Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 21:11:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975286.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_SRR975286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975286_1.fastq.gz SRR975286_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 21:11:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975286.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,515,666
Mapped reads	3,492,388 / 99.34%
Unmapped reads	23,278 / 0.66%
Mapped paired reads	3,492,388 / 99.34%
Mapped reads, first in pair	1,745,801 / 49.66%
Mapped reads, second in pair	1,746,587 / 49.68%
Mapped reads, both in pair	3,485,202 / 99.13%
Mapped reads, singletons	7,186 / 0.2%
Secondary alignments	0
Supplementary alignments	9,760 / 0.28%
Read min/max/mean length	30 / 101 / 101.11
Duplicated reads (estimated)	126,696 / 3.6%
Duplication rate	2.35%
Clipped reads	2,086,071 / 59.34%

2.2. ACGT Content

Number/percentage of A's	93,696,561 / 28.92%
Number/percentage of C's	63,784,284 / 19.69%
Number/percentage of T's	96,054,475 / 29.65%
Number/percentage of G's	70,454,639 / 21.75%
Number/percentage of N's	7,254 / 0%

GC Percentage	41.43%

2.3. Coverage

Mean	0.1047
Standard Deviation	0.9086

2.4. Mapping Quality

Mean Mapping Quality	53.02

2.5. Insert size

Mean	58,762.97
Standard Deviation	2,365,943.92
P25/Median/P75	140 / 172 / 218

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	2,241,347
Insertions	44,115
Mapped reads with at least one insertion	1.24%
Deletions	93,759
Mapped reads with at least one deletion	2.64%
Homopolymer indels	48.21%

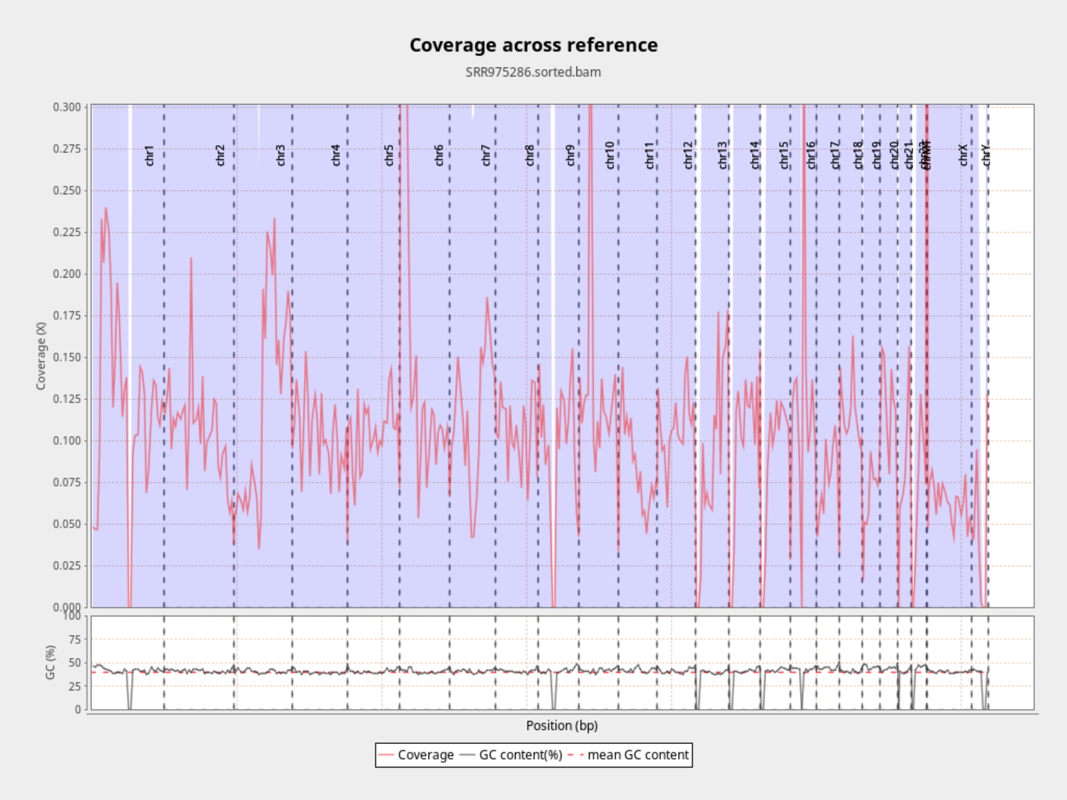
2.7. Chromosome stats

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

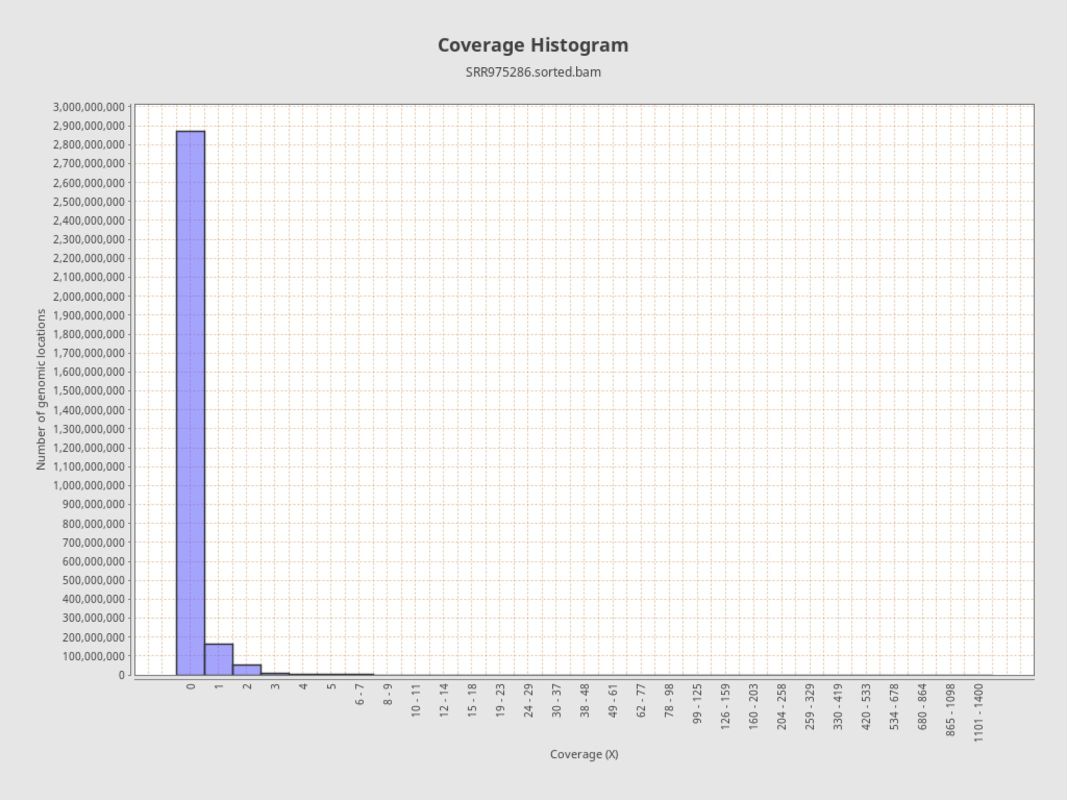
		bases	coverage	deviation
chr1	249250621	30752921	0.1234	0.6457
chr2	243199373	25693969	0.1056	0.8604
chr3	198022430	24444758	0.1234	0.4832
chr4	191154276	19848548	0.1038	0.5754
chr5	180915260	19068275	0.1054	0.4126
chr6	171115067	26291923	0.1537	0.6714
chr7	159138663	18312620	0.1151	0.9688
chr8	146364022	15309593	0.1046	0.4586
chr9	141213431	13433489	0.0951	1.1436
chr10	135534747	17998294	0.1328	2.8459
chr11	135006516	11286186	0.0836	0.6828
chr12	133851895	14581192	0.1089	0.4202
chr13	115169878	10455759	0.0908	0.3871
chr14	107349540	10204800	0.0951	0.4073
chr15	102531392	8967065	0.0875	0.3757
chr16	90354753	11010234	0.1219	1.5528
chr17	81195210	6142524	0.0757	0.5484
chr18	78077248	9188449	0.1177	1.226
chr19	59128983	3910502	0.0661	0.4299
chr20	63025520	7485183	0.1188	0.4544
chr21	48129895	3941885	0.0819	0.4221
chr22	51304566	3515585	0.0685	0.3449
chrMT	16571	26694	1.6109	2.0949
chrX	155270560	9729200	0.0627	0.3927

chrY	59373566	2551911	0.043	0.7312

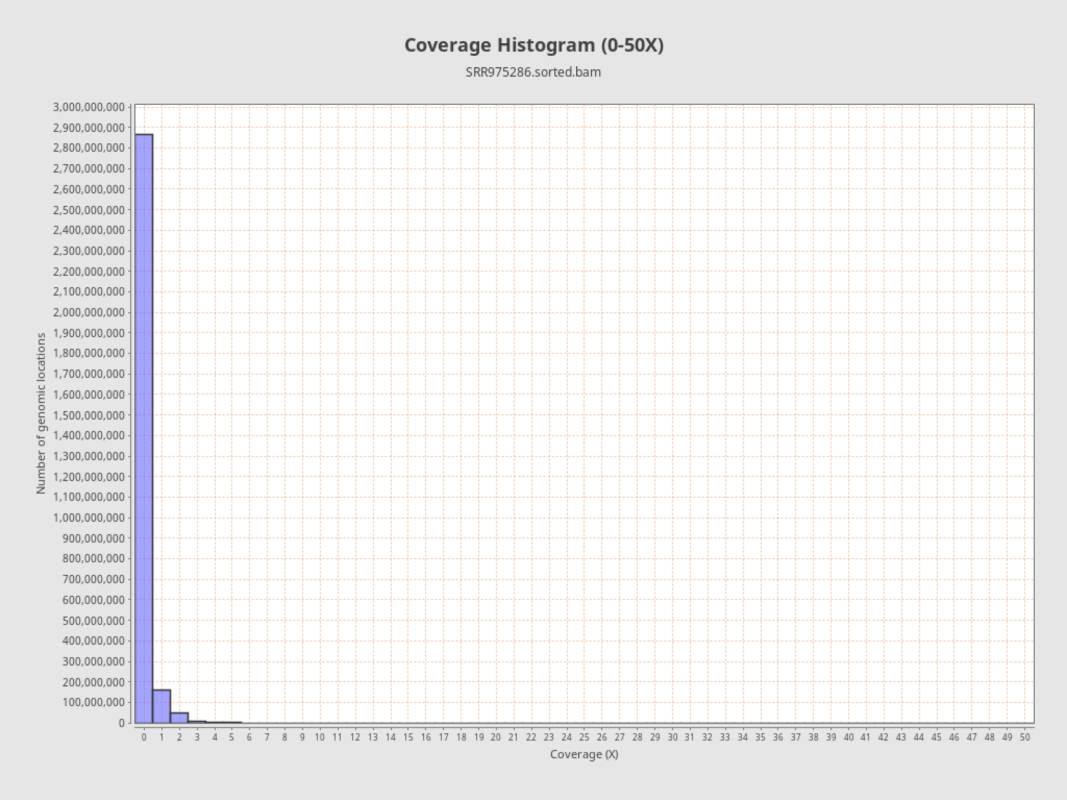
3. Results : Coverage across reference



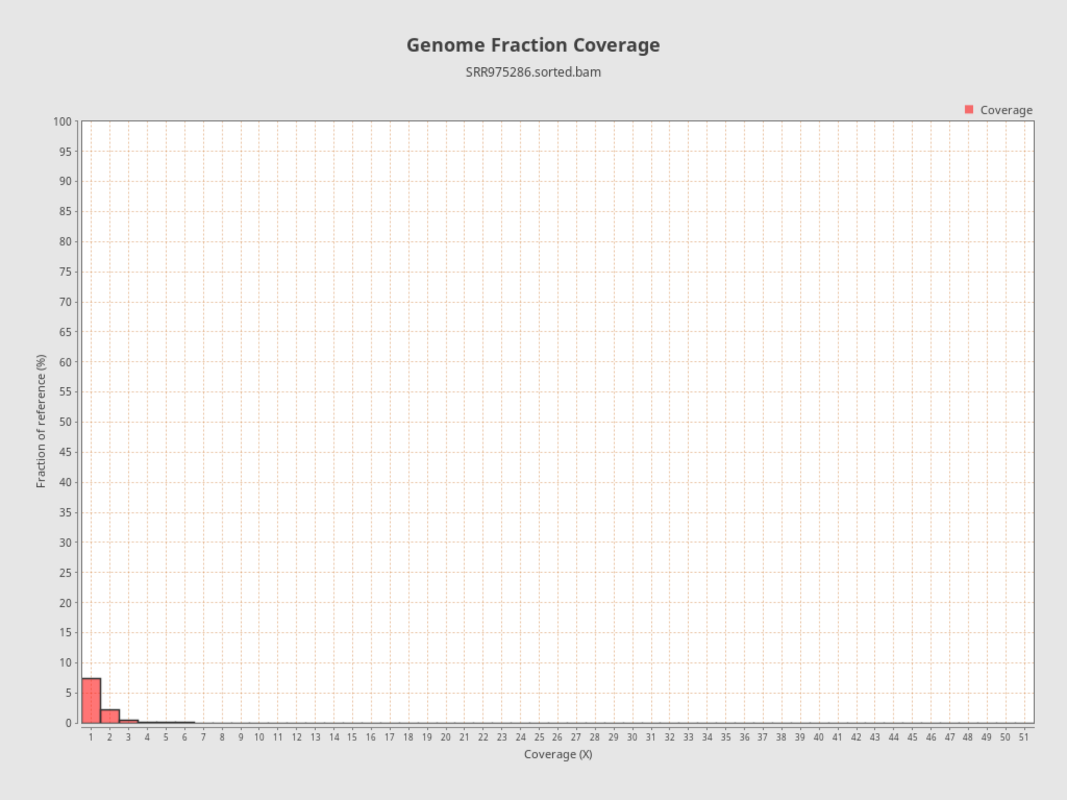
4. Results : Coverage Histogram



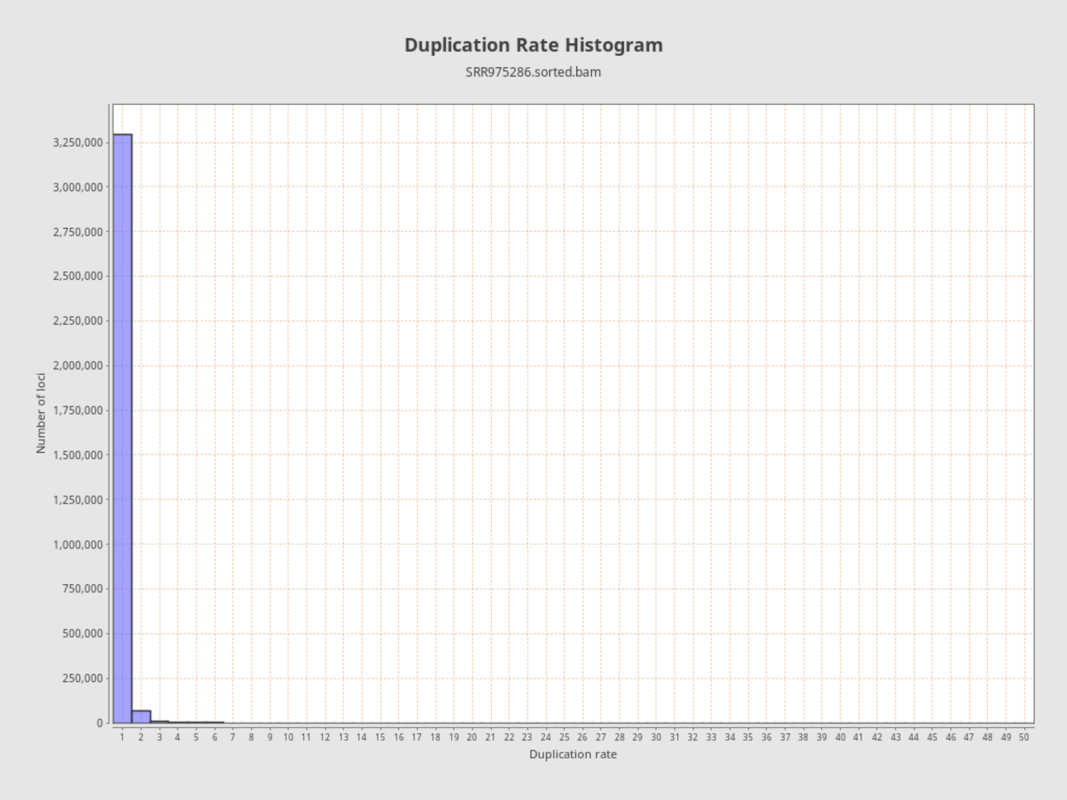
5. Results : Coverage Histogram (0-50X)



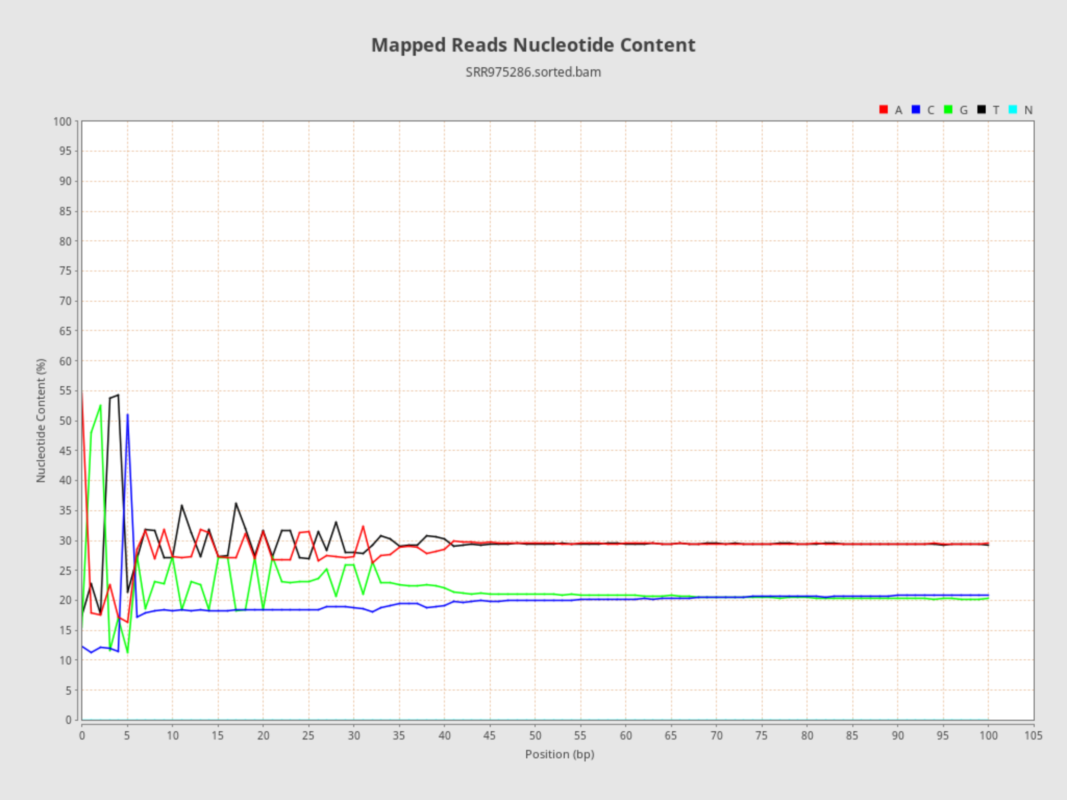
6. Results : Genome Fraction Coverage



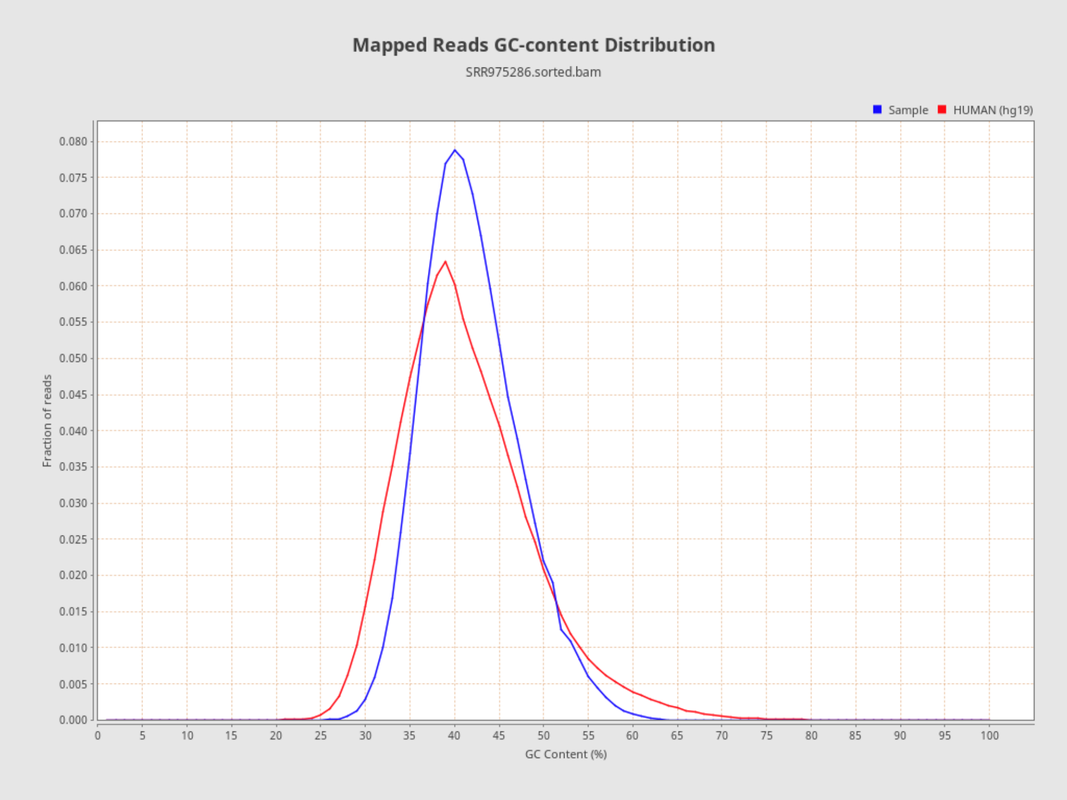
7. Results : Duplication Rate Histogram



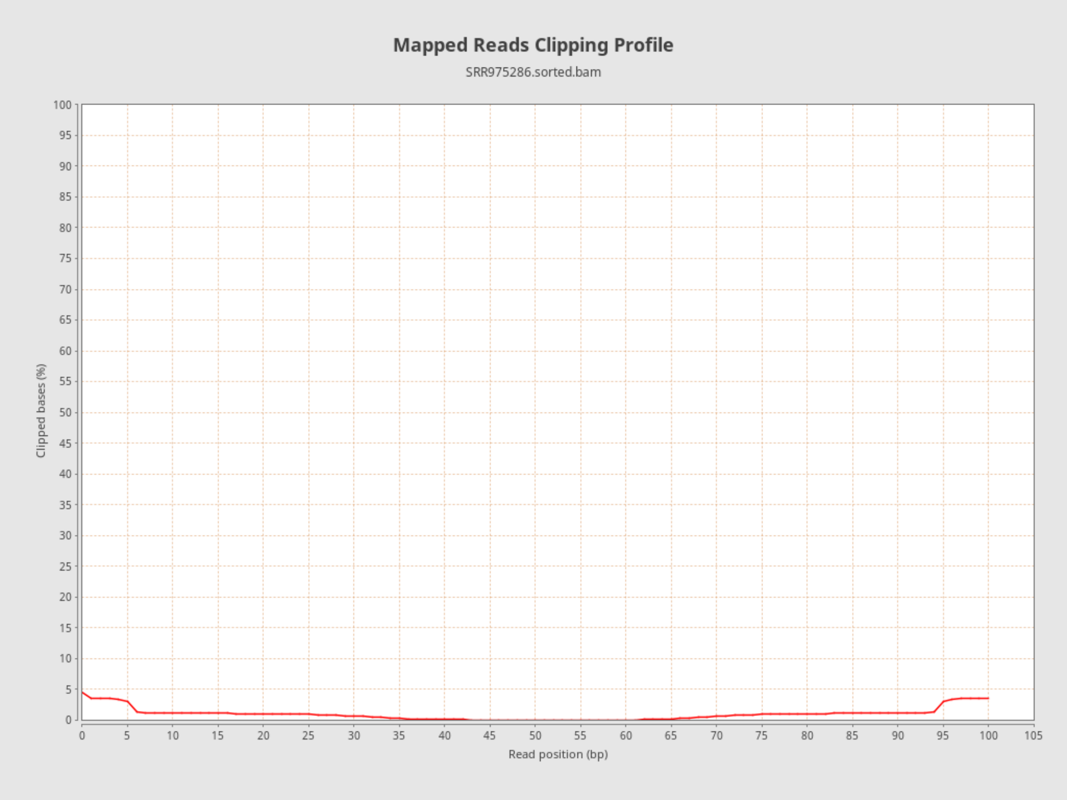
8. Results : Mapped Reads Nucleotide Content



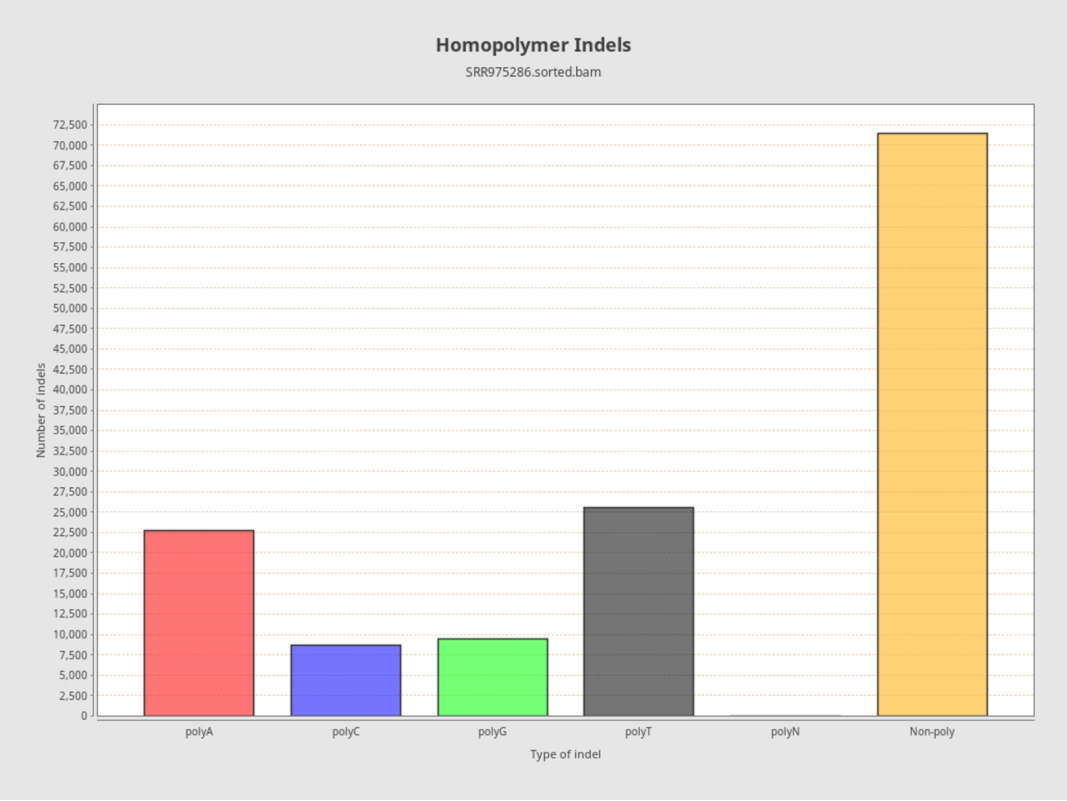
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

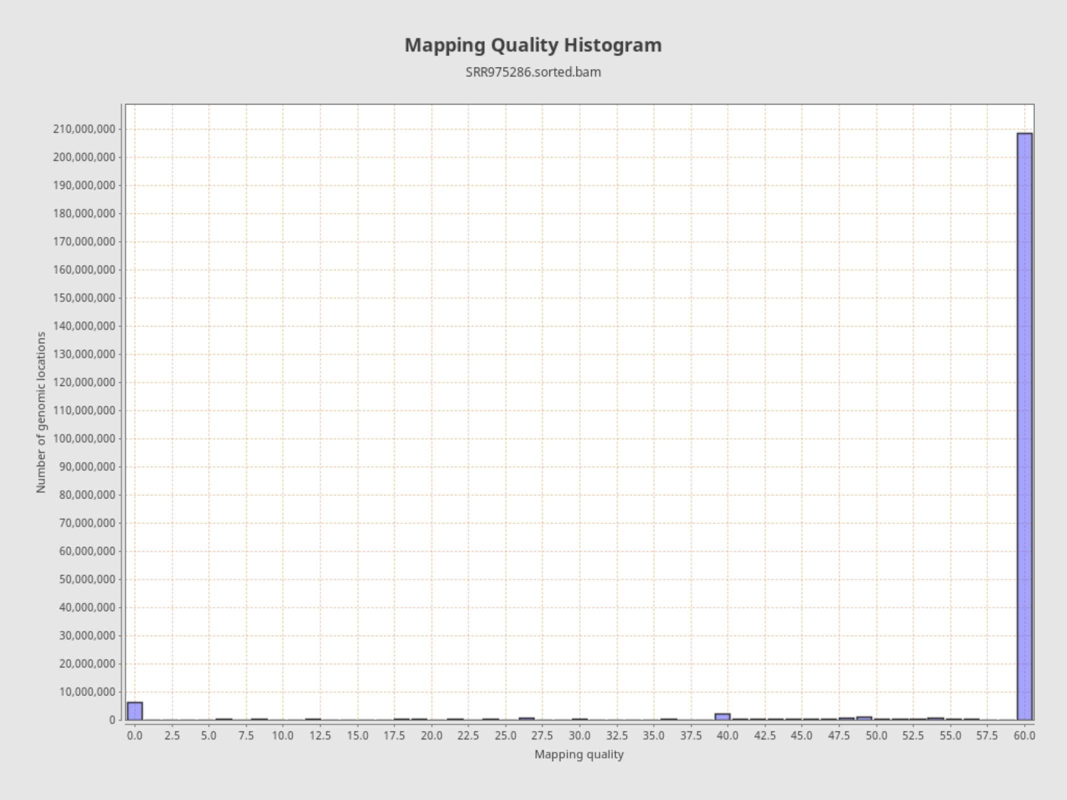


11. Results : Homopolymer Indels

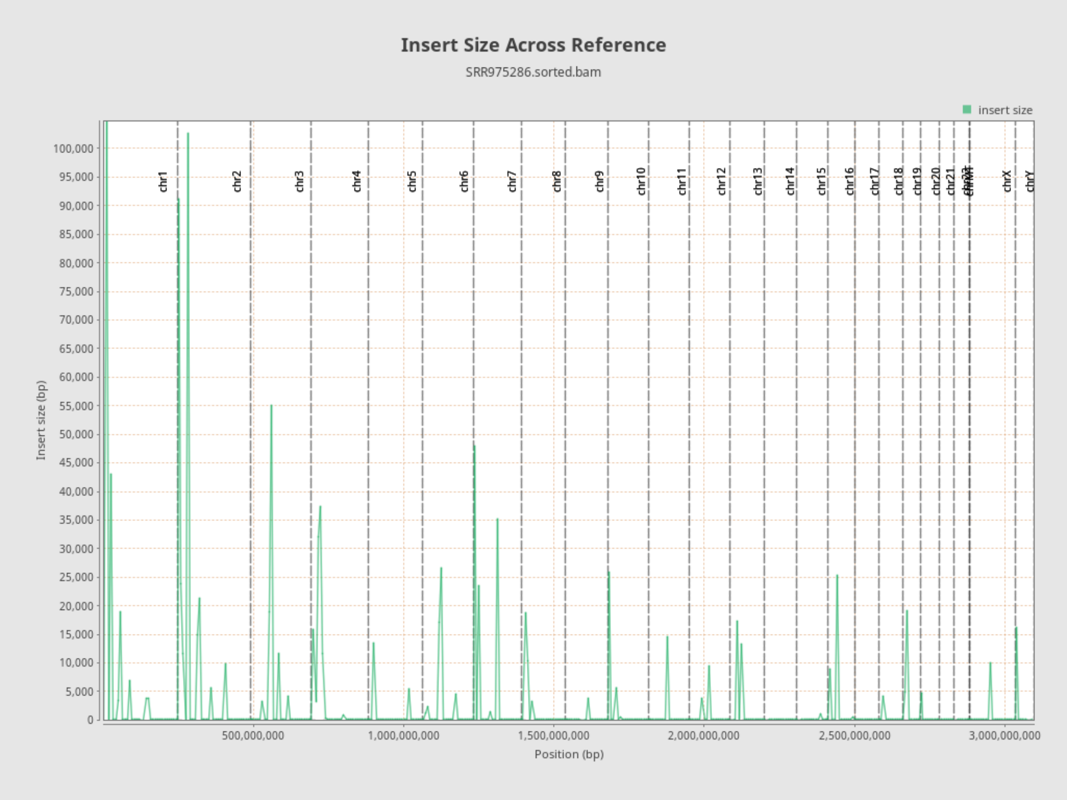


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram