

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 13:55:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038398.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_SRR5038398 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038398_1.fastq.gz SRR5038398_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 13:55:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038398.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,327,614
Mapped reads	14,027,601 / 97.91%
Unmapped reads	300,013 / 2.09%
Mapped paired reads	14,027,601 / 97.91%
Mapped reads, first in pair	7,073,277 / 49.37%
Mapped reads, second in pair	6,954,324 / 48.54%
Mapped reads, both in pair	13,893,284 / 96.97%
Mapped reads, singletons	134,317 / 0.94%
Secondary alignments	0
Supplementary alignments	219,715 / 1.53%
Read min/max/mean length	30 / 150 / 150.8
Duplicated reads (estimated)	2,038,301 / 14.23%
Duplication rate	9.38%
Clipped reads	2,829,809 / 19.75%

2.2. ACGT Content

Number/percentage of A's	595,895,495 / 29.43%
Number/percentage of C's	411,973,754 / 20.35%
Number/percentage of T's	593,873,411 / 29.33%
Number/percentage of G's	422,778,921 / 20.88%
Number/percentage of N's	44,325 / 0%

GC Percentage	41.23%
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2.3. Coverage

Mean	0.6544
Standard Deviation	9.5682

2.4. Mapping Quality

Mean Mapping Quality	53.78
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2.5. Insert size

Mean	74,071.77
Standard Deviation	2,541,088.32
P25/Median/P75	209 / 255 / 313

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	27,311,916
Insertions	355,819
Mapped reads with at least one insertion	2.41%
Deletions	713,399
Mapped reads with at least one deletion	4.9%
Homopolymer indels	48.06%

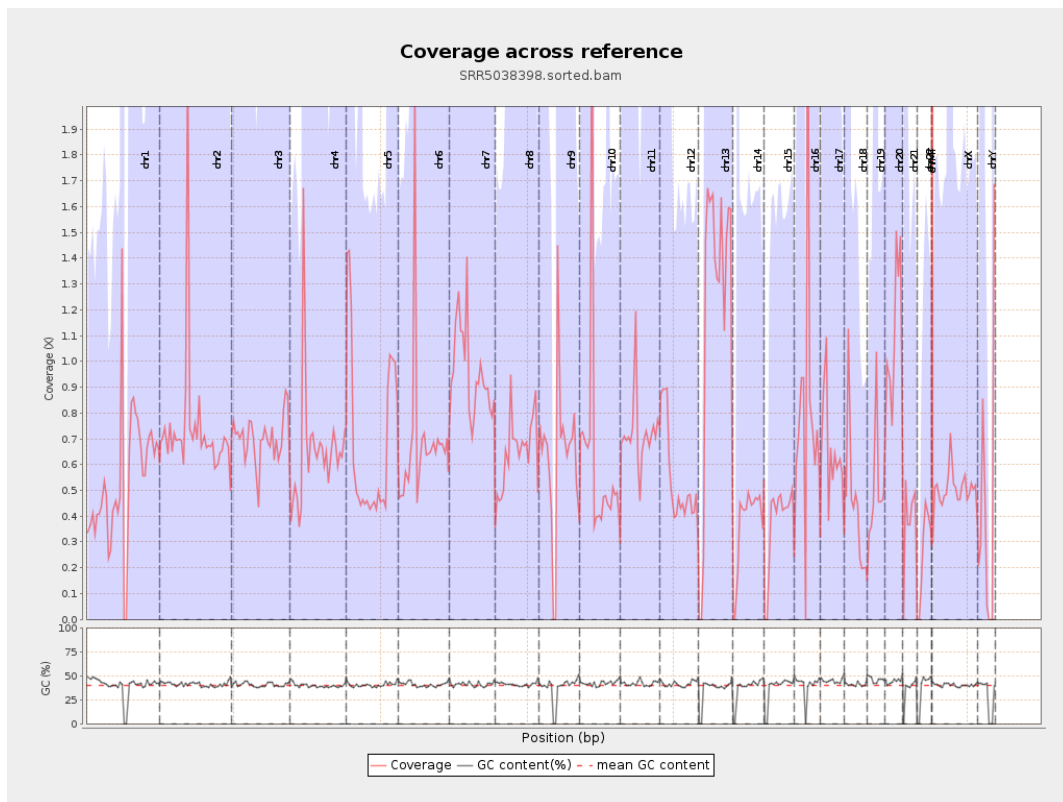
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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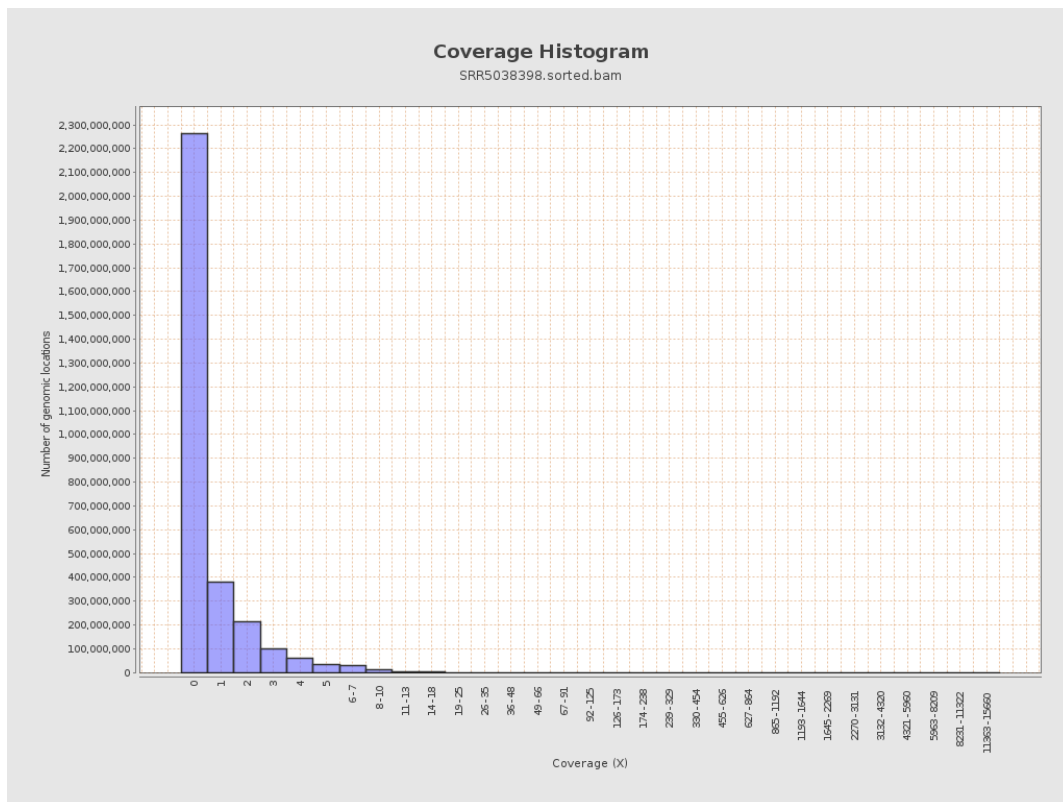
		bases	coverage	deviation
chr1	249250621	134386808	0.5392	15.8612
chr2	243199373	180067737	0.7404	8.9017
chr3	198022430	139150179	0.7027	1.4718
chr4	191154276	123480878	0.646	7.6848
chr5	180915260	124321211	0.6872	1.6005
chr6	171115067	117911064	0.6891	15.0857
chr7	159138663	152025623	0.9553	10.9538
chr8	146364022	95638148	0.6534	2.6445
chr9	141213431	87371497	0.6187	16.5244
chr10	135534747	85535531	0.6311	14.445
chr11	135006516	95655712	0.7085	8.684
chr12	133851895	73746178	0.551	1.3534
chr13	115169878	141739329	1.2307	2.25
chr14	107349540	39807732	0.3708	1.1999
chr15	102531392	38078464	0.3714	1.0179
chr16	90354753	73265382	0.8109	12.2418
chr17	81195210	52284941	0.6439	10.1225
chr18	78077248	34541362	0.4424	13.5676
chr19	59128983	28943166	0.4895	9.3645
chr20	63025520	68870148	1.0927	3.0777
chr21	48129895	18647617	0.3874	3.5522
chr22	51304566	13529595	0.2637	0.8849
chrMT	16571	1699365	102.5505	73.9539
chrX	155270560	77922069	0.5018	2.4318

chrY	59373566	27326527	0.4602	11.7011
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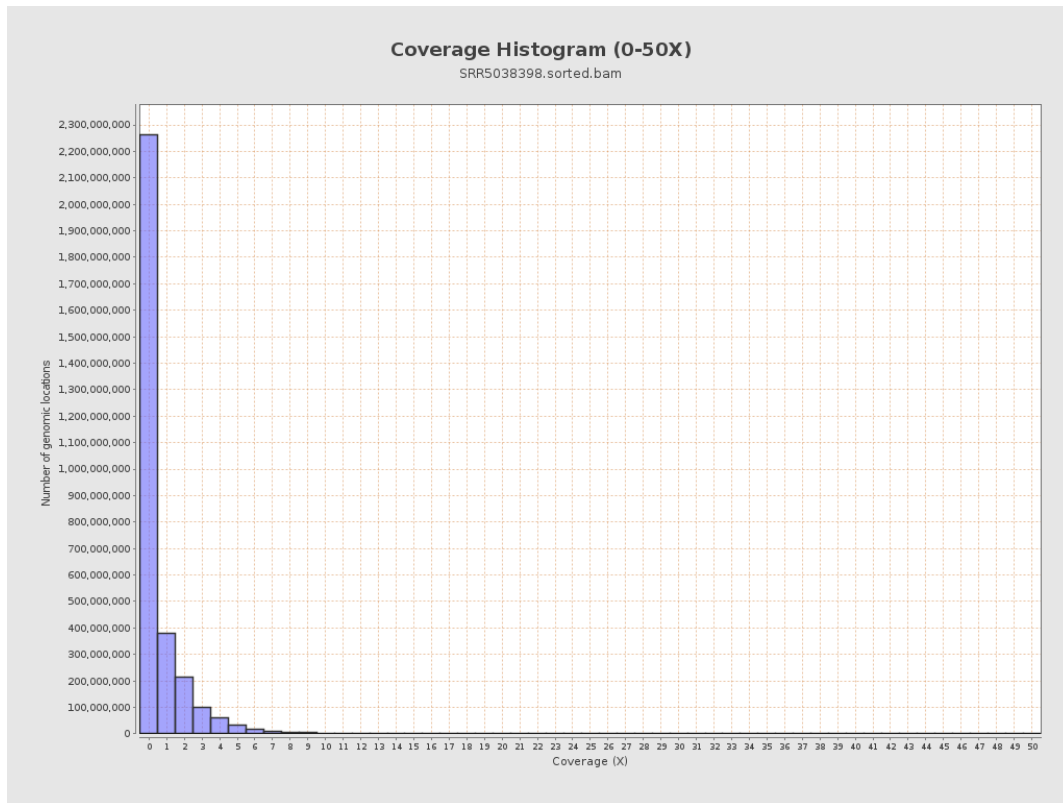
3. Results : Coverage across reference



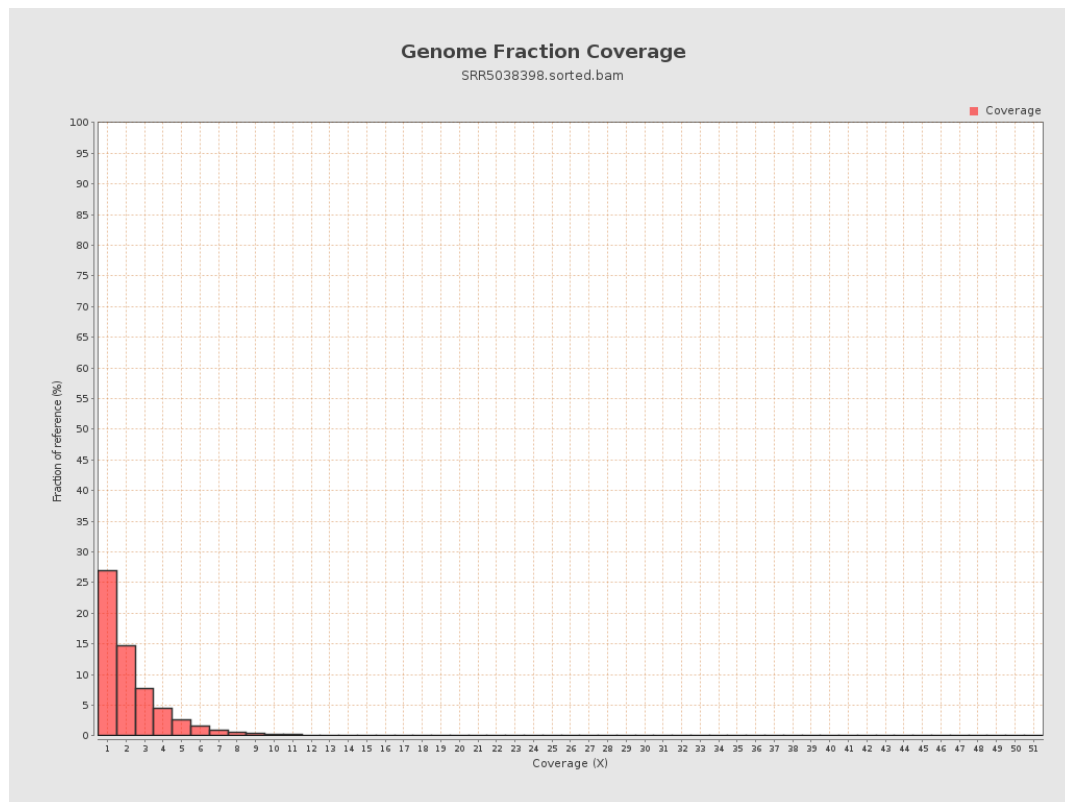
4. Results : Coverage Histogram



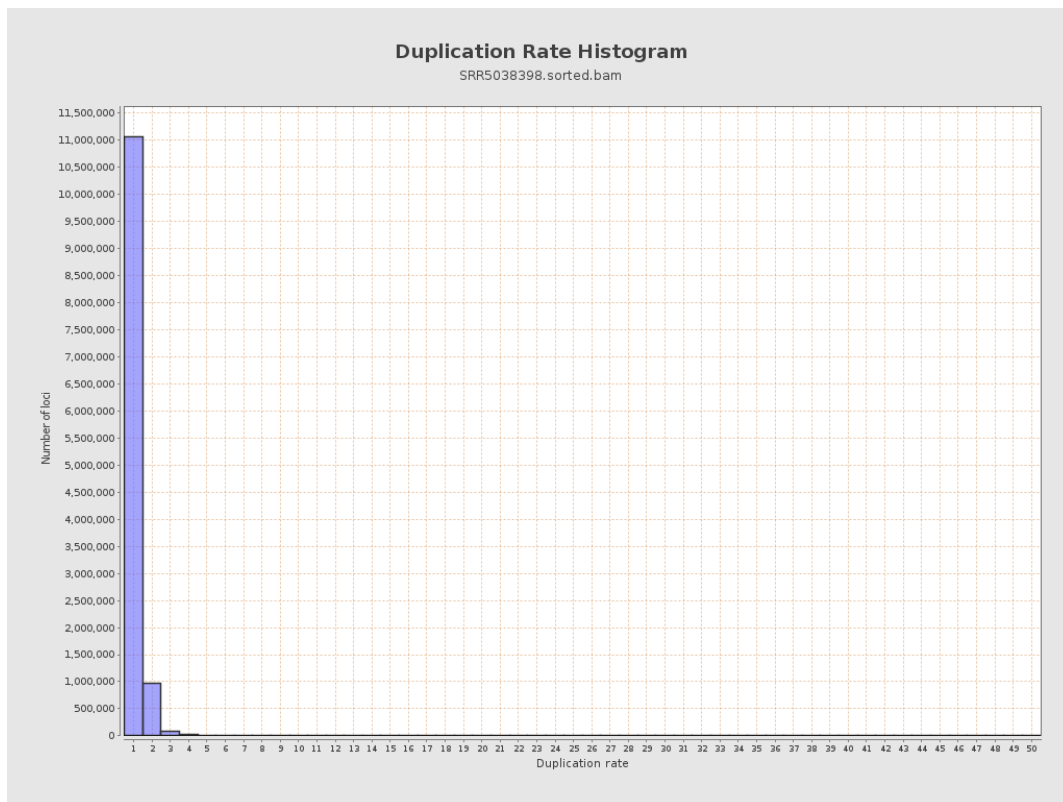
5. Results : Coverage Histogram (0-50X)



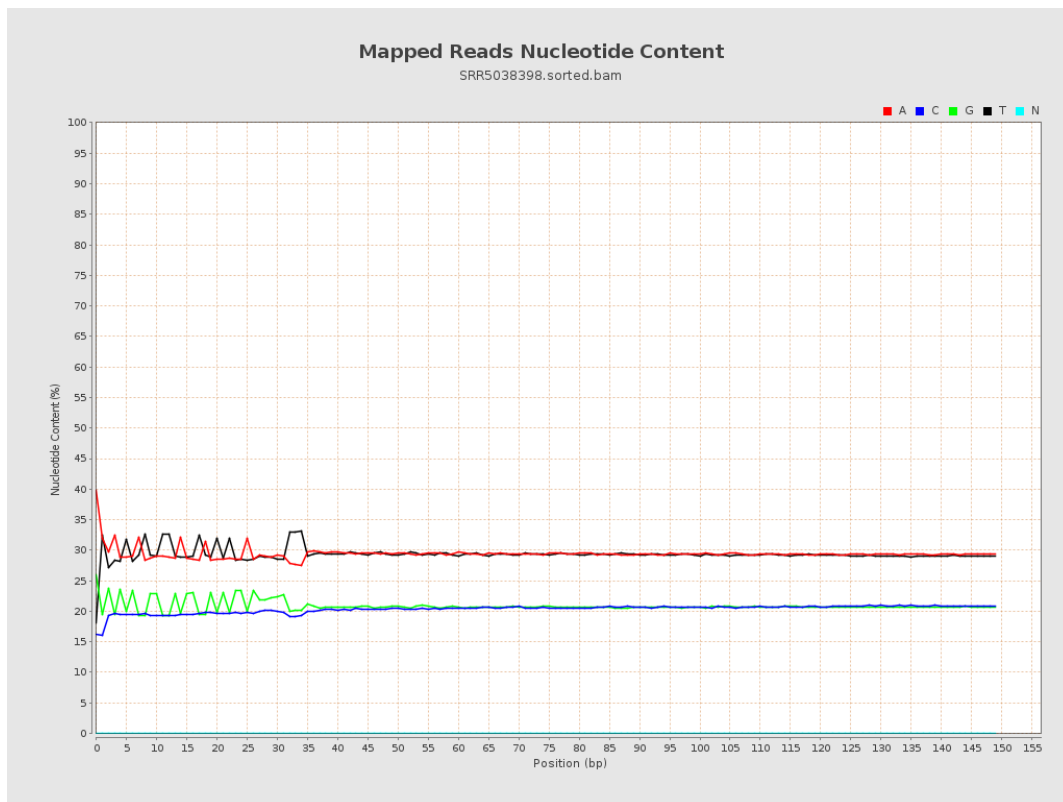
6. Results : Genome Fraction Coverage



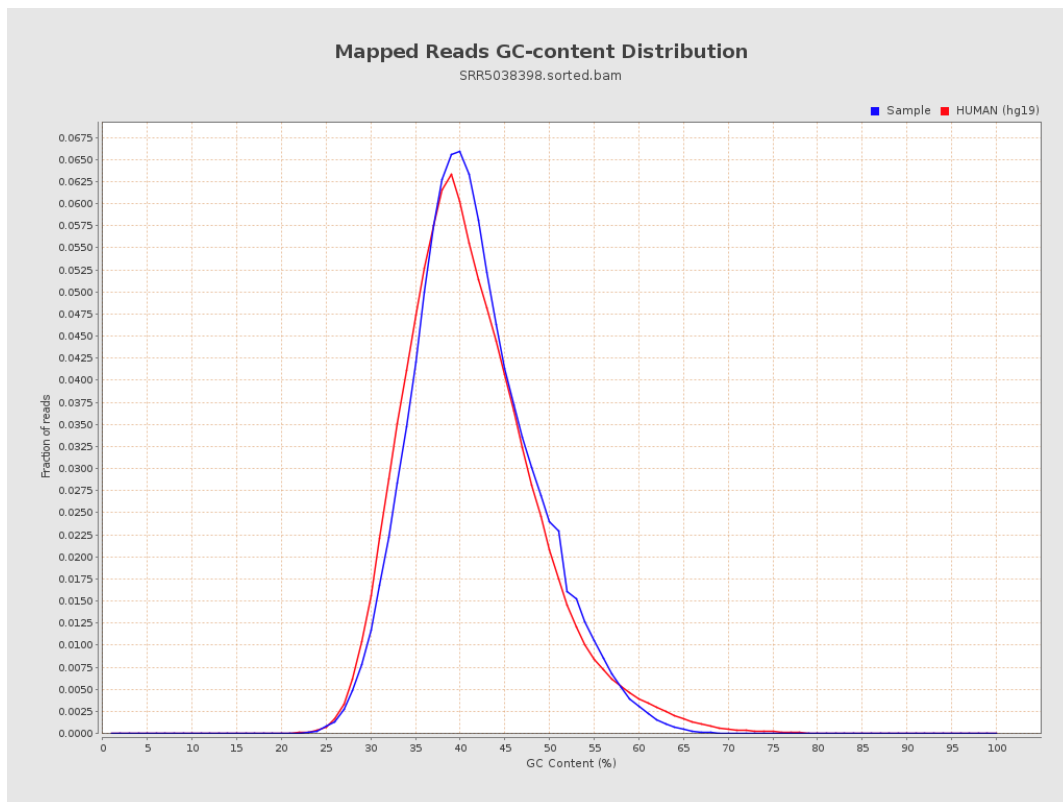
7. Results : Duplication Rate Histogram



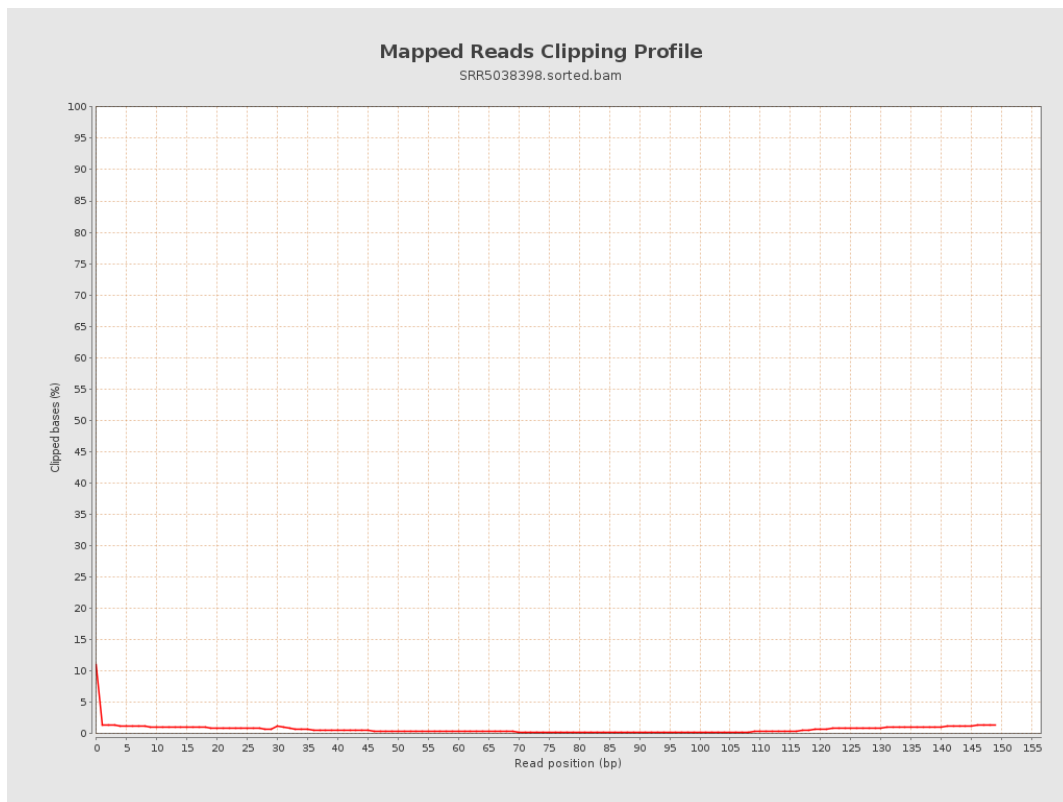
8. Results : Mapped Reads Nucleotide Content



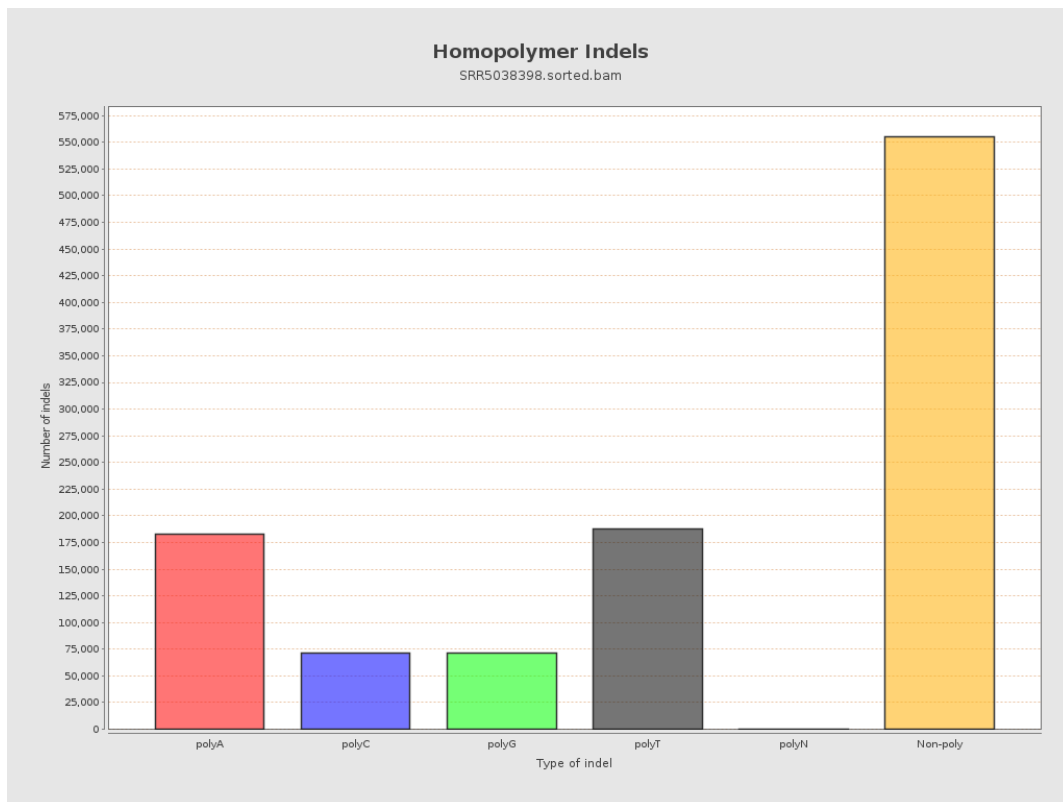
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



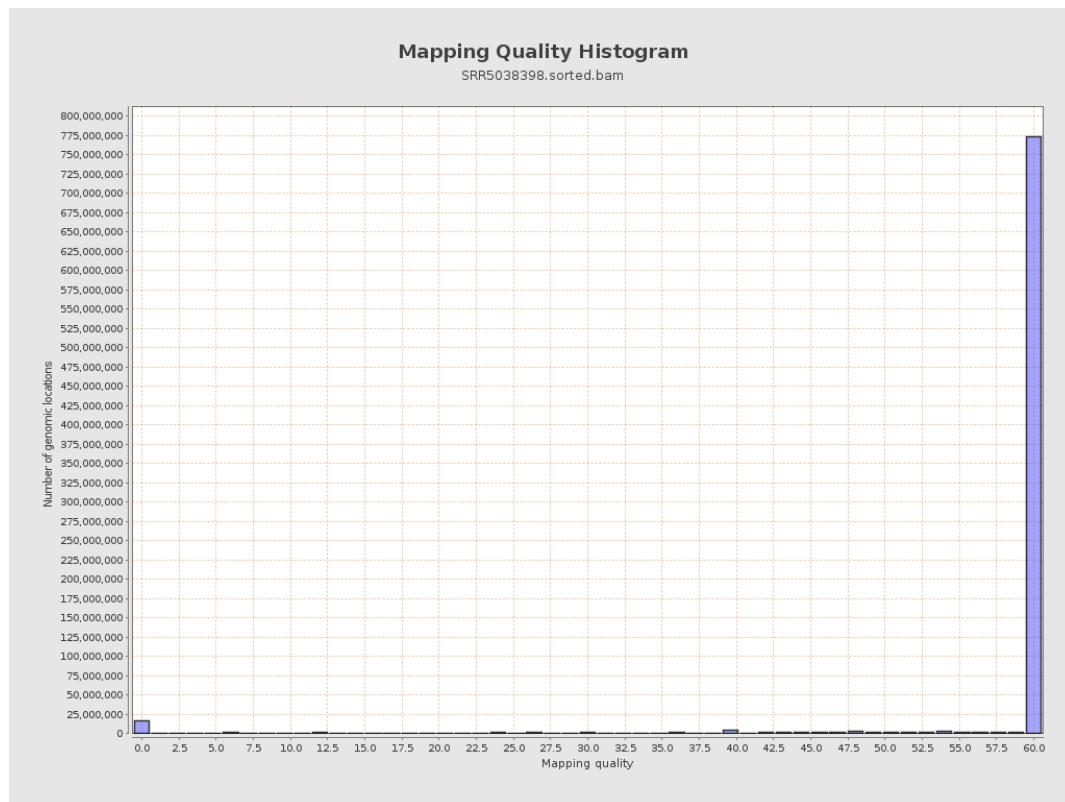
11. Results : Homopolymer Indels



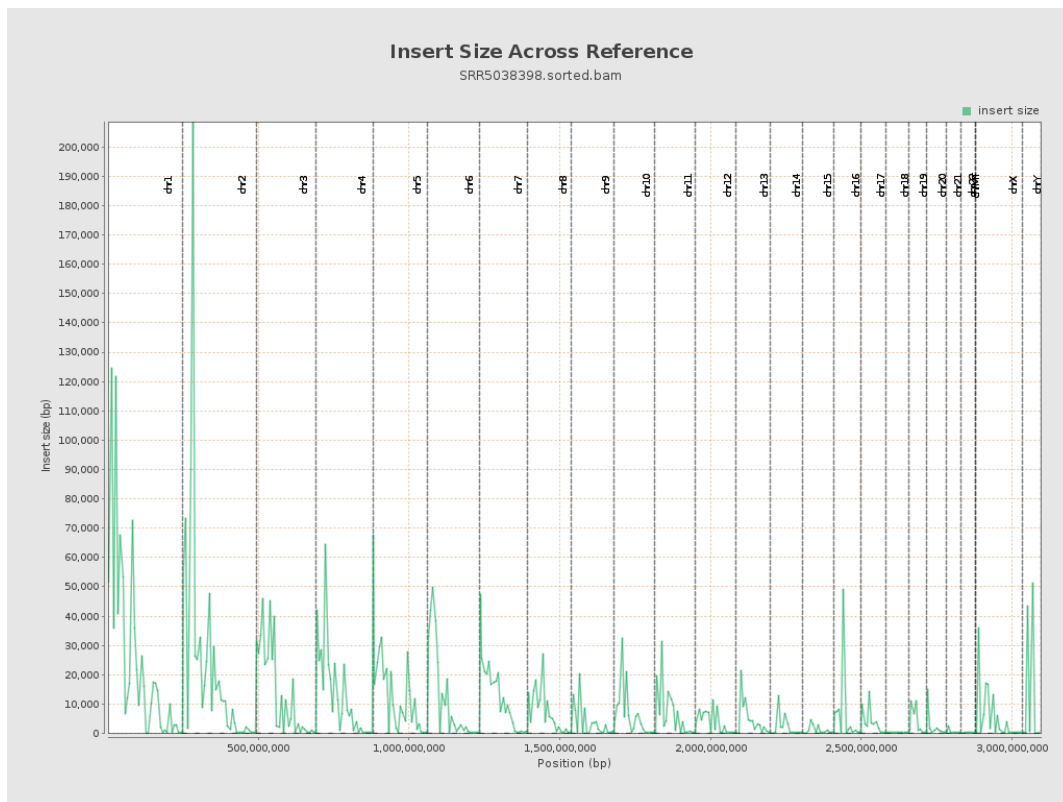
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

