

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:09:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173898.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_SRR10173898 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173898_1.fastq.gz SRR10173898_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:09:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173898.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,093,786
Mapped reads	3,990,150 / 97.47%
Unmapped reads	103,636 / 2.53%
Mapped paired reads	3,990,150 / 97.47%
Mapped reads, first in pair	1,996,581 / 48.77%
Mapped reads, second in pair	1,993,569 / 48.7%
Mapped reads, both in pair	3,916,138 / 95.66%
Mapped reads, singletons	74,012 / 1.81%
Secondary alignments	0
Supplementary alignments	444,060 / 10.85%
Read min/max/mean length	30 / 133 / 128.98
Duplicated reads (estimated)	3,142,349 / 76.76%
Duplication rate	64.21%
Clipped reads	1,709,321 / 41.75%

2.2. ACGT Content

Number/percentage of A's	141,906,229 / 30.03%
Number/percentage of C's	92,555,826 / 19.58%
Number/percentage of T's	141,906,482 / 30.03%
Number/percentage of G's	96,246,948 / 20.36%
Number/percentage of N's	5,140 / 0%

GC Percentage	39.95%
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2.3. Coverage

Mean	0.1528
Standard Deviation	2.2958

2.4. Mapping Quality

Mean Mapping Quality	52.56
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2.5. Insert size

Mean	1,305,556
Standard Deviation	10,642,386.77
P25/Median/P75	149 / 209 / 297

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	4,868,190
Insertions	53,097
Mapped reads with at least one insertion	1.28%
Deletions	109,046
Mapped reads with at least one deletion	2.67%
Homopolymer indels	42.75%

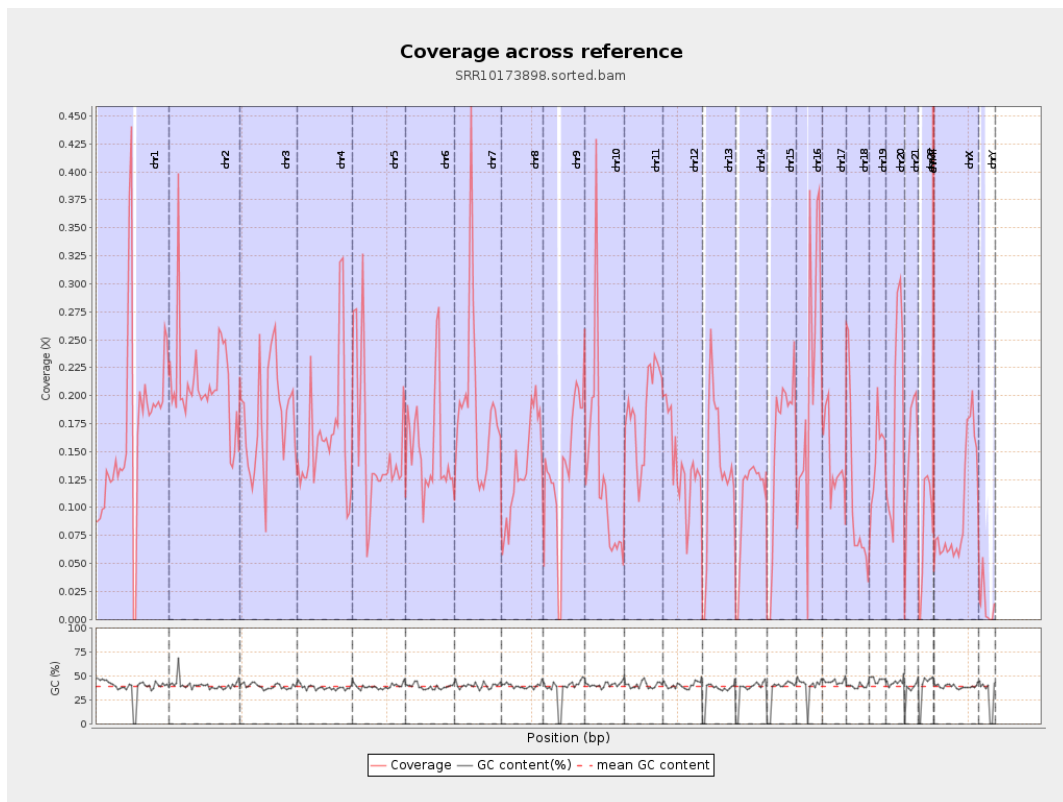
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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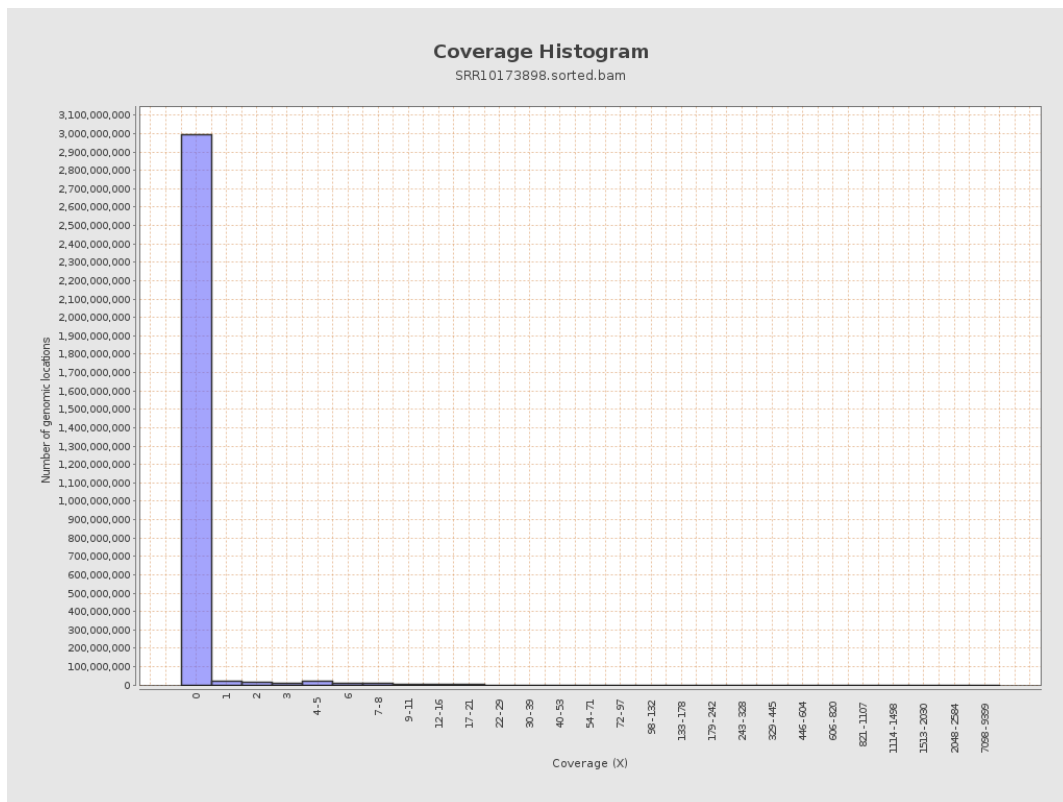
		bases	coverage	deviation
chr1	249250621	41574332	0.1668	1.8337
chr2	243199373	50862726	0.2091	6.6157
chr3	198022430	35835953	0.181	1.2317
chr4	191154276	30777978	0.161	1.4594
chr5	180915260	28339576	0.1566	1.1411
chr6	171115067	26191950	0.1531	1.182
chr7	159138663	29931175	0.1881	1.8592
chr8	146364022	19674531	0.1344	1.165
chr9	141213431	19457931	0.1378	1.2504
chr10	135534747	17232568	0.1271	2.1961
chr11	135006516	25206551	0.1867	1.2582
chr12	133851895	18458557	0.1379	1.066
chr13	115169878	15328621	0.1331	1.0541
chr14	107349540	11425534	0.1064	0.9457
chr15	102531392	15828480	0.1544	1.1211
chr16	90354753	18961256	0.2099	1.8174
chr17	81195210	11230596	0.1383	1.1374
chr18	78077248	8334350	0.1067	1.7045
chr19	59128983	8570662	0.1449	1.7265
chr20	63025520	11387822	0.1807	1.2669
chr21	48129895	7154703	0.1487	1.1722
chr22	51304566	4148882	0.0809	0.7699
chrMT	16571	1238939	74.7655	58.7799
chrX	155270560	14987956	0.0965	0.8981

chrY	59373566	744720	0.0125	0.6746
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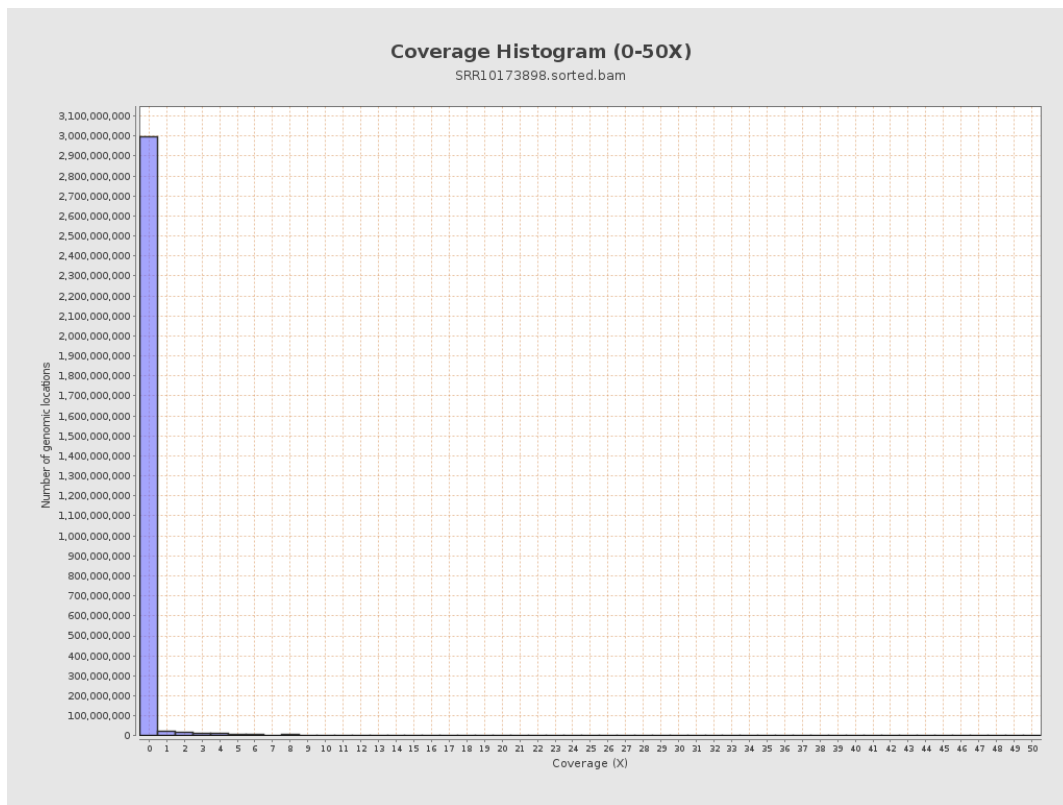
3. Results : Coverage across reference



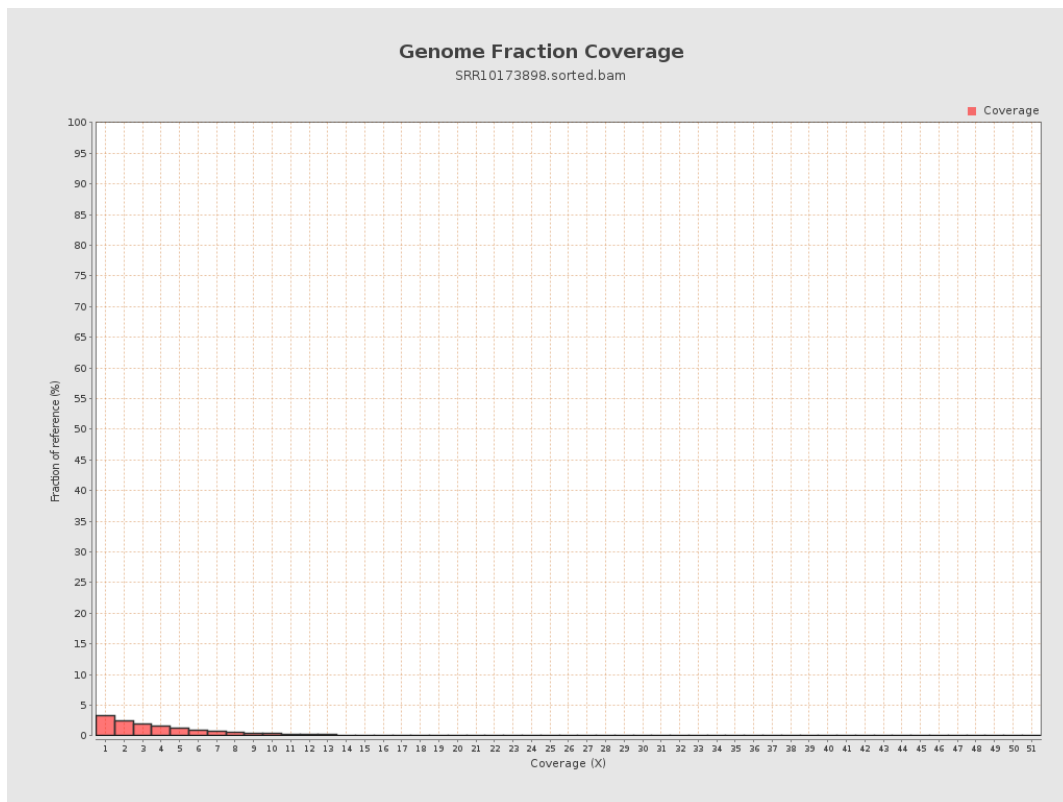
4. Results : Coverage Histogram



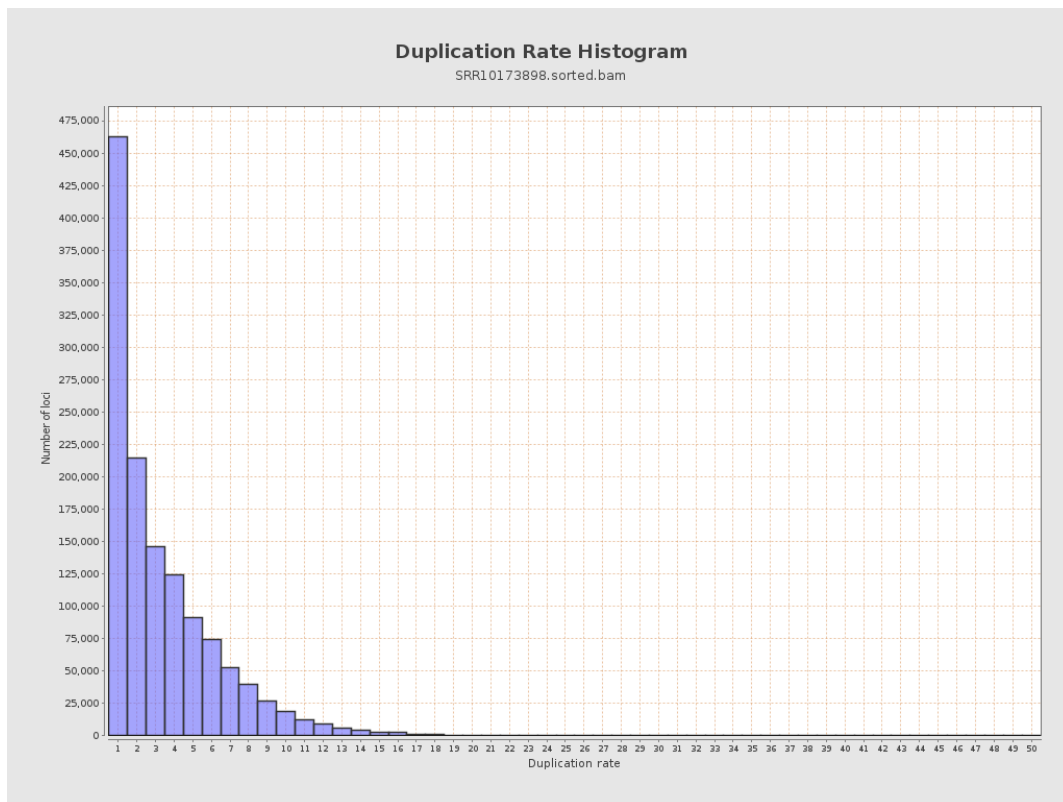
5. Results : Coverage Histogram (0-50X)



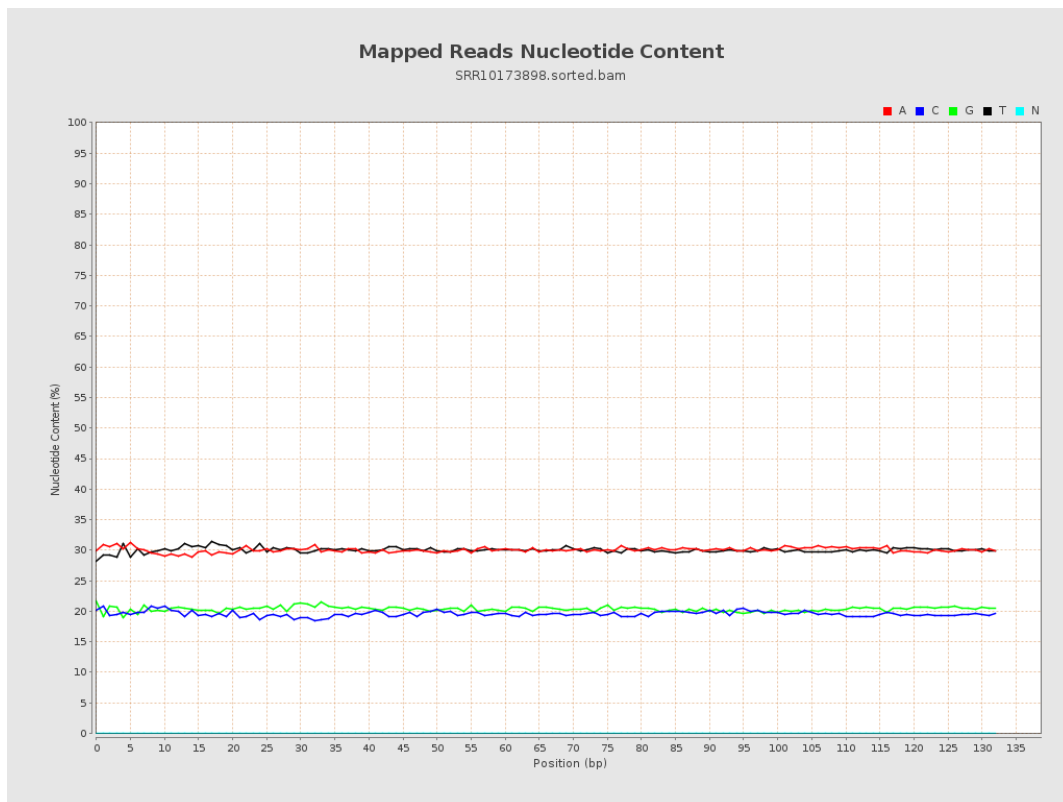
6. Results : Genome Fraction Coverage



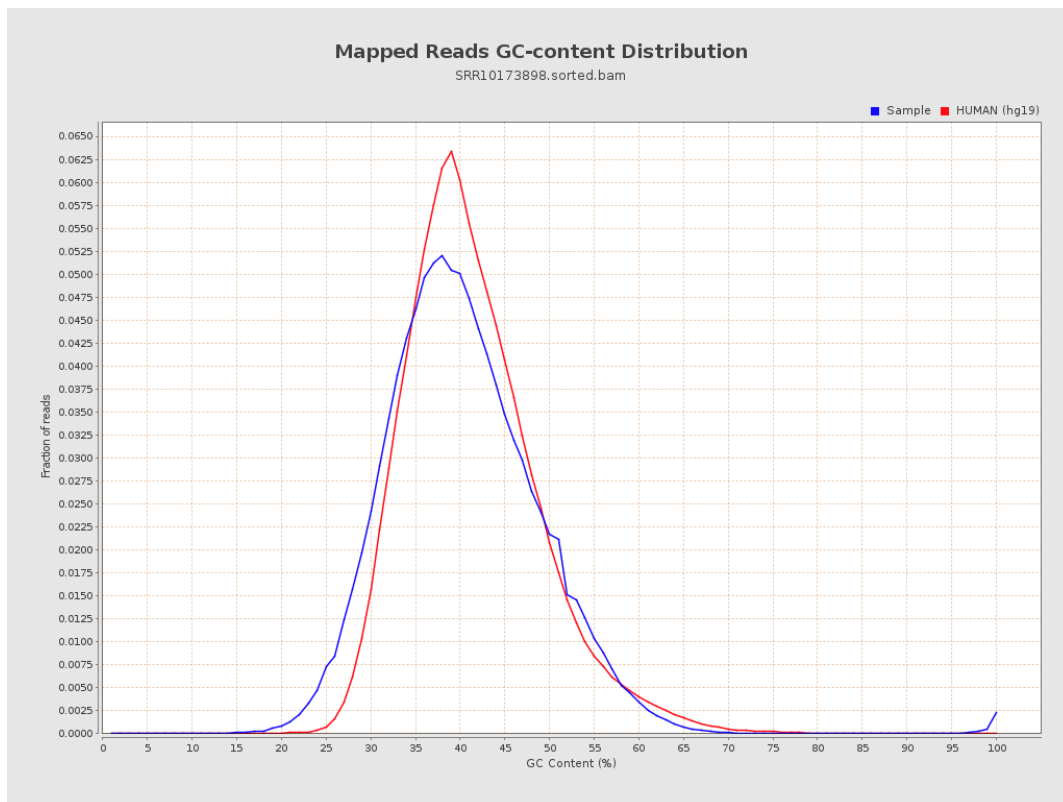
7. Results : Duplication Rate Histogram



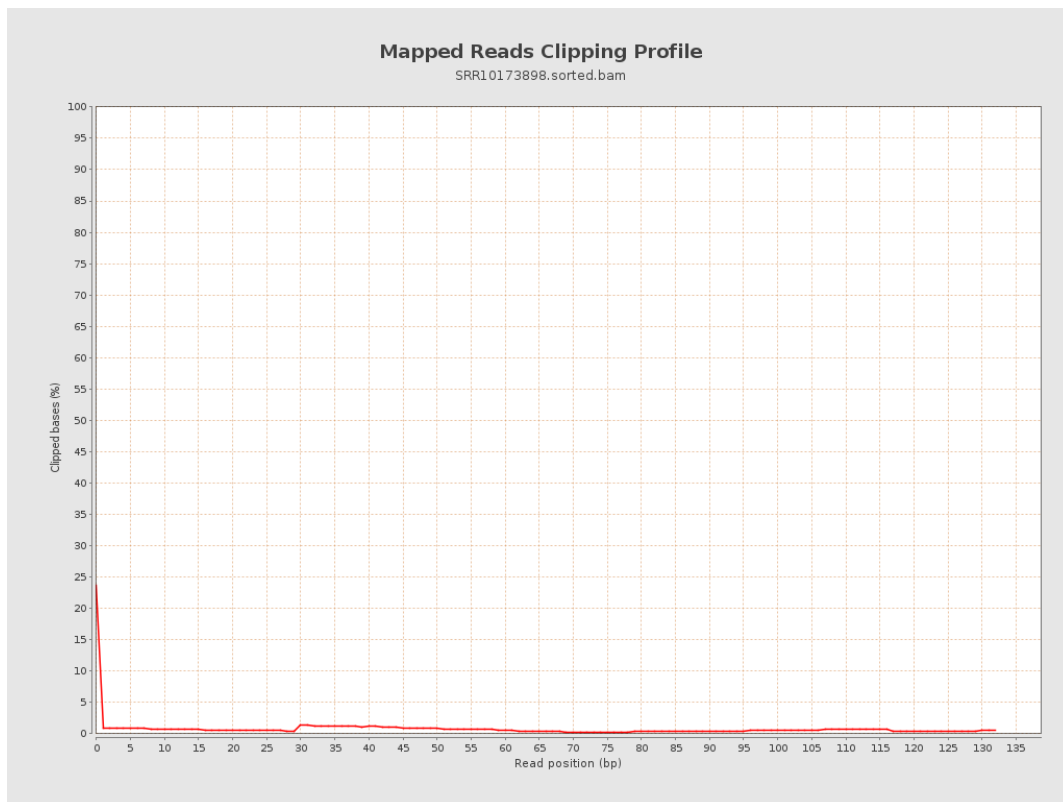
8. Results : Mapped Reads Nucleotide Content



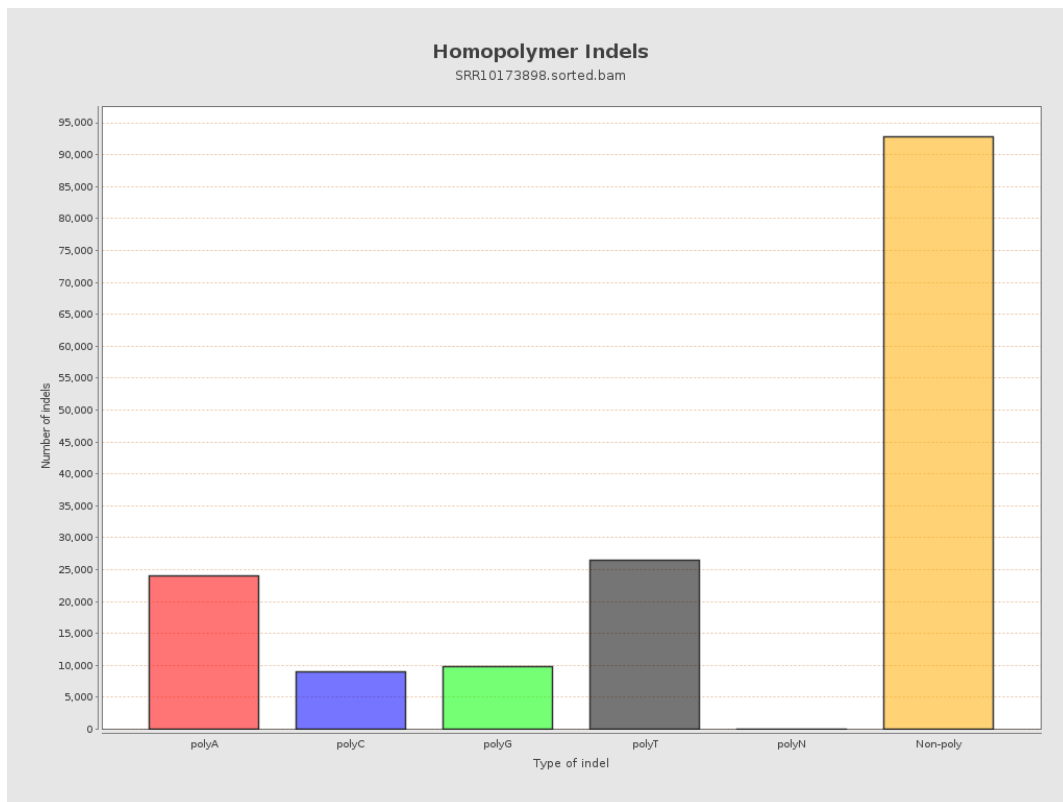
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



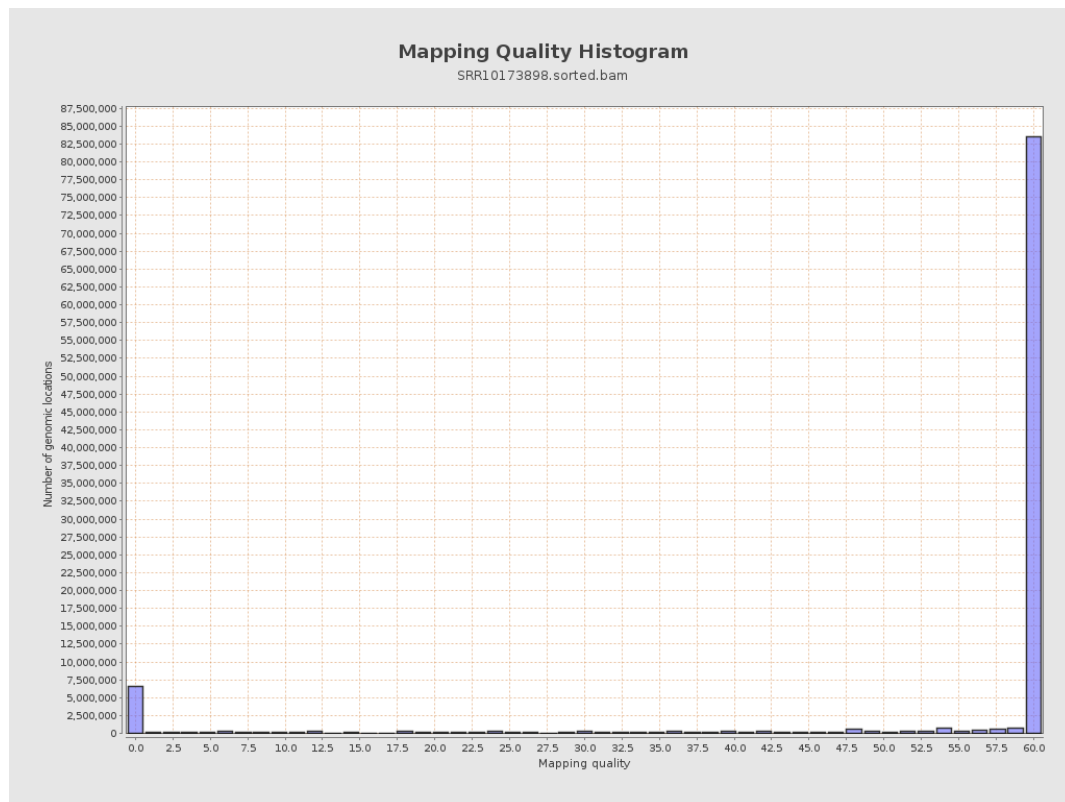
11. Results : Homopolymer Indels



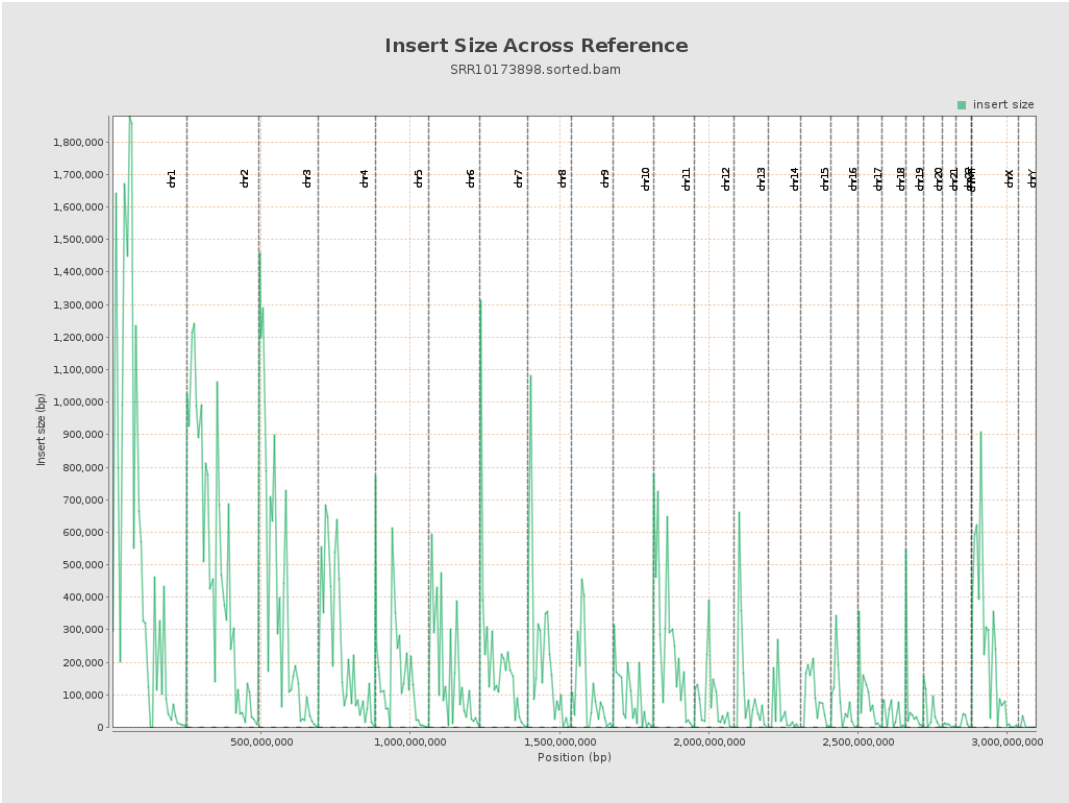
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

