Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 07:46:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094163.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_ERR2094163 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094163_1.fastq.gz ERR2094163_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 07:46:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,022
Mapped reads	719 / 2.87%
Unmapped reads	24,303 / 97.13%
Mapped paired reads	719 / 2.87%
Mapped reads, first in pair	262 / 1.05%
Mapped reads, second in pair	457 / 1.83%
Mapped reads, both in pair	450 / 1.8%
Mapped reads, singletons	269 / 1.08%
Secondary alignments	0
Supplementary alignments	21 / 0.08%
Read min/max/mean length	30 / 151 / 50.96
Duplicated reads (estimated)	509 / 2.03%
Duplication rate	22.08%
Clipped reads	573 / 2.29%

2.2. ACGT Content

Number/percentage of A's	7,079 / 13.59%
Number/percentage of C's	4,907 / 9.42%
Number/percentage of T's	6,195 / 11.9%
Number/percentage of G's	33,890 / 65.08%
Number/percentage of N's	0 / 0%

GC Percentage	74.51%

2.3. Coverage

Mean	0
Standard Deviation	0.0372

2.4. Mapping Quality

Mean Mapping Quality	6.9

2.5. Insert size

Mean	290,076.56
Standard Deviation	4,252,373.32
P25/Median/P75	30 / 31 / 81

2.6. Mismatches and indels

General error rate	3.41%
Mismatches	1,322
Insertions	78
Mapped reads with at least one insertion	7.65%
Deletions	56
Mapped reads with at least one deletion	7.23%
Homopolymer indels	42.54%

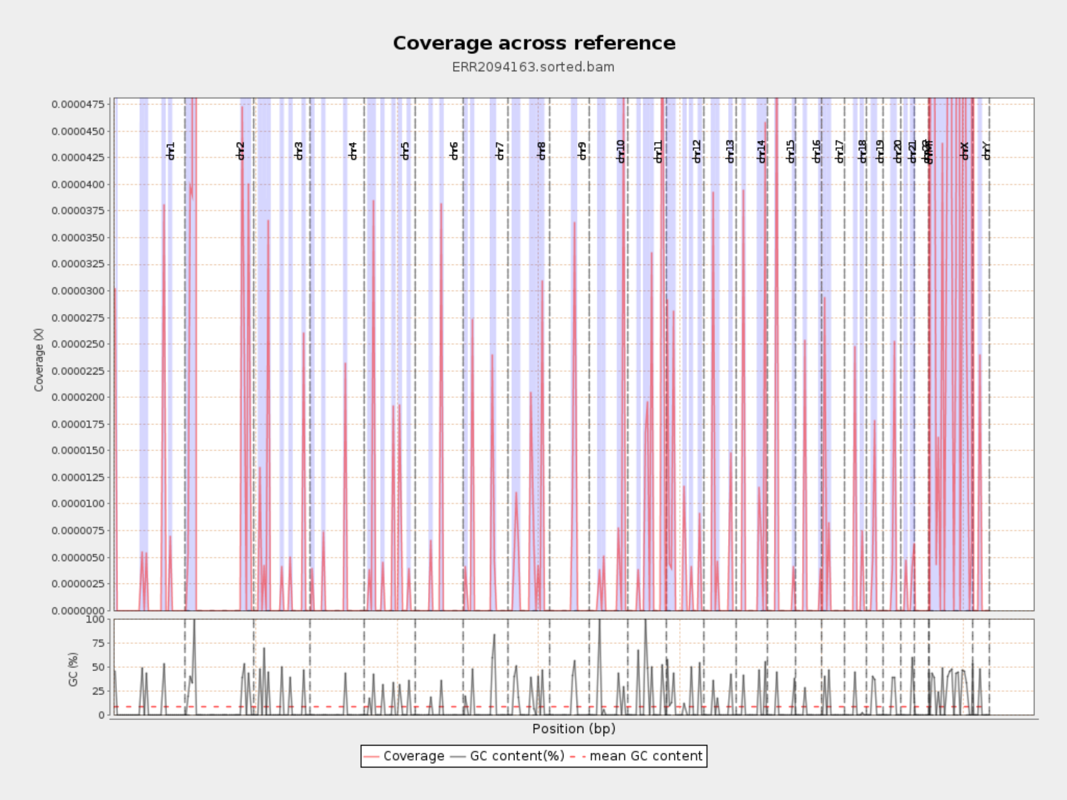
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

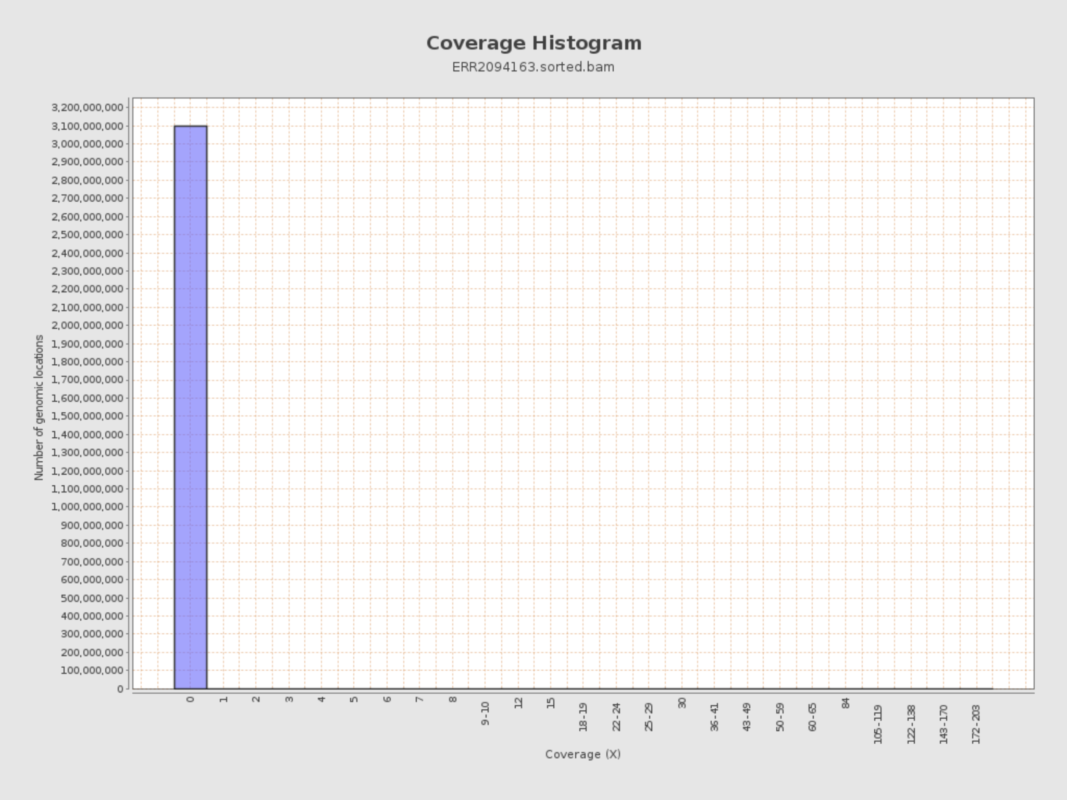
		bases	coverage	deviation
chr1	249250621	668	0	0.0021
chr2	243199373	30946	0.0001	0.1256
chr3	198022430	694	0	0.0024
chr4	191154276	268	0	0.0025
chr5	180915260	693	0	0.0023
chr6	171115067	347	0	0.0019
chr7	159138663	465	0	0.002
chr8	146364022	655	0	0.0025
chr9	141213431	365	0	0.0016
chr10	135534747	515	0	0.0026
chr11	135006516	1094	0	0.004
chr12	133851895	685	0	0.0029
chr13	115169878	455	0	0.0025
chr14	107349540	805	0	0.0039
chr15	102531392	459	0	0.0026
chr16	90354753	228	0	0.002
chr17	81195210	292	0	0.0027
chr18	78077248	250	0	0.0034
chr19	59128983	173	0	0.0021
chr20	63025520	227	0	0.0024
chr21	48129895	100	0	0.0014
chr22	51304566	0	0	0
chrMT	16571	903	0.0545	0.3655
chrX	155270560	10880	0.0001	0.0521

chrY	59373566	186	0	0.0024

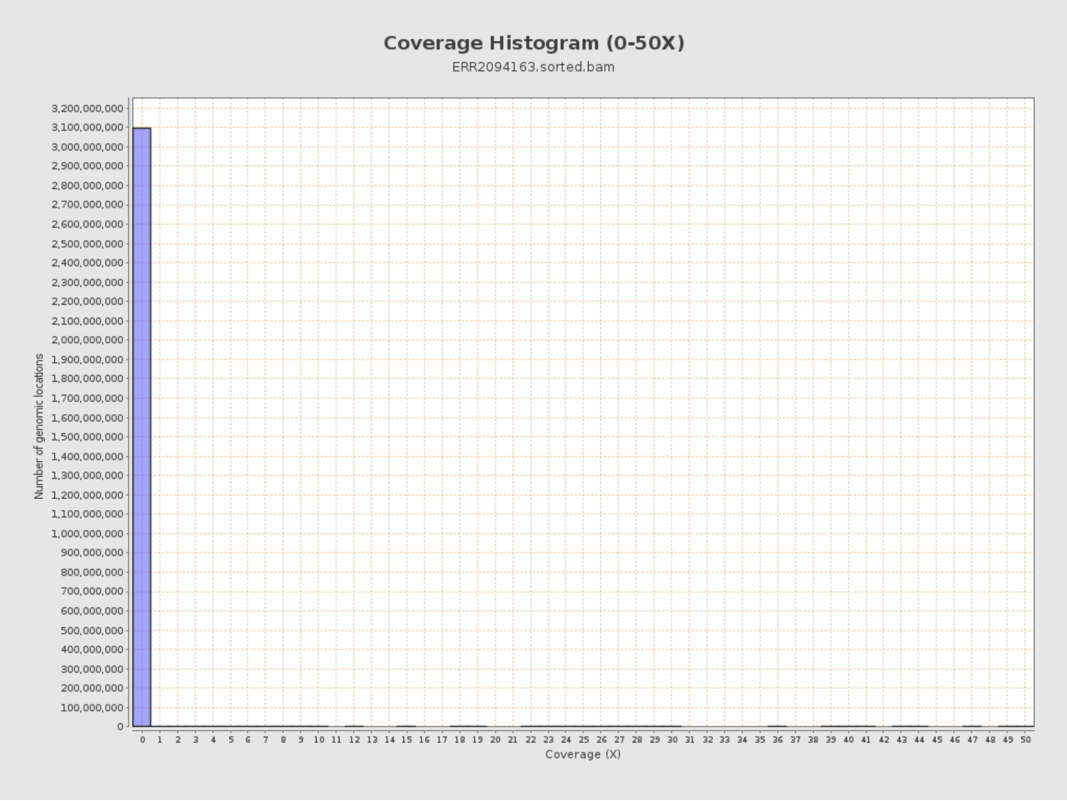
3. Results : Coverage across reference



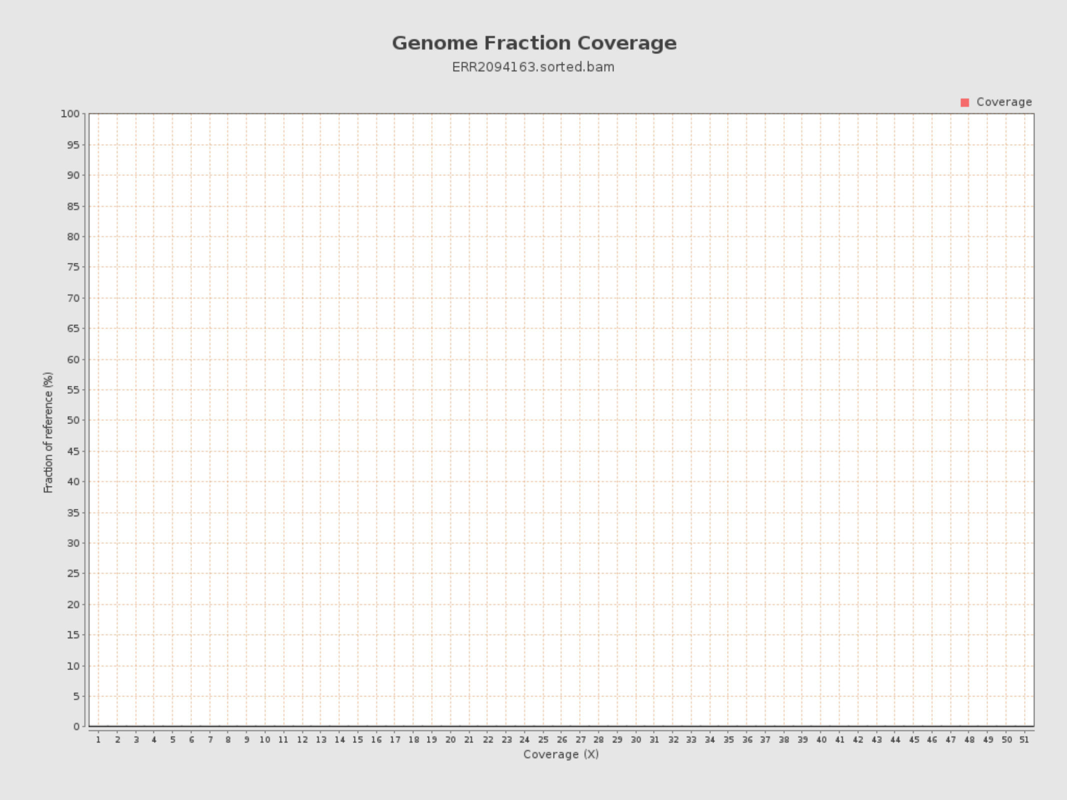
4. Results : Coverage Histogram



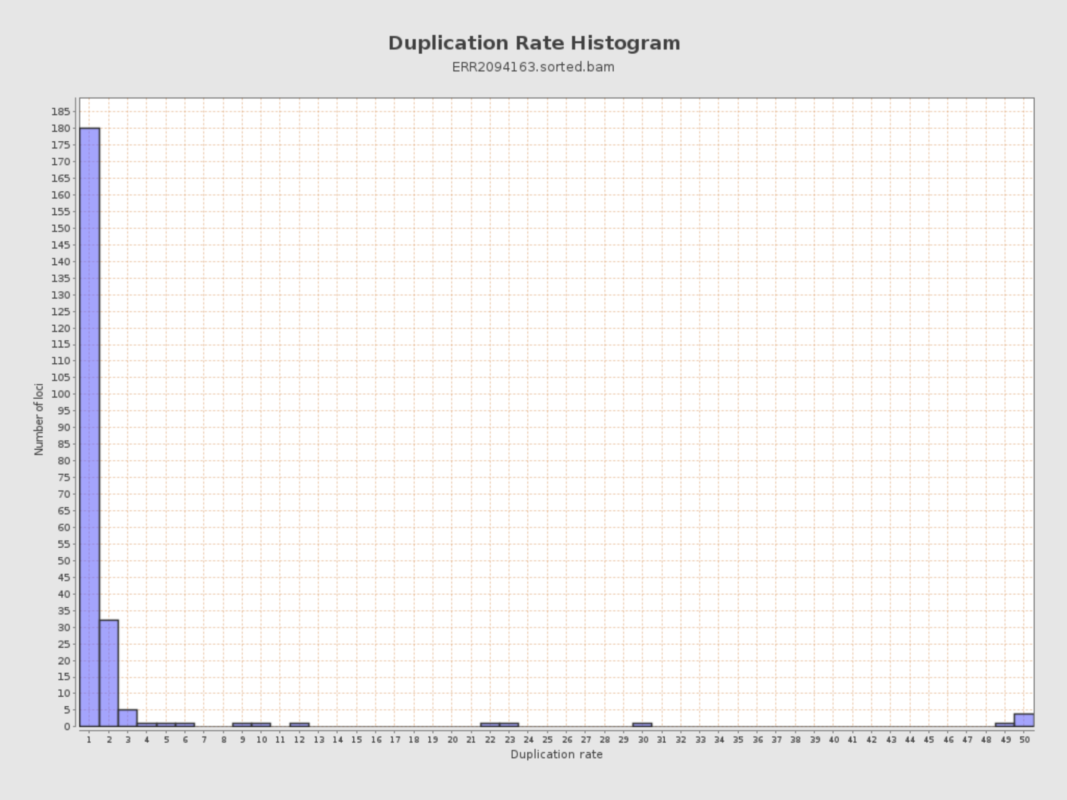
5. Results : Coverage Histogram (0-50X)



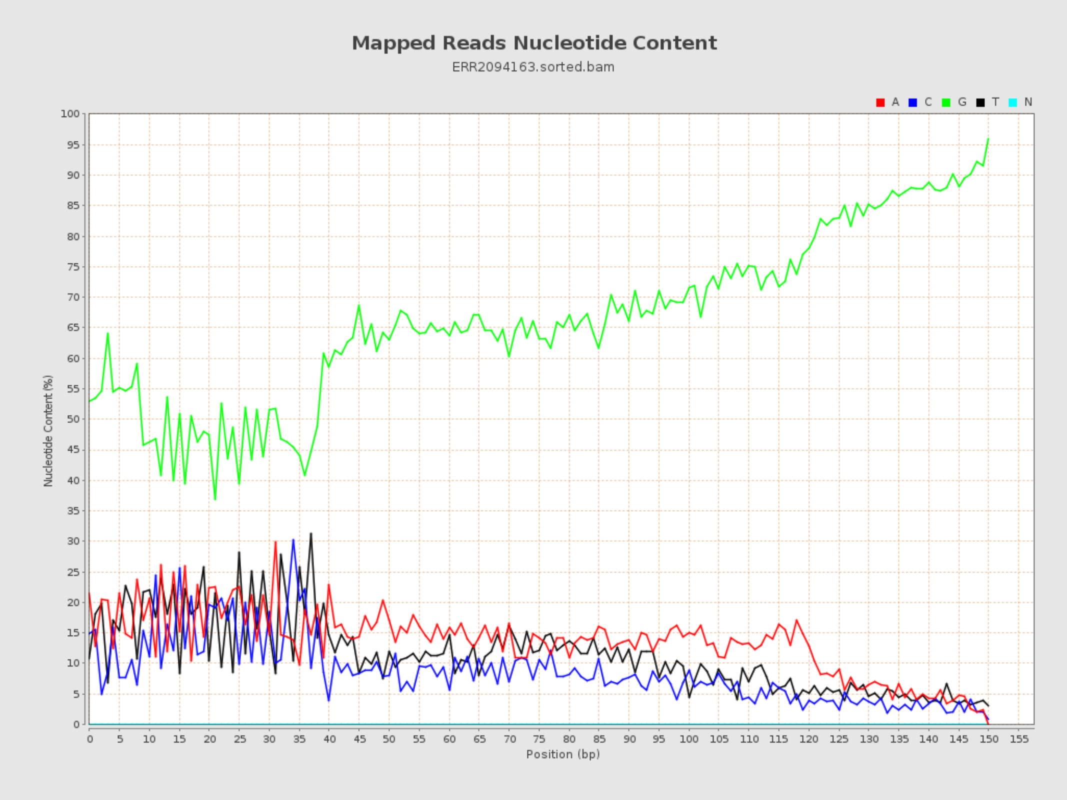
6. Results : Genome Fraction Coverage



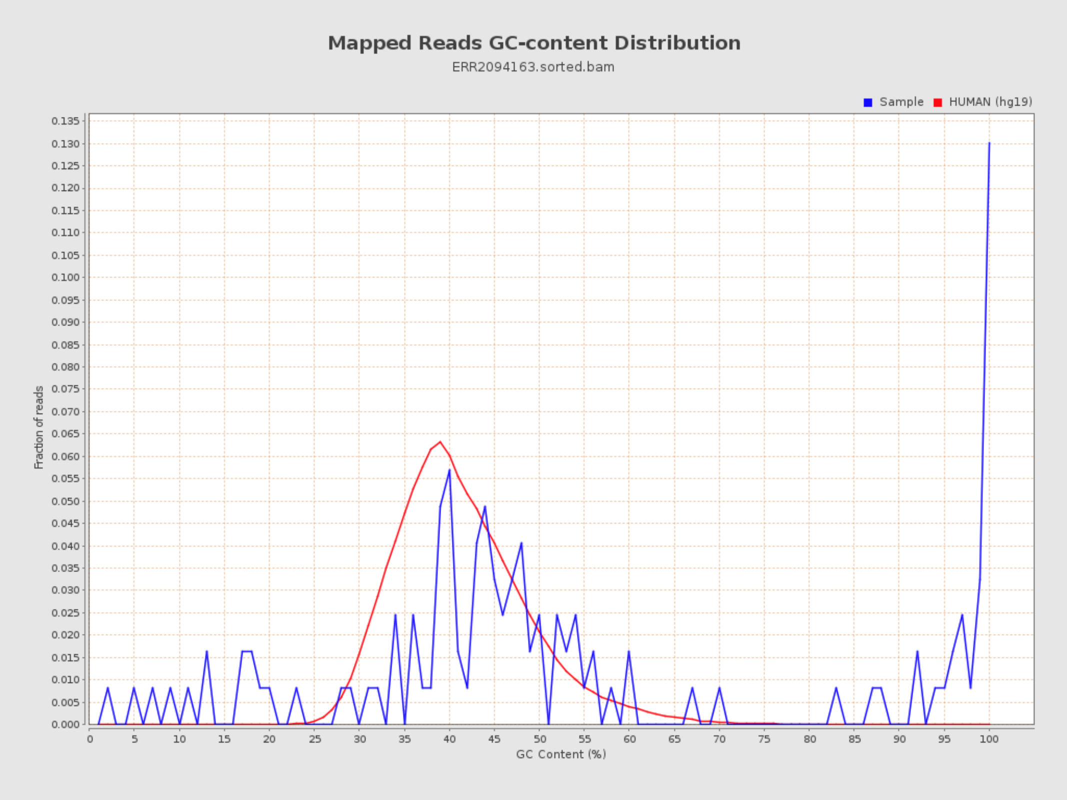
7. Results : Duplication Rate Histogram



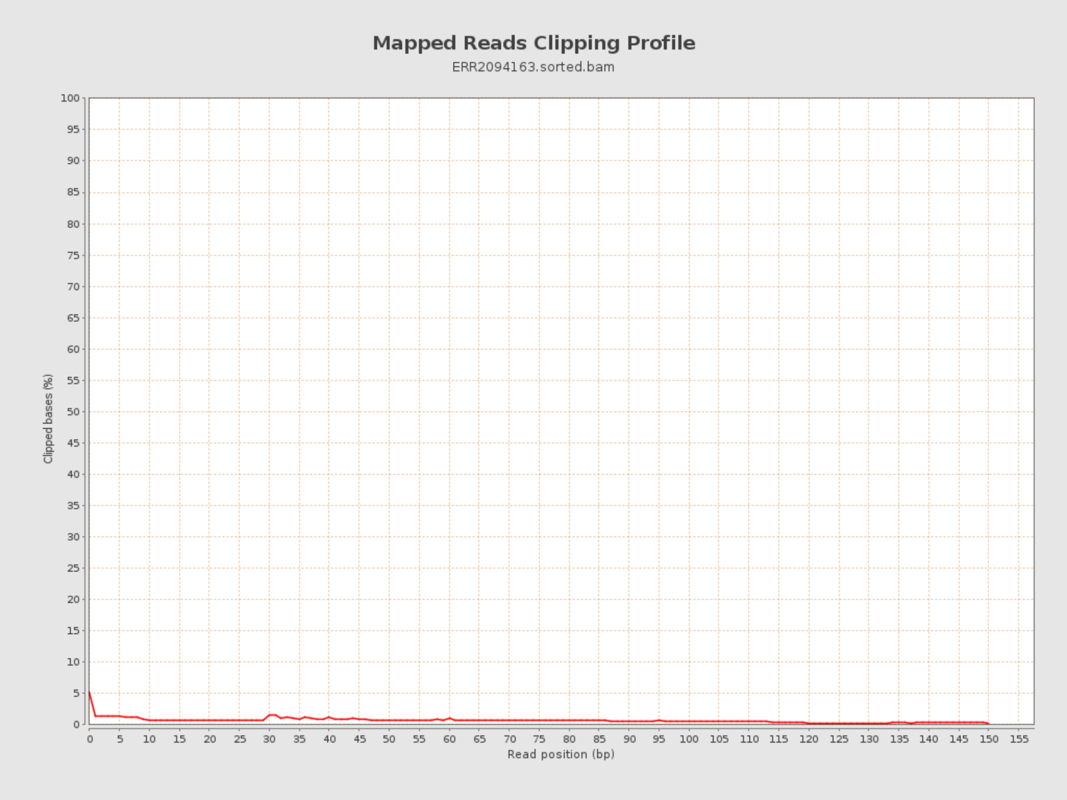
8. Results : Mapped Reads Nucleotide Content



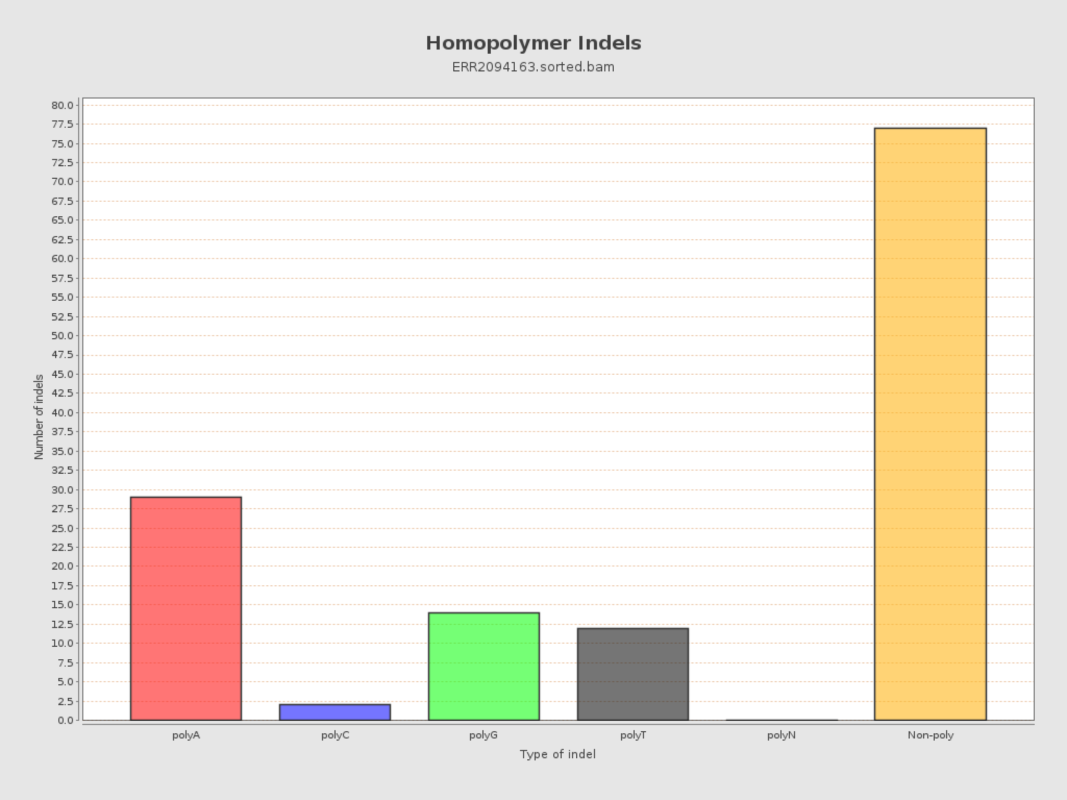
9. Results : Mapped Reads GC-content Distribution



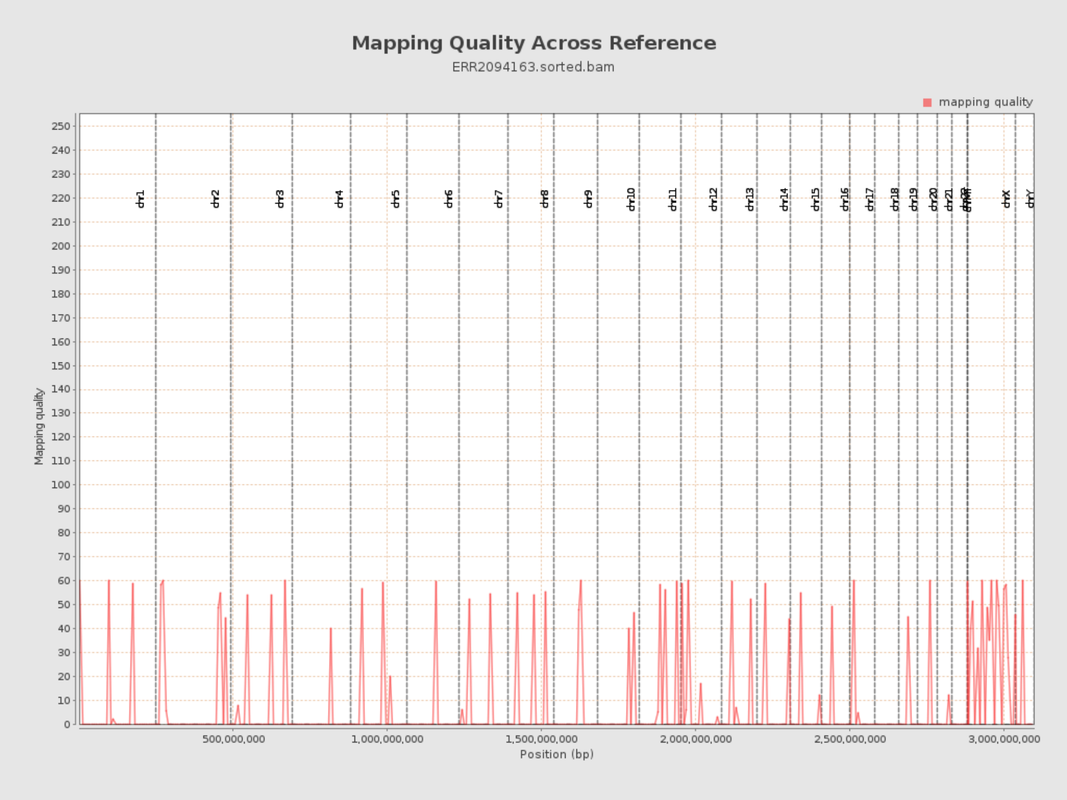
10. Results : Mapped Reads Clipping Profile



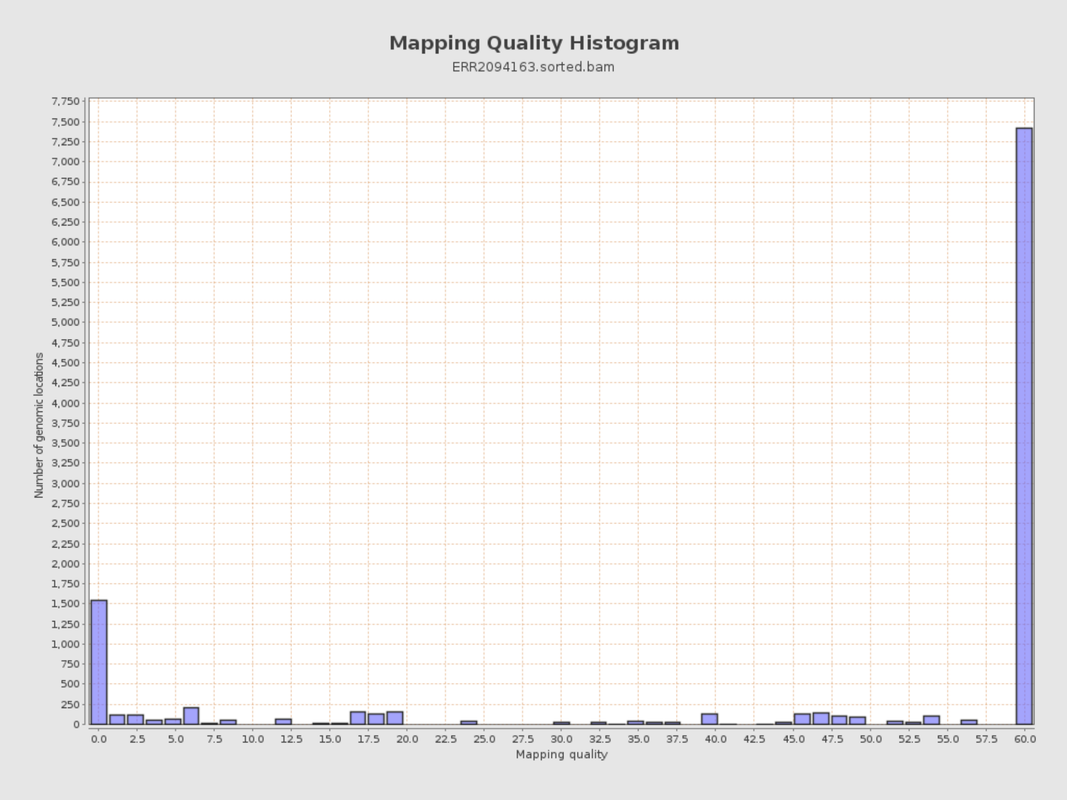
11. Results : Homopolymer Indels



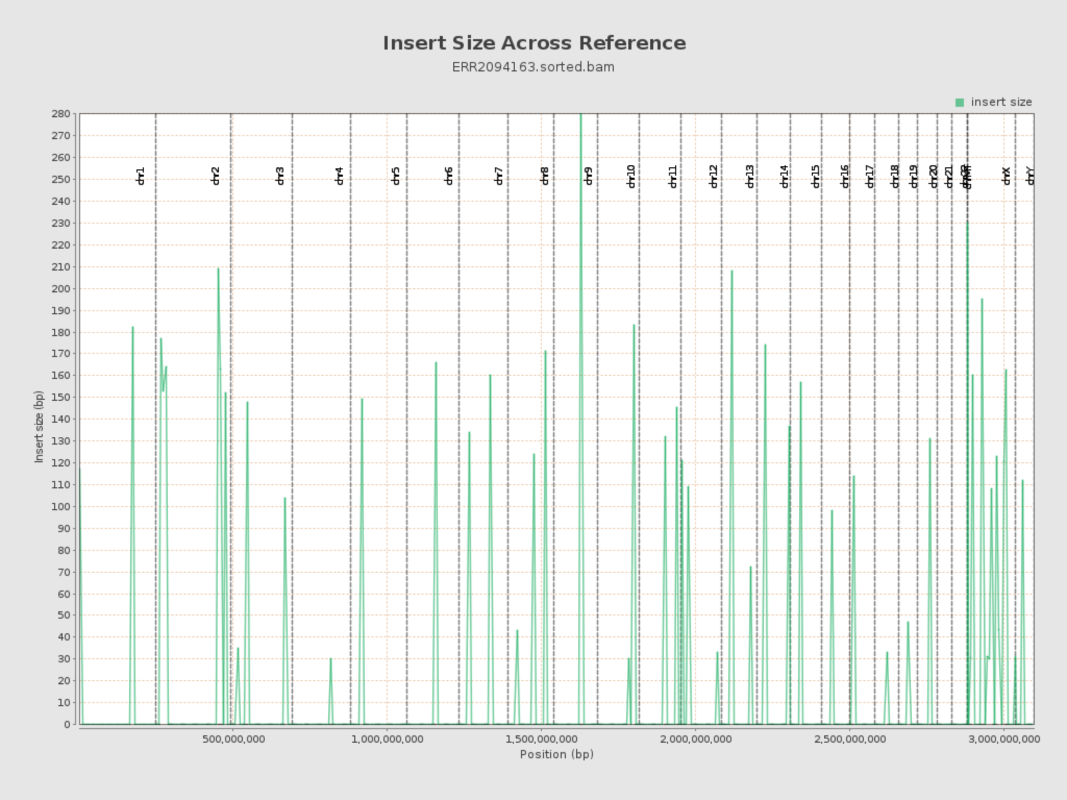
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram