Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/30 04:30:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976573.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_SRR2976573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976573_1.fastq.gz SRR2976573_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 30 04:30:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	289,372,162
Mapped reads	280,299,019 / 96.86%
Unmapped reads	9,073,143 / 3.14%
Mapped paired reads	280,299,019 / 96.86%
Mapped reads, first in pair	143,948,708 / 49.75%
Mapped reads, second in pair	136,350,311 / 47.12%
Mapped reads, both in pair	272,377,630 / 94.13%
Mapped reads, singletons	7,921,389 / 2.74%
Secondary alignments	0
Supplementary alignments	8,630,995 / 2.98%
Read min/max/mean length	20 / 249 / 213.06
Duplicated reads (estimated)	30,792,456 / 10.64%
Duplication rate	9.55%
Clipped reads	57,471,102 / 19.86%

2.2. ACGT Content

Number/percentage of A's	16,548,524,025 / 28.85%
Number/percentage of C's	12,098,563,434 / 21.09%
Number/percentage of T's	16,404,770,228 / 28.6%
Number/percentage of G's	12,240,664,326 / 21.34%
Number/percentage of N's	68,483,343 / 0.12%

GC Percentage	42.43%

2.3. Coverage

Mean	18.5356
Standard Deviation	36.9773

2.4. Mapping Quality

Mean Mapping Quality	55.19

2.5. Insert size

Mean	77,928.76
Standard Deviation	2,706,900.43
P25/Median/P75	497 / 557 / 635

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	577,245,187
Insertions	5,707,998
Mapped reads with at least one insertion	1.93%
Deletions	7,018,063
Mapped reads with at least one deletion	2.38%
Homopolymer indels	45.64%

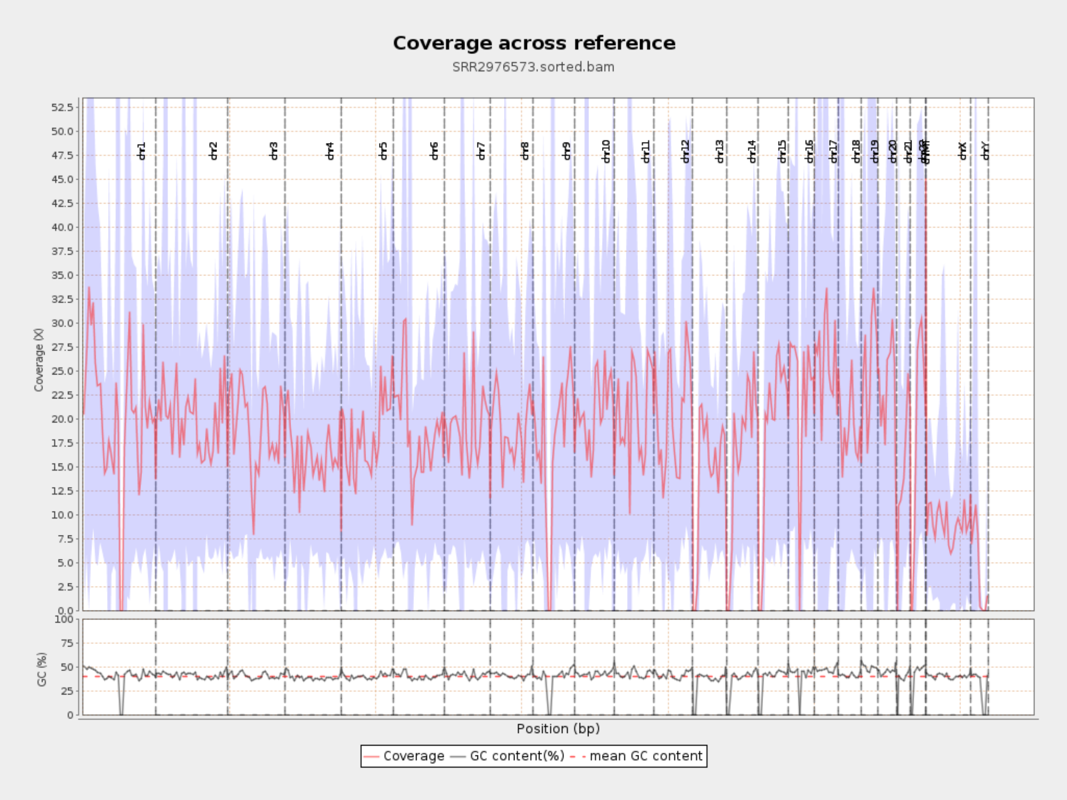
2.7. Chromosome stats

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

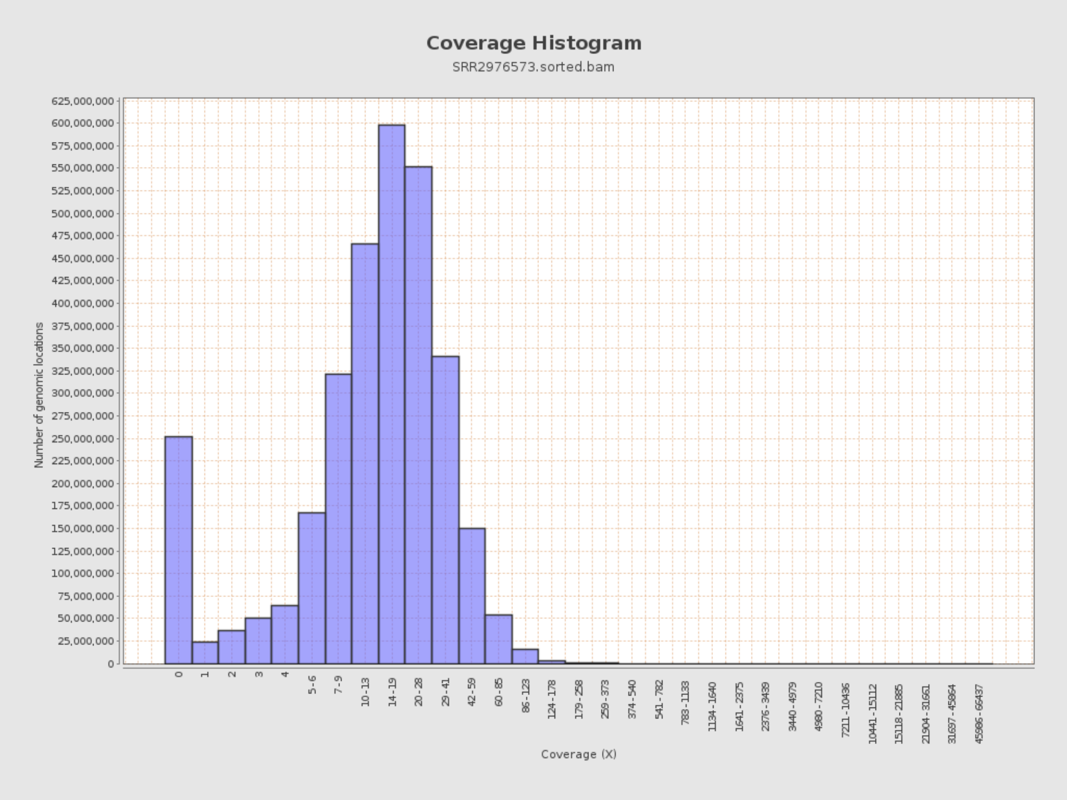
		bases	**coverage**	**deviation**
chr1	249250621	5059716420	20.2997	69.7701
chr2	243199373	4845635383	19.9245	35.6947
chr3	198022430	3756194442	18.9685	16.0001
chr4	191154276	3116384583	16.303	13.5045
chr5	180915260	3333948378	18.4282	15.0087
chr6	171115067	3195916365	18.677	30.2249
chr7	159138663	3075391887	19.3252	21.541
chr8	146364022	2776096908	18.9671	17.8437
chr9	141213431	2493405492	17.657	69.2016
chr10	135534747	2832372982	20.8978	52.882
chr11	135006516	2770007324	20.5176	29.0445
chr12	133851895	2769995038	20.6945	17.9754
chr13	115169878	1662953189	14.4391	12.9068
chr14	107349540	1786056500	16.6378	16.1357
chr15	102531392	1894487157	18.4771	17.6627
chr16	90354753	2024971019	22.4113	22.2187
chr17	81195210	2137967738	26.3312	59.0291
chr18	78077248	1475021265	18.8918	67.5667
chr19	59128983	1515476084	25.63	51.8786
chr20	63025520	1489813100	23.6383	20.2575
chr21	48129895	723379711	15.0297	20.8822
chr22	51304566	962535891	18.7612	21.657
chrMT	16571	747221	45.0921	14.0656
chrX	155270560	1413037957	9.1005	12.3865

chrY	59373566	268997128	4.5306	23.7554

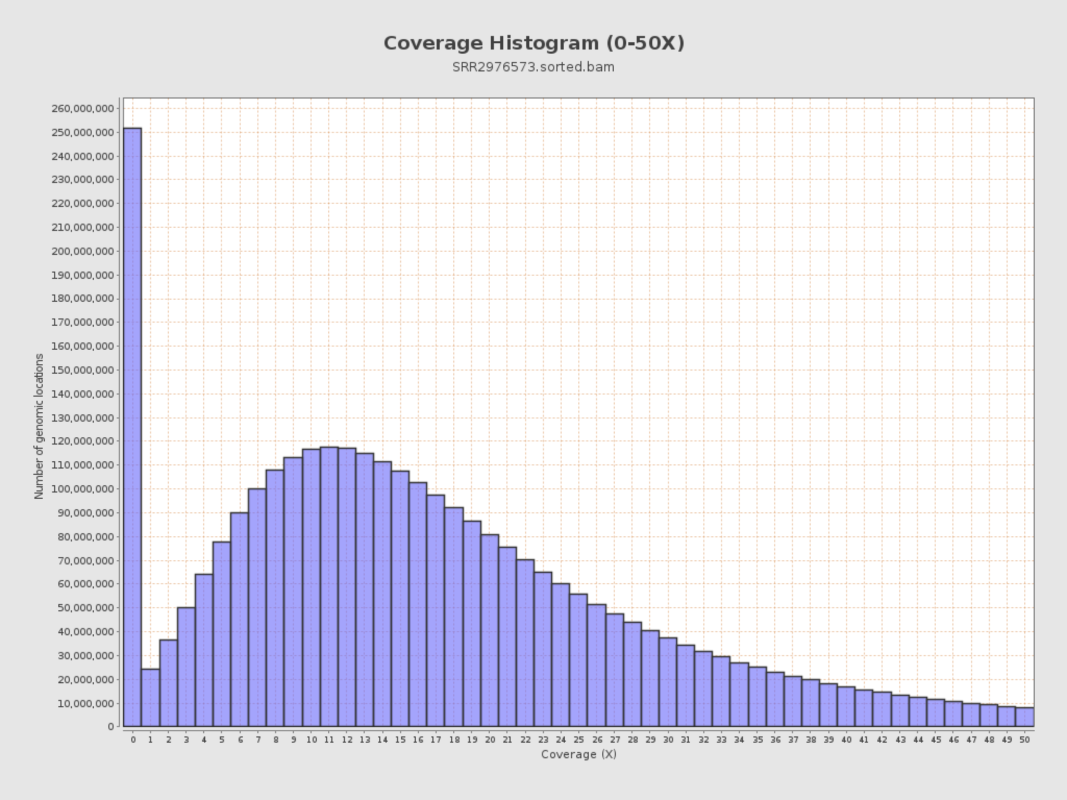
3. Results : Coverage across reference



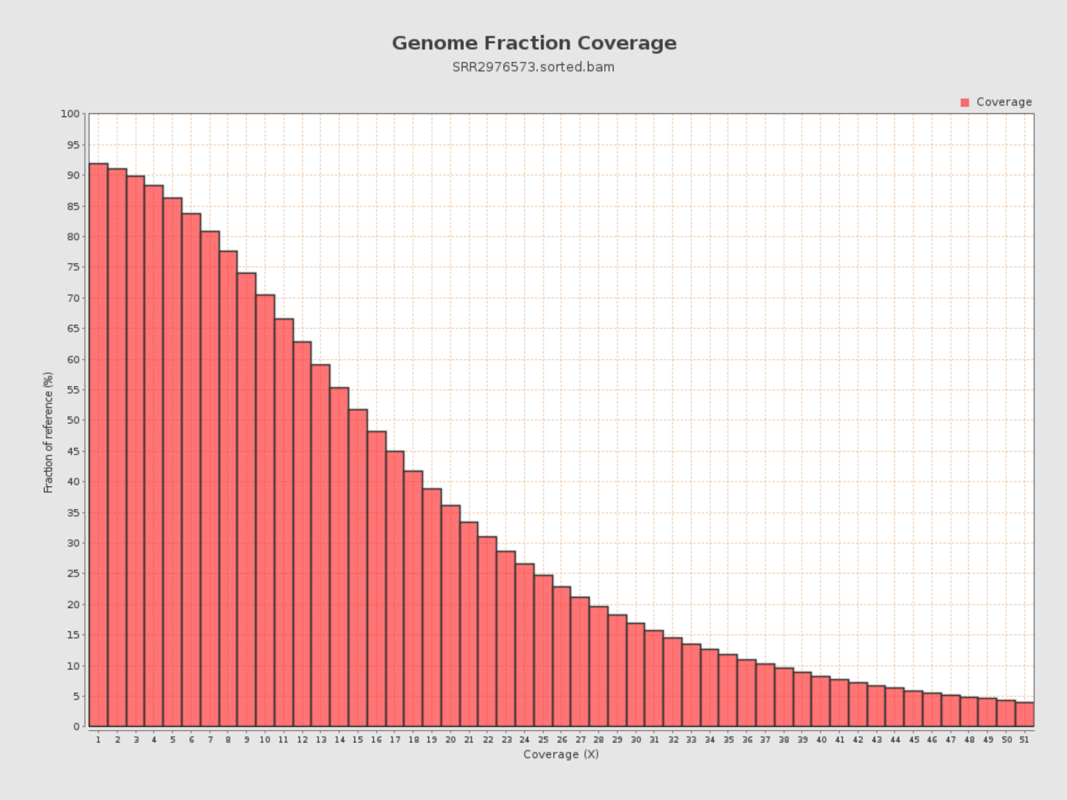
4. Results : Coverage Histogram



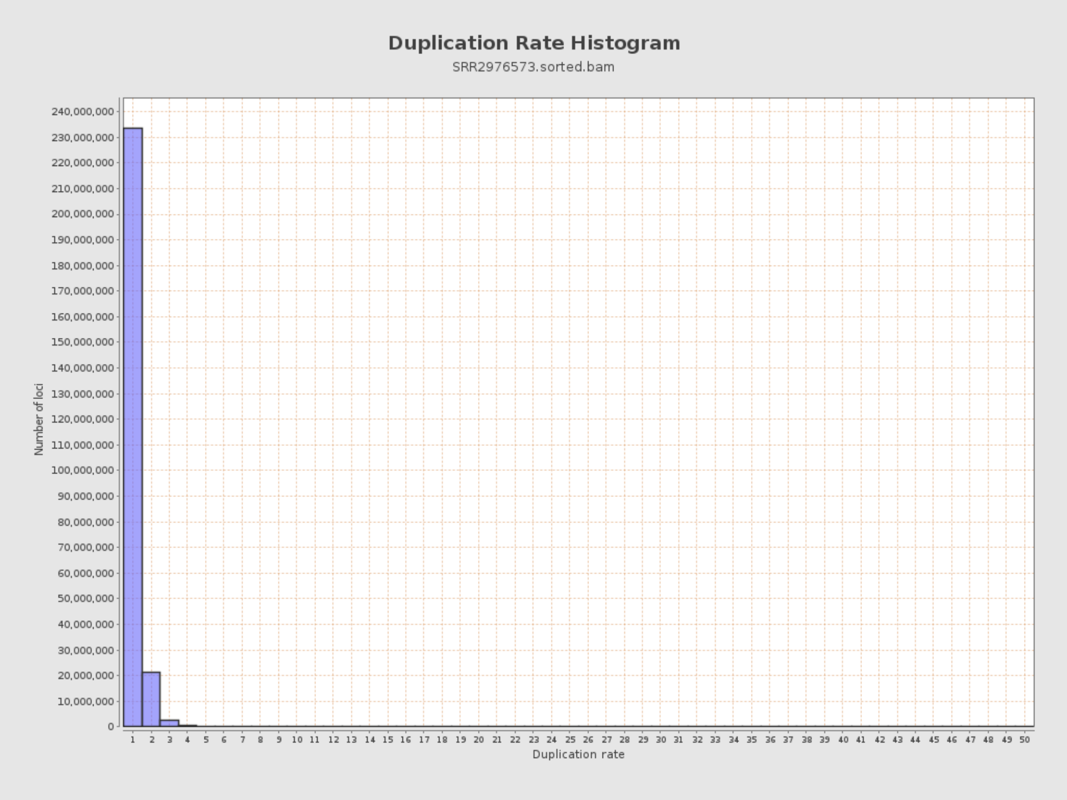
5. Results : Coverage Histogram (0-50X)



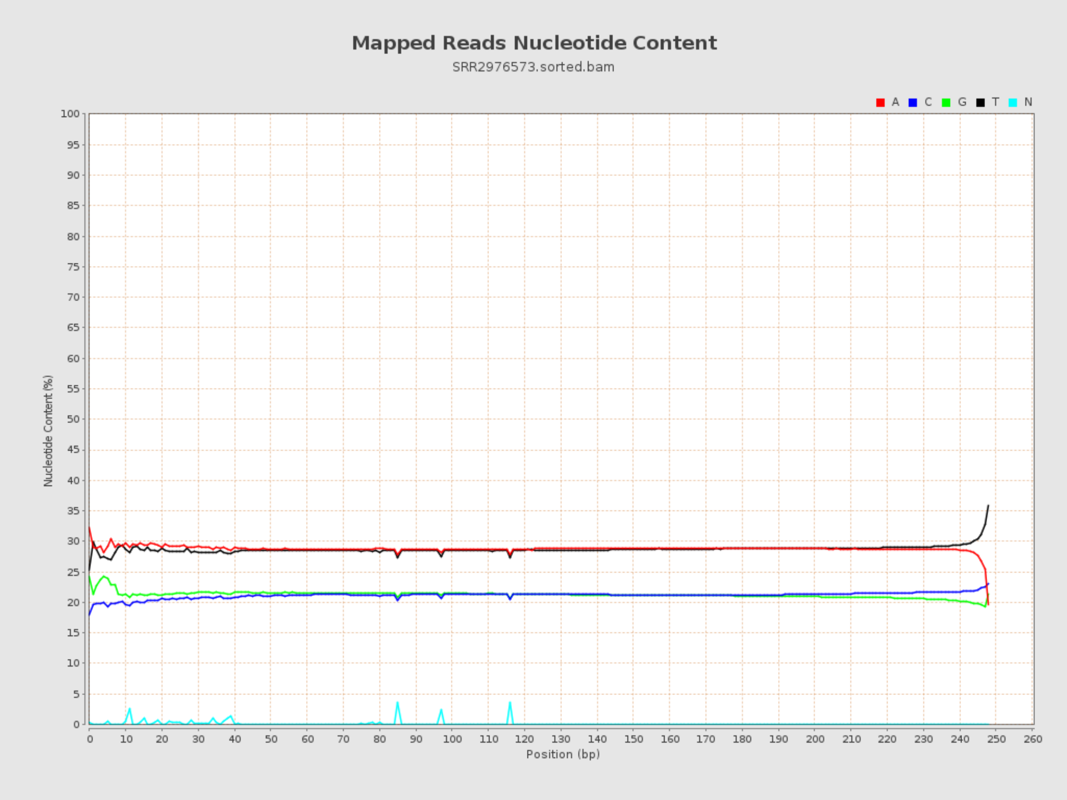
6. Results : Genome Fraction Coverage



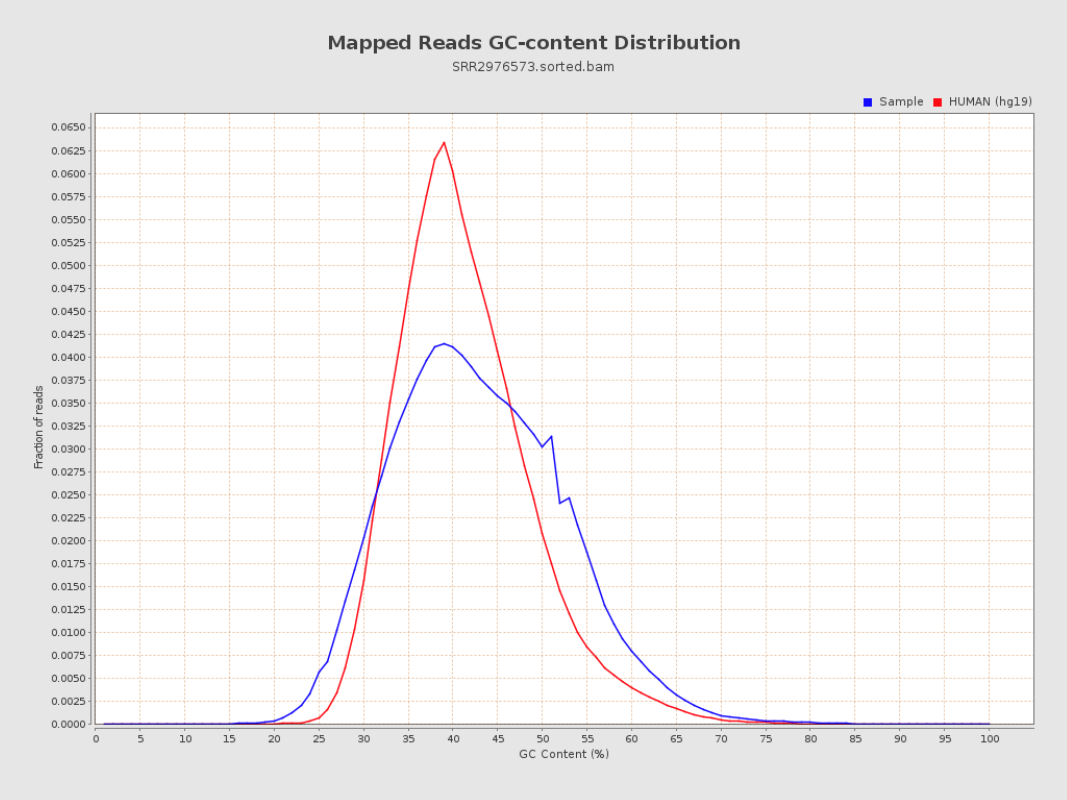
7. Results : Duplication Rate Histogram



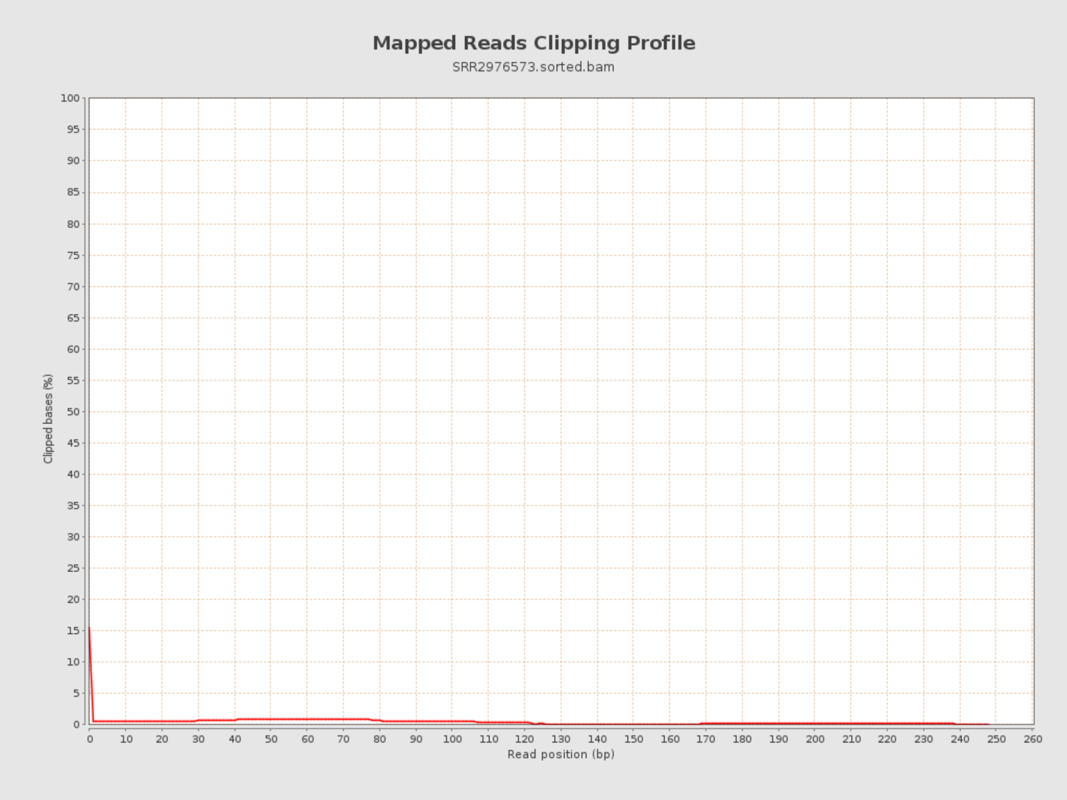
8. Results : Mapped Reads Nucleotide Content



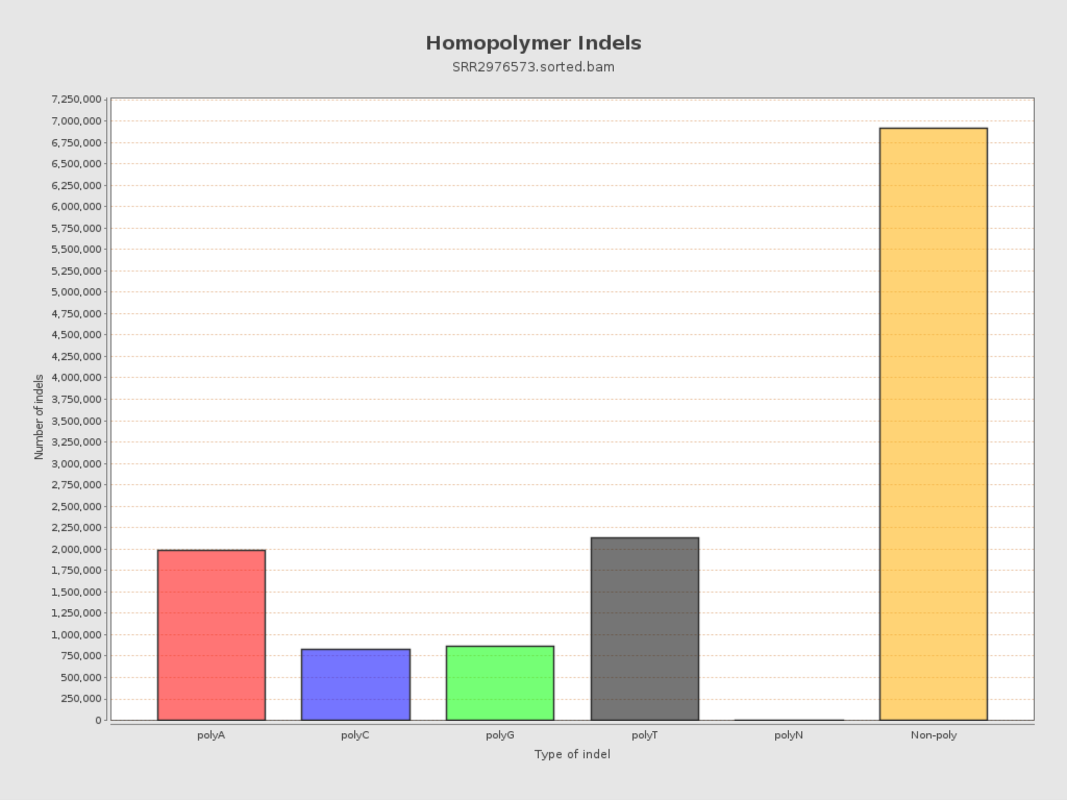
9. Results : Mapped Reads GC-content Distribution



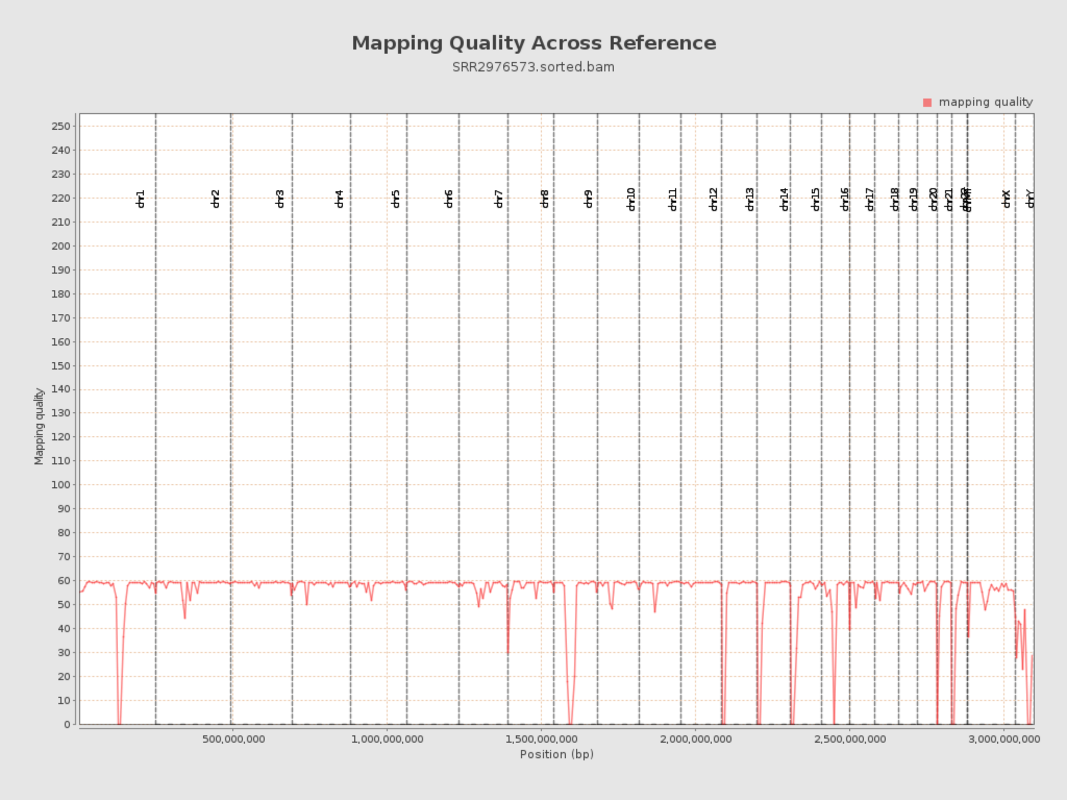
10. Results : Mapped Reads Clipping Profile



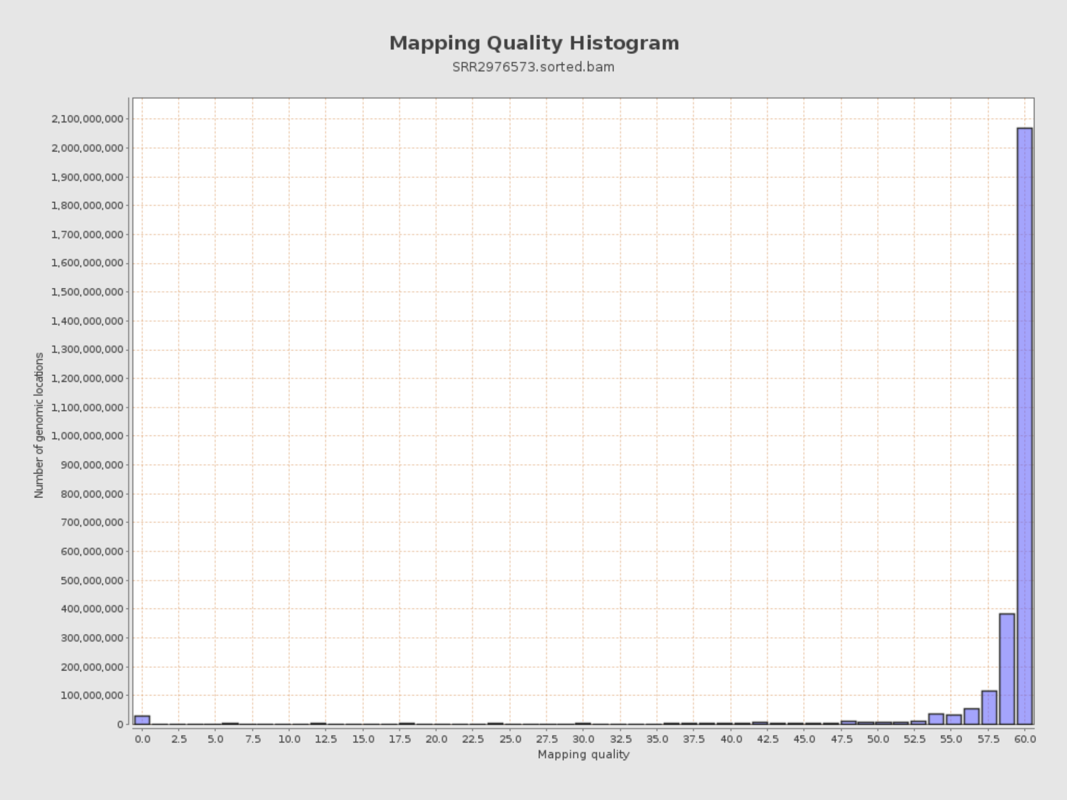
11. Results : Homopolymer Indels



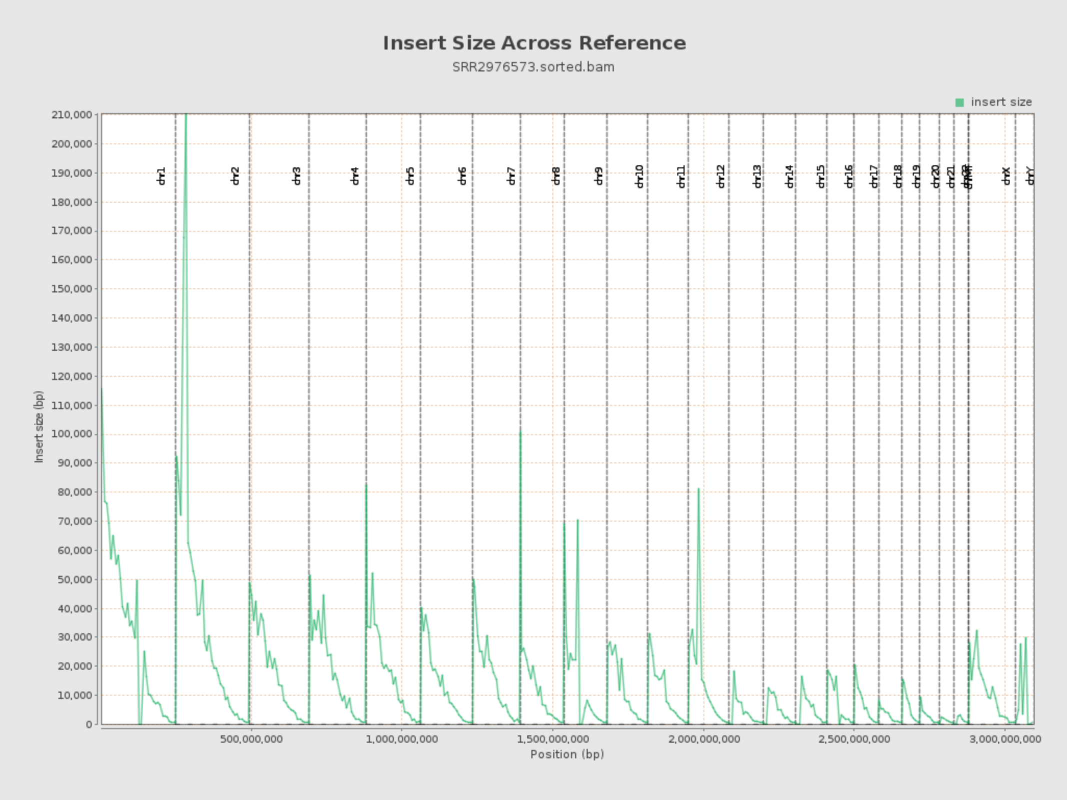
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram