Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:05:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975211.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_SRR975211 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975211_1.fastq.gz SRR975211_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:05:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975211.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,569,912
Mapped reads	2,537,211 / 98.73%
Unmapped reads	32,701 / 1.27%
Mapped paired reads	2,537,211 / 98.73%
Mapped reads, first in pair	1,270,138 / 49.42%
Mapped reads, second in pair	1,267,073 / 49.3%
Mapped reads, both in pair	2,530,470 / 98.47%
Mapped reads, singletons	6,741 / 0.26%
Secondary alignments	0
Supplementary alignments	100,843 / 3.92%
Read min/max/mean length	30 / 151 / 153.05
Duplicated reads (estimated)	620,133 / 24.13%
Duplication rate	26.32%
Clipped reads	2,043,588 / 79.52%

2.2. ACGT Content

Number/percentage of A's	99,028,688 / 28.94%
Number/percentage of C's	71,500,113 / 20.9%
Number/percentage of T's	97,874,593 / 28.6%
Number/percentage of G's	73,747,574 / 21.55%
Number/percentage of N's	16,492 / 0%

GC Percentage	42.45%

2.3. Coverage

Mean	0.1106
Standard Deviation	2.3441

2.4. Mapping Quality

Mean Mapping Quality	53.22

2.5. Insert size

Mean	175,452.7
Standard Deviation	4,121,990.8
P25/Median/P75	125 / 148 / 178

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	3,130,166
Insertions	62,731
Mapped reads with at least one insertion	2.35%
Deletions	65,747
Mapped reads with at least one deletion	2.49%
Homopolymer indels	40.82%

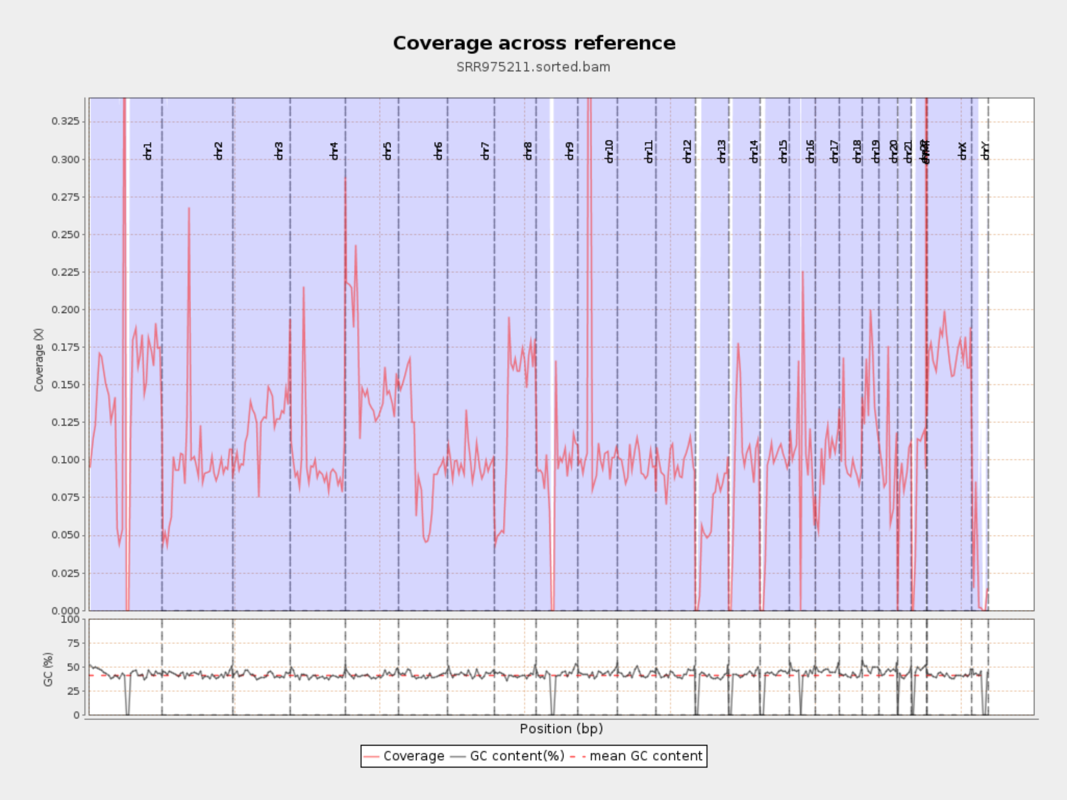
2.7. Chromosome stats

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

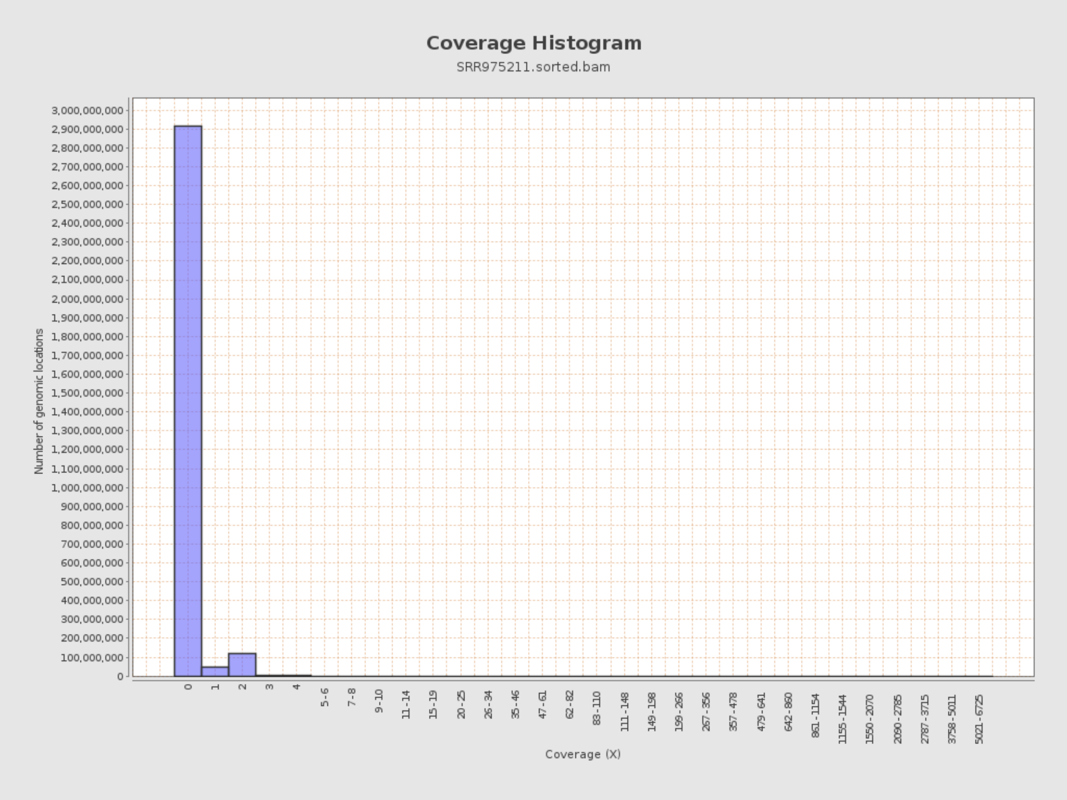
		bases	**coverage**	**deviation**
chr1	249250621	36137248	0.145	6.5764
chr2	243199373	23402979	0.0962	1.0994
chr3	198022430	24270587	0.1226	0.6001
chr4	191154276	18527935	0.0969	0.9631
chr5	180915260	28678310	0.1585	0.5621
chr6	171115067	17323380	0.1012	0.5798
chr7	159138663	15695974	0.0986	0.8142
chr8	146364022	19486753	0.1331	1.2859
chr9	141213431	12693116	0.0899	1.7301
chr10	135534747	17303641	0.1277	5.1176
chr11	135006516	13169545	0.0975	0.676
chr12	133851895	13034407	0.0974	0.4387
chr13	115169878	6858239	0.0595	0.3388
chr14	107349540	10489789	0.0977	0.4428
chr15	102531392	8502916	0.0829	0.3984
chr16	90354753	9666296	0.107	1.0413
chr17	81195210	8055191	0.0992	0.7658
chr18	78077248	7981638	0.1022	1.8364
chr19	59128983	8741022	0.1478	2.8965
chr20	63025520	6148124	0.0975	0.5326
chr21	48129895	4118044	0.0856	0.6796
chr22	51304566	4050594	0.079	0.3904
chrMT	16571	266050	16.0552	7.1304
chrX	155270560	26507063	0.1707	0.7284

chrY	59373566	1227337	0.0207	1.1037

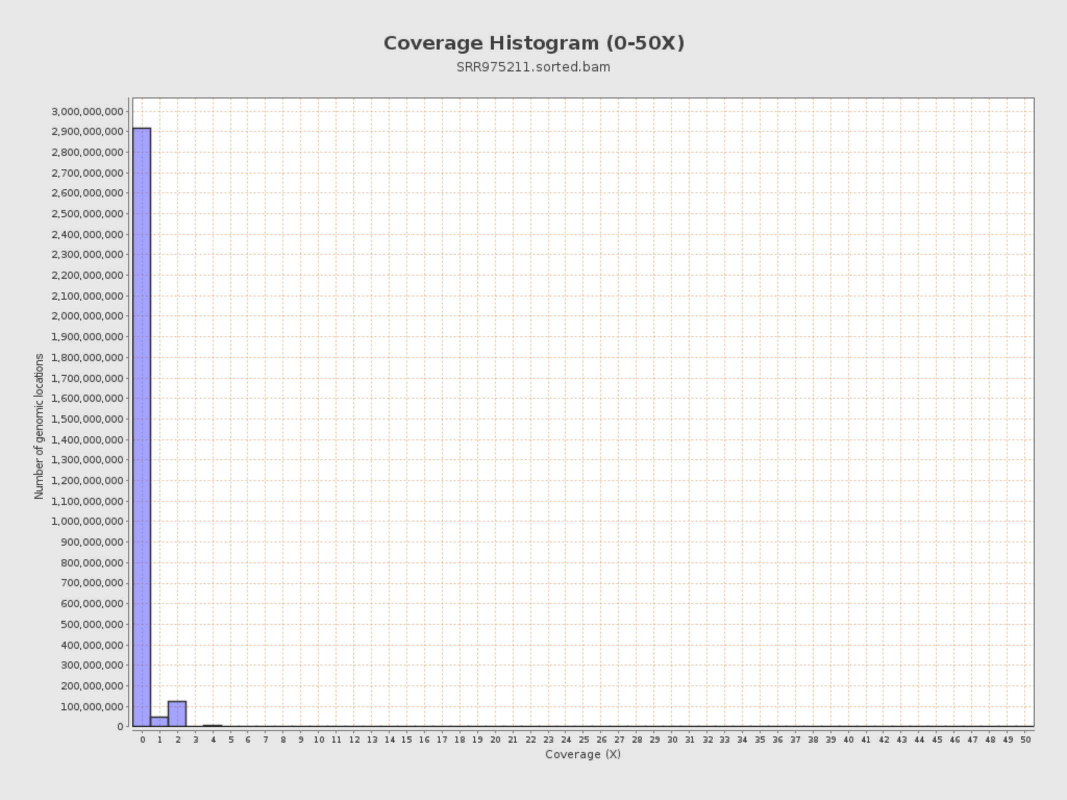
3. Results : Coverage across reference



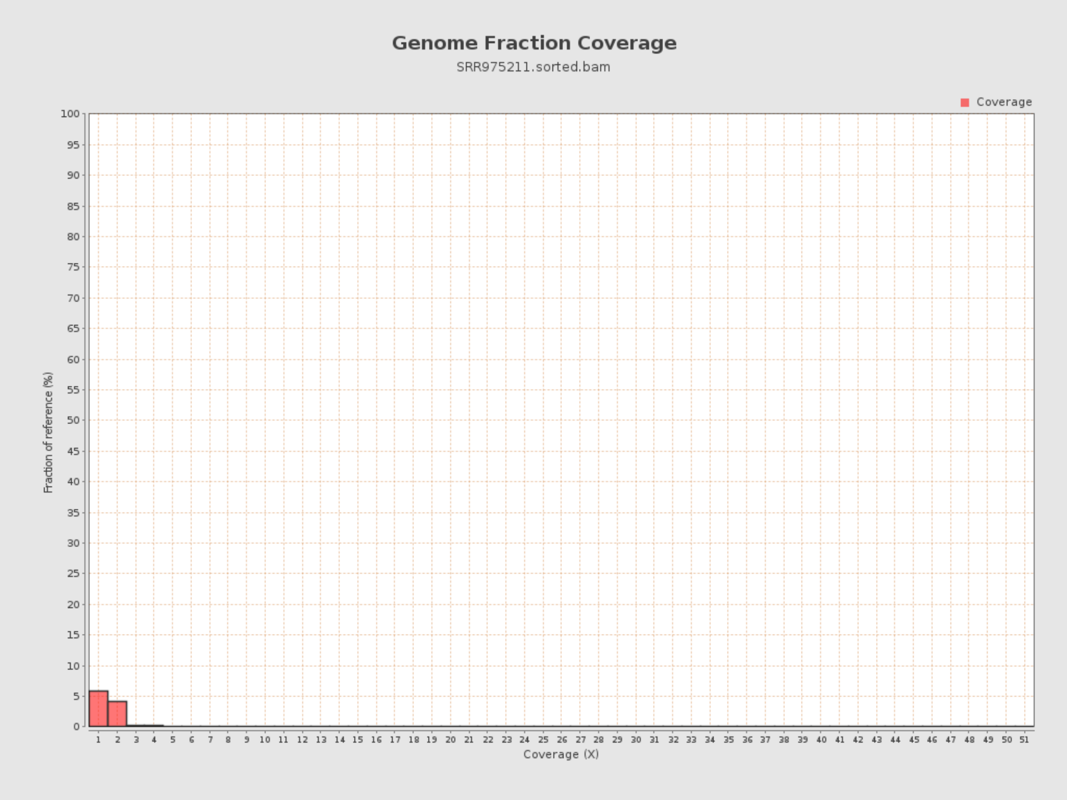
4. Results : Coverage Histogram



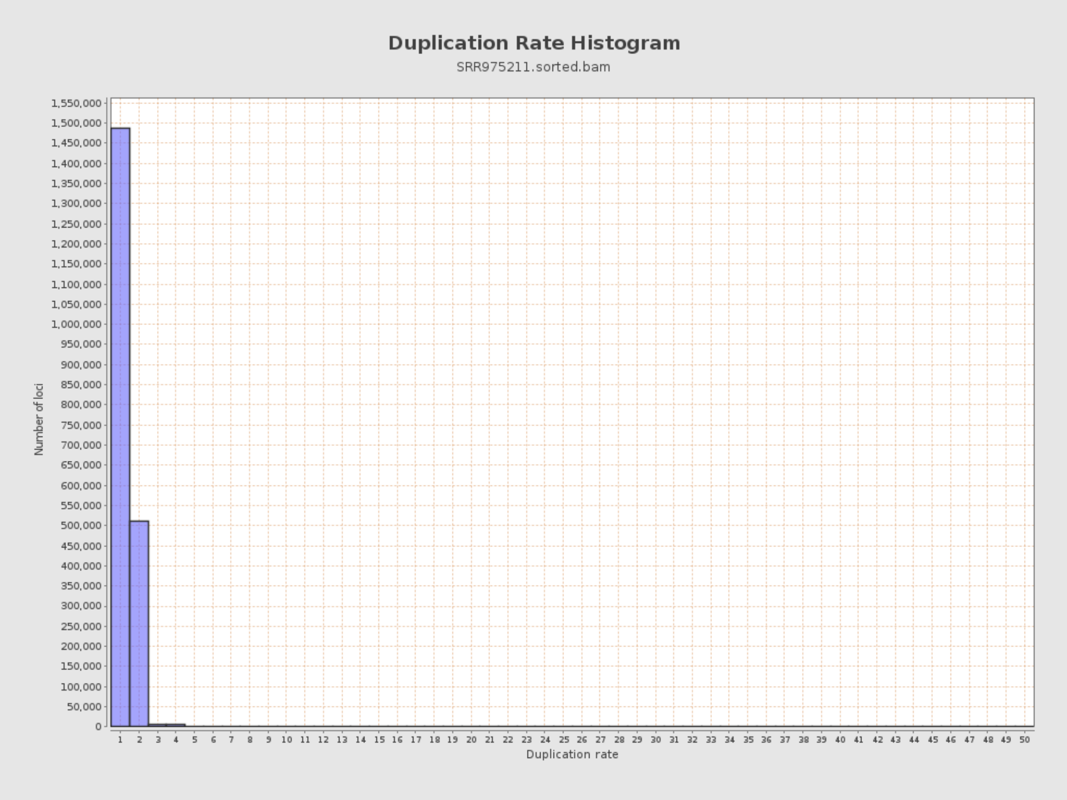
5. Results : Coverage Histogram (0-50X)



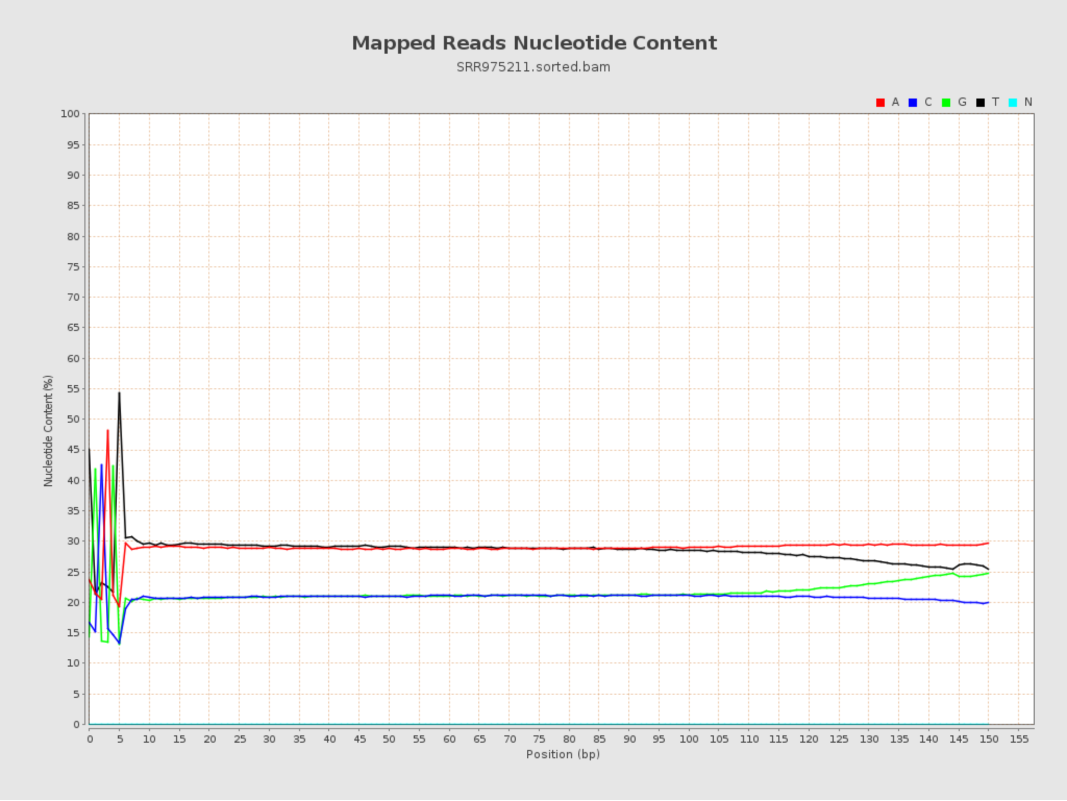
6. Results : Genome Fraction Coverage



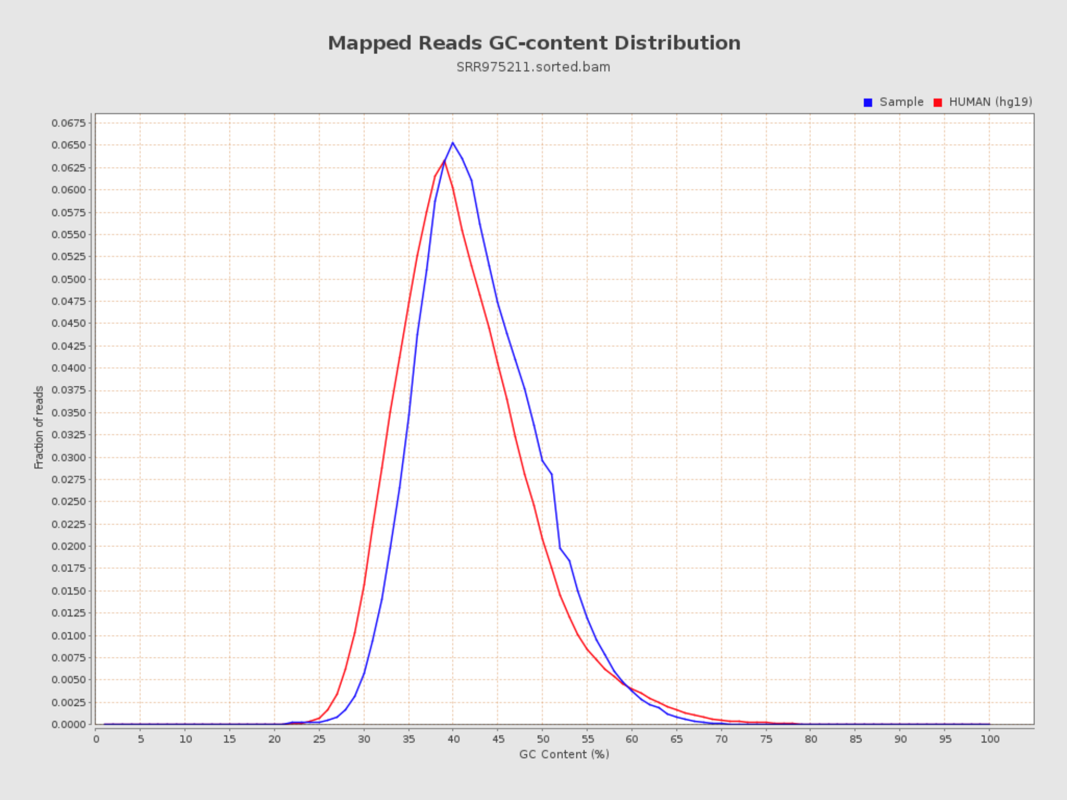
7. Results : Duplication Rate Histogram



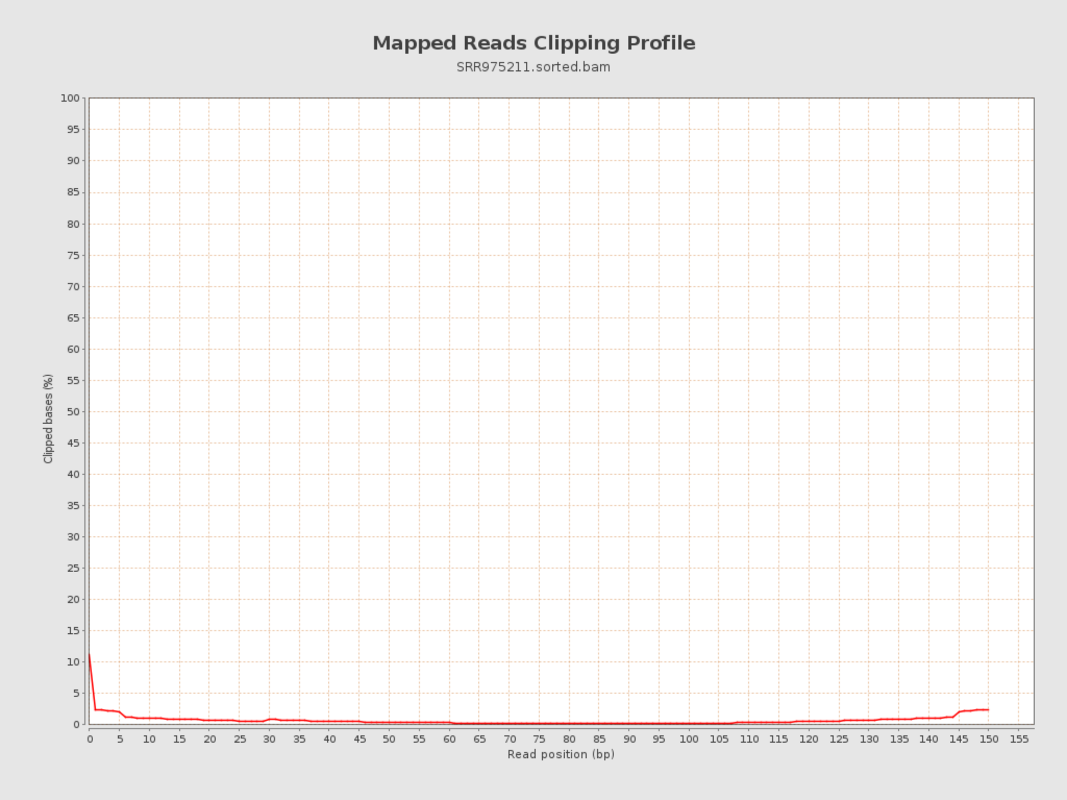
8. Results : Mapped Reads Nucleotide Content



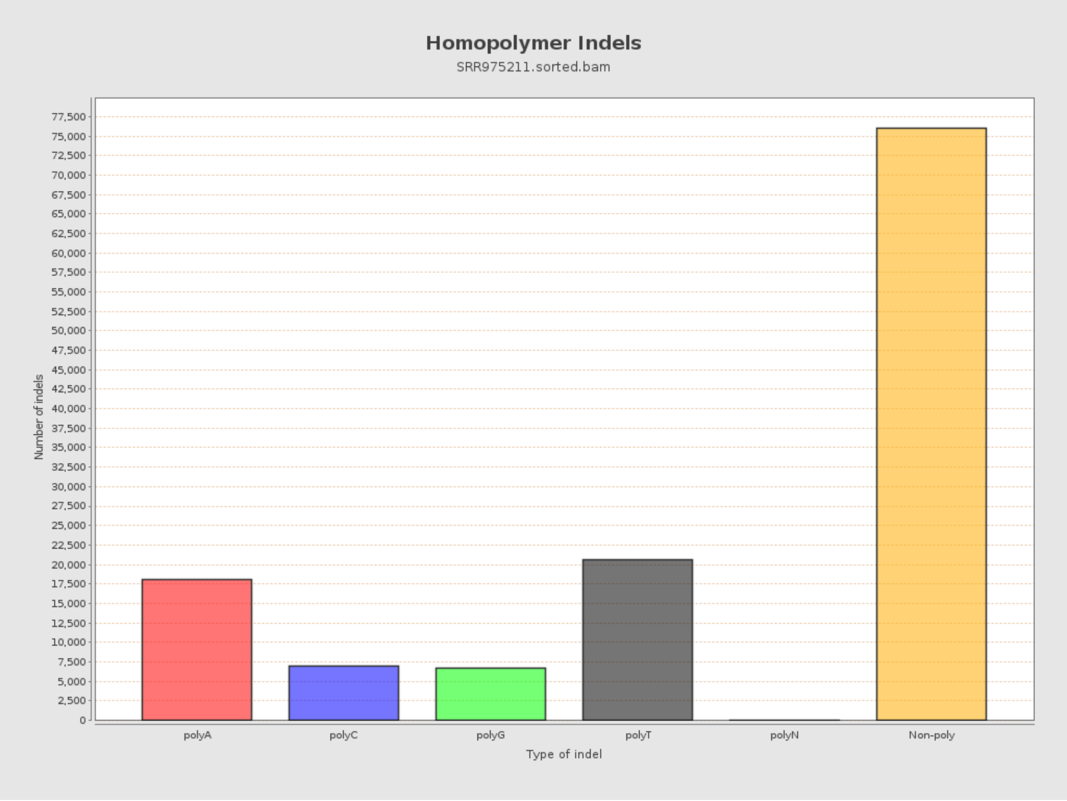
9. Results : Mapped Reads GC-content Distribution



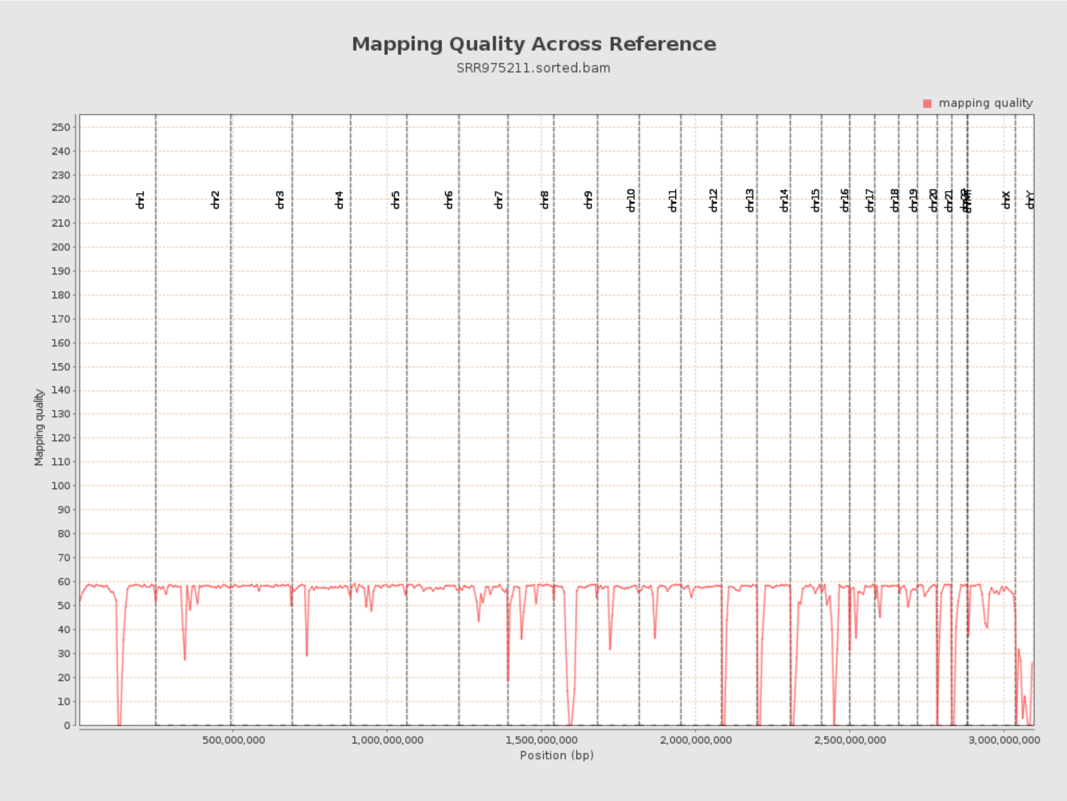
10. Results : Mapped Reads Clipping Profile



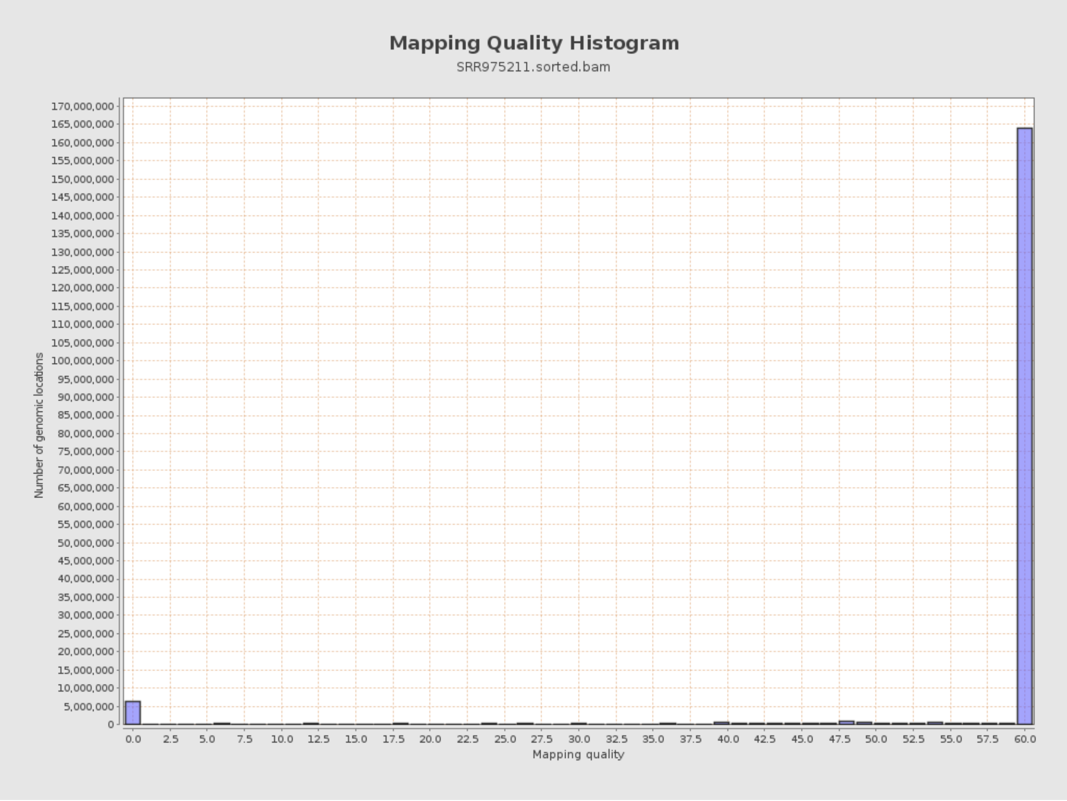
11. Results : Homopolymer Indels



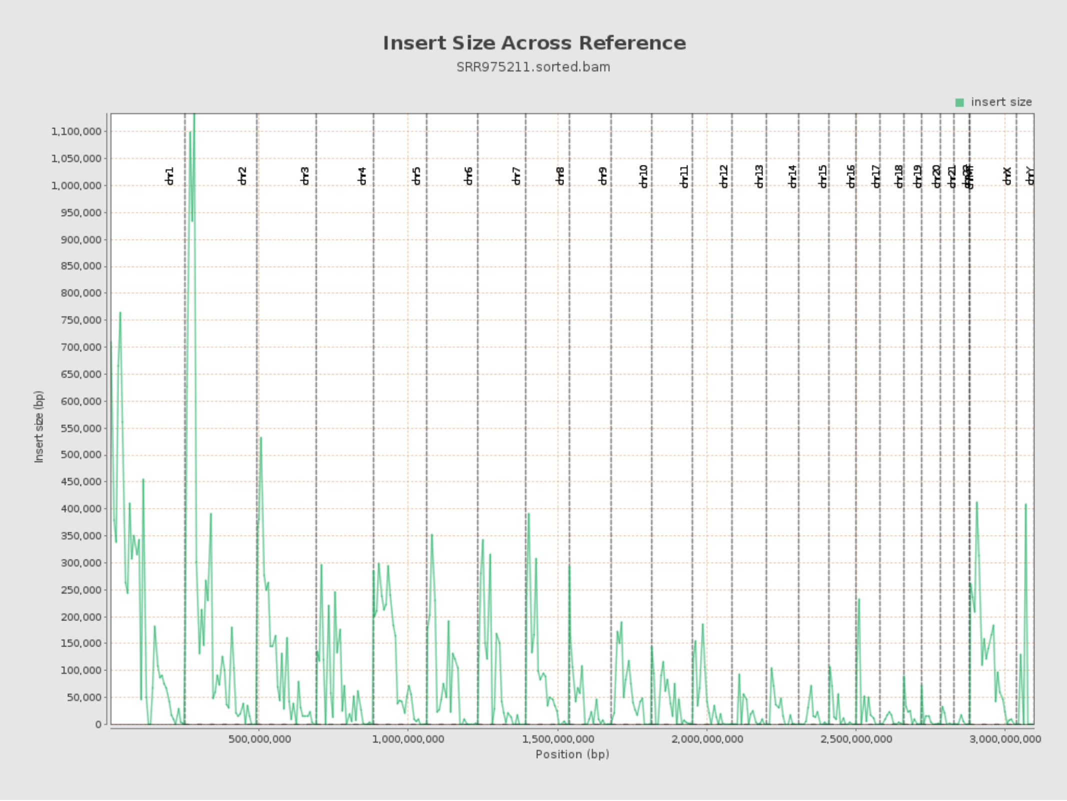
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram