

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:52:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354852.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_SRR22354852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354852_1.fastq.gz SRR22354852_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:51:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,661,322
Mapped reads	22,431,572 / 98.99%
Unmapped reads	229,750 / 1.01%
Mapped paired reads	22,431,572 / 98.99%
Mapped reads, first in pair	11,238,188 / 49.59%
Mapped reads, second in pair	11,193,384 / 49.39%
Mapped reads, both in pair	22,338,382 / 98.57%
Mapped reads, singletons	93,190 / 0.41%
Secondary alignments	0
Supplementary alignments	390,945 / 1.73%
Read min/max/mean length	30 / 150 / 150.76
Duplicated reads (estimated)	7,159,774 / 31.59%
Duplication rate	26.77%
Clipped reads	5,573,386 / 24.59%

2.2. ACGT Content

Number/percentage of A's	901,278,818 / 28.81%
Number/percentage of C's	655,788,131 / 20.96%
Number/percentage of T's	907,287,998 / 29%
Number/percentage of G's	664,436,146 / 21.24%
Number/percentage of N's	52,128 / 0%

GC Percentage	42.2%
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2.3. Coverage

Mean	1.0113
Standard Deviation	19.8069

2.4. Mapping Quality

Mean Mapping Quality	53.96
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2.5. Insert size

Mean	133,878.3
Standard Deviation	4,051,200.7
P25/Median/P75	183 / 291 / 421

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	27,266,397
Insertions	610,629
Mapped reads with at least one insertion	2.48%
Deletions	579,964
Mapped reads with at least one deletion	2.41%
Homopolymer indels	39.6%

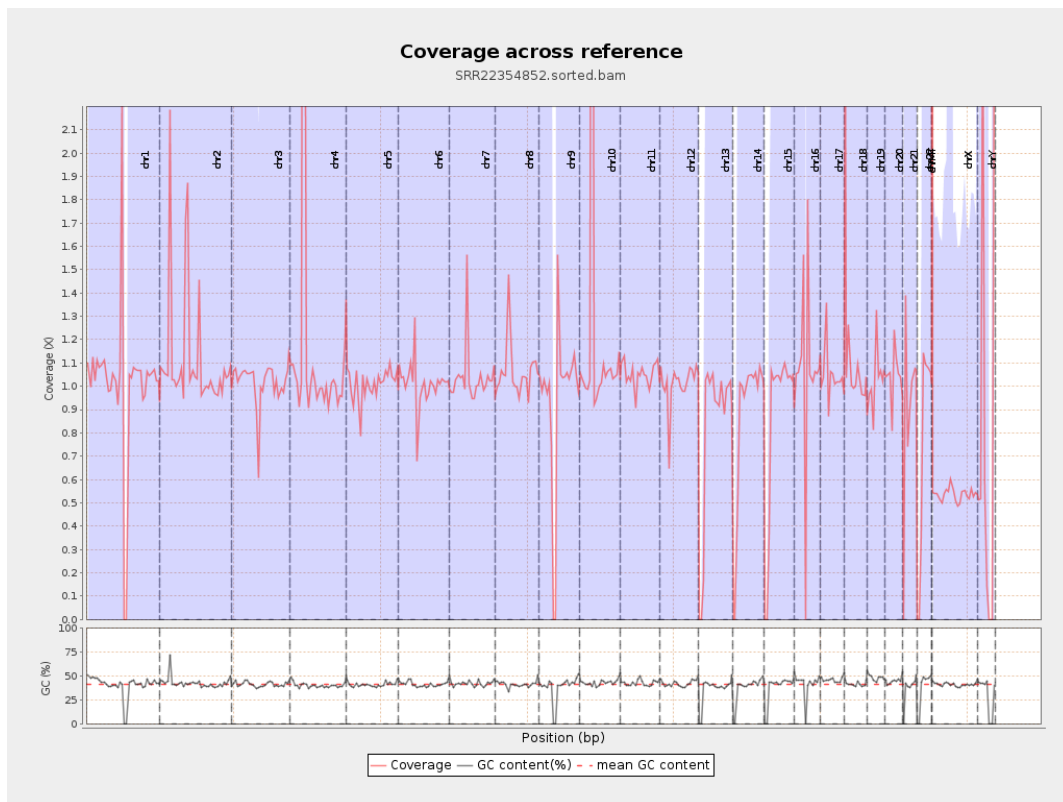
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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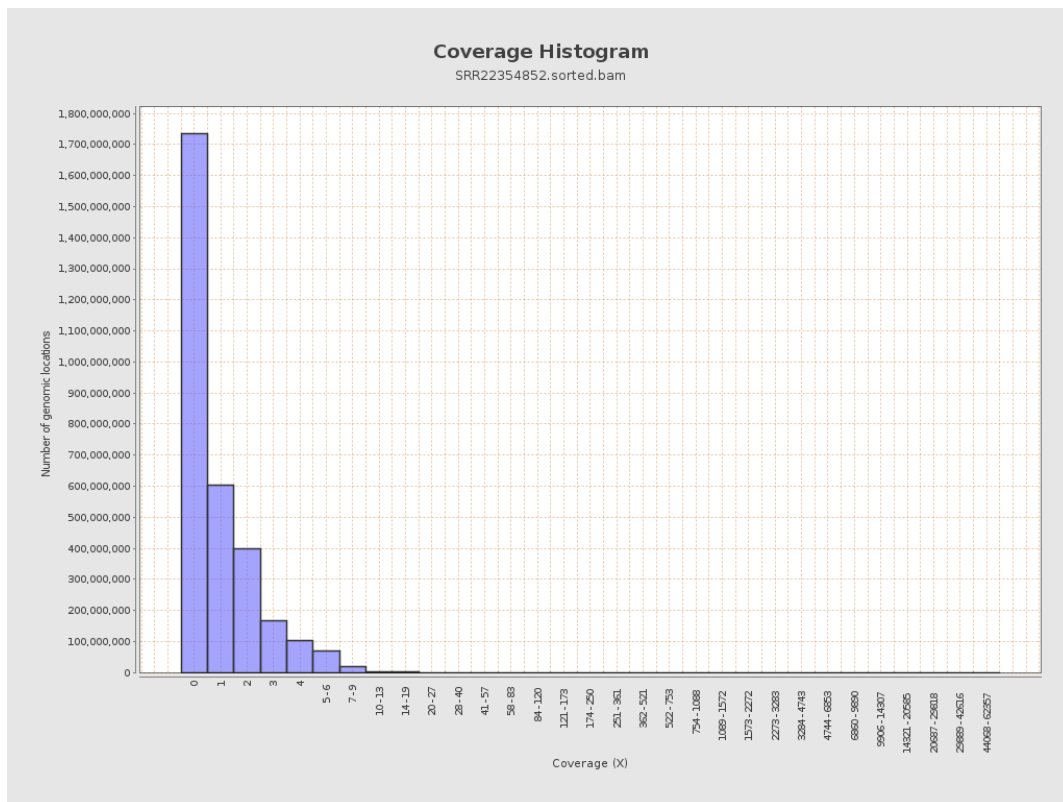
		bases	coverage	deviation
chr1	249250621	253072320	1.0153	28.4742
chr2	243199373	272806848	1.1217	38.1505
chr3	198022430	200693822	1.0135	1.9093
chr4	191154276	221769588	1.1602	29.1111
chr5	180915260	182764360	1.0102	1.6522
chr6	171115067	173159351	1.0119	3.6506
chr7	159138663	165175892	1.0379	12.9394
chr8	146364022	155903032	1.0652	23.2527
chr9	141213431	132056585	0.9352	14.2795
chr10	135534747	178725198	1.3187	36.6151
chr11	135006516	142077452	1.0524	4.2269
chr12	133851895	134943357	1.0082	1.6813
chr13	115169878	94904249	0.824	1.3986
chr14	107349540	92392356	0.8607	2.3866
chr15	102531392	87062534	0.8491	1.4177
chr16	90354753	96668492	1.0699	7.4196
chr17	81195210	84688377	1.043	5.6161
chr18	78077248	86690172	1.1103	16.6957
chr19	59128983	60643048	1.0256	15.6739
chr20	63025520	65989343	1.047	9.2854
chr21	48129895	44969409	0.9343	14.6903
chr22	51304566	38784810	0.756	2.7977
chrMT	16571	29127831	1,757.7594	524.1042
chrX	155270560	83175734	0.5357	1.6424

chrY	59373566	52463913	0.8836	30.8753
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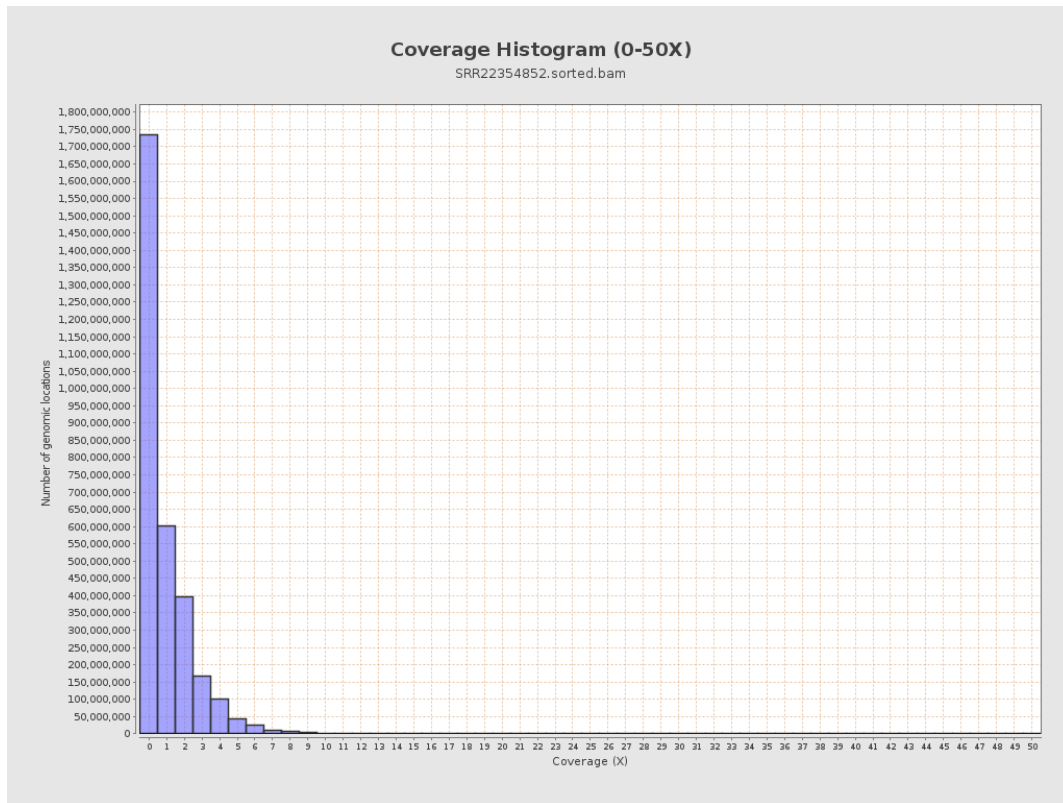
3. Results : Coverage across reference



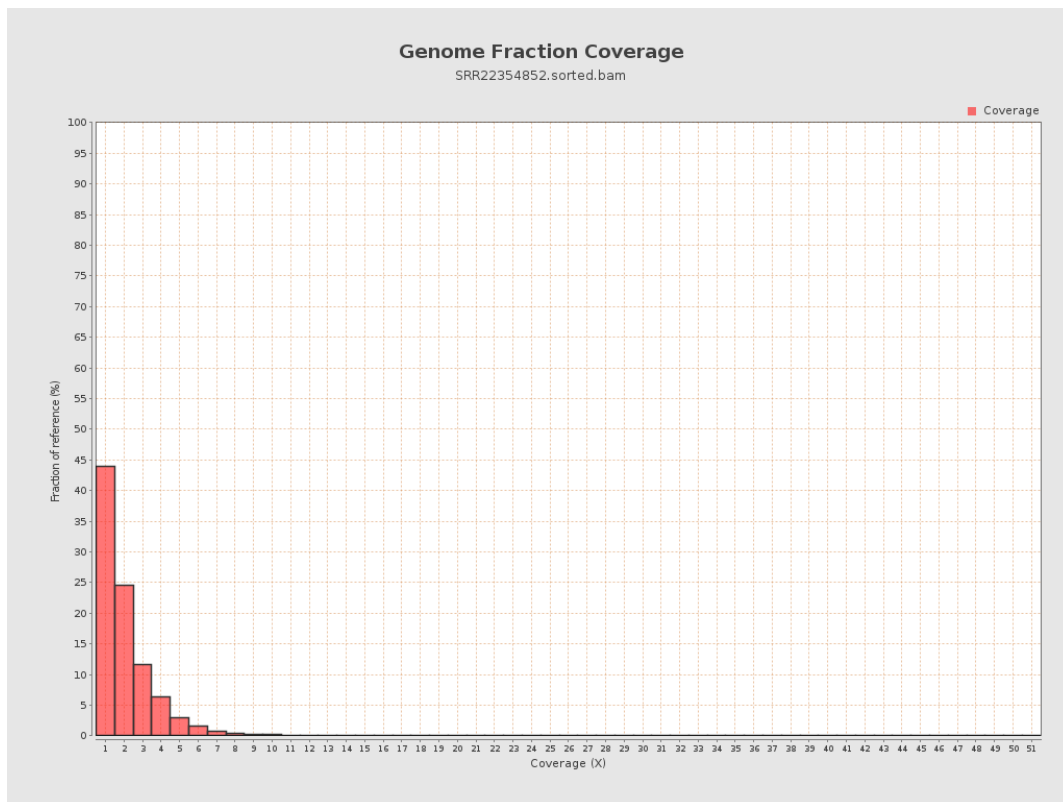
4. Results : Coverage Histogram



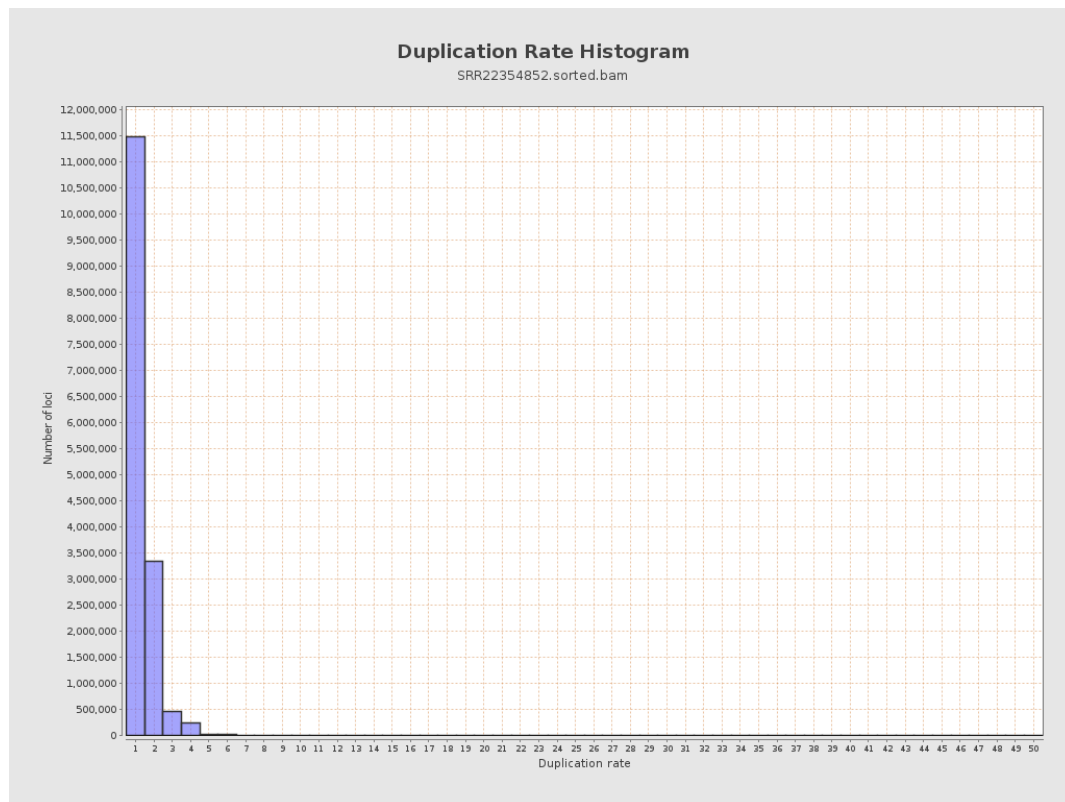
5. Results : Coverage Histogram (0-50X)



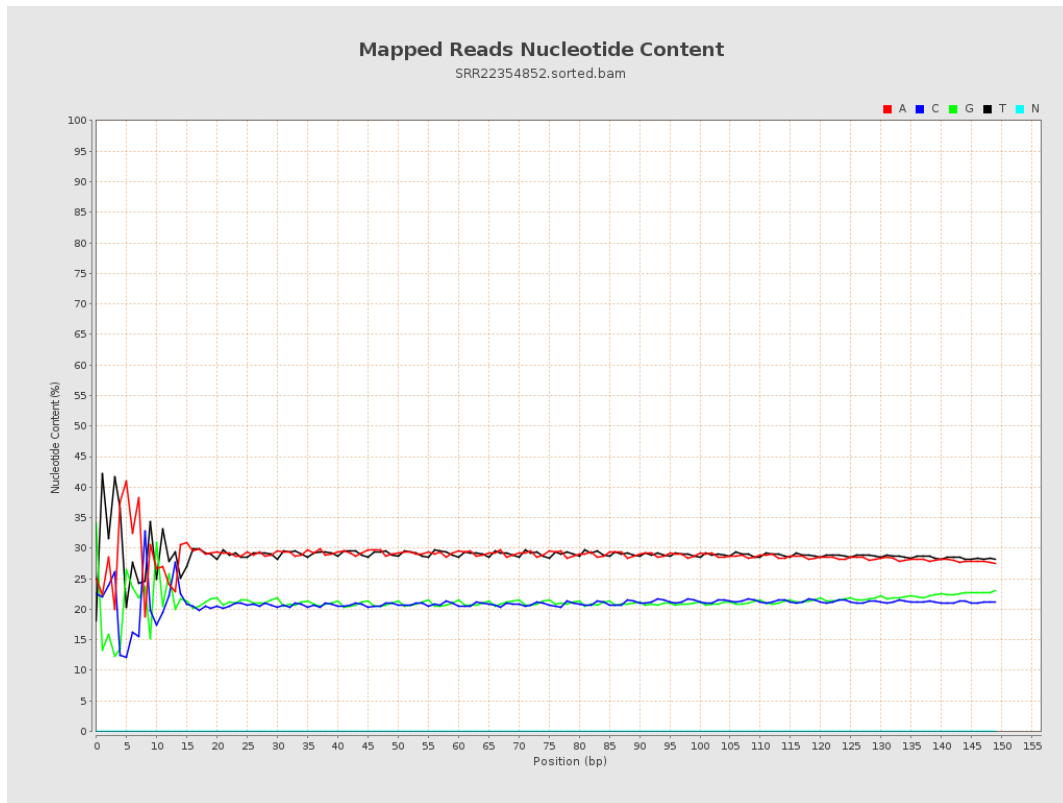
6. Results : Genome Fraction Coverage



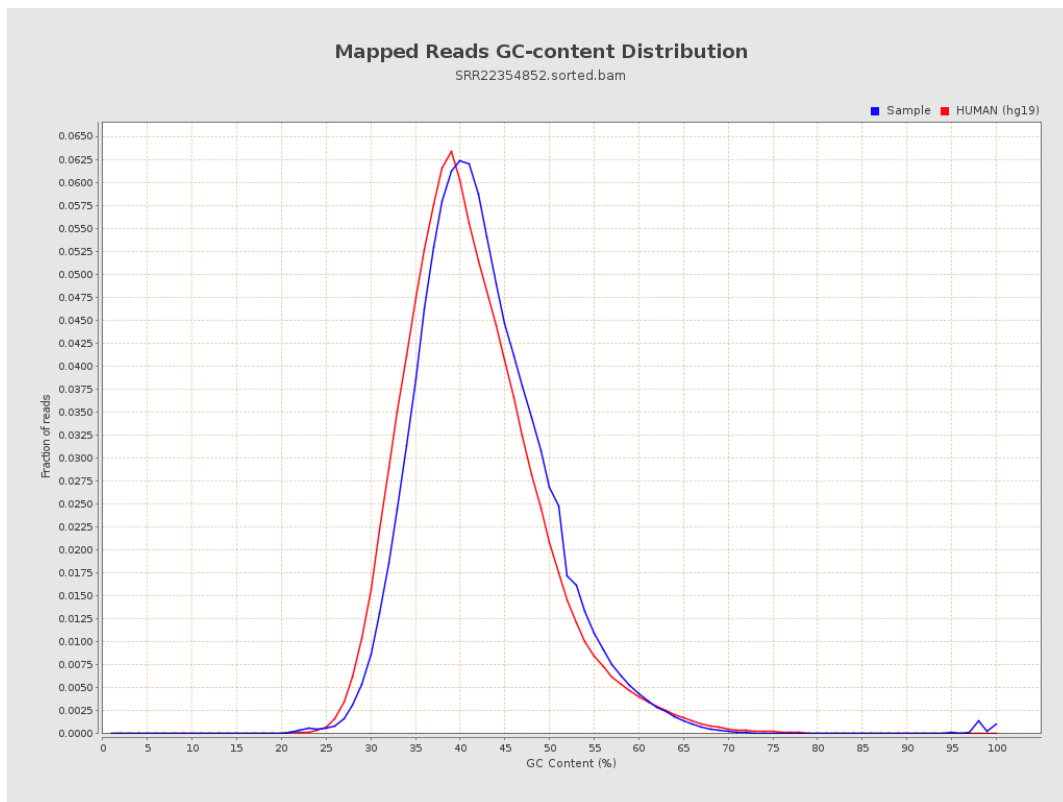
7. Results : Duplication Rate Histogram



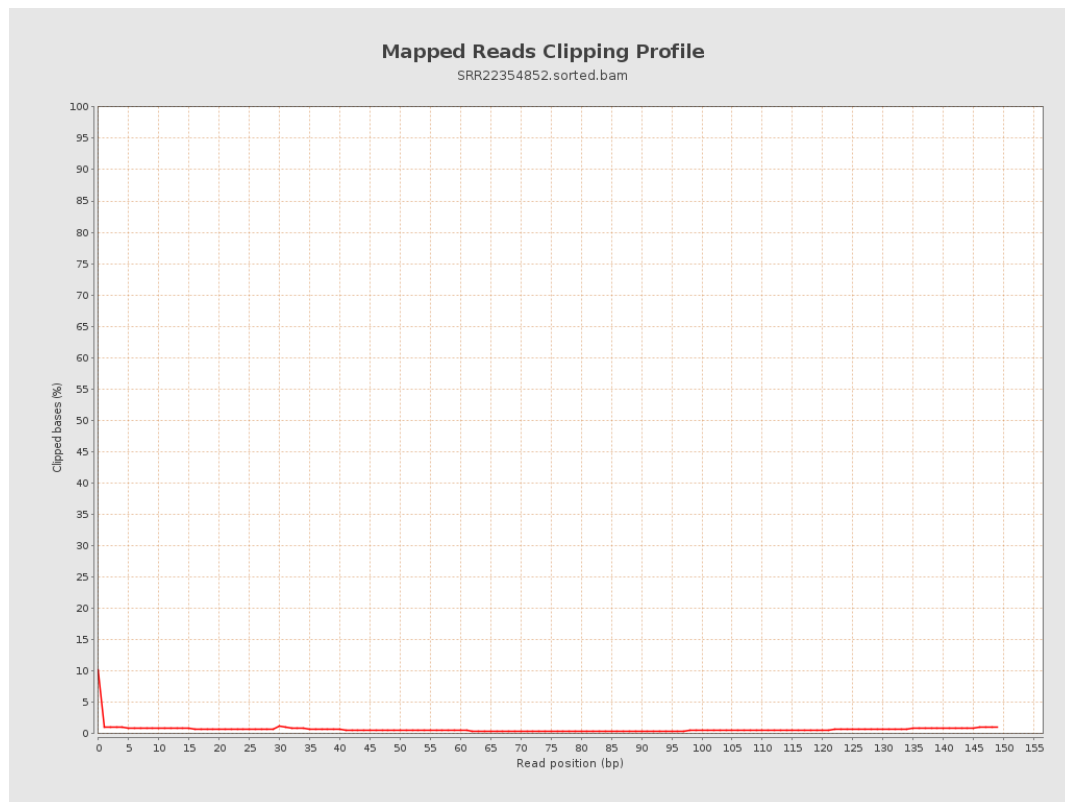
8. Results : Mapped Reads Nucleotide Content



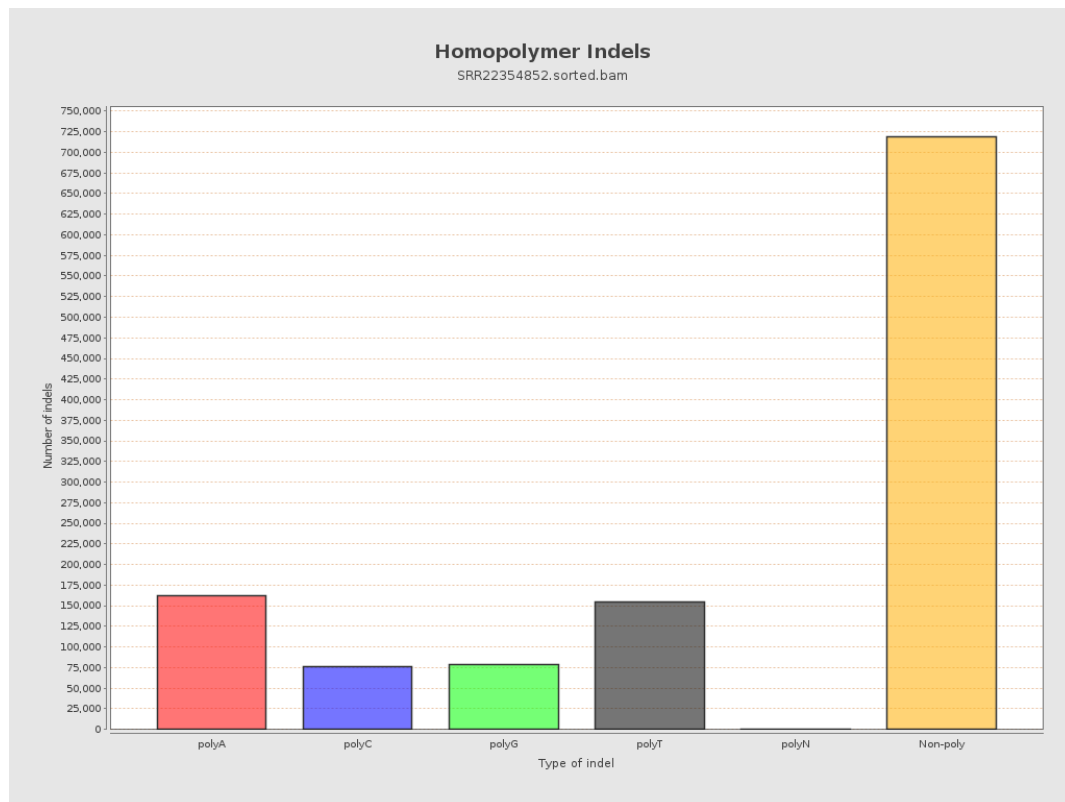
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



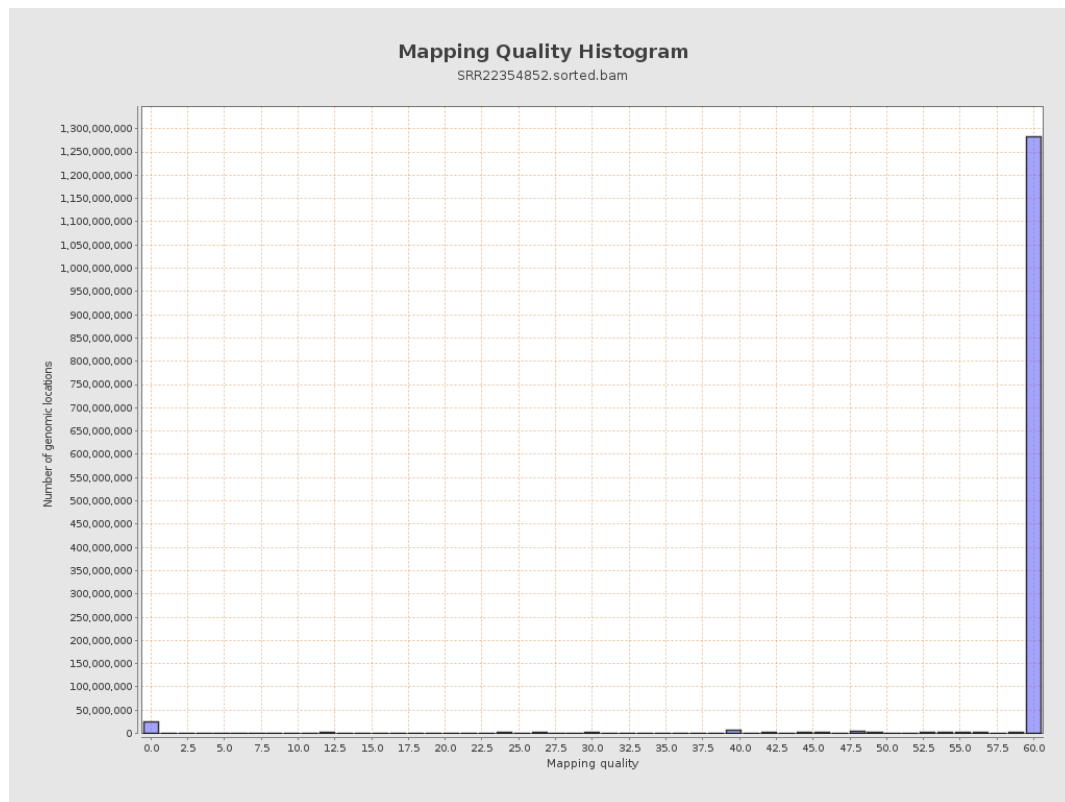
11. Results : Homopolymer Indels



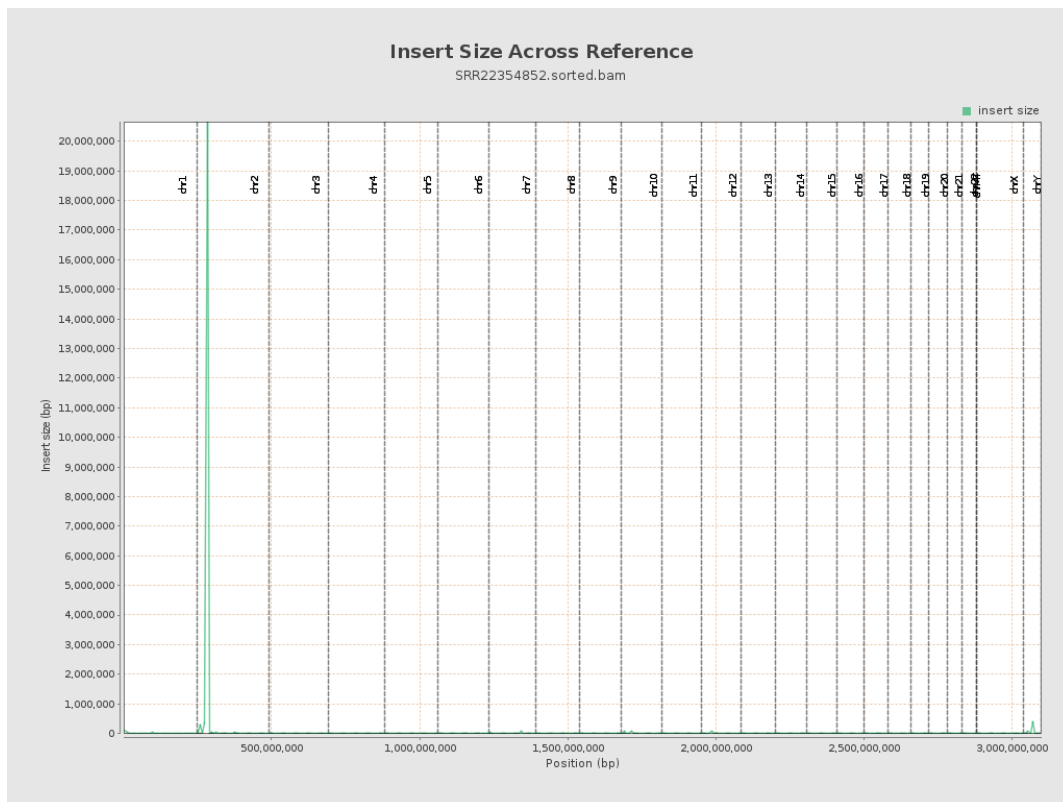
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

