Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:55:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094040.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_ERR2094040 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094040_1.fastq.gz ERR2094040_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:55:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	406,768
Mapped reads	375,851 / 92.4%
Unmapped reads	30,917 / 7.6%
Mapped paired reads	375,851 / 92.4%
Mapped reads, first in pair	188,620 / 46.37%
Mapped reads, second in pair	187,231 / 46.03%
Mapped reads, both in pair	373,228 / 91.75%
Mapped reads, singletons	2,623 / 0.64%
Secondary alignments	0
Supplementary alignments	9,259 / 2.28%
Read min/max/mean length	30 / 151 / 135.7
Duplicated reads (estimated)	363,278 / 89.31%
Duplication rate	51.89%
Clipped reads	153,800 / 37.81%

2.2. ACGT Content

Number/percentage of A's	13,303,407 / 27.92%
Number/percentage of C's	10,500,923 / 22.04%
Number/percentage of T's	13,043,292 / 27.38%
Number/percentage of G's	10,796,036 / 22.66%
Number/percentage of N's	432 / 0%

GC Percentage	44.7%

2.3. Coverage

Mean	0.0159
Standard Deviation	5.6122

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Insert size

Mean	150,516.47
Standard Deviation	4,217,872.8
P25/Median/P75	133 / 167 / 190

2.6. Mismatches and indels

General error rate	5.28%
Mismatches	2,482,471
Insertions	32,557
Mapped reads with at least one insertion	8.49%
Deletions	166,676
Mapped reads with at least one deletion	41.4%
Homopolymer indels	31.79%

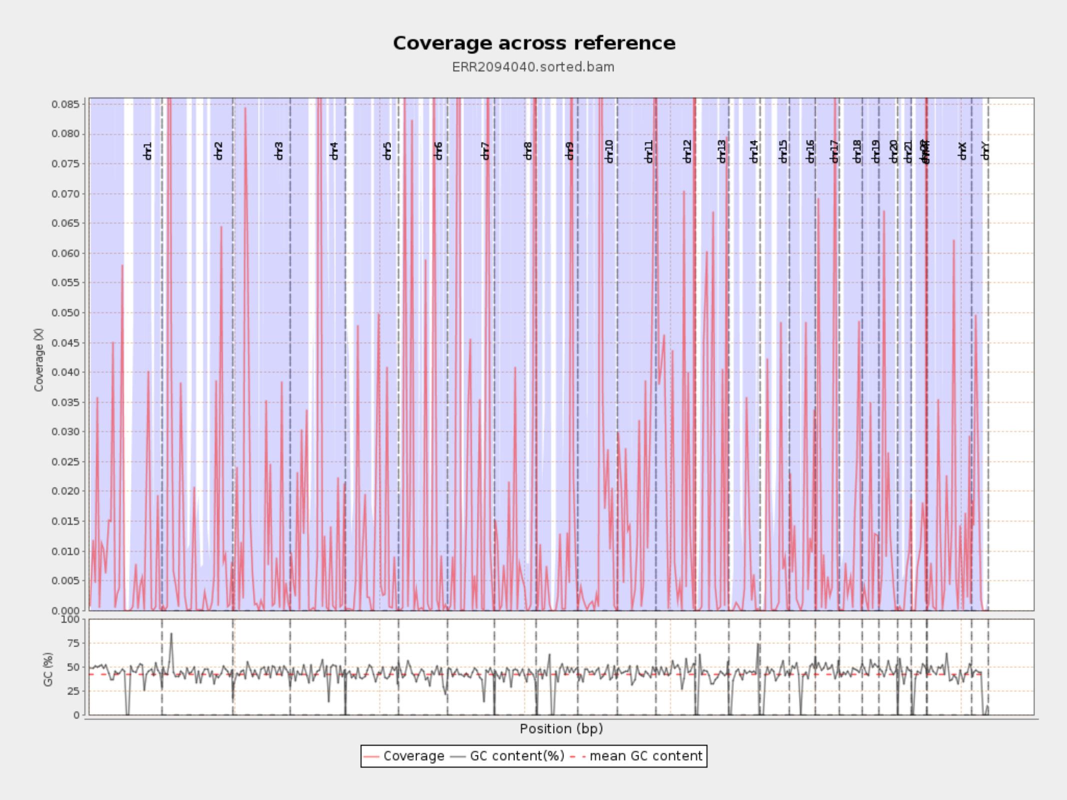
2.7. Chromosome stats

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

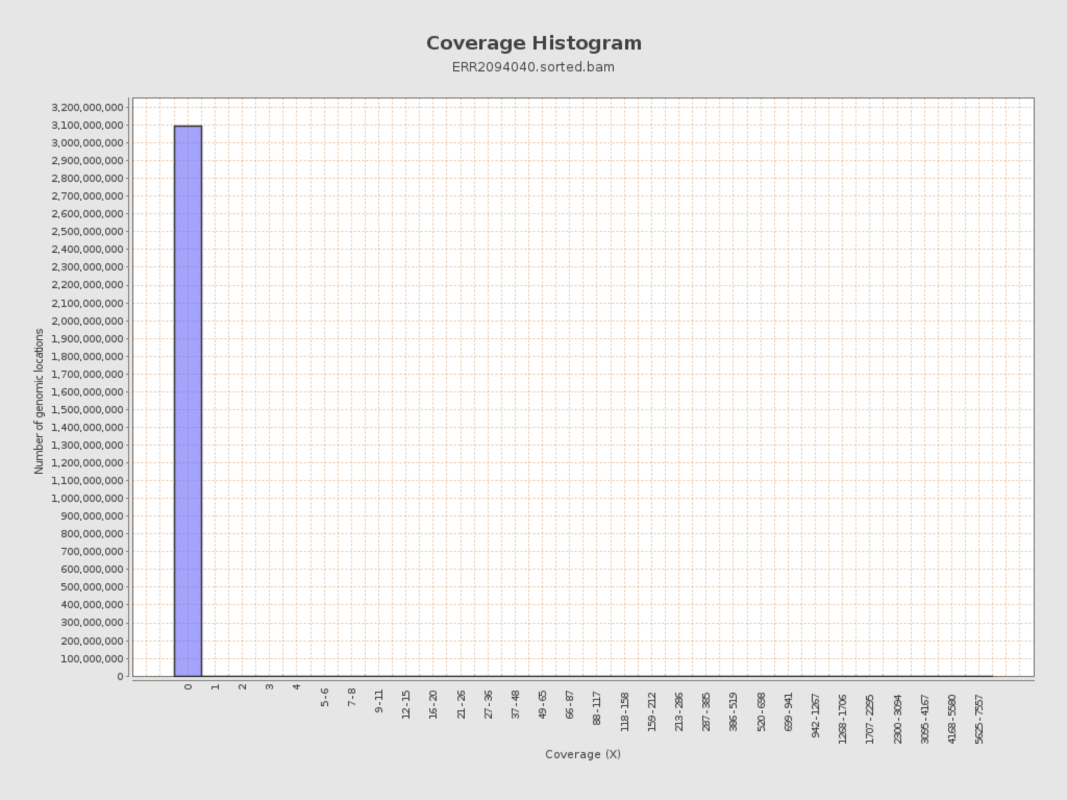
		bases	coverage	deviation
chr1	249250621	2495144	0.01	3.4801
chr2	243199373	3379958	0.0139	4.2496
chr3	198022430	2584728	0.0131	4.1874
chr4	191154276	2935573	0.0154	4.3749
chr5	180915260	1670814	0.0092	3.8721
chr6	171115067	2786655	0.0163	7.7772
chr7	159138663	4062131	0.0255	7.5214
chr8	146364022	2140158	0.0146	5.9055
chr9	141213431	1514547	0.0107	4.7104
chr10	135534747	2378947	0.0176	6.967
chr11	135006516	3150019	0.0233	5.4597
chr12	133851895	4086637	0.0305	7.8496
chr13	115169878	2570646	0.0223	6.2172
chr14	107349540	488704	0.0046	2.3052
chr15	102531392	958968	0.0094	2.5379
chr16	90354753	1137219	0.0126	4.1422
chr17	81195210	1486591	0.0183	6.835
chr18	78077248	833521	0.0107	3.2019
chr19	59128983	516338	0.0087	2.6912
chr20	63025520	983565	0.0156	5.3336
chr21	48129895	230881	0.0048	0.9313
chr22	51304566	388627	0.0076	1.8292
chrMT	16571	4000088	241.3909	979.2363
chrX	155270560	1807886	0.0116	3.6379

chrY	59373566	750500	0.0126	3.2786

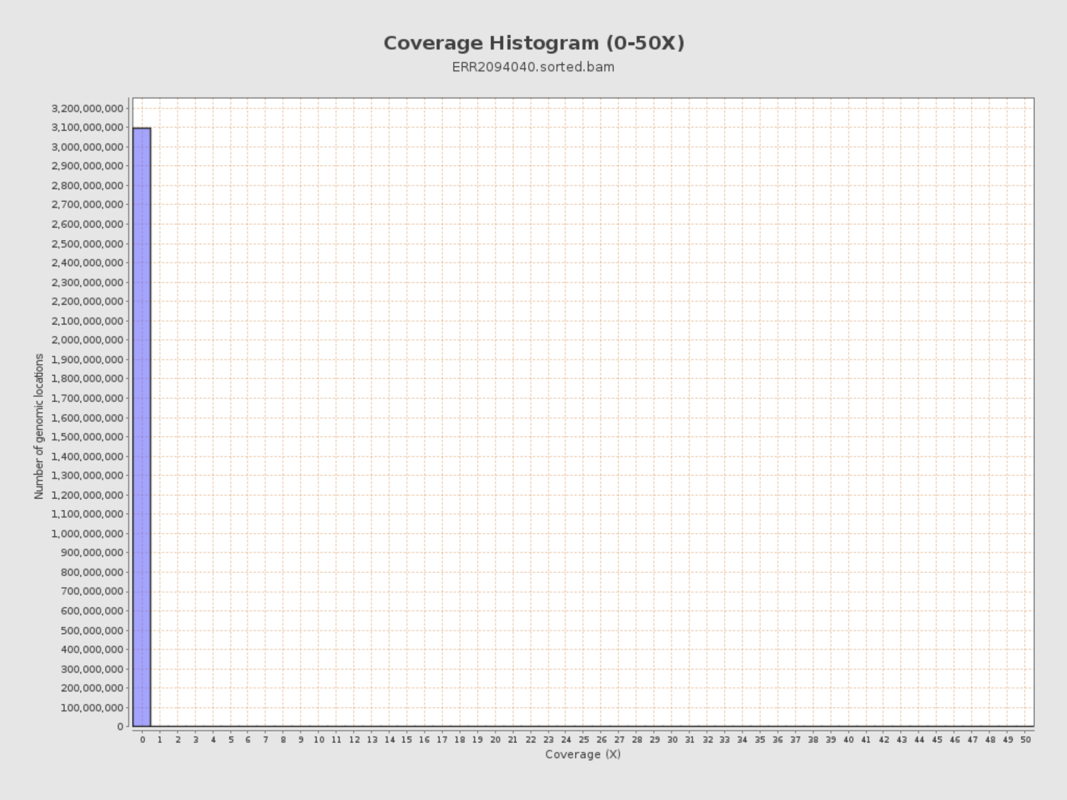
3. Results : Coverage across reference



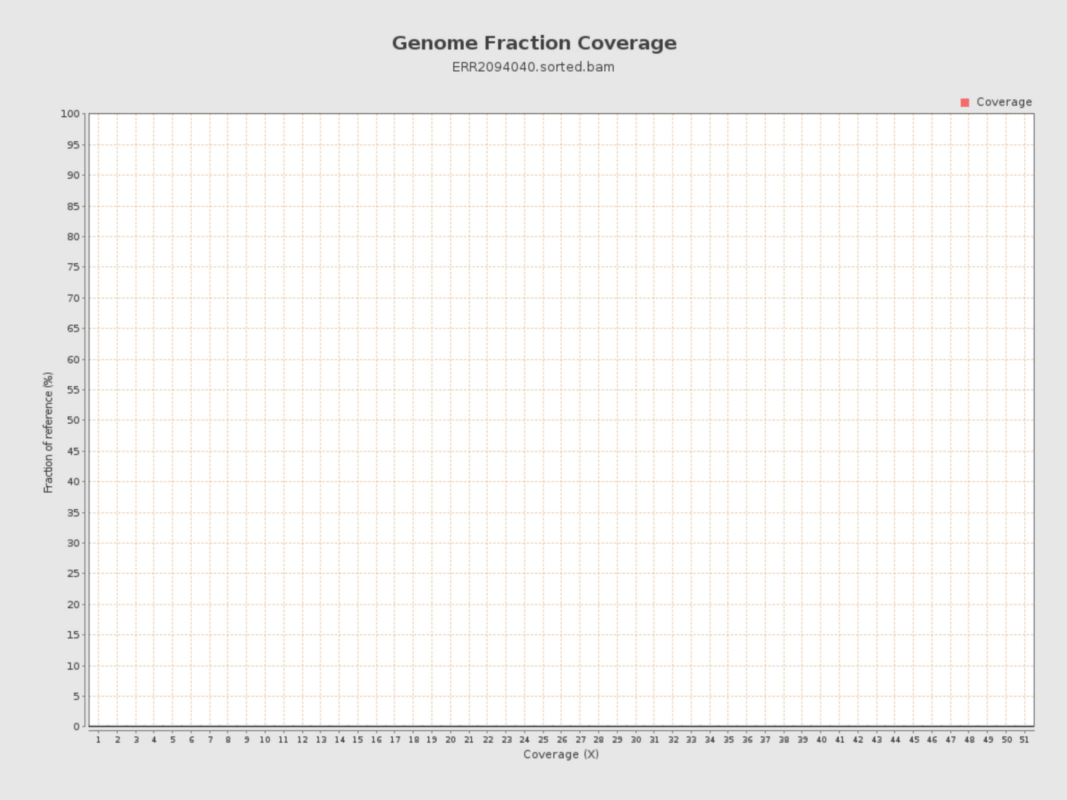
4. Results : Coverage Histogram



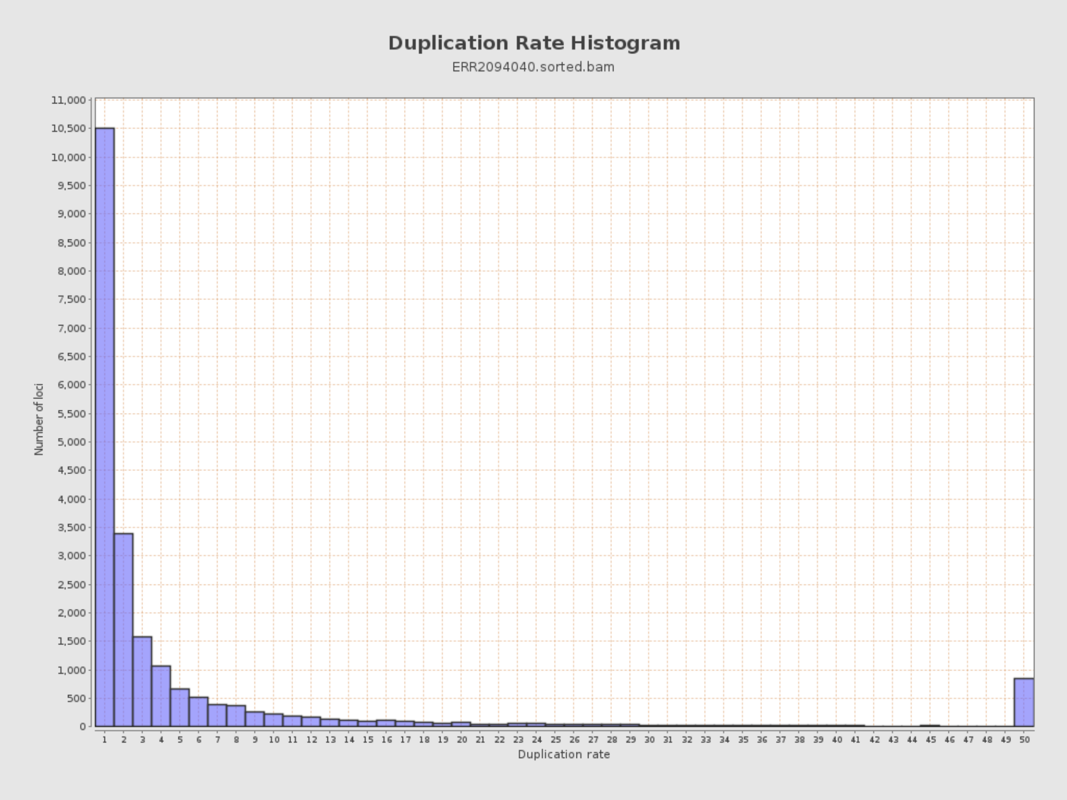
5. Results : Coverage Histogram (0-50X)



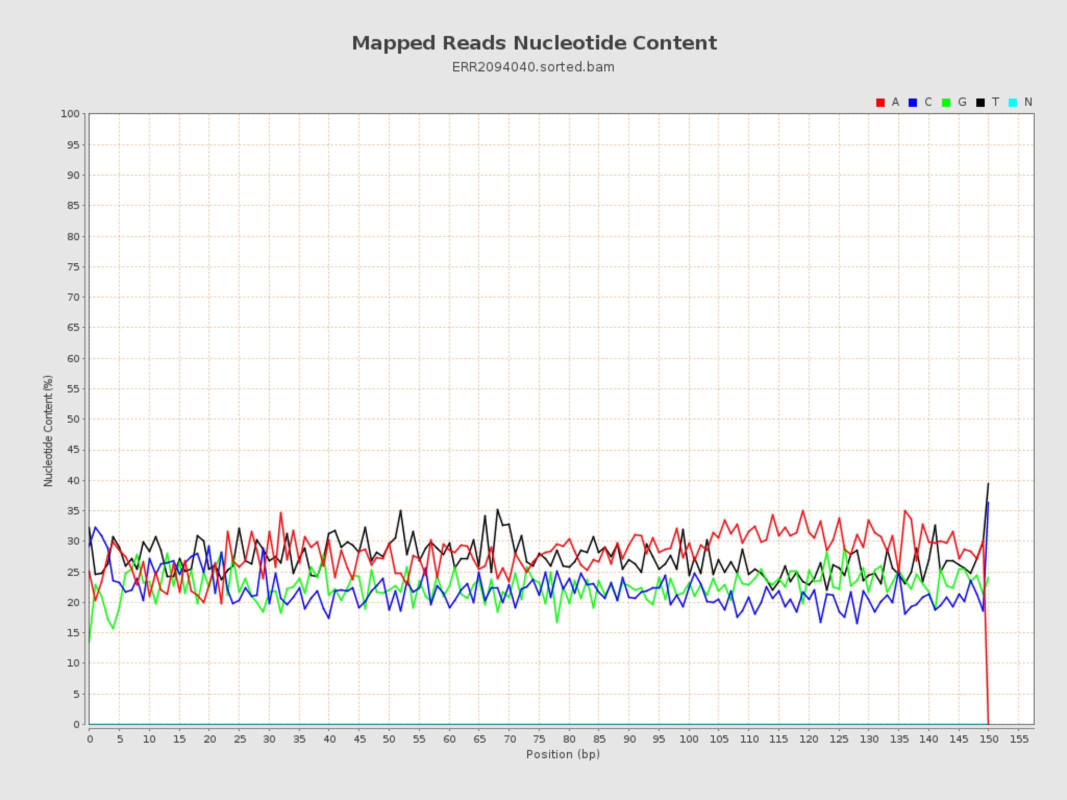
6. Results : Genome Fraction Coverage



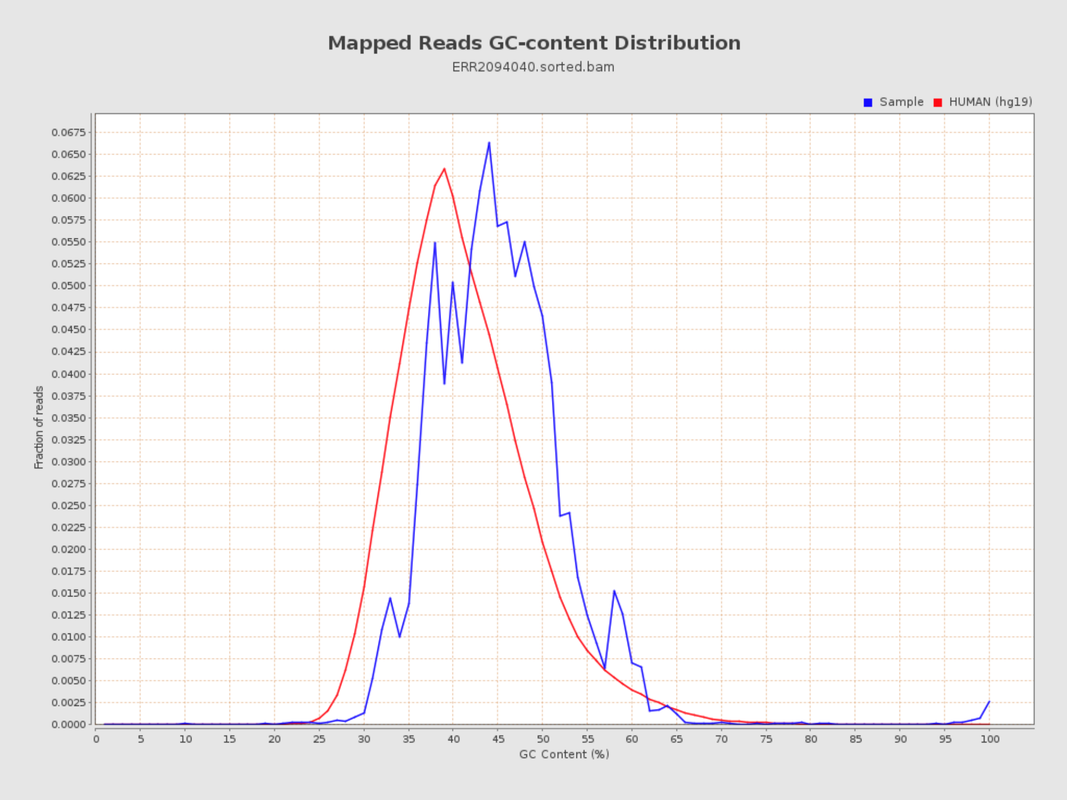
7. Results : Duplication Rate Histogram



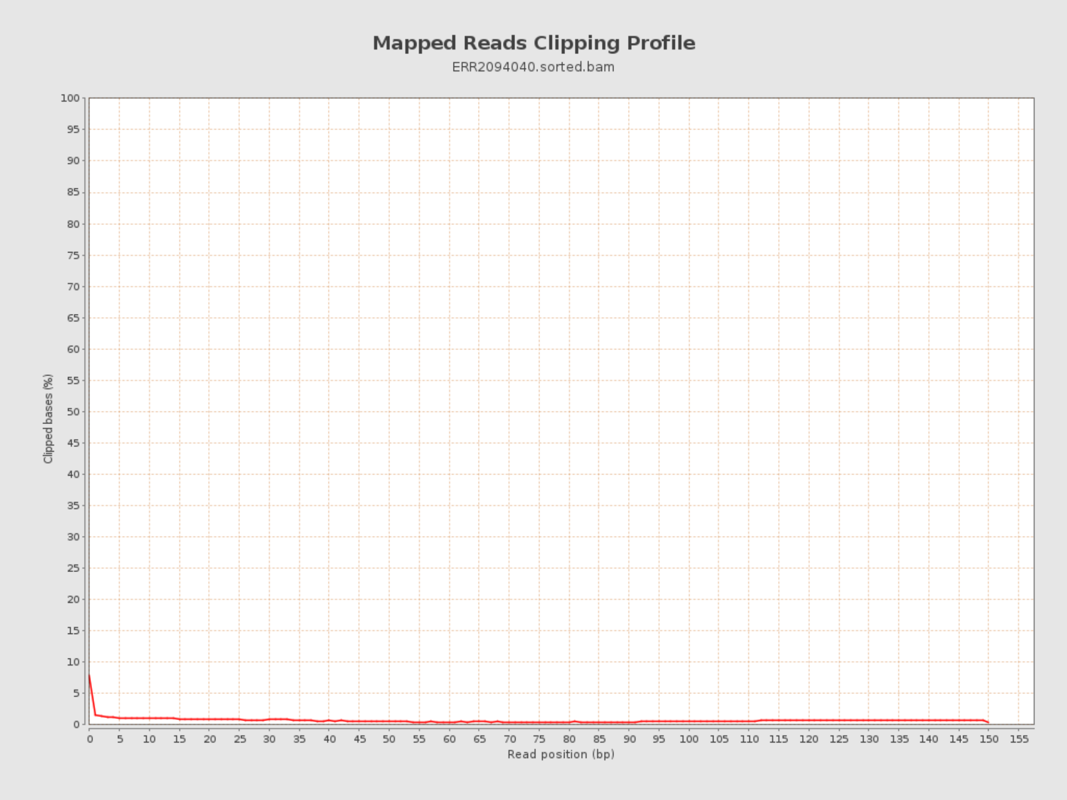
8. Results : Mapped Reads Nucleotide Content



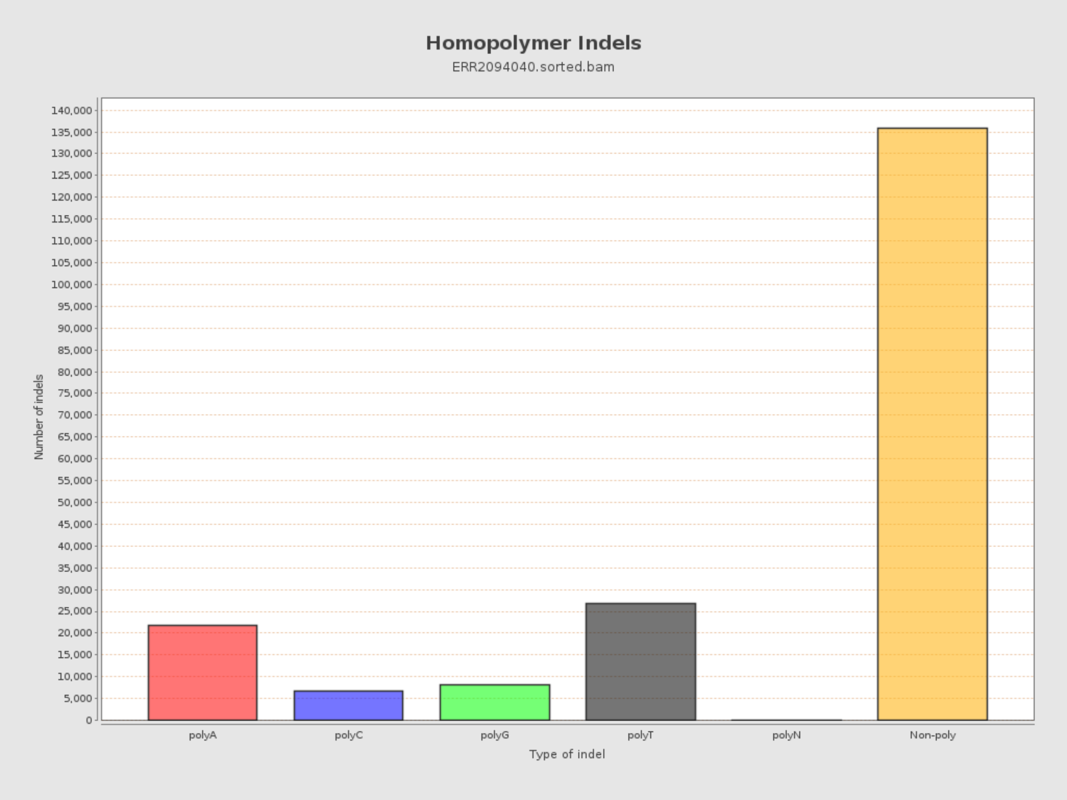
9. Results : Mapped Reads GC-content Distribution



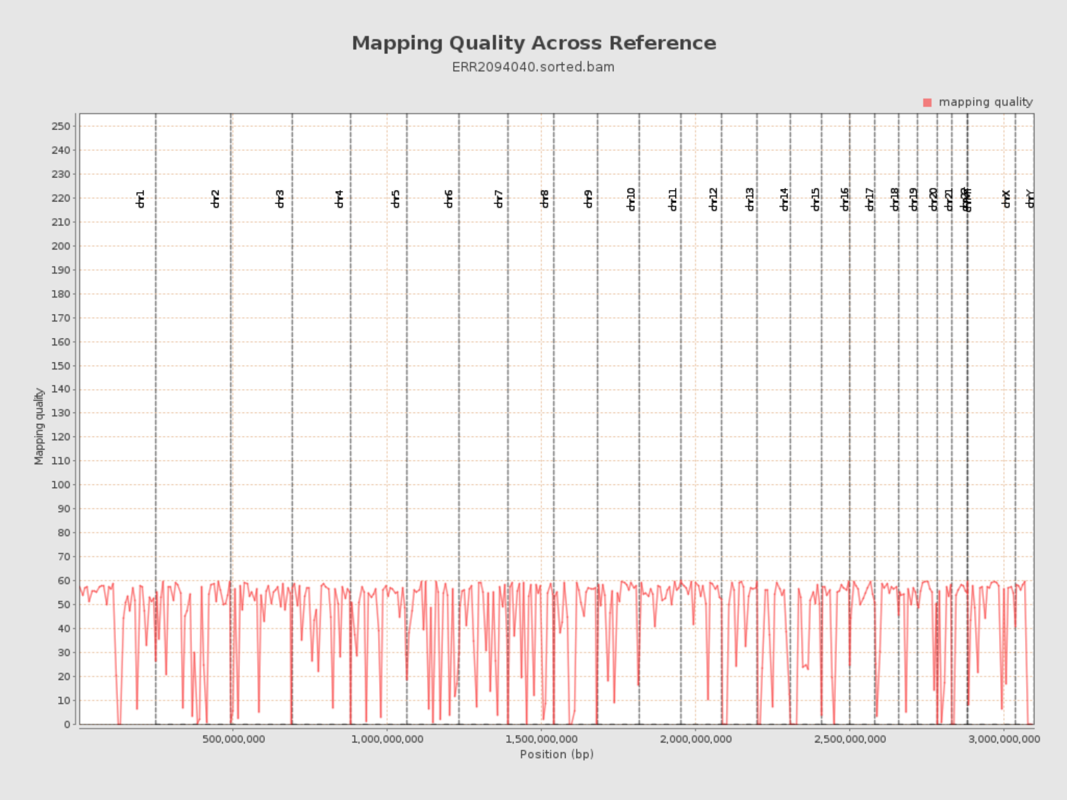
10. Results : Mapped Reads Clipping Profile



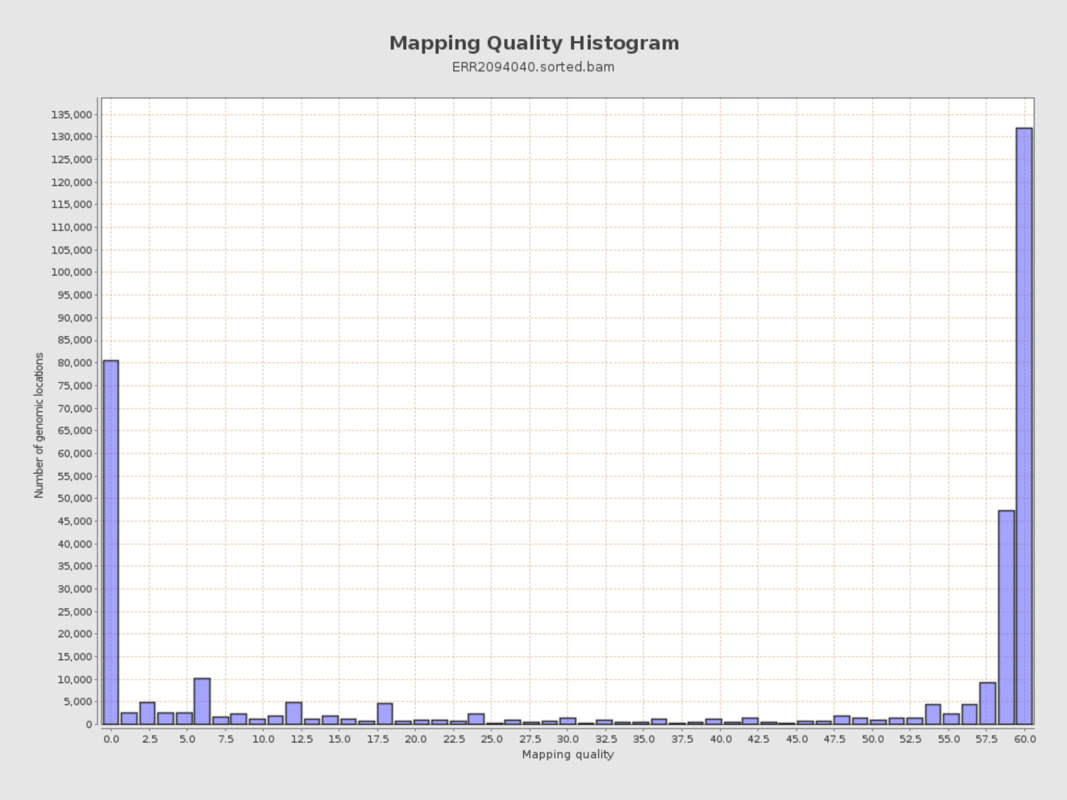
11. Results : Homopolymer Indels



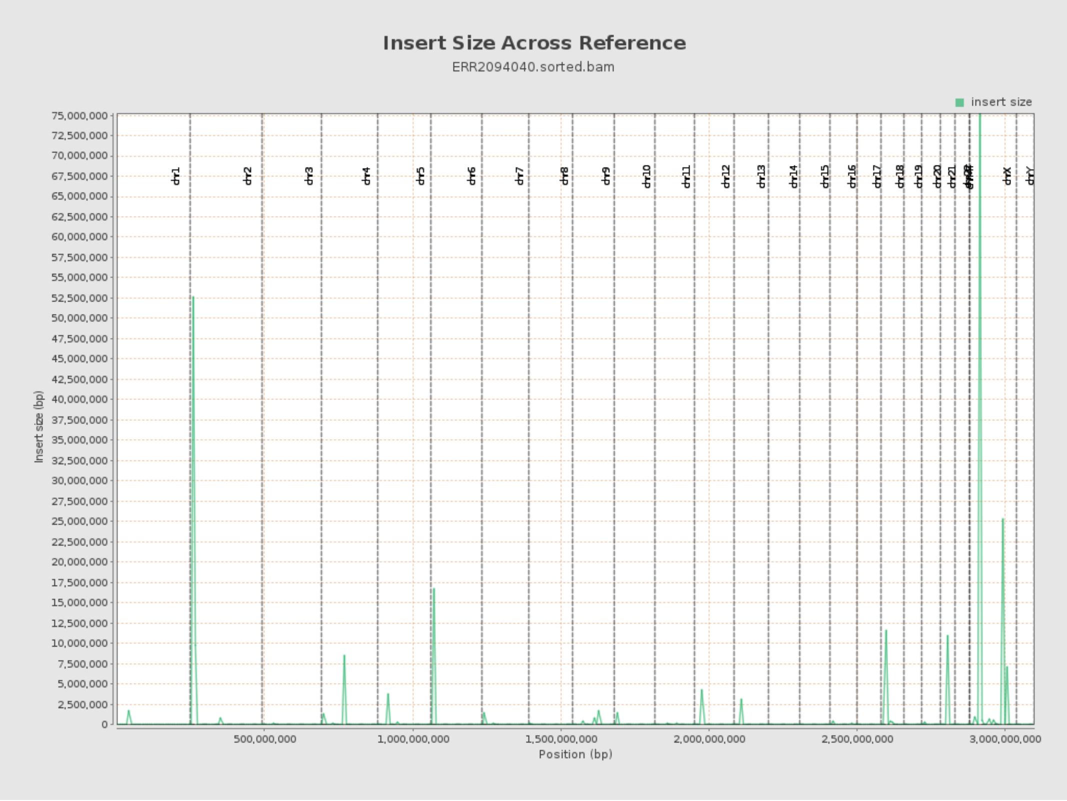
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram