

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 16:45:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472712.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_SRR3472712 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472712_1.fastq.gz SRR3472712_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 16:45:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472712.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	174,910
Mapped reads	173,009 / 98.91%
Unmapped reads	1,901 / 1.09%
Mapped paired reads	173,009 / 98.91%
Mapped reads, first in pair	86,896 / 49.68%
Mapped reads, second in pair	86,113 / 49.23%
Mapped reads, both in pair	171,876 / 98.27%
Mapped reads, singletons	1,133 / 0.65%
Secondary alignments	0
Supplementary alignments	617 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	35,598 / 20.35%
Duplication rate	20.64%
Clipped reads	12,257 / 7.01%

2.2. ACGT Content

Number/percentage of A's	4,718,018 / 27.62%
Number/percentage of C's	3,853,458 / 22.56%
Number/percentage of T's	4,689,814 / 27.46%
Number/percentage of G's	3,815,567 / 22.34%
Number/percentage of N's	3,162 / 0.02%

GC Percentage	44.9%
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2.3. Coverage

Mean	0.0055
Standard Deviation	0.1956

2.4. Mapping Quality

Mean Mapping Quality	54.96
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2.5. Insert size

Mean	22,218.49
Standard Deviation	1,487,026.57
P25/Median/P75	175 / 242 / 325

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	105,866
Insertions	983
Mapped reads with at least one insertion	0.56%
Deletions	949
Mapped reads with at least one deletion	0.54%
Homopolymer indels	44.36%

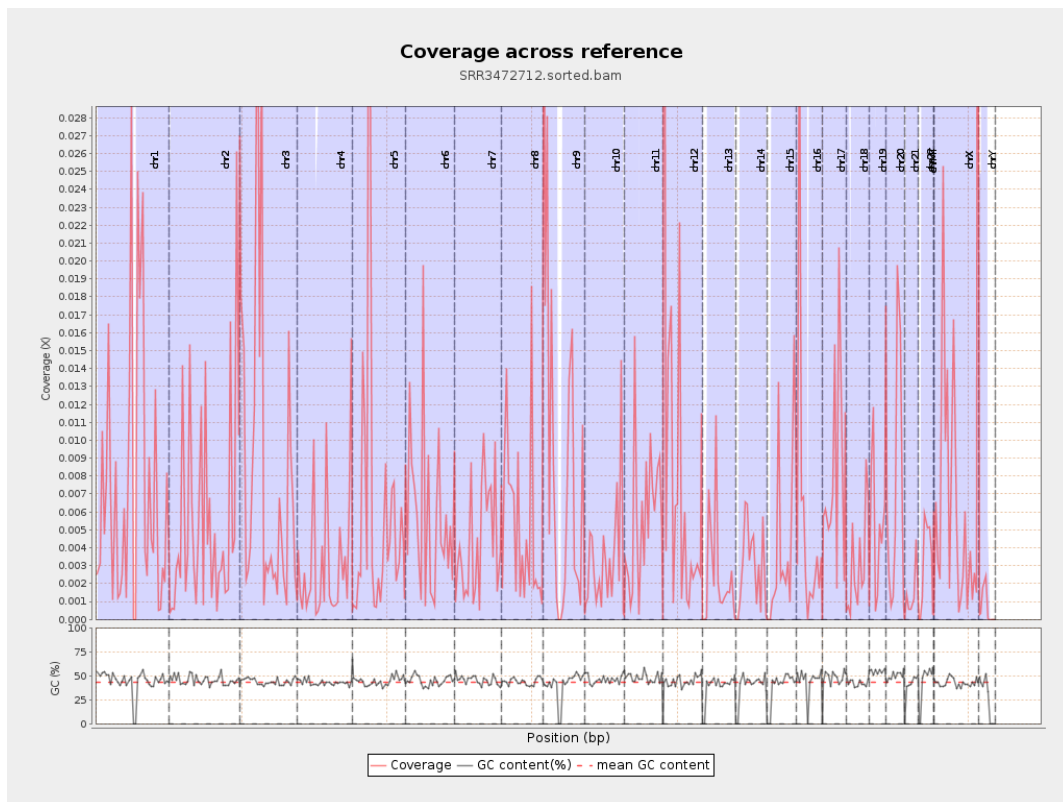
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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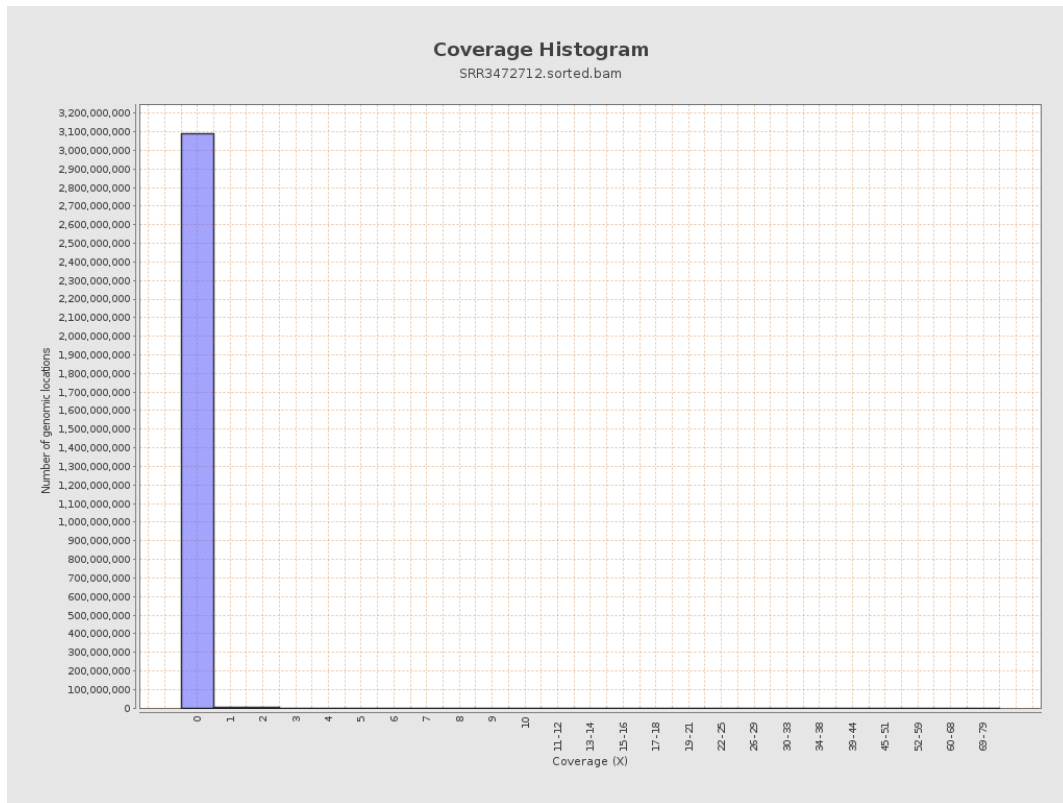
		bases	coverage	deviation
chr1	249250621	1816312	0.0073	0.2342
chr2	243199373	1343279	0.0055	0.2394
chr3	198022430	1733862	0.0088	0.2269
chr4	191154276	594271	0.0031	0.1301
chr5	180915260	1105899	0.0061	0.212
chr6	171115067	982784	0.0057	0.1736
chr7	159138663	682185	0.0043	0.1518
chr8	146364022	754413	0.0052	0.1685
chr9	141213431	1098694	0.0078	0.2096
chr10	135534747	470533	0.0035	0.1486
chr11	135006516	765996	0.0057	0.2368
chr12	133851895	1219533	0.0091	0.3099
chr13	115169878	289780	0.0025	0.1091
chr14	107349540	322905	0.003	0.1084
chr15	102531392	428372	0.0042	0.1658
chr16	90354753	522683	0.0058	0.1836
chr17	81195210	656244	0.0081	0.1914
chr18	78077248	241468	0.0031	0.1125
chr19	59128983	334898	0.0057	0.1572
chr20	63025520	428751	0.0068	0.274
chr21	48129895	68706	0.0014	0.074
chr22	51304566	164268	0.0032	0.1134
chrMT	16571	100	0.006	0.0774
chrX	155270560	1019606	0.0066	0.2118

chrY	59373566	36876	0.0006	0.0511
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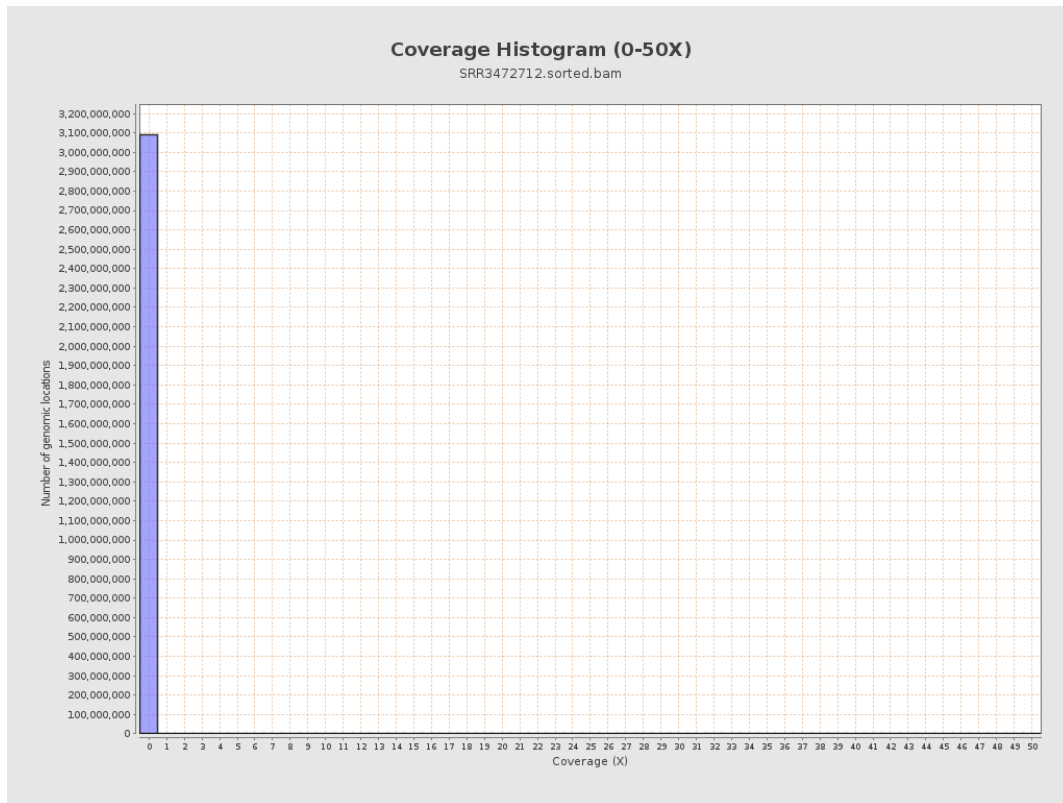
3. Results : Coverage across reference



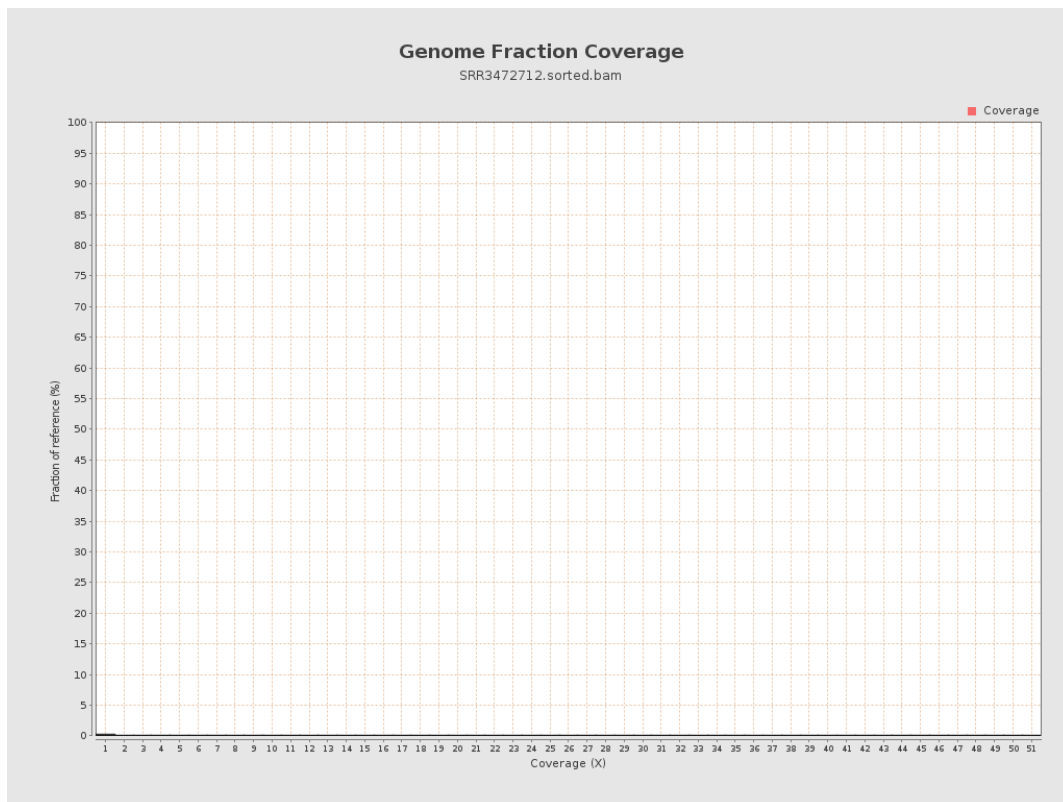
4. Results : Coverage Histogram



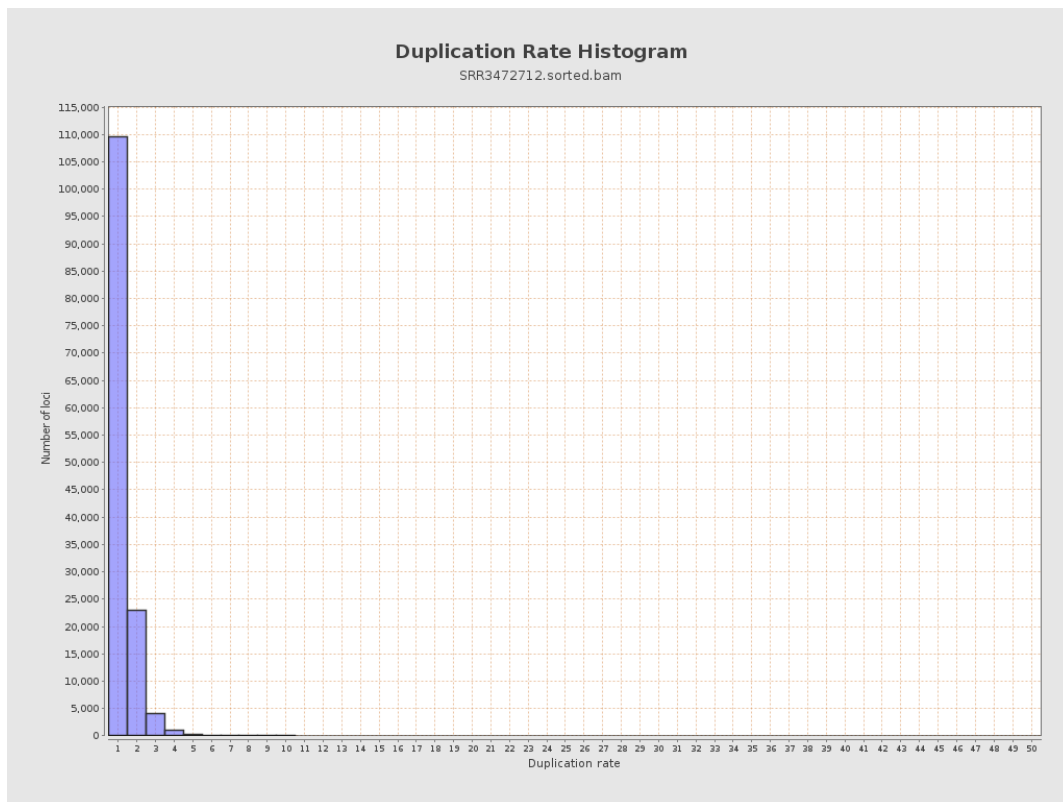
5. Results : Coverage Histogram (0-50X)



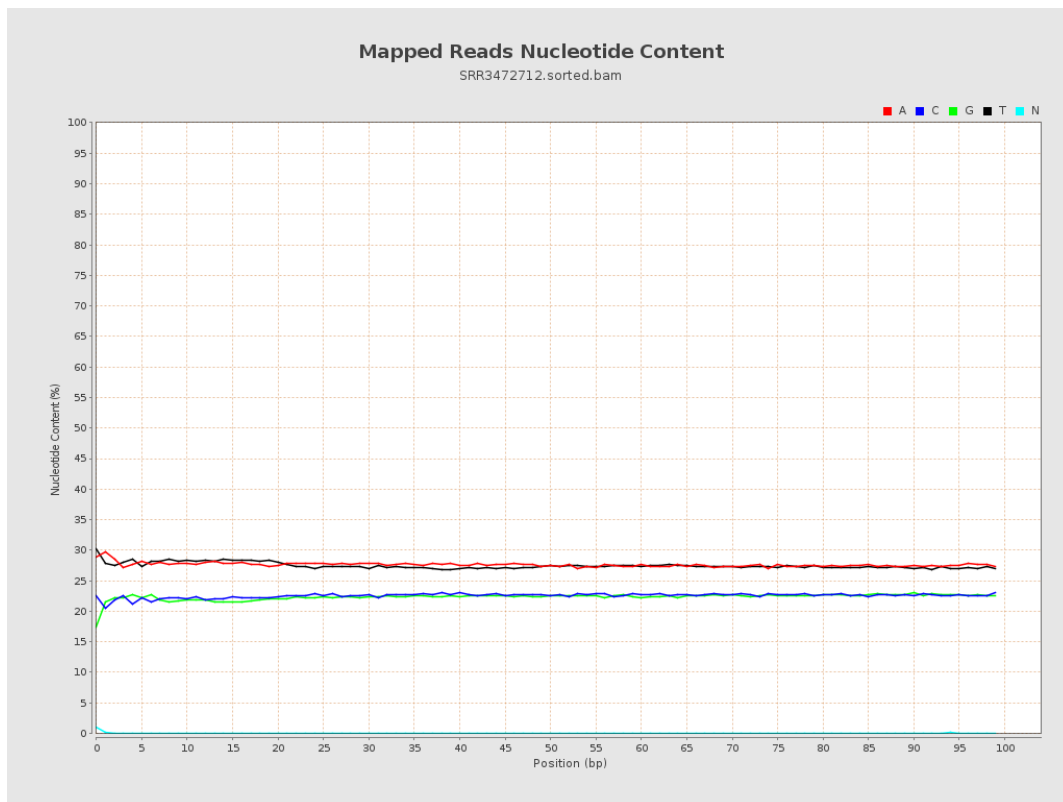
6. Results : Genome Fraction Coverage



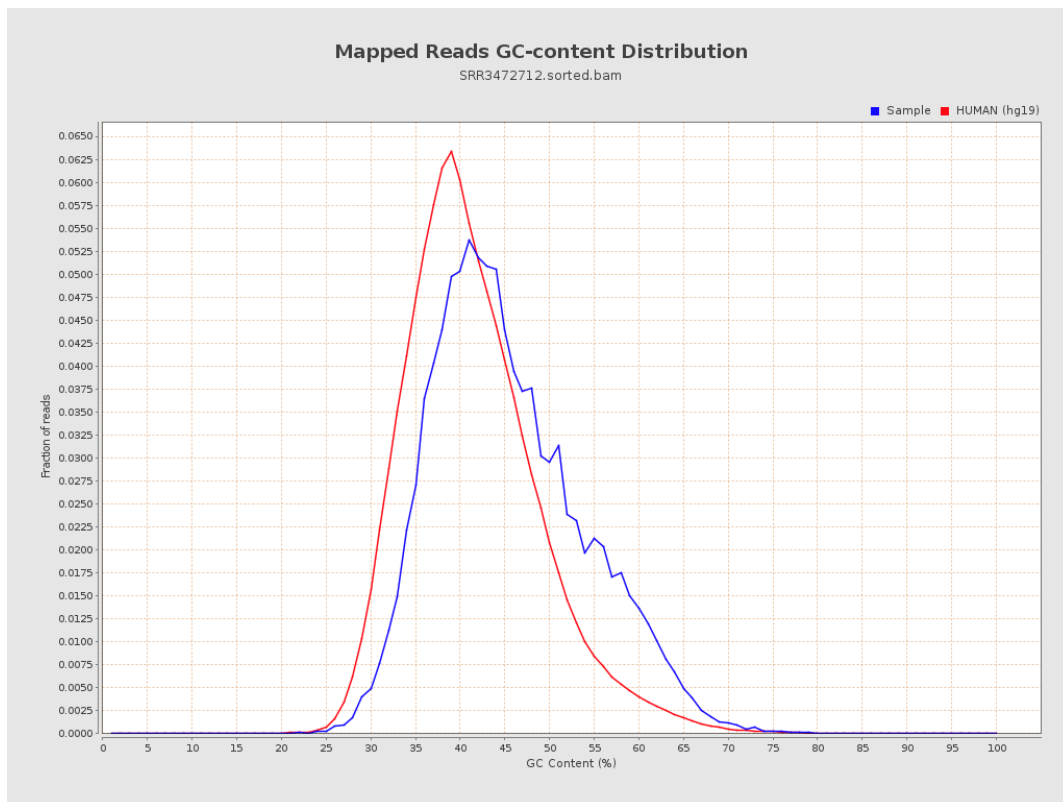
7. Results : Duplication Rate Histogram



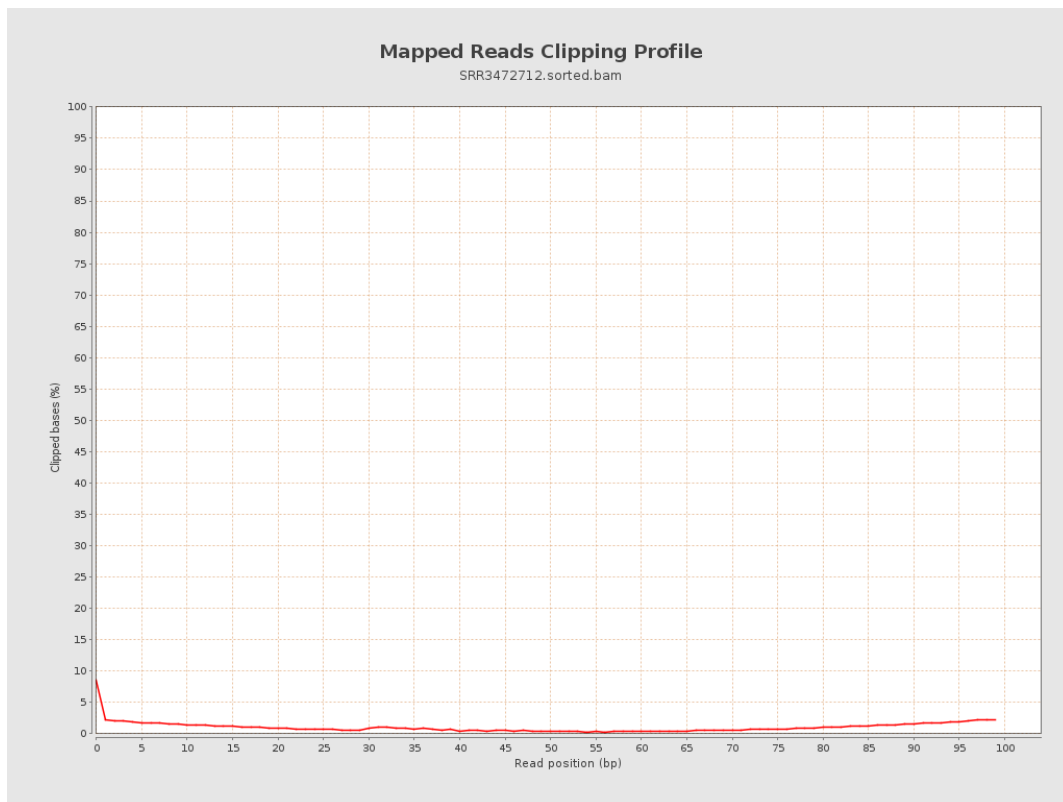
8. Results : Mapped Reads Nucleotide Content



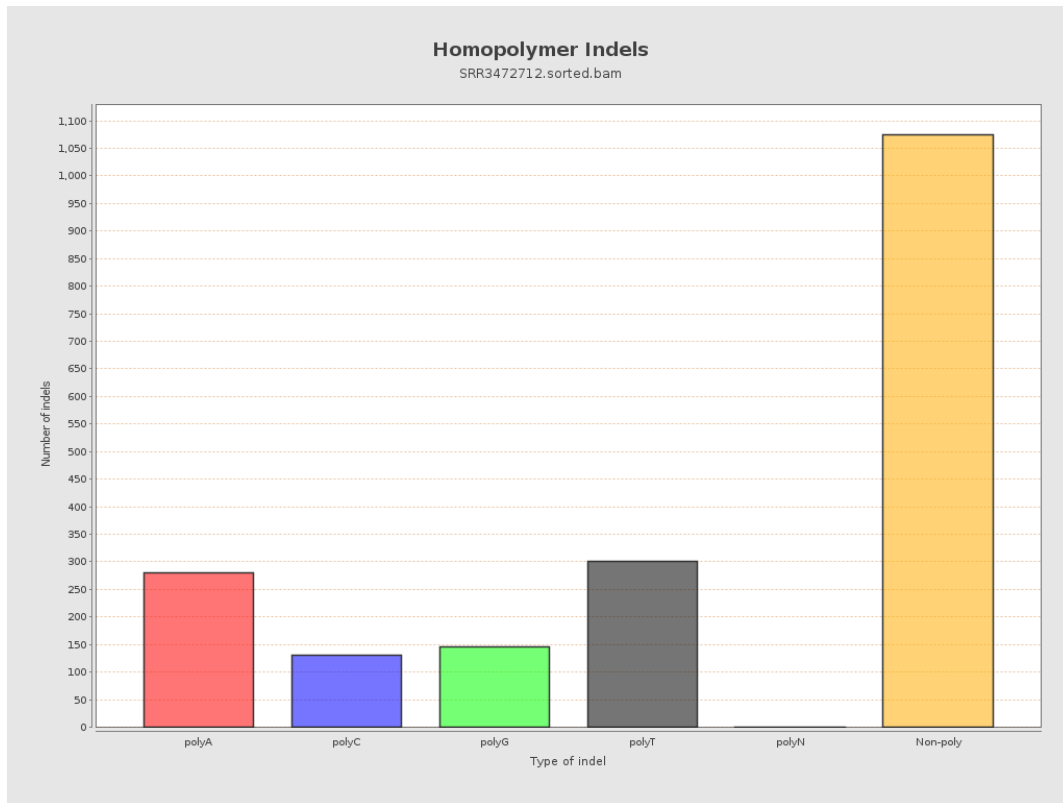
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



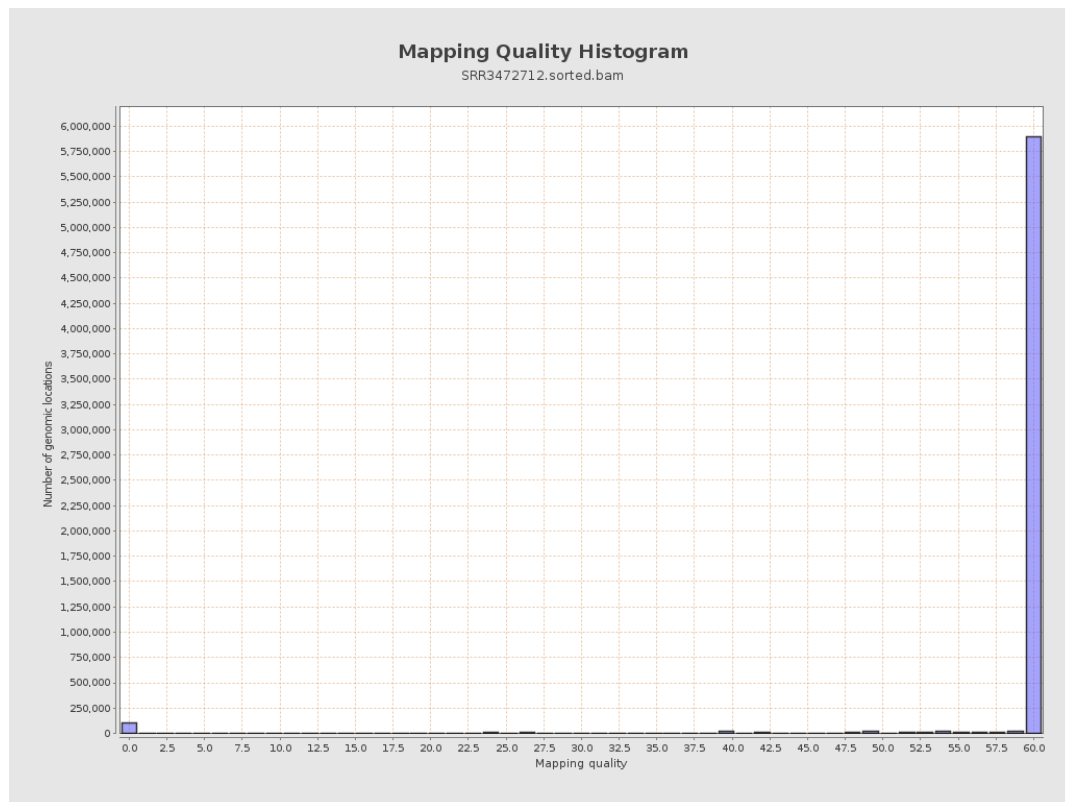
11. Results : Homopolymer Indels



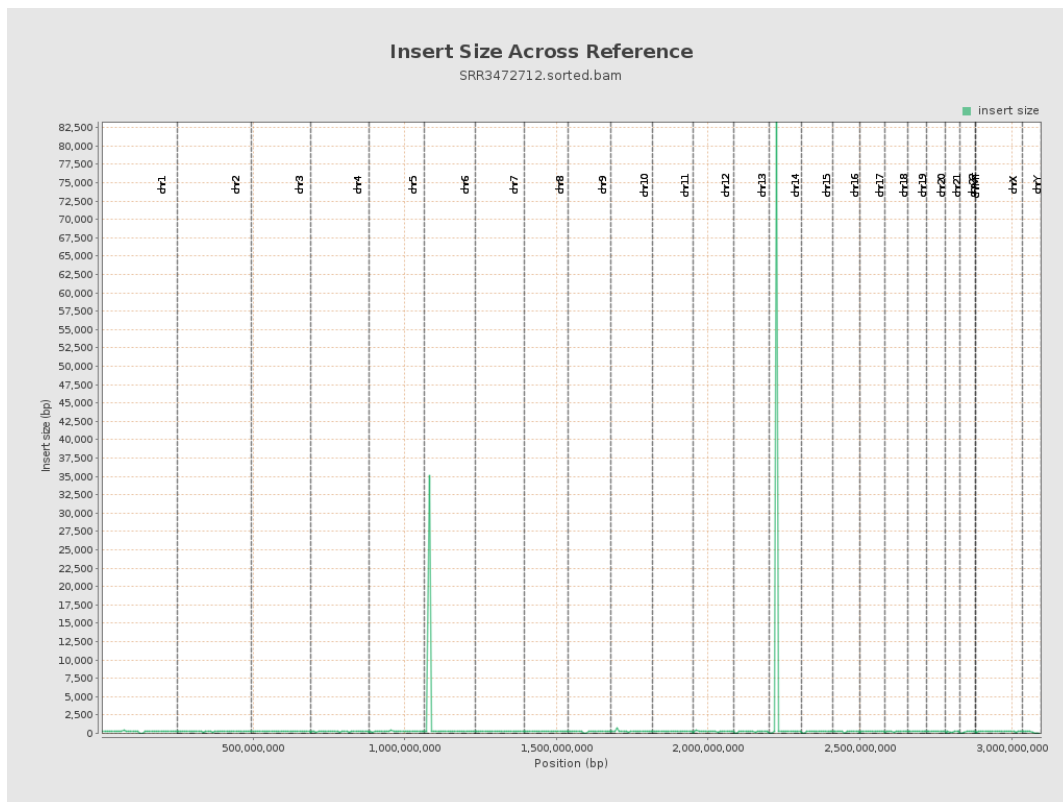
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

