

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:28:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094002.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_ERR2094002 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094002_1.fastq.gz ERR2094002_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:28:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094002.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	461,164
Mapped reads	202,778 / 43.97%
Unmapped reads	258,386 / 56.03%
Mapped paired reads	202,778 / 43.97%
Mapped reads, first in pair	100,800 / 21.86%
Mapped reads, second in pair	101,978 / 22.11%
Mapped reads, both in pair	199,212 / 43.2%
Mapped reads, singletons	3,566 / 0.77%
Secondary alignments	0
Supplementary alignments	304 / 0.07%
Read min/max/mean length	30 / 151 / 100.65
Duplicated reads (estimated)	201,341 / 43.66%
Duplication rate	29.7%
Clipped reads	10,987 / 2.38%

2.2. ACGT Content

Number/percentage of A's	9,070,361 / 30.46%
Number/percentage of C's	5,554,367 / 18.65%
Number/percentage of T's	9,070,304 / 30.46%
Number/percentage of G's	6,085,942 / 20.44%
Number/percentage of N's	522 / 0%

GC Percentage	39.09%
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2.3. Coverage

Mean	0.0096
Standard Deviation	33.0822

2.4. Mapping Quality

Mean Mapping Quality	6.4
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2.5. Insert size

Mean	7,548.68
Standard Deviation	841,993.81
P25/Median/P75	217 / 217 / 217

2.6. Mismatches and indels

General error rate	1.41%
Mismatches	417,594
Insertions	969
Mapped reads with at least one insertion	0.41%
Deletions	4,268
Mapped reads with at least one deletion	2.08%
Homopolymer indels	45.89%

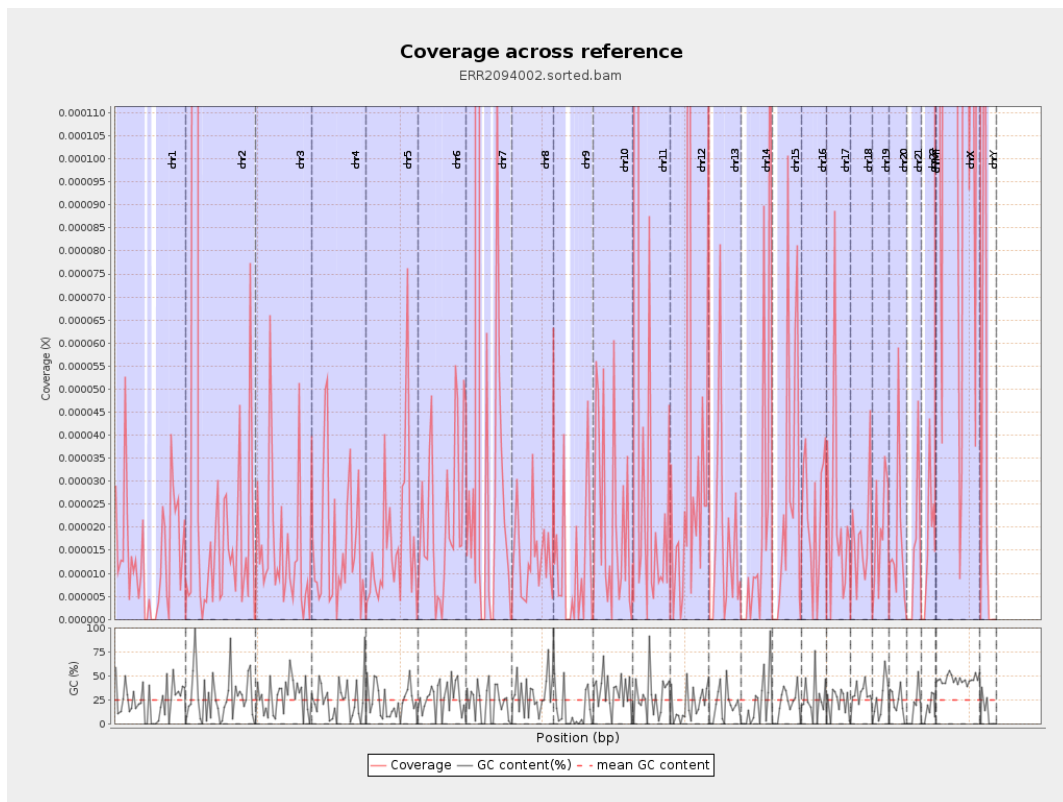
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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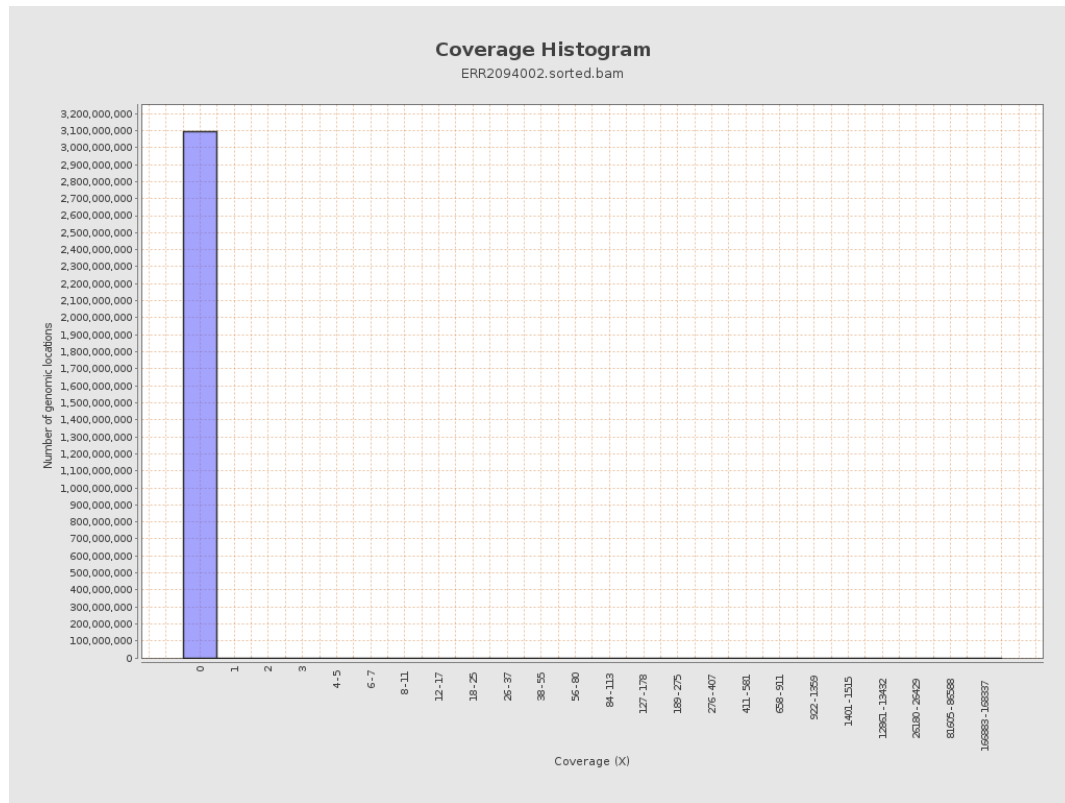
		bases	coverage	deviation
chr1	249250621	3447	0	0.0055
chr2	243199373	246356	0.001	0.9957
chr3	198022430	2890	0	0.0053
chr4	191154276	3087	0	0.0056
chr5	180915260	2953	0	0.0056
chr6	171115067	3731	0	0.0079
chr7	159138663	92529	0.0006	0.6719
chr8	146364022	2029	0	0.0047
chr9	141213431	1639	0	0.0042
chr10	135534747	2908	0	0.0093
chr11	135006516	8495	0.0001	0.0873
chr12	133851895	5173	0	0.0217
chr13	115169878	1919	0	0.0054
chr14	107349540	2725	0	0.0242
chr15	102531392	2692	0	0.0112
chr16	90354753	2070	0	0.0071
chr17	81195210	1898	0	0.0105
chr18	78077248	1340	0	0.005
chr19	59128983	1122	0	0.0059
chr20	63025520	1067	0	0.0051
chr21	48129895	685	0	0.0043
chr22	51304566	823	0	0.0057
chrMT	16571	29296842	1,767.9586	14,188.3631
chrX	155270560	98043	0.0006	0.4831

chrY	59373566	1651	0	0.0155
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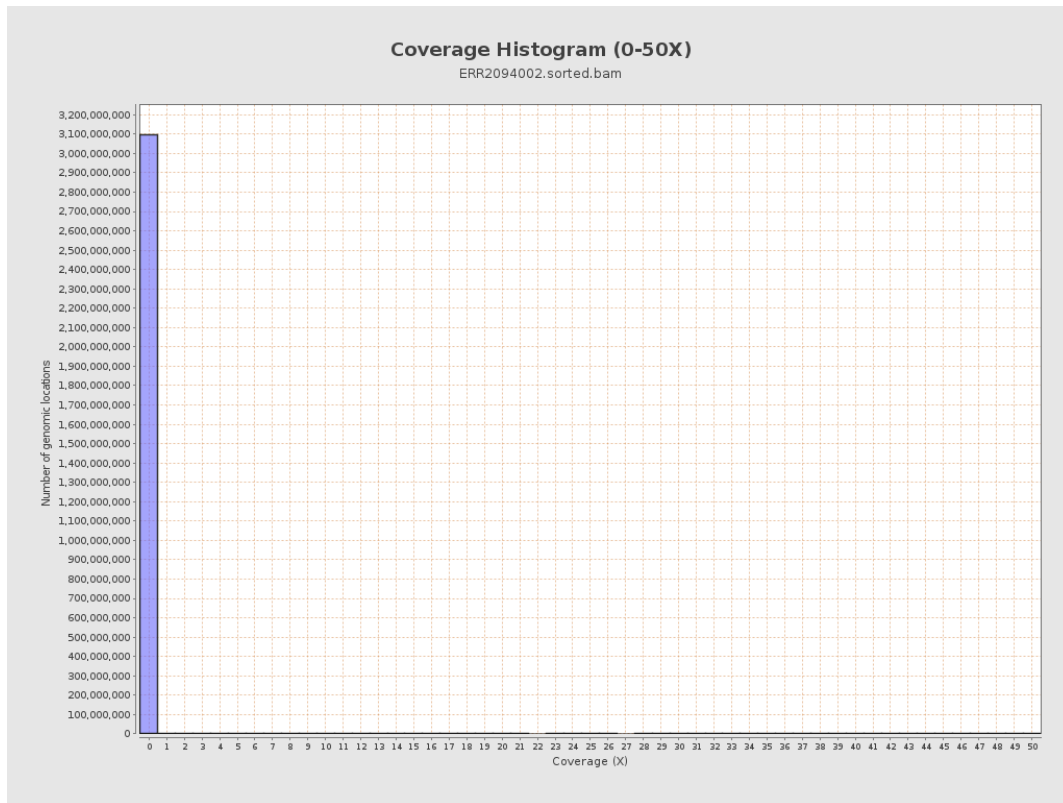
3. Results : Coverage across reference



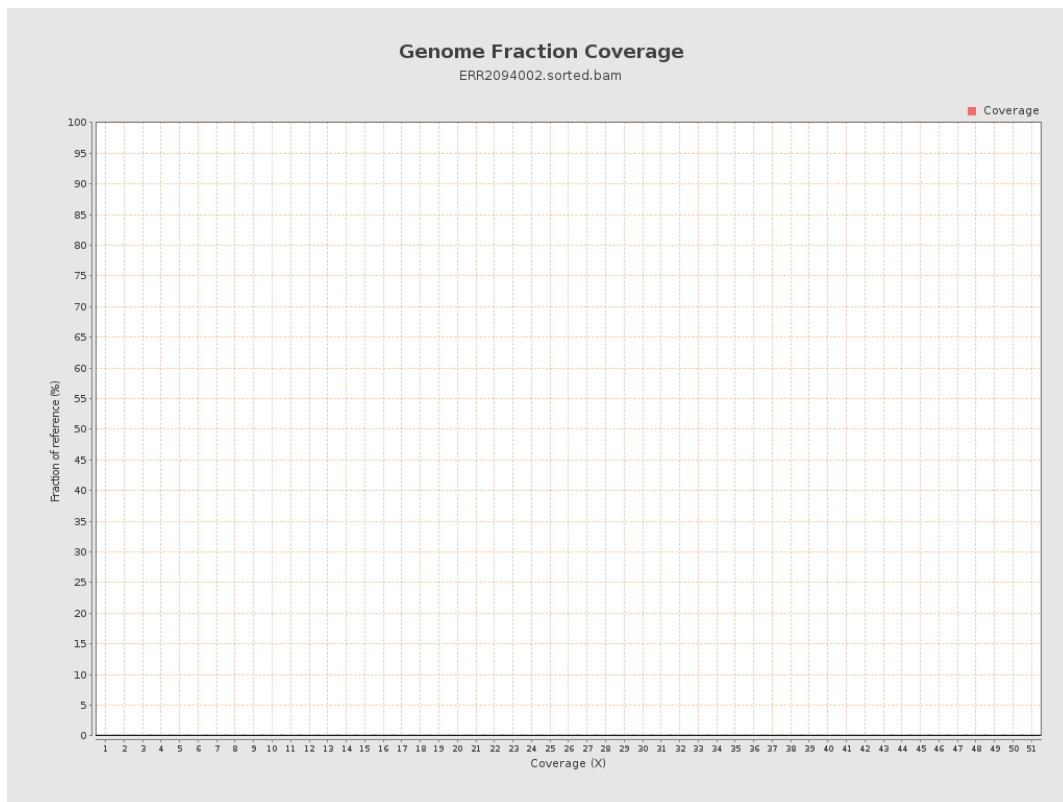
4. Results : Coverage Histogram



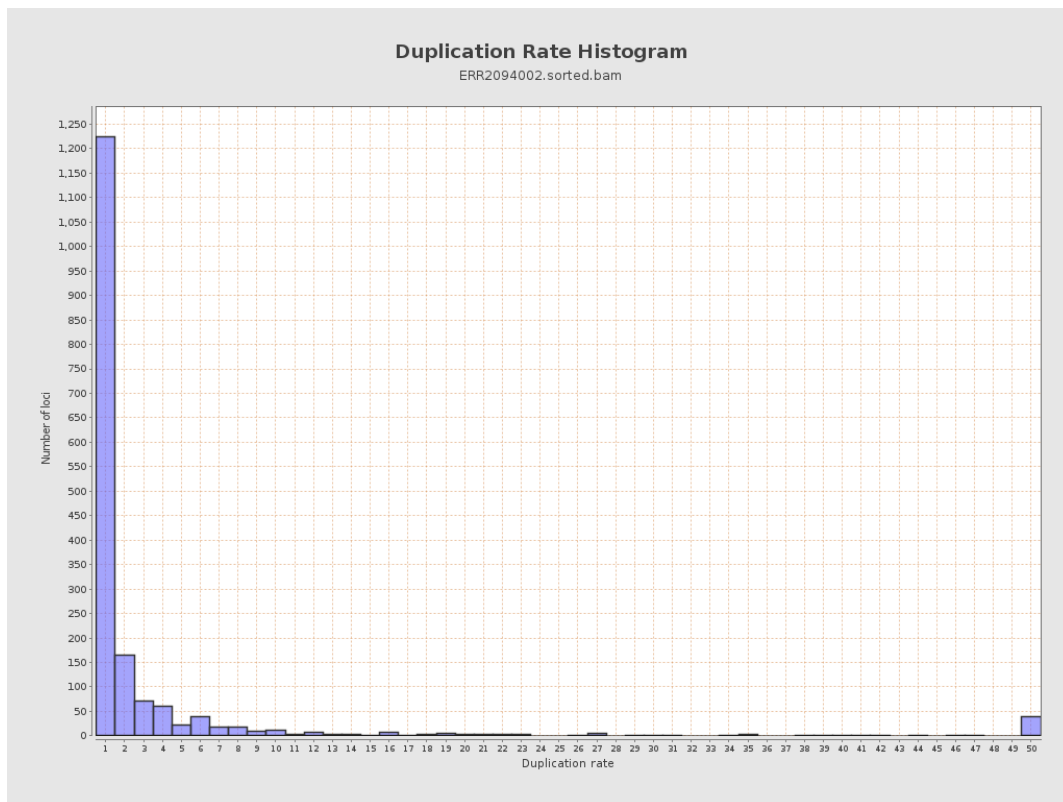
5. Results : Coverage Histogram (0-50X)



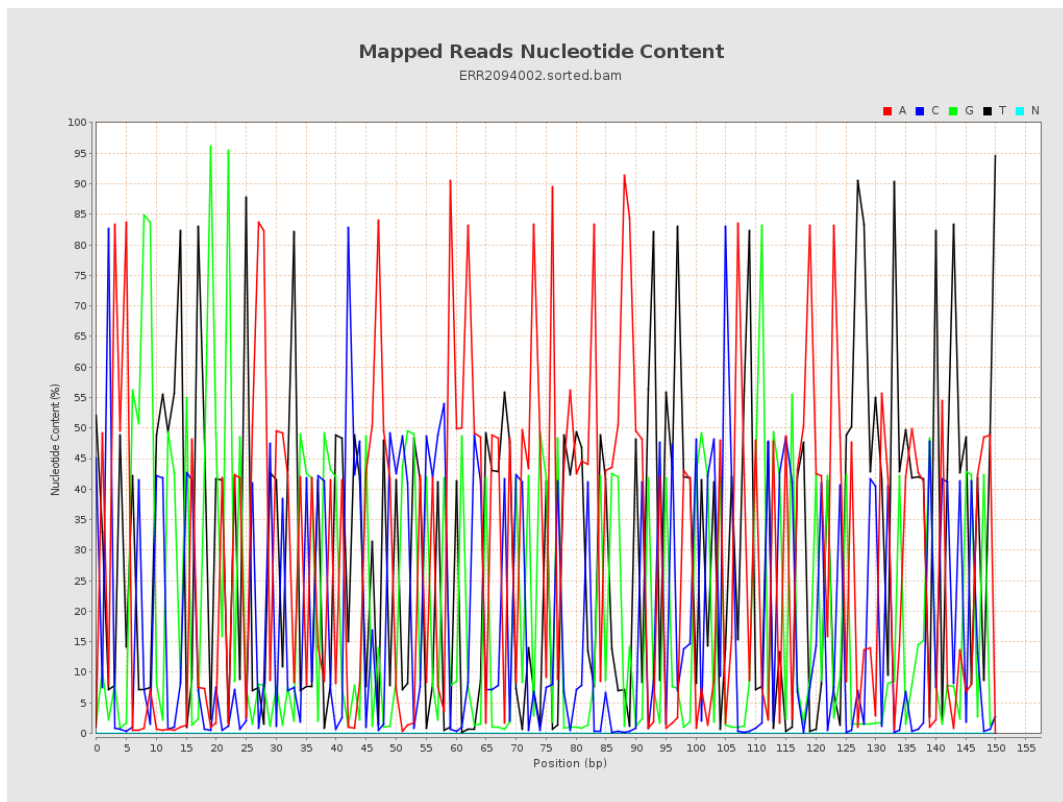
6. Results : Genome Fraction Coverage



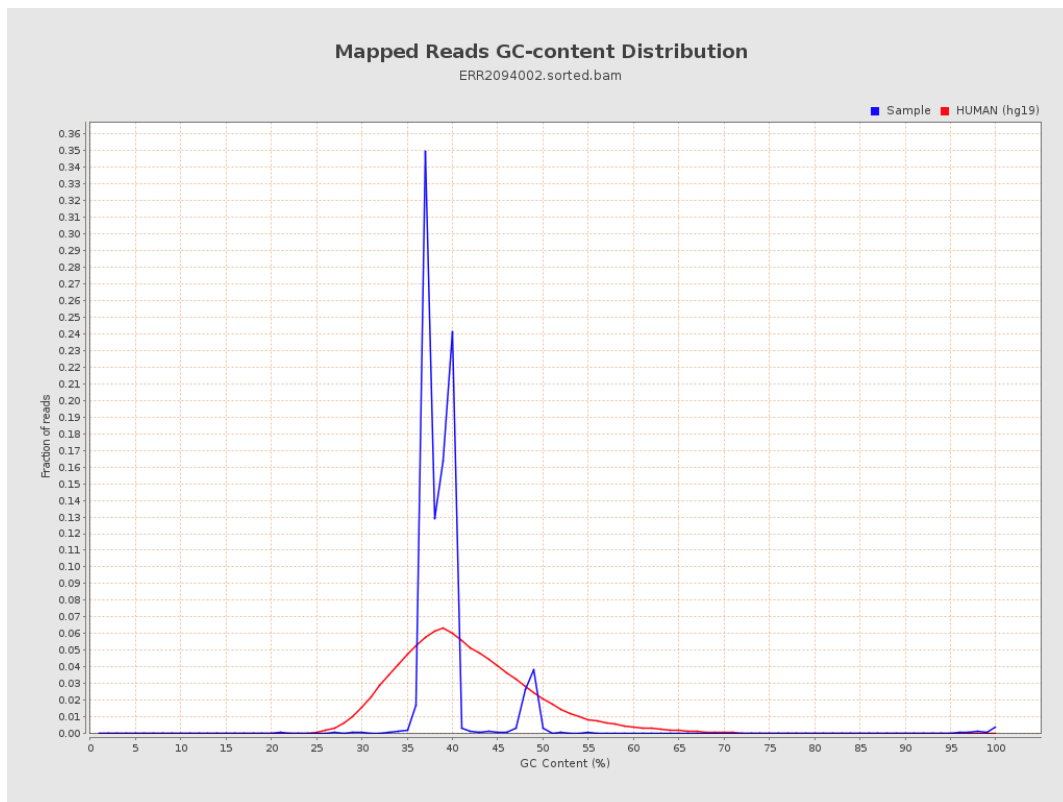
7. Results : Duplication Rate Histogram



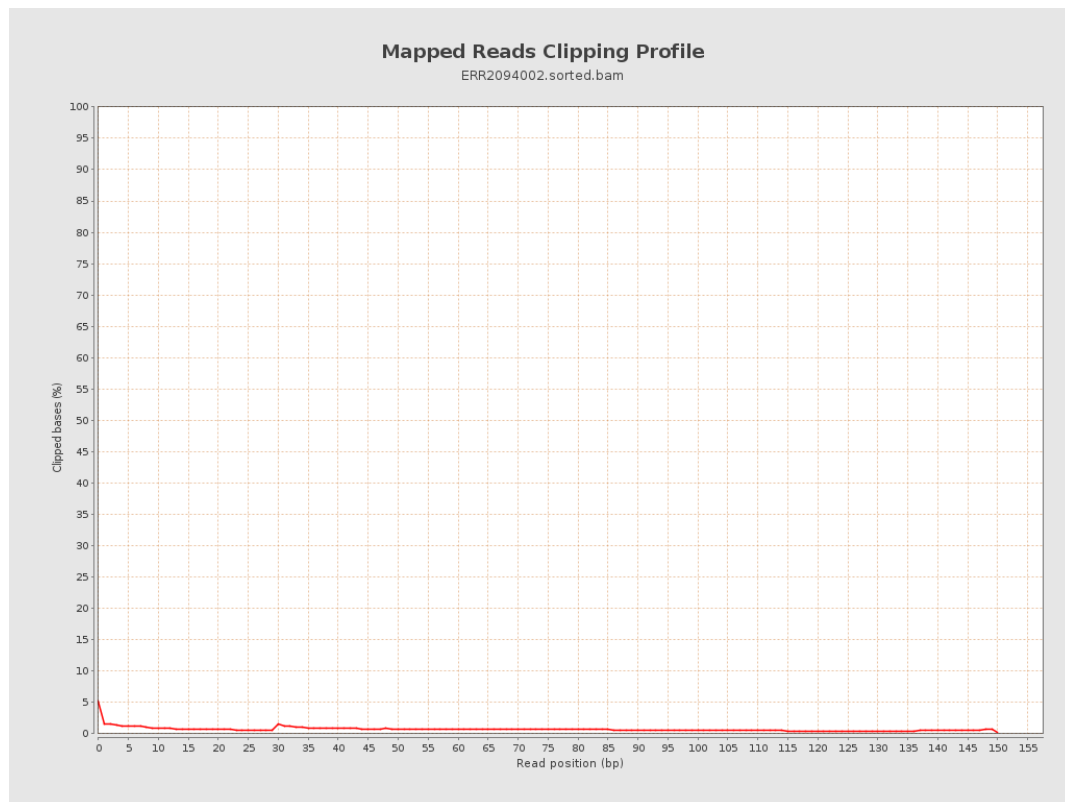
8. Results : Mapped Reads Nucleotide Content



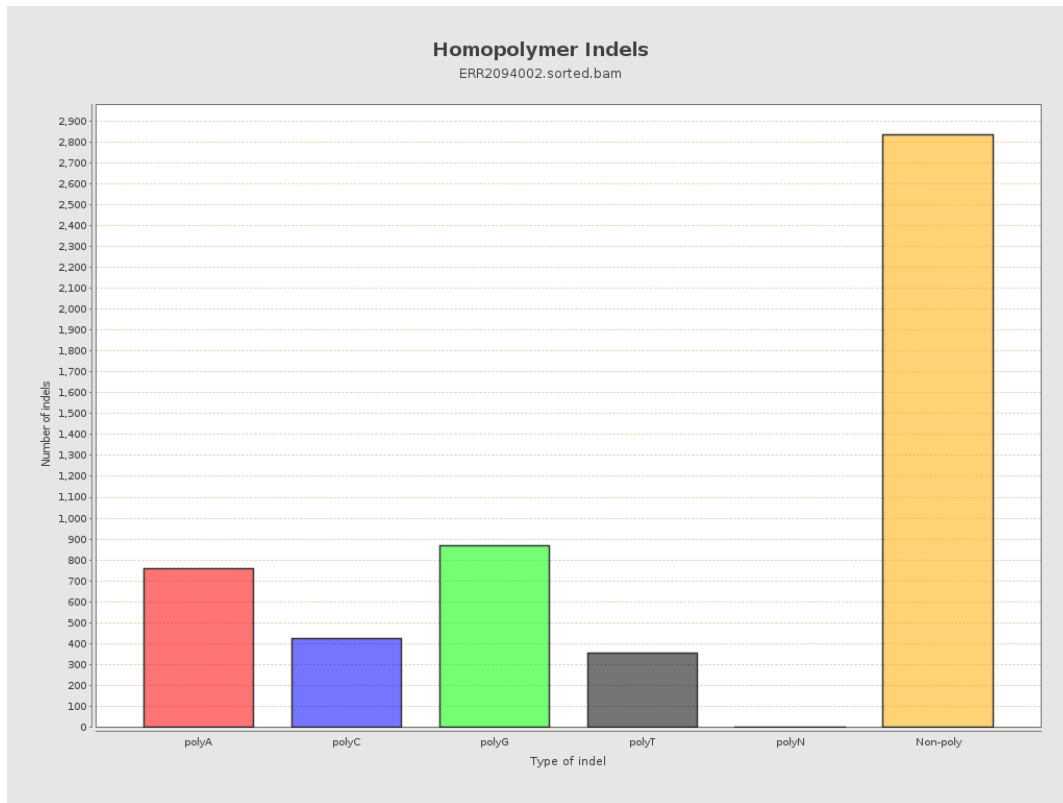
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



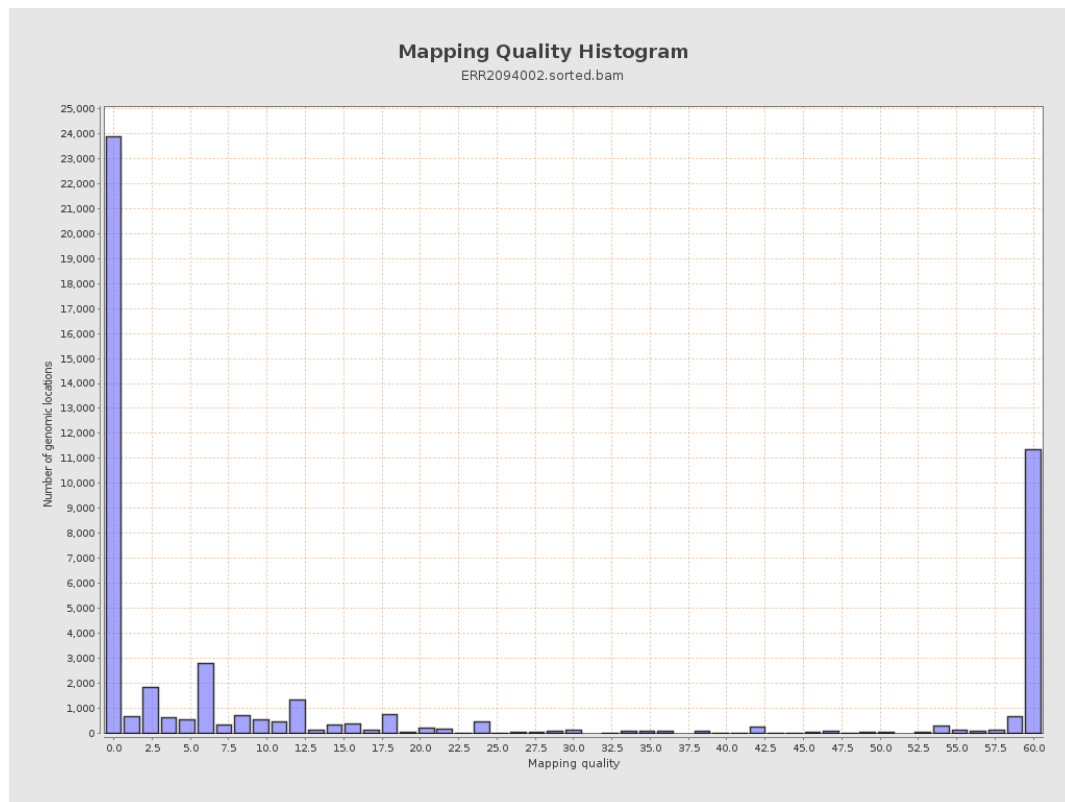
11. Results : Homopolymer Indels



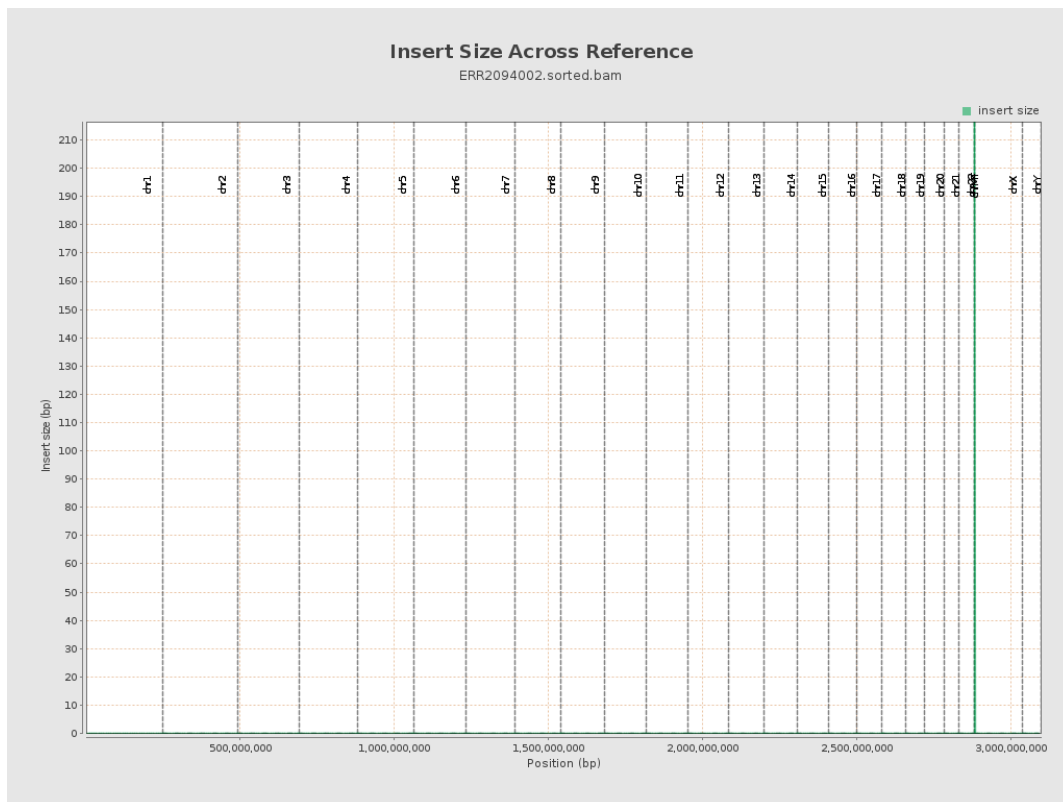
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

