

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 09:52:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1954923.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1954923 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1954923_1.fastq.gz SRR1954923_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 09:52:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1954923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,552,184
Mapped reads	17,088,532 / 97.36%
Unmapped reads	463,652 / 2.64%
Mapped paired reads	17,088,532 / 97.36%
Mapped reads, first in pair	8,712,026 / 49.63%
Mapped reads, second in pair	8,376,506 / 47.72%
Mapped reads, both in pair	16,727,682 / 95.3%
Mapped reads, singletons	360,850 / 2.06%
Secondary alignments	0
Supplementary alignments	41,543 / 0.24%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	751,289 / 4.28%
Duplication rate	3.71%
Clipped reads	4,066,389 / 23.17%

2.2. ACGT Content

Number/percentage of A's	460,337,435 / 28.79%
Number/percentage of C's	315,606,539 / 19.74%
Number/percentage of T's	459,864,305 / 28.76%
Number/percentage of G's	362,794,697 / 22.69%
Number/percentage of N's	101,039 / 0.01%

GC Percentage	42.43%
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2.3. Coverage

Mean	0.5168
Standard Deviation	1.4493

2.4. Mapping Quality

Mean Mapping Quality	54.24
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2.5. Insert size

Mean	28,870.43
Standard Deviation	1,721,580.67
P25/Median/P75	314 / 329 / 343

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	14,191,460
Insertions	261,569
Mapped reads with at least one insertion	1.51%
Deletions	763,517
Mapped reads with at least one deletion	4.36%
Homopolymer indels	54.29%

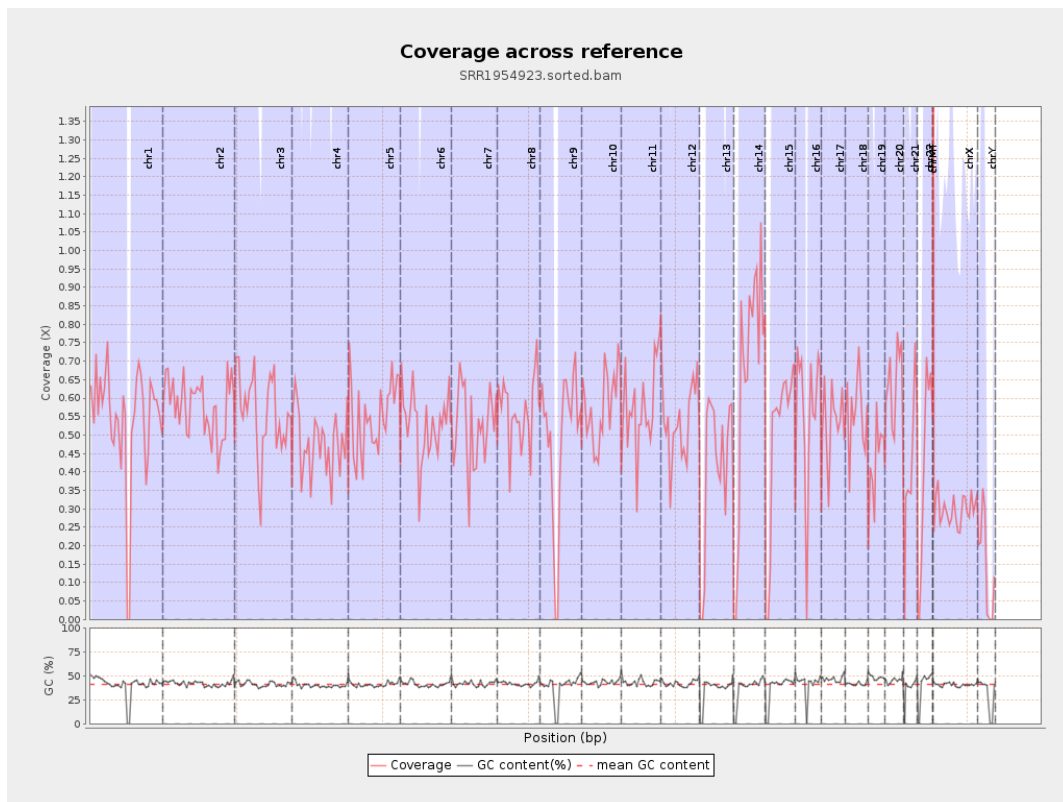
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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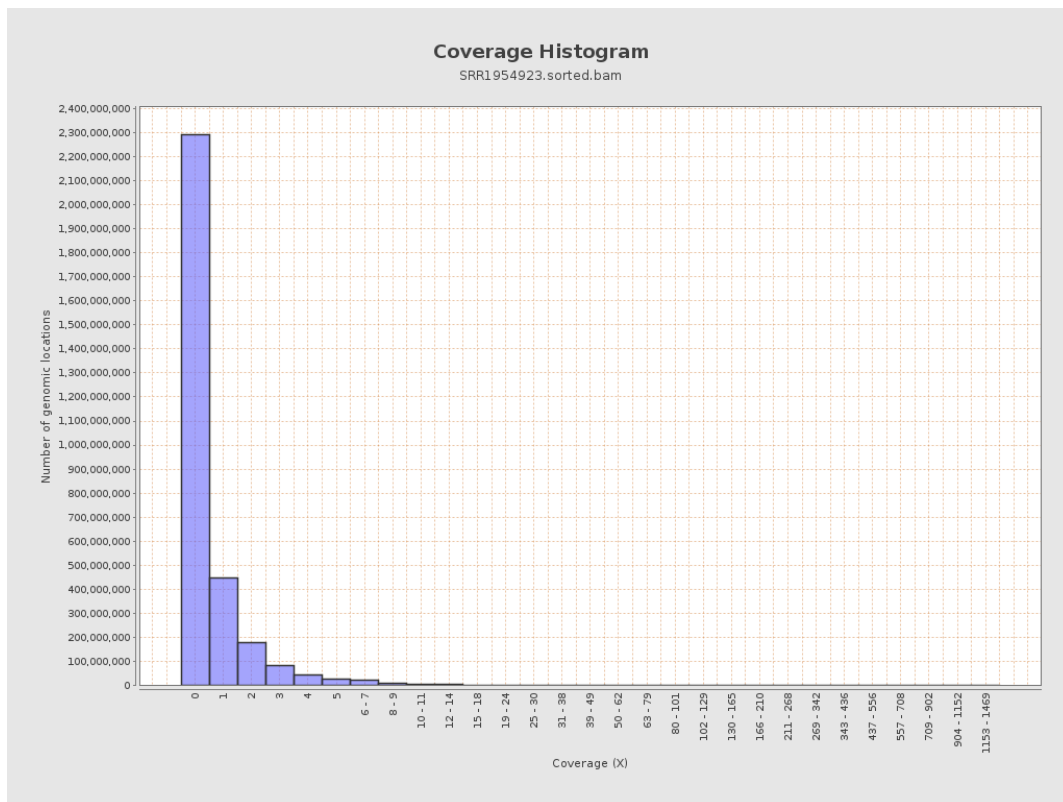
		bases	coverage	deviation
chr1	249250621	134713399	0.5405	1.6117
chr2	243199373	140592169	0.5781	2.2378
chr3	198022430	109917472	0.5551	1.2504
chr4	191154276	91897658	0.4808	1.2571
chr5	180915260	99675129	0.5509	1.2375
chr6	171115067	90452868	0.5286	1.2318
chr7	159138663	83066097	0.522	1.2479
chr8	146364022	82546390	0.564	1.3373
chr9	141213431	69353409	0.4911	1.6806
chr10	135534747	78030827	0.5757	1.4162
chr11	135006516	77514215	0.5742	1.445
chr12	133851895	72168291	0.5392	1.2499
chr13	115169878	47830263	0.4153	1.0766
chr14	107349540	72216302	0.6727	1.5567
chr15	102531392	49878231	0.4865	1.2165
chr16	90354753	49916256	0.5524	1.5615
chr17	81195210	43667667	0.5378	1.3345
chr18	78077248	43298532	0.5546	1.9259
chr19	59128983	25318214	0.4282	1.2809
chr20	63025520	40598388	0.6442	1.4497
chr21	48129895	20534409	0.4266	1.6288
chr22	51304566	21483831	0.4188	1.1724
chrMT	16571	196935	11.8843	7.7185
chrX	155270560	46118583	0.297	0.8473

chrY	59373566	8766912	0.1477	0.9185
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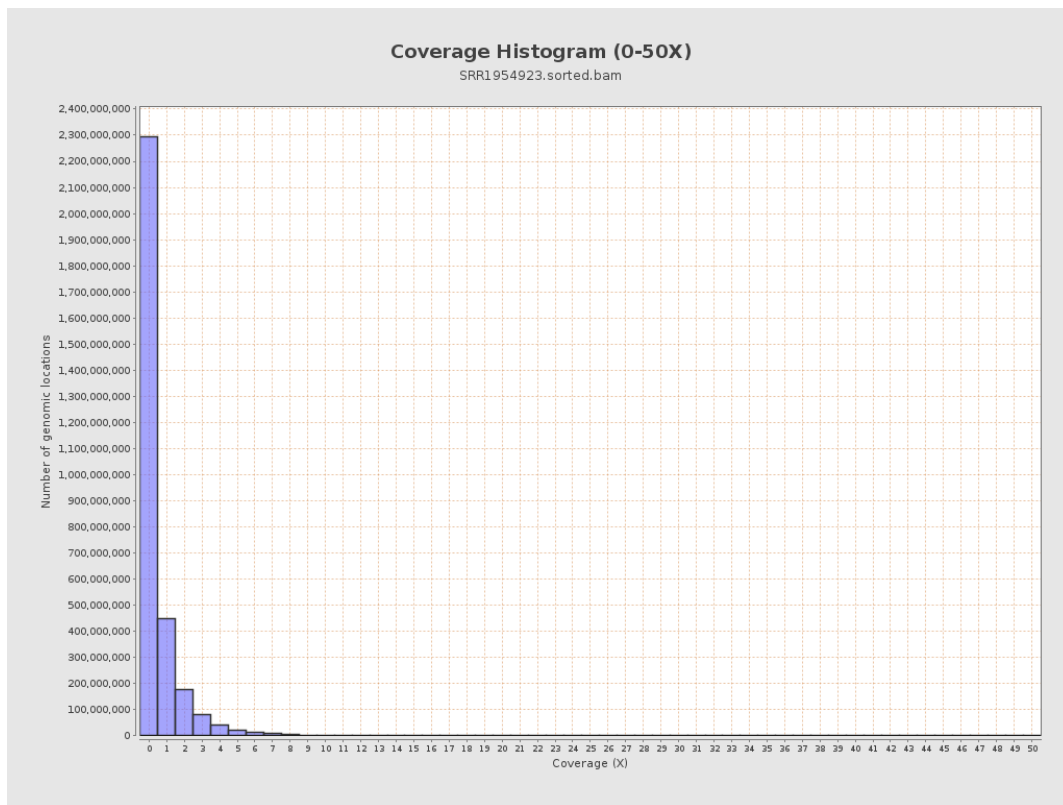
3. Results : Coverage across reference



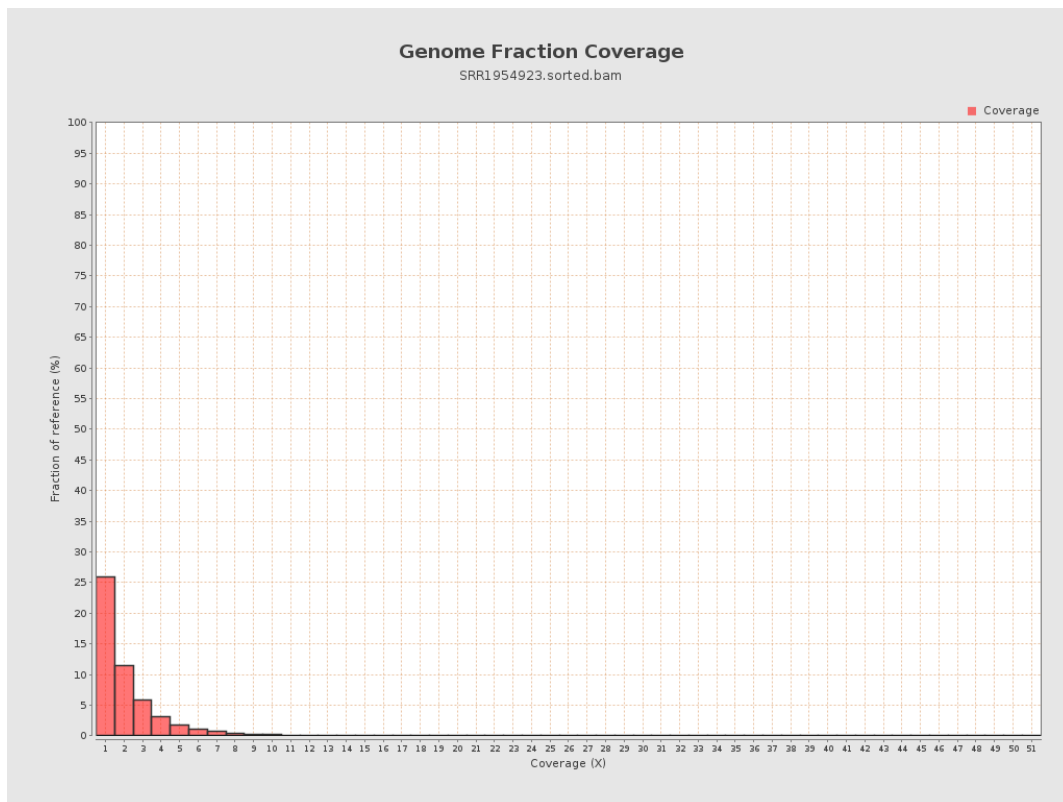
4. Results : Coverage Histogram



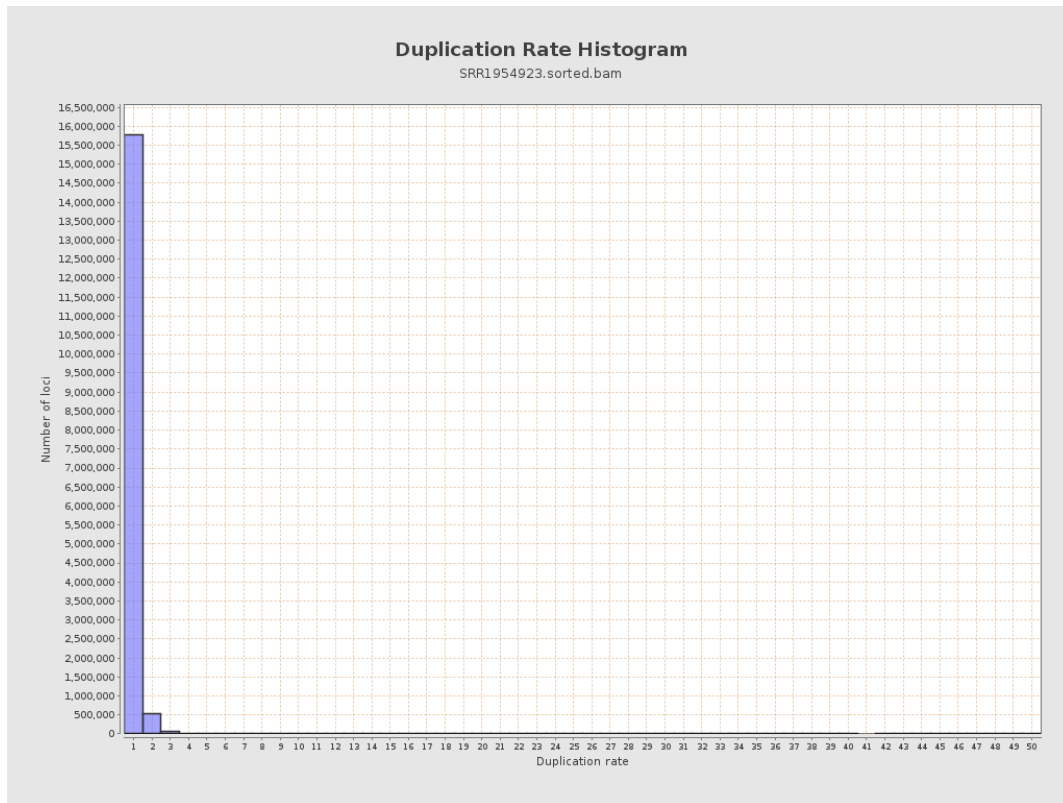
5. Results : Coverage Histogram (0-50X)



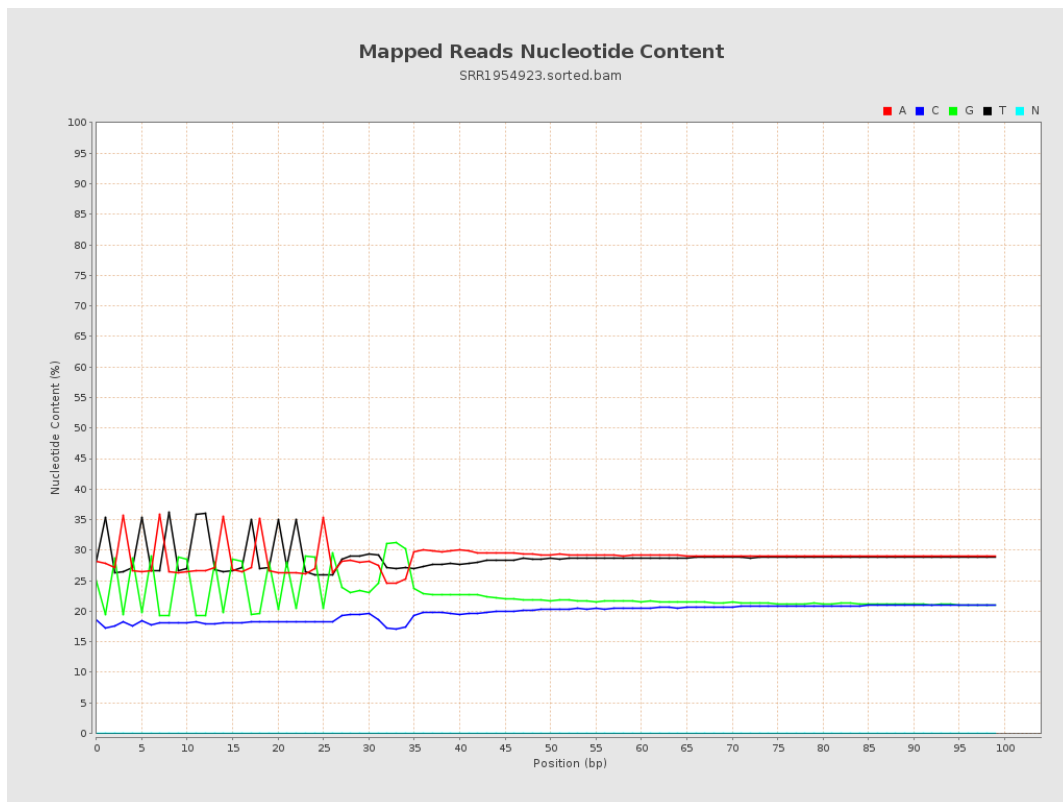
6. Results : Genome Fraction Coverage



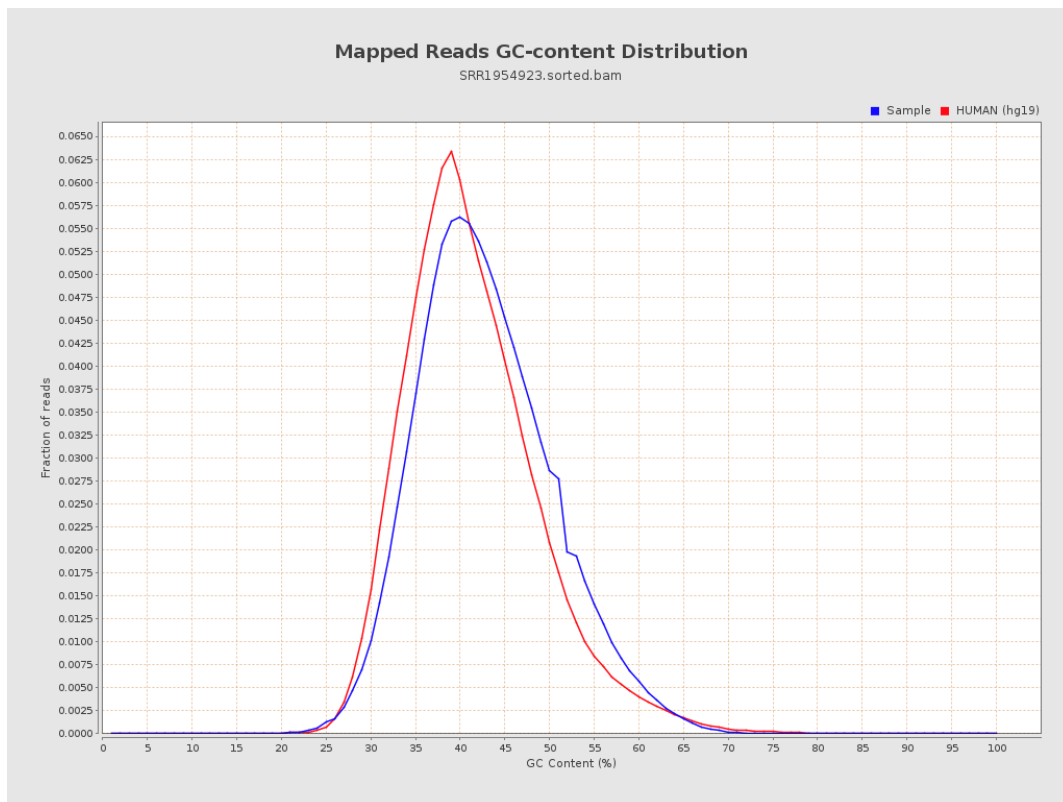
7. Results : Duplication Rate Histogram



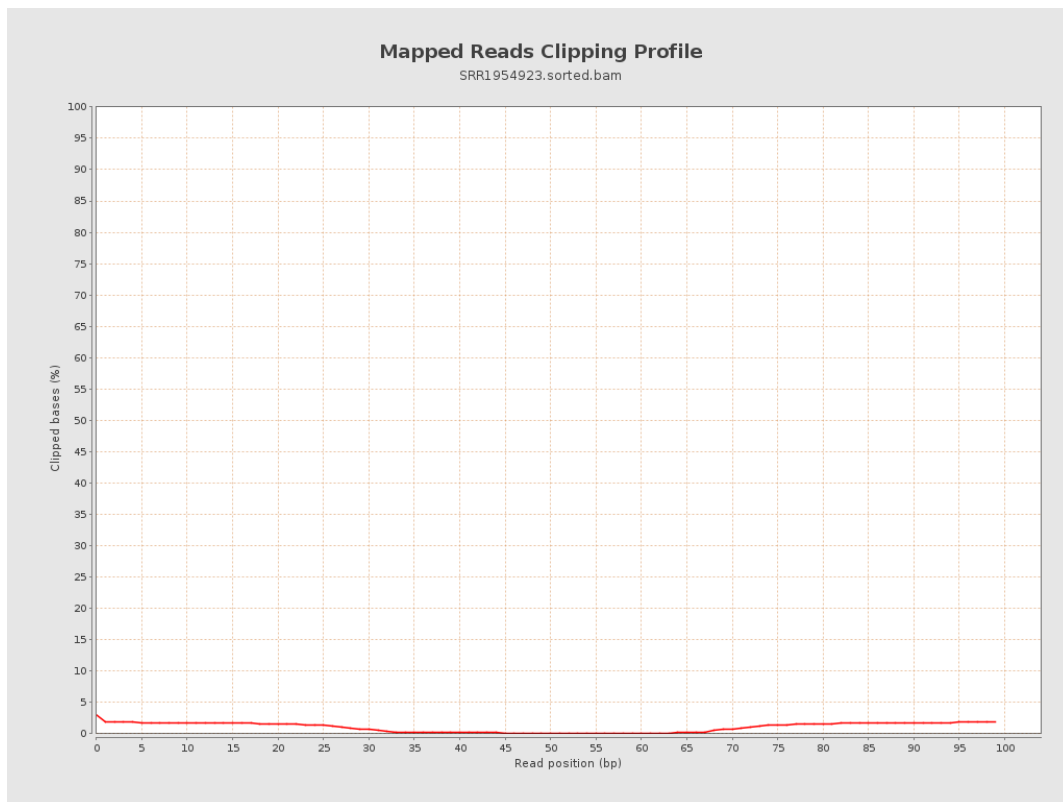
8. Results : Mapped Reads Nucleotide Content



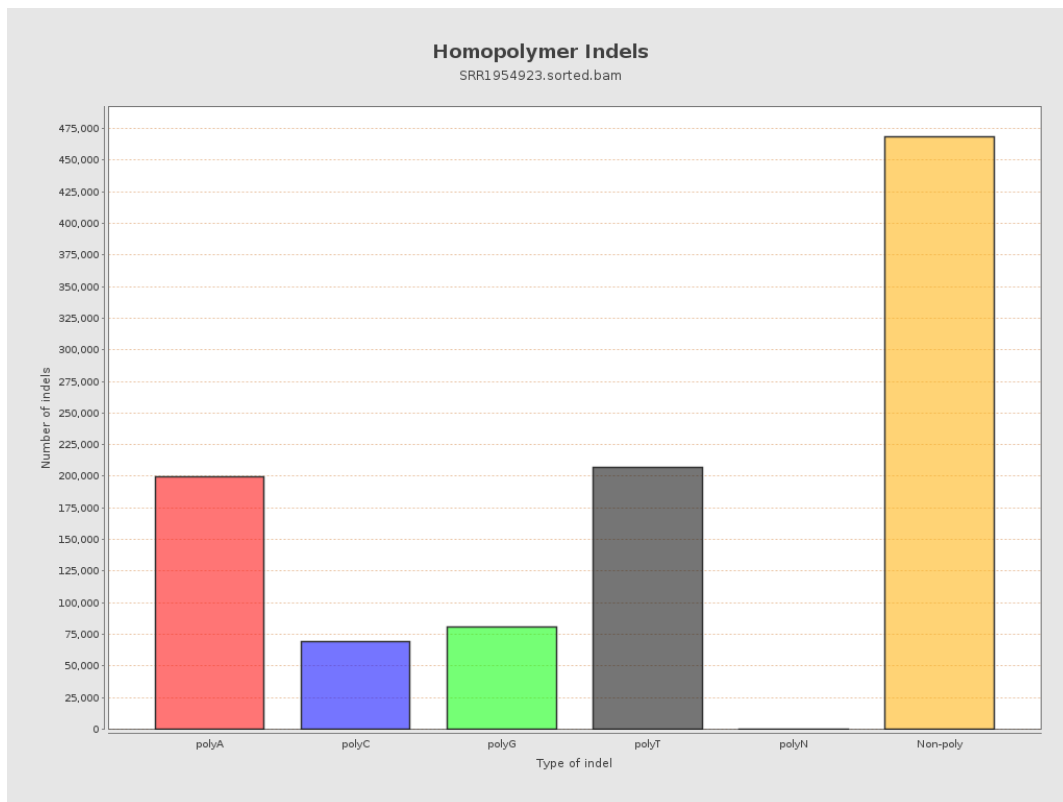
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



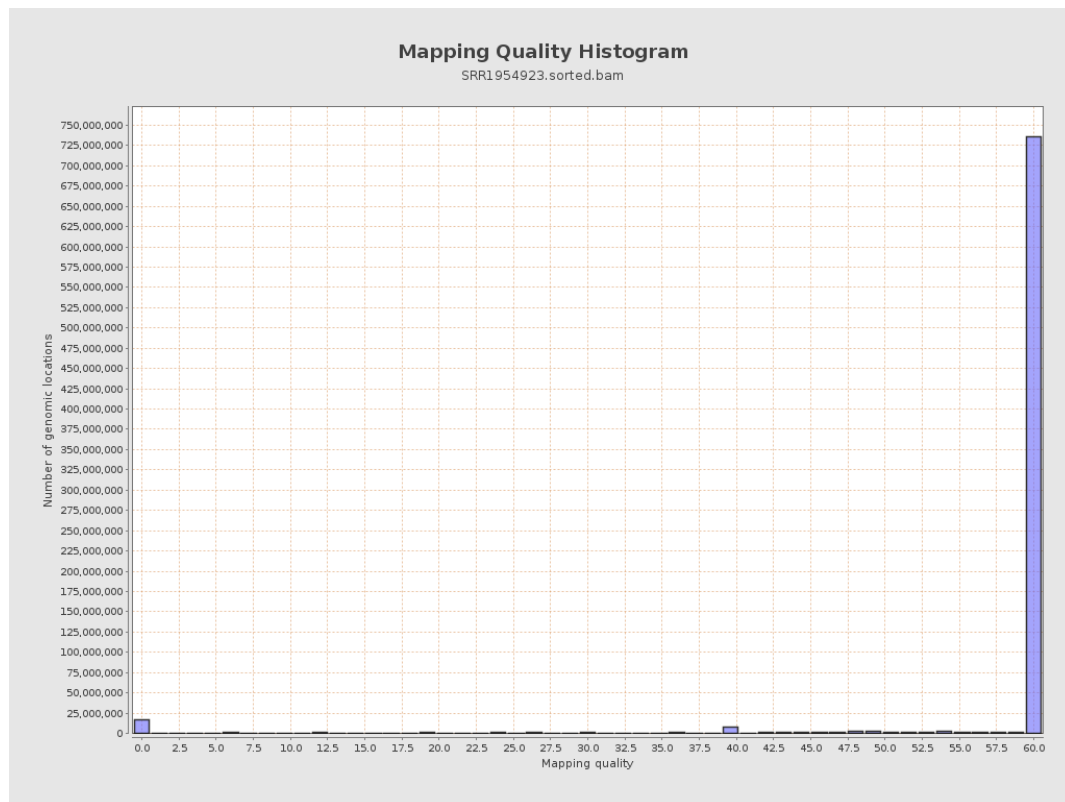
11. Results : Homopolymer Indels



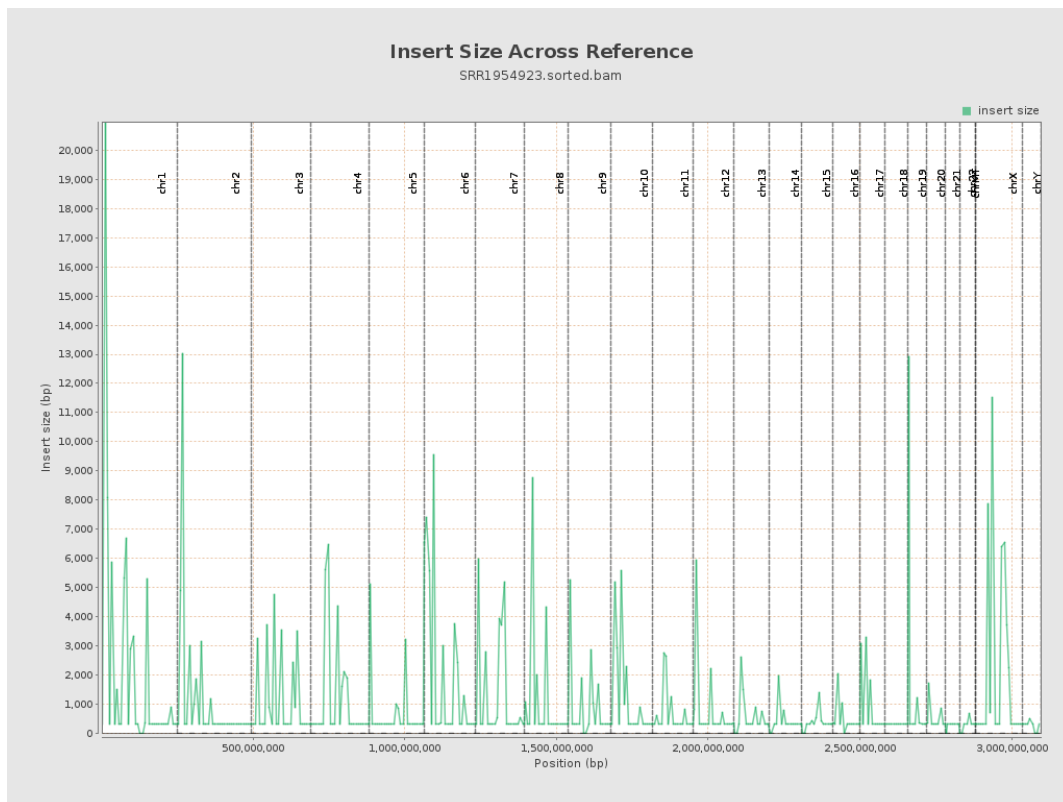
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

