Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:28:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716571.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_SRR9716571 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716571.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:28:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716571.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,052,692
Mapped reads	989,147 / 93.96%
Unmapped reads	63,545 / 6.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,498 / 2.52%
Read min/max/mean length	30 / 101 / 101.92
Duplicated reads (estimated)	29,903 / 2.84%
Duplication rate	2.26%
Clipped reads	1,013,559 / 96.28%

2.2. ACGT Content

Number/percentage of A's	19,100,460 / 25.11%
Number/percentage of C's	15,869,597 / 20.86%
Number/percentage of T's	22,409,315 / 29.46%
Number/percentage of G's	18,692,292 / 24.57%
Number/percentage of N's	2,976 / 0%
GC Percentage	45.43%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2177

2.4. Mapping Quality

Mean Mapping Quality	46.36

2.5. Mismatches and indels

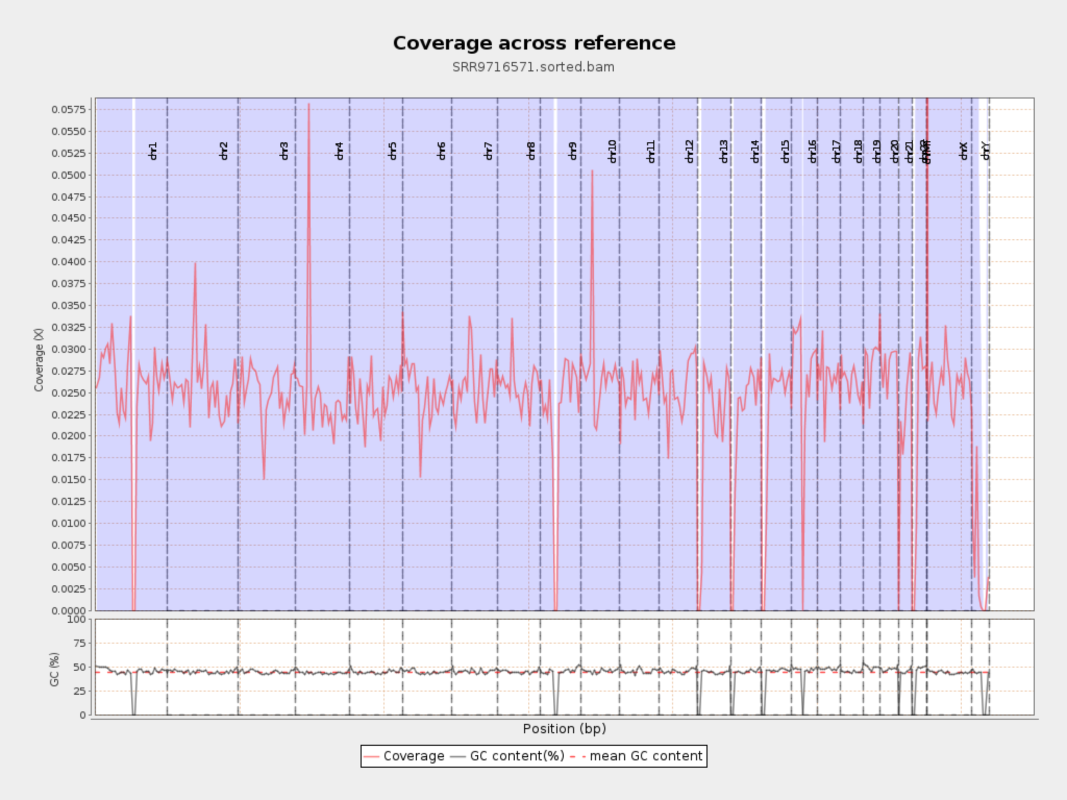
General error rate	0.66%
Mismatches	484,877
Insertions	6,877
Mapped reads with at least one insertion	0.68%
Deletions	14,656
Mapped reads with at least one deletion	1.45%
Homopolymer indels	38.54%

2.6. Chromosome stats

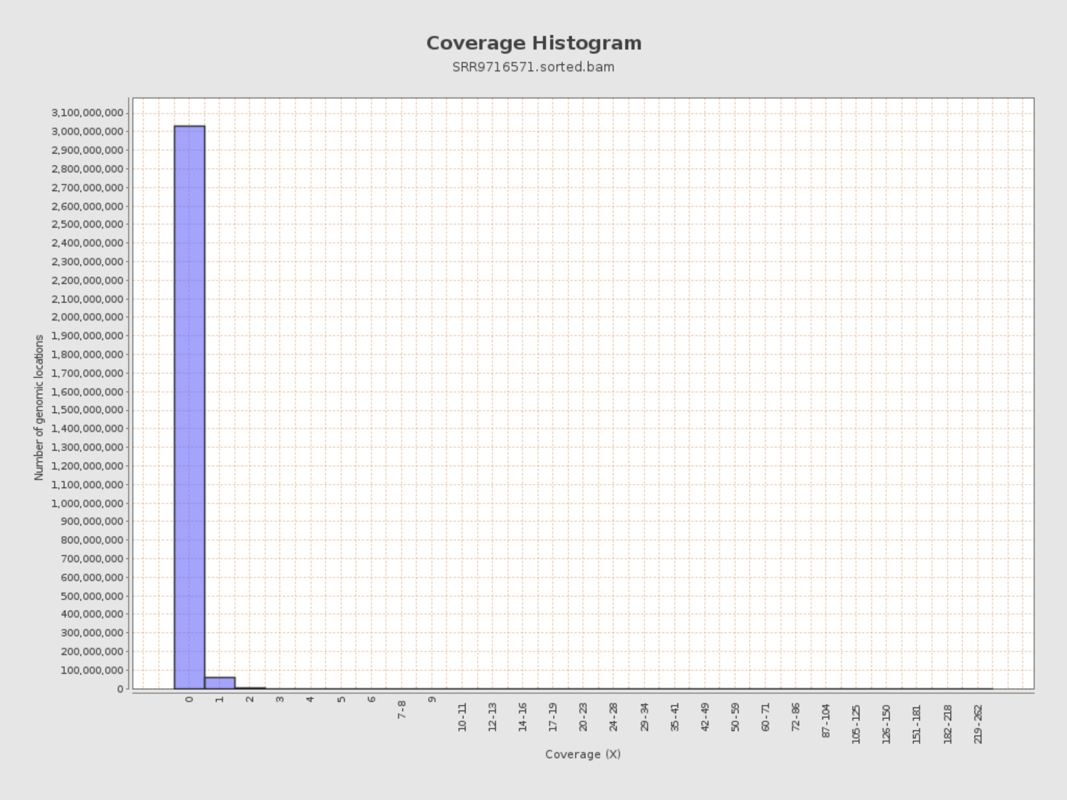
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6245440	0.0251	0.2801
chr2	243199373	6332462	0.026	0.2476
chr3	198022430	4965218	0.0251	0.1721
chr4	191154276	4794467	0.0251	0.2304
chr5	180915260	4463857	0.0247	0.1709
chr6	171115067	4297952	0.0251	0.178
chr7	159138663	4111999	0.0258	0.2543

chr8	146364022	3783685	0.0259	0.2172
chr9	141213431	3146200	0.0223	0.1968
chr10	135534747	3749508	0.0277	0.2917
chr11	135006516	3448398	0.0255	0.2266
chr12	133851895	3460864	0.0259	0.1768
chr13	115169878	2356151	0.0205	0.1565
chr14	107349540	2286427	0.0213	0.1677
chr15	102531392	2221711	0.0217	0.1607
chr16	90354753	2370809	0.0262	0.1893
chr17	81195210	2166613	0.0267	0.1966
chr18	78077248	2050341	0.0263	0.2987
chr19	59128983	1687313	0.0285	0.2417
chr20	63025520	1764841	0.028	0.1923
chr21	48129895	1033085	0.0215	0.1968
chr22	51304566	1023547	0.02	0.1561
chrMT	16571	33253	2.0067	2.0447
chrX	155270560	4035361	0.026	0.2135
chrY	59373566	275460	0.0046	0.1945

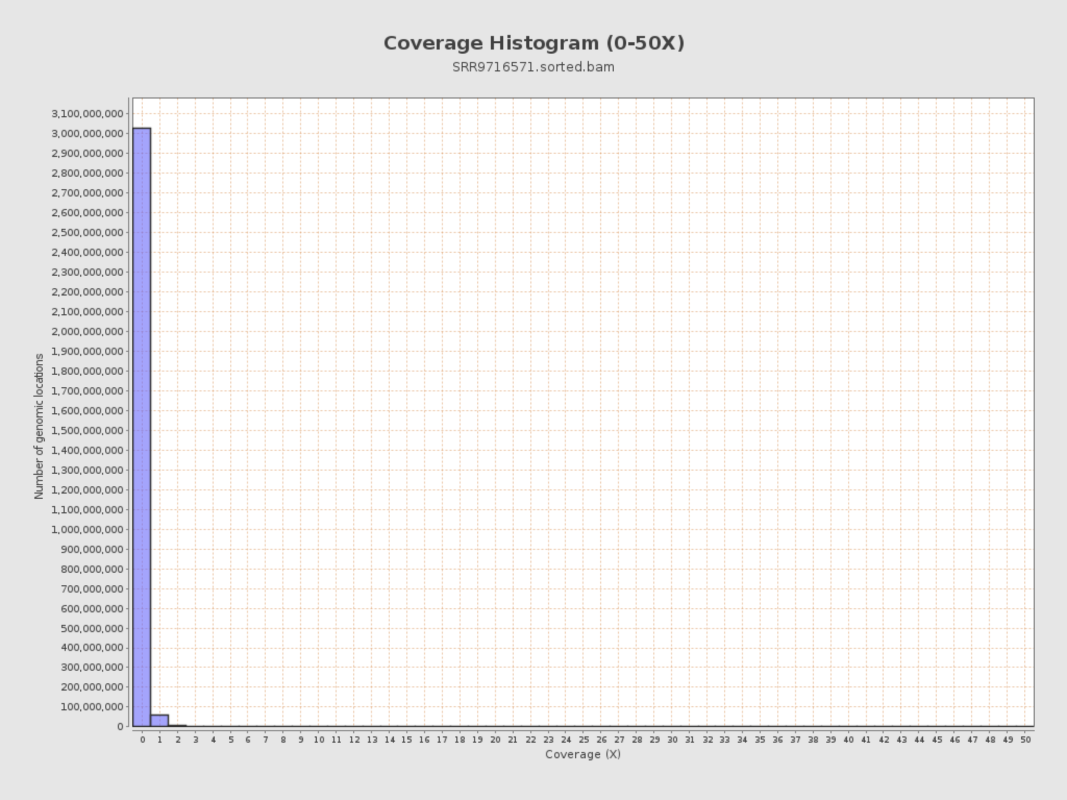
3. Results : Coverage across reference



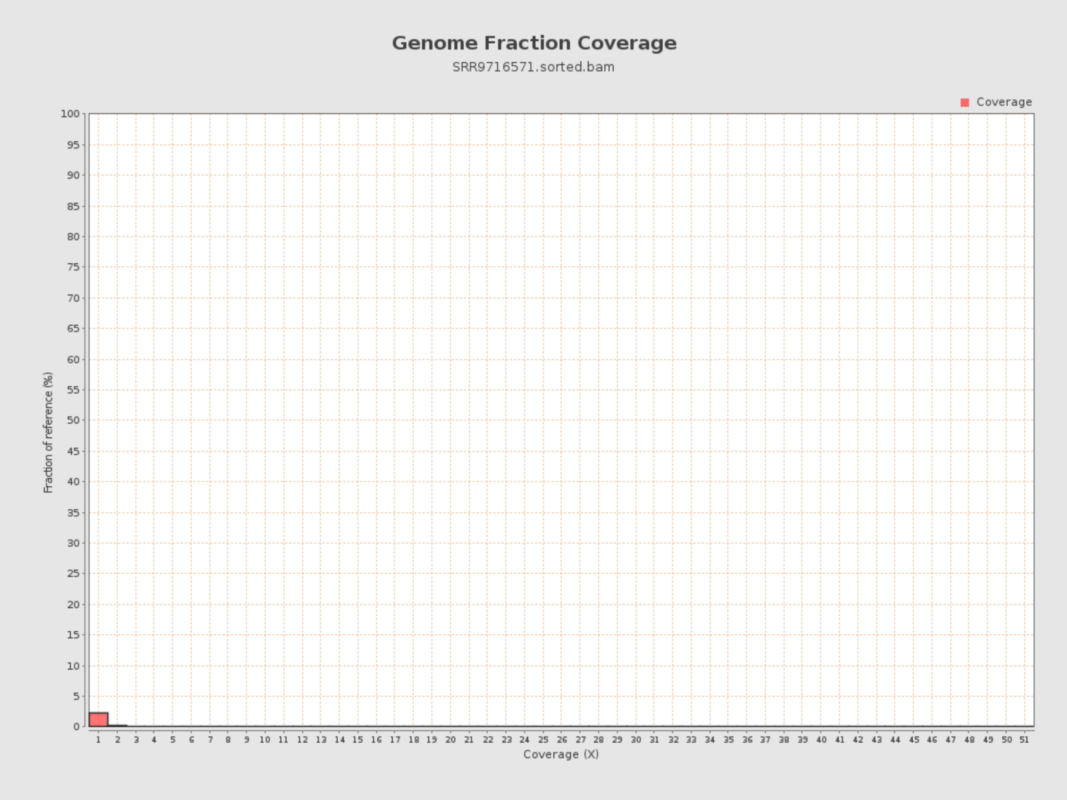
4. Results : Coverage Histogram



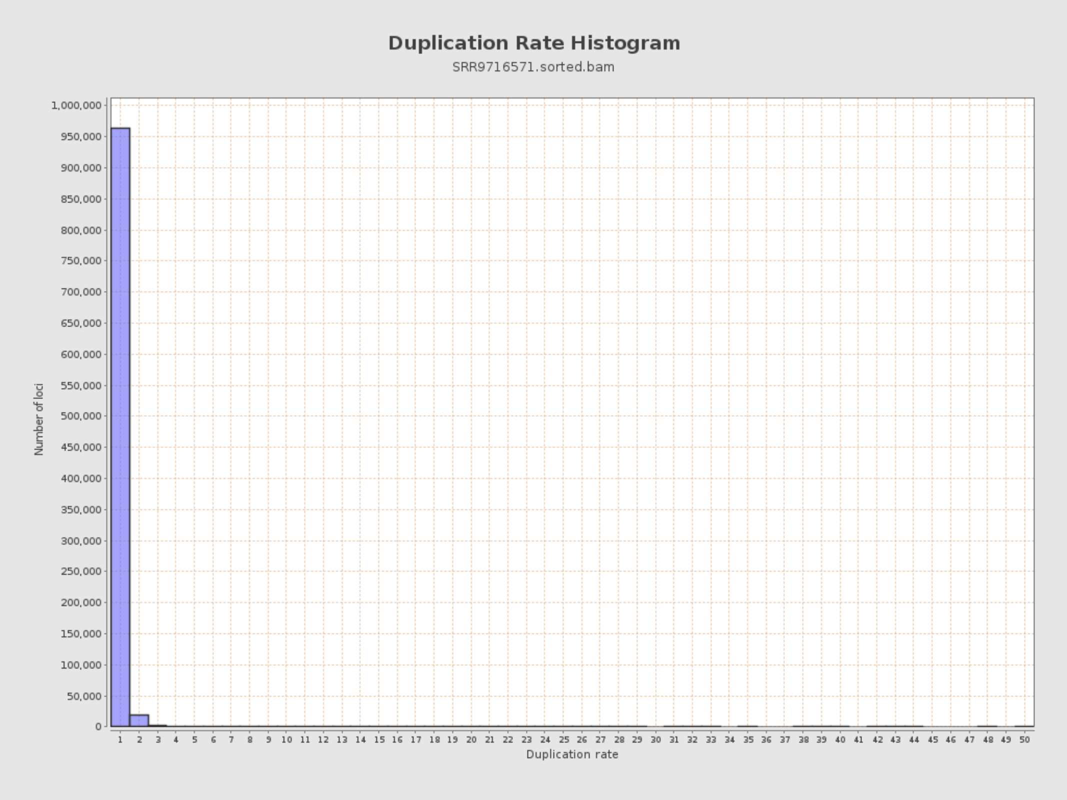
5. Results : Coverage Histogram (0-50X)



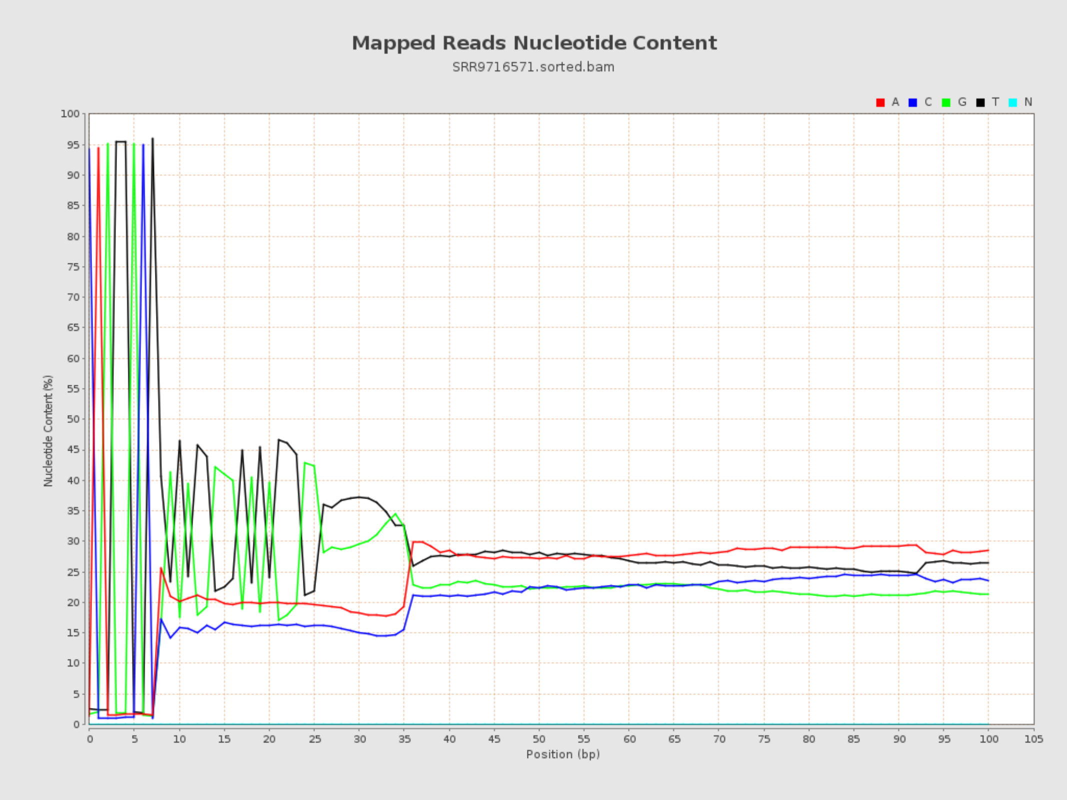
6. Results : Genome Fraction Coverage



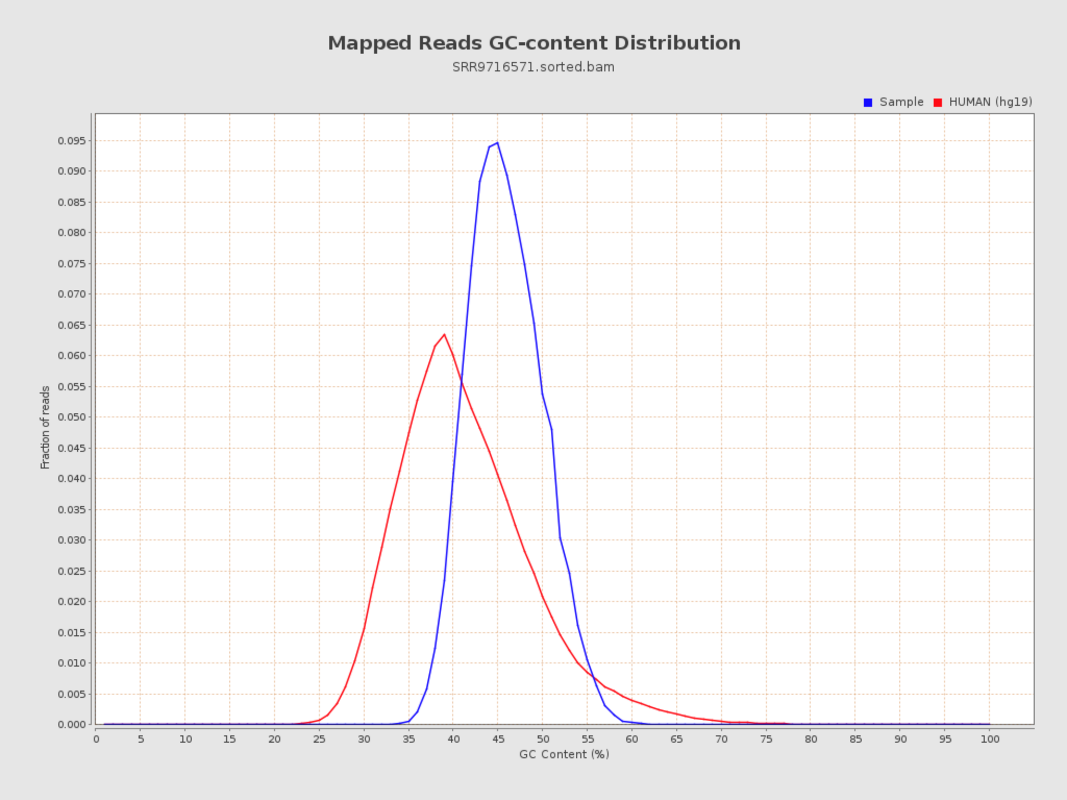
7. Results : Duplication Rate Histogram



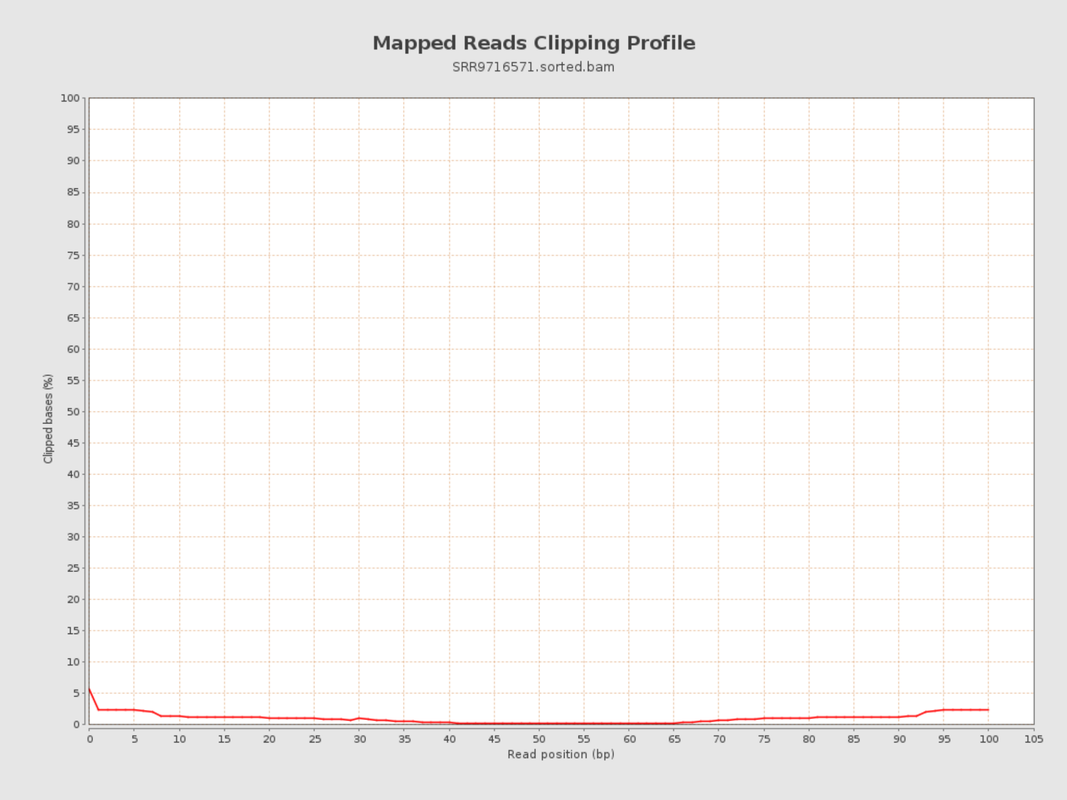
8. Results : Mapped Reads Nucleotide Content



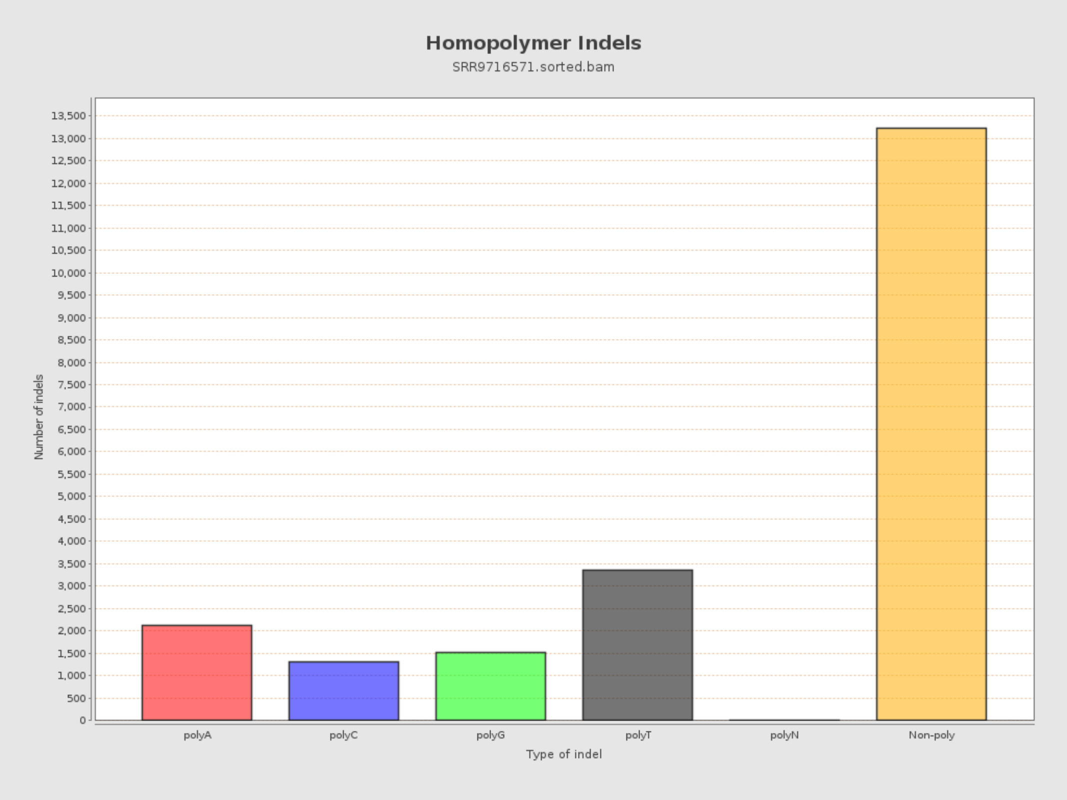
9. Results : Mapped Reads GC-content Distribution



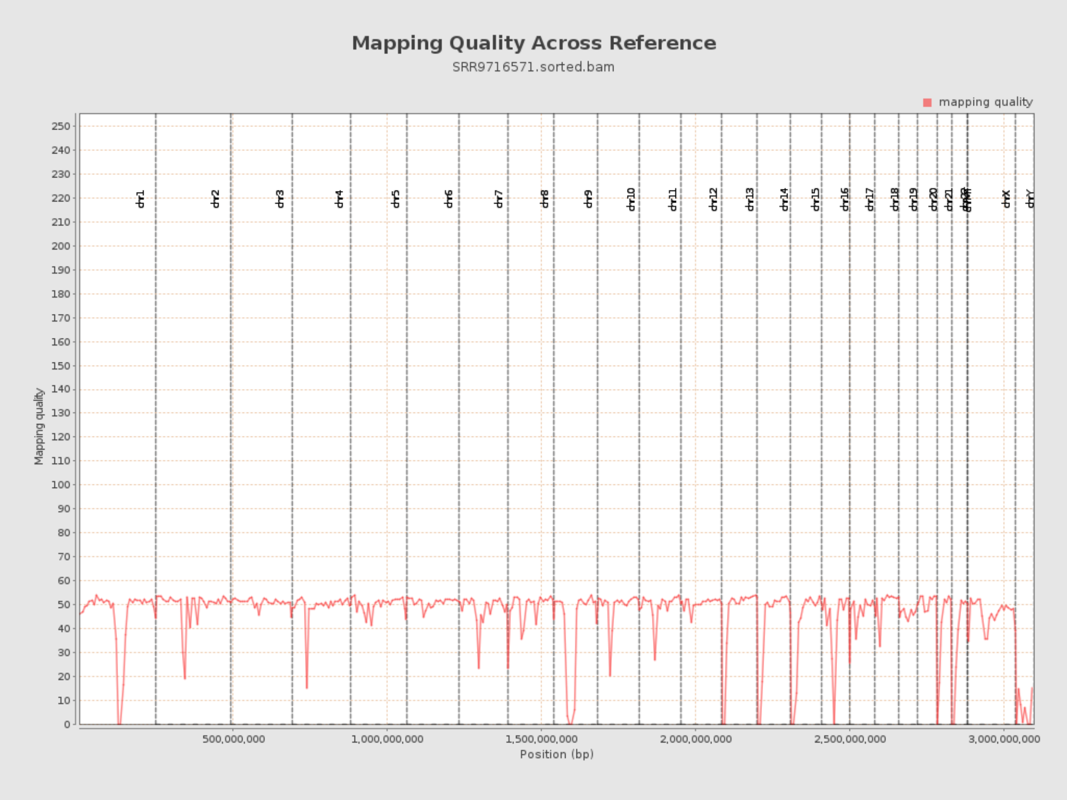
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram