

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 19:13:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038458.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_SRR5038458 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038458_1.fastq.gz SRR5038458_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 19:13:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038458.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	77,682,592
Mapped reads	77,426,964 / 99.67%
Unmapped reads	255,628 / 0.33%
Mapped paired reads	77,426,964 / 99.67%
Mapped reads, first in pair	38,788,135 / 49.93%
Mapped reads, second in pair	38,638,829 / 49.74%
Mapped reads, both in pair	77,252,768 / 99.45%
Mapped reads, singletons	174,196 / 0.22%
Secondary alignments	0
Supplementary alignments	118,884 / 0.15%
Read min/max/mean length	30 / 150 / 150.07
Duplicated reads (estimated)	31,112,818 / 40.05%
Duplication rate	37.99%
Clipped reads	3,108,098 / 4%

2.2. ACGT Content

Number/percentage of A's	2,893,702,646 / 25.07%
Number/percentage of C's	2,876,545,771 / 24.92%
Number/percentage of T's	2,921,946,701 / 25.32%
Number/percentage of G's	2,848,384,983 / 24.68%
Number/percentage of N's	1,064,391 / 0.01%

GC Percentage	49.6%
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2.3. Coverage

Mean	3.7289
Standard Deviation	23.2788

2.4. Mapping Quality

Mean Mapping Quality	55.83
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2.5. Insert size

Mean	17,421.78
Standard Deviation	1,428,244.06
P25/Median/P75	199 / 230 / 270

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	45,863,089
Insertions	537,866
Mapped reads with at least one insertion	0.66%
Deletions	634,016
Mapped reads with at least one deletion	0.8%
Homopolymer indels	46.73%

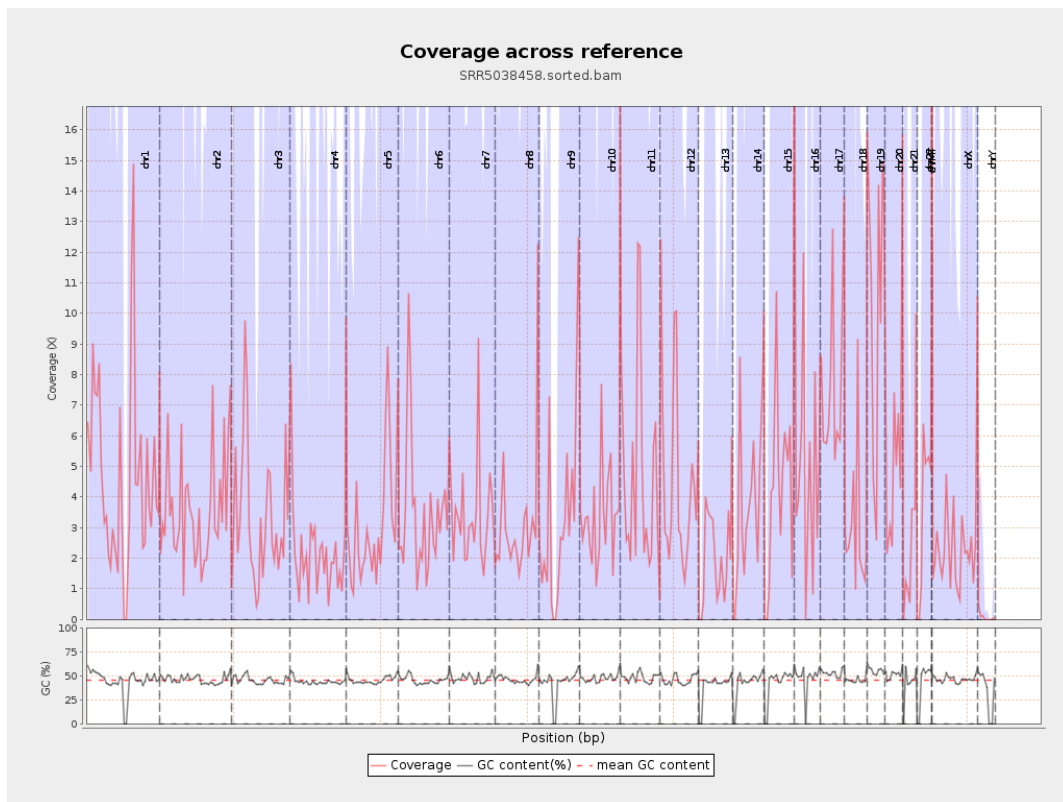
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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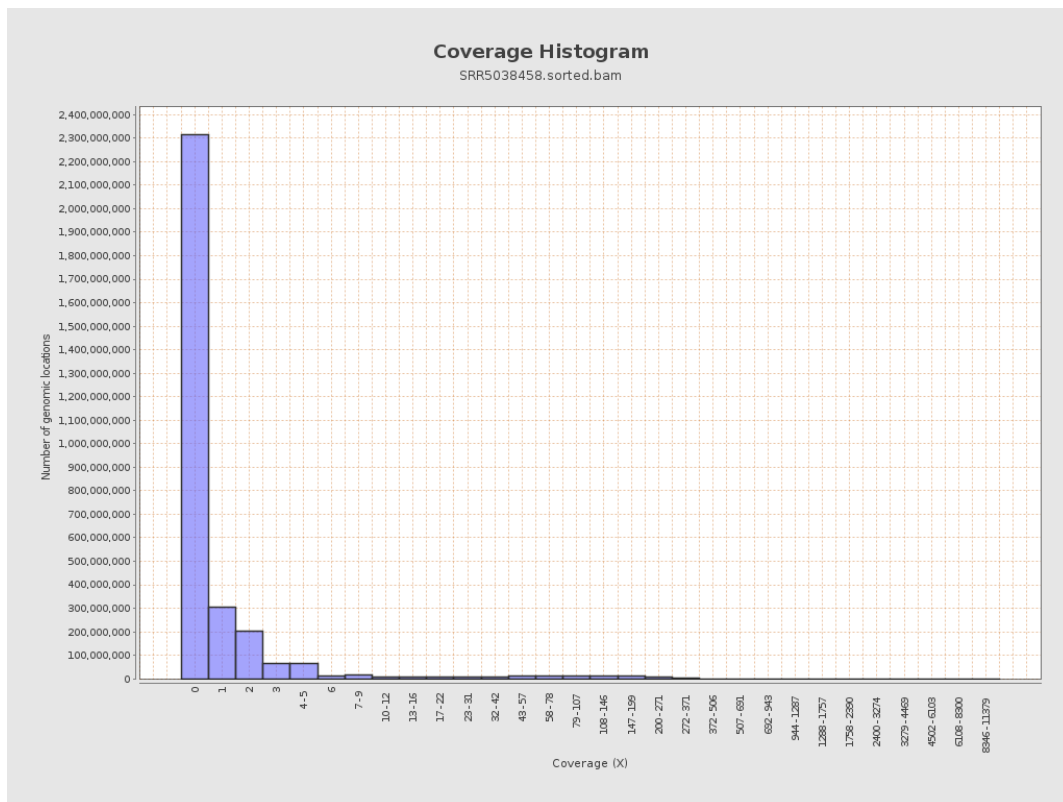
		bases	coverage	deviation
chr1	249250621	1174337623	4.7115	26.6508
chr2	243199373	873554480	3.5919	24.3239
chr3	198022430	667136839	3.369	21.5213
chr4	191154276	403921751	2.1131	15.6292
chr5	180915260	580282059	3.2075	22.0568
chr6	171115067	583359446	3.4092	21.5656
chr7	159138663	546114208	3.4317	20.9771
chr8	146364022	462484436	3.1598	21.9677
chr9	141213431	480974751	3.406	21.9442
chr10	135534747	453718903	3.3476	20.6211
chr11	135006516	680687074	5.0419	27.5294
chr12	133851895	607296424	4.5371	25.2063
chr13	115169878	227336527	1.9739	16.0502
chr14	107349540	398727146	3.7143	23.0515
chr15	102531392	412131435	4.0196	23.2302
chr16	90354753	495129837	5.4798	29.0301
chr17	81195210	629173711	7.7489	33.0343
chr18	78077248	231953561	2.9708	24.7717
chr19	59128983	621678296	10.5139	37.7169
chr20	63025520	328540276	5.2128	29.4434
chr21	48129895	126018004	2.6183	27.039
chr22	51304566	197015145	3.8401	20.0168
chrMT	16571	710629	42.8839	14.7587
chrX	155270560	356254149	2.2944	16.0741

chrY	59373566	4848573	0.0817	2.4057
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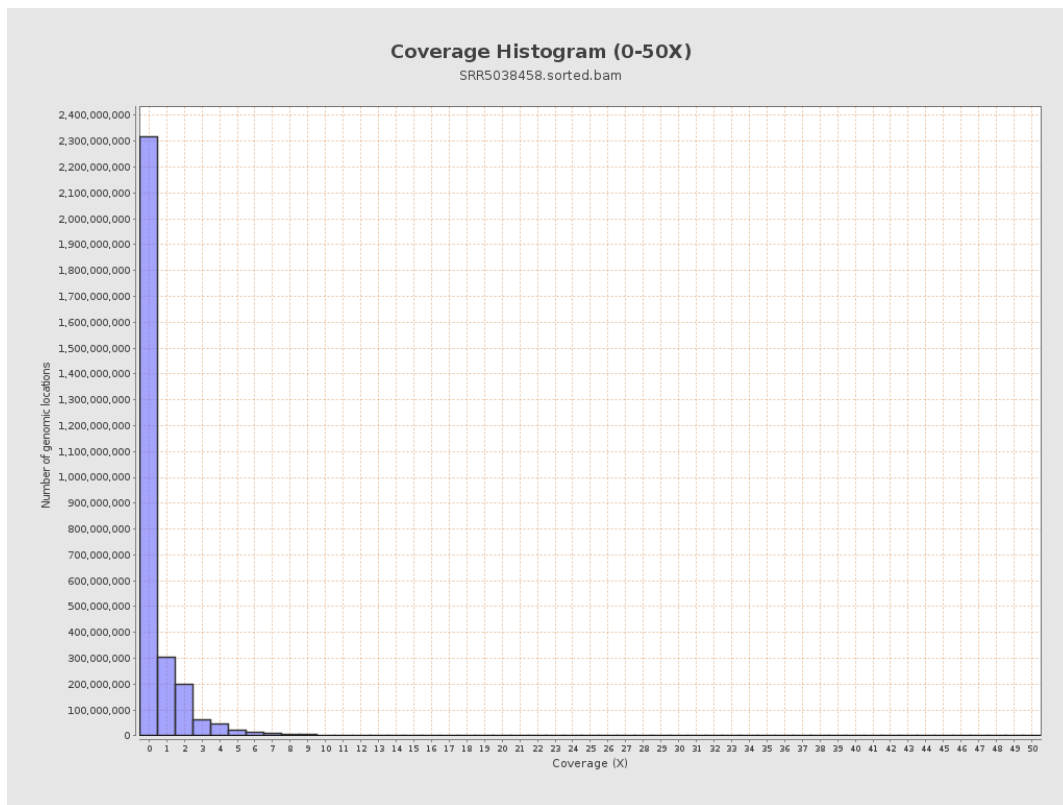
3. Results : Coverage across reference



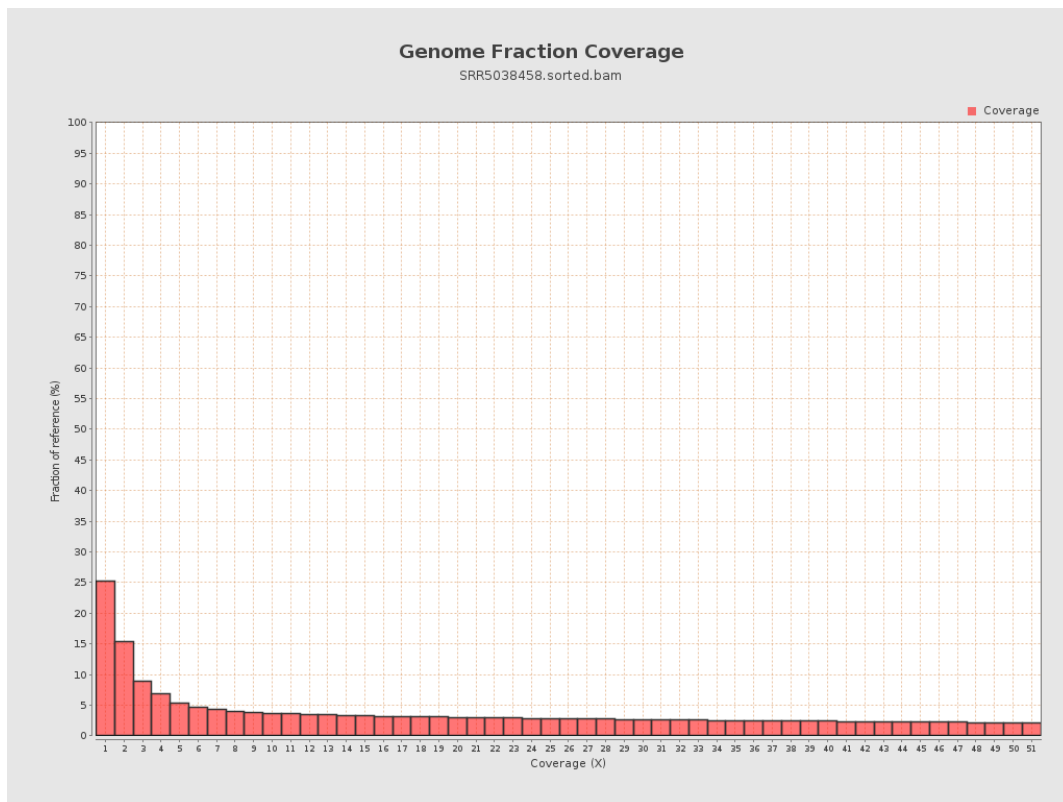
4. Results : Coverage Histogram



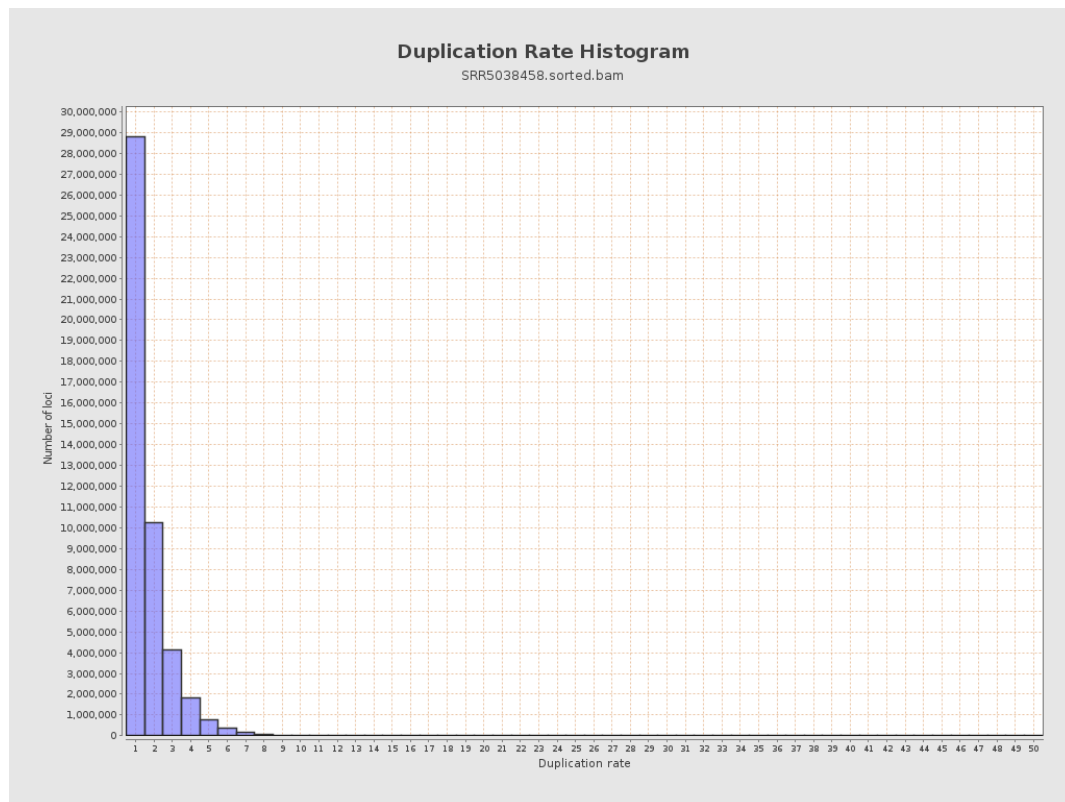
5. Results : Coverage Histogram (0-50X)



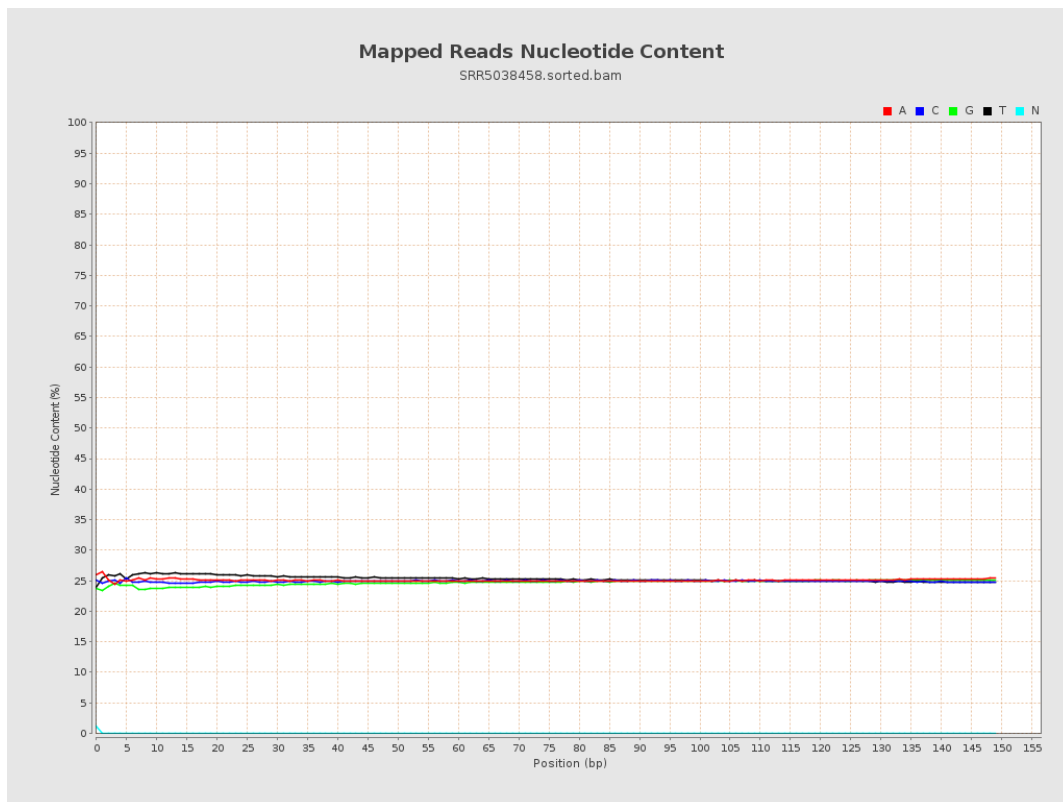
6. Results : Genome Fraction Coverage



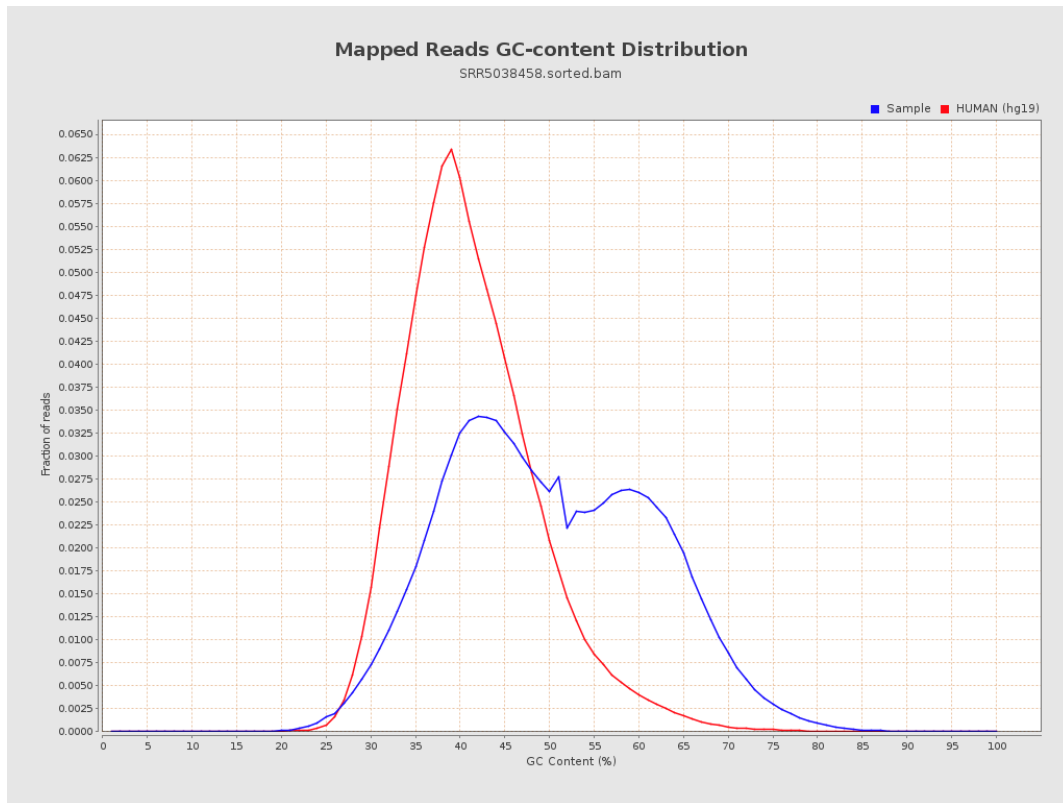
7. Results : Duplication Rate Histogram



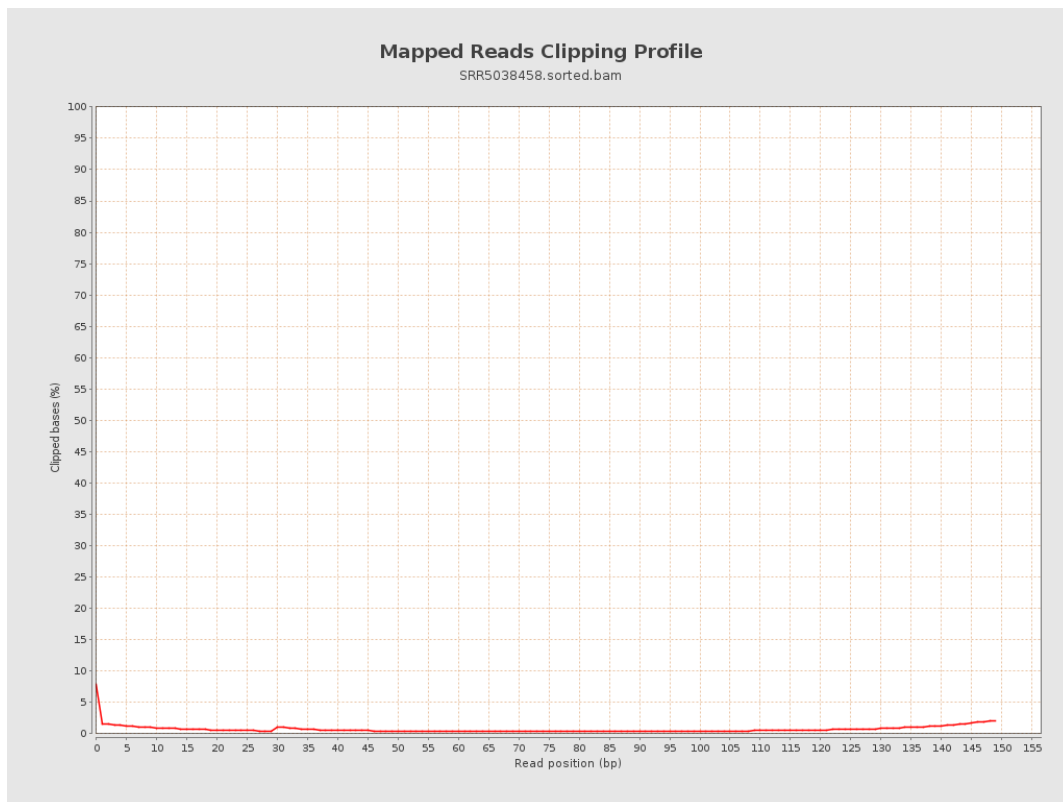
8. Results : Mapped Reads Nucleotide Content



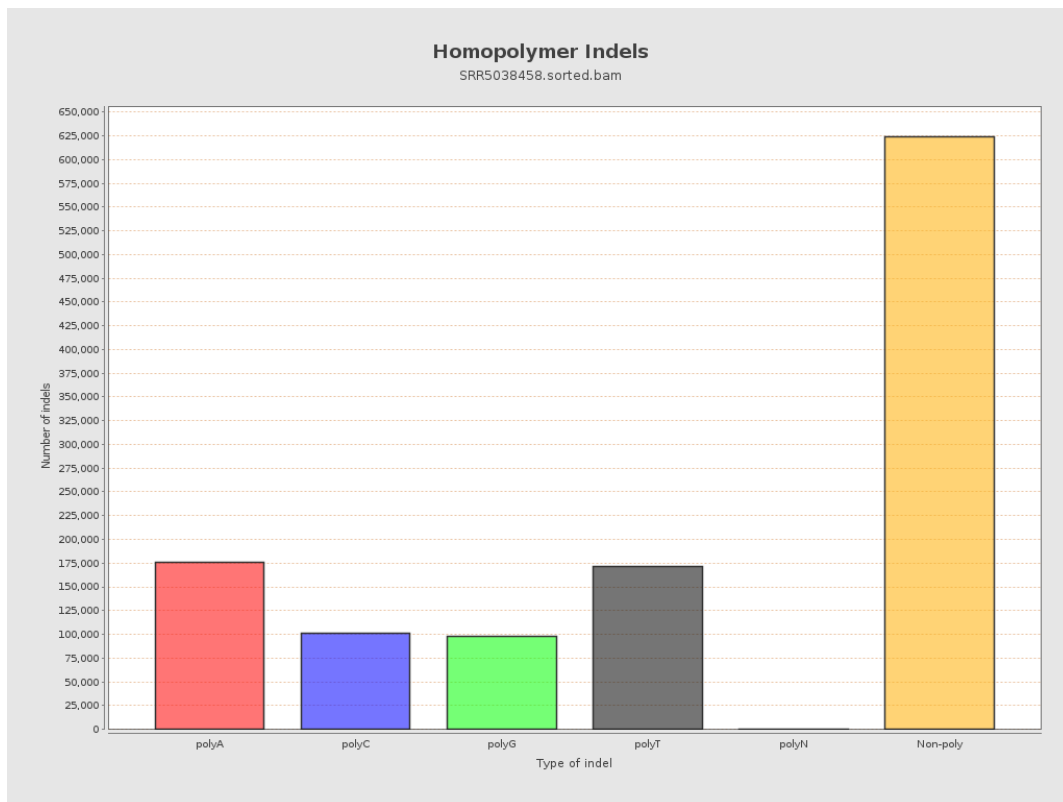
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



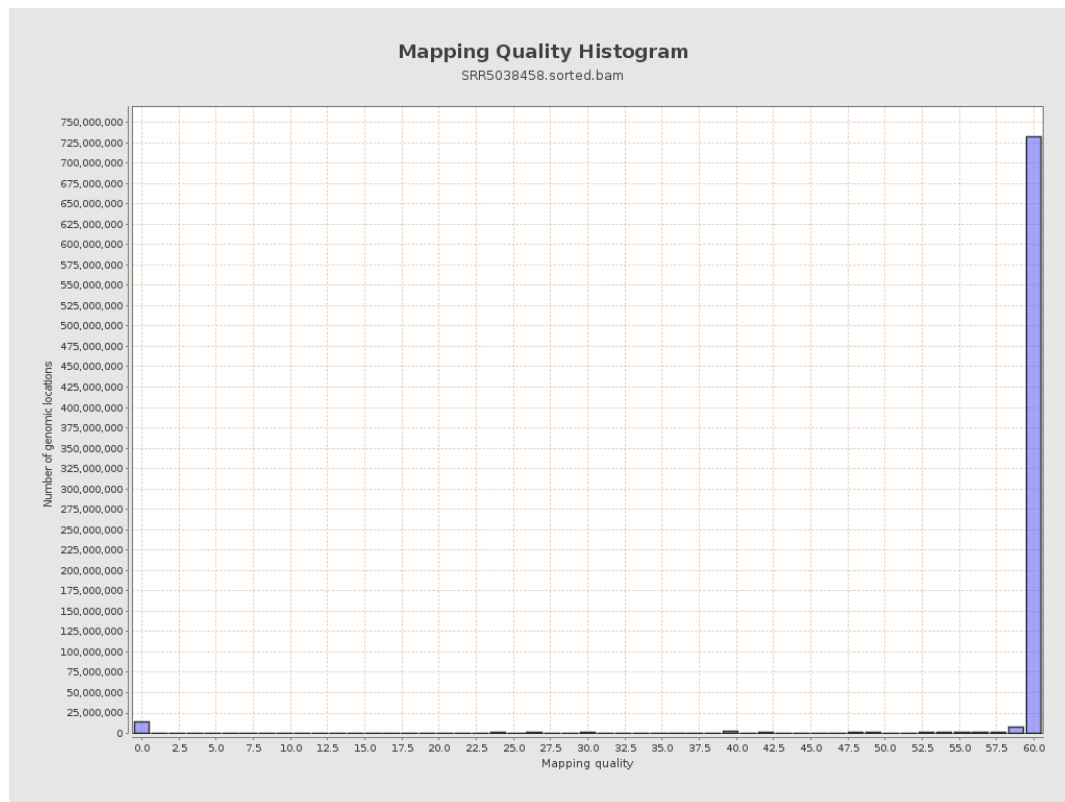
11. Results : Homopolymer Indels



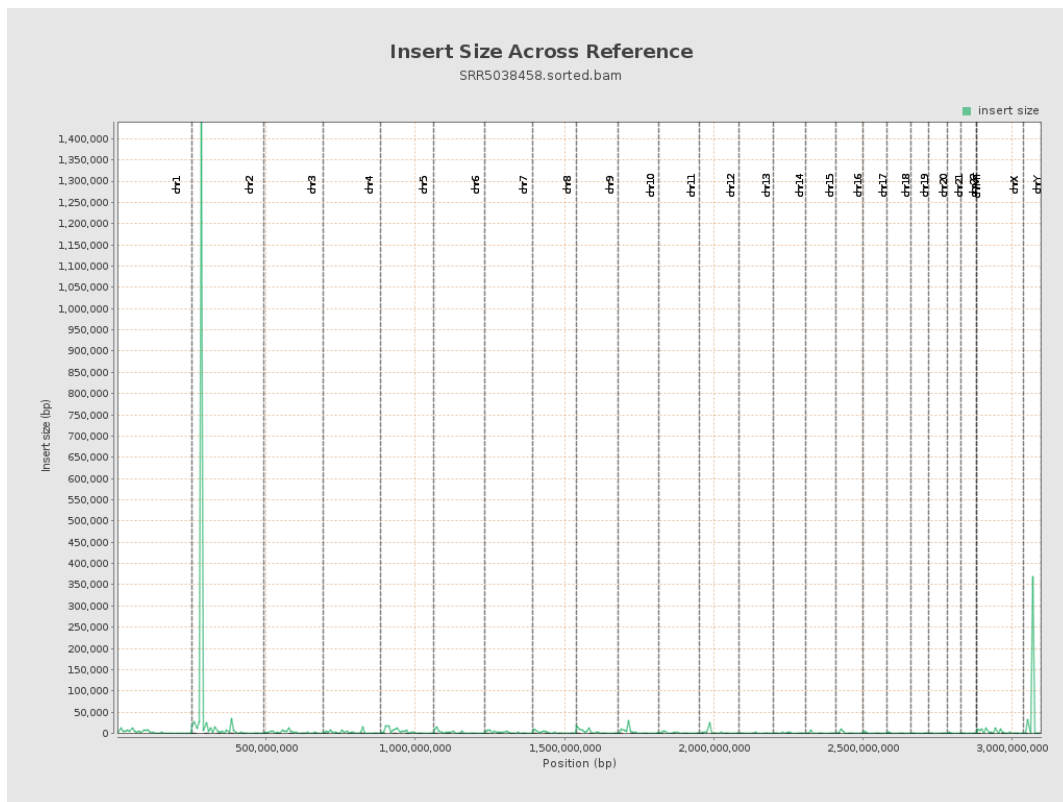
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

