

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 18:08:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975297.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_SRR975297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975297_1.fastq.gz SRR975297_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 18:08:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975297.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	71,037,568
Mapped reads	70,890,983 / 99.79%
Unmapped reads	146,585 / 0.21%
Mapped paired reads	70,890,983 / 99.79%
Mapped reads, first in pair	35,460,278 / 49.92%
Mapped reads, second in pair	35,430,705 / 49.88%
Mapped reads, both in pair	70,822,420 / 99.7%
Mapped reads, singletons	68,563 / 0.1%
Secondary alignments	0
Supplementary alignments	122,033 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	45,918,450 / 64.64%
Duplication rate	48.75%
Clipped reads	40,013,231 / 56.33%

2.2. ACGT Content

Number/percentage of A's	1,761,440,992 / 26.84%
Number/percentage of C's	1,416,288,448 / 21.58%
Number/percentage of T's	1,858,555,201 / 28.31%
Number/percentage of G's	1,527,335,057 / 23.27%
Number/percentage of N's	293,967 / 0%

GC Percentage	44.85%
---------------	--------

2.3. Coverage

Mean	2.121
Standard Deviation	31.1194

2.4. Mapping Quality

Mean Mapping Quality	56.23
----------------------	-------

2.5. Insert size

Mean	77,475.19
Standard Deviation	2,743,162.99
P25/Median/P75	150 / 186 / 234

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	33,881,044
Insertions	556,668
Mapped reads with at least one insertion	0.78%
Deletions	1,309,245
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.21%

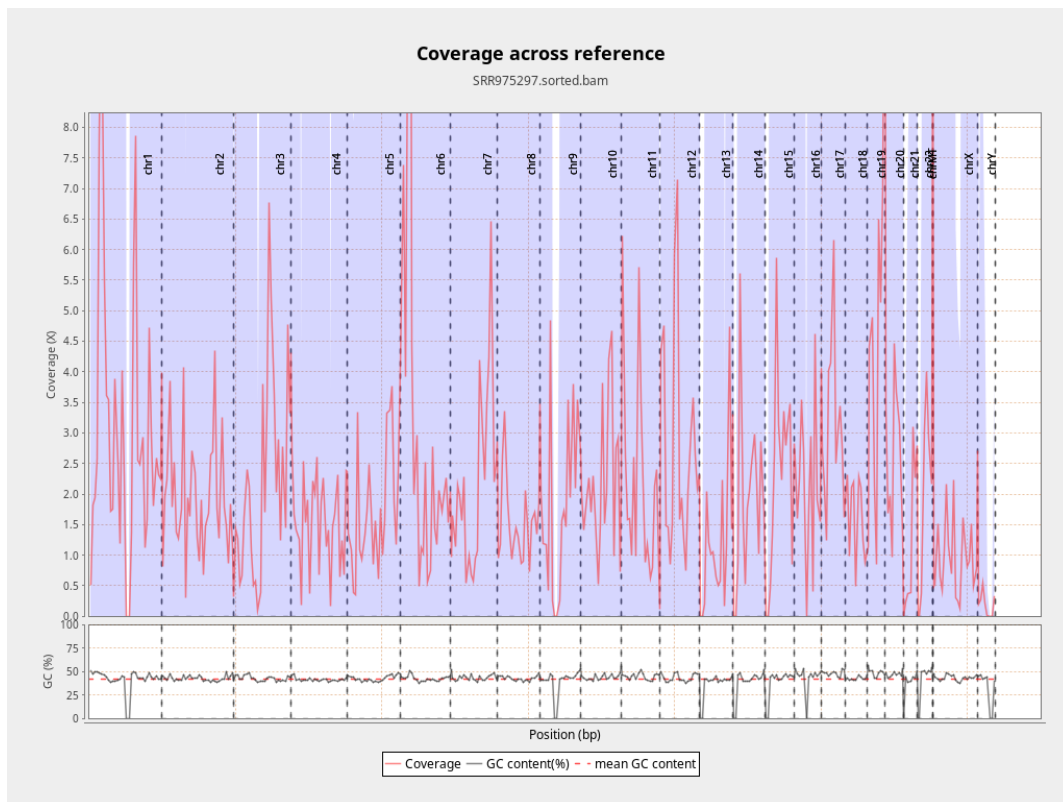
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

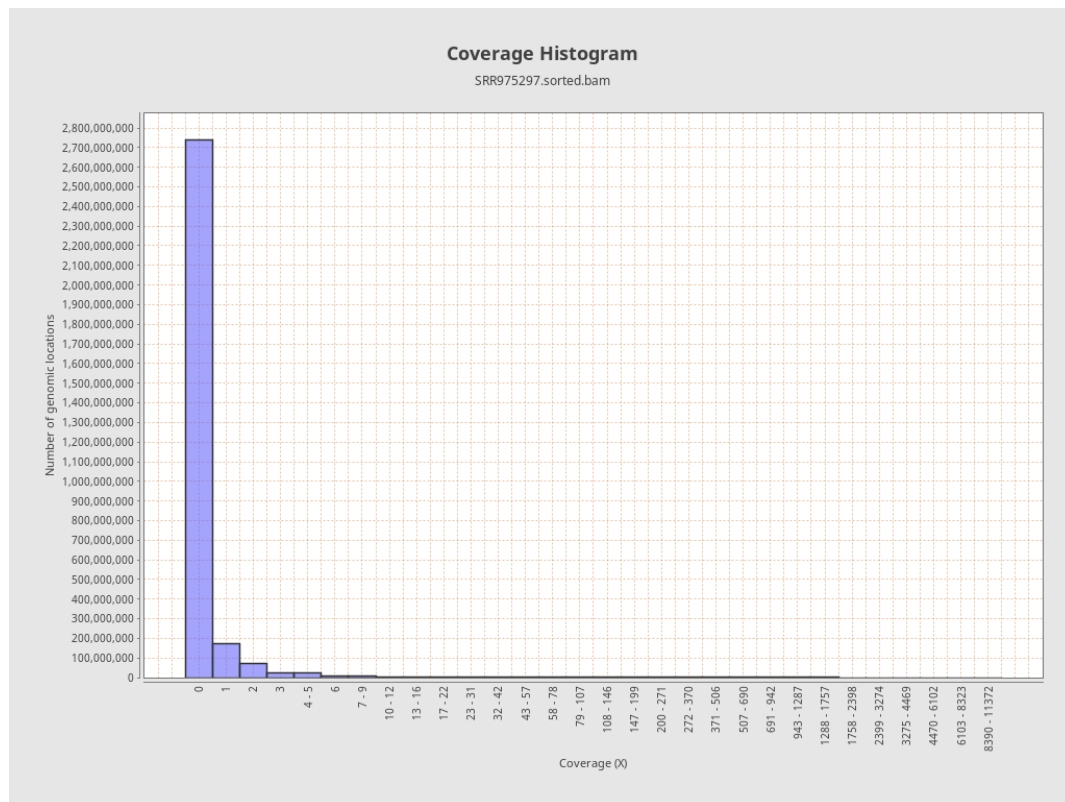
		bases	coverage	deviation
chr1	249250621	762667121	3.0598	38.0348
chr2	243199373	472258111	1.9419	27.2823
chr3	198022430	439157505	2.2177	33.159
chr4	191154276	290065941	1.5174	24.3284
chr5	180915260	312898055	1.7295	25.6418
chr6	171115067	600583688	3.5098	52.5667
chr7	159138663	342921235	2.1549	31.414
chr8	146364022	221661068	1.5145	23.0635
chr9	141213431	259891333	1.8404	27.1996
chr10	135534747	297485634	2.1949	32.9726
chr11	135006516	290956560	2.1551	28.1222
chr12	133851895	363258288	2.7139	32.7849
chr13	115169878	137724460	1.1958	25.3386
chr14	107349540	202998319	1.891	25.92
chr15	102531392	235330831	2.2952	31.615
chr16	90354753	194110436	2.1483	26.6133
chr17	81195210	254157945	3.1302	36.2756
chr18	78077248	124989444	1.6008	27.3052
chr19	59128983	271034203	4.5838	46.4735
chr20	63025520	161894232	2.5687	35.1966
chr21	48129895	62864028	1.3061	21.1338
chr22	51304566	103057008	2.0087	28.0497
chrMT	16571	178616	10.7788	30.3858
chrX	155270560	152211516	0.9803	17.5117

chrY	59373566	11568365	0.1948	5.2357
------	----------	----------	--------	--------

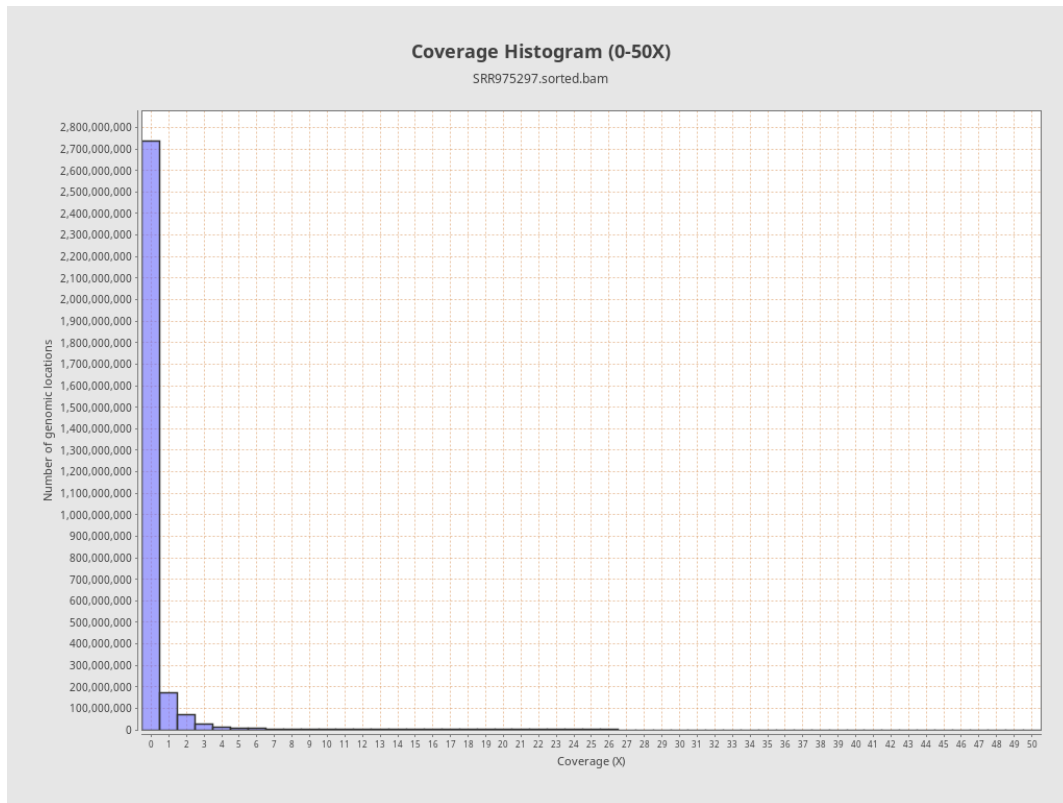
3. Results : Coverage across reference



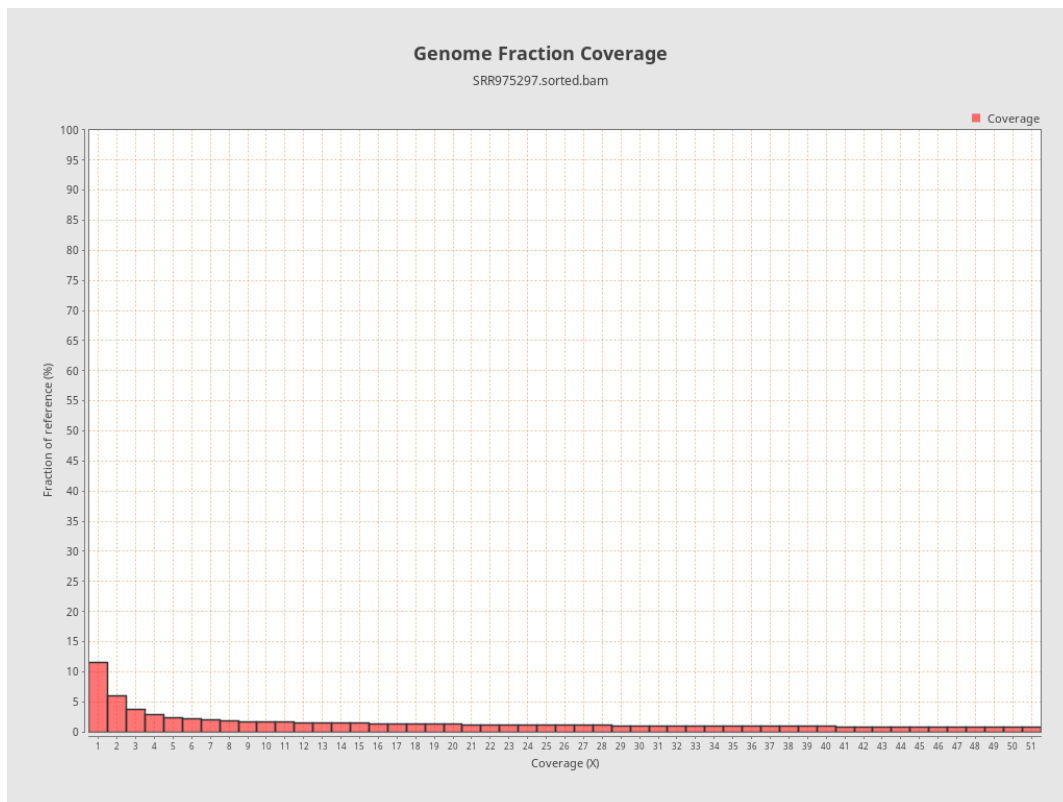
4. Results : Coverage Histogram



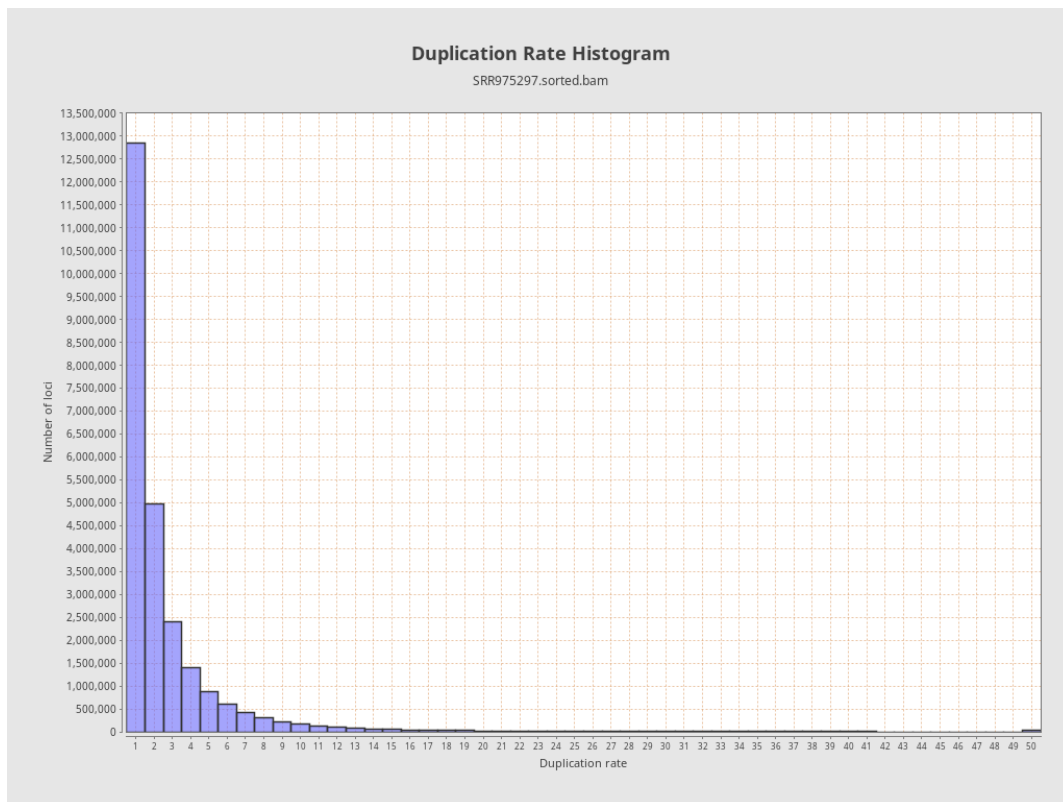
5. Results : Coverage Histogram (0-50X)



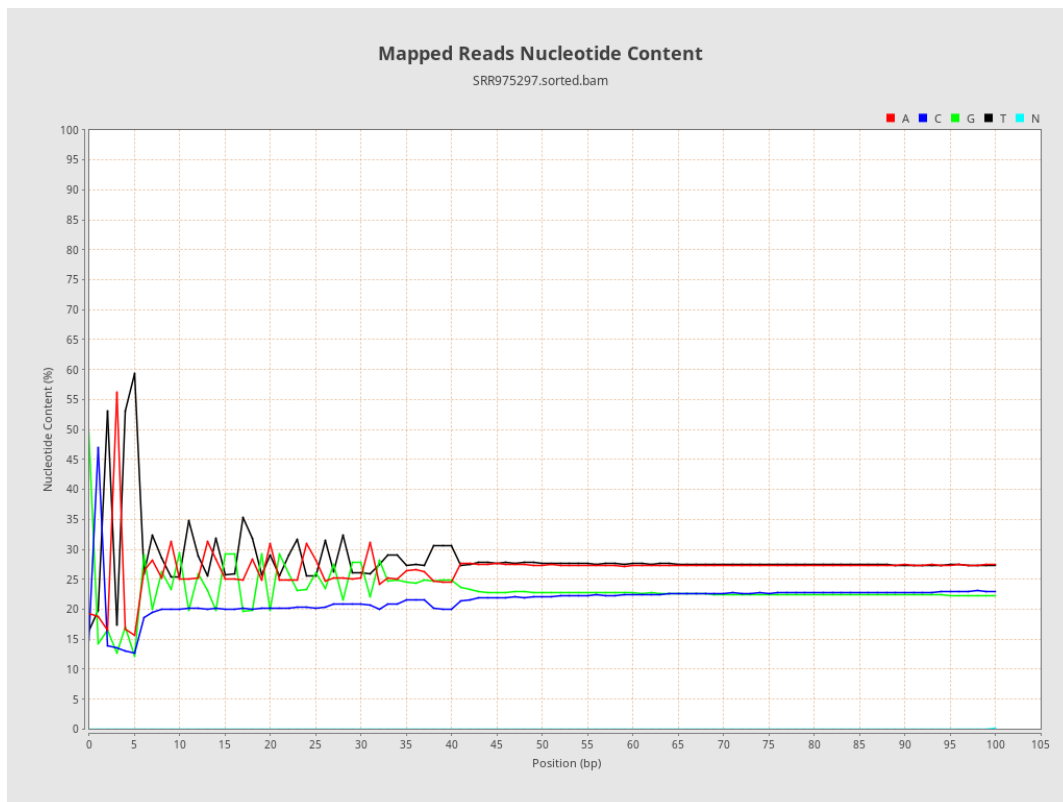
6. Results : Genome Fraction Coverage



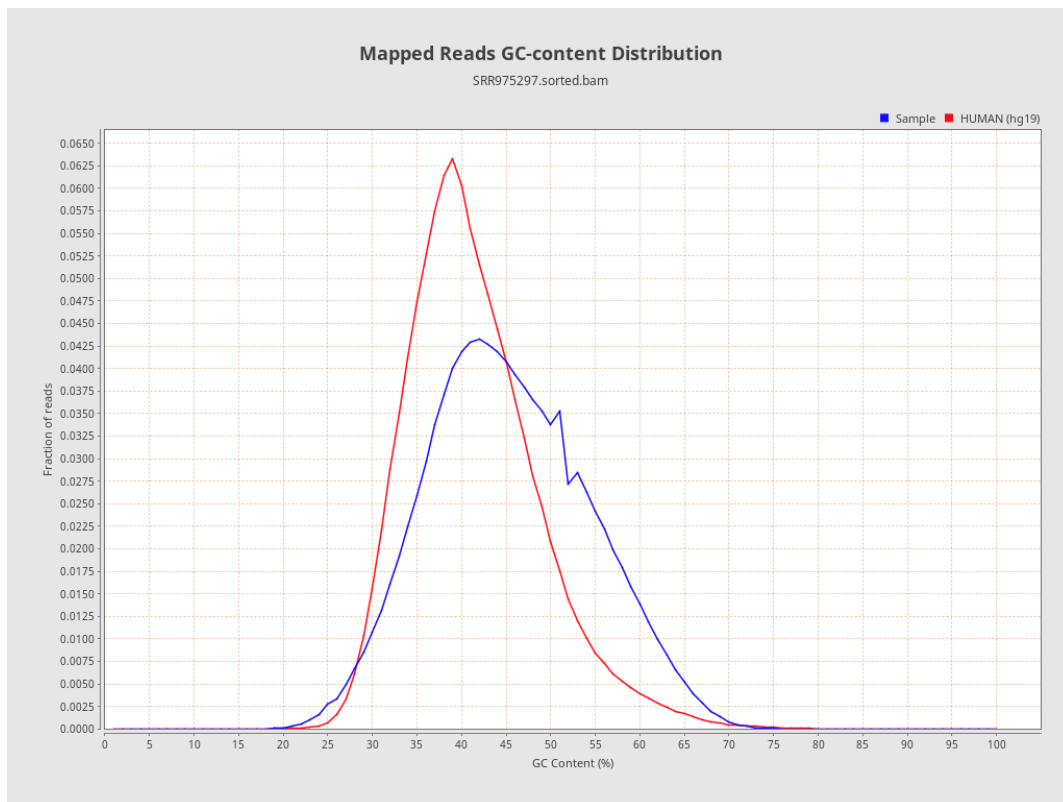
7. Results : Duplication Rate Histogram



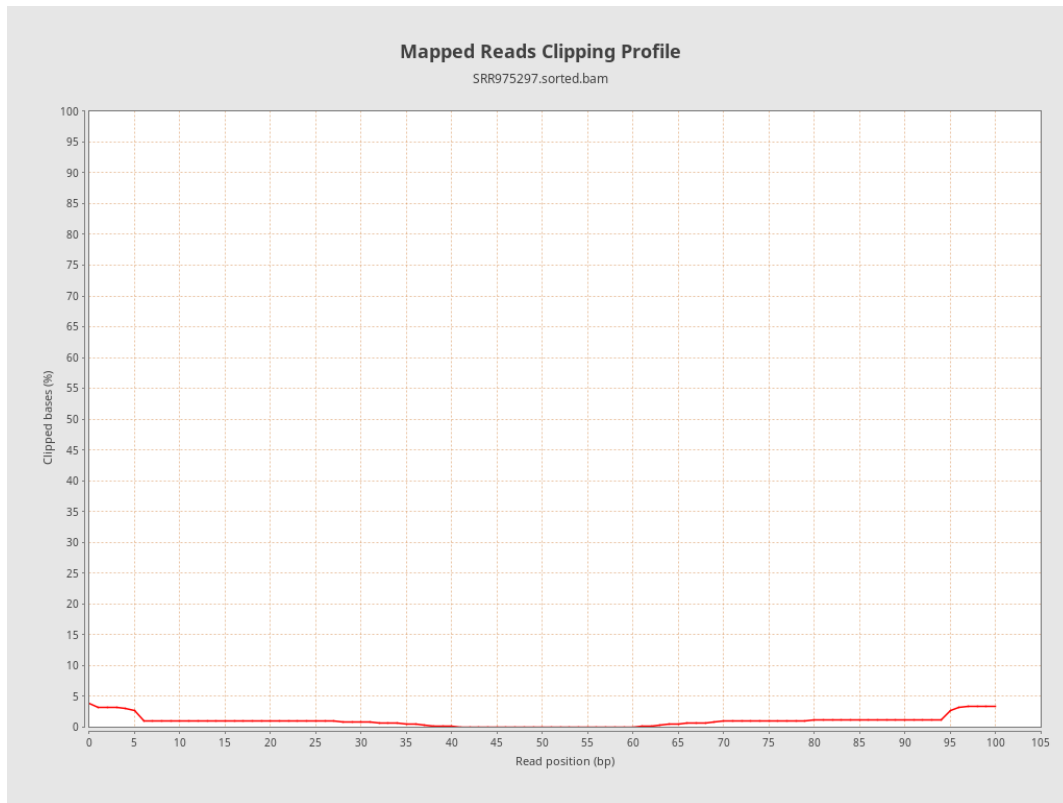
8. Results : Mapped Reads Nucleotide Content



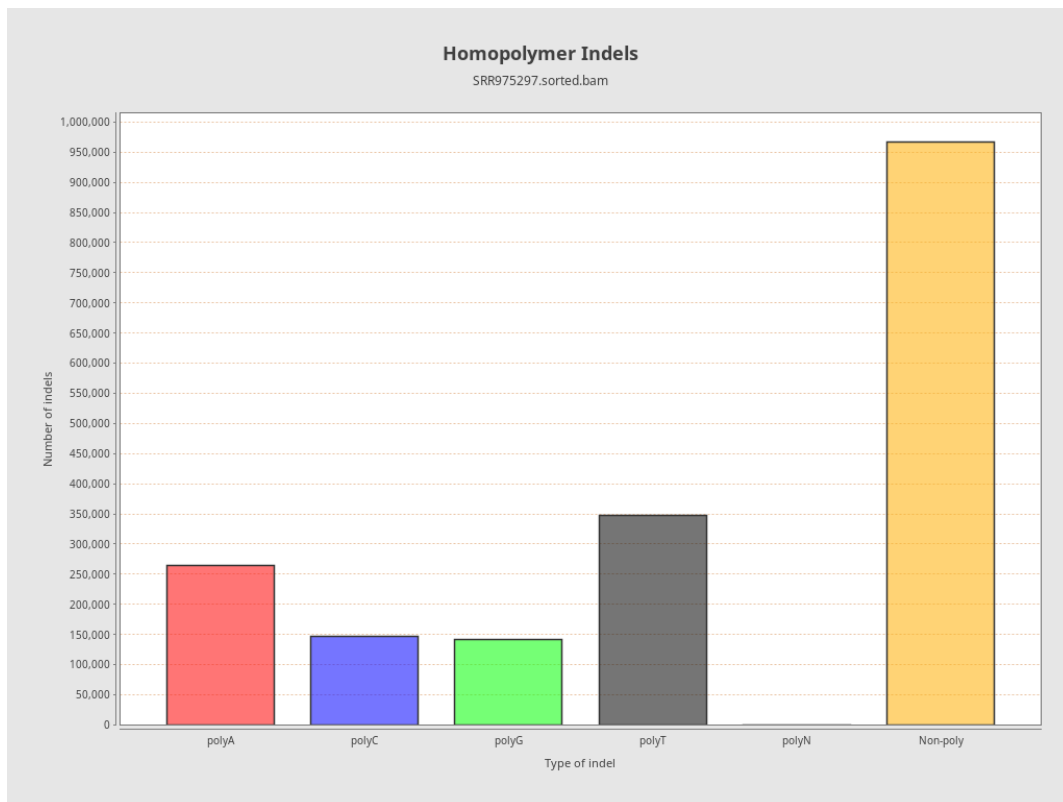
9. Results : Mapped Reads GC-content Distribution



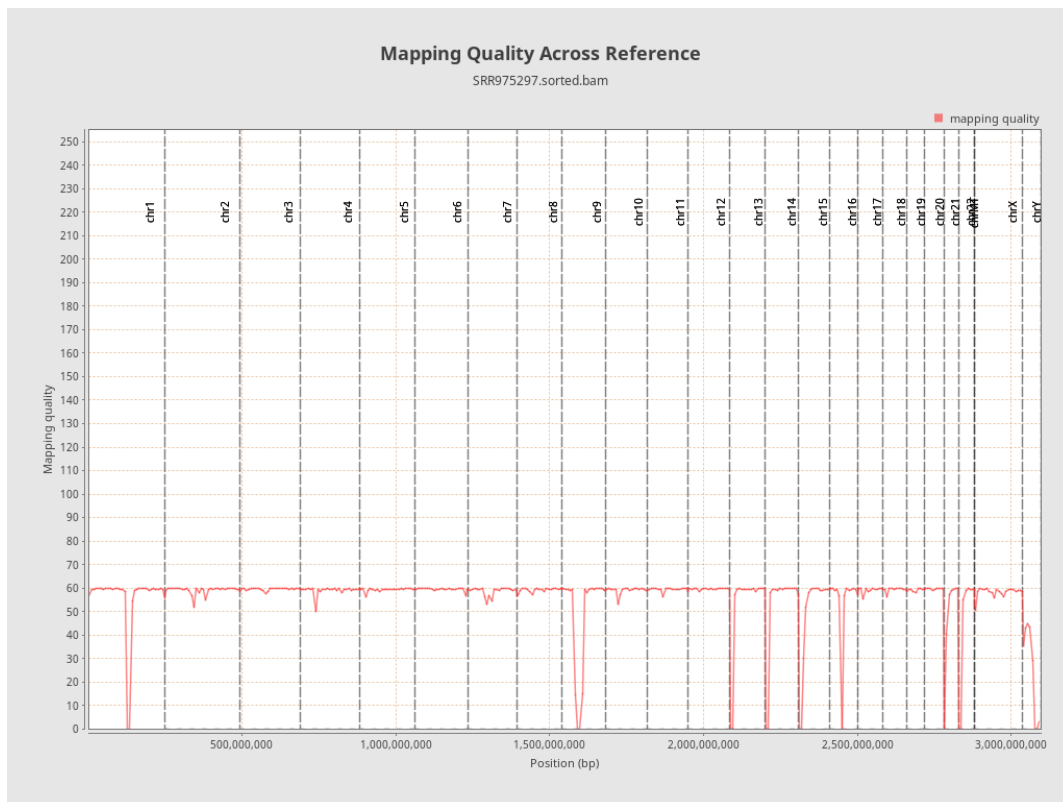
10. Results : Mapped Reads Clipping Profile



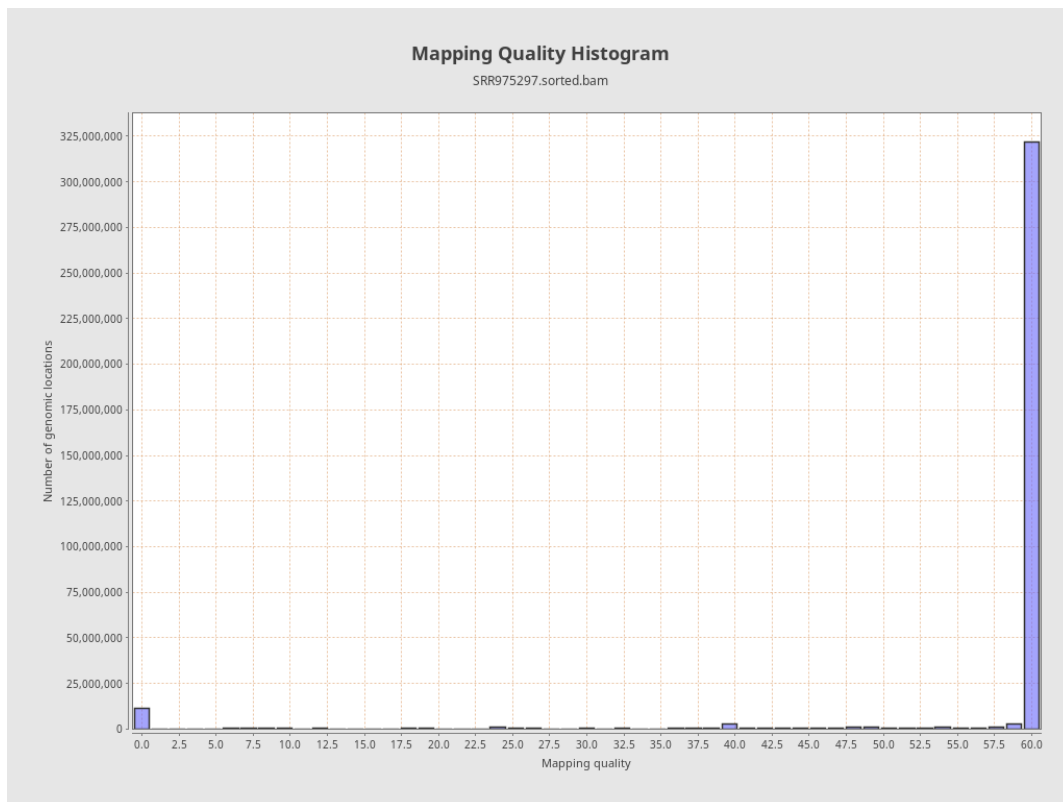
11. Results : Homopolymer Indels



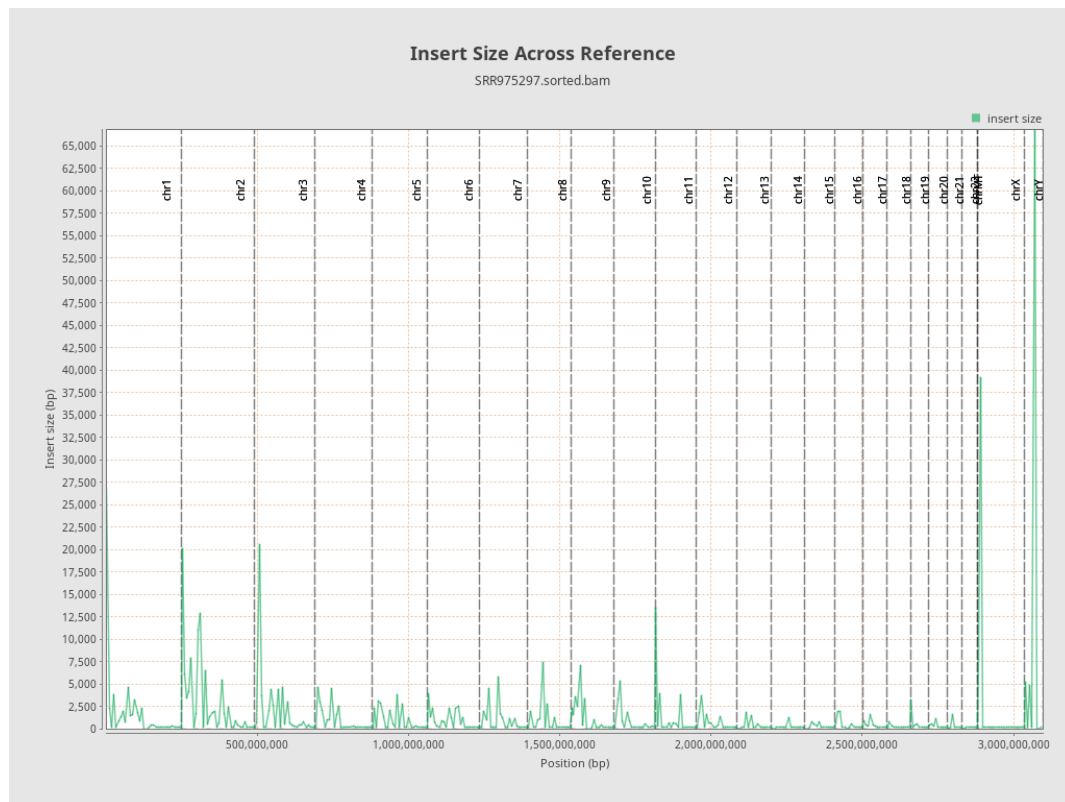
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

