

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 12:32:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038495.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_SRR5038495 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038495_1.fastq.gz SRR5038495_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 12:31:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038495.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	67,579,238
Mapped reads	67,345,350 / 99.65%
Unmapped reads	233,888 / 0.35%
Mapped paired reads	67,345,350 / 99.65%
Mapped reads, first in pair	33,725,844 / 49.91%
Mapped reads, second in pair	33,619,506 / 49.75%
Mapped reads, both in pair	67,220,864 / 99.47%
Mapped reads, singletons	124,486 / 0.18%
Secondary alignments	0
Supplementary alignments	91,903 / 0.14%
Read min/max/mean length	30 / 150 / 150.06
Duplicated reads (estimated)	23,326,717 / 34.52%
Duplication rate	32.99%
Clipped reads	3,124,819 / 4.62%

2.2. ACGT Content

Number/percentage of A's	2,546,749,638 / 25.38%
Number/percentage of C's	2,471,836,223 / 24.64%
Number/percentage of T's	2,566,316,518 / 25.58%
Number/percentage of G's	2,447,379,489 / 24.39%
Number/percentage of N's	970,101 / 0.01%

GC Percentage	49.03%
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2.3. Coverage

Mean	3.2416
Standard Deviation	19.8264

2.4. Mapping Quality

Mean Mapping Quality	55.7
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2.5. Insert size

Mean	18,082.8
Standard Deviation	1,431,859.48
P25/Median/P75	202 / 236 / 277

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	45,609,889
Insertions	532,330
Mapped reads with at least one insertion	0.76%
Deletions	652,032
Mapped reads with at least one deletion	0.94%
Homopolymer indels	46.8%

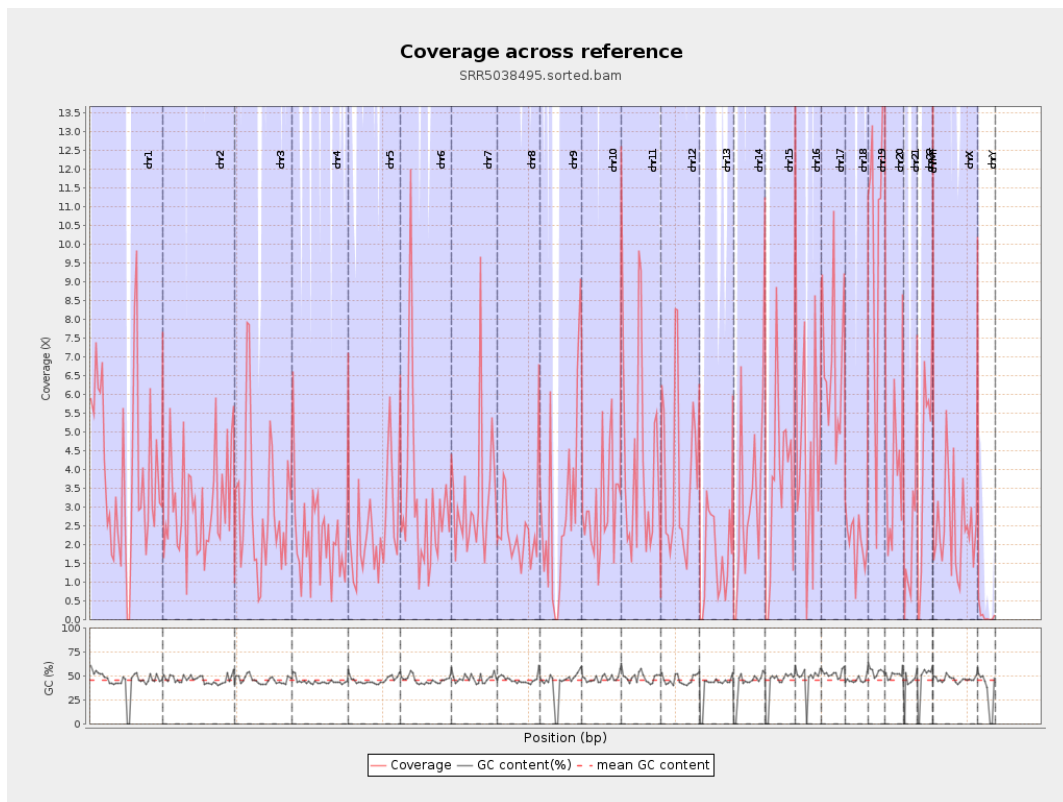
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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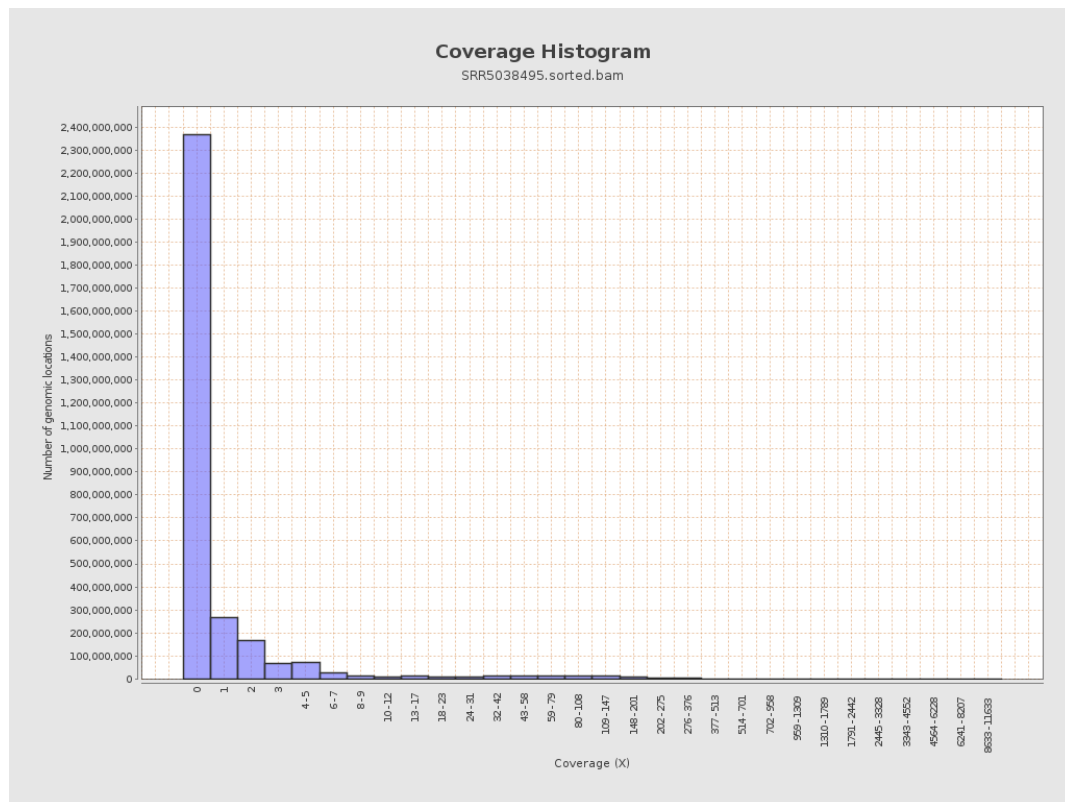
		bases	coverage	deviation
chr1	249250621	967494747	3.8816	21.5482
chr2	243199373	742543069	3.0532	20.7759
chr3	198022430	582615013	2.9422	18.3362
chr4	191154276	413119248	2.1612	15.7266
chr5	180915260	455986652	2.5204	16.6504
chr6	171115067	521316297	3.0466	19.3858
chr7	159138663	514706138	3.2343	21.2188
chr8	146364022	348318938	2.3798	15.8385
chr9	141213431	401870434	2.8458	18.1735
chr10	135534747	407992302	3.0102	18.0985
chr11	135006516	567402806	4.2028	23.3786
chr12	133851895	529194739	3.9536	20.9362
chr13	115169878	193324767	1.6786	13.3702
chr14	107349540	327303531	3.049	18.8893
chr15	102531392	358740606	3.4988	19.7996
chr16	90354753	414468803	4.5871	23.0244
chr17	81195210	550070432	6.7747	28.2608
chr18	78077248	161239416	2.0651	14.5995
chr19	59128983	614054884	10.385	36.811
chr20	63025520	239102727	3.7937	21.3569
chr21	48129895	109212234	2.2691	20.5624
chr22	51304566	211671993	4.1258	21.2212
chrMT	16571	262141	15.8193	7.465
chrX	155270560	397367911	2.5592	17.7078

chrY	59373566	5708855	0.0962	2.4494
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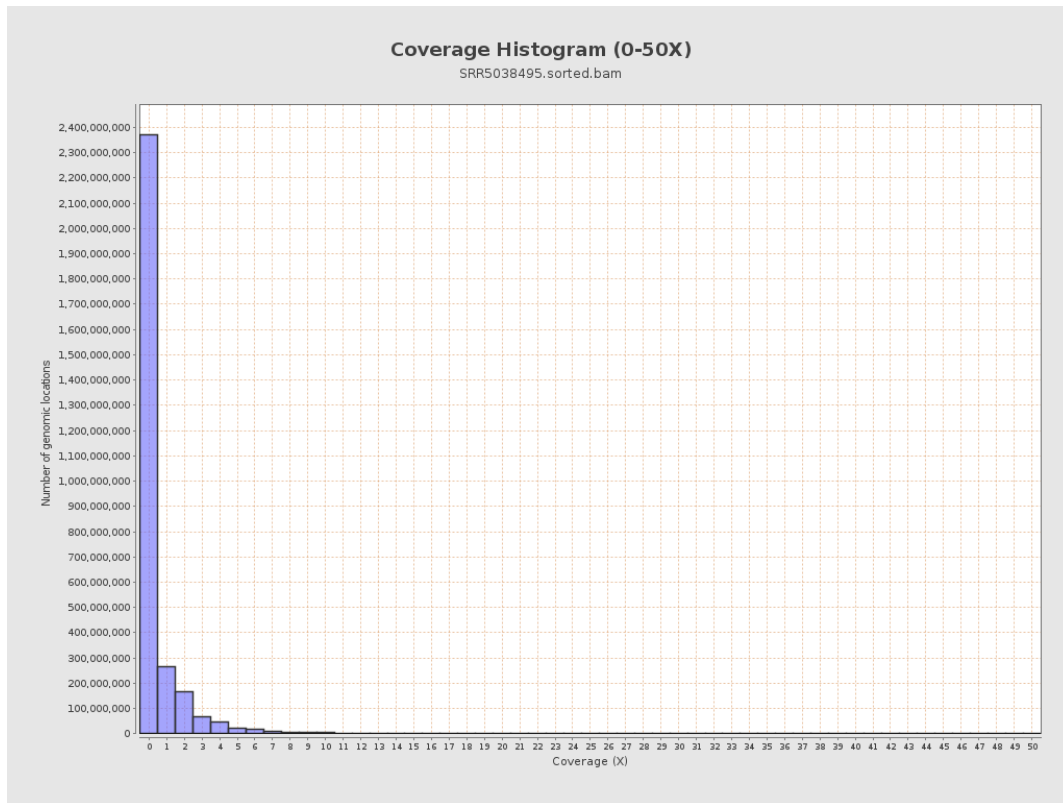
3. Results : Coverage across reference



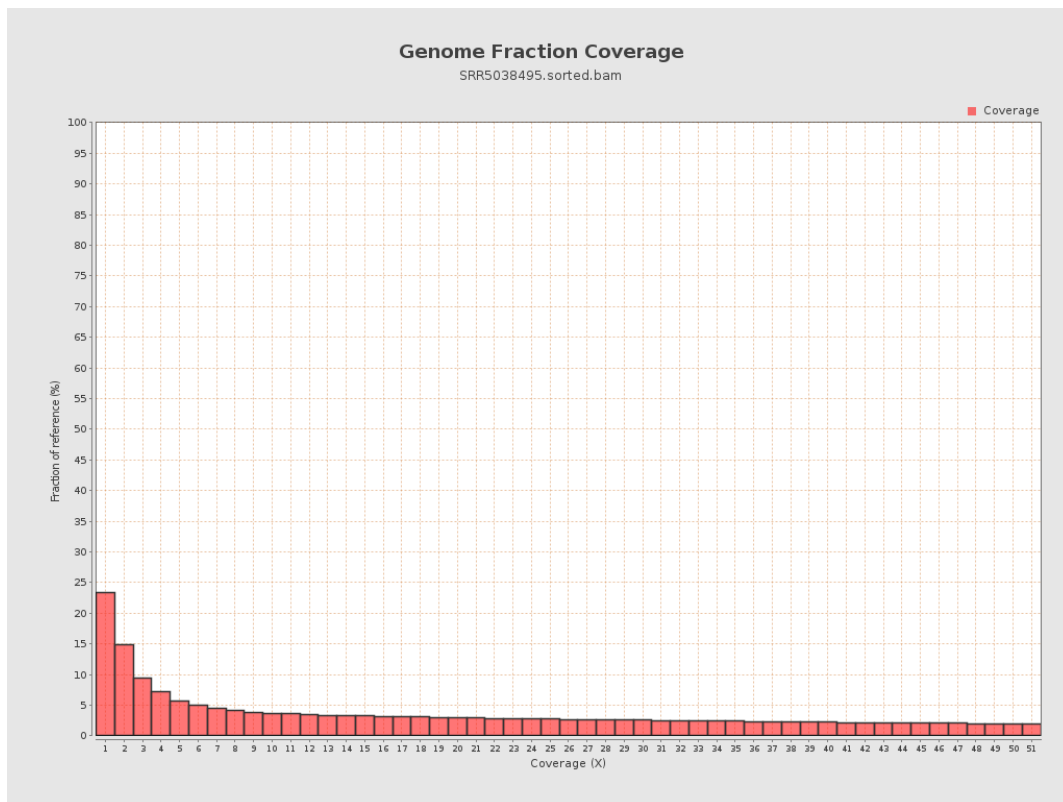
4. Results : Coverage Histogram



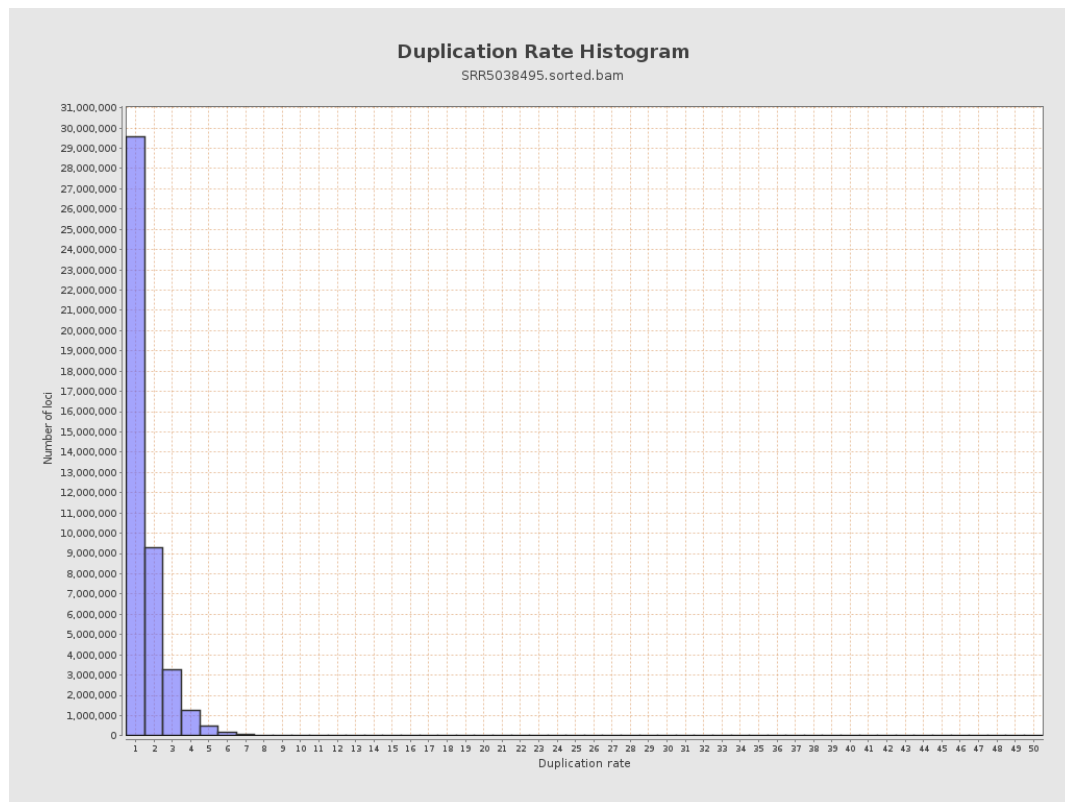
5. Results : Coverage Histogram (0-50X)



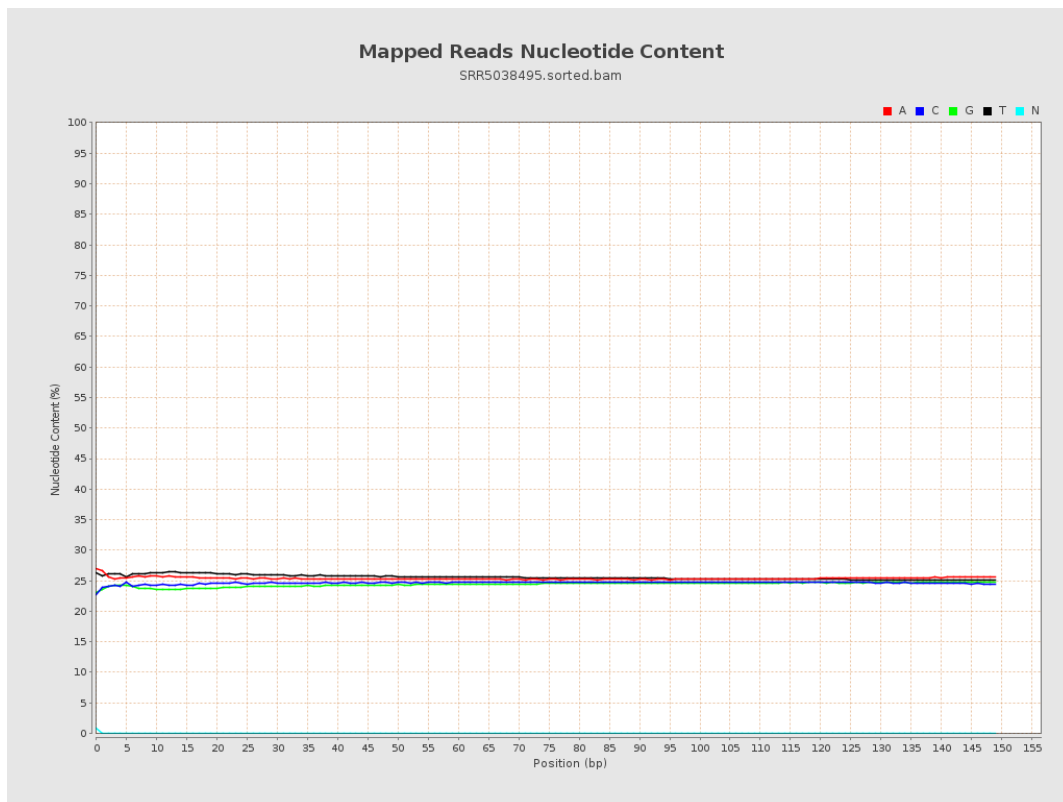
6. Results : Genome Fraction Coverage



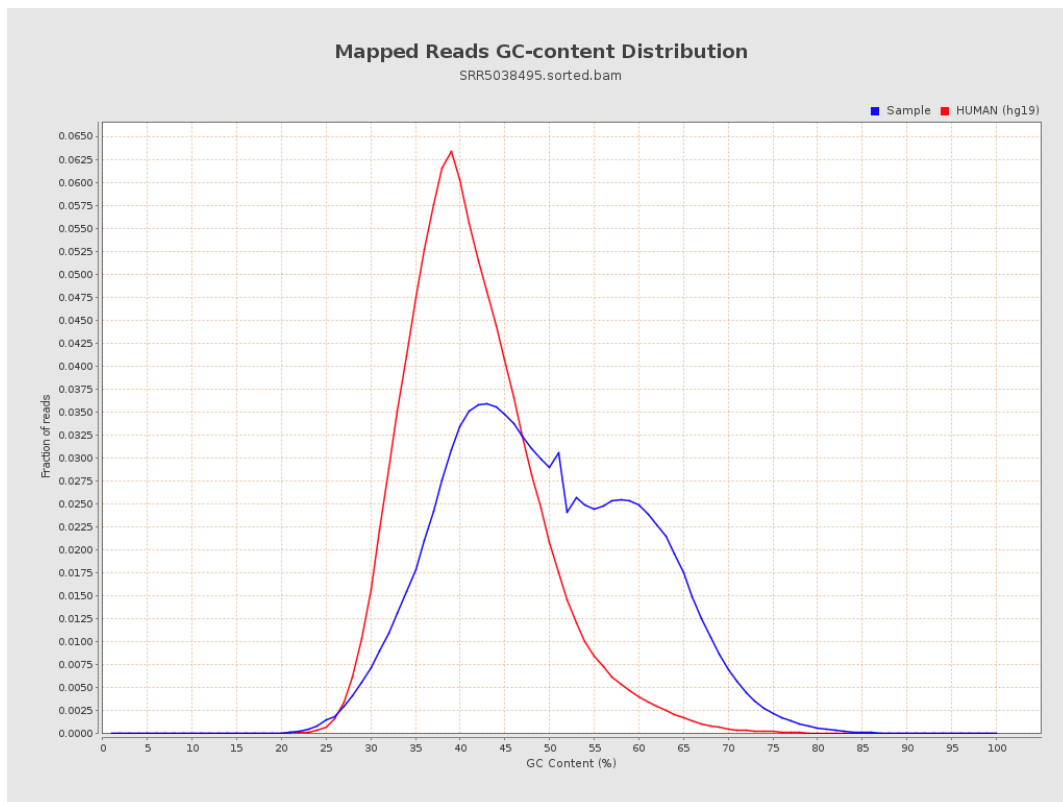
7. Results : Duplication Rate Histogram



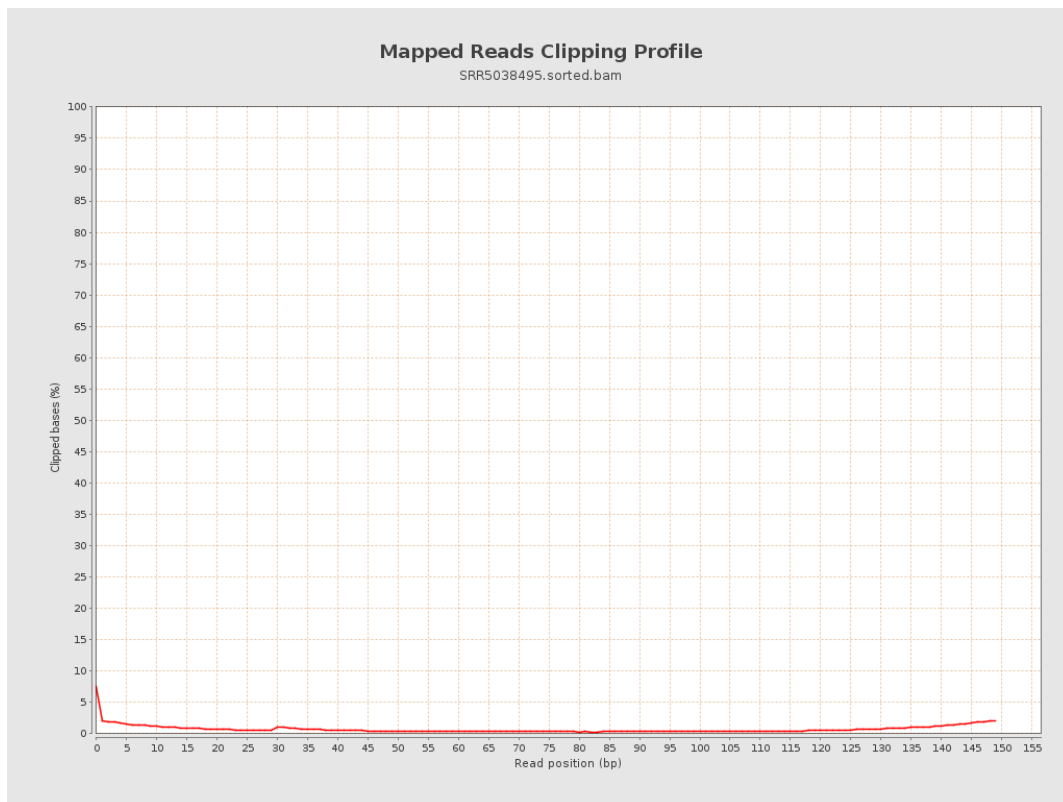
8. Results : Mapped Reads Nucleotide Content



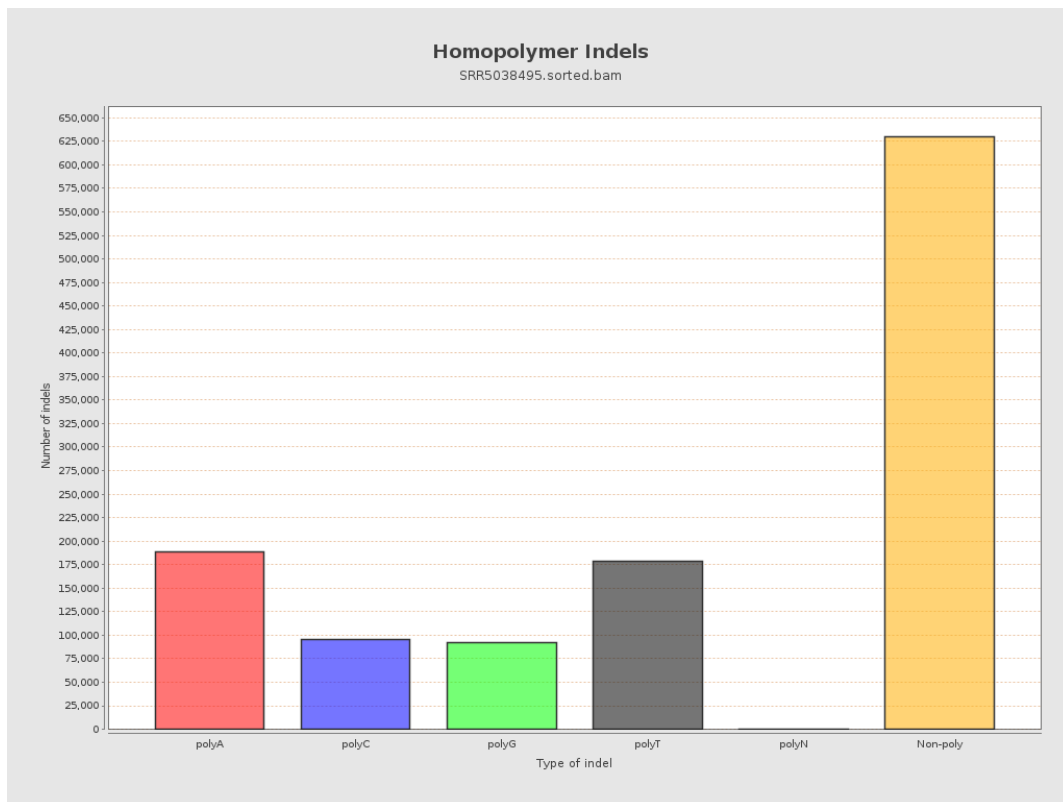
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



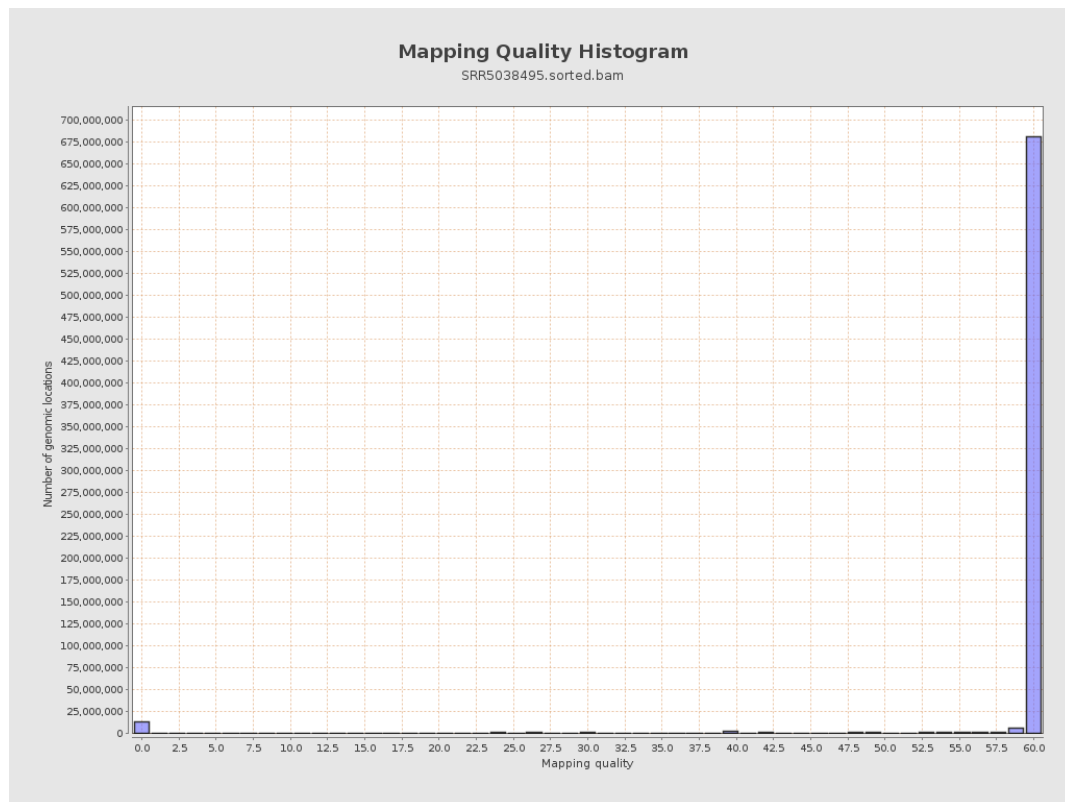
11. Results : Homopolymer Indels



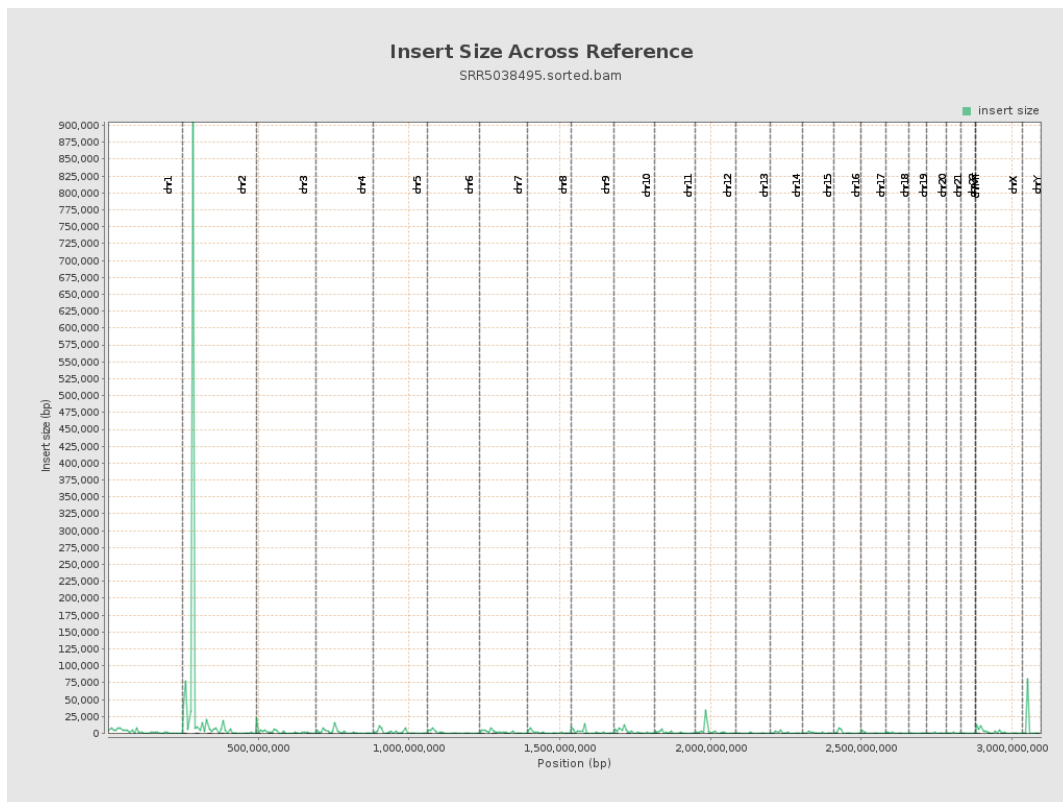
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

