

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:56:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094014.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_ERR2094014 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094014_1.fastq.gz ERR2094014_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:56:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,166
Mapped reads	8,617 / 30.59%
Unmapped reads	19,549 / 69.41%
Mapped paired reads	8,617 / 30.59%
Mapped reads, first in pair	4,248 / 15.08%
Mapped reads, second in pair	4,369 / 15.51%
Mapped reads, both in pair	8,336 / 29.6%
Mapped reads, singletons	281 / 1%
Secondary alignments	0
Supplementary alignments	29 / 0.1%
Read min/max/mean length	30 / 151 / 83.71
Duplicated reads (estimated)	8,278 / 29.39%
Duplication rate	32.61%
Clipped reads	1,041 / 3.7%

2.2. ACGT Content

Number/percentage of A's	320,204 / 25.88%
Number/percentage of C's	250,586 / 20.26%
Number/percentage of T's	354,542 / 28.66%
Number/percentage of G's	311,747 / 25.2%
Number/percentage of N's	7 / 0%

GC Percentage	45.46%
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2.3. Coverage

Mean	0.0004
Standard Deviation	0.9613

2.4. Mapping Quality

Mean Mapping Quality	5.09
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2.5. Insert size

Mean	73,787.9
Standard Deviation	2,549,813.05
P25/Median/P75	237 / 237 / 266

2.6. Mismatches and indels

General error rate	2.72%
Mismatches	33,324
Insertions	96
Mapped reads with at least one insertion	0.97%
Deletions	1,081
Mapped reads with at least one deletion	12.34%
Homopolymer indels	85.22%

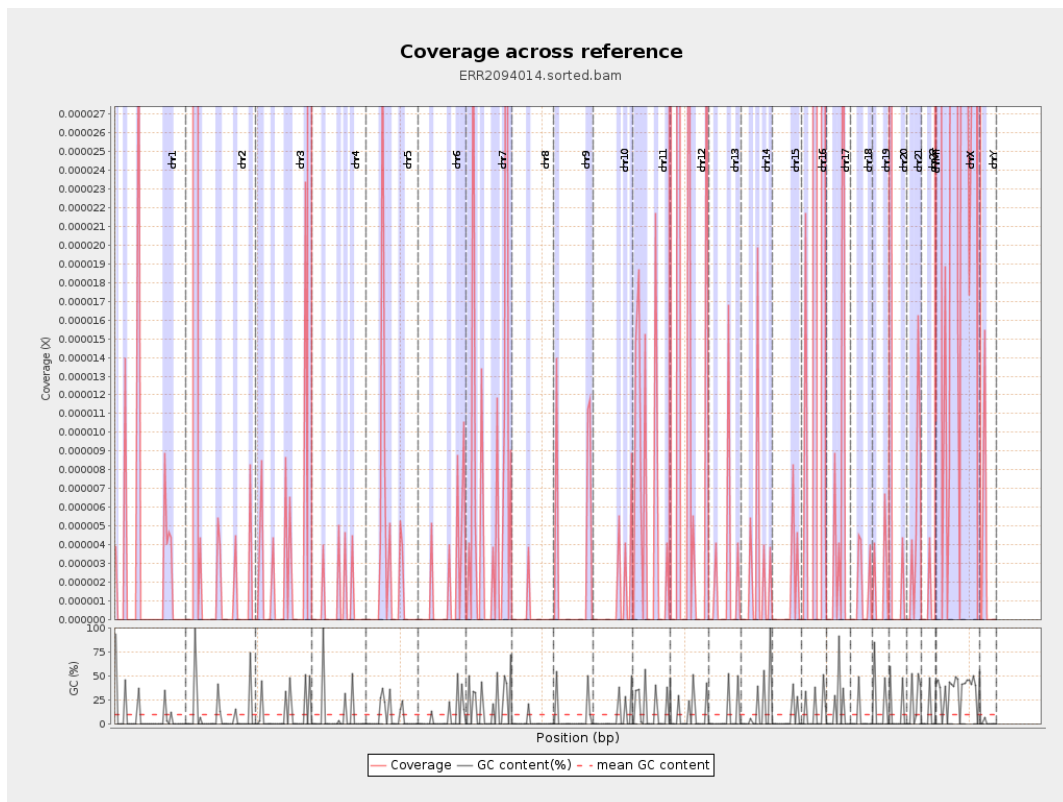
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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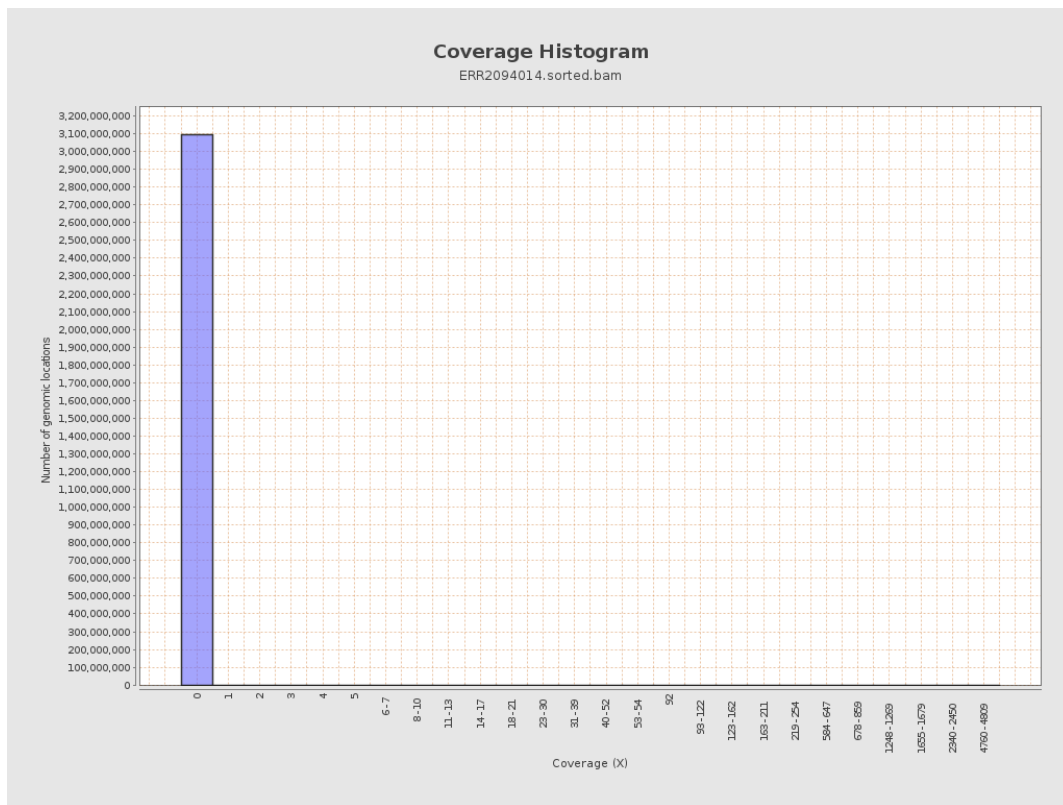
		bases	coverage	deviation
chr1	249250621	570	0	0.002
chr2	243199373	35096	0.0001	0.154
chr3	198022430	13723	0.0001	0.0749
chr4	191154276	141	0	0.0009
chr5	180915260	469	0	0.0019
chr6	171115067	260	0	0.0014
chr7	159138663	1161	0	0.0035
chr8	146364022	30	0	0.0005
chr9	141213431	286	0	0.0014
chr10	135534747	119	0	0.0009
chr11	135006516	918	0	0.003
chr12	133851895	1560	0	0.0071
chr13	115169878	194	0	0.0017
chr14	107349540	257	0	0.0019
chr15	102531392	100	0	0.0013
chr16	90354753	7677	0.0001	0.0479
chr17	81195210	459	0	0.003
chr18	78077248	99	0	0.0011
chr19	59128983	84	0	0.0012
chr20	63025520	1004	0	0.0093
chr21	48129895	240	0	0.0028
chr22	51304566	34	0	0.0008
chrMT	16571	1164751	70.2885	408.9606
chrX	155270560	9115	0.0001	0.0304

chrY	59373566	120	0	0.0014
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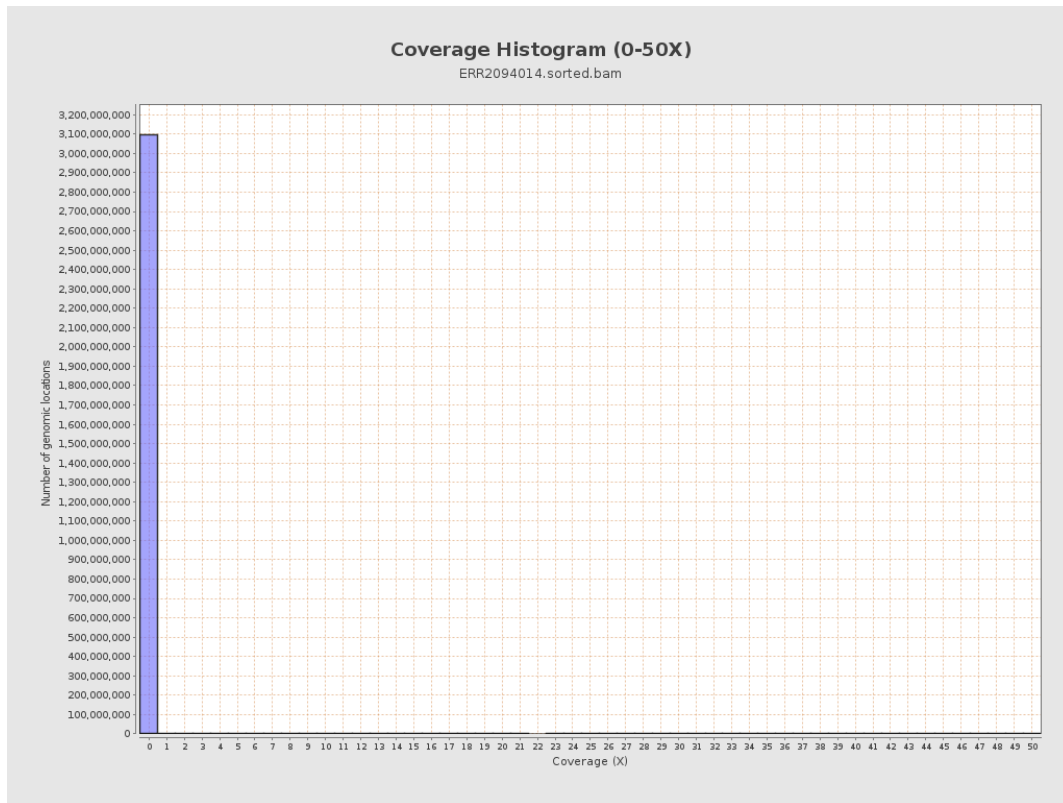
3. Results : Coverage across reference



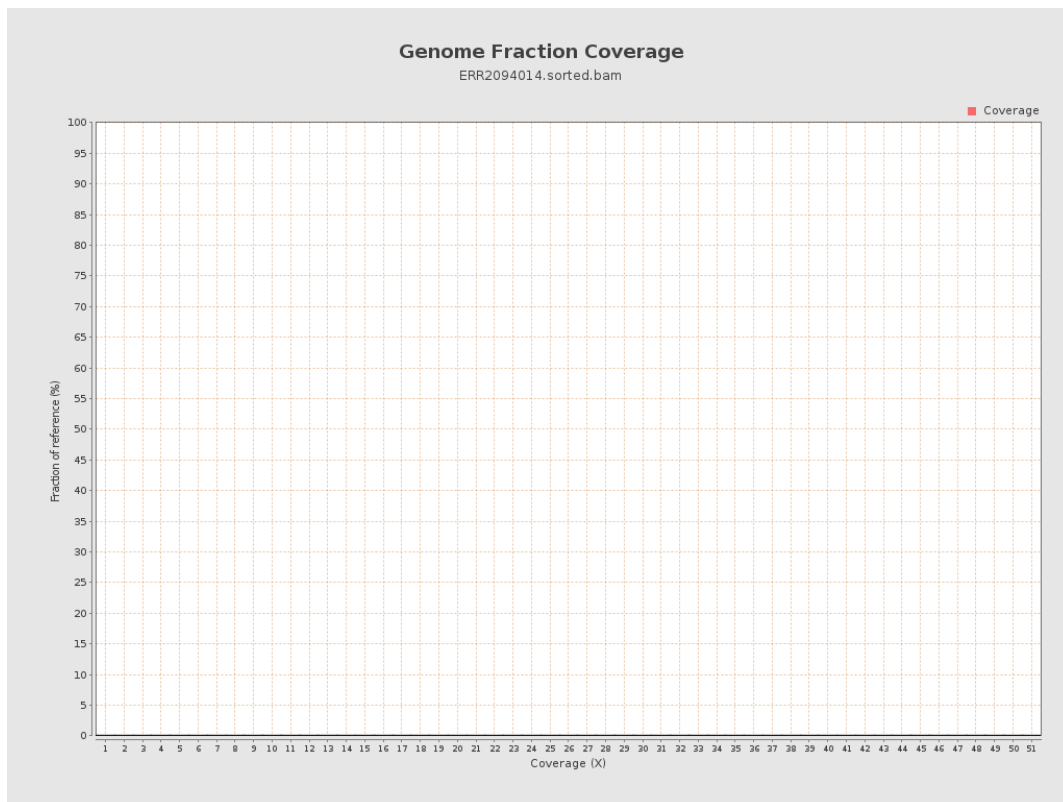
4. Results : Coverage Histogram



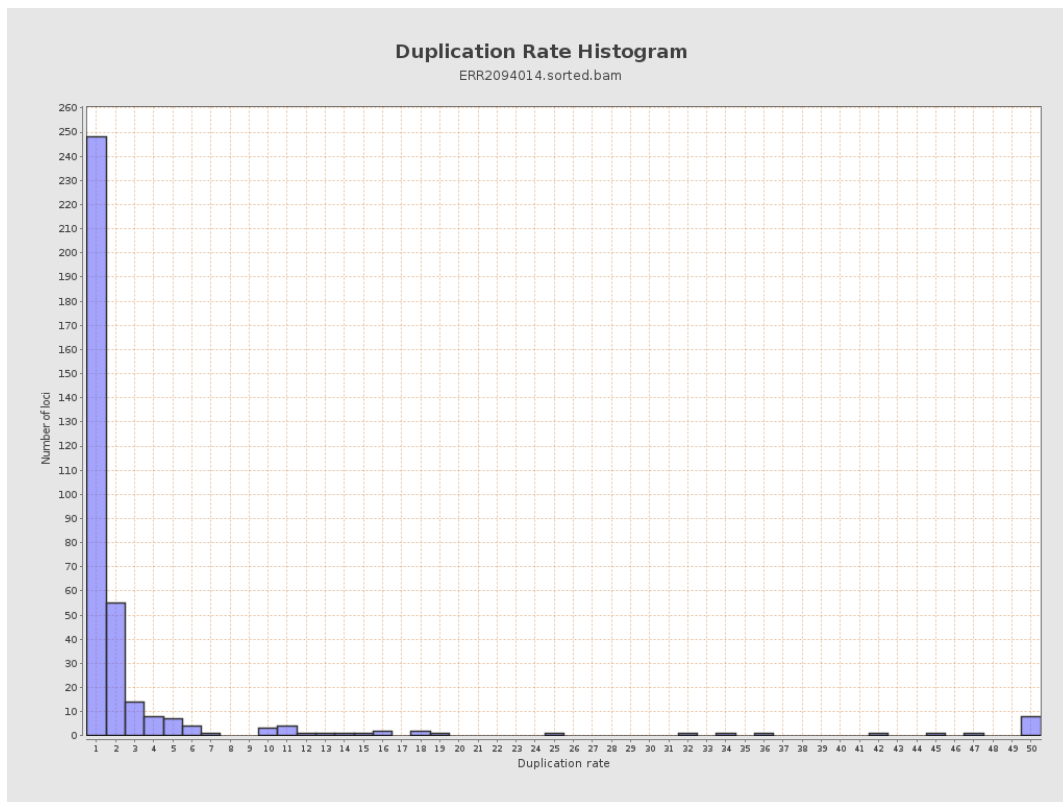
5. Results : Coverage Histogram (0-50X)



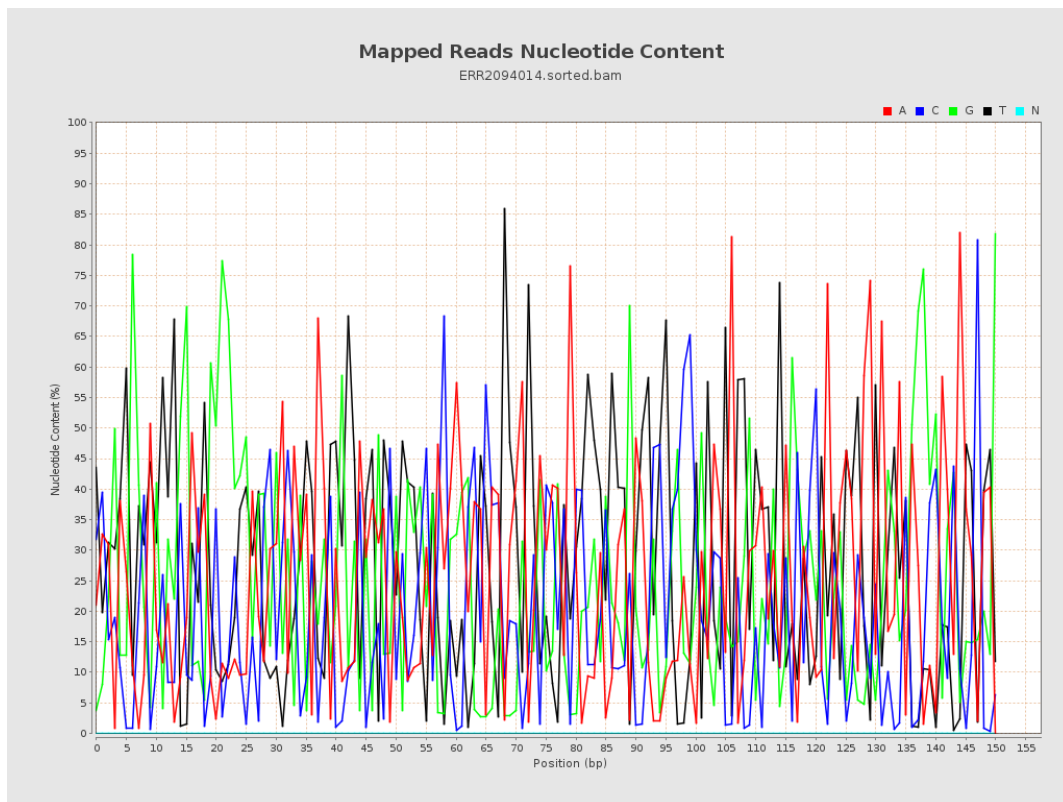
6. Results : Genome Fraction Coverage



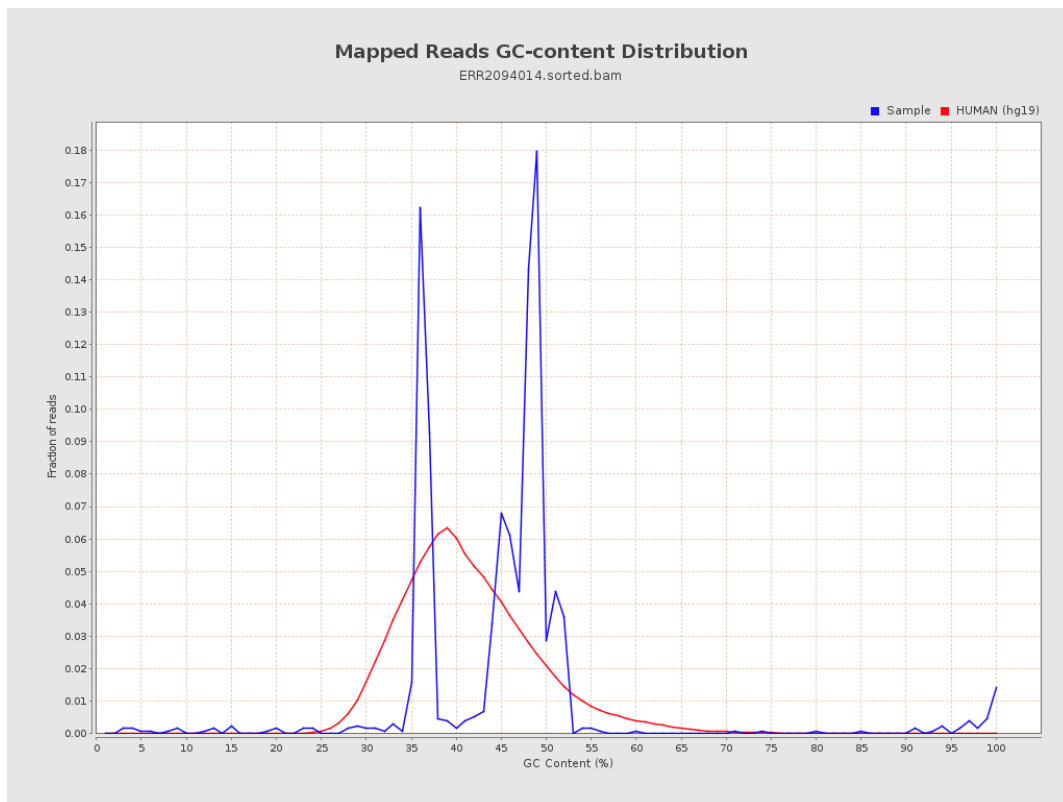
7. Results : Duplication Rate Histogram



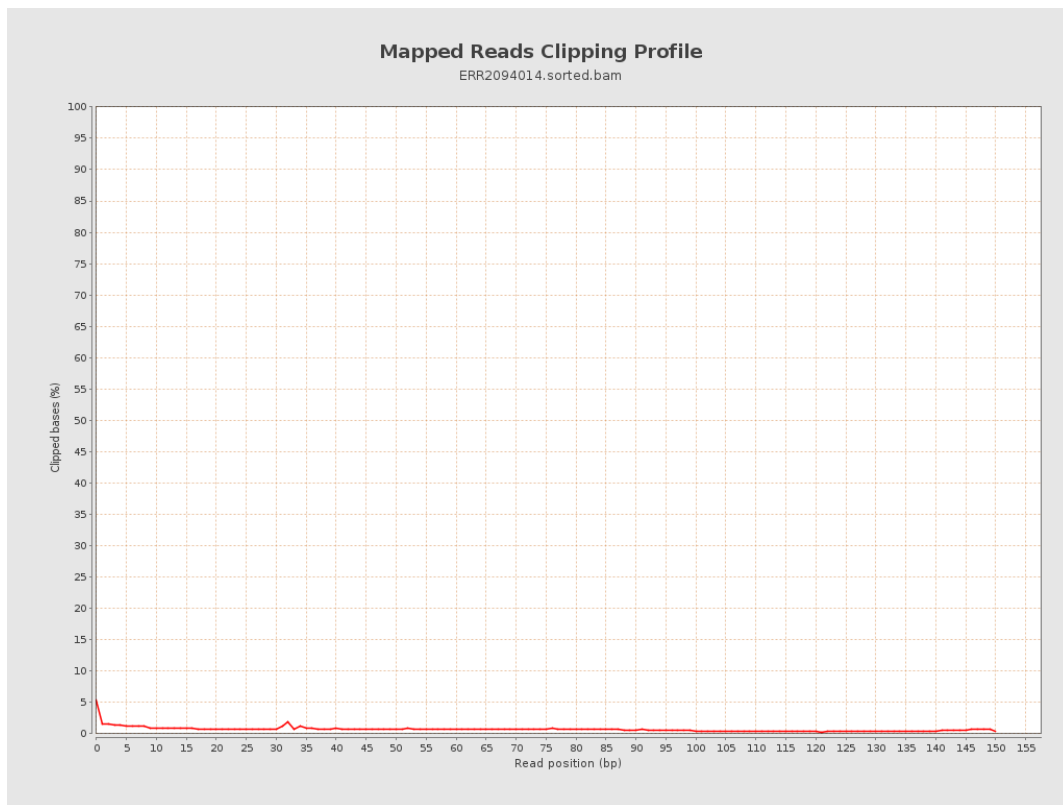
8. Results : Mapped Reads Nucleotide Content



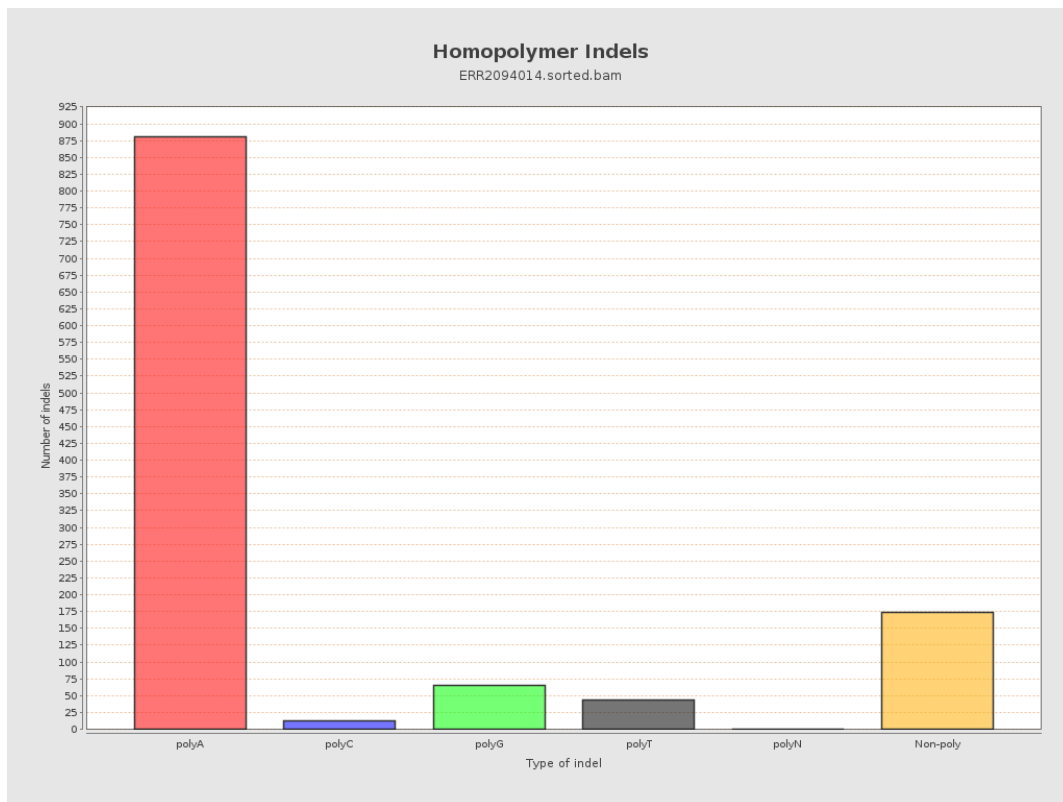
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



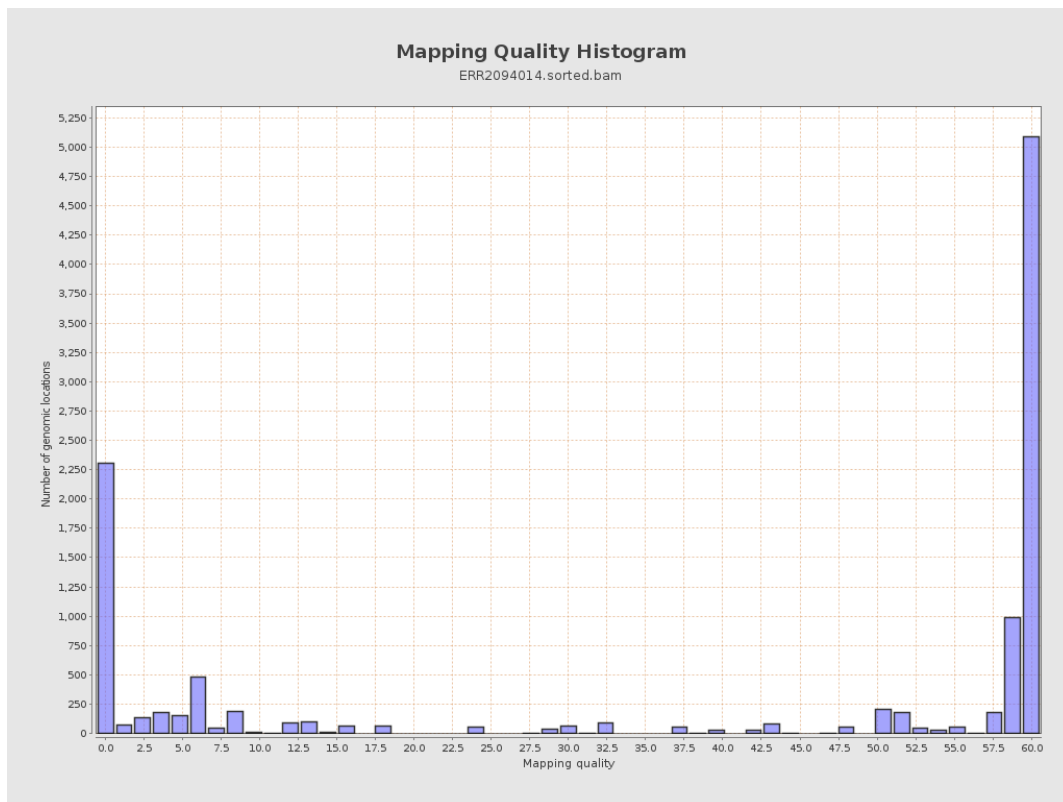
11. Results : Homopolymer Indels



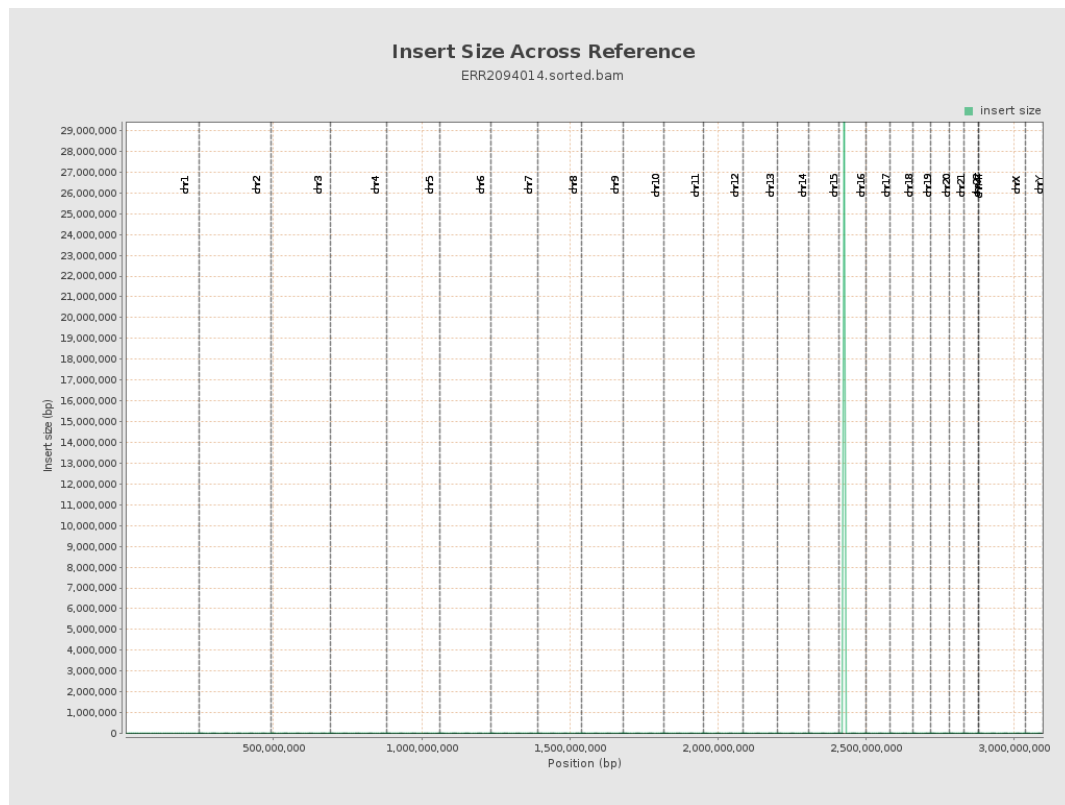
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

