

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 07:35:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094159.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_ERR2094159 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094159_1.fastq.gz ERR2094159_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 07:35:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094159.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,244
Mapped reads	949 / 2.55%
Unmapped reads	36,295 / 97.45%
Mapped paired reads	949 / 2.55%
Mapped reads, first in pair	320 / 0.86%
Mapped reads, second in pair	629 / 1.69%
Mapped reads, both in pair	540 / 1.45%
Mapped reads, singletons	409 / 1.1%
Secondary alignments	0
Supplementary alignments	30 / 0.08%
Read min/max/mean length	30 / 151 / 55.83
Duplicated reads (estimated)	703 / 1.89%
Duplication rate	26.45%
Clipped reads	764 / 2.05%

2.2. ACGT Content

Number/percentage of A's	10,495 / 15.44%
Number/percentage of C's	6,803 / 10.01%
Number/percentage of T's	7,733 / 11.38%
Number/percentage of G's	42,921 / 63.16%
Number/percentage of N's	0 / 0%

GC Percentage	73.18%
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2.3. Coverage

Mean	0
Standard Deviation	0.0466

2.4. Mapping Quality

Mean Mapping Quality	3.72
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2.5. Insert size

Mean	79.83
Standard Deviation	69.74
P25/Median/P75	31 / 34 / 142

2.6. Mismatches and indels

General error rate	2.66%
Mismatches	1,342
Insertions	83
Mapped reads with at least one insertion	5.27%
Deletions	36
Mapped reads with at least one deletion	3.58%
Homopolymer indels	61.34%

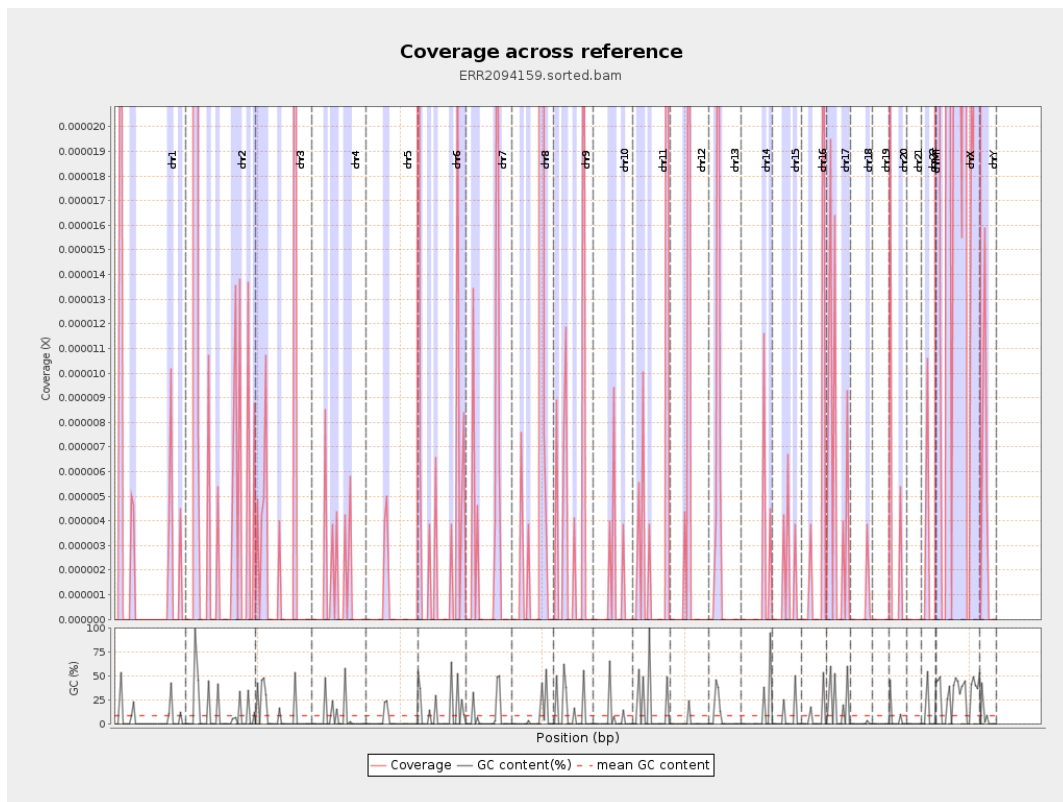
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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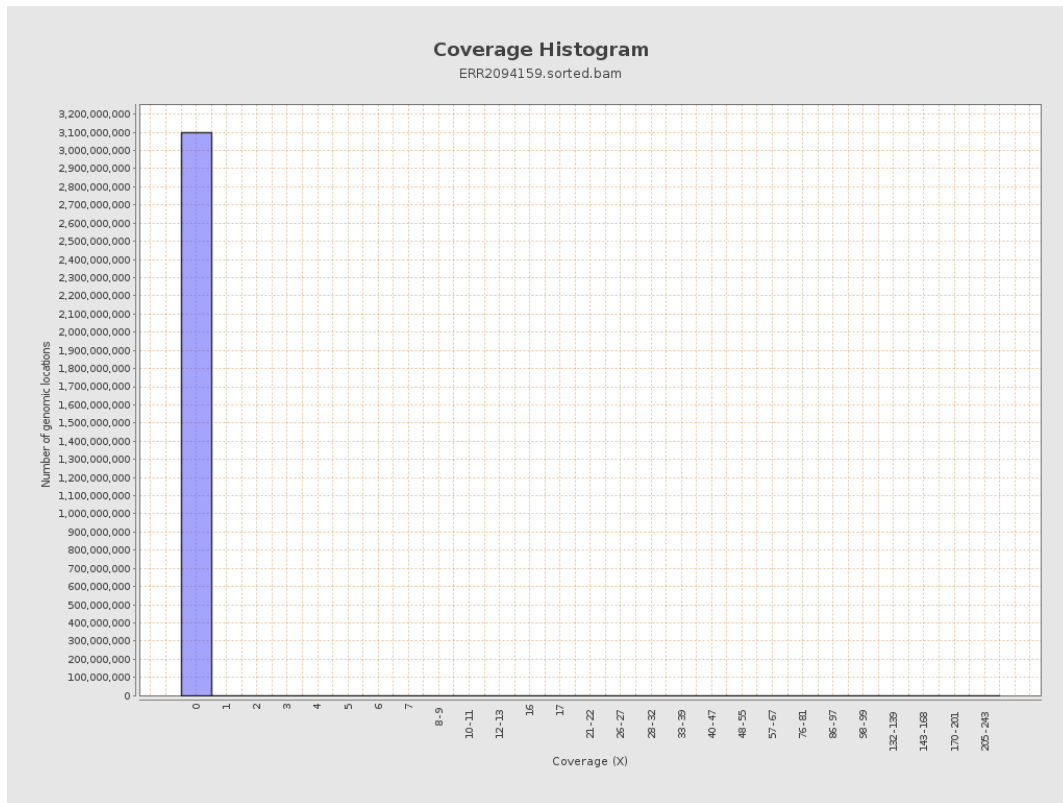
		bases	coverage	deviation
chr1	249250621	538	0	0.0017
chr2	243199373	37559	0.0002	0.1549
chr3	198022430	599	0	0.003
chr4	191154276	208	0	0.0012
chr5	180915260	70	0	0.0006
chr6	171115067	785	0	0.0034
chr7	159138663	488	0	0.0026
chr8	146364022	6125	0	0.0399
chr9	141213431	523	0	0.0024
chr10	135534747	134	0	0.001
chr11	135006516	628	0	0.0032
chr12	133851895	389	0	0.0033
chr13	115169878	378	0	0.0022
chr14	107349540	125	0	0.0017
chr15	102531392	115	0	0.0011
chr16	90354753	302	0	0.0024
chr17	81195210	415	0	0.0031
chr18	78077248	30	0	0.0006
chr19	59128983	0	0	0
chr20	63025520	180	0	0.0022
chr21	48129895	0	0	0
chr22	51304566	82	0	0.0018
chrMT	16571	6283	0.3792	1.5565
chrX	155270560	11988	0.0001	0.0625

chrY	59373566	190	0	0.0023
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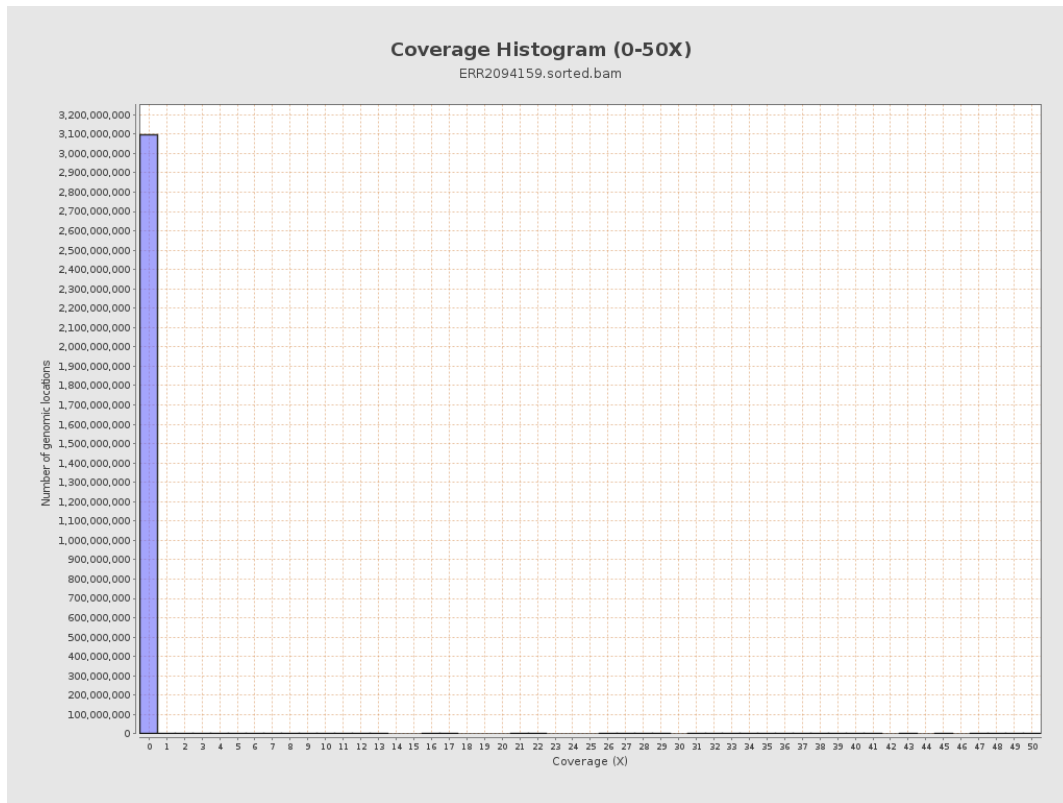
3. Results : Coverage across reference



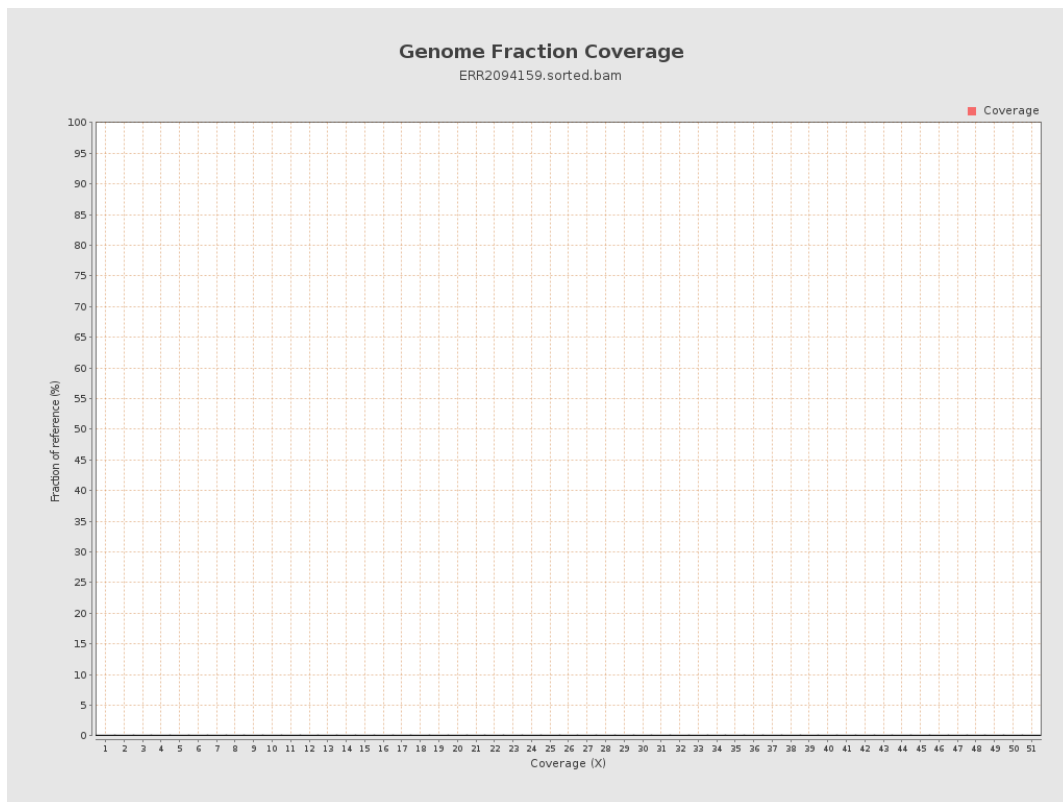
4. Results : Coverage Histogram



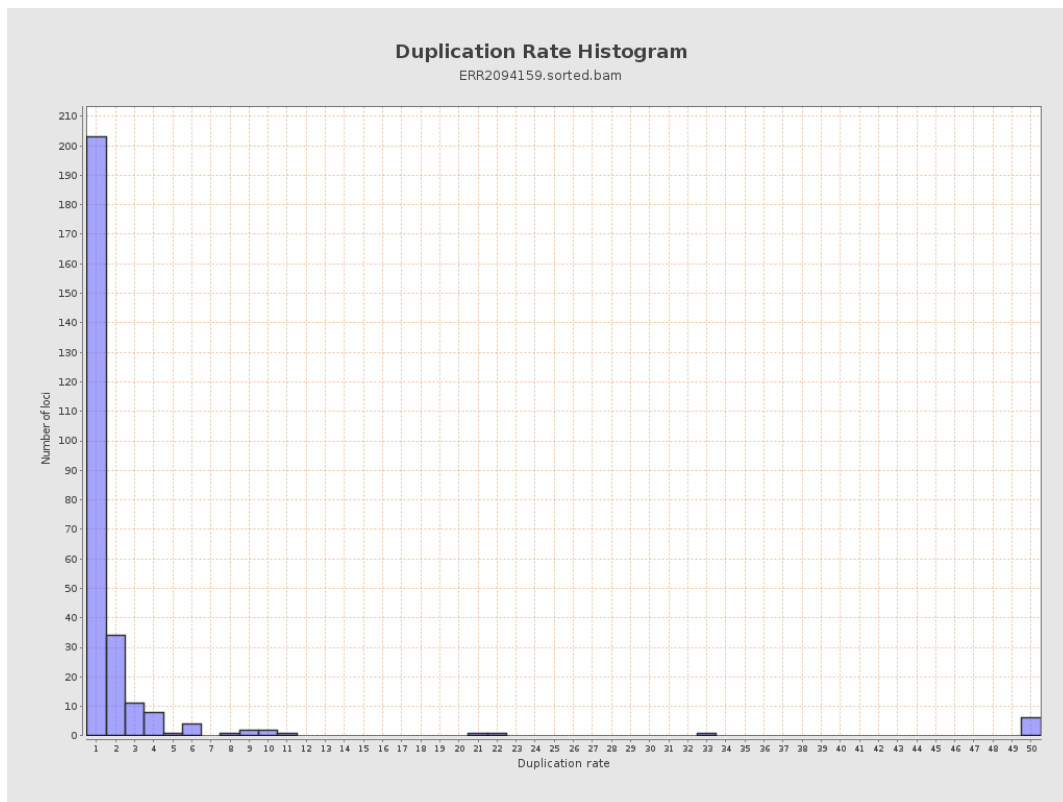
5. Results : Coverage Histogram (0-50X)



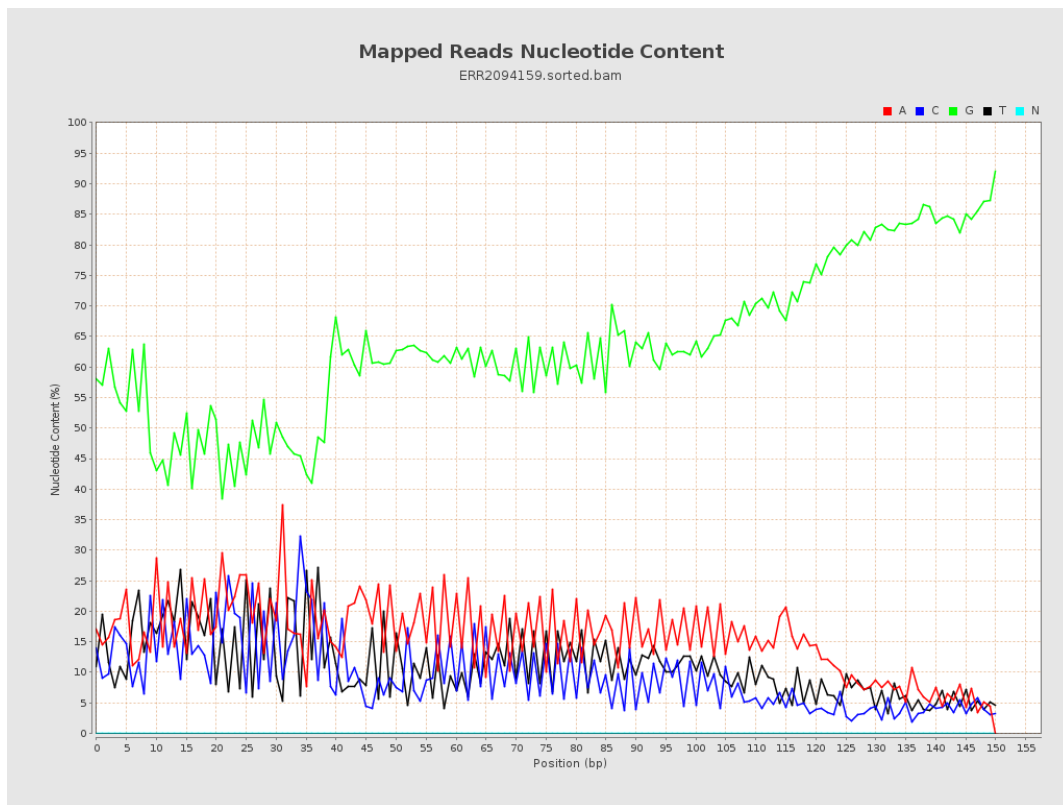
6. Results : Genome Fraction Coverage



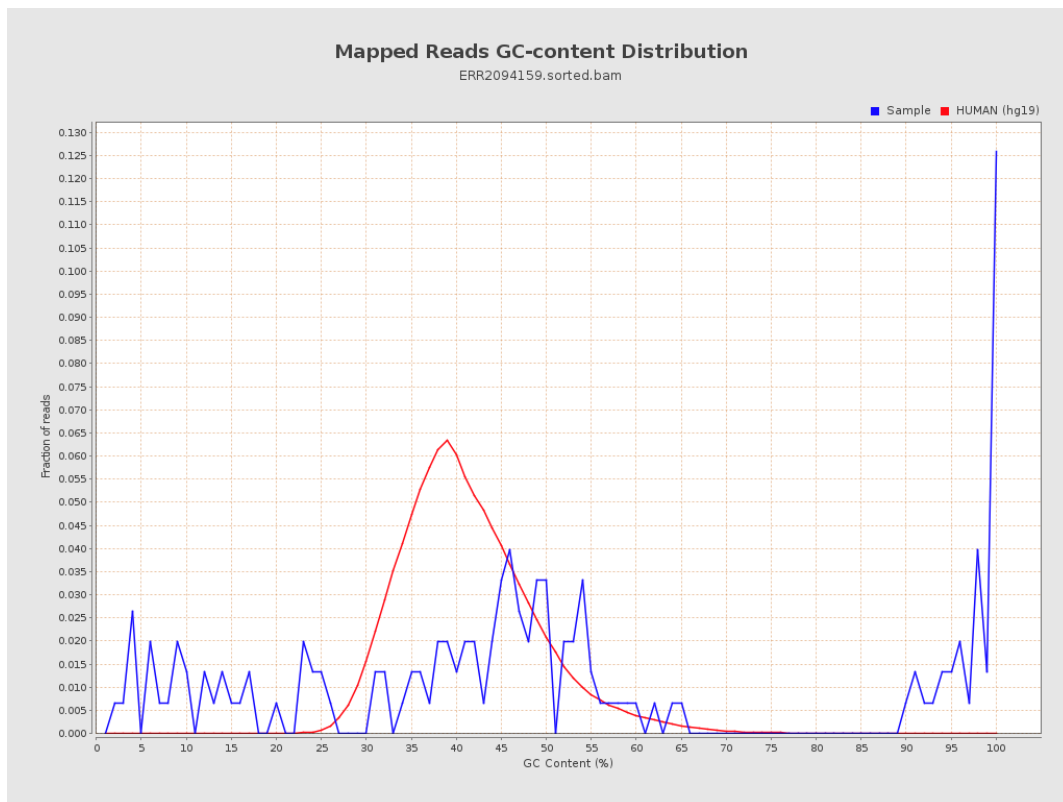
7. Results : Duplication Rate Histogram



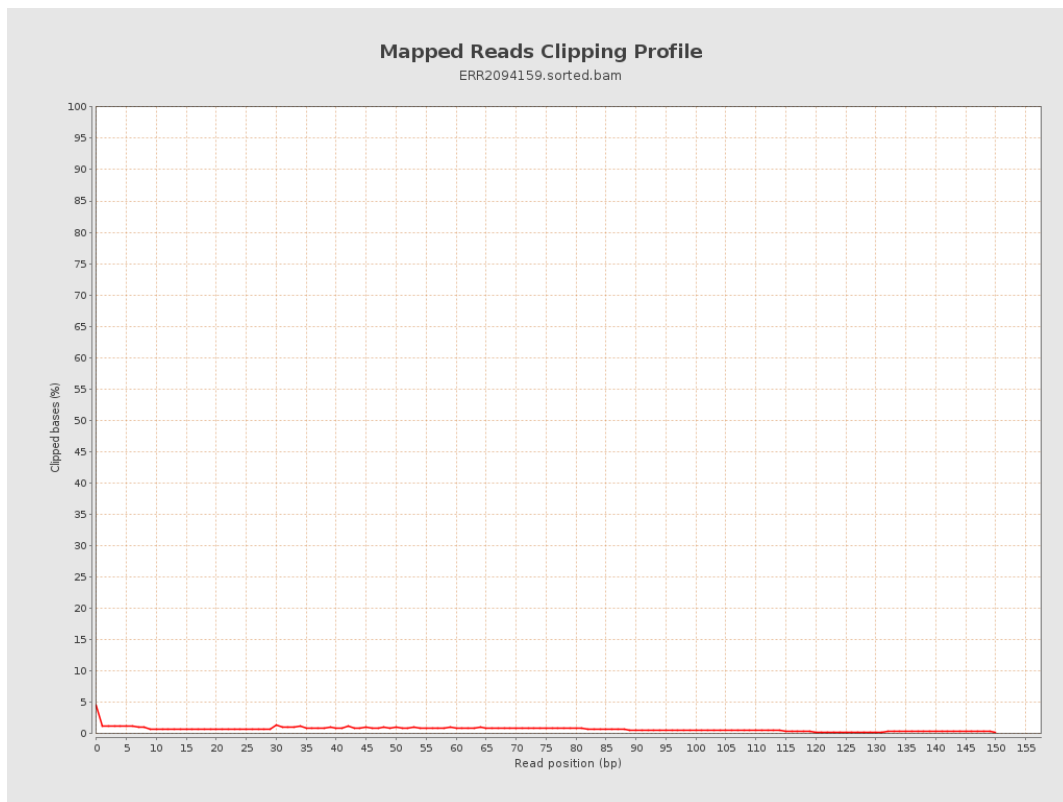
8. Results : Mapped Reads Nucleotide Content



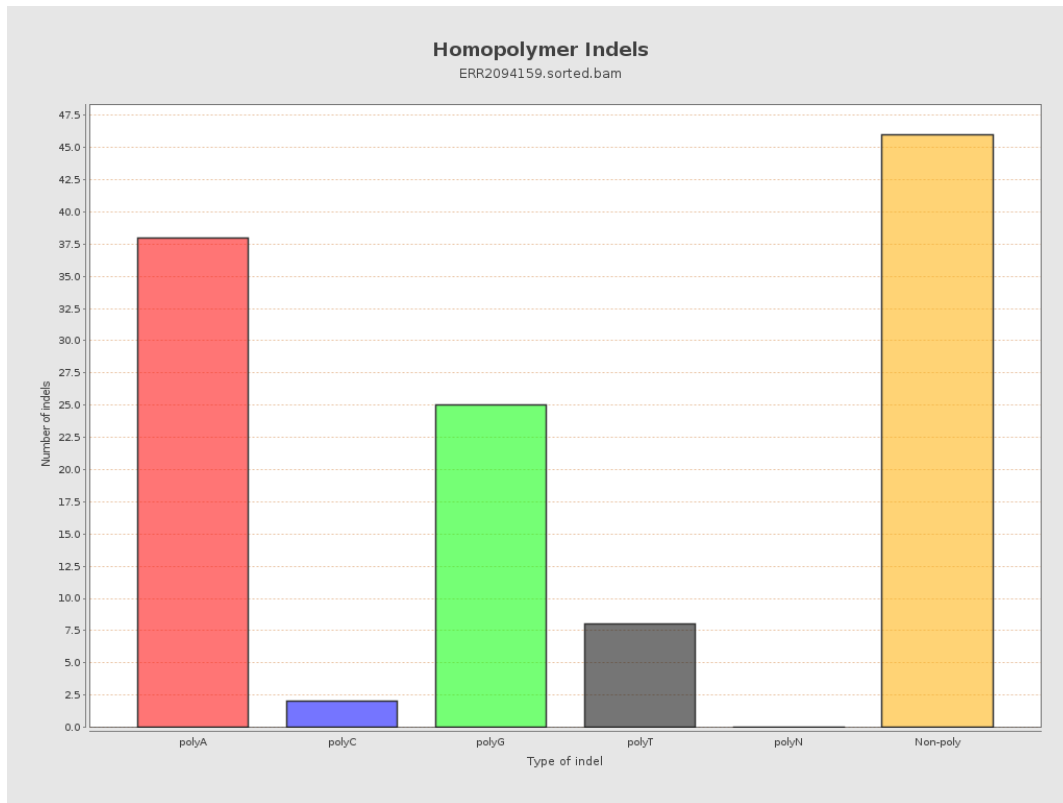
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



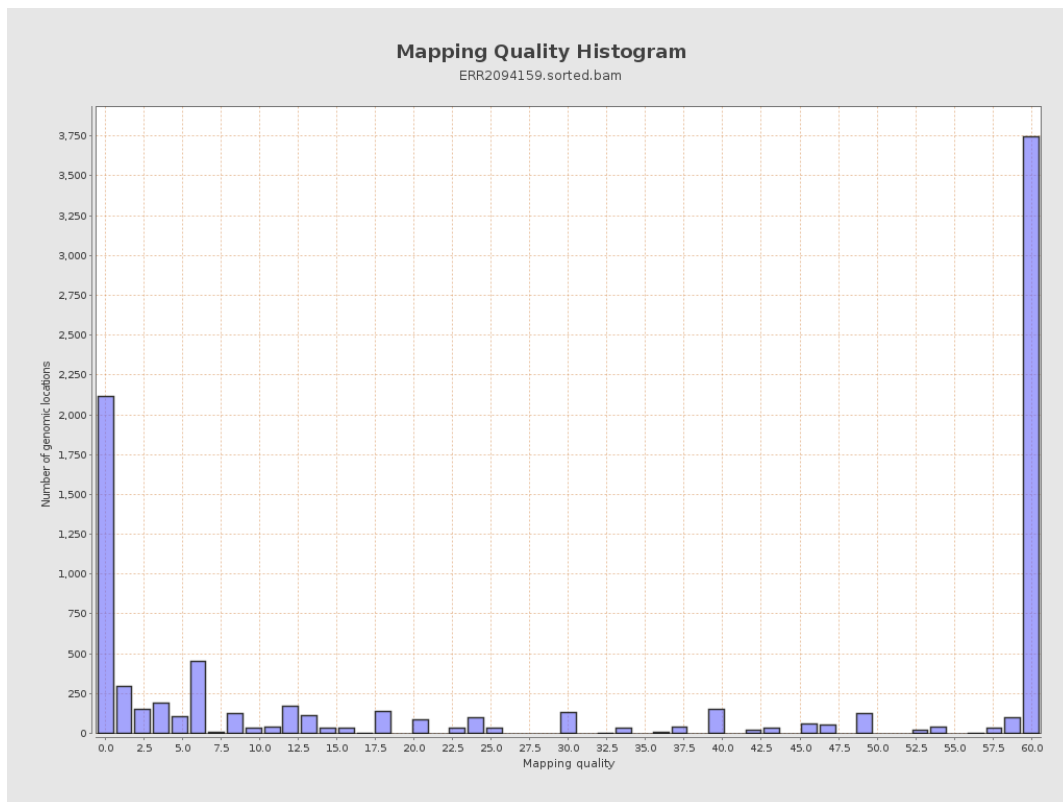
11. Results : Homopolymer Indels



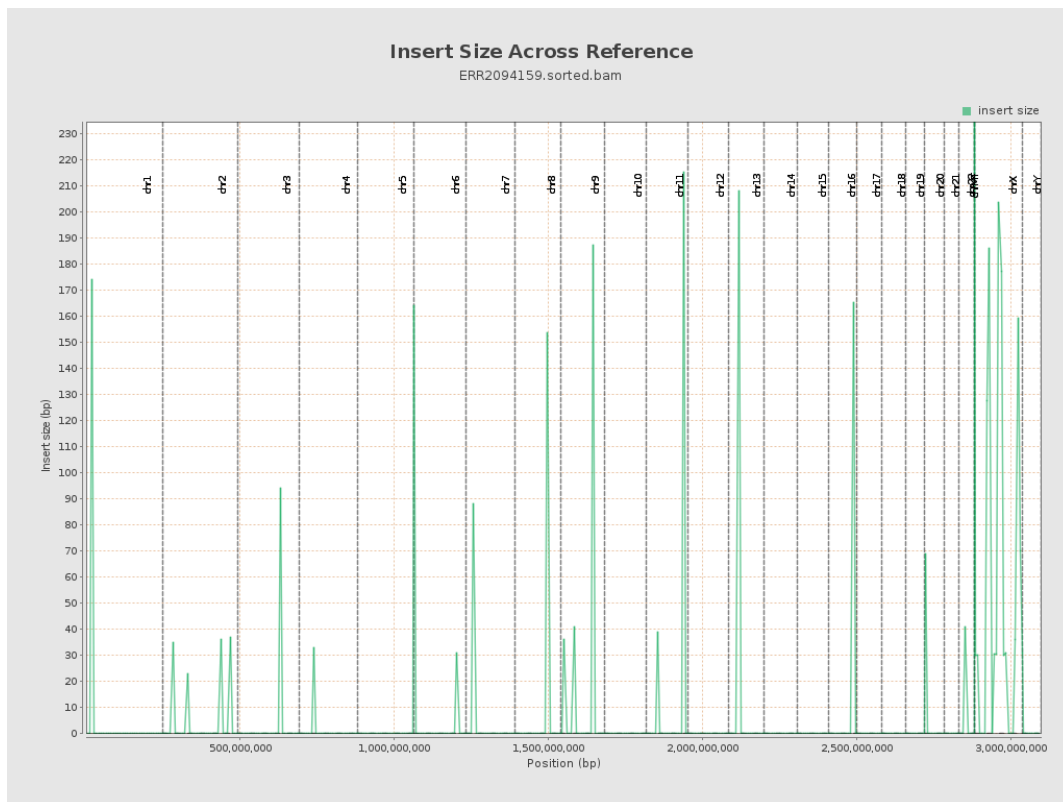
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

