Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 02:43:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174058.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_SRR10174058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174058_1.fastq.gz SRR10174058_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 02:43:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,787,274
Mapped reads	6,595,543 / 97.18%
Unmapped reads	191,731 / 2.82%
Mapped paired reads	6,595,543 / 97.18%
Mapped reads, first in pair	3,302,333 / 48.65%
Mapped reads, second in pair	3,293,210 / 48.52%
Mapped reads, both in pair	6,464,108 / 95.24%
Mapped reads, singletons	131,435 / 1.94%
Secondary alignments	0
Supplementary alignments	667,088 / 9.83%
Read min/max/mean length	30 / 133 / 128.31
Duplicated reads (estimated)	5,246,633 / 77.3%
Duplication rate	65.58%
Clipped reads	2,718,039 / 40.05%

2.2. ACGT Content

Number/percentage of A's	234,402,607 / 30.14%
Number/percentage of C's	151,897,332 / 19.53%
Number/percentage of T's	234,002,190 / 30.09%
Number/percentage of G's	157,436,731 / 20.24%
Number/percentage of N's	9,484 / 0%

GC Percentage	39.77%

2.3. Coverage

Mean	0.2514
Standard Deviation	3.6965

2.4. Mapping Quality

Mean Mapping Quality	52.6

2.5. Insert size

Mean	951,464.98
Standard Deviation	8,636,345.86
P25/Median/P75	146 / 204 / 294

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	7,874,112
Insertions	82,499
Mapped reads with at least one insertion	1.21%
Deletions	180,241
Mapped reads with at least one deletion	2.67%
Homopolymer indels	42.46%

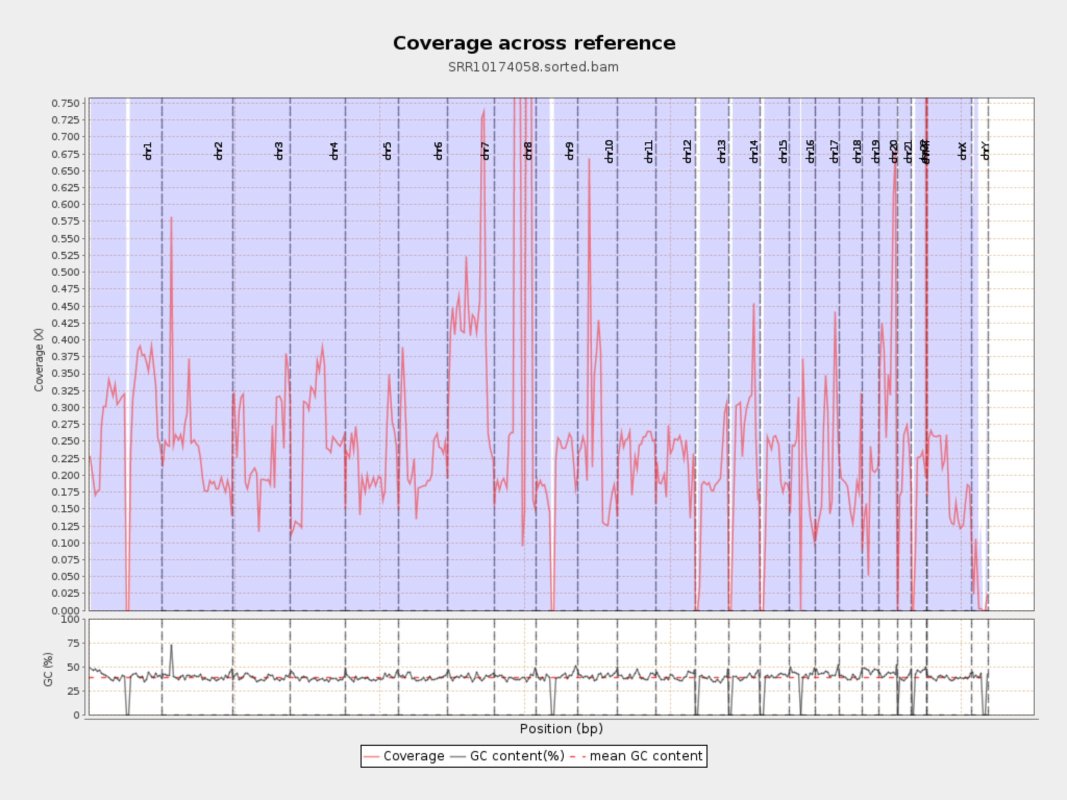
2.7. Chromosome stats

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

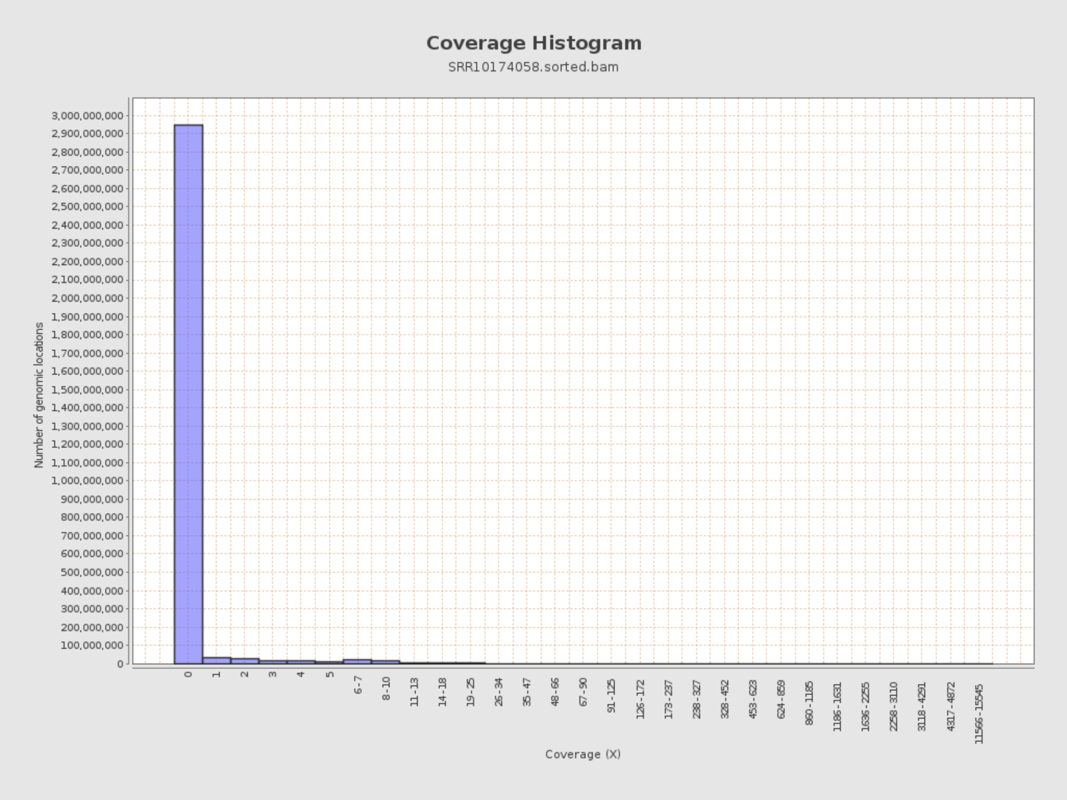
		bases	coverage	deviation
chr1	249250621	71085817	0.2852	2.0434
chr2	243199373	57264104	0.2355	10.866
chr3	198022430	48767164	0.2463	1.497
chr4	191154276	48606063	0.2543	1.9857
chr5	180915260	39870394	0.2204	1.4027
chr6	171115067	38135470	0.2229	1.4814
chr7	159138663	68729338	0.4319	4.0306
chr8	146364022	77690274	0.5308	2.9047
chr9	141213431	26989507	0.1911	1.7062
chr10	135534747	35284235	0.2603	4.7663
chr11	135006516	32576237	0.2413	1.5188
chr12	133851895	29665210	0.2216	1.4085
chr13	115169878	20132983	0.1748	1.2574
chr14	107349540	26106495	0.2432	1.4852
chr15	102531392	18658060	0.182	1.2718
chr16	90354753	17814084	0.1972	1.897
chr17	81195210	19267577	0.2373	1.5518
chr18	78077248	14379085	0.1842	2.2304
chr19	59128983	10126216	0.1713	1.5123
chr20	63025520	26030991	0.413	1.9598
chr21	48129895	9574950	0.1989	1.4598
chr22	51304566	8029242	0.1565	1.1403
chrMT	16571	1846749	111.4446	83.0028
chrX	155270560	30021383	0.1933	1.3147

chrY	59373566	1539149	0.0259	1.128

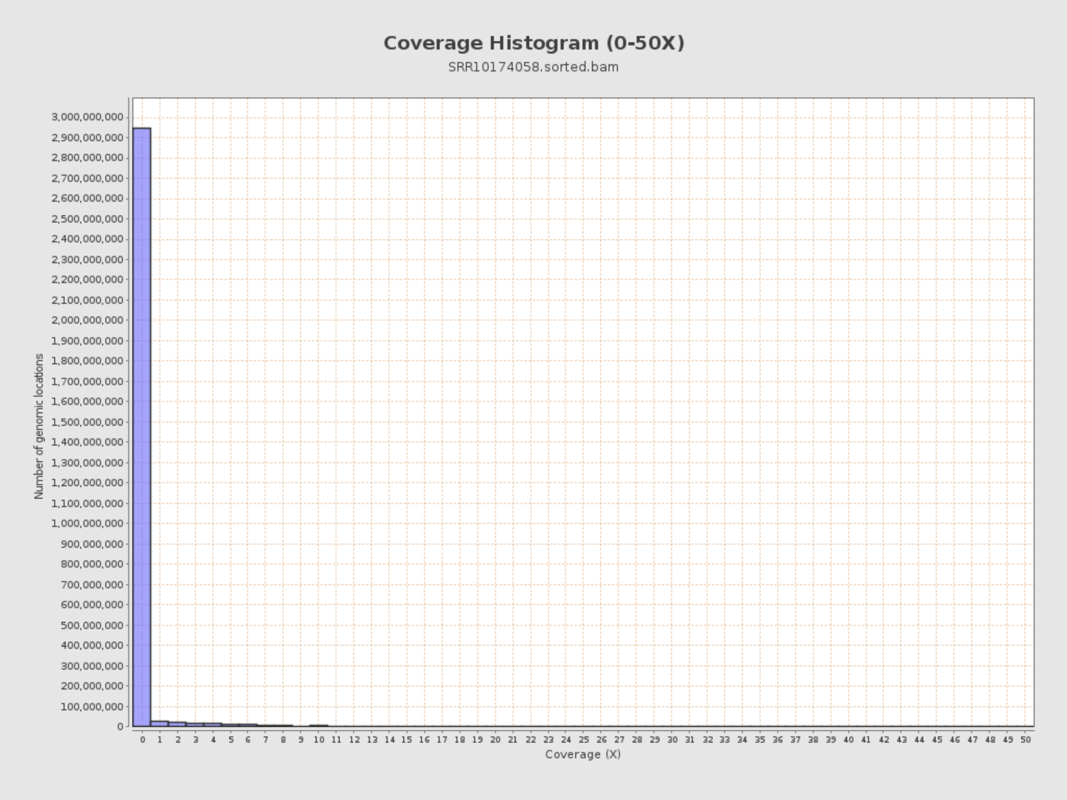
3. Results : Coverage across reference



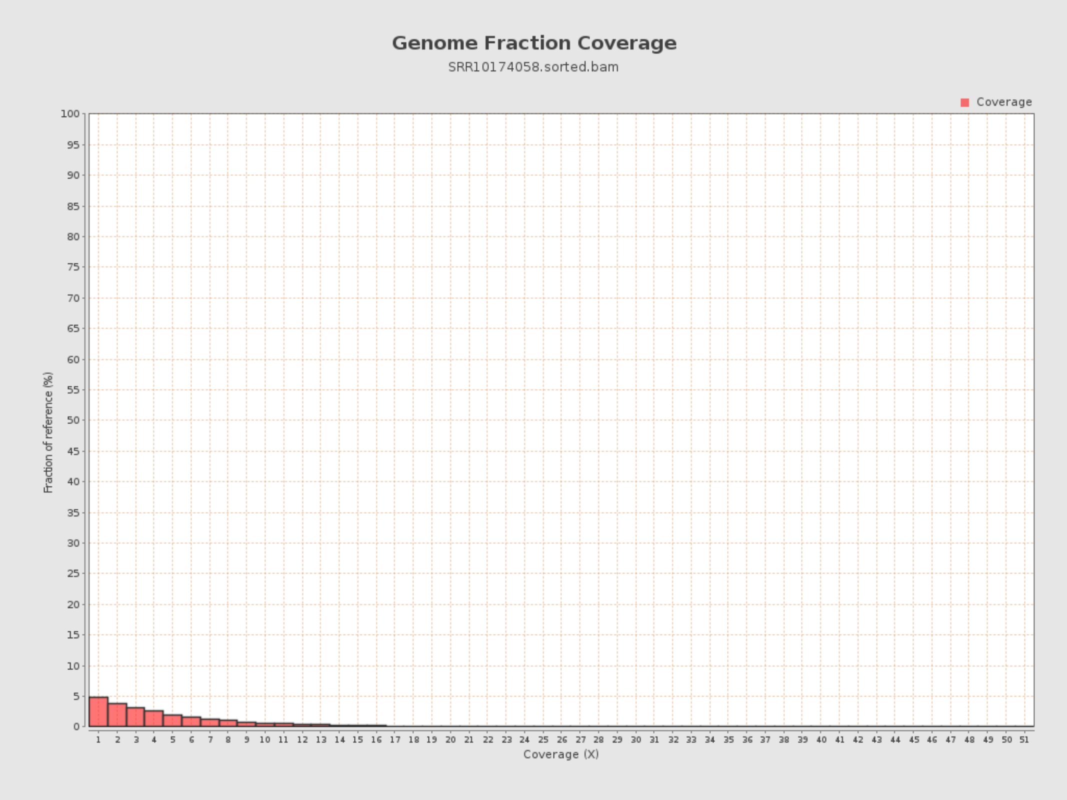
4. Results : Coverage Histogram



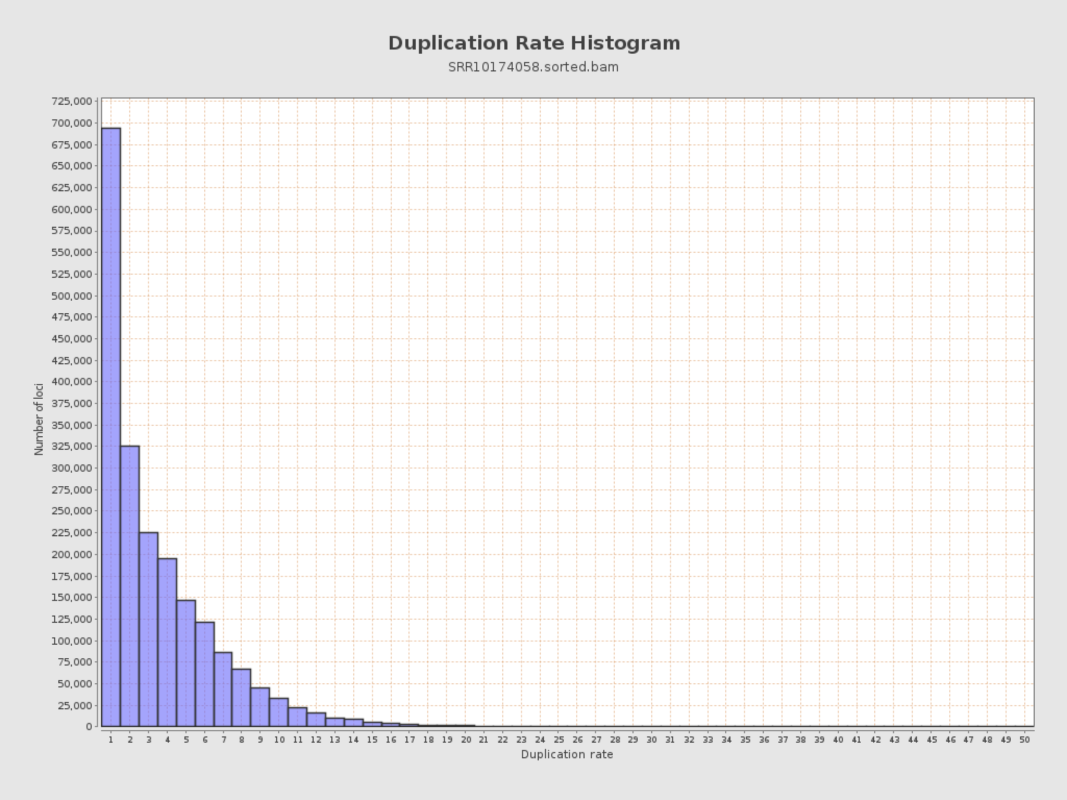
5. Results : Coverage Histogram (0-50X)



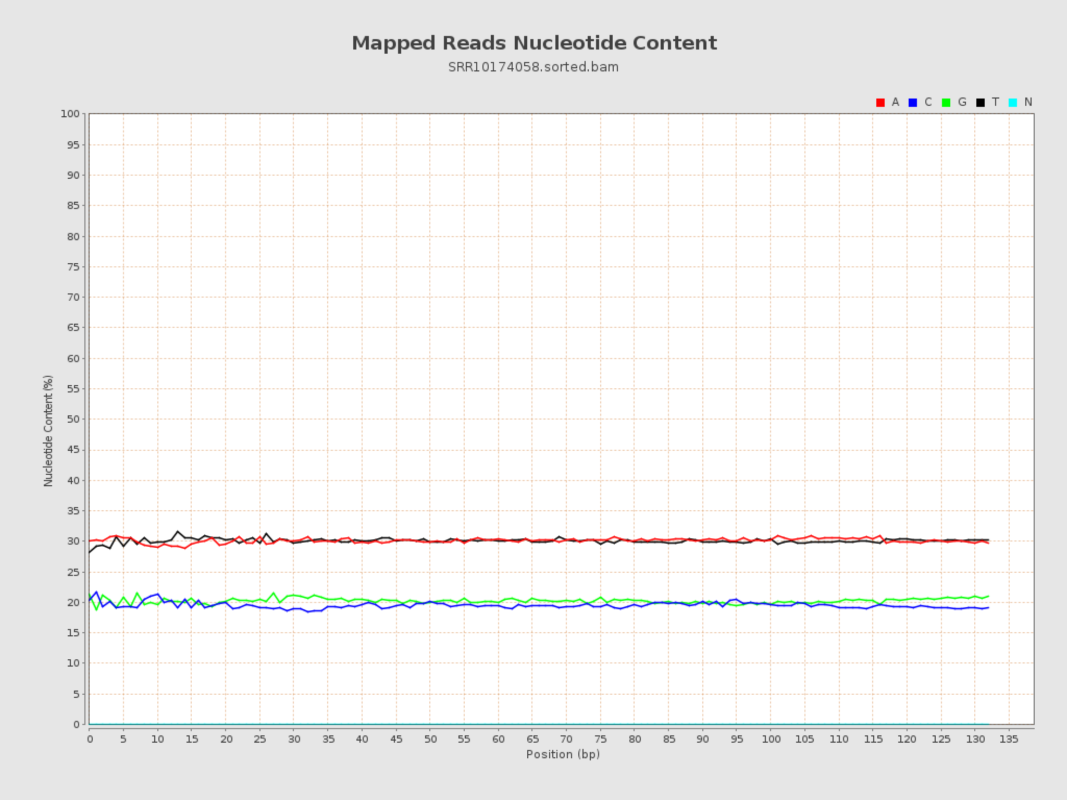
6. Results : Genome Fraction Coverage



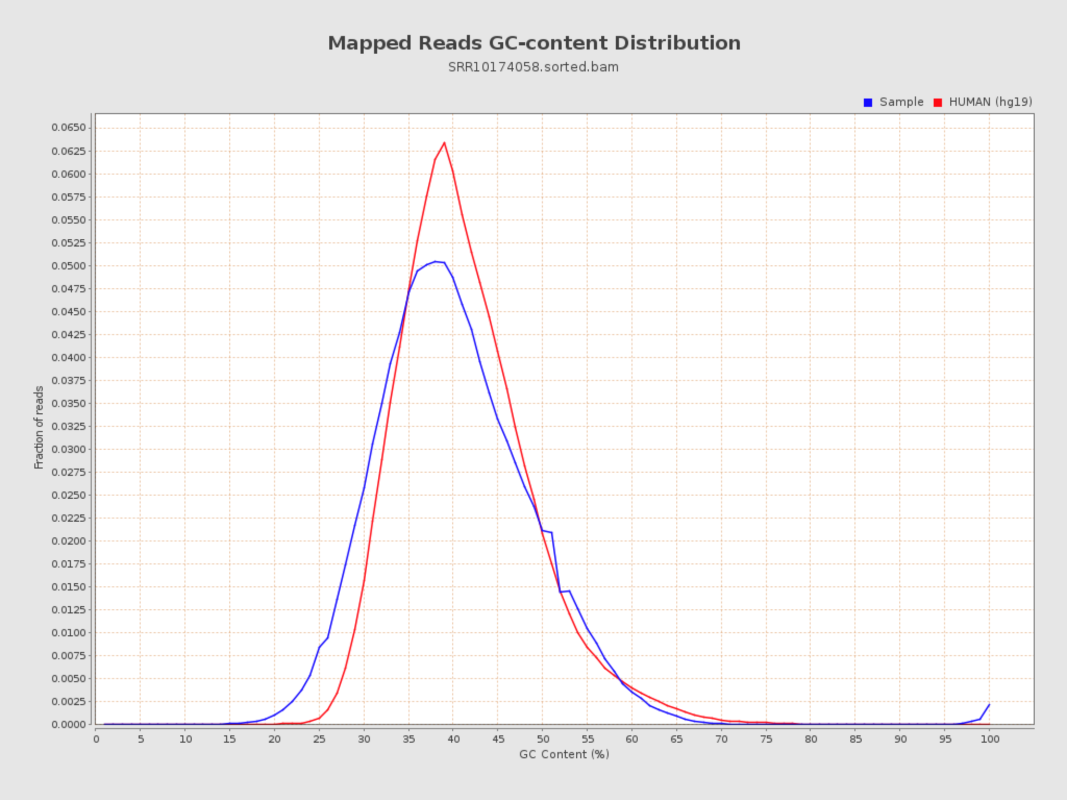
7. Results : Duplication Rate Histogram



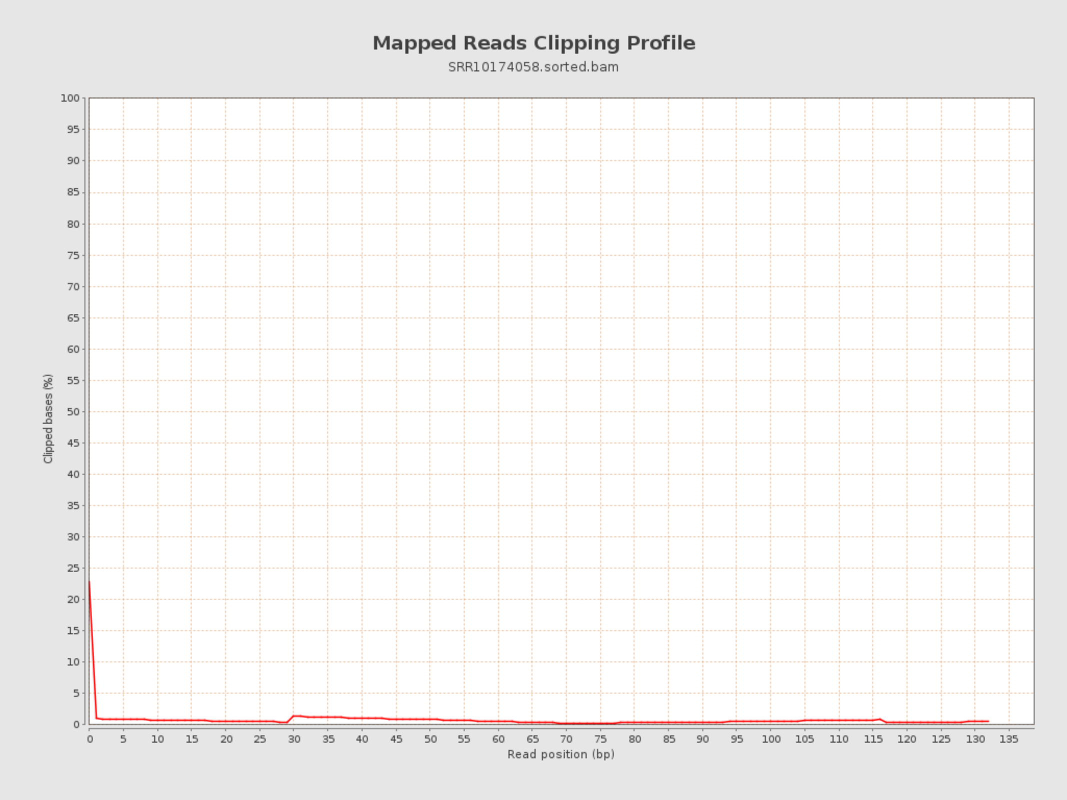
8. Results : Mapped Reads Nucleotide Content



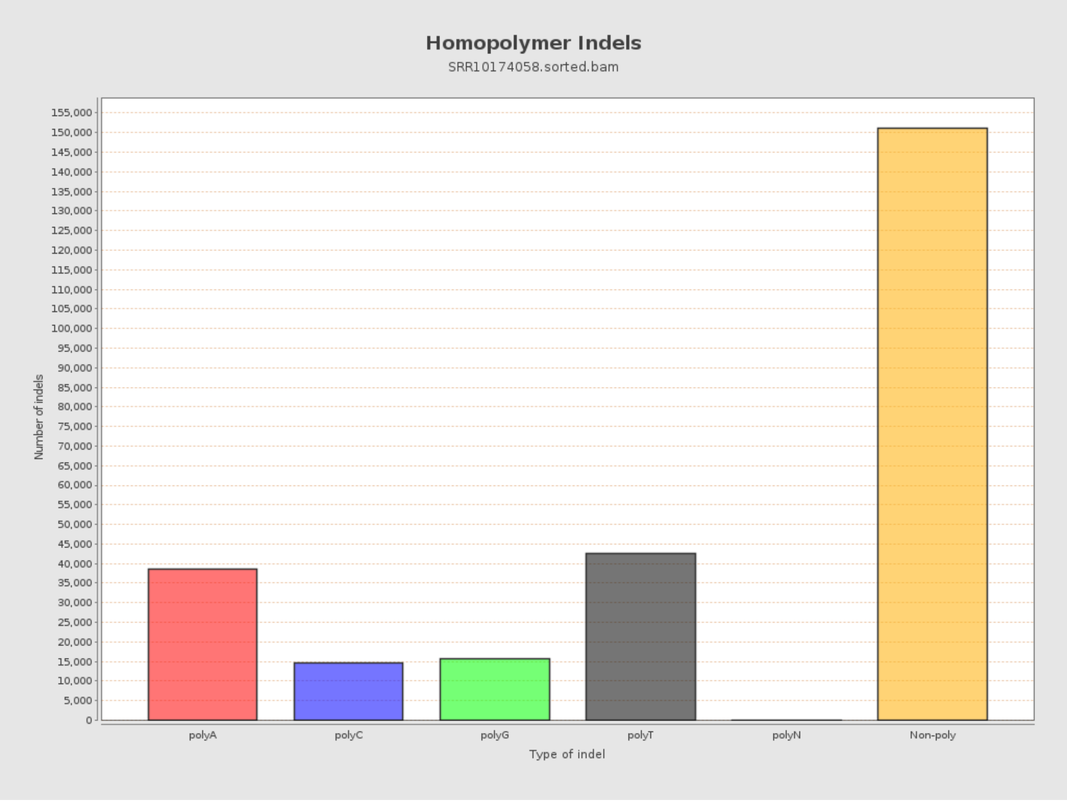
9. Results : Mapped Reads GC-content Distribution



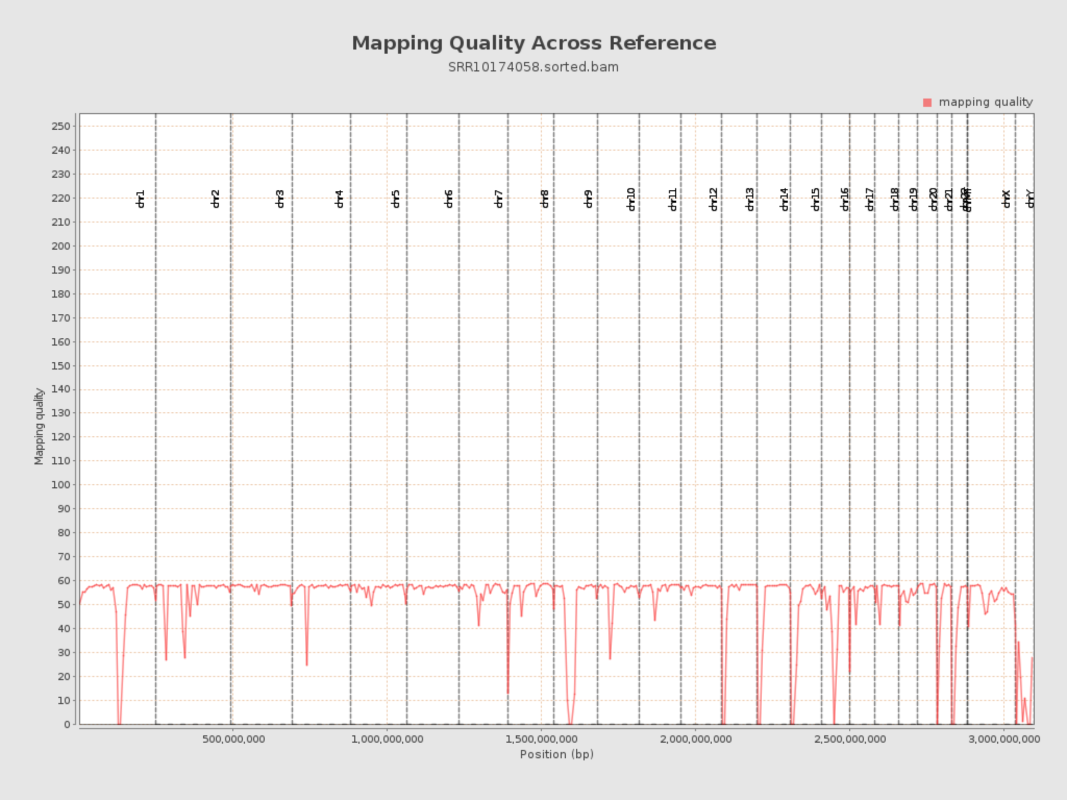
10. Results : Mapped Reads Clipping Profile



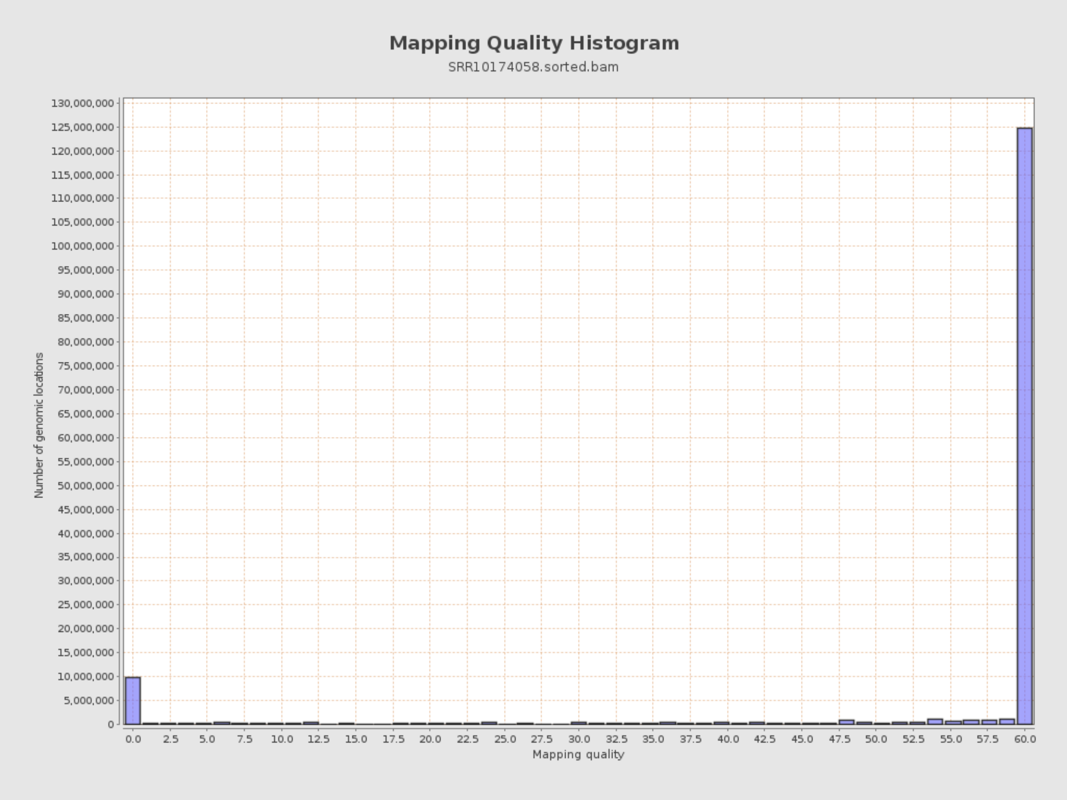
11. Results : Homopolymer Indels



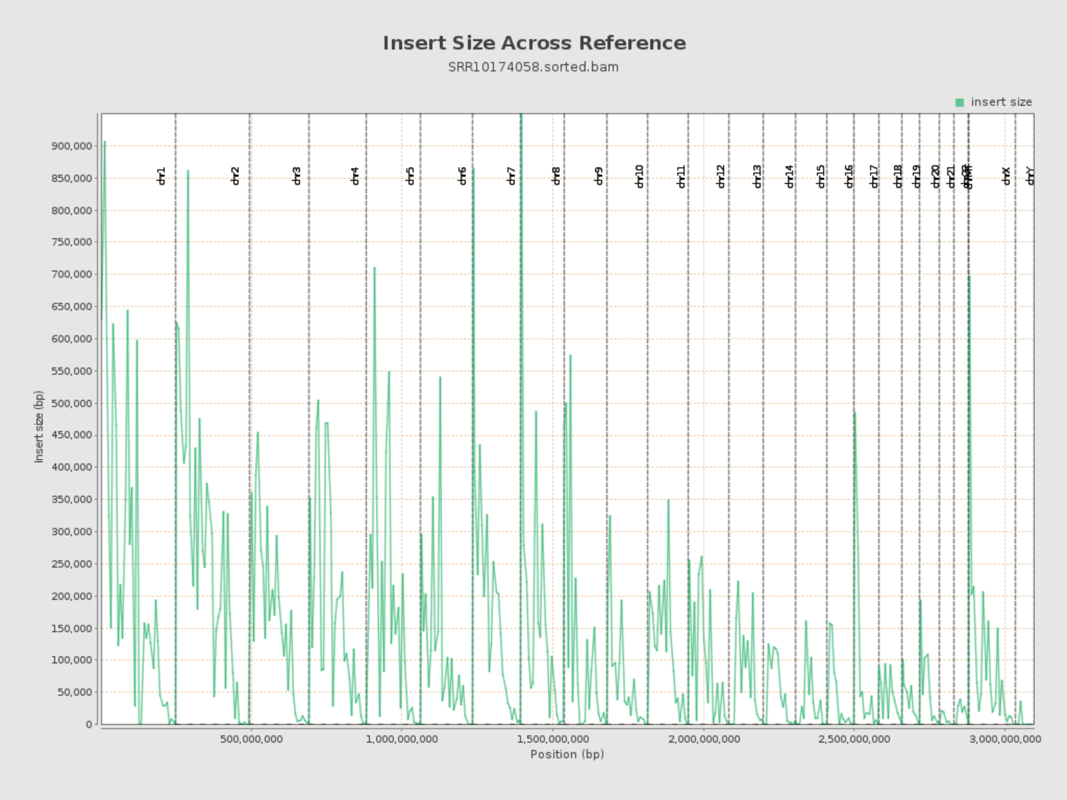
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram