

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 05:40:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472595.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_SRR3472595 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472595_1.fastq.gz SRR3472595_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 05:40:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472595.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,752,098
Mapped reads	10,035,844 / 93.34%
Unmapped reads	716,254 / 6.66%
Mapped paired reads	10,035,844 / 93.34%
Mapped reads, first in pair	5,061,770 / 47.08%
Mapped reads, second in pair	4,974,074 / 46.26%
Mapped reads, both in pair	9,841,830 / 91.53%
Mapped reads, singletons	194,014 / 1.8%
Secondary alignments	0
Supplementary alignments	187,908 / 1.75%
Read min/max/mean length	30 / 100 / 100.67
Duplicated reads (estimated)	1,875,340 / 17.44%
Duplication rate	16.11%
Clipped reads	7,010,223 / 65.2%

2.2. ACGT Content

Number/percentage of A's	215,908,124 / 26.11%
Number/percentage of C's	166,219,282 / 20.1%
Number/percentage of T's	245,012,702 / 29.63%
Number/percentage of G's	199,261,826 / 24.1%
Number/percentage of N's	546,274 / 0.07%

GC Percentage	44.2%
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2.3. Coverage

Mean	0.2672
Standard Deviation	2.0788

2.4. Mapping Quality

Mean Mapping Quality	51.36
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2.5. Insert size

Mean	116,627.69
Standard Deviation	3,263,241.01
P25/Median/P75	92 / 132 / 183

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	9,273,923
Insertions	72,006
Mapped reads with at least one insertion	0.7%
Deletions	190,583
Mapped reads with at least one deletion	1.86%
Homopolymer indels	43.88%

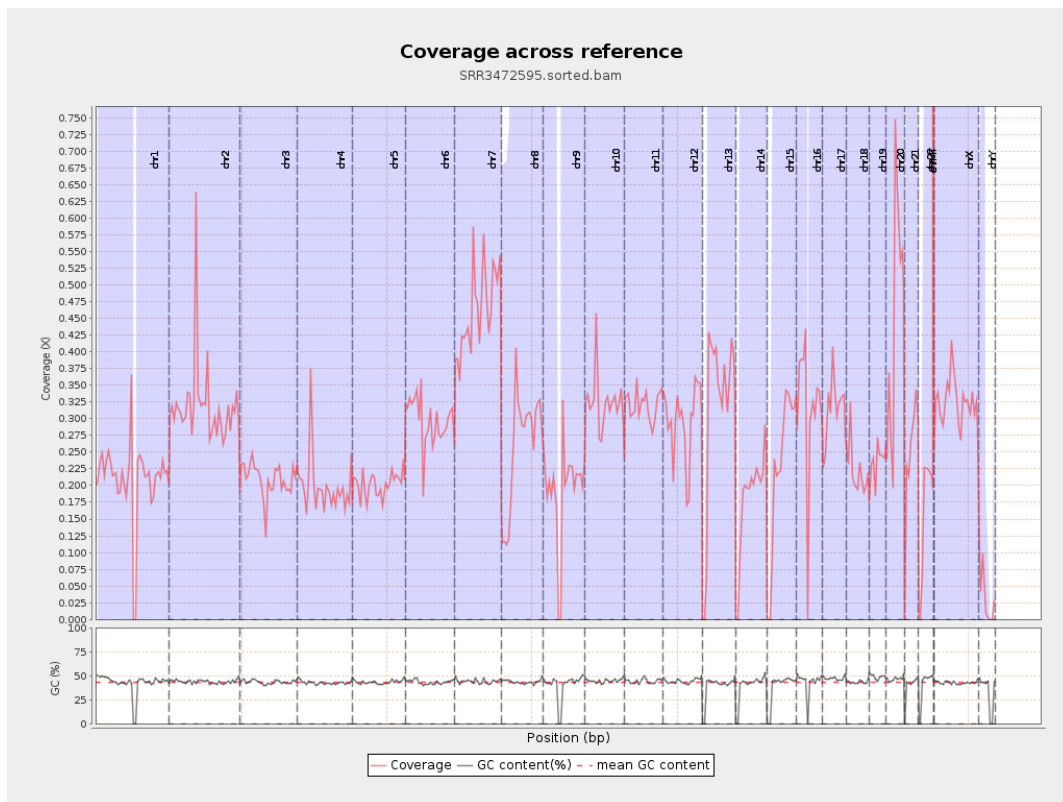
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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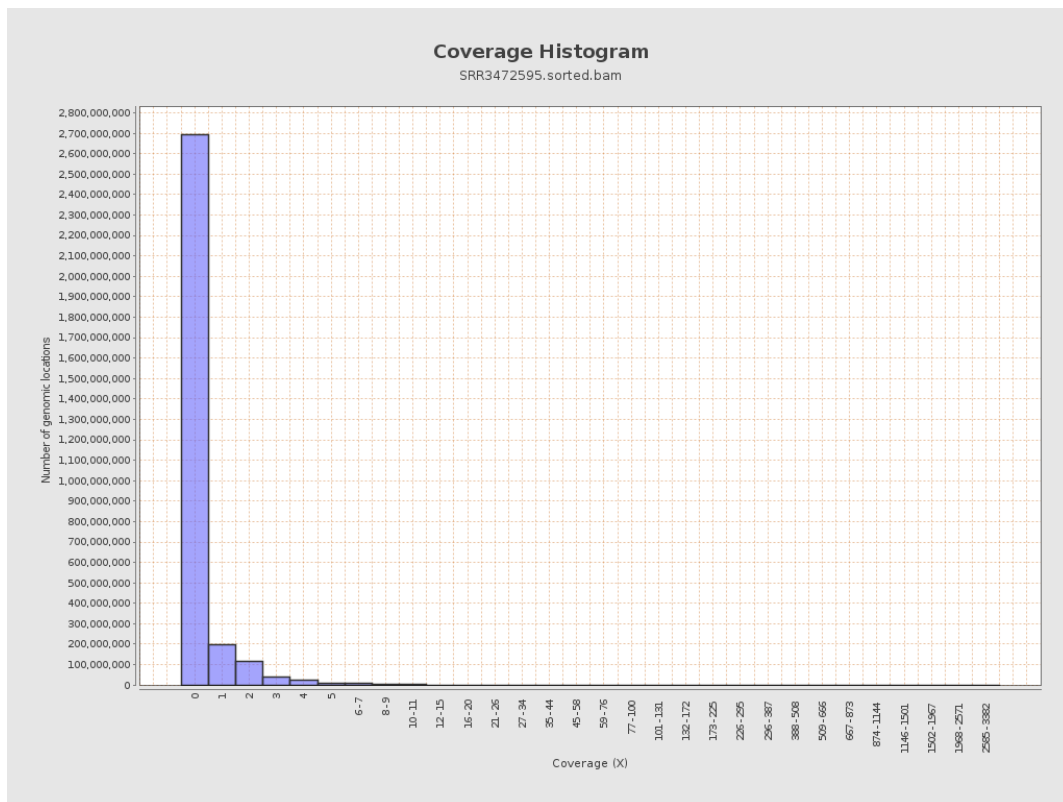
		bases	coverage	deviation
chr1	249250621	52141671	0.2092	2.9605
chr2	243199373	77747526	0.3197	2.6762
chr3	198022430	41425607	0.2092	0.7603
chr4	191154276	37800148	0.1977	1.1405
chr5	180915260	36468463	0.2016	0.764
chr6	171115067	50890589	0.2974	1.3143
chr7	159138663	73945221	0.4647	4.04
chr8	146364022	38071903	0.2601	1.795
chr9	141213431	26939184	0.1908	2.1902
chr10	135534747	43875644	0.3237	2.1594
chr11	135006516	43040599	0.3188	2.2368
chr12	133851895	39444627	0.2947	0.9383
chr13	115169878	36189739	0.3142	0.9741
chr14	107349540	19222311	0.1791	3.3849
chr15	102531392	23445129	0.2287	0.8188
chr16	90354753	28724808	0.3179	1.374
chr17	81195210	25613886	0.3155	1.6634
chr18	78077248	17456590	0.2236	3.4424
chr19	59128983	13934275	0.2357	2.0535
chr20	63025520	28514102	0.4524	1.3765
chr21	48129895	11976723	0.2488	1.0989
chr22	51304566	7812796	0.1523	0.6633
chrMT	16571	248044	14.9686	9.1869
chrX	155270560	50463463	0.325	1.3087

chrY	59373566	1913033	0.0322	0.8822
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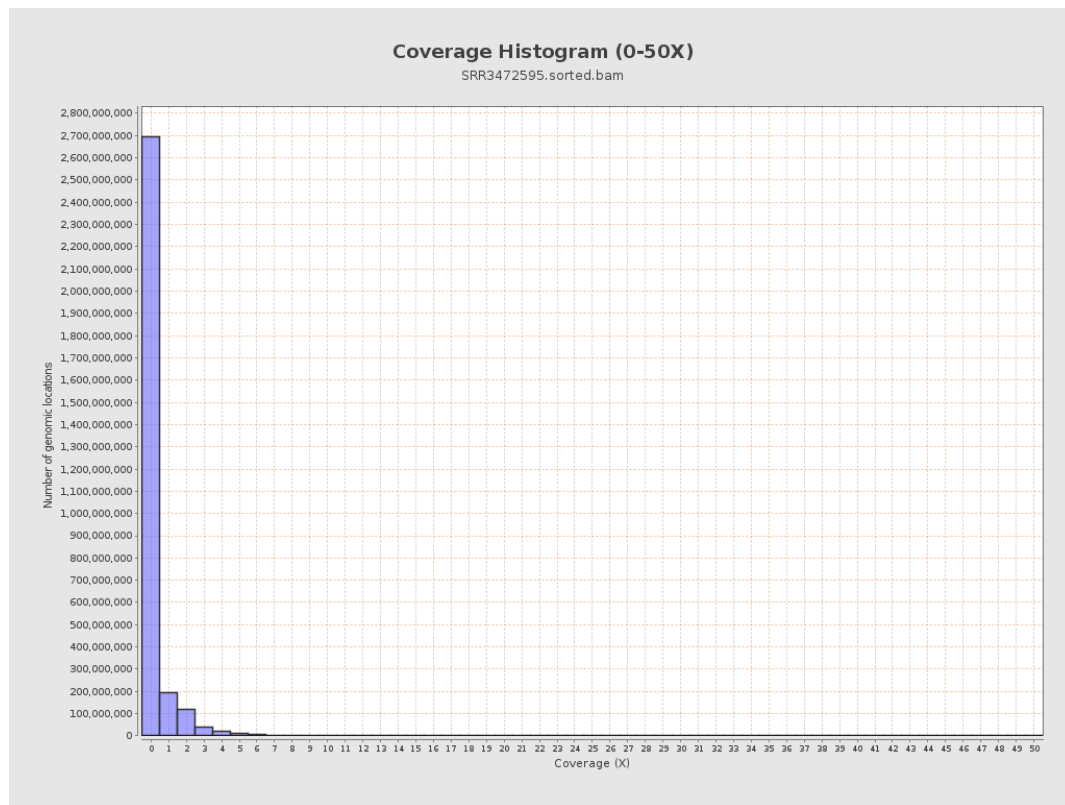
3. Results : Coverage across reference



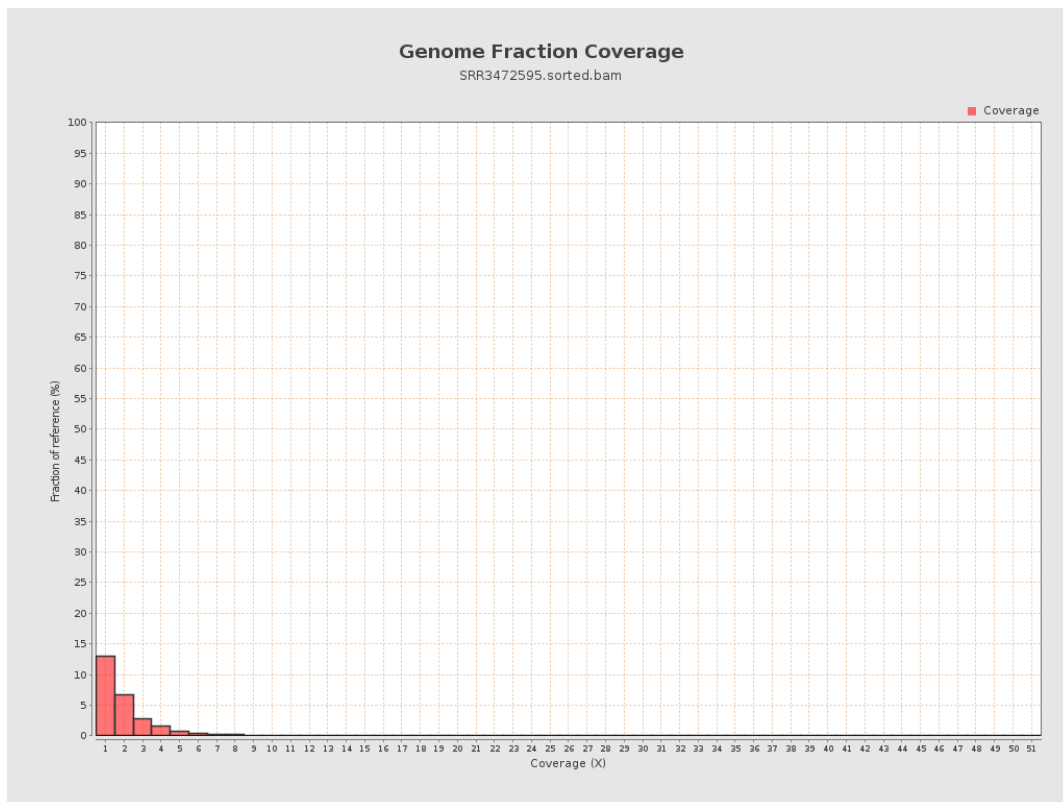
4. Results : Coverage Histogram



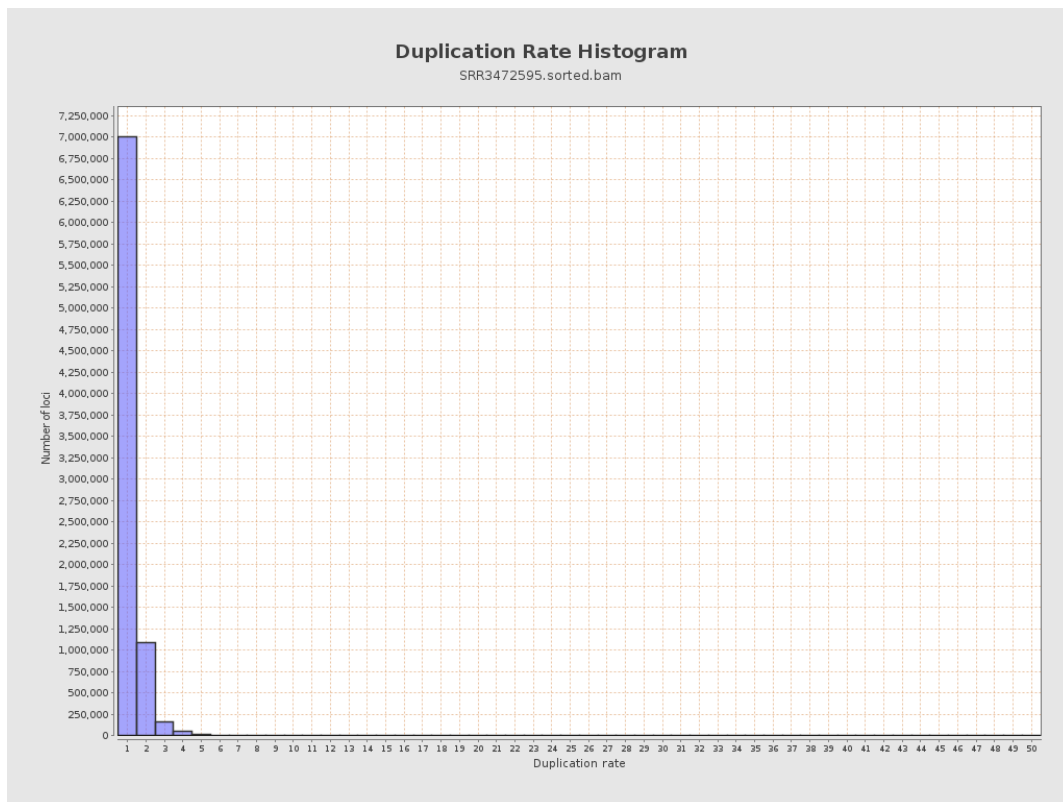
5. Results : Coverage Histogram (0-50X)



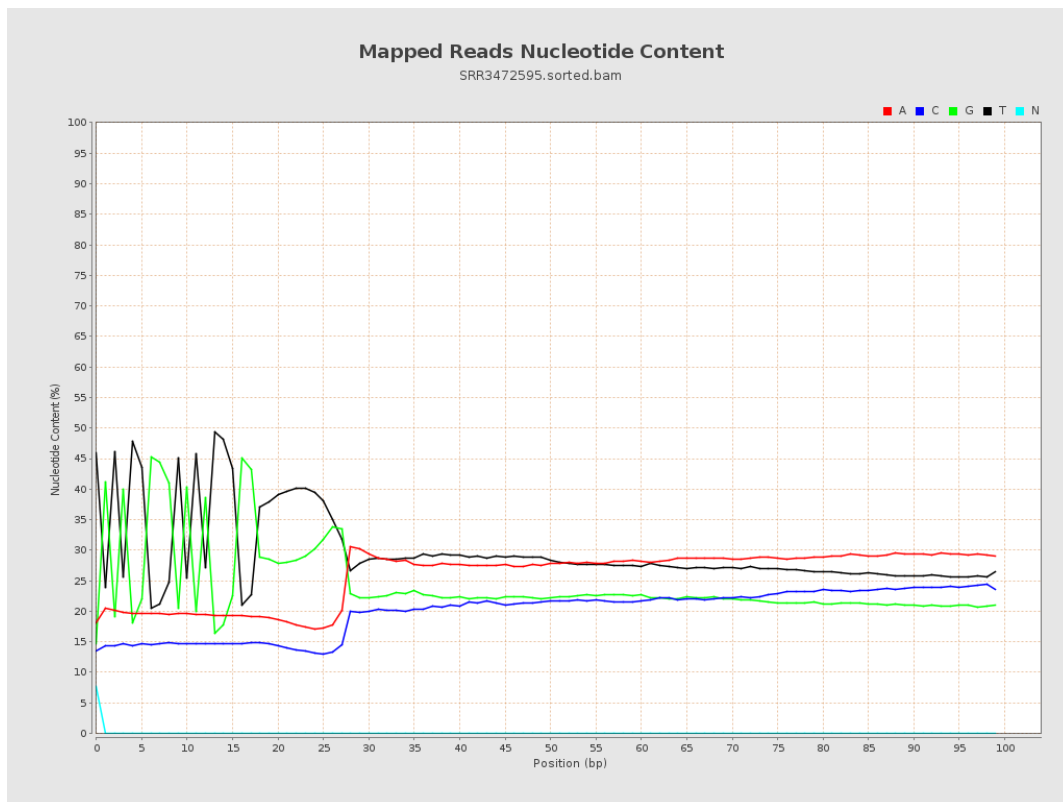
6. Results : Genome Fraction Coverage



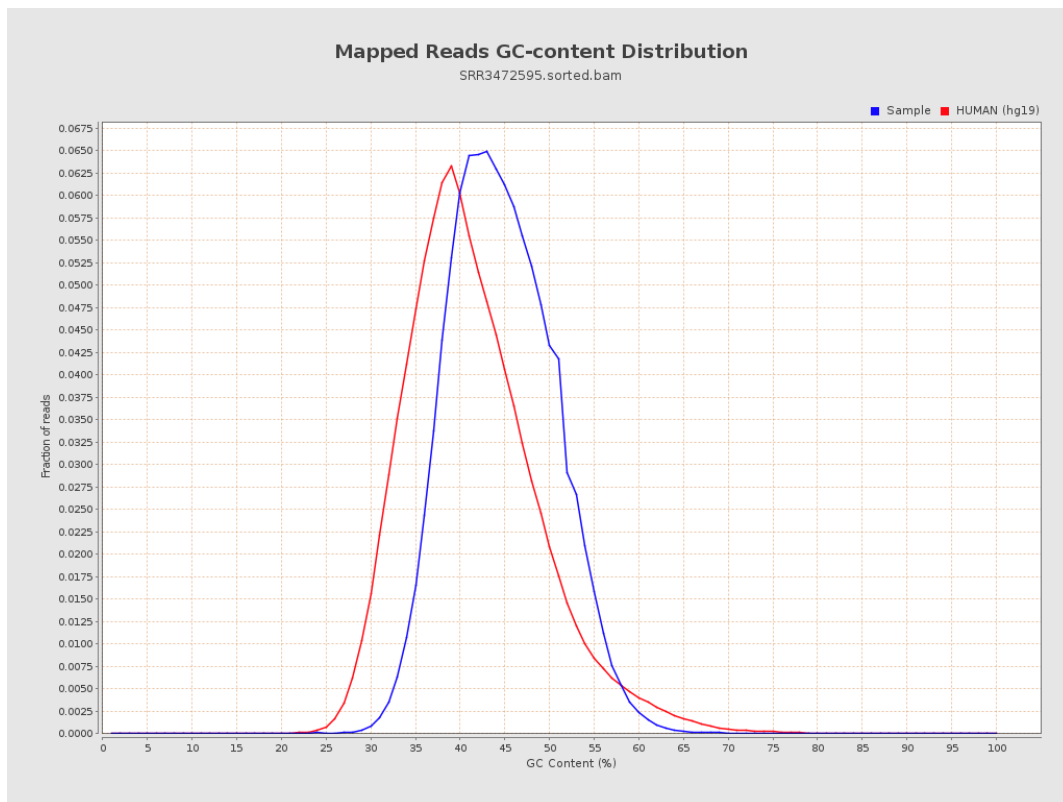
7. Results : Duplication Rate Histogram



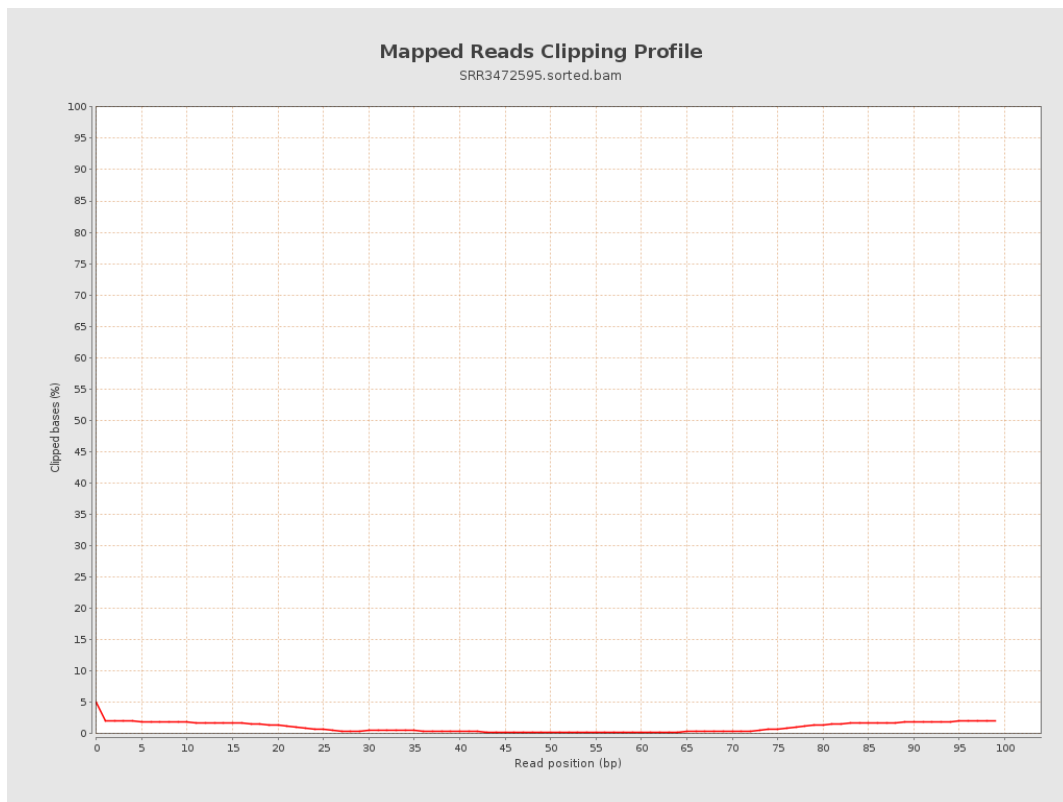
8. Results : Mapped Reads Nucleotide Content



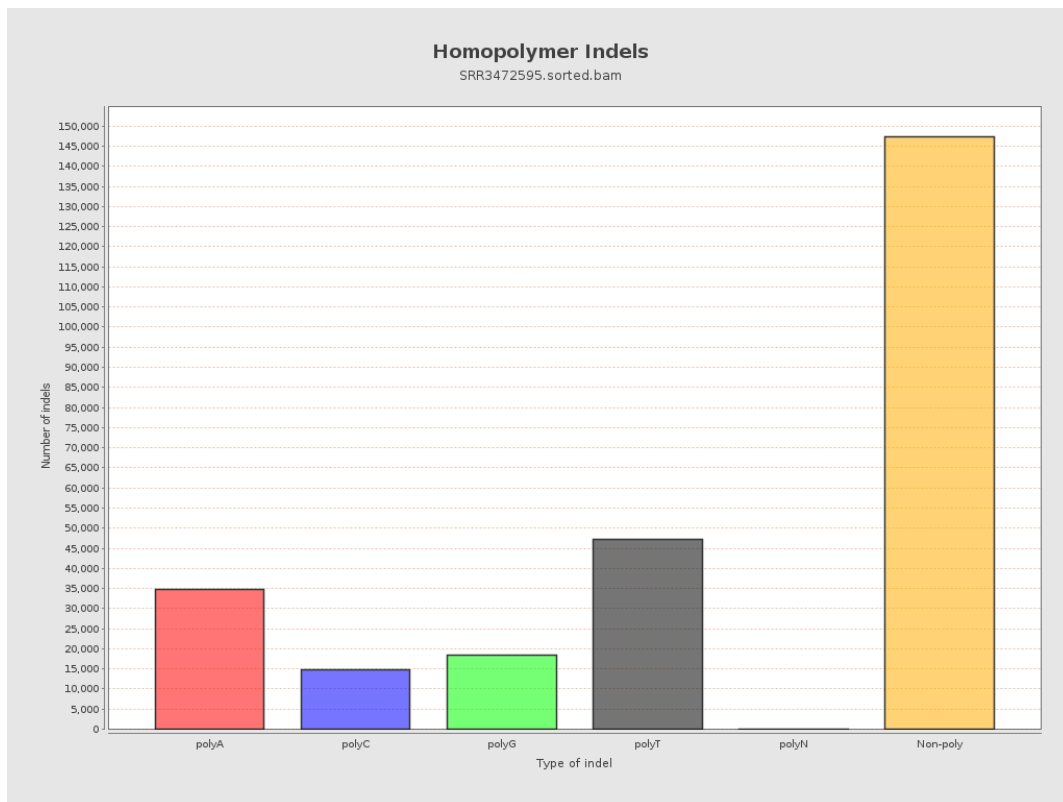
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



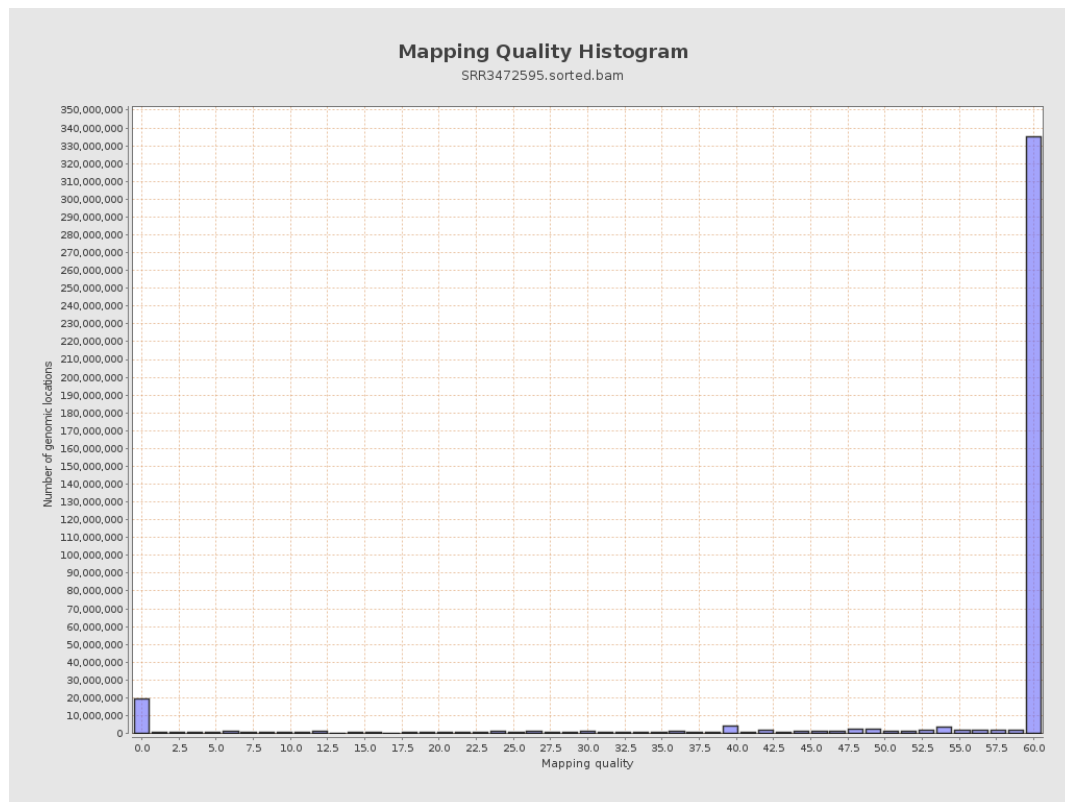
11. Results : Homopolymer Indels



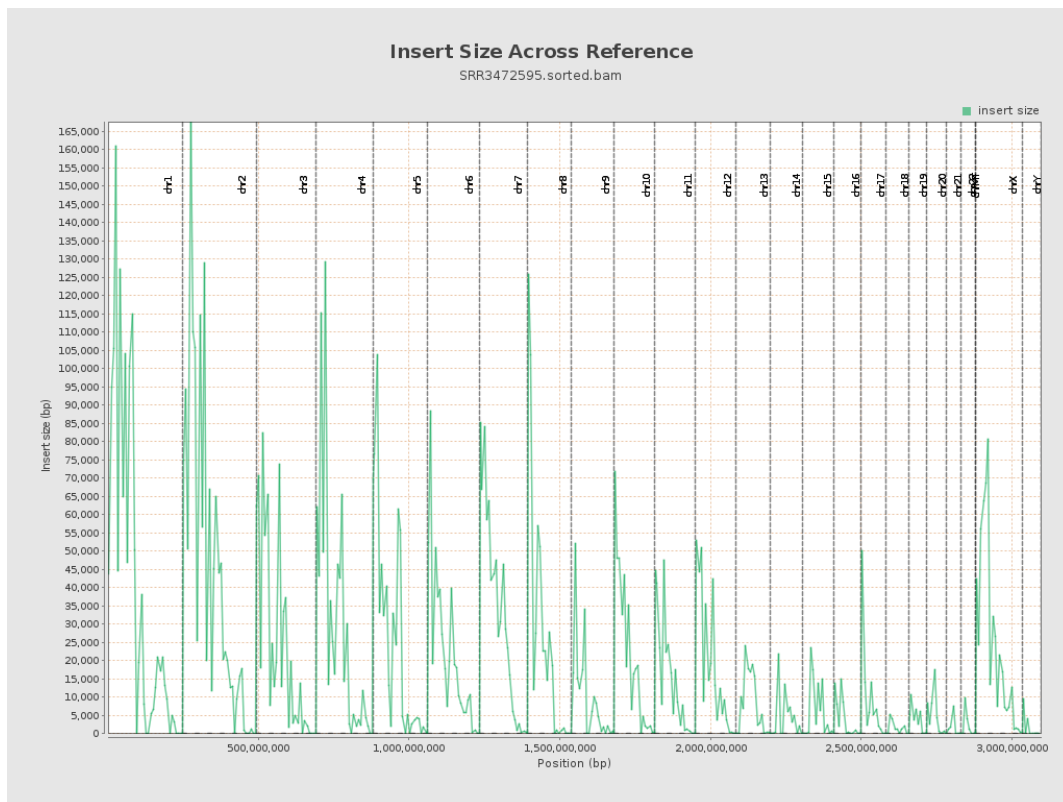
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

