Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:55:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094013.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_ERR2094013 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094013_1.fastq.gz ERR2094013_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:55:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,558
Mapped reads	2,219 / 11.35%
Unmapped reads	17,339 / 88.65%
Mapped paired reads	2,219 / 11.35%
Mapped reads, first in pair	1,039 / 5.31%
Mapped reads, second in pair	1,180 / 6.03%
Mapped reads, both in pair	2,032 / 10.39%
Mapped reads, singletons	187 / 0.96%
Secondary alignments	0
Supplementary alignments	58 / 0.3%
Read min/max/mean length	30 / 151 / 62.13
Duplicated reads (estimated)	1,354 / 6.92%
Duplication rate	27.52%
Clipped reads	908 / 4.64%

2.2. ACGT Content

Number/percentage of A's	70,959 / 26.3%
Number/percentage of C's	55,990 / 20.75%
Number/percentage of T's	68,070 / 25.23%
Number/percentage of G's	74,784 / 27.71%
Number/percentage of N's	30 / 0.01%

GC Percentage	48.46%

2.3. Coverage

Mean	0.0001
Standard Deviation	0.0875

2.4. Mapping Quality

Mean Mapping Quality	17.3

2.5. Insert size

Mean	185,382.92
Standard Deviation	3,076,377.68
P25/Median/P75	137 / 185 / 223

2.6. Mismatches and indels

General error rate	3.06%
Mismatches	7,833
Insertions	136
Mapped reads with at least one insertion	5.45%
Deletions	501
Mapped reads with at least one deletion	21.27%
Homopolymer indels	35.48%

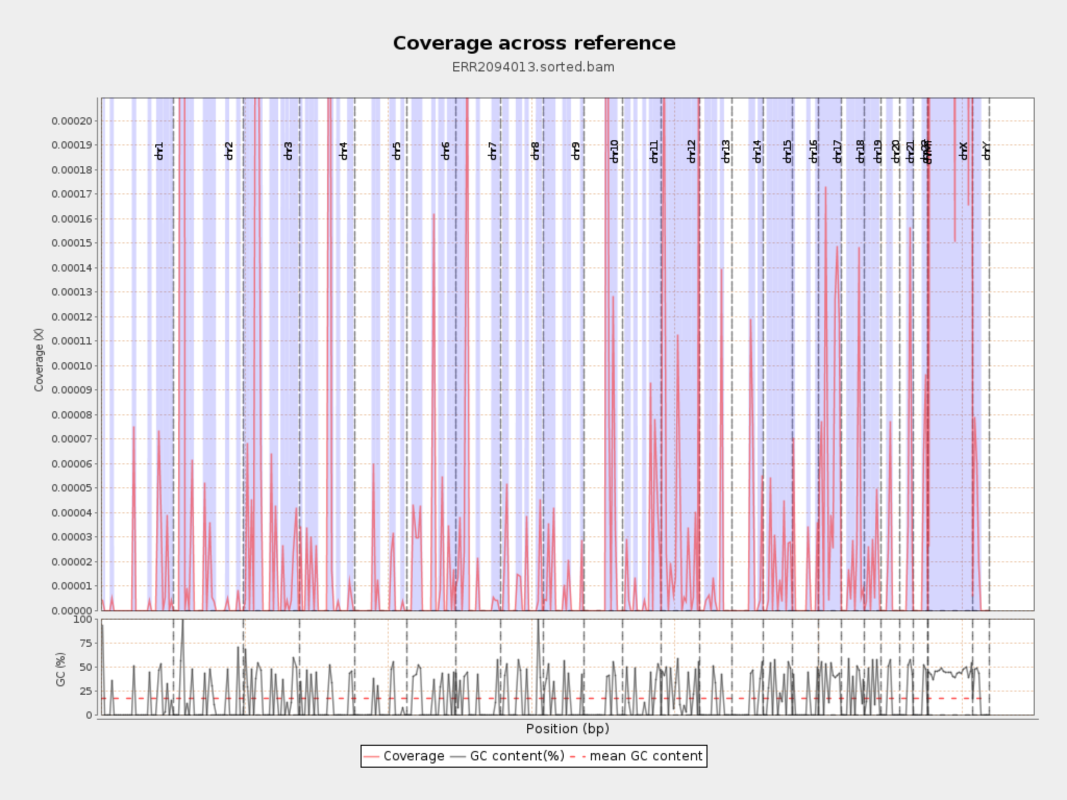
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

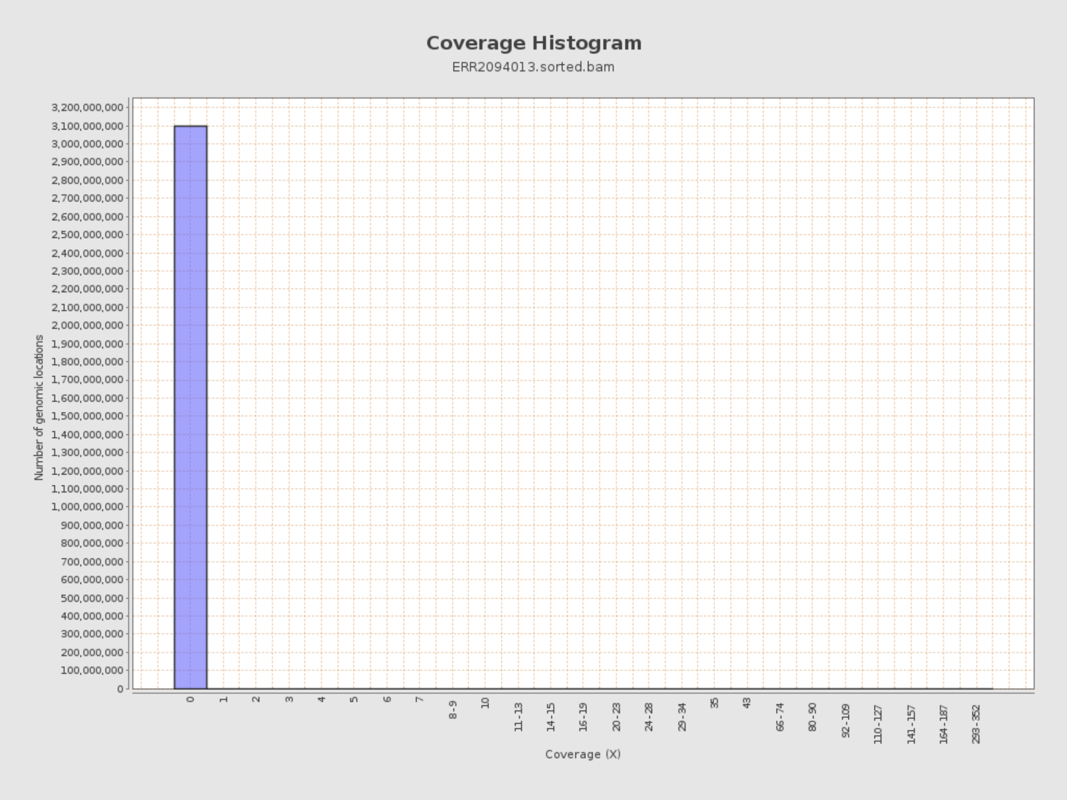
		bases	coverage	deviation
chr1	249250621	1950	0	0.0038
chr2	243199373	23340	0.0001	0.0811
chr3	198022430	7934	0	0.016
chr4	191154276	4192	0	0.0079
chr5	180915260	1024	0	0.003
chr6	171115067	3274	0	0.0076
chr7	159138663	2819	0	0.0096
chr8	146364022	1479	0	0.004
chr9	141213431	1136	0	0.0036
chr10	135534747	5201	0	0.0216
chr11	135006516	2186	0	0.0075
chr12	133851895	5933	0	0.0161
chr13	115169878	1295	0	0.0057
chr14	107349540	1973	0	0.0087
chr15	102531392	1598	0	0.0055
chr16	90354753	886	0	0.0046
chr17	81195210	5923	0.0001	0.0176
chr18	78077248	1845	0	0.009
chr19	59128983	883	0	0.0048
chr20	63025520	790	0	0.0062
chr21	48129895	1597	0	0.0135
chr22	51304566	1242	0	0.0062
chrMT	16571	102770	6.2018	35.2685
chrX	155270560	90886	0.0006	0.0613

chrY	59373566	1255	0	0.0071

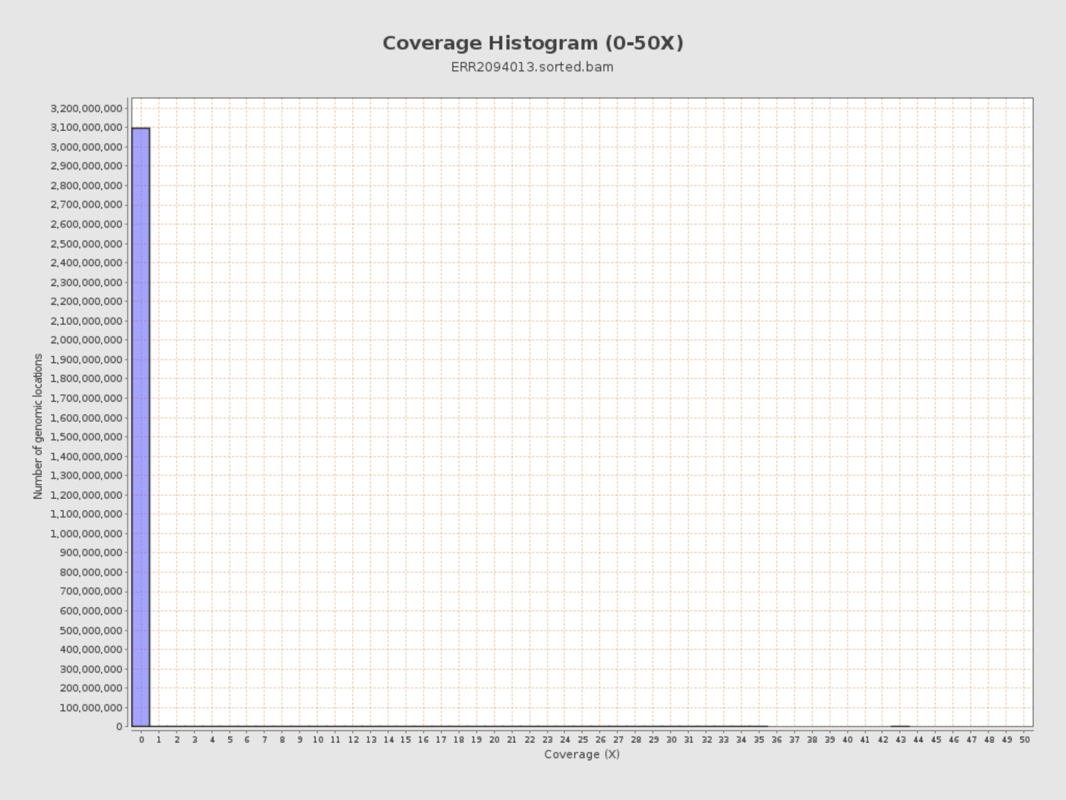
3. Results : Coverage across reference



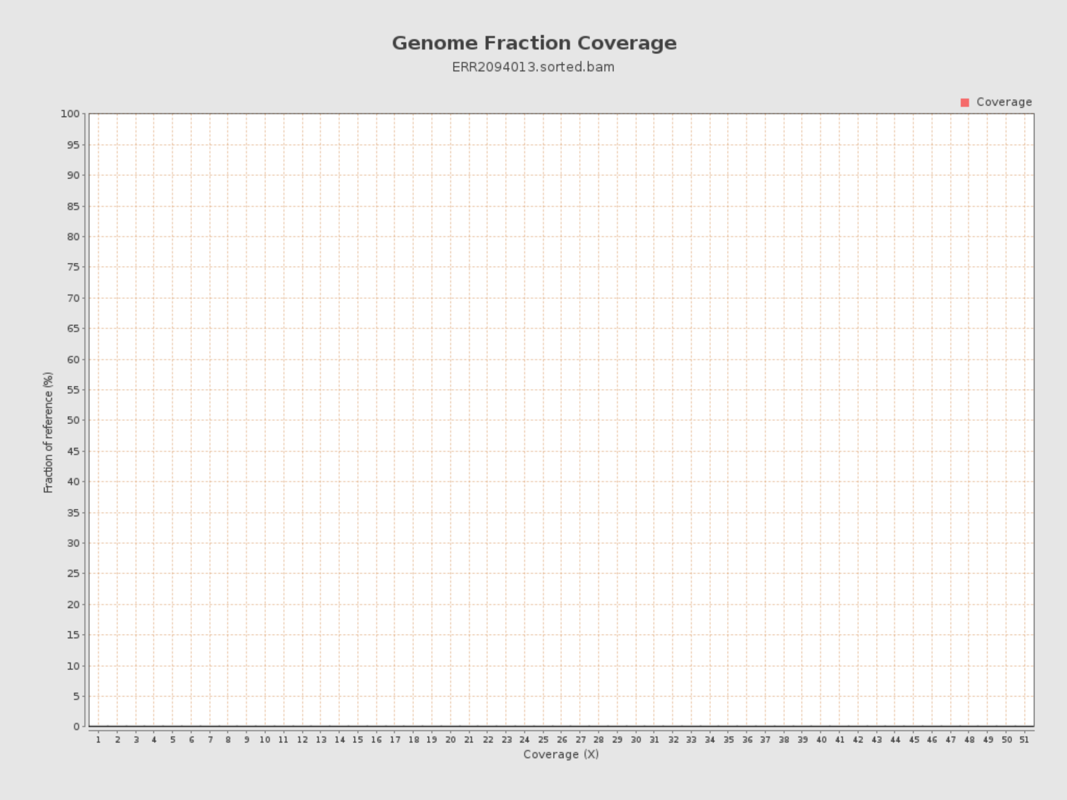
4. Results : Coverage Histogram



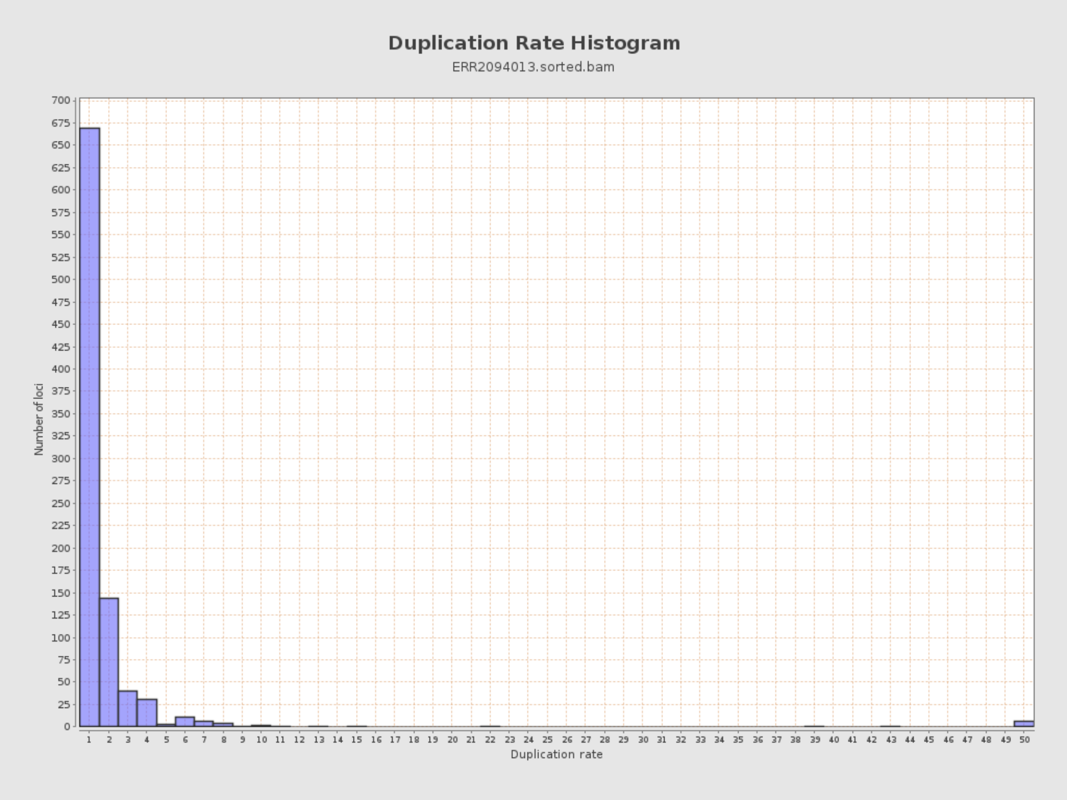
5. Results : Coverage Histogram (0-50X)



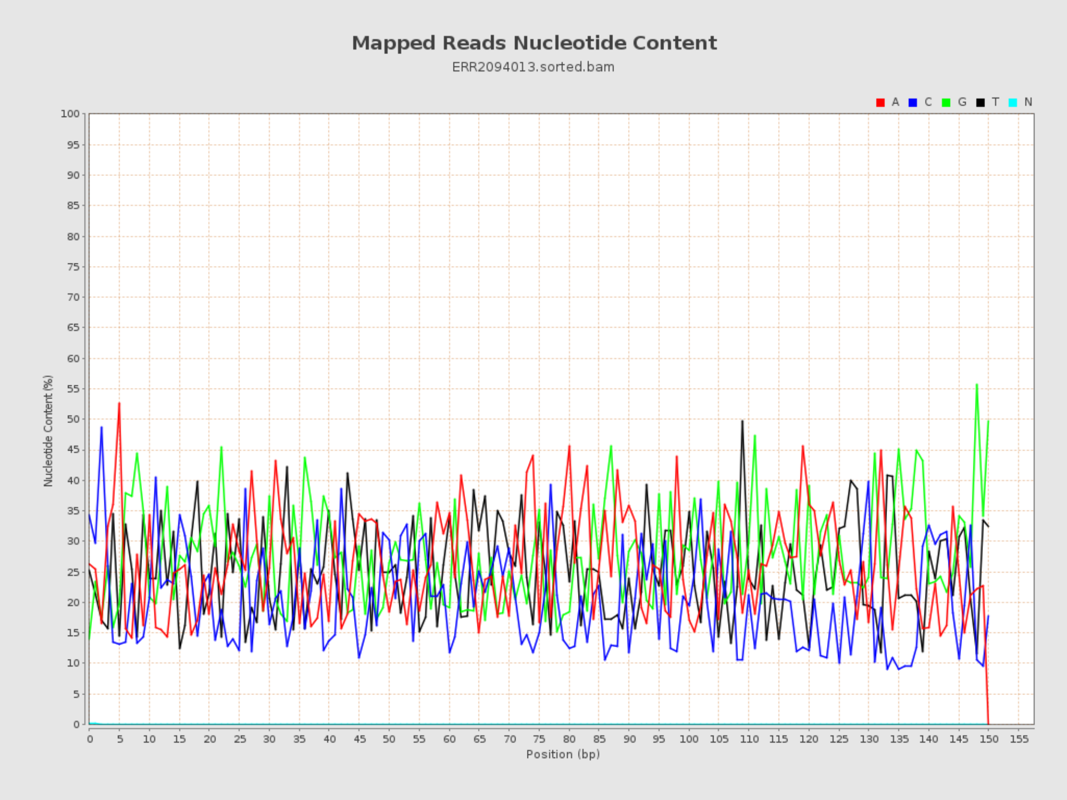
6. Results : Genome Fraction Coverage



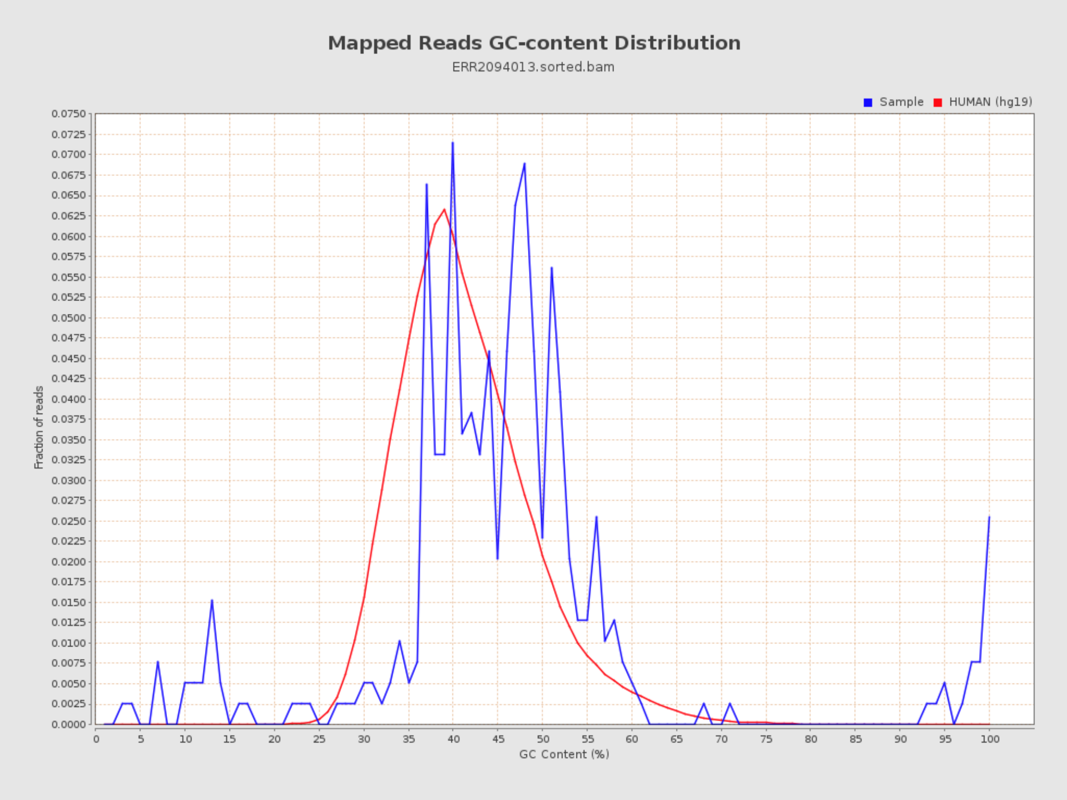
7. Results : Duplication Rate Histogram



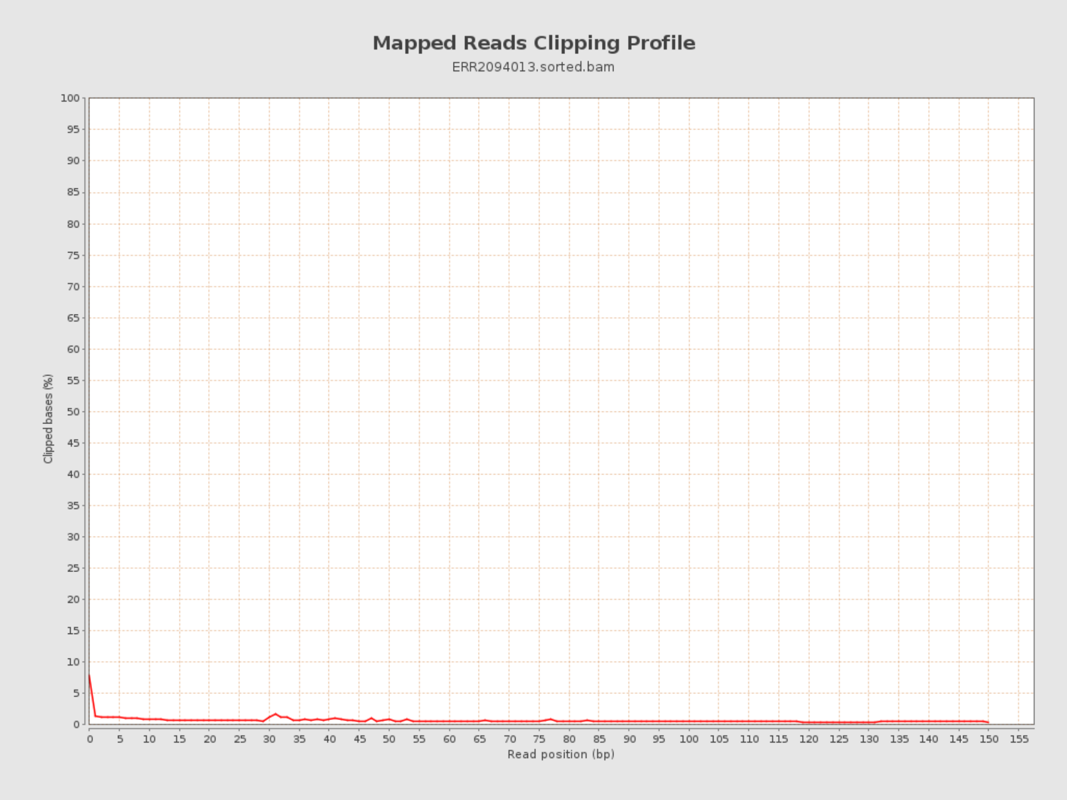
8. Results : Mapped Reads Nucleotide Content



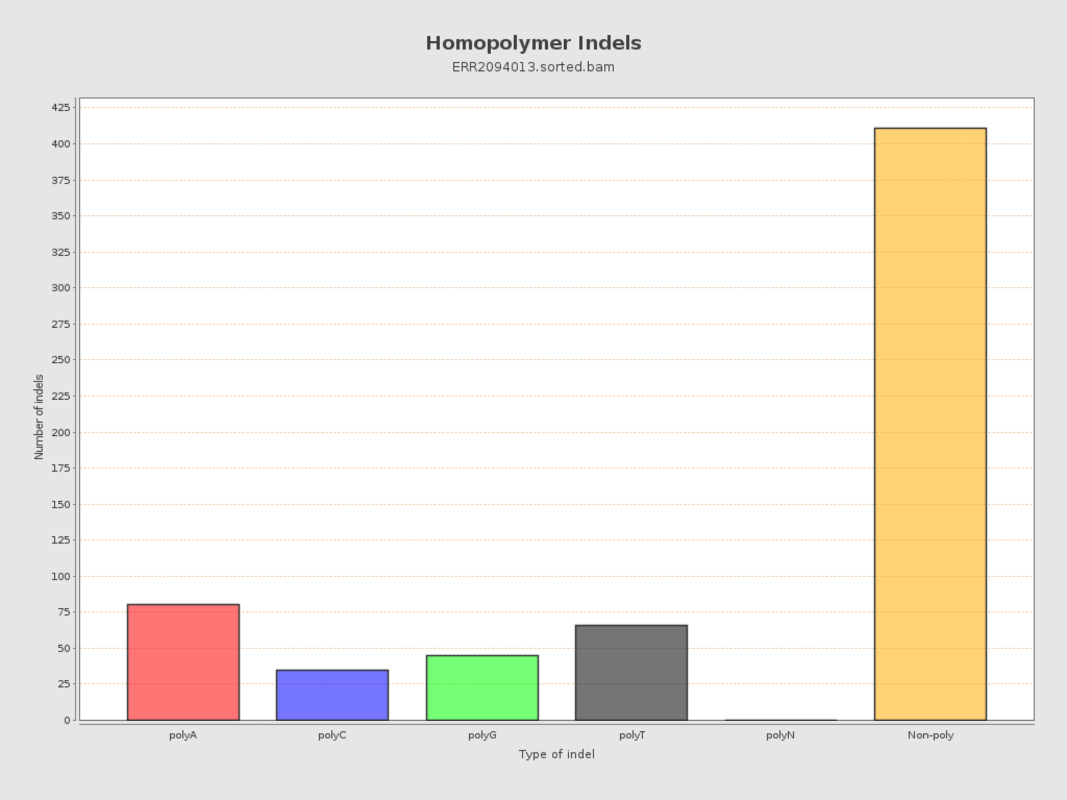
9. Results : Mapped Reads GC-content Distribution



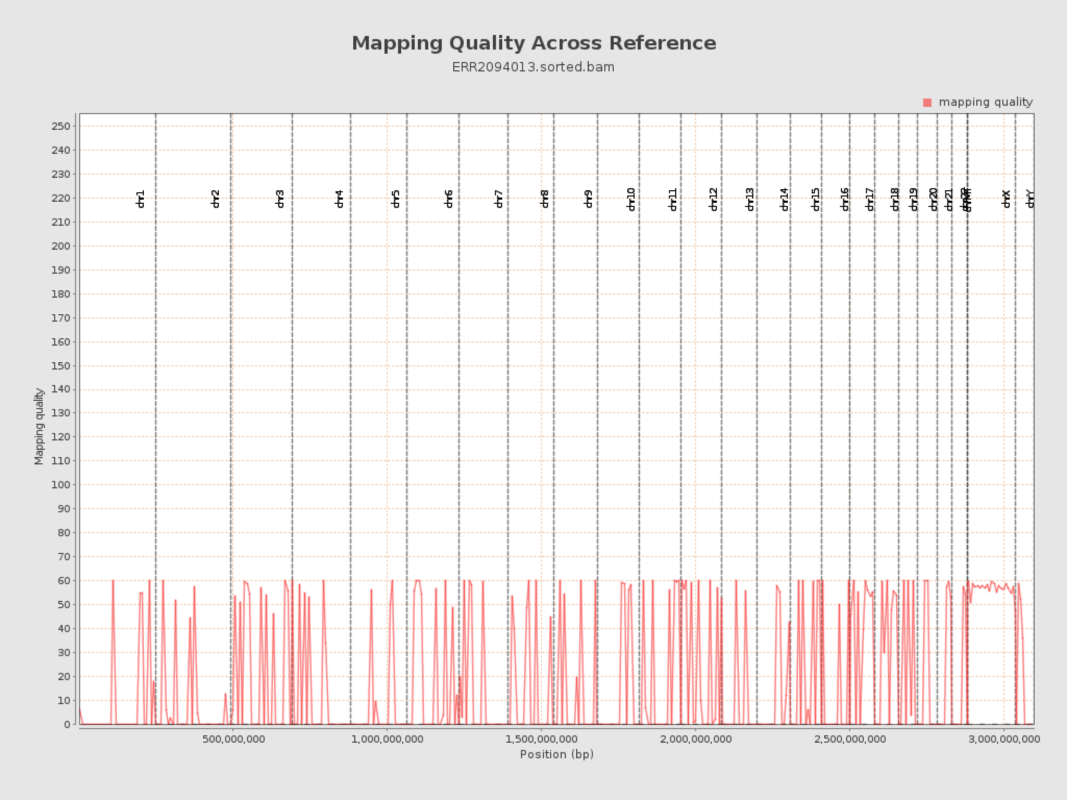
10. Results : Mapped Reads Clipping Profile



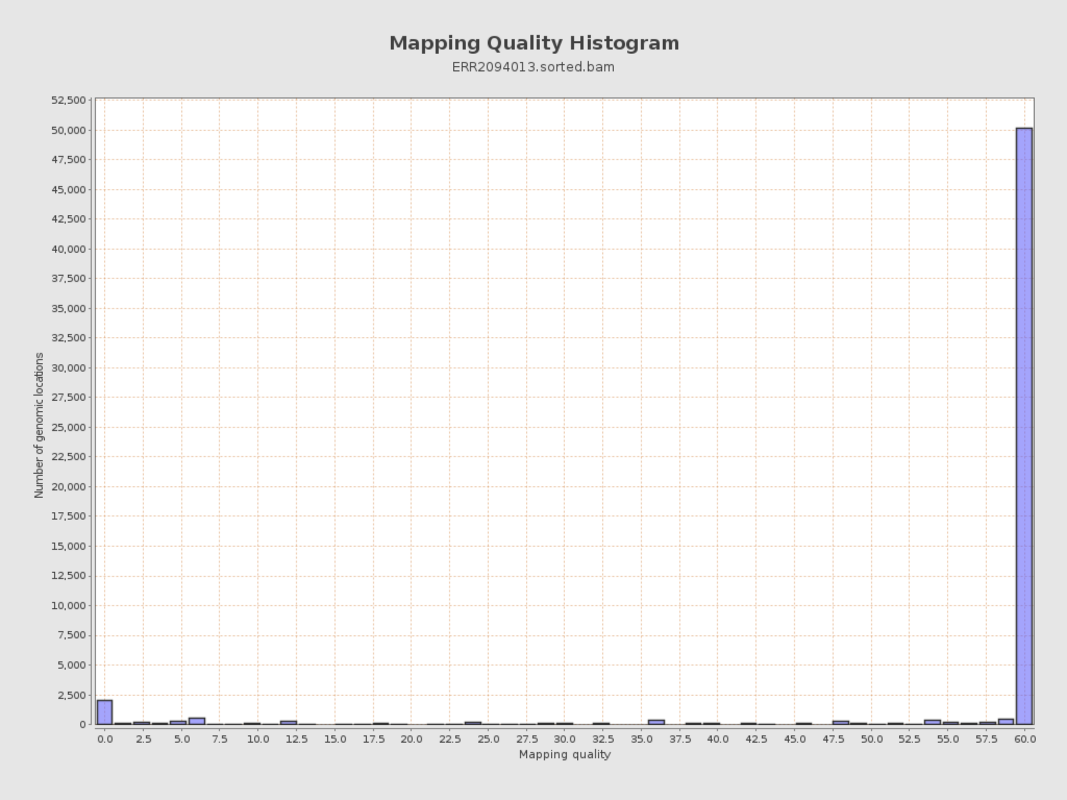
11. Results : Homopolymer Indels



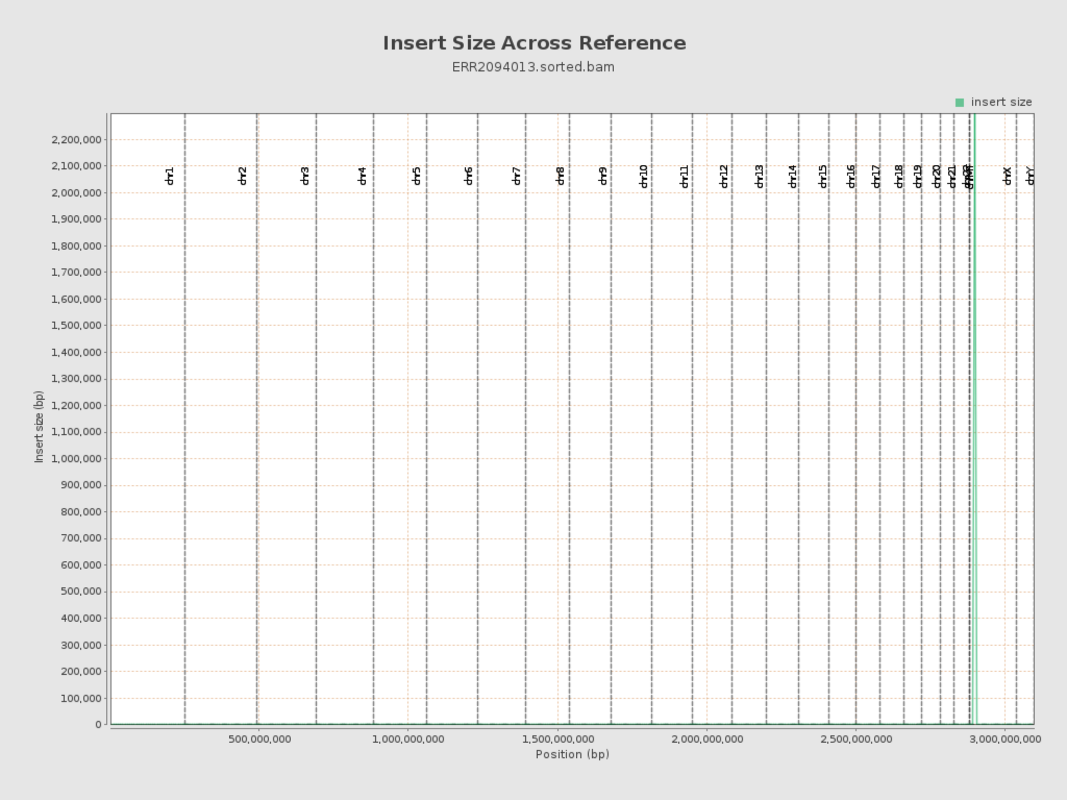
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram