Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 11:34:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038392.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_SRR5038392 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038392_1.fastq.gz SRR5038392_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 11:34:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038392.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,770,586
Mapped reads	18,180,902 / 96.86%
Unmapped reads	589,684 / 3.14%
Mapped paired reads	18,180,902 / 96.86%
Mapped reads, first in pair	9,184,398 / 48.93%
Mapped reads, second in pair	8,996,504 / 47.93%
Mapped reads, both in pair	17,955,174 / 95.66%
Mapped reads, singletons	225,728 / 1.2%
Secondary alignments	0
Supplementary alignments	217,235 / 1.16%
Read min/max/mean length	30 / 150 / 150.58
Duplicated reads (estimated)	3,410,143 / 18.17%
Duplication rate	14.59%
Clipped reads	7,937,050 / 42.28%

2.2. ACGT Content

Number/percentage of A's	685,467,433 / 27.67%
Number/percentage of C's	520,846,771 / 21.03%
Number/percentage of T's	693,088,609 / 27.98%
Number/percentage of G's	577,437,245 / 23.31%
Number/percentage of N's	205,523 / 0.01%

GC Percentage	44.34%

2.3. Coverage

Mean	0.8007
Standard Deviation	6.8813

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	66,448.61
Standard Deviation	2,583,309.85
P25/Median/P75	184 / 230 / 289

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	28,124,256
Insertions	355,332
Mapped reads with at least one insertion	1.87%
Deletions	811,571
Mapped reads with at least one deletion	4.32%
Homopolymer indels	48.17%

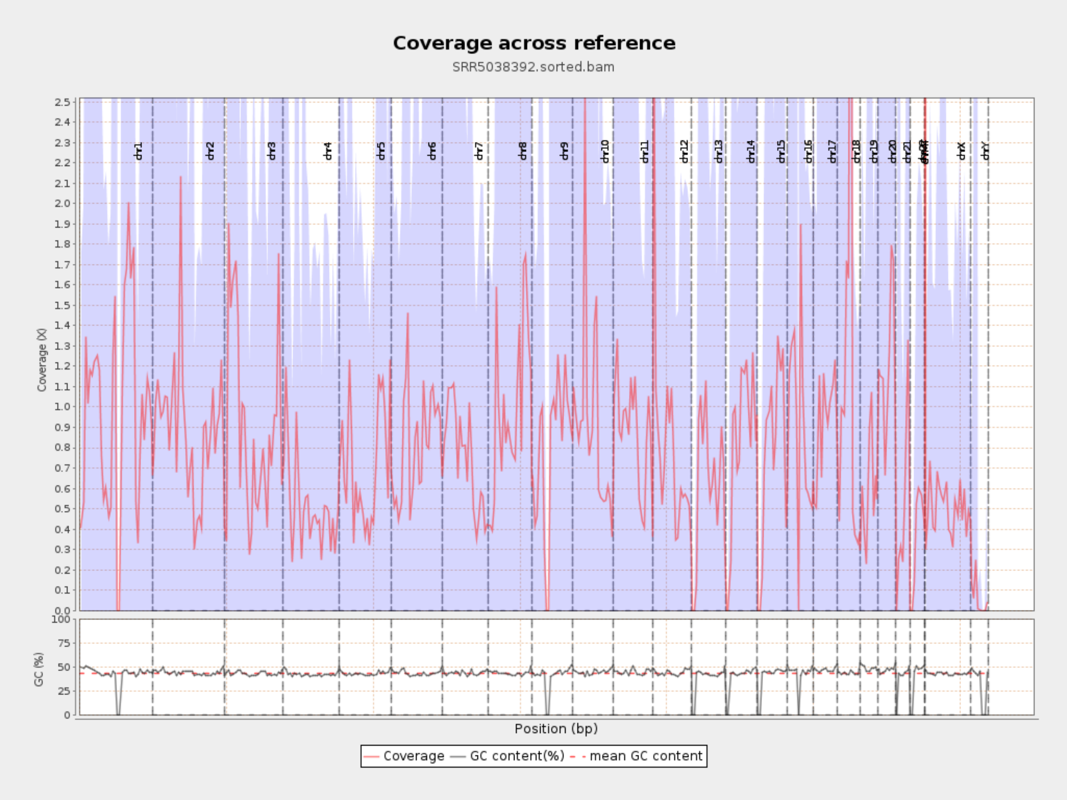
2.7. Chromosome stats

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

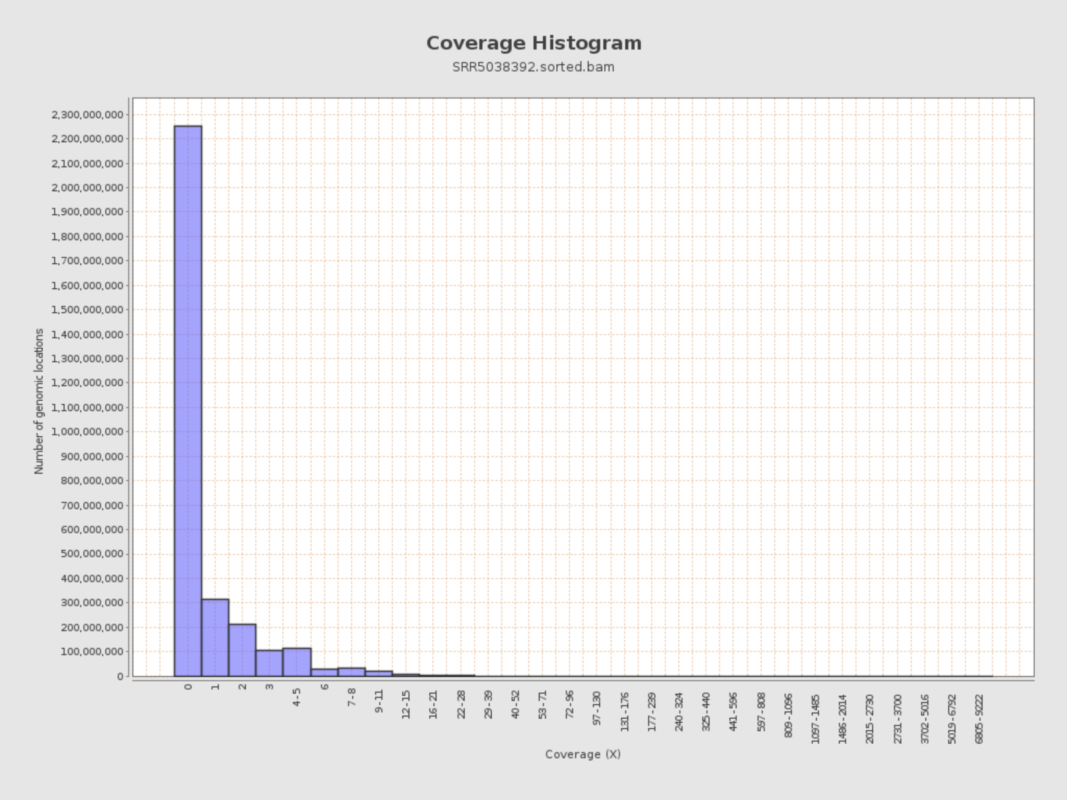
		bases	coverage	deviation
chr1	249250621	244402877	0.9806	9.447
chr2	243199373	219472441	0.9024	8.3252
chr3	198022430	180501872	0.9115	2.0859
chr4	191154276	97532595	0.5102	5.3939
chr5	180915260	129106512	0.7136	1.7044
chr6	171115067	142170968	0.8309	5.9933
chr7	159138663	118606964	0.7453	6.7884
chr8	146364022	146349538	0.9999	3.2283
chr9	141213431	109697235	0.7768	11.2127
chr10	135534747	126738392	0.9351	16.4648
chr11	135006516	119884630	0.888	6.2727
chr12	133851895	110095487	0.8225	2.0954
chr13	115169878	73305015	0.6365	1.609
chr14	107349540	86910636	0.8096	1.9198
chr15	102531392	78015721	0.7609	1.8585
chr16	90354753	80398187	0.8898	7.2061
chr17	81195210	75181358	0.9259	9.9677
chr18	78077248	99685373	1.2768	8.6436
chr19	59128983	35533242	0.6009	4.2472
chr20	63025520	76832025	1.2191	2.863
chr21	48129895	25455438	0.5289	2.8632
chr22	51304566	18593890	0.3624	1.1949
chrMT	16571	2959027	178.5666	118.7597
chrX	155270560	77696168	0.5004	1.8464

chrY	59373566	3446927	0.0581	5.8379

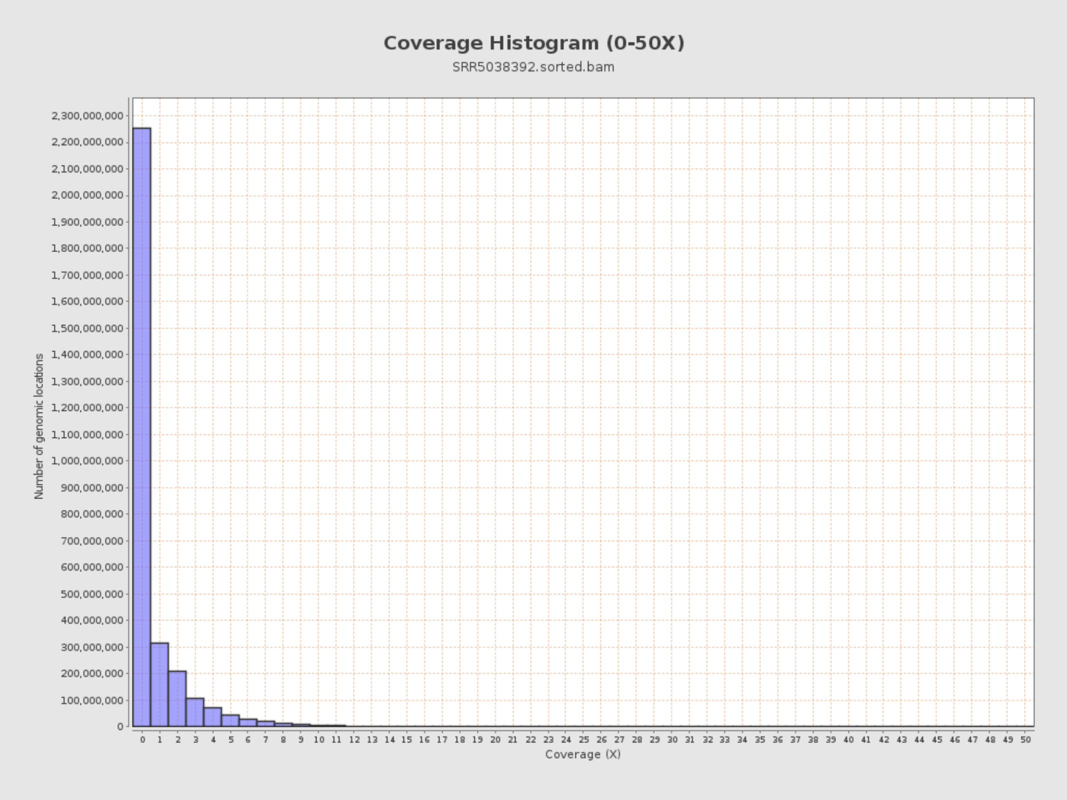
3. Results : Coverage across reference



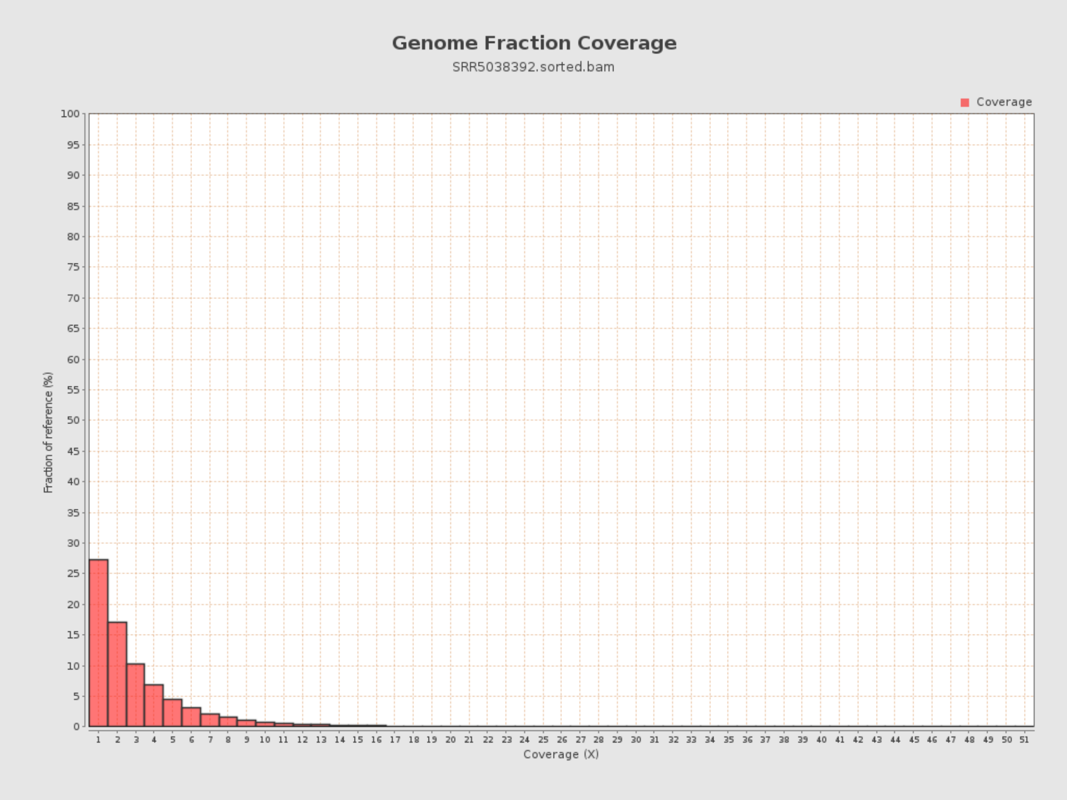
4. Results : Coverage Histogram



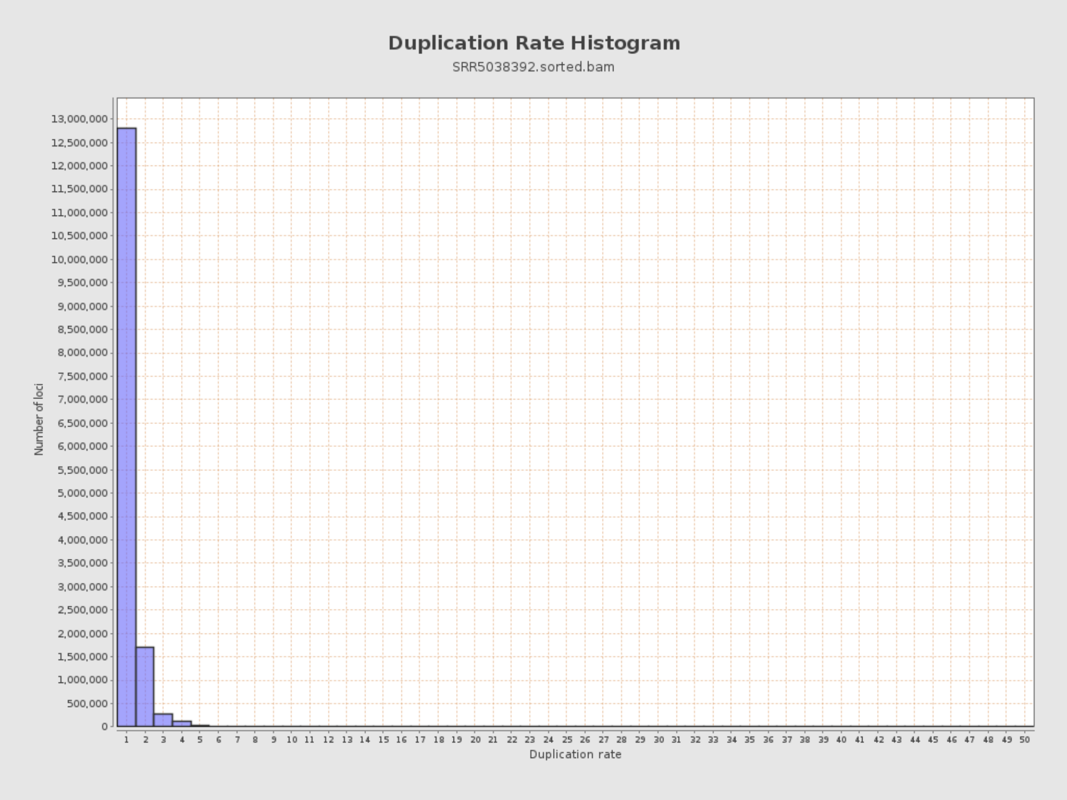
5. Results : Coverage Histogram (0-50X)



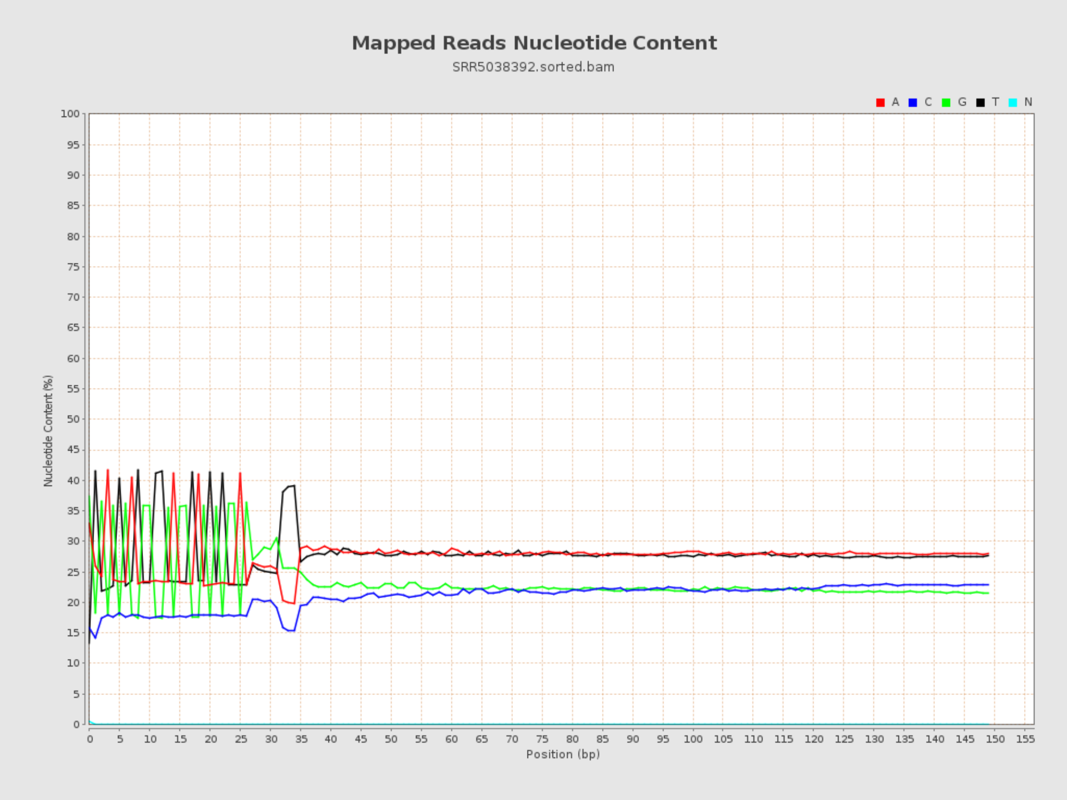
6. Results : Genome Fraction Coverage



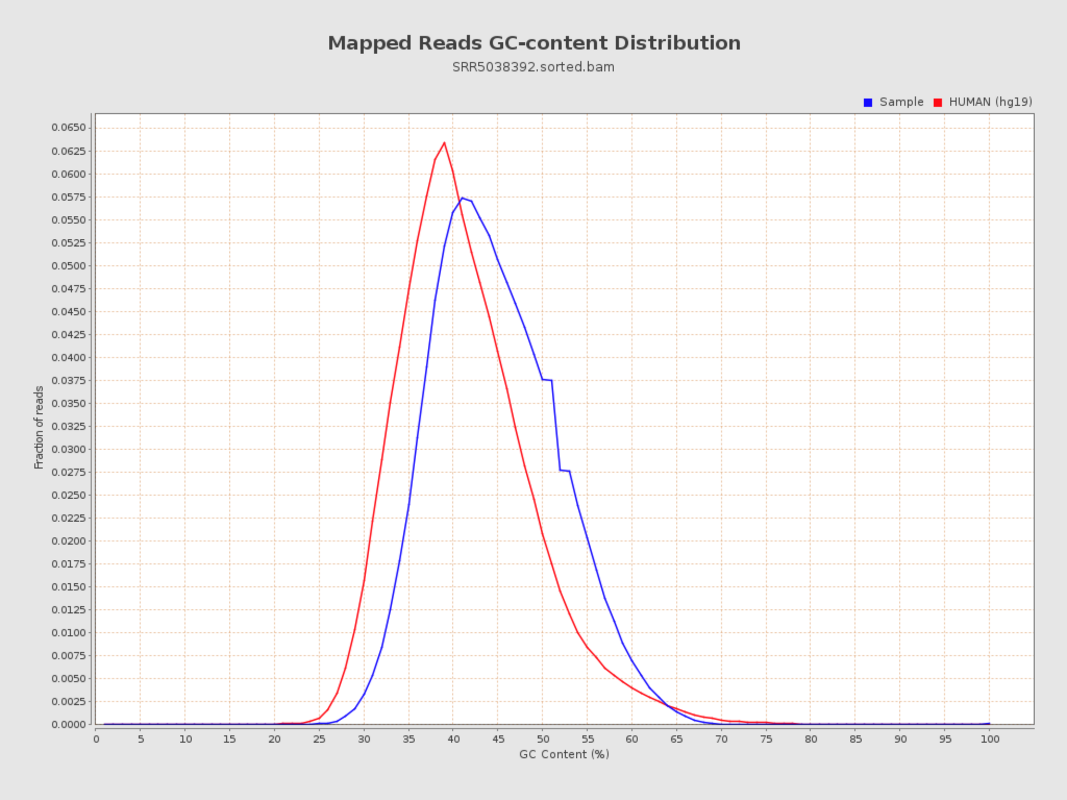
7. Results : Duplication Rate Histogram



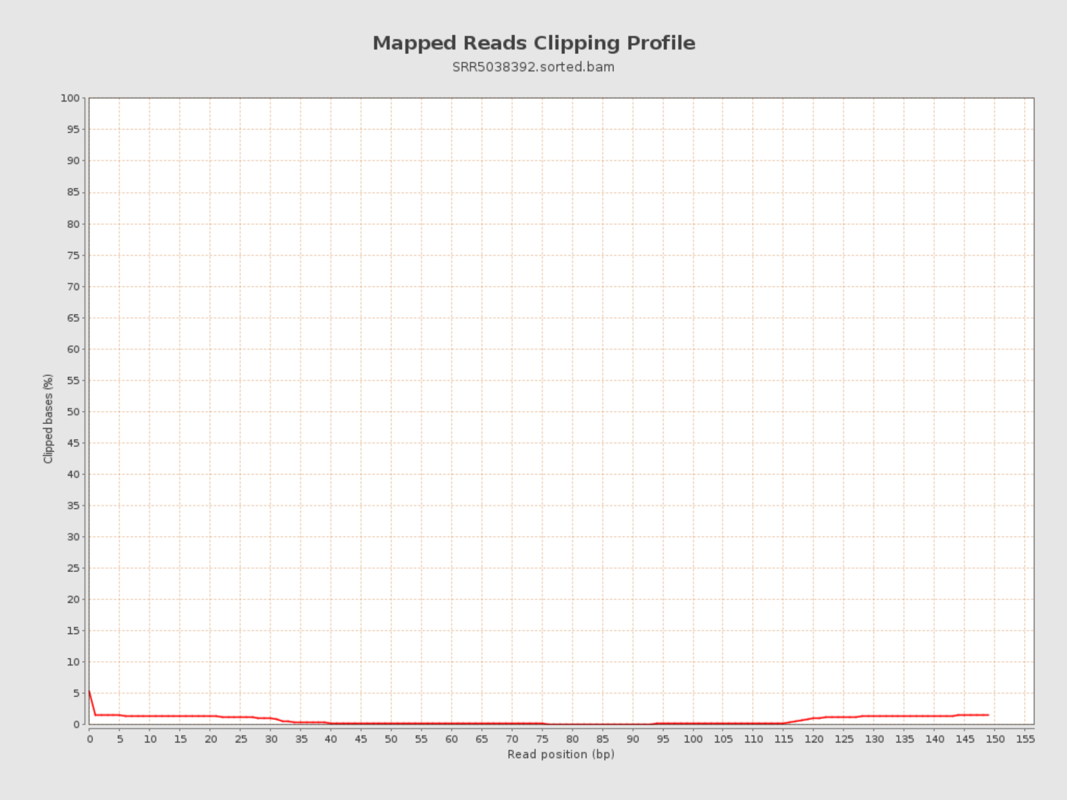
8. Results : Mapped Reads Nucleotide Content



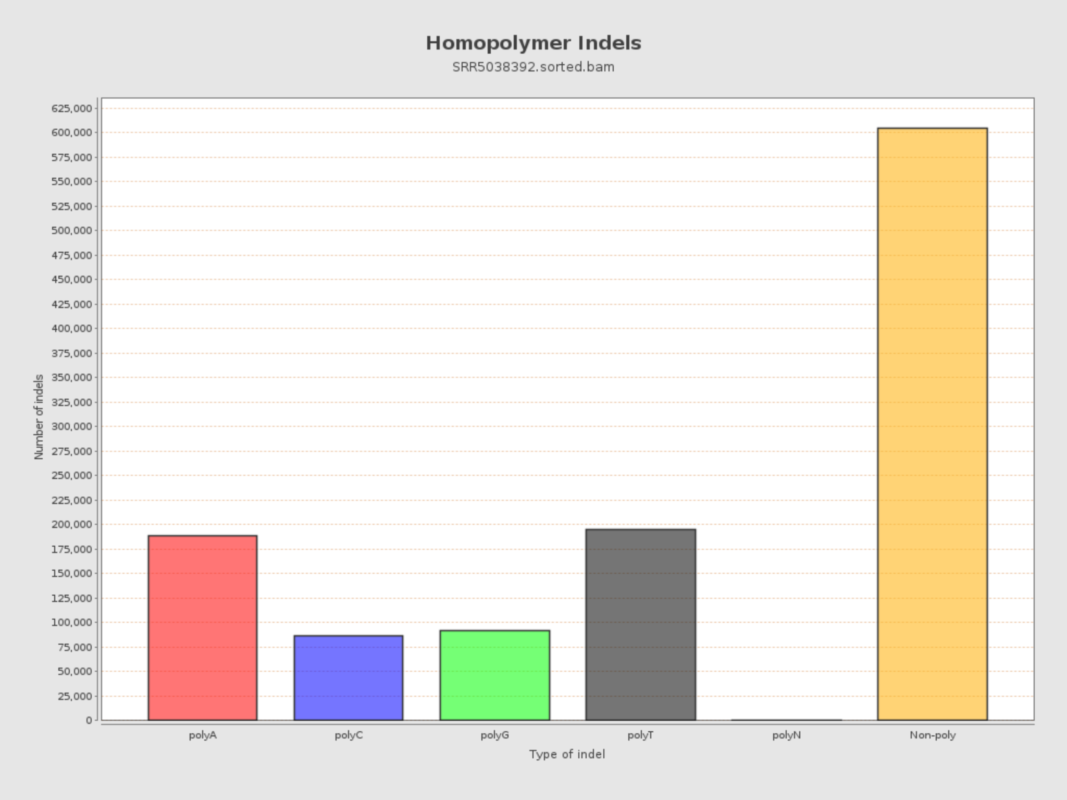
9. Results : Mapped Reads GC-content Distribution



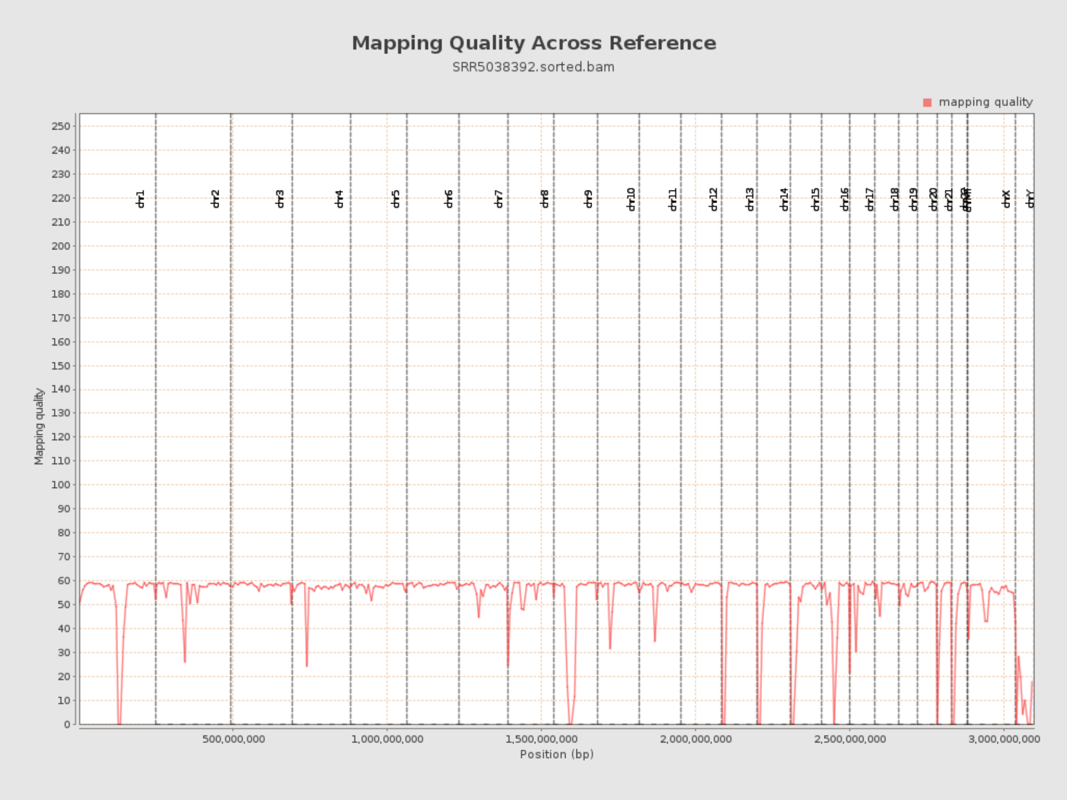
10. Results : Mapped Reads Clipping Profile



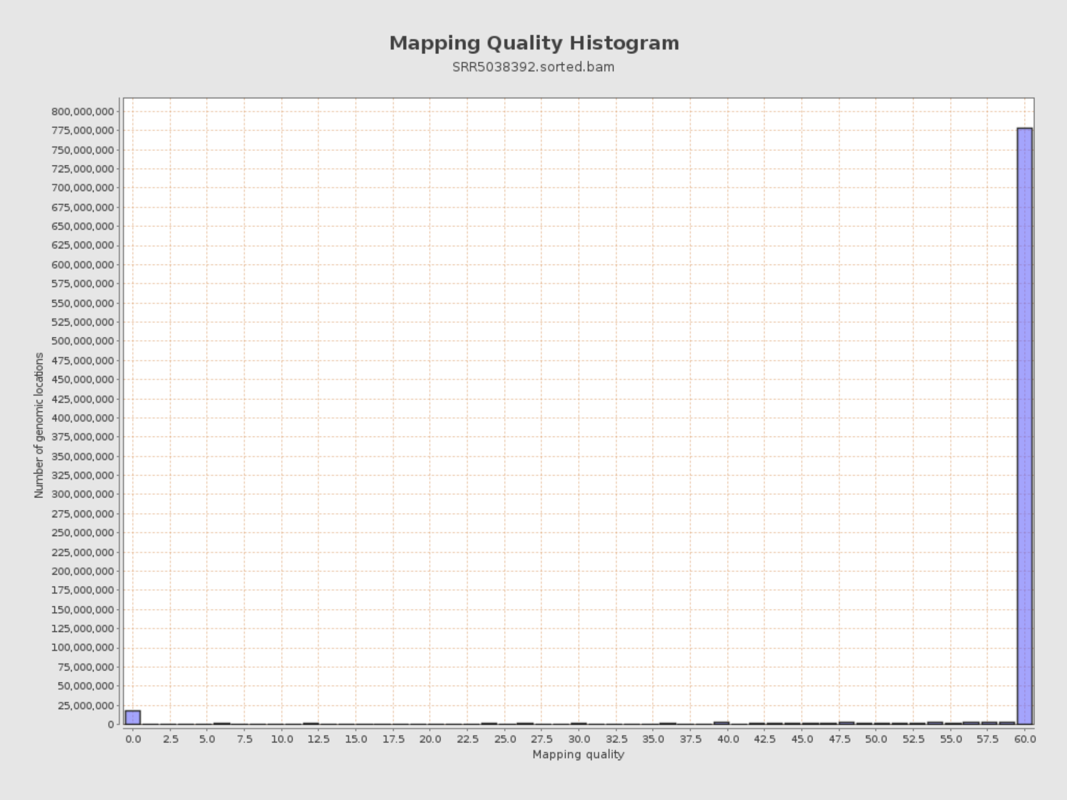
11. Results : Homopolymer Indels



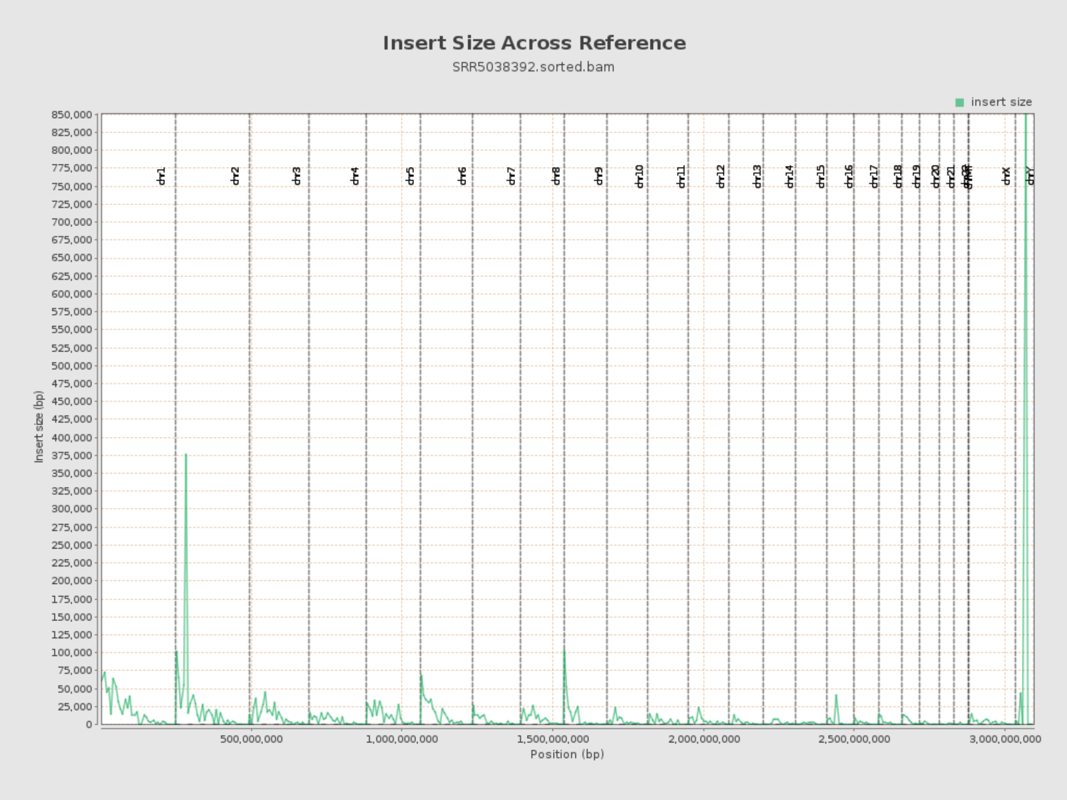
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram