Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 14:03:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975285.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_SRR975285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975285_1.fastq.gz SRR975285_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 14:03:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,449,350
Mapped reads	59,340,998 / 99.82%
Unmapped reads	108,352 / 0.18%
Mapped paired reads	59,340,998 / 99.82%
Mapped reads, first in pair	29,665,535 / 49.9%
Mapped reads, second in pair	29,675,463 / 49.92%
Mapped reads, both in pair	59,300,296 / 99.75%
Mapped reads, singletons	40,702 / 0.07%
Secondary alignments	0
Supplementary alignments	59,904 / 0.1%
Read min/max/mean length	30 / 101 / 101.04
Duplicated reads (estimated)	38,982,523 / 65.57%
Duplication rate	49.05%
Clipped reads	34,397,118 / 57.86%

2.2. ACGT Content

Number/percentage of A's	1,453,595,946 / 26.08%
Number/percentage of C's	1,263,367,261 / 22.66%
Number/percentage of T's	1,500,028,422 / 26.91%
Number/percentage of G's	1,357,362,072 / 24.35%
Number/percentage of N's	178,609 / 0%

GC Percentage	47.01%

2.3. Coverage

Mean	1.8012
Standard Deviation	32.6068

2.4. Mapping Quality

Mean Mapping Quality	56.39

2.5. Insert size

Mean	59,293.42
Standard Deviation	2,406,100.1
P25/Median/P75	153 / 191 / 241

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	32,169,460
Insertions	457,161
Mapped reads with at least one insertion	0.76%
Deletions	1,101,606
Mapped reads with at least one deletion	1.84%
Homopolymer indels	49.05%

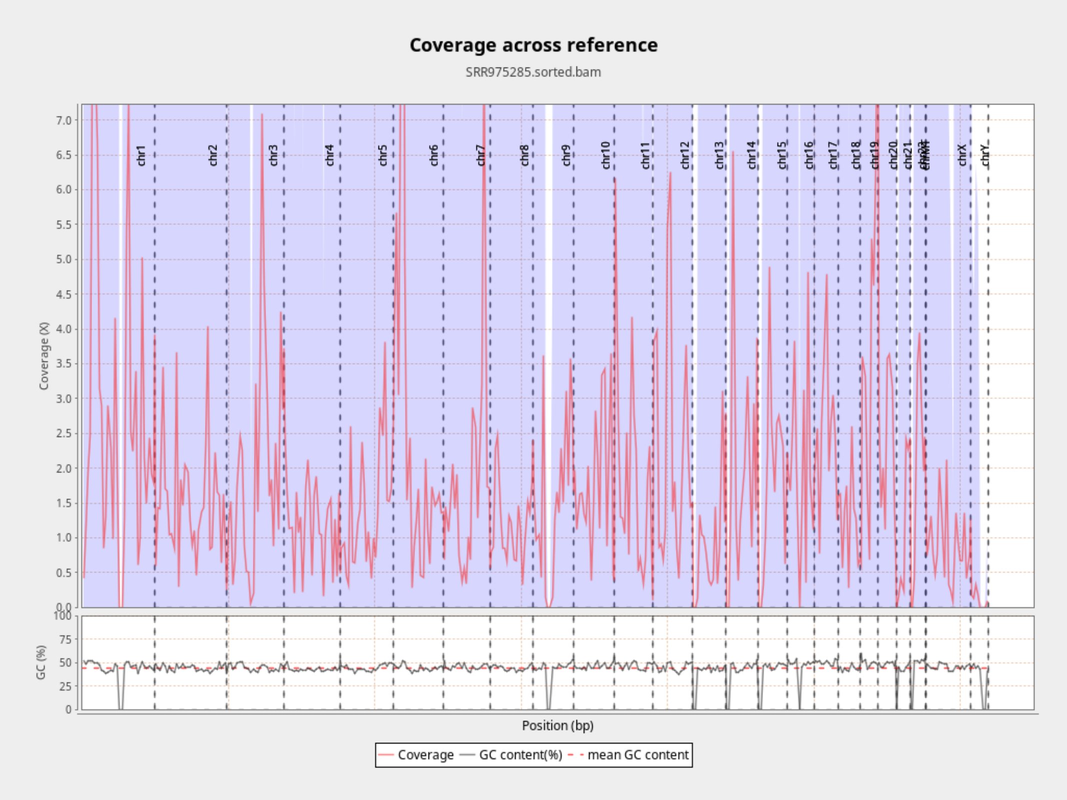
2.7. Chromosome stats

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

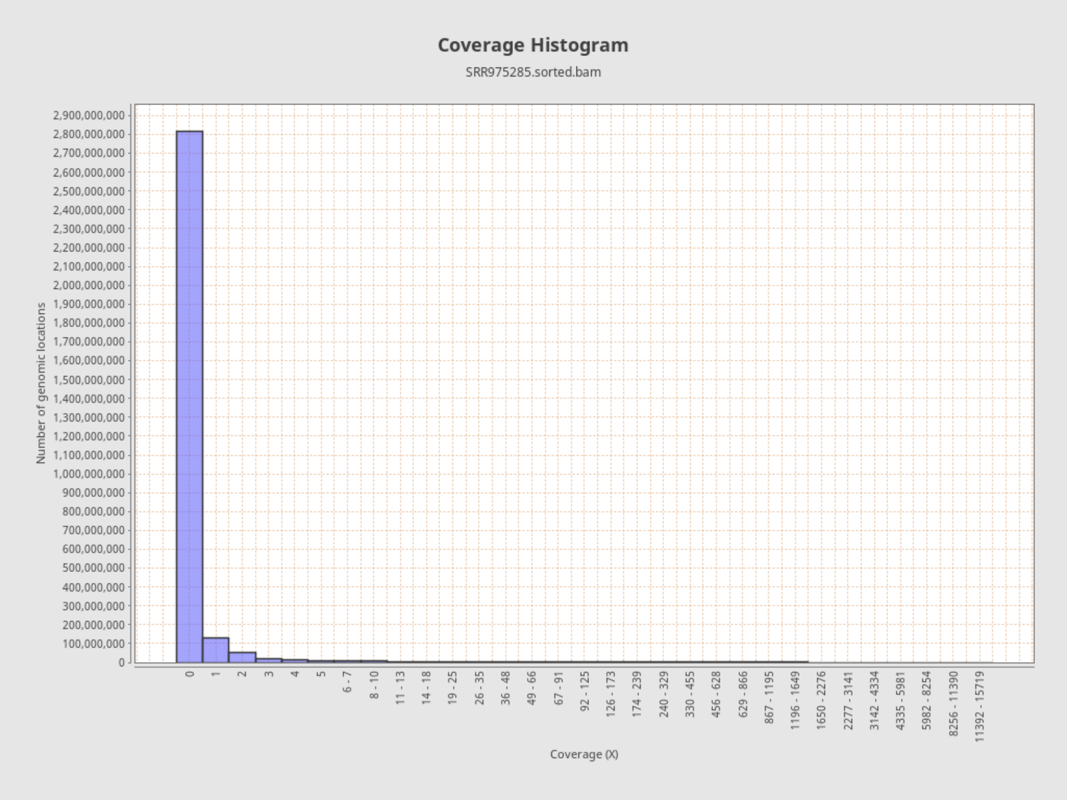
		bases	coverage	deviation
chr1	249250621	684757655	2.7473	43.4159
chr2	243199373	374301799	1.5391	25.6156
chr3	198022430	392636086	1.9828	34.4646
chr4	191154276	229356487	1.1999	24.1611
chr5	180915260	256120349	1.4157	26.203
chr6	171115067	510111144	2.9811	56.6598
chr7	159138663	287507311	1.8066	35.0653
chr8	146364022	172591019	1.1792	22.0696
chr9	141213431	214884407	1.5217	27.0012
chr10	135534747	252017318	1.8594	33.5626
chr11	135006516	249157277	1.8455	30.3081
chr12	133851895	304357385	2.2738	32.9792
chr13	115169878	101001557	0.877	21.3995
chr14	107349540	198702650	1.851	31.5731
chr15	102531392	188557833	1.839	28.1505
chr16	90354753	184871639	2.0461	33.1721
chr17	81195210	209935988	2.5856	36.8085
chr18	78077248	98291490	1.2589	25.2173
chr19	59128983	218885376	3.7018	46.8359
chr20	63025520	145203427	2.3039	36.0329
chr21	48129895	54593601	1.1343	24.8869
chr22	51304566	102985845	2.0073	31.8875
chrMT	16571	29315	1.7691	5.7343
chrX	155270560	138692219	0.8932	18.5776

chrY	59373566	6479135	0.1091	3.7085

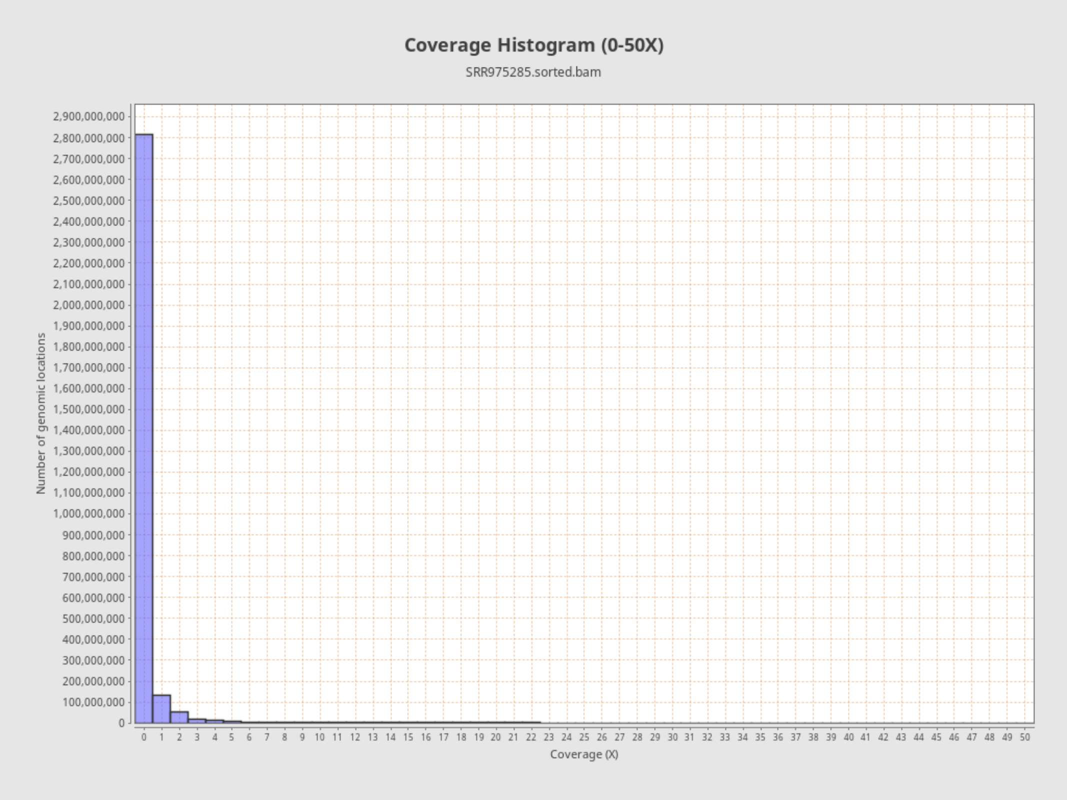
3. Results : Coverage across reference



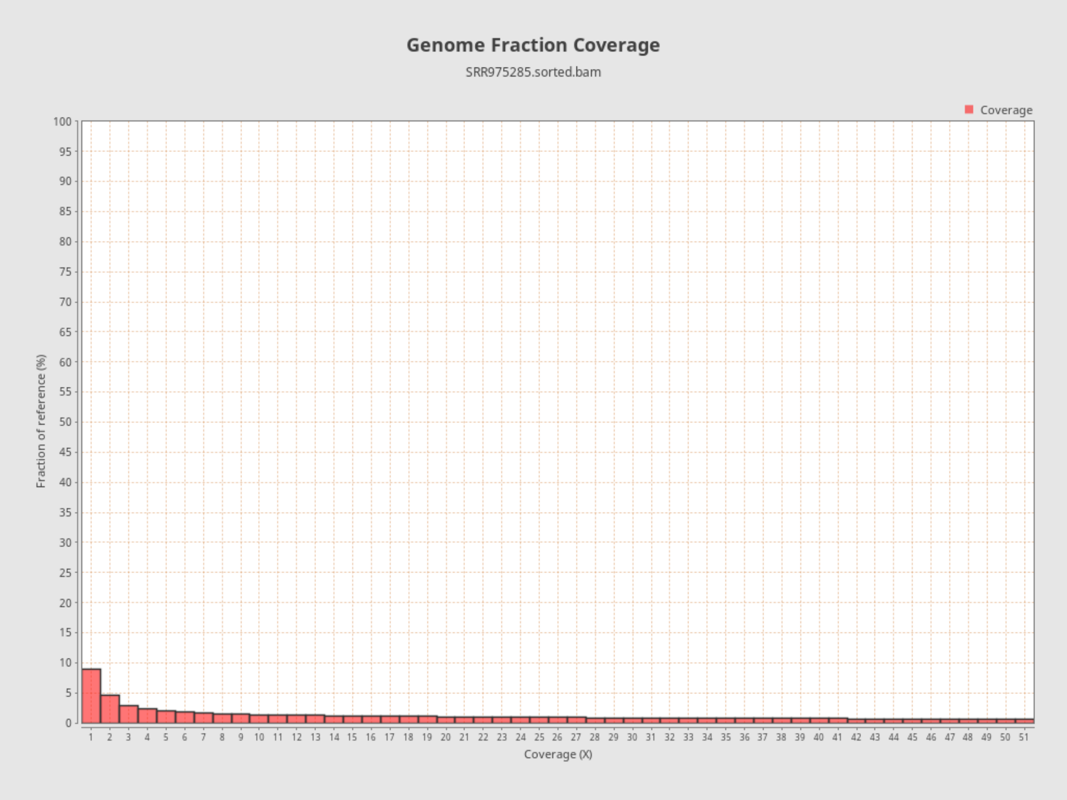
4. Results : Coverage Histogram



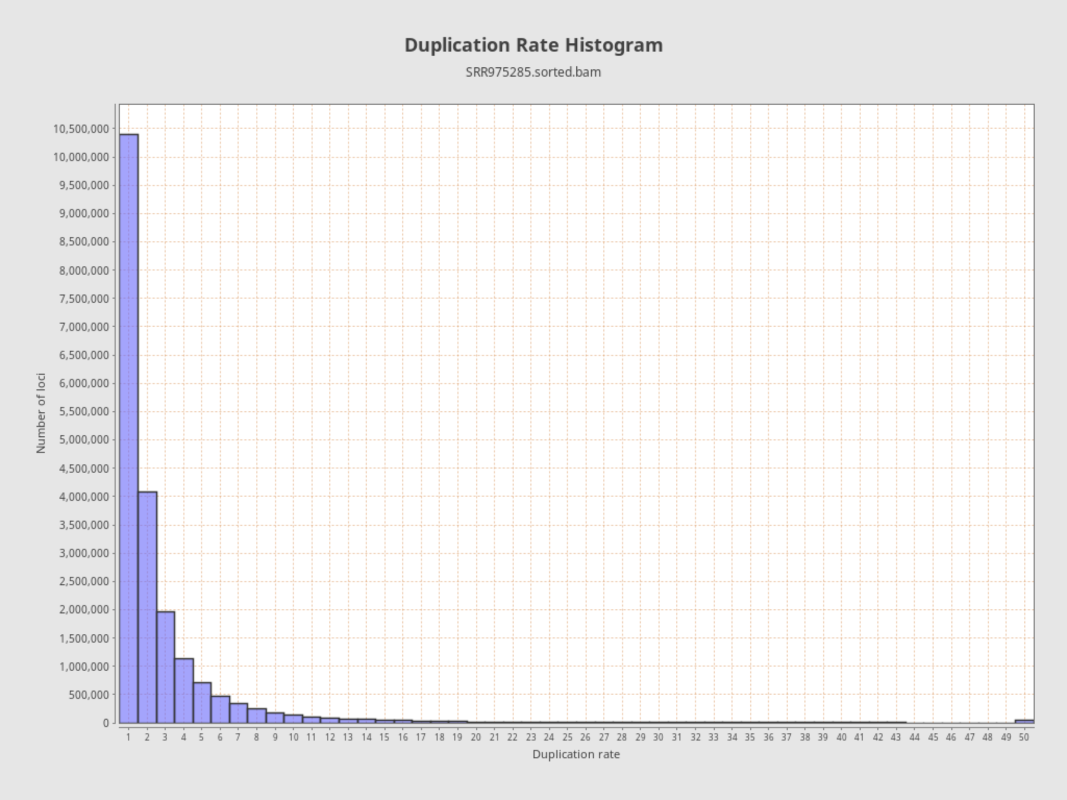
5. Results : Coverage Histogram (0-50X)



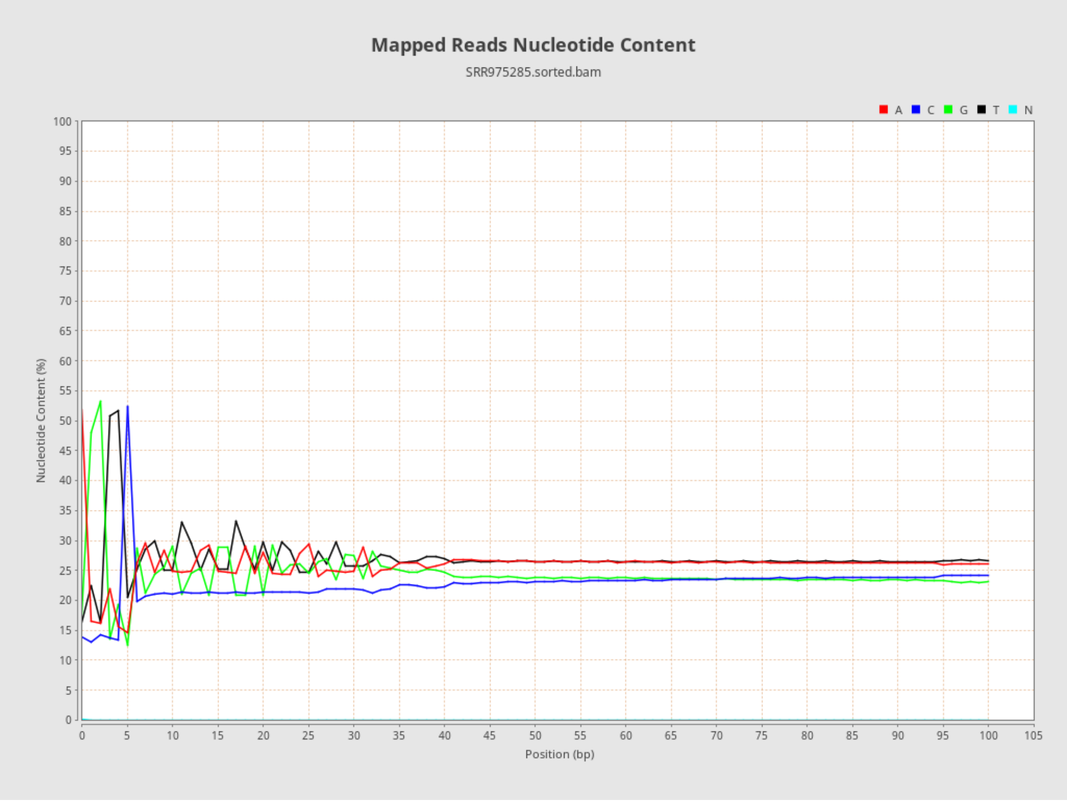
6. Results : Genome Fraction Coverage



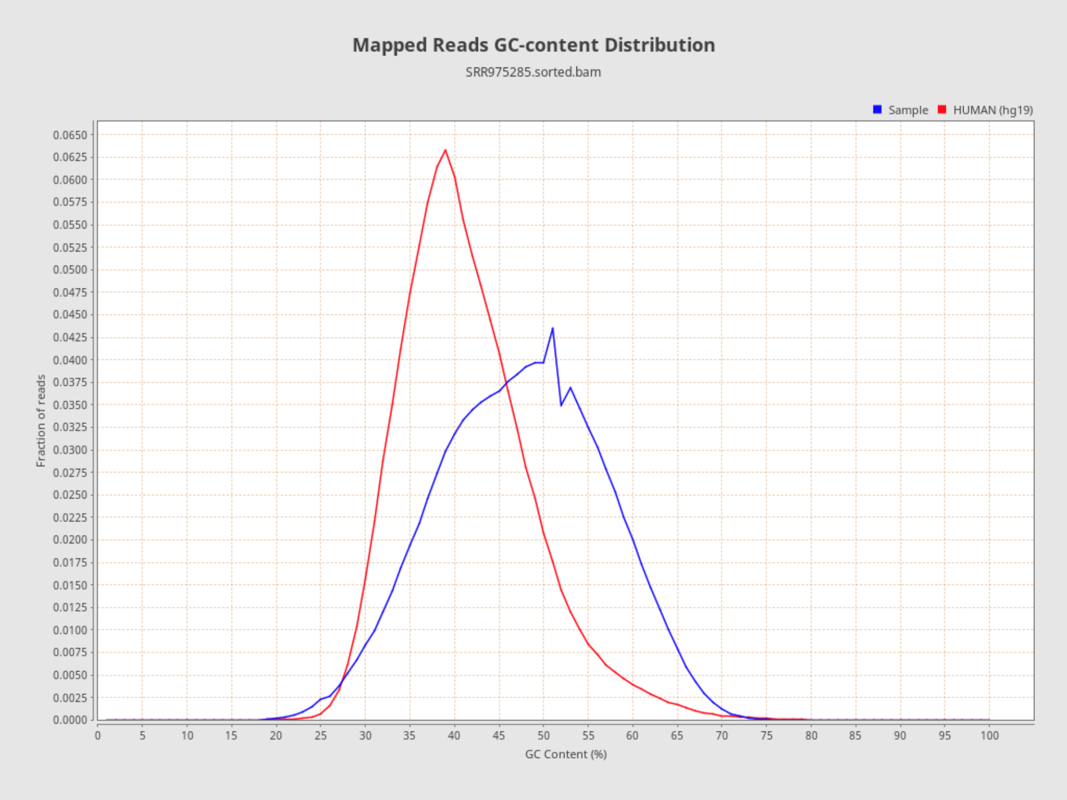
7. Results : Duplication Rate Histogram



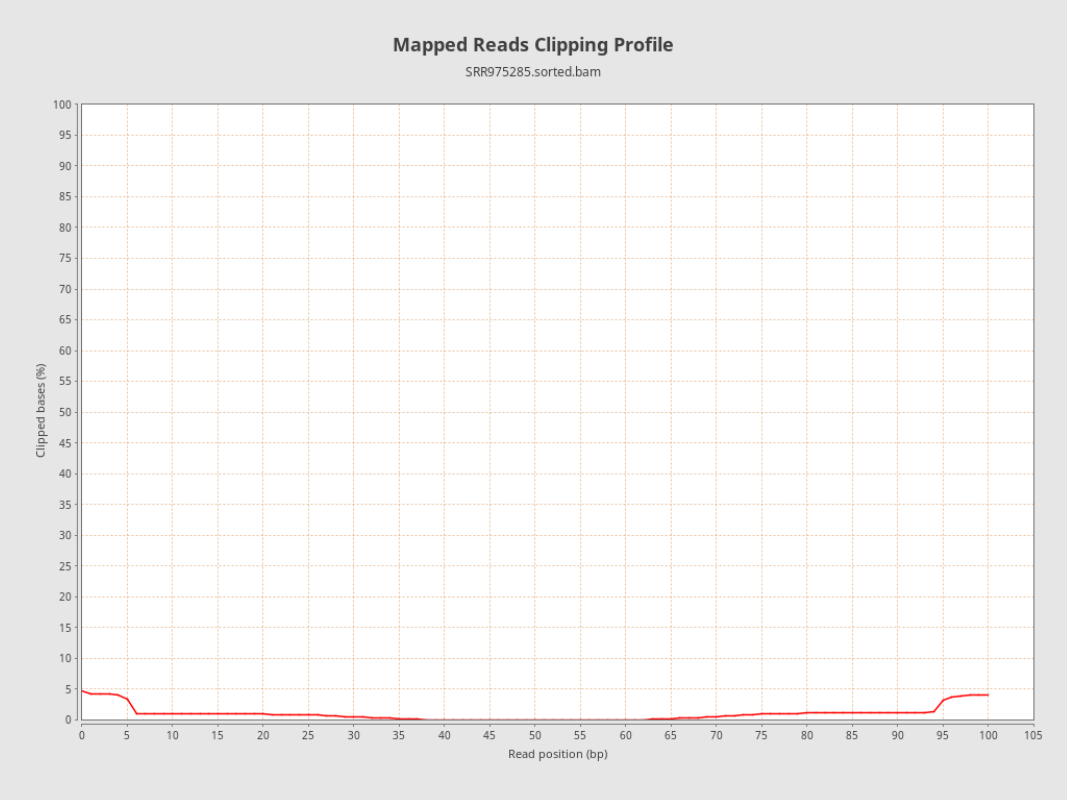
8. Results : Mapped Reads Nucleotide Content



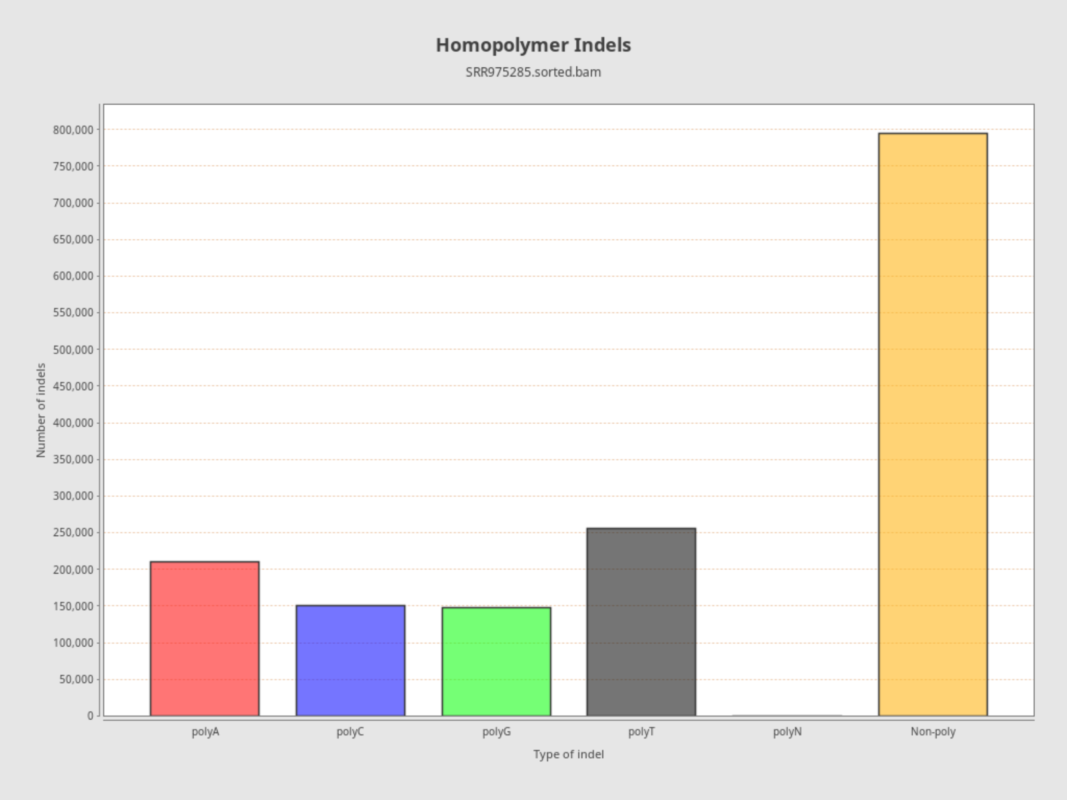
9. Results : Mapped Reads GC-content Distribution



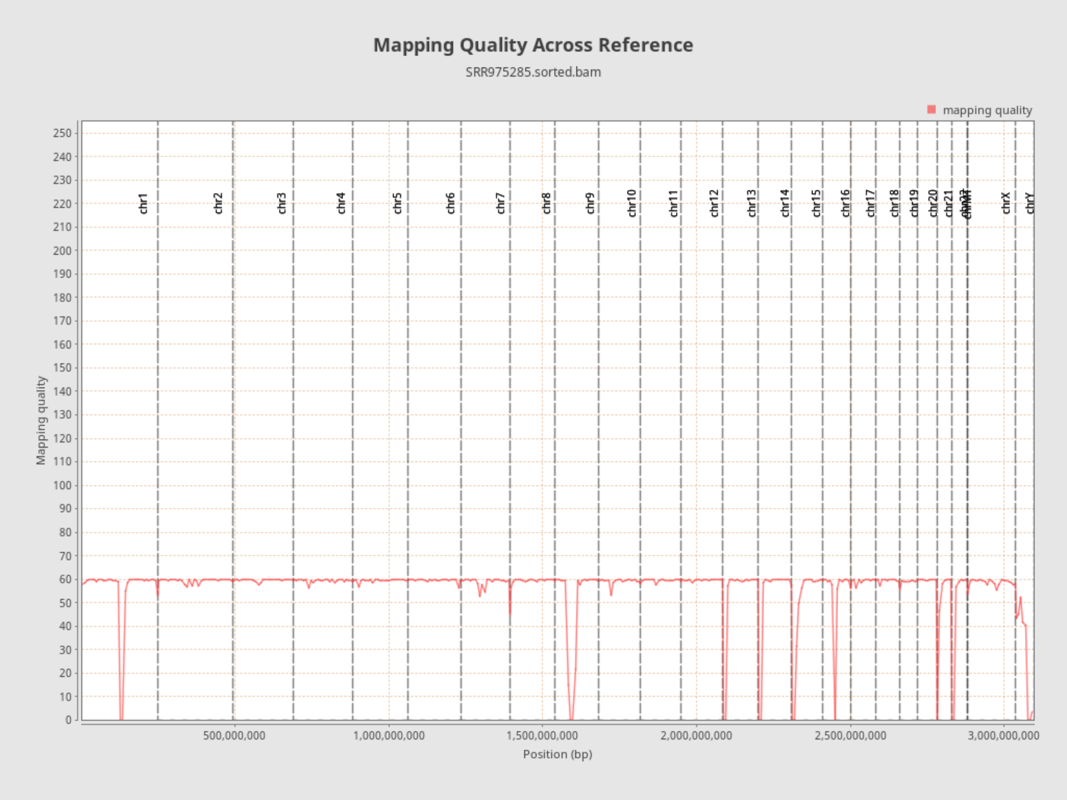
10. Results : Mapped Reads Clipping Profile



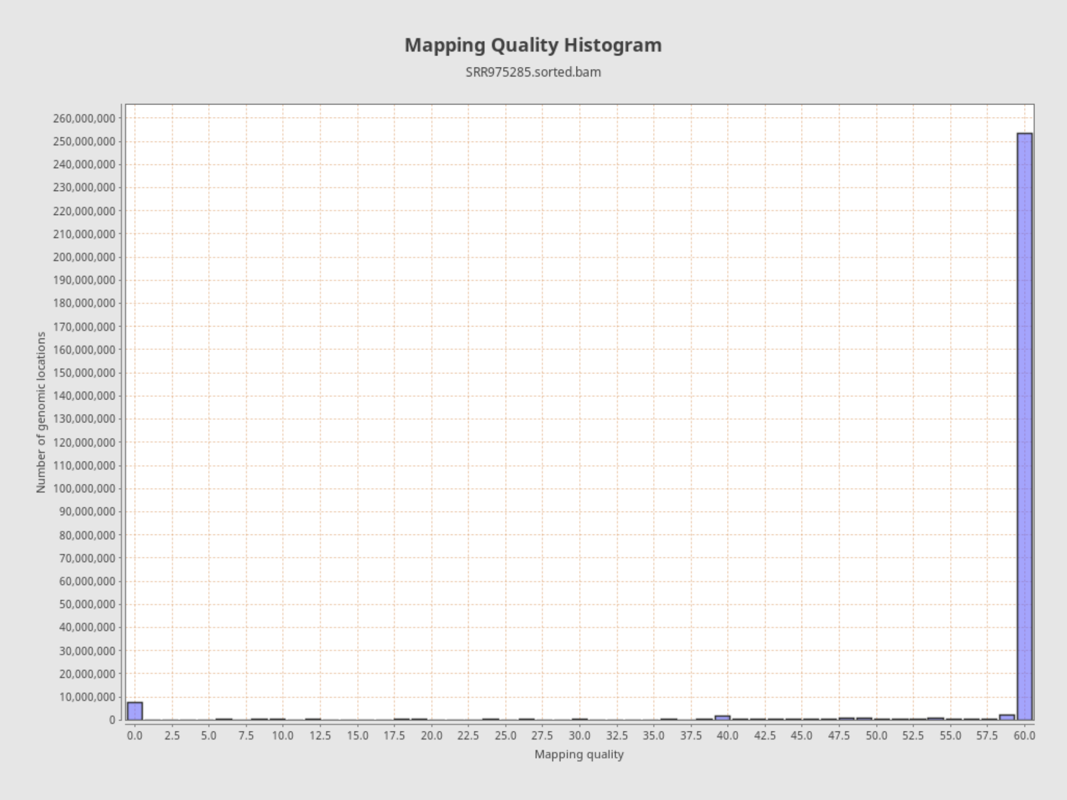
11. Results : Homopolymer Indels



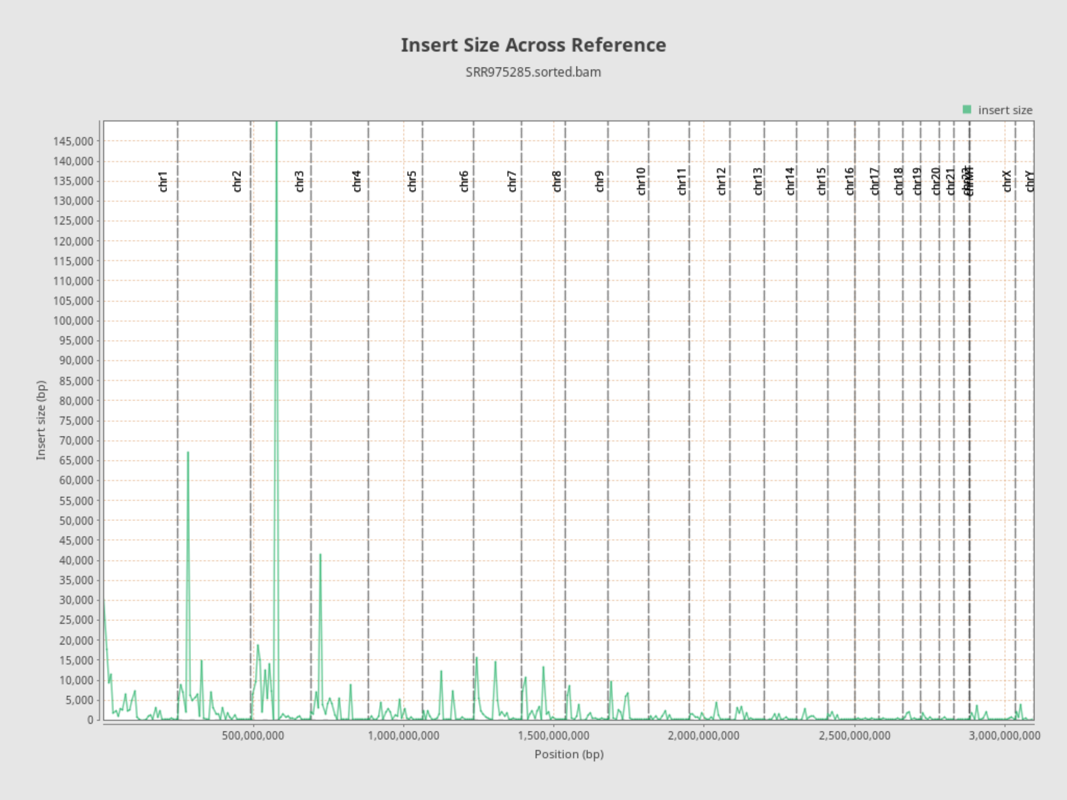
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram