Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:41:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716984.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_SRR9716984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716984.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:41:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,335,013
Mapped reads	3,070,979 / 92.08%
Unmapped reads	264,034 / 7.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,766 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	164,397 / 4.93%
Duplication rate	4.02%
Clipped reads	3,083,316 / 92.45%

2.2. ACGT Content

Number/percentage of A's	44,972,569 / 24.96%
Number/percentage of C's	35,005,233 / 19.43%
Number/percentage of T's	56,466,843 / 31.34%
Number/percentage of G's	43,749,901 / 24.28%
Number/percentage of N's	2,219 / 0%
GC Percentage	43.71%

2.3. Coverage

Mean	0.0582

Standard Deviation	0.4484

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

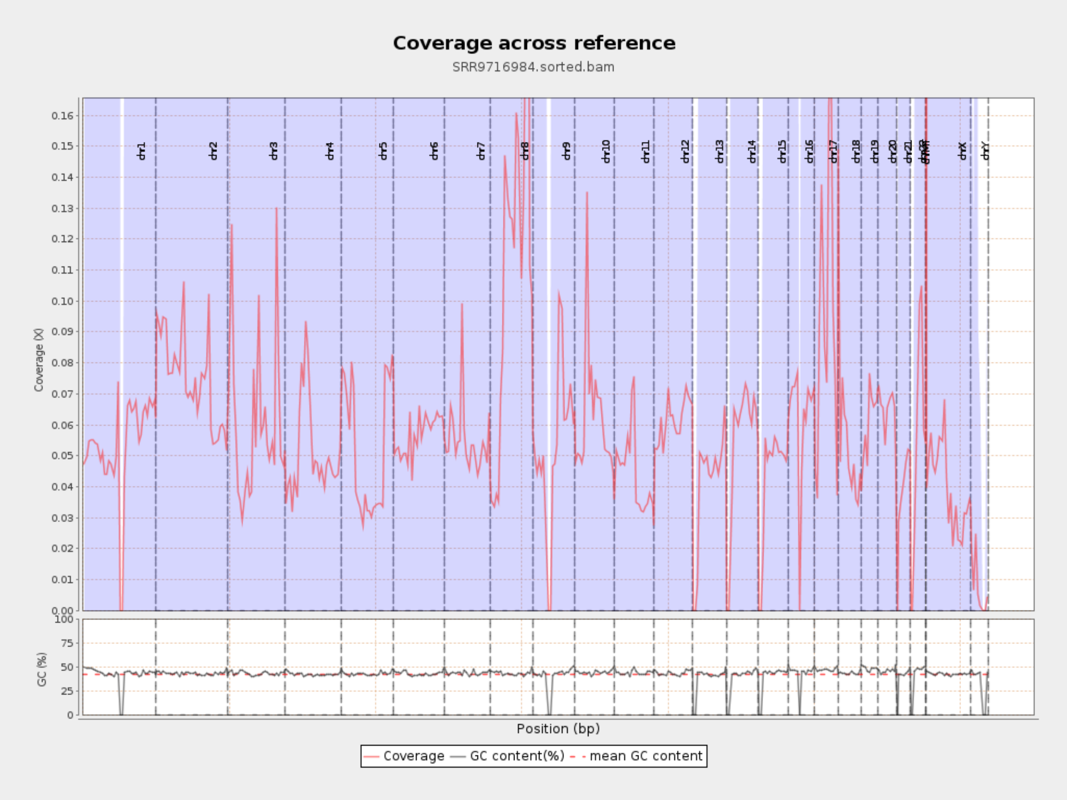
General error rate	0.51%
Mismatches	891,202
Insertions	11,948
Mapped reads with at least one insertion	0.39%
Deletions	32,964
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.06%

2.6. Chromosome stats

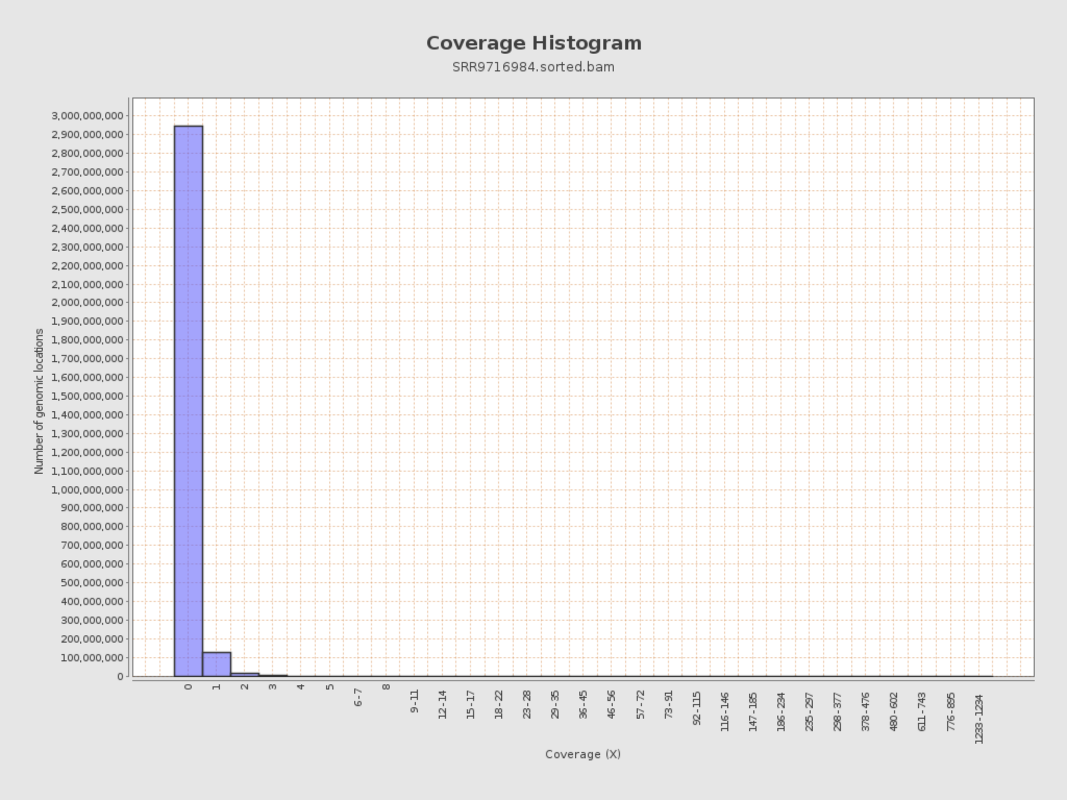
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13274194	0.0533	0.6912
chr2	243199373	18322950	0.0753	0.6361
chr3	198022430	11973730	0.0605	0.2974
chr4	191154276	9817960	0.0514	0.3203
chr5	180915260	9434945	0.0522	0.2679
chr6	171115067	9701962	0.0567	0.3113
chr7	159138663	8821047	0.0554	0.6677

chr8	146364022	17042157	0.1164	0.6185
chr9	141213431	7369358	0.0522	0.3381
chr10	135534747	8461567	0.0624	0.5935
chr11	135006516	6087540	0.0451	0.3439
chr12	133851895	8260633	0.0617	0.3167
chr13	115169878	4766610	0.0414	0.2369
chr14	107349540	5910767	0.0551	0.2858
chr15	102531392	4312189	0.0421	0.2502
chr16	90354753	5522128	0.0611	0.3094
chr17	81195210	7849305	0.0967	0.3949
chr18	78077248	4235338	0.0542	0.5582
chr19	59128983	3599775	0.0609	0.596
chr20	63025520	4106928	0.0652	0.3203
chr21	48129895	1850409	0.0384	0.2616
chr22	51304566	2855081	0.0556	0.2769
chrMT	16571	87047	5.253	3.8017
chrX	155270560	6156173	0.0396	0.2793
chrY	59373566	429449	0.0072	0.1865

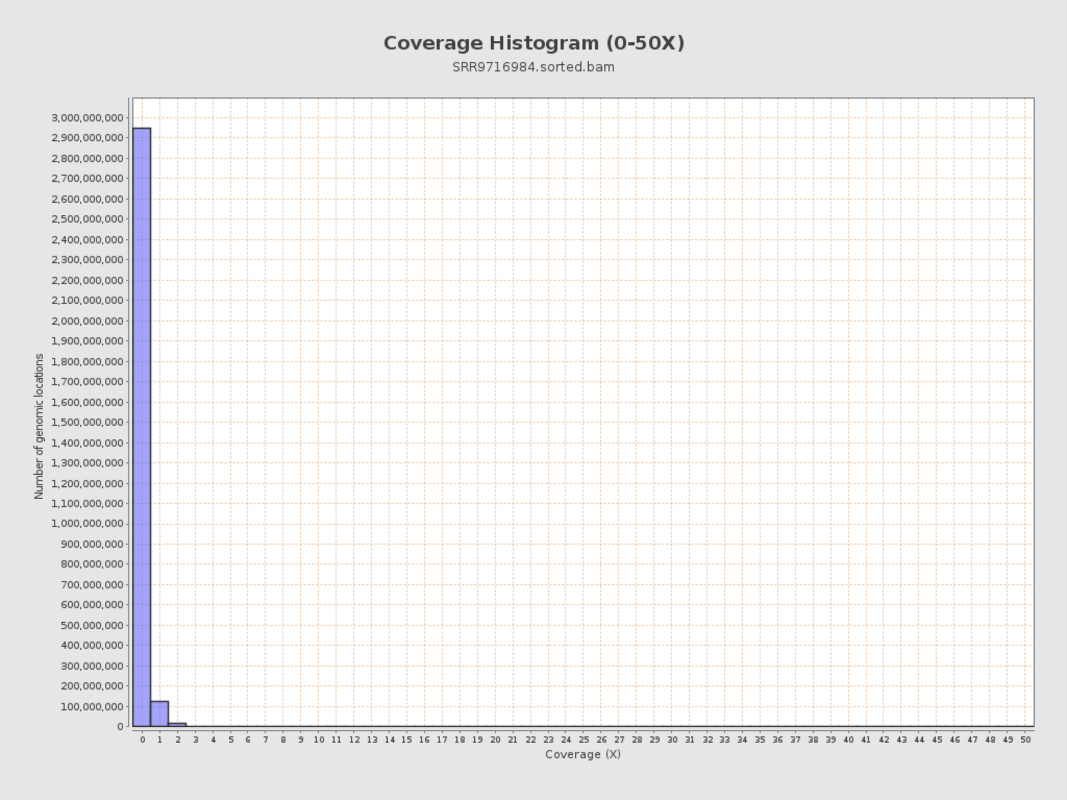
3. Results : Coverage across reference



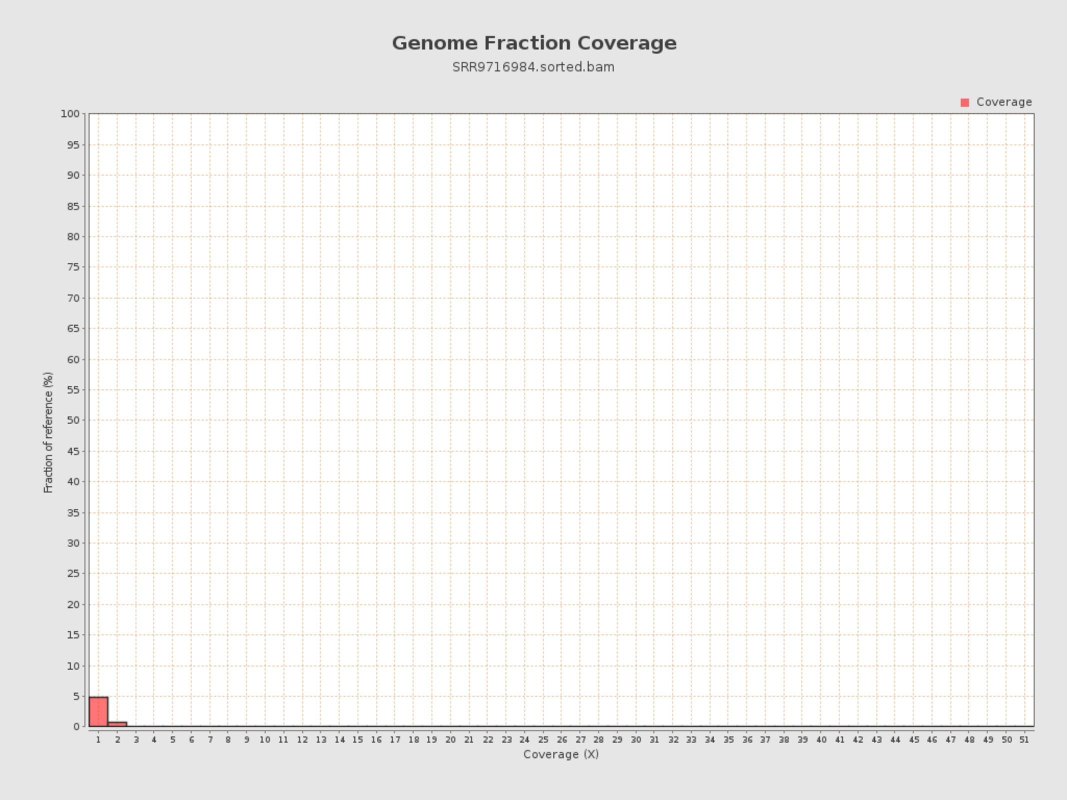
4. Results : Coverage Histogram



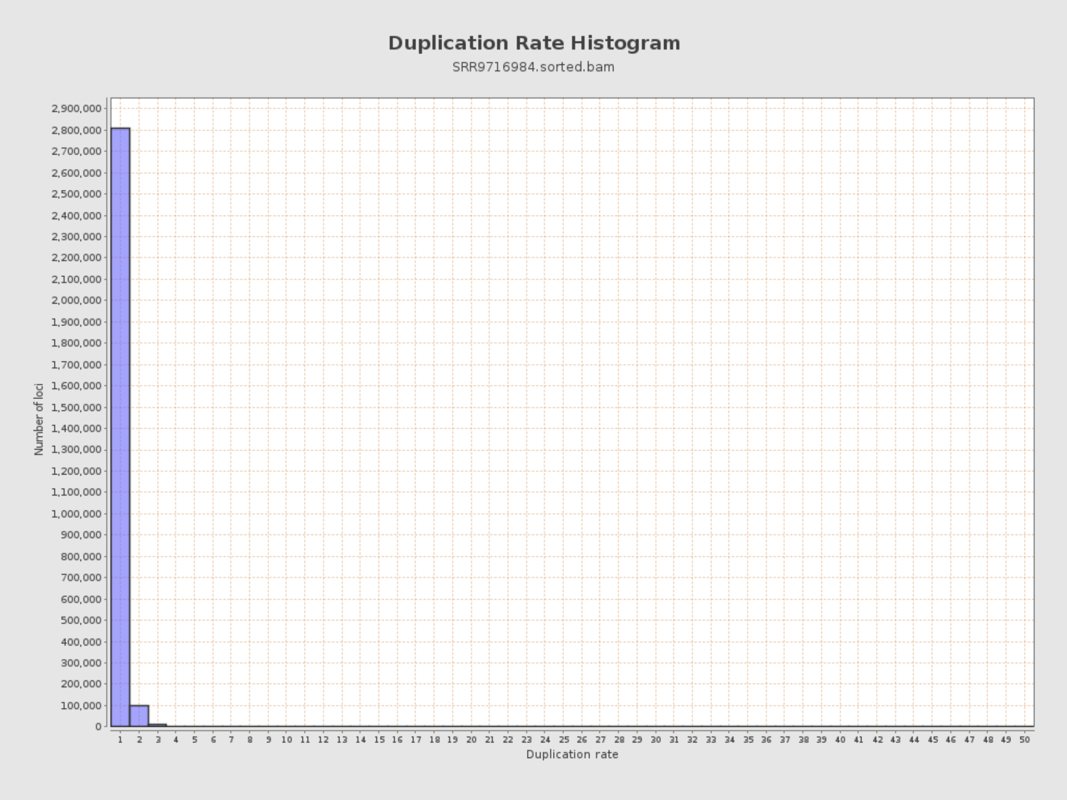
5. Results : Coverage Histogram (0-50X)



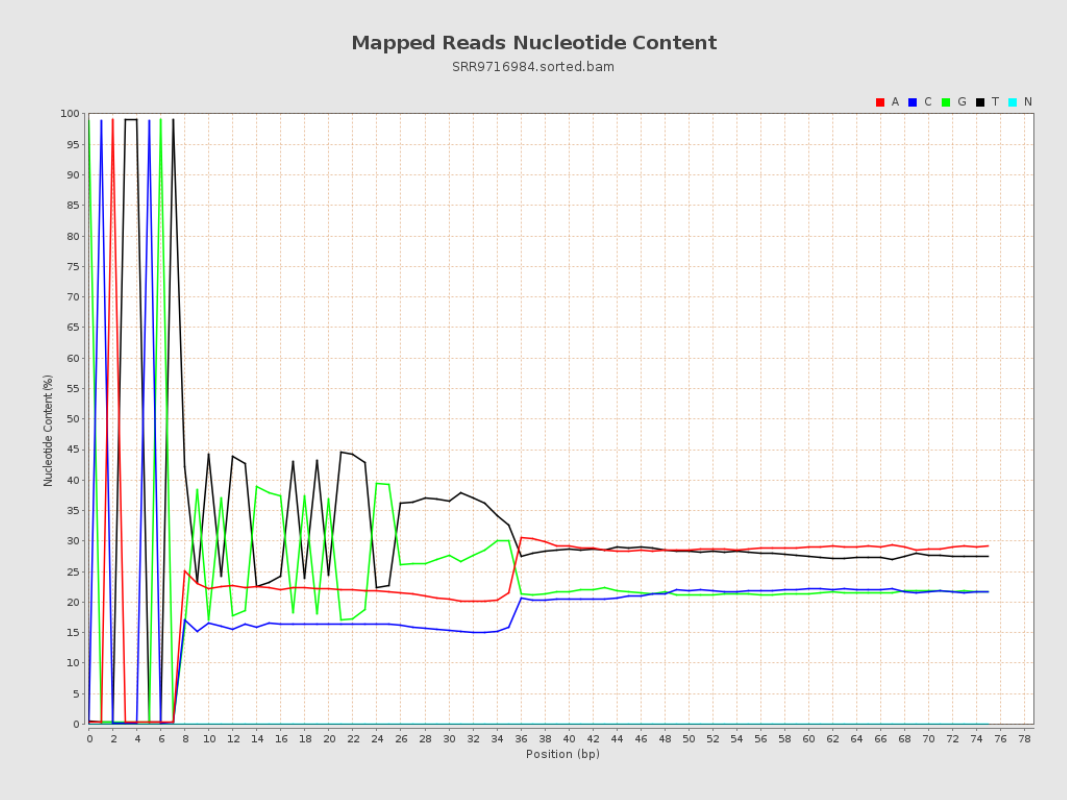
6. Results : Genome Fraction Coverage



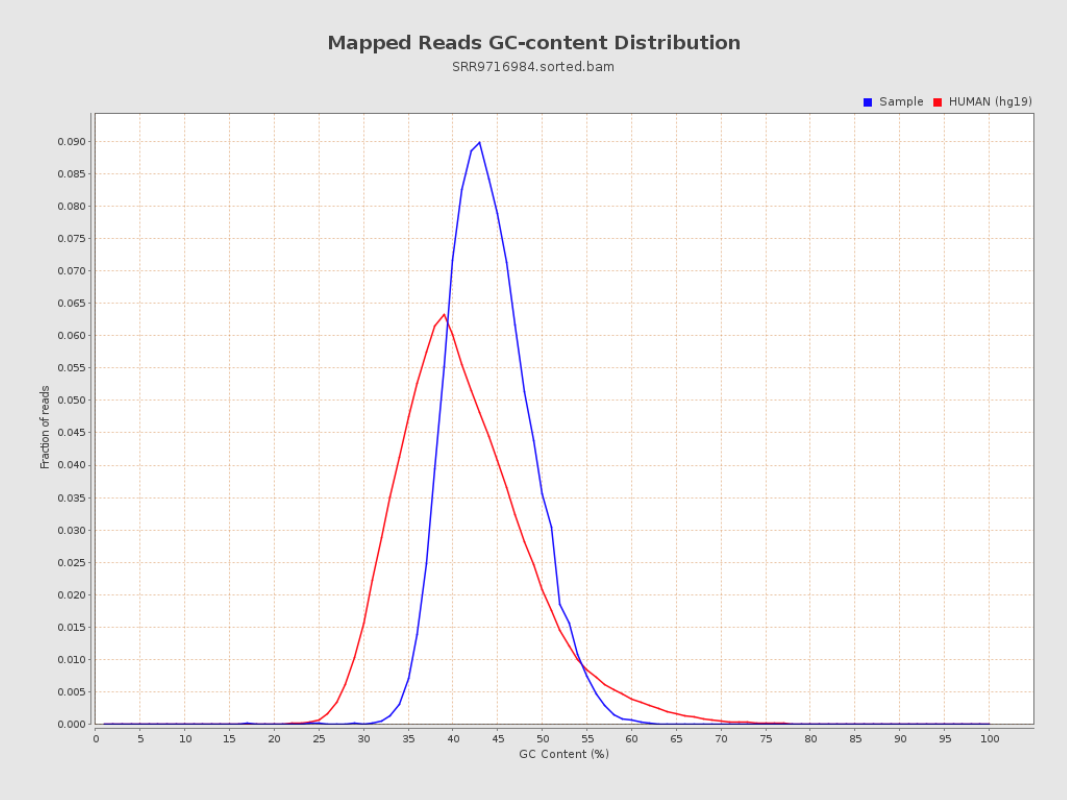
7. Results : Duplication Rate Histogram



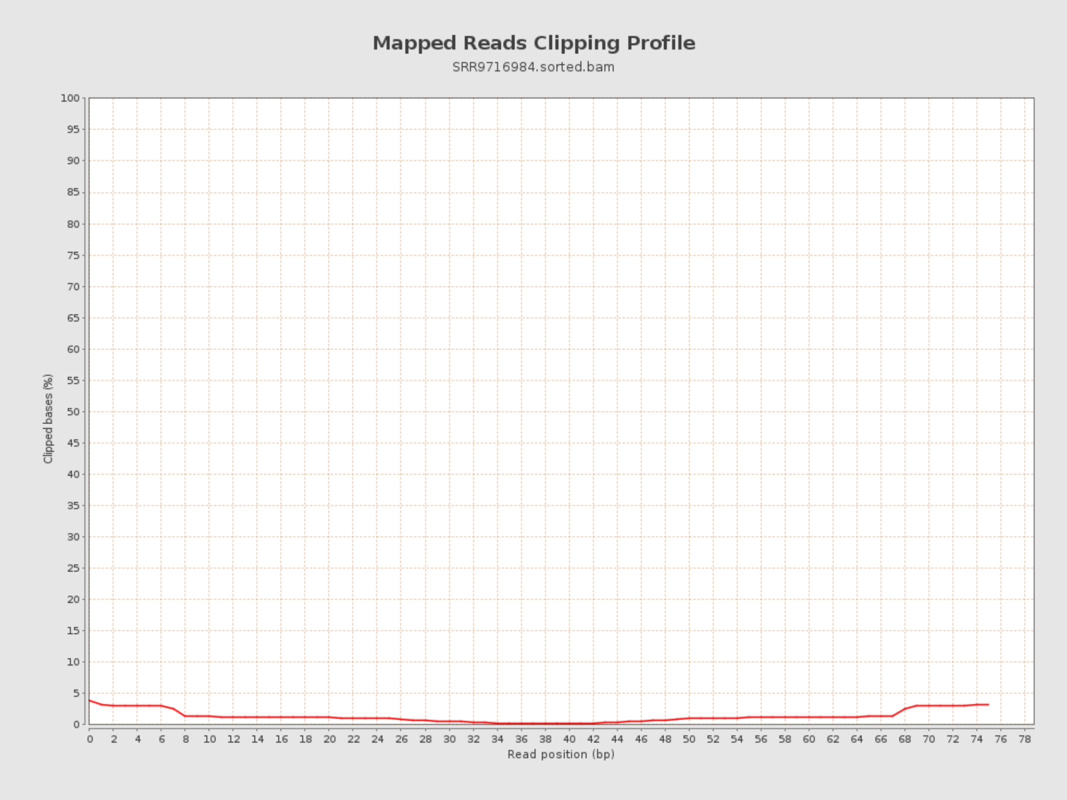
8. Results : Mapped Reads Nucleotide Content



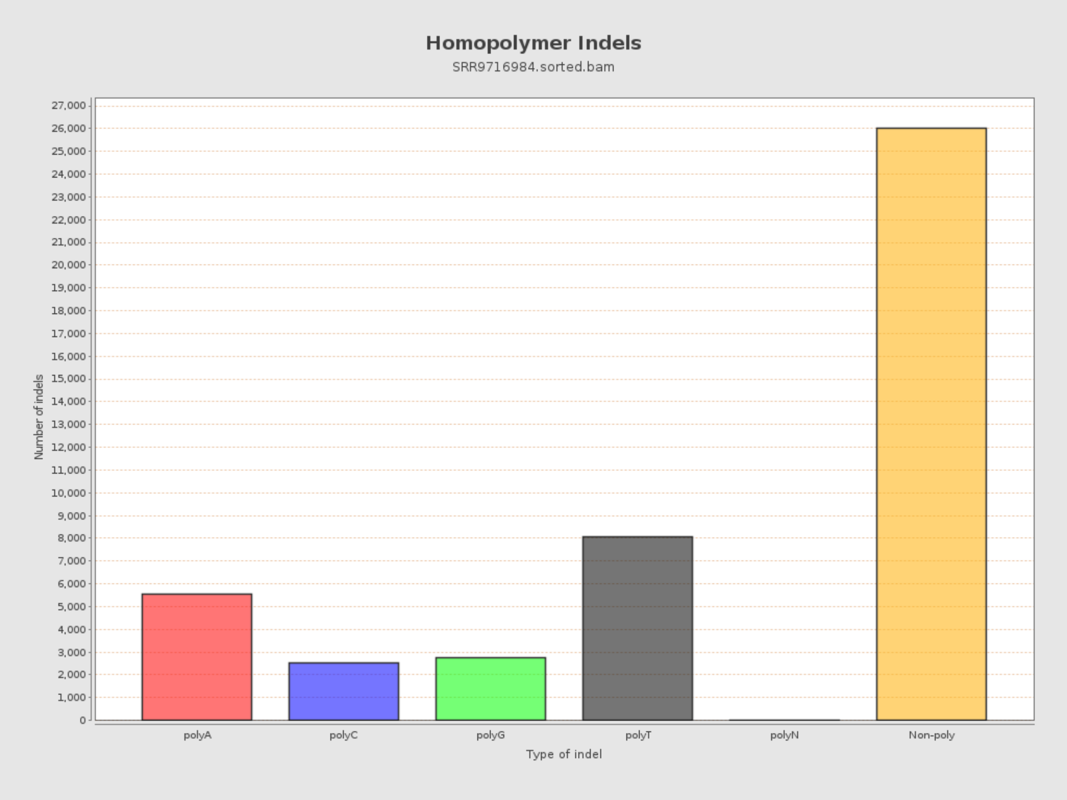
9. Results : Mapped Reads GC-content Distribution



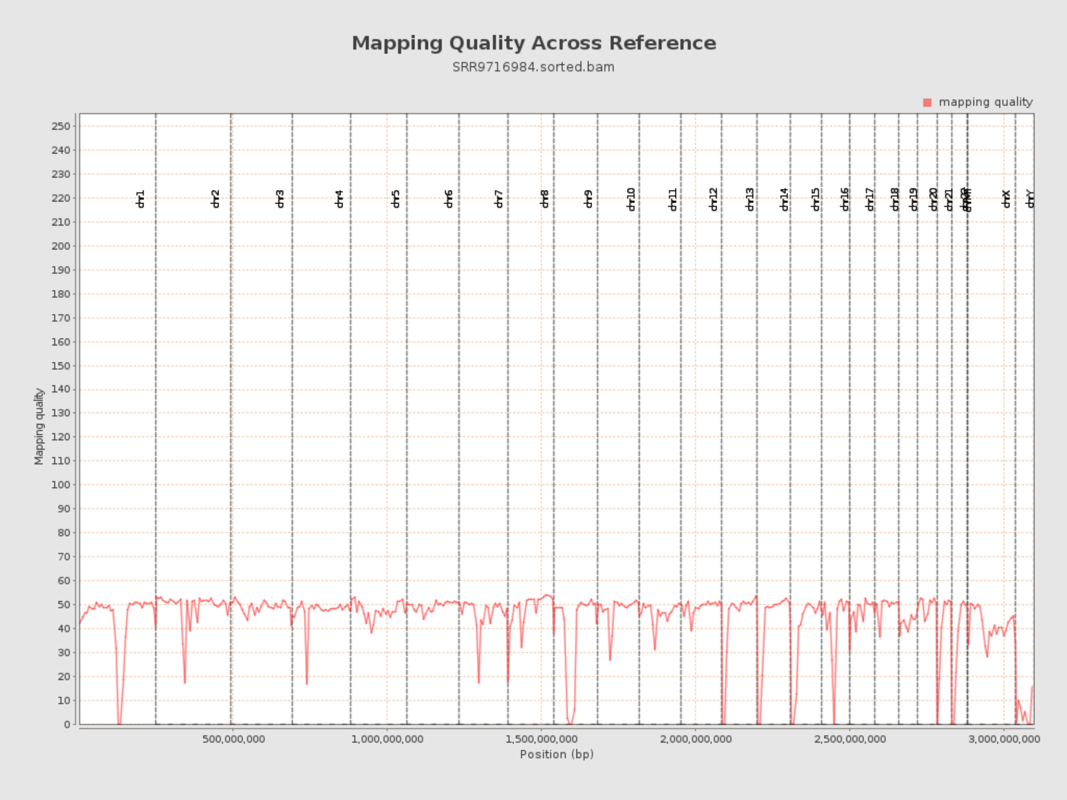
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram