Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 20:07:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174006.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_SRR10174006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174006_1.fastq.gz SRR10174006_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 20:07:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,301,944
Mapped reads	6,158,444 / 97.72%
Unmapped reads	143,500 / 2.28%
Mapped paired reads	6,158,444 / 97.72%
Mapped reads, first in pair	3,081,758 / 48.9%
Mapped reads, second in pair	3,076,686 / 48.82%
Mapped reads, both in pair	6,067,494 / 96.28%
Mapped reads, singletons	90,950 / 1.44%
Secondary alignments	0
Supplementary alignments	538,149 / 8.54%
Read min/max/mean length	30 / 133 / 127.25
Duplicated reads (estimated)	4,753,725 / 75.43%
Duplication rate	66.37%
Clipped reads	2,257,042 / 35.82%

2.2. ACGT Content

Number/percentage of A's	219,551,173 / 30.12%
Number/percentage of C's	142,675,527 / 19.57%
Number/percentage of T's	219,053,011 / 30.05%
Number/percentage of G's	147,680,622 / 20.26%
Number/percentage of N's	9,055 / 0%

GC Percentage	39.83%

2.3. Coverage

Mean	0.2356
Standard Deviation	3.2751

2.4. Mapping Quality

Mean Mapping Quality	53.06

2.5. Insert size

Mean	696,889.69
Standard Deviation	7,837,285.51
P25/Median/P75	141 / 196 / 279

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	7,420,567
Insertions	73,267
Mapped reads with at least one insertion	1.15%
Deletions	199,100
Mapped reads with at least one deletion	3.16%
Homopolymer indels	42.02%

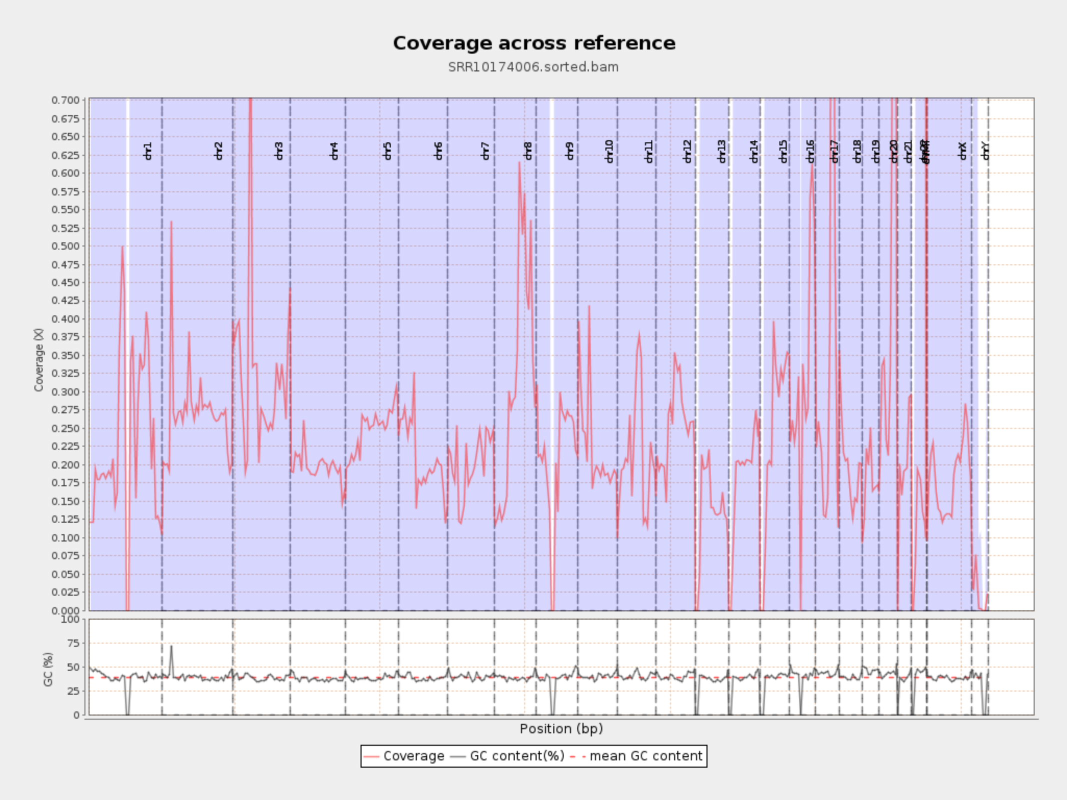
2.7. Chromosome stats

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

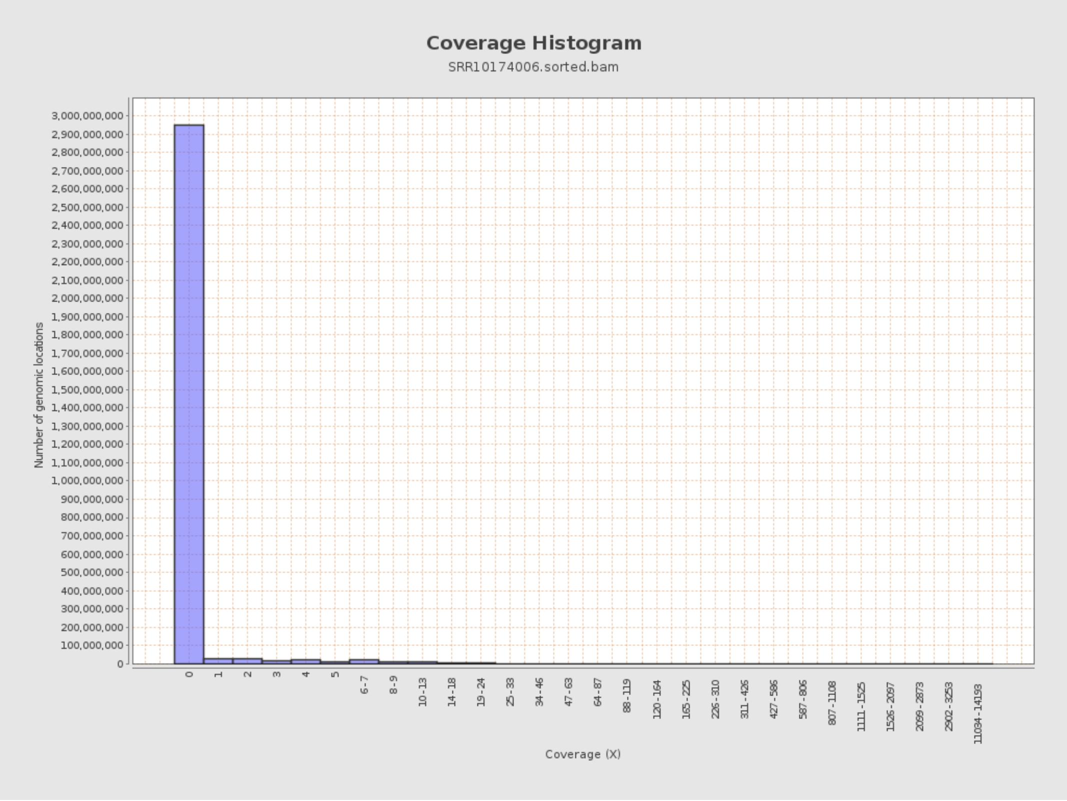
		bases	coverage	deviation
chr1	249250621	56938986	0.2284	2.3493
chr2	243199373	65927191	0.2711	9.9654
chr3	198022430	63655022	0.3215	1.6727
chr4	191154276	37597496	0.1967	1.4321
chr5	180915260	44909597	0.2482	1.4416
chr6	171115067	35784461	0.2091	1.6829
chr7	159138663	32180521	0.2022	1.7746
chr8	146364022	46424991	0.3172	2.1412
chr9	141213431	28667768	0.203	1.6444
chr10	135534747	30512760	0.2251	2.7448
chr11	135006516	29109121	0.2156	1.3952
chr12	133851895	34178006	0.2553	1.4641
chr13	115169878	15507632	0.1347	1.0627
chr14	107349540	19356535	0.1803	1.2241
chr15	102531392	24649267	0.2404	1.4208
chr16	90354753	29630775	0.3279	2.0723
chr17	81195210	29315728	0.3611	1.9695
chr18	78077248	15373978	0.1969	2.2906
chr19	59128983	10699750	0.181	1.818
chr20	63025520	33392088	0.5298	2.34
chr21	48129895	9490606	0.1972	1.3285
chr22	51304566	5576431	0.1087	0.9027
chrMT	16571	1297104	78.2755	70.2947
chrX	155270560	28061734	0.1807	1.2358

chrY	59373566	1201860	0.0202	0.7371

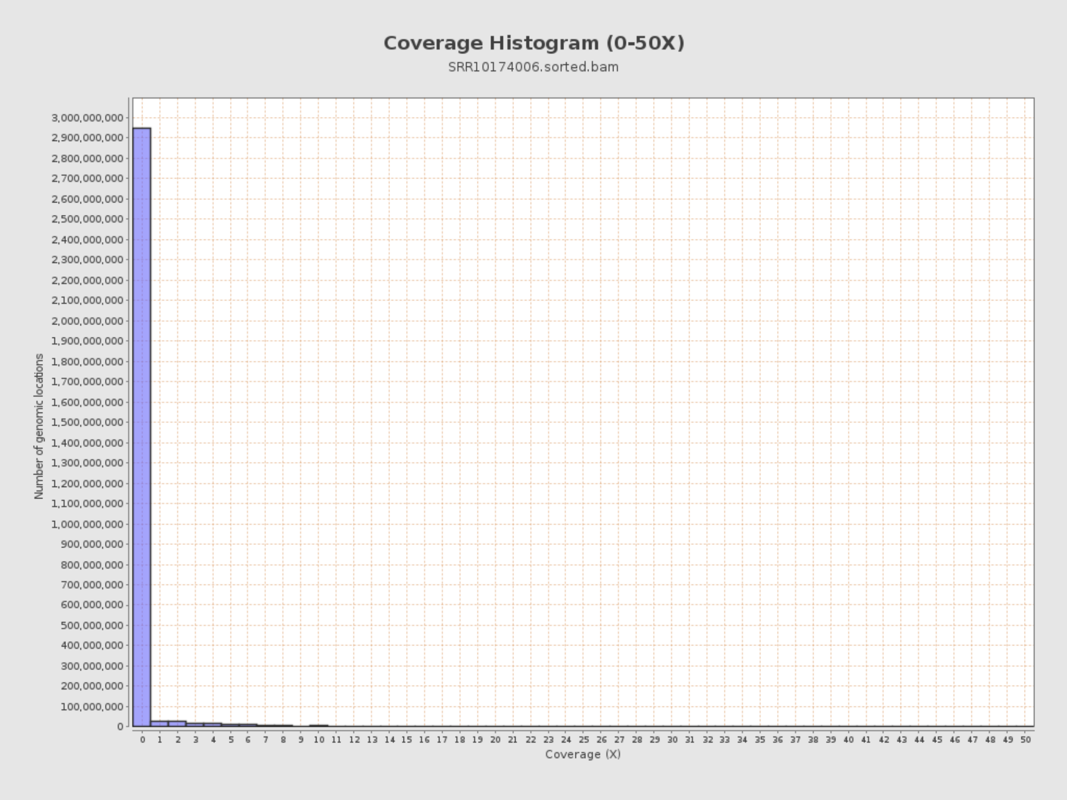
3. Results : Coverage across reference



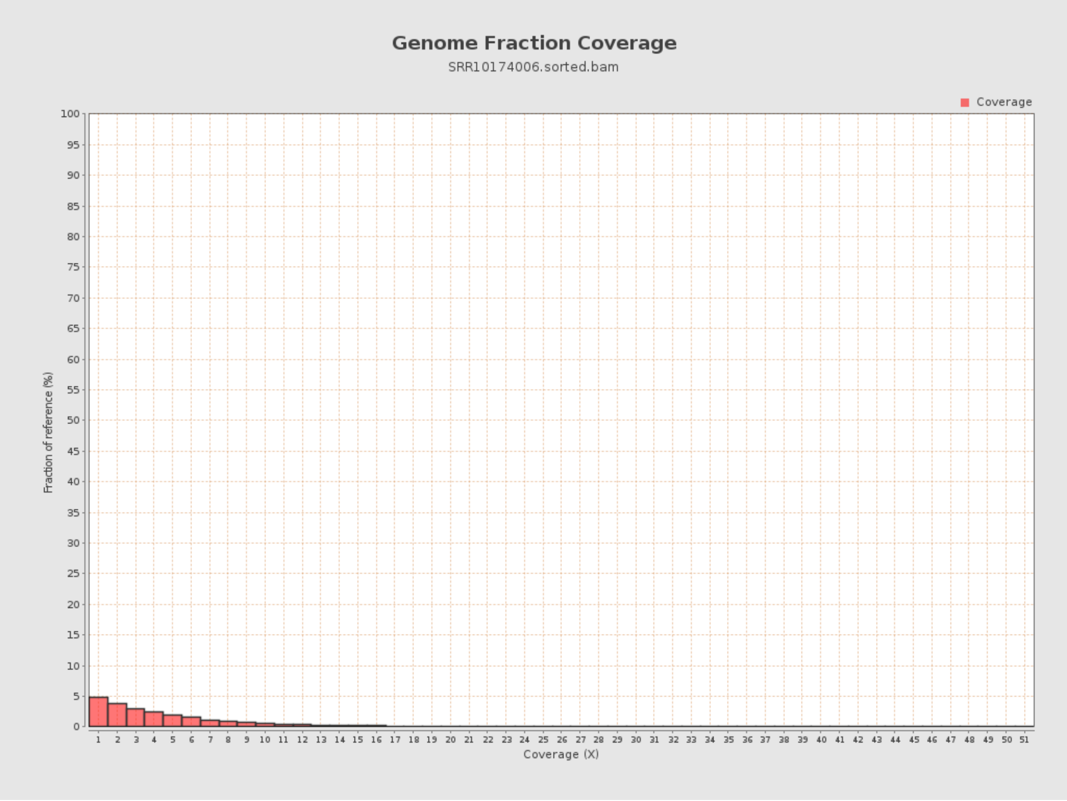
4. Results : Coverage Histogram



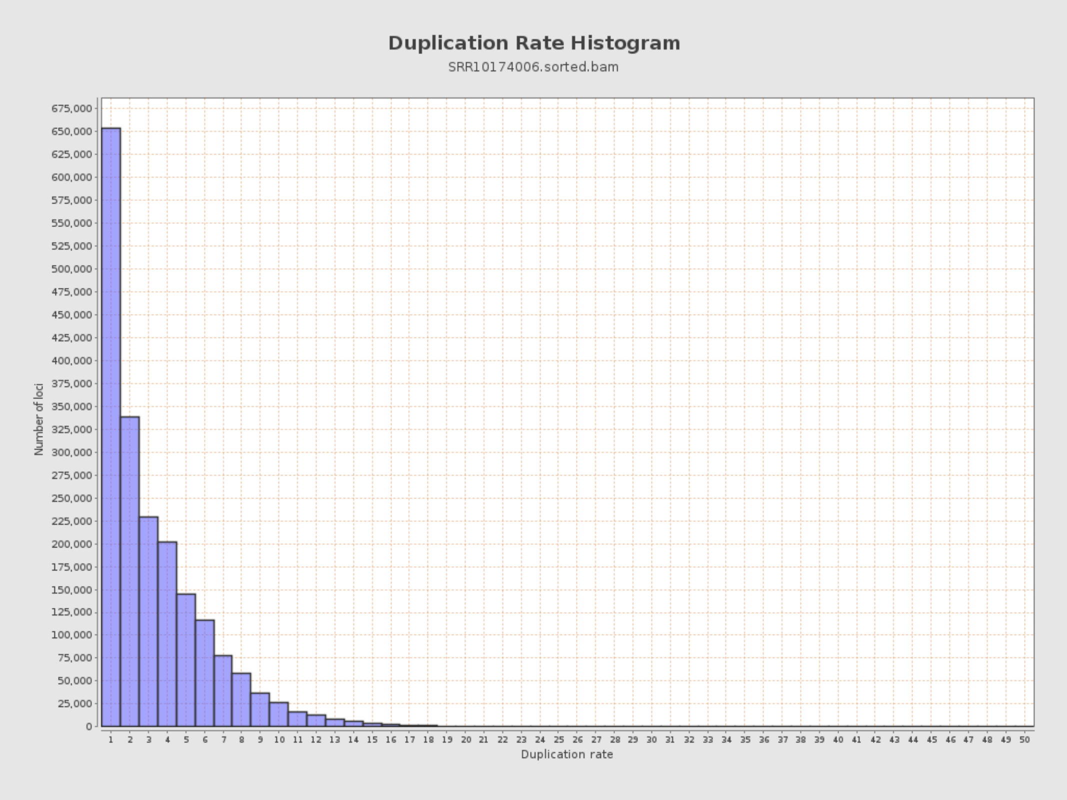
5. Results : Coverage Histogram (0-50X)



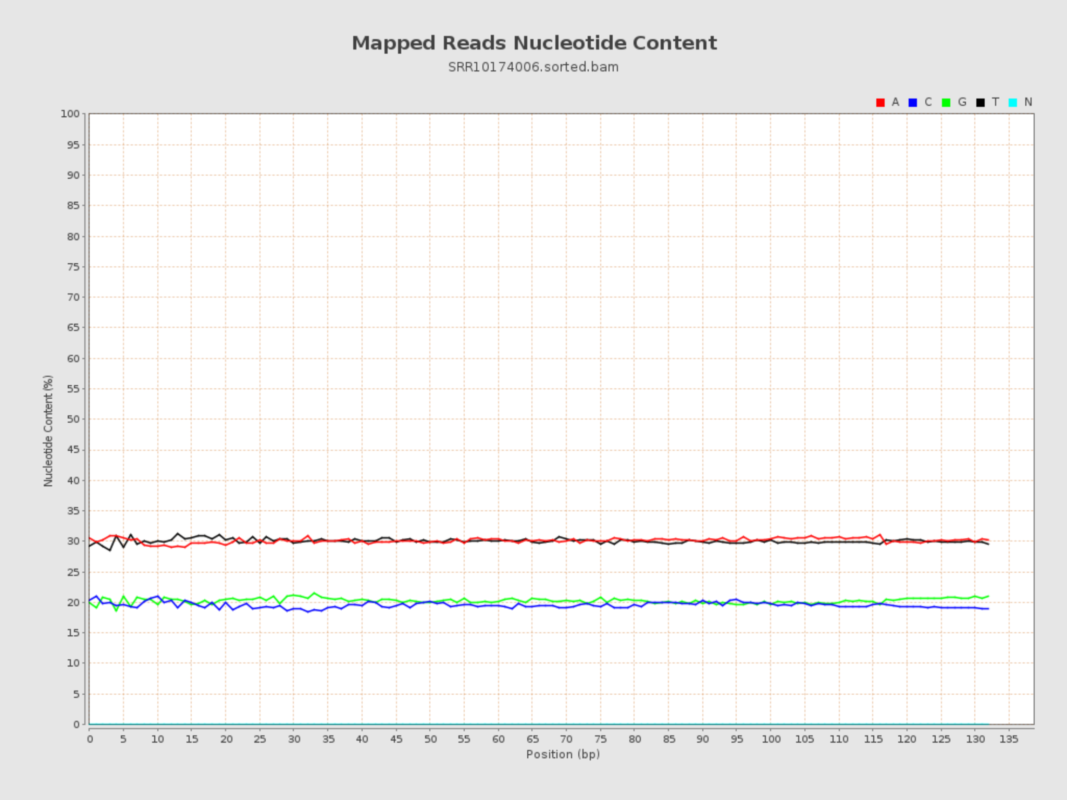
6. Results : Genome Fraction Coverage



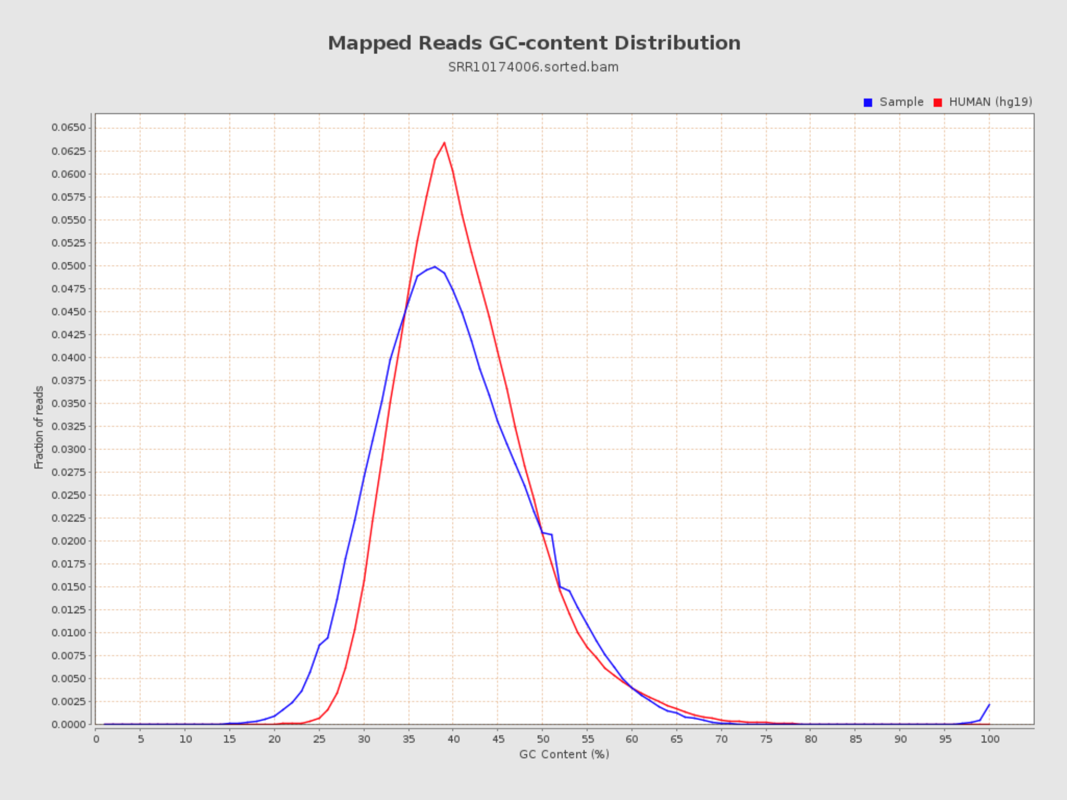
7. Results : Duplication Rate Histogram



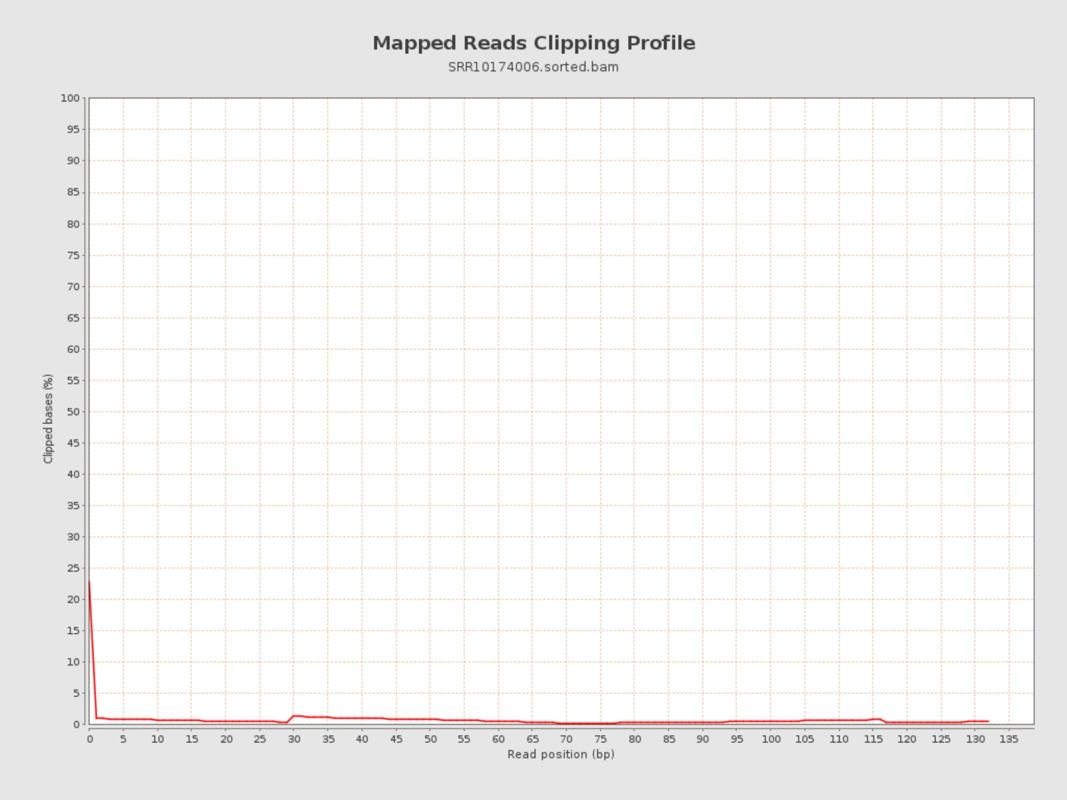
8. Results : Mapped Reads Nucleotide Content



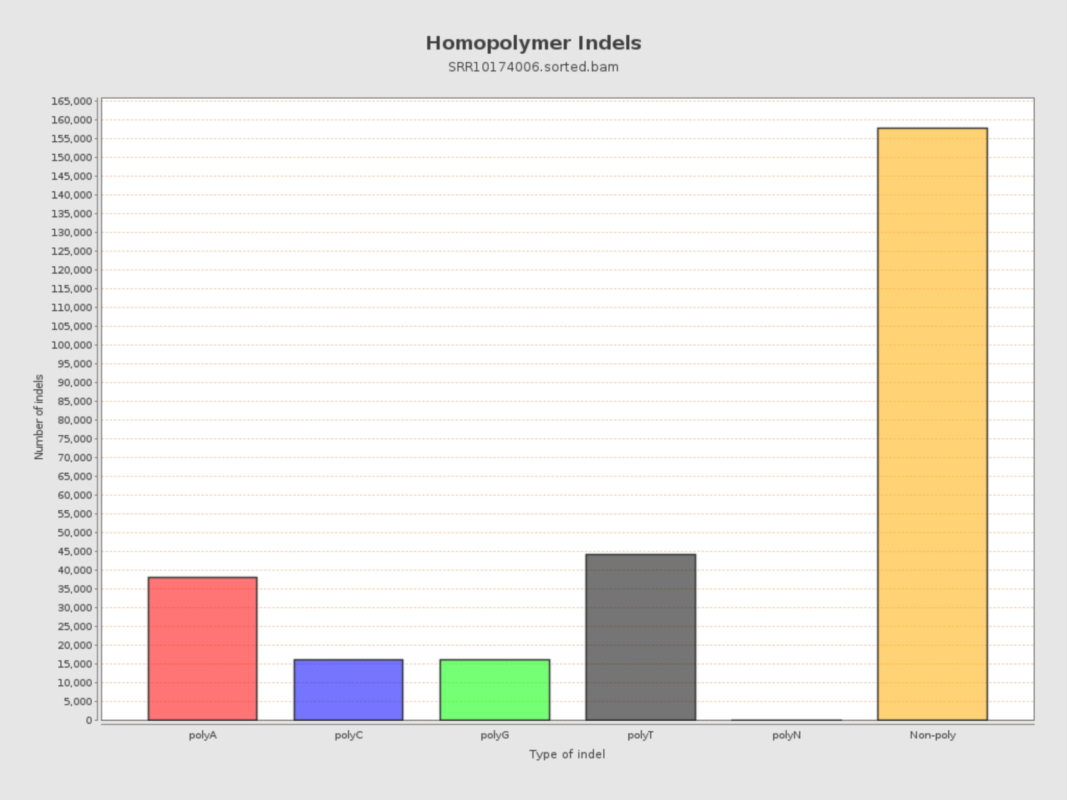
9. Results : Mapped Reads GC-content Distribution



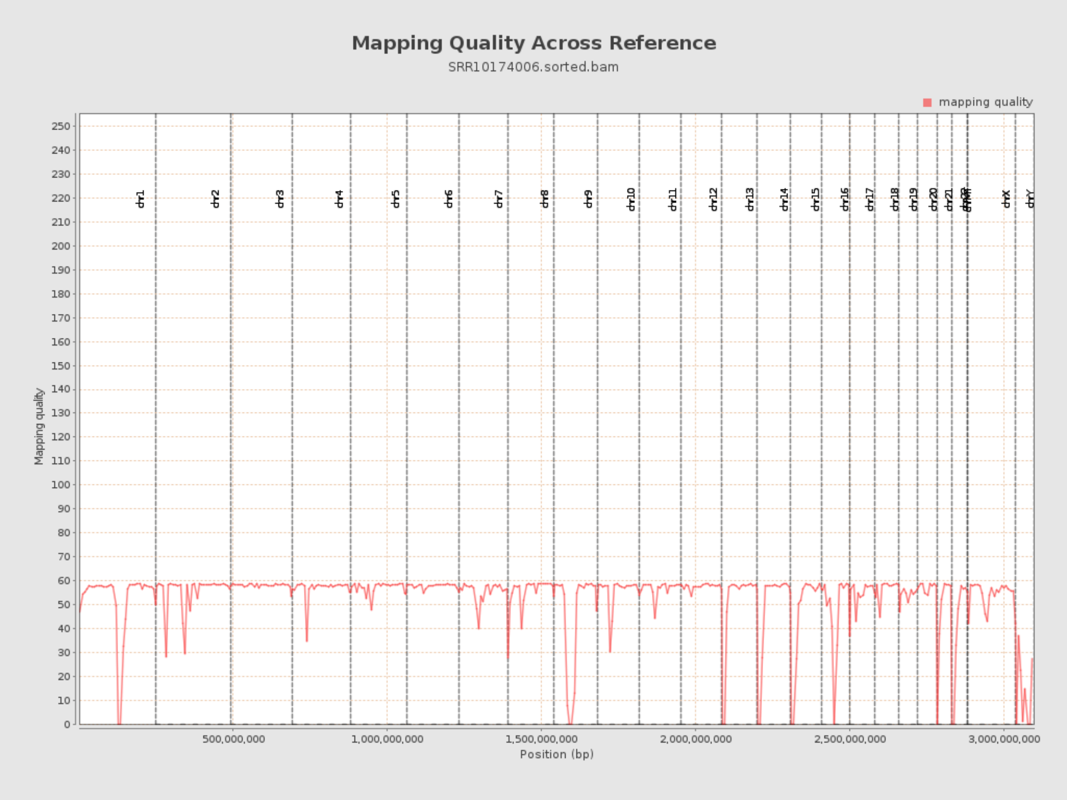
10. Results : Mapped Reads Clipping Profile



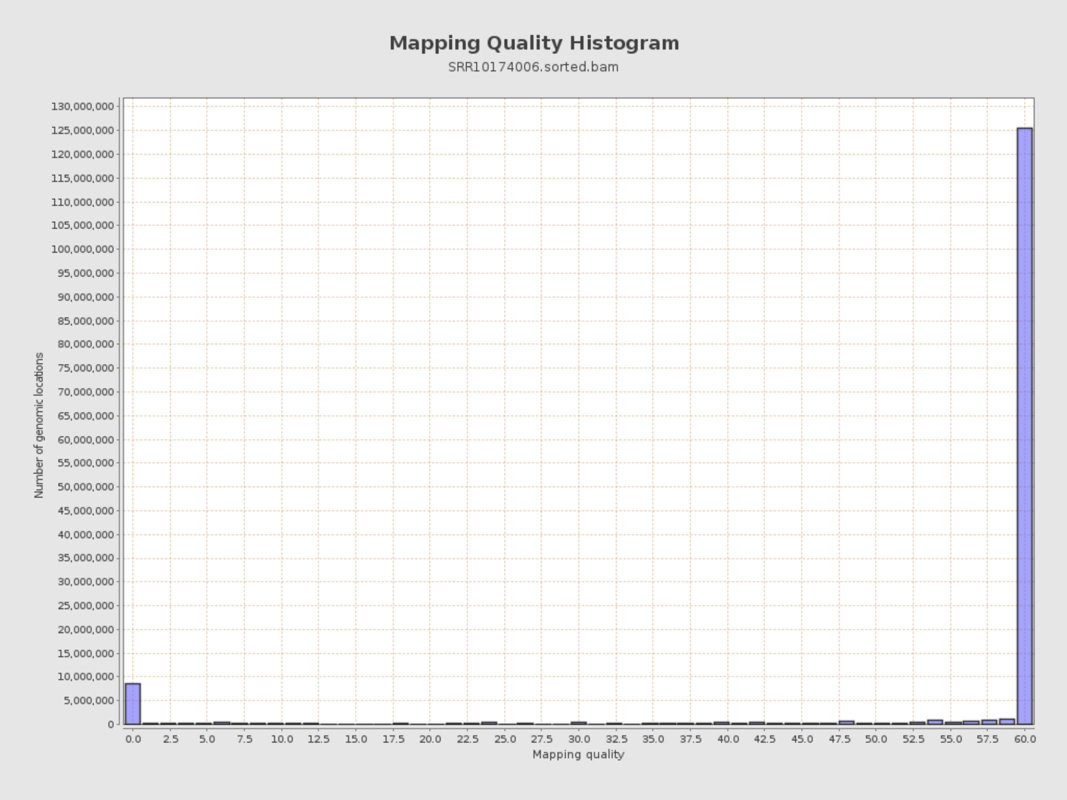
11. Results : Homopolymer Indels



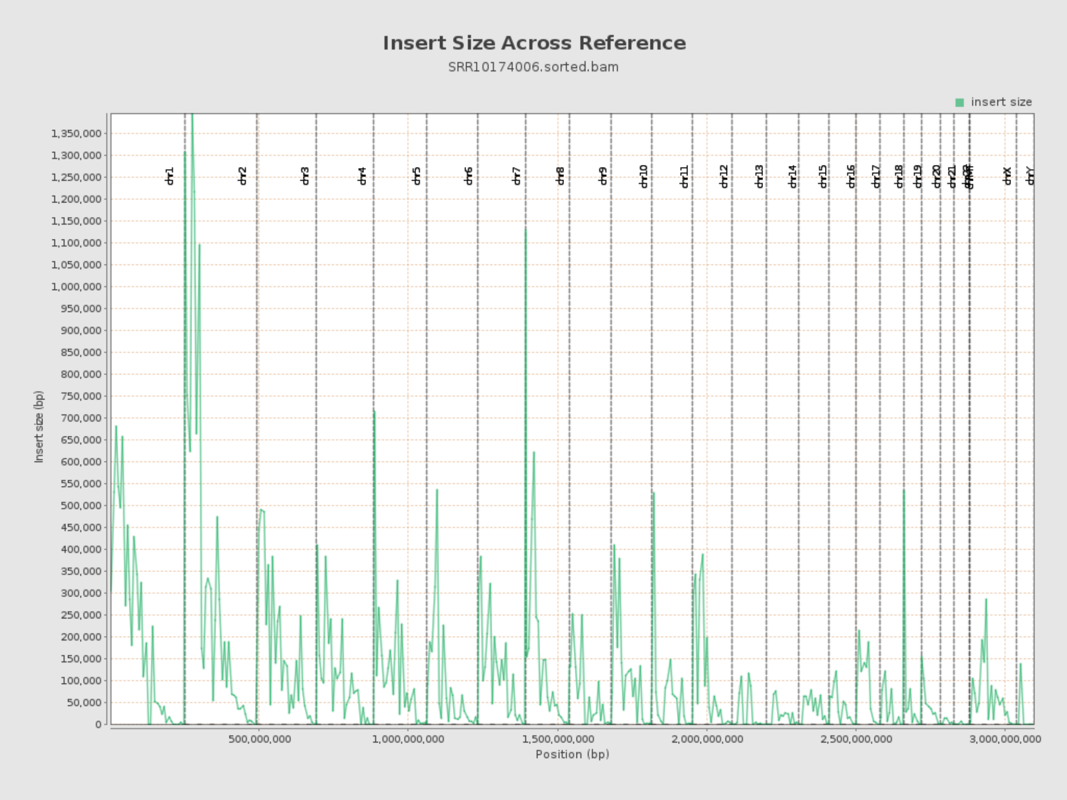
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram