Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:09:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975247.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_SRR975247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975247_1.fastq.gz SRR975247_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:09:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,920,610
Mapped reads	2,889,821 / 98.95%
Unmapped reads	30,789 / 1.05%
Mapped paired reads	2,889,821 / 98.95%
Mapped reads, first in pair	1,447,602 / 49.57%
Mapped reads, second in pair	1,442,219 / 49.38%
Mapped reads, both in pair	2,881,502 / 98.66%
Mapped reads, singletons	8,319 / 0.28%
Secondary alignments	0
Supplementary alignments	117,719 / 4.03%
Read min/max/mean length	30 / 151 / 153.09
Duplicated reads (estimated)	651,187 / 22.3%
Duplication rate	24.16%
Clipped reads	2,285,207 / 78.24%

2.2. ACGT Content

Number/percentage of A's	112,011,695 / 28.44%
Number/percentage of C's	84,540,765 / 21.47%
Number/percentage of T's	110,650,553 / 28.1%
Number/percentage of G's	86,555,098 / 21.98%
Number/percentage of N's	35,884 / 0.01%

GC Percentage	43.45%

2.3. Coverage

Mean	0.1273
Standard Deviation	2.4055

2.4. Mapping Quality

Mean Mapping Quality	53.53

2.5. Insert size

Mean	164,081.71
Standard Deviation	3,854,047.91
P25/Median/P75	128 / 151 / 183

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	3,516,372
Insertions	66,097
Mapped reads with at least one insertion	2.18%
Deletions	68,258
Mapped reads with at least one deletion	2.26%
Homopolymer indels	41.23%

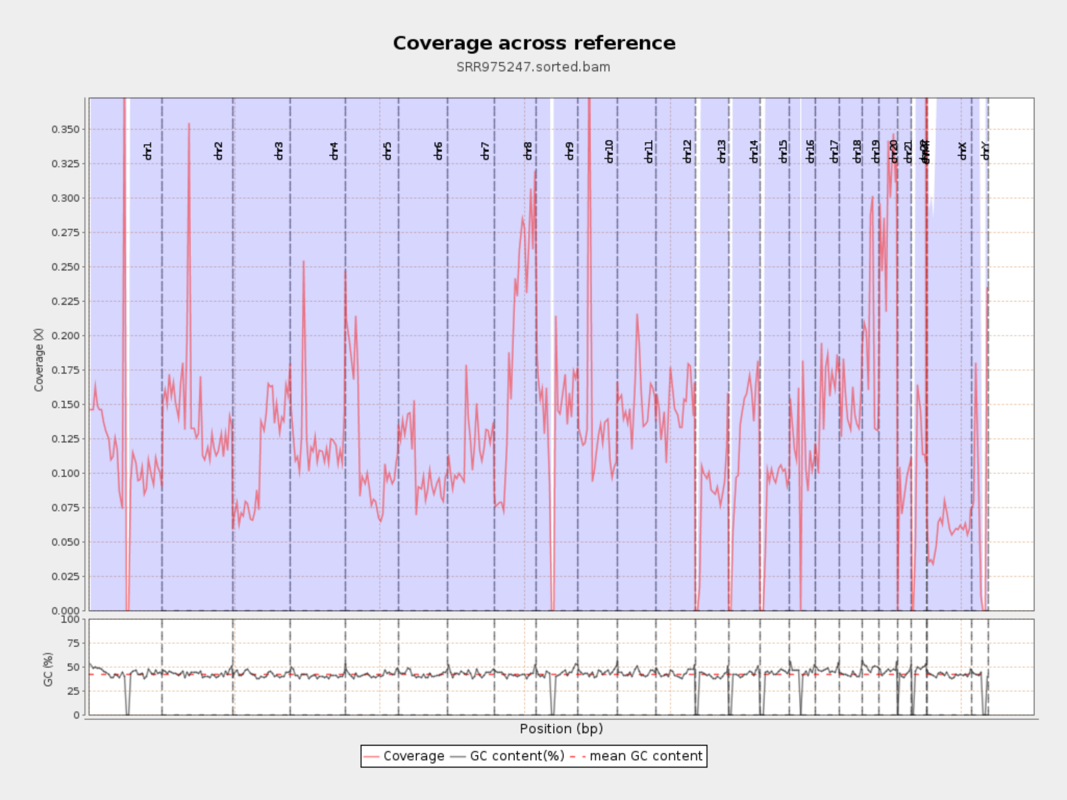
2.7. Chromosome stats

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

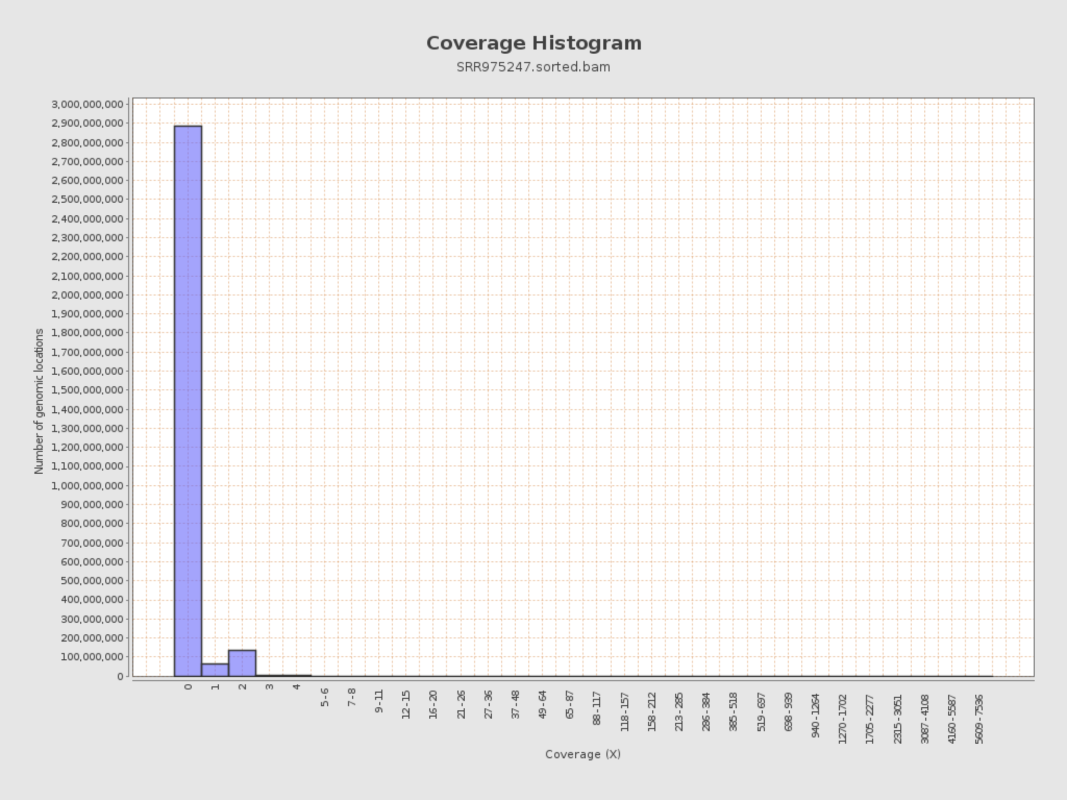
		bases	coverage	deviation
chr1	249250621	29038546	0.1165	7.3923
chr2	243199373	35403499	0.1456	1.4311
chr3	198022430	22085578	0.1115	0.4771
chr4	191154276	23497072	0.1229	1.1866
chr5	180915260	20898325	0.1155	0.4833
chr6	171115067	17994218	0.1052	0.5751
chr7	159138663	18725703	0.1177	1.1816
chr8	146364022	28548886	0.1951	1.2228
chr9	141213431	19496619	0.1381	2.0348
chr10	135534747	18589251	0.1372	2.6208
chr11	135006516	20816530	0.1542	0.8254
chr12	133851895	19921384	0.1488	0.5353
chr13	115169878	9144153	0.0794	0.3903
chr14	107349540	13011048	0.1212	0.4908
chr15	102531392	8297836	0.0809	0.3906
chr16	90354753	10267507	0.1136	0.8167
chr17	81195210	12937127	0.1593	1.1137
chr18	78077248	11569517	0.1482	1.7565
chr19	59128983	11911005	0.2014	3.0027
chr20	63025520	18610706	0.2953	0.8602
chr21	48129895	4090874	0.085	0.8508
chr22	51304566	4727196	0.0921	0.7032
chrMT	16571	445954	26.9117	8.4071
chrX	155270560	8995644	0.0579	0.4311

chrY	59373566	4945694	0.0833	1.5727

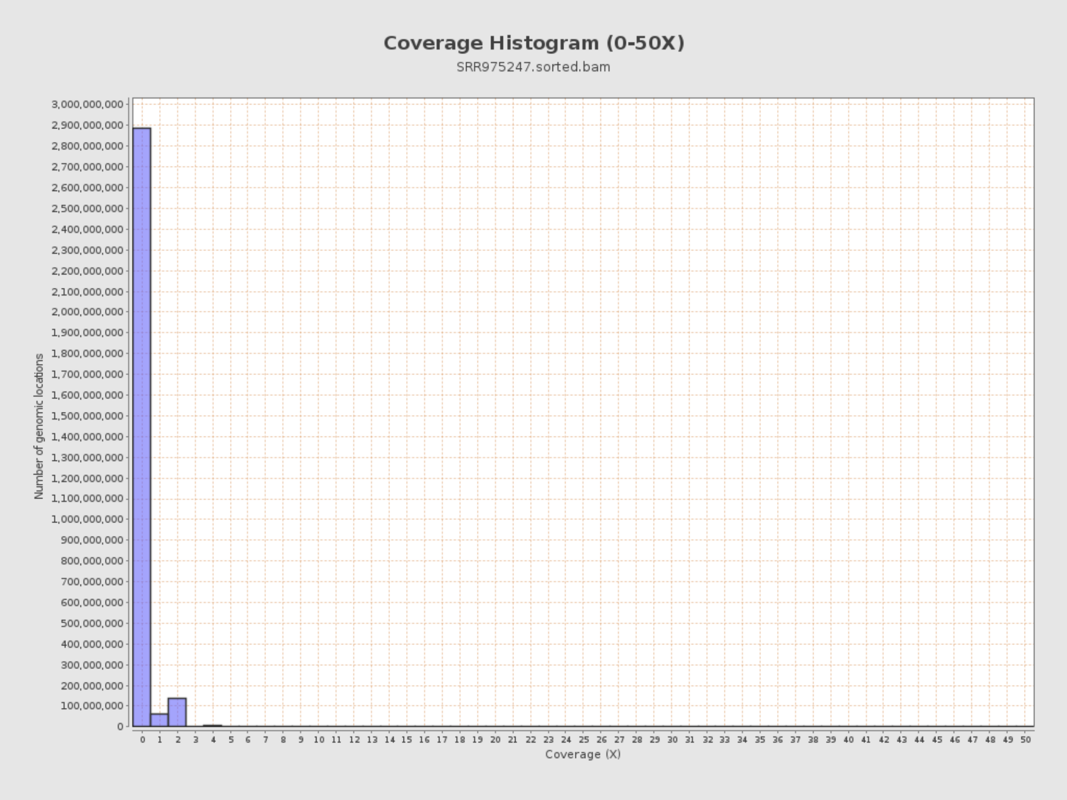
3. Results : Coverage across reference



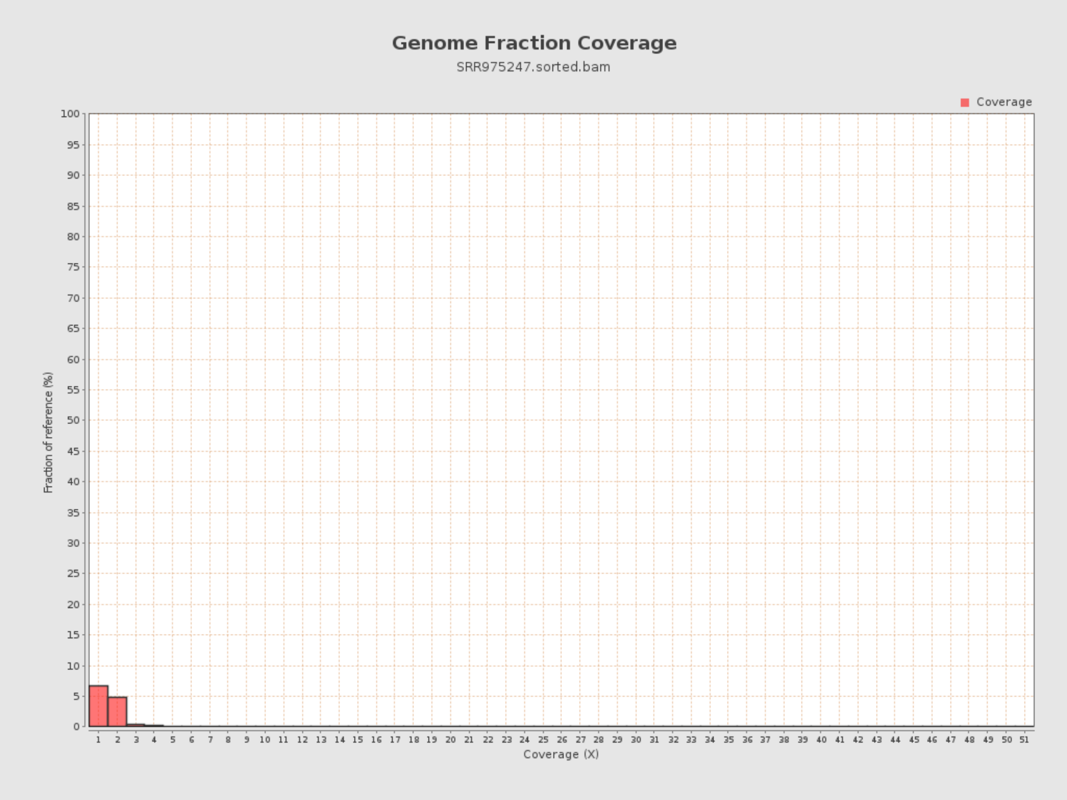
4. Results : Coverage Histogram



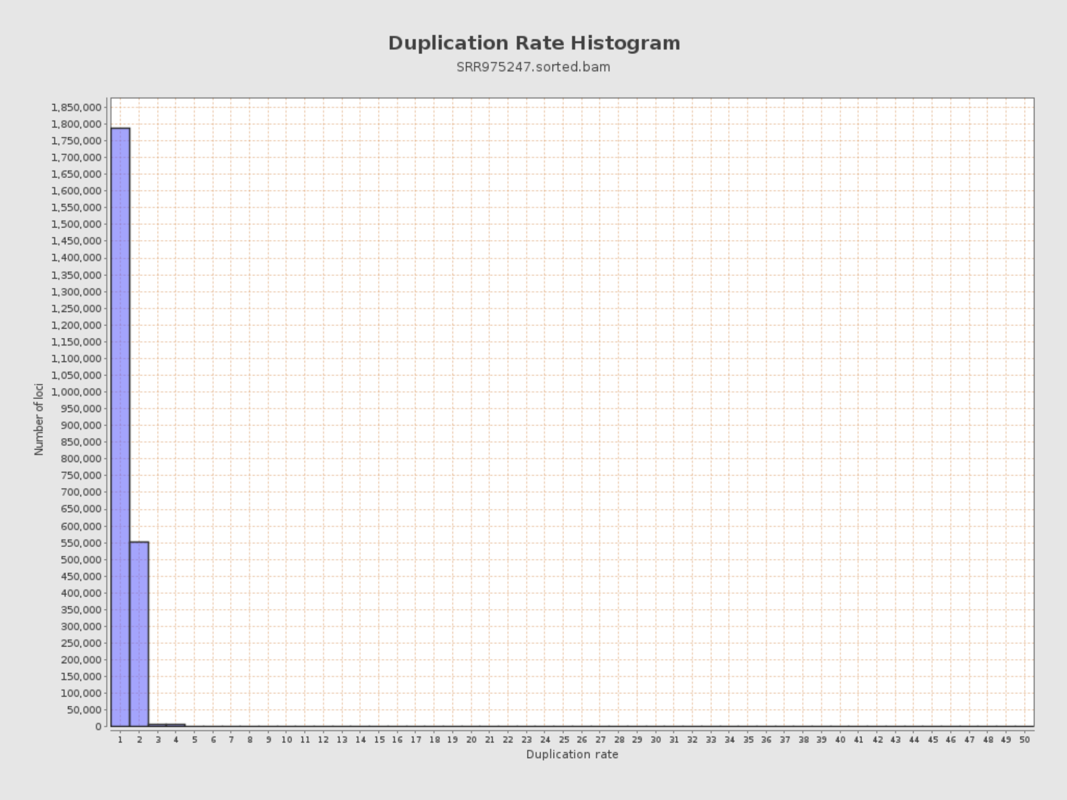
5. Results : Coverage Histogram (0-50X)



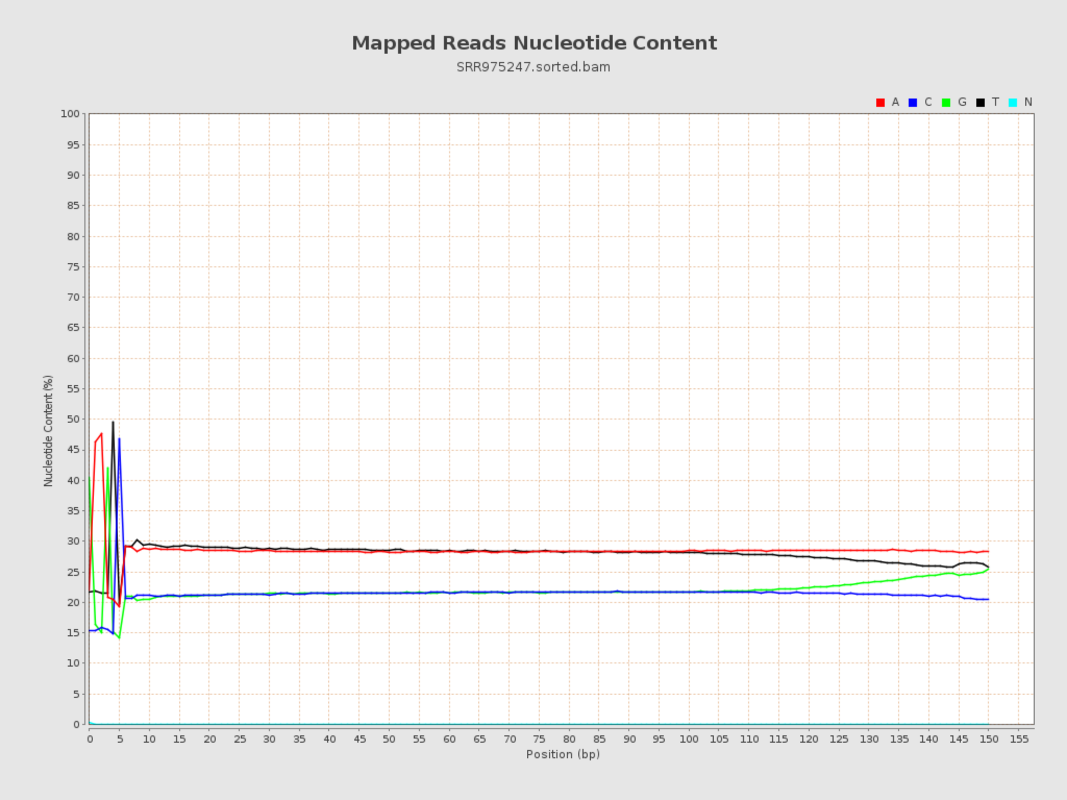
6. Results : Genome Fraction Coverage



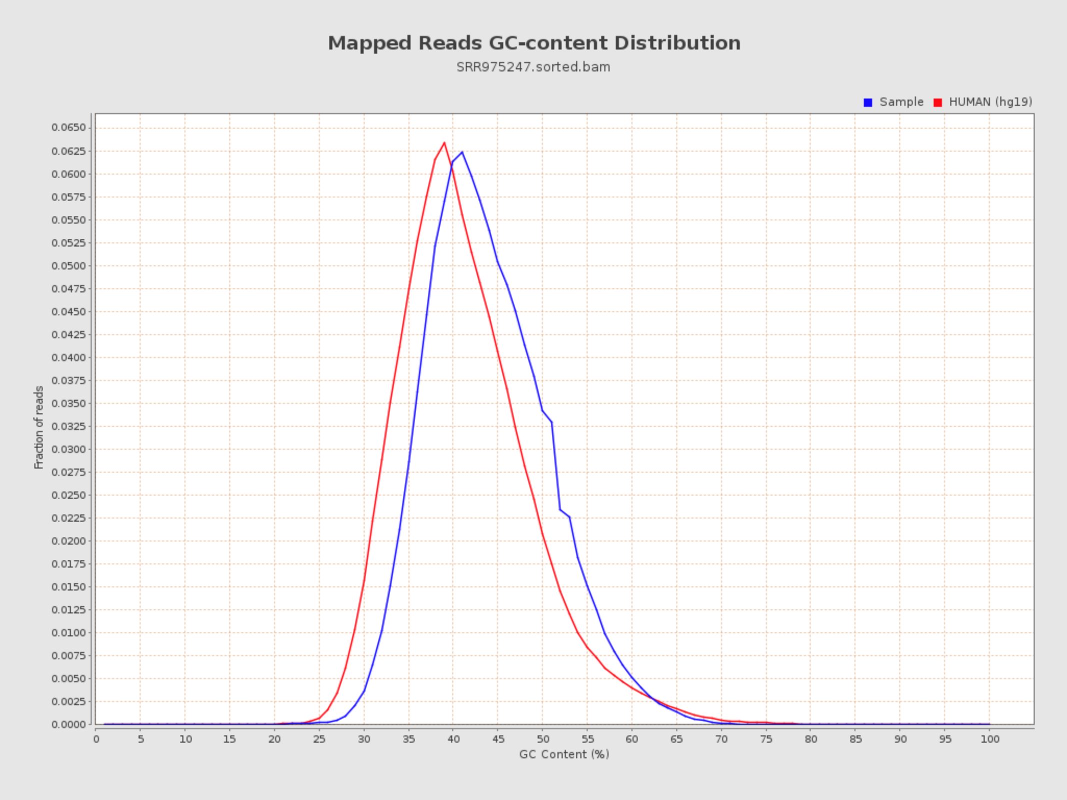
7. Results : Duplication Rate Histogram



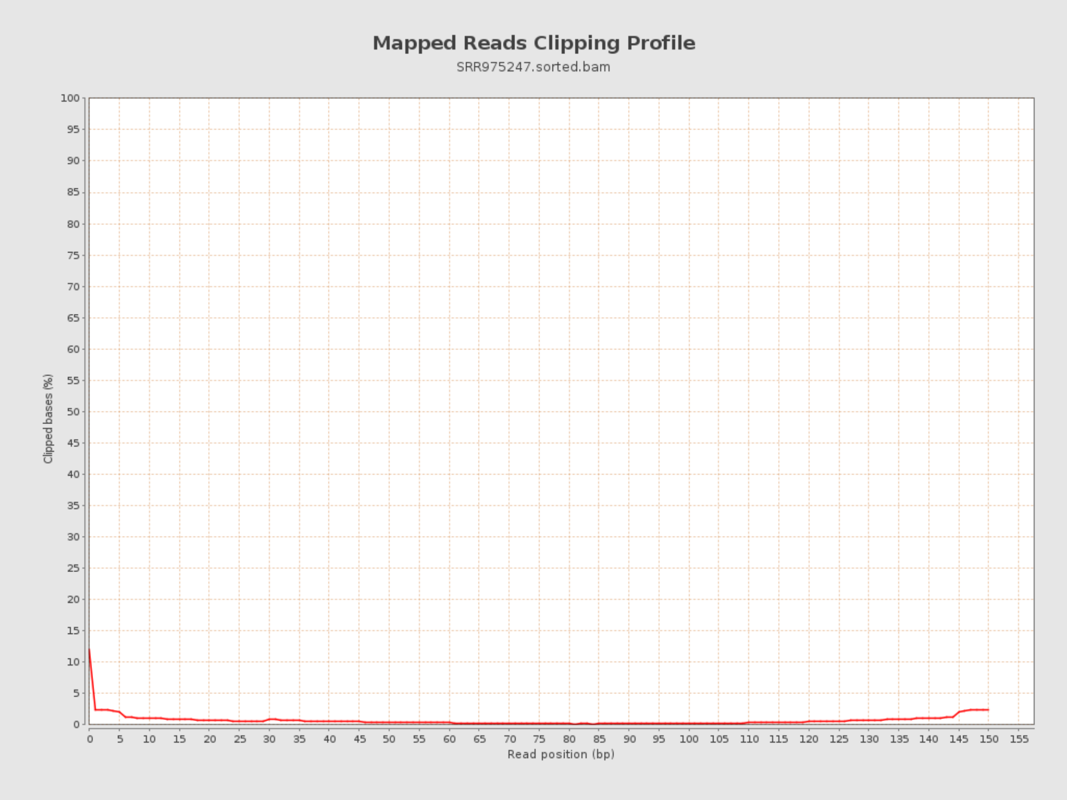
8. Results : Mapped Reads Nucleotide Content



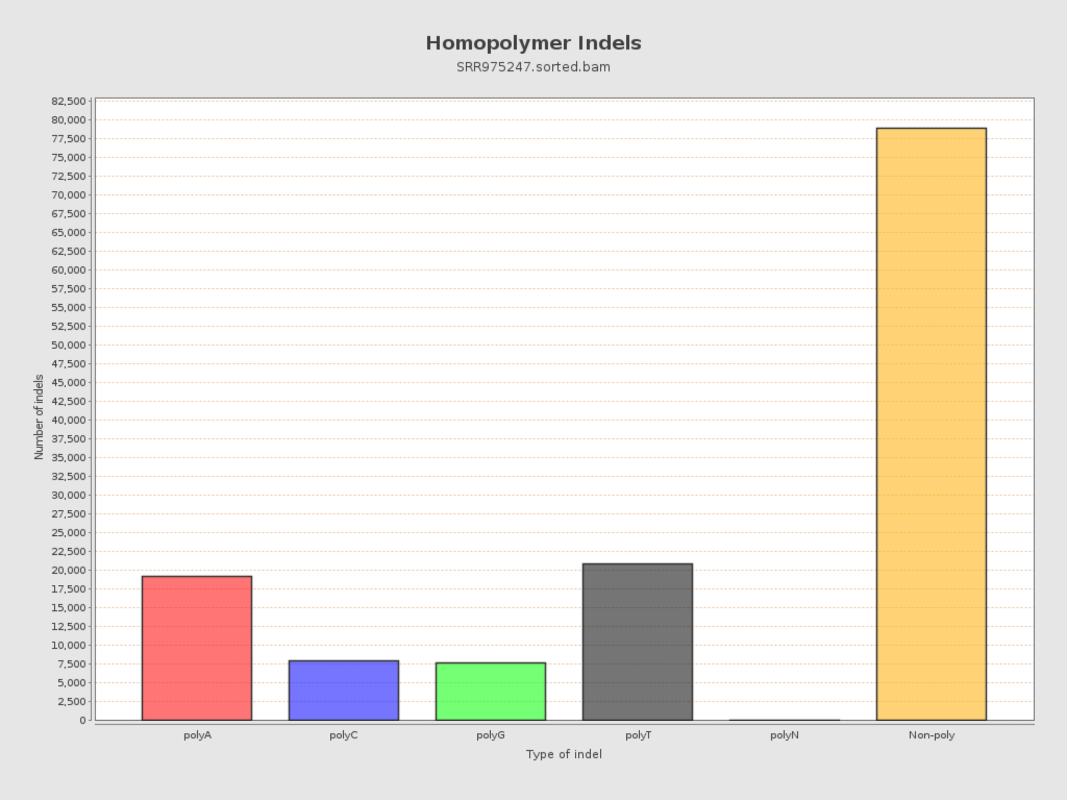
9. Results : Mapped Reads GC-content Distribution



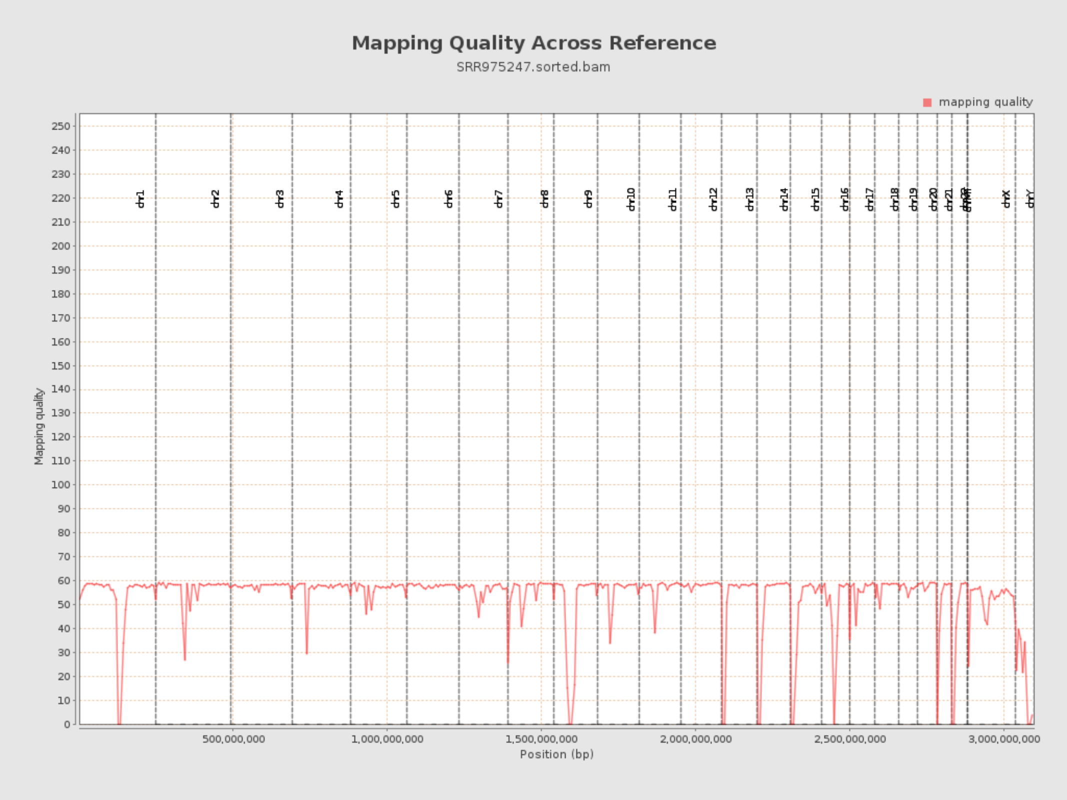
10. Results : Mapped Reads Clipping Profile



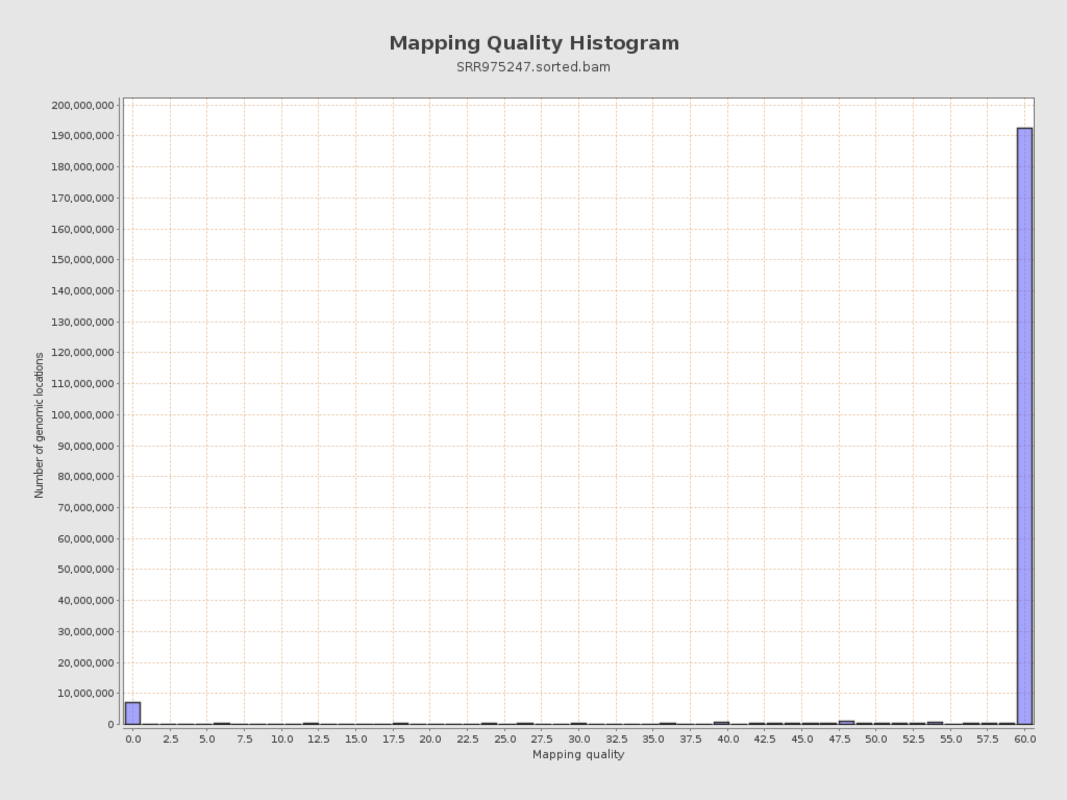
11. Results : Homopolymer Indels



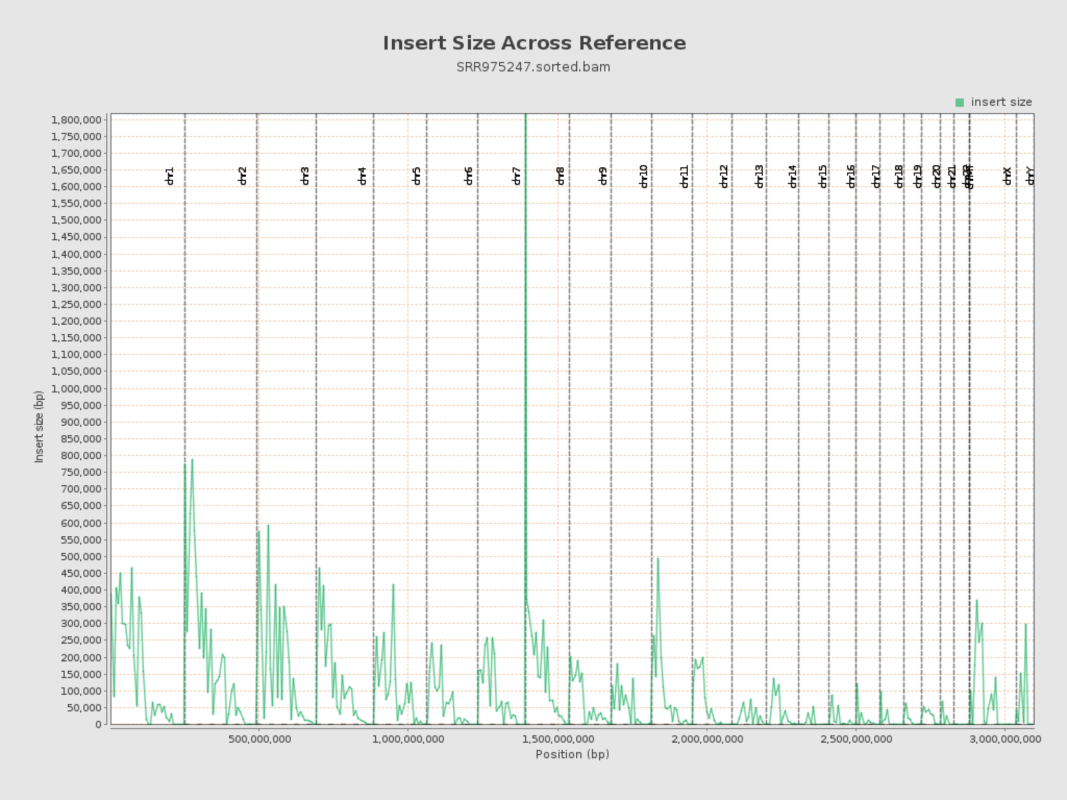
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram