

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 11:48:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038494.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_SRR5038494 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038494_1.fastq.gz SRR5038494_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 11:48:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038494.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,854,548
Mapped reads	11,047,682 / 93.19%
Unmapped reads	806,866 / 6.81%
Mapped paired reads	11,047,682 / 93.19%
Mapped reads, first in pair	5,588,910 / 47.15%
Mapped reads, second in pair	5,458,772 / 46.05%
Mapped reads, both in pair	10,897,614 / 91.93%
Mapped reads, singletons	150,068 / 1.27%
Secondary alignments	0
Supplementary alignments	206,764 / 1.74%
Read min/max/mean length	30 / 150 / 150.89
Duplicated reads (estimated)	1,518,775 / 12.81%
Duplication rate	8.75%
Clipped reads	2,845,085 / 24%

2.2. ACGT Content

Number/percentage of A's	454,709,616 / 28.95%
Number/percentage of C's	322,480,868 / 20.53%
Number/percentage of T's	455,547,677 / 29.01%
Number/percentage of G's	337,635,226 / 21.5%
Number/percentage of N's	33,090 / 0%

GC Percentage	42.03%
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2.3. Coverage

Mean	0.5077
Standard Deviation	6.6329

2.4. Mapping Quality

Mean Mapping Quality	53.74
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2.5. Insert size

Mean	94,575.47
Standard Deviation	2,937,131.64
P25/Median/P75	221 / 263 / 315

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	21,059,739
Insertions	288,827
Mapped reads with at least one insertion	2.43%
Deletions	560,591
Mapped reads with at least one deletion	4.85%
Homopolymer indels	46.37%

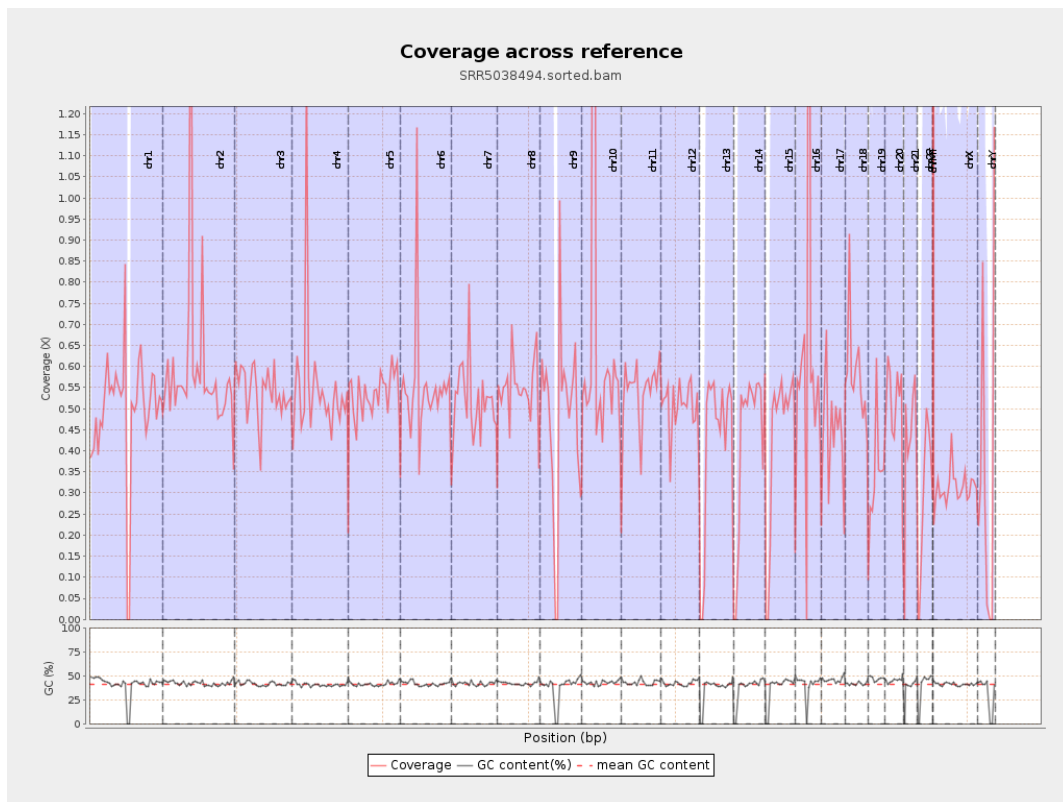
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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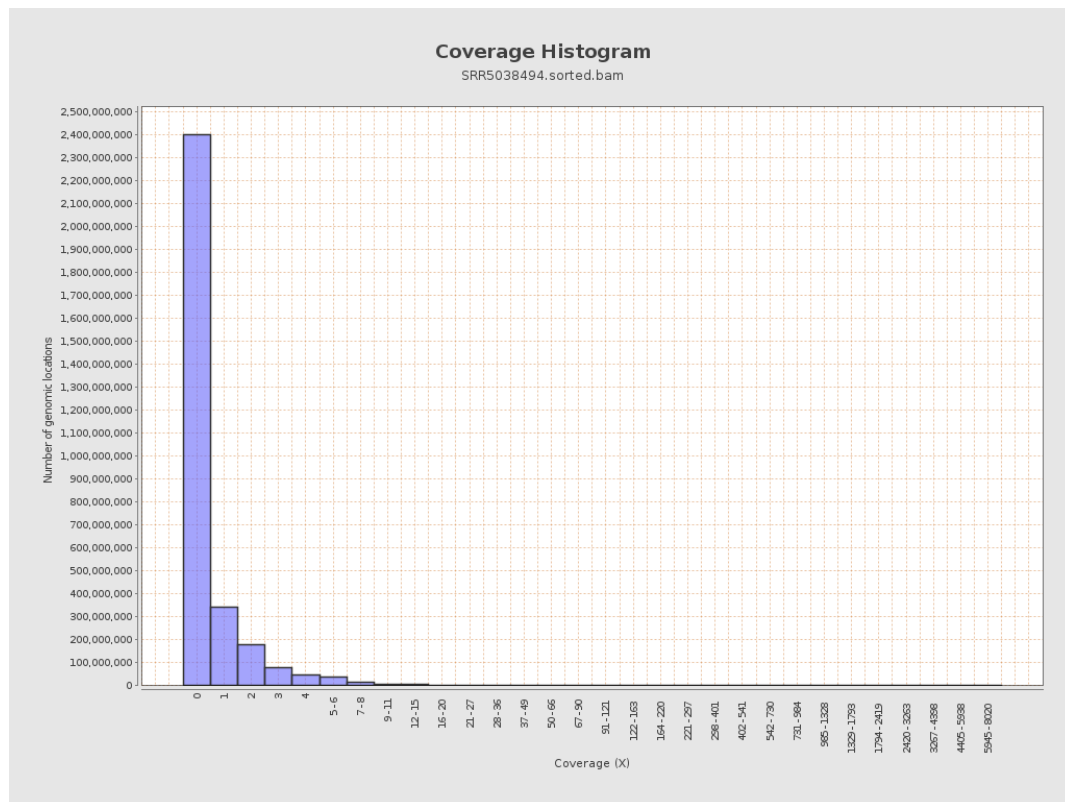
		bases	coverage	deviation
chr1	249250621	123829338	0.4968	5.6179
chr2	243199373	145221683	0.5971	7.9249
chr3	198022430	106834684	0.5395	1.3231
chr4	191154276	105217517	0.5504	5.6996
chr5	180915260	96463097	0.5332	1.3619
chr6	171115067	94132514	0.5501	6.9906
chr7	159138663	82112792	0.516	6.0522
chr8	146364022	80309414	0.5487	1.9458
chr9	141213431	68032979	0.4818	11.4827
chr10	135534747	88000614	0.6493	16.9065
chr11	135006516	73197214	0.5422	3.5527
chr12	133851895	67663153	0.5055	1.2675
chr13	115169878	48507420	0.4212	1.1101
chr14	107349540	46050992	0.429	1.253
chr15	102531392	43669525	0.4259	1.1423
chr16	90354753	58338280	0.6457	12.4889
chr17	81195210	36842641	0.4538	4.3977
chr18	78077248	45673667	0.585	10.1119
chr19	59128983	20605308	0.3485	3.1003
chr20	63025520	32724076	0.5192	1.9575
chr21	48129895	20340330	0.4226	2.889
chr22	51304566	15173750	0.2958	1.0952
chrMT	16571	2521584	152.1685	66.7156
chrX	155270560	48402347	0.3117	1.3592

chrY	59373566	21712548	0.3657	10.0639
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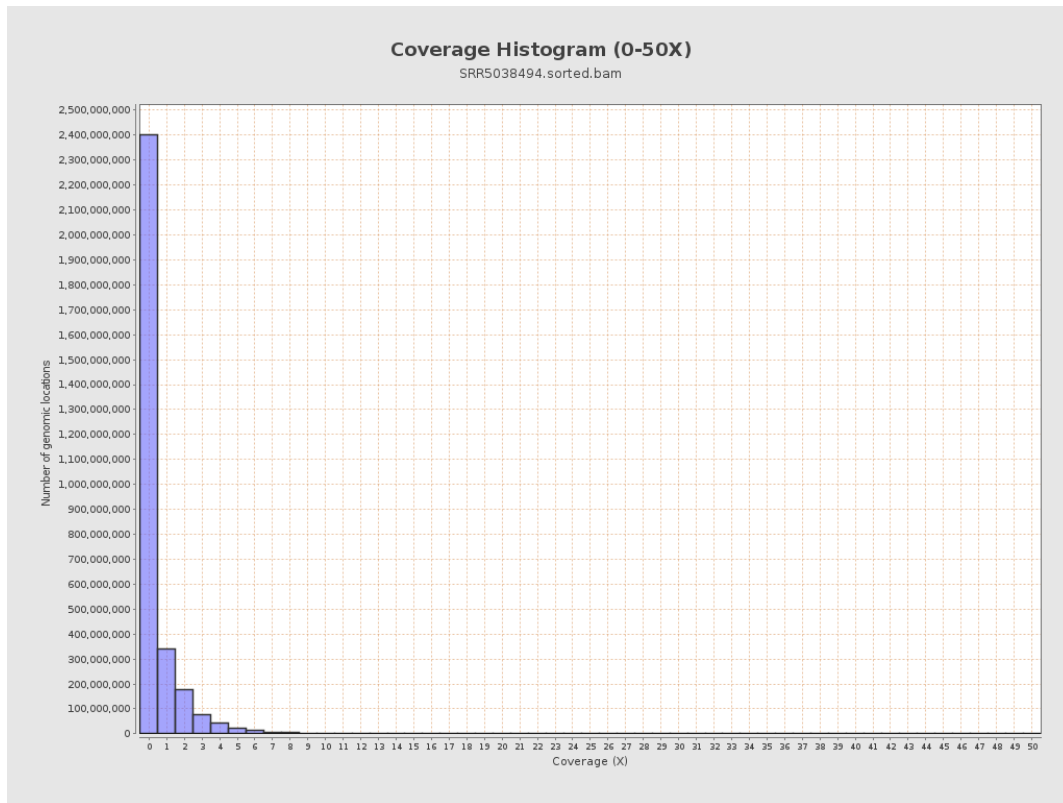
3. Results : Coverage across reference



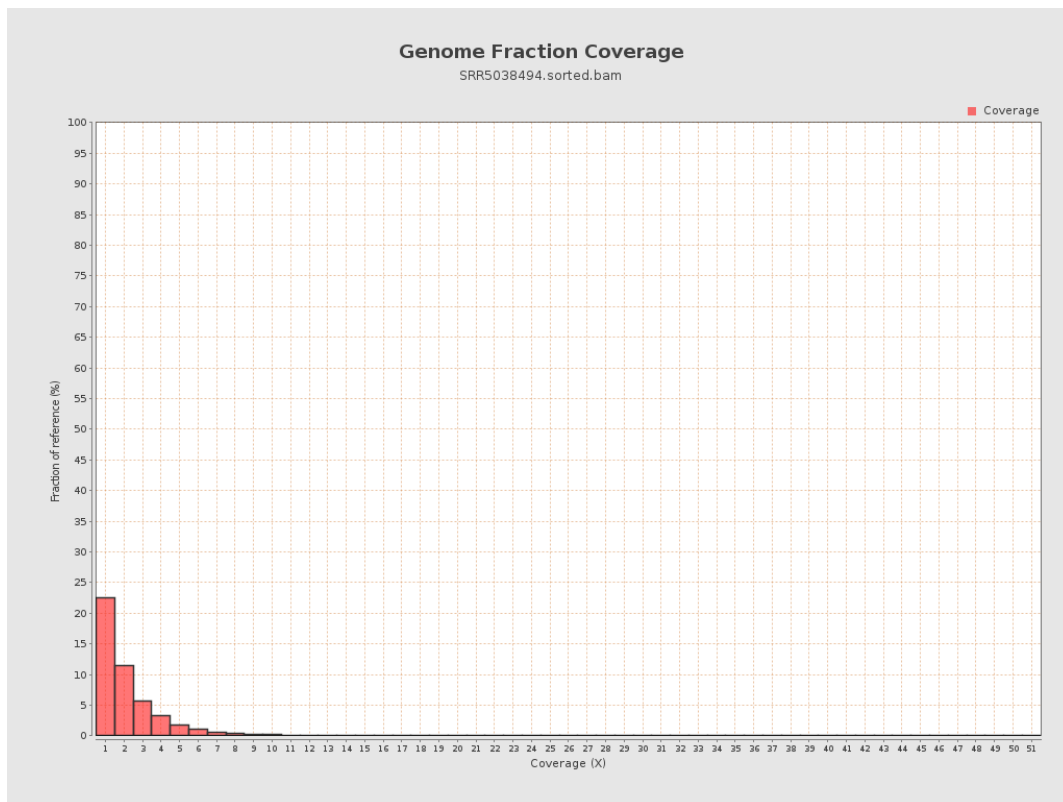
4. Results : Coverage Histogram



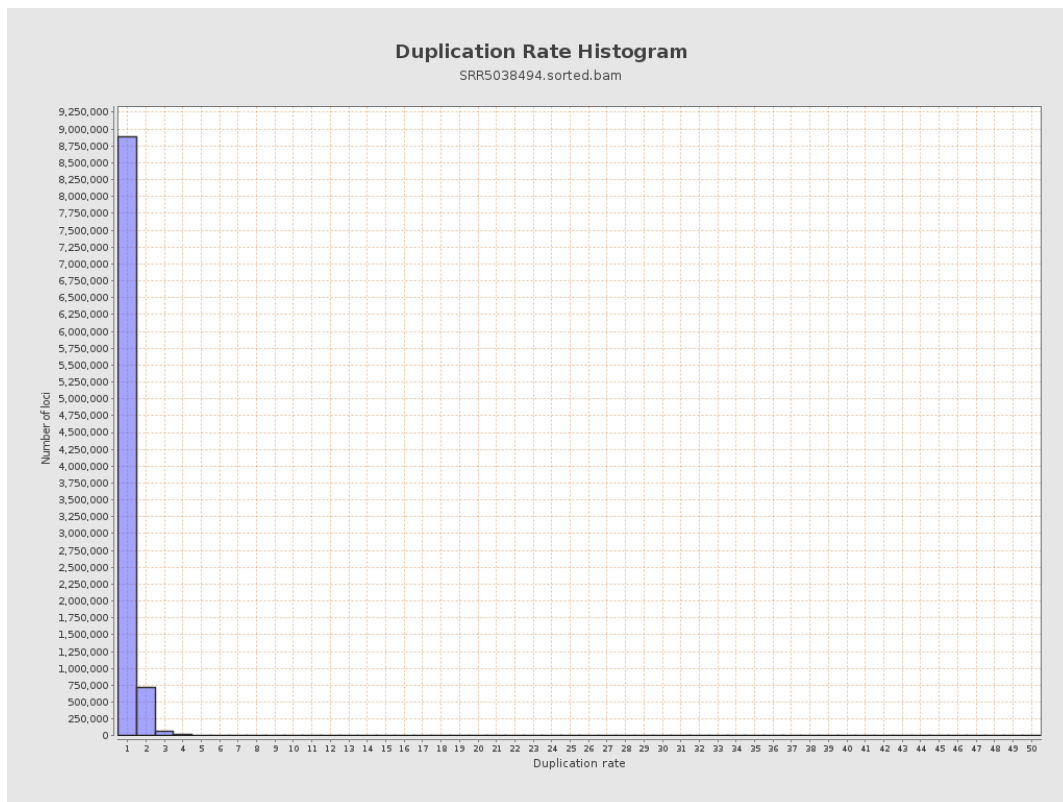
5. Results : Coverage Histogram (0-50X)



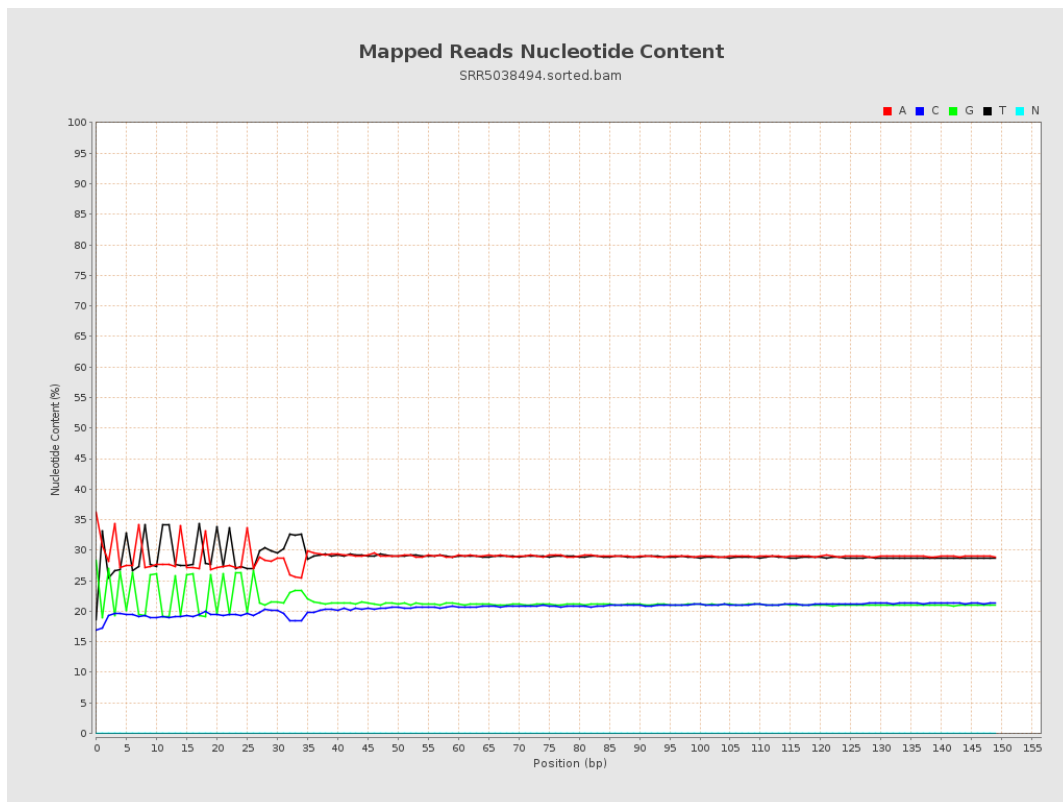
6. Results : Genome Fraction Coverage



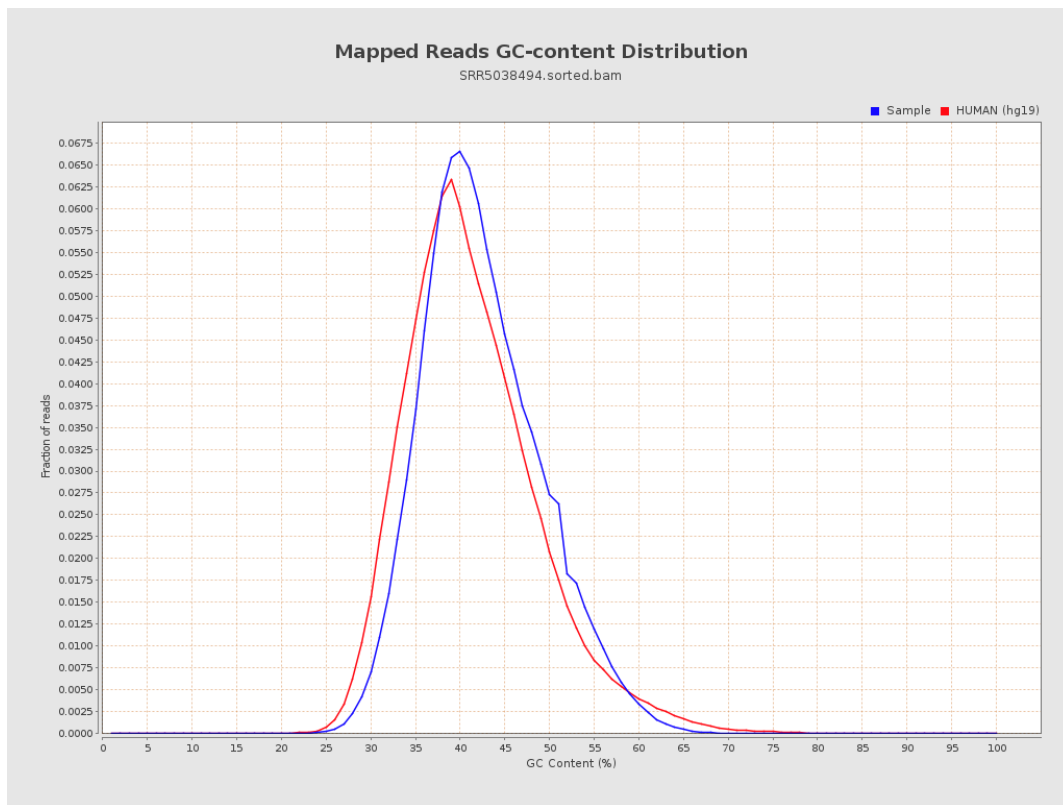
7. Results : Duplication Rate Histogram



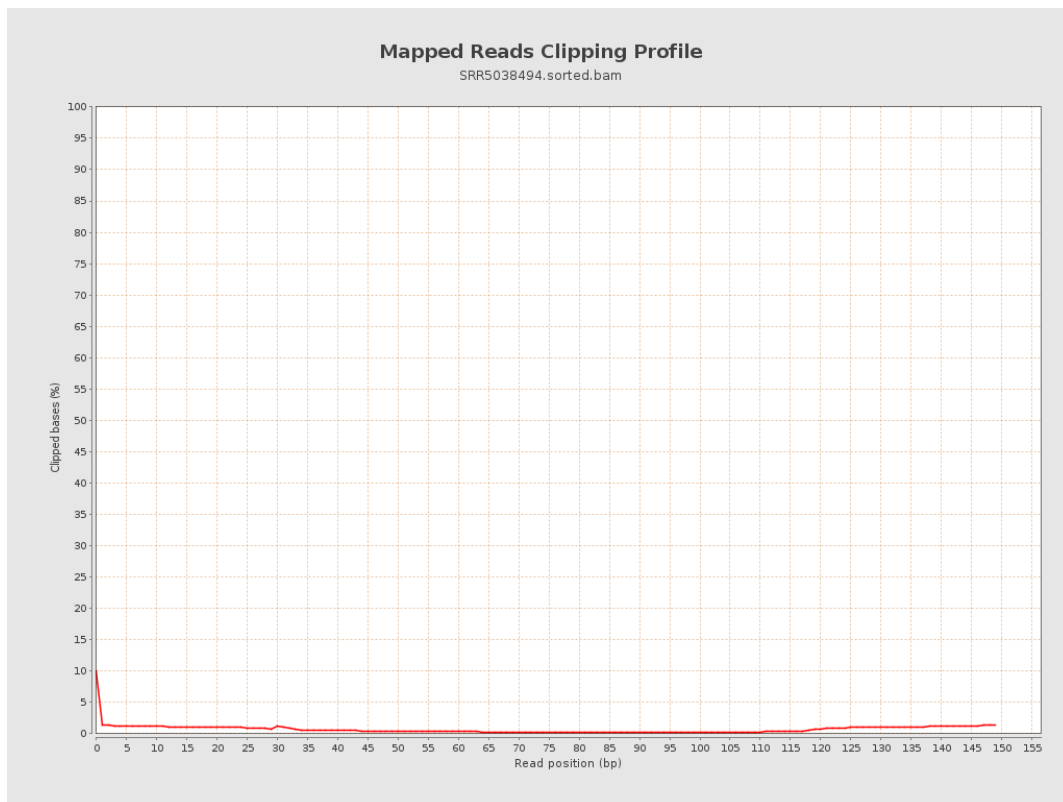
8. Results : Mapped Reads Nucleotide Content



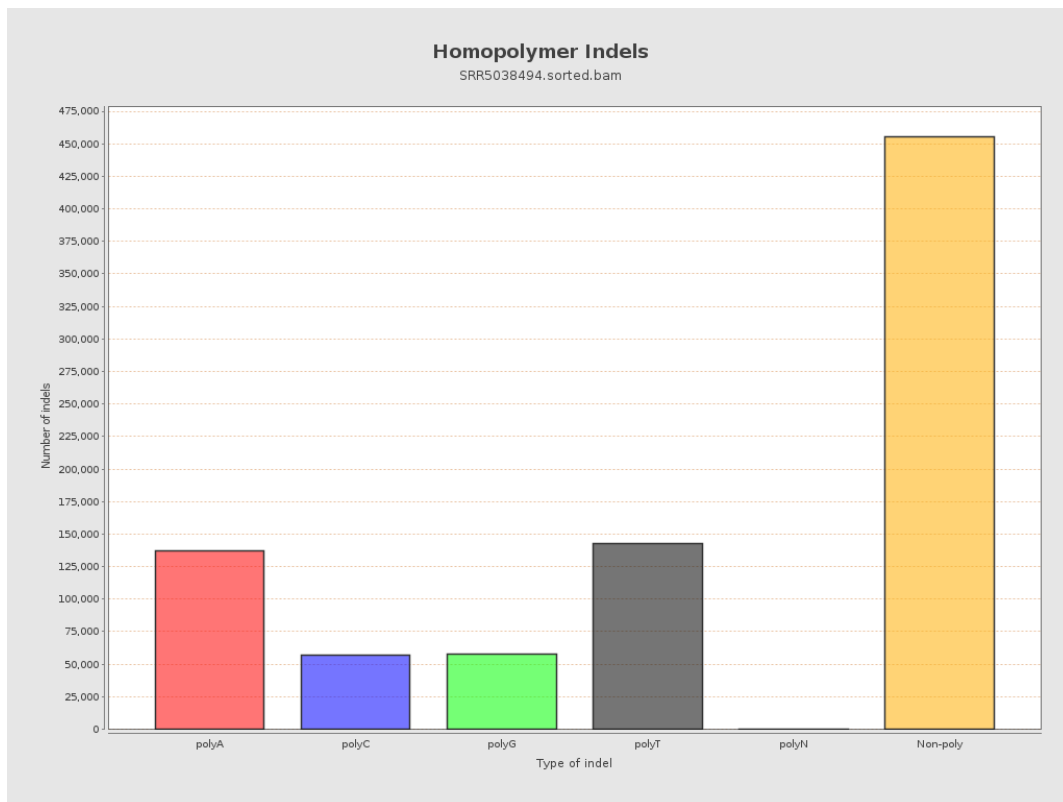
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



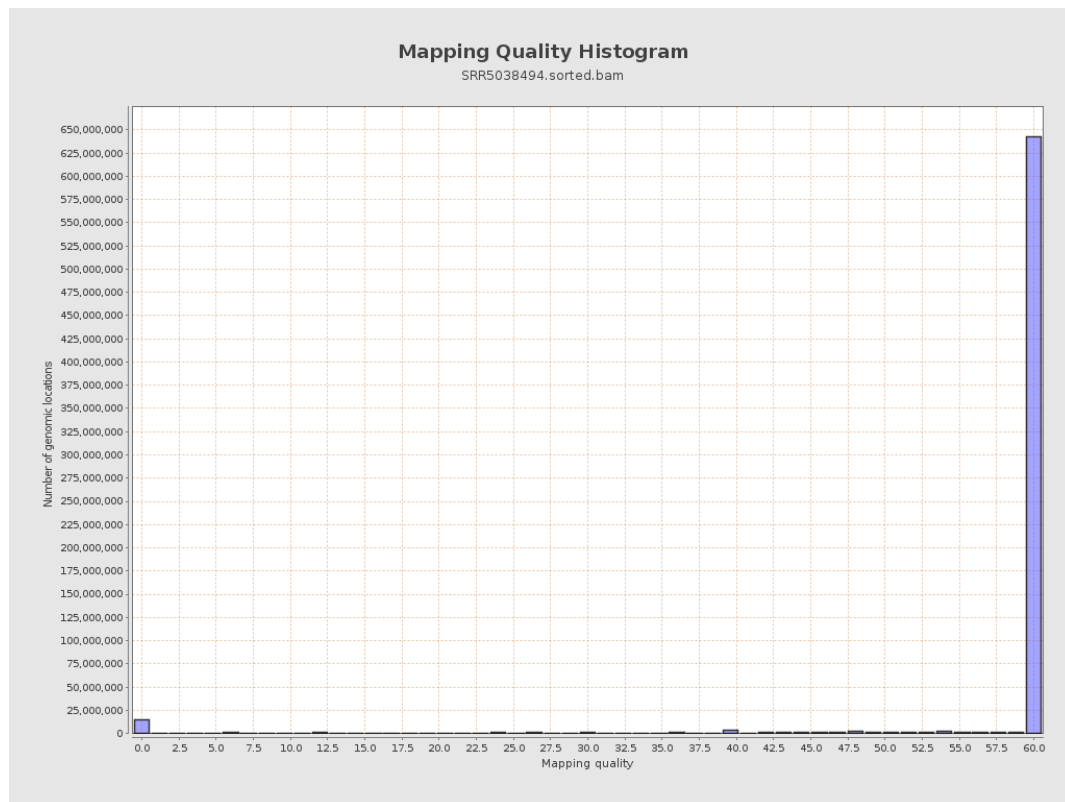
11. Results : Homopolymer Indels



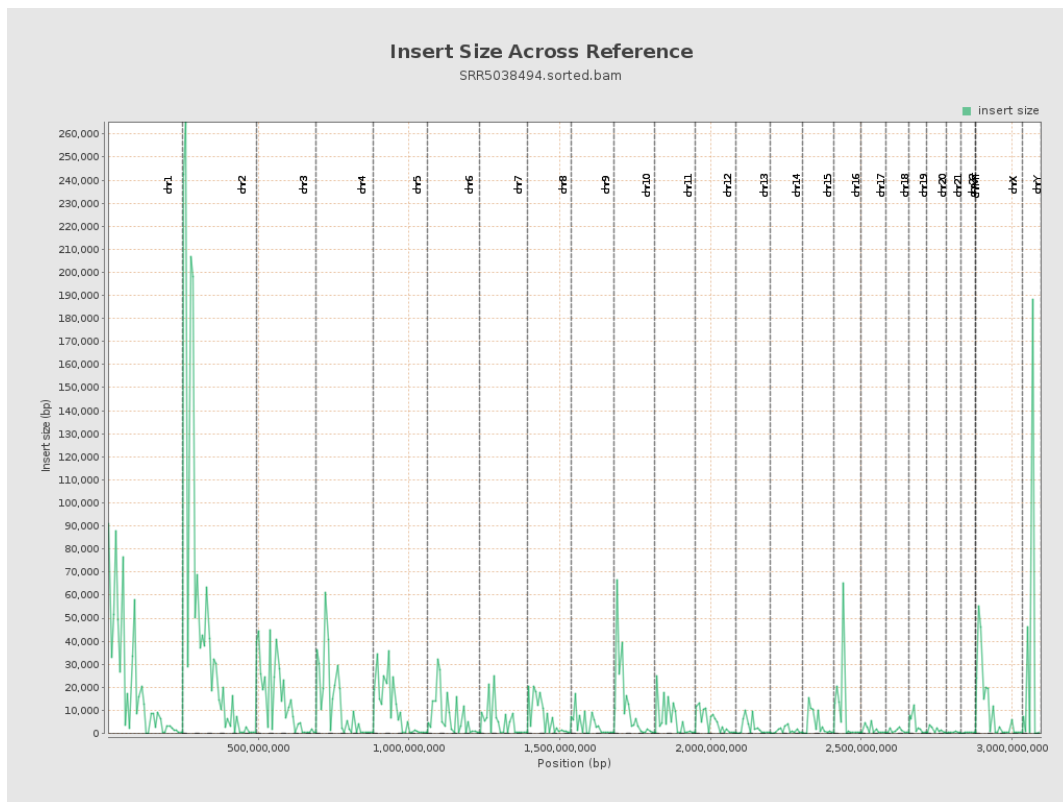
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

