Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 09:33:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617391.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_SRR617391 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617391_1.fastq.gz SRR617391_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 09:33:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617391.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,295,212 / 94.67%
Unmapped reads	1,704,788 / 5.33%
Mapped paired reads	30,295,212 / 94.67%
Mapped reads, first in pair	15,223,390 / 47.57%
Mapped reads, second in pair	15,071,822 / 47.1%
Mapped reads, both in pair	29,867,848 / 93.34%
Mapped reads, singletons	427,364 / 1.34%
Secondary alignments	0
Supplementary alignments	460,650 / 1.44%
Read min/max/mean length	30 / 100 / 100.6
Duplicated reads (estimated)	1,399,378 / 4.37%
Duplication rate	4.2%
Clipped reads	3,143,100 / 9.82%

2.2. ACGT Content

Number/percentage of A's	888,463,223 / 29.77%
Number/percentage of C's	600,341,154 / 20.12%
Number/percentage of T's	879,641,863 / 29.48%
Number/percentage of G's	613,037,527 / 20.54%
Number/percentage of N's	2,750,740 / 0.09%

GC Percentage	40.66%

2.3. Coverage

Mean	0.9642
Standard Deviation	2.9482

2.4. Mapping Quality

Mean Mapping Quality	53.96

2.5. Insert size

Mean	48,733
Standard Deviation	2,102,125
P25/Median/P75	173 / 213 / 278

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	29,889,498
Insertions	257,763
Mapped reads with at least one insertion	0.84%
Deletions	289,745
Mapped reads with at least one deletion	0.94%
Homopolymer indels	44.3%

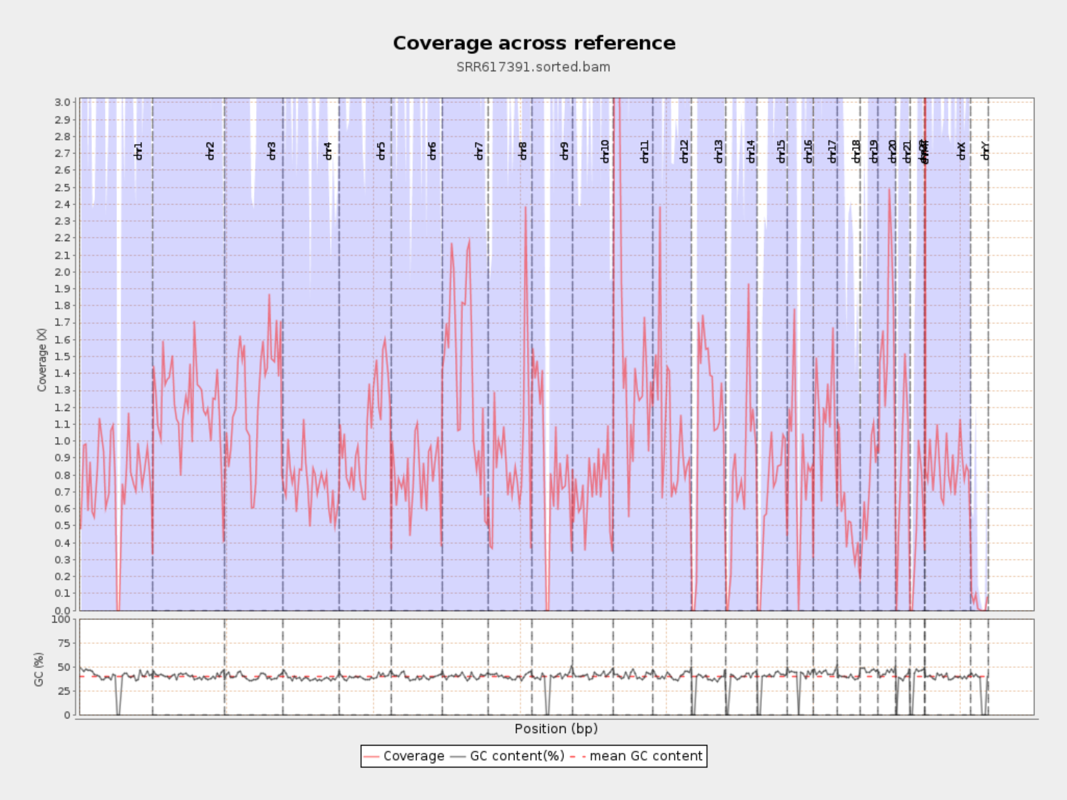
2.7. Chromosome stats

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

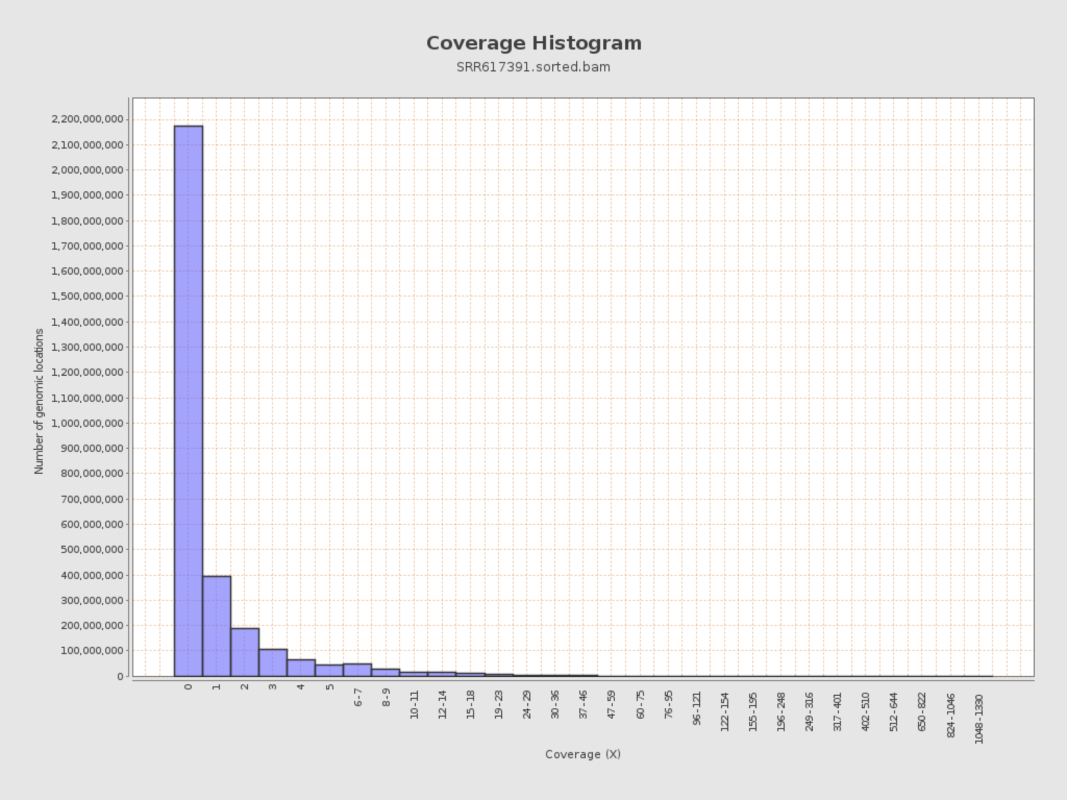
		bases	coverage	deviation
chr1	249250621	192027307	0.7704	2.7734
chr2	243199373	297315754	1.2225	3.0886
chr3	198022430	251911152	1.2721	3.4524
chr4	191154276	143164817	0.7489	2.2892
chr5	180915260	190826808	1.0548	2.8858
chr6	171115067	136616611	0.7984	2.613
chr7	159138663	222998591	1.4013	3.248
chr8	146364022	132193621	0.9032	3.2769
chr9	141213431	119476714	0.8461	2.6398
chr10	135534747	95710525	0.7062	2.4398
chr11	135006516	221545413	1.641	3.8689
chr12	133851895	142695736	1.0661	2.8096
chr13	115169878	129386410	1.1234	2.7946
chr14	107349540	86651694	0.8072	2.9182
chr15	102531392	68432989	0.6674	2.3617
chr16	90354753	75356405	0.834	3.364
chr17	81195210	92474555	1.1389	3.72
chr18	78077248	42663885	0.5464	2.0162
chr19	59128983	42889881	0.7254	2.3698
chr20	63025520	102095999	1.6199	4.8018
chr21	48129895	40713379	0.8459	2.5339
chr22	51304566	24264818	0.473	2.1018
chrMT	16571	182769	11.0294	5.0635
chrX	155270560	130957928	0.8434	2.5755

chrY	59373566	2333703	0.0393	0.5605

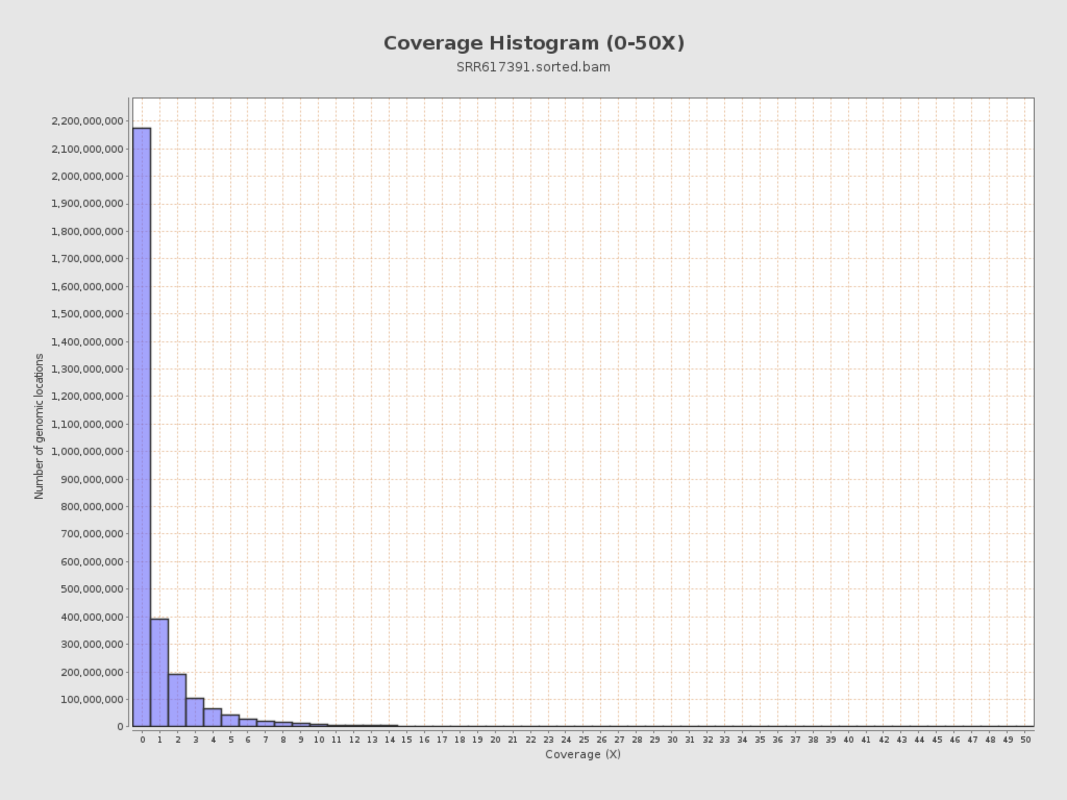
3. Results : Coverage across reference



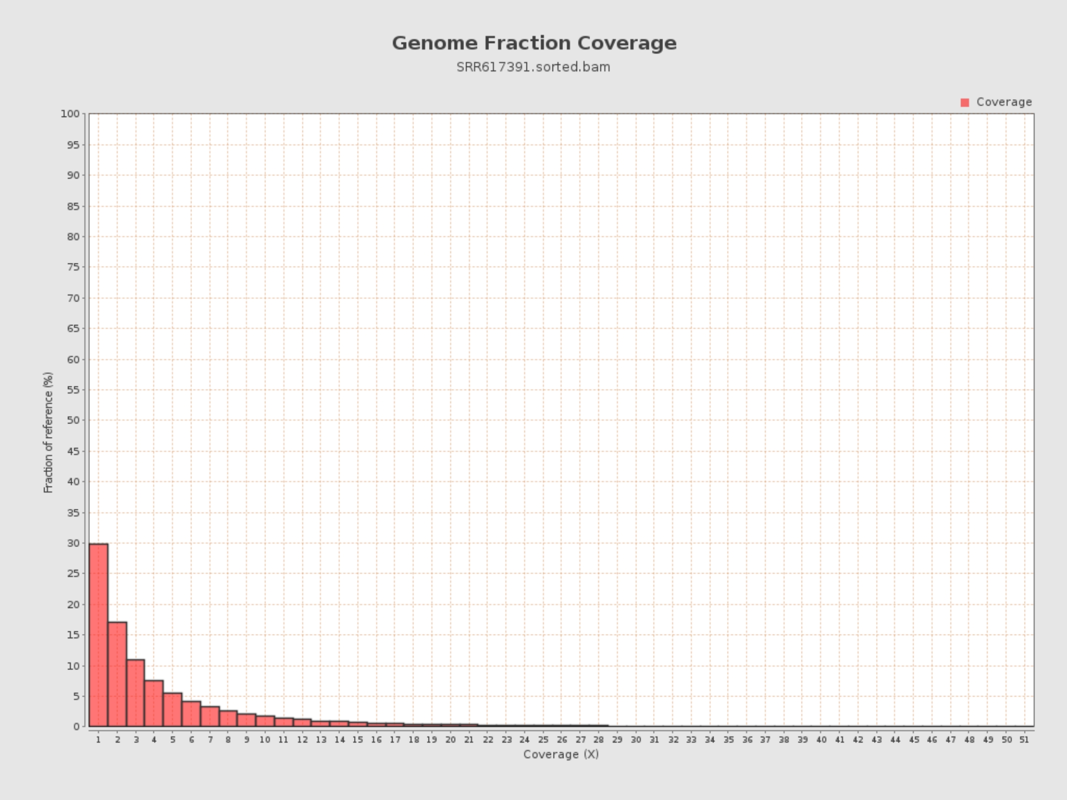
4. Results : Coverage Histogram



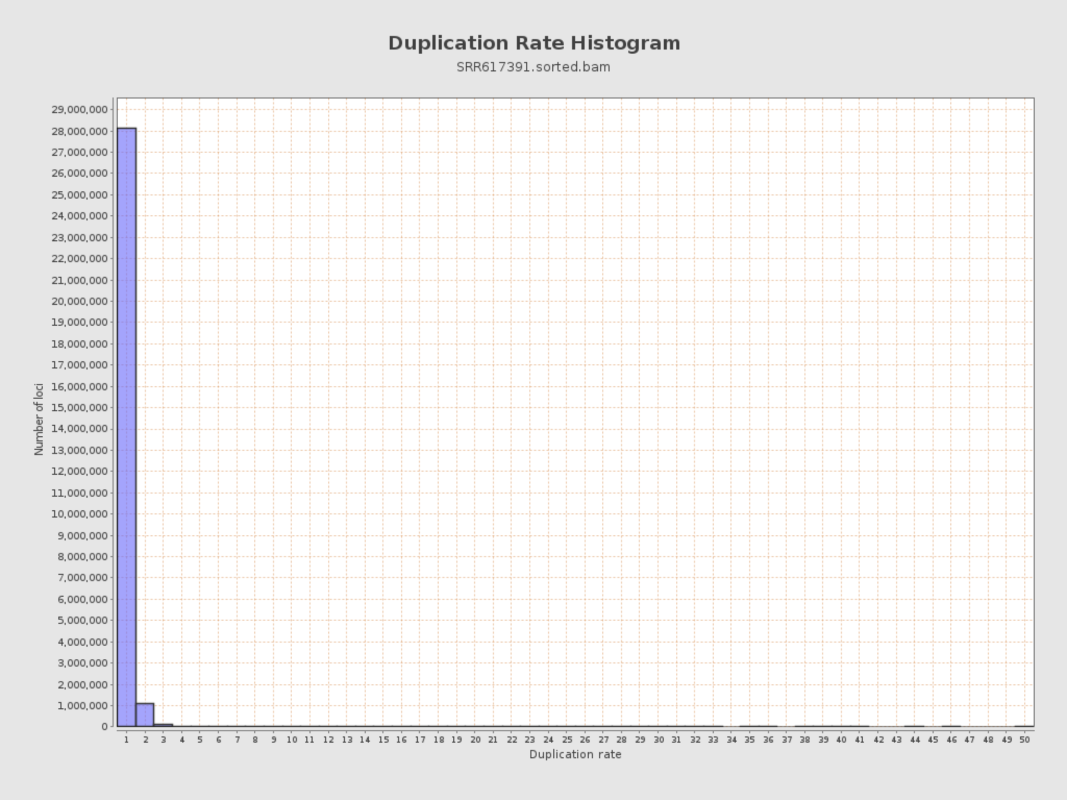
5. Results : Coverage Histogram (0-50X)



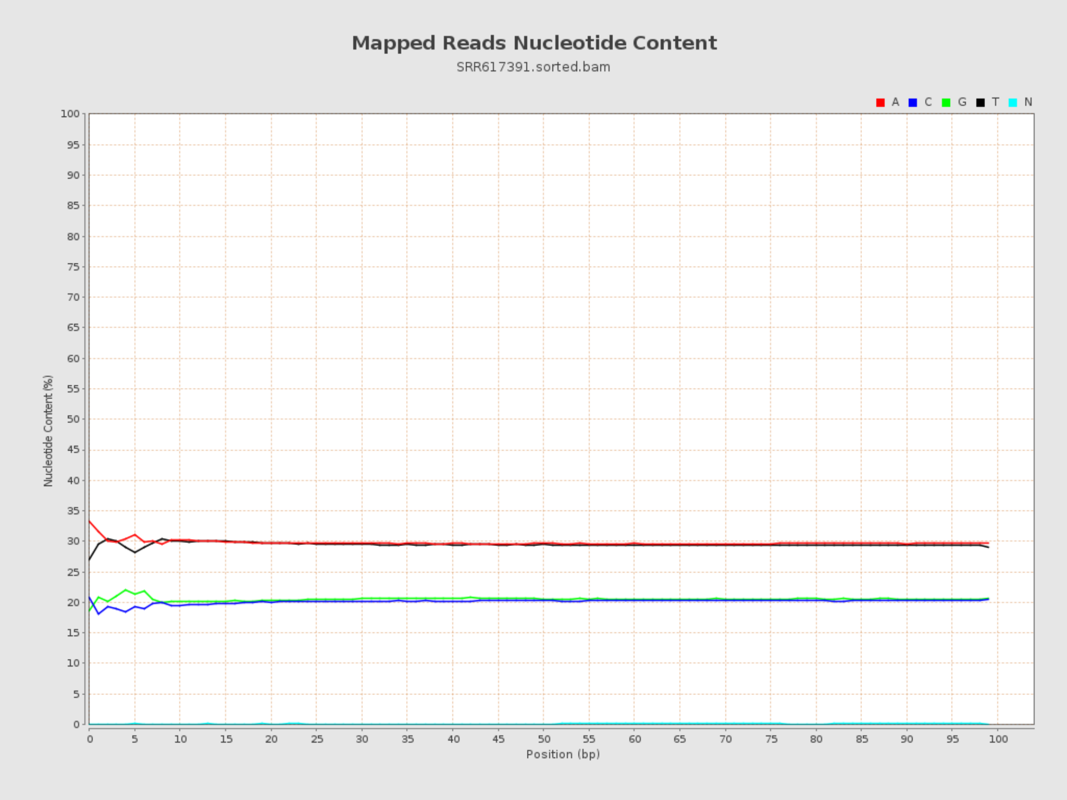
6. Results : Genome Fraction Coverage



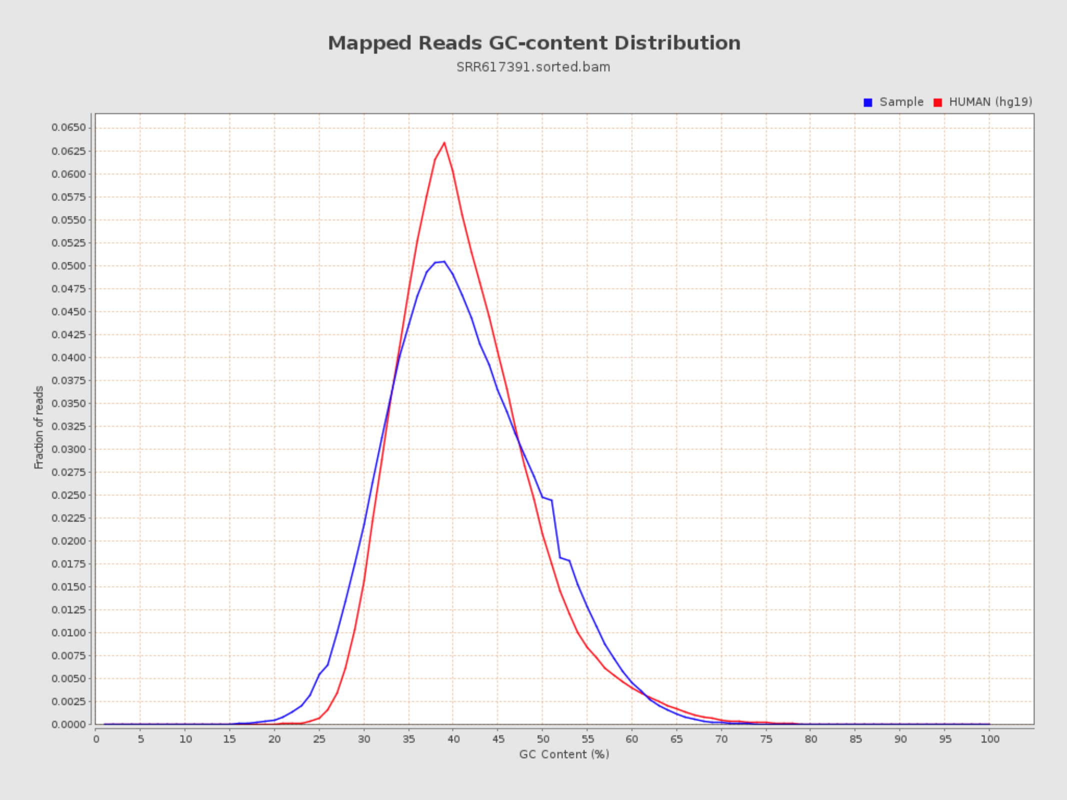
7. Results : Duplication Rate Histogram



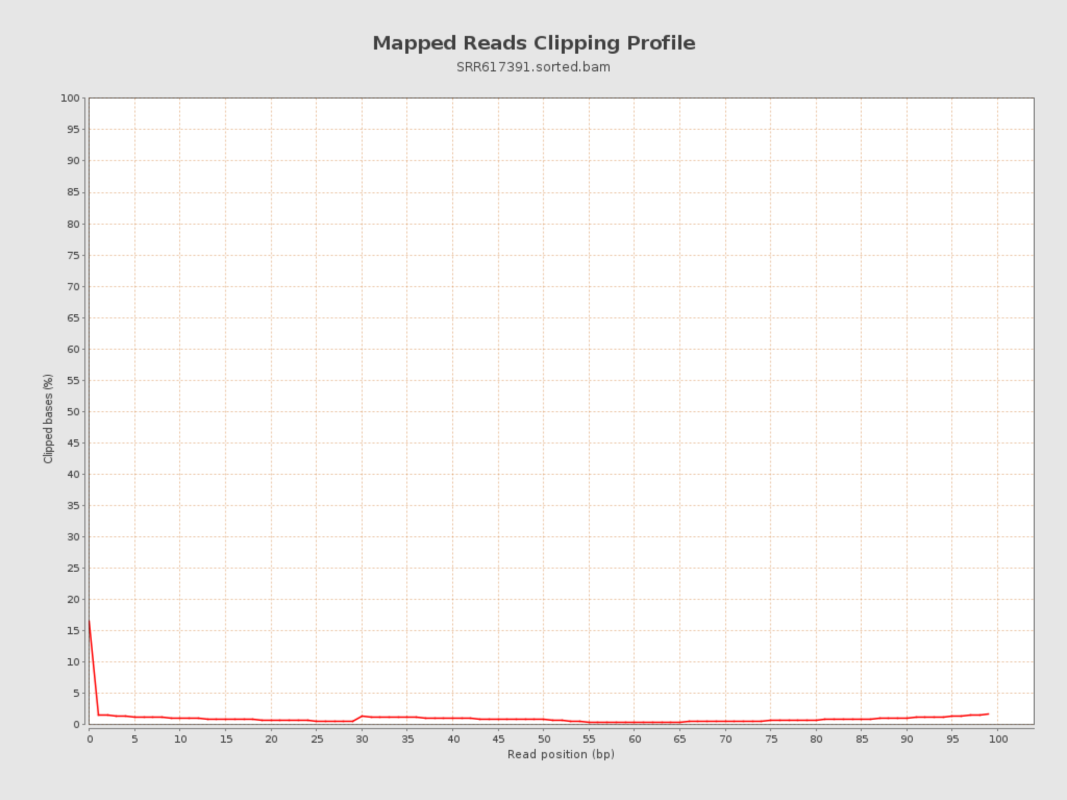
8. Results : Mapped Reads Nucleotide Content



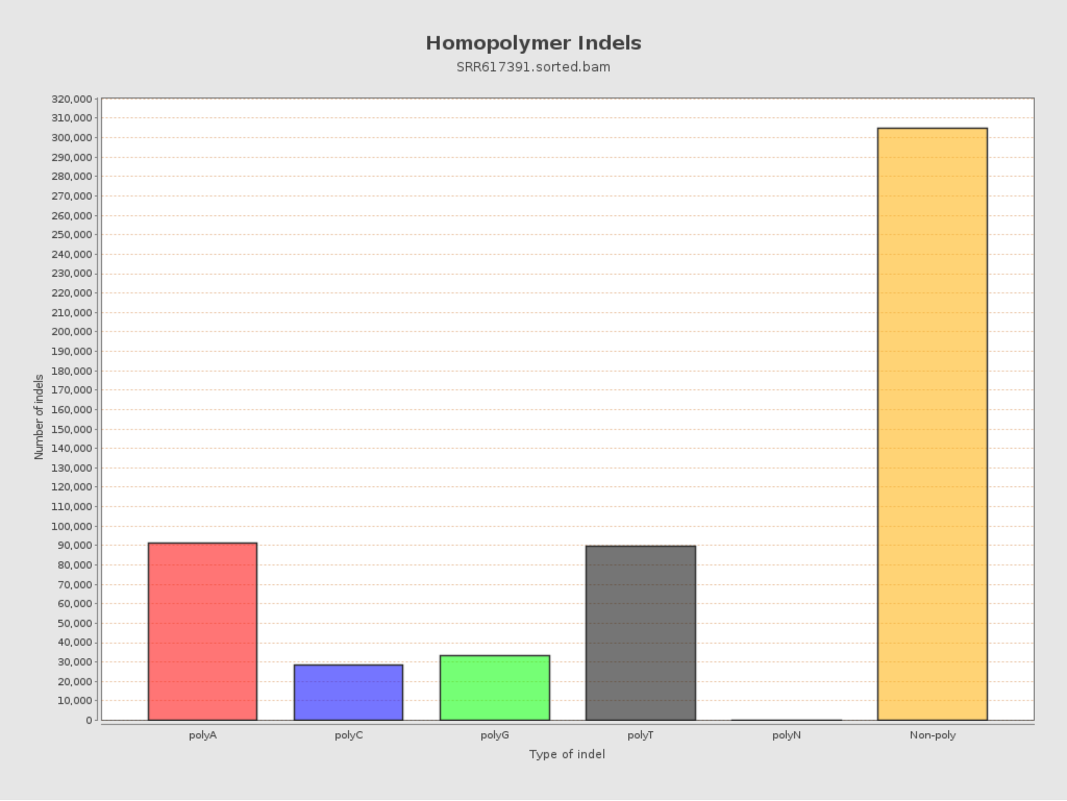
9. Results : Mapped Reads GC-content Distribution



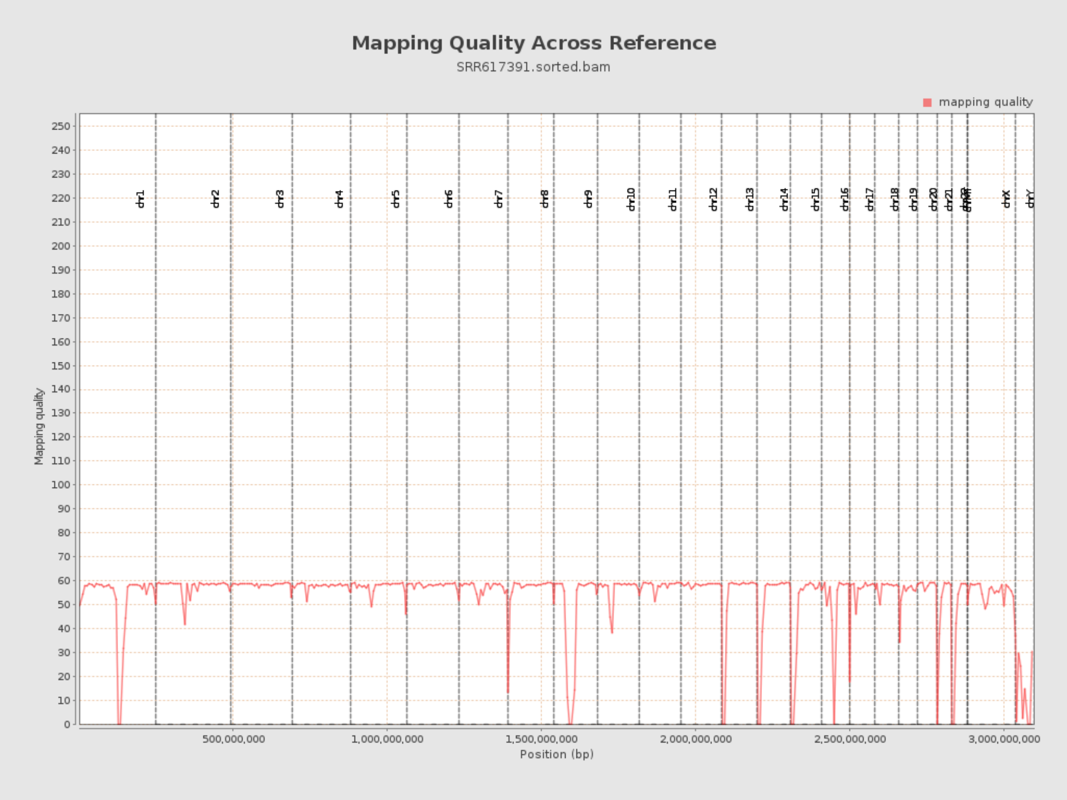
10. Results : Mapped Reads Clipping Profile



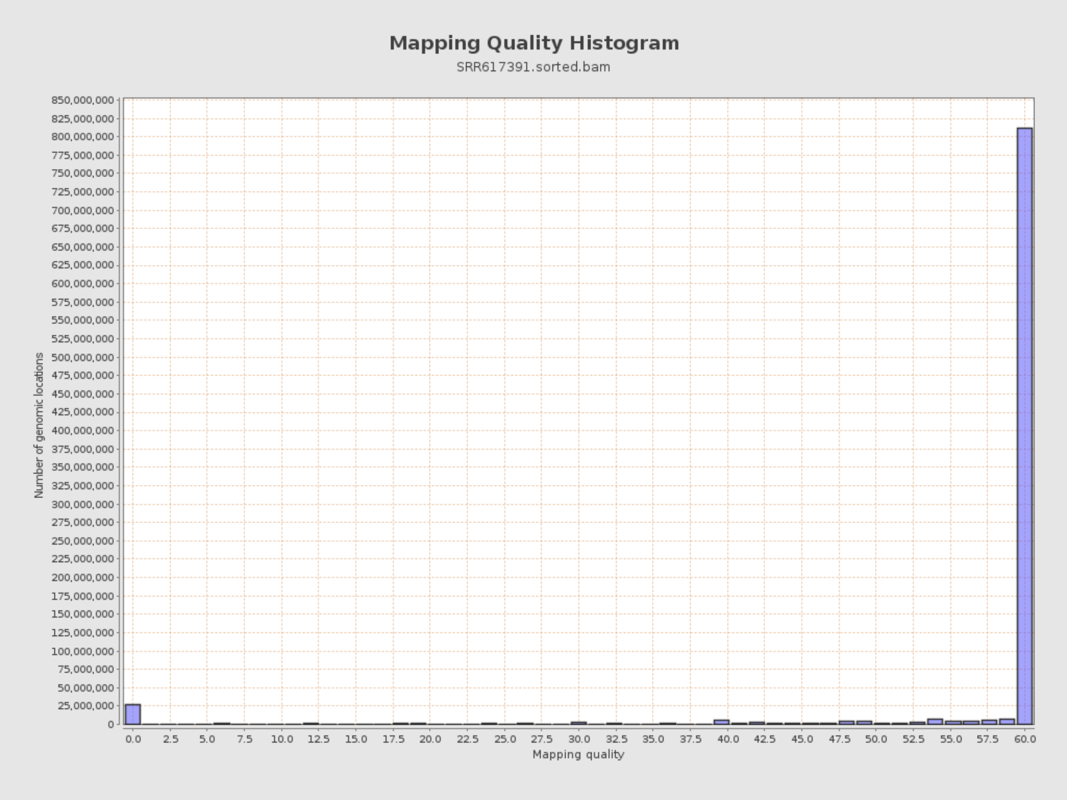
11. Results : Homopolymer Indels



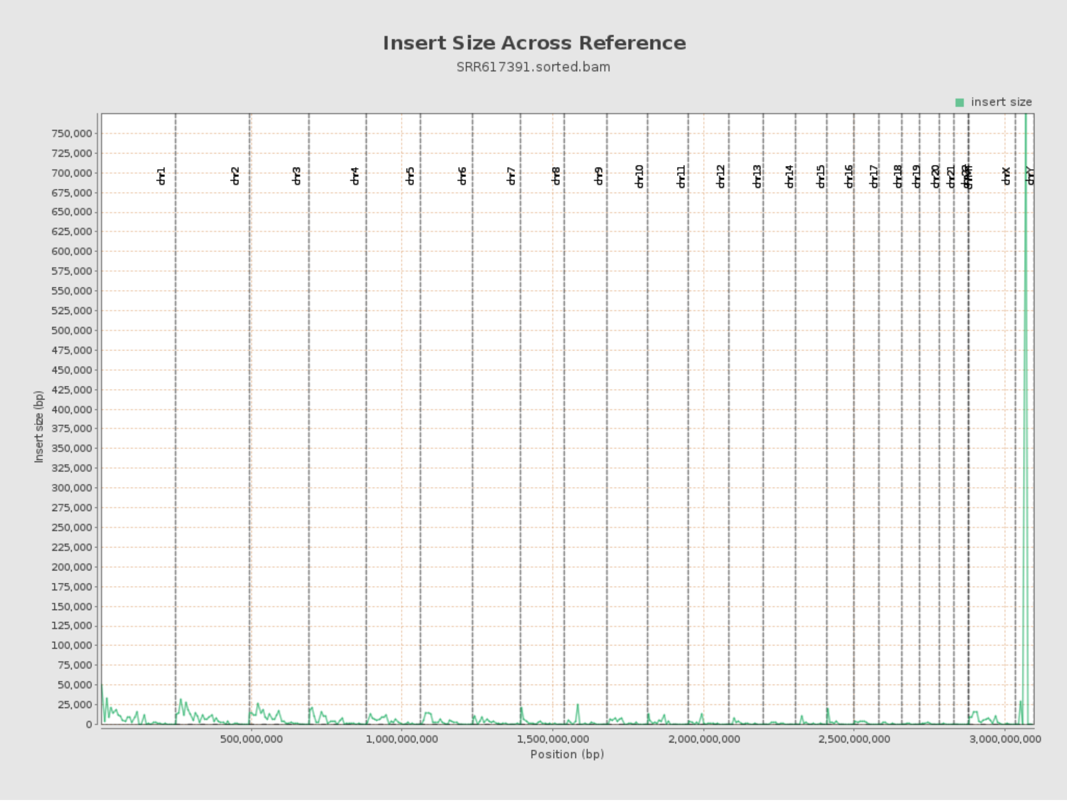
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram