

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 16:52:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173984.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_SRR10173984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173984_1.fastq.gz SRR10173984_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 16:52:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,574,094
Mapped reads	11,307,775 / 97.7%
Unmapped reads	266,319 / 2.3%
Mapped paired reads	11,307,775 / 97.7%
Mapped reads, first in pair	5,656,701 / 48.87%
Mapped reads, second in pair	5,651,074 / 48.83%
Mapped reads, both in pair	11,137,604 / 96.23%
Mapped reads, singletons	170,171 / 1.47%
Secondary alignments	0
Supplementary alignments	1,519,598 / 13.13%
Read min/max/mean length	30 / 133 / 126.05
Duplicated reads (estimated)	9,101,350 / 78.64%
Duplication rate	65.58%
Clipped reads	6,253,742 / 54.03%

2.2. ACGT Content

Number/percentage of A's	381,145,095 / 29.82%
Number/percentage of C's	254,260,759 / 19.89%
Number/percentage of T's	378,120,012 / 29.59%
Number/percentage of G's	264,538,676 / 20.7%
Number/percentage of N's	9,439 / 0%

GC Percentage	40.59%
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2.3. Coverage

Mean	0.4131
Standard Deviation	6.9317

2.4. Mapping Quality

Mean Mapping Quality	52.52
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2.5. Insert size

Mean	951,834.62
Standard Deviation	9,331,725.77
P25/Median/P75	107 / 159 / 246

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	10,912,835
Insertions	139,686
Mapped reads with at least one insertion	1.19%
Deletions	357,542
Mapped reads with at least one deletion	3.08%
Homopolymer indels	41.09%

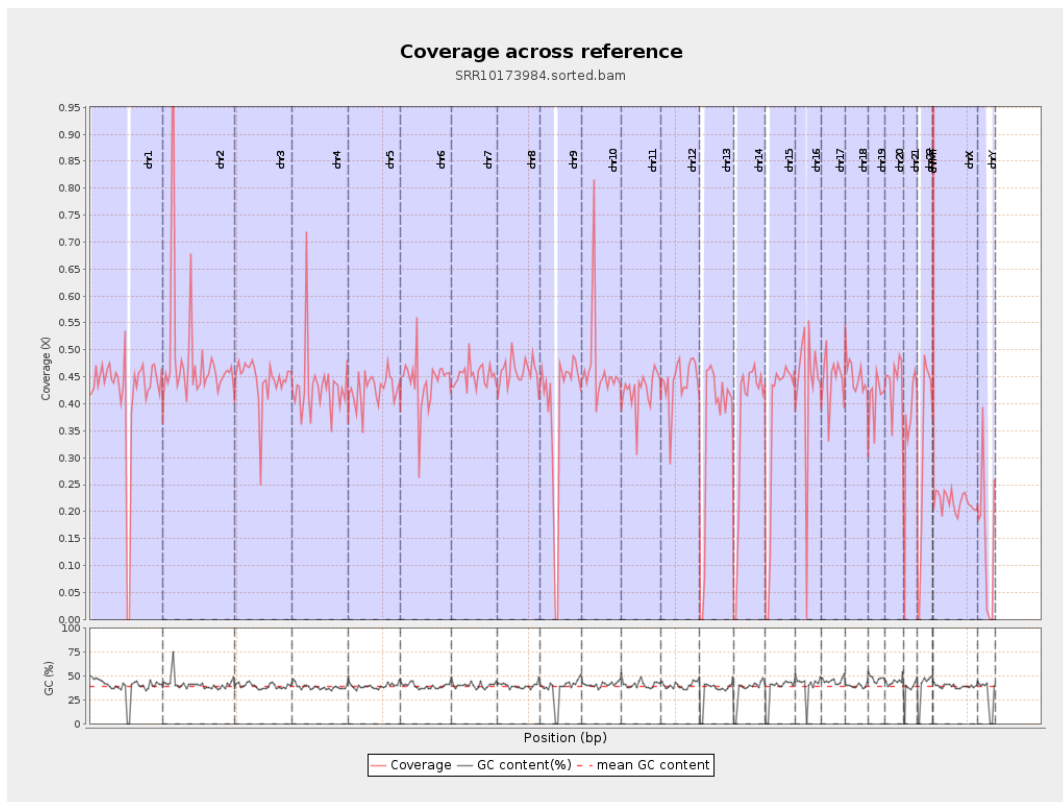
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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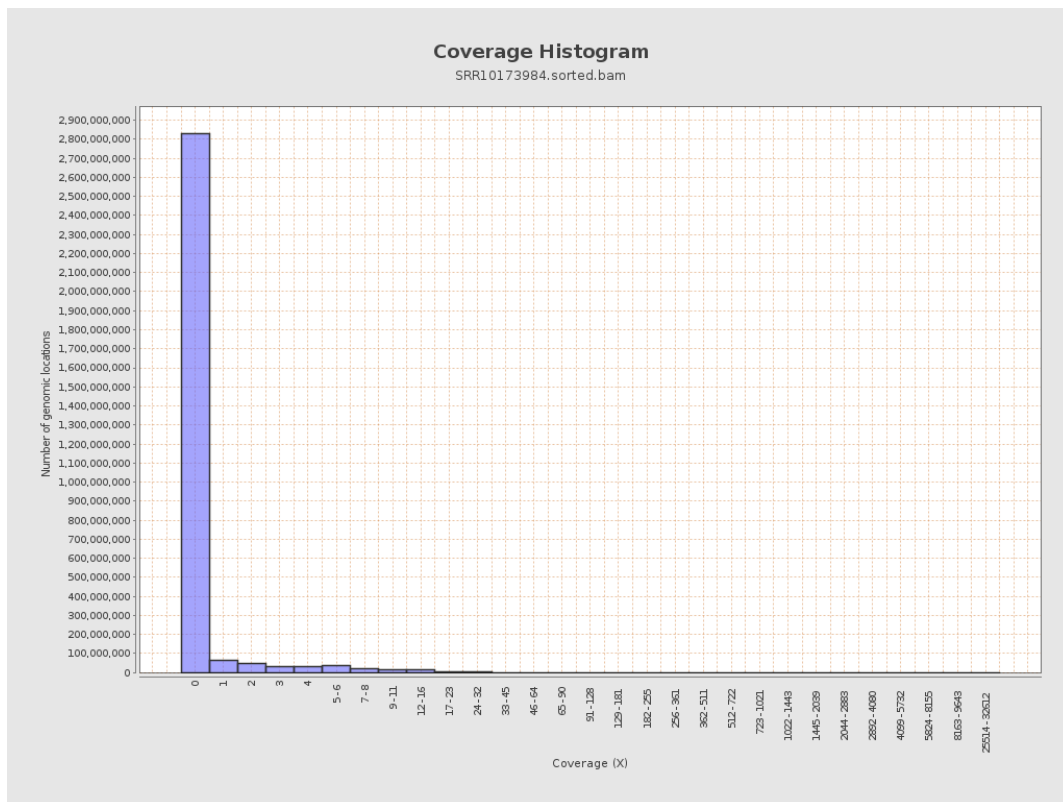
		bases	coverage	deviation
chr1	249250621	104453657	0.4191	3.6085
chr2	243199373	117314404	0.4824	22.7258
chr3	198022430	87708523	0.4429	1.9857
chr4	191154276	82902280	0.4337	3.0659
chr5	180915260	77389500	0.4278	1.9576
chr6	171115067	75399840	0.4406	2.5008
chr7	159138663	71971924	0.4523	3.395
chr8	146364022	67102786	0.4585	4.0575
chr9	141213431	55480139	0.3929	3.2099
chr10	135534747	62915290	0.4642	3.9998
chr11	135006516	57456347	0.4256	2.1239
chr12	133851895	59262043	0.4427	2.0958
chr13	115169878	40906452	0.3552	1.7679
chr14	107349540	39609916	0.369	1.862
chr15	102531392	36953474	0.3604	1.8688
chr16	90354753	38927631	0.4308	2.6091
chr17	81195210	36426541	0.4486	2.4006
chr18	78077248	35339950	0.4526	4.662
chr19	59128983	24402988	0.4127	2.852
chr20	63025520	27913734	0.4429	2.1436
chr21	48129895	17468070	0.3629	2.7286
chr22	51304566	16333232	0.3184	2.2096
chrMT	16571	2507238	151.3028	112.5575
chrX	155270560	33788153	0.2176	1.4127

chrY	59373566	8995041	0.1515	2.3535
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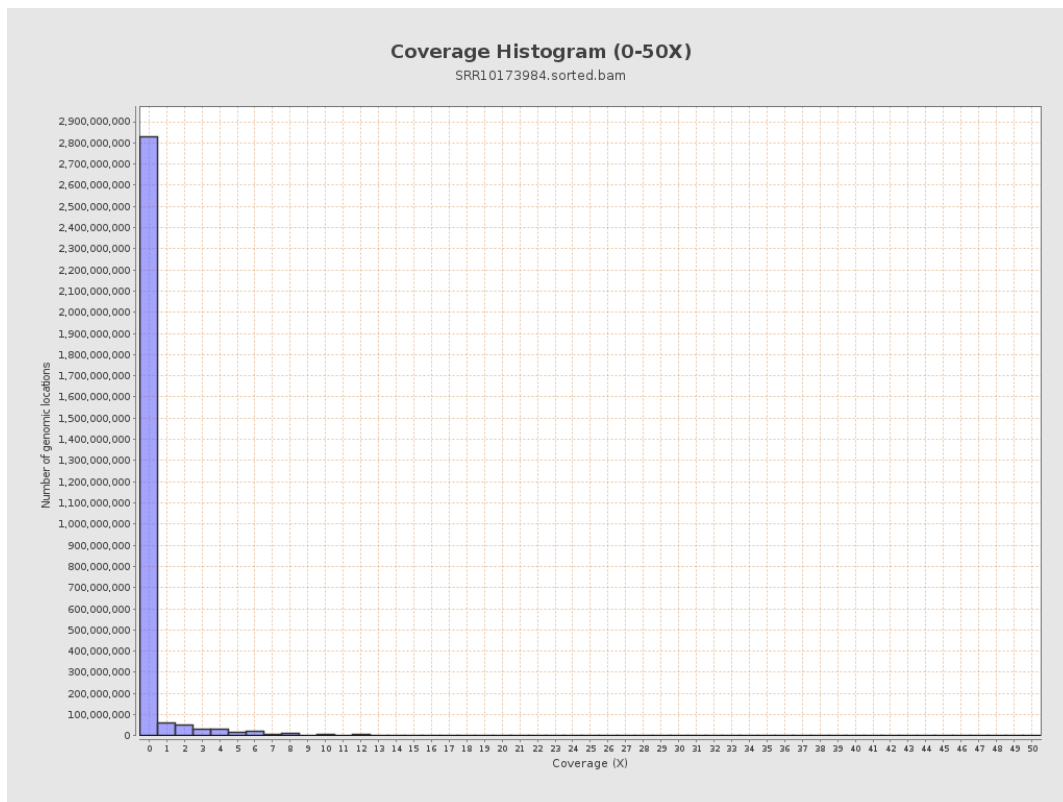
3. Results : Coverage across reference



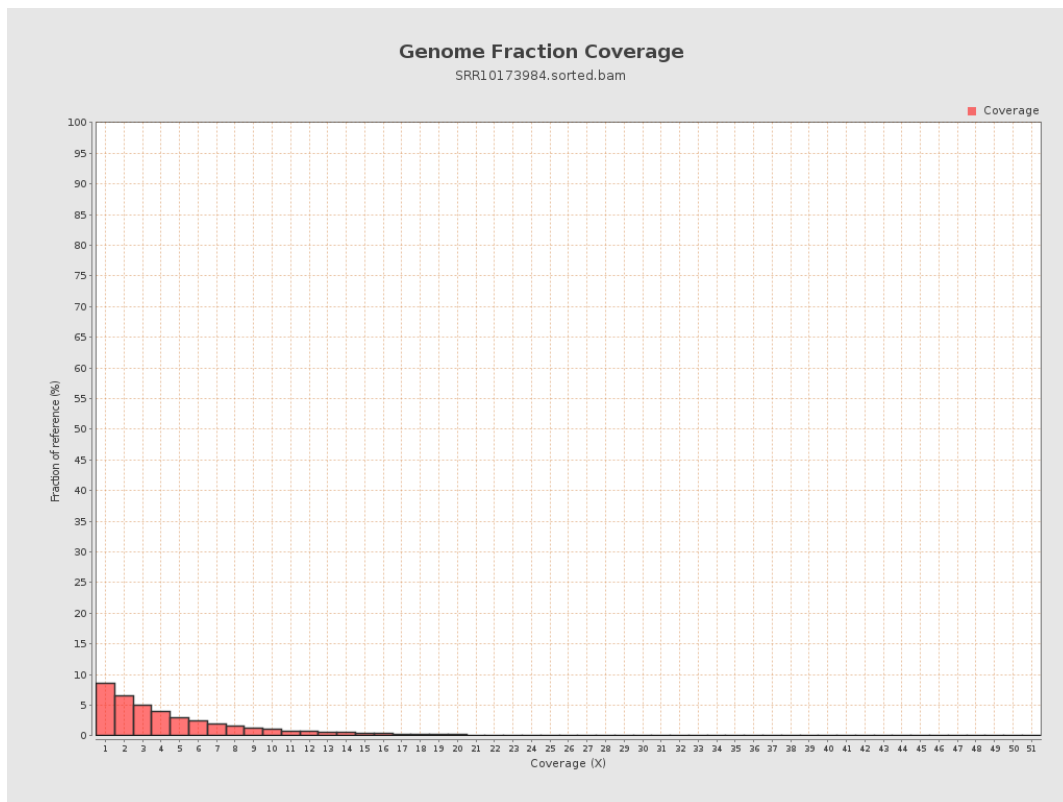
4. Results : Coverage Histogram



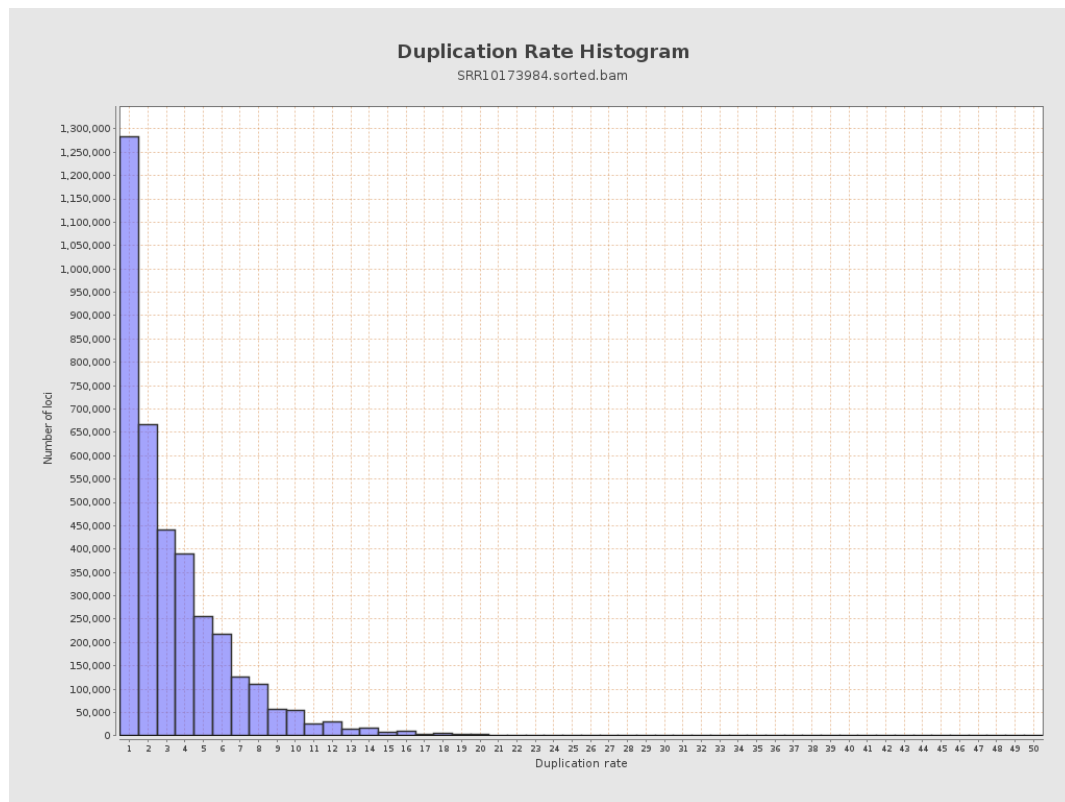
5. Results : Coverage Histogram (0-50X)



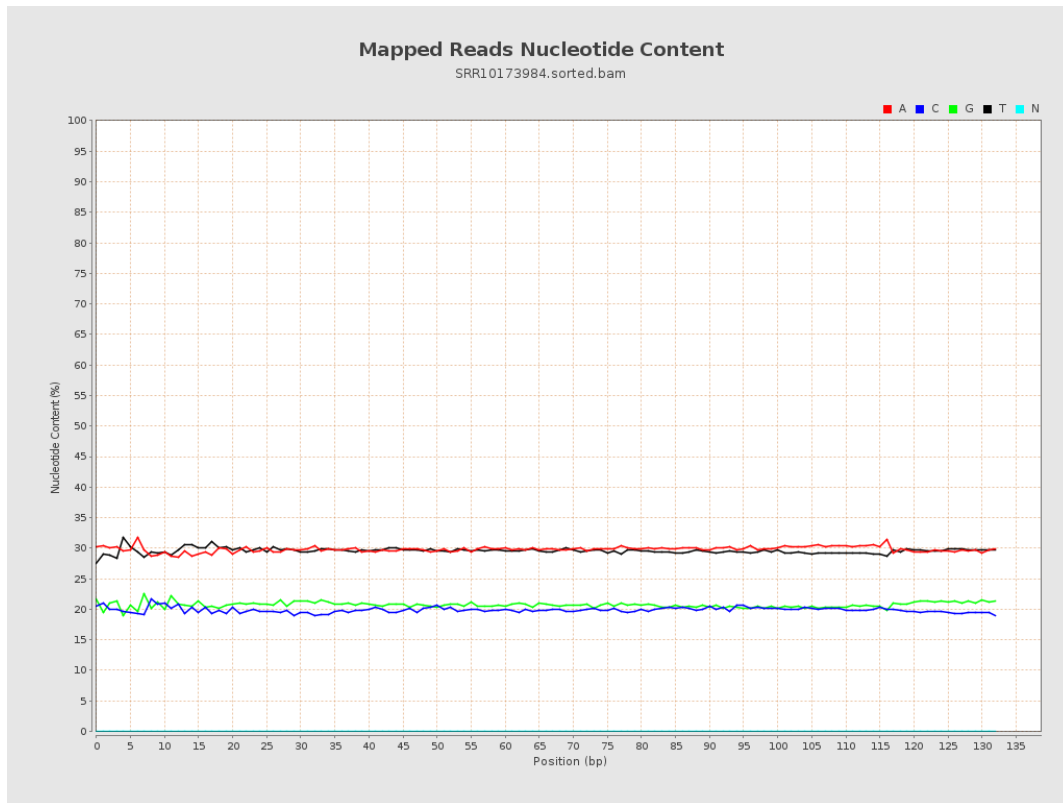
6. Results : Genome Fraction Coverage



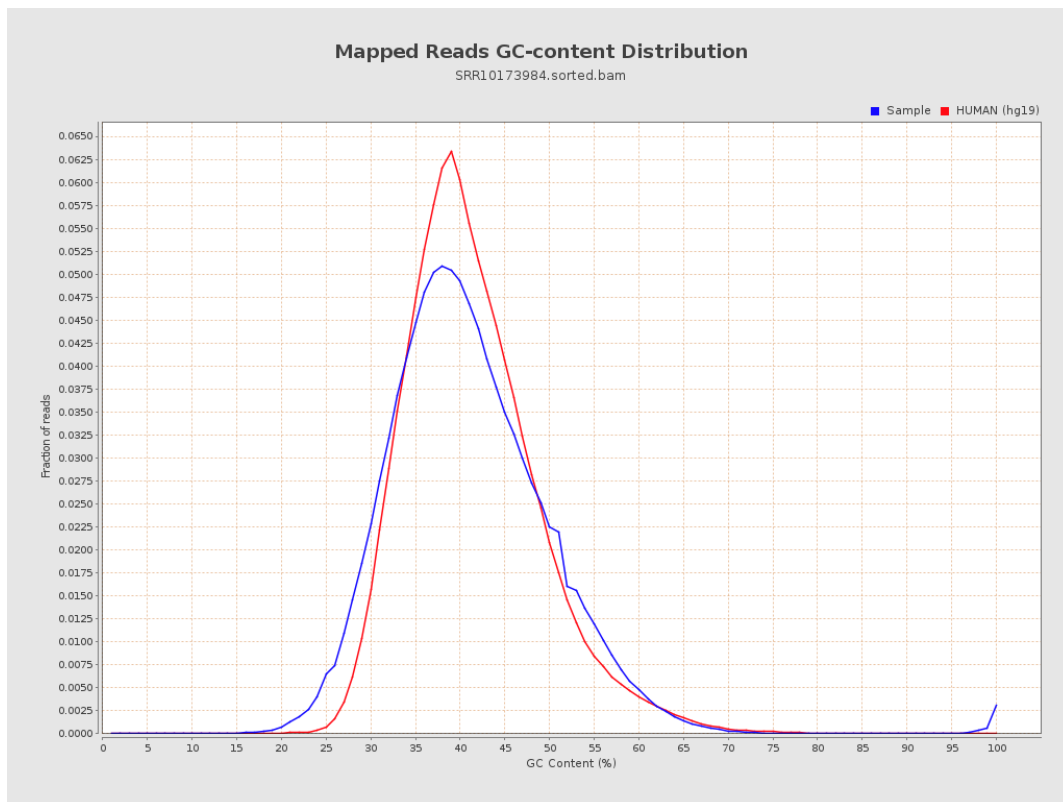
7. Results : Duplication Rate Histogram



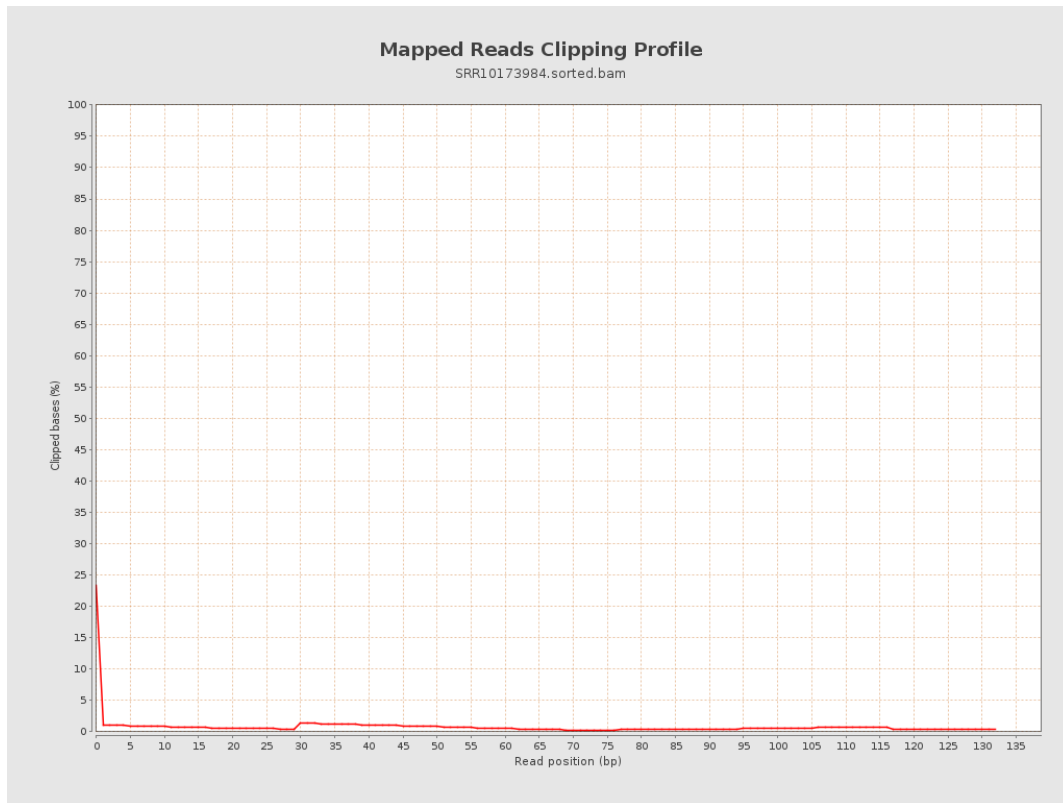
8. Results : Mapped Reads Nucleotide Content



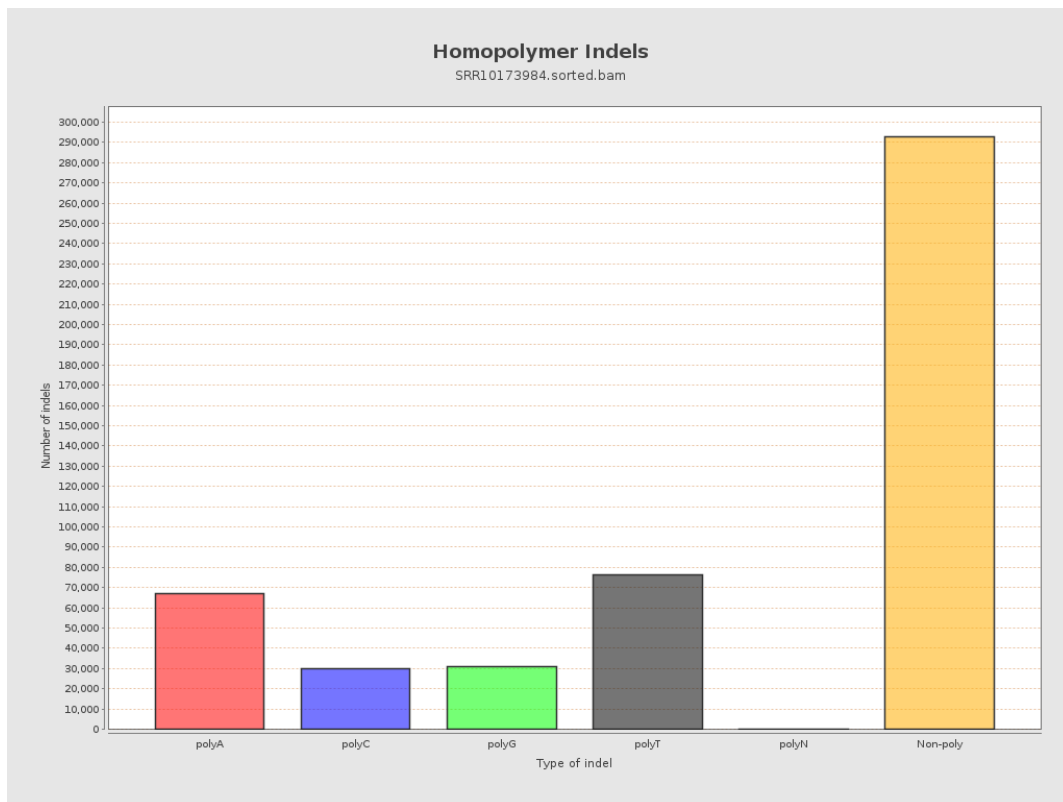
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



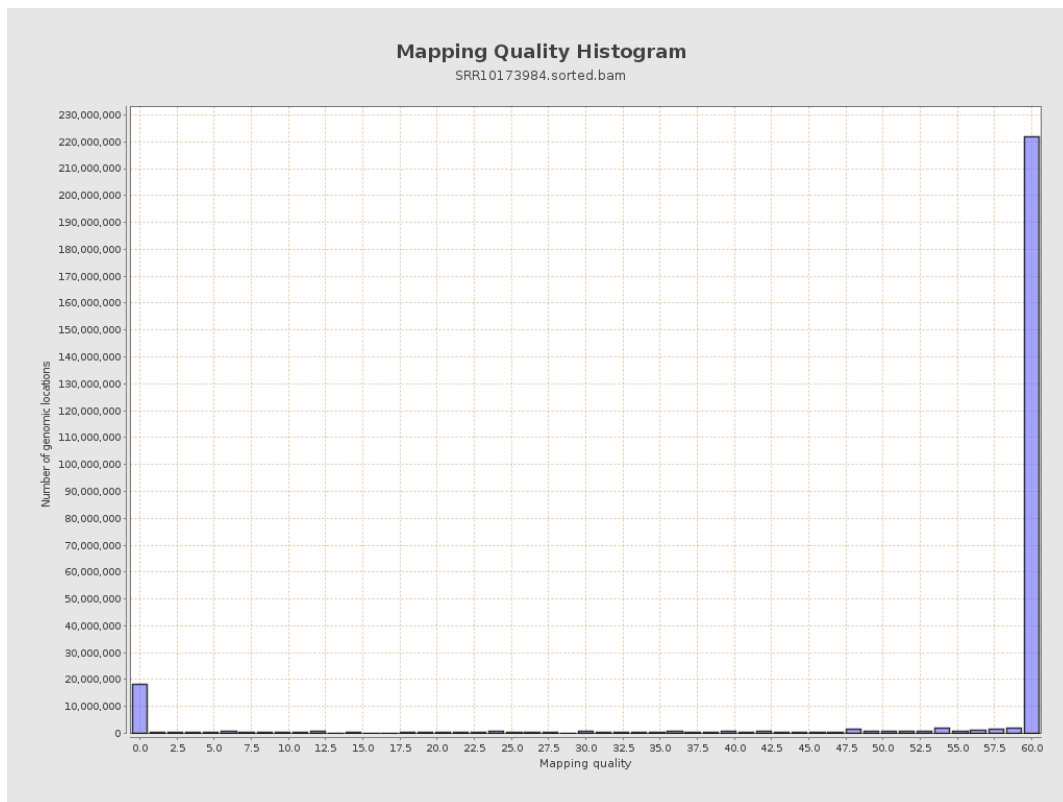
11. Results : Homopolymer Indels



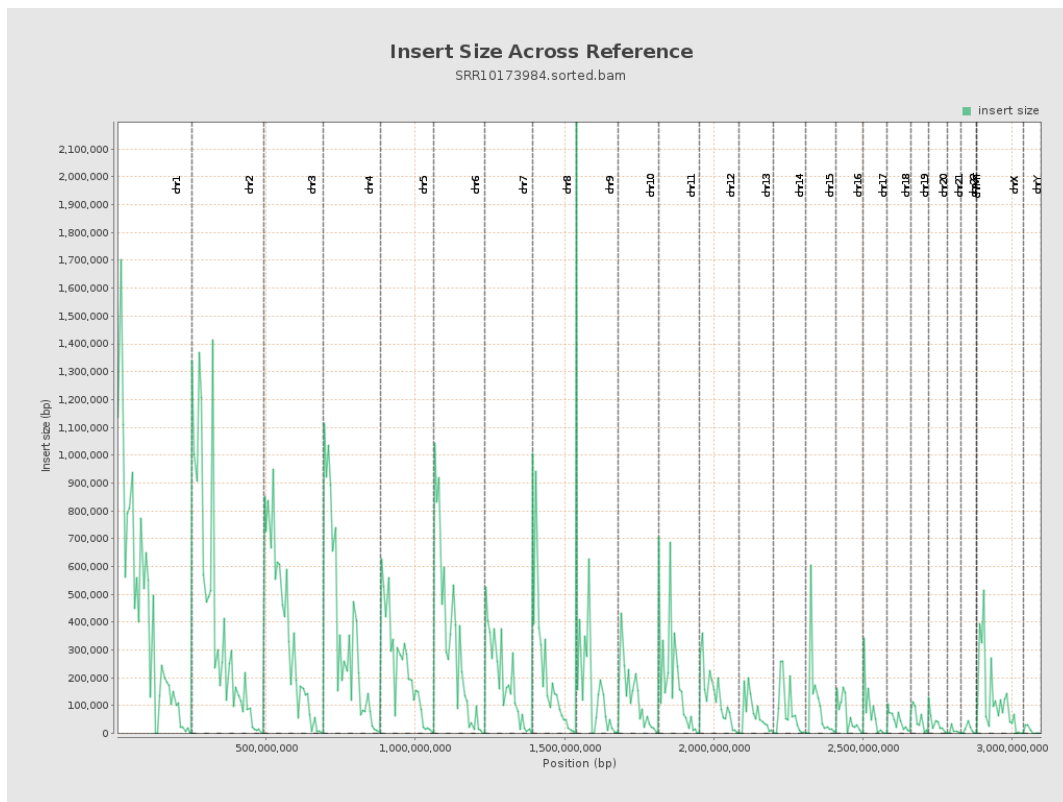
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

