

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:15:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472438.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_SRR3472438 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472438_1.fastq.gz SRR3472438_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:15:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472438.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,262,076
Mapped reads	14,117,962 / 98.99%
Unmapped reads	144,114 / 1.01%
Mapped paired reads	14,117,962 / 98.99%
Mapped reads, first in pair	7,078,057 / 49.63%
Mapped reads, second in pair	7,039,905 / 49.36%
Mapped reads, both in pair	14,047,674 / 98.5%
Mapped reads, singletons	70,288 / 0.49%
Secondary alignments	0
Supplementary alignments	48,798 / 0.34%
Read min/max/mean length	30 / 100 / 99.22
Duplicated reads (estimated)	8,622,778 / 60.46%
Duplication rate	46.9%
Clipped reads	1,029,350 / 7.22%

2.2. ACGT Content

Number/percentage of A's	363,414,684 / 26.29%
Number/percentage of C's	329,188,868 / 23.81%
Number/percentage of T's	363,879,471 / 26.32%
Number/percentage of G's	325,736,966 / 23.56%
Number/percentage of N's	171,016 / 0.01%

GC Percentage	47.38%
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2.3. Coverage

Mean	0.4466
Standard Deviation	14.6328

2.4. Mapping Quality

Mean Mapping Quality	54.79
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2.5. Insert size

Mean	15,644.77
Standard Deviation	1,223,041.72
P25/Median/P75	143 / 195 / 261

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	7,100,916
Insertions	77,288
Mapped reads with at least one insertion	0.54%
Deletions	60,566
Mapped reads with at least one deletion	0.42%
Homopolymer indels	44.5%

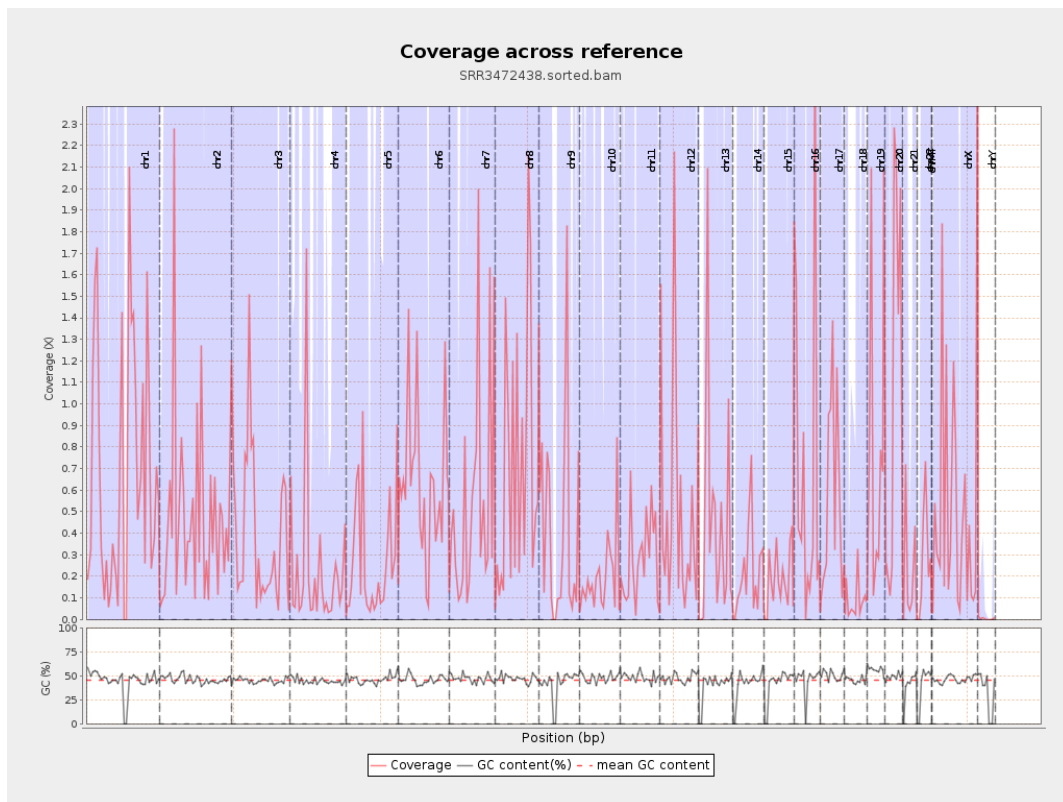
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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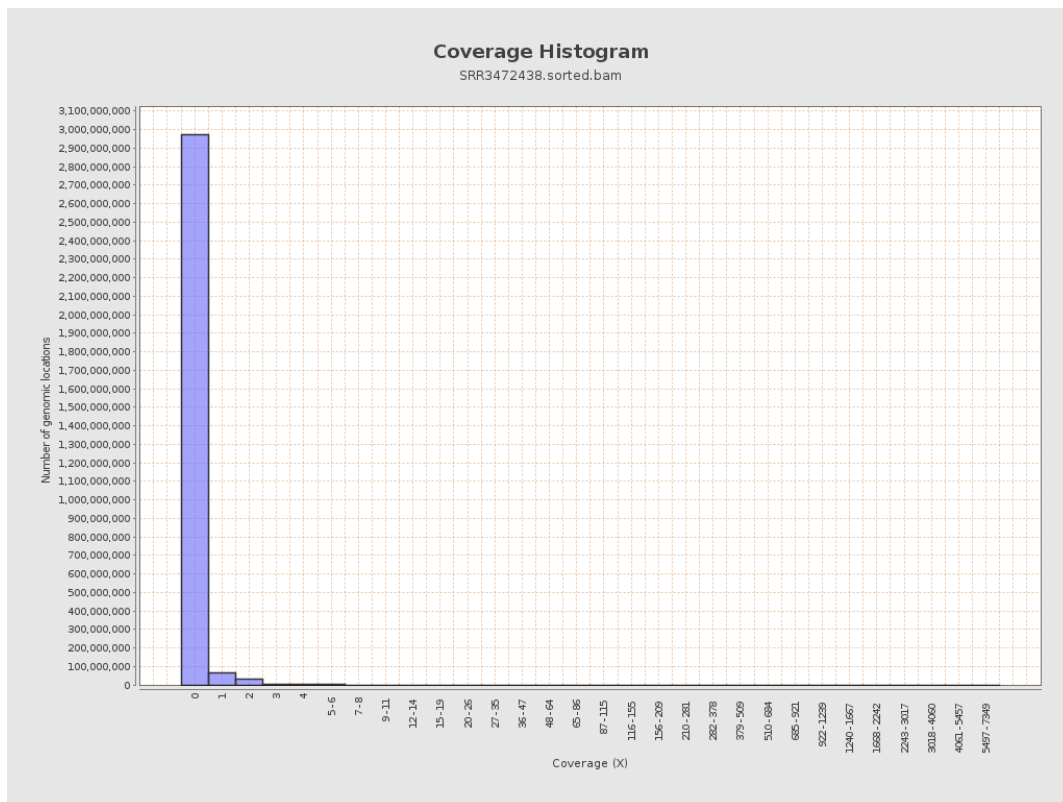
		bases	coverage	deviation
chr1	249250621	174474291	0.7	19.8229
chr2	243199373	115370409	0.4744	18.418
chr3	198022430	81382422	0.411	9.8407
chr4	191154276	41828833	0.2188	9.0455
chr5	180915260	50343955	0.2783	10.5992
chr6	171115067	107471196	0.6281	14.279
chr7	159138663	89548140	0.5627	16.4978
chr8	146364022	104757196	0.7157	20.4932
chr9	141213431	60175086	0.4261	15.6602
chr10	135534747	26882385	0.1983	8.7523
chr11	135006516	38902670	0.2882	9.2895
chr12	133851895	68406249	0.5111	13.7082
chr13	115169878	51427386	0.4465	15.7858
chr14	107349540	22498278	0.2096	6.3703
chr15	102531392	19588126	0.191	6.5716
chr16	90354753	63971839	0.708	19.2849
chr17	81195210	46957677	0.5783	13.5523
chr18	78077248	7154167	0.0916	4.5774
chr19	59128983	43387852	0.7338	17.0624
chr20	63025520	66952760	1.0623	29.1791
chr21	48129895	10810487	0.2246	13.0589
chr22	51304566	14029836	0.2735	9.0841
chrMT	16571	3839	0.2317	0.6227
chrX	155270560	75980682	0.4893	14.9463

chrY	59373566	237308	0.004	0.2694
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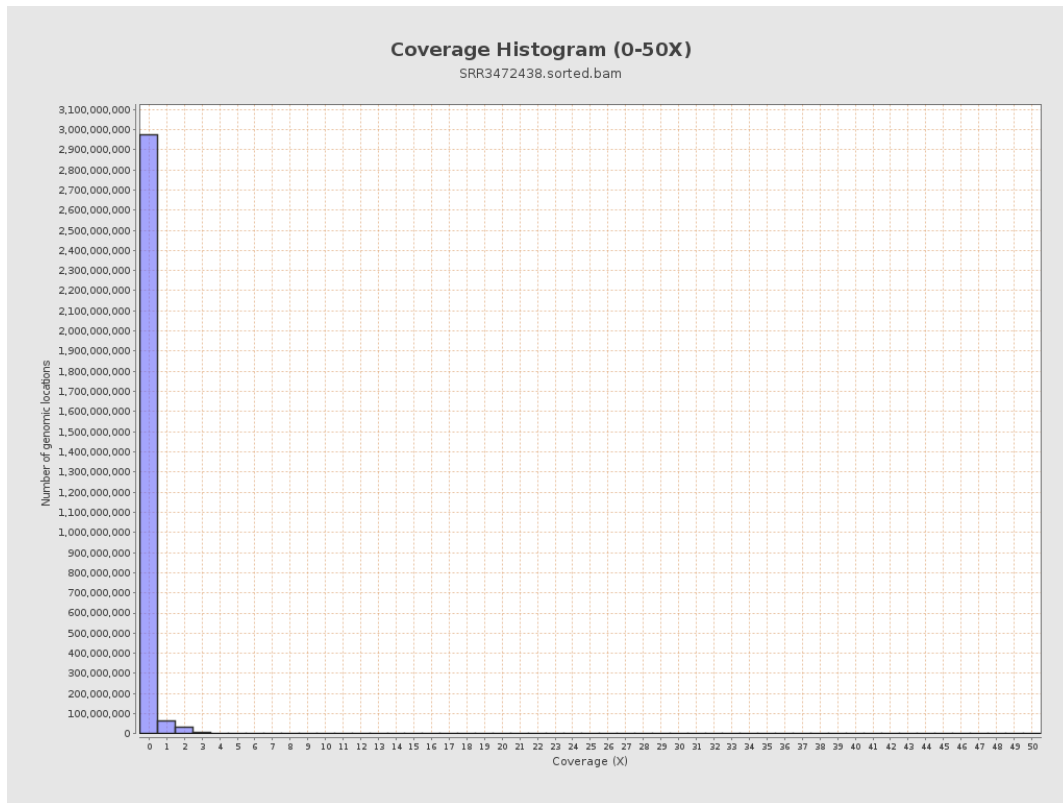
3. Results : Coverage across reference



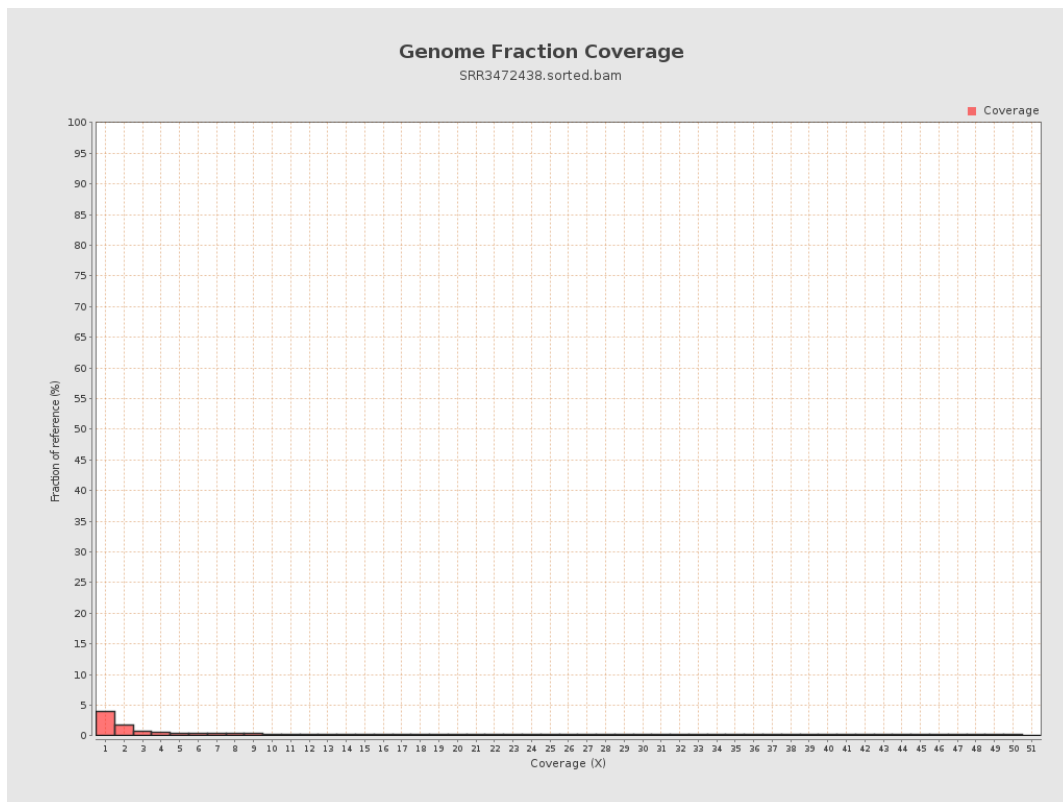
4. Results : Coverage Histogram



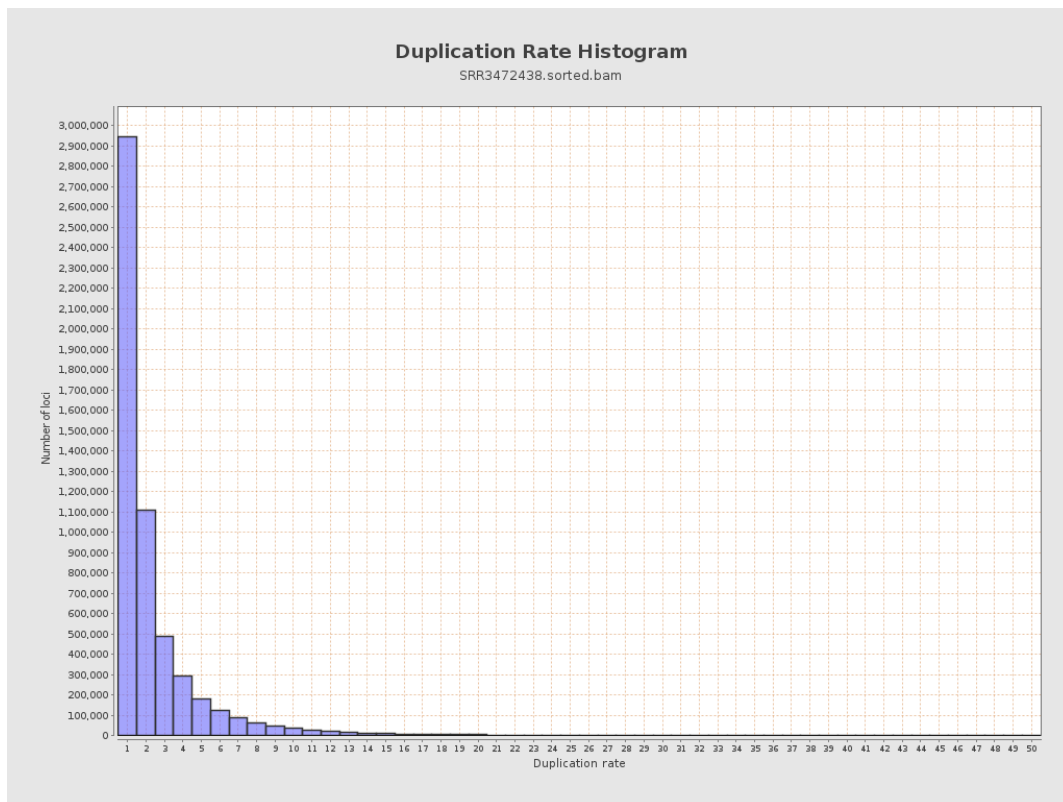
5. Results : Coverage Histogram (0-50X)



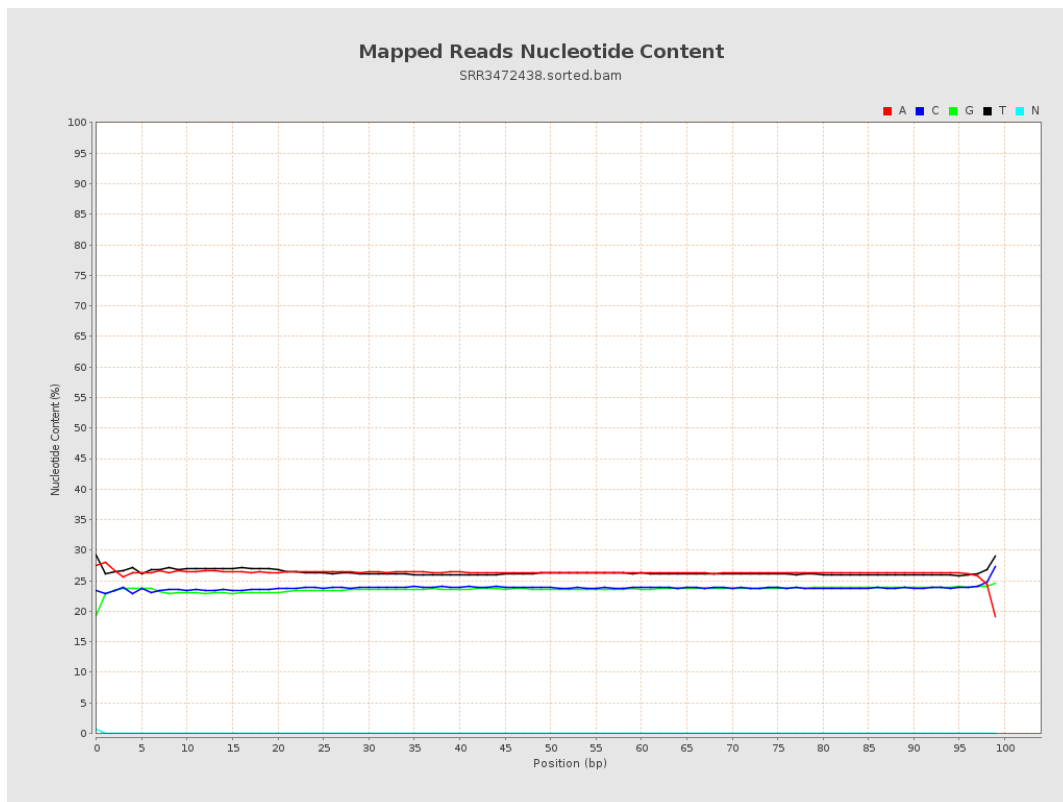
6. Results : Genome Fraction Coverage



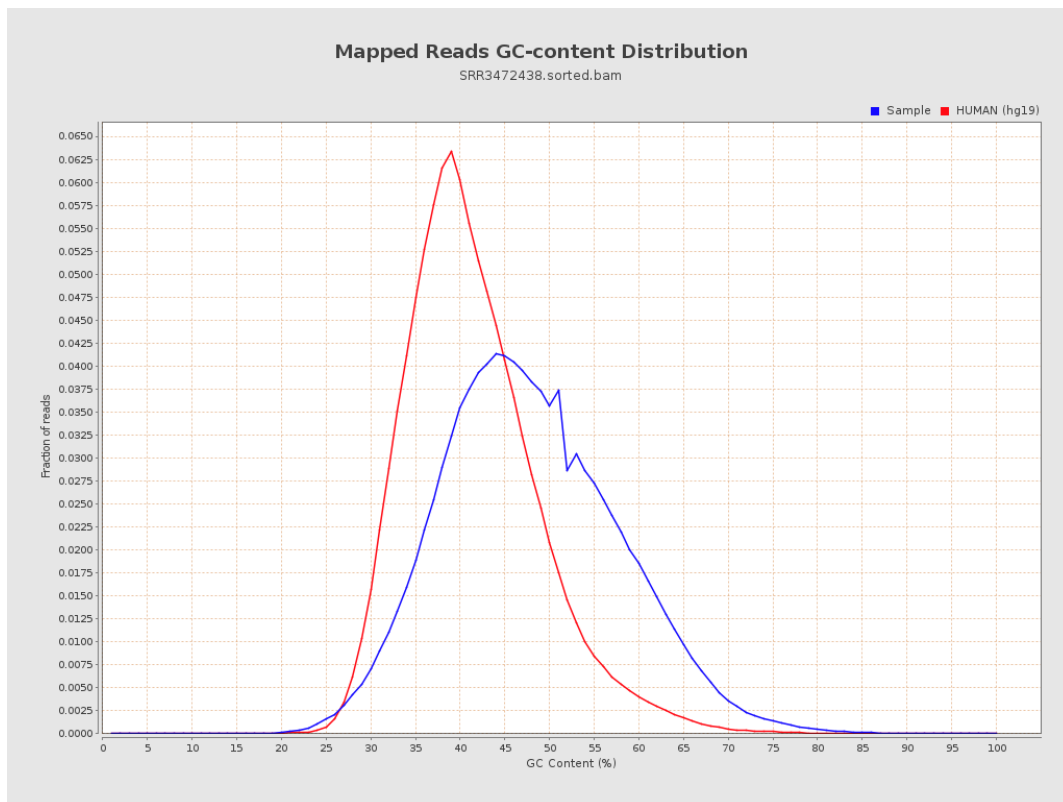
7. Results : Duplication Rate Histogram



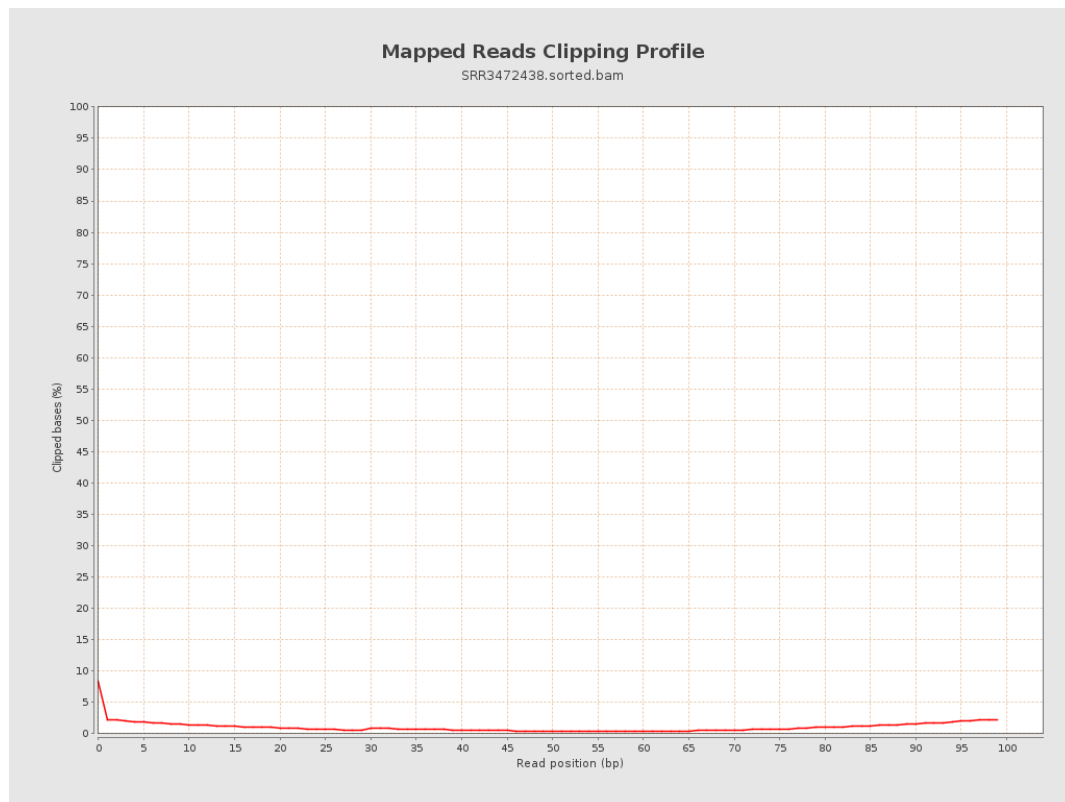
8. Results : Mapped Reads Nucleotide Content



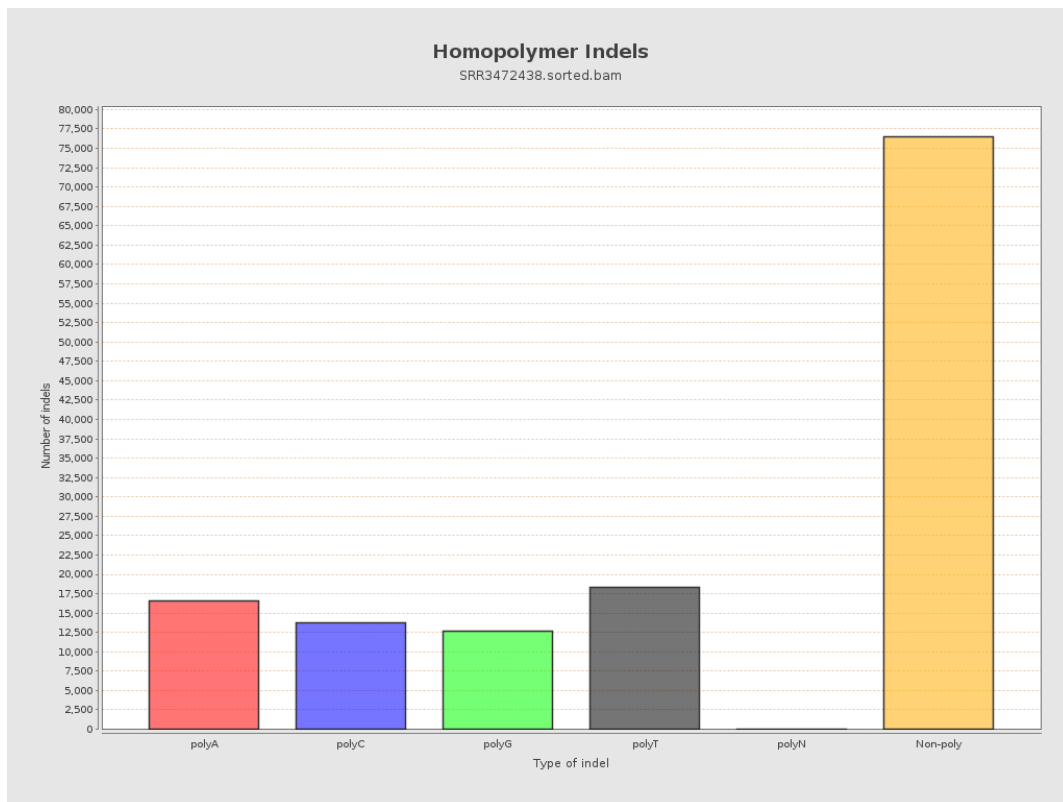
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



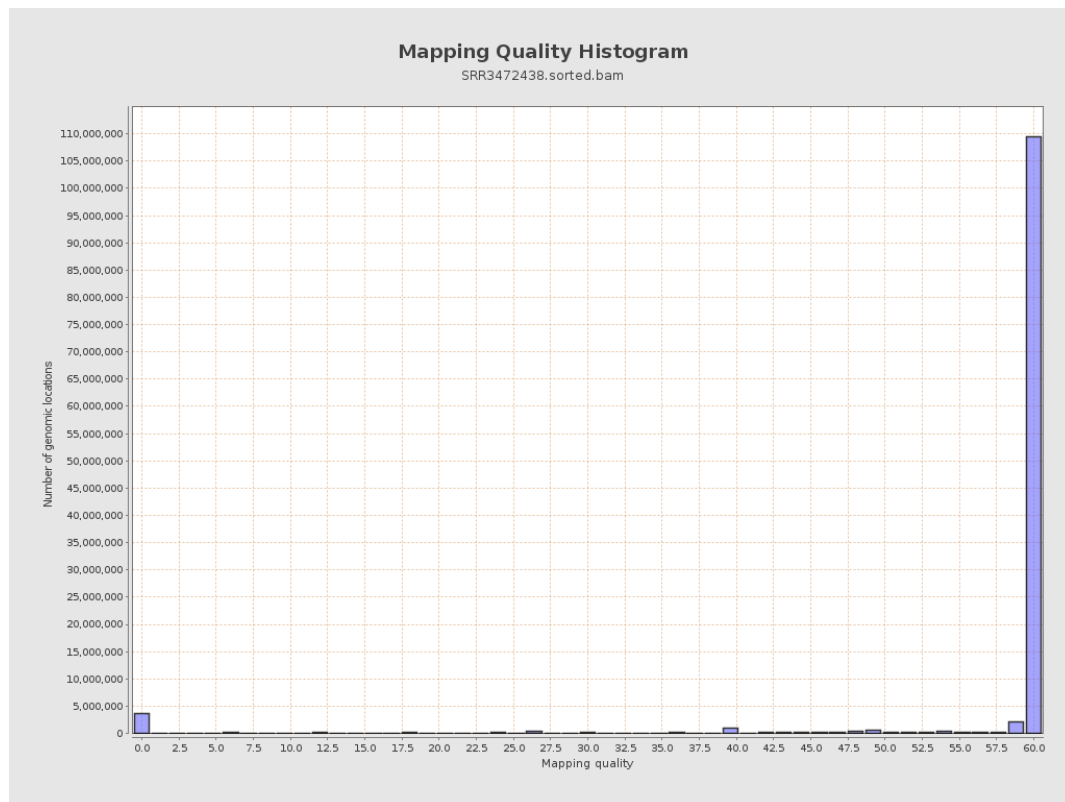
11. Results : Homopolymer Indels



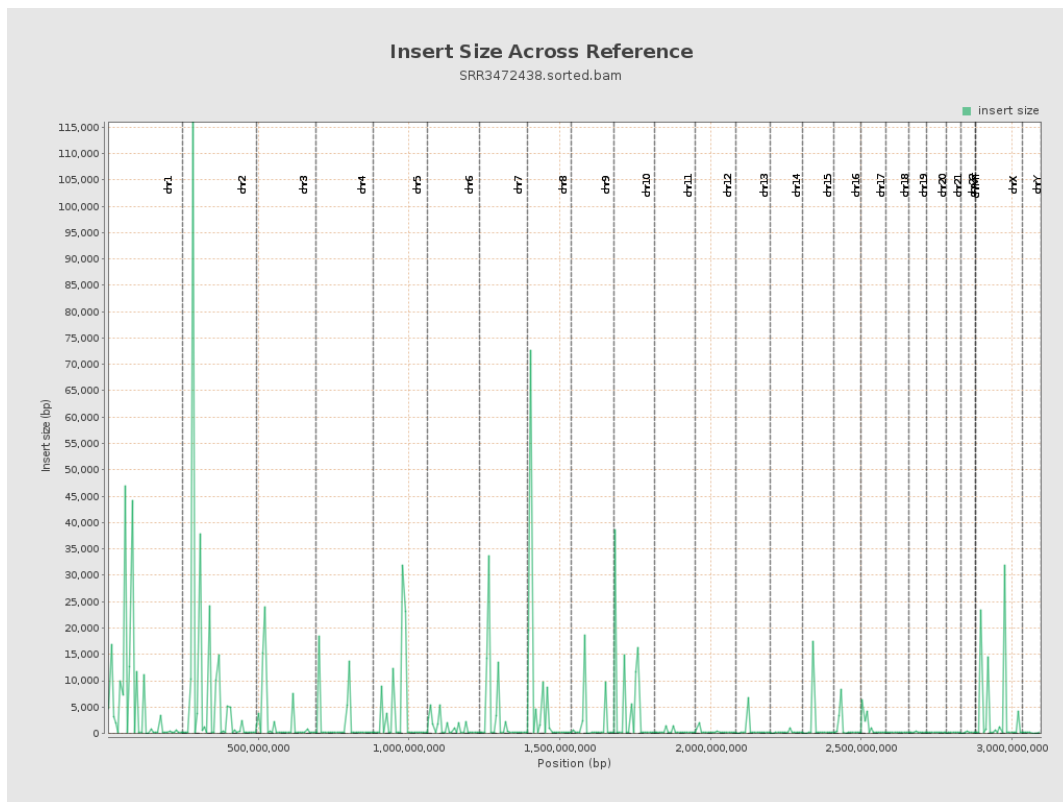
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

