Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 06:03:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975334.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_SRR975334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975334_1.fastq.gz SRR975334_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 06:03:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,126,746
Mapped reads	4,016,423 / 97.33%
Unmapped reads	110,323 / 2.67%
Mapped paired reads	4,016,423 / 97.33%
Mapped reads, first in pair	2,007,206 / 48.64%
Mapped reads, second in pair	2,009,217 / 48.69%
Mapped reads, both in pair	3,995,010 / 96.81%
Mapped reads, singletons	21,413 / 0.52%
Secondary alignments	0
Supplementary alignments	19,296 / 0.47%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	211,941 / 5.14%
Duplication rate	2.61%
Clipped reads	2,498,147 / 60.54%

2.2. ACGT Content

Number/percentage of A's	106,103,959 / 28.9%
Number/percentage of C's	72,596,804 / 19.78%
Number/percentage of T's	109,687,828 / 29.88%
Number/percentage of G's	78,707,839 / 21.44%
Number/percentage of N's	7,277 / 0%

GC Percentage	41.22%

2.3. Coverage

Mean	0.1187
Standard Deviation	1.3539

2.4. Mapping Quality

Mean Mapping Quality	52.79

2.5. Insert size

Mean	79,864.08
Standard Deviation	2,693,411.87
P25/Median/P75	136 / 168 / 212

2.6. Mismatches and indels

General error rate	0.79%
Mismatches	2,777,281
Insertions	55,681
Mapped reads with at least one insertion	1.34%
Deletions	119,380
Mapped reads with at least one deletion	2.91%
Homopolymer indels	46.84%

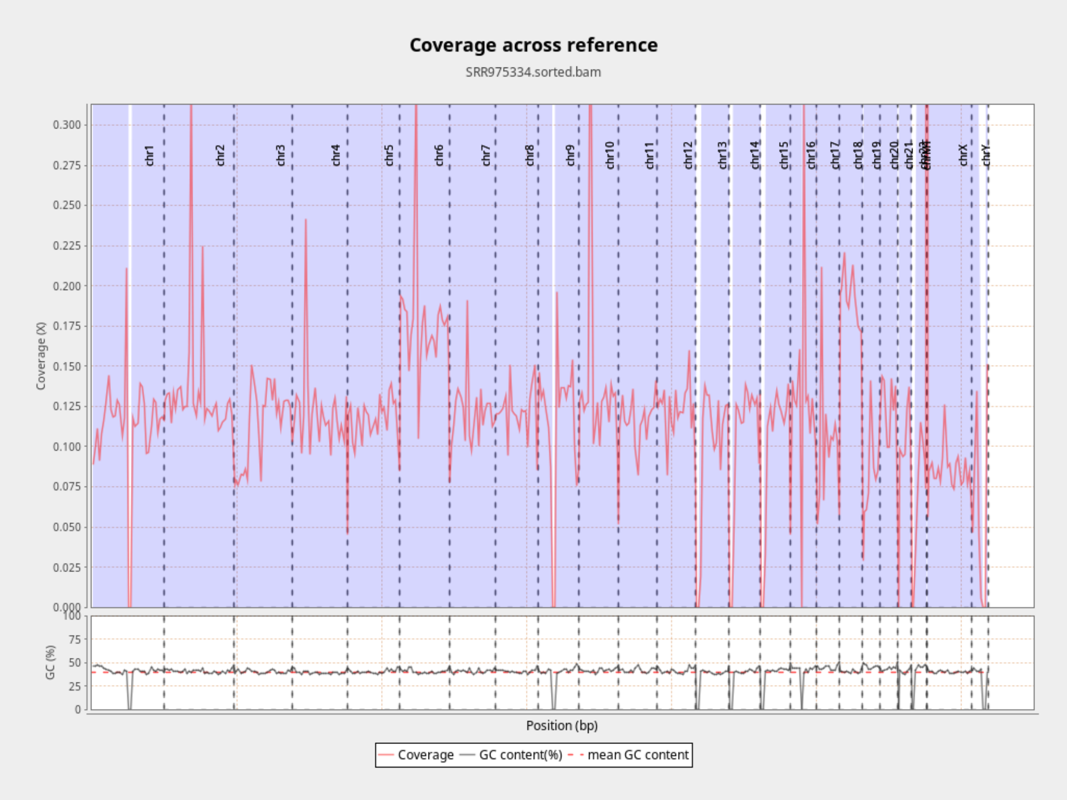
2.7. Chromosome stats

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

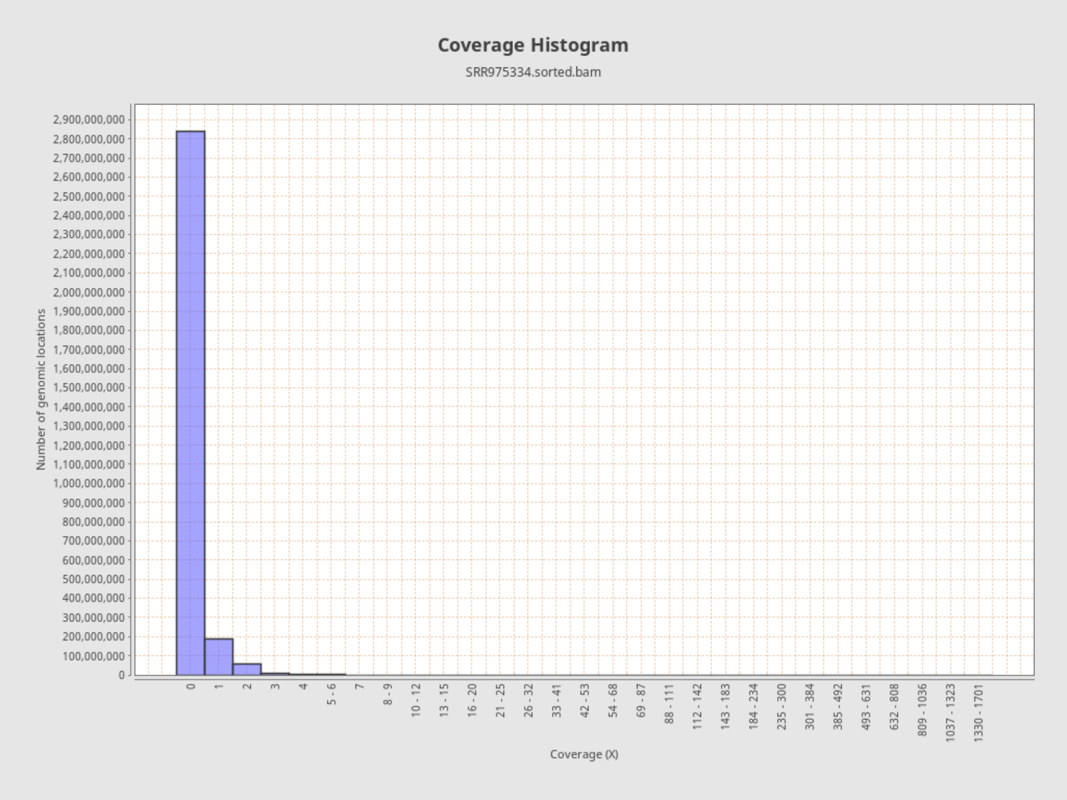
		bases	coverage	deviation
chr1	249250621	27993183	0.1123	1.4547
chr2	243199373	32739116	0.1346	1.6351
chr3	198022430	22723682	0.1148	0.4332
chr4	191154276	23242845	0.1216	0.9233
chr5	180915260	21283763	0.1176	0.4569
chr6	171115067	30423459	0.1778	1.8749
chr7	159138663	19138412	0.1203	1.5482
chr8	146364022	17803376	0.1216	0.5974
chr9	141213431	16166790	0.1145	1.9606
chr10	135534747	19034494	0.1404	2.3684
chr11	135006516	15620409	0.1157	0.9676
chr12	133851895	16534727	0.1235	2.1342
chr13	115169878	11174322	0.097	0.3889
chr14	107349540	11001885	0.1025	0.4462
chr15	102531392	10163723	0.0991	0.3944
chr16	90354753	11664246	0.1291	1.5854
chr17	81195210	8274706	0.1019	1.8219
chr18	78077248	15059180	0.1929	2.1593
chr19	59128983	4810389	0.0814	0.8625
chr20	63025520	7699576	0.1222	0.4889
chr21	48129895	4639938	0.0964	0.5764
chr22	51304566	3470132	0.0676	0.3558
chrMT	16571	89056	5.3742	4.4114
chrX	155270560	13168419	0.0848	0.5659

chrY	59373566	3396520	0.0572	1.5072

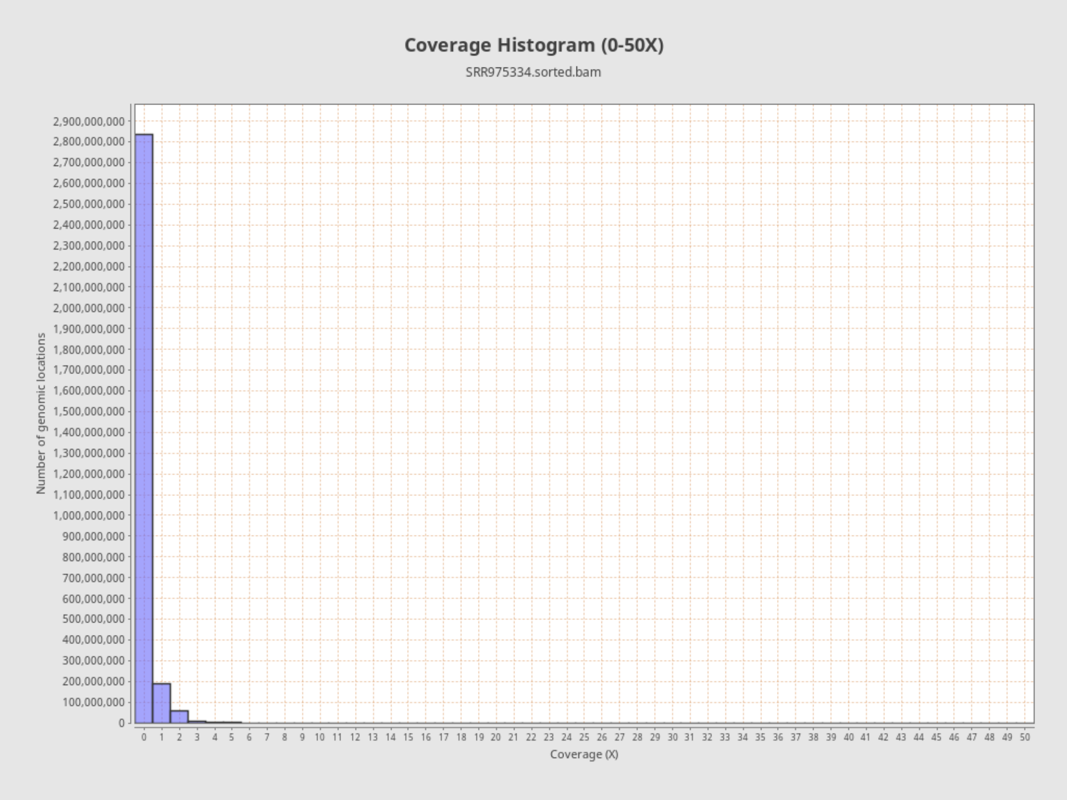
3. Results : Coverage across reference



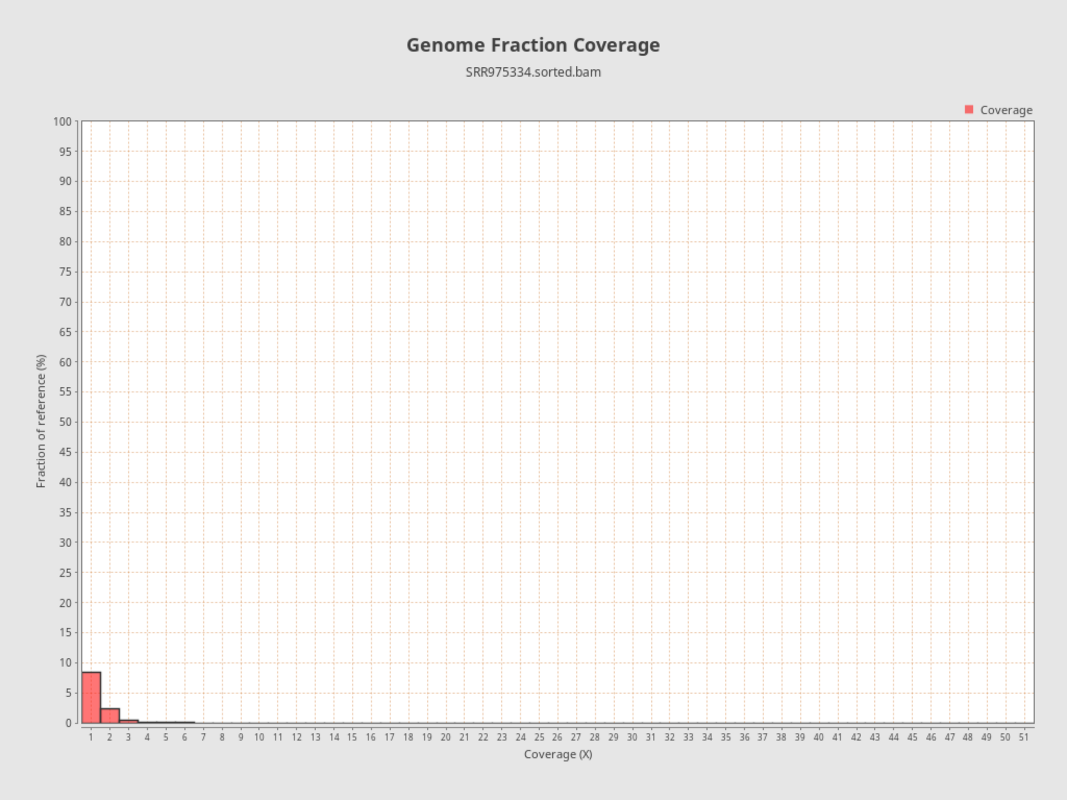
4. Results : Coverage Histogram



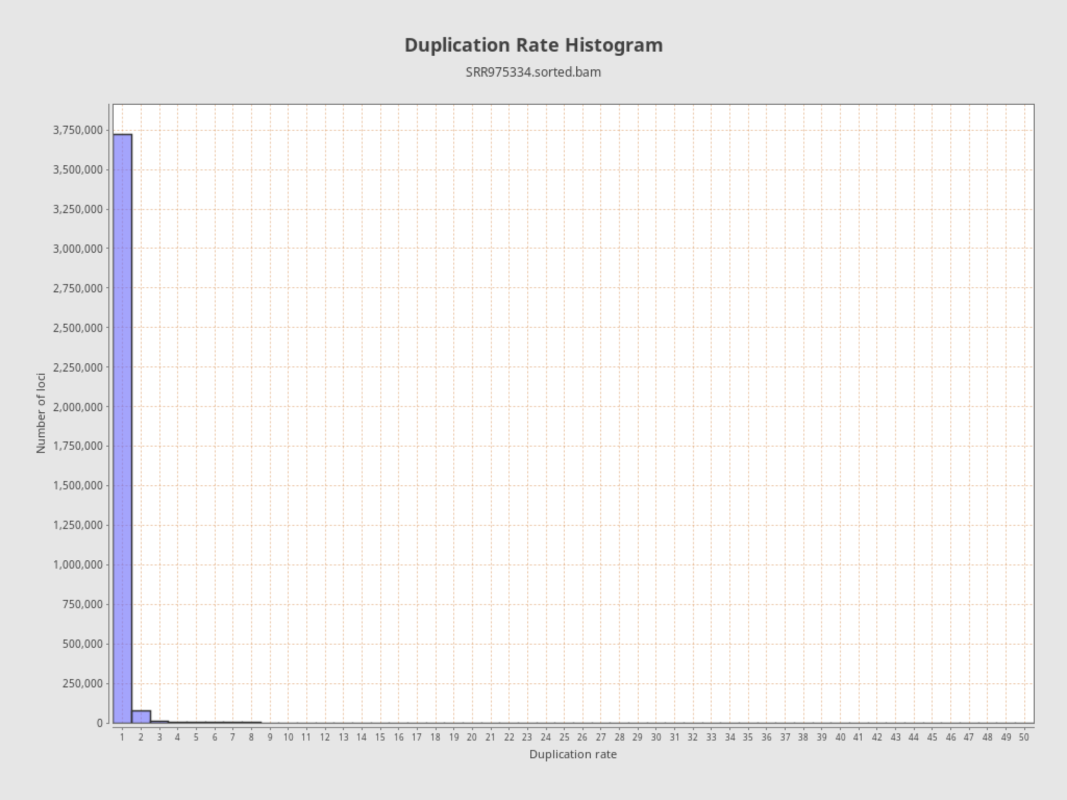
5. Results : Coverage Histogram (0-50X)



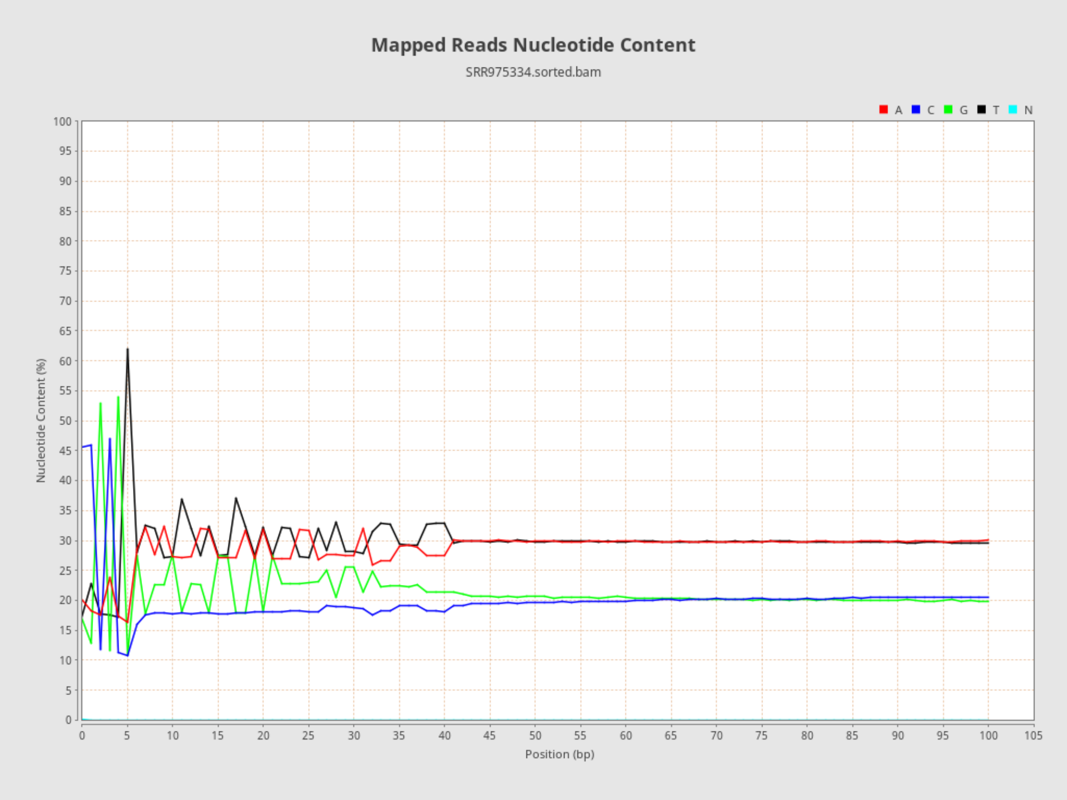
6. Results : Genome Fraction Coverage



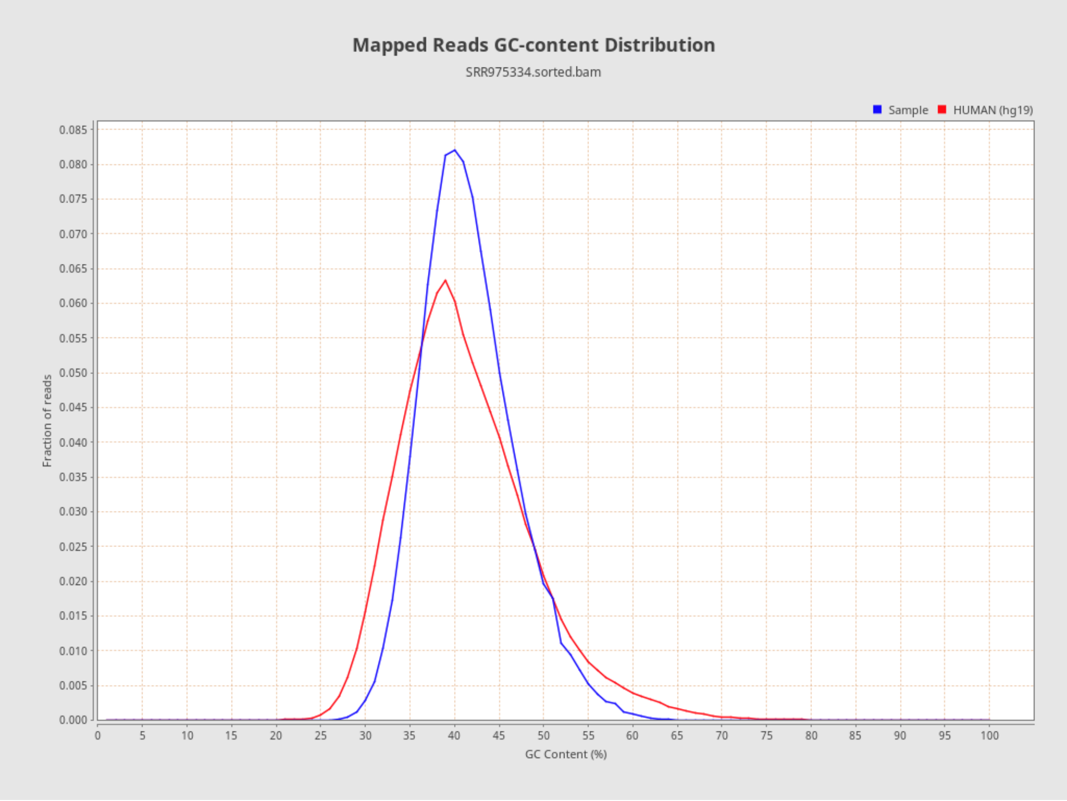
7. Results : Duplication Rate Histogram



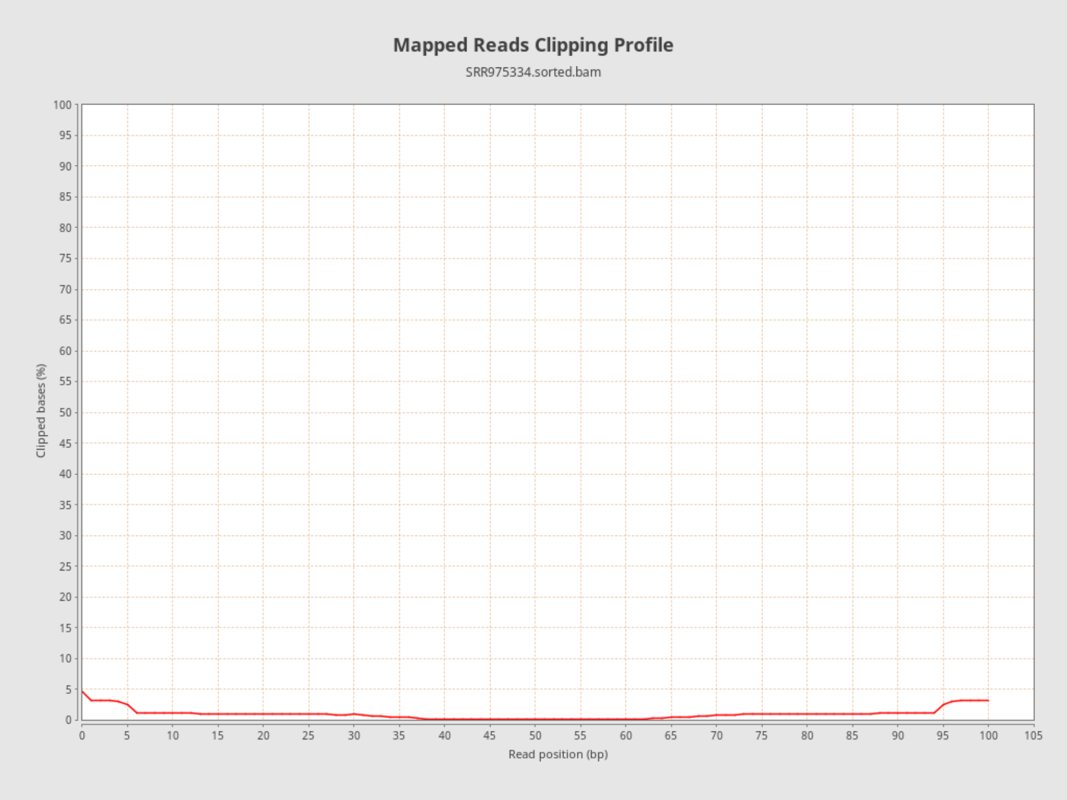
8. Results : Mapped Reads Nucleotide Content



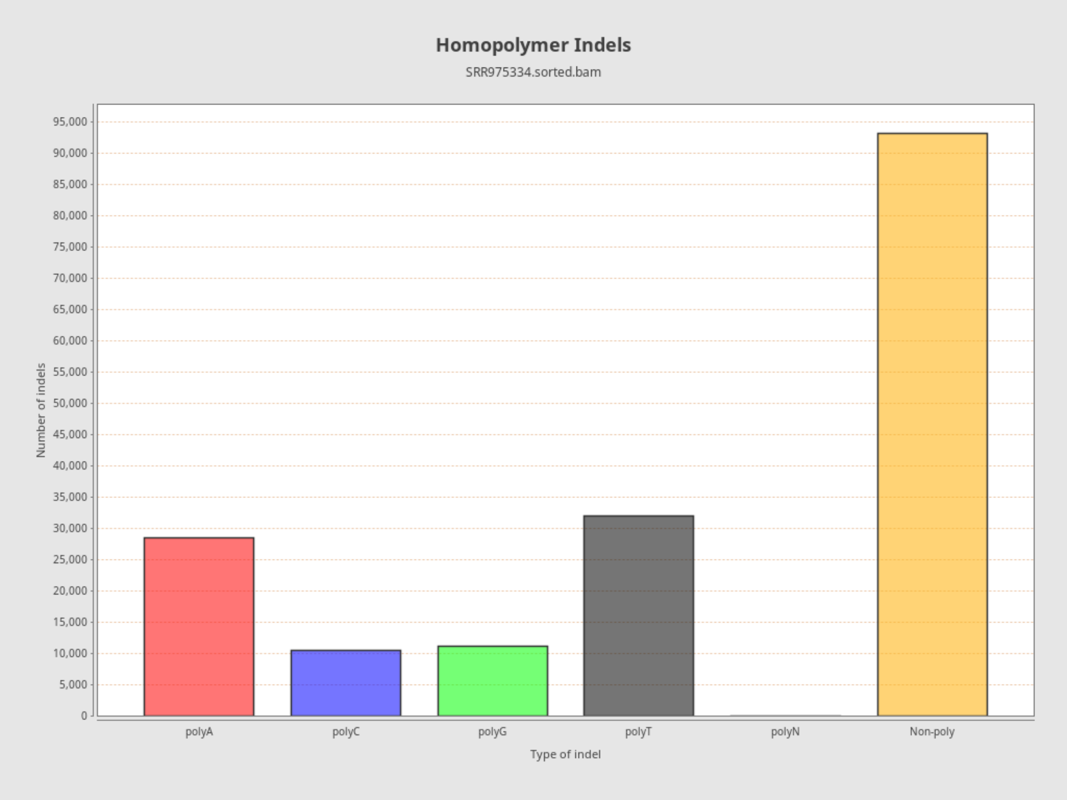
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

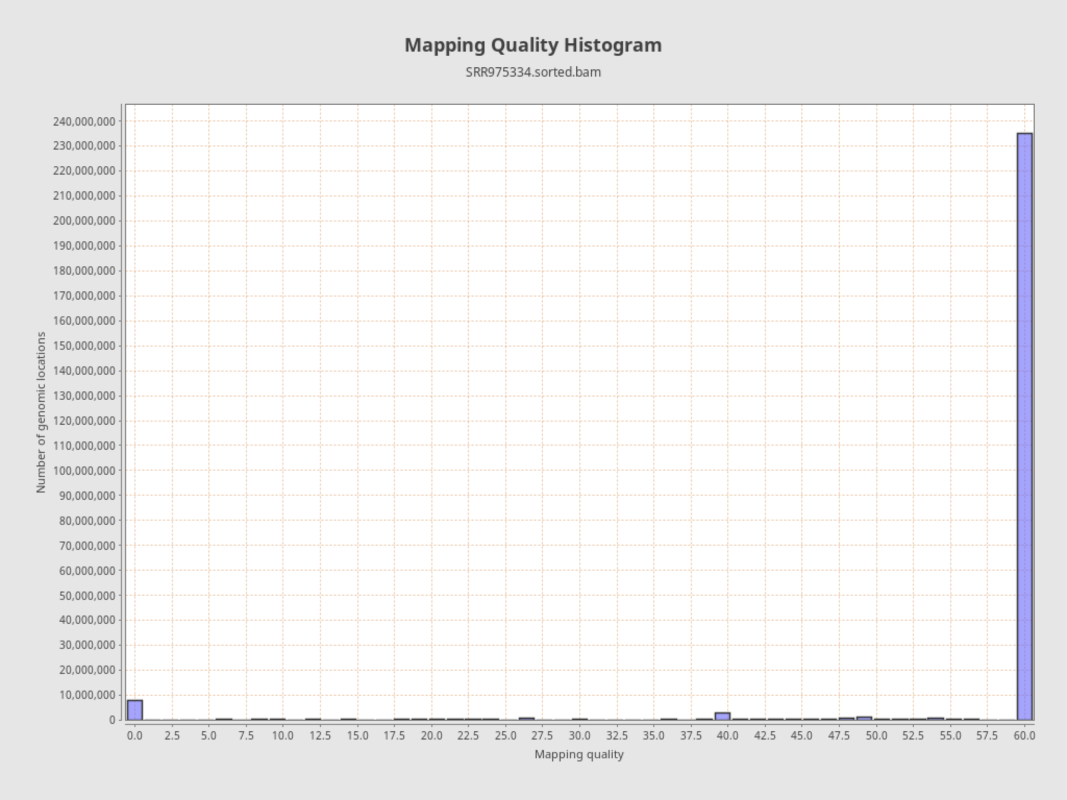


11. Results : Homopolymer Indels

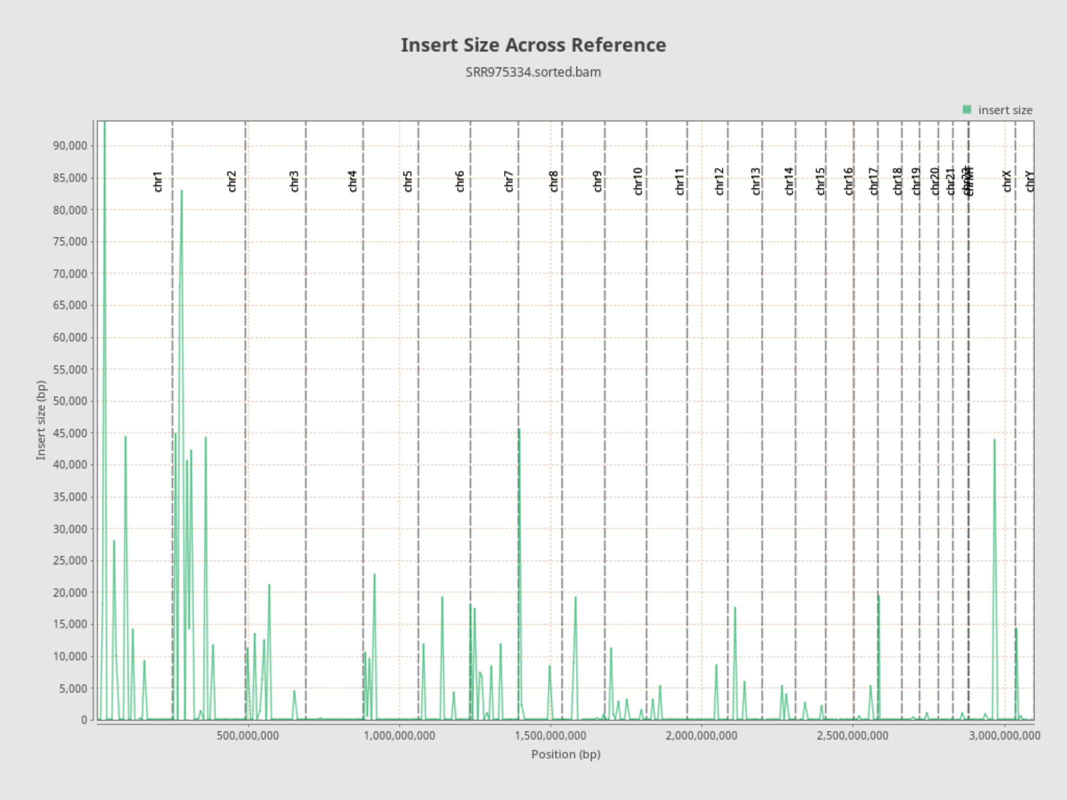


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram