

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 10:55:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173947.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_SRR10173947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173947_1.fastq.gz SRR10173947_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 10:55:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173947.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,573,660
Mapped reads	11,287,444 / 97.53%
Unmapped reads	286,216 / 2.47%
Mapped paired reads	11,287,444 / 97.53%
Mapped reads, first in pair	5,656,056 / 48.87%
Mapped reads, second in pair	5,631,388 / 48.66%
Mapped reads, both in pair	11,102,776 / 95.93%
Mapped reads, singletons	184,668 / 1.6%
Secondary alignments	0
Supplementary alignments	1,485,034 / 12.83%
Read min/max/mean length	30 / 133 / 125.52
Duplicated reads (estimated)	9,225,596 / 79.71%
Duplication rate	66.71%
Clipped reads	5,700,102 / 49.25%

2.2. ACGT Content

Number/percentage of A's	380,746,696 / 29.76%
Number/percentage of C's	255,119,398 / 19.94%
Number/percentage of T's	377,507,535 / 29.51%
Number/percentage of G's	266,054,760 / 20.79%
Number/percentage of N's	9,488 / 0%

GC Percentage	40.73%
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2.3. Coverage

Mean	0.4136
Standard Deviation	7.3302

2.4. Mapping Quality

Mean Mapping Quality	52.65
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2.5. Insert size

Mean	1,185,632.93
Standard Deviation	10,153,355.8
P25/Median/P75	106 / 156 / 240

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	11,112,228
Insertions	137,788
Mapped reads with at least one insertion	1.17%
Deletions	365,206
Mapped reads with at least one deletion	3.16%
Homopolymer indels	40.68%

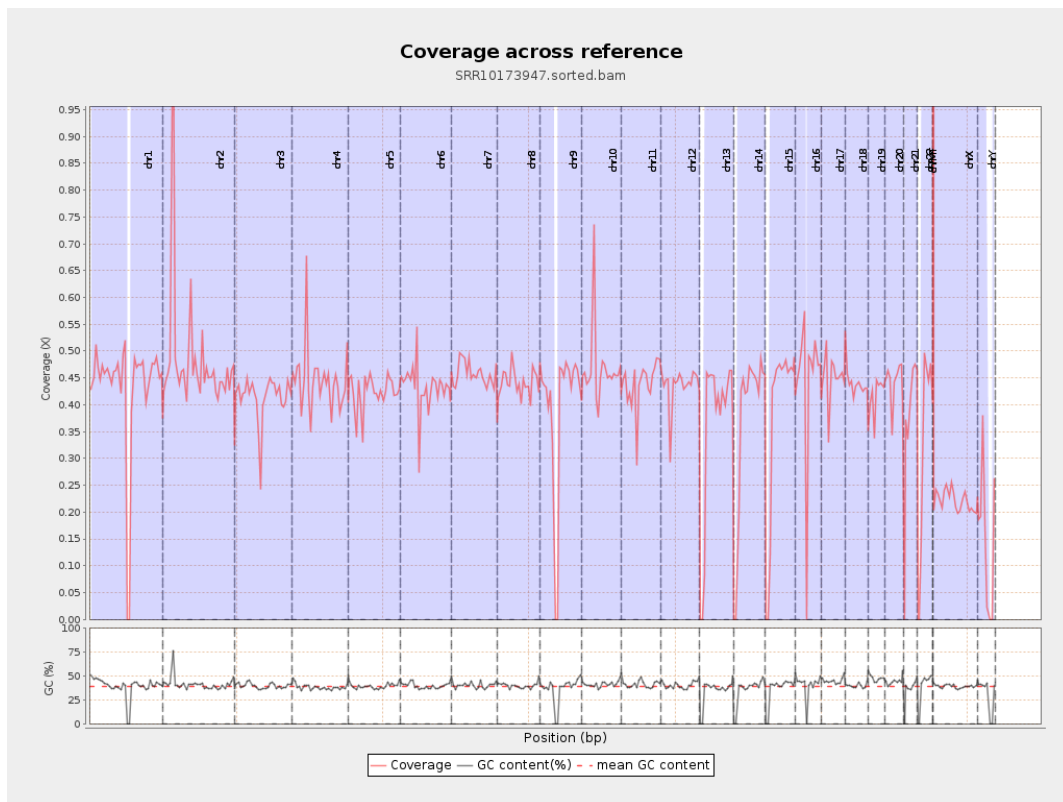
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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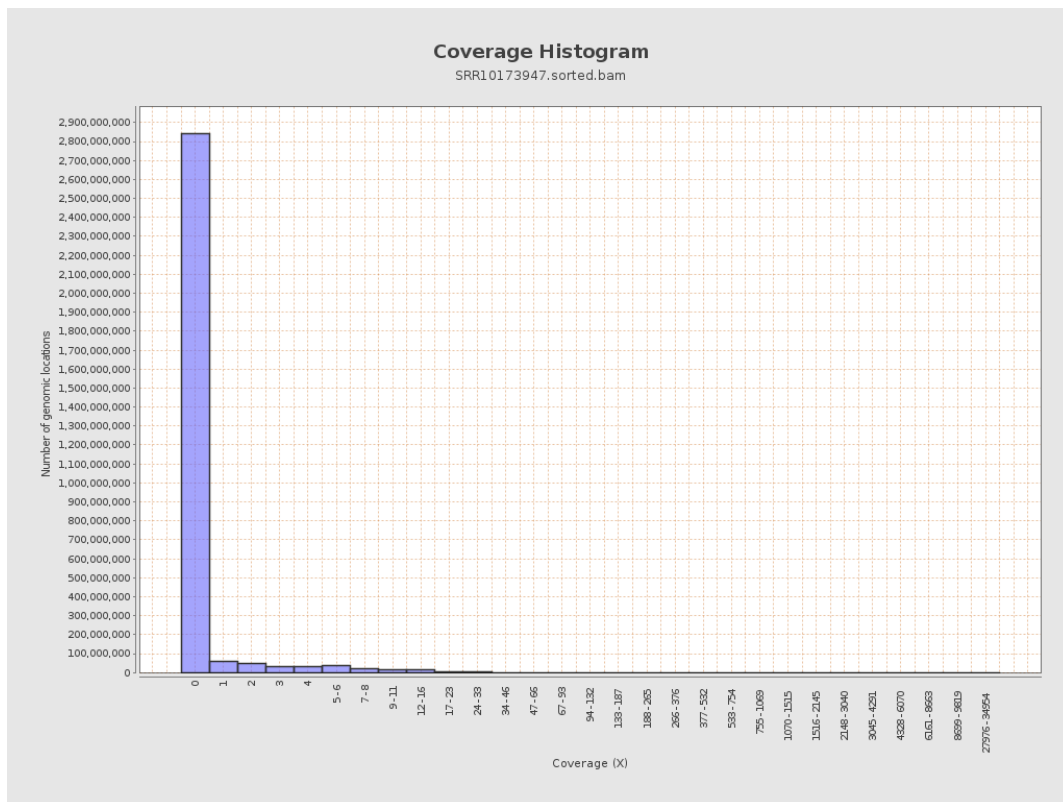
		bases	coverage	deviation
chr1	249250621	107837600	0.4326	3.3148
chr2	243199373	117531435	0.4833	24.4508
chr3	198022430	81743930	0.4128	1.972
chr4	191154276	85063250	0.445	2.7849
chr5	180915260	76785499	0.4244	2.0021
chr6	171115067	73856501	0.4316	2.6241
chr7	159138663	72841338	0.4577	3.1621
chr8	146364022	64597830	0.4414	3.8739
chr9	141213431	55454422	0.3927	3.1972
chr10	135534747	63052394	0.4652	3.6466
chr11	135006516	59079058	0.4376	2.2081
chr12	133851895	58511477	0.4371	2.2346
chr13	115169878	41640238	0.3616	1.8444
chr14	107349540	40049217	0.3731	1.9468
chr15	102531392	38242400	0.373	1.984
chr16	90354753	40111670	0.4439	2.5618
chr17	81195210	36696826	0.452	2.3898
chr18	78077248	34312377	0.4395	3.8584
chr19	59128983	24548821	0.4152	2.5939
chr20	63025520	27905894	0.4428	2.1555
chr21	48129895	18337736	0.381	2.5951
chr22	51304566	16613698	0.3238	2.0908
chrMT	16571	2003566	120.908	90.2741
chrX	155270560	34430893	0.2217	1.4895

chrY	59373566	9031036	0.1521	2.2236
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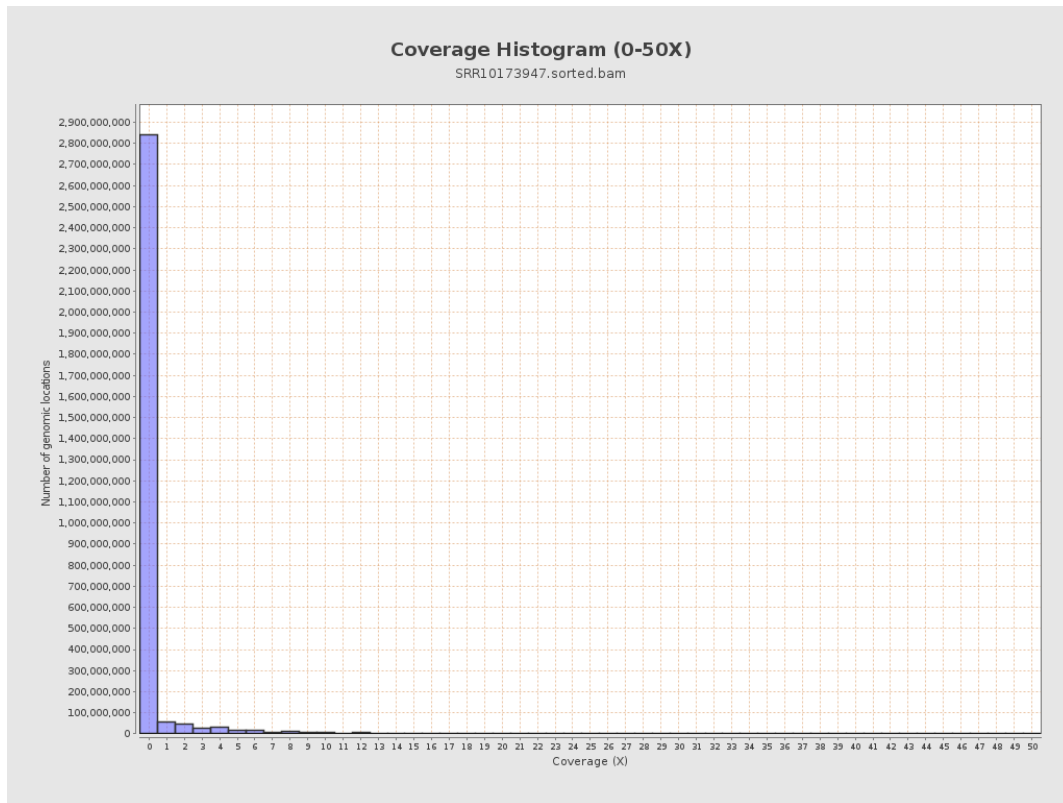
3. Results : Coverage across reference



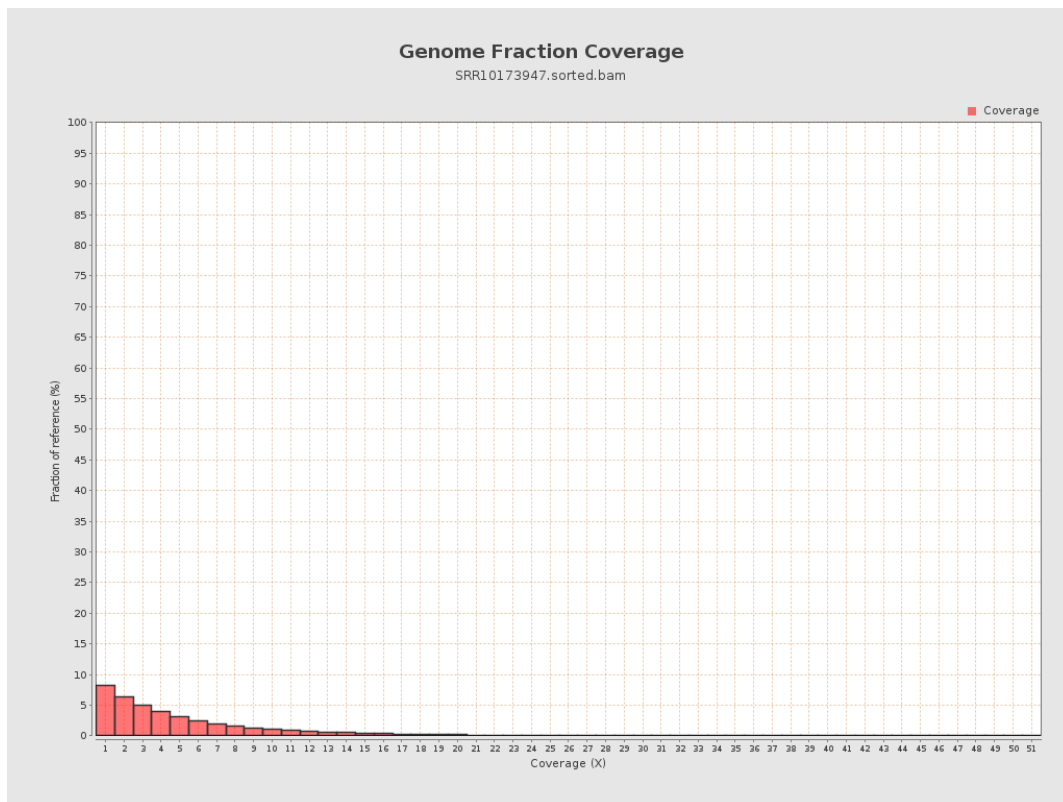
4. Results : Coverage Histogram



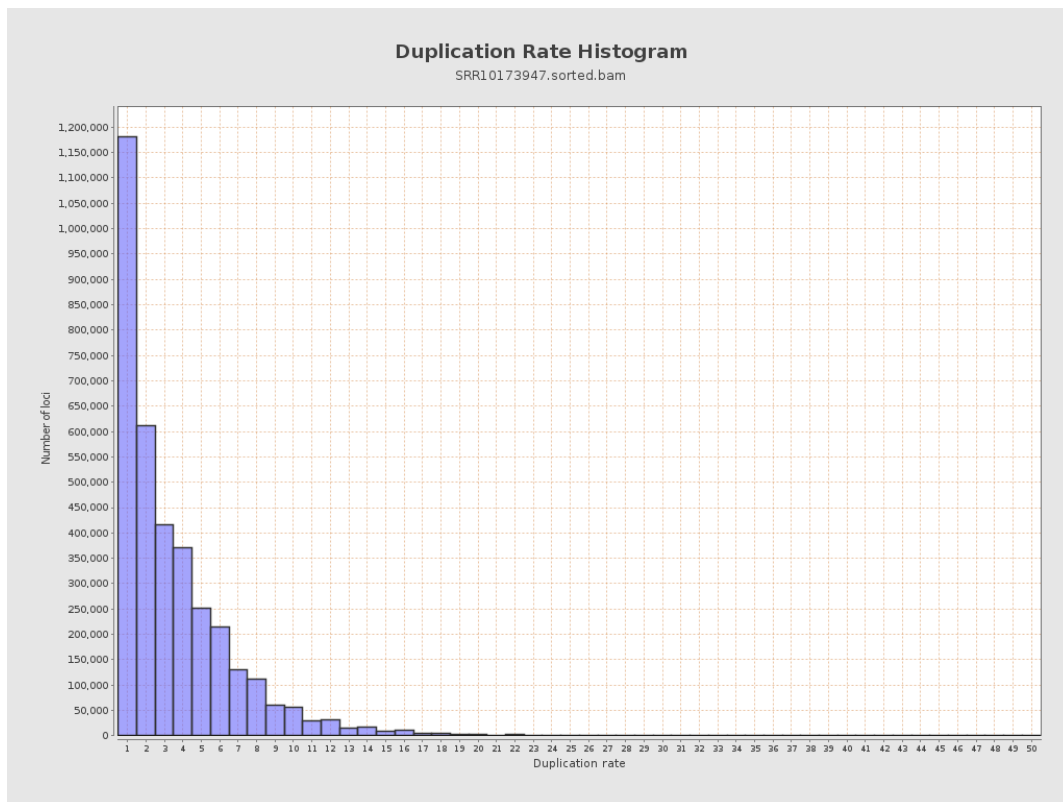
5. Results : Coverage Histogram (0-50X)



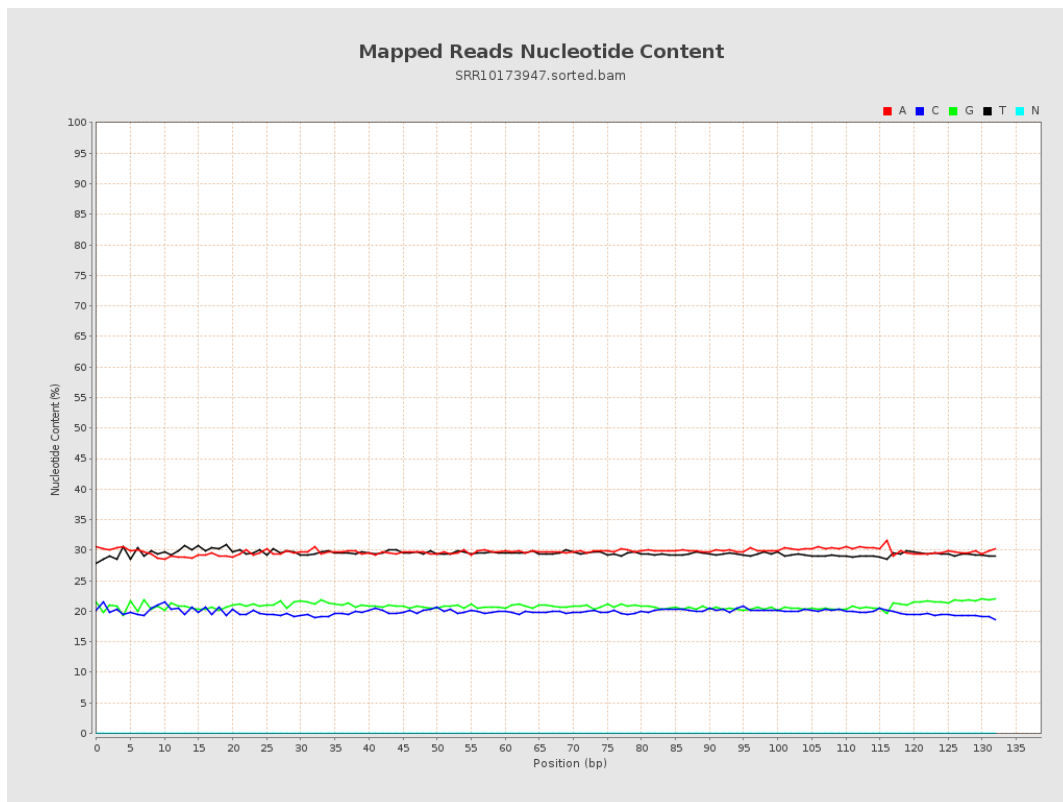
6. Results : Genome Fraction Coverage



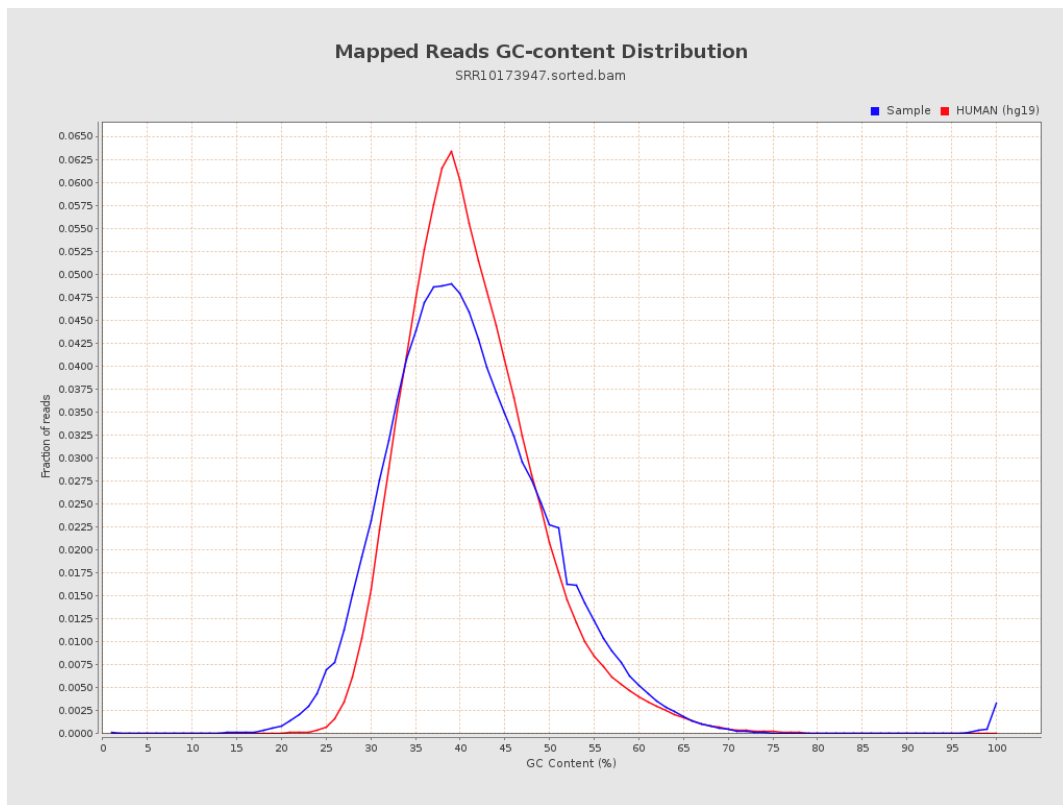
7. Results : Duplication Rate Histogram



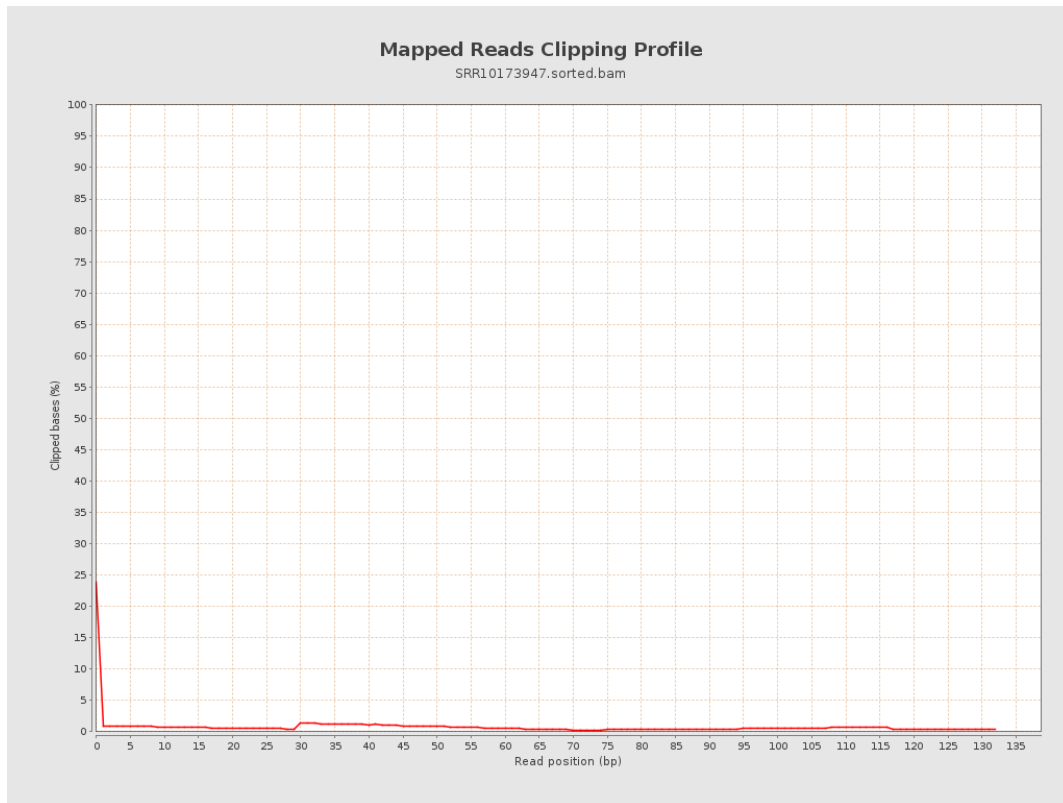
8. Results : Mapped Reads Nucleotide Content



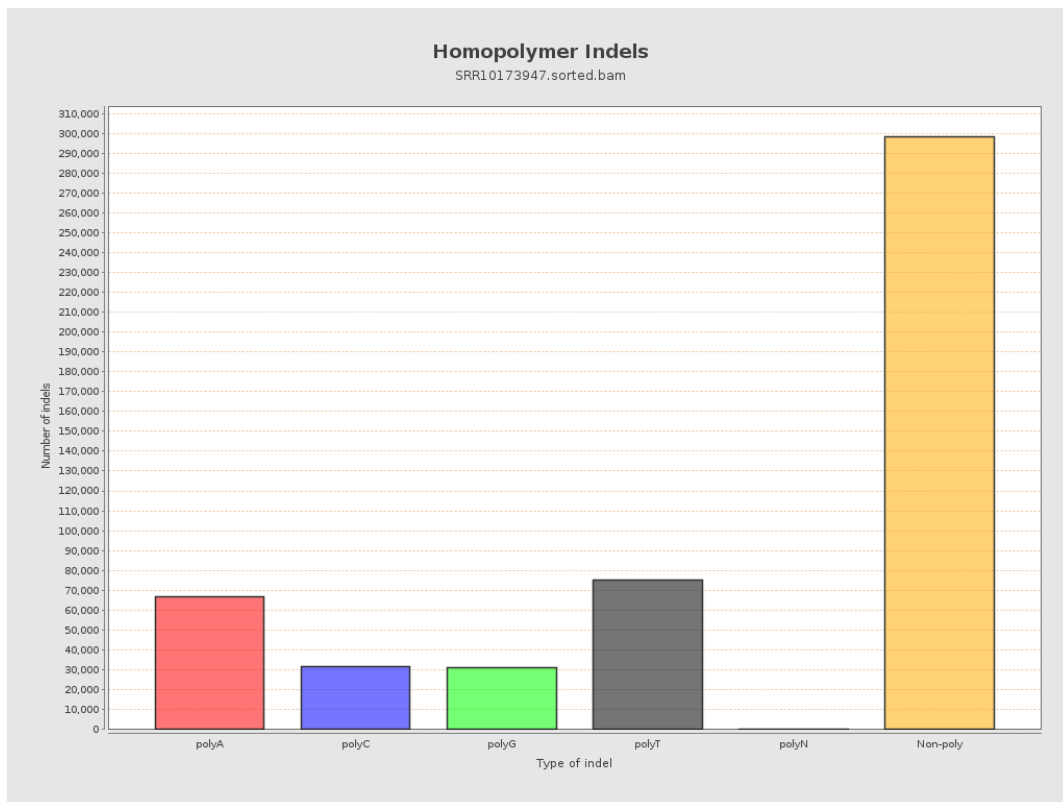
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



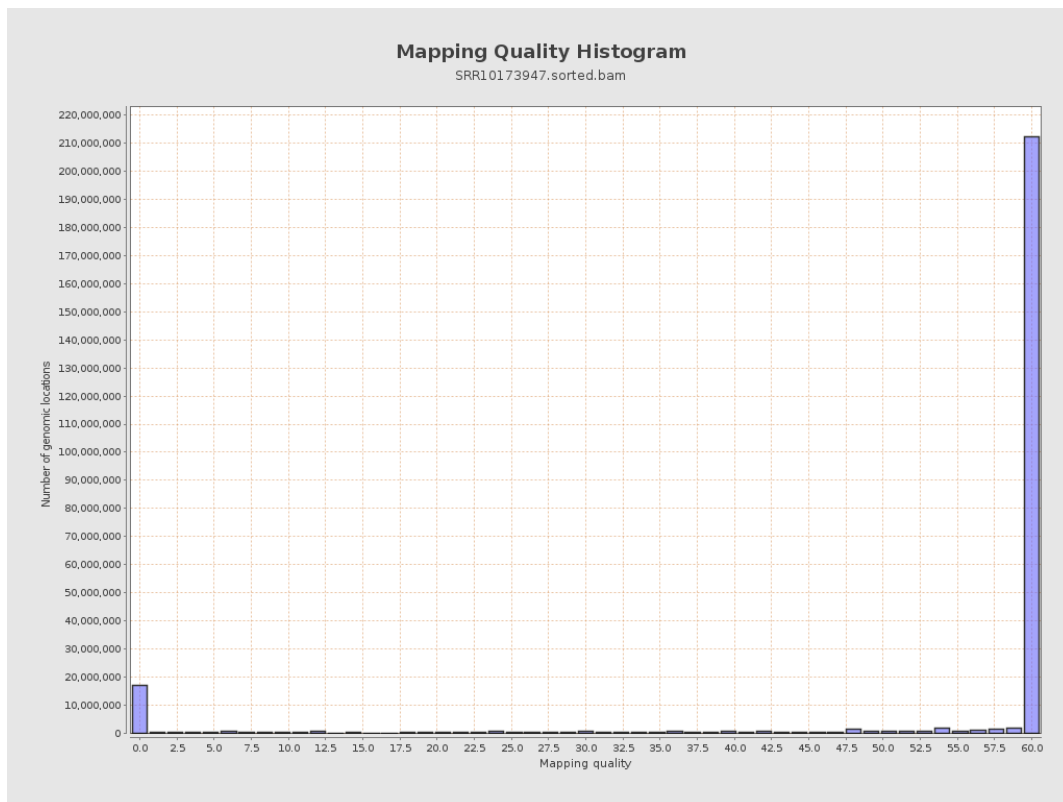
11. Results : Homopolymer Indels



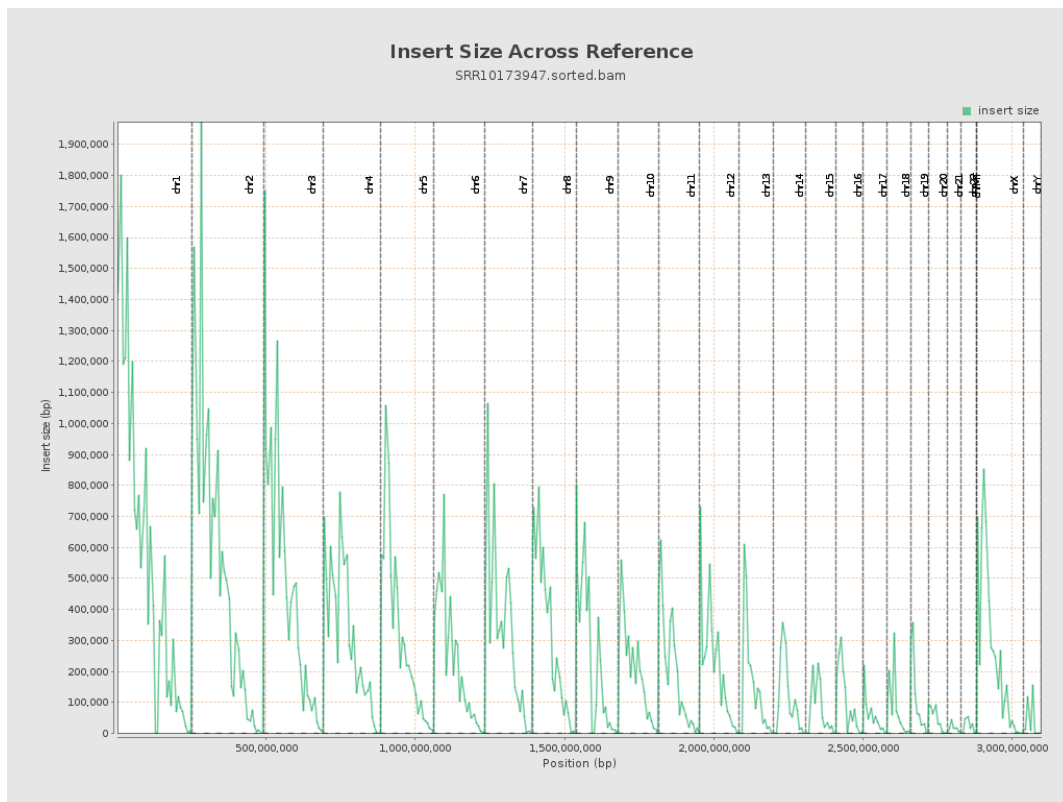
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

