Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:49:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716493.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_SRR9716493 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716493.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:49:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716493.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,126,721
Mapped reads	2,814,364 / 90.01%
Unmapped reads	312,357 / 9.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,161 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	134,802 / 4.31%
Duplication rate	3.46%
Clipped reads	2,821,376 / 90.23%

2.2. ACGT Content

Number/percentage of A's	40,847,658 / 25.23%
Number/percentage of C's	29,963,274 / 18.51%
Number/percentage of T's	51,750,812 / 31.97%
Number/percentage of G's	39,310,842 / 24.28%
Number/percentage of N's	2,709 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0523

Standard Deviation	0.4554

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Mismatches and indels

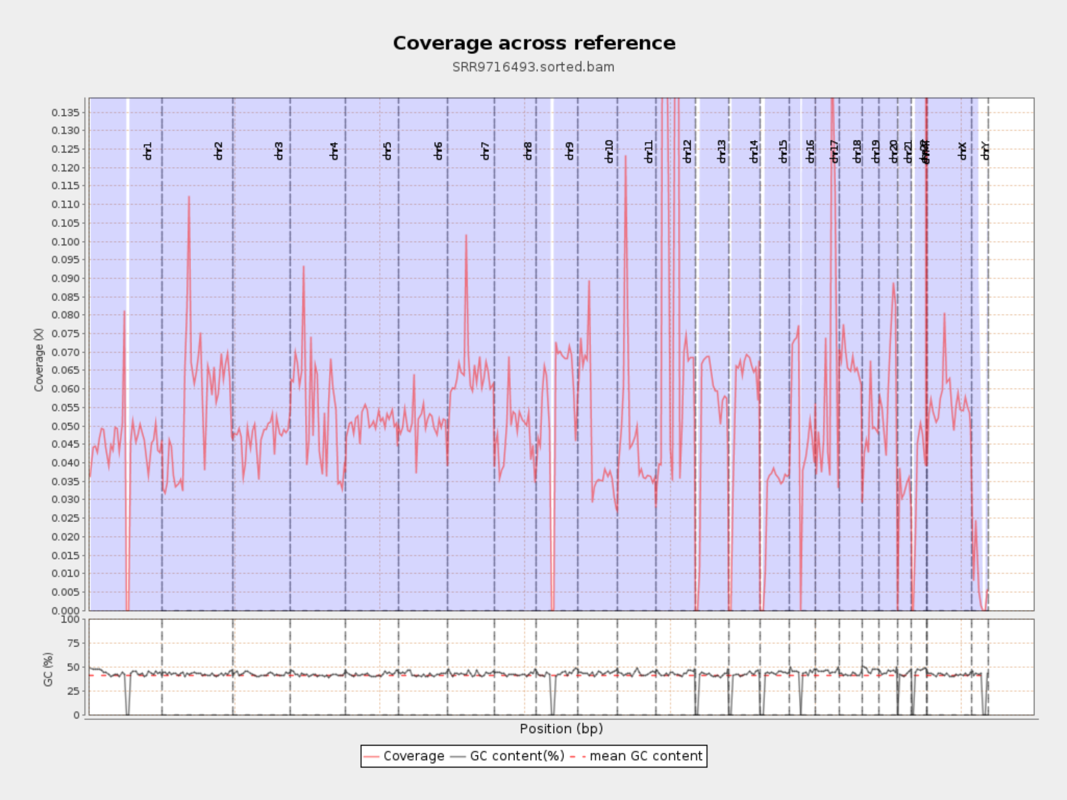
General error rate	0.55%
Mismatches	864,289
Insertions	12,522
Mapped reads with at least one insertion	0.44%
Deletions	27,137
Mapped reads with at least one deletion	0.96%
Homopolymer indels	41.07%

2.6. Chromosome stats

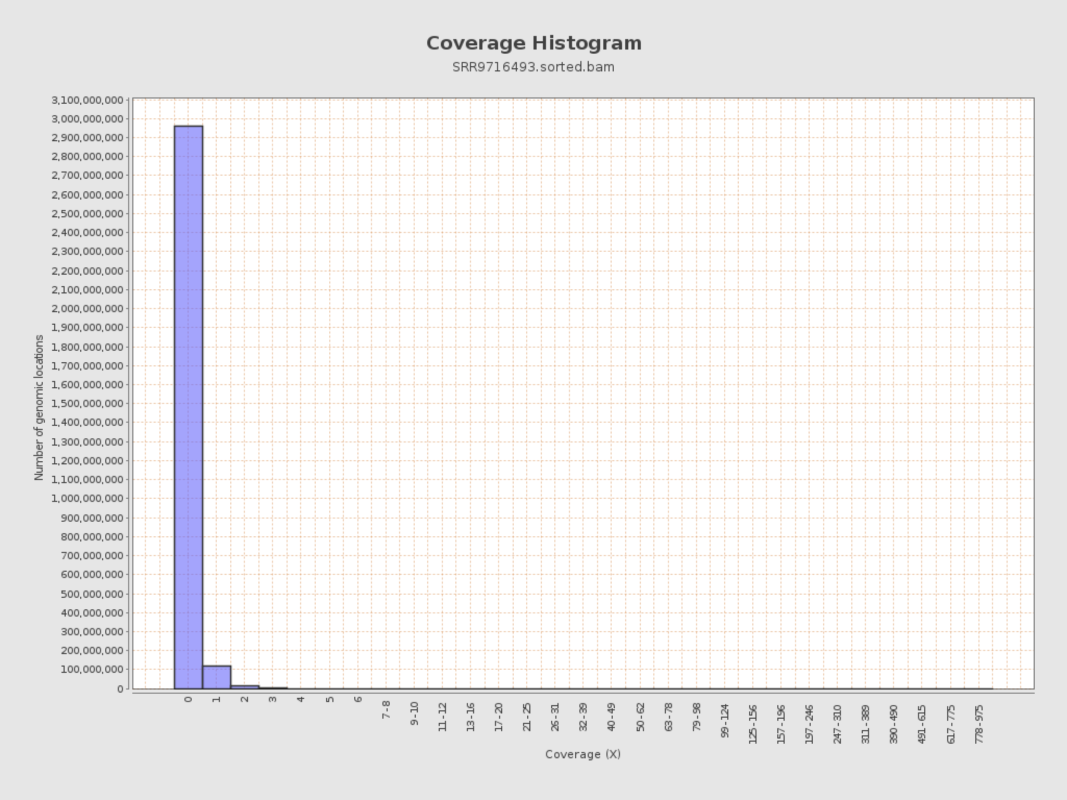
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10918620	0.0438	0.7744
chr2	243199373	13760213	0.0566	0.5281
chr3	198022430	9317024	0.0471	0.2453
chr4	191154276	10464753	0.0547	0.3148
chr5	180915260	9244976	0.0511	0.2653
chr6	171115067	8698855	0.0508	0.3079
chr7	159138663	10299630	0.0647	0.6606

chr8	146364022	7026722	0.048	0.4107
chr9	141213431	7798301	0.0552	0.5232
chr10	135534747	6357122	0.0469	0.4531
chr11	135006516	6506626	0.0482	0.3937
chr12	133851895	12635103	0.0944	0.4172
chr13	115169878	5897243	0.0512	0.2572
chr14	107349540	5910184	0.0551	0.3179
chr15	102531392	2994947	0.0292	0.1961
chr16	90354753	4585165	0.0507	0.2935
chr17	81195210	5091893	0.0627	0.3039
chr18	78077248	5264490	0.0674	0.9163
chr19	59128983	2879068	0.0487	0.6067
chr20	63025520	3955307	0.0628	0.2999
chr21	48129895	1460385	0.0303	0.2648
chr22	51304566	1655373	0.0323	0.201
chrMT	16571	24699	1.4905	1.4786
chrX	155270560	8727304	0.0562	0.3724
chrY	59373566	446800	0.0075	0.166

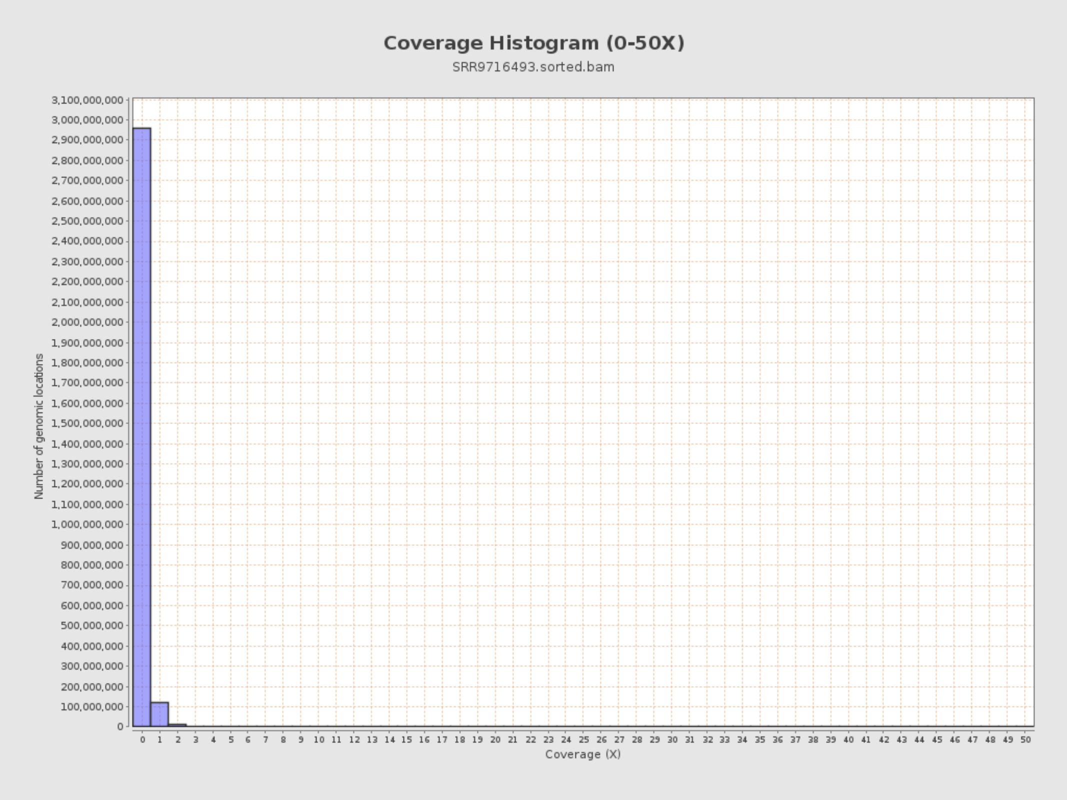
3. Results : Coverage across reference



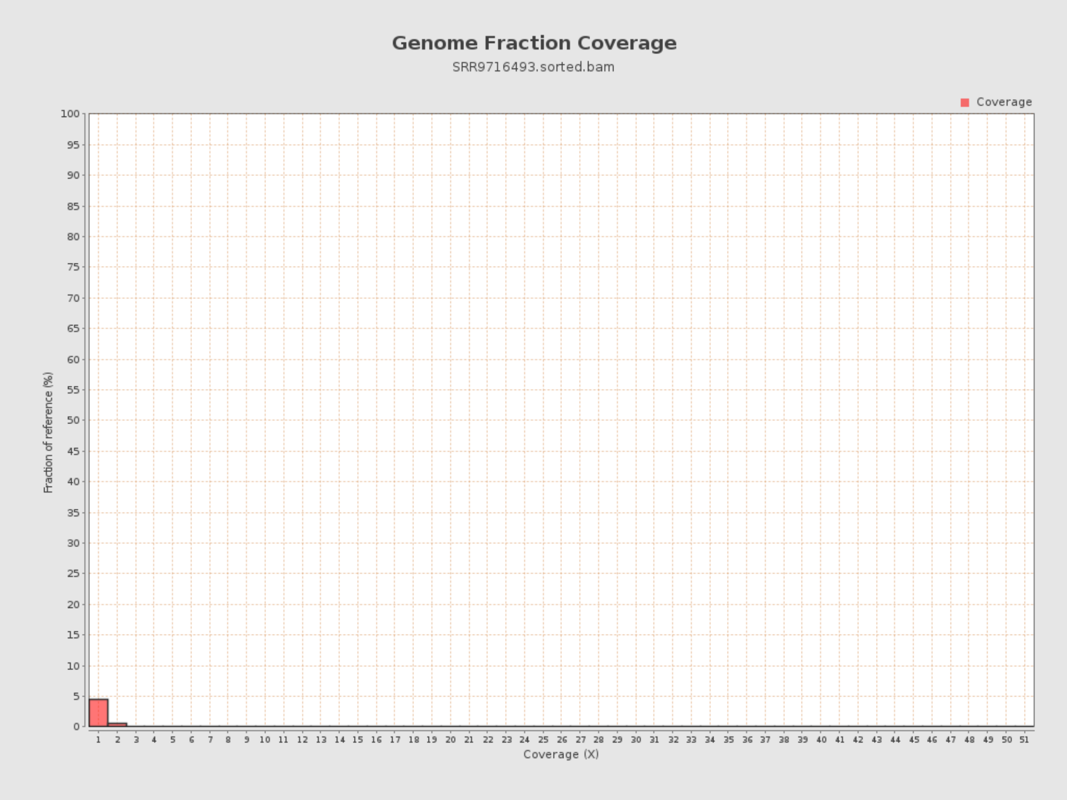
4. Results : Coverage Histogram



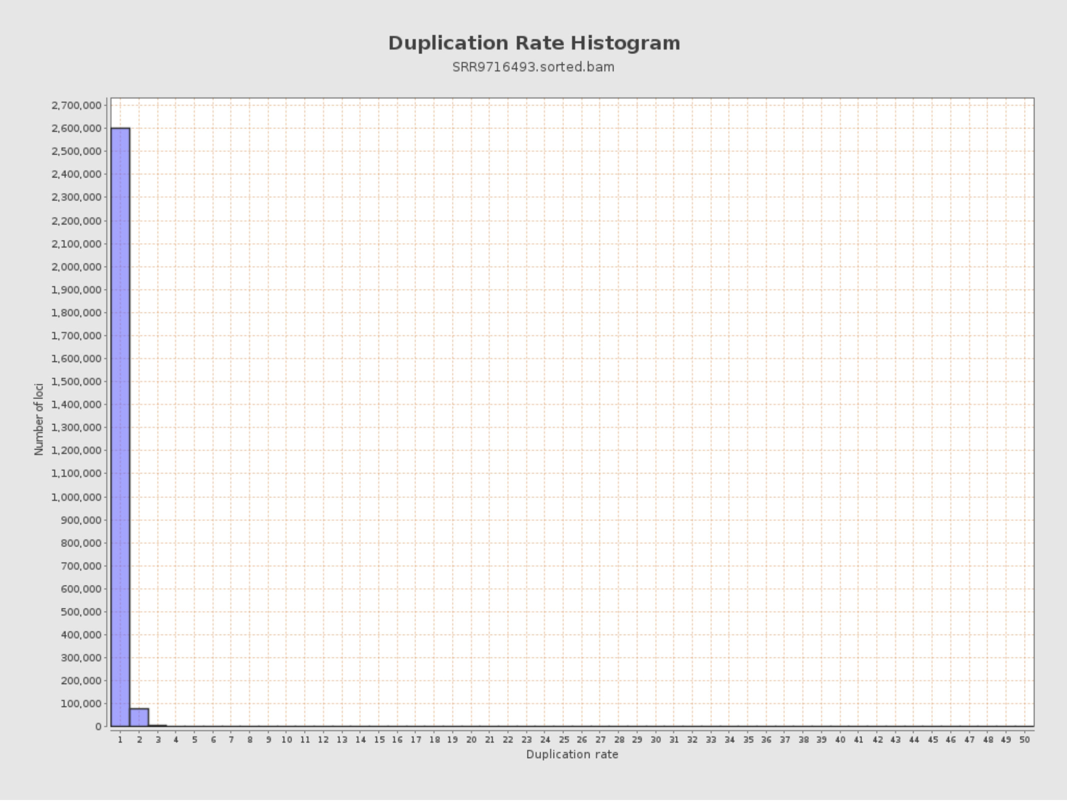
5. Results : Coverage Histogram (0-50X)



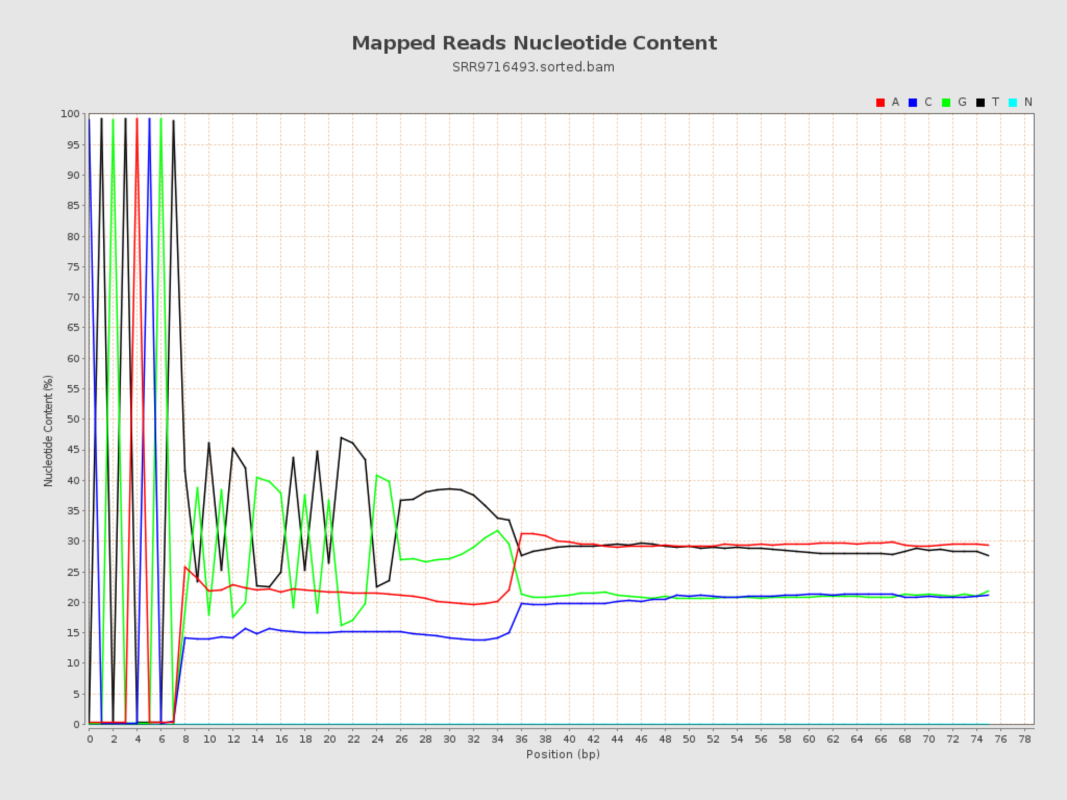
6. Results : Genome Fraction Coverage



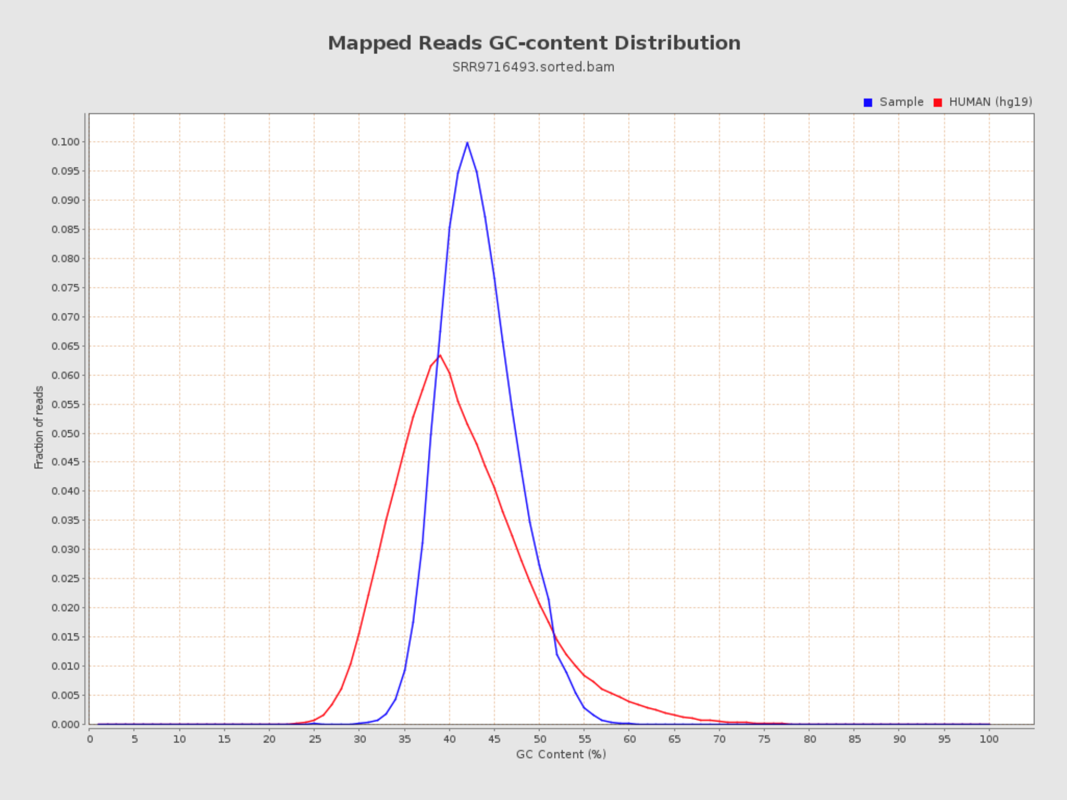
7. Results : Duplication Rate Histogram



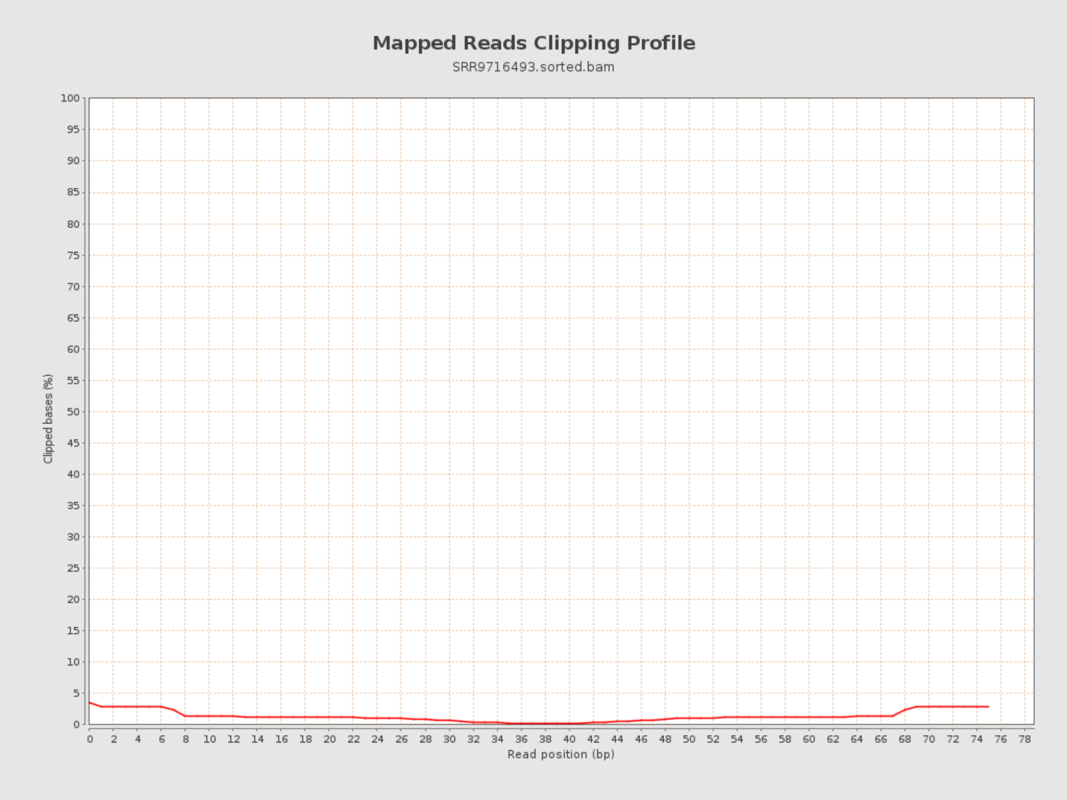
8. Results : Mapped Reads Nucleotide Content



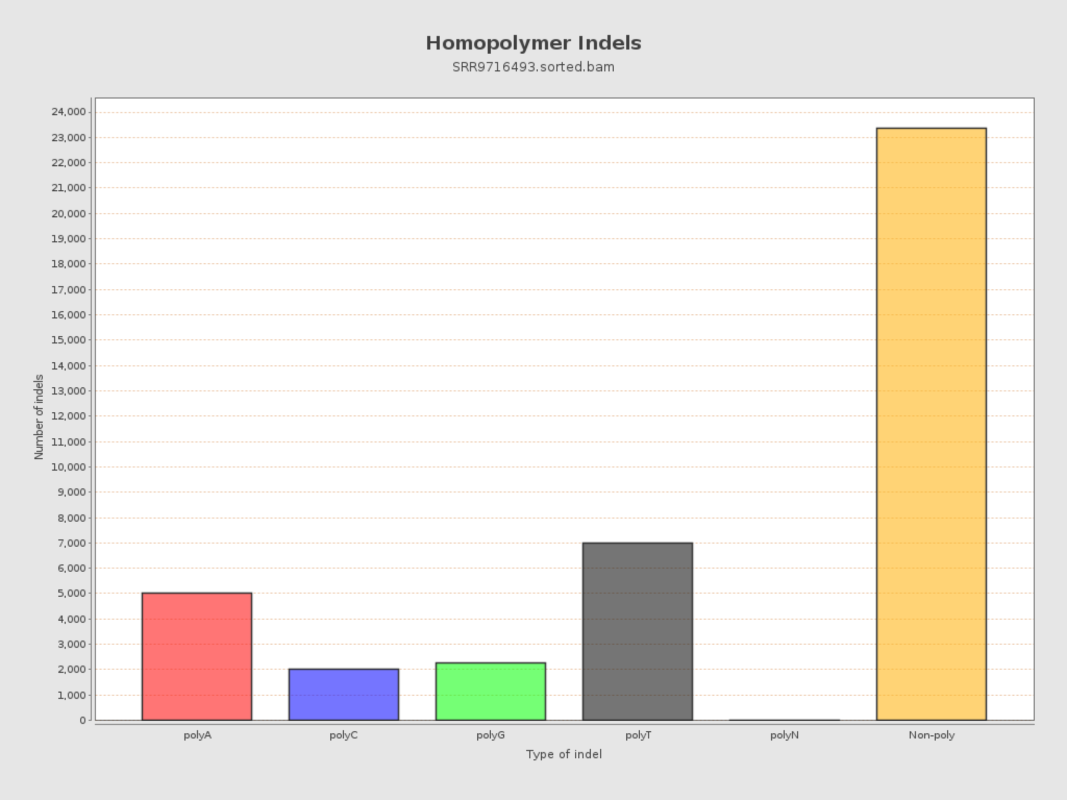
9. Results : Mapped Reads GC-content Distribution



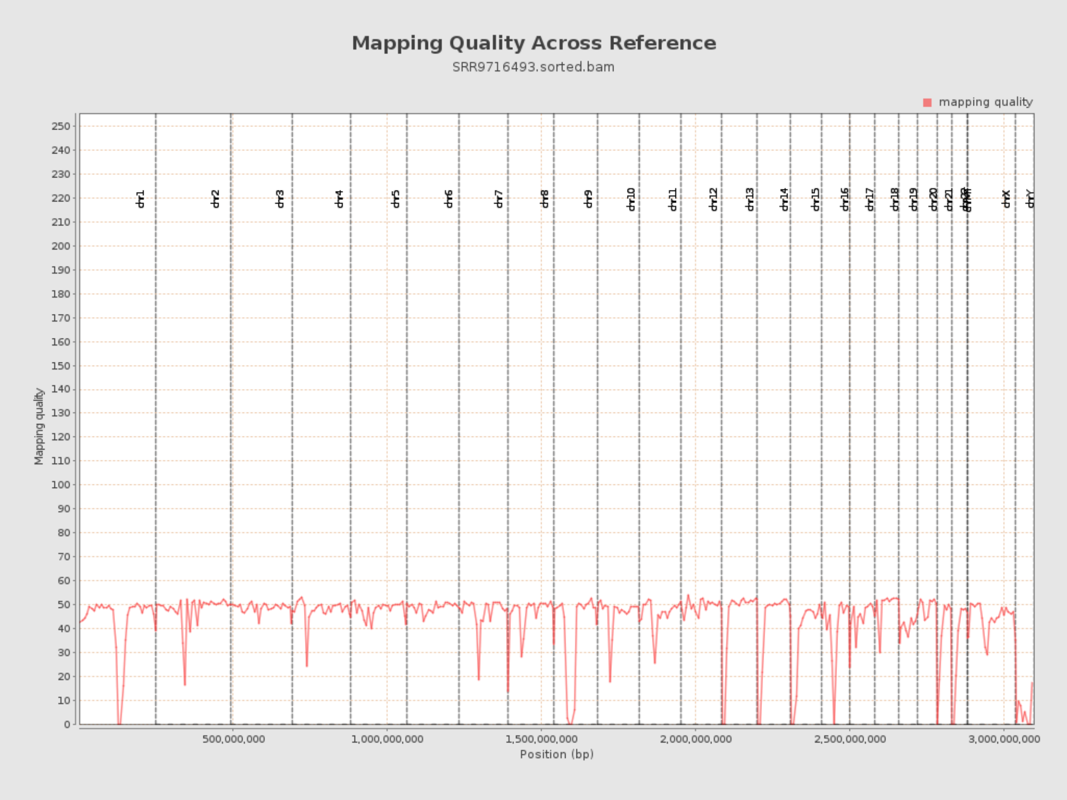
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram