Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 10:25:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617392.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_SRR617392 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617392_1.fastq.gz SRR617392_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 10:25:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617392.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,600,971 / 92.5%
Unmapped reads	2,399,029 / 7.5%
Mapped paired reads	29,600,971 / 92.5%
Mapped reads, first in pair	14,880,059 / 46.5%
Mapped reads, second in pair	14,720,912 / 46%
Mapped reads, both in pair	29,002,640 / 90.63%
Mapped reads, singletons	598,331 / 1.87%
Secondary alignments	0
Supplementary alignments	441,369 / 1.38%
Read min/max/mean length	30 / 100 / 100.57
Duplicated reads (estimated)	1,331,103 / 4.16%
Duplication rate	4.1%
Clipped reads	3,469,639 / 10.84%

2.2. ACGT Content

Number/percentage of A's	869,247,483 / 29.89%
Number/percentage of C's	582,980,698 / 20.05%
Number/percentage of T's	858,474,924 / 29.52%
Number/percentage of G's	594,580,955 / 20.45%
Number/percentage of N's	2,548,485 / 0.09%

GC Percentage	40.5%

2.3. Coverage

Mean	0.9395
Standard Deviation	2.872

2.4. Mapping Quality

Mean Mapping Quality	53.87

2.5. Insert size

Mean	48,265.42
Standard Deviation	2,091,744.34
P25/Median/P75	170 / 208 / 268

2.6. Mismatches and indels

General error rate	1.2%
Mismatches	34,344,378
Insertions	382,699
Mapped reads with at least one insertion	1.28%
Deletions	281,204
Mapped reads with at least one deletion	0.93%
Homopolymer indels	38.88%

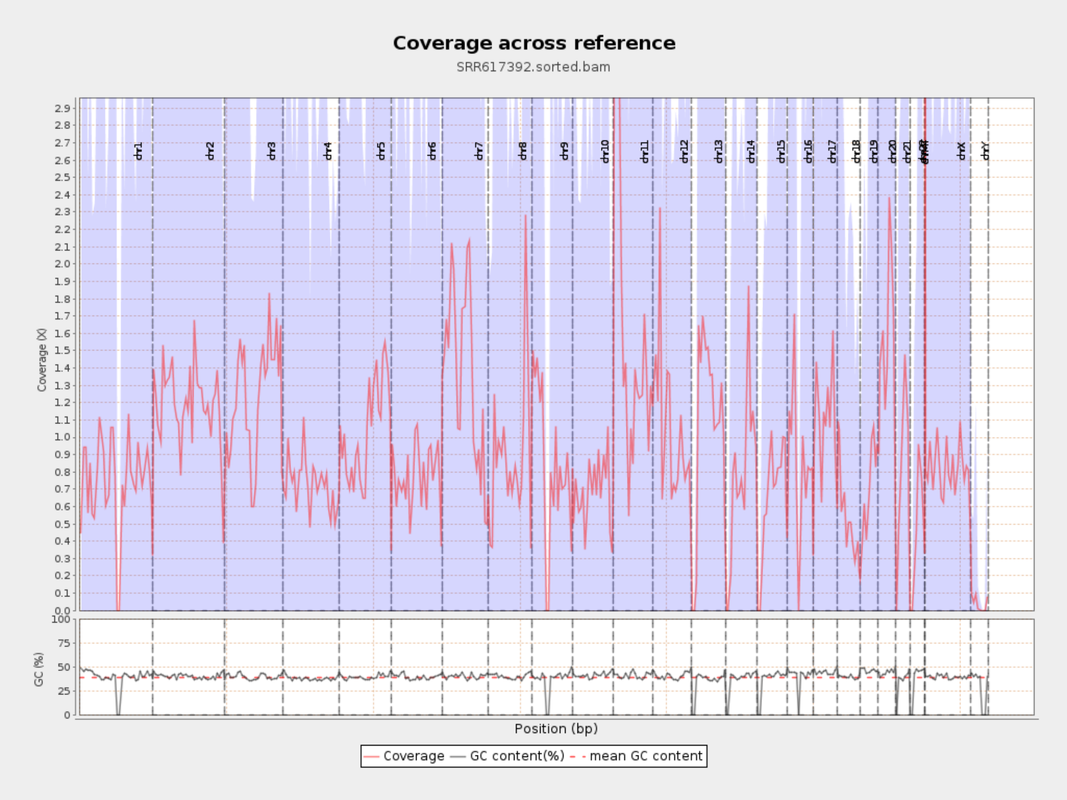
2.7. Chromosome stats

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

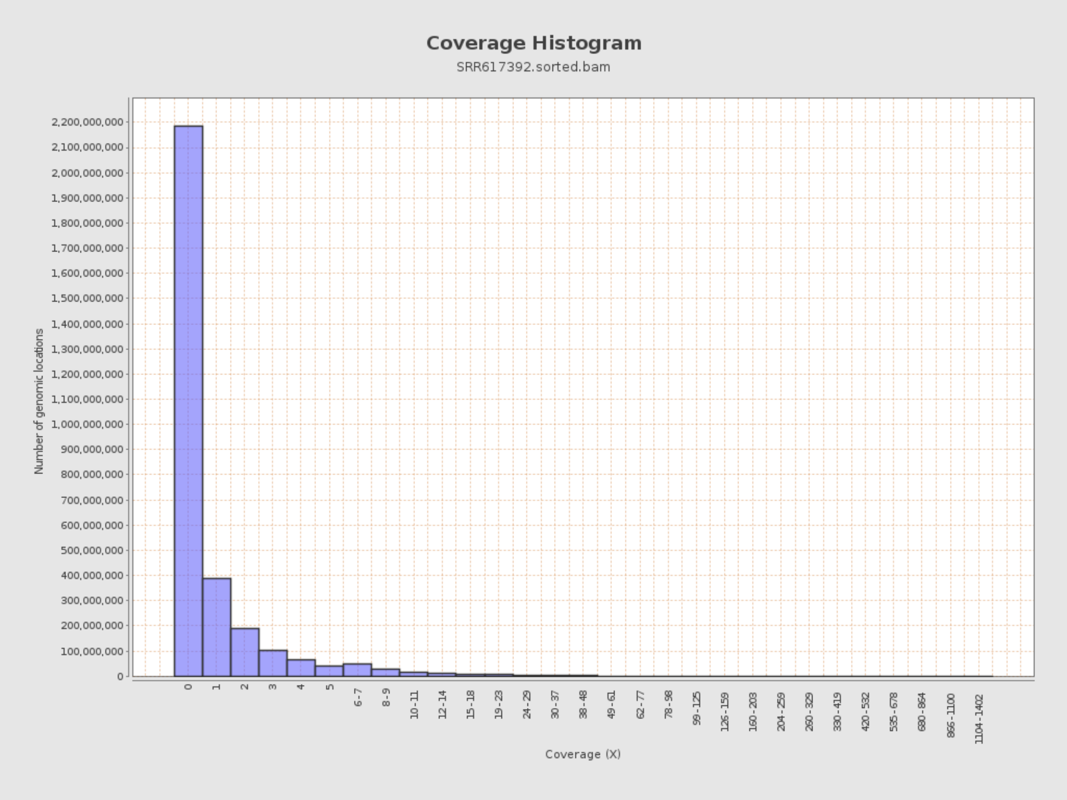
		bases	coverage	deviation
chr1	249250621	186914231	0.7499	2.7005
chr2	243199373	290402408	1.1941	3.0175
chr3	198022430	245782861	1.2412	3.3538
chr4	191154276	140201492	0.7334	2.2373
chr5	180915260	186649412	1.0317	2.8261
chr6	171115067	133641112	0.781	2.5542
chr7	159138663	217654063	1.3677	3.1756
chr8	146364022	128751848	0.8797	3.182
chr9	141213431	116675174	0.8262	2.5828
chr10	135534747	93190451	0.6876	2.3718
chr11	135006516	215968959	1.5997	3.7775
chr12	133851895	138402751	1.034	2.7204
chr13	115169878	126799129	1.101	2.7324
chr14	107349540	84265672	0.785	2.8373
chr15	102531392	66507275	0.6487	2.3061
chr16	90354753	72940651	0.8073	3.2518
chr17	81195210	89126176	1.0977	3.6567
chr18	78077248	41744289	0.5347	1.9723
chr19	59128983	41239188	0.6974	2.2797
chr20	63025520	98481706	1.5626	4.6199
chr21	48129895	39846653	0.8279	2.4665
chr22	51304566	23023542	0.4488	2.0055
chrMT	16571	178292	10.7593	4.8347
chrX	155270560	127785911	0.823	2.5177

chrY	59373566	2285090	0.0385	0.552

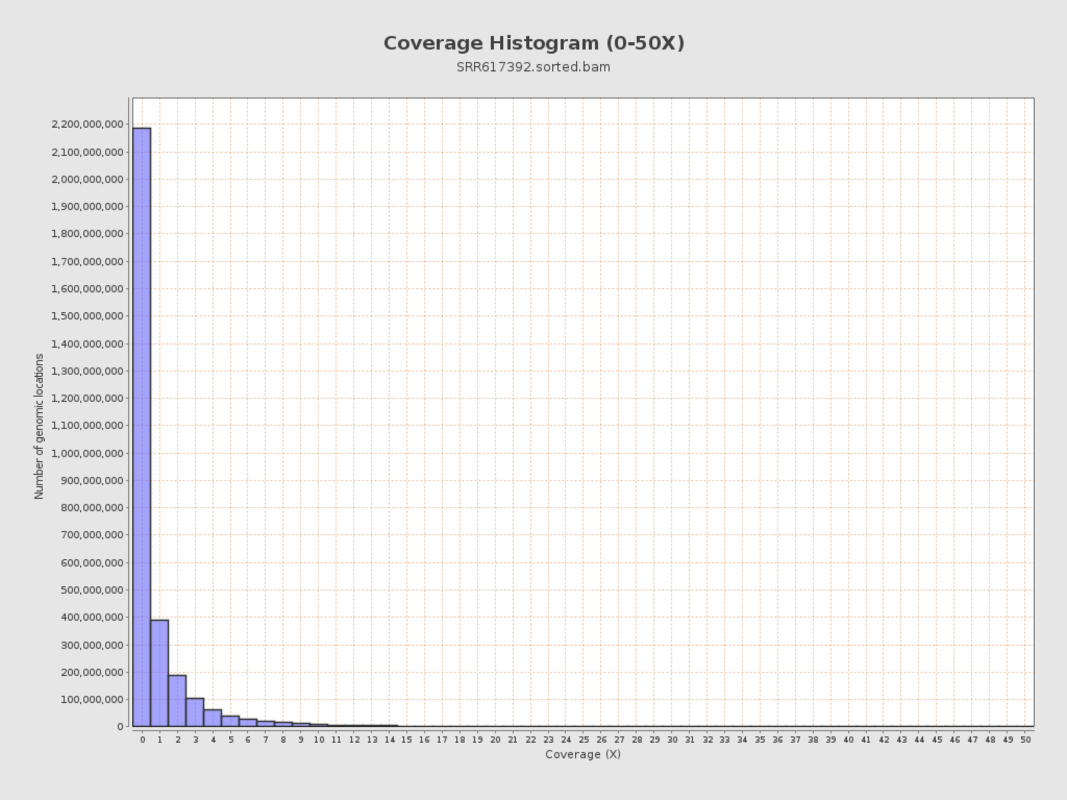
3. Results : Coverage across reference



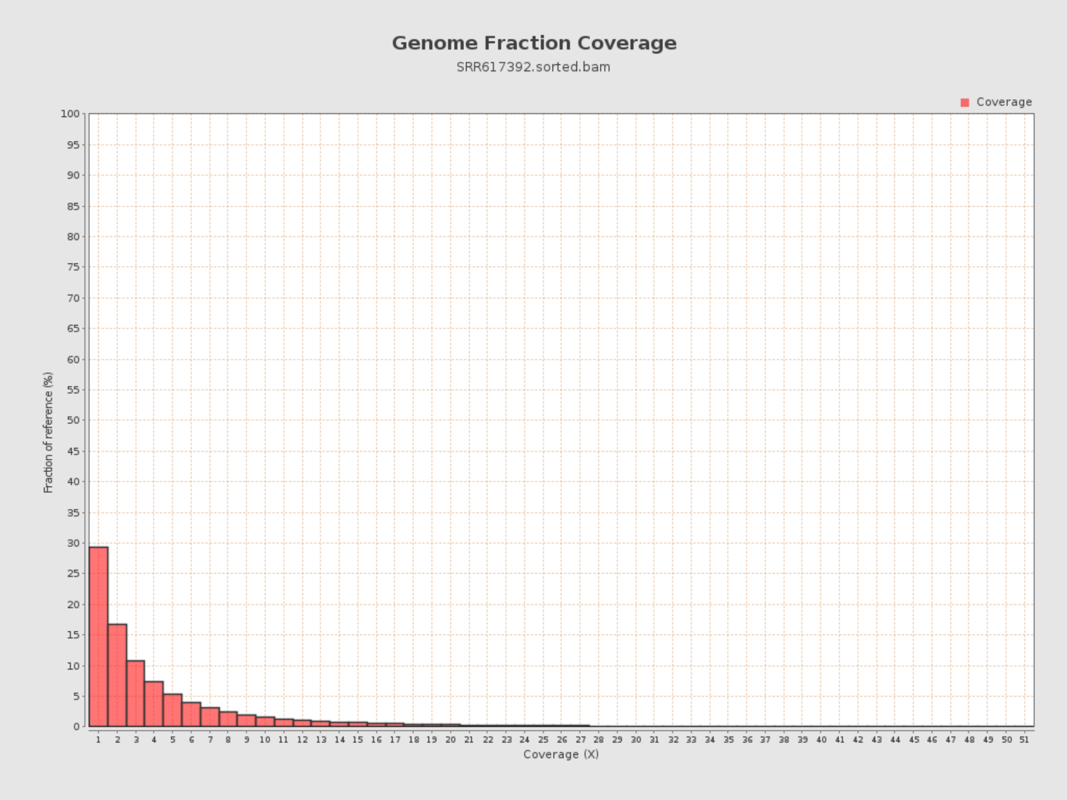
4. Results : Coverage Histogram



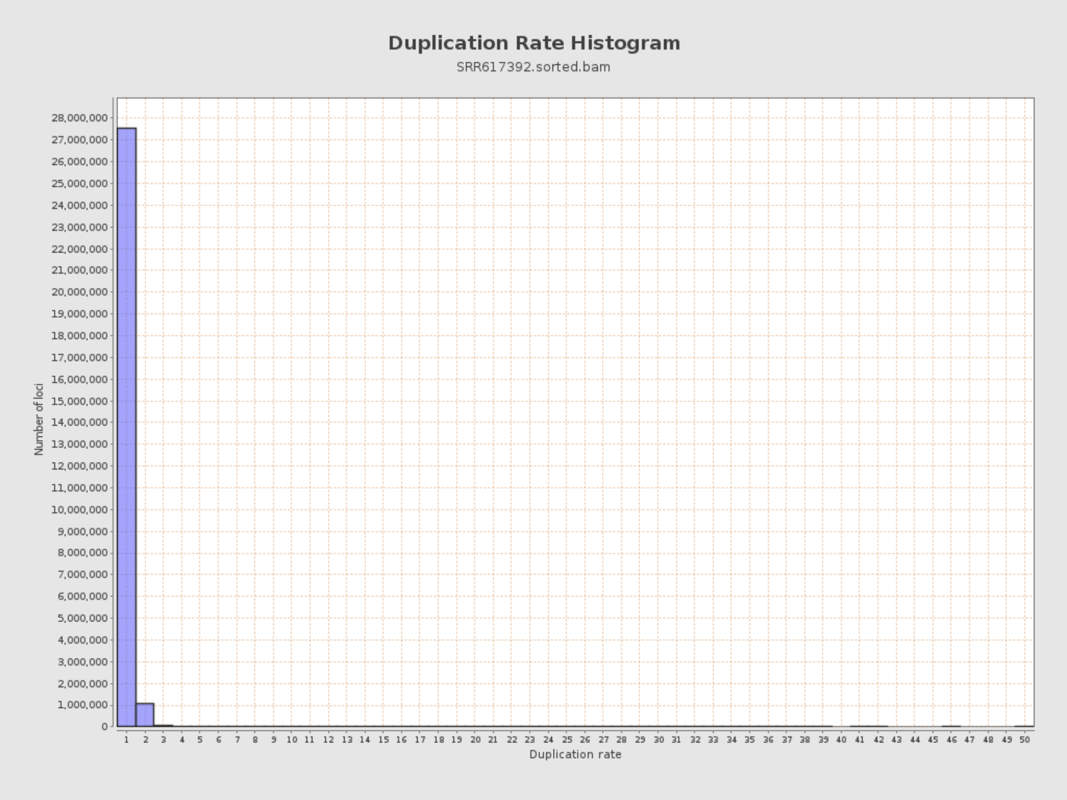
5. Results : Coverage Histogram (0-50X)



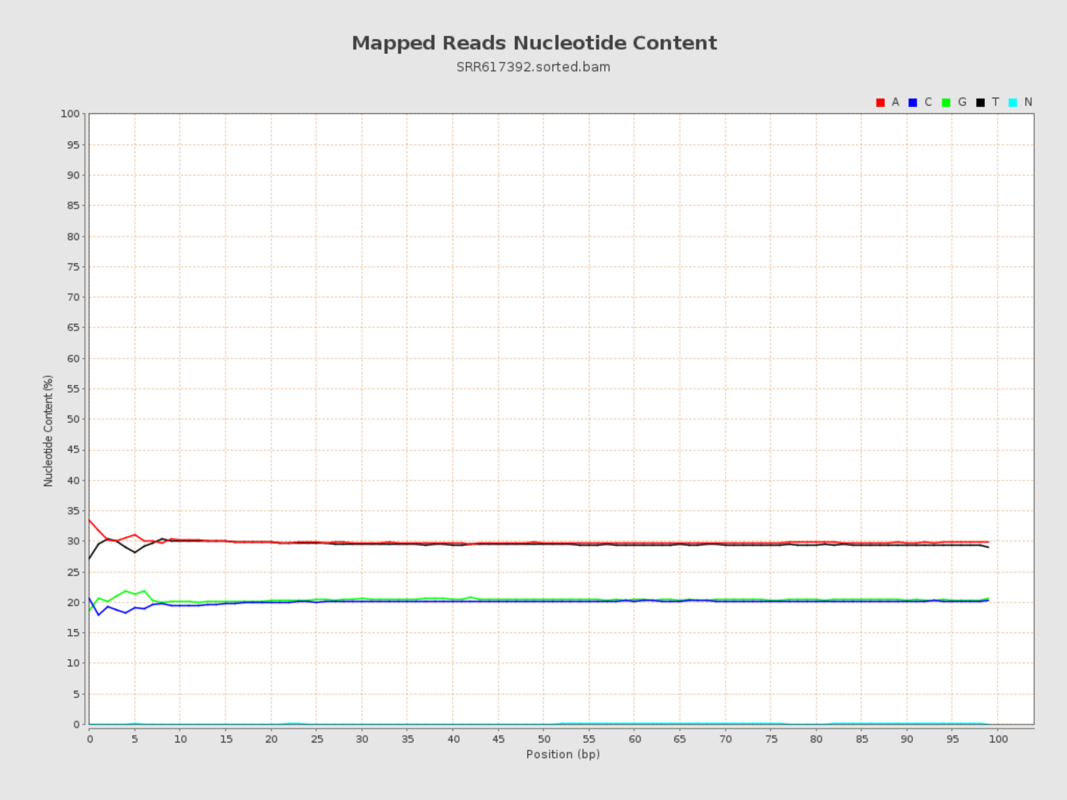
6. Results : Genome Fraction Coverage



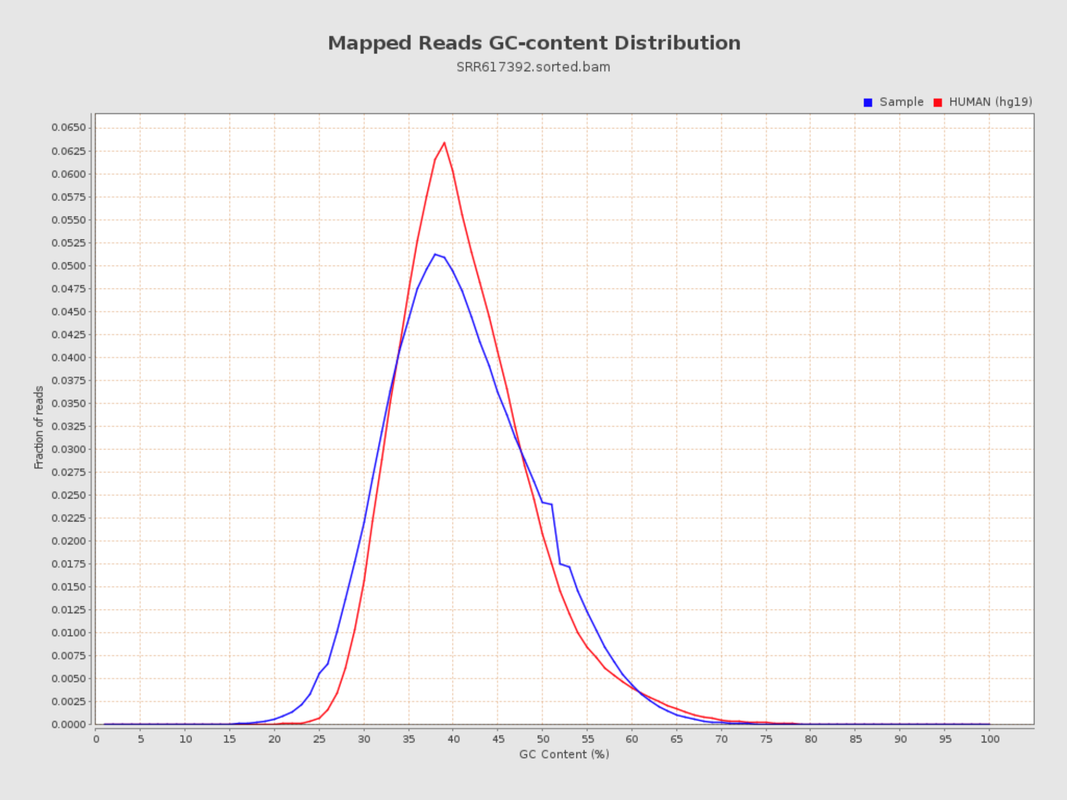
7. Results : Duplication Rate Histogram



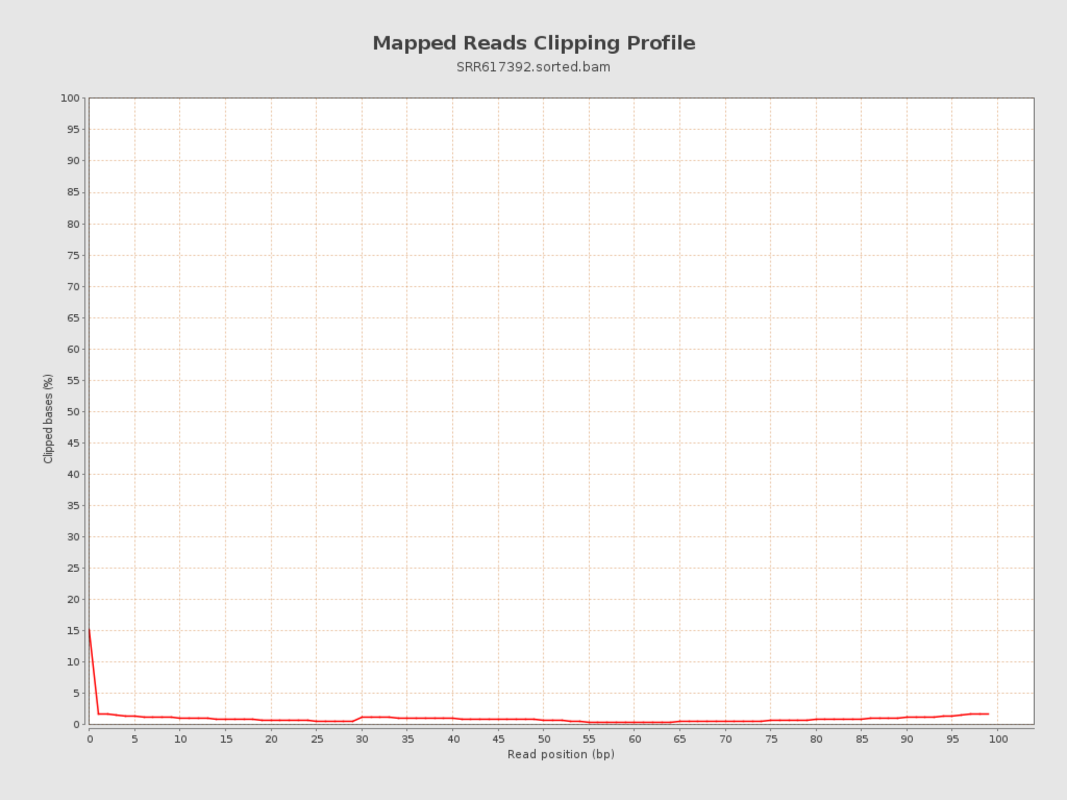
8. Results : Mapped Reads Nucleotide Content



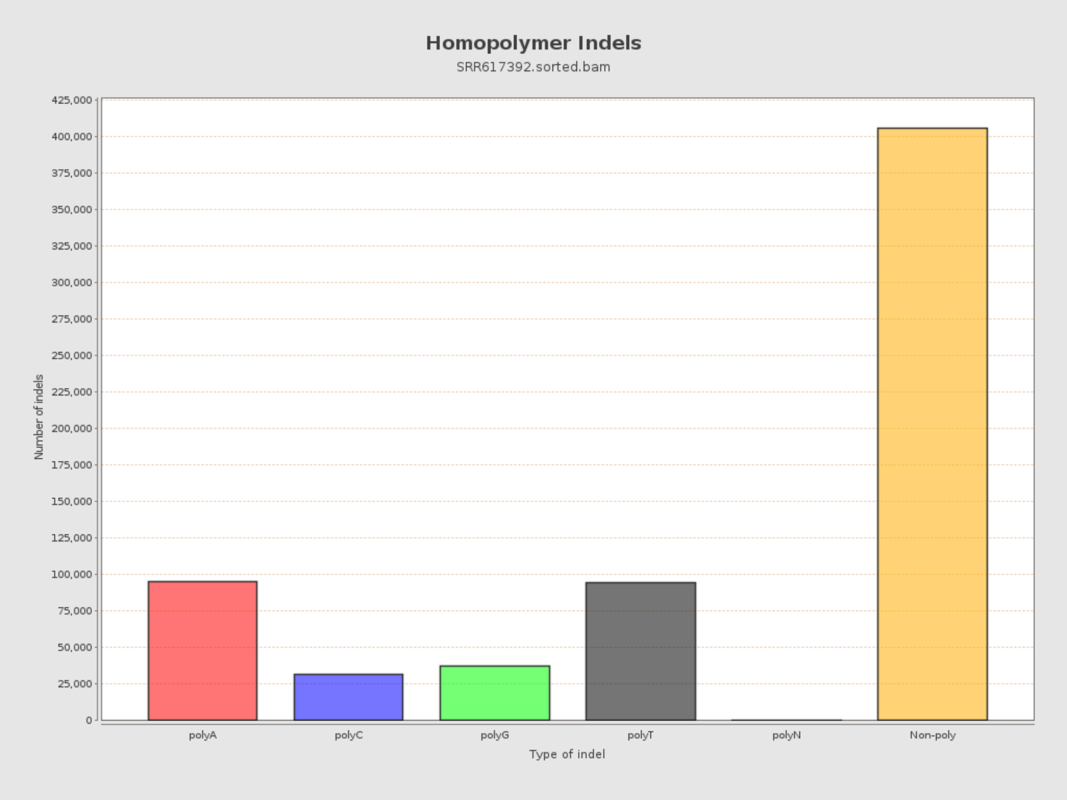
9. Results : Mapped Reads GC-content Distribution



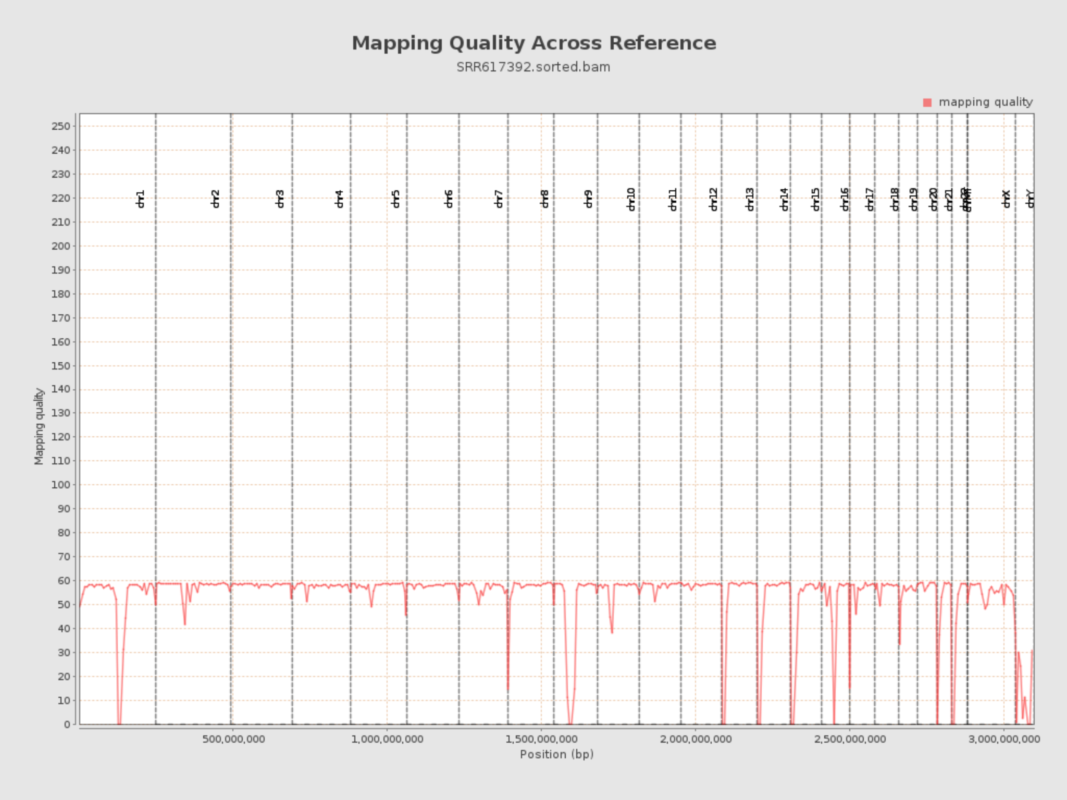
10. Results : Mapped Reads Clipping Profile



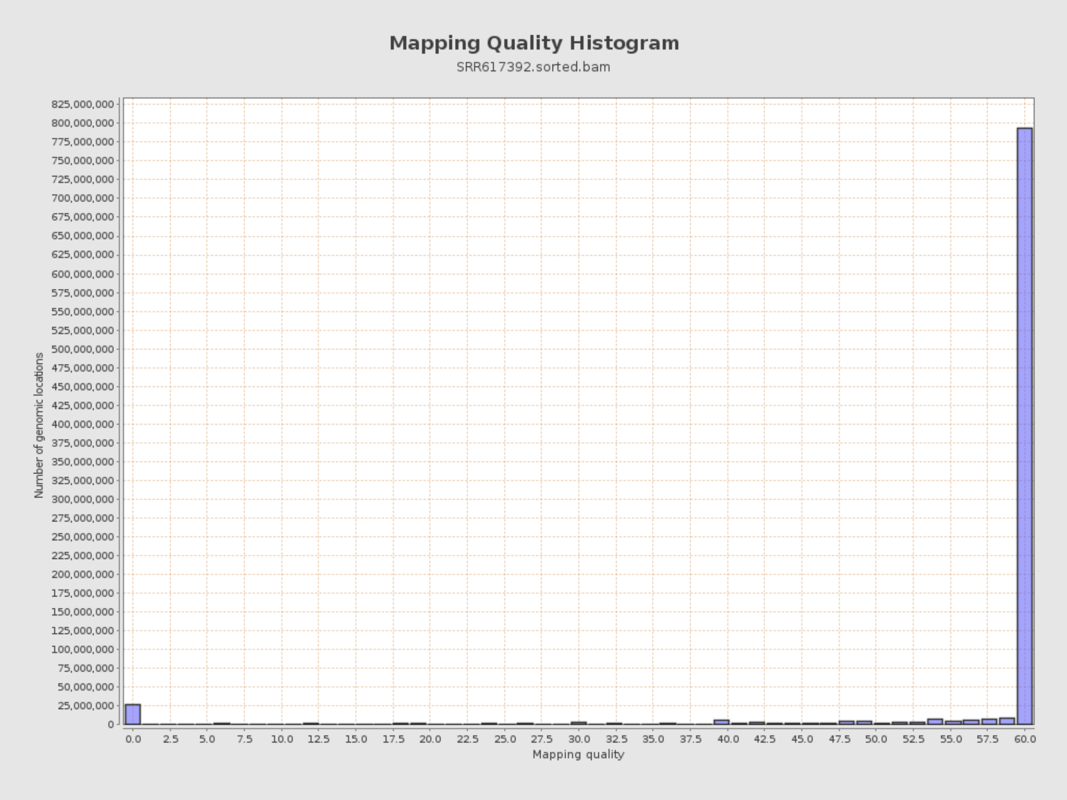
11. Results : Homopolymer Indels



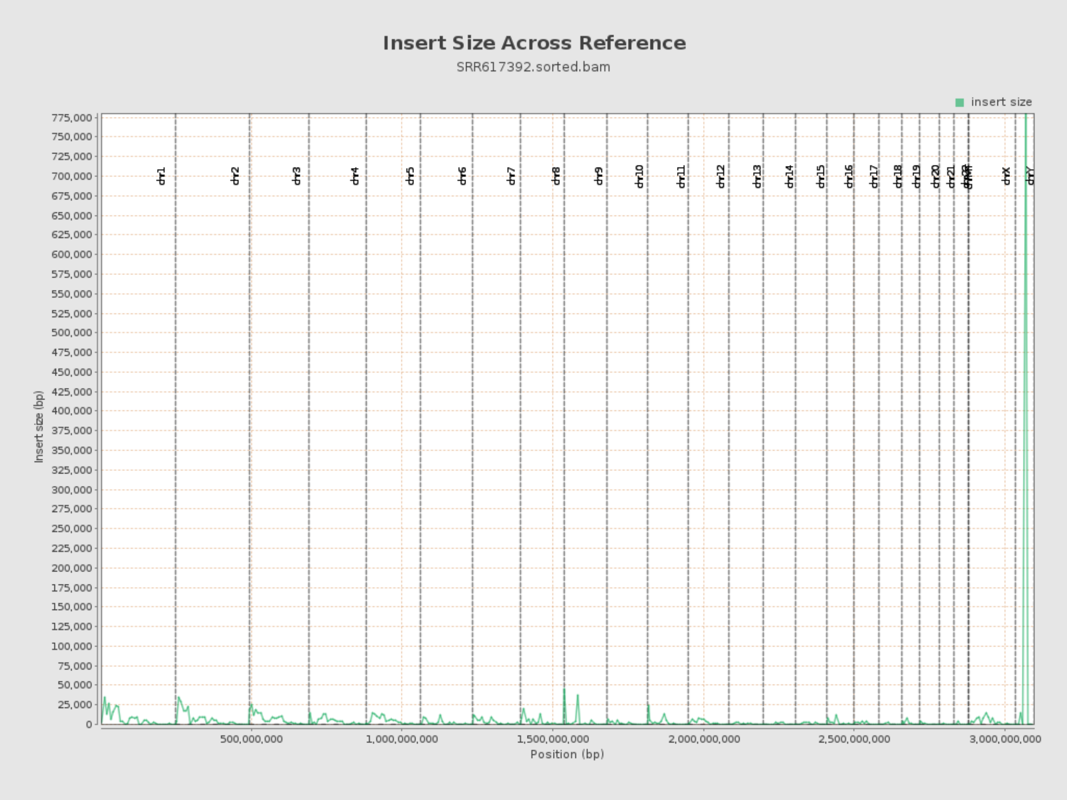
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram