Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/09 02:37:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975315.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_SRR975315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975315_1.fastq.gz SRR975315_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 09 02:37:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975315.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,546,488
Mapped reads	78,396,789 / 99.81%
Unmapped reads	149,699 / 0.19%
Mapped paired reads	78,396,789 / 99.81%
Mapped reads, first in pair	39,212,017 / 49.92%
Mapped reads, second in pair	39,184,772 / 49.89%
Mapped reads, both in pair	78,328,528 / 99.72%
Mapped reads, singletons	68,261 / 0.09%
Secondary alignments	0
Supplementary alignments	136,130 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	51,623,765 / 65.72%
Duplication rate	50.67%
Clipped reads	44,180,671 / 56.25%

2.2. ACGT Content

Number/percentage of A's	1,942,115,850 / 26.56%
Number/percentage of C's	1,653,094,543 / 22.6%
Number/percentage of T's	2,000,165,173 / 27.35%
Number/percentage of G's	1,717,390,798 / 23.48%
Number/percentage of N's	321,970 / 0%

GC Percentage	46.09%

2.3. Coverage

Mean	2.3632
Standard Deviation	32.6034

2.4. Mapping Quality

Mean Mapping Quality	56.04

2.5. Insert size

Mean	86,564.53
Standard Deviation	2,905,582.95
P25/Median/P75	149 / 186 / 234

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	45,607,631
Insertions	638,398
Mapped reads with at least one insertion	0.81%
Deletions	1,789,339
Mapped reads with at least one deletion	2.25%
Homopolymer indels	48.43%

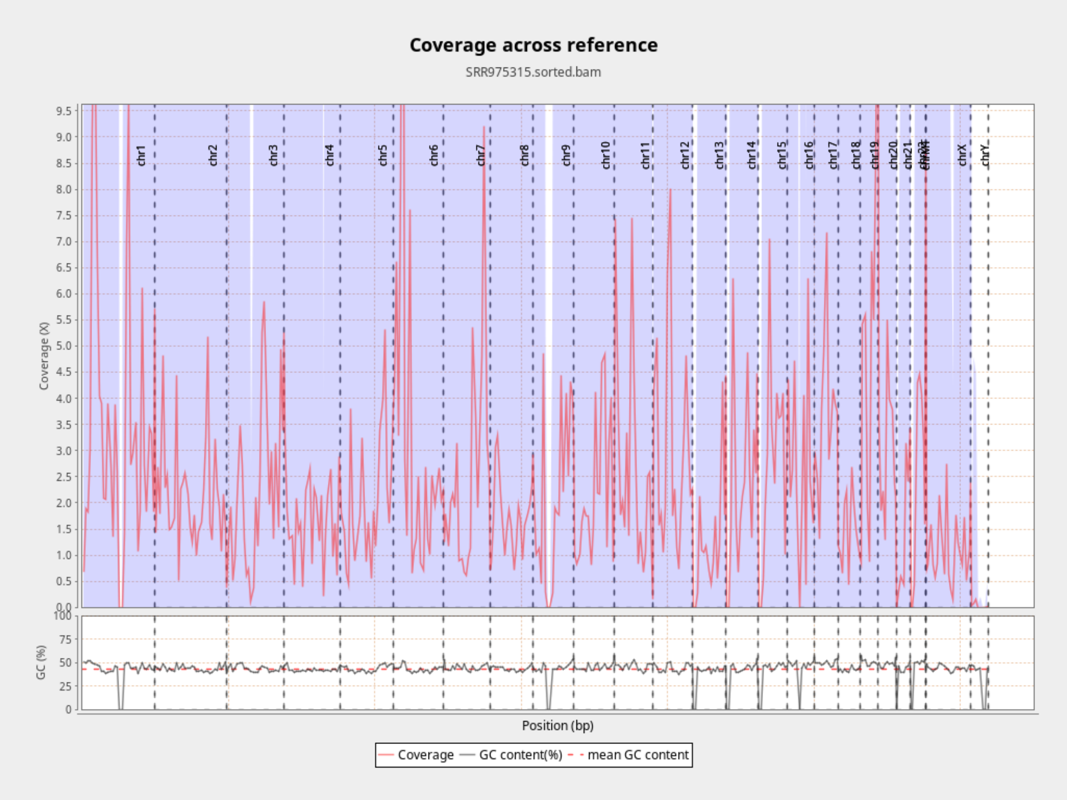
2.7. Chromosome stats

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

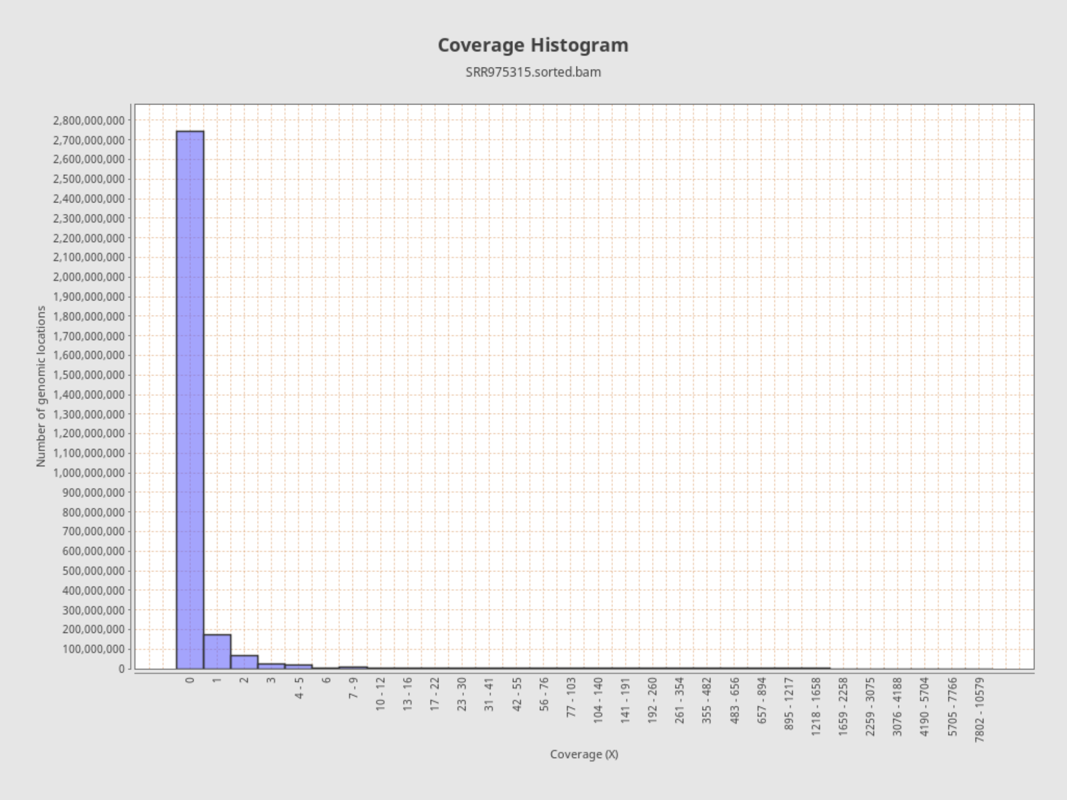
		bases	coverage	deviation
chr1	249250621	870272535	3.4916	42.0479
chr2	243199373	527417636	2.1687	28.0818
chr3	198022430	441041976	2.2272	30.895
chr4	191154276	319124220	1.6695	26.5522
chr5	180915260	368675455	2.0378	30.3979
chr6	171115067	592529555	3.4628	48.2395
chr7	159138663	403423656	2.535	36.2143
chr8	146364022	250258705	1.7098	25.0293
chr9	141213431	294008504	2.082	29.6207
chr10	135534747	302130211	2.2292	30.7785
chr11	135006516	357061281	2.6448	33.0432
chr12	133851895	402486761	3.007	34.7606
chr13	115169878	142494686	1.2373	23.2094
chr14	107349540	244247993	2.2753	31.9776
chr15	102531392	280076769	2.7316	33.8135
chr16	90354753	241110651	2.6685	33.4005
chr17	81195210	299231100	3.6853	38.2552
chr18	78077248	114789232	1.4702	23.1723
chr19	59128983	300895822	5.0888	46.8012
chr20	63025520	189339077	3.0042	39.2082
chr21	48129895	70121506	1.4569	22.3869
chr22	51304566	130401398	2.5417	31.5067
chrMT	16571	145656	8.7898	24.7541
chrX	155270560	172171686	1.1088	18.4077

chrY	59373566	2136503	0.036	2.3295

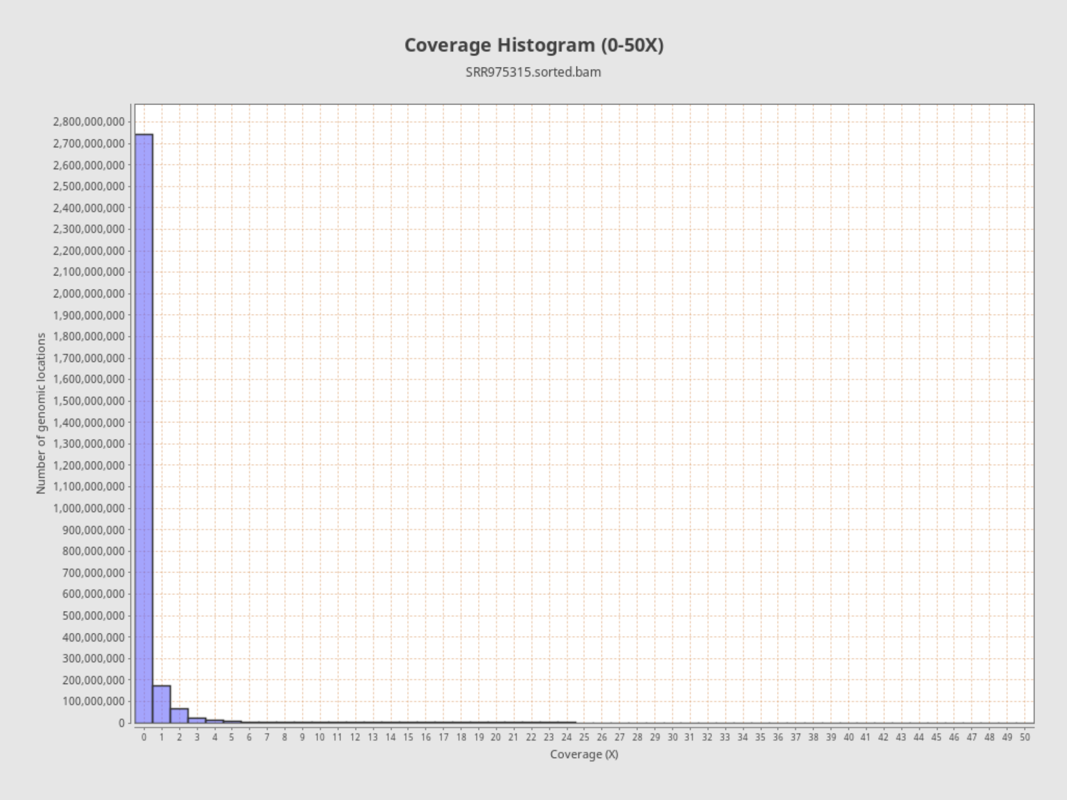
3. Results : Coverage across reference



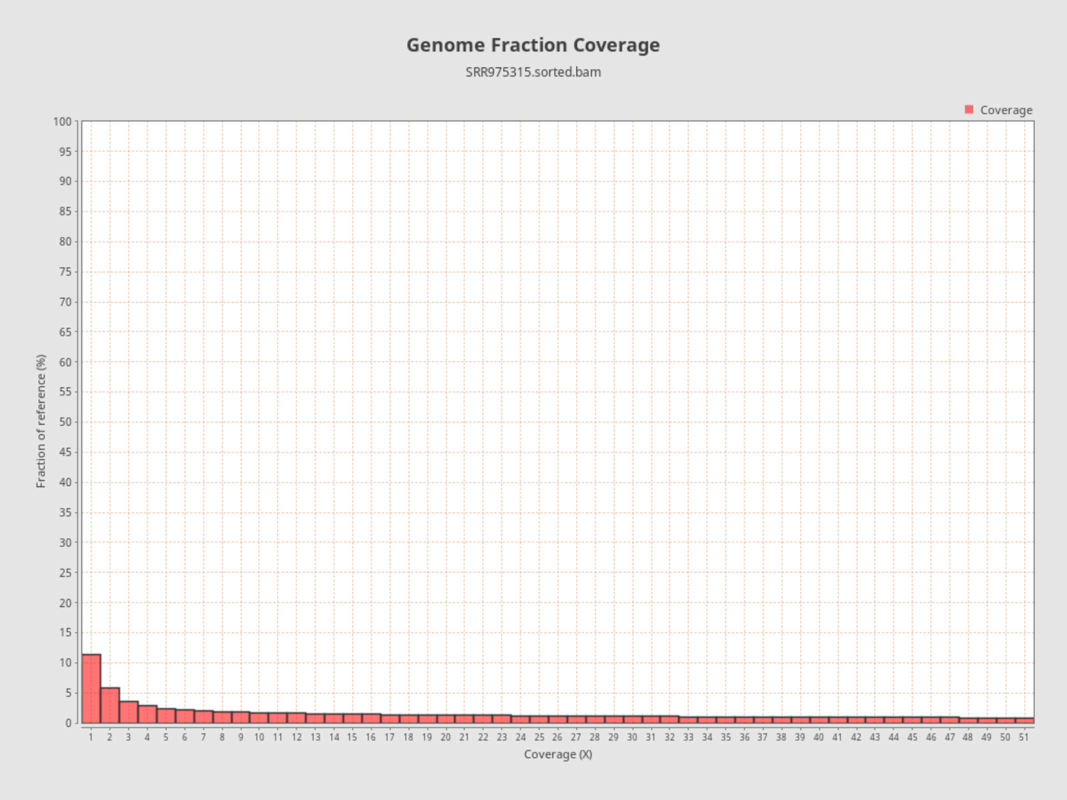
4. Results : Coverage Histogram



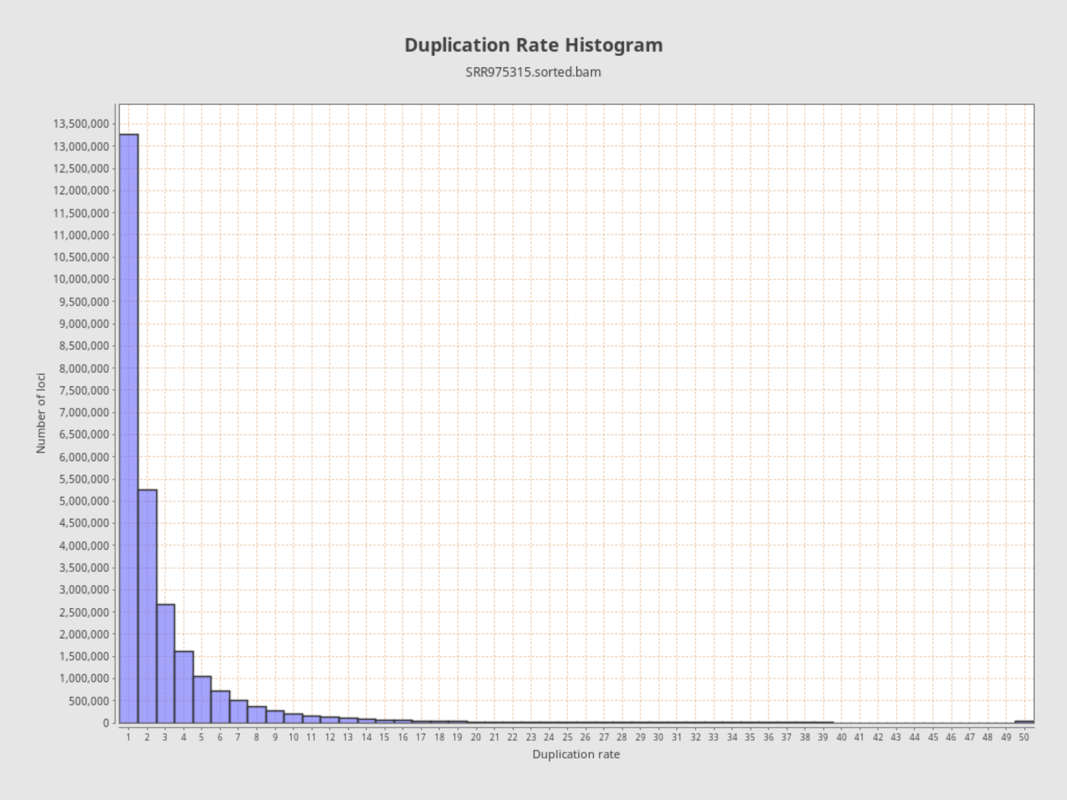
5. Results : Coverage Histogram (0-50X)



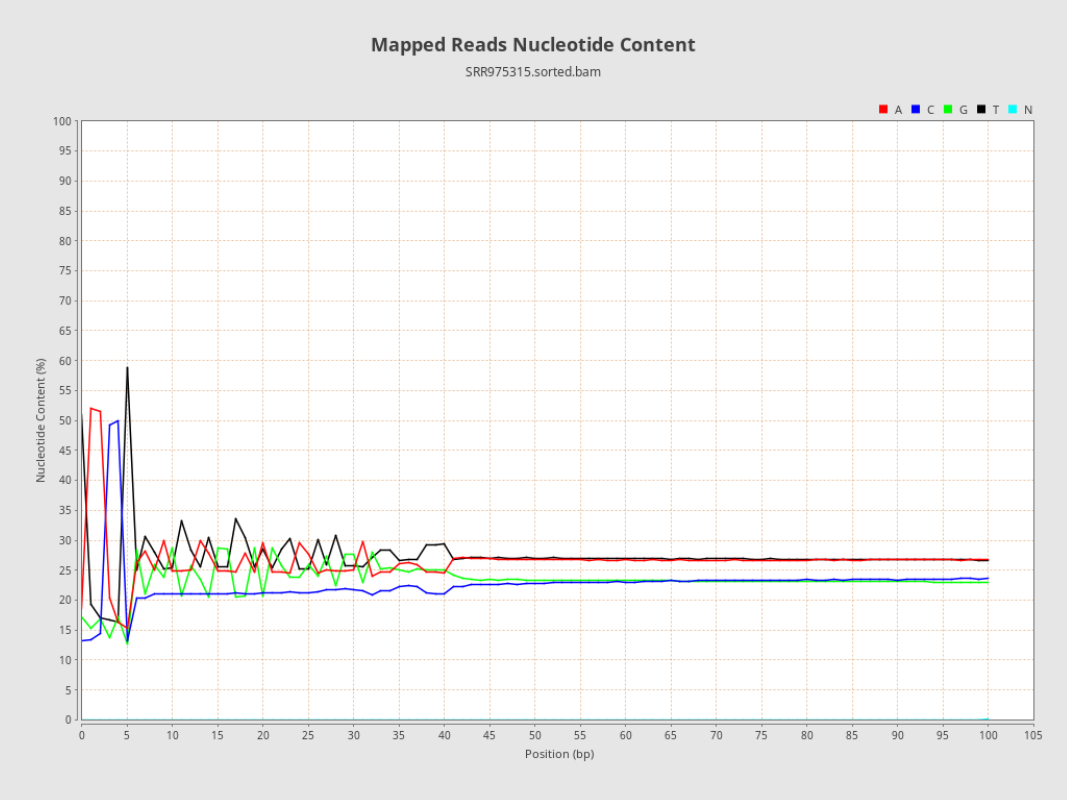
6. Results : Genome Fraction Coverage



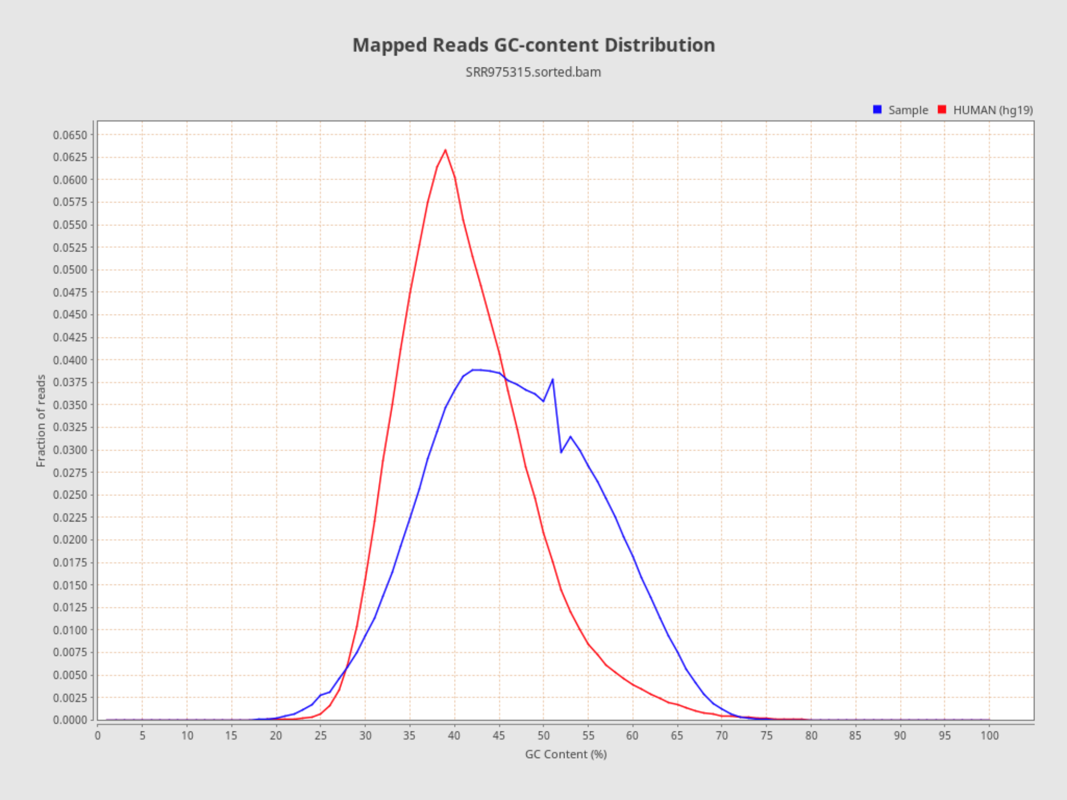
7. Results : Duplication Rate Histogram



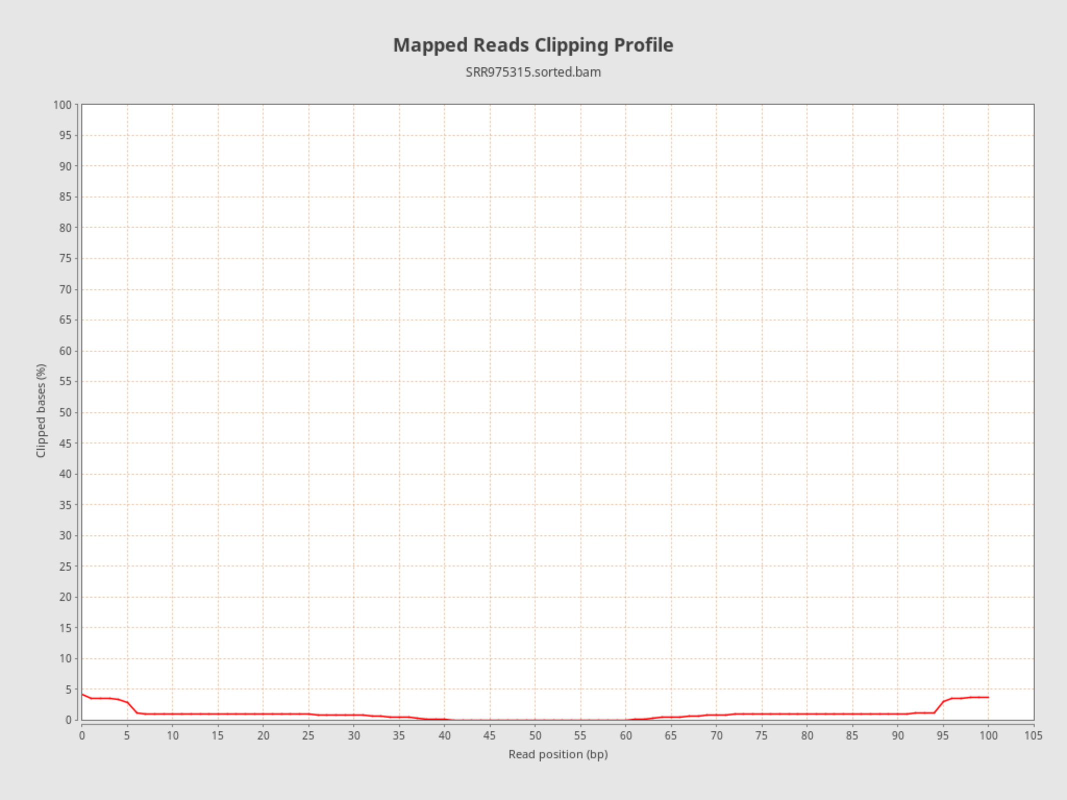
8. Results : Mapped Reads Nucleotide Content



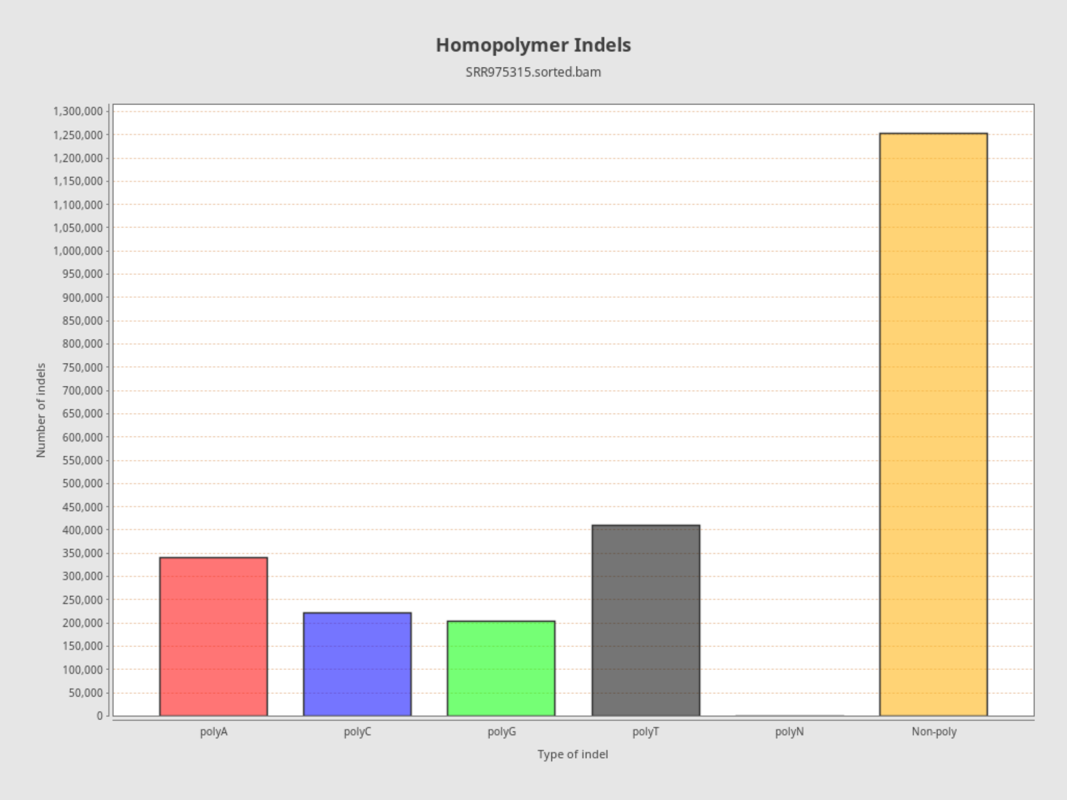
9. Results : Mapped Reads GC-content Distribution



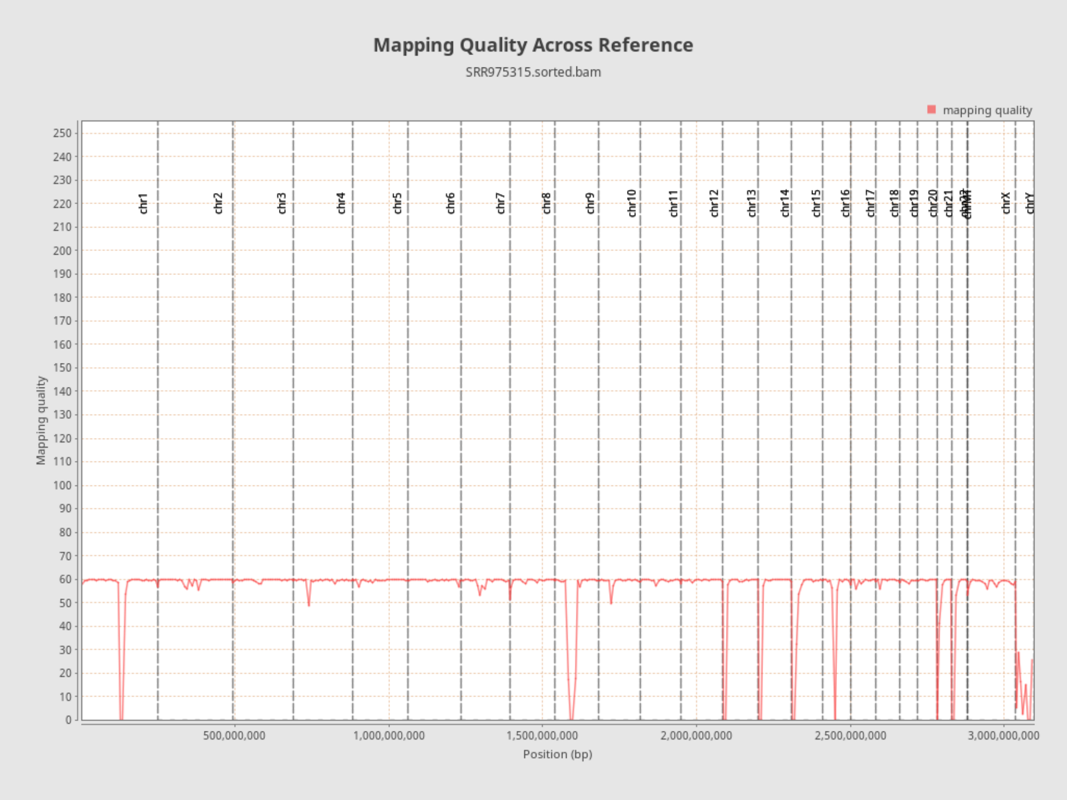
10. Results : Mapped Reads Clipping Profile



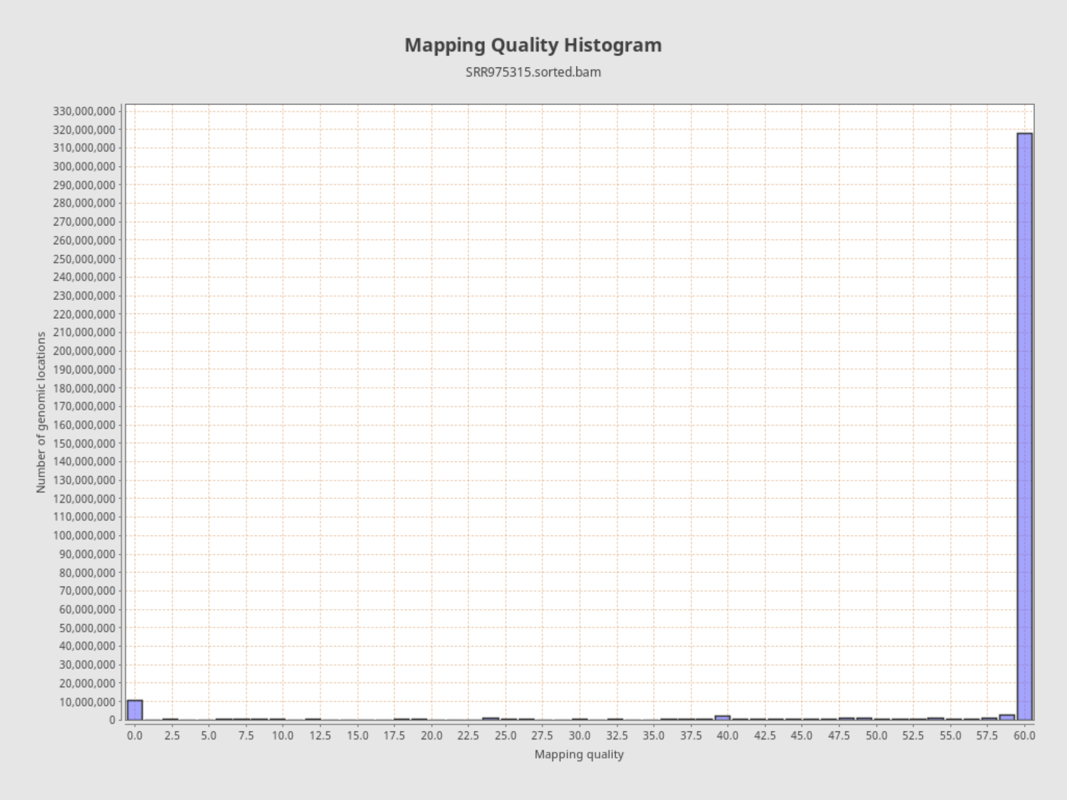
11. Results : Homopolymer Indels



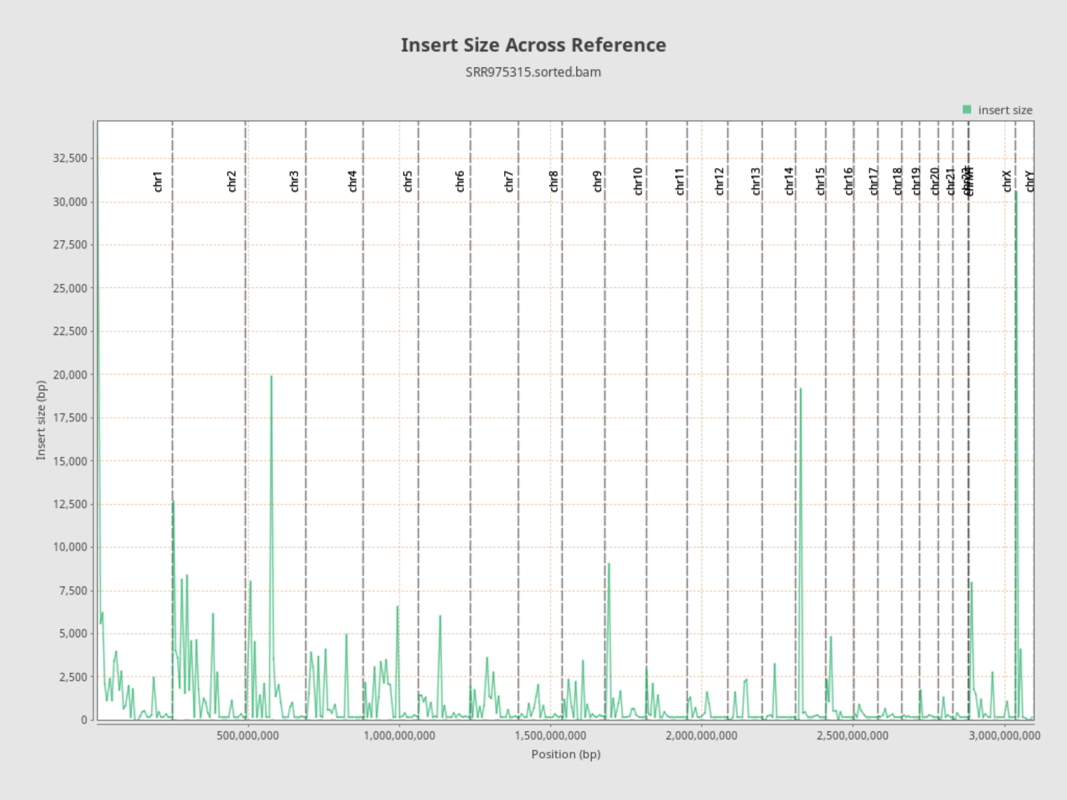
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram