Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 05:05:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038478.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_SRR5038478 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038478_1.fastq.gz SRR5038478_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 05:05:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038478.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,410,332
Mapped reads	10,632,386 / 93.18%
Unmapped reads	777,946 / 6.82%
Mapped paired reads	10,632,386 / 93.18%
Mapped reads, first in pair	5,388,866 / 47.23%
Mapped reads, second in pair	5,243,520 / 45.95%
Mapped reads, both in pair	10,466,002 / 91.72%
Mapped reads, singletons	166,384 / 1.46%
Secondary alignments	0
Supplementary alignments	215,189 / 1.89%
Read min/max/mean length	30 / 150 / 150.96
Duplicated reads (estimated)	1,548,689 / 13.57%
Duplication rate	8.78%
Clipped reads	2,928,620 / 25.67%

2.2. ACGT Content

Number/percentage of A's	436,071,994 / 28.99%
Number/percentage of C's	307,853,972 / 20.47%
Number/percentage of T's	437,574,557 / 29.09%
Number/percentage of G's	322,669,563 / 21.45%
Number/percentage of N's	32,117 / 0%

GC Percentage	41.92%

2.3. Coverage

Mean	0.4863
Standard Deviation	7.2942

2.4. Mapping Quality

Mean Mapping Quality	53.73

2.5. Insert size

Mean	91,303.95
Standard Deviation	2,855,499.88
P25/Median/P75	220 / 261 / 314

2.6. Mismatches and indels

General error rate	1.5%
Mismatches	21,639,970
Insertions	294,599
Mapped reads with at least one insertion	2.57%
Deletions	558,480
Mapped reads with at least one deletion	5.02%
Homopolymer indels	45.99%

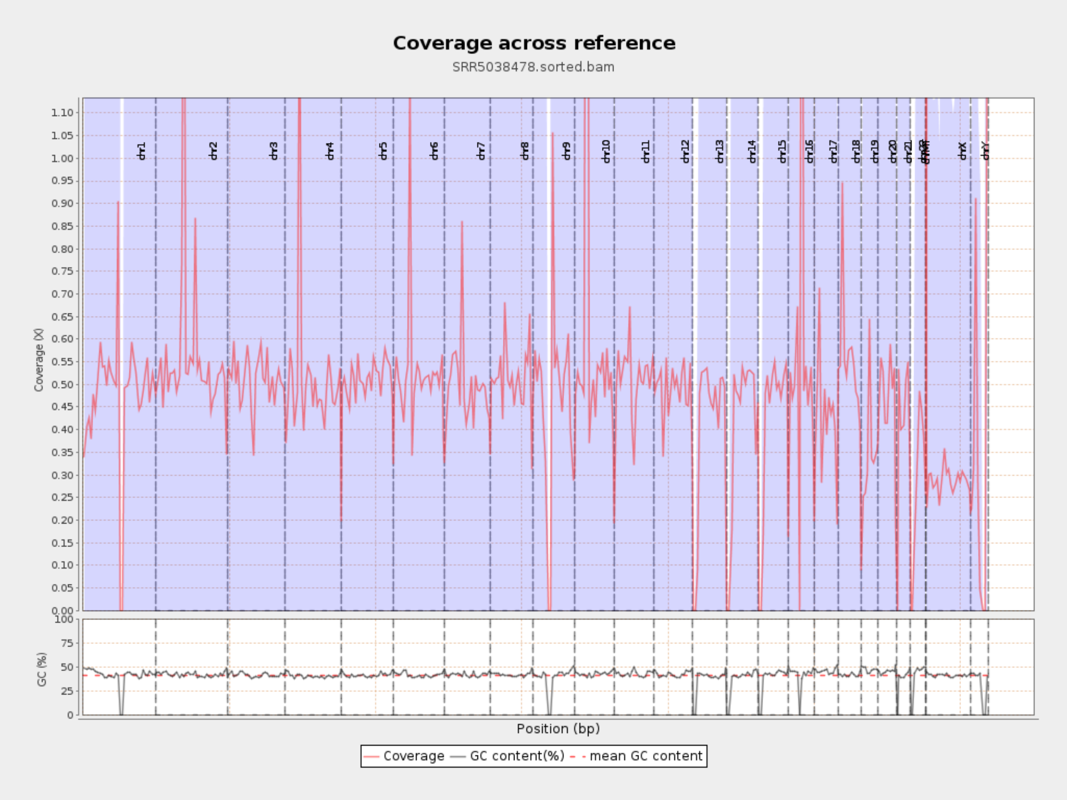
2.7. Chromosome stats

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

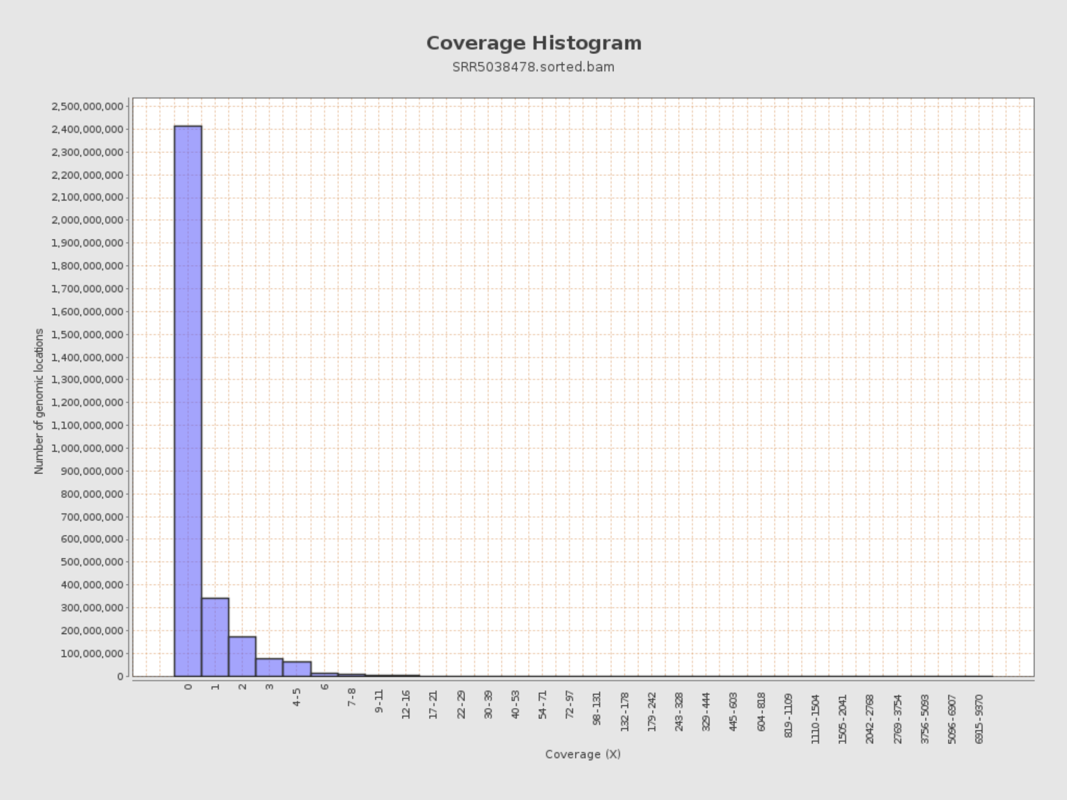
		bases	coverage	deviation
chr1	249250621	118909301	0.4771	7.0381
chr2	243199373	139385980	0.5731	8.2019
chr3	198022430	101215965	0.5111	1.2584
chr4	191154276	99915840	0.5227	6.8655
chr5	180915260	92314603	0.5103	1.3281
chr6	171115067	91120576	0.5325	7.3882
chr7	159138663	79152083	0.4974	6.5603
chr8	146364022	75022902	0.5126	1.8966
chr9	141213431	65924932	0.4668	12.7054
chr10	135534747	85552779	0.6312	19.1797
chr11	135006516	68763670	0.5093	3.8436
chr12	133851895	65586902	0.49	1.2235
chr13	115169878	46667546	0.4052	1.0571
chr14	107349540	43957414	0.4095	1.204
chr15	102531392	41936394	0.409	1.0856
chr16	90354753	54453743	0.6027	12.137
chr17	81195210	35438280	0.4365	4.5855
chr18	78077248	44162533	0.5656	10.7868
chr19	59128983	20196067	0.3416	3.7482
chr20	63025520	30462917	0.4833	2.3316
chr21	48129895	20064653	0.4169	3.2454
chr22	51304566	14442834	0.2815	1.063
chrMT	16571	1870993	112.9077	42.7688
chrX	155270560	44629578	0.2874	1.3522

chrY	59373566	24251728	0.4085	11.6128

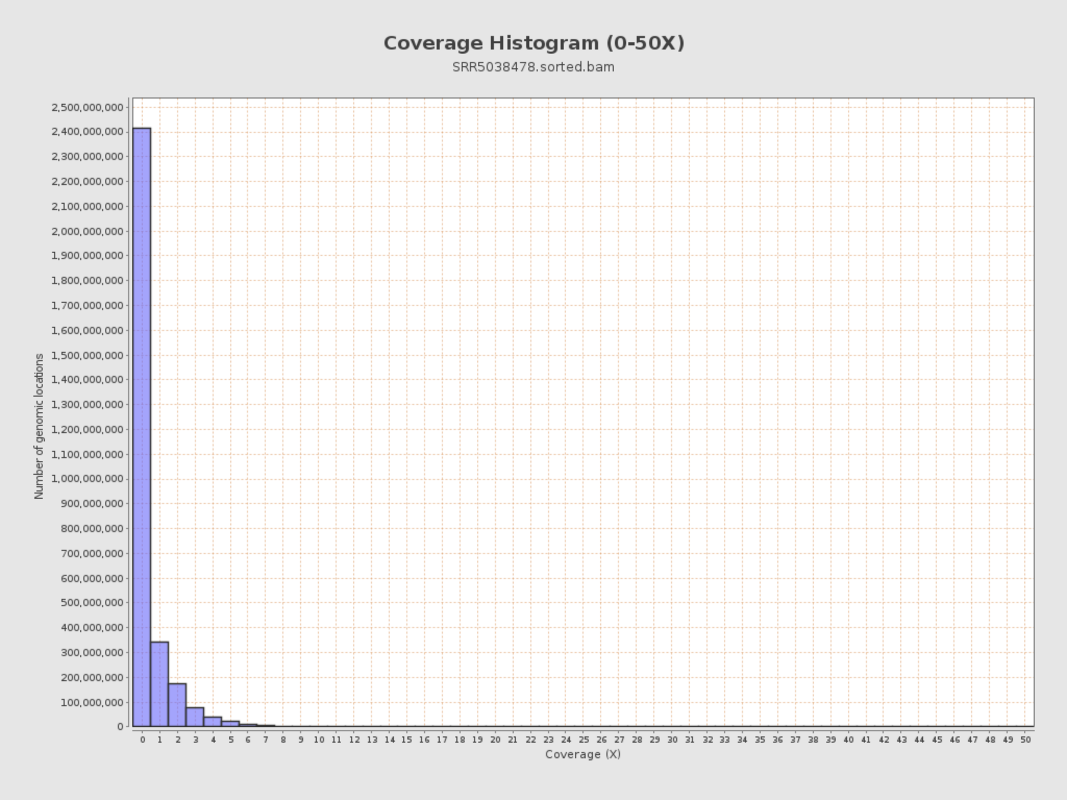
3. Results : Coverage across reference



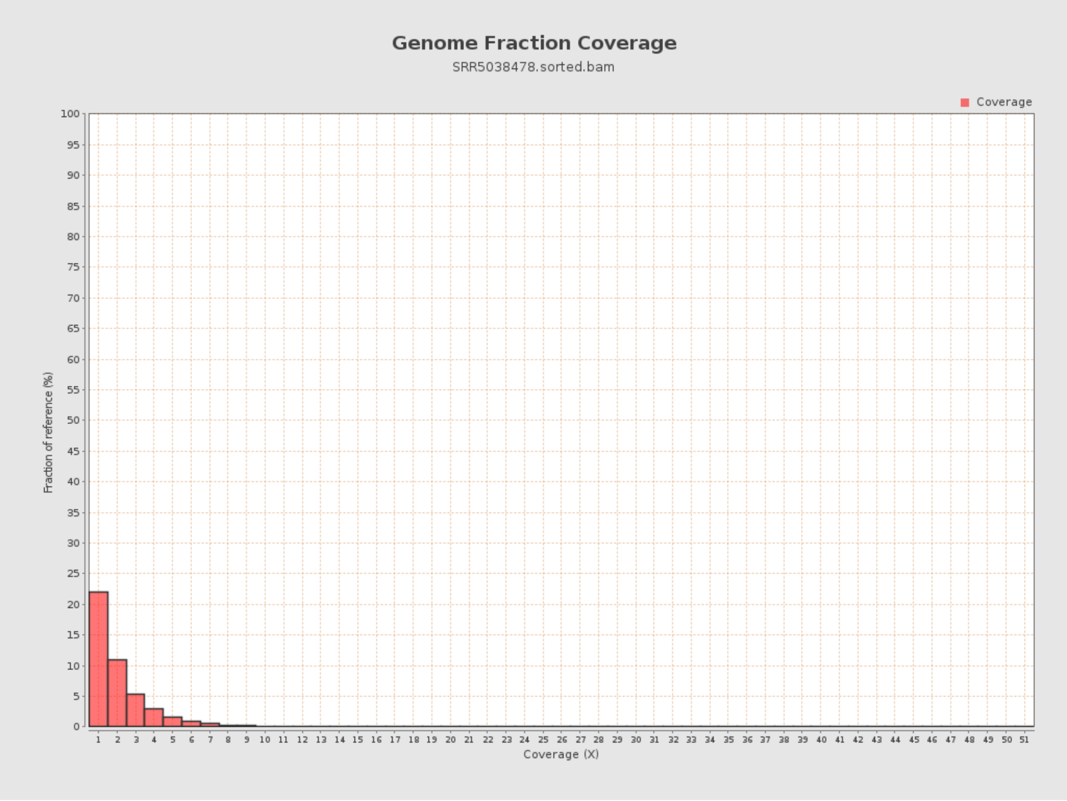
4. Results : Coverage Histogram



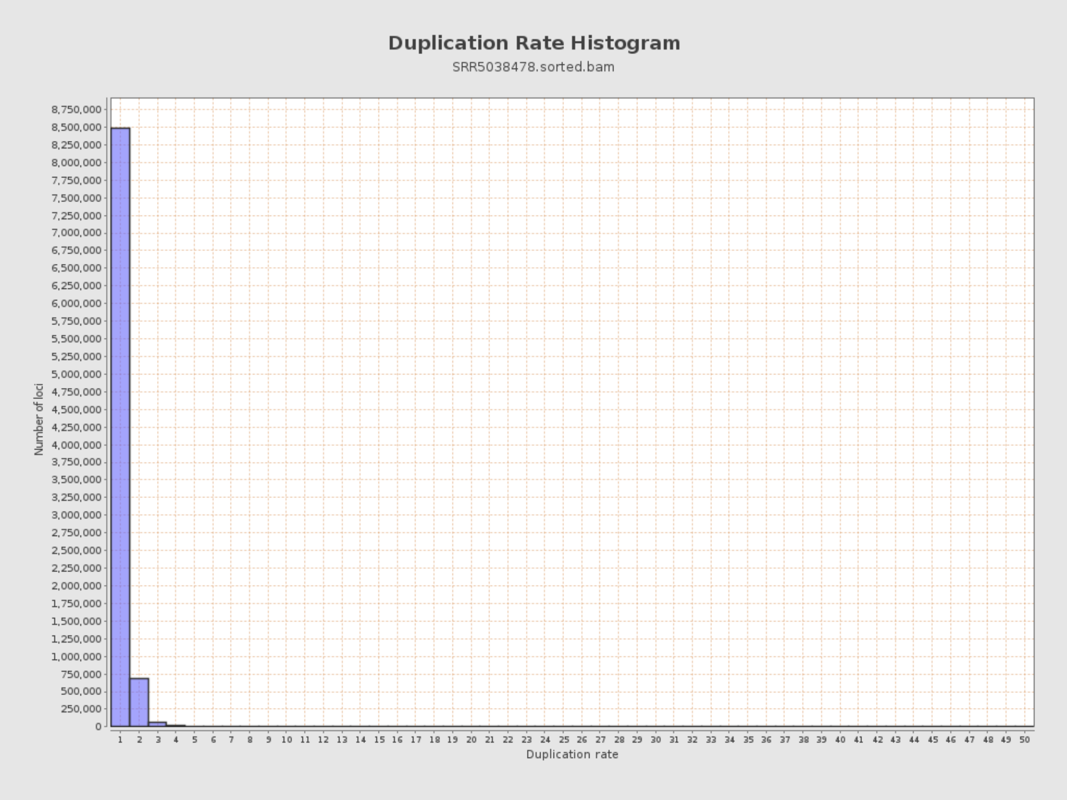
5. Results : Coverage Histogram (0-50X)



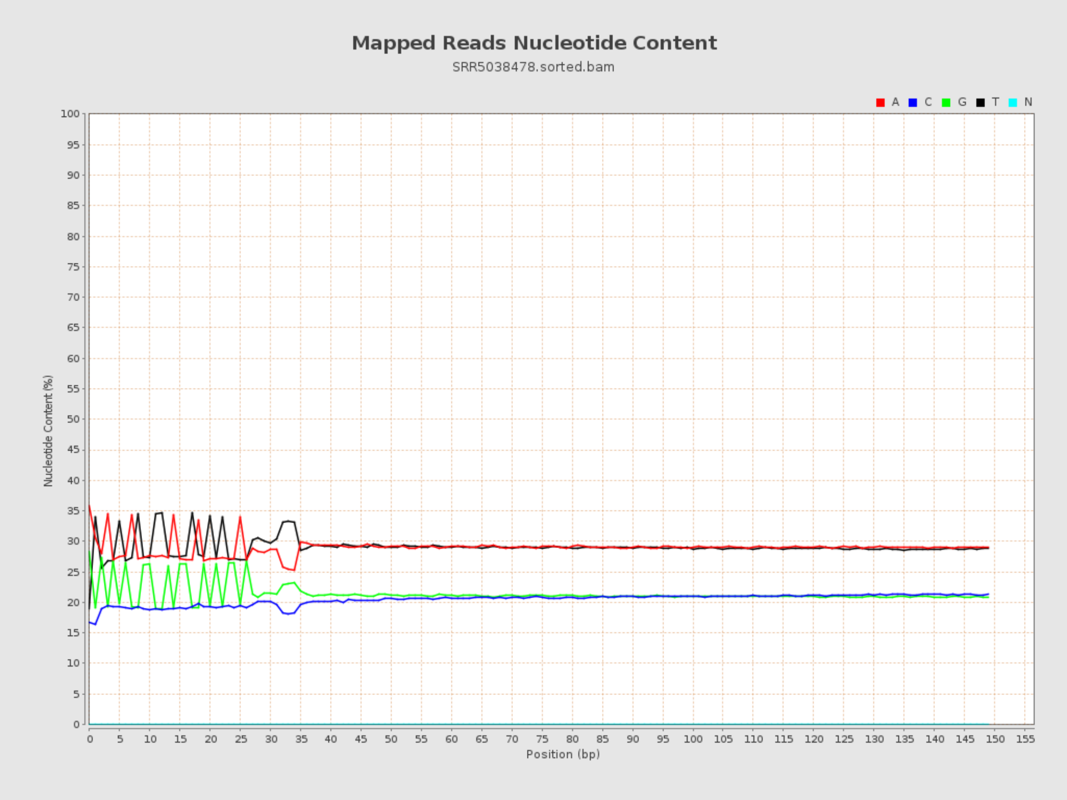
6. Results : Genome Fraction Coverage



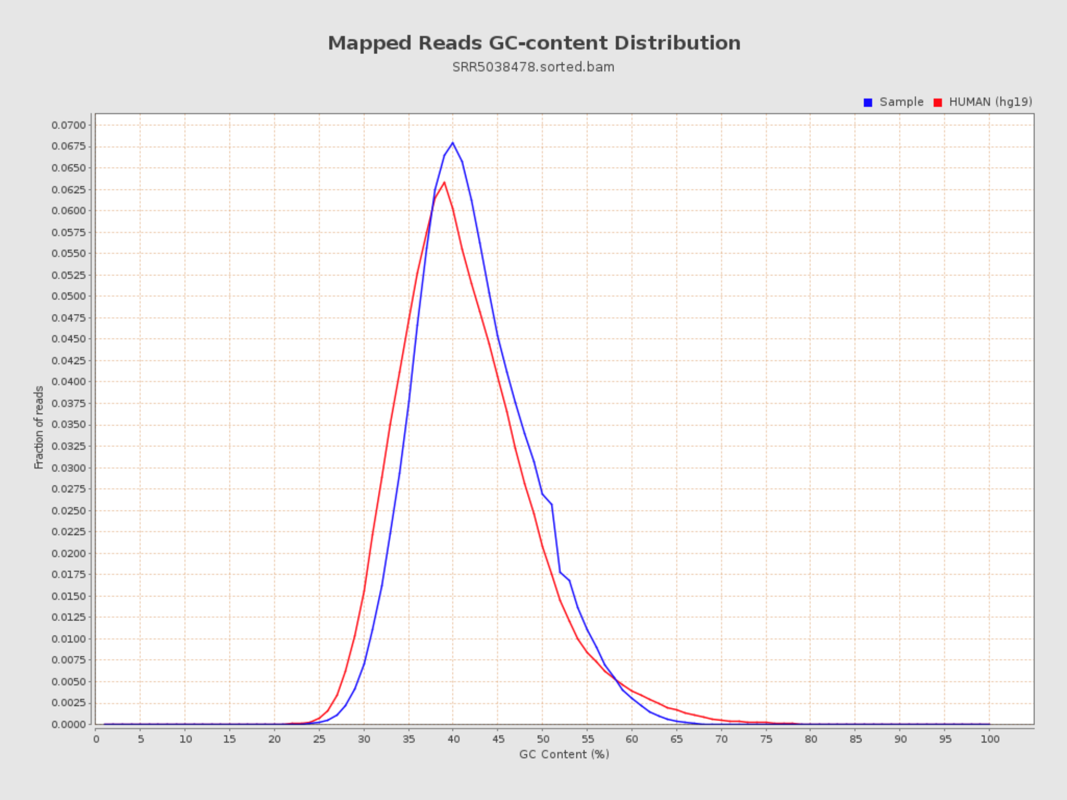
7. Results : Duplication Rate Histogram



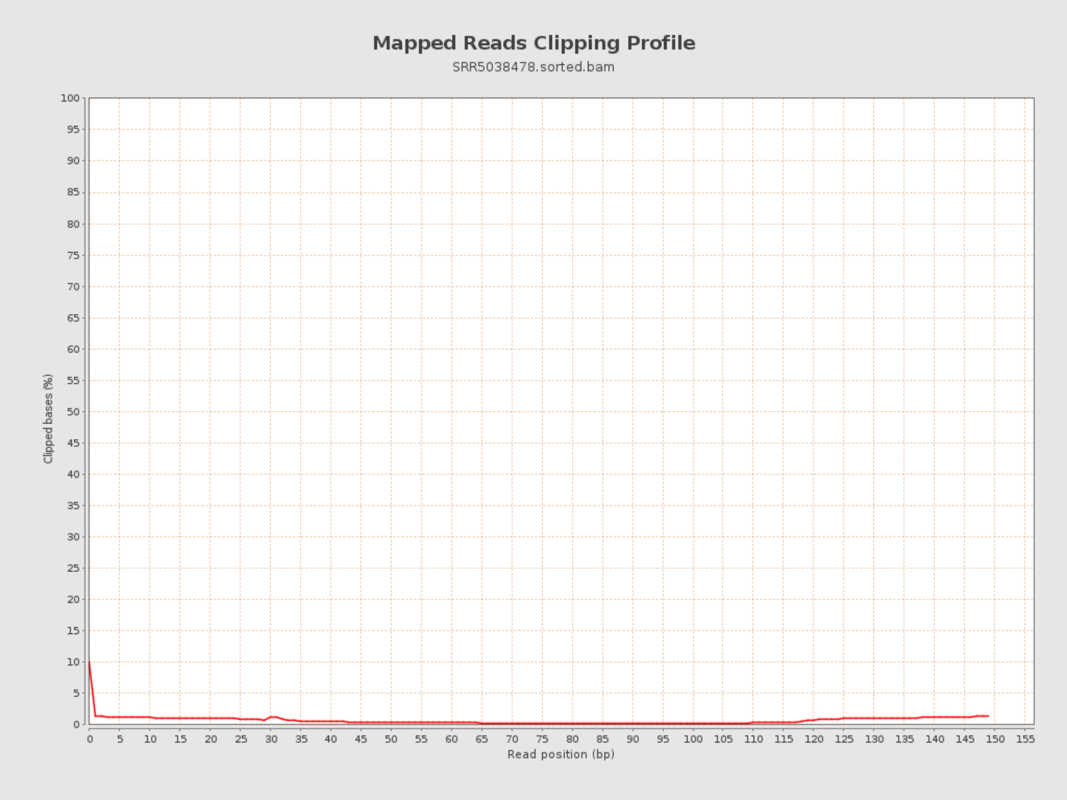
8. Results : Mapped Reads Nucleotide Content



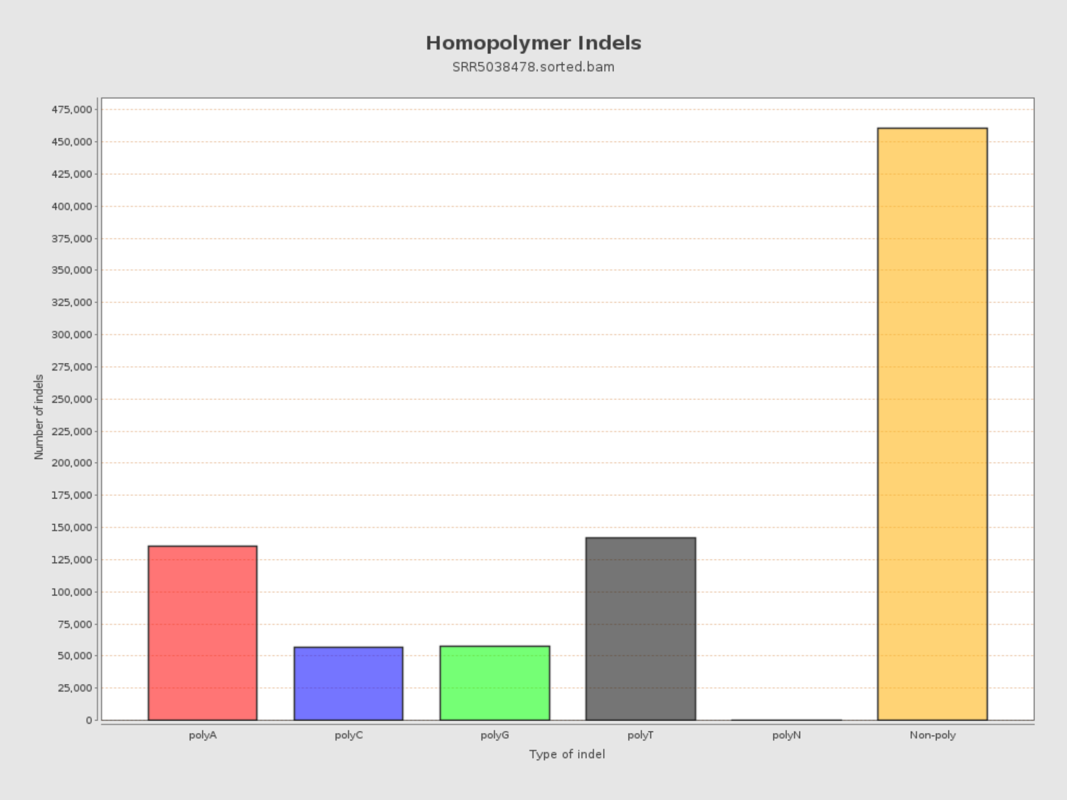
9. Results : Mapped Reads GC-content Distribution



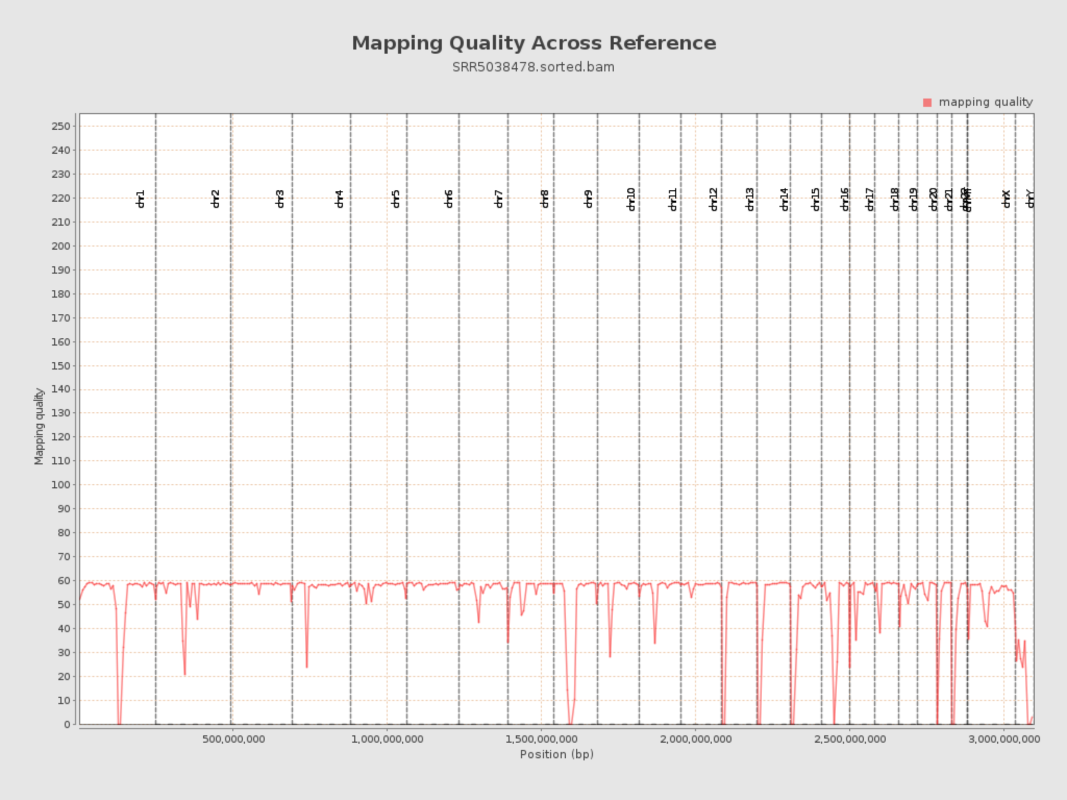
10. Results : Mapped Reads Clipping Profile



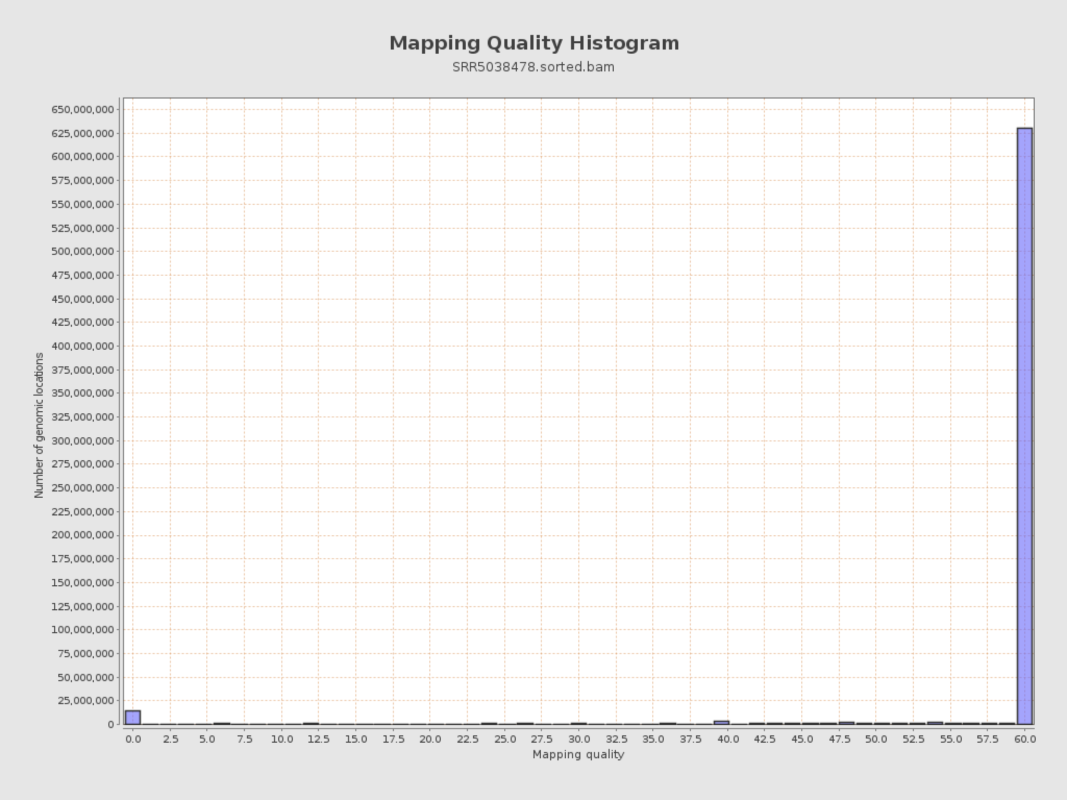
11. Results : Homopolymer Indels



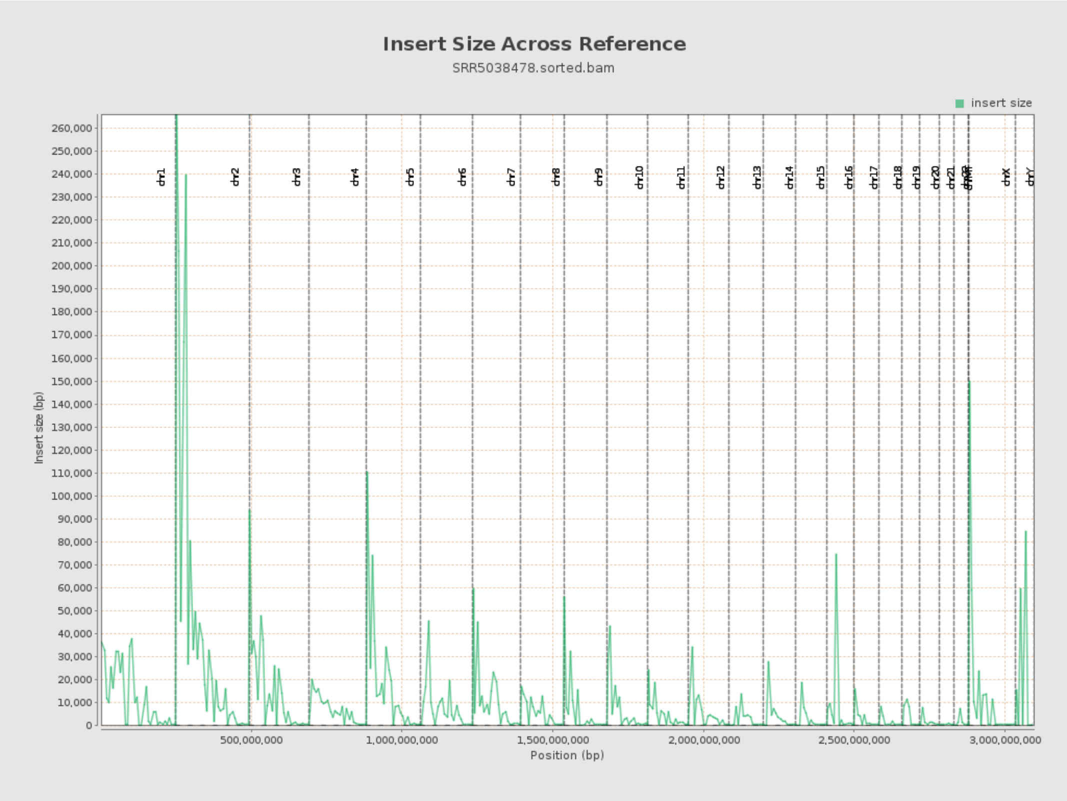
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram