

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 13:43:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038496.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_SRR5038496 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038496_1.fastq.gz SRR5038496_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 13:43:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038496.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	71,676,496
Mapped reads	71,159,795 / 99.28%
Unmapped reads	516,701 / 0.72%
Mapped paired reads	71,159,795 / 99.28%
Mapped reads, first in pair	35,793,480 / 49.94%
Mapped reads, second in pair	35,366,315 / 49.34%
Mapped reads, both in pair	70,705,742 / 98.65%
Mapped reads, singletons	454,053 / 0.63%
Secondary alignments	0
Supplementary alignments	108,590 / 0.15%
Read min/max/mean length	30 / 150 / 150.07
Duplicated reads (estimated)	26,164,571 / 36.5%
Duplication rate	35.02%
Clipped reads	5,143,622 / 7.18%

2.2. ACGT Content

Number/percentage of A's	2,685,389,395 / 25.45%
Number/percentage of C's	2,589,590,363 / 24.54%
Number/percentage of T's	2,705,400,347 / 25.64%
Number/percentage of G's	2,570,996,183 / 24.36%
Number/percentage of N's	814,117 / 0.01%

GC Percentage	48.91%
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2.3. Coverage

Mean	3.4092
Standard Deviation	21.3117

2.4. Mapping Quality

Mean Mapping Quality	55.85
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2.5. Insert size

Mean	18,358.51
Standard Deviation	1,423,927.51
P25/Median/P75	201 / 235 / 275

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	66,074,796
Insertions	546,341
Mapped reads with at least one insertion	0.73%
Deletions	644,161
Mapped reads with at least one deletion	0.88%
Homopolymer indels	45.91%

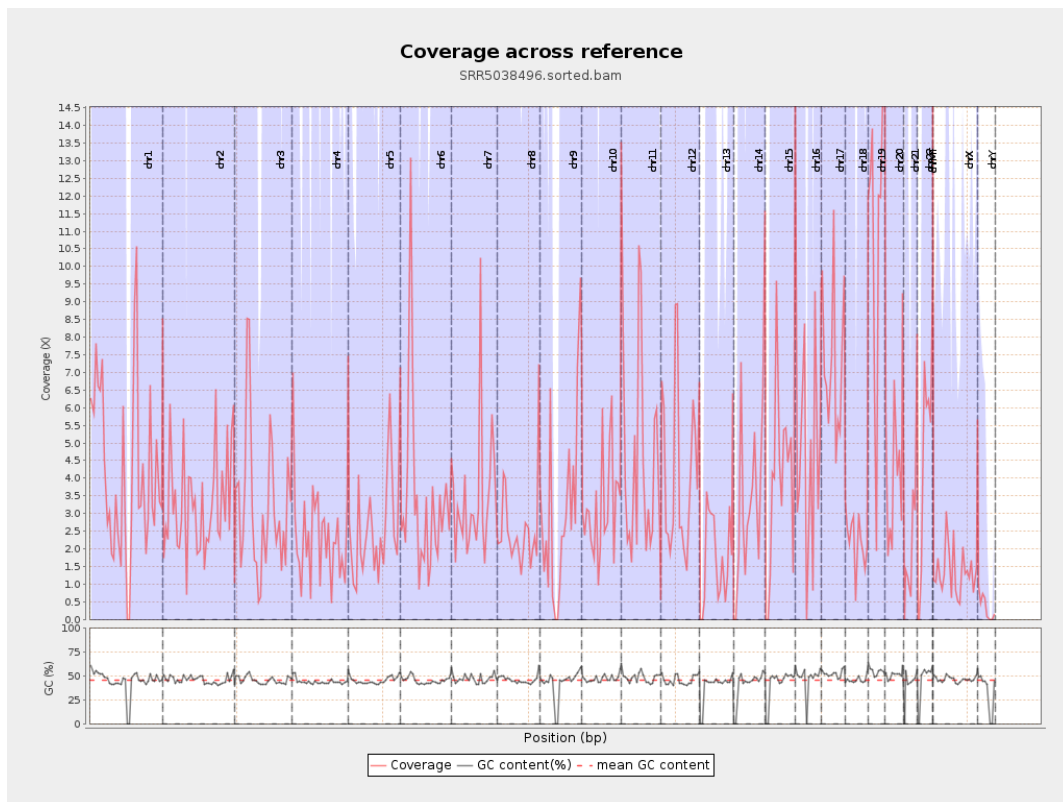
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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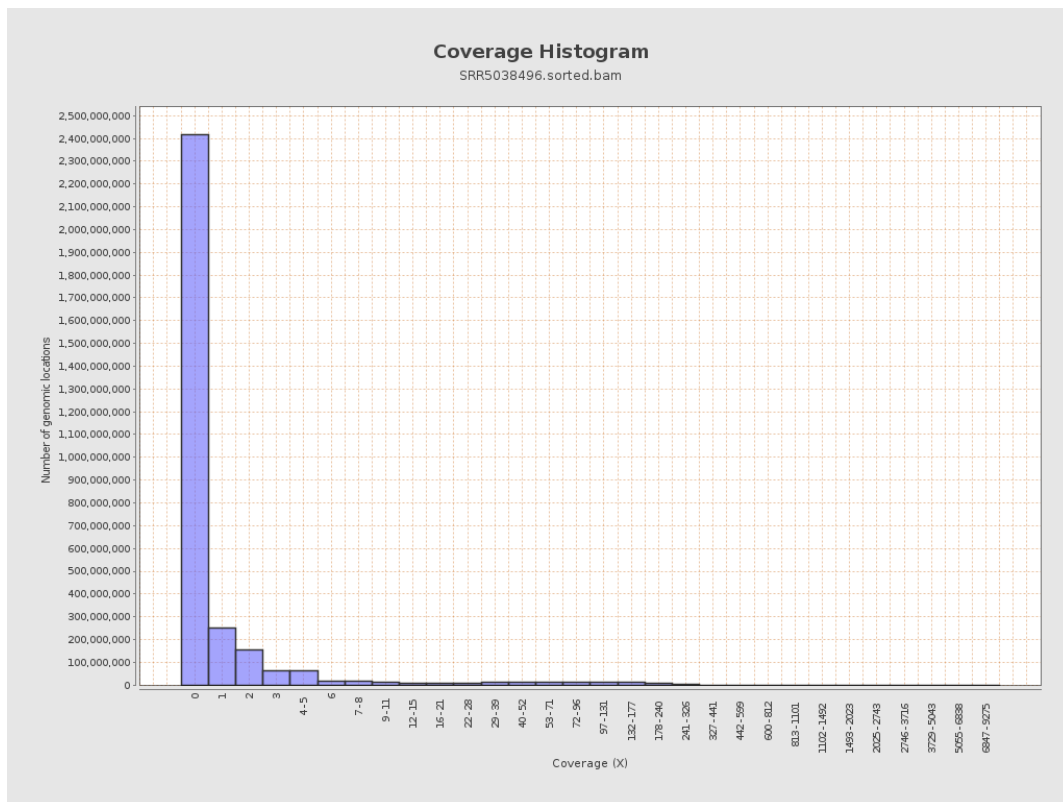
		bases	coverage	deviation
chr1	249250621	1038391013	4.1661	23.4885
chr2	243199373	798479925	3.2832	21.6927
chr3	198022430	626009255	3.1613	20.0712
chr4	191154276	440717504	2.3056	17.2567
chr5	180915260	489211559	2.7041	18.4672
chr6	171115067	561307600	3.2803	21.2894
chr7	159138663	549805458	3.4549	23.1413
chr8	146364022	370210097	2.5294	17.3279
chr9	141213431	430037621	3.0453	19.9105
chr10	135534747	435271841	3.2115	19.7078
chr11	135006516	611055078	4.5261	25.7896
chr12	133851895	568962315	4.2507	22.9823
chr13	115169878	205797783	1.7869	14.7244
chr14	107349540	350602790	3.266	20.5571
chr15	102531392	388193970	3.7861	22.0738
chr16	90354753	442219806	4.8943	25.1338
chr17	81195210	587779906	7.2391	30.7697
chr18	78077248	172517836	2.2096	16.1306
chr19	59128983	649838871	10.9902	39.32
chr20	63025520	254865924	4.0439	23.1624
chr21	48129895	117583149	2.443	24.2274
chr22	51304566	225351004	4.3924	22.9751
chrMT	16571	241682	14.5846	7.9407
chrX	155270560	218680430	1.4084	10.0898

chrY	59373566	20853870	0.3512	5.0352
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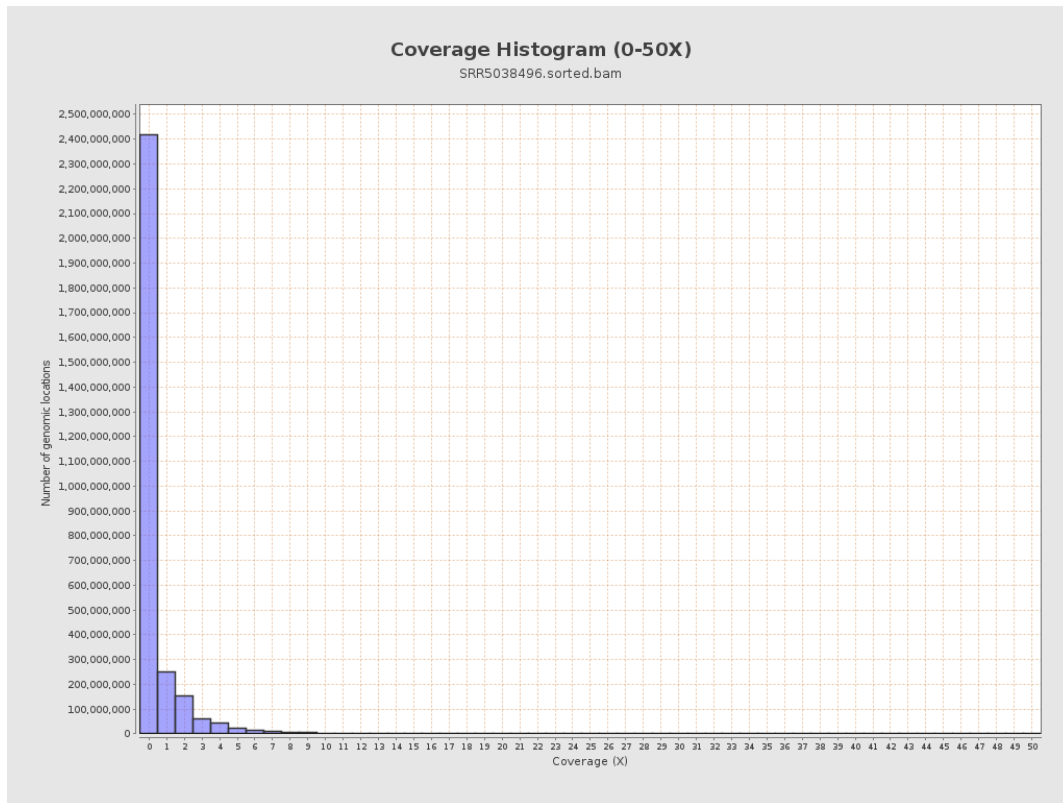
3. Results : Coverage across reference



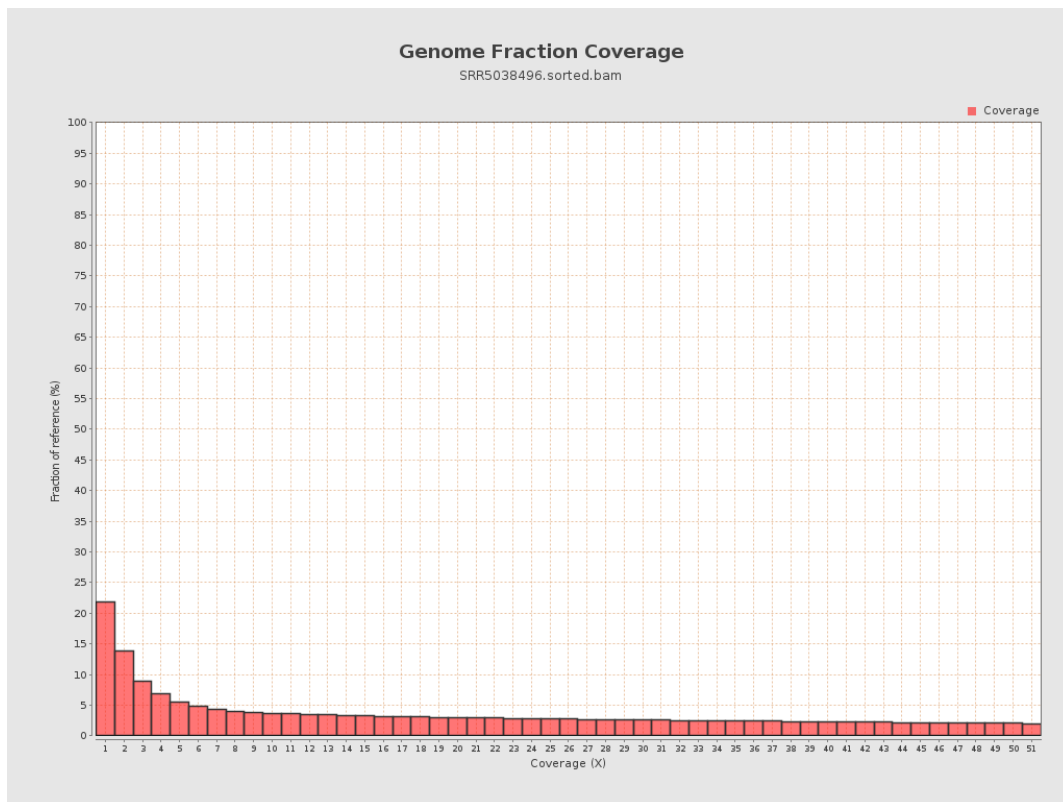
4. Results : Coverage Histogram



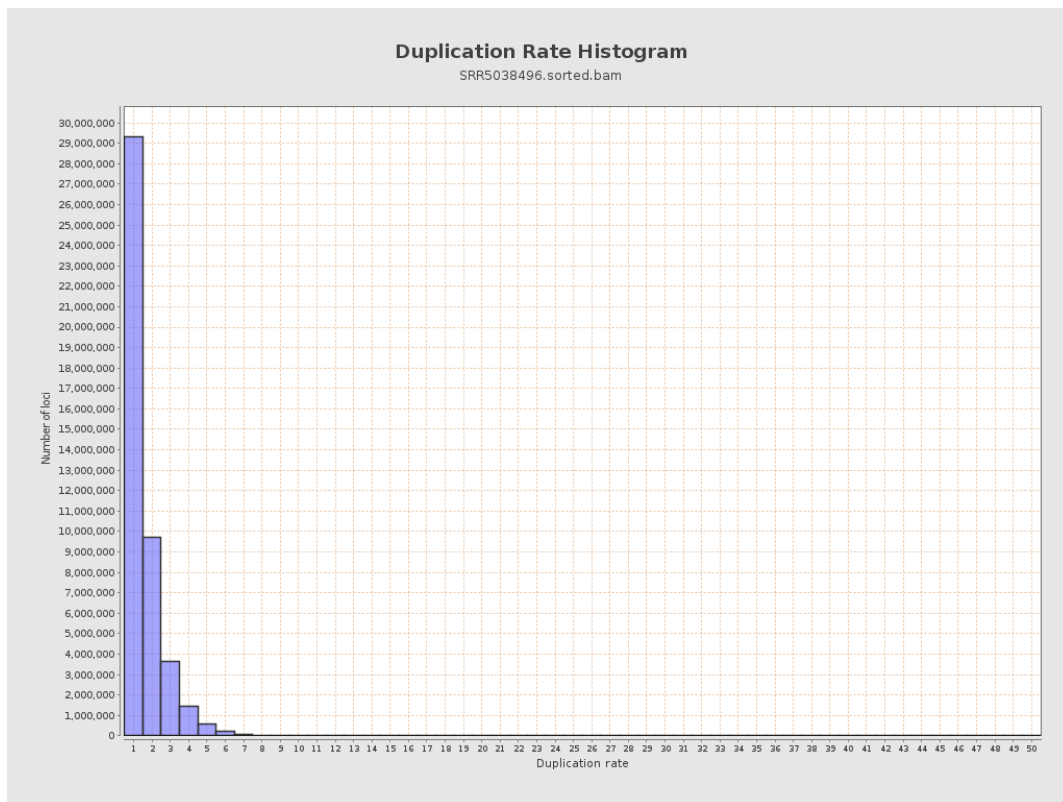
5. Results : Coverage Histogram (0-50X)



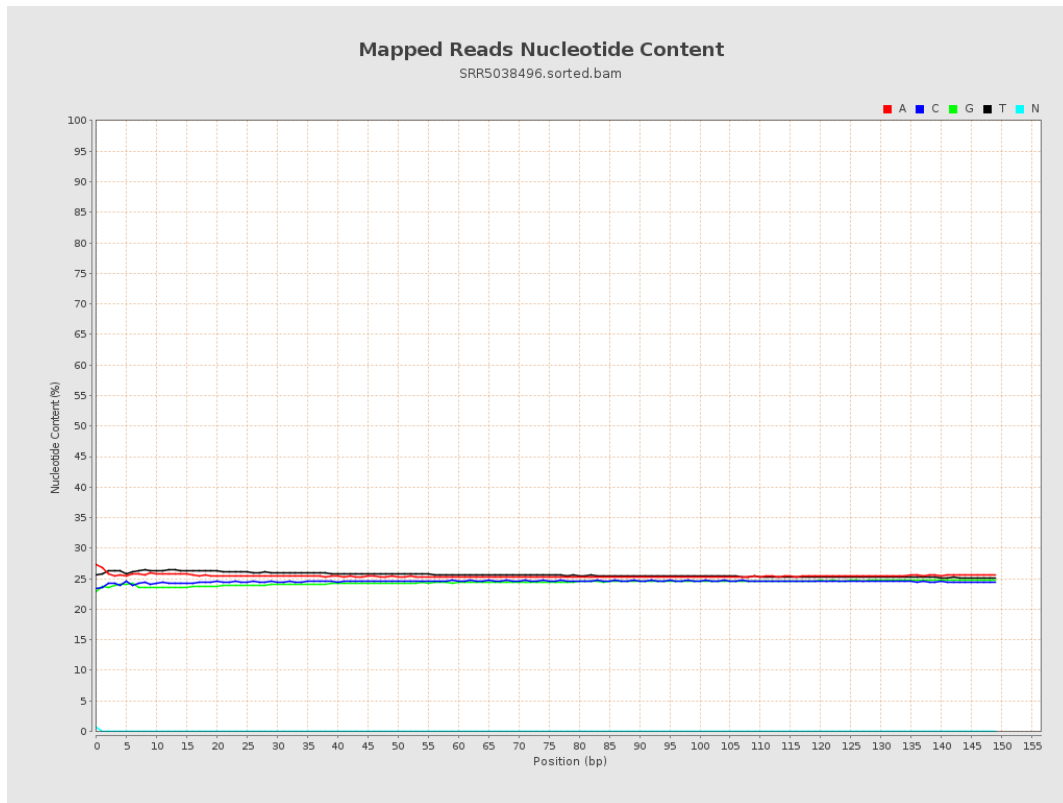
6. Results : Genome Fraction Coverage



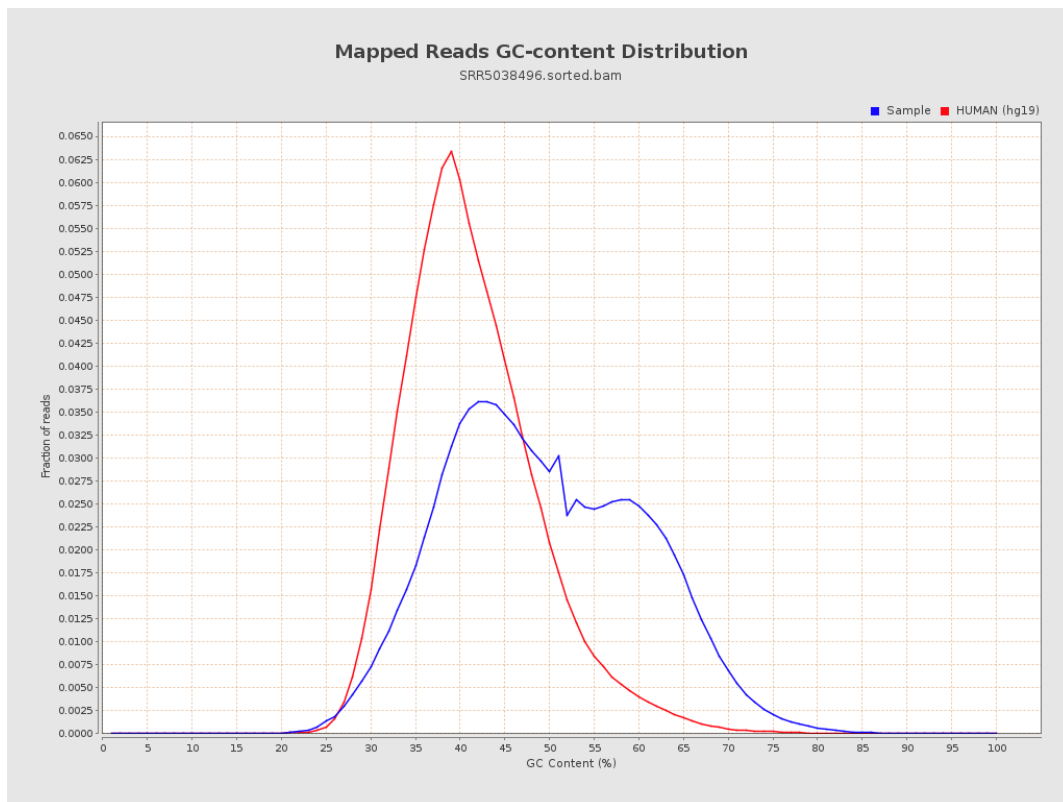
7. Results : Duplication Rate Histogram



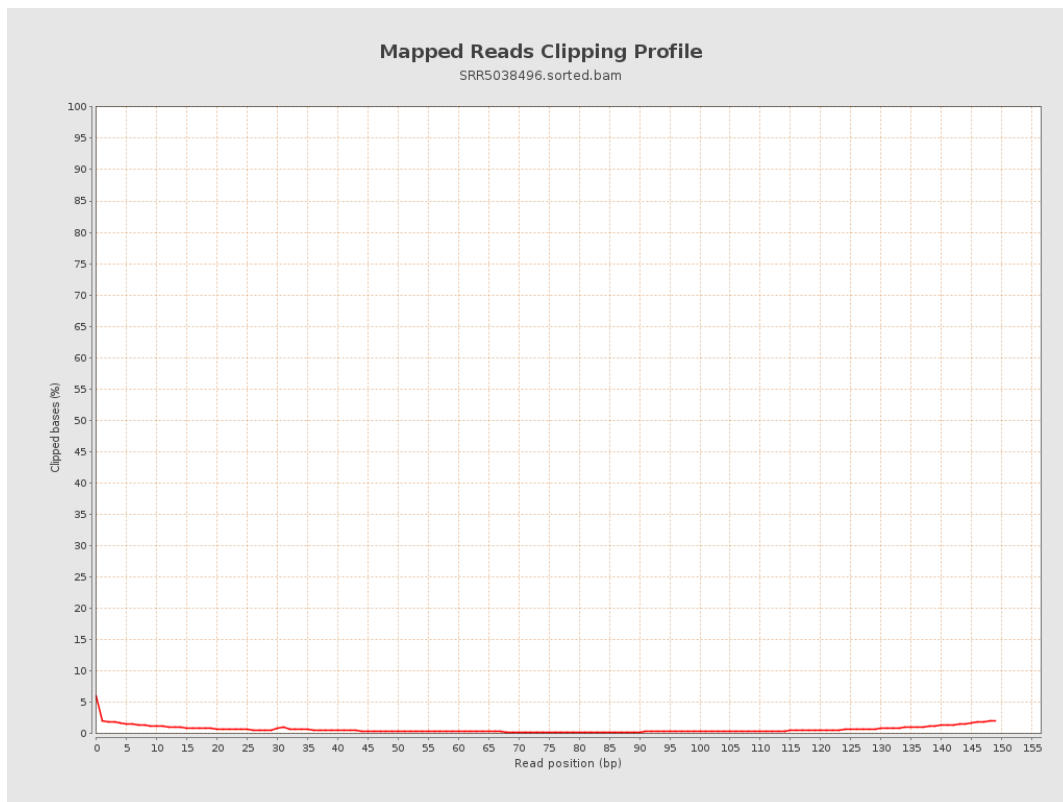
8. Results : Mapped Reads Nucleotide Content



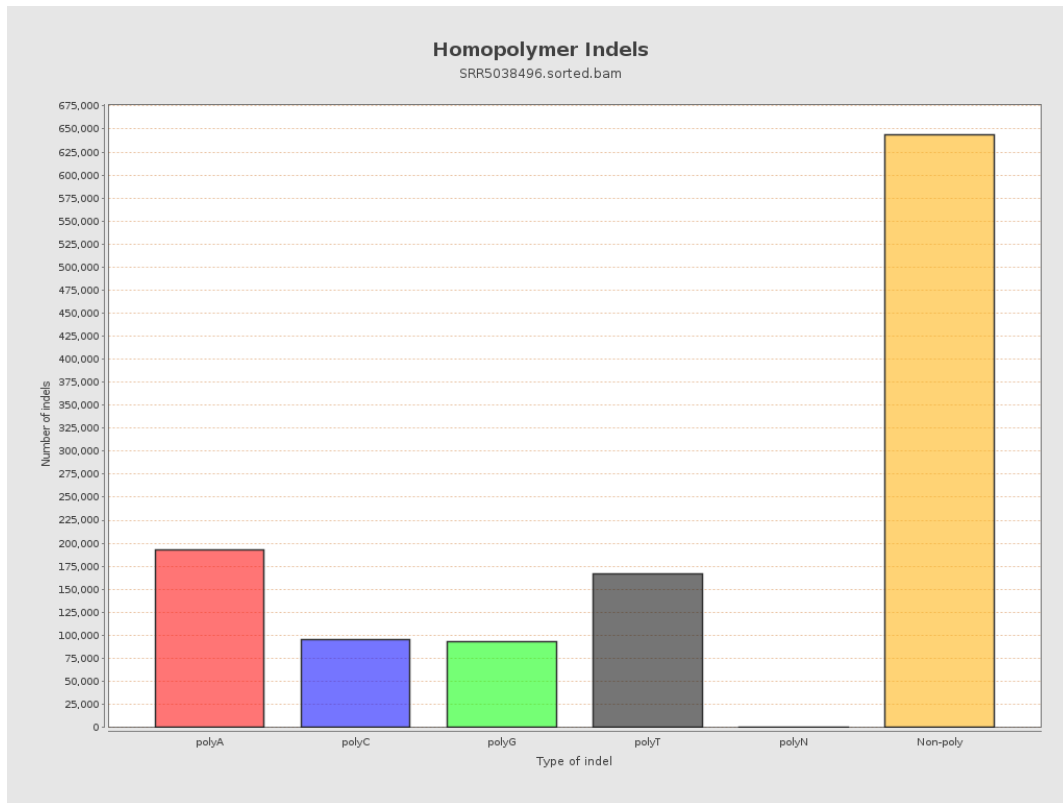
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



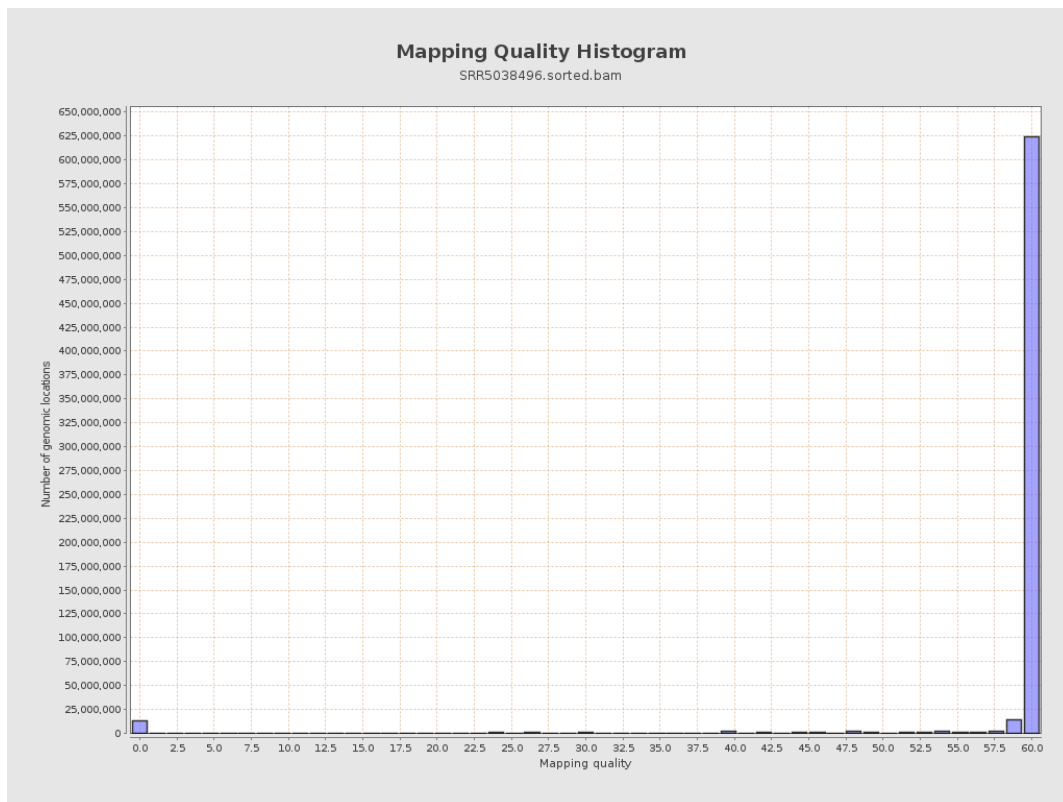
11. Results : Homopolymer Indels



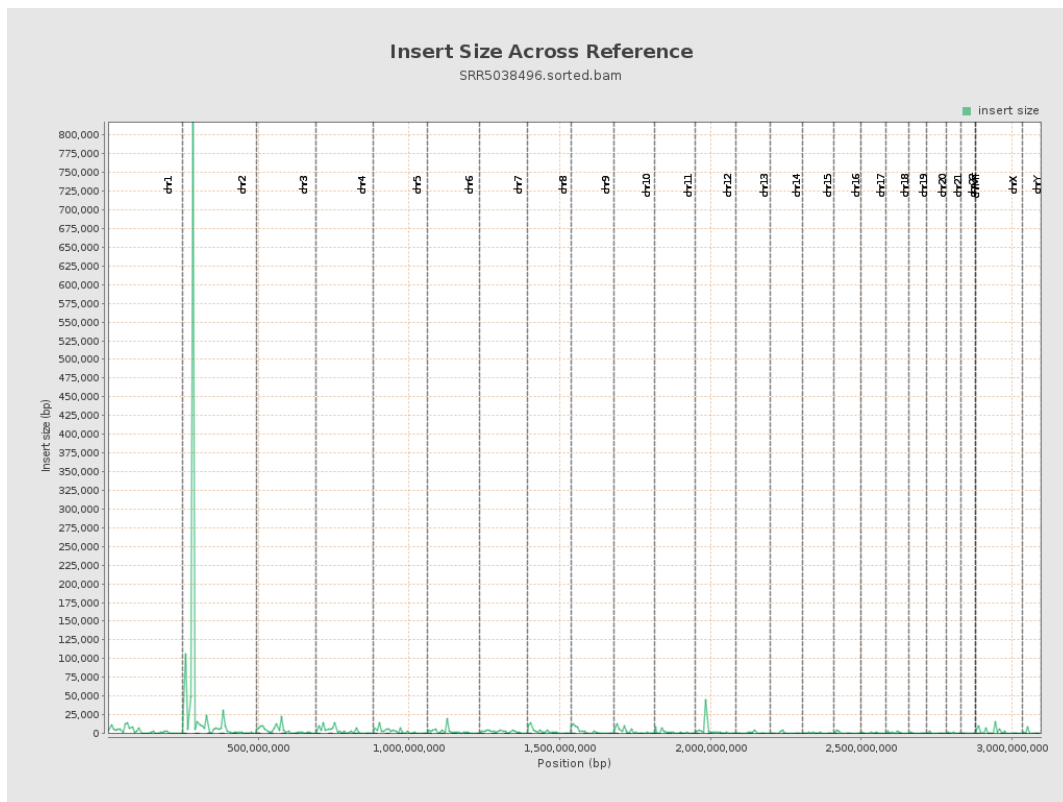
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

