Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:50:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094011.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_ERR2094011 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094011_1.fastq.gz ERR2094011_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:50:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094011.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	420,380
Mapped reads	293,347 / 69.78%
Unmapped reads	127,033 / 30.22%
Mapped paired reads	293,347 / 69.78%
Mapped reads, first in pair	146,804 / 34.92%
Mapped reads, second in pair	146,543 / 34.86%
Mapped reads, both in pair	290,332 / 69.06%
Mapped reads, singletons	3,015 / 0.72%
Secondary alignments	0
Supplementary alignments	4,722 / 1.12%
Read min/max/mean length	30 / 151 / 116.46
Duplicated reads (estimated)	290,294 / 69.06%
Duplication rate	48.51%
Clipped reads	77,063 / 18.33%

2.2. ACGT Content

Number/percentage of A's	11,266,955 / 28.2%
Number/percentage of C's	8,542,964 / 21.38%
Number/percentage of T's	11,212,890 / 28.07%
Number/percentage of G's	8,929,135 / 22.35%
Number/percentage of N's	605 / 0%

GC Percentage	43.73%

2.3. Coverage

Mean	0.0131
Standard Deviation	15.0708

2.4. Mapping Quality

Mean Mapping Quality	30.27

2.5. Insert size

Mean	54,588.19
Standard Deviation	2,661,026.63
P25/Median/P75	156 / 196 / 217

2.6. Mismatches and indels

General error rate	2.79%
Mismatches	1,091,328
Insertions	14,842
Mapped reads with at least one insertion	4.98%
Deletions	69,228
Mapped reads with at least one deletion	21.79%
Homopolymer indels	34.84%

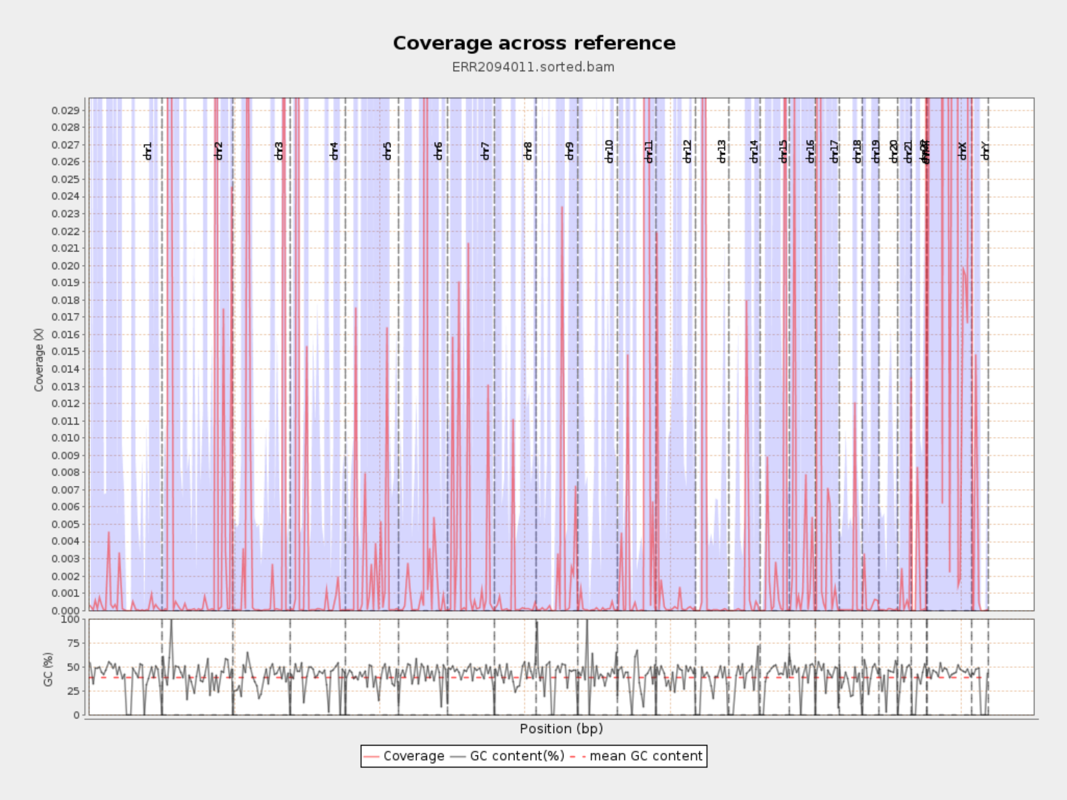
2.7. Chromosome stats

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

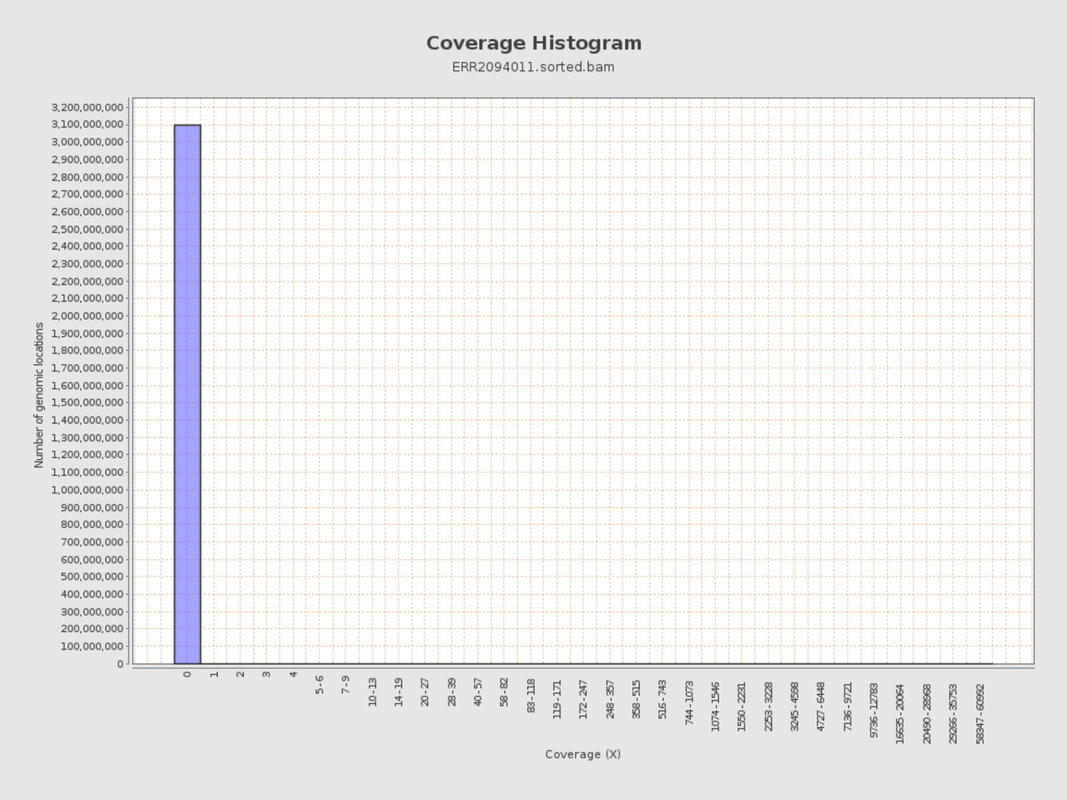
		bases	coverage	deviation
chr1	249250621	103641	0.0004	0.2721
chr2	243199373	2488961	0.0102	7.3649
chr3	198022430	834113	0.0042	2.8323
chr4	191154276	887292	0.0046	4.5548
chr5	180915260	439494	0.0024	1.1107
chr6	171115067	1252661	0.0073	6.727
chr7	159138663	595737	0.0037	1.7236
chr8	146364022	105138	0.0007	0.583
chr9	141213431	304670	0.0022	0.8726
chr10	135534747	21796	0.0002	0.0759
chr11	135006516	1482417	0.011	5.7565
chr12	133851895	191739	0.0014	1.1223
chr13	115169878	594936	0.0052	4.3231
chr14	107349540	152023	0.0014	1.0167
chr15	102531392	462694	0.0045	2.6611
chr16	90354753	376025	0.0042	2.1982
chr17	81195210	952873	0.0117	6.1513
chr18	78077248	95613	0.0012	0.7737
chr19	59128983	38944	0.0007	0.2538
chr20	63025520	3054	0	0.0091
chr21	48129895	90800	0.0019	0.6853
chr22	51304566	66615	0.0013	0.6817
chrMT	16571	18219964	1,099.509	5,864.7086
chrX	155270560	10545832	0.0679	21.898

chrY	59373566	119296	0.002	1.3014

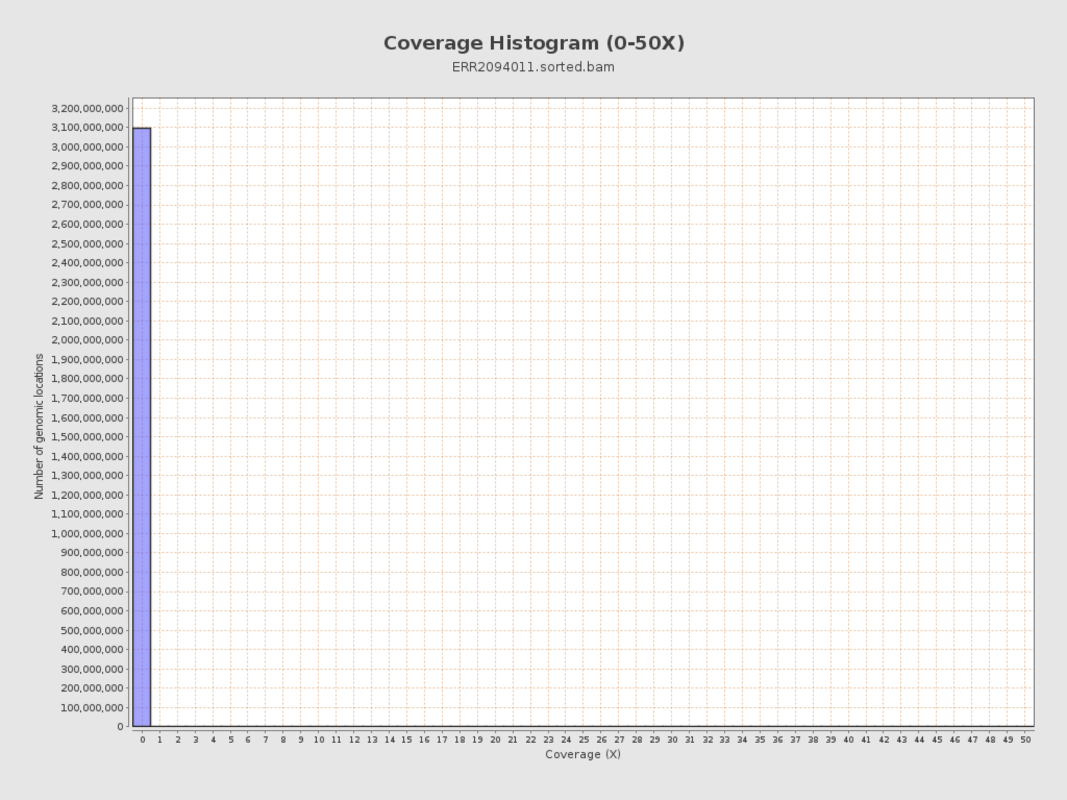
3. Results : Coverage across reference



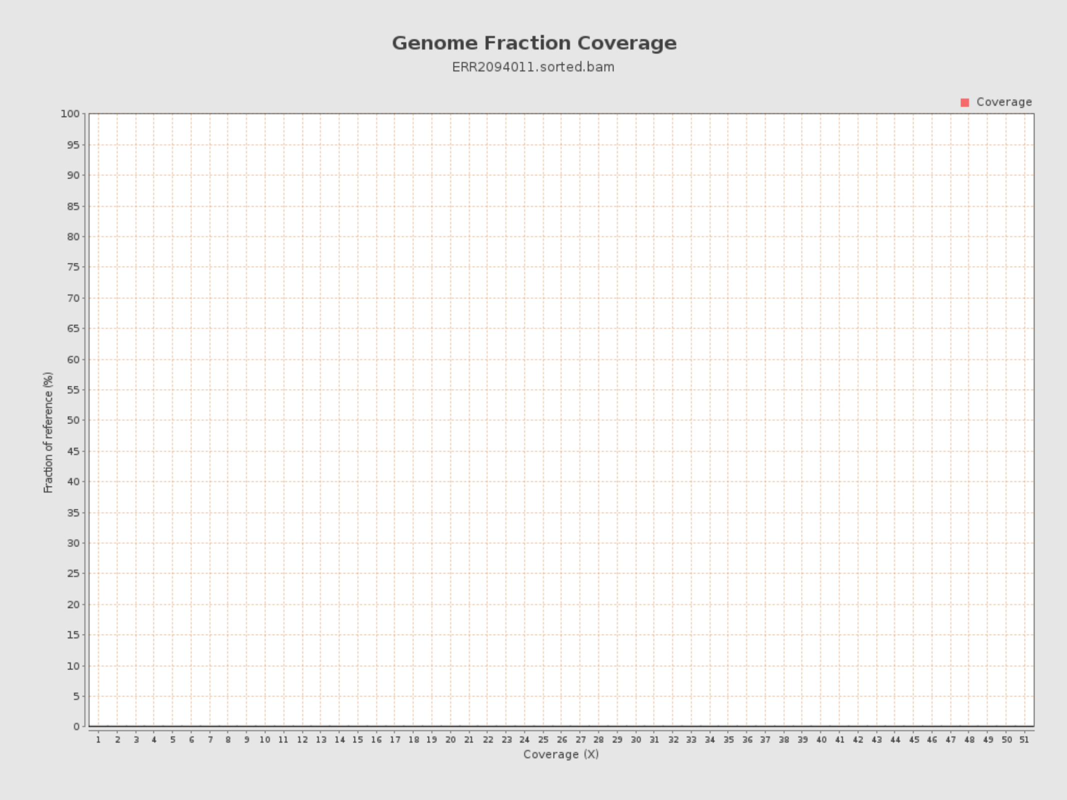
4. Results : Coverage Histogram



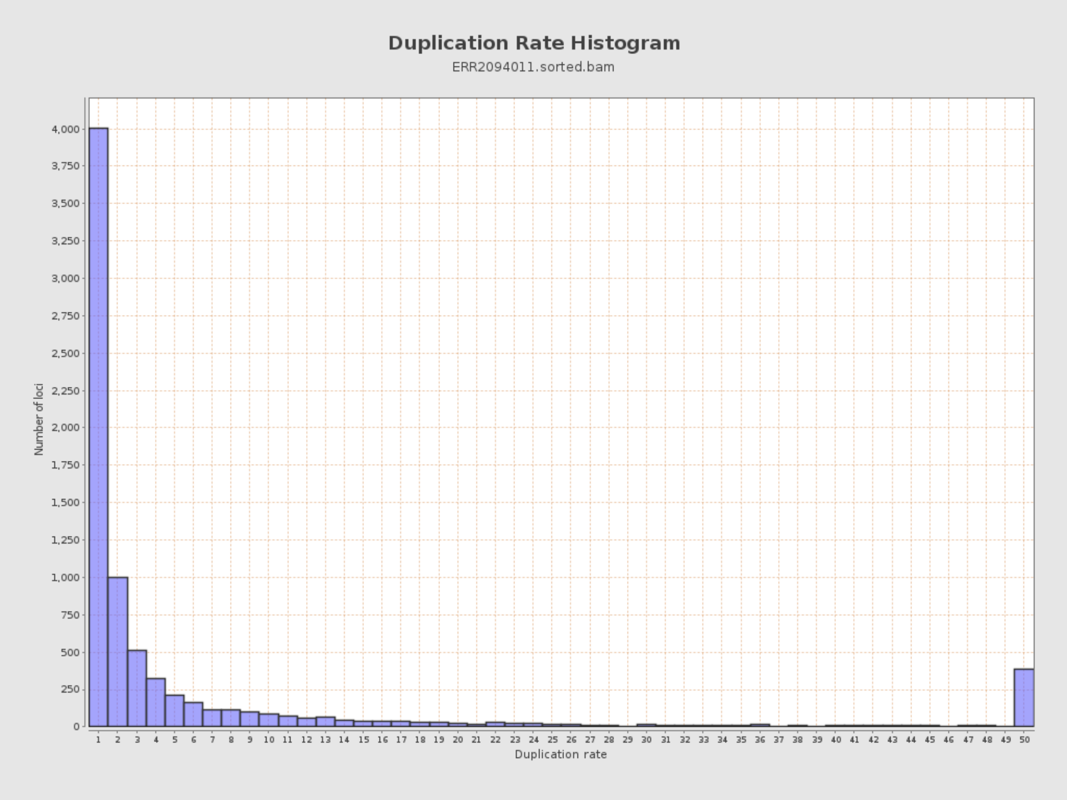
5. Results : Coverage Histogram (0-50X)



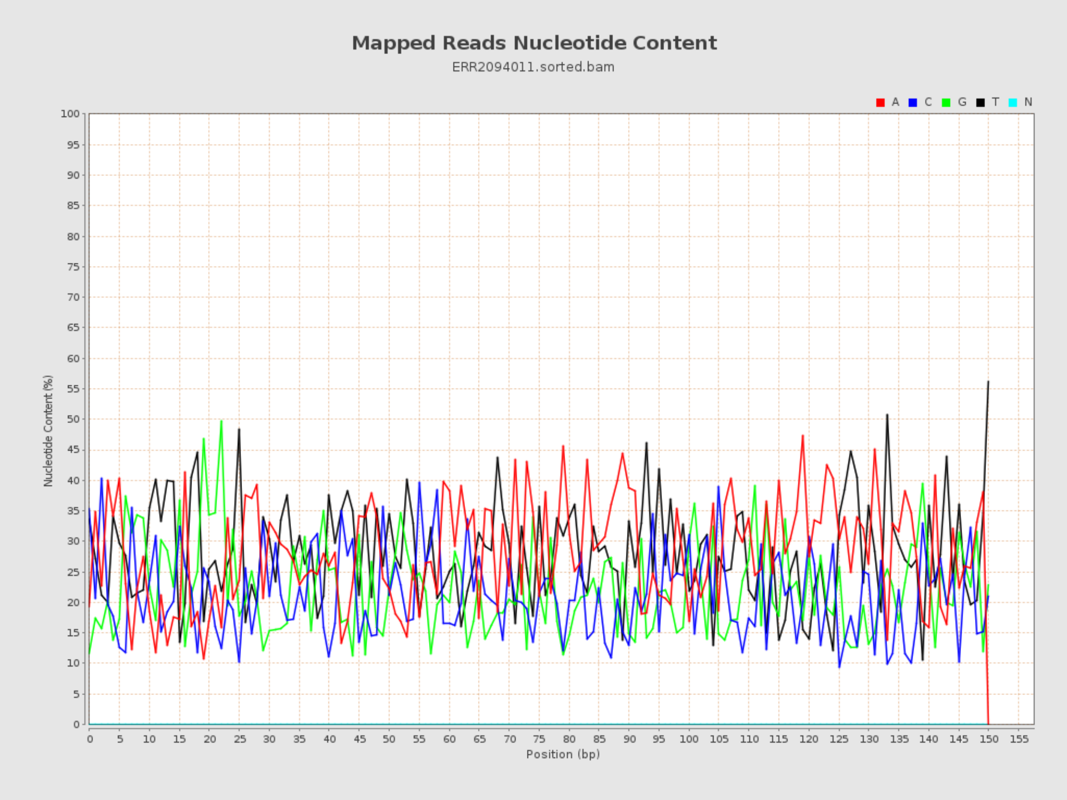
6. Results : Genome Fraction Coverage



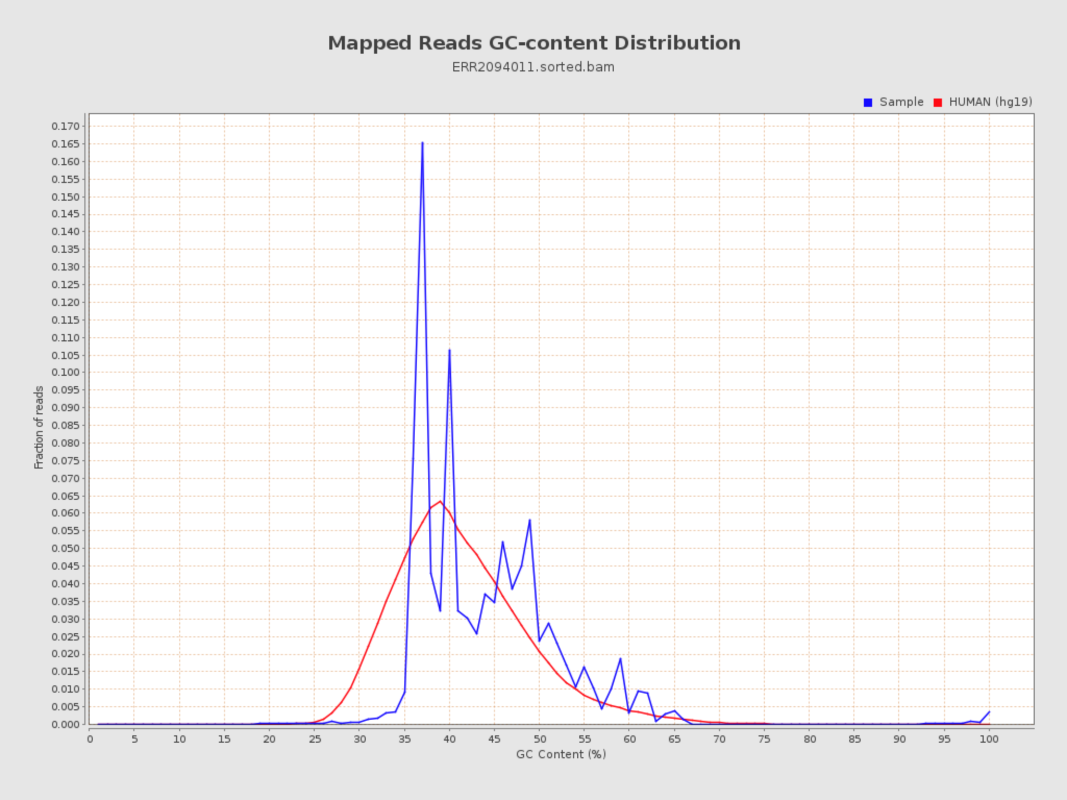
7. Results : Duplication Rate Histogram



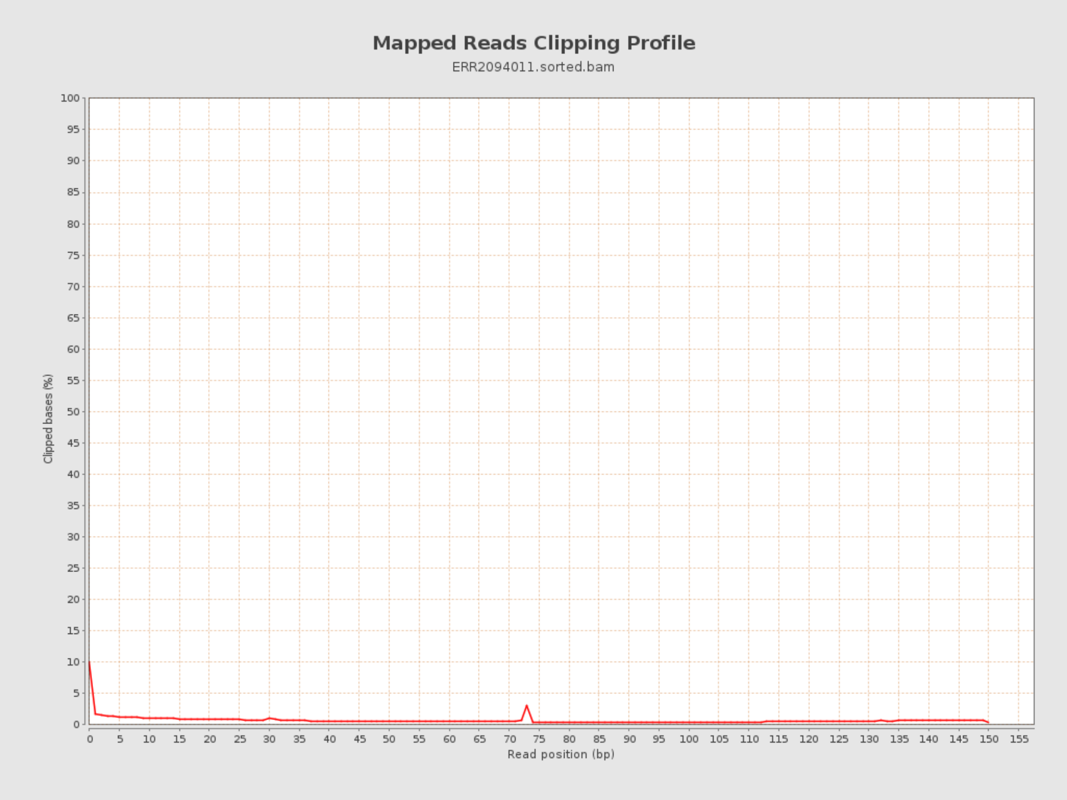
8. Results : Mapped Reads Nucleotide Content



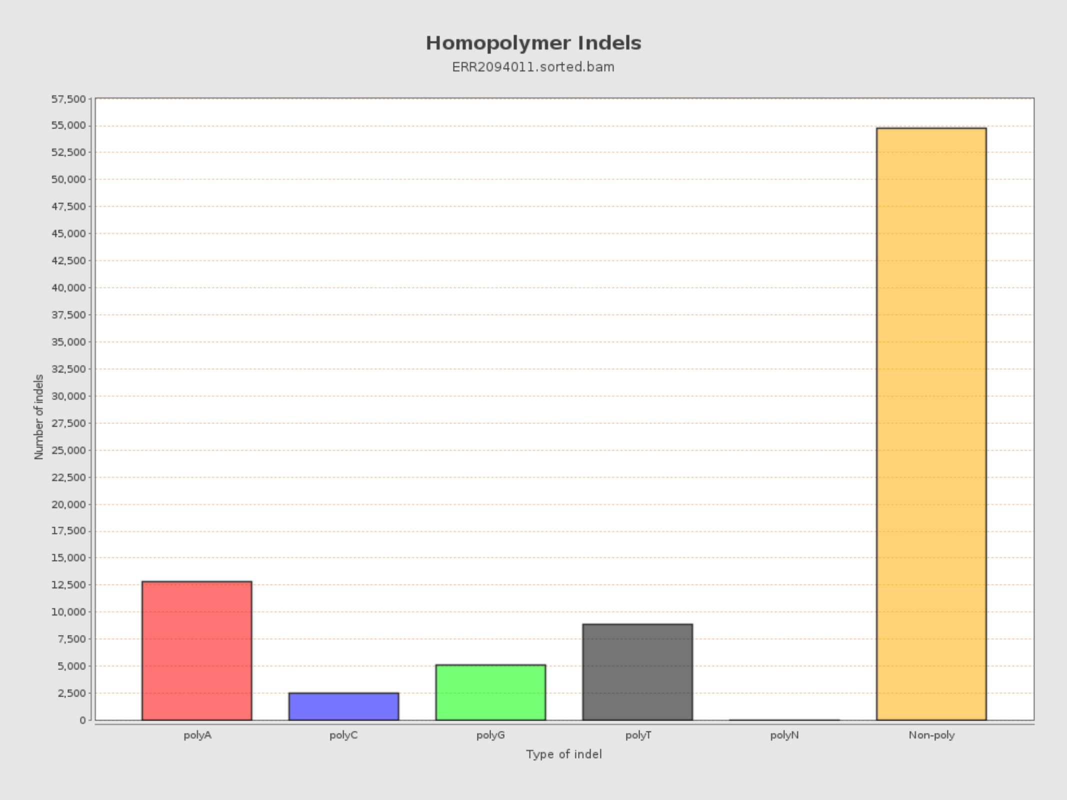
9. Results : Mapped Reads GC-content Distribution



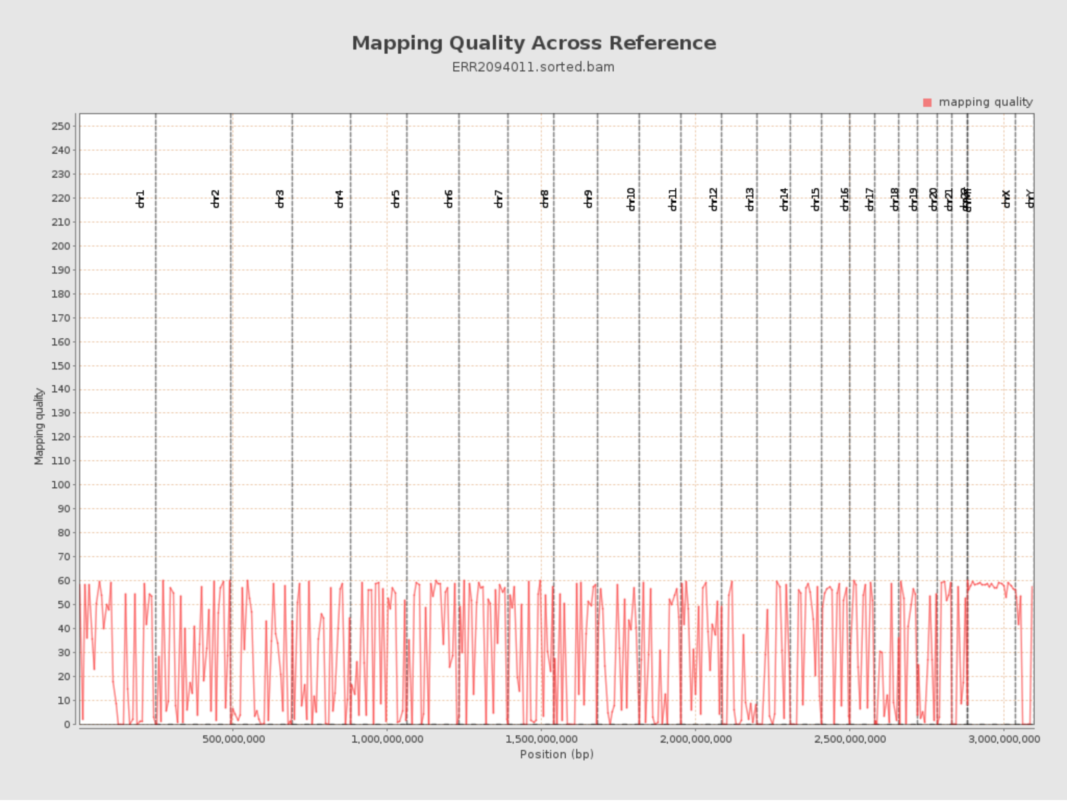
10. Results : Mapped Reads Clipping Profile



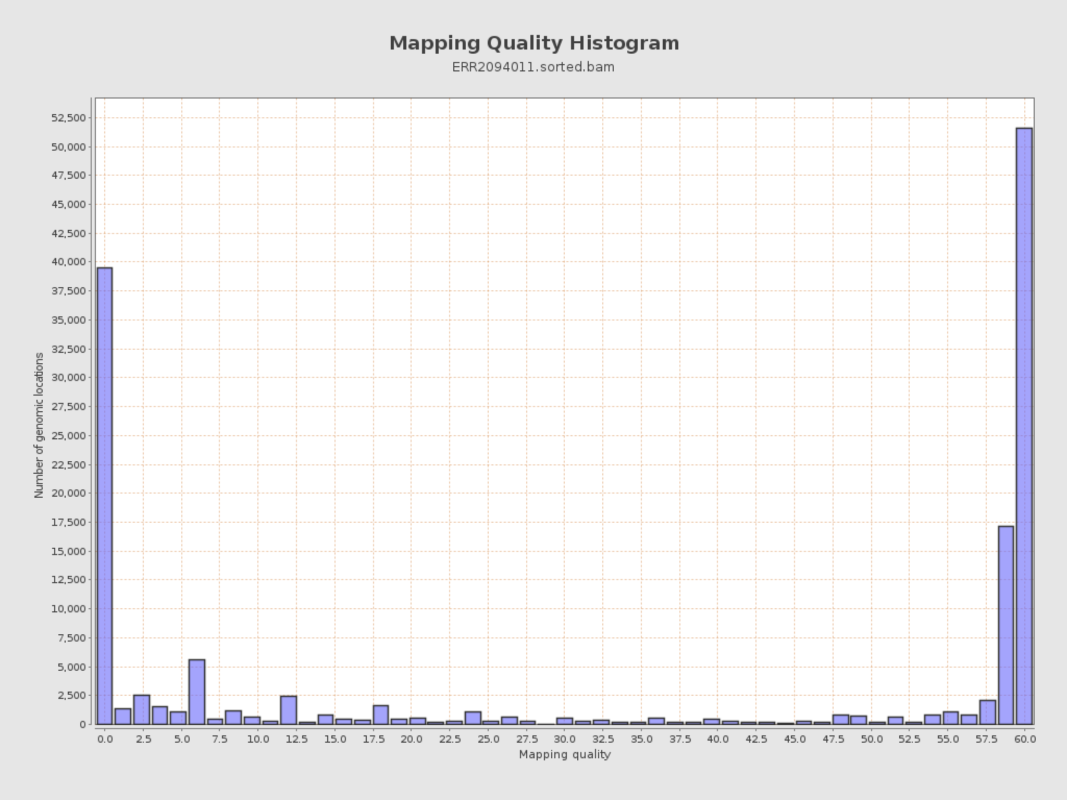
11. Results : Homopolymer Indels



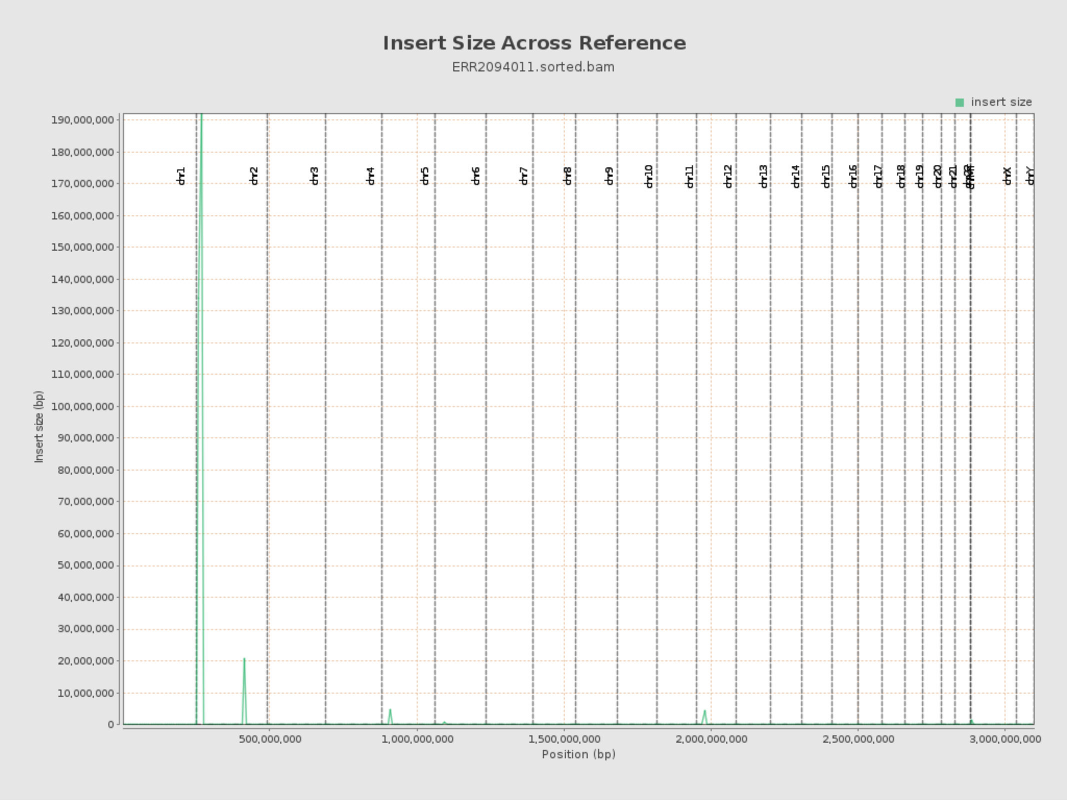
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram