Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 14:56:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617397.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_SRR617397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617397_1.fastq.gz SRR617397_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 14:56:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617397.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,291,123 / 94.66%
Unmapped reads	1,708,877 / 5.34%
Mapped paired reads	30,291,123 / 94.66%
Mapped reads, first in pair	15,205,088 / 47.52%
Mapped reads, second in pair	15,086,035 / 47.14%
Mapped reads, both in pair	29,843,964 / 93.26%
Mapped reads, singletons	447,159 / 1.4%
Secondary alignments	0
Supplementary alignments	459,516 / 1.44%
Read min/max/mean length	30 / 100 / 100.59
Duplicated reads (estimated)	1,395,928 / 4.36%
Duplication rate	4.2%
Clipped reads	3,099,052 / 9.68%

2.2. ACGT Content

Number/percentage of A's	889,355,917 / 29.78%
Number/percentage of C's	600,844,915 / 20.12%
Number/percentage of T's	880,678,268 / 29.49%
Number/percentage of G's	613,195,839 / 20.53%
Number/percentage of N's	2,058,708 / 0.07%

GC Percentage	40.66%

2.3. Coverage

Mean	0.9648
Standard Deviation	2.9499

2.4. Mapping Quality

Mean Mapping Quality	53.97

2.5. Insert size

Mean	47,364.96
Standard Deviation	2,064,302.21
P25/Median/P75	171 / 211 / 274

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	29,805,836
Insertions	745,219
Mapped reads with at least one insertion	2.44%
Deletions	289,718
Mapped reads with at least one deletion	0.94%
Homopolymer indels	35.9%

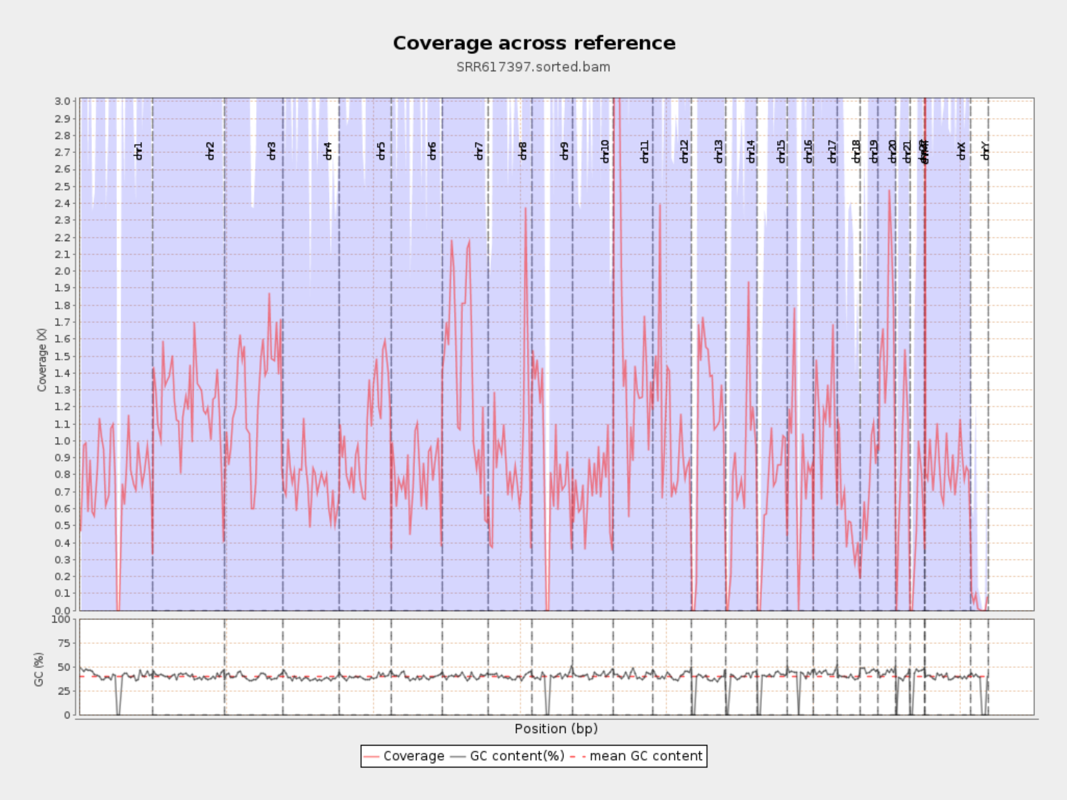
2.7. Chromosome stats

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

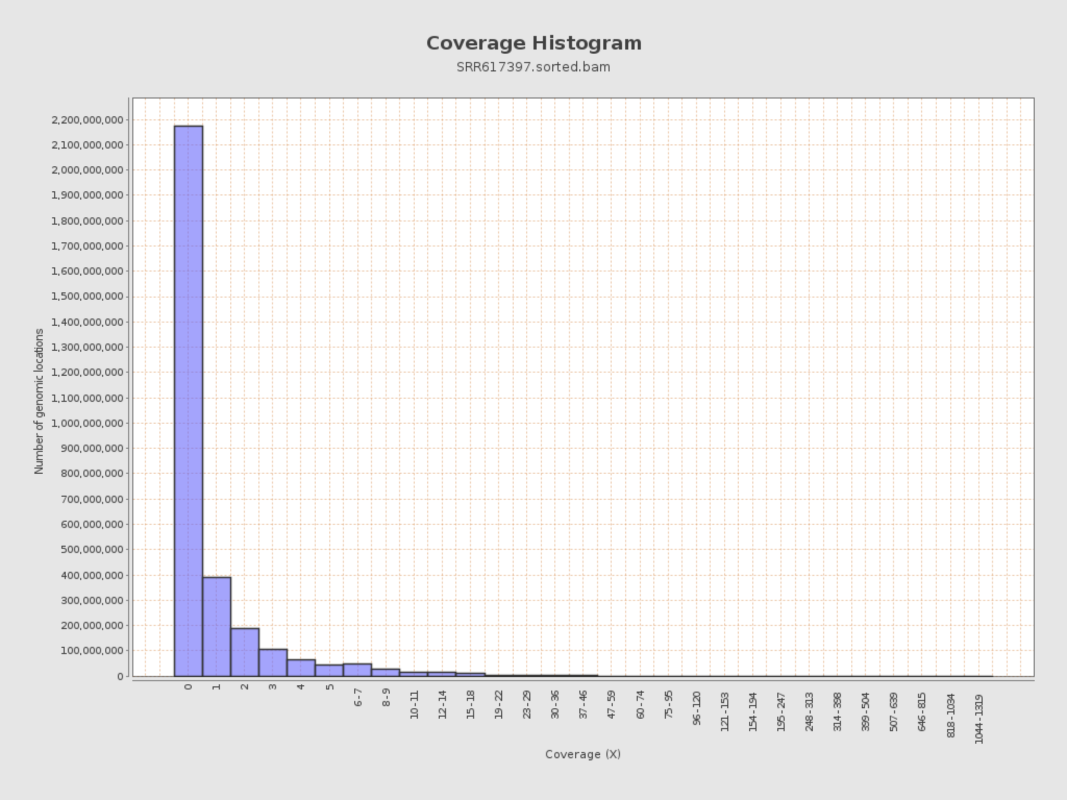
		bases	coverage	deviation
chr1	249250621	192215461	0.7712	2.7654
chr2	243199373	297326109	1.2226	3.0854
chr3	198022430	252267810	1.2739	3.4554
chr4	191154276	143171709	0.749	2.2903
chr5	180915260	191153837	1.0566	2.8914
chr6	171115067	136657986	0.7986	2.6062
chr7	159138663	223578415	1.4049	3.2548
chr8	146364022	131894623	0.9011	3.2969
chr9	141213431	119531698	0.8465	2.6403
chr10	135534747	95718267	0.7062	2.4371
chr11	135006516	221997892	1.6443	3.8783
chr12	133851895	142322489	1.0633	2.8046
chr13	115169878	129414212	1.1237	2.7829
chr14	107349540	86753782	0.8081	2.9254
chr15	102531392	68637719	0.6694	2.3657
chr16	90354753	75268384	0.833	3.3665
chr17	81195210	92362063	1.1375	3.7315
chr18	78077248	42881146	0.5492	2.021
chr19	59128983	42796533	0.7238	2.3634
chr20	63025520	102271627	1.6227	4.7971
chr21	48129895	40907612	0.8499	2.5561
chr22	51304566	24197334	0.4716	2.1027
chrMT	16571	181245	10.9375	5.5041
chrX	155270560	130919474	0.8432	2.575

chrY	59373566	2357574	0.0397	0.5657

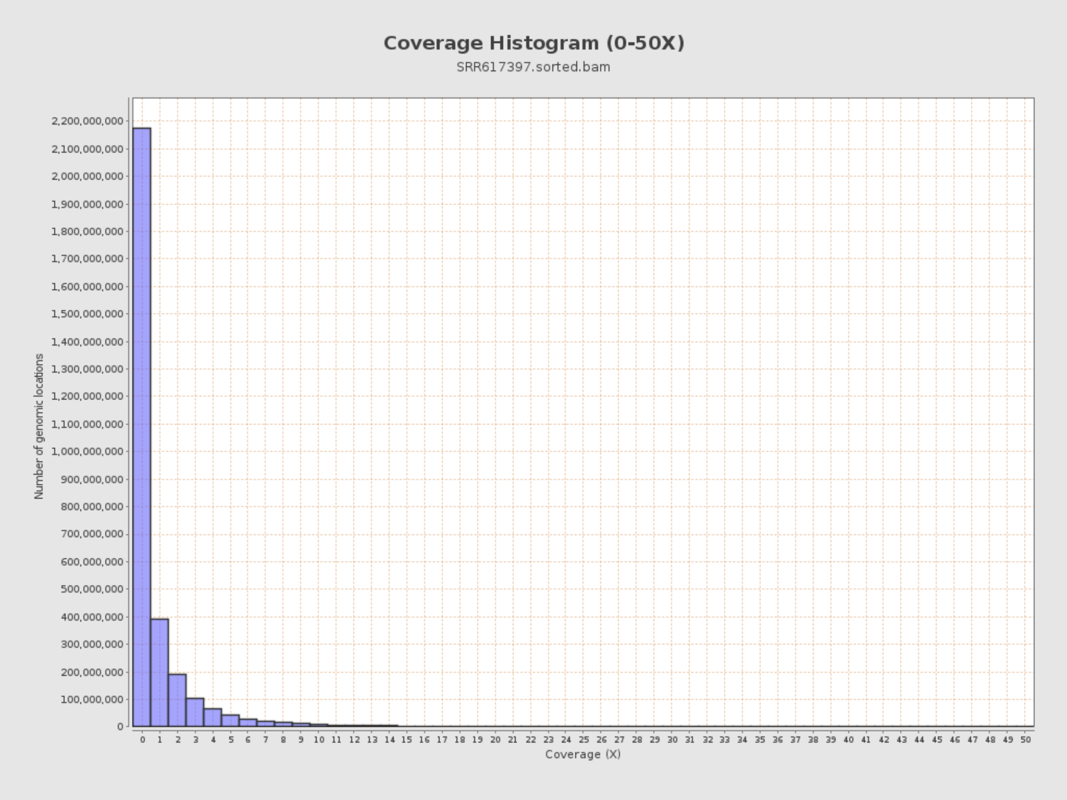
3. Results : Coverage across reference



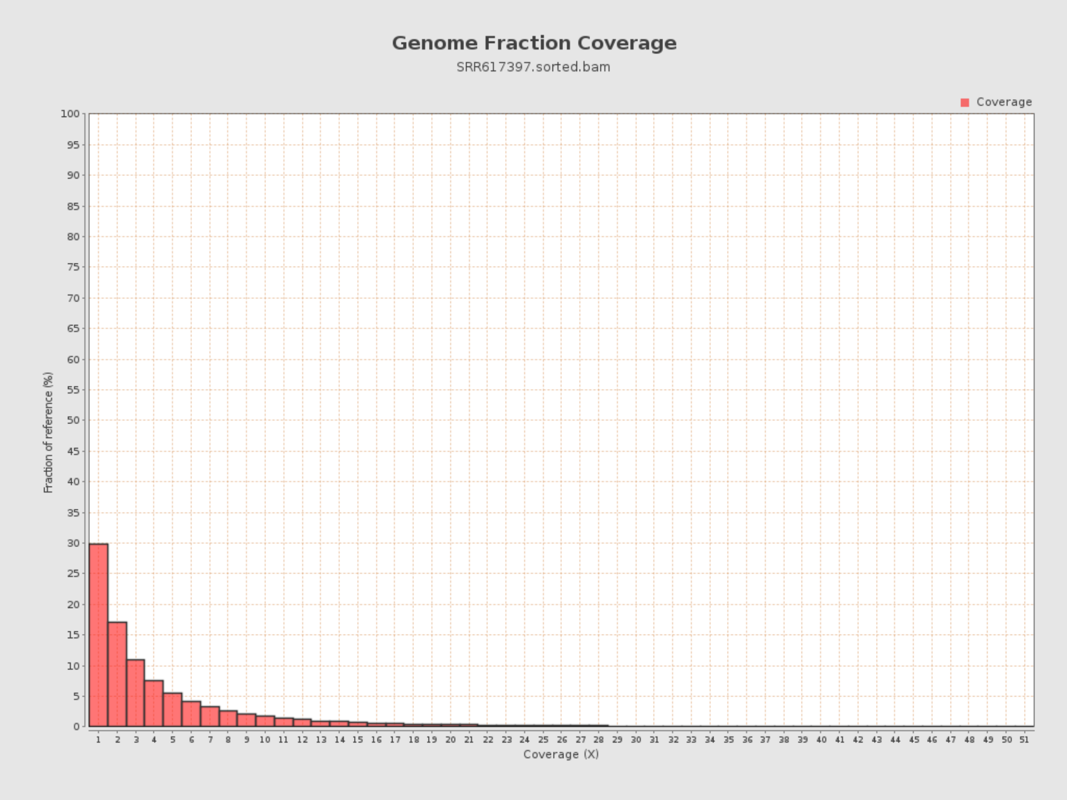
4. Results : Coverage Histogram



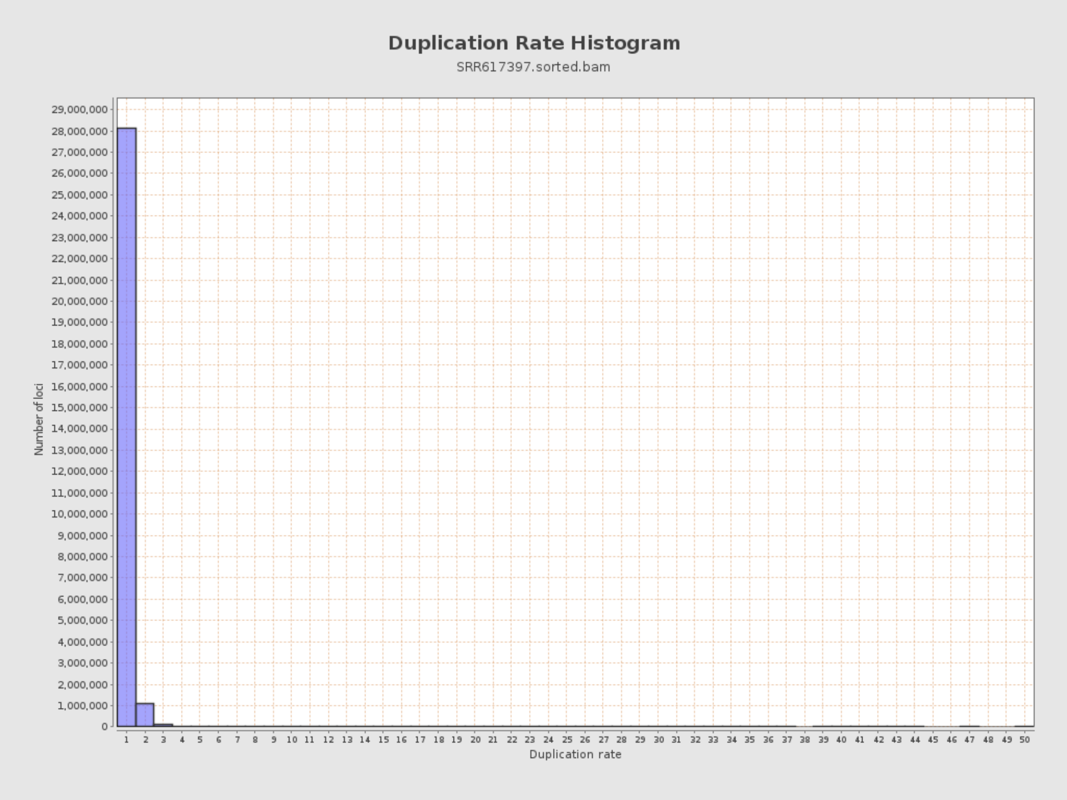
5. Results : Coverage Histogram (0-50X)



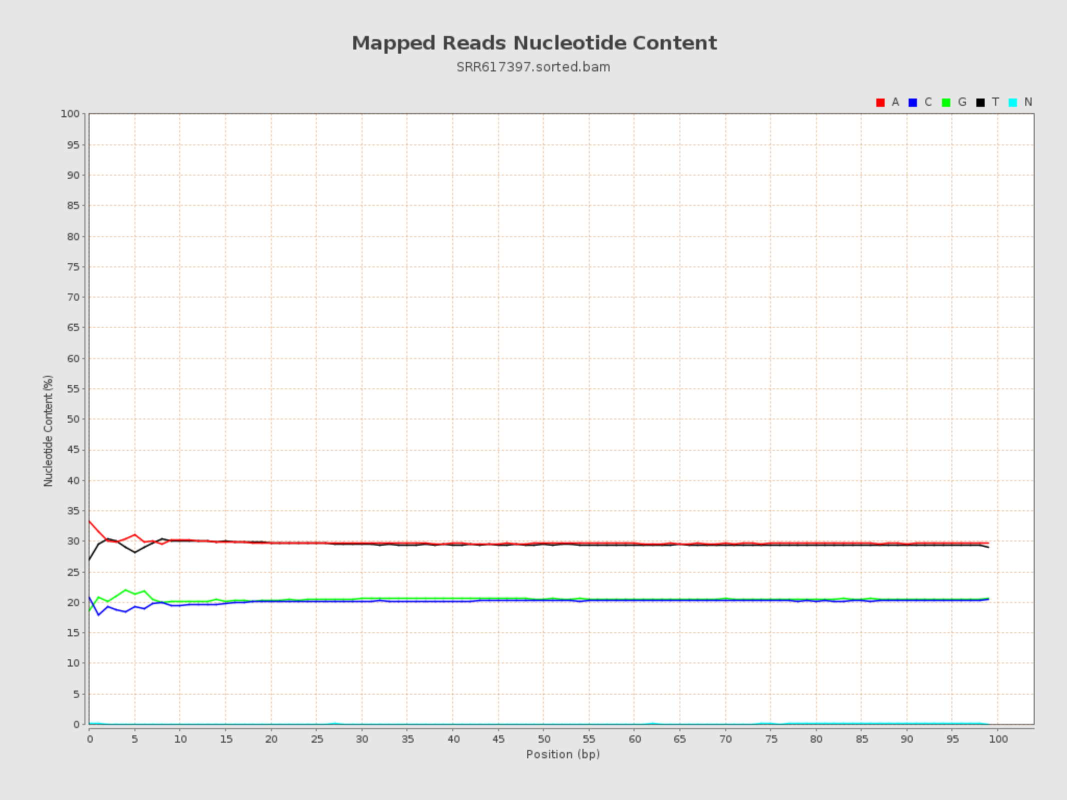
6. Results : Genome Fraction Coverage



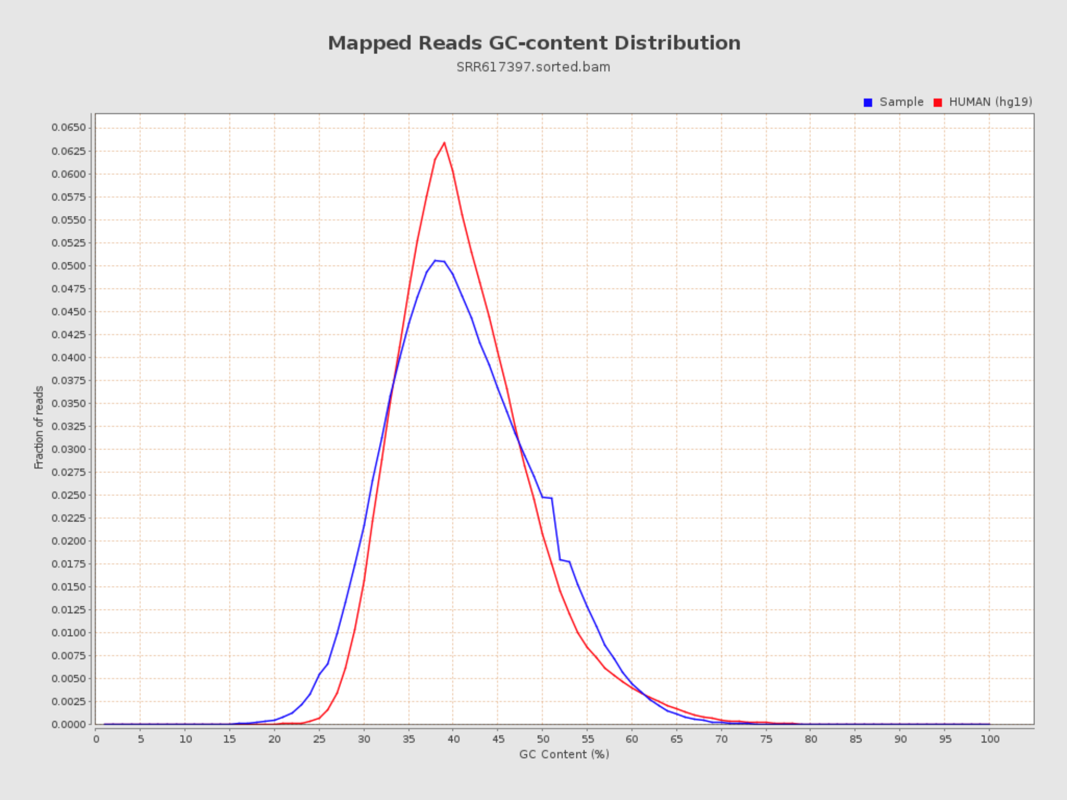
7. Results : Duplication Rate Histogram



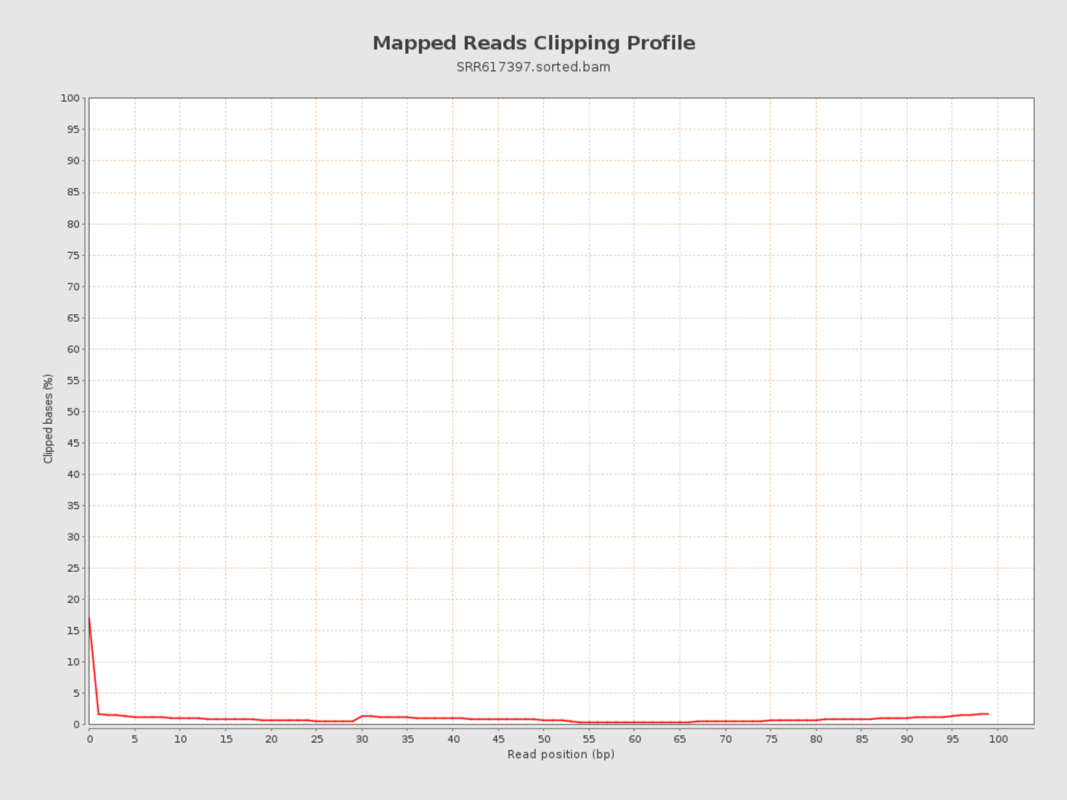
8. Results : Mapped Reads Nucleotide Content



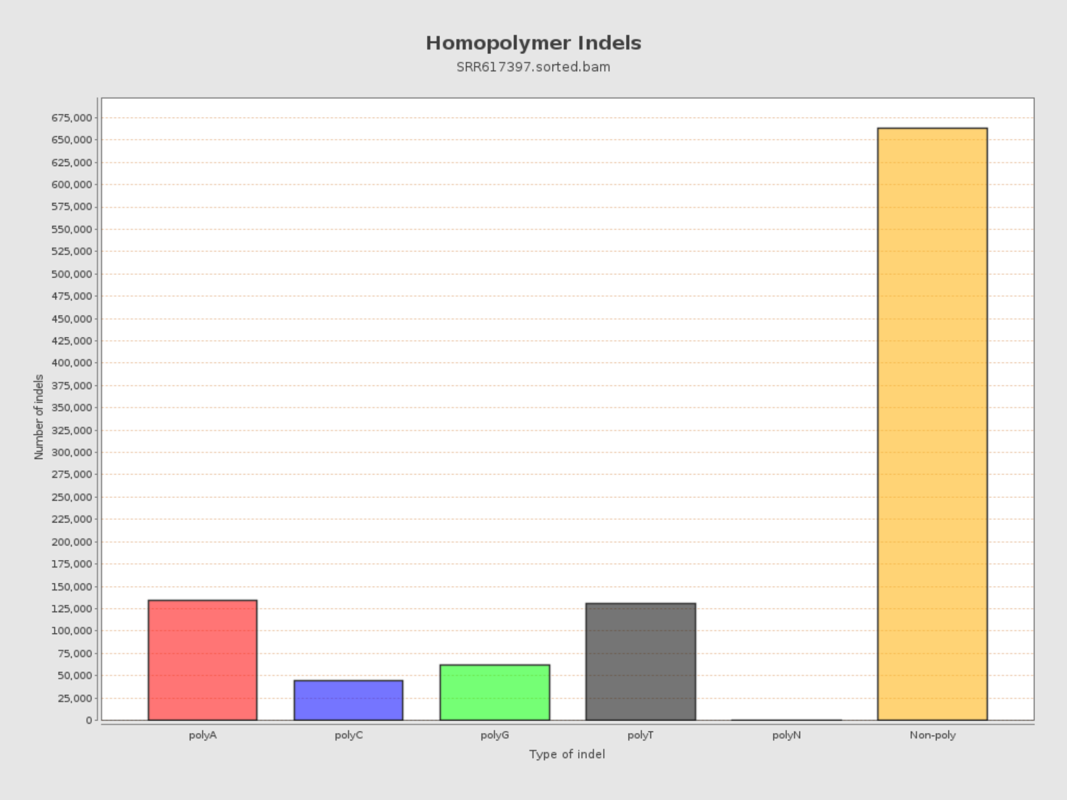
9. Results : Mapped Reads GC-content Distribution



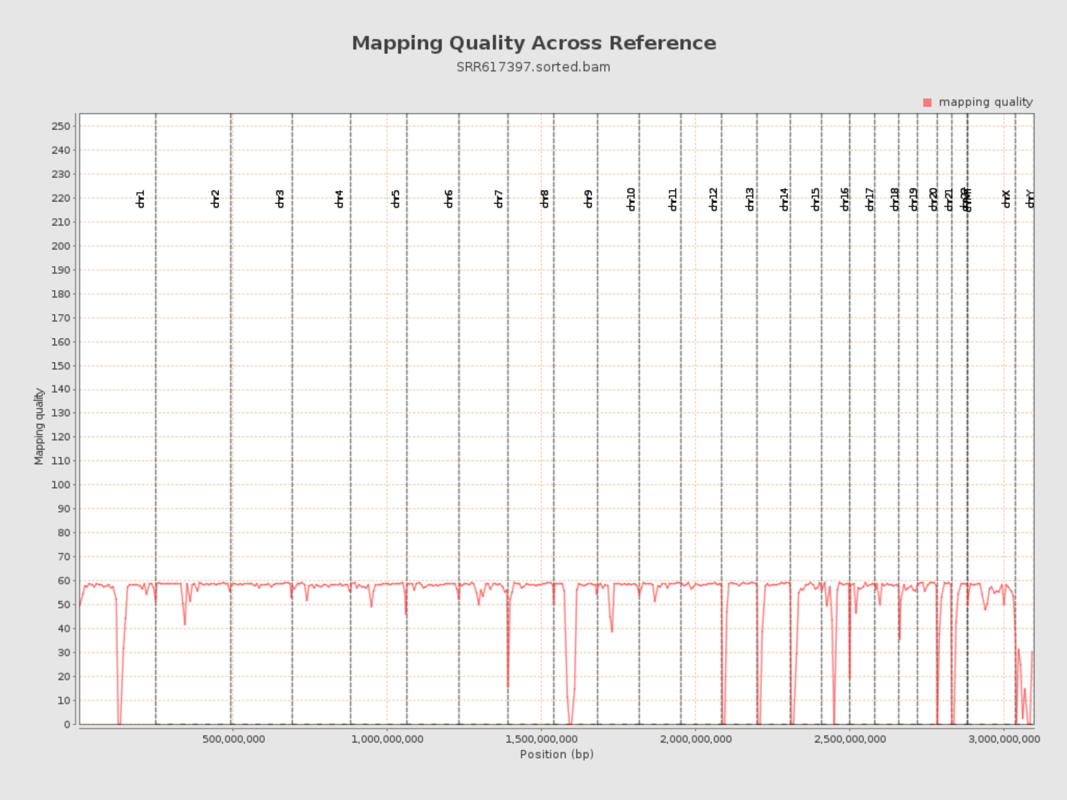
10. Results : Mapped Reads Clipping Profile



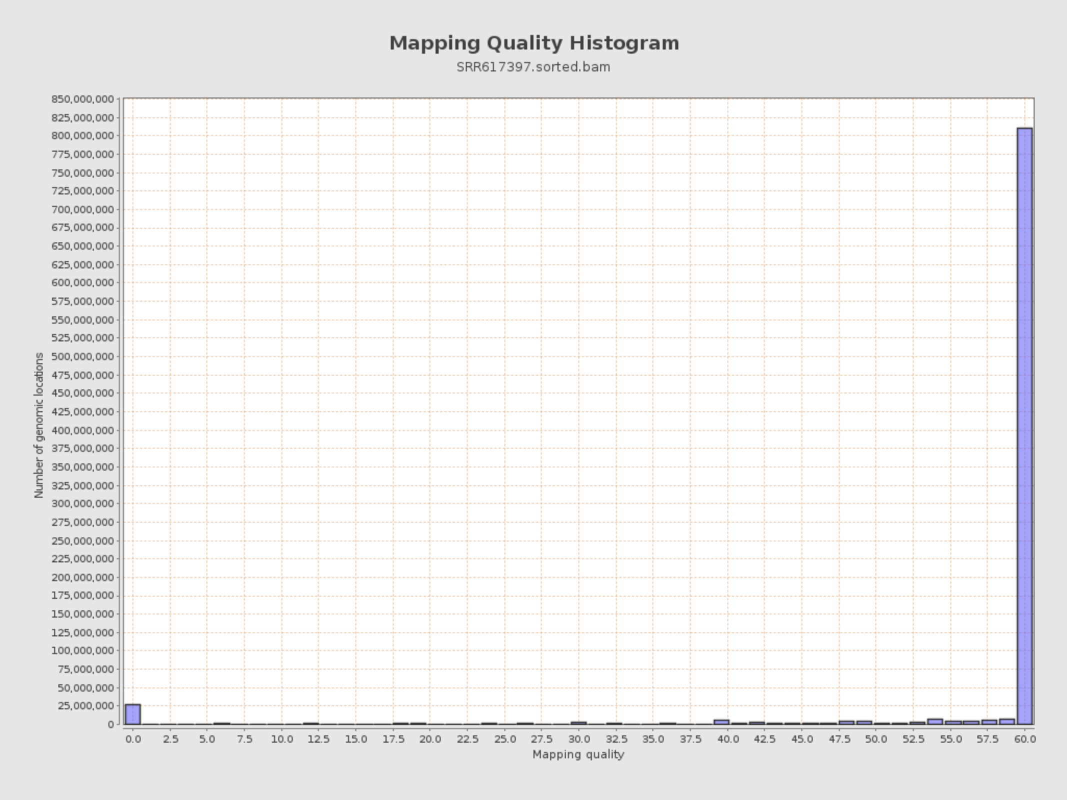
11. Results : Homopolymer Indels



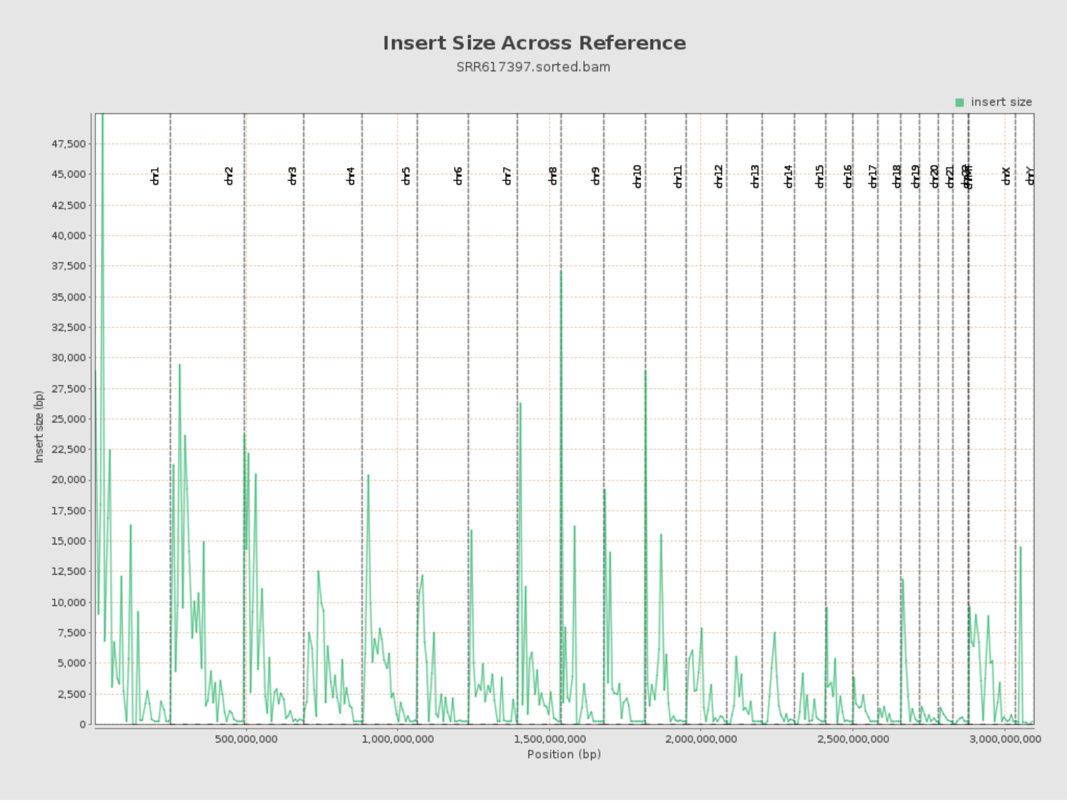
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram