Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:32:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094031.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_ERR2094031 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094031_1.fastq.gz ERR2094031_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:32:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	374,366
Mapped reads	334,972 / 89.48%
Unmapped reads	39,394 / 10.52%
Mapped paired reads	334,972 / 89.48%
Mapped reads, first in pair	168,444 / 44.99%
Mapped reads, second in pair	166,528 / 44.48%
Mapped reads, both in pair	329,276 / 87.96%
Mapped reads, singletons	5,696 / 1.52%
Secondary alignments	0
Supplementary alignments	15,784 / 4.22%
Read min/max/mean length	30 / 151 / 140.81
Duplicated reads (estimated)	313,137 / 83.64%
Duplication rate	43.84%
Clipped reads	159,954 / 42.73%

2.2. ACGT Content

Number/percentage of A's	12,120,911 / 28.36%
Number/percentage of C's	9,245,408 / 21.63%
Number/percentage of T's	11,741,652 / 27.47%
Number/percentage of G's	9,636,231 / 22.54%
Number/percentage of N's	440 / 0%

GC Percentage	44.17%

2.3. Coverage

Mean	0.014
Standard Deviation	6.7975

2.4. Mapping Quality

Mean Mapping Quality	42.85

2.5. Insert size

Mean	362,512.81
Standard Deviation	5,781,272.19
P25/Median/P75	142 / 175 / 217

2.6. Mismatches and indels

General error rate	3.31%
Mismatches	1,358,265
Insertions	24,203
Mapped reads with at least one insertion	7.06%
Deletions	99,619
Mapped reads with at least one deletion	28.48%
Homopolymer indels	31.45%

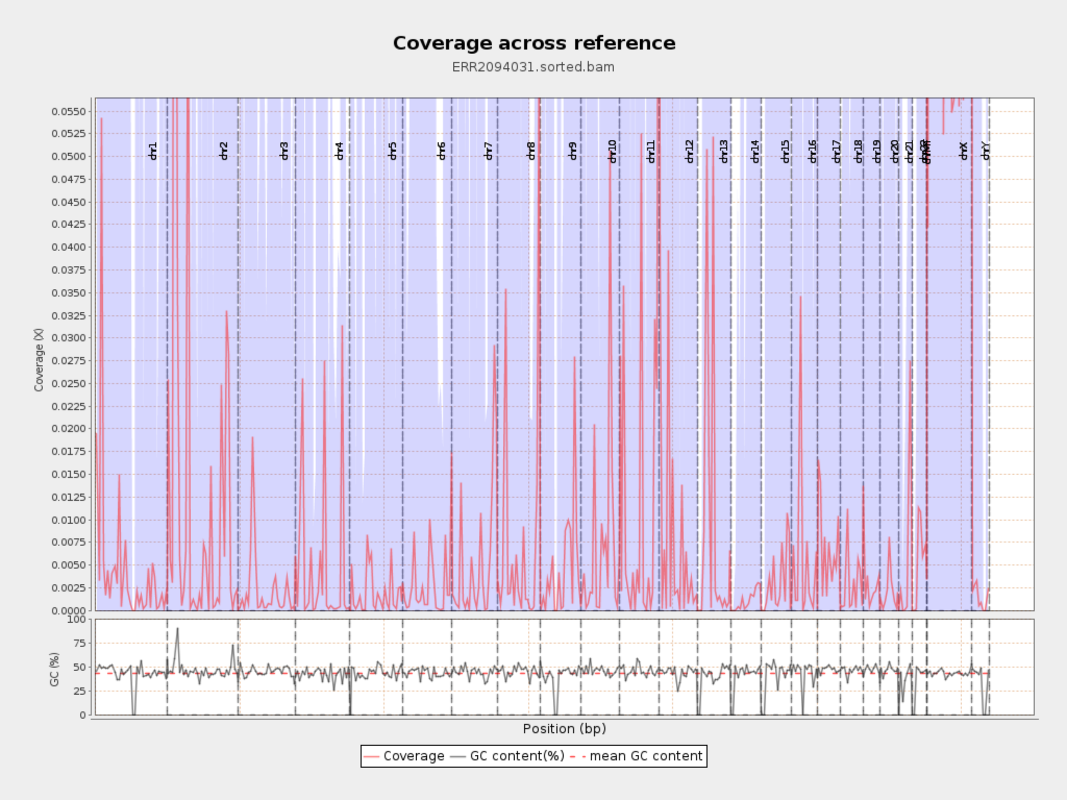
2.7. Chromosome stats

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

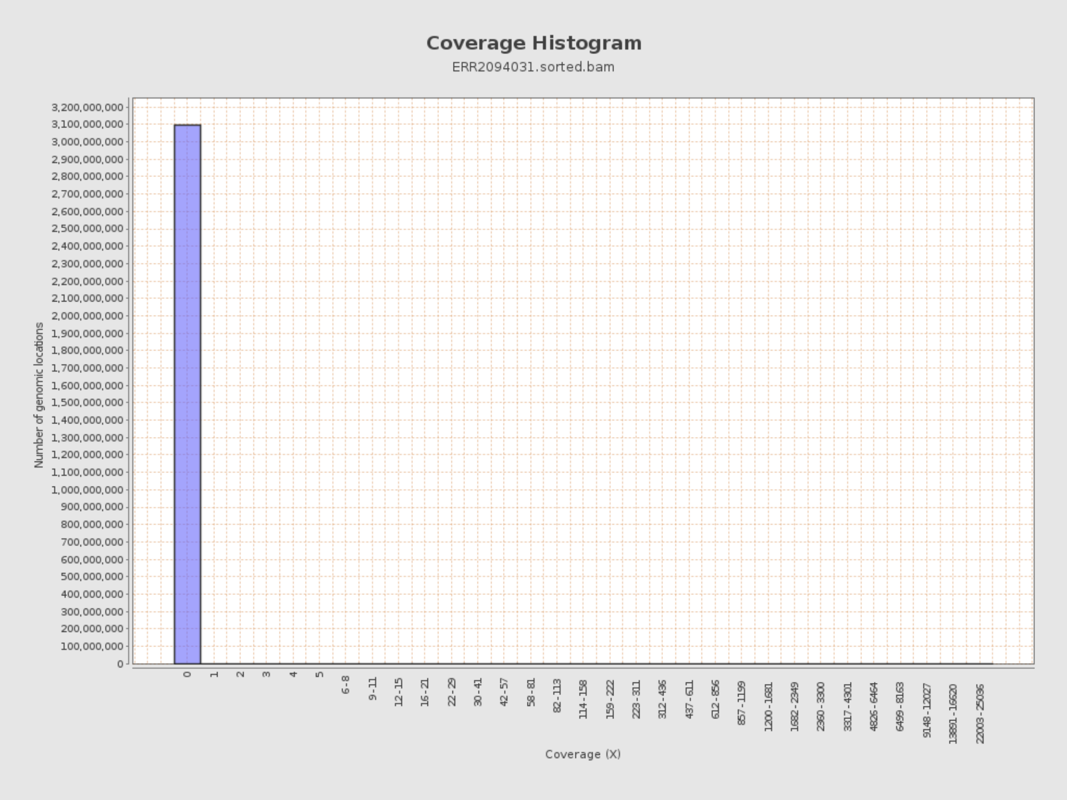
		bases	coverage	deviation
chr1	249250621	1201409	0.0048	1.3005
chr2	243199373	3508746	0.0144	5.051
chr3	198022430	427068	0.0022	0.5095
chr4	191154276	936207	0.0049	1.975
chr5	180915260	376238	0.0021	0.5608
chr6	171115067	481129	0.0028	0.7426
chr7	159138663	889926	0.0056	1.4983
chr8	146364022	1100014	0.0075	2.6743
chr9	141213431	664303	0.0047	1.0863
chr10	135534747	1004965	0.0074	1.9671
chr11	135006516	1482059	0.011	2.9037
chr12	133851895	1027024	0.0077	2.5609
chr13	115169878	1057092	0.0092	4.0297
chr14	107349540	121789	0.0011	0.2106
chr15	102531392	331163	0.0032	0.7187
chr16	90354753	484666	0.0054	1.7916
chr17	81195210	563820	0.0069	1.6169
chr18	78077248	215977	0.0028	0.7957
chr19	59128983	153009	0.0026	0.2622
chr20	63025520	137713	0.0022	0.5664
chr21	48129895	308892	0.0064	1.7364
chr22	51304566	282508	0.0055	1.1938
chrMT	16571	9396754	567.0602	2,540.9011
chrX	155270560	17215354	0.1109	10.2519

chrY	59373566	87470	0.0015	0.1694

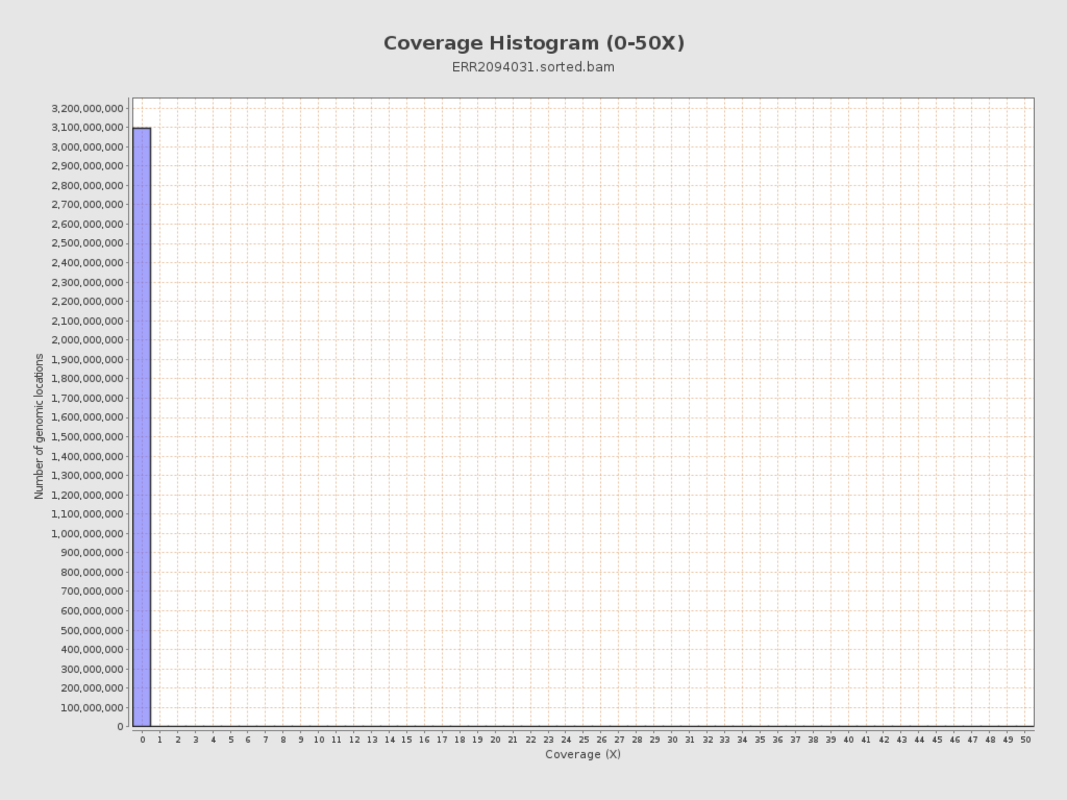
3. Results : Coverage across reference



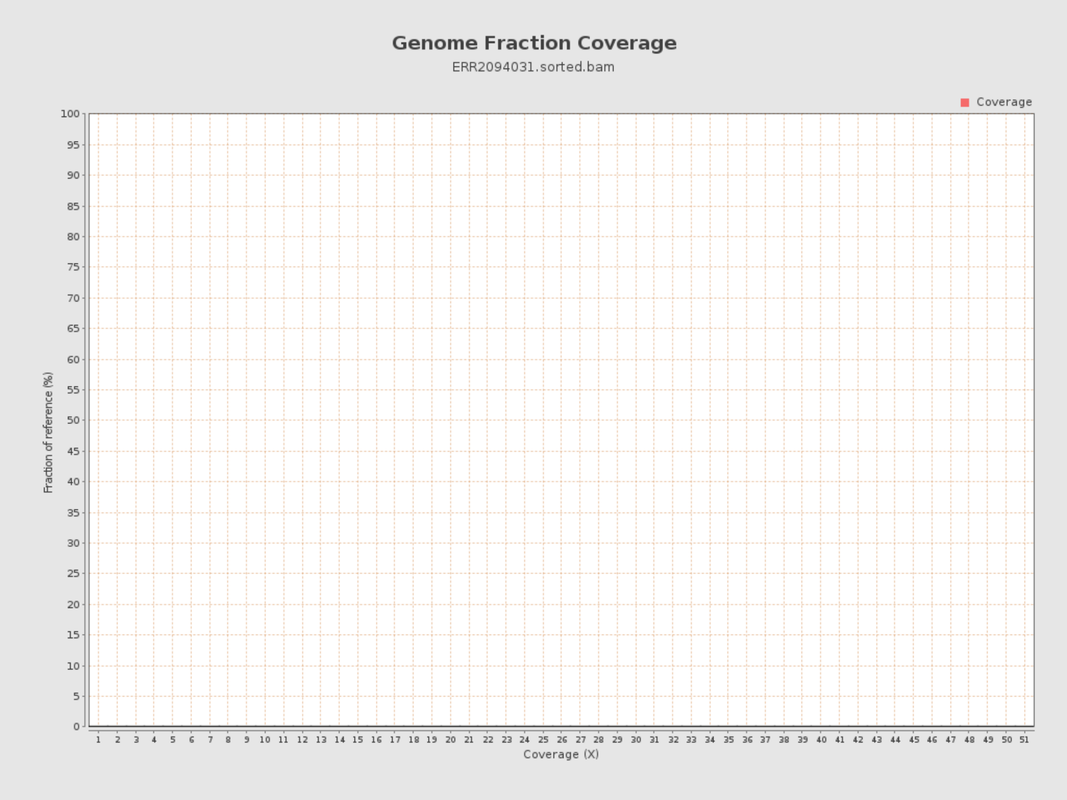
4. Results : Coverage Histogram



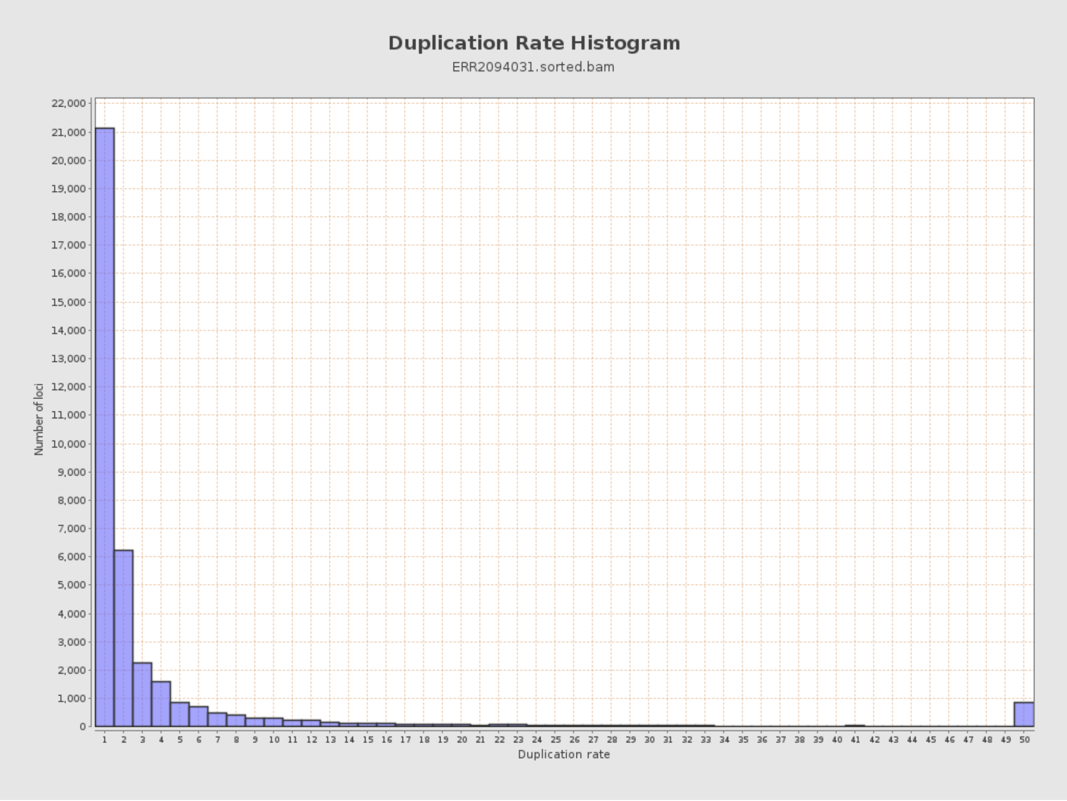
5. Results : Coverage Histogram (0-50X)



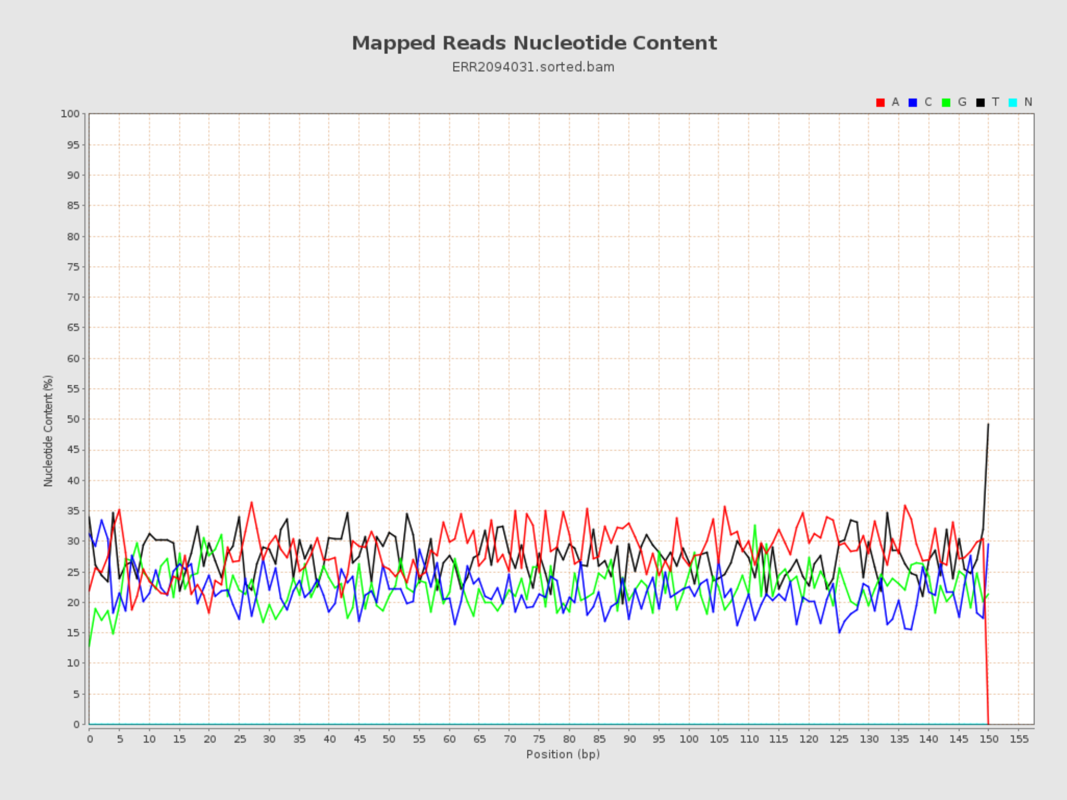
6. Results : Genome Fraction Coverage



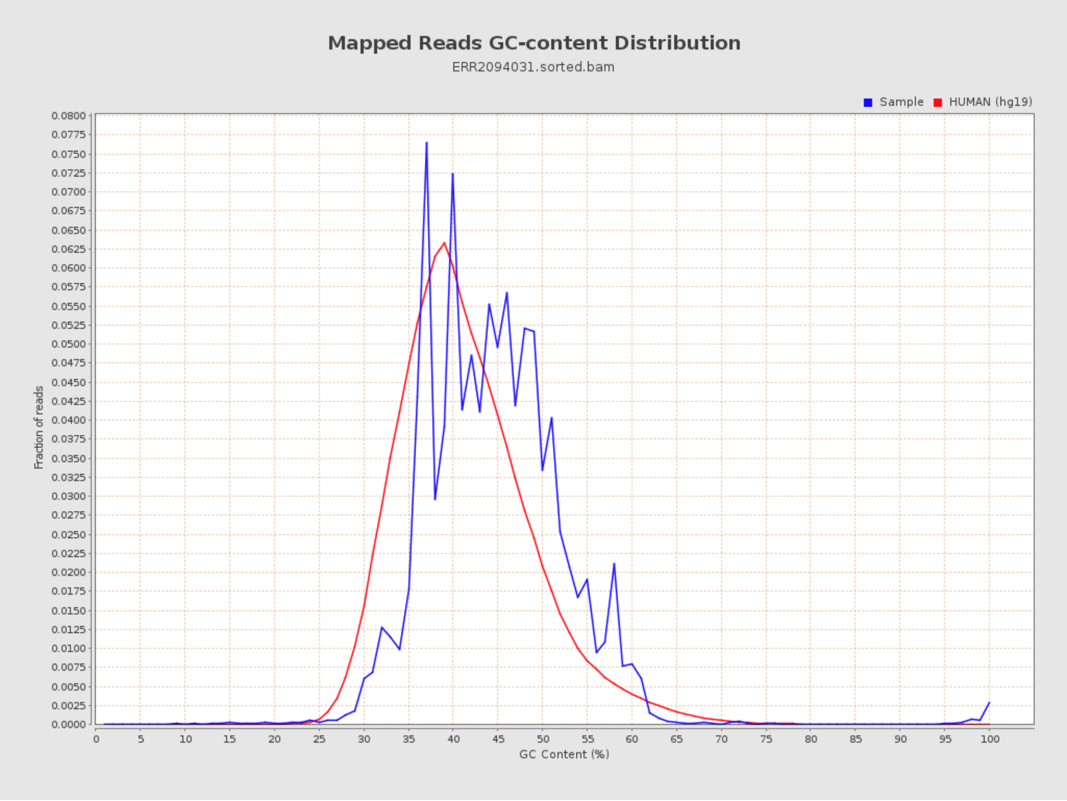
7. Results : Duplication Rate Histogram



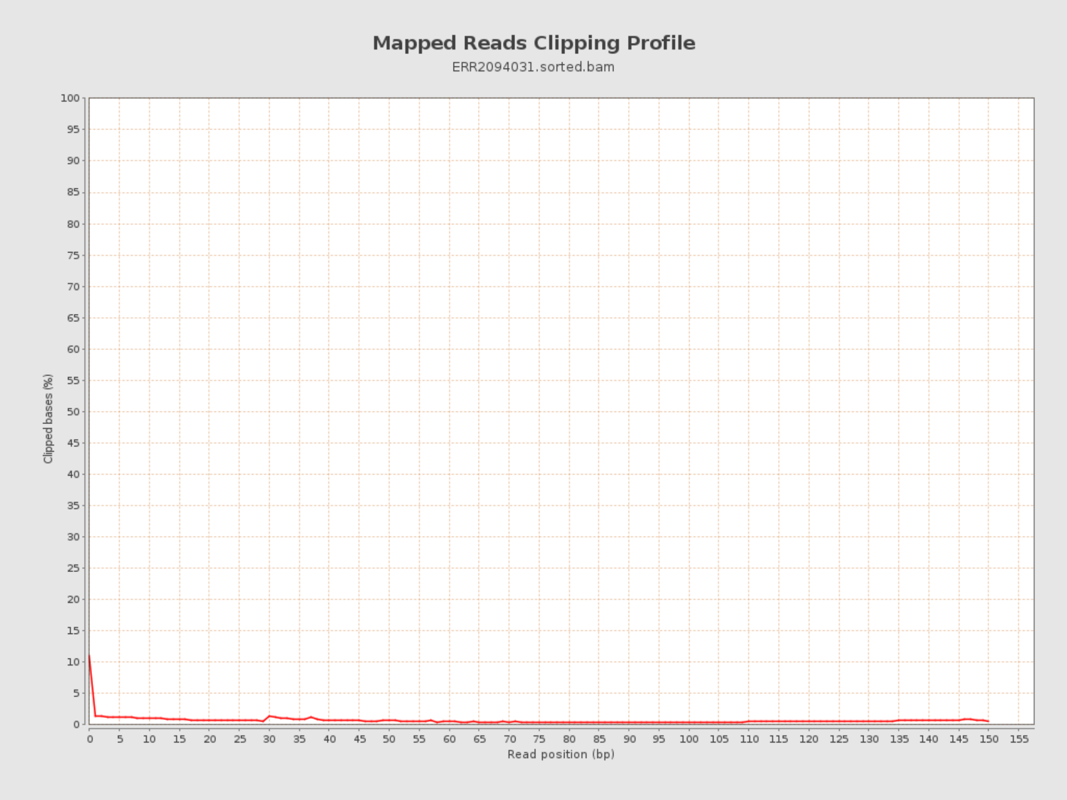
8. Results : Mapped Reads Nucleotide Content



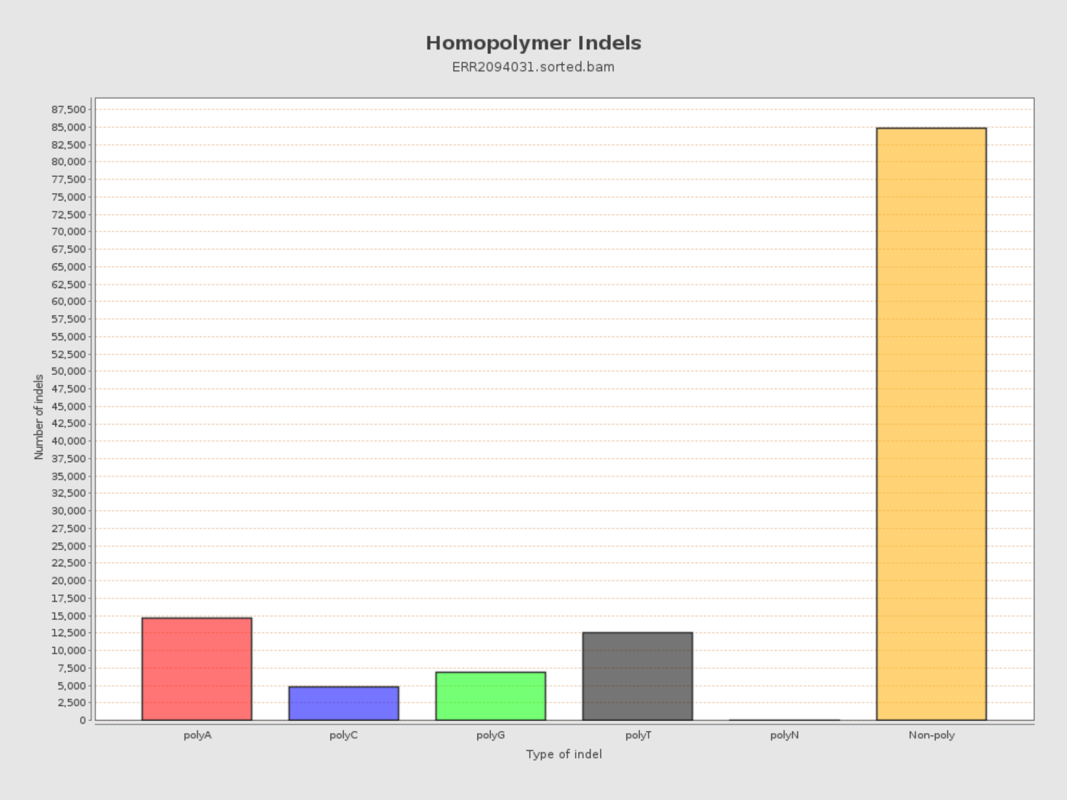
9. Results : Mapped Reads GC-content Distribution



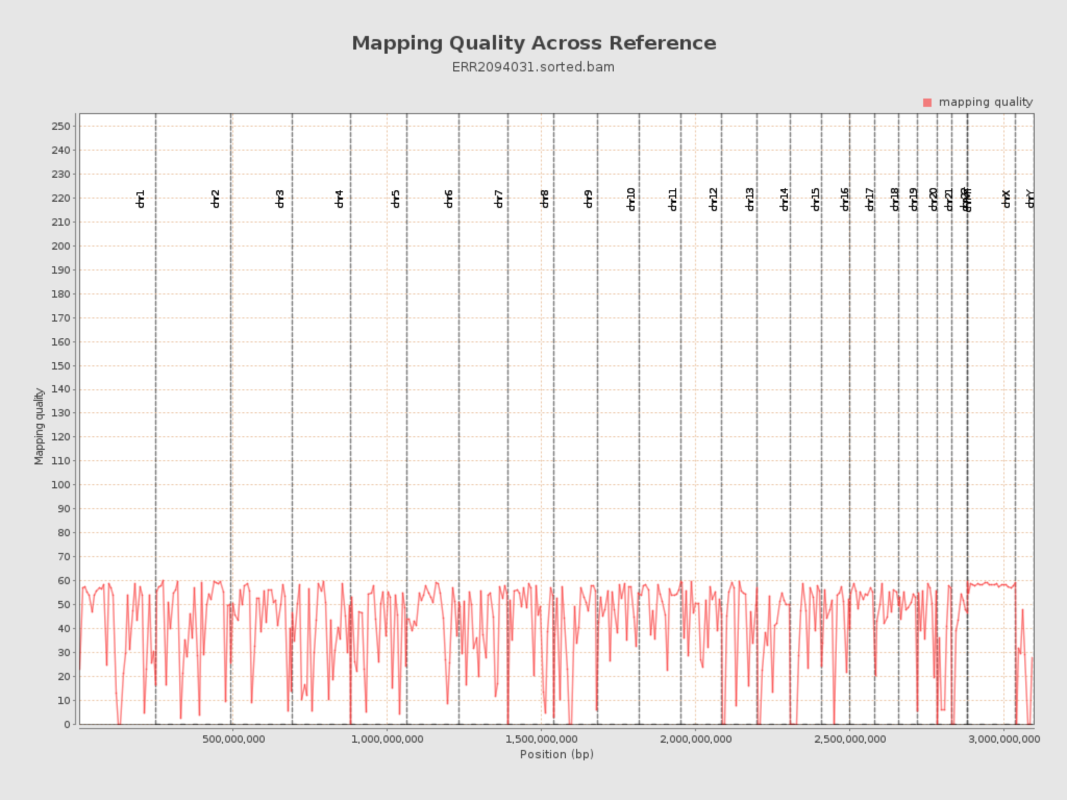
10. Results : Mapped Reads Clipping Profile



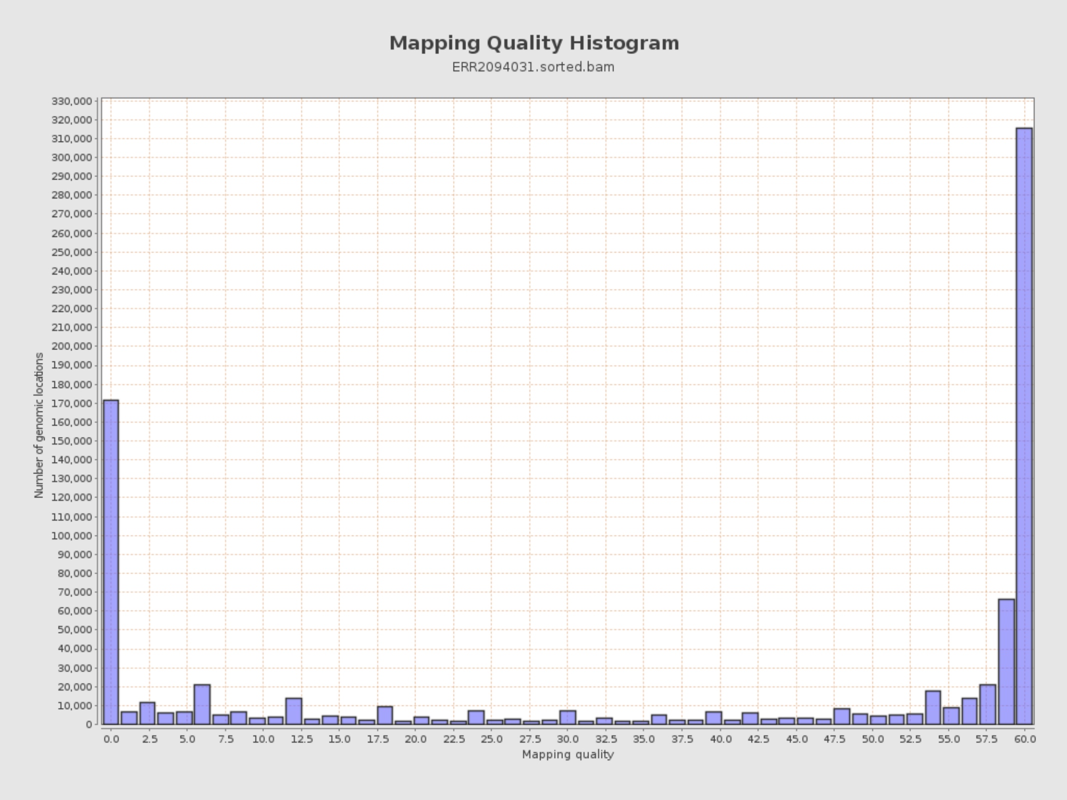
11. Results : Homopolymer Indels



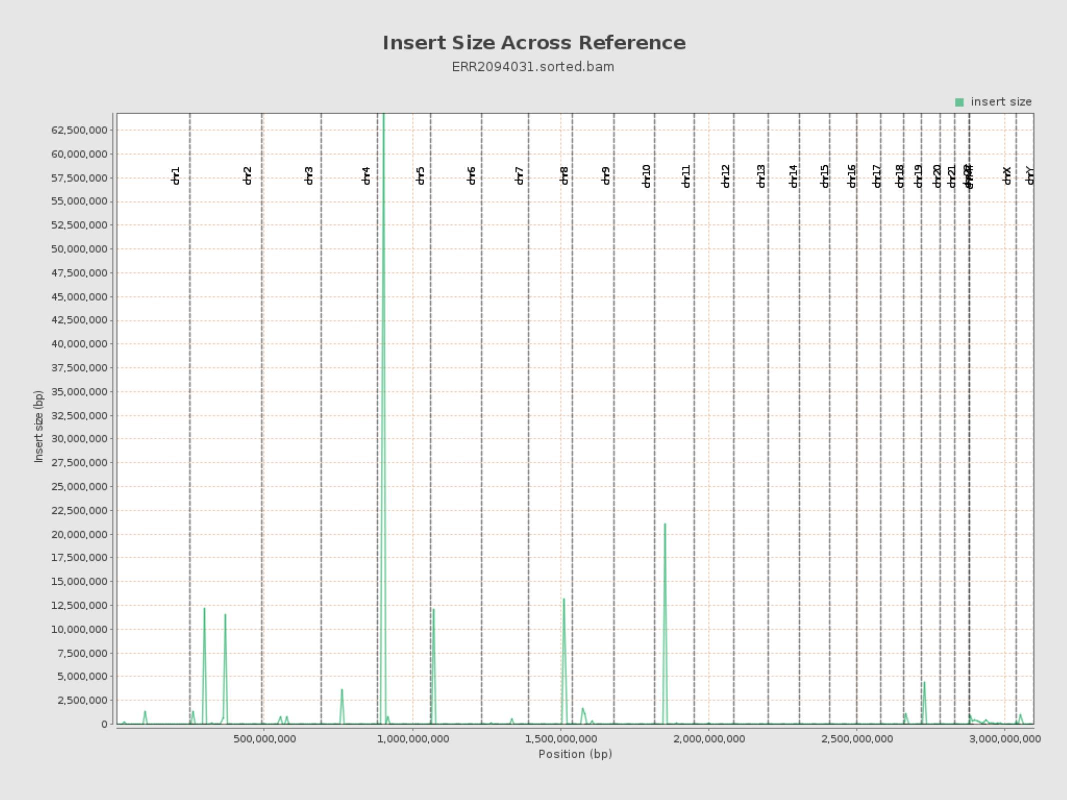
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram