Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 20:51:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617378.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_SRR617378 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617378_1.fastq.gz SRR617378_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 20:51:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617378.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,758,023 / 92.99%
Unmapped reads	2,241,977 / 7.01%
Mapped paired reads	29,758,023 / 92.99%
Mapped reads, first in pair	14,949,052 / 46.72%
Mapped reads, second in pair	14,808,971 / 46.28%
Mapped reads, both in pair	29,180,752 / 91.19%
Mapped reads, singletons	577,271 / 1.8%
Secondary alignments	0
Supplementary alignments	65,216 / 0.2%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,527,546 / 4.77%
Duplication rate	1.47%
Clipped reads	2,622,321 / 8.19%

2.2. ACGT Content

Number/percentage of A's	886,018,105 / 30.38%
Number/percentage of C's	577,416,007 / 19.8%
Number/percentage of T's	872,062,368 / 29.9%
Number/percentage of G's	579,881,676 / 19.88%
Number/percentage of N's	1,405,810 / 0.05%

GC Percentage	39.68%

2.3. Coverage

Mean	0.9425
Standard Deviation	9.6363

2.4. Mapping Quality

Mean Mapping Quality	53.42

2.5. Insert size

Mean	50,344.74
Standard Deviation	2,134,503.7
P25/Median/P75	170 / 209 / 269

2.6. Mismatches and indels

General error rate	1.28%
Mismatches	36,508,727
Insertions	289,708
Mapped reads with at least one insertion	0.94%
Deletions	350,095
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.05%

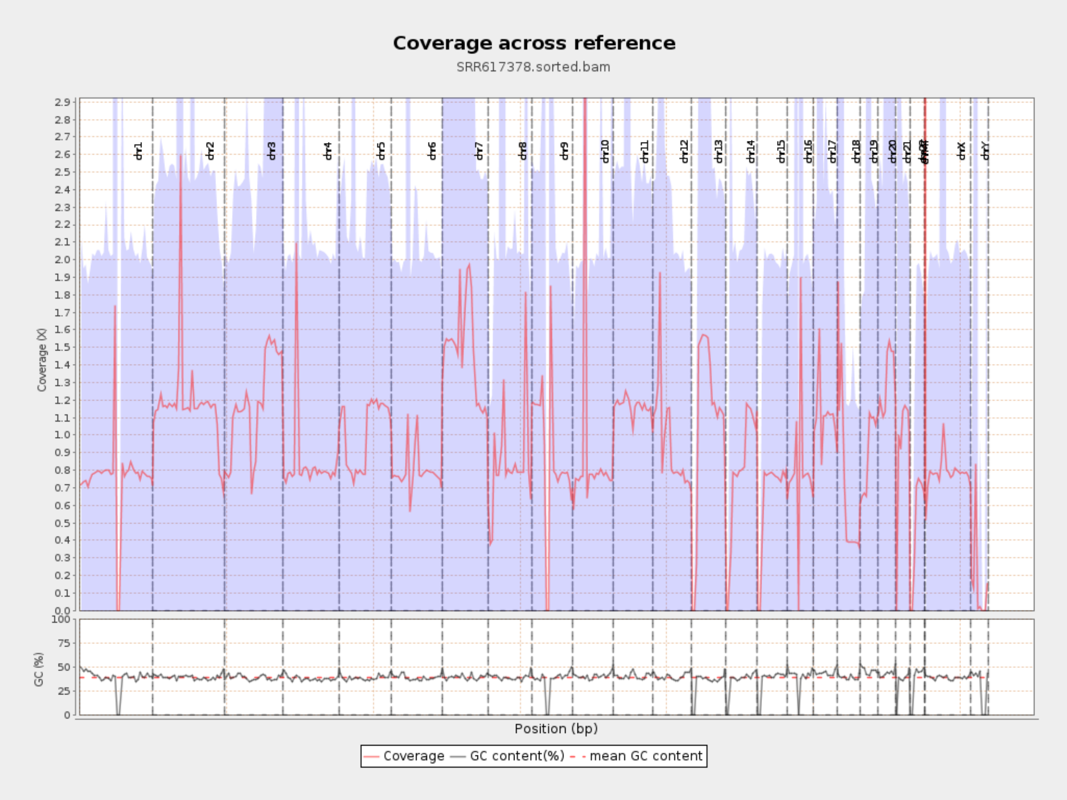
2.7. Chromosome stats

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

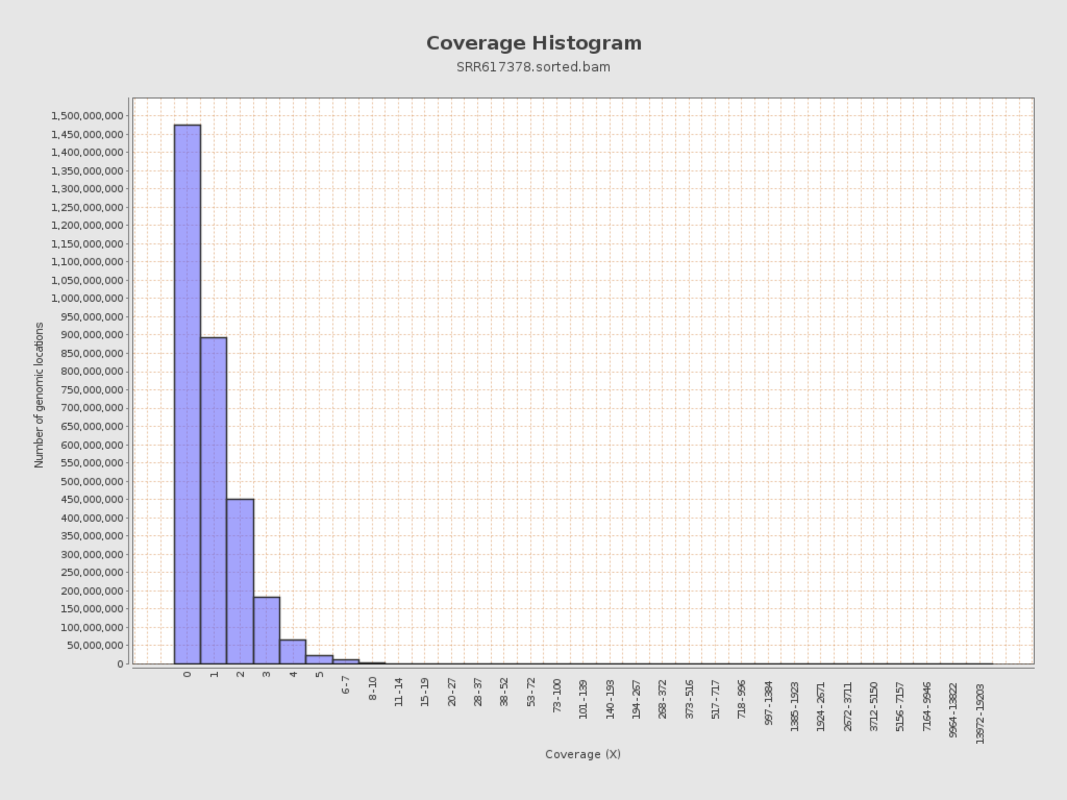
		bases	coverage	deviation
chr1	249250621	189108879	0.7587	19.6726
chr2	243199373	288130793	1.1848	8.5714
chr3	198022430	232766617	1.1755	1.4784
chr4	191154276	160570594	0.84	8.9718
chr5	180915260	183891382	1.0165	1.4531
chr6	171115067	136949330	0.8003	3.6583
chr7	159138663	236760016	1.4878	10.8391
chr8	146364022	123136479	0.8413	7.3324
chr9	141213431	122976148	0.8709	14.6654
chr10	135534747	122955284	0.9072	19.9516
chr11	135006516	156634322	1.1602	5.4918
chr12	133851895	128852632	0.9627	1.353
chr13	115169878	127799127	1.1097	1.2898
chr14	107349540	84069234	0.7831	1.351
chr15	102531392	65315501	0.637	0.9672
chr16	90354753	72899351	0.8068	7.9639
chr17	81195210	89953824	1.1079	7.0529
chr18	78077248	52705748	0.675	15.0172
chr19	59128983	53279339	0.9011	9.3508
chr20	63025520	83061450	1.3179	2.3624
chr21	48129895	46616920	0.9686	3.1768
chr22	51304566	25567429	0.4983	0.8969
chrMT	16571	1946012	117.4348	21.1592
chrX	155270560	121887430	0.785	2.9362

chrY	59373566	9790480	0.1649	7.9741

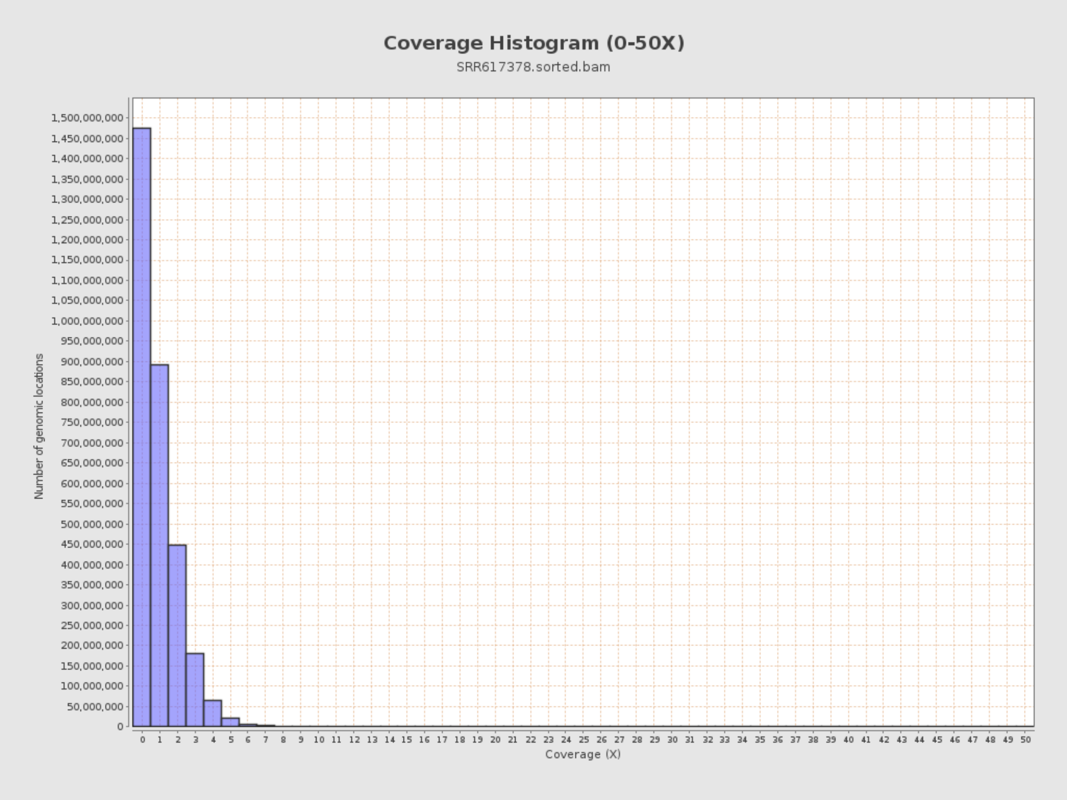
3. Results : Coverage across reference



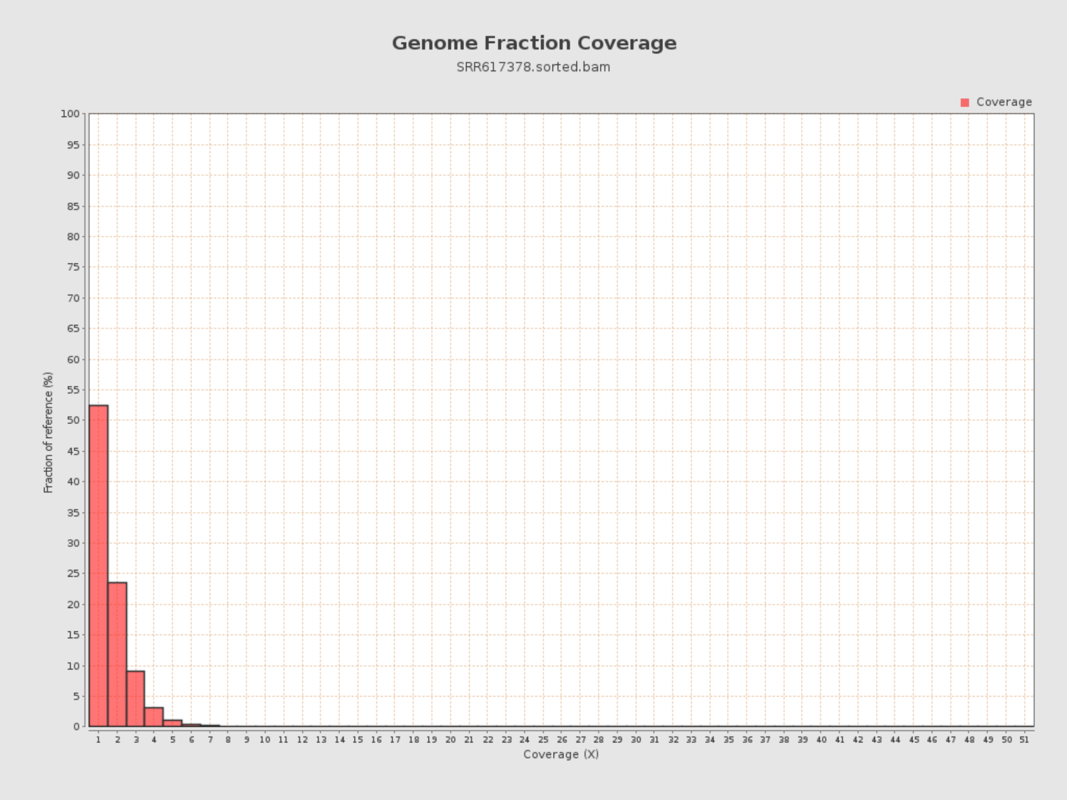
4. Results : Coverage Histogram



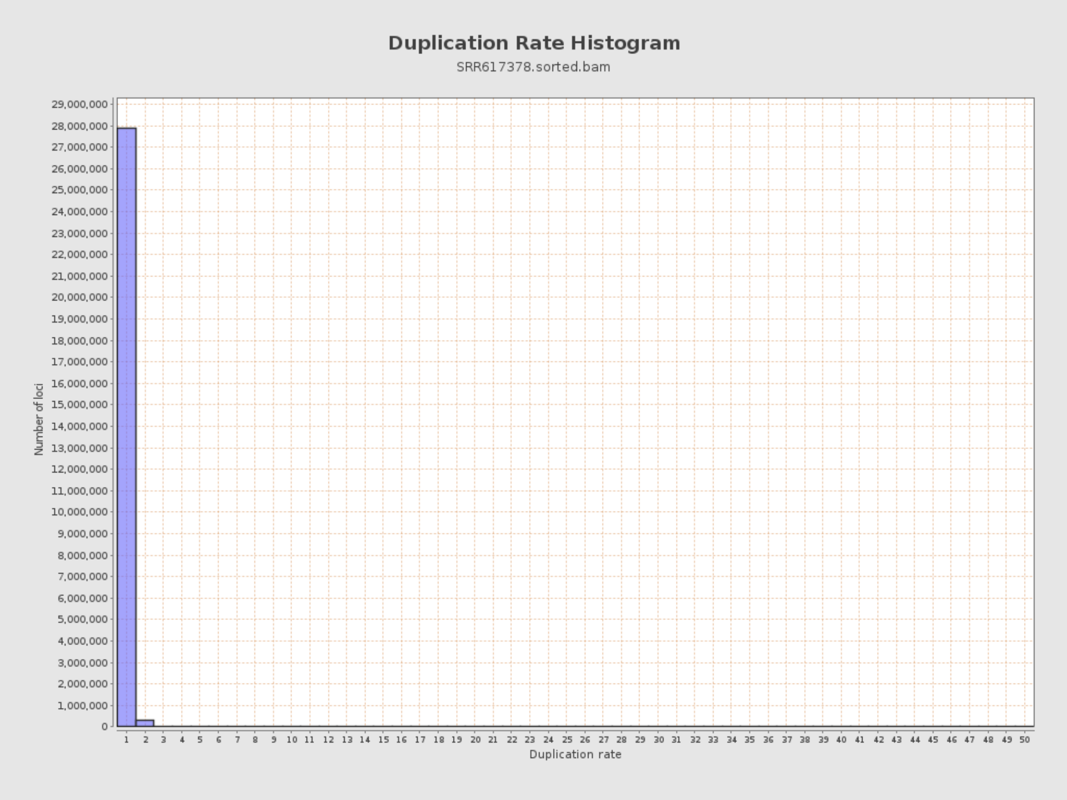
5. Results : Coverage Histogram (0-50X)



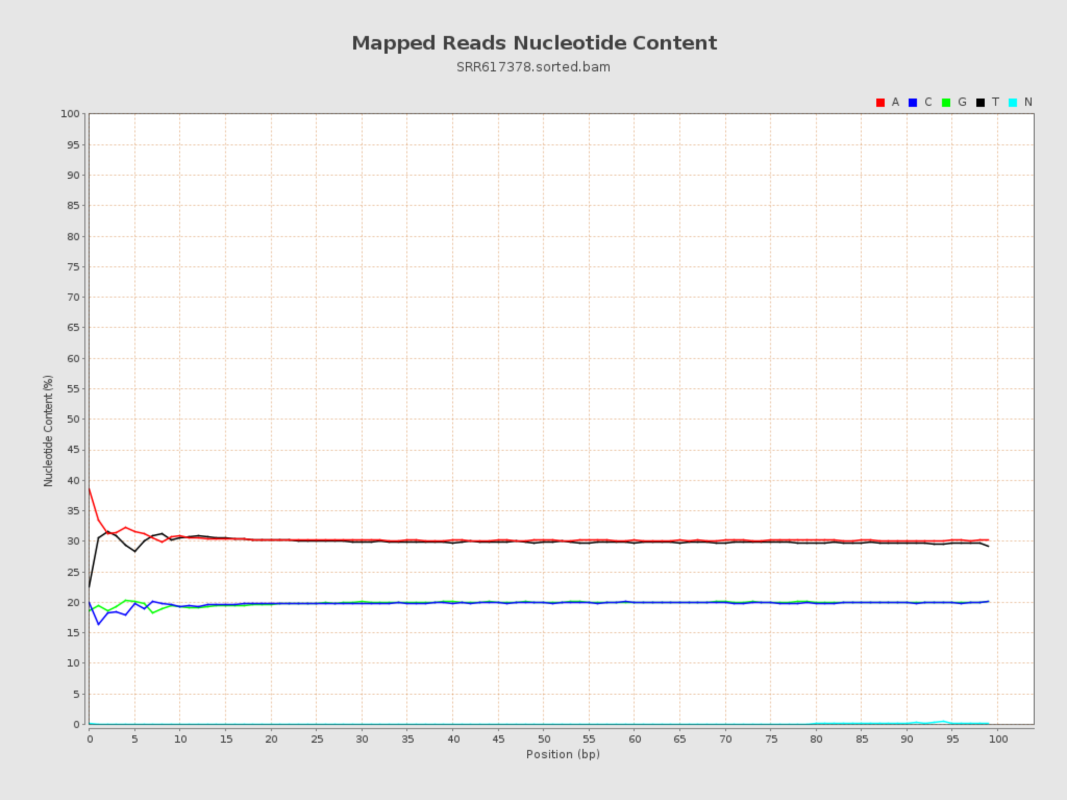
6. Results : Genome Fraction Coverage



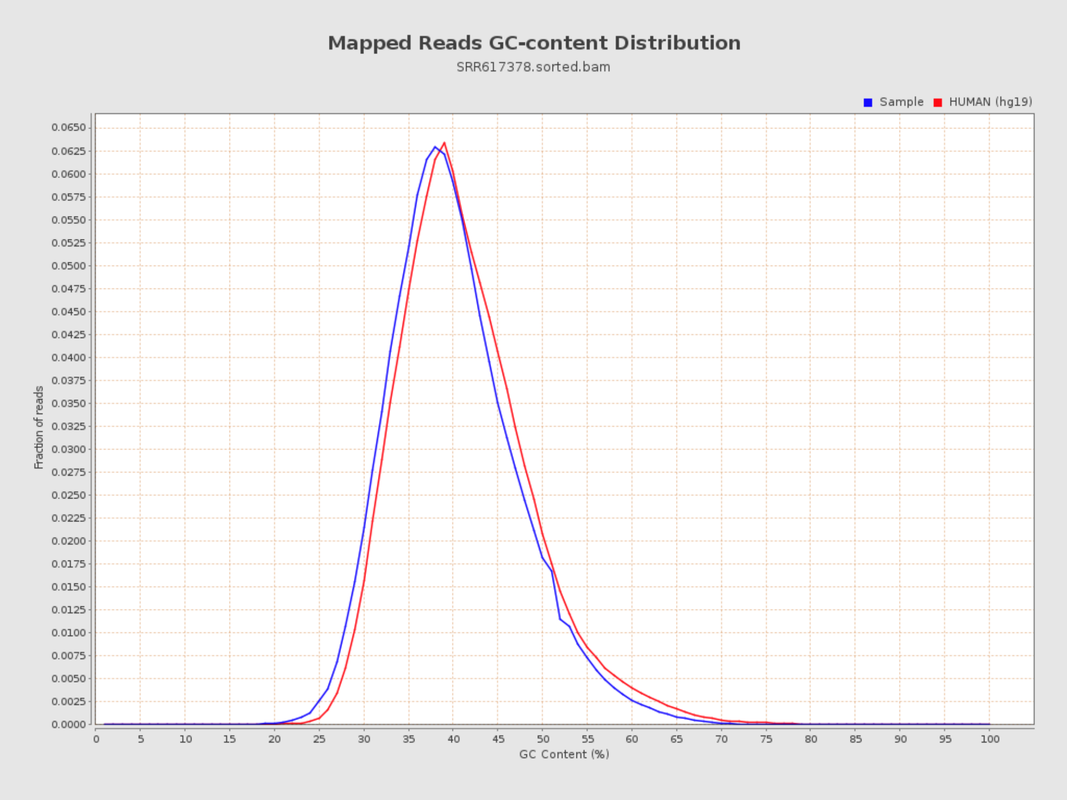
7. Results : Duplication Rate Histogram



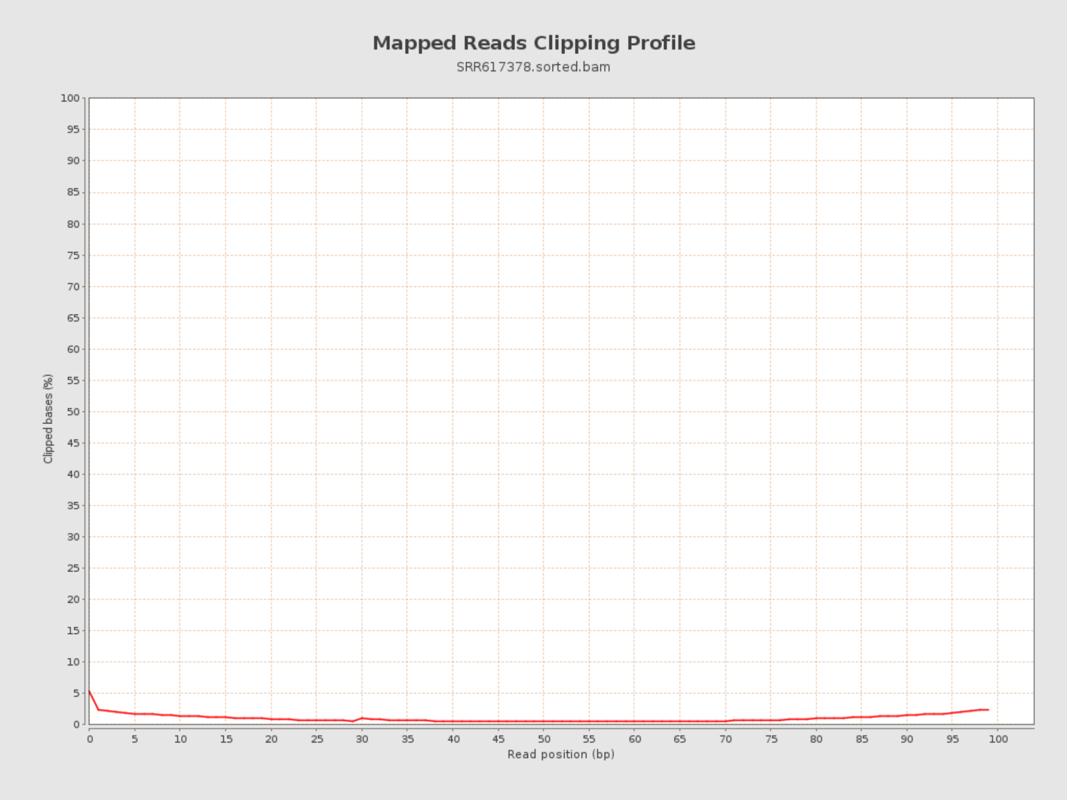
8. Results : Mapped Reads Nucleotide Content



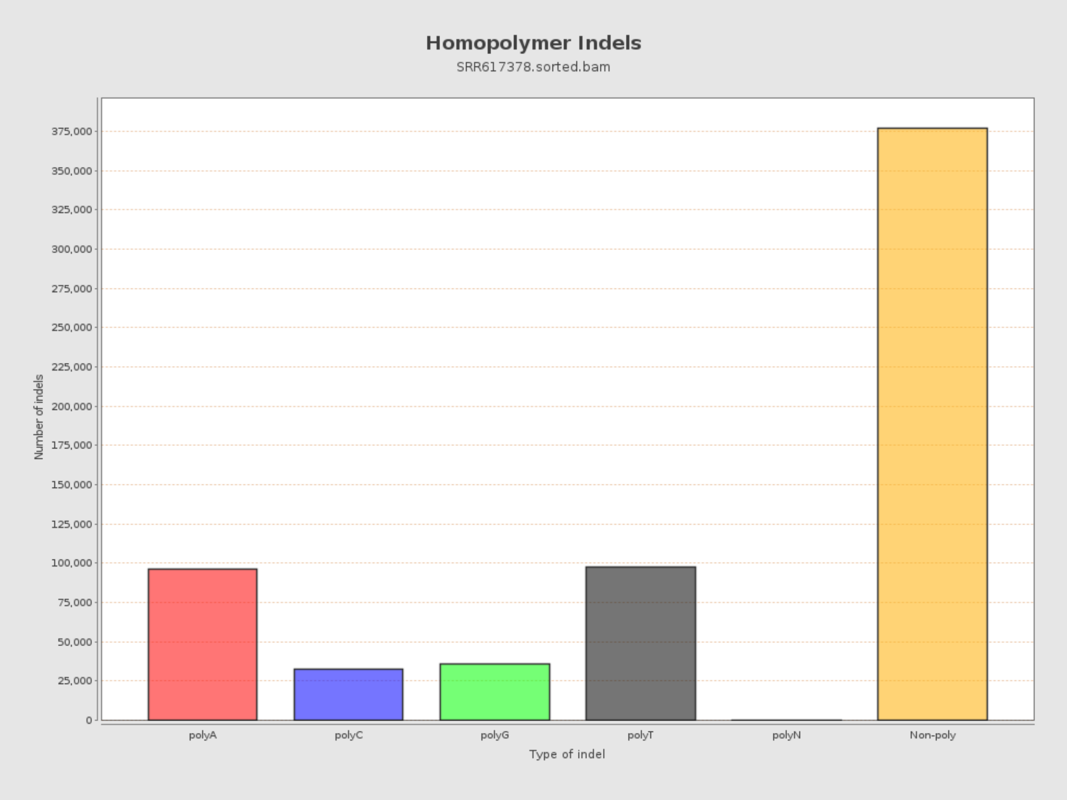
9. Results : Mapped Reads GC-content Distribution



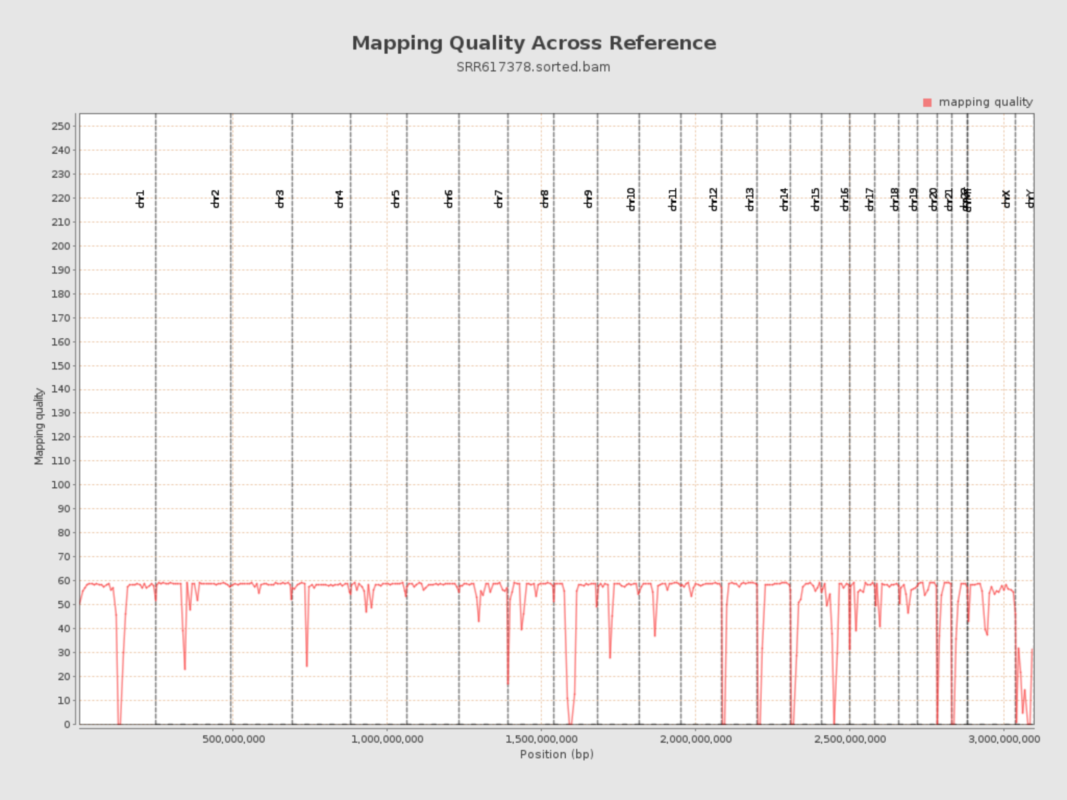
10. Results : Mapped Reads Clipping Profile



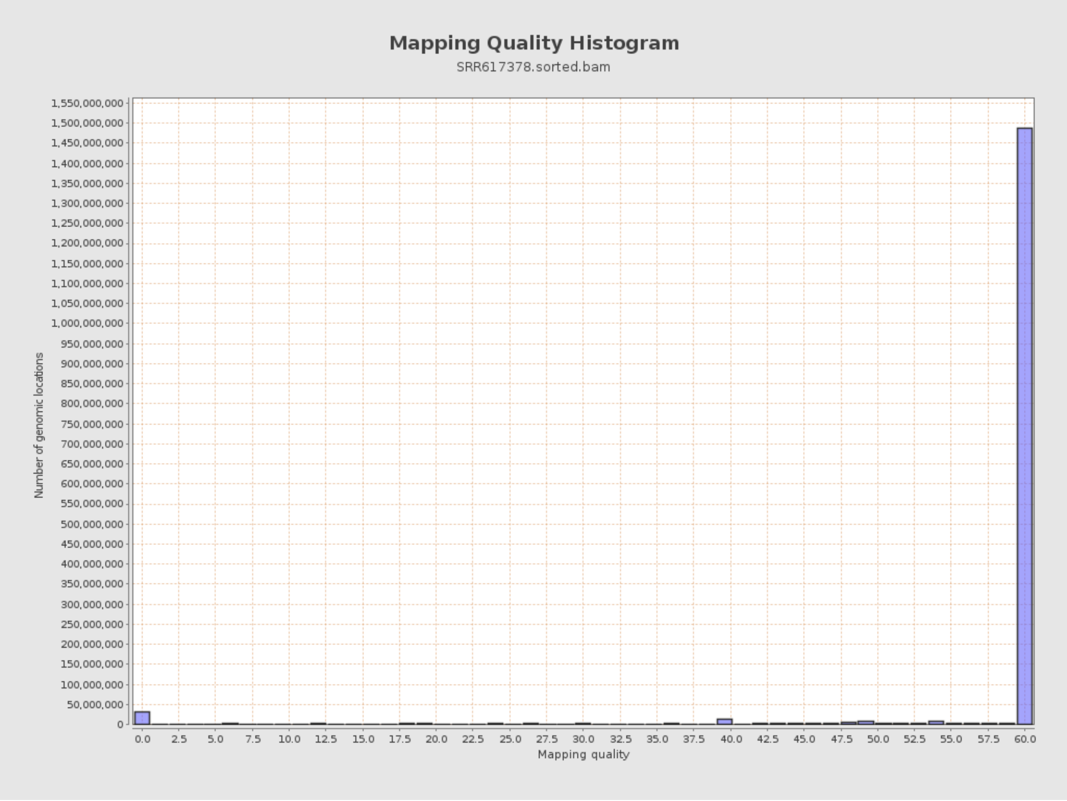
11. Results : Homopolymer Indels



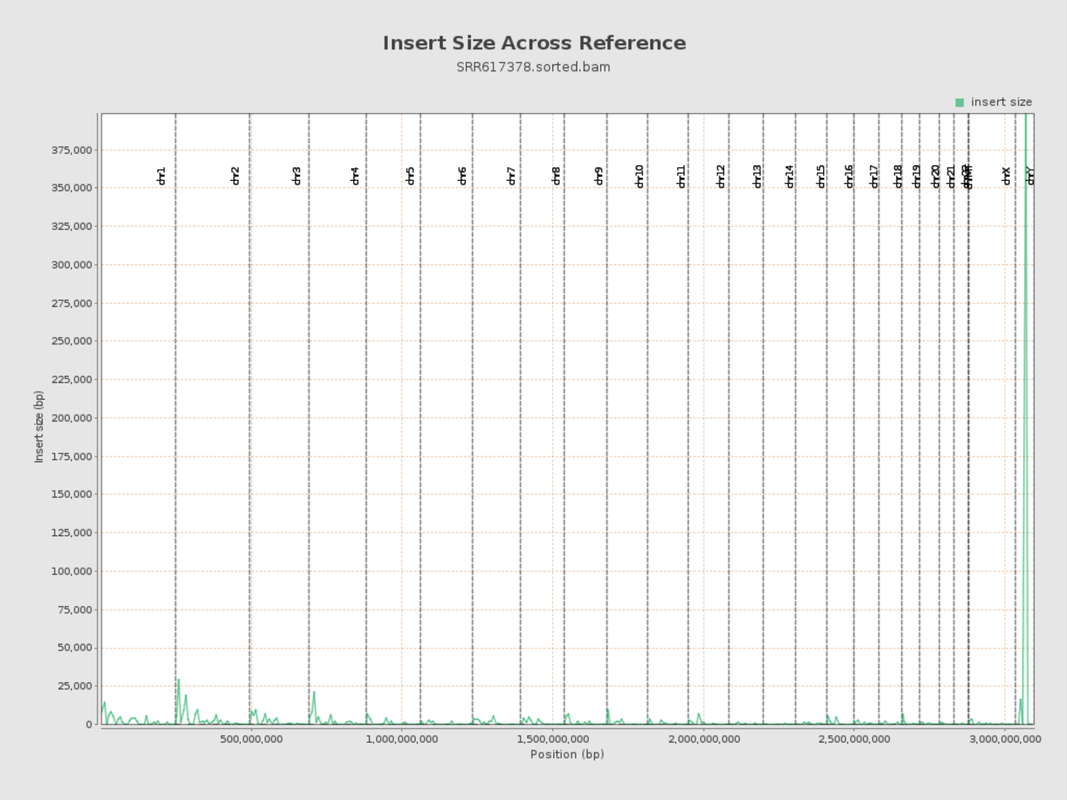
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram