

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/15 15:06:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630861.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630861_1.fastq.gz SRR630861_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 15 15:06:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	62,626,116
Mapped reads	62,080,483 / 99.13%
Unmapped reads	545,633 / 0.87%
Mapped paired reads	62,080,483 / 99.13%
Mapped reads, first in pair	31,213,628 / 49.84%
Mapped reads, second in pair	30,866,855 / 49.29%
Mapped reads, both in pair	61,715,308 / 98.55%
Mapped reads, singletons	365,175 / 0.58%
Secondary alignments	0
Supplementary alignments	302,579 / 0.48%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	12,159,590 / 19.42%
Duplication rate	18.41%
Clipped reads	6,461,077 / 10.32%

2.2. ACGT Content

Number/percentage of A's	1,864,515,975 / 30.85%
Number/percentage of C's	1,158,936,785 / 19.18%
Number/percentage of T's	1,827,064,698 / 30.23%
Number/percentage of G's	1,185,279,997 / 19.61%
Number/percentage of N's	7,338,919 / 0.12%

GC Percentage	38.79%
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2.3. Coverage

Mean	1.9526
Standard Deviation	6.605

2.4. Mapping Quality

Mean Mapping Quality	53.26
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2.5. Insert size

Mean	206,152.95
Standard Deviation	4,277,947.33
P25/Median/P75	156 / 203 / 277

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	50,045,635
Insertions	11,976,107
Mapped reads with at least one insertion	19.14%
Deletions	854,996
Mapped reads with at least one deletion	1.35%
Homopolymer indels	23.25%

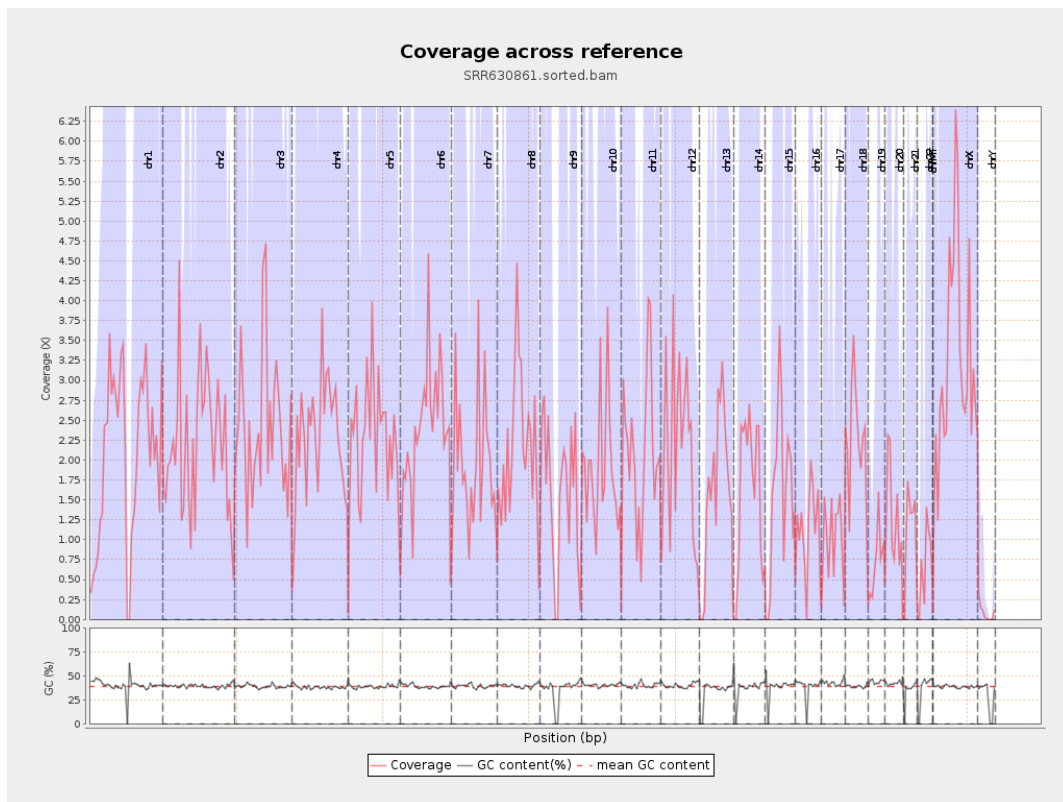
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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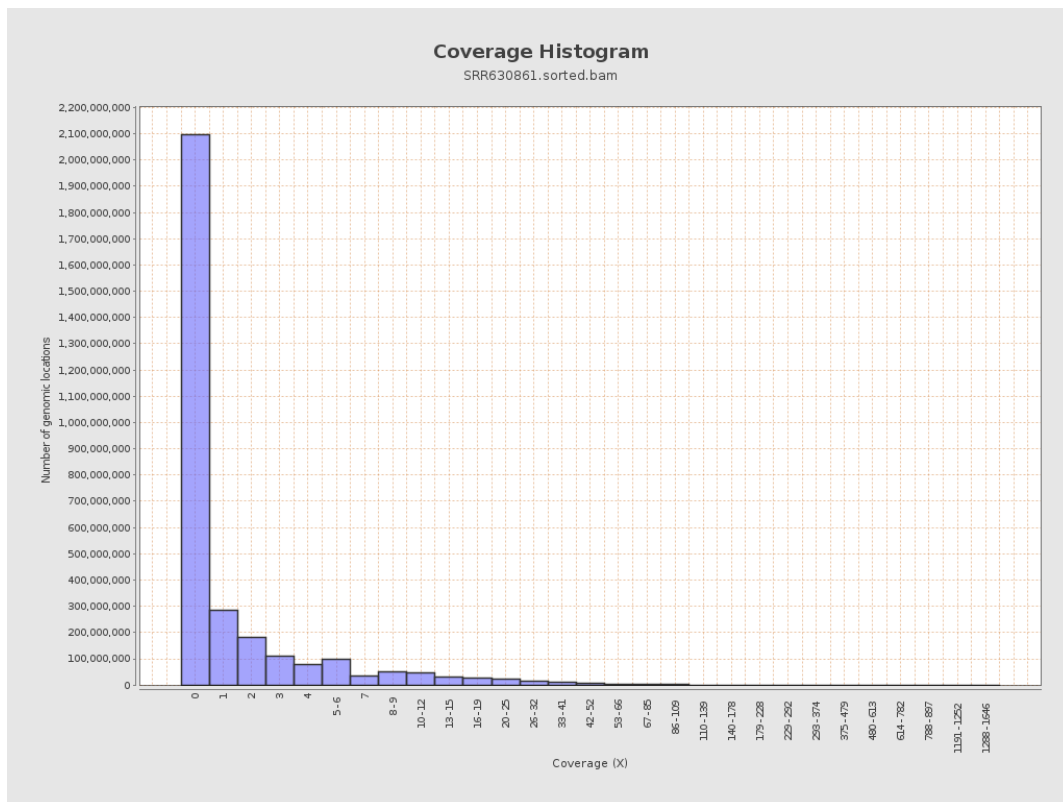
		bases	coverage	deviation
chr1	249250621	514453181	2.064	6.923
chr2	243199373	527202101	2.1678	6.7027
chr3	198022430	473781368	2.3926	8.2513
chr4	191154276	442038133	2.3125	6.2883
chr5	180915260	404556000	2.2362	6.8337
chr6	171115067	411024724	2.402	7.724
chr7	159138663	308117775	1.9362	5.9
chr8	146364022	319409641	2.1823	6.3665
chr9	141213431	223270455	1.5811	5.2679
chr10	135534747	256495496	1.8925	6.4054
chr11	135006516	284073431	2.1041	6.3471
chr12	133851895	278564301	2.0811	6.9223
chr13	115169878	187343107	1.6267	4.8115
chr14	107349540	174700298	1.6274	5.7605
chr15	102531392	157671301	1.5378	6.3637
chr16	90354753	99523128	1.1015	3.8649
chr17	81195210	84376288	1.0392	3.8267
chr18	78077248	178212890	2.2825	7.3285
chr19	59128983	42939320	0.7262	3.7936
chr20	63025520	78854446	1.2512	4.6539
chr21	48129895	53044118	1.1021	3.6625
chr22	51304566	35123727	0.6846	4.0203
chrMT	16571	1286	0.0776	0.3823
chrX	155270560	504988055	3.2523	10.6986

chrY	59373566	4925745	0.083	0.9241
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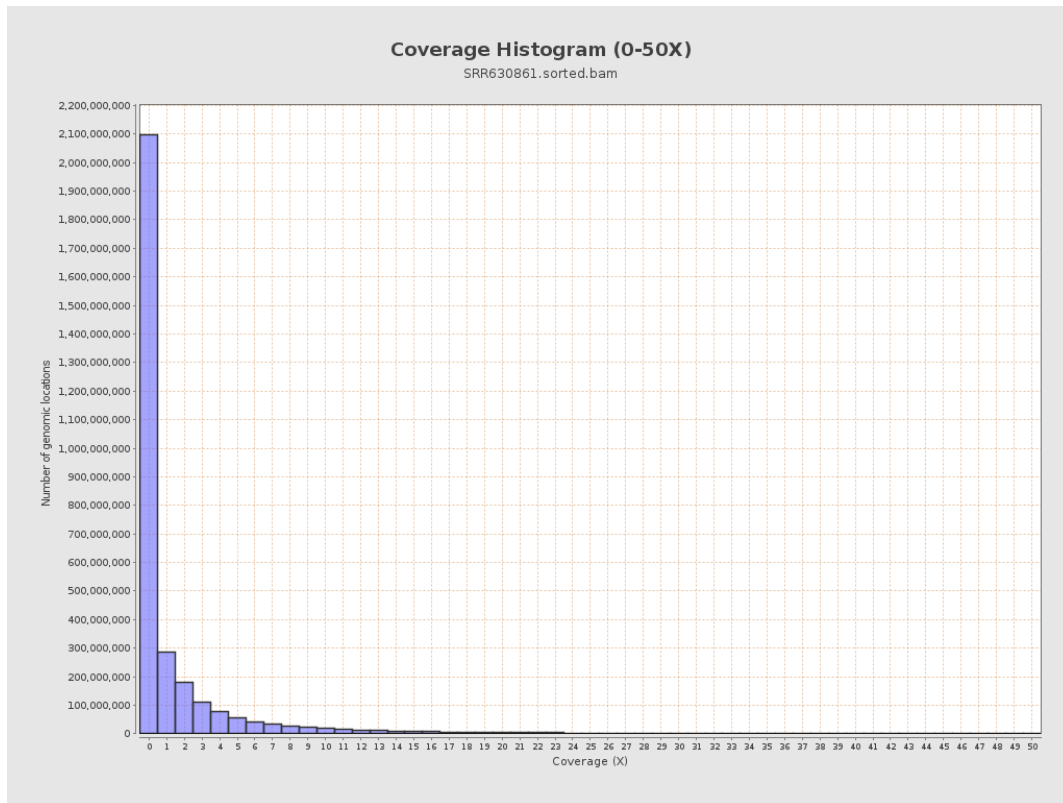
3. Results : Coverage across reference



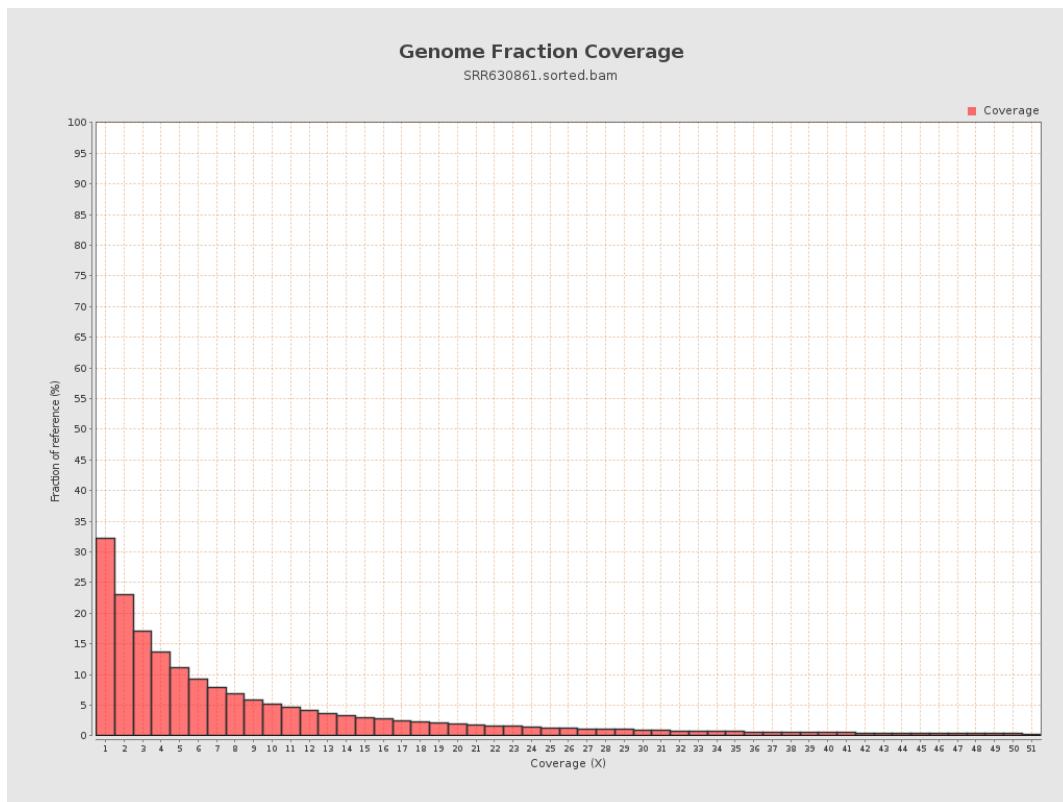
4. Results : Coverage Histogram



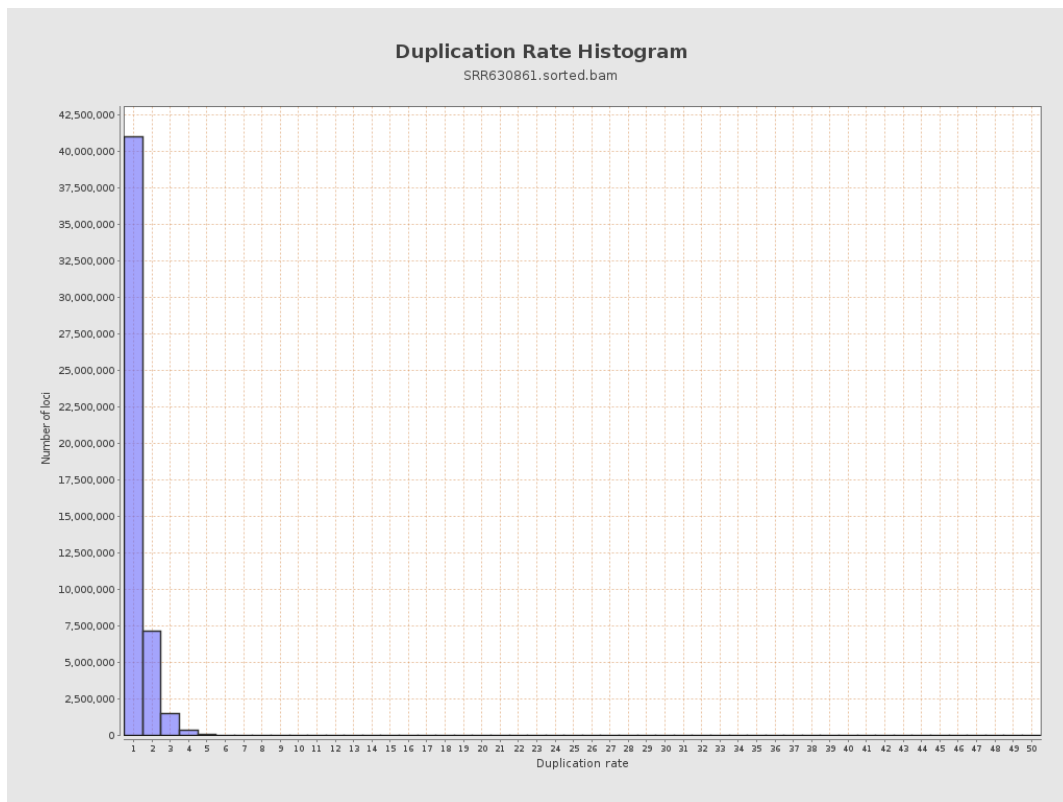
5. Results : Coverage Histogram (0-50X)



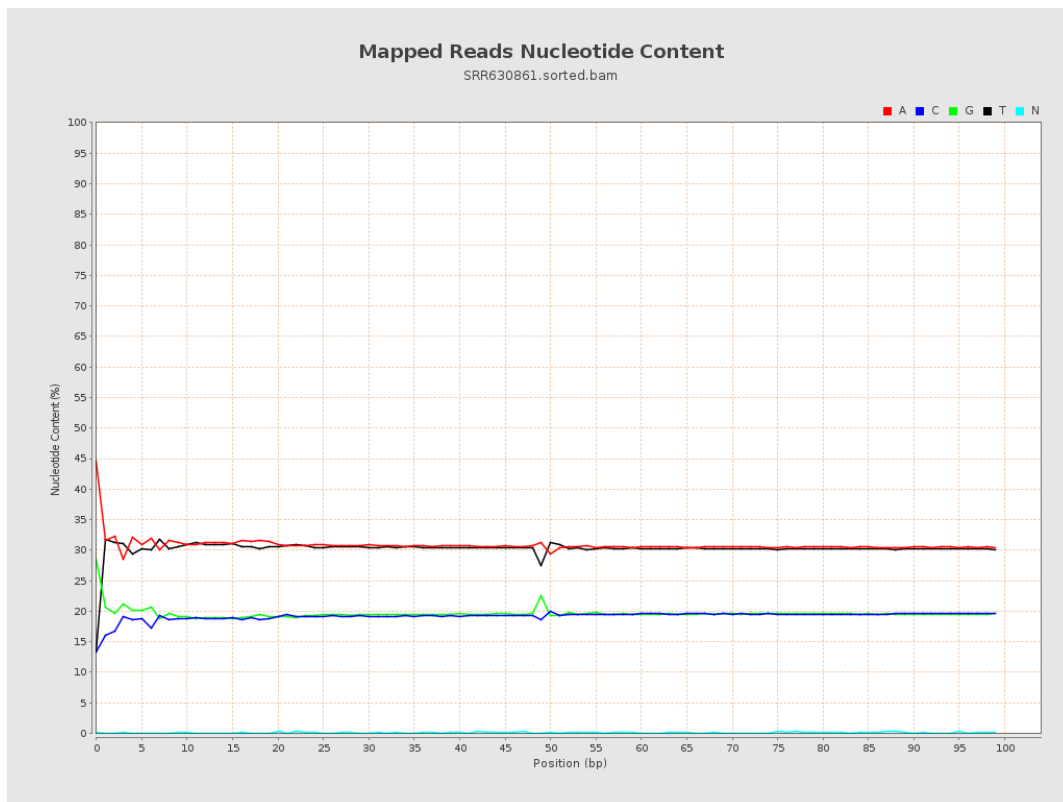
6. Results : Genome Fraction Coverage



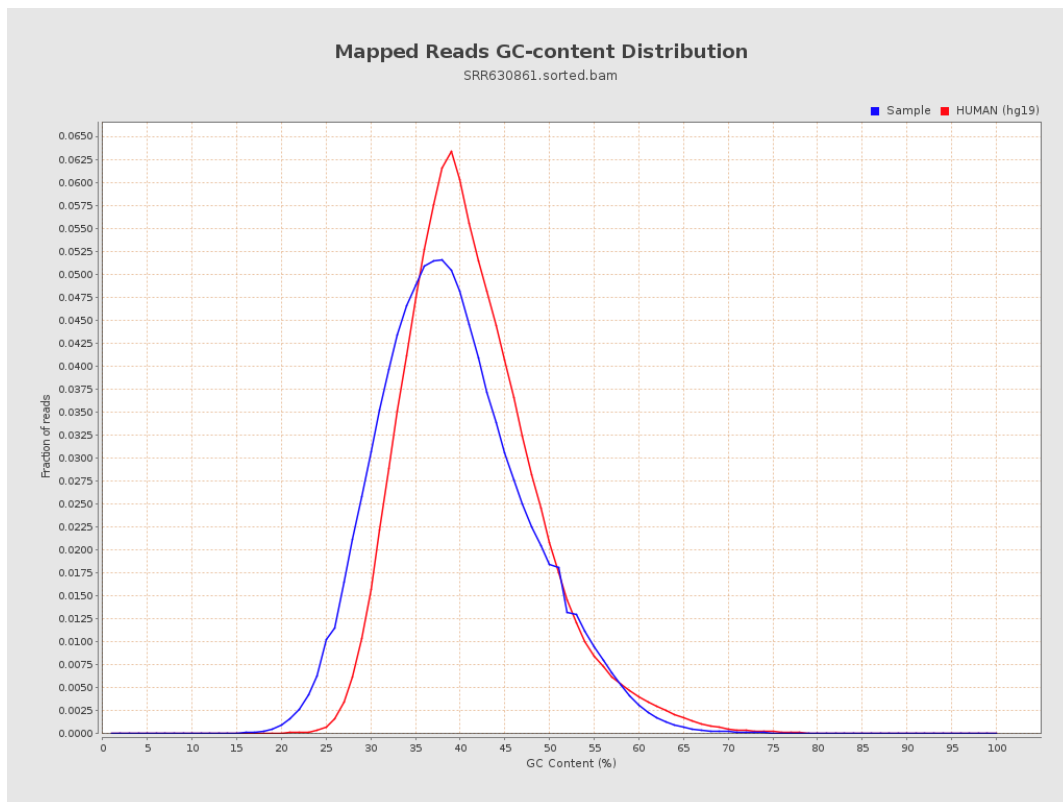
7. Results : Duplication Rate Histogram



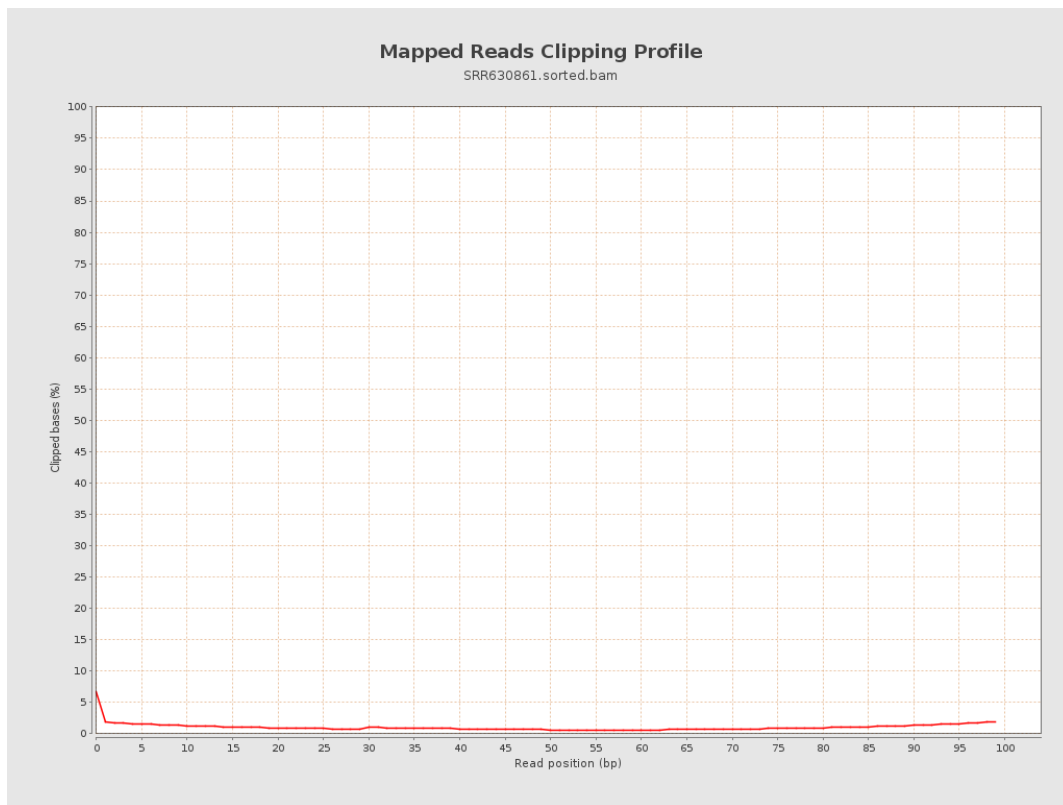
8. Results : Mapped Reads Nucleotide Content



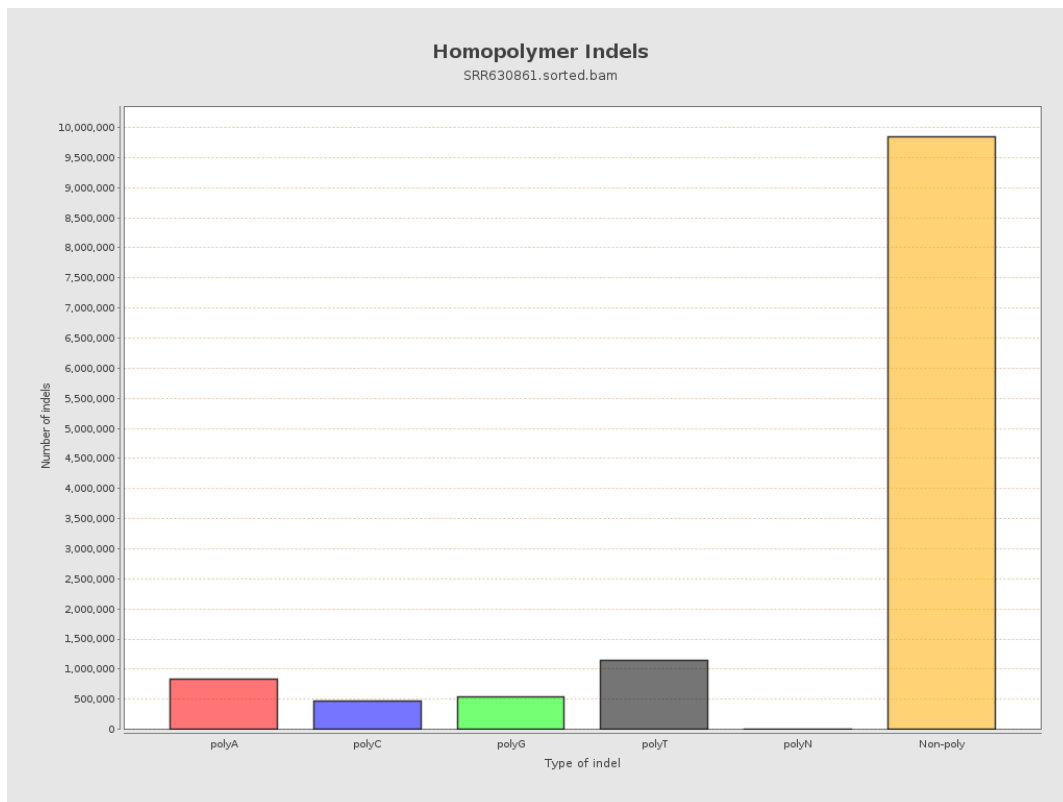
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



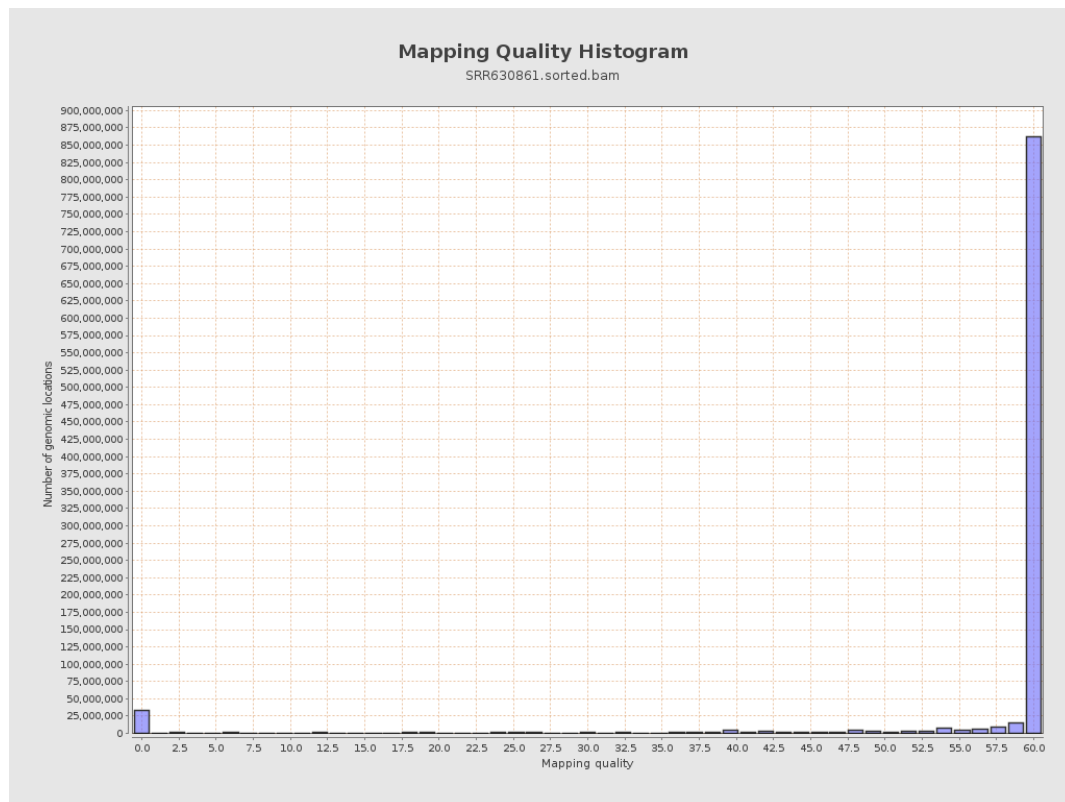
11. Results : Homopolymer Indels



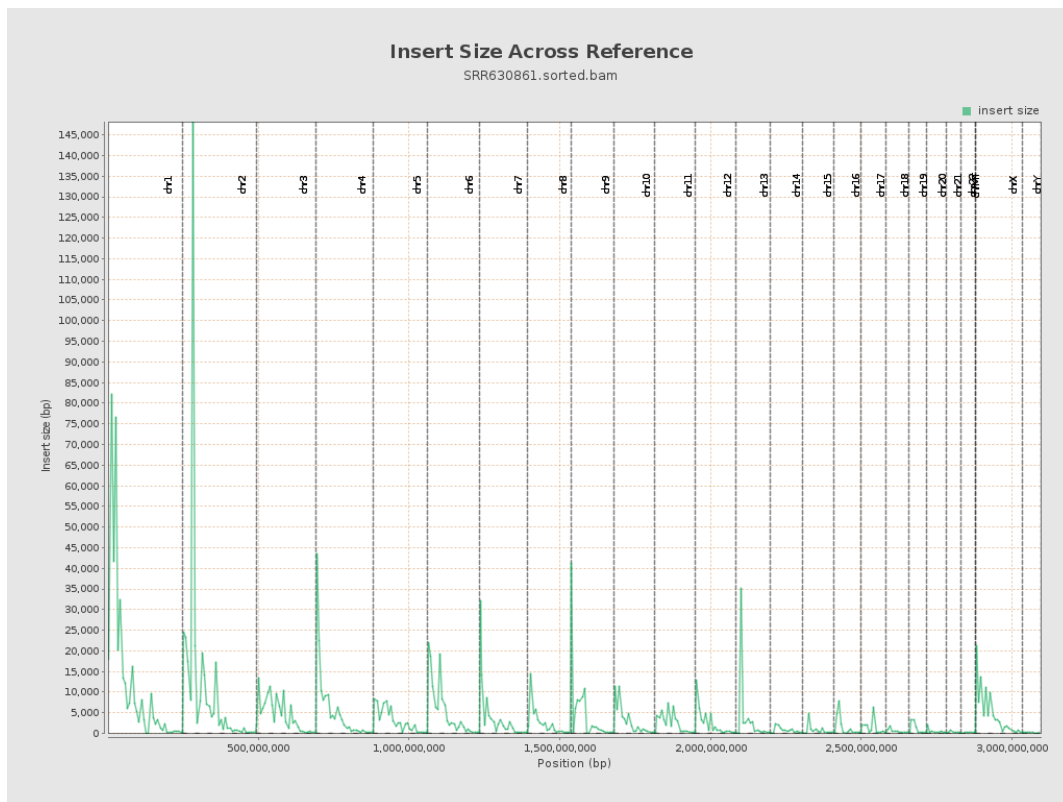
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

