Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/17 10:06:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR631030.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 SRR631030_1.fastq.gz SRR631030_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Mar 17 10:06:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR631030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	107,984,286
Mapped reads	107,638,398 / 99.68%
Unmapped reads	345,888 / 0.32%
Mapped paired reads	107,638,398 / 99.68%
Mapped reads, first in pair	53,943,457 / 49.95%
Mapped reads, second in pair	53,694,941 / 49.72%
Mapped reads, both in pair	107,357,960 / 99.42%
Mapped reads, singletons	280,438 / 0.26%
Secondary alignments	0
Supplementary alignments	619,261 / 0.57%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	26,413,464 / 24.46%
Duplication rate	19.63%
Clipped reads	9,622,502 / 8.91%

2.2. ACGT Content

Number/percentage of A's	3,349,549,488 / 31.3%
Number/percentage of C's	1,984,166,451 / 18.54%
Number/percentage of T's	3,334,936,028 / 31.16%
Number/percentage of G's	1,998,533,210 / 18.68%
Number/percentage of N's	34,194,005 / 0.32%

GC Percentage	37.22%

2.3. Coverage

Mean	3.4576
Standard Deviation	16.5201

2.4. Mapping Quality

Mean Mapping Quality	53.56

2.5. Insert size

Mean	47,042.23
Standard Deviation	2,036,775.85
P25/Median/P75	253 / 316 / 385

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	128,913,593
Insertions	929,232
Mapped reads with at least one insertion	0.85%
Deletions	1,008,593
Mapped reads with at least one deletion	0.91%
Homopolymer indels	43.86%

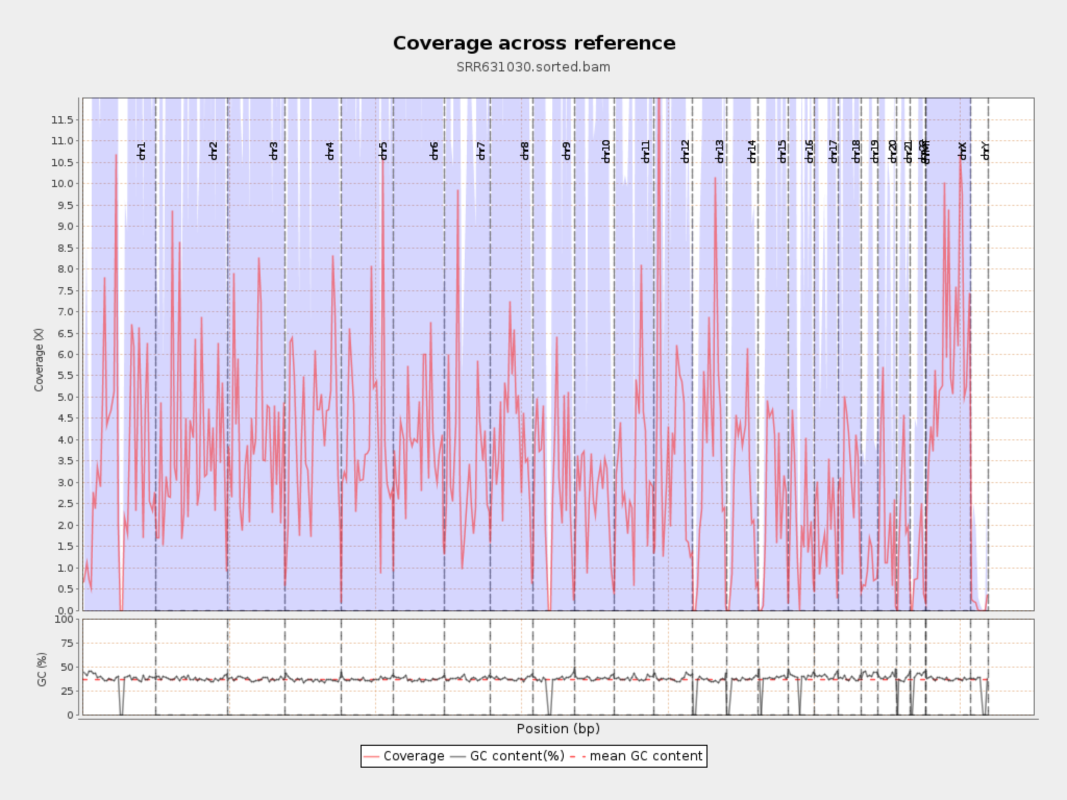
2.7. Chromosome stats

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

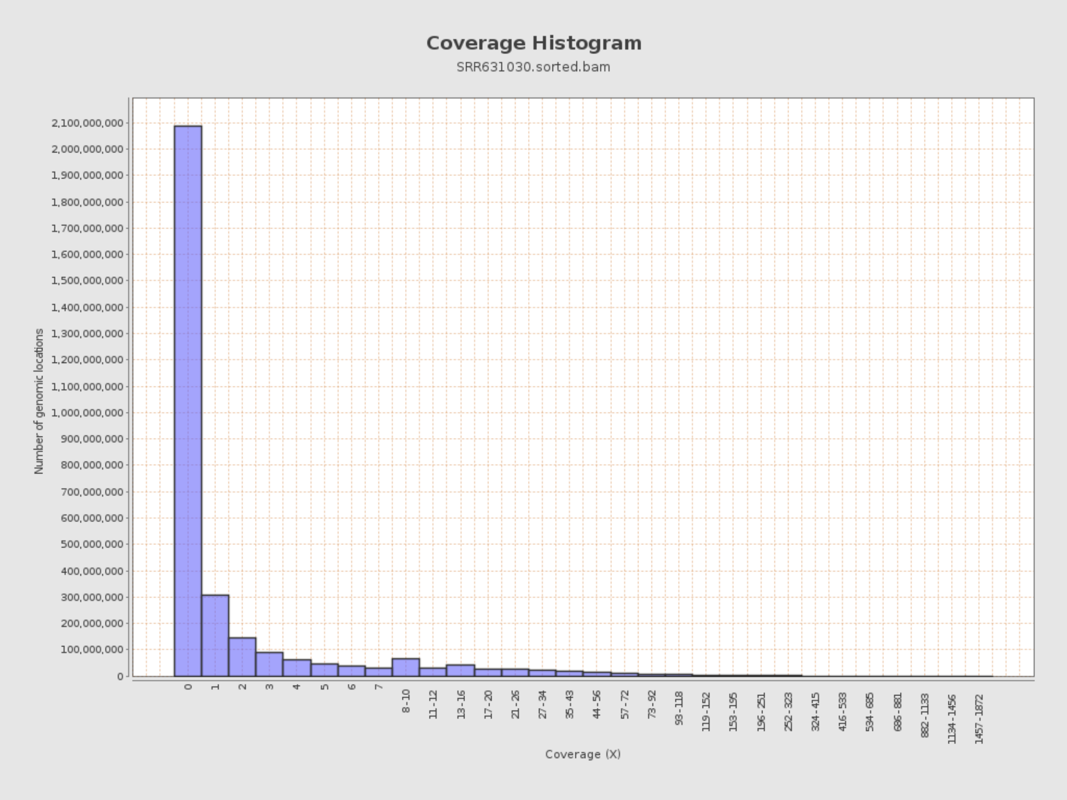
		bases	coverage	deviation
chr1	249250621	883319283	3.5439	20.0661
chr2	243199373	929566596	3.8222	16.2888
chr3	198022430	815934610	4.1204	17.3934
chr4	191154276	830169210	4.3429	15.6692
chr5	180915260	744753562	4.1166	17.6876
chr6	171115067	689087581	4.027	17.0902
chr7	159138663	537082024	3.3749	16.4633
chr8	146364022	594201795	4.0598	16.3216
chr9	141213431	439187797	3.1101	14.6872
chr10	135534747	364258320	2.6876	11.9414
chr11	135006516	453362937	3.3581	14.4081
chr12	133851895	528187067	3.9461	19.4155
chr13	115169878	425820358	3.6973	20.6843
chr14	107349540	306762527	2.8576	16.2879
chr15	102531392	261334183	2.5488	14.3548
chr16	90354753	181191268	2.0053	12.7321
chr17	81195210	161955840	1.9946	9.9981
chr18	78077248	253071734	3.2413	14.0332
chr19	59128983	55606863	0.9404	6.4469
chr20	63025520	147042522	2.3331	14.5564
chr21	48129895	97409550	2.0239	7.4011
chr22	51304566	48018018	0.9359	10.1438
chrMT	16571	3838	0.2316	0.8497
chrX	155270560	948963187	6.1117	24.2813

chrY	59373566	7302709	0.123	1.5464

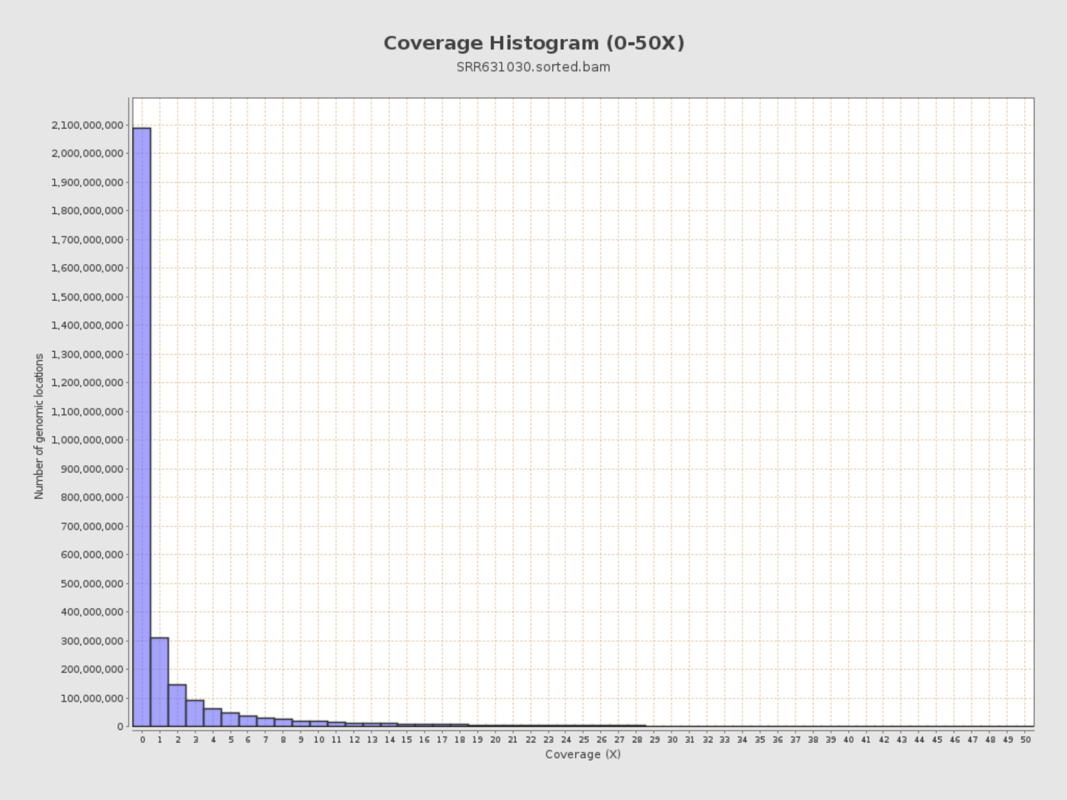
3. Results : Coverage across reference



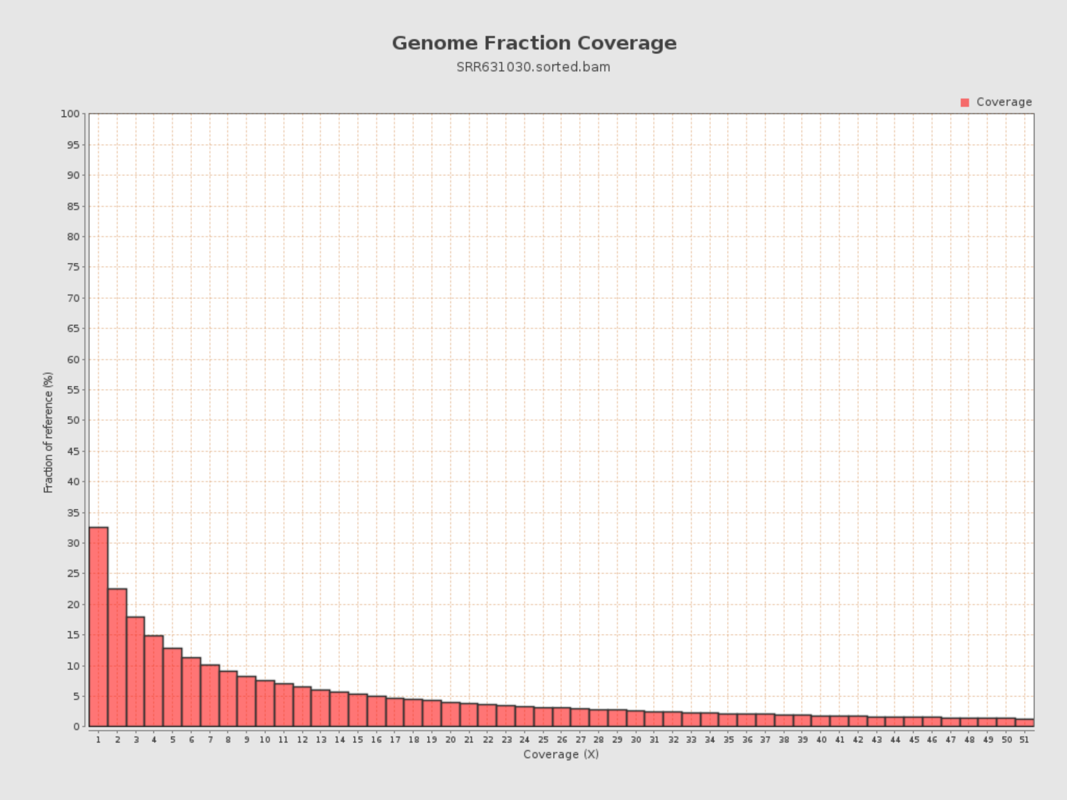
4. Results : Coverage Histogram



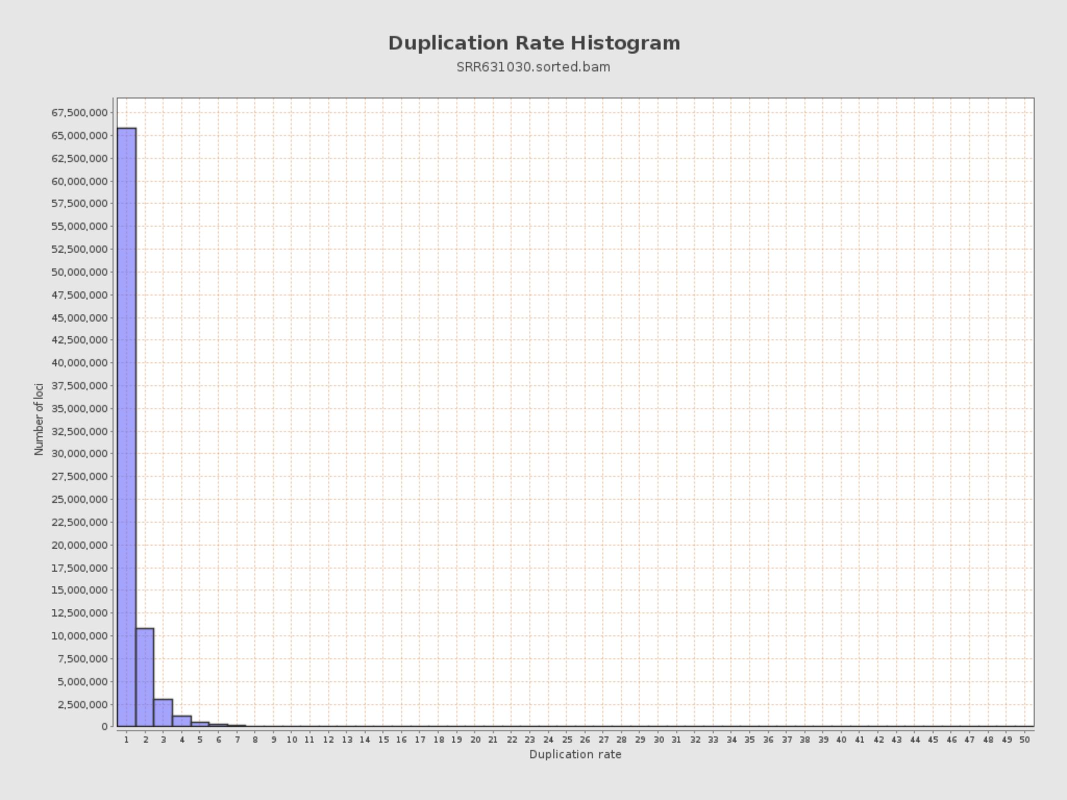
5. Results : Coverage Histogram (0-50X)



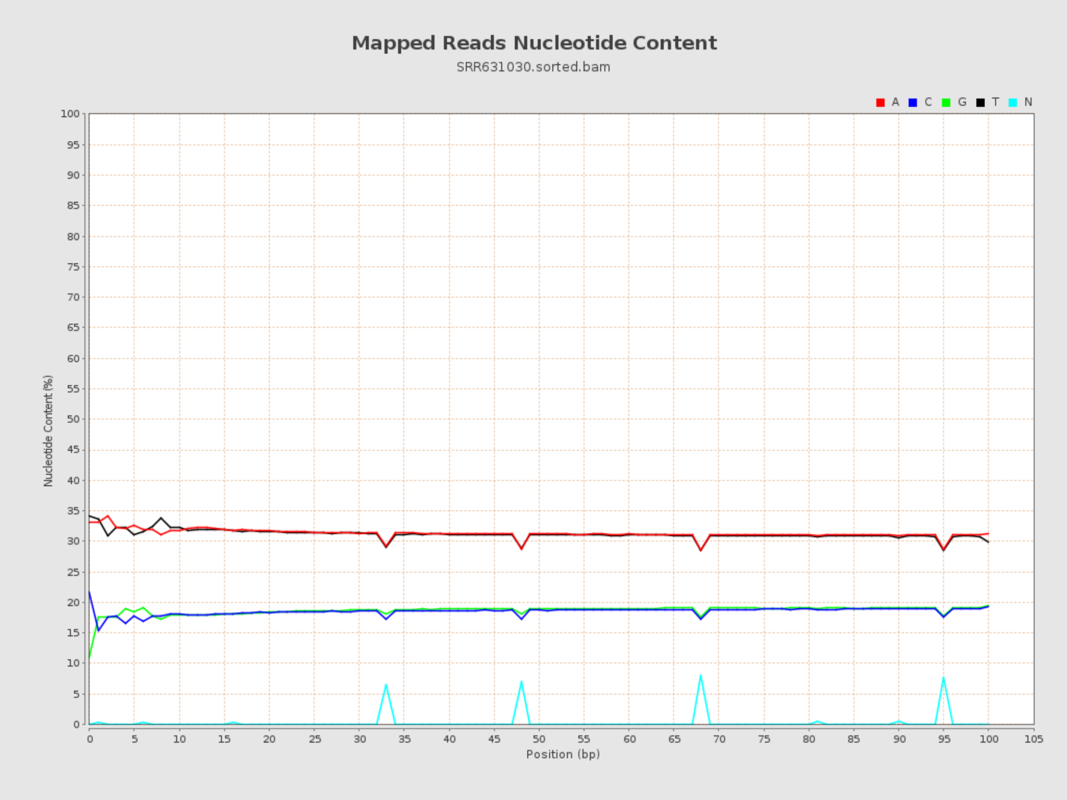
6. Results : Genome Fraction Coverage



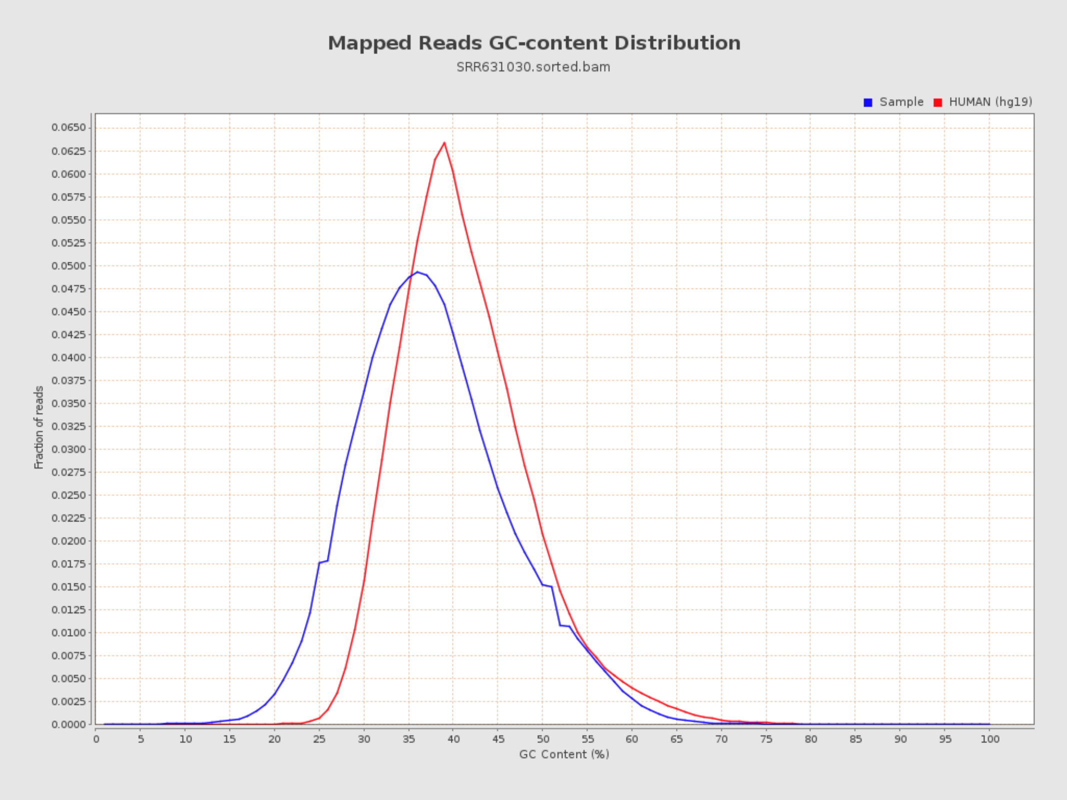
7. Results : Duplication Rate Histogram



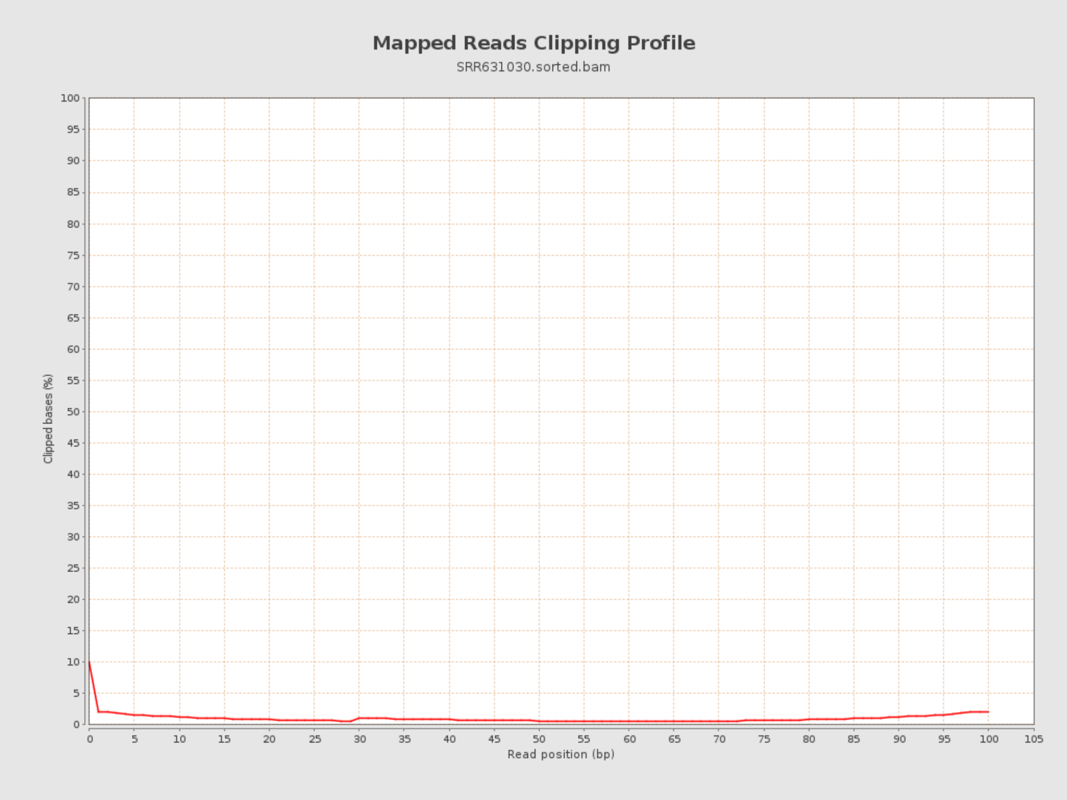
8. Results : Mapped Reads Nucleotide Content



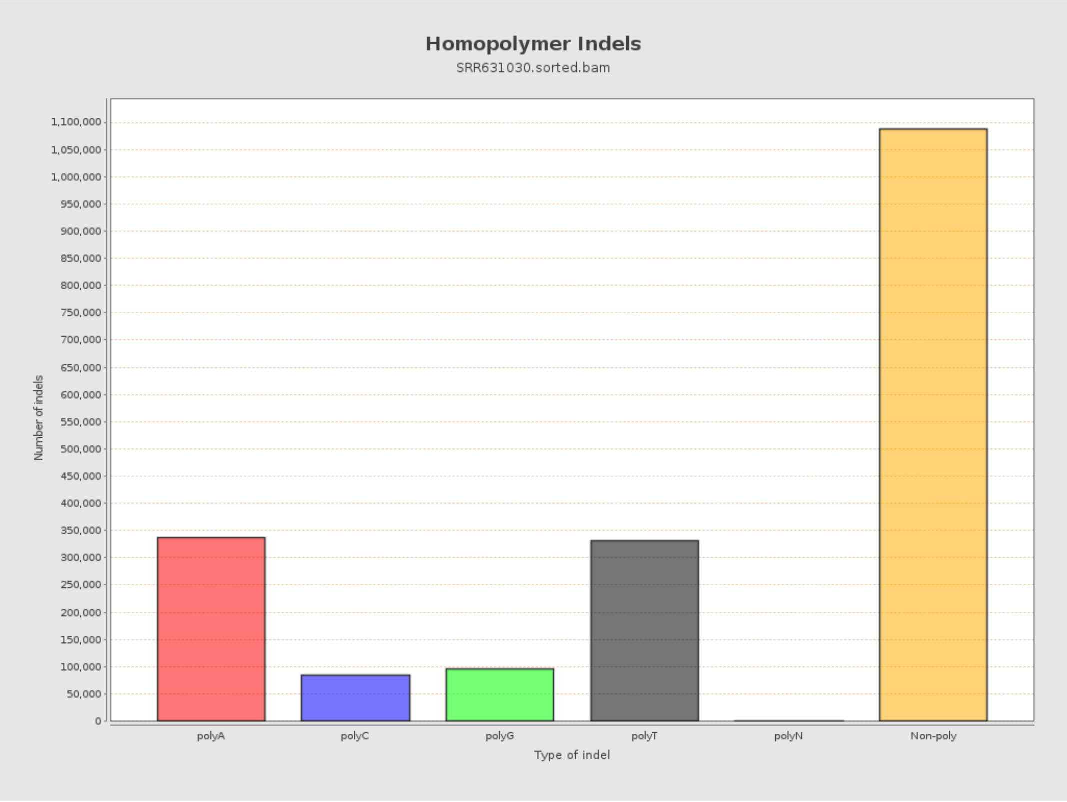
9. Results : Mapped Reads GC-content Distribution



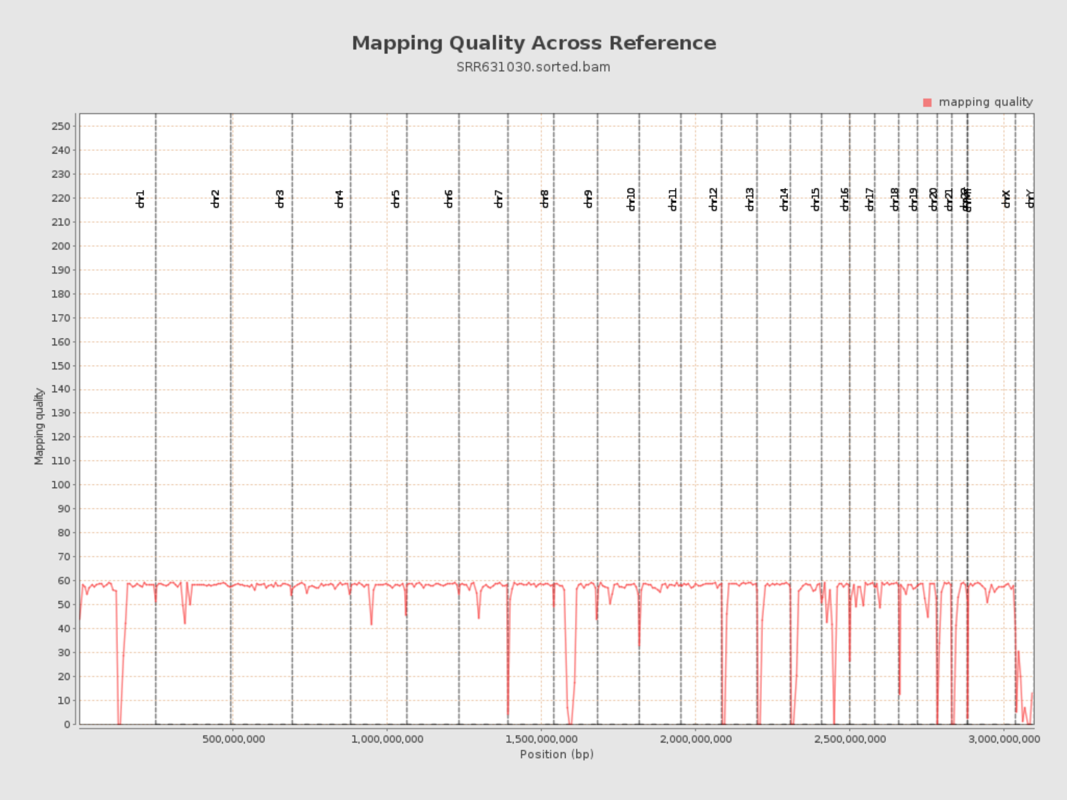
10. Results : Mapped Reads Clipping Profile



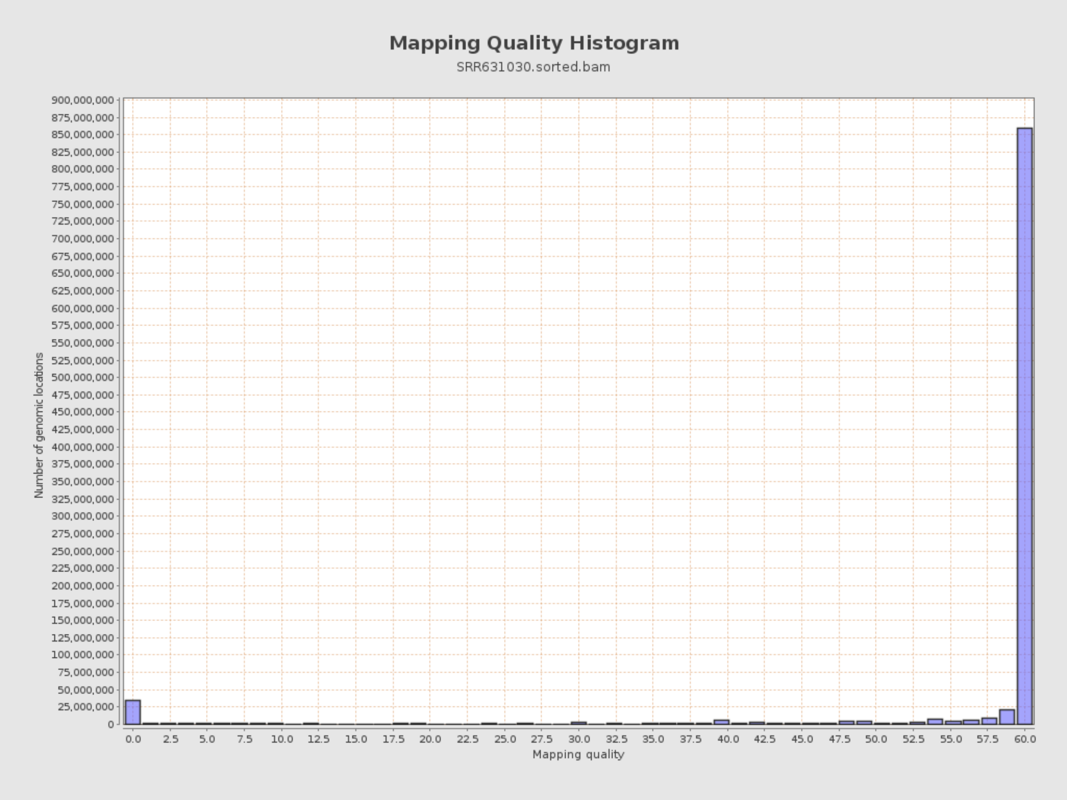
11. Results : Homopolymer Indels



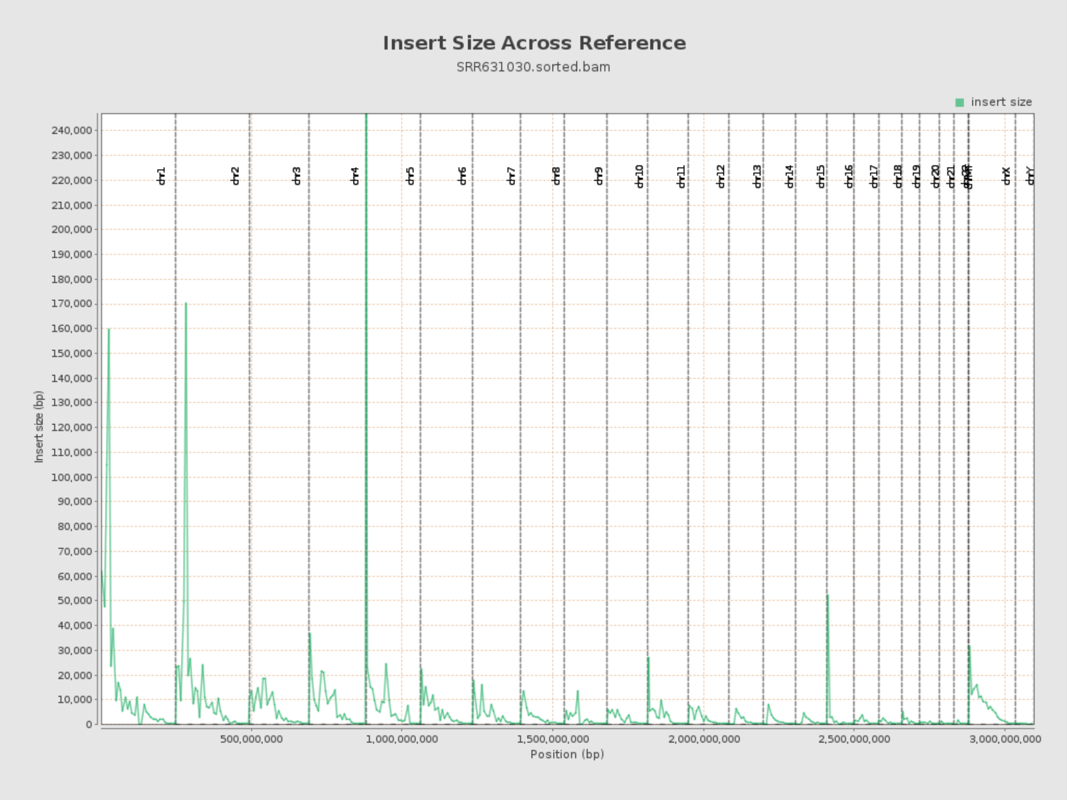
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram