

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 14:58:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472778.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_SRR3472778 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472778_1.fastq.gz SRR3472778_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 14:57:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472778.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,006,458
Mapped reads	17,816,615 / 98.95%
Unmapped reads	189,843 / 1.05%
Mapped paired reads	17,816,615 / 98.95%
Mapped reads, first in pair	8,947,349 / 49.69%
Mapped reads, second in pair	8,869,266 / 49.26%
Mapped reads, both in pair	17,698,180 / 98.29%
Mapped reads, singletons	118,435 / 0.66%
Secondary alignments	0
Supplementary alignments	62,933 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,139,390 / 61.86%
Duplication rate	46.86%
Clipped reads	1,328,805 / 7.38%

2.2. ACGT Content

Number/percentage of A's	491,348,085 / 27.98%
Number/percentage of C's	388,919,287 / 22.14%
Number/percentage of T's	488,447,941 / 27.81%
Number/percentage of G's	387,243,385 / 22.05%
Number/percentage of N's	336,499 / 0.02%

GC Percentage	44.19%
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2.3. Coverage

Mean	0.5674
Standard Deviation	18.2253

2.4. Mapping Quality

Mean Mapping Quality	55.1
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2.5. Insert size

Mean	24,831.01
Standard Deviation	1,560,821.72
P25/Median/P75	188 / 265 / 357

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	11,757,146
Insertions	120,585
Mapped reads with at least one insertion	0.67%
Deletions	102,503
Mapped reads with at least one deletion	0.57%
Homopolymer indels	44.45%

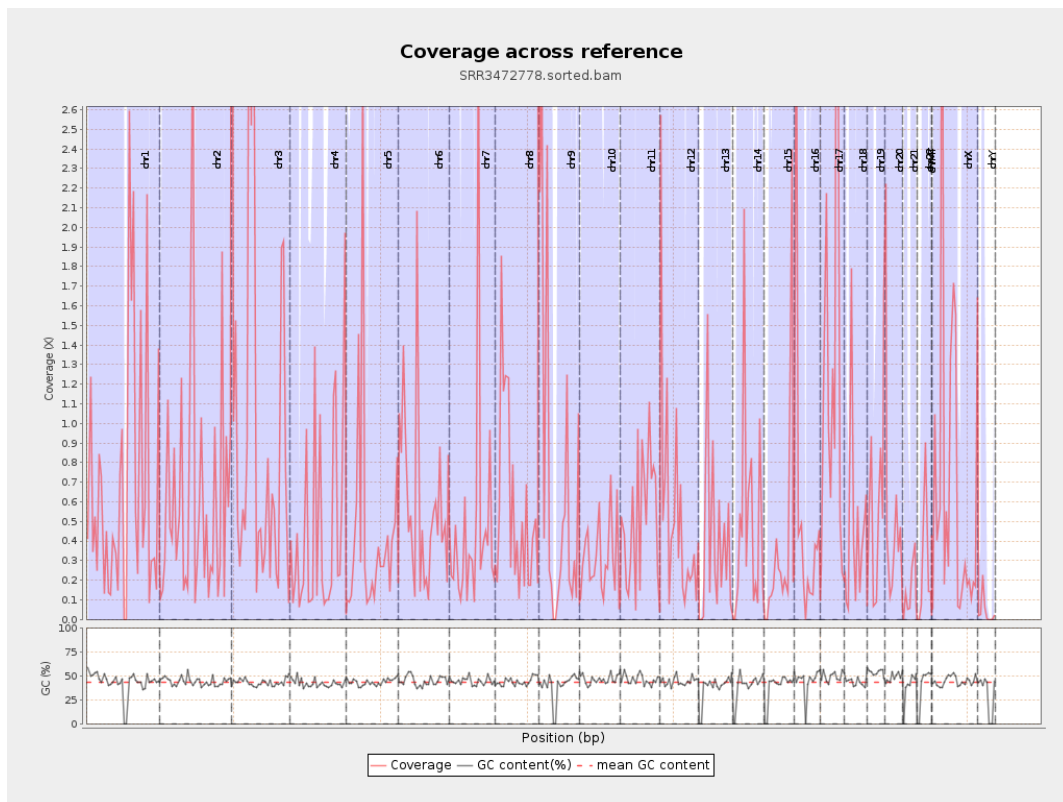
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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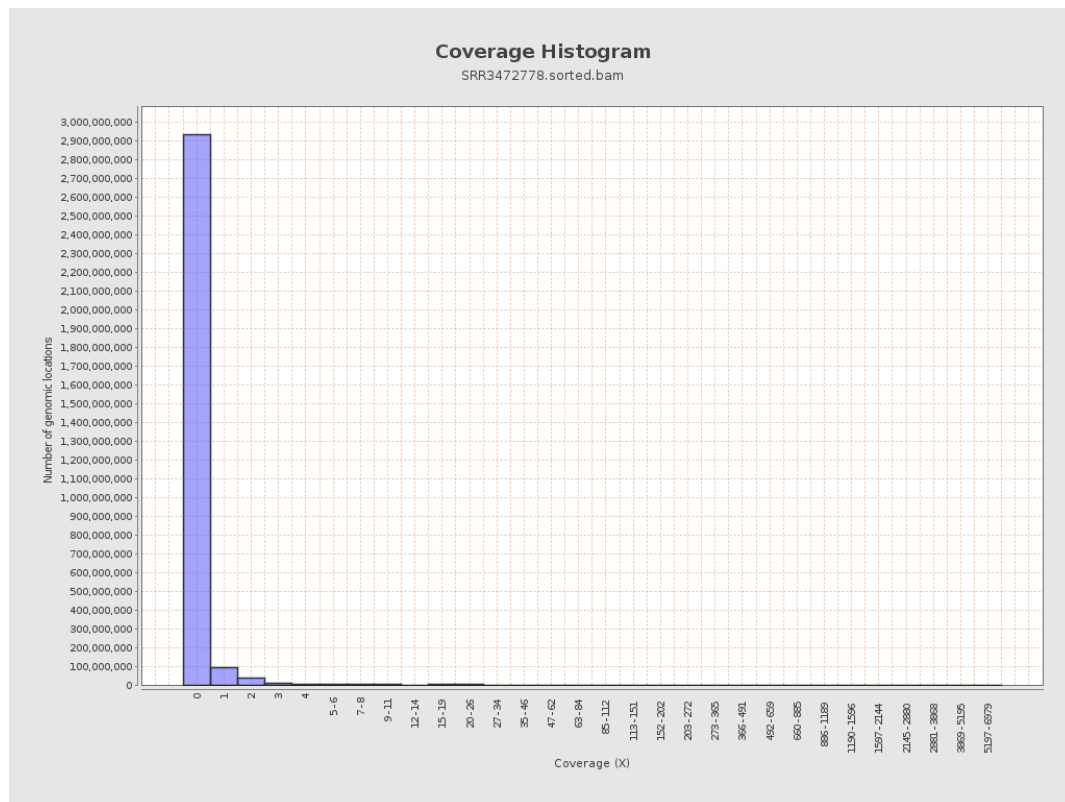
		bases	coverage	deviation
chr1	249250621	169865556	0.6815	20.7195
chr2	243199373	147494208	0.6065	22.8567
chr3	198022430	204720408	1.0338	21.2272
chr4	191154276	86567632	0.4529	19.2937
chr5	180915260	81096516	0.4483	12.4744
chr6	171115067	98770886	0.5772	13.9749
chr7	159138663	75431079	0.474	14.3148
chr8	146364022	83705391	0.5719	16.6827
chr9	141213431	107685464	0.7626	21.5784
chr10	135534747	42473486	0.3134	10.8512
chr11	135006516	70570635	0.5227	16.9026
chr12	133851895	72420076	0.541	14.2934
chr13	115169878	45470747	0.3948	17.1532
chr14	107349540	50355741	0.4691	14.6685
chr15	102531392	42326146	0.4128	14.5935
chr16	90354753	49243642	0.545	14.3808
chr17	81195210	99459963	1.2249	35.3955
chr18	78077248	35094573	0.4495	21.434
chr19	59128983	31813235	0.538	13.6094
chr20	63025520	32374719	0.5137	17.339
chr21	48129895	7326509	0.1522	6.2919
chr22	51304566	13737749	0.2678	6.9473
chrMT	16571	7123	0.4298	1.4992
chrX	155270560	105825148	0.6816	22.9238

chrY	59373566	2717556	0.0458	1.6734
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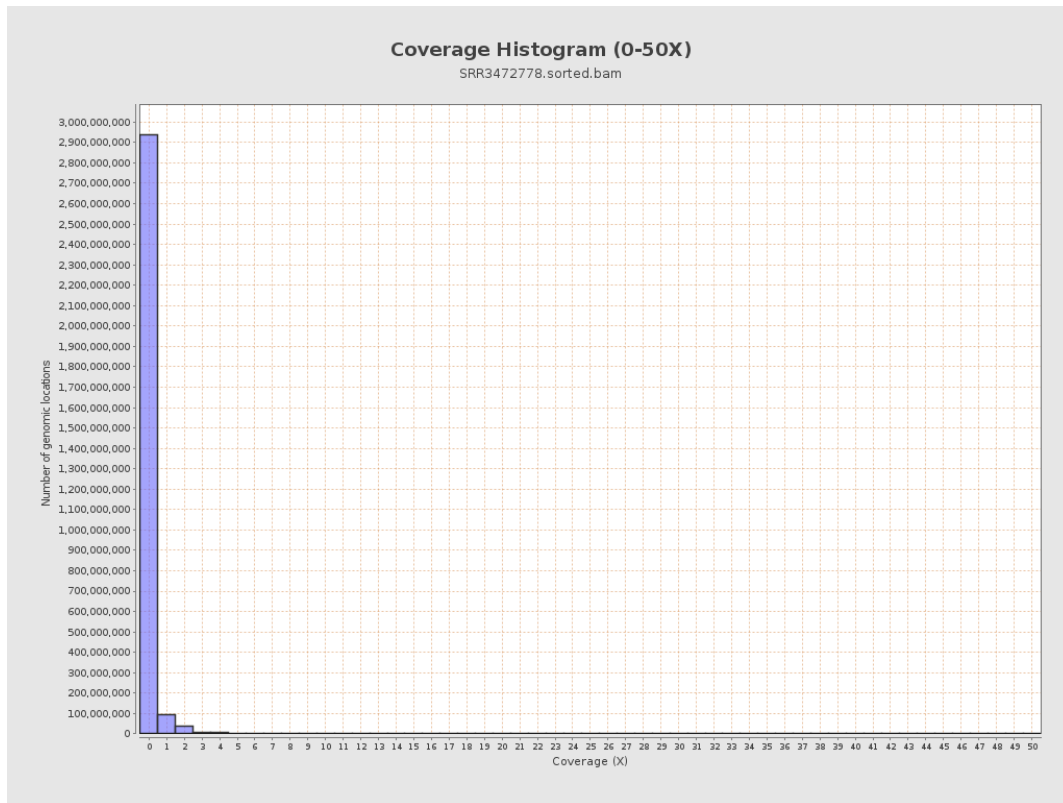
3. Results : Coverage across reference



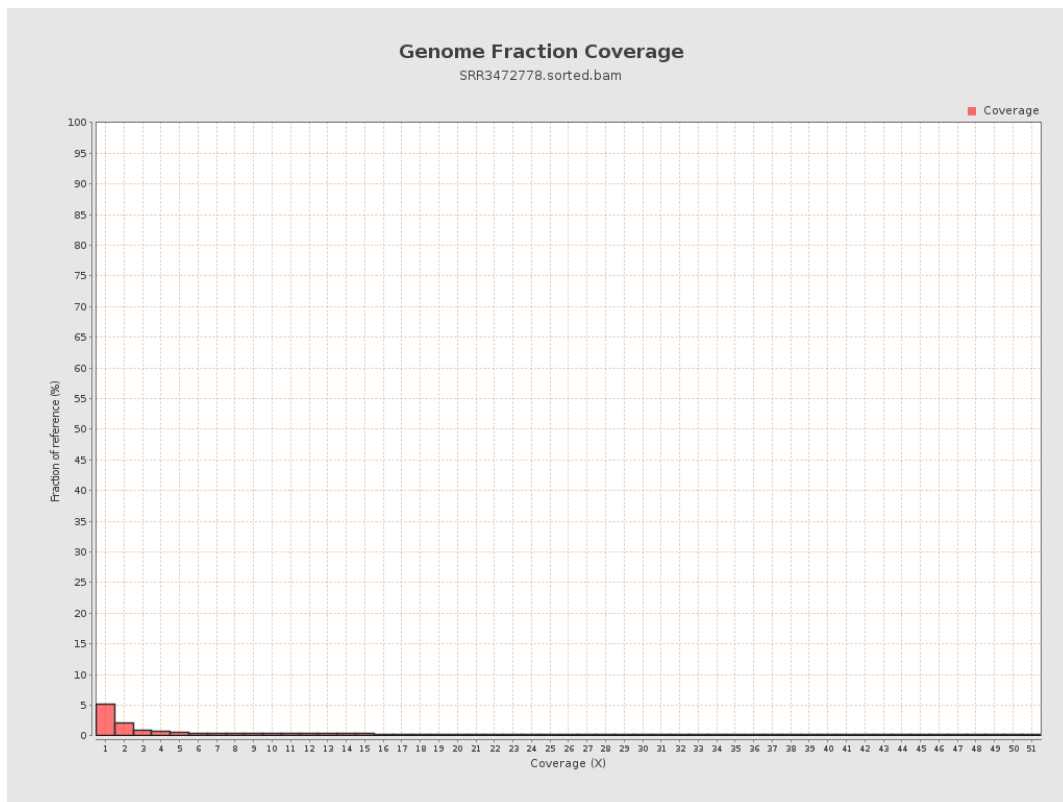
4. Results : Coverage Histogram



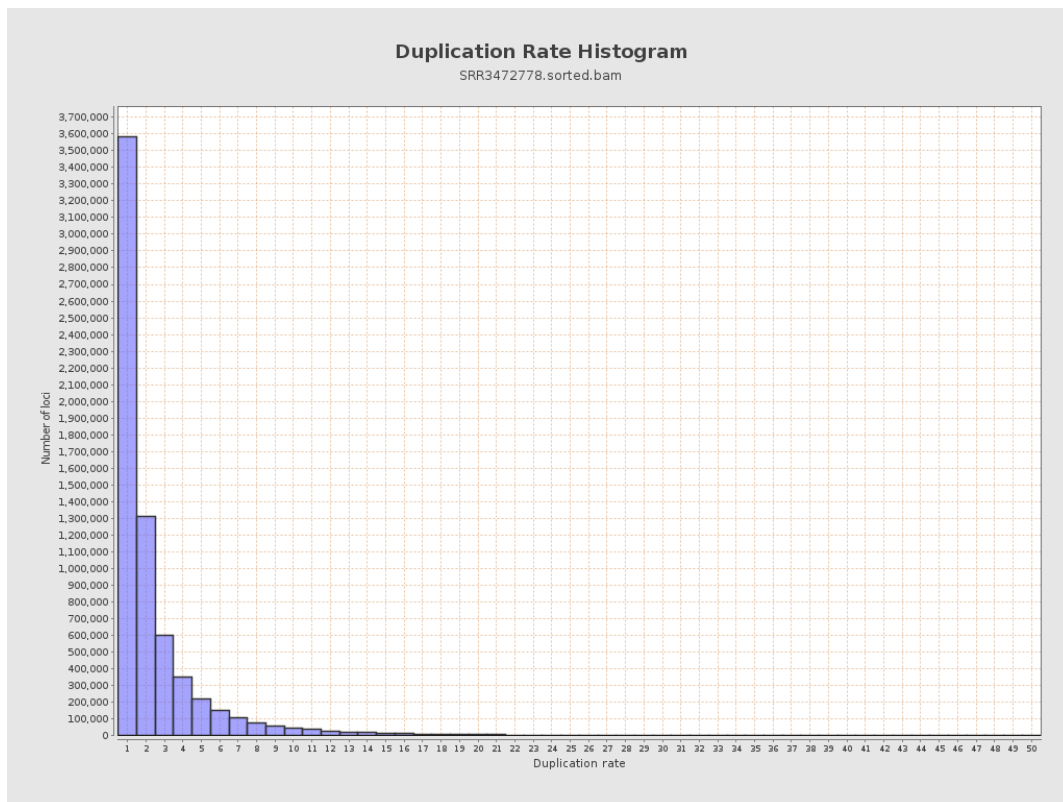
5. Results : Coverage Histogram (0-50X)



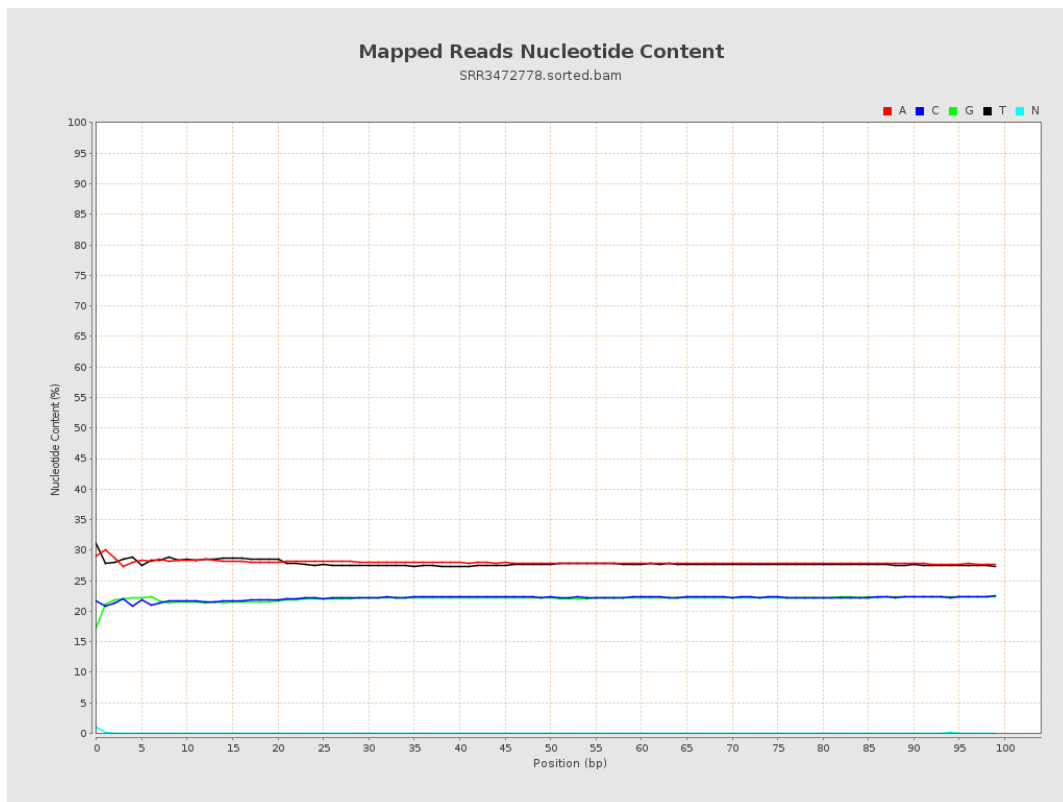
6. Results : Genome Fraction Coverage



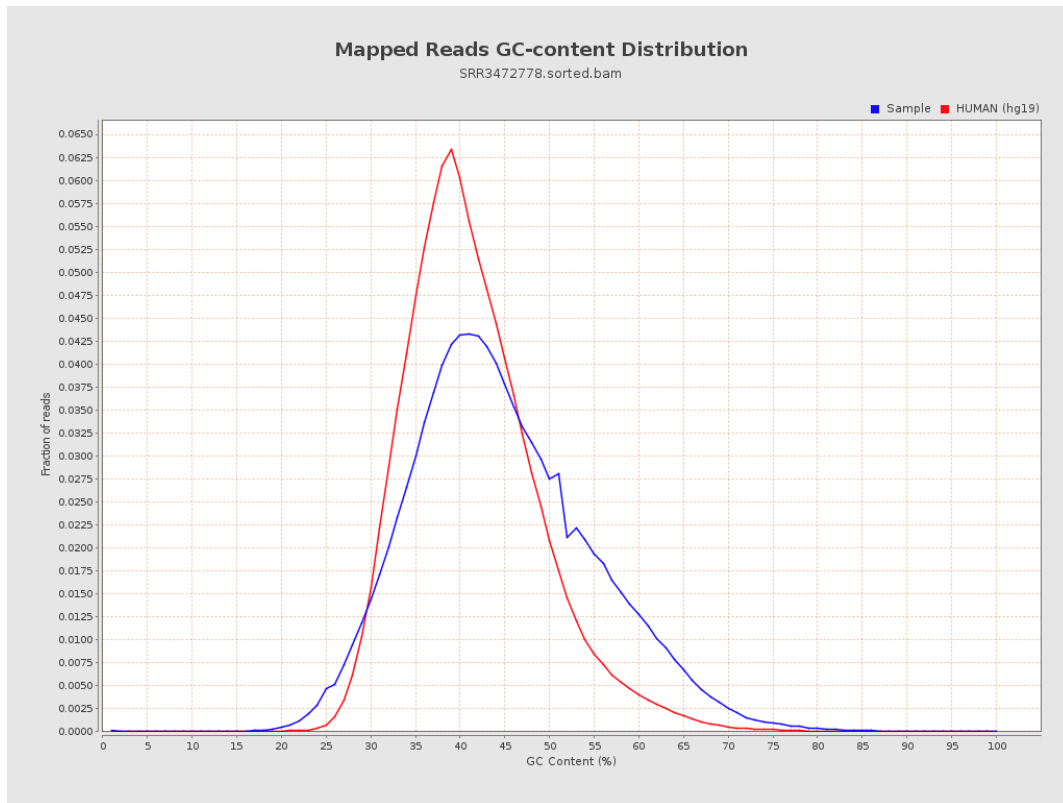
7. Results : Duplication Rate Histogram



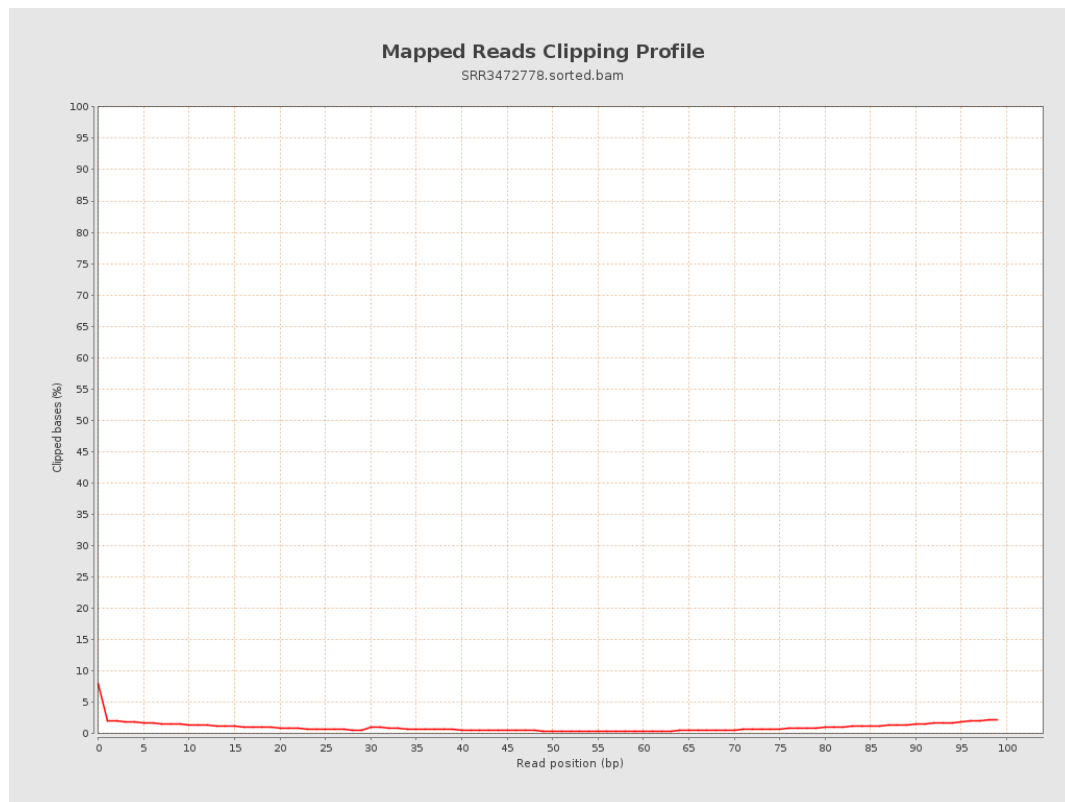
8. Results : Mapped Reads Nucleotide Content



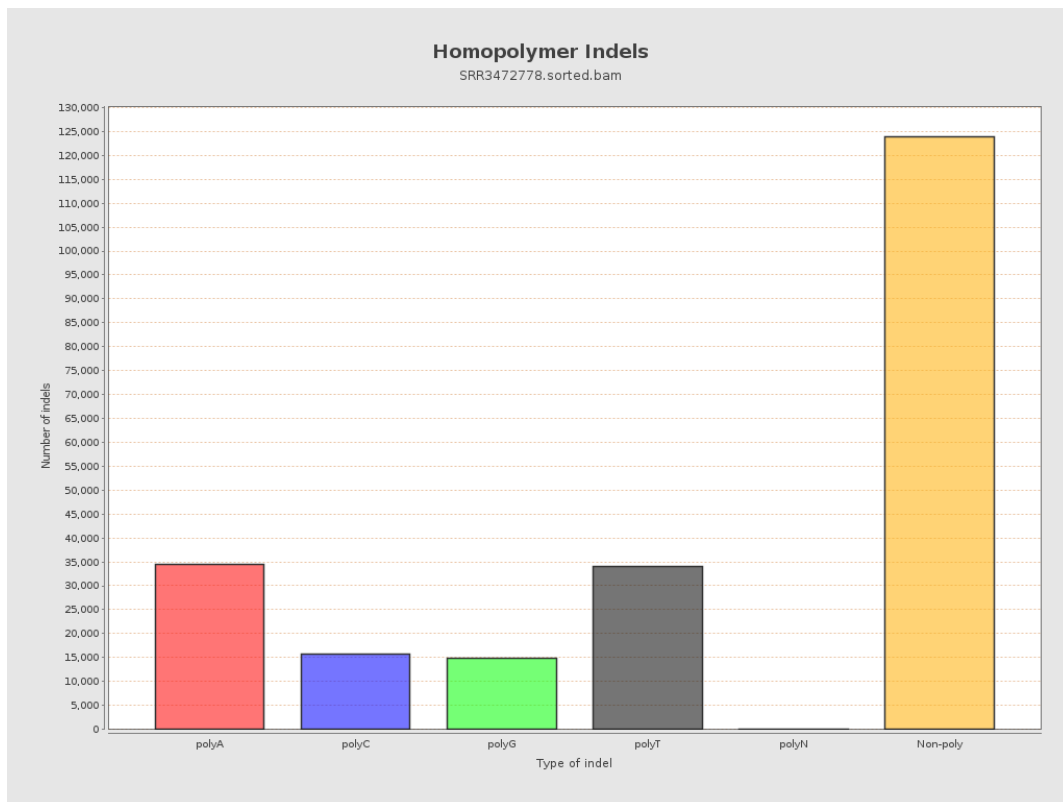
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



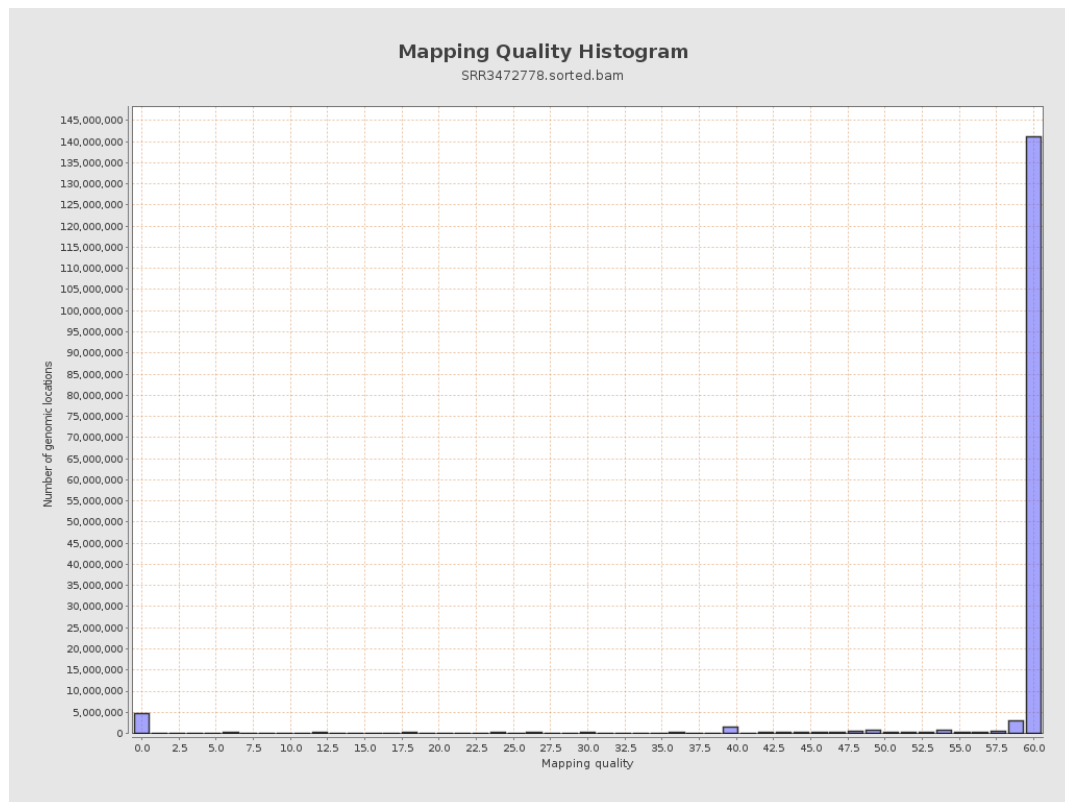
11. Results : Homopolymer Indels



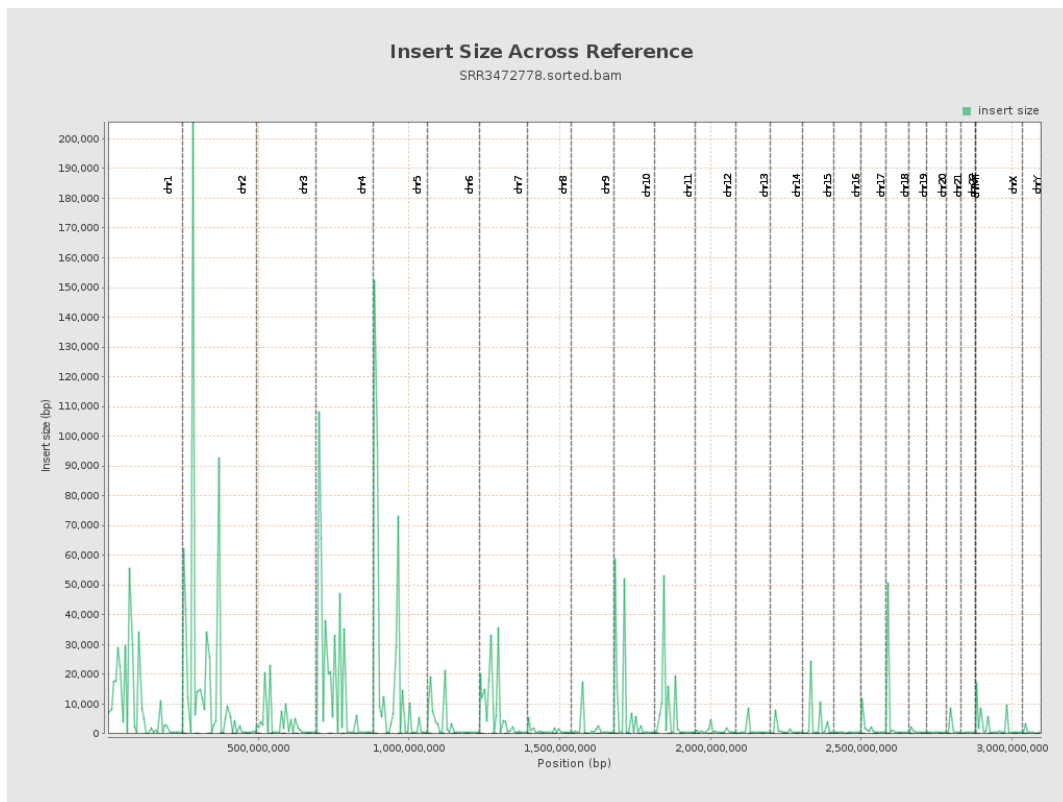
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

