Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 15:03:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038401.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_SRR5038401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038401_1.fastq.gz SRR5038401_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 15:03:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,319,864
Mapped reads	12,012,975 / 97.51%
Unmapped reads	306,889 / 2.49%
Mapped paired reads	12,012,975 / 97.51%
Mapped reads, first in pair	6,089,712 / 49.43%
Mapped reads, second in pair	5,923,263 / 48.08%
Mapped reads, both in pair	11,829,098 / 96.02%
Mapped reads, singletons	183,877 / 1.49%
Secondary alignments	0
Supplementary alignments	234,565 / 1.9%
Read min/max/mean length	30 / 150 / 150.98
Duplicated reads (estimated)	1,753,402 / 14.23%
Duplication rate	7.59%
Clipped reads	2,801,402 / 22.74%

2.2. ACGT Content

Number/percentage of A's	500,003,338 / 29.1%
Number/percentage of C's	353,474,575 / 20.58%
Number/percentage of T's	501,100,842 / 29.17%
Number/percentage of G's	363,345,262 / 21.15%
Number/percentage of N's	35,955 / 0%

GC Percentage	41.73%

2.3. Coverage

Mean	0.5553
Standard Deviation	9.6549

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	103,672.5
Standard Deviation	3,028,492.47
P25/Median/P75	229 / 271 / 325

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	27,034,965
Insertions	317,664
Mapped reads with at least one insertion	2.46%
Deletions	586,723
Mapped reads with at least one deletion	4.68%
Homopolymer indels	45.59%

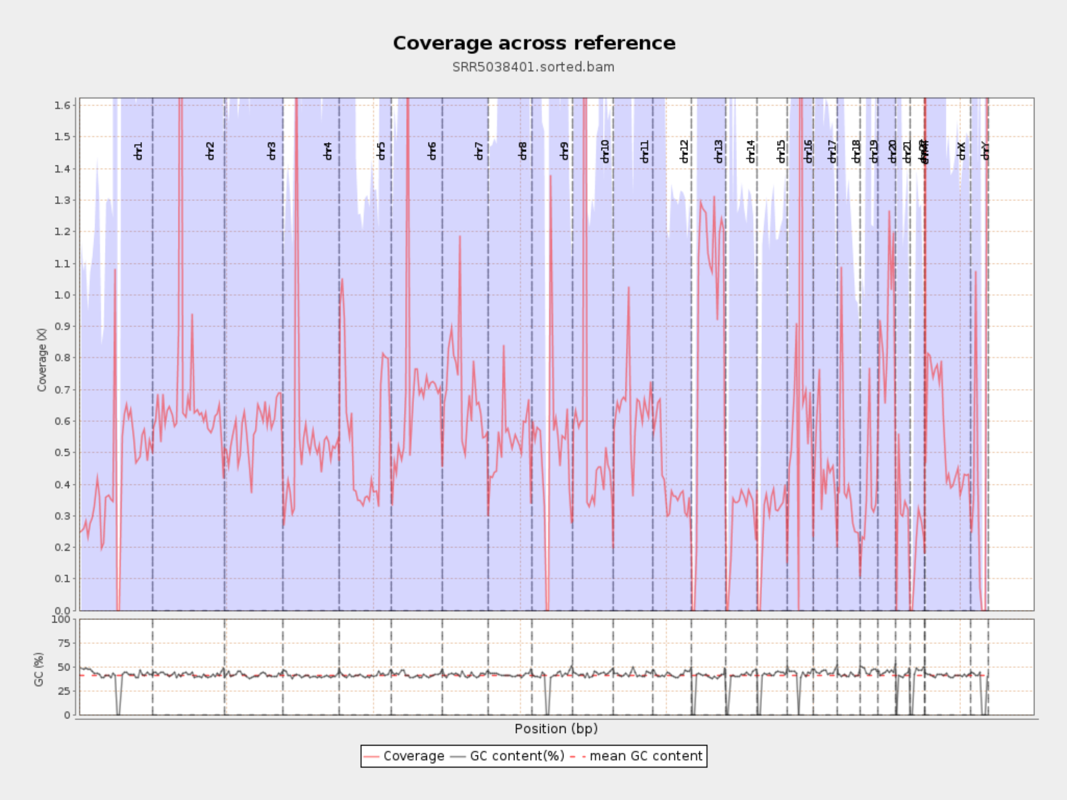
2.7. Chromosome stats

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

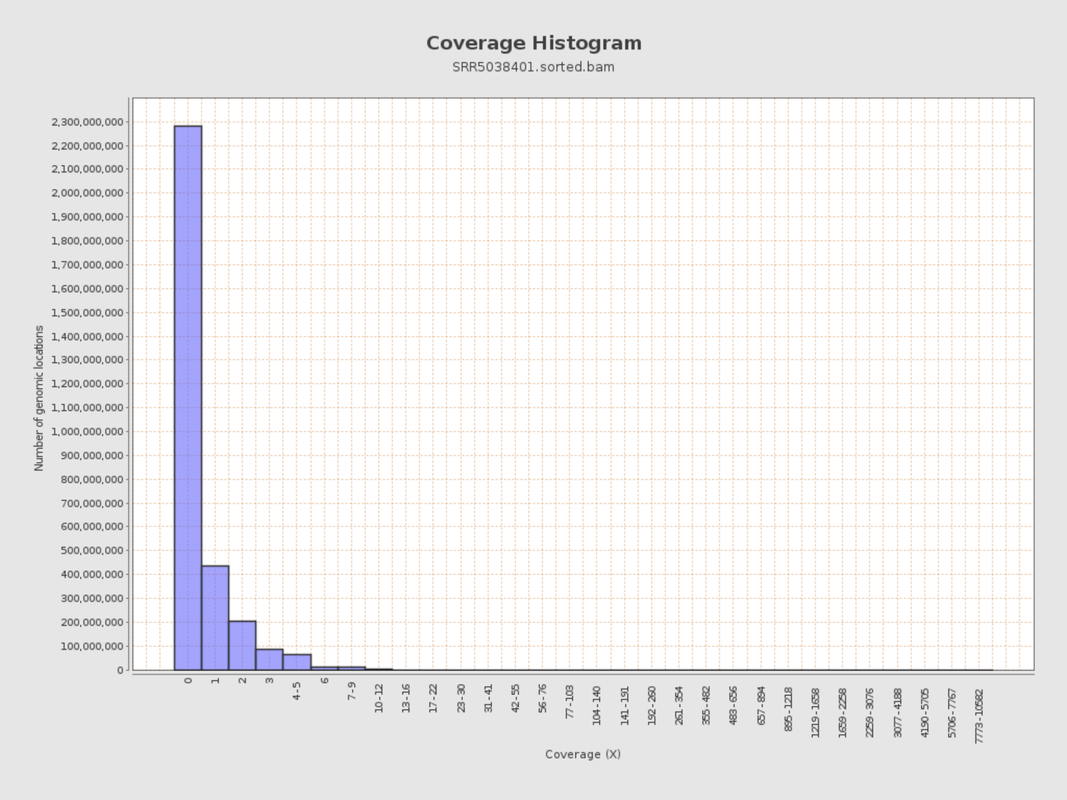
		bases	coverage	deviation
chr1	249250621	103987402	0.4172	11.0929
chr2	243199373	171676109	0.7059	13.0764
chr3	198022430	113460708	0.573	1.2394
chr4	191154276	101961444	0.5334	8.9591
chr5	180915260	100632484	0.5562	1.3394
chr6	171115067	118237151	0.691	14.2177
chr7	159138663	109688752	0.6893	10.1201
chr8	146364022	78307945	0.535	2.7321
chr9	141213431	70750094	0.501	16.38
chr10	135534747	82877220	0.6115	18.8723
chr11	135006516	85505521	0.6333	6.6155
chr12	133851895	55385255	0.4138	1.0678
chr13	115169878	111805381	0.9708	1.7679
chr14	107349540	30971911	0.2885	1.0551
chr15	102531392	29186495	0.2847	0.7976
chr16	90354753	67927248	0.7518	15.1502
chr17	81195210	36552543	0.4502	7.1217
chr18	78077248	31154201	0.399	13.7845
chr19	59128983	20869427	0.3529	6.5681
chr20	63025520	57216444	0.9078	2.8987
chr21	48129895	14865555	0.3089	4.0024
chr22	51304566	9422052	0.1836	0.7971
chrMT	16571	1085414	65.5008	38.996
chrX	155270560	85211491	0.5488	1.9511

chrY	59373566	30453580	0.5129	13.7644

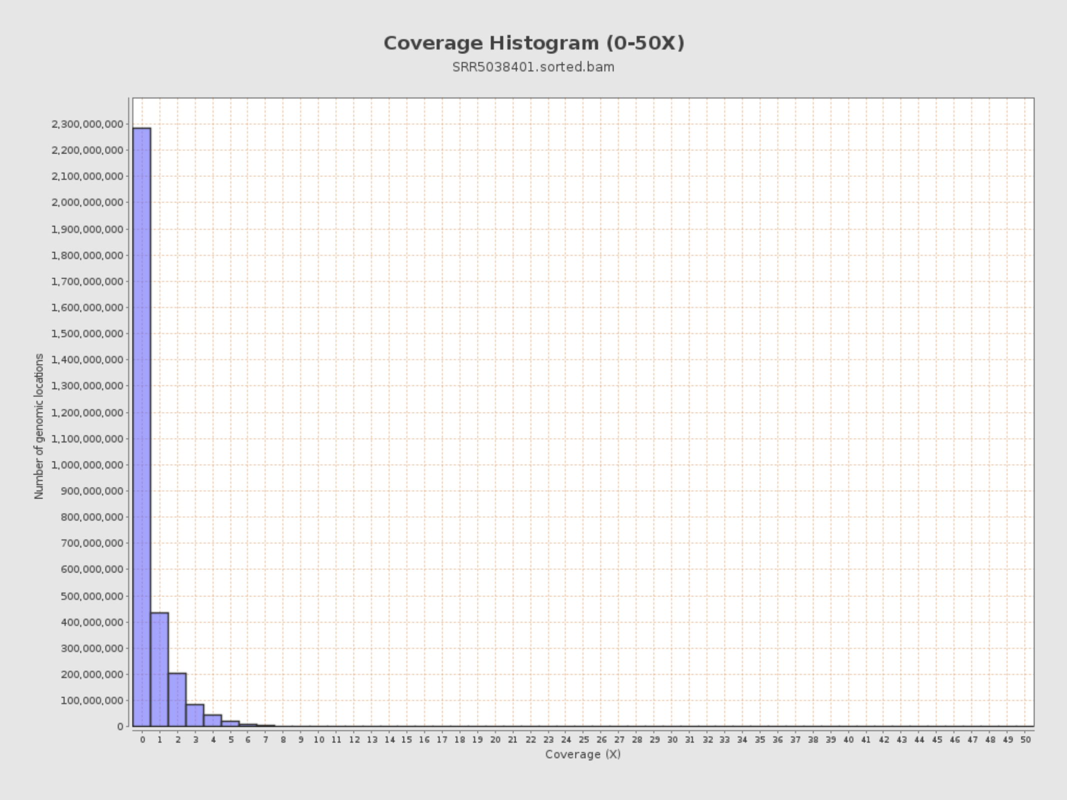
3. Results : Coverage across reference



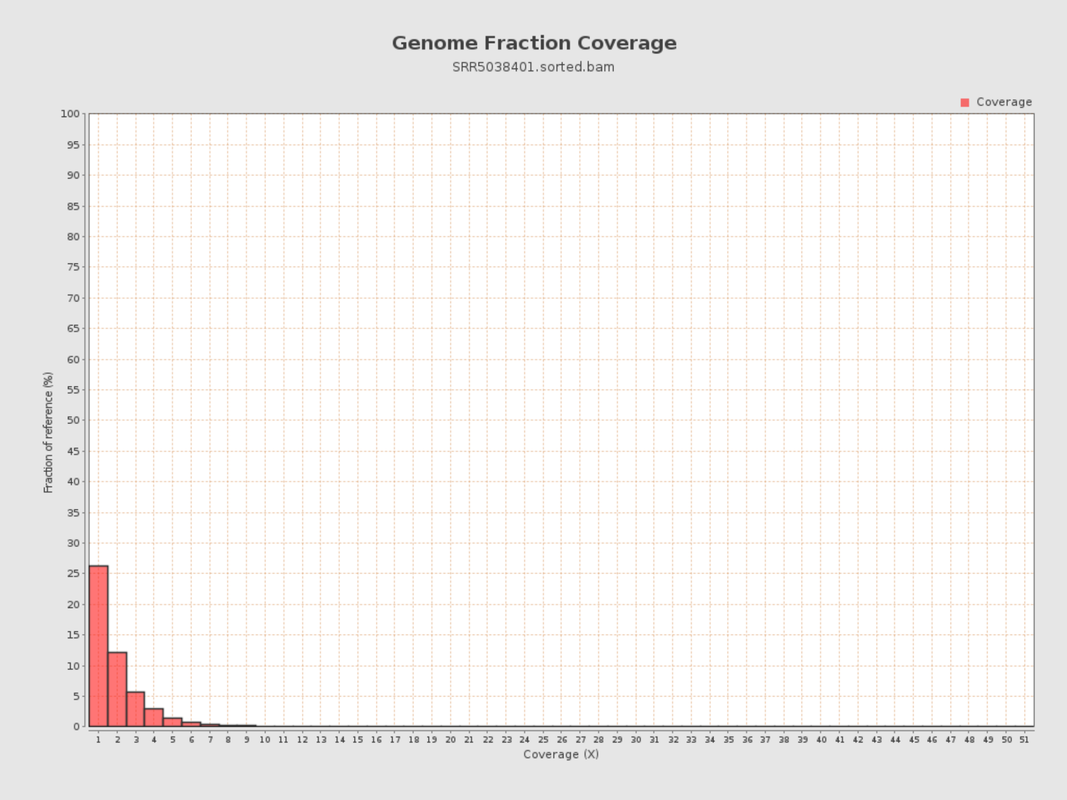
4. Results : Coverage Histogram



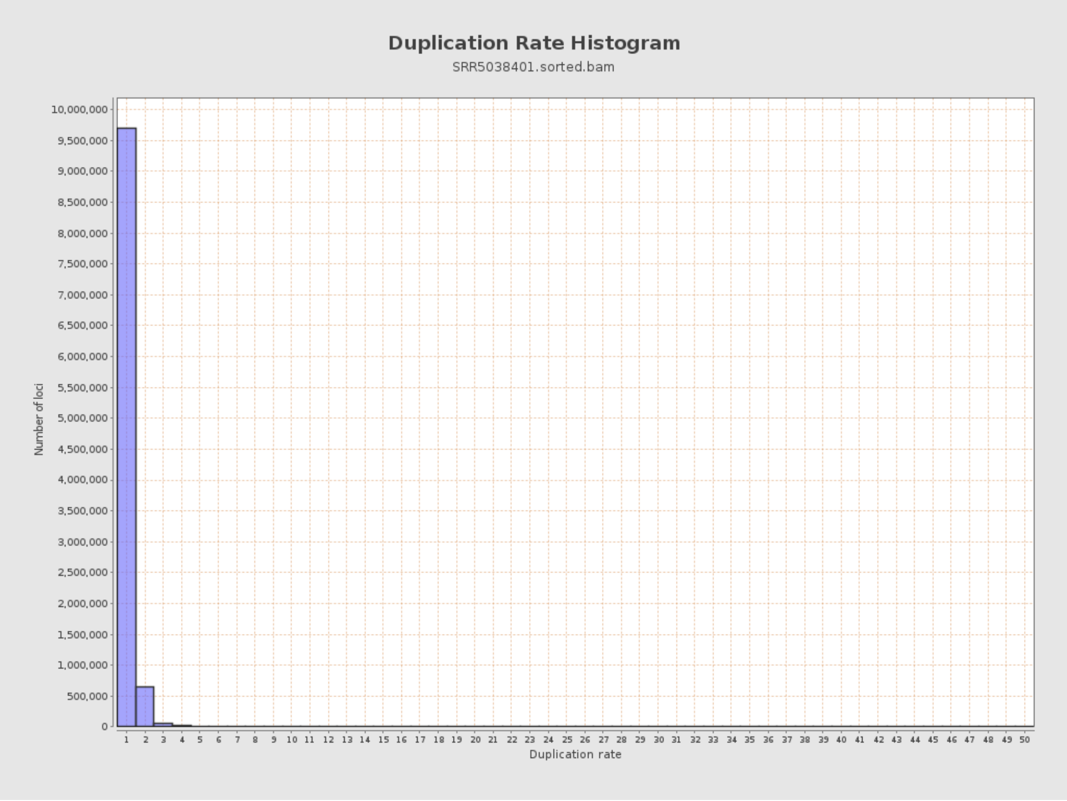
5. Results : Coverage Histogram (0-50X)



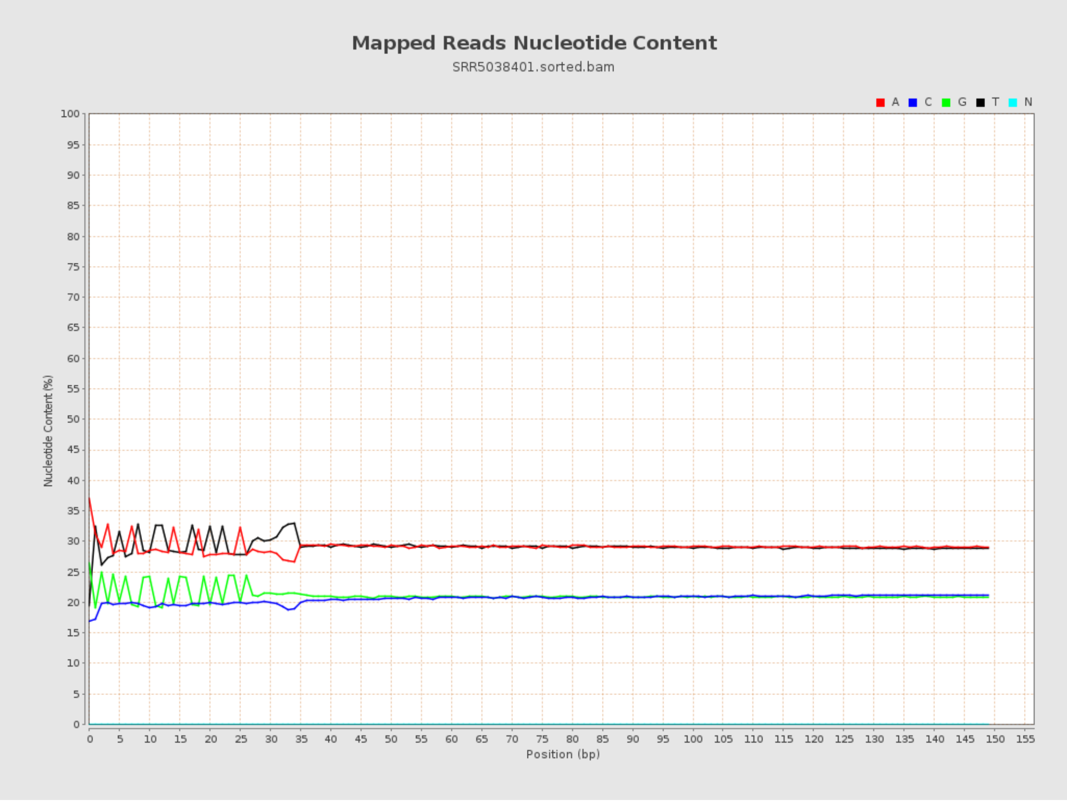
6. Results : Genome Fraction Coverage



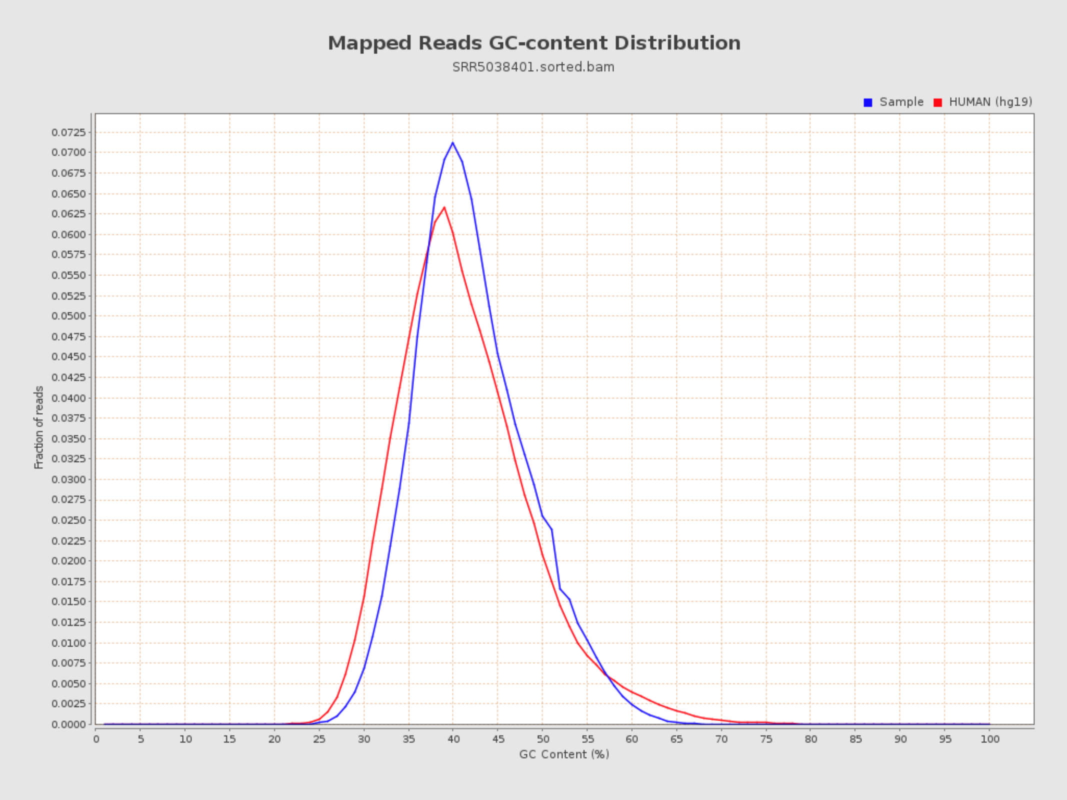
7. Results : Duplication Rate Histogram



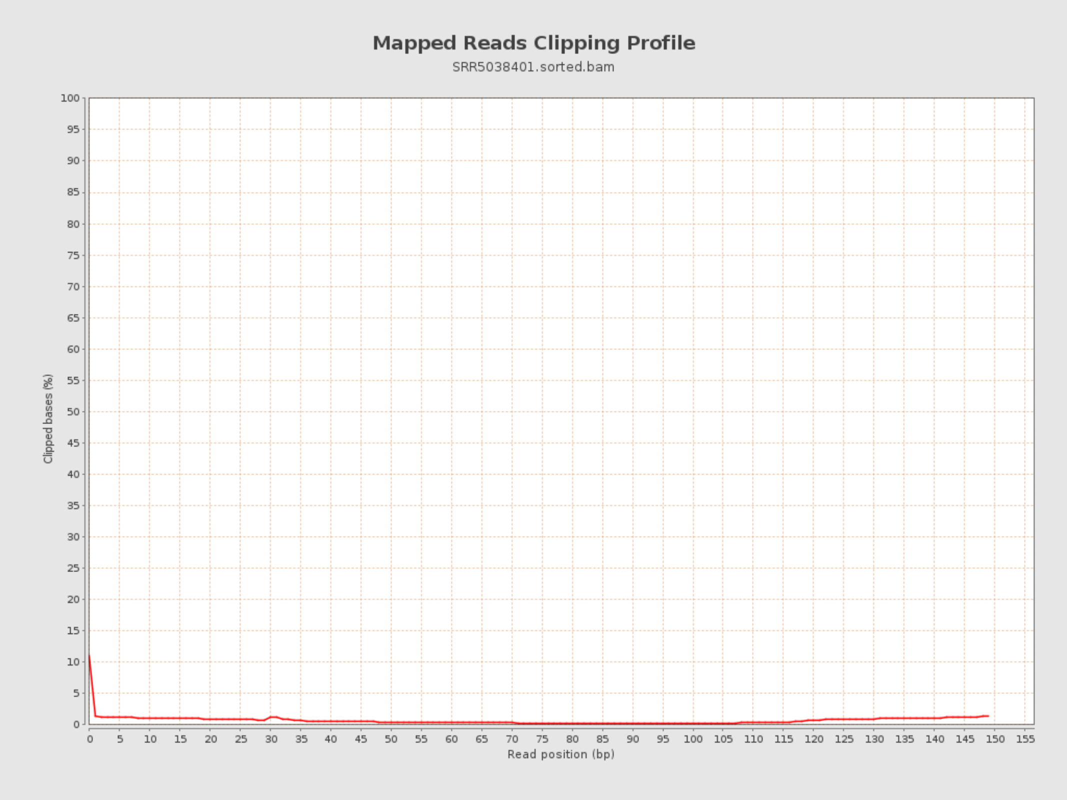
8. Results : Mapped Reads Nucleotide Content



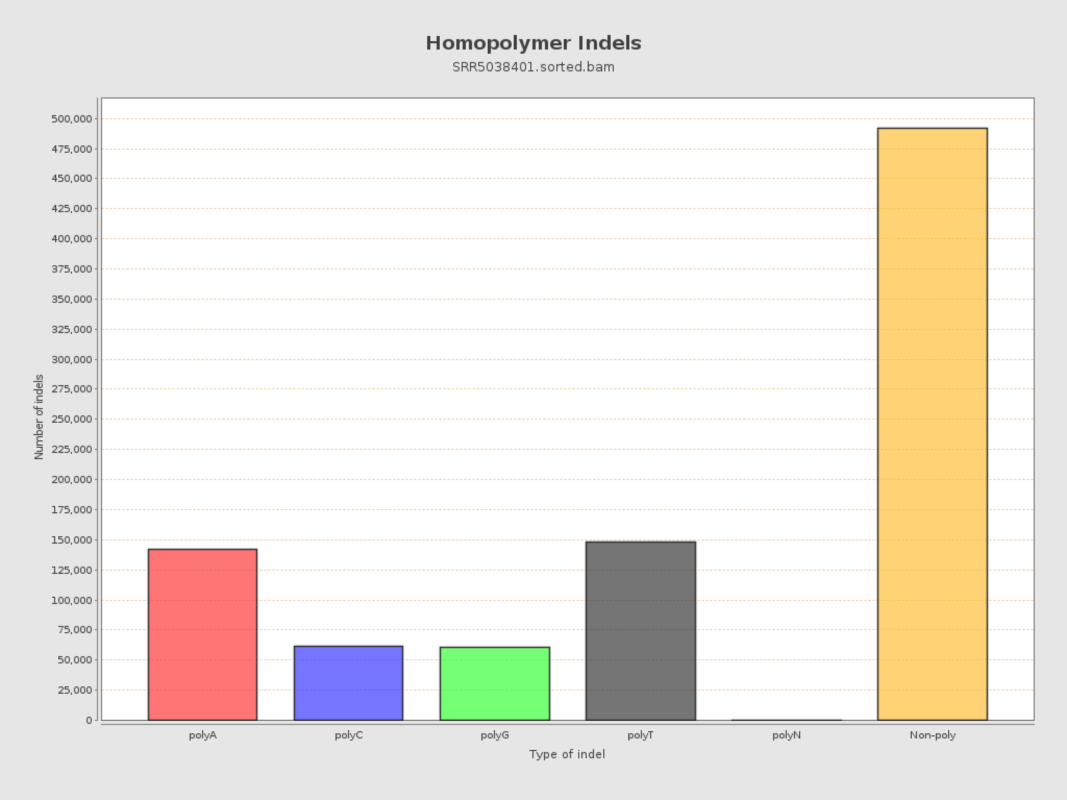
9. Results : Mapped Reads GC-content Distribution



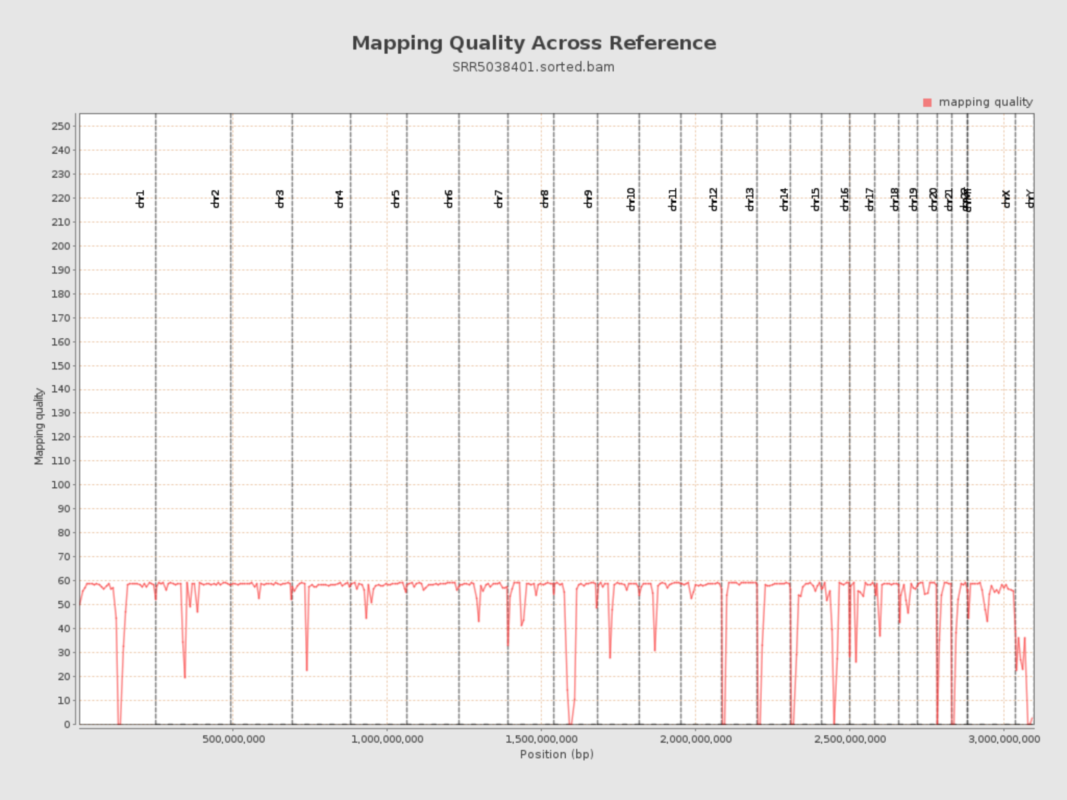
10. Results : Mapped Reads Clipping Profile



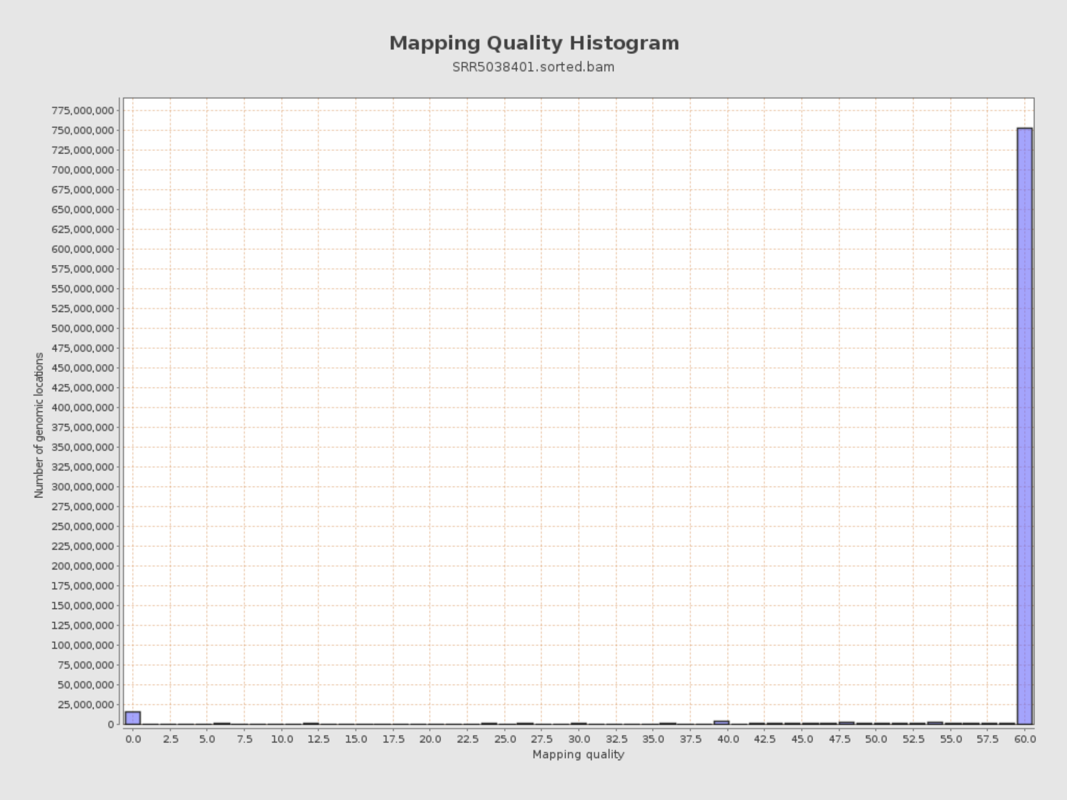
11. Results : Homopolymer Indels



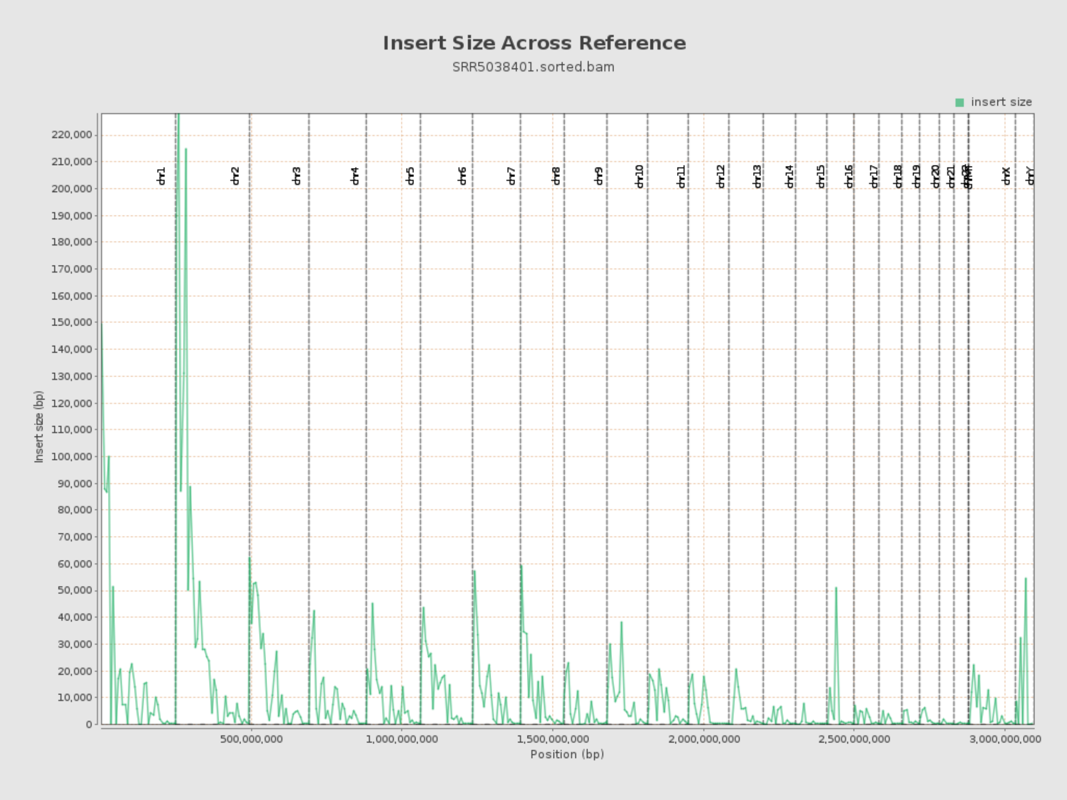
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram