Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 12:10:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617394.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_SRR617394 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617394_1.fastq.gz SRR617394_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 12:10:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617394.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,445,755 / 95.14%
Unmapped reads	1,554,245 / 4.86%
Mapped paired reads	30,445,755 / 95.14%
Mapped reads, first in pair	15,268,508 / 47.71%
Mapped reads, second in pair	15,177,247 / 47.43%
Mapped reads, both in pair	30,030,166 / 93.84%
Mapped reads, singletons	415,589 / 1.3%
Secondary alignments	0
Supplementary alignments	465,402 / 1.45%
Read min/max/mean length	30 / 100 / 100.6
Duplicated reads (estimated)	1,415,445 / 4.42%
Duplication rate	4.23%
Clipped reads	3,129,602 / 9.78%

2.2. ACGT Content

Number/percentage of A's	893,103,583 / 29.75%
Number/percentage of C's	604,363,478 / 20.13%
Number/percentage of T's	884,842,986 / 29.48%
Number/percentage of G's	616,975,093 / 20.55%
Number/percentage of N's	2,353,052 / 0.08%

GC Percentage	40.69%

2.3. Coverage

Mean	0.9698
Standard Deviation	2.9672

2.4. Mapping Quality

Mean Mapping Quality	53.98

2.5. Insert size

Mean	48,231.24
Standard Deviation	2,088,149.34
P25/Median/P75	172 / 213 / 277

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	28,939,628
Insertions	244,404
Mapped reads with at least one insertion	0.79%
Deletions	292,451
Mapped reads with at least one deletion	0.94%
Homopolymer indels	45.04%

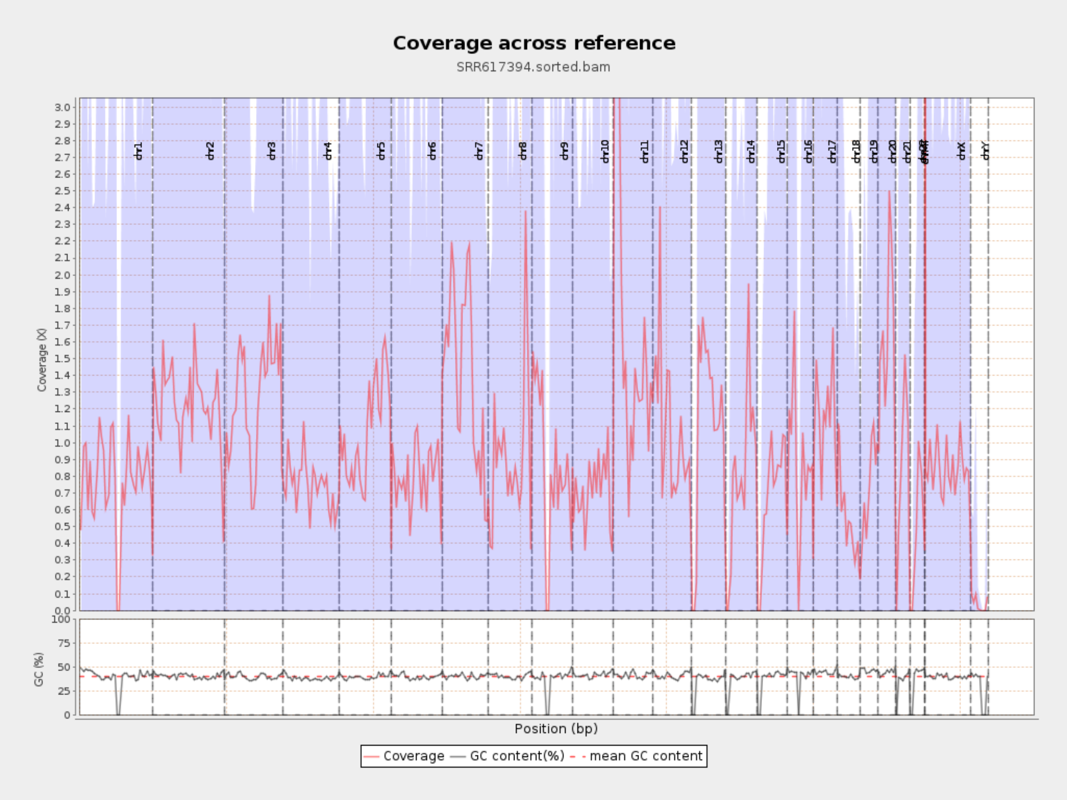
2.7. Chromosome stats

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

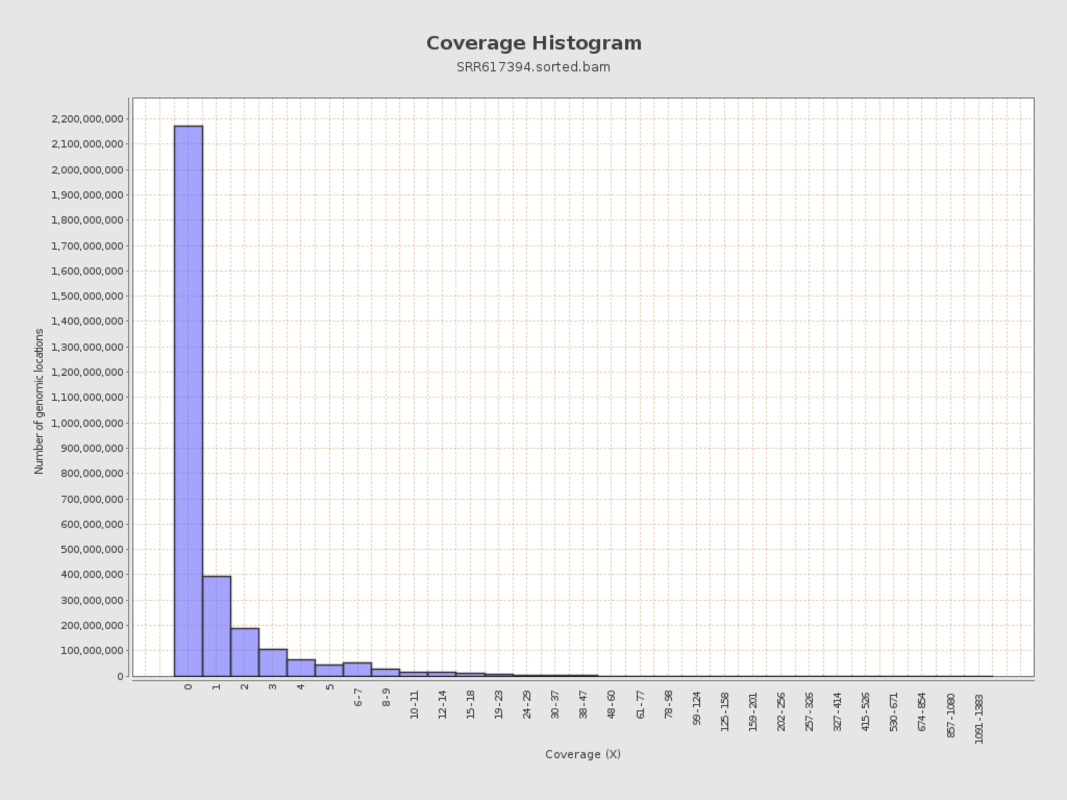
		bases	coverage	deviation
chr1	249250621	193705947	0.7772	2.7765
chr2	243199373	299616229	1.232	3.1072
chr3	198022430	253168002	1.2785	3.4709
chr4	191154276	143682429	0.7517	2.2988
chr5	180915260	192333182	1.0631	2.9181
chr6	171115067	137108474	0.8013	2.63
chr7	159138663	224479348	1.4106	3.2752
chr8	146364022	132709561	0.9067	3.3144
chr9	141213431	119730909	0.8479	2.6474
chr10	135534747	96218324	0.7099	2.4379
chr11	135006516	223013917	1.6519	3.8985
chr12	133851895	143074976	1.0689	2.8115
chr13	115169878	129723874	1.1264	2.7899
chr14	107349540	87257547	0.8128	2.9474
chr15	102531392	69184723	0.6748	2.3902
chr16	90354753	75880949	0.8398	3.3835
chr17	81195210	92893953	1.1441	3.7514
chr18	78077248	42951102	0.5501	2.0341
chr19	59128983	43085984	0.7287	2.3835
chr20	63025520	102880511	1.6324	4.8495
chr21	48129895	41027399	0.8524	2.5553
chr22	51304566	24385053	0.4753	2.1239
chrMT	16571	192995	11.6466	6.0528
chrX	155270560	131641618	0.8478	2.5978

chrY	59373566	2349816	0.0396	0.57

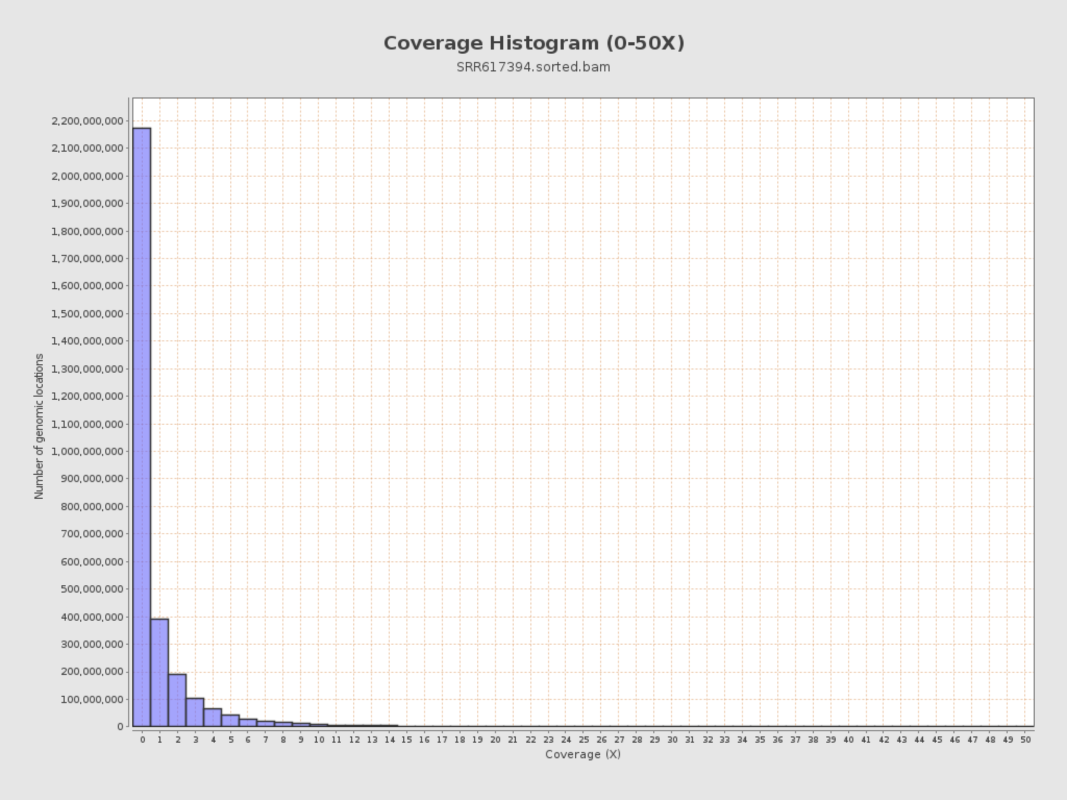
3. Results : Coverage across reference



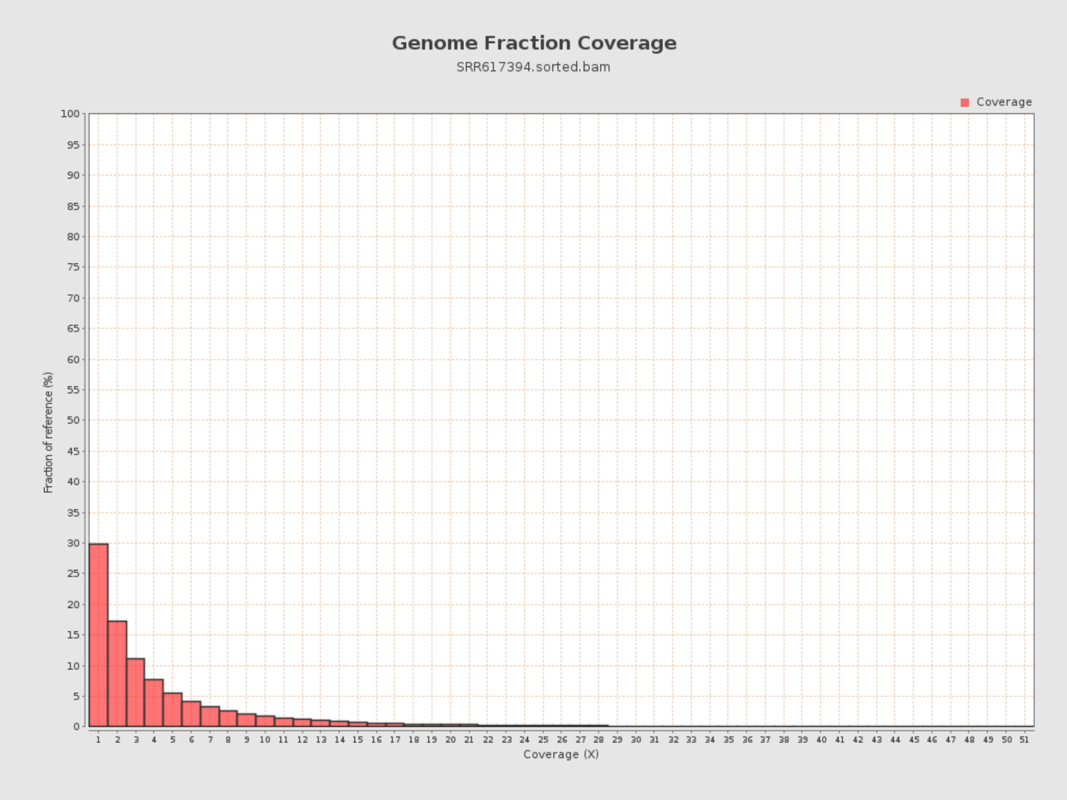
4. Results : Coverage Histogram



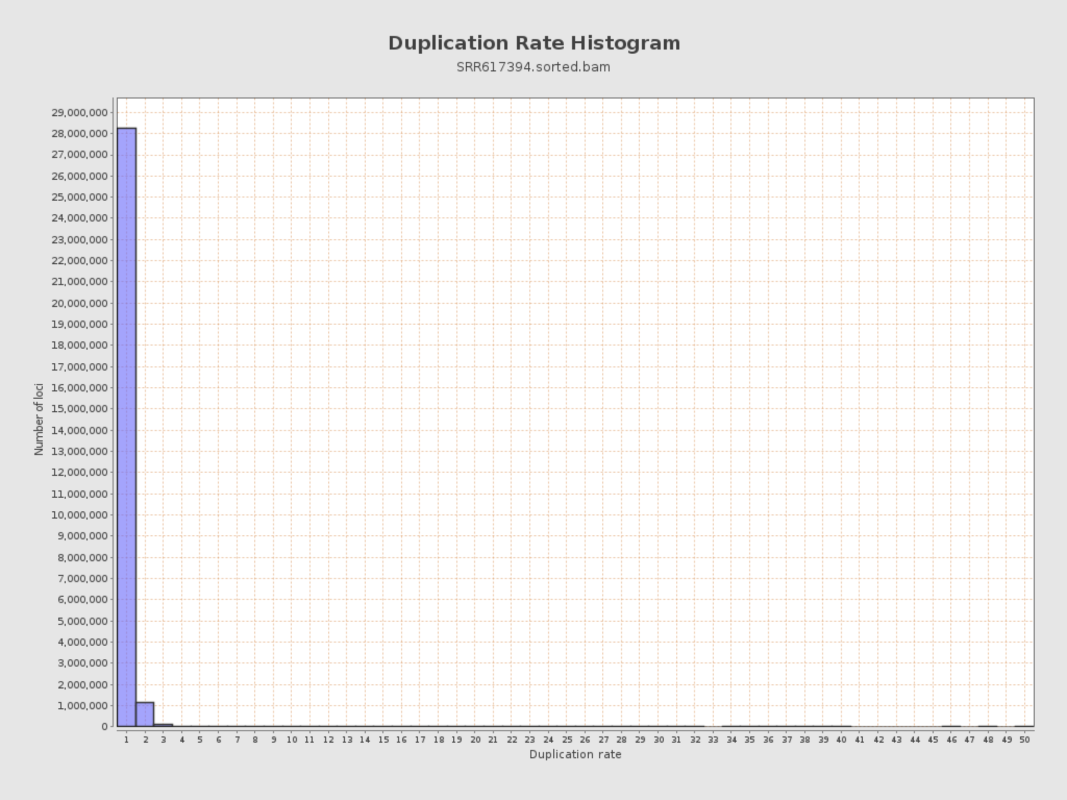
5. Results : Coverage Histogram (0-50X)



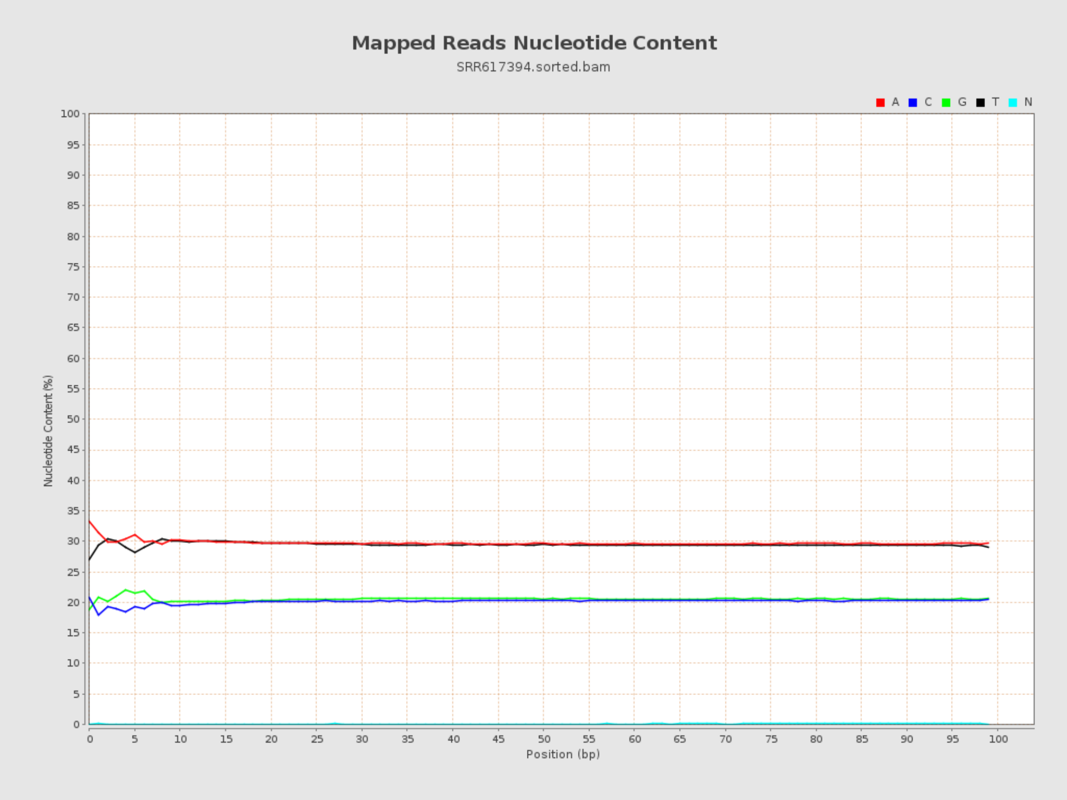
6. Results : Genome Fraction Coverage



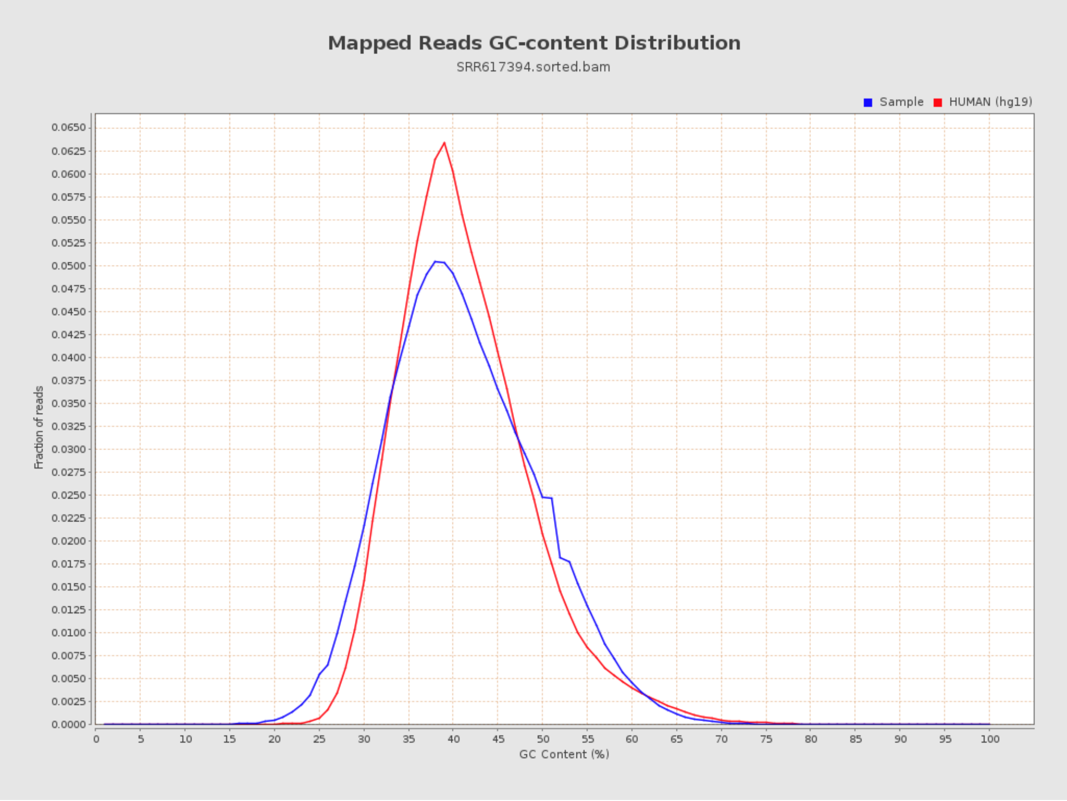
7. Results : Duplication Rate Histogram



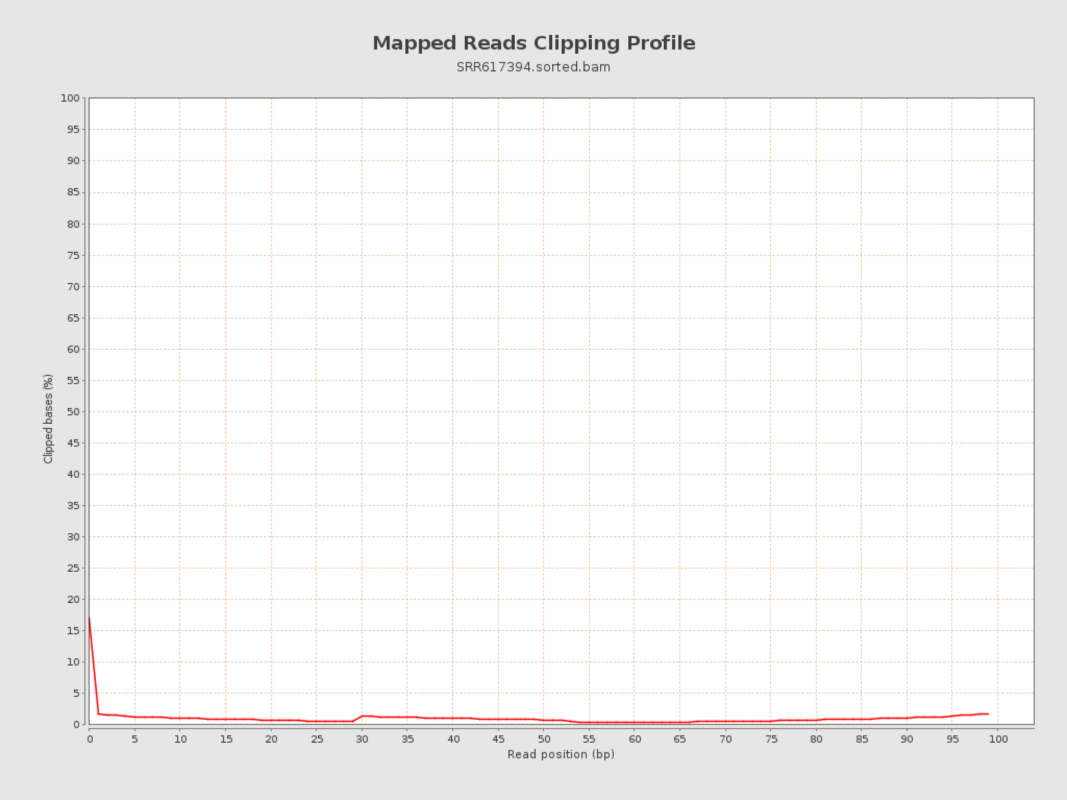
8. Results : Mapped Reads Nucleotide Content



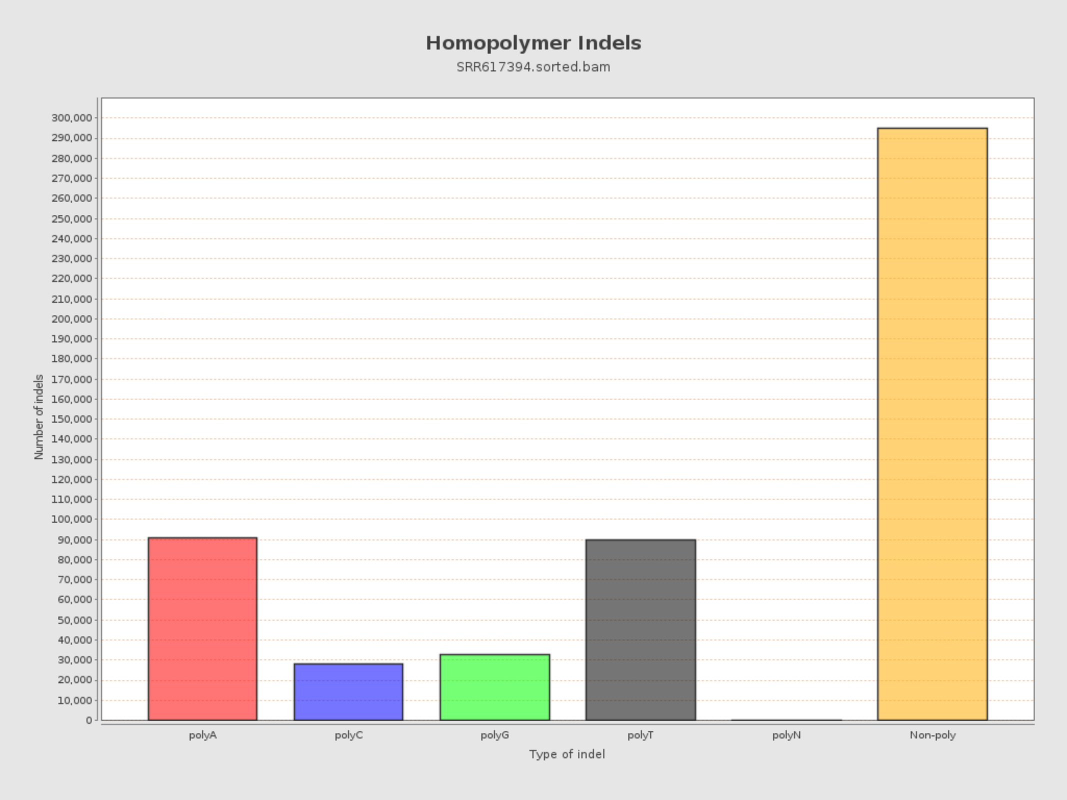
9. Results : Mapped Reads GC-content Distribution



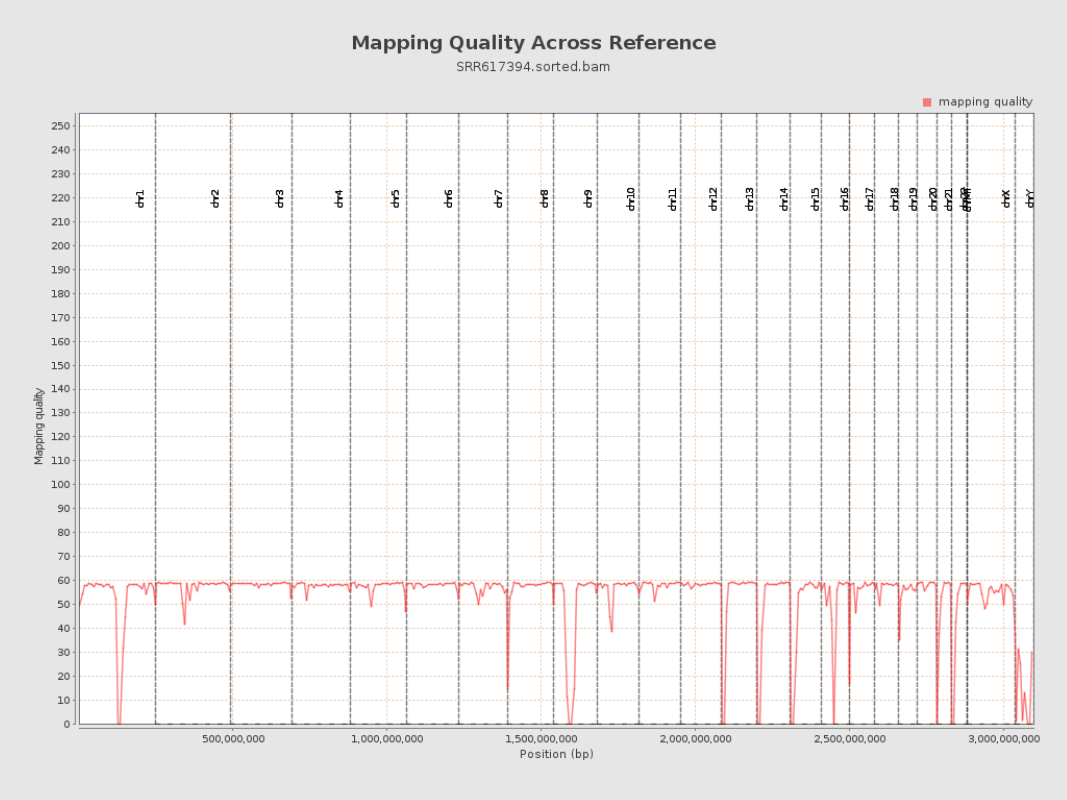
10. Results : Mapped Reads Clipping Profile



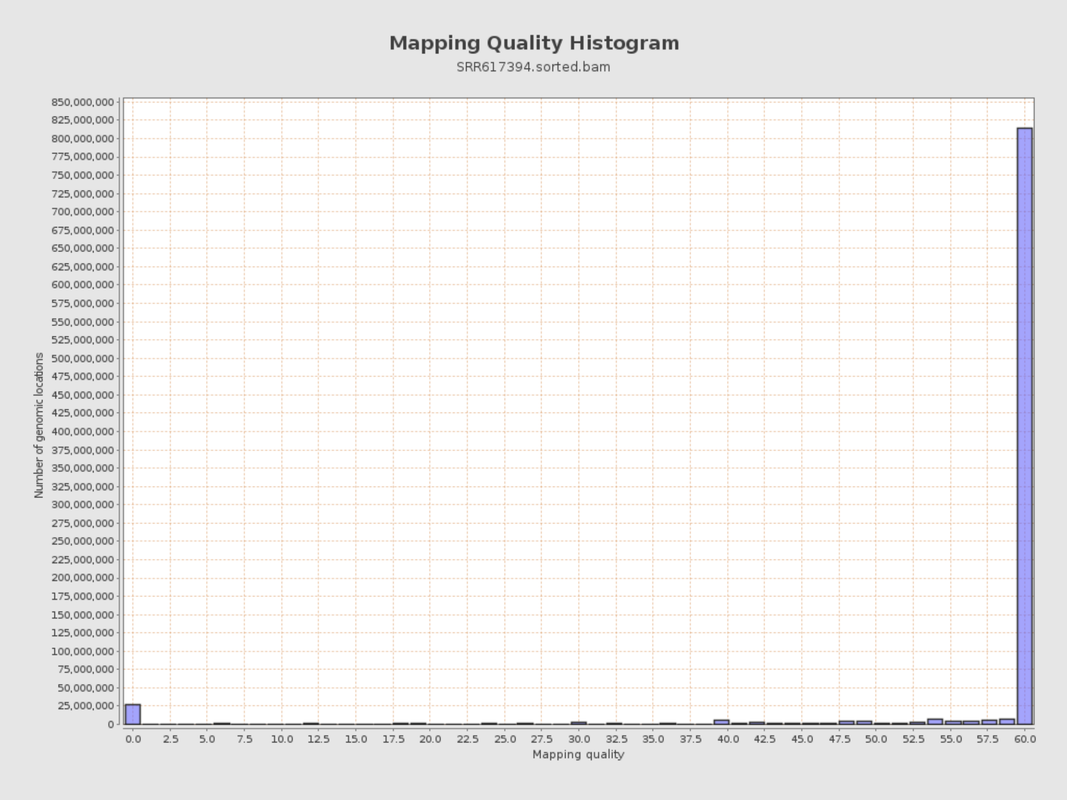
11. Results : Homopolymer Indels



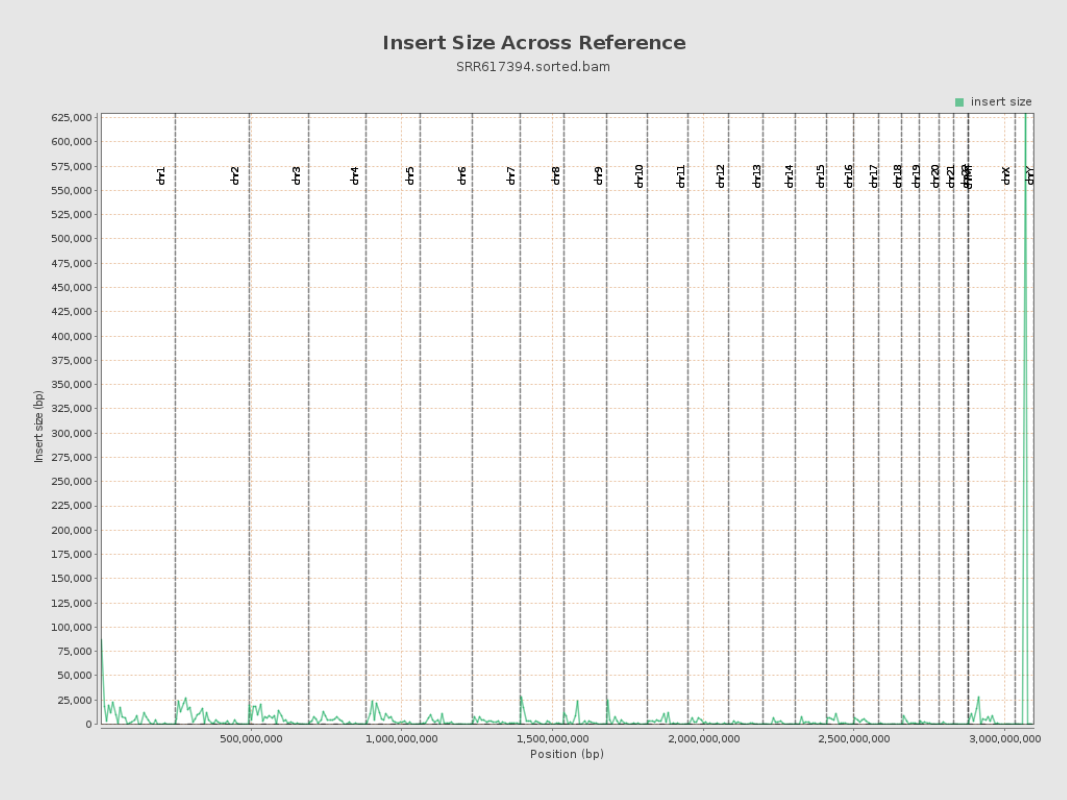
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram