

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 07:37:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438273.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_SRR8438273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438273_1.fastq.gz SRR8438273_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 07:37:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438273.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,399,701,716
Mapped reads	1,394,268,895 / 99.61%
Unmapped reads	5,432,821 / 0.39%
Mapped paired reads	1,394,268,895 / 99.61%
Mapped reads, first in pair	697,498,357 / 49.83%
Mapped reads, second in pair	696,770,538 / 49.78%
Mapped reads, both in pair	1,391,818,876 / 99.44%
Mapped reads, singletons	2,450,019 / 0.18%
Secondary alignments	0
Supplementary alignments	16,862,238 / 1.2%
Read min/max/mean length	30 / 149 / 114.16
Duplicated reads (estimated)	680,672,207 / 48.63%
Duplication rate	46.72%
Clipped reads	265,073,676 / 18.94%

2.2. ACGT Content

Number/percentage of A's	46,658,662,572 / 30.41%
Number/percentage of C's	30,379,901,964 / 19.8%
Number/percentage of T's	45,569,923,196 / 29.7%
Number/percentage of G's	30,839,887,612 / 20.1%
Number/percentage of N's	427,494 / 0%

GC Percentage	39.9%
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2.3. Coverage

Mean	49.5799
Standard Deviation	573.7904

2.4. Mapping Quality

Mean Mapping Quality	53.13
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2.5. Insert size

Mean	86,915.92
Standard Deviation	3,035,549.45
P25/Median/P75	77 / 124 / 197

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	496,816,277
Insertions	21,427,903
Mapped reads with at least one insertion	1.52%
Deletions	15,255,746
Mapped reads with at least one deletion	1.08%
Homopolymer indels	47.8%

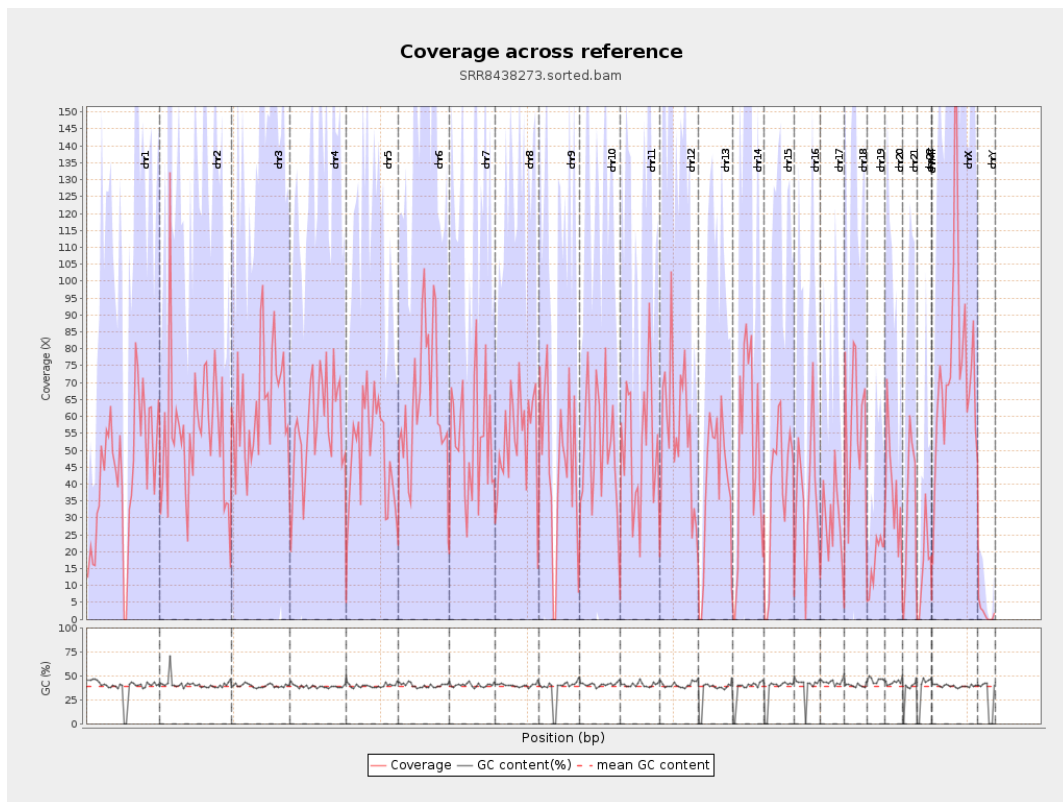
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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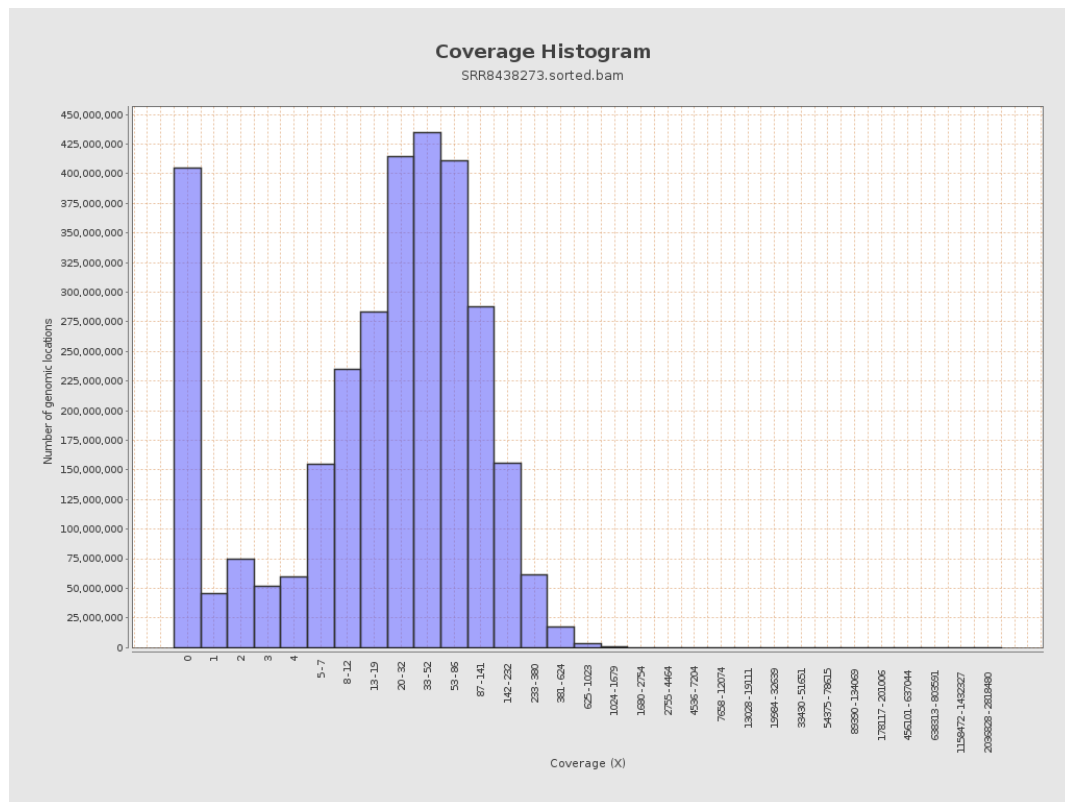
		bases	coverage	deviation
chr1	249250621	10937631722	43.8821	67.8435
chr2	243199373	13301160521	54.6924	2,032.3873
chr3	198022430	12650647857	63.8849	78.0771
chr4	191154276	11065899225	57.8899	70.5152
chr5	180915260	8878856239	49.0774	63.4412
chr6	171115067	11157711192	65.2059	82.5009
chr7	159138663	8421096618	52.9167	70.2566
chr8	146364022	7849570058	53.6305	69.3034
chr9	141213431	6300412160	44.6162	68.4603
chr10	135534747	6998624538	51.6371	68.9199
chr11	135006516	6954489822	51.5123	71.7806
chr12	133851895	7381947692	55.1501	80.7343
chr13	115169878	4644397442	40.3265	58.235
chr14	107349540	5220410568	48.63	73.359
chr15	102531392	3965575531	38.6767	65.0587
chr16	90354753	3177330753	35.1651	57.5091
chr17	81195210	2266785594	27.9177	49.598
chr18	78077248	4536313162	58.1003	70.9538
chr19	59128983	1011691946	17.1099	33.2226
chr20	63025520	2394603425	37.9942	60.1864
chr21	48129895	1688155734	35.075	58.1426
chr22	51304566	782115542	15.2446	37.1404
chrMT	16571	315189	19.0205	12.3612
chrX	155270560	11791410461	75.9411	103.8052

chrY	59373566	106957341	1.8014	10.8617
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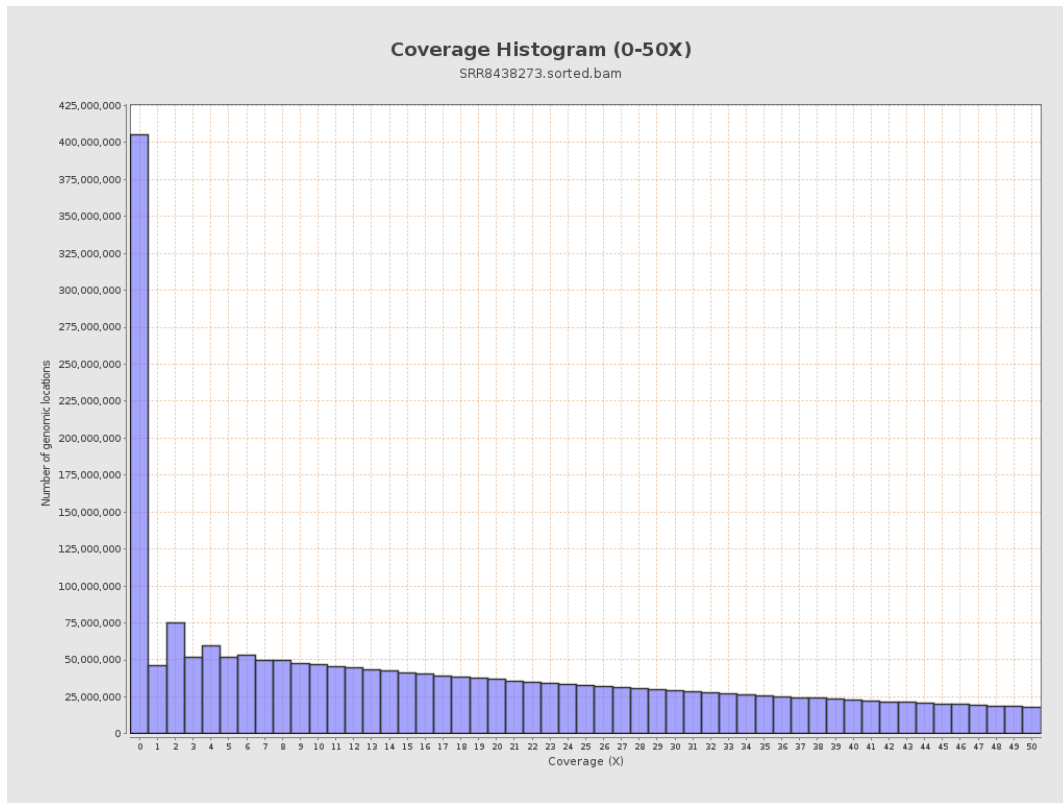
3. Results : Coverage across reference



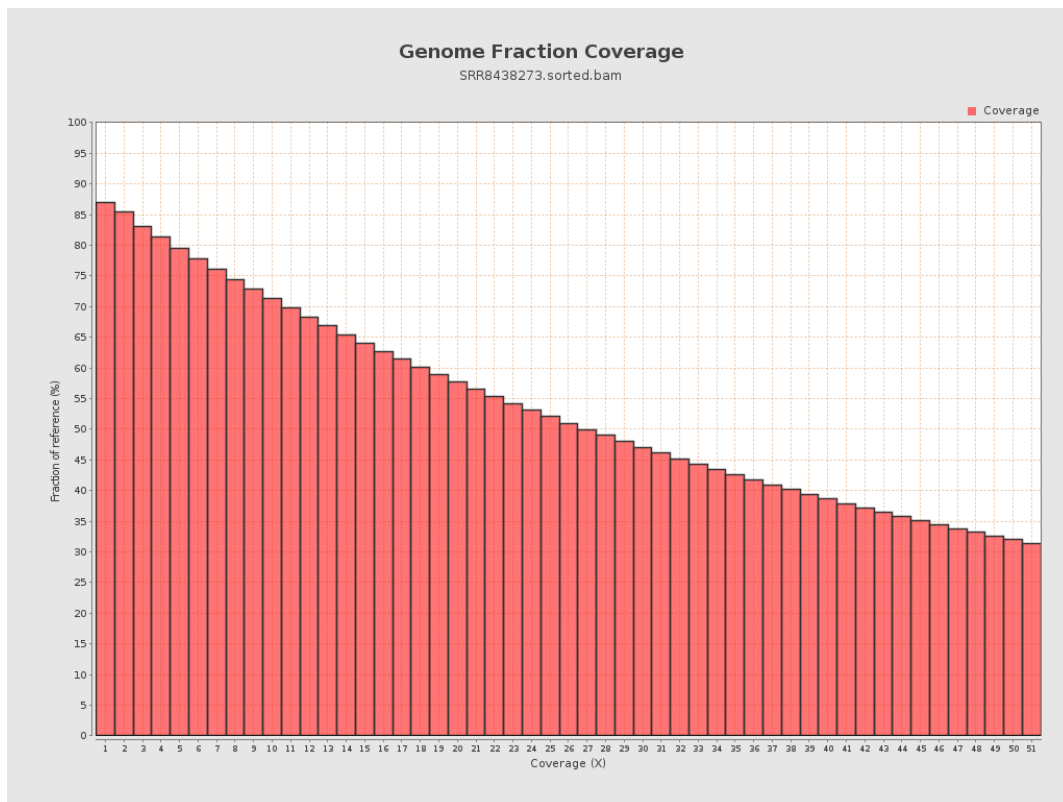
4. Results : Coverage Histogram



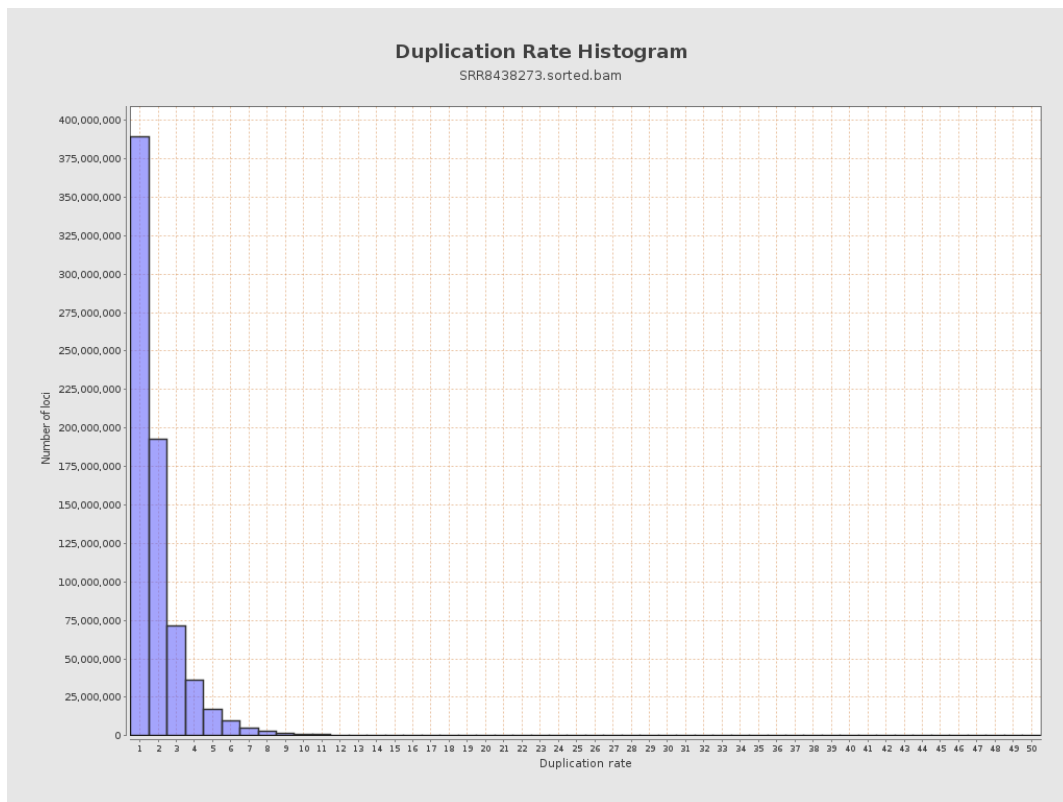
5. Results : Coverage Histogram (0-50X)



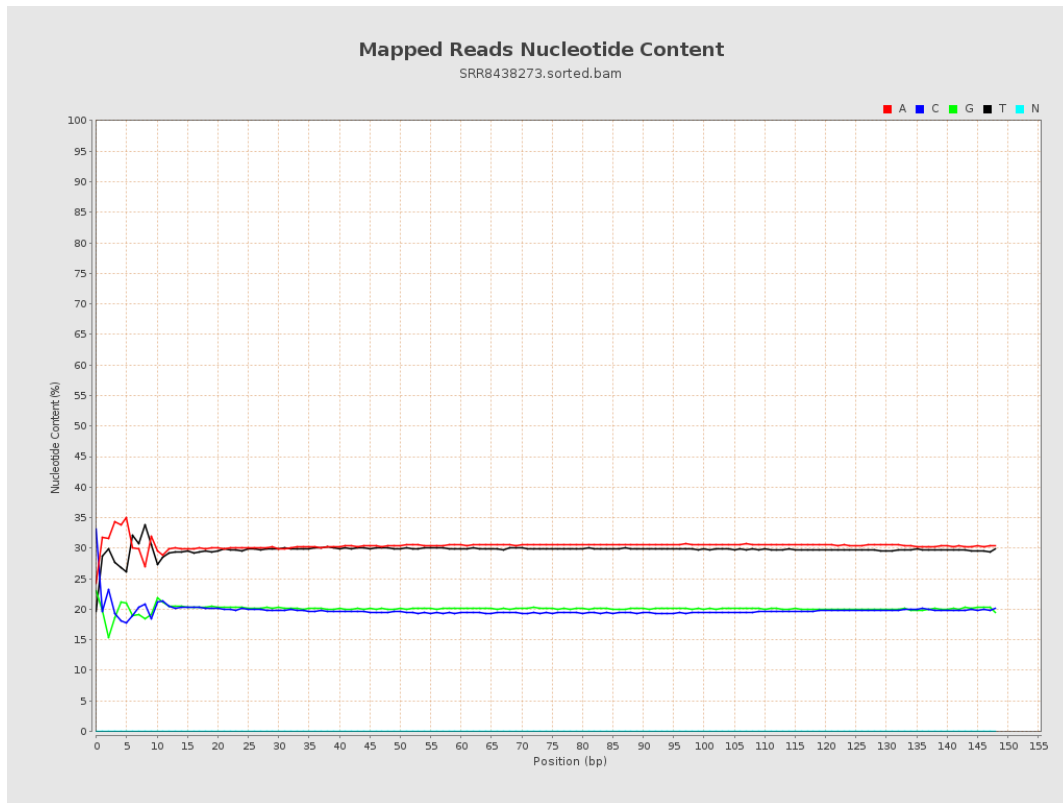
6. Results : Genome Fraction Coverage



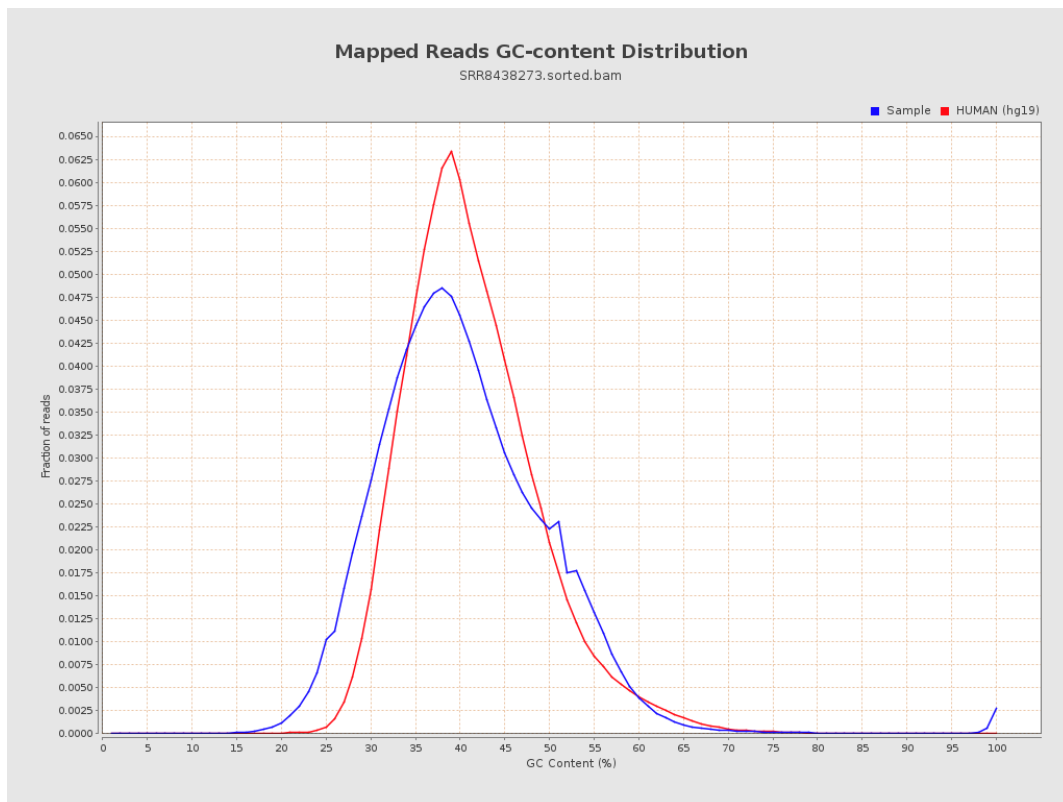
7. Results : Duplication Rate Histogram



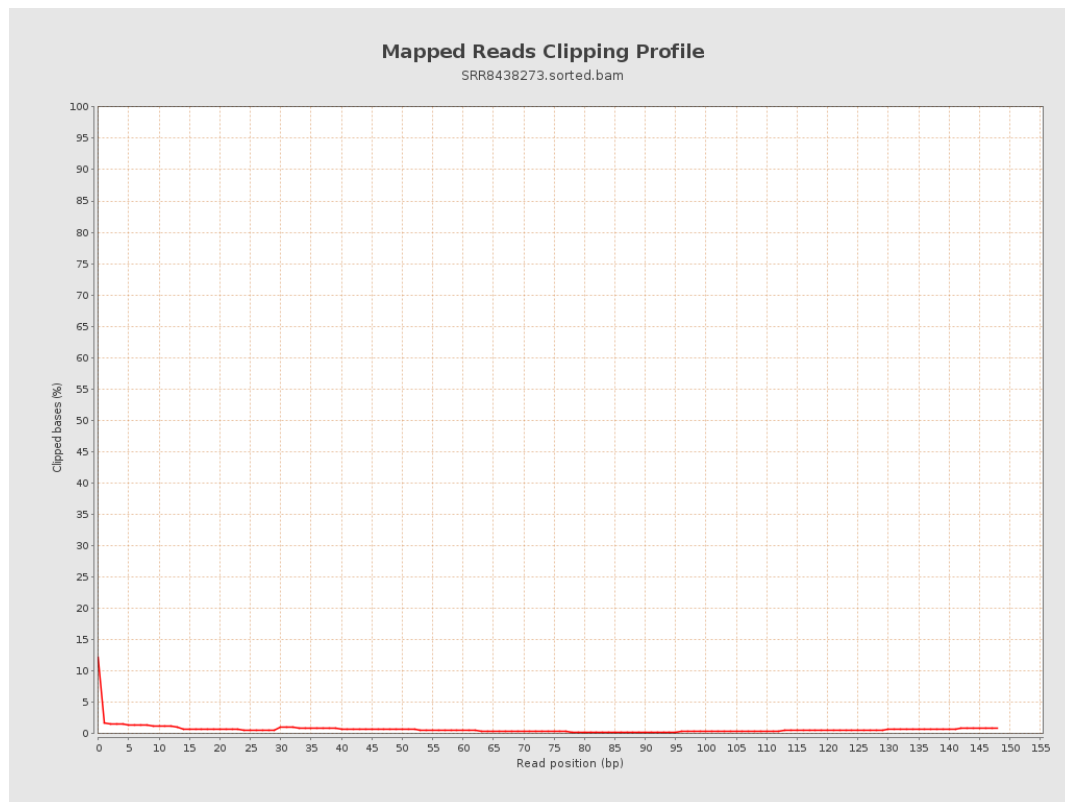
8. Results : Mapped Reads Nucleotide Content



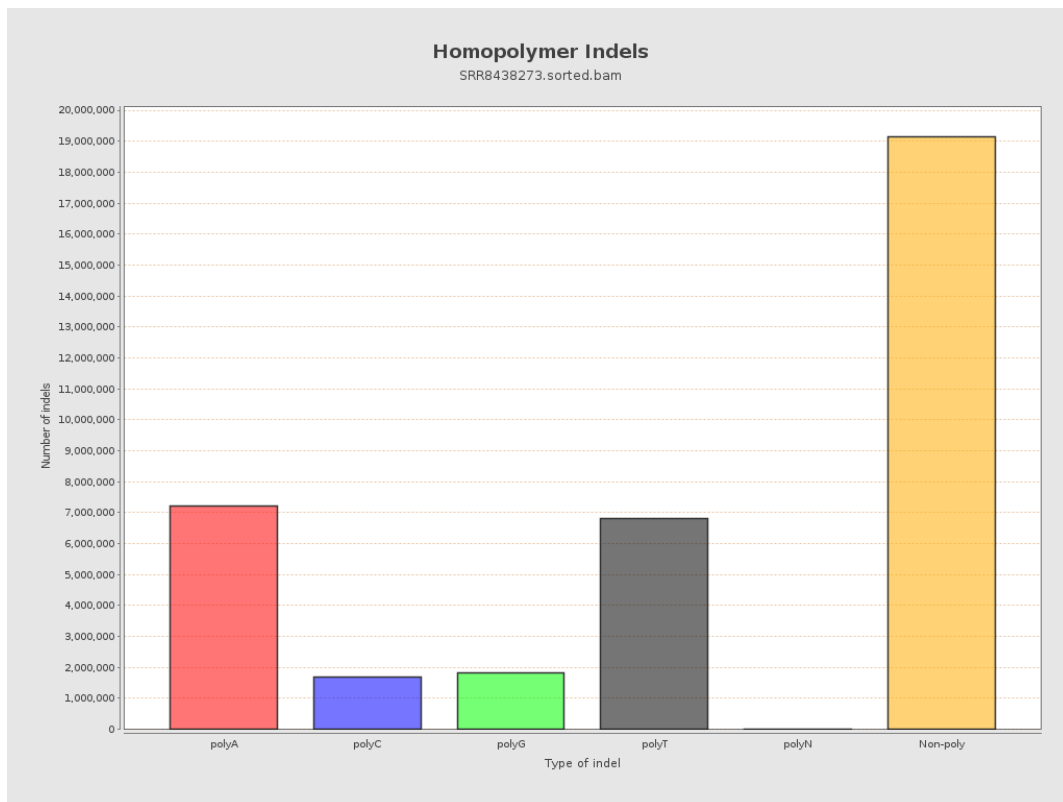
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



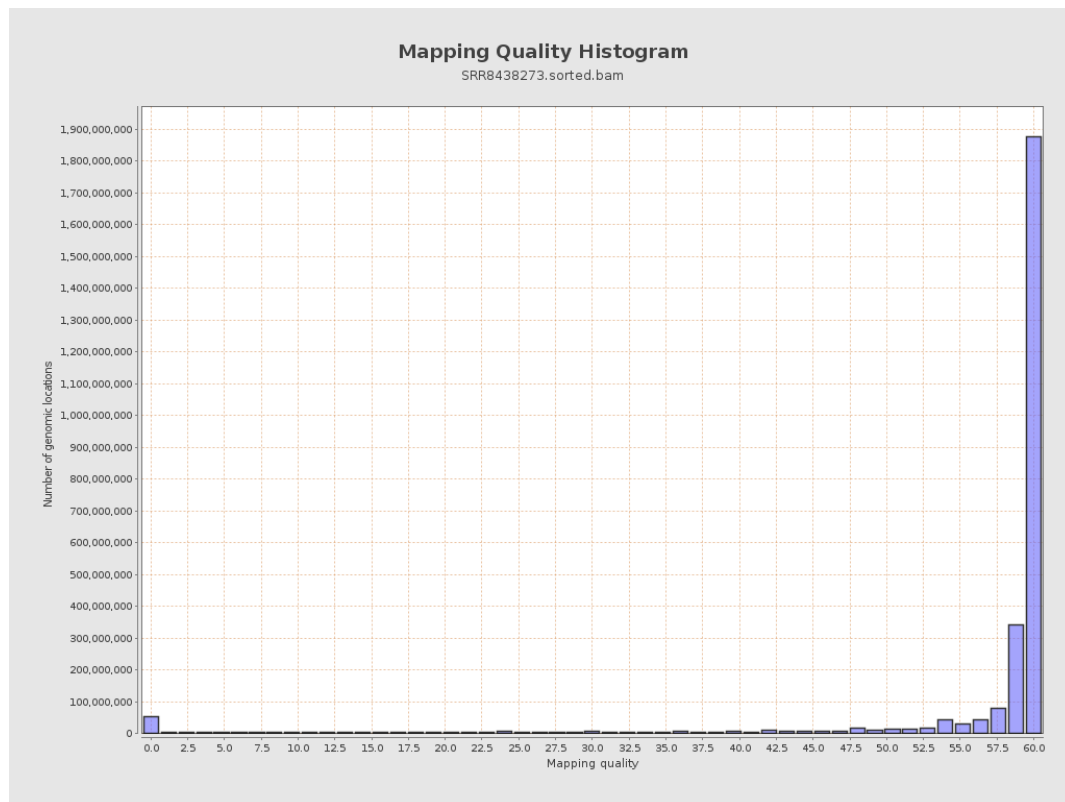
11. Results : Homopolymer Indels



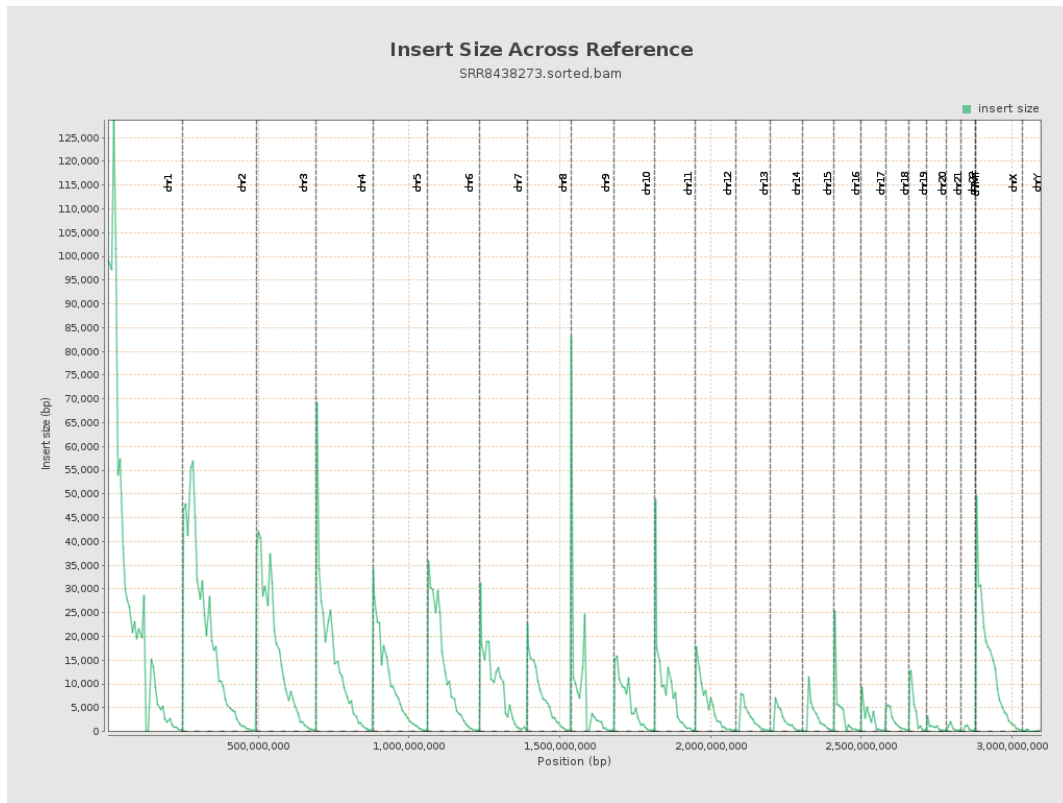
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

