Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:38:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716863.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_SRR9716863 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716863.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:38:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716863.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,529,179
Mapped reads	1,419,781 / 92.85%
Unmapped reads	109,398 / 7.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,832 / 2.02%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	57,300 / 3.75%
Duplication rate	3.14%
Clipped reads	1,448,611 / 94.73%

2.2. ACGT Content

Number/percentage of A's	27,889,811 / 25.5%
Number/percentage of C's	22,106,956 / 20.21%
Number/percentage of T's	32,976,303 / 30.15%
Number/percentage of G's	26,406,015 / 24.14%
Number/percentage of N's	4,367 / 0%
GC Percentage	44.35%

2.3. Coverage

Mean	0.0353

Standard Deviation	0.3019

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

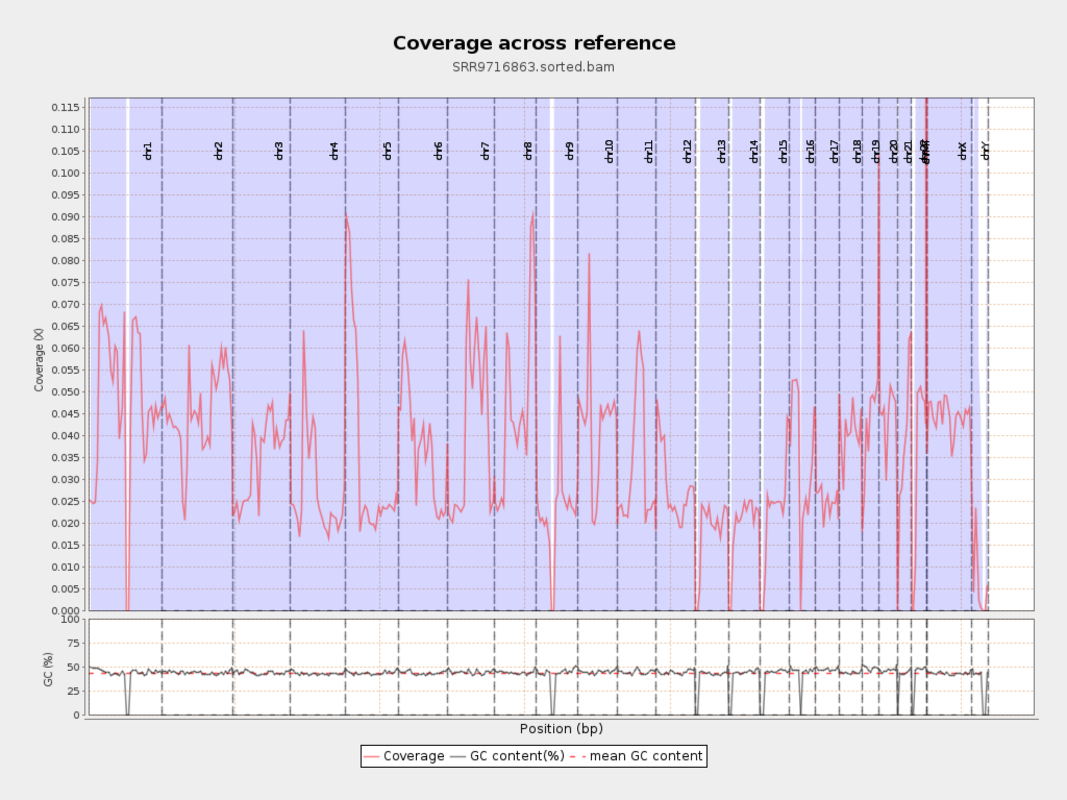
General error rate	0.69%
Mismatches	731,179
Insertions	9,591
Mapped reads with at least one insertion	0.66%
Deletions	21,309
Mapped reads with at least one deletion	1.47%
Homopolymer indels	38.42%

2.6. Chromosome stats

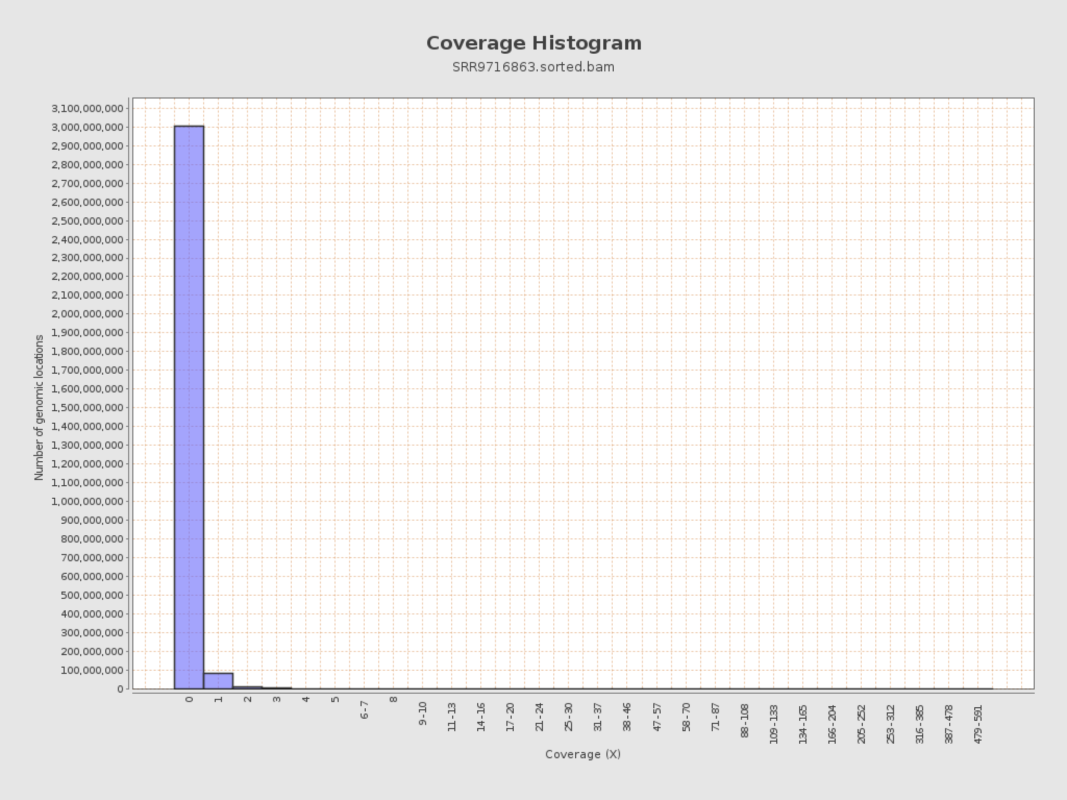
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11787307	0.0473	0.5559
chr2	243199373	11013428	0.0453	0.3283
chr3	198022430	6910574	0.0349	0.2145
chr4	191154276	5183525	0.0271	0.2597
chr5	180915260	6389280	0.0353	0.2173
chr6	171115067	6434393	0.0376	0.2309
chr7	159138663	6644563	0.0418	0.3863

chr8	146364022	6782694	0.0463	0.3282
chr9	141213431	3192577	0.0226	0.2104
chr10	135534747	5772184	0.0426	0.4139
chr11	135006516	4492319	0.0333	0.2529
chr12	133851895	3810138	0.0285	0.1918
chr13	115169878	2063915	0.0179	0.148
chr14	107349540	2071006	0.0193	0.1632
chr15	102531392	2255505	0.022	0.1673
chr16	90354753	3187975	0.0353	0.2266
chr17	81195210	2024289	0.0249	0.202
chr18	78077248	3179194	0.0407	0.3219
chr19	59128983	2632120	0.0445	0.4072
chr20	63025520	2805069	0.0445	0.252
chr21	48129895	1817173	0.0378	0.2605
chr22	51304566	1689453	0.0329	0.2125
chrMT	16571	34043	2.0544	2.1326
chrX	155270560	6886166	0.0443	0.25
chrY	59373566	368887	0.0062	0.2227

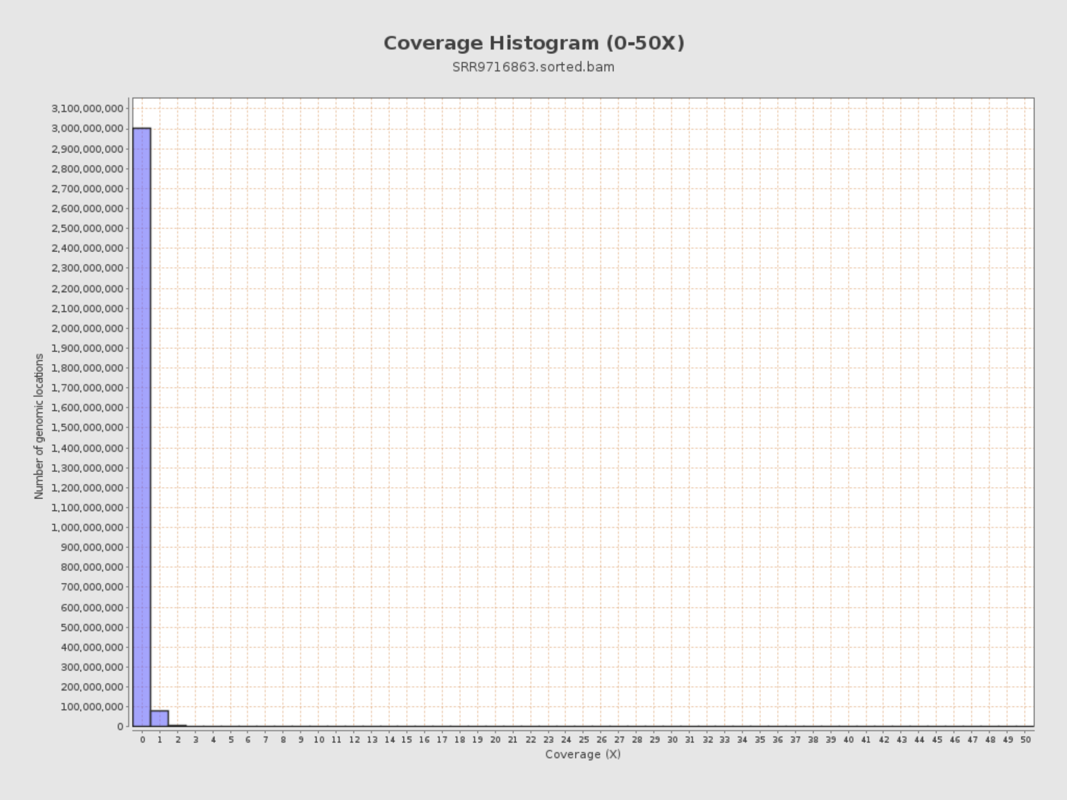
3. Results : Coverage across reference



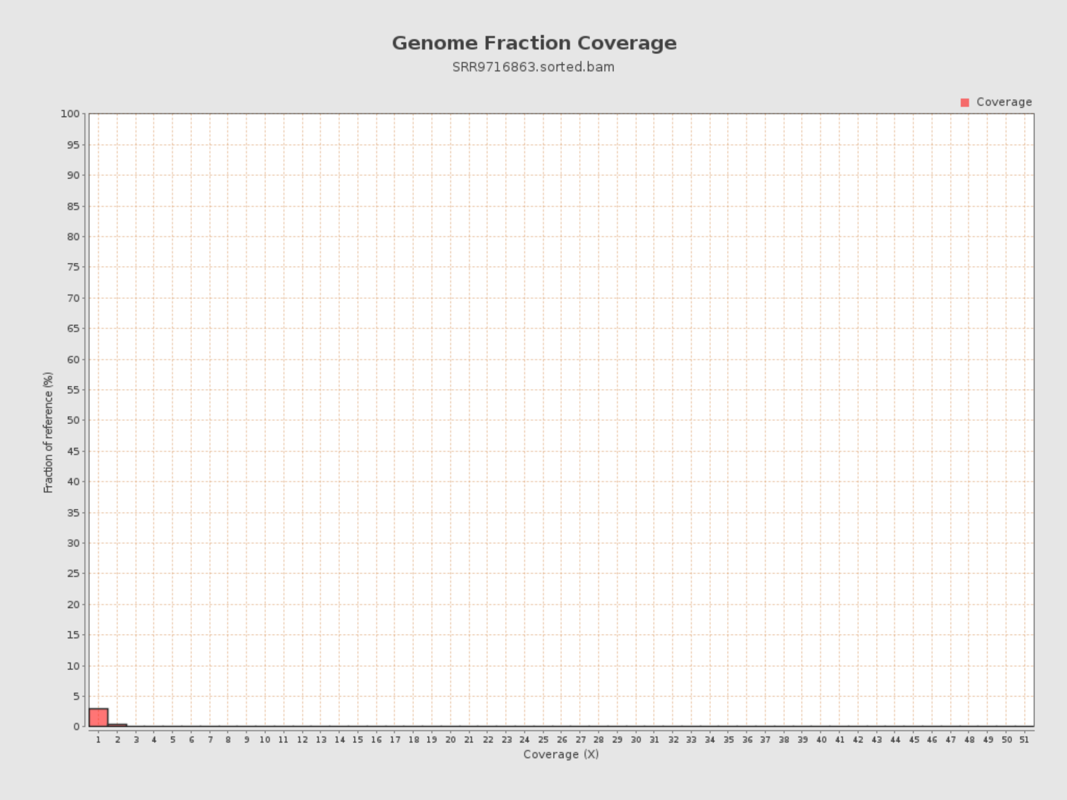
4. Results : Coverage Histogram



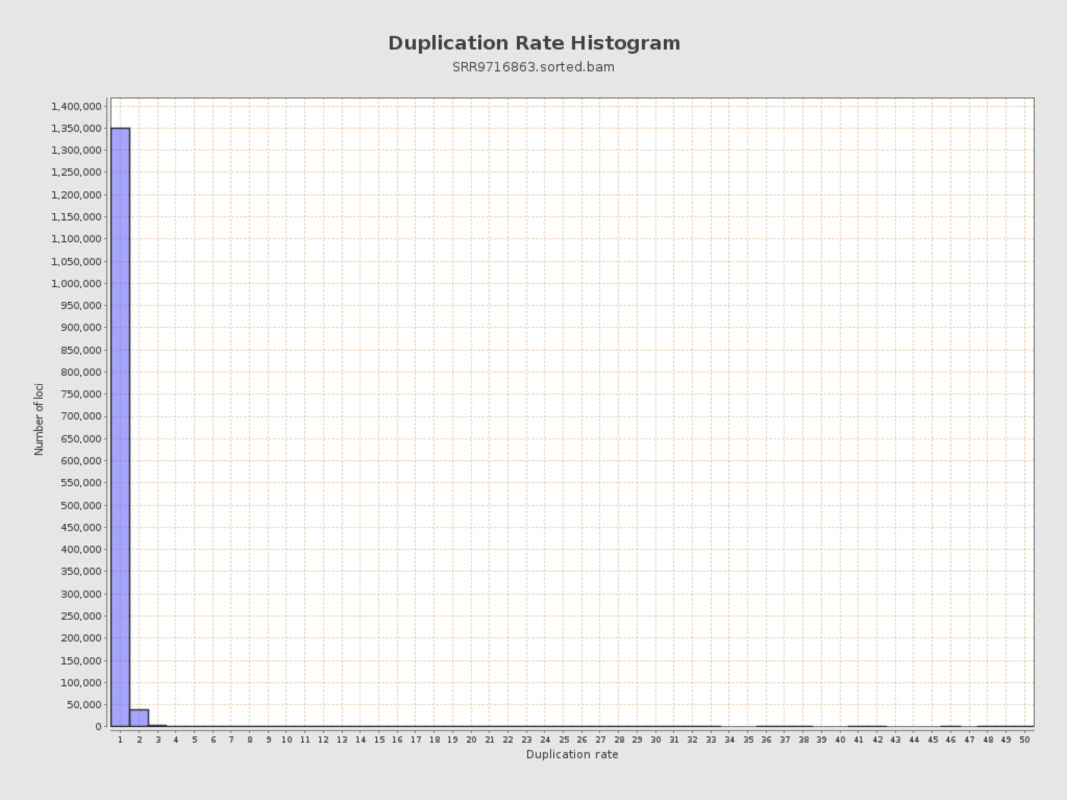
5. Results : Coverage Histogram (0-50X)



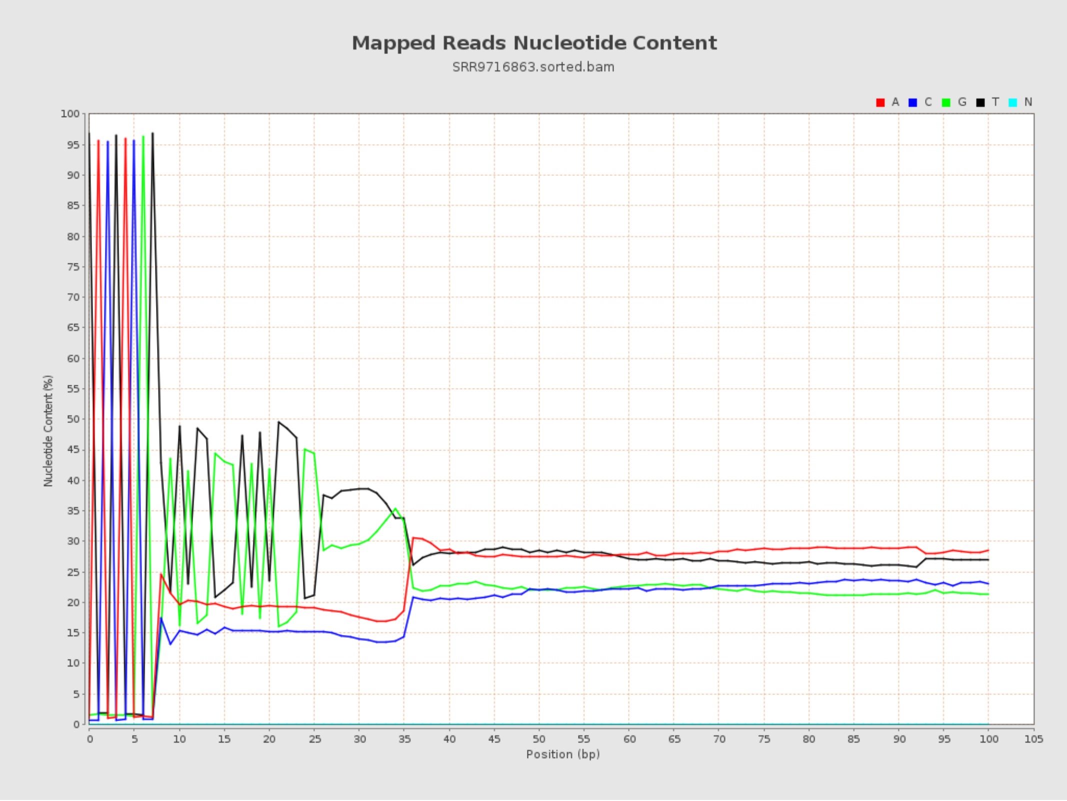
6. Results : Genome Fraction Coverage



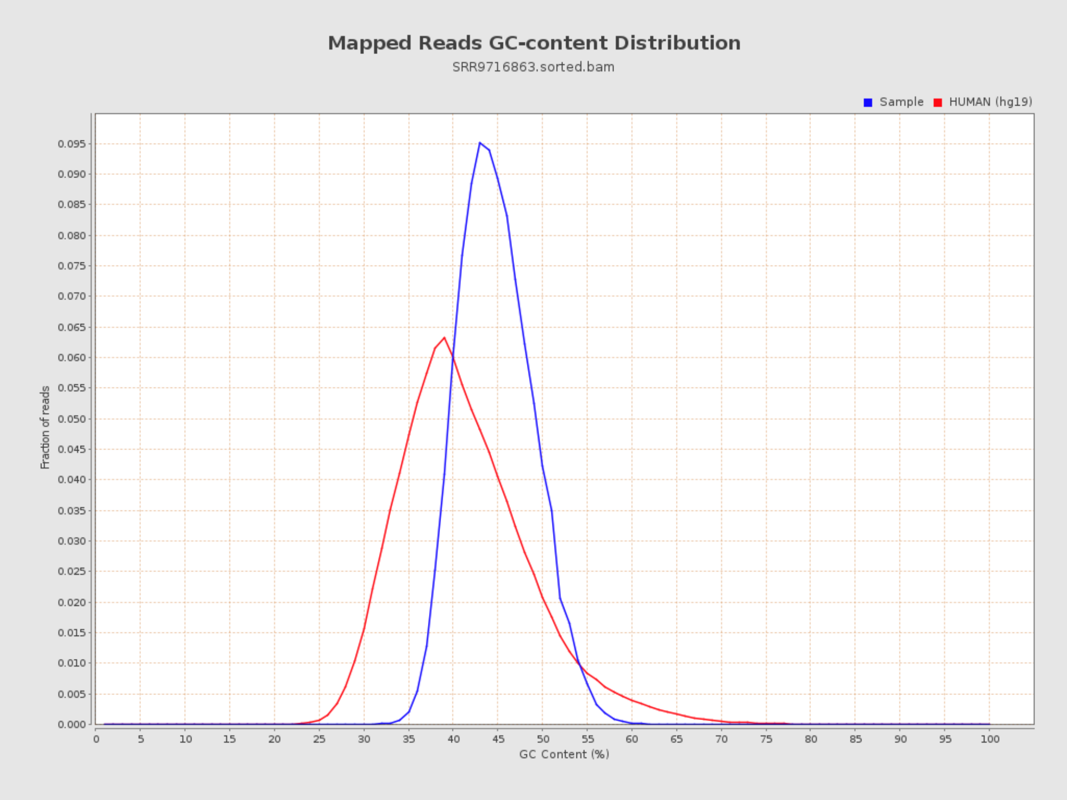
7. Results : Duplication Rate Histogram



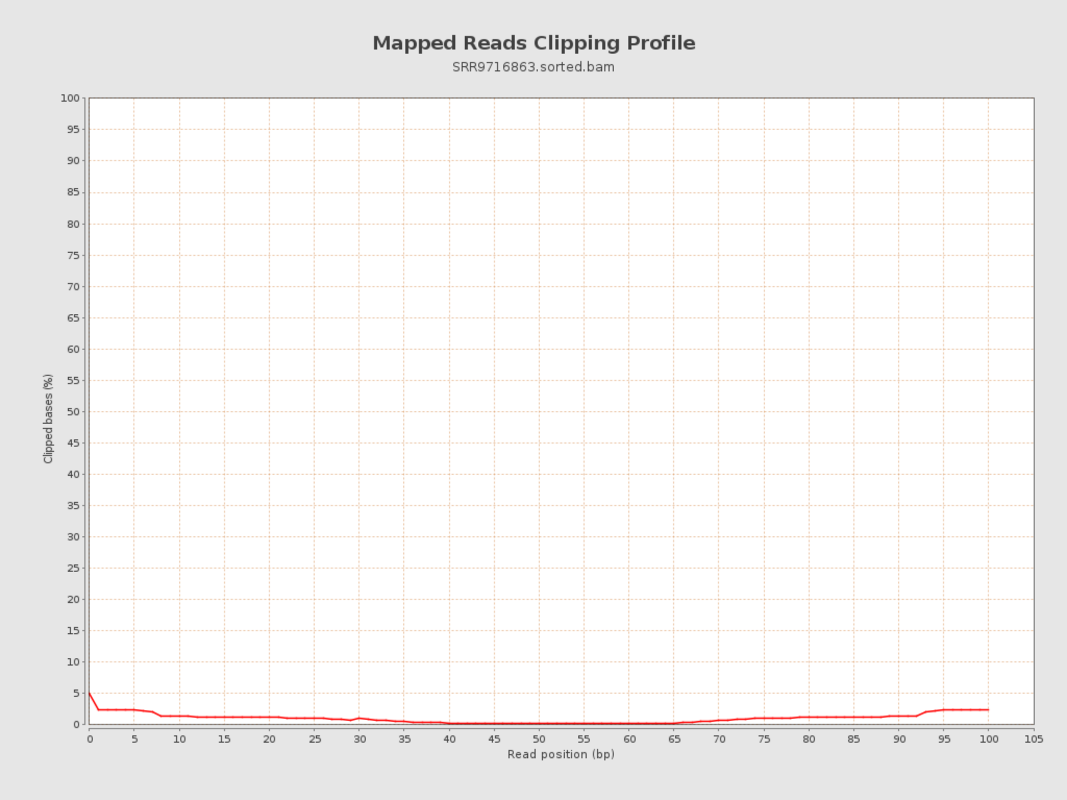
8. Results : Mapped Reads Nucleotide Content



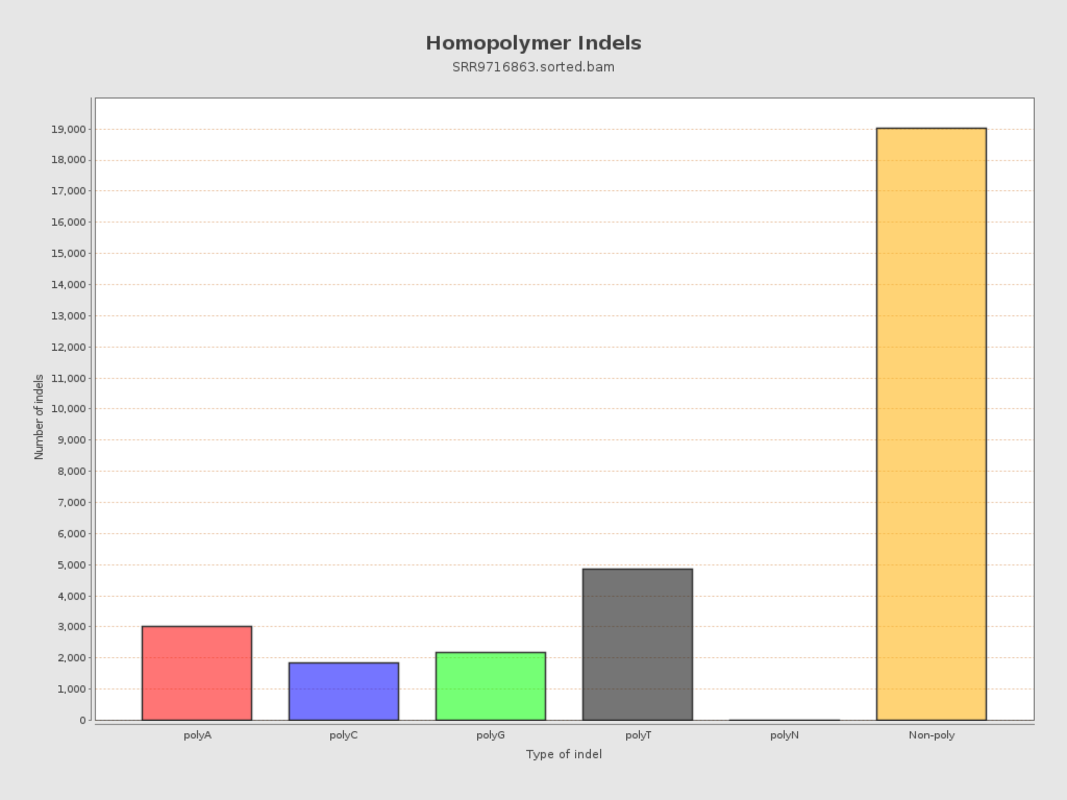
9. Results : Mapped Reads GC-content Distribution



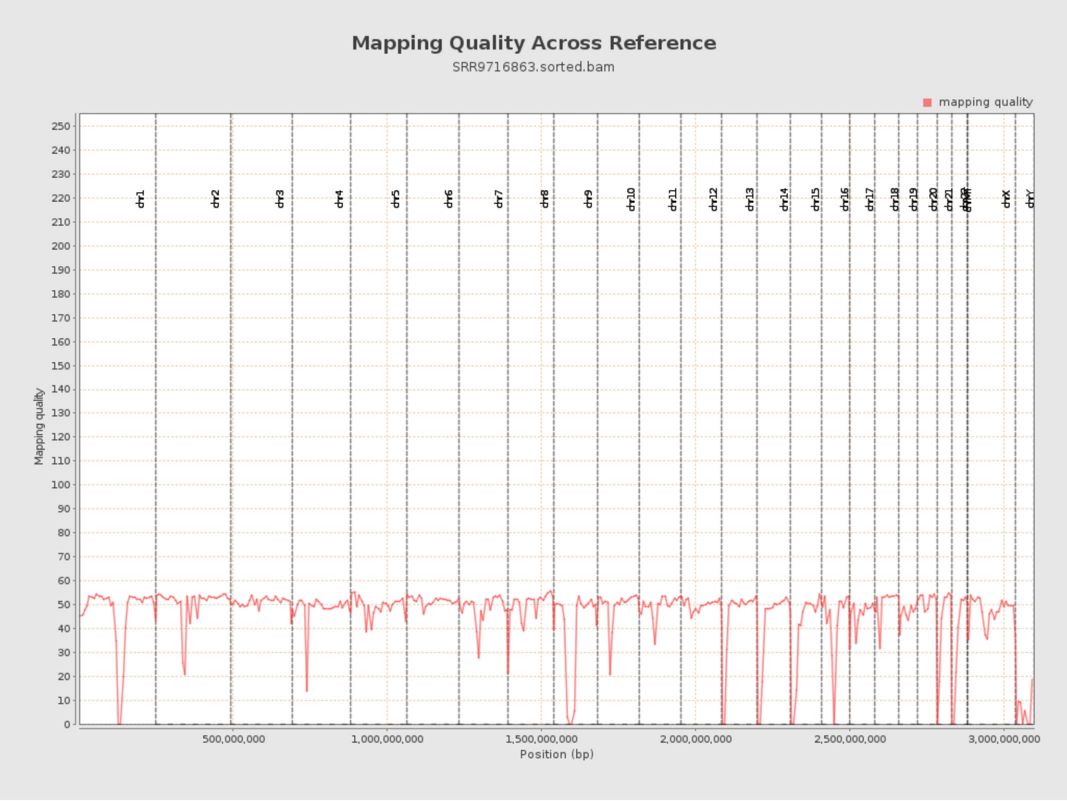
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram