

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 16:11:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173978.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_SRR10173978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173978_1.fastq.gz SRR10173978_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 16:11:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,776,332
Mapped reads	2,721,795 / 98.04%
Unmapped reads	54,537 / 1.96%
Mapped paired reads	2,721,795 / 98.04%
Mapped reads, first in pair	1,361,319 / 49.03%
Mapped reads, second in pair	1,360,476 / 49%
Mapped reads, both in pair	2,691,208 / 96.93%
Mapped reads, singletons	30,587 / 1.1%
Secondary alignments	0
Supplementary alignments	323,146 / 11.64%
Read min/max/mean length	30 / 133 / 123.77
Duplicated reads (estimated)	2,104,609 / 75.81%
Duplication rate	62.36%
Clipped reads	1,280,138 / 46.11%

2.2. ACGT Content

Number/percentage of A's	92,442,035 / 30.09%
Number/percentage of C's	60,707,960 / 19.76%
Number/percentage of T's	91,505,626 / 29.78%
Number/percentage of G's	62,608,430 / 20.38%
Number/percentage of N's	2,531 / 0%

GC Percentage	40.13%
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2.3. Coverage

Mean	0.0993
Standard Deviation	1.7743

2.4. Mapping Quality

Mean Mapping Quality	52.79
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2.5. Insert size

Mean	876,067.37
Standard Deviation	8,723,971.95
P25/Median/P75	102 / 145 / 215

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	2,578,989
Insertions	32,421
Mapped reads with at least one insertion	1.15%
Deletions	86,864
Mapped reads with at least one deletion	3.11%
Homopolymer indels	41.17%

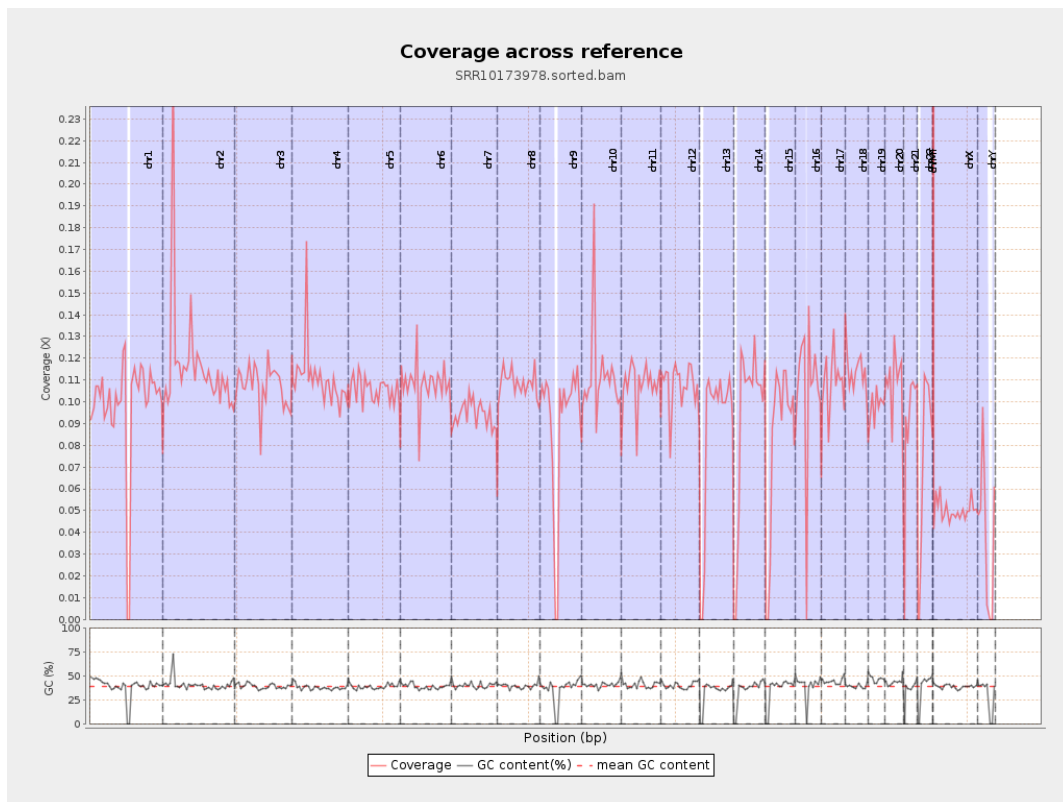
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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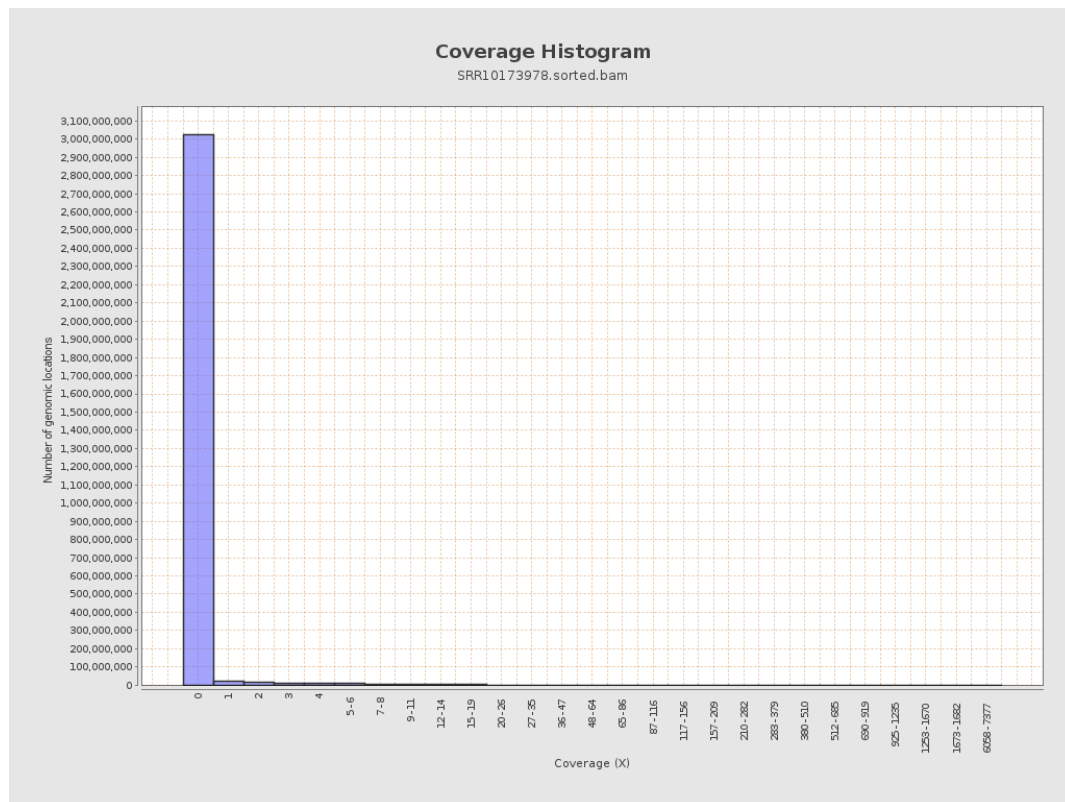
		bases	coverage	deviation
chr1	249250621	24569814	0.0986	1.1204
chr2	243199373	28217517	0.116	5.2391
chr3	198022430	21255717	0.1073	0.9863
chr4	191154276	21130827	0.1105	1.118
chr5	180915260	18993371	0.105	0.9645
chr6	171115067	18542254	0.1084	1.0511
chr7	159138663	14977111	0.0941	1.017
chr8	146364022	15875060	0.1085	1.3505
chr9	141213431	12773405	0.0905	0.9911
chr10	135534747	15082228	0.1113	1.3101
chr11	135006516	14554602	0.1078	0.9867
chr12	133851895	14448953	0.1079	0.9951
chr13	115169878	10056103	0.0873	0.878
chr14	107349540	10078848	0.0939	0.9173
chr15	102531392	8353663	0.0815	0.8459
chr16	90354753	9453006	0.1046	1.0746
chr17	81195210	8910854	0.1097	1.0074
chr18	78077248	8904204	0.114	1.3415
chr19	59128983	5788946	0.0979	0.9968
chr20	63025520	6908352	0.1096	1.0065
chr21	48129895	4376480	0.0909	1.0487
chr22	51304566	3755507	0.0732	0.8467
chrMT	16571	320445	19.3377	19.7935
chrX	155270560	7781641	0.0501	0.665

chrY	59373566	2364416	0.0398	0.6778
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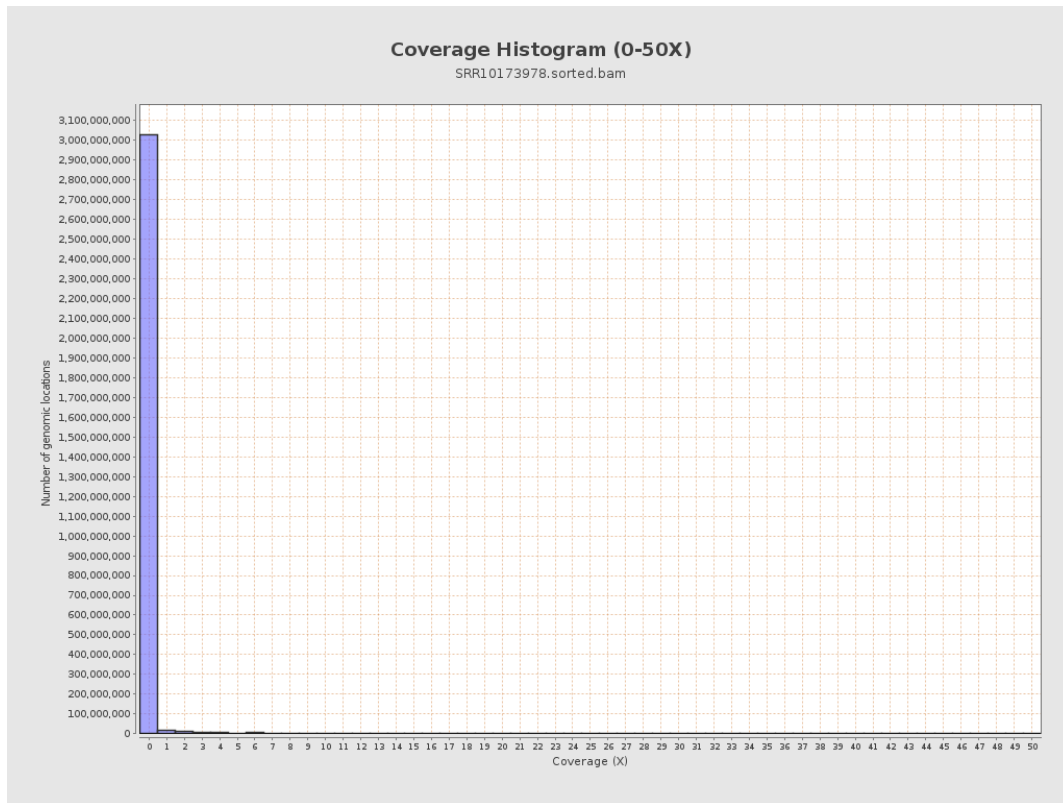
3. Results : Coverage across reference



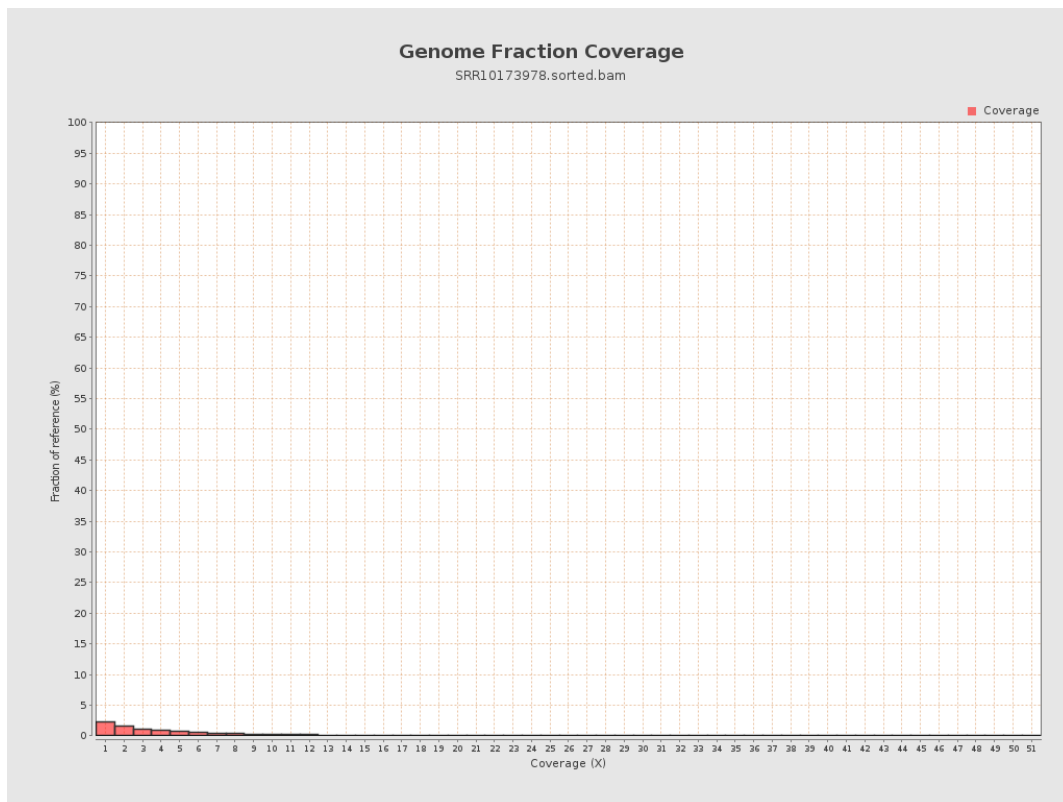
4. Results : Coverage Histogram



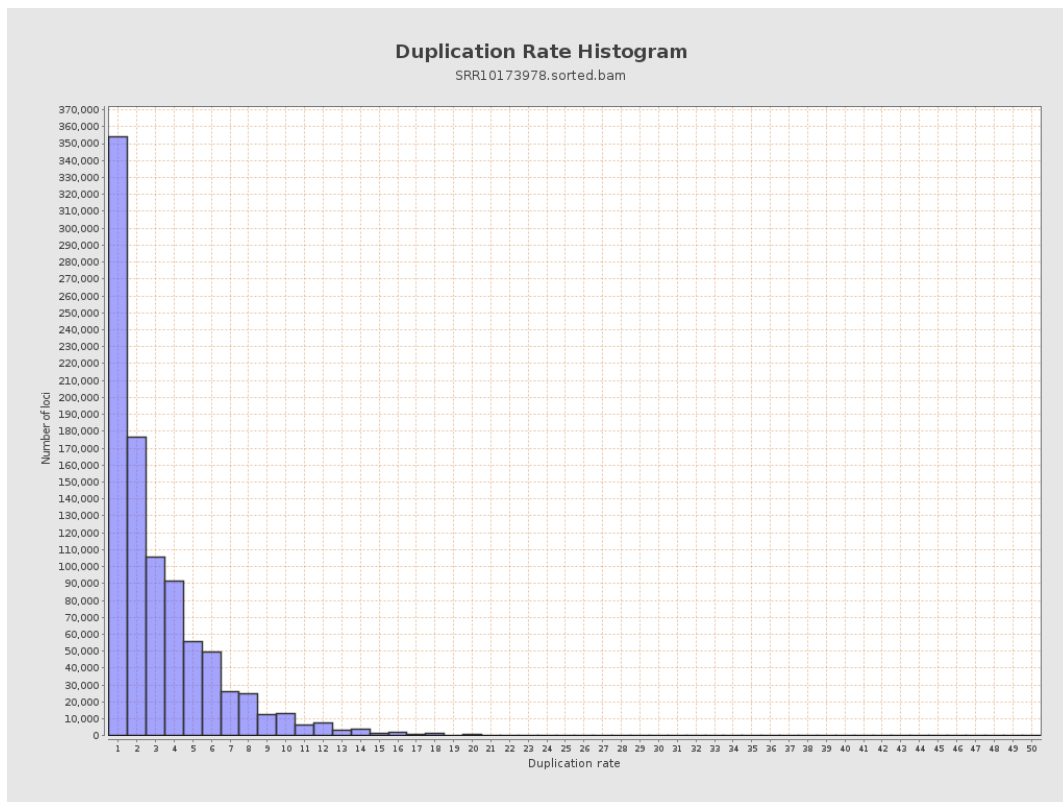
5. Results : Coverage Histogram (0-50X)



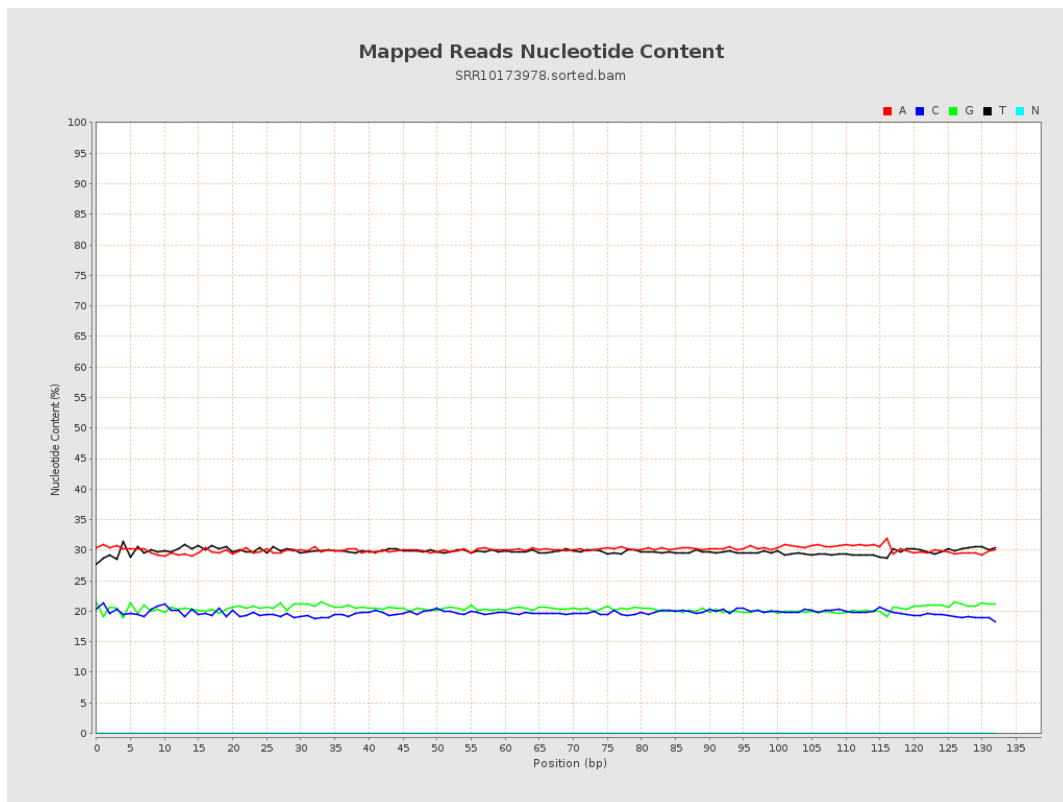
6. Results : Genome Fraction Coverage



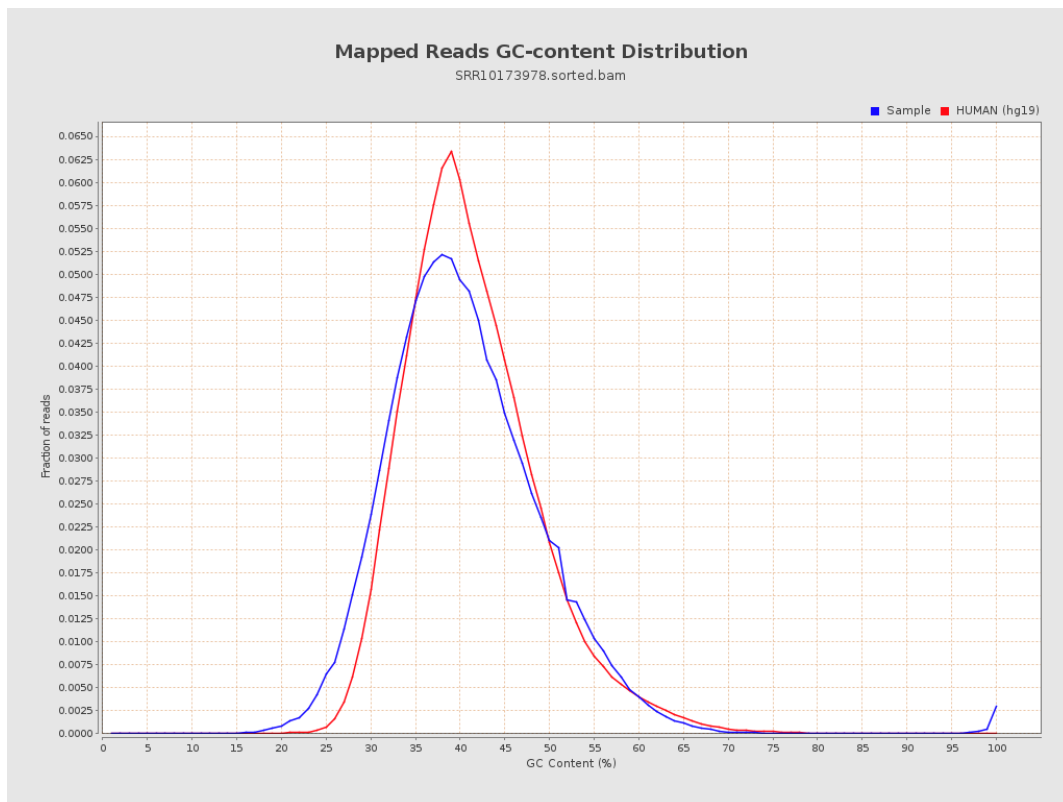
7. Results : Duplication Rate Histogram



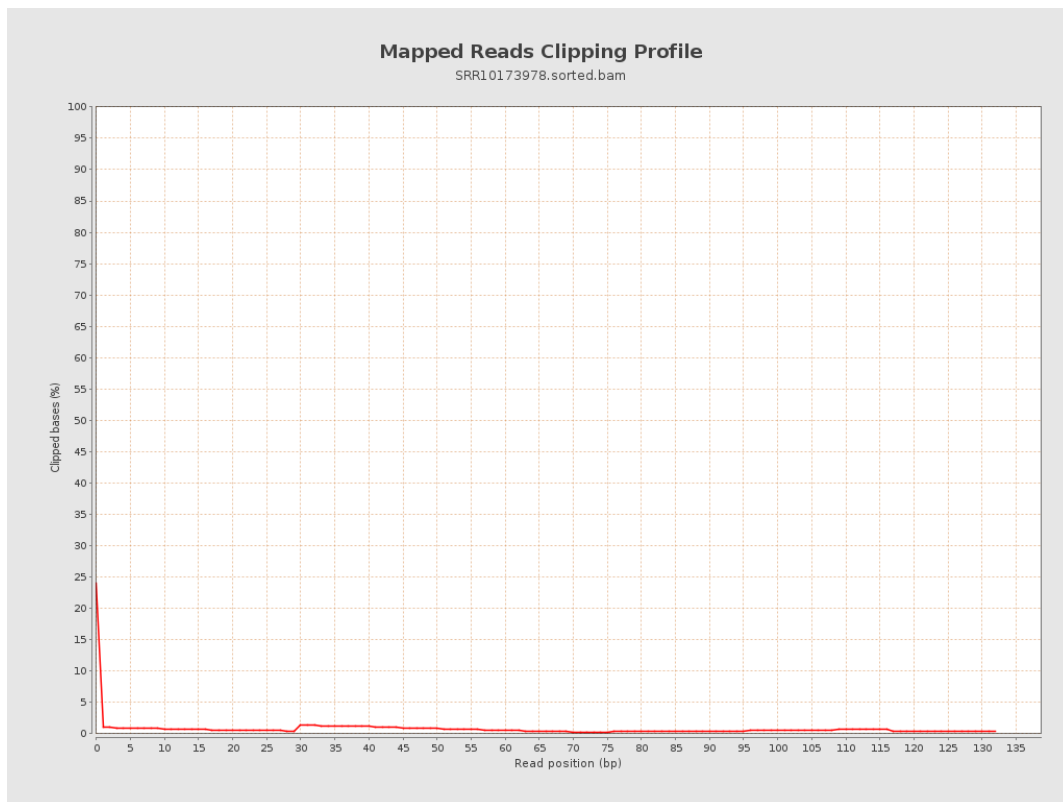
8. Results : Mapped Reads Nucleotide Content



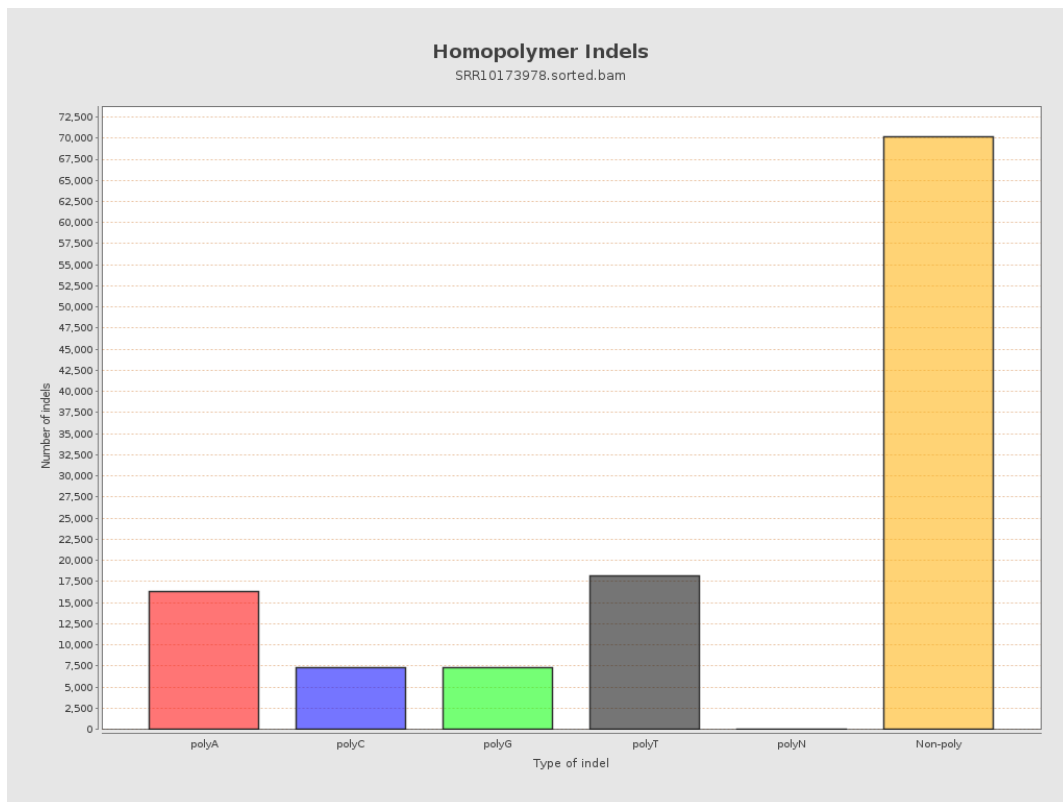
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



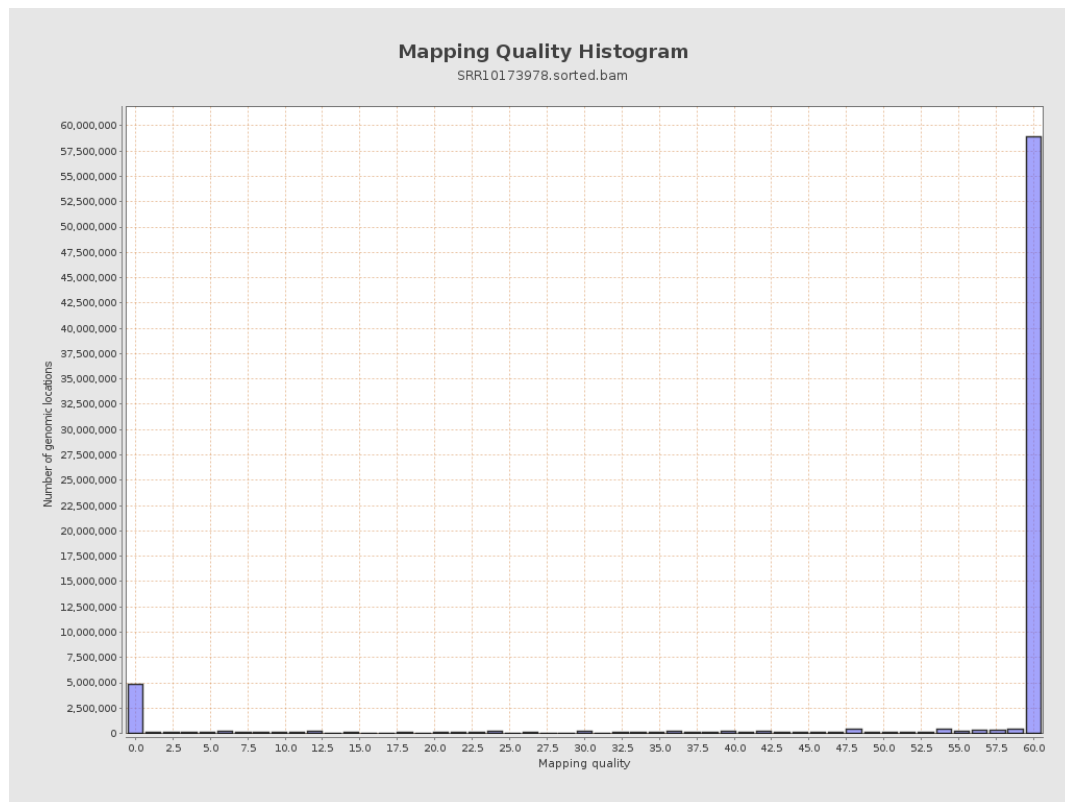
11. Results : Homopolymer Indels



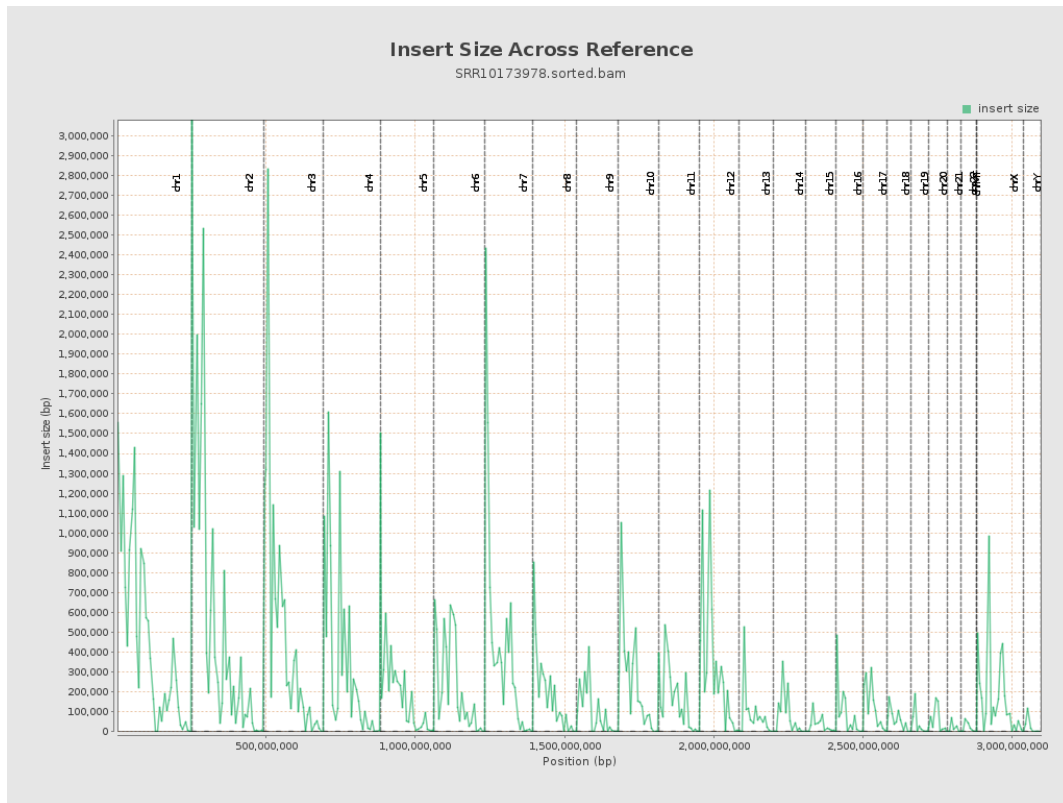
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

