

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 03:42:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174063.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_SRR10174063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174063_1.fastq.gz SRR10174063_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 03:42:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,623,498
Mapped reads	6,444,296 / 97.29%
Unmapped reads	179,202 / 2.71%
Mapped paired reads	6,444,296 / 97.29%
Mapped reads, first in pair	3,229,816 / 48.76%
Mapped reads, second in pair	3,214,480 / 48.53%
Mapped reads, both in pair	6,326,626 / 95.52%
Mapped reads, singletons	117,670 / 1.78%
Secondary alignments	0
Supplementary alignments	651,464 / 9.84%
Read min/max/mean length	30 / 133 / 128.18
Duplicated reads (estimated)	5,117,981 / 77.27%
Duplication rate	66.07%
Clipped reads	2,629,051 / 39.69%

2.2. ACGT Content

Number/percentage of A's	229,213,968 / 30.13%
Number/percentage of C's	148,949,401 / 19.58%
Number/percentage of T's	228,343,476 / 30.01%
Number/percentage of G's	154,248,918 / 20.28%
Number/percentage of N's	9,117 / 0%

GC Percentage	39.85%
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2.3. Coverage

Mean	0.2459
Standard Deviation	3.4897

2.4. Mapping Quality

Mean Mapping Quality	52.73
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2.5. Insert size

Mean	946,216.95
Standard Deviation	8,719,315.23
P25/Median/P75	145 / 203 / 292

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	7,743,349
Insertions	78,836
Mapped reads with at least one insertion	1.18%
Deletions	172,661
Mapped reads with at least one deletion	2.61%
Homopolymer indels	42.83%

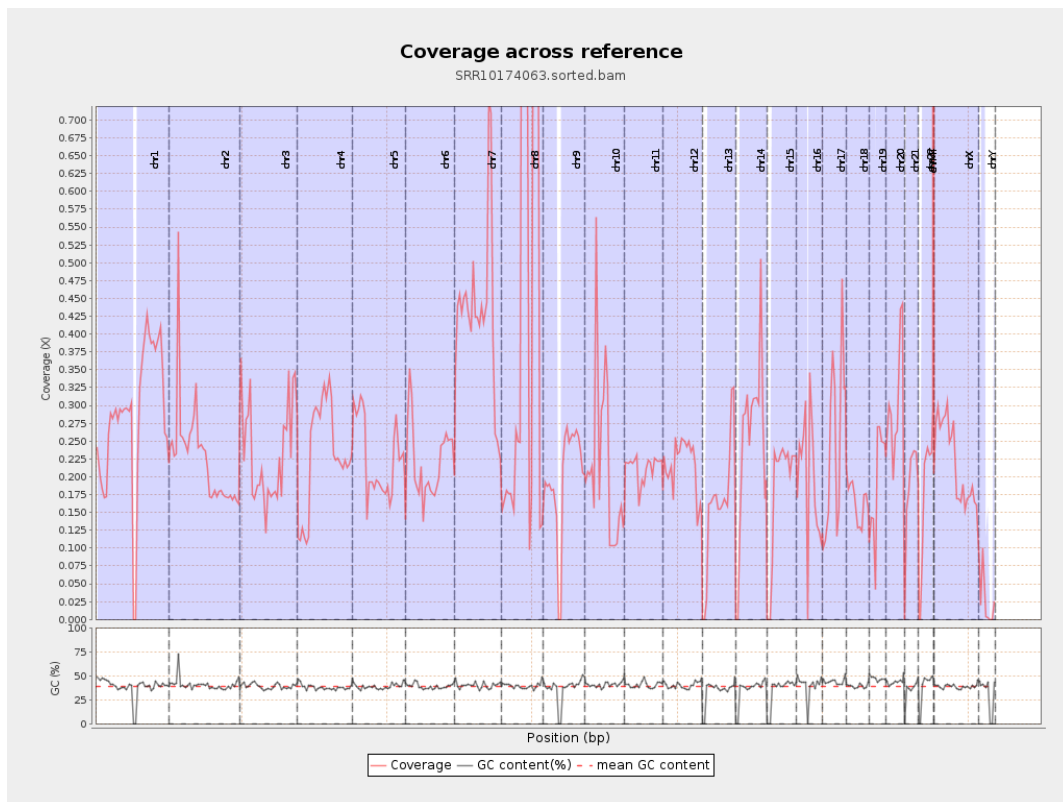
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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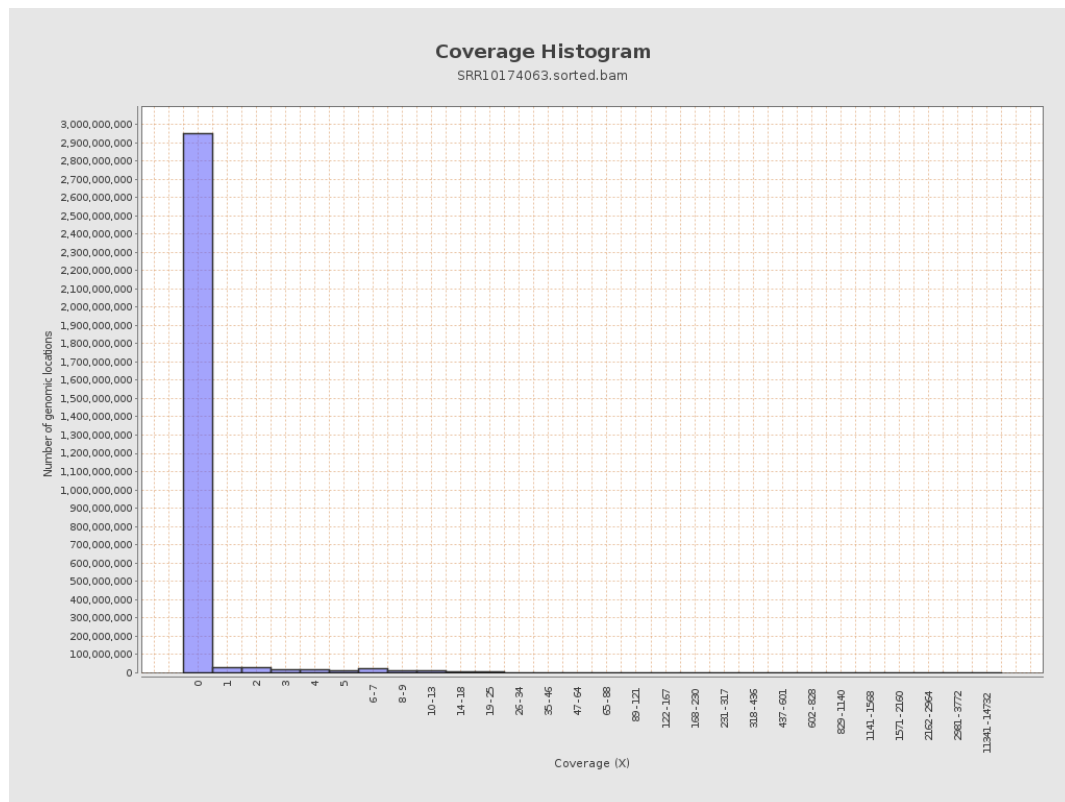
		bases	coverage	deviation
chr1	249250621	70903754	0.2845	2.0215
chr2	243199373	55088238	0.2265	10.2961
chr3	198022430	46188873	0.2333	1.4371
chr4	191154276	43868377	0.2295	1.7561
chr5	180915260	40755775	0.2253	1.3951
chr6	171115067	37424039	0.2187	1.4478
chr7	159138663	68877988	0.4328	3.7151
chr8	146364022	82394946	0.5629	2.7282
chr9	141213431	27833211	0.1971	1.6412
chr10	135534747	29416363	0.217	3.9562
chr11	135006516	28585564	0.2117	1.4115
chr12	133851895	29081136	0.2173	1.378
chr13	115169878	18772894	0.163	1.1991
chr14	107349540	26821422	0.2499	1.4849
chr15	102531392	18844439	0.1838	1.2503
chr16	90354753	17562664	0.1944	1.7573
chr17	81195210	20228616	0.2491	1.6427
chr18	78077248	12930163	0.1656	2.0872
chr19	59128983	11327979	0.1916	1.6238
chr20	63025520	18857098	0.2992	1.6326
chr21	48129895	8913229	0.1852	1.3786
chr22	51304566	8442122	0.1645	1.1575
chrMT	16571	2555555	154.2185	113.8729
chrX	155270560	33984855	0.2189	1.4031

chrY	59373566	1532517	0.0258	0.9429
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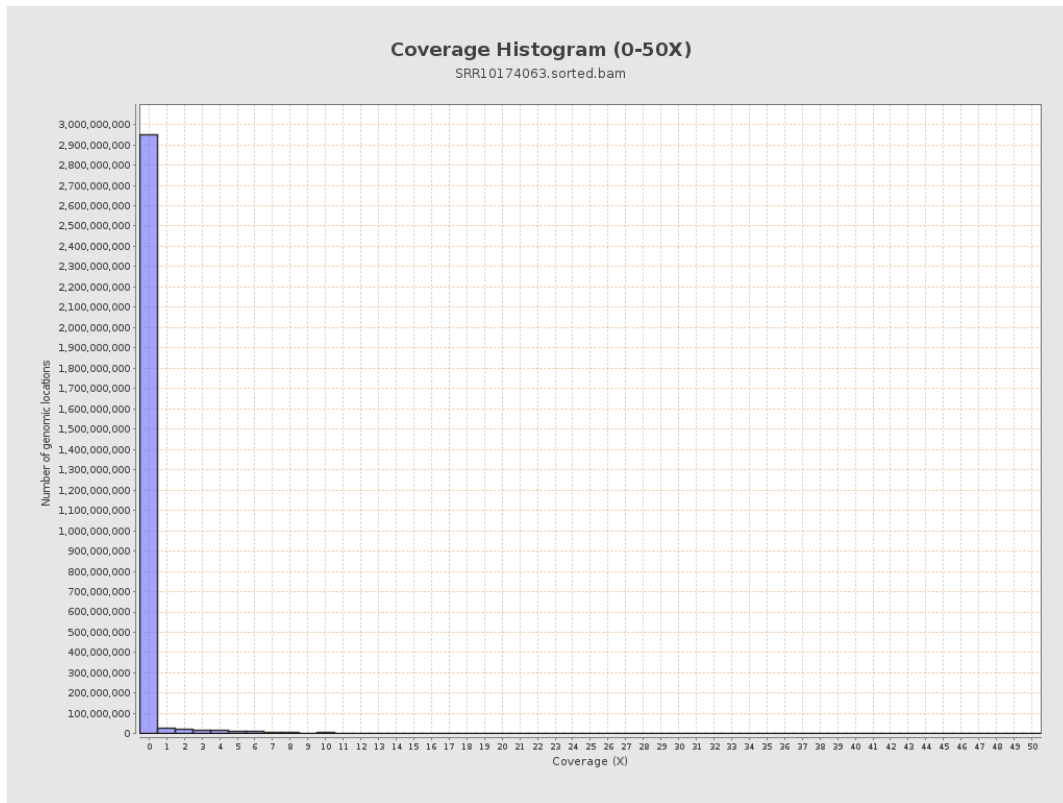
3. Results : Coverage across reference



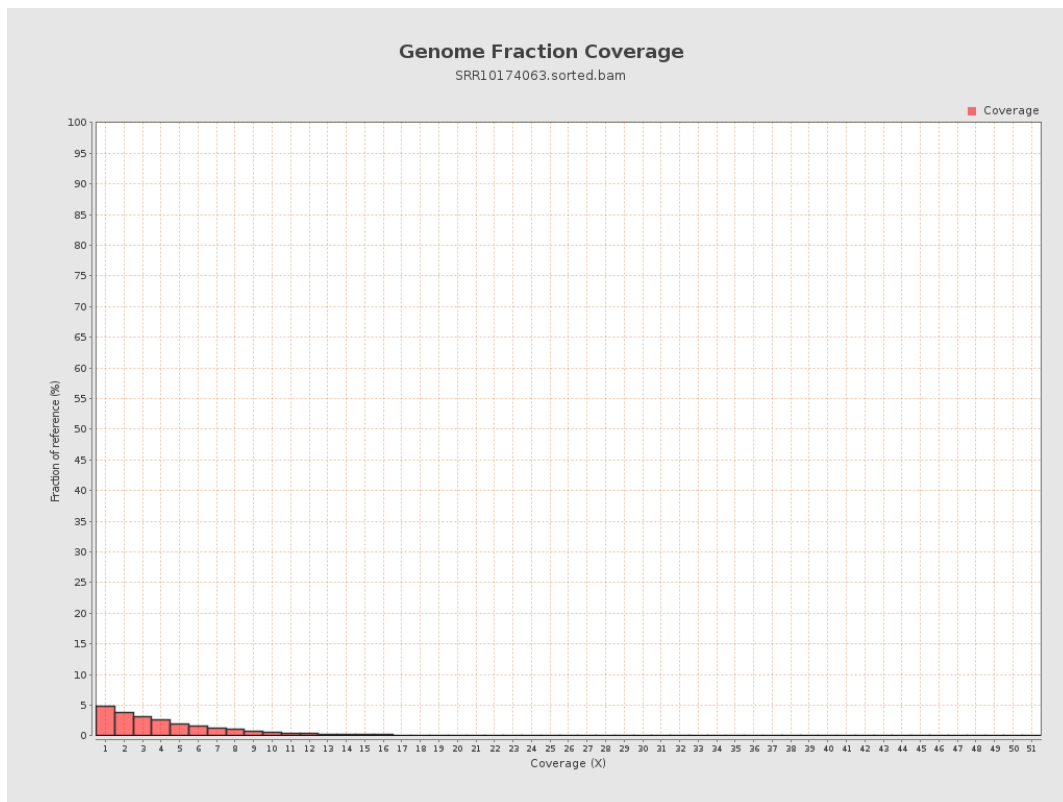
4. Results : Coverage Histogram



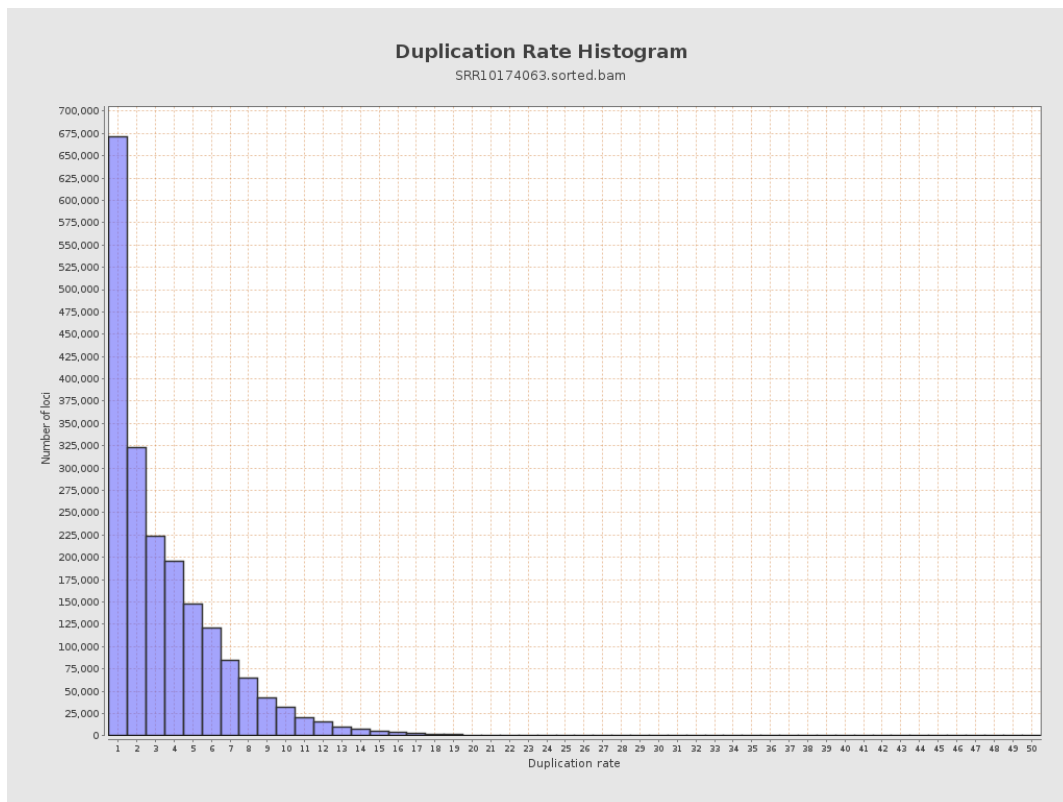
5. Results : Coverage Histogram (0-50X)



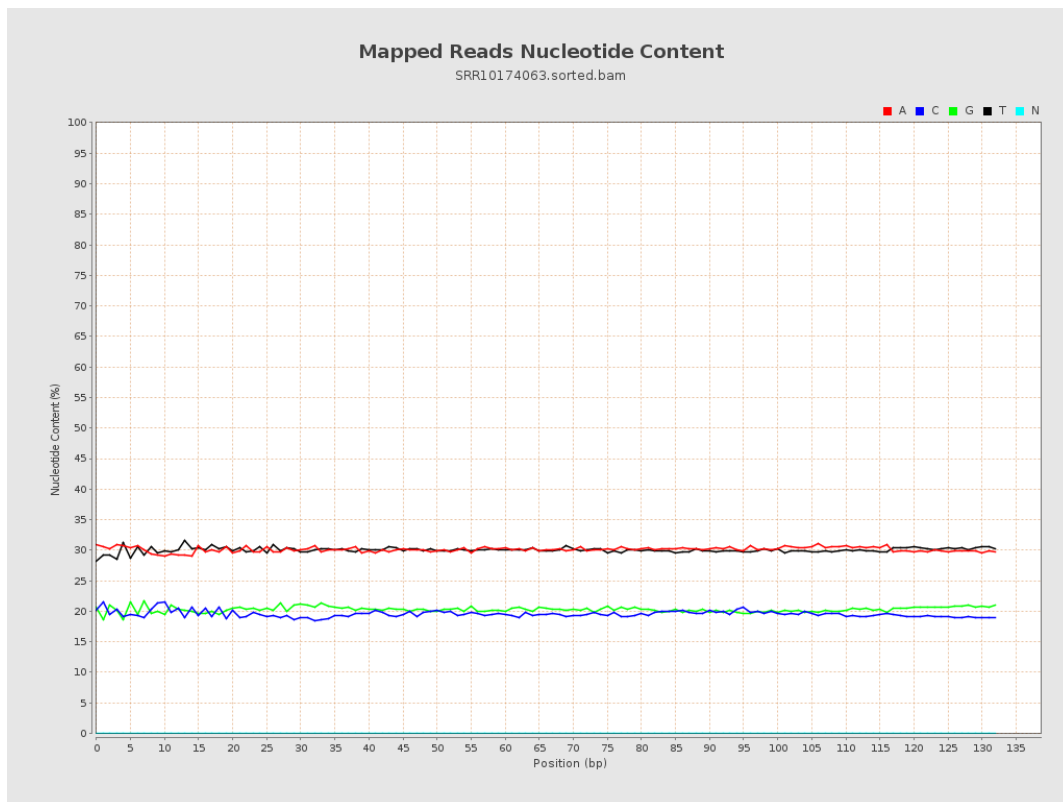
6. Results : Genome Fraction Coverage



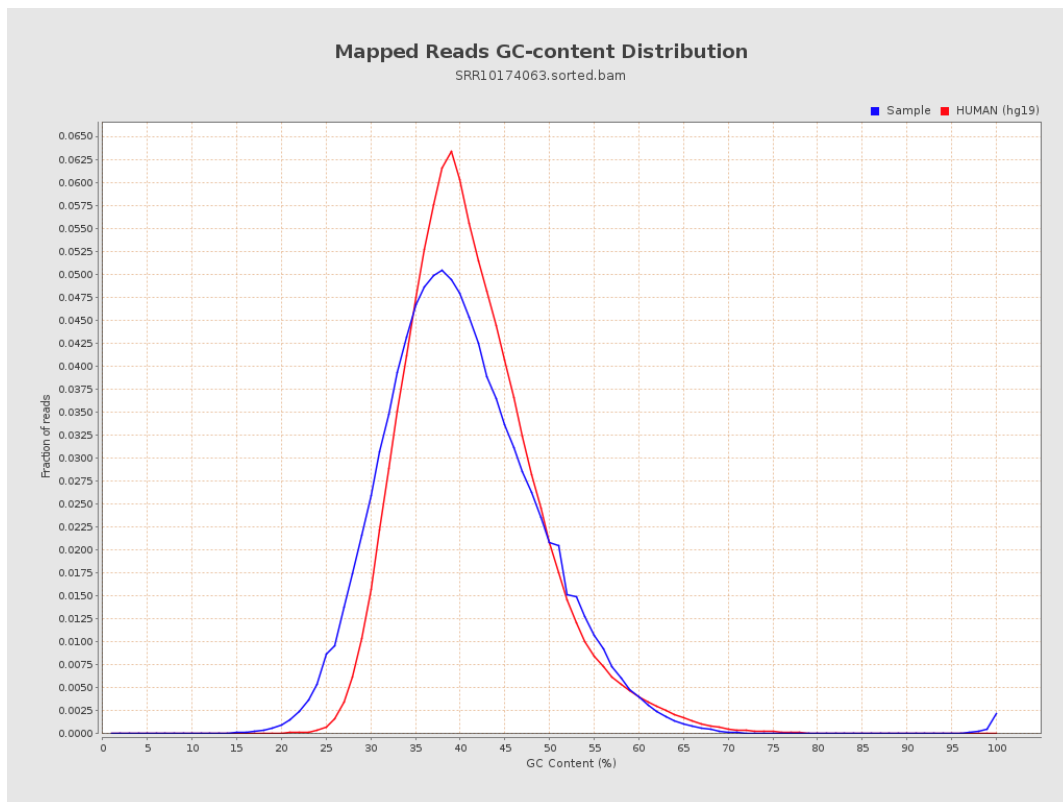
7. Results : Duplication Rate Histogram



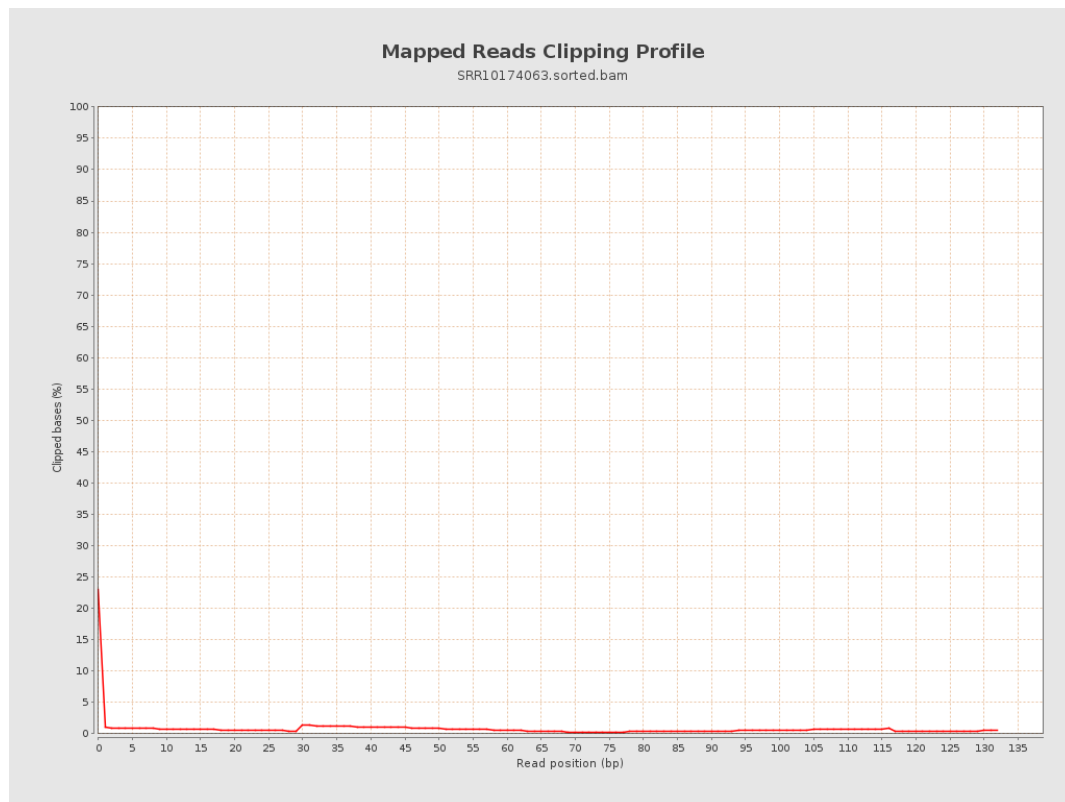
8. Results : Mapped Reads Nucleotide Content



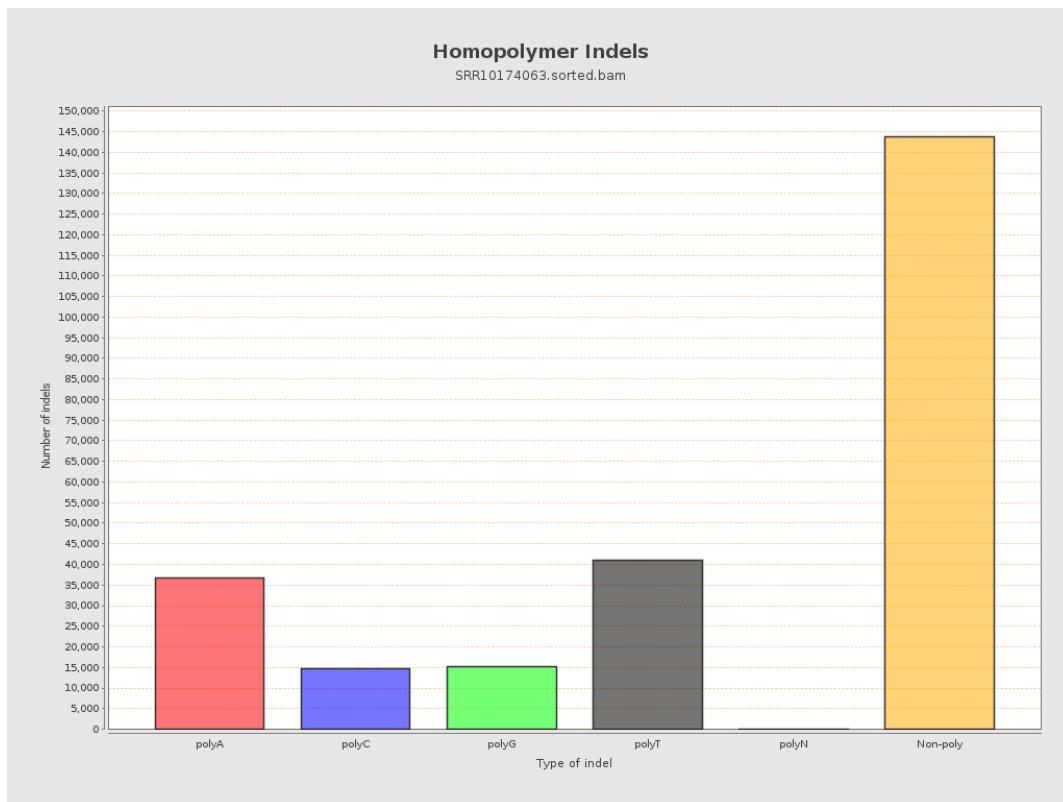
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



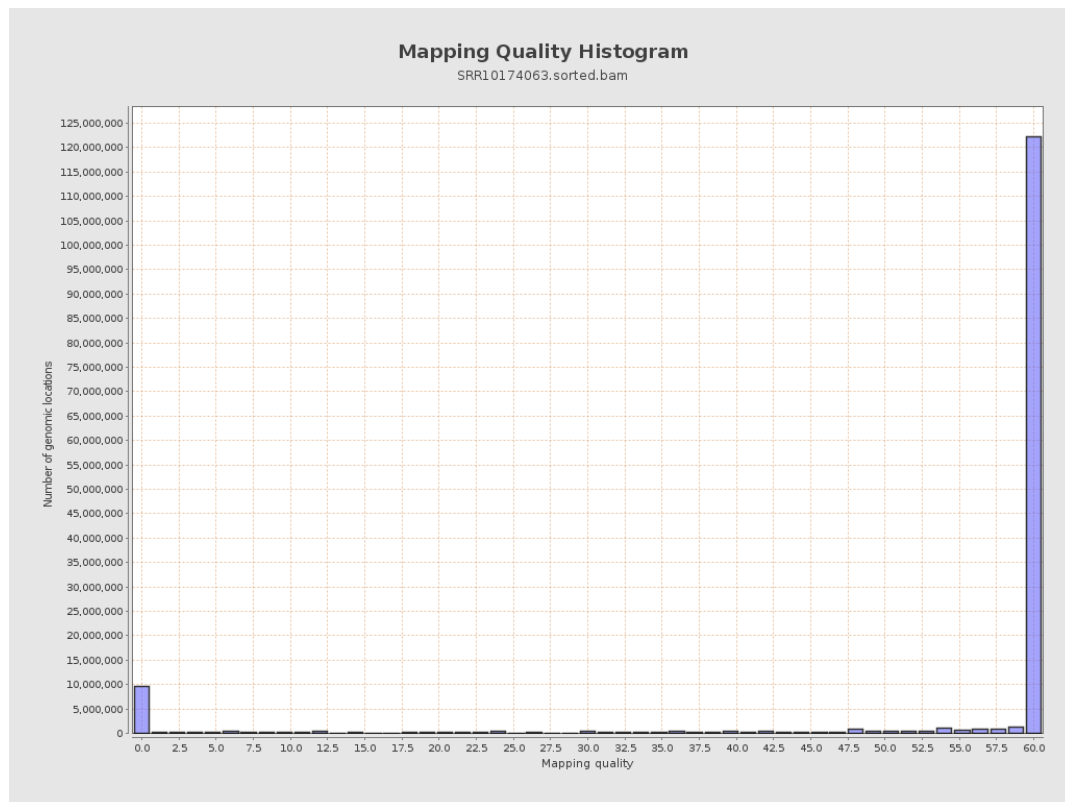
11. Results : Homopolymer Indels



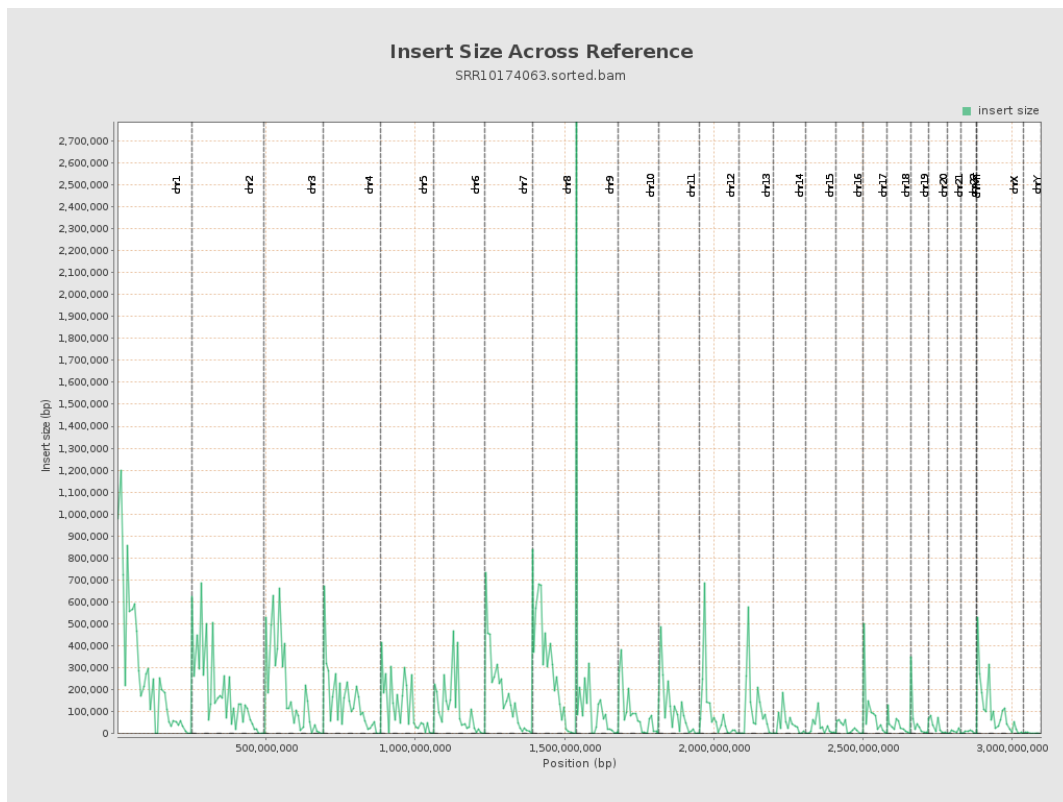
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

