Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/29 21:25:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976572.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_SRR2976572 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976572_1.fastq.gz SRR2976572_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 29 21:25:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976572.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	262,196,872
Mapped reads	260,130,677 / 99.21%
Unmapped reads	2,066,195 / 0.79%
Mapped paired reads	260,130,677 / 99.21%
Mapped reads, first in pair	130,370,106 / 49.72%
Mapped reads, second in pair	129,760,571 / 49.49%
Mapped reads, both in pair	259,121,098 / 98.83%
Mapped reads, singletons	1,009,579 / 0.39%
Secondary alignments	0
Supplementary alignments	8,788,071 / 3.35%
Read min/max/mean length	20 / 249 / 222.75
Duplicated reads (estimated)	27,488,008 / 10.48%
Duplication rate	9.16%
Clipped reads	31,828,121 / 12.14%

2.2. ACGT Content

Number/percentage of A's	16,630,828,412 / 29.06%
Number/percentage of C's	11,967,542,296 / 20.91%
Number/percentage of T's	16,536,236,239 / 28.89%
Number/percentage of G's	12,092,480,453 / 21.13%
Number/percentage of N's	1,795,877 / 0%

GC Percentage	42.04%

2.3. Coverage

Mean	18.493
Standard Deviation	34.4353

2.4. Mapping Quality

Mean Mapping Quality	55.39

2.5. Insert size

Mean	81,260.63
Standard Deviation	2,755,531.33
P25/Median/P75	534 / 589 / 669

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	534,049,673
Insertions	5,722,786
Mapped reads with at least one insertion	2.09%
Deletions	7,057,790
Mapped reads with at least one deletion	2.58%
Homopolymer indels	45.55%

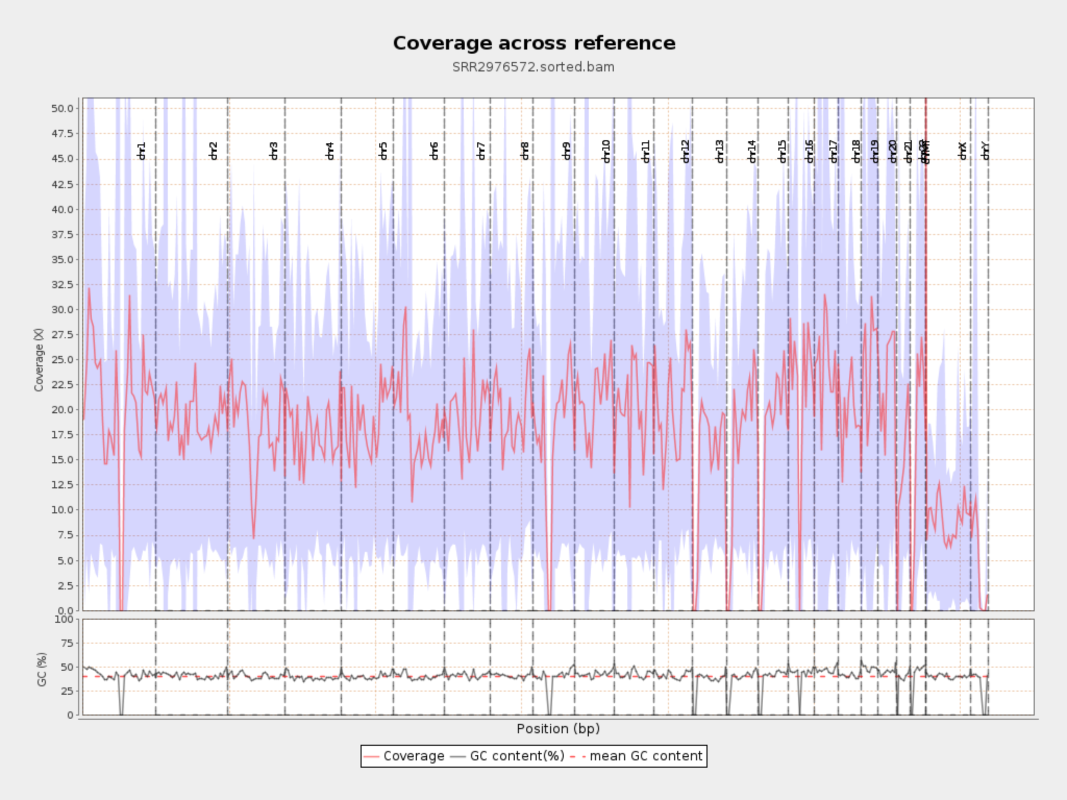
2.7. Chromosome stats

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

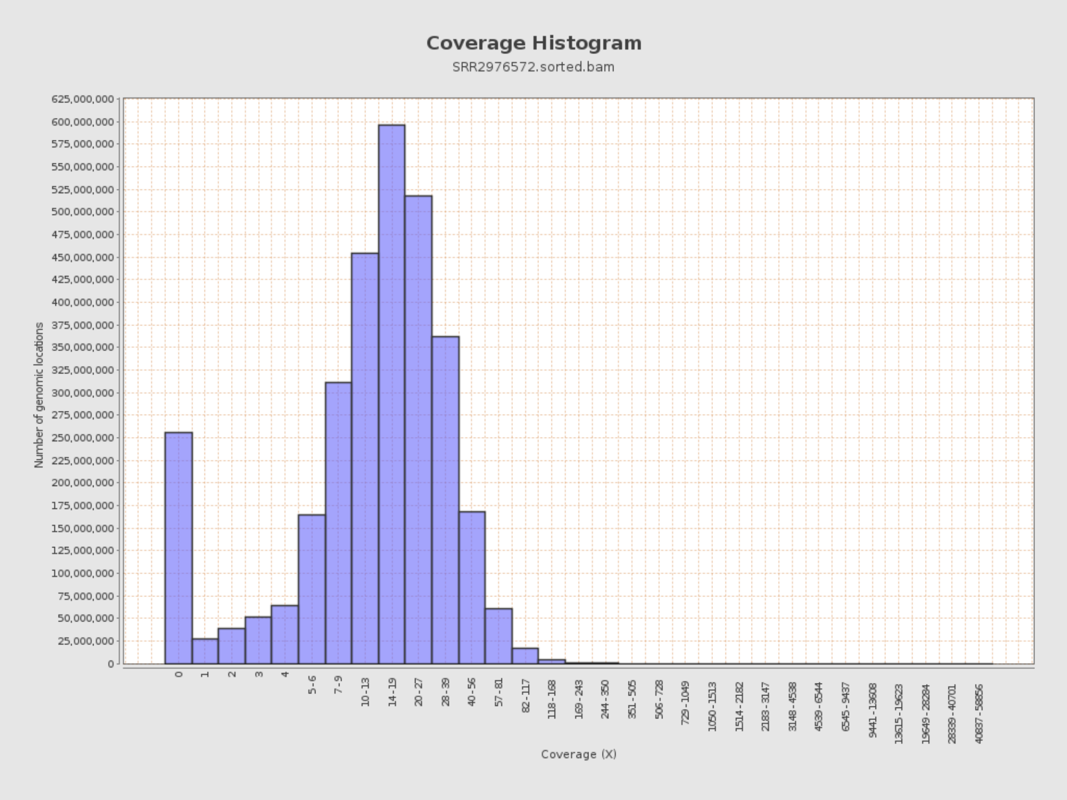
		bases	coverage	deviation
chr1	249250621	5118622496	20.536	62.1178
chr2	243199373	4637088709	19.067	35.4769
chr3	198022430	3650824297	18.4364	15.836
chr4	191154276	3408853949	17.833	14.4227
chr5	180915260	3464369933	19.1491	15.026
chr6	171115067	3173572763	18.5464	28.5006
chr7	159138663	3123430447	19.6271	18.9545
chr8	146364022	2889909804	19.7447	17.4303
chr9	141213431	2465754643	17.4612	65.3379
chr10	135534747	2879954432	21.2488	51.5723
chr11	135006516	2796996495	20.7175	26.731
chr12	133851895	2772858743	20.7159	17.6269
chr13	115169878	1710716838	14.8539	12.9128
chr14	107349540	1817962741	16.935	16.0566
chr15	102531392	1728610083	16.8593	16.3381
chr16	90354753	1966413558	21.7633	21.4425
chr17	81195210	1986322040	24.4635	60.4966
chr18	78077248	1536273390	19.6763	57.5351
chr19	59128983	1472367063	24.9009	43.6309
chr20	63025520	1447570307	22.968	20.0632
chr21	48129895	677577855	14.0781	20.1584
chr22	51304566	845879785	16.4874	19.5076
chrMT	16571	1043256	62.9567	19.7444
chrX	155270560	1402335606	9.0316	10.2306

chrY	59373566	273236112	4.602	20.7484

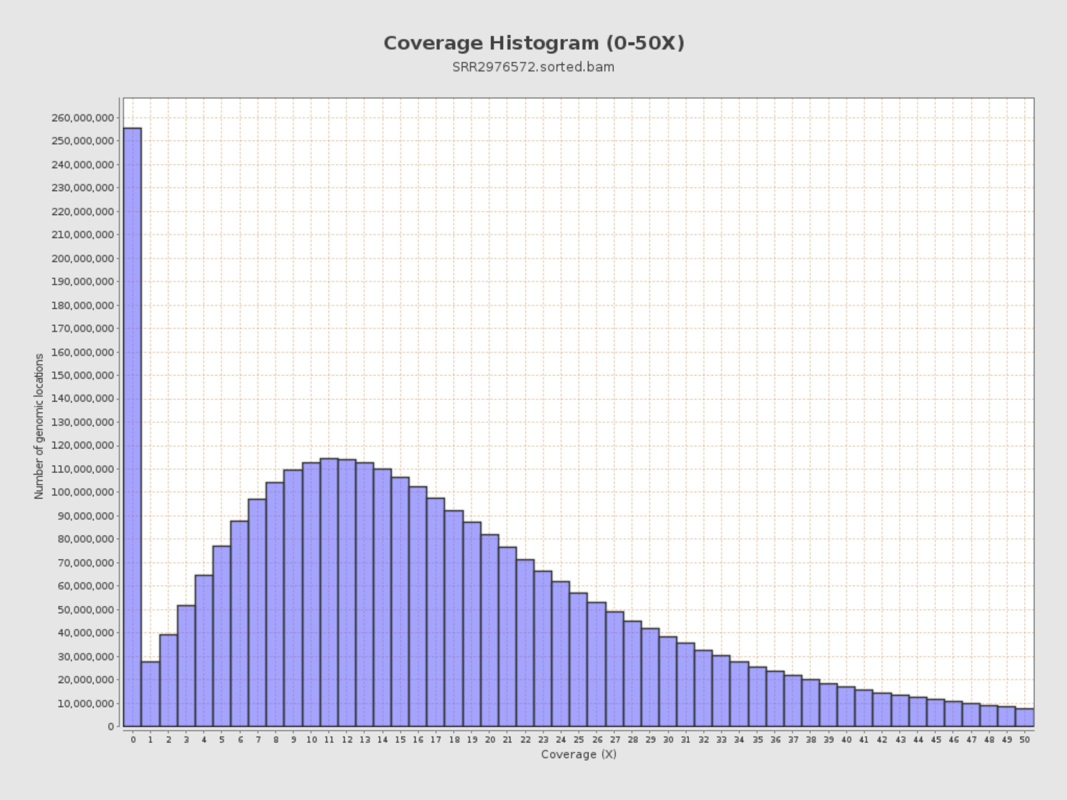
3. Results : Coverage across reference



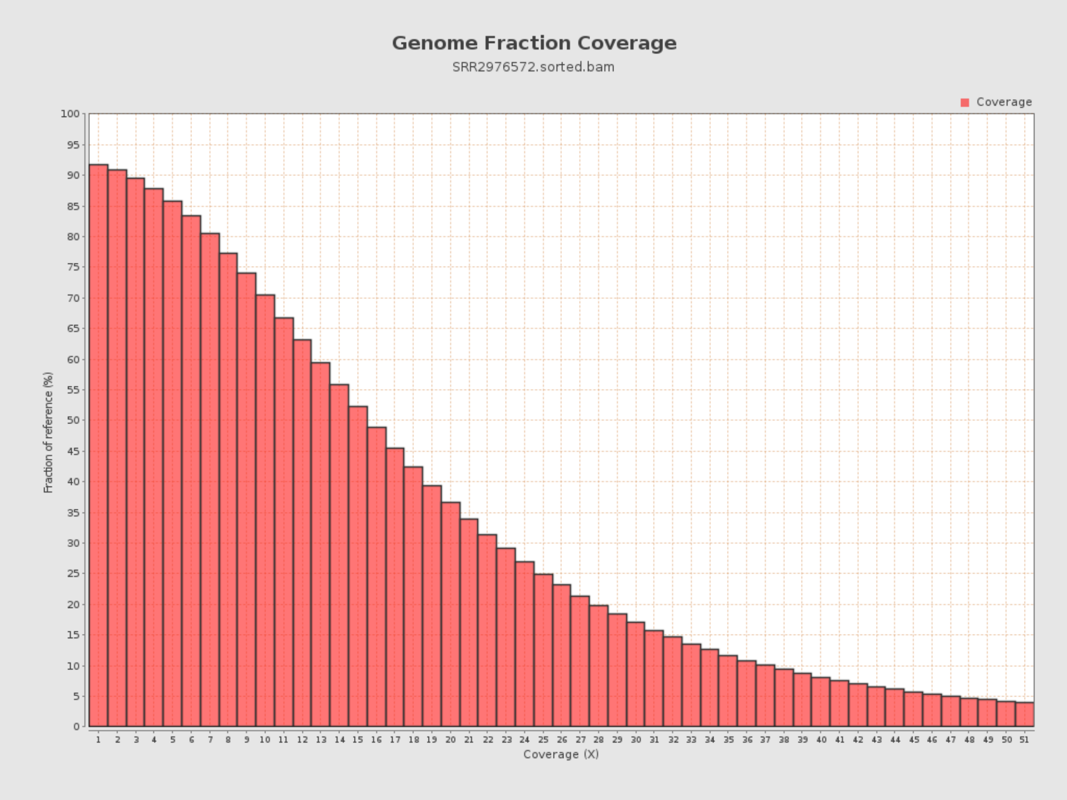
4. Results : Coverage Histogram



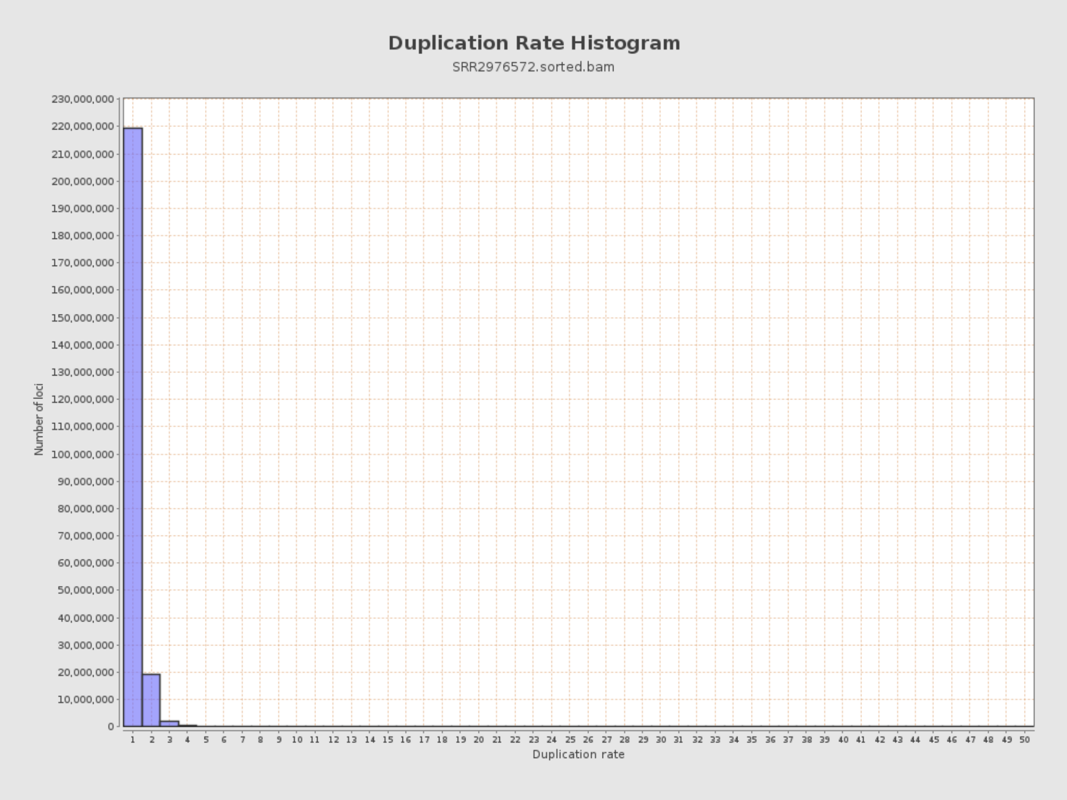
5. Results : Coverage Histogram (0-50X)



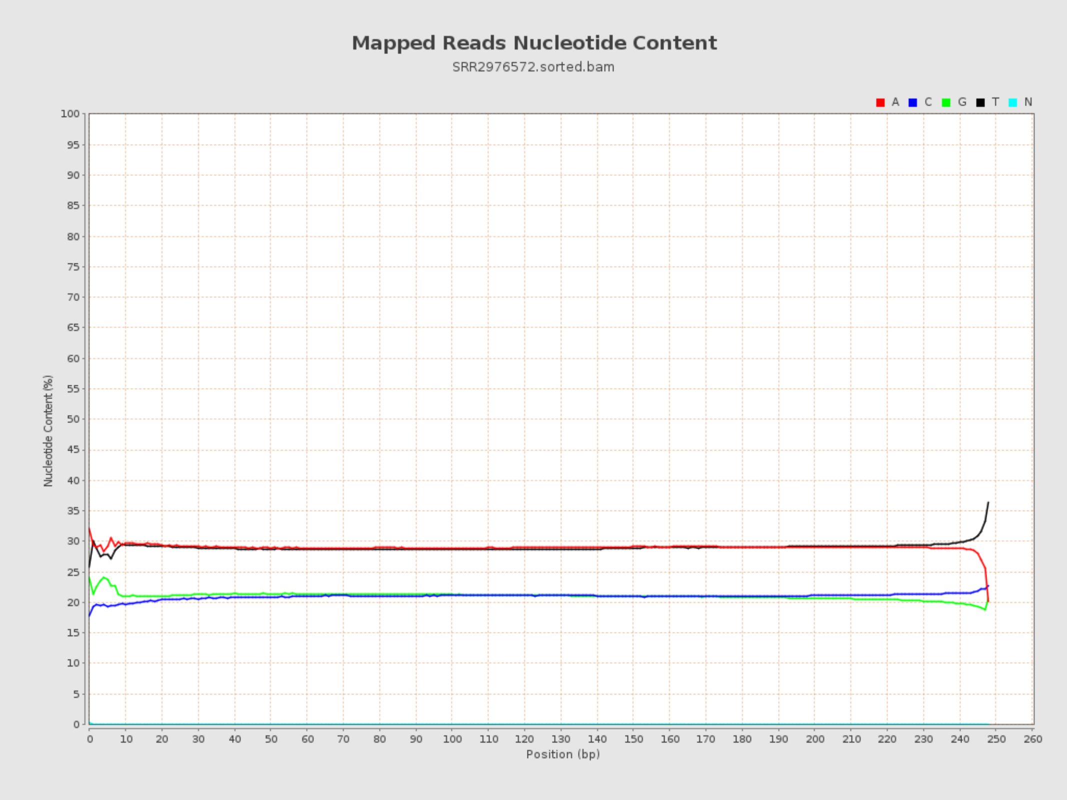
6. Results : Genome Fraction Coverage



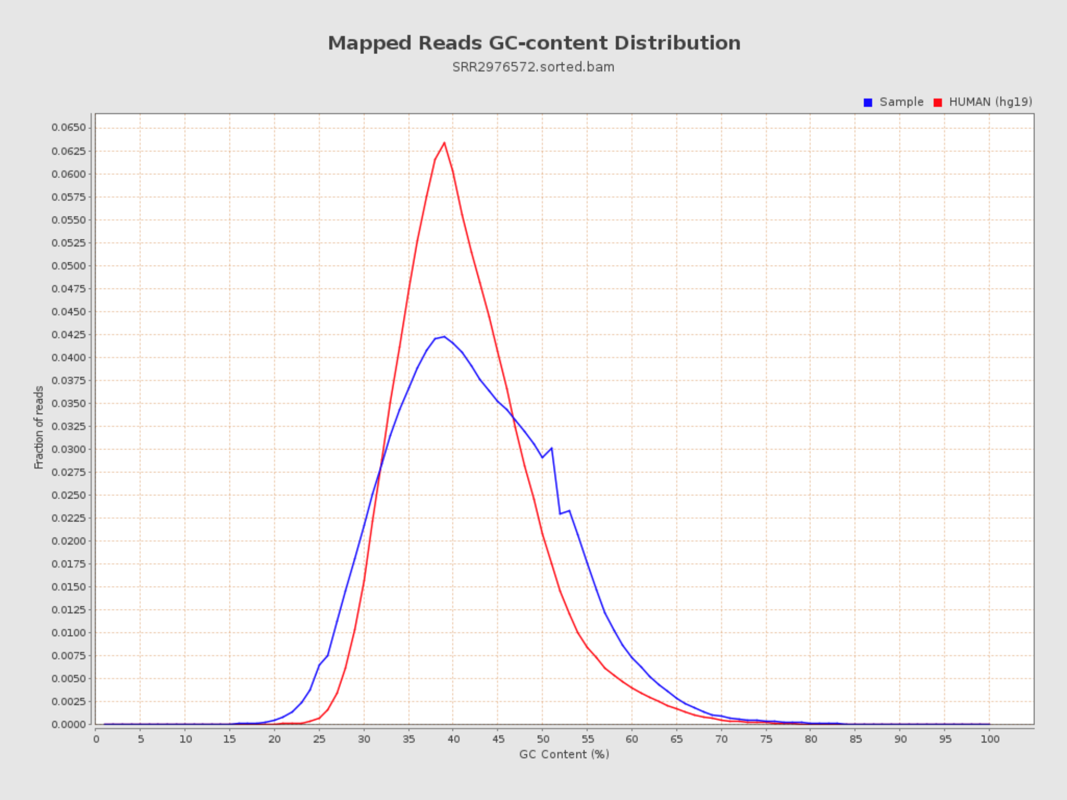
7. Results : Duplication Rate Histogram



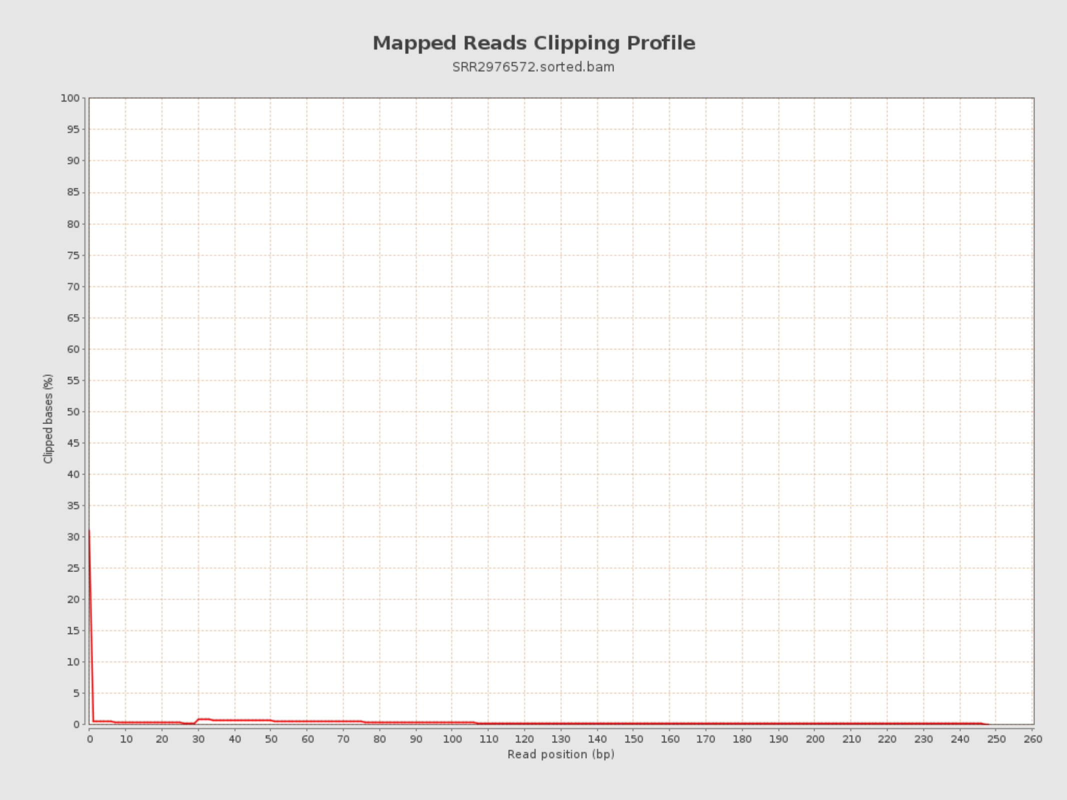
8. Results : Mapped Reads Nucleotide Content



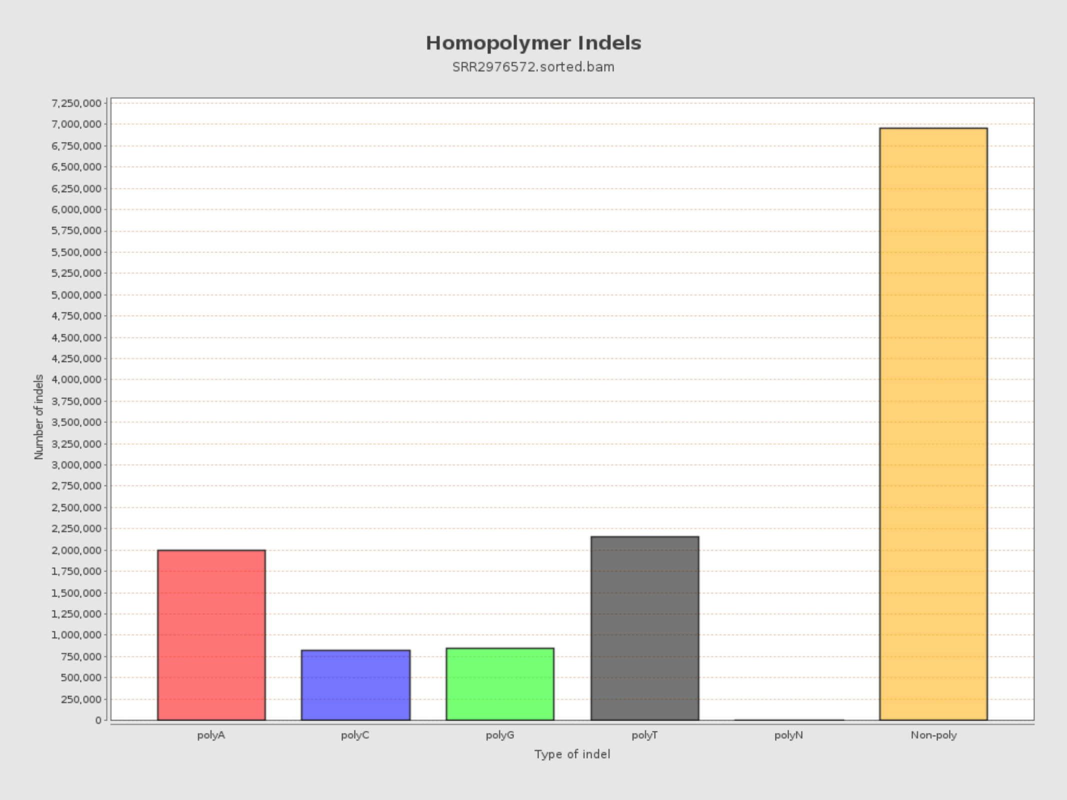
9. Results : Mapped Reads GC-content Distribution



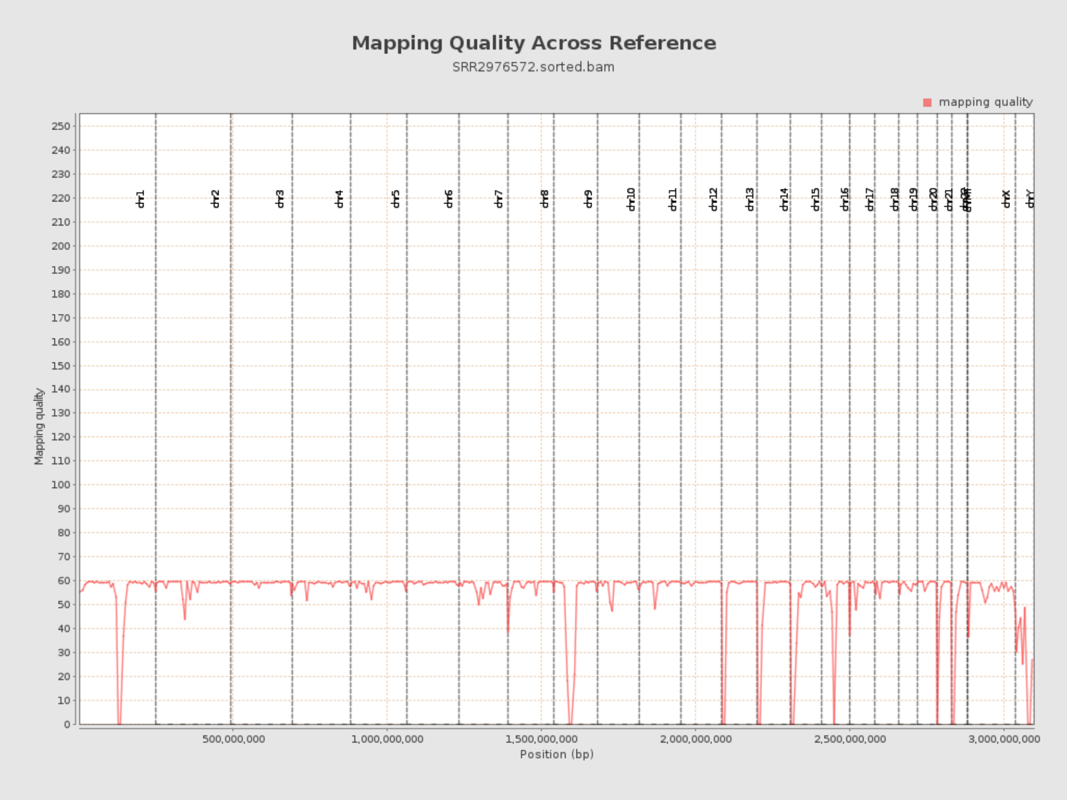
10. Results : Mapped Reads Clipping Profile



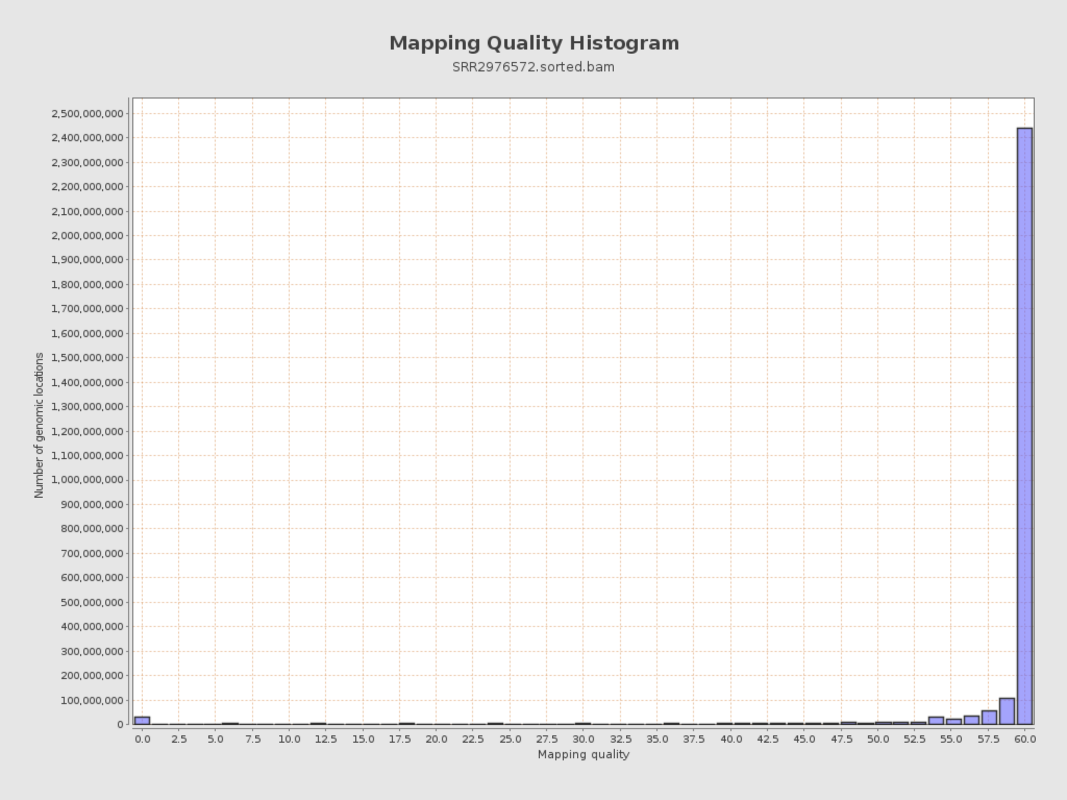
11. Results : Homopolymer Indels



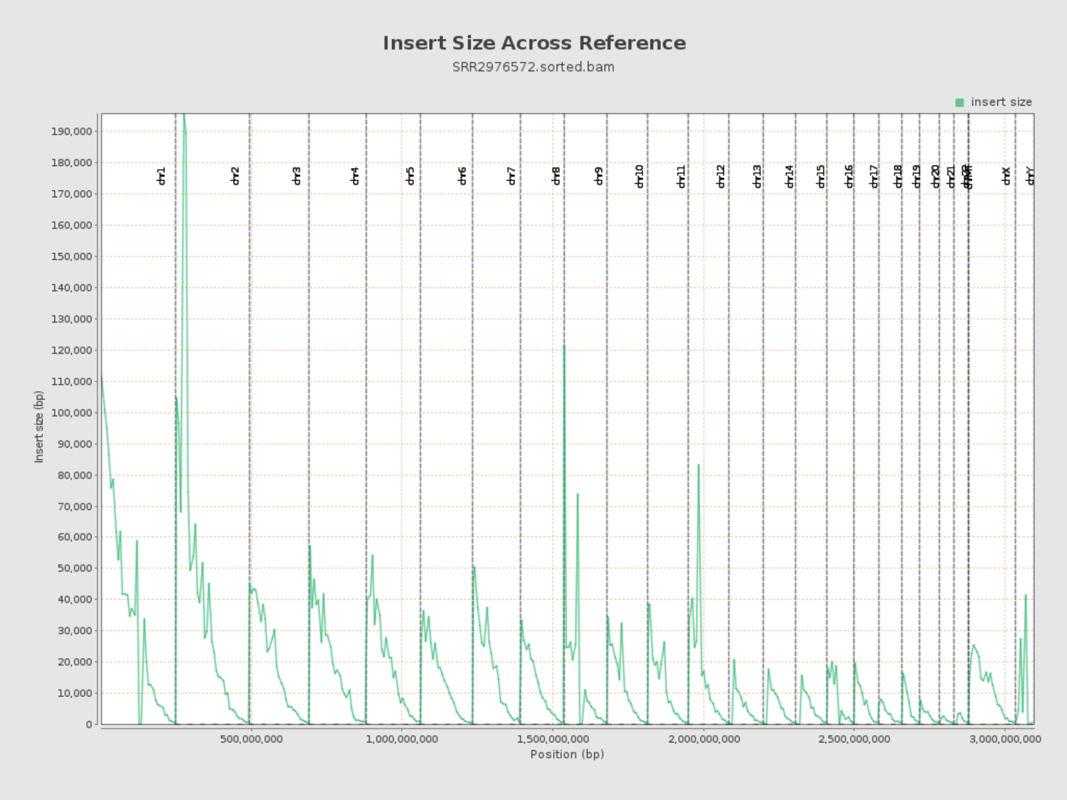
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram