

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 23:46:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038419.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_SRR5038419 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038419_1.fastq.gz SRR5038419_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 23:46:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038419.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,942,040
Mapped reads	14,212,577 / 95.12%
Unmapped reads	729,463 / 4.88%
Mapped paired reads	14,212,577 / 95.12%
Mapped reads, first in pair	7,192,955 / 48.14%
Mapped reads, second in pair	7,019,622 / 46.98%
Mapped reads, both in pair	14,014,078 / 93.79%
Mapped reads, singletons	198,499 / 1.33%
Secondary alignments	0
Supplementary alignments	275,326 / 1.84%
Read min/max/mean length	30 / 150 / 150.96
Duplicated reads (estimated)	2,517,308 / 16.85%
Duplication rate	10.13%
Clipped reads	3,217,450 / 21.53%

2.2. ACGT Content

Number/percentage of A's	602,535,900 / 29.56%
Number/percentage of C's	413,142,290 / 20.27%
Number/percentage of T's	600,979,359 / 29.48%
Number/percentage of G's	421,674,212 / 20.69%
Number/percentage of N's	42,310 / 0%

GC Percentage	40.96%
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2.3. Coverage

Mean	0.6589
Standard Deviation	12.4062

2.4. Mapping Quality

Mean Mapping Quality	53.66
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2.5. Insert size

Mean	79,011.7
Standard Deviation	2,636,643.53
P25/Median/P75	200 / 243 / 298

2.6. Mismatches and indels

General error rate	1.57%
Mismatches	30,914,408
Insertions	391,998
Mapped reads with at least one insertion	2.58%
Deletions	720,849
Mapped reads with at least one deletion	4.87%
Homopolymer indels	46.25%

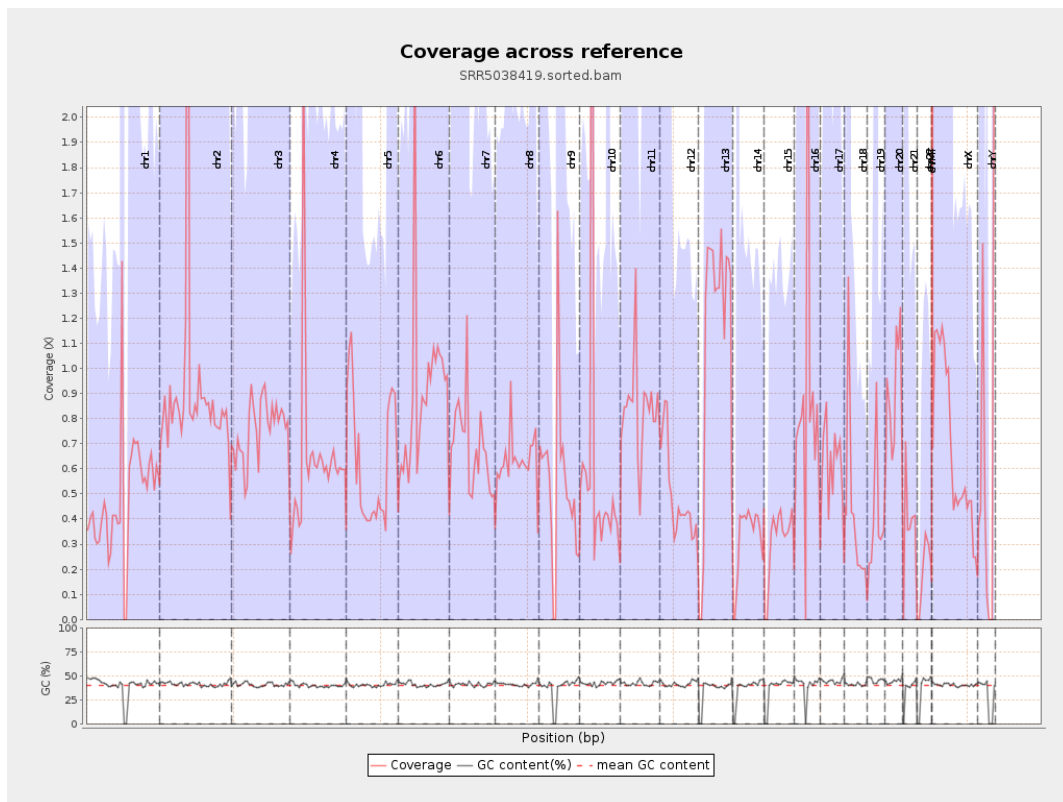
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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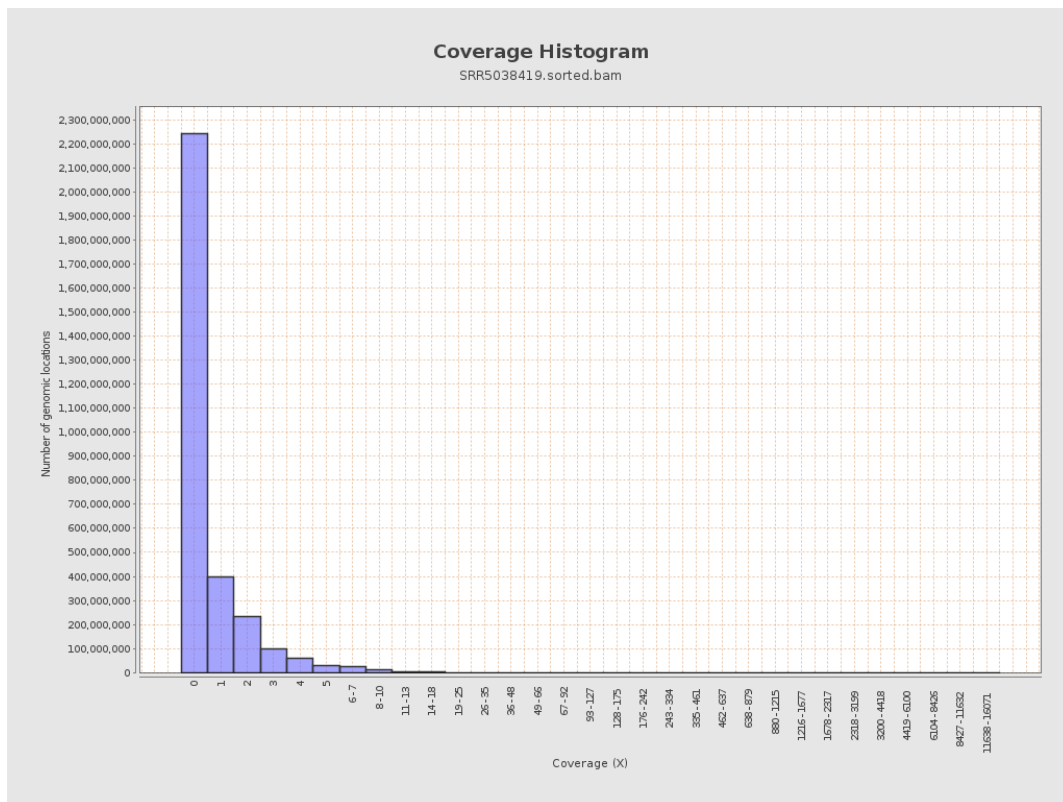
		bases	coverage	deviation
chr1	249250621	121029916	0.4856	16.6758
chr2	243199373	223976725	0.921	16.6647
chr3	198022430	150537456	0.7602	1.5848
chr4	191154276	121195182	0.634	11.7044
chr5	180915260	113913643	0.6297	1.5228
chr6	171115067	156783881	0.9162	17.5286
chr7	159138663	108059246	0.679	9.747
chr8	146364022	92620663	0.6328	3.4133
chr9	141213431	74395534	0.5268	19.8095
chr10	135534747	85516542	0.631	25.2187
chr11	135006516	111144875	0.8233	9.3734
chr12	133851895	65774686	0.4914	1.2696
chr13	115169878	131151152	1.1388	2.017
chr14	107349540	34747290	0.3237	1.301
chr15	102531392	31950622	0.3116	0.8938
chr16	90354753	80503658	0.891	16.8693
chr17	81195210	49293033	0.6071	8.3887
chr18	78077248	31566022	0.4043	17.9169
chr19	59128983	22300538	0.3772	9.3235
chr20	63025520	56117083	0.8904	3.7625
chr21	48129895	18270058	0.3796	5.4301
chr22	51304566	9726361	0.1896	0.7886
chrMT	16571	2101255	126.8032	70.5089
chrX	155270560	106052689	0.683	2.696

chrY	59373566	41153355	0.6931	19.7317
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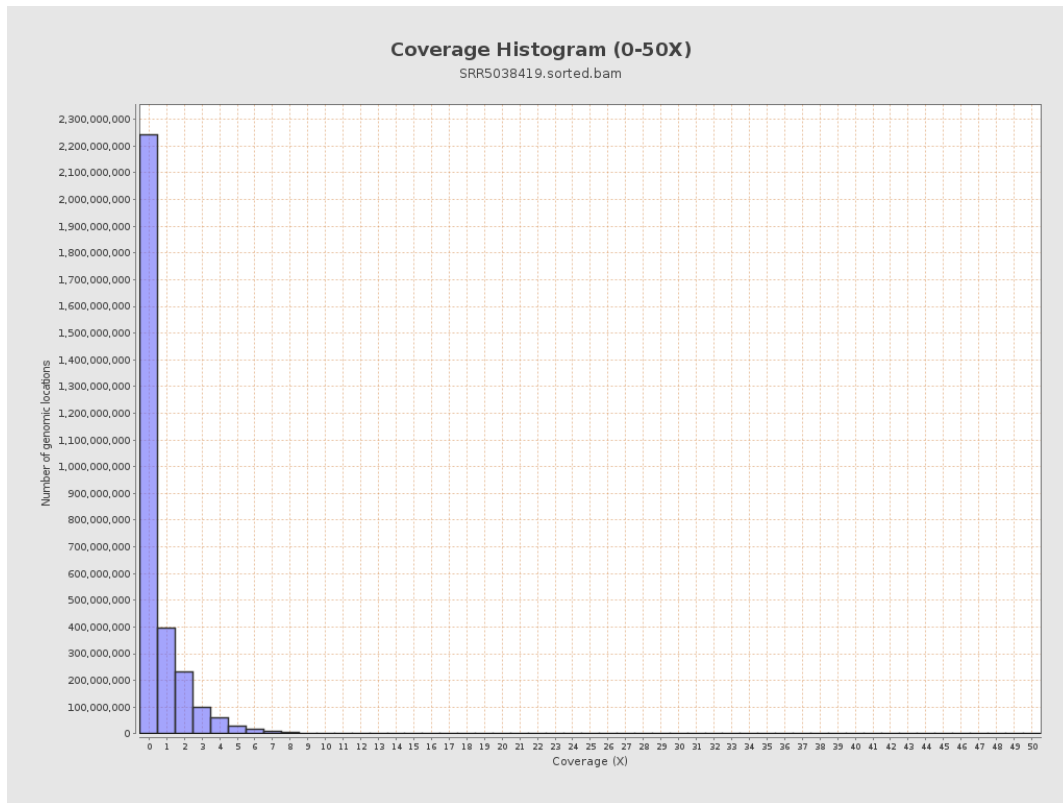
3. Results : Coverage across reference



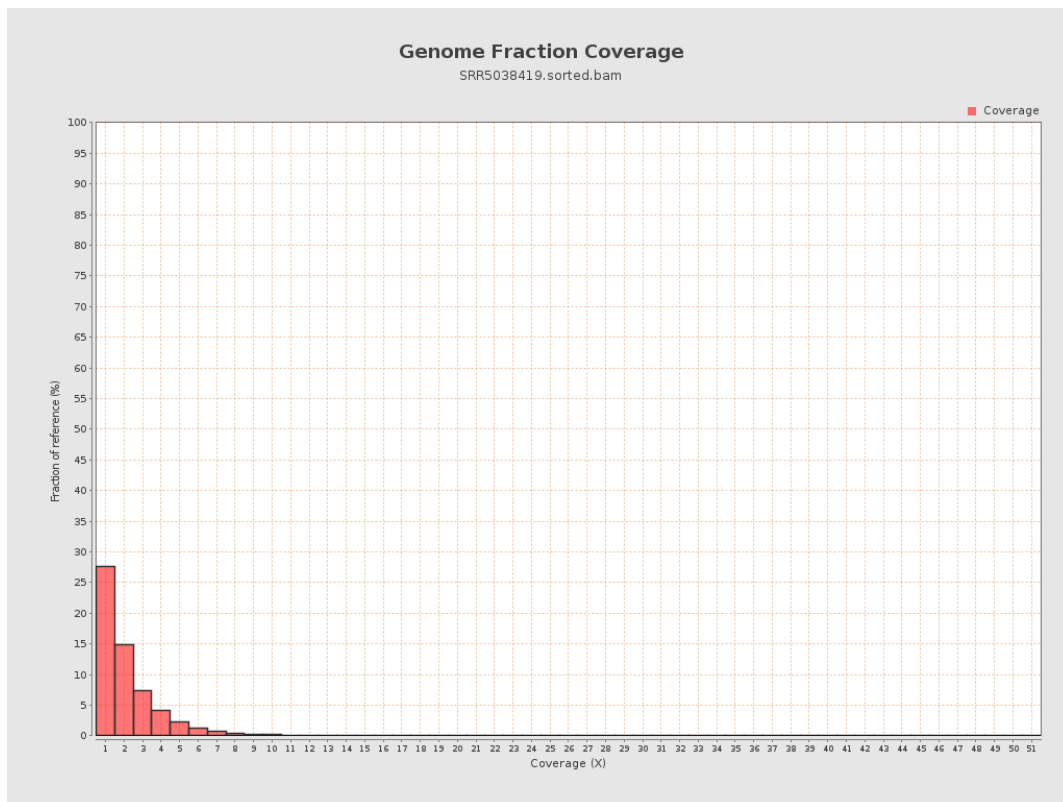
4. Results : Coverage Histogram



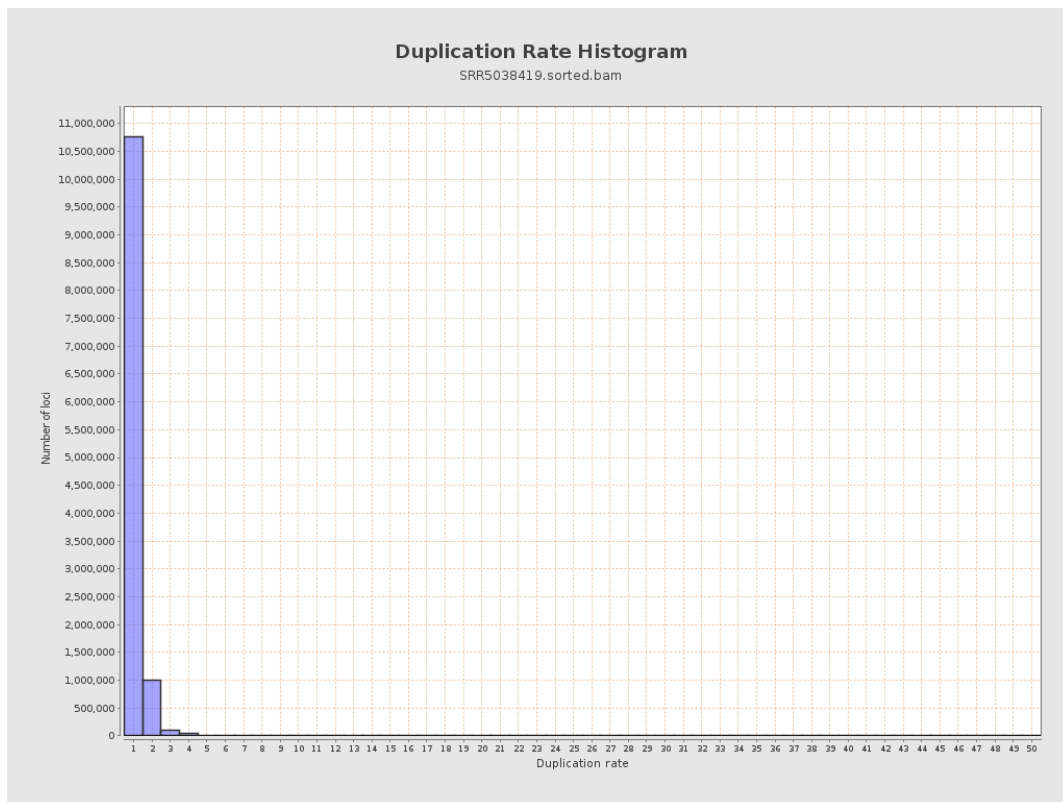
5. Results : Coverage Histogram (0-50X)



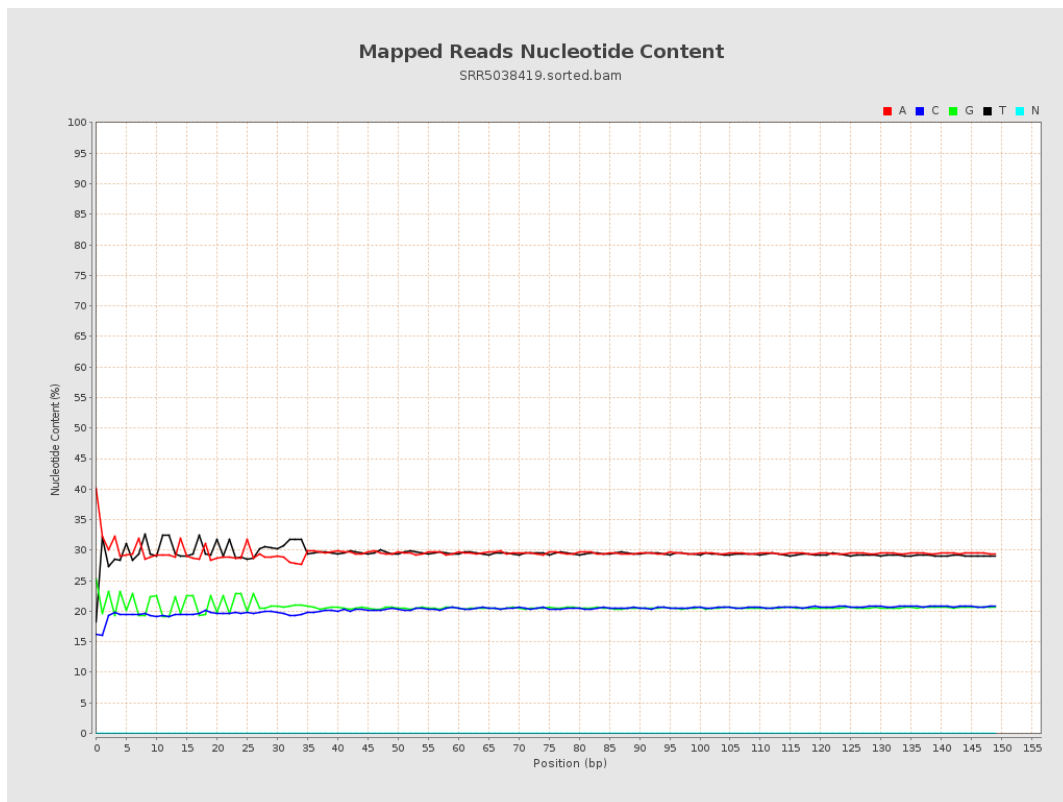
6. Results : Genome Fraction Coverage



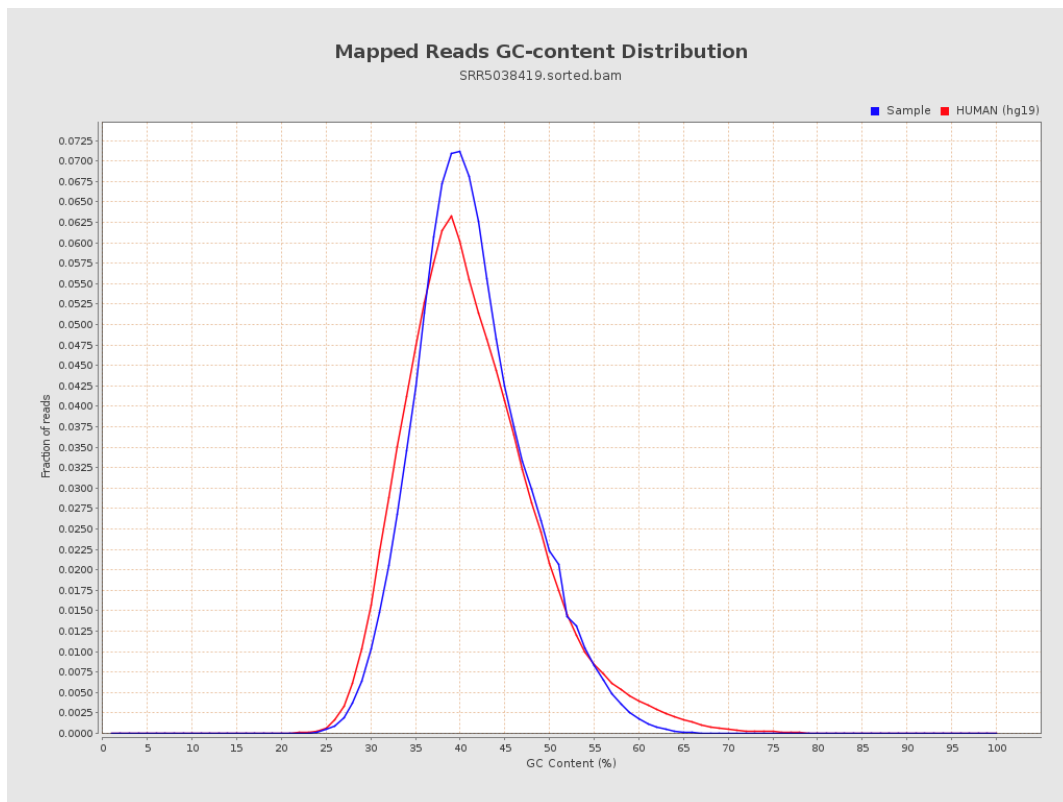
7. Results : Duplication Rate Histogram



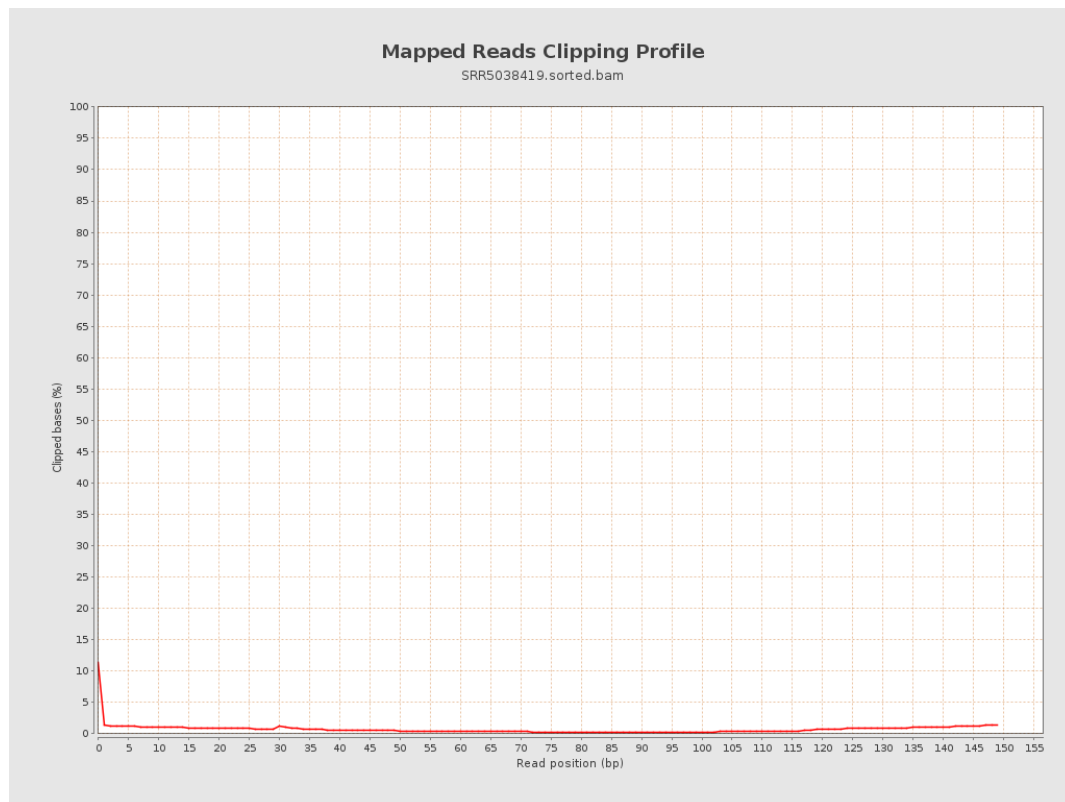
8. Results : Mapped Reads Nucleotide Content



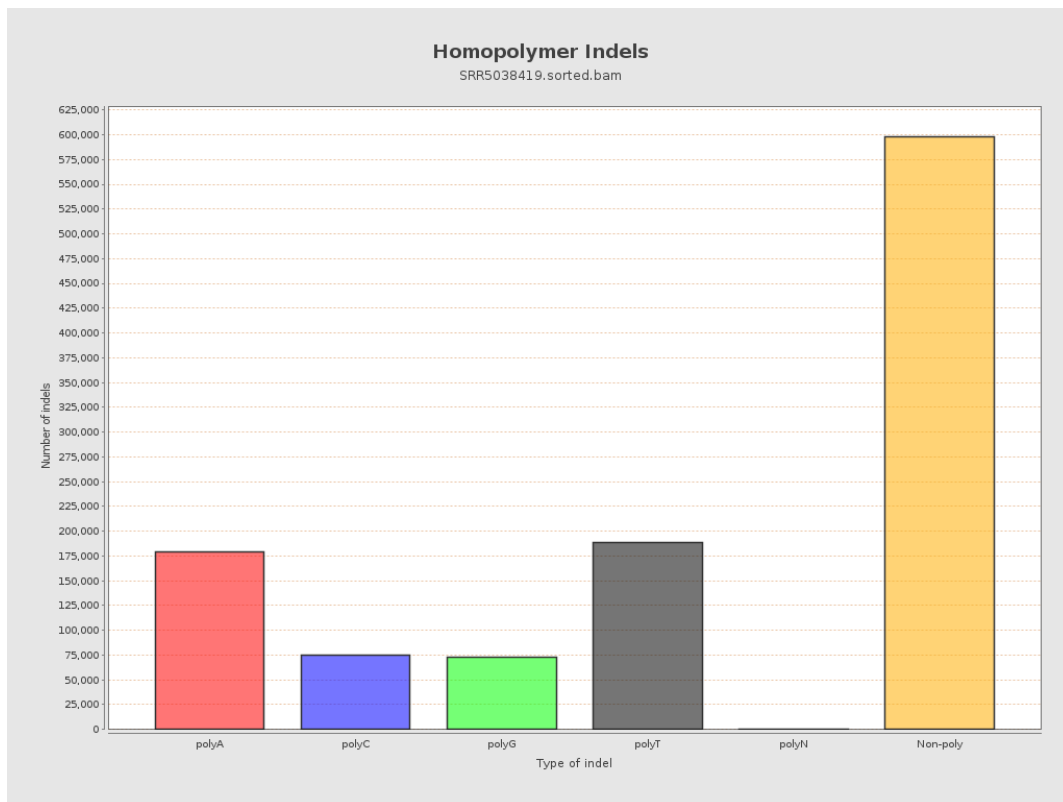
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



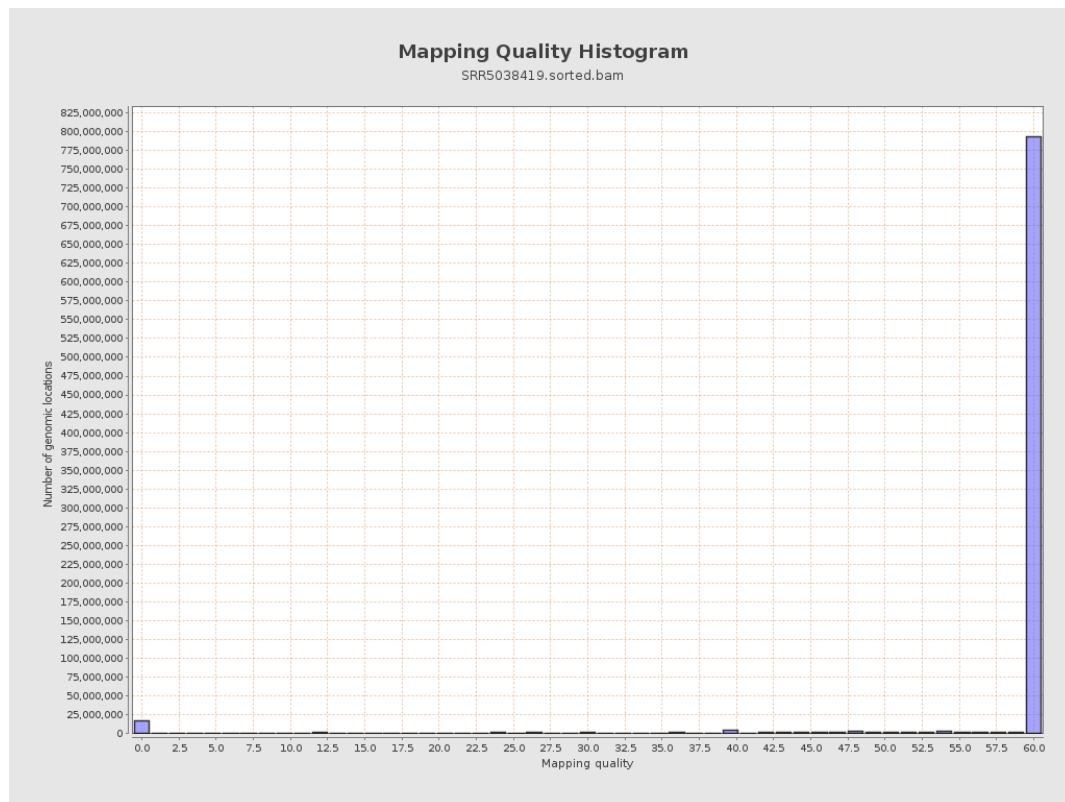
11. Results : Homopolymer Indels



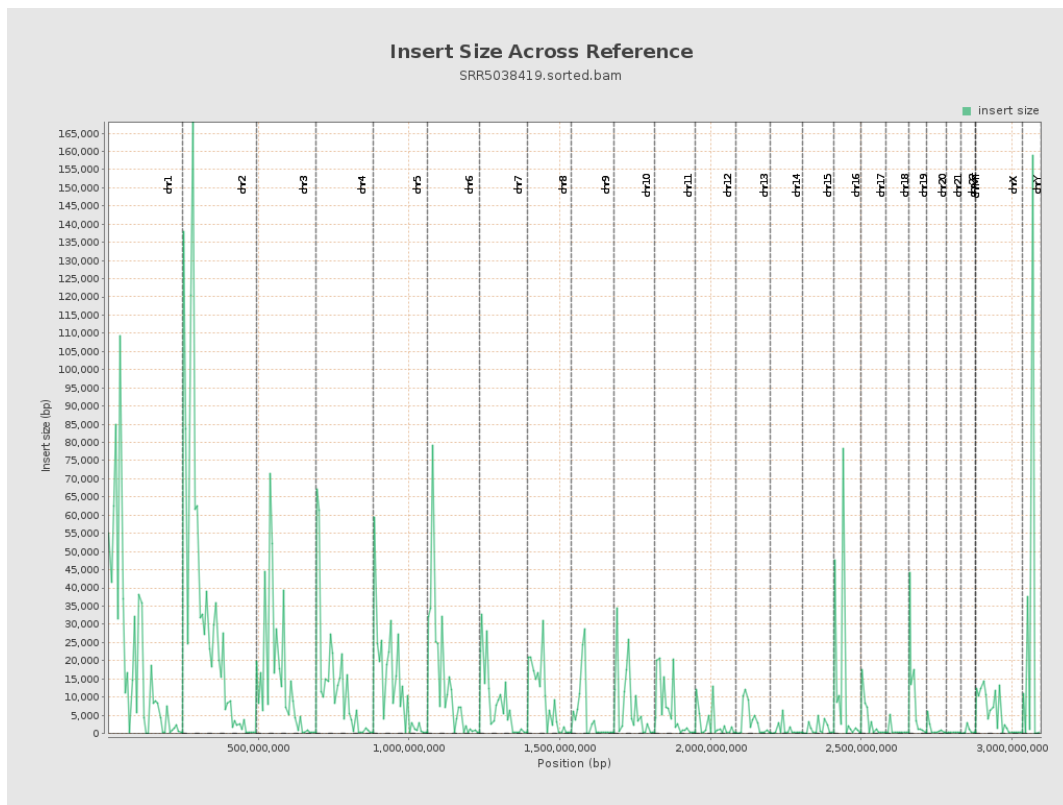
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

