Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 16:50:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975263.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_SRR975263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975263_1.fastq.gz SRR975263_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 16:50:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,540,500
Mapped reads	6,342,761 / 96.98%
Unmapped reads	197,739 / 3.02%
Mapped paired reads	6,342,761 / 96.98%
Mapped reads, first in pair	3,196,026 / 48.87%
Mapped reads, second in pair	3,146,735 / 48.11%
Mapped reads, both in pair	6,271,488 / 95.89%
Mapped reads, singletons	71,273 / 1.09%
Secondary alignments	0
Supplementary alignments	91,940 / 1.41%
Read min/max/mean length	30 / 151 / 151.68
Duplicated reads (estimated)	832,332 / 12.73%
Duplication rate	9.73%
Clipped reads	2,855,255 / 43.65%

2.2. ACGT Content

Number/percentage of A's	247,087,877 / 28.33%
Number/percentage of C's	179,973,164 / 20.64%
Number/percentage of T's	250,110,165 / 28.68%
Number/percentage of G's	194,857,471 / 22.34%
Number/percentage of N's	75,611 / 0.01%

GC Percentage	42.98%

2.3. Coverage

Mean	0.2819
Standard Deviation	2.6889

2.4. Mapping Quality

Mean Mapping Quality	53.55

2.5. Insert size

Mean	63,946.37
Standard Deviation	2,422,728.24
P25/Median/P75	158 / 200 / 259

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	10,145,351
Insertions	170,369
Mapped reads with at least one insertion	2.48%
Deletions	348,073
Mapped reads with at least one deletion	5.24%
Homopolymer indels	46.26%

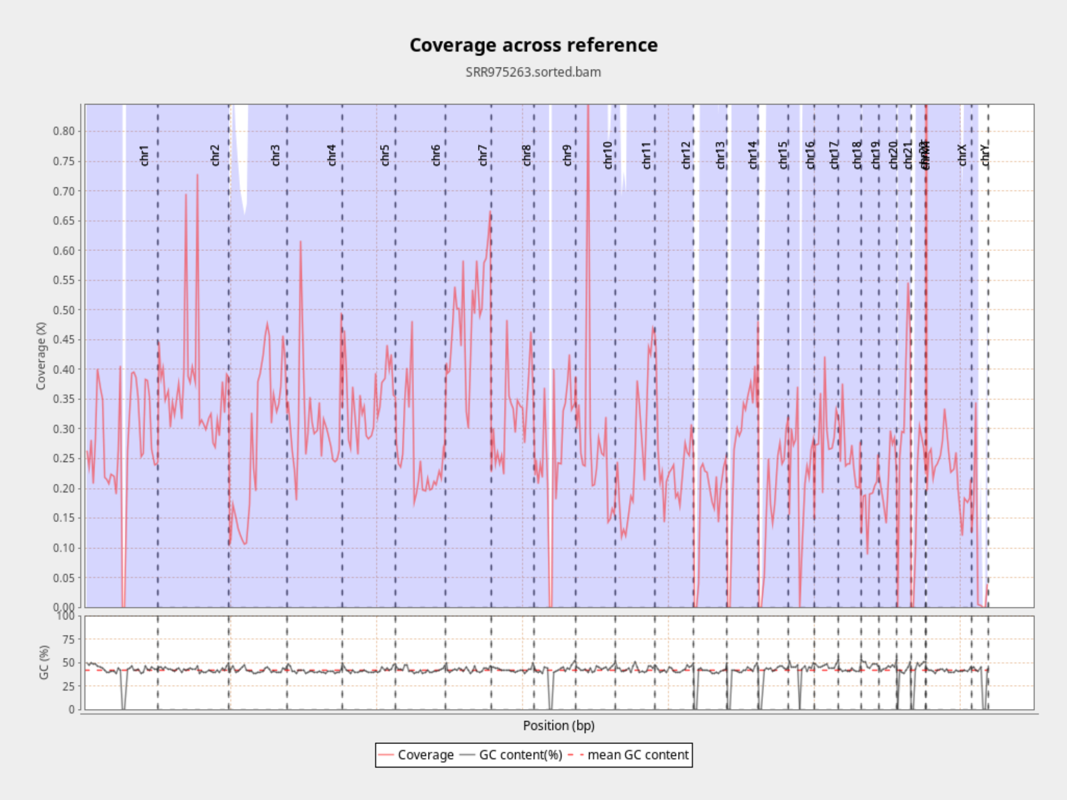
2.7. Chromosome stats

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

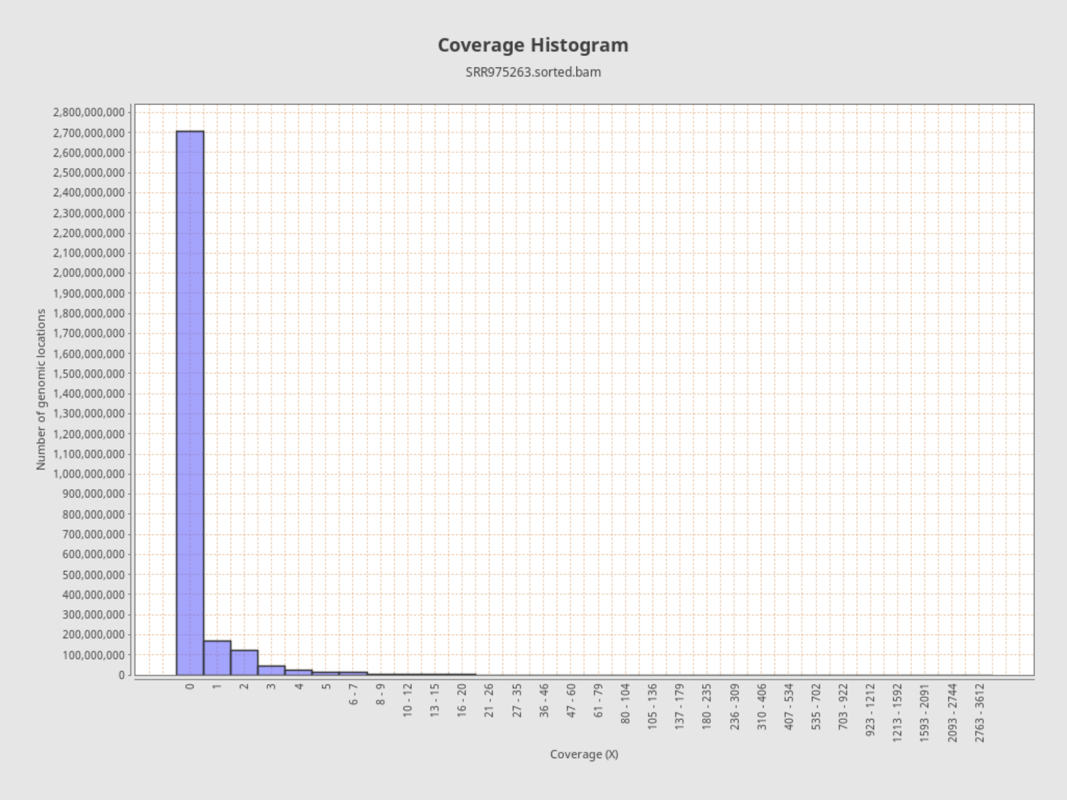
		bases	**coverage**	**deviation**
chr1	249250621	68780390	0.2759	2.7508
chr2	243199373	89787111	0.3692	4.1125
chr3	198022430	55923019	0.2824	0.9435
chr4	191154276	58936012	0.3083	2.5121
chr5	180915260	62825642	0.3473	1.0748
chr6	171115067	43041618	0.2515	2.0092
chr7	159138663	78595541	0.4939	4.6343
chr8	146364022	47590360	0.3252	1.466
chr9	141213431	37039827	0.2623	4.172
chr10	135534747	37448835	0.2763	4.9919
chr11	135006516	35078942	0.2598	1.3068
chr12	133851895	32021245	0.2392	0.8622
chr13	115169878	20197035	0.1754	0.7176
chr14	107349540	29779349	0.2774	1.0188
chr15	102531392	18529764	0.1807	0.7318
chr16	90354753	20382585	0.2256	2.5445
chr17	81195210	24230057	0.2984	2.2482
chr18	78077248	19876148	0.2546	3.897
chr19	59128983	10676799	0.1806	1.5698
chr20	63025520	14287645	0.2267	1.1296
chr21	48129895	16259875	0.3378	1.7498
chr22	51304566	9673989	0.1886	0.8384
chrMT	16571	1132191	68.3236	34.3028
chrX	155270560	35659331	0.2297	1.0356

chrY	59373566	5047551	0.085	4.3182

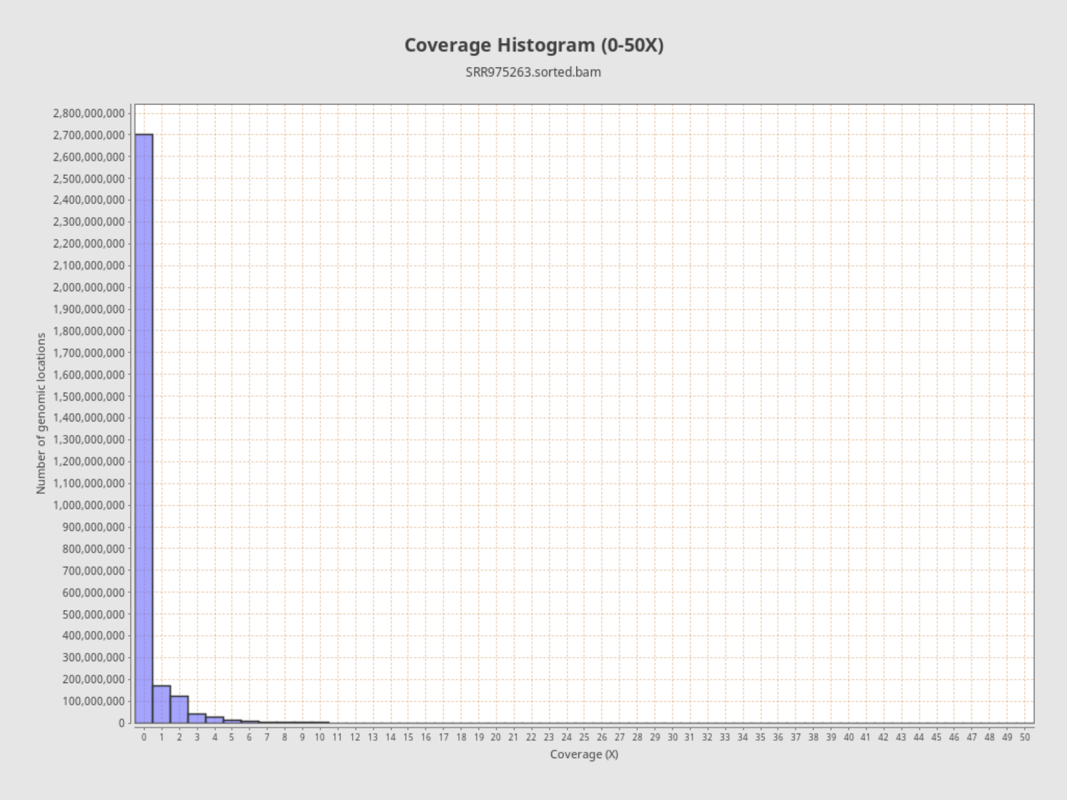
3. Results : Coverage across reference



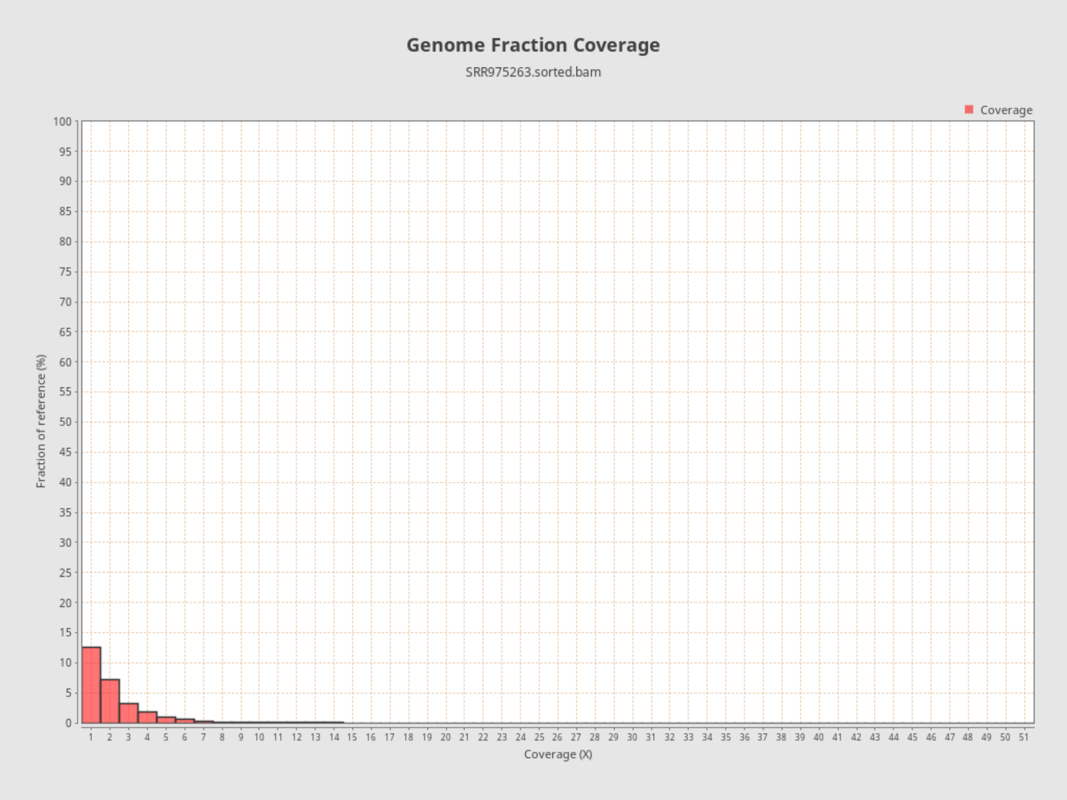
4. Results : Coverage Histogram



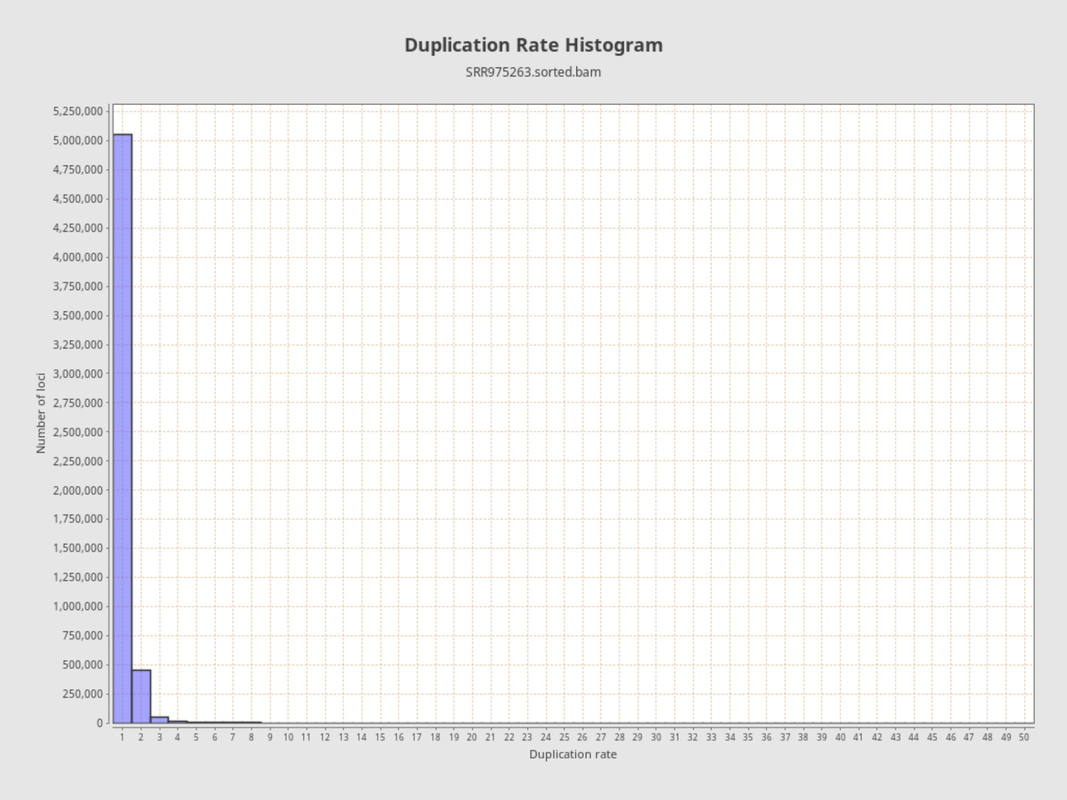
5. Results : Coverage Histogram (0-50X)



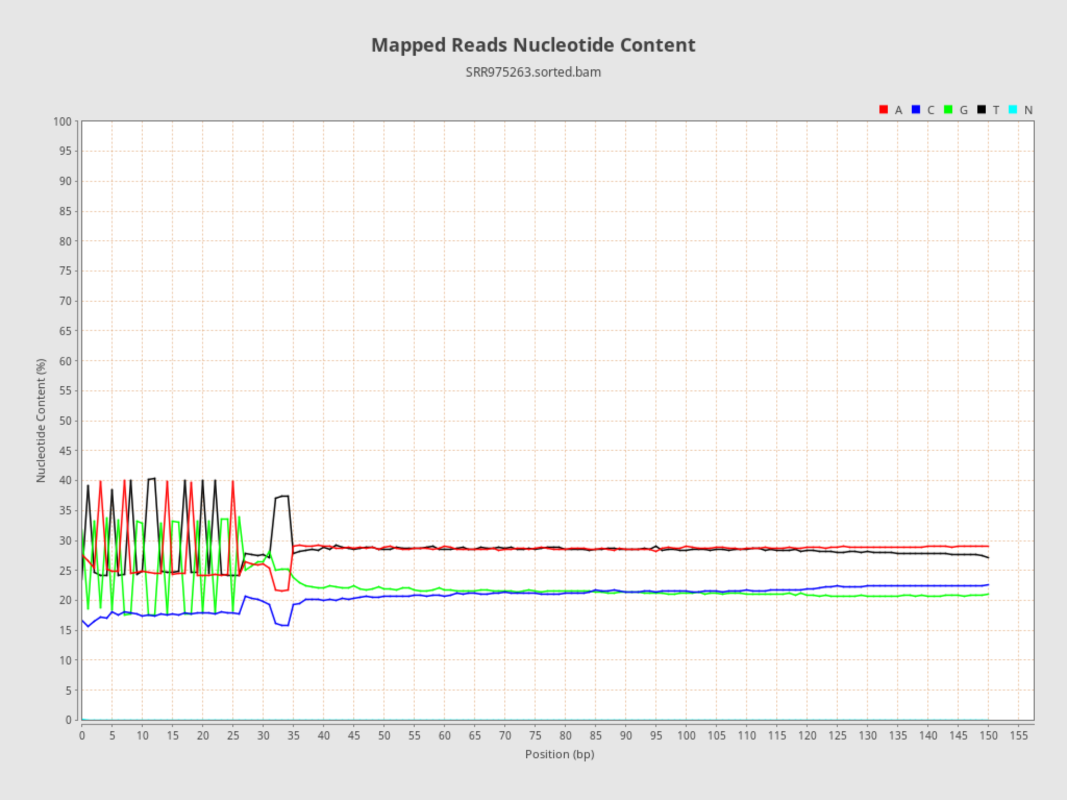
6. Results : Genome Fraction Coverage



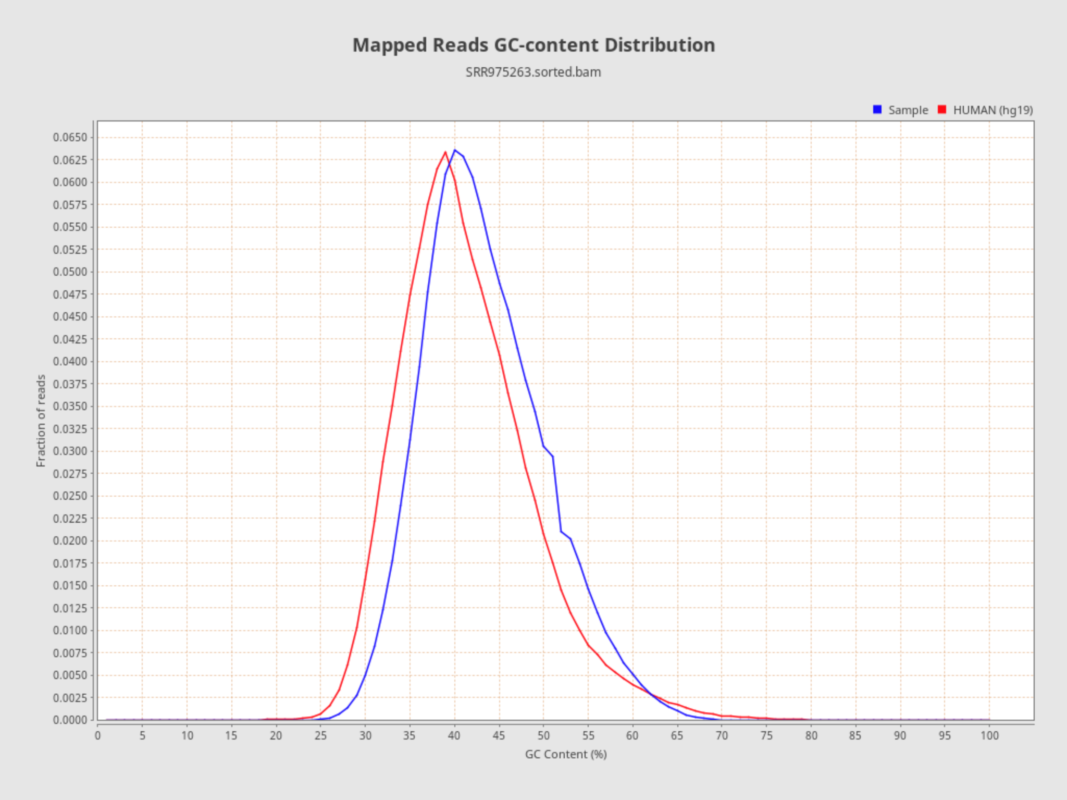
7. Results : Duplication Rate Histogram



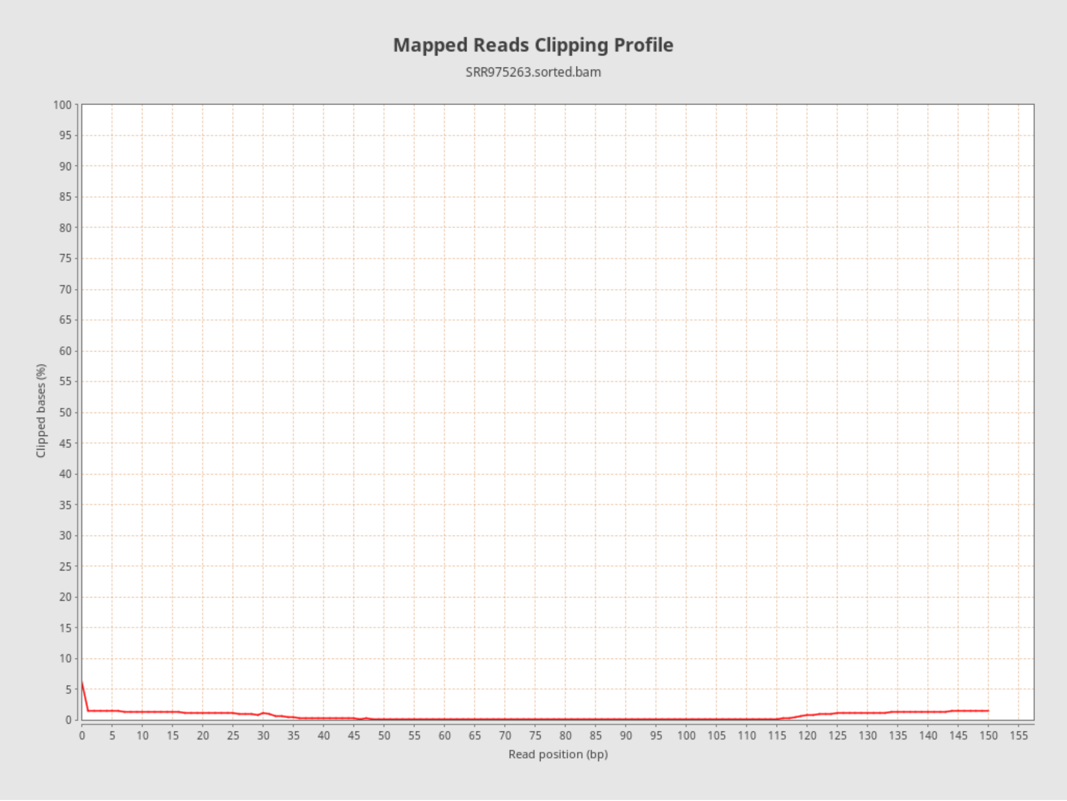
8. Results : Mapped Reads Nucleotide Content



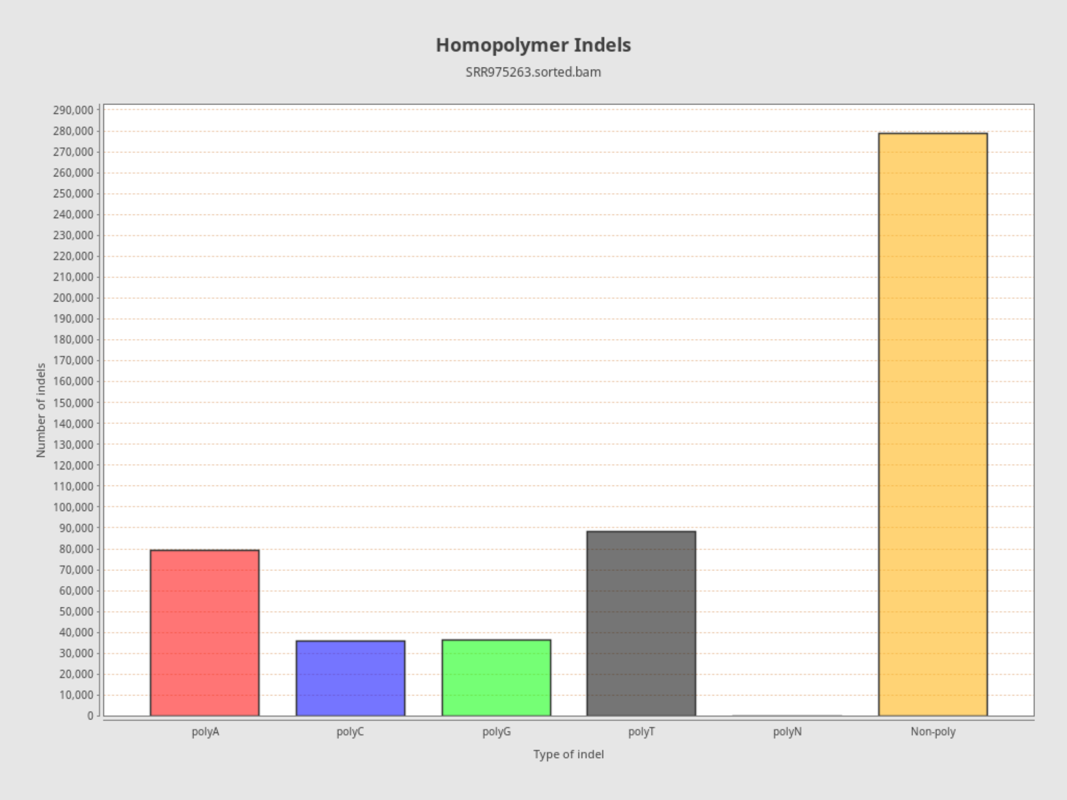
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

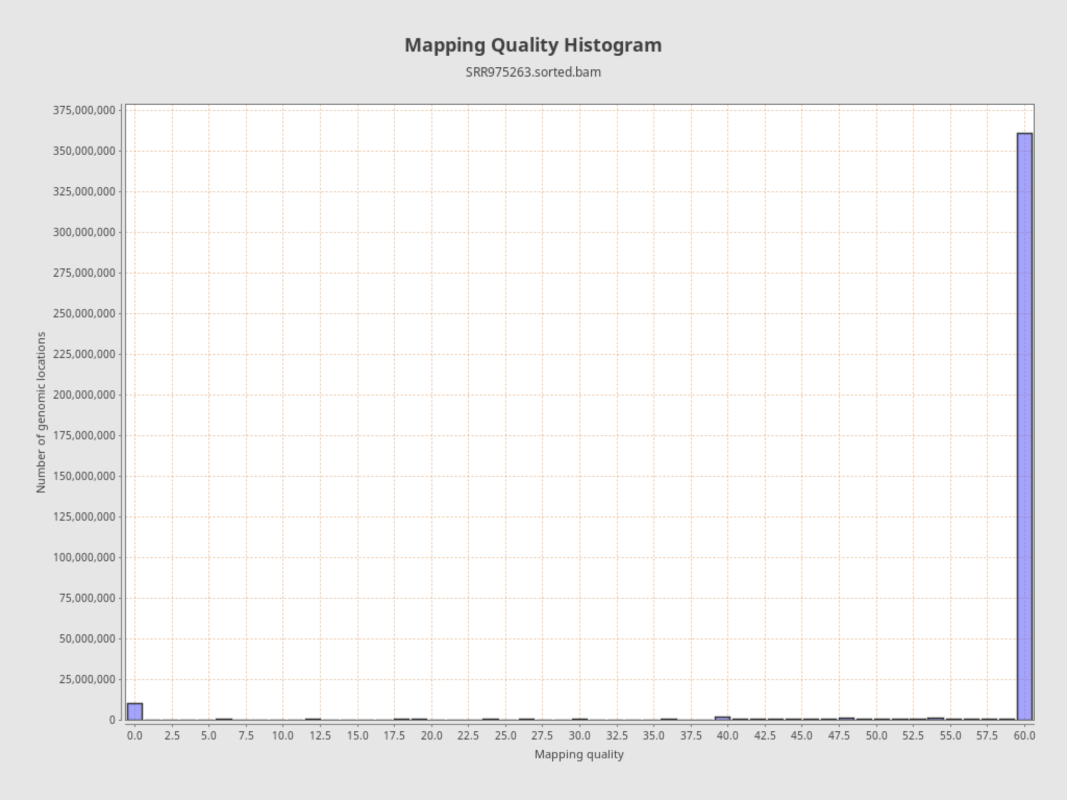


11. Results : Homopolymer Indels

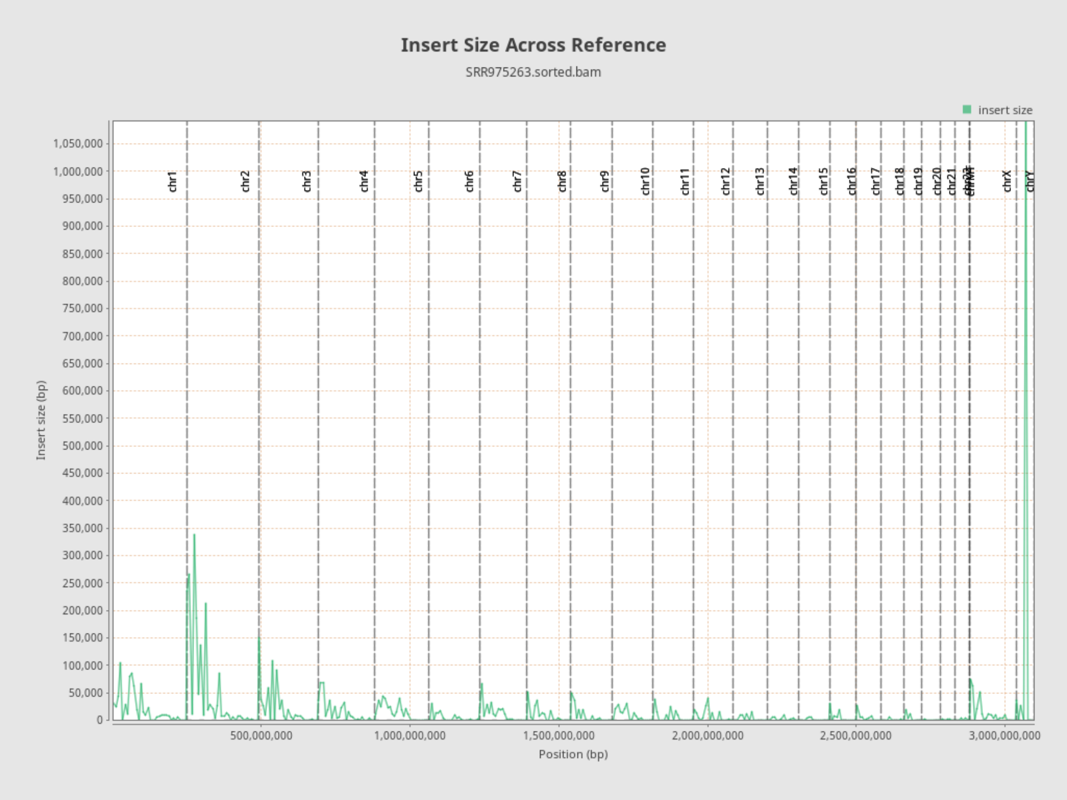


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram