

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 17:59:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173991.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_SRR10173991 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173991_1.fastq.gz SRR10173991_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 17:59:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173991.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,273,844
Mapped reads	3,214,190 / 98.18%
Unmapped reads	59,654 / 1.82%
Mapped paired reads	3,214,190 / 98.18%
Mapped reads, first in pair	1,605,119 / 49.03%
Mapped reads, second in pair	1,609,071 / 49.15%
Mapped reads, both in pair	3,176,746 / 97.03%
Mapped reads, singletons	37,444 / 1.14%
Secondary alignments	0
Supplementary alignments	388,636 / 11.87%
Read min/max/mean length	30 / 133 / 125.47
Duplicated reads (estimated)	2,574,507 / 78.64%
Duplication rate	65.82%
Clipped reads	1,457,888 / 44.53%

2.2. ACGT Content

Number/percentage of A's	110,402,857 / 29.89%
Number/percentage of C's	73,530,619 / 19.91%
Number/percentage of T's	109,389,670 / 29.62%
Number/percentage of G's	75,991,986 / 20.58%
Number/percentage of N's	2,914 / 0%

GC Percentage	40.49%
---------------	--------

2.3. Coverage

Mean	0.1194
Standard Deviation	2.1506

2.4. Mapping Quality

Mean Mapping Quality	52.69
----------------------	-------

2.5. Insert size

Mean	1,021,468.57
Standard Deviation	9,530,858.92
P25/Median/P75	111 / 161 / 242

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	3,042,508
Insertions	40,285
Mapped reads with at least one insertion	1.2%
Deletions	90,449
Mapped reads with at least one deletion	2.74%
Homopolymer indels	42.25%

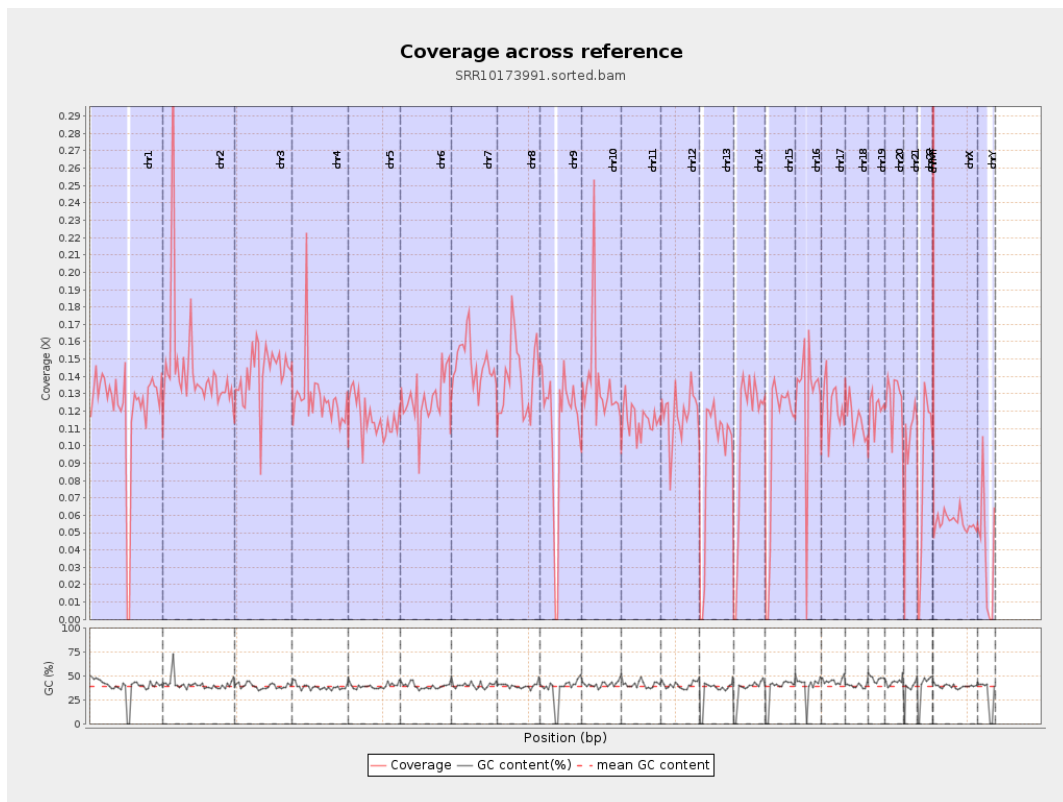
2.7. Chromosome stats

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

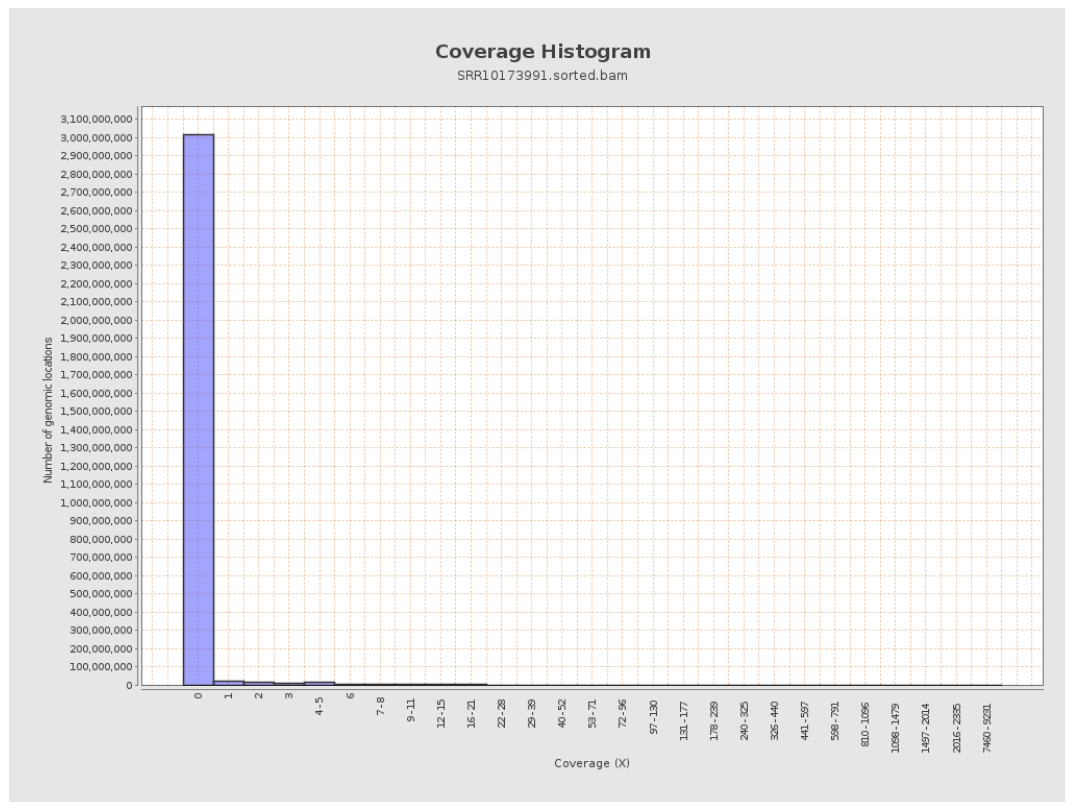
		bases	coverage	deviation
chr1	249250621	30404596	0.122	1.19
chr2	243199373	34967787	0.1438	6.5098
chr3	198022430	28096052	0.1419	1.1448
chr4	191154276	24509768	0.1282	1.3163
chr5	180915260	20972050	0.1159	1.02
chr6	171115067	21646542	0.1265	1.1161
chr7	159138663	23422836	0.1472	1.5201
chr8	146364022	20390379	0.1393	1.5056
chr9	141213431	15815966	0.112	1.3208
chr10	135534747	18399575	0.1358	1.5542
chr11	135006516	15487676	0.1147	1.0367
chr12	133851895	15908414	0.1189	1.054
chr13	115169878	10769638	0.0935	0.9225
chr14	107349540	11678545	0.1088	1.0039
chr15	102531392	10522868	0.1026	0.9596
chr16	90354753	11568711	0.128	1.1898
chr17	81195210	10043031	0.1237	1.1376
chr18	78077248	9010548	0.1154	1.485
chr19	59128983	7146691	0.1209	1.16
chr20	63025520	8025532	0.1273	1.0994
chr21	48129895	4844493	0.1007	1.1116
chr22	51304566	4402032	0.0858	0.9376
chrMT	16571	396738	23.9417	29.0605
chrX	155270560	8699688	0.056	0.7092

chrY	59373566	2407137	0.0405	0.72
------	----------	---------	--------	------

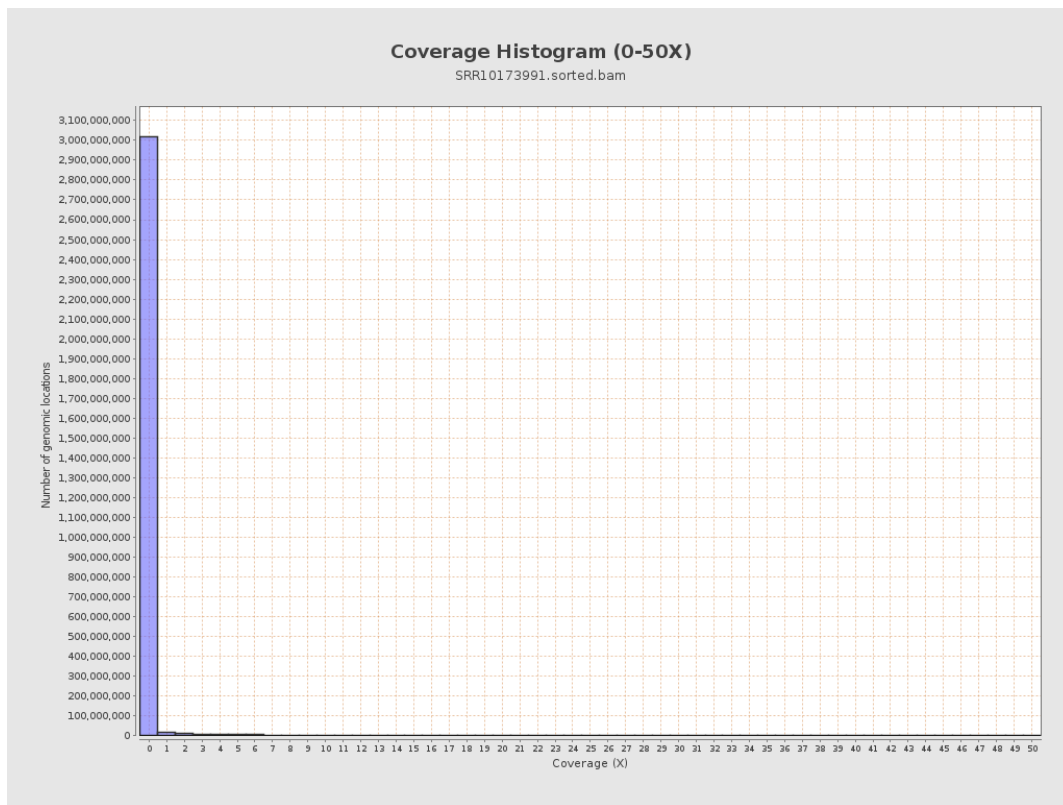
3. Results : Coverage across reference



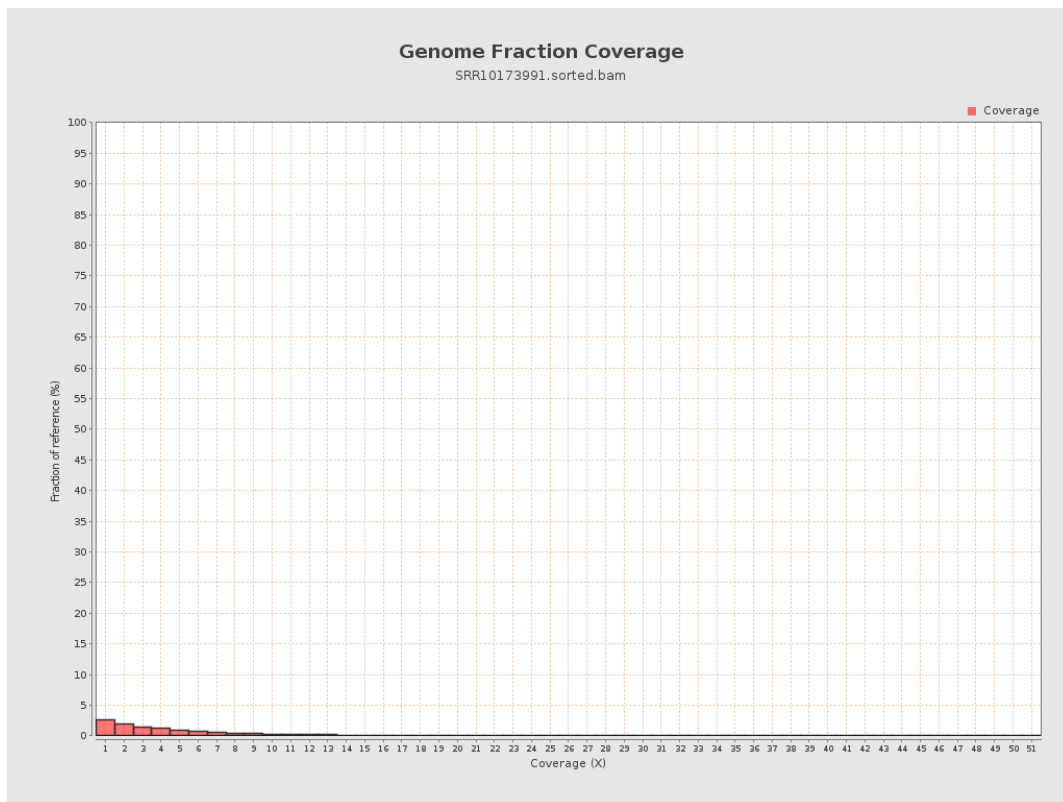
4. Results : Coverage Histogram



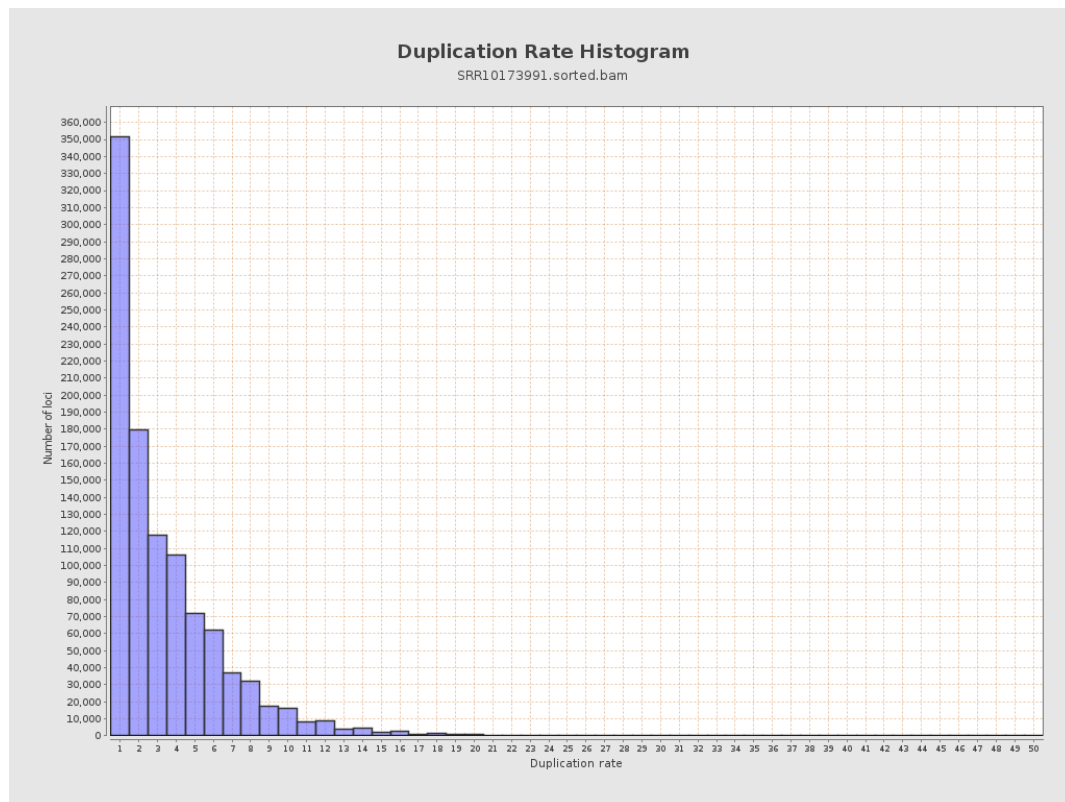
5. Results : Coverage Histogram (0-50X)



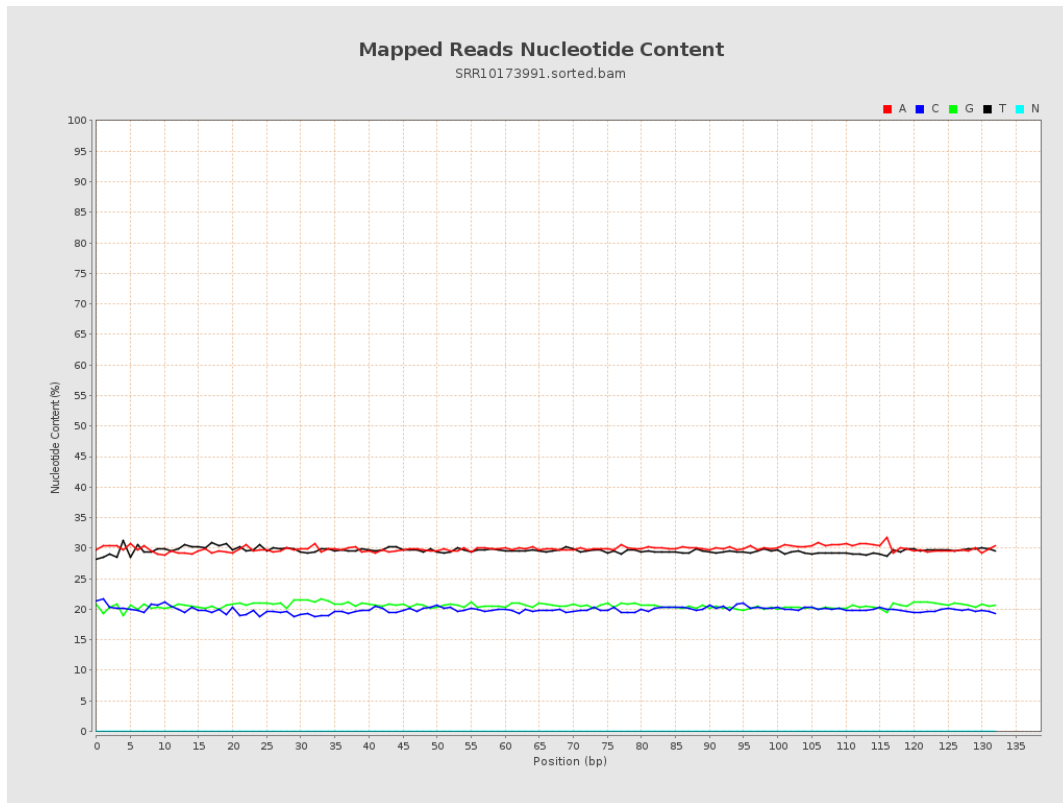
6. Results : Genome Fraction Coverage



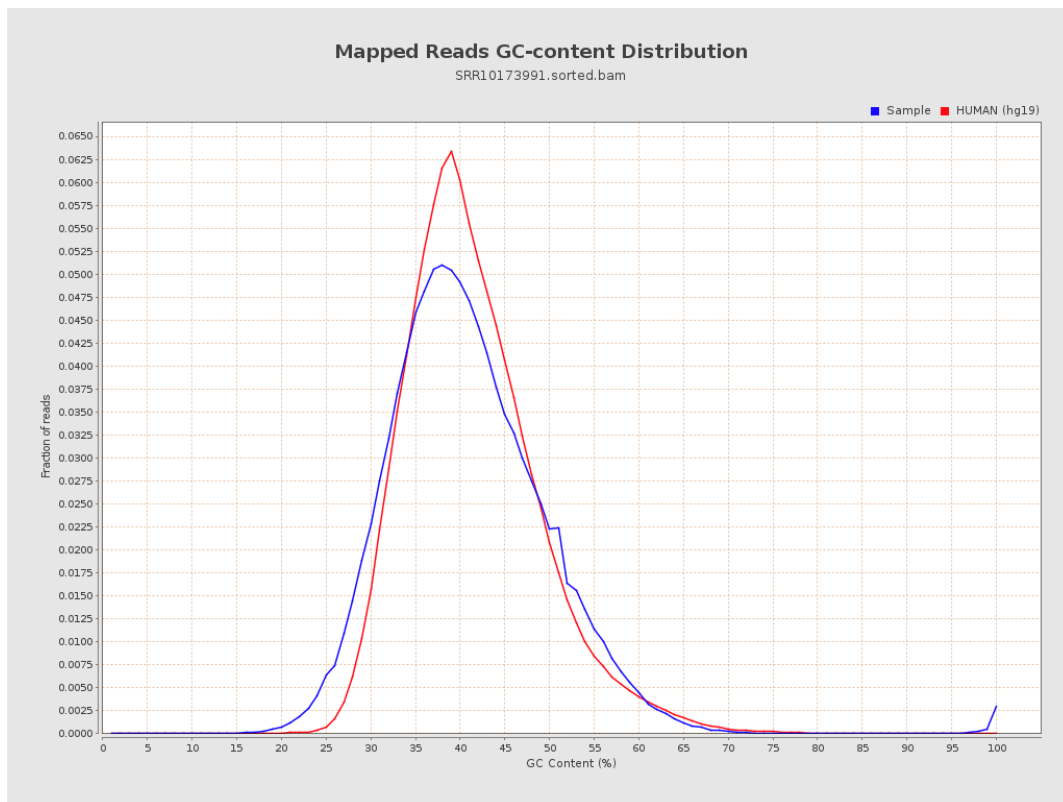
7. Results : Duplication Rate Histogram



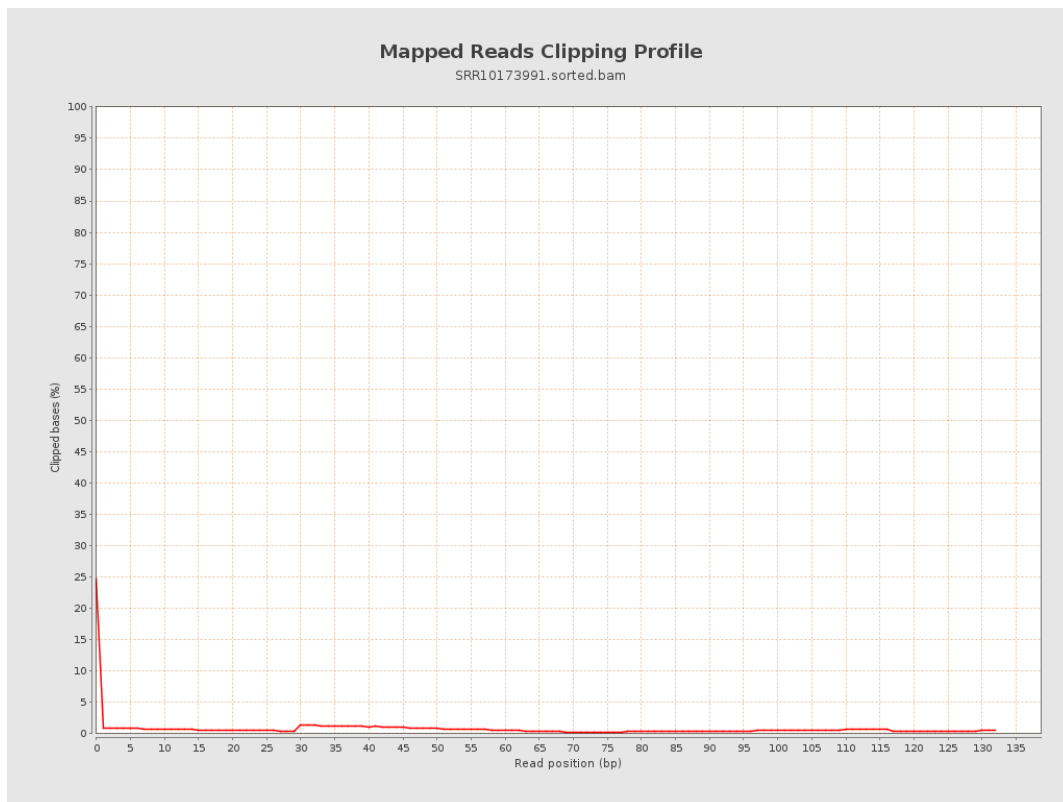
8. Results : Mapped Reads Nucleotide Content



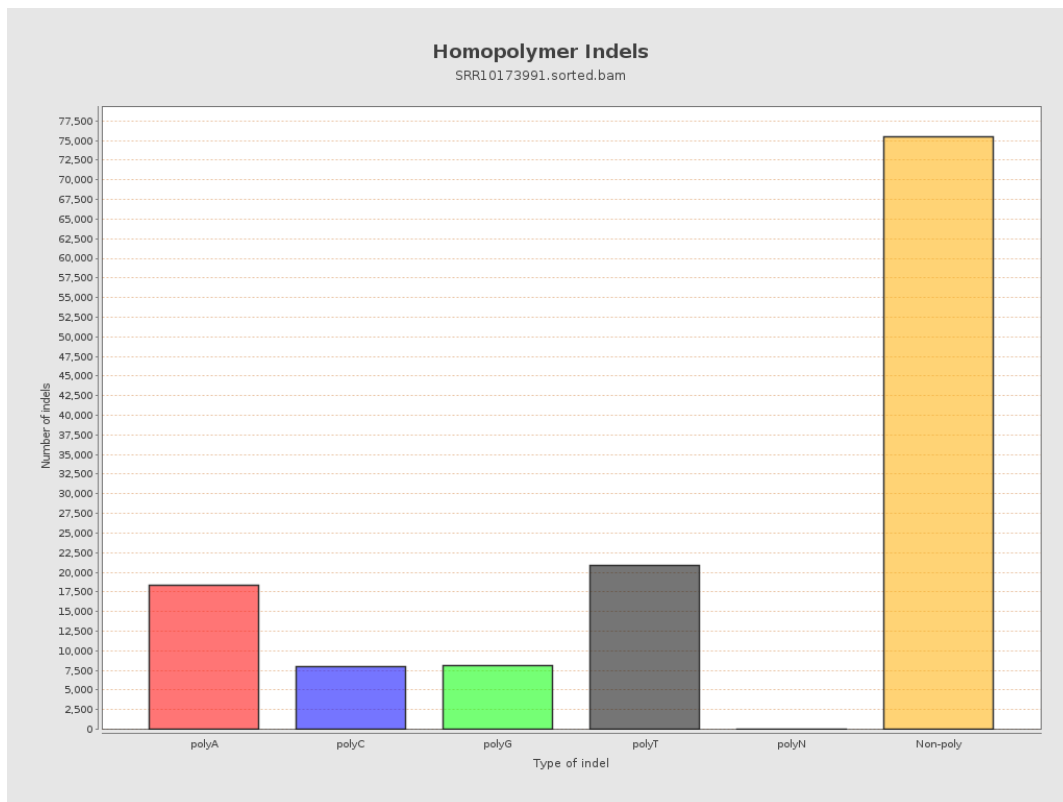
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



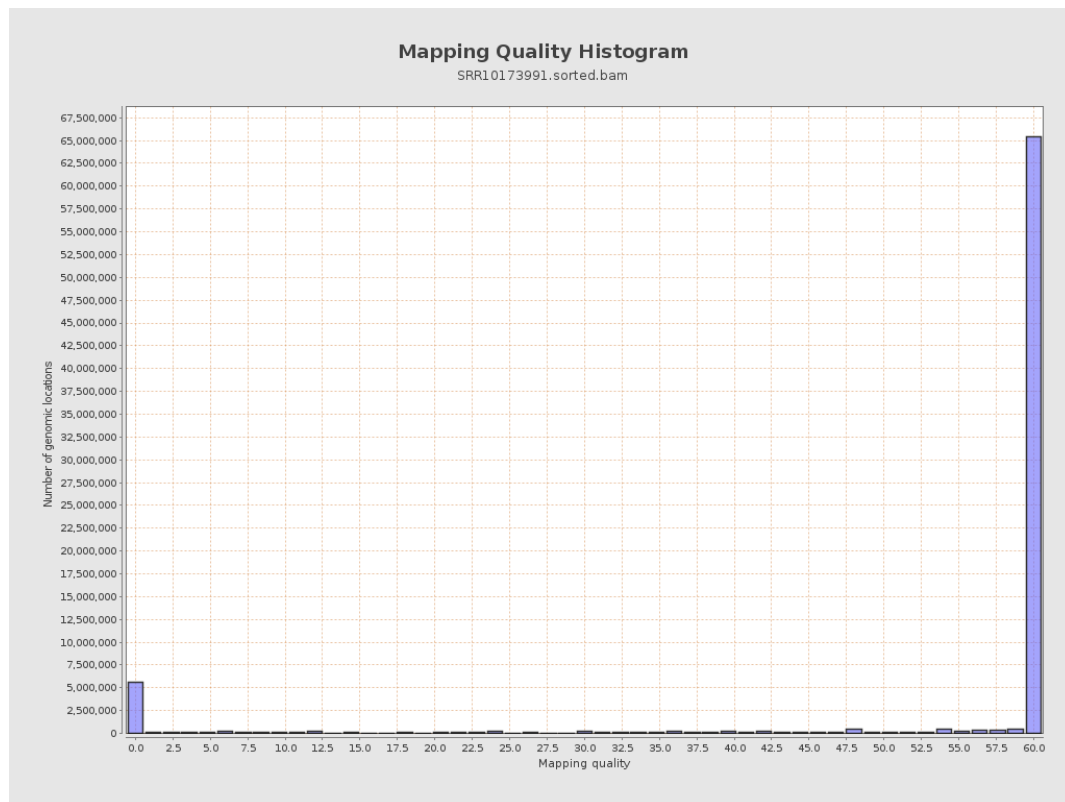
11. Results : Homopolymer Indels



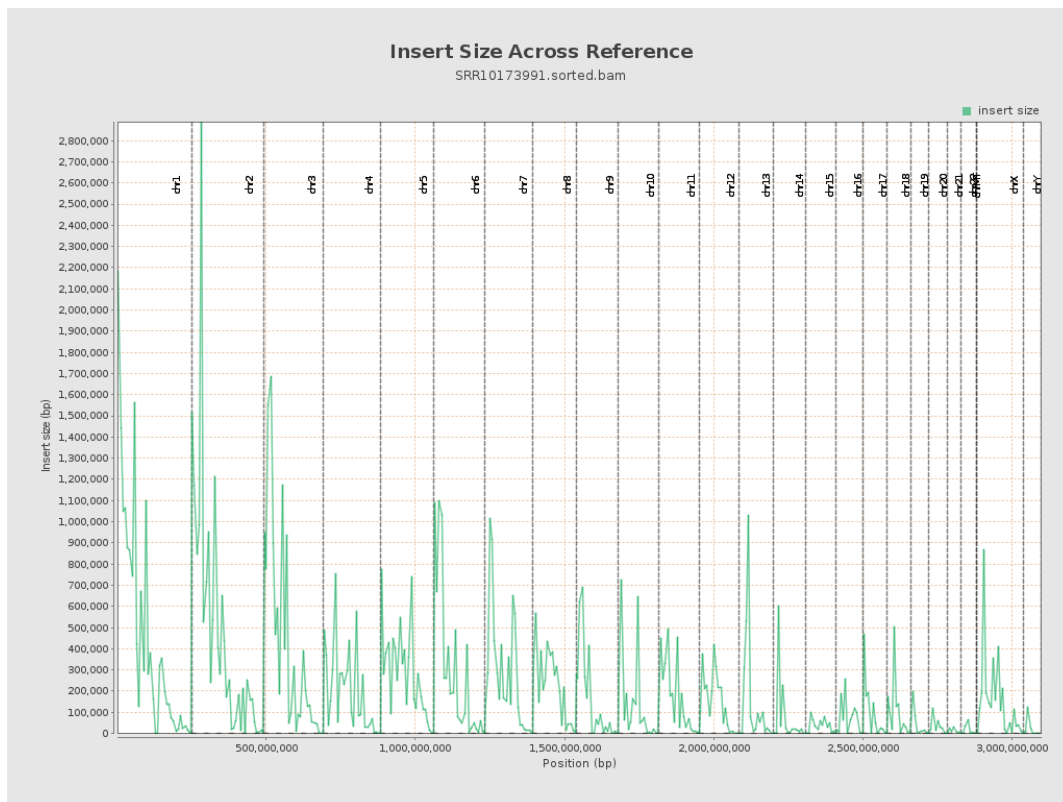
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

