

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 10:00:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1954924.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_SRR1954924 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1954924_1.fastq.gz SRR1954924_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 10:00:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1954924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,092,594
Mapped reads	17,644,813 / 97.53%
Unmapped reads	447,781 / 2.47%
Mapped paired reads	17,644,813 / 97.53%
Mapped reads, first in pair	8,981,655 / 49.64%
Mapped reads, second in pair	8,663,158 / 47.88%
Mapped reads, both in pair	17,300,360 / 95.62%
Mapped reads, singletons	344,453 / 1.9%
Secondary alignments	0
Supplementary alignments	43,458 / 0.24%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	796,175 / 4.4%
Duplication rate	3.8%
Clipped reads	4,179,885 / 23.1%

2.2. ACGT Content

Number/percentage of A's	475,938,062 / 28.82%
Number/percentage of C's	325,565,805 / 19.72%
Number/percentage of T's	475,472,549 / 28.79%
Number/percentage of G's	374,295,083 / 22.67%
Number/percentage of N's	48,068 / 0%

GC Percentage	42.38%
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2.3. Coverage

Mean	0.5338
Standard Deviation	1.4901

2.4. Mapping Quality

Mean Mapping Quality	54.26
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2.5. Insert size

Mean	30,048.36
Standard Deviation	1,734,453.53
P25/Median/P75	314 / 329 / 343

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	14,147,178
Insertions	269,991
Mapped reads with at least one insertion	1.51%
Deletions	789,658
Mapped reads with at least one deletion	4.37%
Homopolymer indels	54.35%

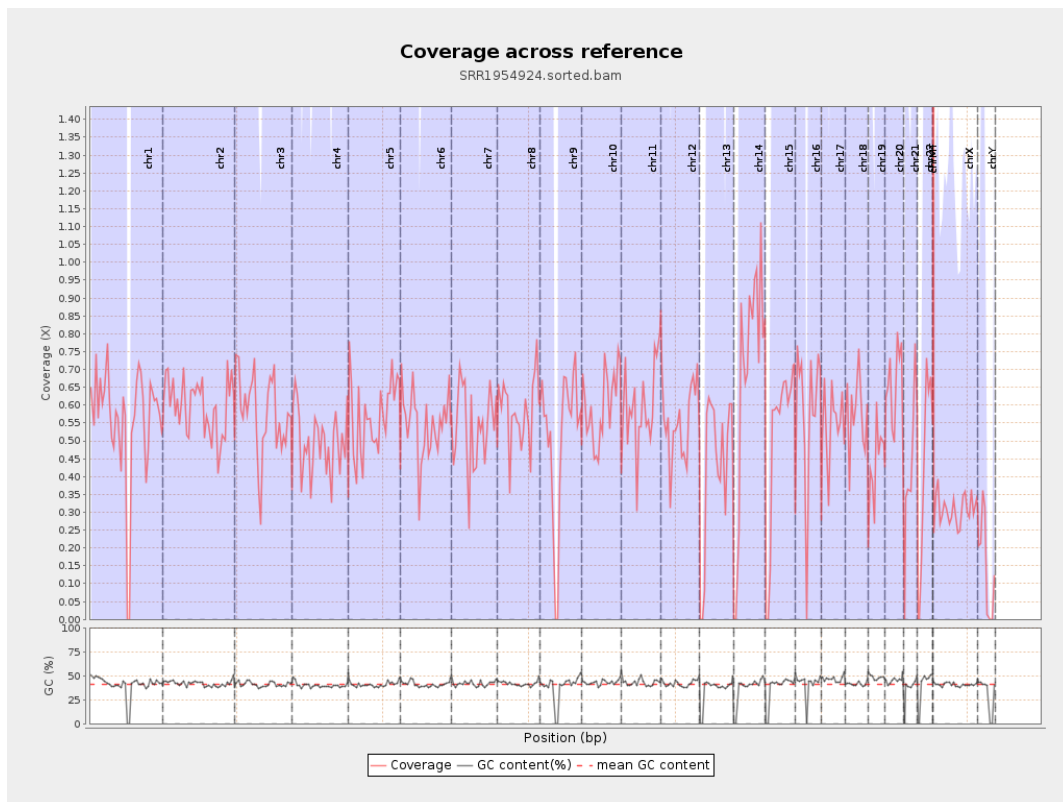
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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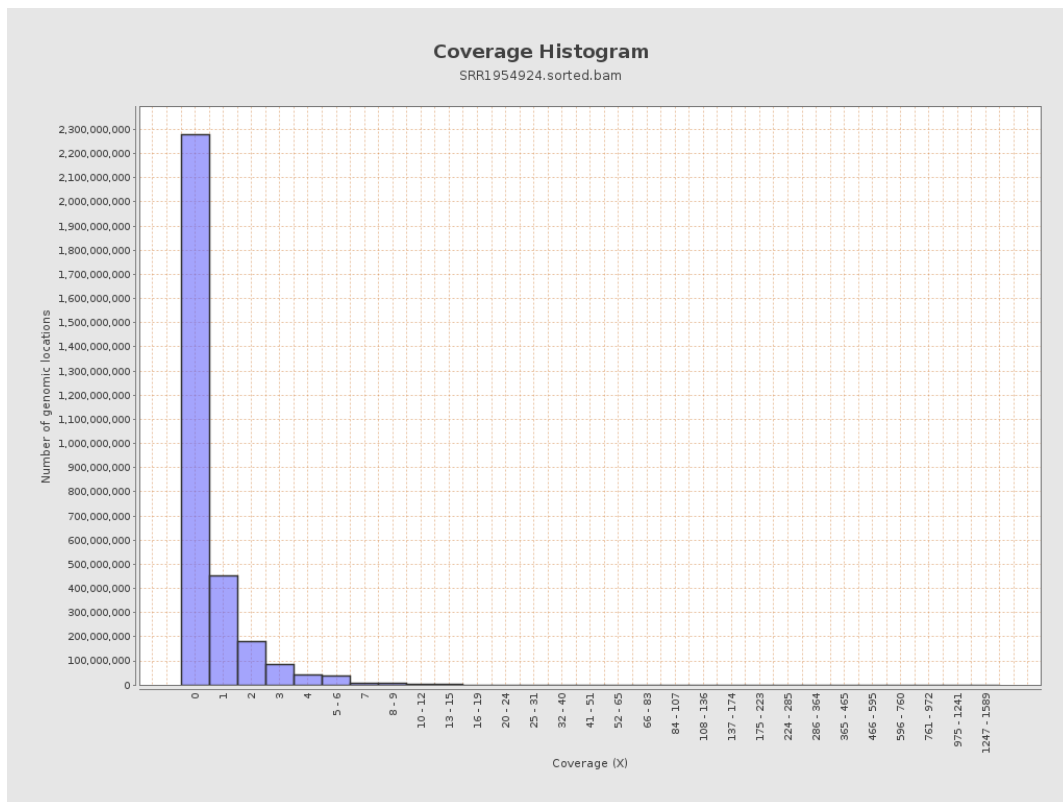
		bases	coverage	deviation
chr1	249250621	138768544	0.5567	1.6465
chr2	243199373	145153117	0.5968	2.2928
chr3	198022430	113443091	0.5729	1.2834
chr4	191154276	95354439	0.4988	1.3023
chr5	180915260	103123352	0.57	1.2721
chr6	171115067	93622621	0.5471	1.2635
chr7	159138663	85753107	0.5389	1.2883
chr8	146364022	85273069	0.5826	1.3716
chr9	141213431	71839427	0.5087	1.7447
chr10	135534747	80720608	0.5956	1.4599
chr11	135006516	80237362	0.5943	1.4791
chr12	133851895	74518778	0.5567	1.2847
chr13	115169878	49676985	0.4313	1.1077
chr14	107349540	74505149	0.694	1.5964
chr15	102531392	51665592	0.5039	1.2565
chr16	90354753	51426364	0.5692	1.6266
chr17	81195210	44685077	0.5503	1.3678
chr18	78077248	44737793	0.573	2.0017
chr19	59128983	25848781	0.4372	1.3057
chr20	63025520	41745615	0.6624	1.4767
chr21	48129895	21212929	0.4407	1.6912
chr22	51304566	22003090	0.4289	1.187
chrMT	16571	207556	12.5253	9.3174
chrX	155270560	47875661	0.3083	0.8731

chrY	59373566	9003813	0.1516	0.9281
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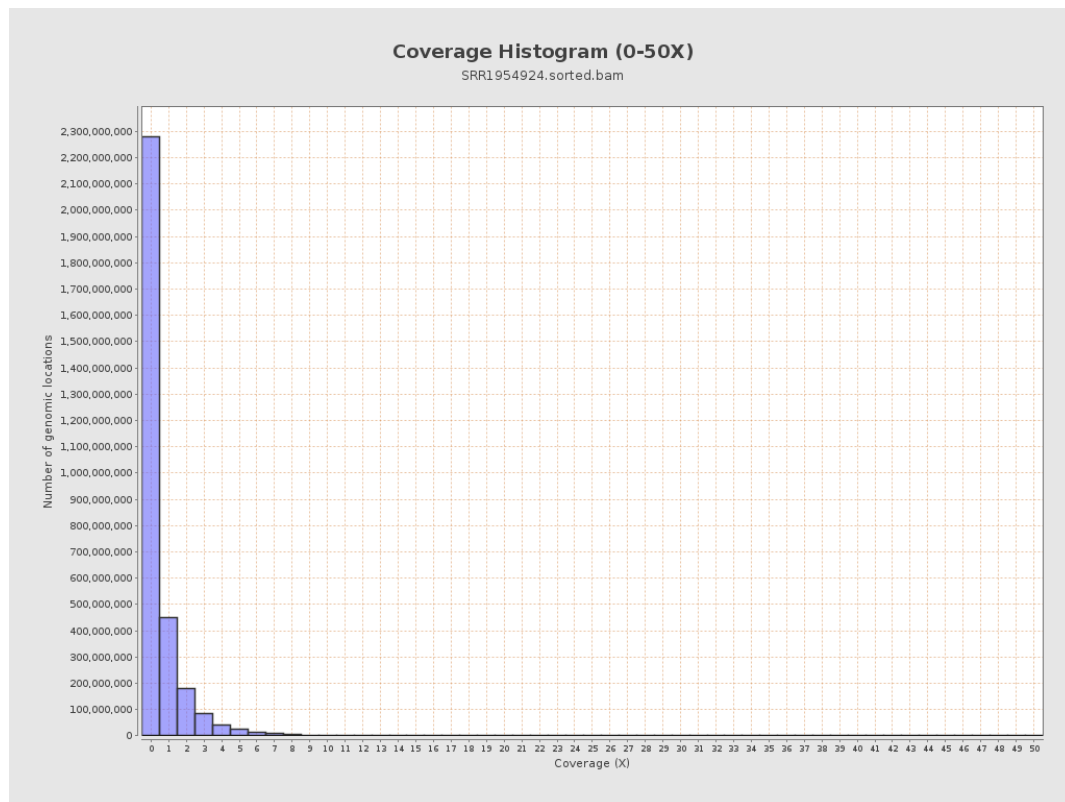
3. Results : Coverage across reference



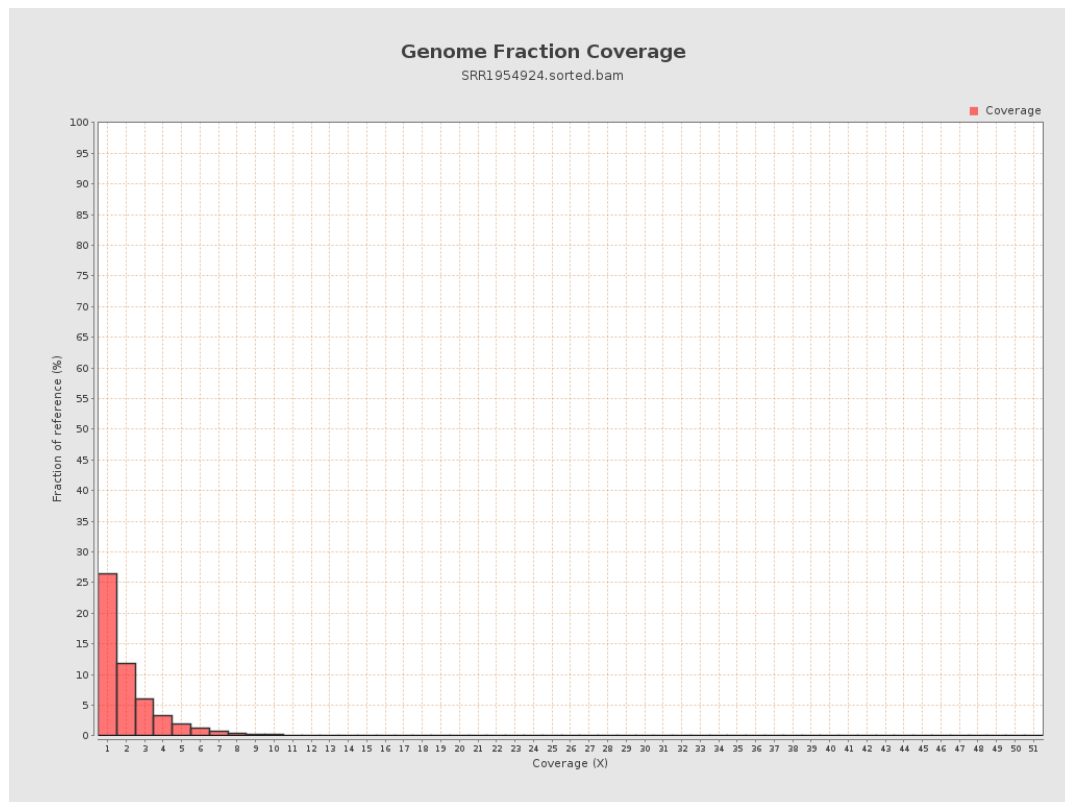
4. Results : Coverage Histogram



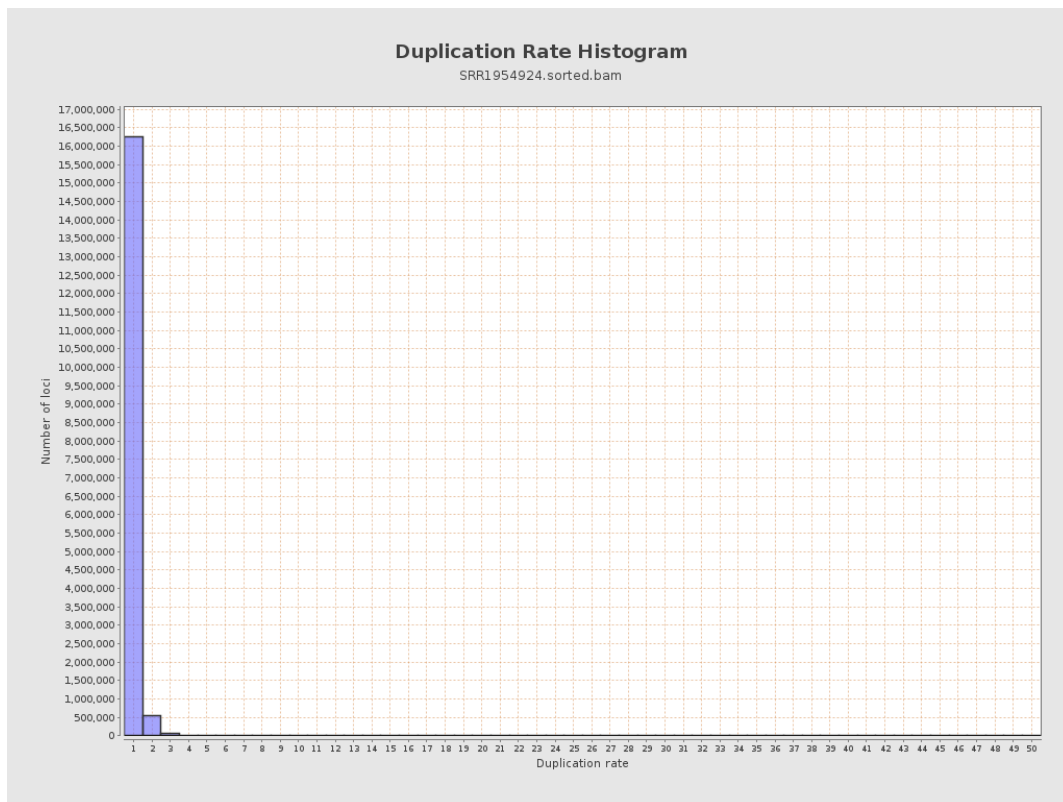
5. Results : Coverage Histogram (0-50X)



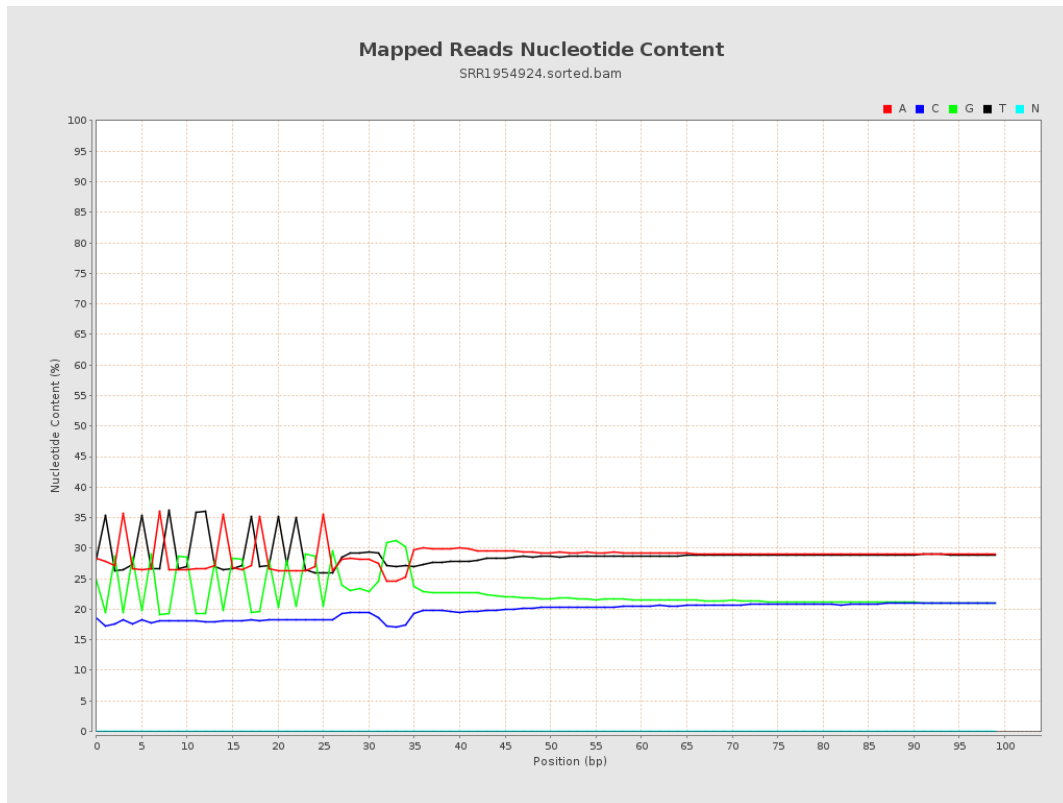
6. Results : Genome Fraction Coverage



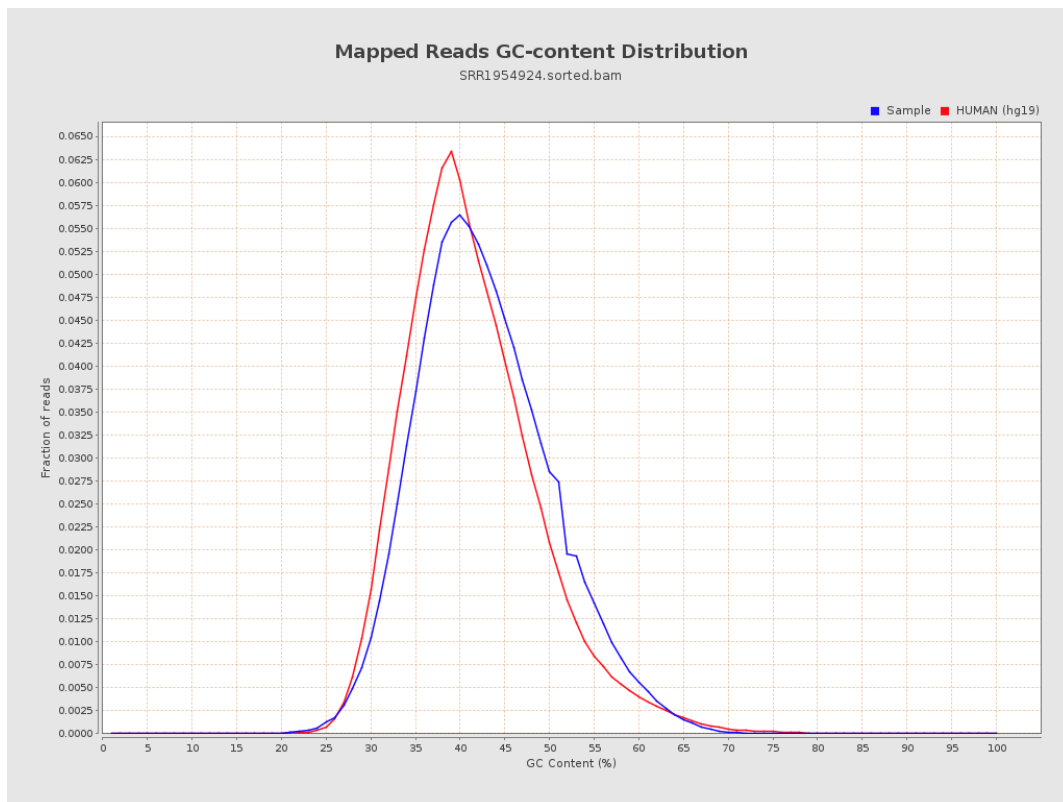
7. Results : Duplication Rate Histogram



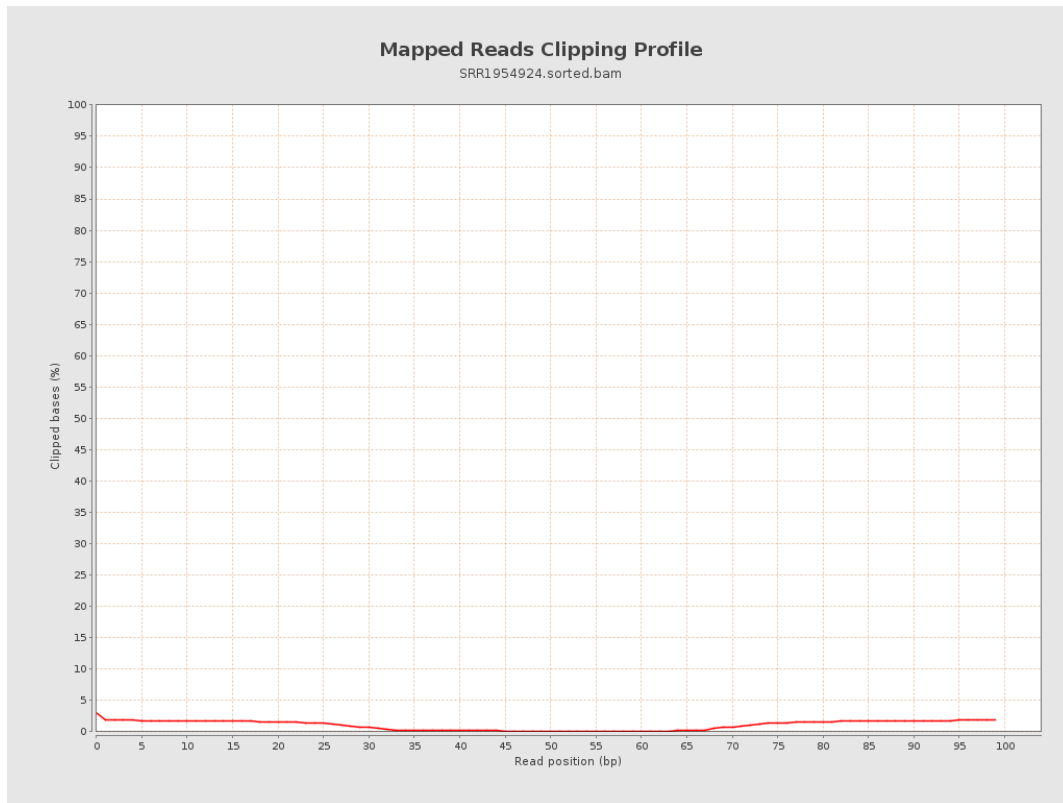
8. Results : Mapped Reads Nucleotide Content



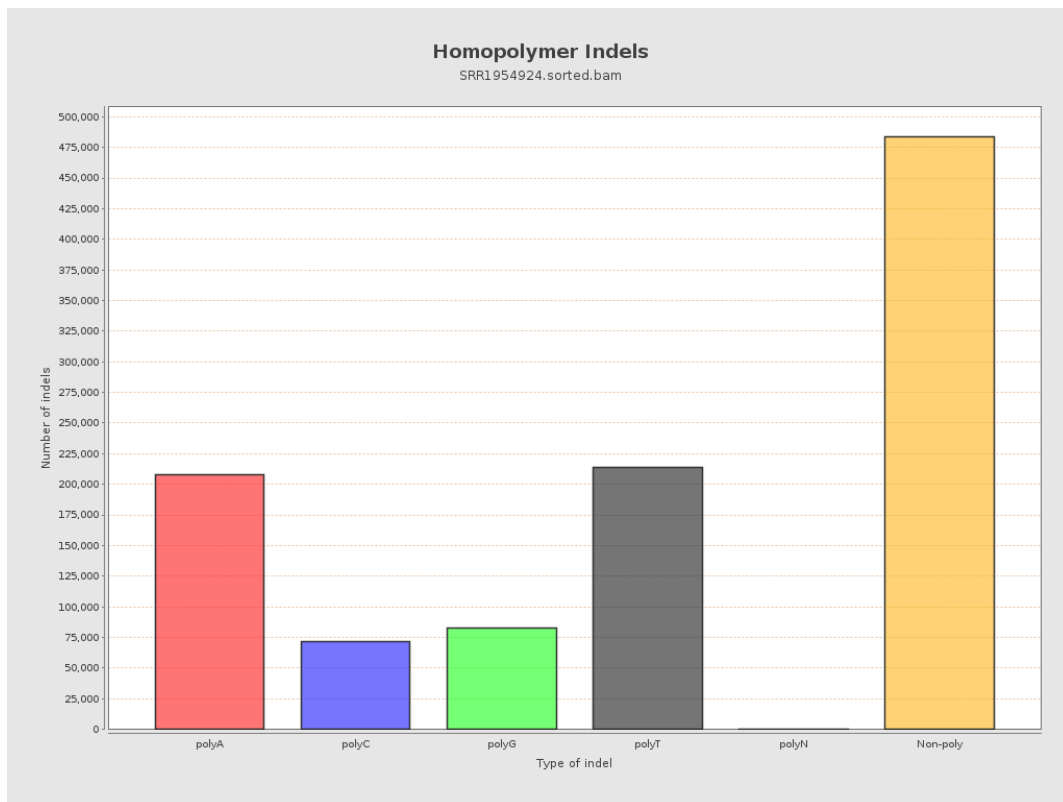
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



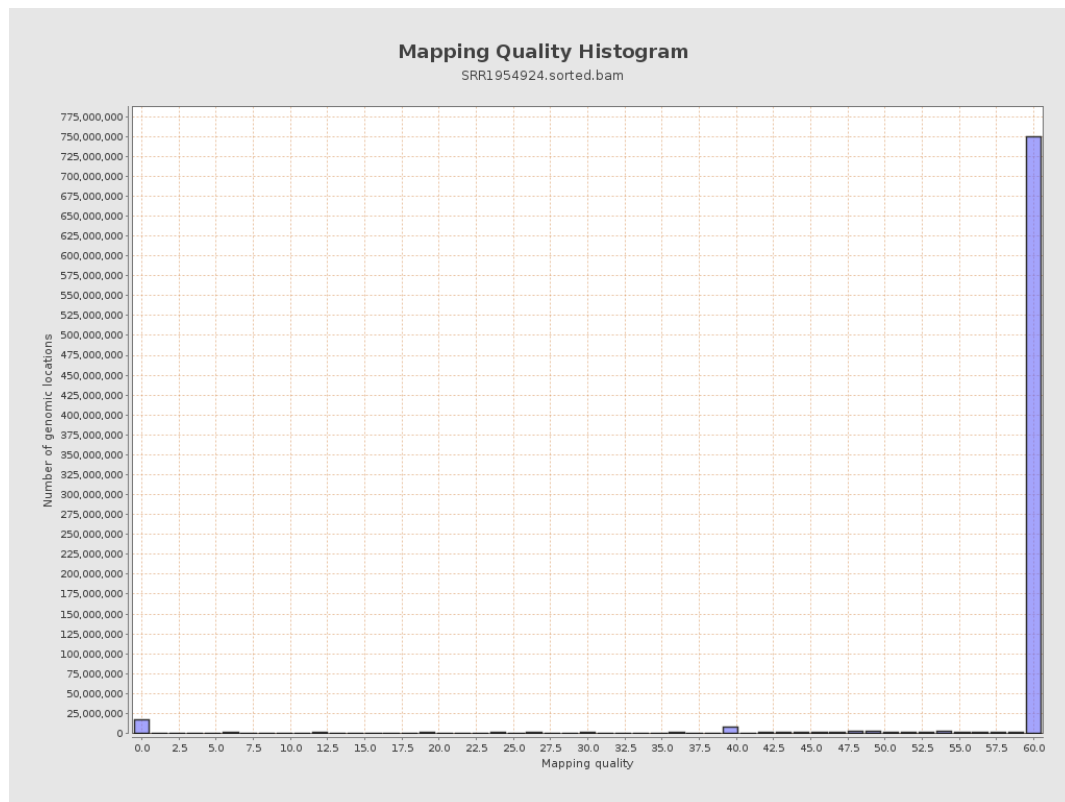
11. Results : Homopolymer Indels



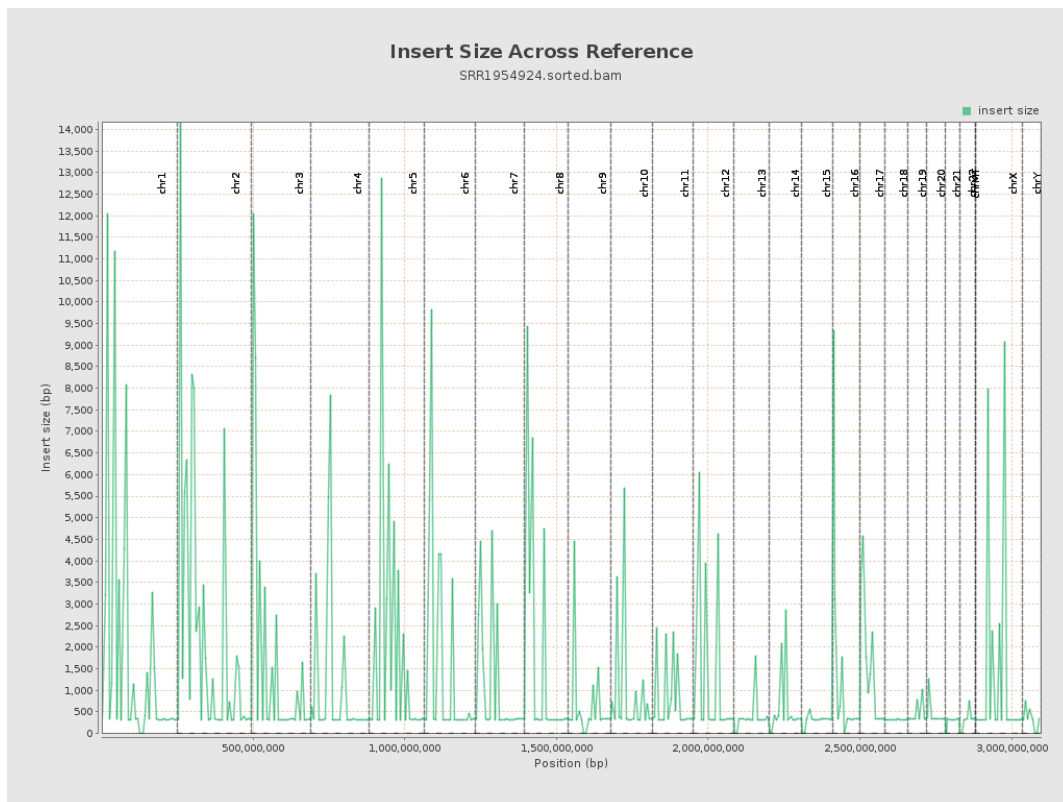
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

