Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/15 04:33:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630498.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 SRR630498_1.fastq.gz SRR630498_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 15 04:33:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630498.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	99,433,784
Mapped reads	99,091,196 / 99.66%
Unmapped reads	342,588 / 0.34%
Mapped paired reads	99,091,196 / 99.66%
Mapped reads, first in pair	49,661,406 / 49.94%
Mapped reads, second in pair	49,429,790 / 49.71%
Mapped reads, both in pair	98,825,300 / 99.39%
Mapped reads, singletons	265,896 / 0.27%
Secondary alignments	0
Supplementary alignments	589,228 / 0.59%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	18,123,717 / 18.23%
Duplication rate	15.56%
Clipped reads	9,364,272 / 9.42%

2.2. ACGT Content

Number/percentage of A's	3,065,070,486 / 31.15%
Number/percentage of C's	1,839,343,541 / 18.69%
Number/percentage of T's	3,048,655,520 / 30.98%
Number/percentage of G's	1,855,212,650 / 18.85%
Number/percentage of N's	31,353,071 / 0.32%

GC Percentage	37.55%

2.3. Coverage

Mean	3.1792
Standard Deviation	12.2427

2.4. Mapping Quality

Mean Mapping Quality	53.7

2.5. Insert size

Mean	49,079.99
Standard Deviation	2,100,549.81
P25/Median/P75	252 / 316 / 386

2.6. Mismatches and indels

General error rate	1.25%
Mismatches	121,297,799
Insertions	872,881
Mapped reads with at least one insertion	0.87%
Deletions	944,391
Mapped reads with at least one deletion	0.93%
Homopolymer indels	43.91%

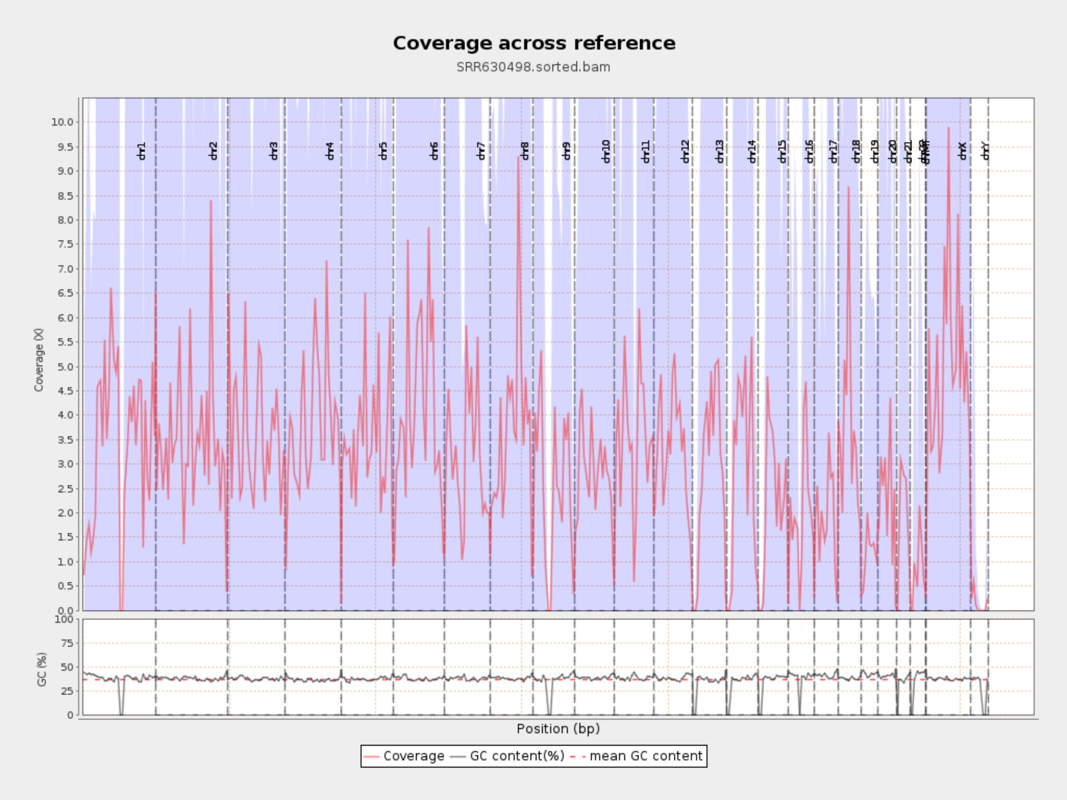
2.7. Chromosome stats

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

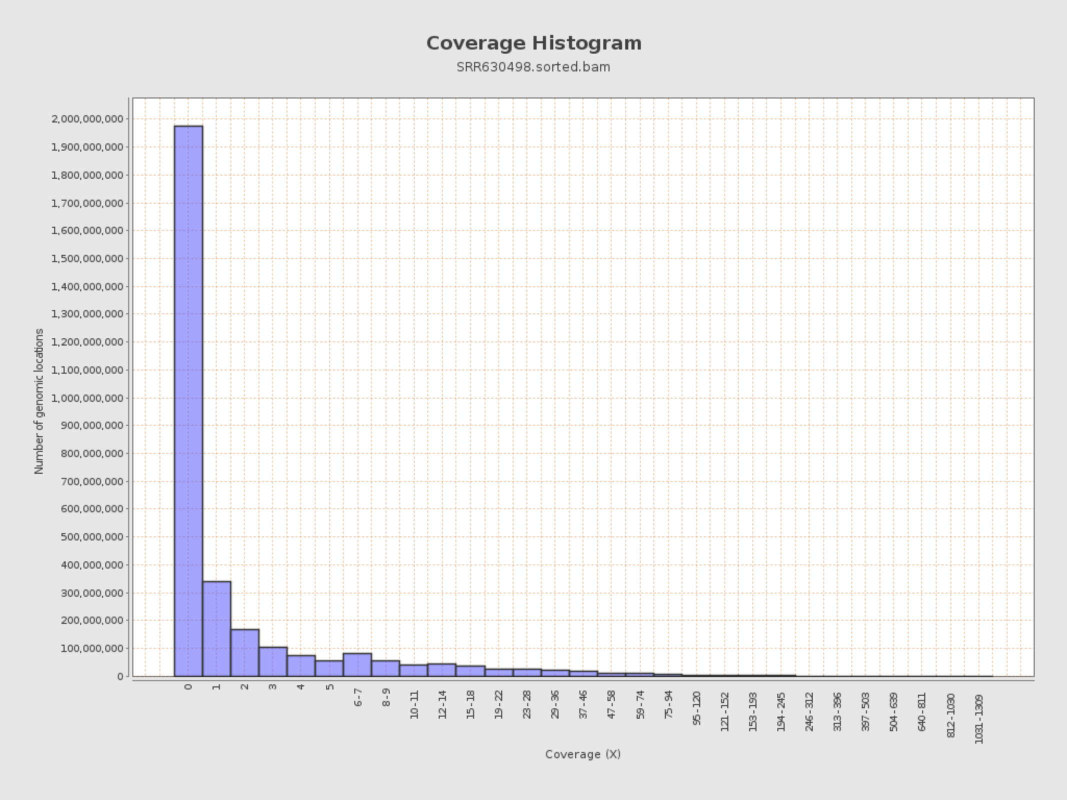
		bases	coverage	deviation
chr1	249250621	842275728	3.3792	13.6581
chr2	243199373	841842187	3.4615	13.3934
chr3	198022430	716931353	3.6205	12.5111
chr4	191154276	736521389	3.853	13.61
chr5	180915260	622725393	3.4421	12.7484
chr6	171115067	708038468	4.1378	14.0814
chr7	159138663	496189574	3.118	10.9535
chr8	146364022	544259662	3.7185	14.7575
chr9	141213431	368495976	2.6095	10.8512
chr10	135534747	389442337	2.8734	9.2027
chr11	135006516	473408752	3.5066	12.7458
chr12	133851895	443226464	3.3113	11.4262
chr13	115169878	328539556	2.8527	10.678
chr14	107349540	313256162	2.9181	11.048
chr15	102531392	229900696	2.2422	9.1972
chr16	90354753	180883602	2.0019	7.5411
chr17	81195210	159415286	1.9634	7.8645
chr18	78077248	296426469	3.7966	14.5023
chr19	59128983	70166342	1.1867	4.8583
chr20	63025520	150382824	2.3861	9.4814
chr21	48129895	90560588	1.8816	6.9438
chr22	51304566	44703293	0.8713	4.9588
chrMT	16571	4159	0.251	0.8707
chrX	155270560	785477445	5.0588	18.0391

chrY	59373566	8659297	0.1458	2.7365

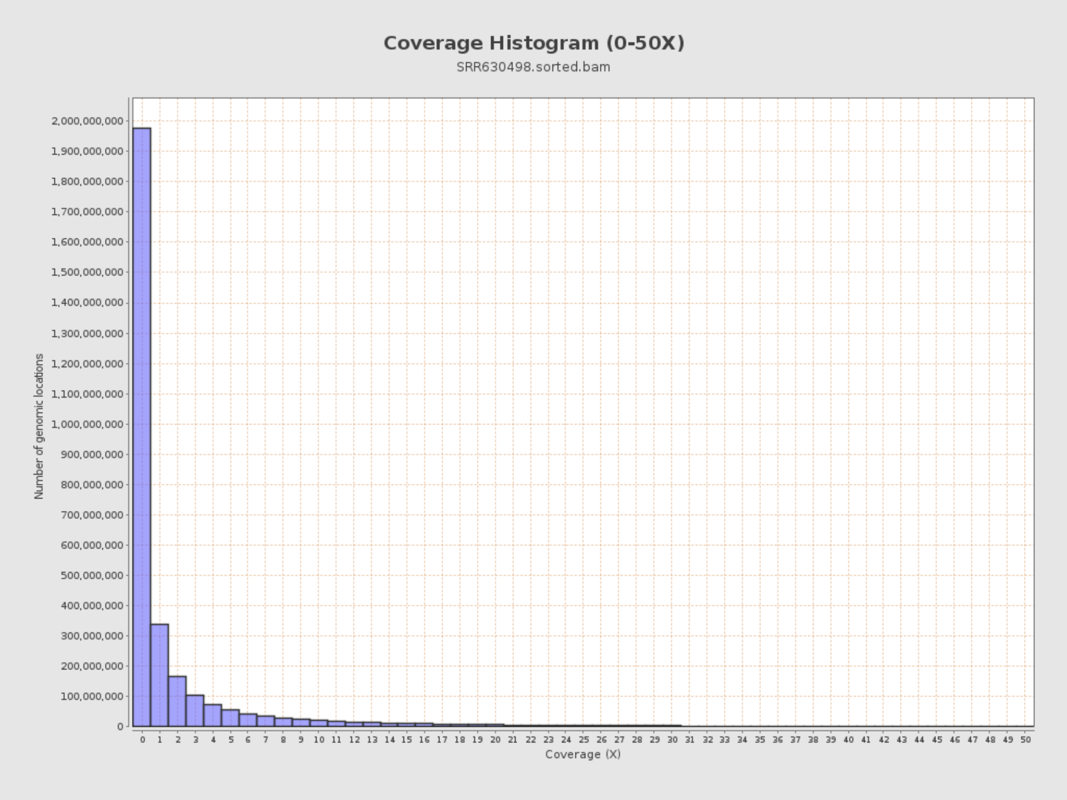
3. Results : Coverage across reference



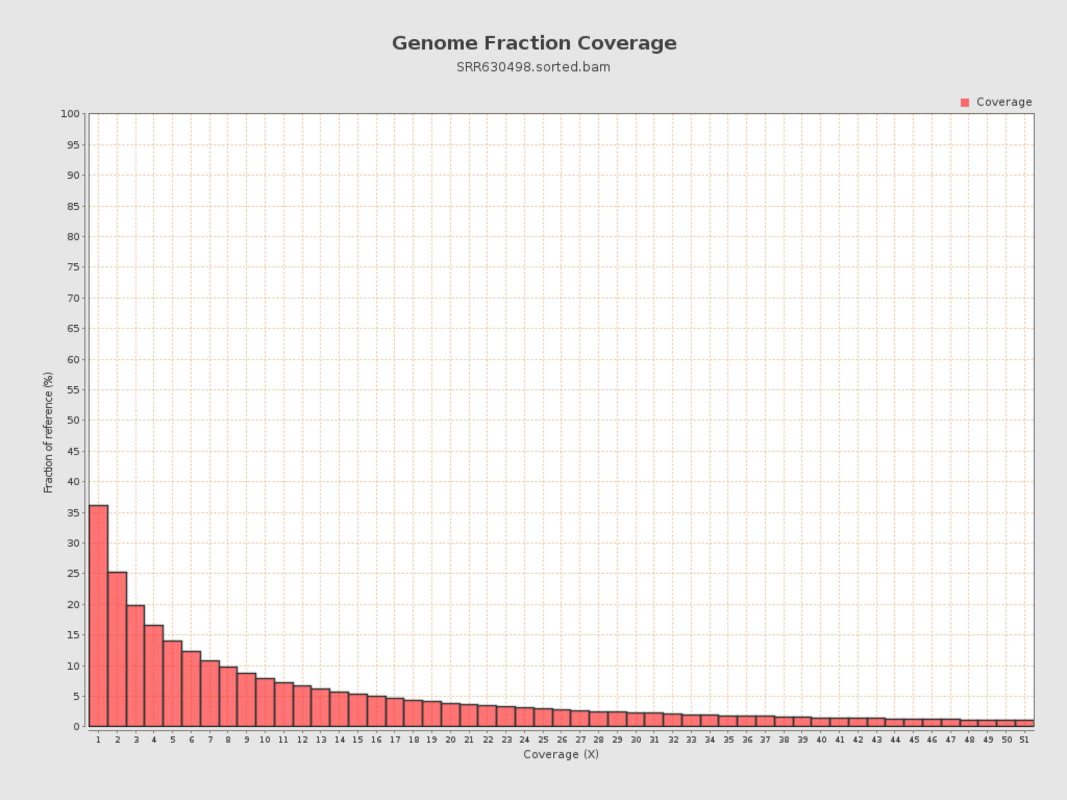
4. Results : Coverage Histogram



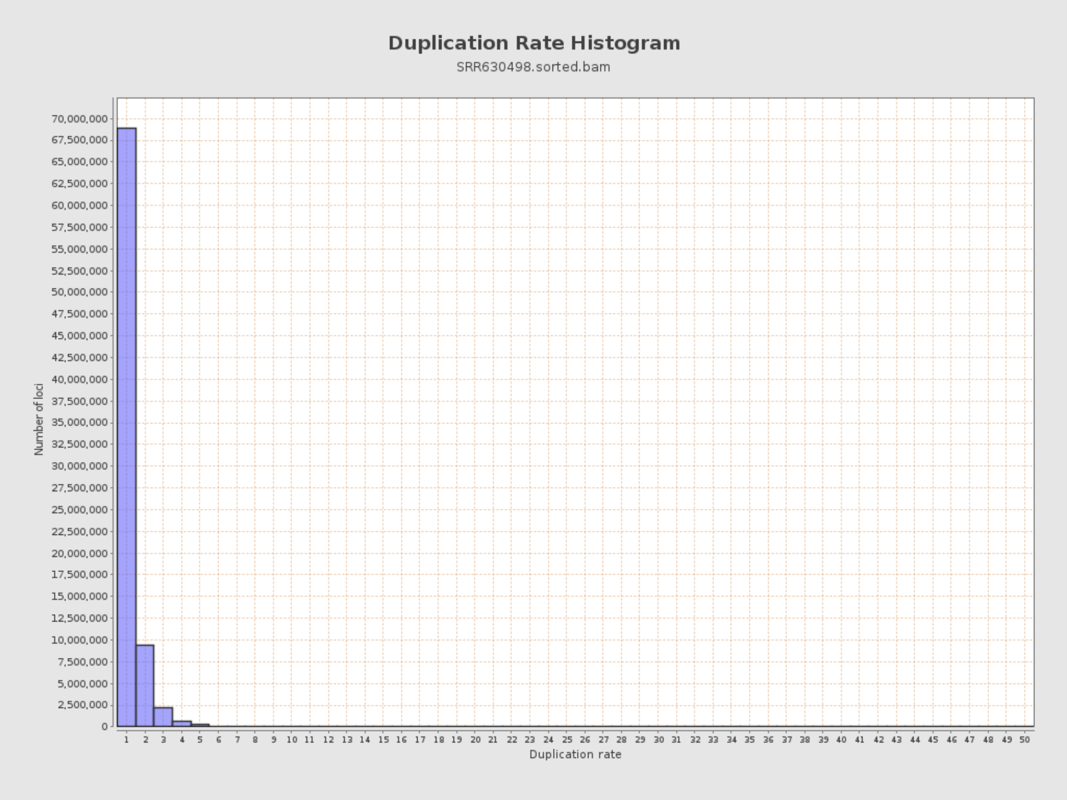
5. Results : Coverage Histogram (0-50X)



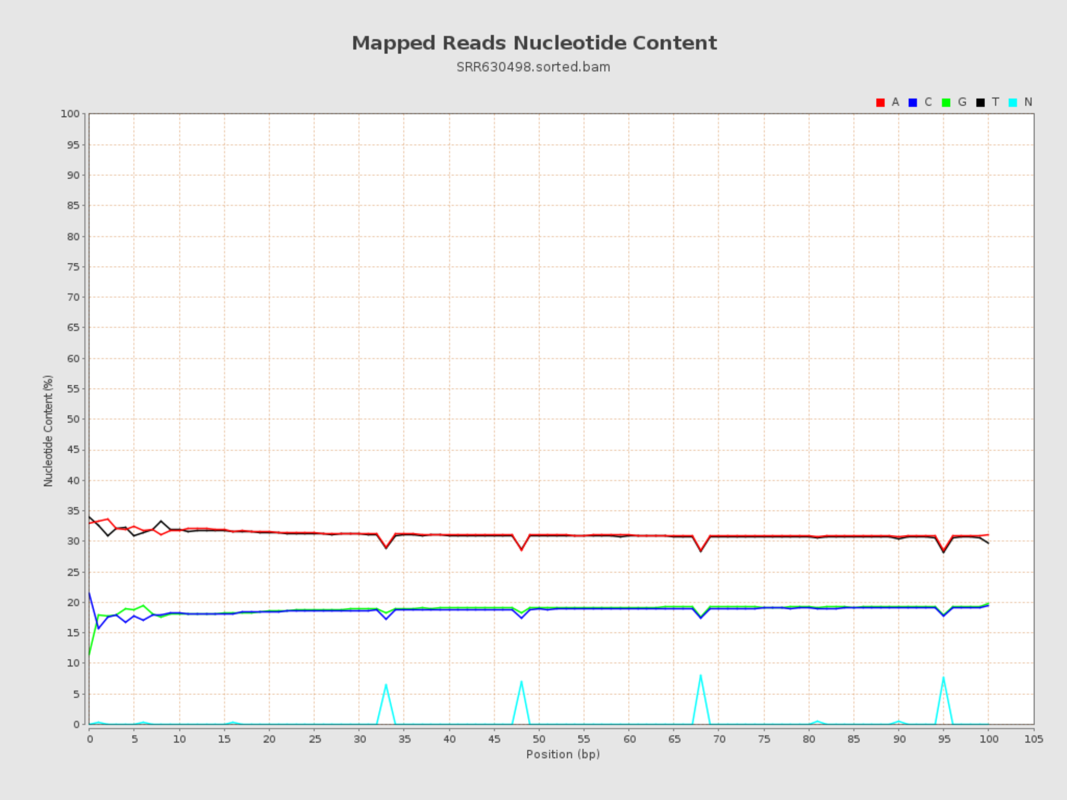
6. Results : Genome Fraction Coverage



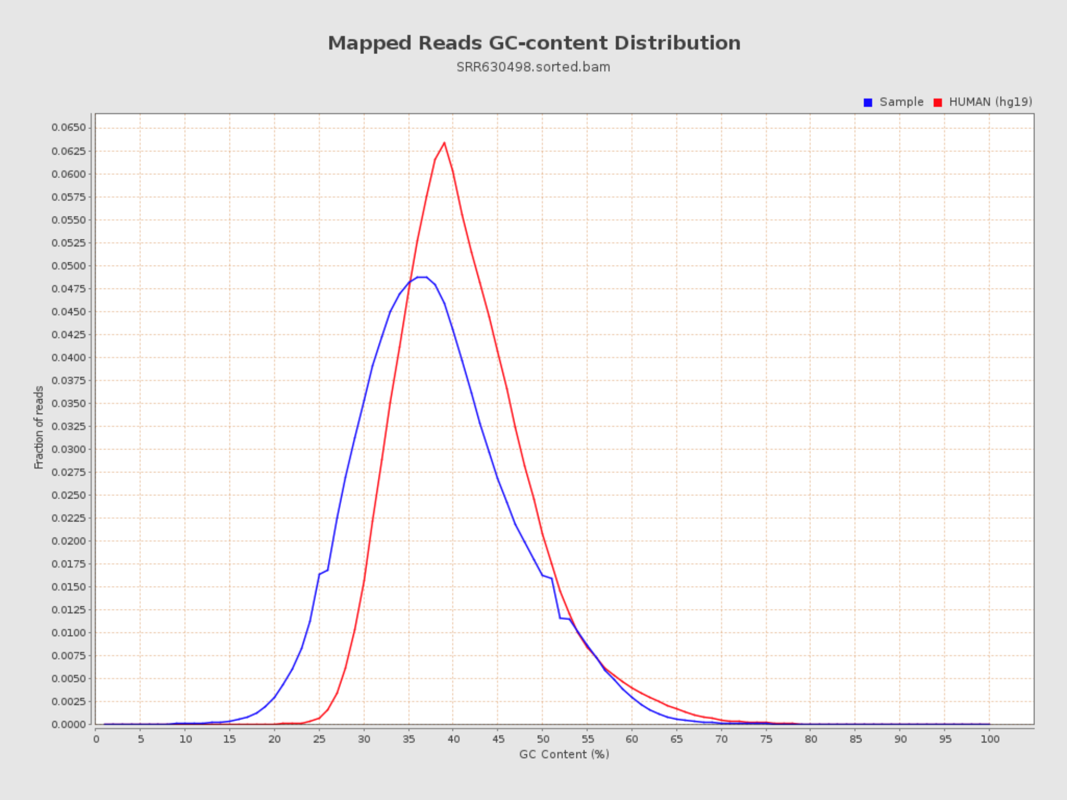
7. Results : Duplication Rate Histogram



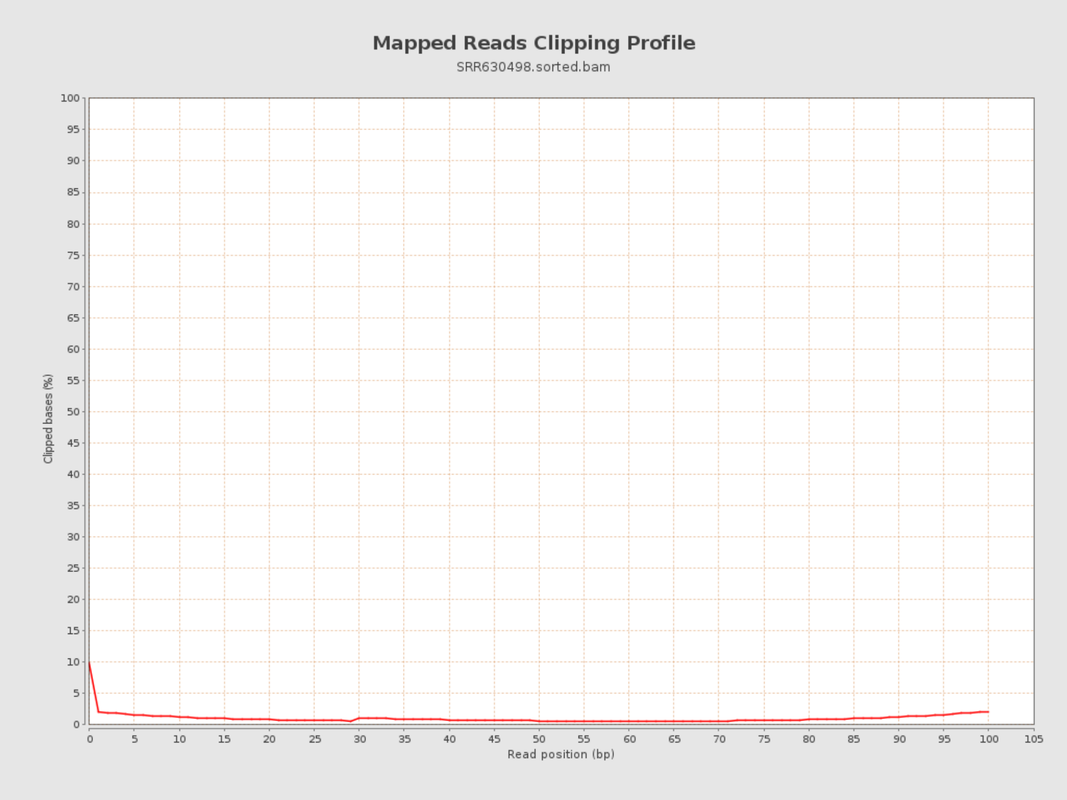
8. Results : Mapped Reads Nucleotide Content



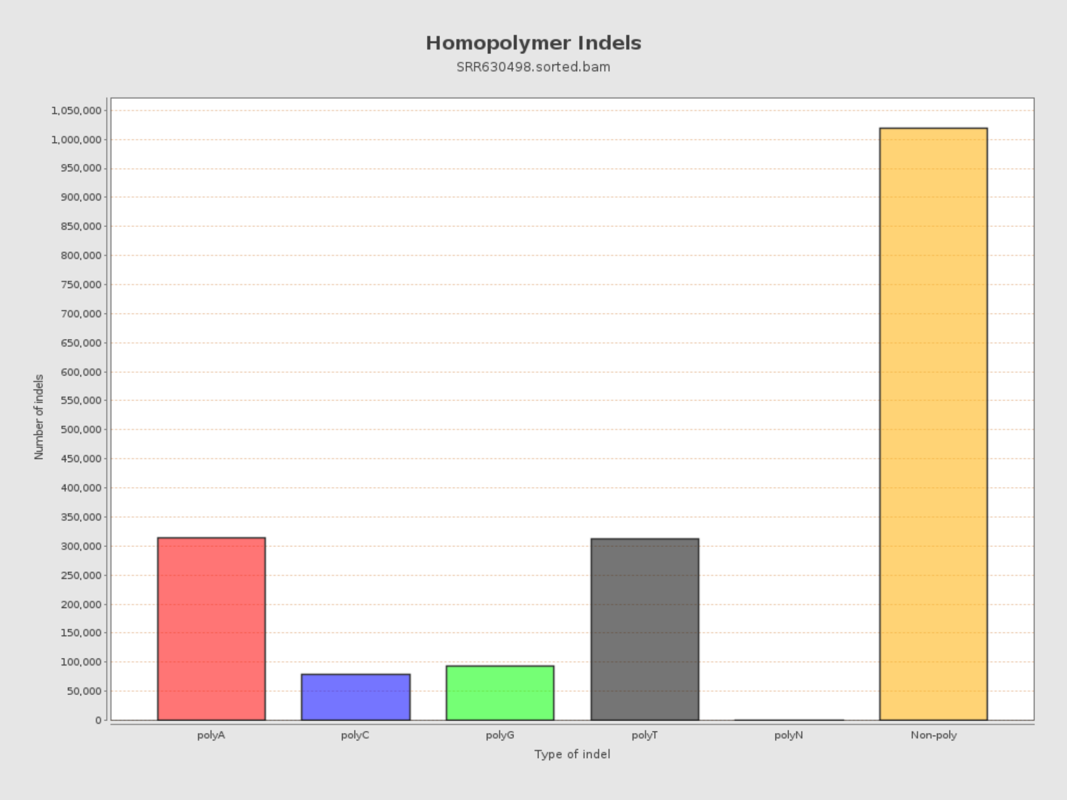
9. Results : Mapped Reads GC-content Distribution



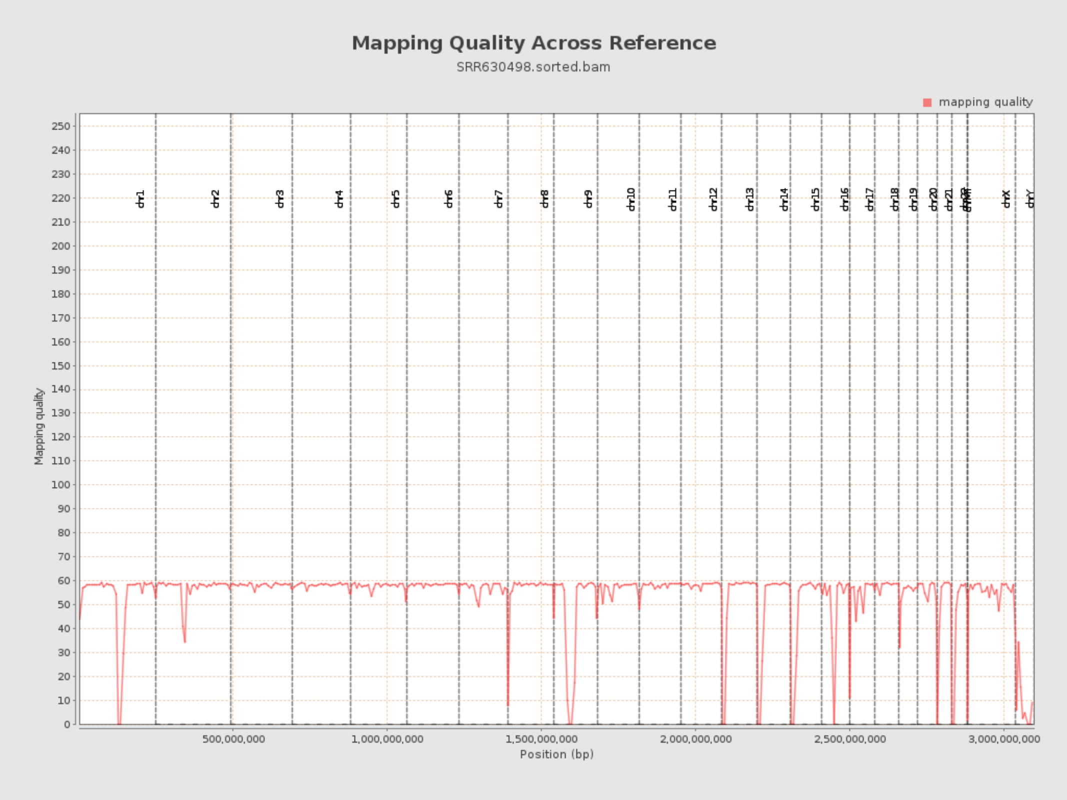
10. Results : Mapped Reads Clipping Profile



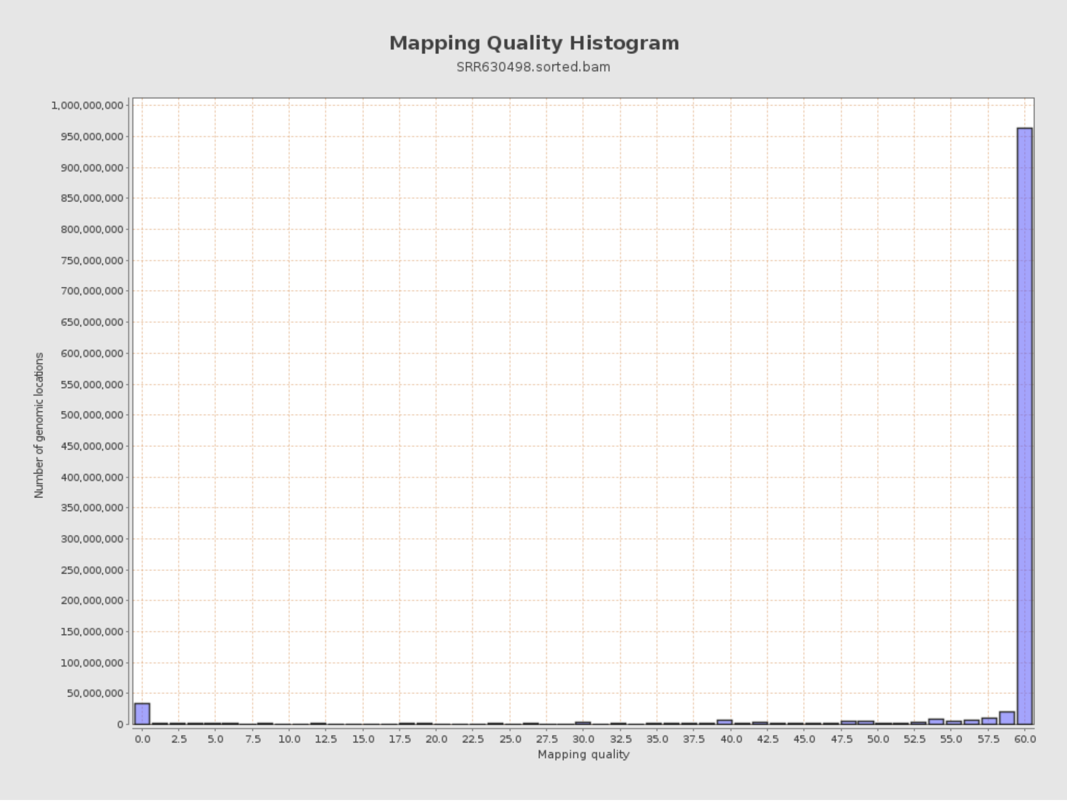
11. Results : Homopolymer Indels



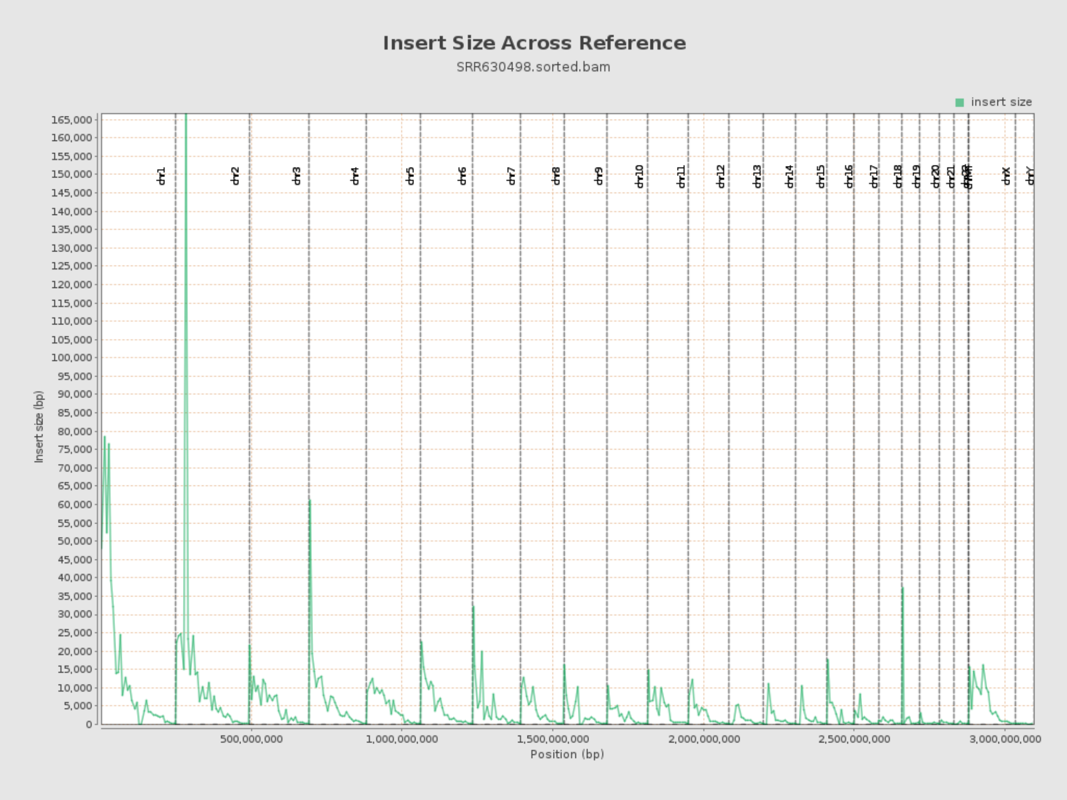
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram