Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 03:51:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174064.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_SRR10174064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174064_1.fastq.gz SRR10174064_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 03:51:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,018,980
Mapped reads	2,955,939 / 97.91%
Unmapped reads	63,041 / 2.09%
Mapped paired reads	2,955,939 / 97.91%
Mapped reads, first in pair	1,478,882 / 48.99%
Mapped reads, second in pair	1,477,057 / 48.93%
Mapped reads, both in pair	2,913,534 / 96.51%
Mapped reads, singletons	42,405 / 1.4%
Secondary alignments	0
Supplementary alignments	274,771 / 9.1%
Read min/max/mean length	30 / 133 / 127.82
Duplicated reads (estimated)	2,258,123 / 74.8%
Duplication rate	65.14%
Clipped reads	1,110,870 / 36.8%

2.2. ACGT Content

Number/percentage of A's	105,736,809 / 30.15%
Number/percentage of C's	68,449,997 / 19.52%
Number/percentage of T's	105,638,297 / 30.12%
Number/percentage of G's	70,837,139 / 20.2%
Number/percentage of N's	4,395 / 0%

GC Percentage	39.72%

2.3. Coverage

Mean	0.1133
Standard Deviation	1.768

2.4. Mapping Quality

Mean Mapping Quality	52.93

2.5. Insert size

Mean	961,313.02
Standard Deviation	9,262,986.51
P25/Median/P75	143 / 195 / 274

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	3,251,893
Insertions	36,054
Mapped reads with at least one insertion	1.18%
Deletions	72,041
Mapped reads with at least one deletion	2.38%
Homopolymer indels	43.54%

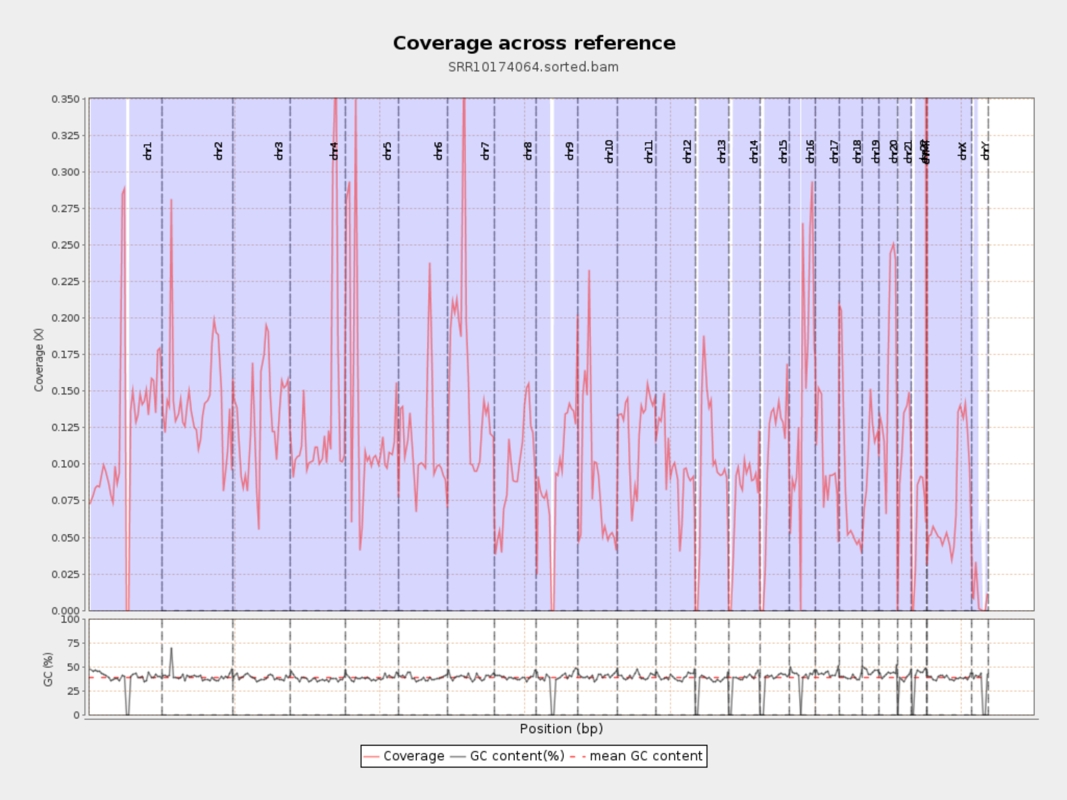
2.7. Chromosome stats

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

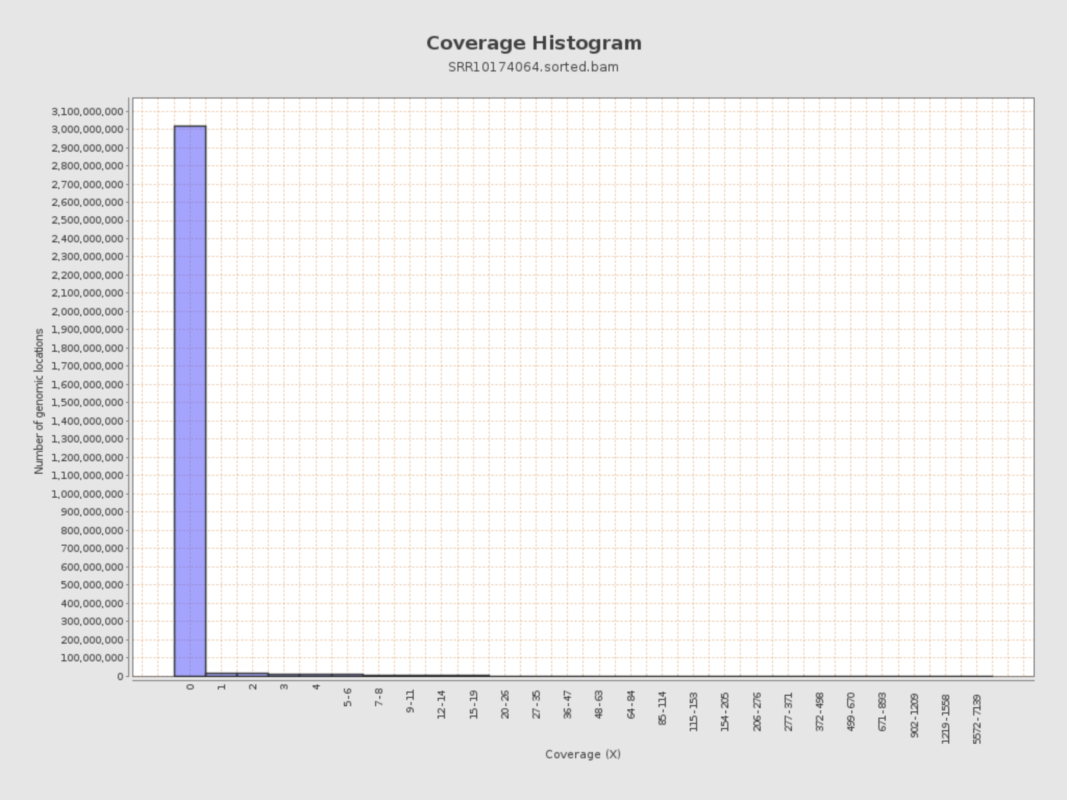
		bases	coverage	deviation
chr1	249250621	30115140	0.1208	1.1623
chr2	243199373	34547720	0.1421	5.0444
chr3	198022430	26030406	0.1315	1.041
chr4	191154276	24734164	0.1294	1.0931
chr5	180915260	24050282	0.1329	1.0547
chr6	171115067	19679297	0.115	0.9777
chr7	159138663	25563804	0.1606	1.6031
chr8	146364022	14016571	0.0958	0.9625
chr9	141213431	13181713	0.0933	0.9513
chr10	135534747	12126542	0.0895	1.51
chr11	135006516	16724658	0.1239	0.9989
chr12	133851895	13087514	0.0978	0.8856
chr13	115169878	11534271	0.1002	0.9148
chr14	107349540	8162931	0.076	0.779
chr15	102531392	10669940	0.1041	0.9064
chr16	90354753	13667353	0.1513	1.3746
chr17	81195210	7960614	0.098	0.9353
chr18	78077248	6547746	0.0839	1.1849
chr19	59128983	6379961	0.1079	1.3457
chr20	63025520	10651485	0.169	1.1615
chr21	48129895	5315768	0.1104	0.9625
chr22	51304566	3001836	0.0585	0.6579
chrMT	16571	1271910	76.7552	63.9682
chrX	155270560	11347087	0.0731	0.7679

chrY	59373566	474480	0.008	0.355

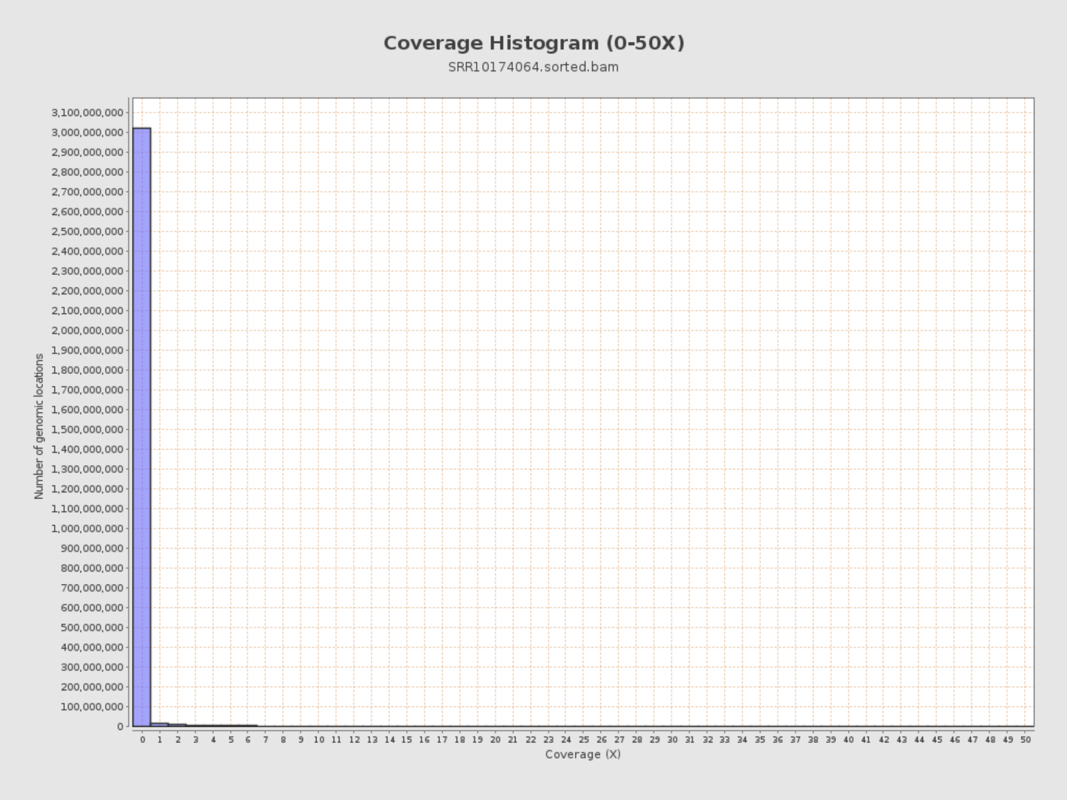
3. Results : Coverage across reference



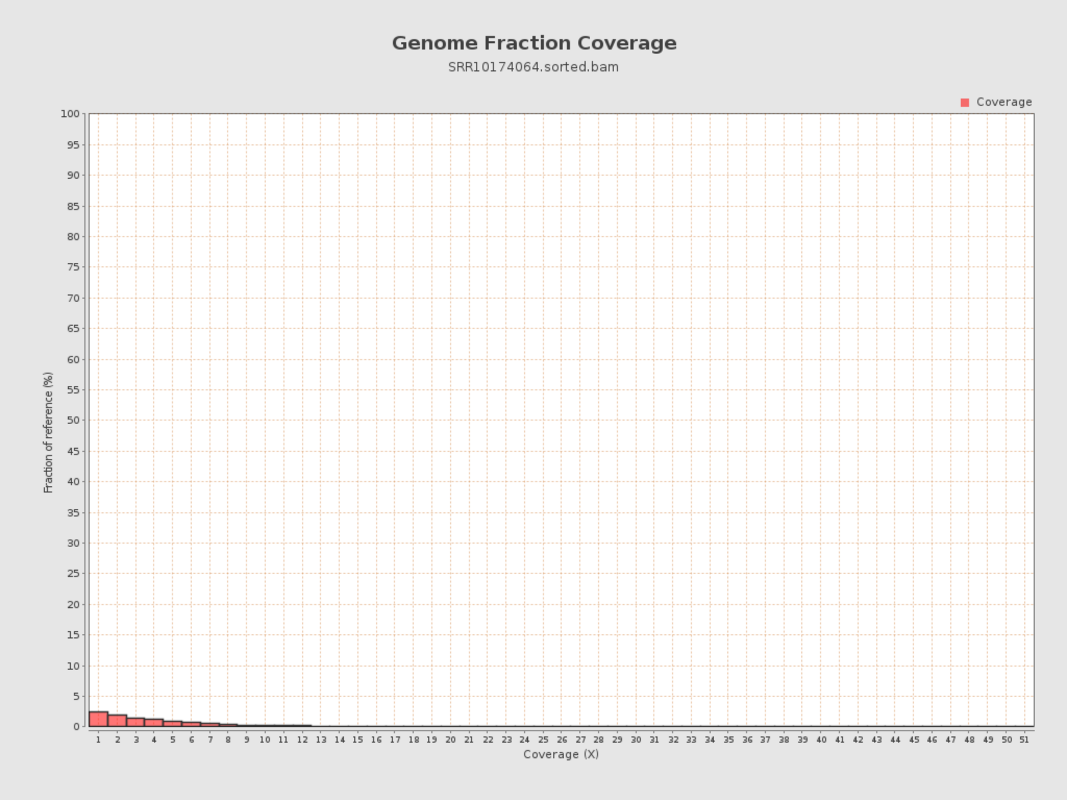
4. Results : Coverage Histogram



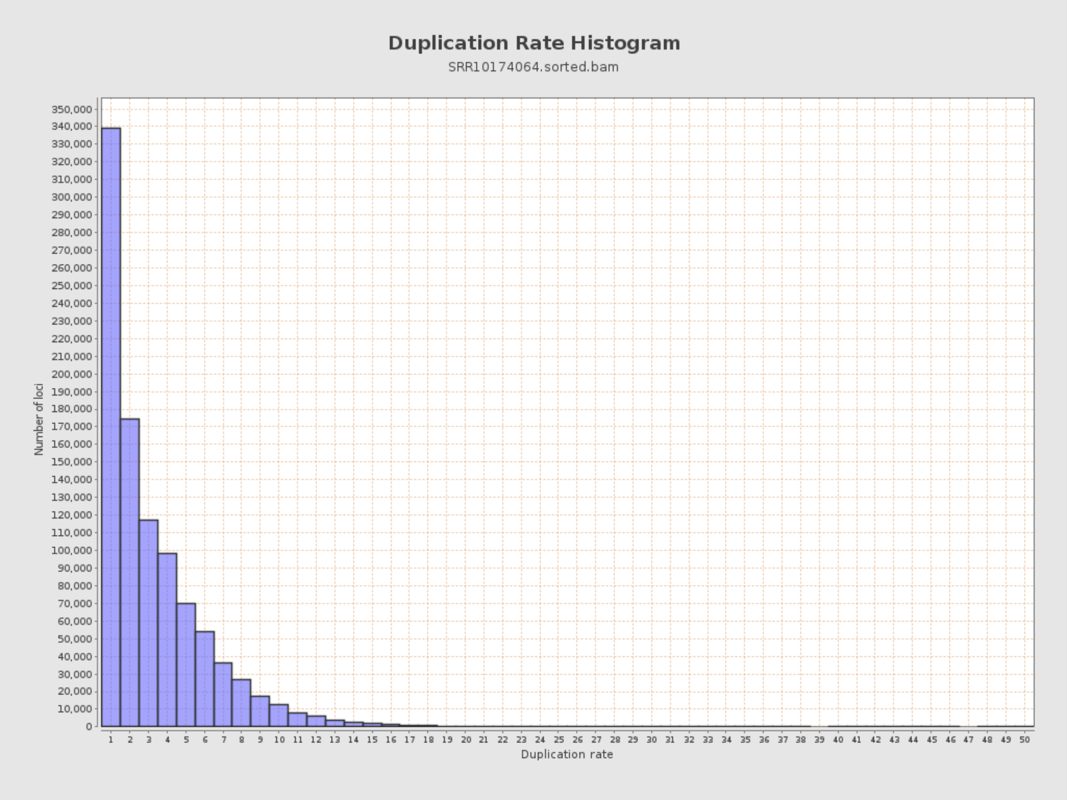
5. Results : Coverage Histogram (0-50X)



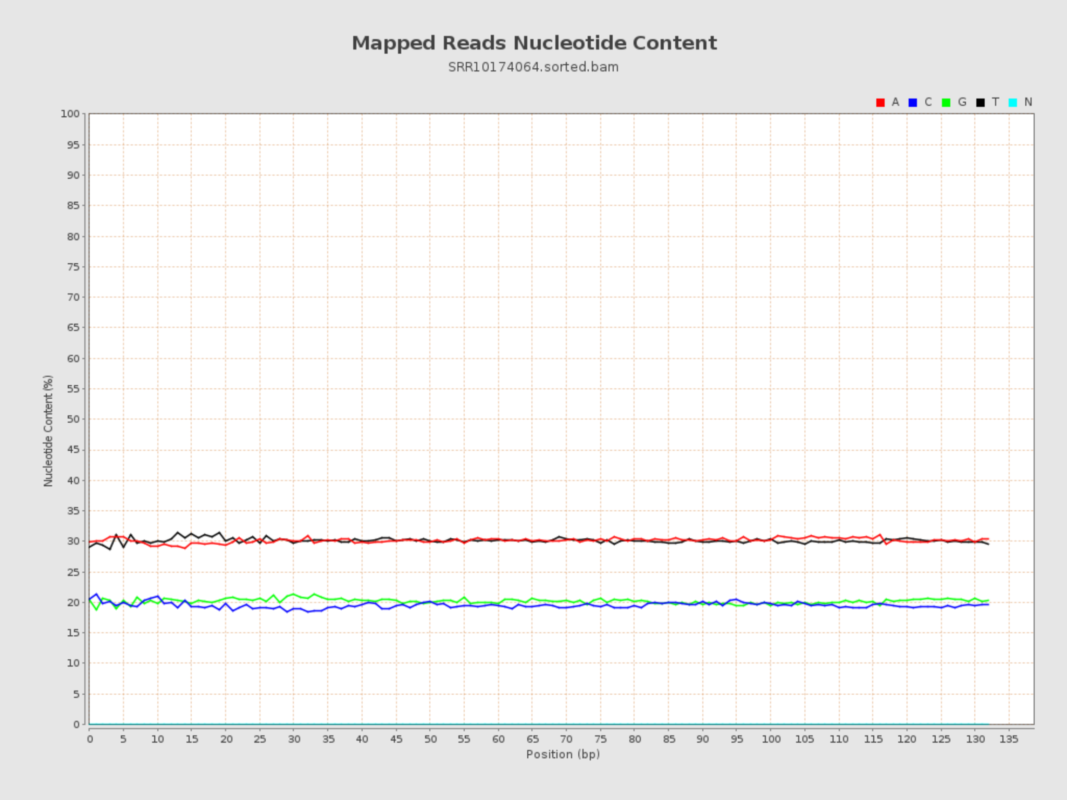
6. Results : Genome Fraction Coverage



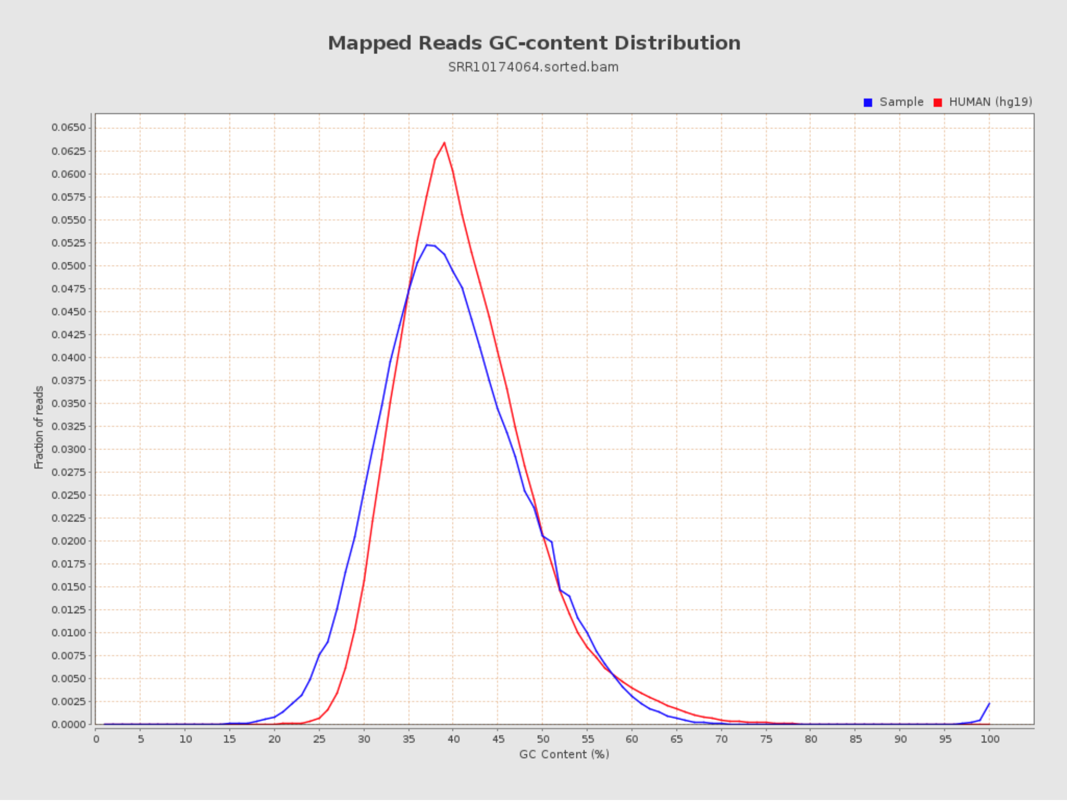
7. Results : Duplication Rate Histogram



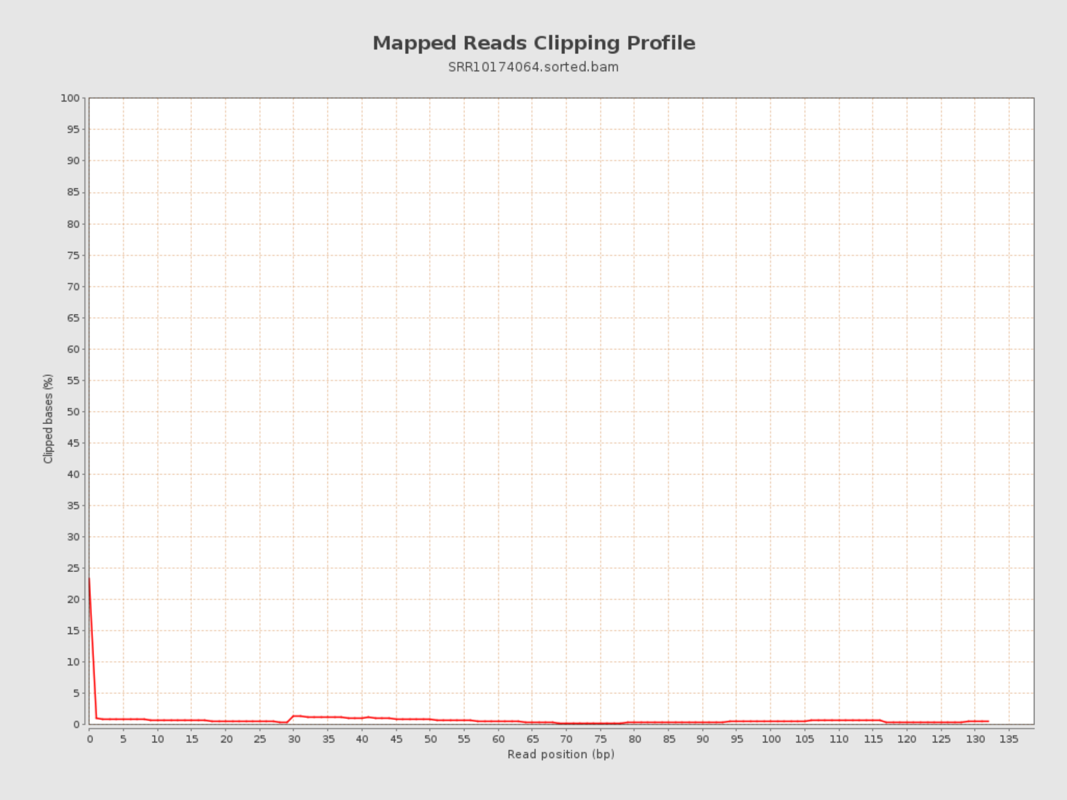
8. Results : Mapped Reads Nucleotide Content



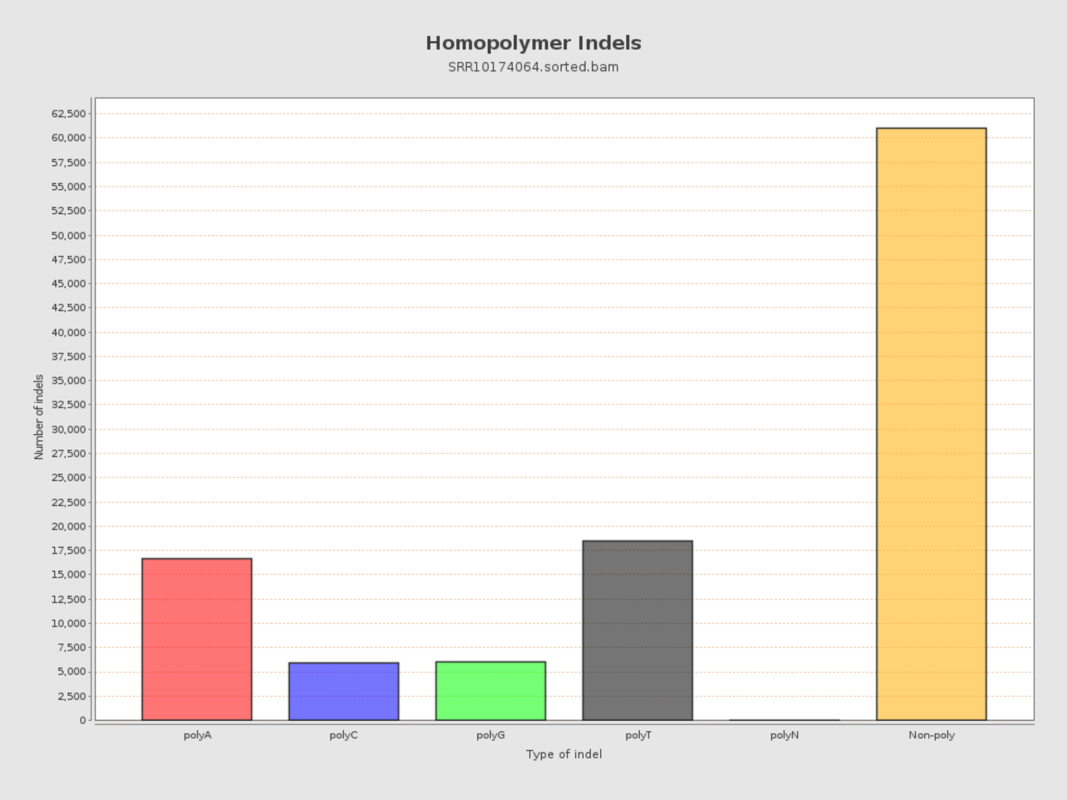
9. Results : Mapped Reads GC-content Distribution



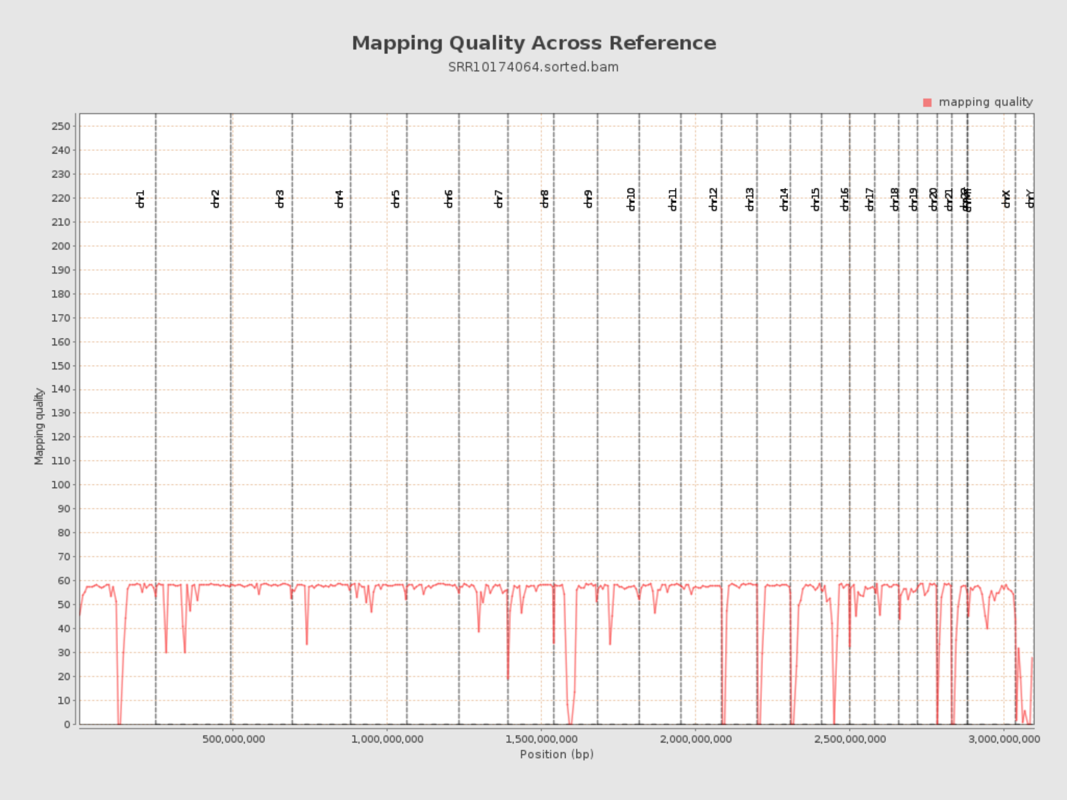
10. Results : Mapped Reads Clipping Profile



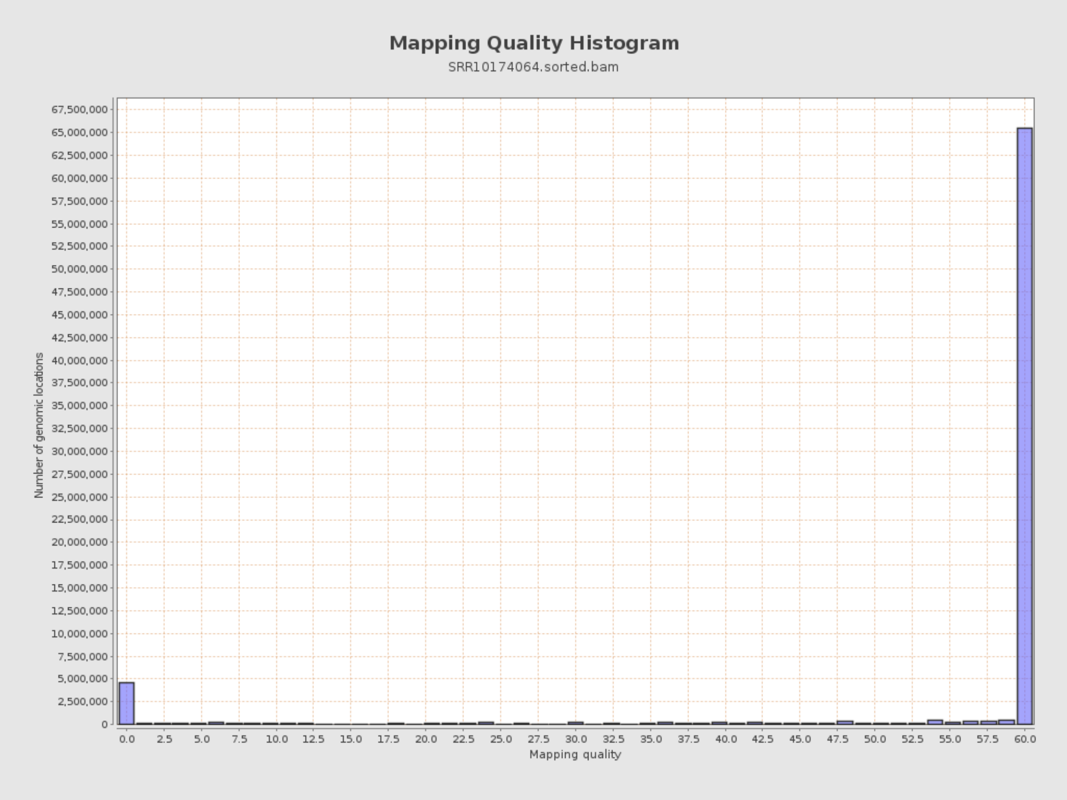
11. Results : Homopolymer Indels



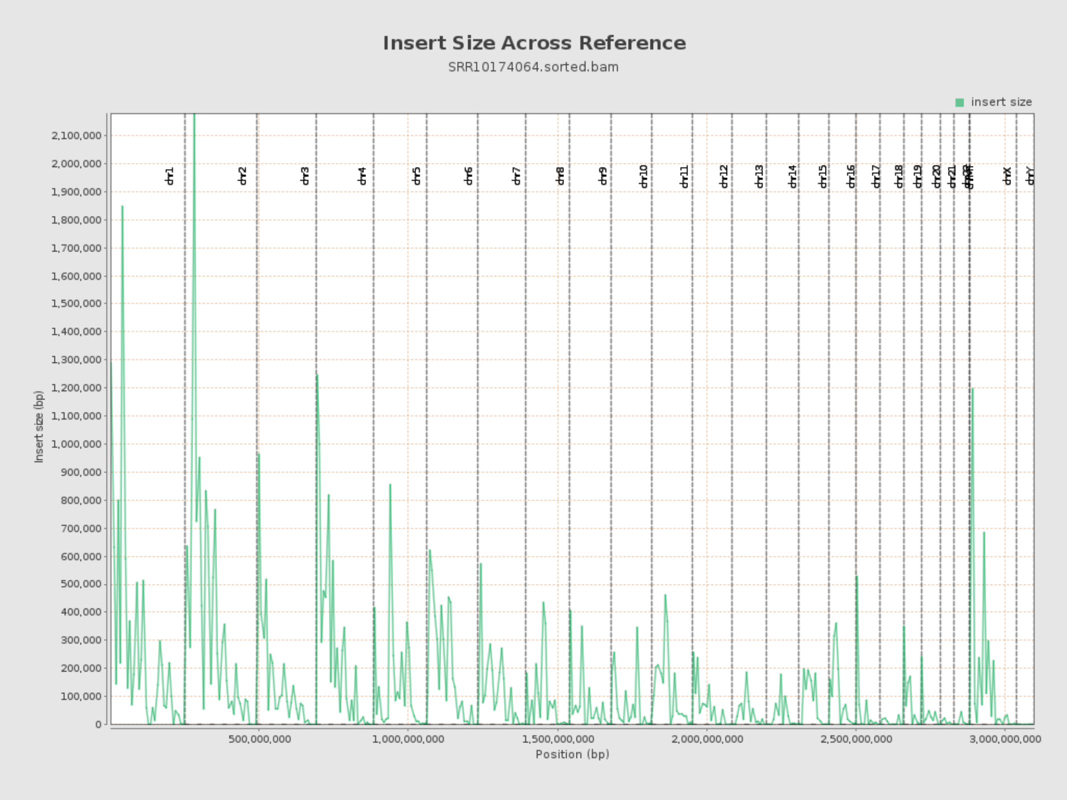
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram