260	8072832	0.0446	0.2447
chr6	171115067	7860384	0.0459	0.3174
chr7	159138663	7578366	0.0476	0.644

chr8	146364022	6961227	0.0476	0.6622
chr9	141213431	5829891	0.0413	0.5738
chr10	135534747	6441983	0.0475	0.4818
chr11	135006516	6149998	0.0456	0.4841
chr12	133851895	6165703	0.0461	0.2546
chr13	115169878	4287153	0.0372	0.2173
chr14	107349540	4107041	0.0383	0.3329
chr15	102531392	3883952	0.0379	0.2268
chr16	90354753	3941939	0.0436	0.2891
chr17	81195210	3709299	0.0457	0.2794
chr18	78077248	3832453	0.0491	1.1024
chr19	59128983	2859205	0.0484	0.6008
chr20	63025520	2720383	0.0432	0.2608
chr21	48129895	1754420	0.0365	0.2435
chr22	51304566	1492602	0.0291	0.1919
chrMT	16571	13628	0.8224	1.1783
chrX	155270560	7908902	0.0509	0.3786
chrY	59373566	372429	0.0063	0.1794

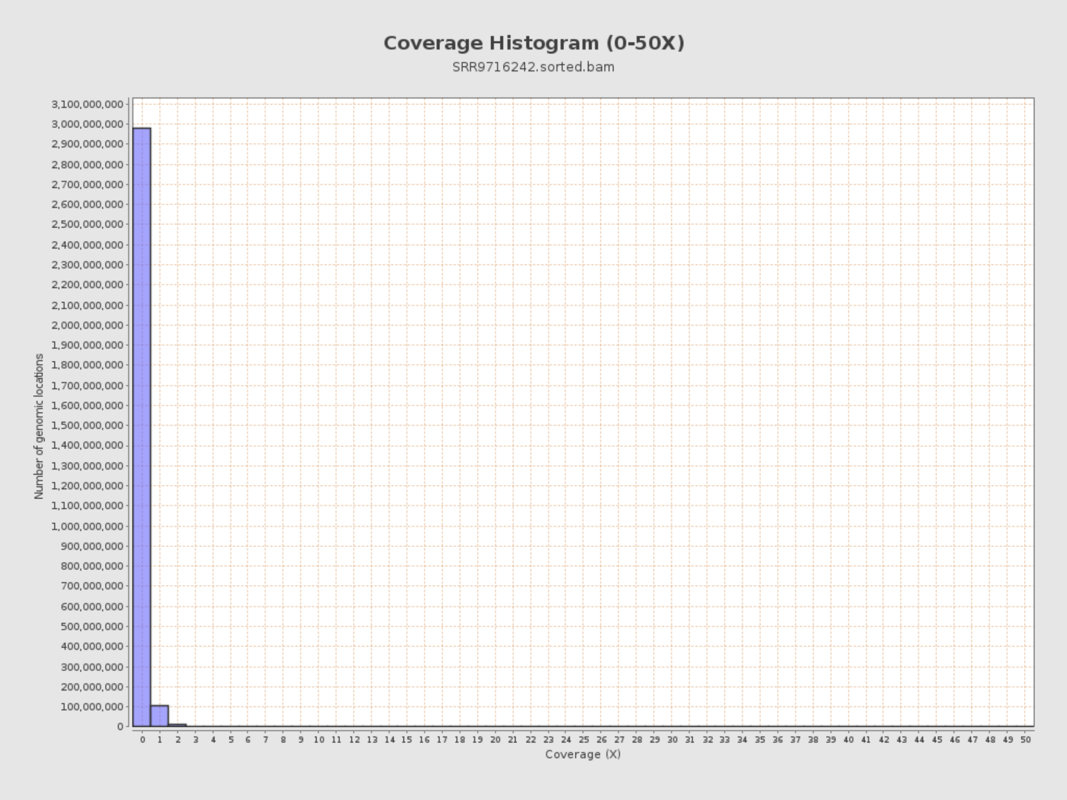
3. Results : Coverage across reference



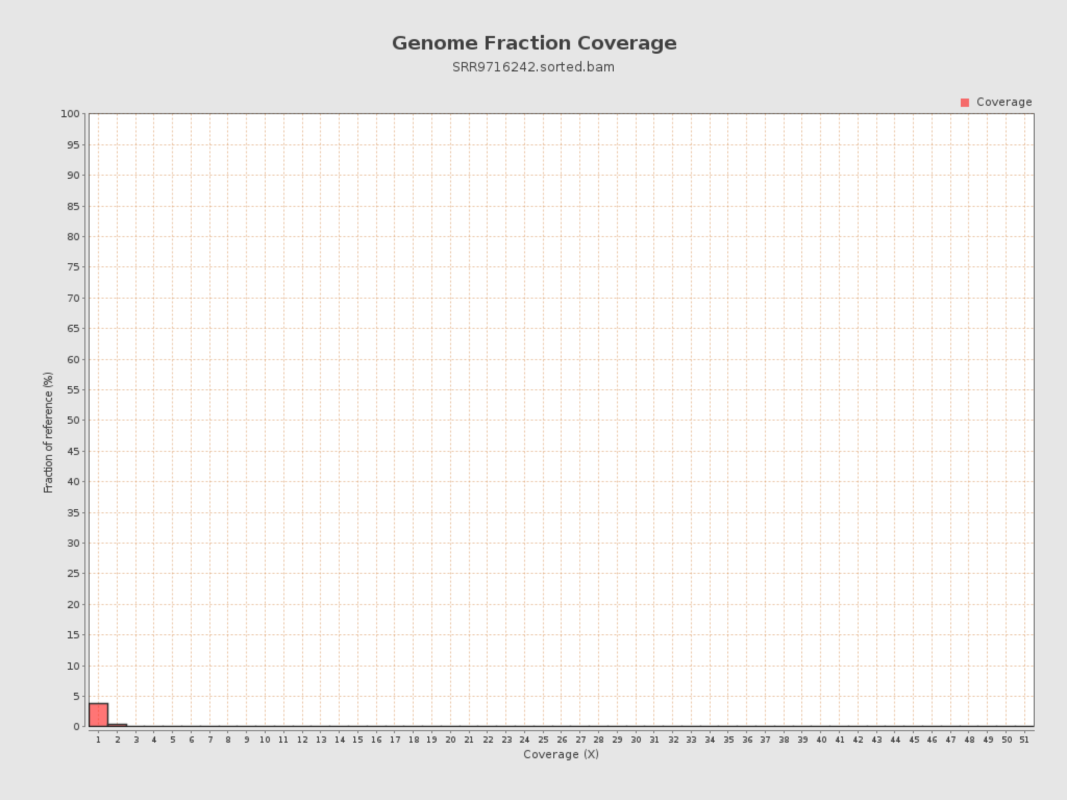
4. Results : Coverage Histogram



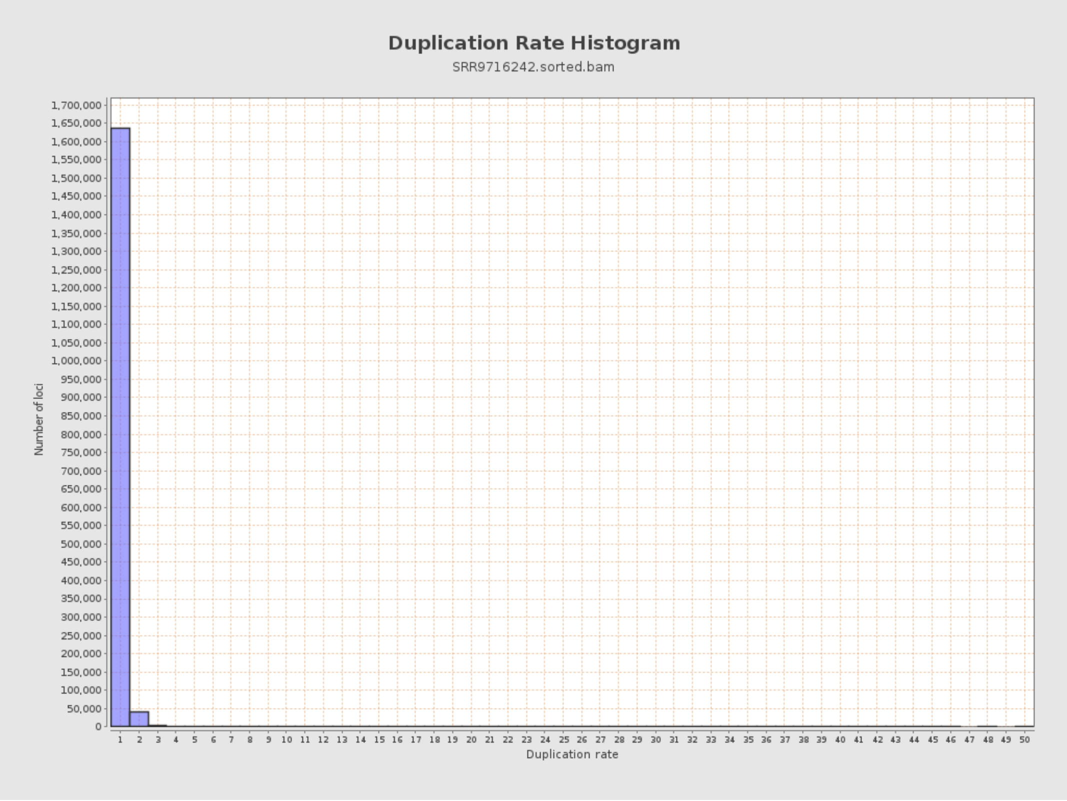
5. Results : Coverage Histogram (0-50X)



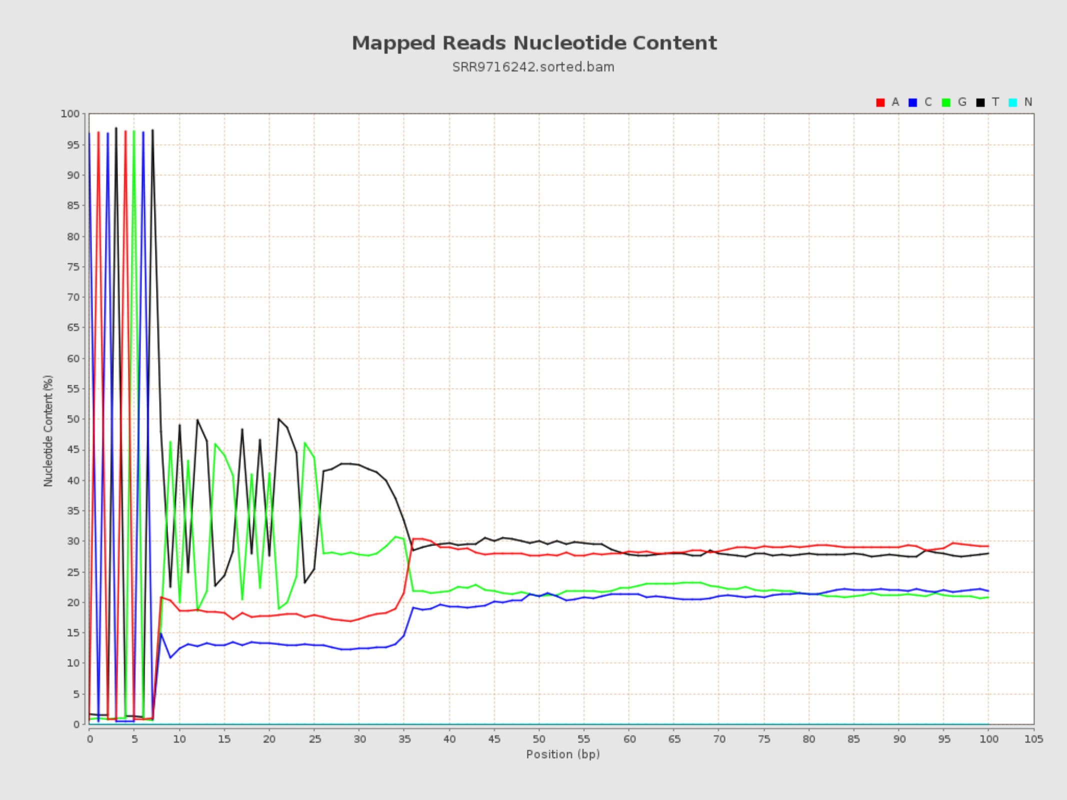
6. Results : Genome Fraction Coverage



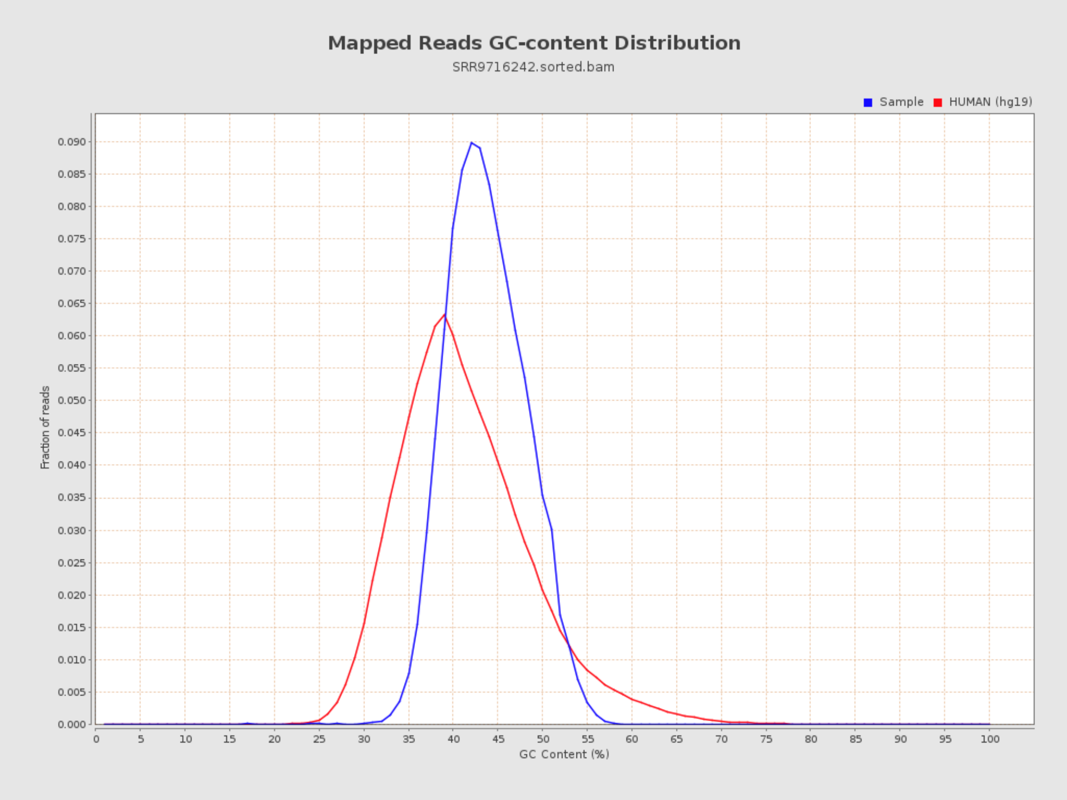
7. Results : Duplication Rate Histogram



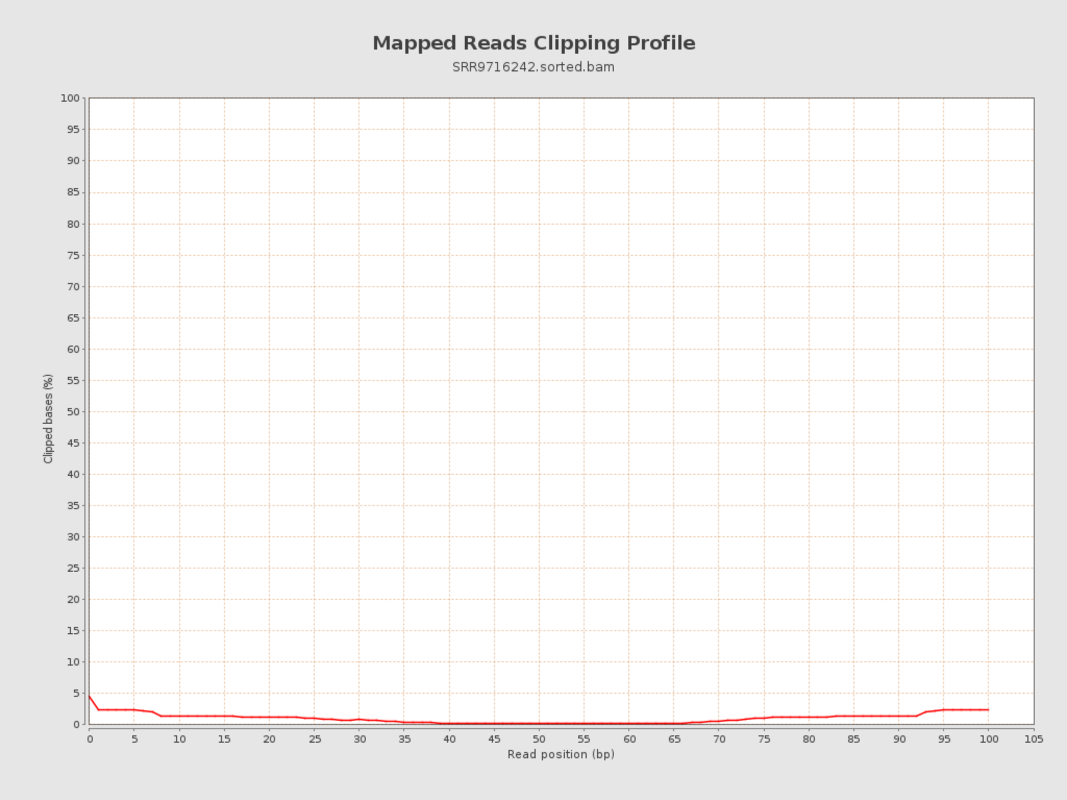
8. Results : Mapped Reads Nucleotide Content



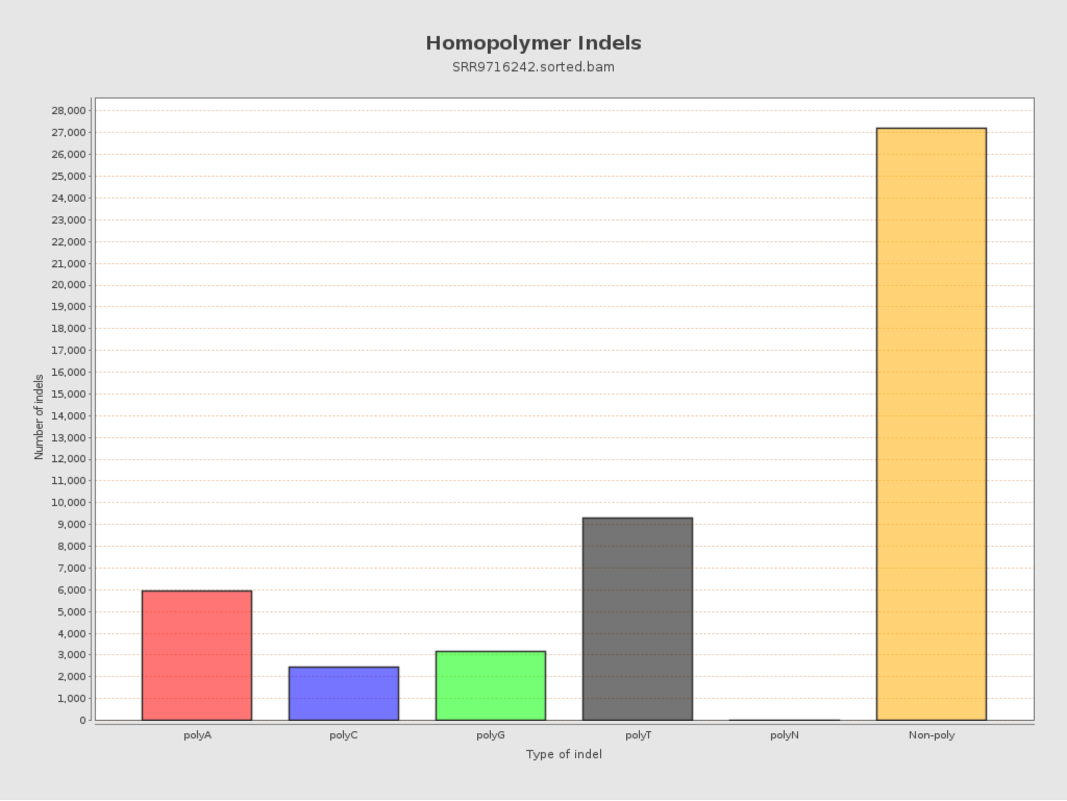
9. Results : Mapped Reads GC-content Distribution



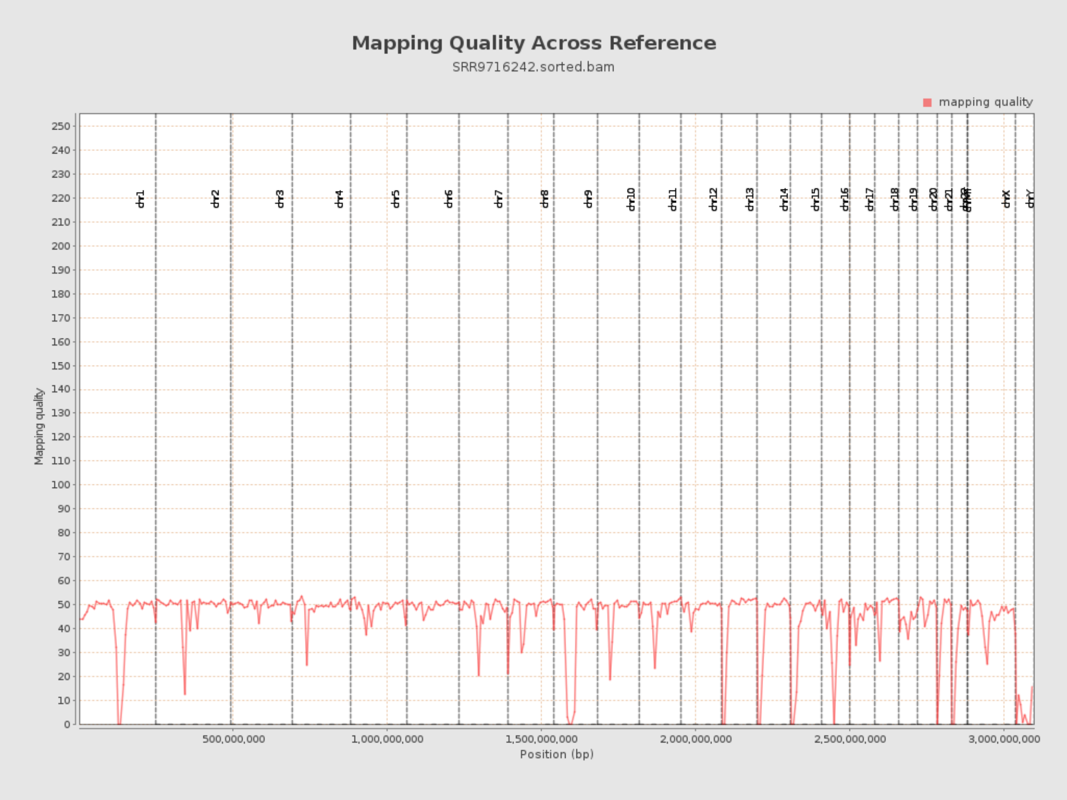
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram