

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:12:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173879.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_SRR10173879 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173879_1.fastq.gz SRR10173879_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:12:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173879.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,815,154
Mapped reads	1,768,740 / 97.44%
Unmapped reads	46,414 / 2.56%
Mapped paired reads	1,768,740 / 97.44%
Mapped reads, first in pair	885,651 / 48.79%
Mapped reads, second in pair	883,089 / 48.65%
Mapped reads, both in pair	1,739,388 / 95.83%
Mapped reads, singletons	29,352 / 1.62%
Secondary alignments	0
Supplementary alignments	171,538 / 9.45%
Read min/max/mean length	30 / 133 / 128
Duplicated reads (estimated)	1,328,402 / 73.18%
Duplication rate	62.83%
Clipped reads	721,999 / 39.78%

2.2. ACGT Content

Number/percentage of A's	63,370,975 / 30.34%
Number/percentage of C's	40,419,123 / 19.35%
Number/percentage of T's	63,217,507 / 30.27%
Number/percentage of G's	41,853,199 / 20.04%
Number/percentage of N's	1,980 / 0%

GC Percentage	39.39%
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2.3. Coverage

Mean	0.0675
Standard Deviation	1.1486

2.4. Mapping Quality

Mean Mapping Quality	53.08
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2.5. Insert size

Mean	1,064,995.5
Standard Deviation	9,732,605.62
P25/Median/P75	142 / 197 / 280

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	2,153,738
Insertions	22,936
Mapped reads with at least one insertion	1.25%
Deletions	48,336
Mapped reads with at least one deletion	2.66%
Homopolymer indels	43.31%

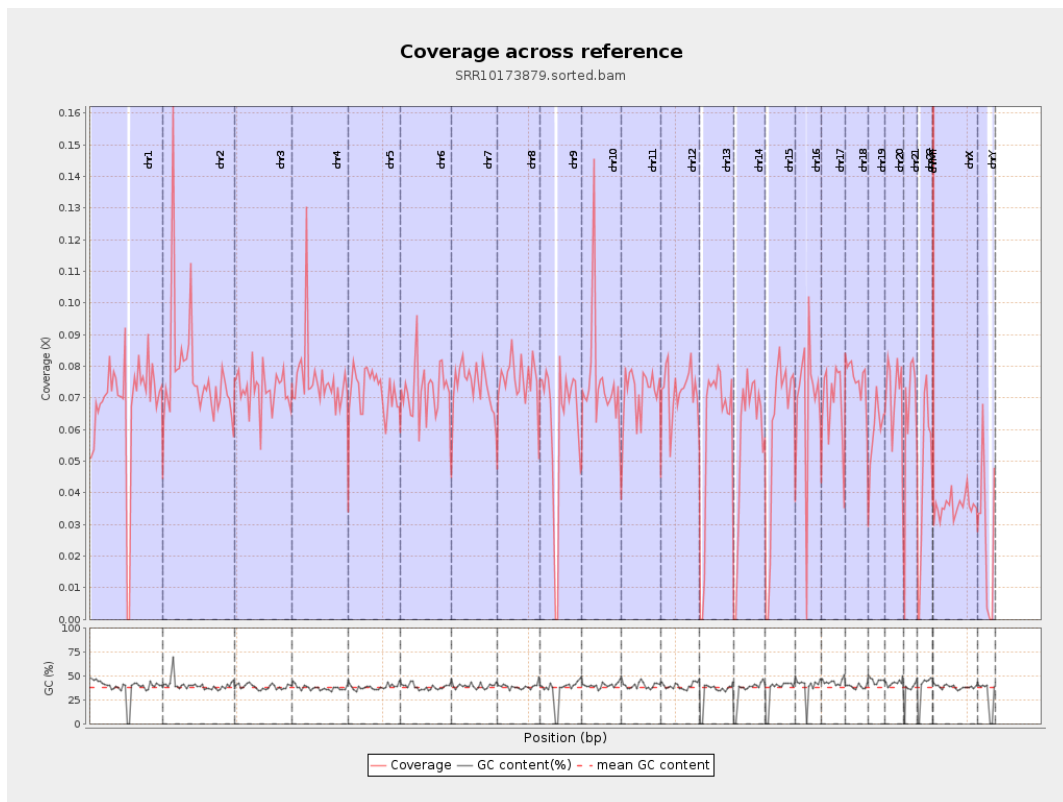
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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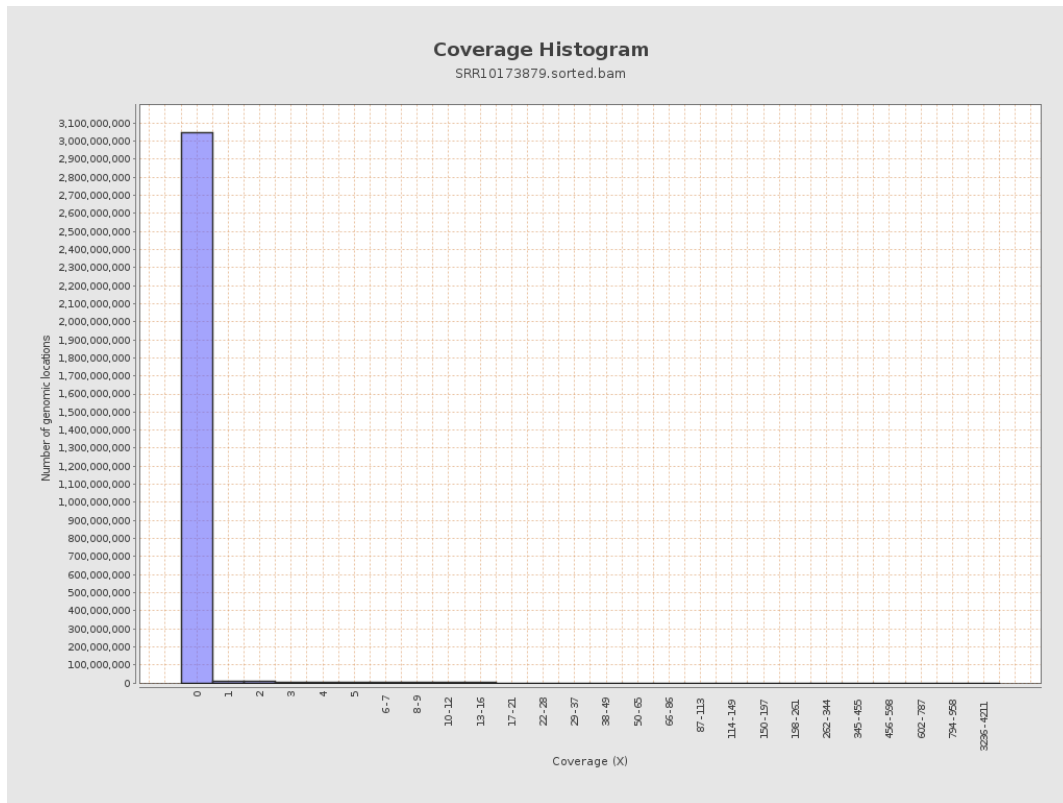
		bases	coverage	deviation
chr1	249250621	16956323	0.068	0.9037
chr2	243199373	18750962	0.0771	3.0033
chr3	198022430	14349388	0.0725	0.7584
chr4	191154276	14489544	0.0758	0.8728
chr5	180915260	13016719	0.0719	0.7515
chr6	171115067	12390251	0.0724	0.802
chr7	159138663	11663407	0.0733	0.8582
chr8	146364022	11074915	0.0757	1.022
chr9	141213431	8786540	0.0622	0.8227
chr10	135534747	10150513	0.0749	1.0675
chr11	135006516	9659111	0.0715	0.7521
chr12	133851895	9726688	0.0727	0.7588
chr13	115169878	6904764	0.06	0.6855
chr14	107349540	6175379	0.0575	0.6668
chr15	102531392	6064577	0.0591	0.675
chr16	90354753	6146983	0.068	0.7856
chr17	81195210	5637907	0.0694	0.7803
chr18	78077248	5953317	0.0762	1.0645
chr19	59128983	3554049	0.0601	0.7476
chr20	63025520	4515587	0.0716	0.7488
chr21	48129895	3133814	0.0651	0.8792
chr22	51304566	2344376	0.0457	0.6143
chrMT	16571	326041	19.6754	17.2209
chrX	155270560	5546329	0.0357	0.5358

chrY	59373566	1663073	0.028	0.5557
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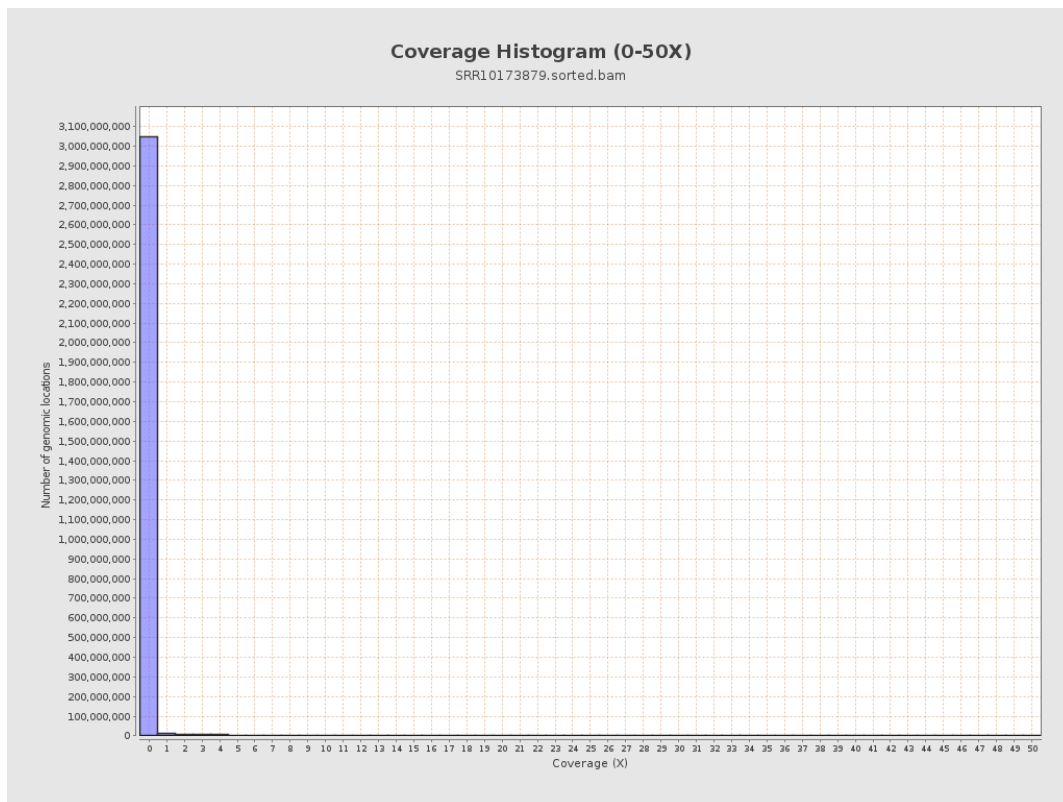
3. Results : Coverage across reference



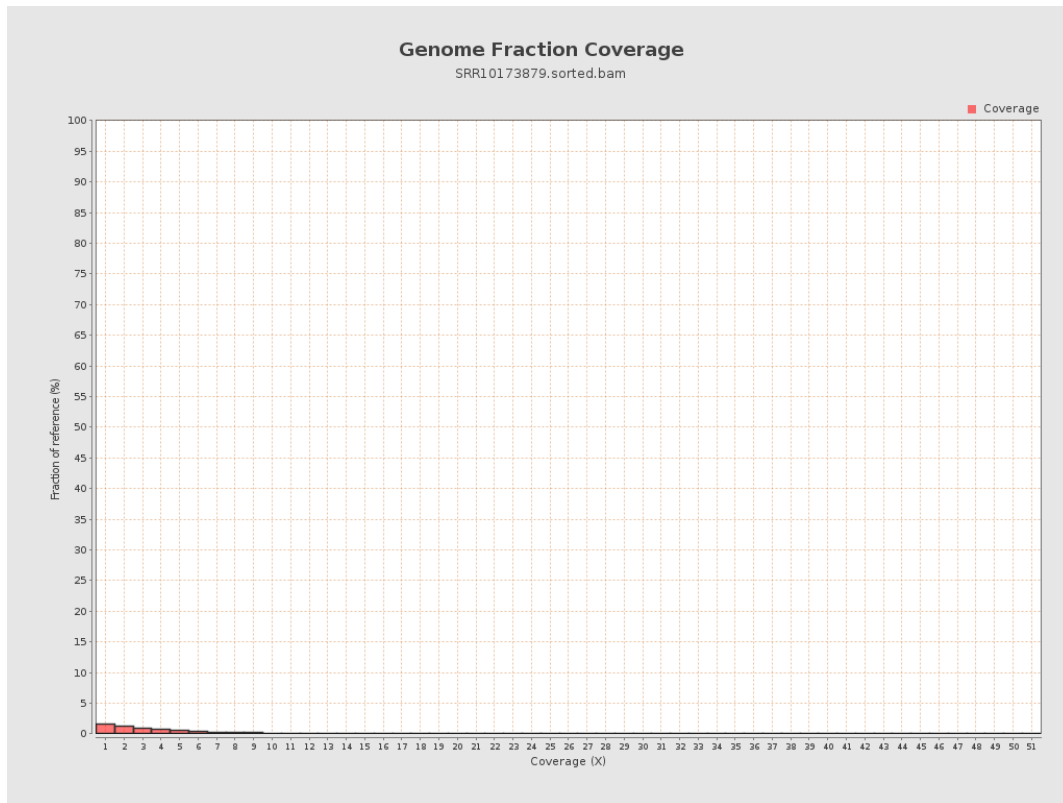
4. Results : Coverage Histogram



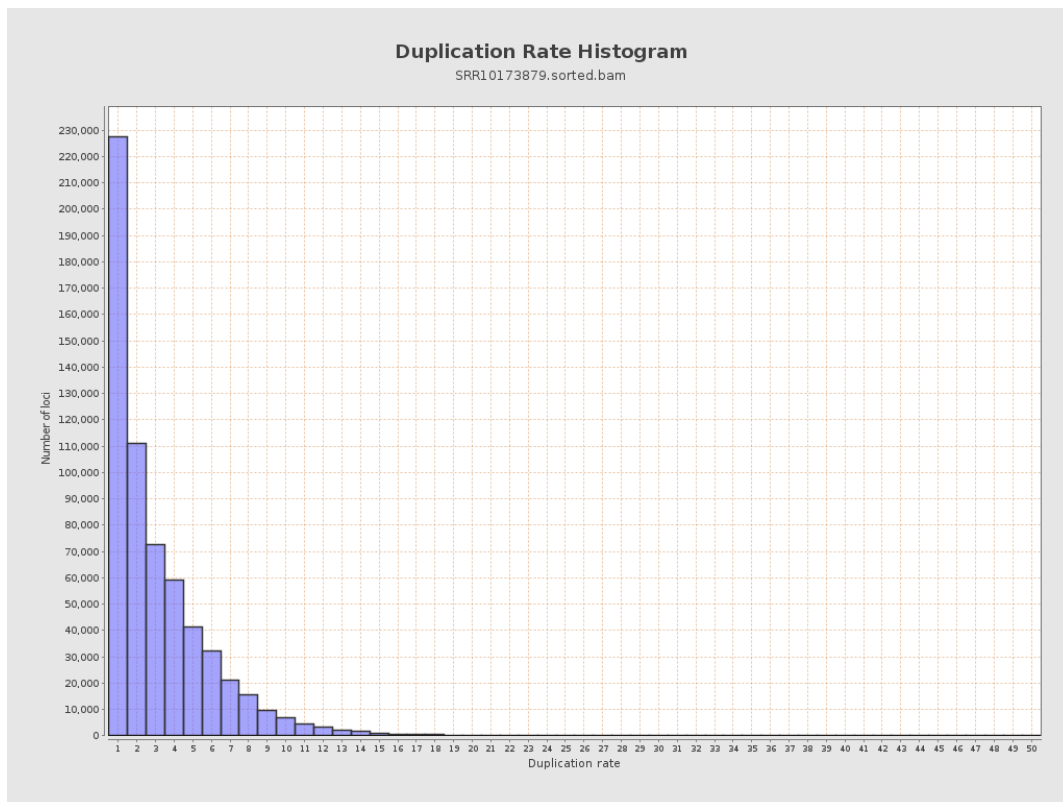
5. Results : Coverage Histogram (0-50X)



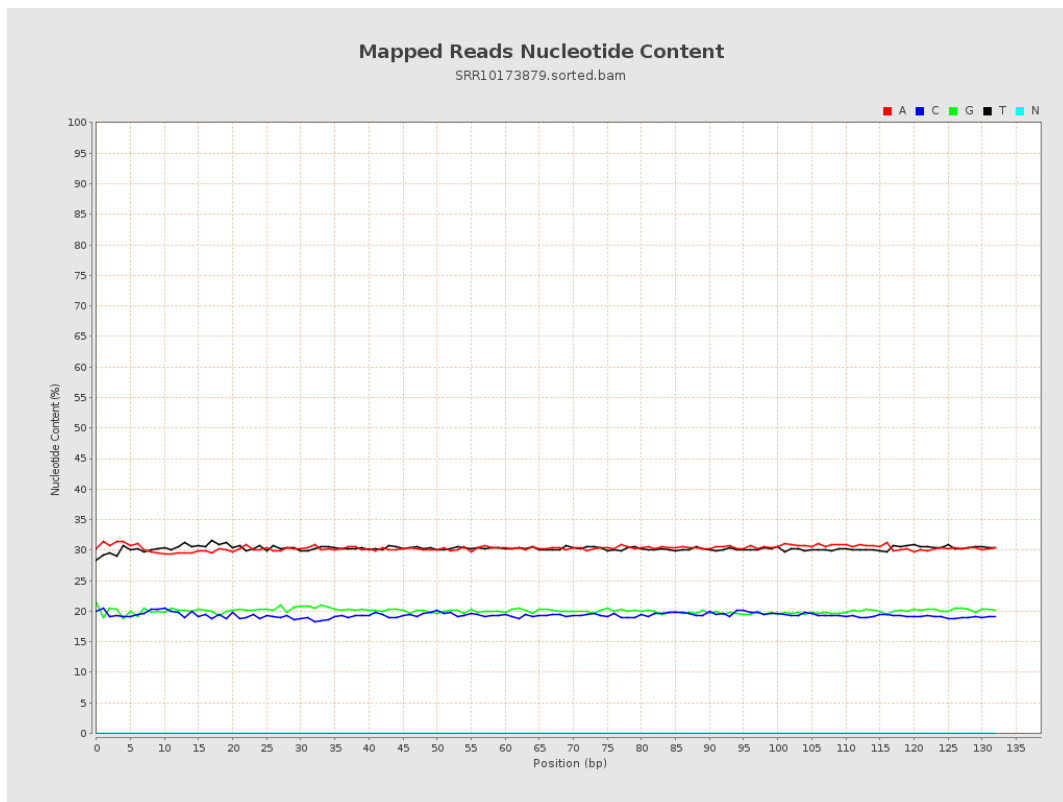
6. Results : Genome Fraction Coverage



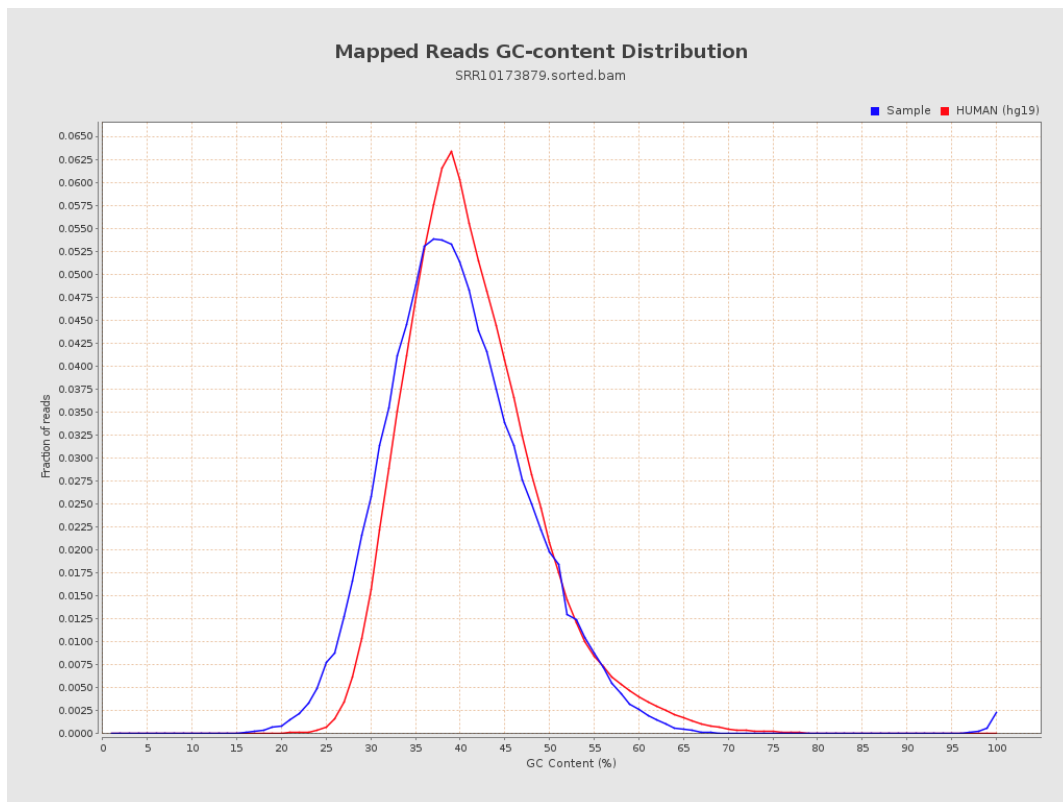
7. Results : Duplication Rate Histogram



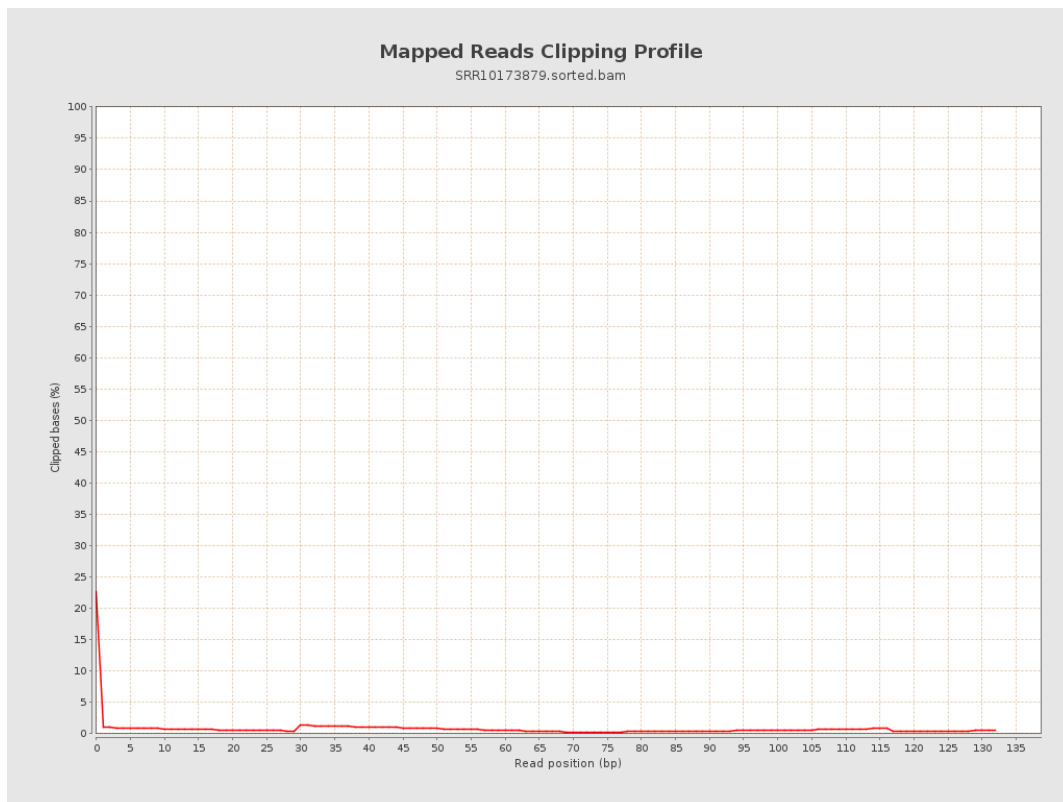
8. Results : Mapped Reads Nucleotide Content



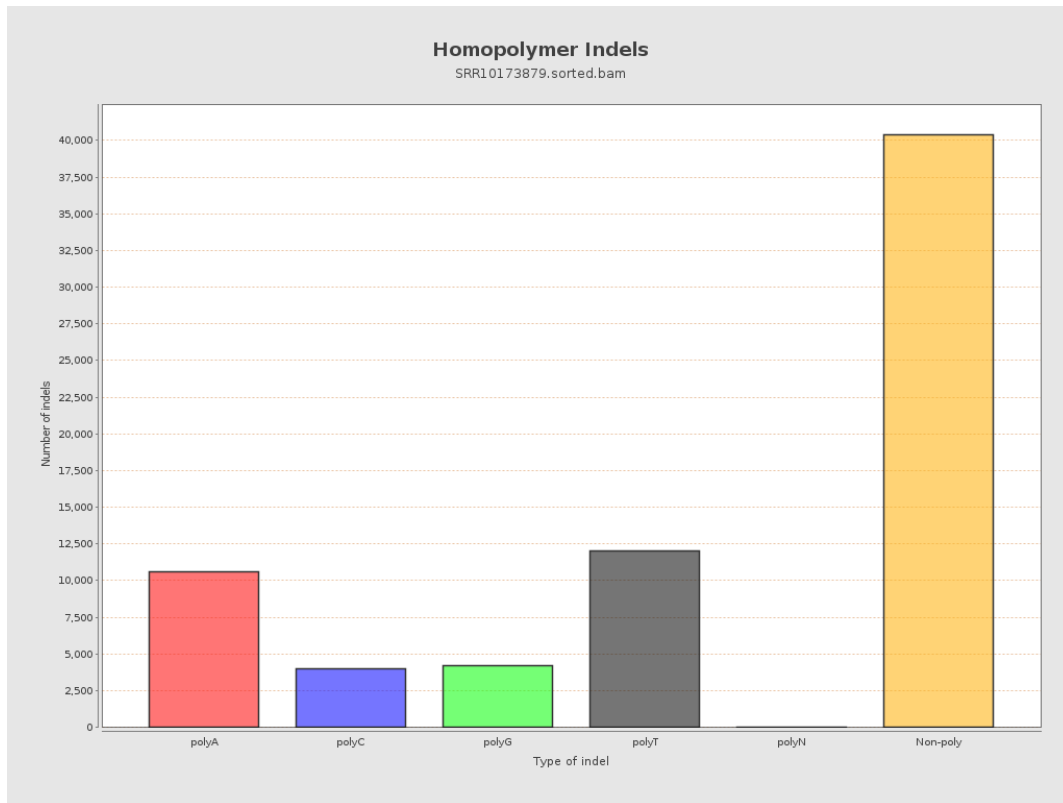
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



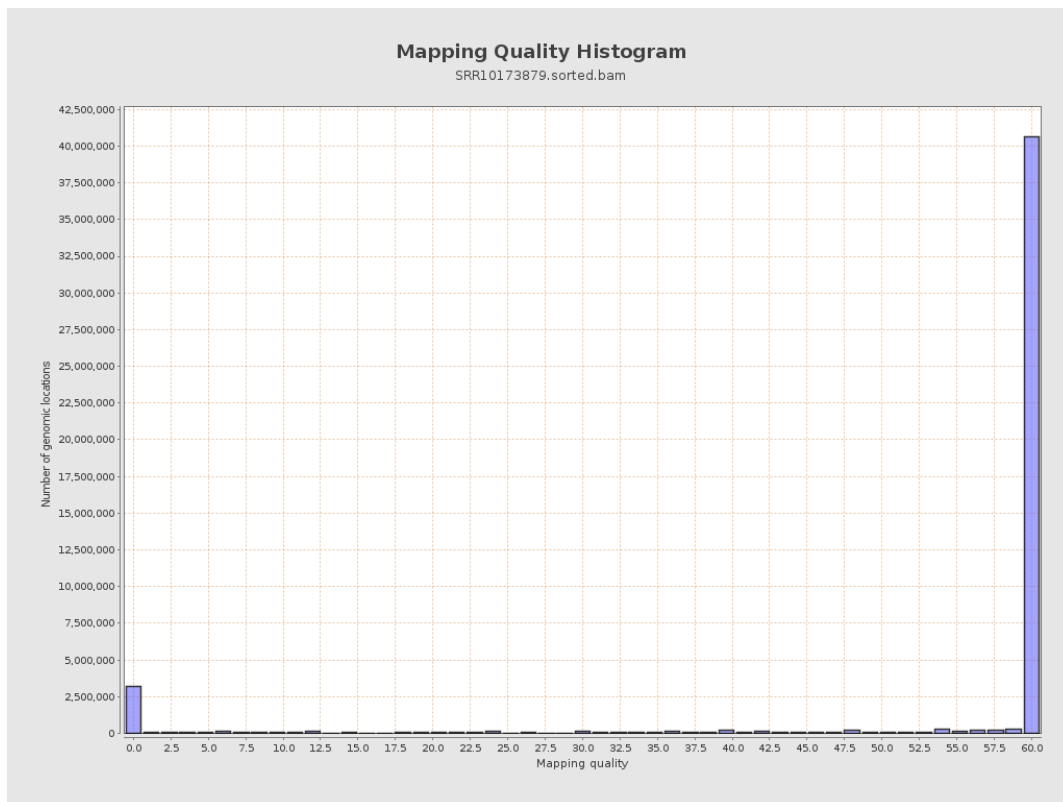
11. Results : Homopolymer Indels



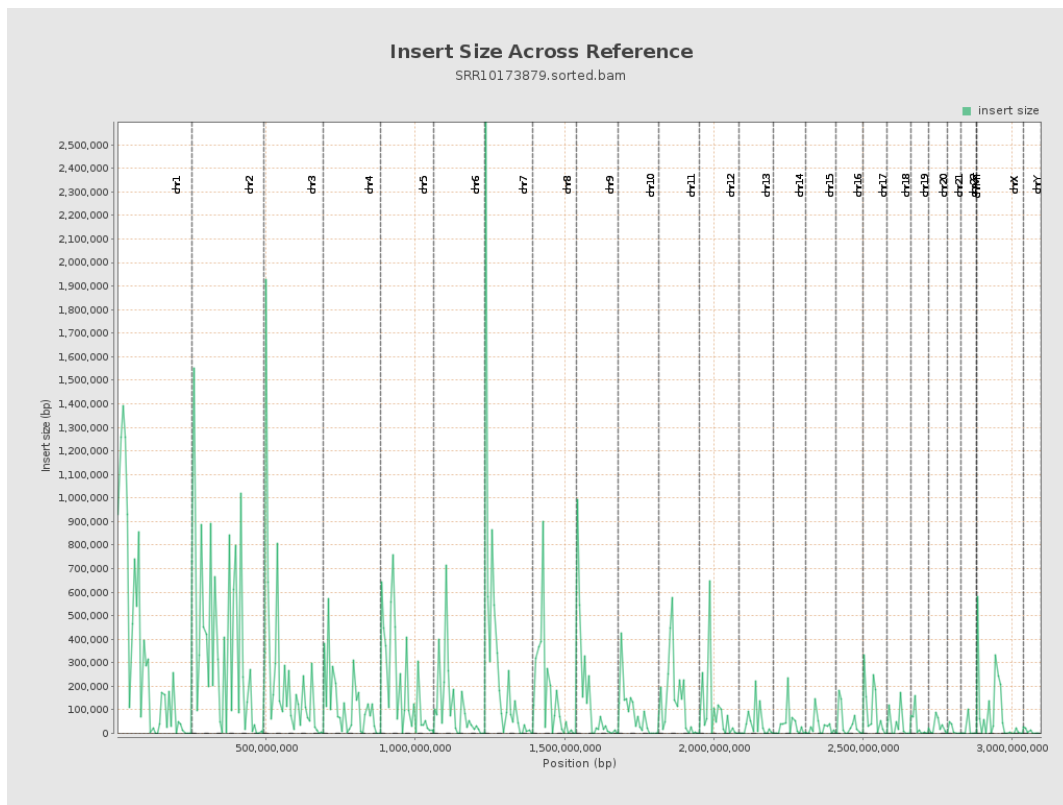
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

