Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:57:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094120.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_ERR2094120 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094120_1.fastq.gz ERR2094120_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:57:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	970,798
Mapped reads	906,544 / 93.38%
Unmapped reads	64,254 / 6.62%
Mapped paired reads	906,544 / 93.38%
Mapped reads, first in pair	454,681 / 46.84%
Mapped reads, second in pair	451,863 / 46.55%
Mapped reads, both in pair	902,182 / 92.93%
Mapped reads, singletons	4,362 / 0.45%
Secondary alignments	0
Supplementary alignments	14,159 / 1.46%
Read min/max/mean length	30 / 151 / 144.29
Duplicated reads (estimated)	912,568 / 94%
Duplication rate	42.72%
Clipped reads	185,104 / 19.07%

2.2. ACGT Content

Number/percentage of A's	36,871,048 / 28.08%
Number/percentage of C's	27,350,610 / 20.83%
Number/percentage of T's	38,006,833 / 28.94%
Number/percentage of G's	29,085,909 / 22.15%
Number/percentage of N's	1,580 / 0%

GC Percentage	42.98%

2.3. Coverage

Mean	0.0426
Standard Deviation	66.1078

2.4. Mapping Quality

Mean Mapping Quality	14.8

2.5. Insert size

Mean	33,446.73
Standard Deviation	1,816,527.5
P25/Median/P75	217 / 237 / 261

2.6. Mismatches and indels

General error rate	2.03%
Mismatches	2,596,293
Insertions	43,053
Mapped reads with at least one insertion	4.69%
Deletions	118,911
Mapped reads with at least one deletion	12.83%
Homopolymer indels	57.77%

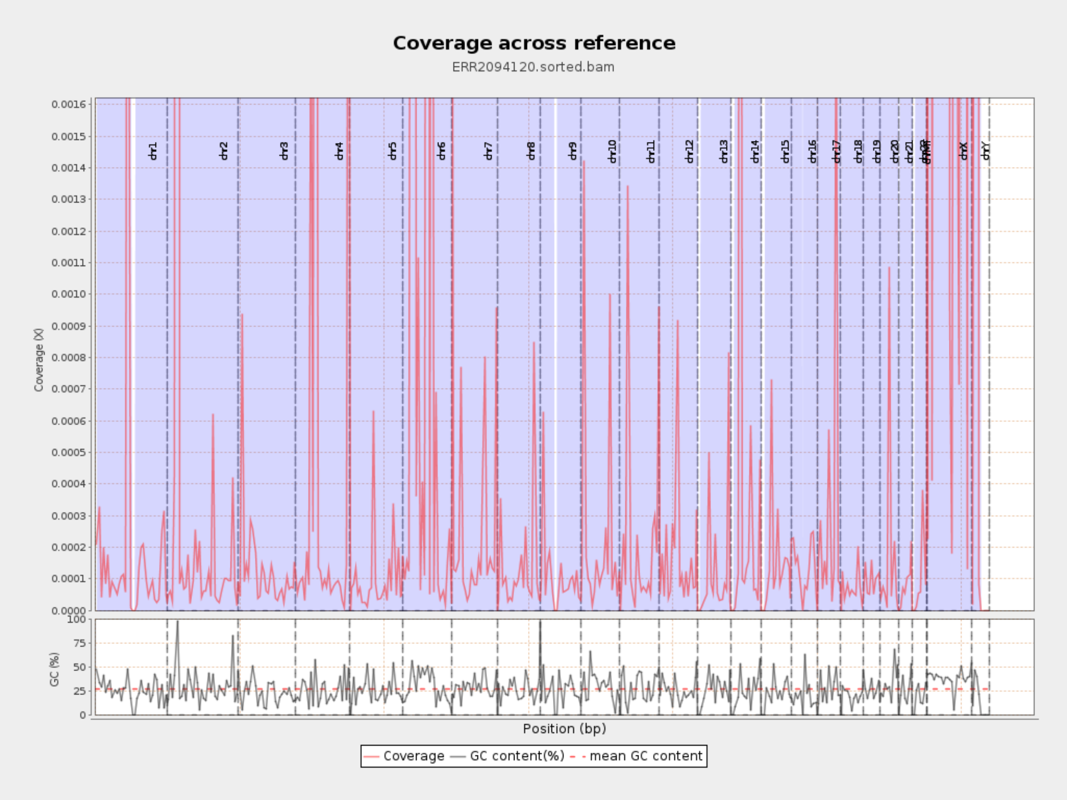
2.7. Chromosome stats

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

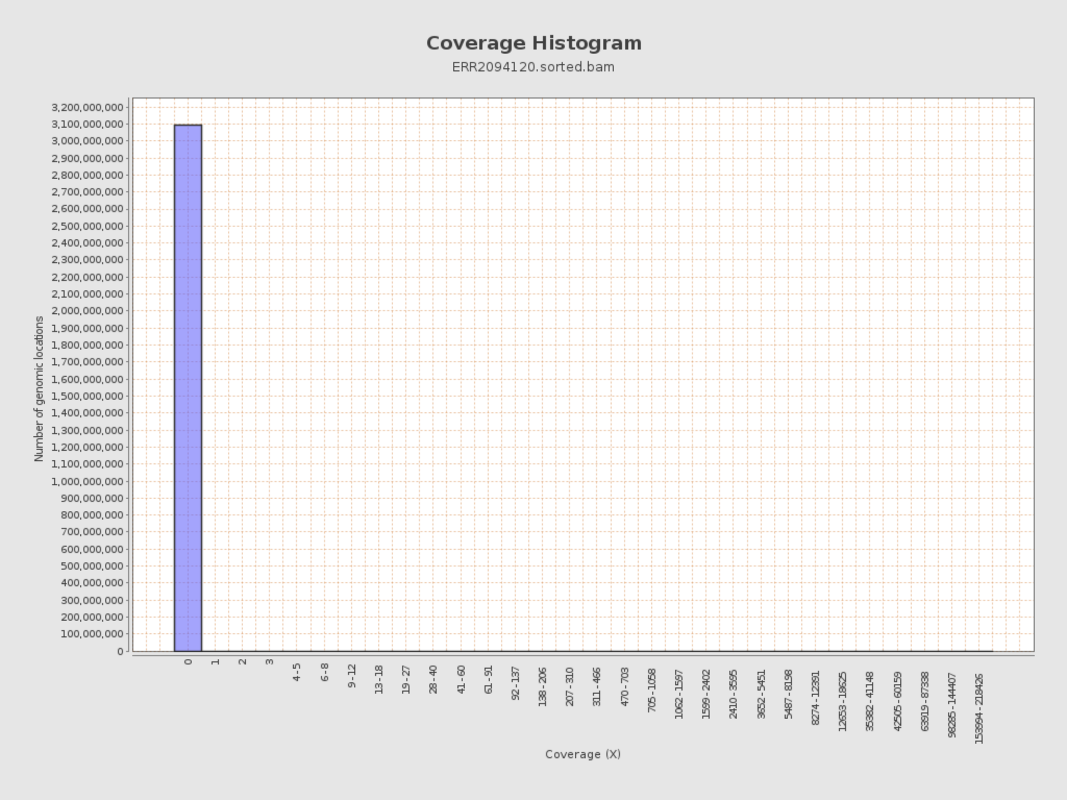
		bases	coverage	deviation
chr1	249250621	53326	0.0002	0.1077
chr2	243199373	441955	0.0018	1.6366
chr3	198022430	26253	0.0001	0.0667
chr4	191154276	104395	0.0005	0.581
chr5	180915260	18902	0.0001	0.0429
chr6	171115067	333565	0.0019	0.7506
chr7	159138663	44230	0.0003	0.147
chr8	146364022	20105	0.0001	0.0837
chr9	141213431	15706	0.0001	0.0519
chr10	135534747	32259	0.0002	0.1623
chr11	135006516	26362	0.0002	0.1317
chr12	133851895	22240	0.0002	0.0591
chr13	115169878	16007	0.0001	0.0944
chr14	107349540	60591	0.0006	0.3269
chr15	102531392	15983	0.0002	0.0959
chr16	90354753	12227	0.0001	0.0314
chr17	81195210	28160	0.0003	0.1349
chr18	78077248	5783	0.0001	0.0189
chr19	59128983	5659	0.0001	0.0174
chr20	63025520	12144	0.0002	0.1087
chr21	48129895	3868	0.0001	0.0216
chr22	51304566	5266	0.0001	0.0552
chrMT	16571	109692409	6,619.5407	27,249.5633
chrX	155270560	20467199	0.1318	56.6391

chrY	59373566	260196	0.0044	2.7702

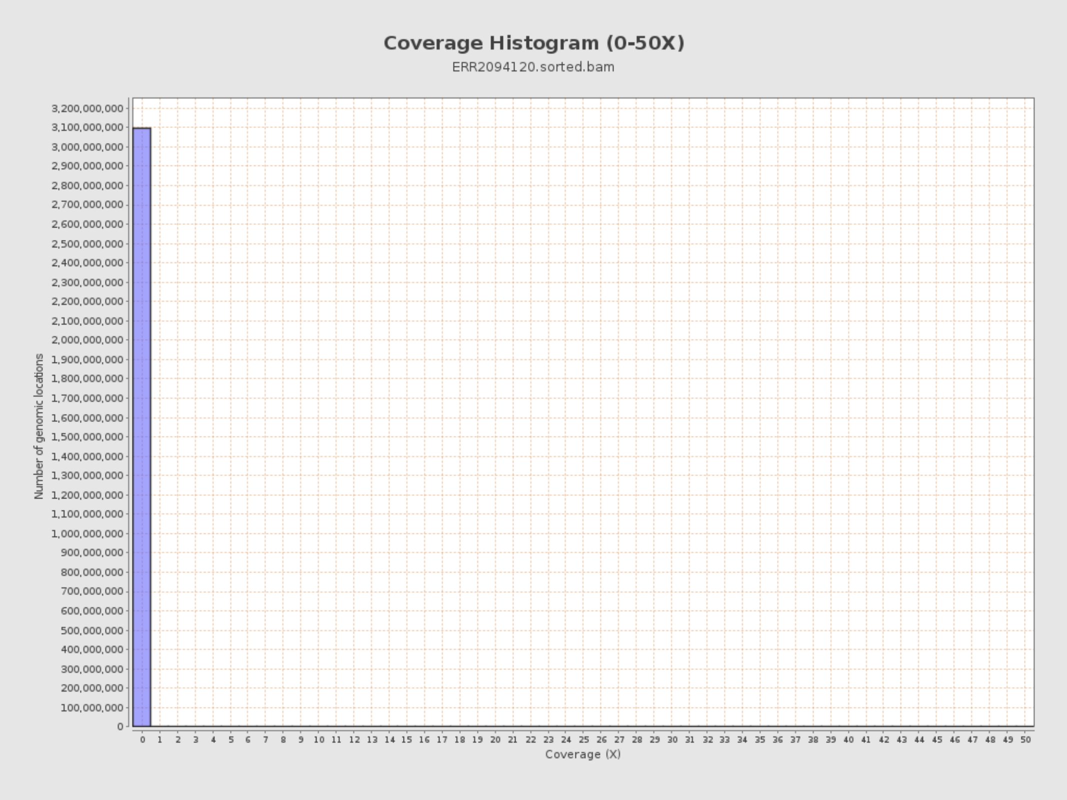
3. Results : Coverage across reference



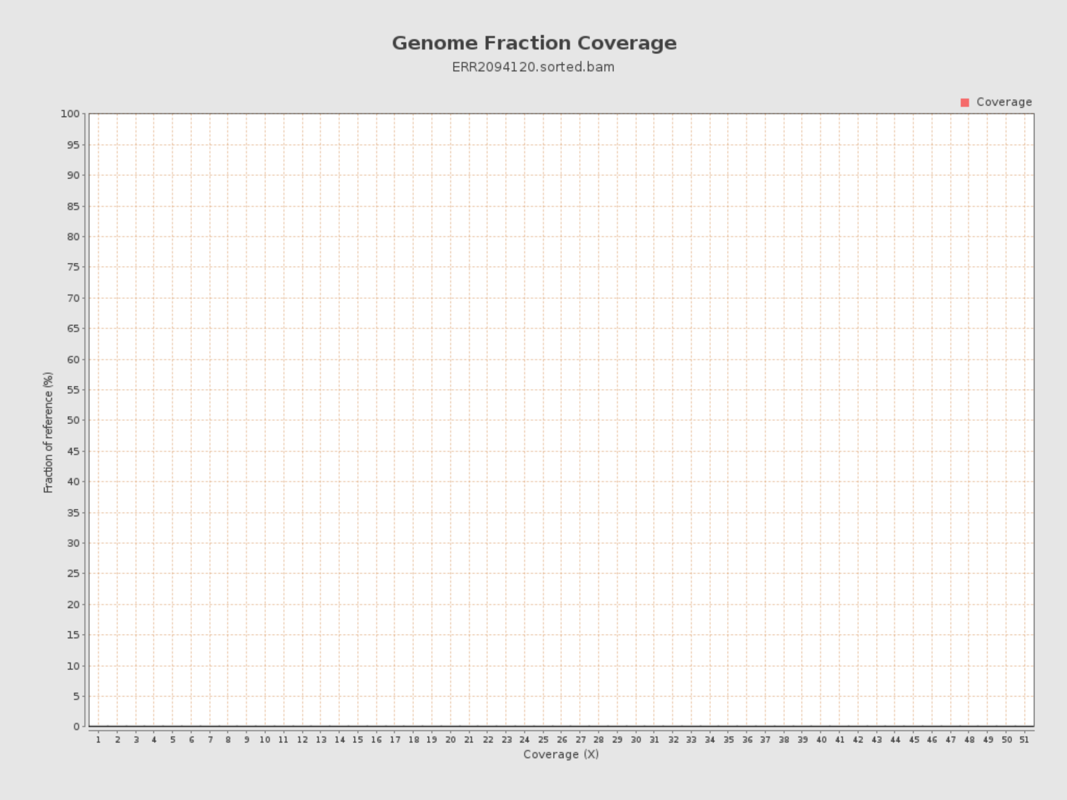
4. Results : Coverage Histogram



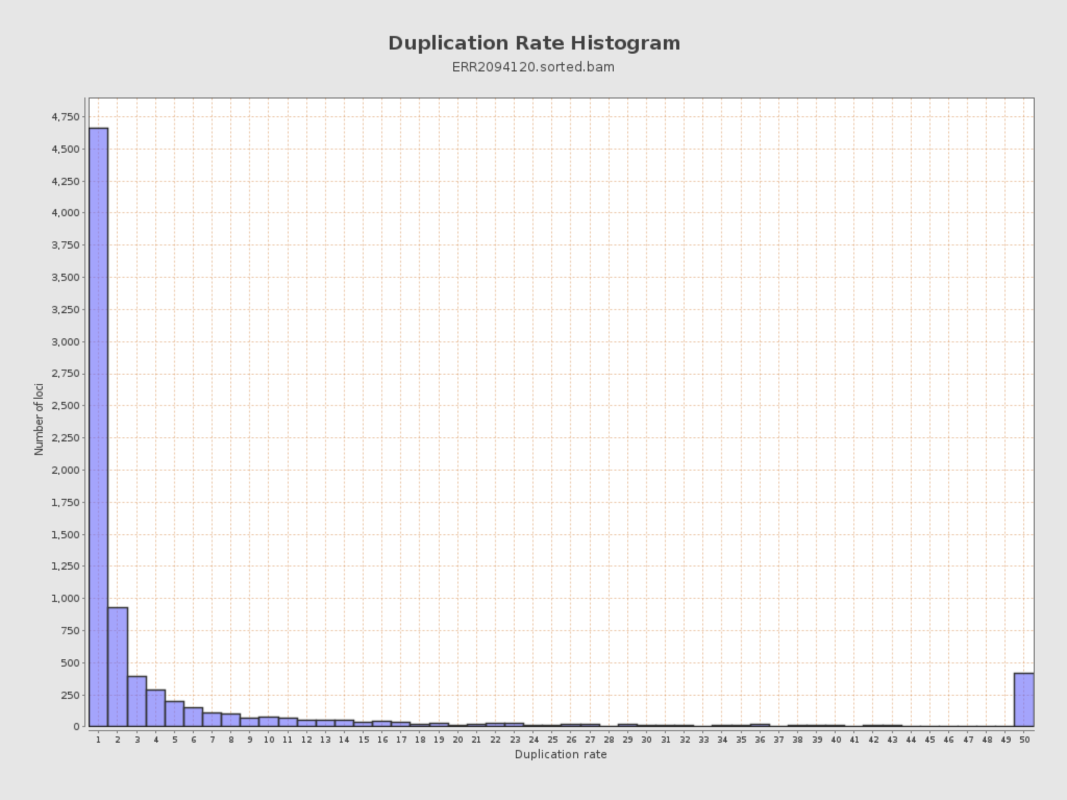
5. Results : Coverage Histogram (0-50X)



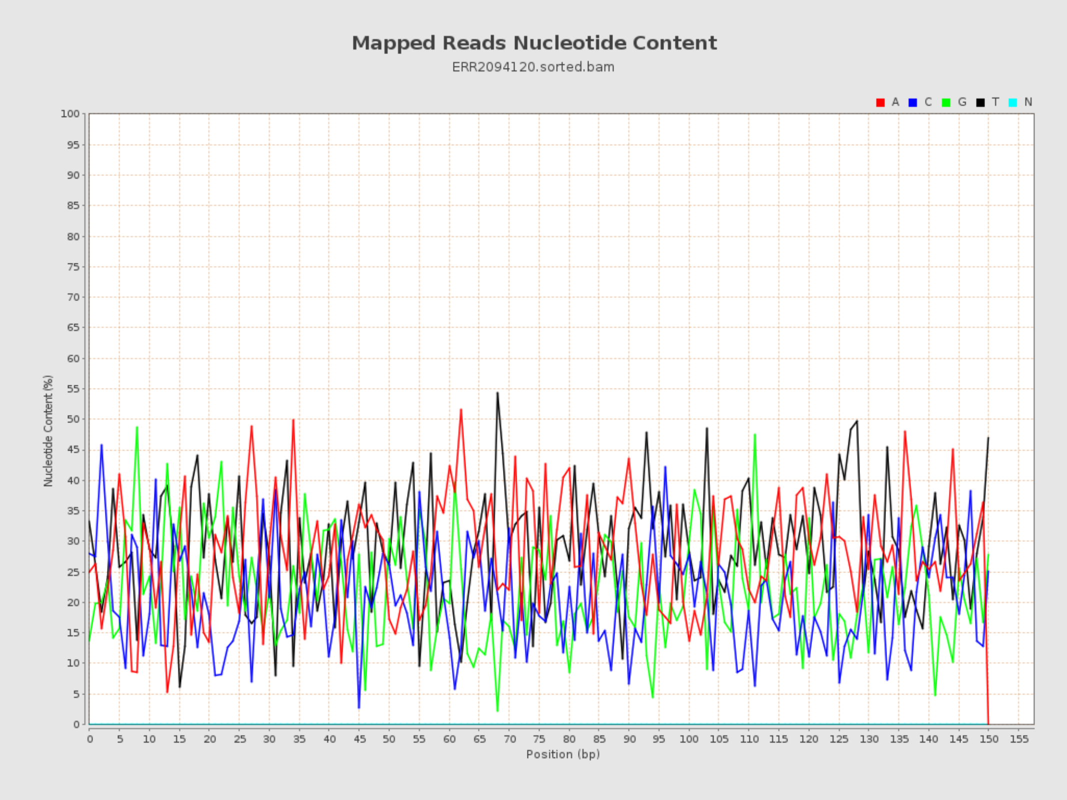
6. Results : Genome Fraction Coverage



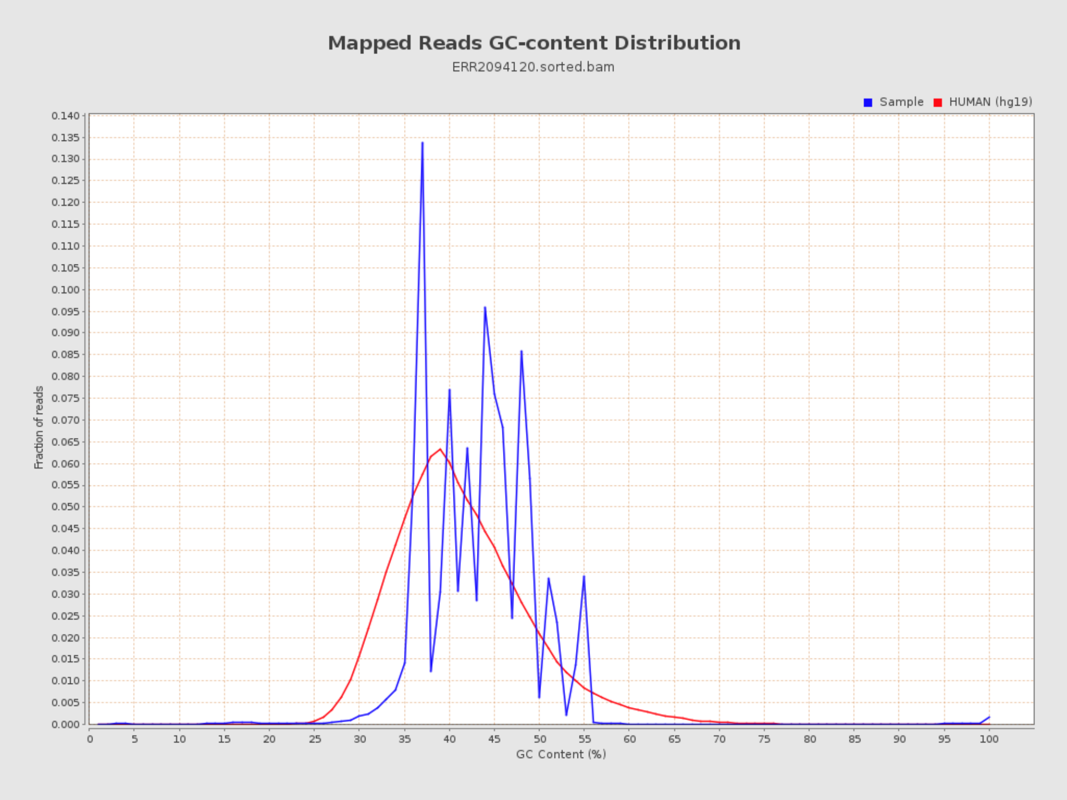
7. Results : Duplication Rate Histogram



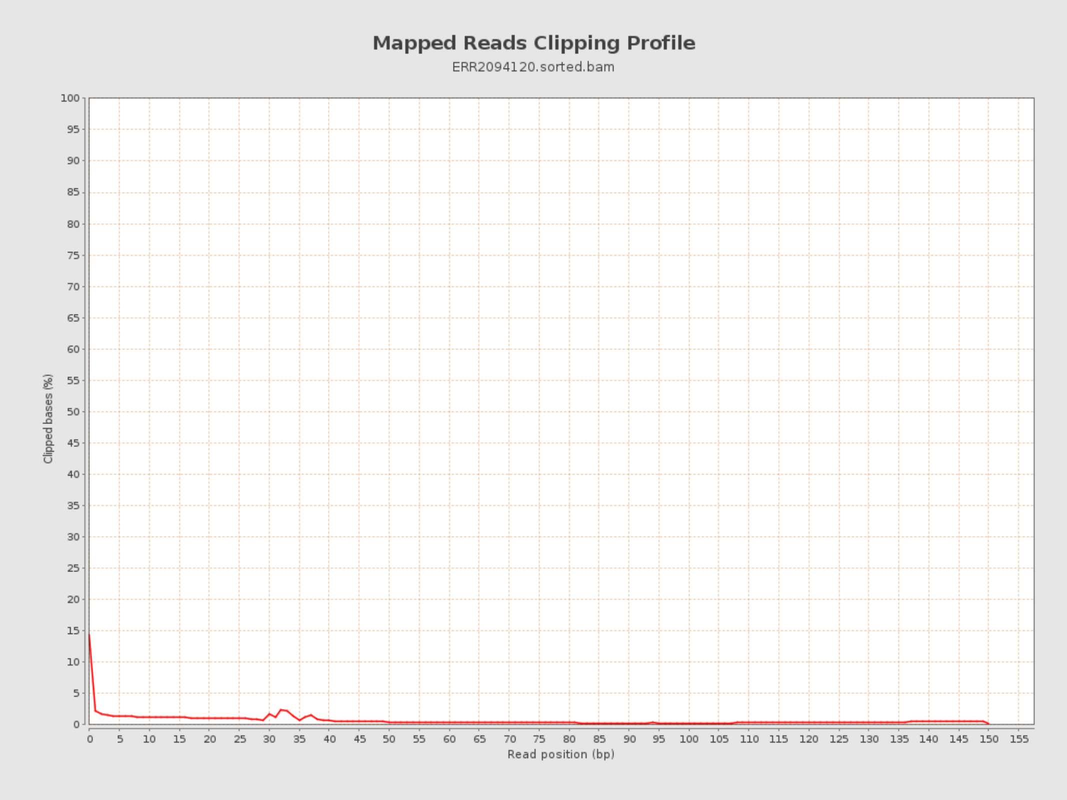
8. Results : Mapped Reads Nucleotide Content



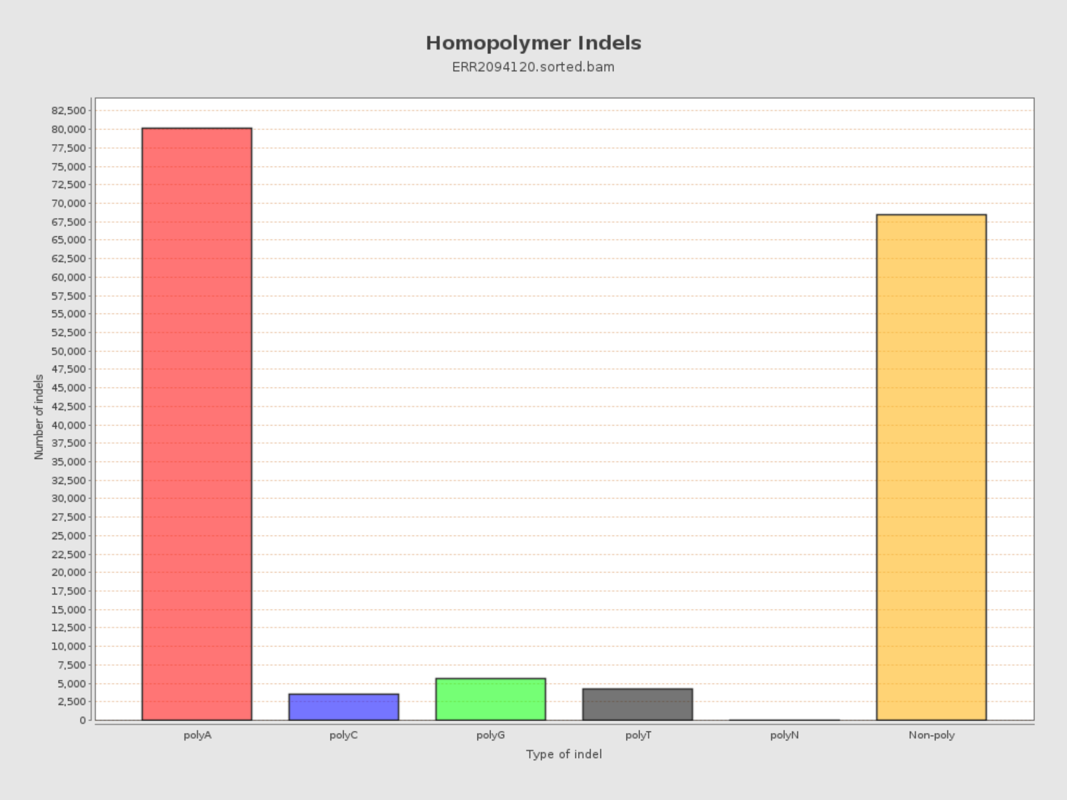
9. Results : Mapped Reads GC-content Distribution



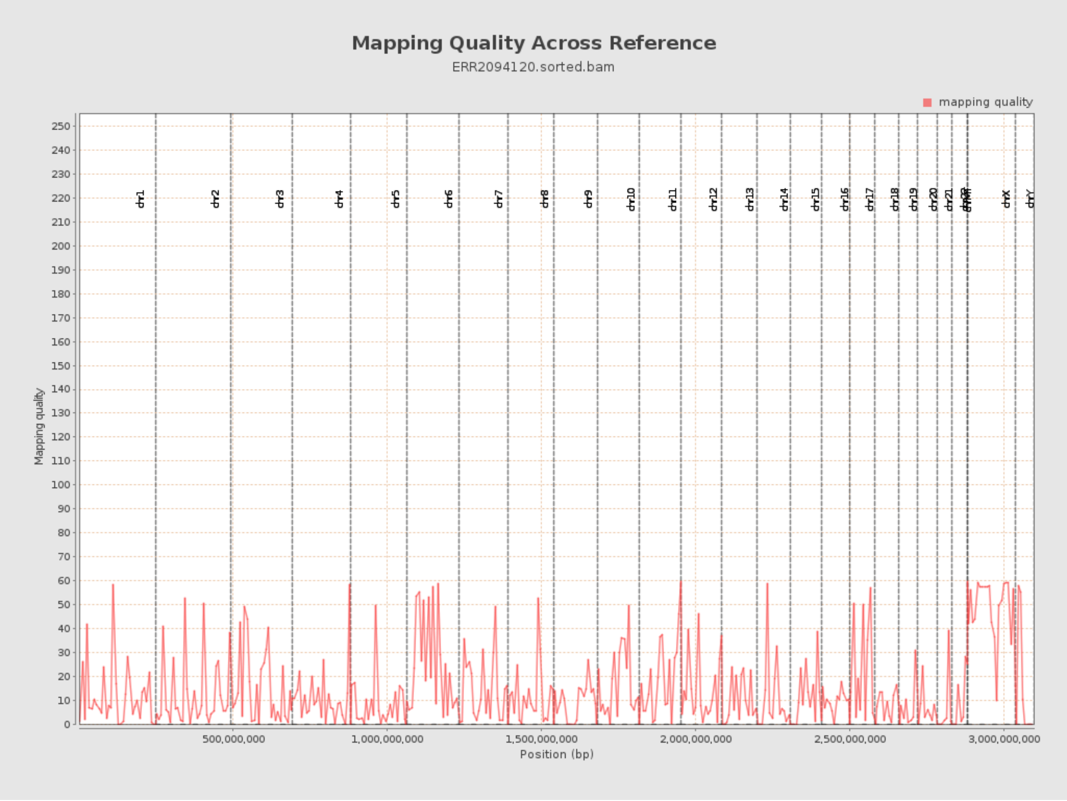
10. Results : Mapped Reads Clipping Profile



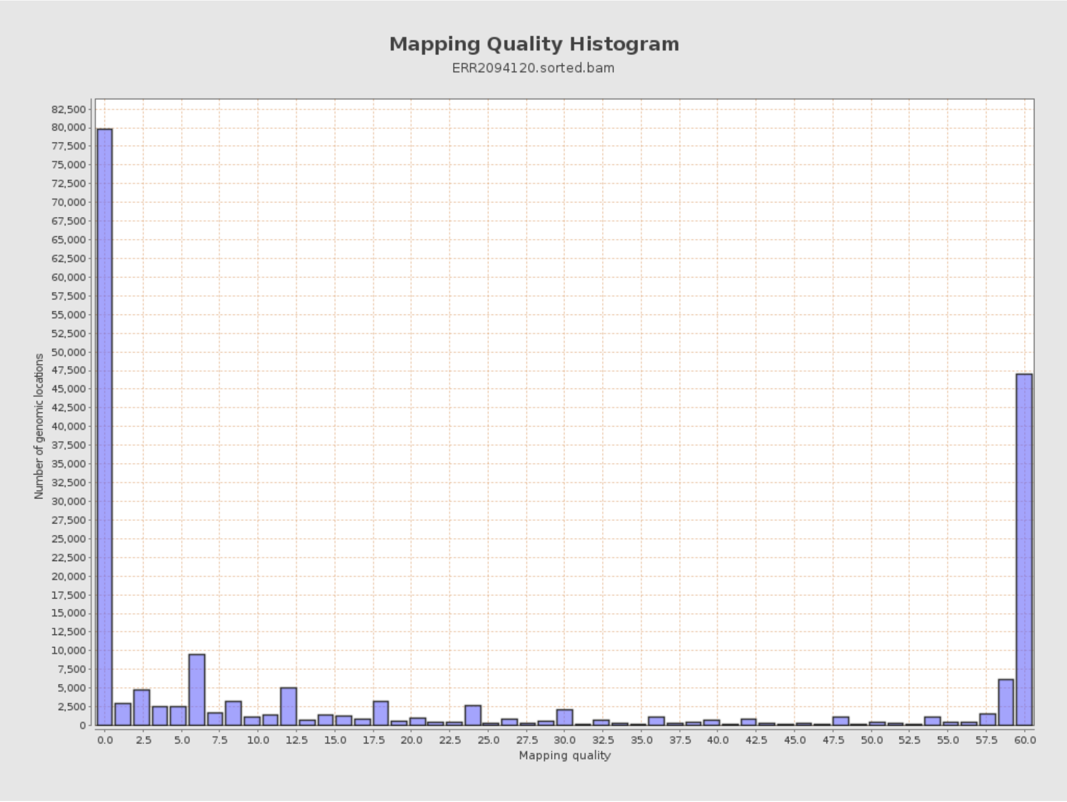
11. Results : Homopolymer Indels



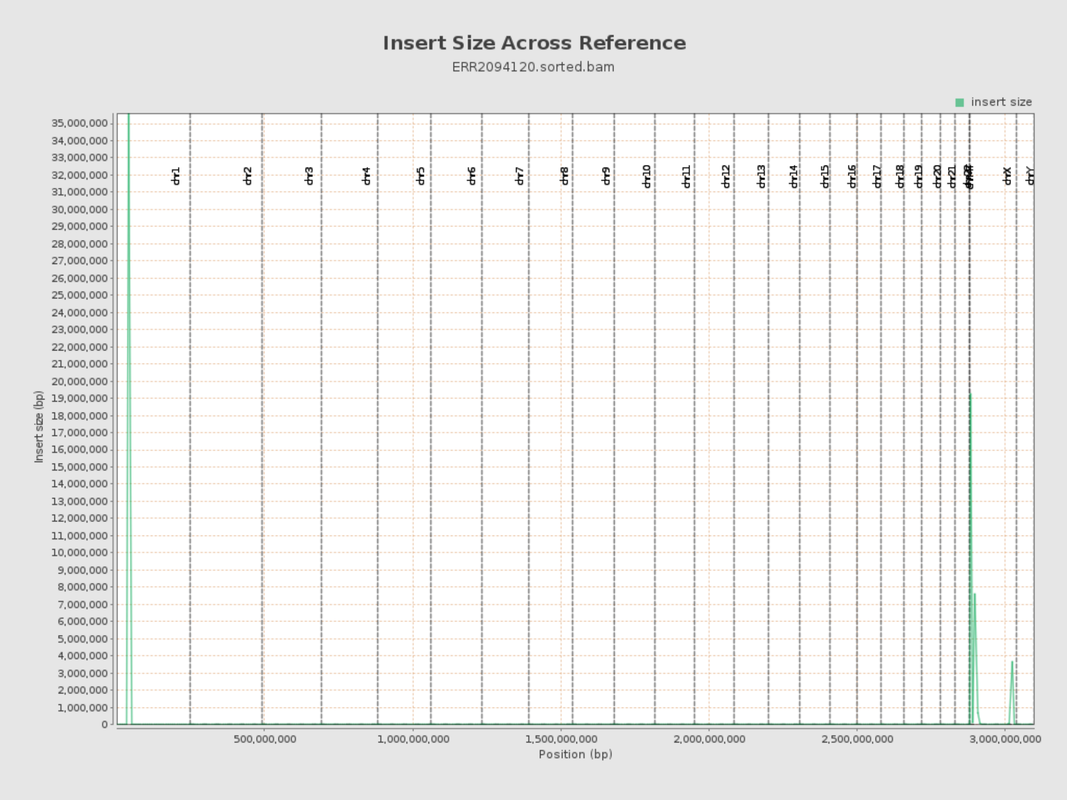
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram