

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 07:31:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354878.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_SRR22354878 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354878_1.fastq.gz SRR22354878_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 07:31:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354878.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,677,640
Mapped reads	20,582,377 / 99.54%
Unmapped reads	95,263 / 0.46%
Mapped paired reads	20,582,377 / 99.54%
Mapped reads, first in pair	10,295,848 / 49.79%
Mapped reads, second in pair	10,286,529 / 49.75%
Mapped reads, both in pair	20,541,954 / 99.34%
Mapped reads, singletons	40,423 / 0.2%
Secondary alignments	0
Supplementary alignments	113,448 / 0.55%
Read min/max/mean length	30 / 150 / 150.27
Duplicated reads (estimated)	5,222,636 / 25.26%
Duplication rate	23.34%
Clipped reads	1,046,397 / 5.06%

2.2. ACGT Content

Number/percentage of A's	873,312,478 / 28.6%
Number/percentage of C's	653,685,066 / 21.4%
Number/percentage of T's	868,516,284 / 28.44%
Number/percentage of G's	658,474,110 / 21.56%
Number/percentage of N's	40,836 / 0%

GC Percentage	42.96%
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2.3. Coverage

Mean	0.987
Standard Deviation	11.8008

2.4. Mapping Quality

Mean Mapping Quality	54.49
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2.5. Insert size

Mean	38,275.35
Standard Deviation	1,928,375.13
P25/Median/P75	260 / 303 / 351

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	17,408,598
Insertions	452,972
Mapped reads with at least one insertion	2.05%
Deletions	458,000
Mapped reads with at least one deletion	2.12%
Homopolymer indels	45.13%

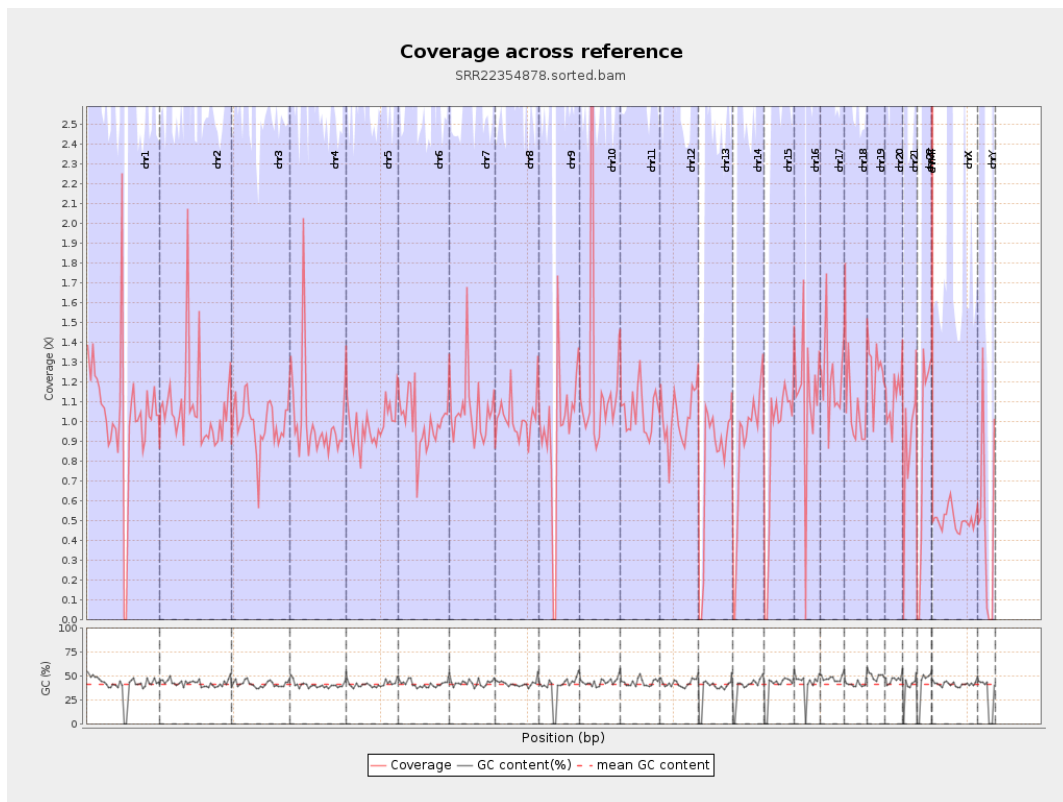
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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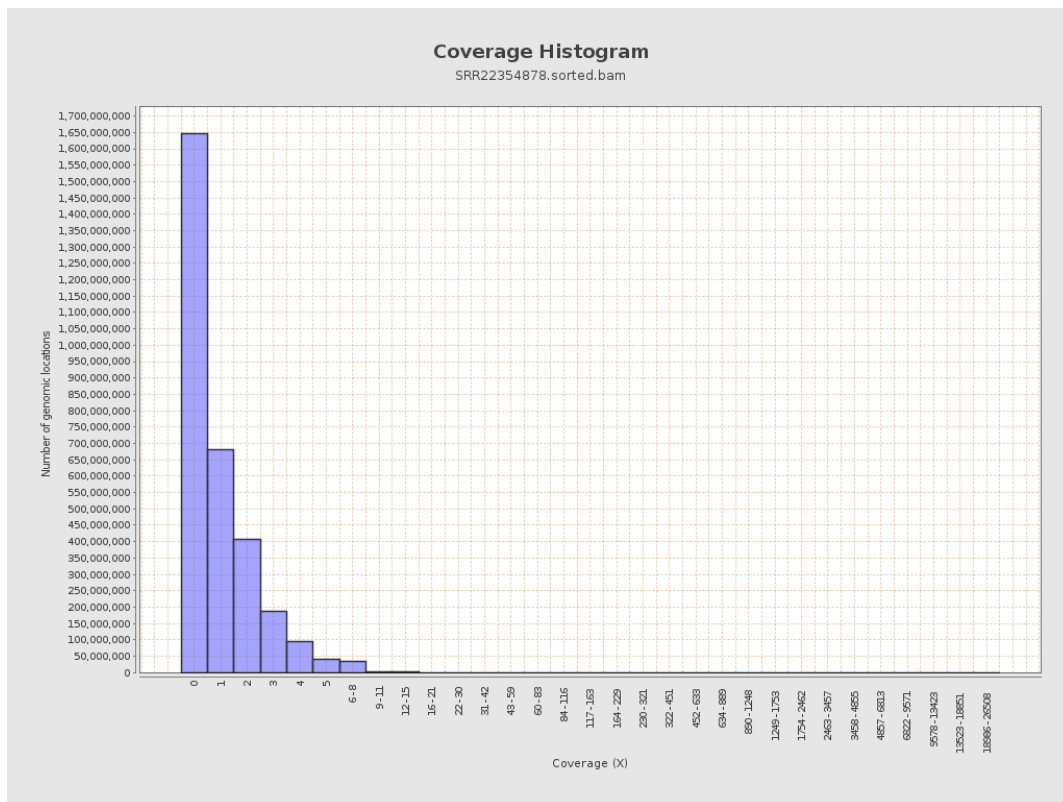
		bases	coverage	deviation
chr1	249250621	258118621	1.0356	27.3558
chr2	243199373	260761324	1.0722	8.6284
chr3	198022430	195977301	0.9897	1.4969
chr4	191154276	190575814	0.997	10.1607
chr5	180915260	178087063	0.9844	1.5698
chr6	171115067	169755577	0.9921	3.9556
chr7	159138663	168524396	1.059	13.5067
chr8	146364022	149518312	1.0216	5.8654
chr9	141213431	134814471	0.9547	17.6397
chr10	135534747	164761381	1.2156	24.1668
chr11	135006516	143161240	1.0604	5.4385
chr12	133851895	135879950	1.0152	1.6656
chr13	115169878	91615604	0.7955	1.3237
chr14	107349540	93453740	0.8706	1.5255
chr15	102531392	89940080	0.8772	1.387
chr16	90354753	102640292	1.136	4.6115
chr17	81195210	98578062	1.2141	7.04
chr18	78077248	83089790	1.0642	12.8763
chr19	59128983	75191116	1.2716	12.304
chr20	63025520	70410852	1.1172	3.884
chr21	48129895	43132766	0.8962	5.1917
chr22	51304566	45398262	0.8849	2.613
chrMT	16571	4651880	280.7242	33.2929
chrX	155270560	77981058	0.5022	2.1221

chrY	59373566	29320928	0.4938	11.9328
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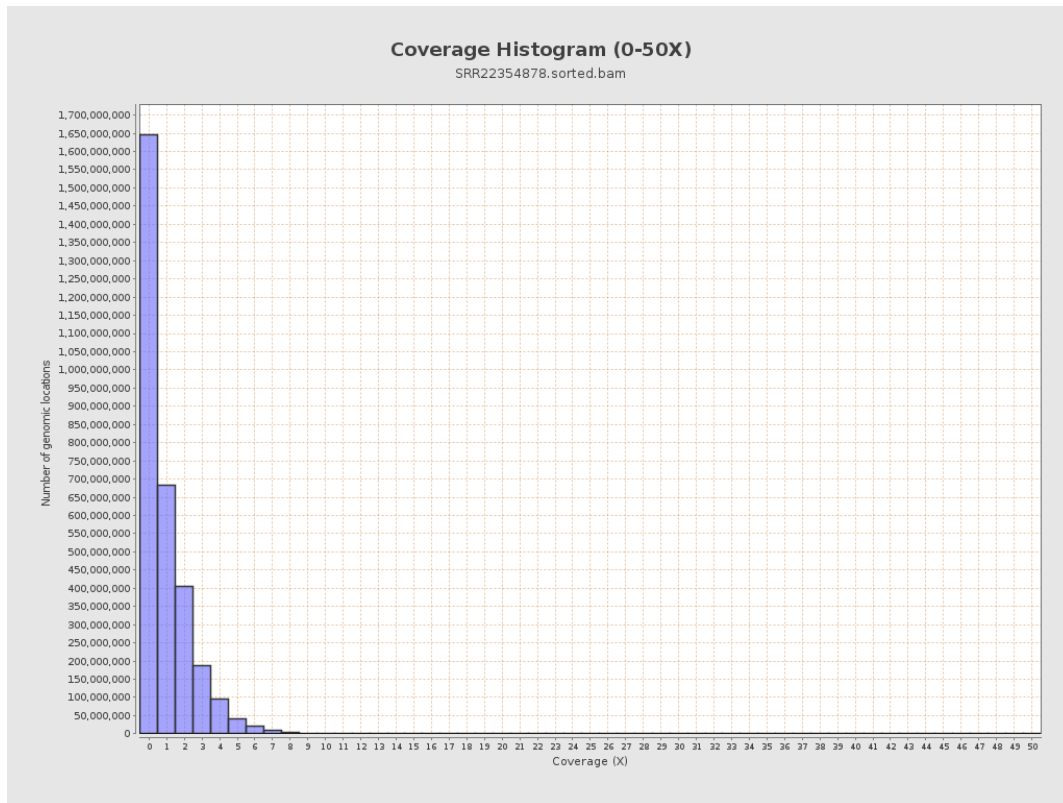
3. Results : Coverage across reference



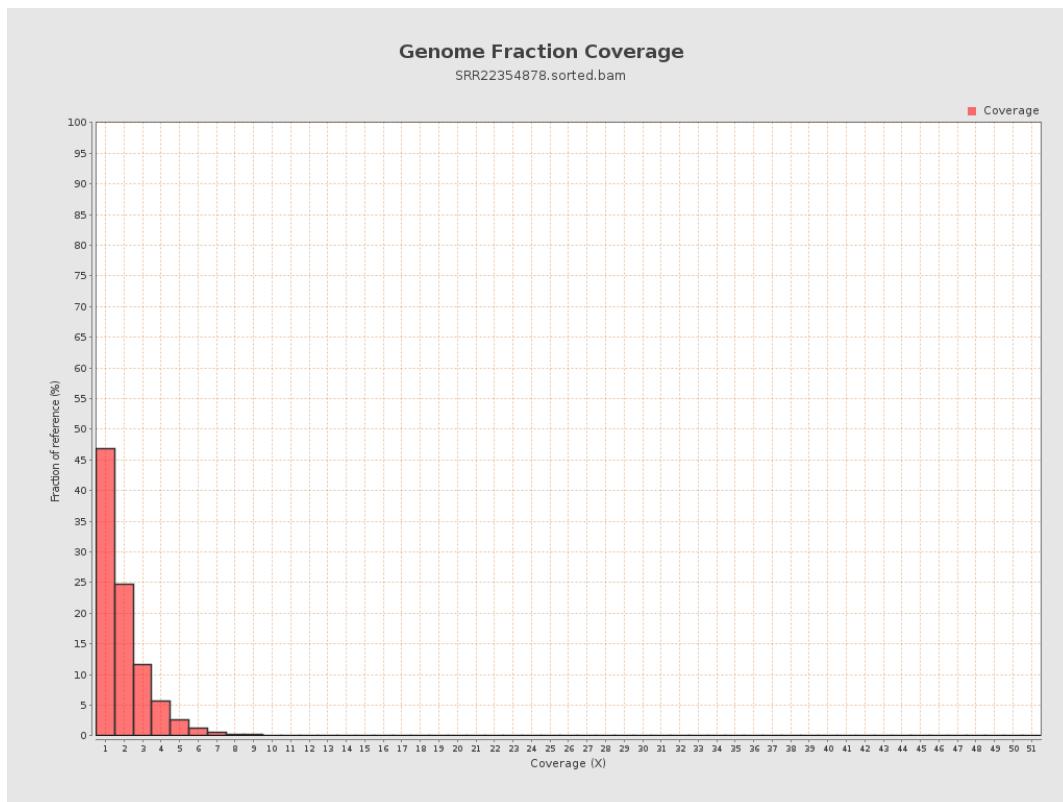
4. Results : Coverage Histogram



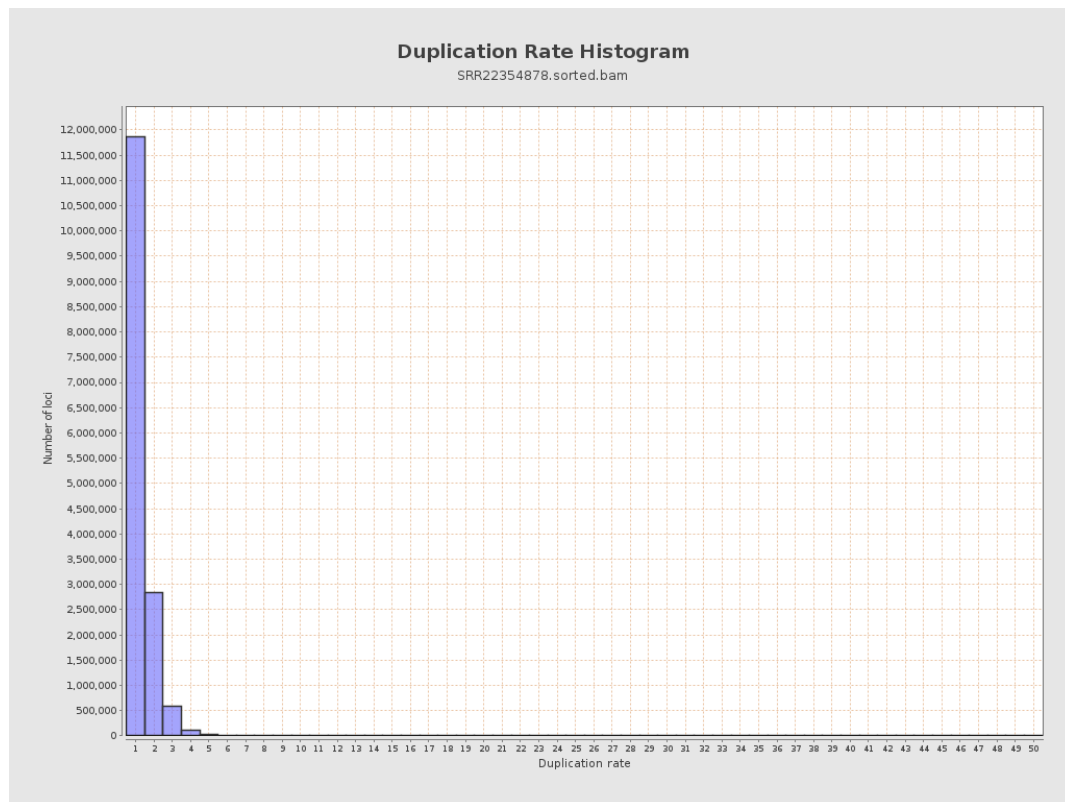
5. Results : Coverage Histogram (0-50X)



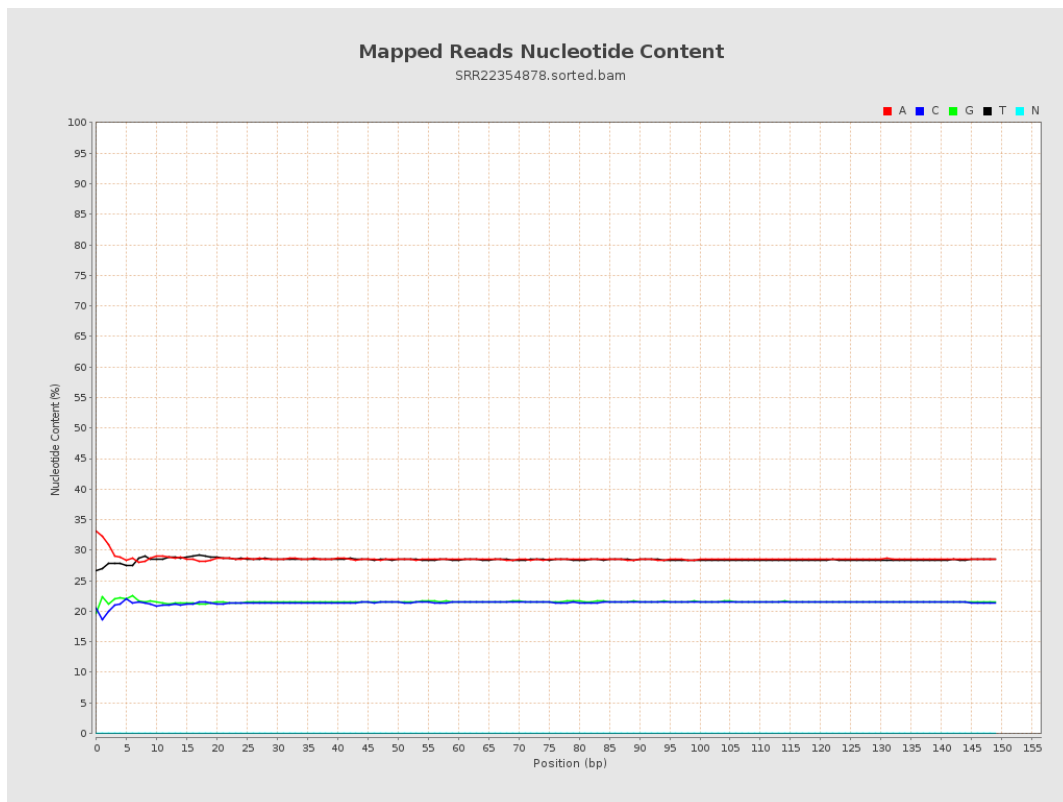
6. Results : Genome Fraction Coverage



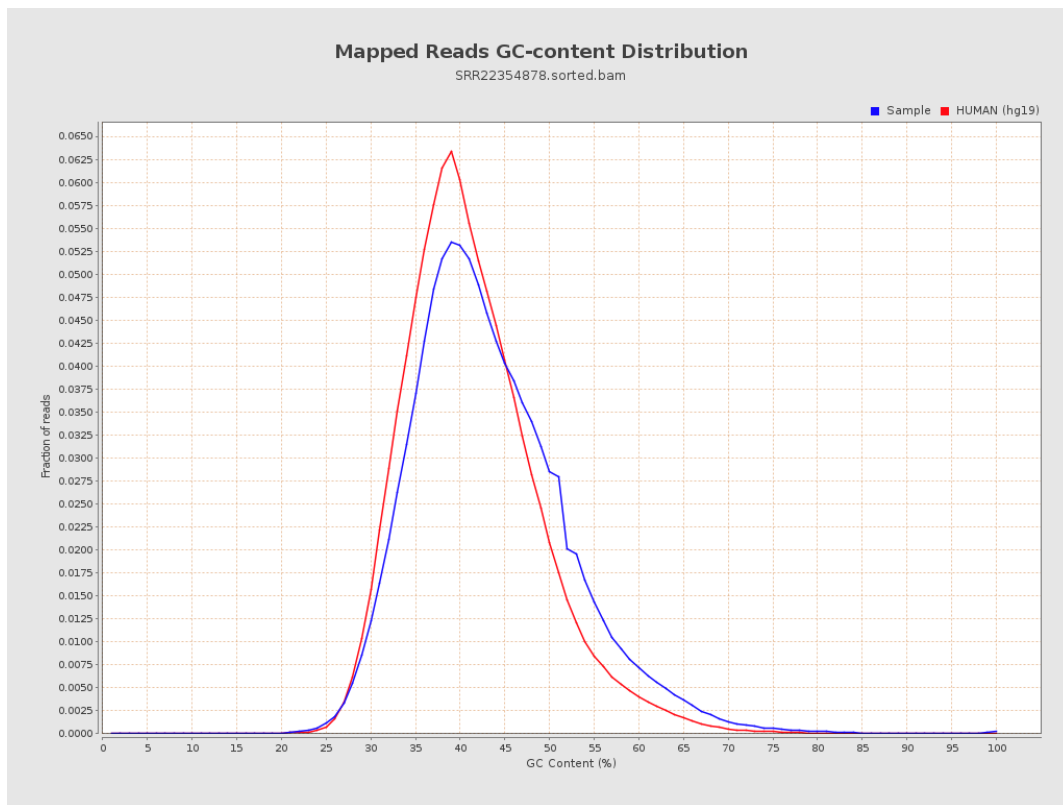
7. Results : Duplication Rate Histogram



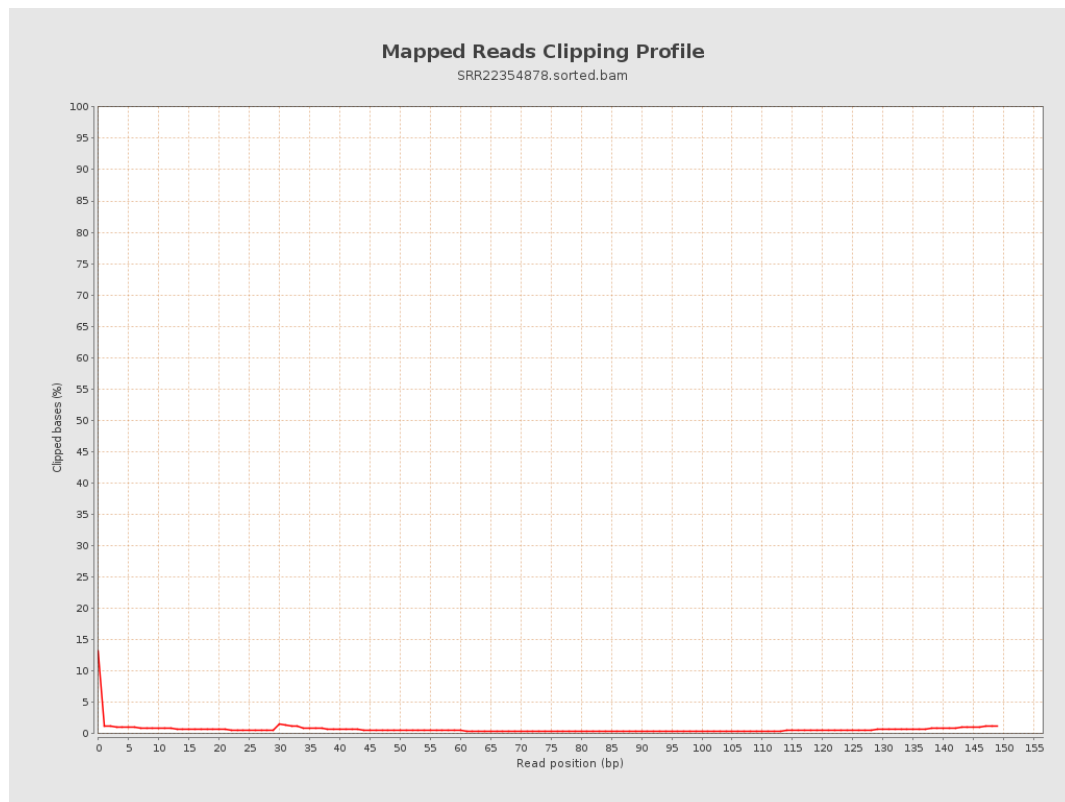
8. Results : Mapped Reads Nucleotide Content



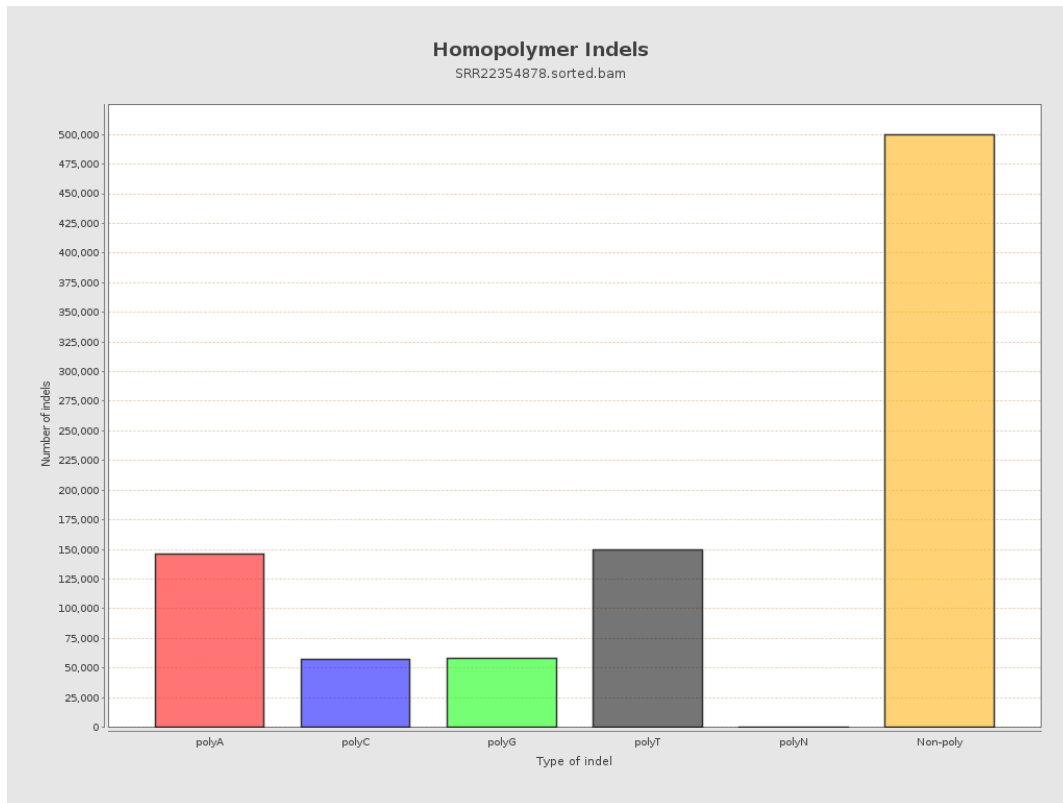
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



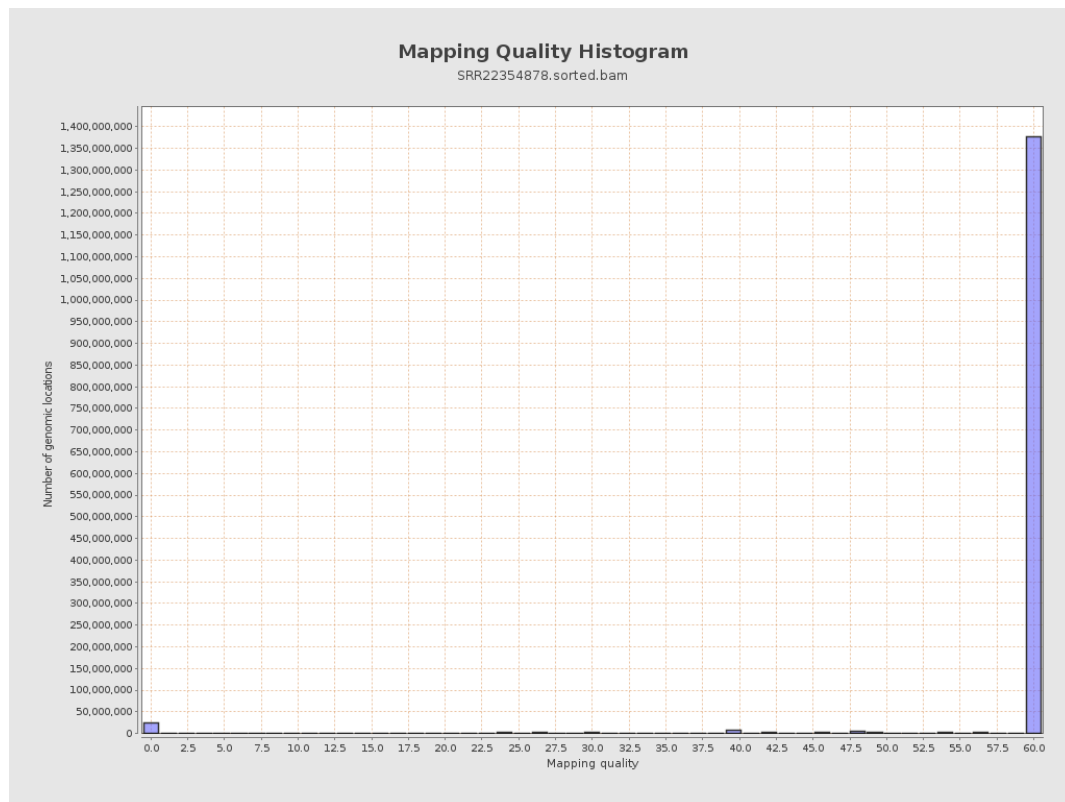
11. Results : Homopolymer Indels



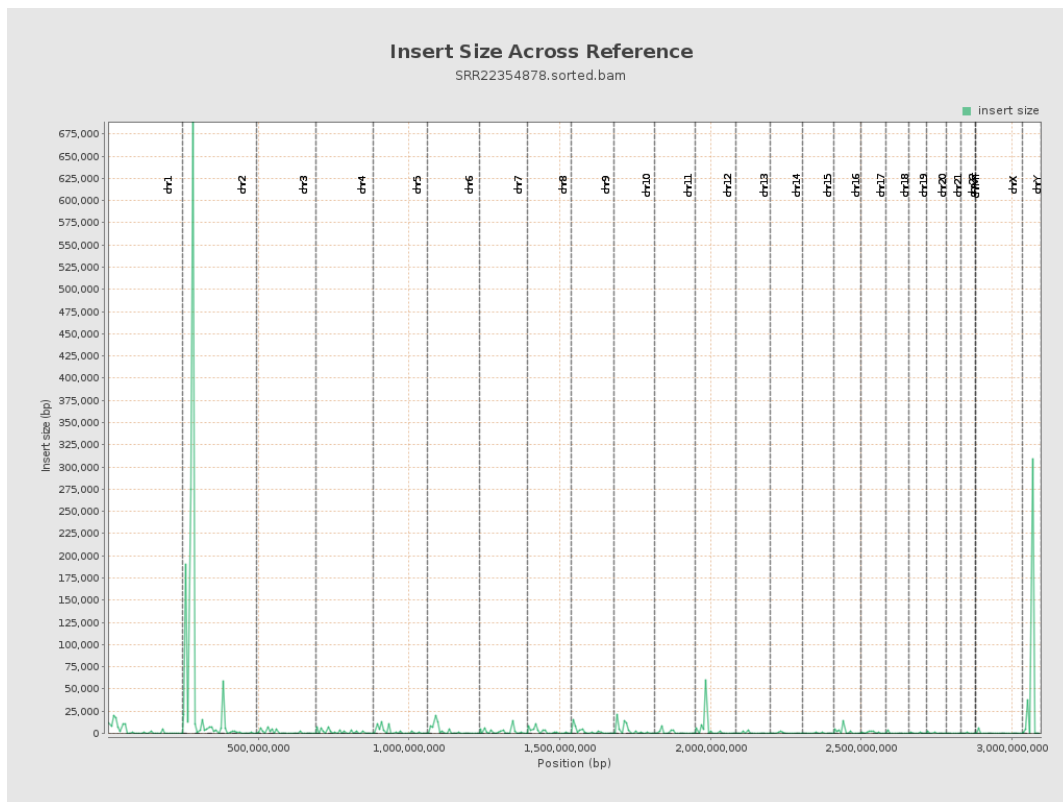
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

