

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 10:15:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173943.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_SRR10173943 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173943_1.fastq.gz SRR10173943_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 10:15:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,246,646
Mapped reads	4,141,522 / 97.52%
Unmapped reads	105,124 / 2.48%
Mapped paired reads	4,141,522 / 97.52%
Mapped reads, first in pair	2,073,449 / 48.83%
Mapped reads, second in pair	2,068,073 / 48.7%
Mapped reads, both in pair	4,080,118 / 96.08%
Mapped reads, singletons	61,404 / 1.45%
Secondary alignments	0
Supplementary alignments	517,523 / 12.19%
Read min/max/mean length	30 / 133 / 125.24
Duplicated reads (estimated)	3,276,632 / 77.16%
Duplication rate	65.16%
Clipped reads	2,004,335 / 47.2%

2.2. ACGT Content

Number/percentage of A's	141,991,026 / 30.17%
Number/percentage of C's	92,181,948 / 19.58%
Number/percentage of T's	140,804,283 / 29.91%
Number/percentage of G's	95,710,832 / 20.33%
Number/percentage of N's	3,769 / 0%

GC Percentage	39.92%
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2.3. Coverage

Mean	0.1522
Standard Deviation	2.9635

2.4. Mapping Quality

Mean Mapping Quality	52.59
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2.5. Insert size

Mean	1,224,646.48
Standard Deviation	10,543,518.75
P25/Median/P75	108 / 157 / 242

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	4,137,556
Insertions	50,881
Mapped reads with at least one insertion	1.19%
Deletions	137,844
Mapped reads with at least one deletion	3.25%
Homopolymer indels	41.36%

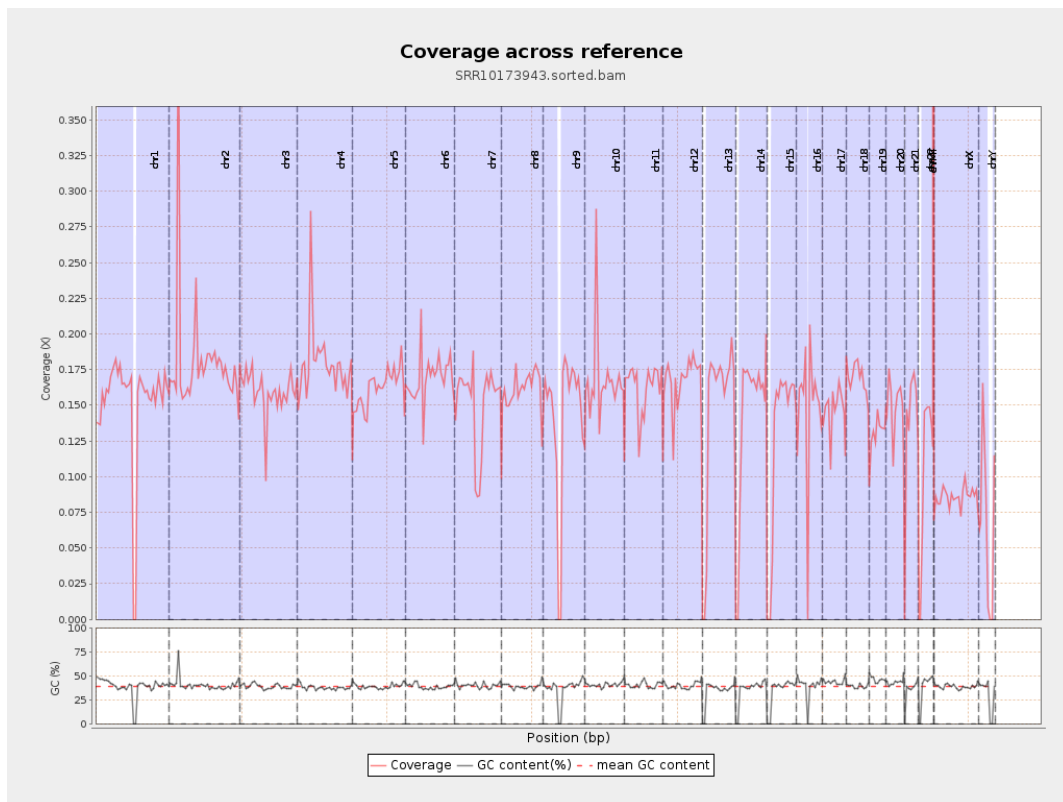
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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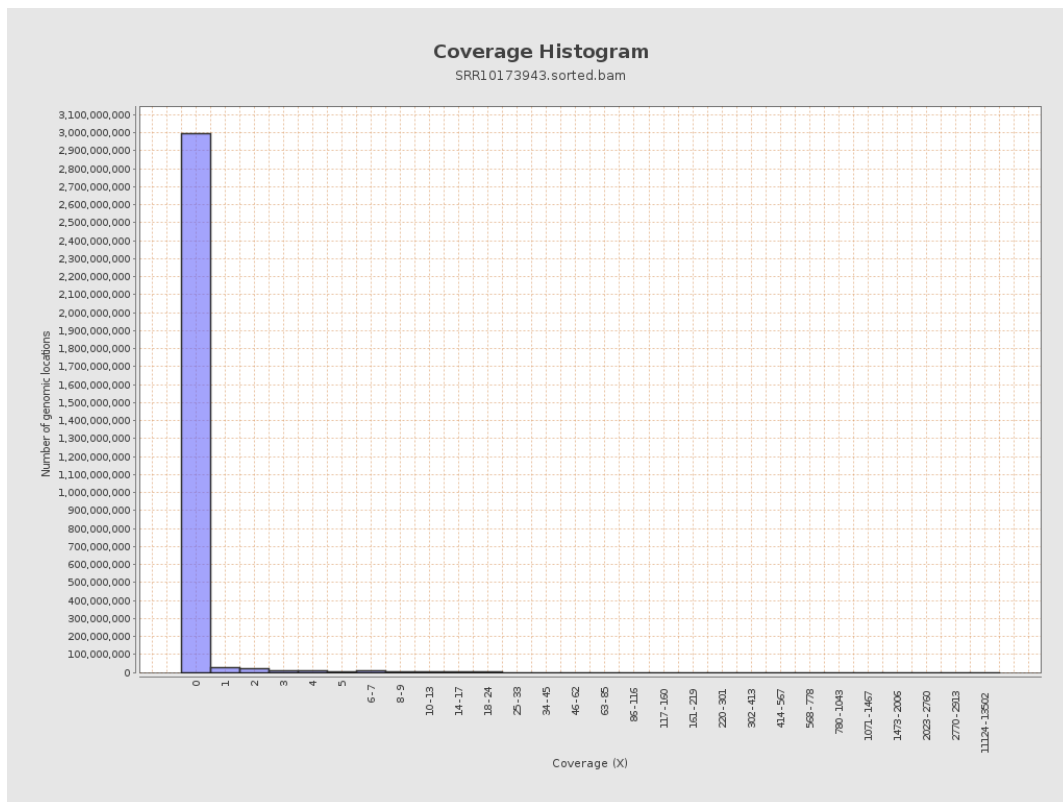
		bases	coverage	deviation
chr1	249250621	37912863	0.1521	1.4524
chr2	243199373	44191399	0.1817	9.4892
chr3	198022430	31648748	0.1598	1.18
chr4	191154276	34206134	0.1789	1.544
chr5	180915260	29351397	0.1622	1.1931
chr6	171115067	28973970	0.1693	1.3249
chr7	159138663	24025143	0.151	1.5
chr8	146364022	23656831	0.1616	1.855
chr9	141213431	20045218	0.1419	1.4209
chr10	135534747	22688723	0.1674	1.7152
chr11	135006516	21908587	0.1623	1.2378
chr12	133851895	22350876	0.167	1.2394
chr13	115169878	16668769	0.1447	1.1363
chr14	107349540	15089440	0.1406	1.1206
chr15	102531392	13115816	0.1279	1.061
chr16	90354753	13350236	0.1478	1.3195
chr17	81195210	11807774	0.1454	1.1793
chr18	78077248	13222485	0.1694	1.8916
chr19	59128983	7788289	0.1317	1.146
chr20	63025520	9378882	0.1488	1.1823
chr21	48129895	6625319	0.1377	1.4686
chr22	51304566	5197903	0.1013	1.0598
chrMT	16571	681309	41.1145	38.7585
chrX	155270560	13342656	0.0859	0.8655

chrY	59373566	3795714	0.0639	1.0786
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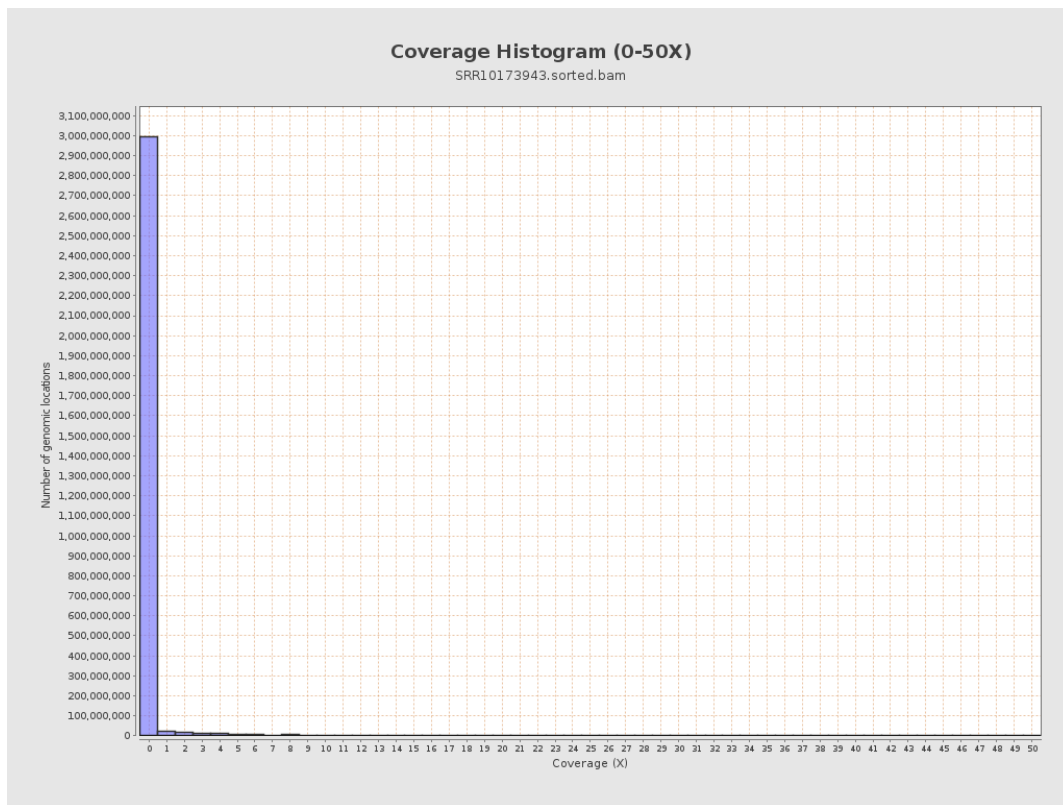
3. Results : Coverage across reference



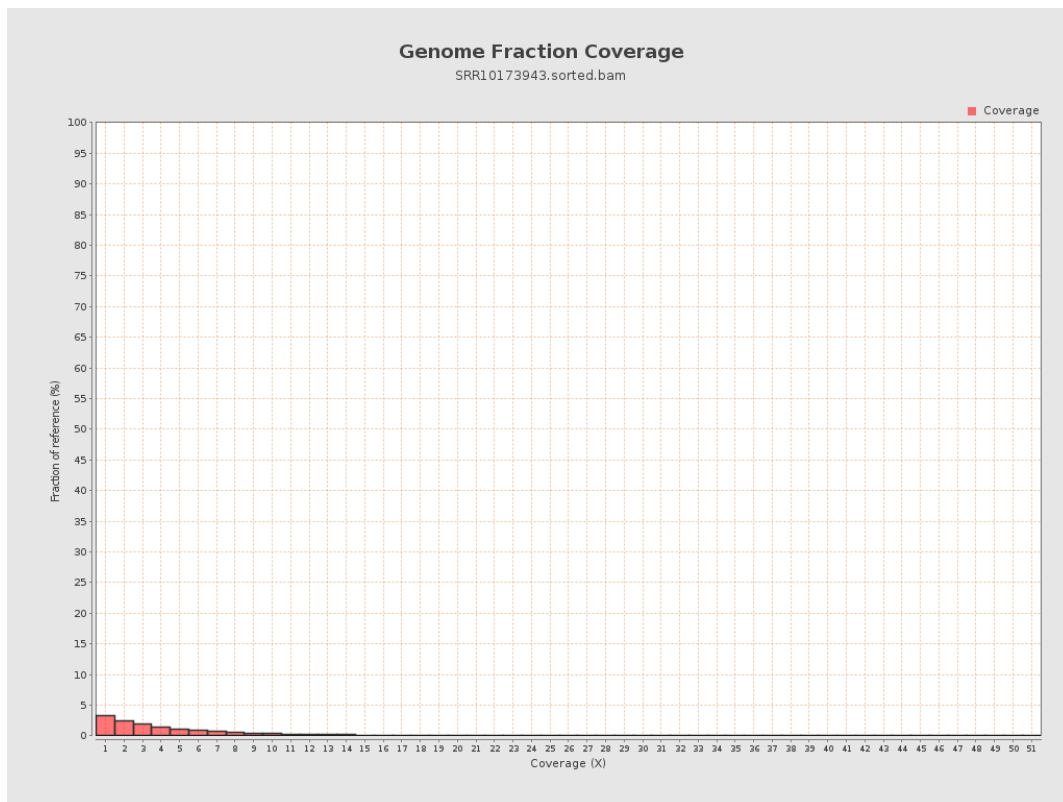
4. Results : Coverage Histogram



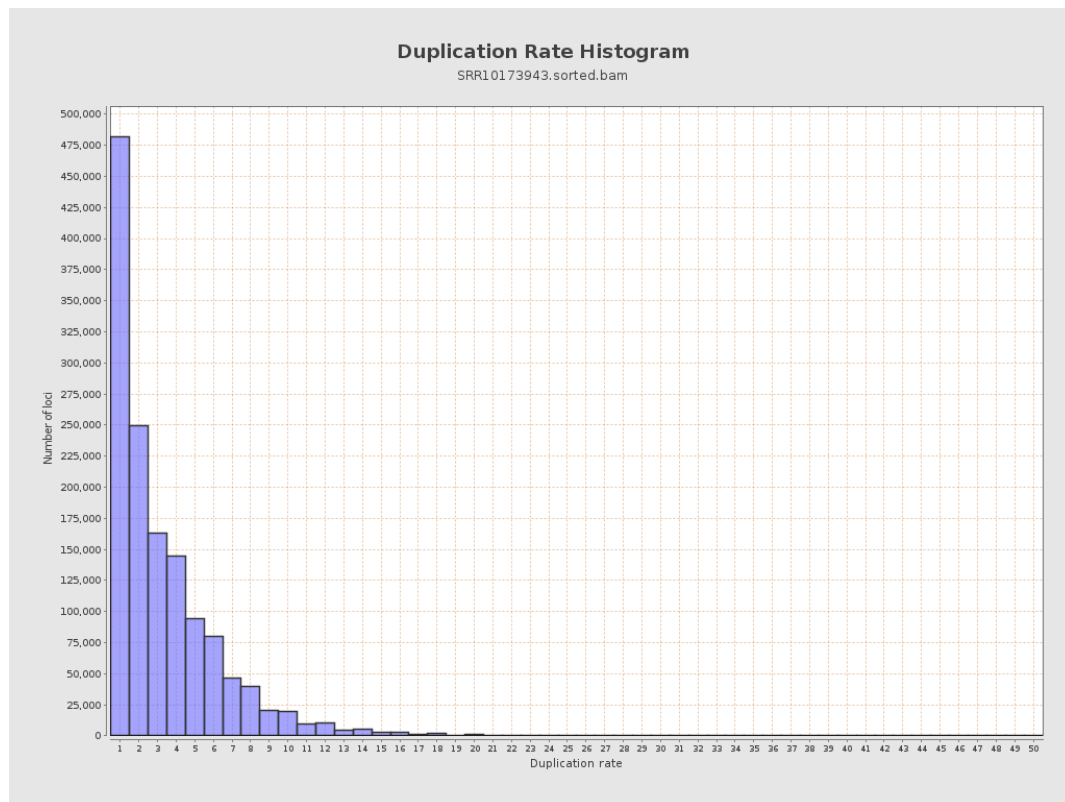
5. Results : Coverage Histogram (0-50X)



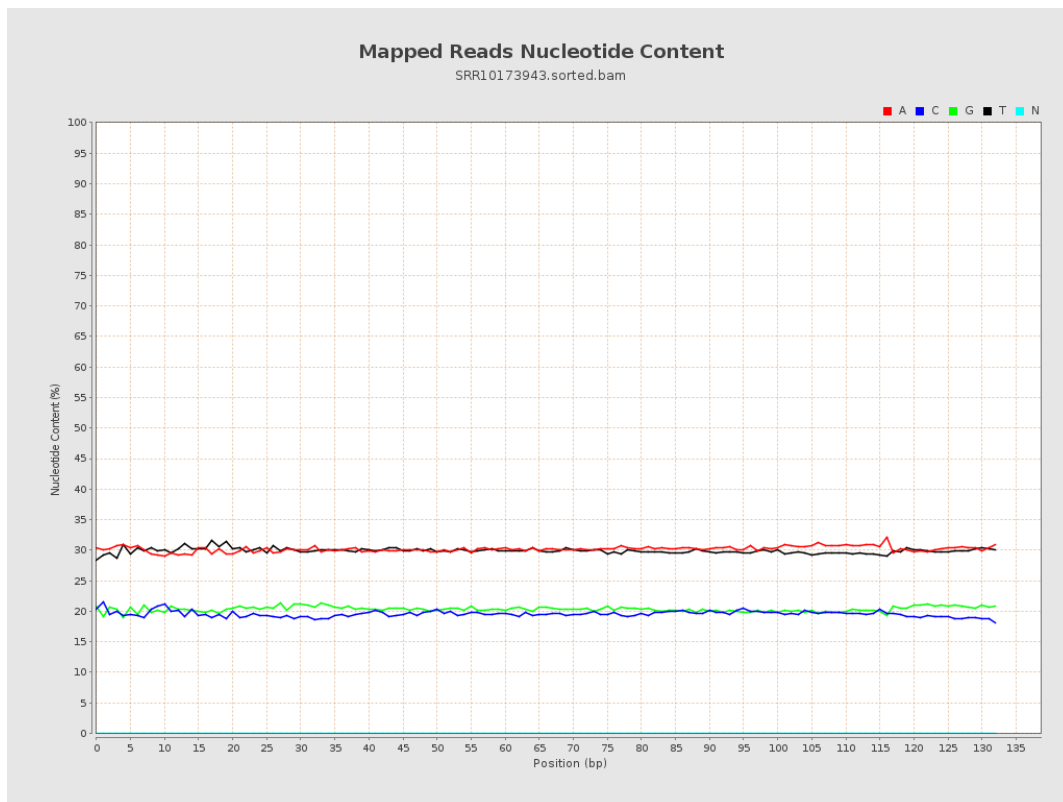
6. Results : Genome Fraction Coverage



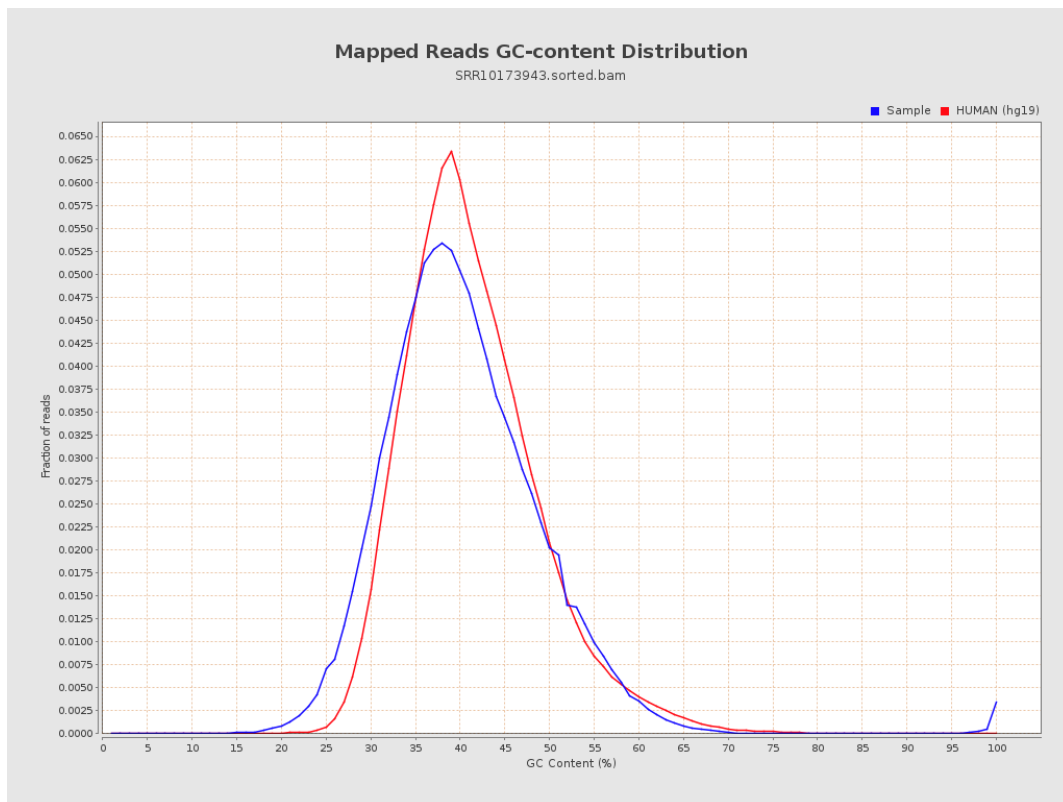
7. Results : Duplication Rate Histogram



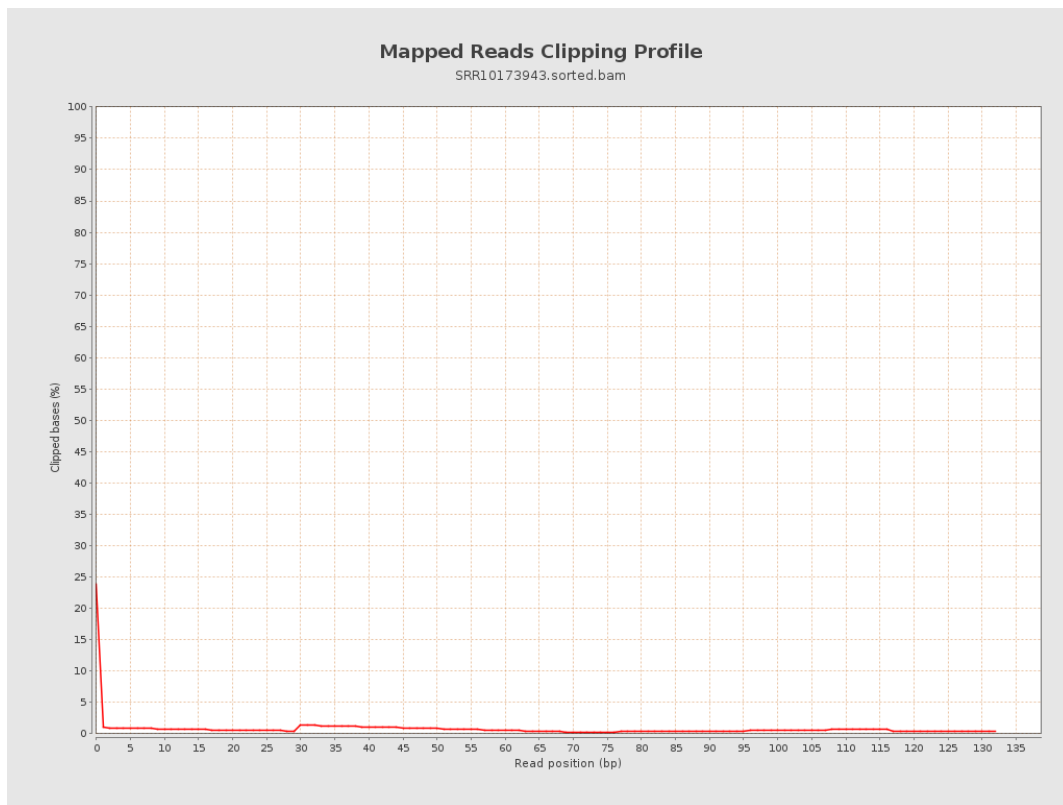
8. Results : Mapped Reads Nucleotide Content



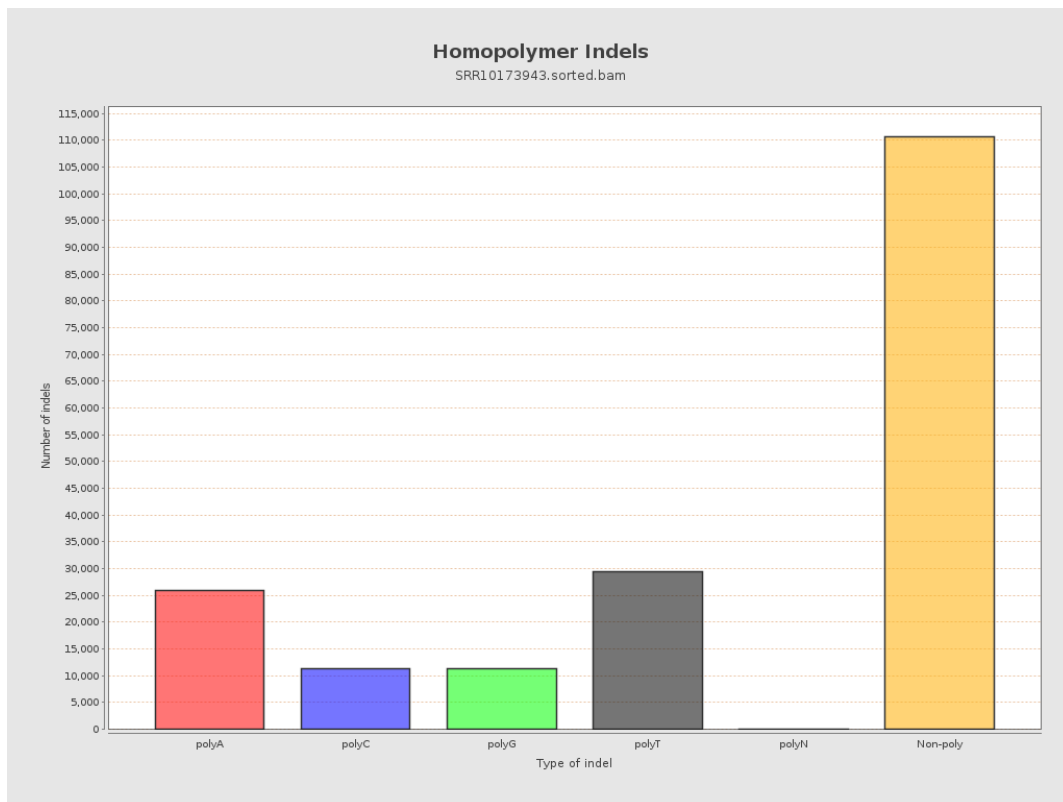
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



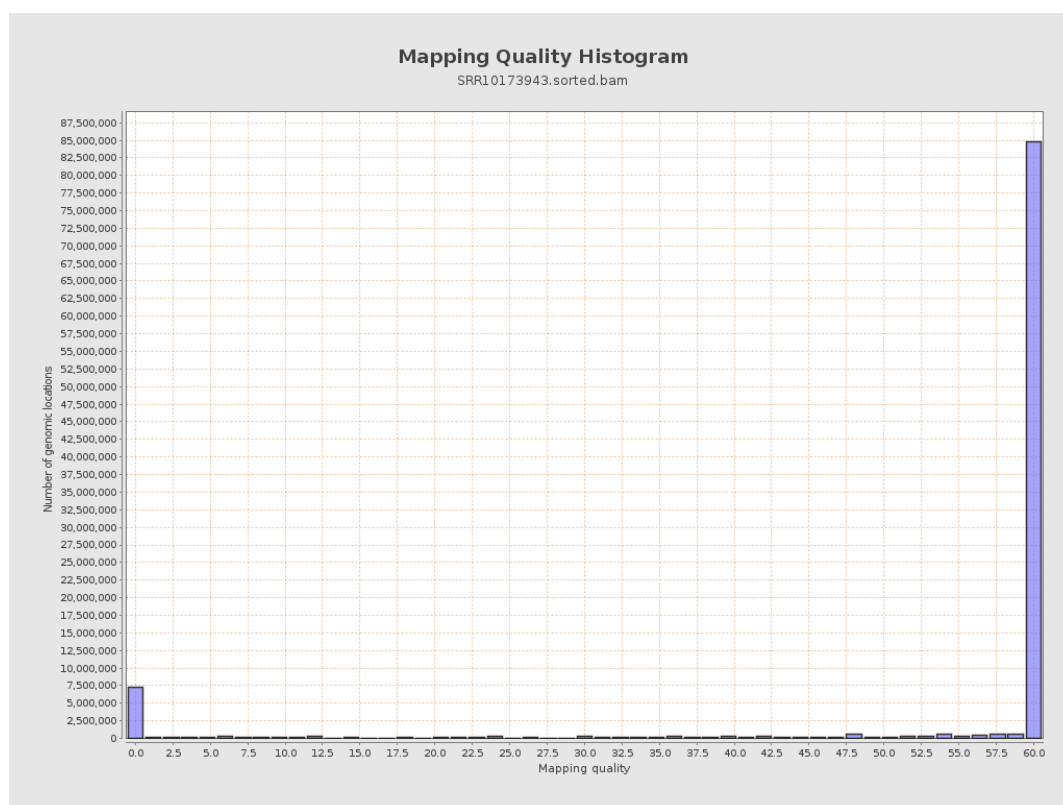
11. Results : Homopolymer Indels



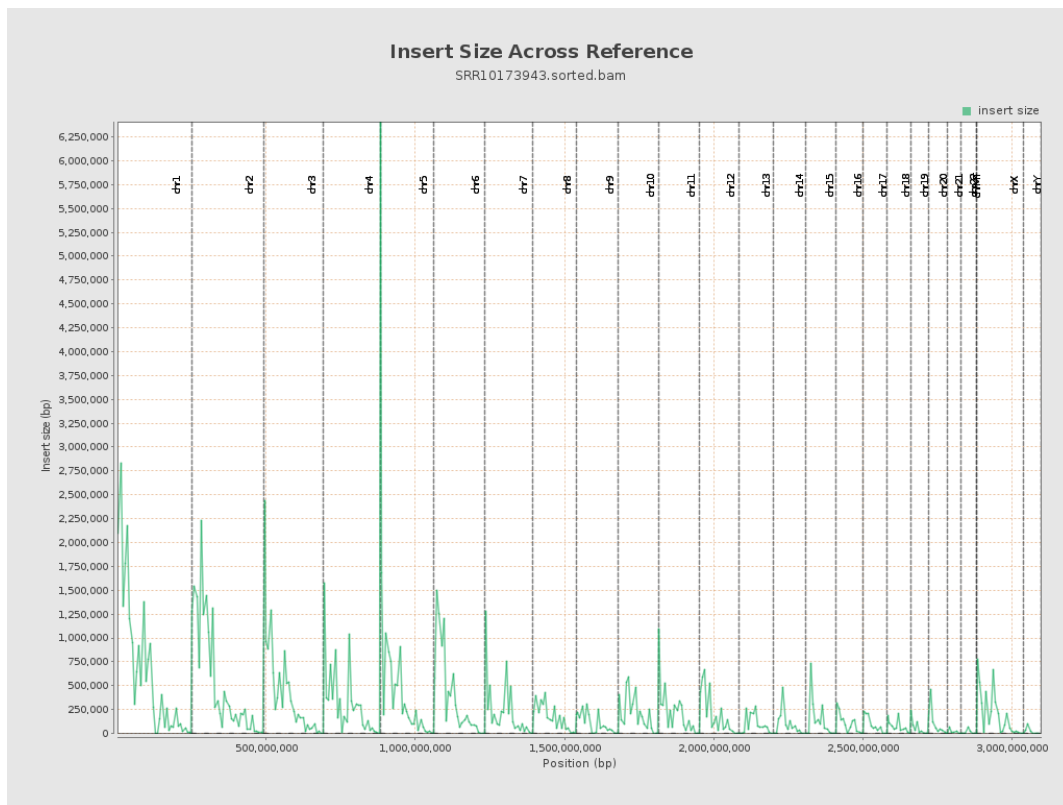
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

