Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:42:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094035.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_ERR2094035 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094035_1.fastq.gz ERR2094035_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:42:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	349,008
Mapped reads	314,917 / 90.23%
Unmapped reads	34,091 / 9.77%
Mapped paired reads	314,917 / 90.23%
Mapped reads, first in pair	158,599 / 45.44%
Mapped reads, second in pair	156,318 / 44.79%
Mapped reads, both in pair	309,040 / 88.55%
Mapped reads, singletons	5,877 / 1.68%
Secondary alignments	0
Supplementary alignments	18,232 / 5.22%
Read min/max/mean length	30 / 151 / 139.8
Duplicated reads (estimated)	287,616 / 82.41%
Duplication rate	43.78%
Clipped reads	165,213 / 47.34%

2.2. ACGT Content

Number/percentage of A's	11,009,820 / 28.23%
Number/percentage of C's	8,643,946 / 22.17%
Number/percentage of T's	10,400,222 / 26.67%
Number/percentage of G's	8,940,346 / 22.93%
Number/percentage of N's	396 / 0%

GC Percentage	45.09%

2.3. Coverage

Mean	0.0128
Standard Deviation	3.8533

2.4. Mapping Quality

Mean Mapping Quality	44.02

2.5. Insert size

Mean	579,756.48
Standard Deviation	7,107,502.42
P25/Median/P75	129 / 165 / 206

2.6. Mismatches and indels

General error rate	3.71%
Mismatches	1,386,546
Insertions	26,052
Mapped reads with at least one insertion	8.06%
Deletions	102,866
Mapped reads with at least one deletion	31.36%
Homopolymer indels	29.16%

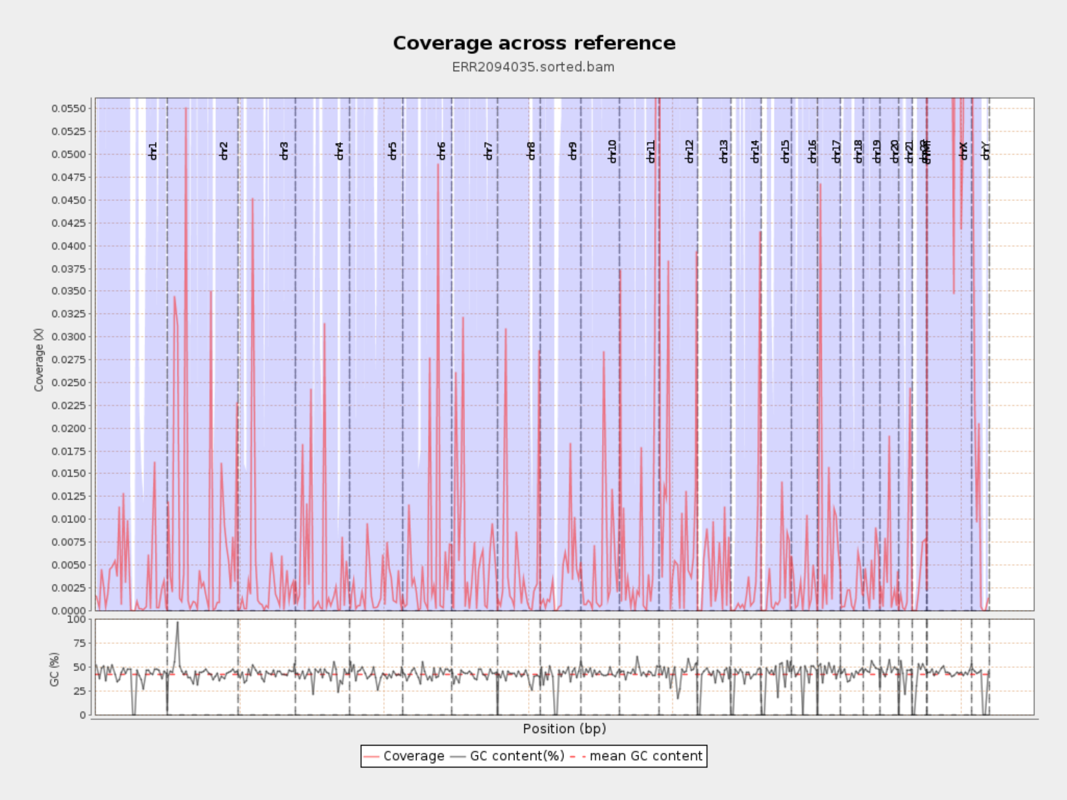
2.7. Chromosome stats

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

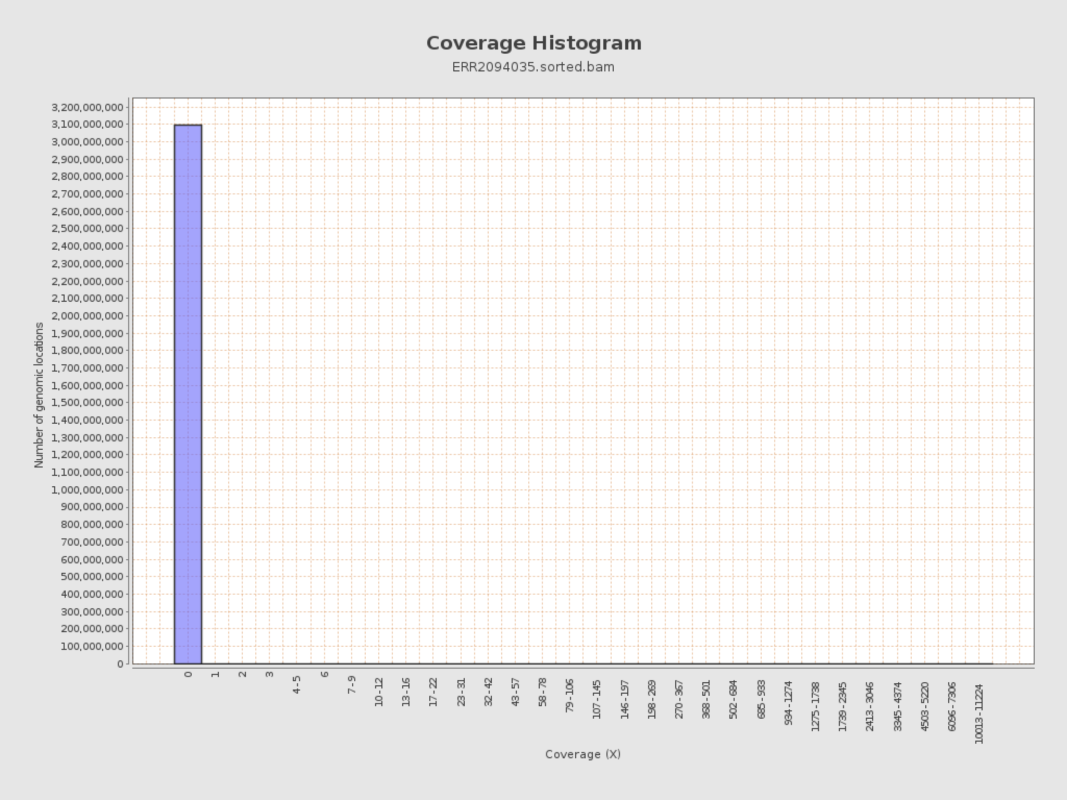
		bases	**coverage**	**deviation**
chr1	249250621	835644	0.0034	0.9764
chr2	243199373	2024318	0.0083	2.3638
chr3	198022430	717965	0.0036	1.4117
chr4	191154276	919973	0.0048	1.3604
chr5	180915260	444513	0.0025	0.6504
chr6	171115067	1002402	0.0059	2.0541
chr7	159138663	1042787	0.0066	1.6374
chr8	146364022	721349	0.0049	1.7782
chr9	141213431	503343	0.0036	0.8422
chr10	135534747	692089	0.0051	1.4222
chr11	135006516	1584690	0.0117	3.225
chr12	133851895	1257435	0.0094	2.3757
chr13	115169878	485375	0.0042	0.9811
chr14	107349540	506801	0.0047	0.7902
chr15	102531392	308029	0.003	0.9131
chr16	90354753	261795	0.0029	0.7295
chr17	81195210	796137	0.0098	1.9087
chr18	78077248	155094	0.002	0.4528
chr19	59128983	226872	0.0038	0.6794
chr20	63025520	290953	0.0046	1.2943
chr21	48129895	259711	0.0054	0.9462
chr22	51304566	173579	0.0034	0.5635
chrMT	16571	5015133	302.6452	1,276.0077
chrX	155270560	18826553	0.1212	7.903

chrY	59373566	715879	0.0121	2.5473

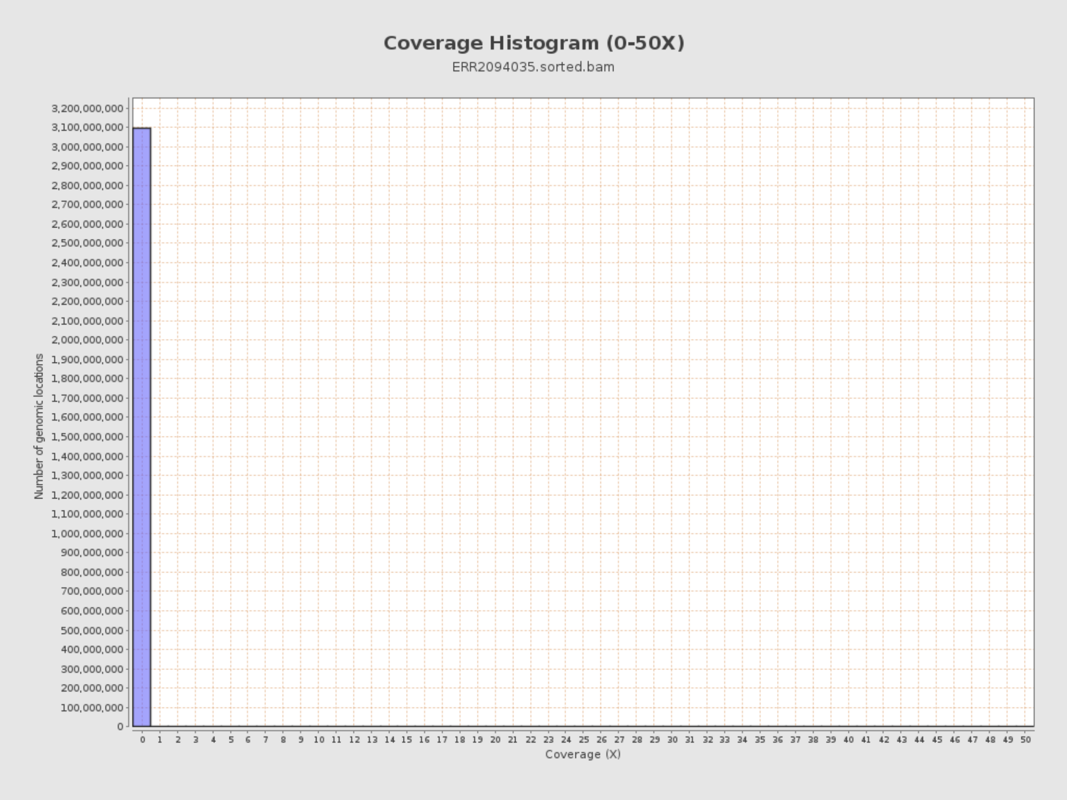
3. Results : Coverage across reference



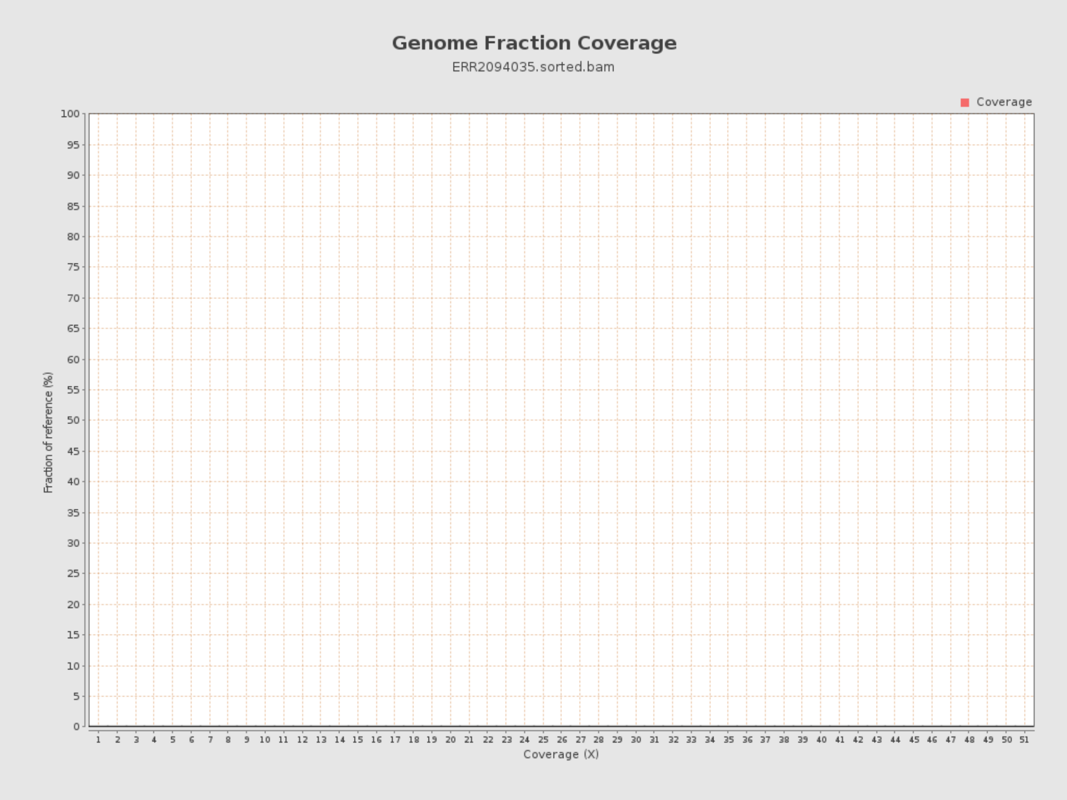
4. Results : Coverage Histogram



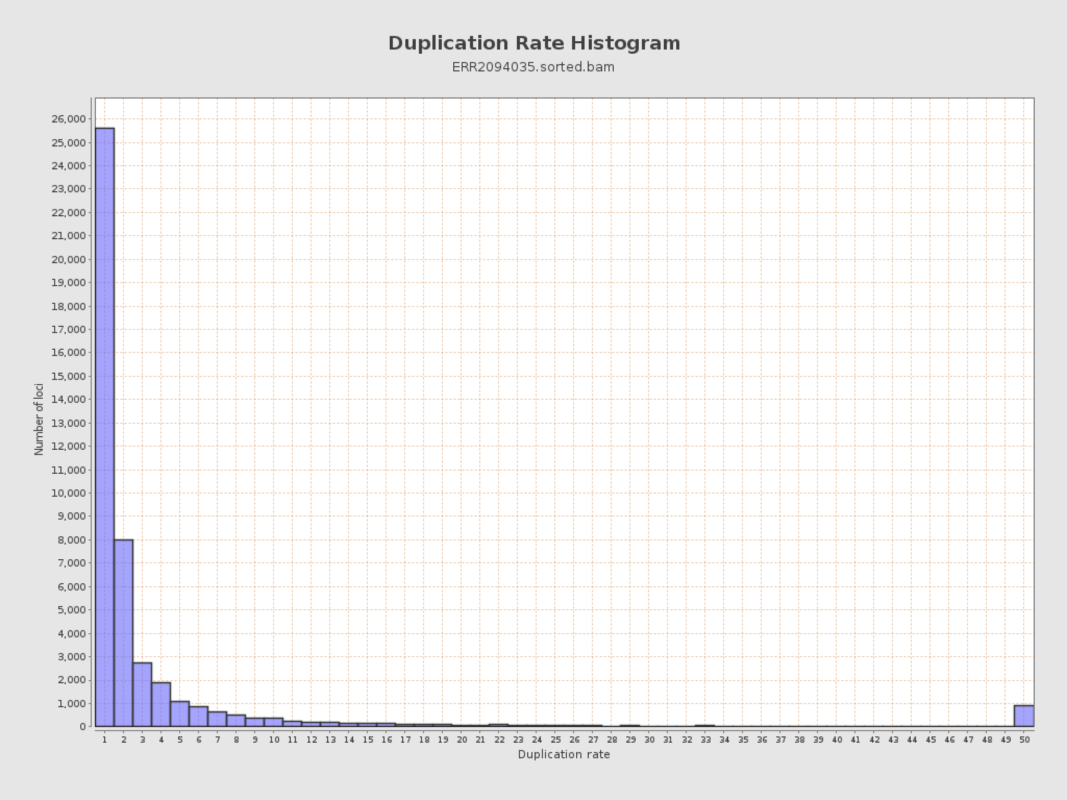
5. Results : Coverage Histogram (0-50X)



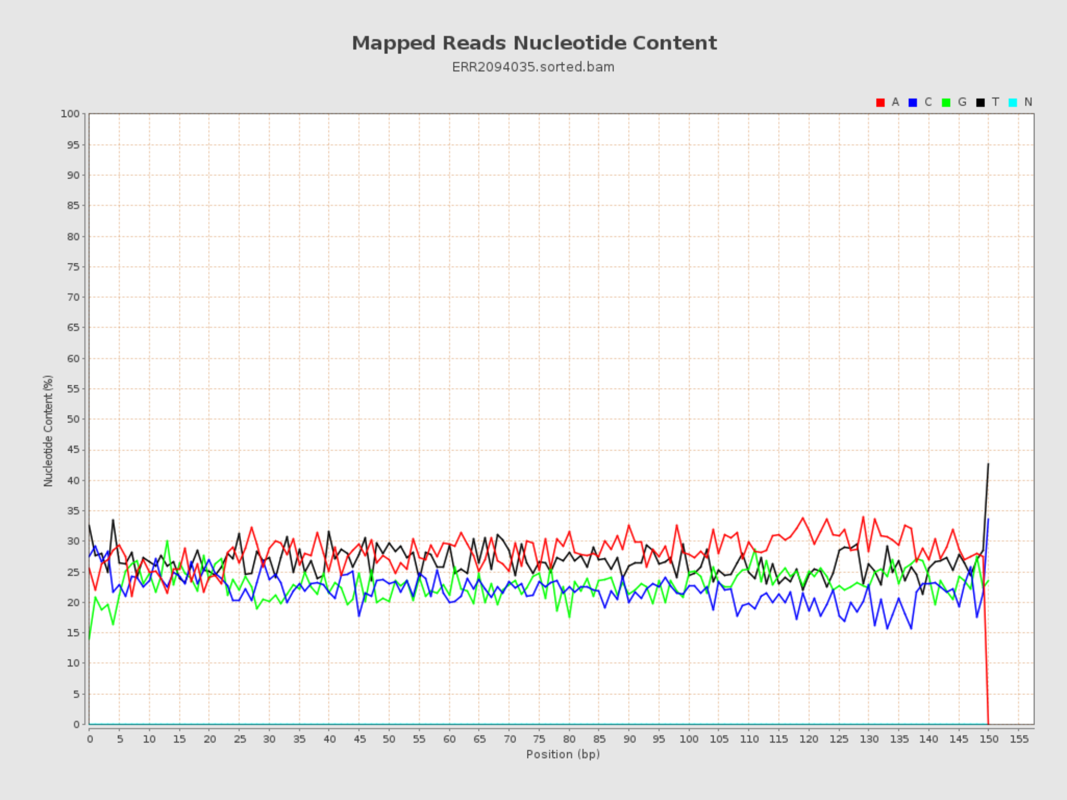
6. Results : Genome Fraction Coverage



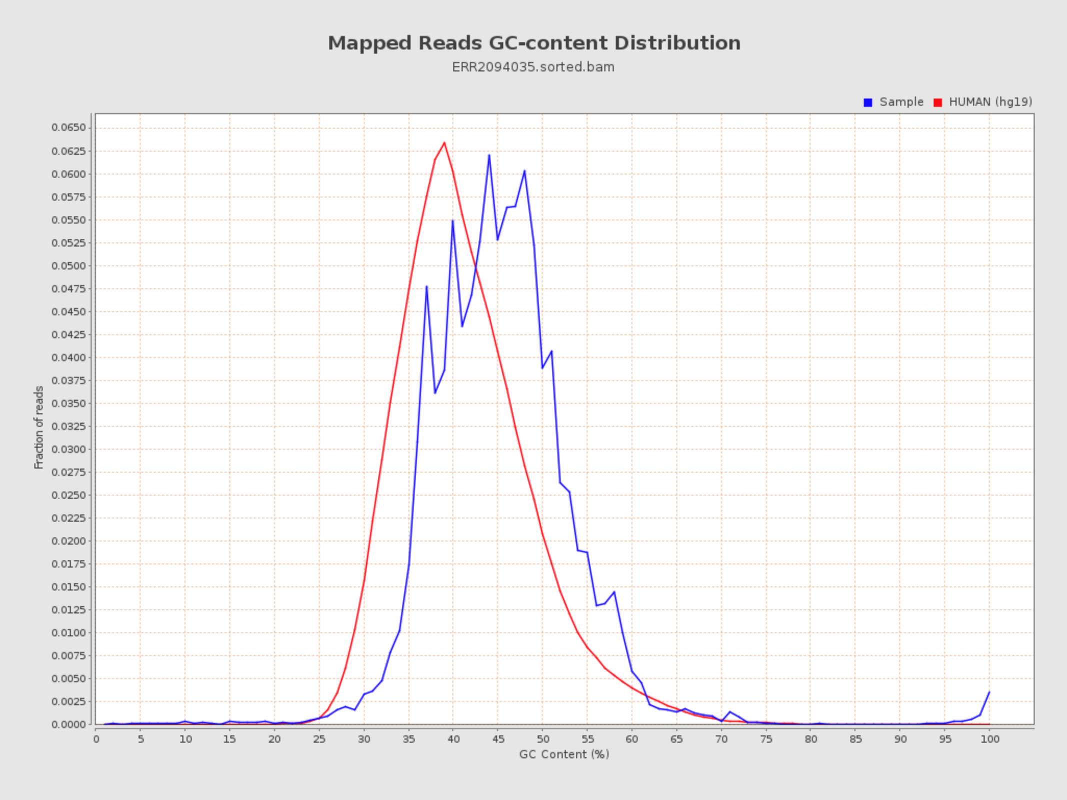
7. Results : Duplication Rate Histogram



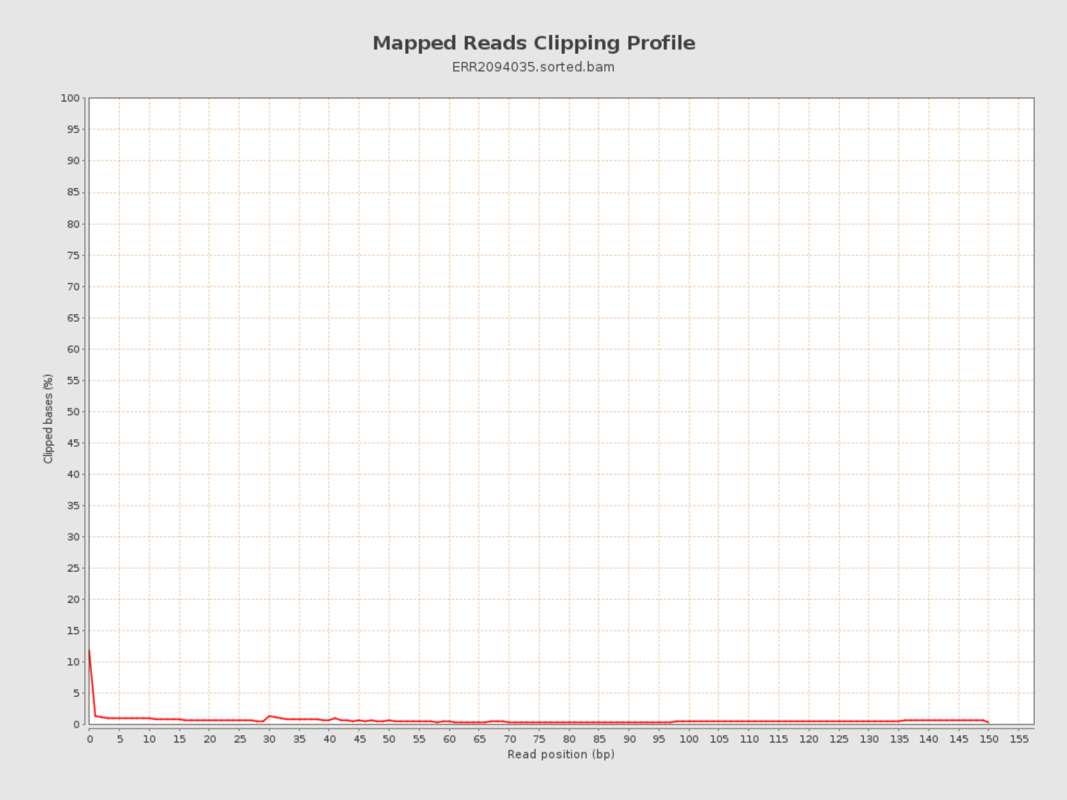
8. Results : Mapped Reads Nucleotide Content



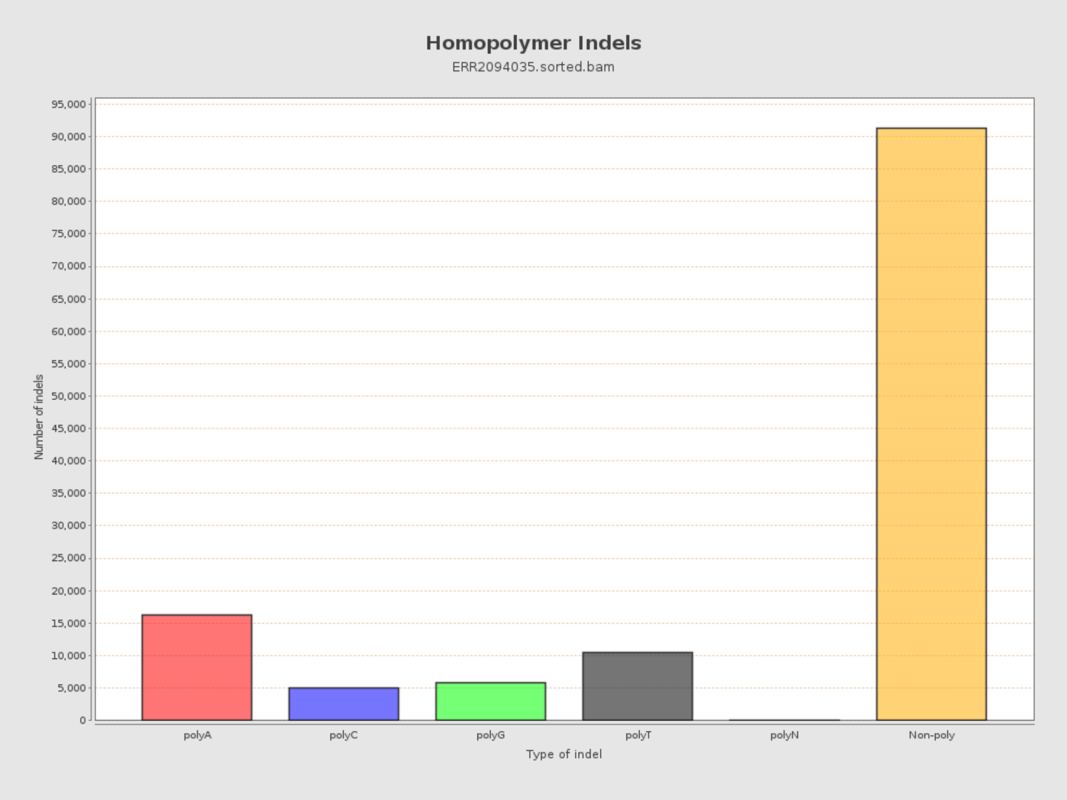
9. Results : Mapped Reads GC-content Distribution



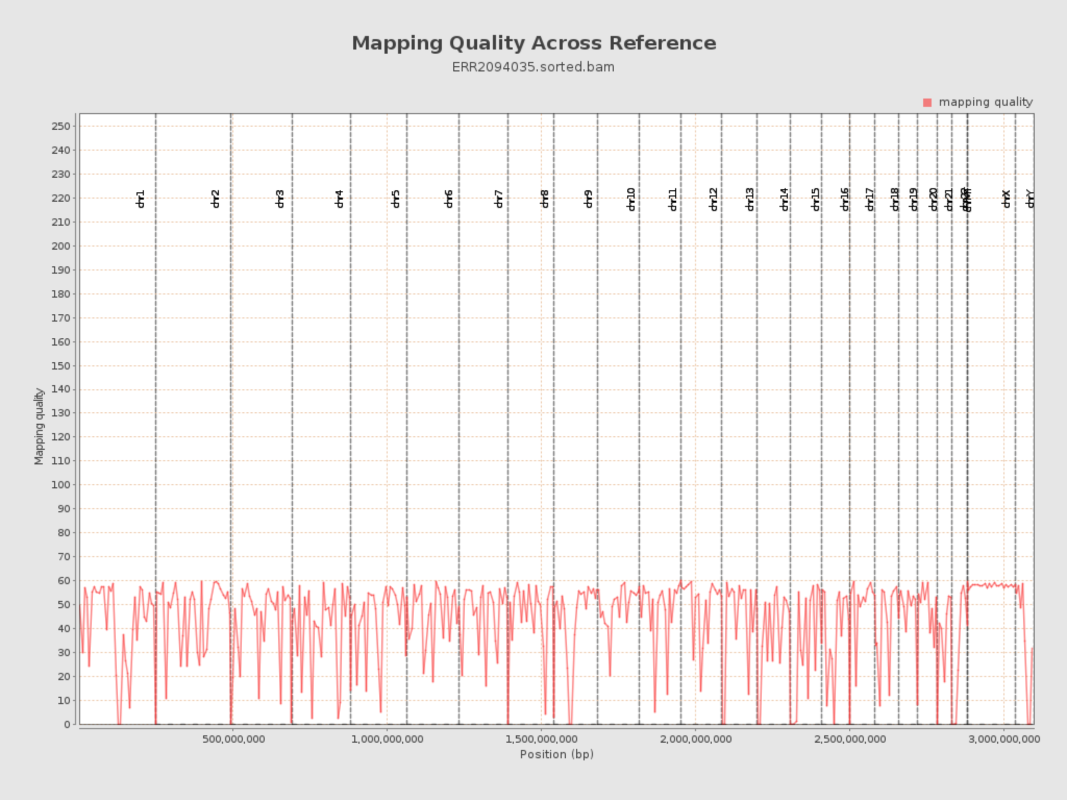
10. Results : Mapped Reads Clipping Profile



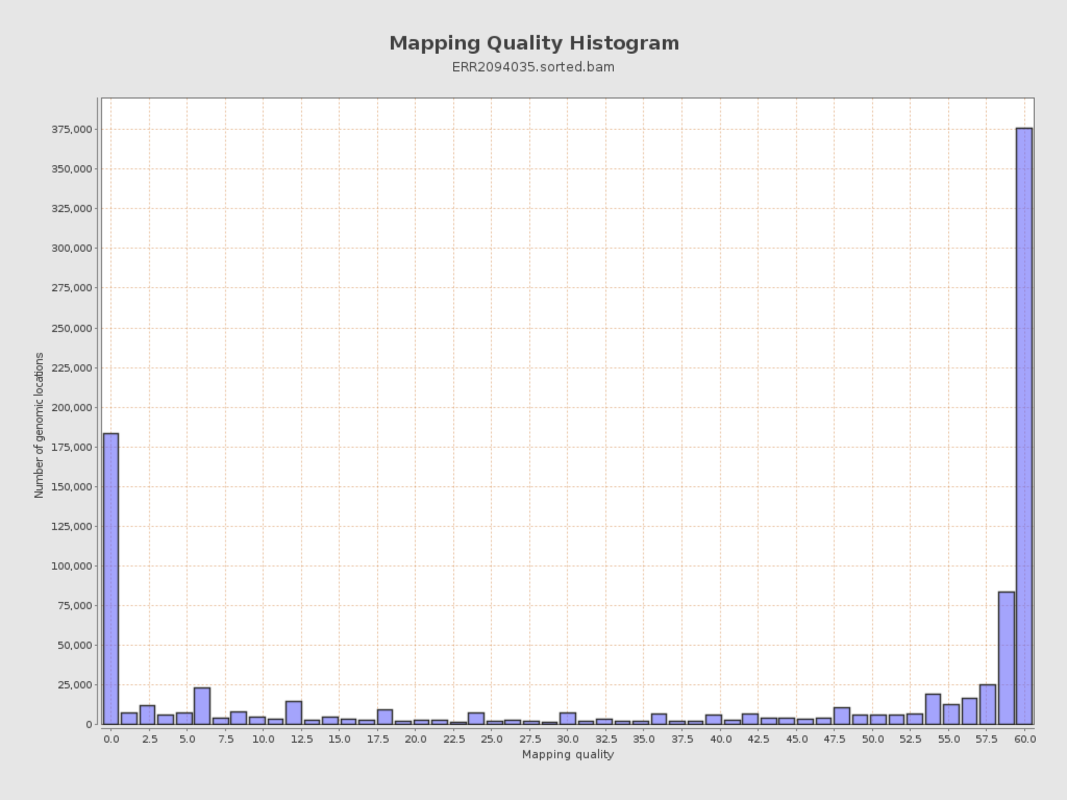
11. Results : Homopolymer Indels



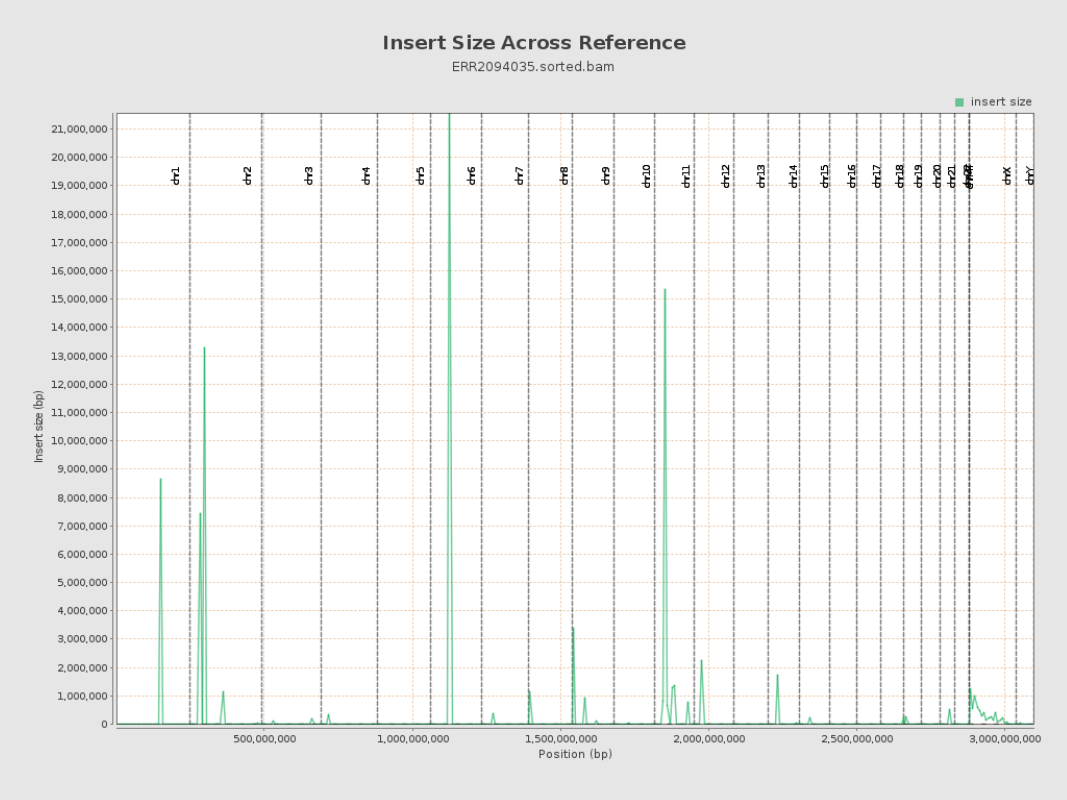
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram