

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 09:25:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173938.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_SRR10173938 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173938_1.fastq.gz SRR10173938_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 09:25:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173938.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,404,292
Mapped reads	4,294,025 / 97.5%
Unmapped reads	110,267 / 2.5%
Mapped paired reads	4,294,025 / 97.5%
Mapped reads, first in pair	2,150,173 / 48.82%
Mapped reads, second in pair	2,143,852 / 48.68%
Mapped reads, both in pair	4,224,732 / 95.92%
Mapped reads, singletons	69,293 / 1.57%
Secondary alignments	0
Supplementary alignments	566,253 / 12.86%
Read min/max/mean length	30 / 133 / 125.35
Duplicated reads (estimated)	3,457,360 / 78.5%
Duplication rate	64.38%
Clipped reads	2,223,117 / 50.48%

2.2. ACGT Content

Number/percentage of A's	144,648,752 / 29.81%
Number/percentage of C's	96,578,680 / 19.9%
Number/percentage of T's	143,381,006 / 29.55%
Number/percentage of G's	100,612,589 / 20.74%
Number/percentage of N's	3,666 / 0%

GC Percentage	40.64%
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2.3. Coverage

Mean	0.1569
Standard Deviation	2.9697

2.4. Mapping Quality

Mean Mapping Quality	52.57
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2.5. Insert size

Mean	1,226,403.97
Standard Deviation	9,951,199.2
P25/Median/P75	105 / 153 / 237

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	4,272,135
Insertions	53,006
Mapped reads with at least one insertion	1.19%
Deletions	149,083
Mapped reads with at least one deletion	3.39%
Homopolymer indels	40.87%

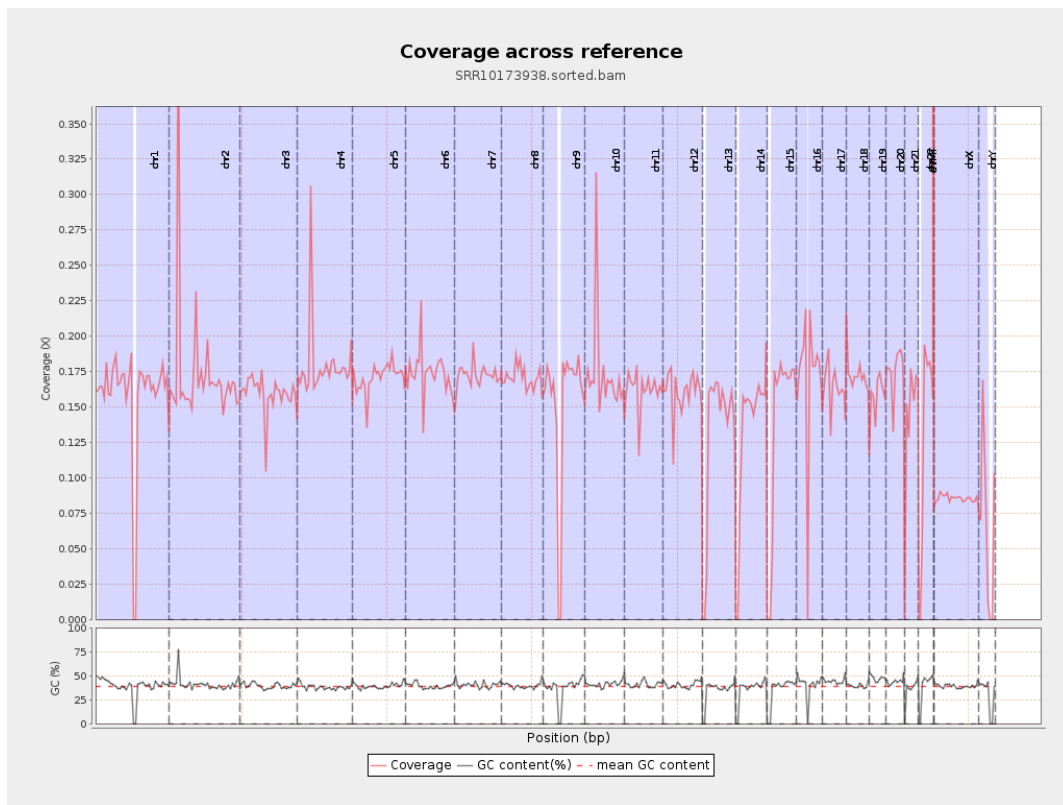
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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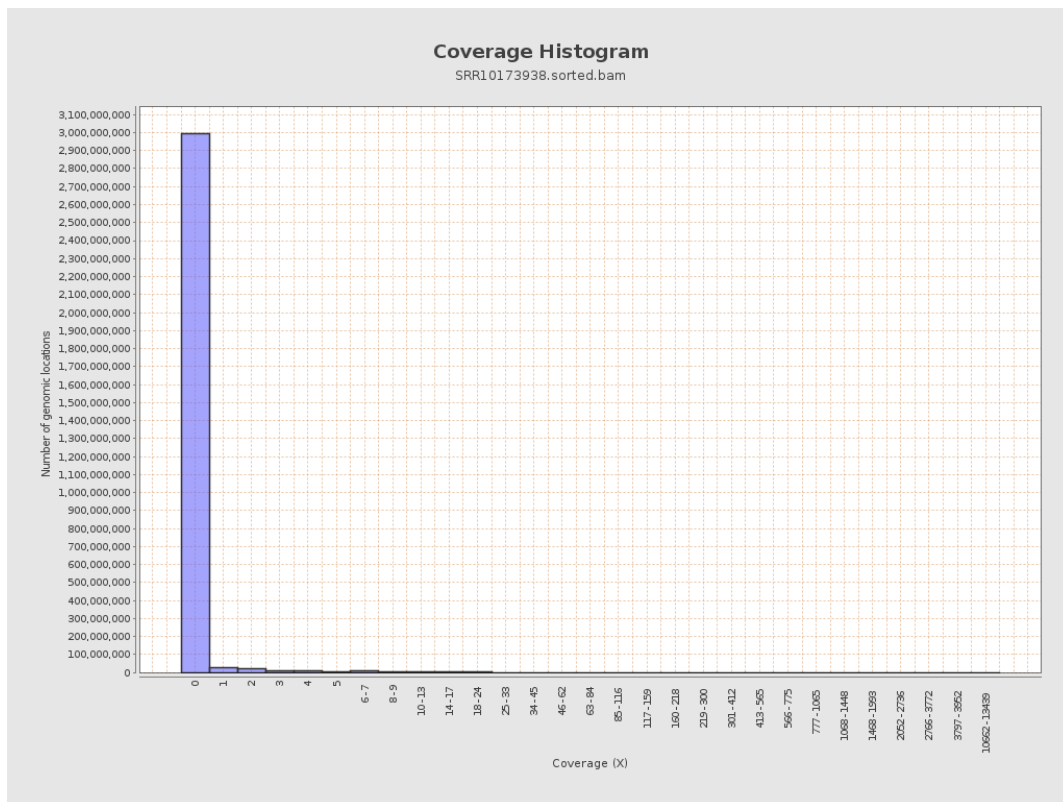
		bases	coverage	deviation
chr1	249250621	39330491	0.1578	1.4962
chr2	243199373	42316749	0.174	9.4373
chr3	198022430	31606458	0.1596	1.2221
chr4	191154276	34243148	0.1791	1.6338
chr5	180915260	30951025	0.1711	1.2739
chr6	171115067	29734525	0.1738	1.4176
chr7	159138663	27490124	0.1727	1.6452
chr8	146364022	25012635	0.1709	1.7555
chr9	141213431	21426512	0.1517	1.4762
chr10	135534747	23445616	0.173	1.832
chr11	135006516	21886693	0.1621	1.2658
chr12	133851895	21497157	0.1606	1.2443
chr13	115169878	15005568	0.1303	1.1064
chr14	107349540	14108531	0.1314	1.1048
chr15	102531392	14214224	0.1386	1.1516
chr16	90354753	15390653	0.1703	1.4034
chr17	81195210	13230627	0.1629	1.248
chr18	78077248	13476925	0.1726	1.8291
chr19	59128983	9364365	0.1584	1.3118
chr20	63025520	11006753	0.1746	1.3141
chr21	48129895	6910745	0.1436	1.4048
chr22	51304566	6417429	0.1251	1.2034
chrMT	16571	520653	31.4195	29.2062
chrX	155270560	13266238	0.0854	0.8929

chrY	59373566	3726364	0.0628	1.0327
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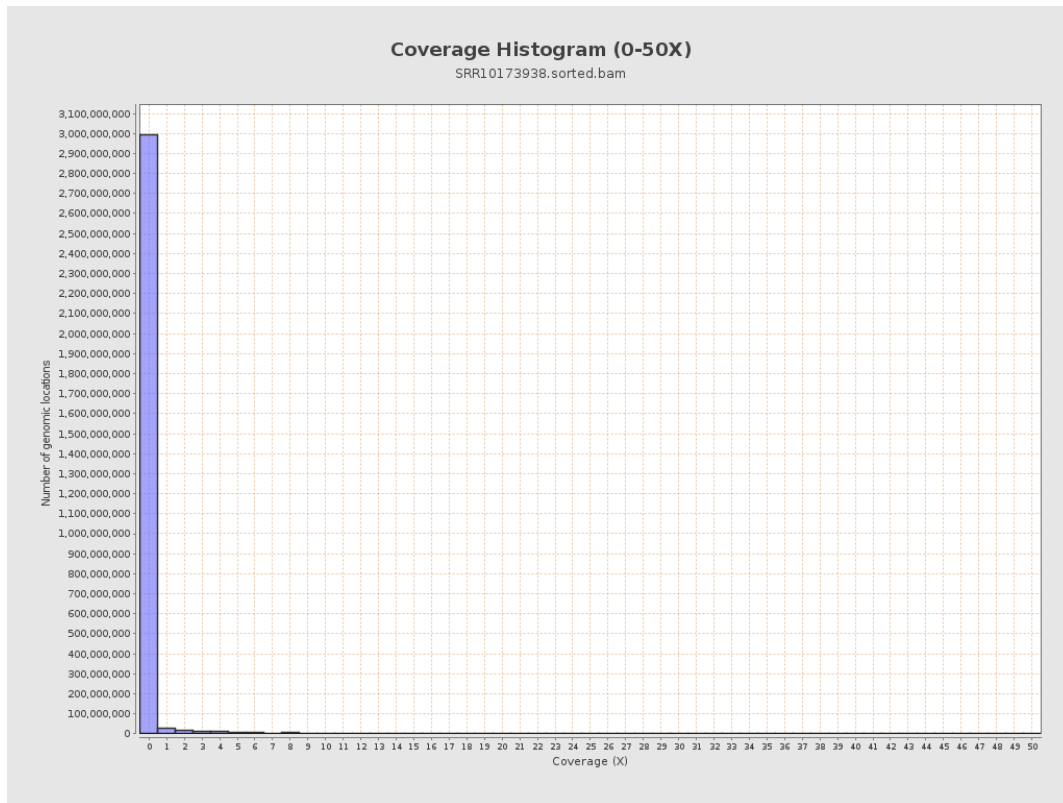
3. Results : Coverage across reference



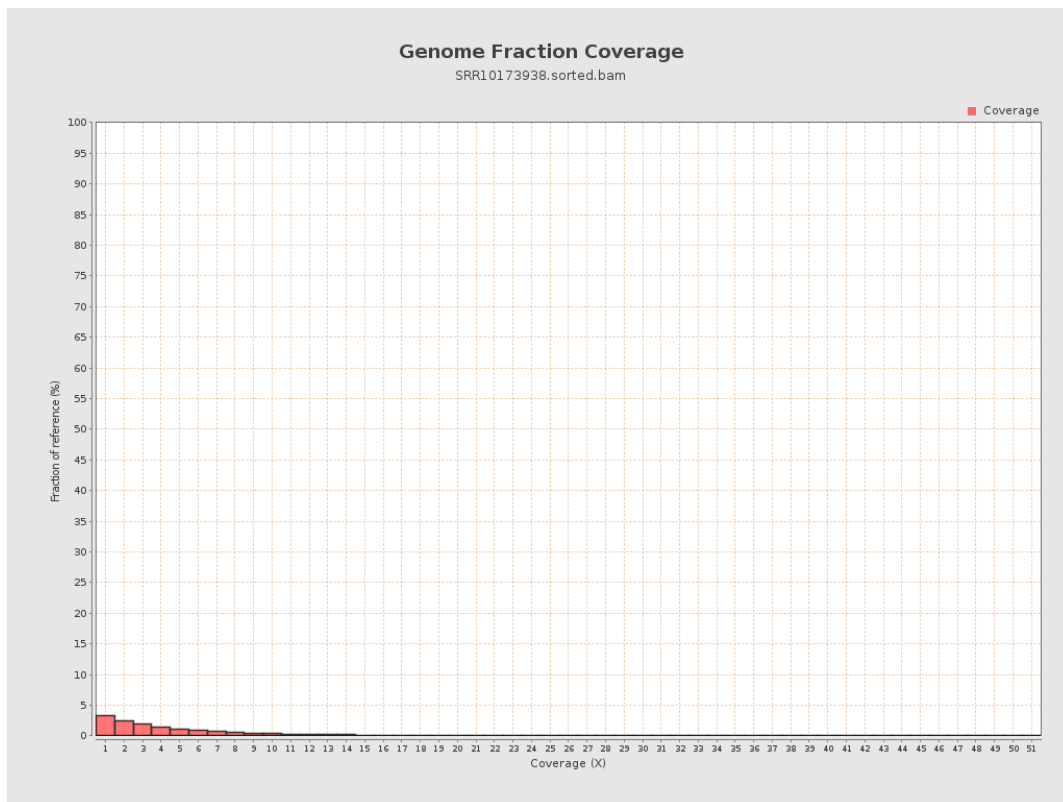
4. Results : Coverage Histogram



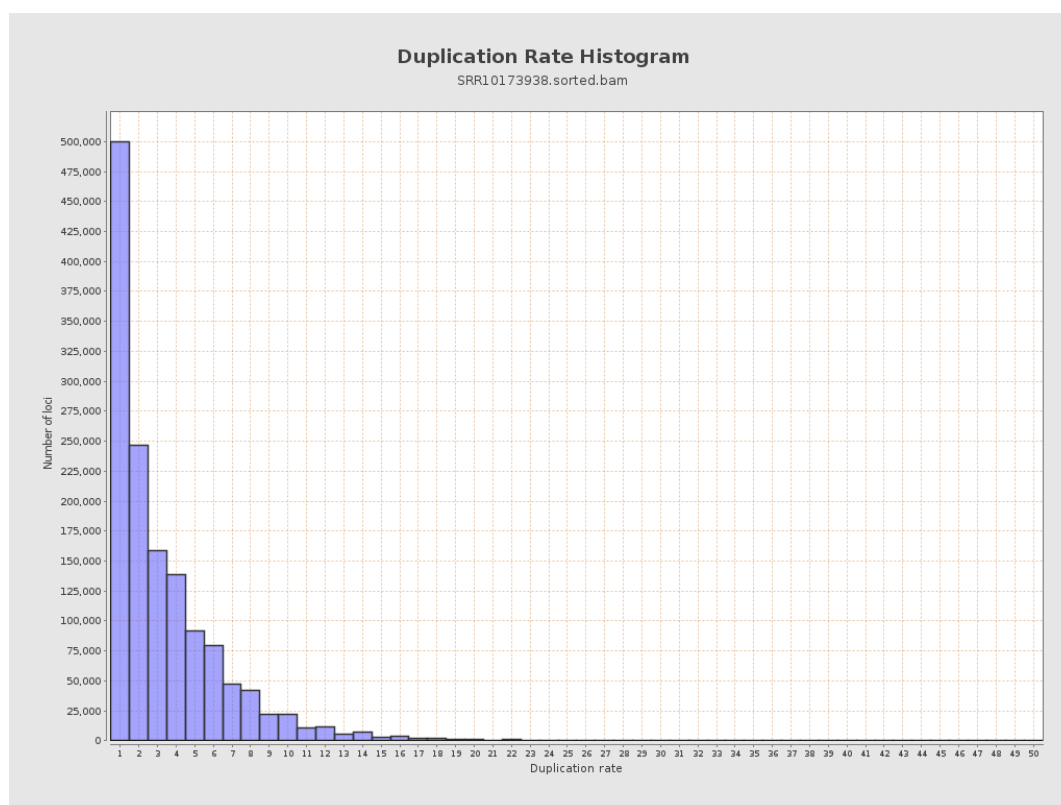
5. Results : Coverage Histogram (0-50X)



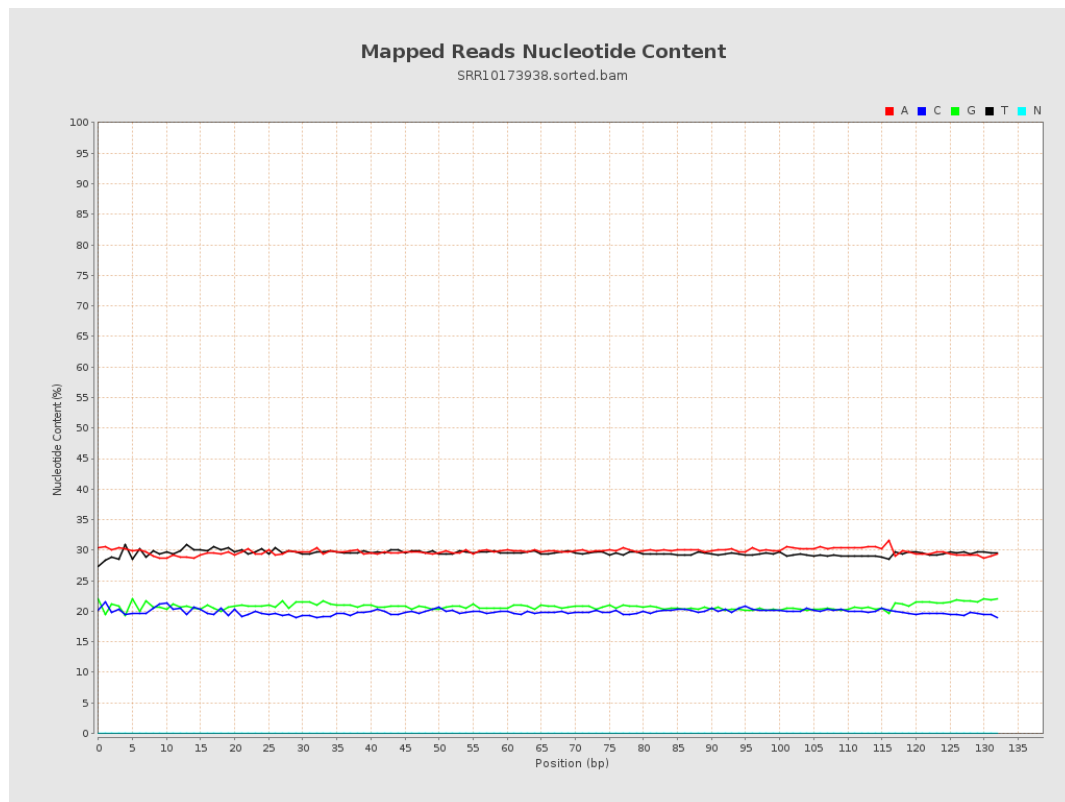
6. Results : Genome Fraction Coverage



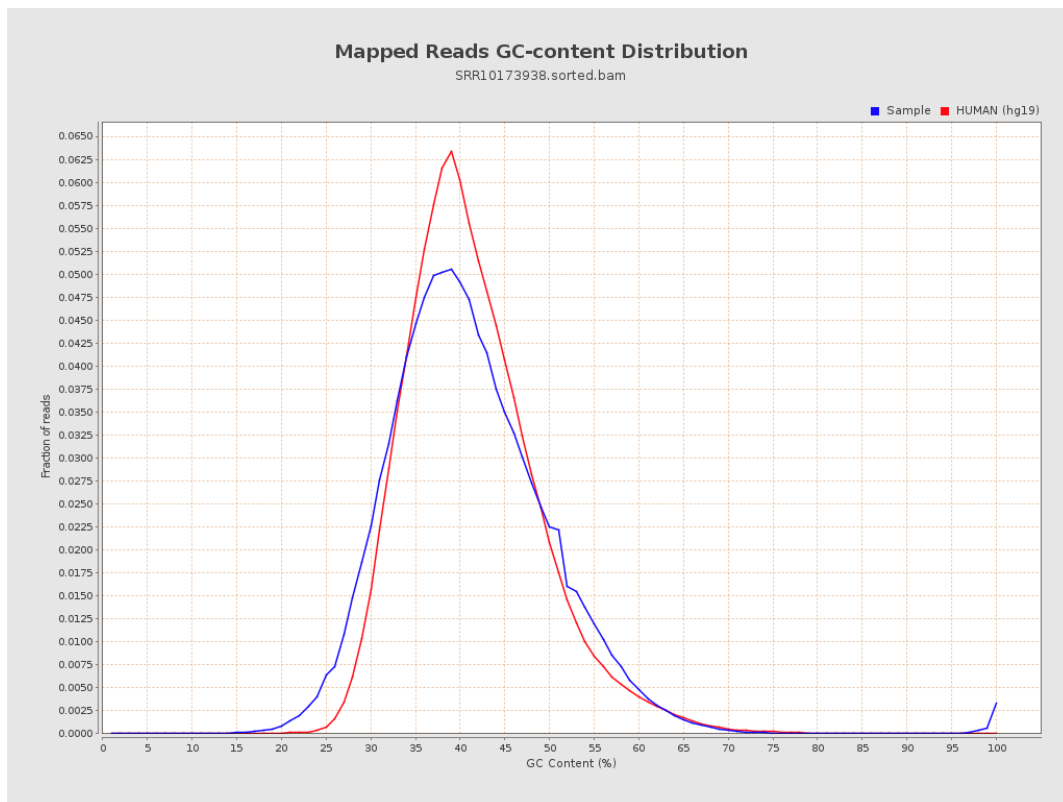
7. Results : Duplication Rate Histogram



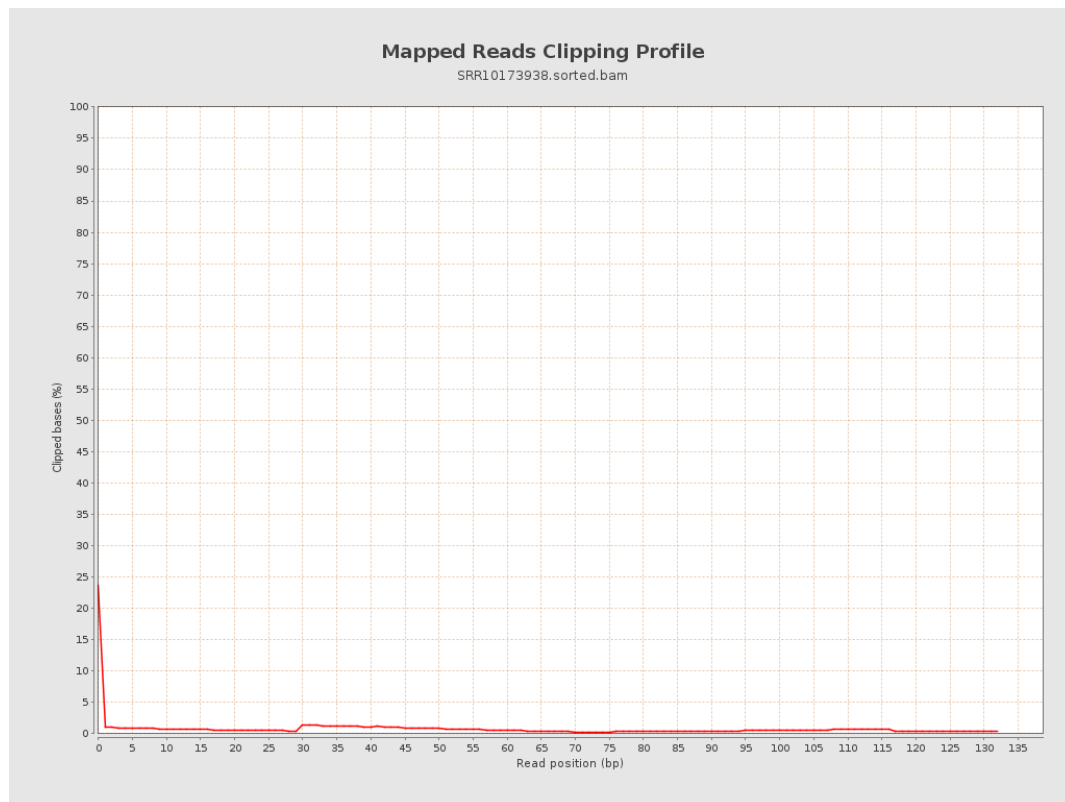
8. Results : Mapped Reads Nucleotide Content



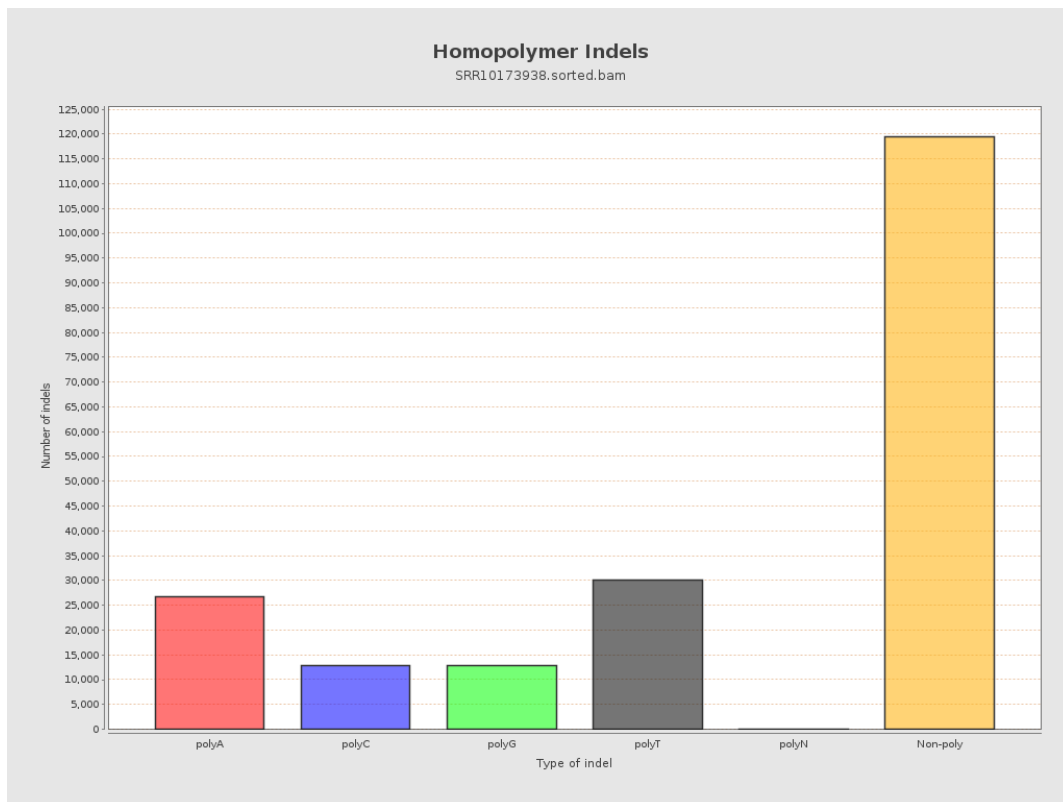
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



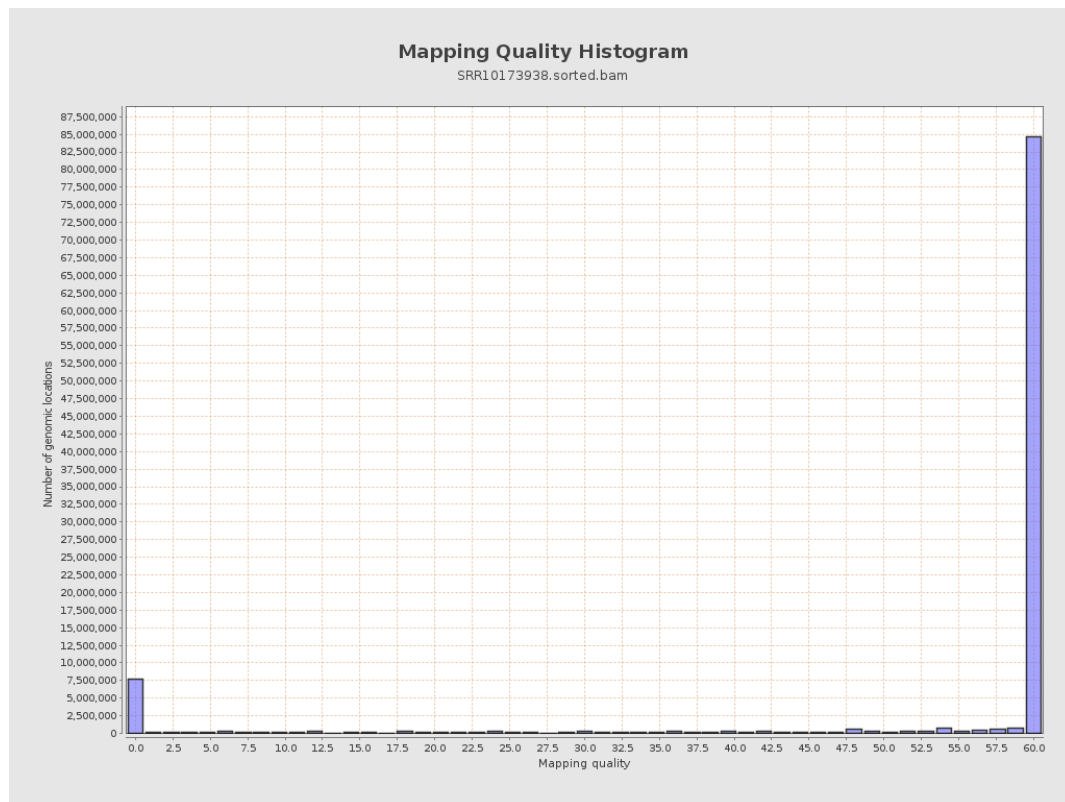
11. Results : Homopolymer Indels



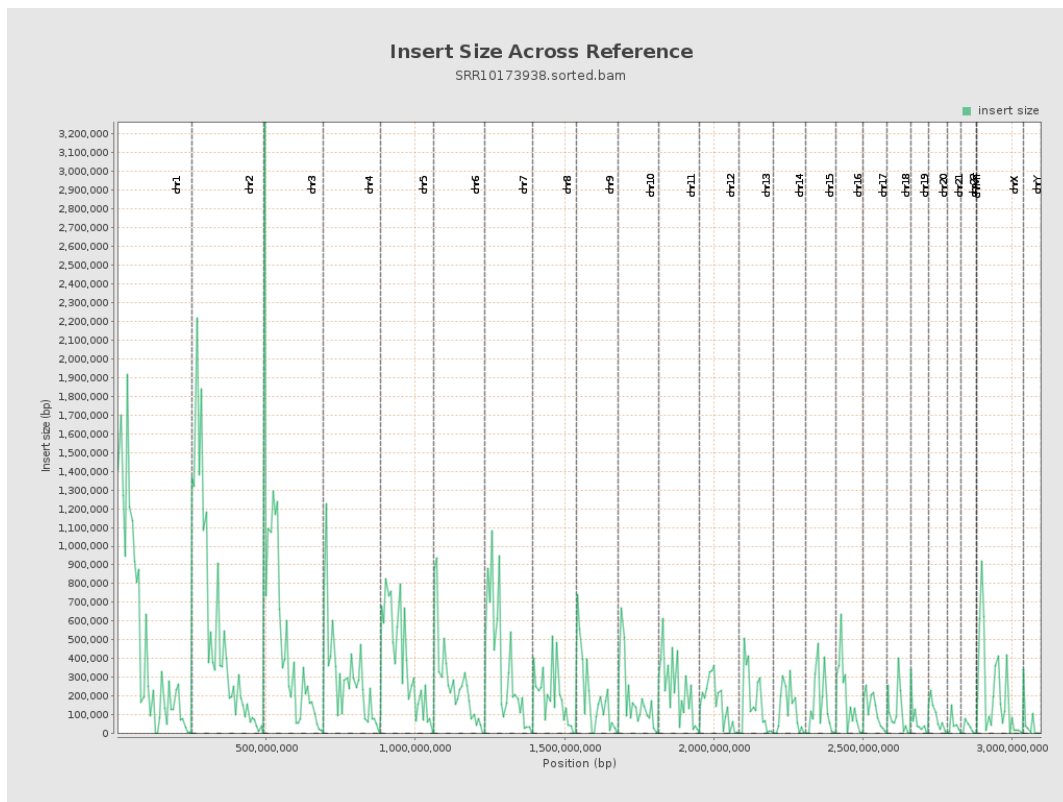
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

