Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 02:26:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975314.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_SRR975314 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975314_1.fastq.gz SRR975314_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 02:26:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975314.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,587,888
Mapped reads	2,561,296 / 98.97%
Unmapped reads	26,592 / 1.03%
Mapped paired reads	2,561,296 / 98.97%
Mapped reads, first in pair	1,283,082 / 49.58%
Mapped reads, second in pair	1,278,214 / 49.39%
Mapped reads, both in pair	2,552,944 / 98.65%
Mapped reads, singletons	8,352 / 0.32%
Secondary alignments	0
Supplementary alignments	27,619 / 1.07%
Read min/max/mean length	30 / 151 / 151.52
Duplicated reads (estimated)	381,091 / 14.73%
Duplication rate	14.82%
Clipped reads	1,844,050 / 71.26%

2.2. ACGT Content

Number/percentage of A's	99,719,149 / 28.88%
Number/percentage of C's	70,765,724 / 20.5%
Number/percentage of T's	100,397,319 / 29.08%
Number/percentage of G's	74,363,536 / 21.54%
Number/percentage of N's	22,926 / 0.01%

GC Percentage	42.03%

2.3. Coverage

Mean	0.1116
Standard Deviation	1.1475

2.4. Mapping Quality

Mean Mapping Quality	53.78

2.5. Insert size

Mean	75,248.77
Standard Deviation	2,620,284.4
P25/Median/P75	136 / 169 / 214

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	3,405,163
Insertions	60,513
Mapped reads with at least one insertion	2.25%
Deletions	123,245
Mapped reads with at least one deletion	4.65%
Homopolymer indels	46.92%

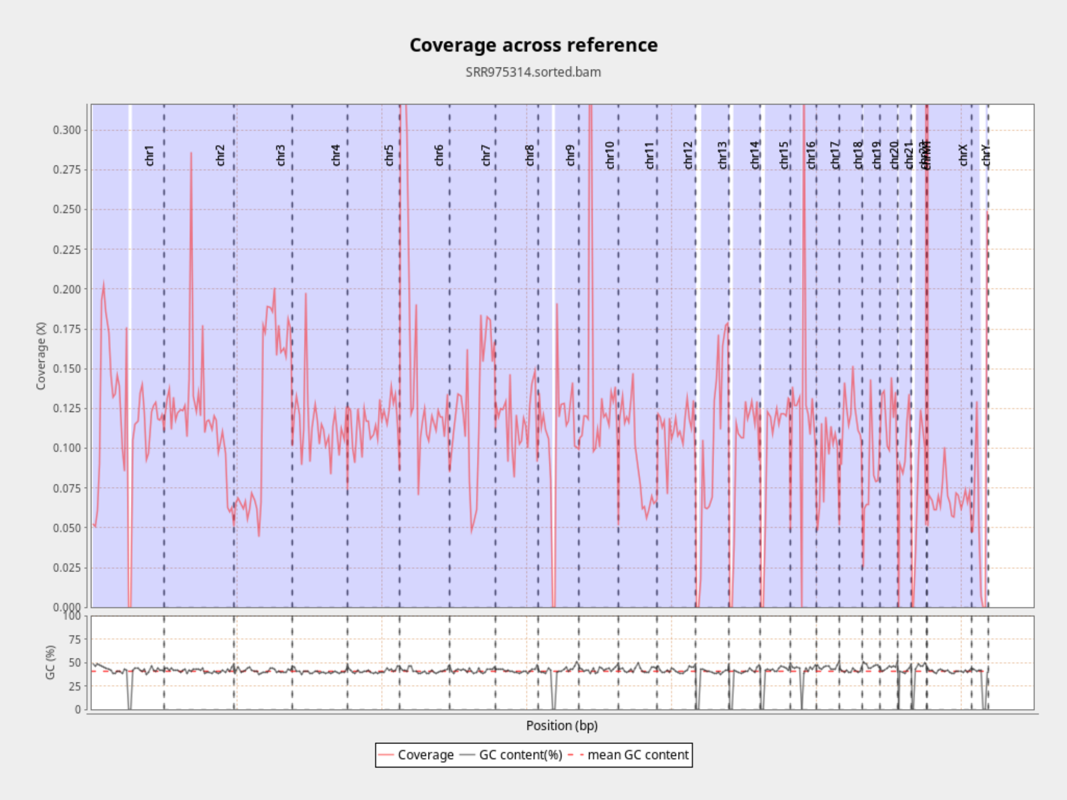
2.7. Chromosome stats

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

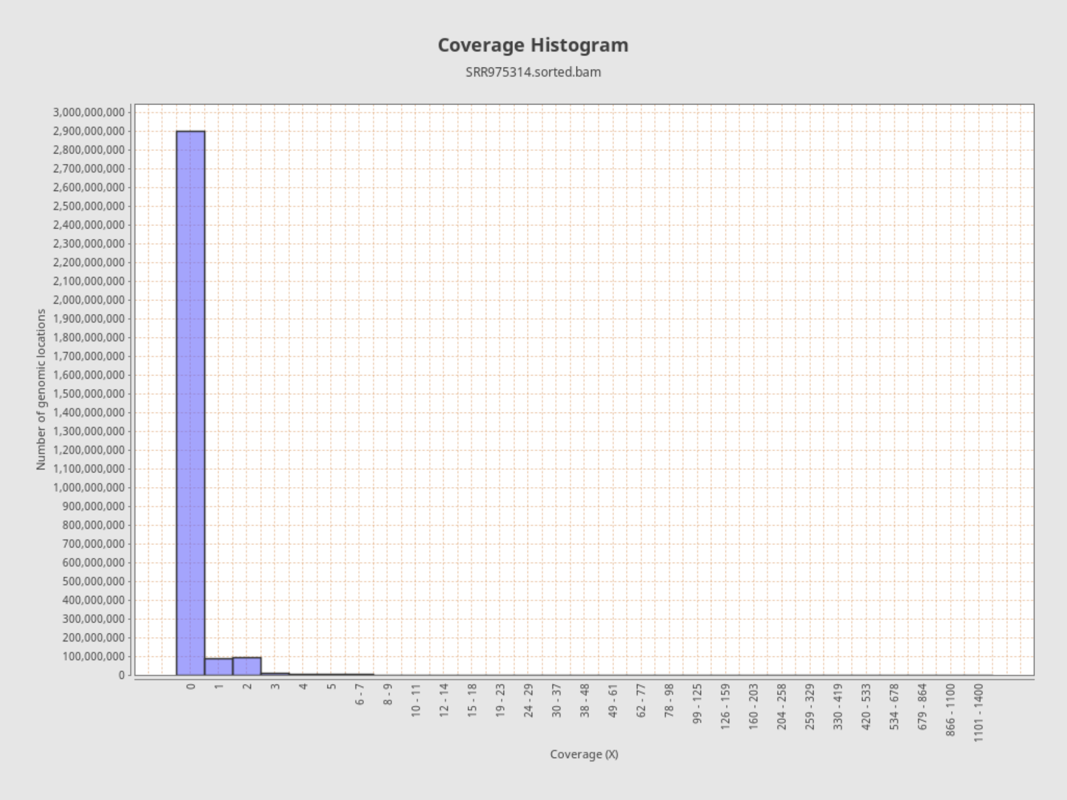
		bases	coverage	deviation
chr1	249250621	29017970	0.1164	1.1538
chr2	243199373	29177713	0.12	1.1772
chr3	198022430	23992029	0.1212	0.4995
chr4	191154276	21873433	0.1144	0.7674
chr5	180915260	21071948	0.1165	0.472
chr6	171115067	27034244	0.158	0.9796
chr7	159138663	19937208	0.1253	1.2869
chr8	146364022	17061947	0.1166	0.5669
chr9	141213431	15188159	0.1076	1.8991
chr10	135534747	18417428	0.1359	2.9025
chr11	135006516	12496959	0.0926	1.1719
chr12	133851895	15103758	0.1128	0.4623
chr13	115169878	11456556	0.0995	0.4382
chr14	107349540	10299436	0.0959	0.4402
chr15	102531392	10089116	0.0984	0.4338
chr16	90354753	11511455	0.1274	1.6111
chr17	81195210	7432242	0.0915	1.0612
chr18	78077248	9313136	0.1193	1.7244
chr19	59128983	4712086	0.0797	0.7645
chr20	63025520	7546974	0.1197	0.5189
chr21	48129895	4417854	0.0918	0.5752
chr22	51304566	3695385	0.072	0.374
chrMT	16571	53922	3.254	2.745
chrX	155270560	10520814	0.0678	0.4889

chrY	59373566	4080516	0.0687	1.4903

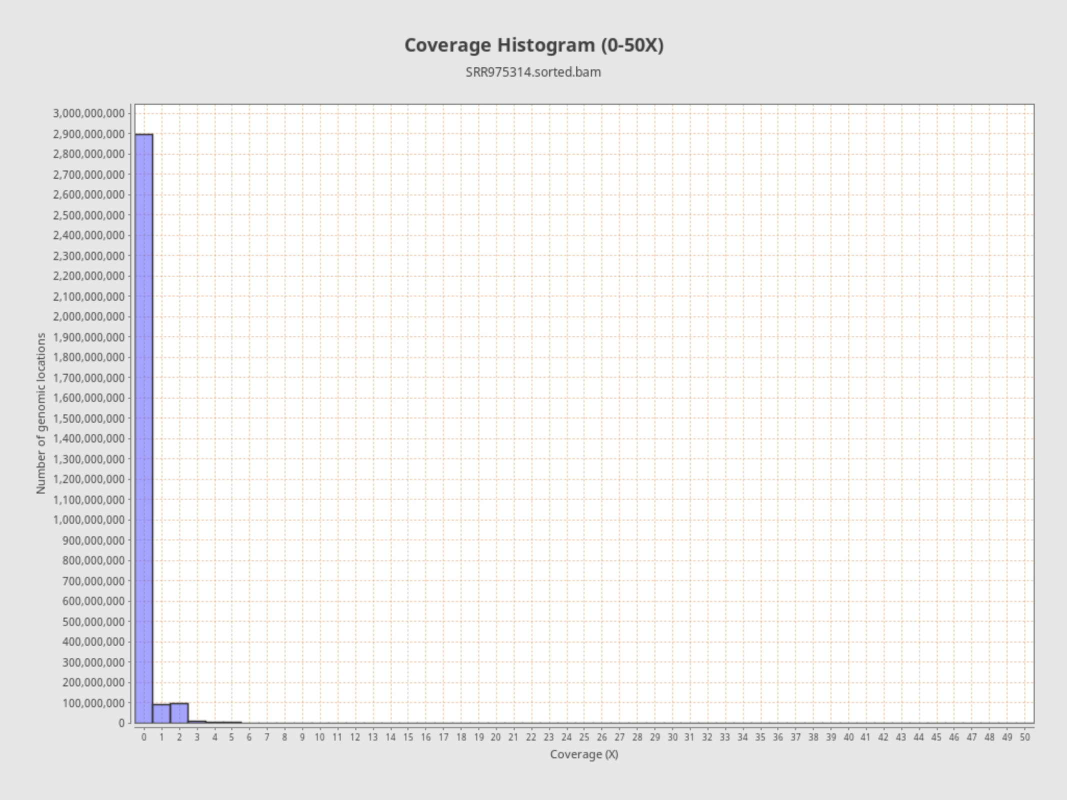
3. Results : Coverage across reference



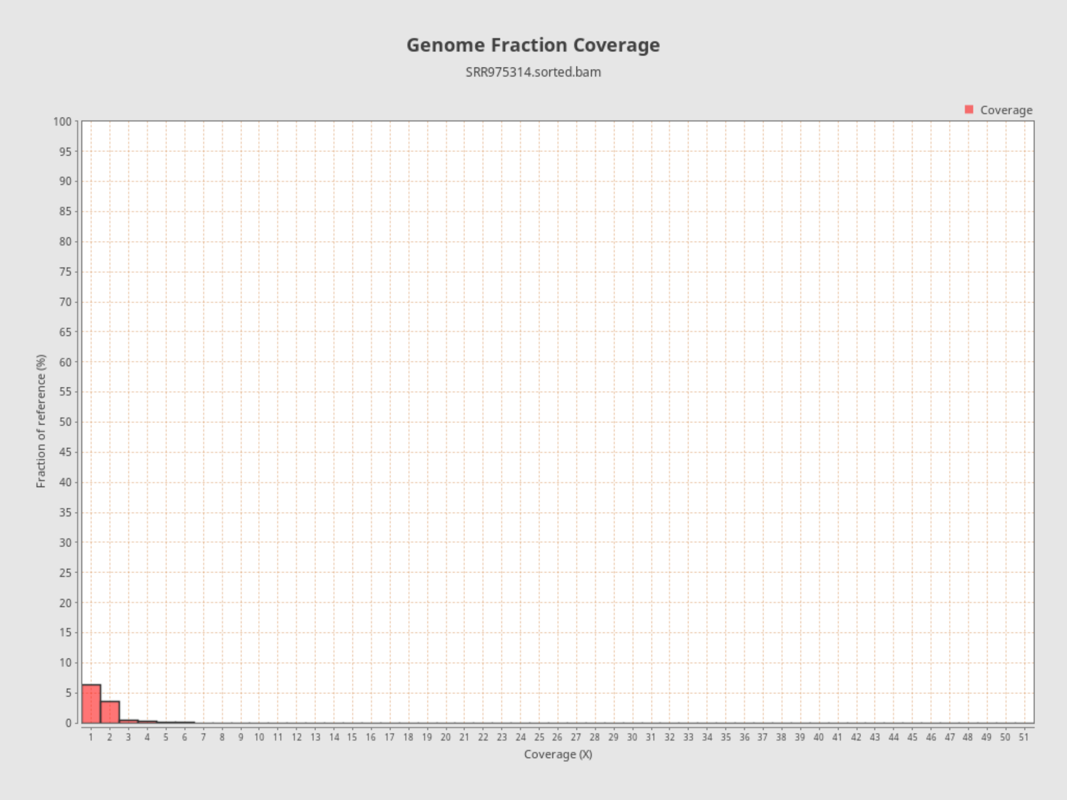
4. Results : Coverage Histogram



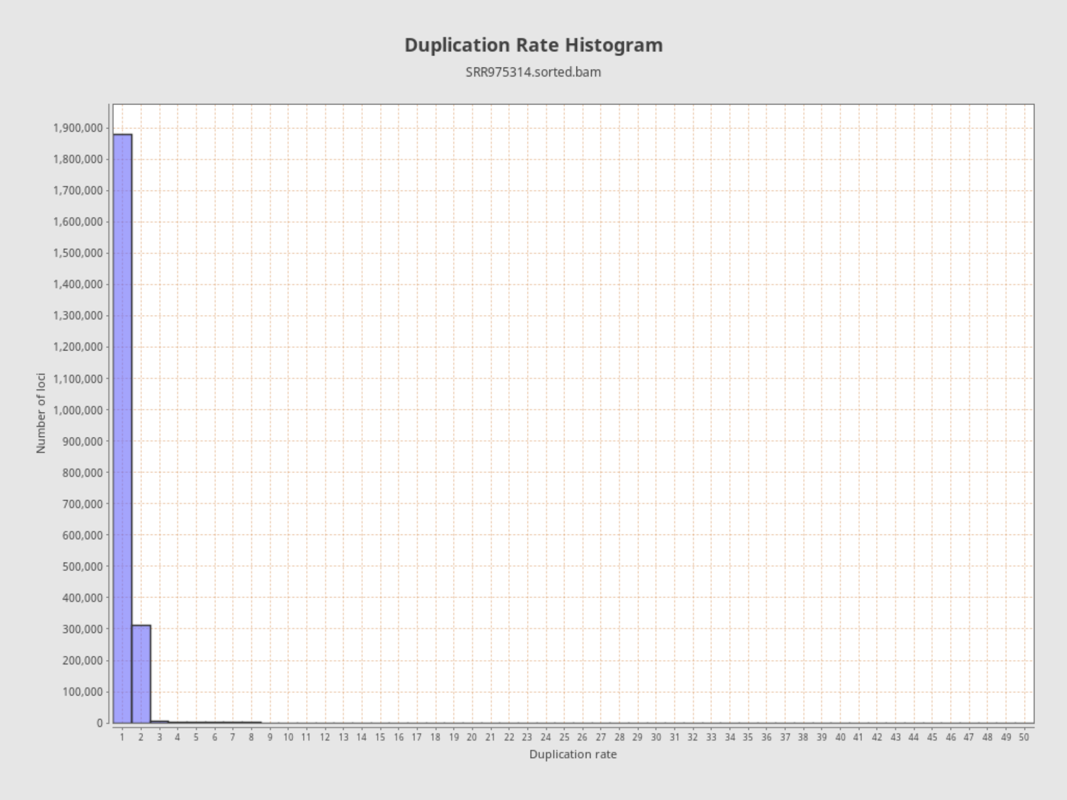
5. Results : Coverage Histogram (0-50X)



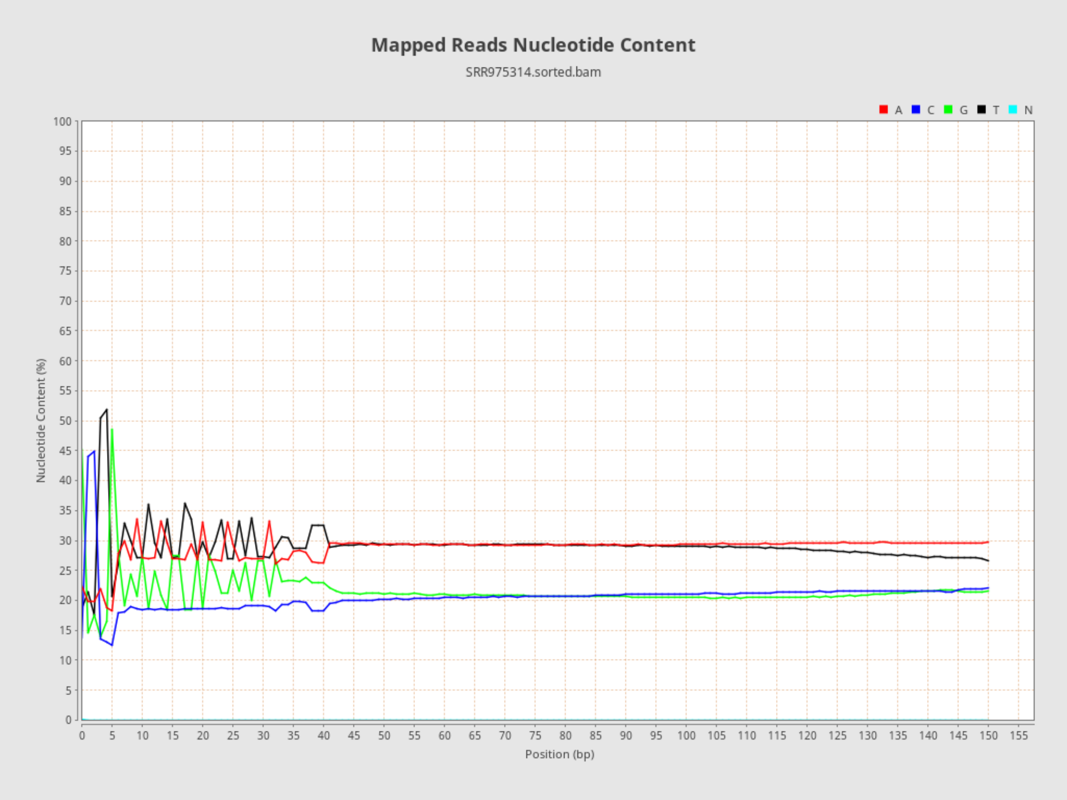
6. Results : Genome Fraction Coverage



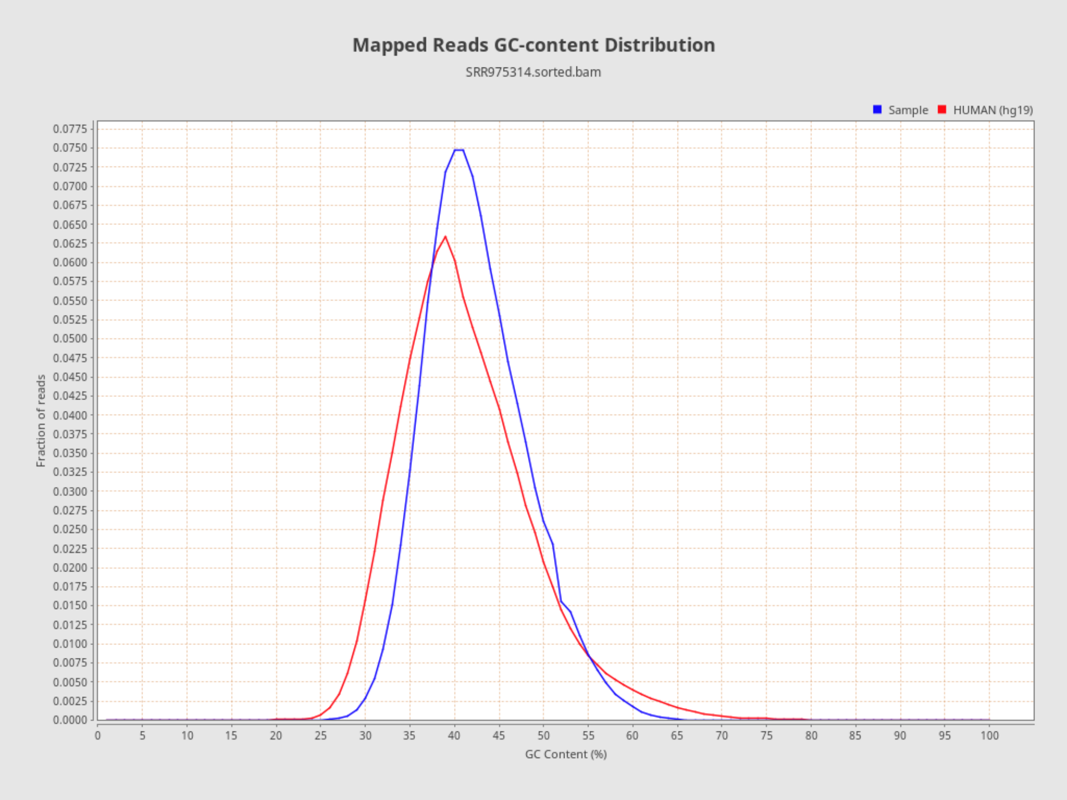
7. Results : Duplication Rate Histogram



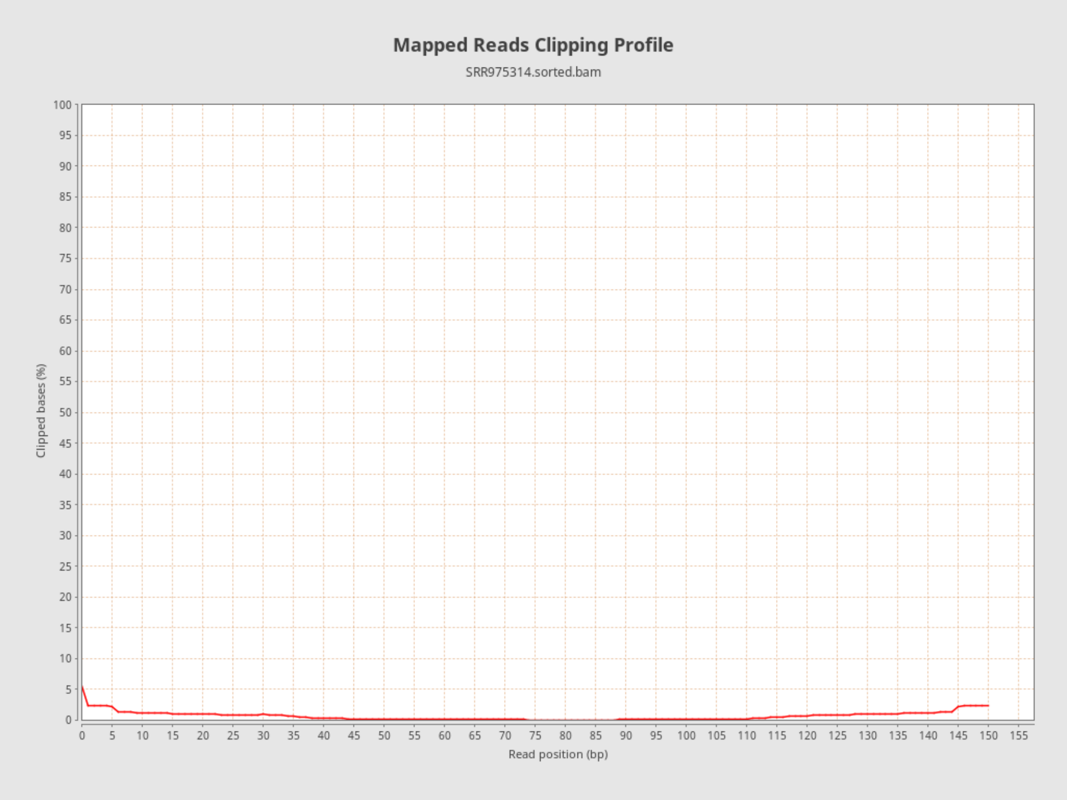
8. Results : Mapped Reads Nucleotide Content



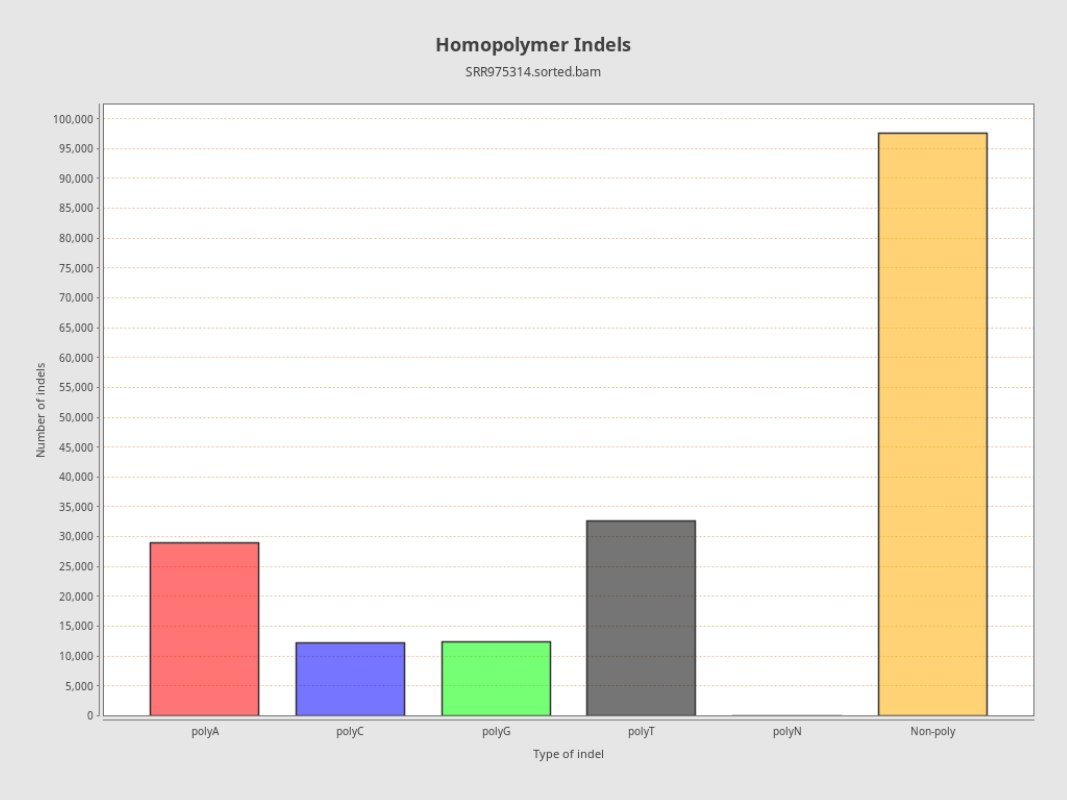
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

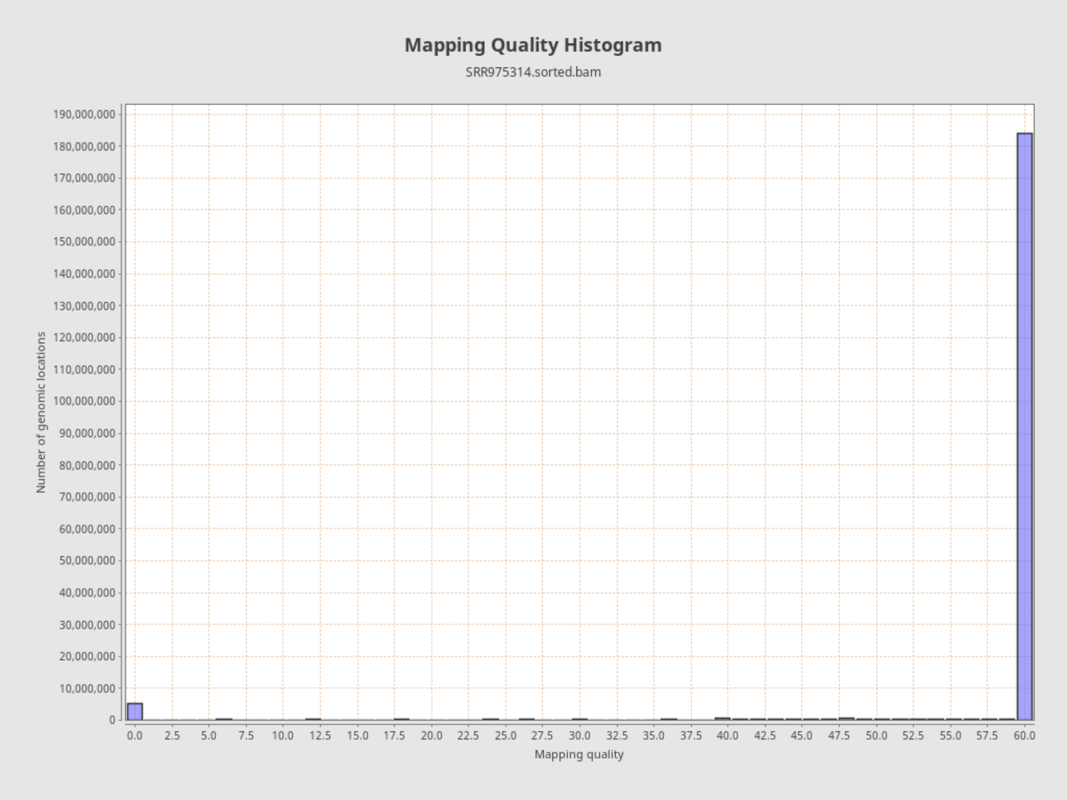


11. Results : Homopolymer Indels

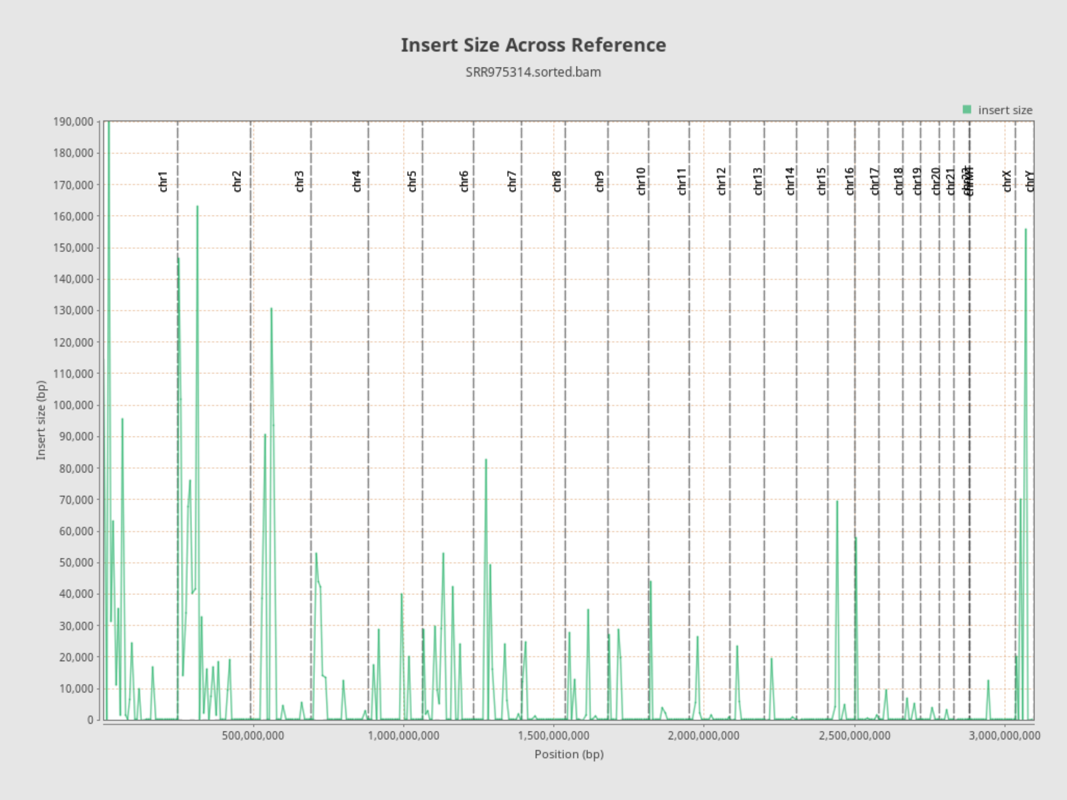


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram