

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 08:49:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354881.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_SRR22354881 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354881_1.fastq.gz SRR22354881_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 08:49:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354881.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,157,704
Mapped reads	19,016,419 / 99.26%
Unmapped reads	141,285 / 0.74%
Mapped paired reads	19,016,419 / 99.26%
Mapped reads, first in pair	9,518,740 / 49.69%
Mapped reads, second in pair	9,497,679 / 49.58%
Mapped reads, both in pair	18,973,152 / 99.04%
Mapped reads, singletons	43,267 / 0.23%
Secondary alignments	0
Supplementary alignments	419,167 / 2.19%
Read min/max/mean length	30 / 150 / 150.86
Duplicated reads (estimated)	6,689,542 / 34.92%
Duplication rate	32.8%
Clipped reads	7,271,336 / 37.96%

2.2. ACGT Content

Number/percentage of A's	719,883,151 / 28.41%
Number/percentage of C's	535,576,290 / 21.14%
Number/percentage of T's	727,986,159 / 28.73%
Number/percentage of G's	550,109,069 / 21.71%
Number/percentage of N's	11,782 / 0%

GC Percentage	42.85%
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2.3. Coverage

Mean	0.8189
Standard Deviation	18.9448

2.4. Mapping Quality

Mean Mapping Quality	53.98
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2.5. Insert size

Mean	197,056.04
Standard Deviation	5,065,630.94
P25/Median/P75	128 / 196 / 283

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	19,595,437
Insertions	487,070
Mapped reads with at least one insertion	2.38%
Deletions	502,615
Mapped reads with at least one deletion	2.51%
Homopolymer indels	43.66%

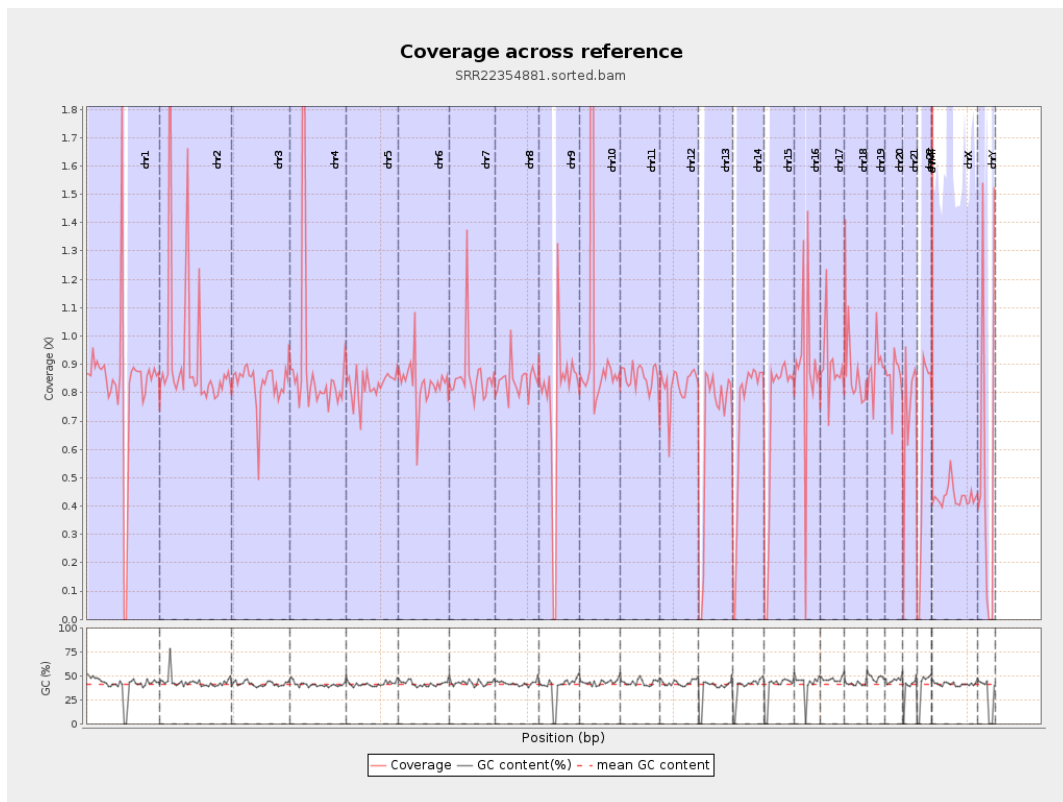
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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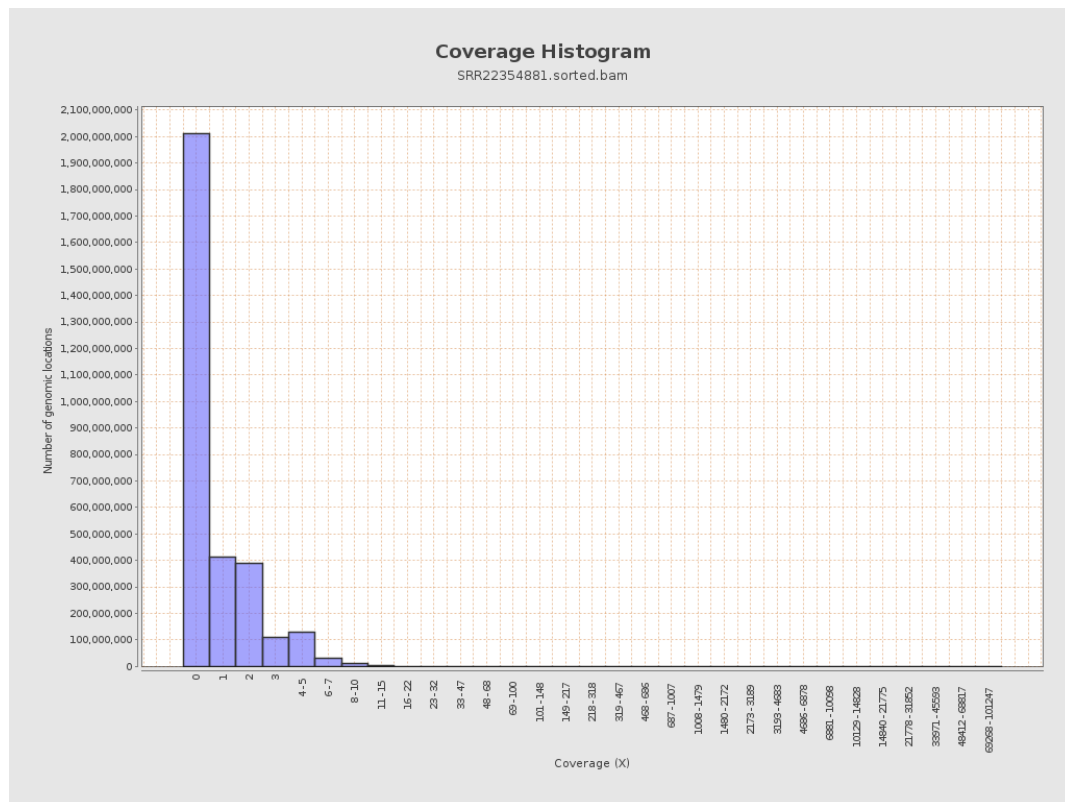
		bases	coverage	deviation
chr1	249250621	207822250	0.8338	22.0317
chr2	243199373	227172247	0.9341	54.4605
chr3	198022430	164694507	0.8317	1.7985
chr4	191154276	171246753	0.8959	13.8604
chr5	180915260	149611261	0.827	1.4919
chr6	171115067	142680968	0.8338	3.2577
chr7	159138663	136974827	0.8607	11.9607
chr8	146364022	123678313	0.845	3.2102
chr9	141213431	108589385	0.769	12.0347
chr10	135534747	142959690	1.0548	30.8664
chr11	135006516	115839228	0.858	4.2712
chr12	133851895	110531154	0.8258	1.5003
chr13	115169878	77702133	0.6747	1.3076
chr14	107349540	76471592	0.7124	3.0658
chr15	102531392	71869765	0.701	1.3276
chr16	90354753	80057038	0.886	5.666
chr17	81195210	72269435	0.8901	4.9651
chr18	78077248	68371219	0.8757	10.4085
chr19	59128983	52667519	0.8907	11.2568
chr20	63025520	53863245	0.8546	4.4297
chr21	48129895	35503814	0.7377	6.9016
chr22	51304566	31608391	0.6161	2.5477
chrMT	16571	12443852	750.9415	166.4804
chrX	155270560	67249595	0.4331	1.7115

chrY	59373566	33128390	0.558	16.5016
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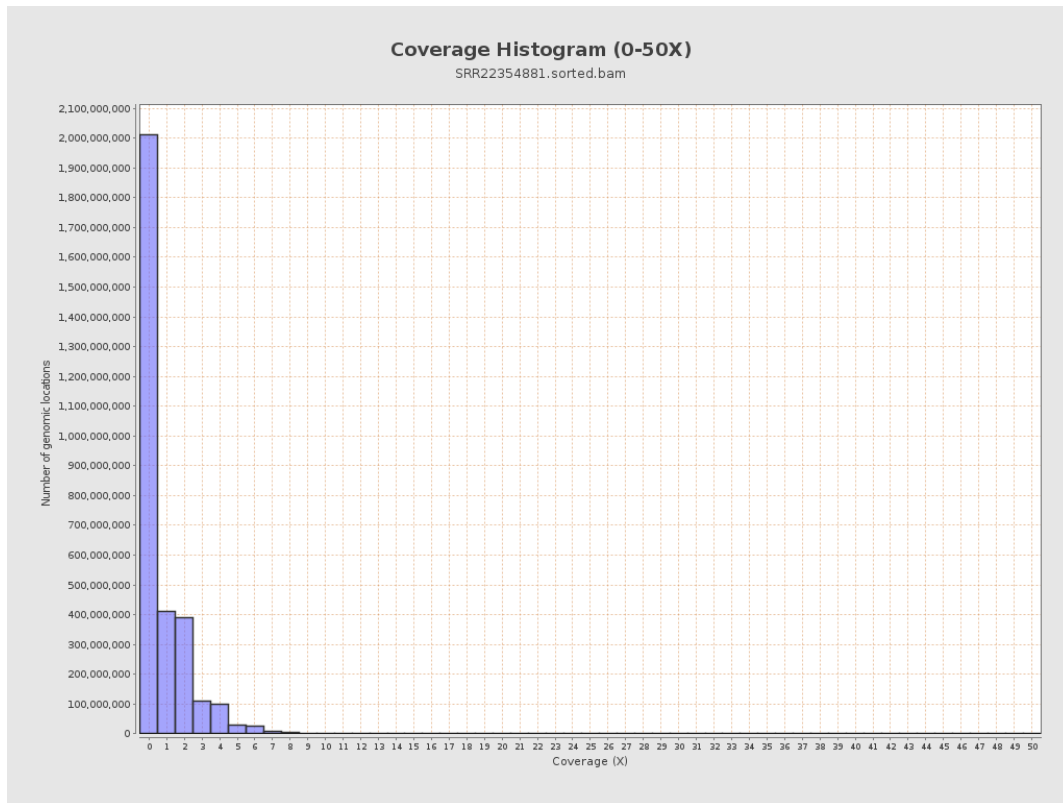
3. Results : Coverage across reference



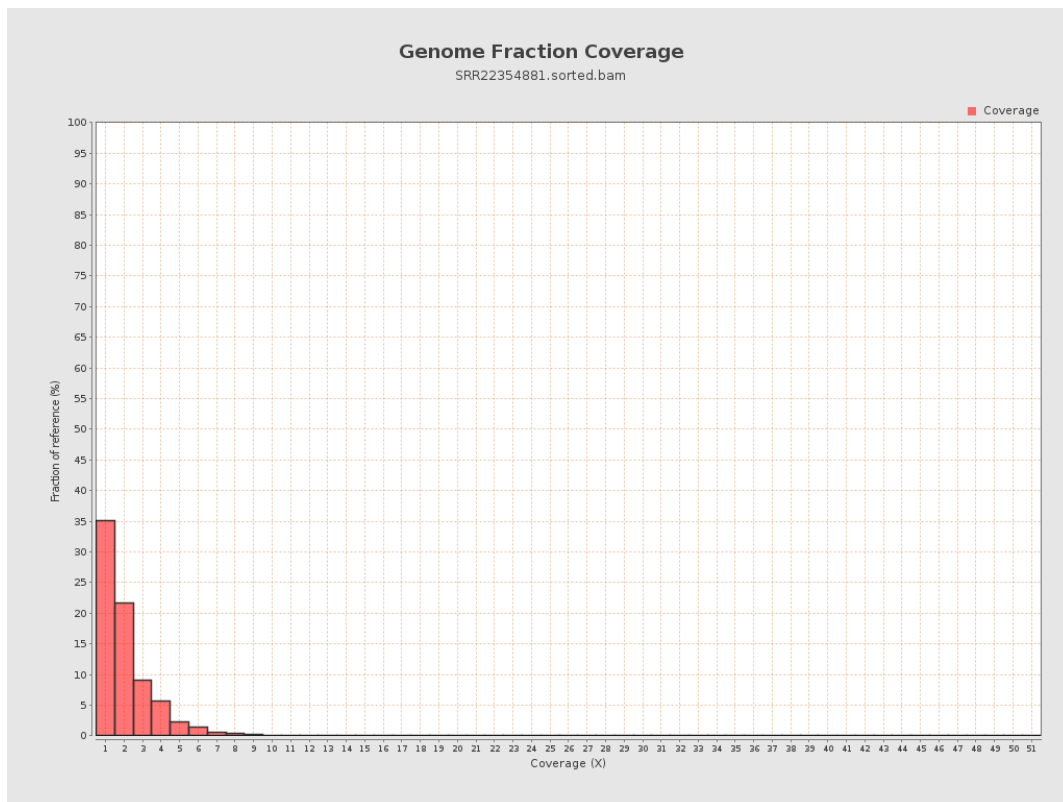
4. Results : Coverage Histogram



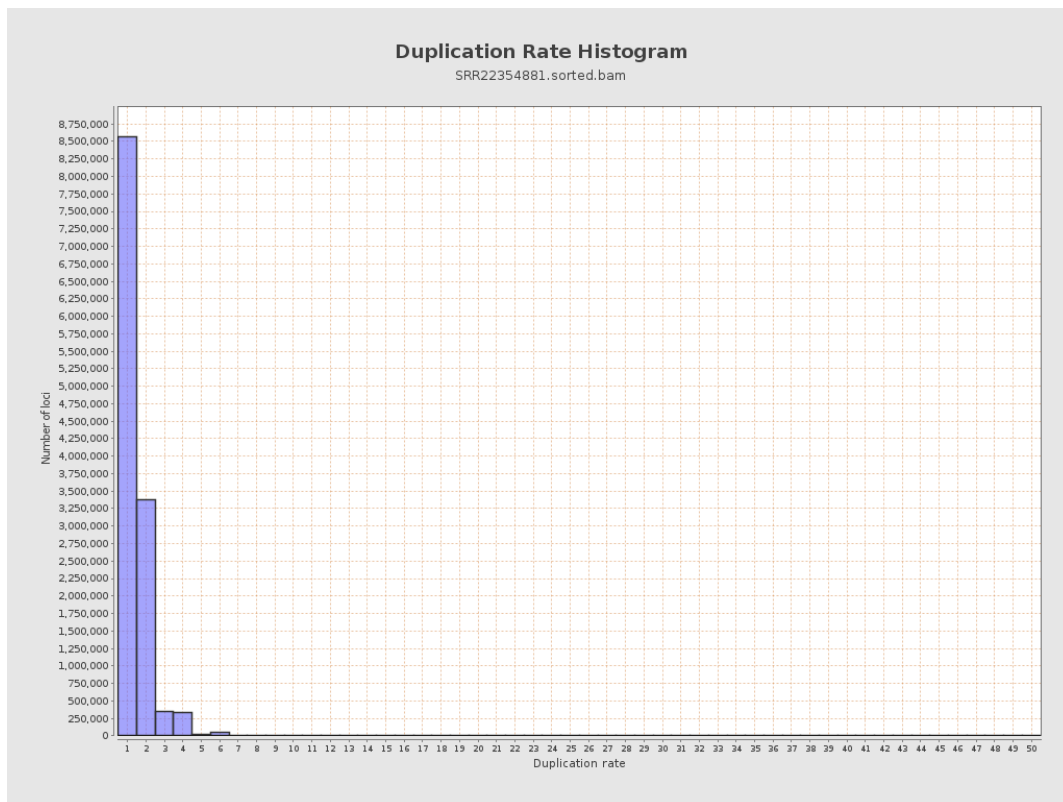
5. Results : Coverage Histogram (0-50X)



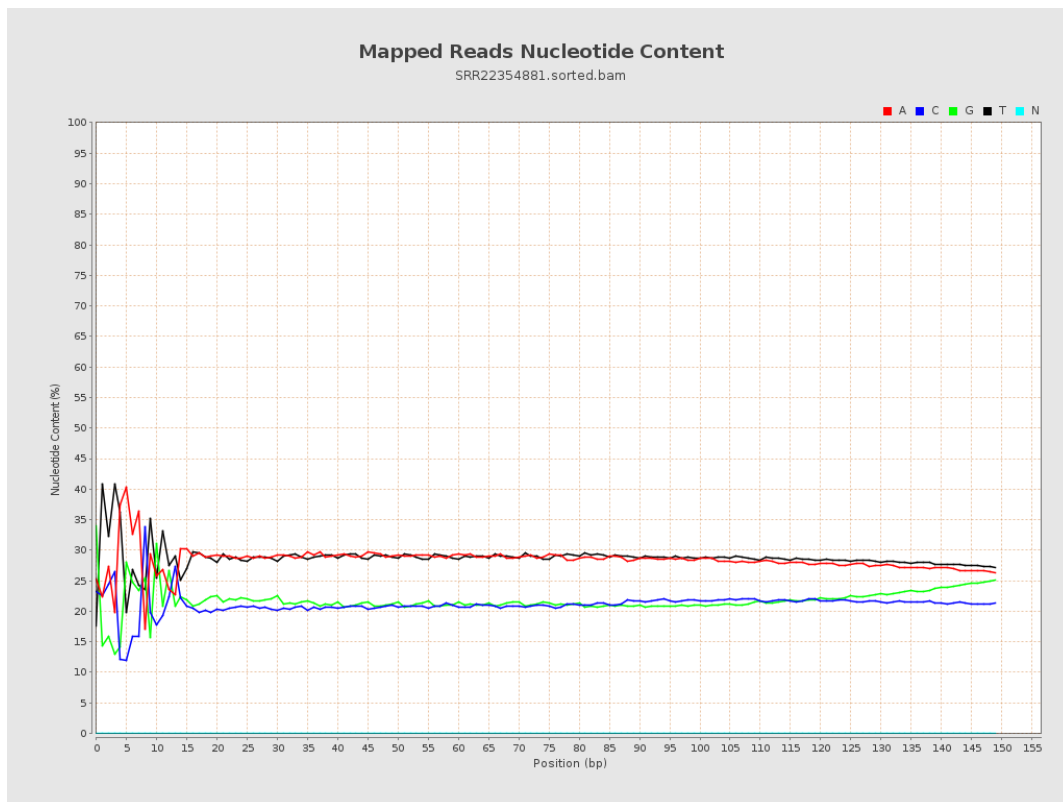
6. Results : Genome Fraction Coverage



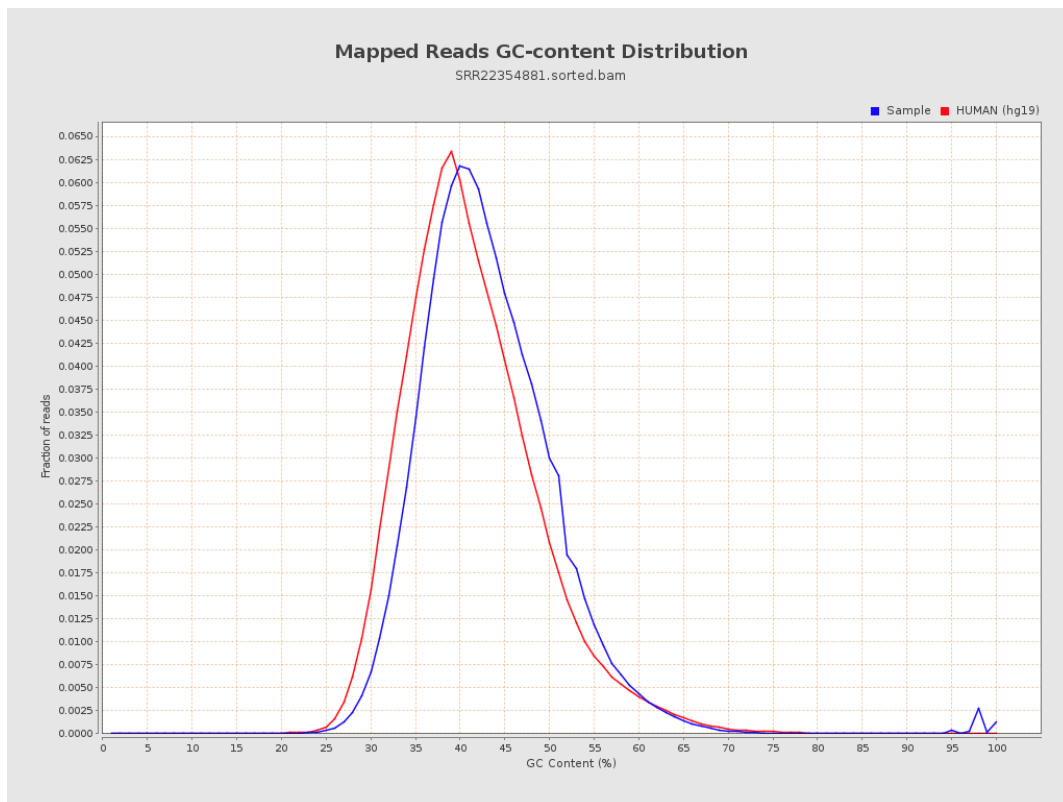
7. Results : Duplication Rate Histogram



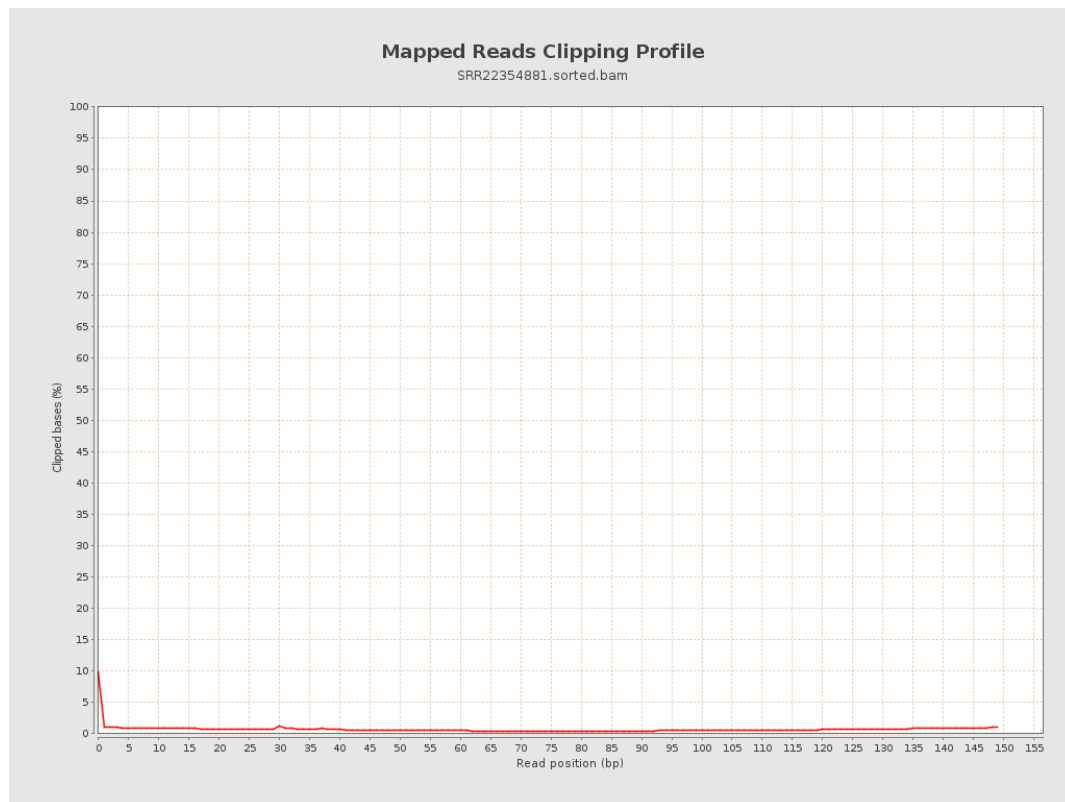
8. Results : Mapped Reads Nucleotide Content



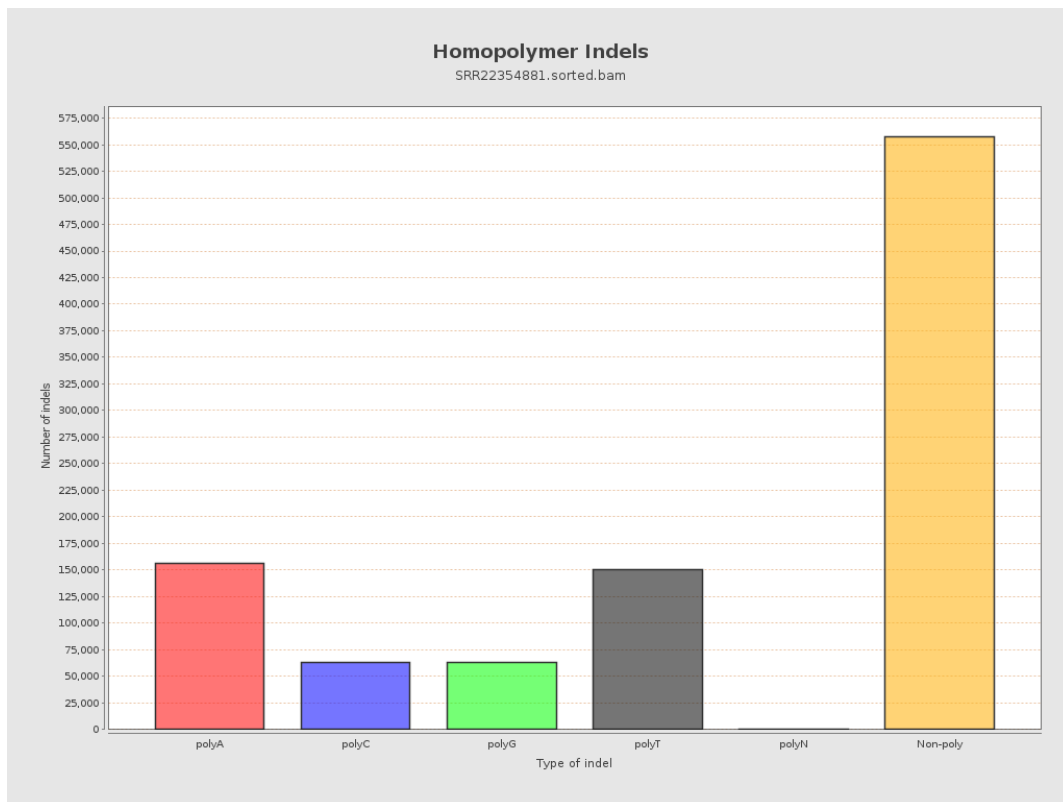
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



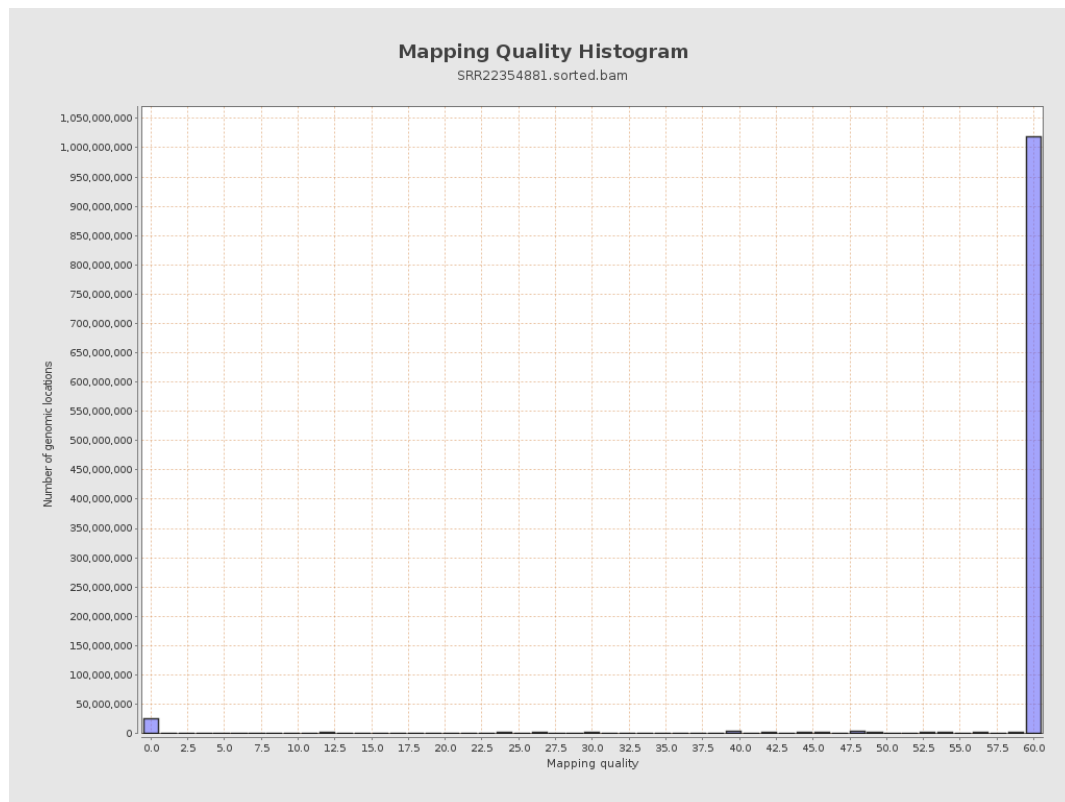
11. Results : Homopolymer Indels



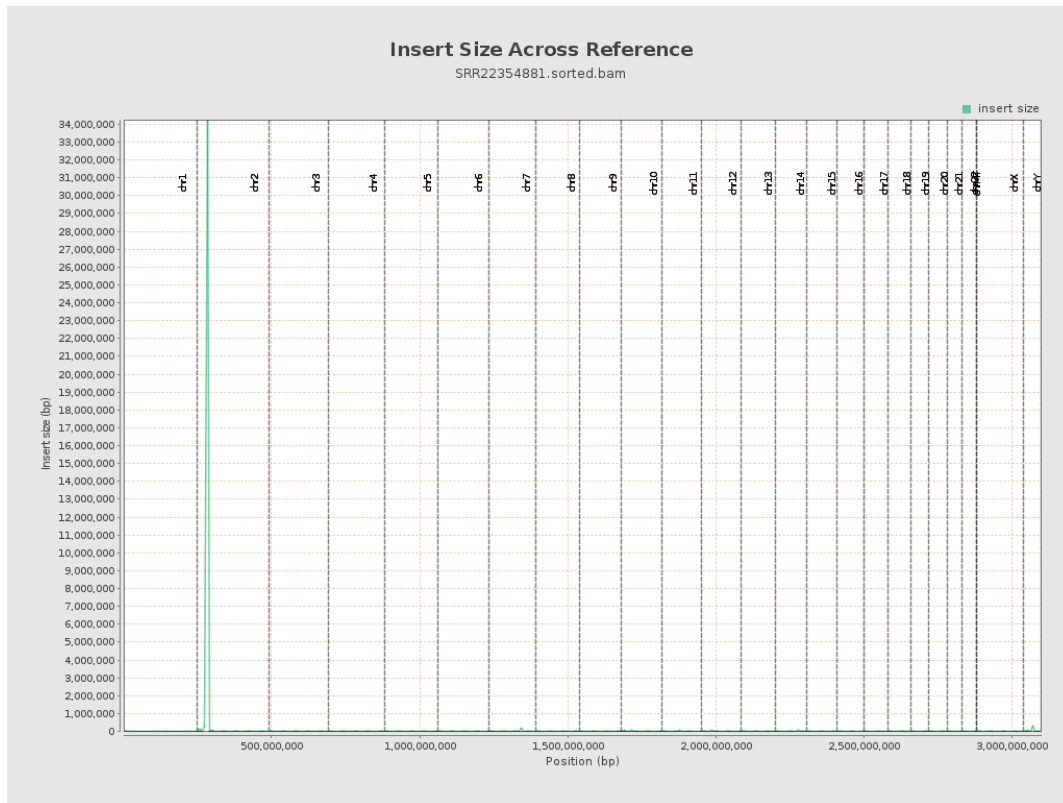
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

