

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 22:09:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472653.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_SRR3472653 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472653_1.fastq.gz SRR3472653_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 22:09:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472653.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,772,664
Mapped reads	17,629,567 / 99.19%
Unmapped reads	143,097 / 0.81%
Mapped paired reads	17,629,567 / 99.19%
Mapped reads, first in pair	8,838,077 / 49.73%
Mapped reads, second in pair	8,791,490 / 49.47%
Mapped reads, both in pair	17,529,618 / 98.63%
Mapped reads, singletons	99,949 / 0.56%
Secondary alignments	0
Supplementary alignments	111,119 / 0.63%
Read min/max/mean length	30 / 101 / 99.87
Duplicated reads (estimated)	12,335,082 / 69.4%
Duplication rate	49.61%
Clipped reads	1,235,650 / 6.95%

2.2. ACGT Content

Number/percentage of A's	479,283,848 / 27.59%
Number/percentage of C's	391,701,067 / 22.55%
Number/percentage of T's	480,107,702 / 27.63%
Number/percentage of G's	385,935,214 / 22.21%
Number/percentage of N's	332,584 / 0.02%

GC Percentage	44.76%
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2.3. Coverage

Mean	0.5613
Standard Deviation	26.1844

2.4. Mapping Quality

Mean Mapping Quality	54.77
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2.5. Insert size

Mean	24,218.55
Standard Deviation	1,528,208.63
P25/Median/P75	162 / 222 / 296

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	10,637,721
Insertions	118,122
Mapped reads with at least one insertion	0.66%
Deletions	93,804
Mapped reads with at least one deletion	0.52%
Homopolymer indels	44.49%

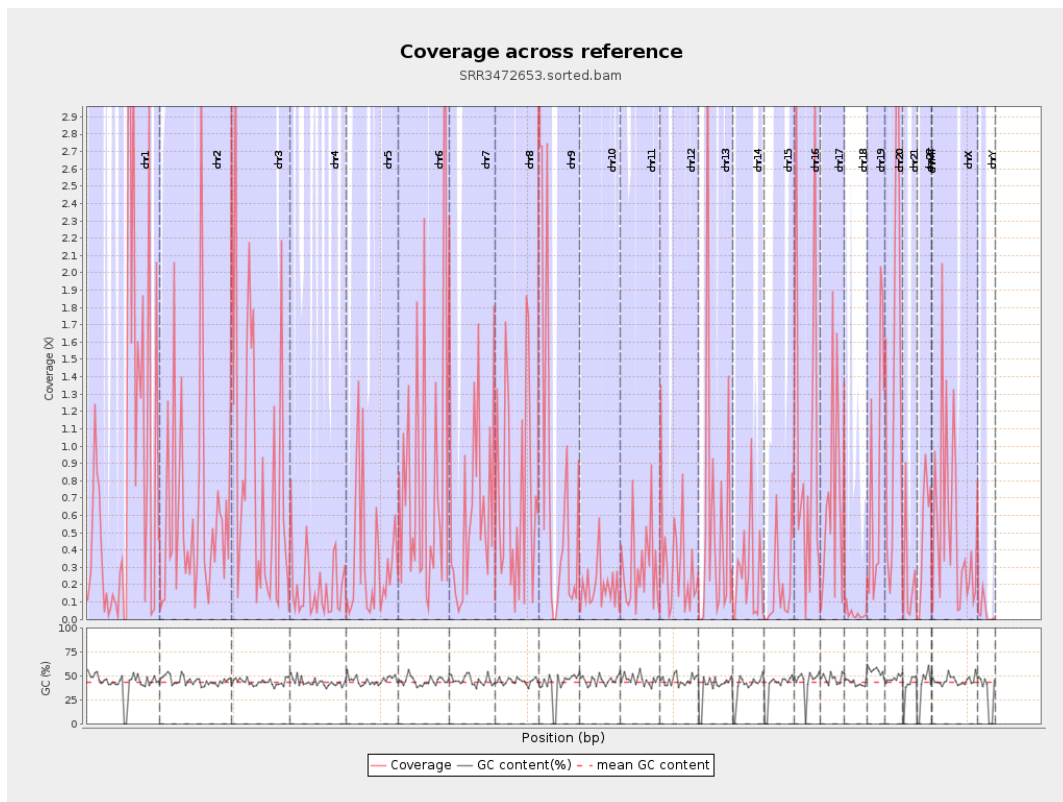
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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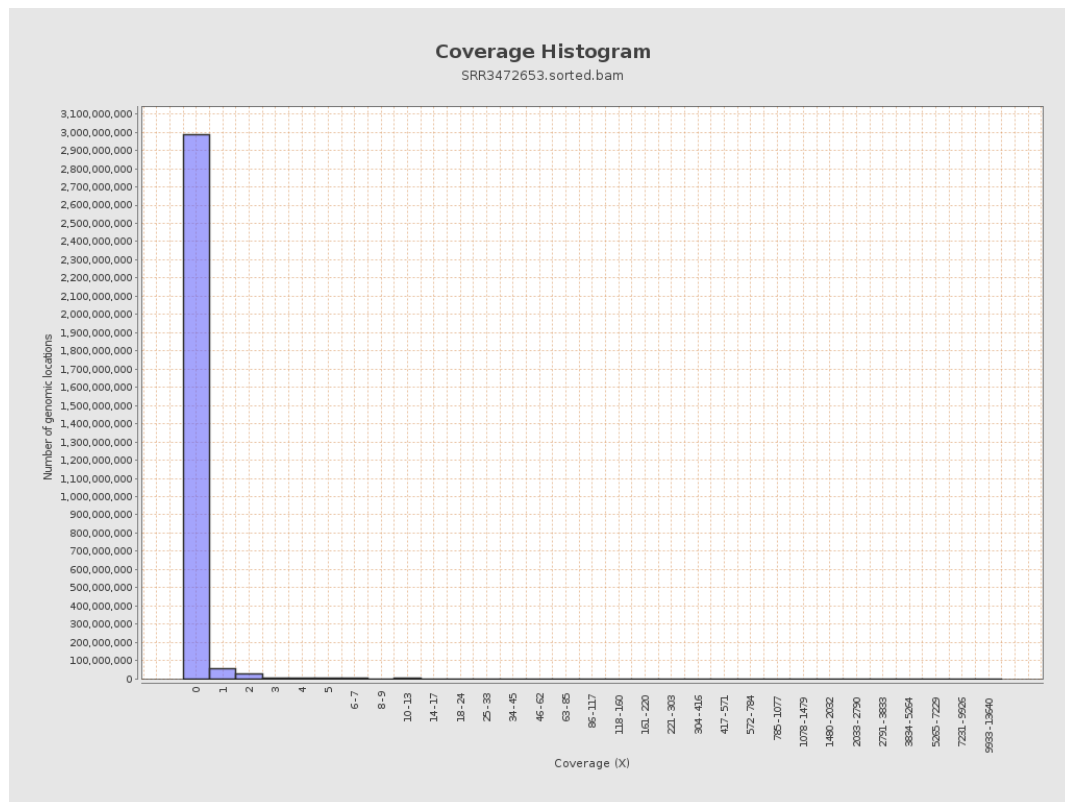
		bases	coverage	deviation
chr1	249250621	212460712	0.8524	45.0367
chr2	243199373	147399146	0.6061	25.3006
chr3	198022430	174017107	0.8788	35.0453
chr4	191154276	35231368	0.1843	7.9704
chr5	180915260	62009139	0.3428	15.0584
chr6	171115067	143612829	0.8393	30.4381
chr7	159138663	105651623	0.6639	30.0279
chr8	146364022	107275525	0.7329	27.4768
chr9	141213431	112442290	0.7963	24.6419
chr10	135534747	25550832	0.1885	10.1557
chr11	135006516	39807044	0.2949	11.4374
chr12	133851895	44951635	0.3358	12.9756
chr13	115169878	64909551	0.5636	26.6283
chr14	107349540	26609165	0.2479	10.793
chr15	102531392	20087295	0.1959	14.7109
chr16	90354753	94290773	1.0436	34.7425
chr17	81195210	56973925	0.7017	20.434
chr18	78077248	2528083	0.0324	1.2737
chr19	59128983	50590912	0.8556	37.6121
chr20	63025520	89089708	1.4135	55.1656
chr21	48129895	11099546	0.2306	16.2617
chr22	51304566	25630796	0.4996	17.7347
chrMT	16571	5996	0.3618	0.6929
chrX	155270560	82558269	0.5317	17.4724

chrY	59373566	2789084	0.047	4.0425
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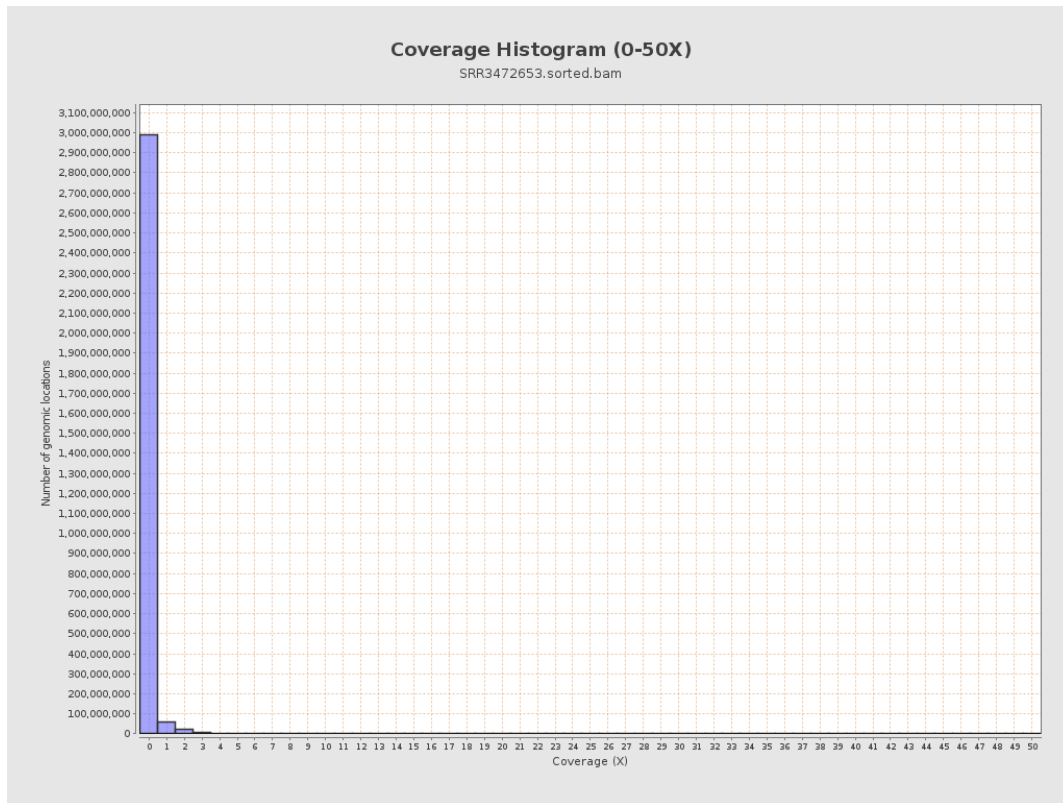
3. Results : Coverage across reference



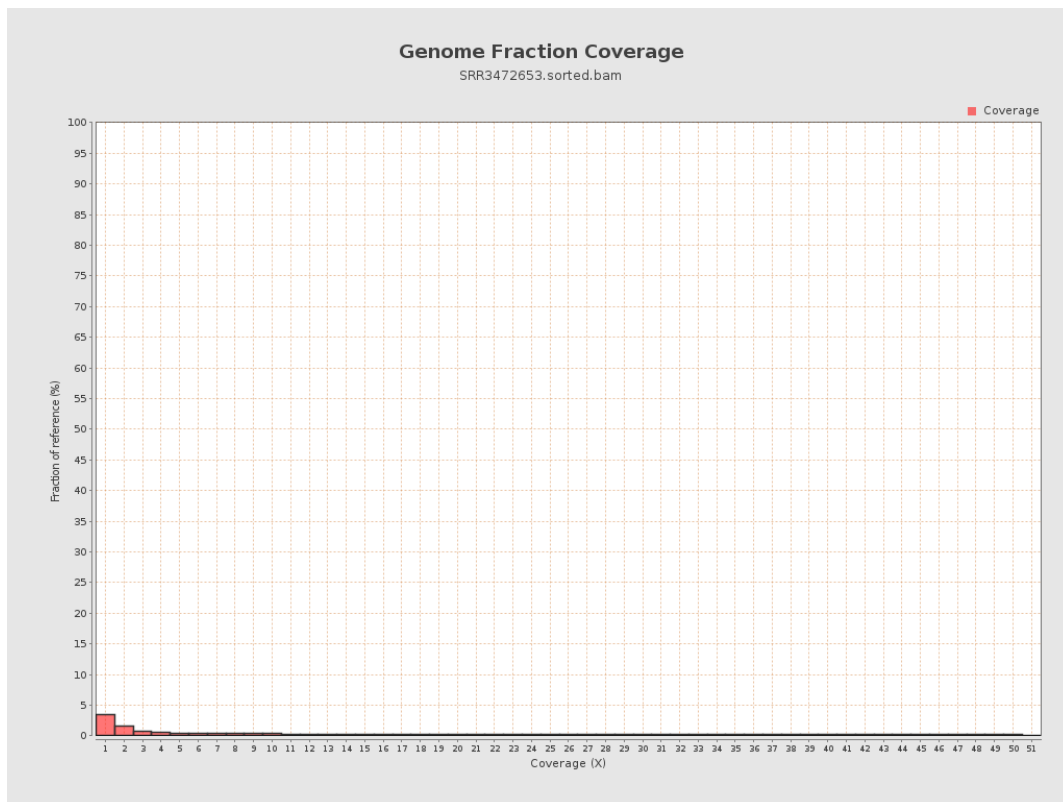
4. Results : Coverage Histogram



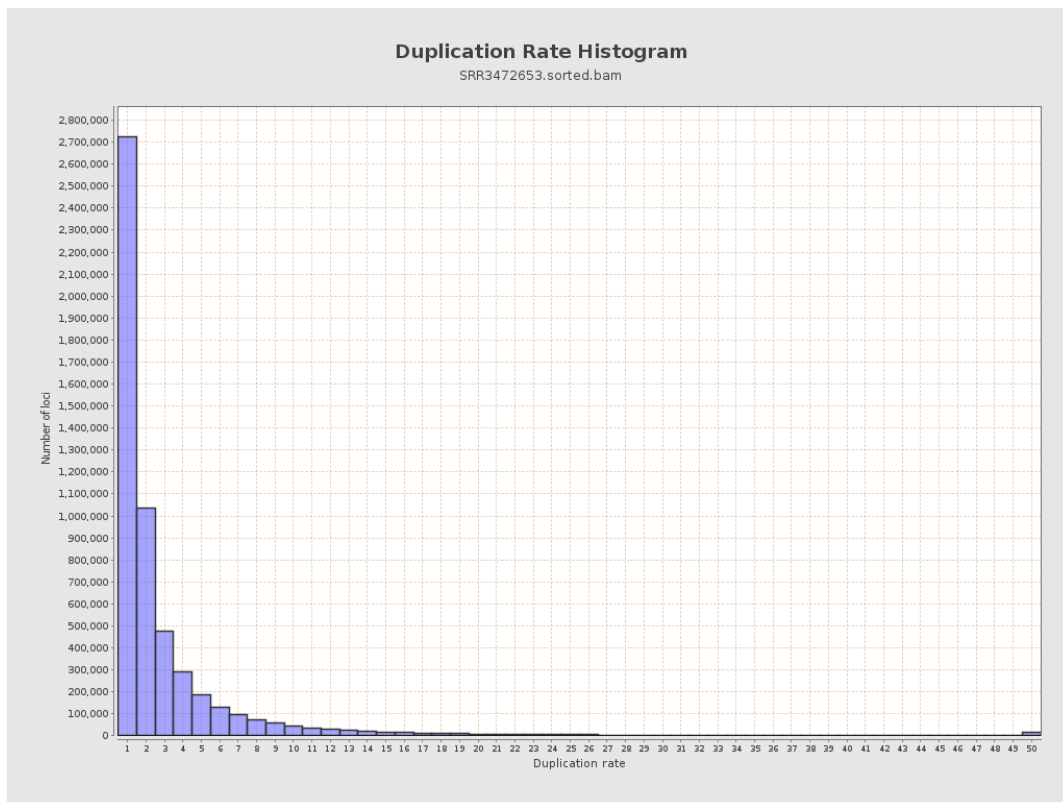
5. Results : Coverage Histogram (0-50X)



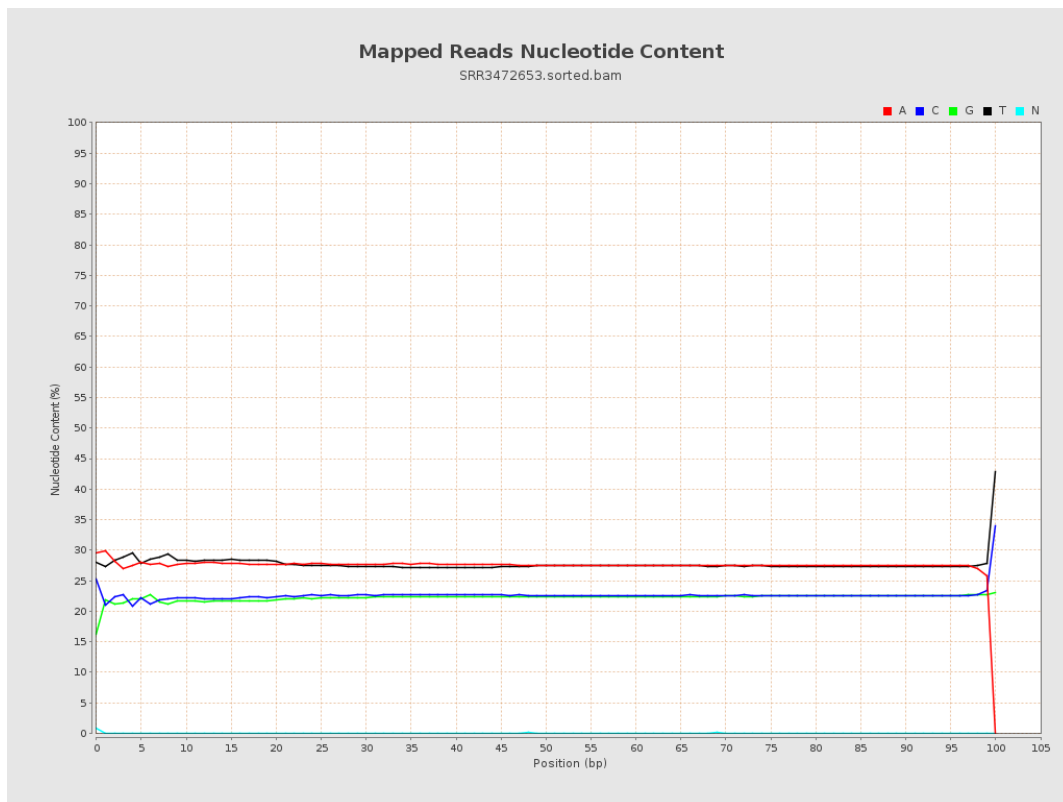
6. Results : Genome Fraction Coverage



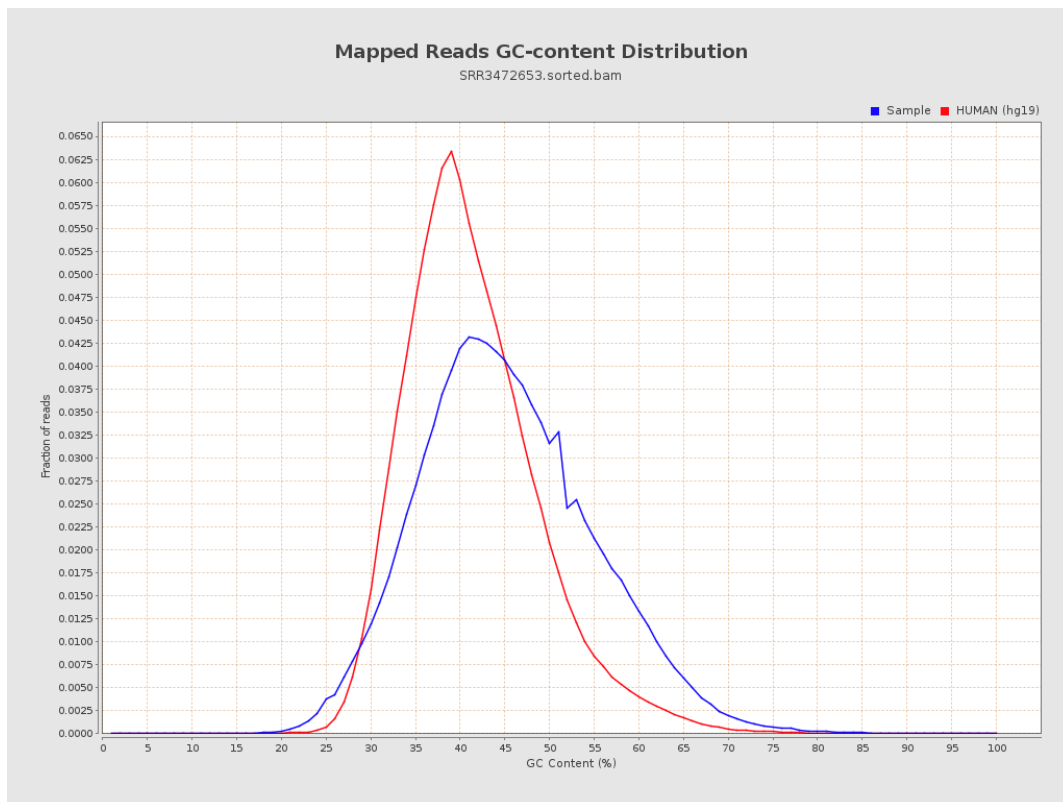
7. Results : Duplication Rate Histogram



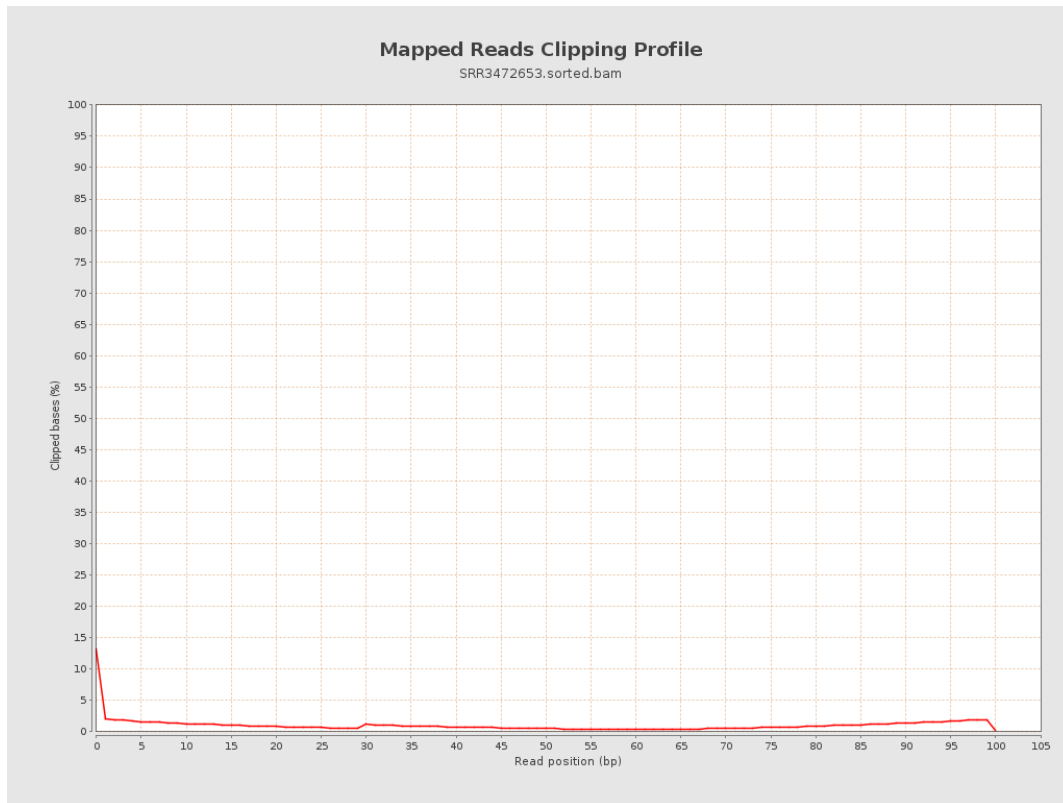
8. Results : Mapped Reads Nucleotide Content



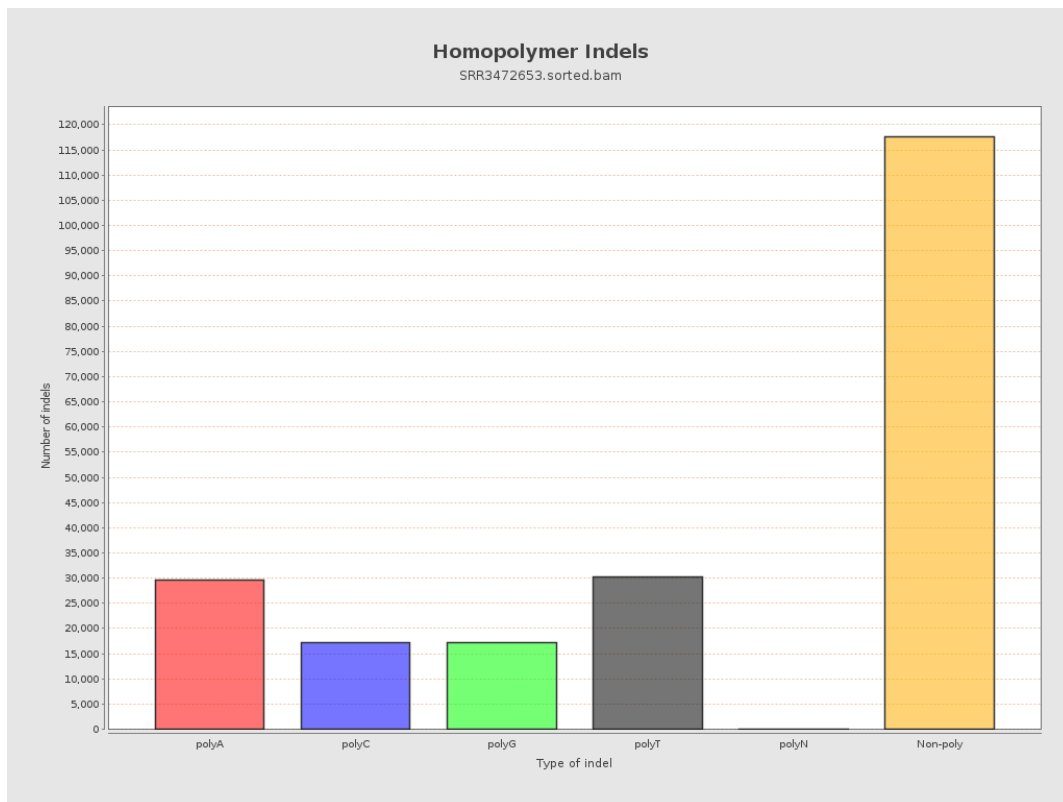
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



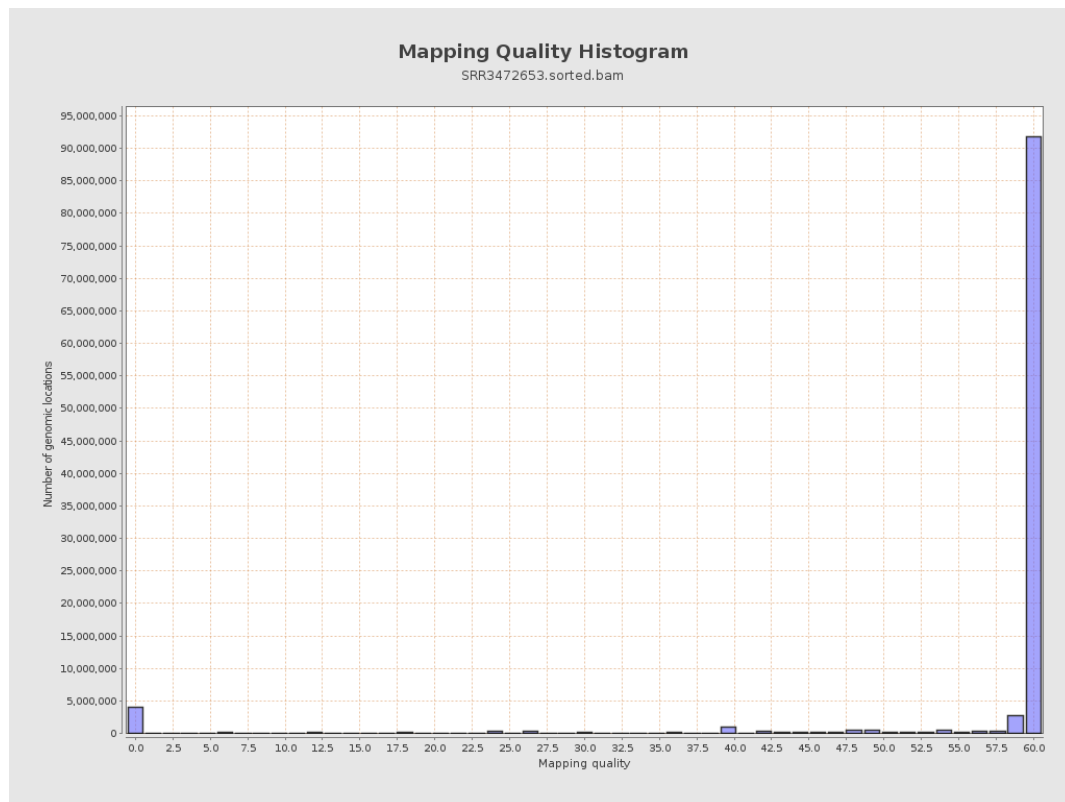
11. Results : Homopolymer Indels



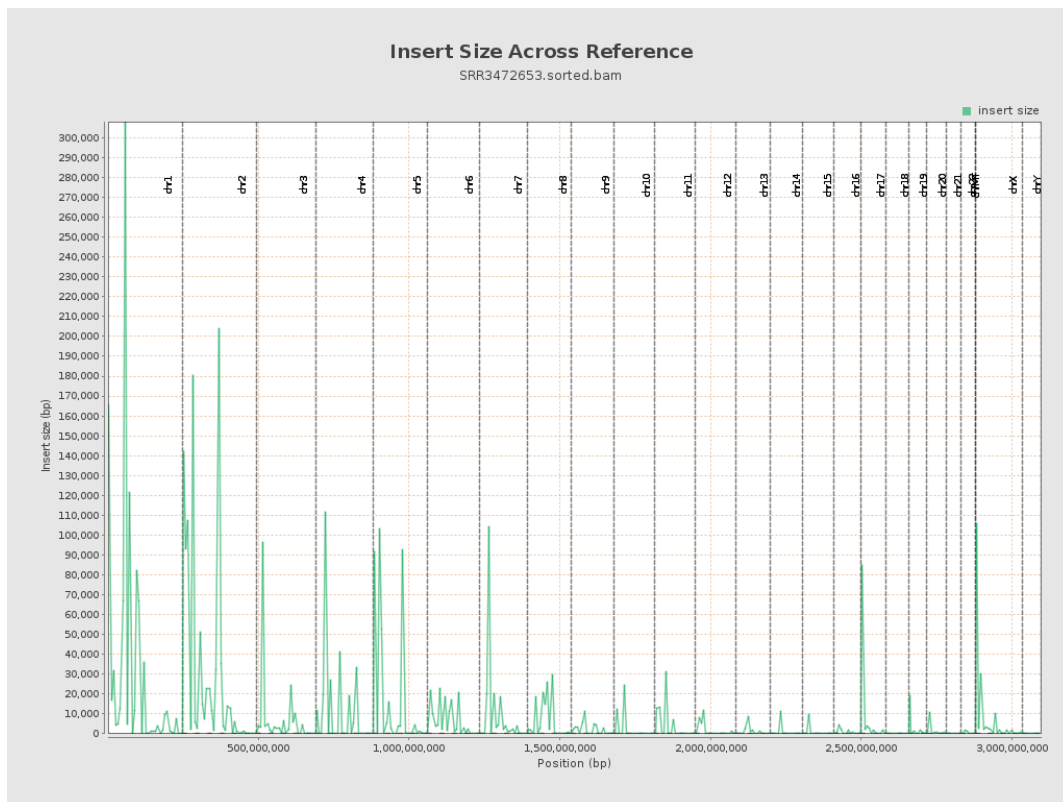
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

