Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 21:55:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716563.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_SRR9716563 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716563.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 21:55:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716563.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,901,262
Mapped reads	16,476,162 / 97.48%
Unmapped reads	425,100 / 2.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,589 / 0.05%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	860,003 / 5.09%
Duplication rate	1.88%
Clipped reads	16,368,673 / 96.85%

2.2. ACGT Content

Number/percentage of A's	319,613,692 / 28.48%
Number/percentage of C's	232,233,829 / 20.7%
Number/percentage of T's	338,319,408 / 30.15%
Number/percentage of G's	231,844,683 / 20.66%
Number/percentage of N's	56,762 / 0.01%
GC Percentage	41.36%

2.3. Coverage

Mean	0.3625

Standard Deviation	4.0863

2.4. Mapping Quality

Mean Mapping Quality	49.19

2.5. Mismatches and indels

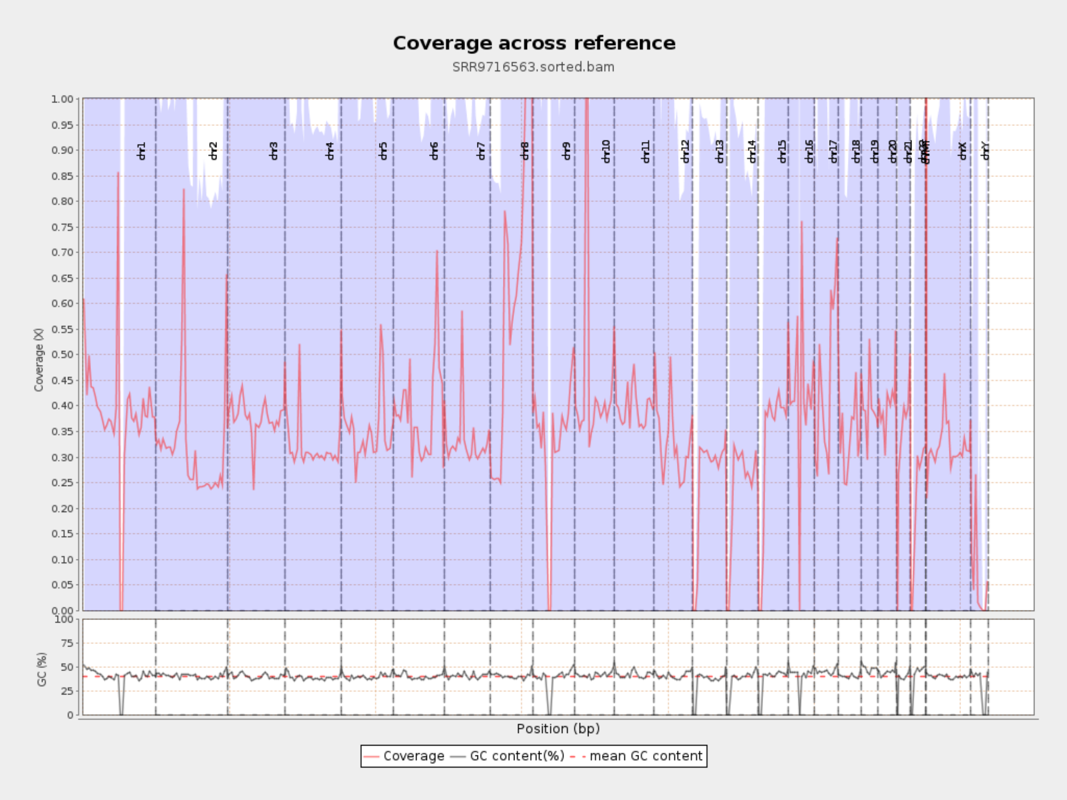
General error rate	0.31%
Mismatches	3,315,356
Insertions	99,959
Mapped reads with at least one insertion	0.6%
Deletions	99,382
Mapped reads with at least one deletion	0.6%
Homopolymer indels	38.64%

2.6. Chromosome stats

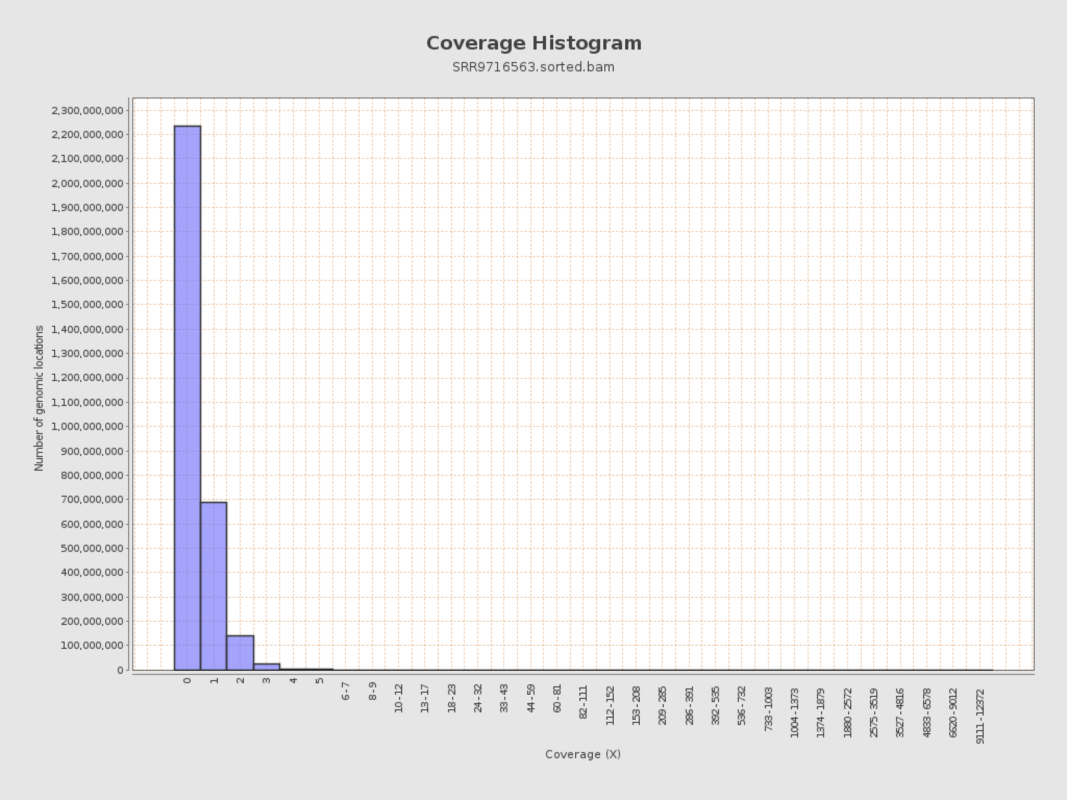
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	96457270	0.387	10.42
chr2	243199373	77812912	0.32	2.2213
chr3	198022430	74695395	0.3772	1.2435
chr4	191154276	61026194	0.3193	1.3797
chr5	180915260	64451843	0.3563	0.7705
chr6	171115067	67038371	0.3918	1.5733
chr7	159138663	53262627	0.3347	3.7676

chr8	146364022	96484837	0.6592	2.6766
chr9	141213431	46492471	0.3292	2.0863
chr10	135534747	59516338	0.4391	7.2643
chr11	135006516	53808341	0.3986	1.8266
chr12	133851895	44709933	0.334	0.8142
chr13	115169878	29378654	0.2551	0.6128
chr14	107349540	25984016	0.2421	0.9947
chr15	102531392	32595244	0.3179	0.6162
chr16	90354753	38875656	0.4303	2.8821
chr17	81195210	35988732	0.4432	1.593
chr18	78077248	26778298	0.343	4.4763
chr19	59128983	23528268	0.3979	7.5552
chr20	63025520	25186368	0.3996	0.8491
chr21	48129895	16163929	0.3358	1.4049
chr22	51304566	10769457	0.2099	0.5563
chrMT	16571	7747827	467.5534	97.3789
chrX	155270560	49915551	0.3215	1.3432
chrY	59373566	3589904	0.0605	2.224

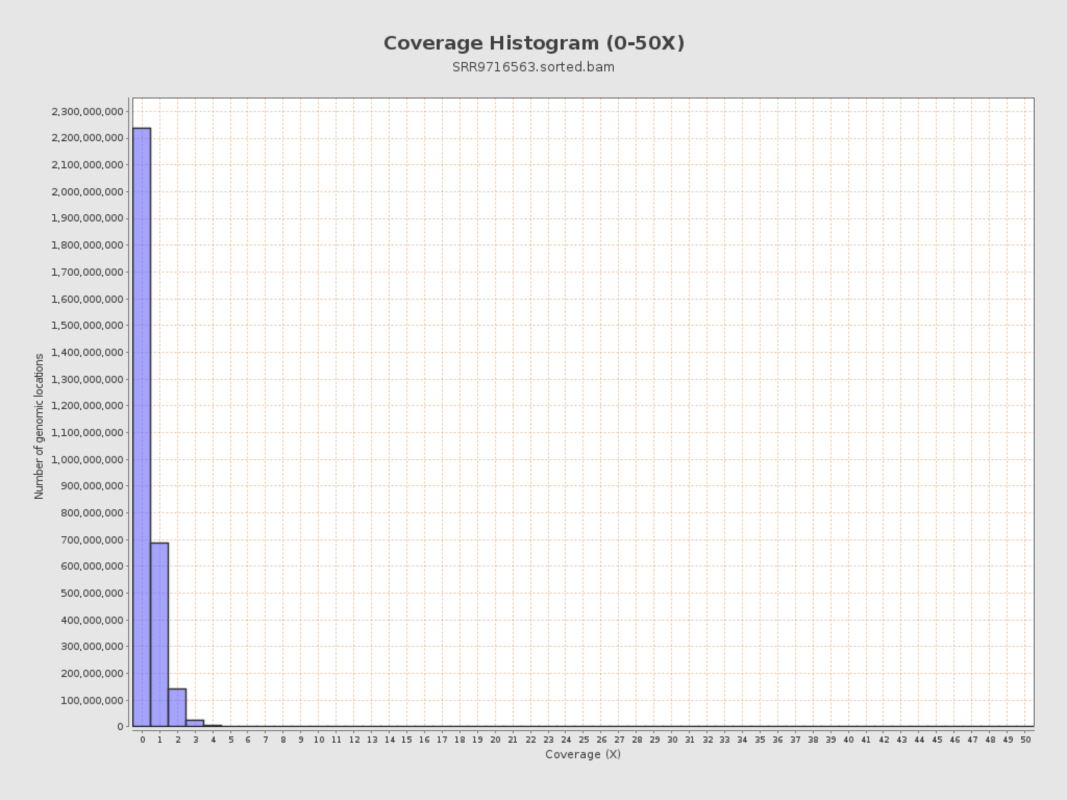
3. Results : Coverage across reference



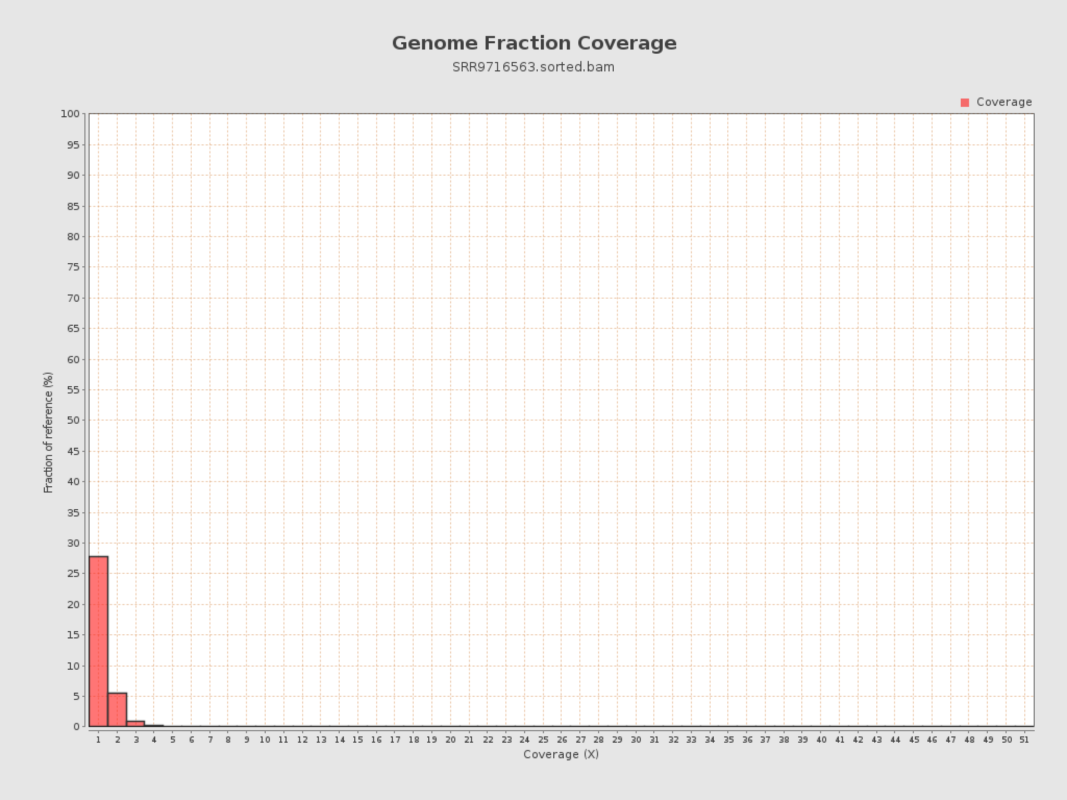
4. Results : Coverage Histogram



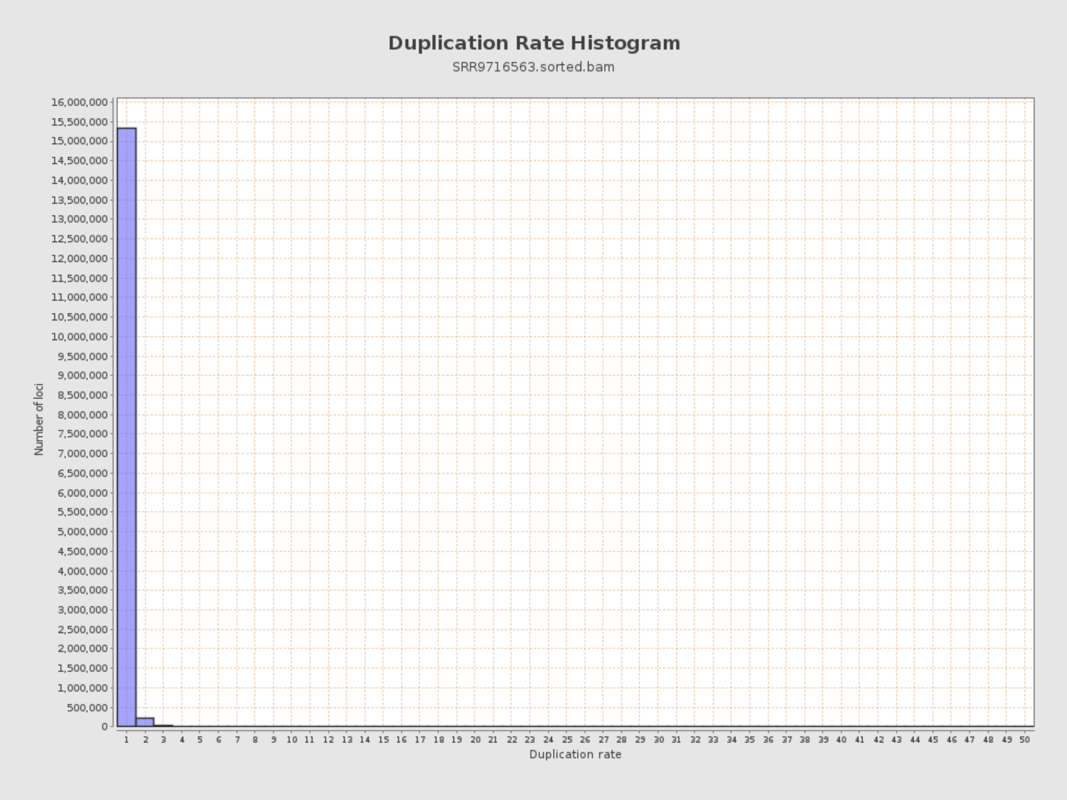
5. Results : Coverage Histogram (0-50X)



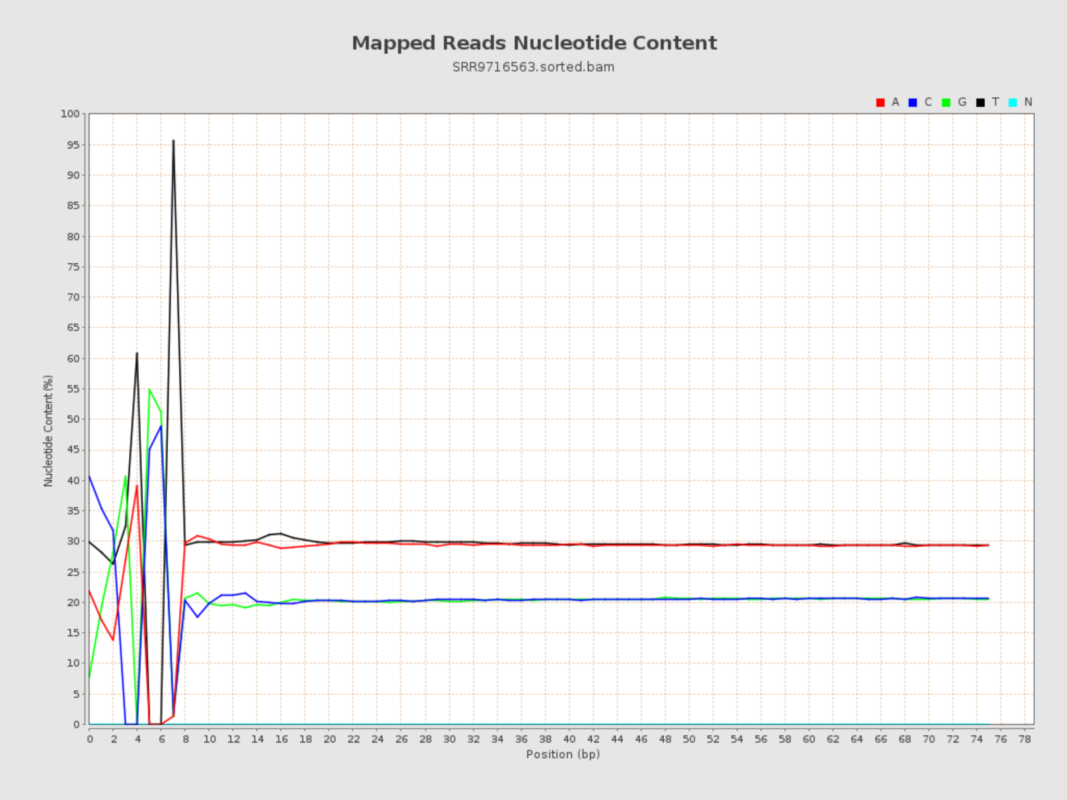
6. Results : Genome Fraction Coverage



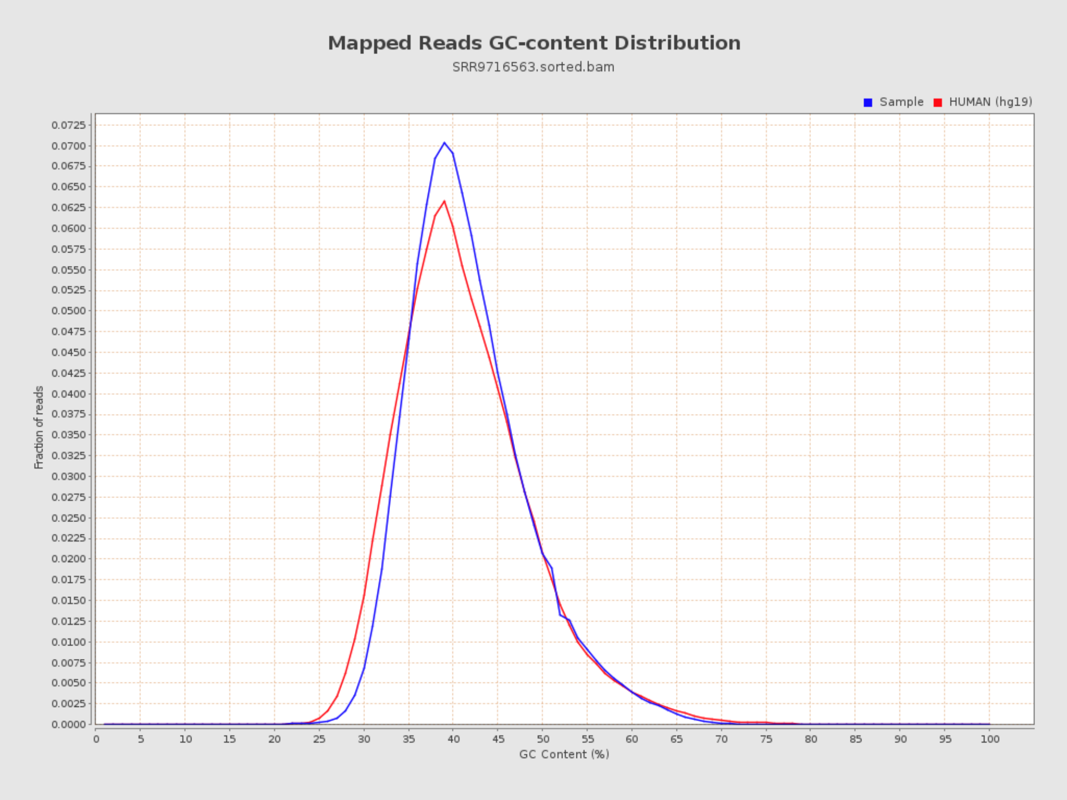
7. Results : Duplication Rate Histogram



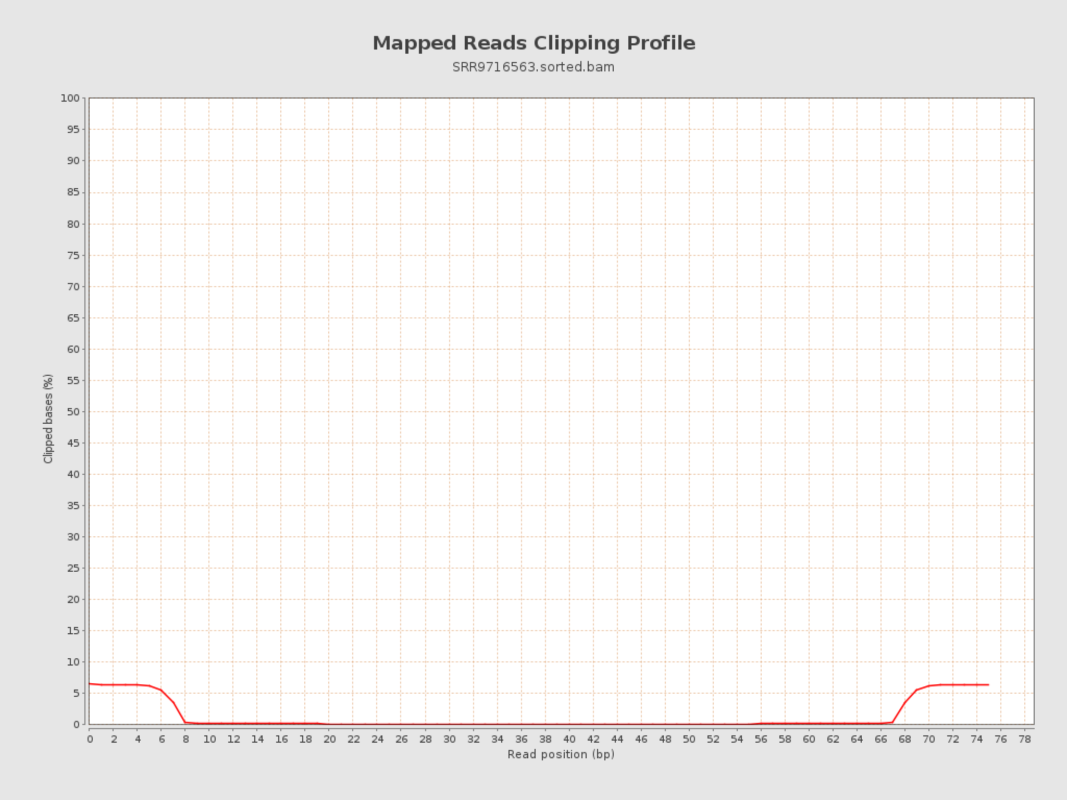
8. Results : Mapped Reads Nucleotide Content



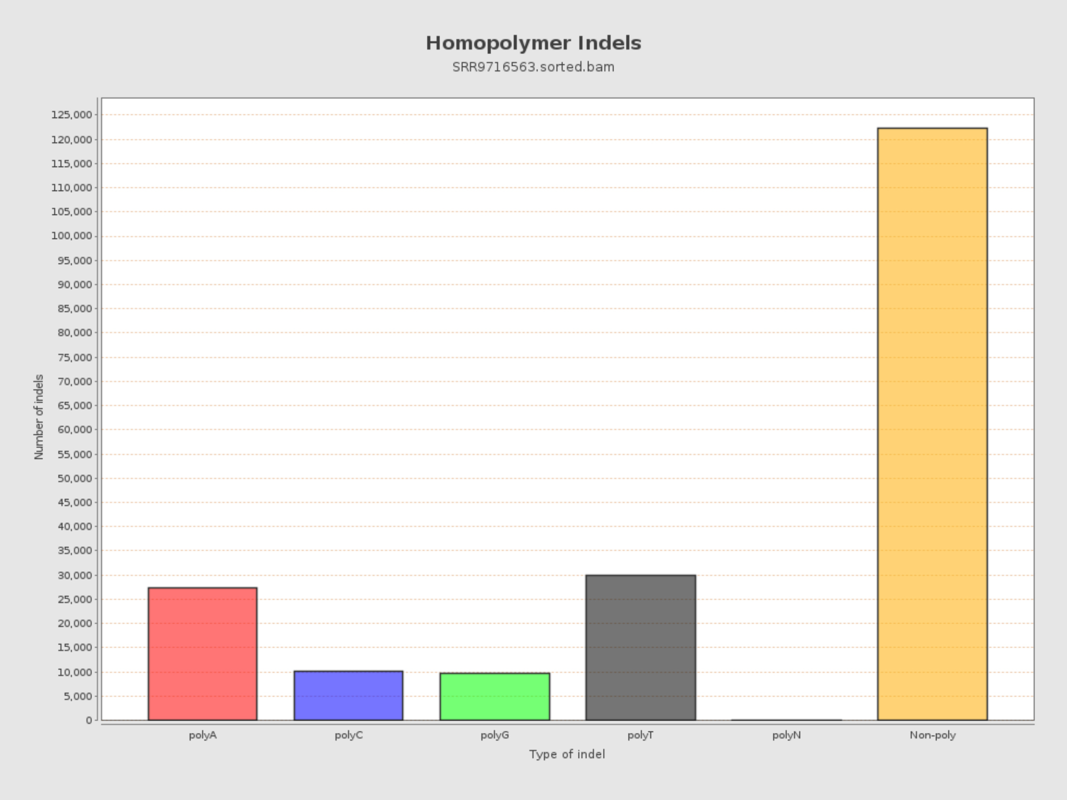
9. Results : Mapped Reads GC-content Distribution



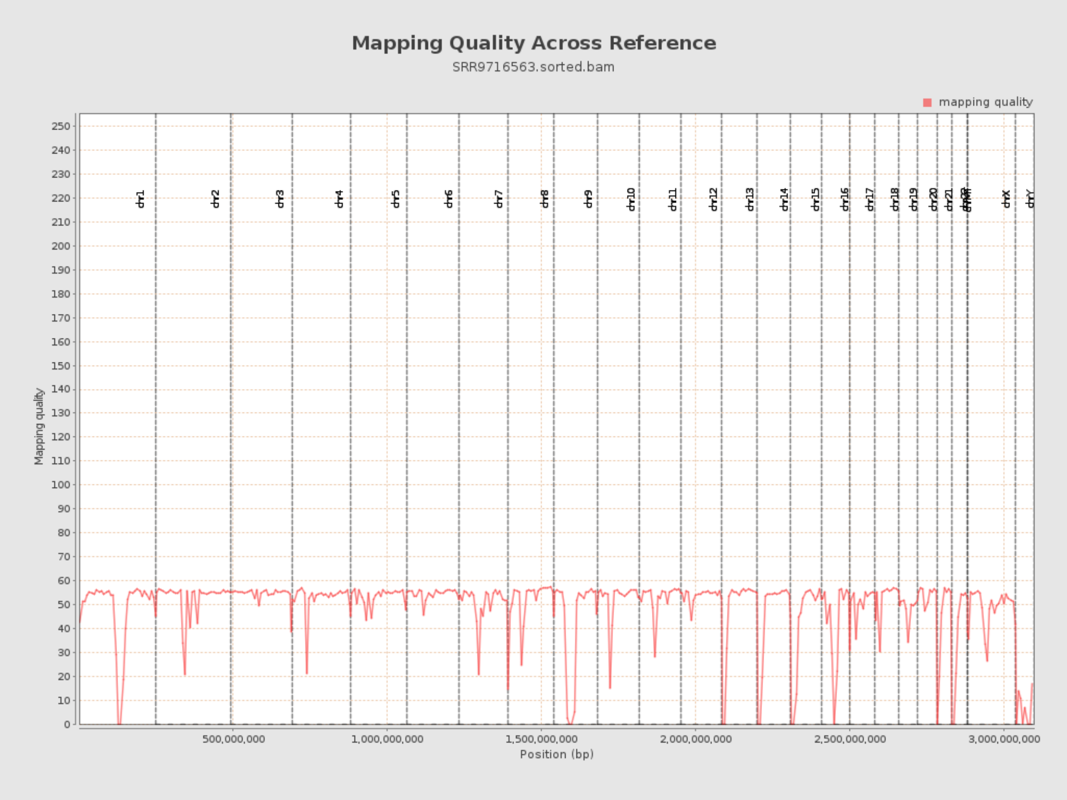
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram