Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 06:18:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038481.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_SRR5038481 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038481_1.fastq.gz SRR5038481_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 06:18:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038481.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,697,270
Mapped reads	11,352,386 / 97.05%
Unmapped reads	344,884 / 2.95%
Mapped paired reads	11,352,386 / 97.05%
Mapped reads, first in pair	5,759,561 / 49.24%
Mapped reads, second in pair	5,592,825 / 47.81%
Mapped reads, both in pair	11,171,780 / 95.51%
Mapped reads, singletons	180,606 / 1.54%
Secondary alignments	0
Supplementary alignments	204,119 / 1.75%
Read min/max/mean length	30 / 150 / 150.9
Duplicated reads (estimated)	1,603,719 / 13.71%
Duplication rate	8.55%
Clipped reads	3,227,932 / 27.6%

2.2. ACGT Content

Number/percentage of A's	464,551,533 / 28.94%
Number/percentage of C's	329,100,692 / 20.5%
Number/percentage of T's	465,412,374 / 29%
Number/percentage of G's	345,972,467 / 21.55%
Number/percentage of N's	33,893 / 0%

GC Percentage	42.06%

2.3. Coverage

Mean	0.5189
Standard Deviation	7.9221

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	84,610.25
Standard Deviation	2,738,930.74
P25/Median/P75	214 / 253 / 304

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	24,138,383
Insertions	286,848
Mapped reads with at least one insertion	2.37%
Deletions	565,035
Mapped reads with at least one deletion	4.78%
Homopolymer indels	46.74%

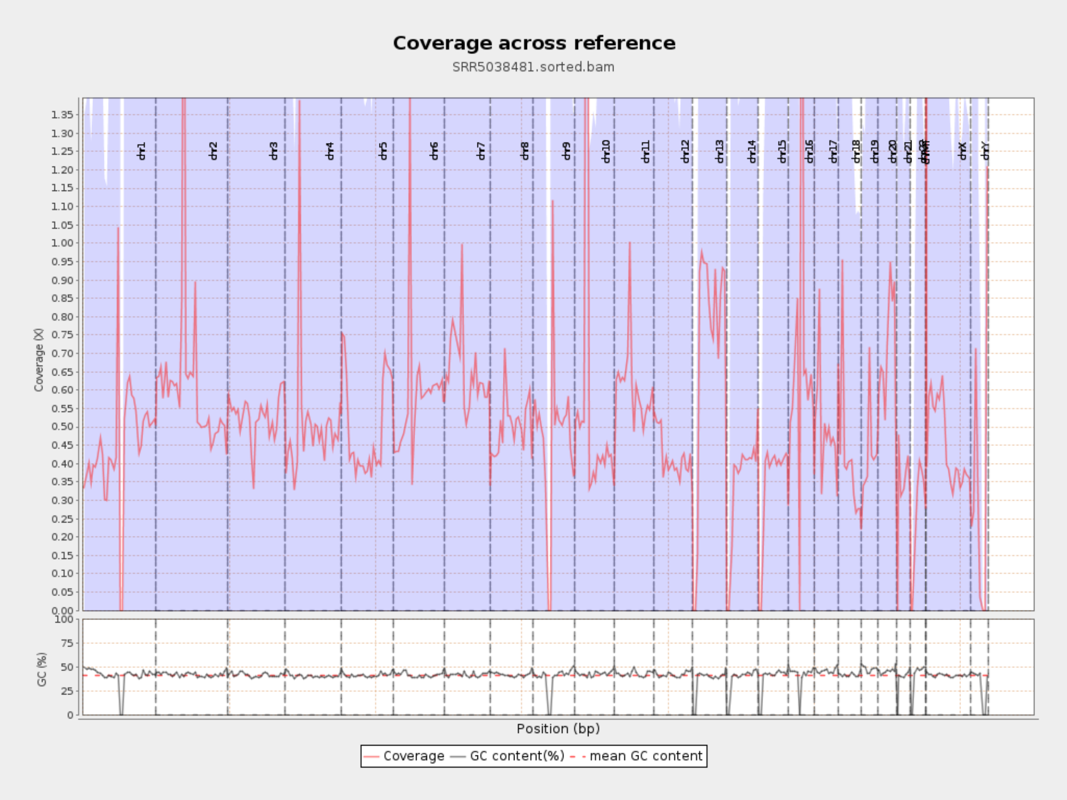
2.7. Chromosome stats

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

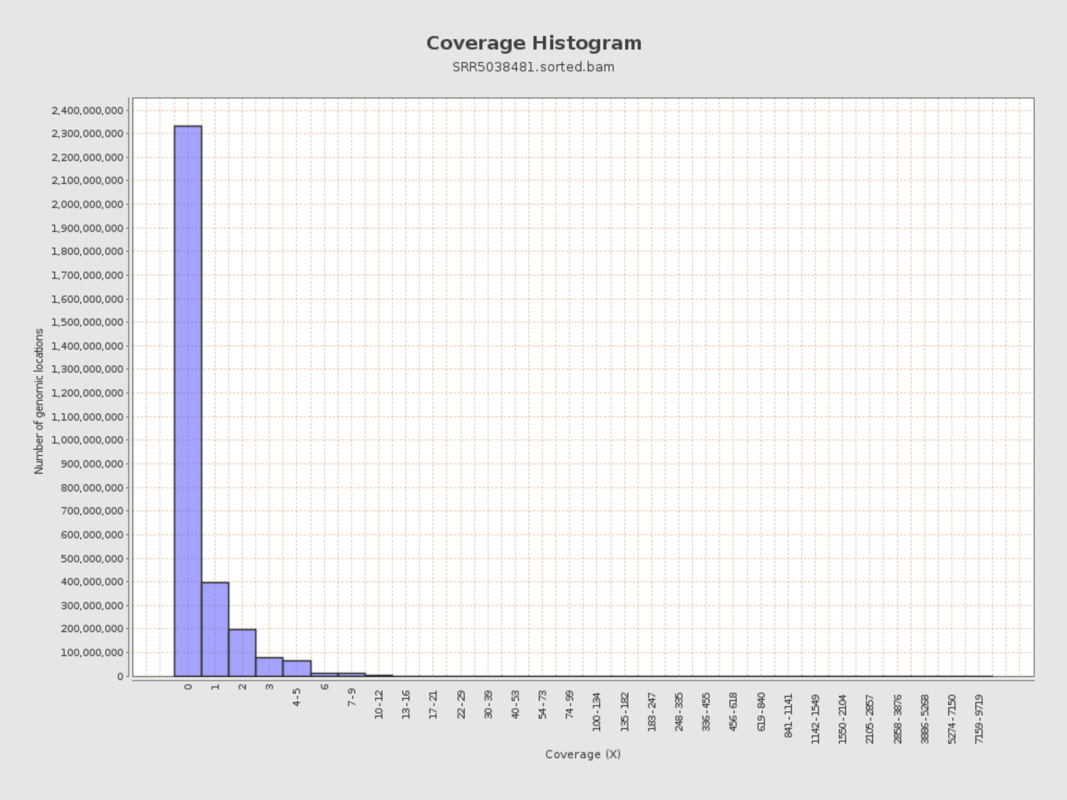
		bases	coverage	deviation
chr1	249250621	111622650	0.4478	10.0913
chr2	243199373	153672518	0.6319	8.651
chr3	198022430	104324914	0.5268	1.2172
chr4	191154276	97224977	0.5086	6.0916
chr5	180915260	90121591	0.4981	1.2074
chr6	171115067	100357010	0.5865	9.9614
chr7	159138663	104201677	0.6548	6.793
chr8	146364022	73457534	0.5019	2.019
chr9	141213431	67190316	0.4758	12.1923
chr10	135534747	77231003	0.5698	19.3528
chr11	135006516	82081265	0.608	7.0449
chr12	133851895	56331465	0.4208	1.0622
chr13	115169878	83320745	0.7235	1.4664
chr14	107349540	36473682	0.3398	1.0525
chr15	102531392	34527667	0.3368	0.8965
chr16	90354753	66016440	0.7306	13.2759
chr17	81195210	41173010	0.5071	7.5644
chr18	78077248	33362802	0.4273	11.0474
chr19	59128983	25074631	0.4241	6.0842
chr20	63025520	45669557	0.7246	2.3094
chr21	48129895	16476726	0.3423	2.6836
chr22	51304566	13083955	0.255	0.8504
chrMT	16571	2176295	131.3315	94.0143
chrX	155270560	70016860	0.4509	1.8919

chrY	59373566	21040362	0.3544	9.2191

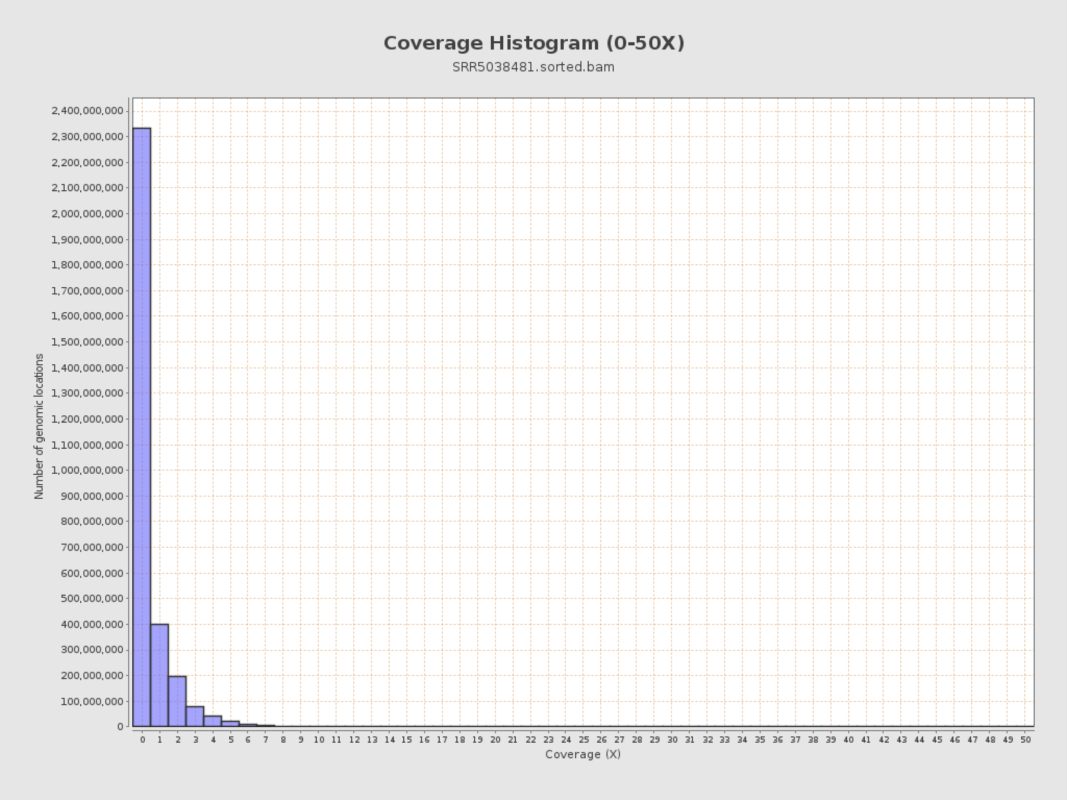
3. Results : Coverage across reference



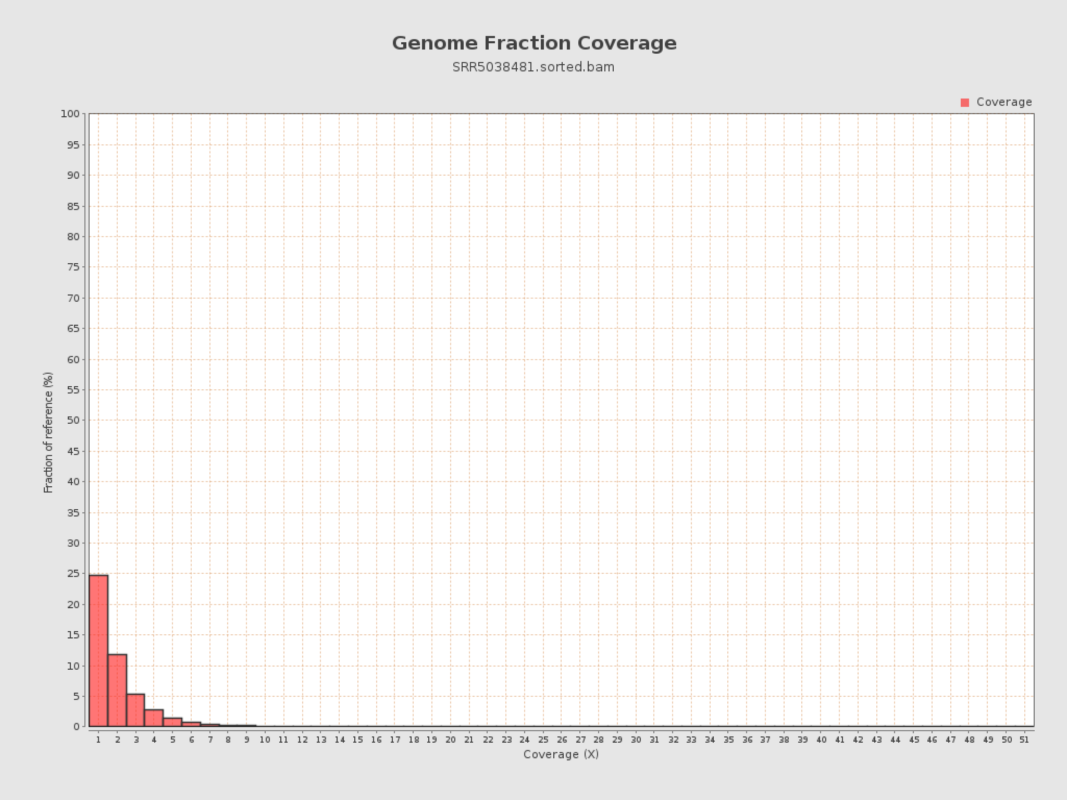
4. Results : Coverage Histogram



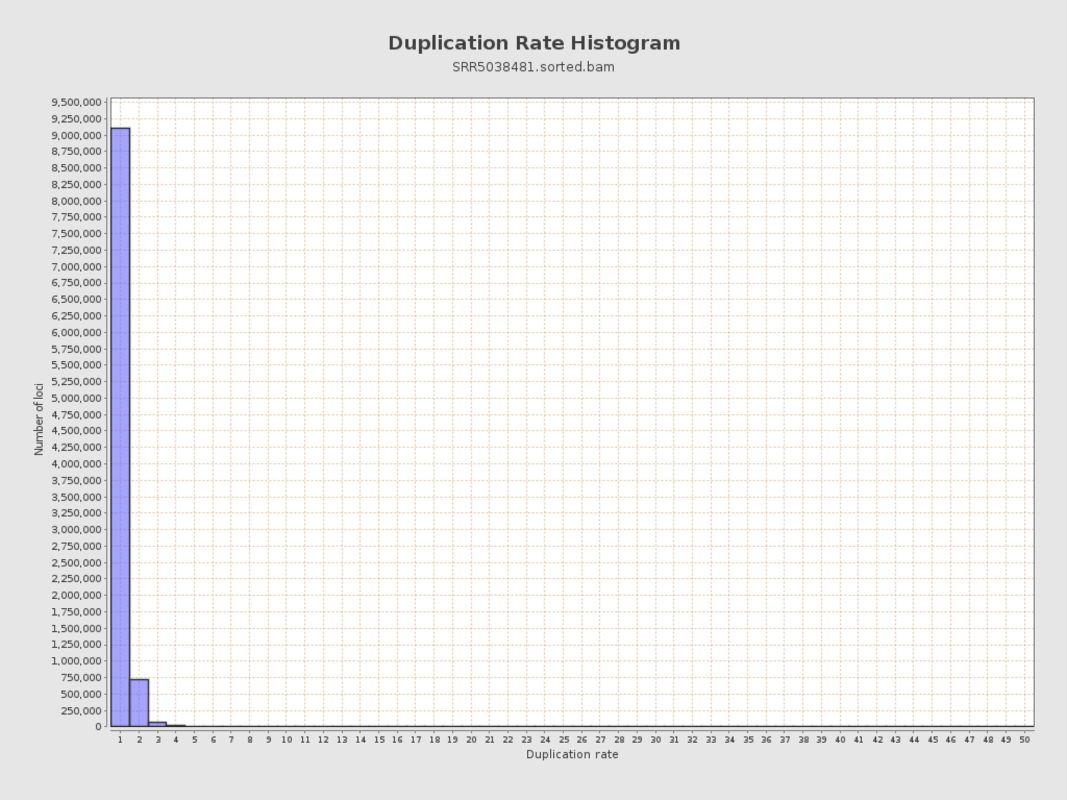
5. Results : Coverage Histogram (0-50X)



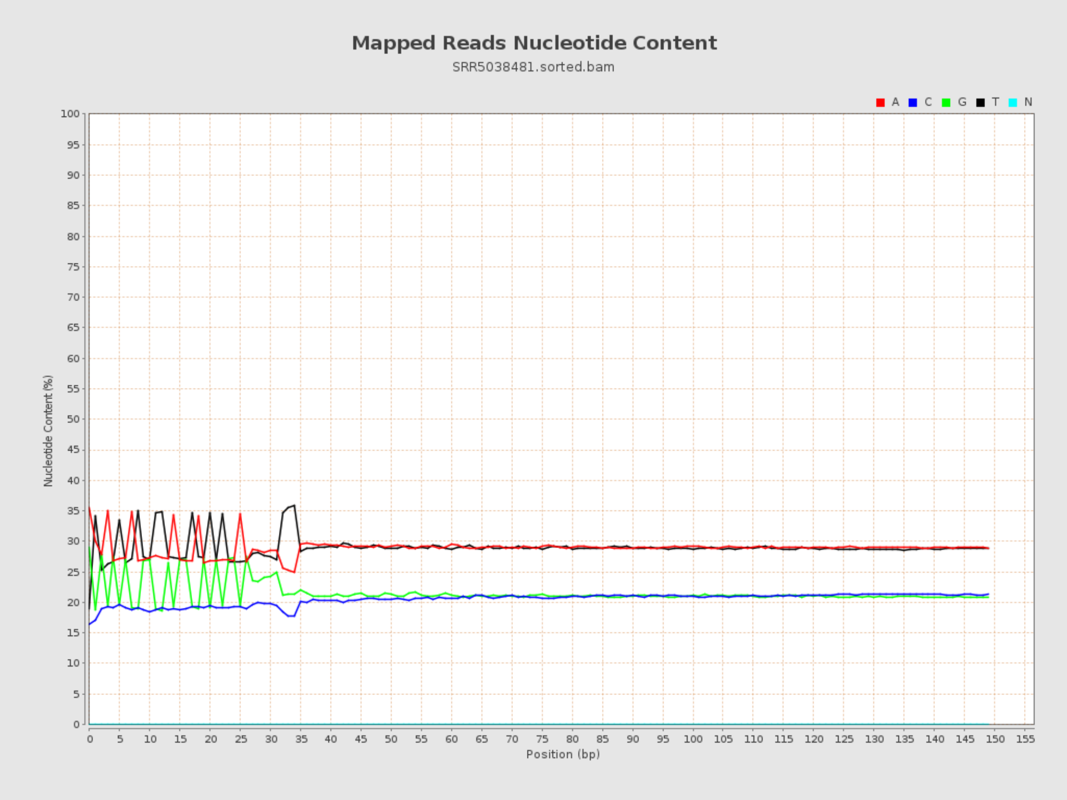
6. Results : Genome Fraction Coverage



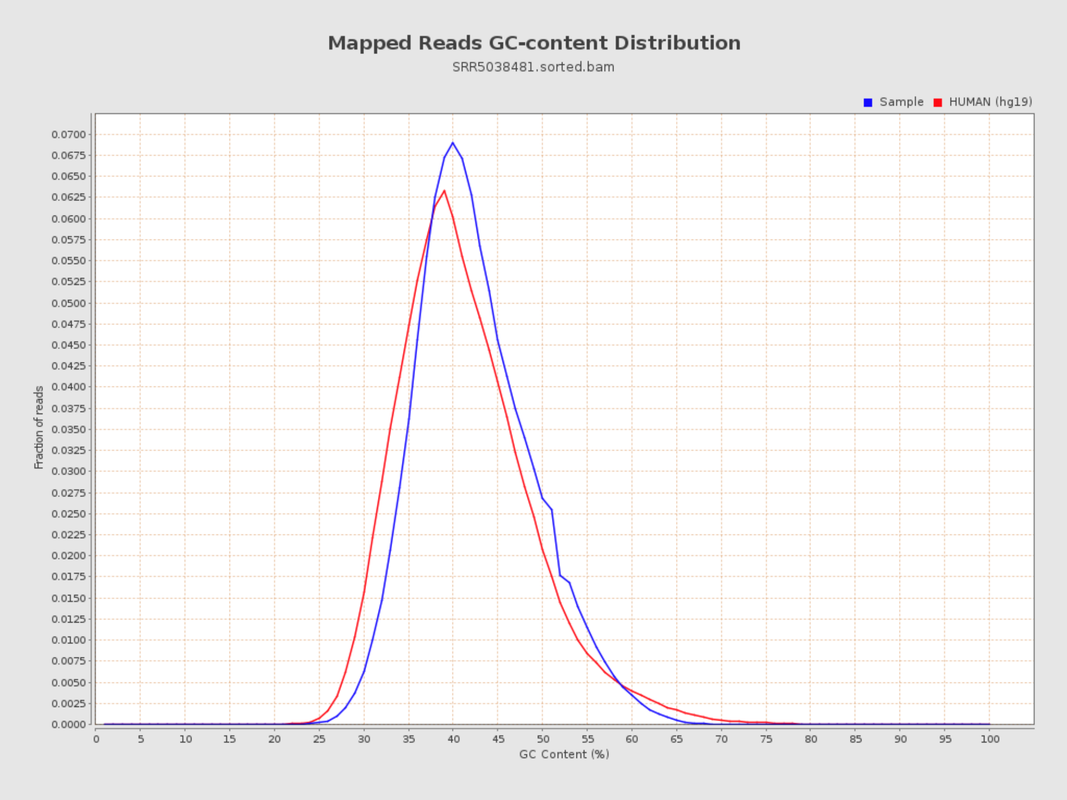
7. Results : Duplication Rate Histogram



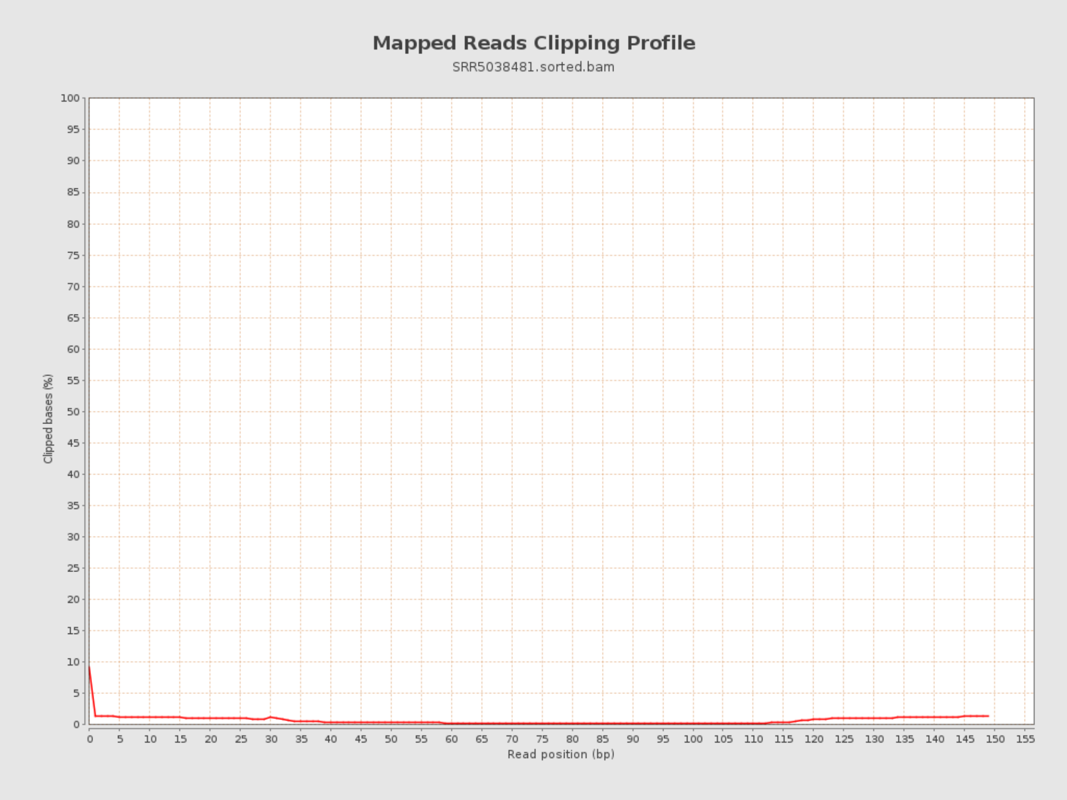
8. Results : Mapped Reads Nucleotide Content



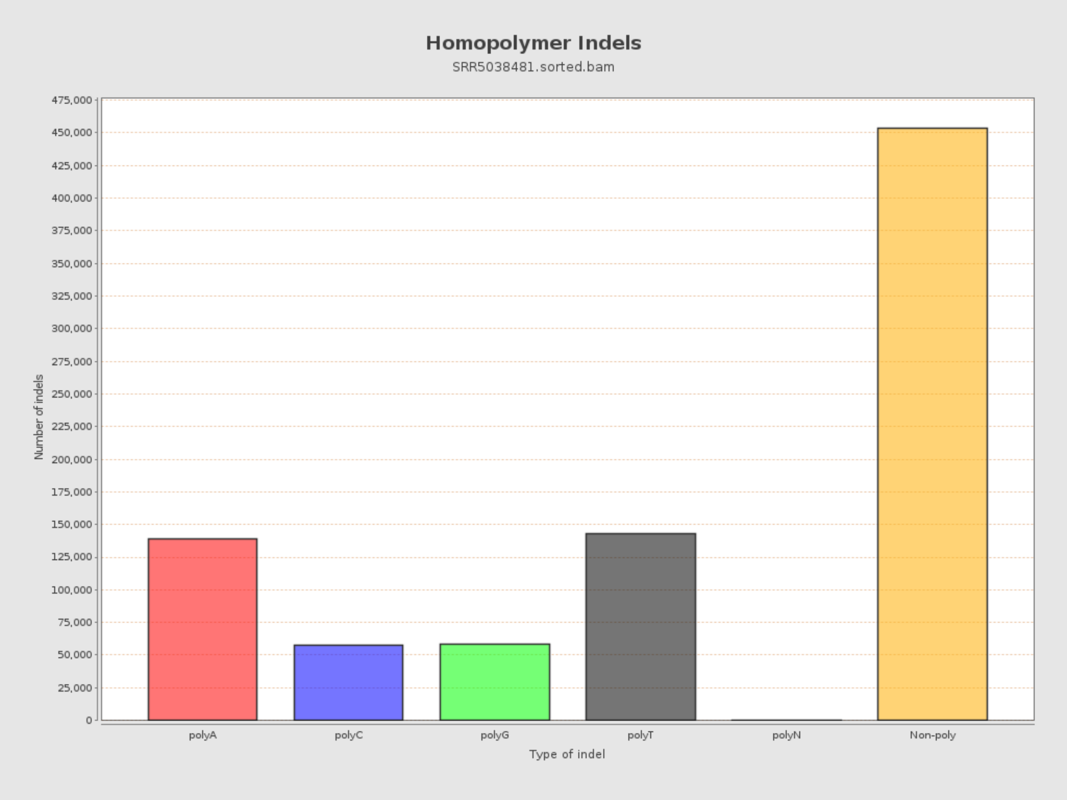
9. Results : Mapped Reads GC-content Distribution



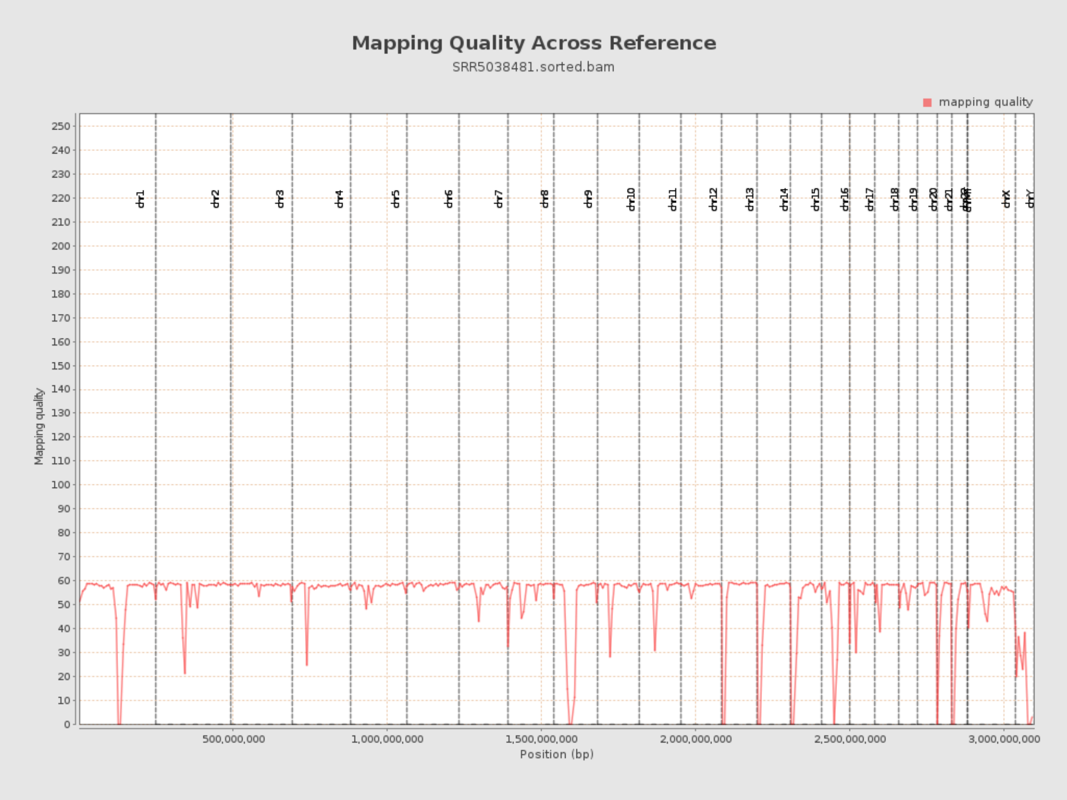
10. Results : Mapped Reads Clipping Profile



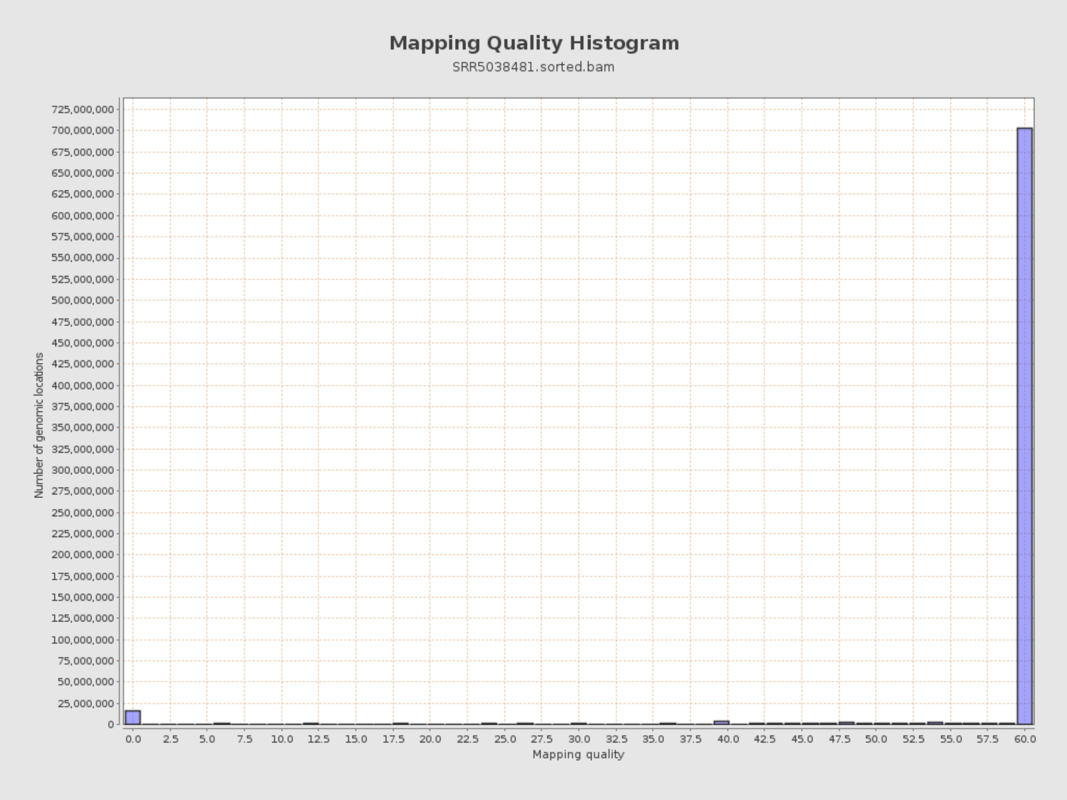
11. Results : Homopolymer Indels



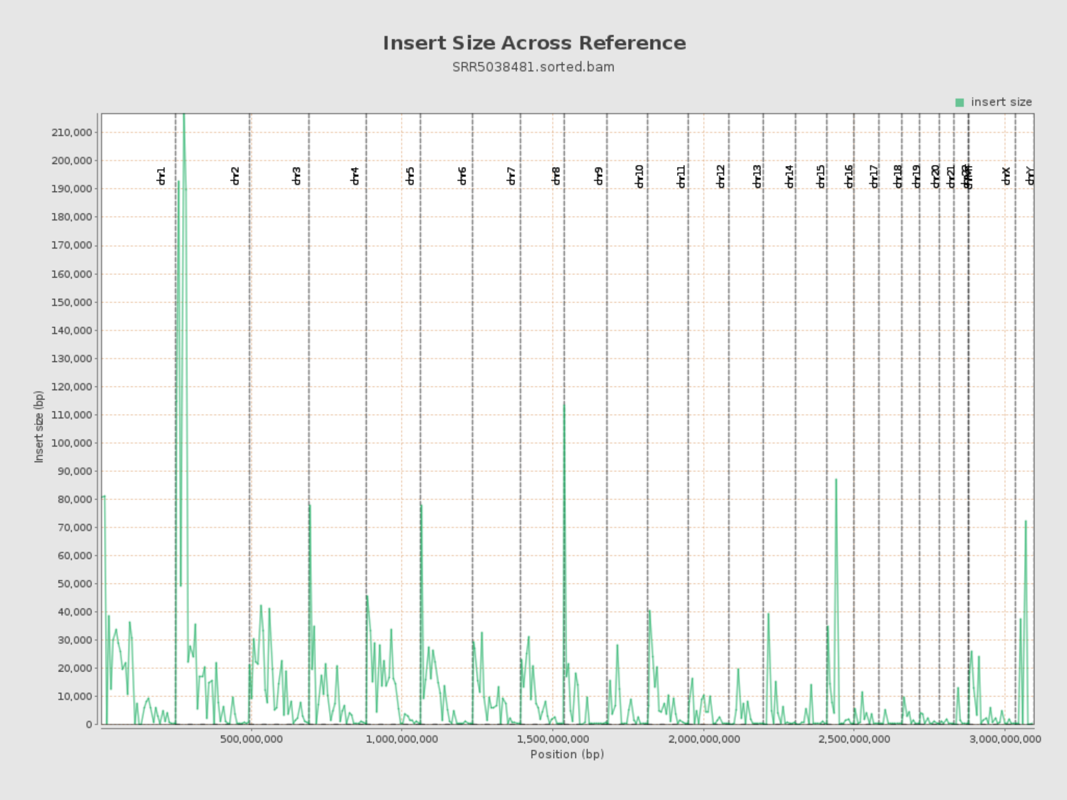
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram