

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:37:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094112.sorted.bam -c -nw 400 -hm 3
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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_ERR2094112 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094112_1.fastq.gz ERR2094112_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:37:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	307,974
Mapped reads	291,068 / 94.51%
Unmapped reads	16,906 / 5.49%
Mapped paired reads	291,068 / 94.51%
Mapped reads, first in pair	146,147 / 47.45%
Mapped reads, second in pair	144,921 / 47.06%
Mapped reads, both in pair	288,988 / 93.84%
Mapped reads, singletons	2,080 / 0.68%
Secondary alignments	0
Supplementary alignments	20,396 / 6.62%
Read min/max/mean length	30 / 151 / 135.22
Duplicated reads (estimated)	276,490 / 89.78%
Duplication rate	52.36%
Clipped reads	151,419 / 49.17%

2.2. ACGT Content

Number/percentage of A's	9,867,626 / 28.31%
Number/percentage of C's	7,651,898 / 21.95%
Number/percentage of T's	9,369,470 / 26.88%
Number/percentage of G's	7,964,040 / 22.85%
Number/percentage of N's	358 / 0%

GC Percentage	44.8%
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2.3. Coverage

Mean	0.0115
Standard Deviation	2.7981

2.4. Mapping Quality

Mean Mapping Quality	40.14
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2.5. Insert size

Mean	1,665,398.36
Standard Deviation	11,529,664.97
P25/Median/P75	110 / 142 / 170

2.6. Mismatches and indels

General error rate	3.43%
Mismatches	1,151,229
Insertions	22,366
Mapped reads with at least one insertion	7.6%
Deletions	93,804
Mapped reads with at least one deletion	31.27%
Homopolymer indels	28.54%

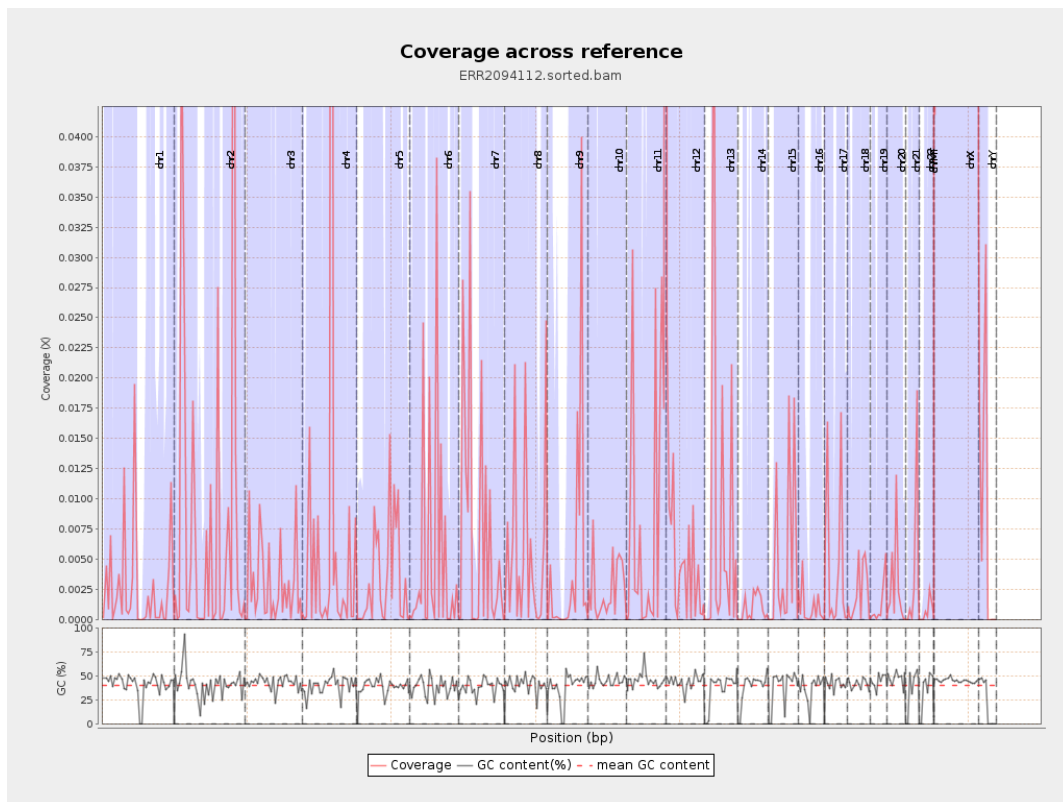
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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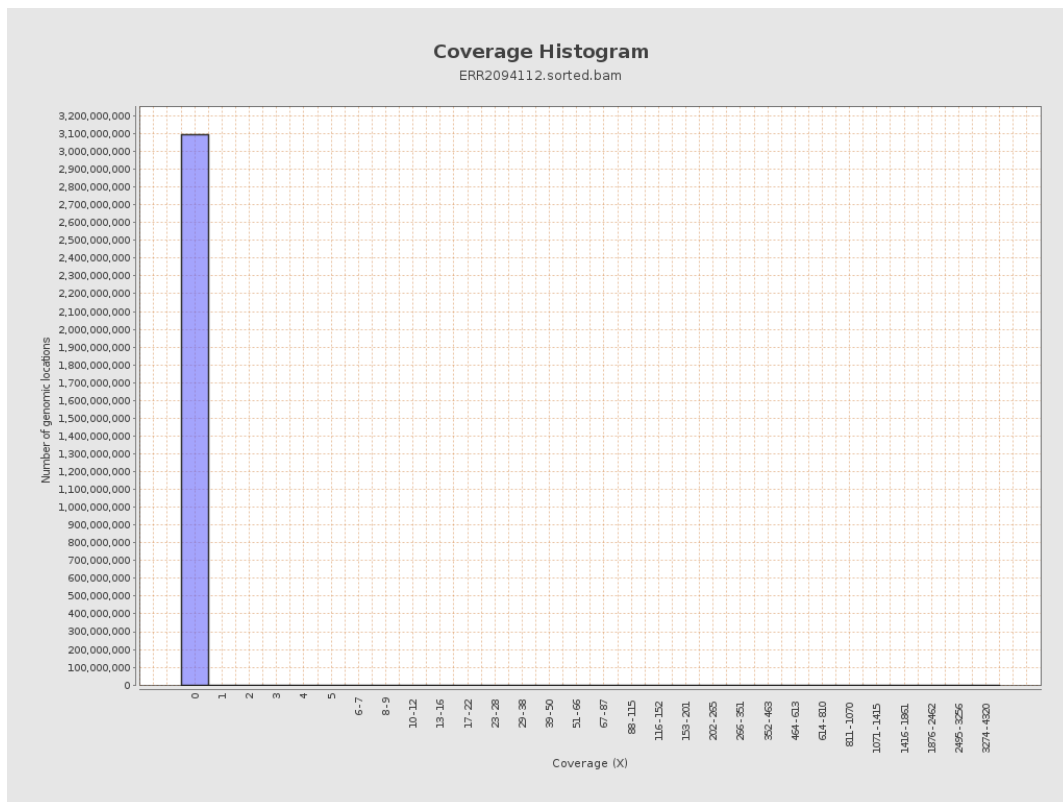
		bases	coverage	deviation
chr1	249250621	640335	0.0026	1.0263
chr2	243199373	2189516	0.009	3.765
chr3	198022430	589426	0.003	0.8185
chr4	191154276	1569405	0.0082	2.4283
chr5	180915260	658997	0.0036	1.274
chr6	171115067	923197	0.0054	1.8685
chr7	159138663	1084949	0.0068	2.2063
chr8	146364022	841044	0.0057	1.859
chr9	141213431	609701	0.0043	1.5302
chr10	135534747	335817	0.0025	0.6596
chr11	135006516	1384722	0.0103	3.3534
chr12	133851895	701353	0.0052	1.1642
chr13	115169878	912547	0.0079	2.4829
chr14	107349540	98355	0.0009	0.2792
chr15	102531392	491666	0.0048	1.3653
chr16	90354753	92774	0.001	0.3807
chr17	81195210	375952	0.0046	1.5458
chr18	78077248	183681	0.0024	0.6307
chr19	59128983	72666	0.0012	0.4194
chr20	63025520	179806	0.0029	0.8763
chr21	48129895	186538	0.0039	1.5136
chr22	51304566	33835	0.0007	0.1851
chrMT	16571	26355	1.5904	7.8904
chrX	155270560	20823205	0.1341	9.3281

chrY	59373566	506672	0.0085	1.7128
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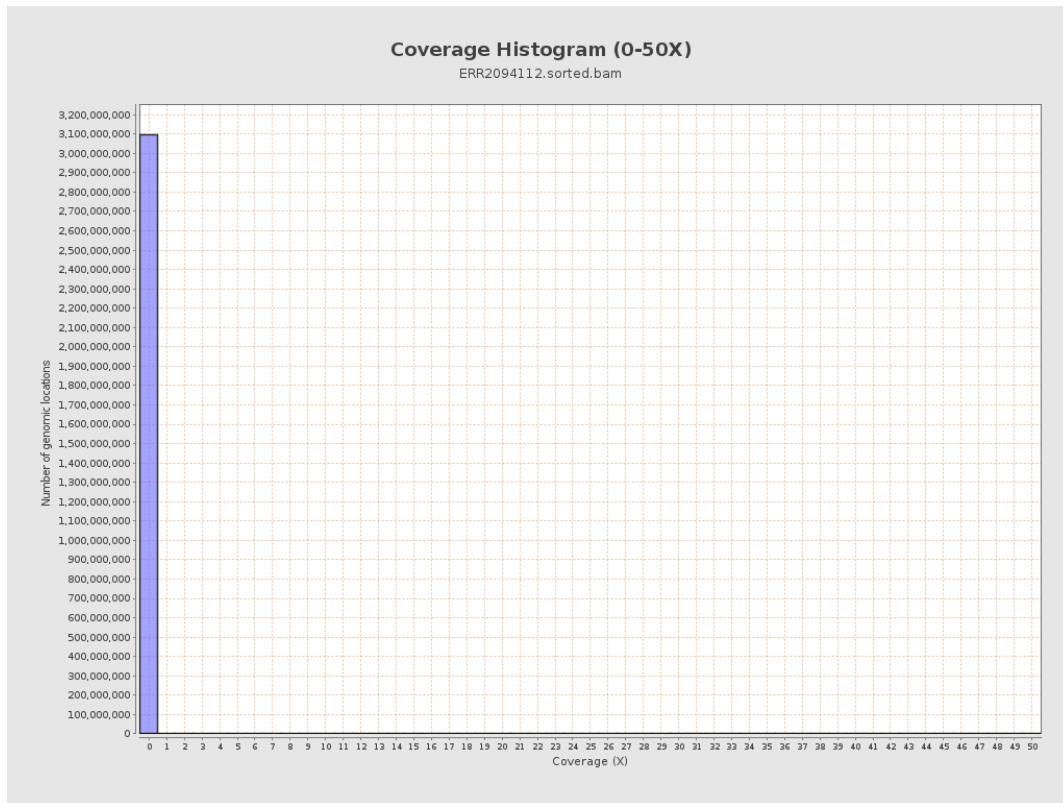
3. Results : Coverage across reference



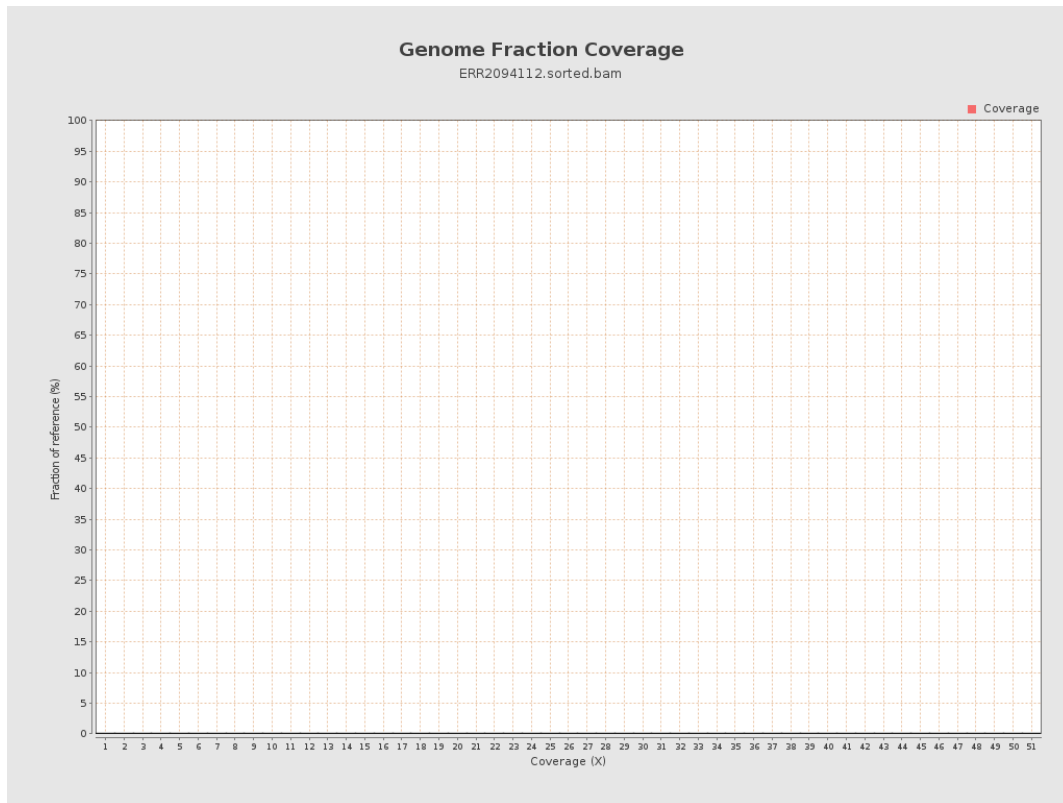
4. Results : Coverage Histogram



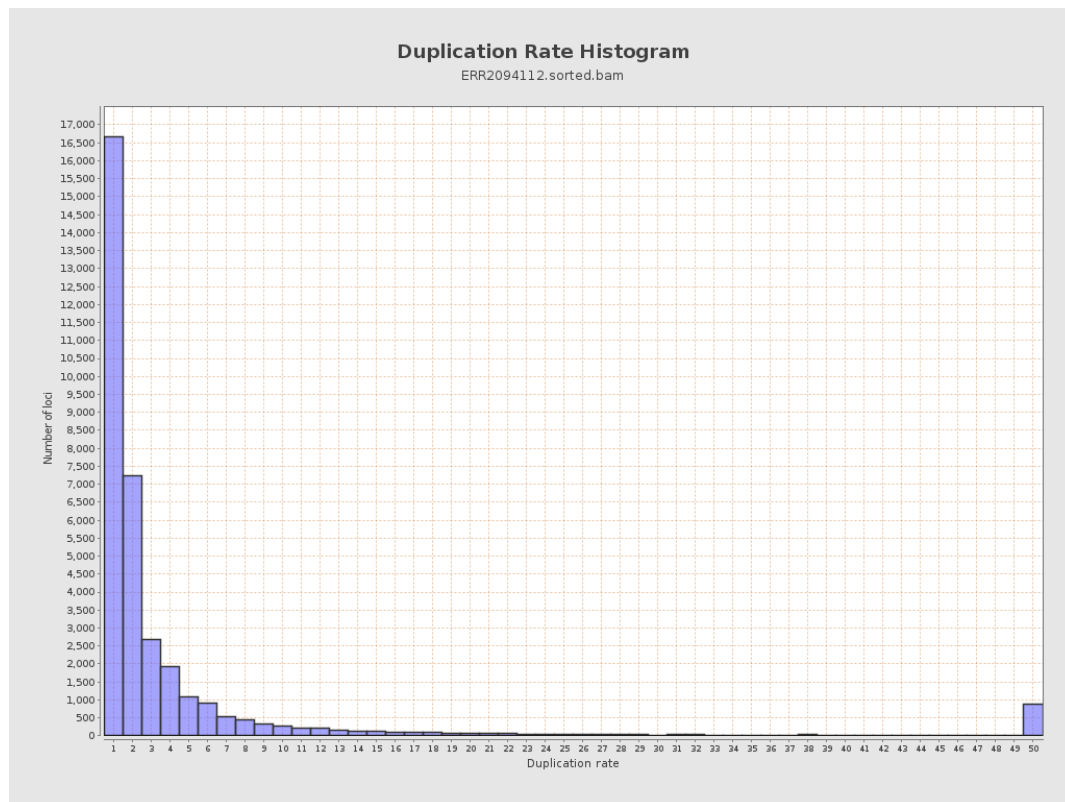
5. Results : Coverage Histogram (0-50X)



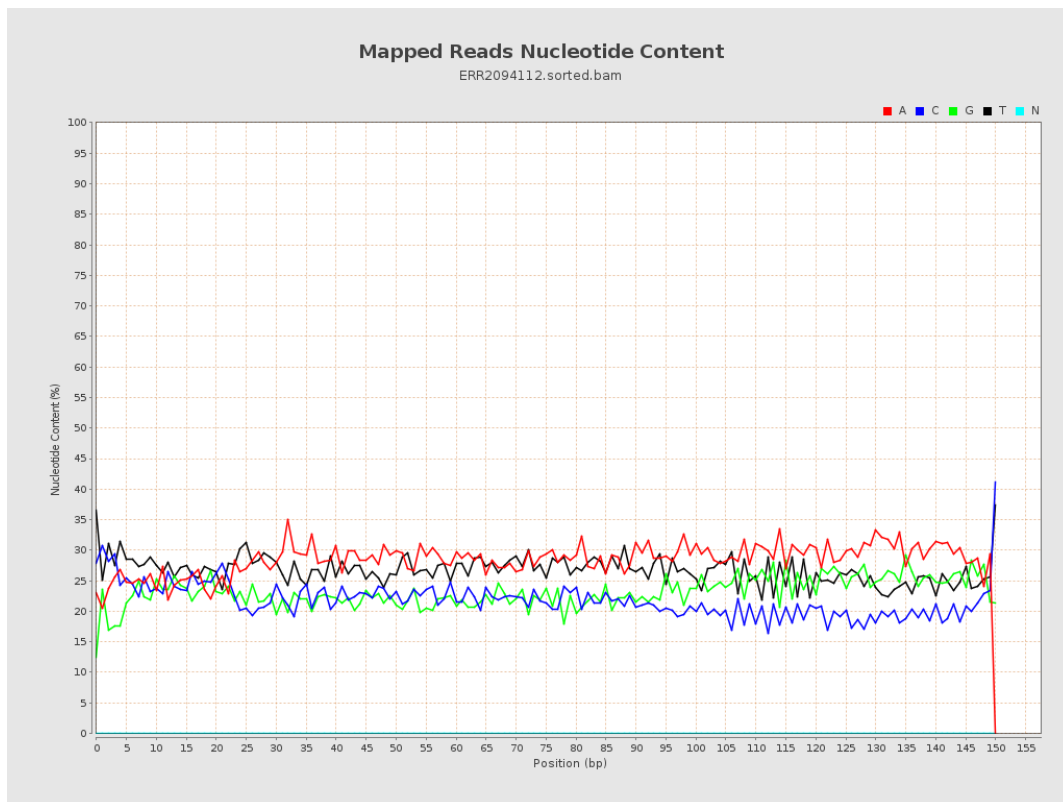
6. Results : Genome Fraction Coverage



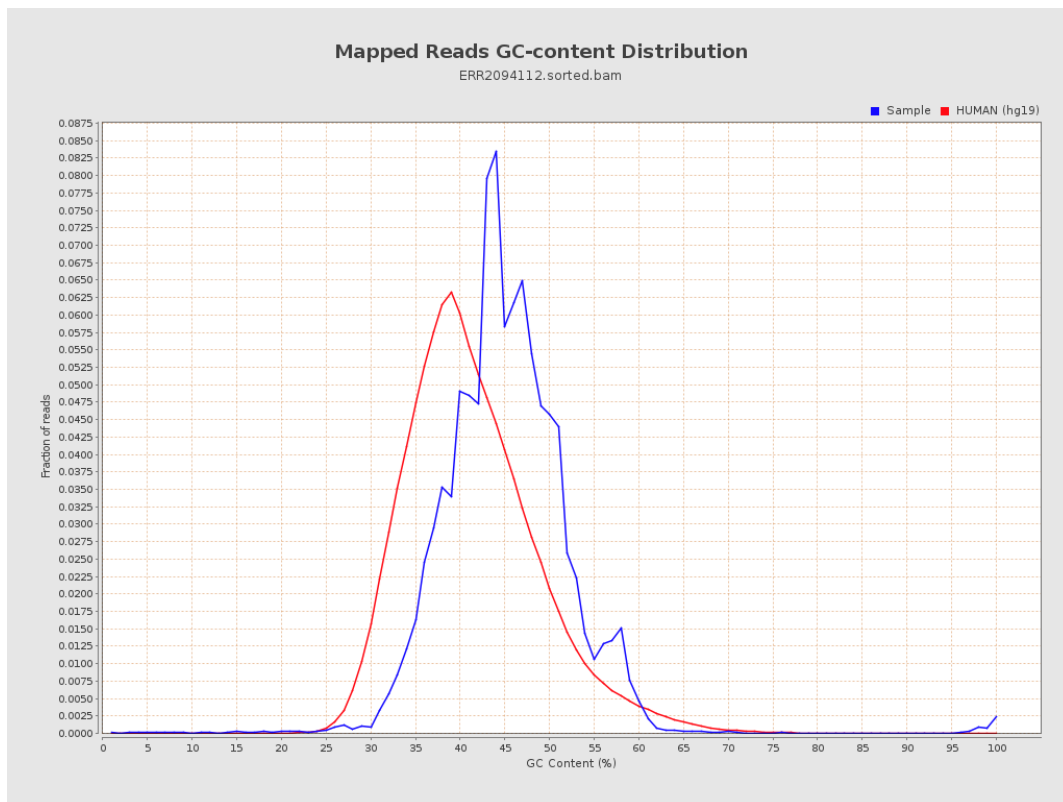
7. Results : Duplication Rate Histogram



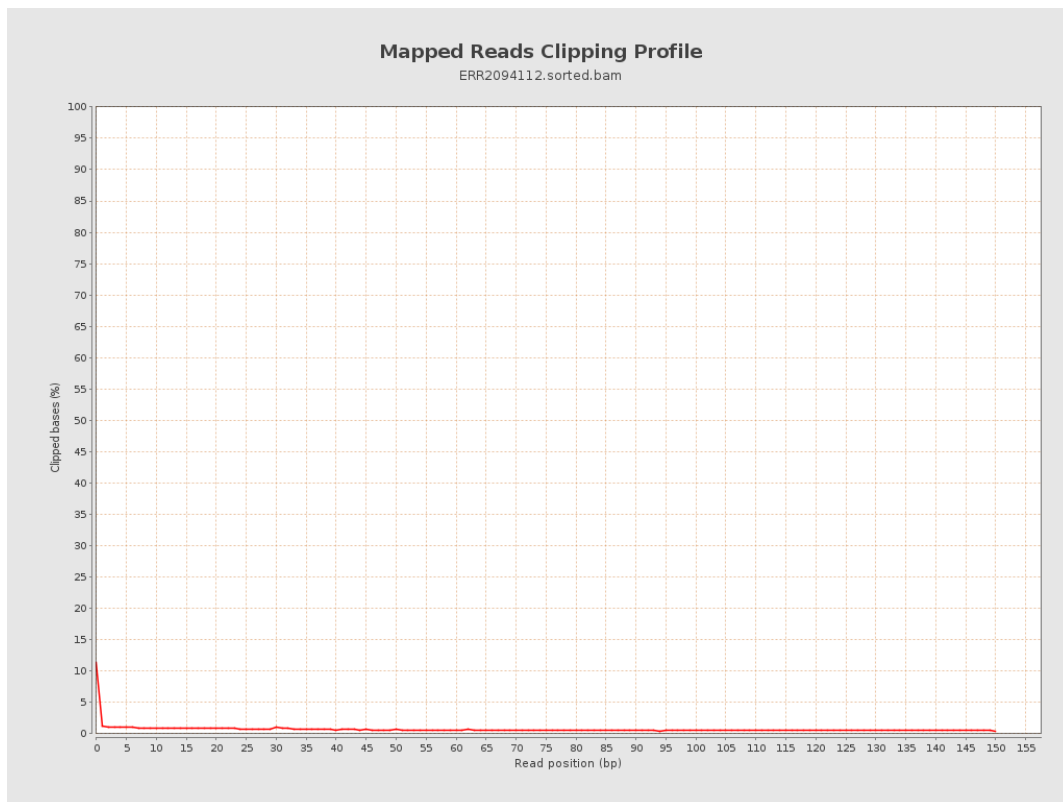
8. Results : Mapped Reads Nucleotide Content



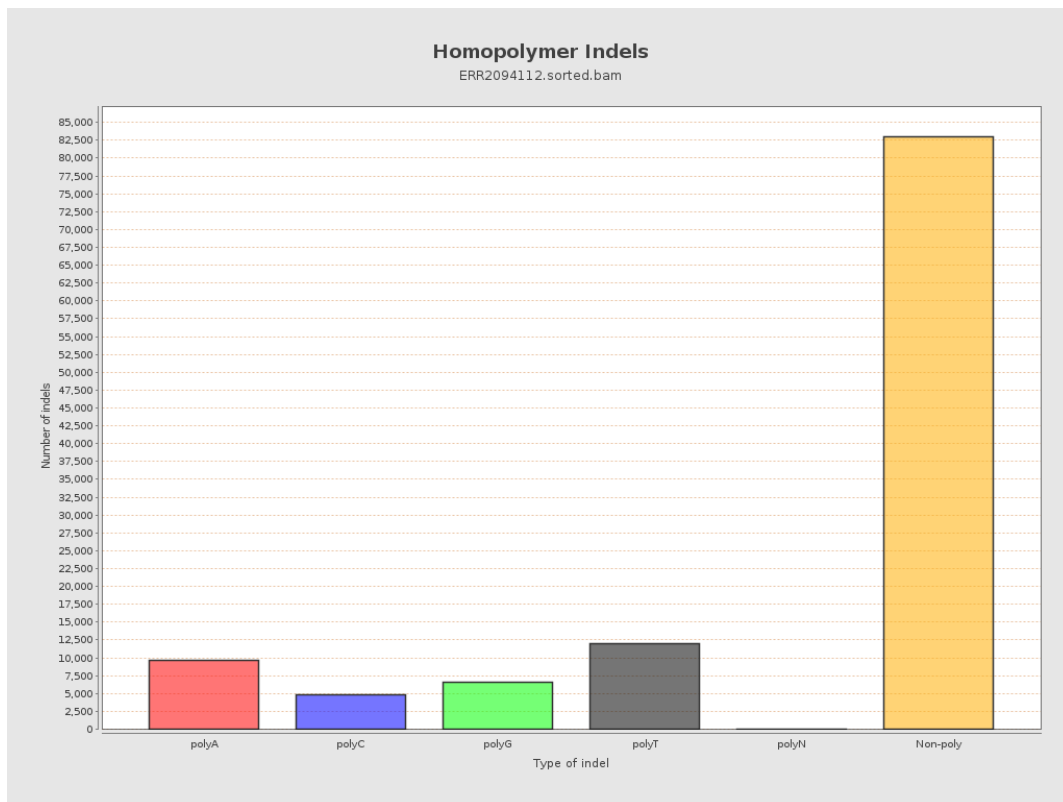
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



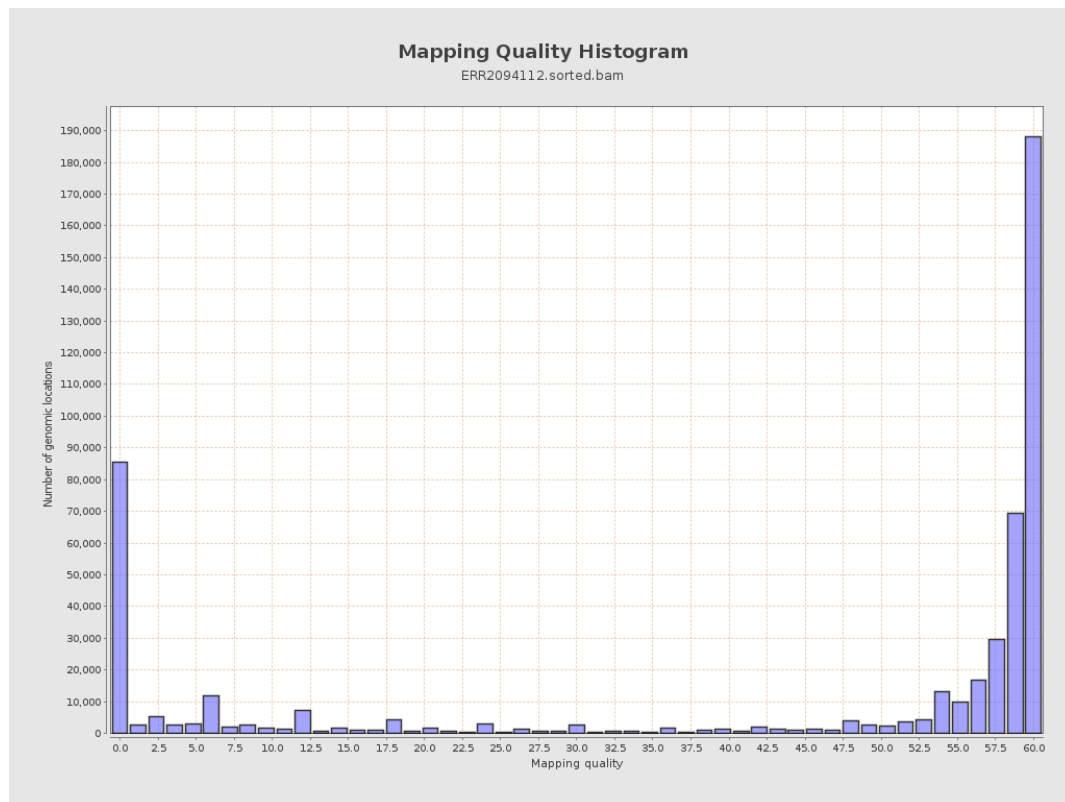
11. Results : Homopolymer Indels



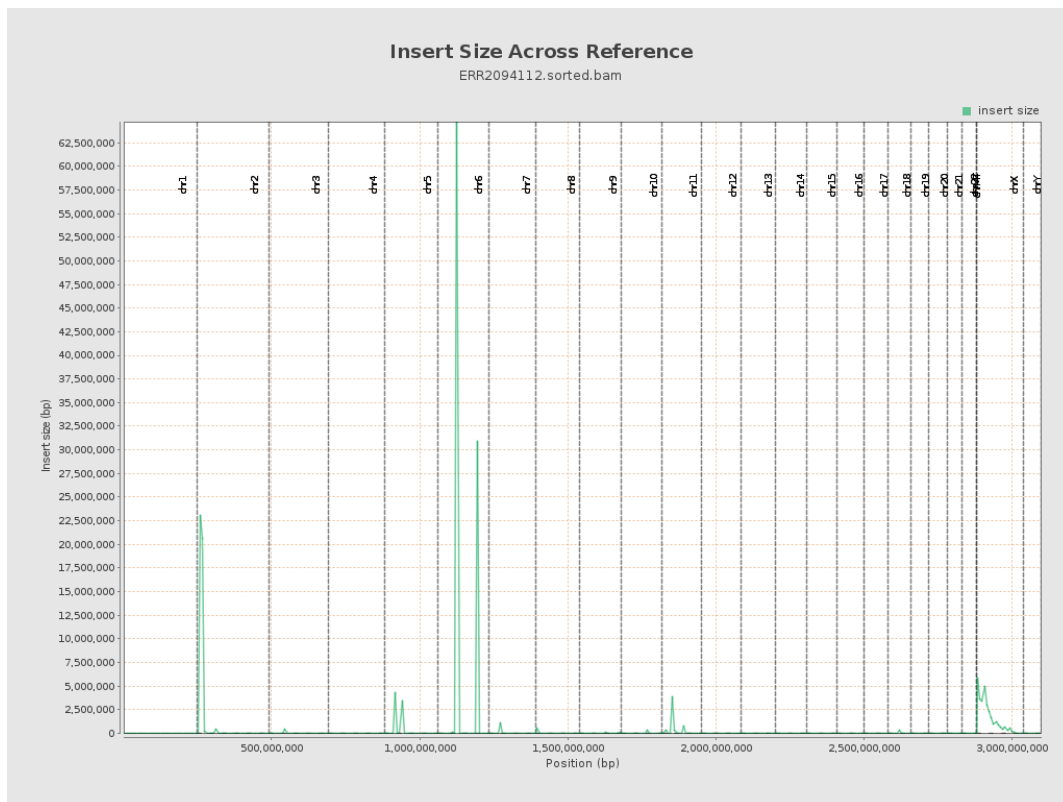
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

