

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:59:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472399.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_SRR3472399 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472399_1.fastq.gz SRR3472399_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:59:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472399.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,608,772
Mapped reads	32,237,253 / 98.86%
Unmapped reads	371,519 / 1.14%
Mapped paired reads	32,237,253 / 98.86%
Mapped reads, first in pair	16,225,312 / 49.76%
Mapped reads, second in pair	16,011,941 / 49.1%
Mapped reads, both in pair	31,957,060 / 98%
Mapped reads, singletons	280,193 / 0.86%
Secondary alignments	0
Supplementary alignments	48,630 / 0.15%
Read min/max/mean length	30 / 100 / 99.51
Duplicated reads (estimated)	20,285,849 / 62.21%
Duplication rate	51.3%
Clipped reads	1,643,528 / 5.04%

2.2. ACGT Content

Number/percentage of A's	893,629,043 / 28.15%
Number/percentage of C's	694,077,500 / 21.87%
Number/percentage of T's	898,096,794 / 28.29%
Number/percentage of G's	688,065,451 / 21.68%
Number/percentage of N's	436,812 / 0.01%

GC Percentage	43.54%
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2.3. Coverage

Mean	1.0255
Standard Deviation	19.636

2.4. Mapping Quality

Mean Mapping Quality	54.76
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2.5. Insert size

Mean	44,694.67
Standard Deviation	2,081,458.76
P25/Median/P75	168 / 235 / 319

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	16,884,753
Insertions	156,192
Mapped reads with at least one insertion	0.48%
Deletions	190,960
Mapped reads with at least one deletion	0.58%
Homopolymer indels	45.72%

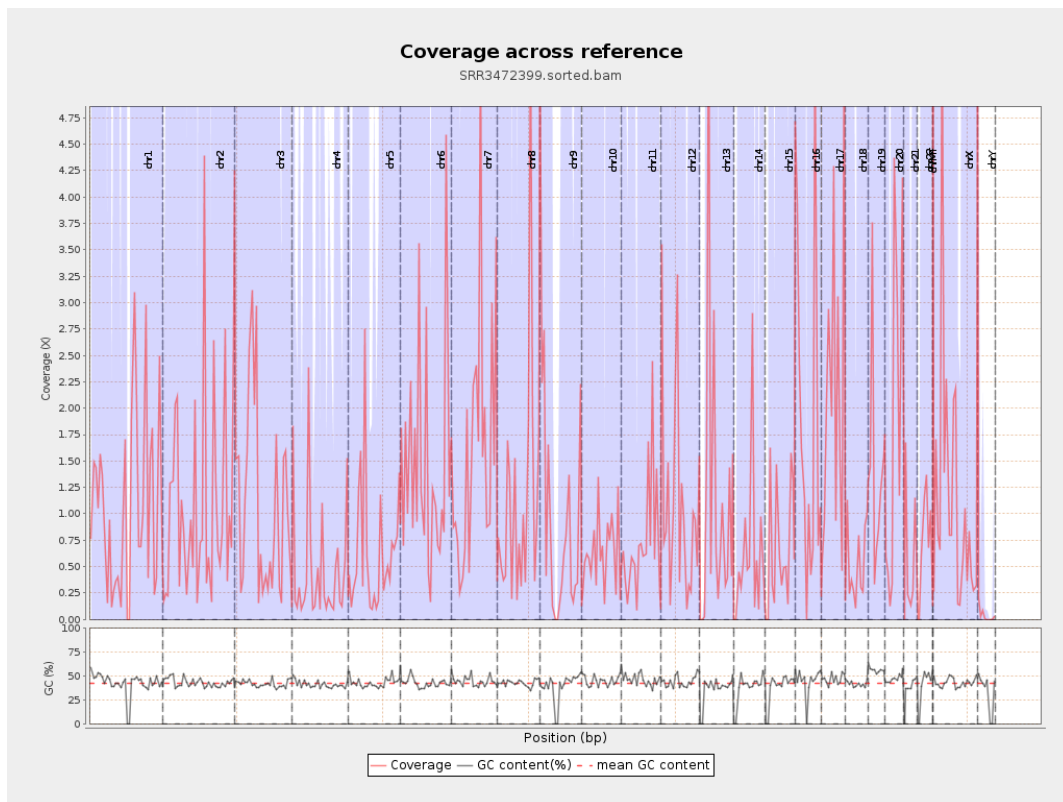
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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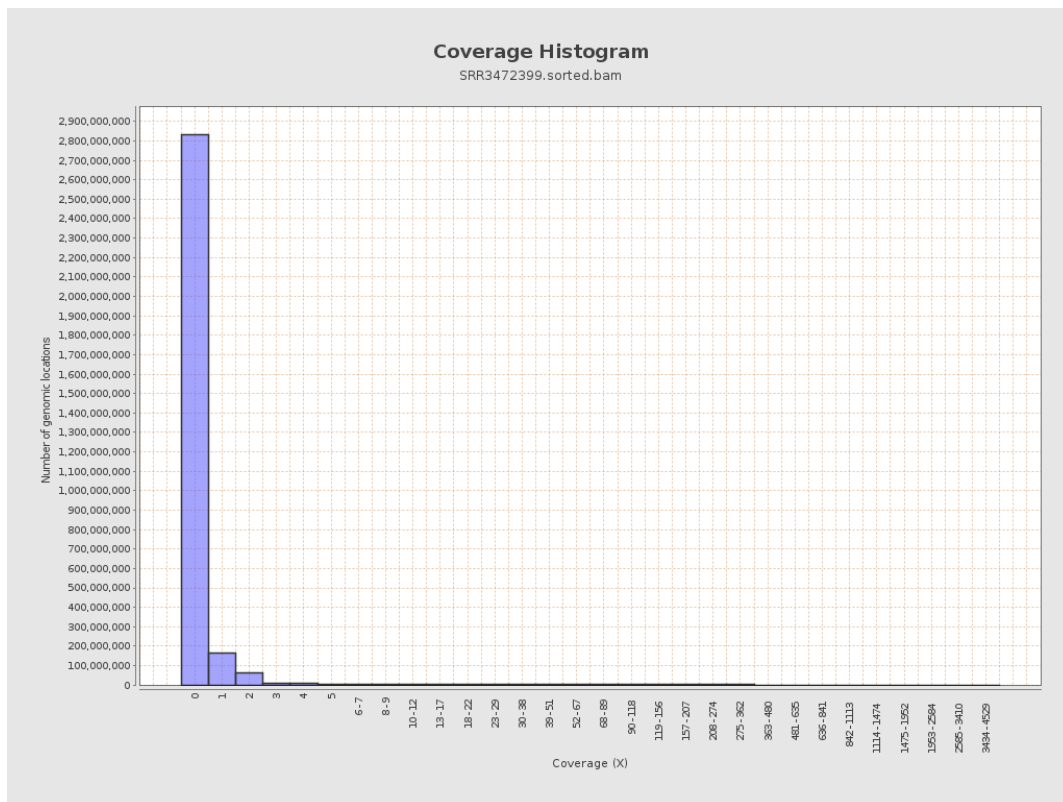
		bases	coverage	deviation
chr1	249250621	262864966	1.0546	17.5513
chr2	243199373	259666125	1.0677	21.4799
chr3	198022430	223058451	1.1264	16.6765
chr4	191154276	91407026	0.4782	11.4702
chr5	180915260	116329901	0.643	12.9079
chr6	171115067	245449840	1.4344	21.8365
chr7	159138663	261053215	1.6404	31.042
chr8	146364022	167047459	1.1413	20.4936
chr9	141213431	118719686	0.8407	13.3953
chr10	135534747	87417729	0.645	13.8165
chr11	135006516	97823034	0.7246	14.5141
chr12	133851895	150109712	1.1215	17.5772
chr13	115169878	128360577	1.1145	27.9443
chr14	107349540	65296248	0.6083	12.0618
chr15	102531392	67380116	0.6572	14.9081
chr16	90354753	166200639	1.8394	30.1779
chr17	81195210	168338409	2.0733	30.3652
chr18	78077248	39583232	0.507	9.9108
chr19	59128983	83336970	1.4094	18.3536
chr20	63025520	115456008	1.8319	34.2764
chr21	48129895	28500920	0.5922	21.9702
chr22	51304566	37790378	0.7366	14.7617
chrMT	16571	129924	7.8404	3.8196
chrX	155270560	191280081	1.2319	18.755

chrY	59373566	2155971	0.0363	1.5766
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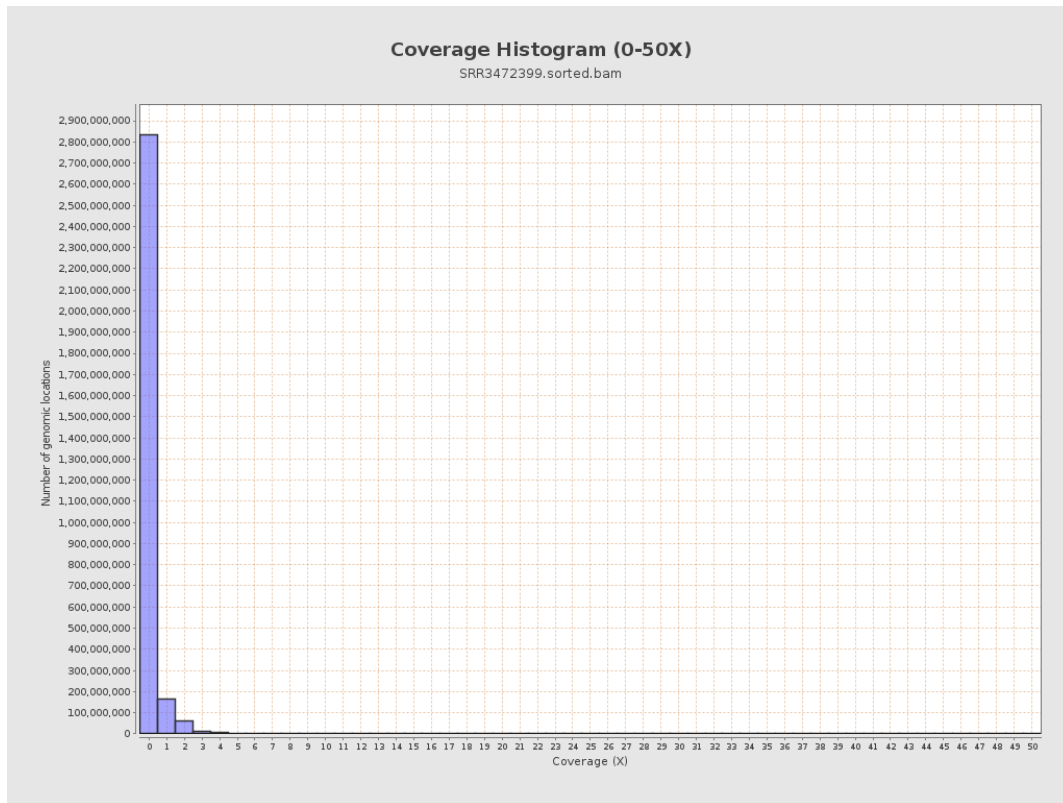
3. Results : Coverage across reference



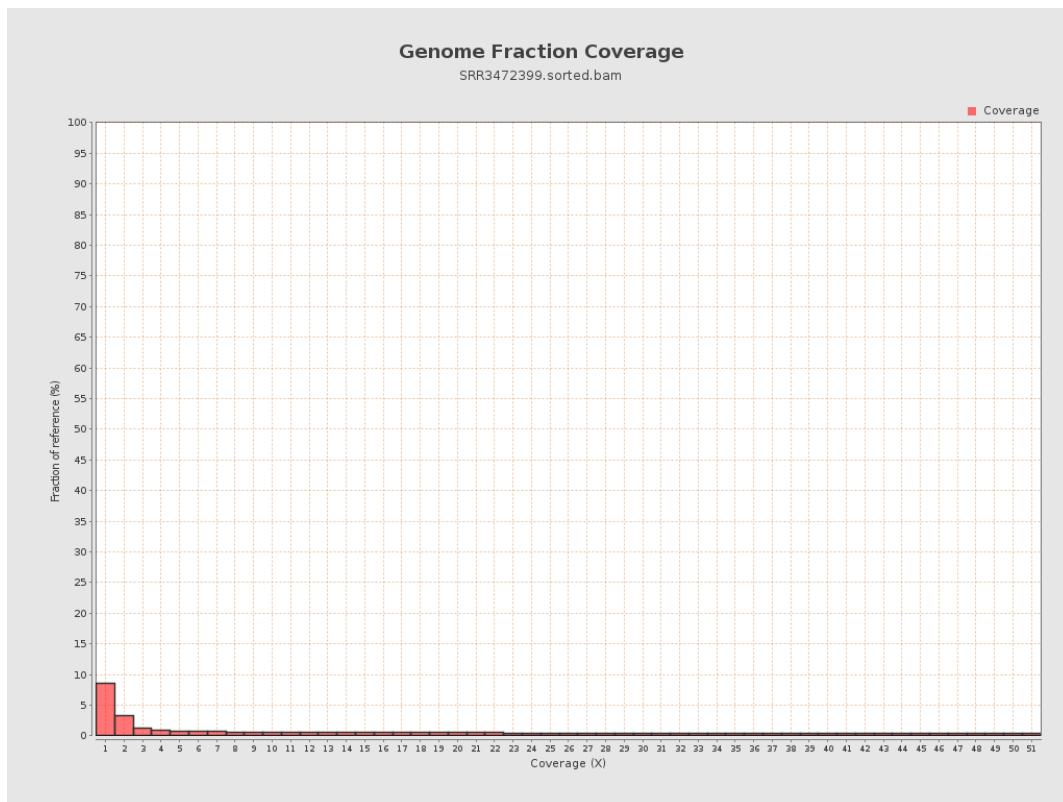
4. Results : Coverage Histogram



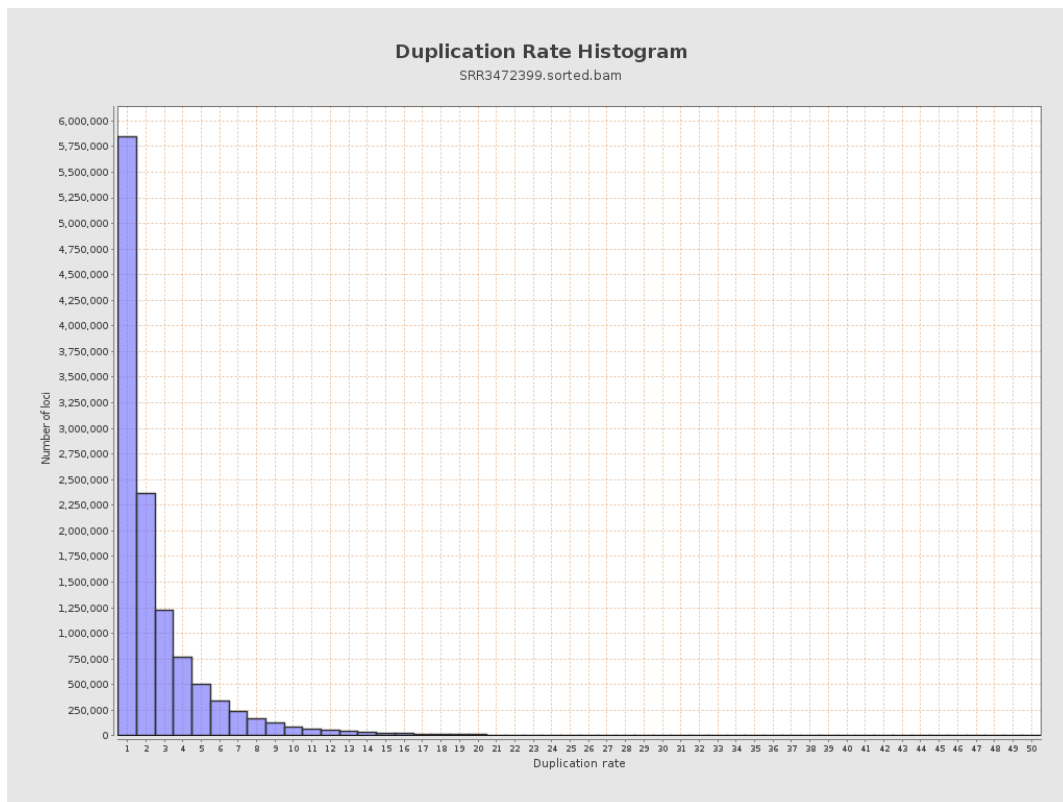
5. Results : Coverage Histogram (0-50X)



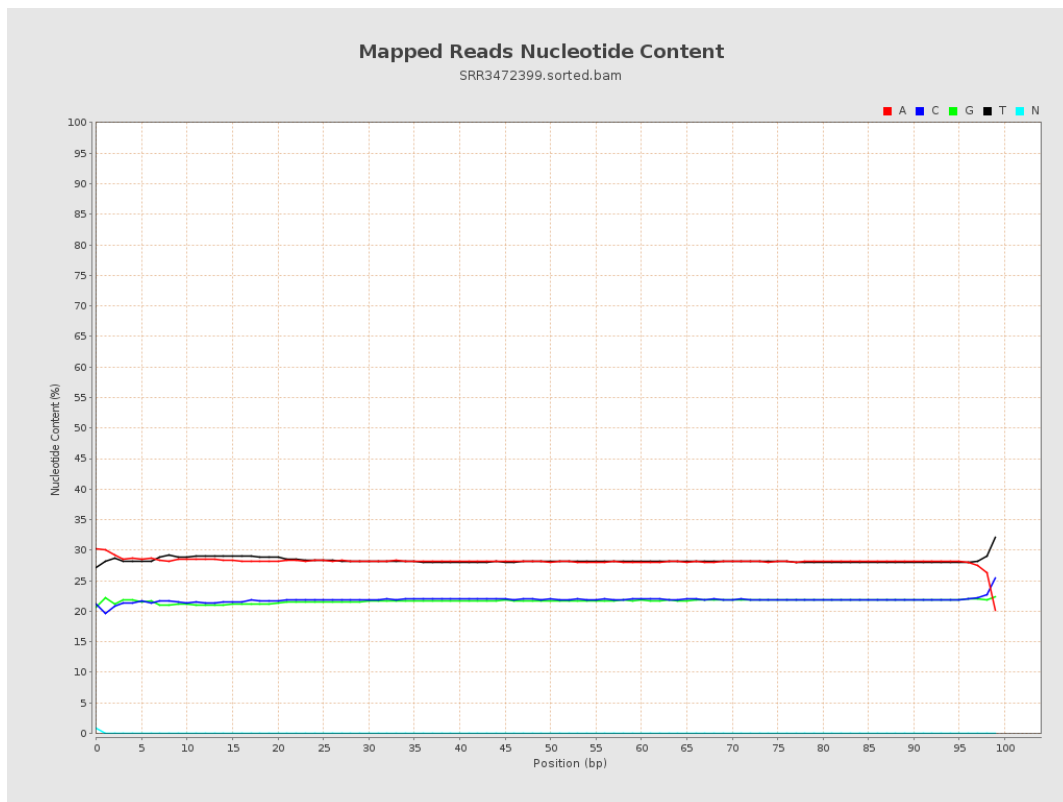
6. Results : Genome Fraction Coverage



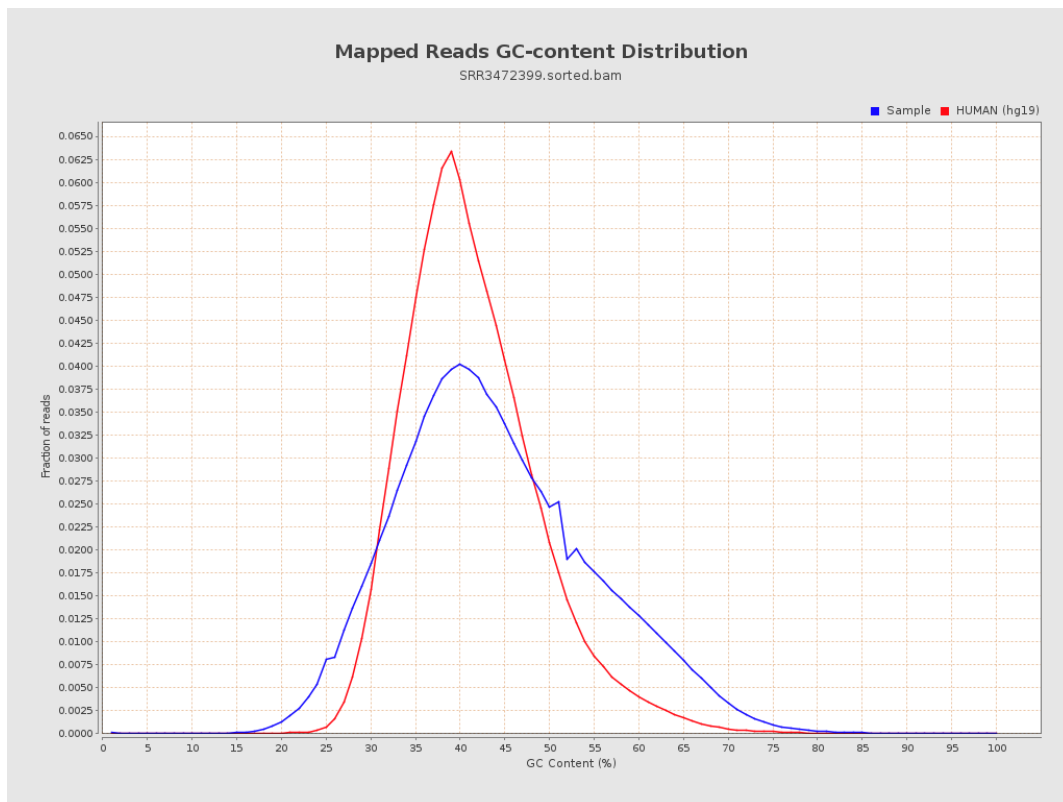
7. Results : Duplication Rate Histogram



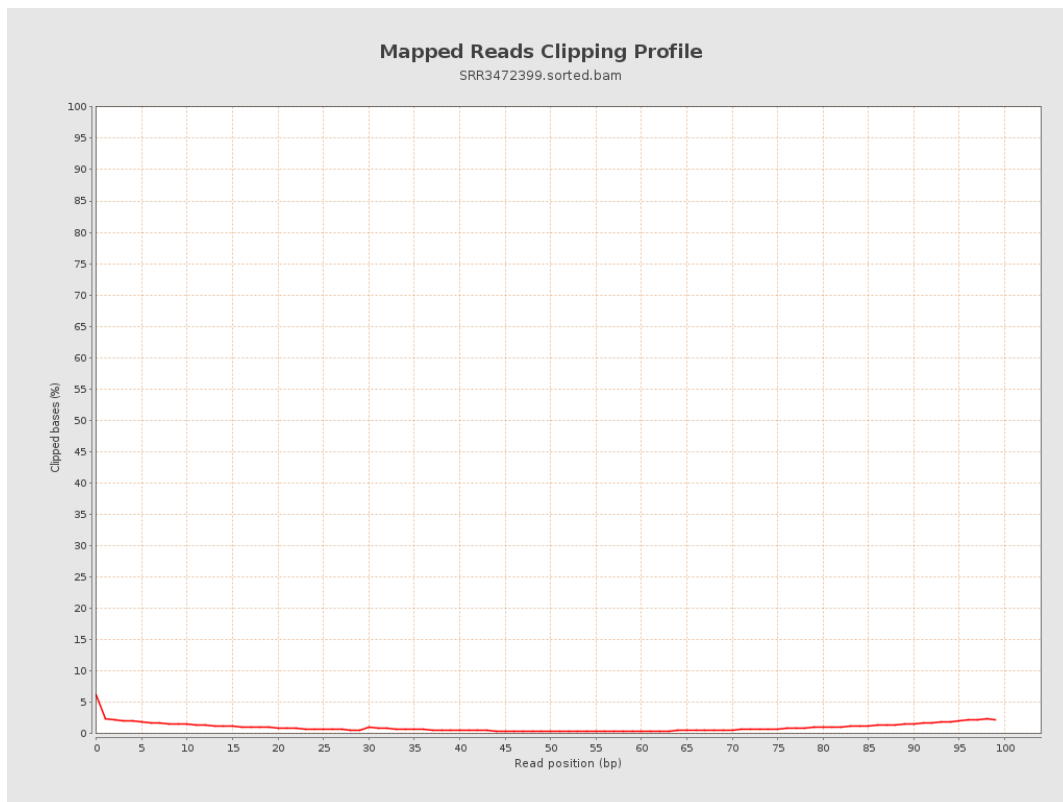
8. Results : Mapped Reads Nucleotide Content



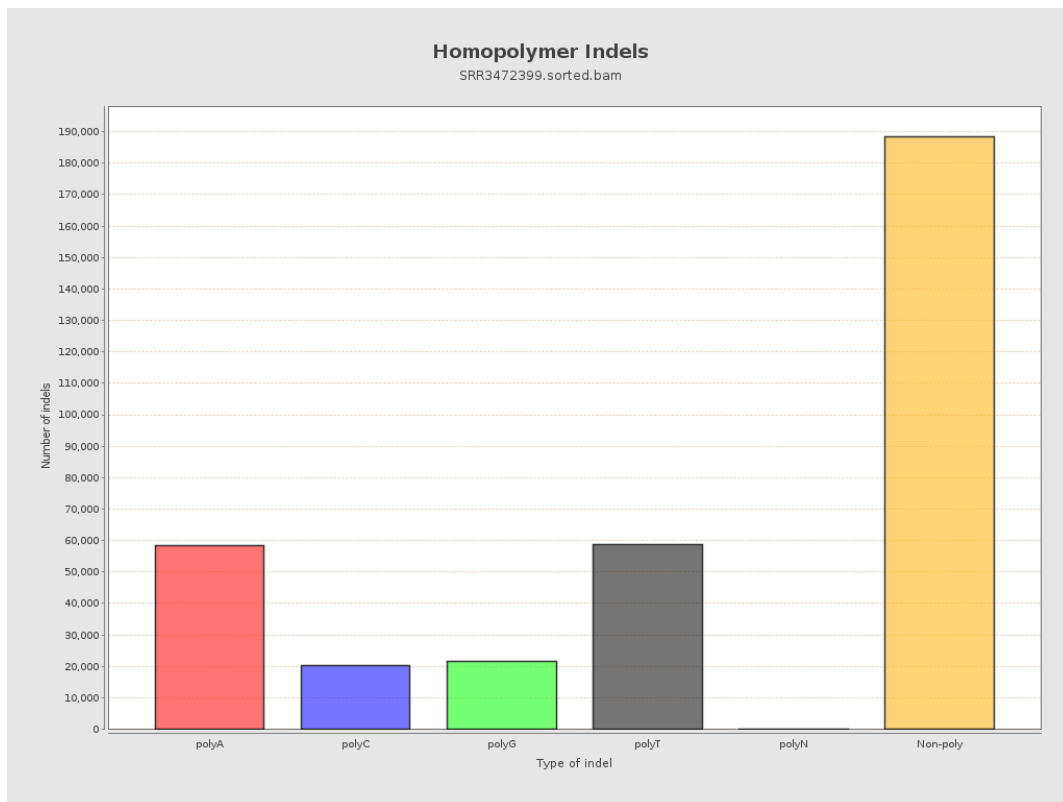
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



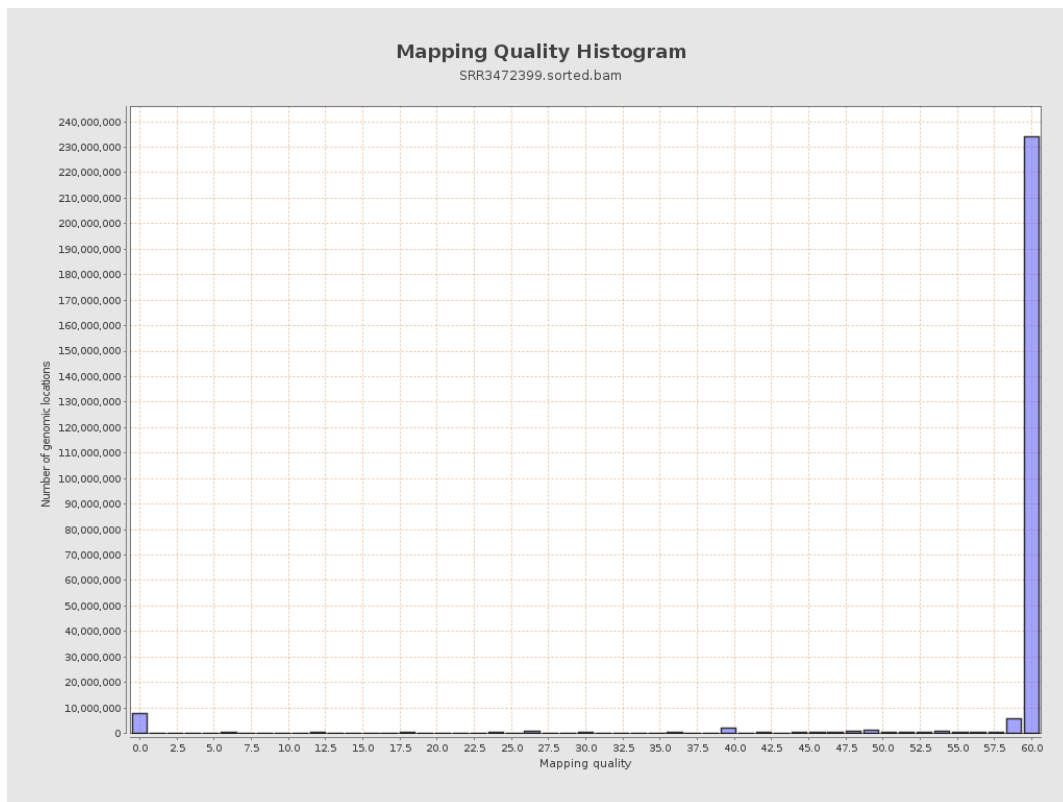
11. Results : Homopolymer Indels



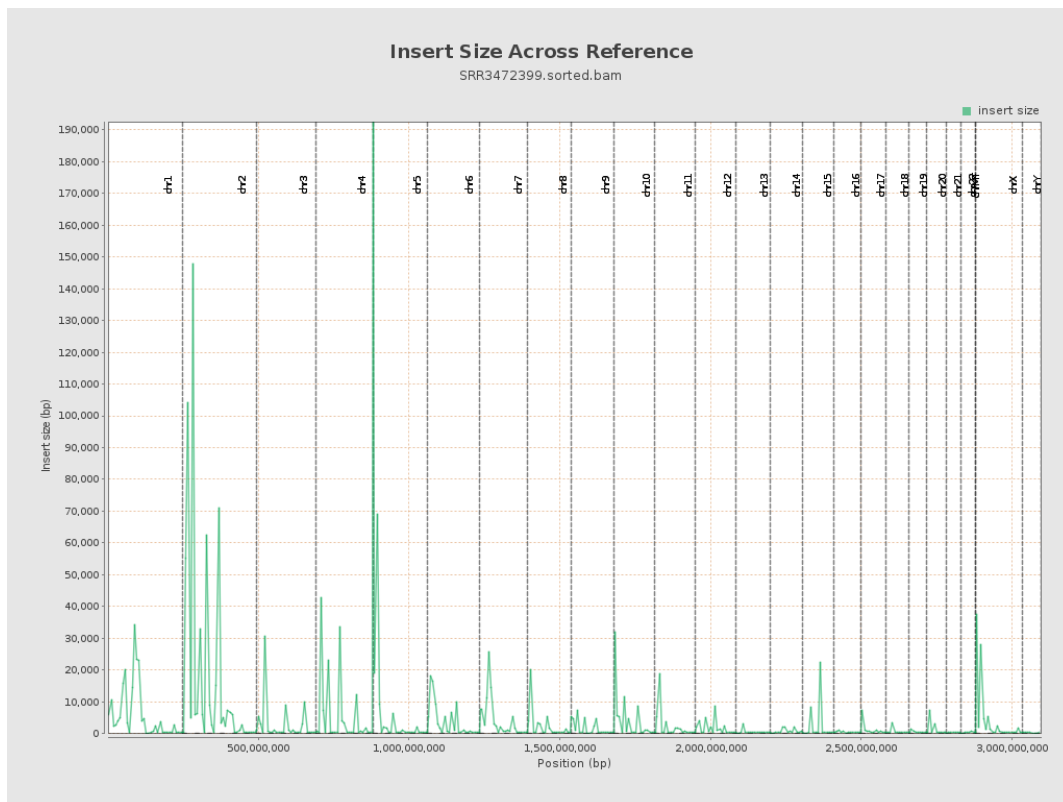
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

