

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 03:03:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975317.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_SRR975317 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975317_1.fastq.gz SRR975317_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 03:03:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975317.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,595,698
Mapped reads	47,386,726 / 99.56%
Unmapped reads	208,972 / 0.44%
Mapped paired reads	47,386,726 / 99.56%
Mapped reads, first in pair	23,765,890 / 49.93%
Mapped reads, second in pair	23,620,836 / 49.63%
Mapped reads, both in pair	47,211,764 / 99.19%
Mapped reads, singletons	174,962 / 0.37%
Secondary alignments	0
Supplementary alignments	224,418 / 0.47%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	22,592,835 / 47.47%
Duplication rate	53.15%
Clipped reads	24,519,233 / 51.52%

2.2. ACGT Content

Number/percentage of A's	1,221,112,260 / 26.38%
Number/percentage of C's	1,083,371,044 / 23.4%
Number/percentage of T's	1,256,298,581 / 27.14%
Number/percentage of G's	1,067,574,635 / 23.06%
Number/percentage of N's	1,010,954 / 0.02%

GC Percentage	46.46%
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2.3. Coverage

Mean	1.4956
Standard Deviation	11.0086

2.4. Mapping Quality

Mean Mapping Quality	56.4
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2.5. Insert size

Mean	141,084.02
Standard Deviation	3,702,702.44
P25/Median/P75	198 / 247 / 310

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	25,292,721
Insertions	371,577
Mapped reads with at least one insertion	0.78%
Deletions	276,271
Mapped reads with at least one deletion	0.57%
Homopolymer indels	35.12%

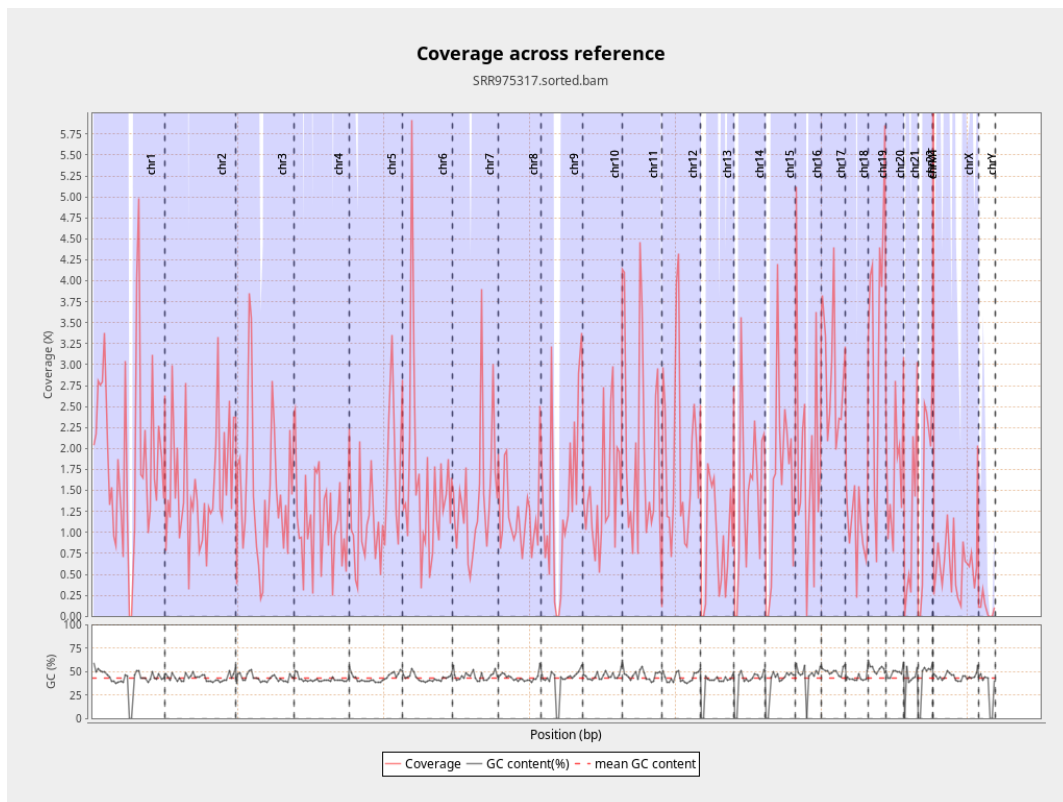
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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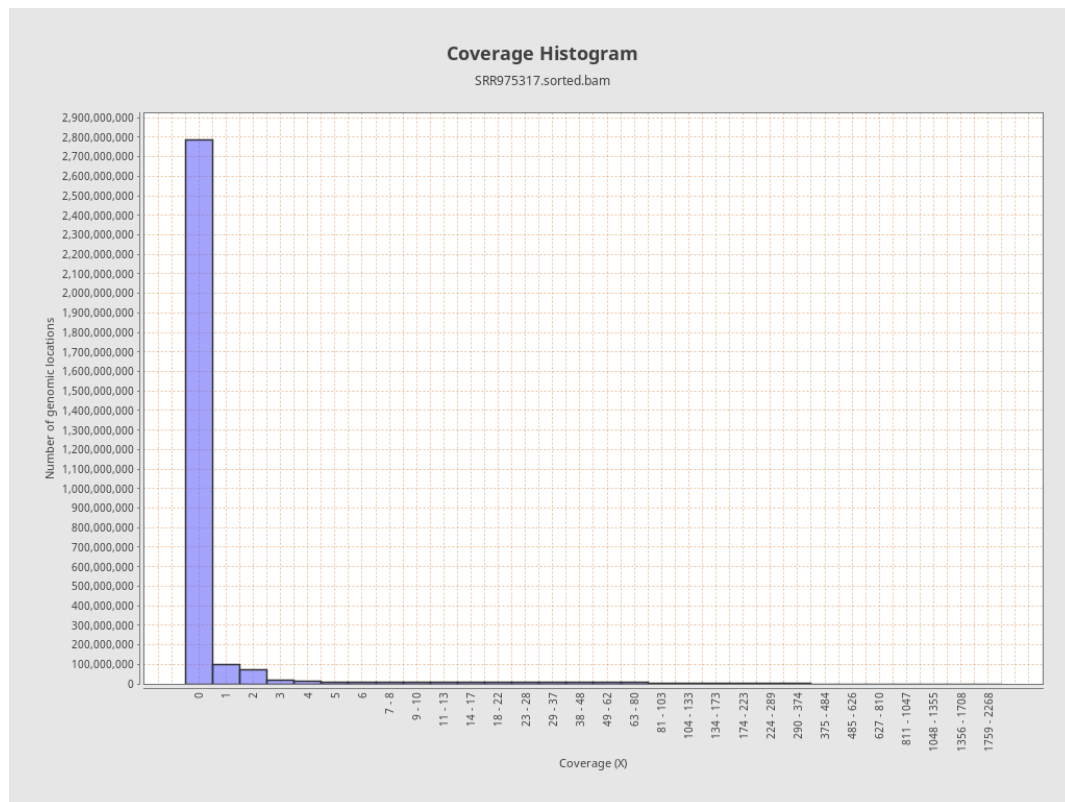
		bases	coverage	deviation
chr1	249250621	471069244	1.8899	12.7211
chr2	243199373	374785833	1.5411	11.2447
chr3	198022430	298844048	1.5091	11.0261
chr4	191154276	215851641	1.1292	9.7836
chr5	180915260	236935182	1.3096	10.3741
chr6	171115067	269362065	1.5742	11.902
chr7	159138663	227460651	1.4293	11.0517
chr8	146364022	173738661	1.187	9.6417
chr9	141213431	186979908	1.3241	10.2161
chr10	135534747	201013174	1.4831	11.0878
chr11	135006516	269498380	1.9962	13.0587
chr12	133851895	253598089	1.8946	12.3669
chr13	115169878	102207573	0.8875	8.5852
chr14	107349540	155692910	1.4503	11.0028
chr15	102531392	167392776	1.6326	11.617
chr16	90354753	161631414	1.7889	11.4974
chr17	81195210	233097097	2.8708	14.9778
chr18	78077248	82348381	1.0547	9.1707
chr19	59128983	205218203	3.4707	15.4812
chr20	63025520	109430123	1.7363	11.5545
chr21	48129895	50832462	1.0562	9.6665
chr22	51304566	80796775	1.5748	10.2084
chrMT	16571	360242	21.7393	32.9324
chrX	155270560	95899005	0.6176	5.4187

chrY	59373566	5898635	0.0993	1.6021
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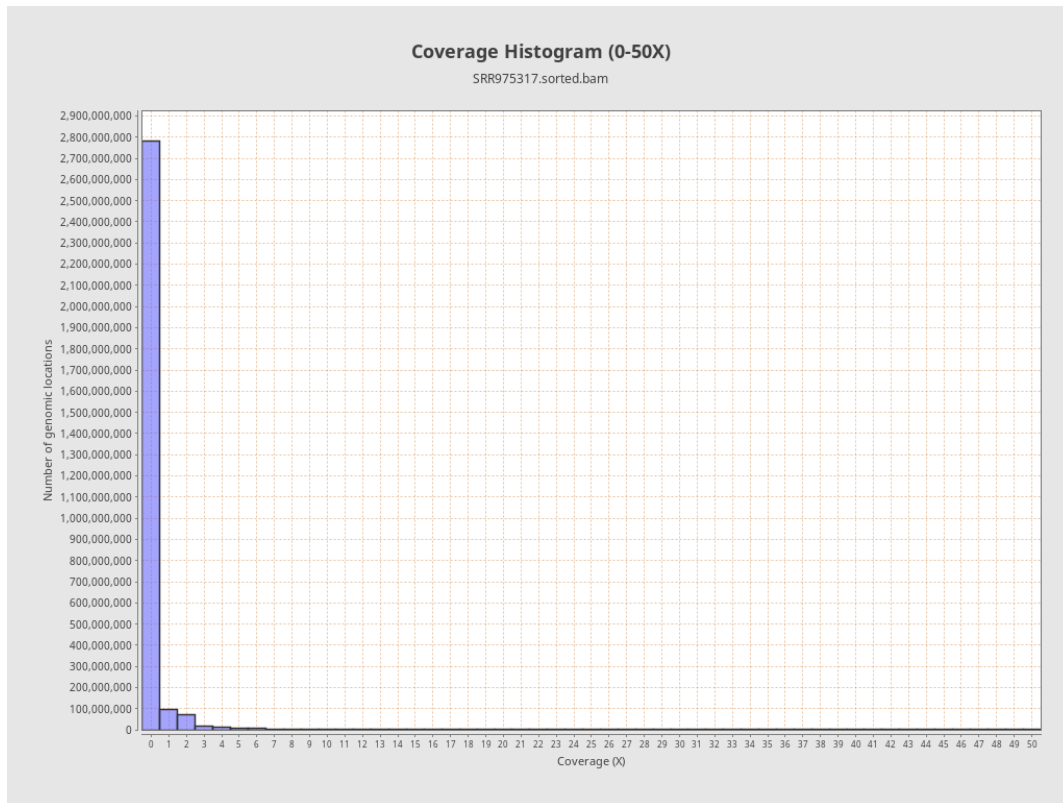
3. Results : Coverage across reference



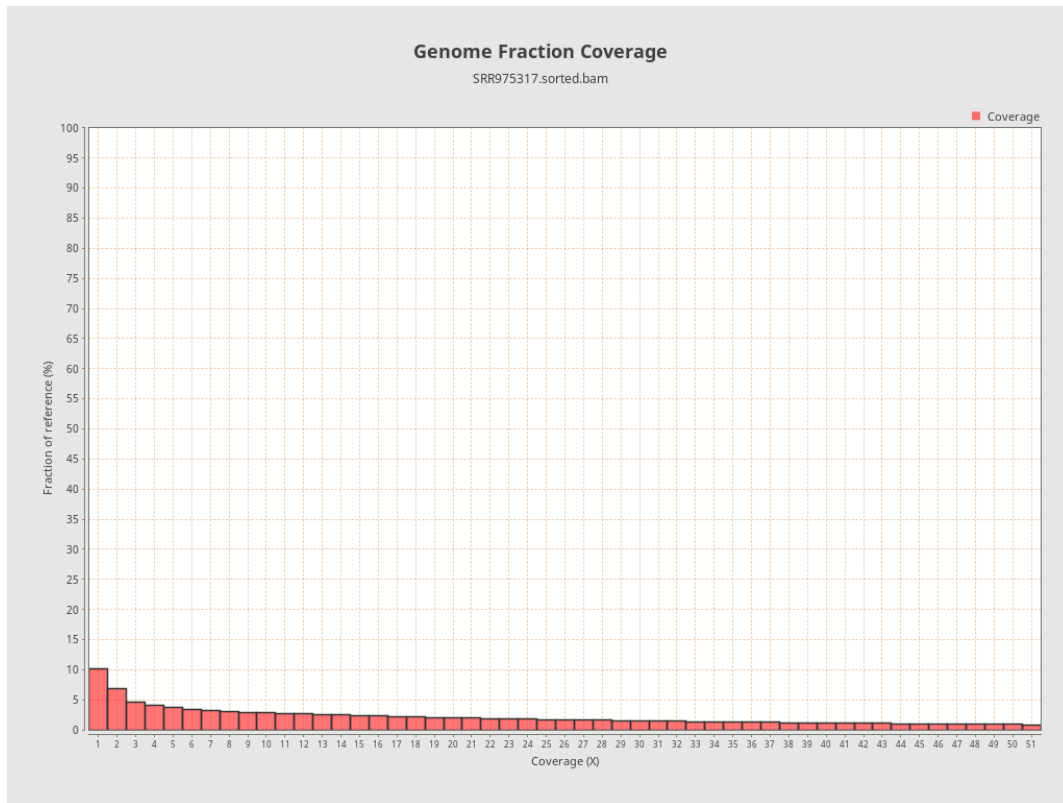
4. Results : Coverage Histogram



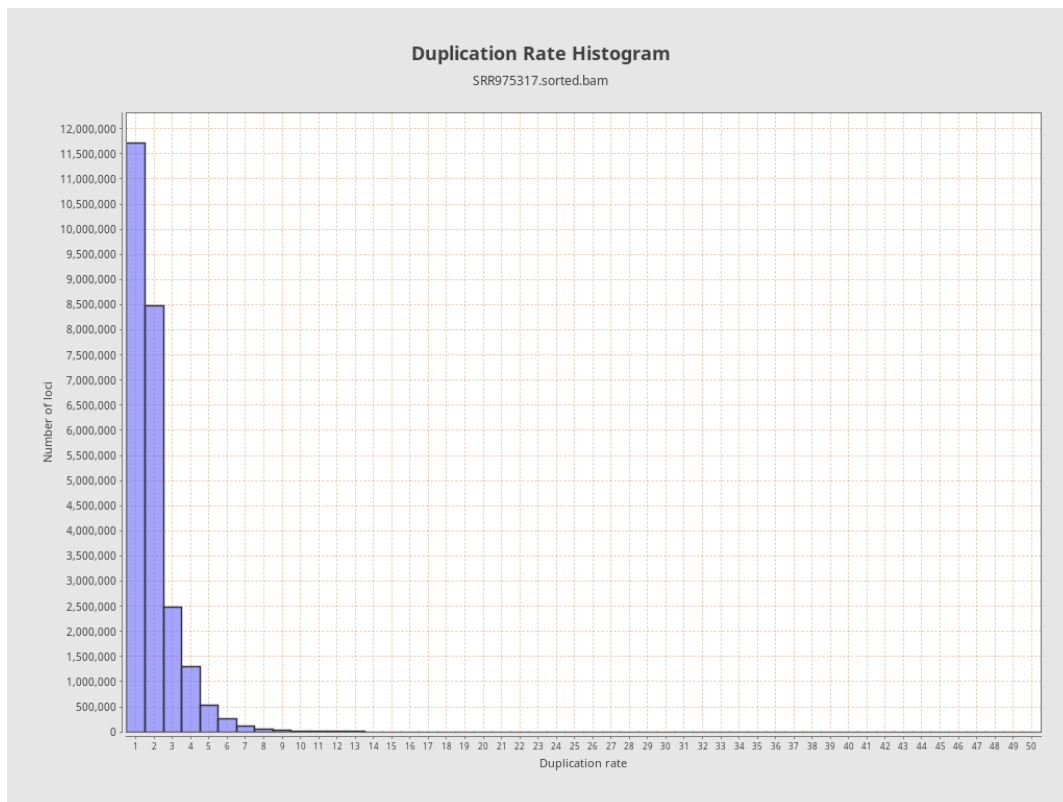
5. Results : Coverage Histogram (0-50X)



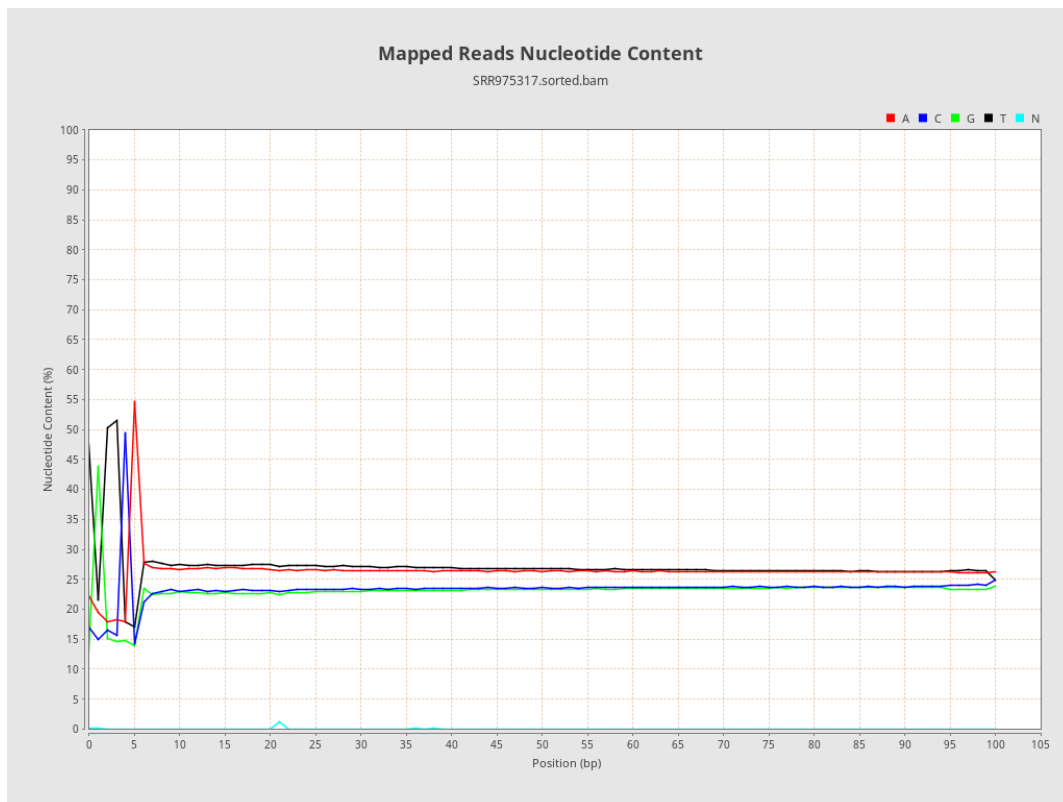
6. Results : Genome Fraction Coverage



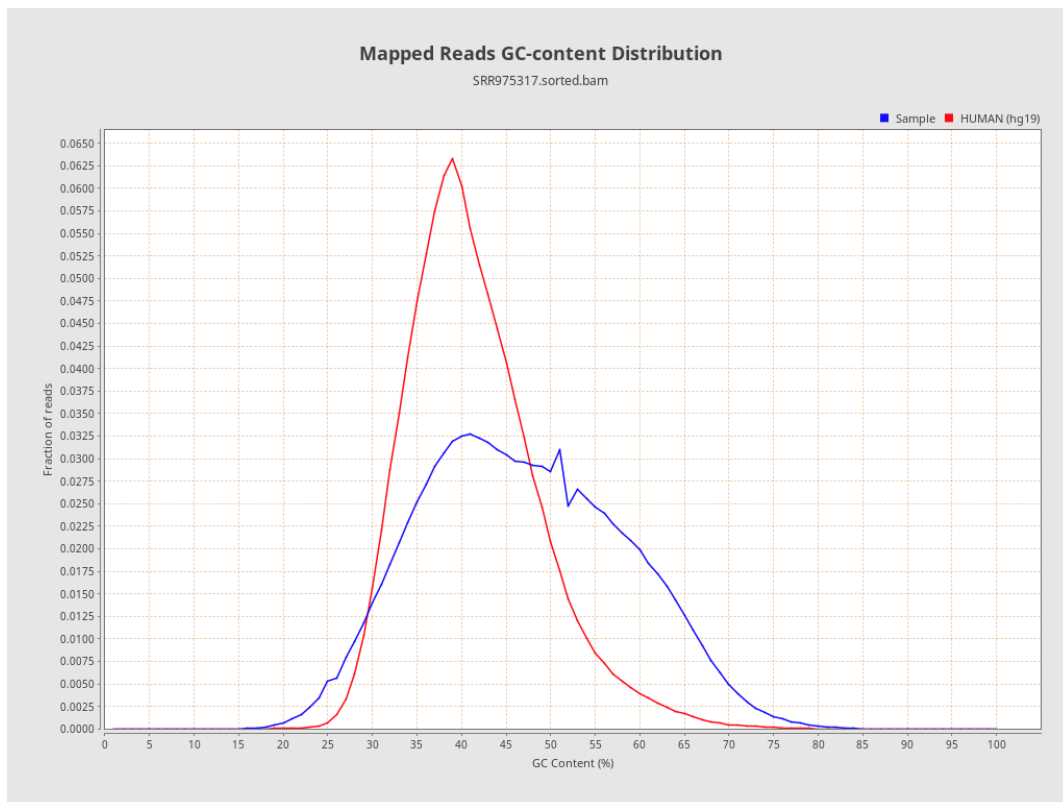
7. Results : Duplication Rate Histogram



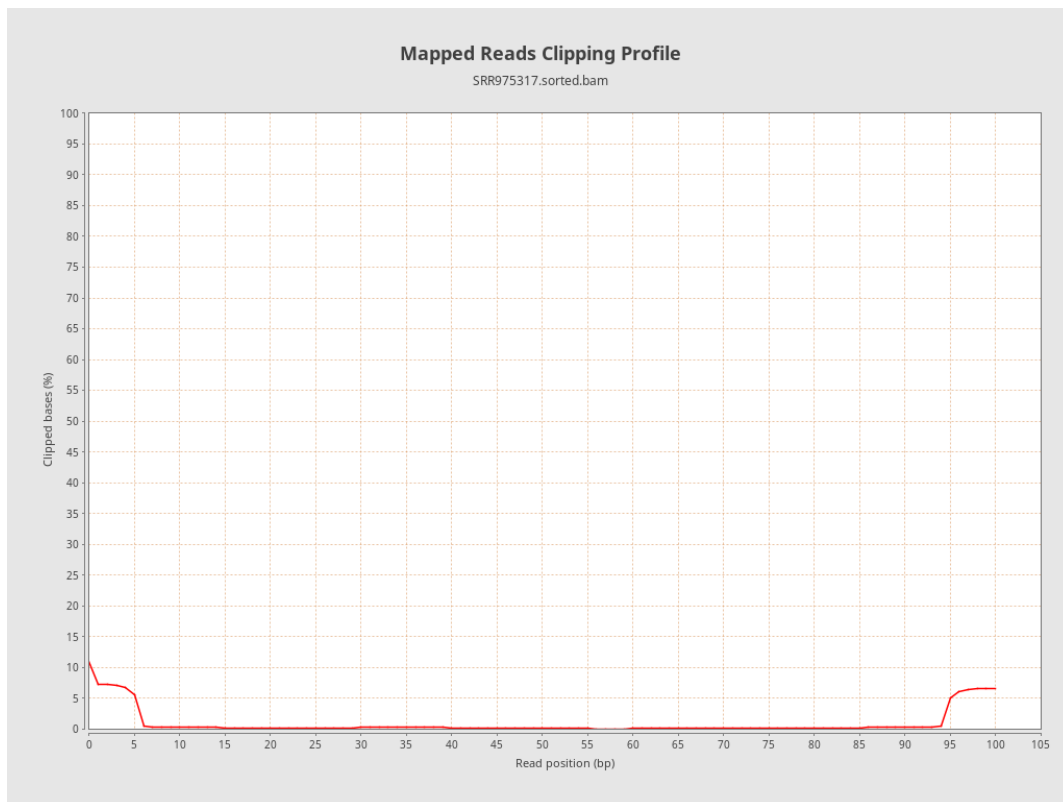
8. Results : Mapped Reads Nucleotide Content



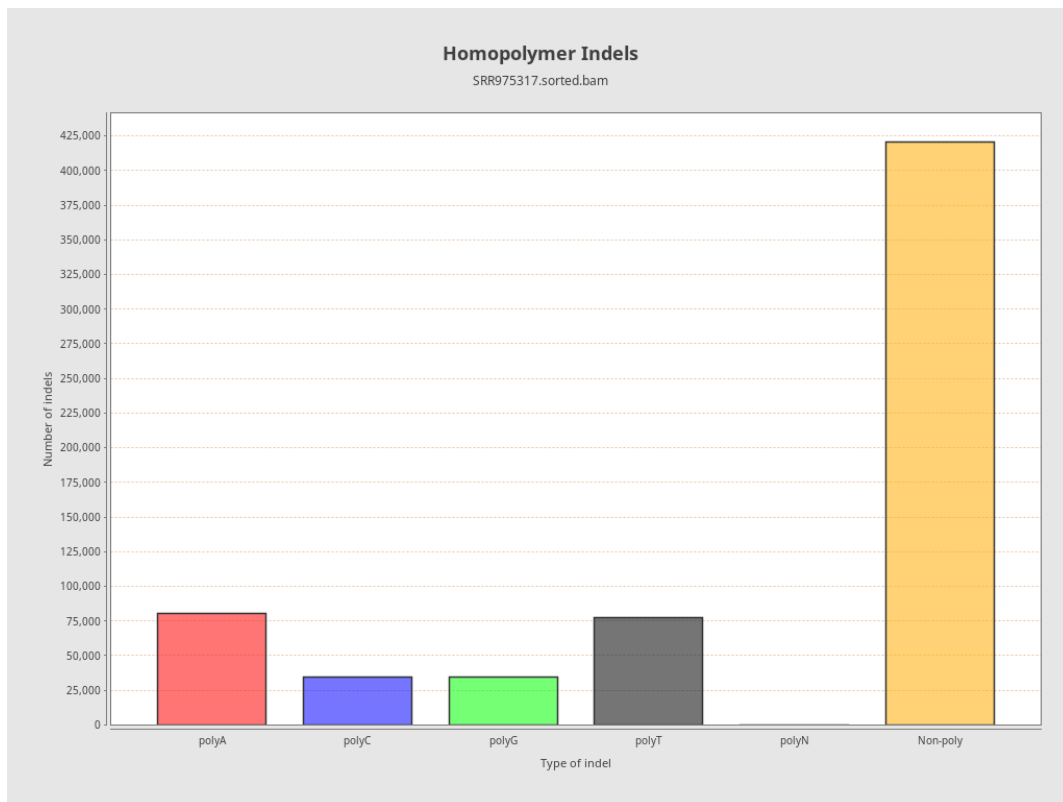
9. Results : Mapped Reads GC-content Distribution



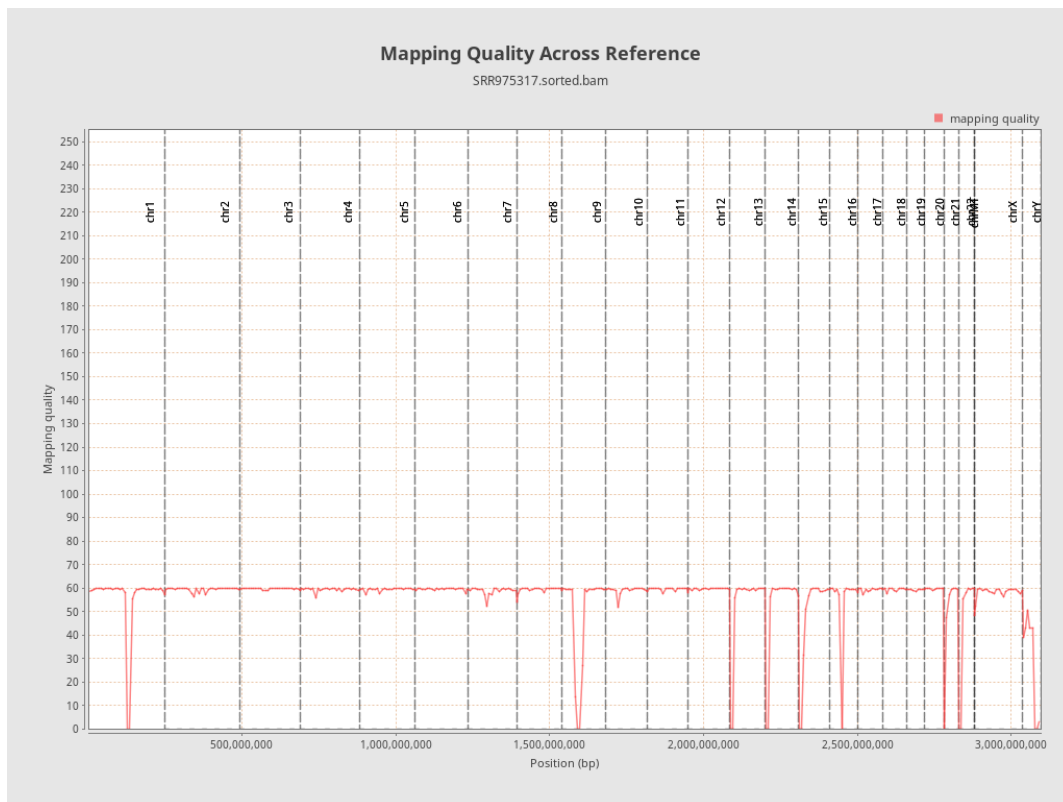
10. Results : Mapped Reads Clipping Profile



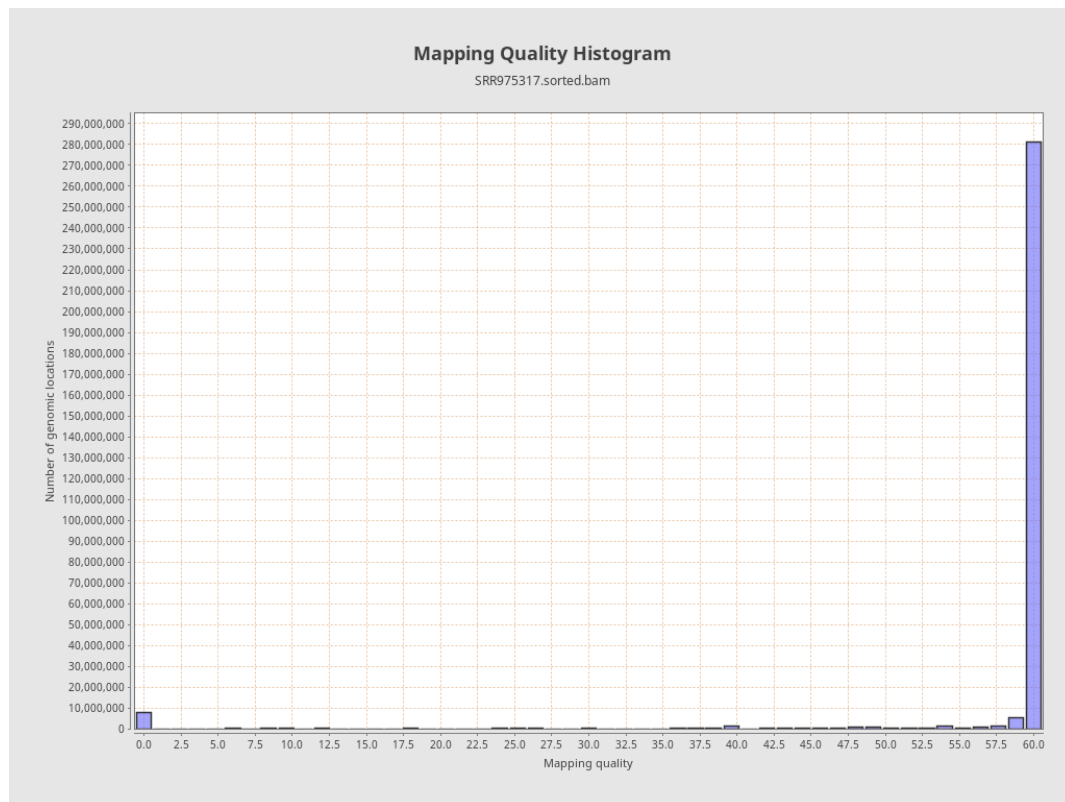
11. Results : Homopolymer Indels



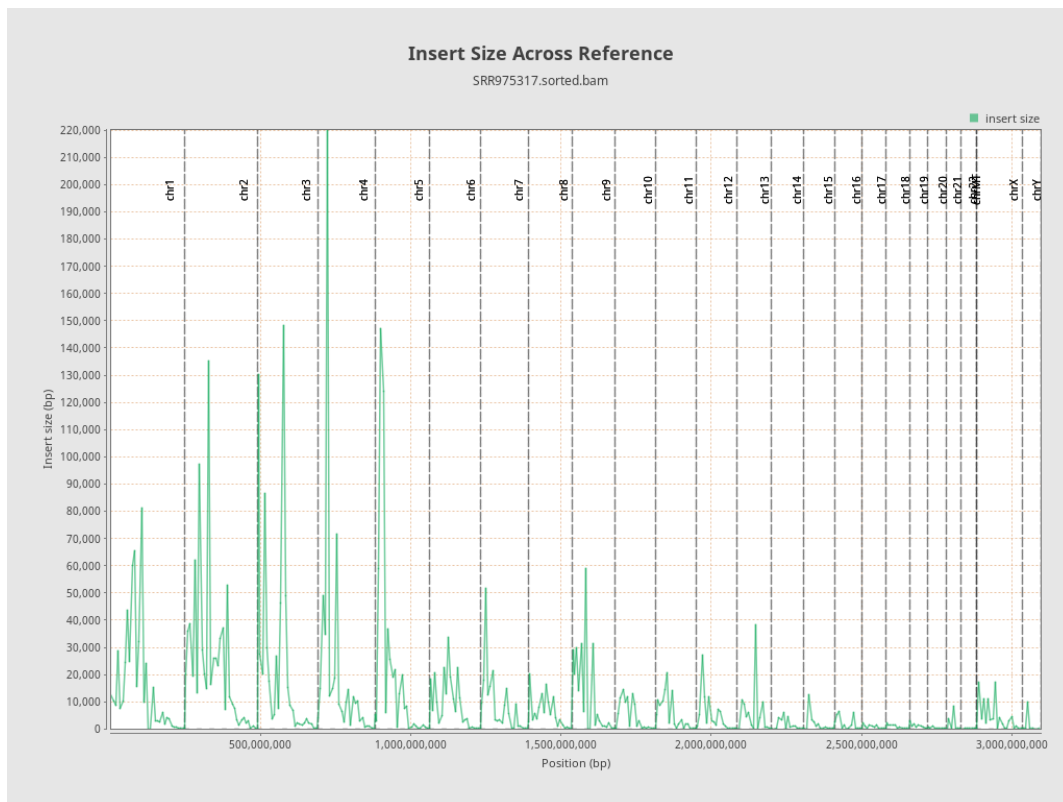
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

