Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 15:31:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975249.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_SRR975249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975249_1.fastq.gz SRR975249_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 15:31:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975249.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,368,800
Mapped reads	4,335,699 / 99.24%
Unmapped reads	33,101 / 0.76%
Mapped paired reads	4,335,699 / 99.24%
Mapped reads, first in pair	2,167,521 / 49.61%
Mapped reads, second in pair	2,168,178 / 49.63%
Mapped reads, both in pair	4,325,192 / 99%
Mapped reads, singletons	10,507 / 0.24%
Secondary alignments	0
Supplementary alignments	10,118 / 0.23%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	181,995 / 4.17%
Duplication rate	2.32%
Clipped reads	2,588,661 / 59.25%

2.2. ACGT Content

Number/percentage of A's	117,832,145 / 29.5%
Number/percentage of C's	76,968,131 / 19.27%
Number/percentage of T's	119,080,451 / 29.82%
Number/percentage of G's	85,492,346 / 21.41%
Number/percentage of N's	5,953 / 0%

GC Percentage	40.68%

2.3. Coverage

Mean	0.1291
Standard Deviation	1.4381

2.4. Mapping Quality

Mean Mapping Quality	52.92

2.5. Insert size

Mean	55,176.95
Standard Deviation	2,252,456.03
P25/Median/P75	142 / 177 / 226

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	2,836,413
Insertions	64,966
Mapped reads with at least one insertion	1.48%
Deletions	117,095
Mapped reads with at least one deletion	2.65%
Homopolymer indels	45.34%

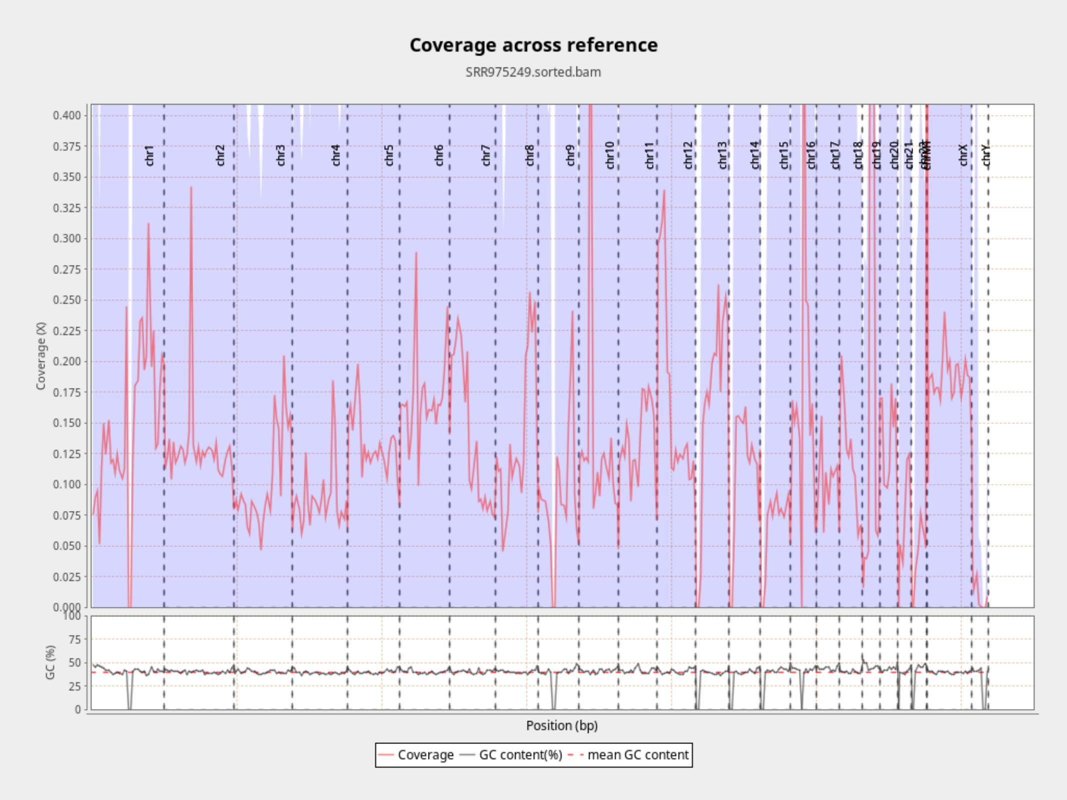
2.7. Chromosome stats

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

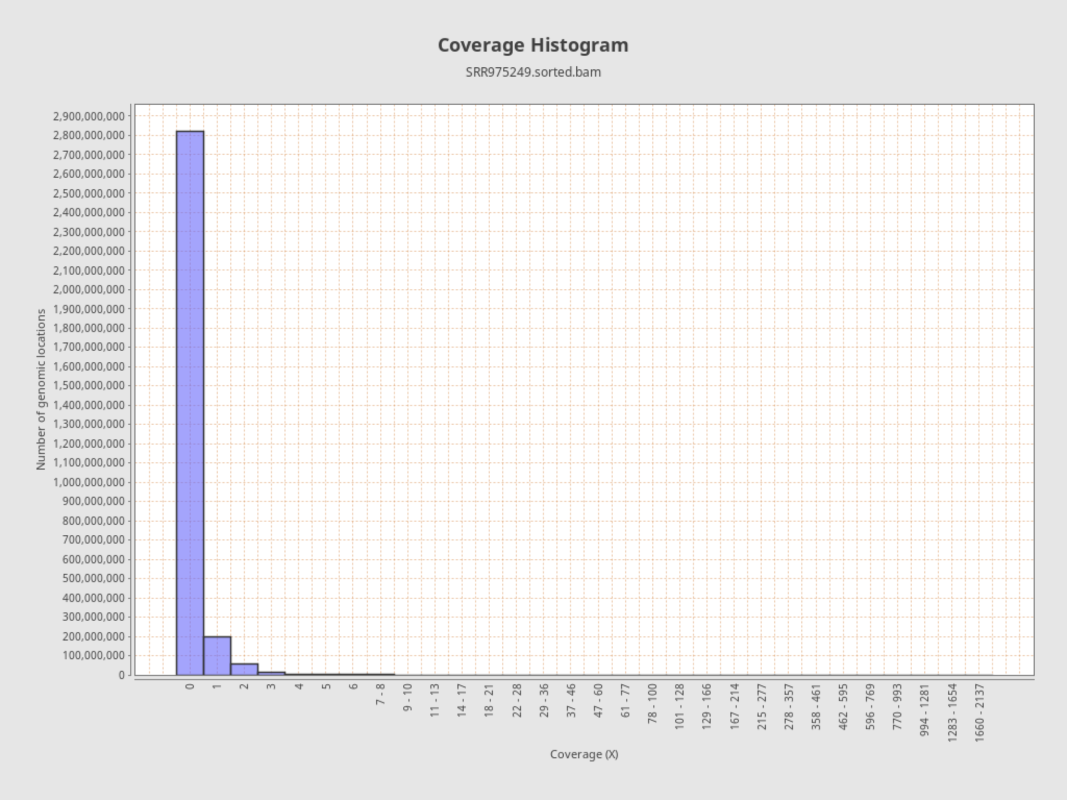
		bases	coverage	deviation
chr1	249250621	36116513	0.1449	2.1665
chr2	243199373	31491565	0.1295	1.2894
chr3	198022430	20404158	0.103	0.456
chr4	191154276	17058950	0.0892	0.5419
chr5	180915260	24183798	0.1337	0.4585
chr6	171115067	29152228	0.1704	1.4303
chr7	159138663	21998997	0.1382	1.7126
chr8	146364022	20113243	0.1374	0.5587
chr9	141213431	13174985	0.0933	1.0707
chr10	135534747	18562587	0.137	4.28
chr11	135006516	18245689	0.1351	0.8702
chr12	133851895	22769902	0.1701	0.5398
chr13	115169878	19128889	0.1661	0.529
chr14	107349540	11843250	0.1103	0.4325
chr15	102531392	6705358	0.0654	0.3149
chr16	90354753	16168696	0.1789	2.4549
chr17	81195210	8381533	0.1032	1.1119
chr18	78077248	9476914	0.1214	1.4012
chr19	59128983	10924593	0.1848	1.095
chr20	63025520	8693333	0.1379	0.4787
chr21	48129895	3524136	0.0732	0.3573
chr22	51304566	2234438	0.0436	0.2593
chrMT	16571	16781	1.0127	1.3168
chrX	155270560	28632883	0.1844	0.7194

chrY	59373566	562212	0.0095	0.2511

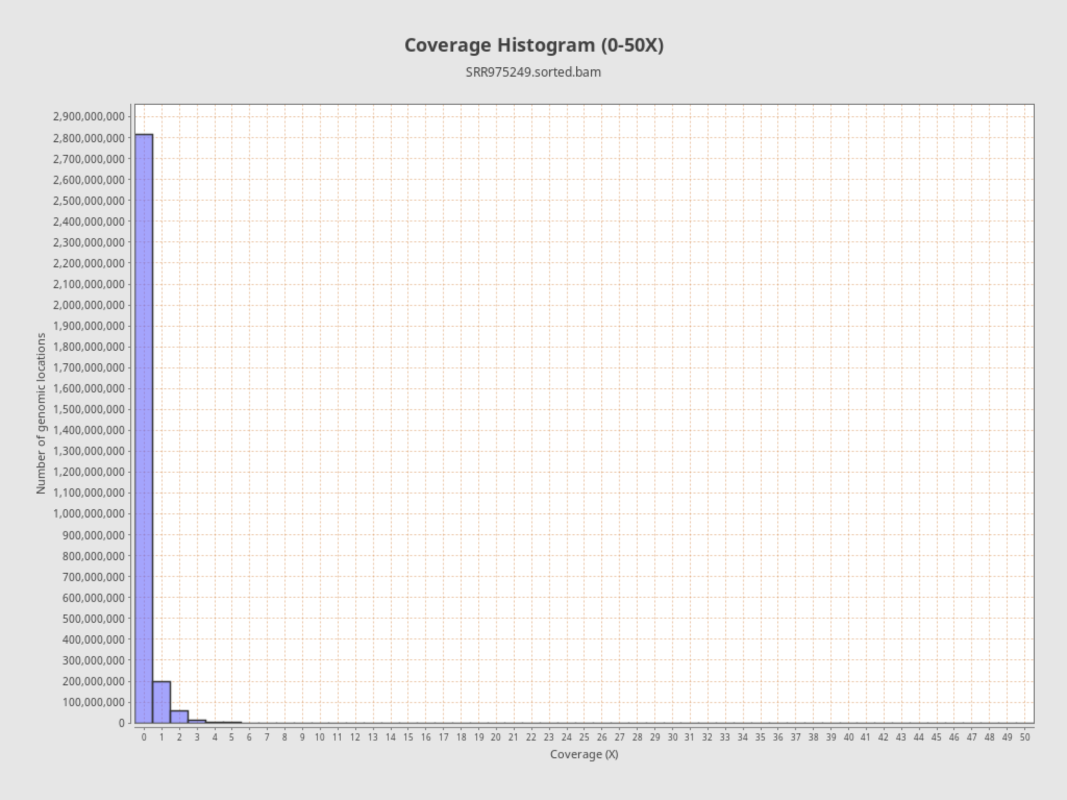
3. Results : Coverage across reference



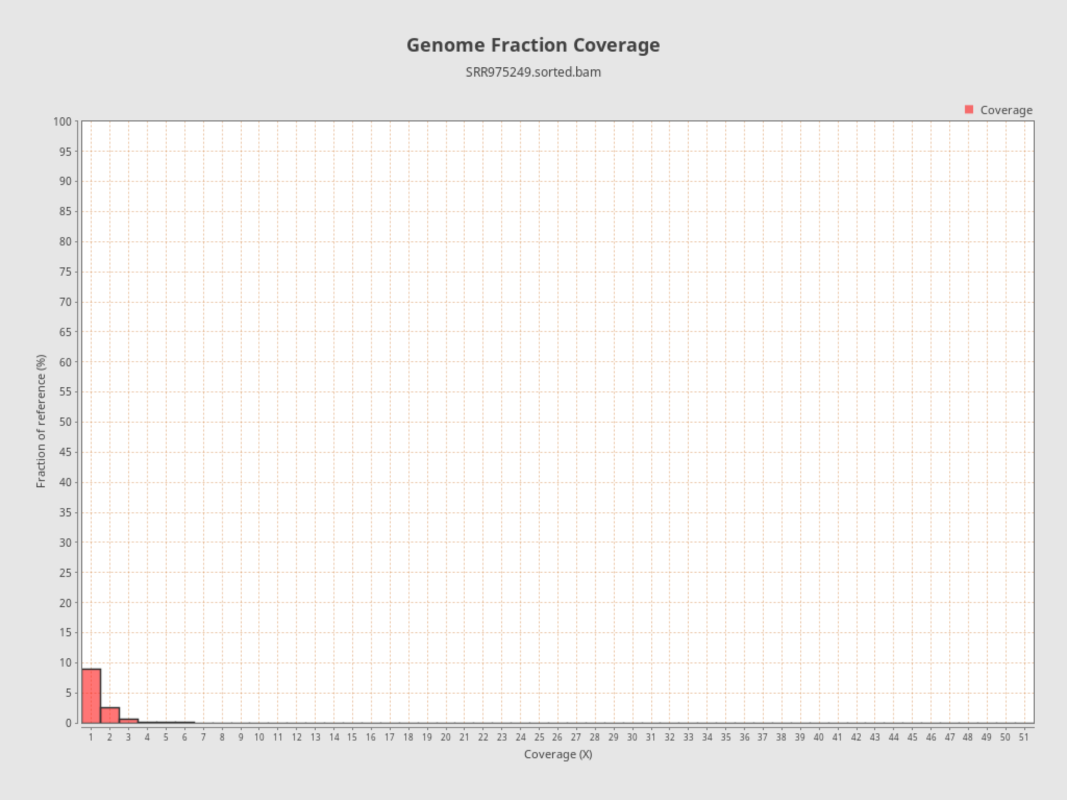
4. Results : Coverage Histogram



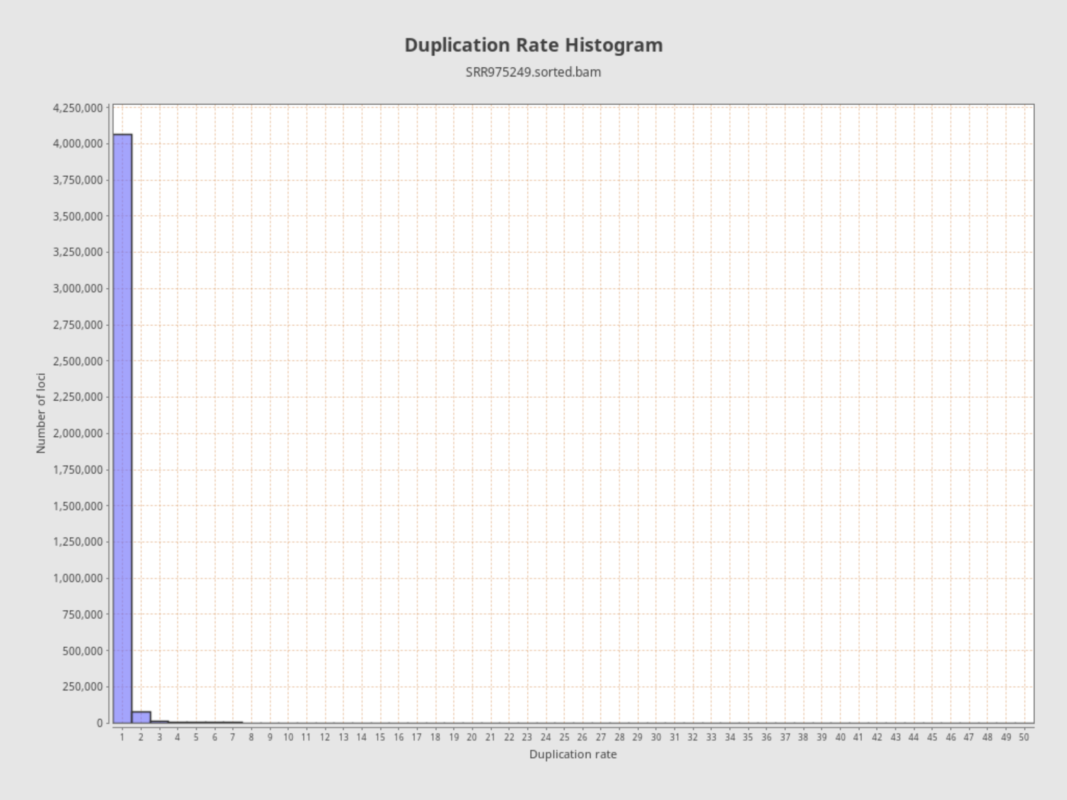
5. Results : Coverage Histogram (0-50X)



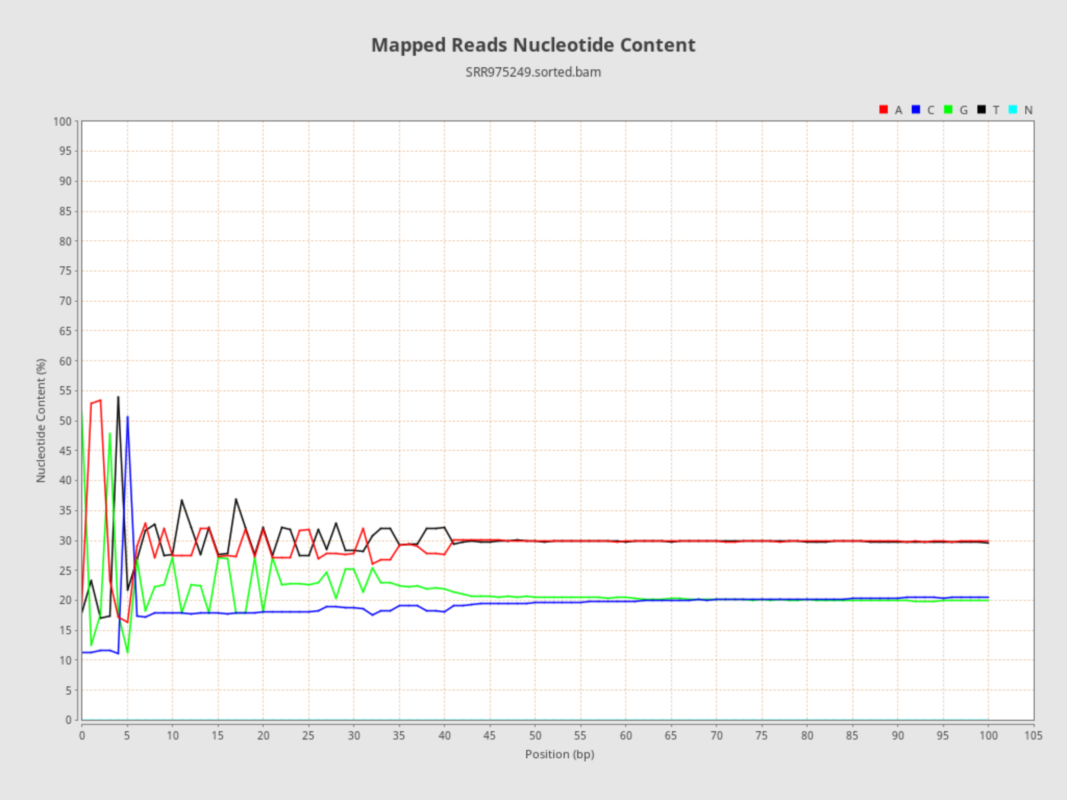
6. Results : Genome Fraction Coverage



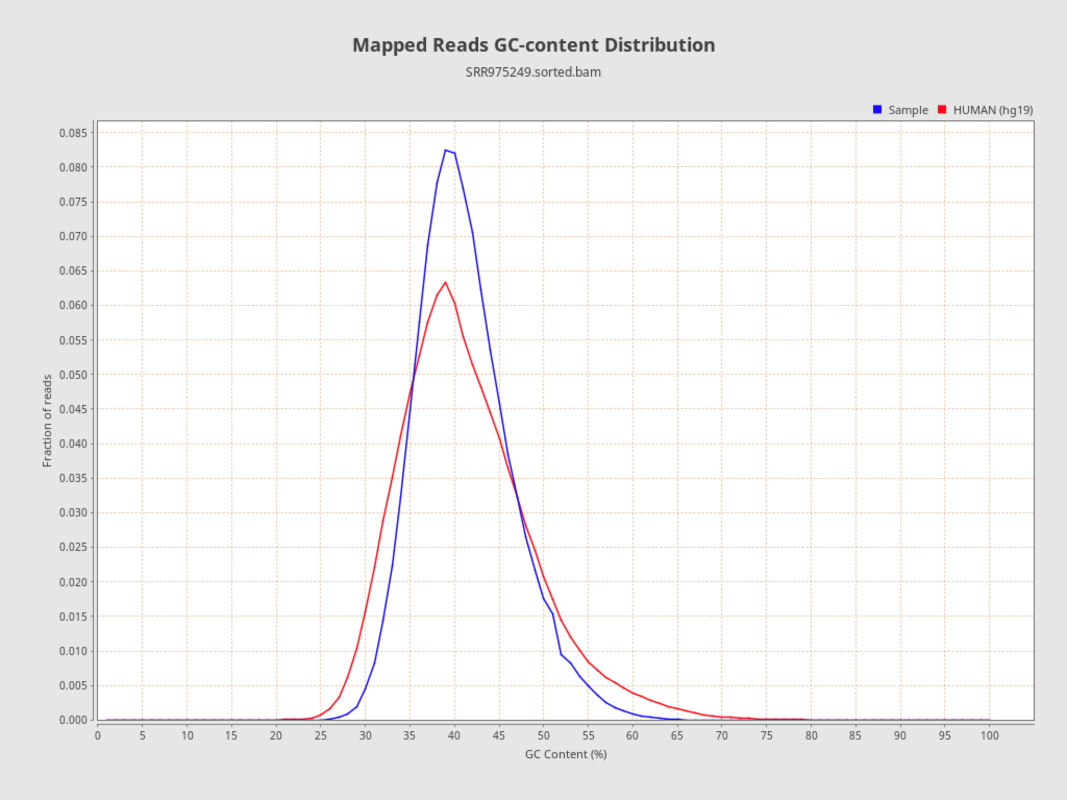
7. Results : Duplication Rate Histogram



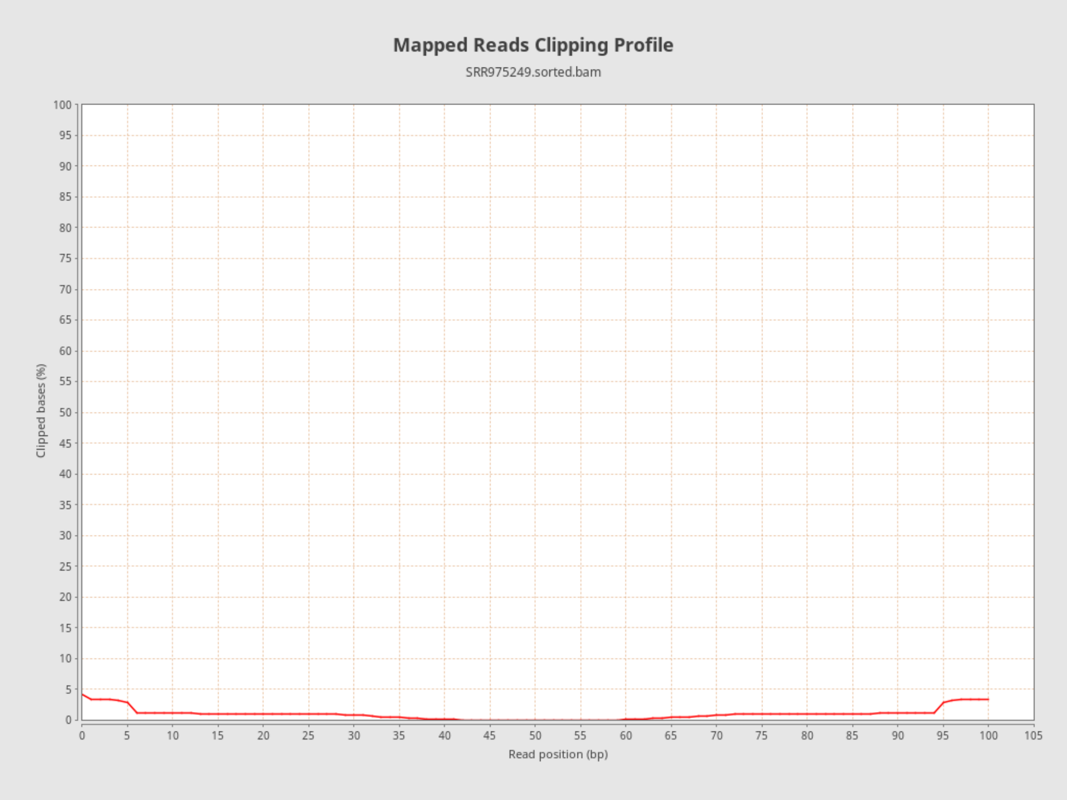
8. Results : Mapped Reads Nucleotide Content



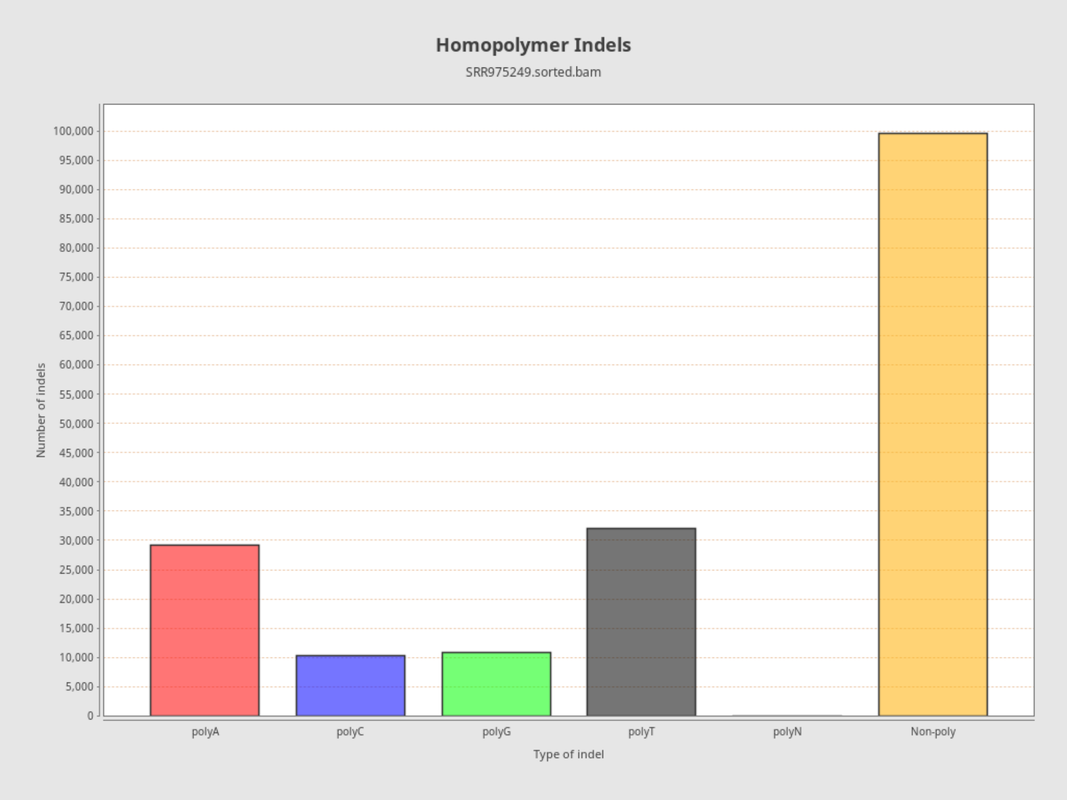
9. Results : Mapped Reads GC-content Distribution



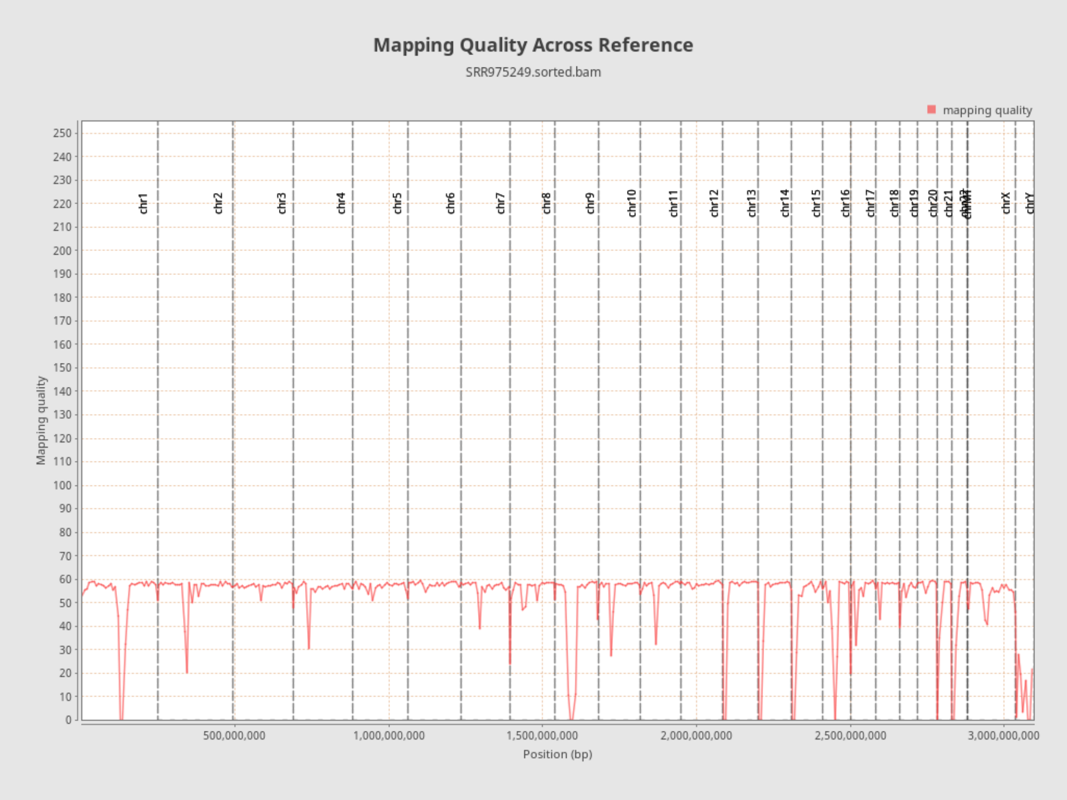
10. Results : Mapped Reads Clipping Profile



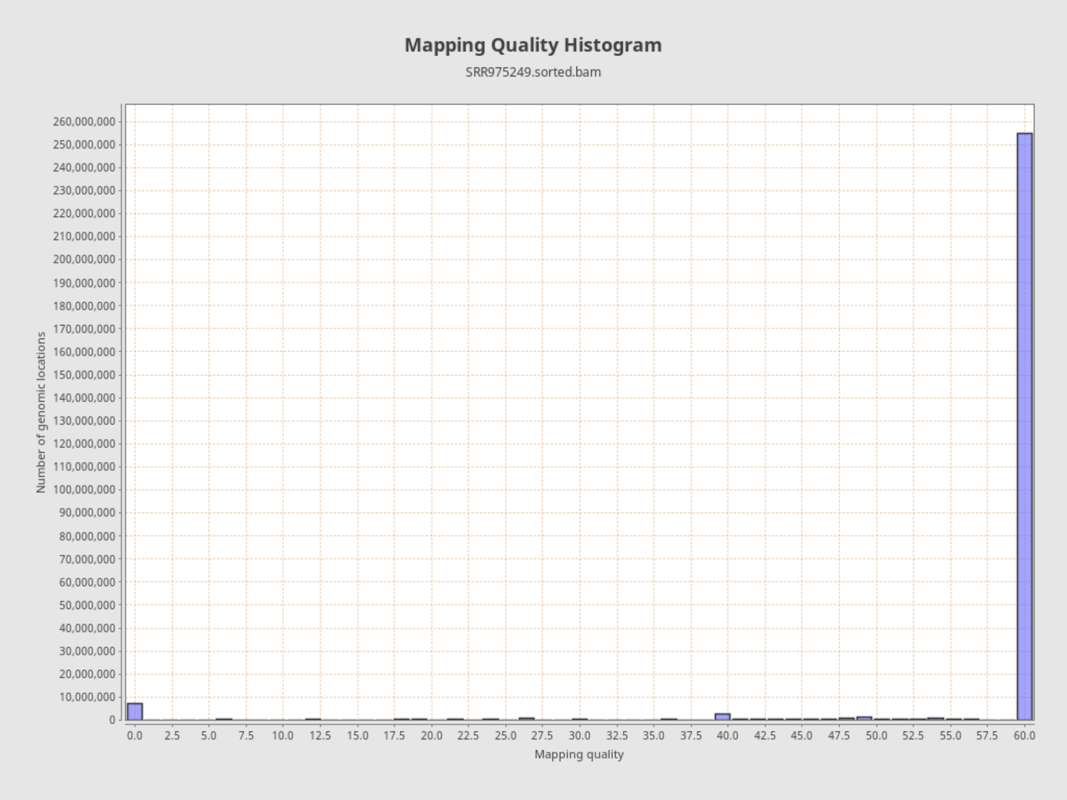
11. Results : Homopolymer Indels



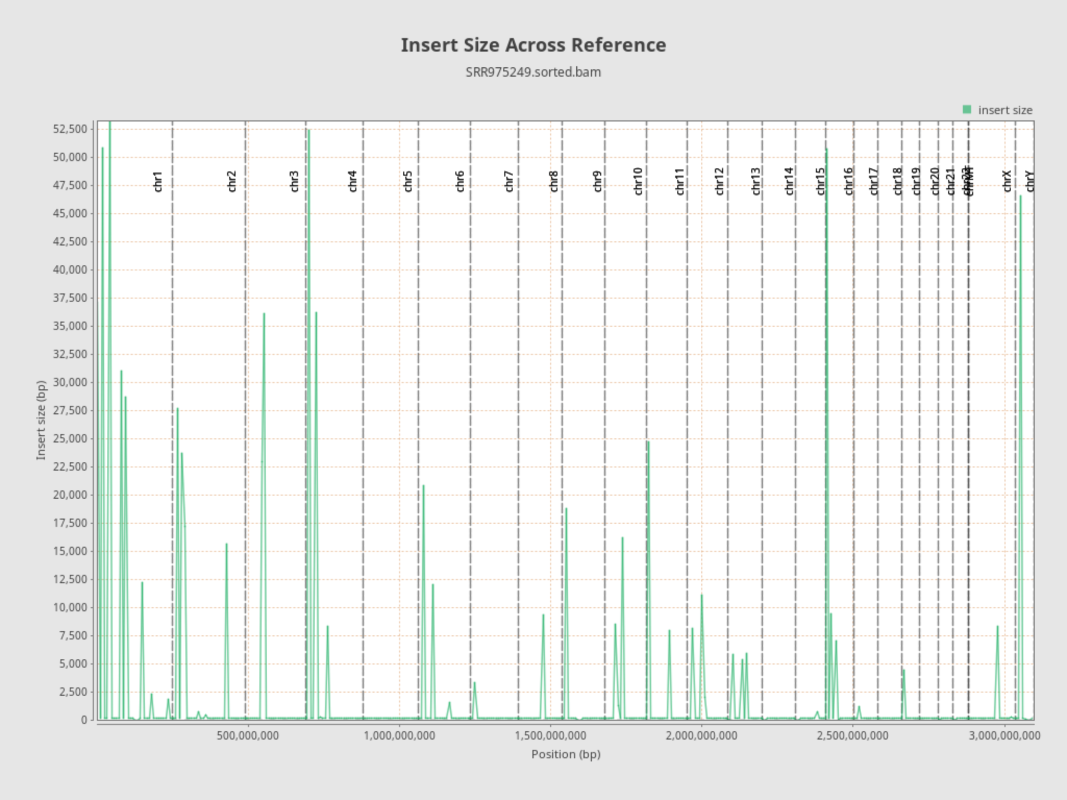
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram