

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 02:07:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174054.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_SRR10174054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174054_1.fastq.gz SRR10174054_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 02:07:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,160,804
Mapped reads	5,047,330 / 97.8%
Unmapped reads	113,474 / 2.2%
Mapped paired reads	5,047,330 / 97.8%
Mapped reads, first in pair	2,518,242 / 48.8%
Mapped reads, second in pair	2,529,088 / 49.01%
Mapped reads, both in pair	4,970,242 / 96.31%
Mapped reads, singletons	77,088 / 1.49%
Secondary alignments	0
Supplementary alignments	558,200 / 10.82%
Read min/max/mean length	30 / 133 / 128.85
Duplicated reads (estimated)	4,033,729 / 78.16%
Duplication rate	66.13%
Clipped reads	2,025,207 / 39.24%

2.2. ACGT Content

Number/percentage of A's	181,829,016 / 30.25%
Number/percentage of C's	116,529,065 / 19.38%
Number/percentage of T's	182,050,415 / 30.28%
Number/percentage of G's	120,733,758 / 20.08%
Number/percentage of N's	7,571 / 0%

GC Percentage	39.47%
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2.3. Coverage

Mean	0.1943
Standard Deviation	2.8486

2.4. Mapping Quality

Mean Mapping Quality	52.67
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2.5. Insert size

Mean	1,119,215.08
Standard Deviation	9,859,992.79
P25/Median/P75	148 / 206 / 298

2.6. Mismatches and indels

General error rate	1%
Mismatches	5,882,456
Insertions	62,321
Mapped reads with at least one insertion	1.19%
Deletions	109,438
Mapped reads with at least one deletion	2.11%
Homopolymer indels	44.5%

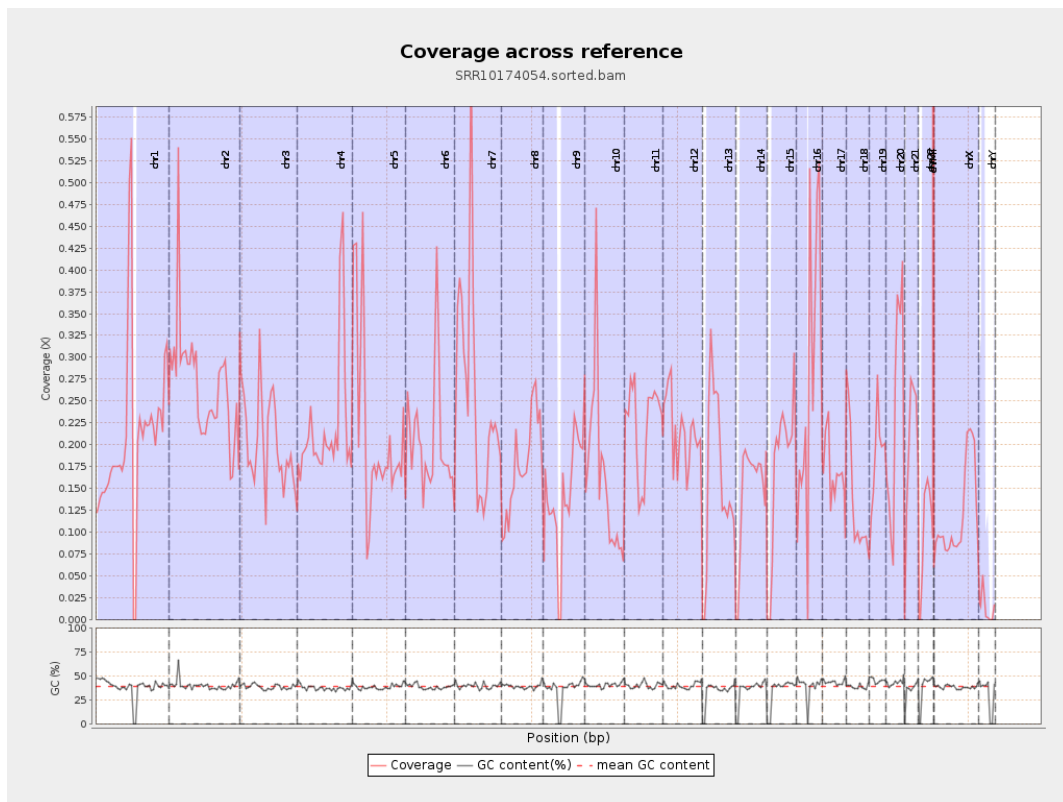
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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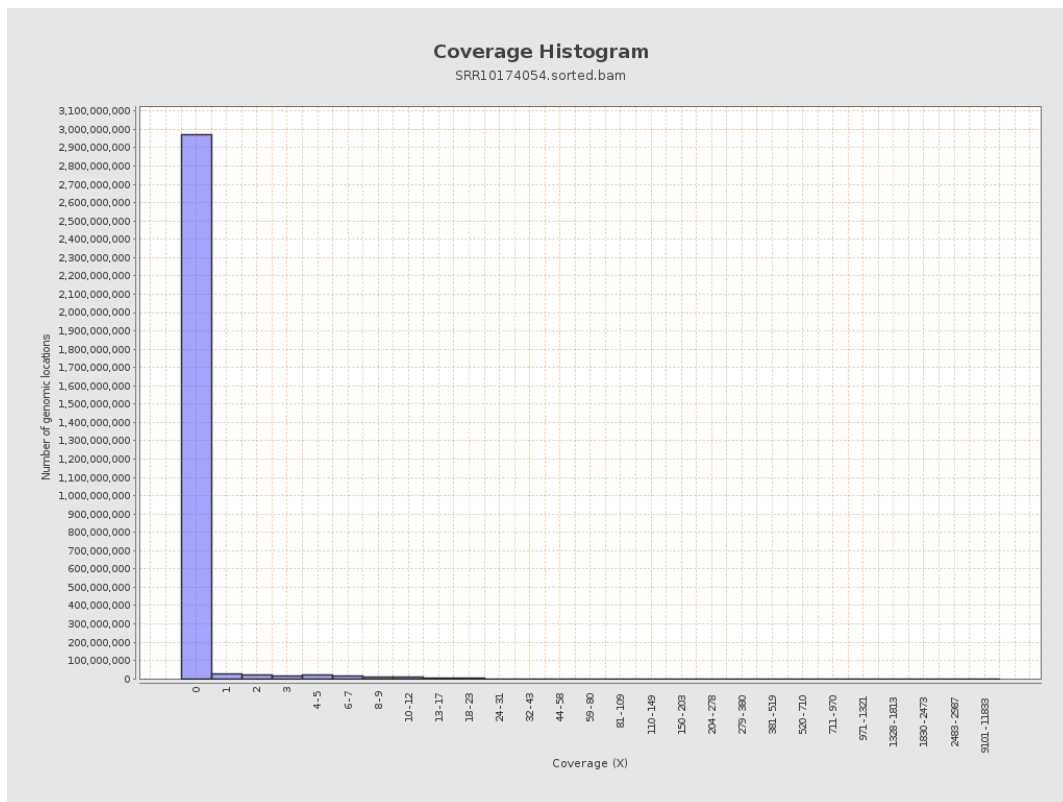
		bases	coverage	deviation
chr1	249250621	51686366	0.2074	2.064
chr2	243199373	64899385	0.2669	8.3703
chr3	198022430	40458151	0.2043	1.3306
chr4	191154276	41306504	0.2161	1.5477
chr5	180915260	38655370	0.2137	1.3534
chr6	171115067	35211097	0.2058	1.3995
chr7	159138663	40729623	0.2559	2.6588
chr8	146364022	26077855	0.1782	1.6078
chr9	141213431	20201508	0.1431	1.4234
chr10	135534747	22128749	0.1633	2.6532
chr11	135006516	30235012	0.224	1.4112
chr12	133851895	28397019	0.2122	1.3567
chr13	115169878	18283839	0.1588	1.1749
chr14	107349540	15580243	0.1451	1.116
chr15	102531392	17868232	0.1743	1.207
chr16	90354753	24780354	0.2743	2.2117
chr17	81195210	13402008	0.1651	1.4069
chr18	78077248	10578977	0.1355	1.8317
chr19	59128983	11023034	0.1864	2.3968
chr20	63025520	14747235	0.234	1.4116
chr21	48129895	9513578	0.1977	1.3406
chr22	51304566	5073100	0.0989	0.8675
chrMT	16571	1341548	80.9576	76.5053
chrX	155270560	18494366	0.1191	1.0136

chrY	59373566	769773	0.013	0.5197
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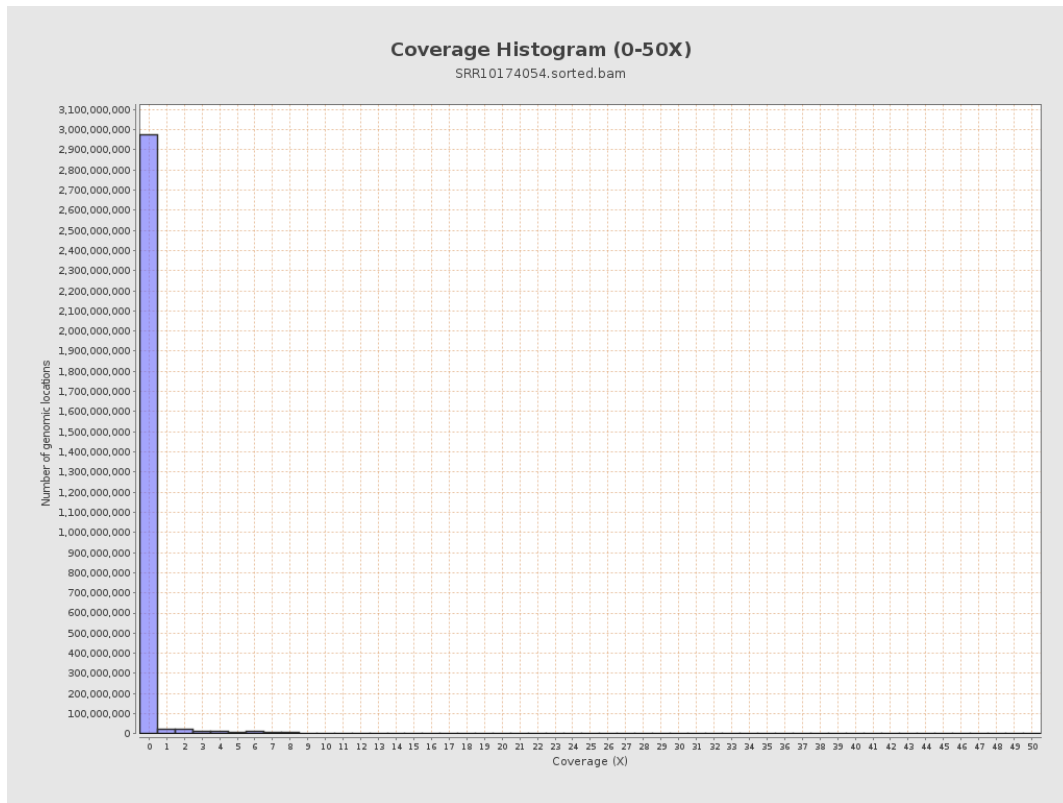
3. Results : Coverage across reference



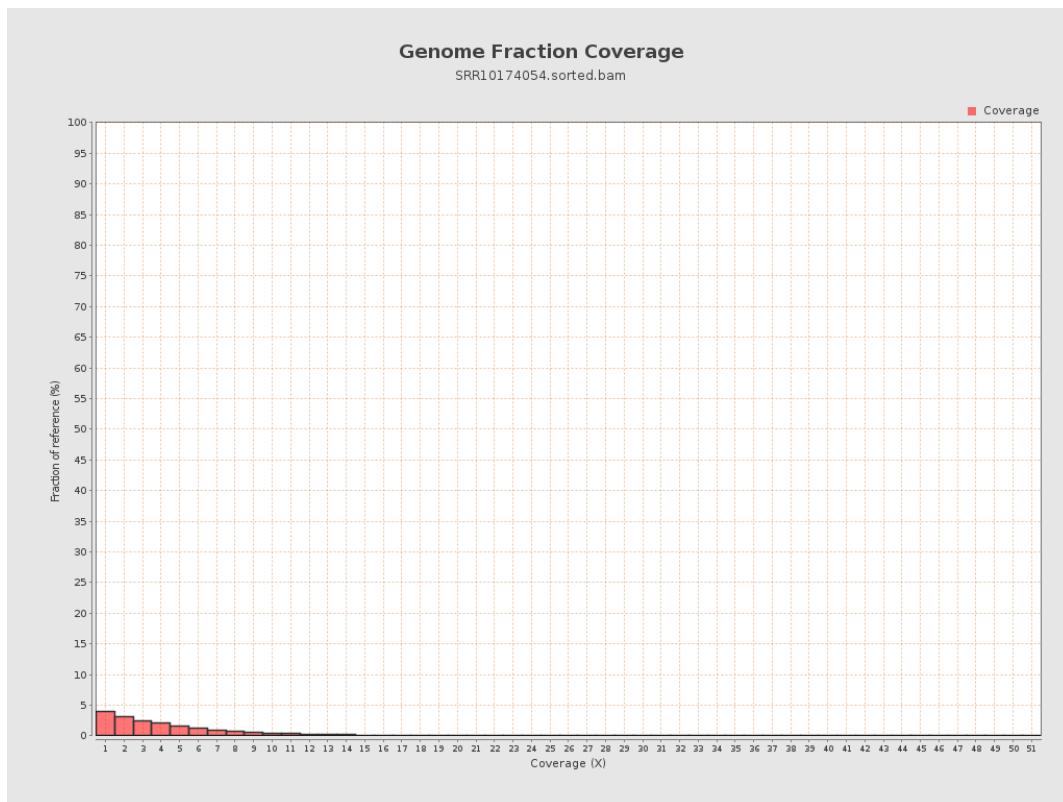
4. Results : Coverage Histogram



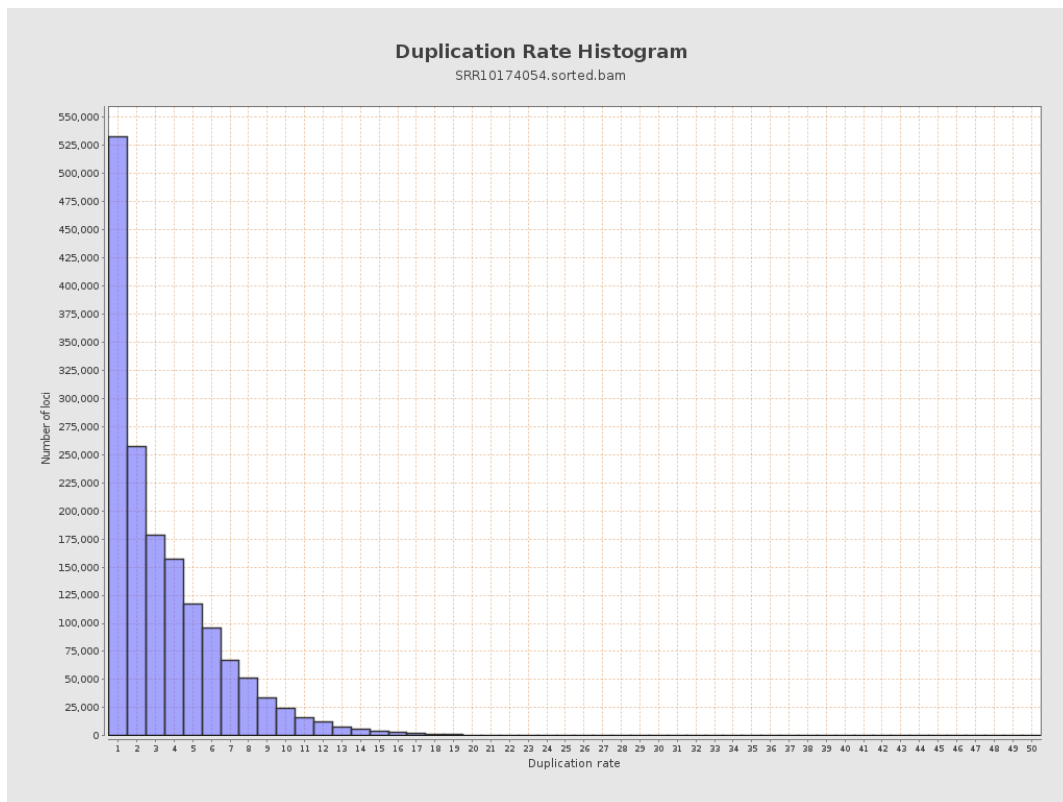
5. Results : Coverage Histogram (0-50X)



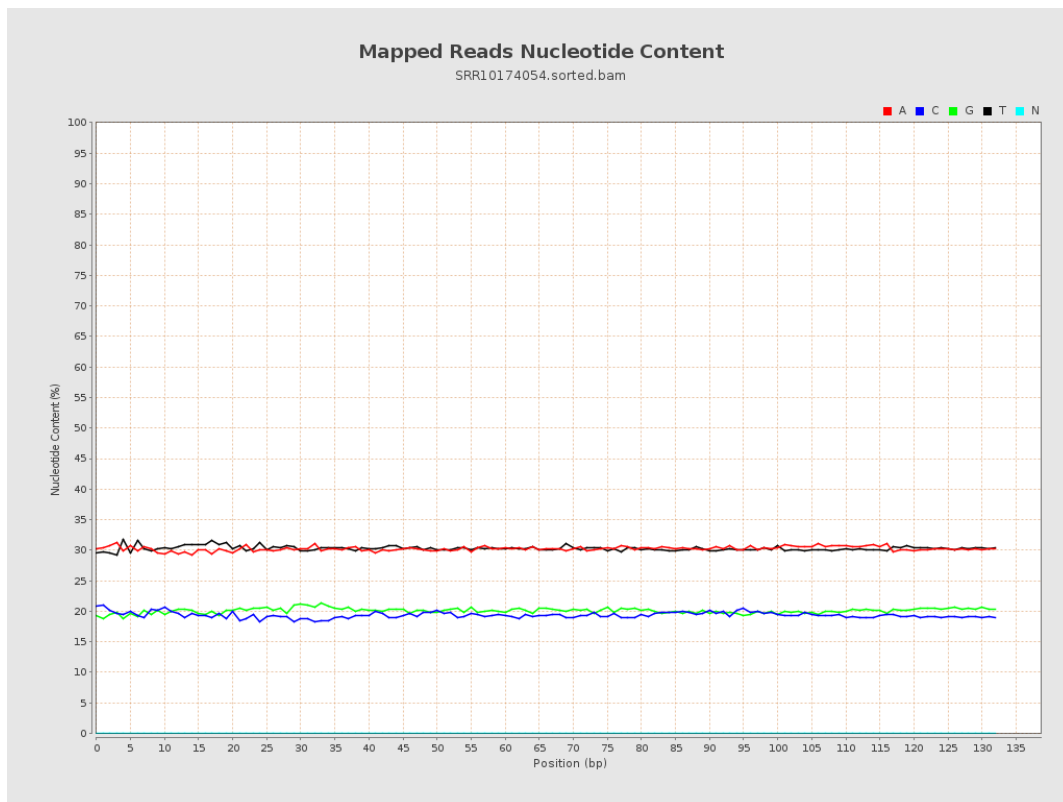
6. Results : Genome Fraction Coverage



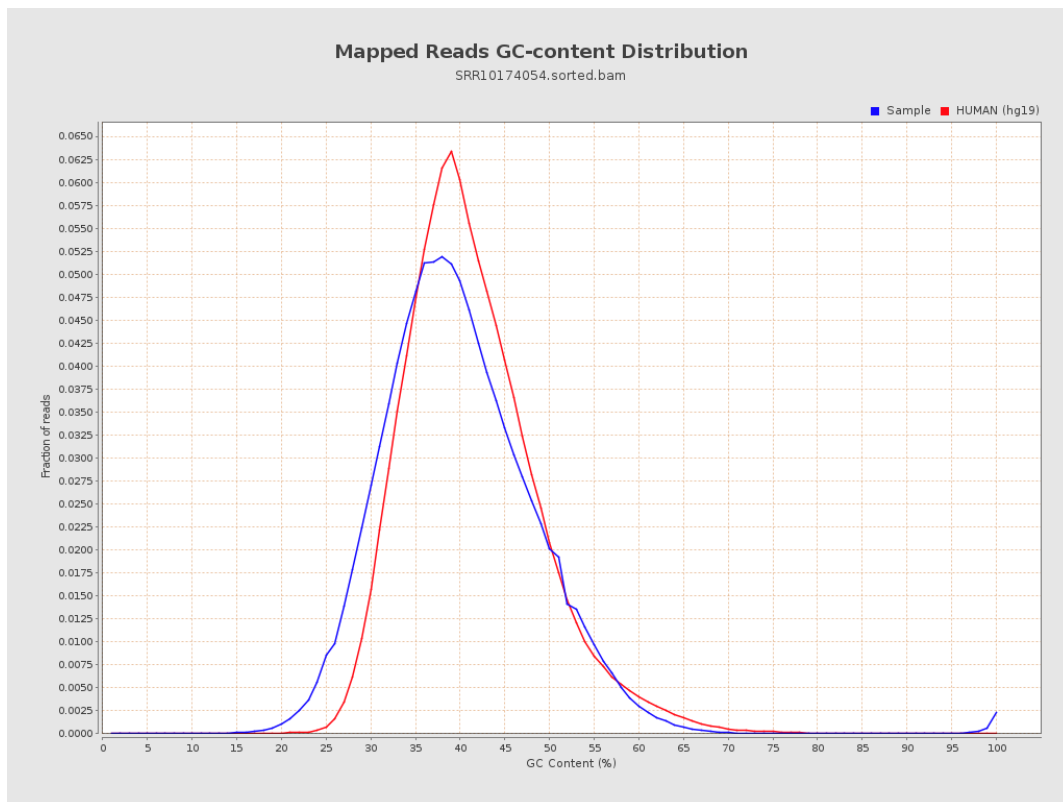
7. Results : Duplication Rate Histogram



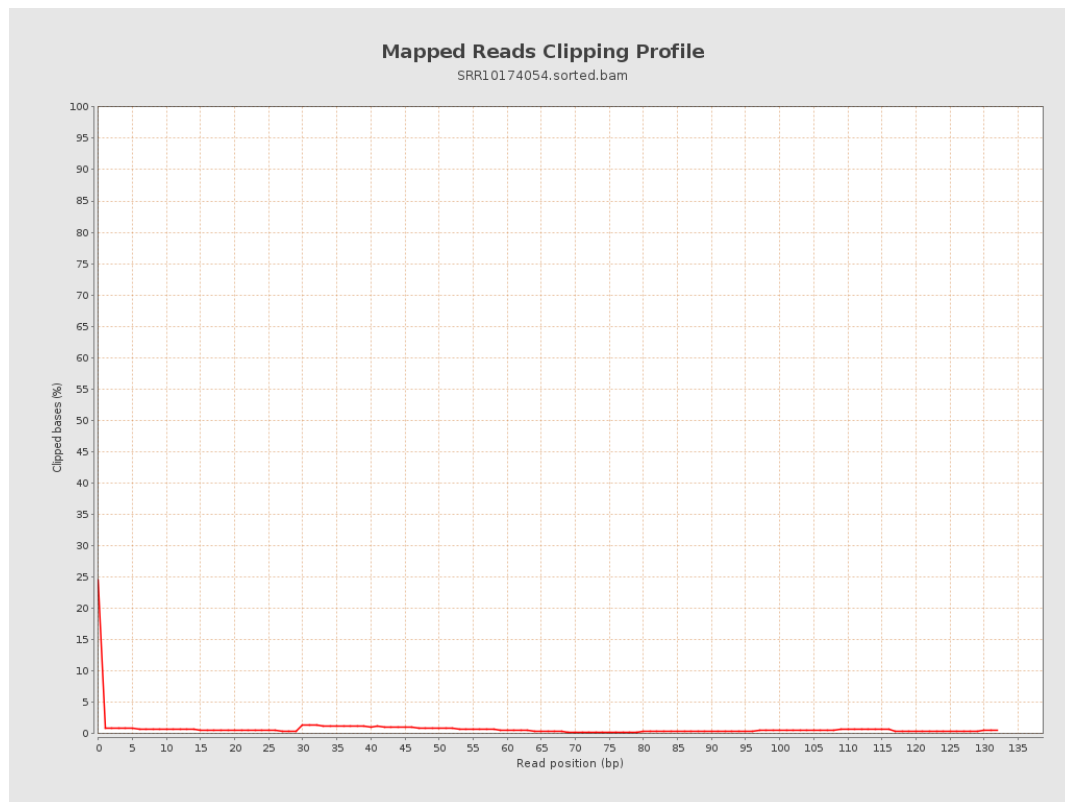
8. Results : Mapped Reads Nucleotide Content



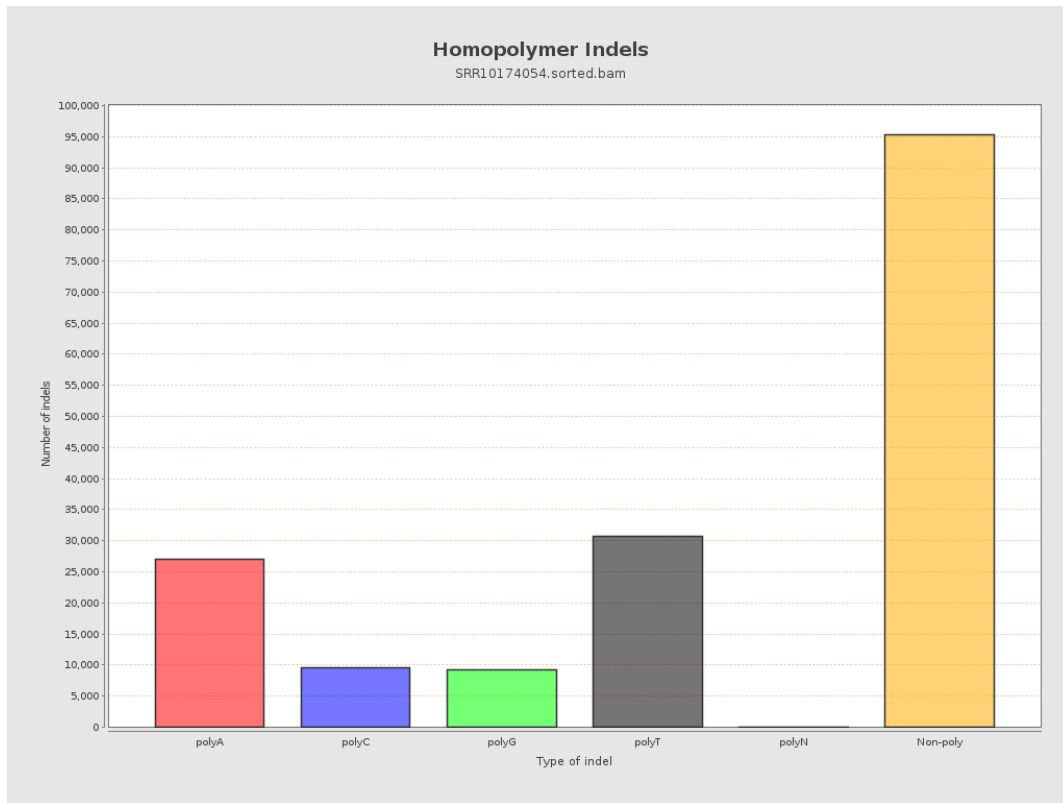
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



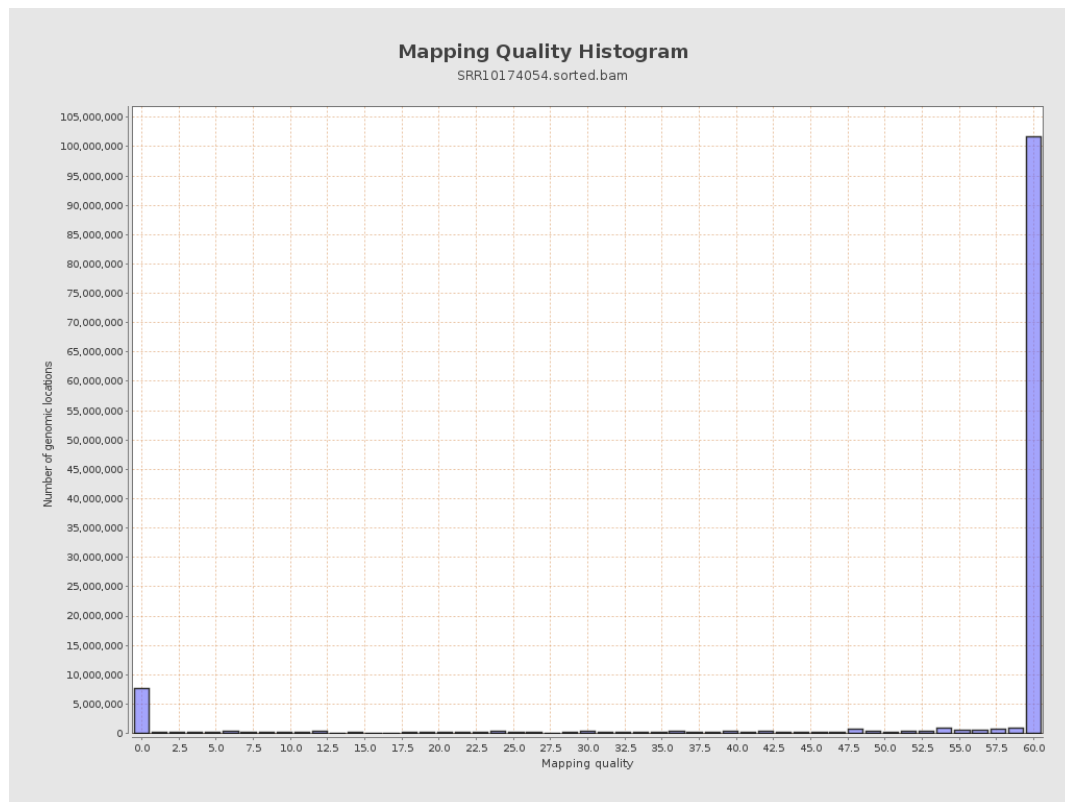
11. Results : Homopolymer Indels



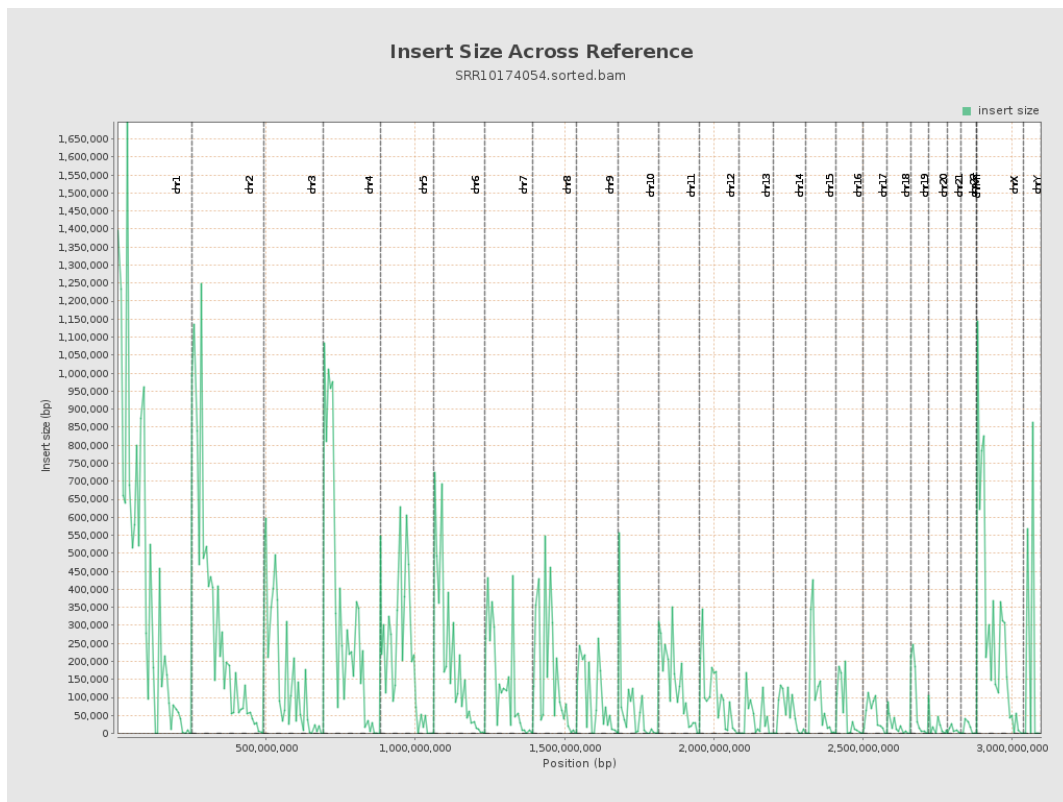
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

