Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:46:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094132.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_ERR2094132 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094132_1.fastq.gz ERR2094132_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:46:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094132.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	478,504
Mapped reads	430,132 / 89.89%
Unmapped reads	48,372 / 10.11%
Mapped paired reads	430,132 / 89.89%
Mapped reads, first in pair	215,731 / 45.08%
Mapped reads, second in pair	214,401 / 44.81%
Mapped reads, both in pair	426,836 / 89.2%
Mapped reads, singletons	3,296 / 0.69%
Secondary alignments	0
Supplementary alignments	6,043 / 1.26%
Read min/max/mean length	30 / 151 / 141.21
Duplicated reads (estimated)	426,612 / 89.16%
Duplication rate	42.32%
Clipped reads	128,934 / 26.95%

2.2. ACGT Content

Number/percentage of A's	16,748,112 / 27.69%
Number/percentage of C's	12,963,644 / 21.43%
Number/percentage of T's	17,213,830 / 28.46%
Number/percentage of G's	13,556,644 / 22.41%
Number/percentage of N's	671 / 0%

GC Percentage	43.85%

2.3. Coverage

Mean	0.0196
Standard Deviation	26.8588

2.4. Mapping Quality

Mean Mapping Quality	26.45

2.5. Insert size

Mean	92,114.01
Standard Deviation	3,329,713.07
P25/Median/P75	212 / 231 / 261

2.6. Mismatches and indels

General error rate	2.04%
Mismatches	1,208,806
Insertions	20,524
Mapped reads with at least one insertion	4.65%
Deletions	61,607
Mapped reads with at least one deletion	13.89%
Homopolymer indels	50.13%

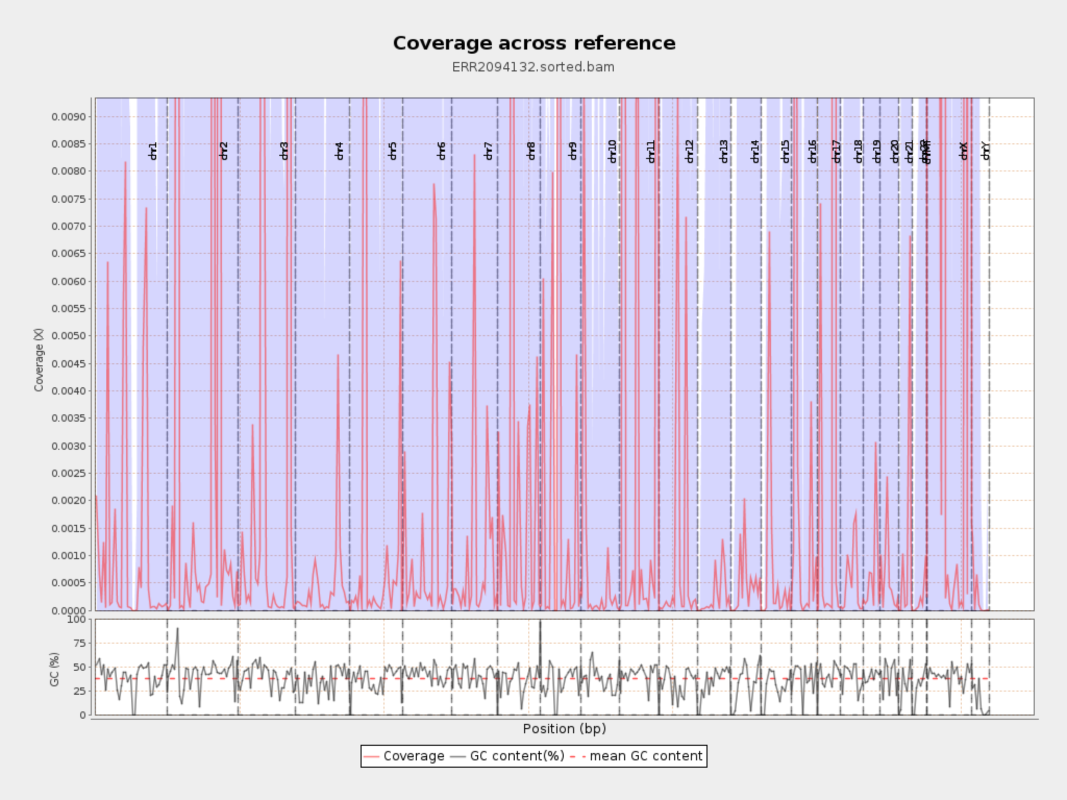
2.7. Chromosome stats

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

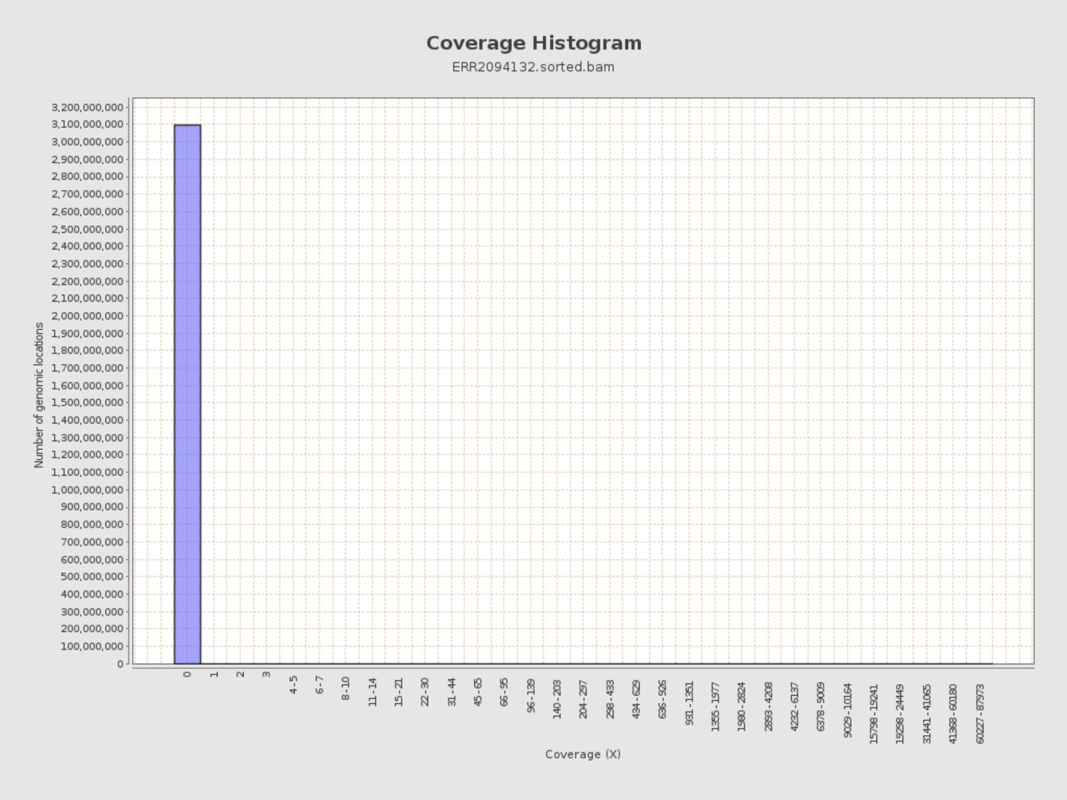
		bases	coverage	deviation
chr1	249250621	319387	0.0013	0.5903
chr2	243199373	1470265	0.006	4.0943
chr3	198022430	1355212	0.0068	6.0625
chr4	191154276	93078	0.0005	0.1566
chr5	180915260	290729	0.0016	1.0271
chr6	171115067	229532	0.0013	0.52
chr7	159138663	154165	0.001	0.4367
chr8	146364022	708684	0.0048	3.4116
chr9	141213431	508765	0.0036	1.6666
chr10	135534747	108394	0.0008	0.4336
chr11	135006516	1459855	0.0108	5.494
chr12	133851895	144720	0.0011	0.7188
chr13	115169878	32069	0.0003	0.0938
chr14	107349540	53249	0.0005	0.1503
chr15	102531392	78405	0.0008	0.4567
chr16	90354753	251115	0.0028	1.5804
chr17	81195210	1558456	0.0192	9.5707
chr18	78077248	45098	0.0006	0.1681
chr19	59128983	40140	0.0007	0.2204
chr20	63025520	40522	0.0006	0.1794
chr21	48129895	62878	0.0013	0.4619
chr22	51304566	11623	0.0002	0.0488
chrMT	16571	45210446	2,728.2871	11,124.9392
chrX	155270560	6580537	0.0424	14.6843

chrY	59373566	13266	0.0002	0.0873

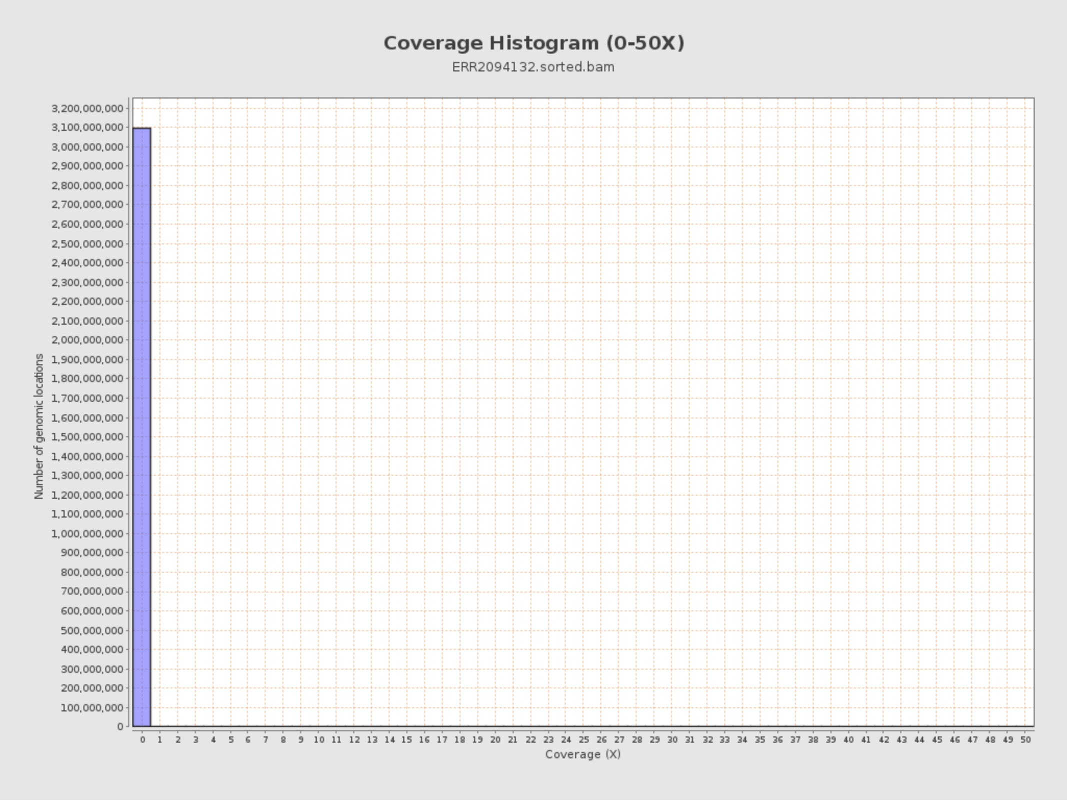
3. Results : Coverage across reference



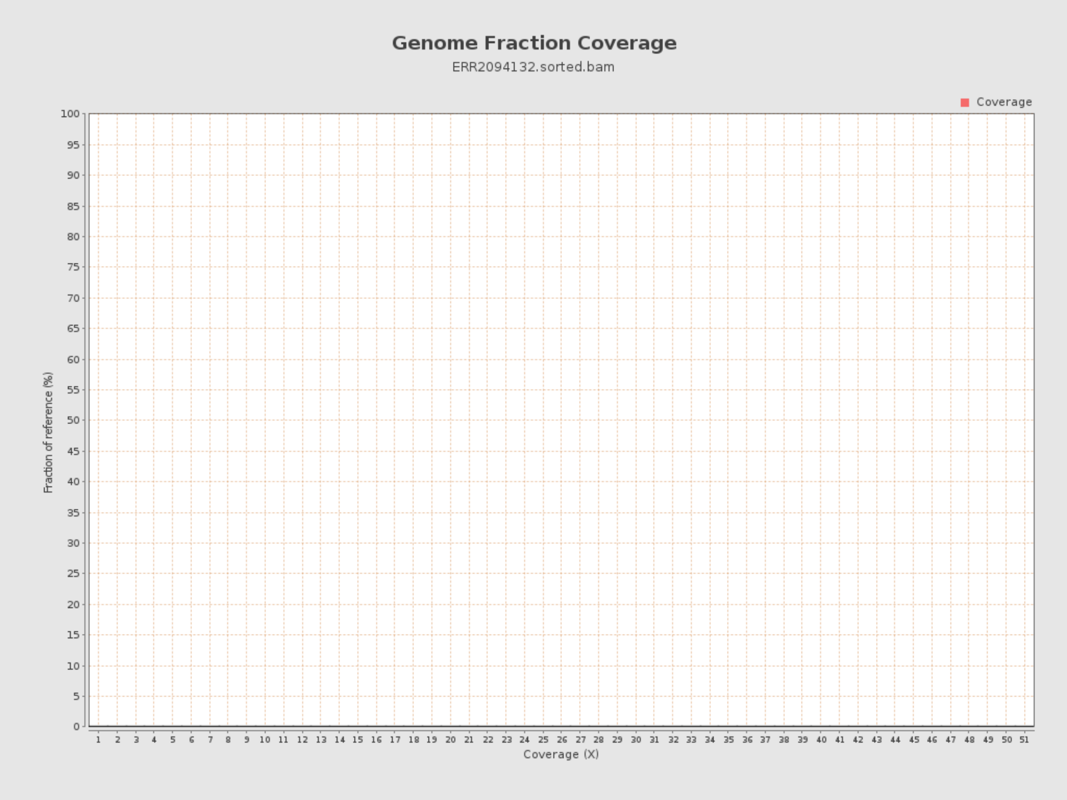
4. Results : Coverage Histogram



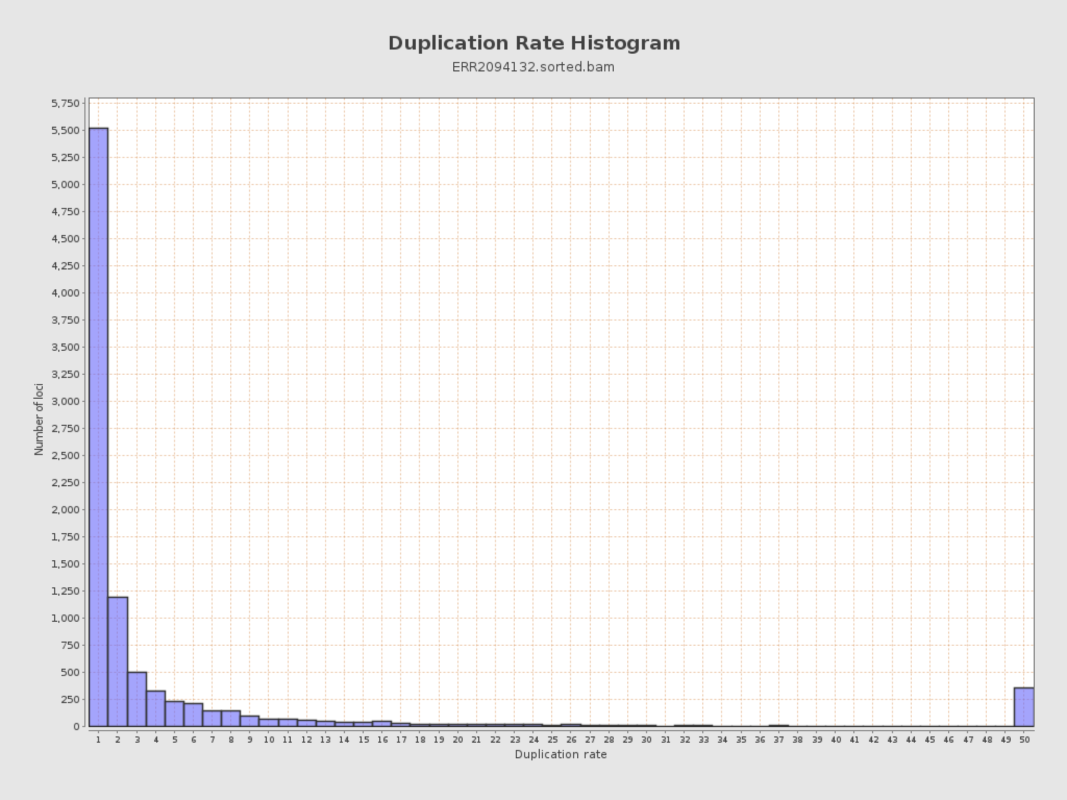
5. Results : Coverage Histogram (0-50X)



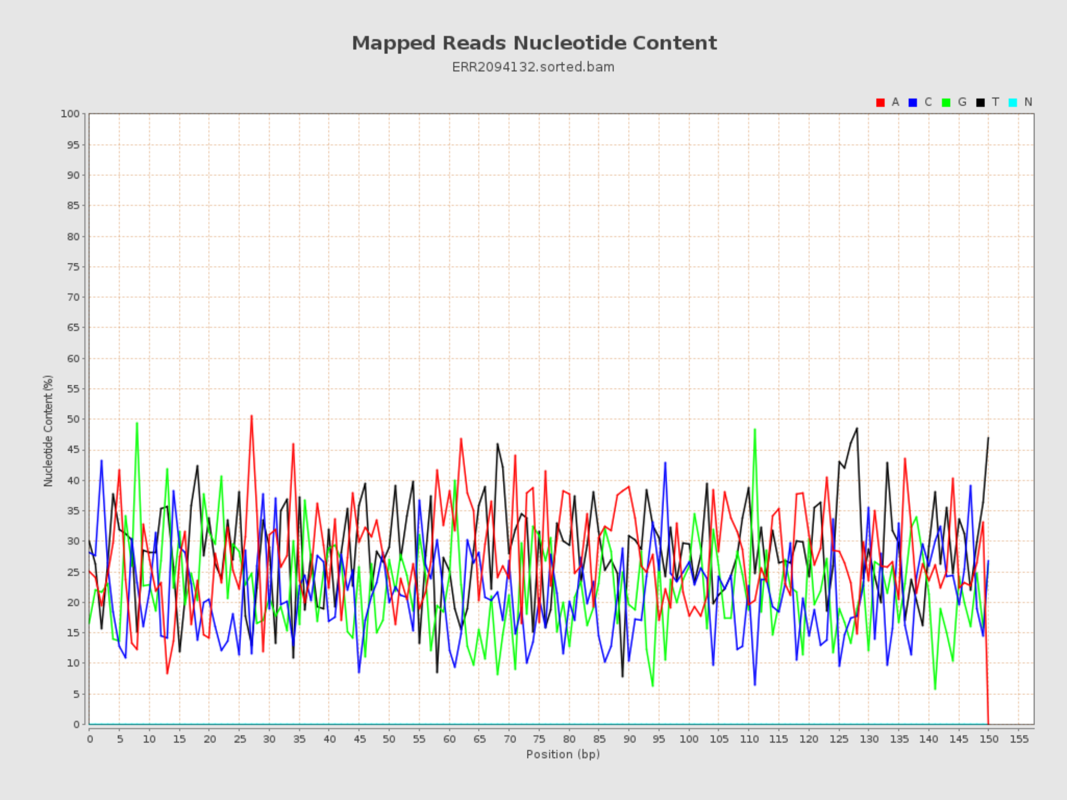
6. Results : Genome Fraction Coverage



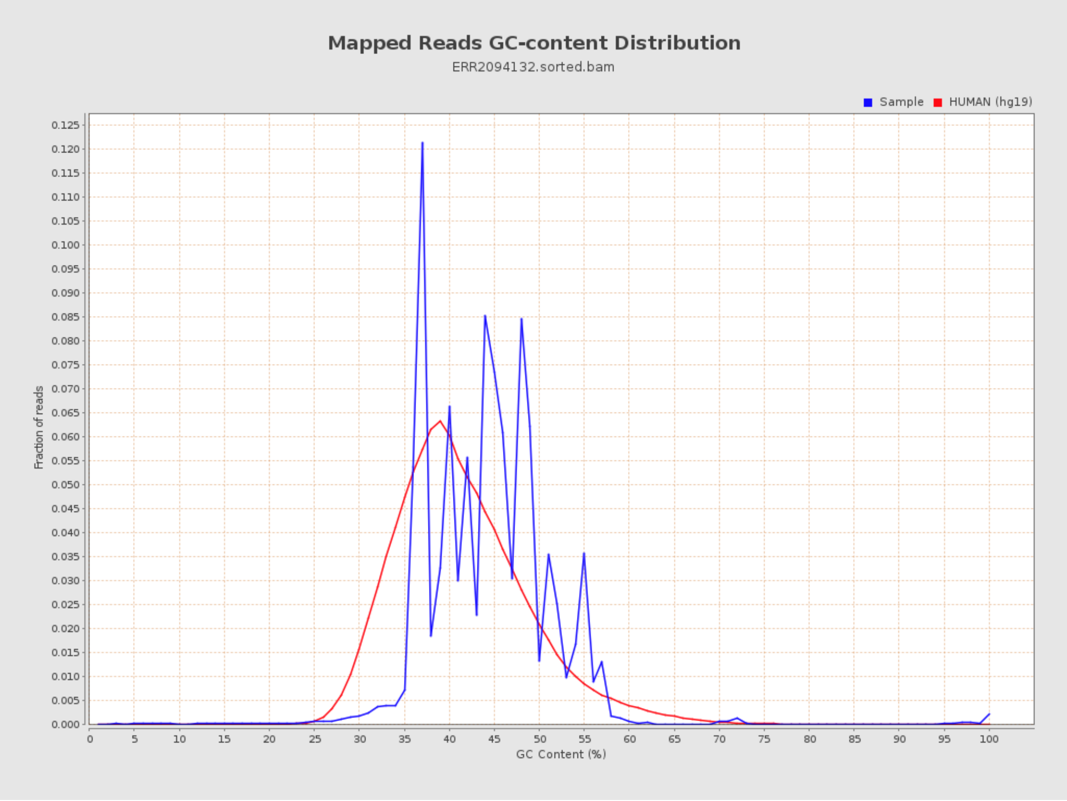
7. Results : Duplication Rate Histogram



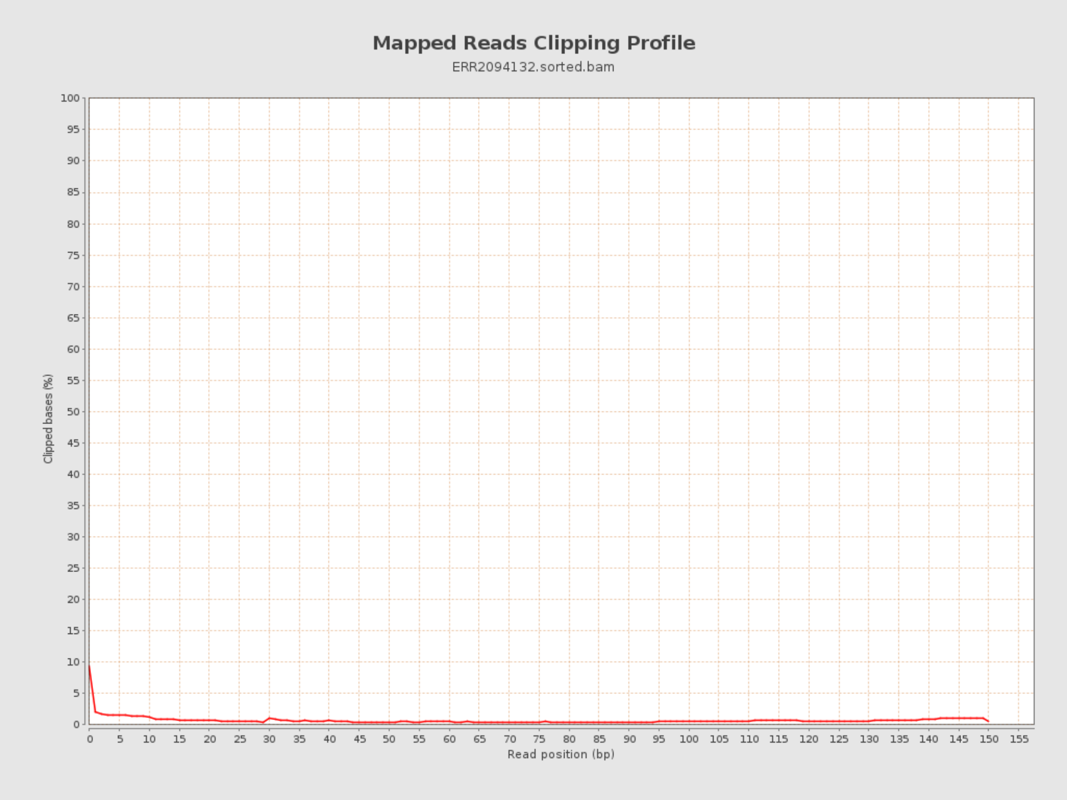
8. Results : Mapped Reads Nucleotide Content



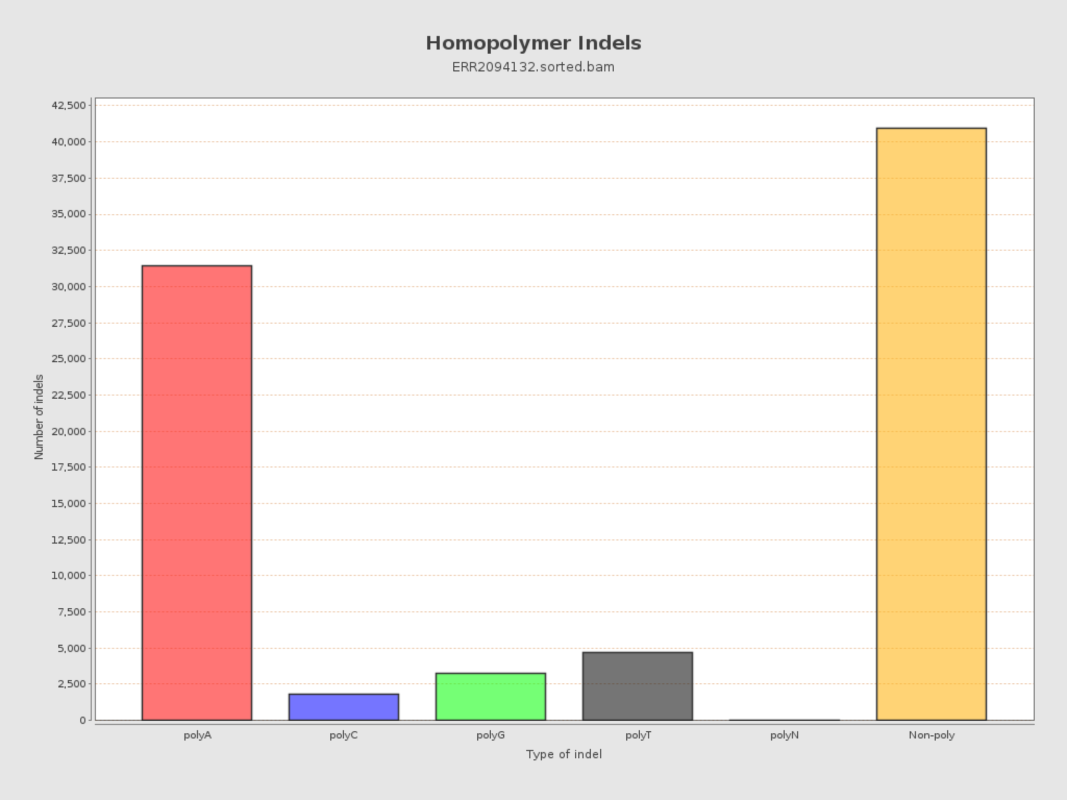
9. Results : Mapped Reads GC-content Distribution



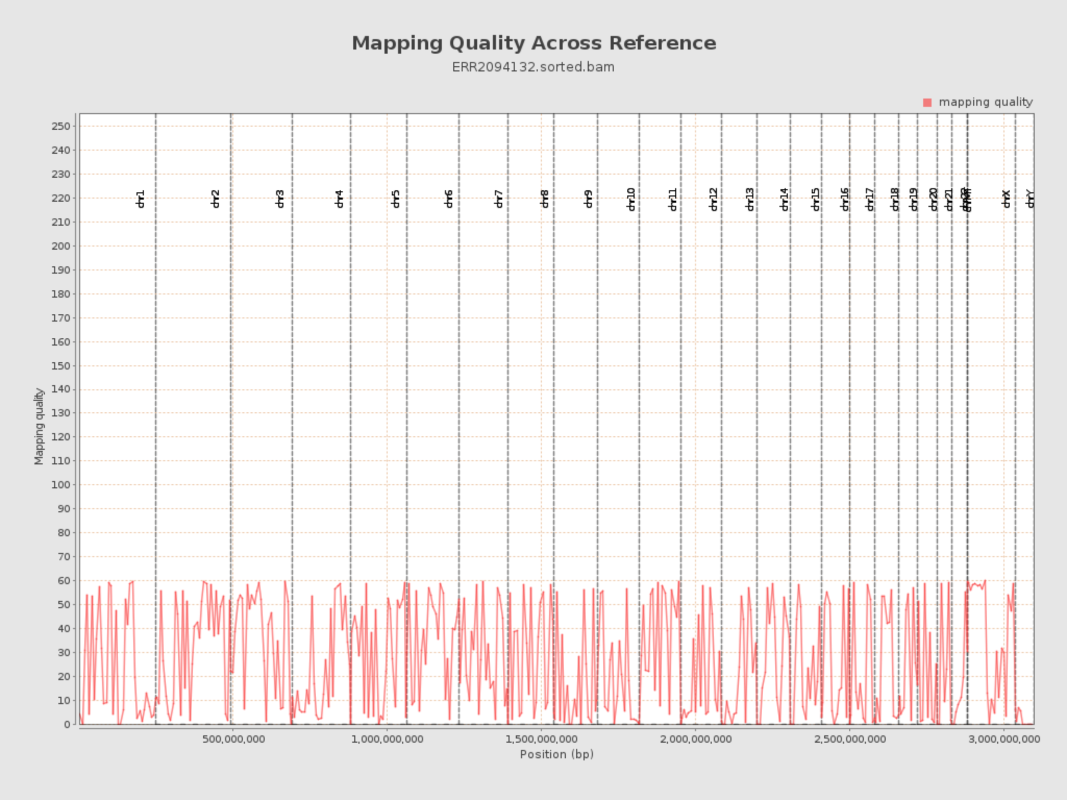
10. Results : Mapped Reads Clipping Profile



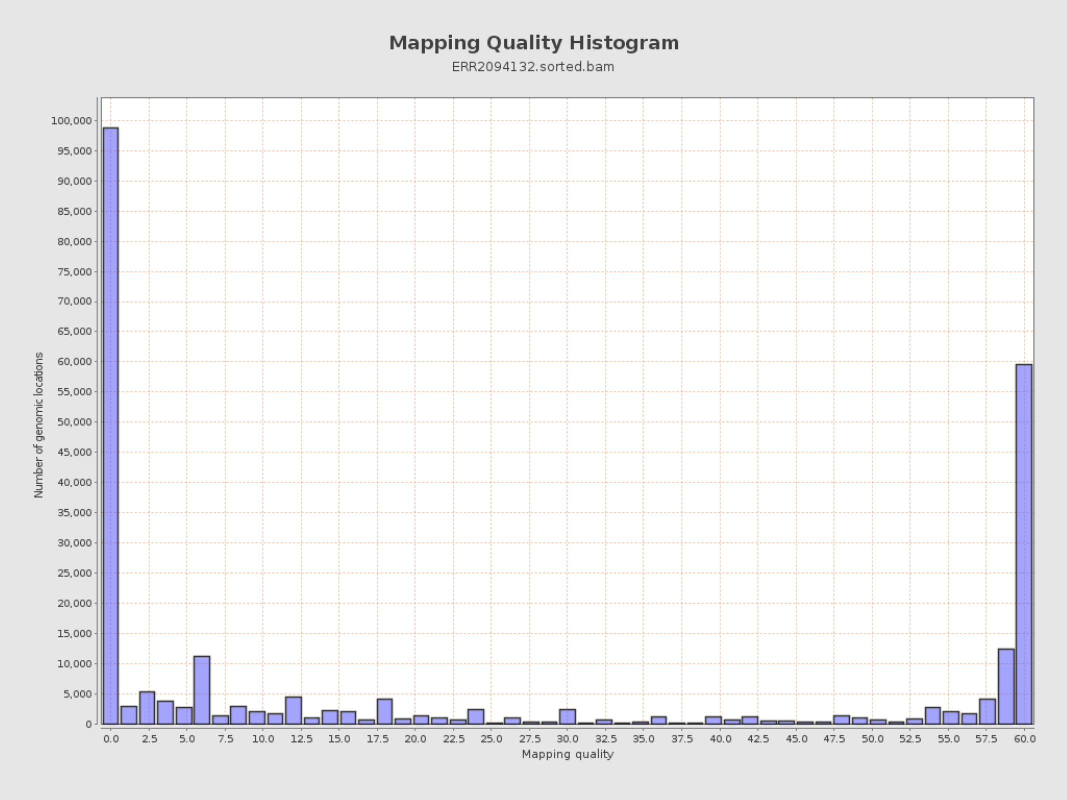
11. Results : Homopolymer Indels



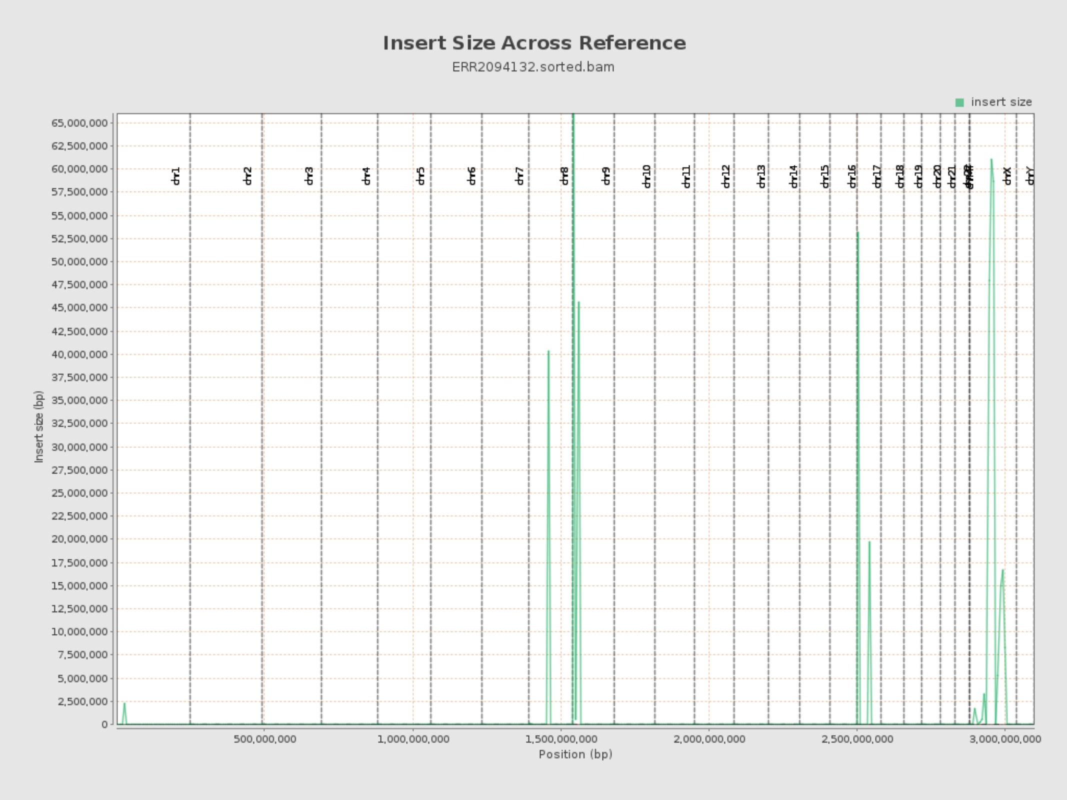
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram