Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/17 19:01:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR631031.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR631031_1.fastq.gz SRR631031_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Mar 17 19:01:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR631031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	111,523,710
Mapped reads	111,266,249 / 99.77%
Unmapped reads	257,461 / 0.23%
Mapped paired reads	111,266,249 / 99.77%
Mapped reads, first in pair	55,717,912 / 49.96%
Mapped reads, second in pair	55,548,337 / 49.81%
Mapped reads, both in pair	111,073,164 / 99.6%
Mapped reads, singletons	193,085 / 0.17%
Secondary alignments	0
Supplementary alignments	662,227 / 0.59%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	27,275,992 / 24.46%
Duplication rate	20.55%
Clipped reads	7,404,561 / 6.64%

2.2. ACGT Content

Number/percentage of A's	3,463,442,044 / 31.17%
Number/percentage of C's	2,086,817,657 / 18.78%
Number/percentage of T's	3,450,280,312 / 31.05%
Number/percentage of G's	2,109,991,726 / 18.99%
Number/percentage of N's	939,459 / 0.01%

GC Percentage	37.77%

2.3. Coverage

Mean	3.5901
Standard Deviation	16.1863

2.4. Mapping Quality

Mean Mapping Quality	53.92

2.5. Insert size

Mean	33,362.24
Standard Deviation	1,713,691.59
P25/Median/P75	202 / 239 / 294

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	76,497,932
Insertions	937,959
Mapped reads with at least one insertion	0.83%
Deletions	1,015,892
Mapped reads with at least one deletion	0.89%
Homopolymer indels	44.94%

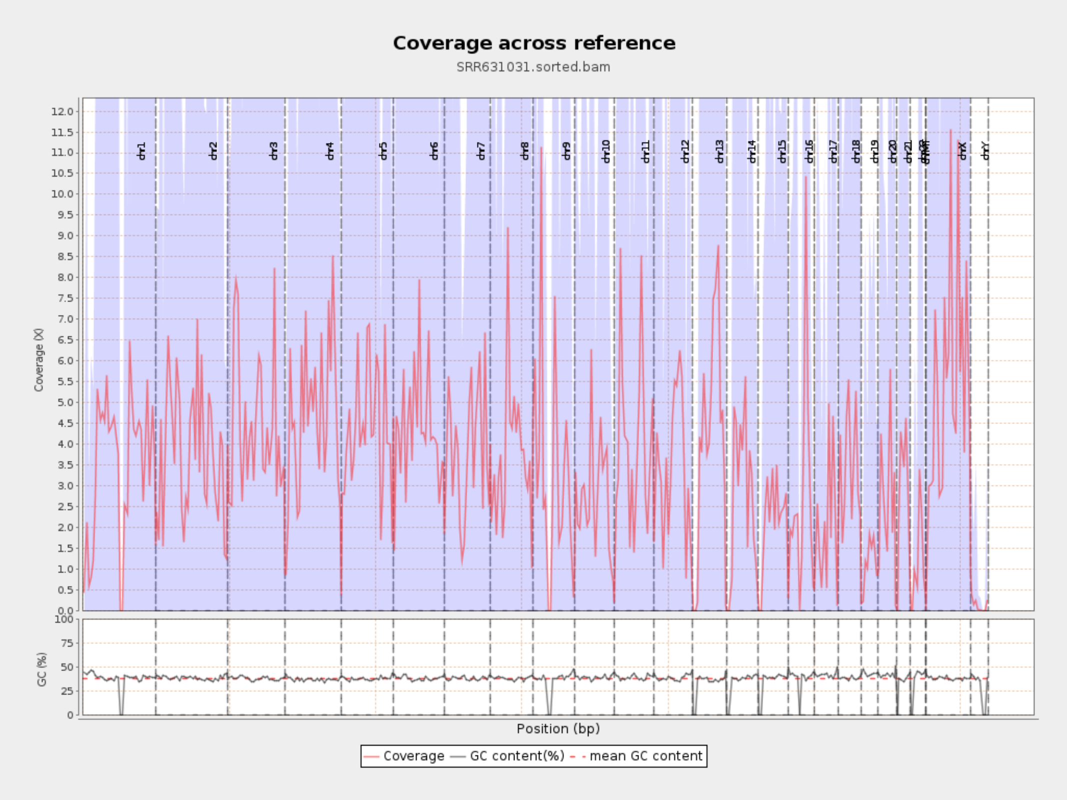
2.7. Chromosome stats

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

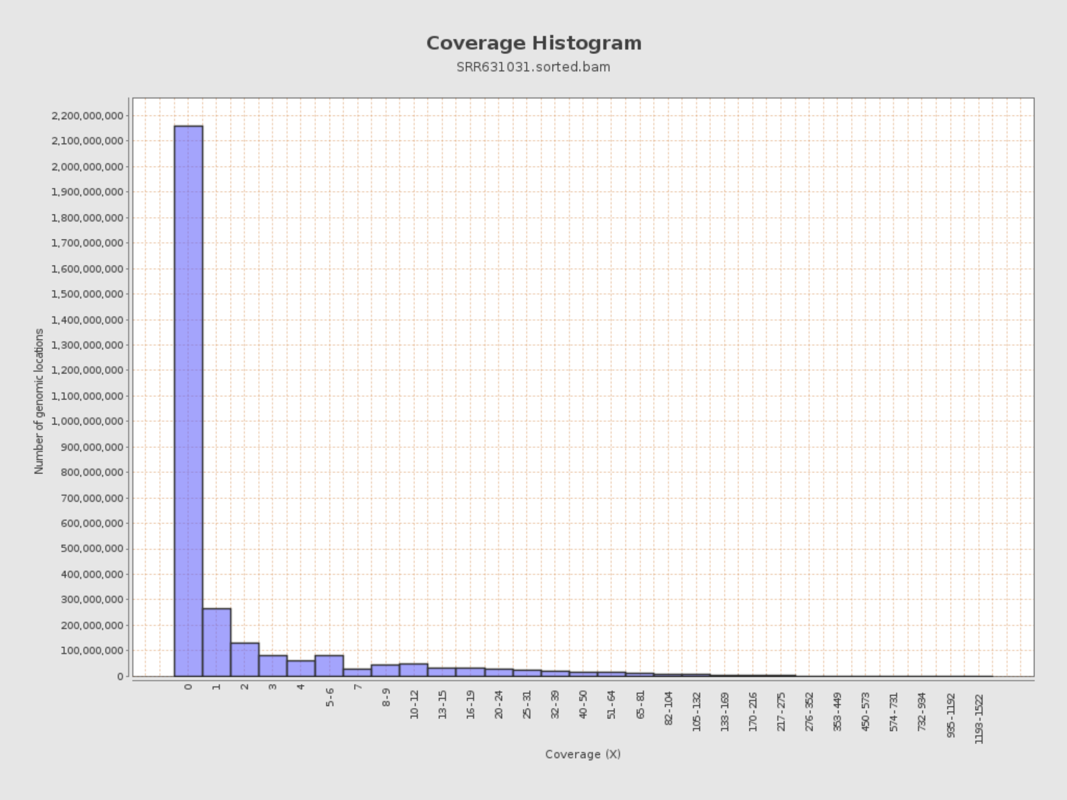
		bases	coverage	deviation
chr1	249250621	867257455	3.4795	15.3918
chr2	243199373	926771249	3.8107	16.3231
chr3	198022430	878901996	4.4384	16.5693
chr4	191154276	902095422	4.7192	19.8922
chr5	180915260	784960146	4.3388	16.8617
chr6	171115067	751168845	4.3898	17.421
chr7	159138663	609472255	3.8298	17.8936
chr8	146364022	538043847	3.6761	14.8452
chr9	141213431	478315934	3.3872	19.5608
chr10	135534747	378569194	2.7932	11.1873
chr11	135006516	540527659	4.0037	15.7979
chr12	133851895	459822973	3.4353	15.0847
chr13	115169878	488808707	4.2442	19.9438
chr14	107349540	299681154	2.7916	13.7512
chr15	102531392	220275706	2.1484	10.0333
chr16	90354753	246227563	2.7251	14.924
chr17	81195210	172179231	2.1206	10.68
chr18	78077248	271395629	3.476	17.2292
chr19	59128983	67716631	1.1452	5.614
chr20	63025520	174243576	2.7647	12.4537
chr21	48129895	136610617	2.8384	11.739
chr22	51304566	63827883	1.2441	8.2313
chrMT	16571	481	0.029	0.2403
chrX	155270560	849642370	5.472	22.868

chrY	59373566	7247251	0.1221	2.098

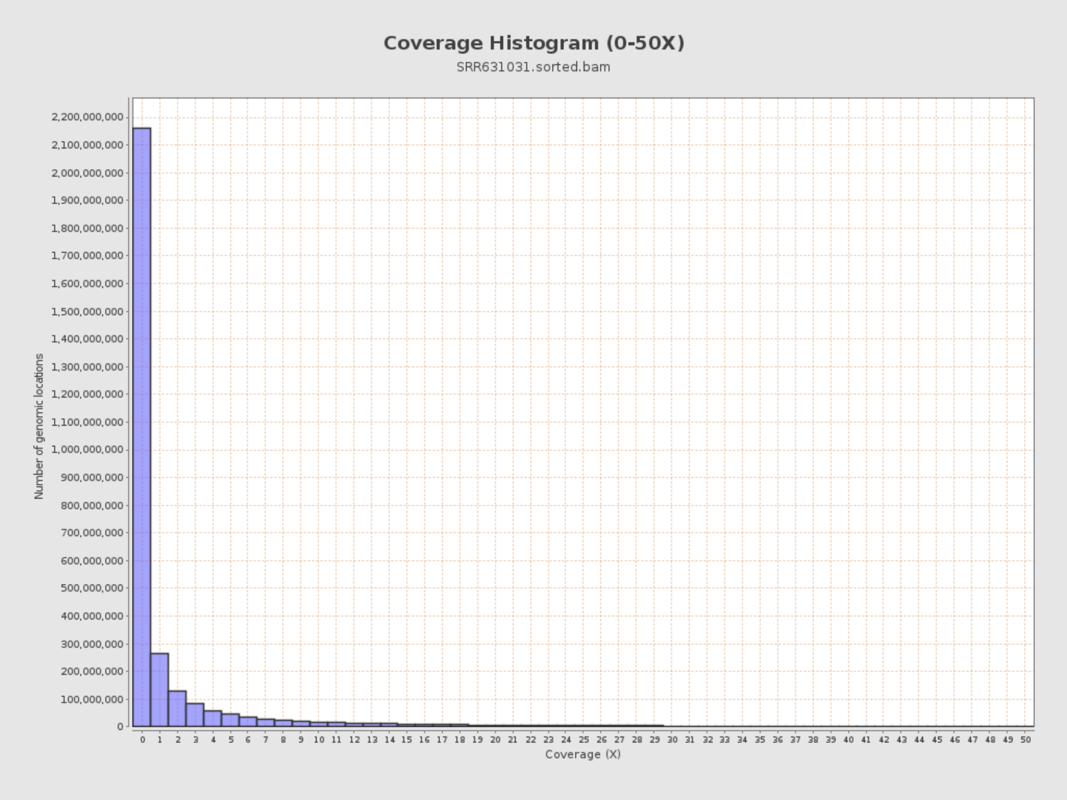
3. Results : Coverage across reference



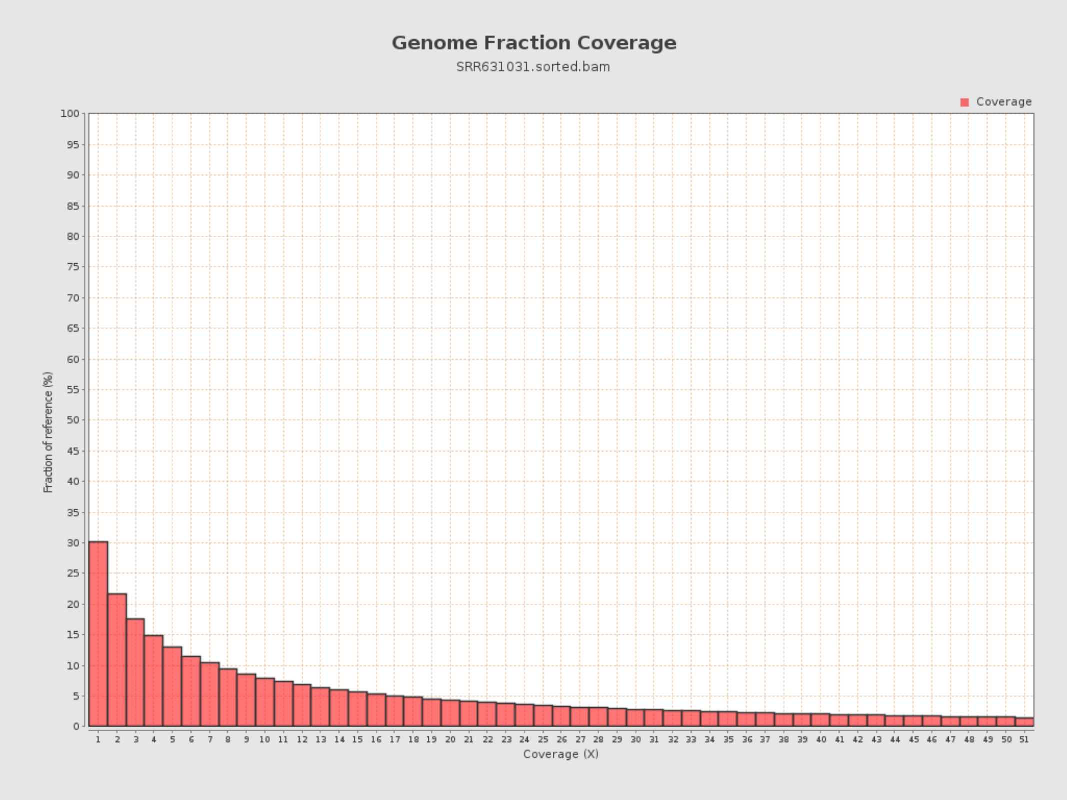
4. Results : Coverage Histogram



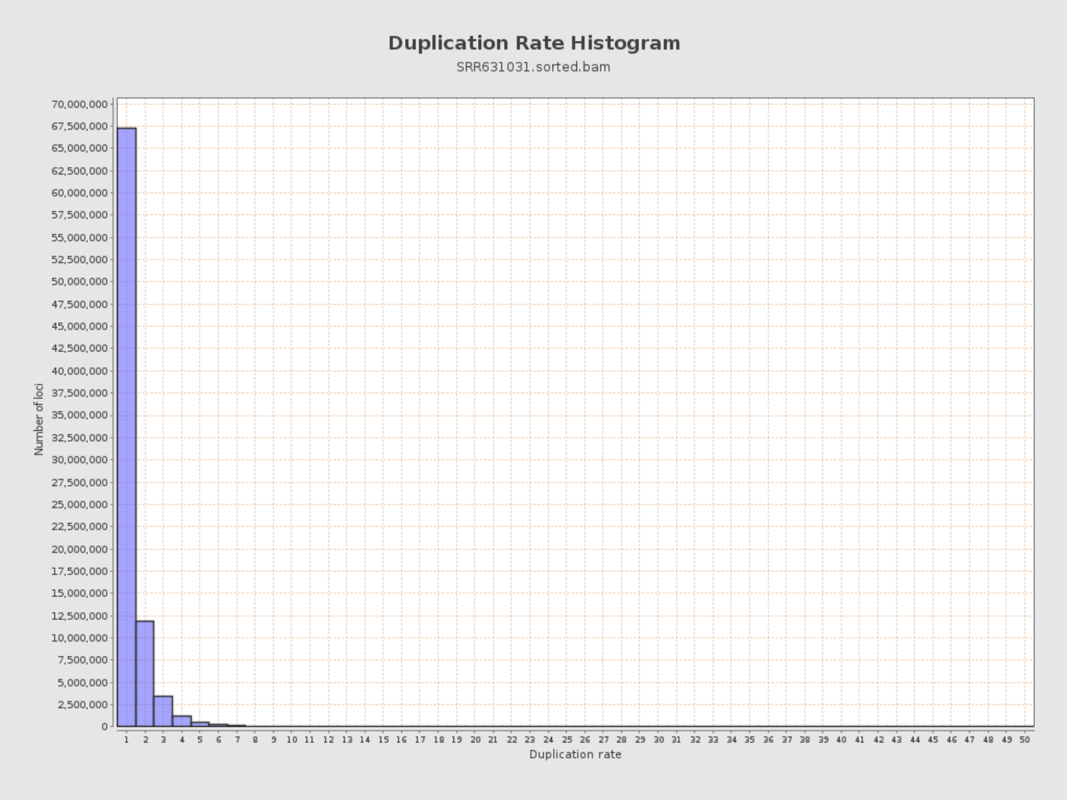
5. Results : Coverage Histogram (0-50X)



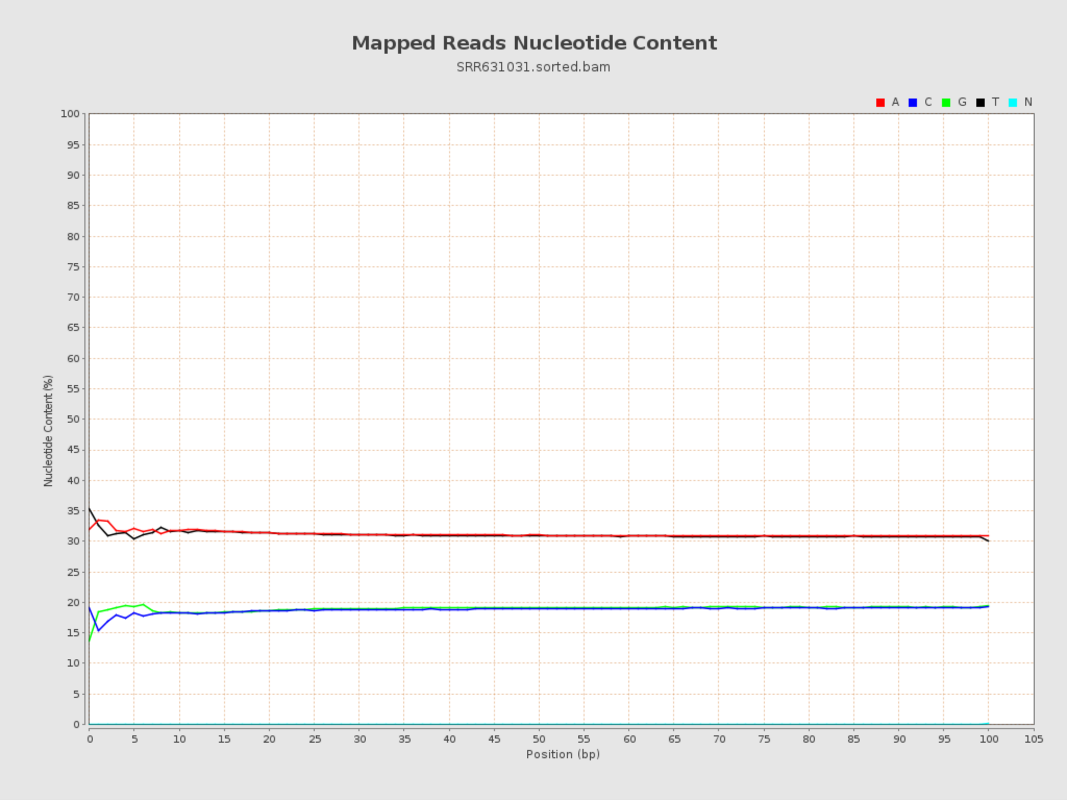
6. Results : Genome Fraction Coverage



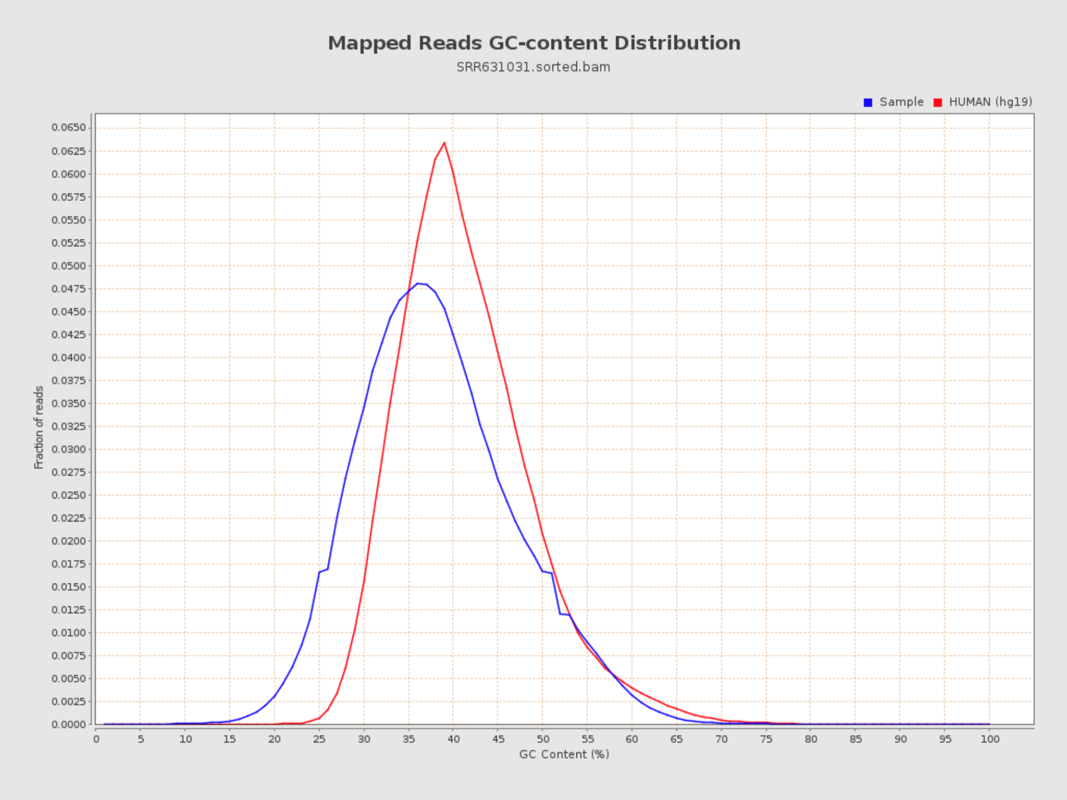
7. Results : Duplication Rate Histogram



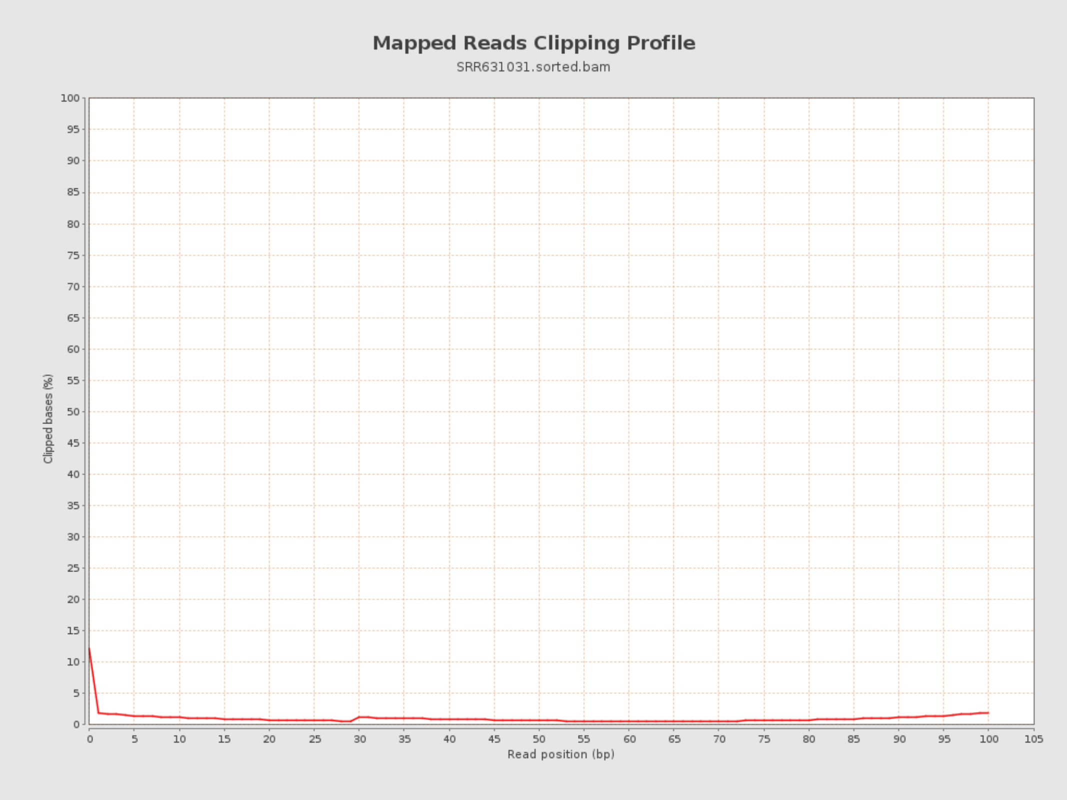
8. Results : Mapped Reads Nucleotide Content



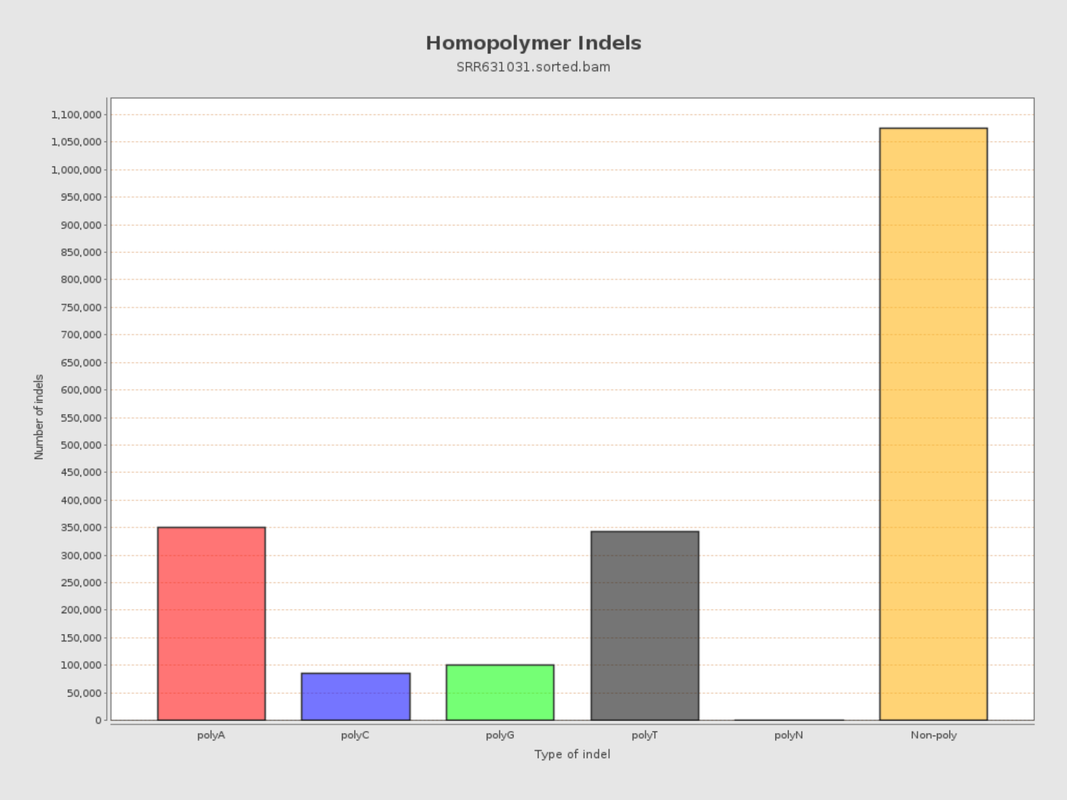
9. Results : Mapped Reads GC-content Distribution



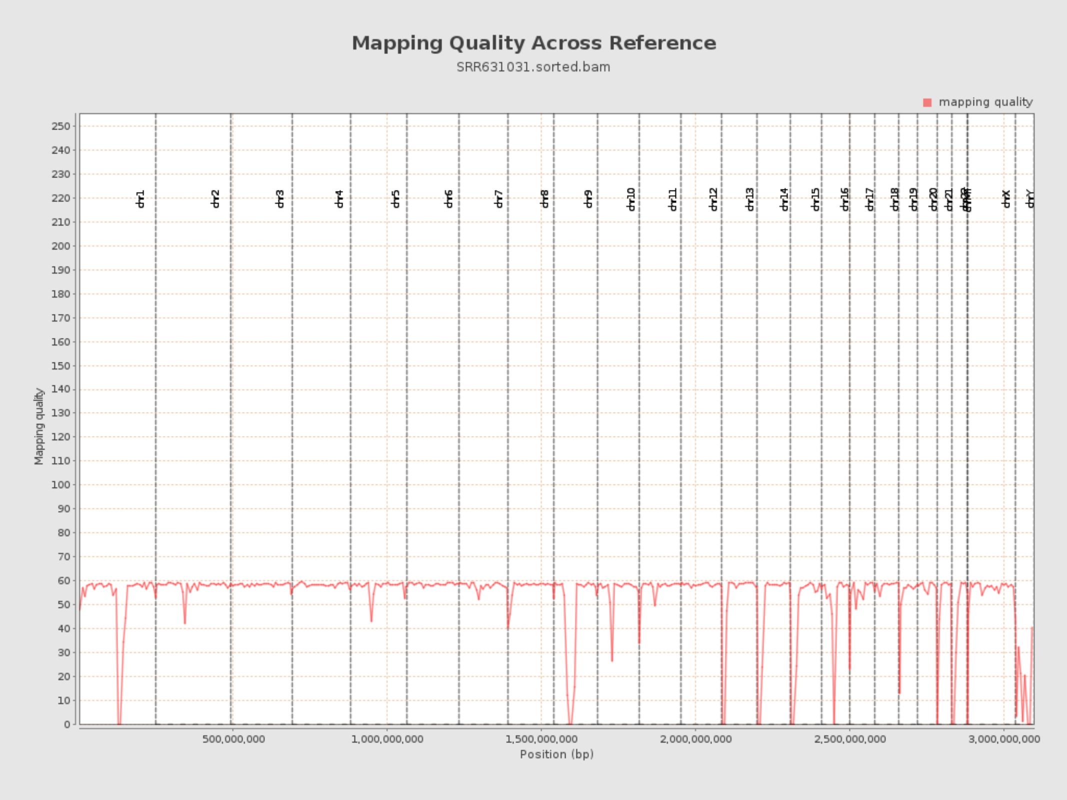
10. Results : Mapped Reads Clipping Profile



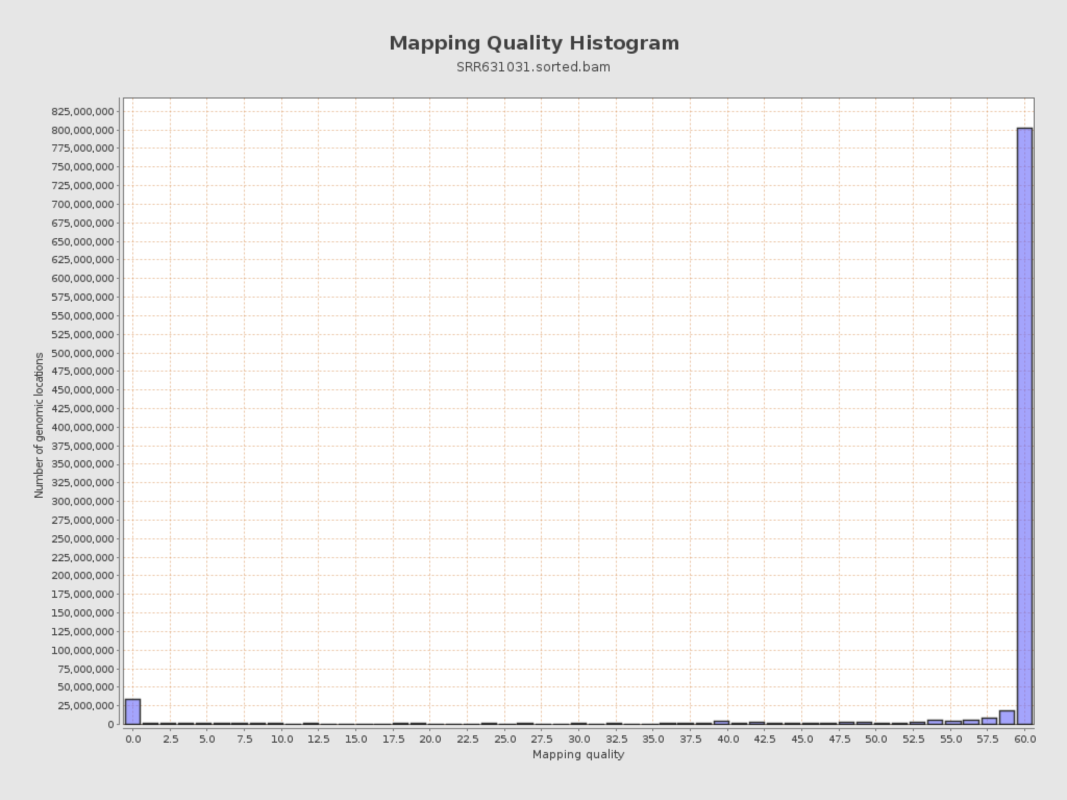
11. Results : Homopolymer Indels



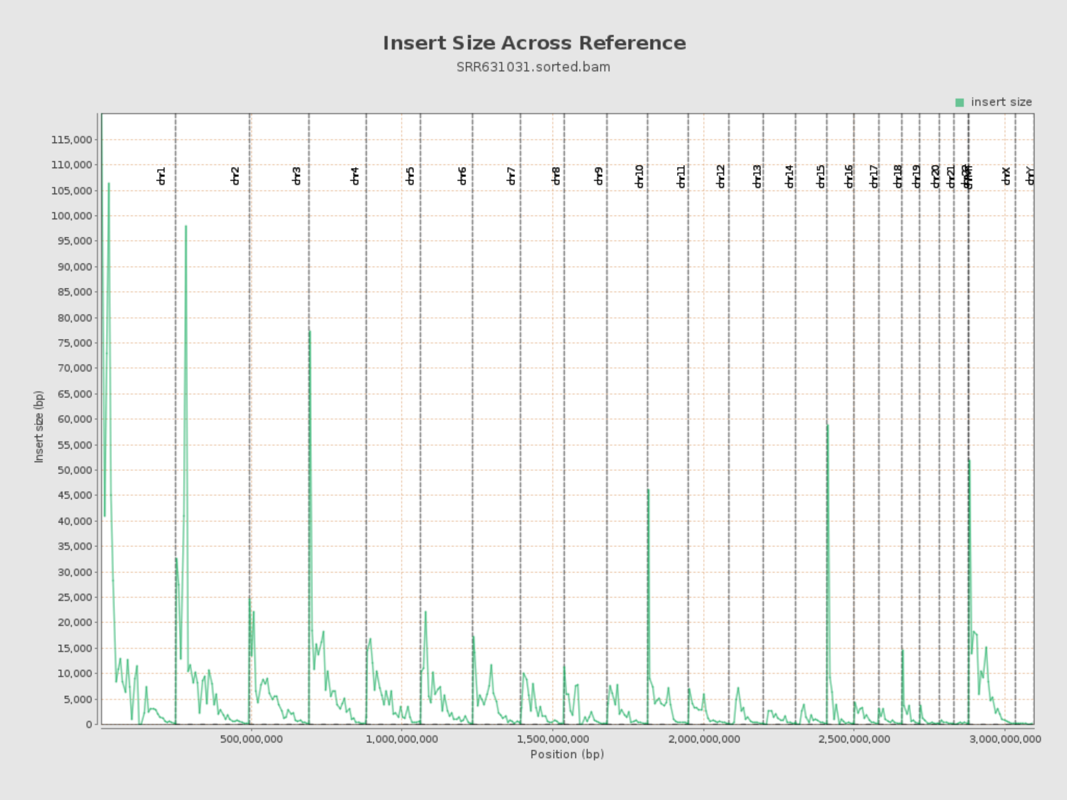
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram