Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:12:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094103.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_ERR2094103 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094103_1.fastq.gz ERR2094103_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:12:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	361,876
Mapped reads	351,116 / 97.03%
Unmapped reads	10,760 / 2.97%
Mapped paired reads	351,116 / 97.03%
Mapped reads, first in pair	176,550 / 48.79%
Mapped reads, second in pair	174,566 / 48.24%
Mapped reads, both in pair	348,236 / 96.23%
Mapped reads, singletons	2,880 / 0.8%
Secondary alignments	0
Supplementary alignments	27,558 / 7.62%
Read min/max/mean length	30 / 151 / 144.71
Duplicated reads (estimated)	334,371 / 92.4%
Duplication rate	51.68%
Clipped reads	197,674 / 54.62%

2.2. ACGT Content

Number/percentage of A's	12,926,423 / 29.22%
Number/percentage of C's	9,321,678 / 21.07%
Number/percentage of T's	12,099,473 / 27.35%
Number/percentage of G's	9,884,524 / 22.35%
Number/percentage of N's	454 / 0%

GC Percentage	43.42%

2.3. Coverage

Mean	0.0145
Standard Deviation	2.8156

2.4. Mapping Quality

Mean Mapping Quality	40.12

2.5. Insert size

Mean	1,829,975.21
Standard Deviation	11,768,228.49
P25/Median/P75	127 / 163 / 192

2.6. Mismatches and indels

General error rate	3.45%
Mismatches	1,456,342
Insertions	29,757
Mapped reads with at least one insertion	8.34%
Deletions	108,897
Mapped reads with at least one deletion	29.76%
Homopolymer indels	28.61%

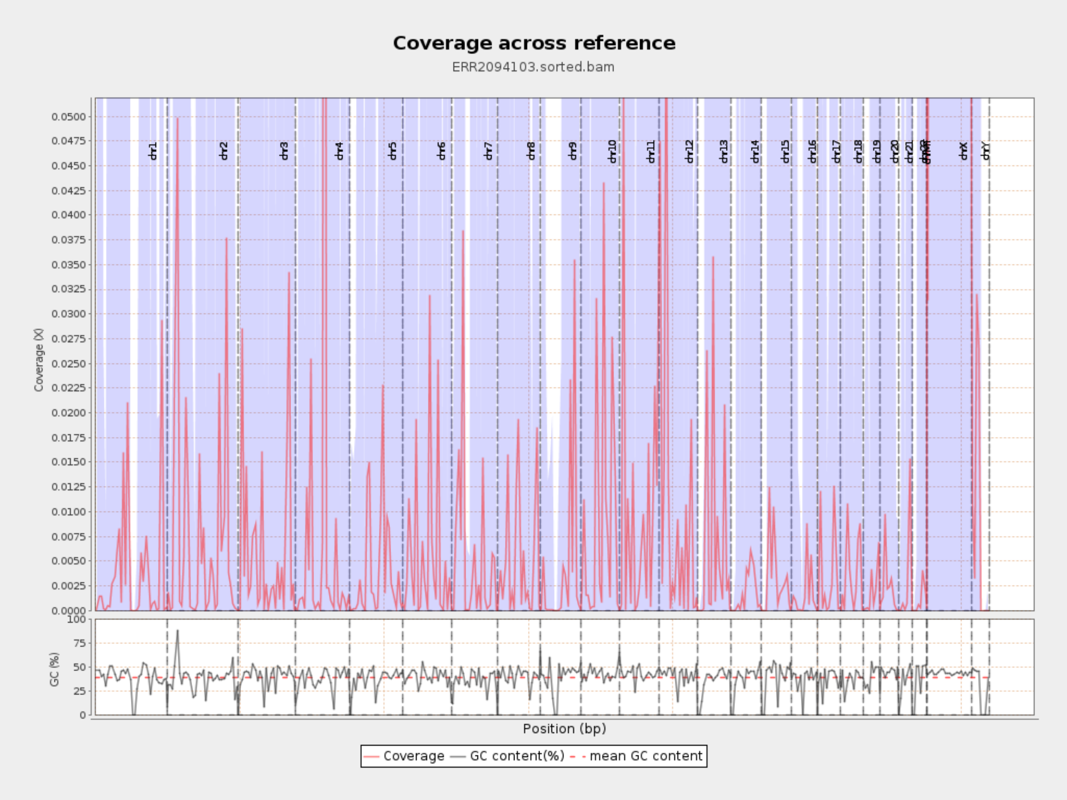
2.7. Chromosome stats

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

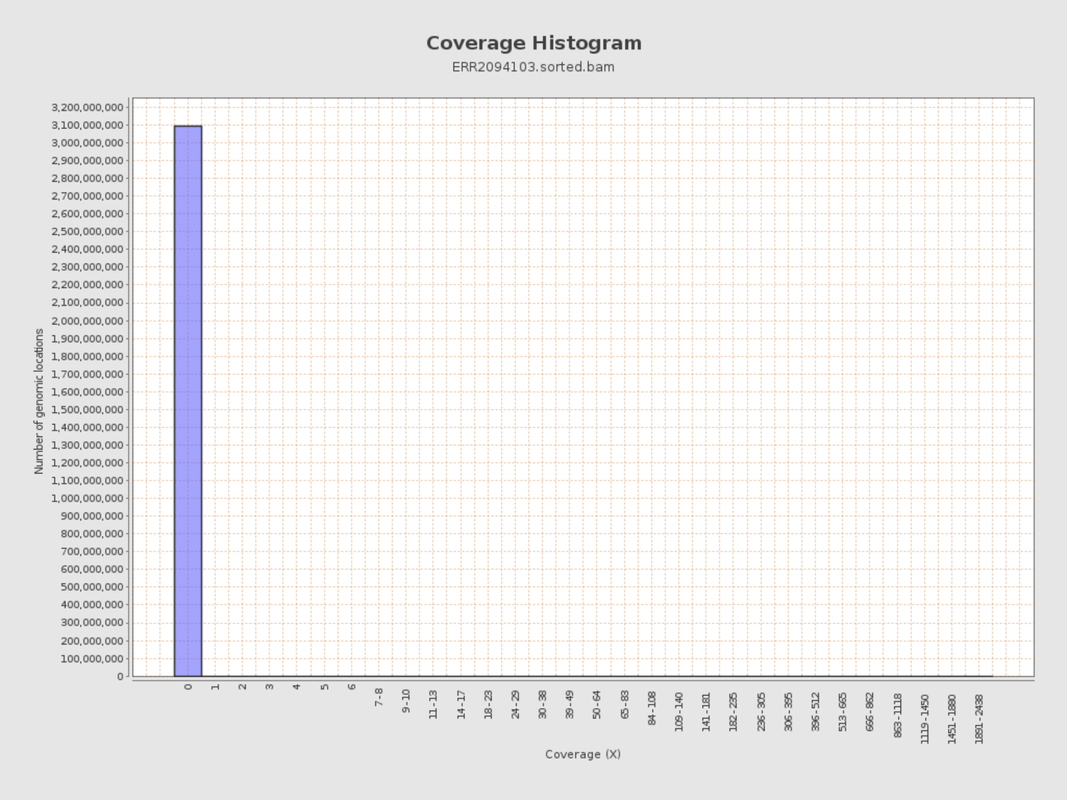
		bases	coverage	deviation
chr1	249250621	914274	0.0037	1.42
chr2	243199373	1865713	0.0077	2.1894
chr3	198022430	1225417	0.0062	2.1208
chr4	191154276	1968379	0.0103	2.8774
chr5	180915260	771150	0.0043	1.4119
chr6	171115067	980880	0.0057	1.7308
chr7	159138663	855965	0.0054	1.6059
chr8	146364022	748416	0.0051	1.3426
chr9	141213431	617717	0.0044	1.4838
chr10	135534747	1216558	0.009	2.8762
chr11	135006516	1282697	0.0095	2.3611
chr12	133851895	1495273	0.0112	2.7538
chr13	115169878	816112	0.0071	2.1309
chr14	107349540	191133	0.0018	0.5647
chr15	102531392	335713	0.0033	0.7776
chr16	90354753	157531	0.0017	0.5945
chr17	81195210	278584	0.0034	0.9536
chr18	78077248	284028	0.0036	0.8587
chr19	59128983	110904	0.0019	0.6029
chr20	63025520	156113	0.0025	0.8372
chr21	48129895	157224	0.0033	0.8024
chr22	51304566	51824	0.001	0.2898
chrMT	16571	392787	23.7033	110.4604
chrX	155270560	27610737	0.1778	9.6087

chrY	59373566	534026	0.009	1.9154

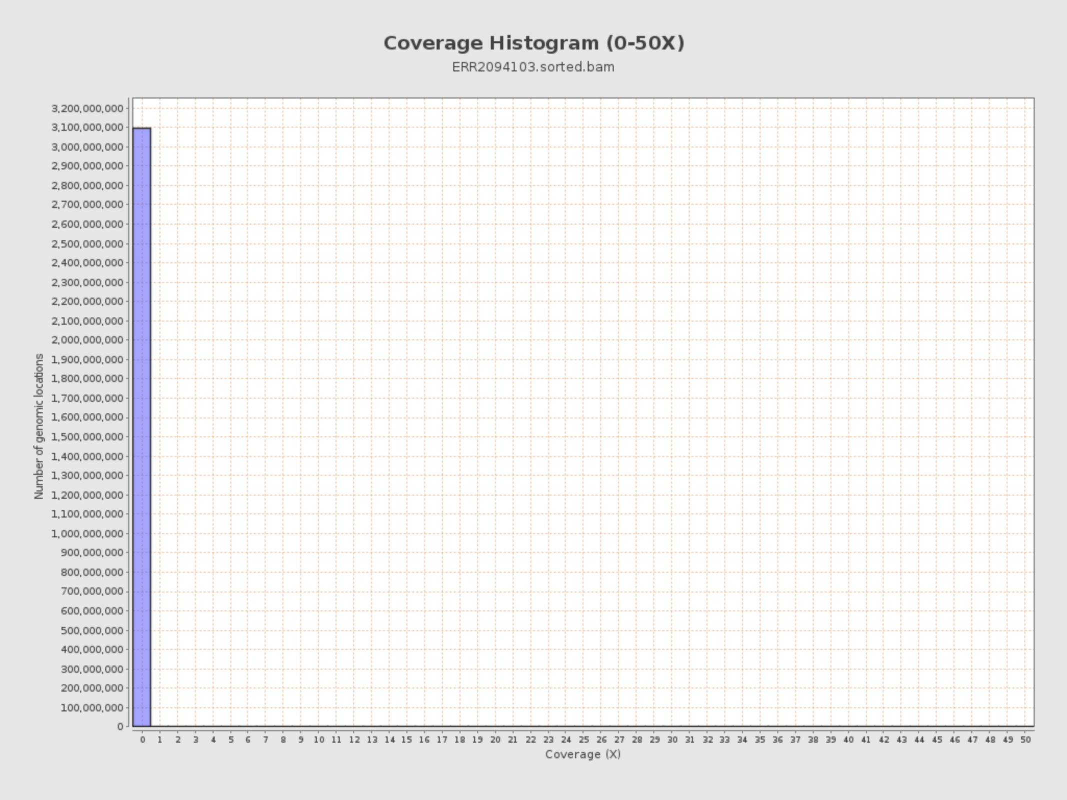
3. Results : Coverage across reference



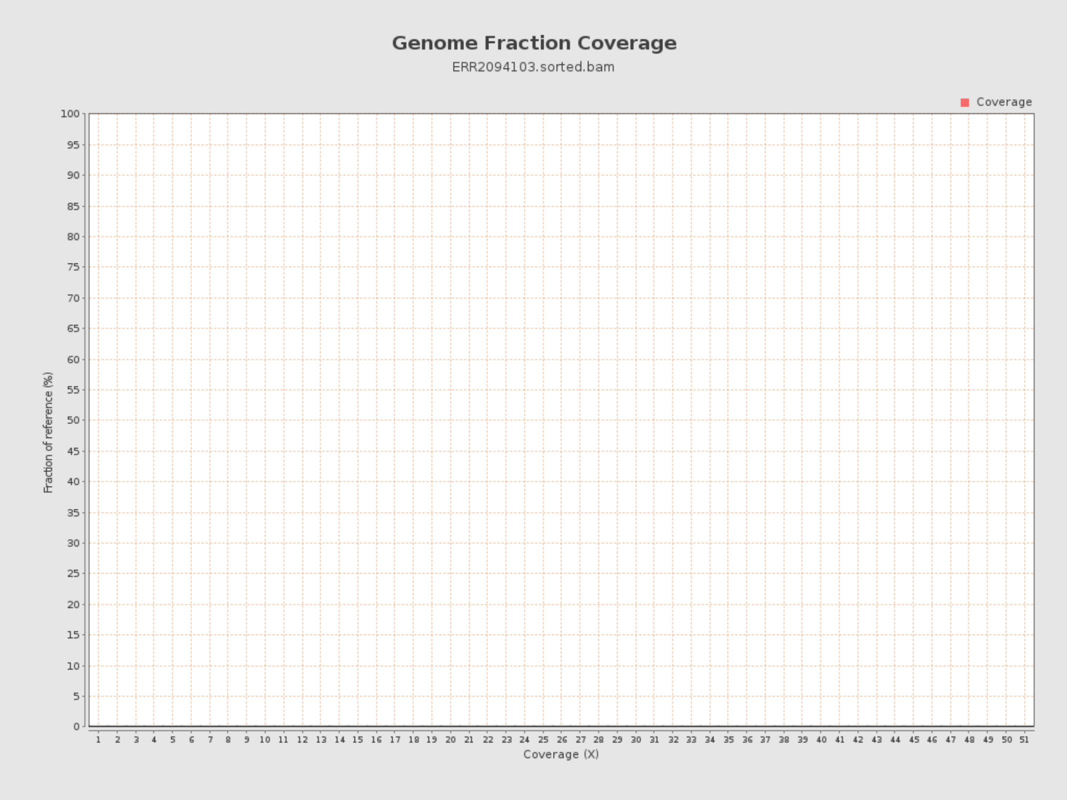
4. Results : Coverage Histogram



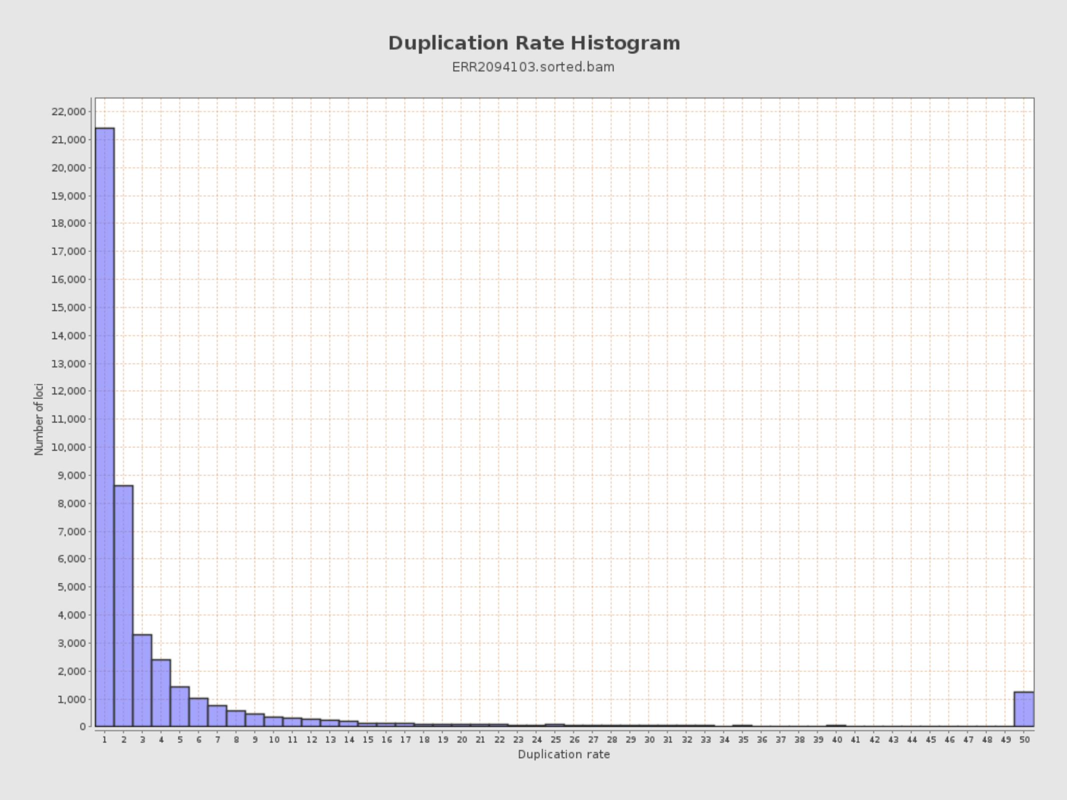
5. Results : Coverage Histogram (0-50X)



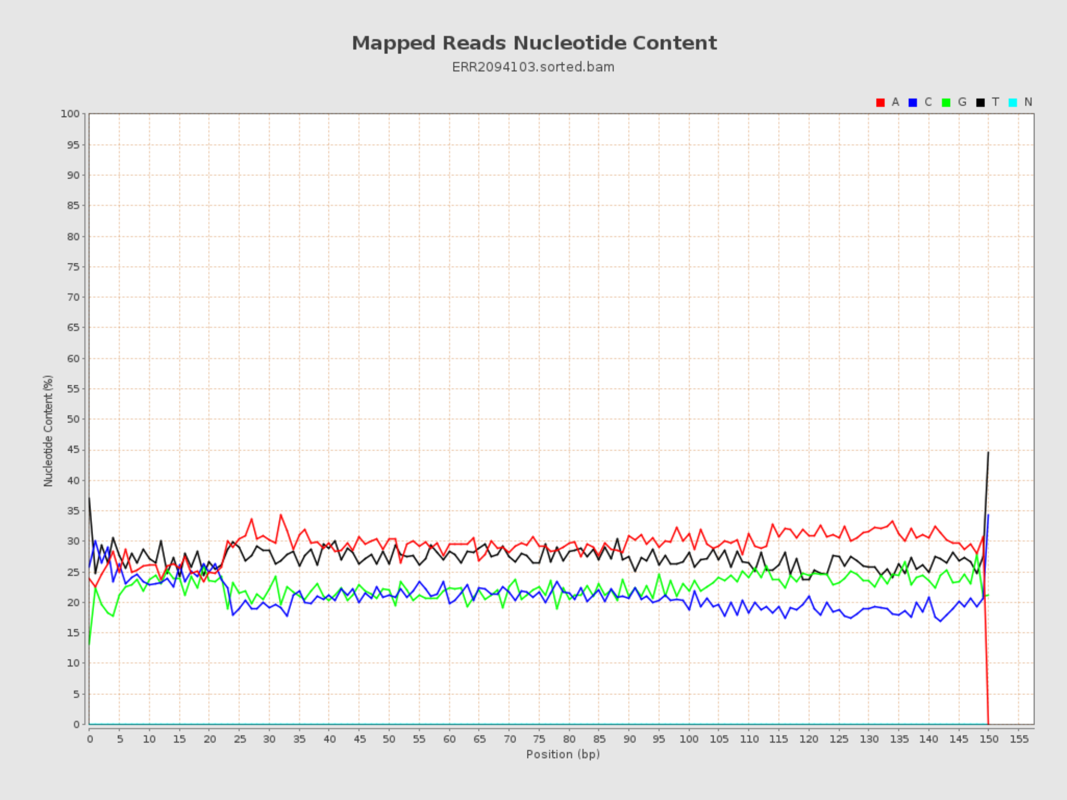
6. Results : Genome Fraction Coverage



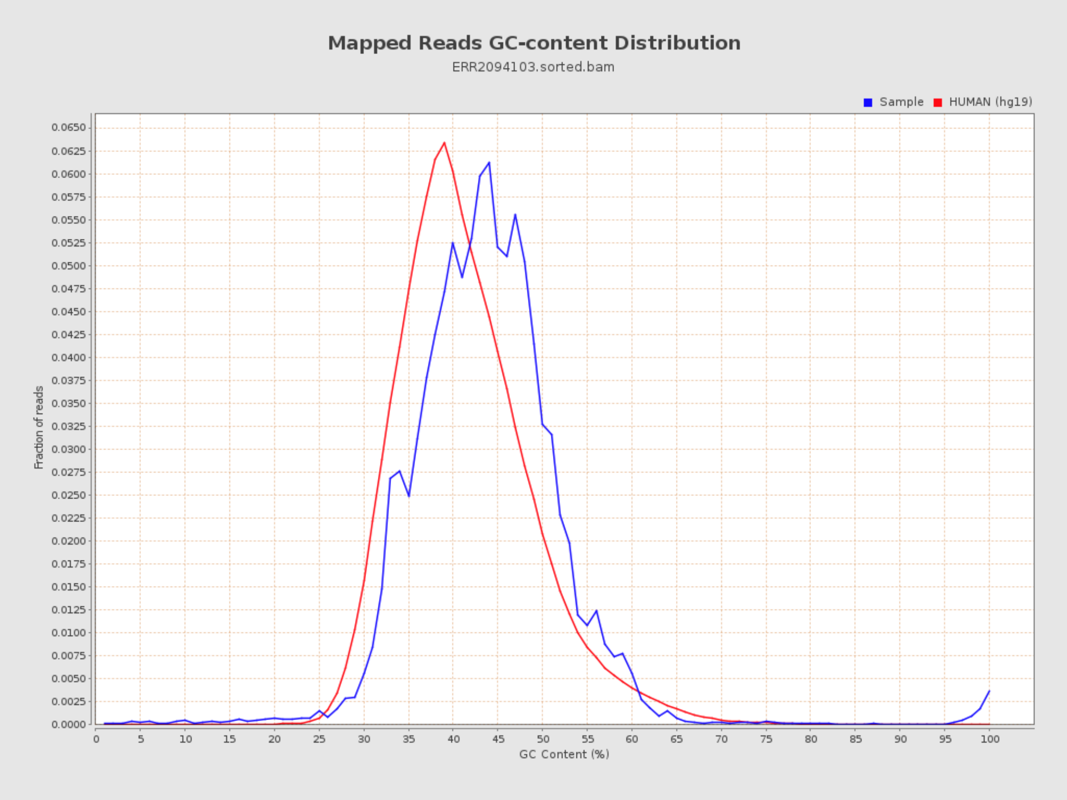
7. Results : Duplication Rate Histogram



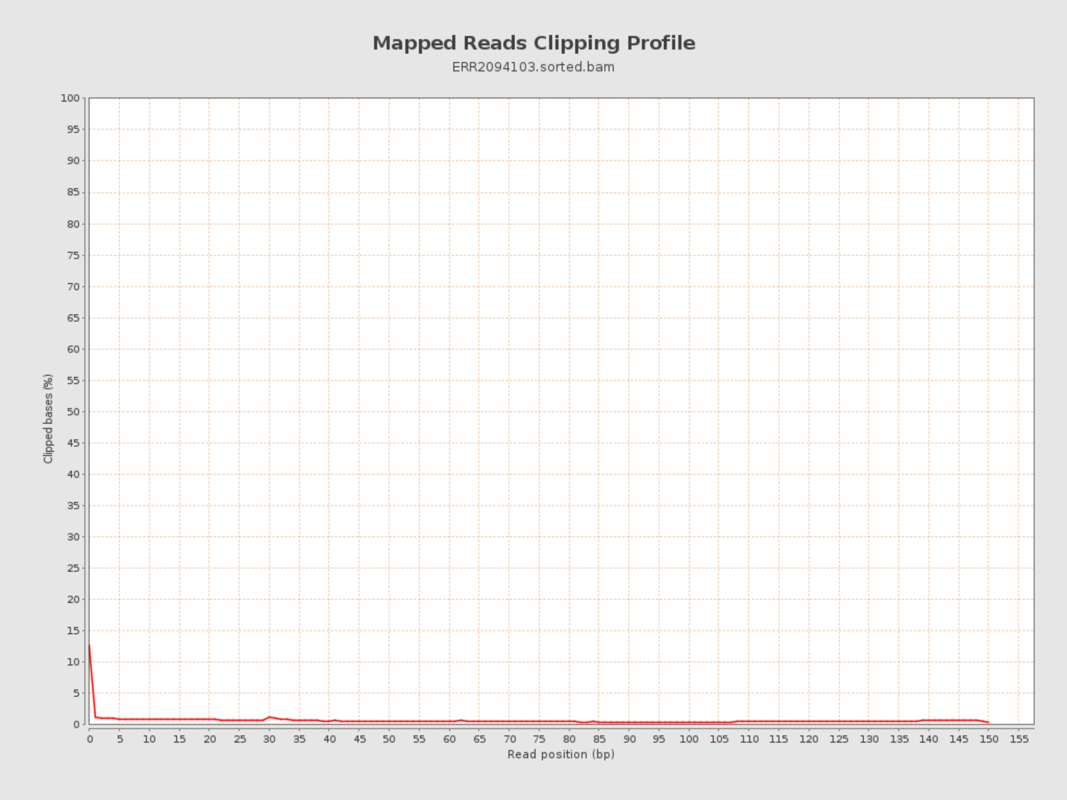
8. Results : Mapped Reads Nucleotide Content



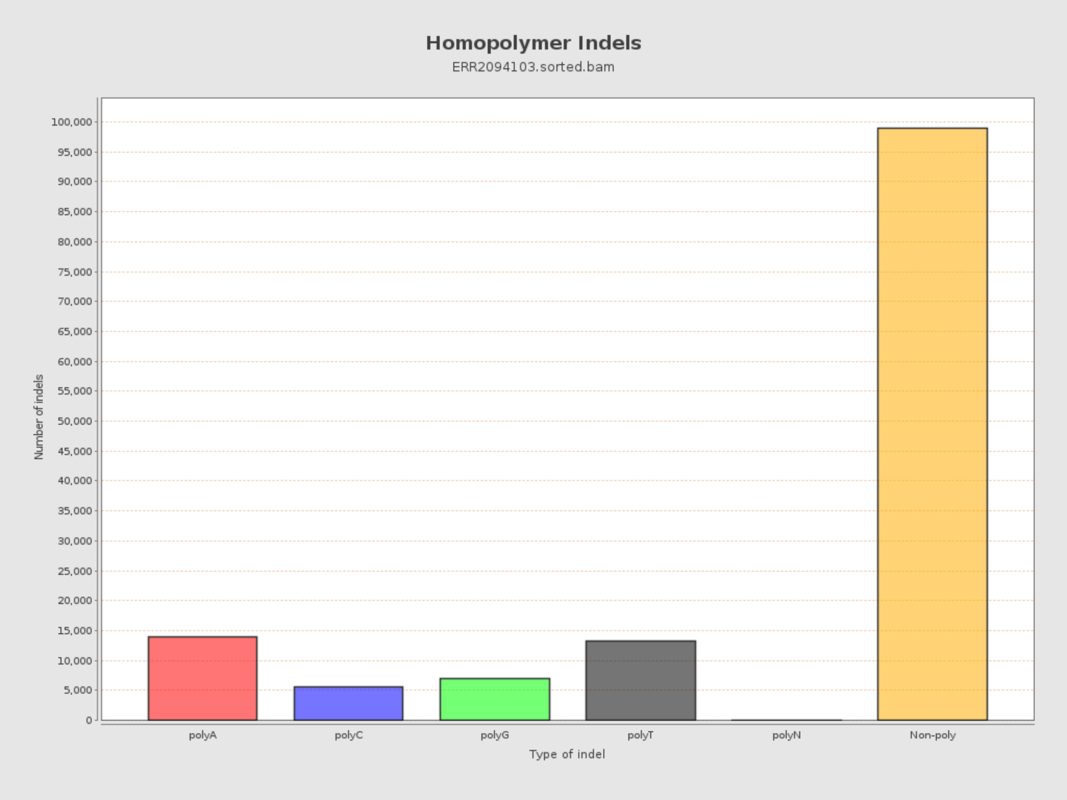
9. Results : Mapped Reads GC-content Distribution



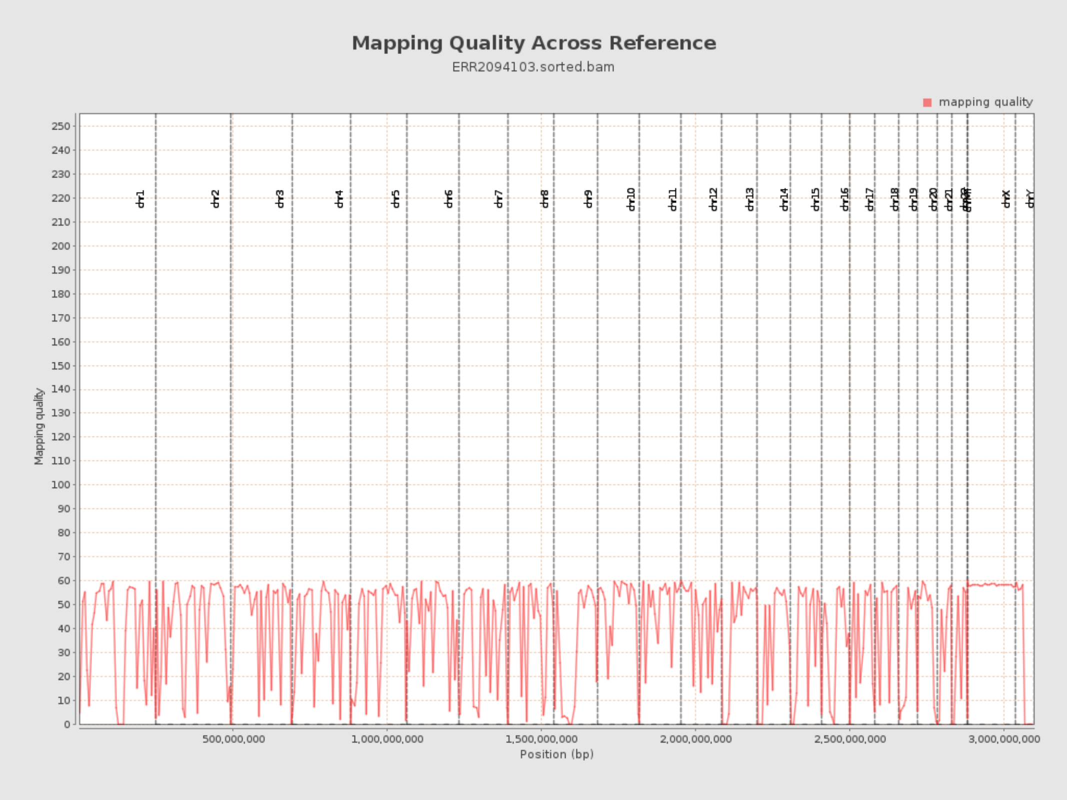
10. Results : Mapped Reads Clipping Profile



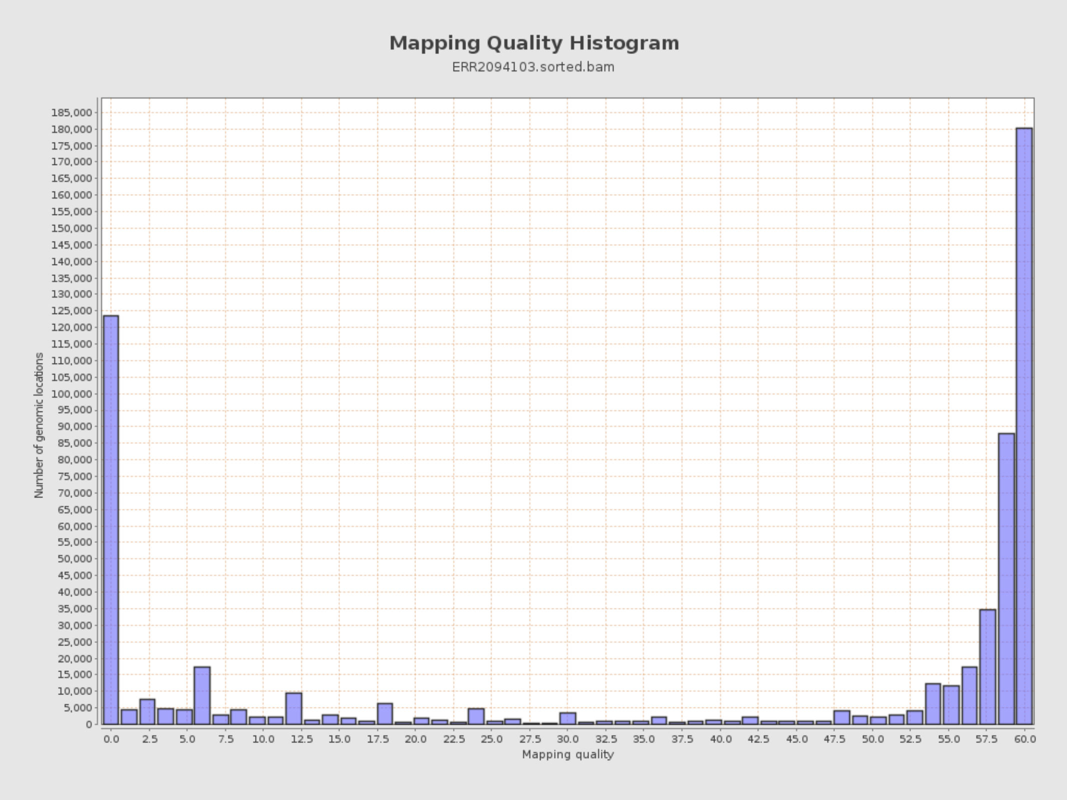
11. Results : Homopolymer Indels



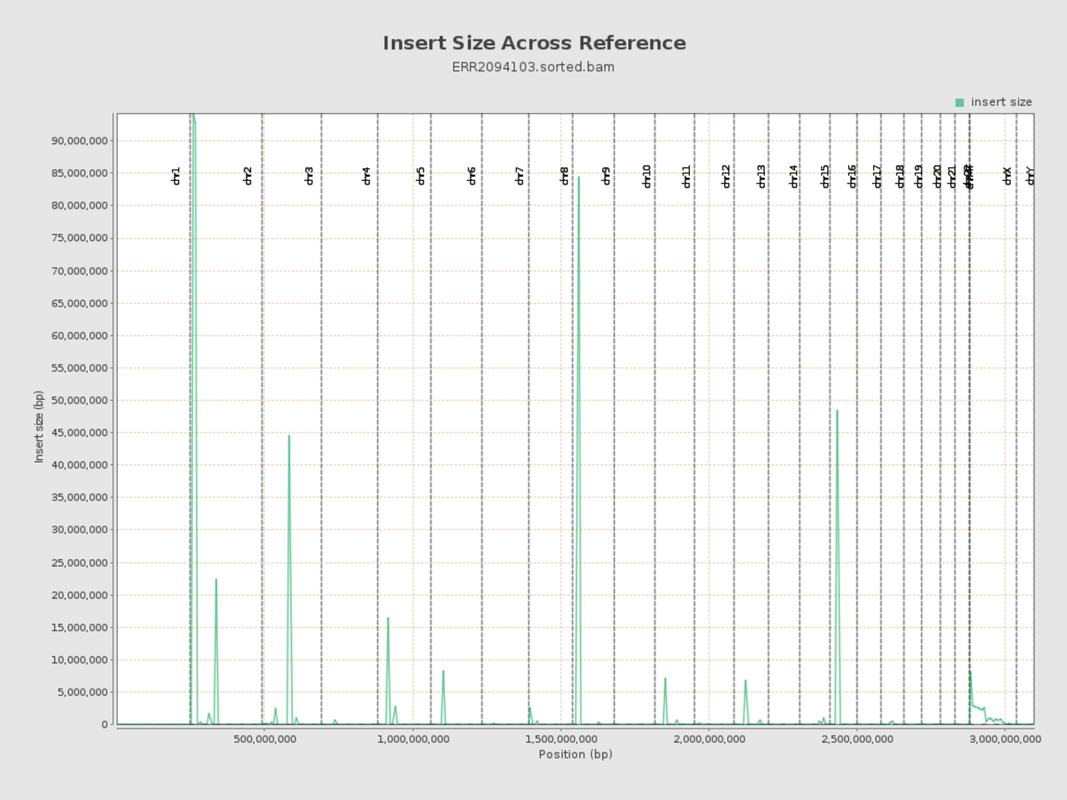
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram