

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:00:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094096.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_ERR2094096 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094096_1.fastq.gz ERR2094096_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:00:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	170
Mapped reads	134 / 78.82%
Unmapped reads	36 / 21.18%
Mapped paired reads	134 / 78.82%
Mapped reads, first in pair	68 / 40%
Mapped reads, second in pair	66 / 38.82%
Mapped reads, both in pair	122 / 71.76%
Mapped reads, singletons	12 / 7.06%
Secondary alignments	0
Supplementary alignments	10 / 5.88%
Read min/max/mean length	30 / 151 / 136.24
Duplicated reads (estimated)	17 / 10%
Duplication rate	11.02%
Clipped reads	100 / 58.82%

2.2. ACGT Content

Number/percentage of A's	4,689 / 29.97%
Number/percentage of C's	3,301 / 21.1%
Number/percentage of T's	4,145 / 26.49%
Number/percentage of G's	3,510 / 22.44%
Number/percentage of N's	0 / 0%

GC Percentage	43.53%
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2.3. Coverage

Mean	0
Standard Deviation	0.0031

2.4. Mapping Quality

Mean Mapping Quality	6.17
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2.5. Insert size

Mean	3,856,437.07
Standard Deviation	14,172,425.21
P25/Median/P75	145 / 167 / 197

2.6. Mismatches and indels

General error rate	3.85%
Mismatches	567
Insertions	17
Mapped reads with at least one insertion	12.69%
Deletions	41
Mapped reads with at least one deletion	27.61%
Homopolymer indels	39.66%

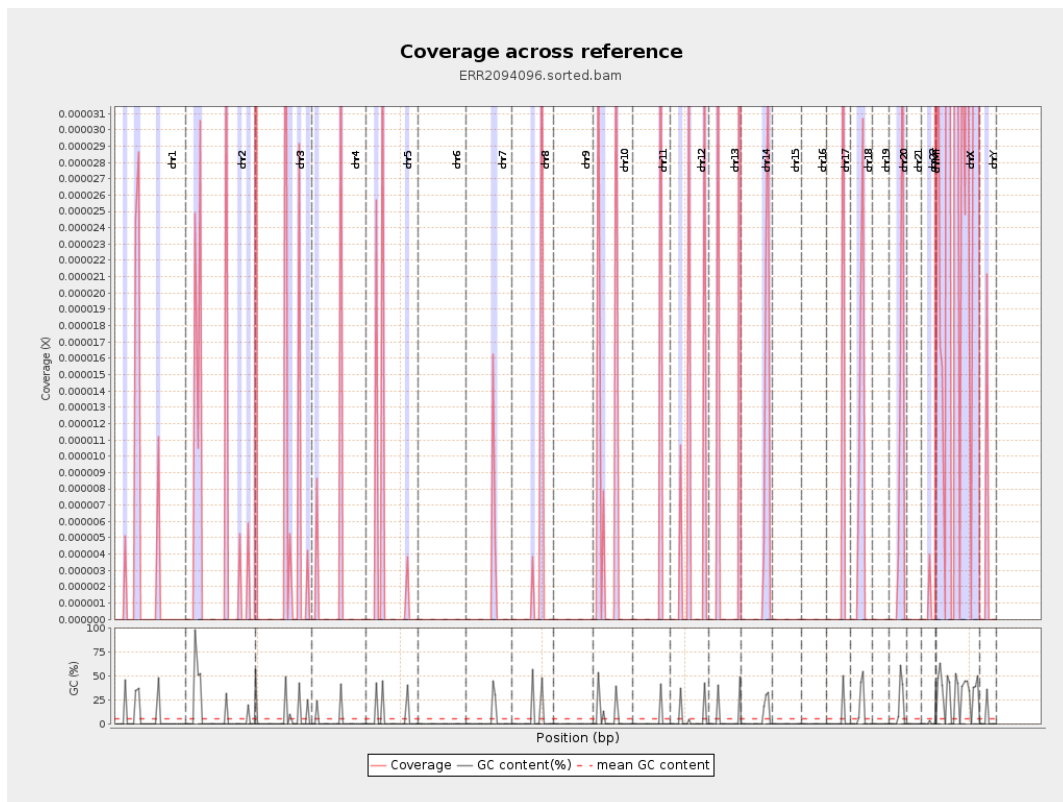
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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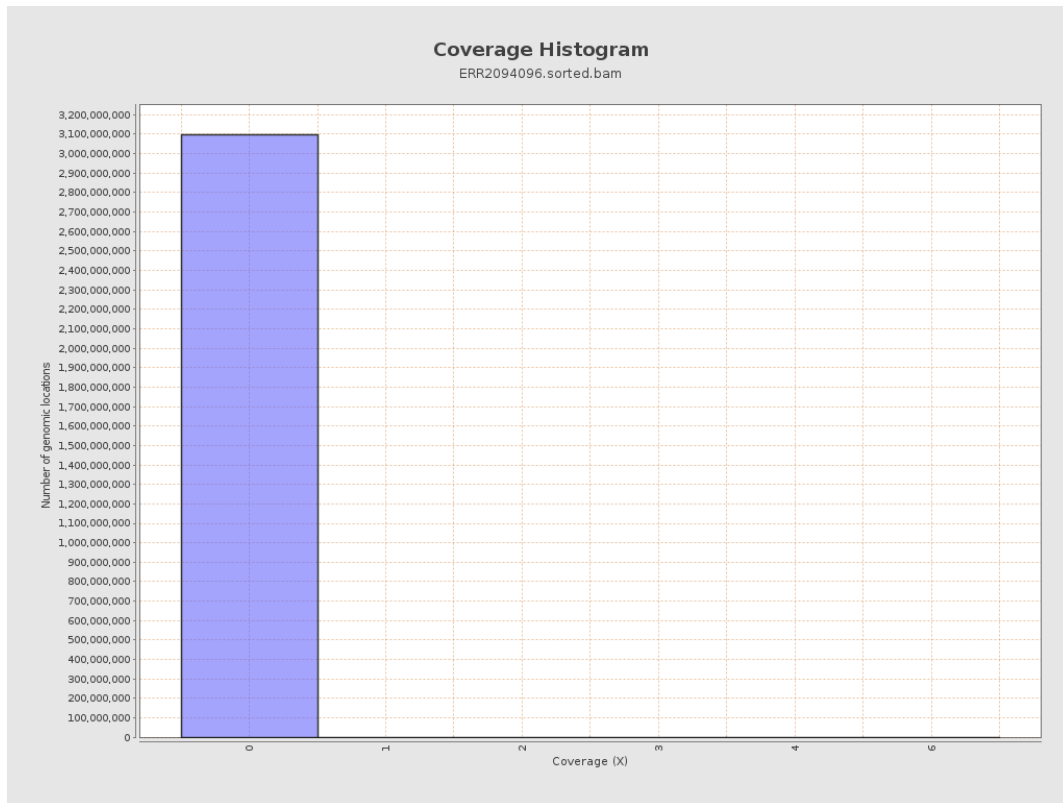
		bases	coverage	deviation
chr1	249250621	539	0	0.002
chr2	243199373	893	0	0.0024
chr3	198022430	938	0	0.0029
chr4	191154276	367	0	0.0017
chr5	180915260	526	0	0.0023
chr6	171115067	0	0	0
chr7	159138663	163	0	0.001
chr8	146364022	341	0	0.002
chr9	141213431	0	0	0
chr10	135534747	649	0	0.003
chr11	135006516	331	0	0.002
chr12	133851895	627	0	0.0032
chr13	115169878	907	0	0.0046
chr14	107349540	472	0	0.0026
chr15	102531392	0	0	0
chr16	90354753	0	0	0
chr17	81195210	337	0	0.0026
chr18	78077248	461	0	0.0027
chr19	59128983	0	0	0
chr20	63025520	449	0	0.0029
chr21	48129895	0	0	0
chr22	51304566	31	0	0.0008
chrMT	16571	1350	0.0815	0.3532
chrX	155270560	6376	0	0.0089

chrY	59373566	164	0	0.002
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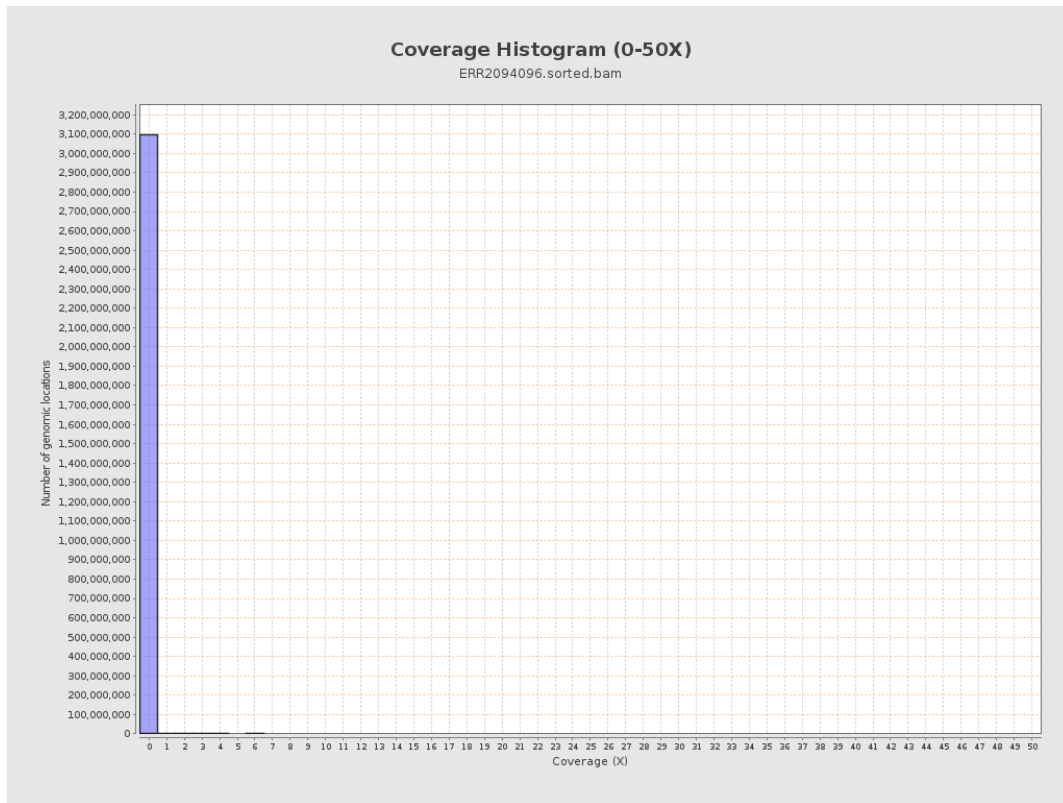
3. Results : Coverage across reference



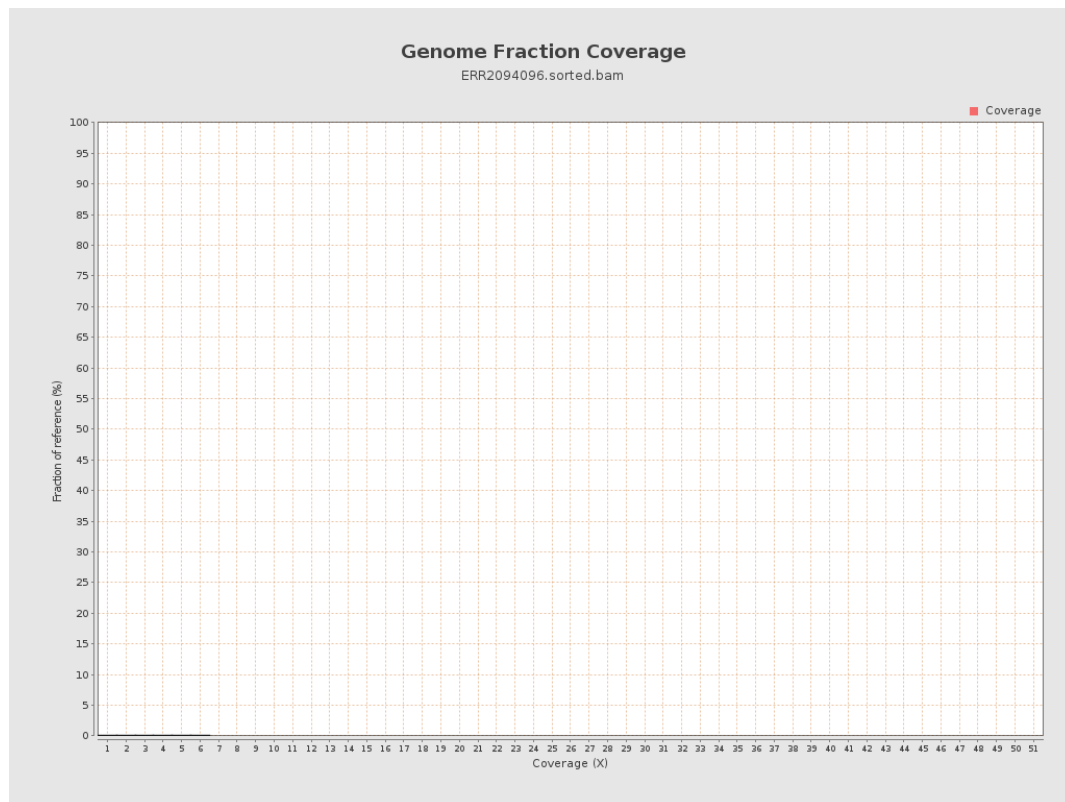
4. Results : Coverage Histogram



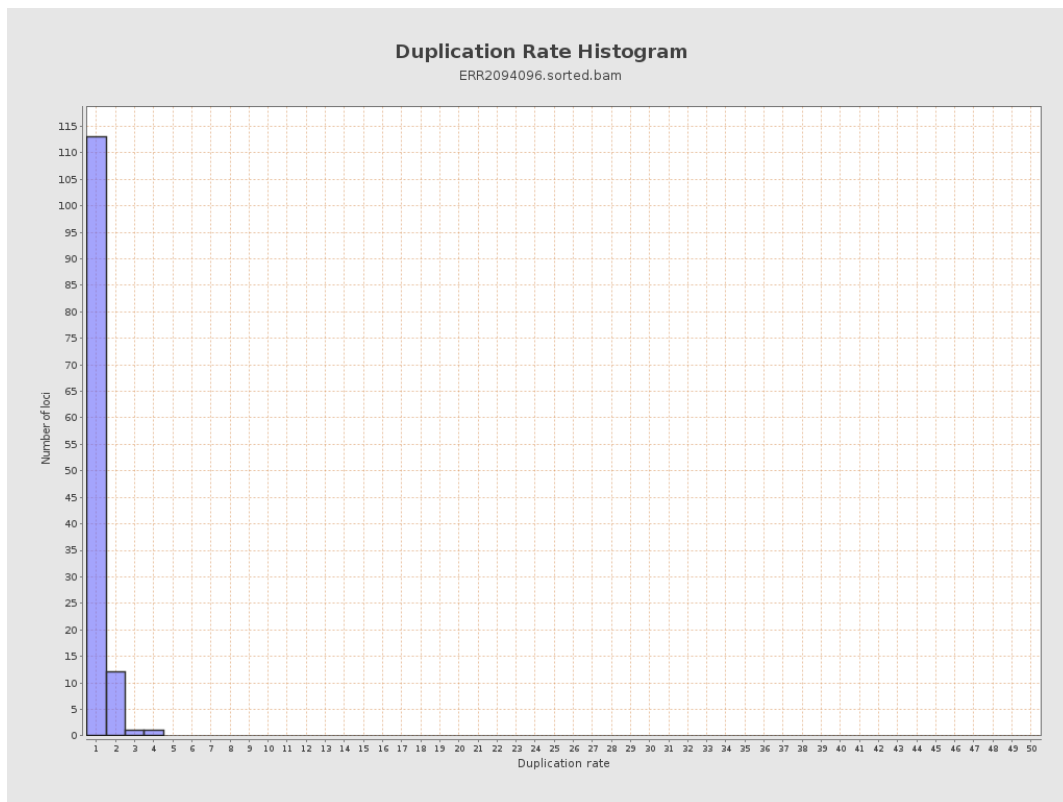
5. Results : Coverage Histogram (0-50X)



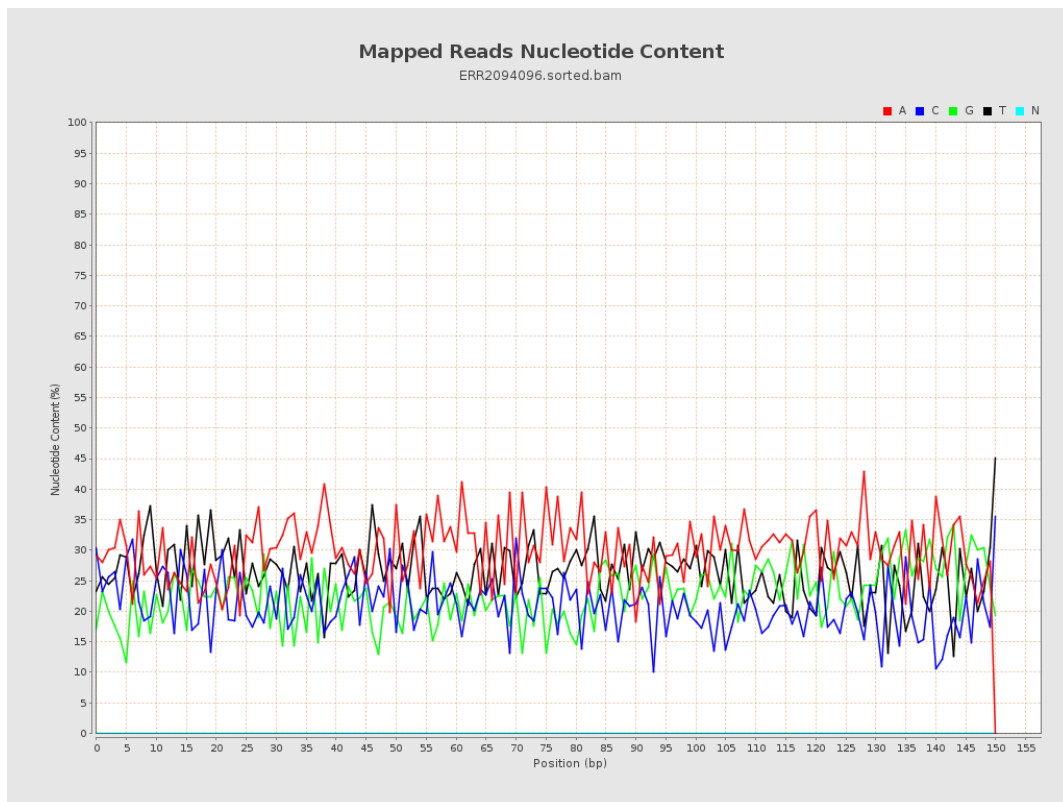
6. Results : Genome Fraction Coverage



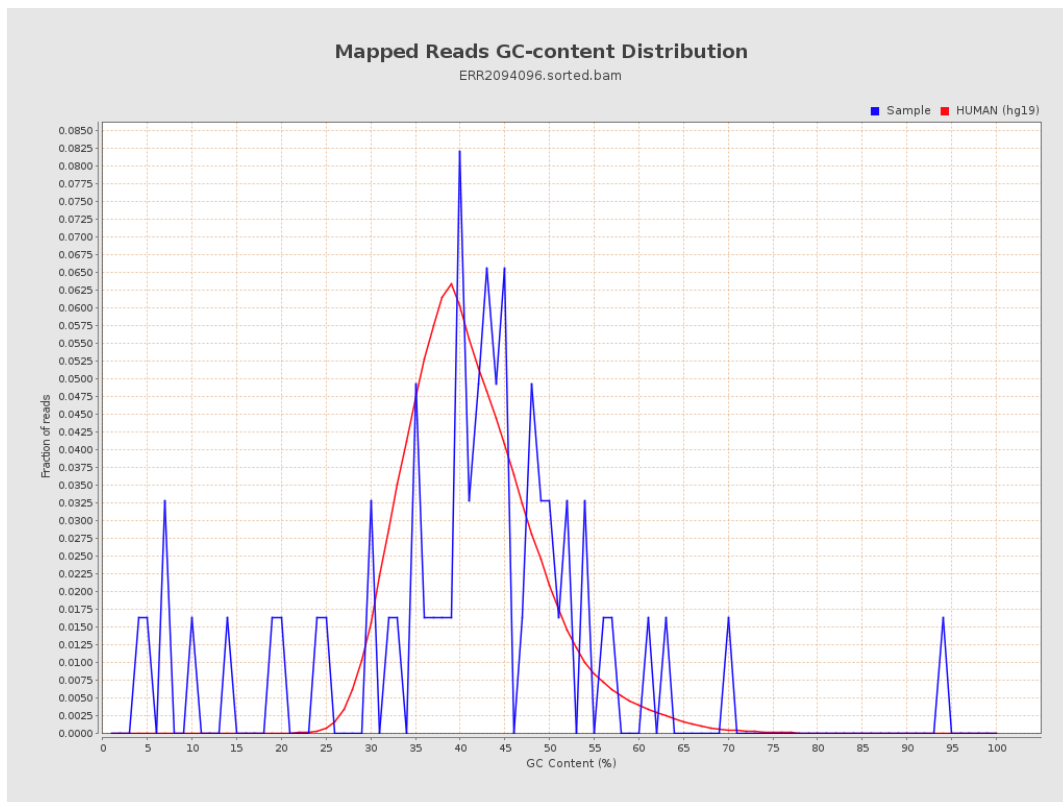
7. Results : Duplication Rate Histogram



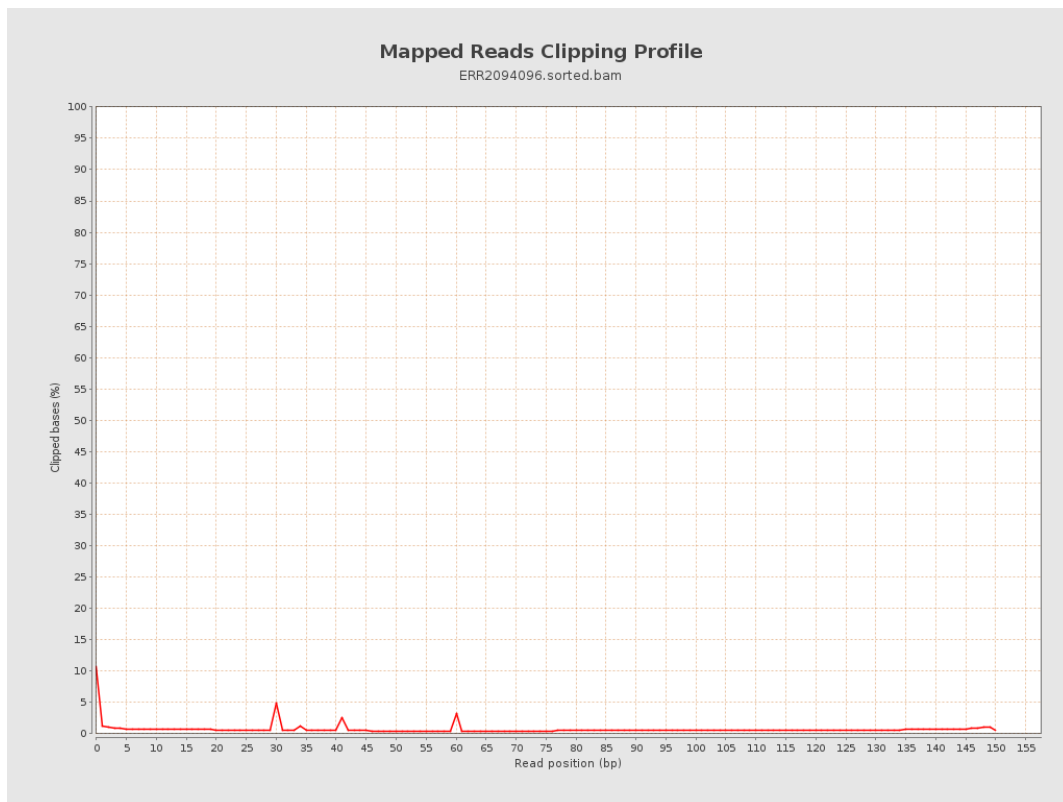
8. Results : Mapped Reads Nucleotide Content



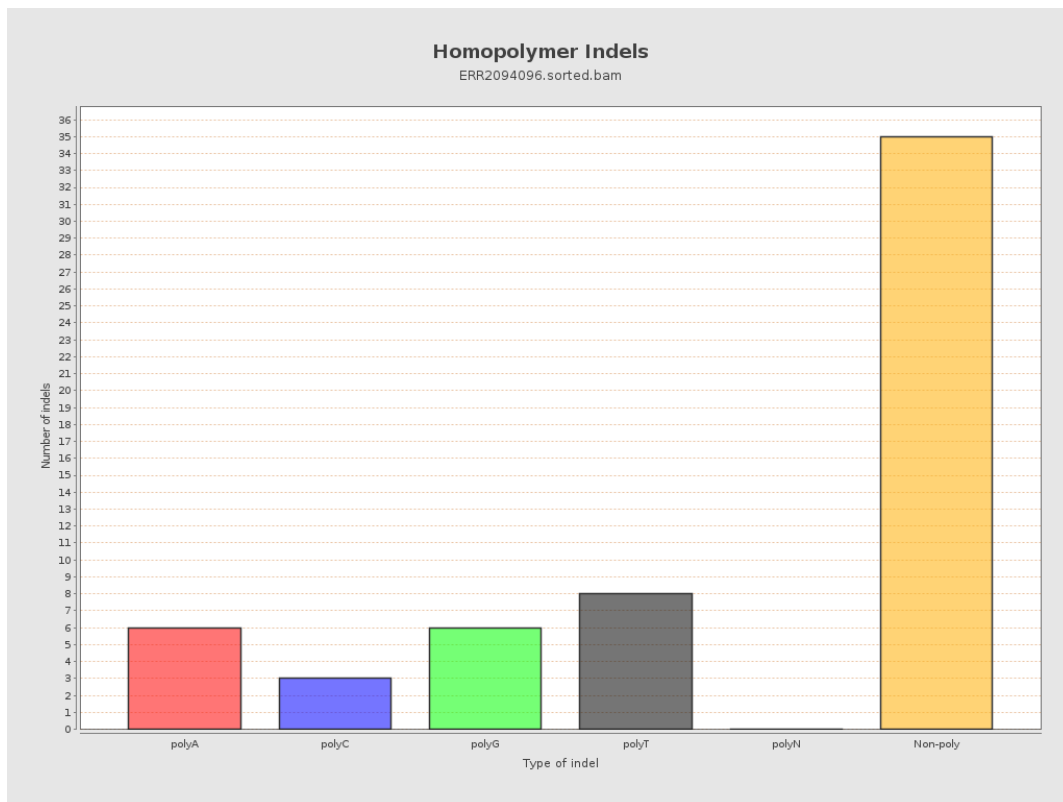
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



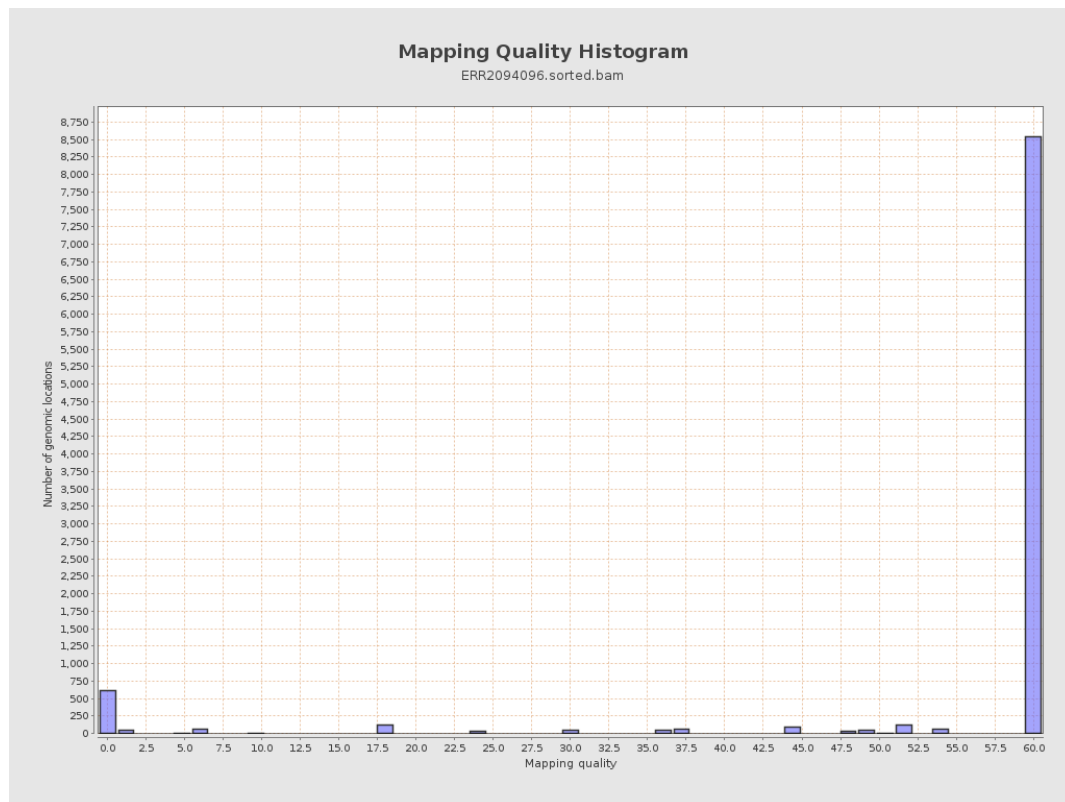
11. Results : Homopolymer Indels



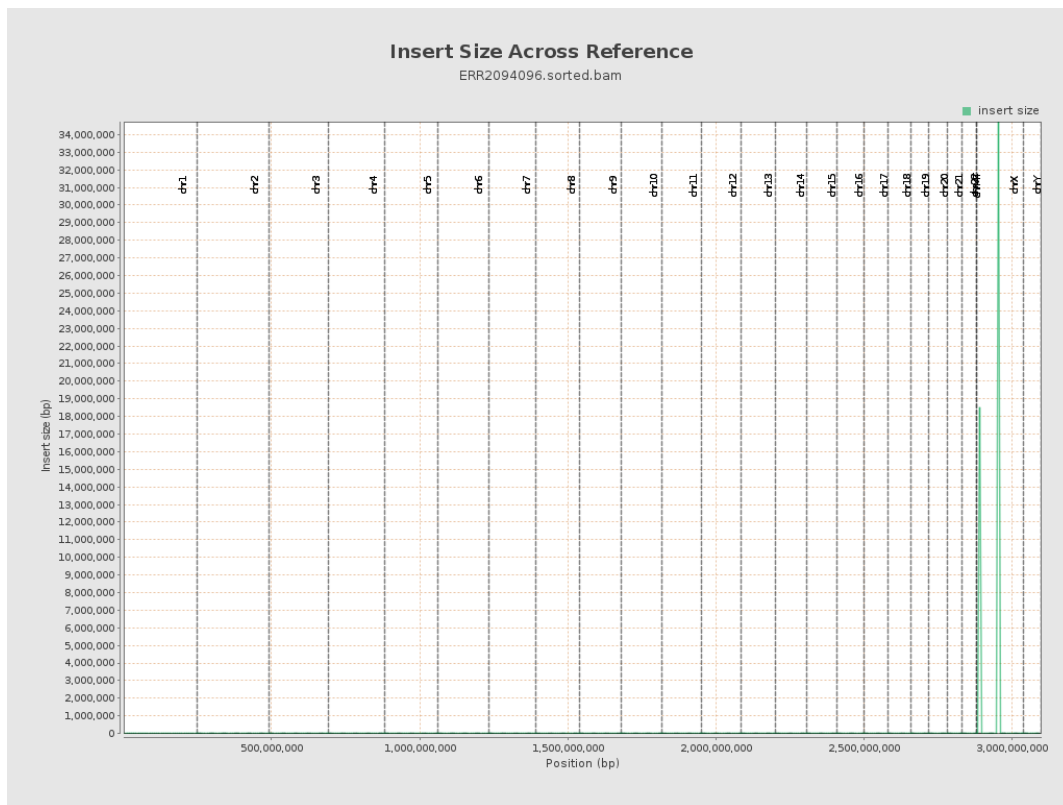
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

