

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 17:43:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038455.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_SRR5038455 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038455_1.fastq.gz SRR5038455_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 17:43:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038455.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,820,854
Mapped reads	17,818,694 / 94.68%
Unmapped reads	1,002,160 / 5.32%
Mapped paired reads	17,818,694 / 94.68%
Mapped reads, first in pair	9,020,746 / 47.93%
Mapped reads, second in pair	8,797,948 / 46.75%
Mapped reads, both in pair	17,517,442 / 93.07%
Mapped reads, singletons	301,252 / 1.6%
Secondary alignments	0
Supplementary alignments	371,931 / 1.98%
Read min/max/mean length	30 / 150 / 150.97
Duplicated reads (estimated)	4,680,050 / 24.87%
Duplication rate	18.4%
Clipped reads	9,722,679 / 51.66%

2.2. ACGT Content

Number/percentage of A's	663,606,974 / 28.25%
Number/percentage of C's	474,454,061 / 20.2%
Number/percentage of T's	674,809,464 / 28.73%
Number/percentage of G's	536,123,512 / 22.82%
Number/percentage of N's	182,179 / 0.01%

GC Percentage	43.02%
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2.3. Coverage

Mean	0.7595
Standard Deviation	11.8062

2.4. Mapping Quality

Mean Mapping Quality	53.16
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2.5. Insert size

Mean	93,384.29
Standard Deviation	2,905,806.57
P25/Median/P75	174 / 222 / 281

2.6. Mismatches and indels

General error rate	1.44%
Mismatches	32,278,729
Insertions	502,467
Mapped reads with at least one insertion	2.63%
Deletions	910,569
Mapped reads with at least one deletion	4.88%
Homopolymer indels	45.65%

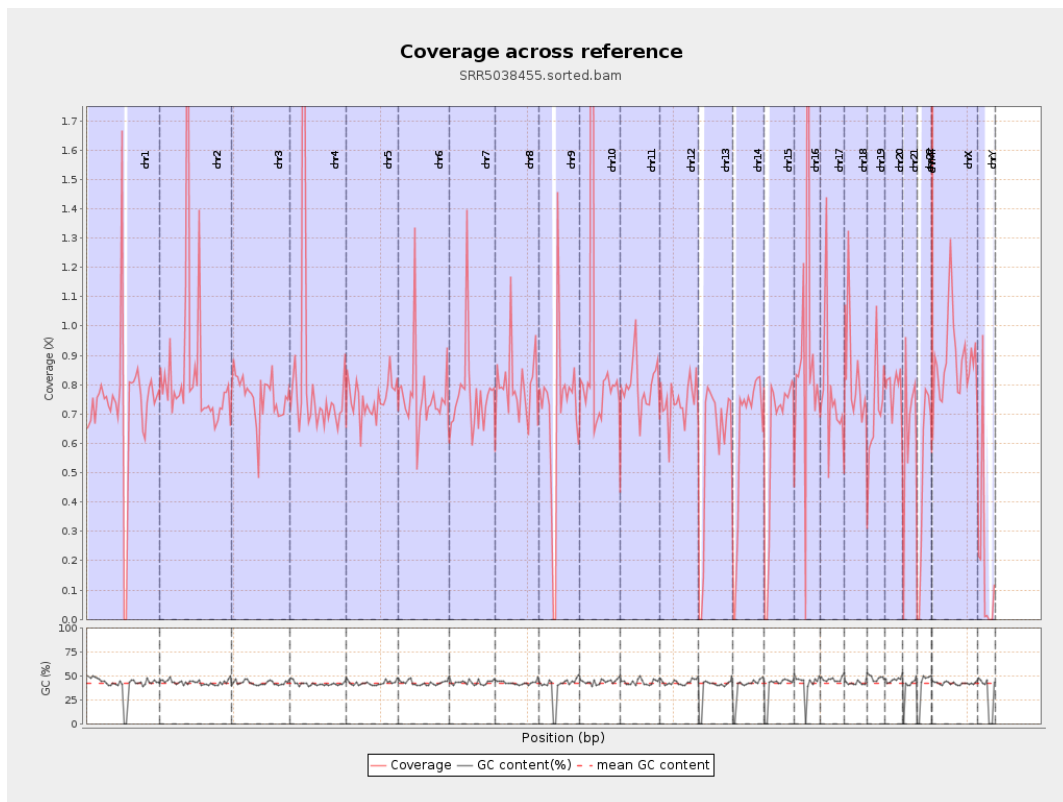
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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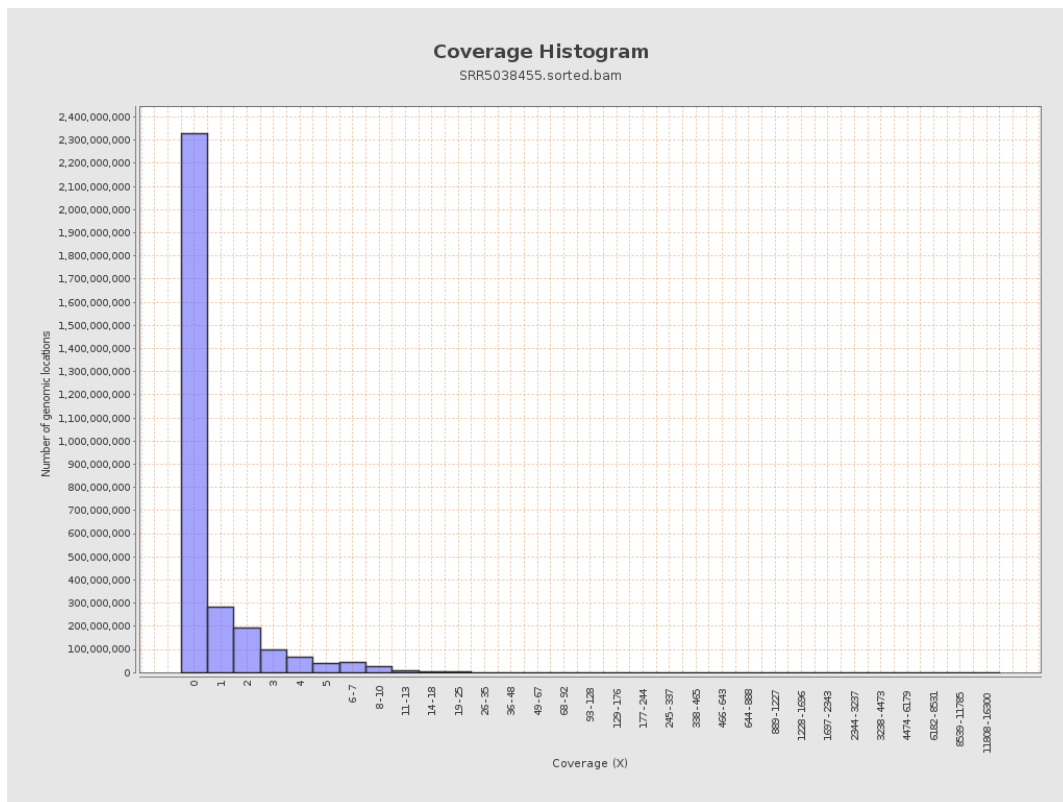
		bases	coverage	deviation
chr1	249250621	182451222	0.732	16.2261
chr2	243199373	206297688	0.8483	12.9123
chr3	198022430	150457164	0.7598	2.0275
chr4	191154276	156546395	0.819	13.4723
chr5	180915260	136464674	0.7543	1.9421
chr6	171115067	130730341	0.764	6.8488
chr7	159138663	122005093	0.7667	10.356
chr8	146364022	116818781	0.7981	3.6694
chr9	141213431	97301920	0.689	15.8778
chr10	135534747	136696510	1.0086	32.9896
chr11	135006516	106864650	0.7916	6.5352
chr12	133851895	99356400	0.7423	2.0085
chr13	115169878	68150527	0.5917	1.6263
chr14	107349540	67517482	0.6289	1.9855
chr15	102531392	62690990	0.6114	1.6637
chr16	90354753	85452667	0.9457	15.4637
chr17	81195210	61747832	0.7605	11.6937
chr18	78077248	65011445	0.8327	14.161
chr19	59128983	41699246	0.7052	7.646
chr20	63025520	49408170	0.7839	4.2254
chr21	48129895	32020476	0.6653	6.4734
chr22	51304566	25588897	0.4988	1.8271
chrMT	16571	1628588	98.2794	64.3657
chrX	155270560	136937132	0.8819	3.7104

chrY	59373566	11296708	0.1903	15.4101
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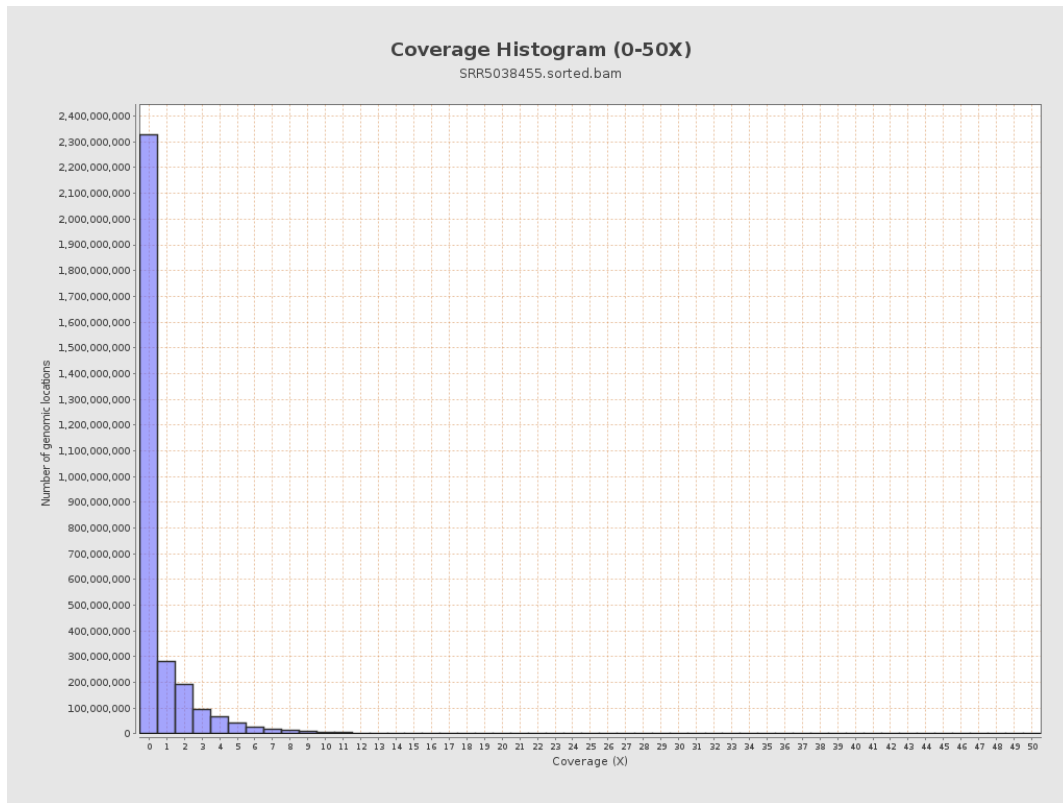
3. Results : Coverage across reference



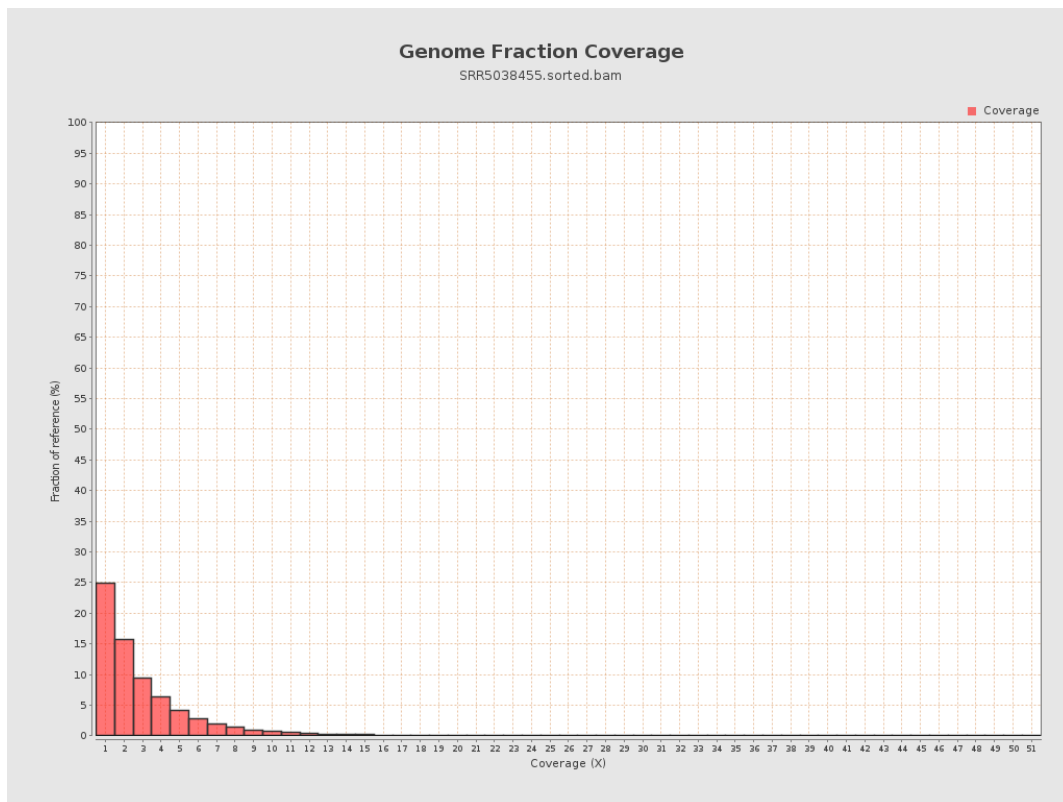
4. Results : Coverage Histogram



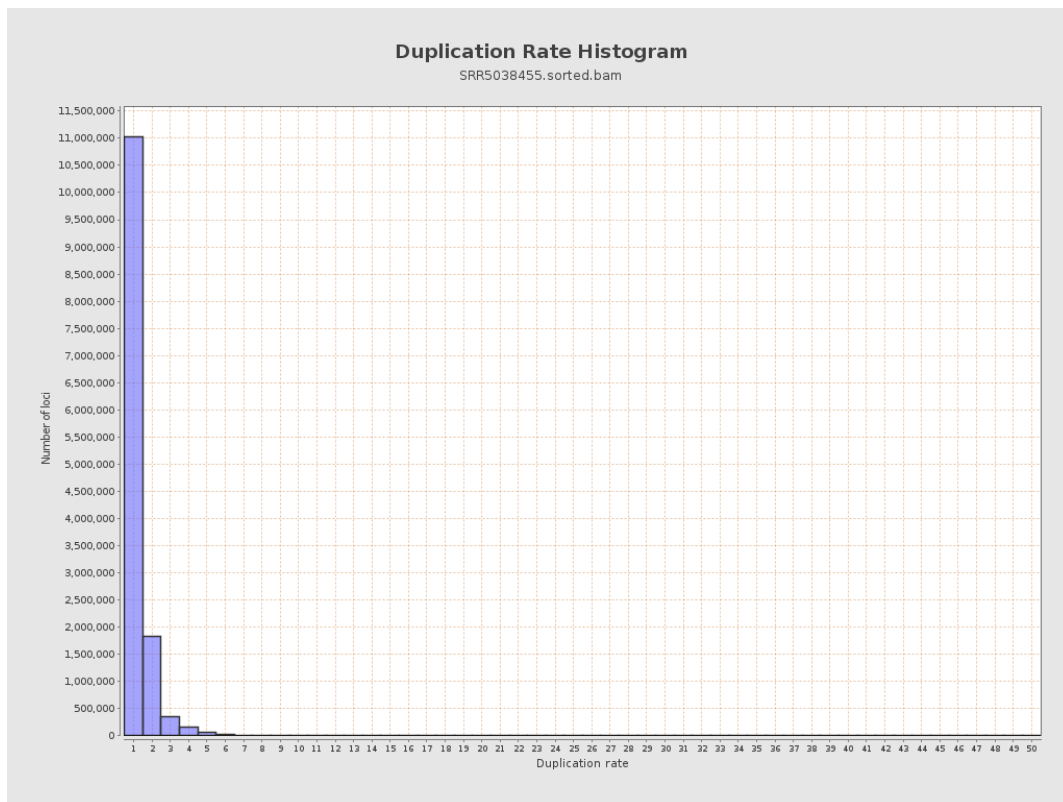
5. Results : Coverage Histogram (0-50X)



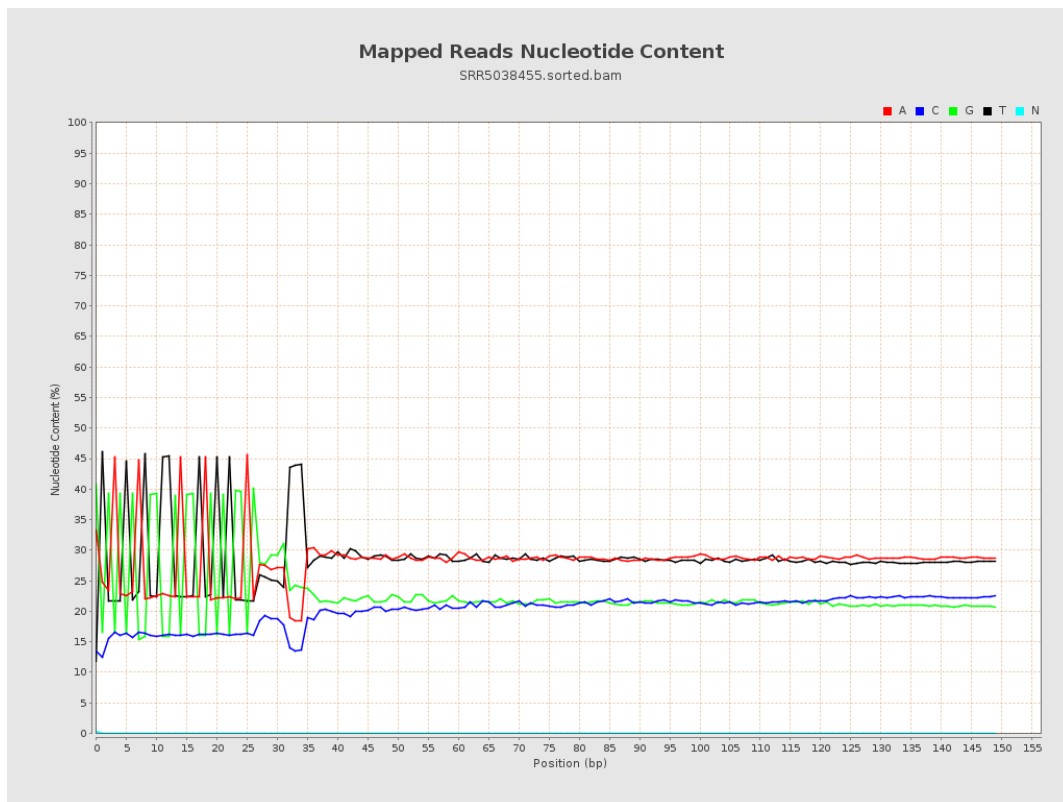
6. Results : Genome Fraction Coverage



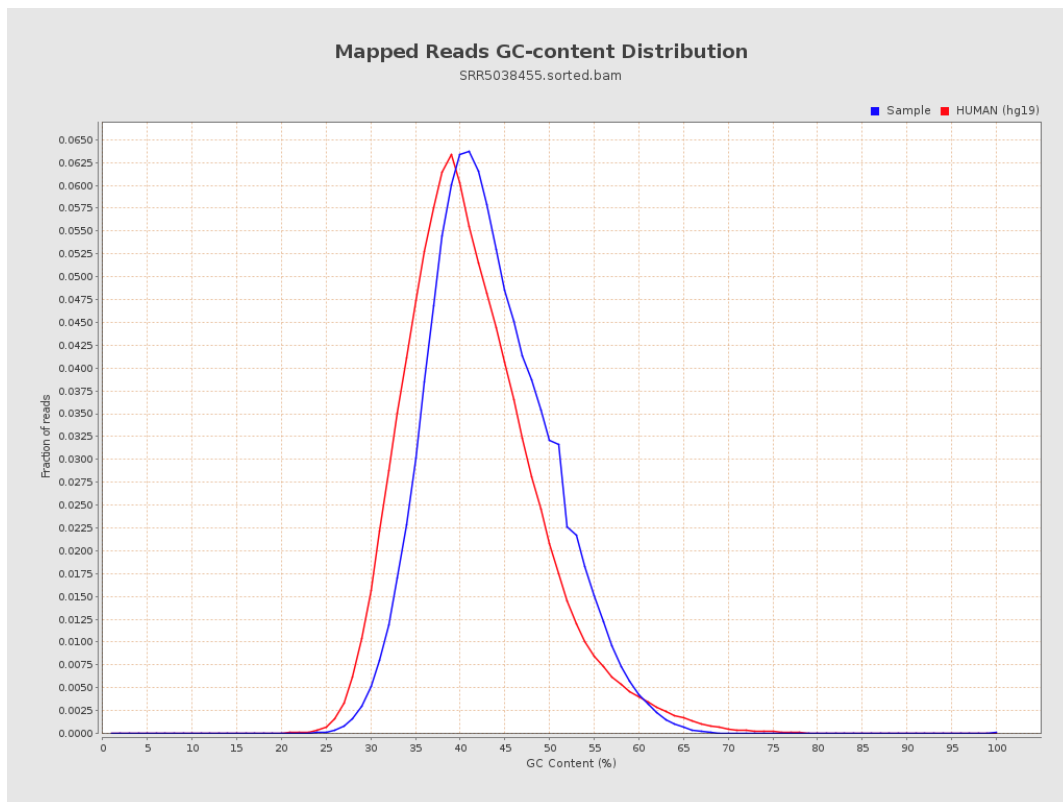
7. Results : Duplication Rate Histogram



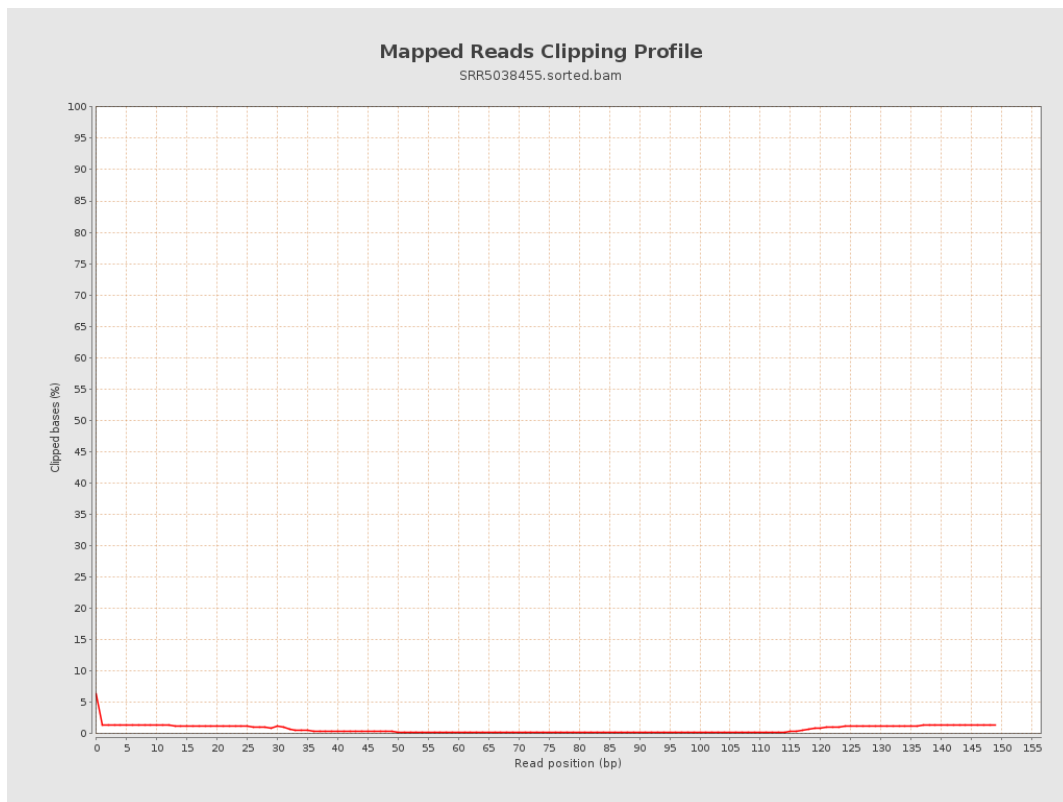
8. Results : Mapped Reads Nucleotide Content



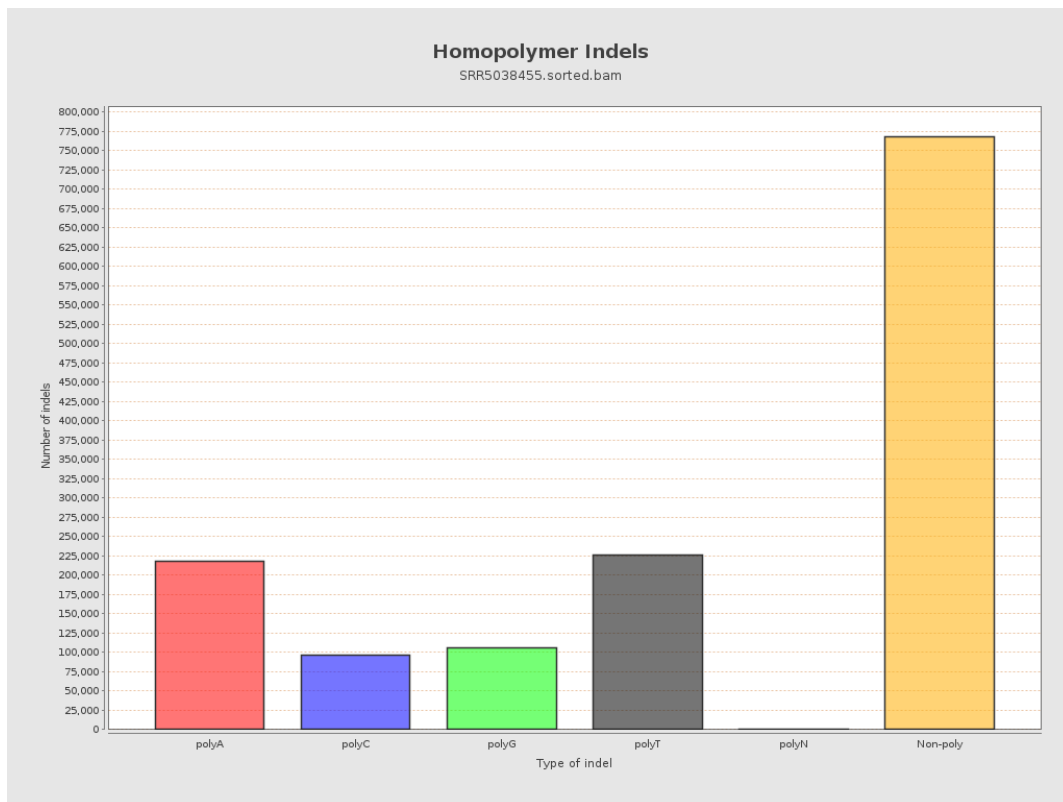
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



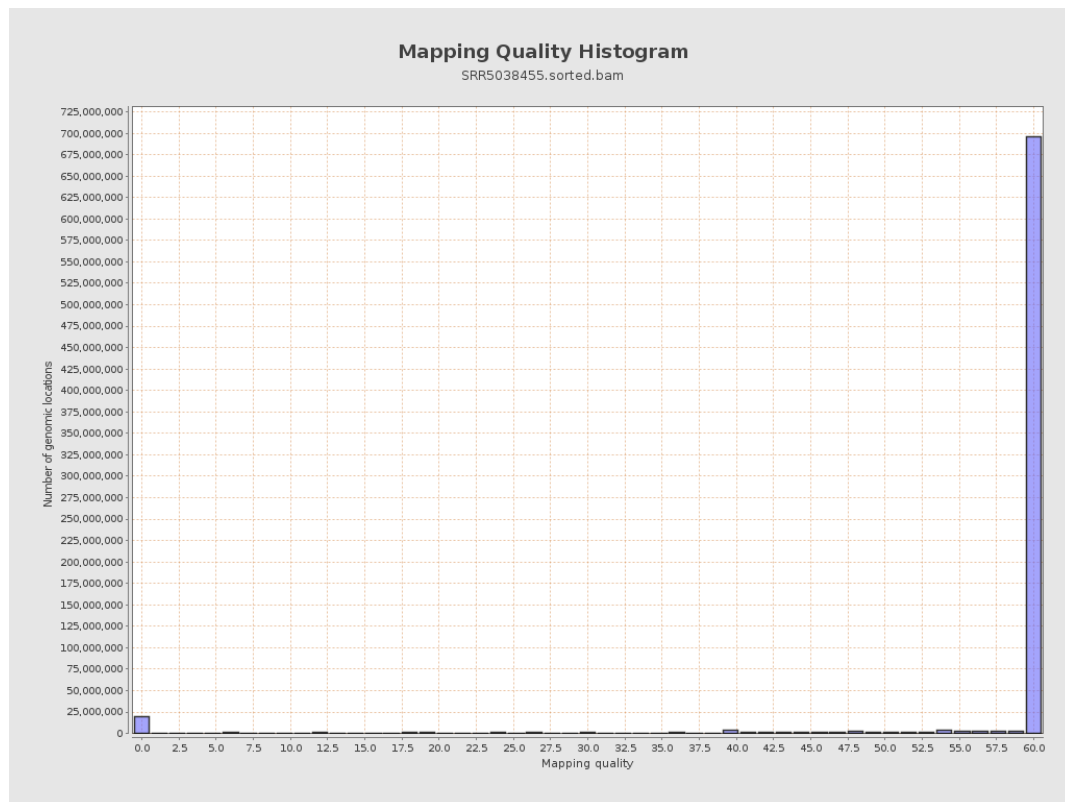
11. Results : Homopolymer Indels



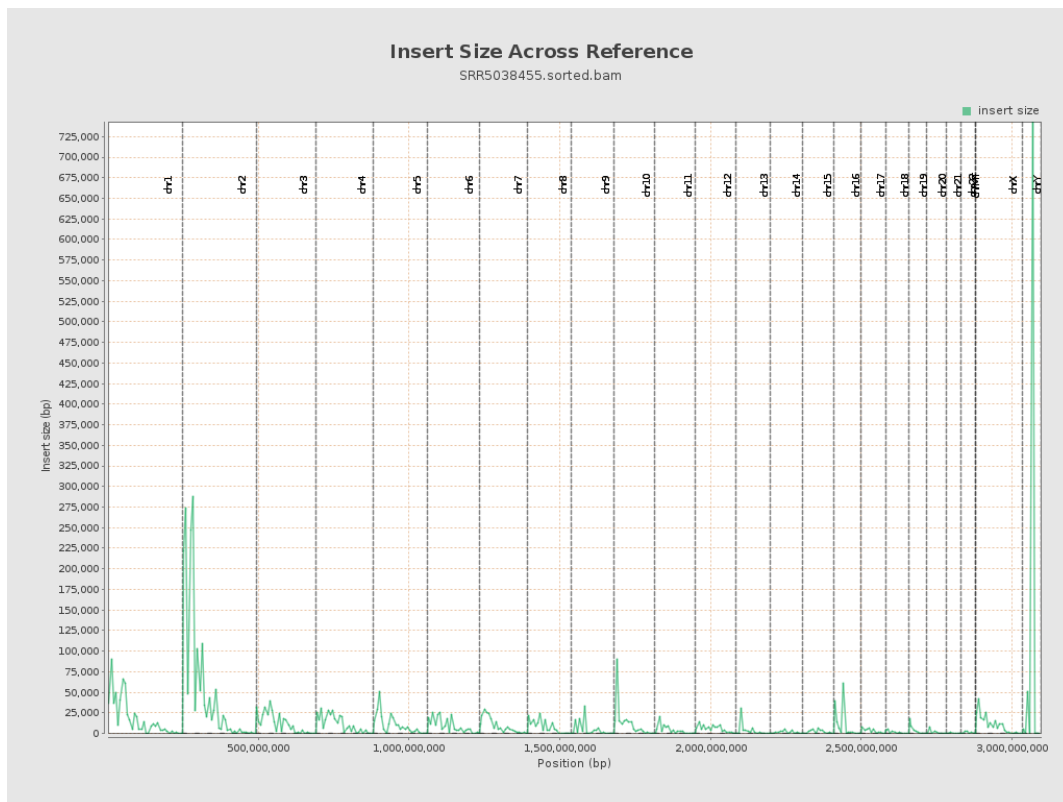
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

