Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 03:27:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094136.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_ERR2094136 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094136_1.fastq.gz ERR2094136_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 03:27:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	471,618
Mapped reads	438,770 / 93.04%
Unmapped reads	32,848 / 6.96%
Mapped paired reads	438,770 / 93.04%
Mapped reads, first in pair	220,716 / 46.8%
Mapped reads, second in pair	218,054 / 46.24%
Mapped reads, both in pair	433,612 / 91.94%
Mapped reads, singletons	5,158 / 1.09%
Secondary alignments	0
Supplementary alignments	8,648 / 1.83%
Read min/max/mean length	30 / 151 / 141.86
Duplicated reads (estimated)	422,809 / 89.65%
Duplication rate	53.92%
Clipped reads	255,065 / 54.08%

2.2. ACGT Content

Number/percentage of A's	14,848,450 / 26.24%
Number/percentage of C's	13,001,991 / 22.97%
Number/percentage of T's	14,929,402 / 26.38%
Number/percentage of G's	13,812,497 / 24.41%
Number/percentage of N's	604 / 0%

GC Percentage	47.38%

2.3. Coverage

Mean	0.0183
Standard Deviation	17.519

2.4. Mapping Quality

Mean Mapping Quality	35.07

2.5. Insert size

Mean	37,288.08
Standard Deviation	1,695,031.75
P25/Median/P75	131 / 212 / 238

2.6. Mismatches and indels

General error rate	1.6%
Mismatches	877,372
Insertions	16,258
Mapped reads with at least one insertion	3.62%
Deletions	39,990
Mapped reads with at least one deletion	8.94%
Homopolymer indels	53.71%

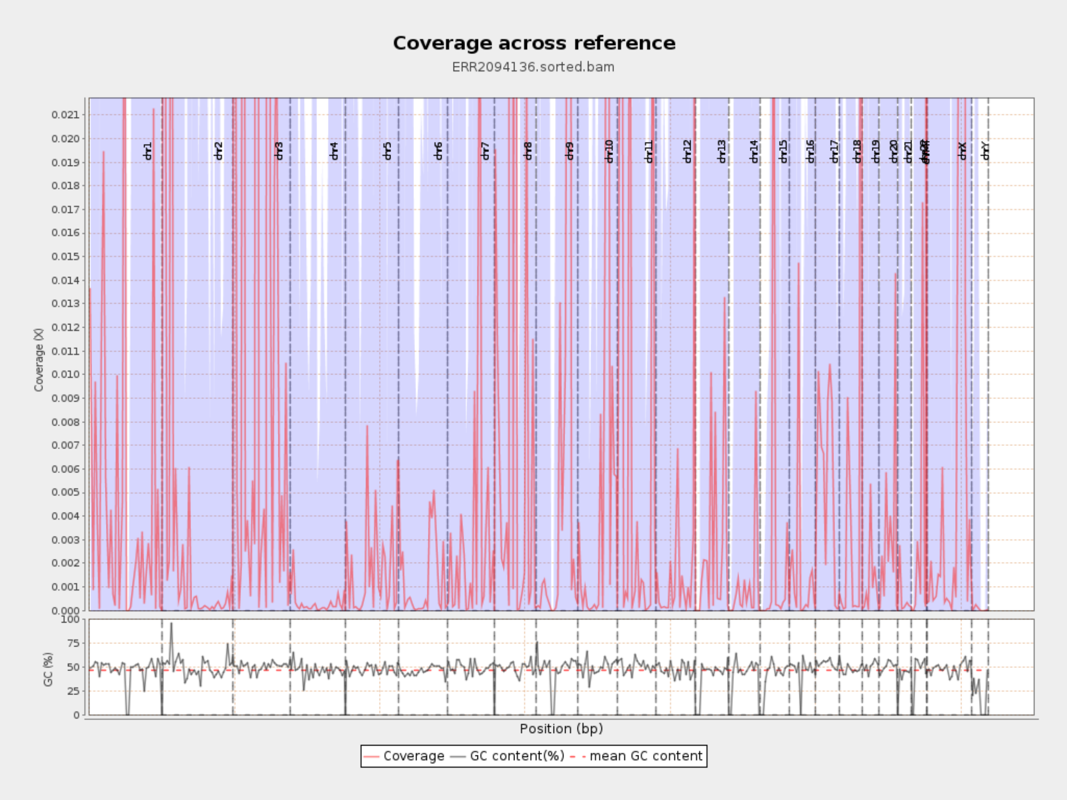
2.7. Chromosome stats

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

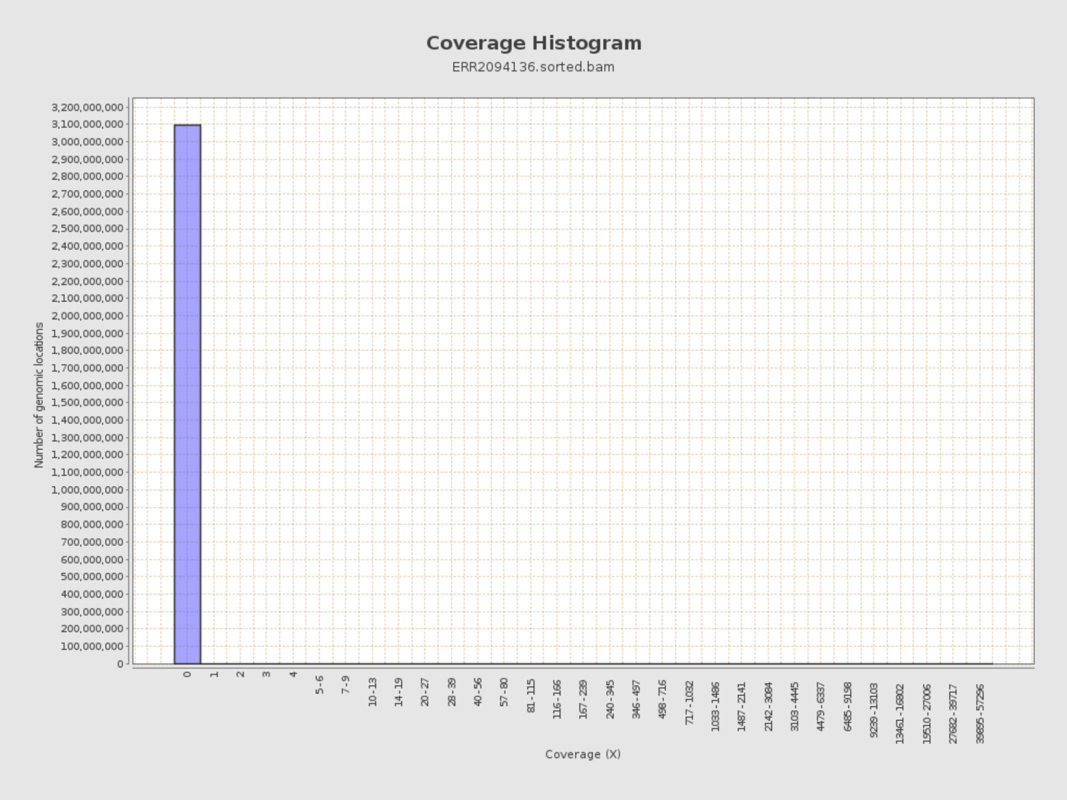
		bases	coverage	deviation
chr1	249250621	1278885	0.0051	0.8898
chr2	243199373	1006828	0.0041	1.4342
chr3	198022430	5562260	0.0281	7.6463
chr4	191154276	61115	0.0003	0.0729
chr5	180915260	296636	0.0016	0.3467
chr6	171115067	237364	0.0014	0.2716
chr7	159138663	527517	0.0033	1.7212
chr8	146364022	7179986	0.0491	12.2846
chr9	141213431	1329051	0.0094	2.4306
chr10	135534747	765996	0.0057	0.6934
chr11	135006516	1106856	0.0082	1.5497
chr12	133851895	228440	0.0017	0.2945
chr13	115169878	341692	0.003	0.6448
chr14	107349540	124045	0.0012	0.2576
chr15	102531392	290632	0.0028	0.5097
chr16	90354753	178875	0.002	0.4994
chr17	81195210	451304	0.0056	0.7186
chr18	78077248	384667	0.0049	1.2859
chr19	59128983	74534	0.0013	0.1915
chr20	63025520	239792	0.0038	0.5281
chr21	48129895	27905	0.0006	0.1187
chr22	51304566	167533	0.0033	1.3496
chrMT	16571	32760834	1,976.998	7,141.8614
chrX	155270560	2148411	0.0138	4.8968

chrY	59373566	3772	0.0001	0.0178

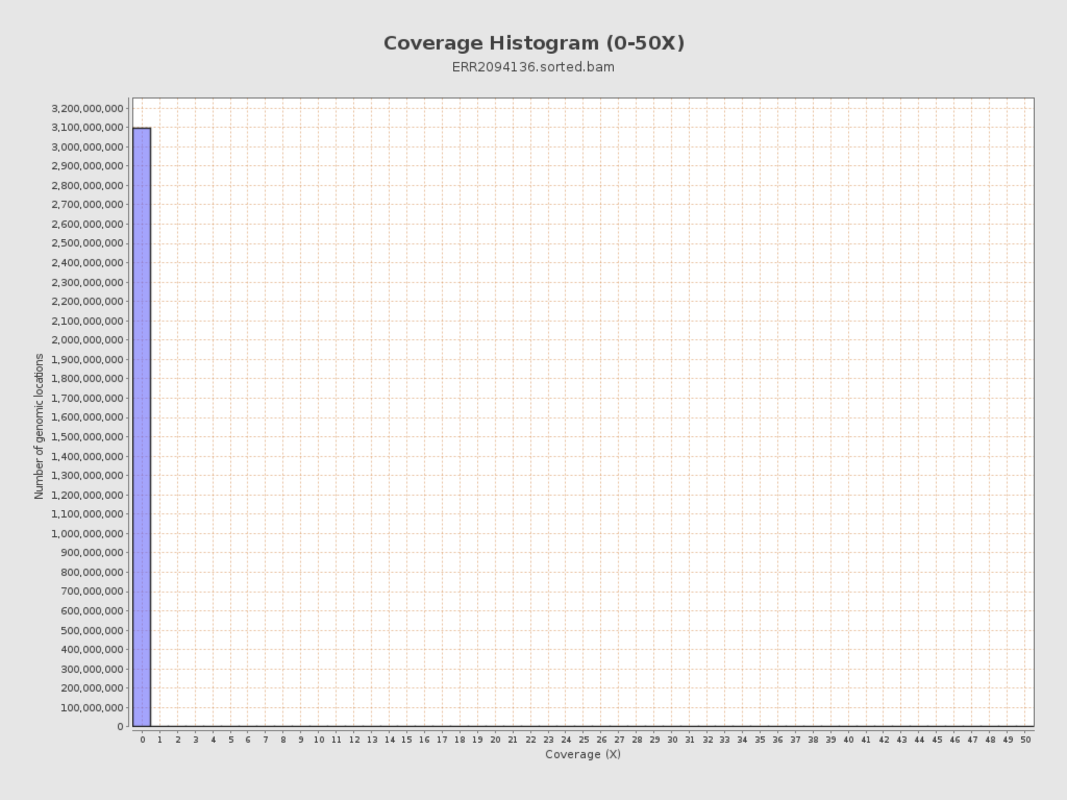
3. Results : Coverage across reference



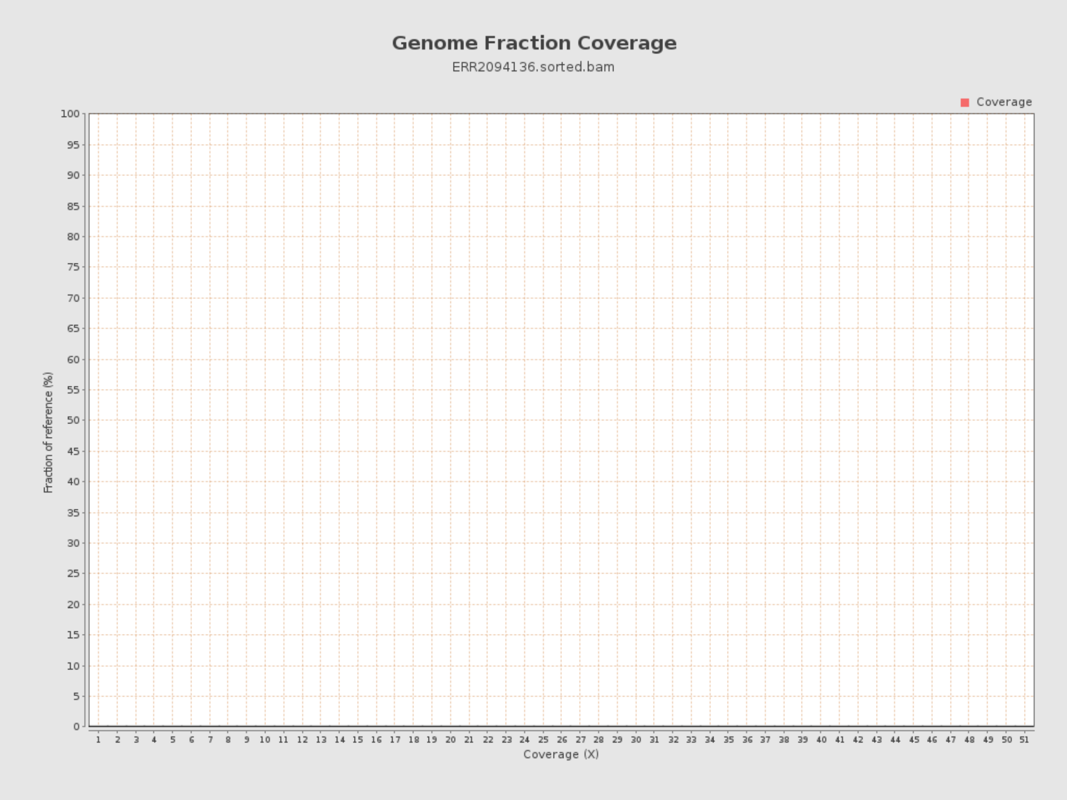
4. Results : Coverage Histogram



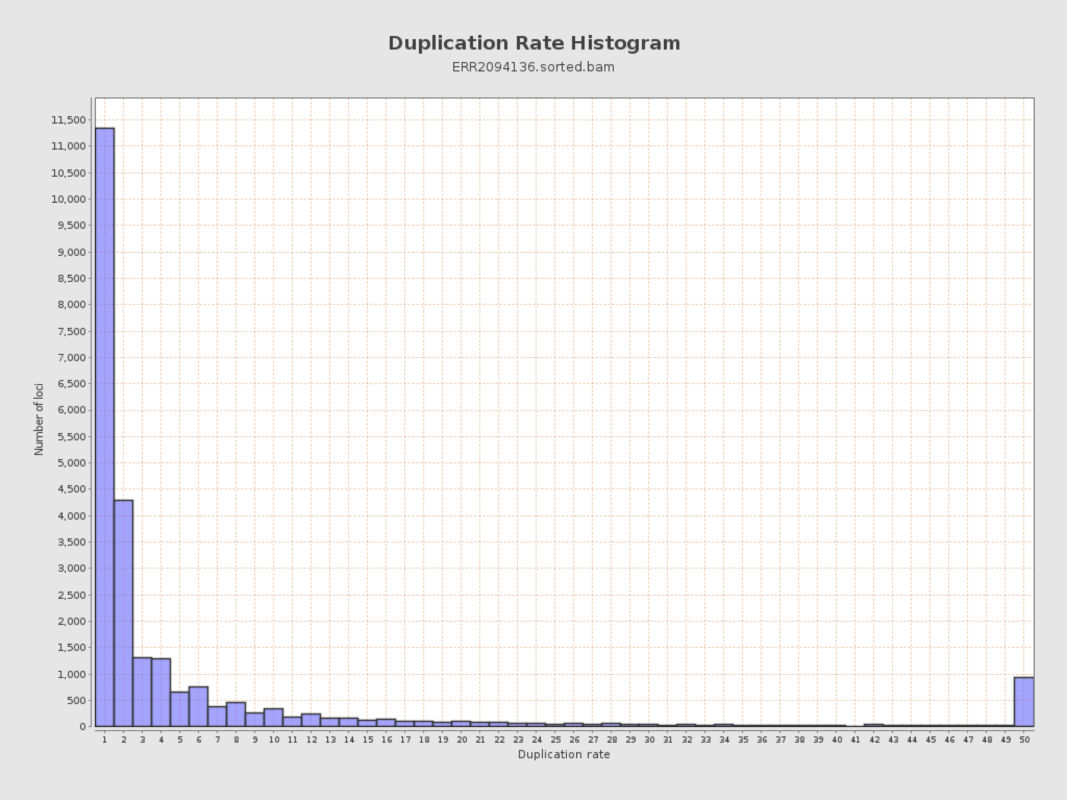
5. Results : Coverage Histogram (0-50X)



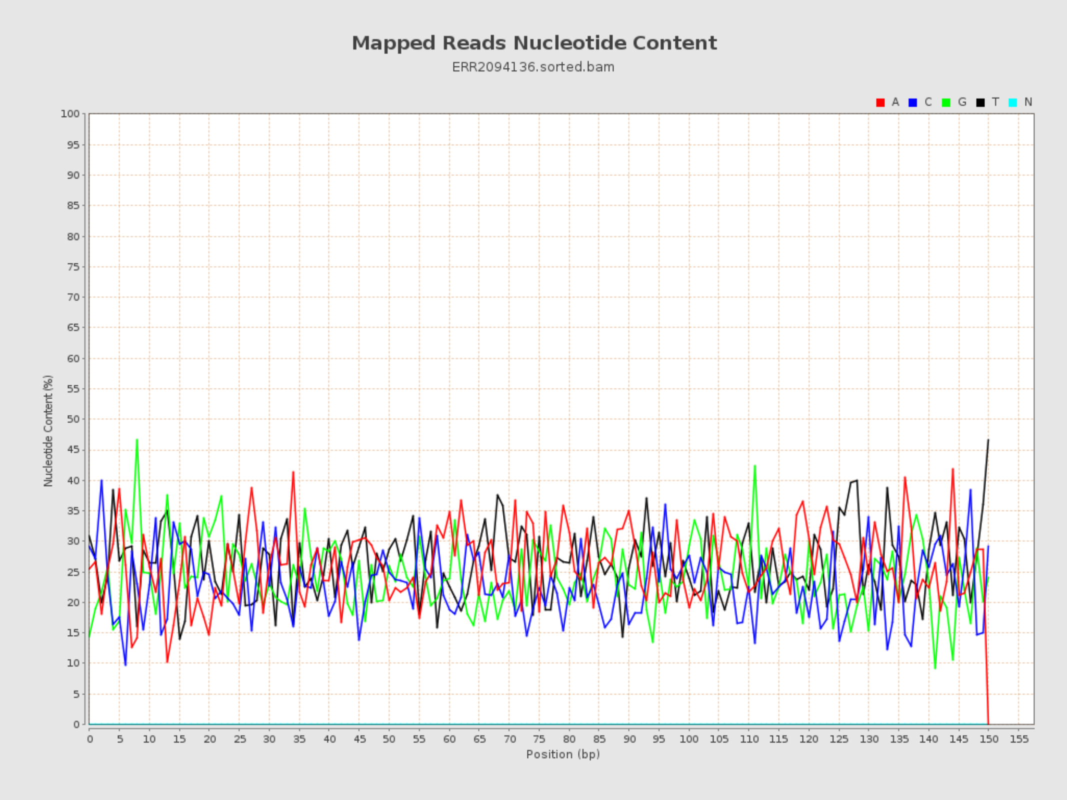
6. Results : Genome Fraction Coverage



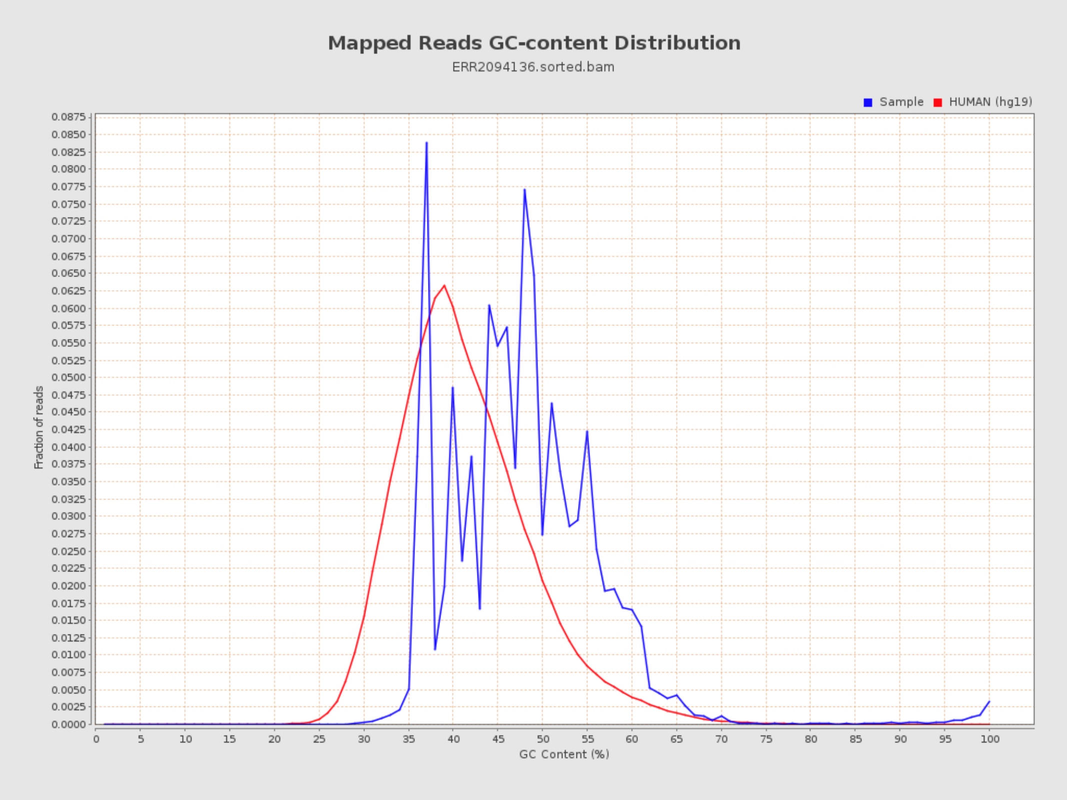
7. Results : Duplication Rate Histogram



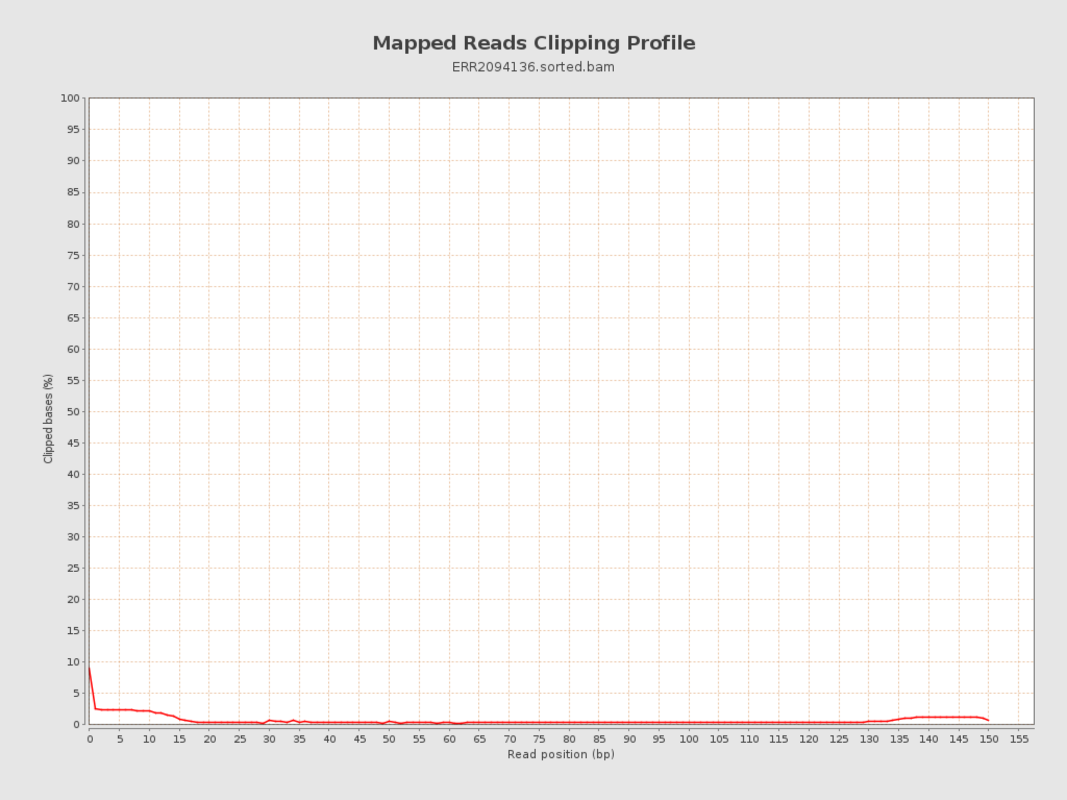
8. Results : Mapped Reads Nucleotide Content



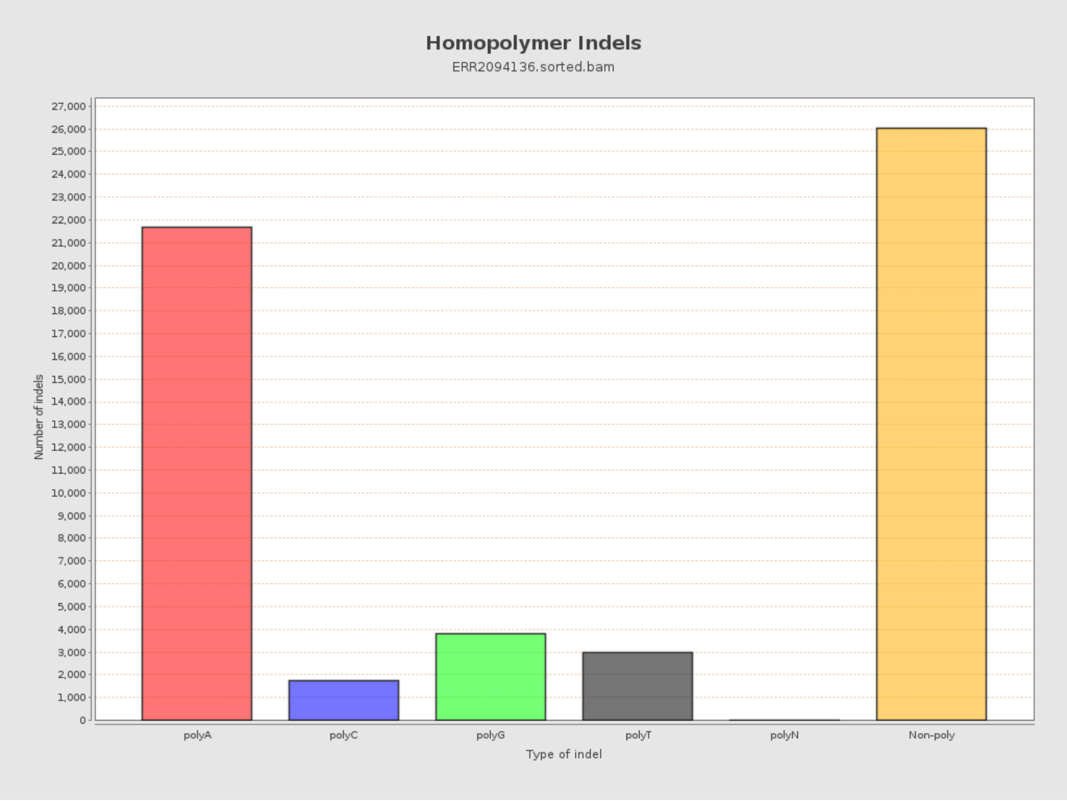
9. Results : Mapped Reads GC-content Distribution



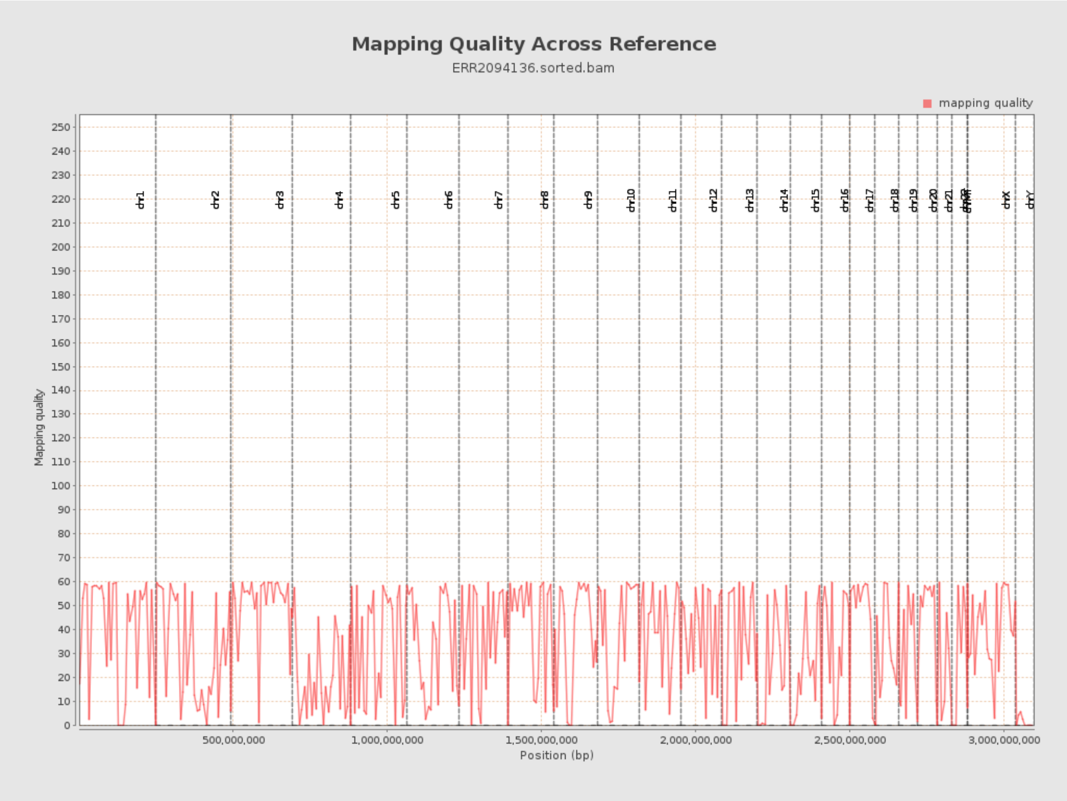
10. Results : Mapped Reads Clipping Profile



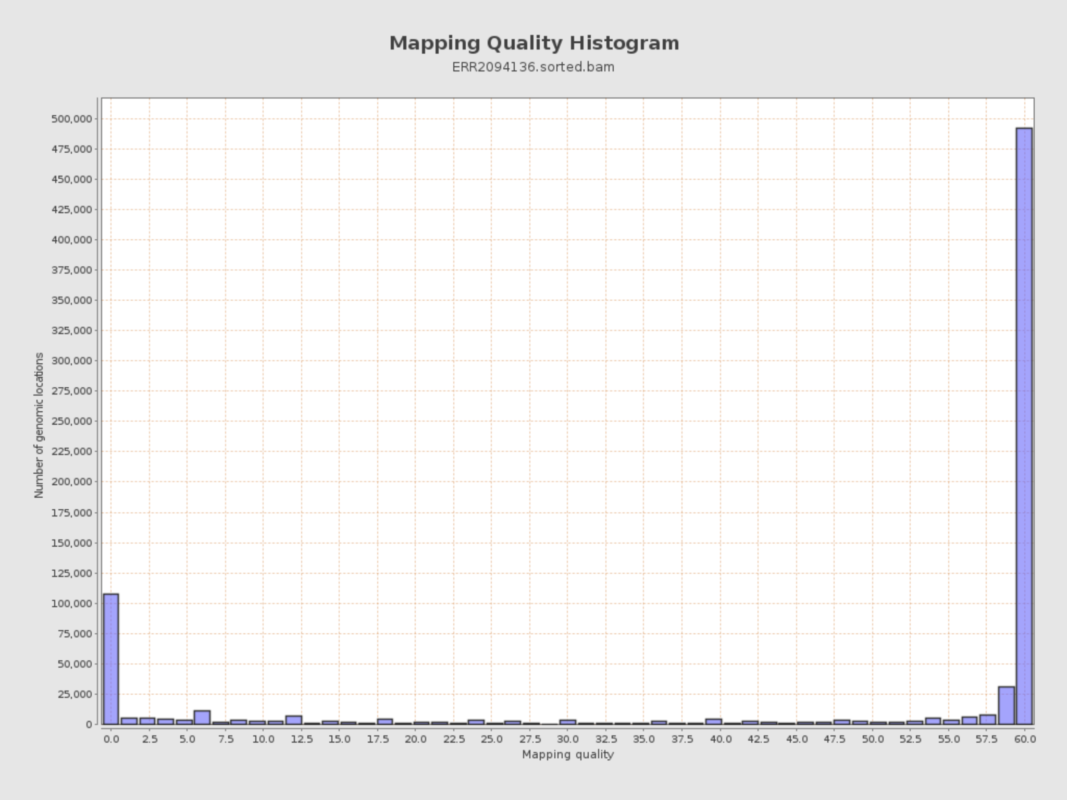
11. Results : Homopolymer Indels



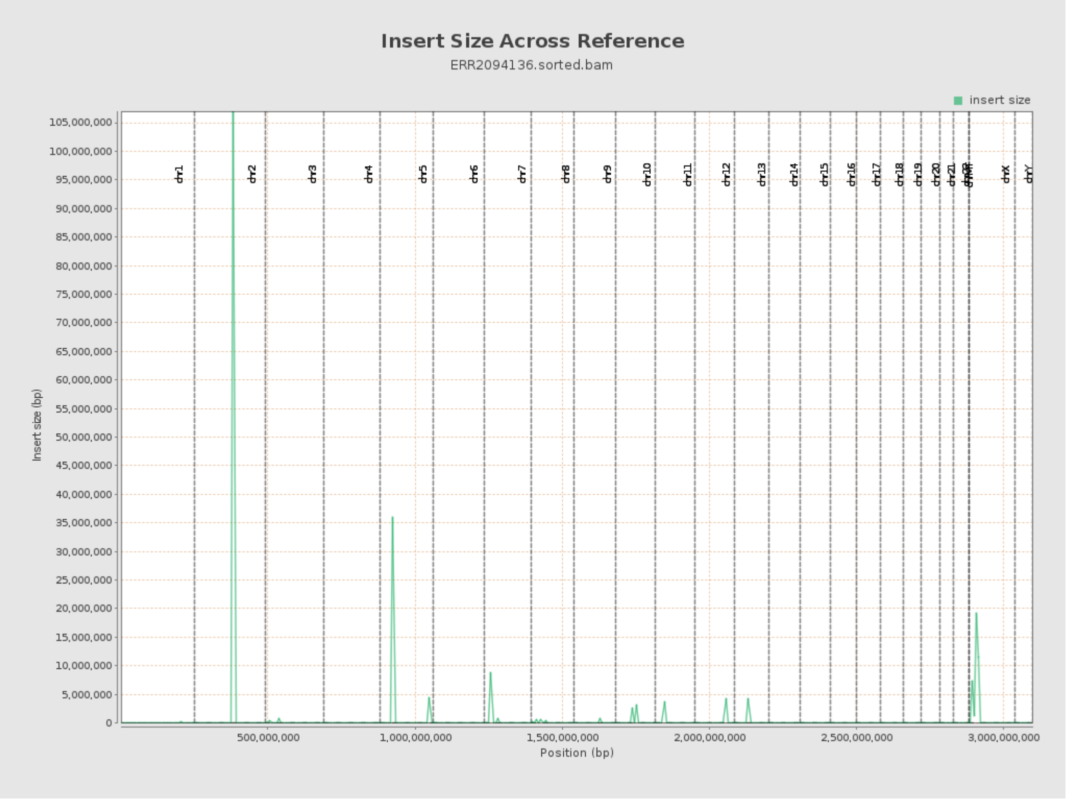
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram