

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 09:04:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173935.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_SRR10173935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173935_1.fastq.gz SRR10173935_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 09:04:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,402,228
Mapped reads	4,304,099 / 97.77%
Unmapped reads	98,129 / 2.23%
Mapped paired reads	4,304,099 / 97.77%
Mapped reads, first in pair	2,155,670 / 48.97%
Mapped reads, second in pair	2,148,429 / 48.8%
Mapped reads, both in pair	4,246,056 / 96.45%
Mapped reads, singletons	58,043 / 1.32%
Secondary alignments	0
Supplementary alignments	492,249 / 11.18%
Read min/max/mean length	30 / 133 / 124.16
Duplicated reads (estimated)	3,436,980 / 78.07%
Duplication rate	66.01%
Clipped reads	2,019,992 / 45.89%

2.2. ACGT Content

Number/percentage of A's	145,833,210 / 29.98%
Number/percentage of C's	96,221,790 / 19.78%
Number/percentage of T's	144,581,387 / 29.72%
Number/percentage of G's	99,847,847 / 20.52%
Number/percentage of N's	3,734 / 0%

GC Percentage	40.3%
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2.3. Coverage

Mean	0.1573
Standard Deviation	2.9255

2.4. Mapping Quality

Mean Mapping Quality	52.86
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2.5. Insert size

Mean	773,328.44
Standard Deviation	8,293,003.7
P25/Median/P75	105 / 151 / 225

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	4,109,147
Insertions	51,618
Mapped reads with at least one insertion	1.16%
Deletions	146,472
Mapped reads with at least one deletion	3.32%
Homopolymer indels	40.54%

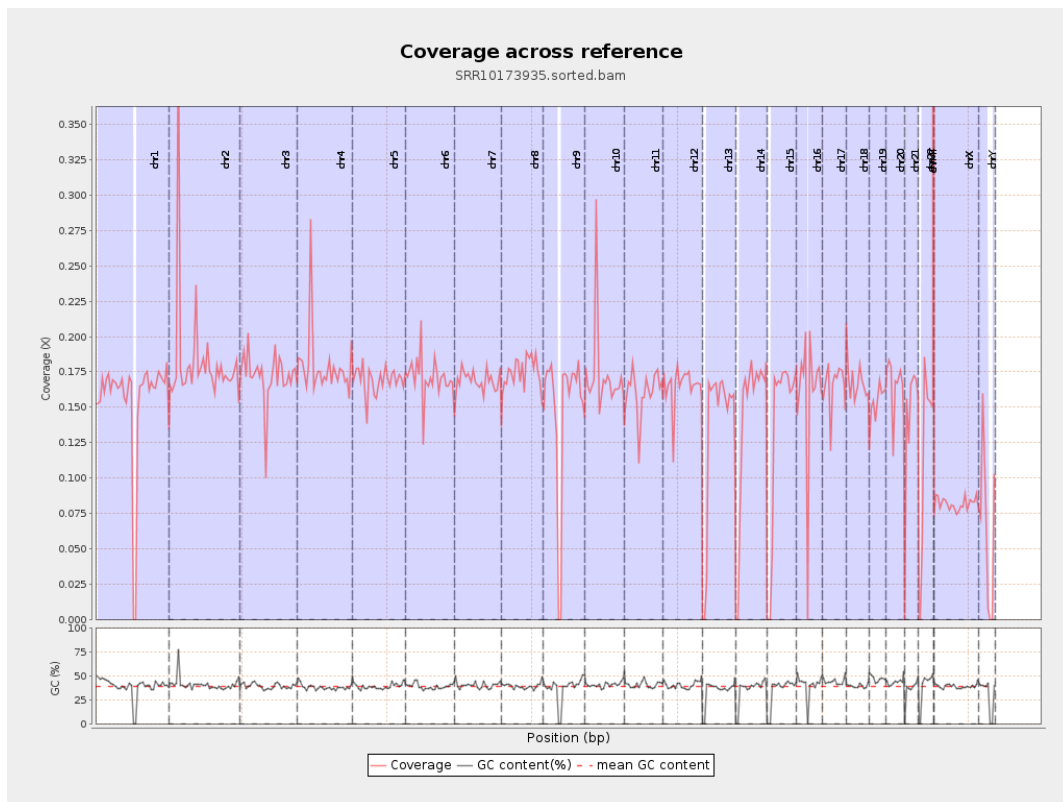
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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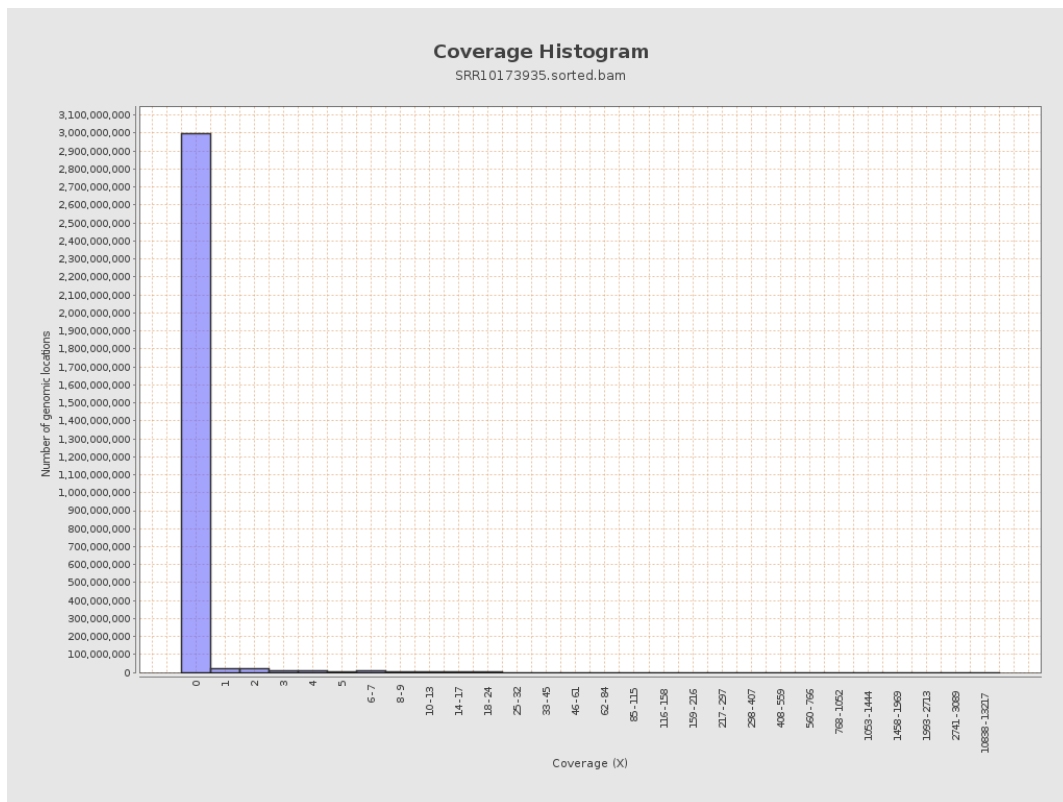
		bases	coverage	deviation
chr1	249250621	38734150	0.1554	1.4255
chr2	243199373	44575231	0.1833	9.293
chr3	198022430	34072972	0.1721	1.2819
chr4	191154276	34093910	0.1784	1.5245
chr5	180915260	30550951	0.1689	1.255
chr6	171115067	29224726	0.1708	1.3462
chr7	159138663	26928990	0.1692	1.5633
chr8	146364022	25571121	0.1747	1.8522
chr9	141213431	21045658	0.149	1.3655
chr10	135534747	23322079	0.1721	1.8167
chr11	135006516	21742095	0.161	1.2513
chr12	133851895	22107185	0.1652	1.2861
chr13	115169878	15397915	0.1337	1.1226
chr14	107349540	15221536	0.1418	1.1703
chr15	102531392	13949858	0.1361	1.1479
chr16	90354753	14400422	0.1594	1.3848
chr17	81195210	13355707	0.1645	1.3022
chr18	78077248	13110346	0.1679	1.6391
chr19	59128983	9133952	0.1545	1.2707
chr20	63025520	10406608	0.1651	1.2771
chr21	48129895	6885086	0.1431	1.4138
chr22	51304566	5768870	0.1124	1.1943
chrMT	16571	866269	52.2762	48.7012
chrX	155270560	12712336	0.0819	0.8693

chrY	59373566	3639395	0.0613	1.0538
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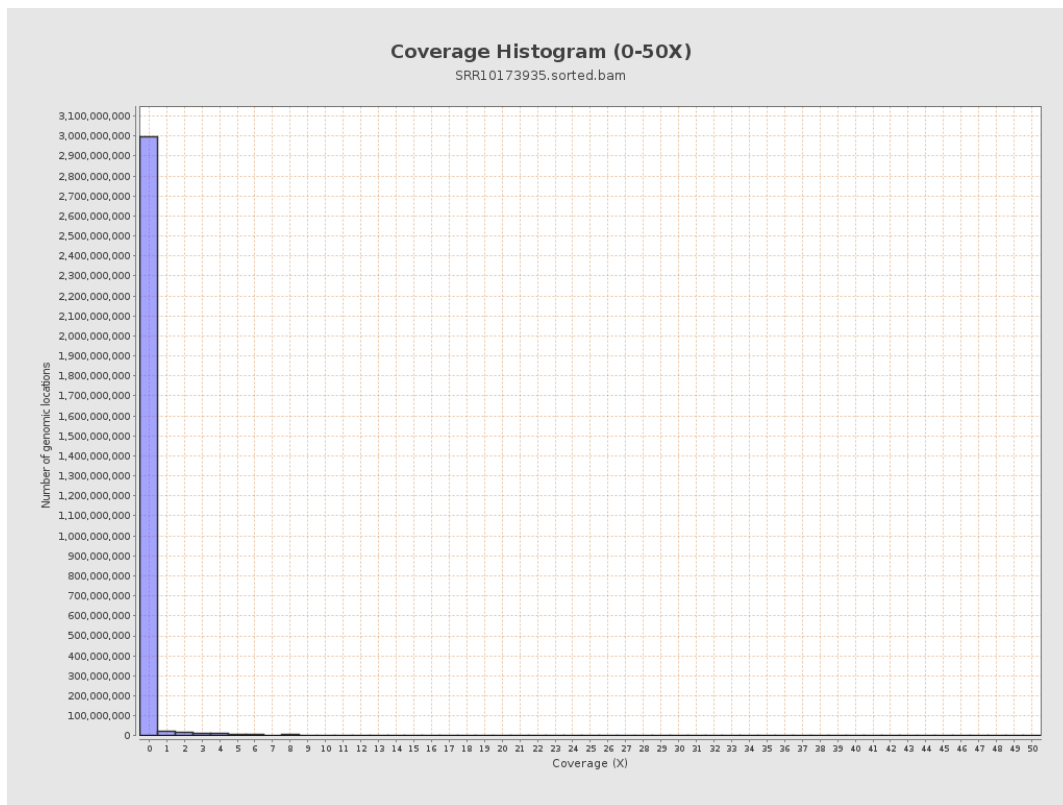
3. Results : Coverage across reference



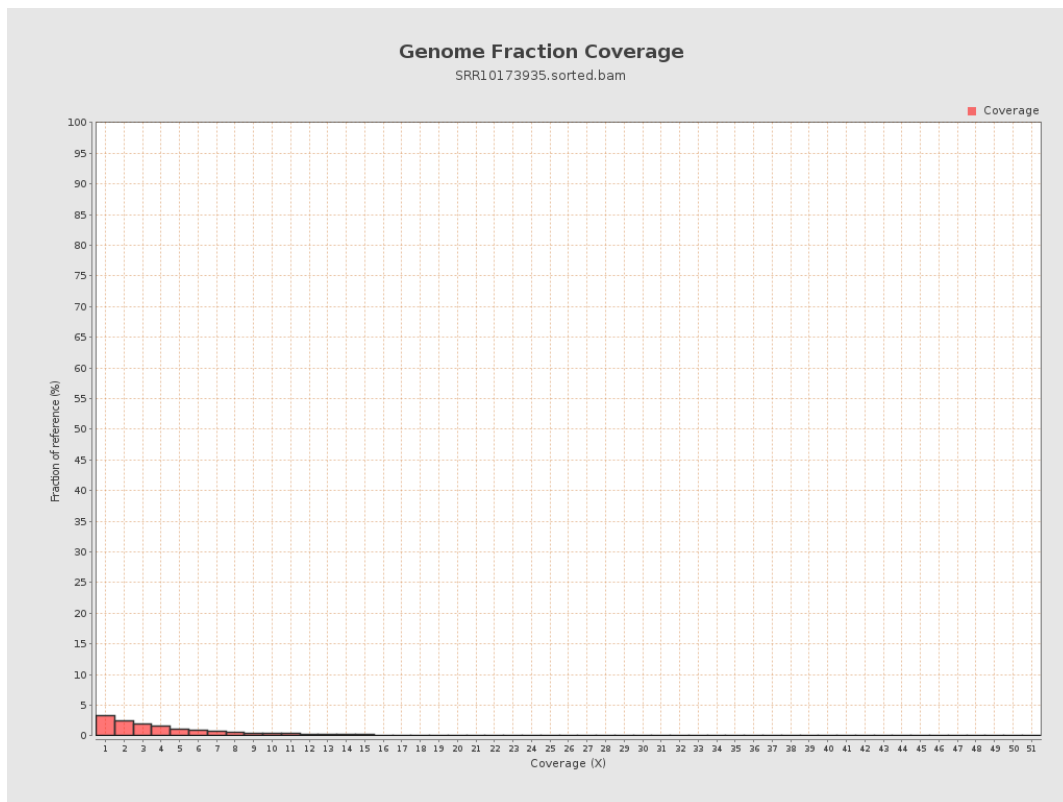
4. Results : Coverage Histogram



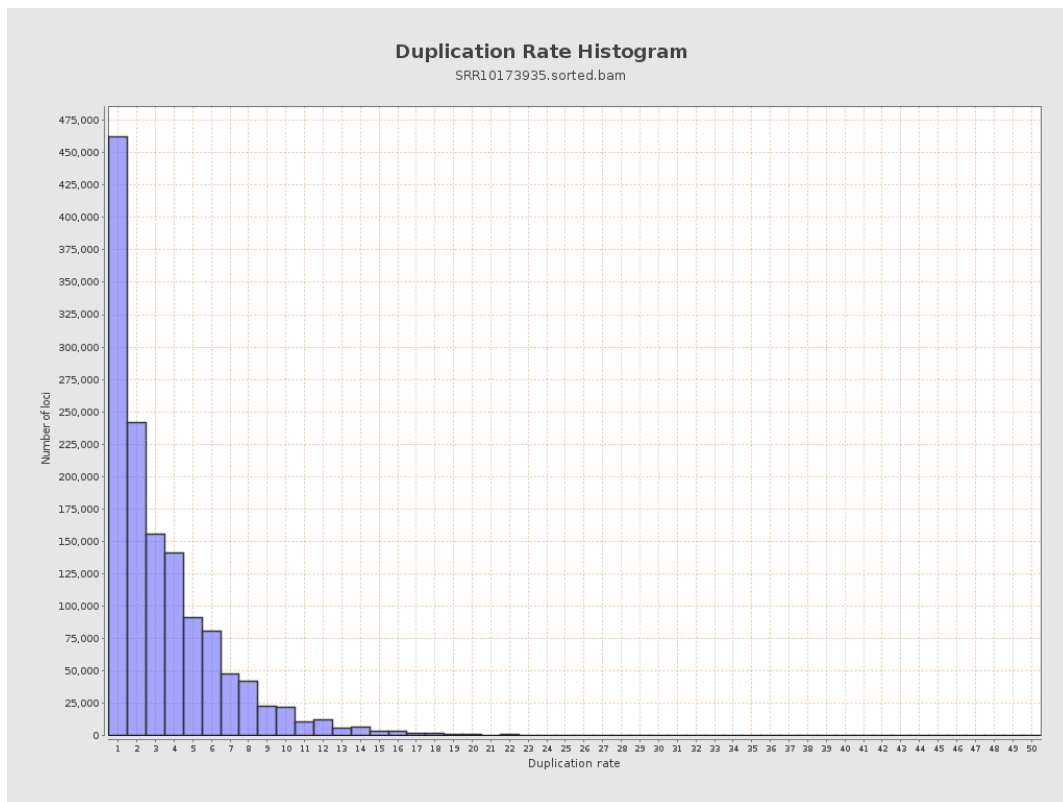
5. Results : Coverage Histogram (0-50X)



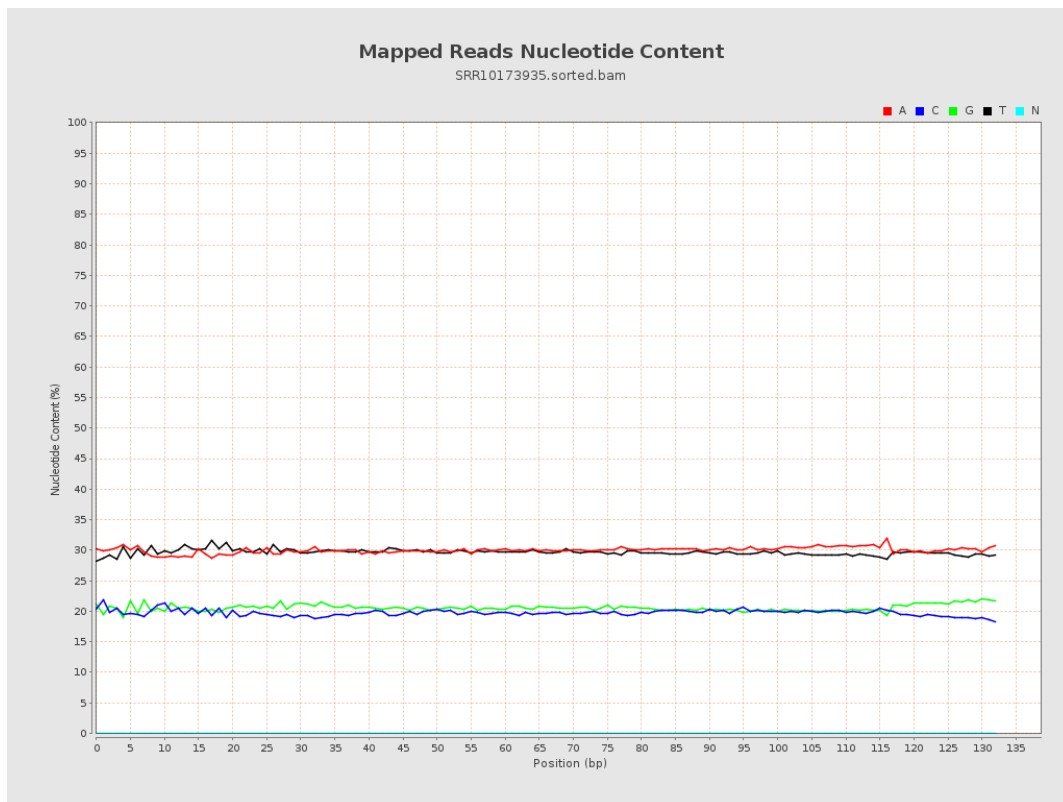
6. Results : Genome Fraction Coverage



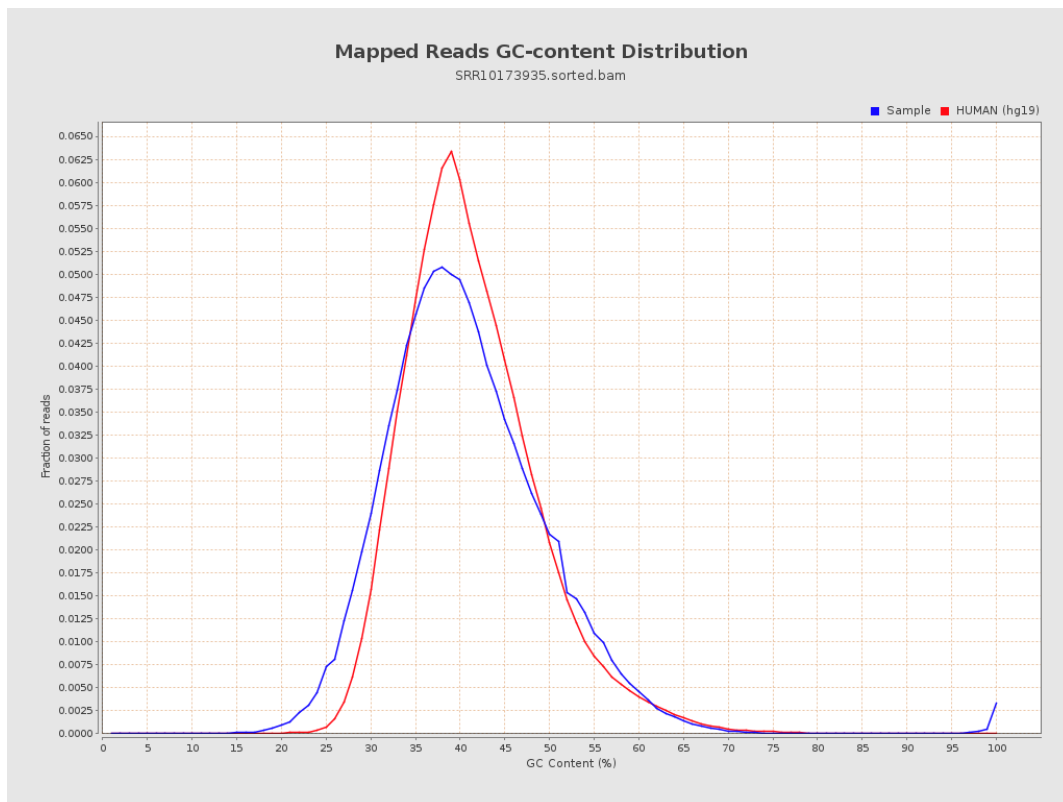
7. Results : Duplication Rate Histogram



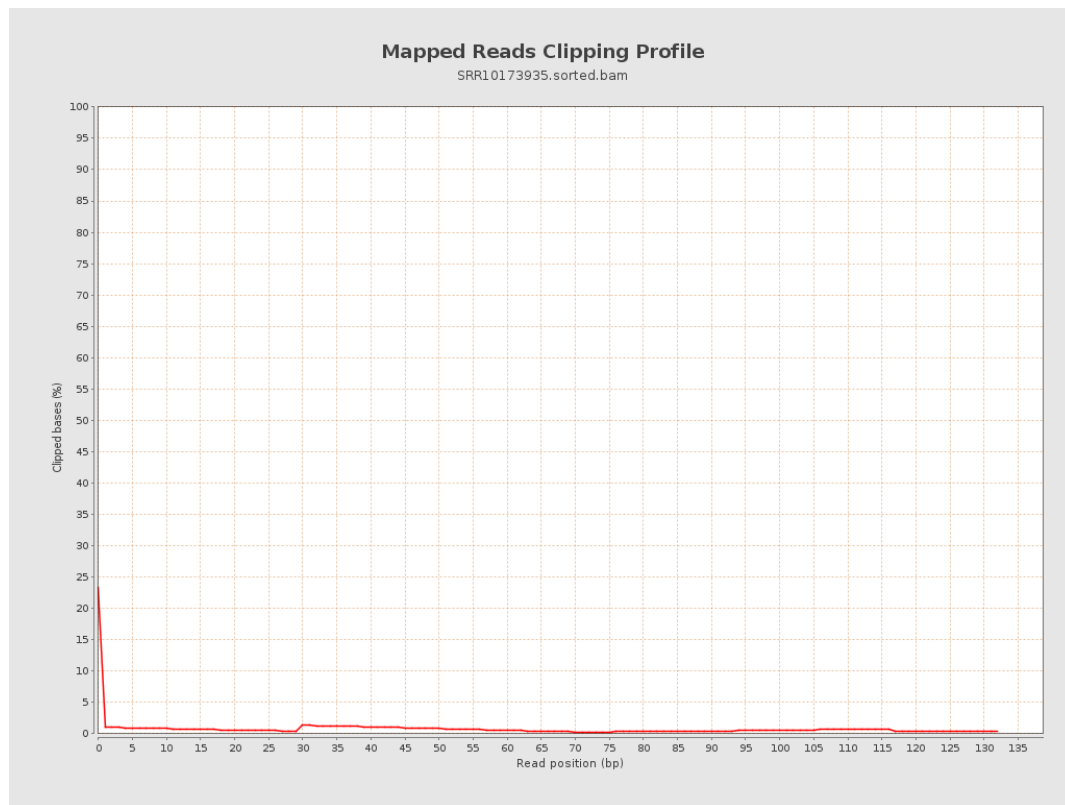
8. Results : Mapped Reads Nucleotide Content



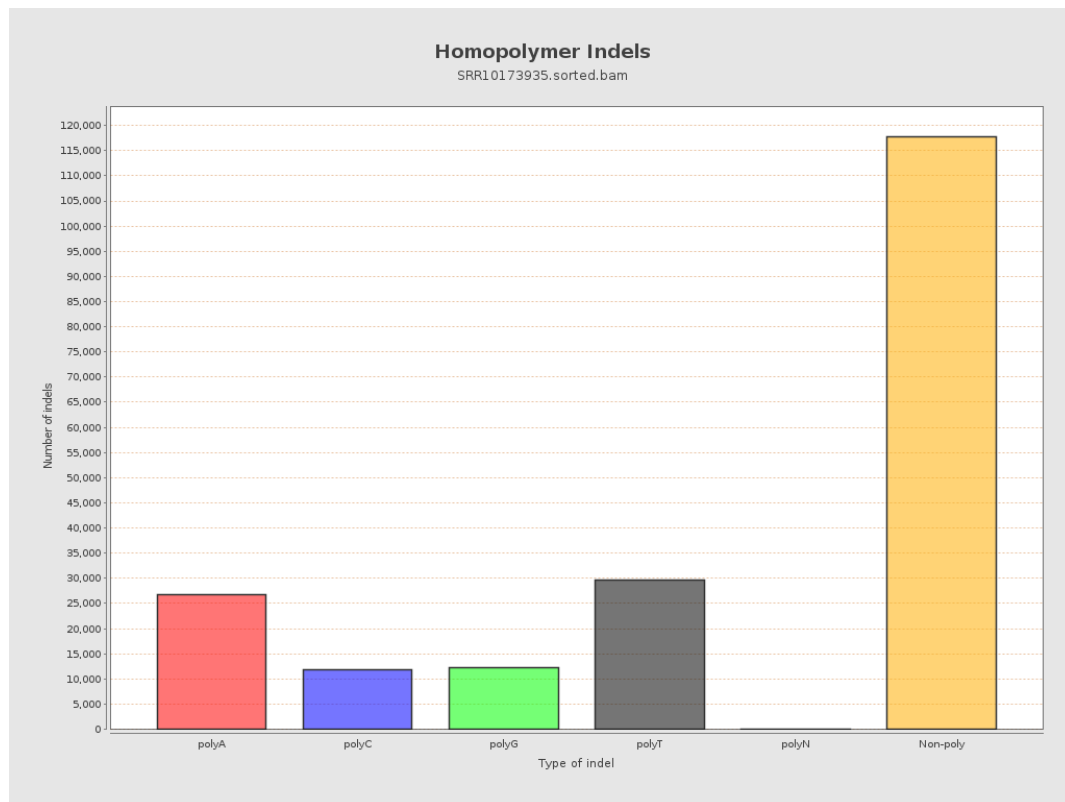
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



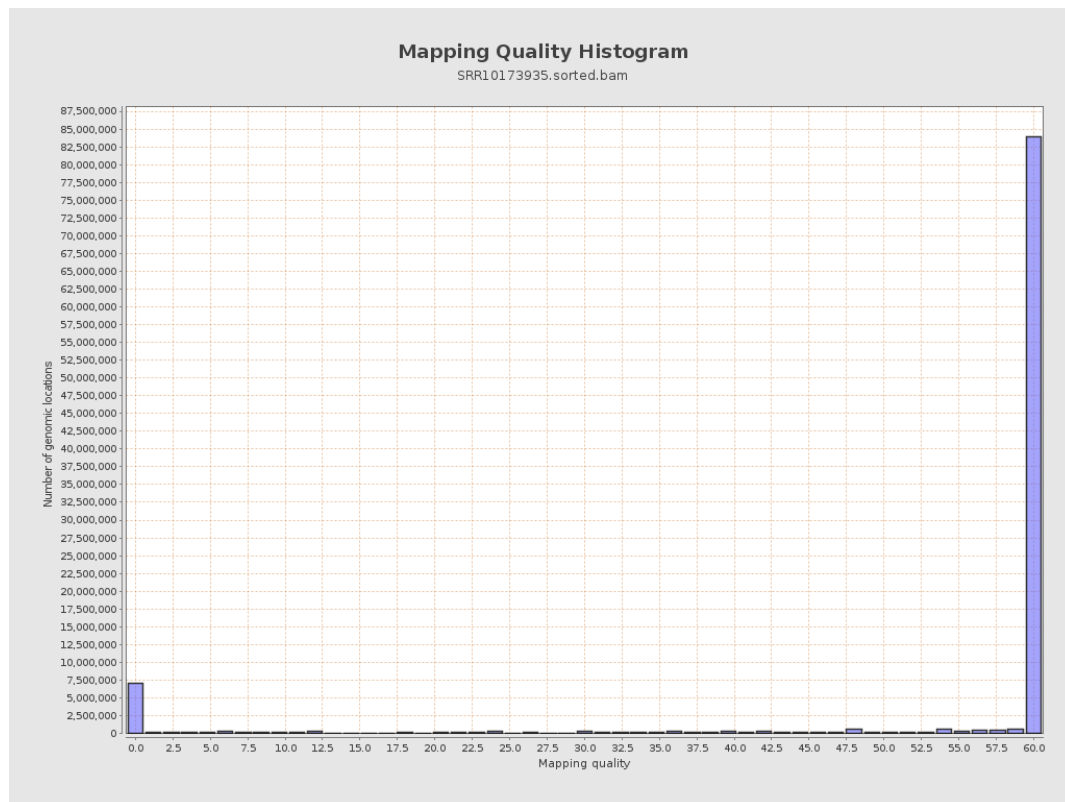
11. Results : Homopolymer Indels



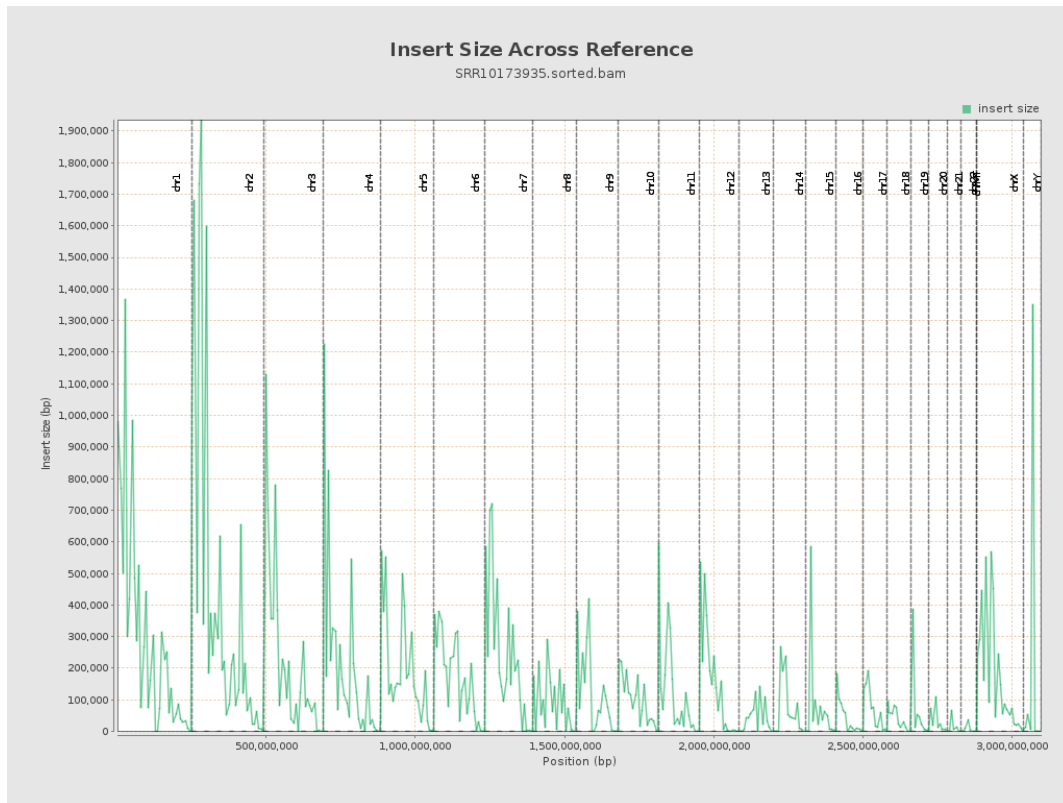
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

