

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 09:41:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124954.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_SRR3124954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124954_1.fastq.gz SRR3124954_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 09:41:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,145,168
Mapped reads	6,070,454 / 98.78%
Unmapped reads	74,714 / 1.22%
Mapped paired reads	6,070,454 / 98.78%
Mapped reads, first in pair	3,040,940 / 49.49%
Mapped reads, second in pair	3,029,514 / 49.3%
Mapped reads, both in pair	6,047,916 / 98.42%
Mapped reads, singletons	22,538 / 0.37%
Secondary alignments	0
Supplementary alignments	23,121 / 0.38%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	450,909 / 7.34%
Duplication rate	4.99%
Clipped reads	2,875,368 / 46.79%

2.2. ACGT Content

Number/percentage of A's	149,035,585 / 28.25%
Number/percentage of C's	97,715,838 / 18.52%
Number/percentage of T's	158,252,856 / 30%
Number/percentage of G's	122,575,747 / 23.23%
Number/percentage of N's	7,591 / 0%

GC Percentage	41.75%
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2.3. Coverage

Mean	0.1705
Standard Deviation	1.5932

2.4. Mapping Quality

Mean Mapping Quality	52.79
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2.5. Insert size

Mean	27,587.99
Standard Deviation	1,549,498.53
P25/Median/P75	146 / 200 / 282

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	3,784,207
Insertions	65,334
Mapped reads with at least one insertion	1.06%
Deletions	166,116
Mapped reads with at least one deletion	2.69%
Homopolymer indels	48.06%

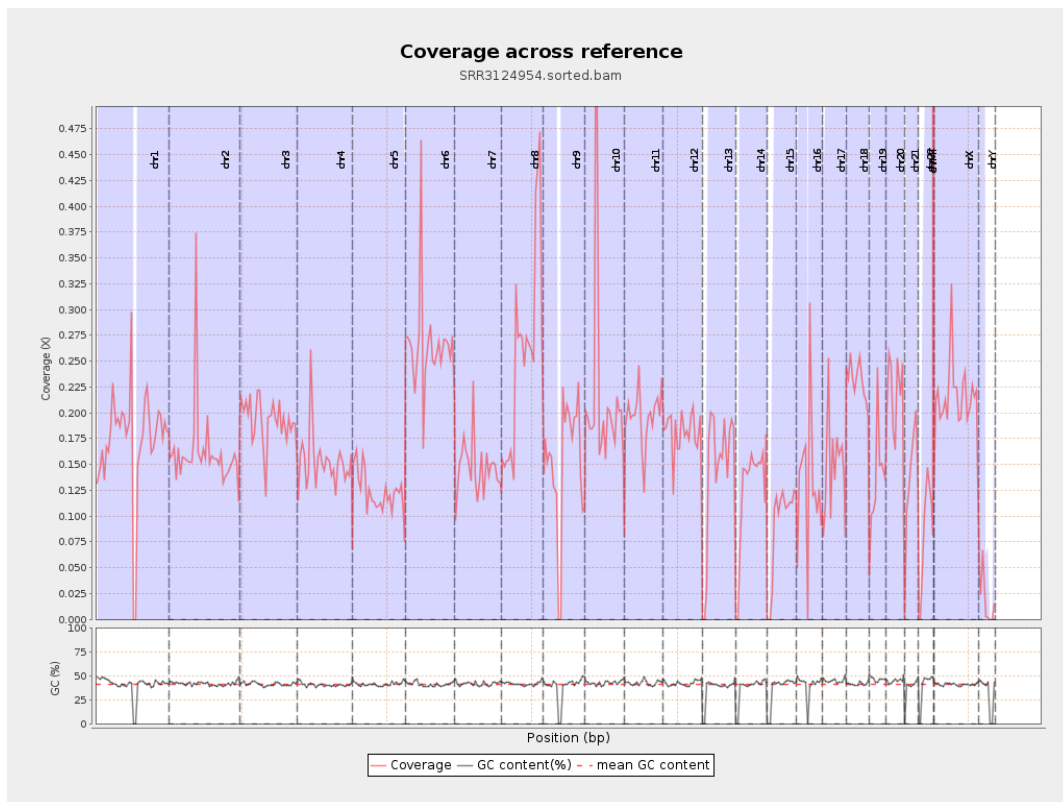
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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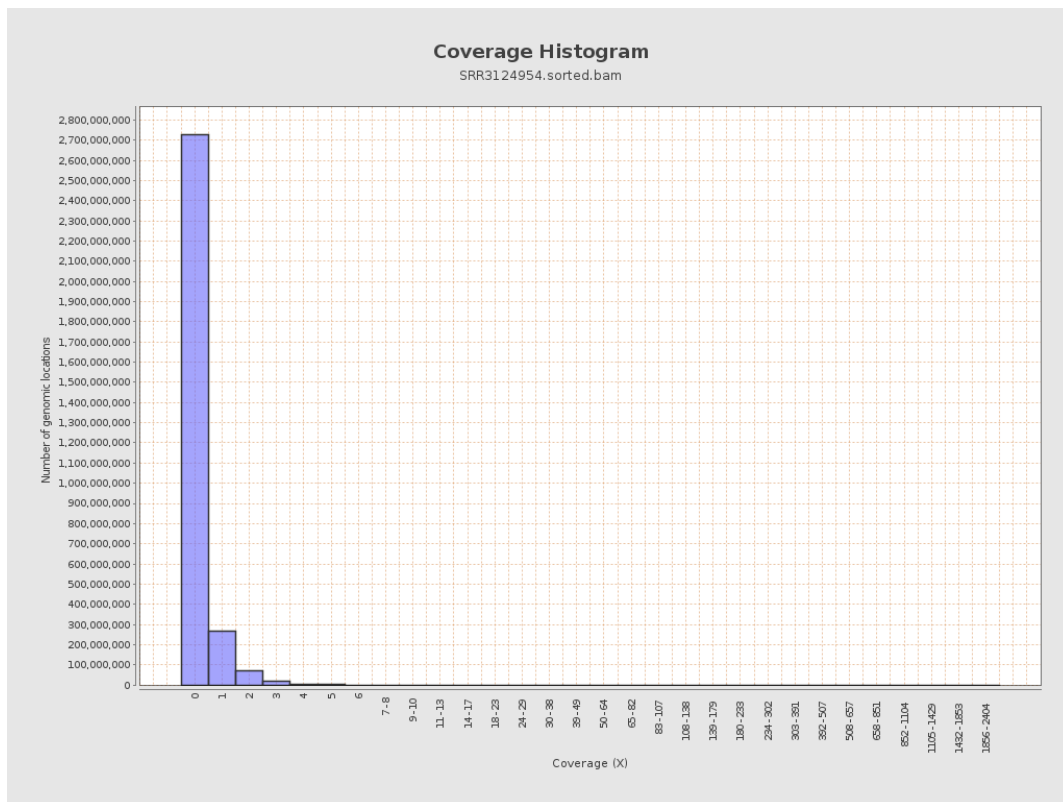
		bases	coverage	deviation
chr1	249250621	43188334	0.1733	1.8133
chr2	243199373	39299056	0.1616	1.5556
chr3	198022430	38085951	0.1923	0.568
chr4	191154276	29086298	0.1522	0.8865
chr5	180915260	22309272	0.1233	0.4495
chr6	171115067	45368501	0.2651	2.4591
chr7	159138663	23488073	0.1476	1.8572
chr8	146364022	38032465	0.2598	0.9524
chr9	141213431	21610980	0.153	1.9247
chr10	135534747	28934447	0.2135	3.8505
chr11	135006516	26216211	0.1942	1.9039
chr12	133851895	24079901	0.1799	0.5454
chr13	115169878	16419348	0.1426	0.4775
chr14	107349540	13190753	0.1229	0.5218
chr15	102531392	9373165	0.0914	0.3927
chr16	90354753	11859654	0.1313	1.5433
chr17	81195210	11851667	0.146	2.0654
chr18	78077248	18131316	0.2322	2.3425
chr19	59128983	8226195	0.1391	1.1695
chr20	63025520	13639624	0.2164	0.6394
chr21	48129895	6523773	0.1355	0.5803
chr22	51304566	4317582	0.0842	0.3715
chrMT	16571	77322	4.6661	3.6836
chrX	155270560	33483249	0.2156	1.0859

chrY	59373566	1060008	0.0179	0.8072
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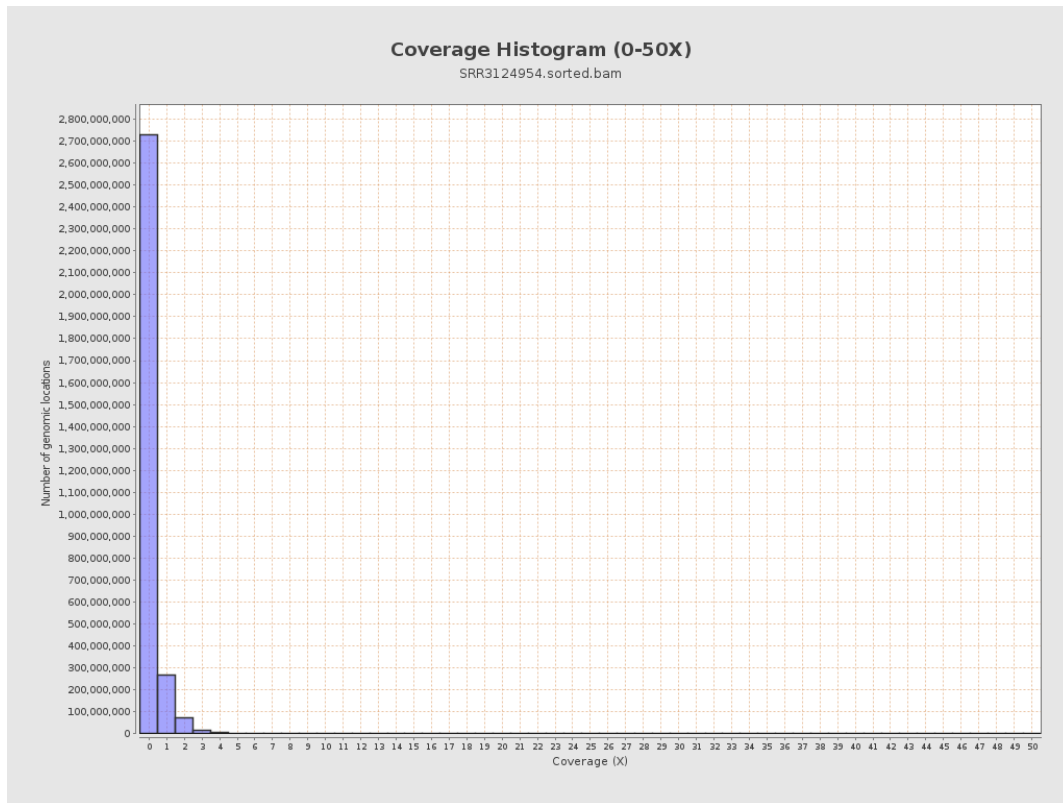
3. Results : Coverage across reference



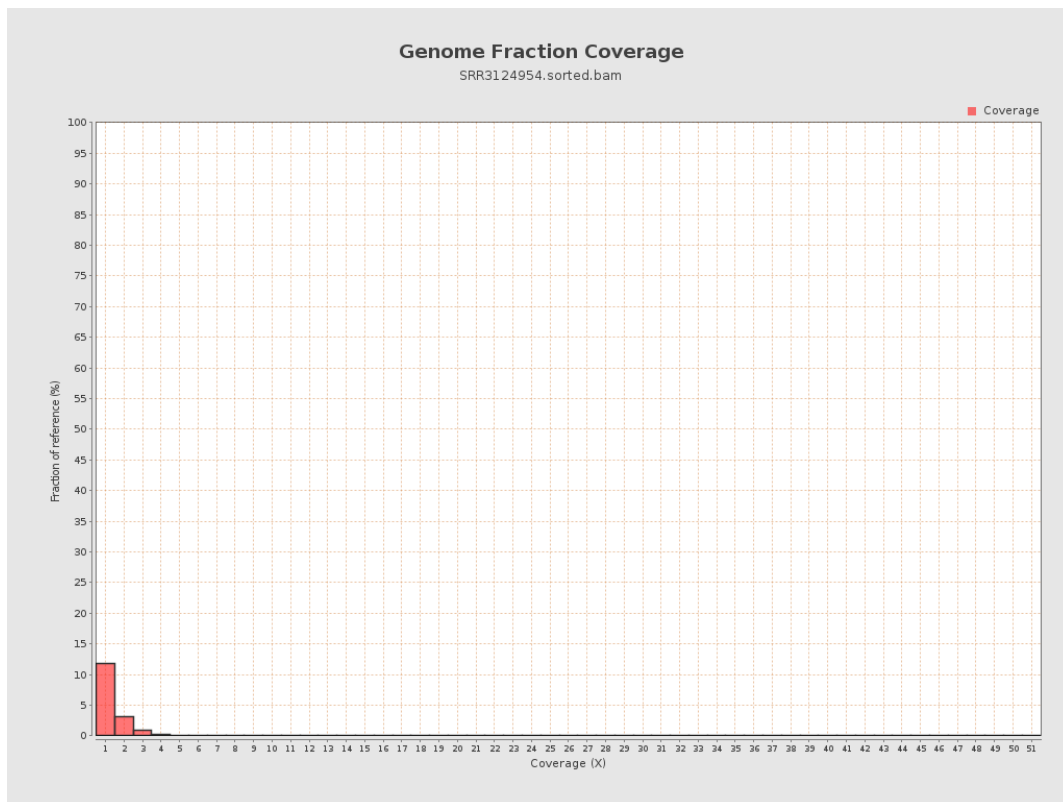
4. Results : Coverage Histogram



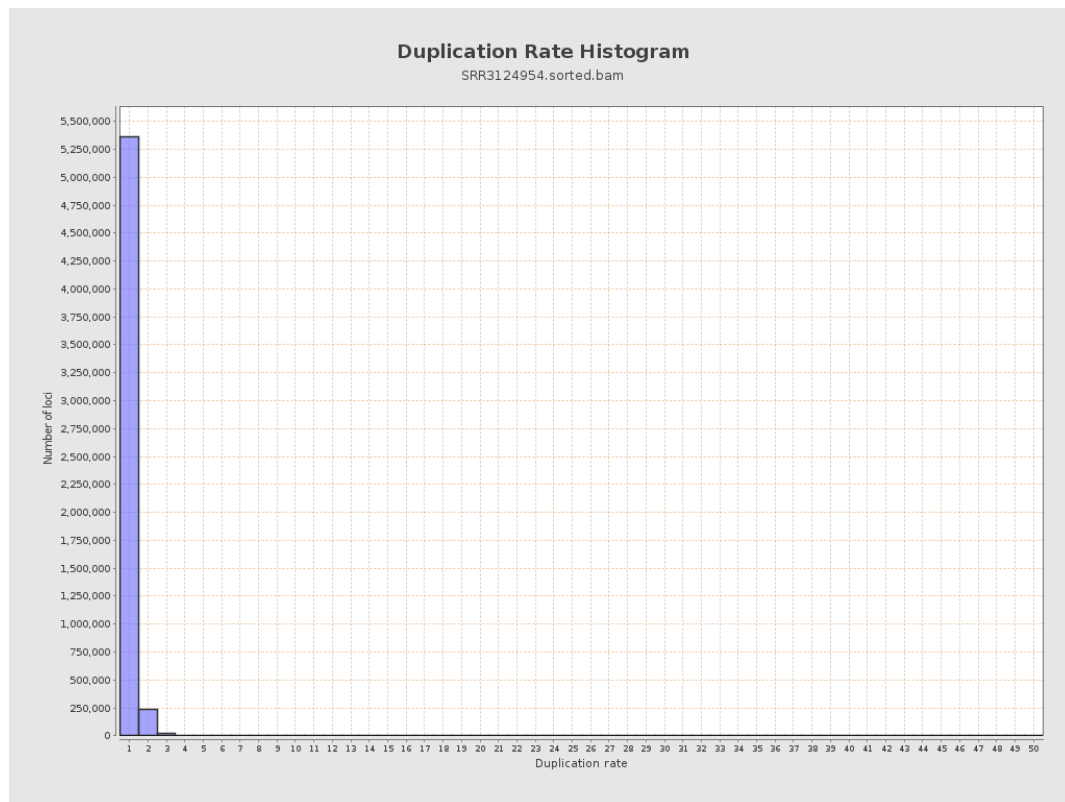
5. Results : Coverage Histogram (0-50X)



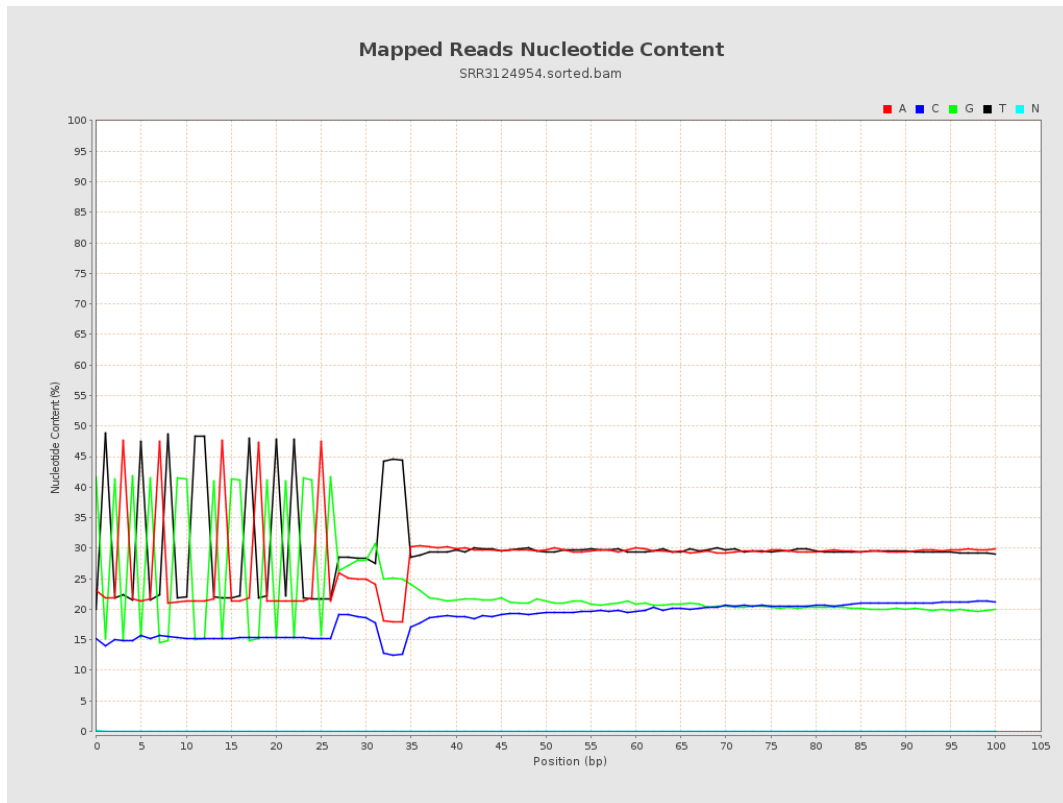
6. Results : Genome Fraction Coverage



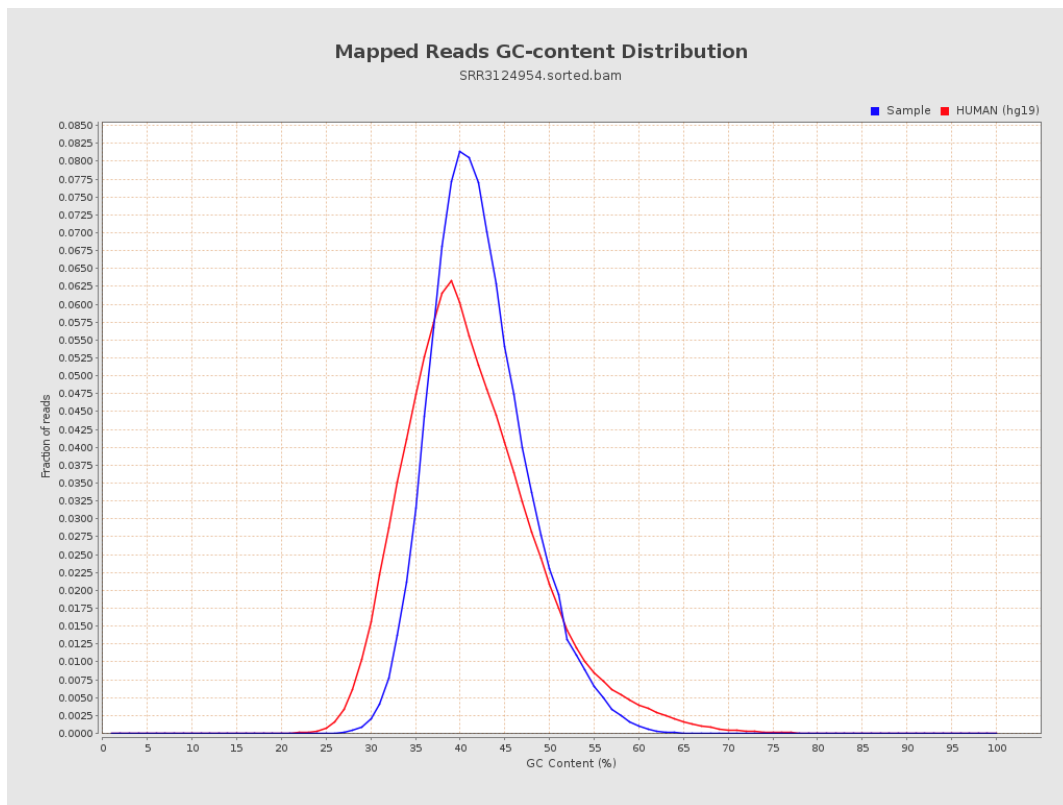
7. Results : Duplication Rate Histogram



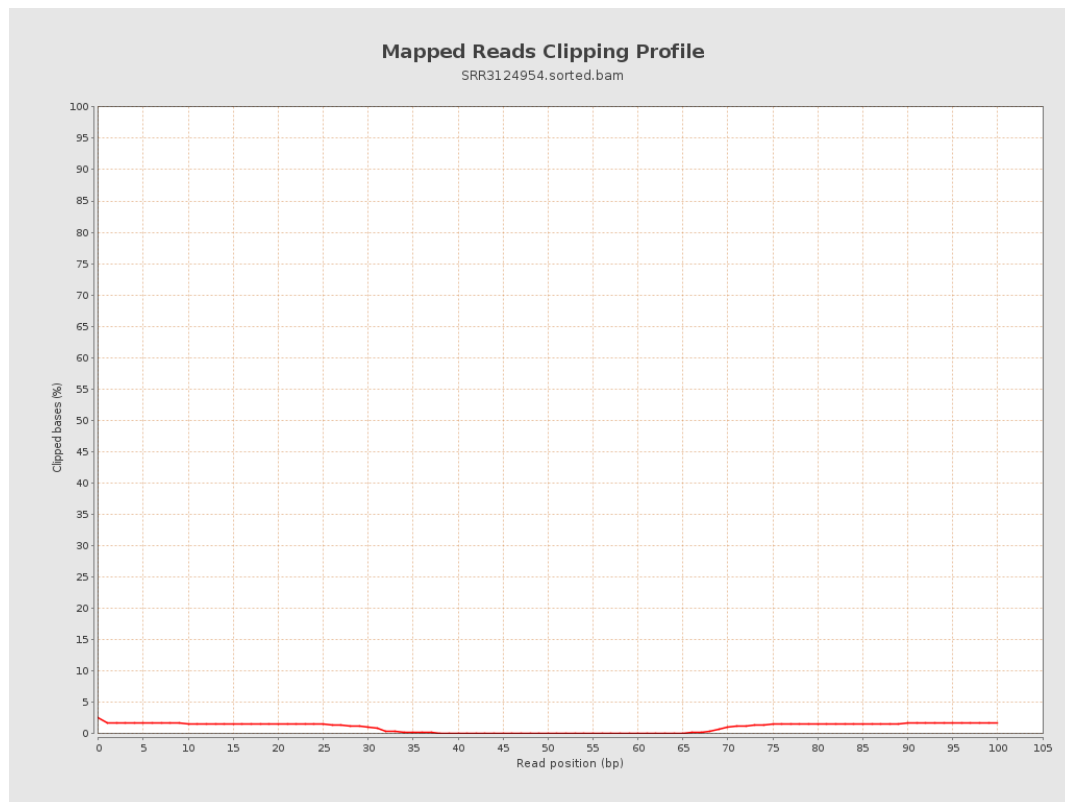
8. Results : Mapped Reads Nucleotide Content



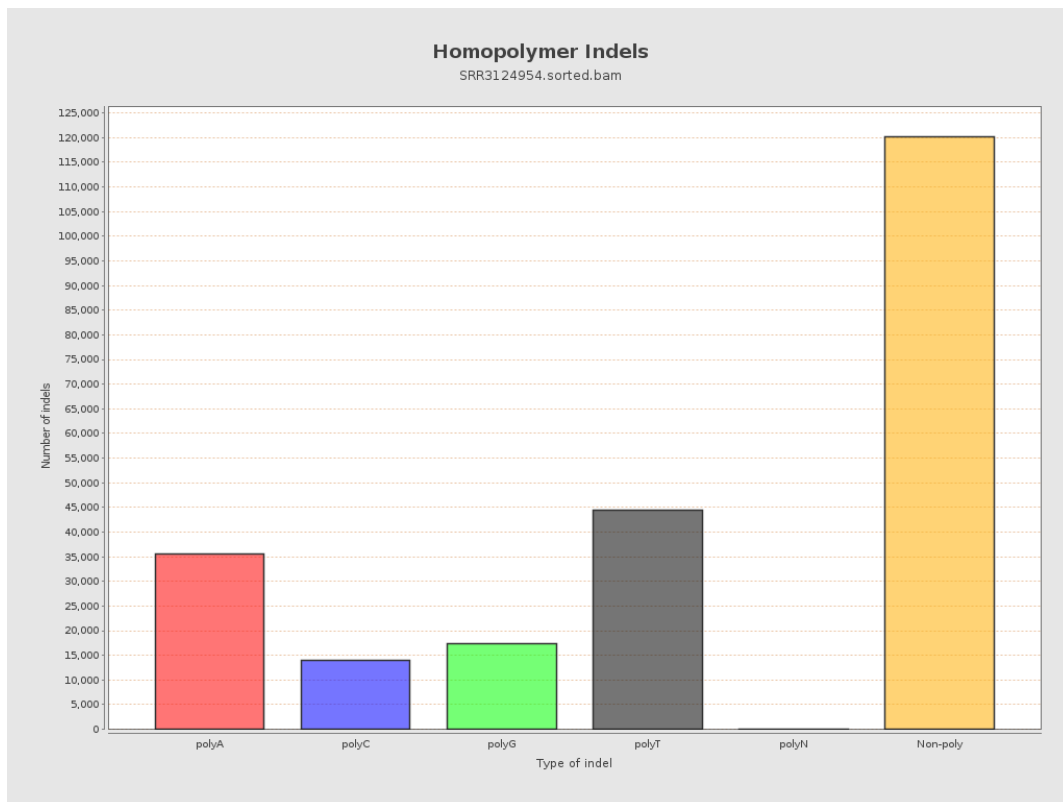
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



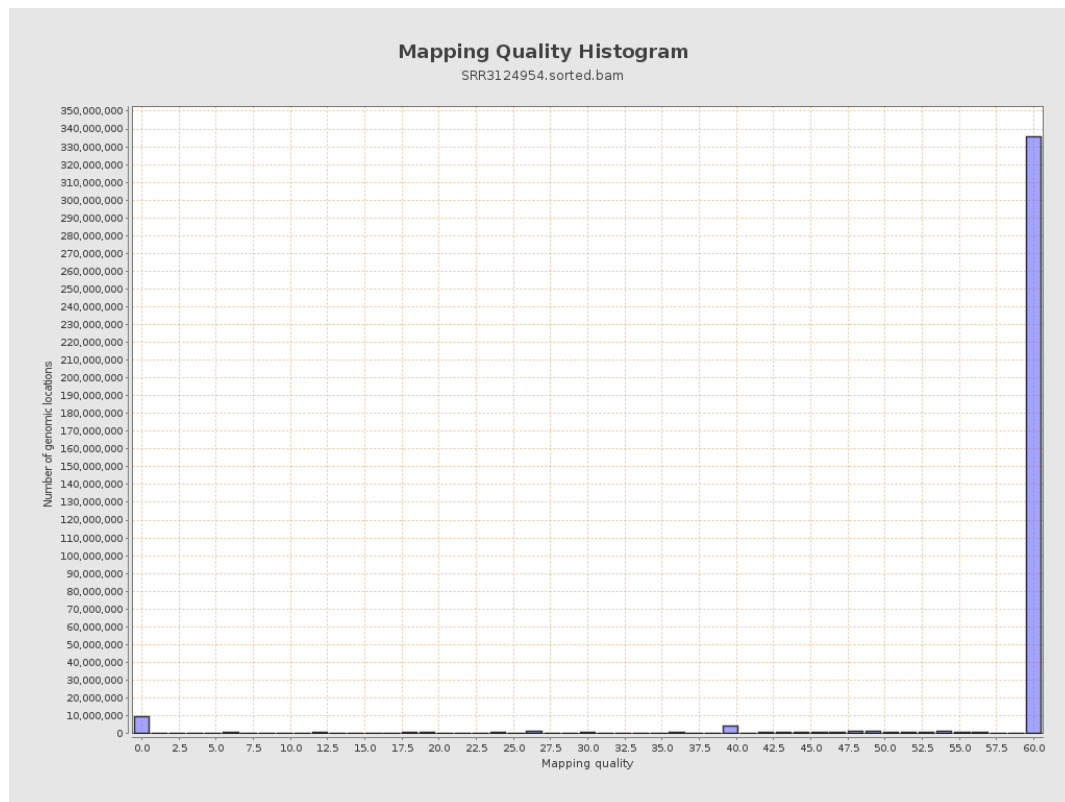
11. Results : Homopolymer Indels



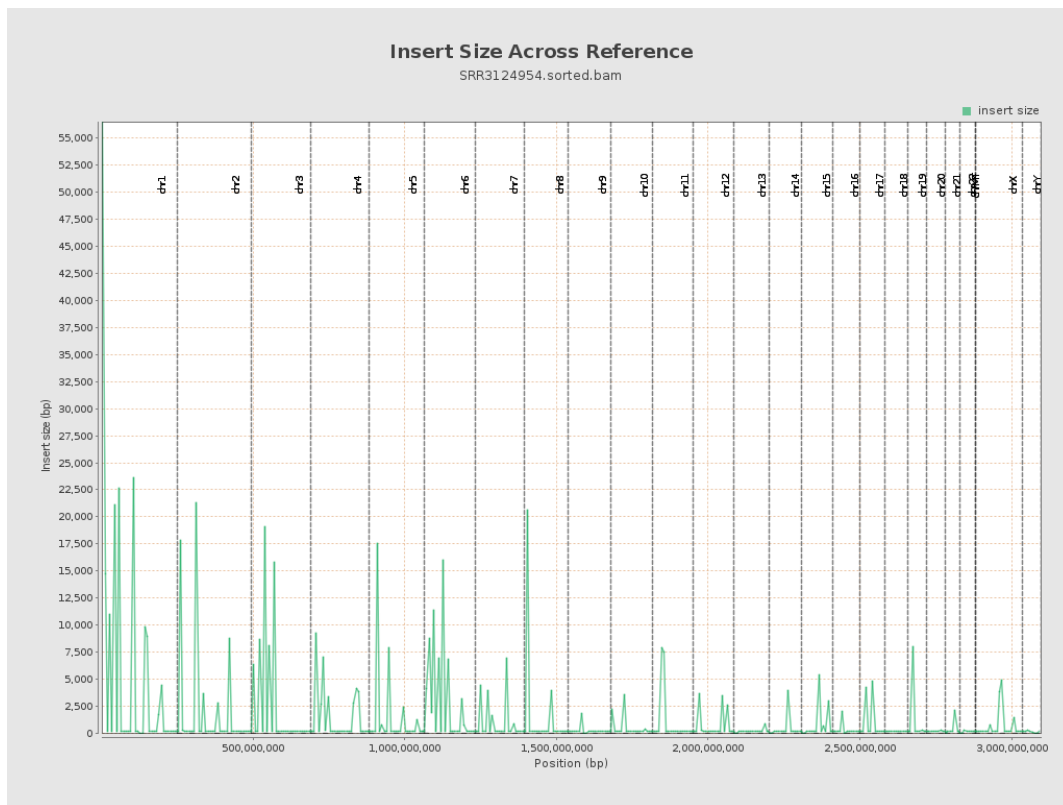
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

