Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 23:52:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264630.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1264630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264630_1.fastq.gz SRR1264630_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 23:52:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264630.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,830,176,318
Mapped reads	1,817,650,518 / 99.32%
Unmapped reads	12,525,800 / 0.68%
Mapped paired reads	1,817,650,518 / 99.32%
Mapped reads, first in pair	912,822,306 / 49.88%
Mapped reads, second in pair	904,828,212 / 49.44%
Mapped reads, both in pair	1,808,293,024 / 98.8%
Mapped reads, singletons	9,357,494 / 0.51%
Secondary alignments	0
Supplementary alignments	10,698,105 / 0.58%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	799,548,869 / 43.69%
Duplication rate	43.31%
Clipped reads	74,904,103 / 4.09%

2.2. ACGT Content

Number/percentage of A's	56,587,480,003 / 31.01%
Number/percentage of C's	34,560,398,776 / 18.94%
Number/percentage of T's	56,472,256,241 / 30.94%
Number/percentage of G's	34,851,417,510 / 19.1%
Number/percentage of N's	36,330,881 / 0.02%

GC Percentage	38.03%

2.3. Coverage

Mean	58.969
Standard Deviation	63.8368

2.4. Mapping Quality

Mean Mapping Quality	54.49

2.5. Insert size

Mean	70,910.66
Standard Deviation	2,566,463.05
P25/Median/P75	276 / 304 / 338

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	765,640,701
Insertions	20,182,302
Mapped reads with at least one insertion	1.1%
Deletions	18,894,857
Mapped reads with at least one deletion	1.02%
Homopolymer indels	48.58%

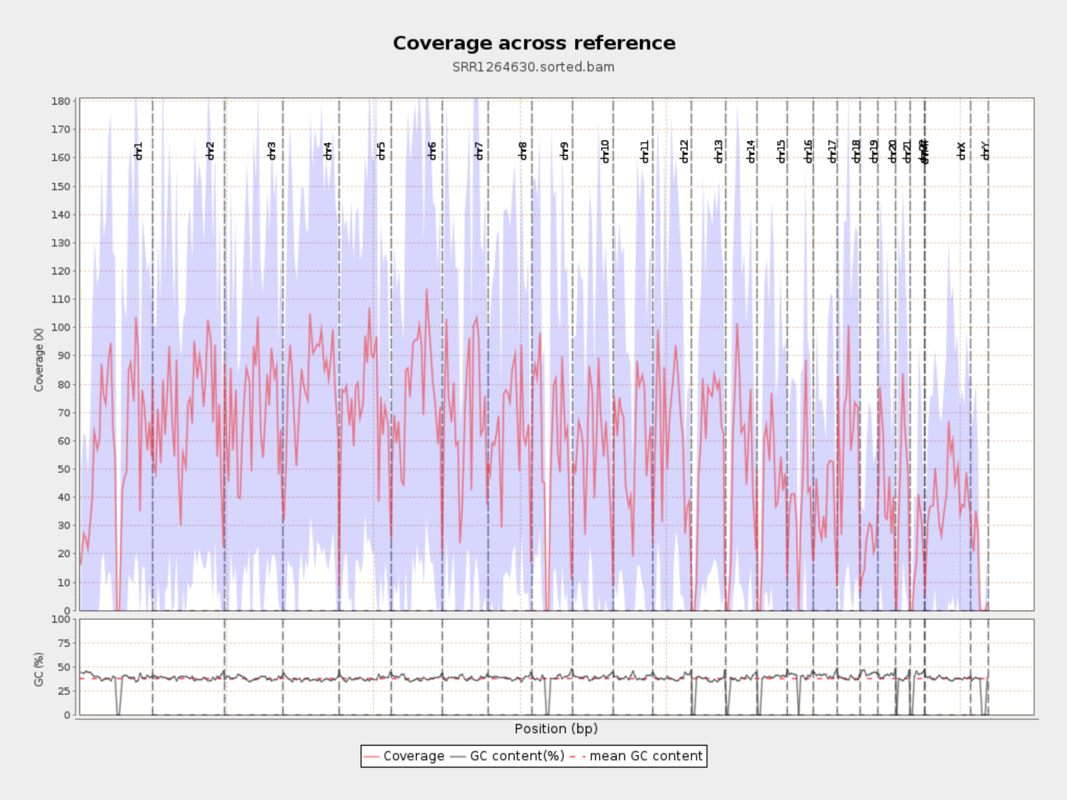
2.7. Chromosome stats

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

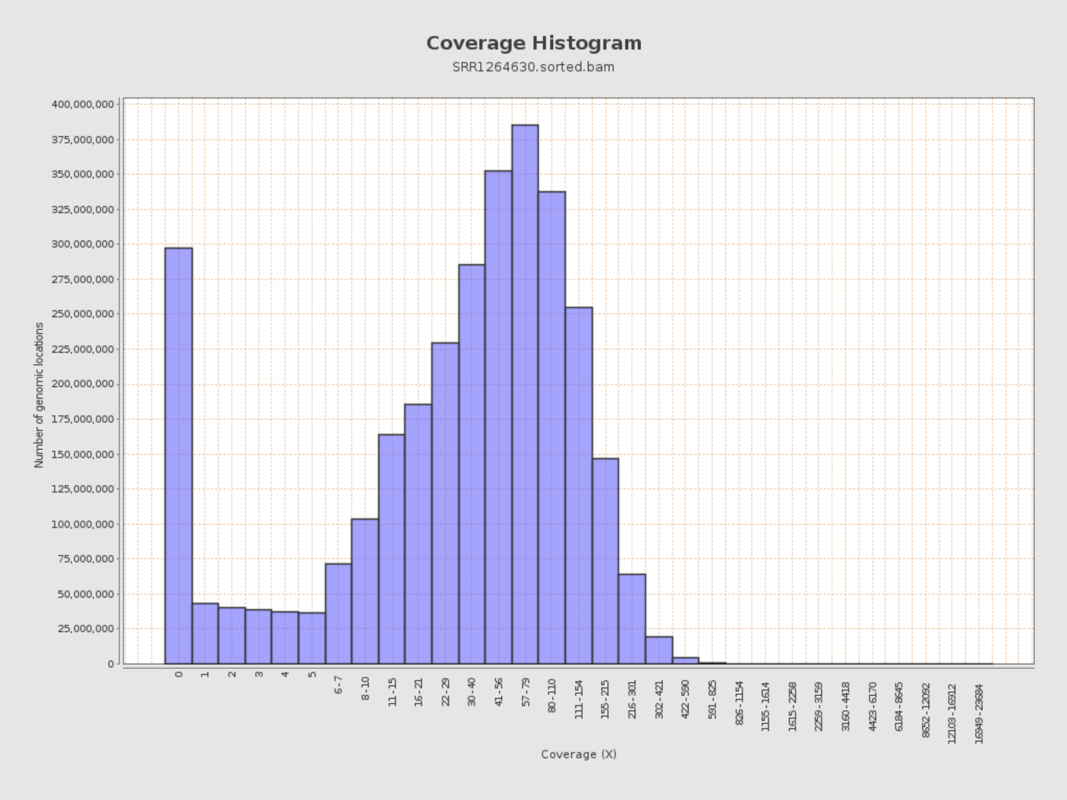
		bases	coverage	deviation
chr1	249250621	14272066750	57.2599	65.3269
chr2	243199373	16904465309	69.5087	66.5825
chr3	198022430	13895602412	70.1719	63.4139
chr4	191154276	15440790704	80.7766	68.3382
chr5	180915260	13168320328	72.7872	64.7342
chr6	171115067	13384517661	78.2194	72.0125
chr7	159138663	11026588404	69.2892	70.0738
chr8	146364022	9458699454	64.6245	61.4207
chr9	141213431	7939994125	56.2269	66.9087
chr10	135534747	7862569157	58.0115	59.7223
chr11	135006516	8164082020	60.4718	61.6727
chr12	133851895	8447025941	63.1073	66.2911
chr13	115169878	6693689299	58.1201	62.5226
chr14	107349540	5657843783	52.7049	62.218
chr15	102531392	4437634083	43.2807	55.498
chr16	90354753	3326940793	36.8209	48.0903
chr17	81195210	2854228132	35.1527	47.6261
chr18	78077248	5143234480	65.8737	62.6346
chr19	59128983	1281537192	21.6736	33.4795
chr20	63025520	2769093625	43.9361	60.5678
chr21	48129895	2296742682	47.7197	67.2596
chr22	51304566	942397128	18.3687	34.6414
chrMT	16571	89934	5.4272	7.7872
chrX	155270560	6371937616	41.0376	45.2818

chrY	59373566	809864584	13.6402	32.4831

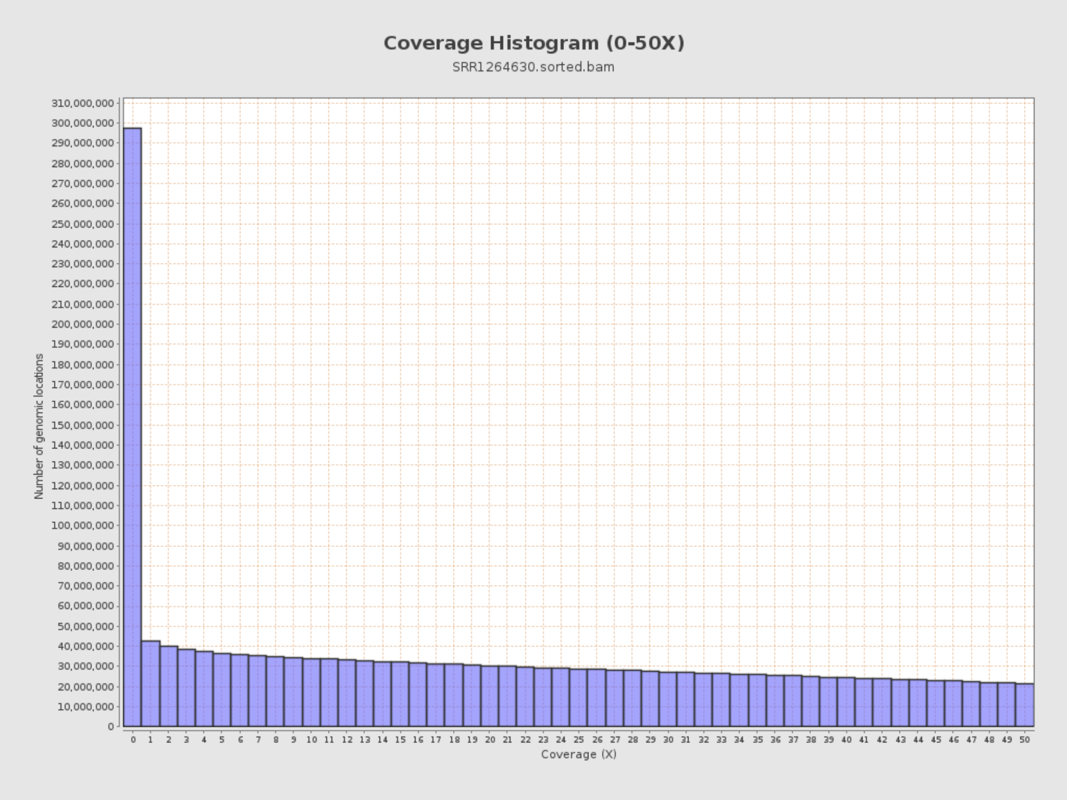
3. Results : Coverage across reference



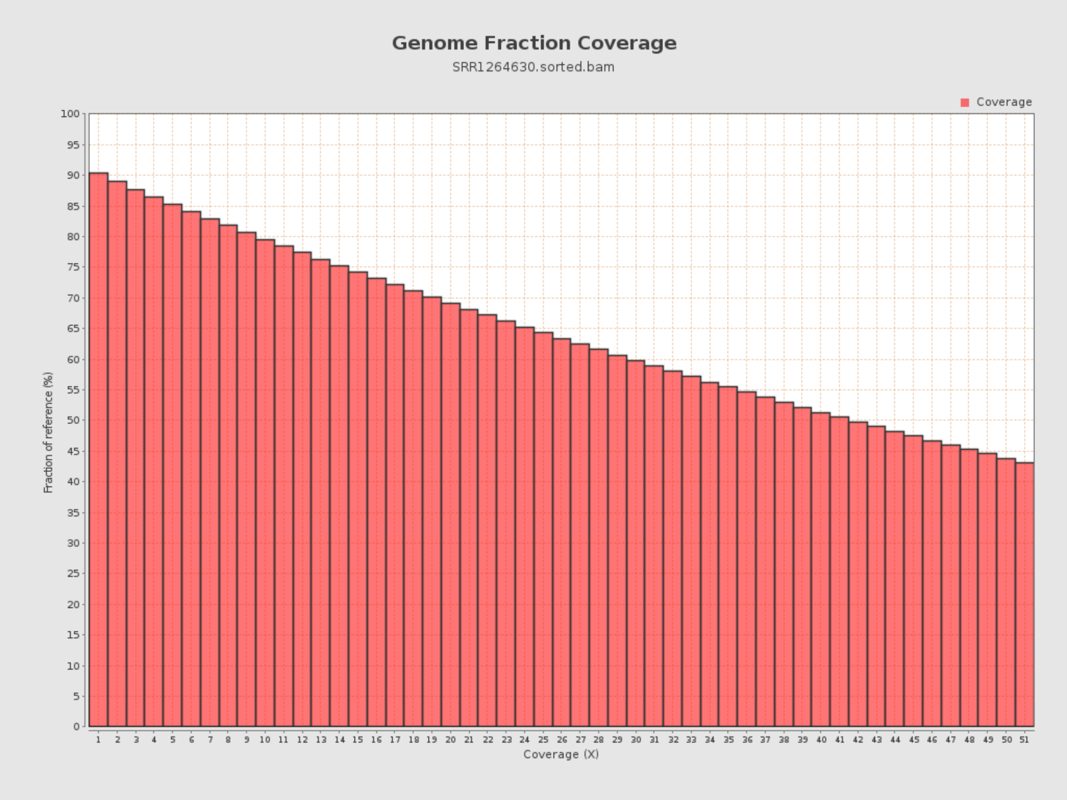
4. Results : Coverage Histogram



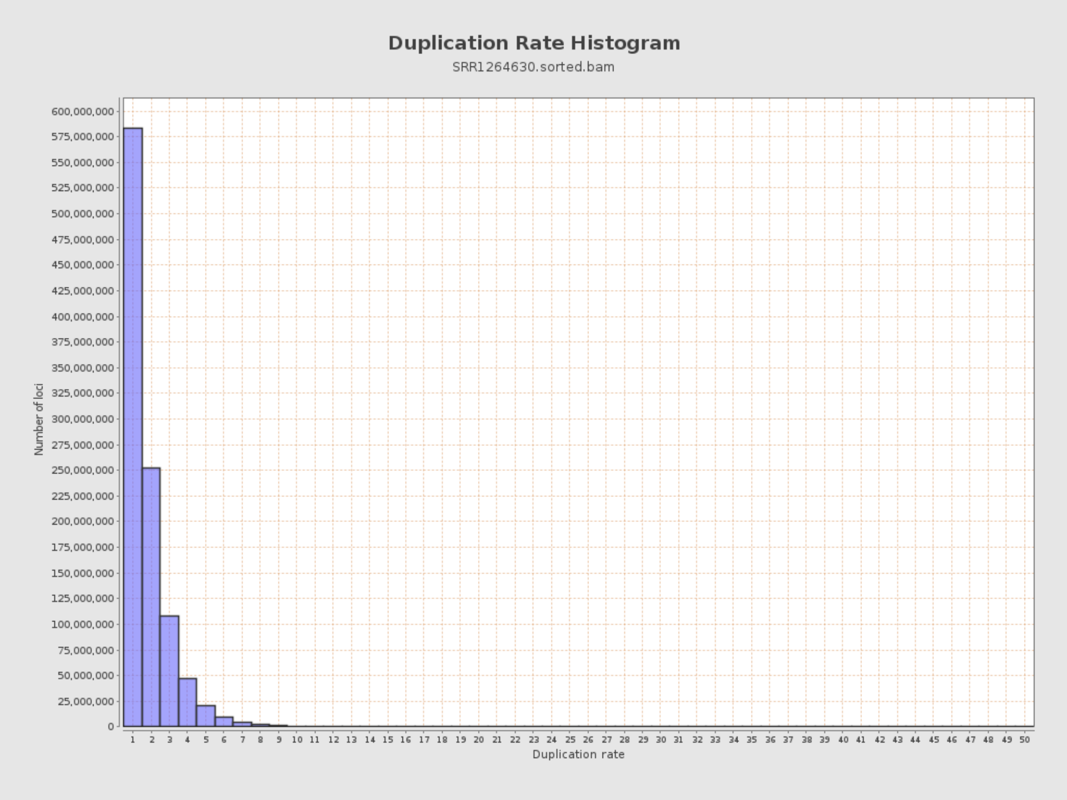
5. Results : Coverage Histogram (0-50X)



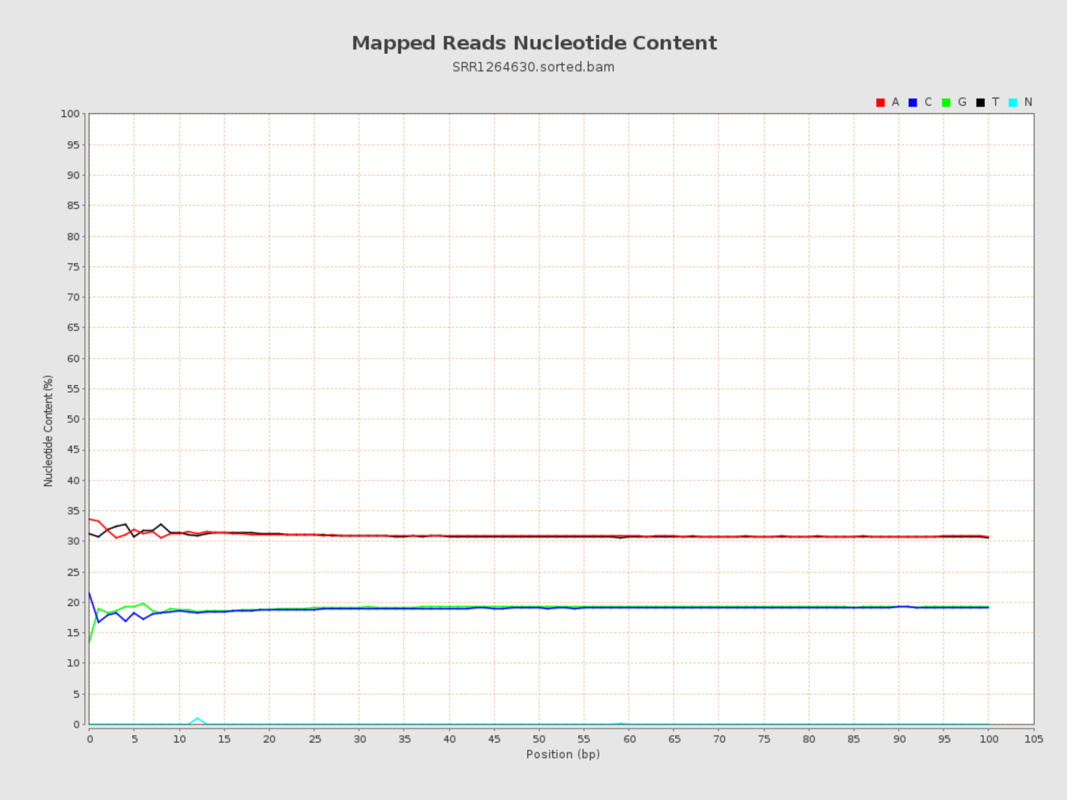
6. Results : Genome Fraction Coverage



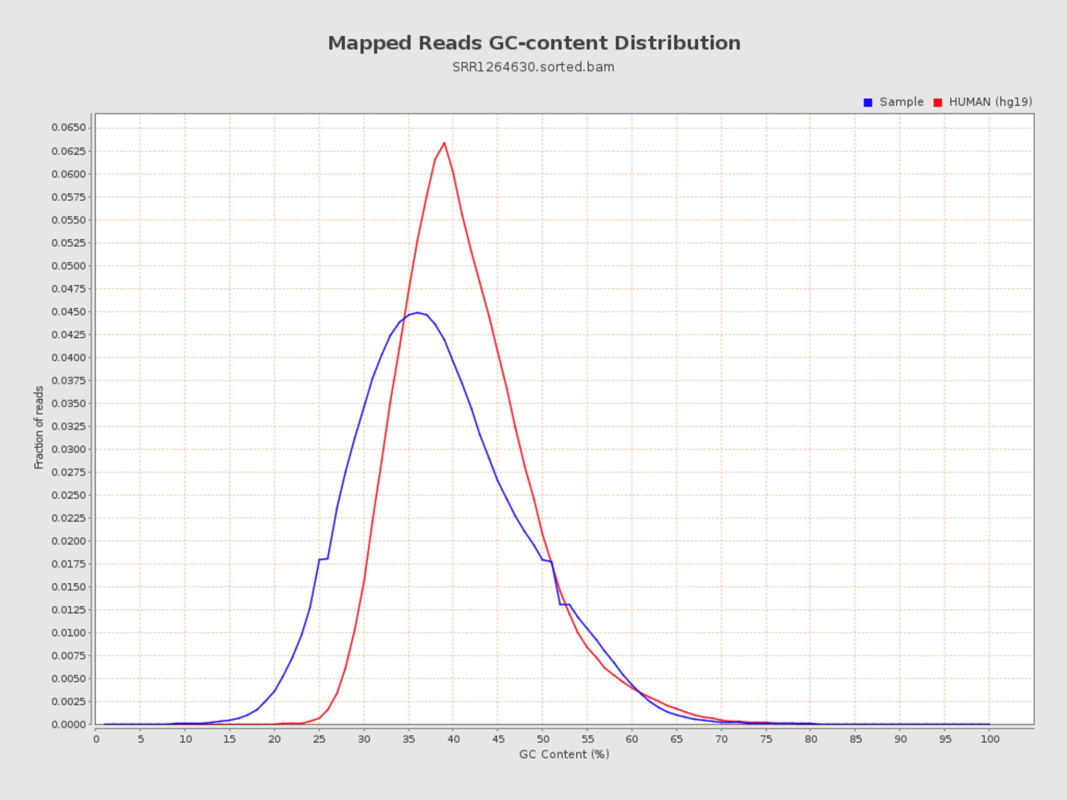
7. Results : Duplication Rate Histogram



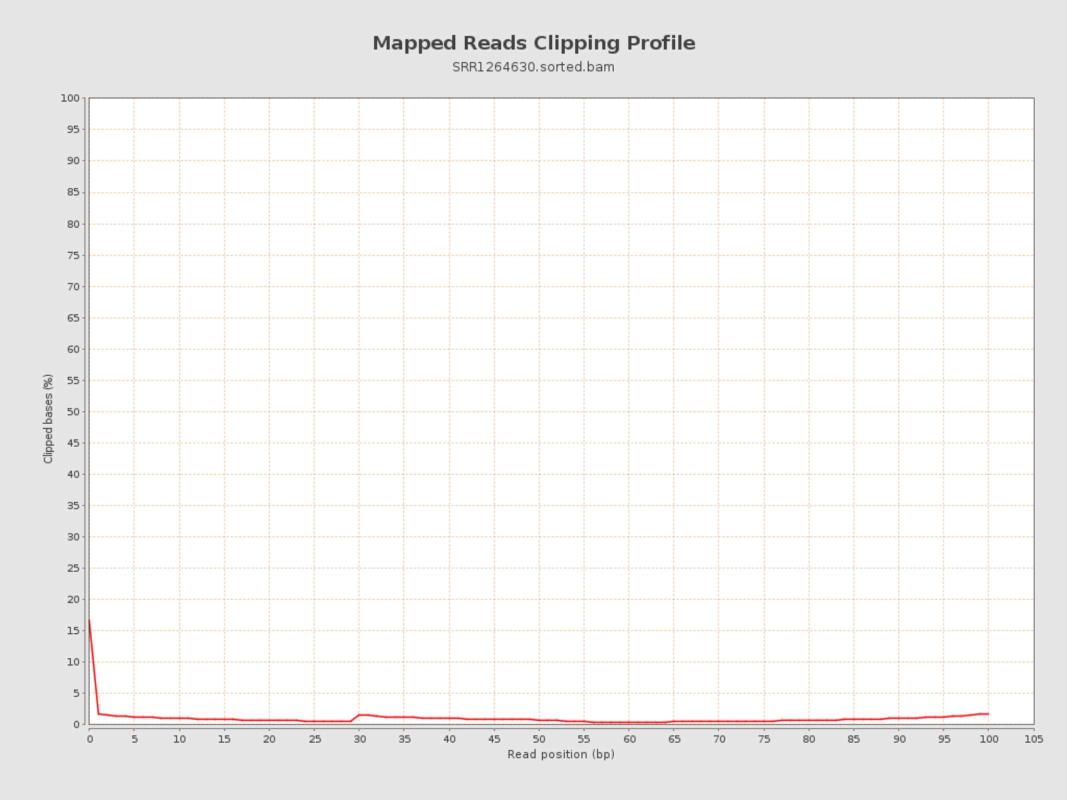
8. Results : Mapped Reads Nucleotide Content



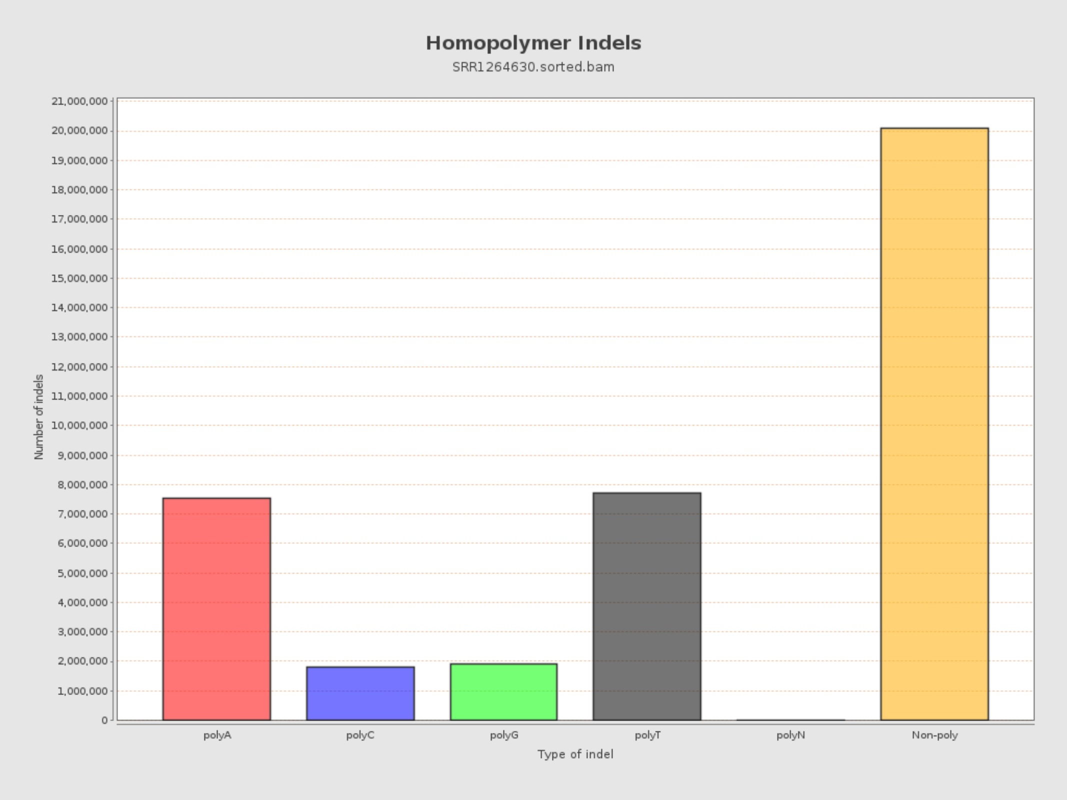
9. Results : Mapped Reads GC-content Distribution



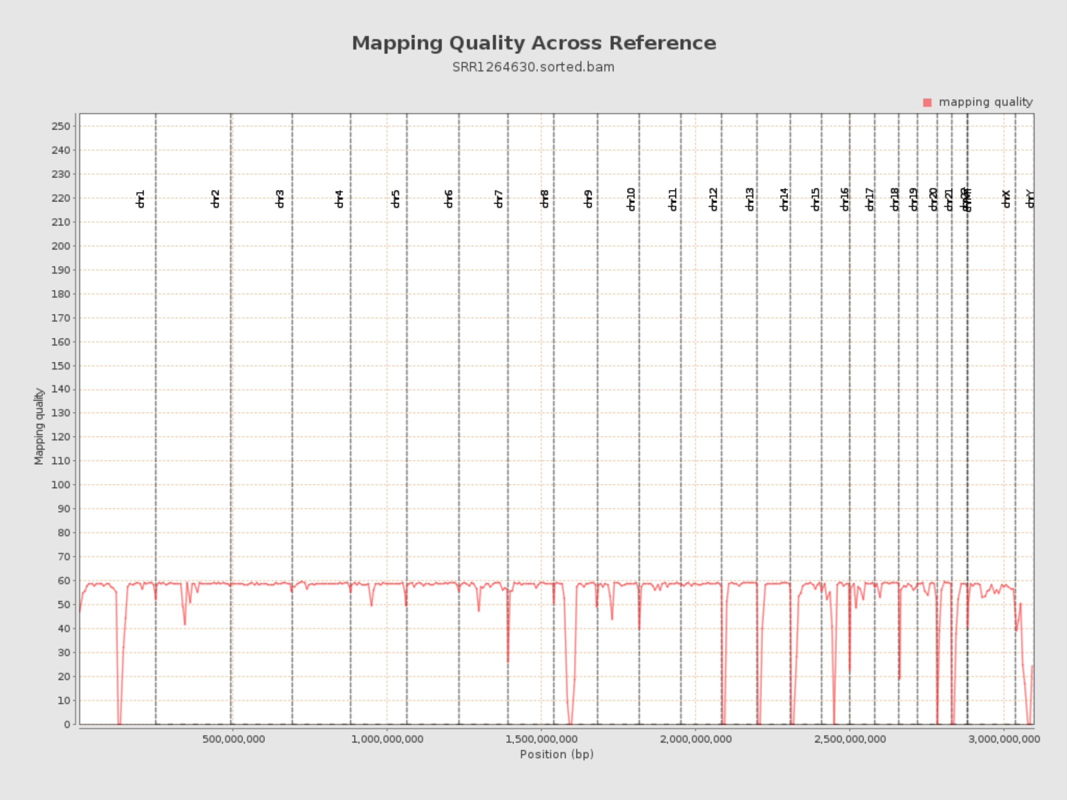
10. Results : Mapped Reads Clipping Profile



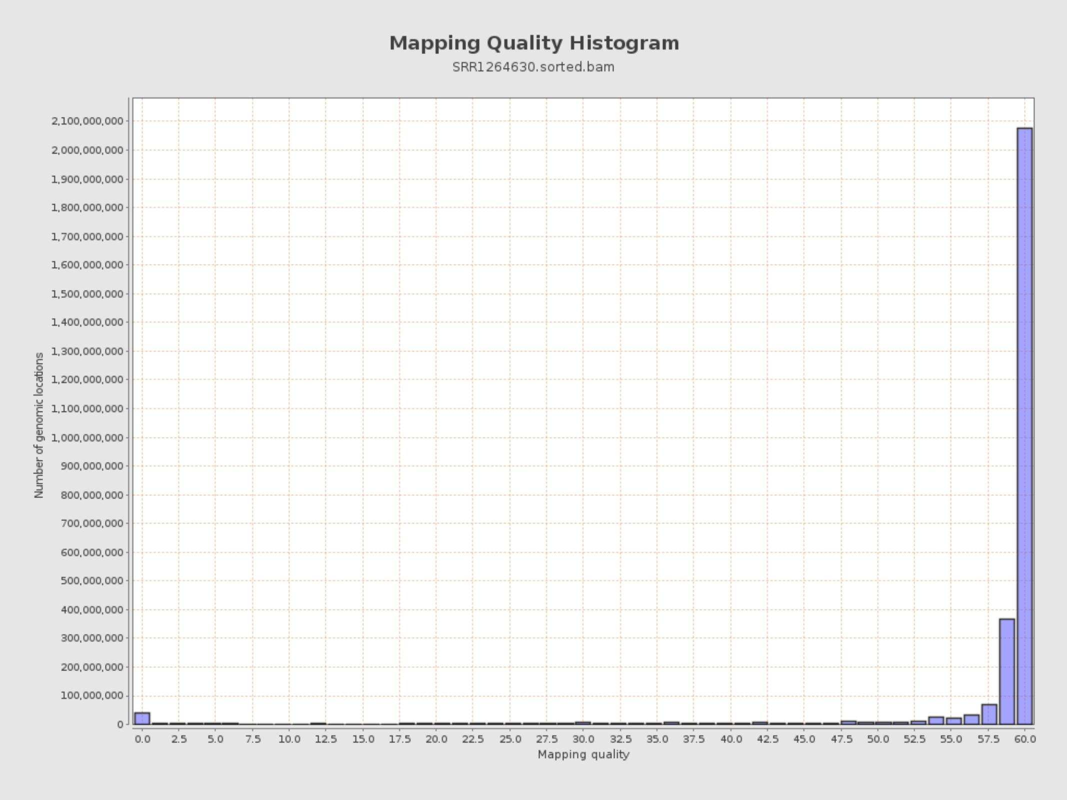
11. Results : Homopolymer Indels



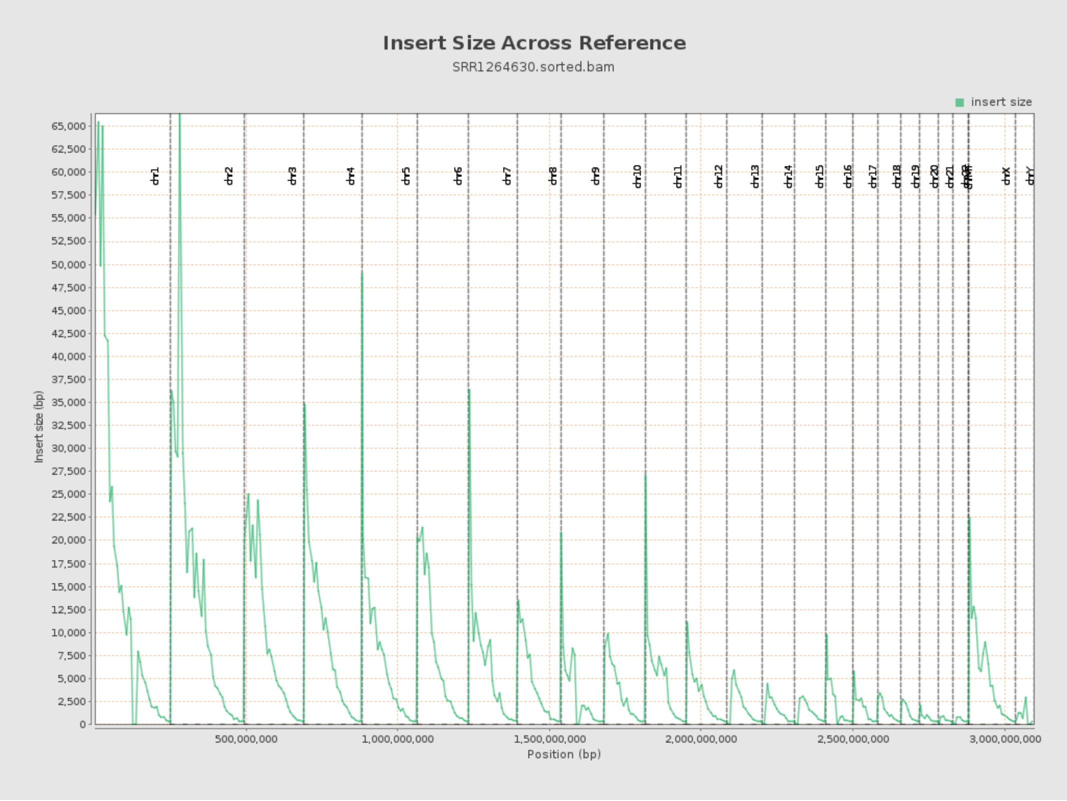
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram