Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 15:04:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975289.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_SRR975289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975289_1.fastq.gz SRR975289_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 15:04:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	54,349,888
Mapped reads	54,214,862 / 99.75%
Unmapped reads	135,026 / 0.25%
Mapped paired reads	54,214,862 / 99.75%
Mapped reads, first in pair	27,105,755 / 49.87%
Mapped reads, second in pair	27,109,107 / 49.88%
Mapped reads, both in pair	54,168,262 / 99.67%
Mapped reads, singletons	46,600 / 0.09%
Secondary alignments	0
Supplementary alignments	98,847 / 0.18%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	33,901,001 / 62.38%
Duplication rate	47.52%
Clipped reads	33,255,499 / 61.19%

2.2. ACGT Content

Number/percentage of A's	1,306,352,601 / 26.08%
Number/percentage of C's	1,101,675,309 / 21.99%
Number/percentage of T's	1,388,620,971 / 27.72%
Number/percentage of G's	1,212,636,028 / 24.21%
Number/percentage of N's	158,647 / 0%

GC Percentage	46.2%

2.3. Coverage

Mean	1.6187
Standard Deviation	26.1514

2.4. Mapping Quality

Mean Mapping Quality	56.05

2.5. Insert size

Mean	41,093.26
Standard Deviation	2,006,800.48
P25/Median/P75	150 / 189 / 241

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	32,497,959
Insertions	508,758
Mapped reads with at least one insertion	0.93%
Deletions	1,199,896
Mapped reads with at least one deletion	2.18%
Homopolymer indels	46.91%

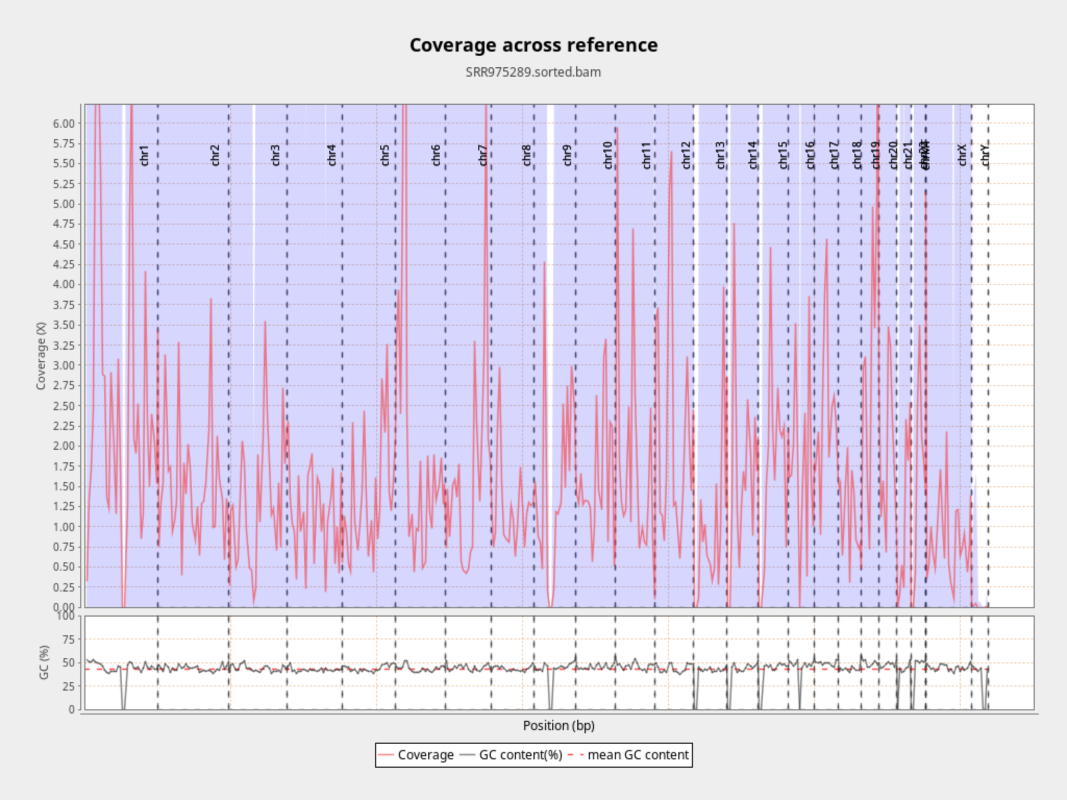
2.7. Chromosome stats

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

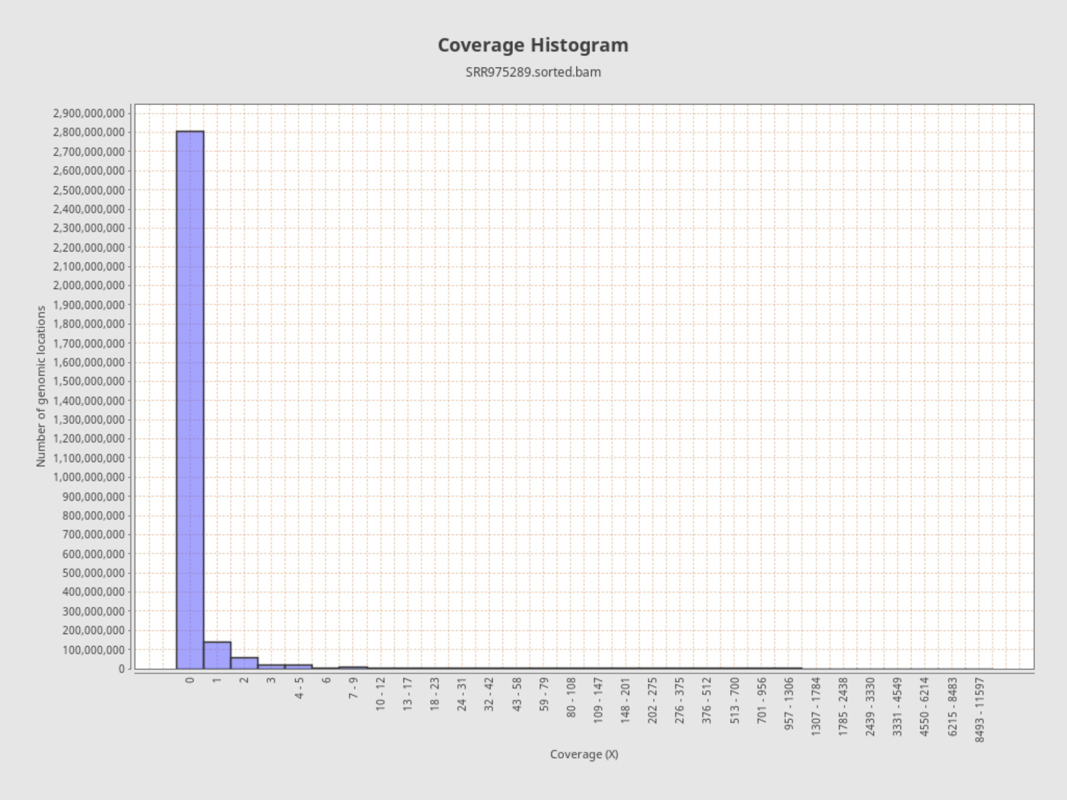
		bases	coverage	deviation
chr1	249250621	620998229	2.4915	35.8189
chr2	243199373	368146116	1.5138	23.2142
chr3	198022430	265073560	1.3386	21.0593
chr4	191154276	220694271	1.1545	19.4997
chr5	180915260	250298349	1.3835	22.7323
chr6	171115067	380315322	2.2226	34.7673
chr7	159138663	269577838	1.694	27.1755
chr8	146364022	182839133	1.2492	20.8867
chr9	141213431	202628269	1.4349	23.1975
chr10	135534747	219145695	1.6169	24.759
chr11	135006516	250040539	1.8521	28.1022
chr12	133851895	293804424	2.195	30.3956
chr13	115169878	108189731	0.9394	23.7994
chr14	107349540	167888450	1.5639	25.0763
chr15	102531392	178670292	1.7426	26.8999
chr16	90354753	159555756	1.7659	25.2927
chr17	81195210	200426556	2.4685	32.5988
chr18	78077248	92006478	1.1784	21.0887
chr19	59128983	187884643	3.1775	38.9327
chr20	63025520	127271107	2.0194	29.9852
chr21	48129895	51817911	1.0766	22.5249
chr22	51304566	82853451	1.6149	25.4936
chrMT	16571	85310	5.1482	9.3724
chrX	155270560	130072152	0.8377	16.8216

chrY	59373566	838153	0.0141	0.7758

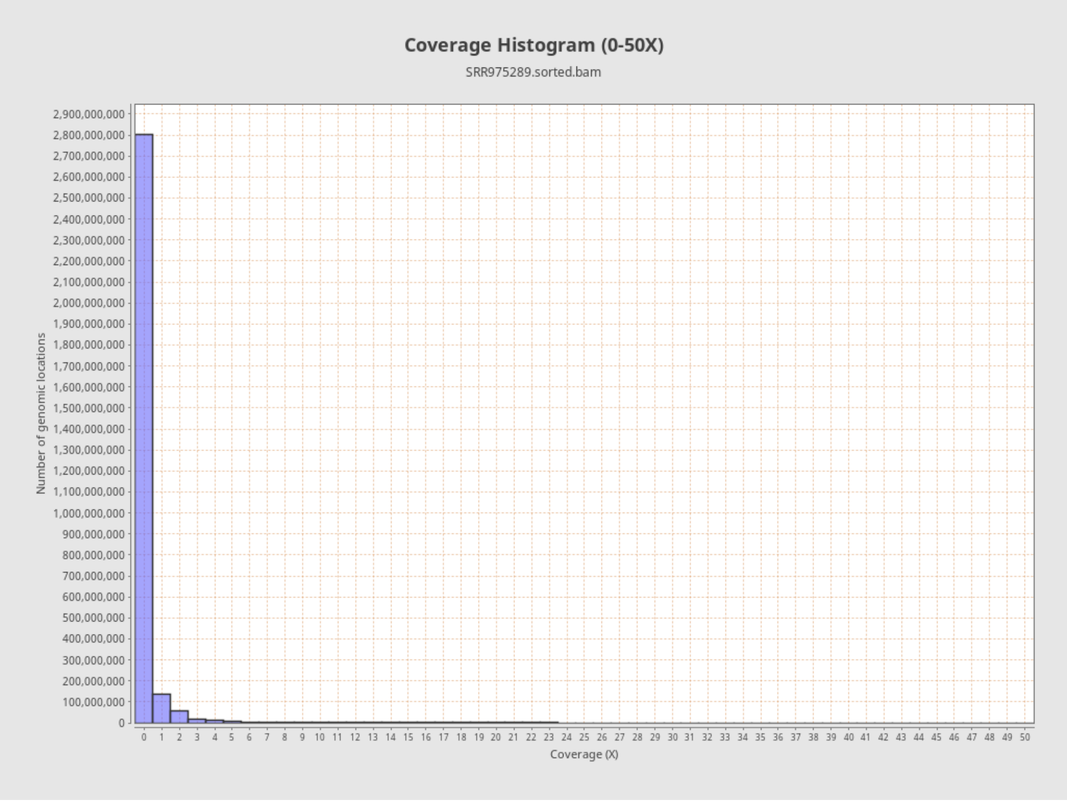
3. Results : Coverage across reference



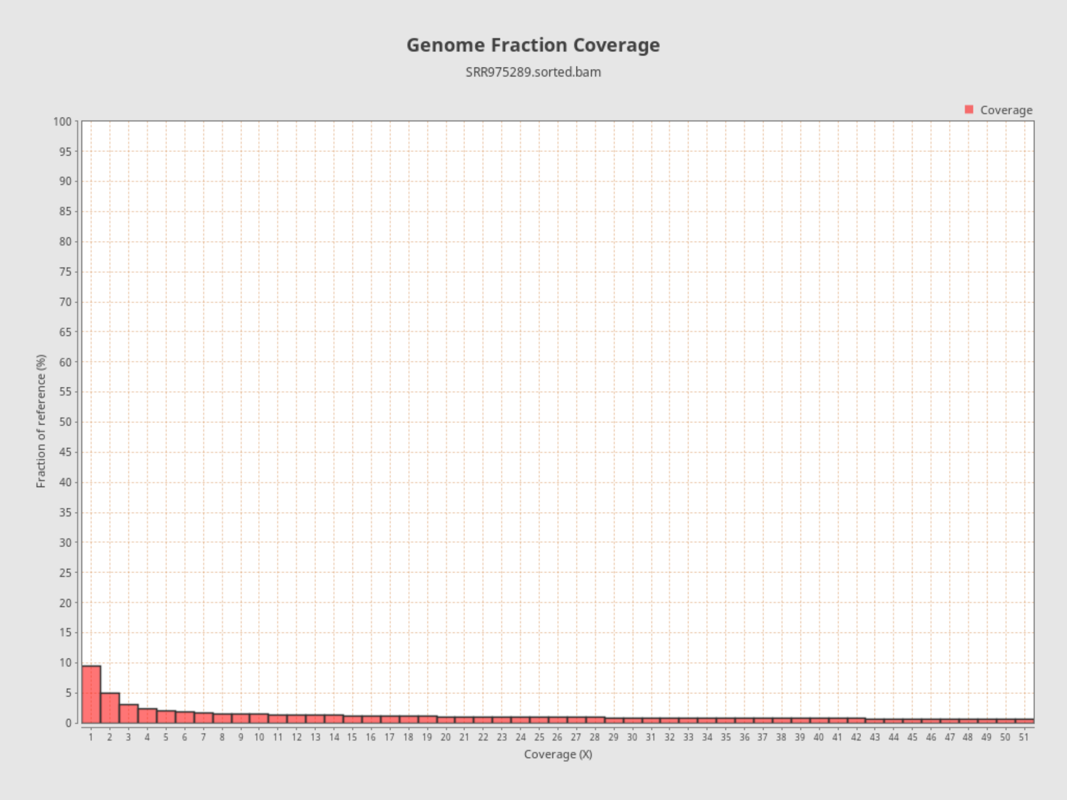
4. Results : Coverage Histogram



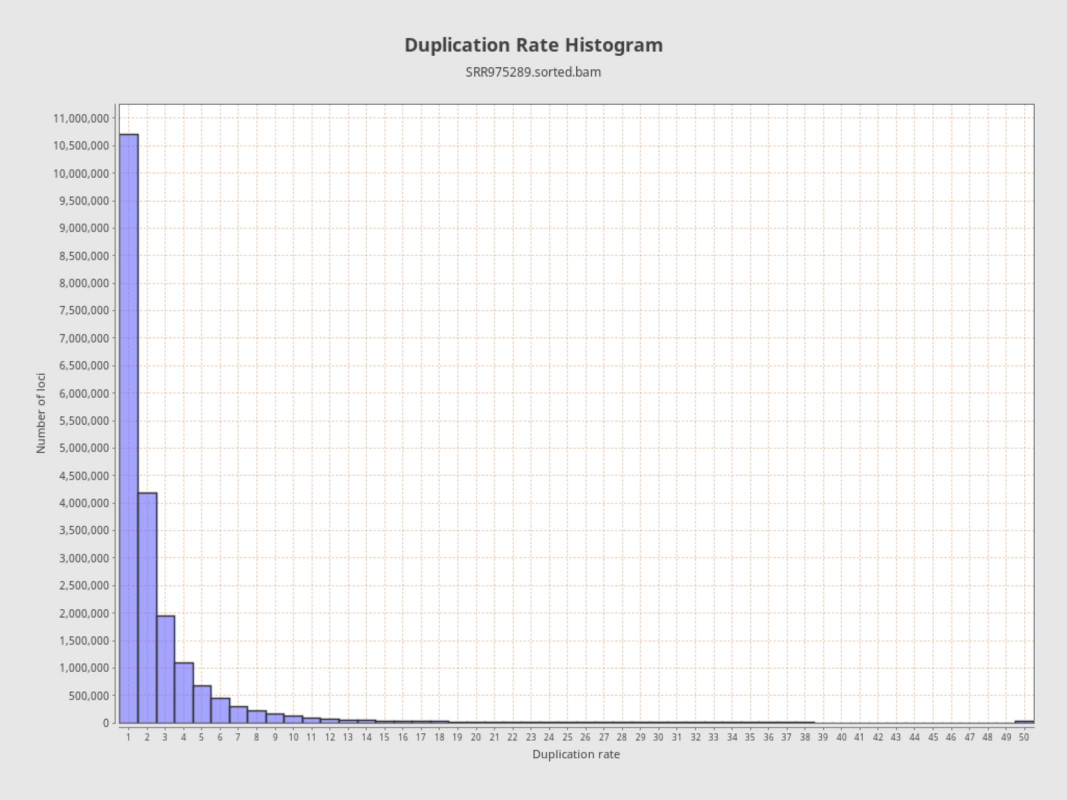
5. Results : Coverage Histogram (0-50X)



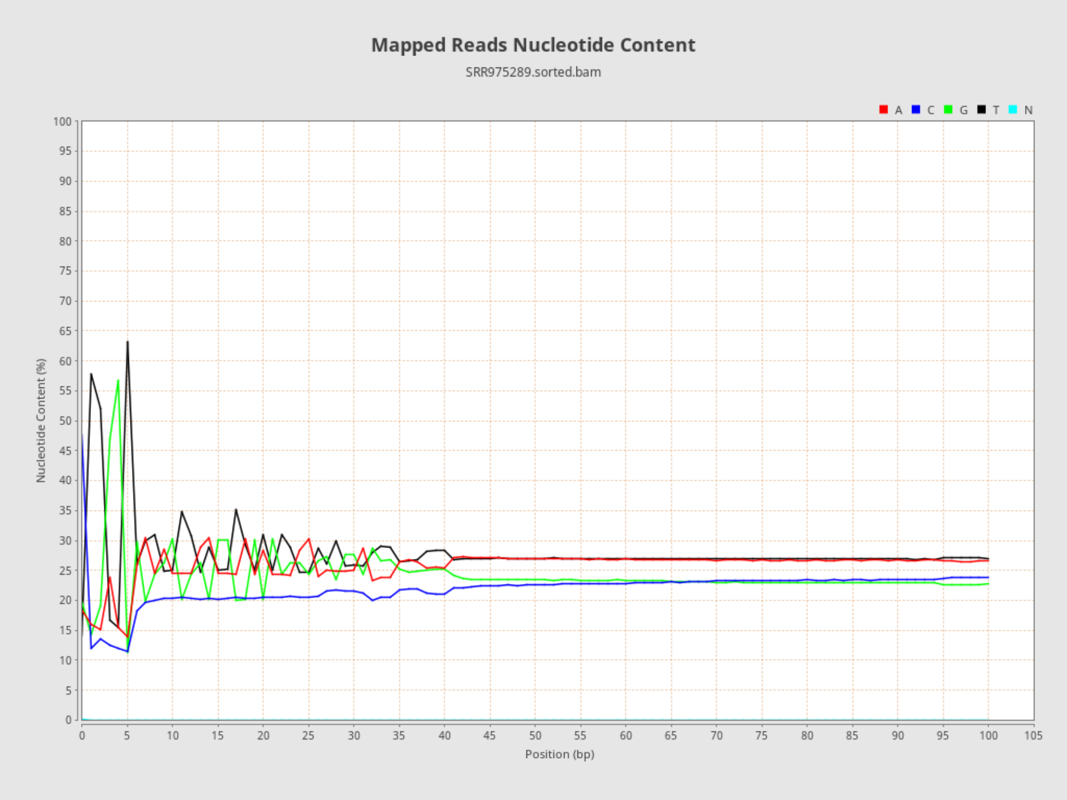
6. Results : Genome Fraction Coverage



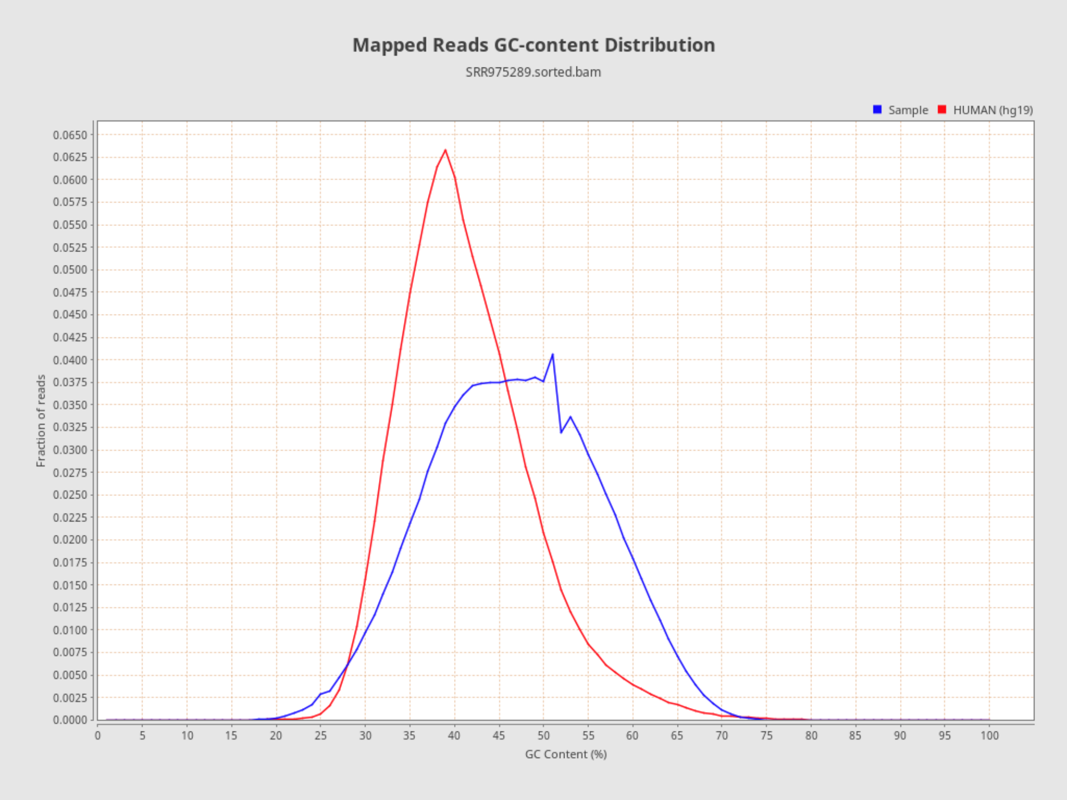
7. Results : Duplication Rate Histogram



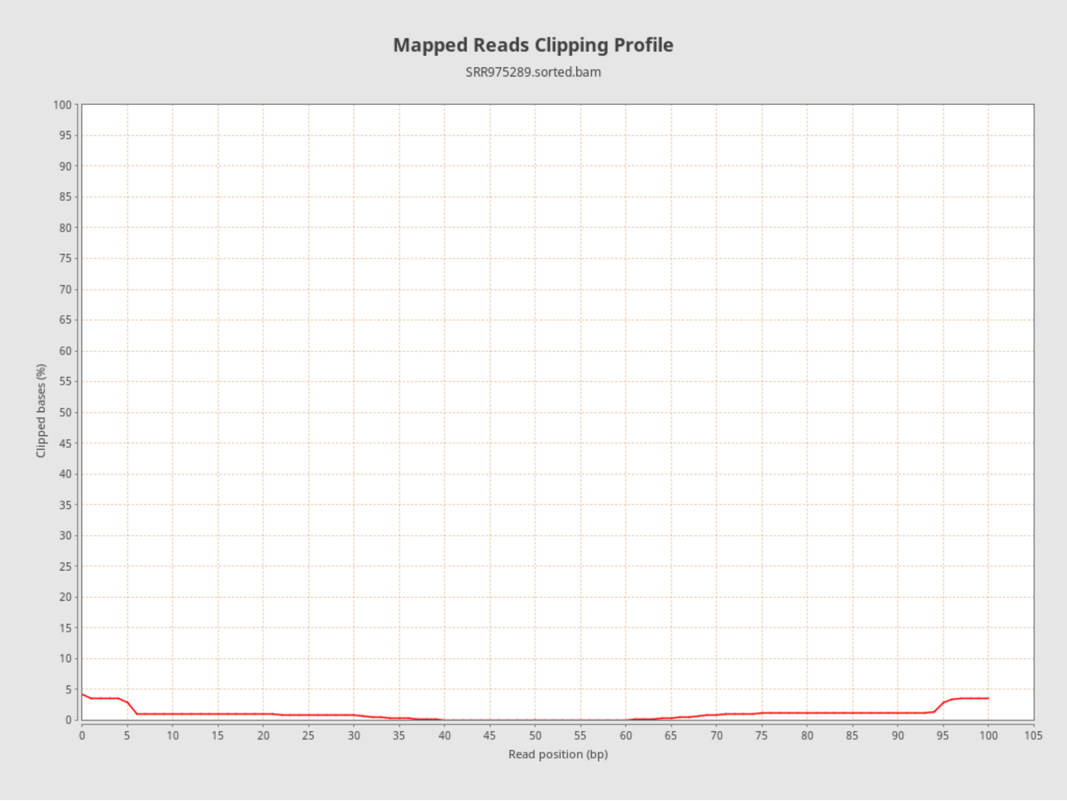
8. Results : Mapped Reads Nucleotide Content



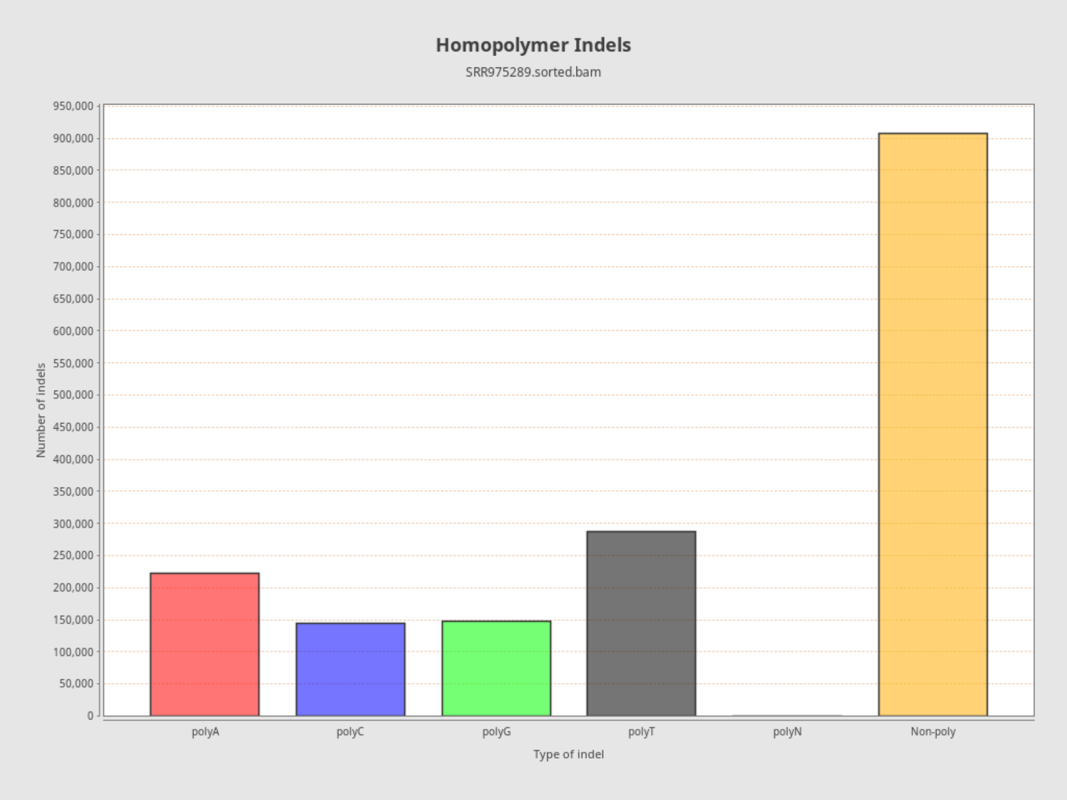
9. Results : Mapped Reads GC-content Distribution



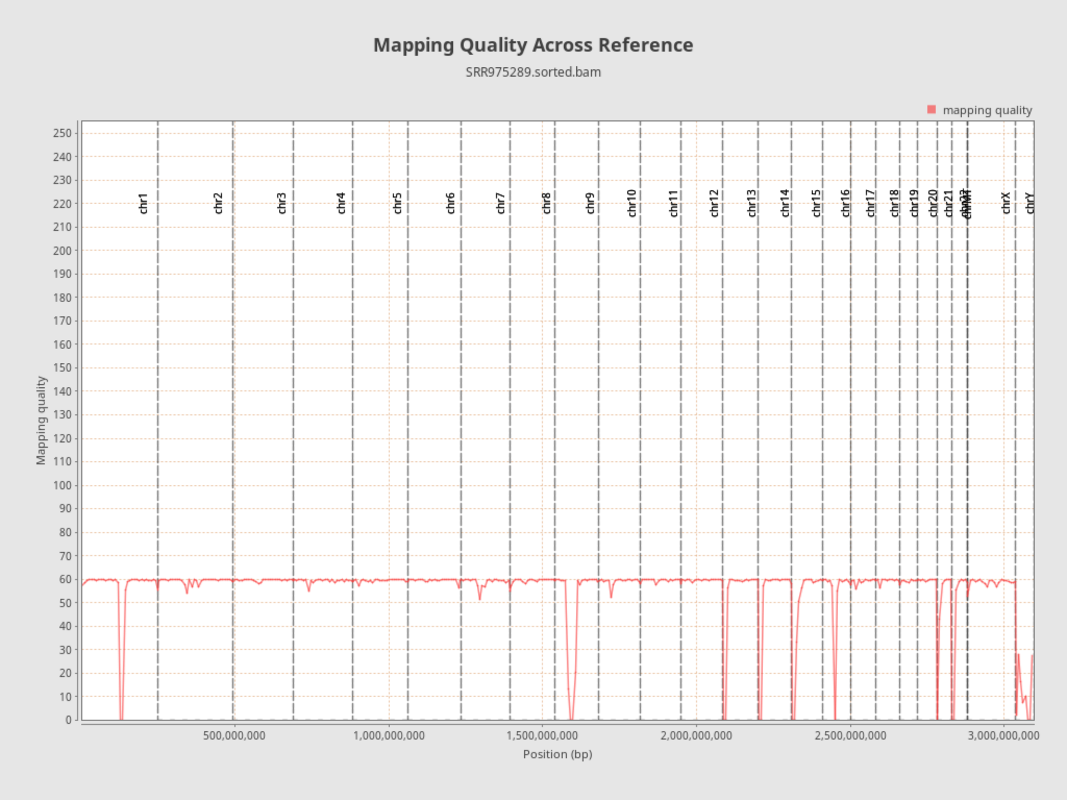
10. Results : Mapped Reads Clipping Profile



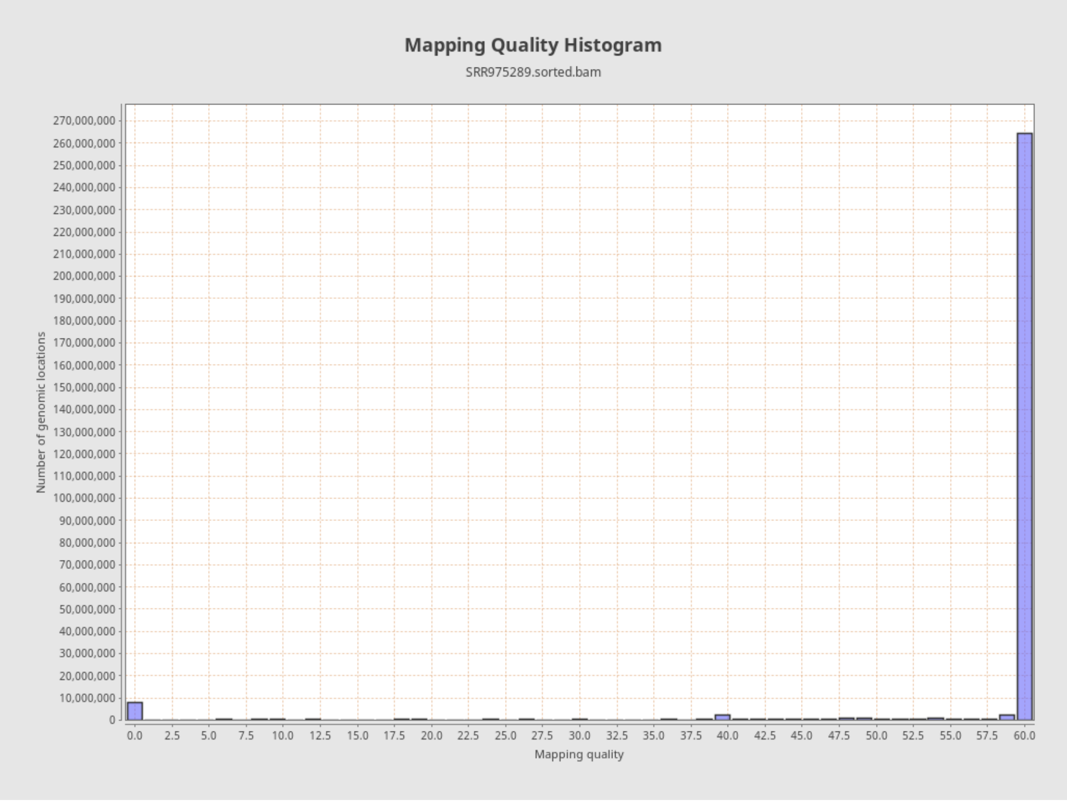
11. Results : Homopolymer Indels



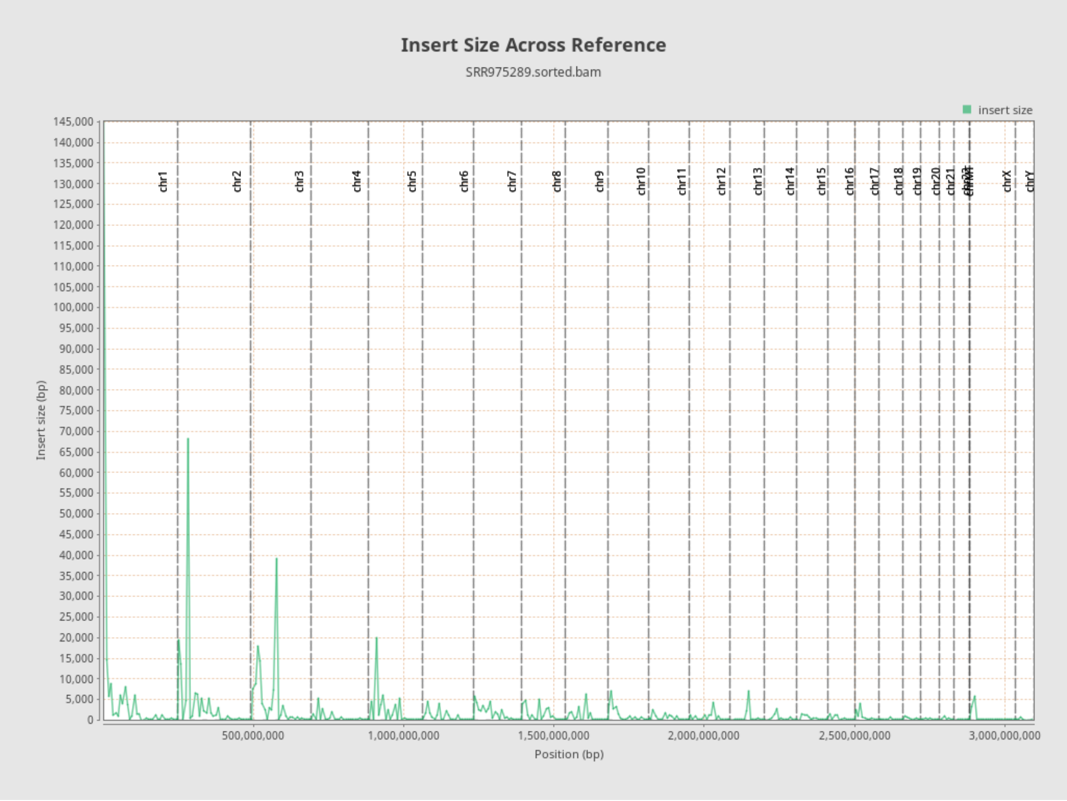
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram