Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 14:36:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975243.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_SRR975243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975243_1.fastq.gz SRR975243_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 14:36:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,721,364
Mapped reads	2,696,017 / 99.07%
Unmapped reads	25,347 / 0.93%
Mapped paired reads	2,696,017 / 99.07%
Mapped reads, first in pair	1,347,895 / 49.53%
Mapped reads, second in pair	1,348,122 / 49.54%
Mapped reads, both in pair	2,689,770 / 98.84%
Mapped reads, singletons	6,247 / 0.23%
Secondary alignments	0
Supplementary alignments	25,079 / 0.92%
Read min/max/mean length	30 / 101 / 101.38
Duplicated reads (estimated)	66,188 / 2.43%
Duplication rate	1.25%
Clipped reads	1,425,522 / 52.38%

2.2. ACGT Content

Number/percentage of A's	77,727,095 / 29.63%
Number/percentage of C's	53,456,707 / 20.38%
Number/percentage of T's	77,898,543 / 29.7%
Number/percentage of G's	53,218,093 / 20.29%
Number/percentage of N's	3,755 / 0%

GC Percentage	40.67%

2.3. Coverage

Mean	0.0848
Standard Deviation	0.9003

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	123,525.12
Standard Deviation	3,385,550.33
P25/Median/P75	146 / 177 / 221

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	1,249,865
Insertions	33,310
Mapped reads with at least one insertion	1.21%
Deletions	33,124
Mapped reads with at least one deletion	1.19%
Homopolymer indels	38.24%

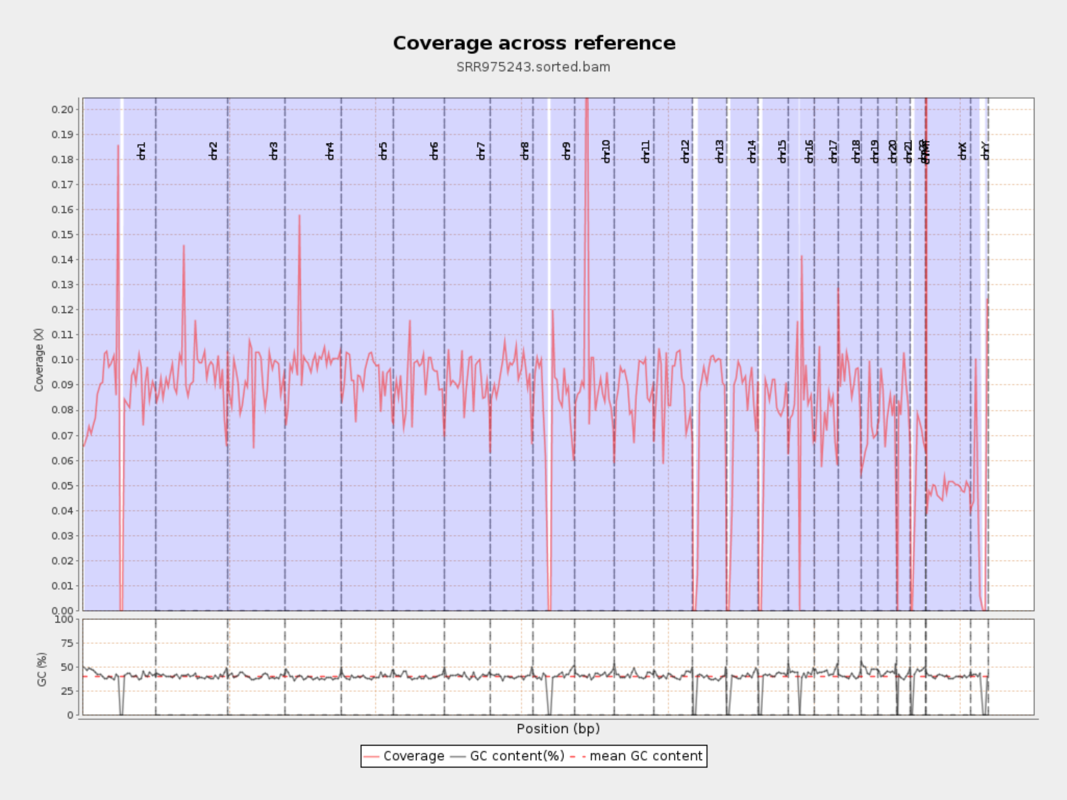
2.7. Chromosome stats

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

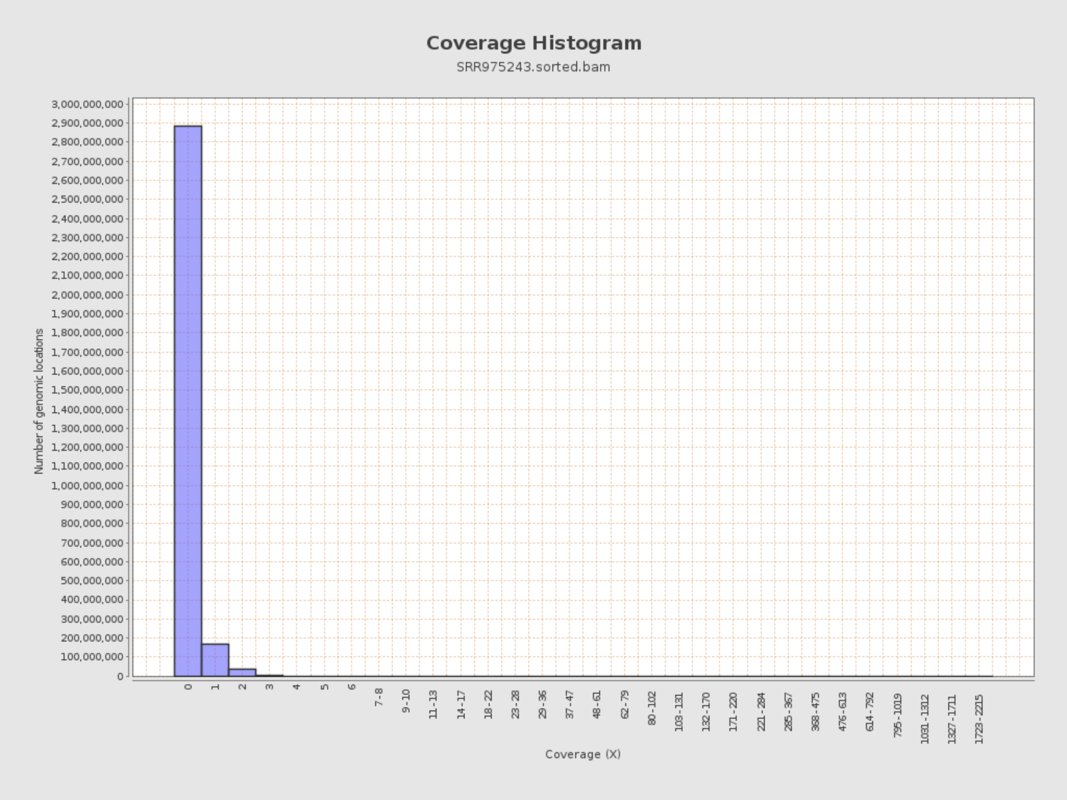
		bases	coverage	deviation
chr1	249250621	21260890	0.0853	2.2408
chr2	243199373	23109476	0.095	0.571
chr3	198022430	18369436	0.0928	0.3587
chr4	191154276	19150845	0.1002	0.6317
chr5	180915260	16792460	0.0928	0.3489
chr6	171115067	15872273	0.0928	0.401
chr7	159138663	14536364	0.0913	0.6665
chr8	146364022	13793647	0.0942	1.0834
chr9	141213431	11083339	0.0785	0.9377
chr10	135534747	13151515	0.097	1.5502
chr11	135006516	11954427	0.0885	0.4408
chr12	133851895	11781746	0.088	0.3386
chr13	115169878	9120323	0.0792	0.3206
chr14	107349540	8024099	0.0747	0.3206
chr15	102531392	7241117	0.0706	0.3022
chr16	90354753	7389479	0.0818	0.5998
chr17	81195210	6323238	0.0779	0.5773
chr18	78077248	7462266	0.0956	0.9641
chr19	59128983	4200200	0.071	0.9793
chr20	63025520	5073686	0.0805	0.3541
chr21	48129895	3721477	0.0773	0.4359
chr22	51304566	2620328	0.0511	0.3653
chrMT	16571	131302	7.9236	3.6237
chrX	155270560	7511564	0.0484	0.2894

chrY	59373566	2706873	0.0456	0.751

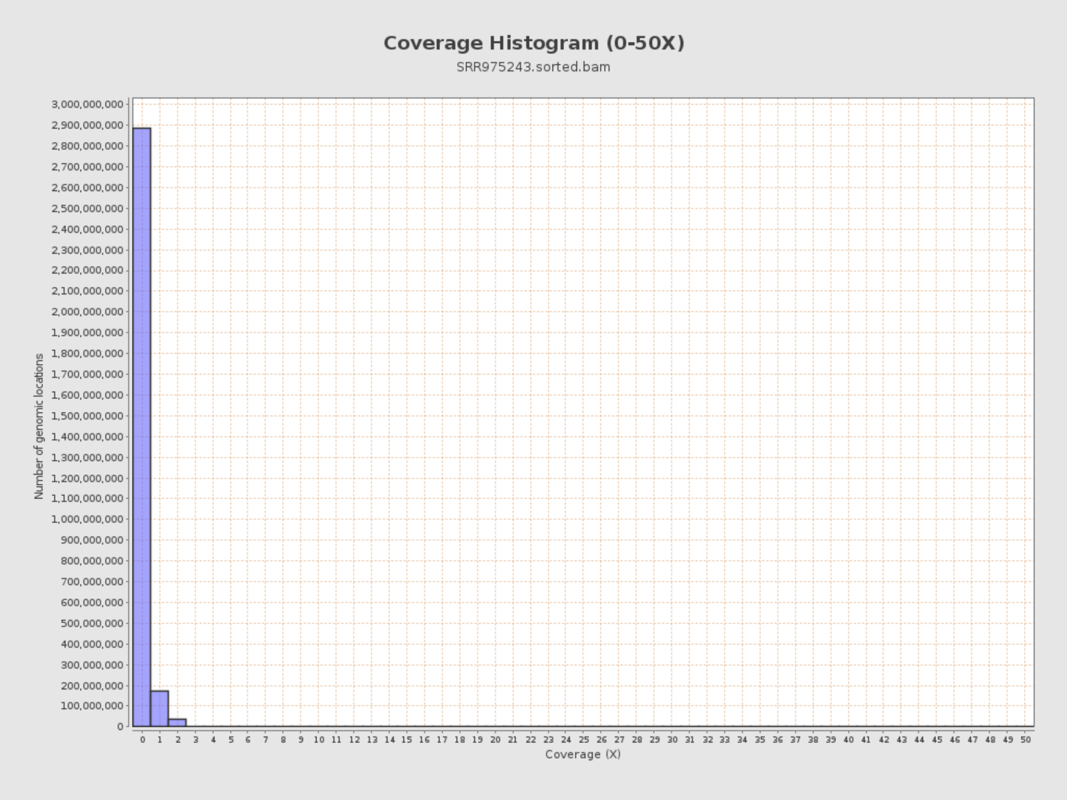
3. Results : Coverage across reference



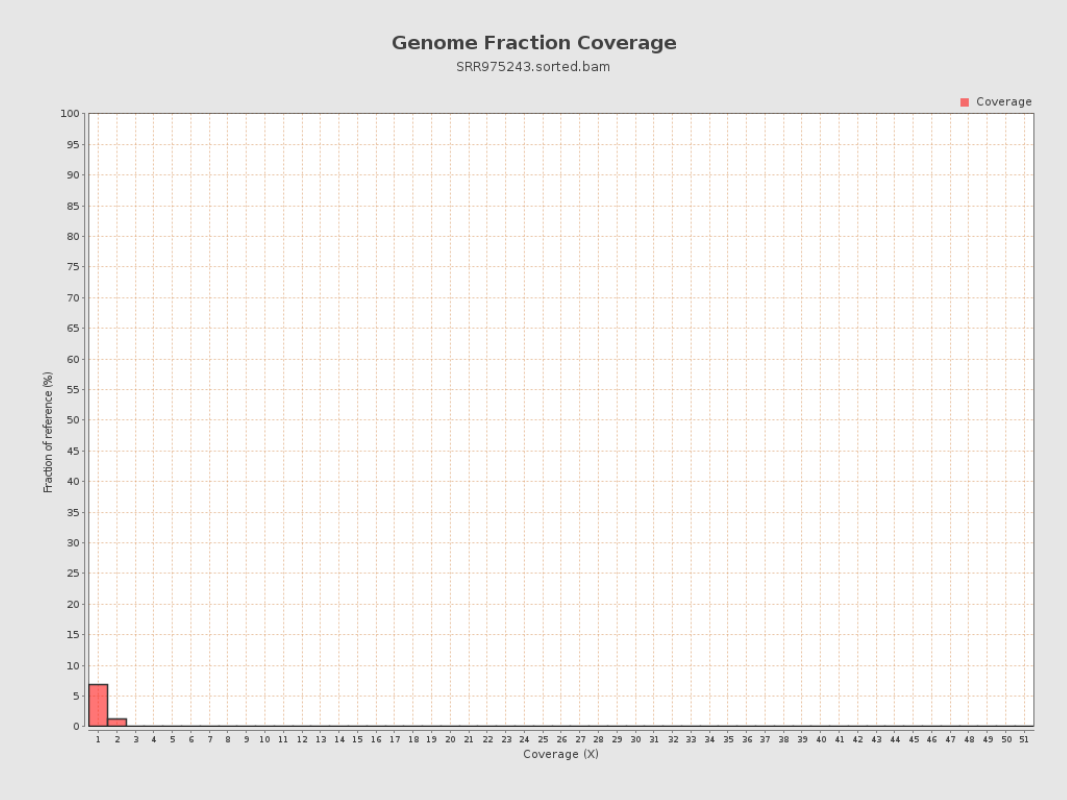
4. Results : Coverage Histogram



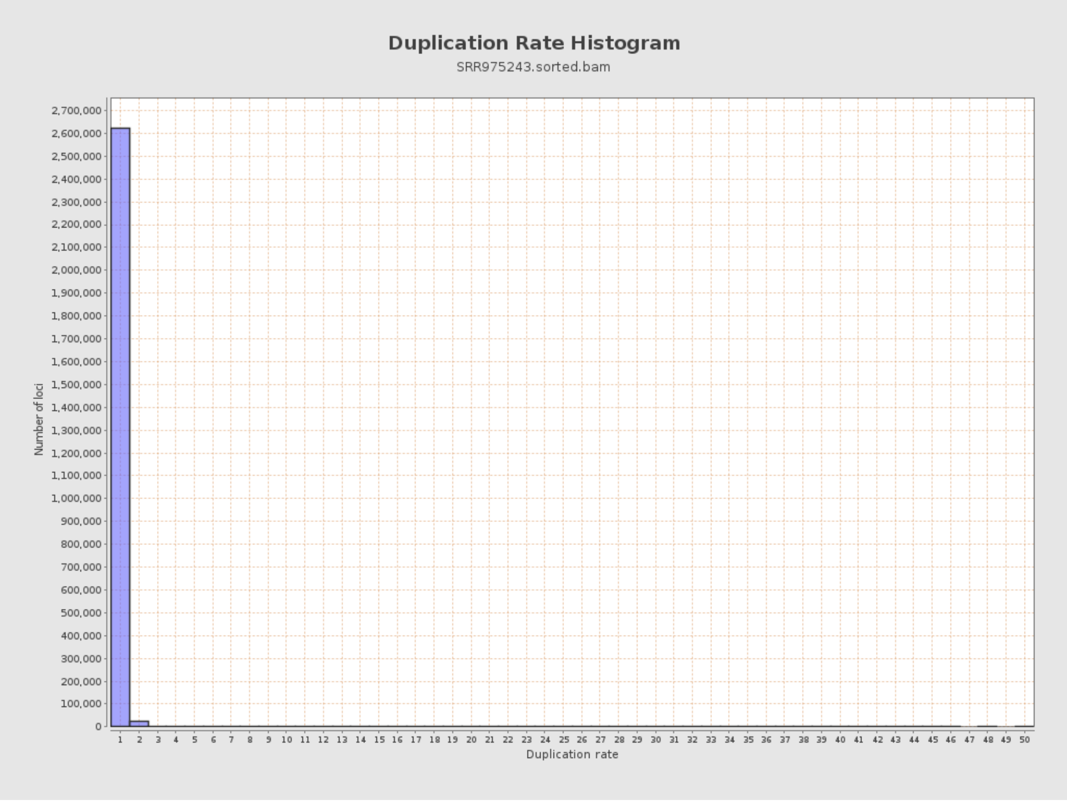
5. Results : Coverage Histogram (0-50X)



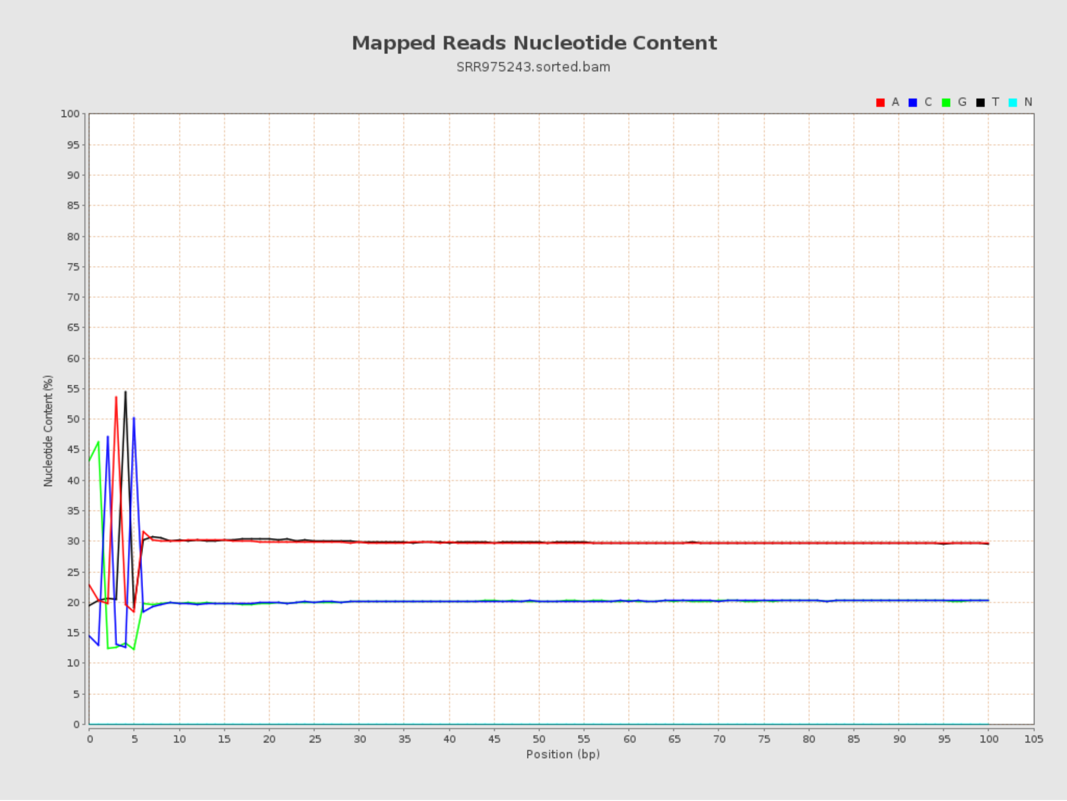
6. Results : Genome Fraction Coverage



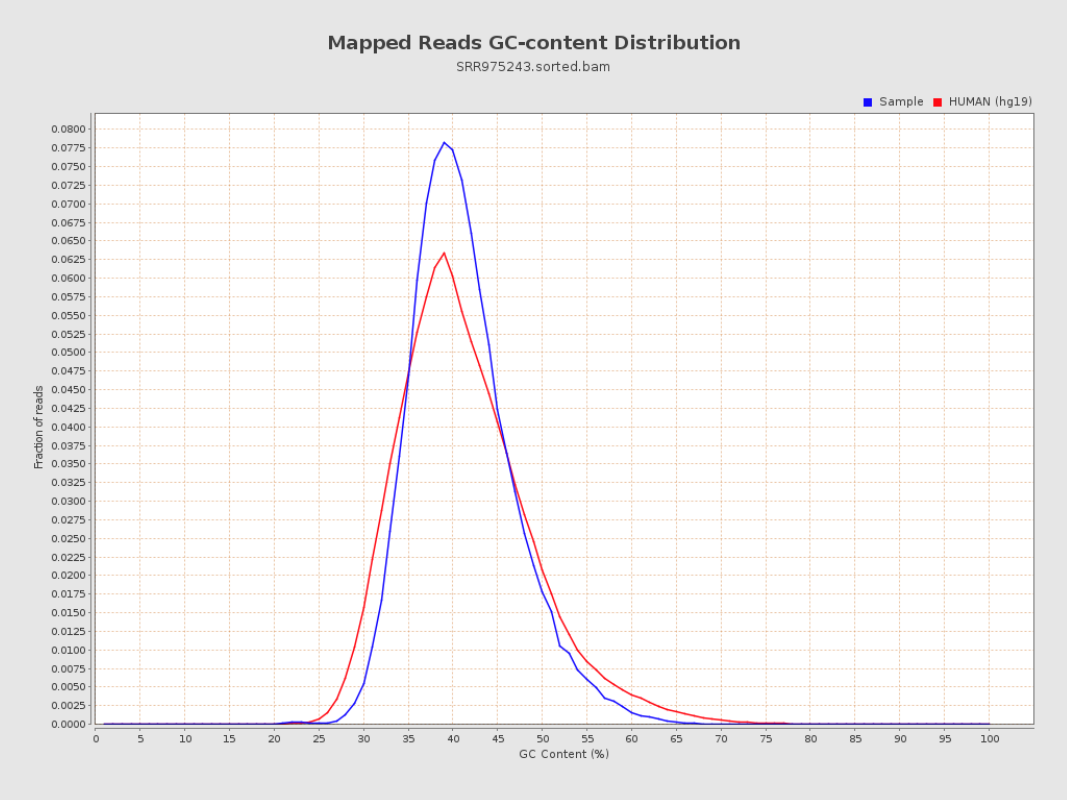
7. Results : Duplication Rate Histogram



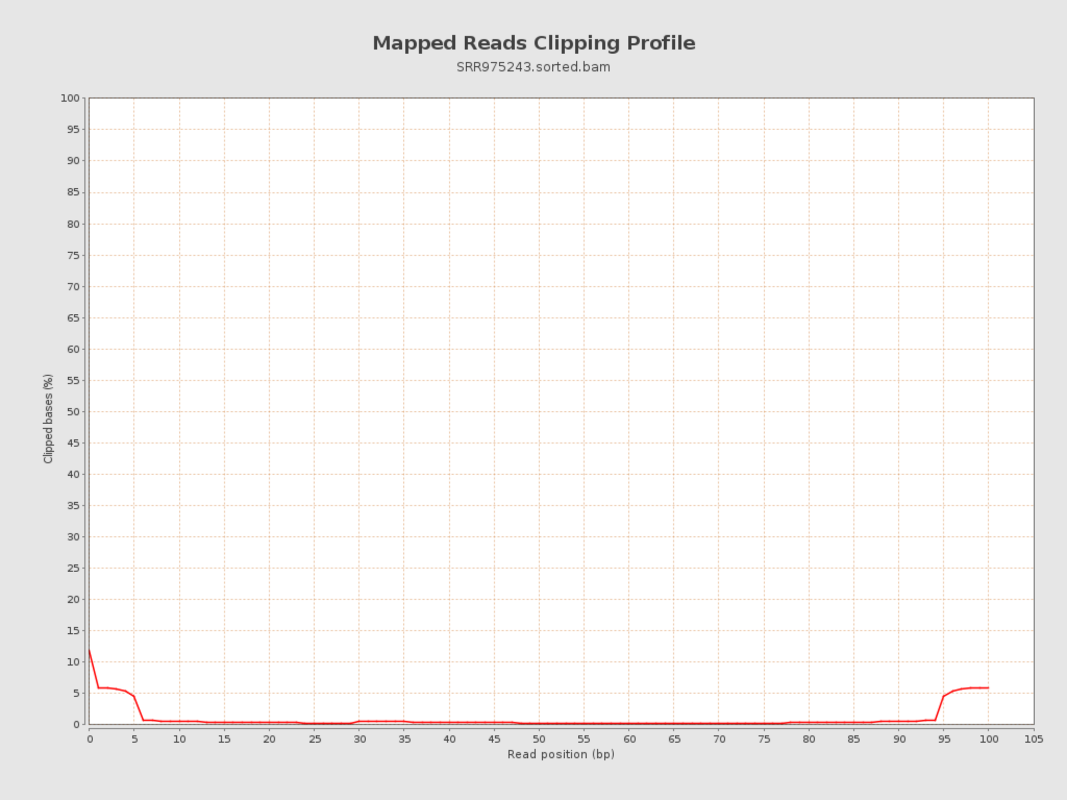
8. Results : Mapped Reads Nucleotide Content



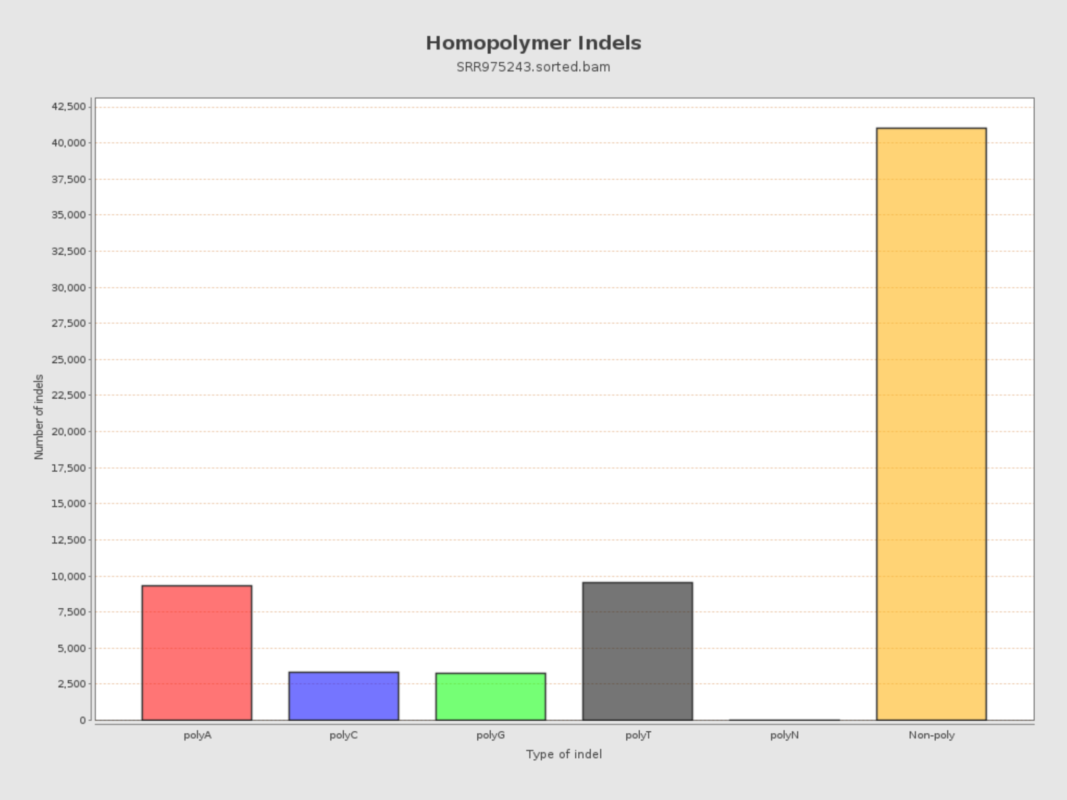
9. Results : Mapped Reads GC-content Distribution



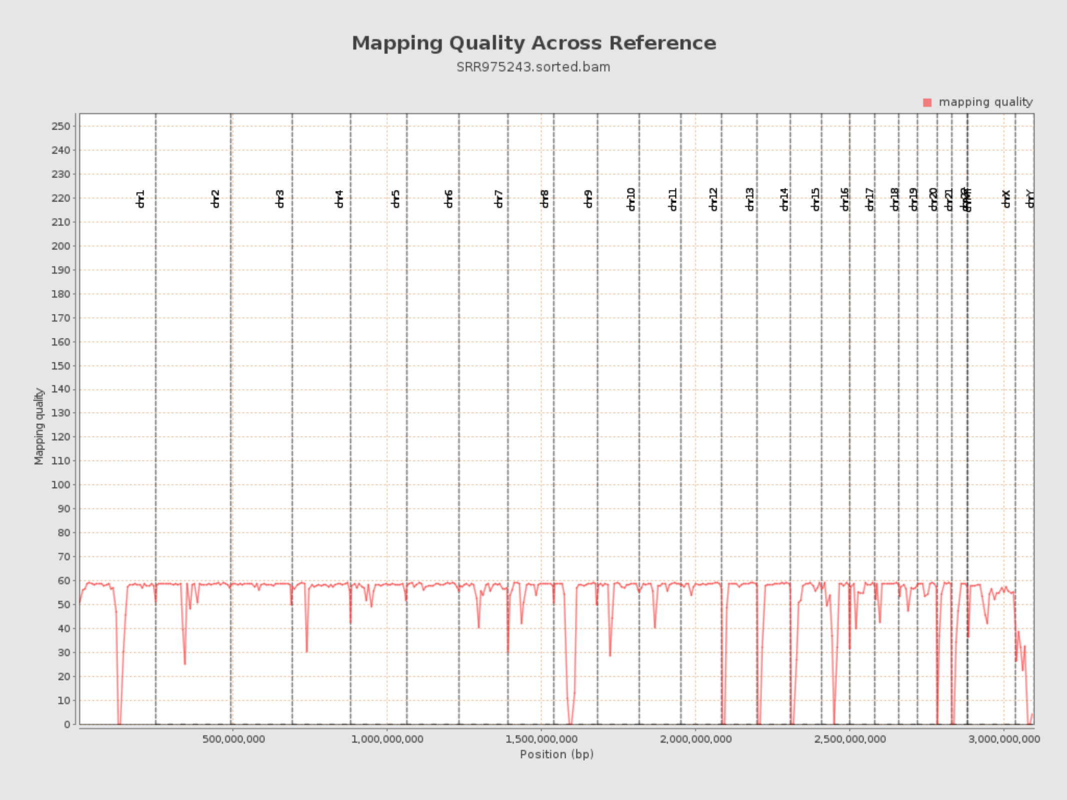
10. Results : Mapped Reads Clipping Profile



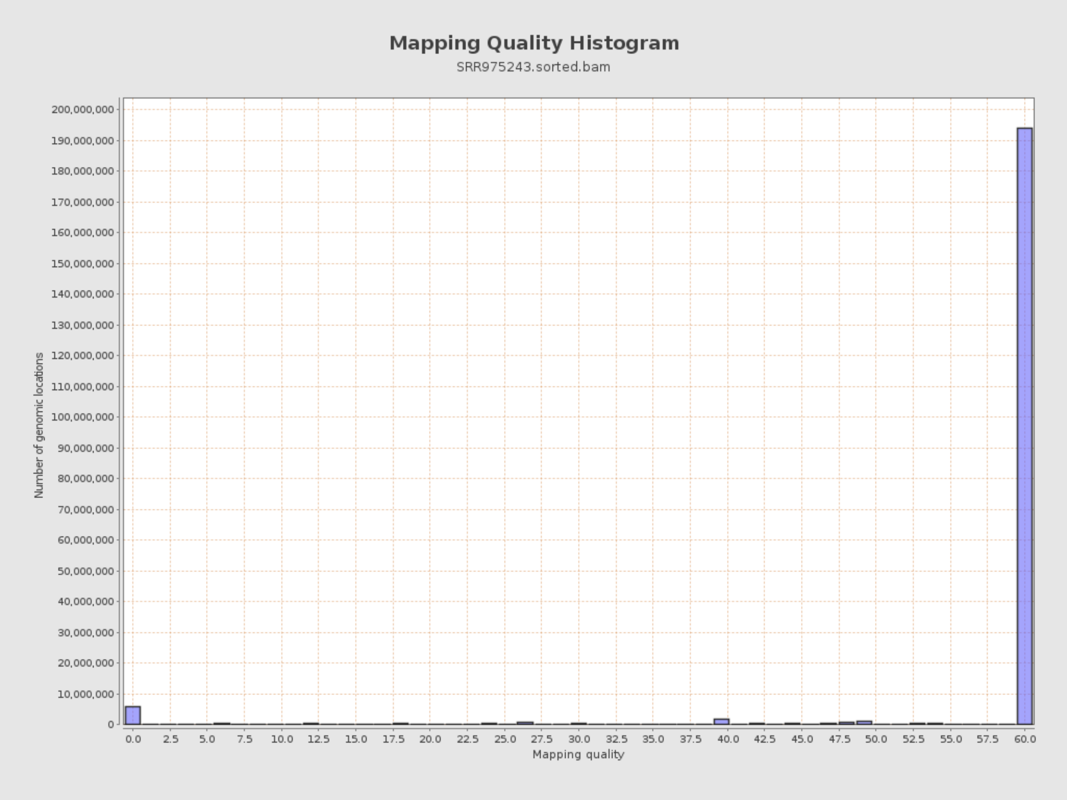
11. Results : Homopolymer Indels



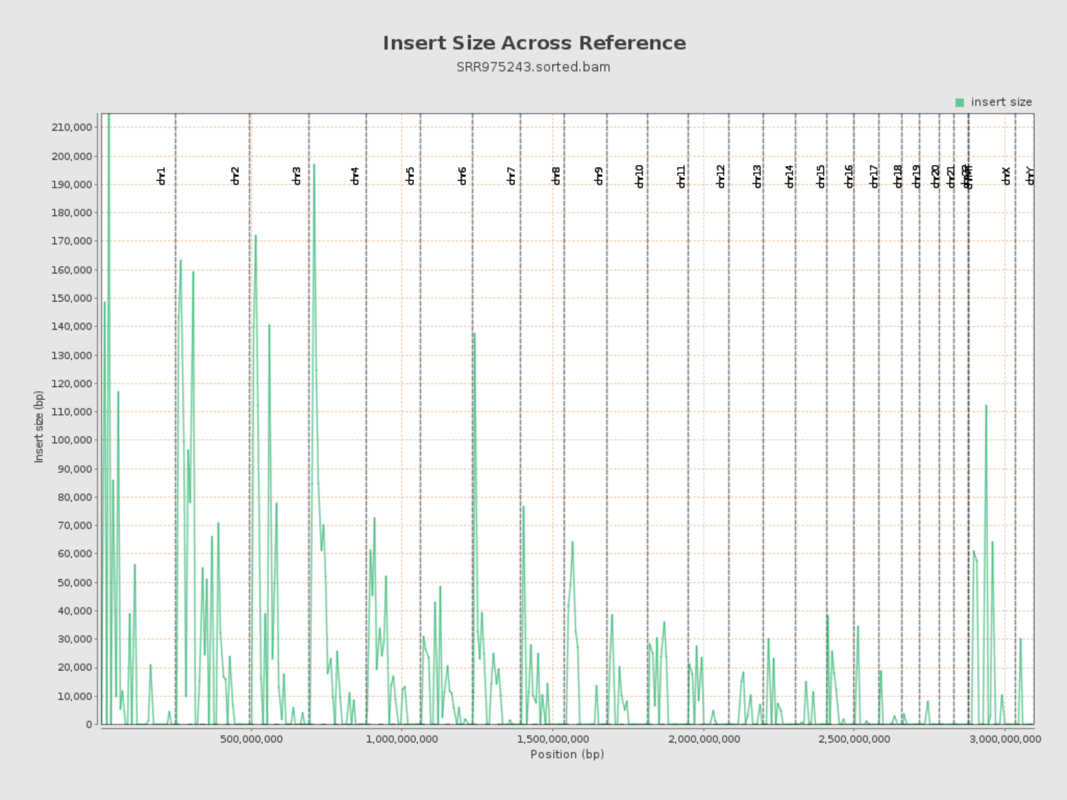
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram