Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/18 04:15:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365365.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_SRR5365365 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365365_1.fastq.gz SRR5365365_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Nov 18 04:15:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365365.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	576,647,552
Mapped reads	492,000,162 / 85.32%
Unmapped reads	84,647,390 / 14.68%
Mapped paired reads	492,000,162 / 85.32%
Mapped reads, first in pair	244,637,639 / 42.42%
Mapped reads, second in pair	247,362,523 / 42.9%
Mapped reads, both in pair	477,682,998 / 82.84%
Mapped reads, singletons	14,317,164 / 2.48%
Secondary alignments	0
Supplementary alignments	19,466,705 / 3.38%
Read min/max/mean length	30 / 150 / 151.6
Duplicated reads (estimated)	348,903,867 / 60.51%
Duplication rate	46.32%
Clipped reads	379,647,921 / 65.84%

2.2. ACGT Content

Number/percentage of A's	17,226,597,478 / 28.01%
Number/percentage of C's	12,832,781,921 / 20.86%
Number/percentage of T's	17,564,677,315 / 28.56%
Number/percentage of G's	13,883,316,082 / 22.57%
Number/percentage of N's	1,846,524 / 0%

GC Percentage	43.43%

2.3. Coverage

Mean	19.8801
Standard Deviation	194.6026

2.4. Mapping Quality

Mean Mapping Quality	53.09

2.5. Insert size

Mean	125,830.62
Standard Deviation	3,457,232.42
P25/Median/P75	118 / 149 / 186

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	635,465,000
Insertions	6,051,219
Mapped reads with at least one insertion	1.17%
Deletions	15,844,016
Mapped reads with at least one deletion	3.12%
Homopolymer indels	43.08%

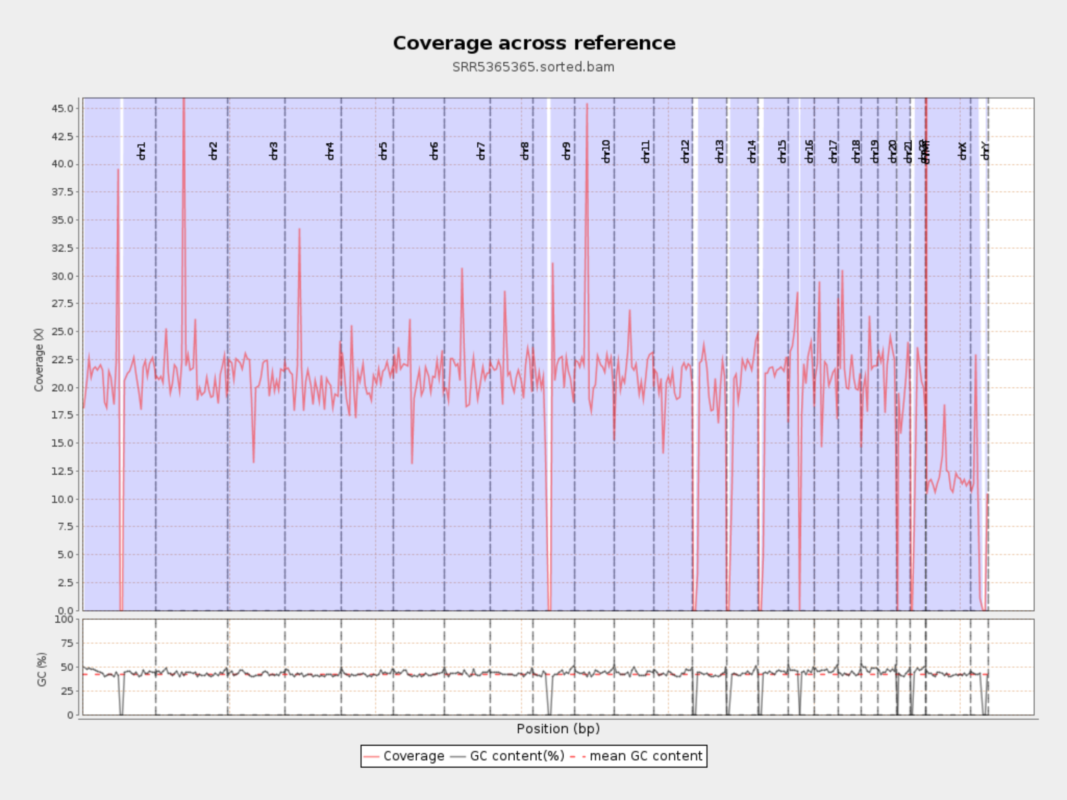
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

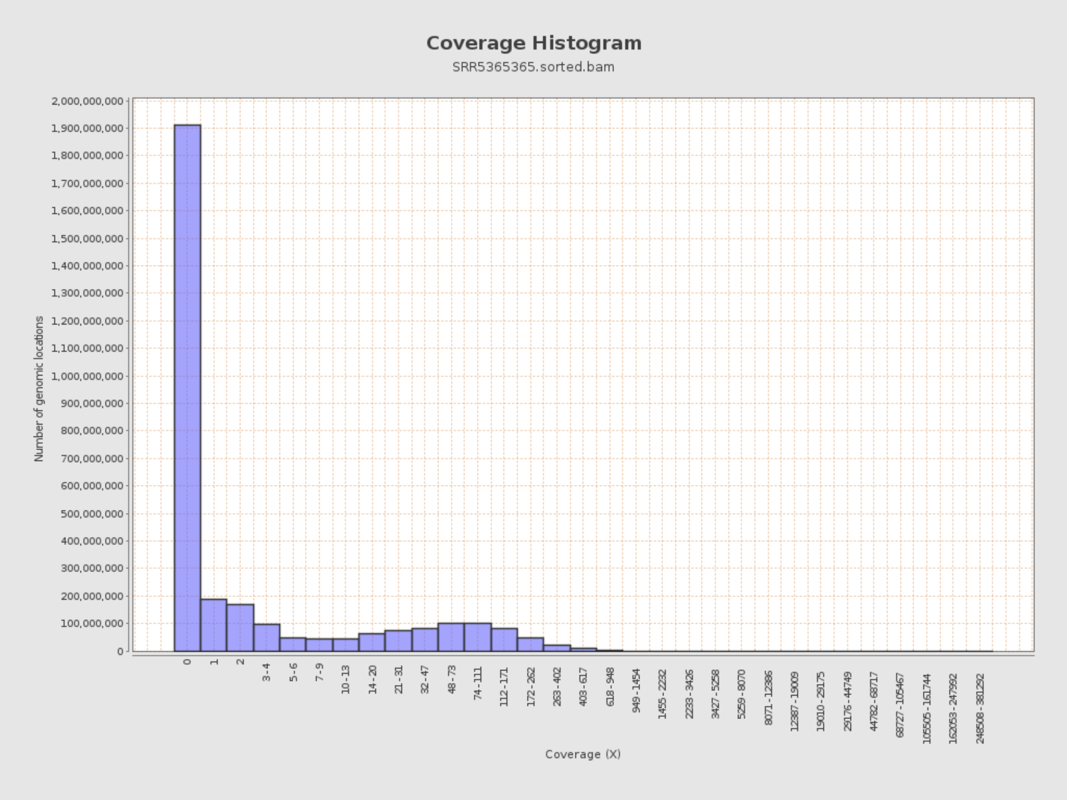
		bases	coverage	deviation
chr1	249250621	5054381077	20.2783	385.4979
chr2	243199373	5335236742	21.9377	243.2352
chr3	198022430	4167743888	21.0468	63.3595
chr4	191154276	3980662555	20.8243	109.2753
chr5	180915260	3754453989	20.7526	75.7448
chr6	171115067	3615158146	21.1271	100.3914
chr7	159138663	3399180867	21.3599	235.6167
chr8	146364022	3147758996	21.5064	110.7984
chr9	141213431	2685339518	19.0162	272.7475
chr10	135534747	3088591087	22.7882	236.5017
chr11	135006516	2905580191	21.5218	278.4166
chr12	133851895	2734209179	20.4271	63.2703
chr13	115169878	1965851341	17.0691	56.3038
chr14	107349540	1950808263	18.1725	162.6417
chr15	102531392	1776767808	17.329	58.5739
chr16	90354753	1856097188	20.5423	82.8188
chr17	81195210	1729775345	21.3039	158.8033
chr18	78077248	1727902924	22.1307	311.8853
chr19	59128983	1255612825	21.2352	217.6969
chr20	63025520	1389643910	22.0489	83.1872
chr21	48129895	864583755	17.9635	103.6843
chr22	51304566	760055959	14.8146	80.2158
chrMT	16571	39685969	2,394.9049	1,396.008
chrX	155270560	1862262925	11.9937	84.9728

chrY	59373566	495208030	8.3405	134.1935

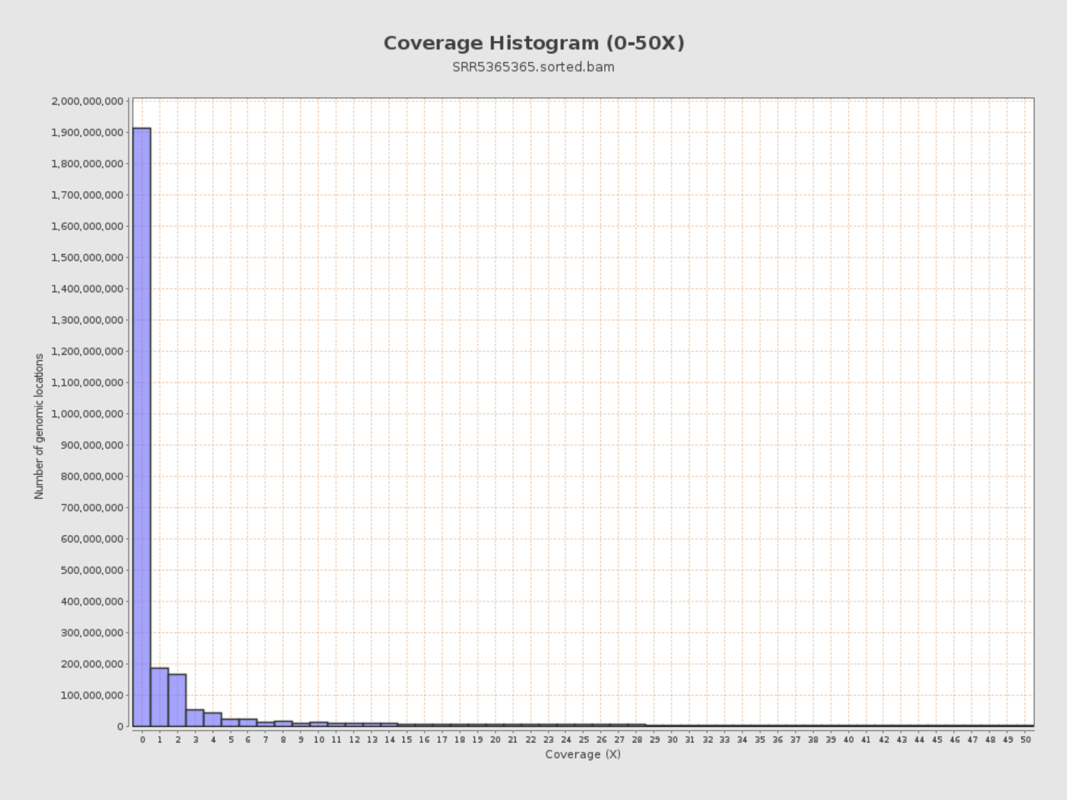
3. Results : Coverage across reference



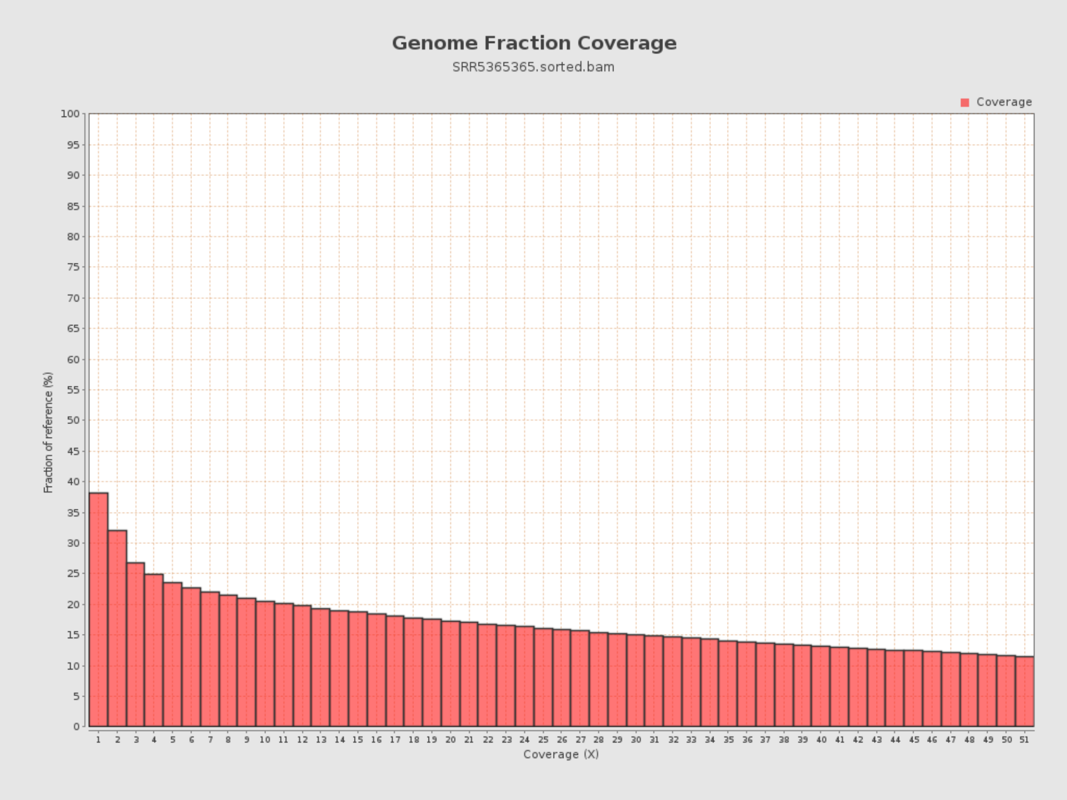
4. Results : Coverage Histogram



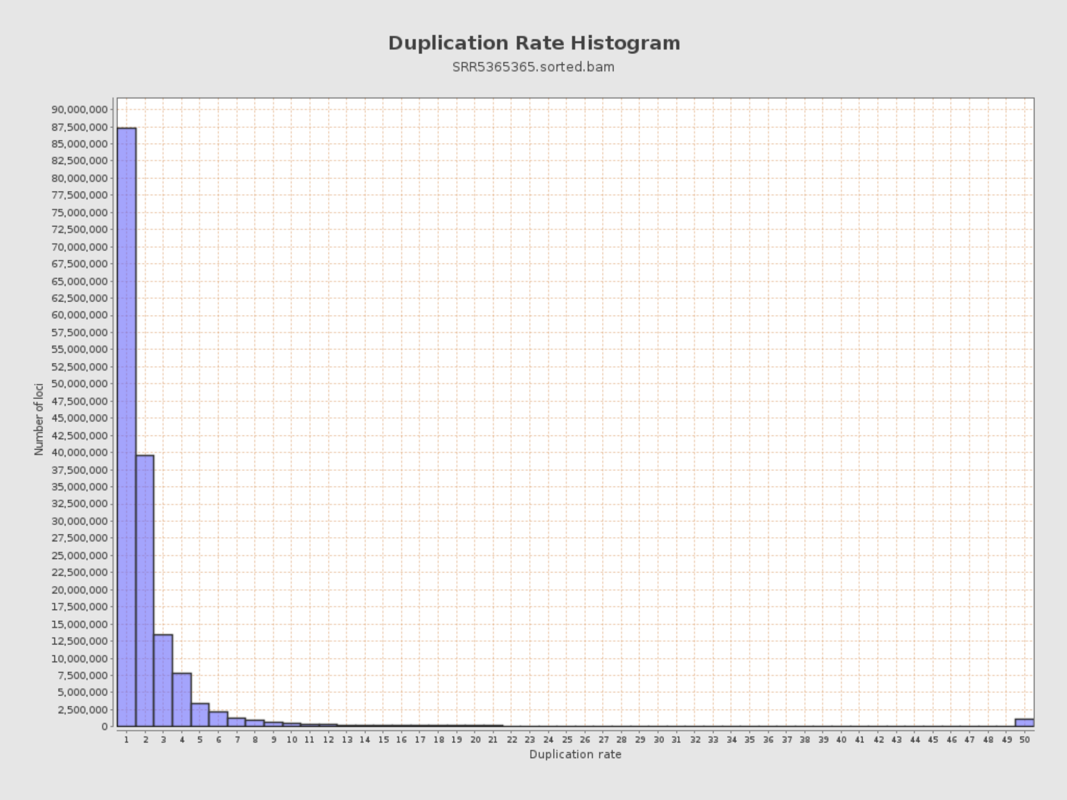
5. Results : Coverage Histogram (0-50X)



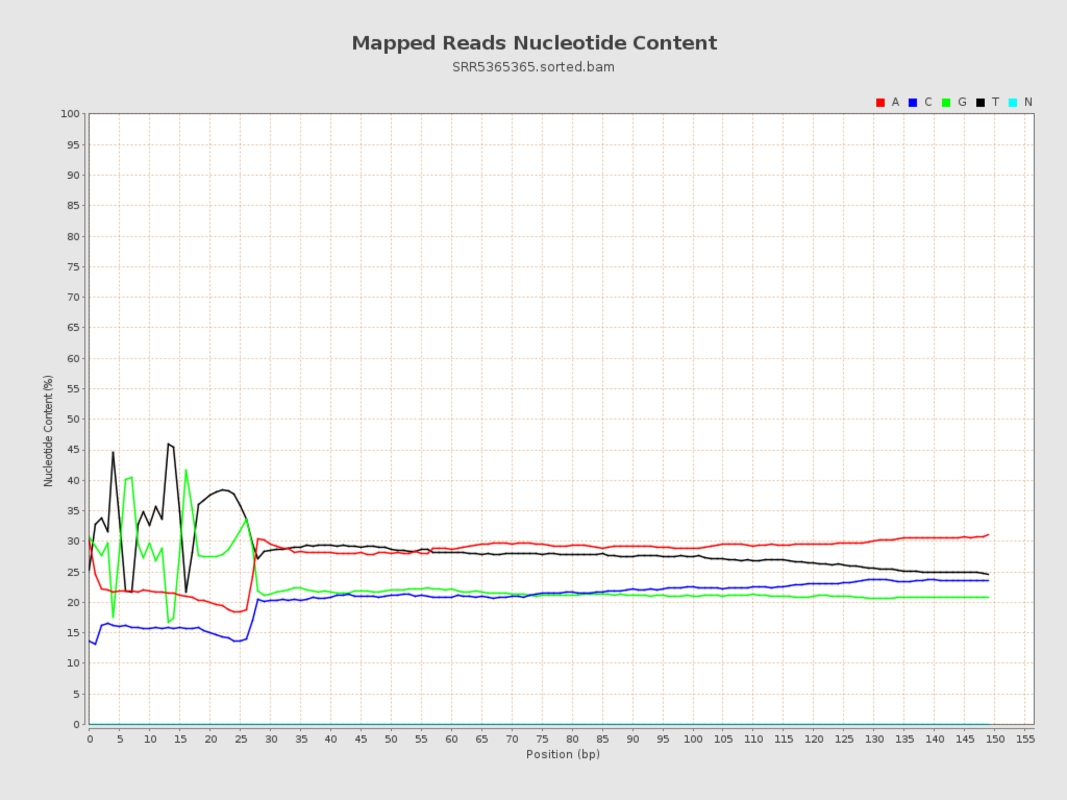
6. Results : Genome Fraction Coverage



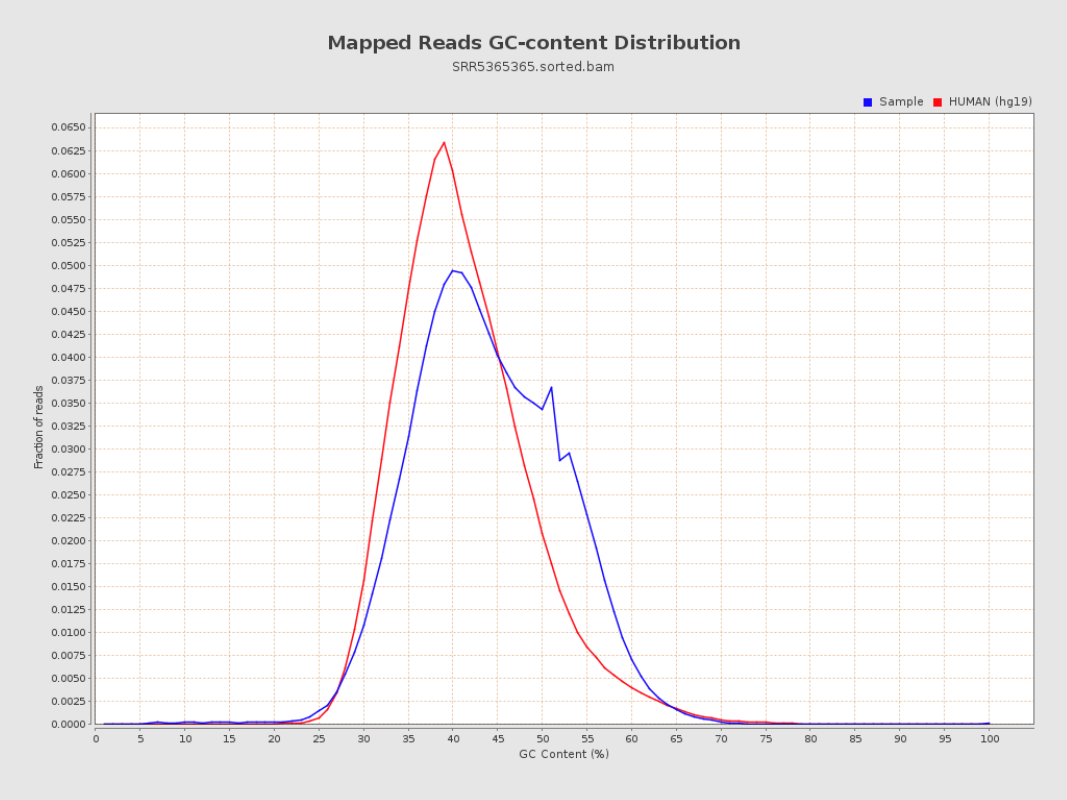
7. Results : Duplication Rate Histogram



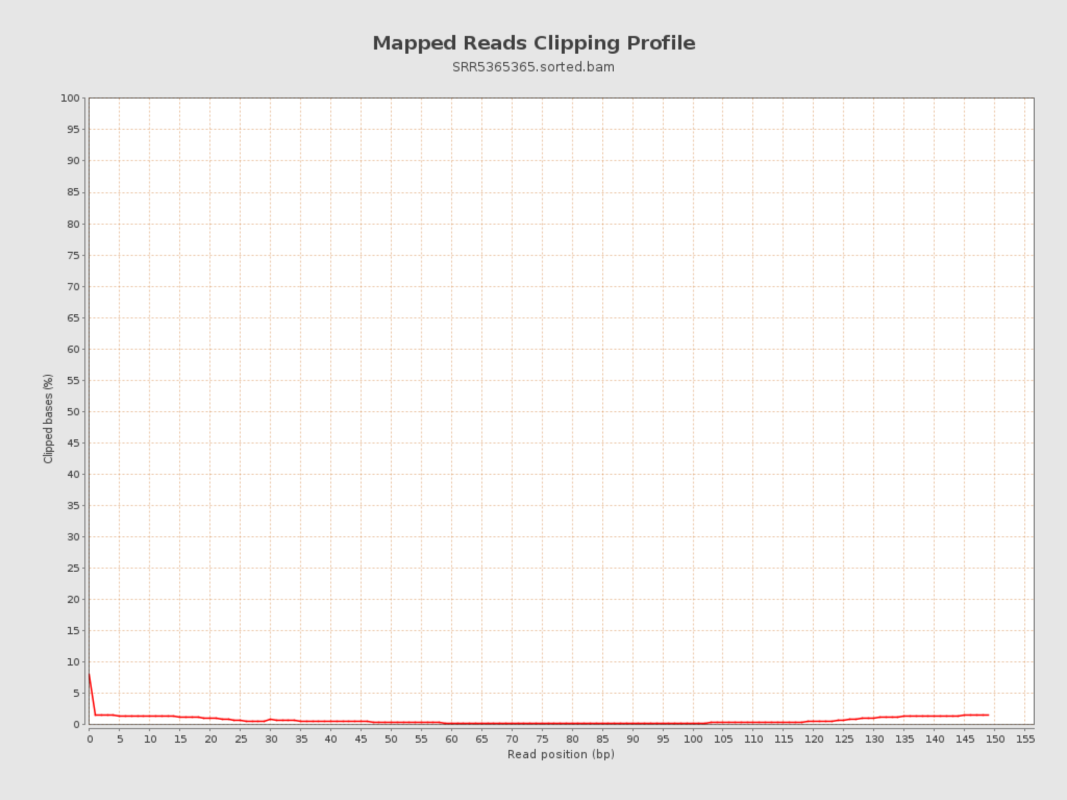
8. Results : Mapped Reads Nucleotide Content



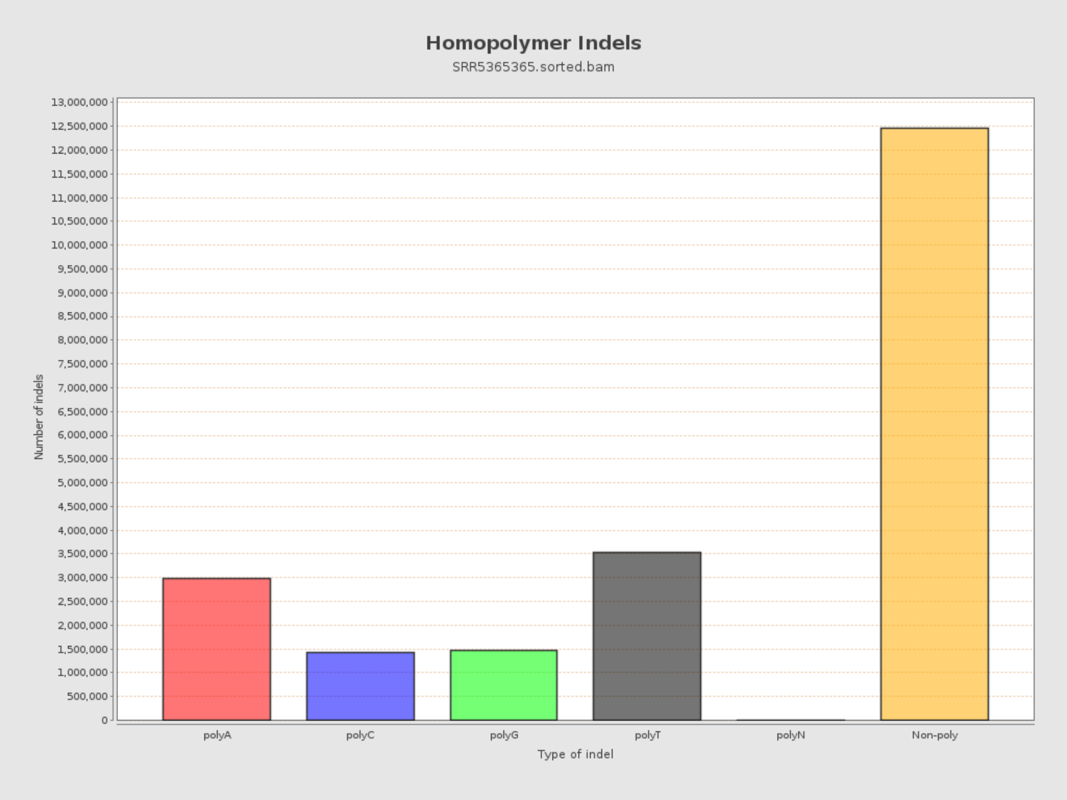
9. Results : Mapped Reads GC-content Distribution



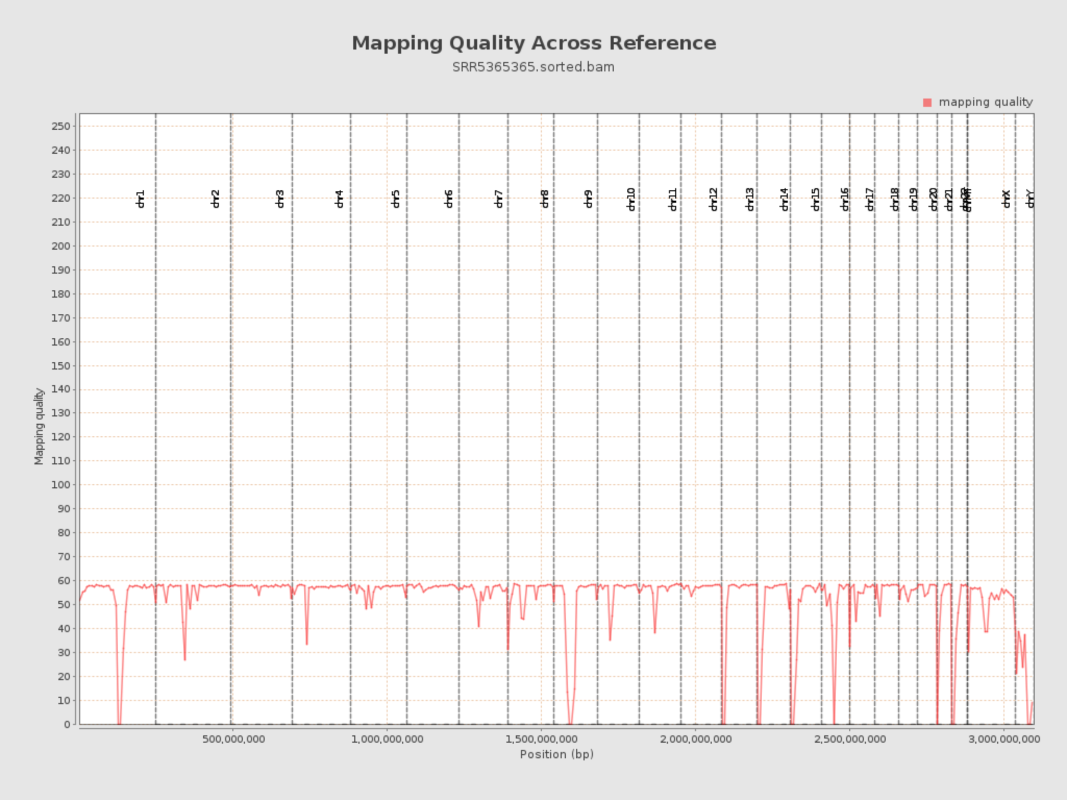
10. Results : Mapped Reads Clipping Profile



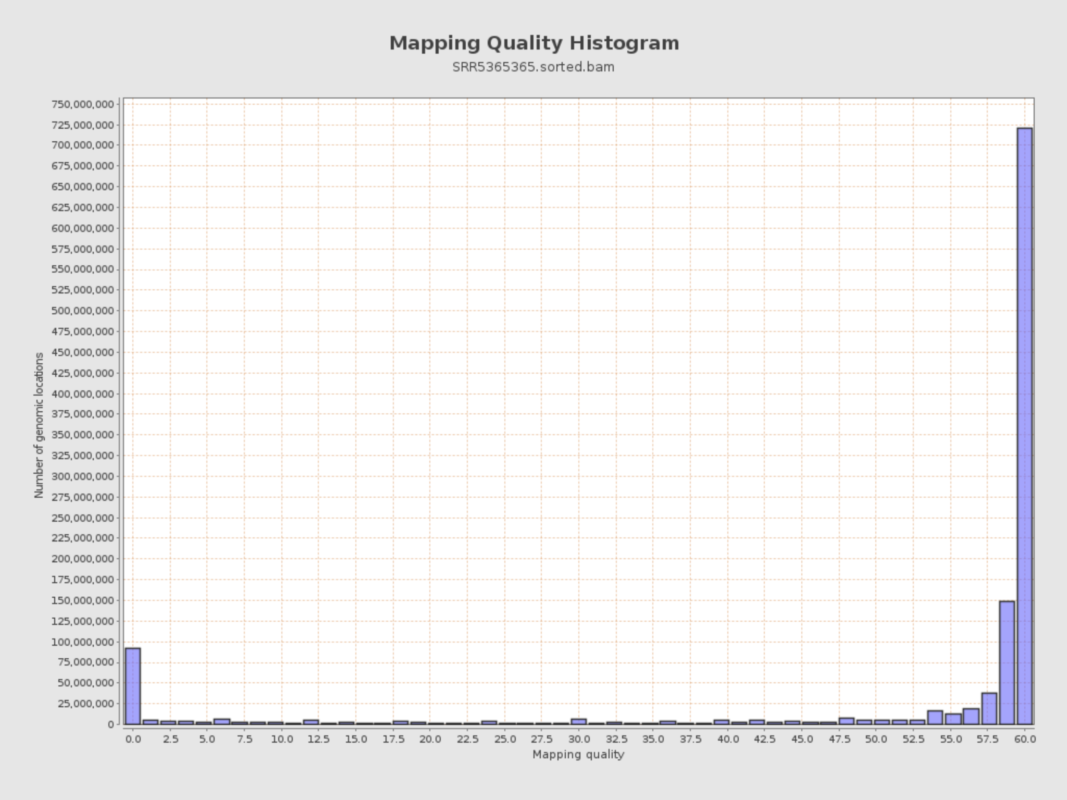
11. Results : Homopolymer Indels



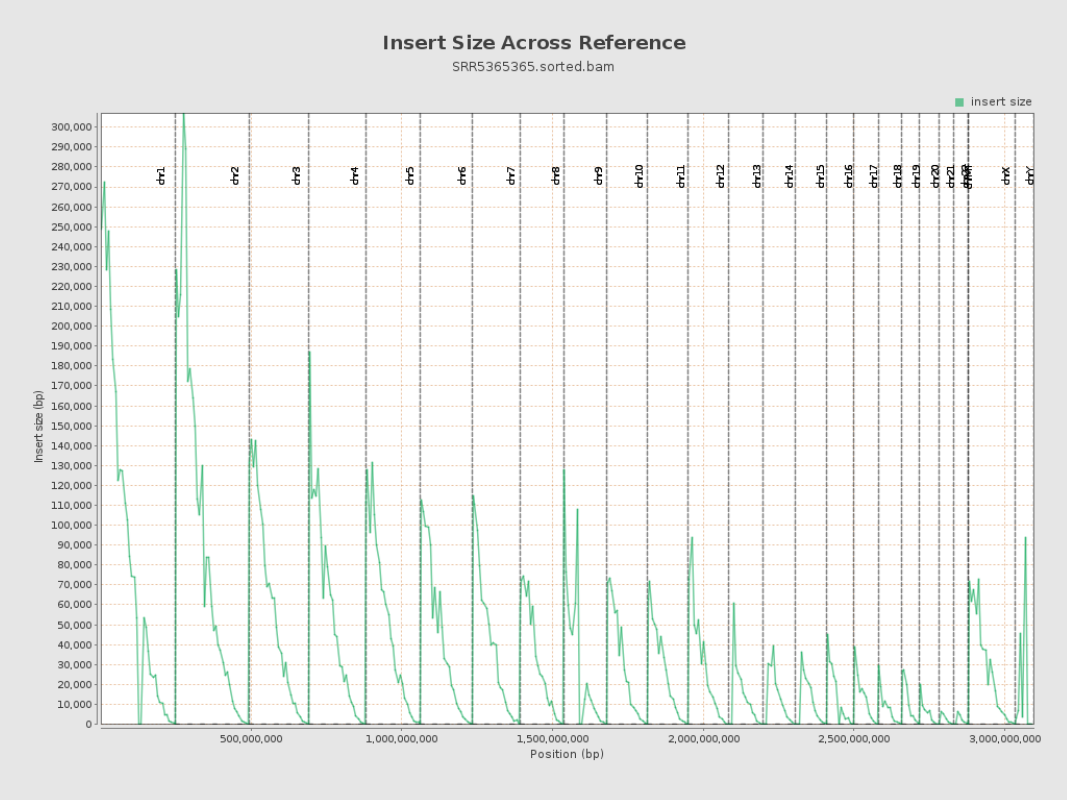
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram