Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:02:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094019.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_ERR2094019 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094019_1.fastq.gz ERR2094019_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:02:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,194
Mapped reads	15,102 / 57.65%
Unmapped reads	11,092 / 42.35%
Mapped paired reads	15,102 / 57.65%
Mapped reads, first in pair	7,533 / 28.76%
Mapped reads, second in pair	7,569 / 28.9%
Mapped reads, both in pair	14,894 / 56.86%
Mapped reads, singletons	208 / 0.79%
Secondary alignments	0
Supplementary alignments	24 / 0.09%
Read min/max/mean length	30 / 151 / 111.03
Duplicated reads (estimated)	14,651 / 55.93%
Duplication rate	32.42%
Clipped reads	1,012 / 3.86%

2.2. ACGT Content

Number/percentage of A's	644,270 / 28.95%
Number/percentage of C's	444,467 / 19.97%
Number/percentage of T's	656,905 / 29.51%
Number/percentage of G's	480,141 / 21.57%
Number/percentage of N's	13 / 0%

GC Percentage	41.54%

2.3. Coverage

Mean	0.0007
Standard Deviation	1.682

2.4. Mapping Quality

Mean Mapping Quality	7.48

2.5. Insert size

Mean	7,954.82
Standard Deviation	614,744.45
P25/Median/P75	217 / 217 / 237

2.6. Mismatches and indels

General error rate	1.76%
Mismatches	38,898
Insertions	152
Mapped reads with at least one insertion	0.92%
Deletions	975
Mapped reads with at least one deletion	6.36%
Homopolymer indels	74.36%

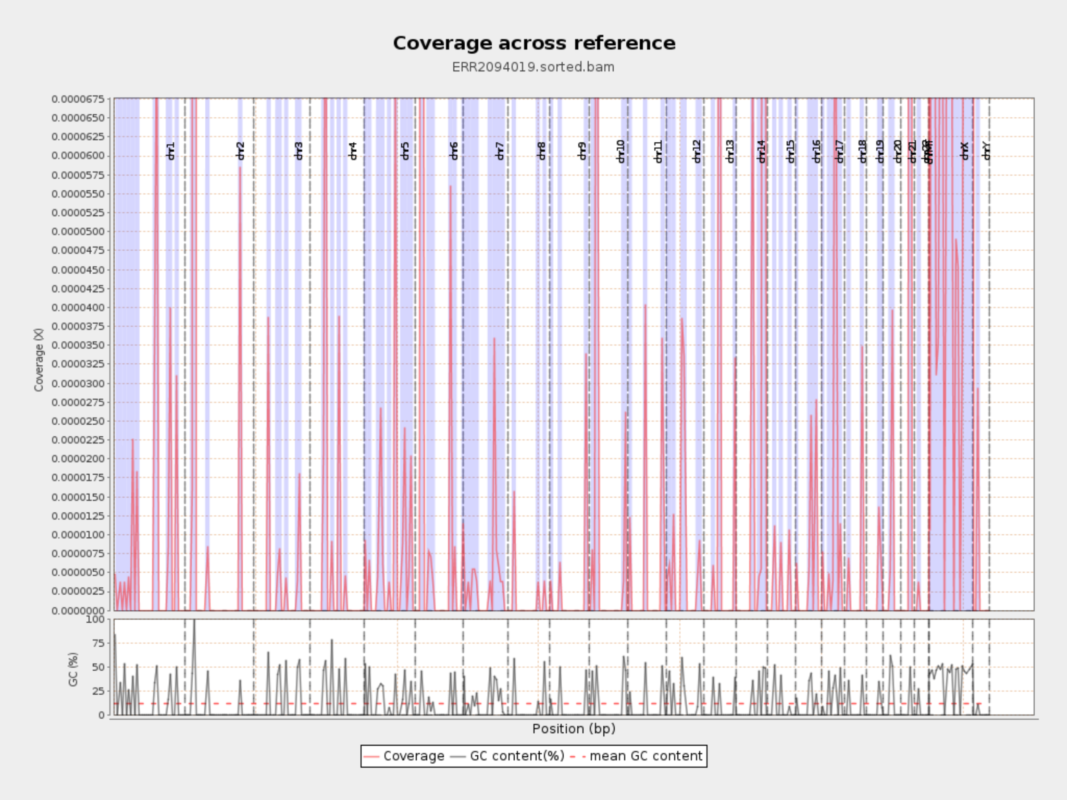
2.7. Chromosome stats

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

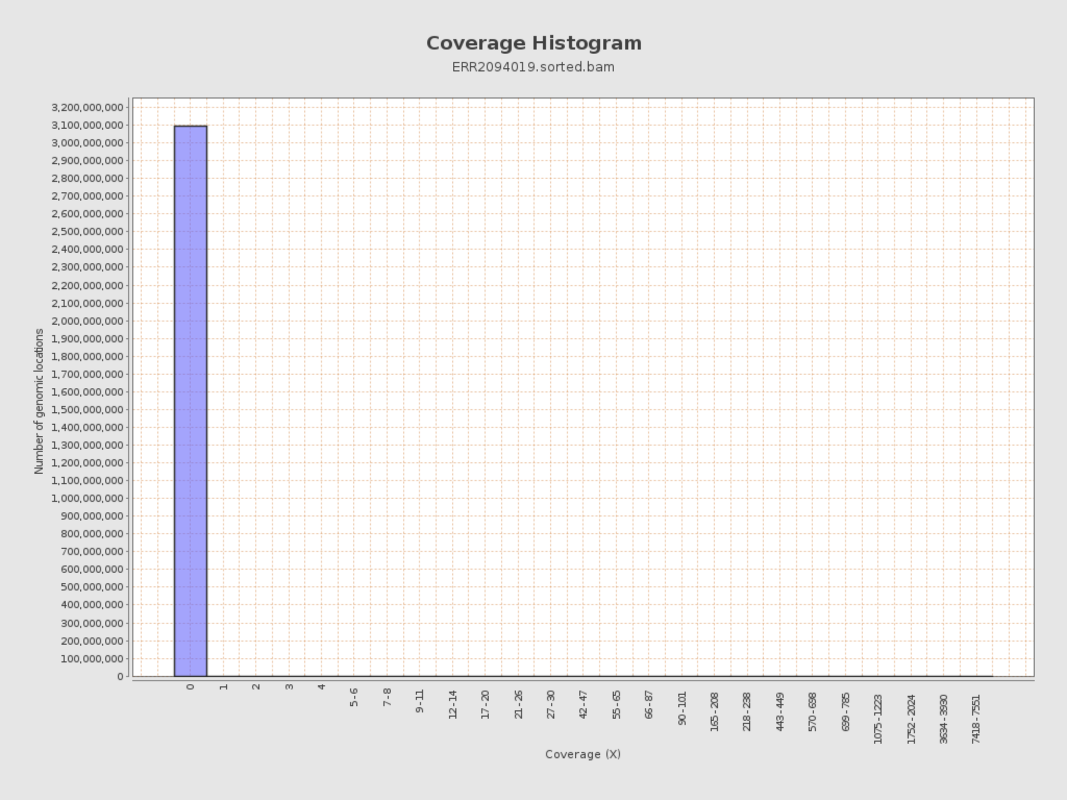
		bases	coverage	deviation
chr1	249250621	1976	0	0.004
chr2	243199373	16078	0.0001	0.064
chr3	198022430	606	0	0.0024
chr4	191154276	1394	0	0.0055
chr5	180915260	1450	0	0.0041
chr6	171115067	2854	0	0.0068
chr7	159138663	653	0	0.0022
chr8	146364022	183	0	0.0011
chr9	141213431	344	0	0.0019
chr10	135534747	1303	0	0.0062
chr11	135006516	688	0	0.003
chr12	133851895	844	0	0.0034
chr13	115169878	1549	0	0.0088
chr14	107349540	3763	0	0.01
chr15	102531392	240	0	0.0015
chr16	90354753	488	0	0.0028
chr17	81195210	1011	0	0.0089
chr18	78077248	324	0	0.0027
chr19	59128983	136	0	0.0015
chr20	63025520	351	0	0.003
chr21	48129895	3116	0.0001	0.0287
chr22	51304566	30	0	0.0008
chrMT	16571	2172091	131.0778	715.0364
chrX	155270560	15369	0.0001	0.0289

chrY	59373566	228	0	0.0031

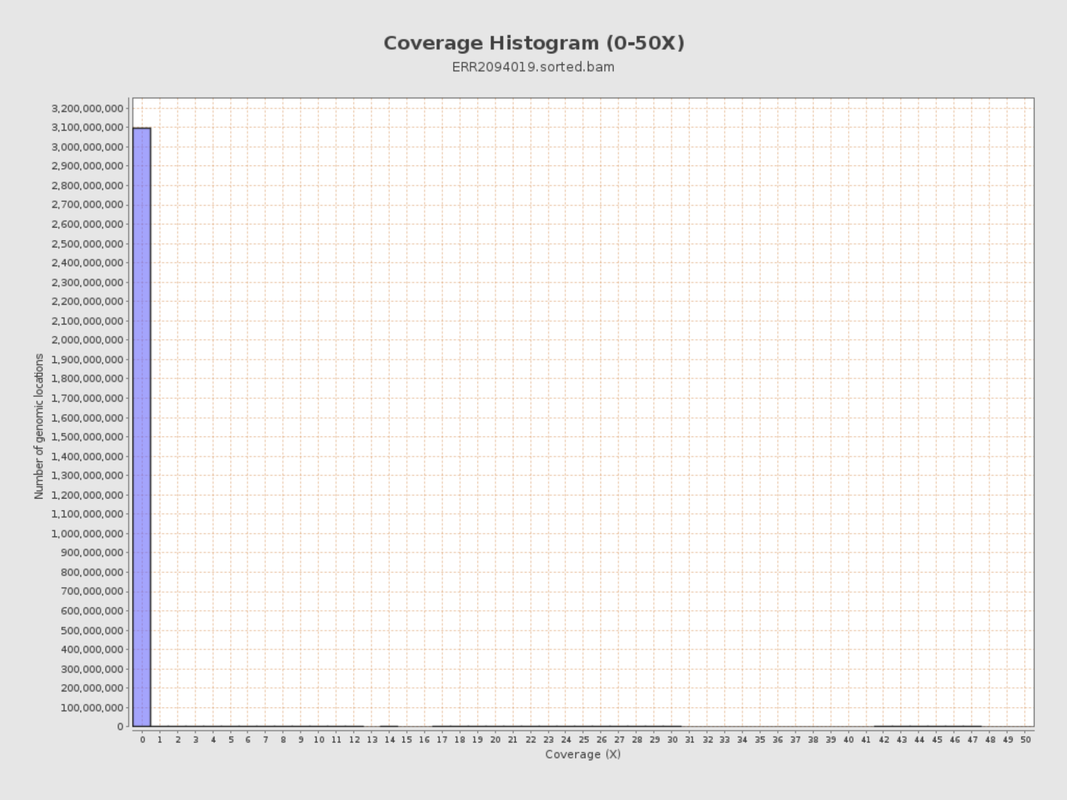
3. Results : Coverage across reference



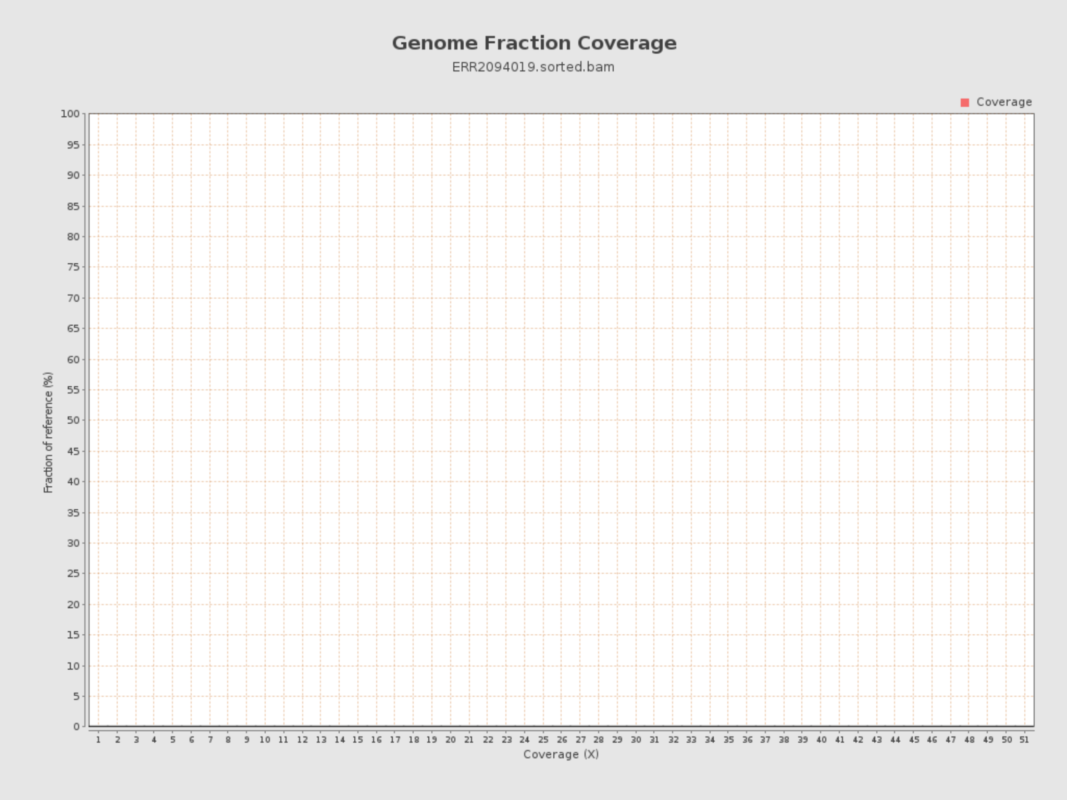
4. Results : Coverage Histogram



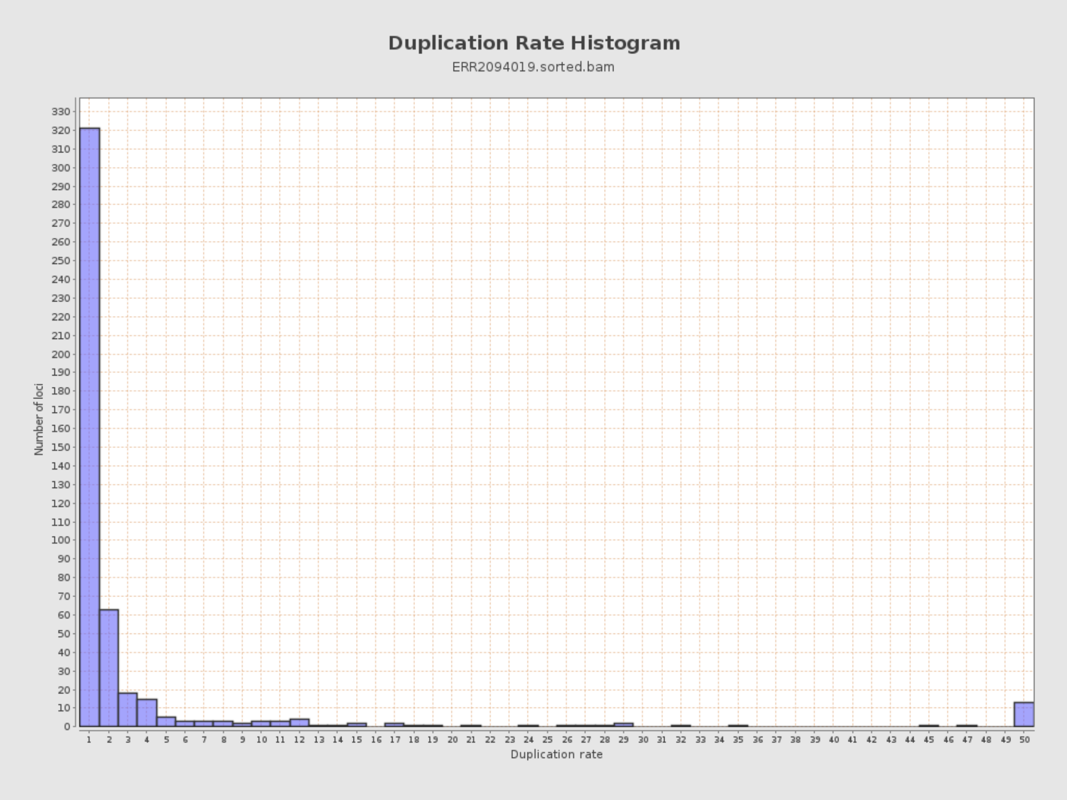
5. Results : Coverage Histogram (0-50X)



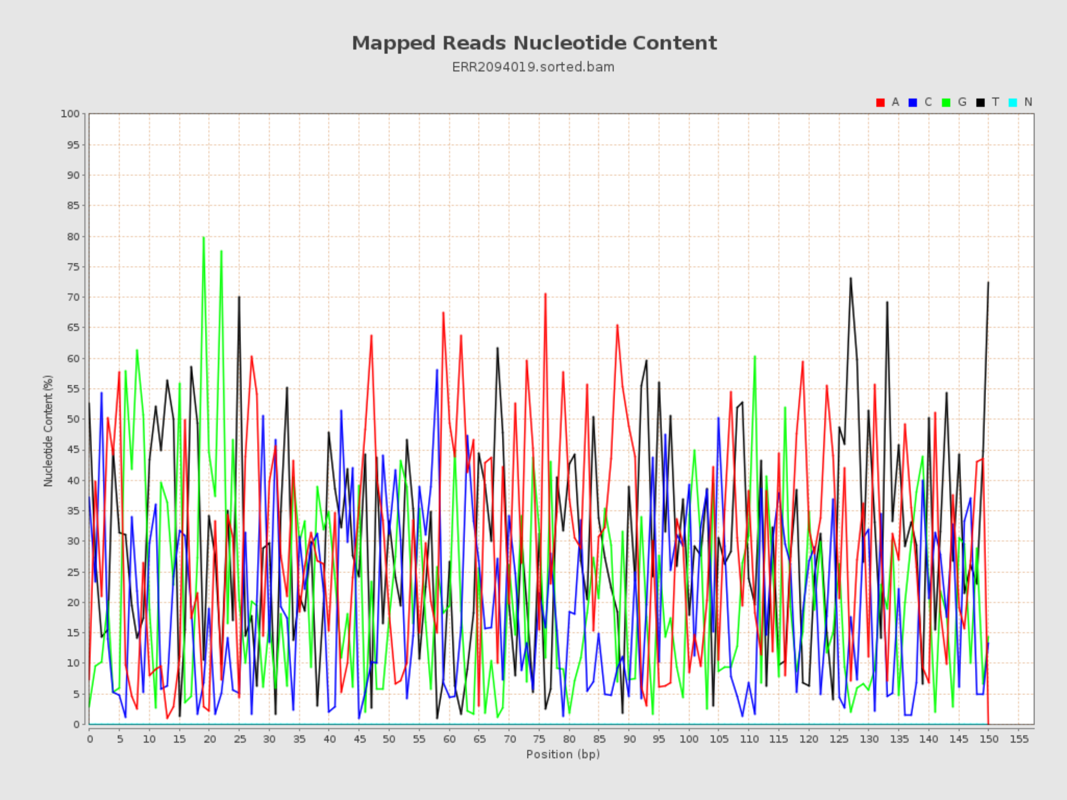
6. Results : Genome Fraction Coverage



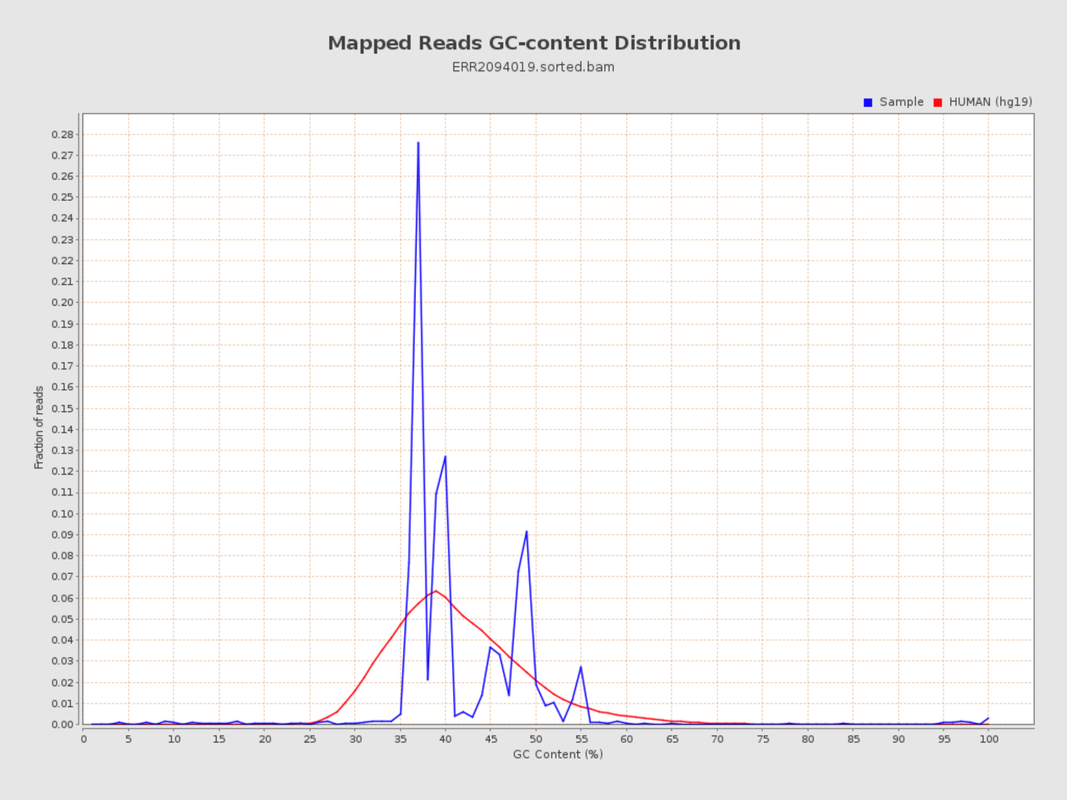
7. Results : Duplication Rate Histogram



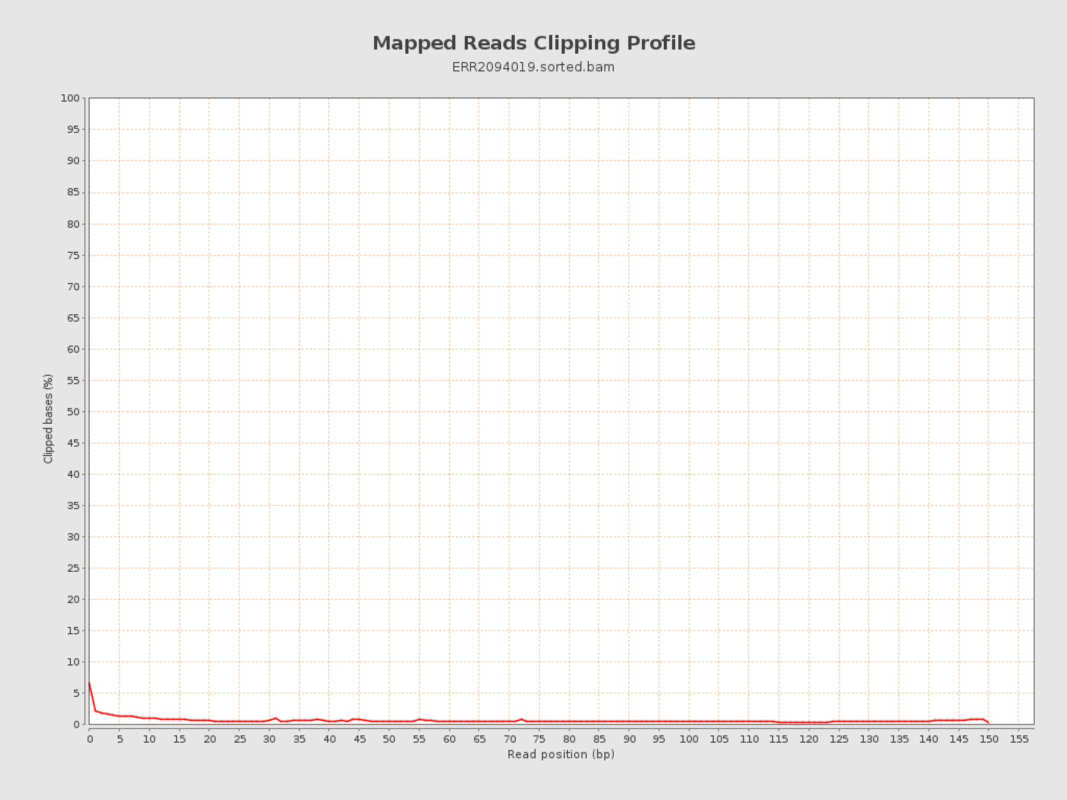
8. Results : Mapped Reads Nucleotide Content



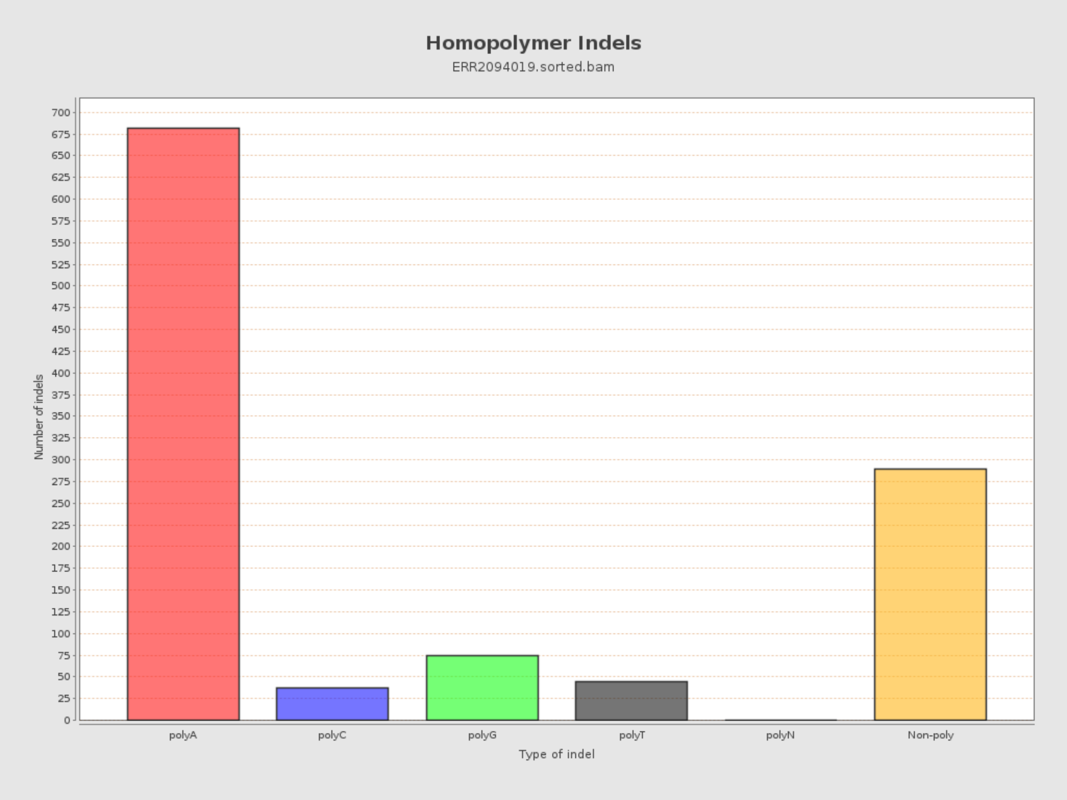
9. Results : Mapped Reads GC-content Distribution



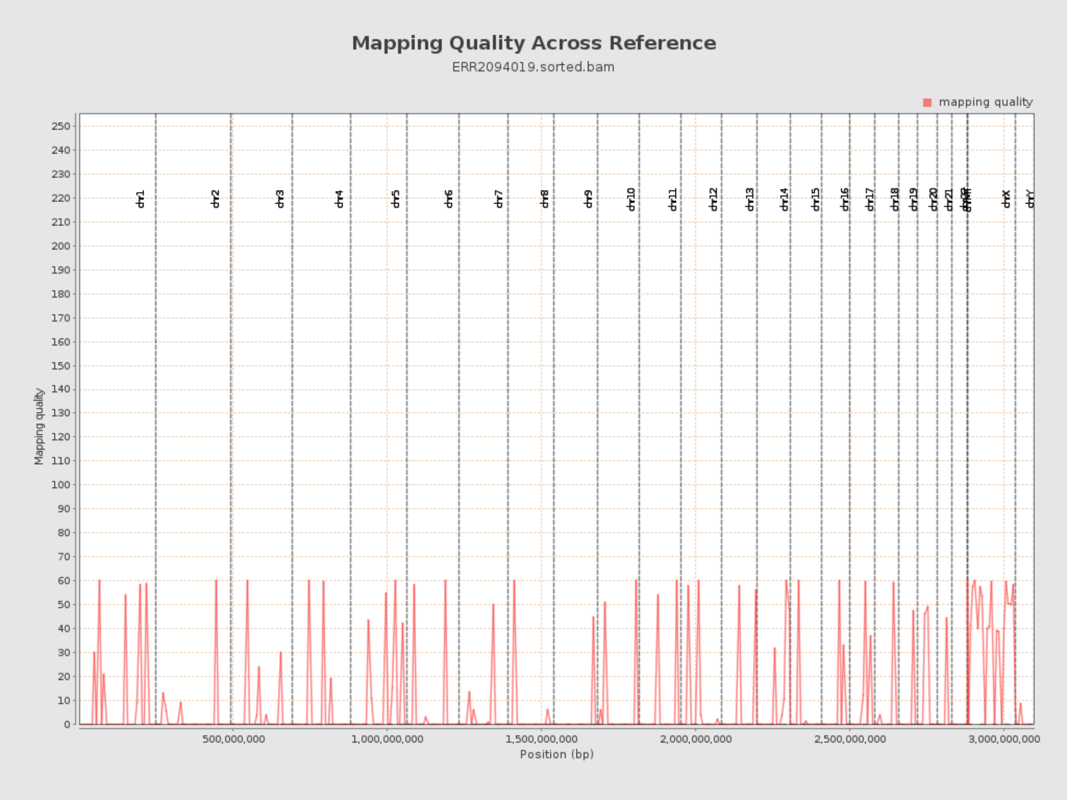
10. Results : Mapped Reads Clipping Profile



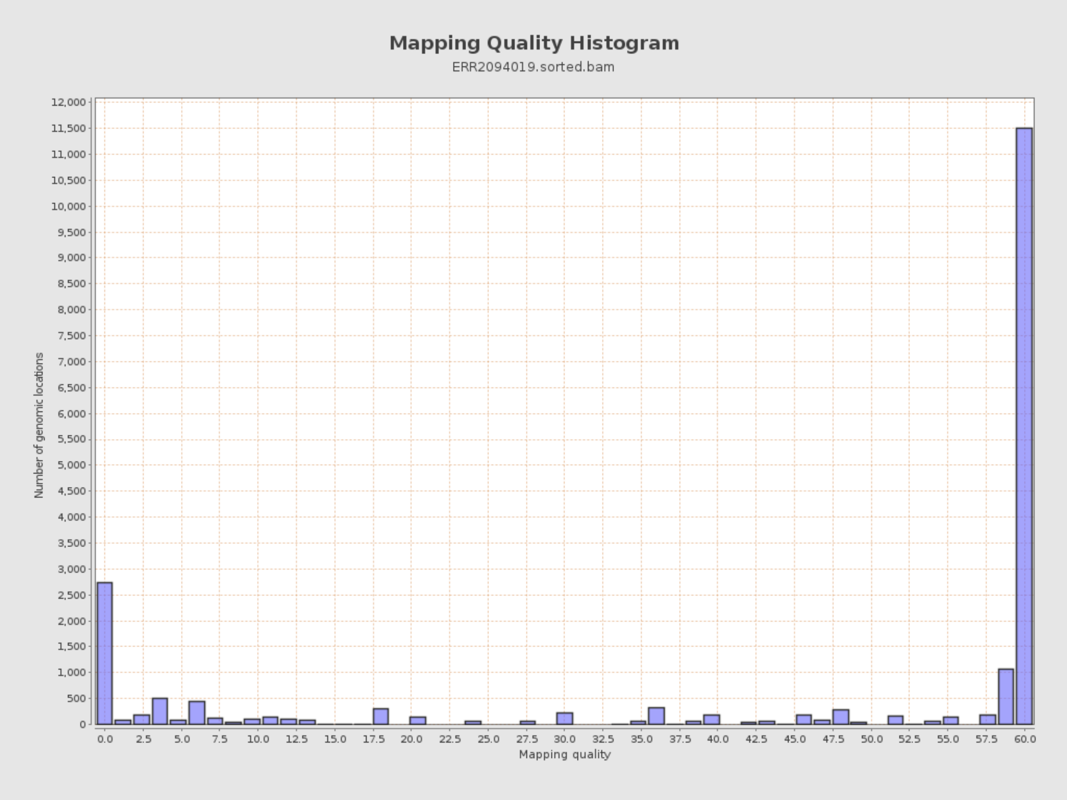
11. Results : Homopolymer Indels



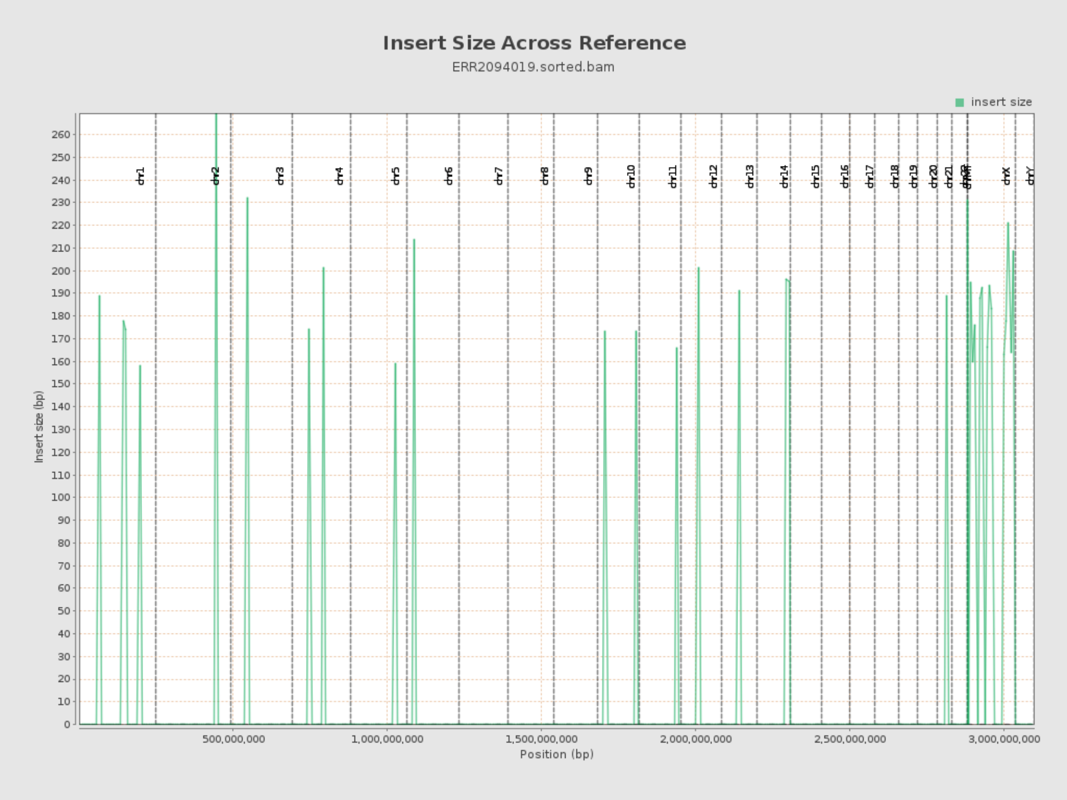
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram