Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 08:49:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617364.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_SRR617364 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617364_1.fastq.gz SRR617364_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 08:49:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617364.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,643,063 / 92.63%
Unmapped reads	2,356,937 / 7.37%
Mapped paired reads	29,643,063 / 92.63%
Mapped reads, first in pair	14,940,884 / 46.69%
Mapped reads, second in pair	14,702,179 / 45.94%
Mapped reads, both in pair	28,951,346 / 90.47%
Mapped reads, singletons	691,717 / 2.16%
Secondary alignments	0
Supplementary alignments	67,898 / 0.21%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	1,518,532 / 4.75%
Duplication rate	1.48%
Clipped reads	2,695,326 / 8.42%

2.2. ACGT Content

Number/percentage of A's	880,467,947 / 30.33%
Number/percentage of C's	575,892,838 / 19.84%
Number/percentage of T's	866,533,429 / 29.85%
Number/percentage of G's	578,940,608 / 19.94%
Number/percentage of N's	1,540,321 / 0.05%

GC Percentage	39.78%

2.3. Coverage

Mean	0.9381
Standard Deviation	9.5755

2.4. Mapping Quality

Mean Mapping Quality	53.39

2.5. Insert size

Mean	48,934.81
Standard Deviation	2,088,653.75
P25/Median/P75	169 / 207 / 267

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	38,101,505
Insertions	290,522
Mapped reads with at least one insertion	0.95%
Deletions	352,826
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.22%

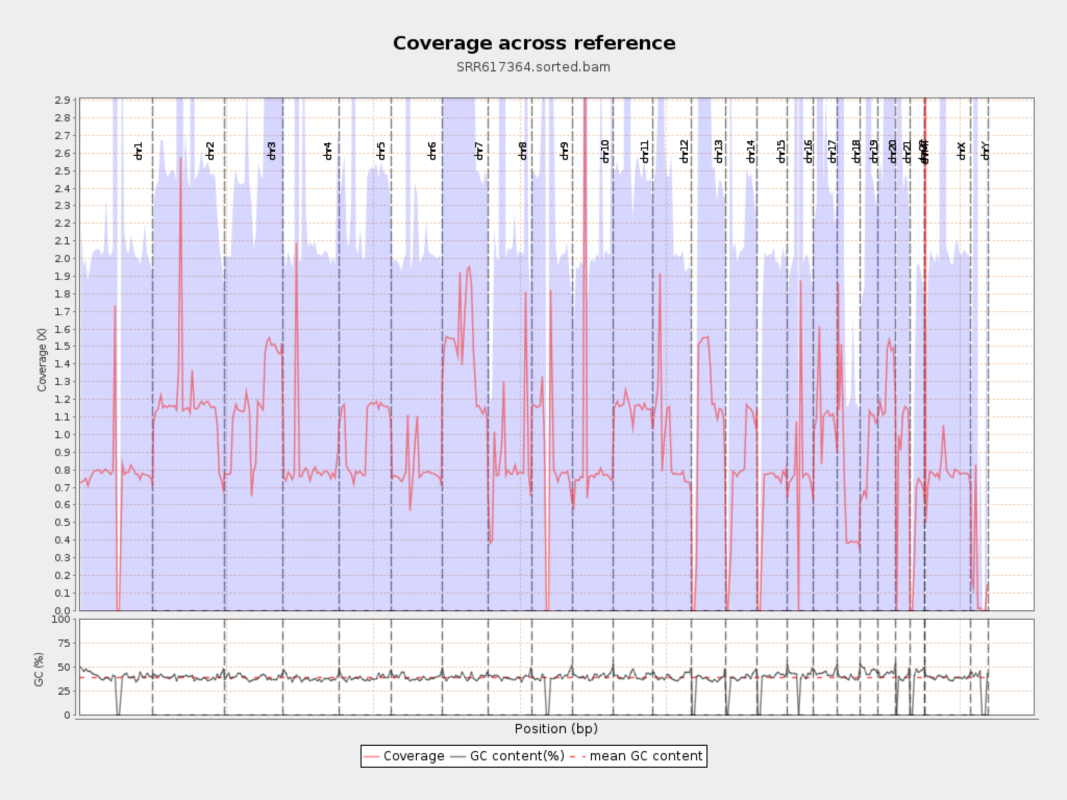
2.7. Chromosome stats

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

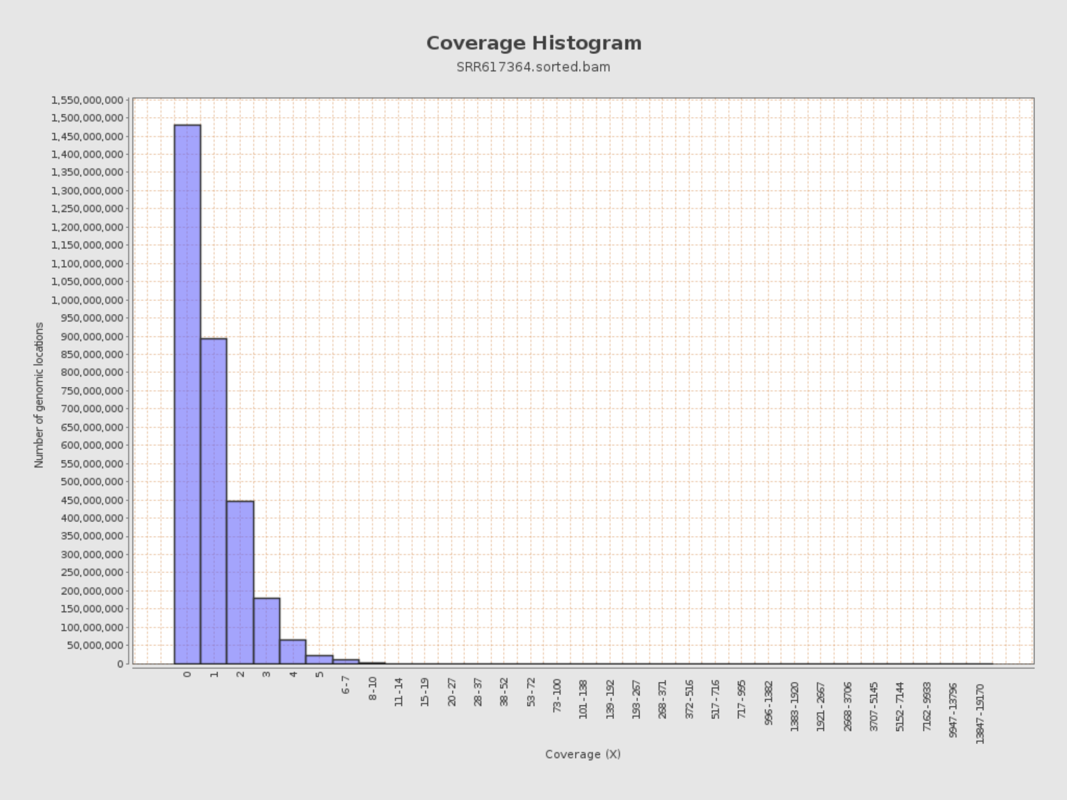
		bases	coverage	deviation
chr1	249250621	188638437	0.7568	19.6684
chr2	243199373	286446678	1.1778	8.5562
chr3	198022430	231323478	1.1682	1.4873
chr4	191154276	159334335	0.8335	8.8807
chr5	180915260	182554743	1.0091	1.4473
chr6	171115067	136535730	0.7979	3.6071
chr7	159138663	235964857	1.4828	10.6652
chr8	146364022	122497854	0.8369	7.3363
chr9	141213431	122218987	0.8655	14.3286
chr10	135534747	122458317	0.9035	19.9273
chr11	135006516	155831969	1.1543	5.4452
chr12	133851895	128274056	0.9583	1.3657
chr13	115169878	127055610	1.1032	1.2847
chr14	107349540	83820761	0.7808	1.3349
chr15	102531392	65057977	0.6345	0.9684
chr16	90354753	72500164	0.8024	7.856
chr17	81195210	89949274	1.1078	7.0404
chr18	78077248	52511636	0.6726	14.763
chr19	59128983	53514579	0.905	9.3059
chr20	63025520	83112882	1.3187	2.3782
chr21	48129895	46246251	0.9609	3.0902
chr22	51304566	25507647	0.4972	0.8994
chrMT	16571	1980775	119.5326	20.3382
chrX	155270560	121175148	0.7804	2.9145

chrY	59373566	9706723	0.1635	7.8321

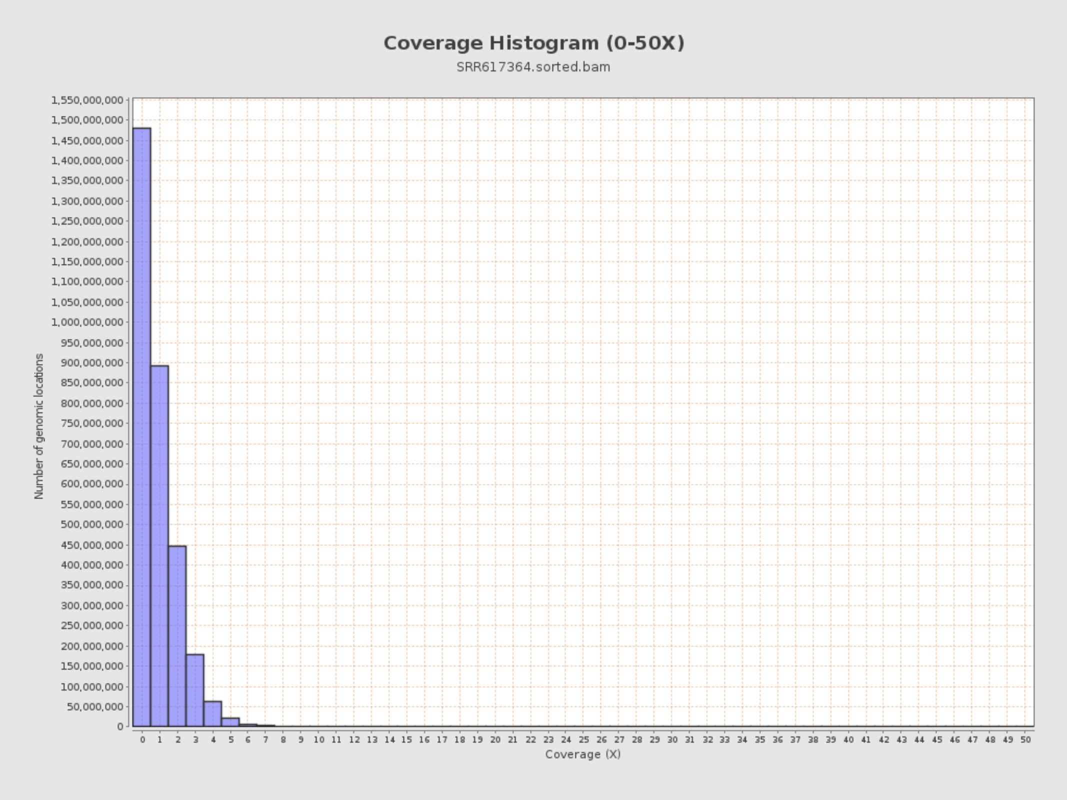
3. Results : Coverage across reference



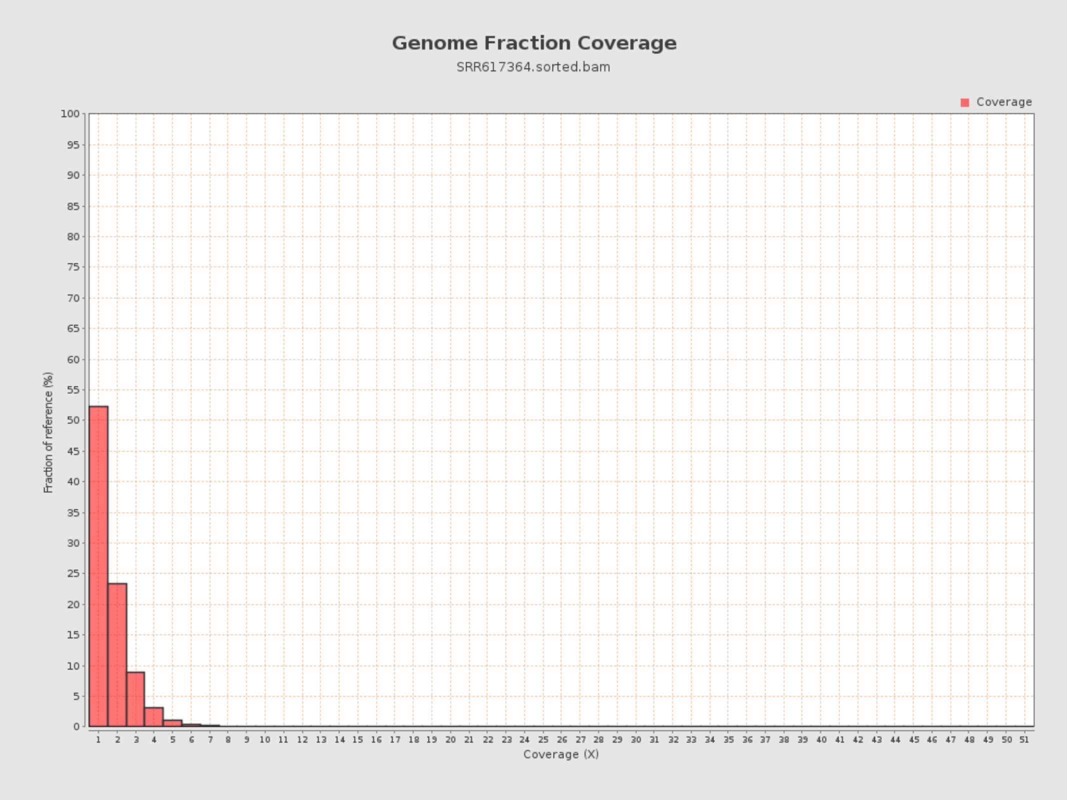
4. Results : Coverage Histogram



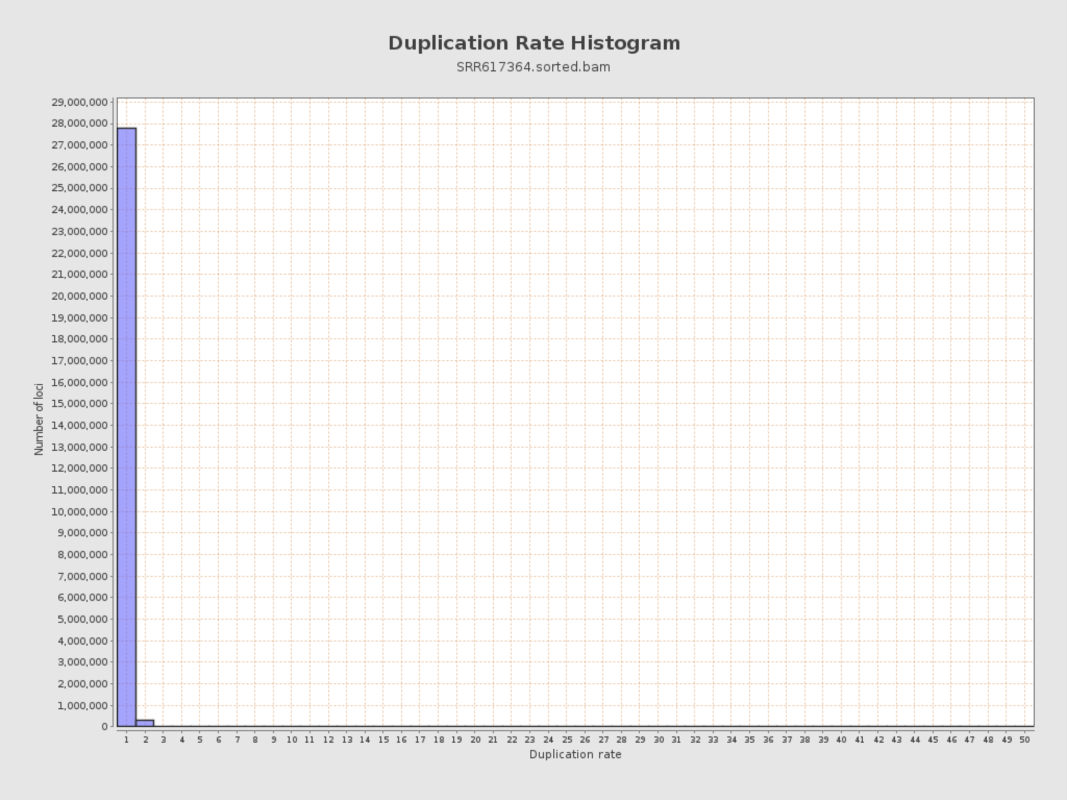
5. Results : Coverage Histogram (0-50X)



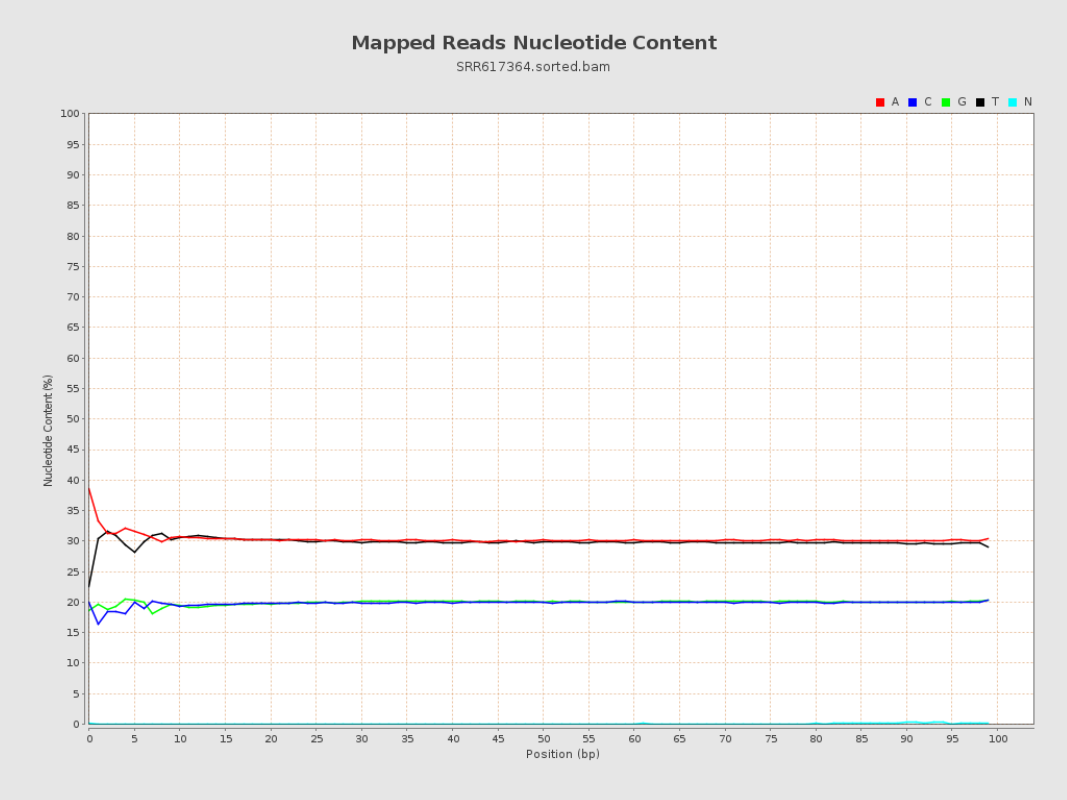
6. Results : Genome Fraction Coverage



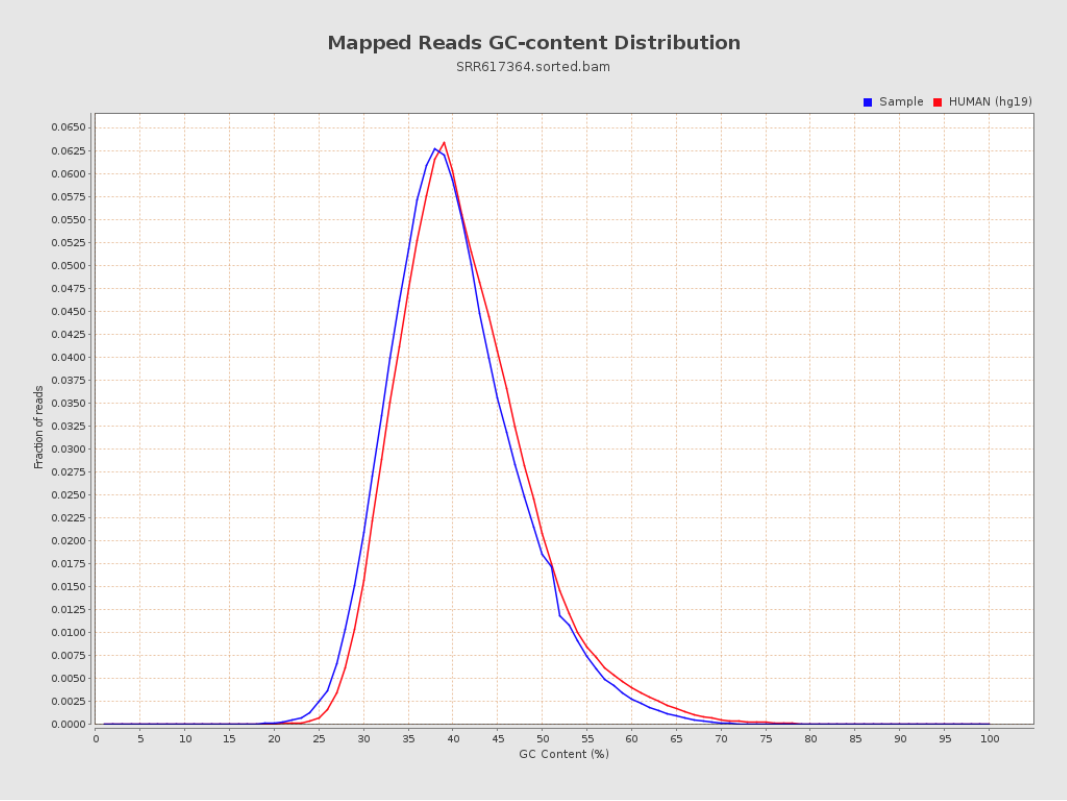
7. Results : Duplication Rate Histogram



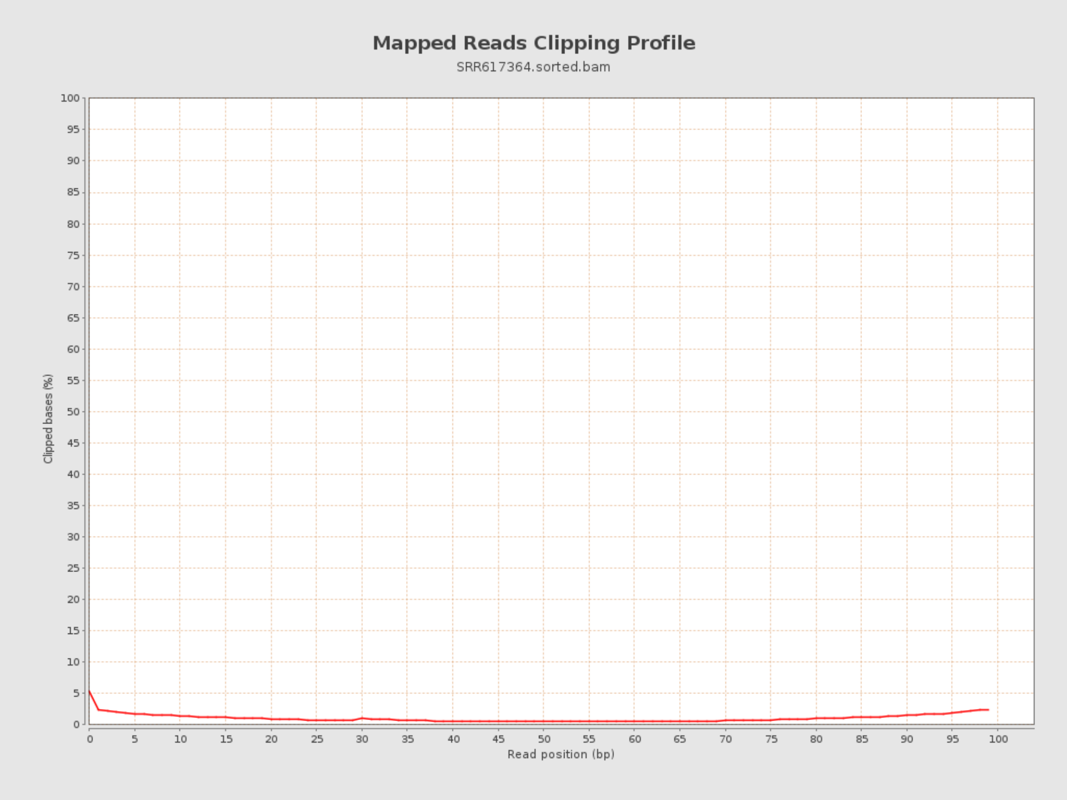
8. Results : Mapped Reads Nucleotide Content



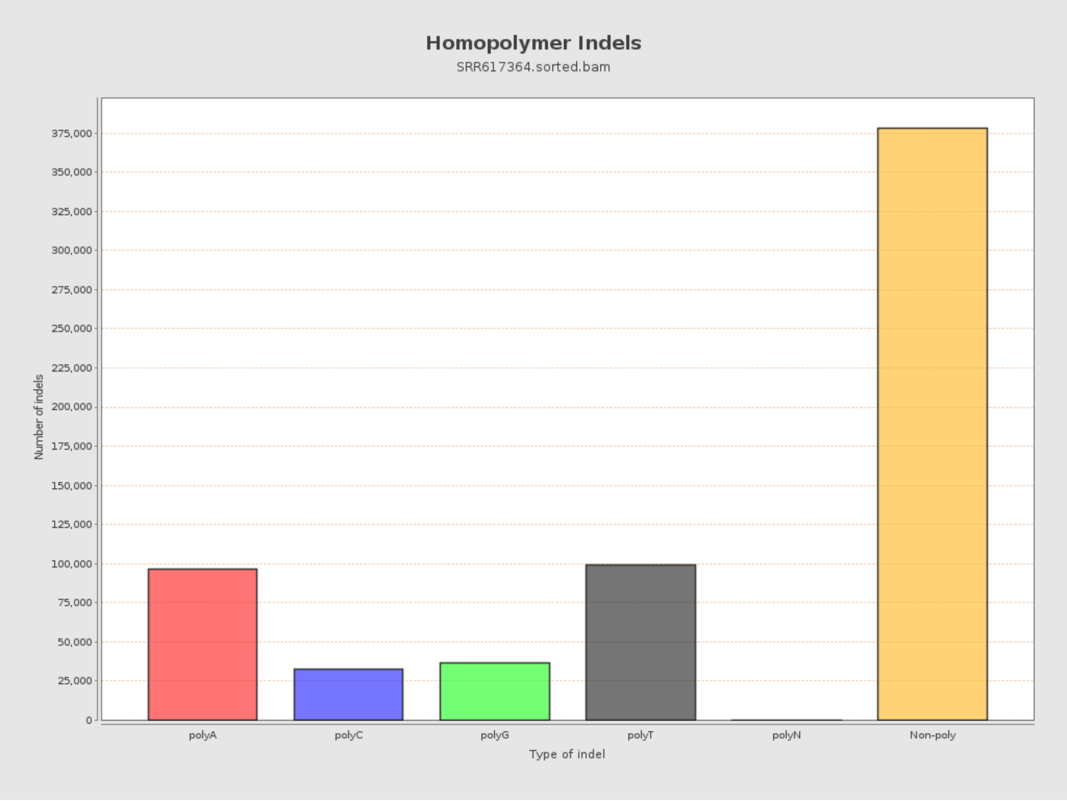
9. Results : Mapped Reads GC-content Distribution



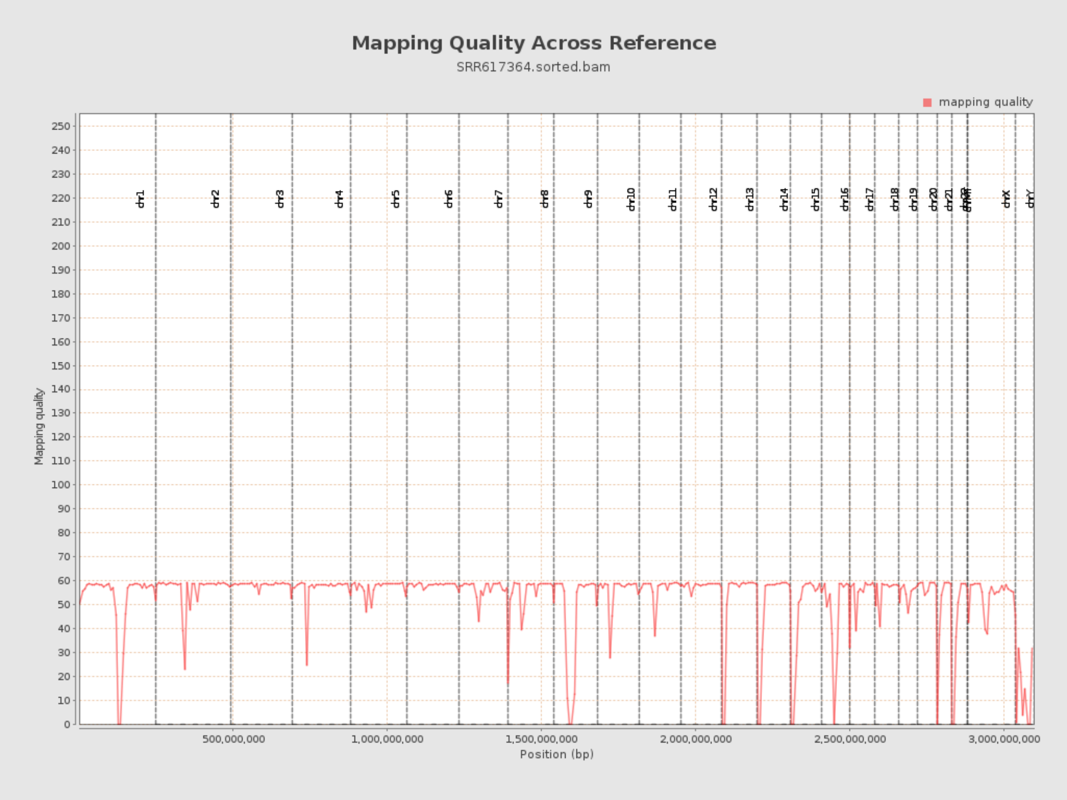
10. Results : Mapped Reads Clipping Profile



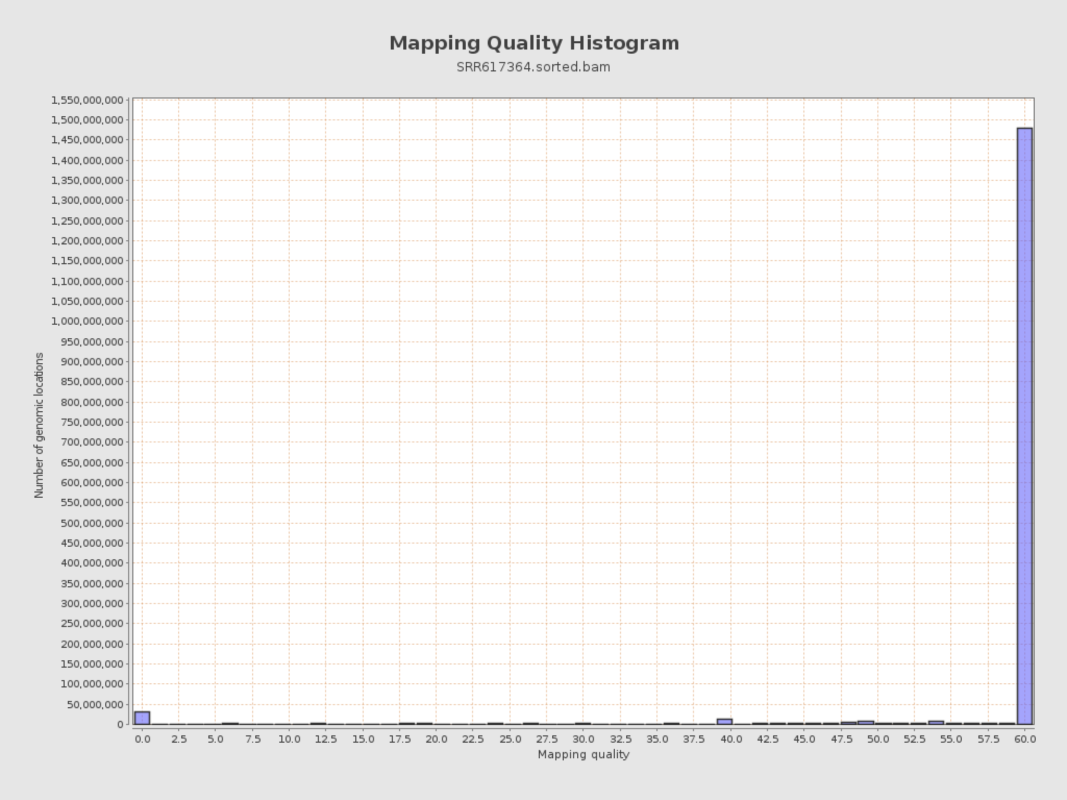
11. Results : Homopolymer Indels



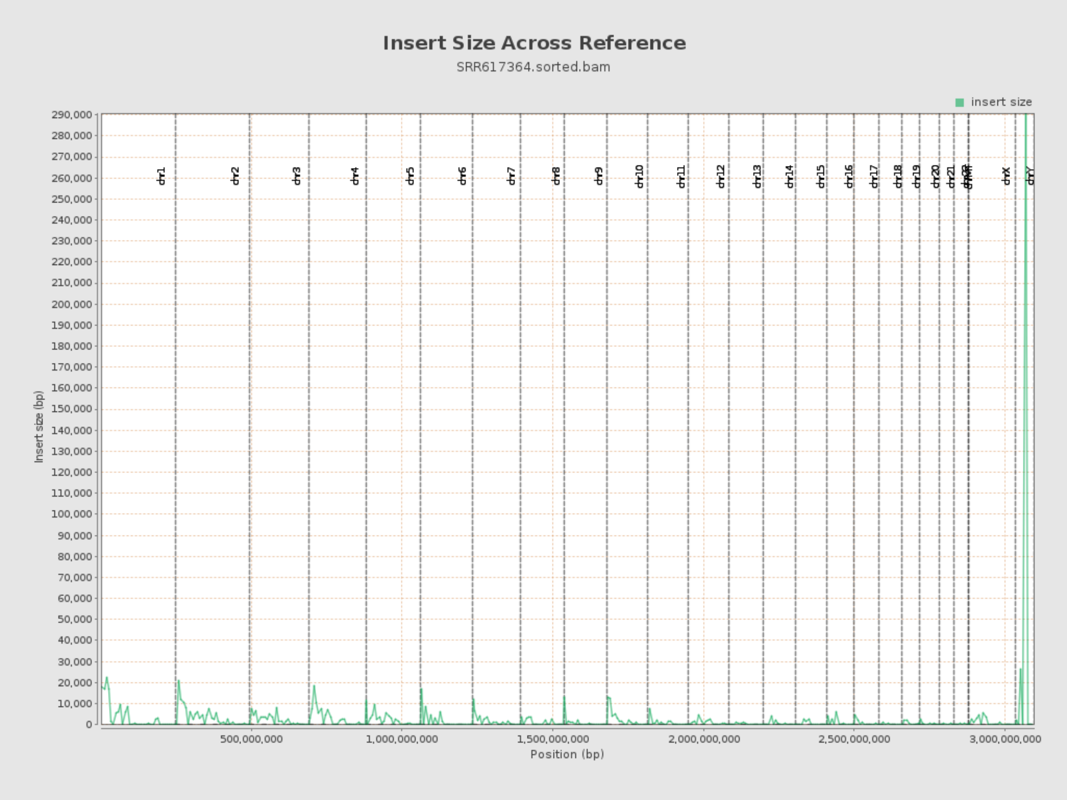
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram