

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 15:20:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173973.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_SRR10173973 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173973_1.fastq.gz SRR10173973_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 15:20:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173973.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,183,314
Mapped reads	4,108,021 / 98.2%
Unmapped reads	75,293 / 1.8%
Mapped paired reads	4,108,021 / 98.2%
Mapped reads, first in pair	2,053,577 / 49.09%
Mapped reads, second in pair	2,054,444 / 49.11%
Mapped reads, both in pair	4,060,572 / 97.07%
Mapped reads, singletons	47,449 / 1.13%
Secondary alignments	0
Supplementary alignments	518,185 / 12.39%
Read min/max/mean length	30 / 133 / 124.97
Duplicated reads (estimated)	3,305,056 / 79.01%
Duplication rate	65.24%
Clipped reads	1,953,283 / 46.69%

2.2. ACGT Content

Number/percentage of A's	138,611,150 / 29.63%
Number/percentage of C's	94,122,247 / 20.12%
Number/percentage of T's	137,404,383 / 29.38%
Number/percentage of G's	97,596,311 / 20.87%
Number/percentage of N's	3,386 / 0%

GC Percentage	40.99%
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2.3. Coverage

Mean	0.1512
Standard Deviation	2.6578

2.4. Mapping Quality

Mean Mapping Quality	52.81
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2.5. Insert size

Mean	976,394.91
Standard Deviation	9,131,589.08
P25/Median/P75	106 / 153 / 230

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	3,760,477
Insertions	48,574
Mapped reads with at least one insertion	1.14%
Deletions	135,662
Mapped reads with at least one deletion	3.22%
Homopolymer indels	41.6%

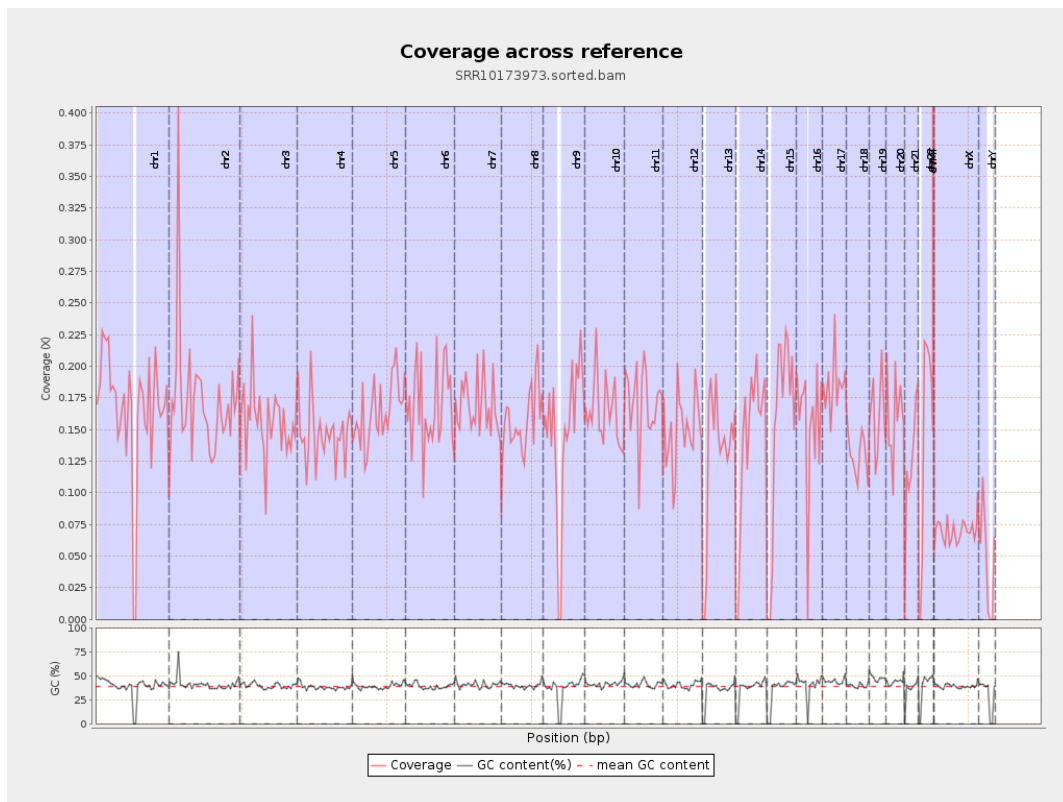
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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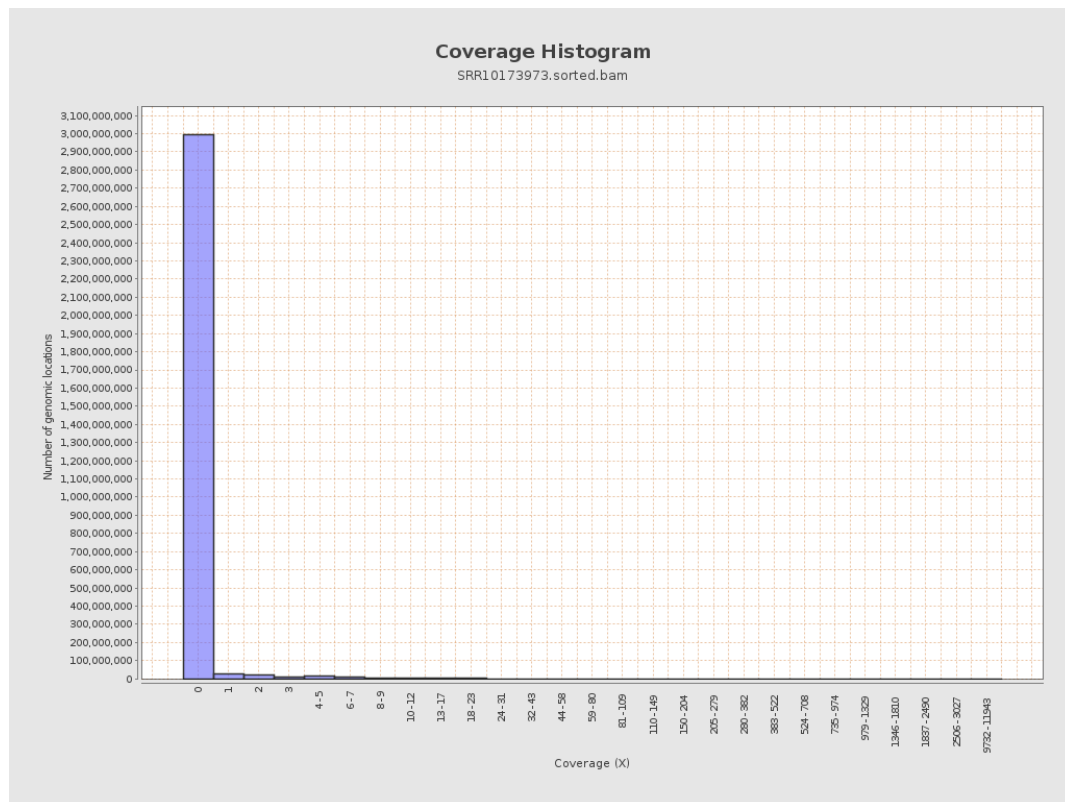
		bases	coverage	deviation
chr1	249250621	41348227	0.1659	1.3941
chr2	243199373	42245585	0.1737	8.406
chr3	198022430	30782597	0.1555	1.1986
chr4	191154276	27811608	0.1455	1.3307
chr5	180915260	29665867	0.164	1.252
chr6	171115067	28917001	0.169	1.3595
chr7	159138663	26883184	0.1689	1.4183
chr8	146364022	23100121	0.1578	1.4411
chr9	141213431	20704112	0.1466	1.2966
chr10	135534747	22156192	0.1635	1.5366
chr11	135006516	23195900	0.1718	1.2869
chr12	133851895	20083832	0.15	1.2075
chr13	115169878	14701202	0.1276	1.0936
chr14	107349540	15081319	0.1405	1.1515
chr15	102531392	15638017	0.1525	1.2178
chr16	90354753	13845891	0.1532	1.2486
chr17	81195210	15054010	0.1854	1.3212
chr18	78077248	10233923	0.1311	1.388
chr19	59128983	9498751	0.1606	1.2558
chr20	63025520	10052863	0.1595	1.2375
chr21	48129895	6003205	0.1247	1.2088
chr22	51304566	7099861	0.1384	1.241
chrMT	16571	530163	31.9934	29.218
chrX	155270560	10734277	0.0691	0.7969

chrY	59373566	2690723	0.0453	0.8163
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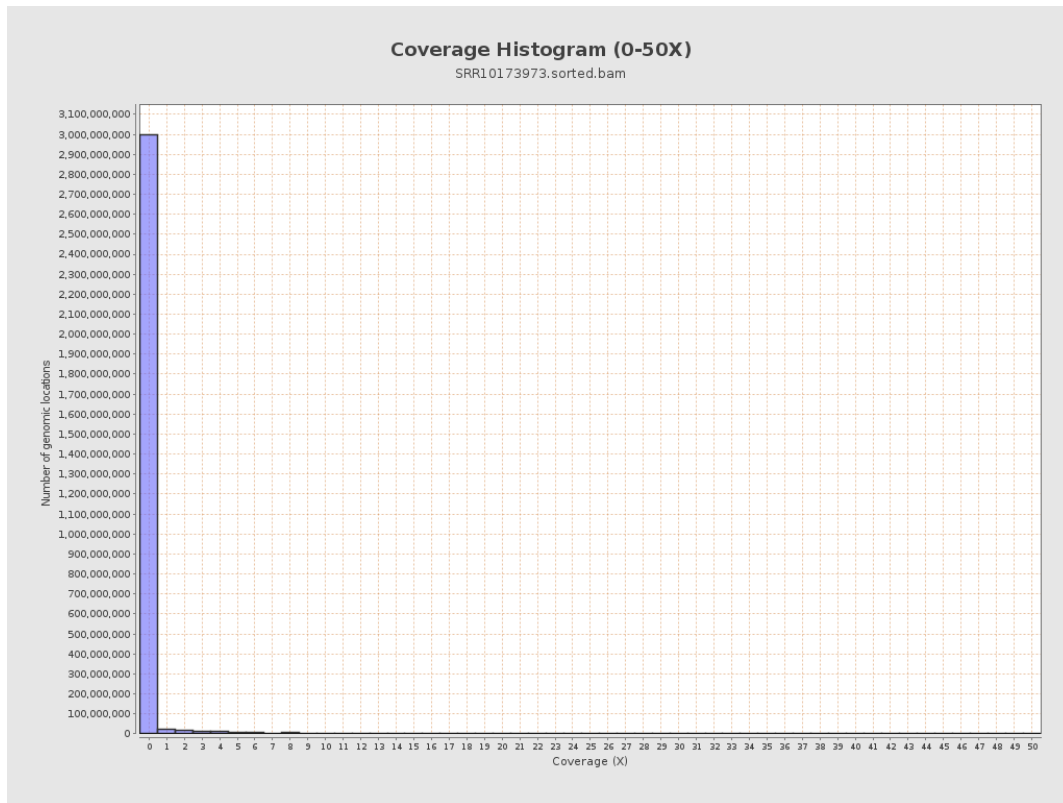
3. Results : Coverage across reference



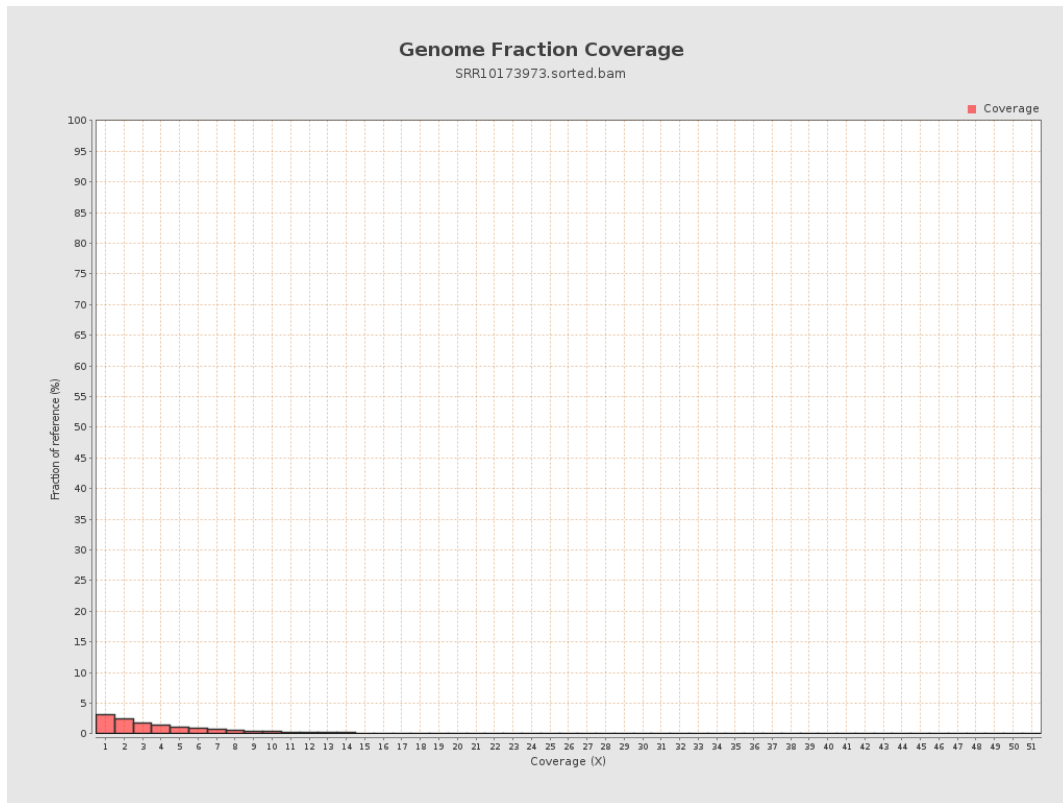
4. Results : Coverage Histogram



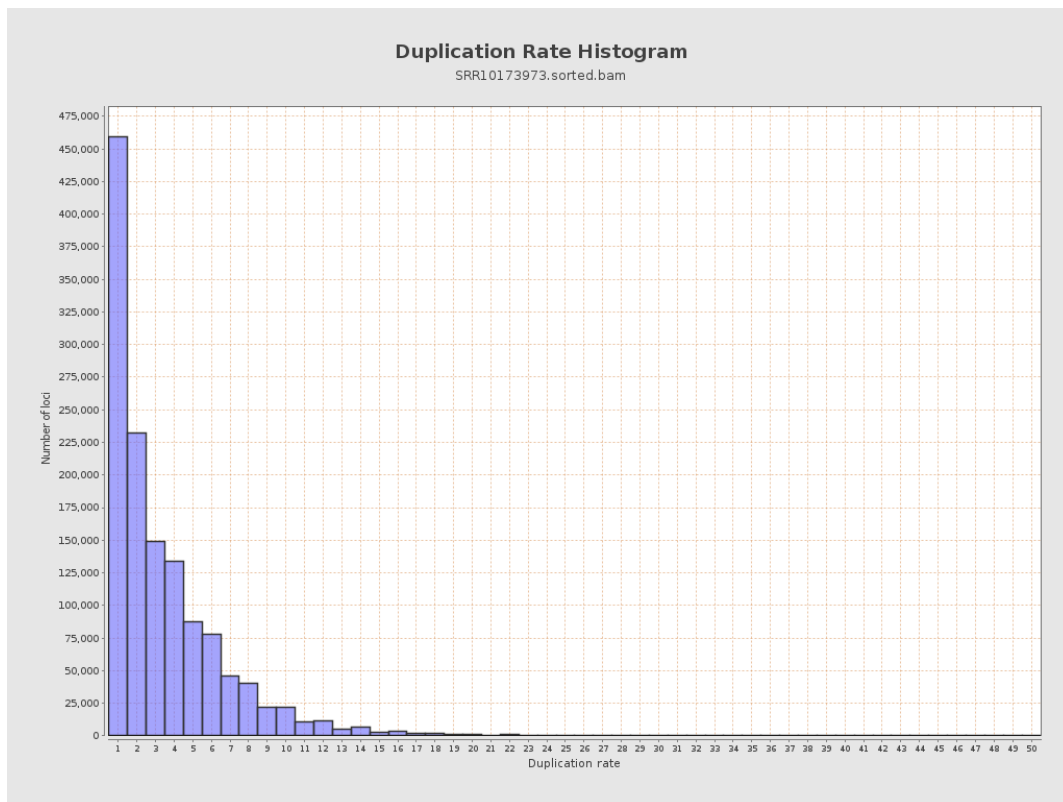
5. Results : Coverage Histogram (0-50X)



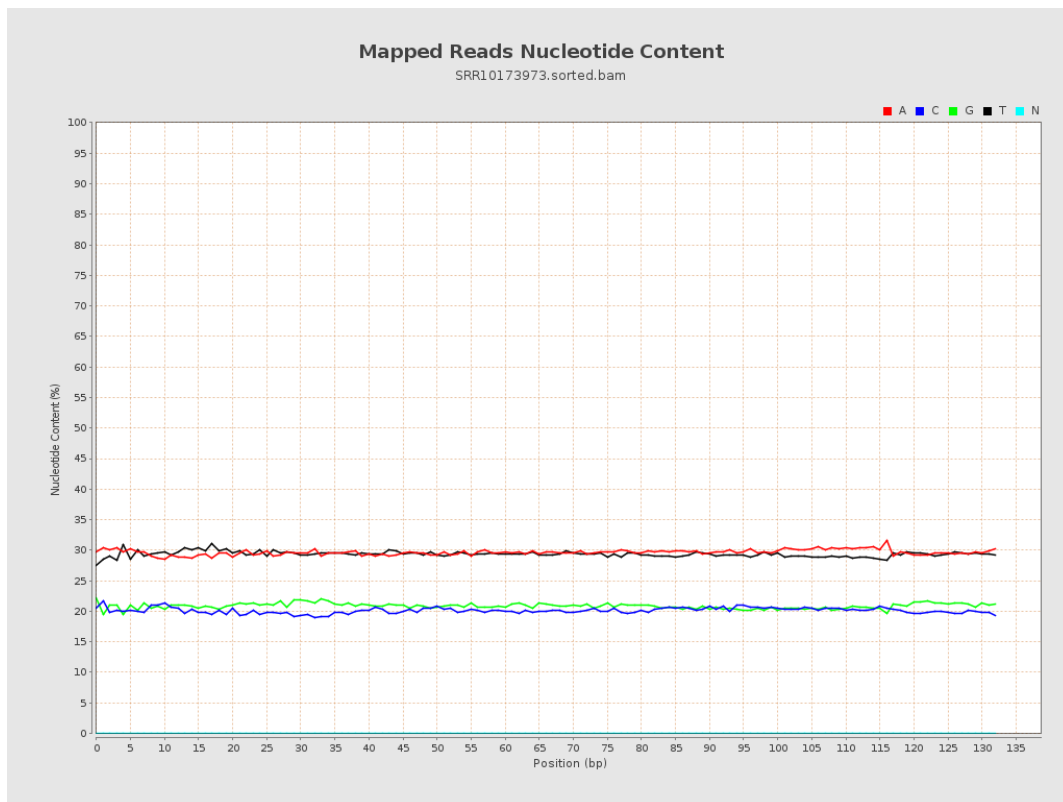
6. Results : Genome Fraction Coverage



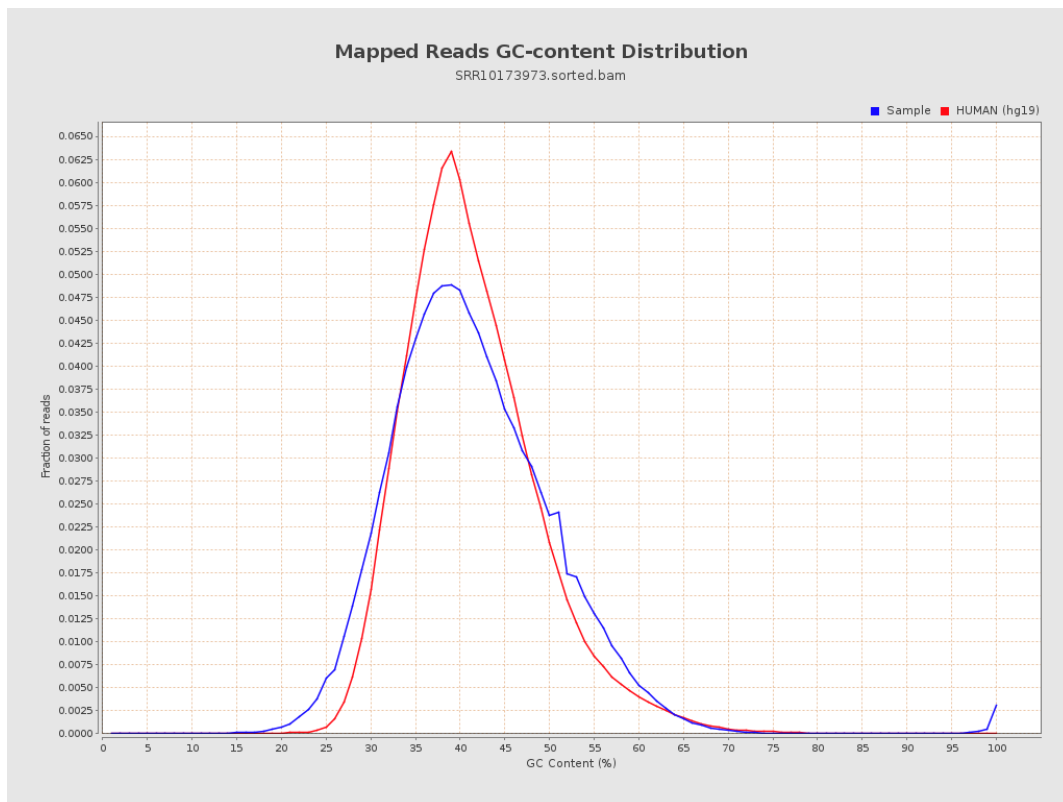
7. Results : Duplication Rate Histogram



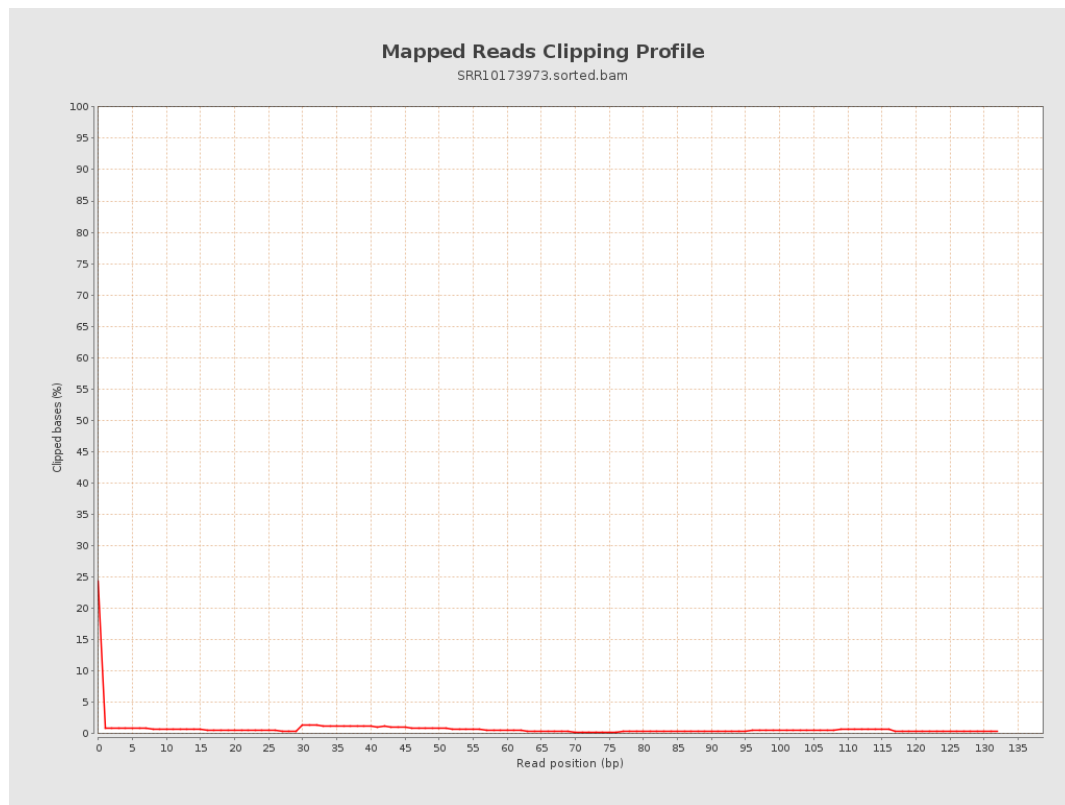
8. Results : Mapped Reads Nucleotide Content



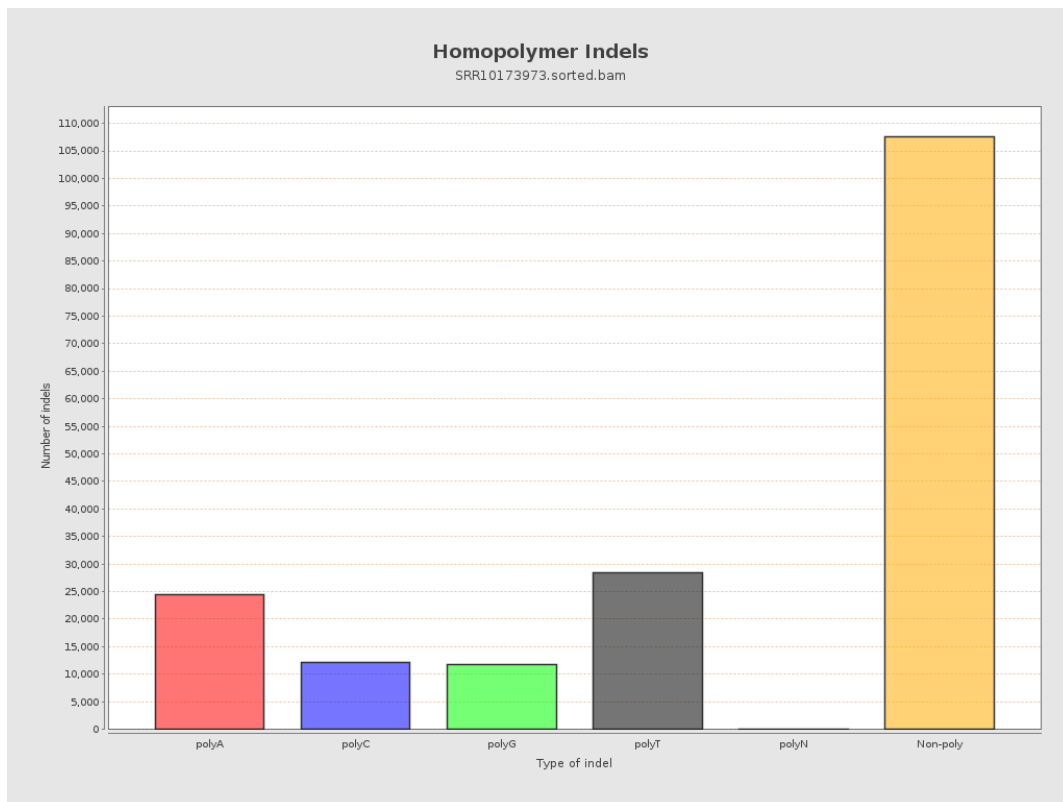
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



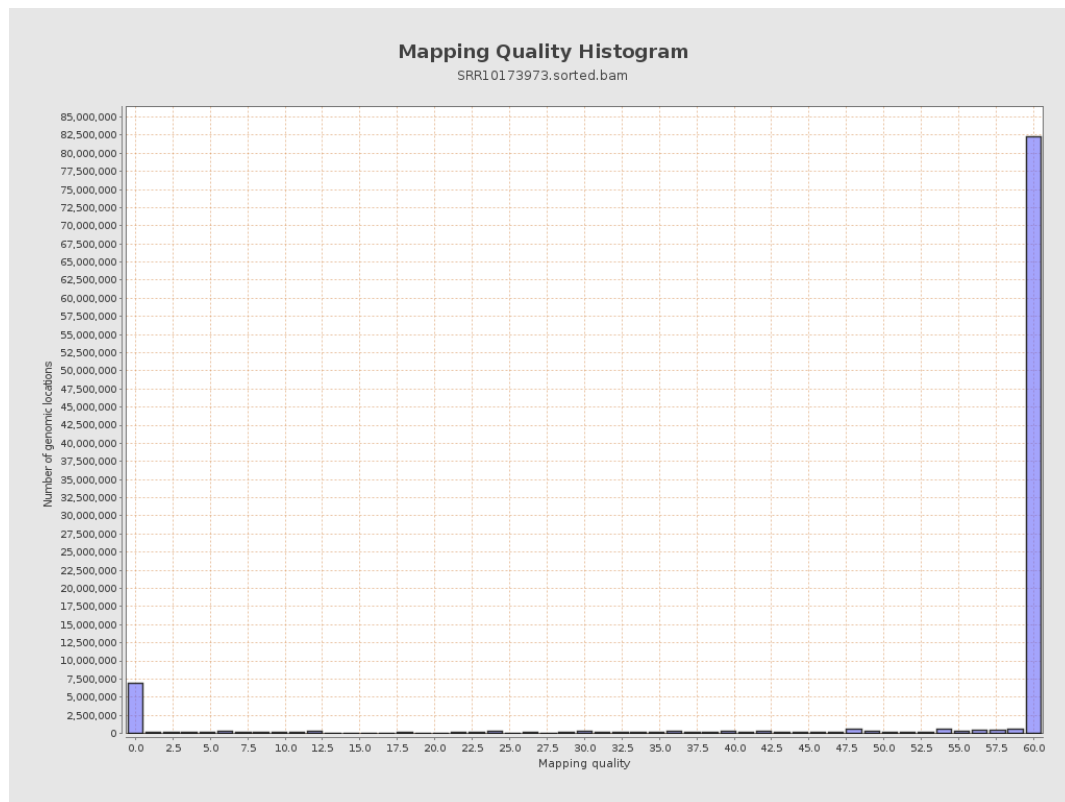
11. Results : Homopolymer Indels



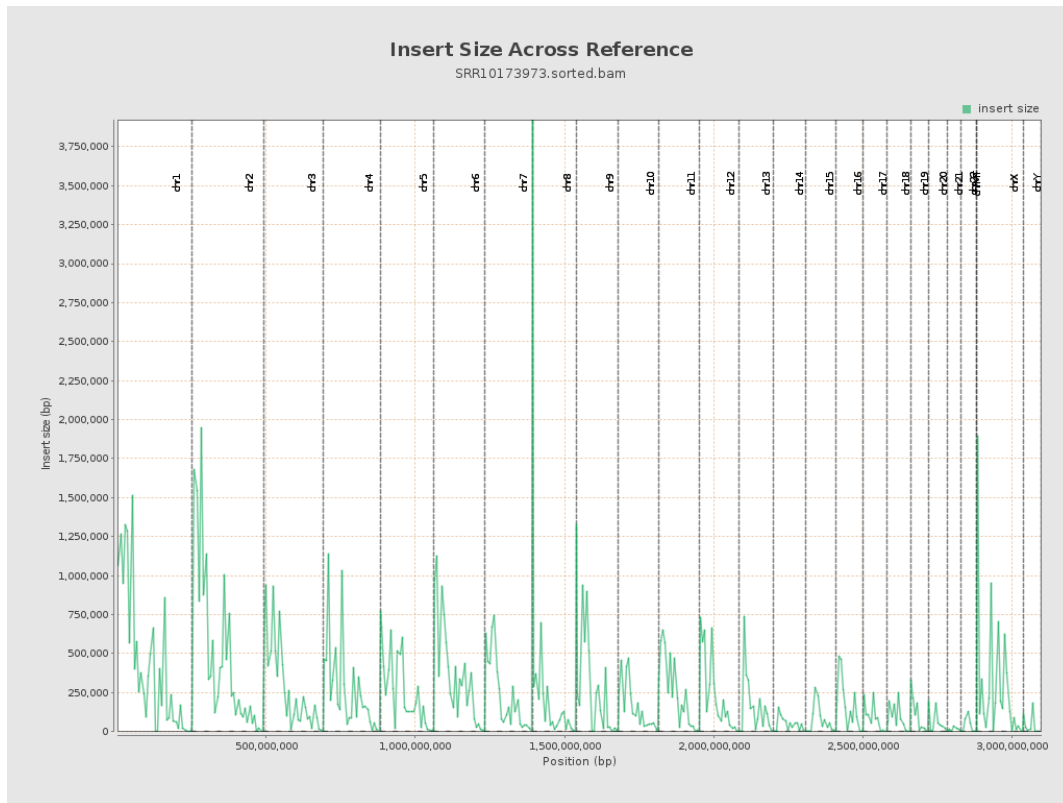
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

