Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 06:27:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975337.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_SRR975337 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975337_1.fastq.gz SRR975337_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 06:27:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975337.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,534,996
Mapped reads	4,364,044 / 96.23%
Unmapped reads	170,952 / 3.77%
Mapped paired reads	4,364,044 / 96.23%
Mapped reads, first in pair	2,179,998 / 48.07%
Mapped reads, second in pair	2,184,046 / 48.16%
Mapped reads, both in pair	4,320,494 / 95.27%
Mapped reads, singletons	43,550 / 0.96%
Secondary alignments	0
Supplementary alignments	25,072 / 0.55%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	289,559 / 6.38%
Duplication rate	3.32%
Clipped reads	2,782,295 / 61.35%

2.2. ACGT Content

Number/percentage of A's	118,932,135 / 30.17%
Number/percentage of C's	73,852,818 / 18.74%
Number/percentage of T's	119,298,932 / 30.26%
Number/percentage of G's	82,094,415 / 20.83%
Number/percentage of N's	7,999 / 0%

GC Percentage	39.56%

2.3. Coverage

Mean	0.1274
Standard Deviation	1.574

2.4. Mapping Quality

Mean Mapping Quality	52.6

2.5. Insert size

Mean	74,974.51
Standard Deviation	2,577,116.95
P25/Median/P75	134 / 167 / 213

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	2,976,030
Insertions	75,467
Mapped reads with at least one insertion	1.68%
Deletions	134,053
Mapped reads with at least one deletion	3%
Homopolymer indels	45.27%

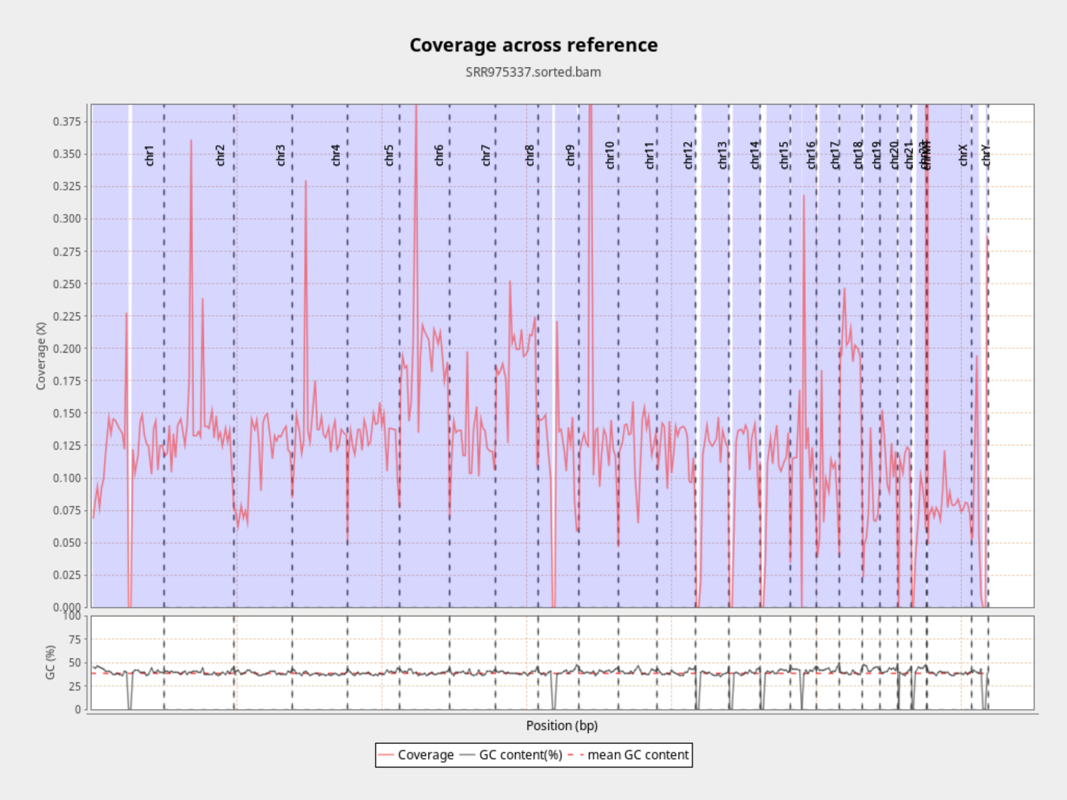
2.7. Chromosome stats

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

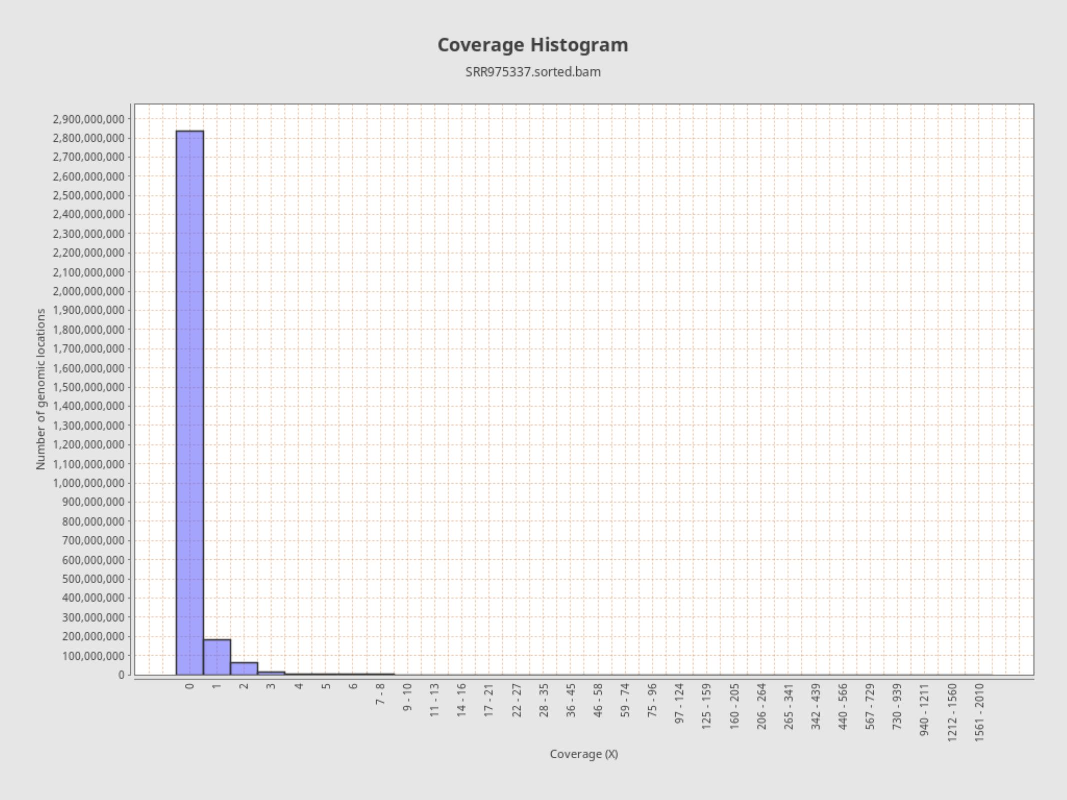
		bases	coverage	deviation
chr1	249250621	29062967	0.1166	1.6716
chr2	243199373	34815405	0.1432	1.9768
chr3	198022430	22870851	0.1155	0.4725
chr4	191154276	27068201	0.1416	1.7923
chr5	180915260	23940646	0.1323	0.5772
chr6	171115067	34073425	0.1991	2.1535
chr7	159138663	20352286	0.1279	1.4921
chr8	146364022	28281543	0.1932	0.8524
chr9	141213431	16248074	0.1151	2.7061
chr10	135534747	19847368	0.1464	3.0815
chr11	135006516	17216006	0.1275	1.0474
chr12	133851895	16381304	0.1224	0.4674
chr13	115169878	12215995	0.1061	0.4245
chr14	107349540	11283603	0.1051	0.5168
chr15	102531392	9896729	0.0965	0.4036
chr16	90354753	10992117	0.1217	1.6508
chr17	81195210	7479721	0.0921	1.5878
chr18	78077248	15745483	0.2017	2.5826
chr19	59128983	4271181	0.0722	1.0123
chr20	63025520	7026705	0.1115	0.5427
chr21	48129895	4859244	0.101	0.6337
chr22	51304566	3057928	0.0596	0.3866
chrMT	16571	113336	6.8394	5.0732
chrX	155270560	12153424	0.0783	0.5622

chrY	59373566	5180644	0.0873	2.4416

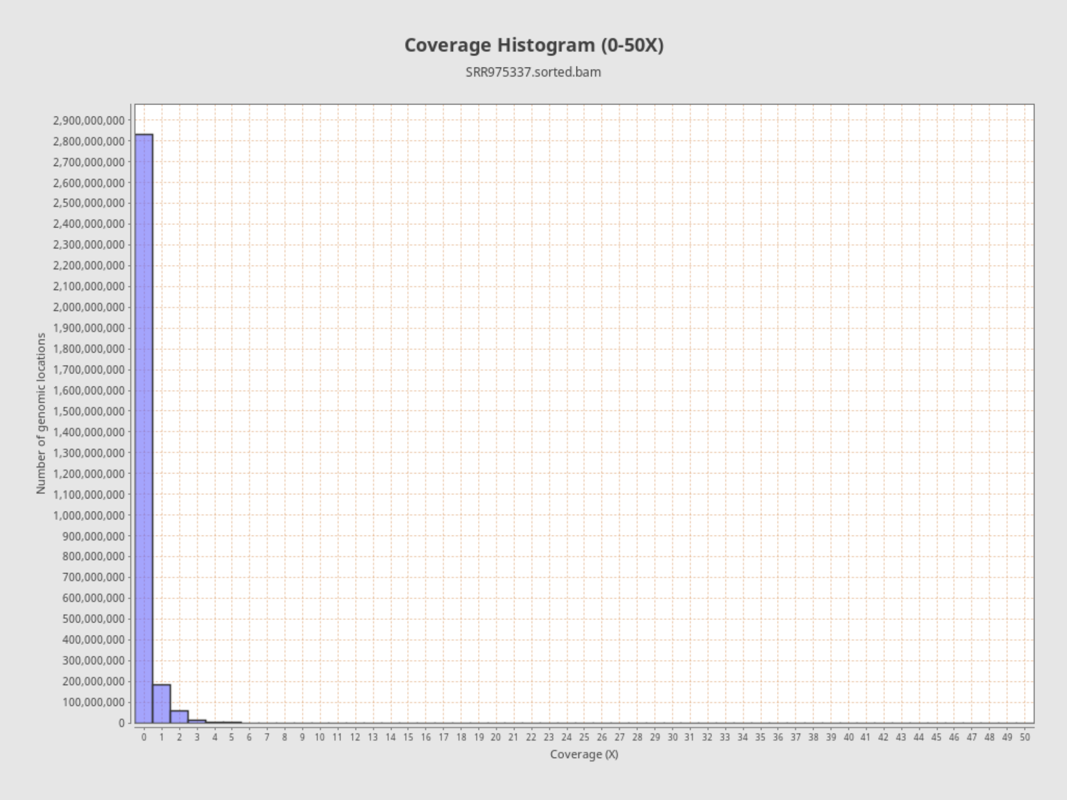
3. Results : Coverage across reference



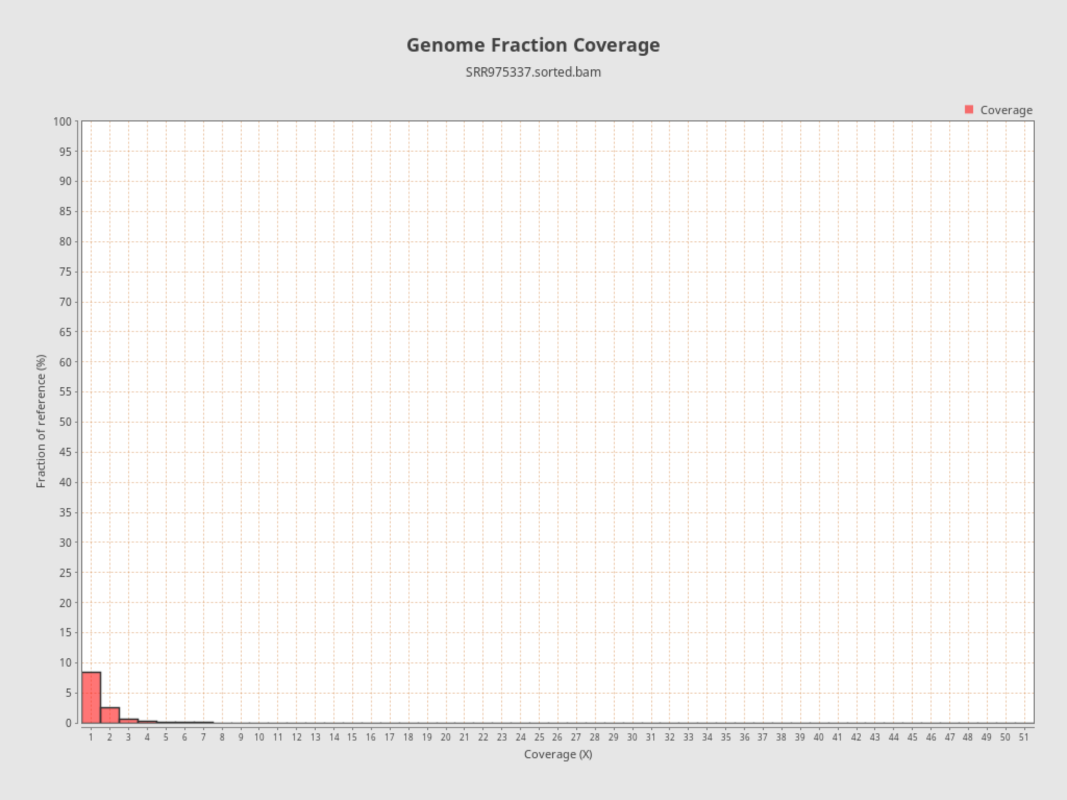
4. Results : Coverage Histogram



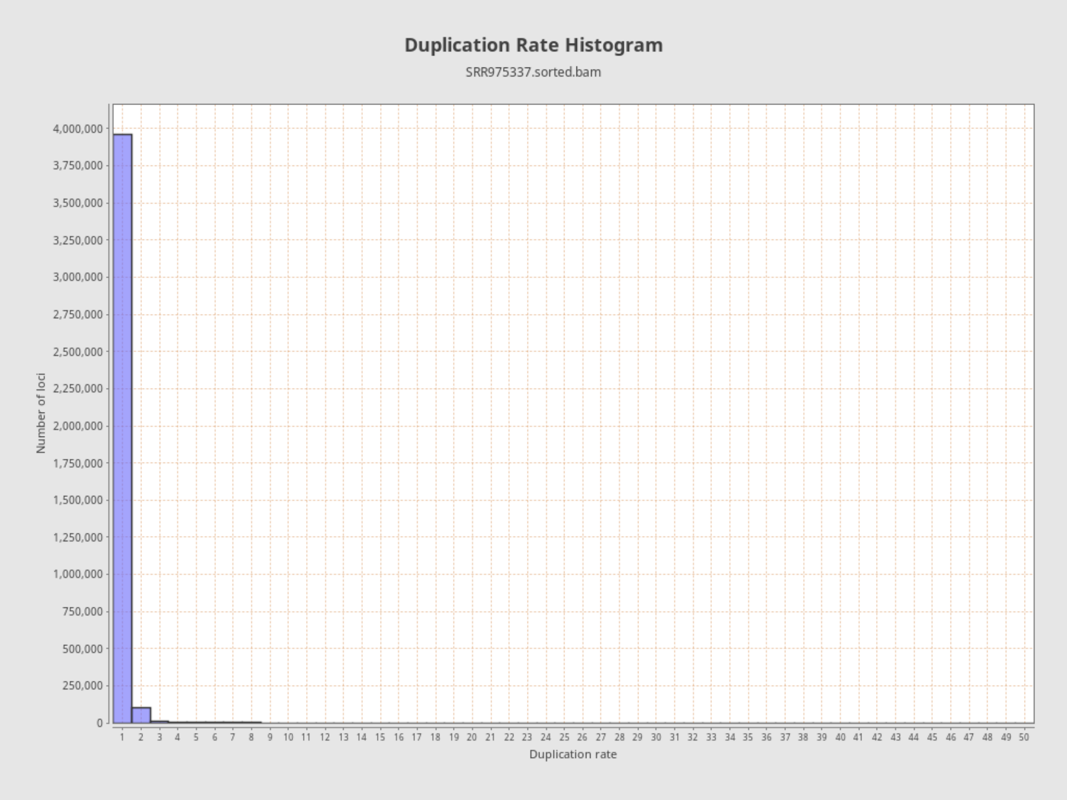
5. Results : Coverage Histogram (0-50X)



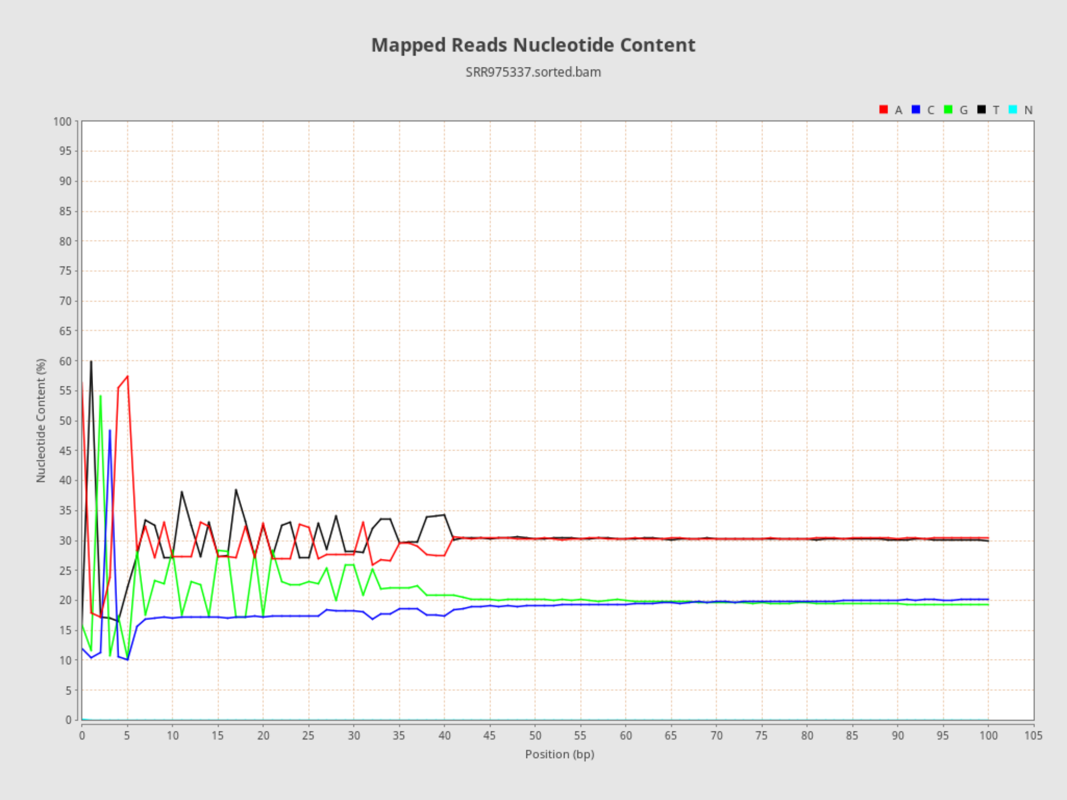
6. Results : Genome Fraction Coverage



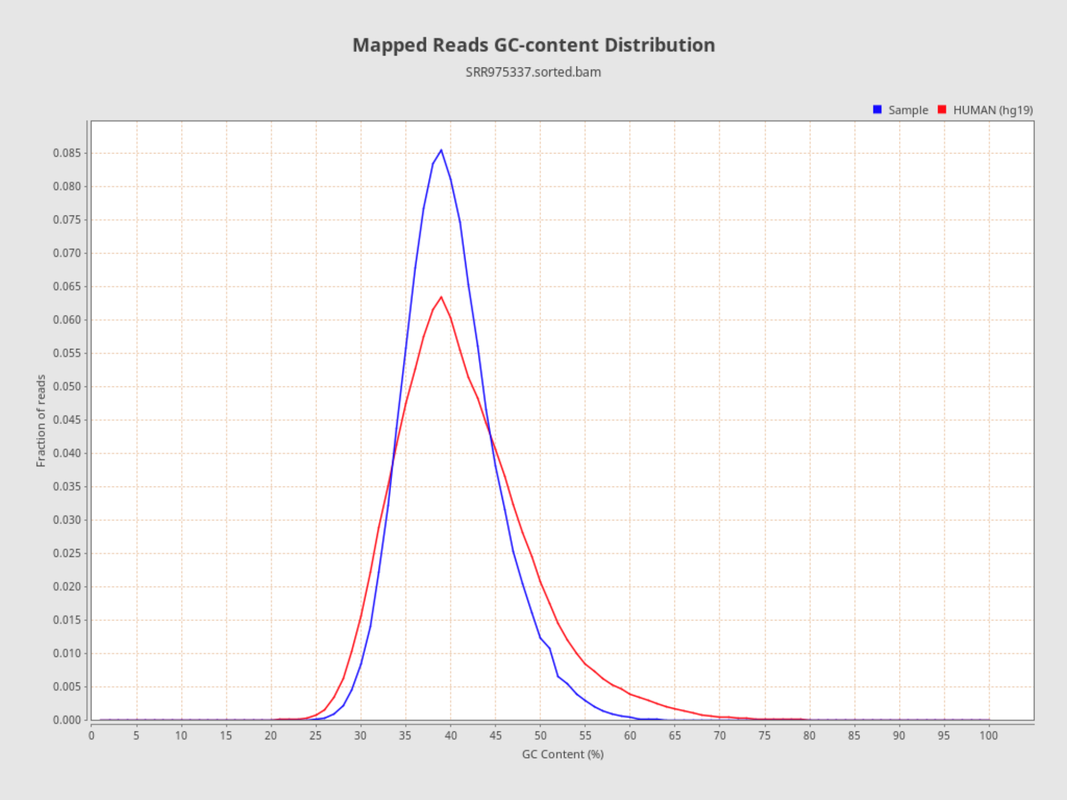
7. Results : Duplication Rate Histogram



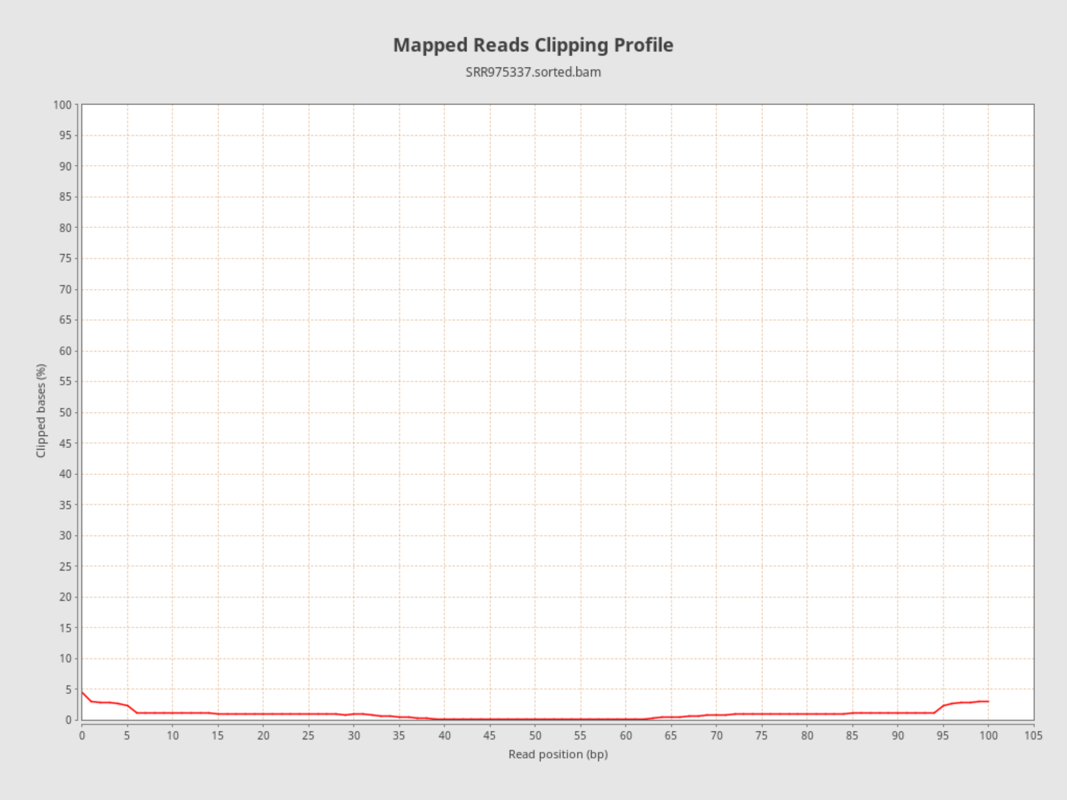
8. Results : Mapped Reads Nucleotide Content



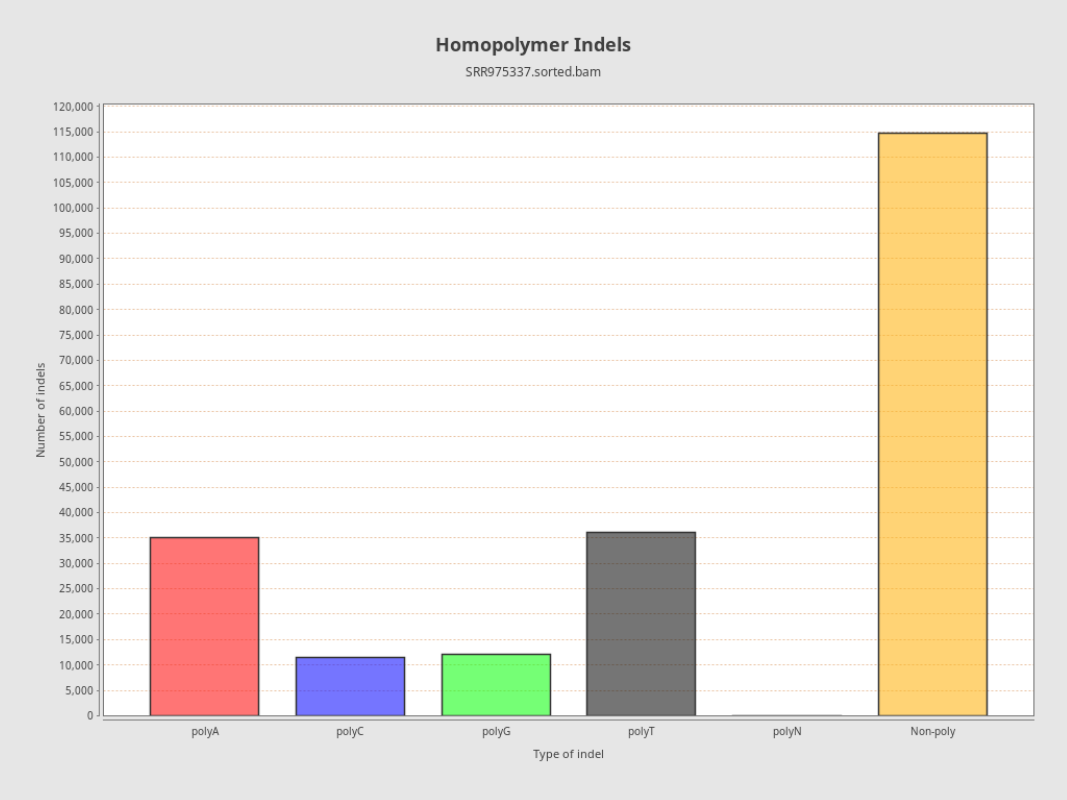
9. Results : Mapped Reads GC-content Distribution



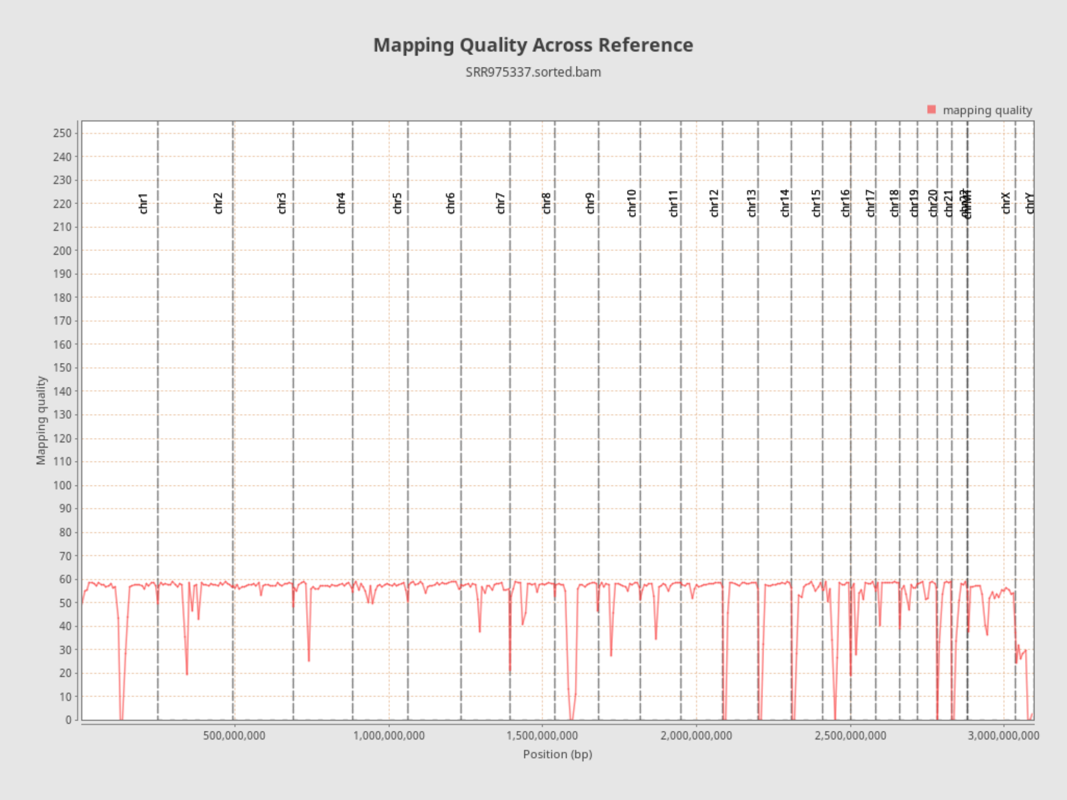
10. Results : Mapped Reads Clipping Profile



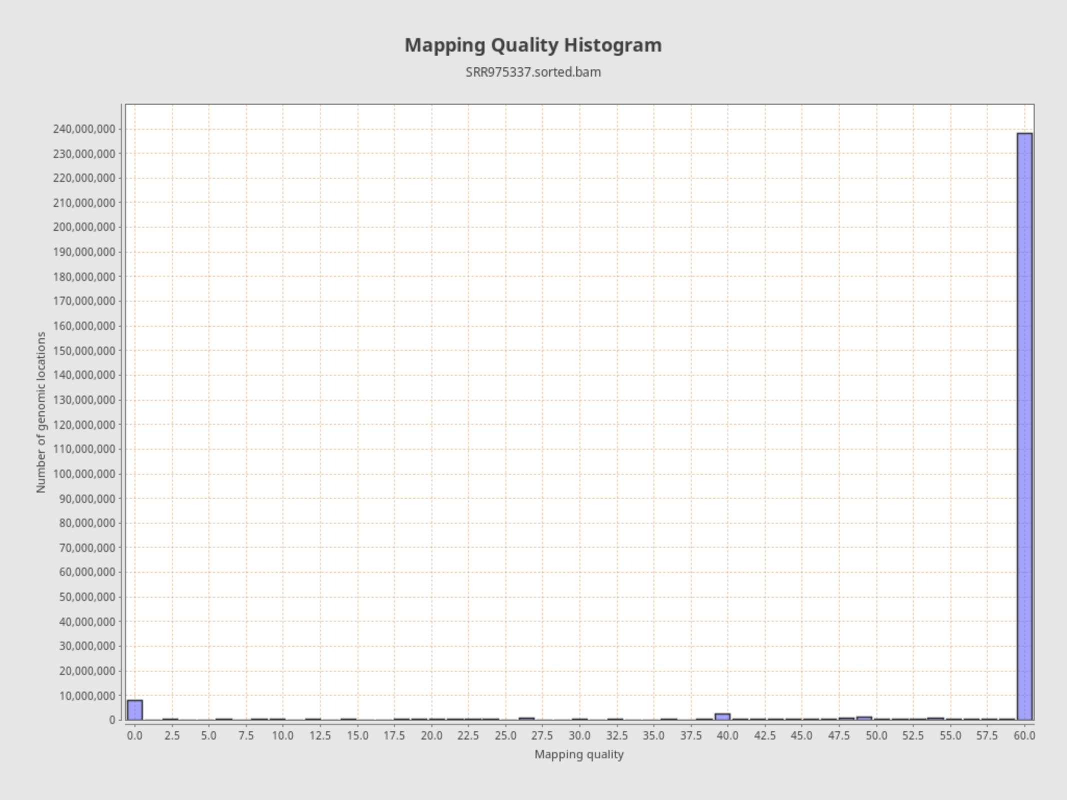
11. Results : Homopolymer Indels



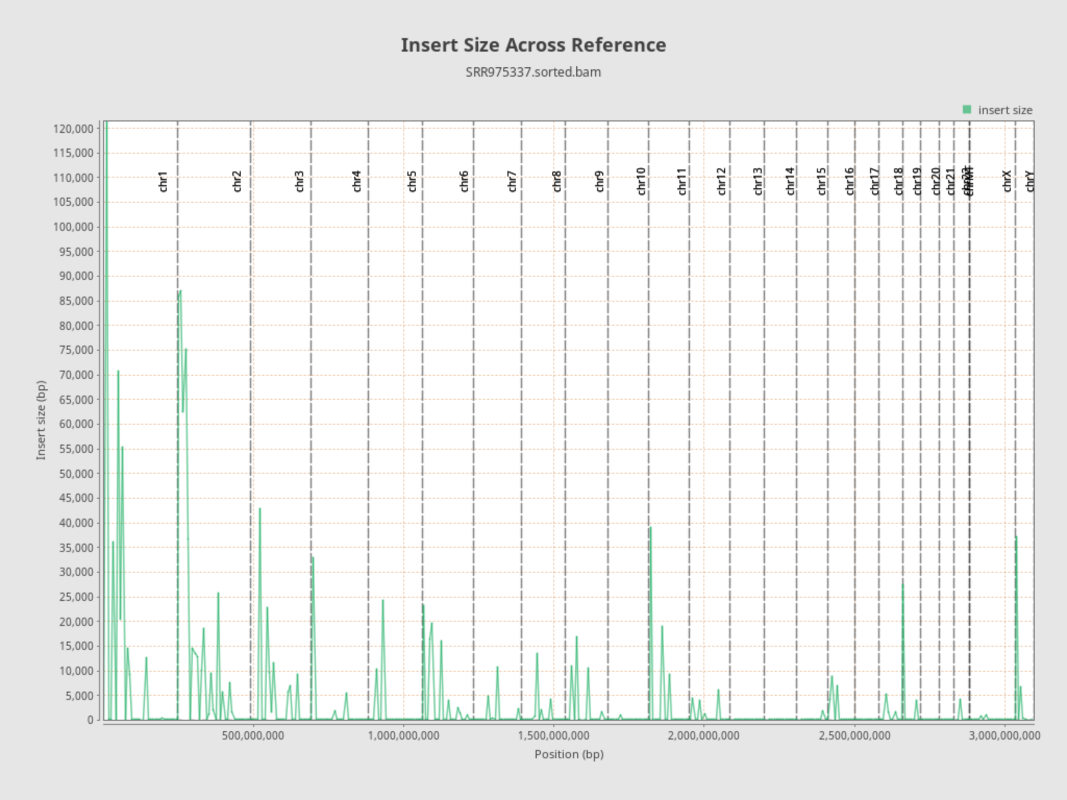
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram