Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:04:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094020.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_ERR2094020 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094020_1.fastq.gz ERR2094020_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:04:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	577,080
Mapped reads	438,157 / 75.93%
Unmapped reads	138,923 / 24.07%
Mapped paired reads	438,157 / 75.93%
Mapped reads, first in pair	219,536 / 38.04%
Mapped reads, second in pair	218,621 / 37.88%
Mapped reads, both in pair	434,014 / 75.21%
Mapped reads, singletons	4,143 / 0.72%
Secondary alignments	0
Supplementary alignments	12,456 / 2.16%
Read min/max/mean length	30 / 151 / 125.44
Duplicated reads (estimated)	437,604 / 75.83%
Duplication rate	39.8%
Clipped reads	153,735 / 26.64%

2.2. ACGT Content

Number/percentage of A's	17,387,024 / 29.64%
Number/percentage of C's	12,174,097 / 20.75%
Number/percentage of T's	16,663,567 / 28.41%
Number/percentage of G's	12,431,968 / 21.19%
Number/percentage of N's	766 / 0%

GC Percentage	41.95%

2.3. Coverage

Mean	0.0192
Standard Deviation	19.4648

2.4. Mapping Quality

Mean Mapping Quality	23.32

2.5. Insert size

Mean	170,443.69
Standard Deviation	3,854,176.04
P25/Median/P75	151 / 191 / 217

2.6. Mismatches and indels

General error rate	2.72%
Mismatches	1,557,698
Insertions	20,278
Mapped reads with at least one insertion	4.52%
Deletions	120,207
Mapped reads with at least one deletion	26.48%
Homopolymer indels	22.9%

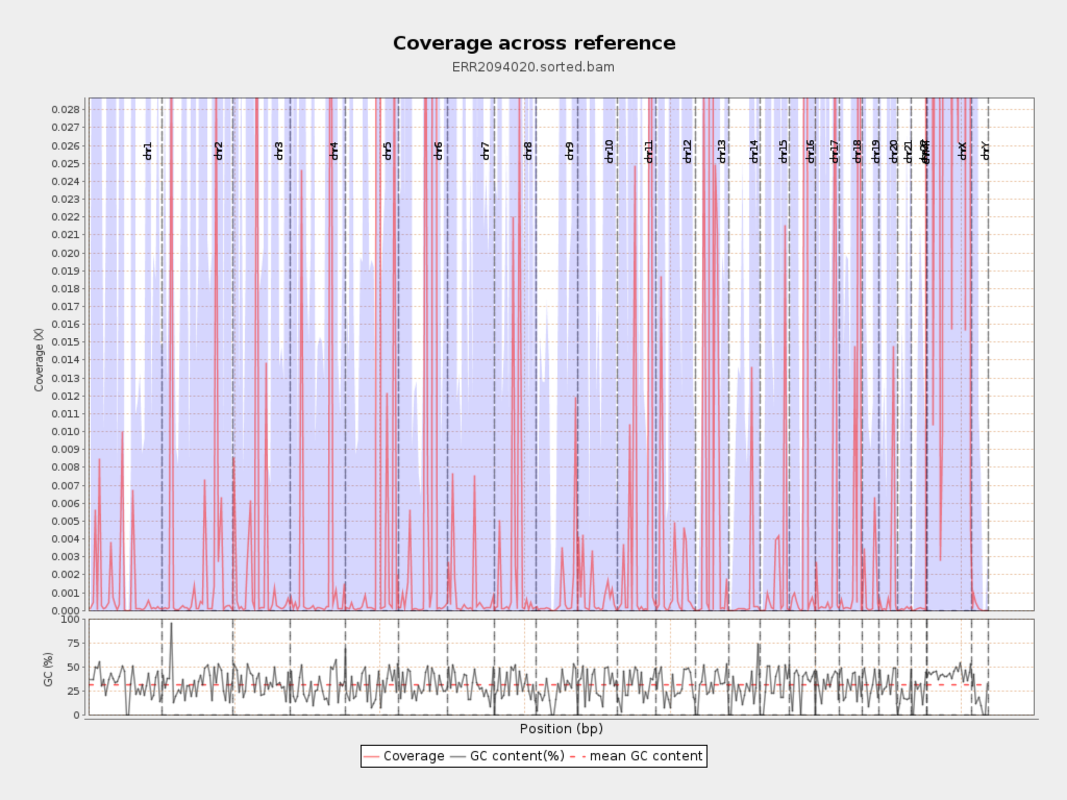
2.7. Chromosome stats

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

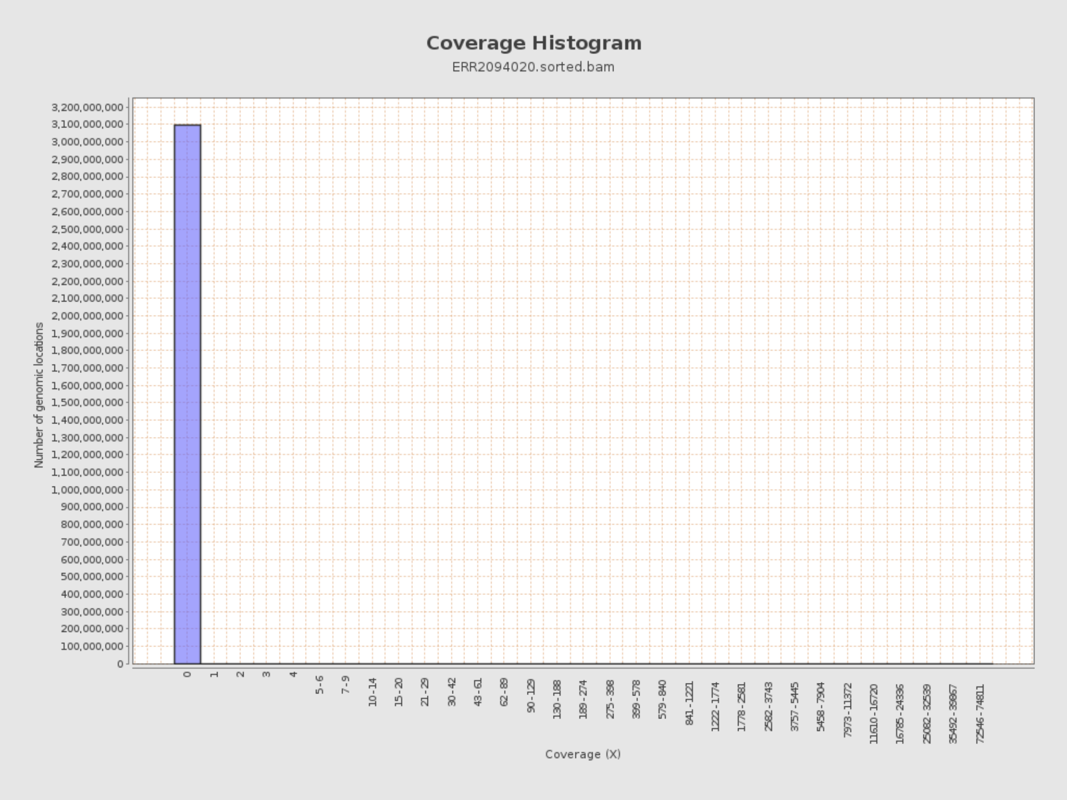
		bases	**coverage**	**deviation**
chr1	249250621	307668	0.0012	0.6638
chr2	243199373	678492	0.0028	1.7102
chr3	198022430	614717	0.0031	1.8647
chr4	191154276	671486	0.0035	2.7799
chr5	180915260	2298392	0.0127	12.0097
chr6	171115067	2079793	0.0122	11.2447
chr7	159138663	173461	0.0011	0.5751
chr8	146364022	474769	0.0032	1.6331
chr9	141213431	147947	0.001	0.5257
chr10	135534747	137122	0.001	0.331
chr11	135006516	781724	0.0058	3.3786
chr12	133851895	276304	0.0021	1.0265
chr13	115169878	4822698	0.0419	27.3133
chr14	107349540	114702	0.0011	1.0264
chr15	102531392	247243	0.0024	1.311
chr16	90354753	764721	0.0085	6.6123
chr17	81195210	299705	0.0037	2.3789
chr18	78077248	648619	0.0083	4.8394
chr19	59128983	81970	0.0014	0.4868
chr20	63025520	127757	0.002	1.5095
chr21	48129895	4989	0.0001	0.0177
chr22	51304566	3504	0.0001	0.0131
chrMT	16571	24118767	1,455.4805	7,120.3253
chrX	155270560	19422357	0.1251	31.3081

chrY	59373566	11776	0.0002	0.0875

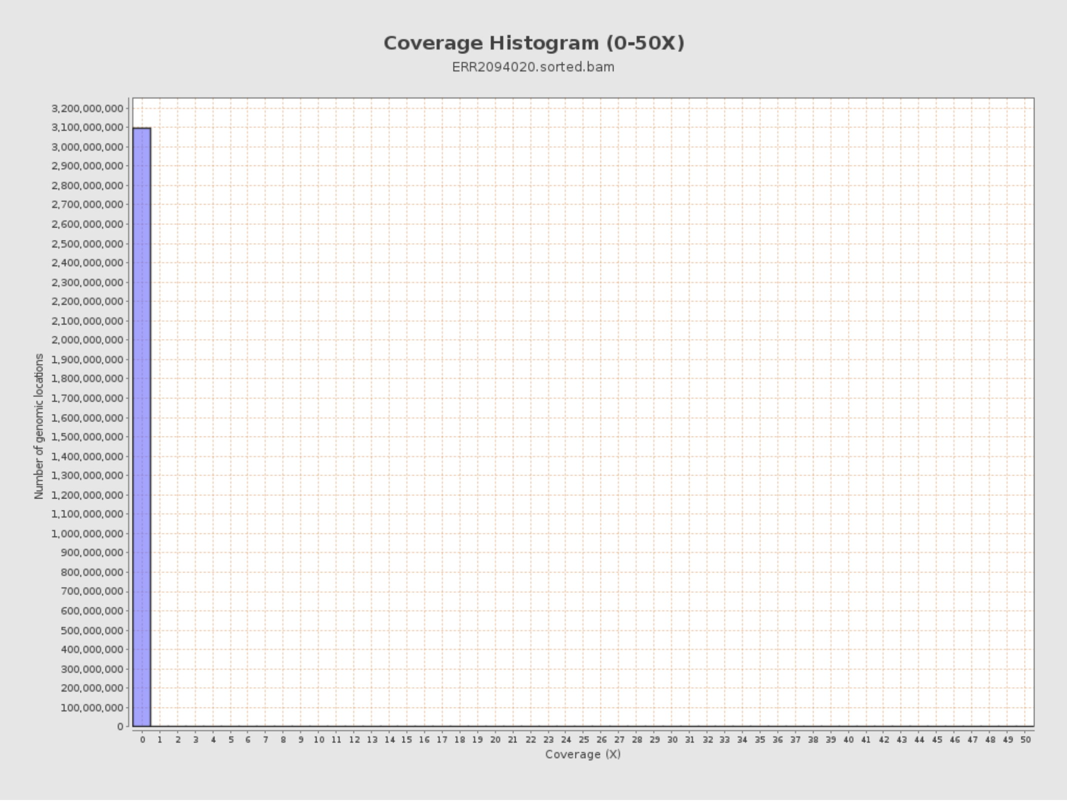
3. Results : Coverage across reference



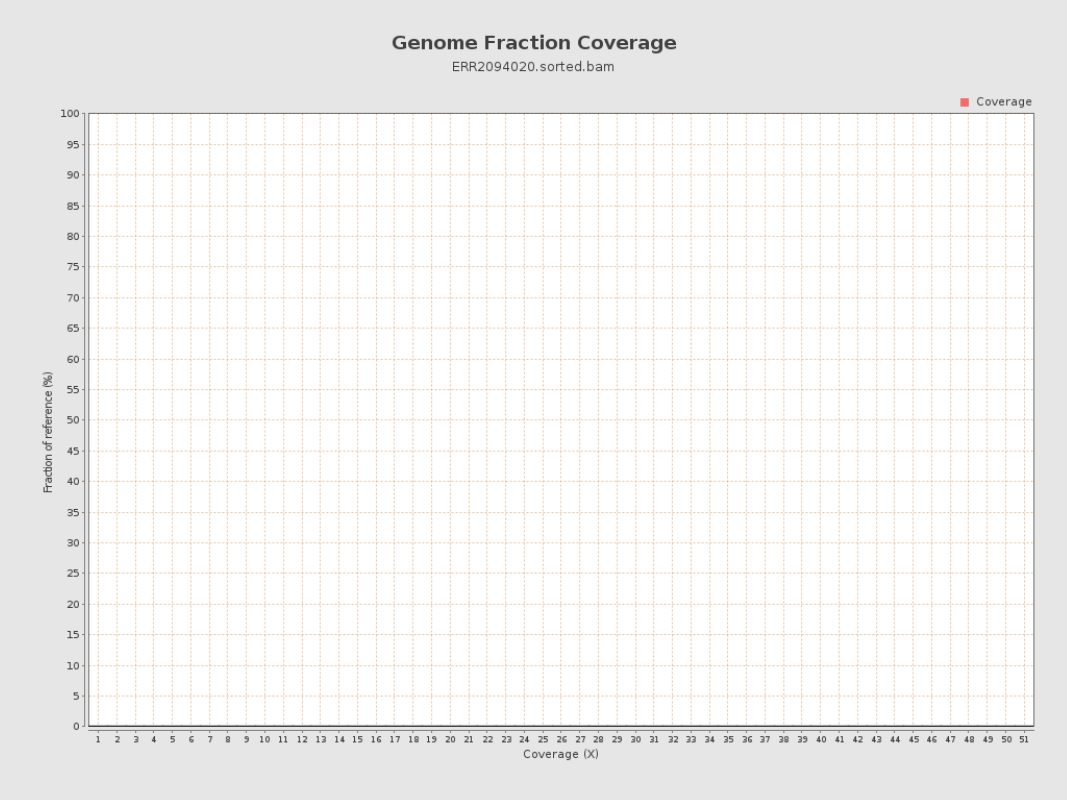
4. Results : Coverage Histogram



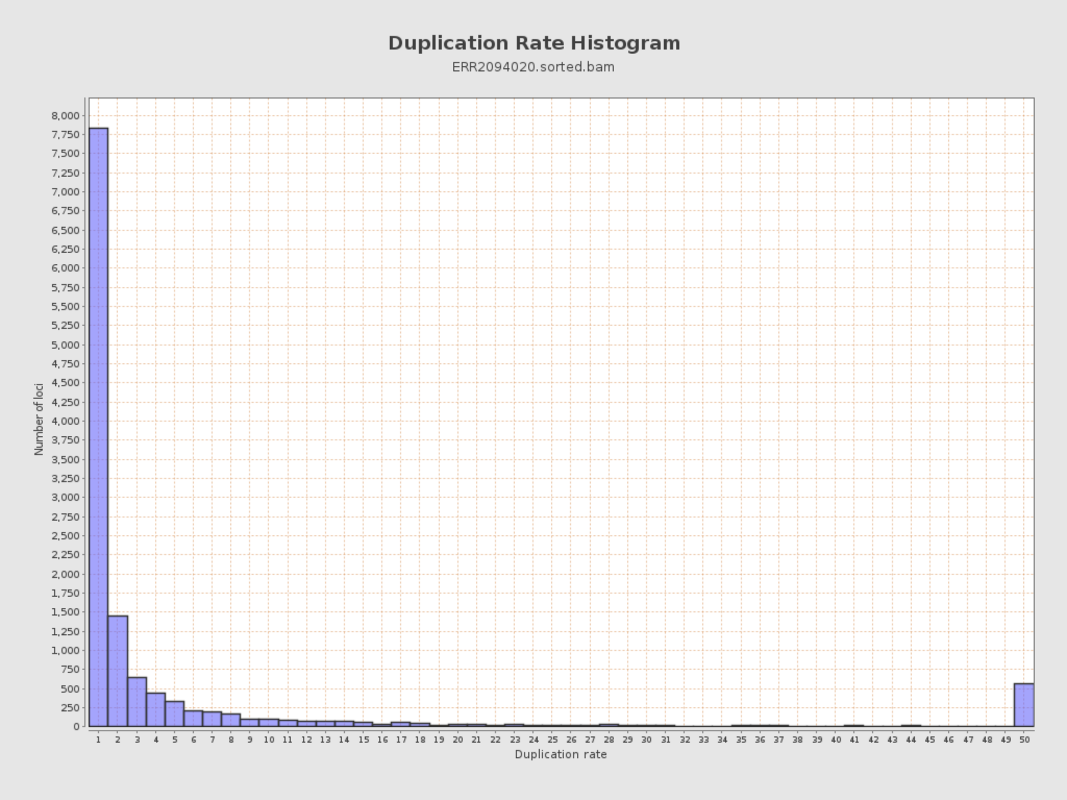
5. Results : Coverage Histogram (0-50X)



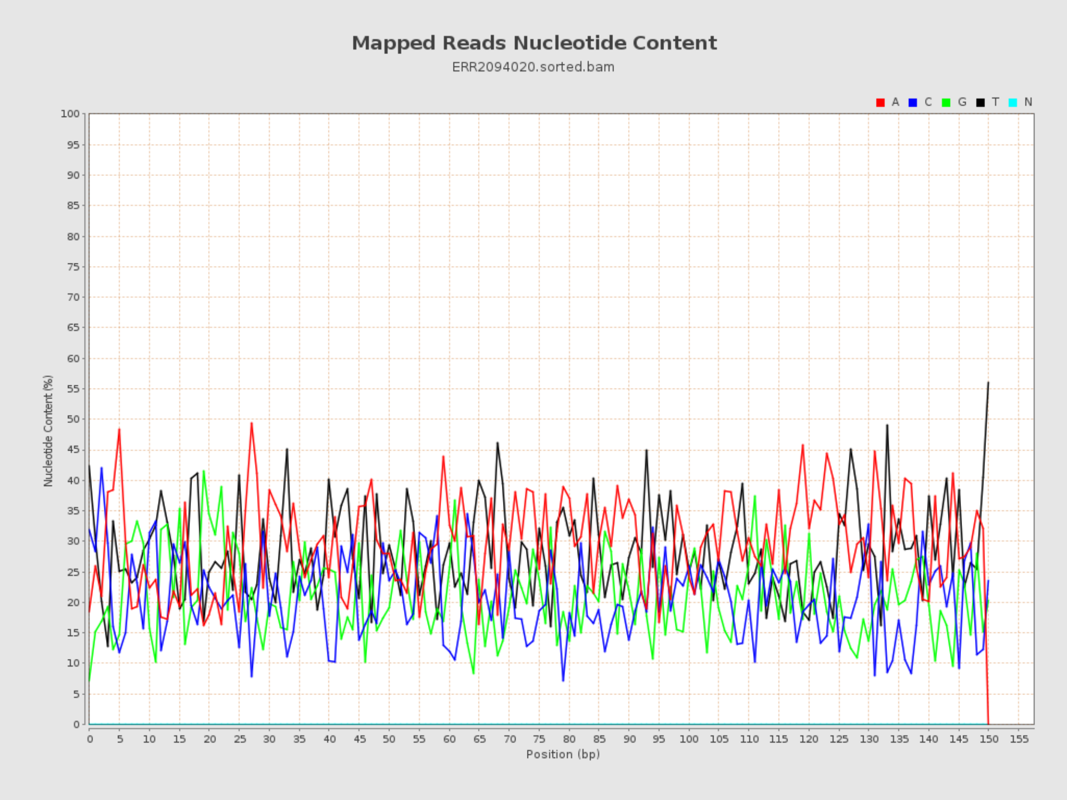
6. Results : Genome Fraction Coverage



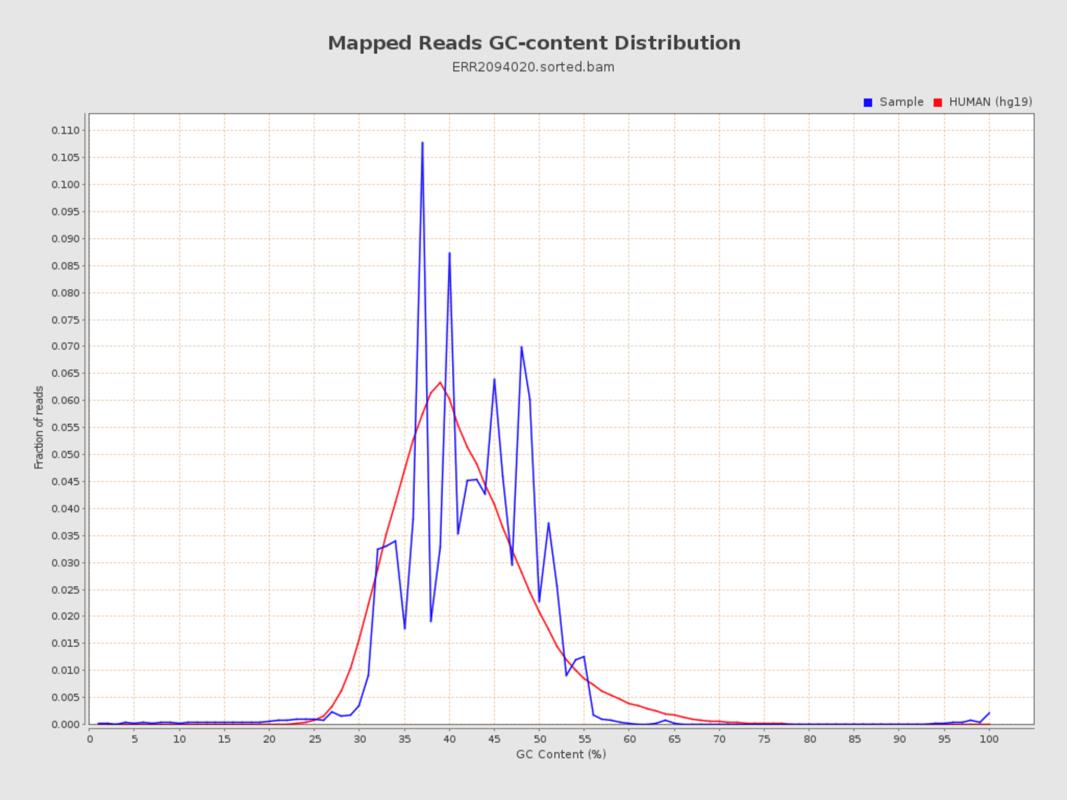
7. Results : Duplication Rate Histogram



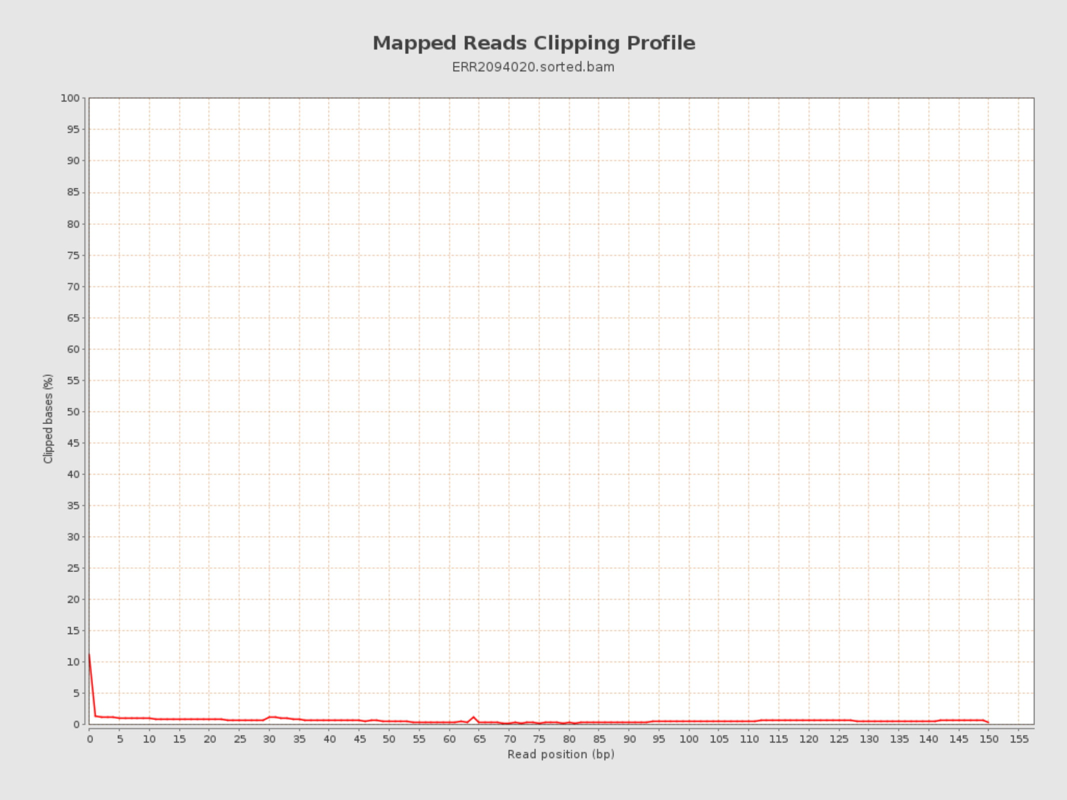
8. Results : Mapped Reads Nucleotide Content



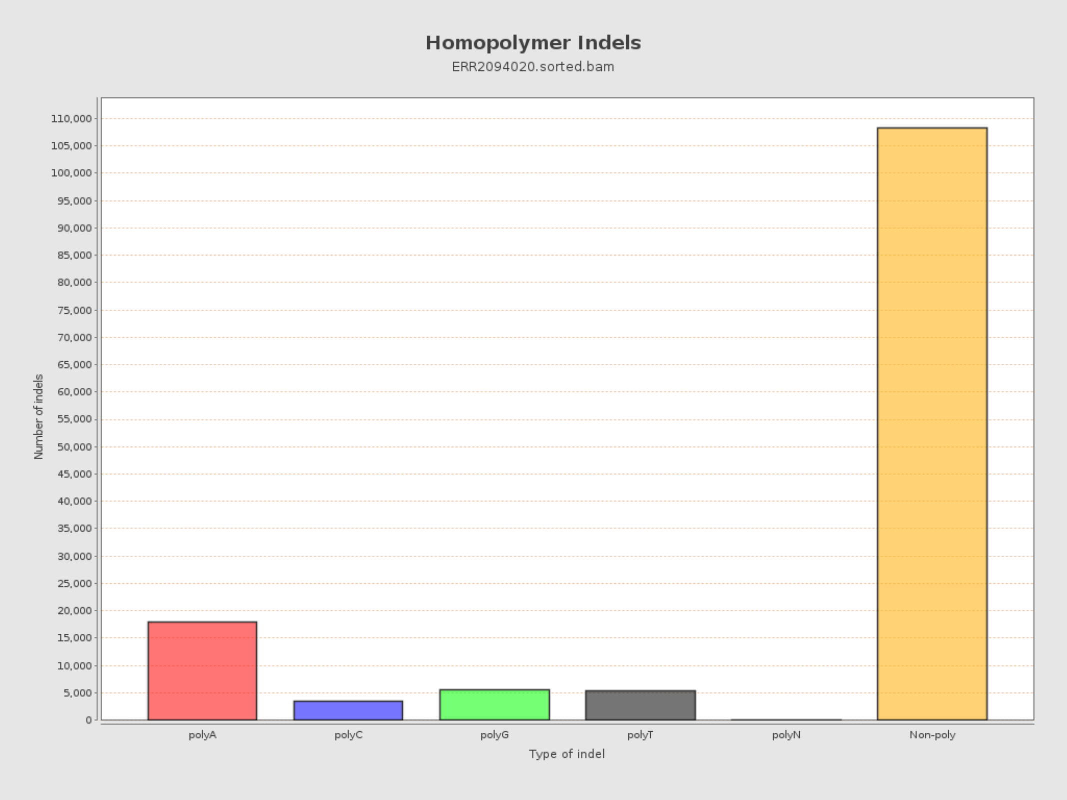
9. Results : Mapped Reads GC-content Distribution



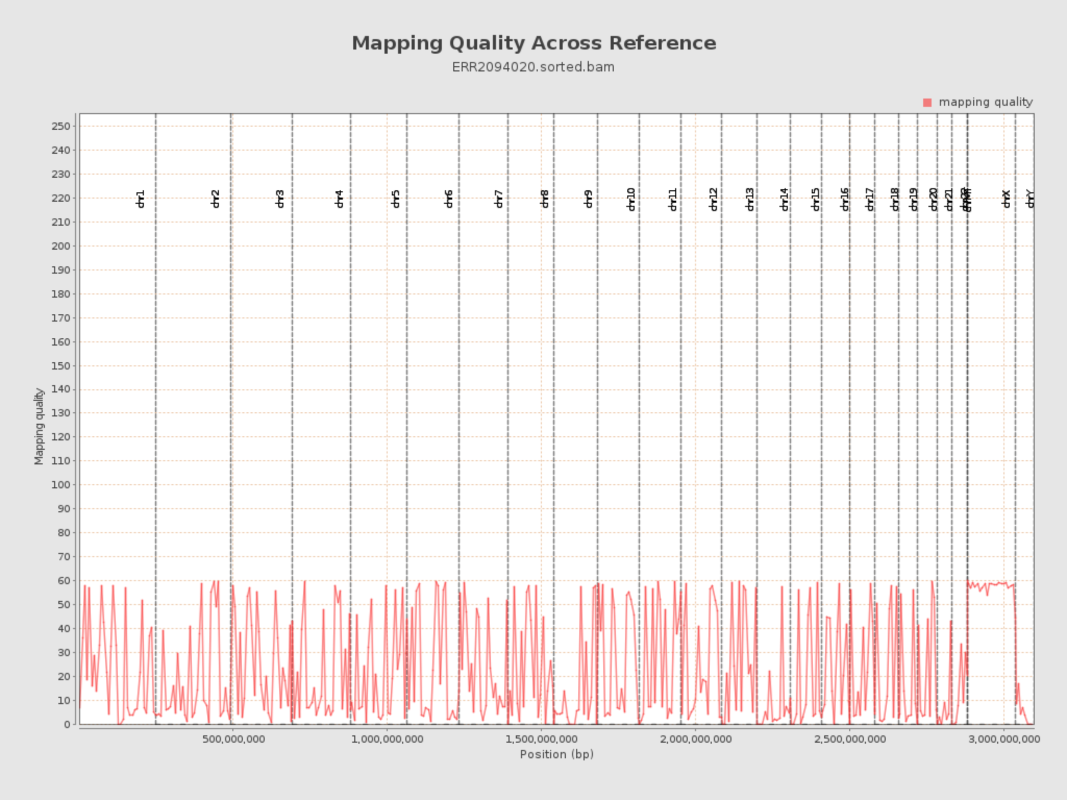
10. Results : Mapped Reads Clipping Profile



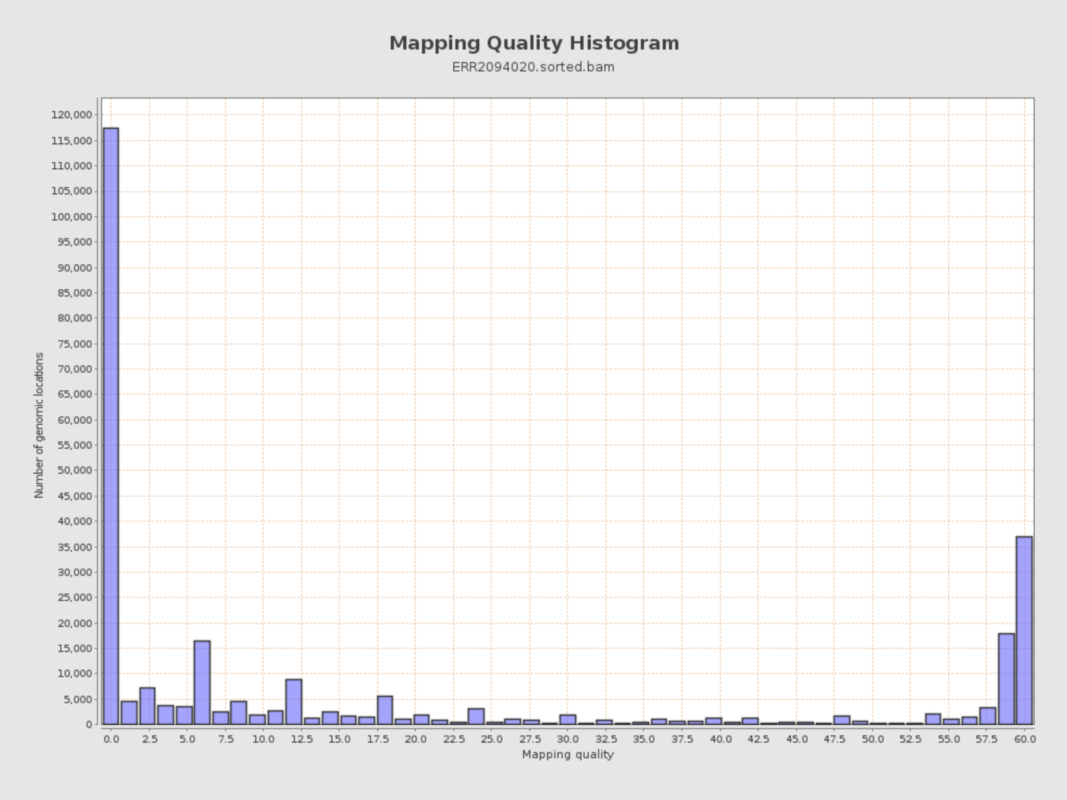
11. Results : Homopolymer Indels



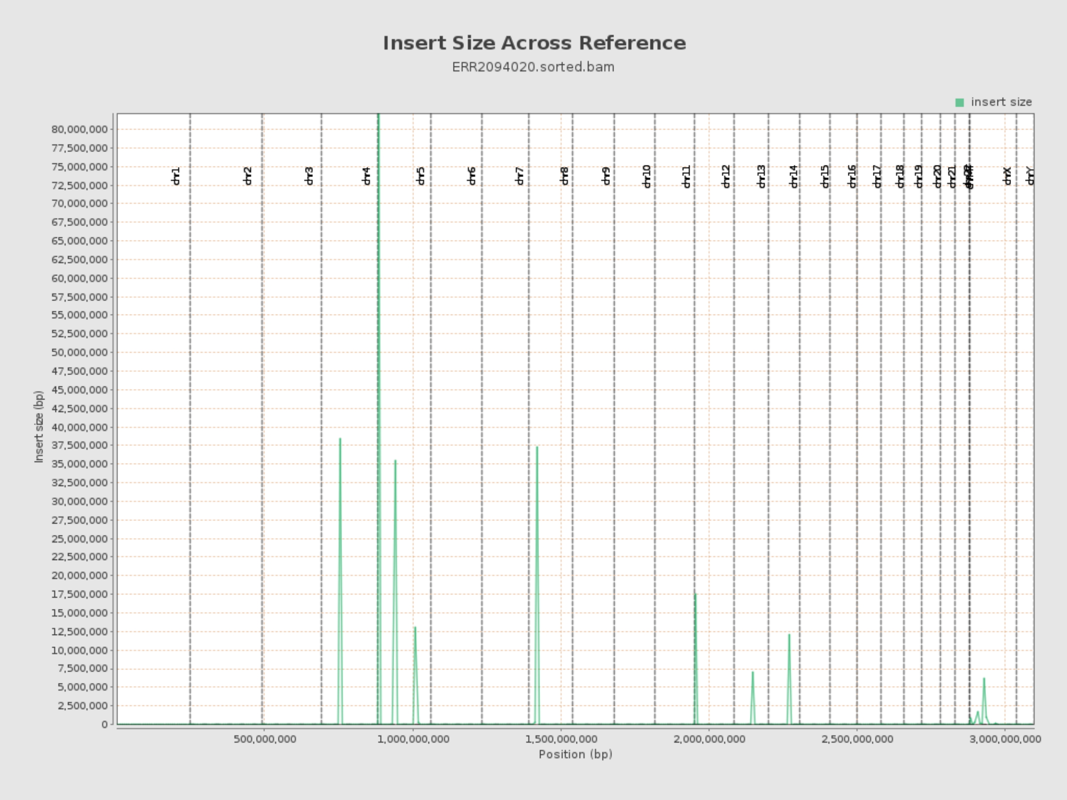
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram