Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:10:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716375.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_SRR9716375 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716375.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:09:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716375.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,321,458
Mapped reads	2,119,778 / 91.31%
Unmapped reads	201,680 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,119 / 1.99%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	89,013 / 3.83%
Duplication rate	3.03%
Clipped reads	2,161,827 / 93.12%

2.2. ACGT Content

Number/percentage of A's	43,415,752 / 26.19%
Number/percentage of C's	32,903,507 / 19.85%
Number/percentage of T's	50,445,220 / 30.43%
Number/percentage of G's	38,985,039 / 23.52%
Number/percentage of N's	11,157 / 0.01%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.4437

2.4. Mapping Quality

Mean Mapping Quality	47.22

2.5. Mismatches and indels

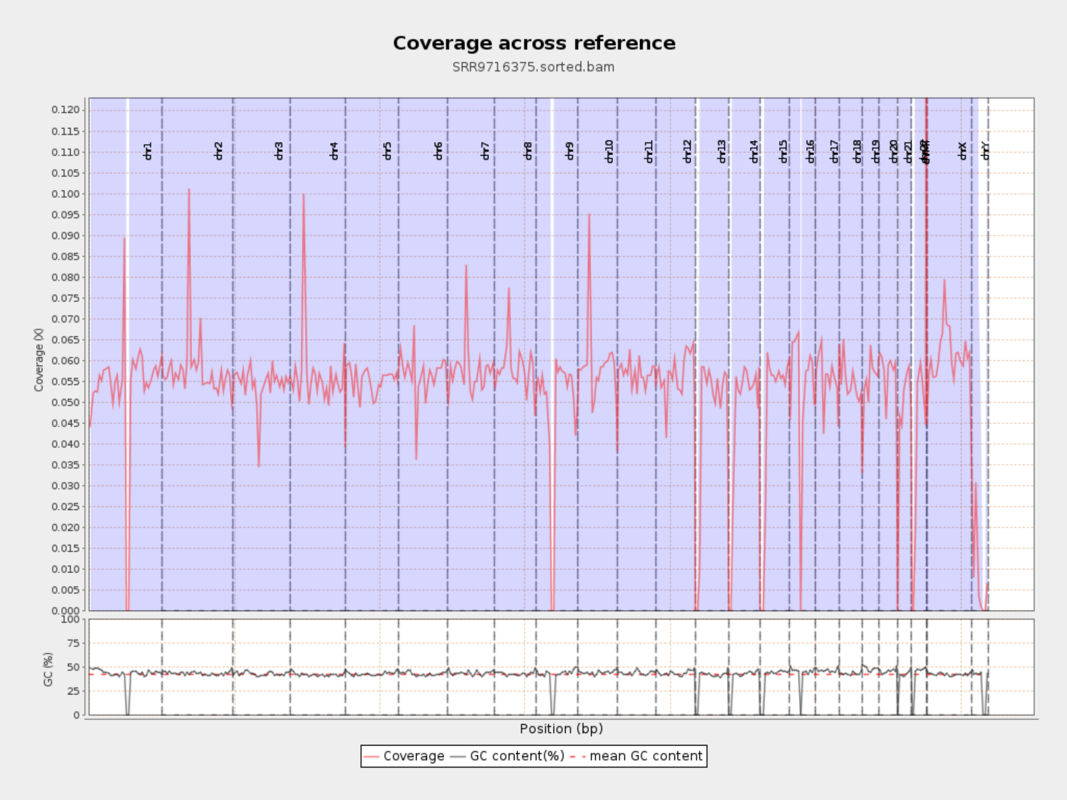
General error rate	0.7%
Mismatches	1,126,252
Insertions	13,462
Mapped reads with at least one insertion	0.63%
Deletions	39,342
Mapped reads with at least one deletion	1.83%
Homopolymer indels	43.4%

2.6. Chromosome stats

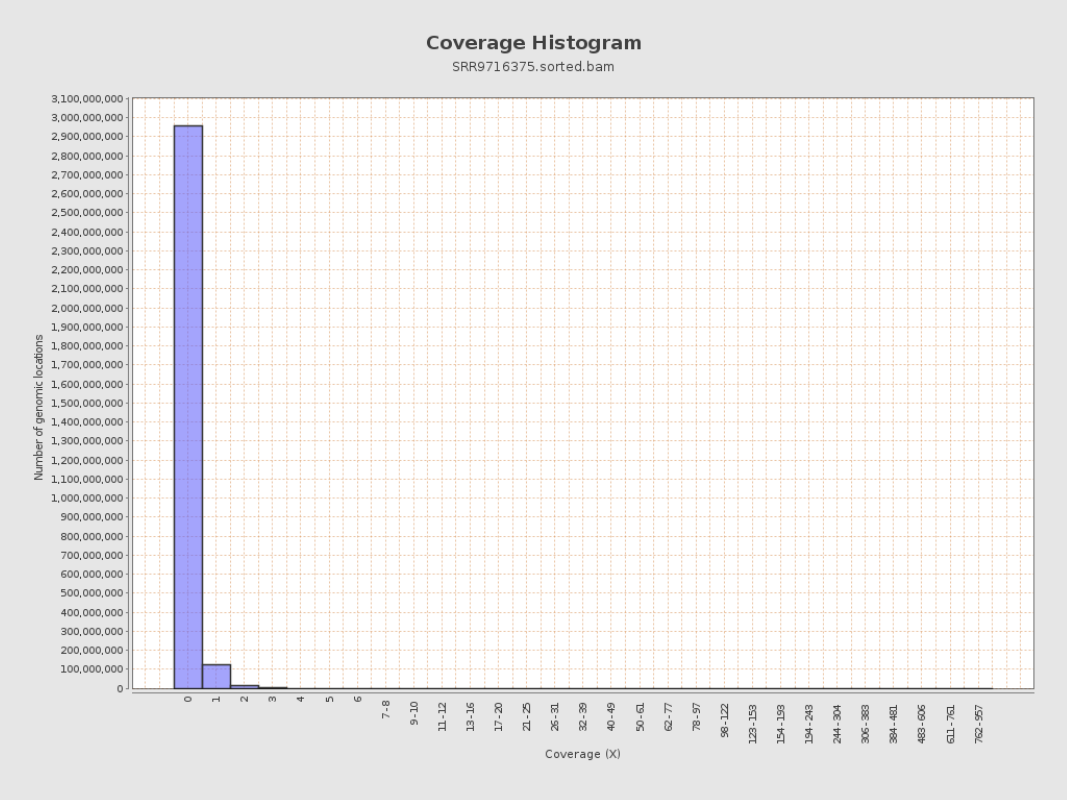
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13269004	0.0532	0.8253
chr2	243199373	14100606	0.058	0.5237
chr3	198022430	10743890	0.0543	0.263
chr4	191154276	10810915	0.0566	0.3356
chr5	180915260	9980303	0.0552	0.2699
chr6	171115067	9684014	0.0566	0.3054
chr7	159138663	9207014	0.0579	0.5854

chr8	146364022	8513067	0.0582	0.56
chr9	141213431	6749328	0.0478	0.3997
chr10	135534747	8042873	0.0593	0.4603
chr11	135006516	7637777	0.0566	0.427
chr12	133851895	7586906	0.0567	0.2732
chr13	115169878	5239177	0.0455	0.2404
chr14	107349540	4880568	0.0455	0.2613
chr15	102531392	4749841	0.0463	0.2458
chr16	90354753	4825613	0.0534	0.2895
chr17	81195210	4499197	0.0554	0.3141
chr18	78077248	4303348	0.0551	0.6448
chr19	59128983	3264383	0.0552	0.6004
chr20	63025520	3578327	0.0568	0.2847
chr21	48129895	2244149	0.0466	0.2858
chr22	51304566	1913622	0.0373	0.2198
chrMT	16571	16130	0.9734	1.1776
chrX	155270560	9499506	0.0612	0.3309
chrY	59373566	495154	0.0083	0.261

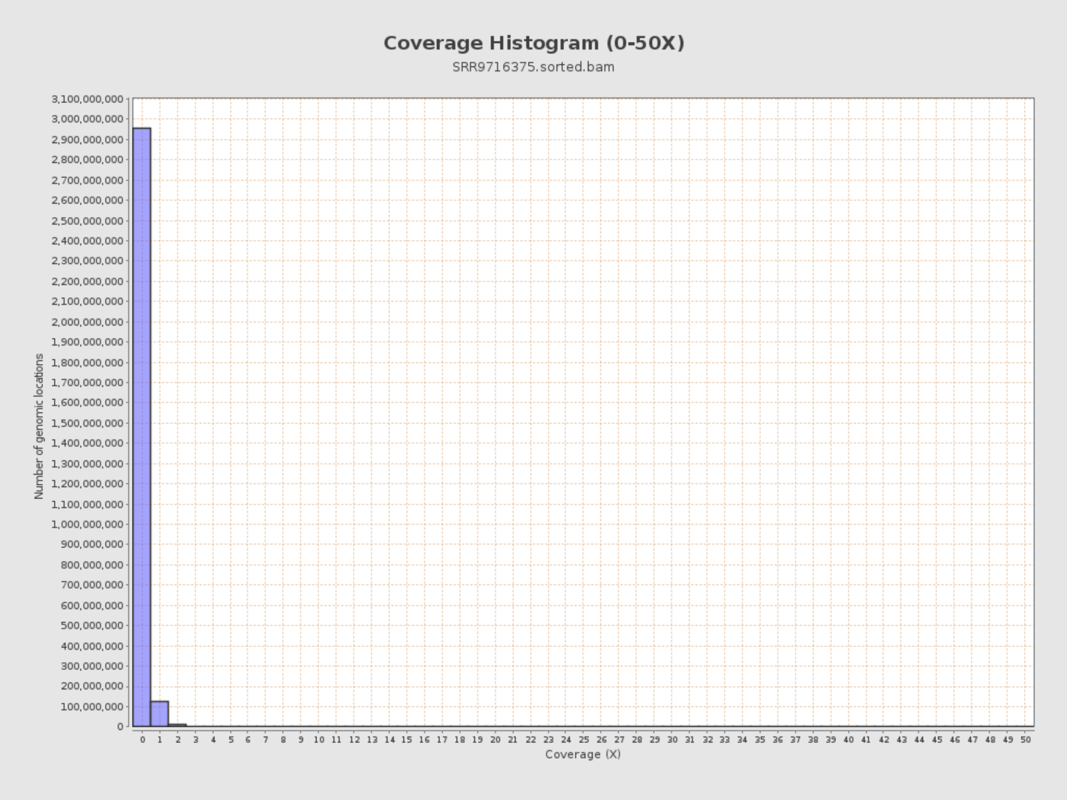
3. Results : Coverage across reference



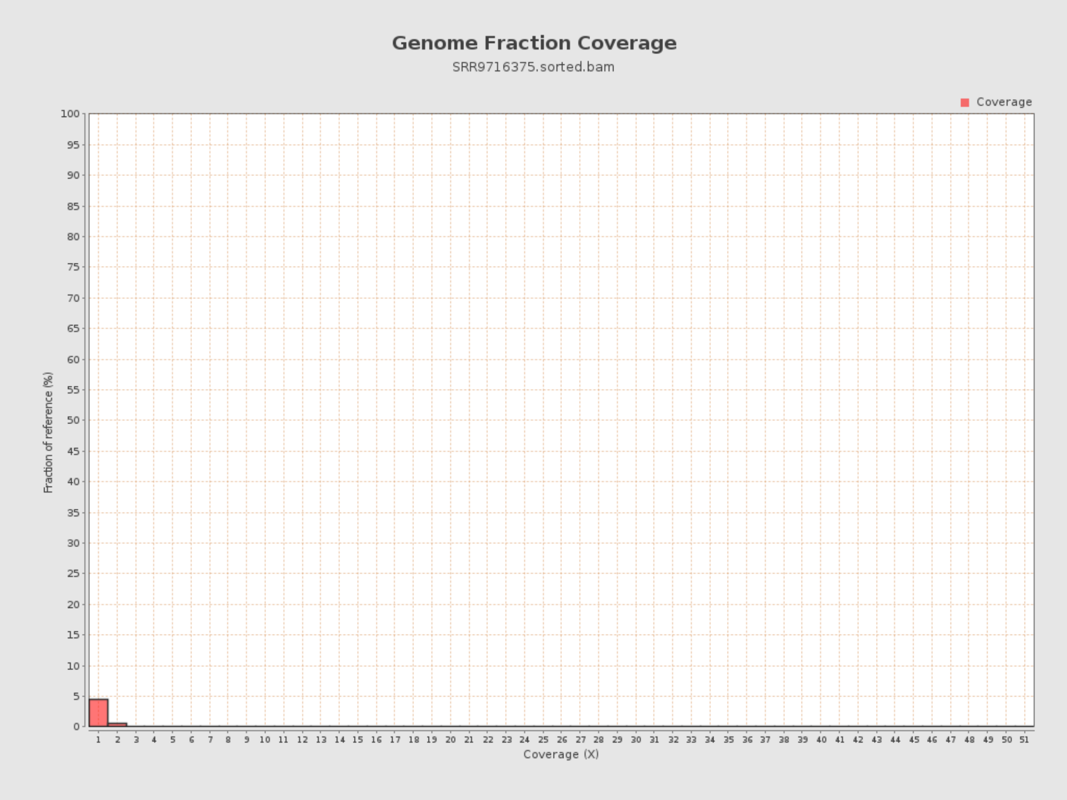
4. Results : Coverage Histogram



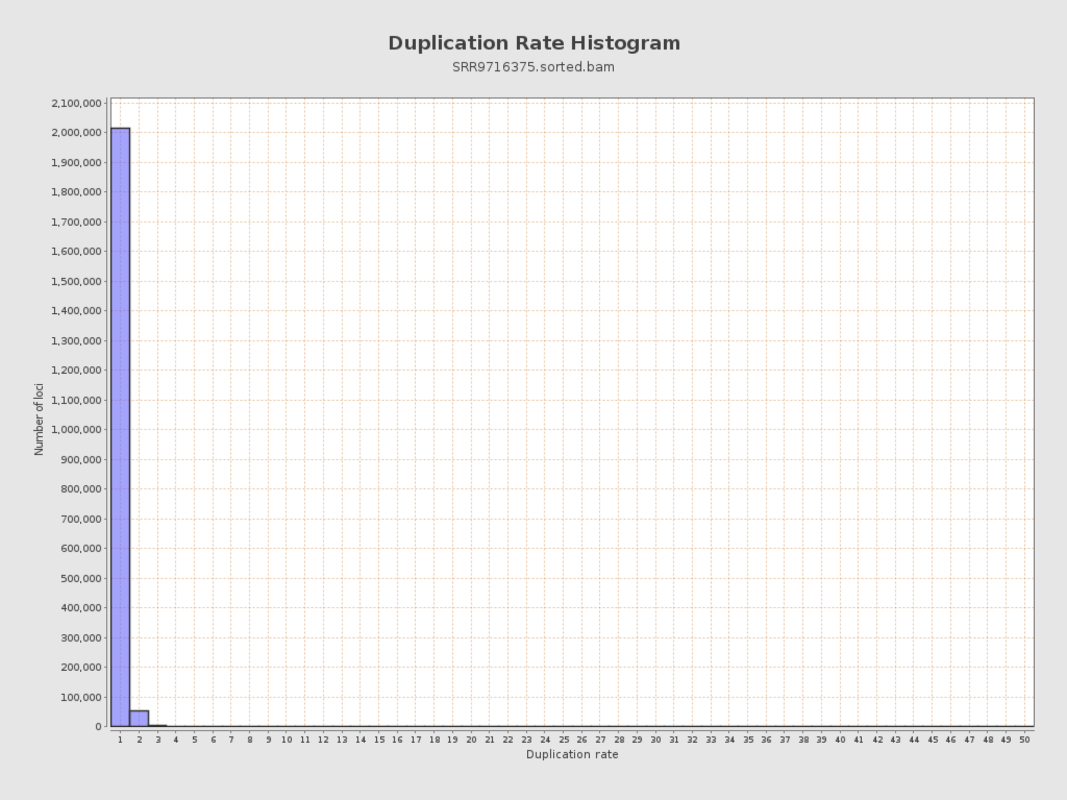
5. Results : Coverage Histogram (0-50X)



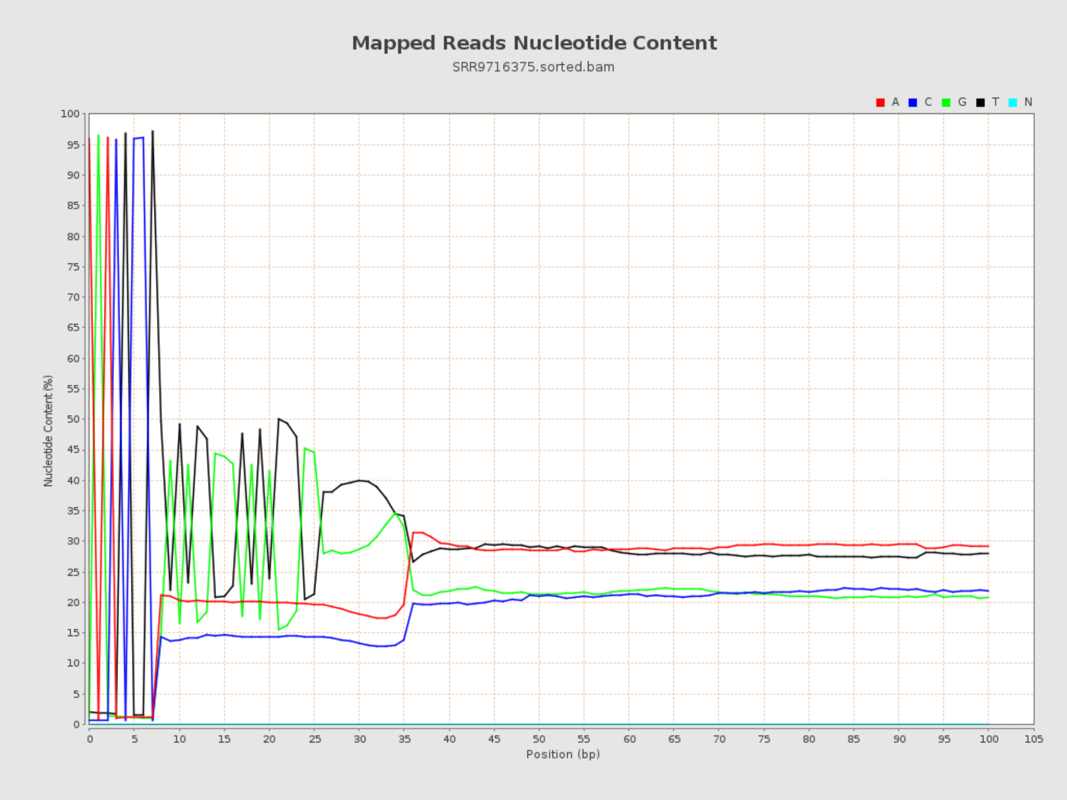
6. Results : Genome Fraction Coverage



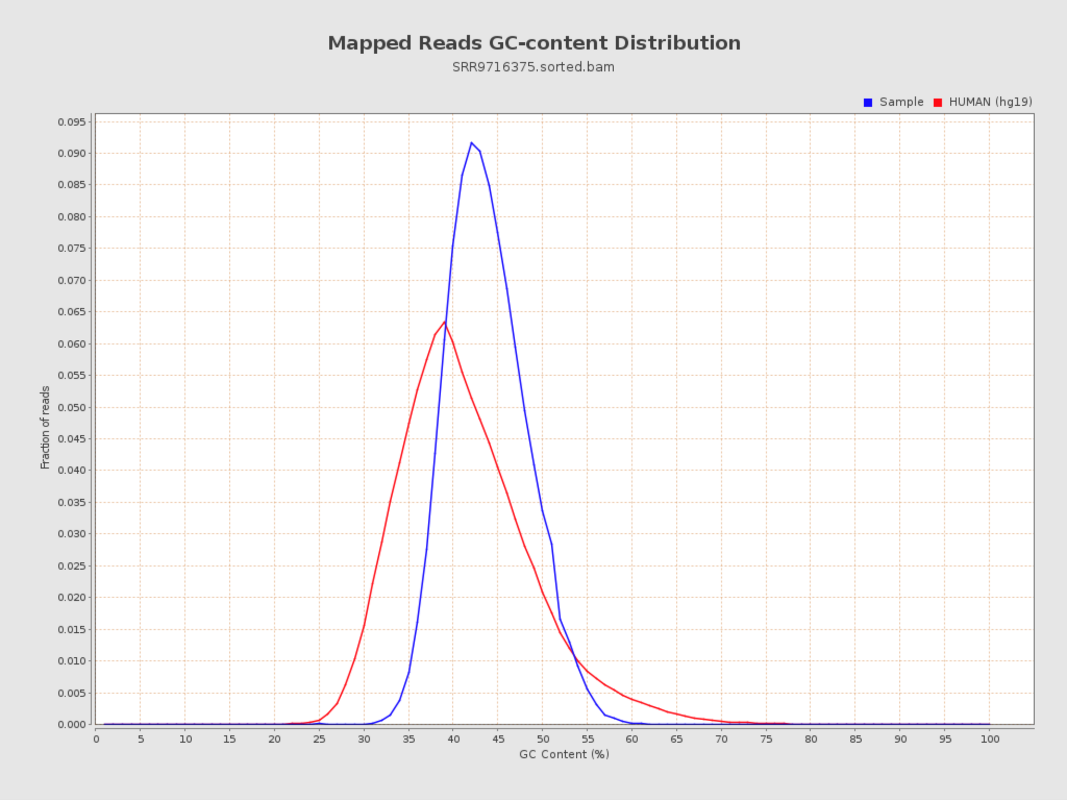
7. Results : Duplication Rate Histogram



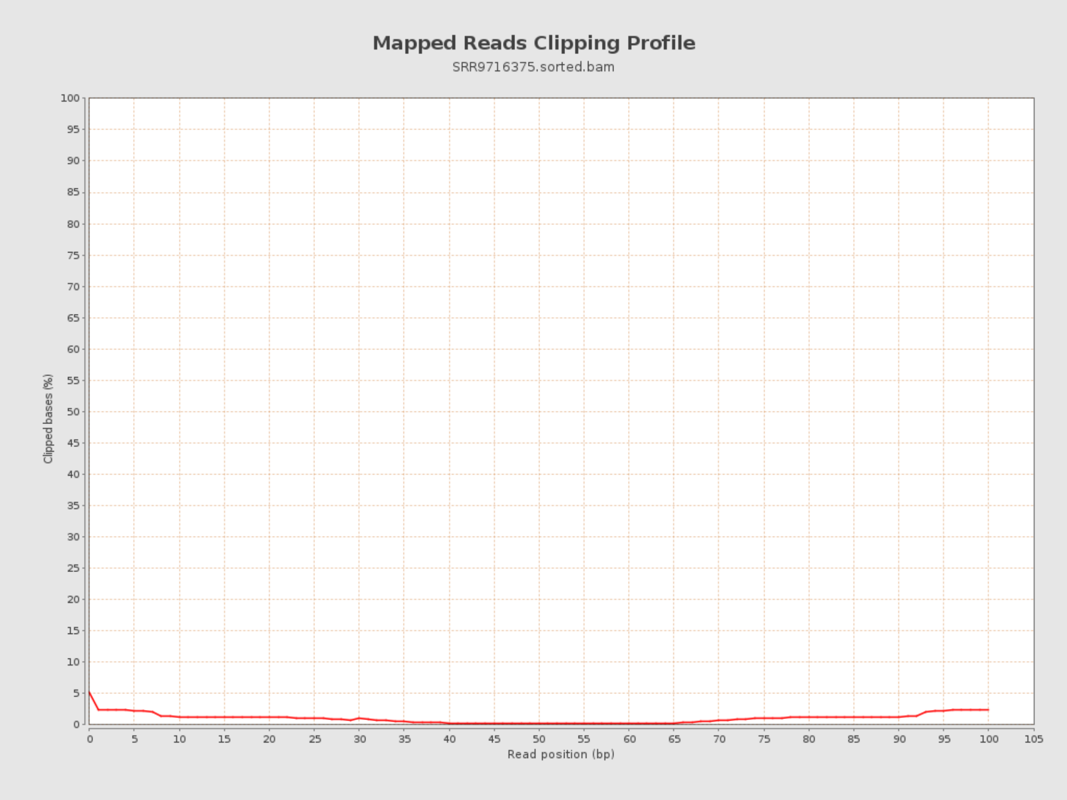
8. Results : Mapped Reads Nucleotide Content



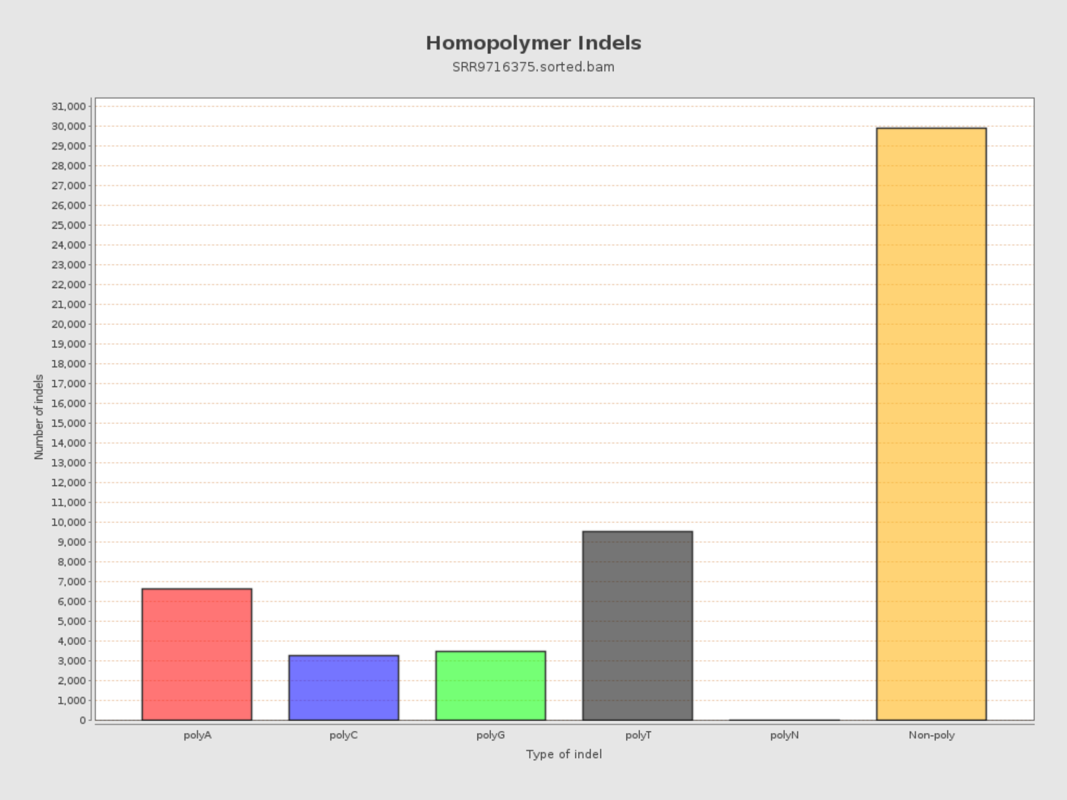
9. Results : Mapped Reads GC-content Distribution



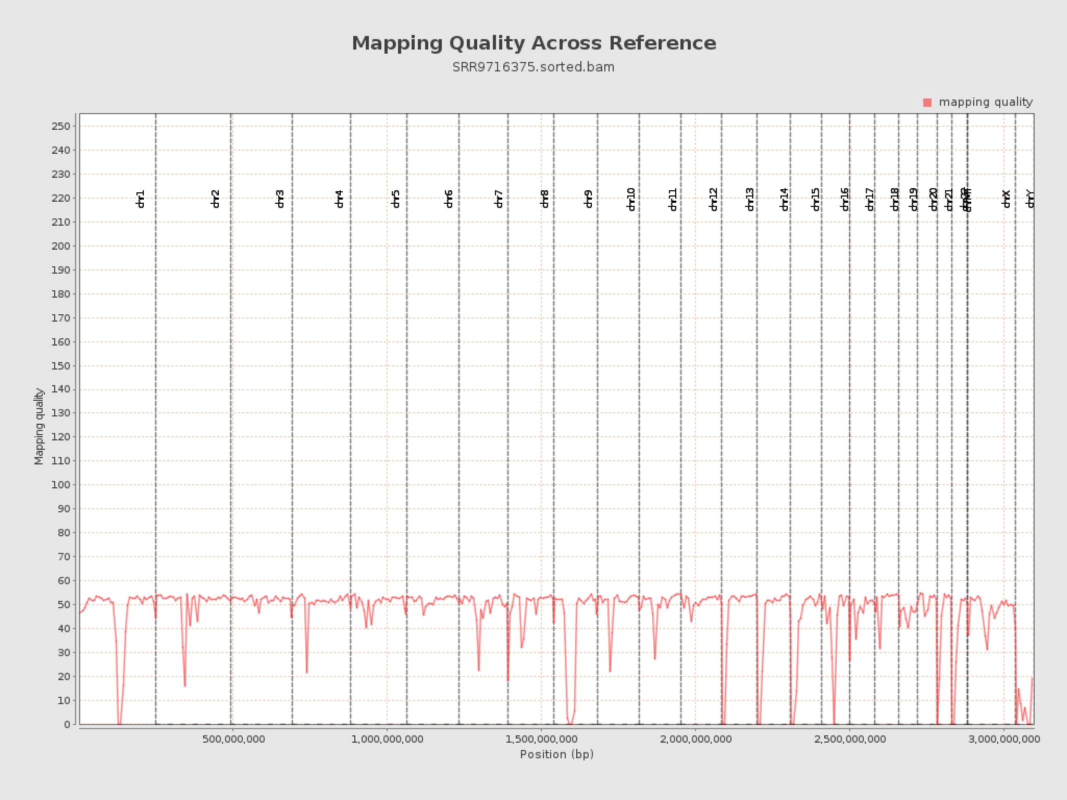
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram