Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/14 19:26:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630491.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 SRR630491_1.fastq.gz SRR630491_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 14 19:26:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630491.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	267,169,308
Mapped reads	264,538,926 / 99.02%
Unmapped reads	2,630,382 / 0.98%
Mapped paired reads	264,538,926 / 99.02%
Mapped reads, first in pair	133,304,043 / 49.89%
Mapped reads, second in pair	131,234,883 / 49.12%
Mapped reads, both in pair	262,323,530 / 98.19%
Mapped reads, singletons	2,215,396 / 0.83%
Secondary alignments	0
Supplementary alignments	596,538 / 0.22%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	45,961,708 / 17.2%
Duplication rate	12.27%
Clipped reads	30,755,934 / 11.51%

2.2. ACGT Content

Number/percentage of A's	7,866,112,958 / 30.51%
Number/percentage of C's	5,072,985,185 / 19.68%
Number/percentage of T's	7,764,376,932 / 30.12%
Number/percentage of G's	5,069,064,345 / 19.66%
Number/percentage of N's	6,293,986 / 0.02%

GC Percentage	39.34%

2.3. Coverage

Mean	8.33
Standard Deviation	106.059

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	45,192.26
Standard Deviation	2,011,213.46
P25/Median/P75	337 / 392 / 462

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	269,868,669
Insertions	3,001,150
Mapped reads with at least one insertion	1.1%
Deletions	3,791,741
Mapped reads with at least one deletion	1.39%
Homopolymer indels	42.07%

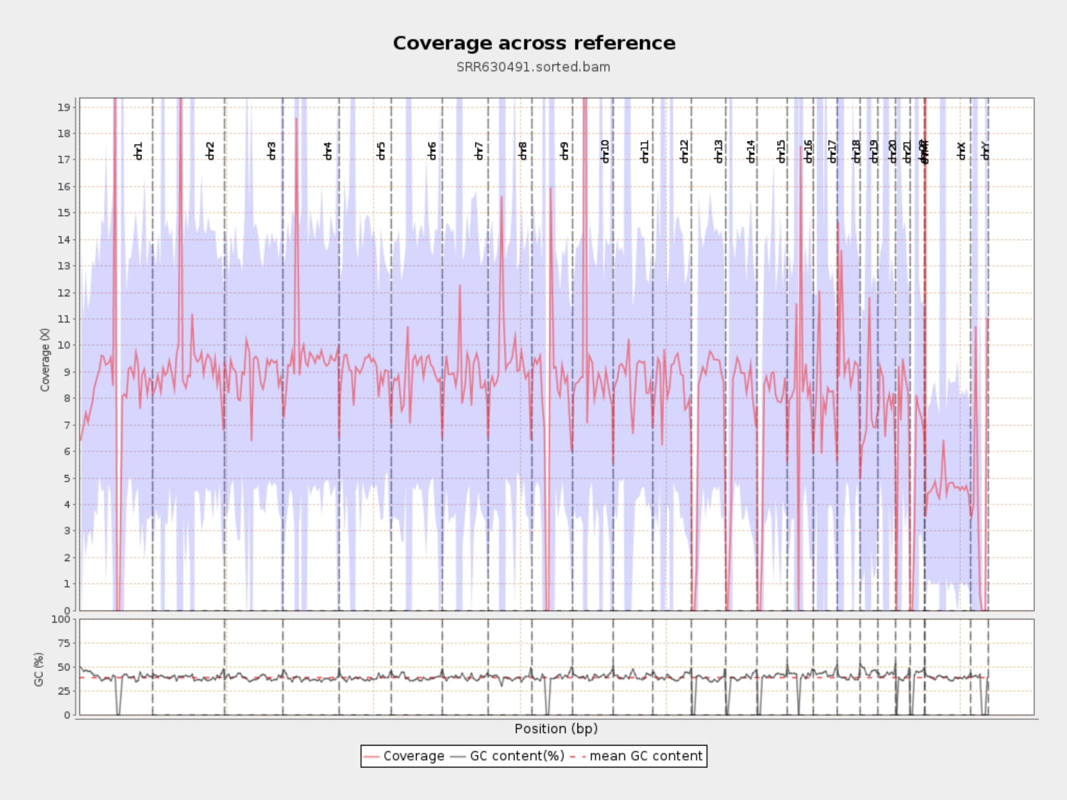
2.7. Chromosome stats

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

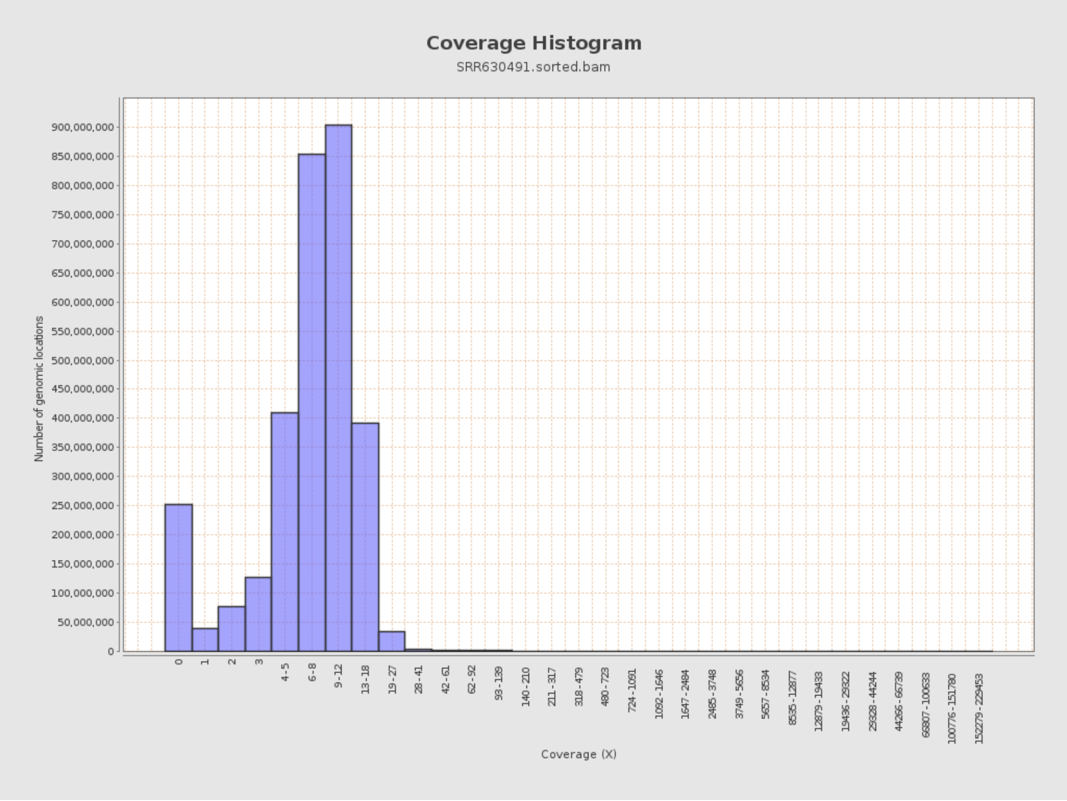
		bases	coverage	deviation
chr1	249250621	2084341616	8.3624	236.3068
chr2	243199373	2286052570	9.3999	68.2678
chr3	198022430	1769929155	8.938	8.1387
chr4	191154276	1855978475	9.7093	75.9855
chr5	180915260	1622165291	8.9664	6.9558
chr6	171115067	1530666375	8.9452	19.8872
chr7	159138663	1419942248	8.9227	69.8261
chr8	146364022	1380718815	9.4335	219.5058
chr9	141213431	1121249978	7.9401	147.1341
chr10	135534747	1348845598	9.952	166.6228
chr11	135006516	1174284381	8.698	46.9029
chr12	133851895	1147358909	8.5719	9.6873
chr13	115169878	876783904	7.613	5.1738
chr14	107349540	775048193	7.2199	9.9245
chr15	102531392	695054719	6.7789	5.5689
chr16	90354753	760247354	8.414	68.9438
chr17	81195210	641354120	7.8989	54.898
chr18	78077248	756603839	9.6905	147.2115
chr19	59128983	434567626	7.3495	118.4548
chr20	63025520	496840161	7.8832	17.3853
chr21	48129895	365136291	7.5865	25.1495
chr22	51304566	263332171	5.1327	21.6147
chrMT	16571	4154977	250.7379	37.9084
chrX	155270560	721604249	4.6474	17.9393

chrY	59373566	254805292	4.2916	68.2265

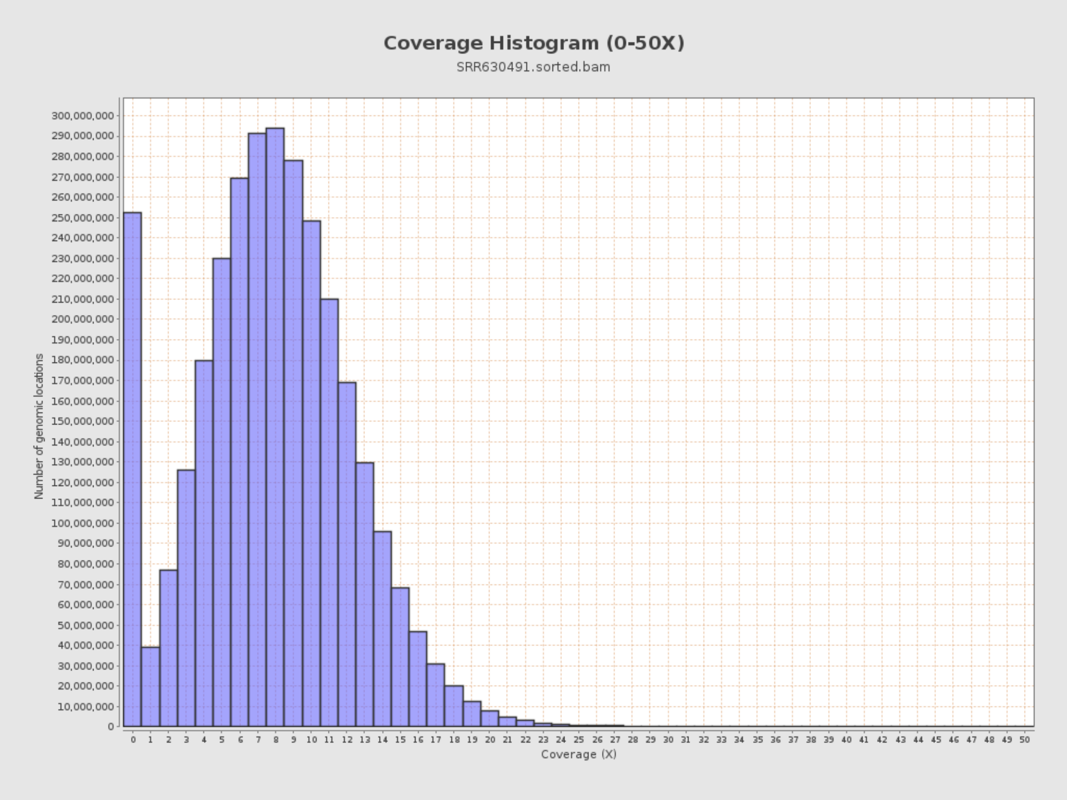
3. Results : Coverage across reference



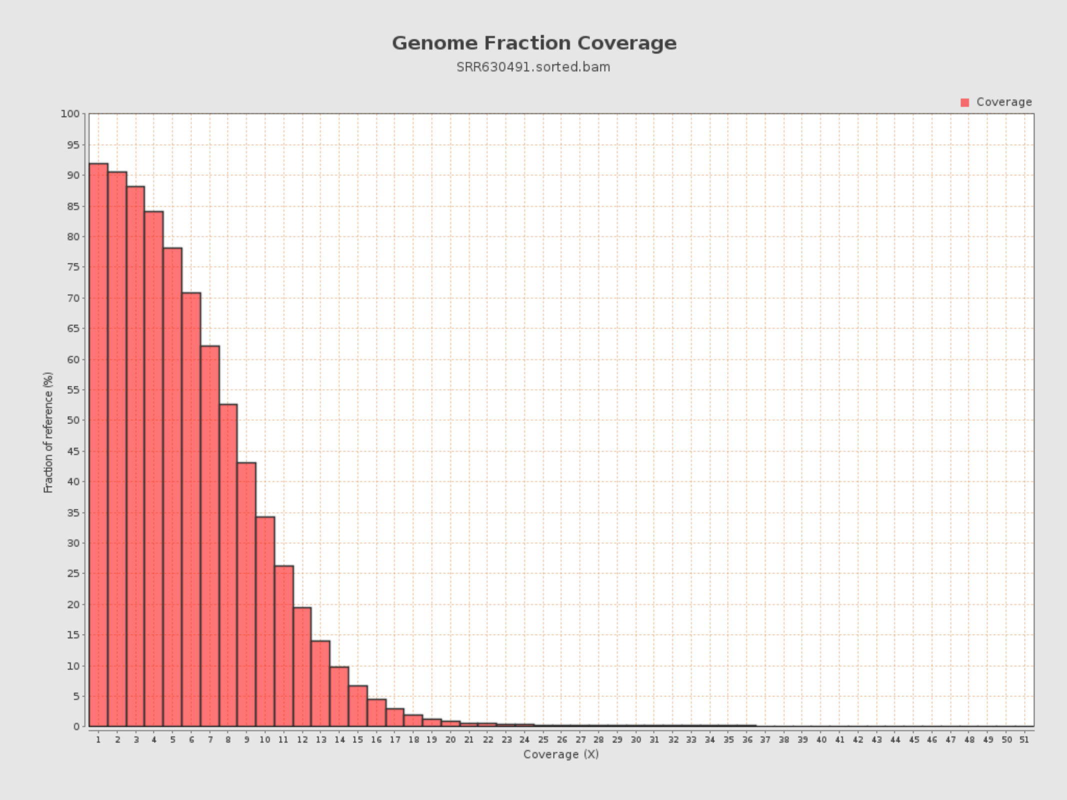
4. Results : Coverage Histogram



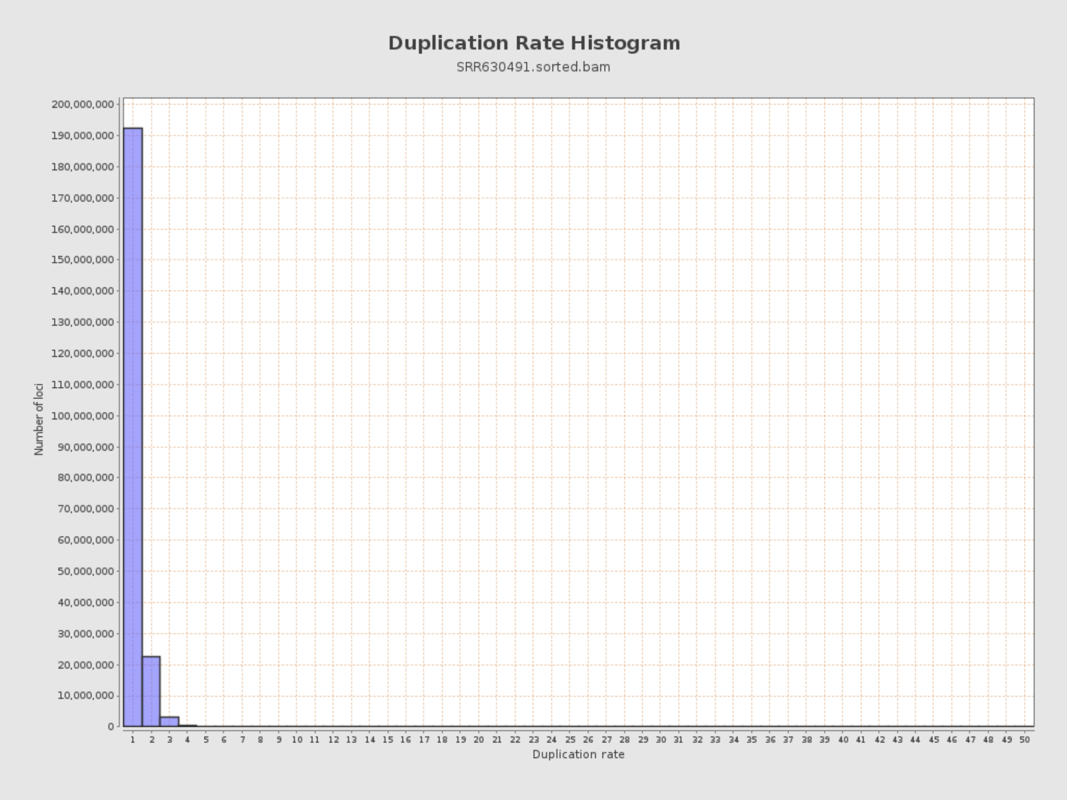
5. Results : Coverage Histogram (0-50X)



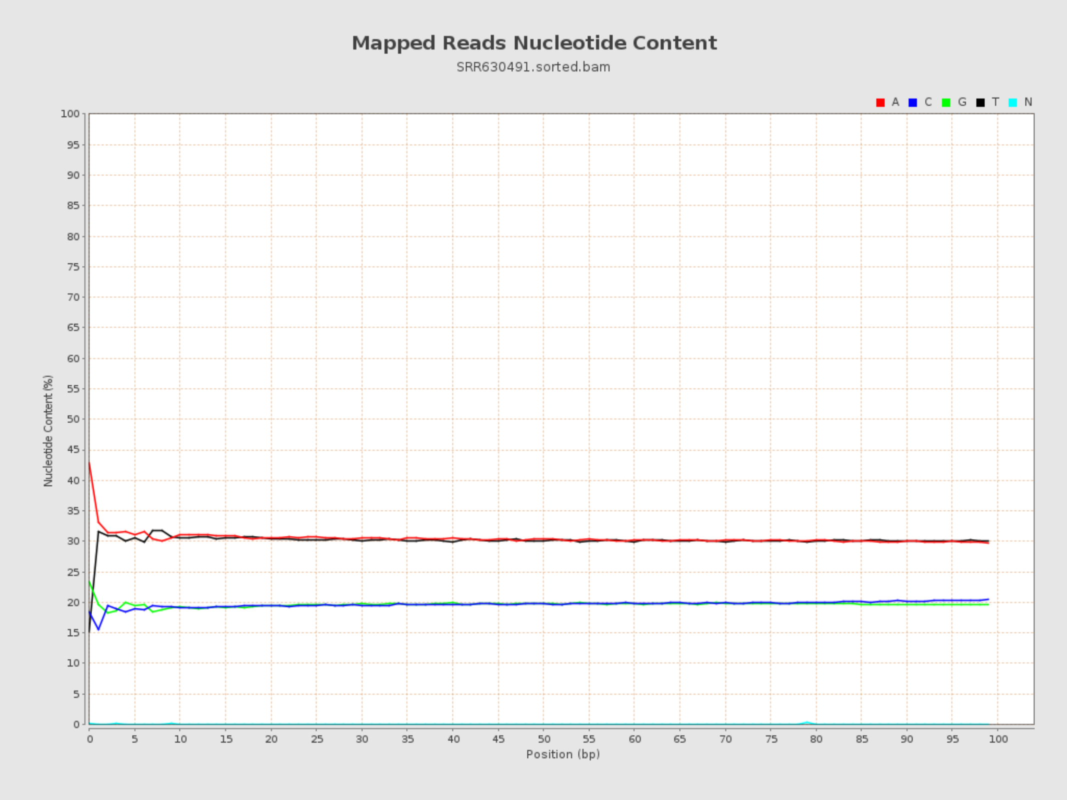
6. Results : Genome Fraction Coverage



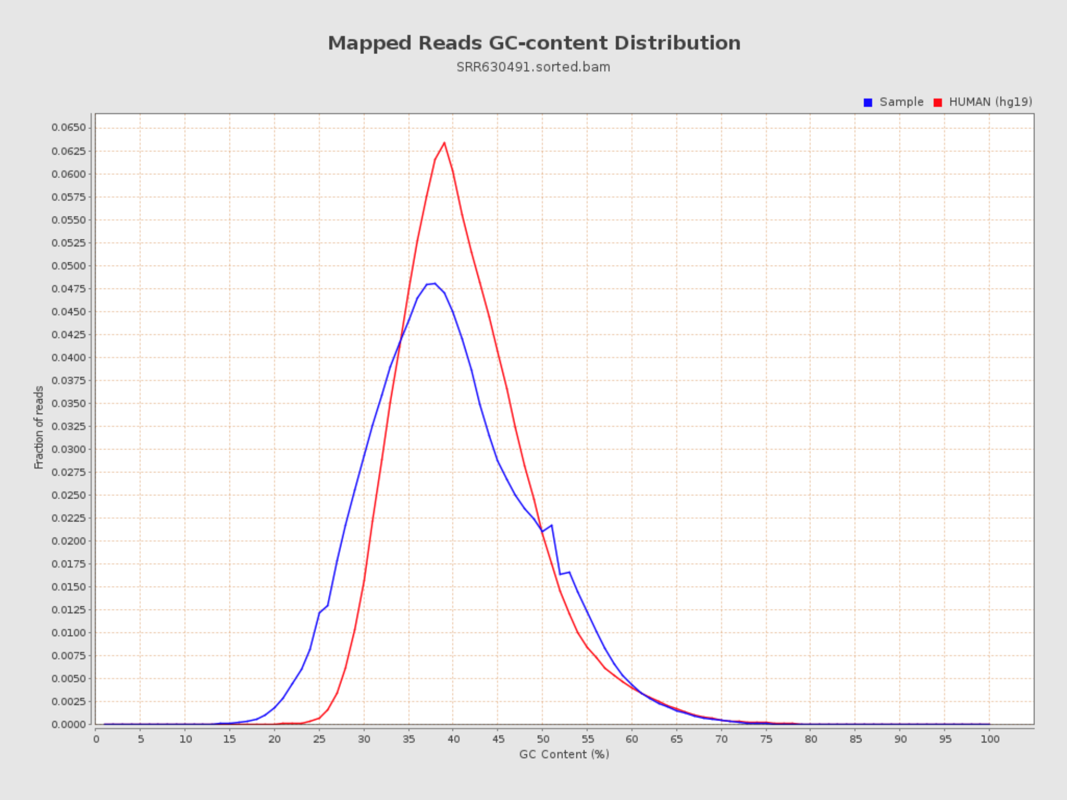
7. Results : Duplication Rate Histogram



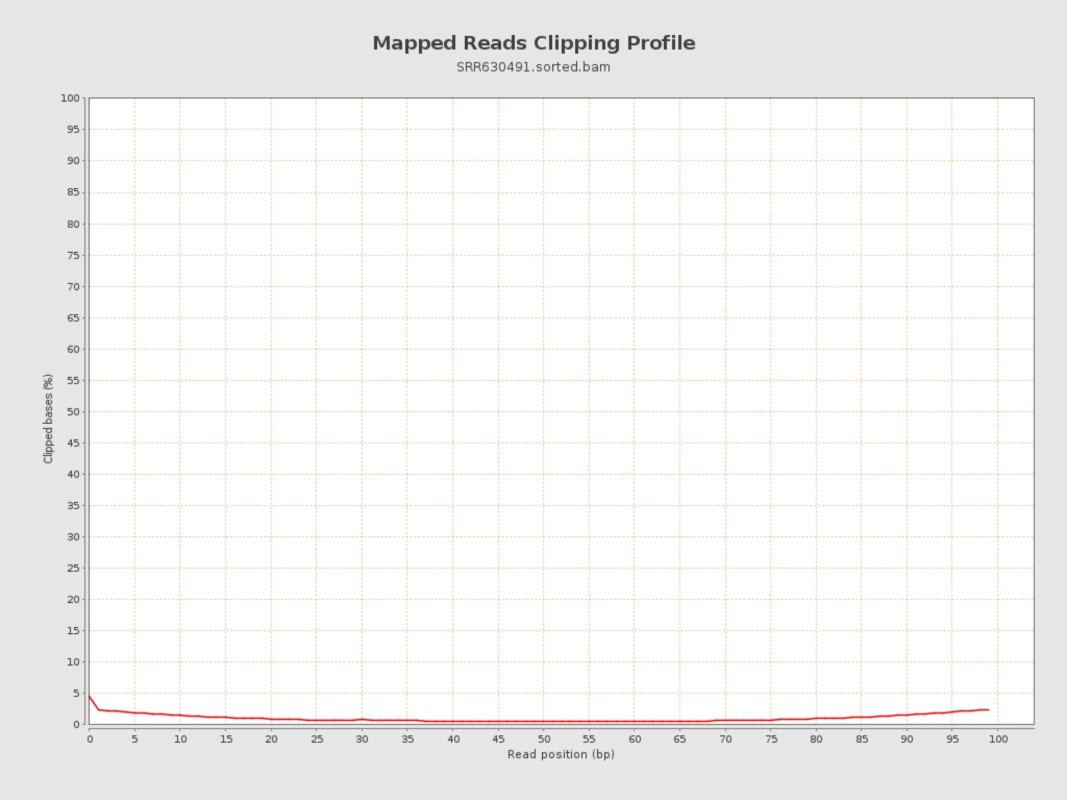
8. Results : Mapped Reads Nucleotide Content



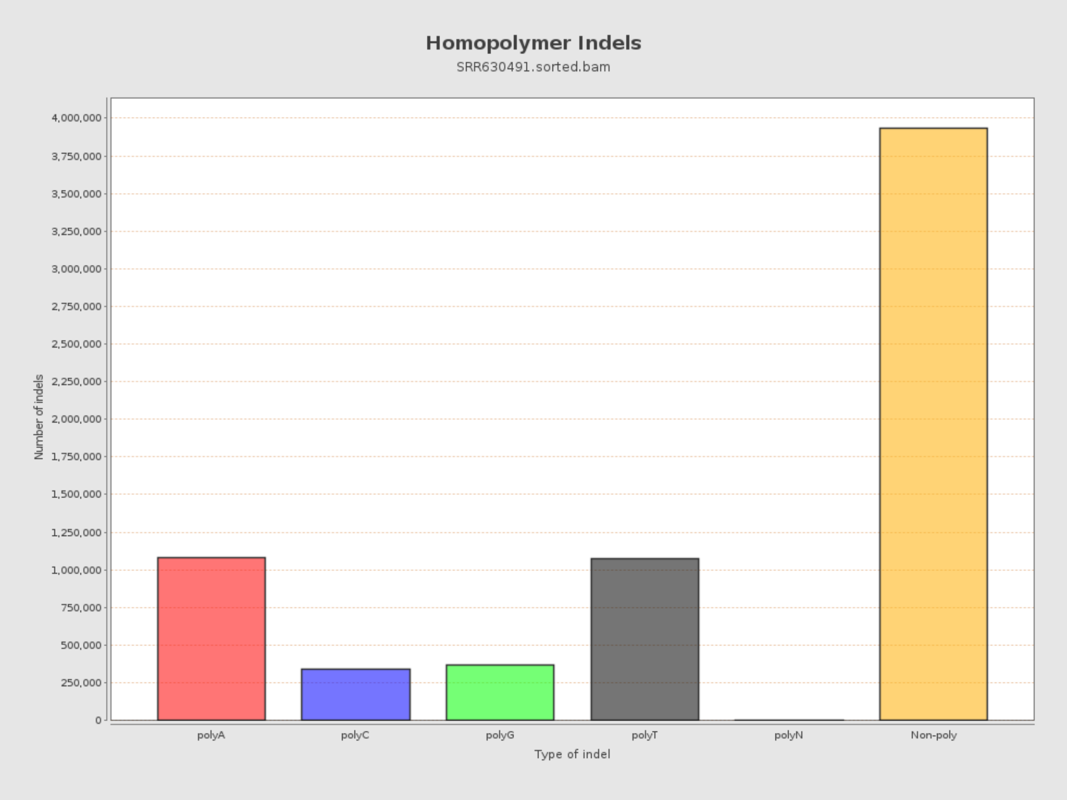
9. Results : Mapped Reads GC-content Distribution



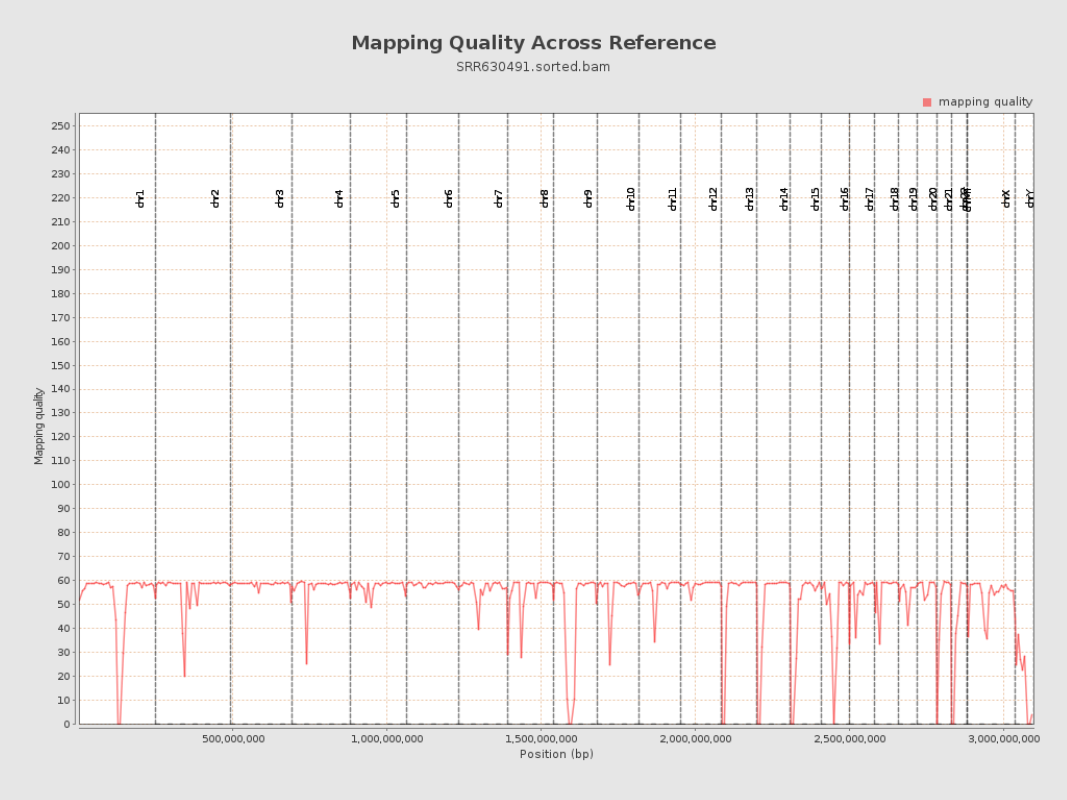
10. Results : Mapped Reads Clipping Profile



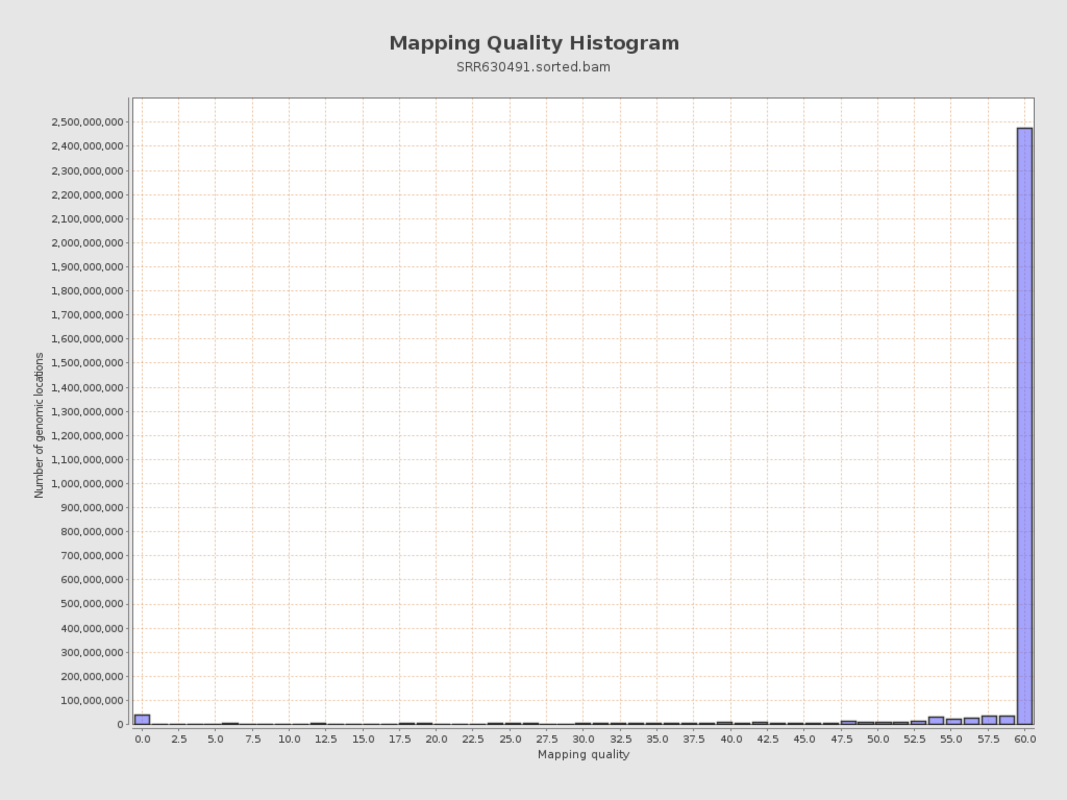
11. Results : Homopolymer Indels



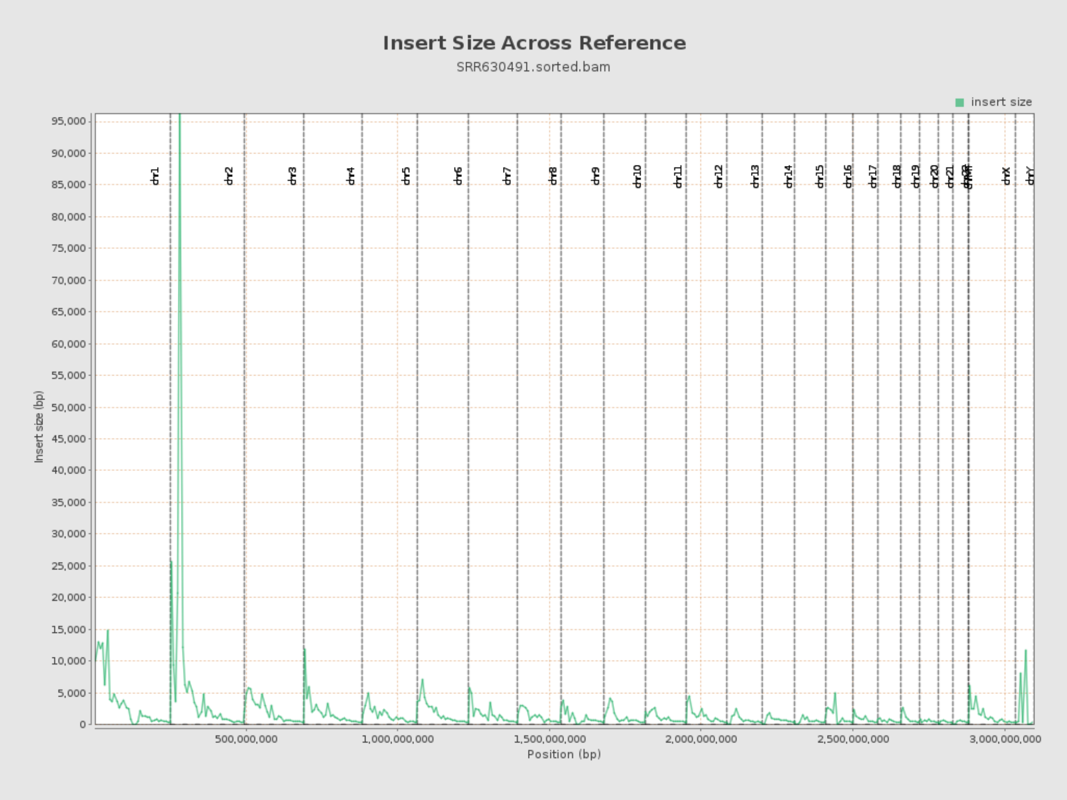
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram