

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 07:40:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094161.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_ERR2094161 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094161_1.fastq.gz ERR2094161_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 07:40:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,512
Mapped reads	27,430 / 64.52%
Unmapped reads	15,082 / 35.48%
Mapped paired reads	27,430 / 64.52%
Mapped reads, first in pair	13,767 / 32.38%
Mapped reads, second in pair	13,663 / 32.14%
Mapped reads, both in pair	26,858 / 63.18%
Mapped reads, singletons	572 / 1.35%
Secondary alignments	0
Supplementary alignments	72 / 0.17%
Read min/max/mean length	30 / 151 / 121.28
Duplicated reads (estimated)	26,534 / 62.42%
Duplication rate	35.43%
Clipped reads	4,396 / 10.34%

2.2. ACGT Content

Number/percentage of A's	1,095,656 / 27.69%
Number/percentage of C's	760,347 / 19.22%
Number/percentage of T's	1,187,033 / 30%
Number/percentage of G's	913,629 / 23.09%
Number/percentage of N's	24 / 0%

GC Percentage	42.31%
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2.3. Coverage

Mean	0.0013
Standard Deviation	2.7358

2.4. Mapping Quality

Mean Mapping Quality	12.73
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2.5. Insert size

Mean	103,841.37
Standard Deviation	2,303,018.14
P25/Median/P75	231 / 237 / 237

2.6. Mismatches and indels

General error rate	2.69%
Mismatches	106,105
Insertions	378
Mapped reads with at least one insertion	1.28%
Deletions	7,681
Mapped reads with at least one deletion	27.26%
Homopolymer indels	55.63%

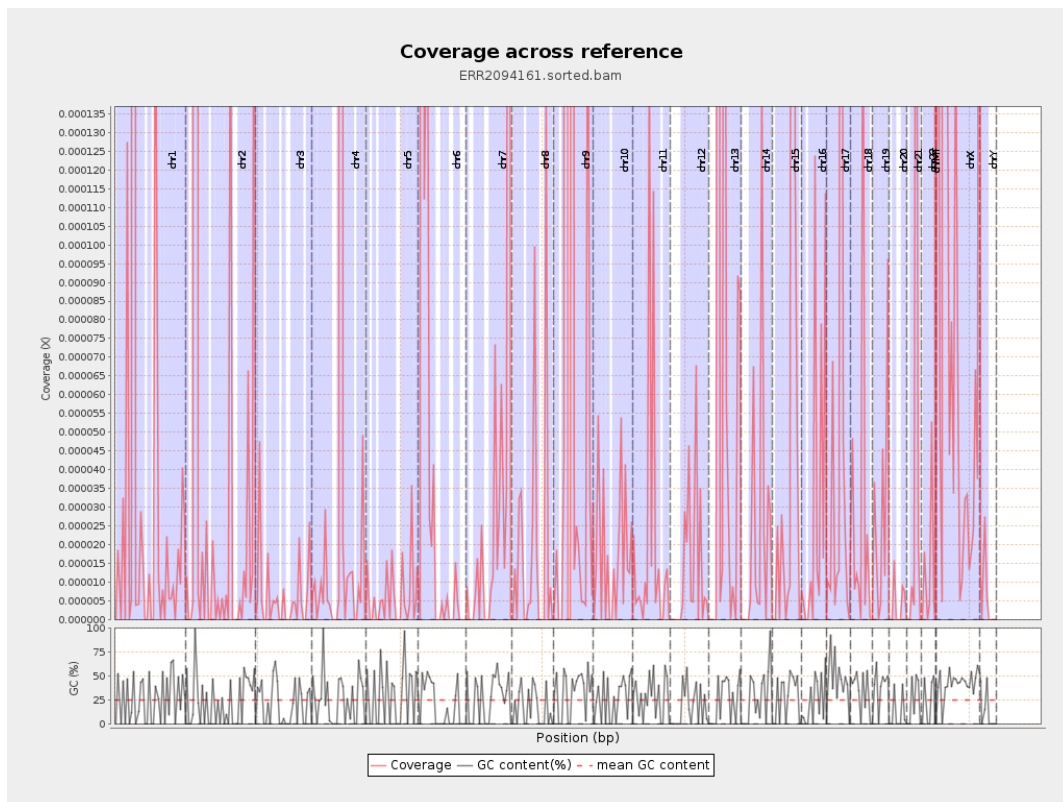
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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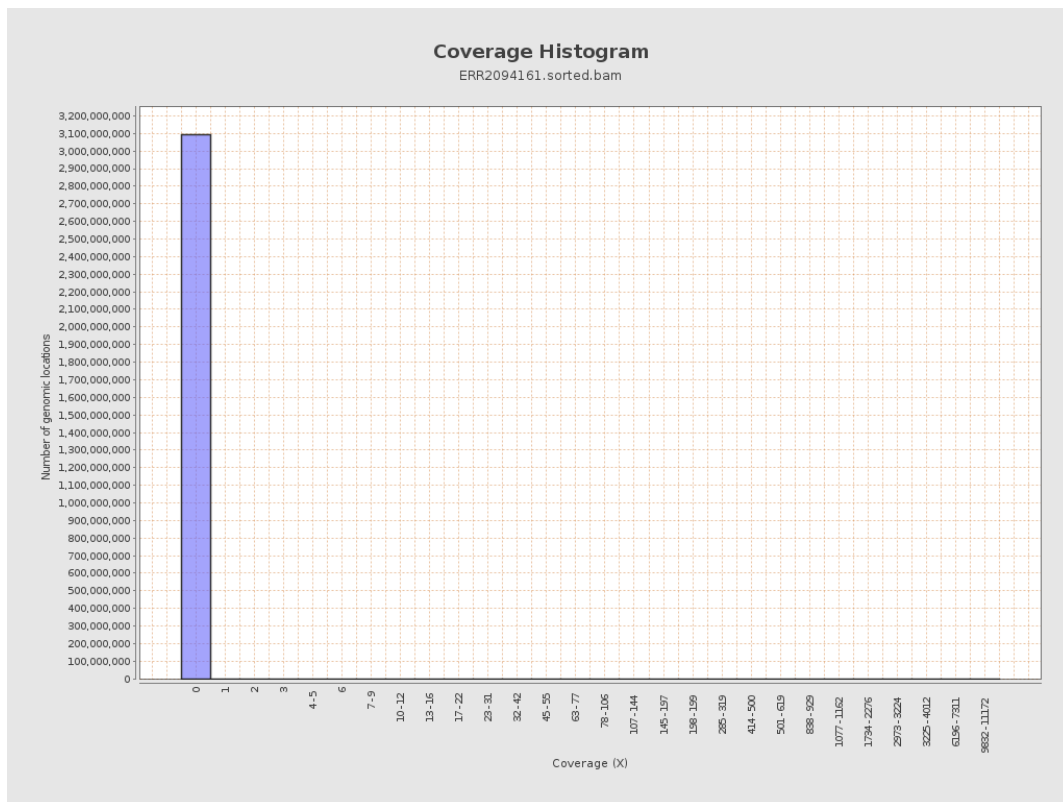
		bases	coverage	deviation
chr1	249250621	32408	0.0001	0.1403
chr2	243199373	28447	0.0001	0.1003
chr3	198022430	1303	0	0.0032
chr4	191154276	343724	0.0018	1.8595
chr5	180915260	1115	0	0.0029
chr6	171115067	16778	0.0001	0.0904
chr7	159138663	6499	0	0.0272
chr8	146364022	2934	0	0.011
chr9	141213431	28459	0.0002	0.1295
chr10	135534747	2360	0	0.0057
chr11	135006516	2893	0	0.0108
chr12	133851895	1726	0	0.0051
chr13	115169878	9100	0.0001	0.04
chr14	107349540	2515	0	0.0126
chr15	102531392	9269	0.0001	0.0584
chr16	90354753	2878	0	0.0166
chr17	81195210	5374	0.0001	0.0321
chr18	78077248	2367	0	0.0194
chr19	59128983	1629	0	0.013
chr20	63025520	248	0	0.0022
chr21	48129895	2357	0	0.0418
chr22	51304566	620	0	0.0082
chrMT	16571	3376818	203.7788	1,146.2597
chrX	155270560	84140	0.0005	0.5008

chrY	59373566	320	0	0.0033
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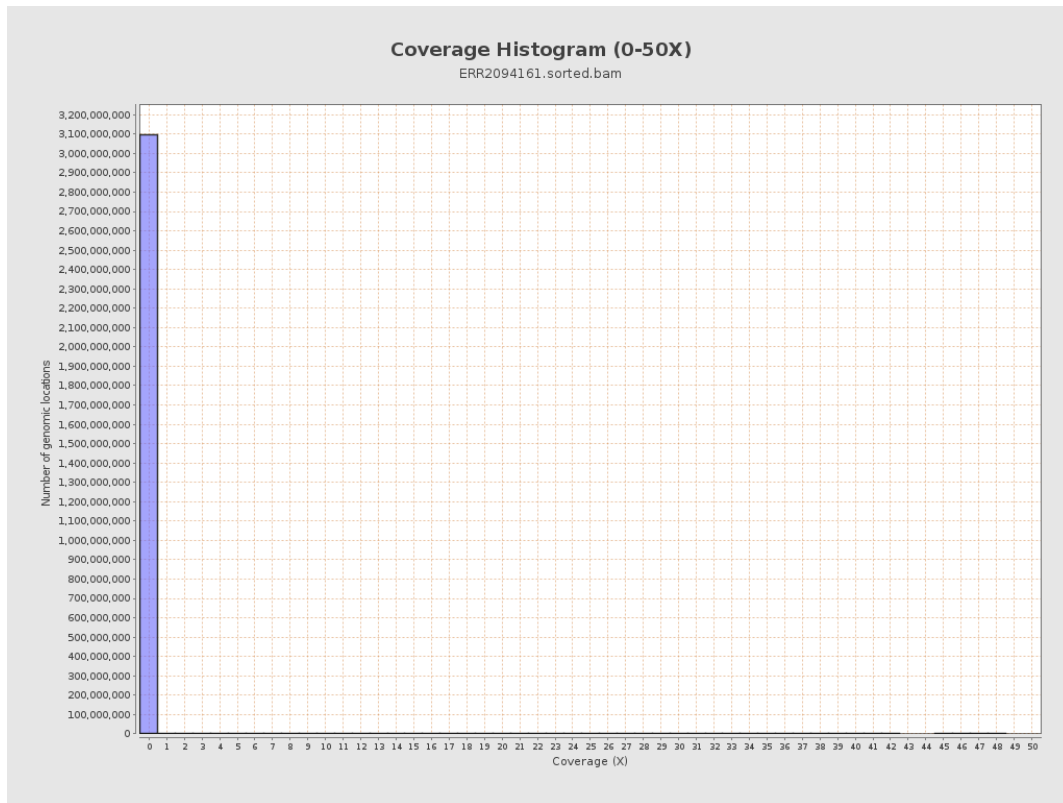
3. Results : Coverage across reference



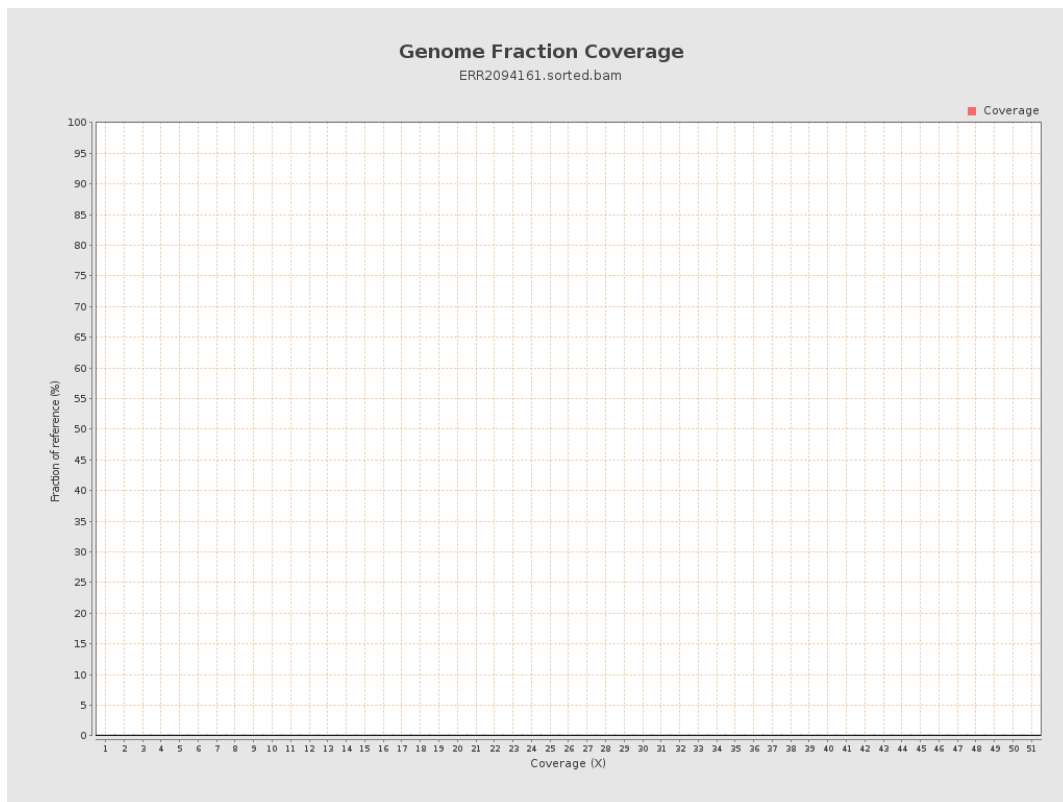
4. Results : Coverage Histogram



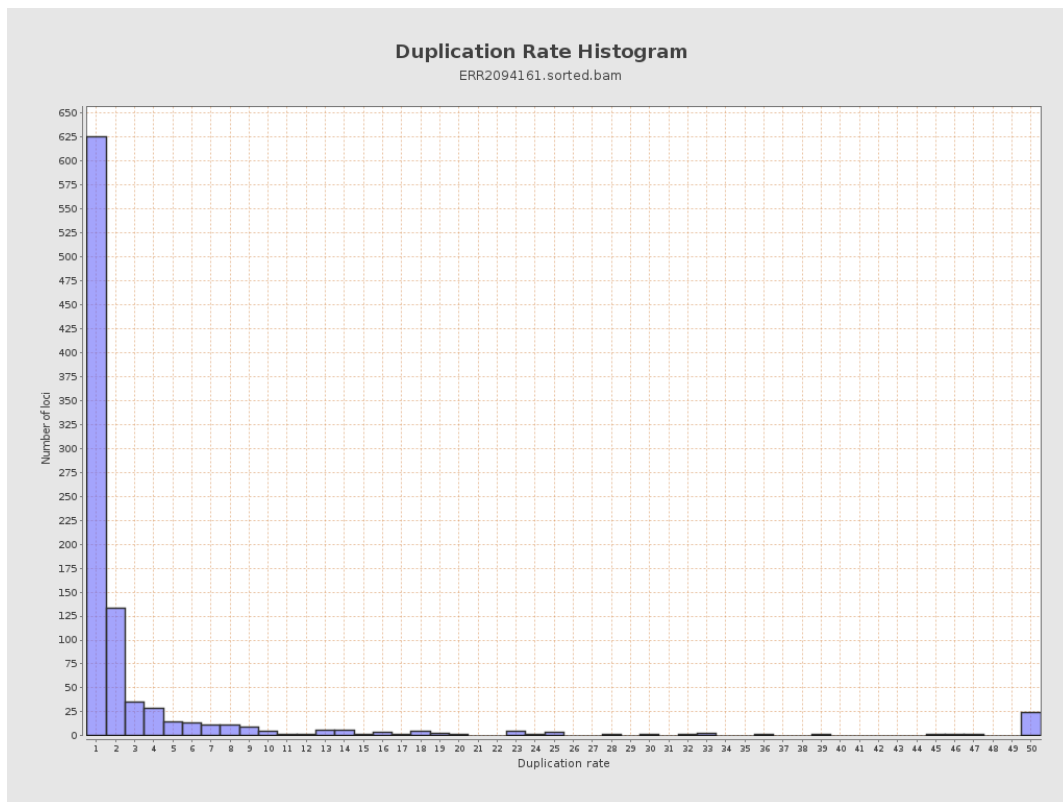
5. Results : Coverage Histogram (0-50X)



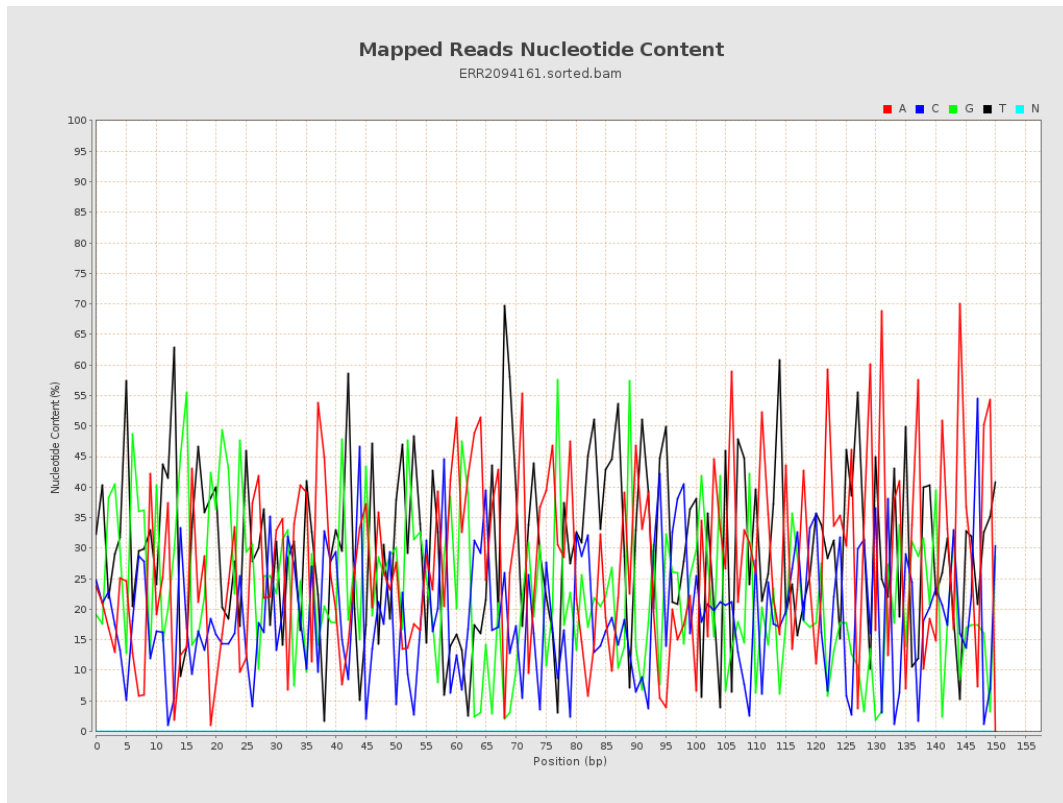
6. Results : Genome Fraction Coverage



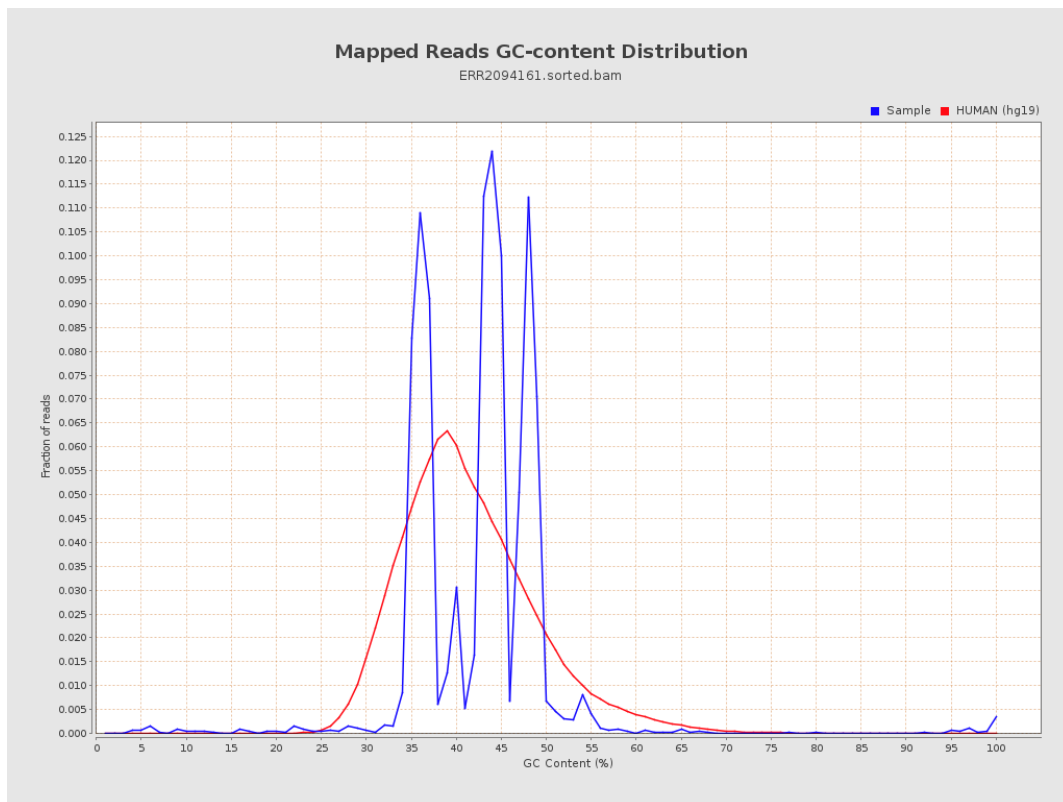
7. Results : Duplication Rate Histogram



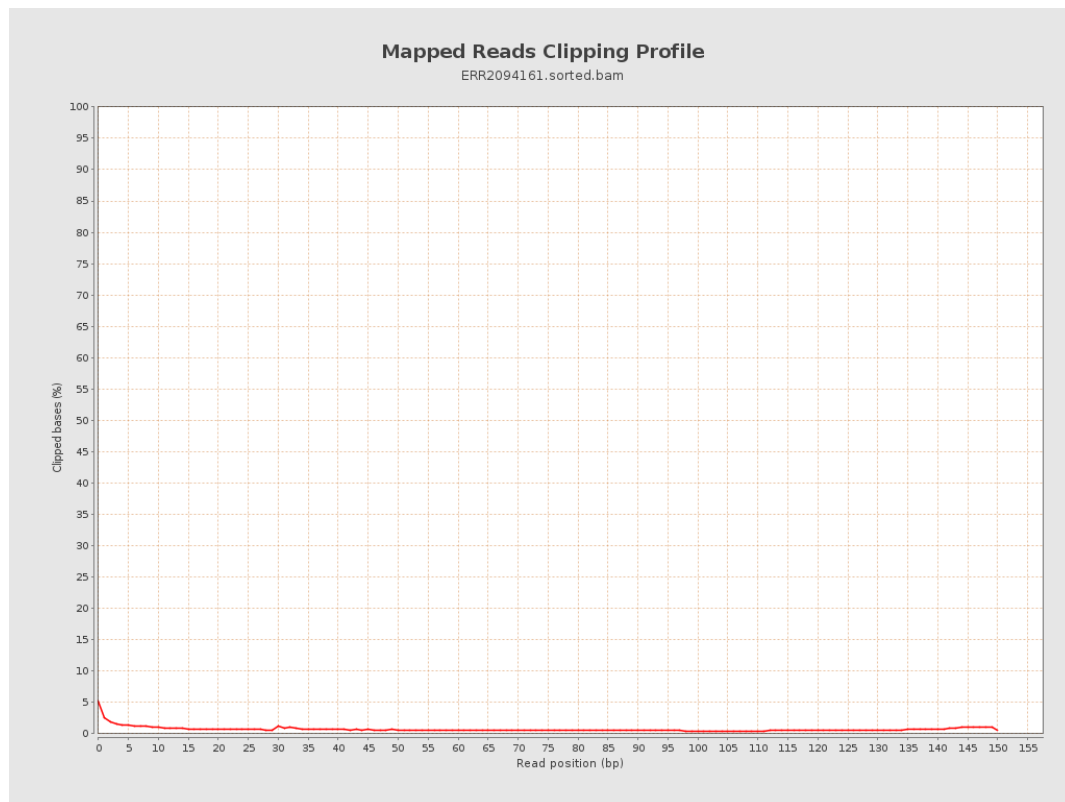
8. Results : Mapped Reads Nucleotide Content



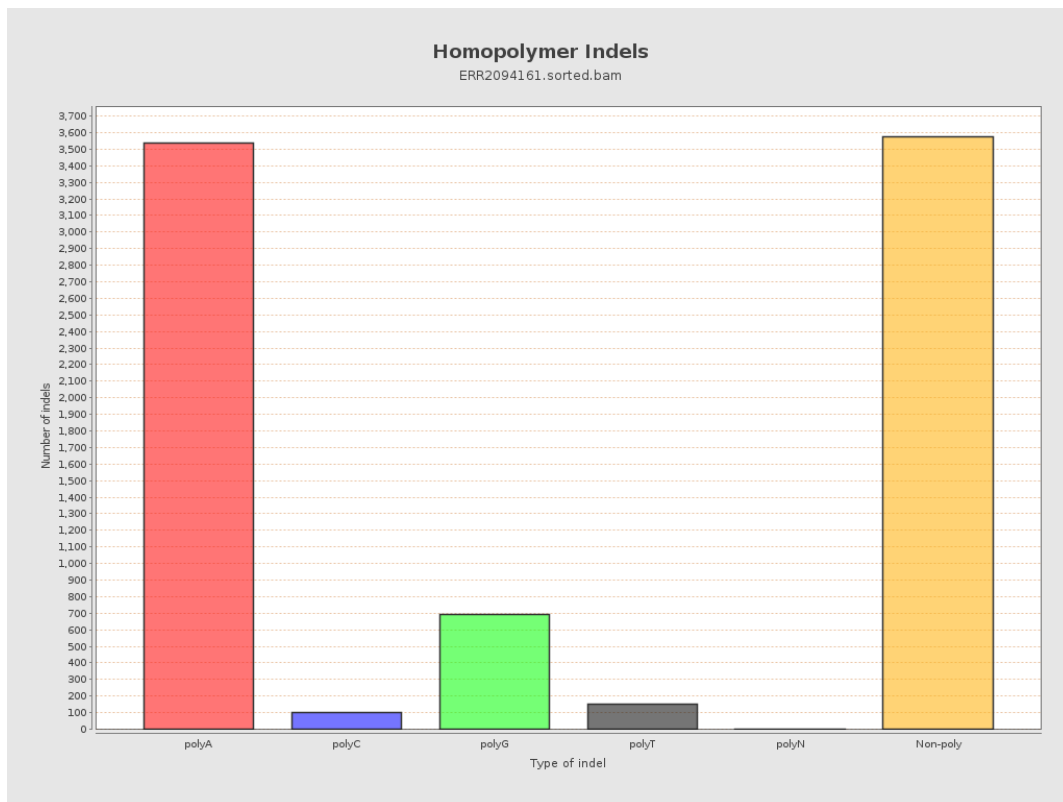
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



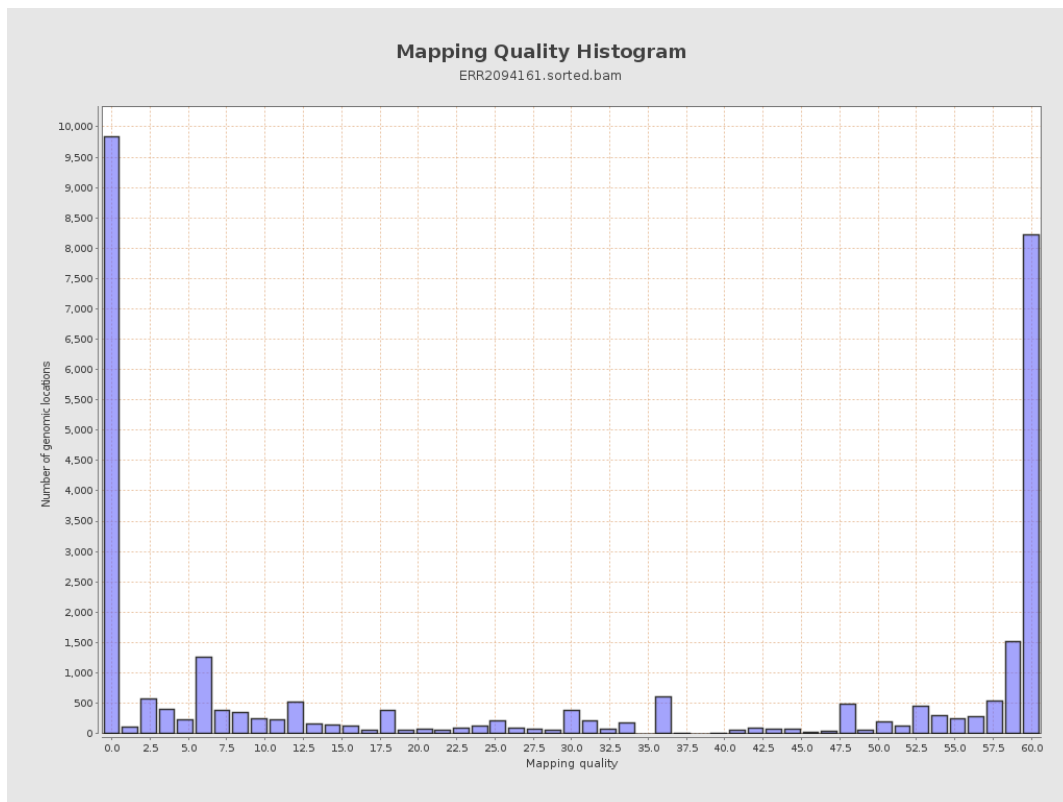
11. Results : Homopolymer Indels



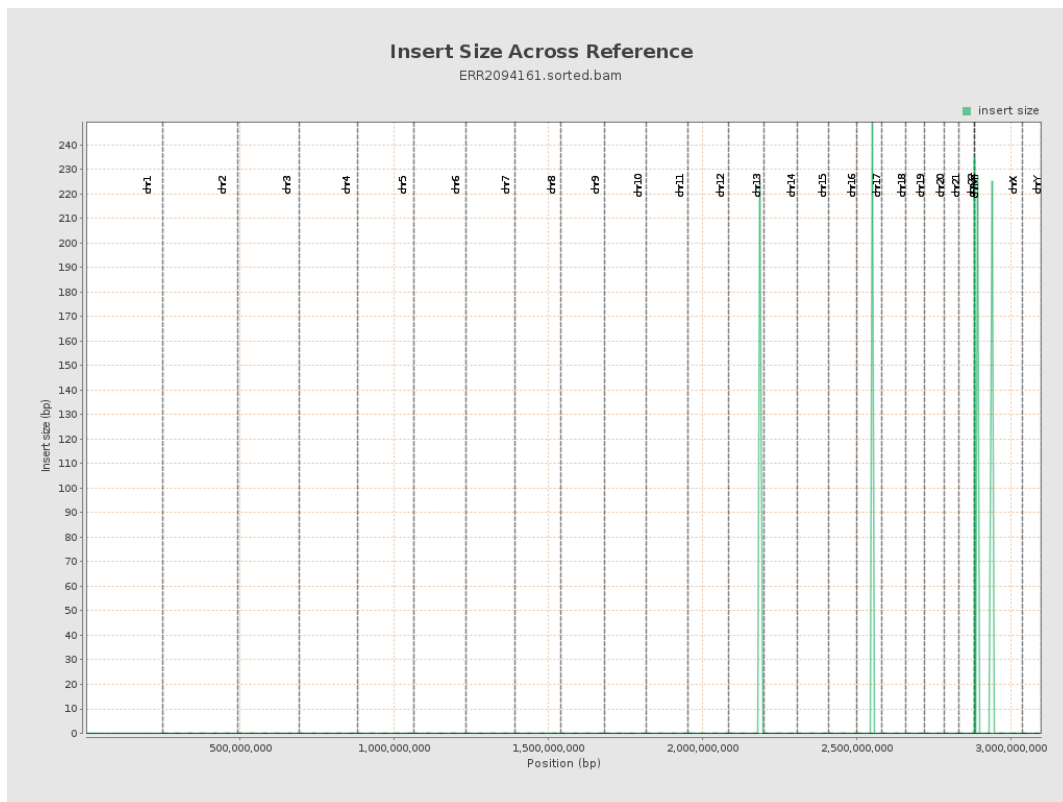
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

