Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/15 02:21:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630496.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 SRR630496_1.fastq.gz SRR630496_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 15 02:21:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630496.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	77,153,952
Mapped reads	76,860,749 / 99.62%
Unmapped reads	293,203 / 0.38%
Mapped paired reads	76,860,749 / 99.62%
Mapped reads, first in pair	38,516,061 / 49.92%
Mapped reads, second in pair	38,344,688 / 49.7%
Mapped reads, both in pair	76,657,942 / 99.36%
Mapped reads, singletons	202,807 / 0.26%
Secondary alignments	0
Supplementary alignments	437,128 / 0.57%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	13,922,365 / 18.04%
Duplication rate	15.19%
Clipped reads	7,004,909 / 9.08%

2.2. ACGT Content

Number/percentage of A's	2,384,597,436 / 31.23%
Number/percentage of C's	1,421,540,279 / 18.61%
Number/percentage of T's	2,373,213,895 / 31.08%
Number/percentage of G's	1,433,053,297 / 18.77%
Number/percentage of N's	24,395,698 / 0.32%

GC Percentage	37.38%

2.3. Coverage

Mean	2.4674
Standard Deviation	11.0066

2.4. Mapping Quality

Mean Mapping Quality	53.85

2.5. Insert size

Mean	41,207.12
Standard Deviation	1,897,800.7
P25/Median/P75	259 / 323 / 392

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	93,112,007
Insertions	668,737
Mapped reads with at least one insertion	0.86%
Deletions	724,046
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.83%

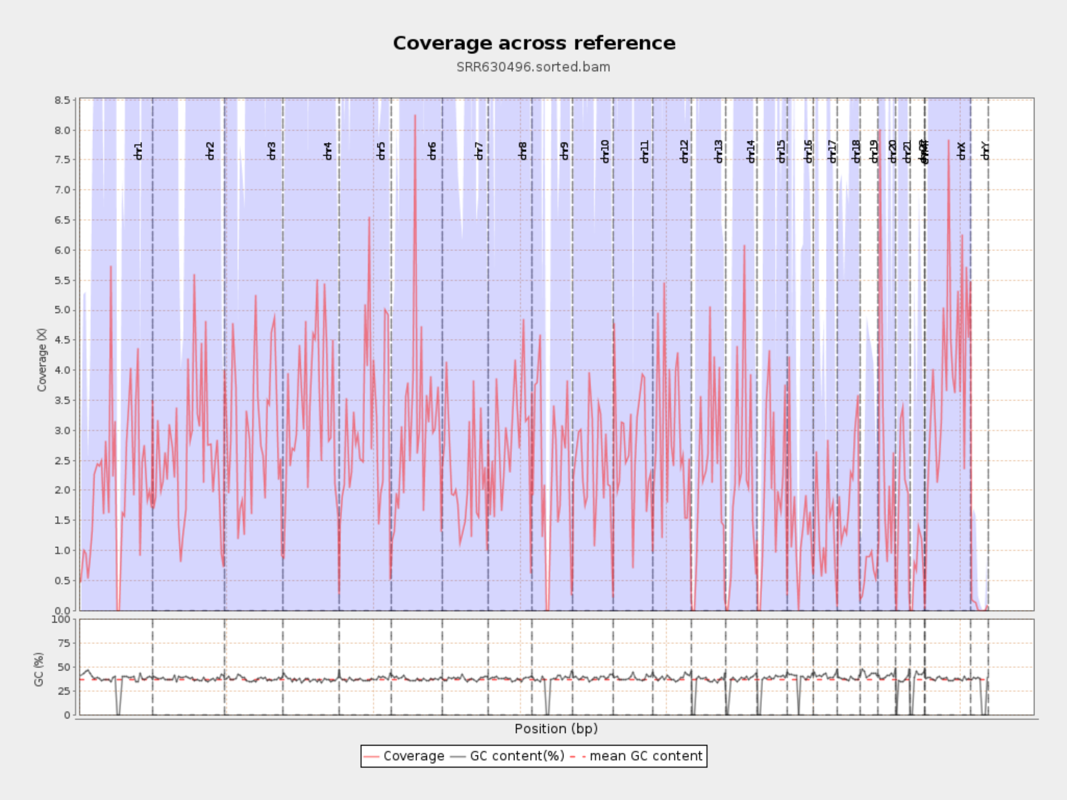
2.7. Chromosome stats

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

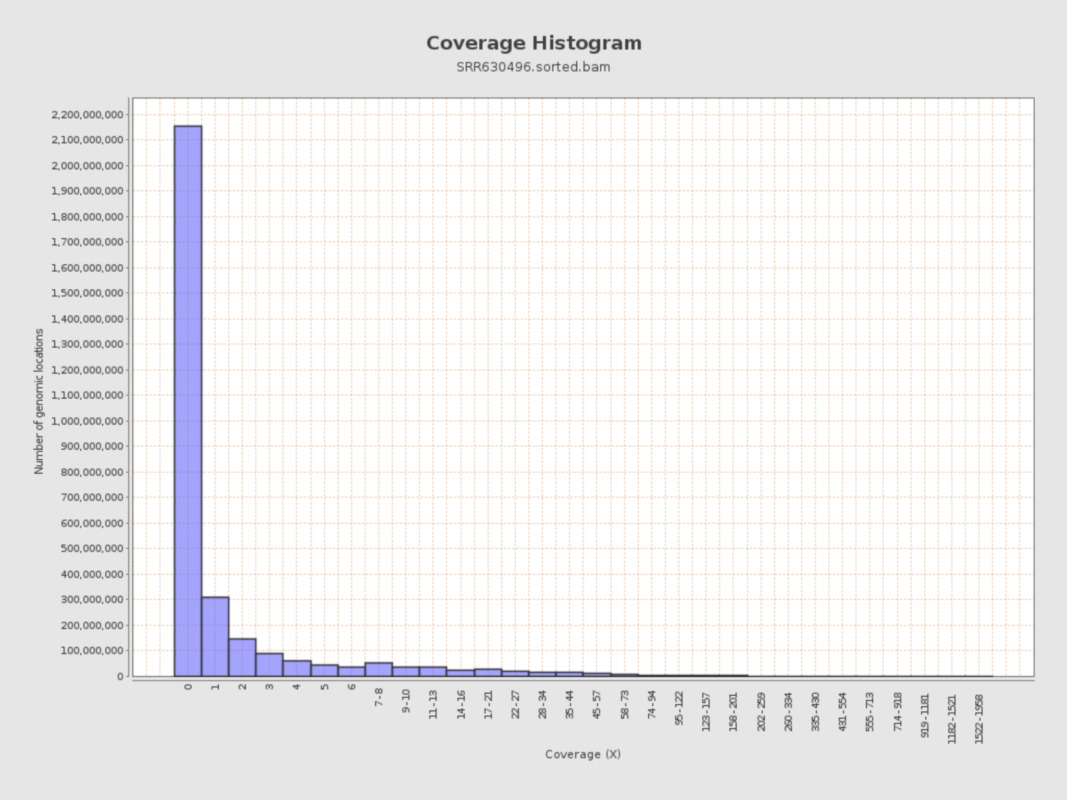
		bases	coverage	deviation
chr1	249250621	523203488	2.0991	9.476
chr2	243199373	630583180	2.5929	10.0926
chr3	198022430	592417211	2.9917	11.2001
chr4	191154276	644495003	3.3716	12.4085
chr5	180915260	536914708	2.9678	12.7017
chr6	171115067	527854983	3.0848	13.3026
chr7	159138663	349087078	2.1936	9.9914
chr8	146364022	413701617	2.8265	10.5111
chr9	141213431	315058560	2.2311	8.9154
chr10	135534747	329413877	2.4305	9.7364
chr11	135006516	366923363	2.7178	10.5569
chr12	133851895	381548523	2.8505	11.1384
chr13	115169878	265811902	2.308	9.1198
chr14	107349540	229148271	2.1346	13.203
chr15	102531392	209003495	2.0384	8.9068
chr16	90354753	125238052	1.3861	12.0173
chr17	81195210	107224987	1.3206	6.734
chr18	78077248	151032254	1.9344	6.8947
chr19	59128983	38261689	0.6471	2.8928
chr20	63025520	155798450	2.472	19.0563
chr21	48129895	97614651	2.0282	9.0274
chr22	51304566	35941371	0.7005	3.5341
chrMT	16571	573	0.0346	0.3342
chrX	155270560	608208617	3.9171	16.0028

chrY	59373566	3928354	0.0662	0.9072

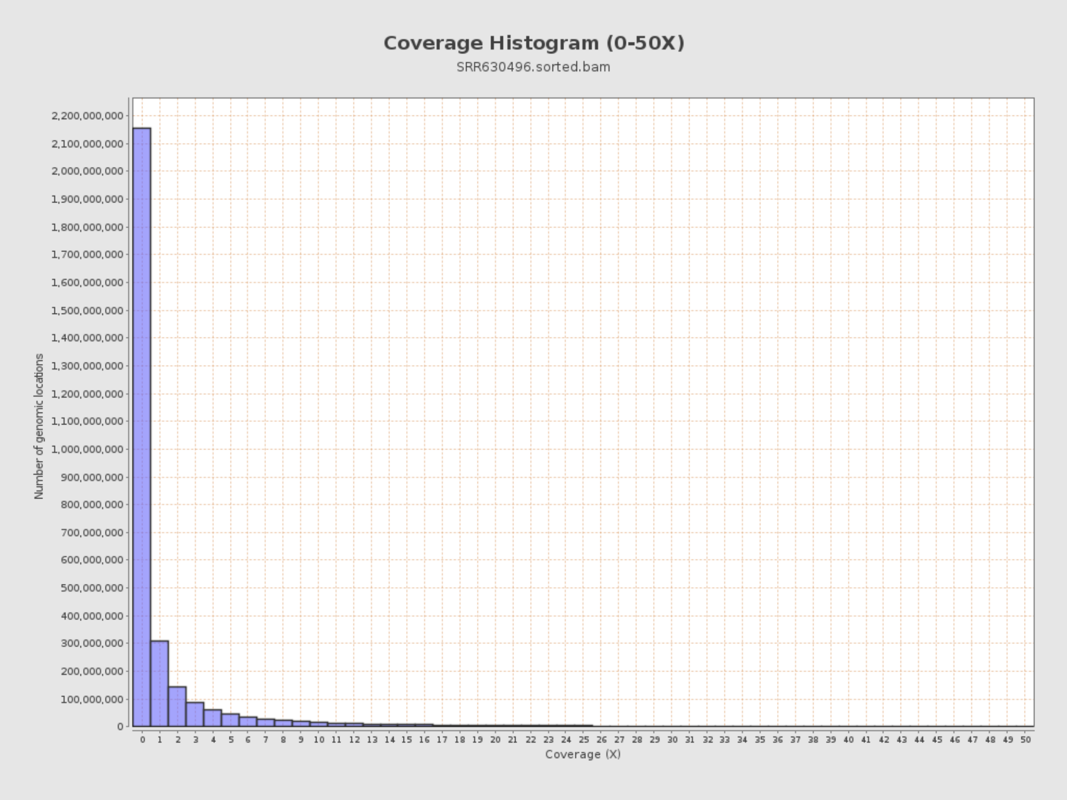
3. Results : Coverage across reference



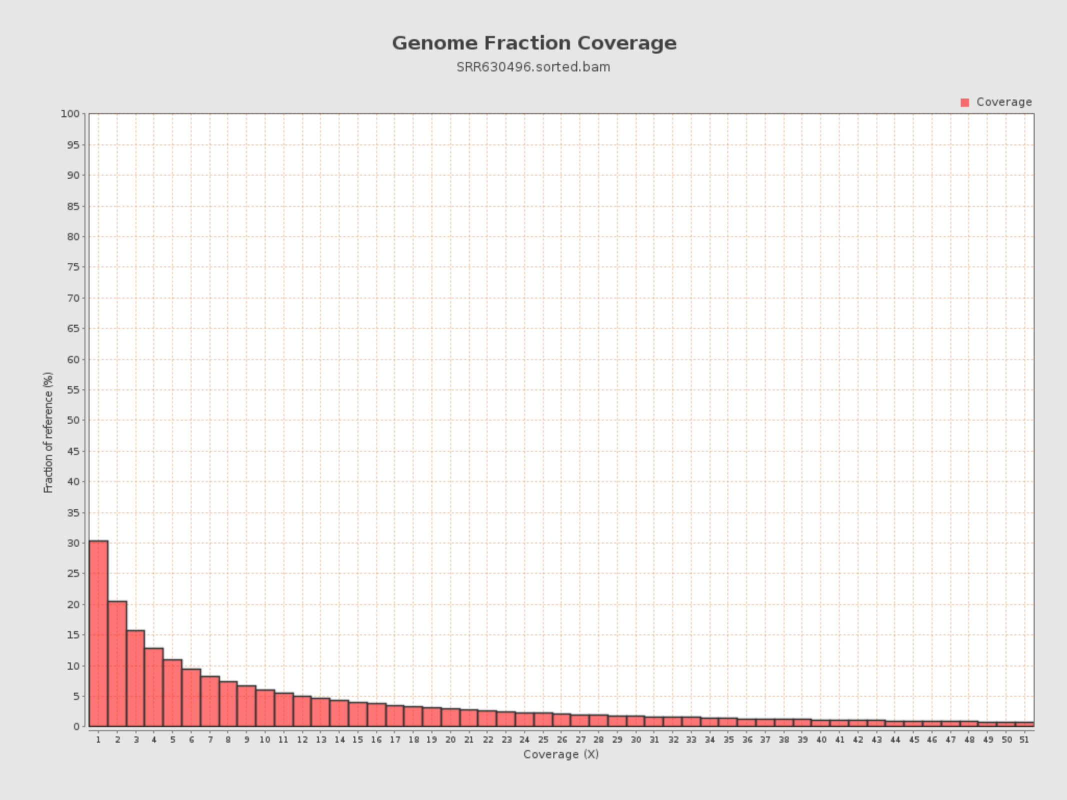
4. Results : Coverage Histogram



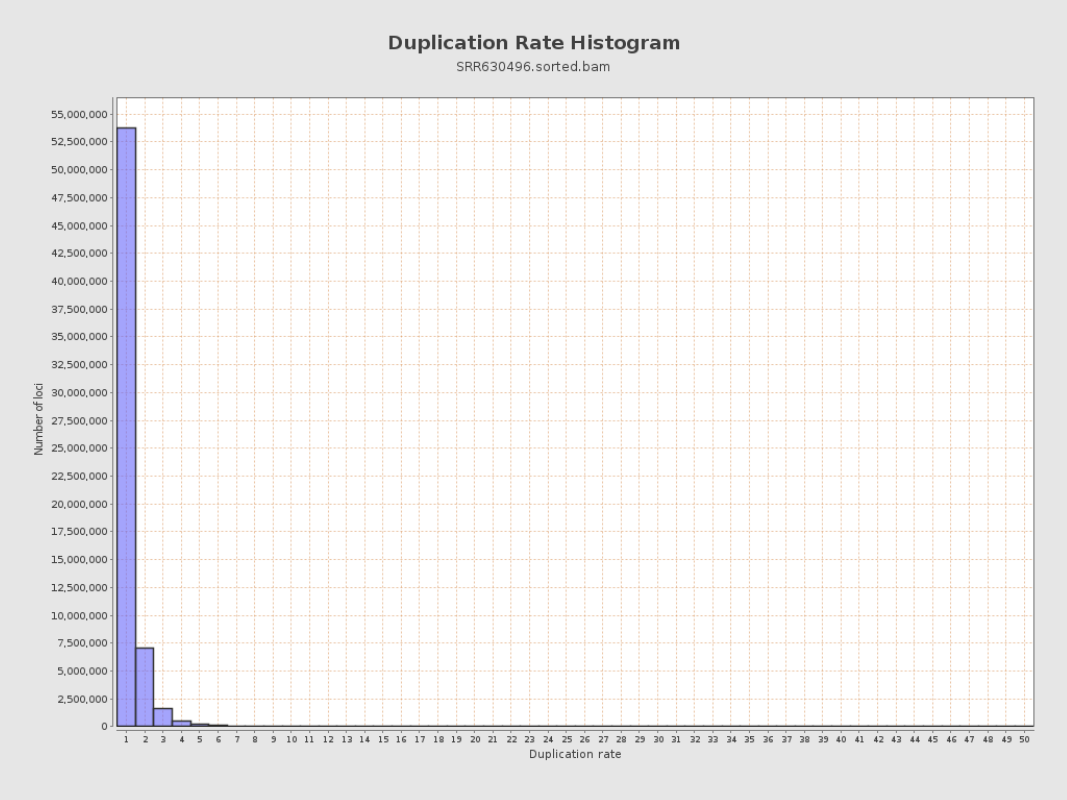
5. Results : Coverage Histogram (0-50X)



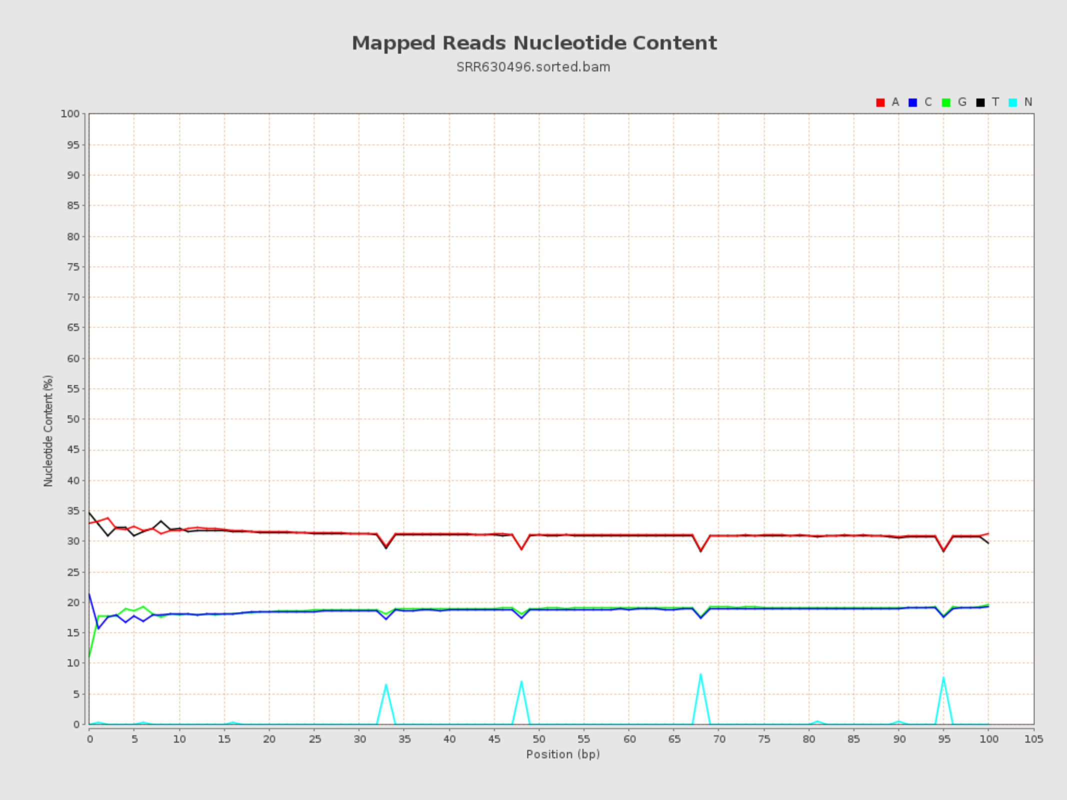
6. Results : Genome Fraction Coverage



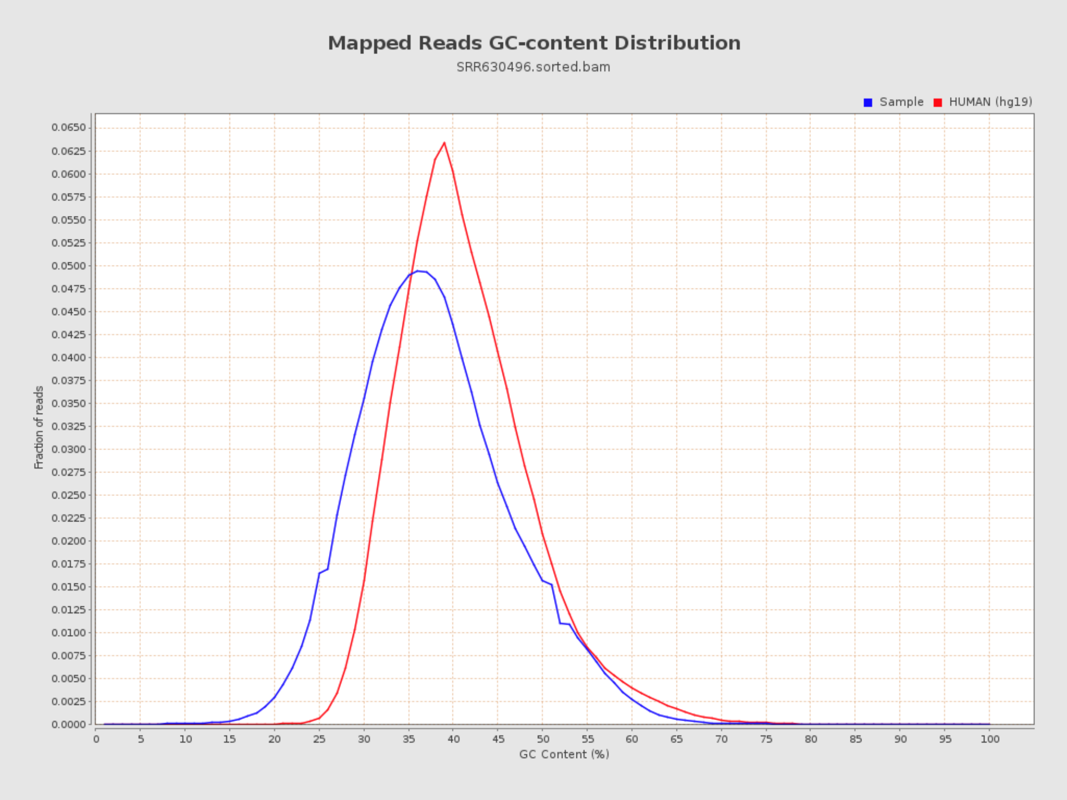
7. Results : Duplication Rate Histogram



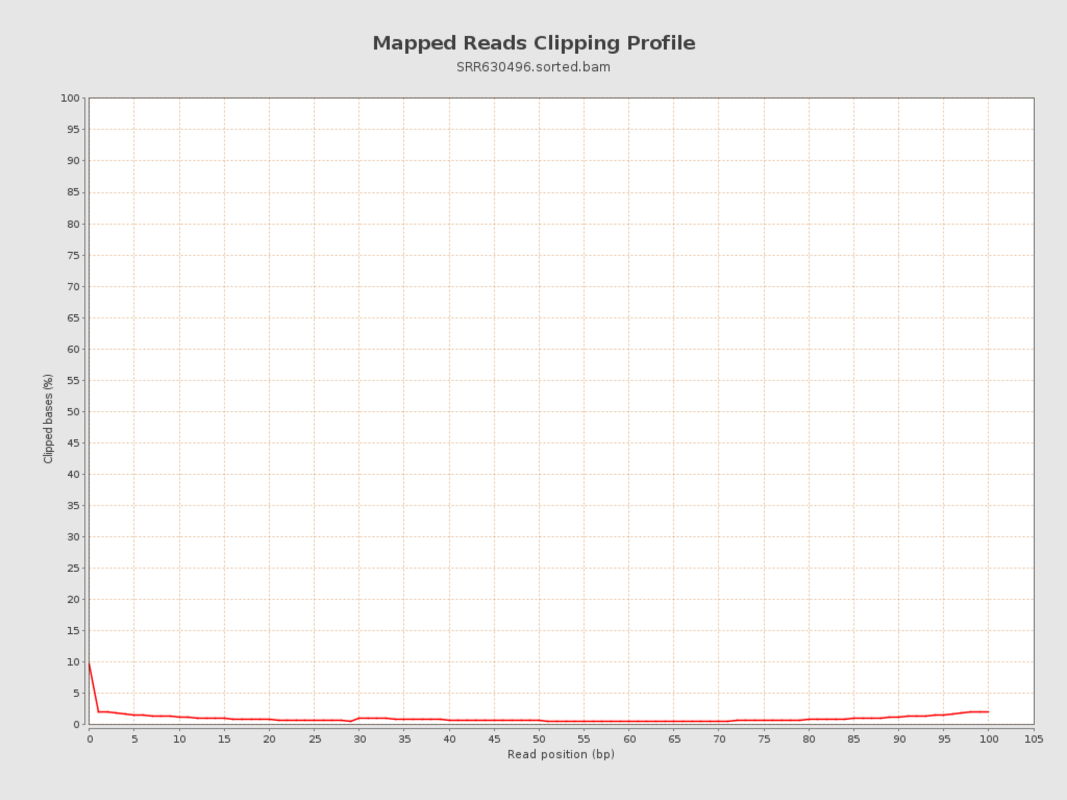
8. Results : Mapped Reads Nucleotide Content



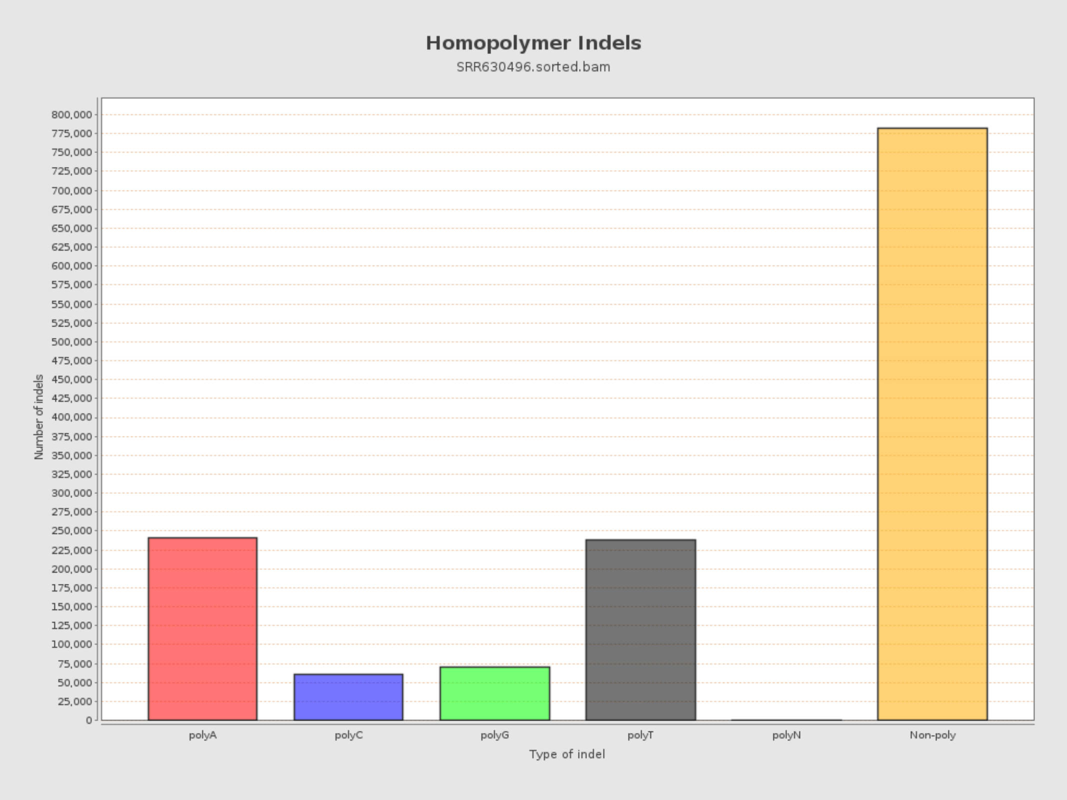
9. Results : Mapped Reads GC-content Distribution



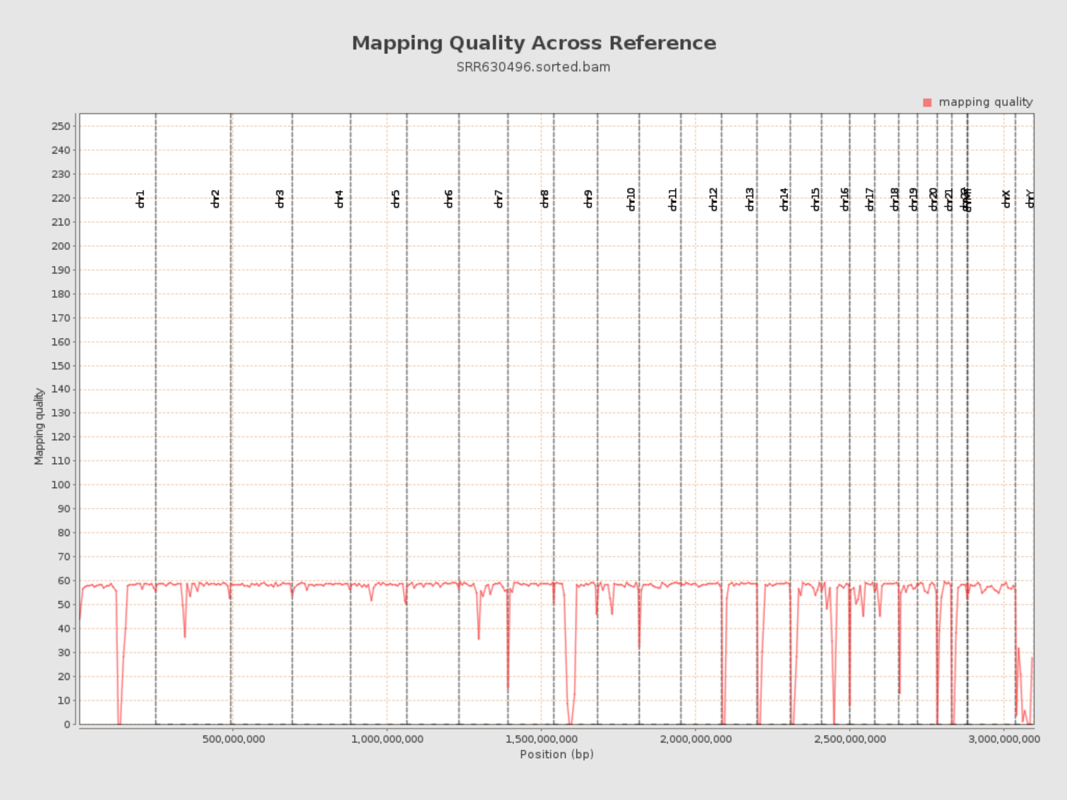
10. Results : Mapped Reads Clipping Profile



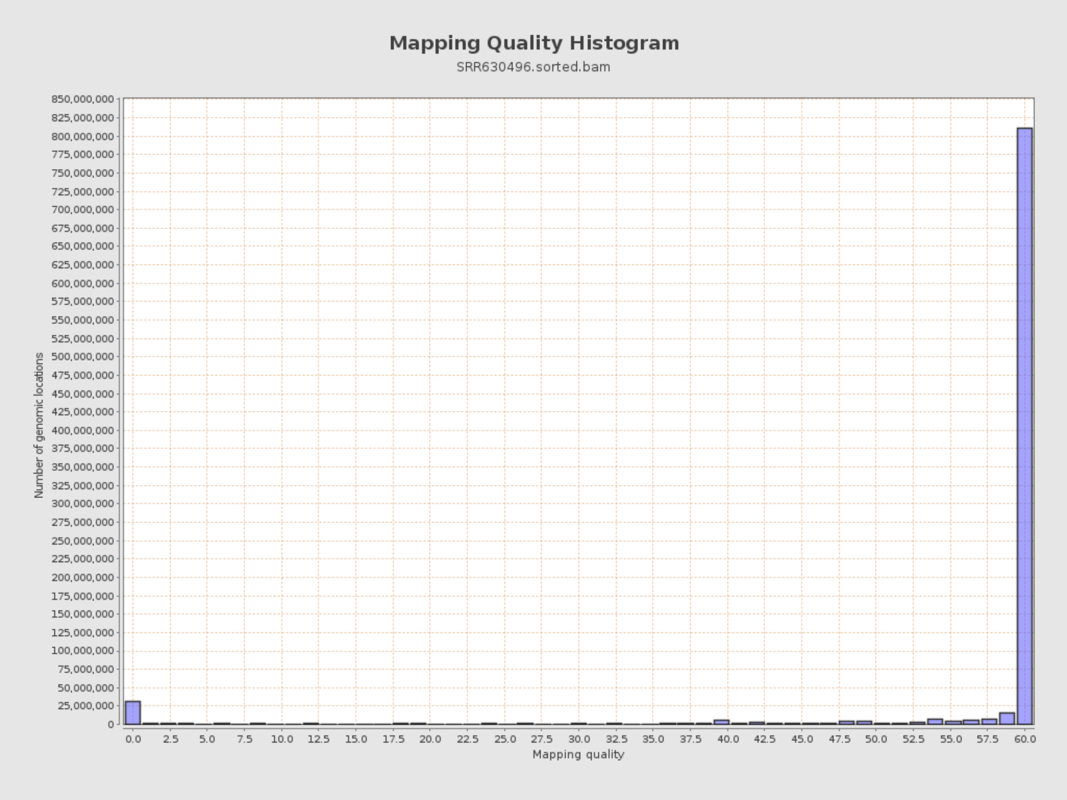
11. Results : Homopolymer Indels



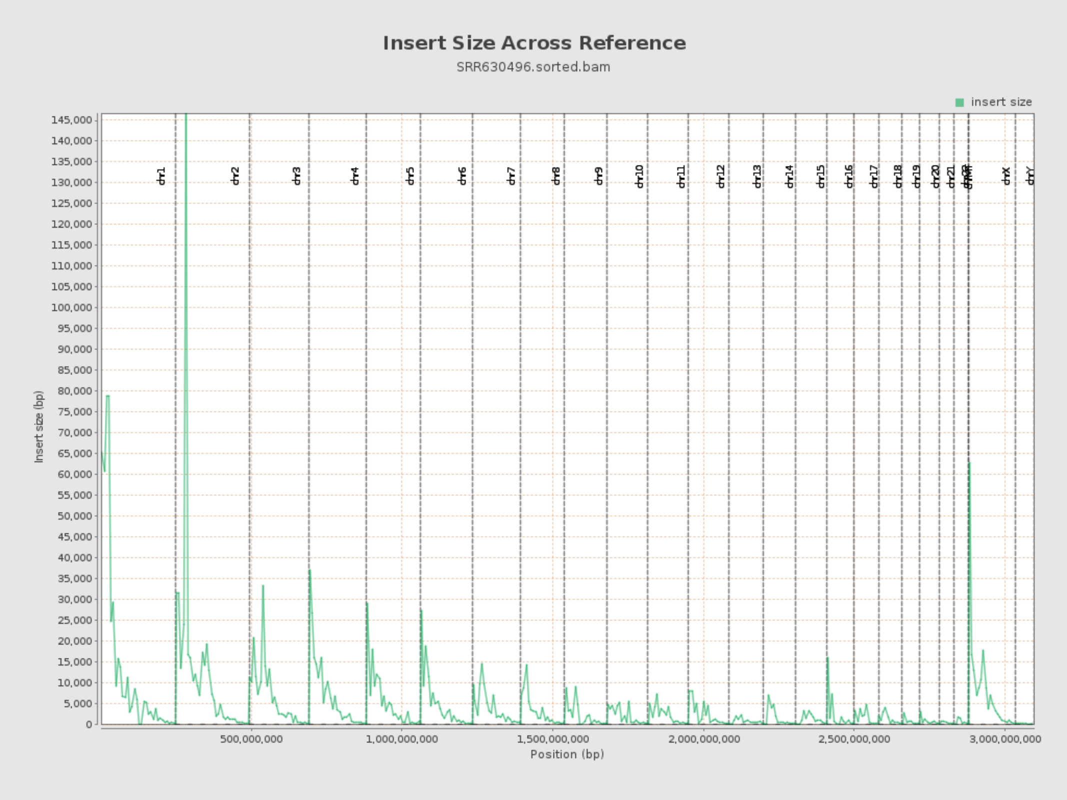
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram