Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 06:01:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094153.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_ERR2094153 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094153_1.fastq.gz ERR2094153_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 06:01:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094153.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,450
Mapped reads	1,035 / 5.32%
Unmapped reads	18,415 / 94.68%
Mapped paired reads	1,035 / 5.32%
Mapped reads, first in pair	456 / 2.34%
Mapped reads, second in pair	579 / 2.98%
Mapped reads, both in pair	830 / 4.27%
Mapped reads, singletons	205 / 1.05%
Secondary alignments	0
Supplementary alignments	26 / 0.13%
Read min/max/mean length	30 / 151 / 65.26
Duplicated reads (estimated)	445 / 2.29%
Duplication rate	25.32%
Clipped reads	553 / 2.84%

2.2. ACGT Content

Number/percentage of A's	25,993 / 23.6%
Number/percentage of C's	21,194 / 19.24%
Number/percentage of T's	24,299 / 22.06%
Number/percentage of G's	38,659 / 35.1%
Number/percentage of N's	0 / 0%

GC Percentage	54.34%

2.3. Coverage

Mean	0
Standard Deviation	0.0227

2.4. Mapping Quality

Mean Mapping Quality	12.73

2.5. Insert size

Mean	543,429.09
Standard Deviation	6,547,710.03
P25/Median/P75	111 / 154 / 190

2.6. Mismatches and indels

General error rate	4.46%
Mismatches	4,627
Insertions	85
Mapped reads with at least one insertion	6.67%
Deletions	347
Mapped reads with at least one deletion	31.59%
Homopolymer indels	33.1%

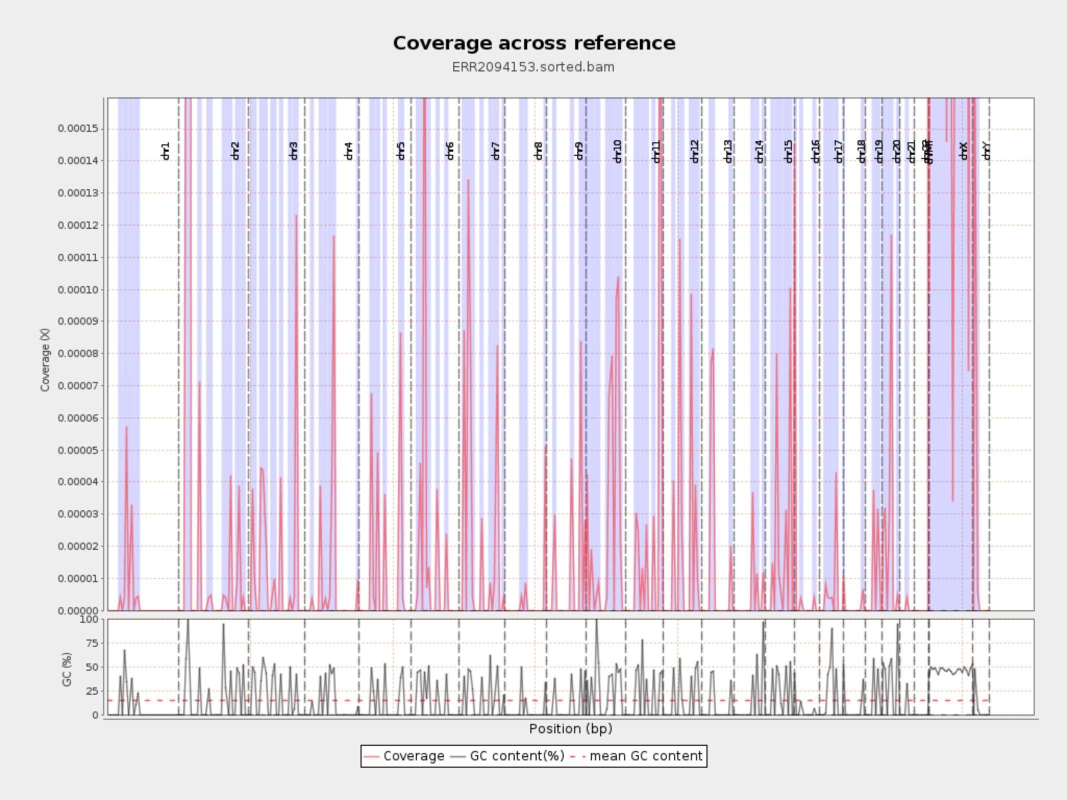
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

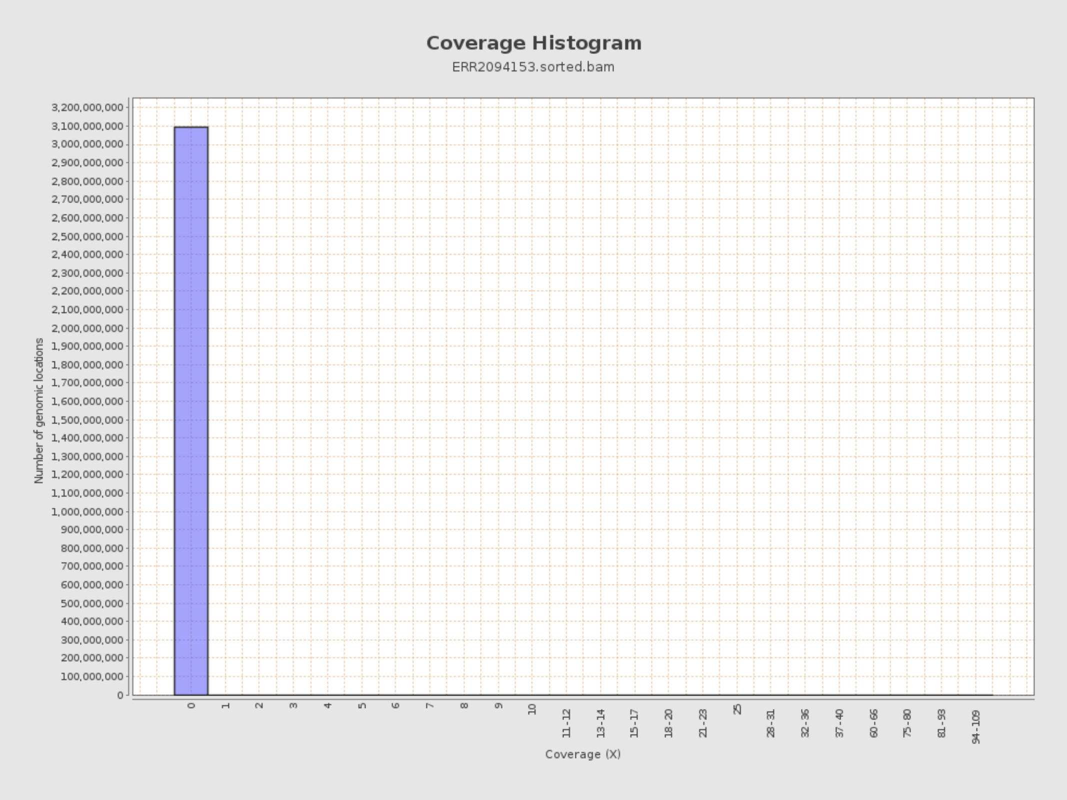
		bases	coverage	deviation
chr1	249250621	828	0	0.0022
chr2	243199373	19990	0.0001	0.0709
chr3	198022430	2656	0	0.0061
chr4	191154276	1666	0	0.0037
chr5	180915260	1916	0	0.0059
chr6	171115067	2853	0	0.0113
chr7	159138663	3434	0	0.0077
chr8	146364022	448	0	0.0022
chr9	141213431	1465	0	0.0053
chr10	135534747	3415	0	0.0082
chr11	135006516	3354	0	0.0116
chr12	133851895	2524	0	0.0079
chr13	115169878	1385	0	0.0053
chr14	107349540	468	0	0.0032
chr15	102531392	1887	0	0.0056
chr16	90354753	764	0	0.0072
chr17	81195210	486	0	0.003
chr18	78077248	89	0	0.0011
chr19	59128983	535	0	0.0038
chr20	63025520	1557	0	0.0097
chr21	48129895	31	0	0.0008
chr22	51304566	0	0	0
chrMT	16571	3815	0.2302	1.1193
chrX	155270560	55896	0.0004	0.0389

chrY	59373566	1431	0	0.0107

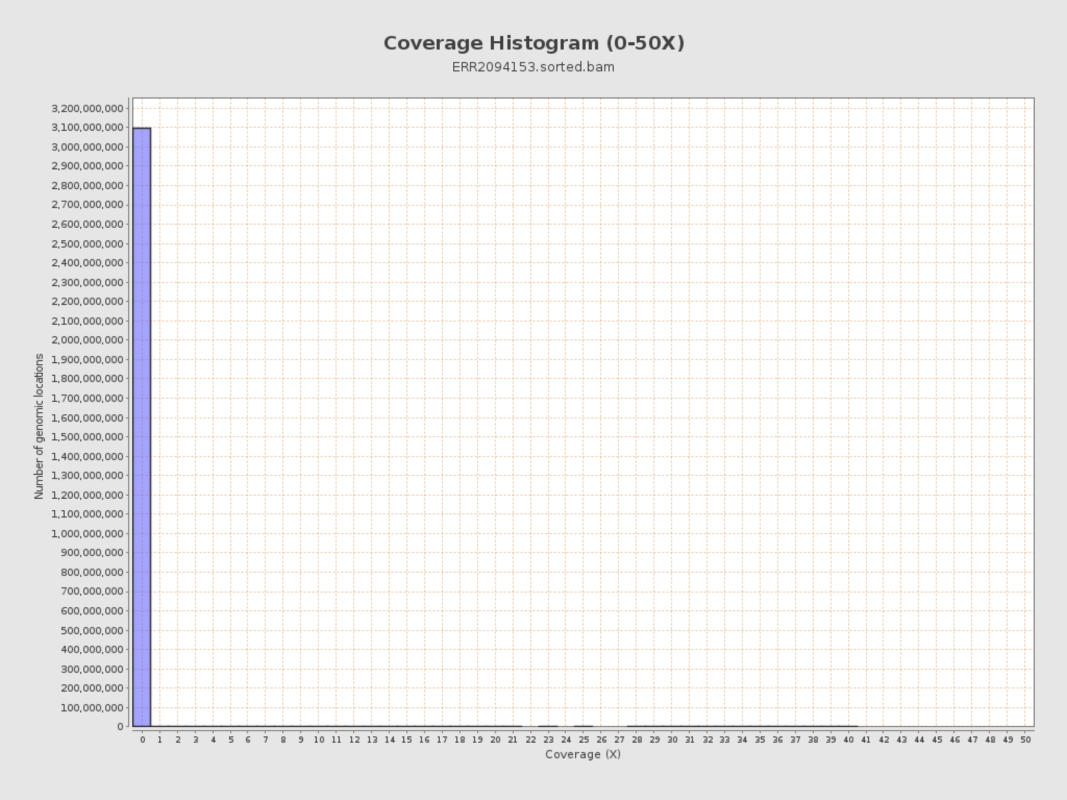
3. Results : Coverage across reference



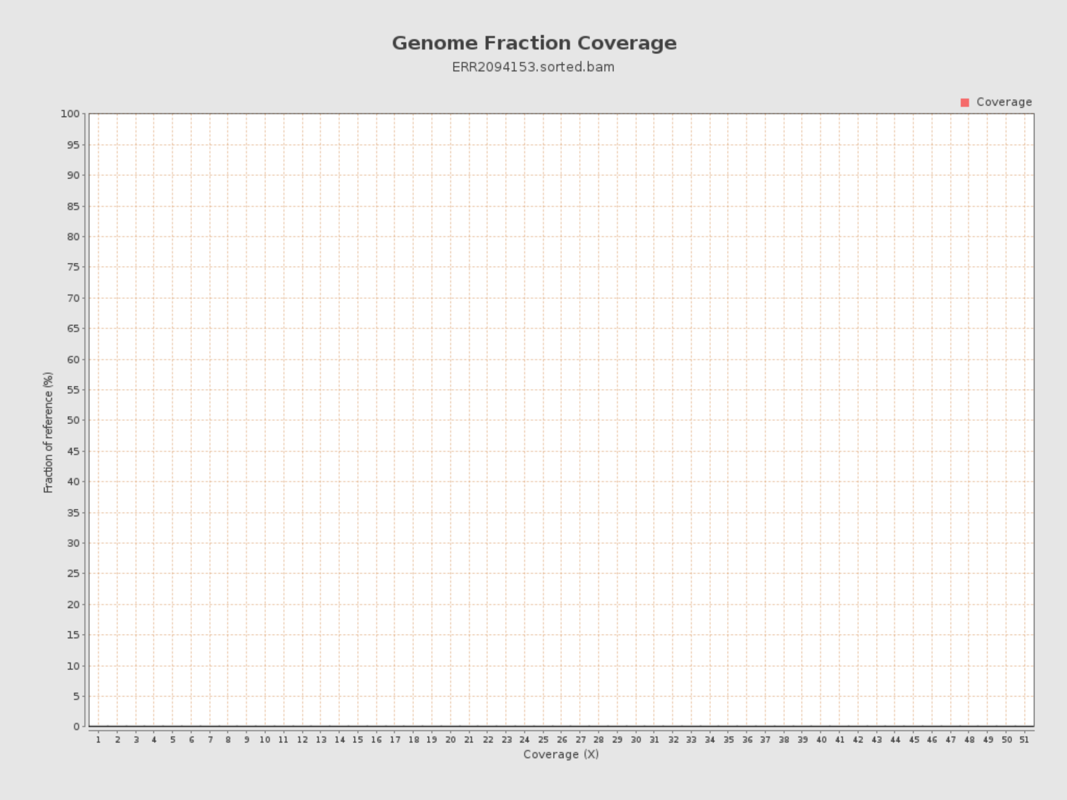
4. Results : Coverage Histogram



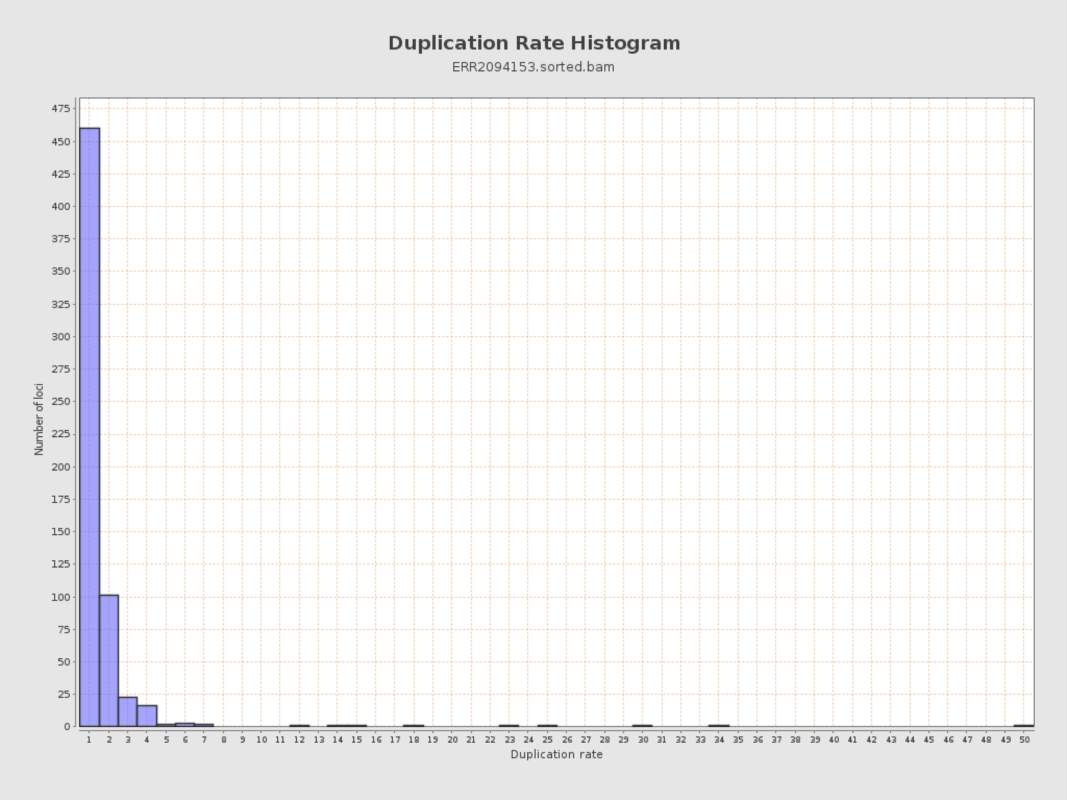
5. Results : Coverage Histogram (0-50X)



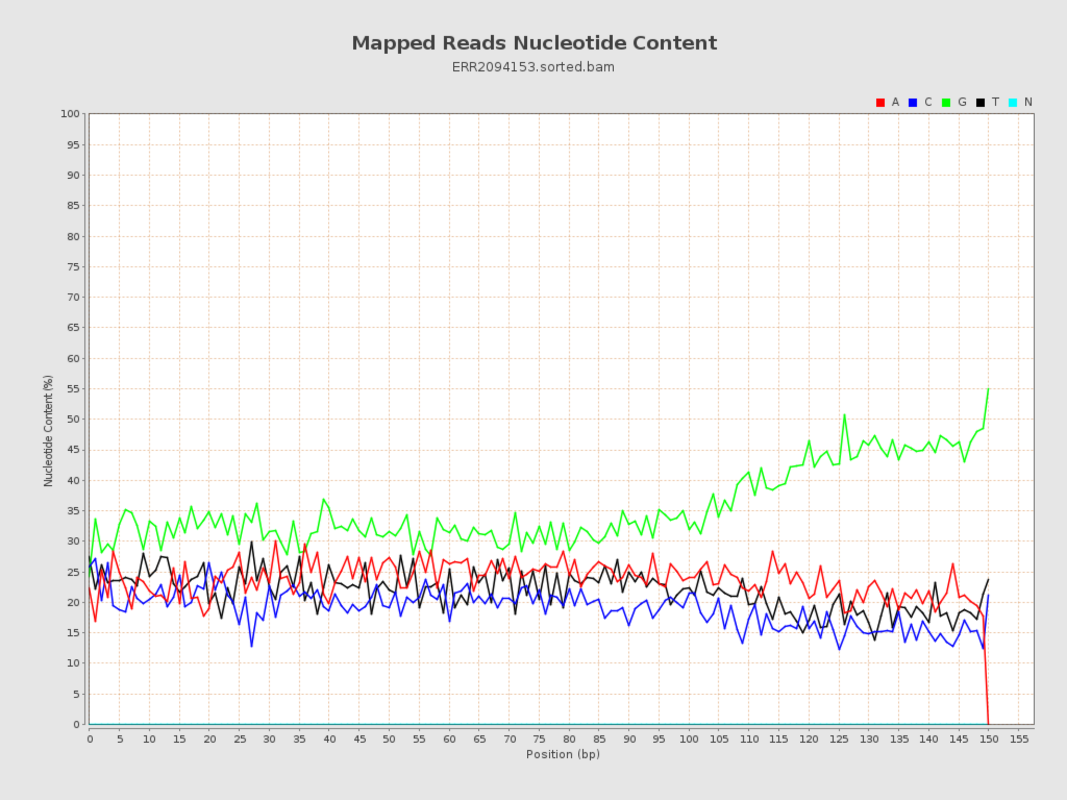
6. Results : Genome Fraction Coverage



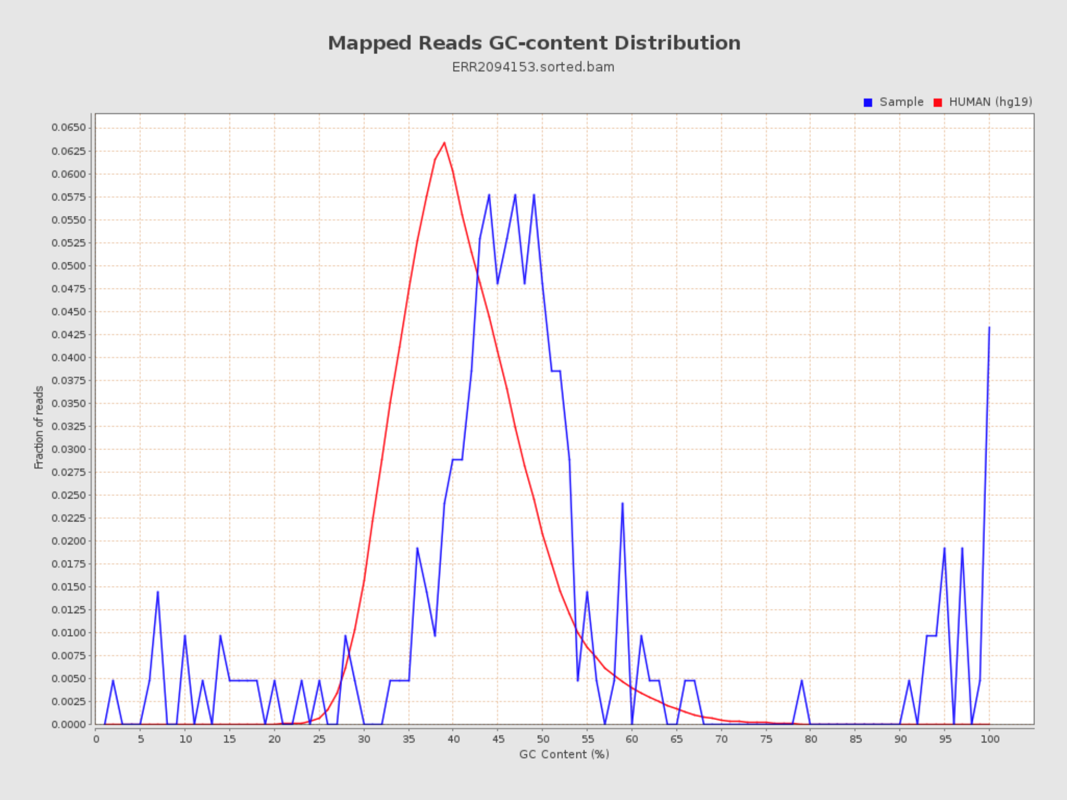
7. Results : Duplication Rate Histogram



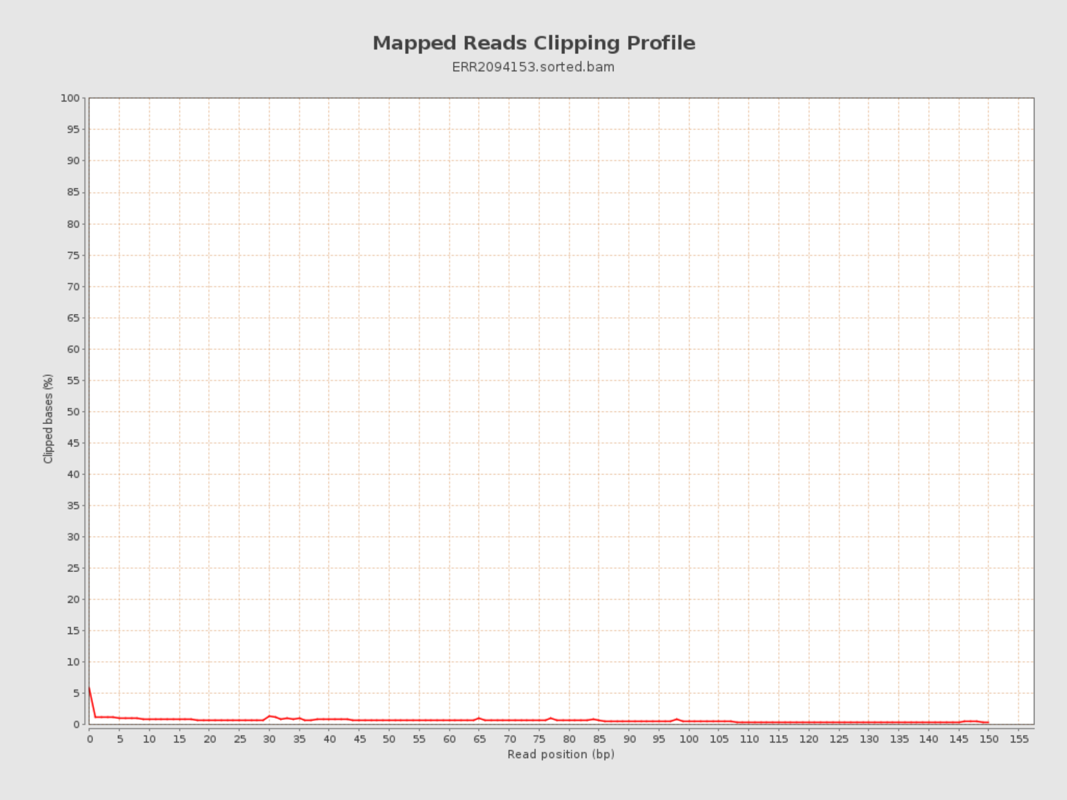
8. Results : Mapped Reads Nucleotide Content



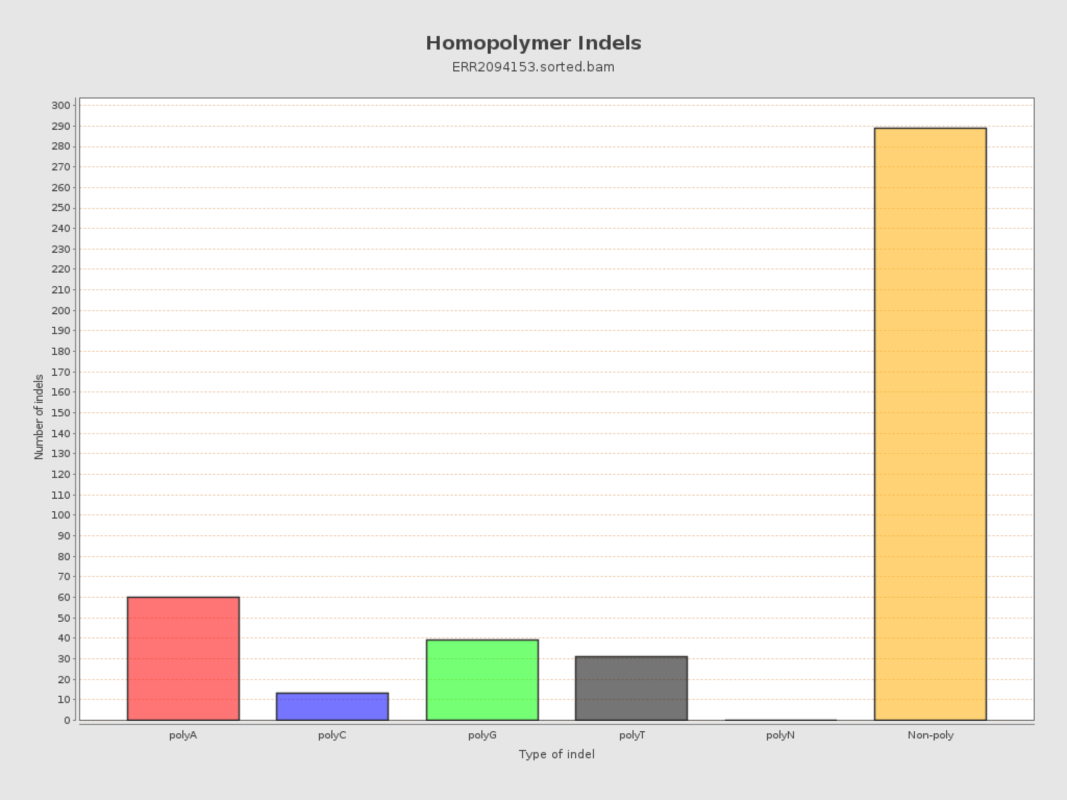
9. Results : Mapped Reads GC-content Distribution



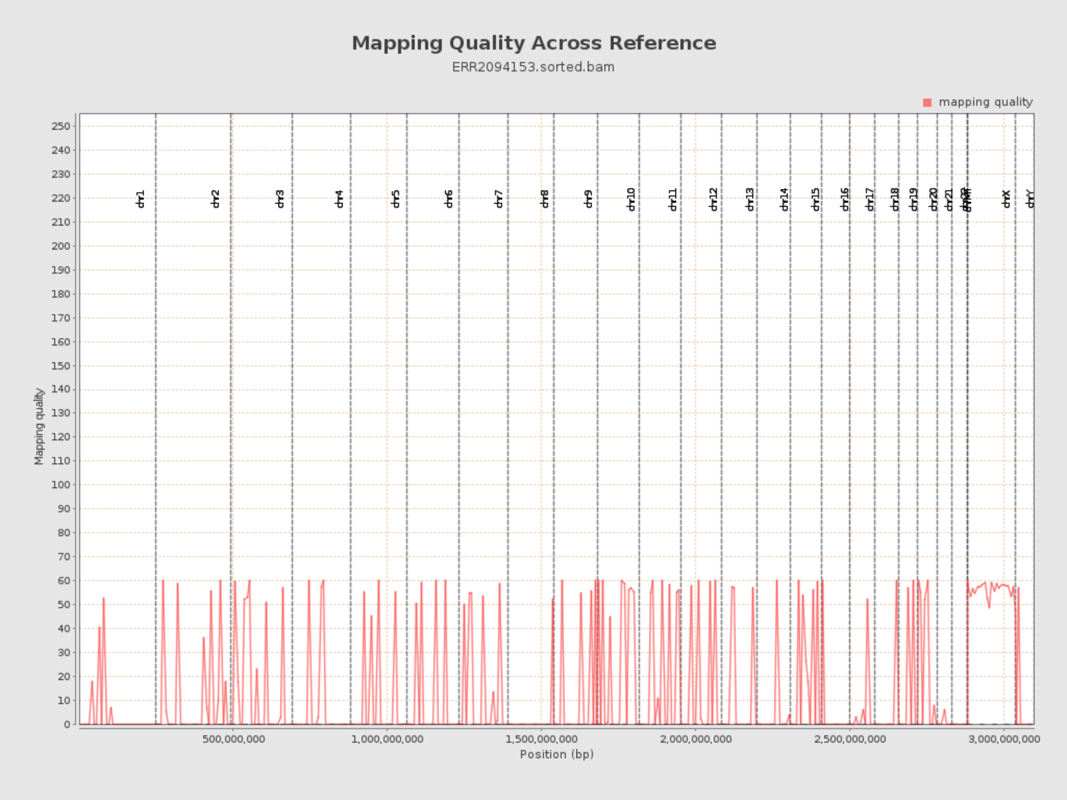
10. Results : Mapped Reads Clipping Profile



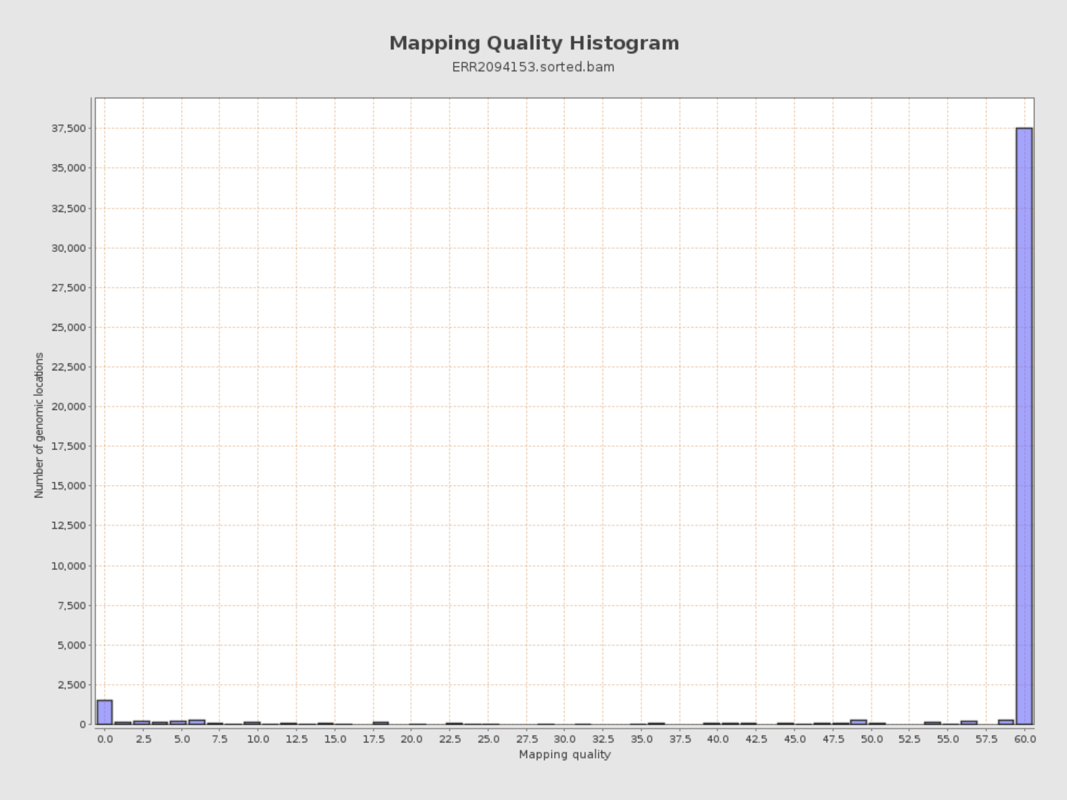
11. Results : Homopolymer Indels



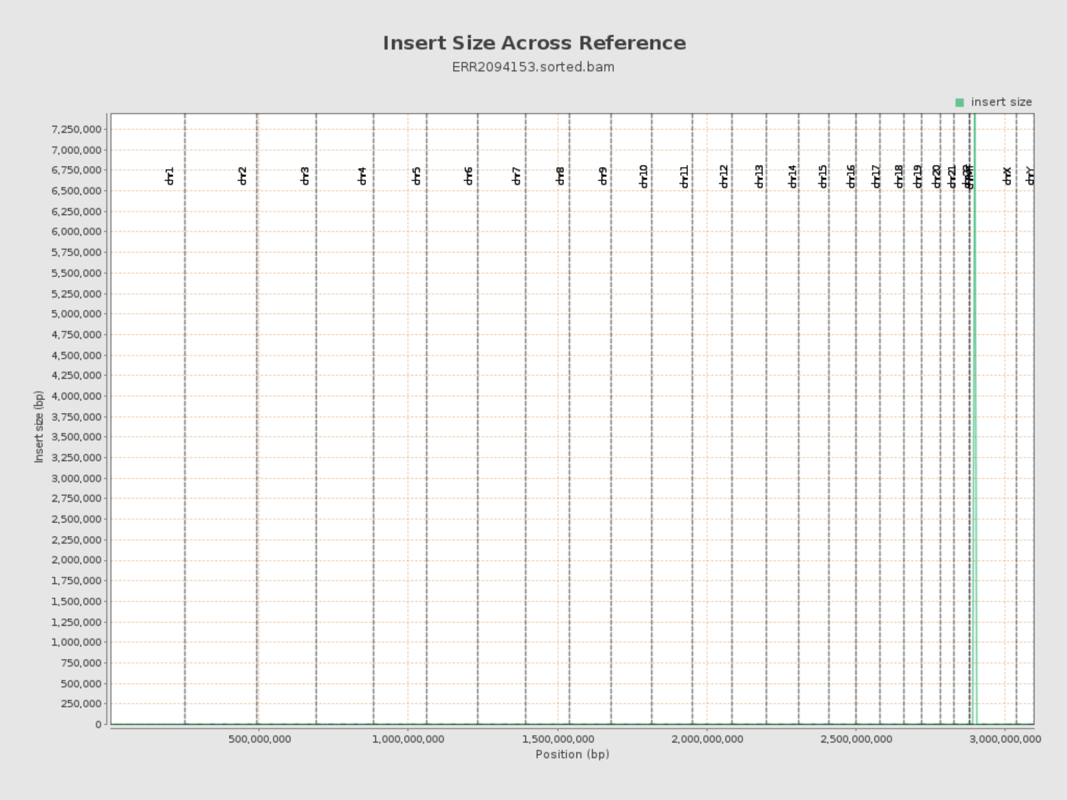
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram