Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 14:11:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173964.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_SRR10173964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173964_1.fastq.gz SRR10173964_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 14:11:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,858,742
Mapped reads	4,761,912 / 98.01%
Unmapped reads	96,830 / 1.99%
Mapped paired reads	4,761,912 / 98.01%
Mapped reads, first in pair	2,379,344 / 48.97%
Mapped reads, second in pair	2,382,568 / 49.04%
Mapped reads, both in pair	4,699,472 / 96.72%
Mapped reads, singletons	62,440 / 1.29%
Secondary alignments	0
Supplementary alignments	637,066 / 13.11%
Read min/max/mean length	30 / 133 / 125.89
Duplicated reads (estimated)	3,838,201 / 79%
Duplication rate	65.06%
Clipped reads	2,474,803 / 50.94%

2.2. ACGT Content

Number/percentage of A's	162,163,009 / 29.97%
Number/percentage of C's	106,796,156 / 19.74%
Number/percentage of T's	160,972,680 / 29.75%
Number/percentage of G's	111,093,866 / 20.53%
Number/percentage of N's	4,112 / 0%

GC Percentage	40.27%

2.3. Coverage

Mean	0.1749
Standard Deviation	3.1077

2.4. Mapping Quality

Mean Mapping Quality	52.61

2.5. Insert size

Mean	1,284,709.66
Standard Deviation	10,008,860.73
P25/Median/P75	108 / 161 / 254

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	4,473,564
Insertions	59,071
Mapped reads with at least one insertion	1.19%
Deletions	145,915
Mapped reads with at least one deletion	2.99%
Homopolymer indels	41.48%

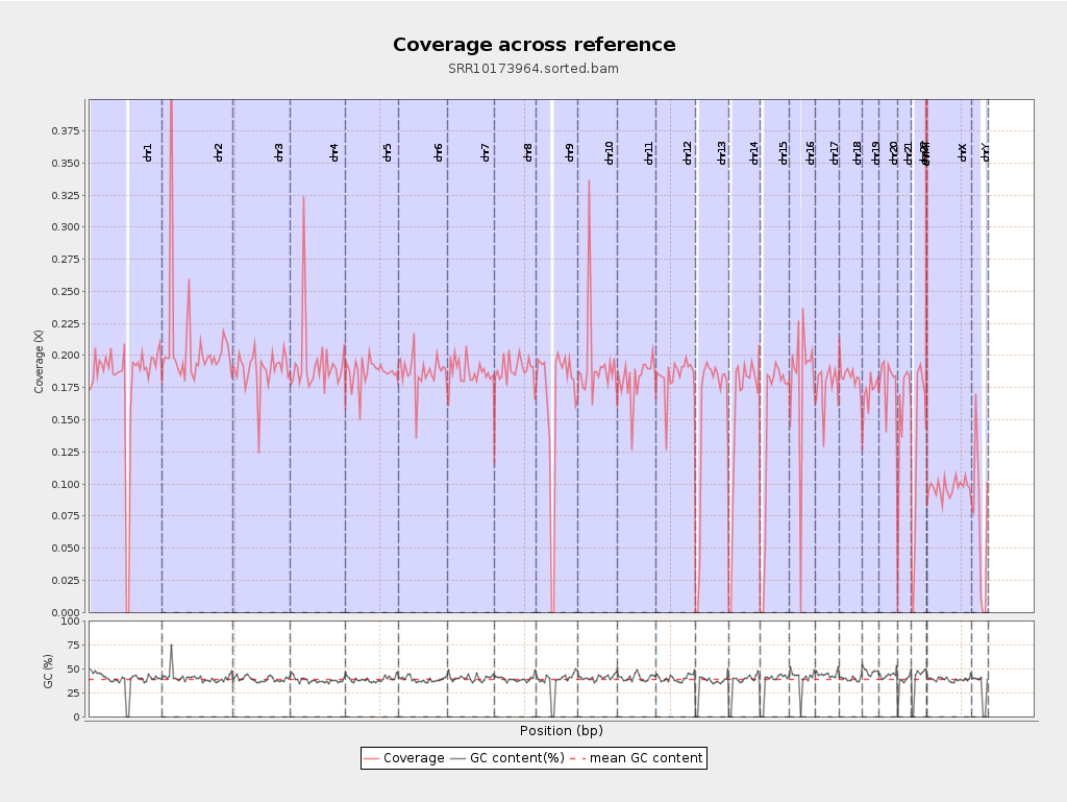
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

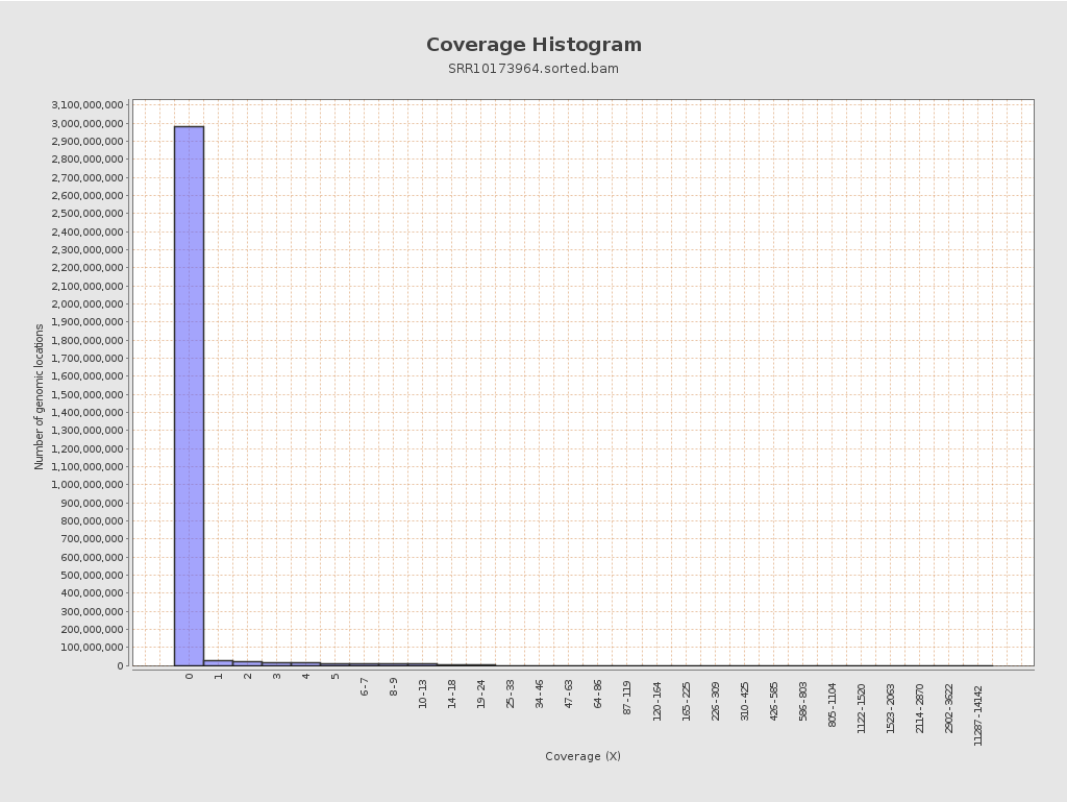
		bases	coverage	deviation
chr1	249250621	44830670	0.1799	1.6017
chr2	243199373	50666953	0.2083	9.8931
chr3	198022430	37460266	0.1892	1.3166
chr4	191154276	36960508	0.1934	1.6436
chr5	180915260	33847534	0.1871	1.3027
chr6	171115067	32037251	0.1872	1.421
chr7	159138663	29887272	0.1878	1.5316
chr8	146364022	27653963	0.1889	1.9134
chr9	141213431	23345047	0.1653	1.5302
chr10	135534747	26180555	0.1932	1.8871
chr11	135006516	24565142	0.182	1.3064
chr12	133851895	24643190	0.1841	1.3307
chr13	115169878	17715561	0.1538	1.1911
chr14	107349540	16529741	0.154	1.178
chr15	102531392	15117695	0.1474	1.165
chr16	90354753	16255354	0.1799	1.5036
chr17	81195210	14299797	0.1761	1.2937
chr18	78077248	14381553	0.1842	1.9338
chr19	59128983	10137416	0.1714	1.3795
chr20	63025520	11306363	0.1794	1.3029
chr21	48129895	7439380	0.1546	1.4892
chr22	51304566	6469832	0.1261	1.2281
chrMT	16571	656327	39.607	35.6518
chrX	155270560	15069855	0.0971	0.9338

chrY	59373566	3928075	0.0662	1.1665

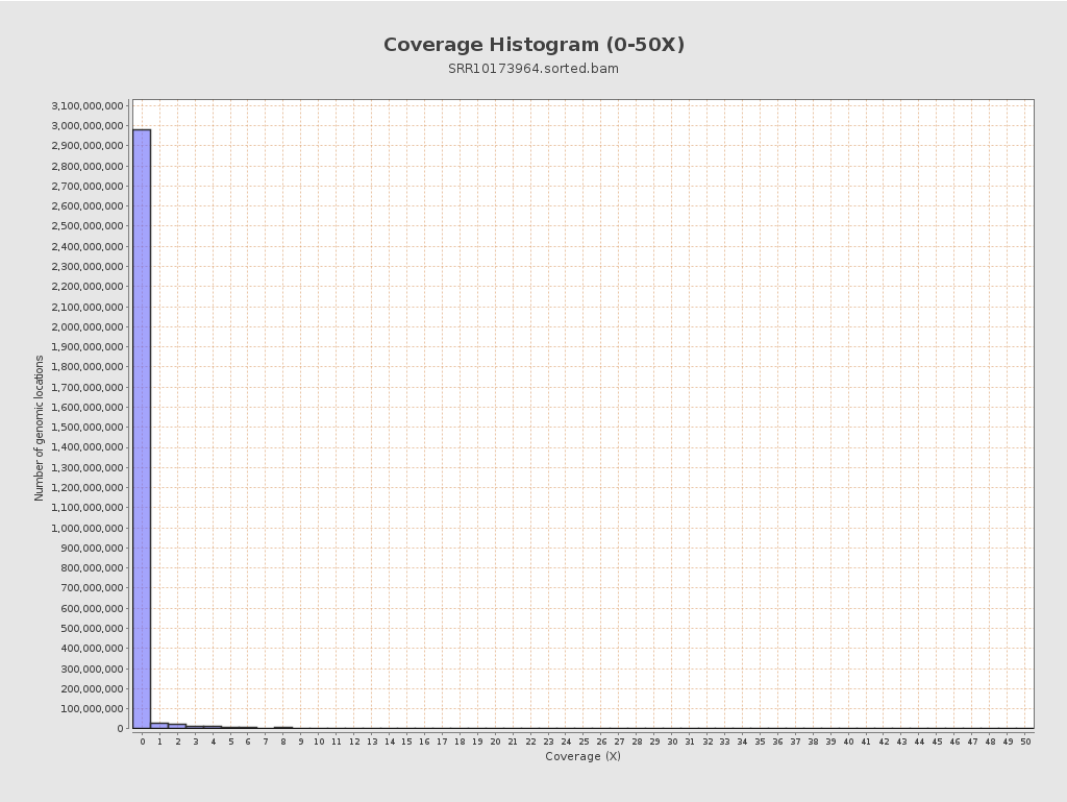
3. Results : Coverage across reference



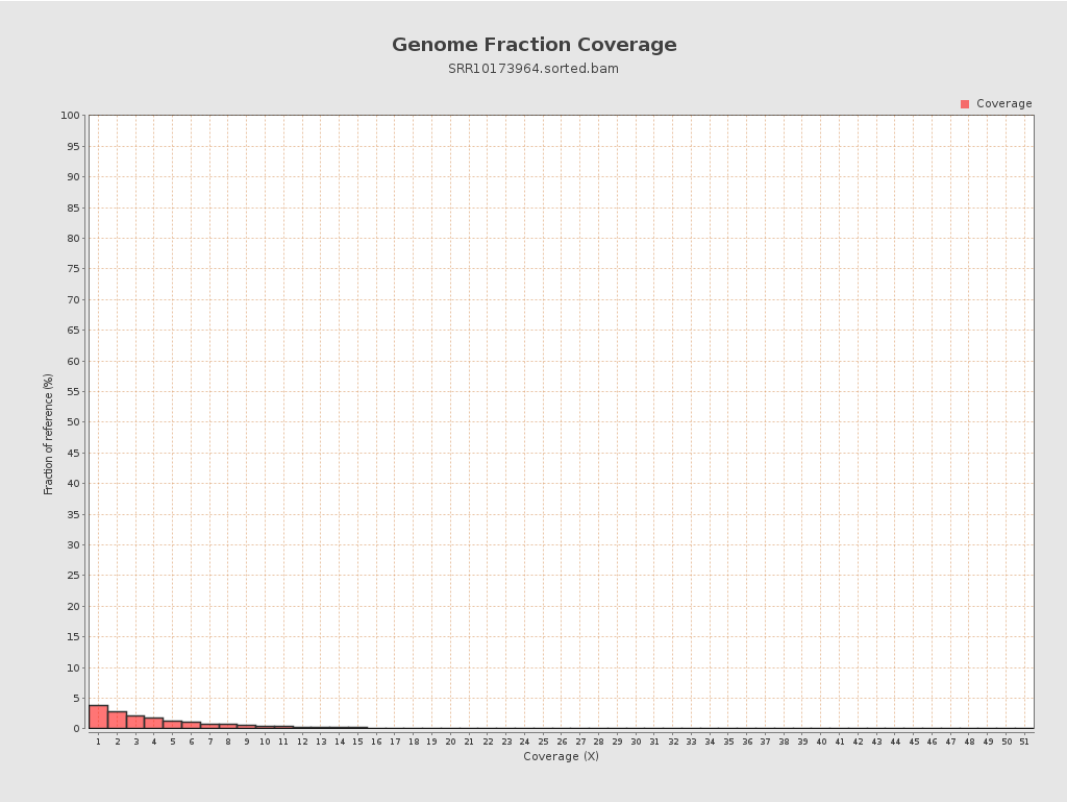
4. Results : Coverage Histogram



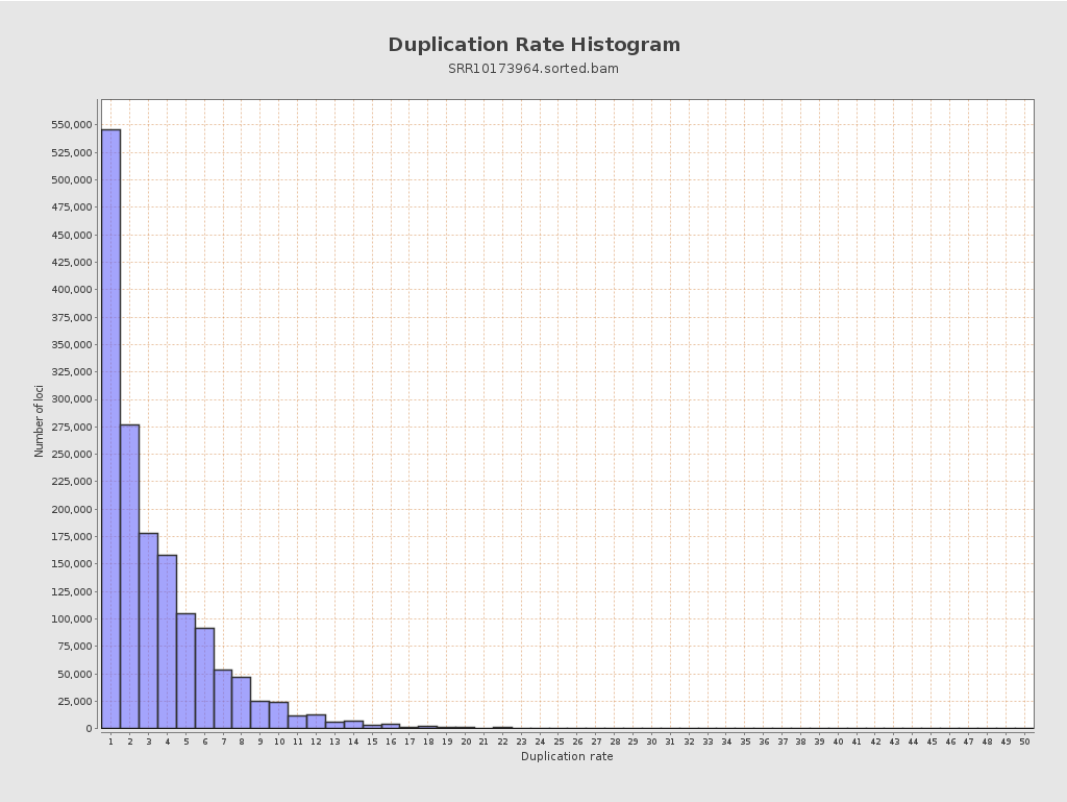
5. Results : Coverage Histogram (0-50X)



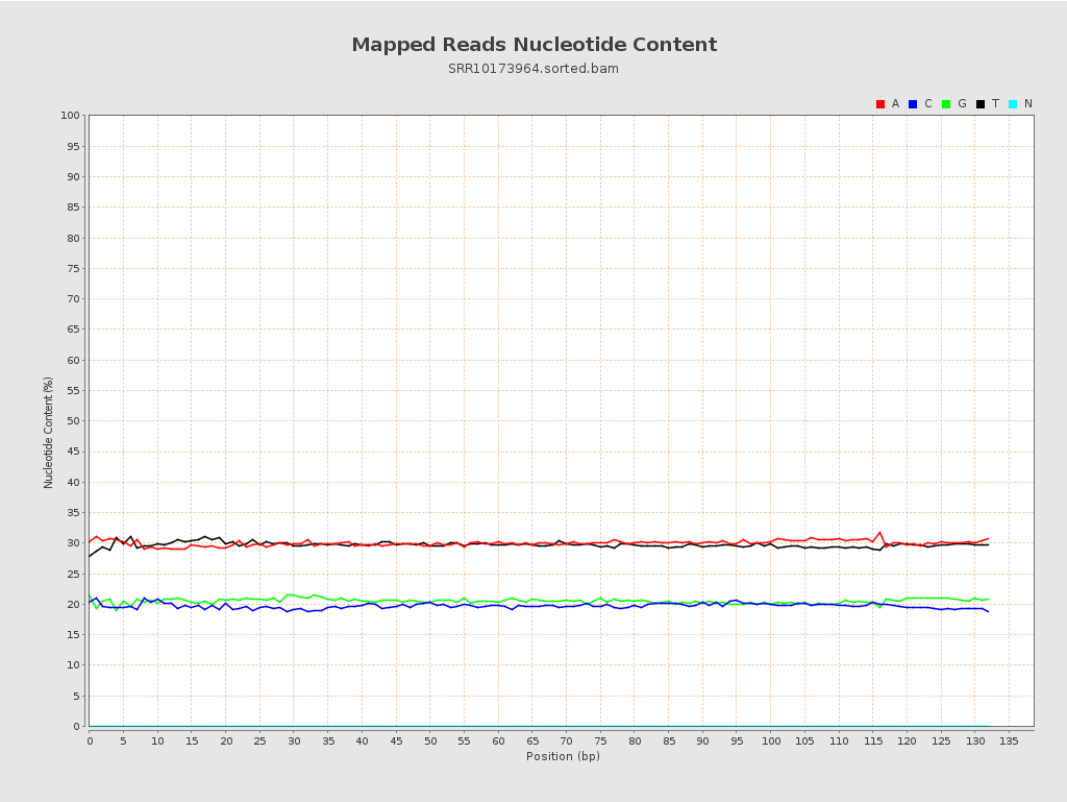
6. Results : Genome Fraction Coverage



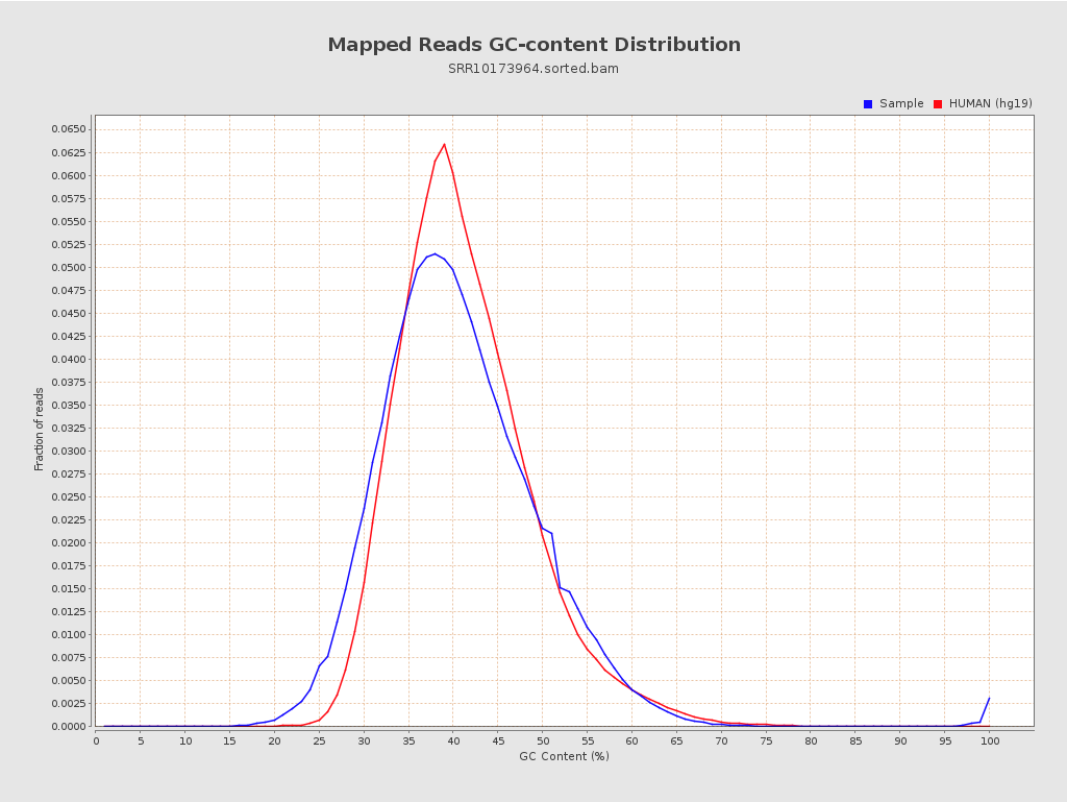
7. Results : Duplication Rate Histogram



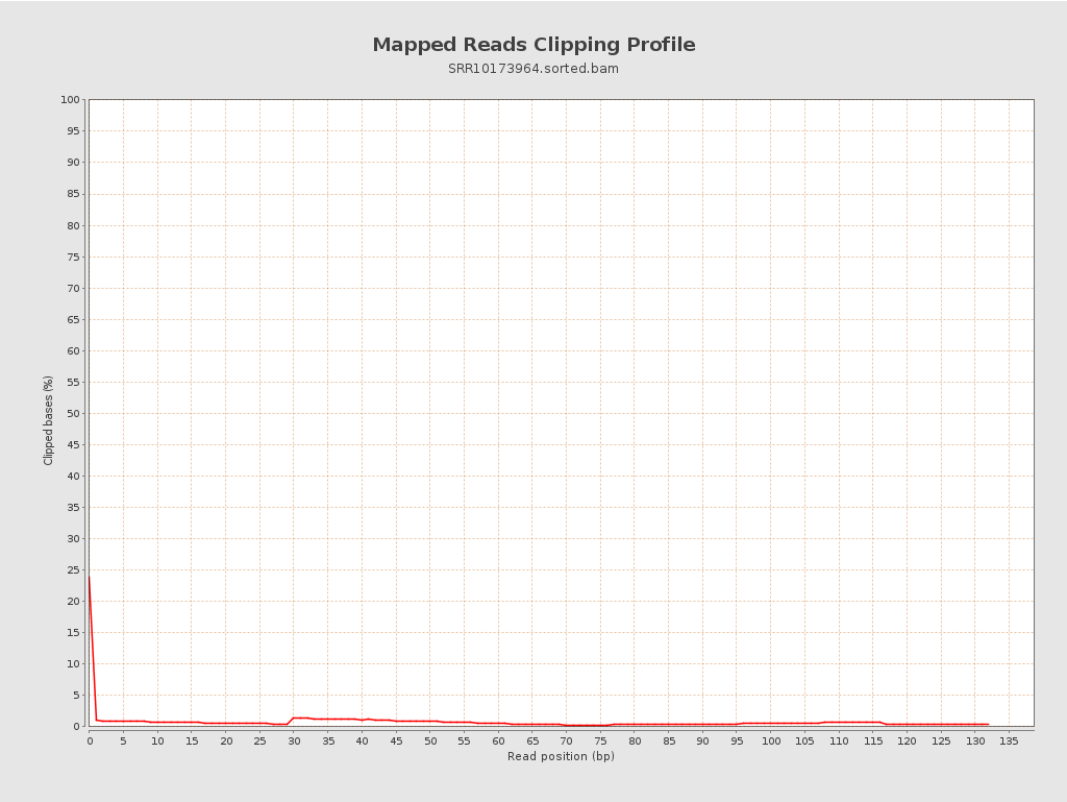
8. Results : Mapped Reads Nucleotide Content



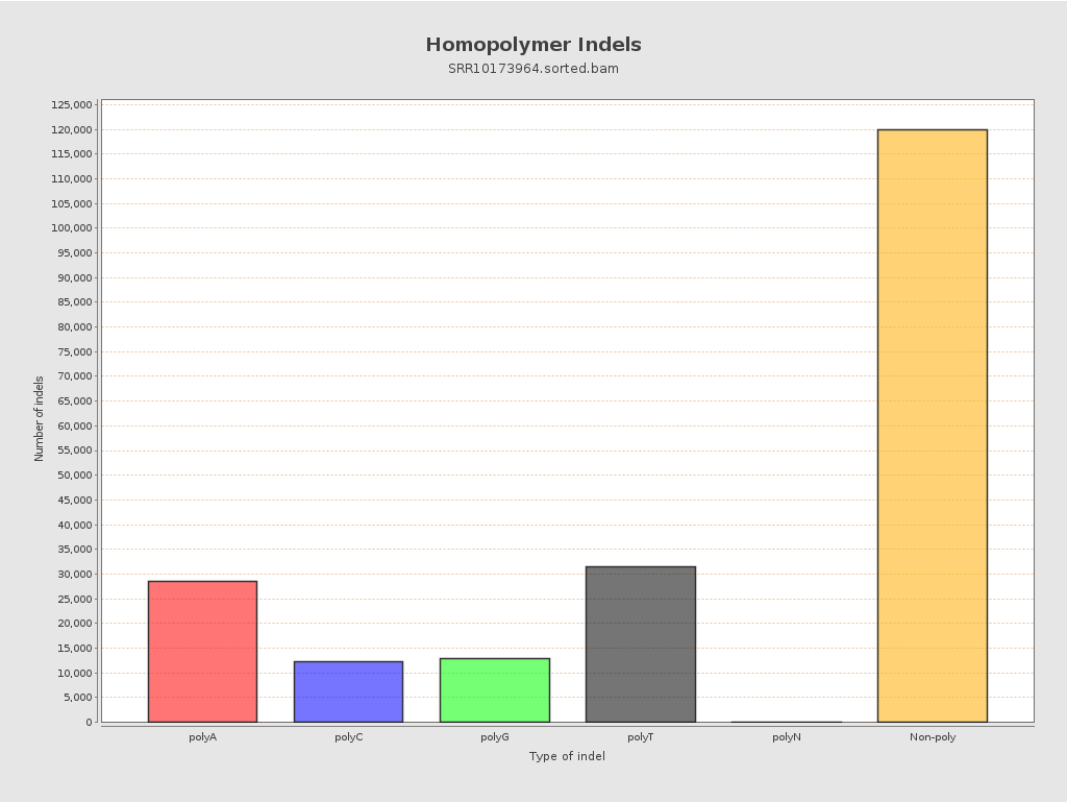
9. Results : Mapped Reads GC-content Distribution



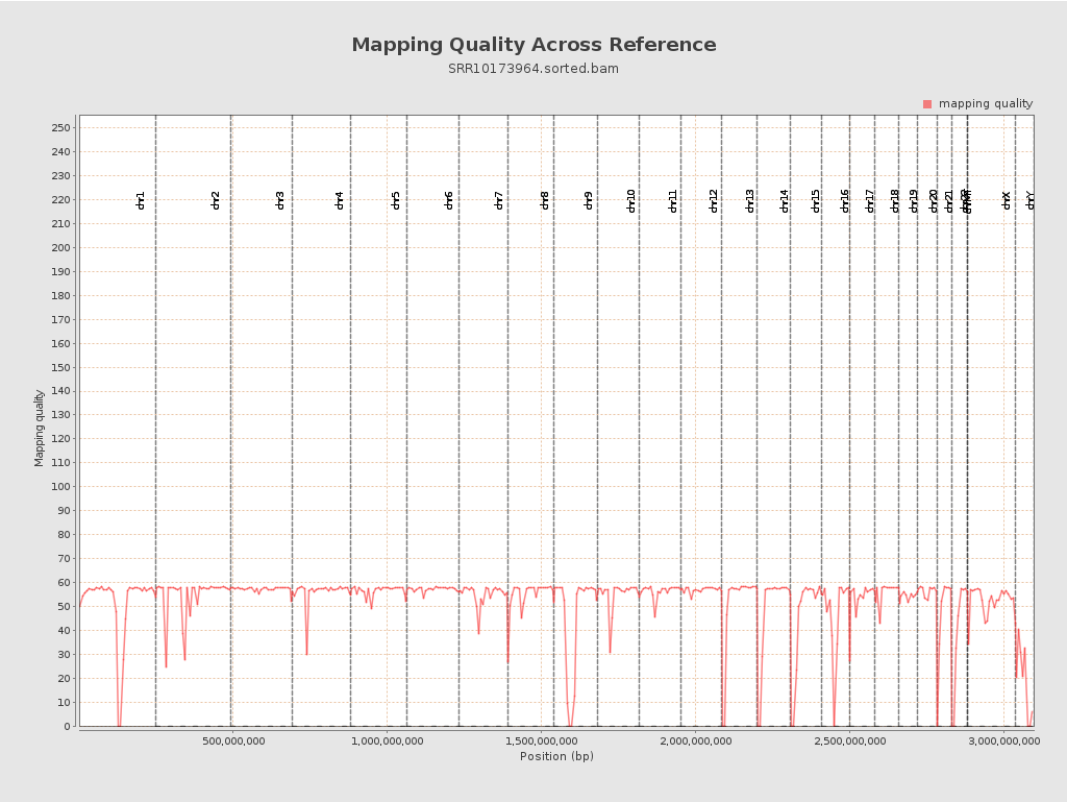
10. Results : Mapped Reads Clipping Profile



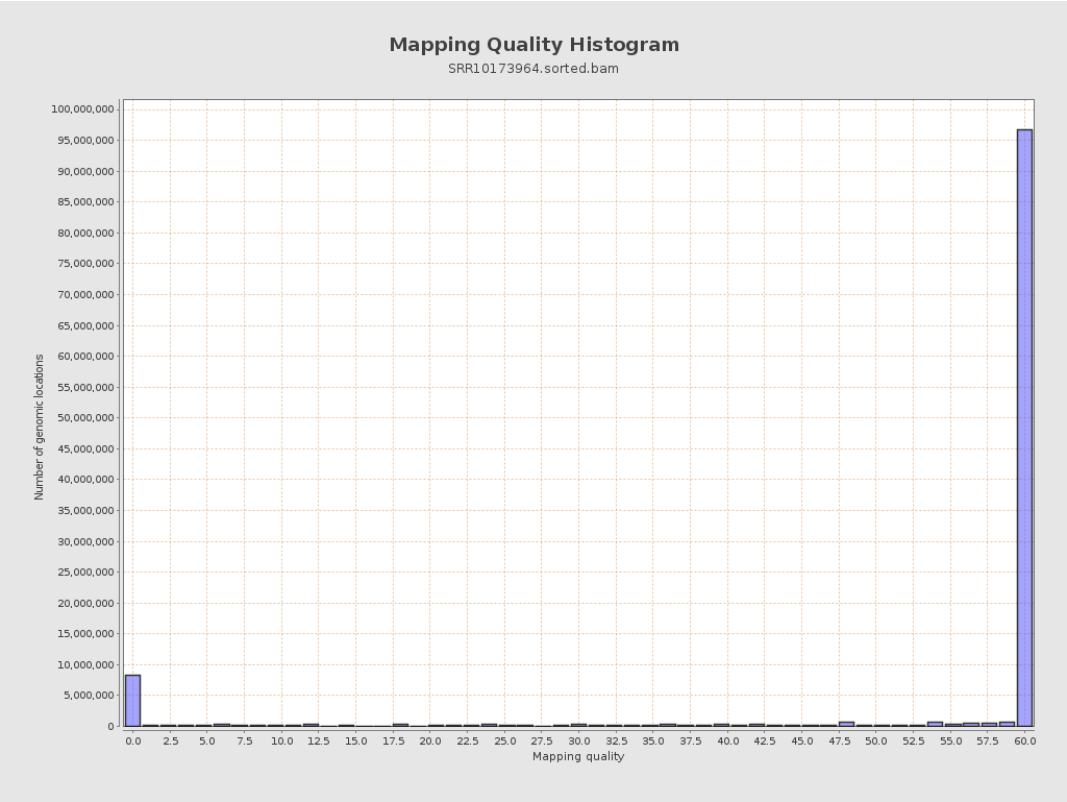
11. Results : Homopolymer Indels



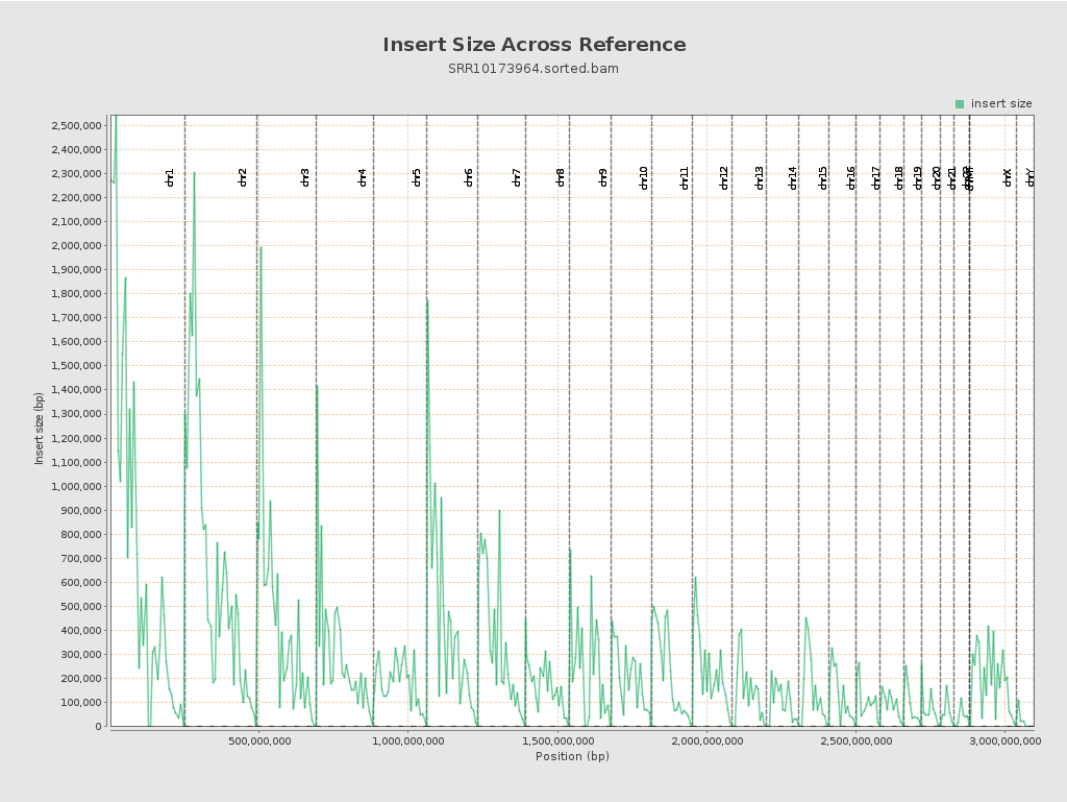
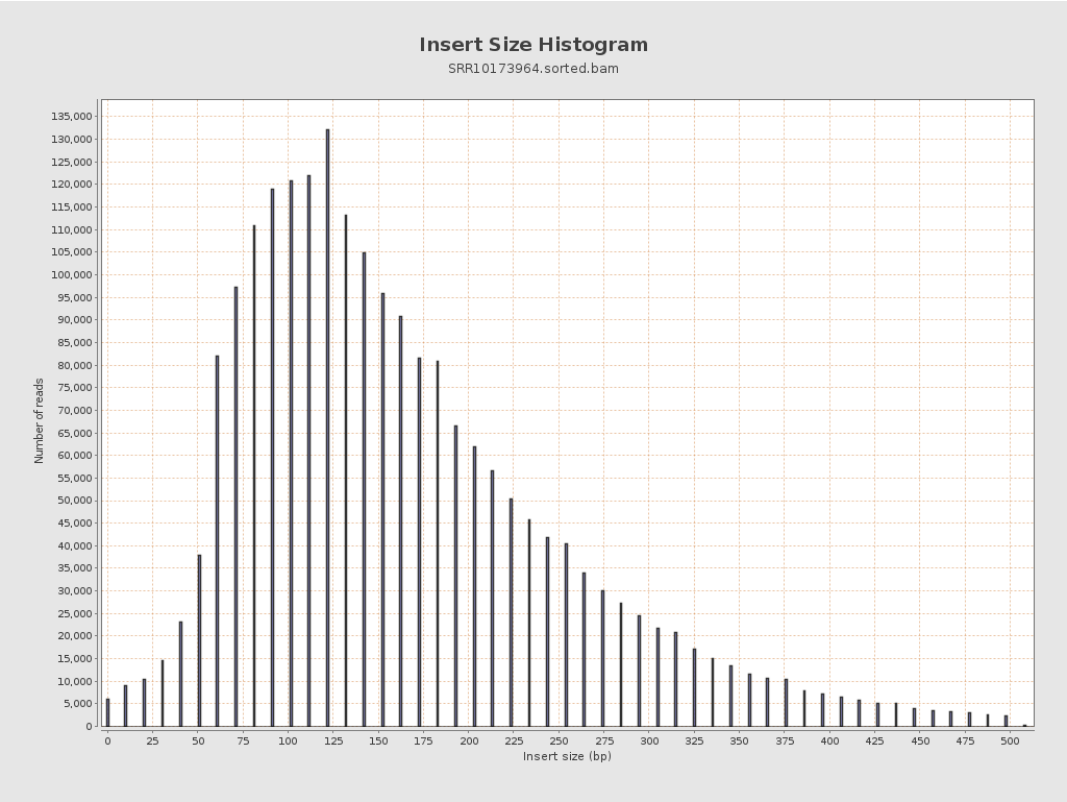
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram