Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:43:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717046.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_SRR9717046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:43:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,596,873
Mapped reads	1,491,136 / 93.38%
Unmapped reads	105,737 / 6.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,090 / 2.76%
Read min/max/mean length	30 / 101 / 101.99
Duplicated reads (estimated)	32,152 / 2.01%
Duplication rate	1.4%
Clipped reads	1,532,418 / 95.96%

2.2. ACGT Content

Number/percentage of A's	27,937,657 / 25.15%
Number/percentage of C's	23,218,632 / 20.9%
Number/percentage of T's	32,856,771 / 29.58%
Number/percentage of G's	27,058,989 / 24.36%
Number/percentage of N's	13,029 / 0.01%
GC Percentage	45.26%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.2892

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

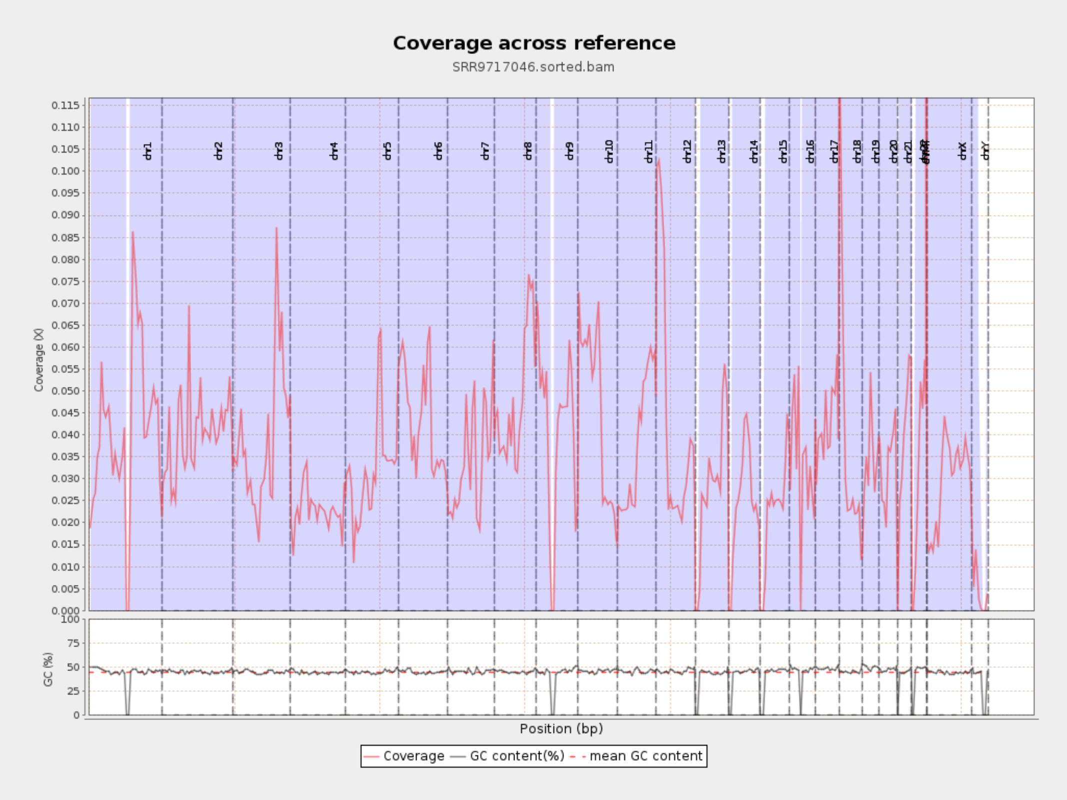
General error rate	0.78%
Mismatches	843,672
Insertions	9,486
Mapped reads with at least one insertion	0.63%
Deletions	21,618
Mapped reads with at least one deletion	1.43%
Homopolymer indels	40.02%

2.6. Chromosome stats

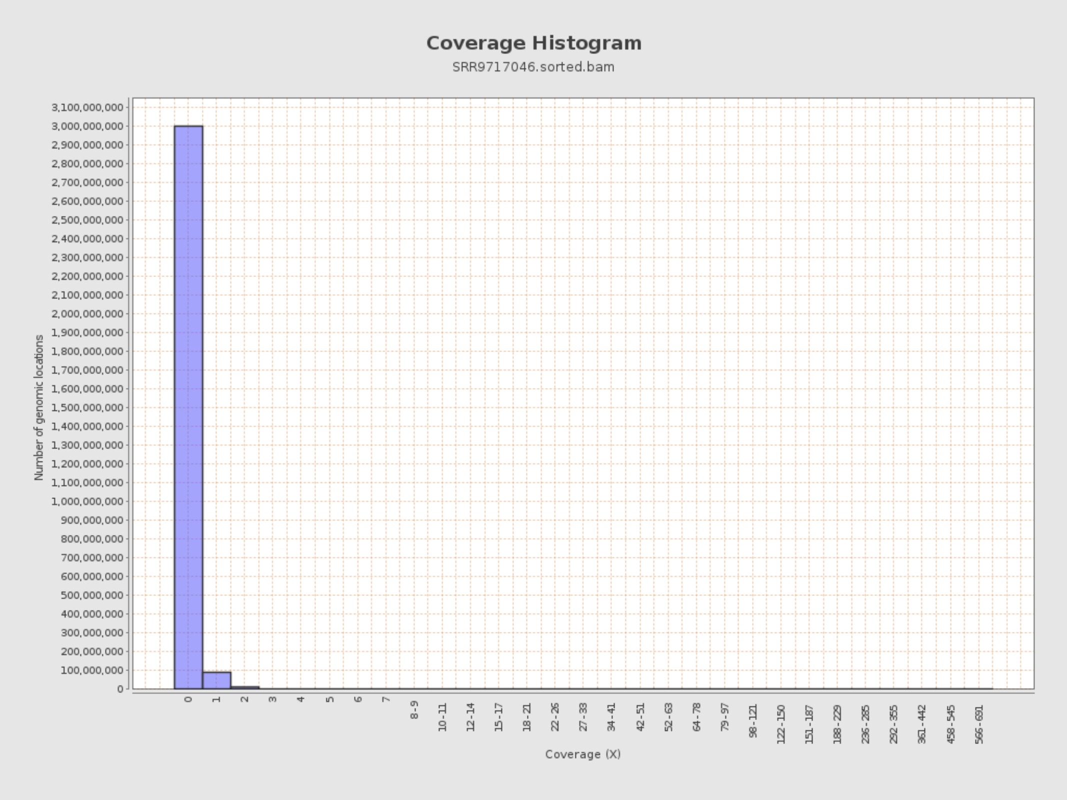
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10245003	0.0411	0.3252
chr2	243199373	9855603	0.0405	0.4977
chr3	198022430	7674252	0.0388	0.2154
chr4	191154276	4337657	0.0227	0.1725
chr5	180915260	5706057	0.0315	0.1924
chr6	171115067	7498574	0.0438	0.2447
chr7	159138663	5454373	0.0343	0.3523

chr8	146364022	7120118	0.0486	0.3917
chr9	141213431	5725452	0.0405	0.294
chr10	135534747	6368536	0.047	0.3155
chr11	135006516	5143949	0.0381	0.2704
chr12	133851895	5834174	0.0436	0.2341
chr13	115169878	3333370	0.0289	0.1853
chr14	107349540	2656962	0.0248	0.1835
chr15	102531392	2299451	0.0224	0.1613
chr16	90354753	2962375	0.0328	0.215
chr17	81195210	3445478	0.0424	0.2505
chr18	78077248	3030007	0.0388	0.4132
chr19	59128983	2031172	0.0344	0.3122
chr20	63025520	2054617	0.0326	0.2012
chr21	48129895	1845973	0.0384	0.225
chr22	51304566	1545664	0.0301	0.1935
chrMT	16571	101522	6.1265	5.6019
chrX	155270560	4579634	0.0295	0.2189
chrY	59373566	272465	0.0046	0.1343

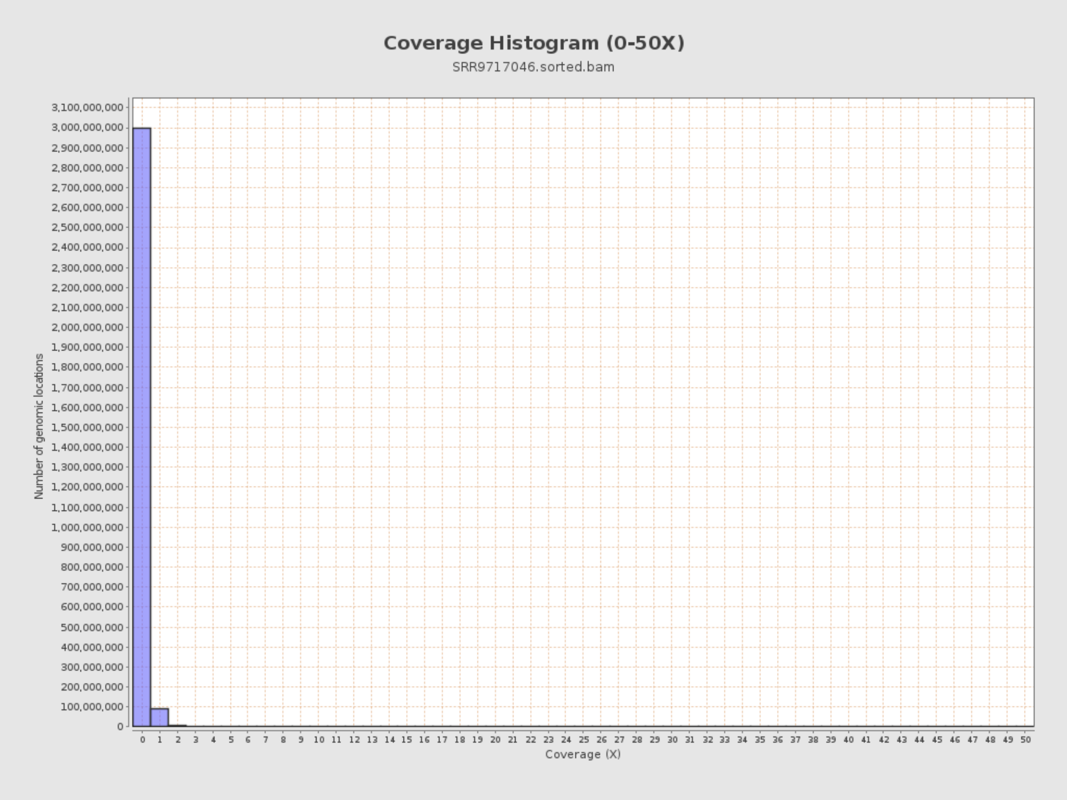
3. Results : Coverage across reference



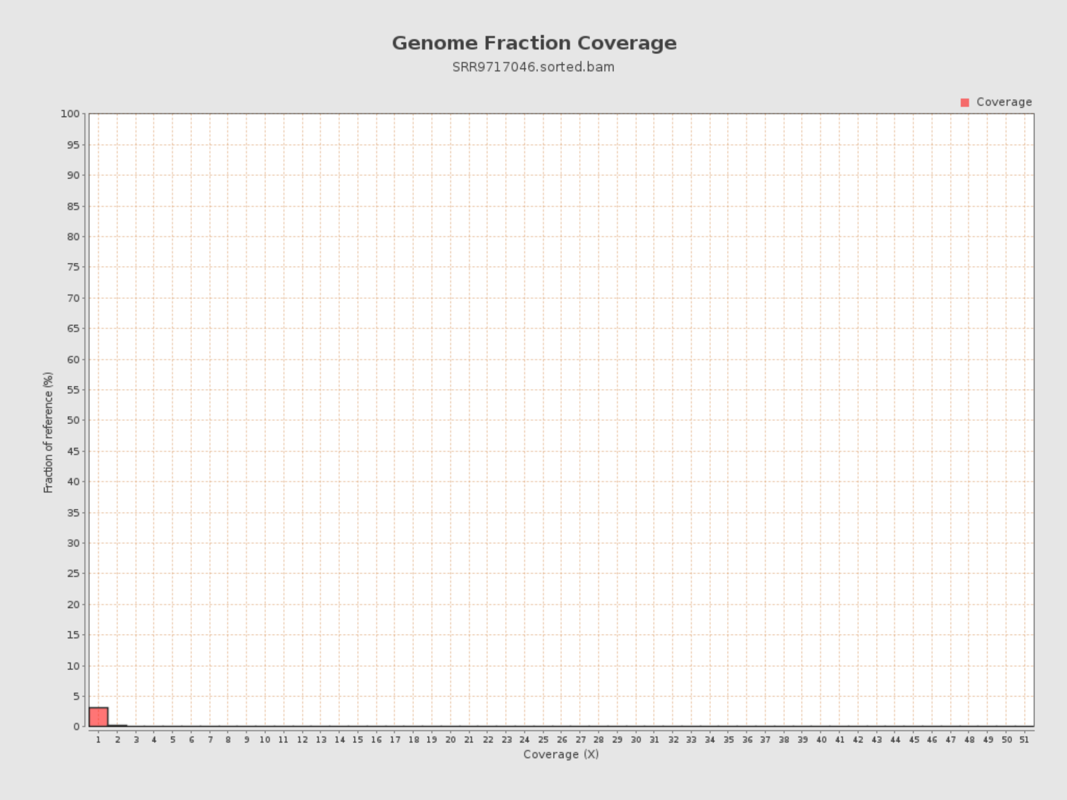
4. Results : Coverage Histogram



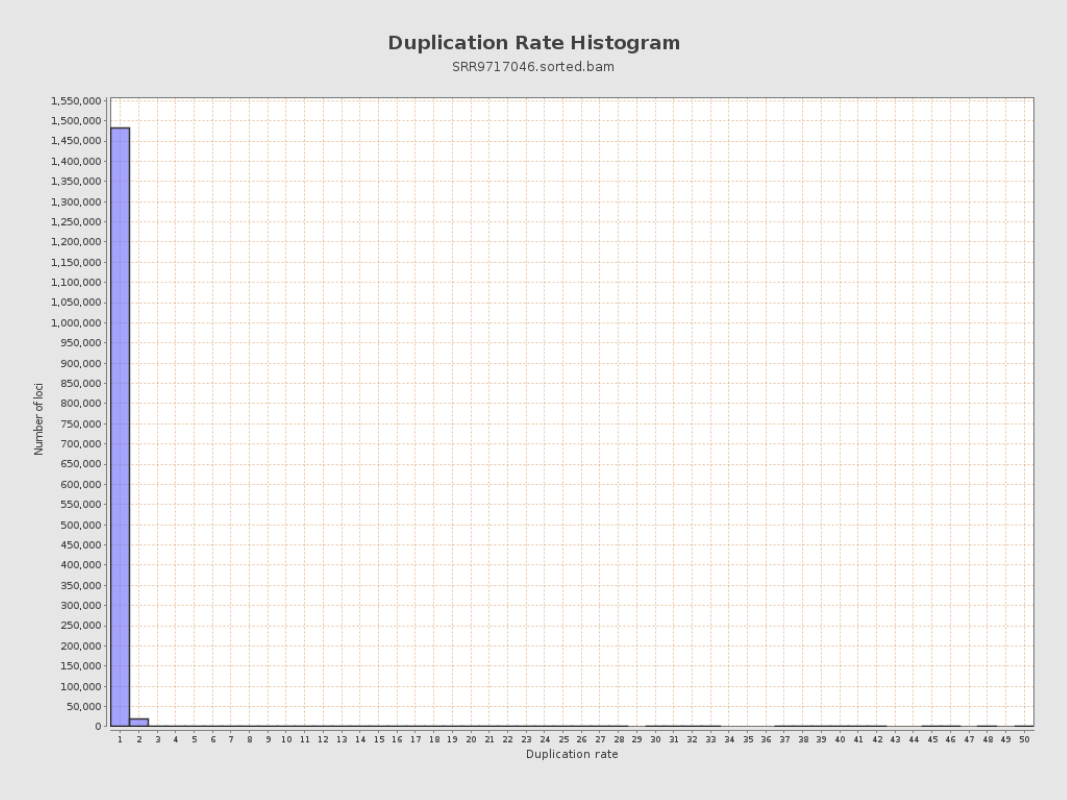
5. Results : Coverage Histogram (0-50X)



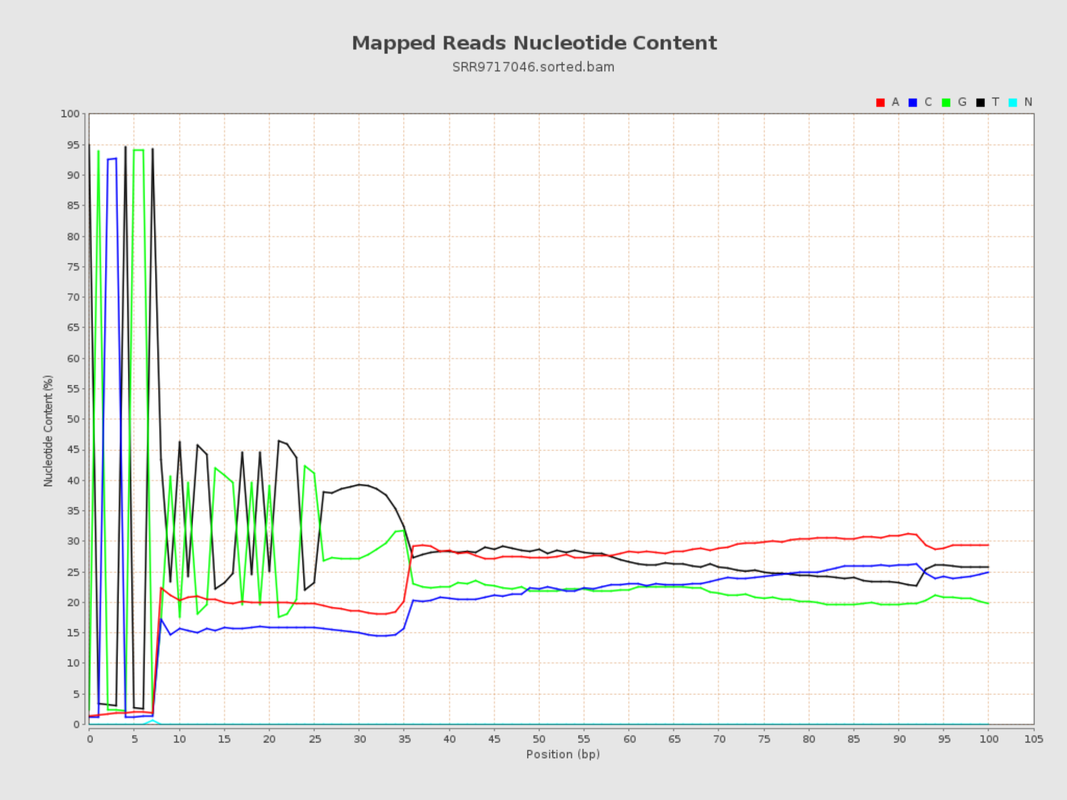
6. Results : Genome Fraction Coverage



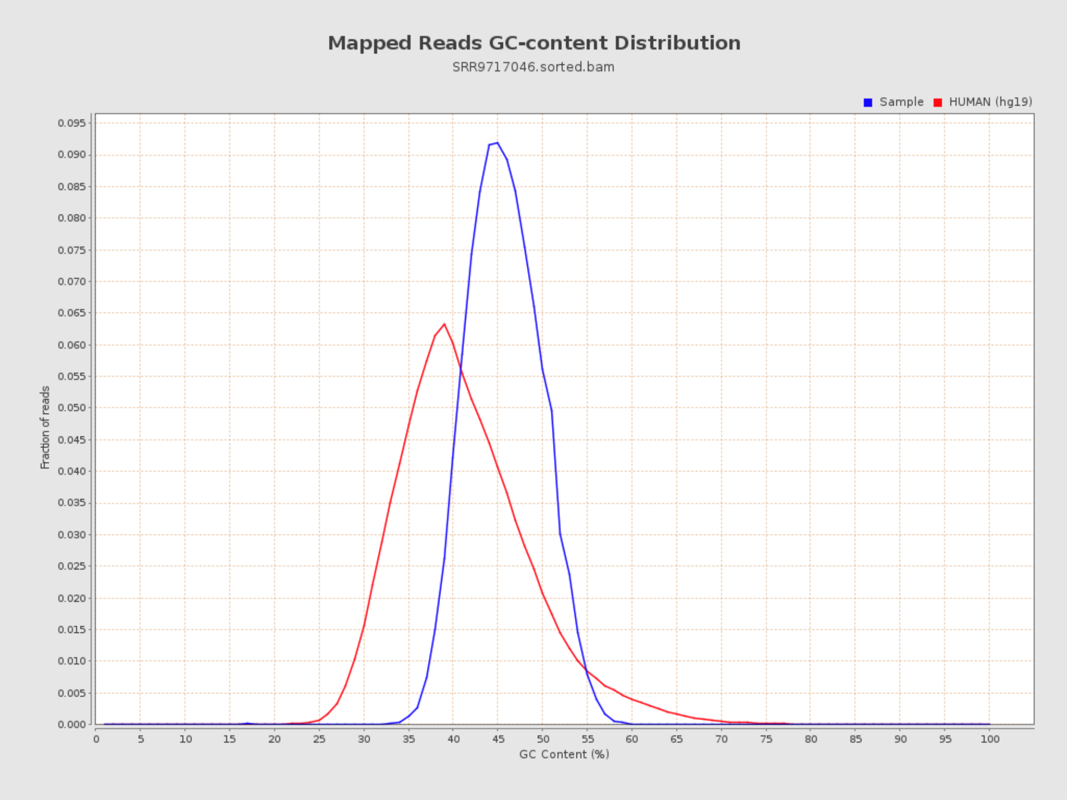
7. Results : Duplication Rate Histogram



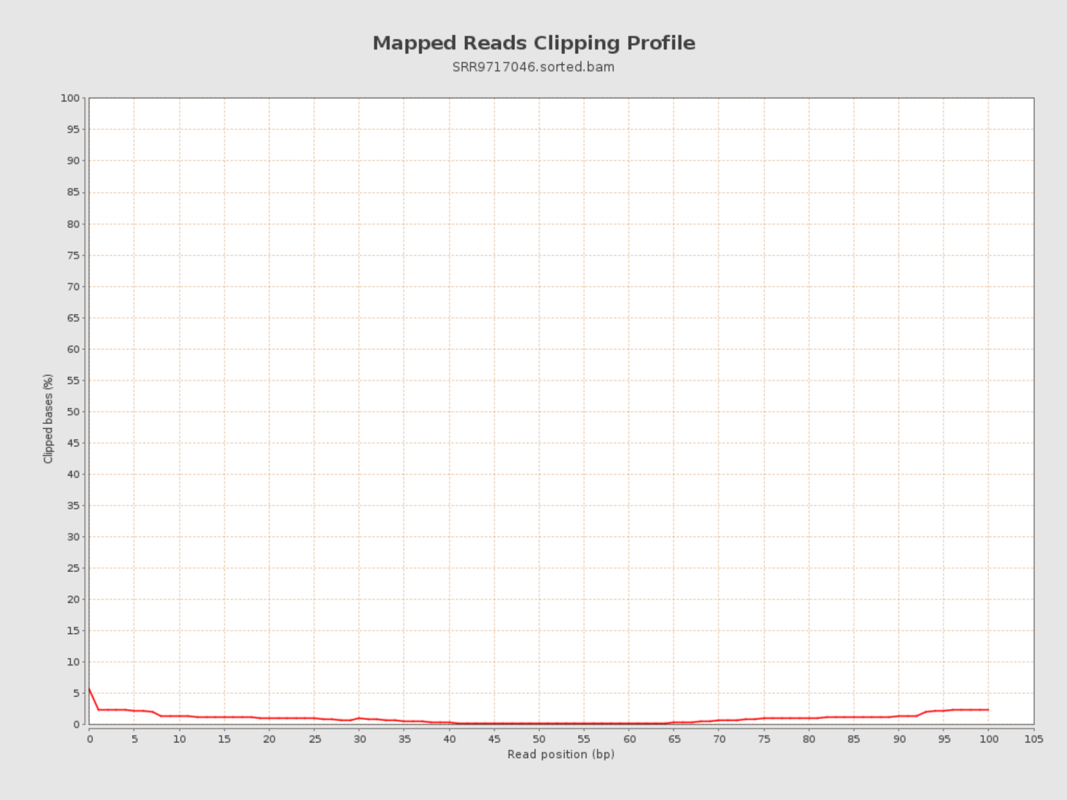
8. Results : Mapped Reads Nucleotide Content



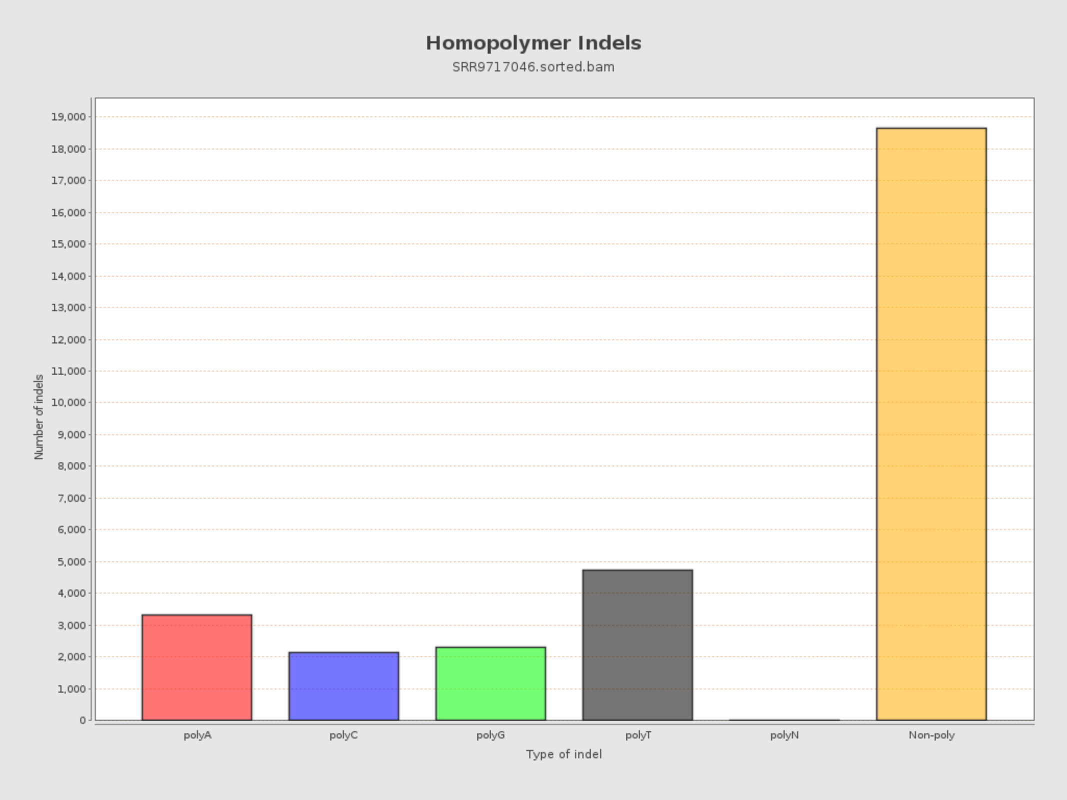
9. Results : Mapped Reads GC-content Distribution



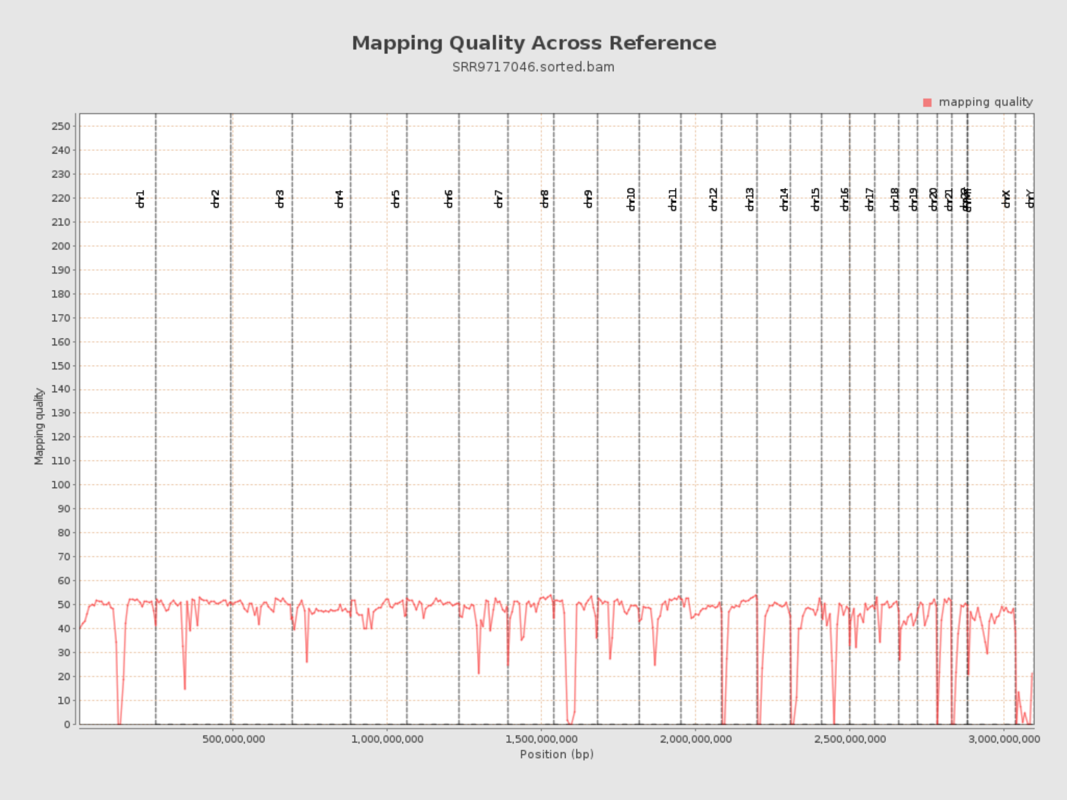
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram