

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:44:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472538.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_SRR3472538 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472538_1.fastq.gz SRR3472538_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:44:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472538.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,166,650
Mapped reads	16,946,620 / 98.72%
Unmapped reads	220,030 / 1.28%
Mapped paired reads	16,946,620 / 98.72%
Mapped reads, first in pair	8,499,013 / 49.51%
Mapped reads, second in pair	8,447,607 / 49.21%
Mapped reads, both in pair	16,838,740 / 98.09%
Mapped reads, singletons	107,880 / 0.63%
Secondary alignments	0
Supplementary alignments	60,311 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	10,533,931 / 61.36%
Duplication rate	46.82%
Clipped reads	1,328,803 / 7.74%

2.2. ACGT Content

Number/percentage of A's	462,671,173 / 27.74%
Number/percentage of C's	373,678,162 / 22.4%
Number/percentage of T's	459,670,315 / 27.56%
Number/percentage of G's	371,703,804 / 22.28%
Number/percentage of N's	258,607 / 0.02%

GC Percentage	44.69%
---------------	--------

2.3. Coverage

Mean	0.5389
Standard Deviation	17.7545

2.4. Mapping Quality

Mean Mapping Quality	54.97
----------------------	-------

2.5. Insert size

Mean	26,887.79
Standard Deviation	1,600,158.38
P25/Median/P75	172 / 238 / 321

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	9,905,039
Insertions	93,916
Mapped reads with at least one insertion	0.55%
Deletions	81,381
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.8%

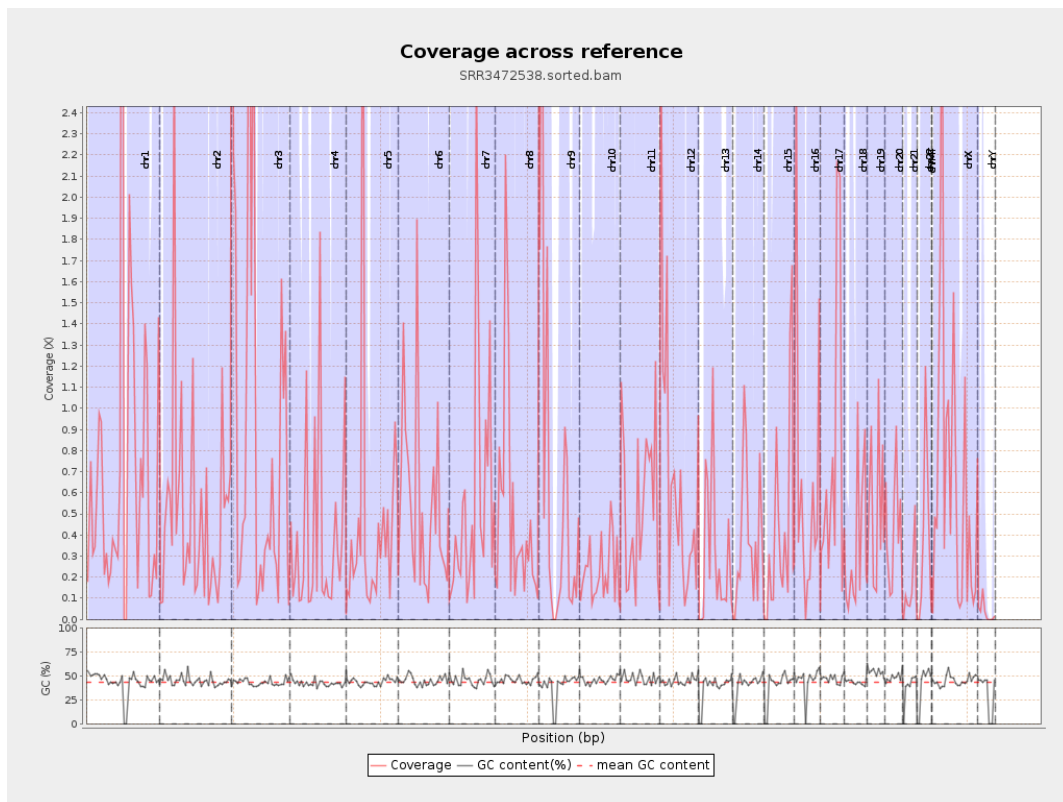
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

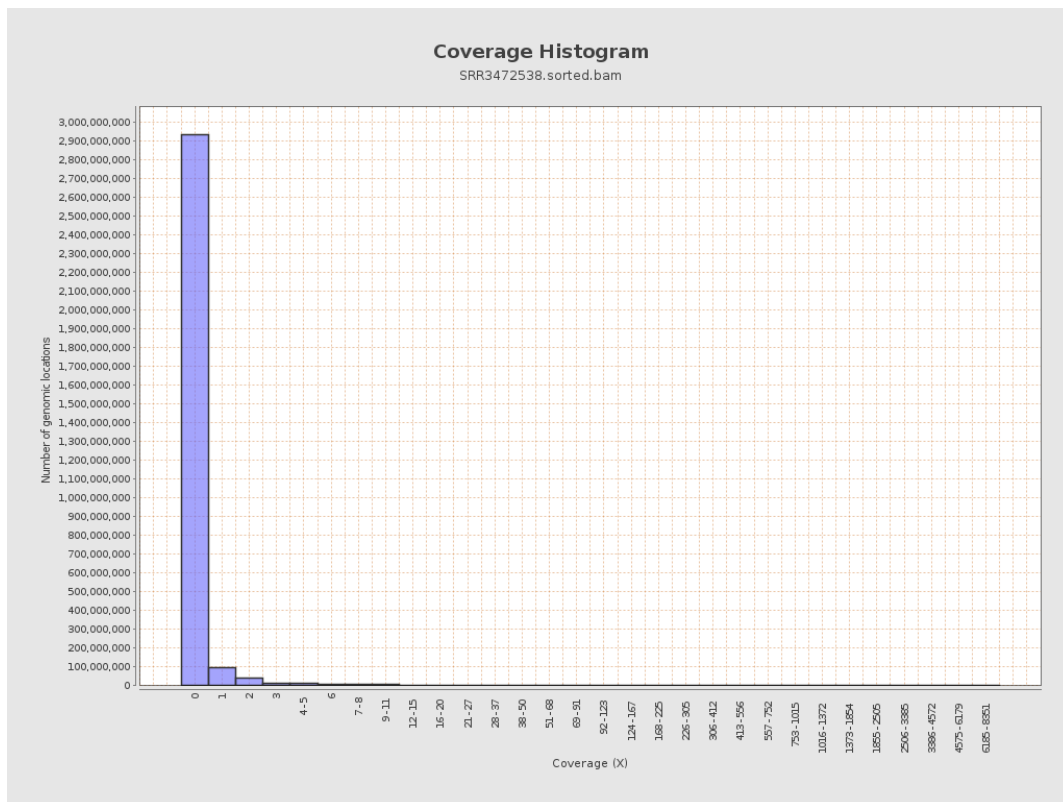
		bases	coverage	deviation
chr1	249250621	189878395	0.7618	25.9758
chr2	243199373	123382256	0.5073	18.8939
chr3	198022430	190936115	0.9642	22.4341
chr4	191154276	72270459	0.3781	14.1297
chr5	180915260	85989089	0.4753	15.5991
chr6	171115067	92309267	0.5395	15.3467
chr7	159138663	92433183	0.5808	21.2448
chr8	146364022	71892341	0.4912	14.7269
chr9	141213431	93779752	0.6641	16.054
chr10	135534747	31129759	0.2297	7.0509
chr11	135006516	73292640	0.5429	14.8846
chr12	133851895	91472153	0.6834	21.1302
chr13	115169878	34406667	0.2987	9.9682
chr14	107349540	40859492	0.3806	12.2027
chr15	102531392	45892183	0.4476	12.8356
chr16	90354753	57988309	0.6418	19.3215
chr17	81195210	60472559	0.7448	22.5329
chr18	78077248	26752983	0.3426	12.2483
chr19	59128983	32903498	0.5565	14.1647
chr20	63025520	27141093	0.4306	11.0659
chr21	48129895	7507036	0.156	5.1356
chr22	51304566	18331488	0.3573	11.1392
chrMT	16571	3371	0.2034	0.5339
chrX	155270560	105040435	0.6765	25.8611

chrY	59373566	2104550	0.0354	1.5082
------	----------	---------	--------	--------

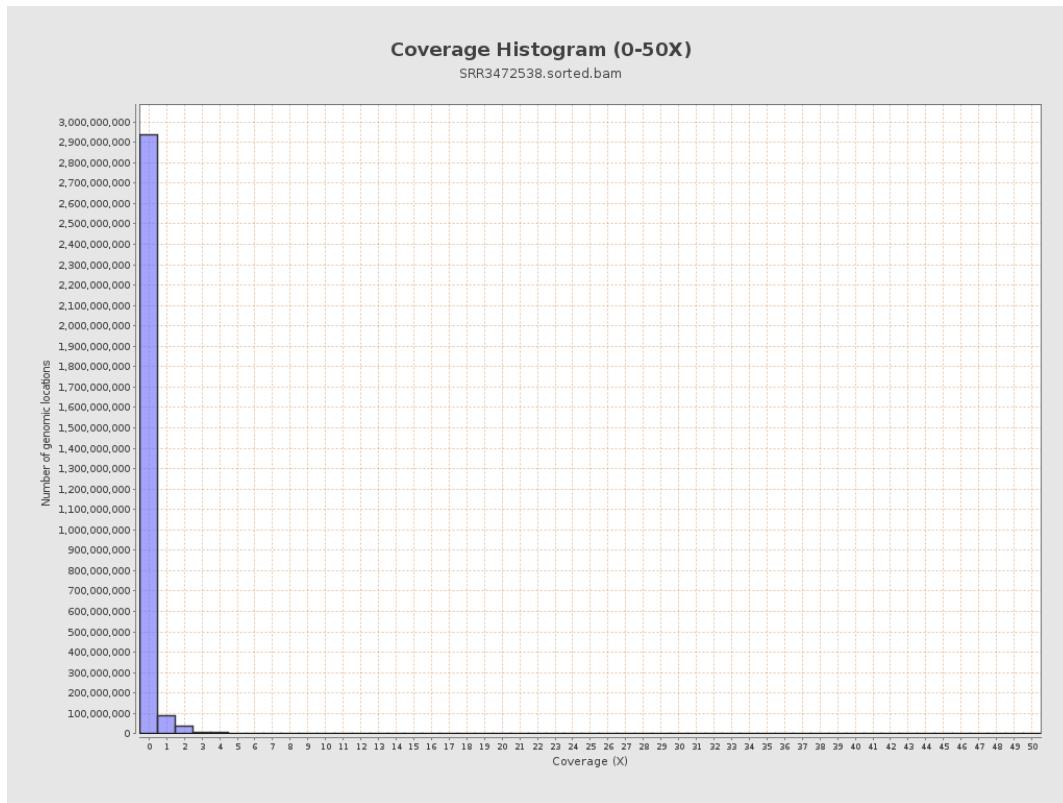
3. Results : Coverage across reference



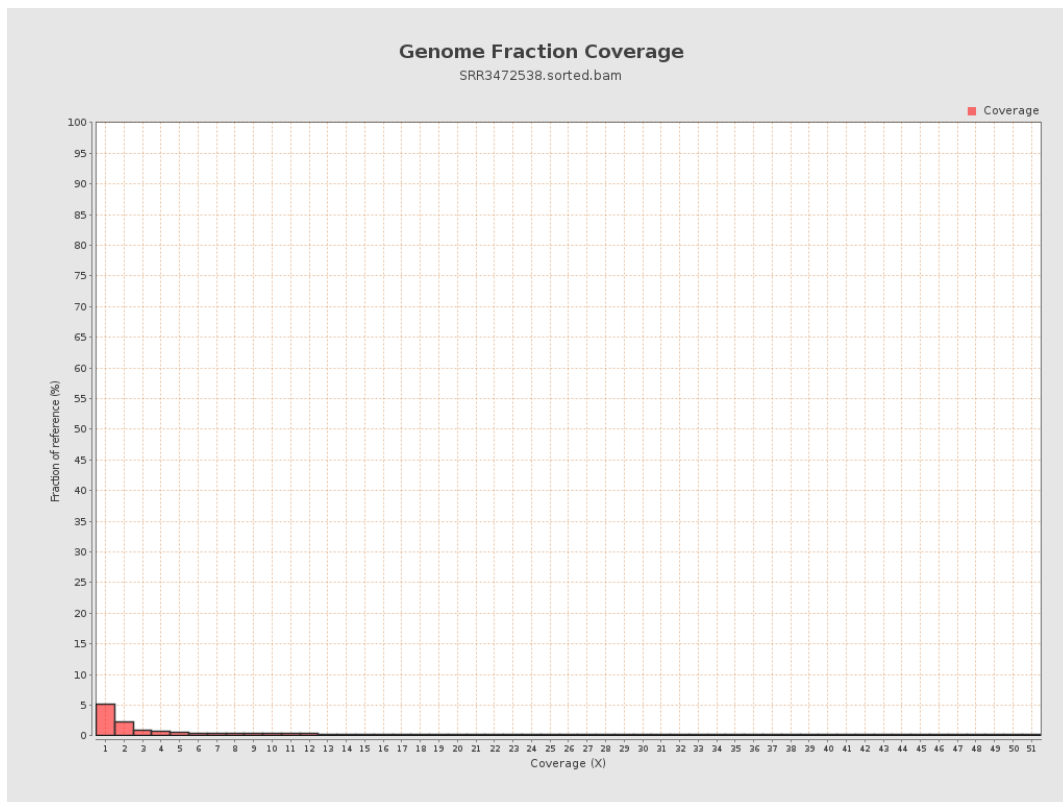
4. Results : Coverage Histogram



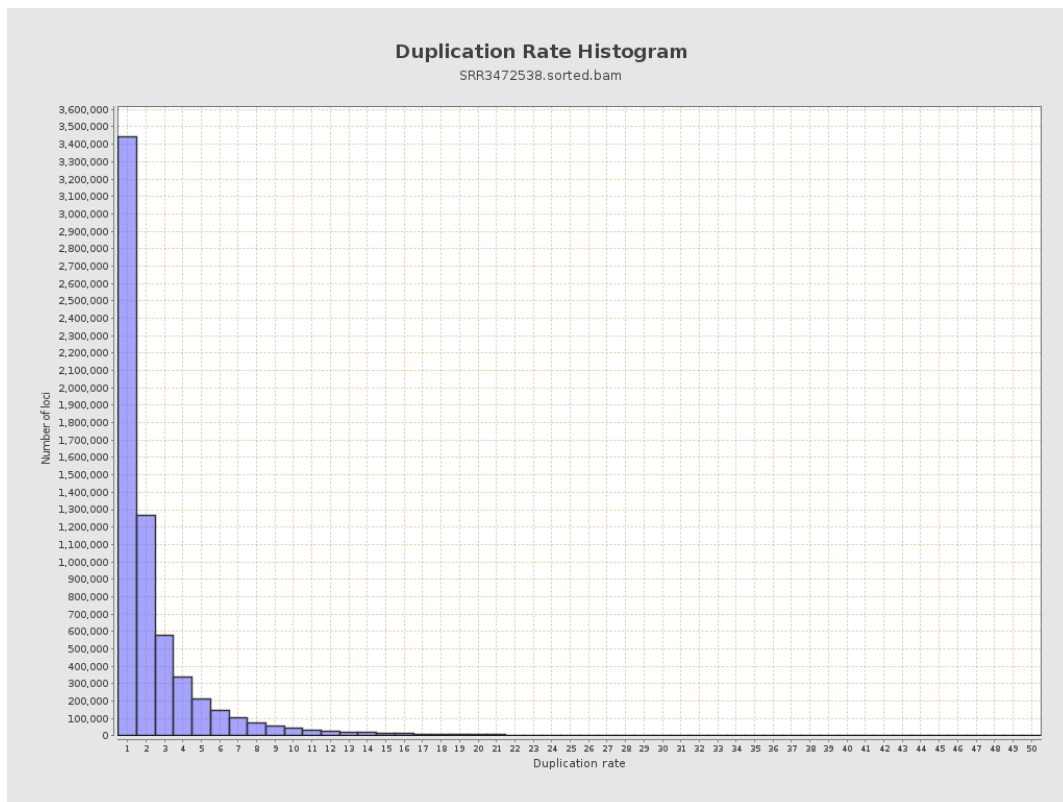
5. Results : Coverage Histogram (0-50X)



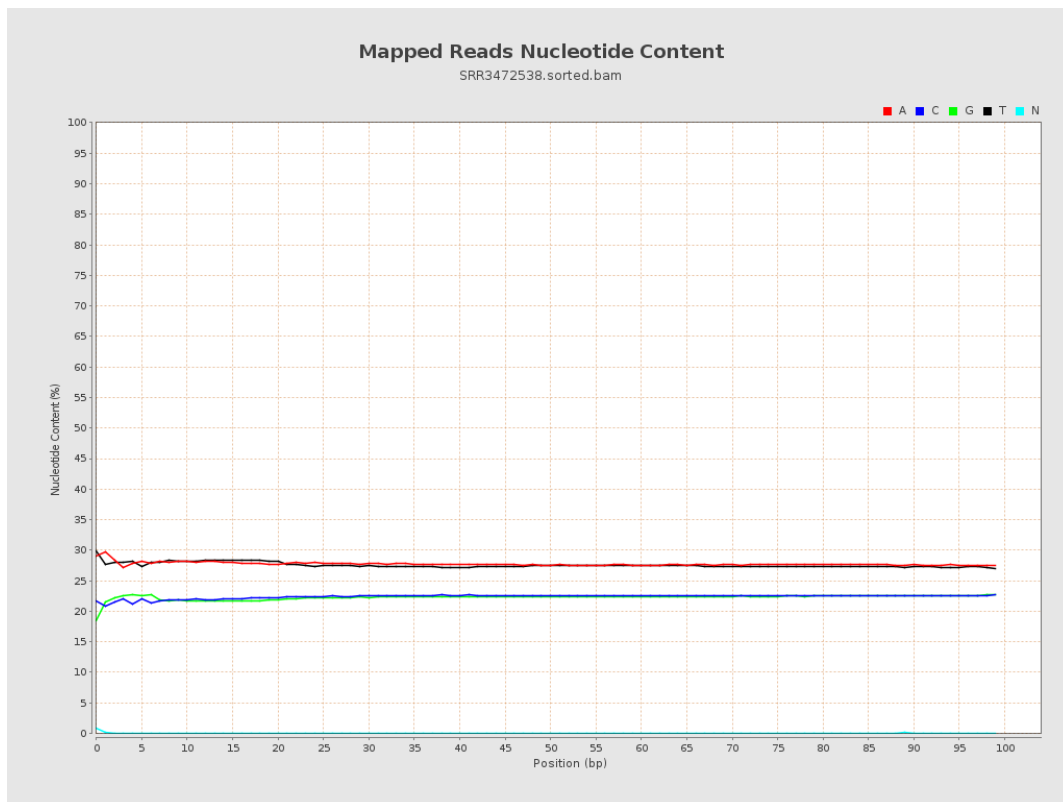
6. Results : Genome Fraction Coverage



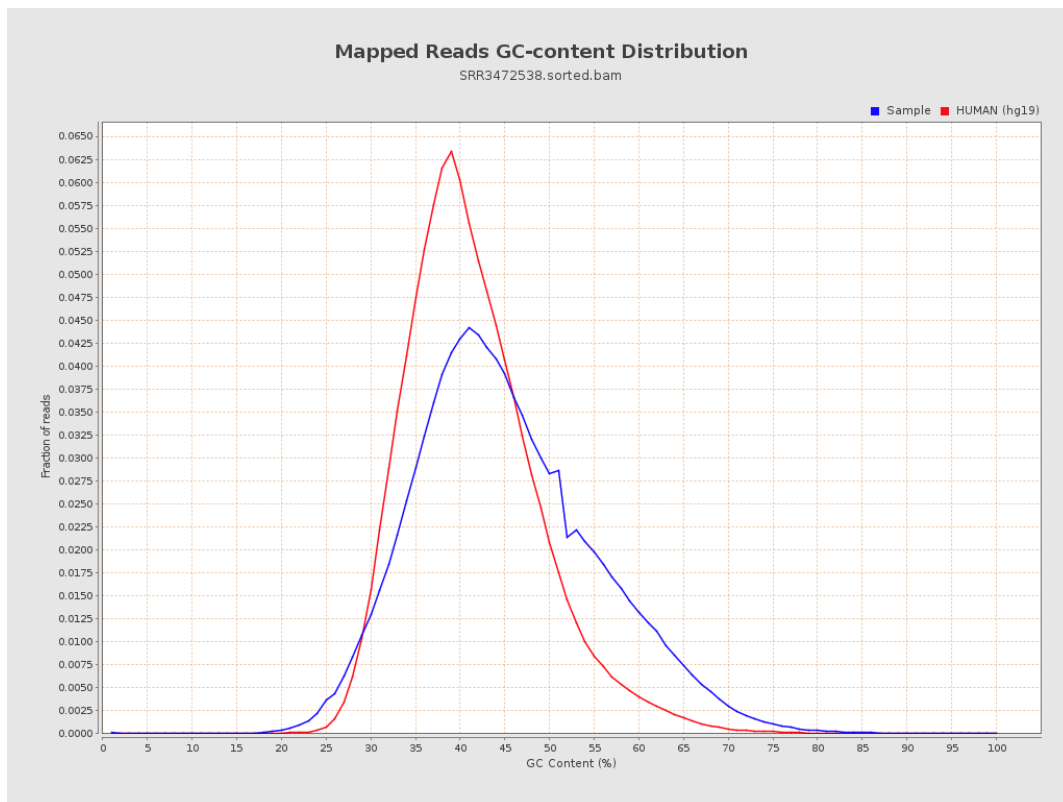
7. Results : Duplication Rate Histogram



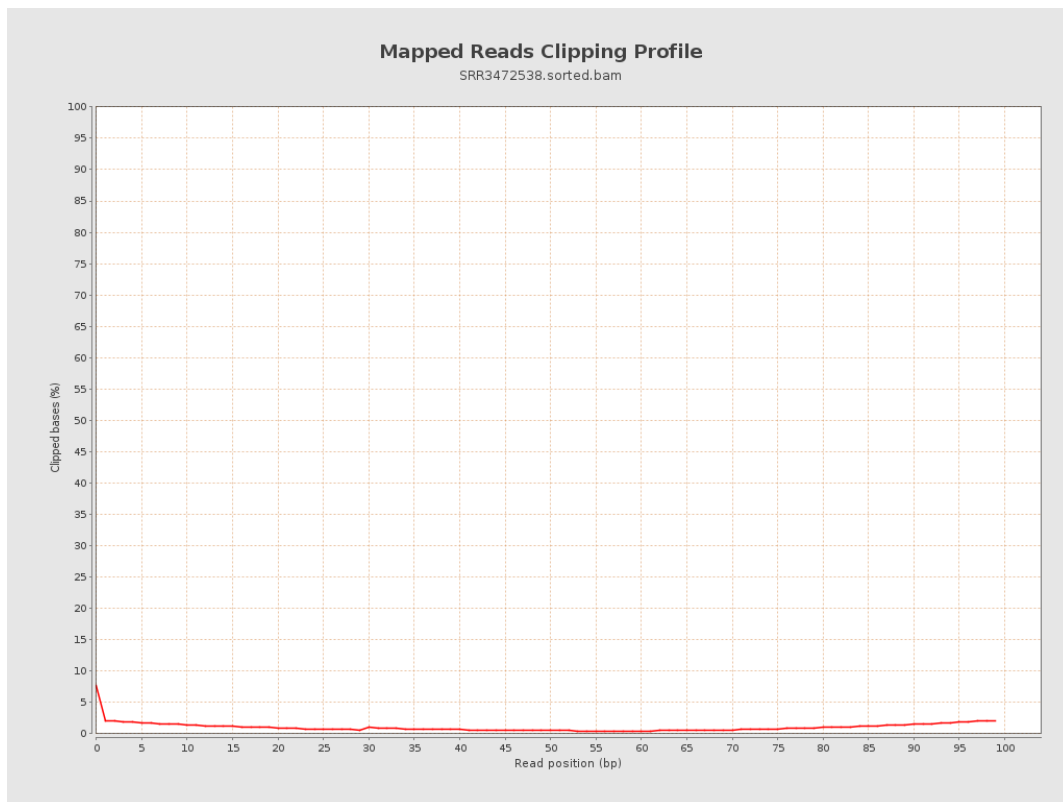
8. Results : Mapped Reads Nucleotide Content



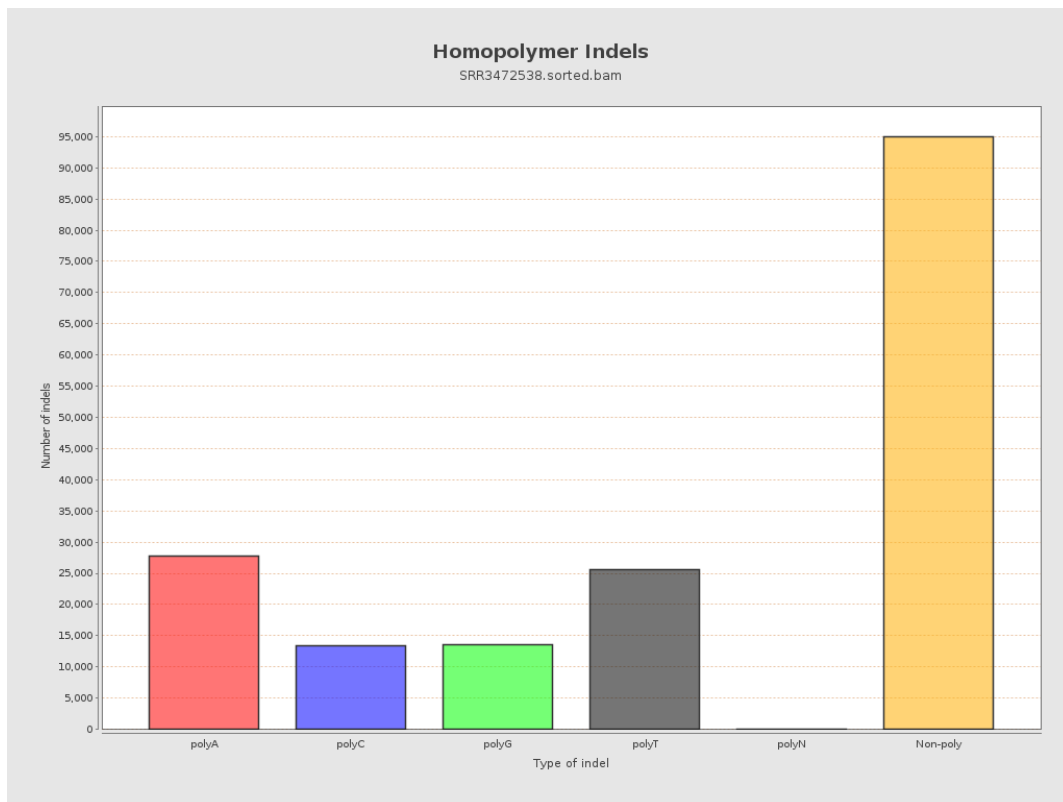
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



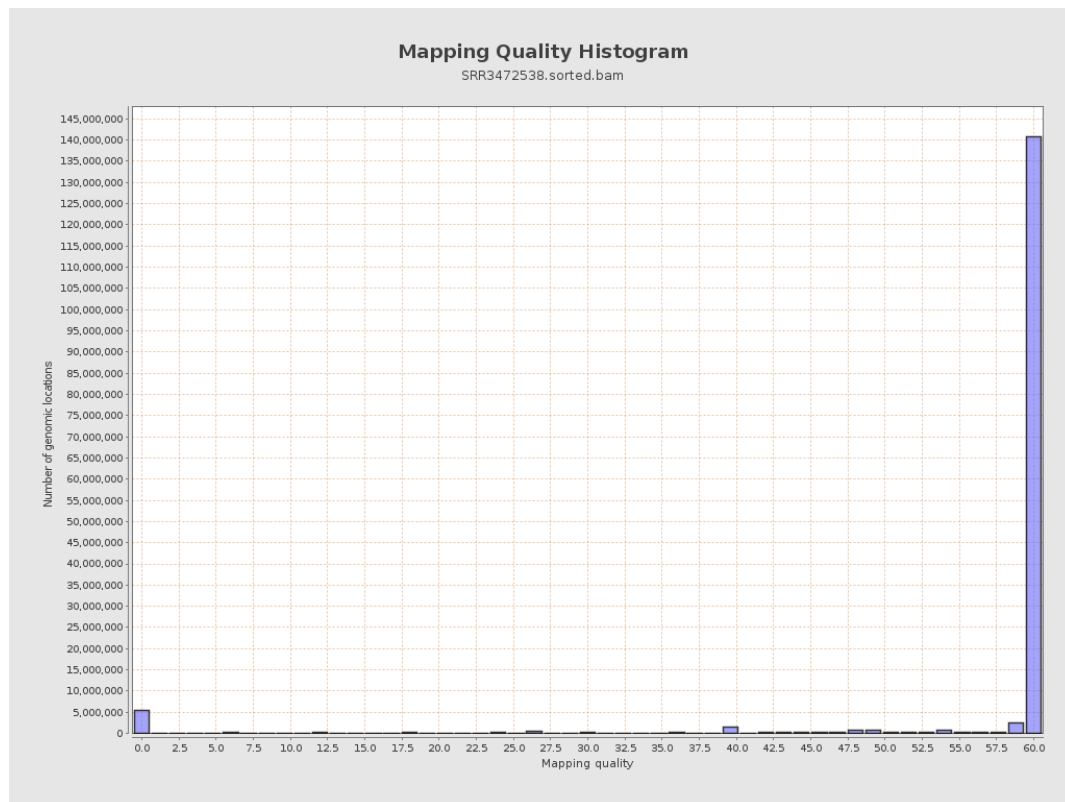
11. Results : Homopolymer Indels



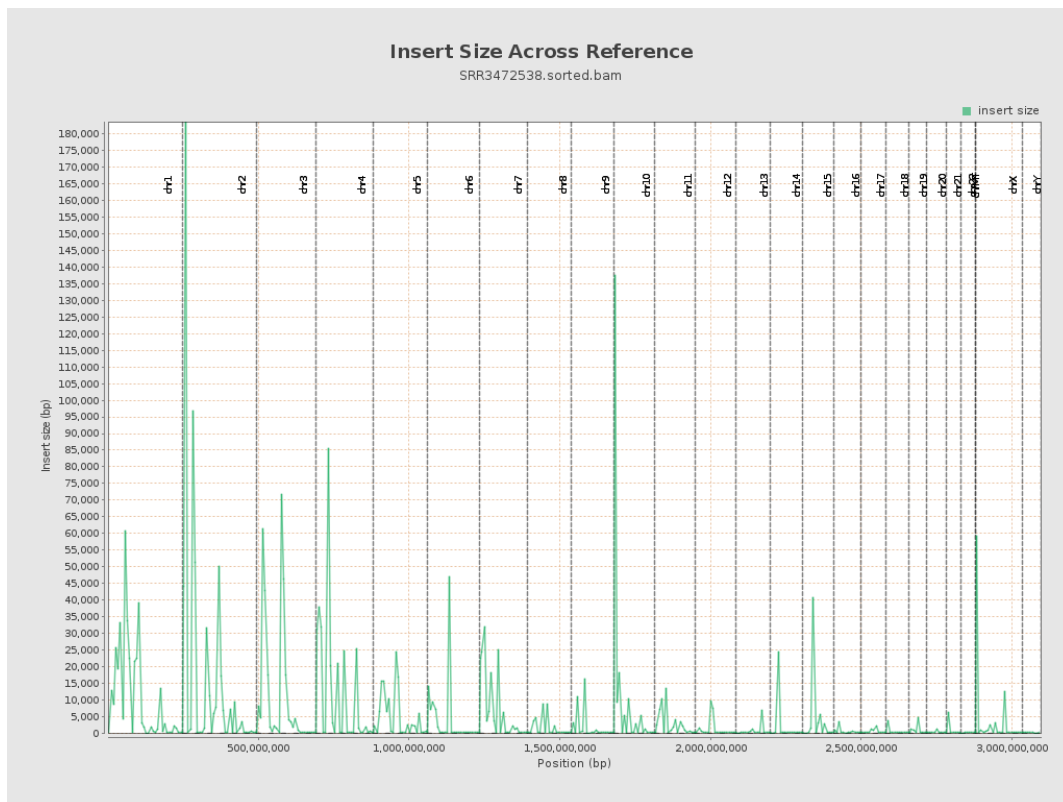
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

