Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/23 07:47:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976563.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_SRR2976563 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976563_1.fastq.gz SRR2976563_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 23 07:47:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976563.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	378,668,658
Mapped reads	375,539,683 / 99.17%
Unmapped reads	3,128,975 / 0.83%
Mapped paired reads	375,539,683 / 99.17%
Mapped reads, first in pair	188,846,400 / 49.87%
Mapped reads, second in pair	186,693,283 / 49.3%
Mapped reads, both in pair	373,035,086 / 98.51%
Mapped reads, singletons	2,504,597 / 0.66%
Secondary alignments	0
Supplementary alignments	12,801,002 / 3.38%
Read min/max/mean length	20 / 249 / 231.09
Duplicated reads (estimated)	61,515,664 / 16.25%
Duplication rate	14.3%
Clipped reads	42,990,185 / 11.35%

2.2. ACGT Content

Number/percentage of A's	25,067,467,018 / 29.2%
Number/percentage of C's	17,865,028,744 / 20.81%
Number/percentage of T's	24,841,394,026 / 28.94%
Number/percentage of G's	18,065,538,413 / 21.05%
Number/percentage of N's	1,762,740 / 0%

GC Percentage	41.86%

2.3. Coverage

Mean	27.7385
Standard Deviation	47.6202

2.4. Mapping Quality

Mean Mapping Quality	55.48

2.5. Insert size

Mean	77,925.71
Standard Deviation	2,712,283.01
P25/Median/P75	489 / 538 / 613

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	677,116,270
Insertions	8,156,613
Mapped reads with at least one insertion	2.06%
Deletions	10,405,823
Mapped reads with at least one deletion	2.64%
Homopolymer indels	46.54%

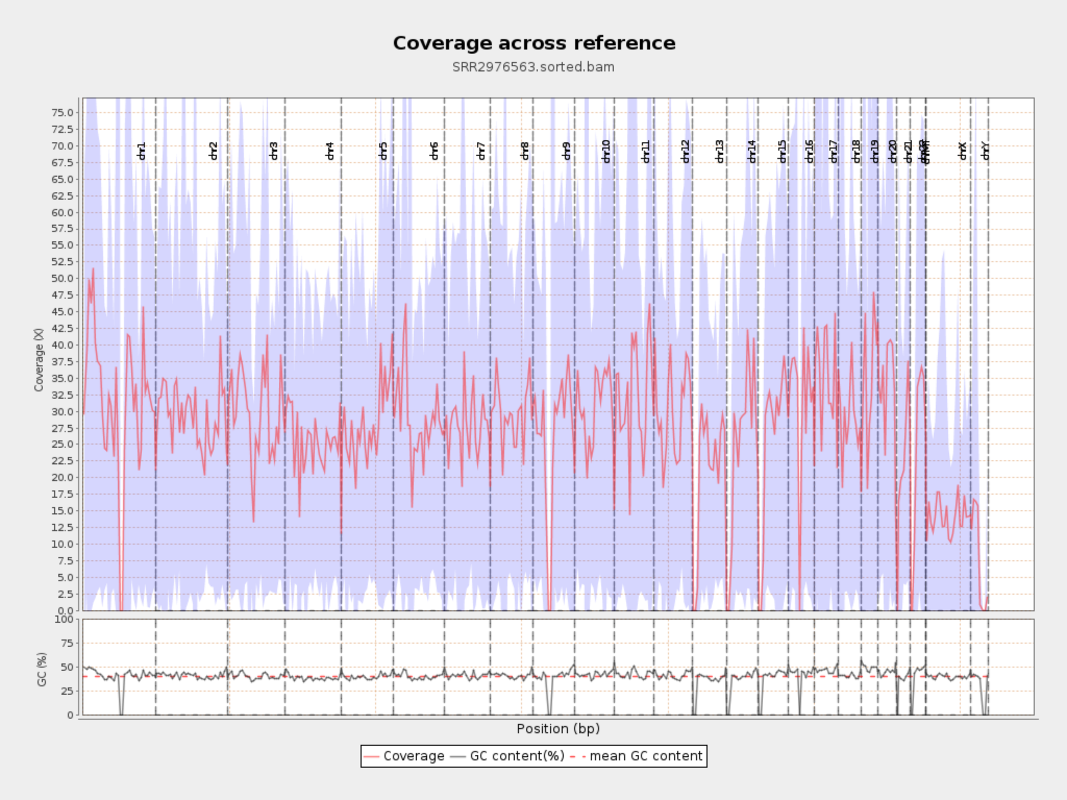
2.7. Chromosome stats

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

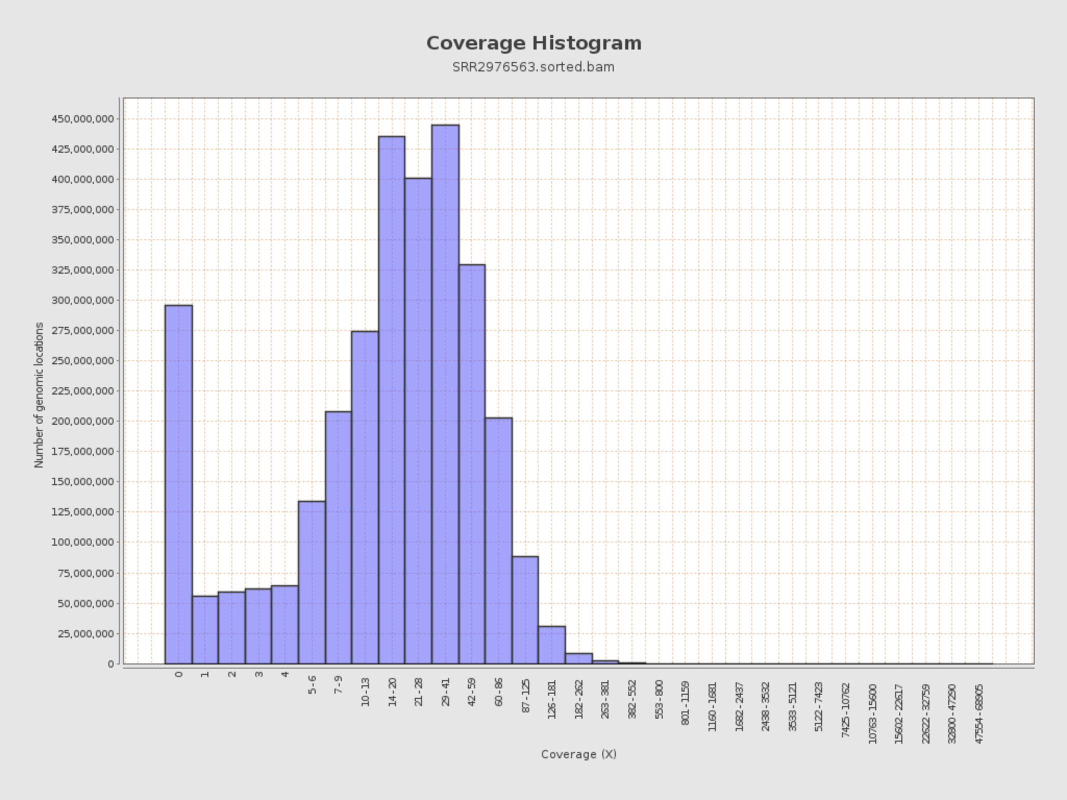
		bases	coverage	deviation
chr1	249250621	7875813248	31.598	77.4667
chr2	243199373	7147815522	29.3908	35.6799
chr3	198022430	5888793988	29.738	28.8845
chr4	191154276	4892727561	25.5957	25.1426
chr5	180915260	5119443075	28.2975	28.2655
chr6	171115067	4947415261	28.9128	37.7131
chr7	159138663	4437770741	27.8862	30.0819
chr8	146364022	4352352704	29.7365	32.4909
chr9	141213431	3715667689	26.3124	87.0527
chr10	135534747	4209657033	31.0596	71.8758
chr11	135006516	4311974255	31.939	42.9645
chr12	133851895	4072800427	30.4277	30.9587
chr13	115169878	2422451339	21.0337	23.1057
chr14	107349540	2747493612	25.5939	29.8099
chr15	102531392	2605402463	25.4108	30.374
chr16	90354753	2832924452	31.3534	35.2459
chr17	81195210	2891594099	35.6129	88.0228
chr18	78077248	2253519617	28.8627	76.4056
chr19	59128983	2041895493	34.5329	65.5611
chr20	63025520	2144517961	34.0262	35.5359
chr21	48129895	1085756696	22.5589	32.1195
chr22	51304566	1217108010	23.7232	33.19
chrMT	16571	310046	18.7102	9.9551
chrX	155270560	2189834069	14.1033	21.0006

chrY	59373566	464788338	7.8282	29.8947

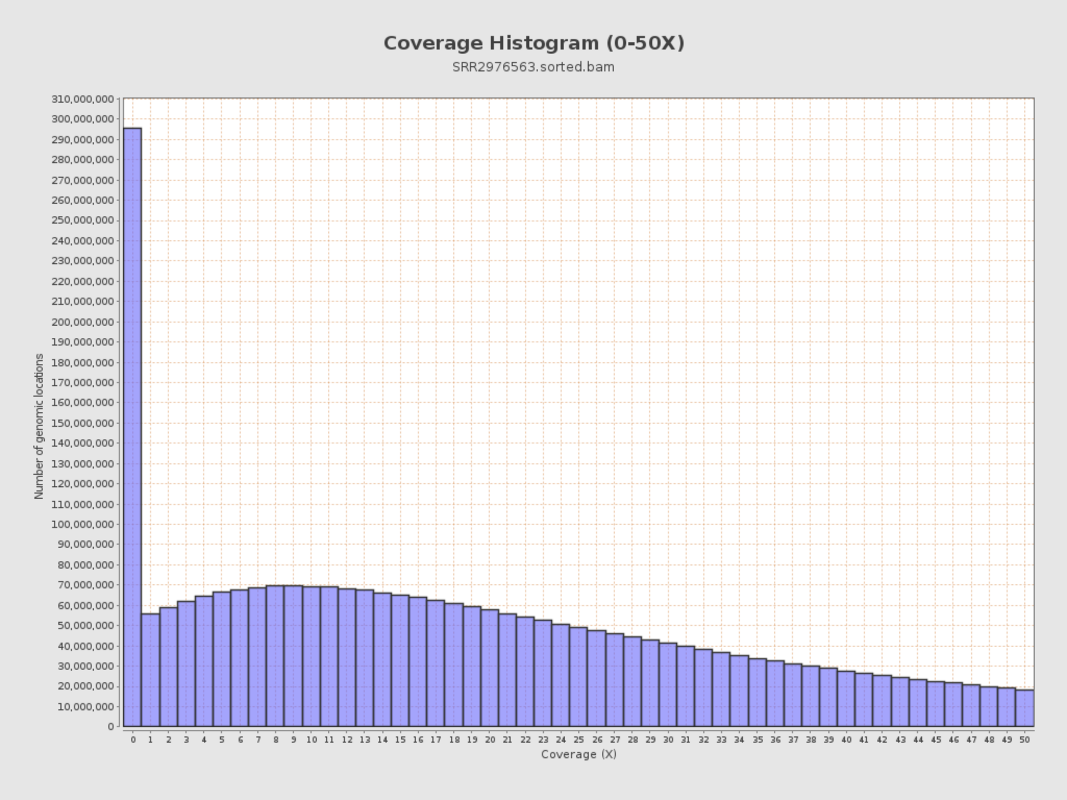
3. Results : Coverage across reference



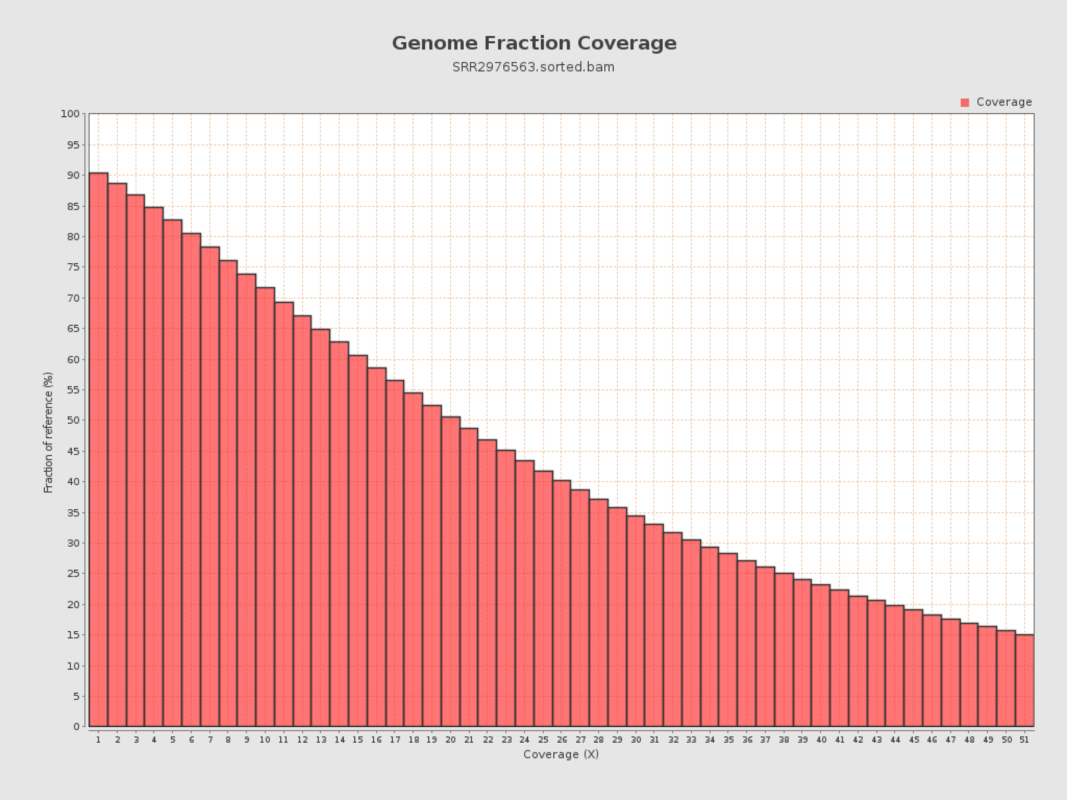
4. Results : Coverage Histogram



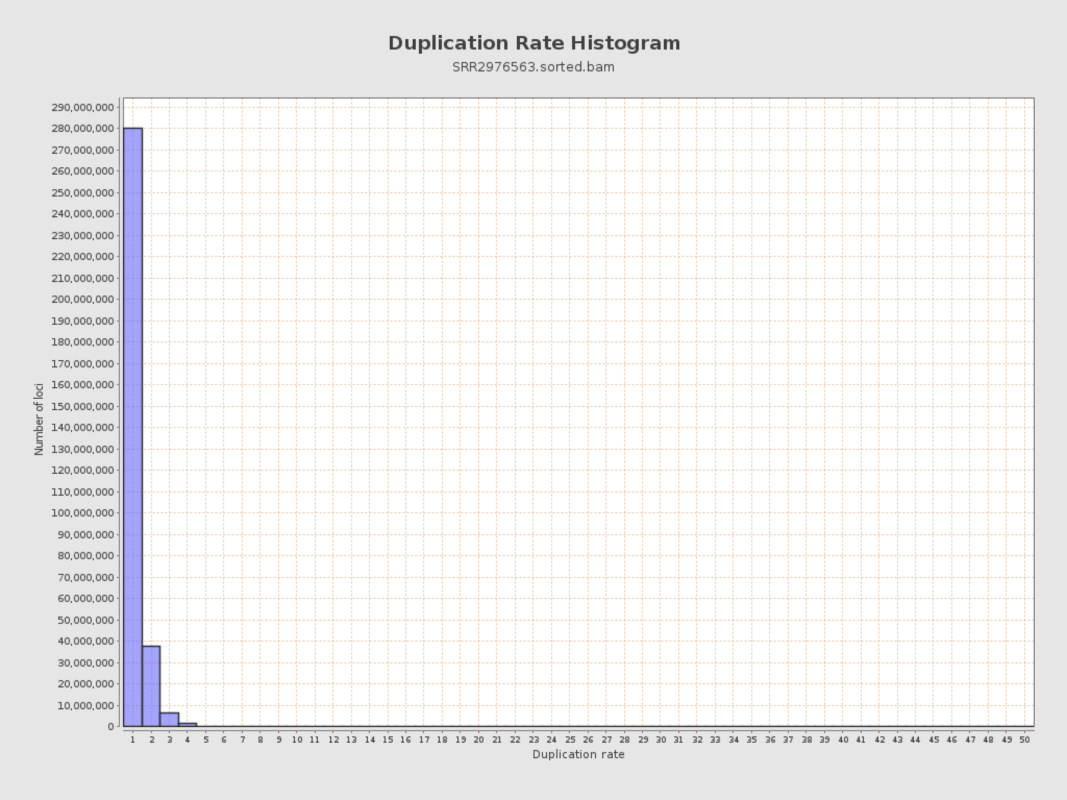
5. Results : Coverage Histogram (0-50X)



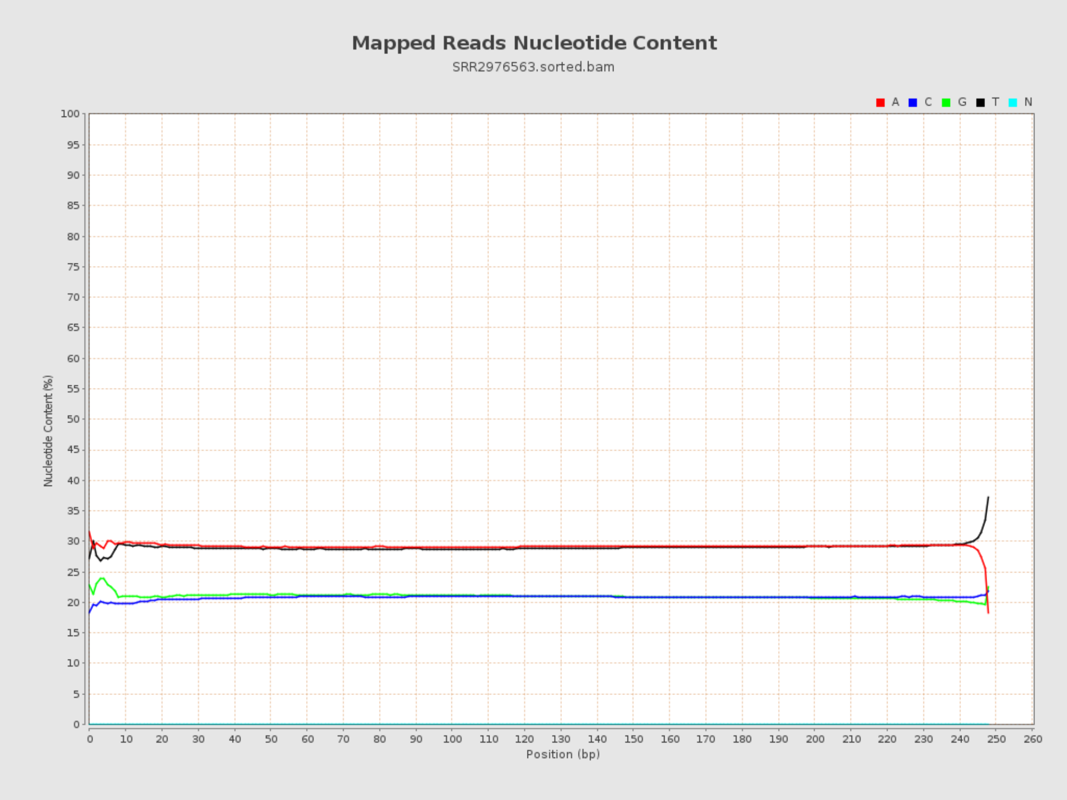
6. Results : Genome Fraction Coverage



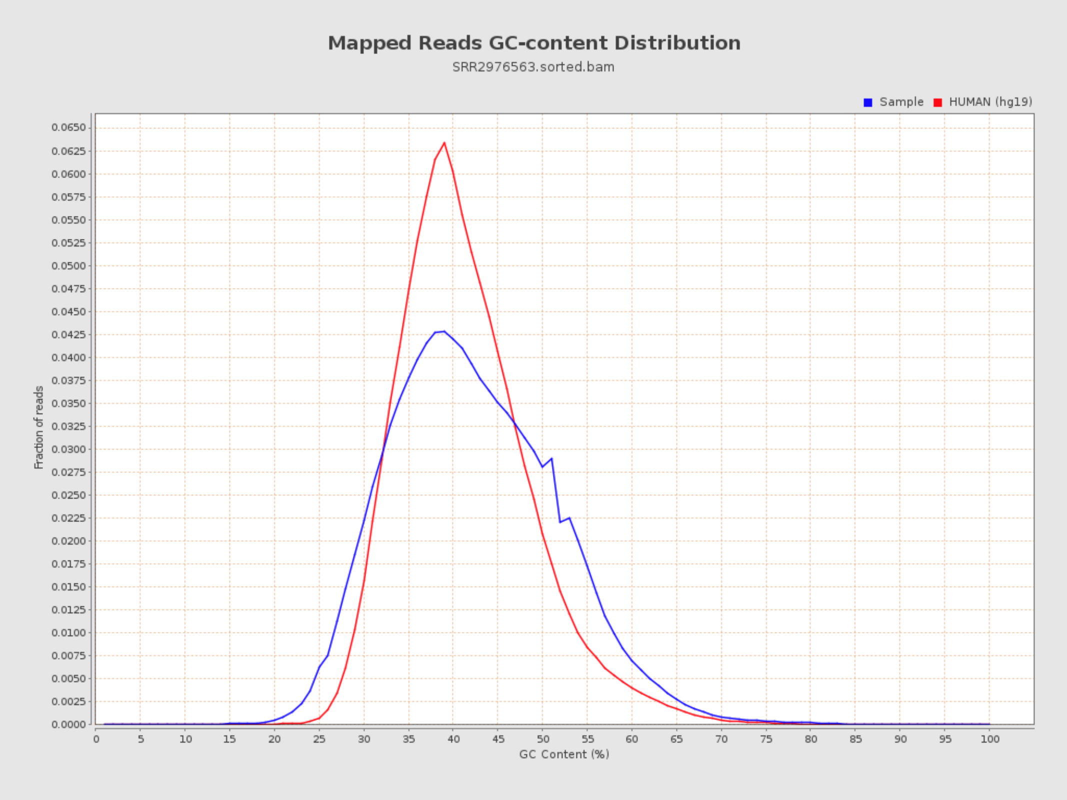
7. Results : Duplication Rate Histogram



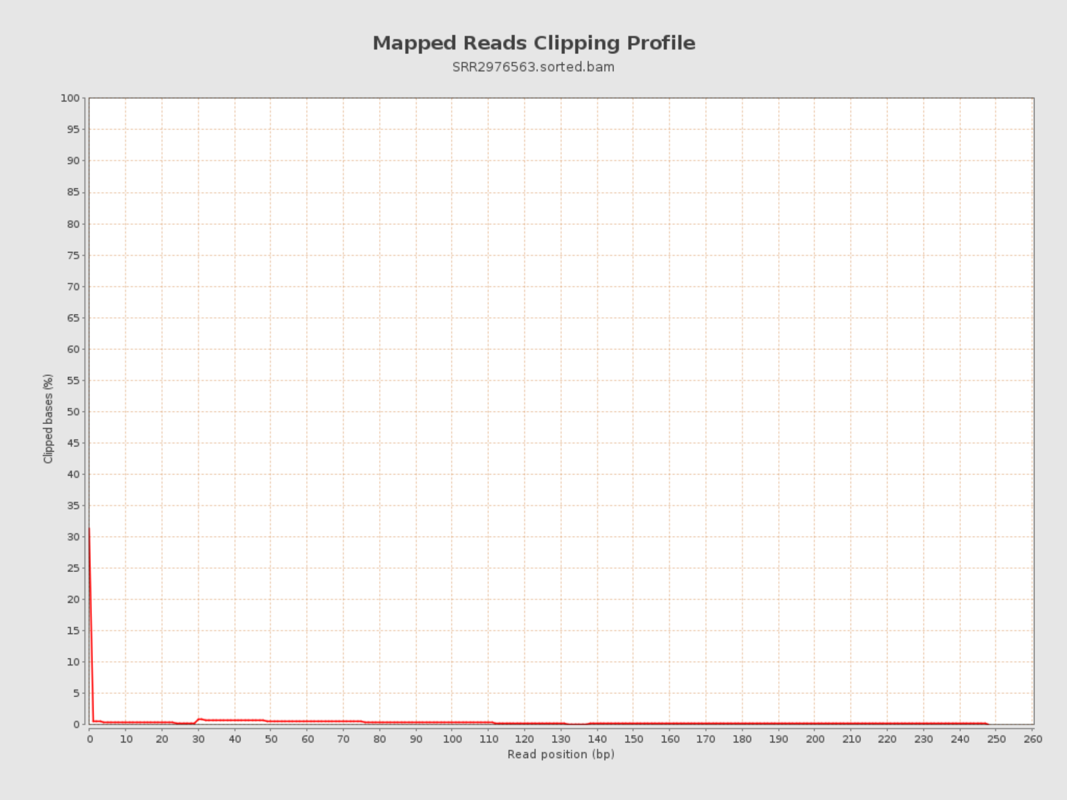
8. Results : Mapped Reads Nucleotide Content



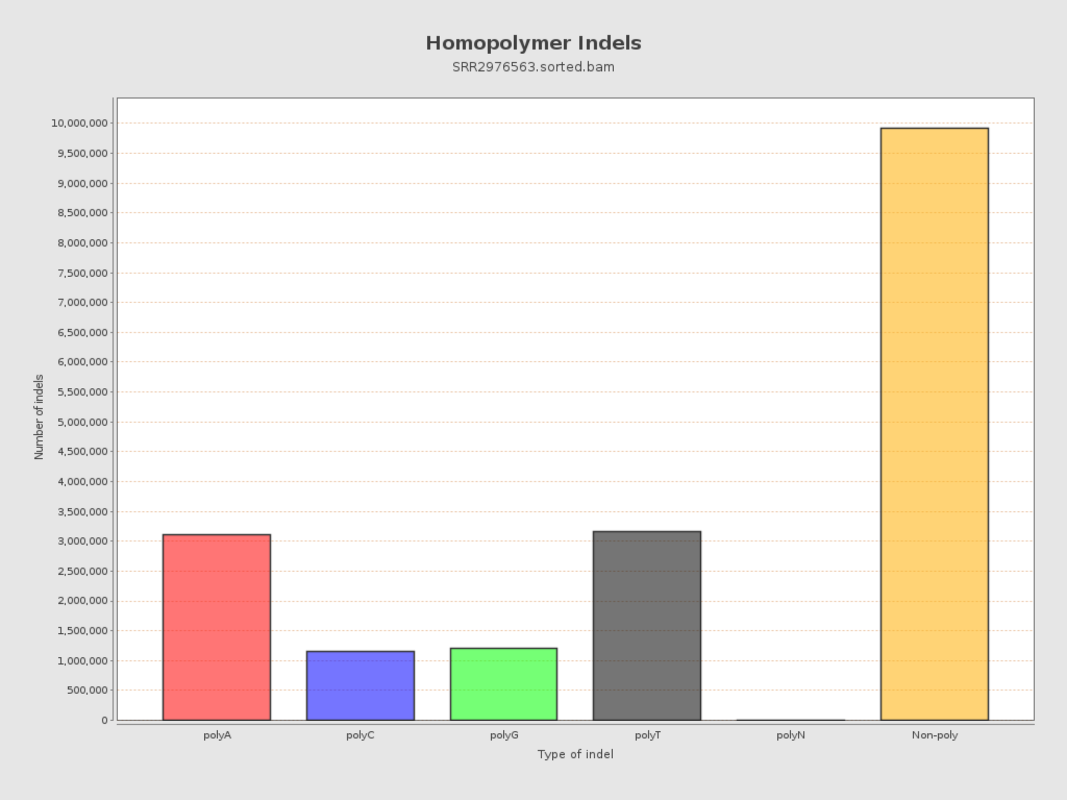
9. Results : Mapped Reads GC-content Distribution



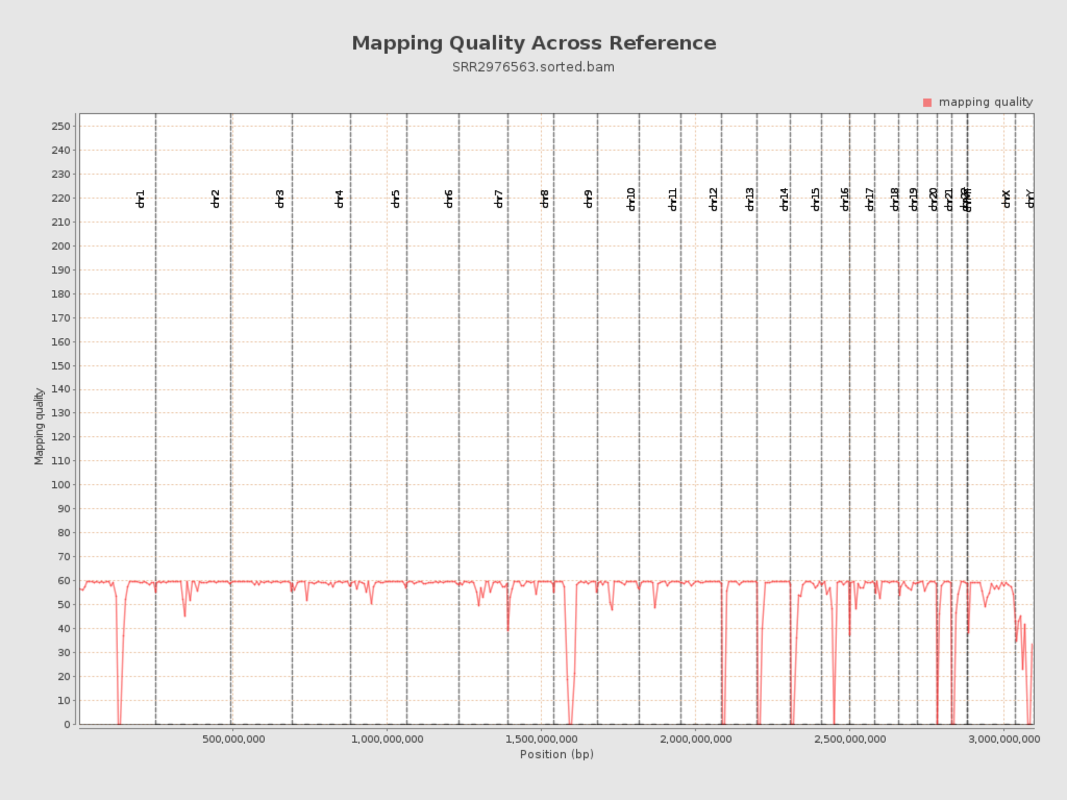
10. Results : Mapped Reads Clipping Profile



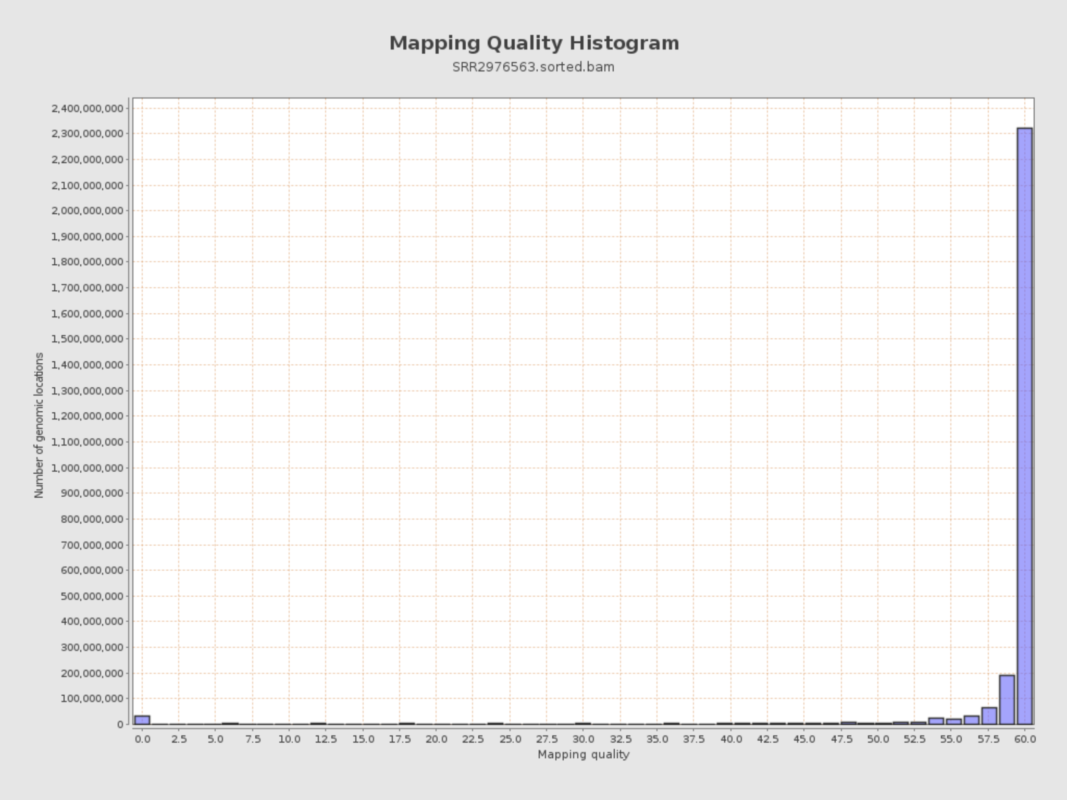
11. Results : Homopolymer Indels



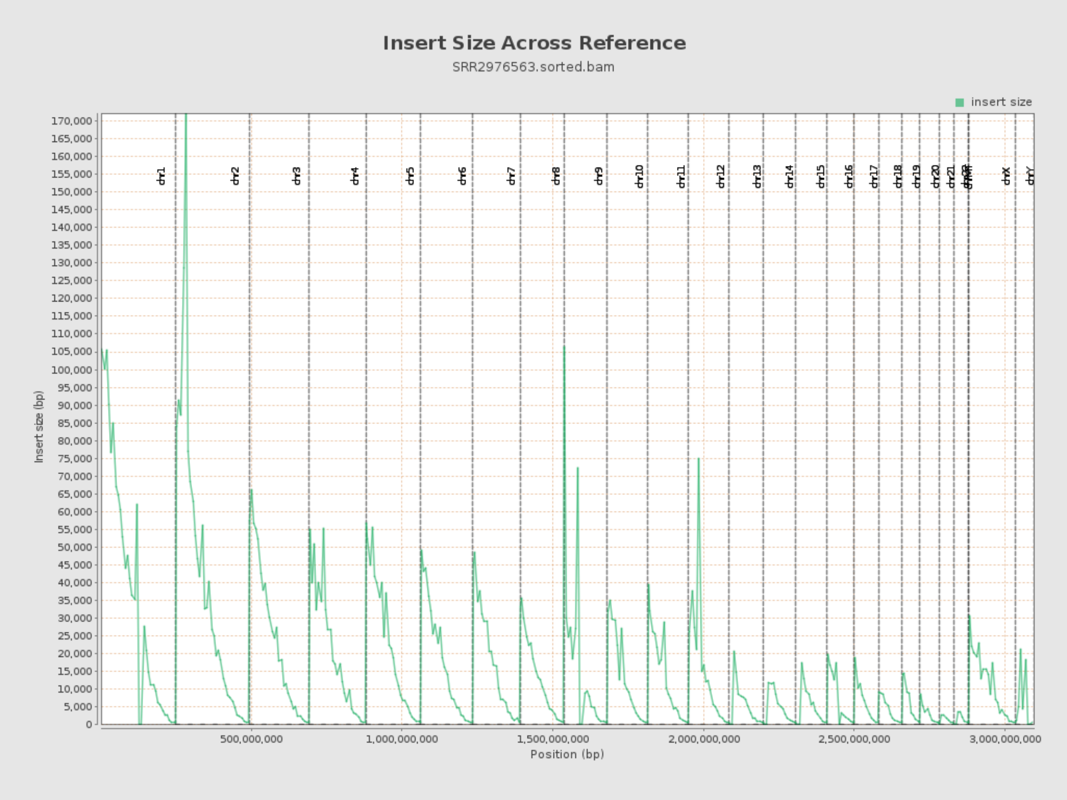
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram