Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/15 00:21:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630495.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 SRR630495_1.fastq.gz SRR630495_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 15 00:21:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630495.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	103,479,816
Mapped reads	103,146,198 / 99.68%
Unmapped reads	333,618 / 0.32%
Mapped paired reads	103,146,198 / 99.68%
Mapped reads, first in pair	51,667,361 / 49.93%
Mapped reads, second in pair	51,478,837 / 49.75%
Mapped reads, both in pair	102,929,674 / 99.47%
Mapped reads, singletons	216,524 / 0.21%
Secondary alignments	0
Supplementary alignments	524,245 / 0.51%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	15,991,532 / 15.45%
Duplication rate	13.57%
Clipped reads	6,551,255 / 6.33%

2.2. ACGT Content

Number/percentage of A's	3,206,903,891 / 31.13%
Number/percentage of C's	1,937,359,659 / 18.81%
Number/percentage of T's	3,196,536,724 / 31.03%
Number/percentage of G's	1,958,381,317 / 19.01%
Number/percentage of N's	878,328 / 0.01%

GC Percentage	37.82%

2.3. Coverage

Mean	3.3279
Standard Deviation	11.1293

2.4. Mapping Quality

Mean Mapping Quality	53.96

2.5. Insert size

Mean	32,942.88
Standard Deviation	1,721,931.64
P25/Median/P75	201 / 238 / 292

2.6. Mismatches and indels

General error rate	0.71%
Mismatches	71,119,185
Insertions	880,684
Mapped reads with at least one insertion	0.84%
Deletions	944,420
Mapped reads with at least one deletion	0.89%
Homopolymer indels	44.63%

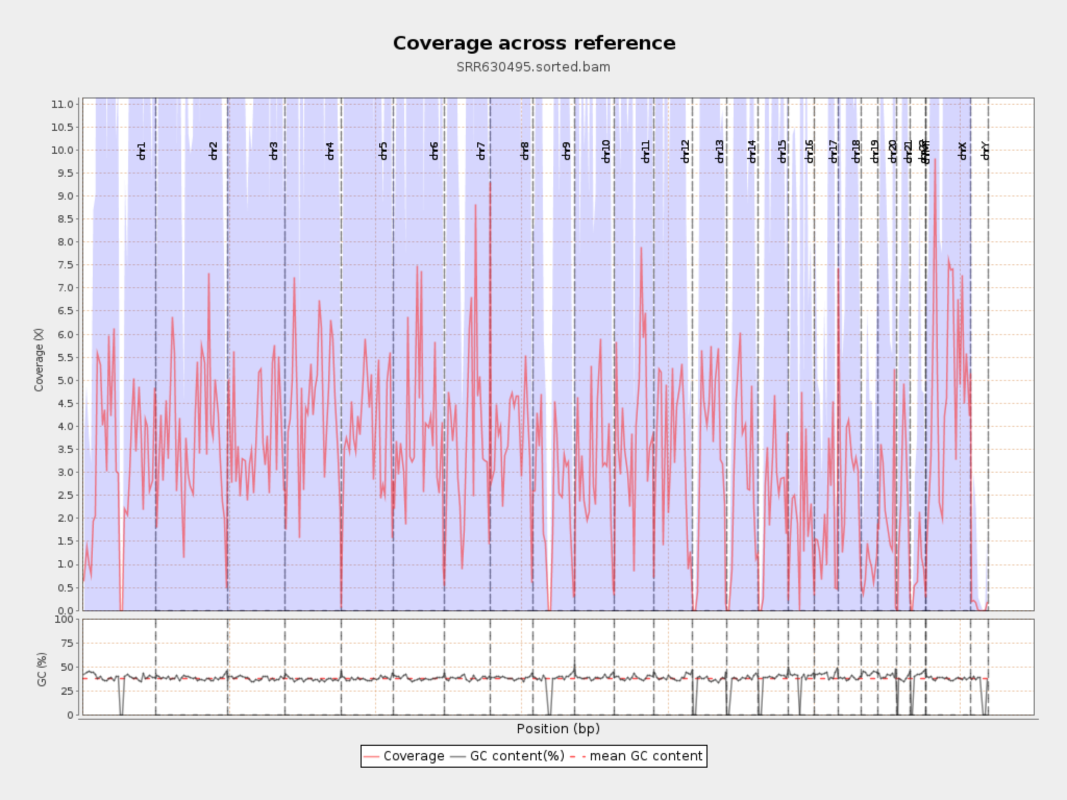
2.7. Chromosome stats

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

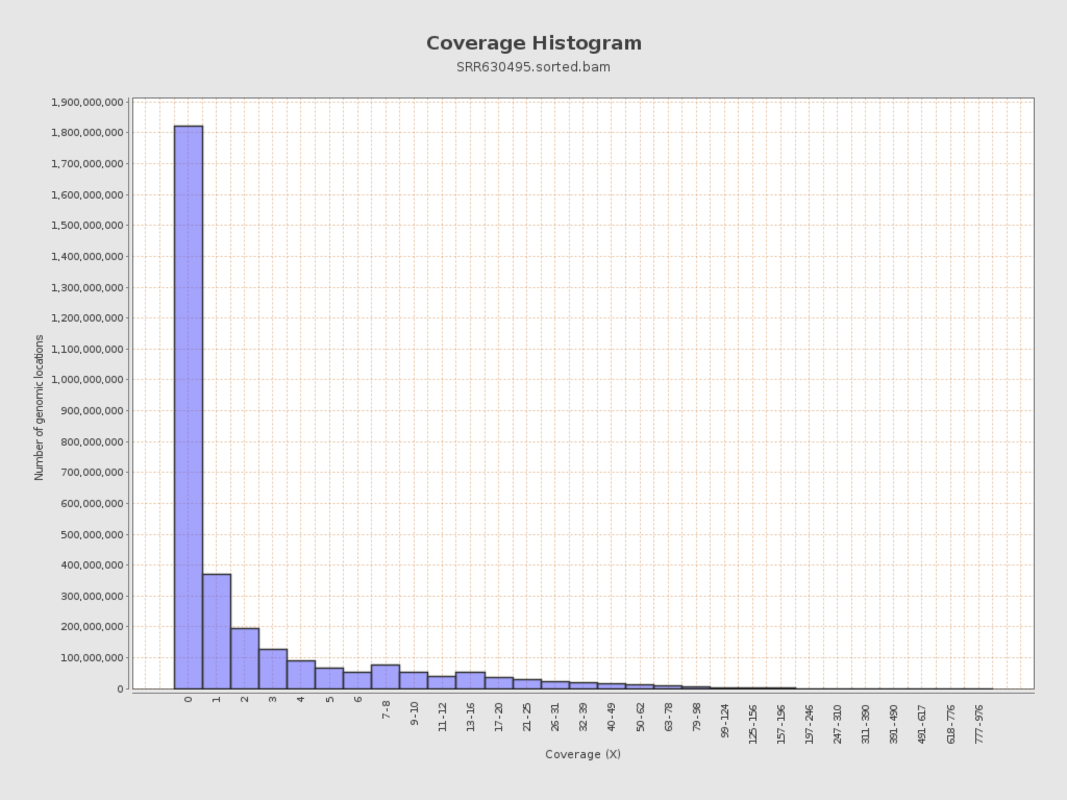
		bases	coverage	deviation
chr1	249250621	794464757	3.1874	11.3729
chr2	243199373	918053465	3.7749	11.5834
chr3	198022430	745121085	3.7628	10.7596
chr4	191154276	851008915	4.4519	12.7573
chr5	180915260	703839420	3.8904	11.5008
chr6	171115067	670329398	3.9174	12.537
chr7	159138663	590448277	3.7103	13.7449
chr8	146364022	552211122	3.7729	10.8785
chr9	141213431	352724786	2.4978	8.0989
chr10	135534747	432100083	3.1881	9.9851
chr11	135006516	539367115	3.9951	12.7174
chr12	133851895	465635418	3.4787	10.1257
chr13	115169878	393155691	3.4137	10.6835
chr14	107349540	321024262	2.9905	10.2763
chr15	102531392	238121903	2.3224	8.1872
chr16	90354753	180705642	2	10.8444
chr17	81195210	153157893	1.8863	7.363
chr18	78077248	244007815	3.1252	9.15
chr19	59128983	54501417	0.9217	3.5645
chr20	63025520	155496363	2.4672	9.4725
chr21	48129895	112425864	2.3359	8.6728
chr22	51304566	42210750	0.8227	3.6741
chrMT	16571	5845	0.3527	1.6547
chrX	155270560	786390516	5.0646	16.3033

chrY	59373566	5692995	0.0959	1.3998

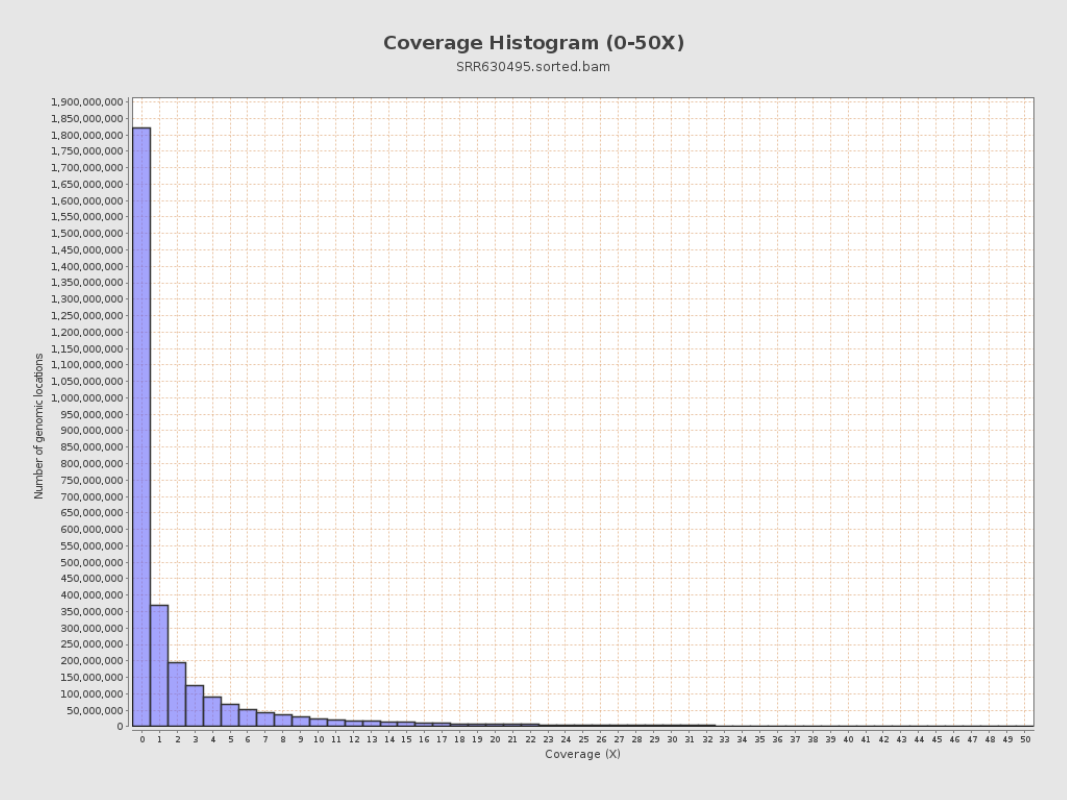
3. Results : Coverage across reference



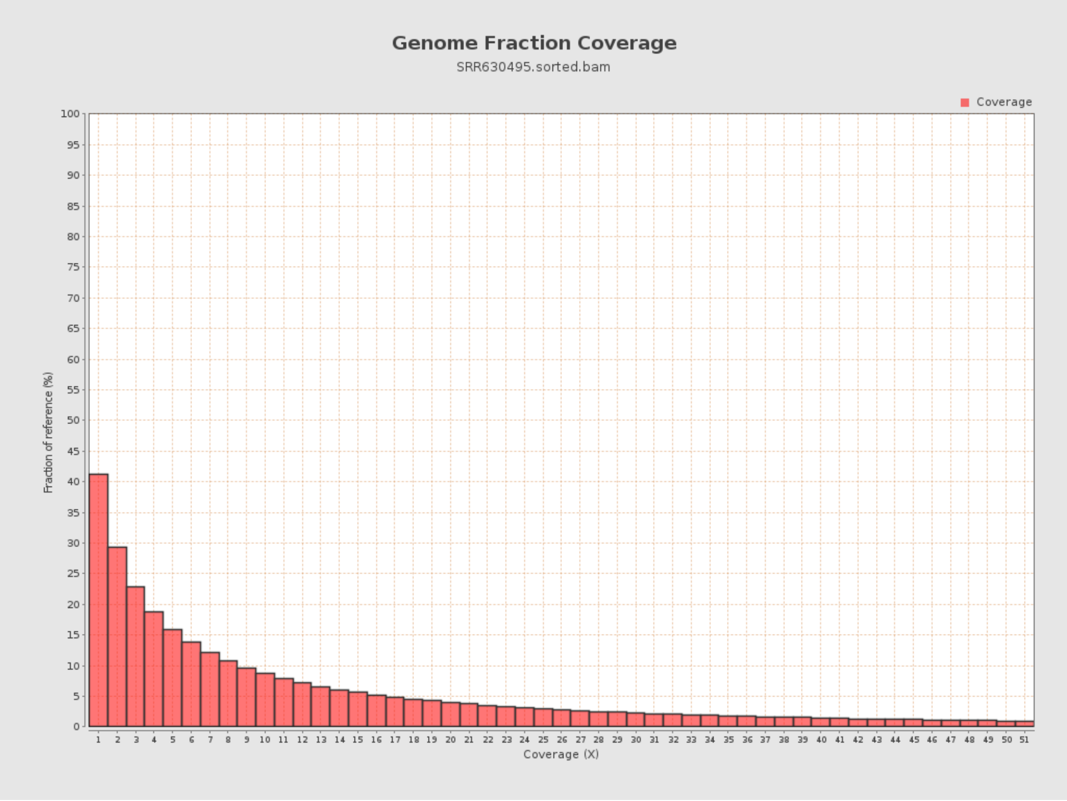
4. Results : Coverage Histogram



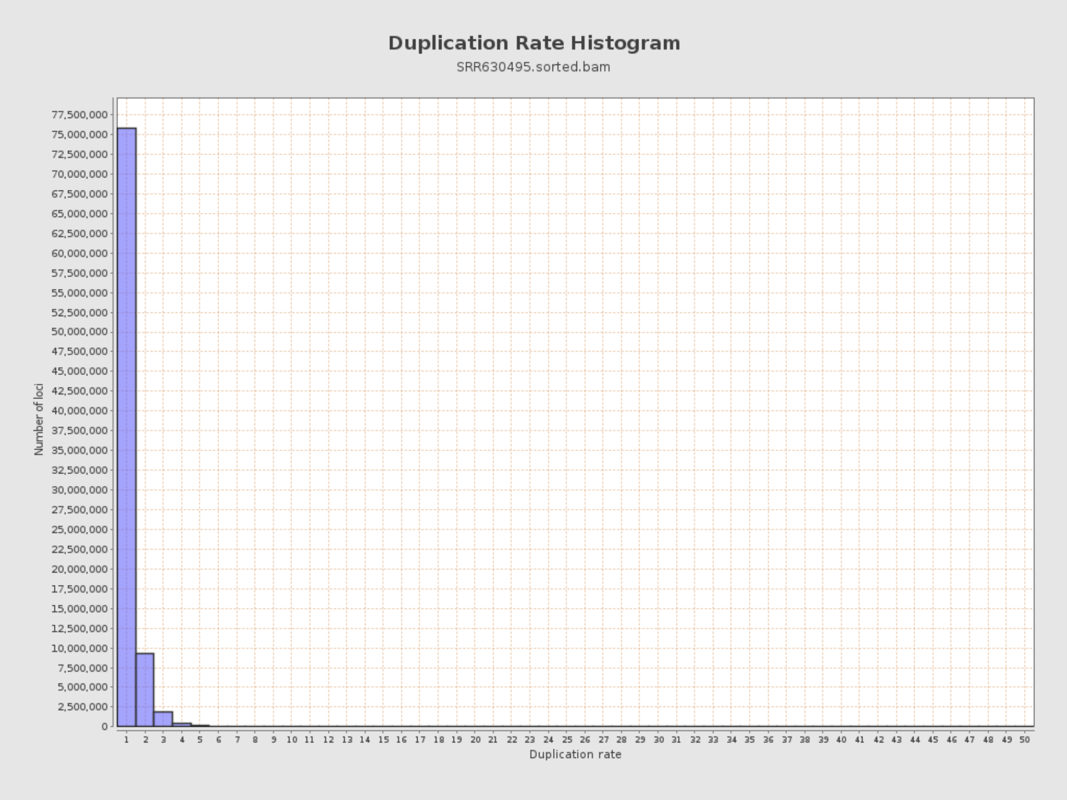
5. Results : Coverage Histogram (0-50X)



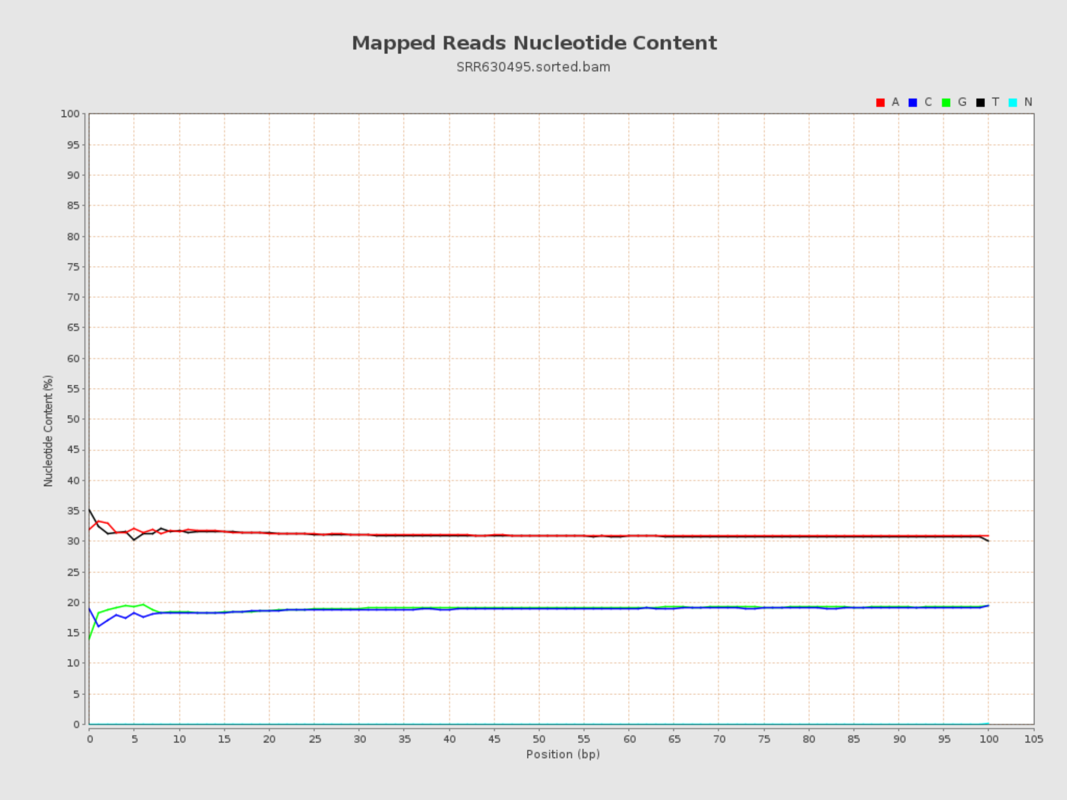
6. Results : Genome Fraction Coverage



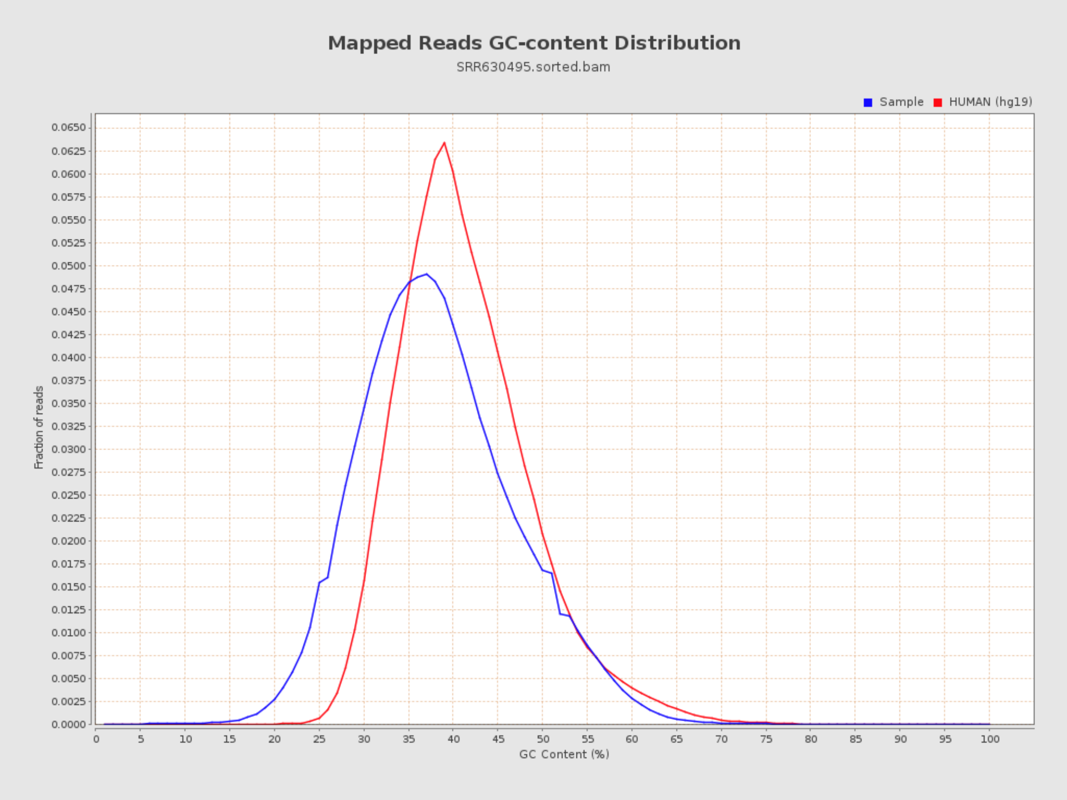
7. Results : Duplication Rate Histogram



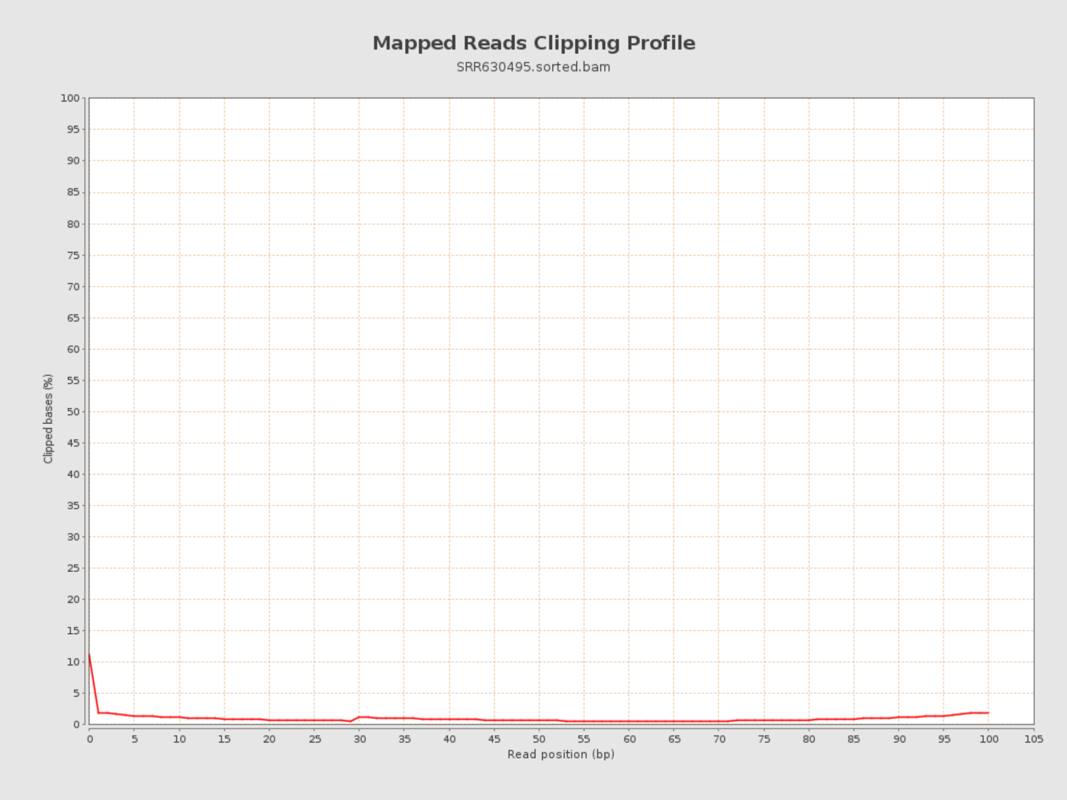
8. Results : Mapped Reads Nucleotide Content



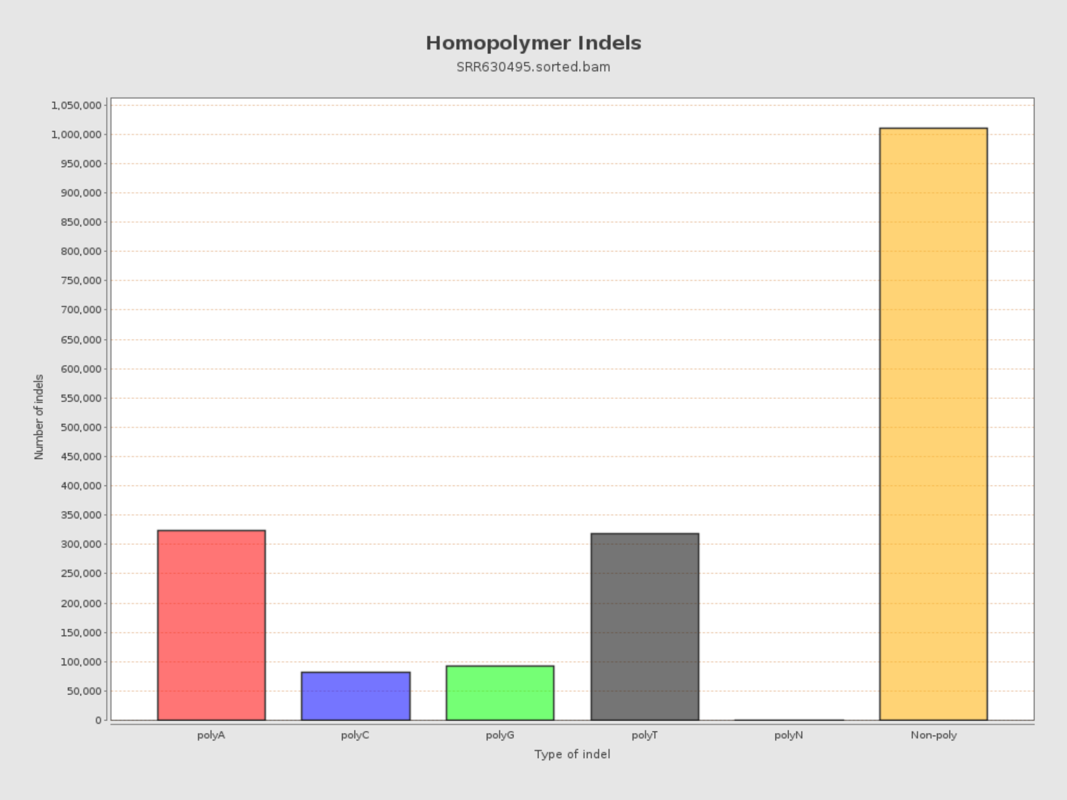
9. Results : Mapped Reads GC-content Distribution



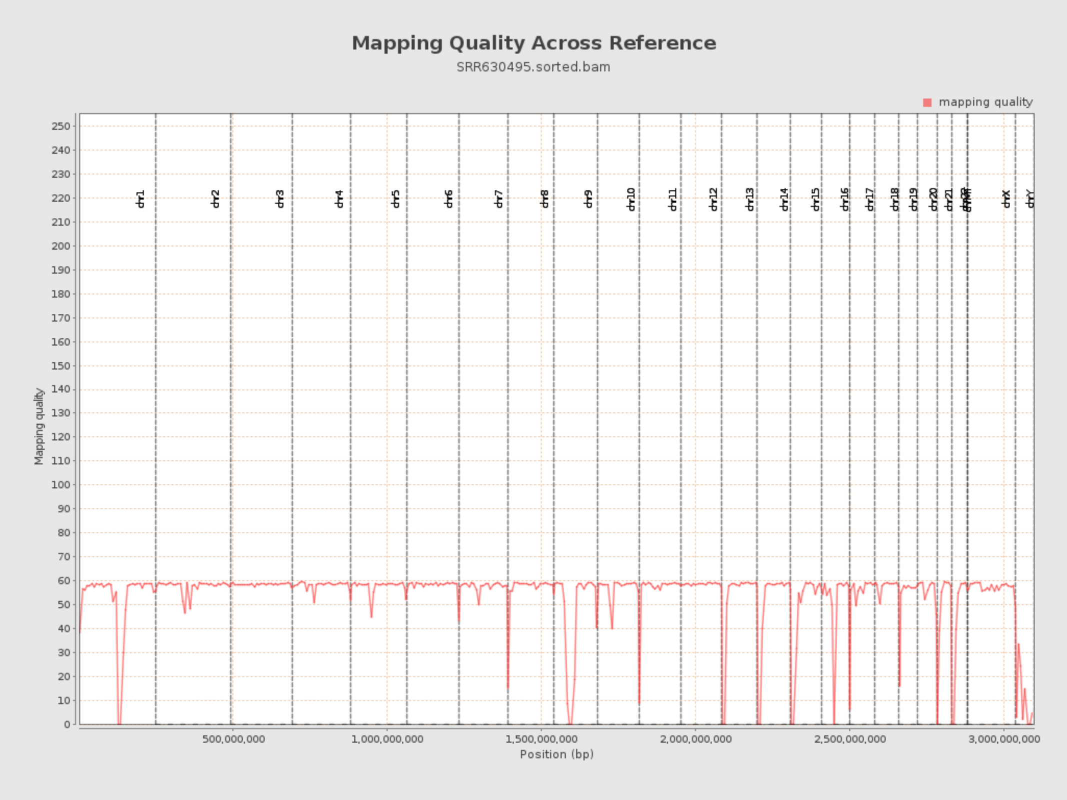
10. Results : Mapped Reads Clipping Profile



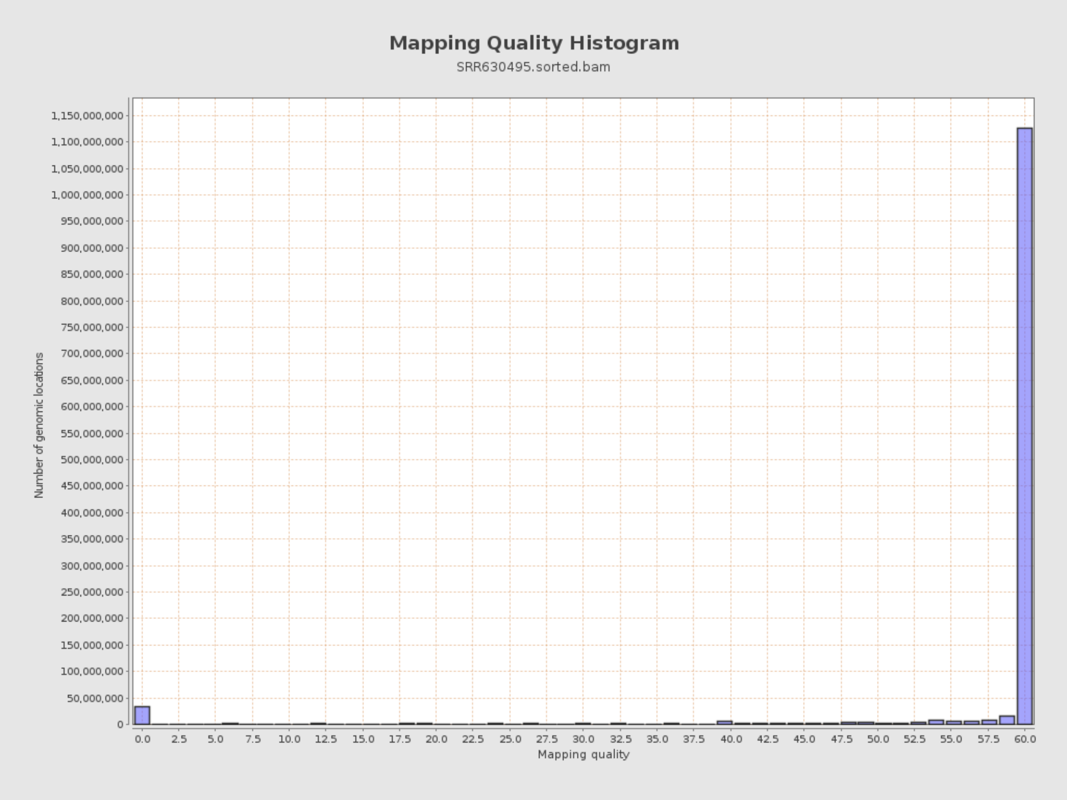
11. Results : Homopolymer Indels



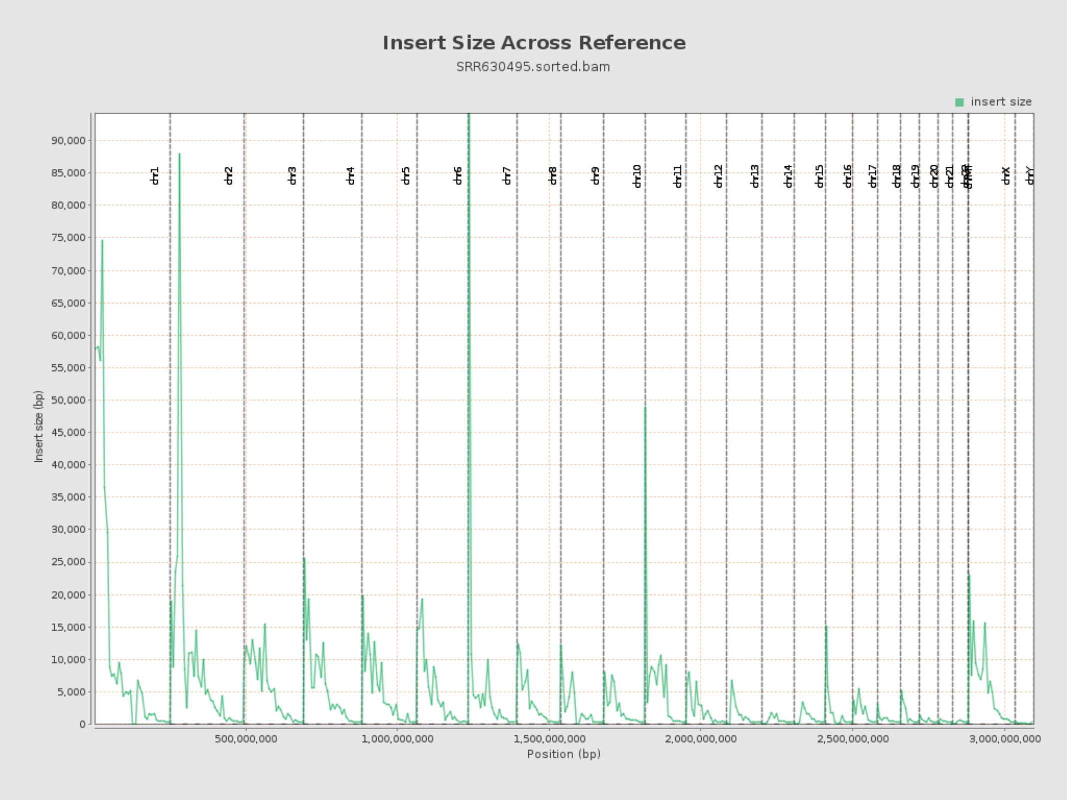
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram