Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/15 06:42:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630499.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 SRR630499_1.fastq.gz SRR630499_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 15 06:42:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630499.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	95,335,640
Mapped reads	95,009,101 / 99.66%
Unmapped reads	326,539 / 0.34%
Mapped paired reads	95,009,101 / 99.66%
Mapped reads, first in pair	47,625,255 / 49.96%
Mapped reads, second in pair	47,383,846 / 49.7%
Mapped reads, both in pair	94,743,606 / 99.38%
Mapped reads, singletons	265,495 / 0.28%
Secondary alignments	0
Supplementary alignments	540,604 / 0.57%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	17,739,614 / 18.61%
Duplication rate	16.09%
Clipped reads	6,974,211 / 7.32%

2.2. ACGT Content

Number/percentage of A's	2,959,297,321 / 31.24%
Number/percentage of C's	1,773,191,728 / 18.72%
Number/percentage of T's	2,944,580,896 / 31.09%
Number/percentage of G's	1,794,595,225 / 18.95%
Number/percentage of N's	793,542 / 0.01%

GC Percentage	37.66%

2.3. Coverage

Mean	3.0605
Standard Deviation	12.1247

2.4. Mapping Quality

Mean Mapping Quality	54

2.5. Insert size

Mean	43,710.17
Standard Deviation	1,990,903.29
P25/Median/P75	255 / 319 / 390

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	76,589,019
Insertions	814,618
Mapped reads with at least one insertion	0.84%
Deletions	864,441
Mapped reads with at least one deletion	0.89%
Homopolymer indels	44.95%

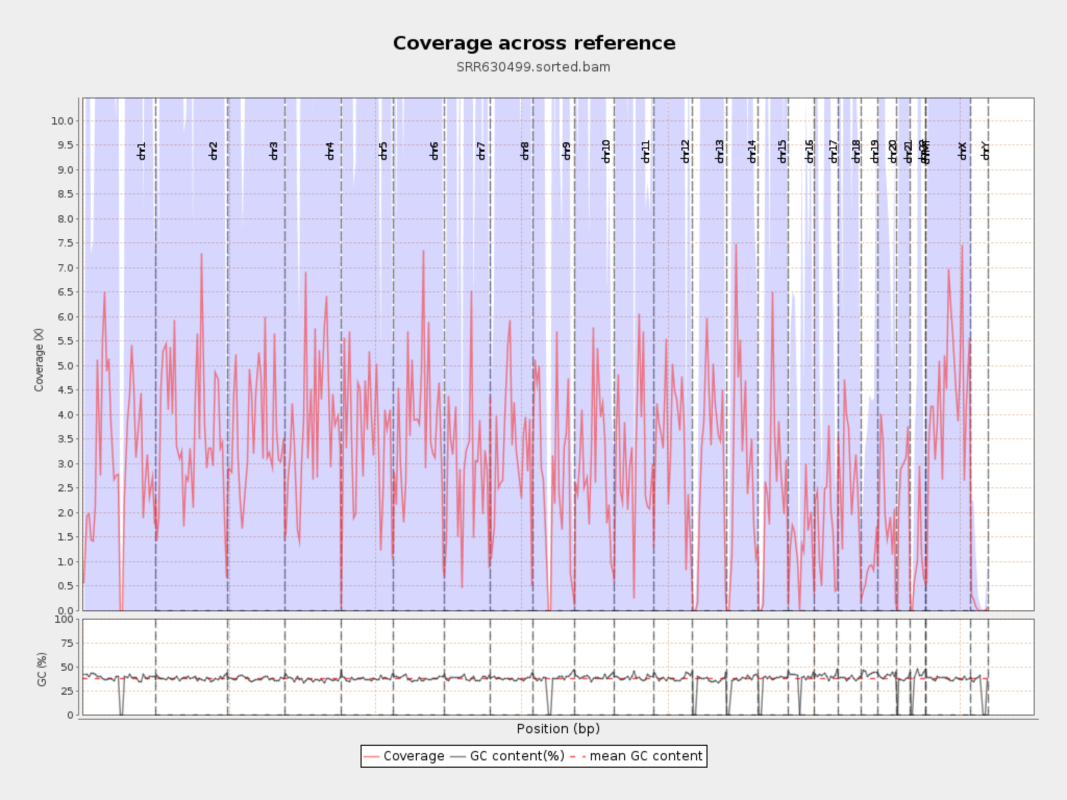
2.7. Chromosome stats

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

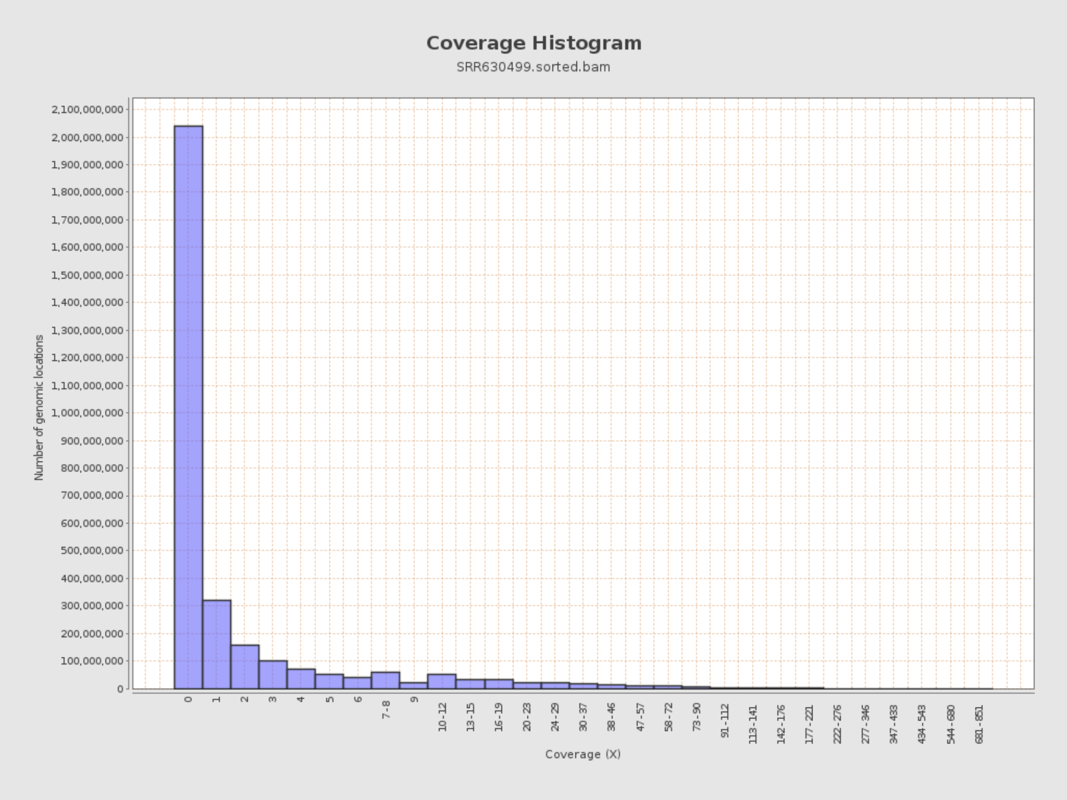
		bases	coverage	deviation
chr1	249250621	762490946	3.0591	12.3528
chr2	243199373	895979748	3.6841	14.8293
chr3	198022430	723632273	3.6543	12.6136
chr4	191154276	734894460	3.8445	12.7686
chr5	180915260	630572939	3.4855	13.5401
chr6	171115067	653052599	3.8165	13.8092
chr7	159138663	452915964	2.846	9.9971
chr8	146364022	470817237	3.2168	11.687
chr9	141213431	389323427	2.757	11.7098
chr10	135534747	408477189	3.0138	11.4015
chr11	135006516	421540662	3.1224	11.8485
chr12	133851895	457194348	3.4157	11.8631
chr13	115169878	354290289	3.0762	11.781
chr14	107349540	330665135	3.0803	12.8307
chr15	102531392	248188291	2.4206	13.2555
chr16	90354753	121425156	1.3439	5.1397
chr17	81195210	148744113	1.8319	9.0869
chr18	78077248	221472782	2.8366	8.7566
chr19	59128983	49636232	0.8395	3.9541
chr20	63025520	135464408	2.1494	9.0922
chr21	48129895	116281303	2.416	11.086
chr22	51304566	50550460	0.9853	7.8936
chrMT	16571	17143	1.0345	5.5642
chrX	155270560	692178709	4.4579	16.0645

chrY	59373566	4589779	0.0773	1.0498

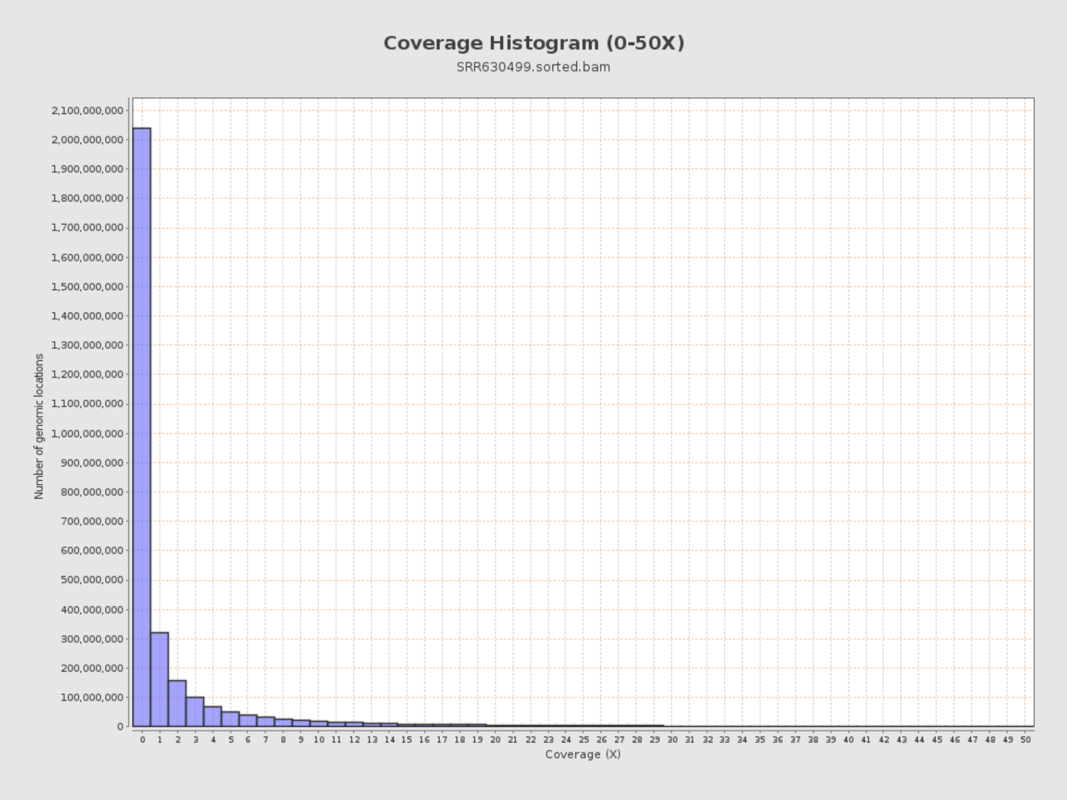
3. Results : Coverage across reference



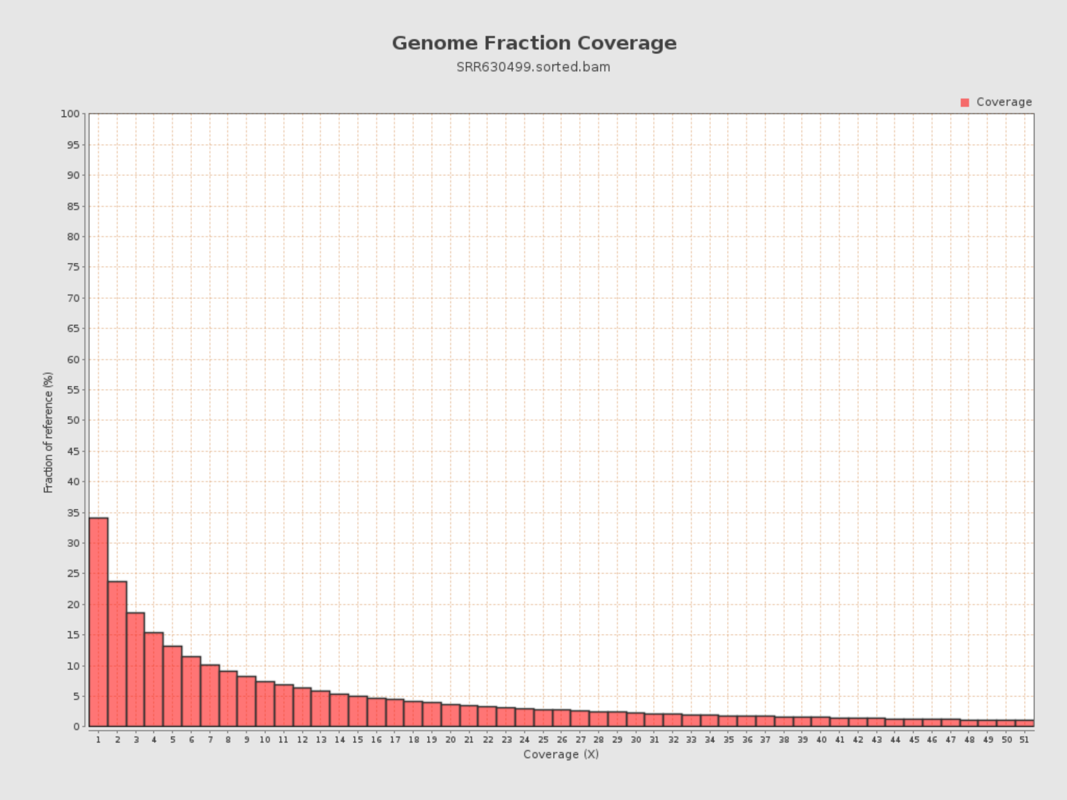
4. Results : Coverage Histogram



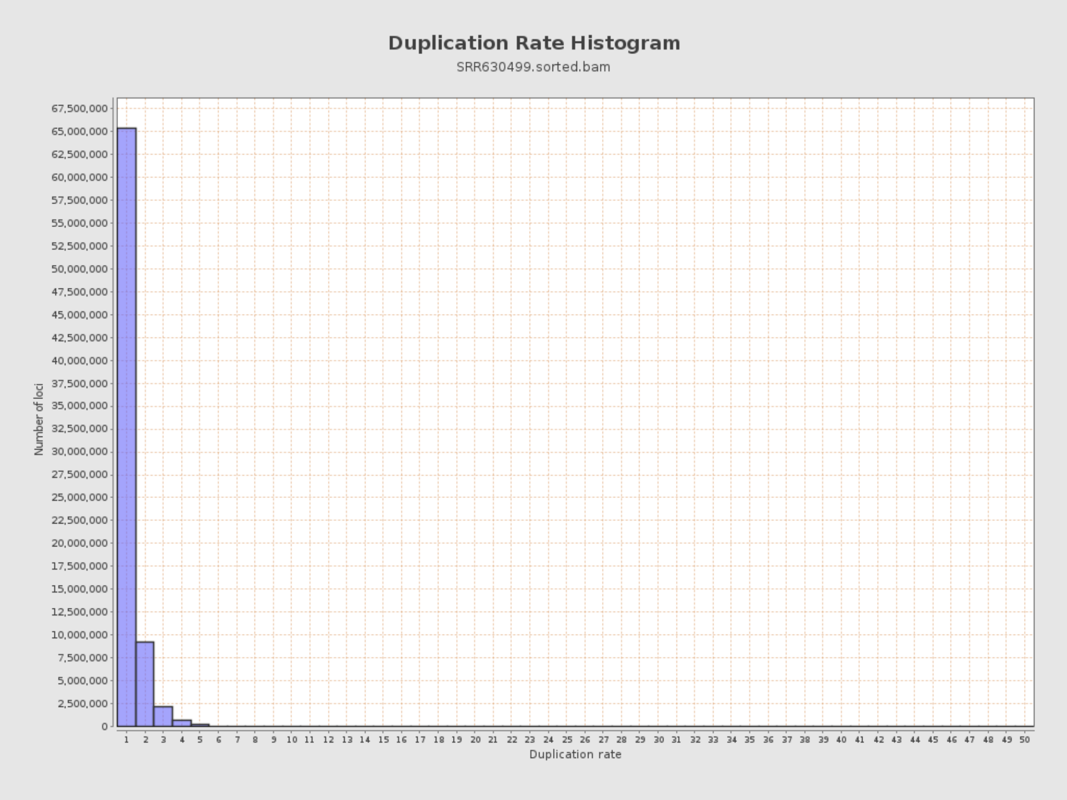
5. Results : Coverage Histogram (0-50X)



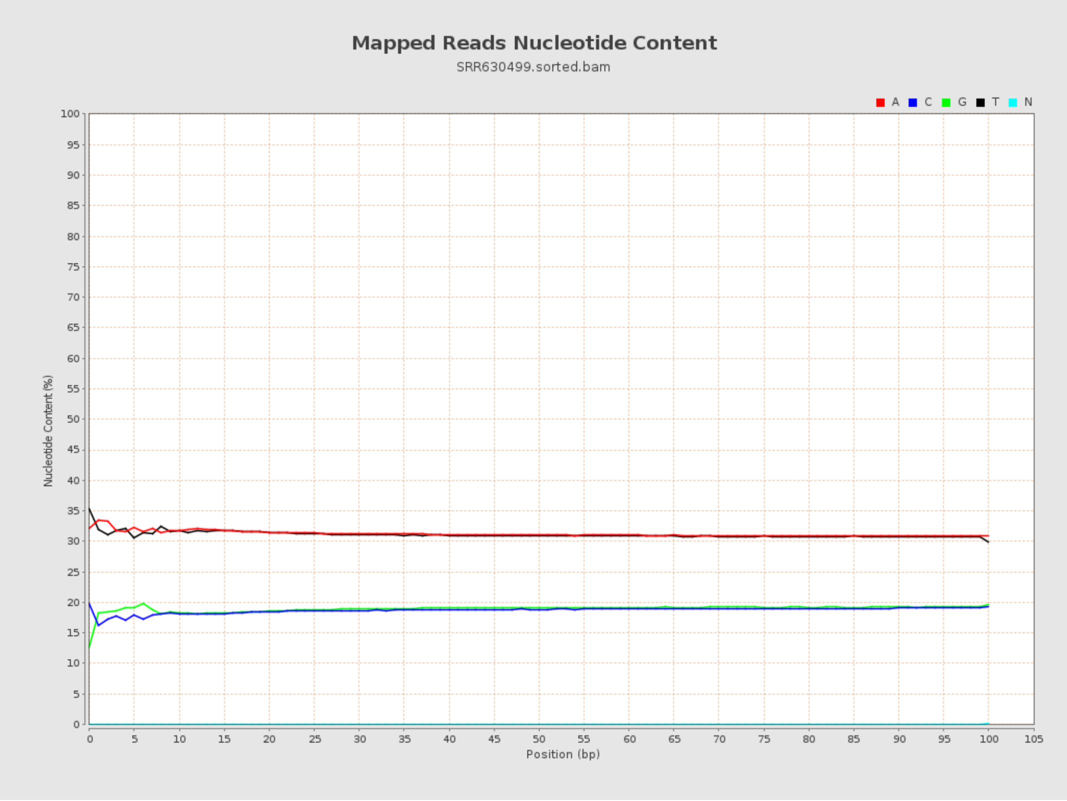
6. Results : Genome Fraction Coverage



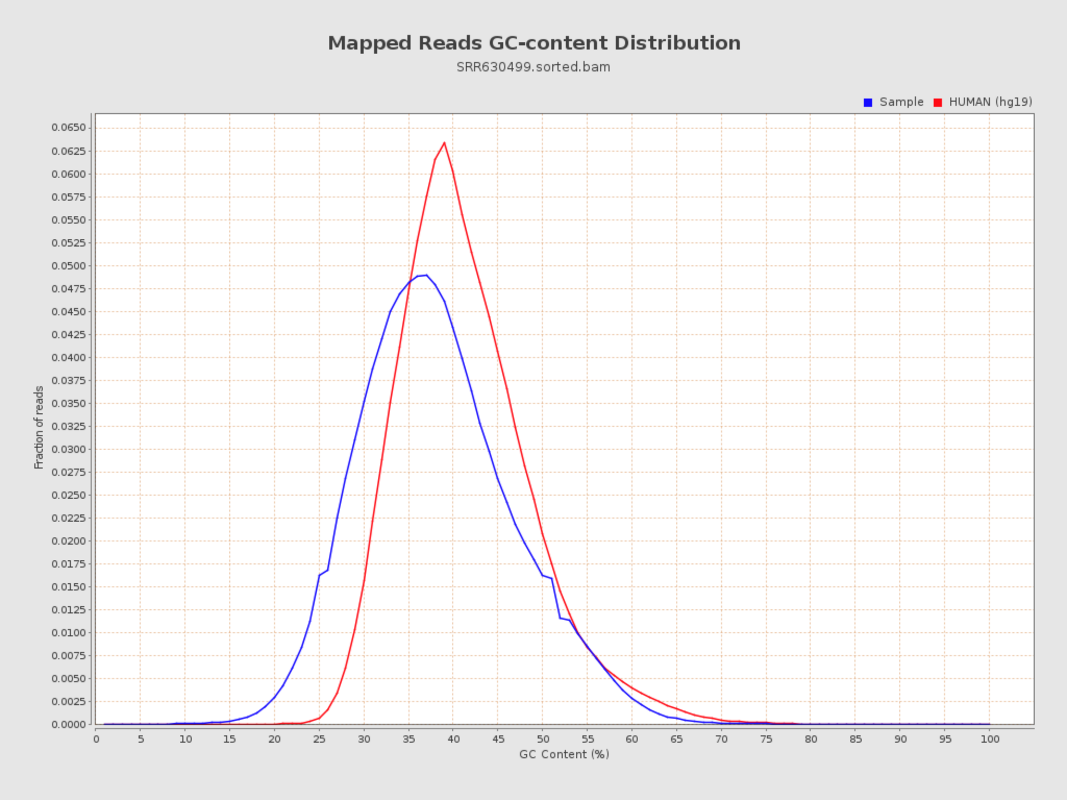
7. Results : Duplication Rate Histogram



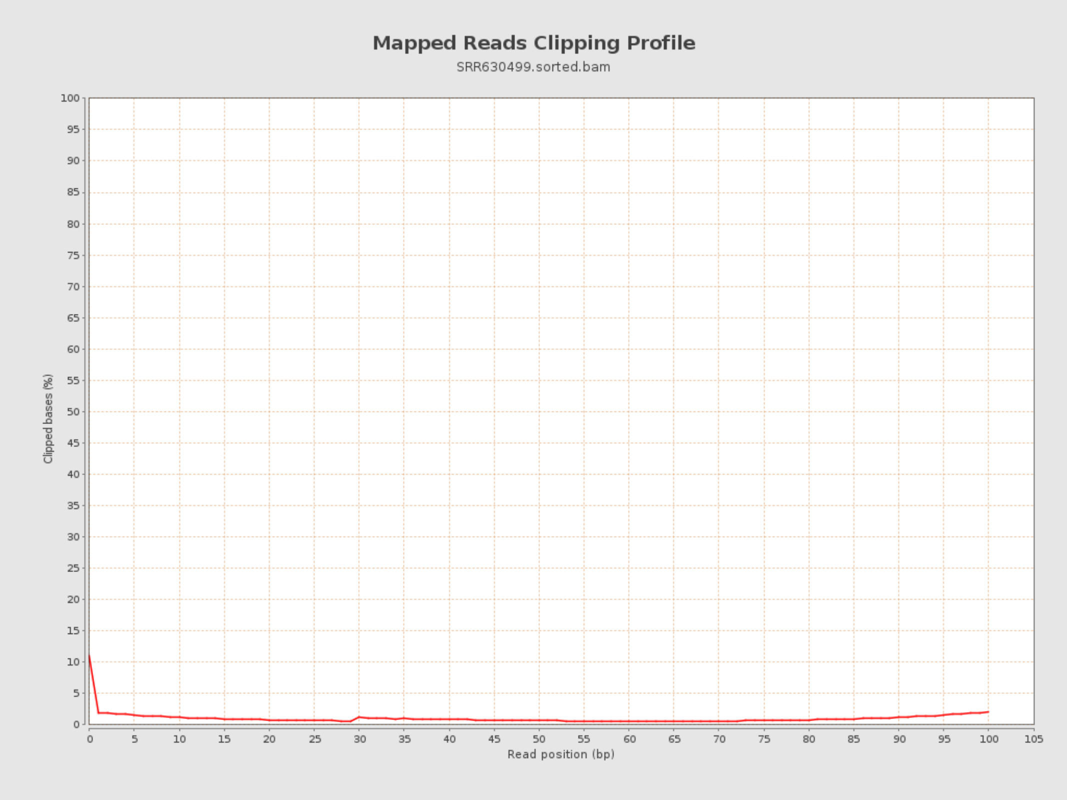
8. Results : Mapped Reads Nucleotide Content



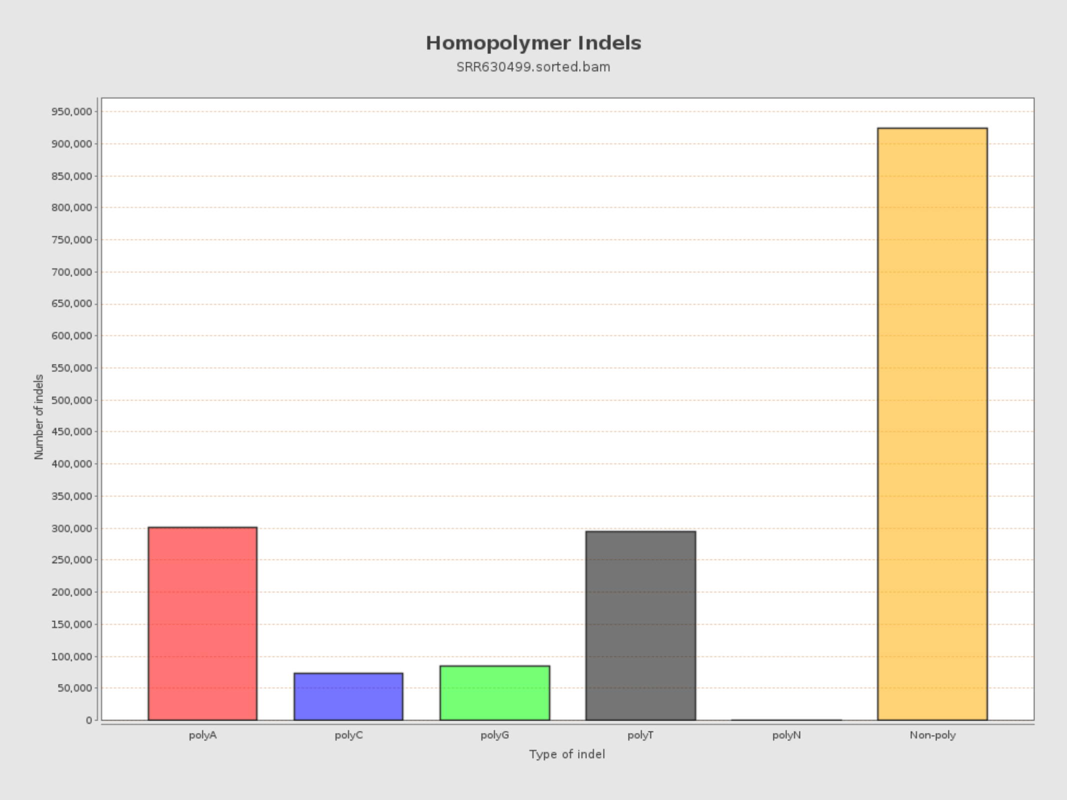
9. Results : Mapped Reads GC-content Distribution



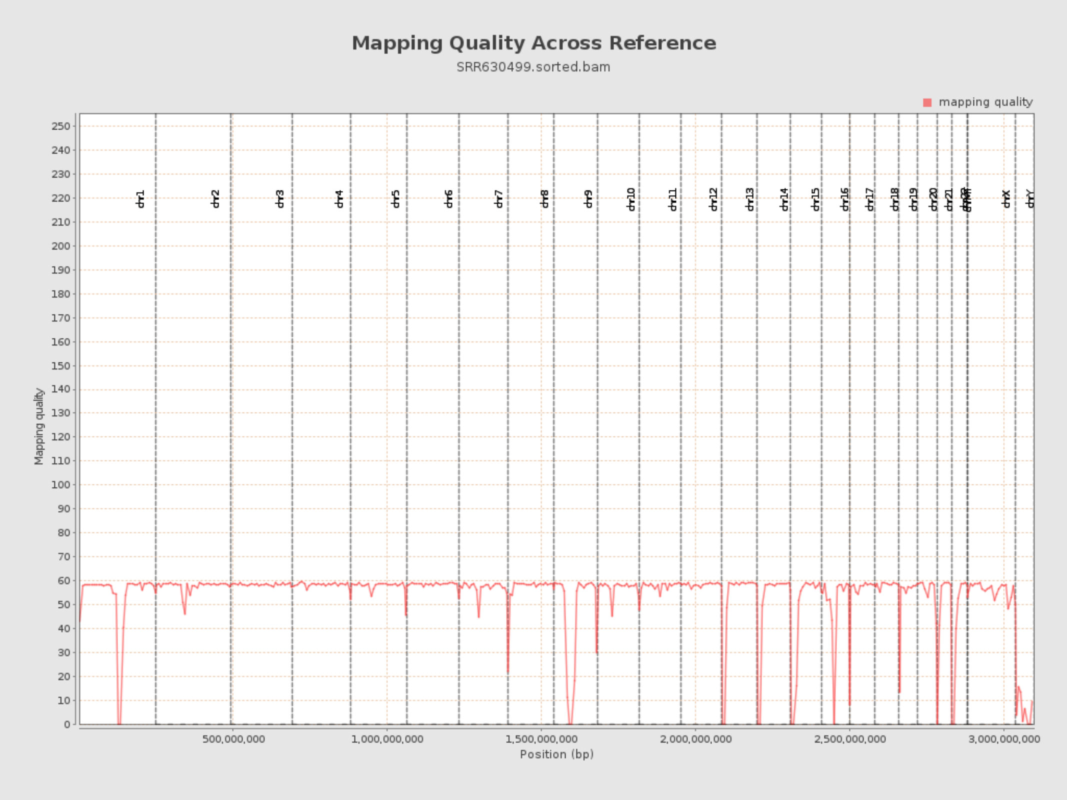
10. Results : Mapped Reads Clipping Profile



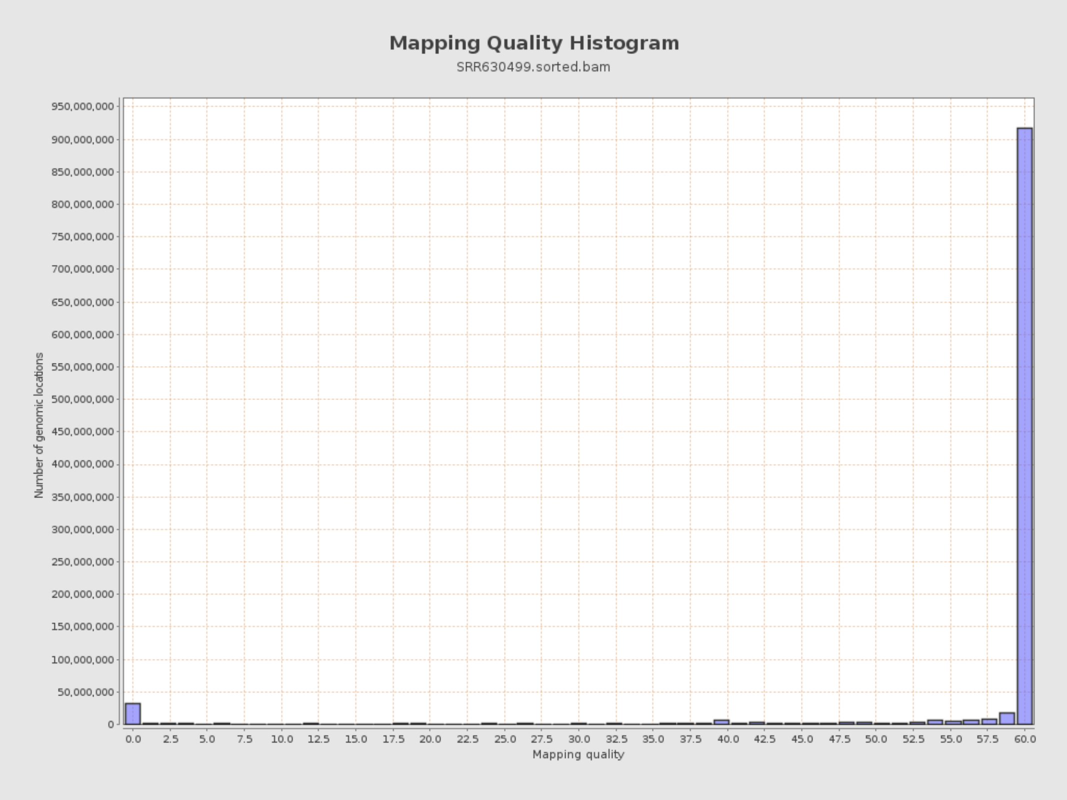
11. Results : Homopolymer Indels



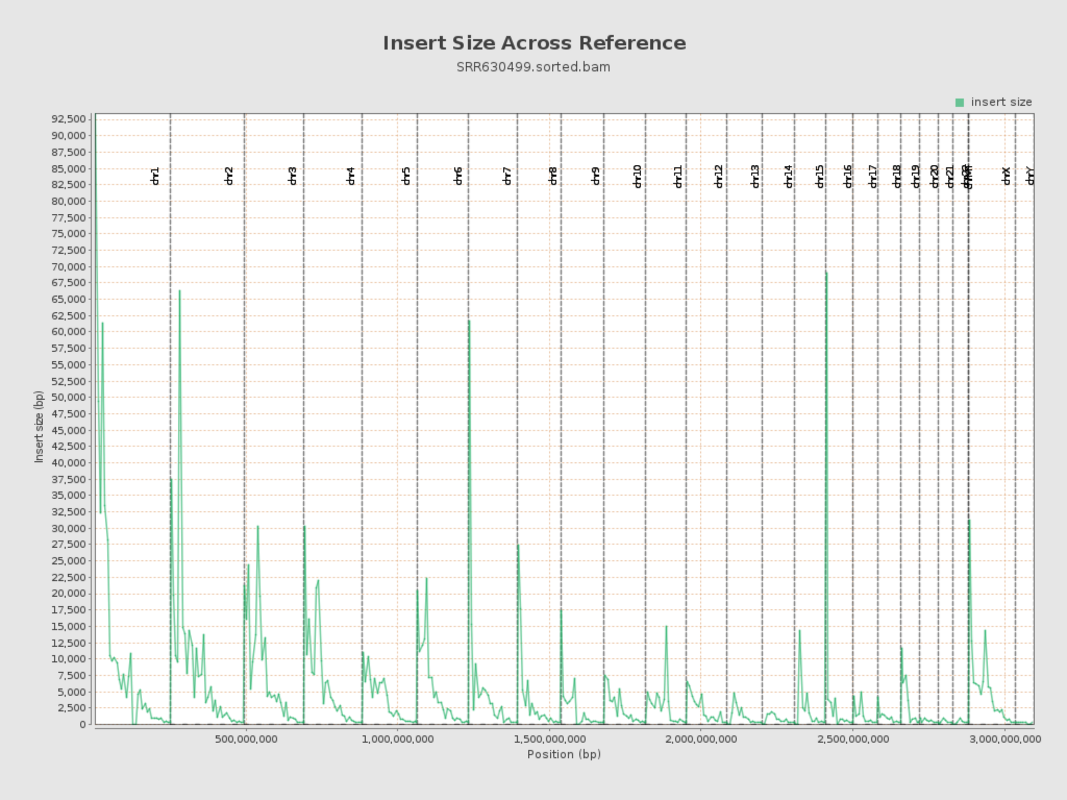
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram