Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:20:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716451.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_SRR9716451 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716451.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:20:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716451.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,315,162
Mapped reads	1,224,498 / 93.11%
Unmapped reads	90,664 / 6.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,539 / 1.49%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	46,595 / 3.54%
Duplication rate	2.38%
Clipped reads	1,243,015 / 94.51%

2.2. ACGT Content

Number/percentage of A's	24,131,017 / 24.96%
Number/percentage of C's	19,123,481 / 19.78%
Number/percentage of T's	29,734,665 / 30.75%
Number/percentage of G's	23,697,795 / 24.51%
Number/percentage of N's	5,701 / 0.01%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.3494

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

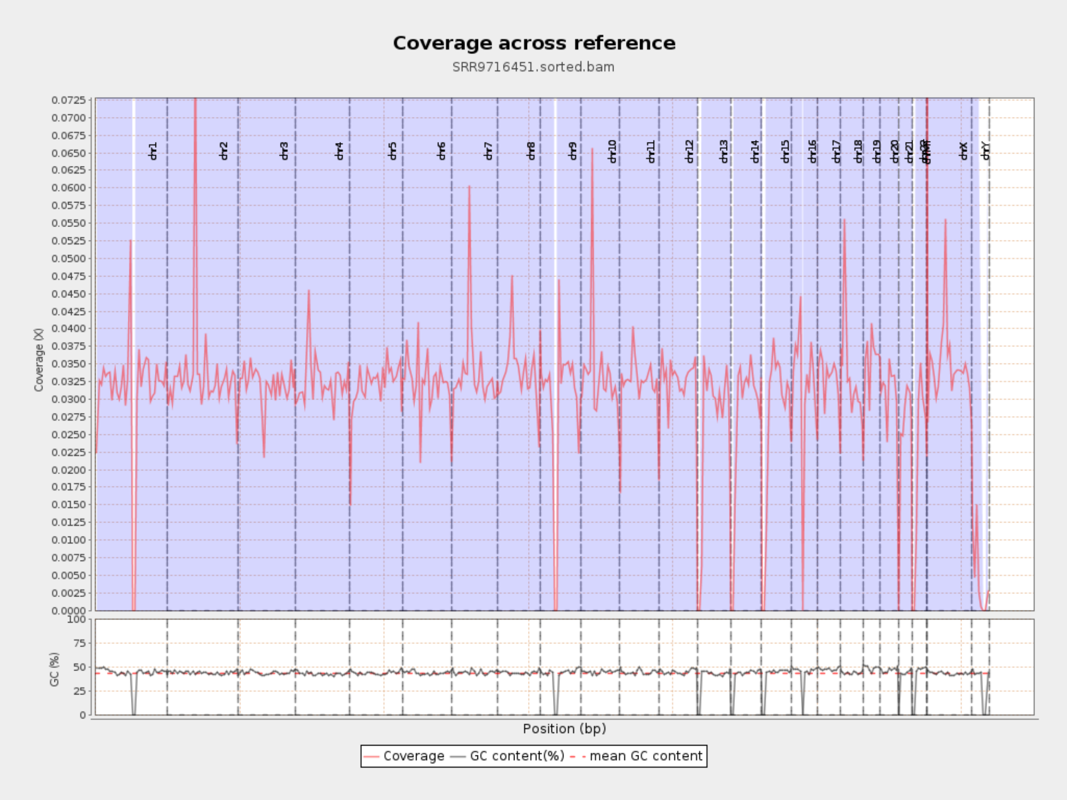
General error rate	0.81%
Mismatches	763,985
Insertions	8,563
Mapped reads with at least one insertion	0.69%
Deletions	23,165
Mapped reads with at least one deletion	1.86%
Homopolymer indels	44.34%

2.6. Chromosome stats

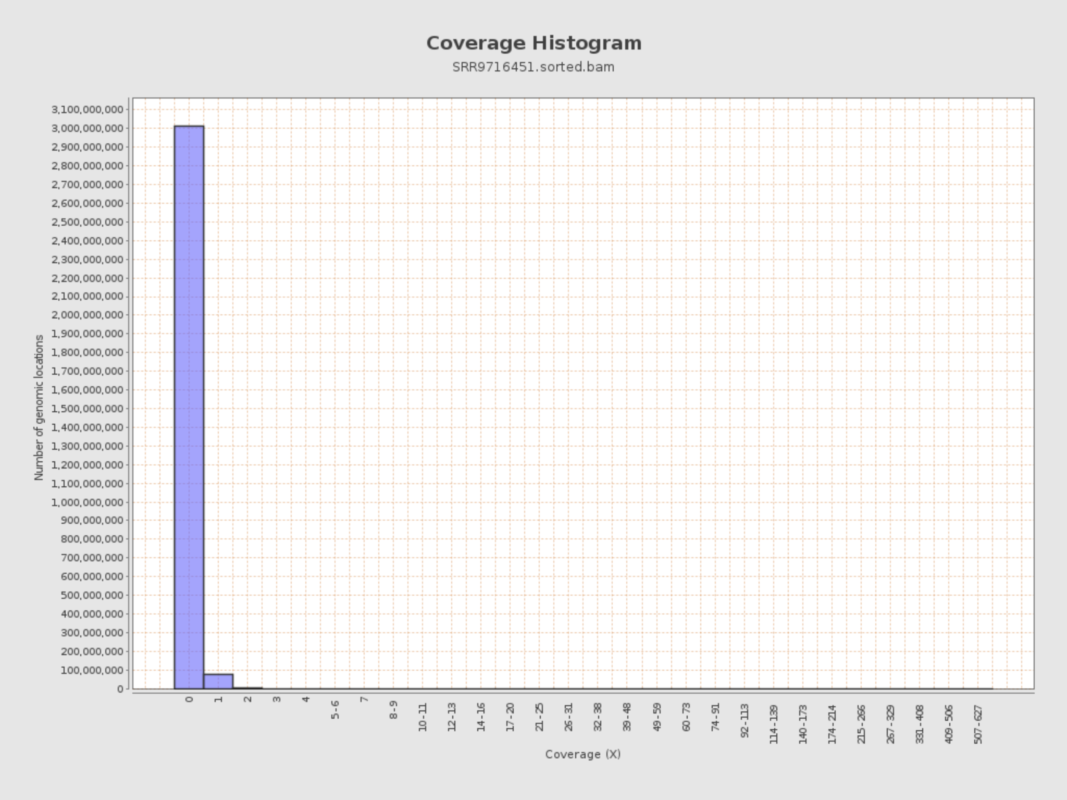
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7724850	0.031	0.5232
chr2	243199373	8241139	0.0339	0.4914
chr3	198022430	6350330	0.0321	0.2006
chr4	191154276	6263169	0.0328	0.2191
chr5	180915260	5893552	0.0326	0.2049
chr6	171115067	5533291	0.0323	0.2365
chr7	159138663	5396158	0.0339	0.4625

chr8	146364022	4962955	0.0339	0.4452
chr9	141213431	4143688	0.0293	0.4052
chr10	135534747	4592964	0.0339	0.3708
chr11	135006516	4437335	0.0329	0.3387
chr12	133851895	4401880	0.0329	0.2052
chr13	115169878	3012748	0.0262	0.1765
chr14	107349540	2879471	0.0268	0.2435
chr15	102531392	2739710	0.0267	0.1819
chr16	90354753	2796947	0.031	0.2218
chr17	81195210	2683262	0.033	0.2177
chr18	78077248	2625732	0.0336	0.7247
chr19	59128983	2095424	0.0354	0.4074
chr20	63025520	1932430	0.0307	0.2035
chr21	48129895	1232671	0.0256	0.188
chr22	51304566	1077373	0.021	0.1594
chrMT	16571	2608	0.1574	0.4496
chrX	155270560	5453342	0.0351	0.2723
chrY	59373566	260384	0.0044	0.1279

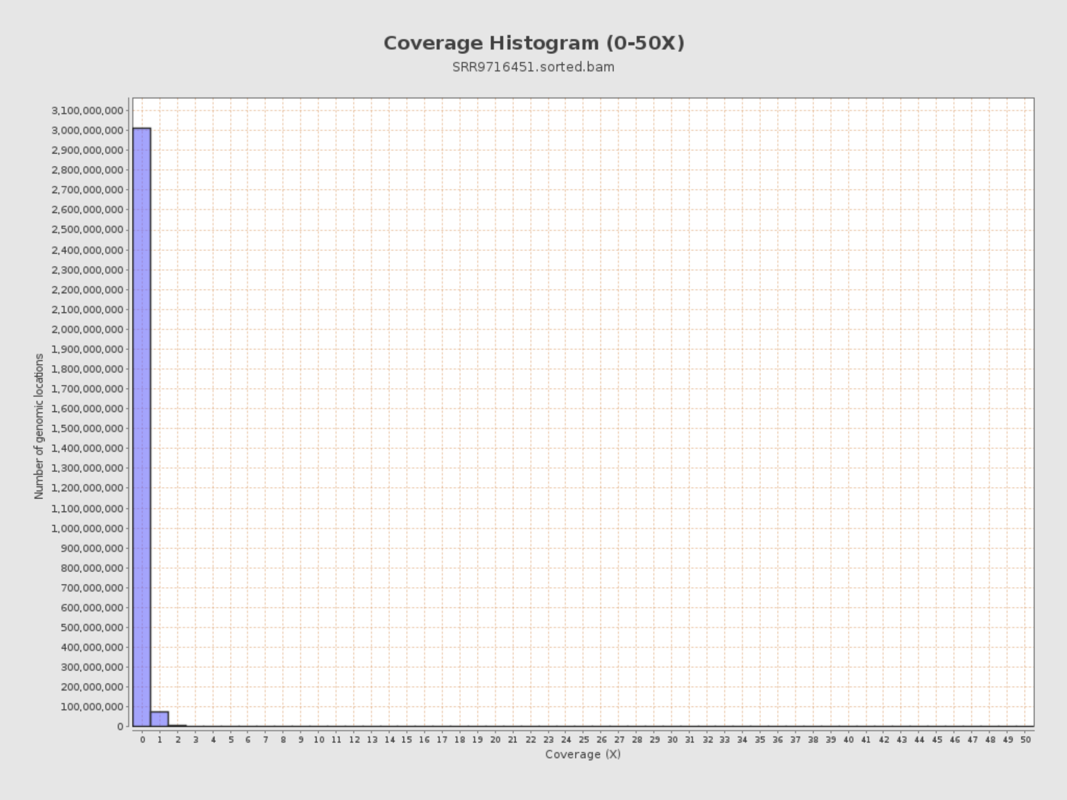
3. Results : Coverage across reference



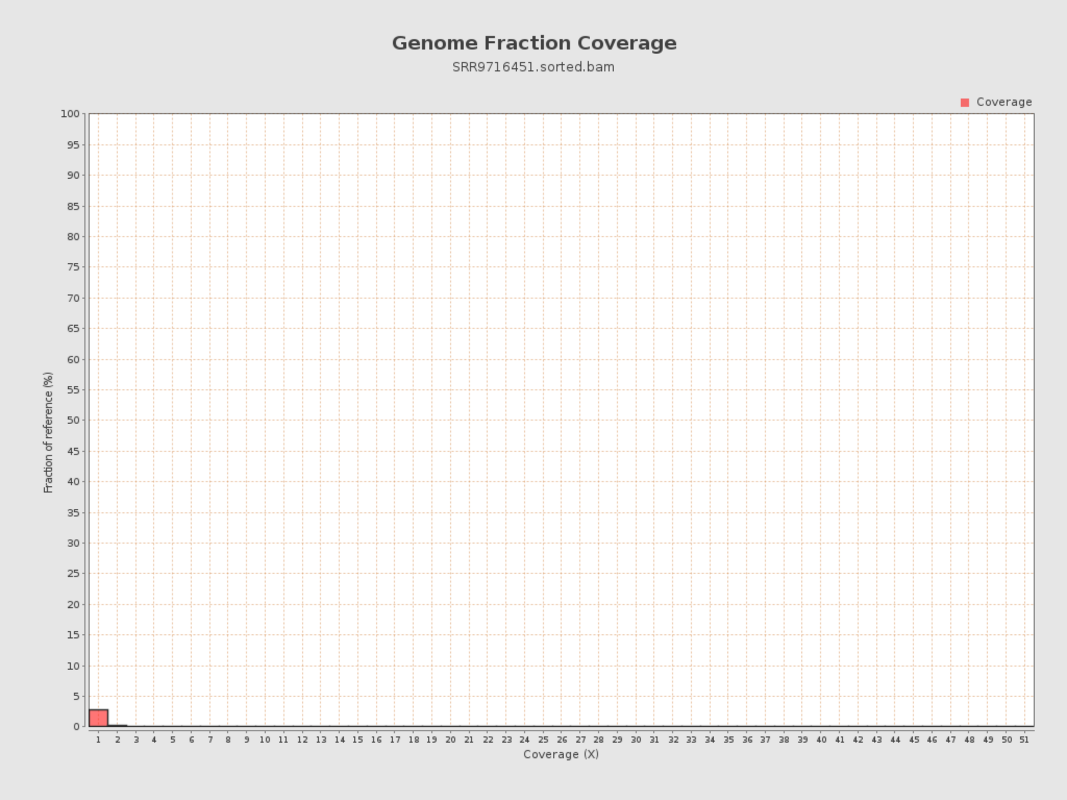
4. Results : Coverage Histogram



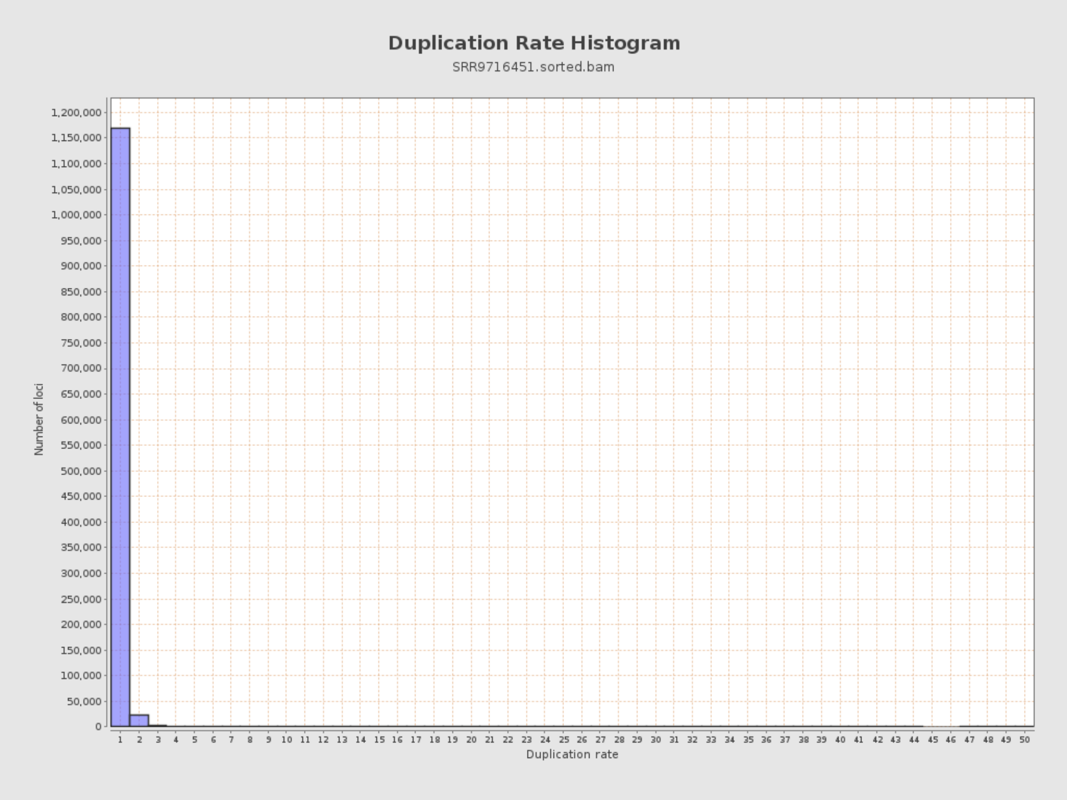
5. Results : Coverage Histogram (0-50X)



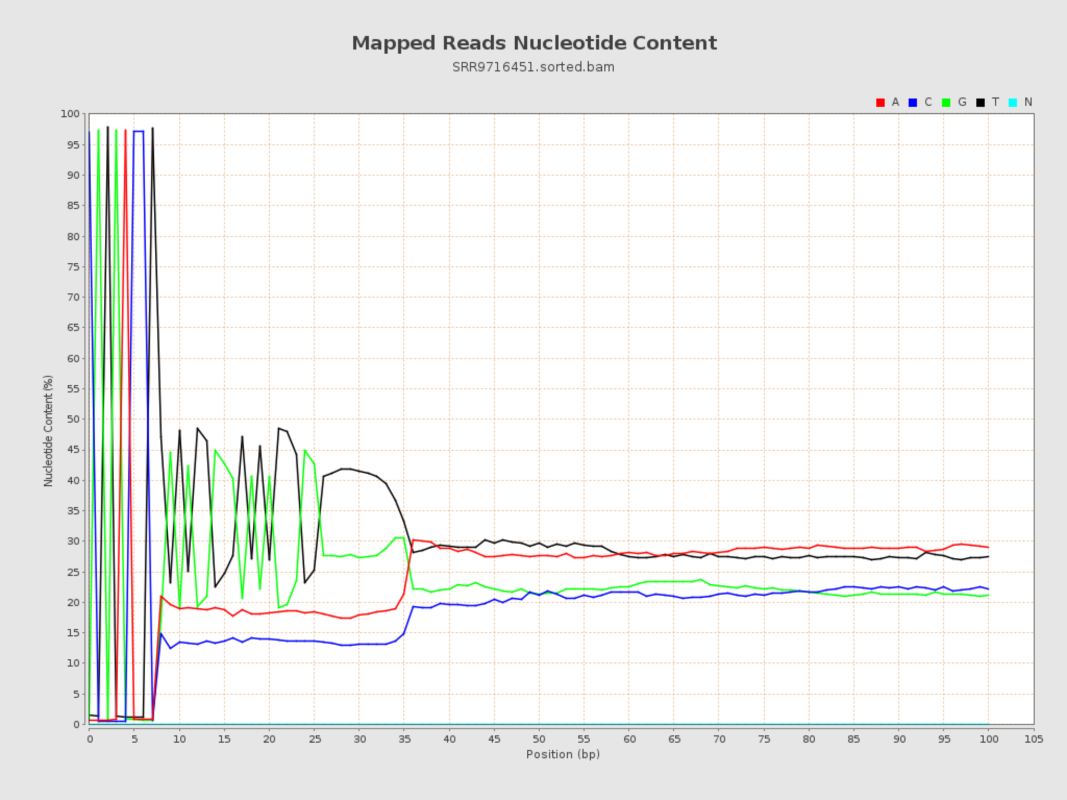
6. Results : Genome Fraction Coverage



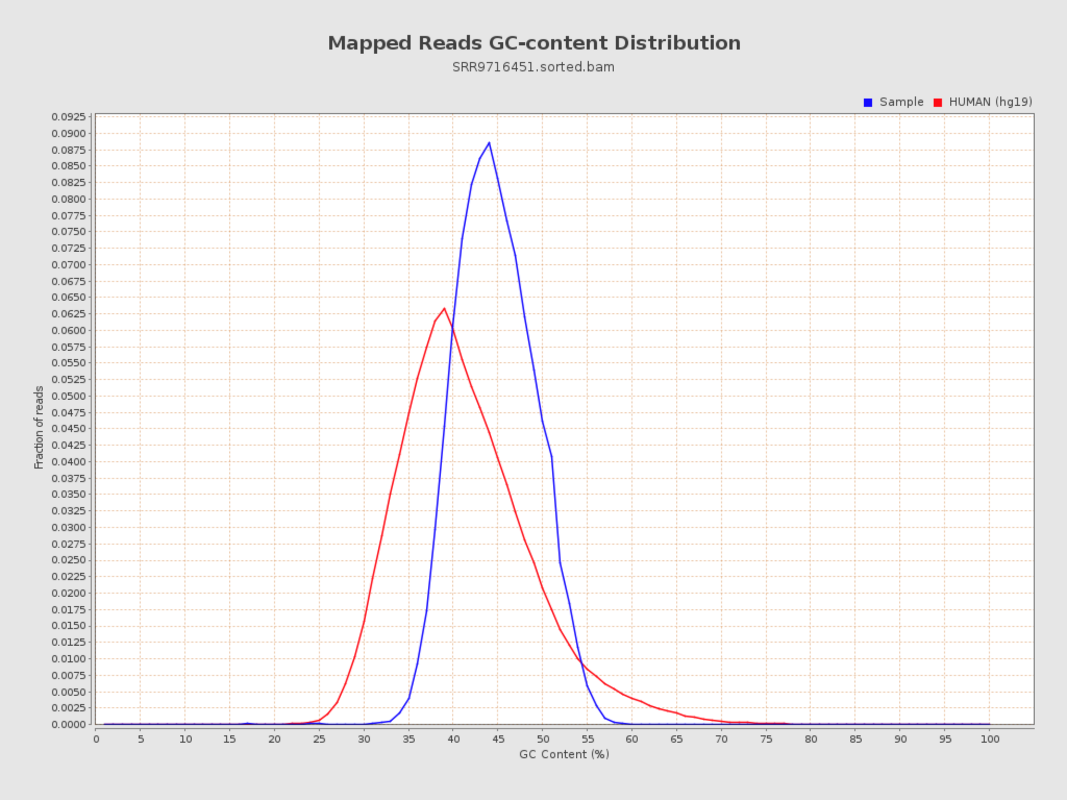
7. Results : Duplication Rate Histogram



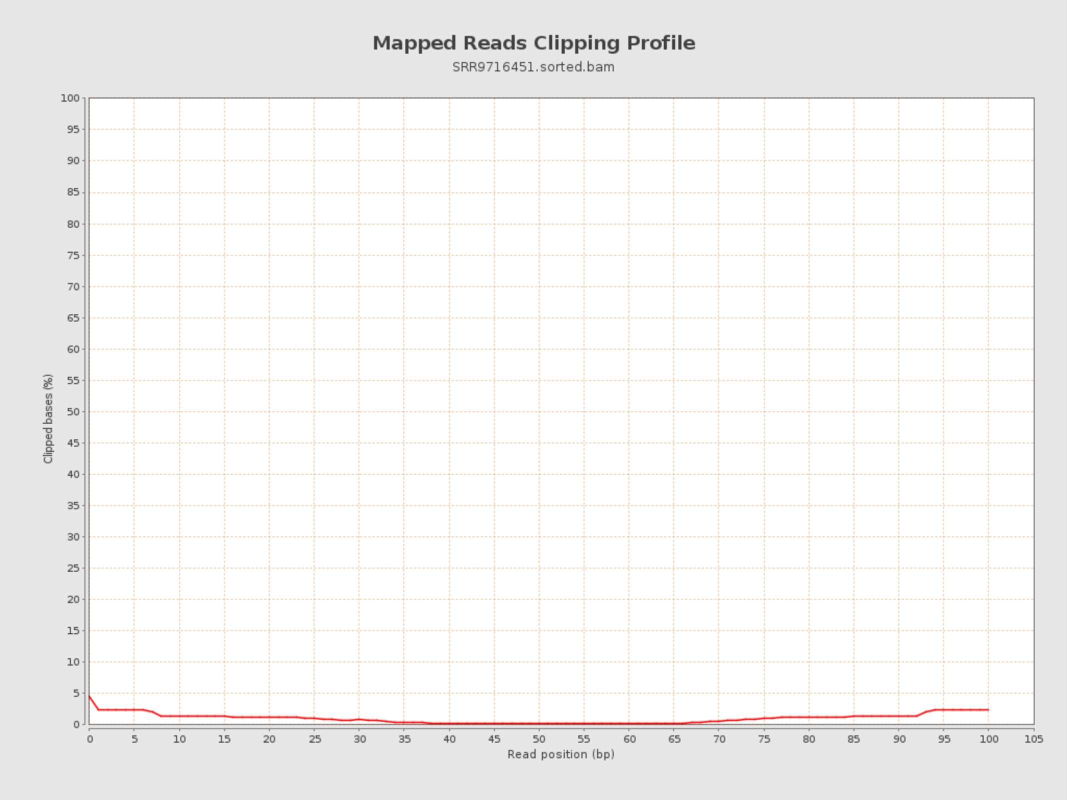
8. Results : Mapped Reads Nucleotide Content



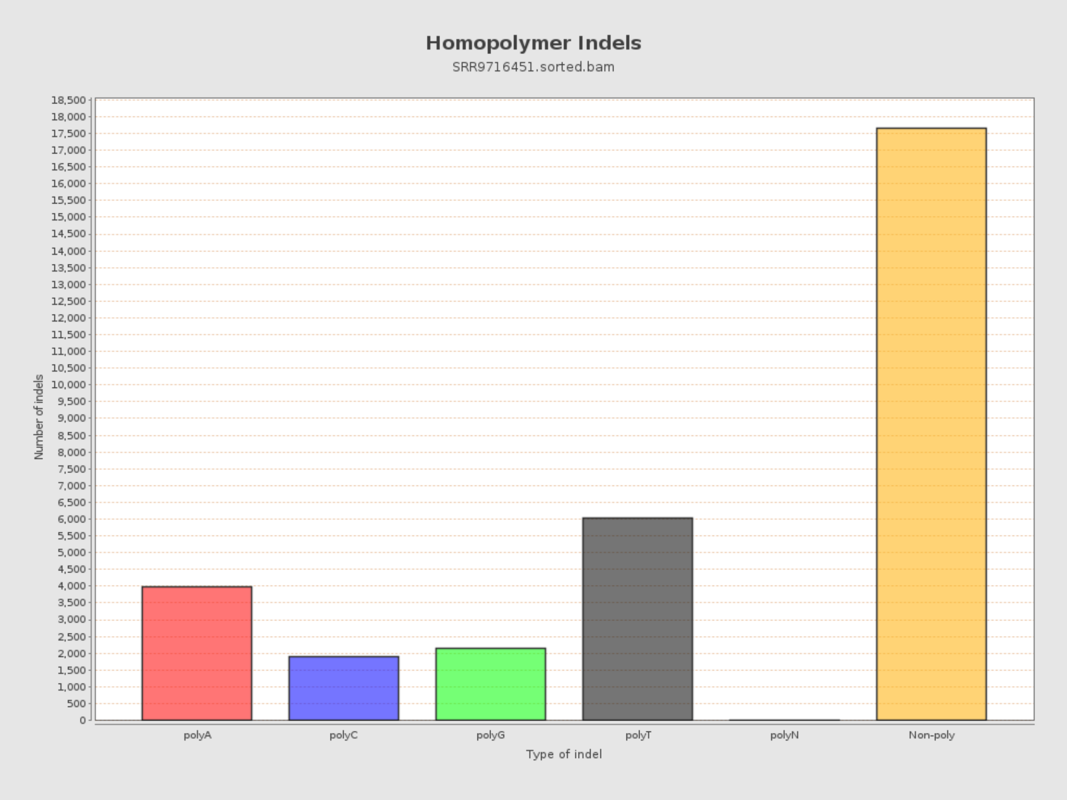
9. Results : Mapped Reads GC-content Distribution



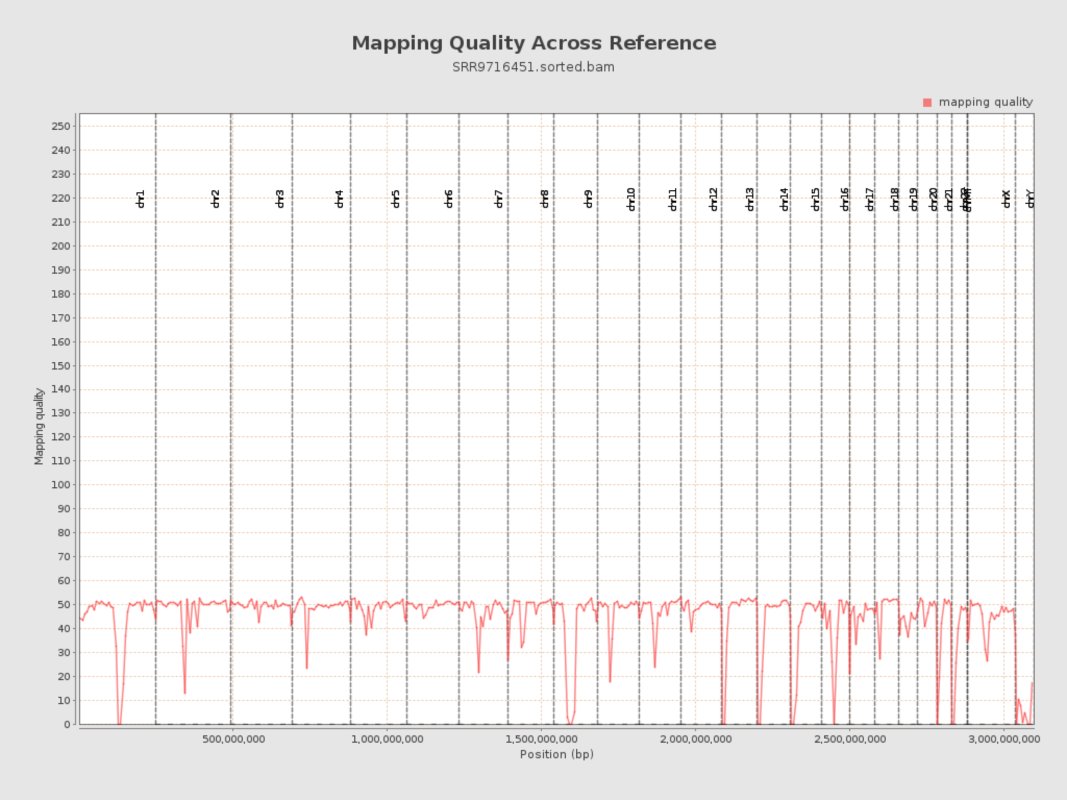
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram