

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:21:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094128.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_ERR2094128 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094128_1.fastq.gz ERR2094128_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:21:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094128.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	419,560
Mapped reads	376,934 / 89.84%
Unmapped reads	42,626 / 10.16%
Mapped paired reads	376,934 / 89.84%
Mapped reads, first in pair	189,741 / 45.22%
Mapped reads, second in pair	187,193 / 44.62%
Mapped reads, both in pair	372,916 / 88.88%
Mapped reads, singletons	4,018 / 0.96%
Secondary alignments	0
Supplementary alignments	5,654 / 1.35%
Read min/max/mean length	30 / 151 / 139.4
Duplicated reads (estimated)	367,384 / 87.56%
Duplication rate	44.57%
Clipped reads	97,554 / 23.25%

2.2. ACGT Content

Number/percentage of A's	14,516,998 / 27.33%
Number/percentage of C's	11,459,525 / 21.58%
Number/percentage of T's	14,743,573 / 27.76%
Number/percentage of G's	12,387,409 / 23.32%
Number/percentage of N's	636 / 0%

GC Percentage	44.9%
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2.3. Coverage

Mean	0.0173
Standard Deviation	23.2538

2.4. Mapping Quality

Mean Mapping Quality	39.05
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2.5. Insert size

Mean	92,597.91
Standard Deviation	2,838,246.12
P25/Median/P75	203 / 217 / 256

2.6. Mismatches and indels

General error rate	2.33%
Mismatches	1,189,978
Insertions	23,976
Mapped reads with at least one insertion	6.24%
Deletions	66,081
Mapped reads with at least one deletion	16.92%
Homopolymer indels	46.71%

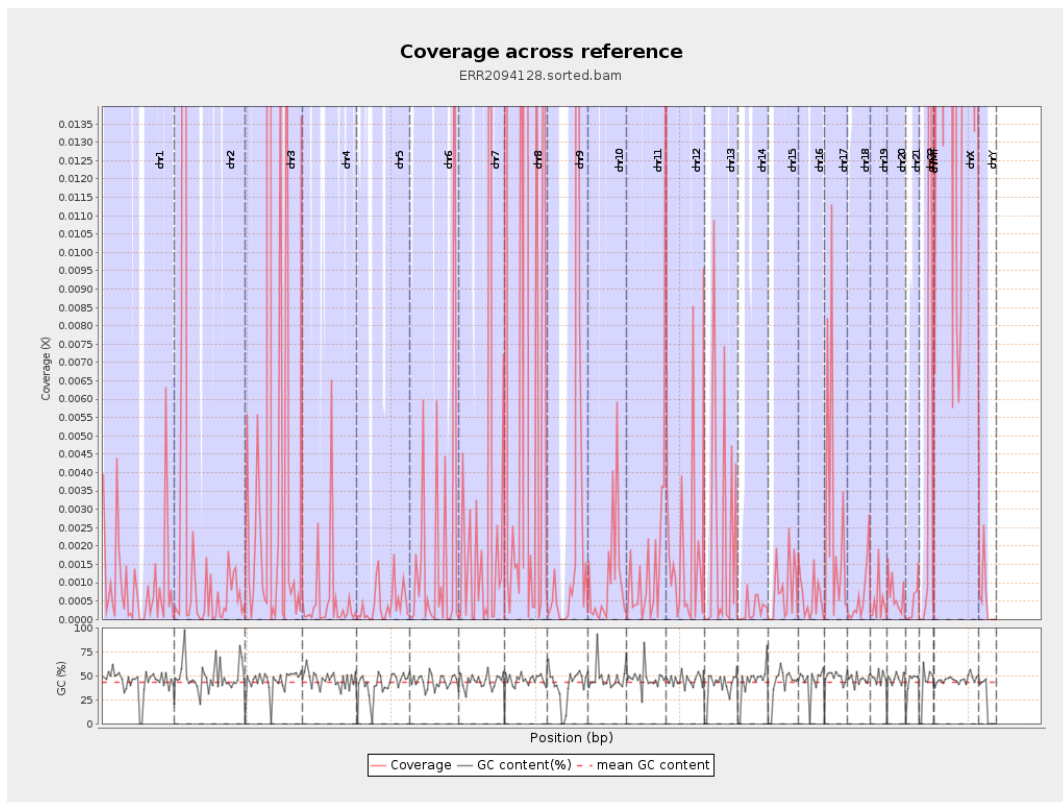
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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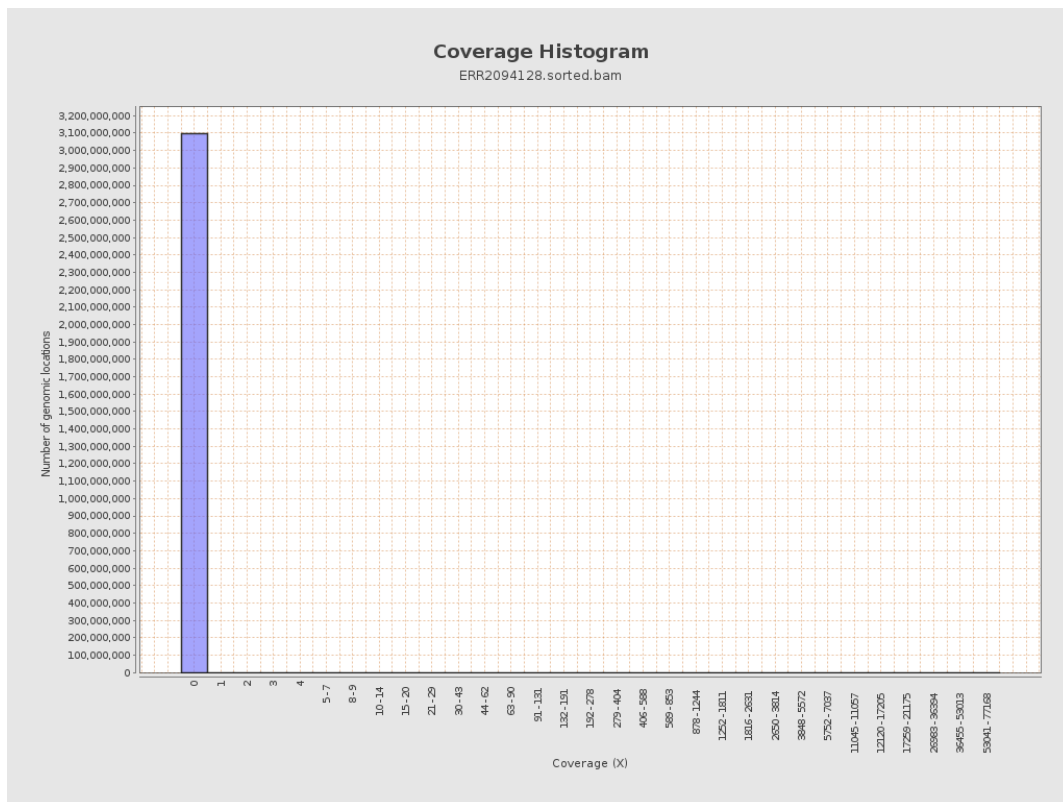
		bases	coverage	deviation
chr1	249250621	229190	0.0009	0.3008
chr2	243199373	644981	0.0027	1.6097
chr3	198022430	2536426	0.0128	10.0679
chr4	191154276	108174	0.0006	0.236
chr5	180915260	79480	0.0004	0.1131
chr6	171115067	340092	0.002	1.2909
chr7	159138663	497454	0.0031	2.1203
chr8	146364022	1802260	0.0123	6.0146
chr9	141213431	561208	0.004	2.4692
chr10	135534747	149401	0.0011	0.286
chr11	135006516	169256	0.0013	0.2424
chr12	133851895	233008	0.0017	0.5318
chr13	115169878	250288	0.0022	0.6327
chr14	107349540	29157	0.0003	0.0733
chr15	102531392	80085	0.0008	0.1905
chr16	90354753	56427	0.0006	0.1474
chr17	81195210	225524	0.0028	0.5841
chr18	78077248	48327	0.0006	0.1589
chr19	59128983	27096	0.0005	0.1386
chr20	63025520	43362	0.0007	0.1349
chr21	48129895	20147	0.0004	0.0751
chr22	51304566	235395	0.0046	2.4126
chrMT	16571	39579773	2,388.4963	9,654.2342
chrX	155270560	5513545	0.0355	6.591

chrY	59373566	32844	0.0006	0.1775
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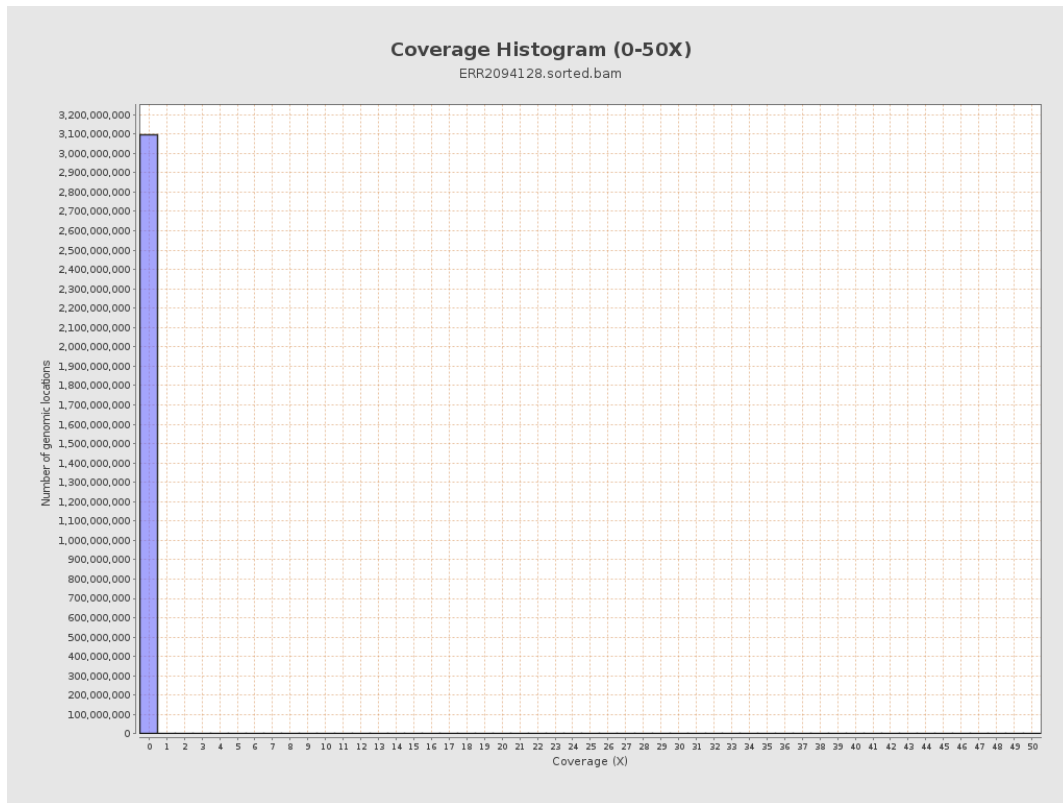
3. Results : Coverage across reference



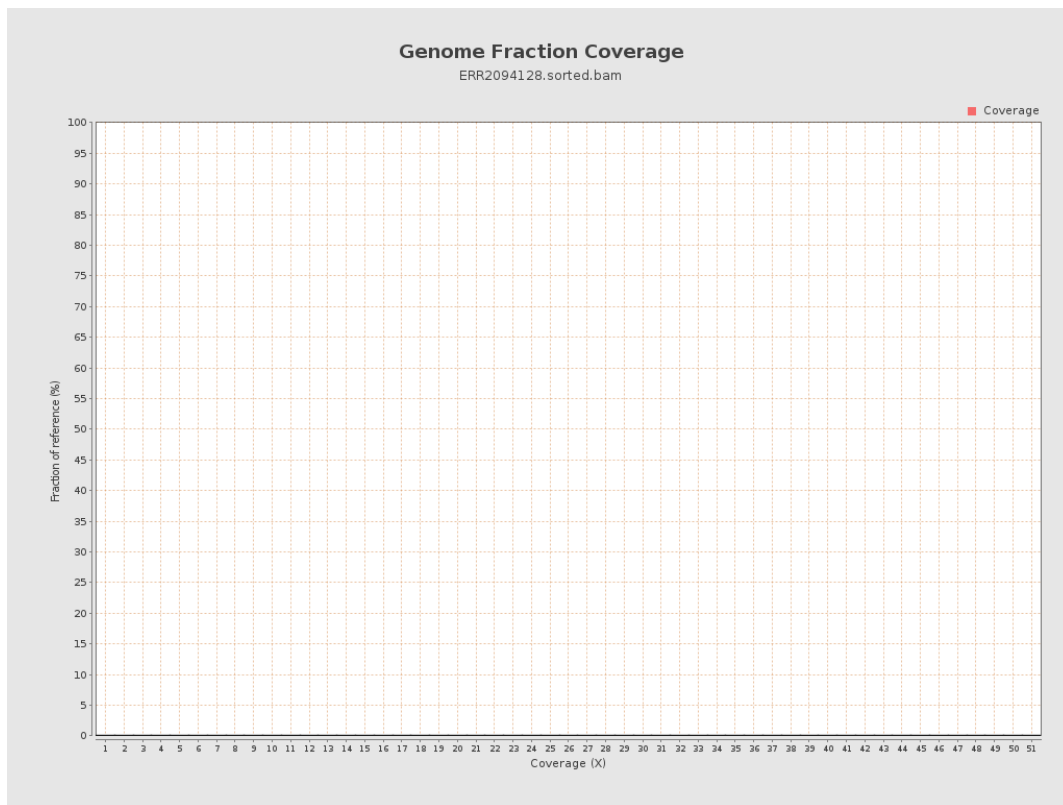
4. Results : Coverage Histogram



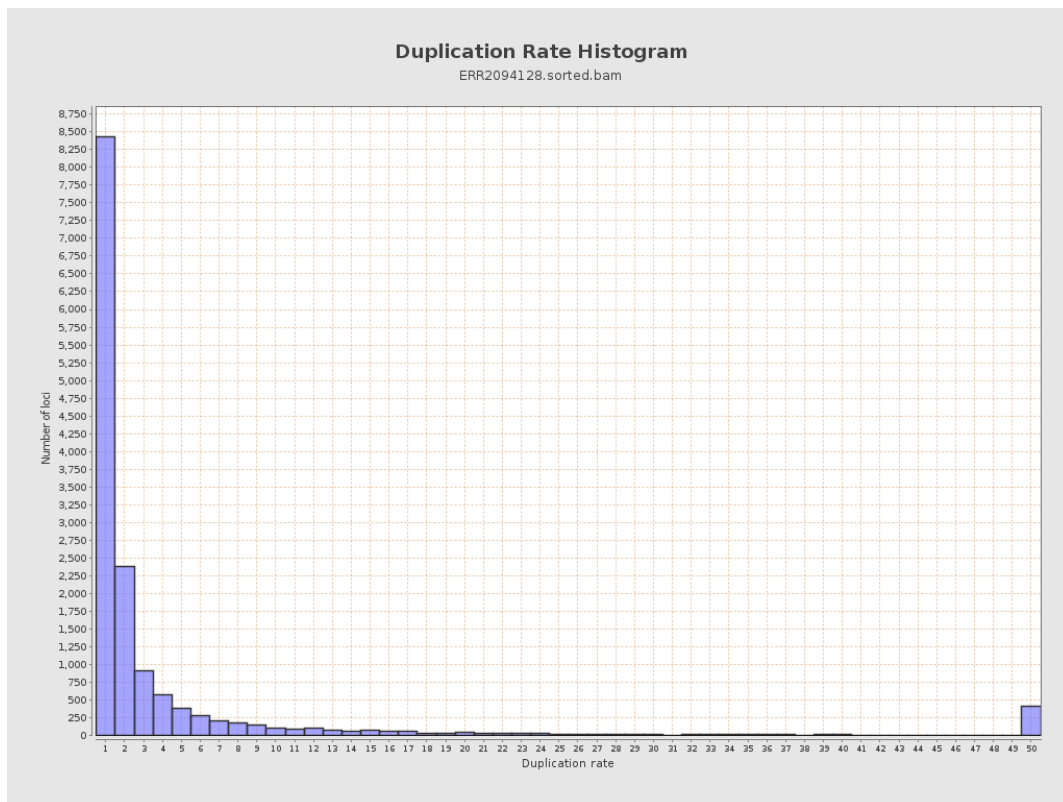
5. Results : Coverage Histogram (0-50X)



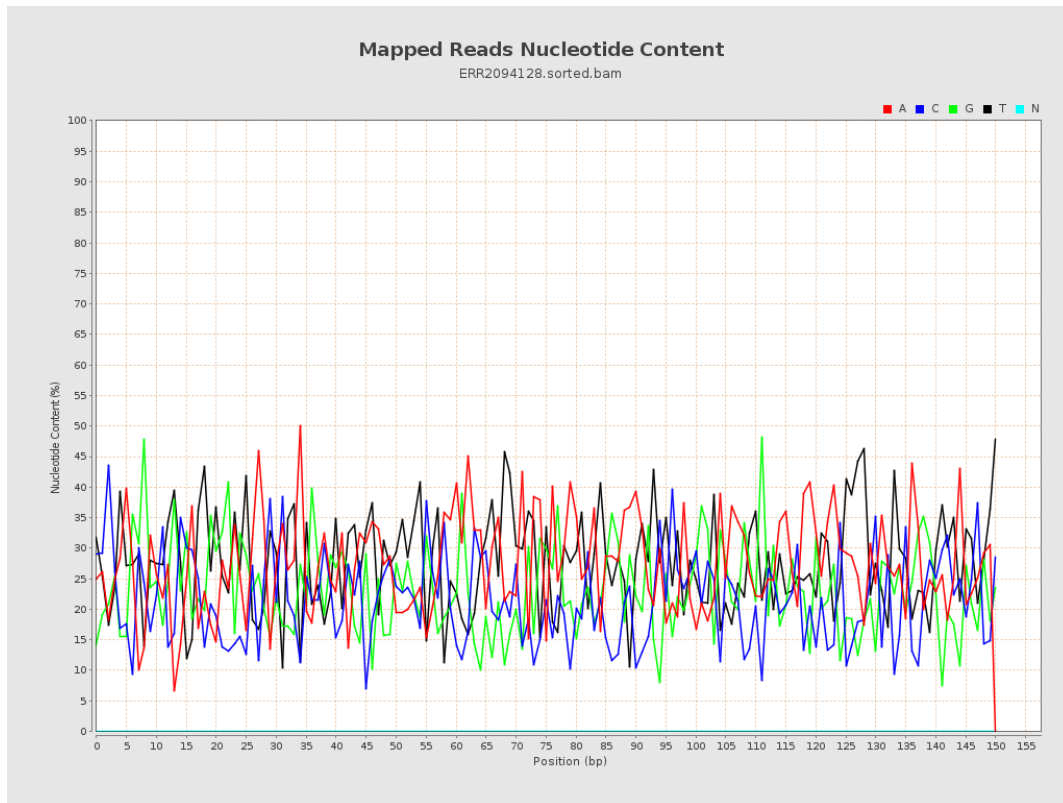
6. Results : Genome Fraction Coverage



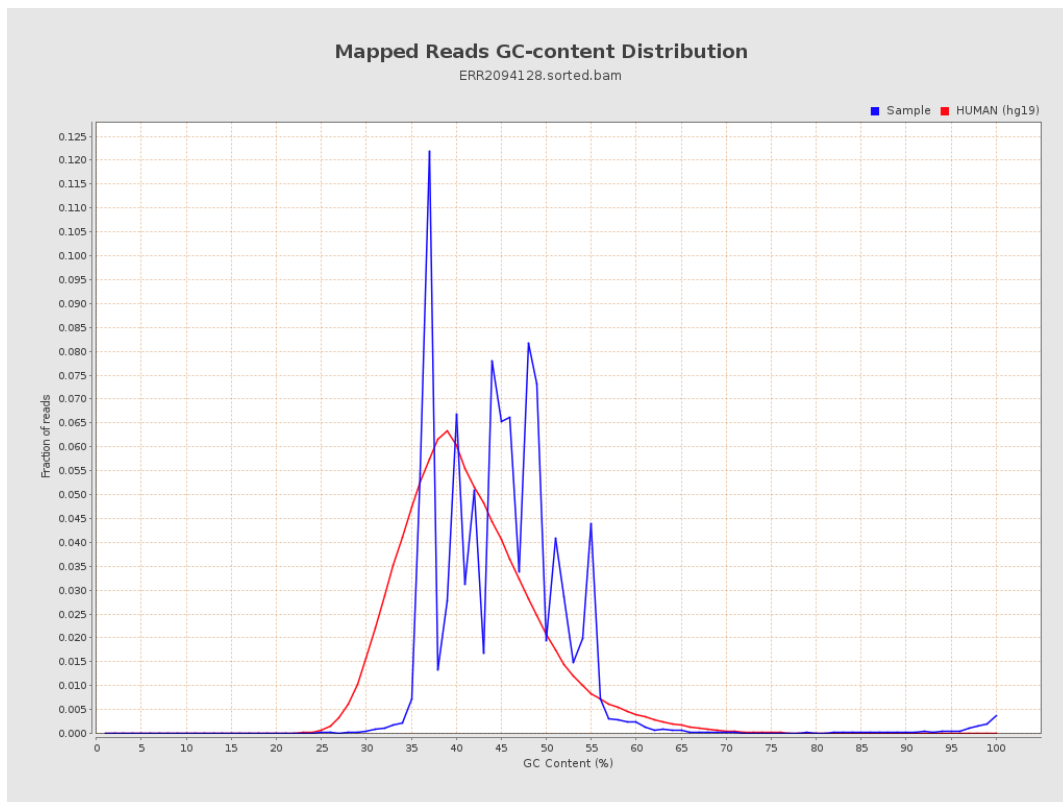
7. Results : Duplication Rate Histogram



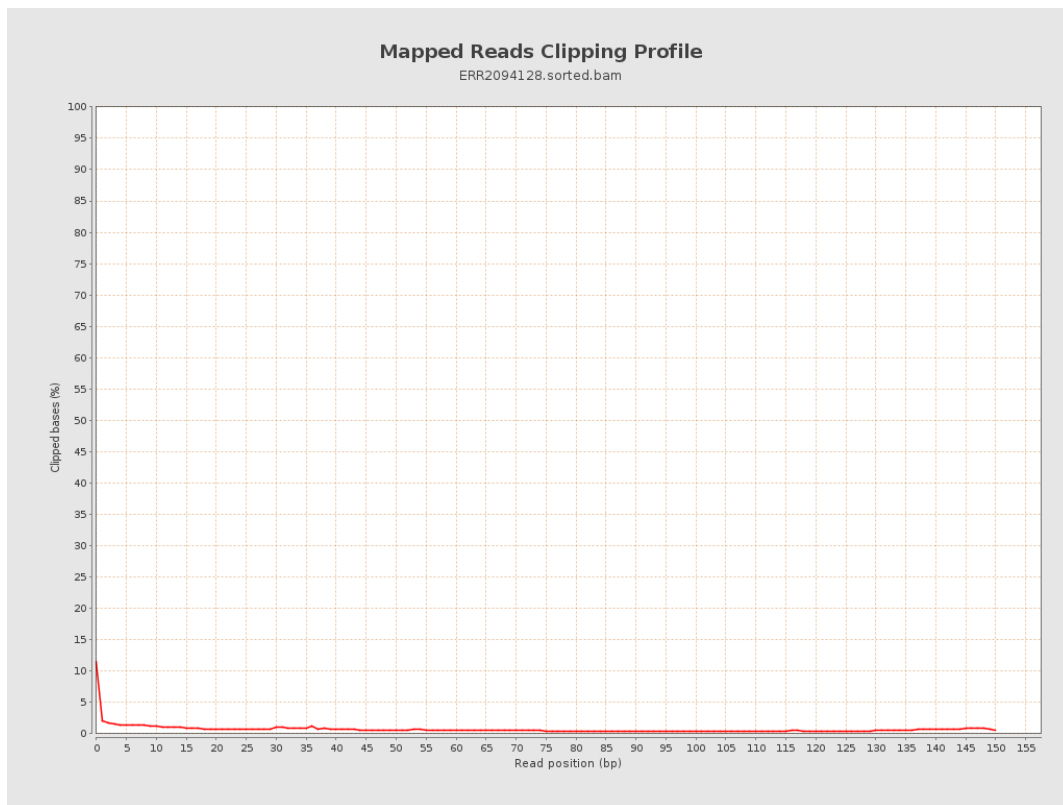
8. Results : Mapped Reads Nucleotide Content



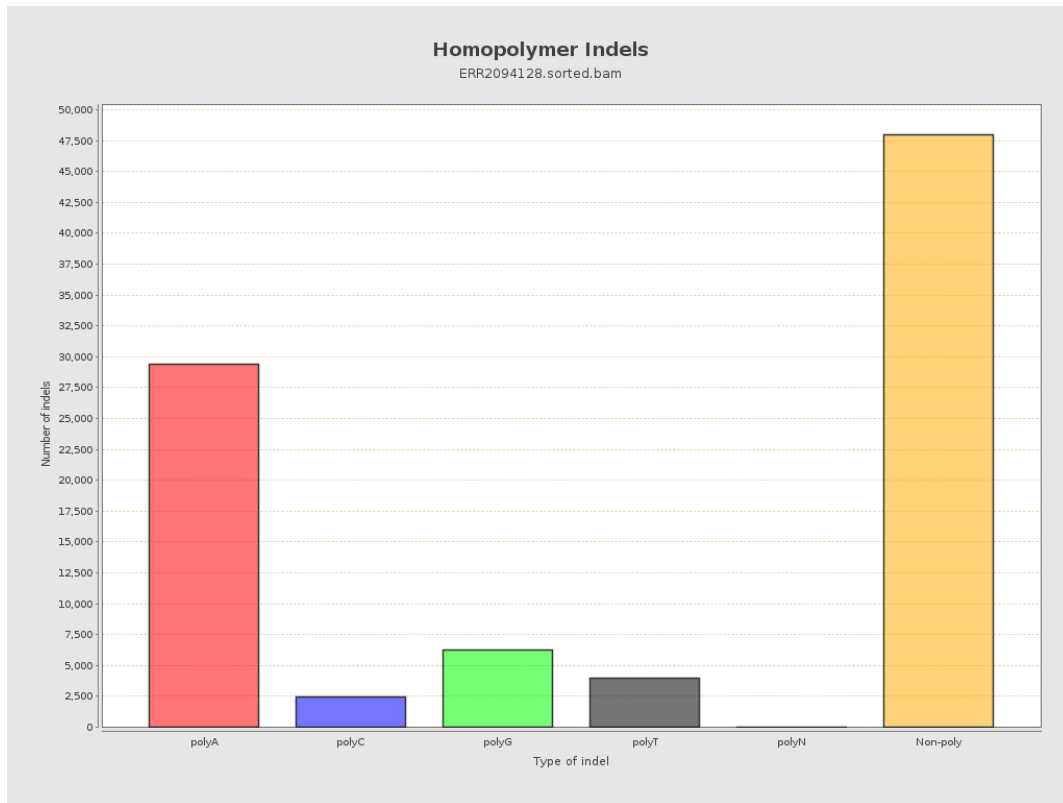
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



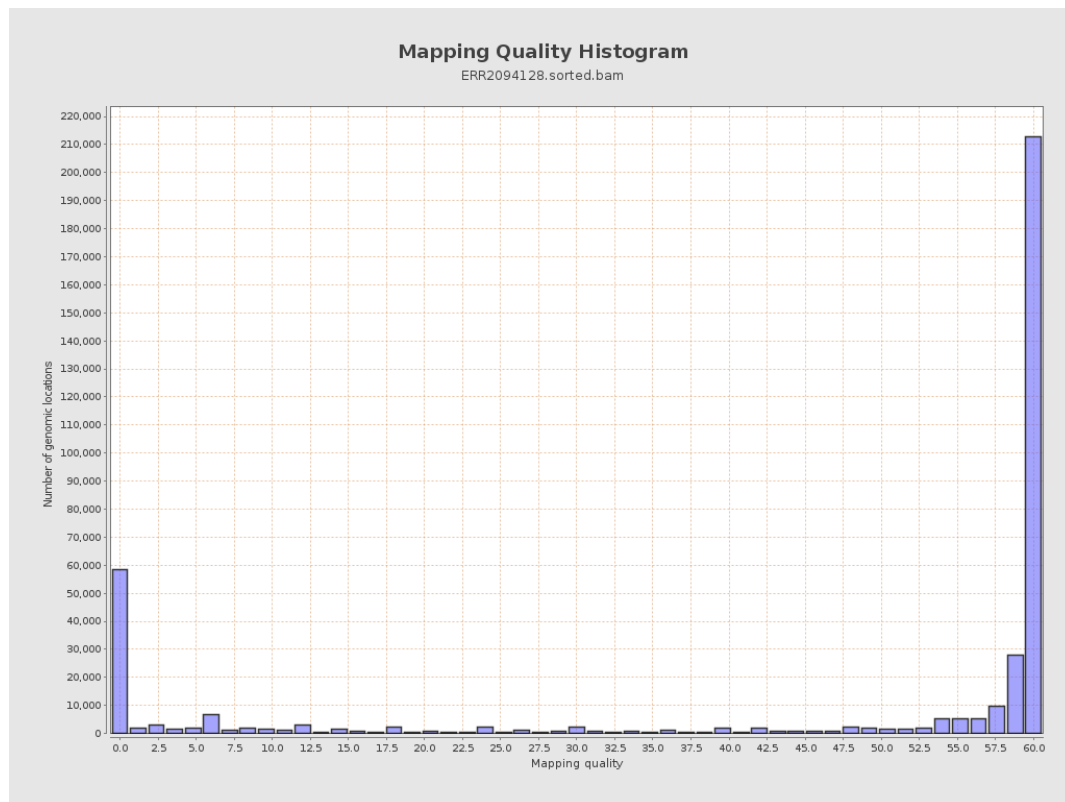
11. Results : Homopolymer Indels



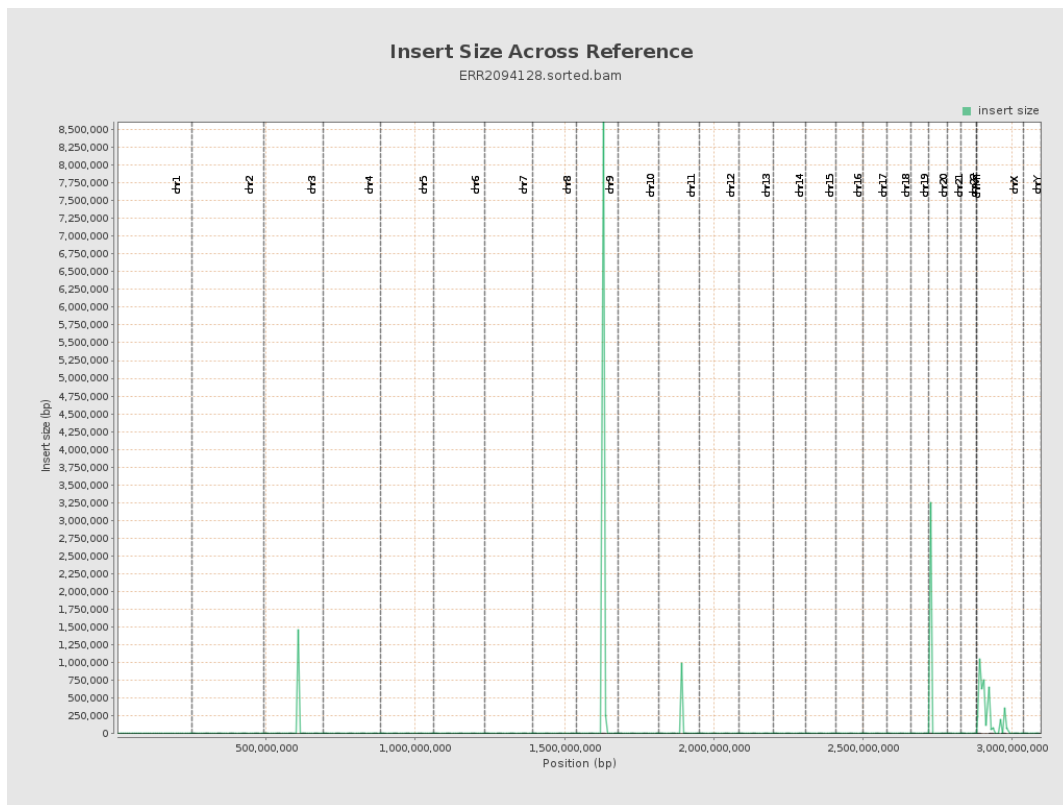
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

