

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 10:21:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173944.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_SRR10173944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173944_1.fastq.gz SRR10173944_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 10:21:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,928,160
Mapped reads	3,839,980 / 97.76%
Unmapped reads	88,180 / 2.24%
Mapped paired reads	3,839,980 / 97.76%
Mapped reads, first in pair	1,923,802 / 48.97%
Mapped reads, second in pair	1,916,178 / 48.78%
Mapped reads, both in pair	3,787,704 / 96.42%
Mapped reads, singletons	52,276 / 1.33%
Secondary alignments	0
Supplementary alignments	484,245 / 12.33%
Read min/max/mean length	30 / 133 / 123.89
Duplicated reads (estimated)	3,012,657 / 76.69%
Duplication rate	63.82%
Clipped reads	2,057,727 / 52.38%

2.2. ACGT Content

Number/percentage of A's	128,500,474 / 30.03%
Number/percentage of C's	84,365,844 / 19.71%
Number/percentage of T's	127,445,877 / 29.78%
Number/percentage of G's	87,614,703 / 20.47%
Number/percentage of N's	3,201 / 0%

GC Percentage	40.19%
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2.3. Coverage

Mean	0.1383
Standard Deviation	2.6977

2.4. Mapping Quality

Mean Mapping Quality	52.69
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2.5. Insert size

Mean	988,779.82
Standard Deviation	8,853,713.77
P25/Median/P75	99 / 142 / 213

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	3,694,632
Insertions	47,640
Mapped reads with at least one insertion	1.19%
Deletions	149,233
Mapped reads with at least one deletion	3.79%
Homopolymer indels	40.28%

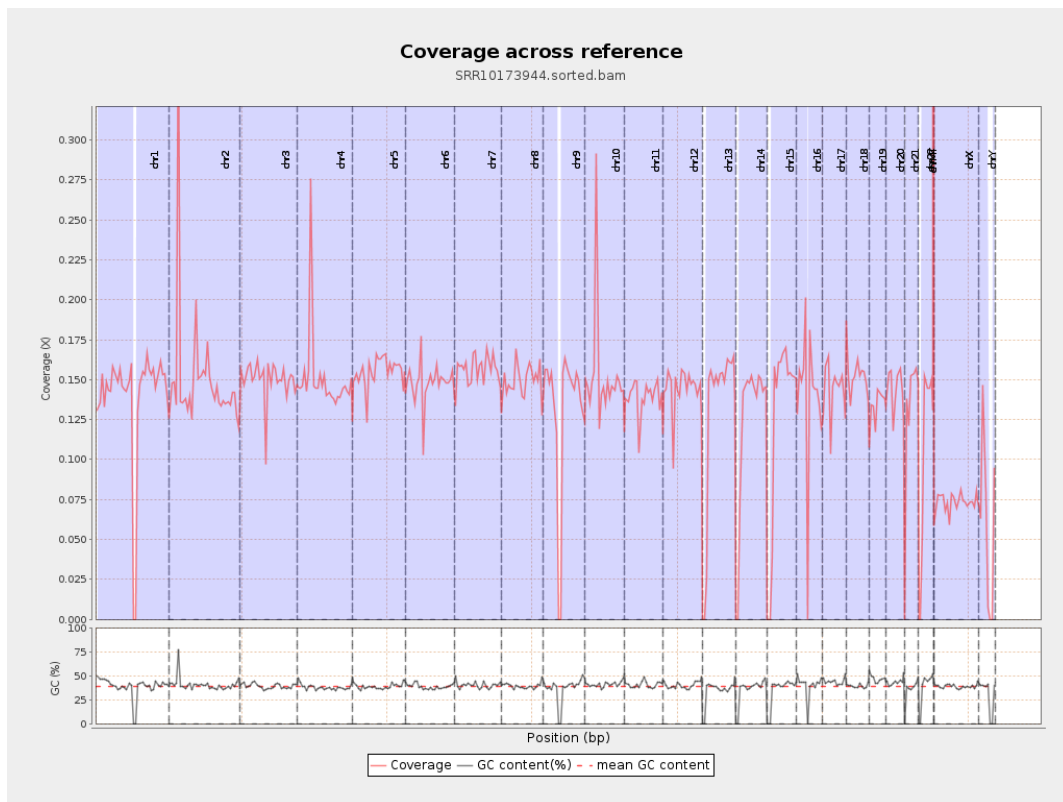
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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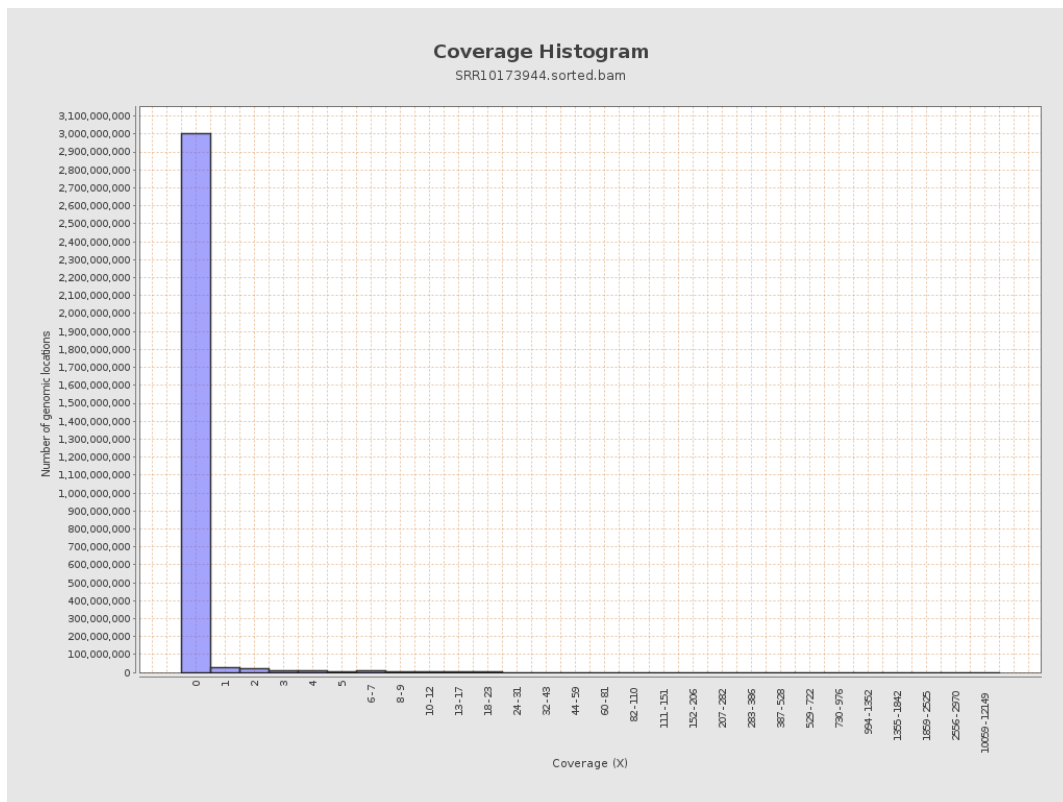
		bases	coverage	deviation
chr1	249250621	34836895	0.1398	1.3457
chr2	243199373	36760374	0.1512	8.562
chr3	198022430	29714335	0.1501	1.1623
chr4	191154276	28702369	0.1502	1.4706
chr5	180915260	28034856	0.155	1.1856
chr6	171115067	25362849	0.1482	1.2386
chr7	159138663	24995545	0.1571	1.4355
chr8	146364022	21869373	0.1494	1.6506
chr9	141213431	18542130	0.1313	1.2978
chr10	135534747	20595697	0.152	1.7851
chr11	135006516	18774923	0.1391	1.136
chr12	133851895	19298153	0.1442	1.1605
chr13	115169878	14855914	0.129	1.0863
chr14	107349540	13225317	0.1232	1.0717
chr15	102531392	12930325	0.1261	1.0701
chr16	90354753	12534537	0.1387	1.2801
chr17	81195210	11608894	0.143	1.1503
chr18	78077248	11867322	0.152	1.5134
chr19	59128983	7937346	0.1342	1.1706
chr20	63025520	9068992	0.1439	1.1508
chr21	48129895	6328018	0.1315	1.2805
chr22	51304566	5262458	0.1026	1.0662
chrMT	16571	408252	24.6365	24.1024
chrX	155270560	11367462	0.0732	0.7957

chrY	59373566	3395645	0.0572	1.0713
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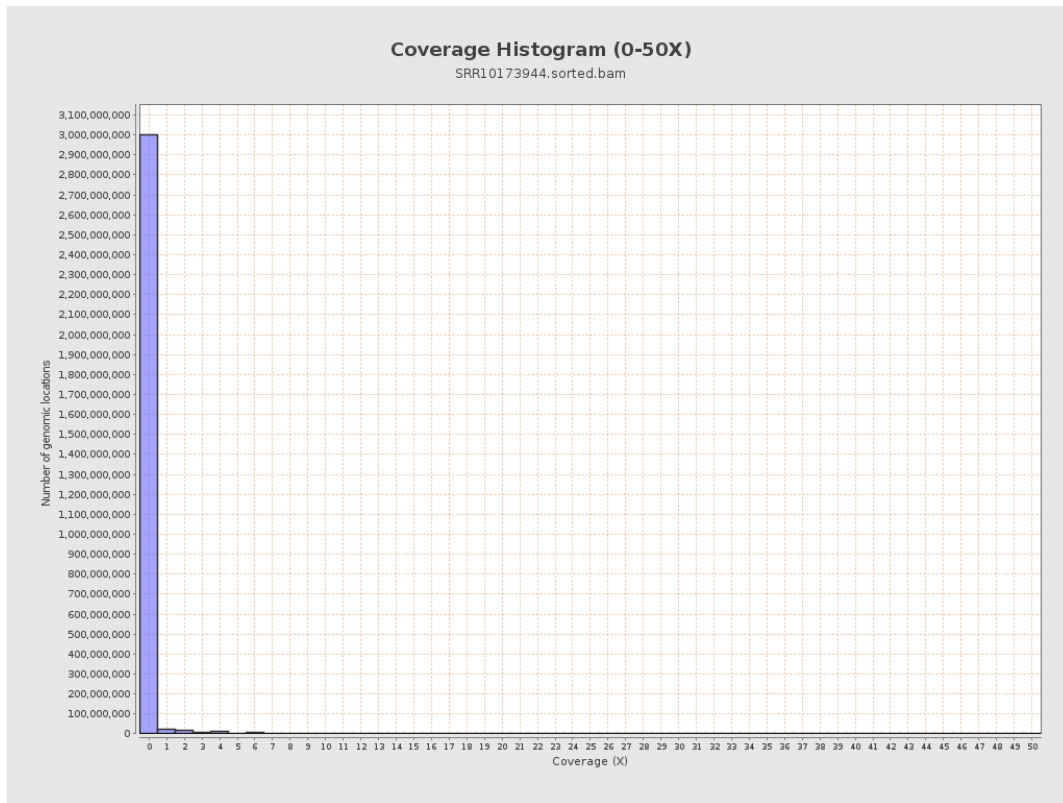
3. Results : Coverage across reference



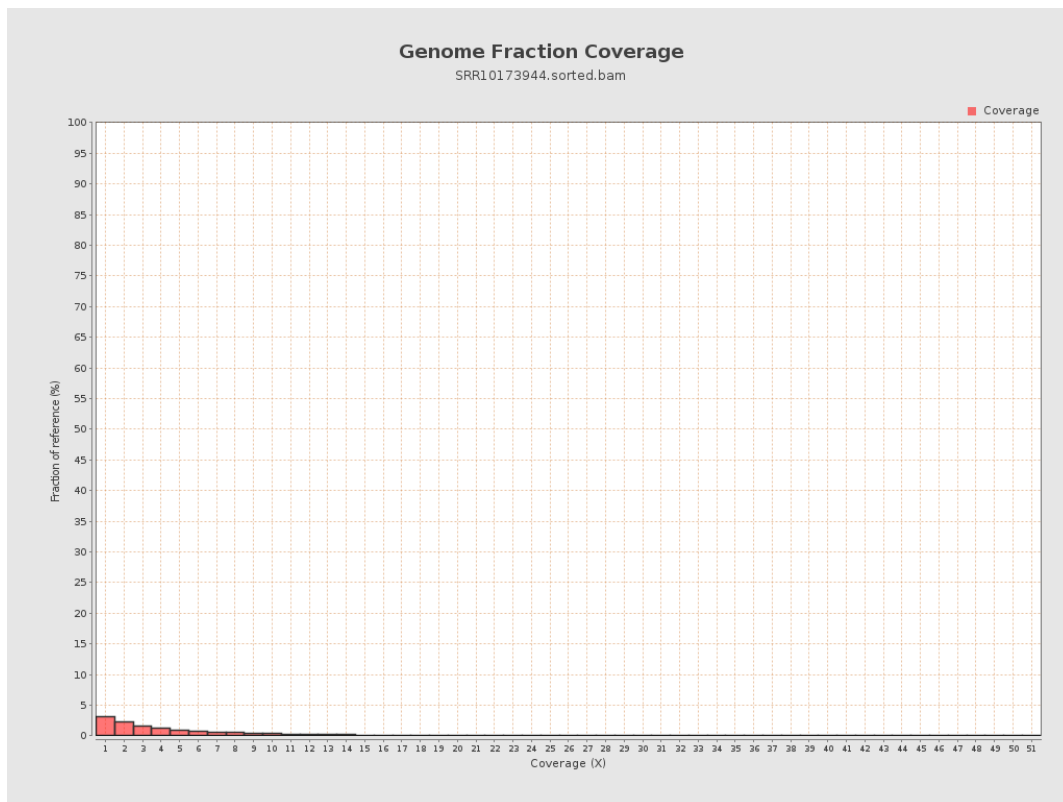
4. Results : Coverage Histogram



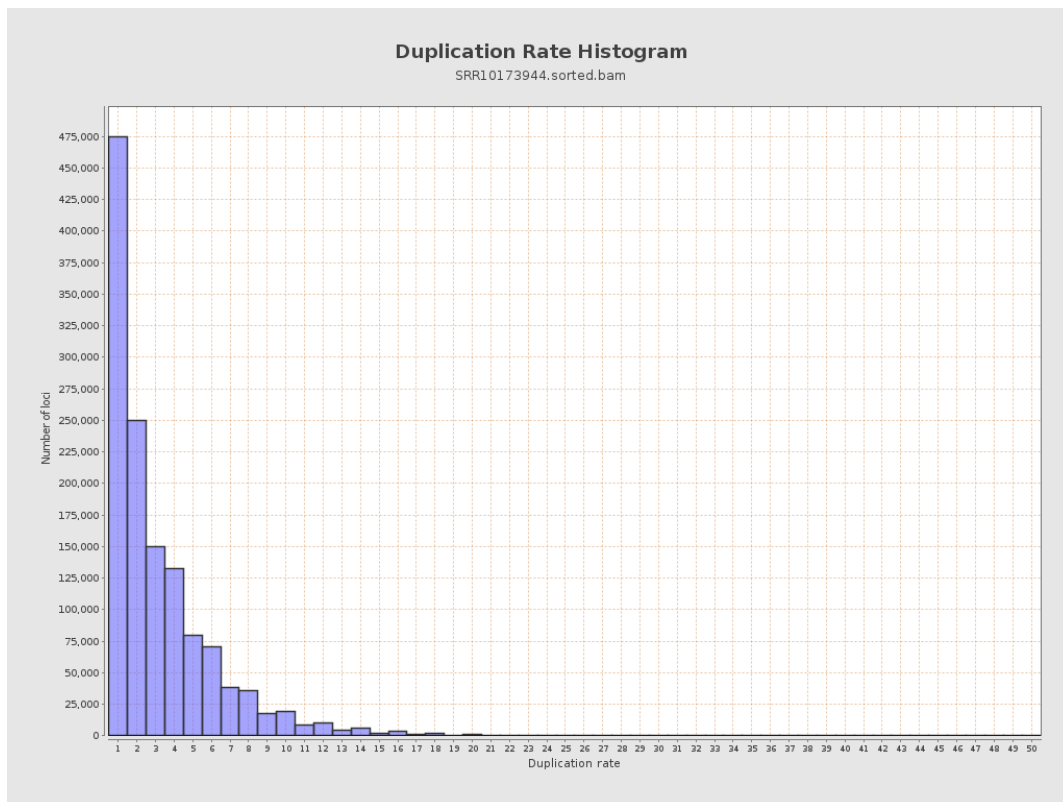
5. Results : Coverage Histogram (0-50X)



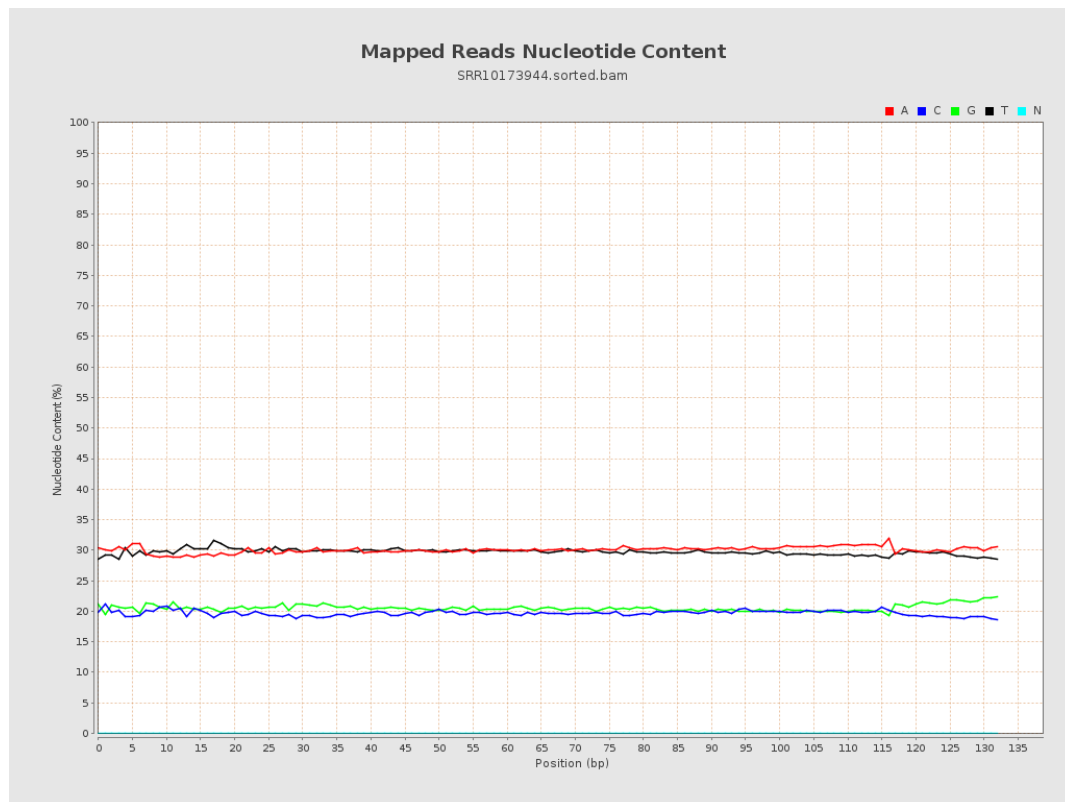
6. Results : Genome Fraction Coverage



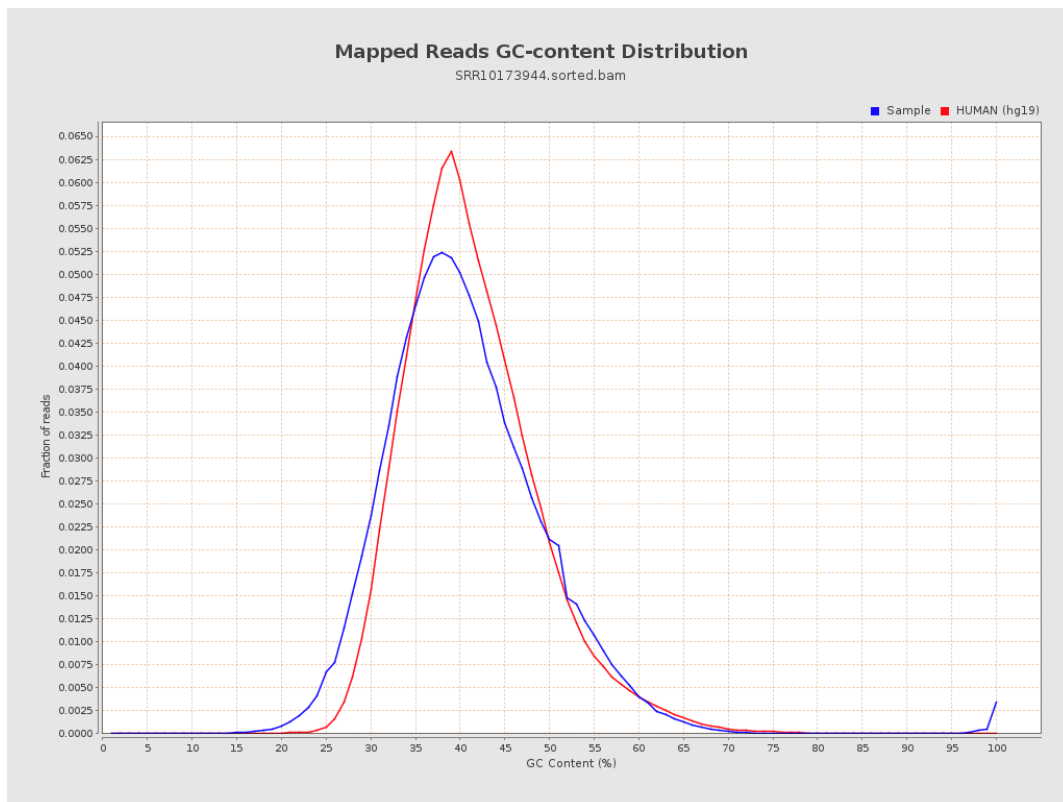
7. Results : Duplication Rate Histogram



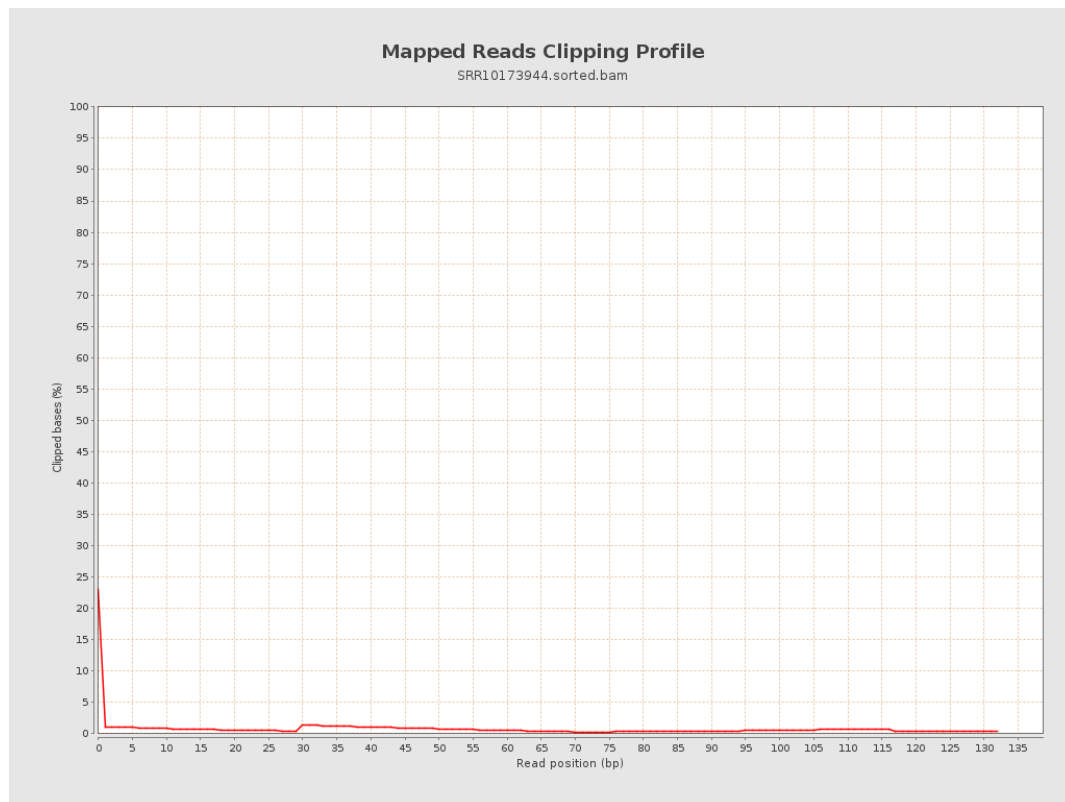
8. Results : Mapped Reads Nucleotide Content



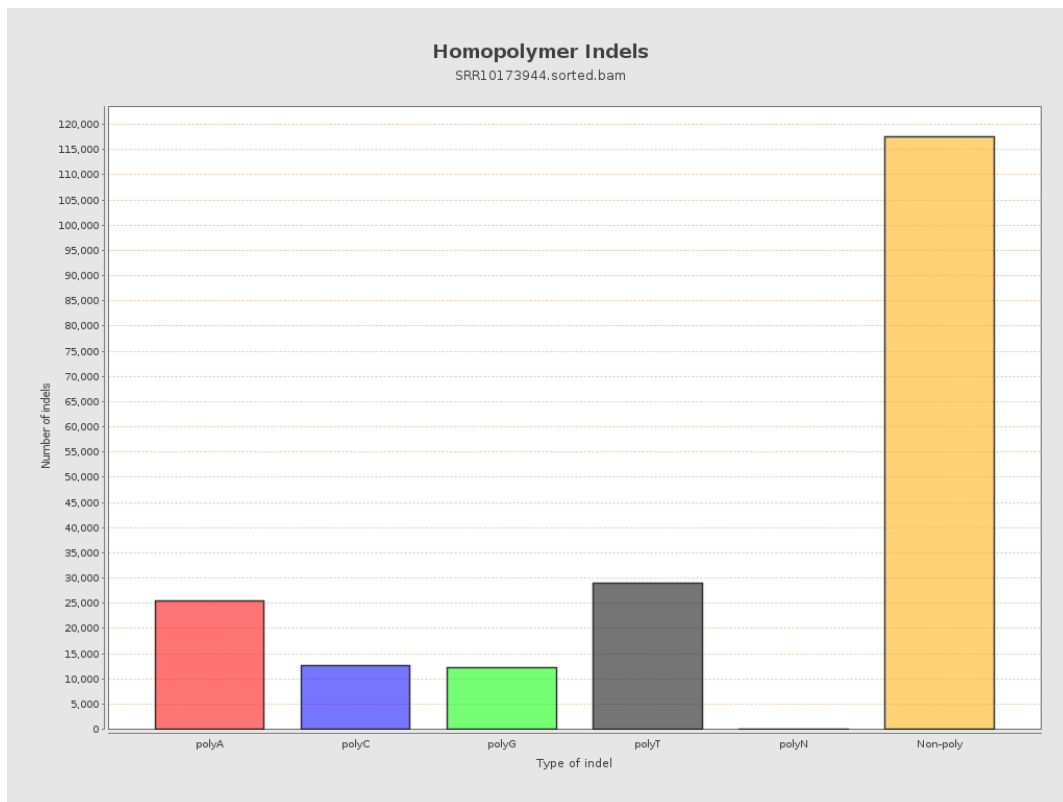
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



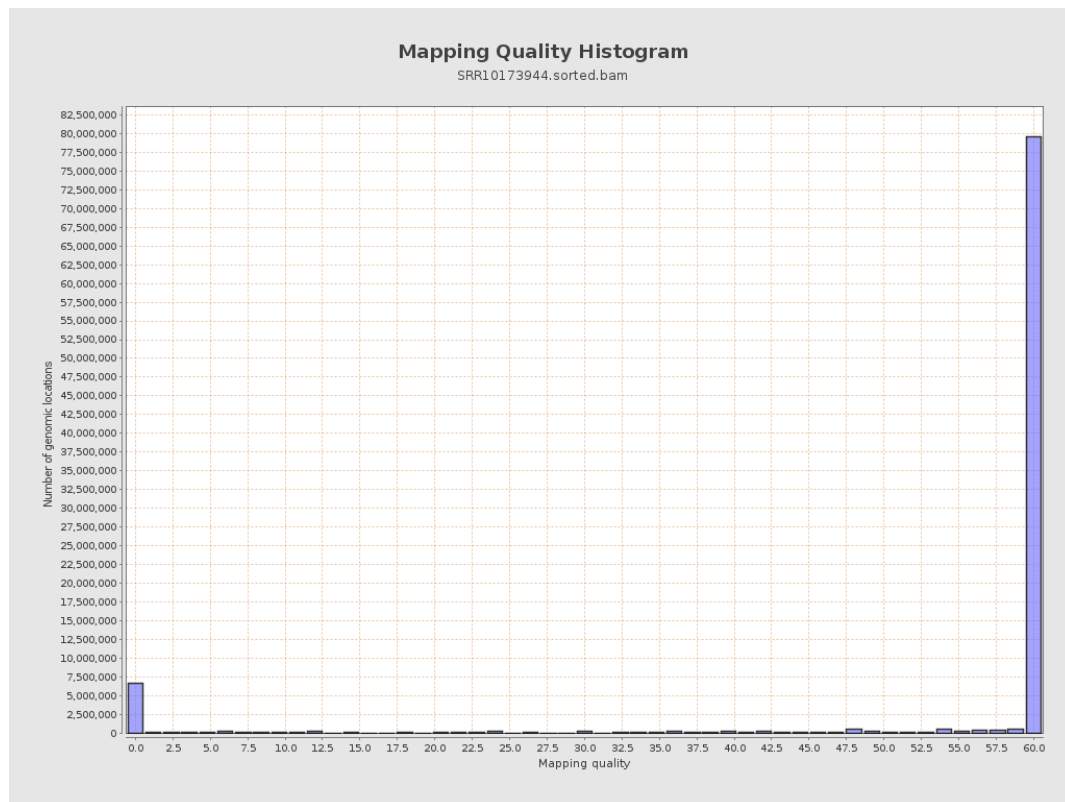
11. Results : Homopolymer Indels



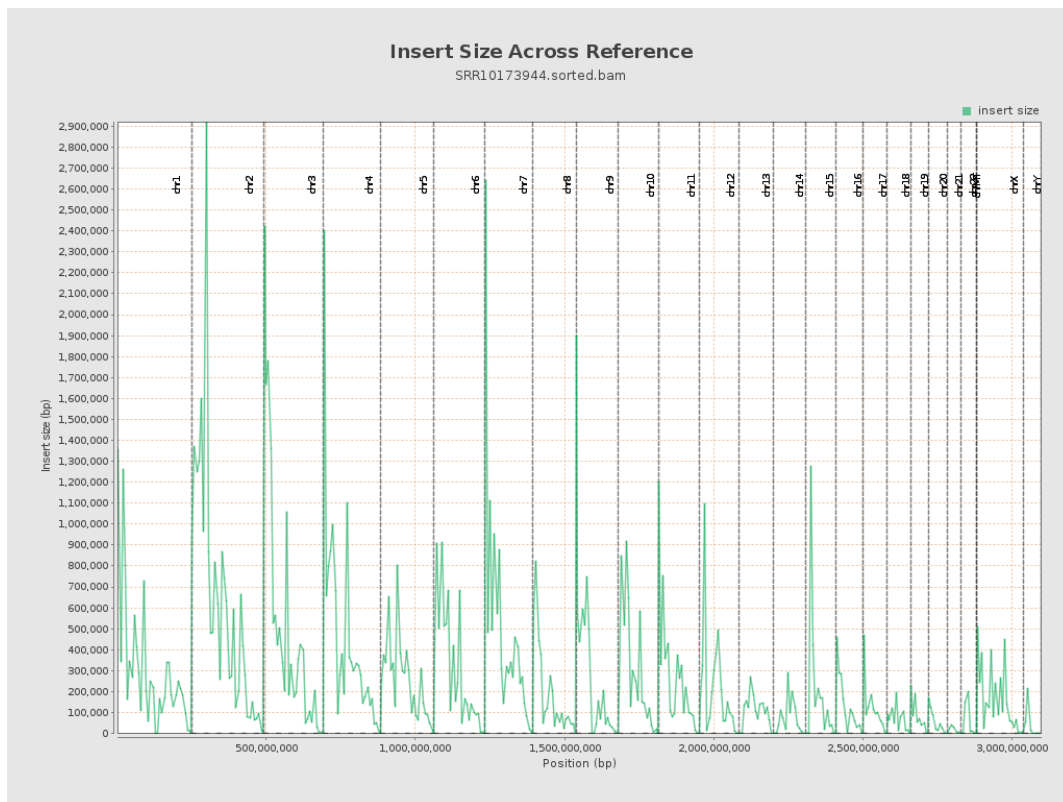
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

