Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/15 00:59:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365360.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_SRR5365360 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365360_1.fastq.gz SRR5365360_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Nov 15 00:59:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365360.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	549,833,842
Mapped reads	474,905,948 / 86.37%
Unmapped reads	74,927,894 / 13.63%
Mapped paired reads	474,905,948 / 86.37%
Mapped reads, first in pair	234,857,819 / 42.71%
Mapped reads, second in pair	240,048,129 / 43.66%
Mapped reads, both in pair	460,468,010 / 83.75%
Mapped reads, singletons	14,437,938 / 2.63%
Secondary alignments	0
Supplementary alignments	16,962,567 / 3.09%
Read min/max/mean length	30 / 150 / 151.52
Duplicated reads (estimated)	259,078,804 / 47.12%
Duplication rate	42.24%
Clipped reads	343,048,510 / 62.39%

2.2. ACGT Content

Number/percentage of A's	15,798,582,635 / 26.34%
Number/percentage of C's	13,519,709,720 / 22.54%
Number/percentage of T's	15,879,561,733 / 26.48%
Number/percentage of G's	14,769,481,800 / 24.63%
Number/percentage of N's	1,701,468 / 0%

GC Percentage	47.17%

2.3. Coverage

Mean	19.3815
Standard Deviation	153.8487

2.4. Mapping Quality

Mean Mapping Quality	52.59

2.5. Insert size

Mean	182,680.01
Standard Deviation	4,274,350.31
P25/Median/P75	124 / 156 / 195

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	671,954,042
Insertions	7,535,524
Mapped reads with at least one insertion	1.49%
Deletions	16,335,179
Mapped reads with at least one deletion	3.32%
Homopolymer indels	40.62%

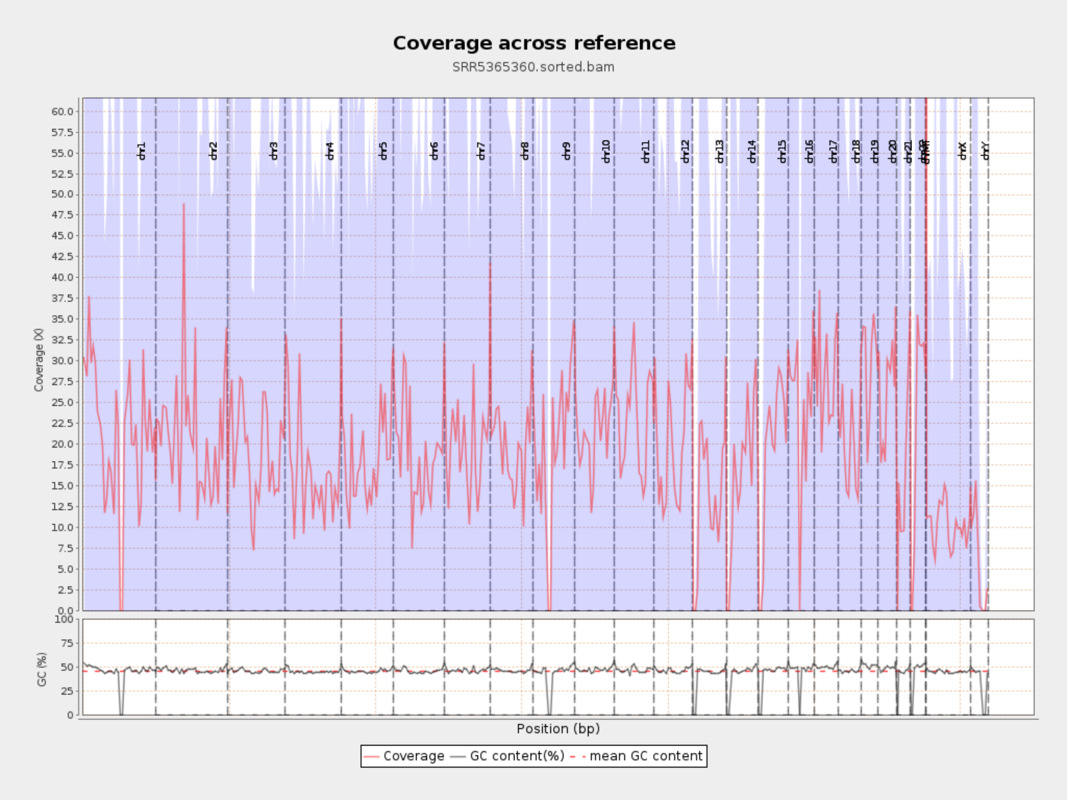
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

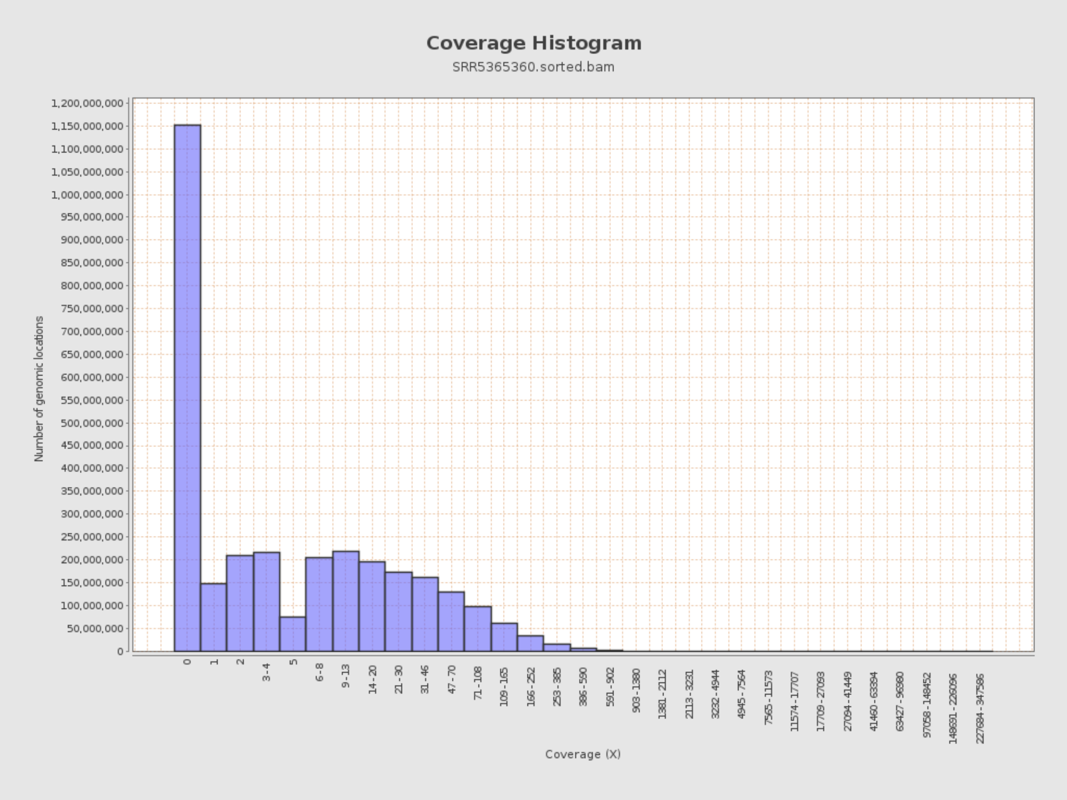
		bases	coverage	deviation
chr1	249250621	5268727367	21.1383	108.7263
chr2	243199373	5159568218	21.2154	266.0592
chr3	198022430	3754141347	18.9582	50.166
chr4	191154276	3200644842	16.7438	96.5032
chr5	180915260	3339670729	18.4599	66.5186
chr6	171115067	3191433849	18.6508	154.1805
chr7	159138663	3139476188	19.7279	126.0033
chr8	146364022	2862915188	19.5602	99.0499
chr9	141213431	2741067970	19.4108	238.2401
chr10	135534747	2907264740	21.4503	69.7526
chr11	135006516	3127779582	23.1676	329.1812
chr12	133851895	2710154927	20.2474	52.3868
chr13	115169878	1565263304	13.5909	41.0604
chr14	107349540	1801718304	16.7837	56.5069
chr15	102531392	1926196411	18.7864	51.2522
chr16	90354753	2180818989	24.1362	114.5717
chr17	81195210	2299183785	28.3167	270.7116
chr18	78077248	1518160074	19.4443	297.607
chr19	59128983	1759596590	29.7586	95.0791
chr20	63025520	1639724130	26.0168	73.1658
chr21	48129895	815060793	16.9346	124.5855
chr22	51304566	1131293213	22.0505	81.3296
chrMT	16571	11702555	706.2069	1,980.1419
chrX	155270560	1592980003	10.2594	73.3121

chrY	59373566	354789475	5.9755	96.6758

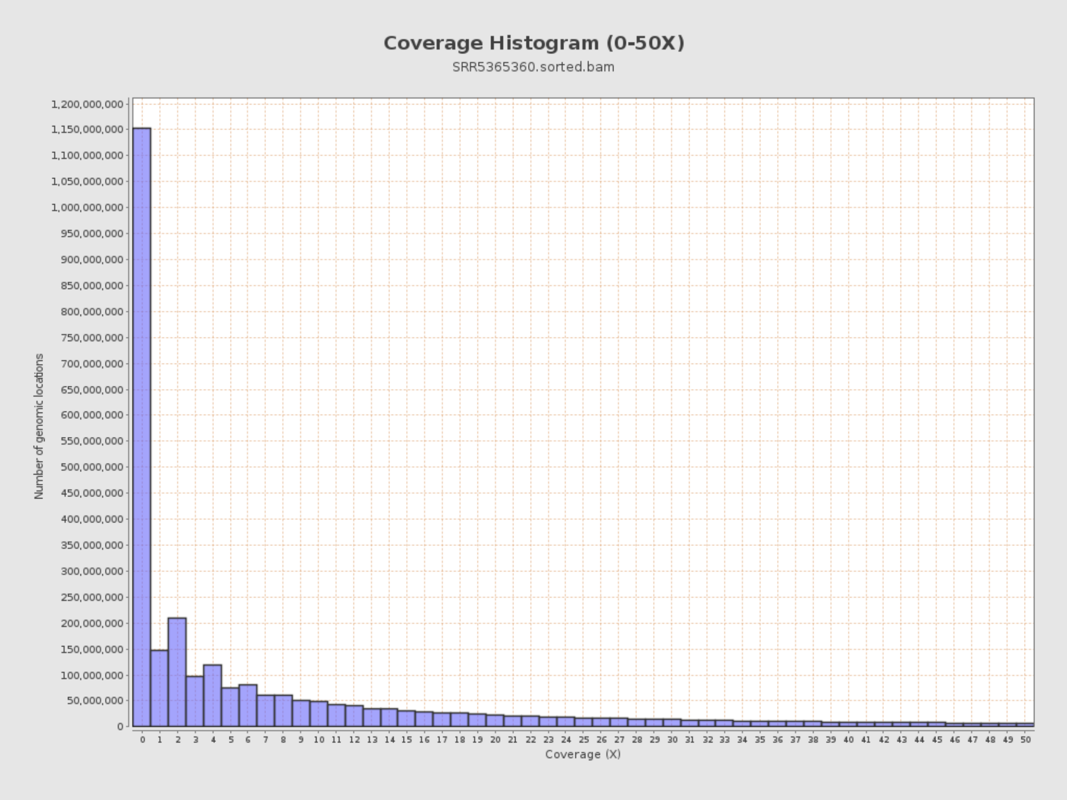
3. Results : Coverage across reference



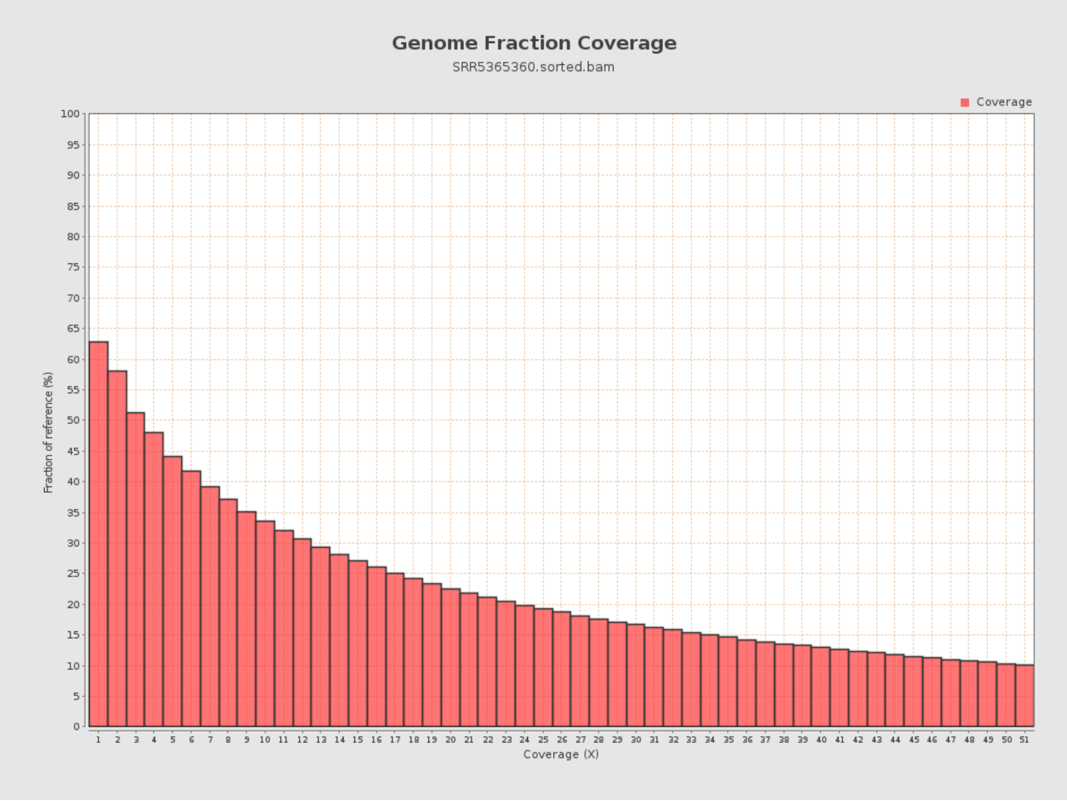
4. Results : Coverage Histogram



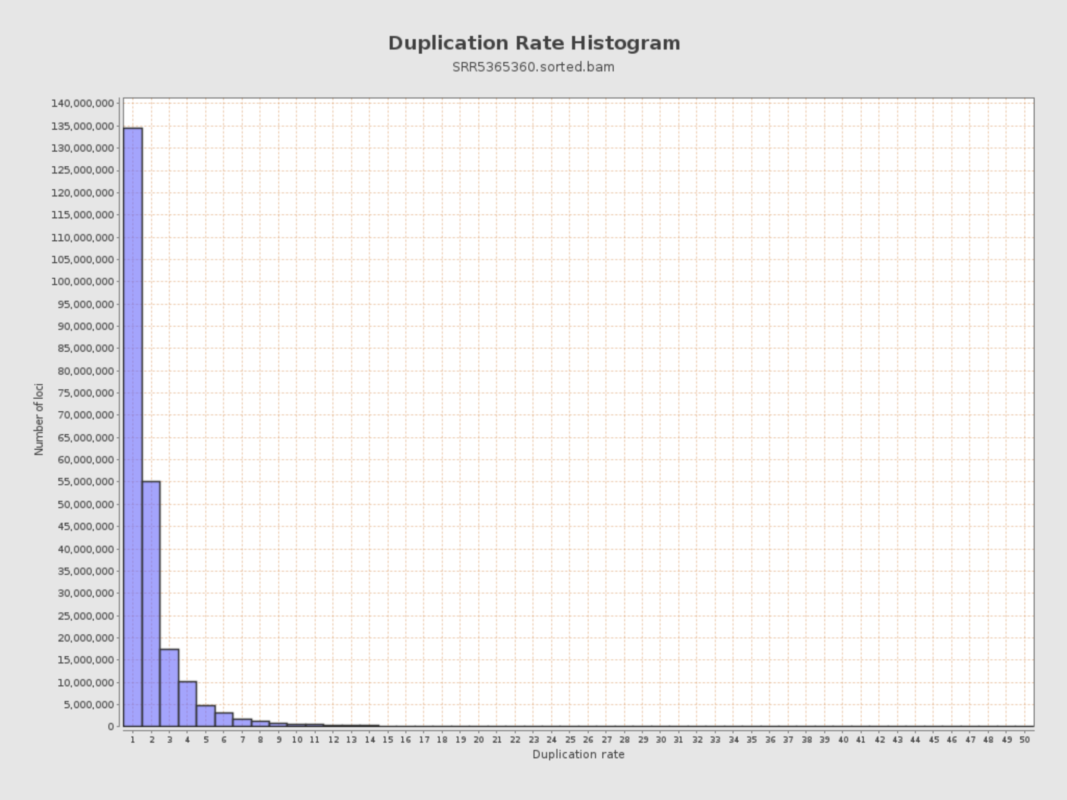
5. Results : Coverage Histogram (0-50X)



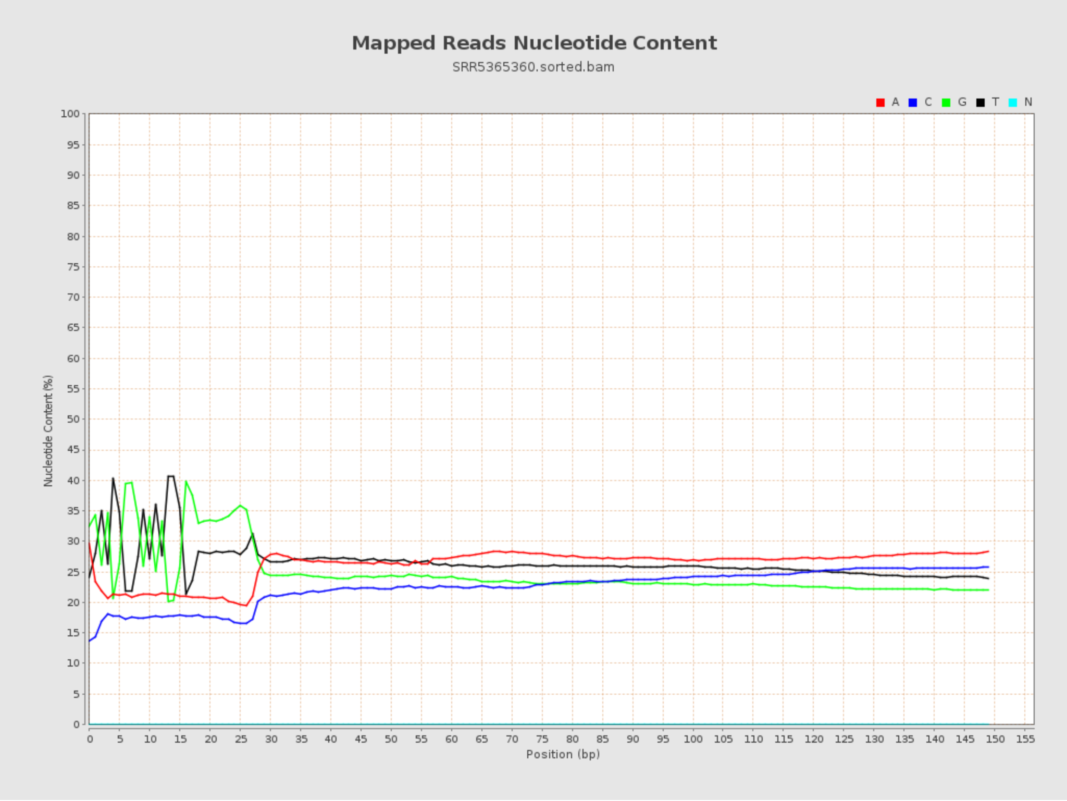
6. Results : Genome Fraction Coverage



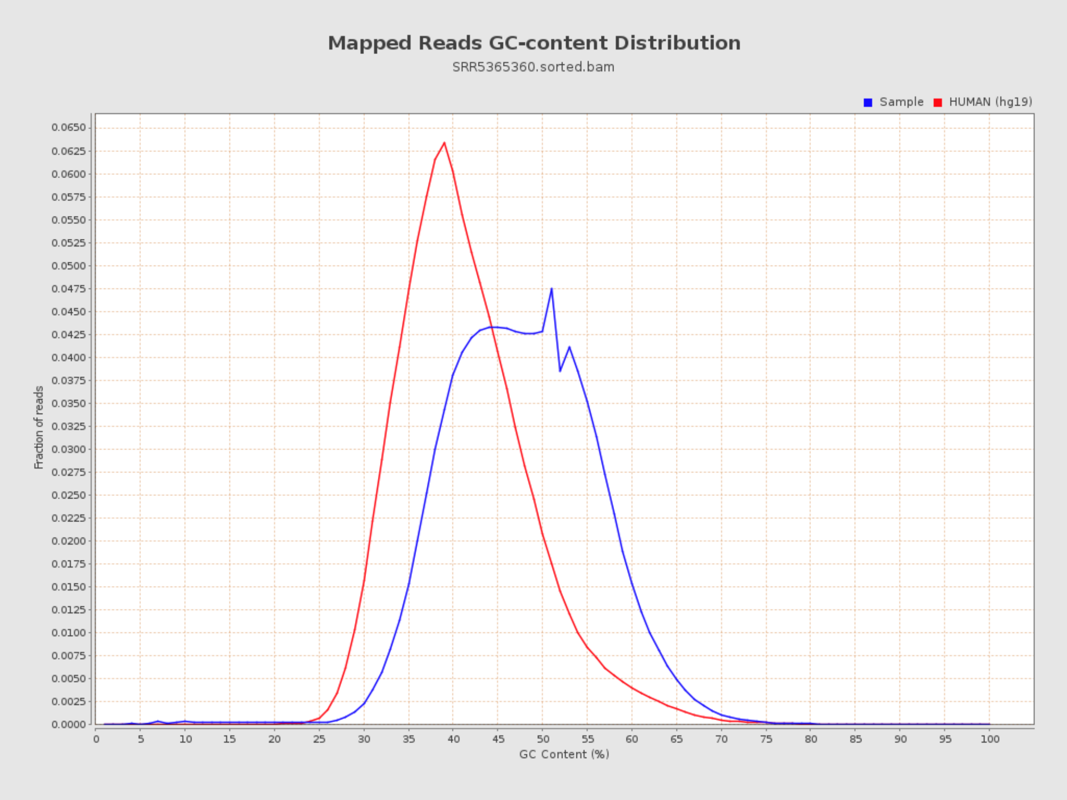
7. Results : Duplication Rate Histogram



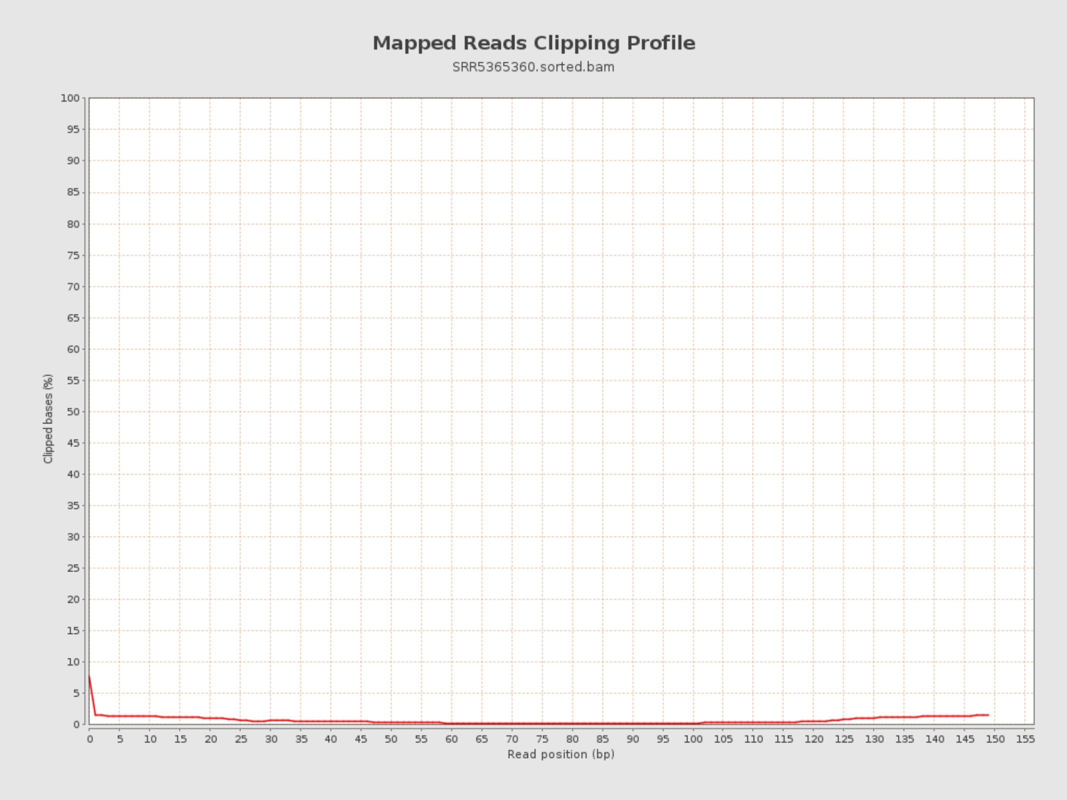
8. Results : Mapped Reads Nucleotide Content



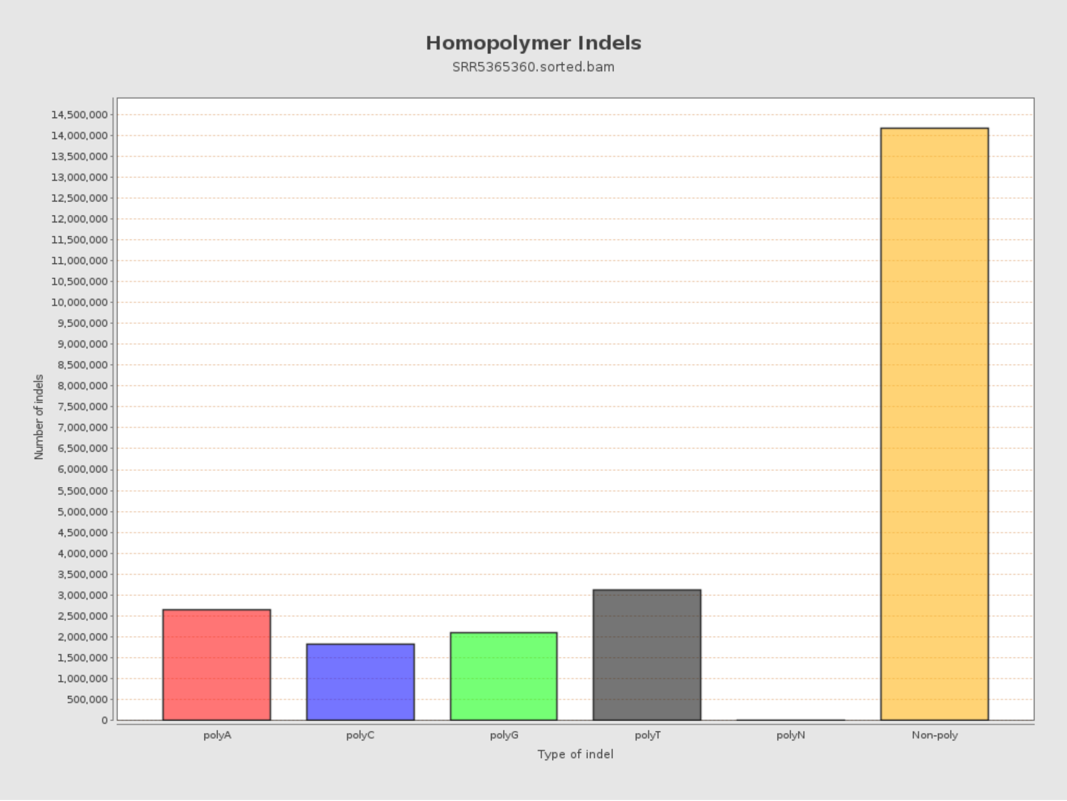
9. Results : Mapped Reads GC-content Distribution



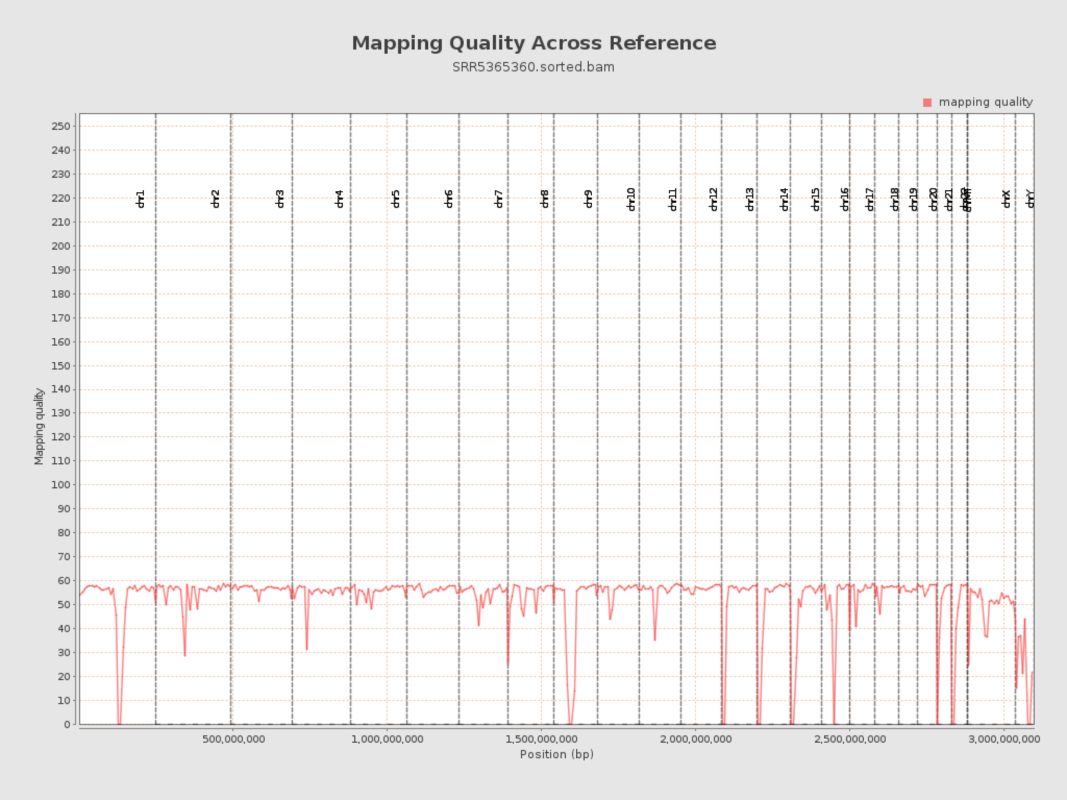
10. Results : Mapped Reads Clipping Profile



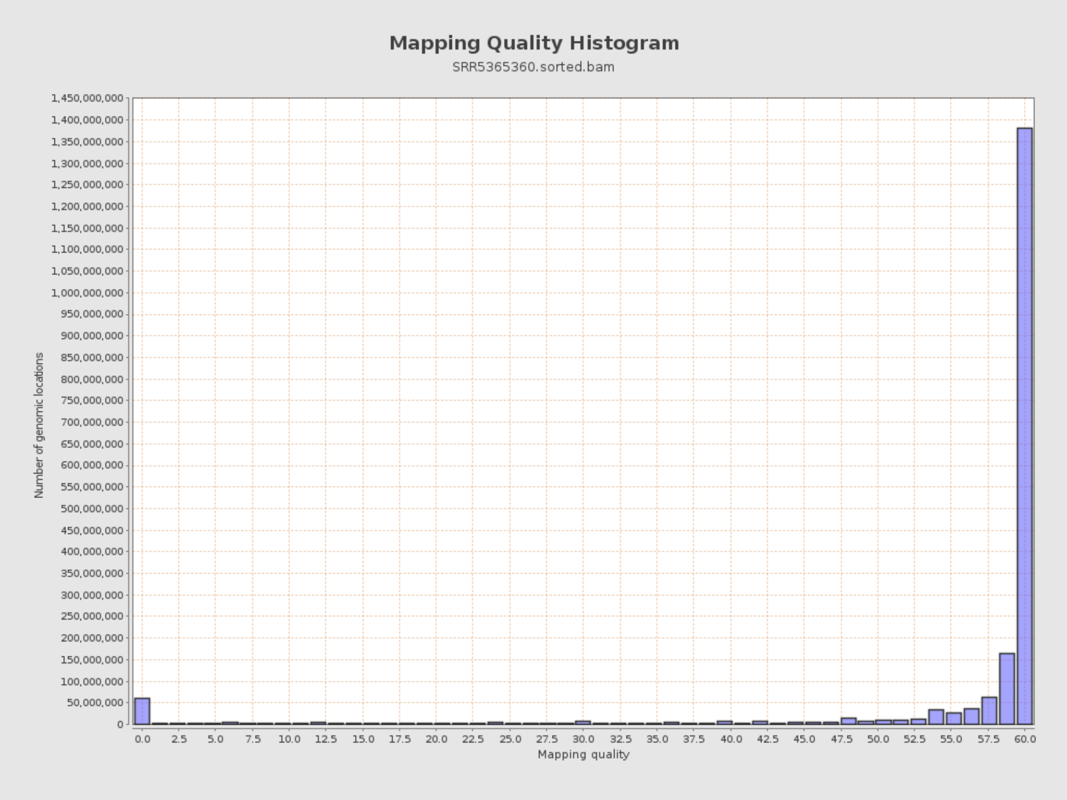
11. Results : Homopolymer Indels



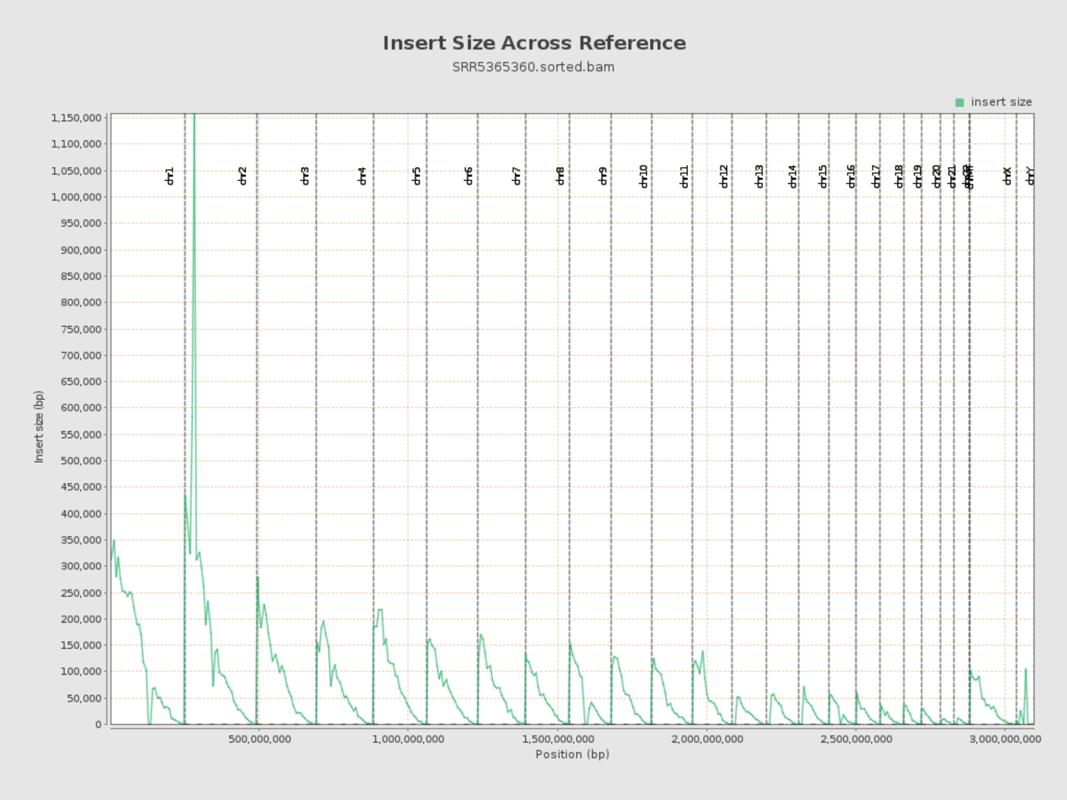
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram