Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:07:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094021.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_ERR2094021 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094021_1.fastq.gz ERR2094021_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:07:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	422,474
Mapped reads	380,092 / 89.97%
Unmapped reads	42,382 / 10.03%
Mapped paired reads	380,092 / 89.97%
Mapped reads, first in pair	190,971 / 45.2%
Mapped reads, second in pair	189,121 / 44.77%
Mapped reads, both in pair	375,916 / 88.98%
Mapped reads, singletons	4,176 / 0.99%
Secondary alignments	0
Supplementary alignments	18,803 / 4.45%
Read min/max/mean length	30 / 151 / 135.41
Duplicated reads (estimated)	353,139 / 83.59%
Duplication rate	47.49%
Clipped reads	181,614 / 42.99%

2.2. ACGT Content

Number/percentage of A's	13,083,920 / 27.72%
Number/percentage of C's	10,531,746 / 22.32%
Number/percentage of T's	12,460,836 / 26.4%
Number/percentage of G's	11,118,755 / 23.56%
Number/percentage of N's	431 / 0%

GC Percentage	45.87%

2.3. Coverage

Mean	0.0156
Standard Deviation	4.4125

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Insert size

Mean	642,330.07
Standard Deviation	7,207,733.44
P25/Median/P75	124 / 159 / 201

2.6. Mismatches and indels

General error rate	3.87%
Mismatches	1,771,802
Insertions	28,282
Mapped reads with at least one insertion	7.32%
Deletions	137,984
Mapped reads with at least one deletion	35.07%
Homopolymer indels	29.45%

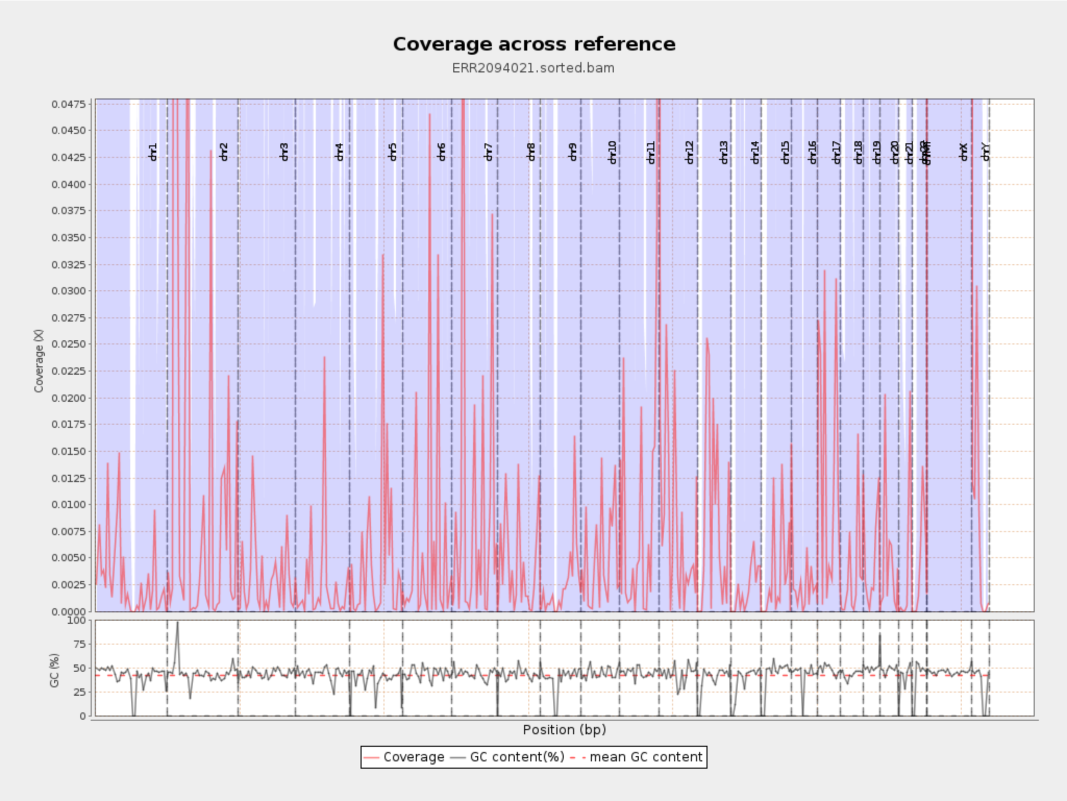
2.7. Chromosome stats

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

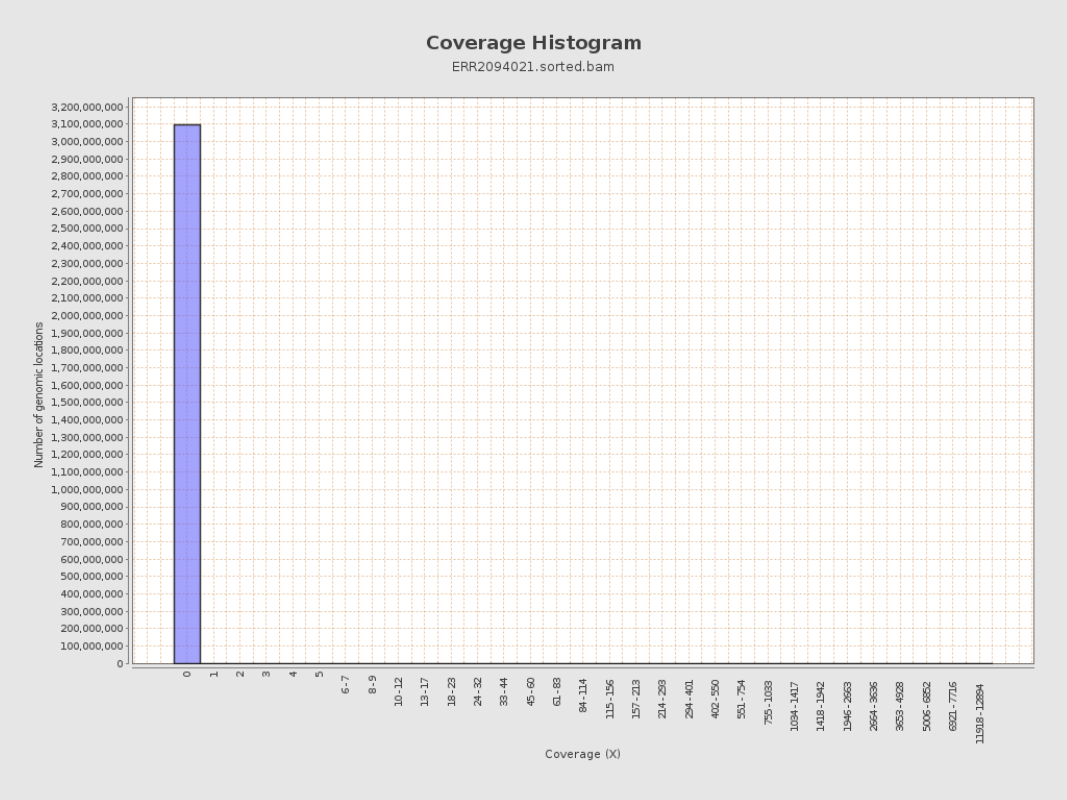
		bases	coverage	deviation
chr1	249250621	790425	0.0032	1.0145
chr2	243199373	3319994	0.0137	3.6025
chr3	198022430	594294	0.003	0.7706
chr4	191154276	528705	0.0028	0.7017
chr5	180915260	898854	0.005	1.9972
chr6	171115067	1130276	0.0066	2.5963
chr7	159138663	1593104	0.01	2.947
chr8	146364022	637034	0.0044	1.1566
chr9	141213431	381557	0.0027	0.6822
chr10	135534747	652527	0.0048	1.0763
chr11	135006516	1327312	0.0098	2.368
chr12	133851895	1060665	0.0079	1.8696
chr13	115169878	996417	0.0087	1.9337
chr14	107349540	224920	0.0021	0.5936
chr15	102531392	359784	0.0035	0.8246
chr16	90354753	258904	0.0029	0.7685
chr17	81195210	1141422	0.0141	2.942
chr18	78077248	265211	0.0034	1.1307
chr19	59128983	259929	0.0044	0.8971
chr20	63025520	306072	0.0049	1.6029
chr21	48129895	204611	0.0043	1.3664
chr22	51304566	219093	0.0043	0.7393
chrMT	16571	5273838	318.2571	1,377.1777
chrX	155270560	25352607	0.1633	10.3588

chrY	59373566	468544	0.0079	2.0816

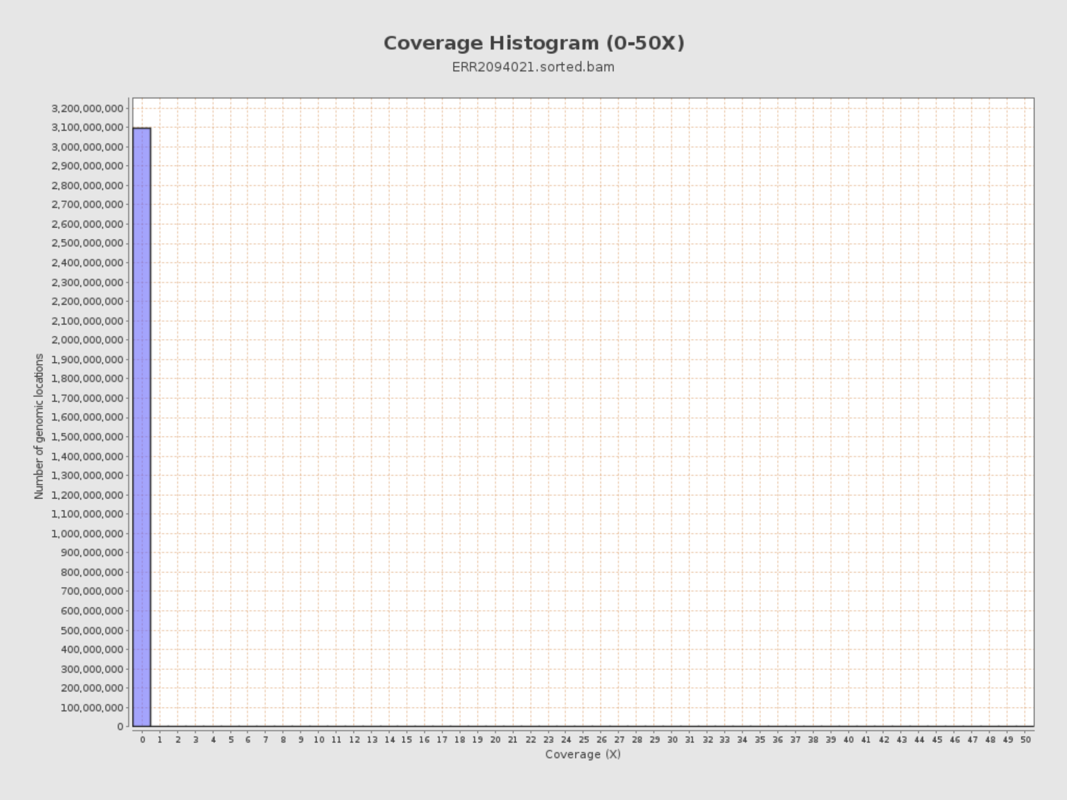
3. Results : Coverage across reference



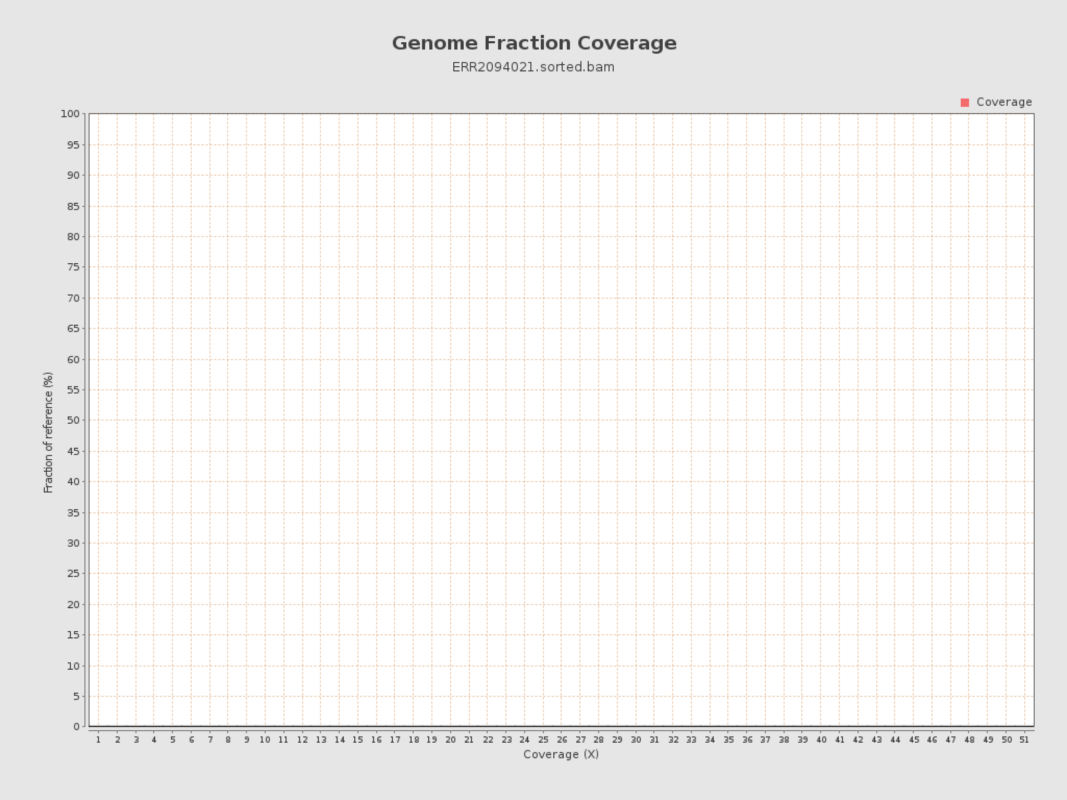
4. Results : Coverage Histogram



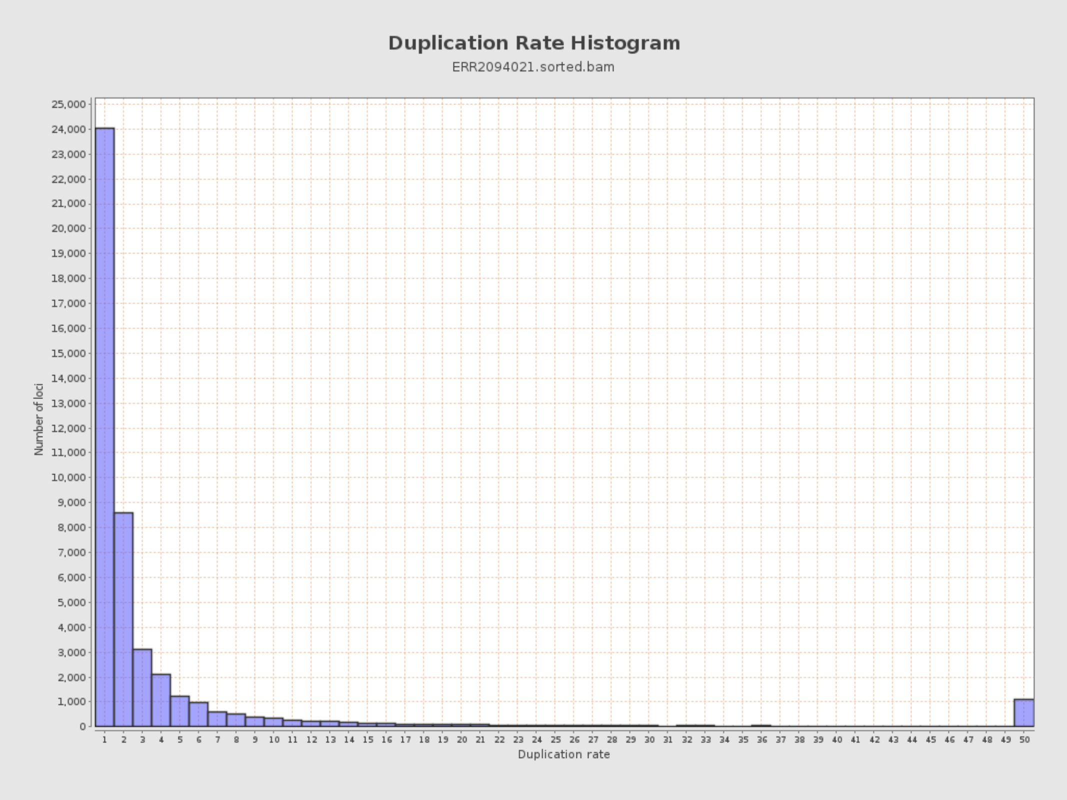
5. Results : Coverage Histogram (0-50X)



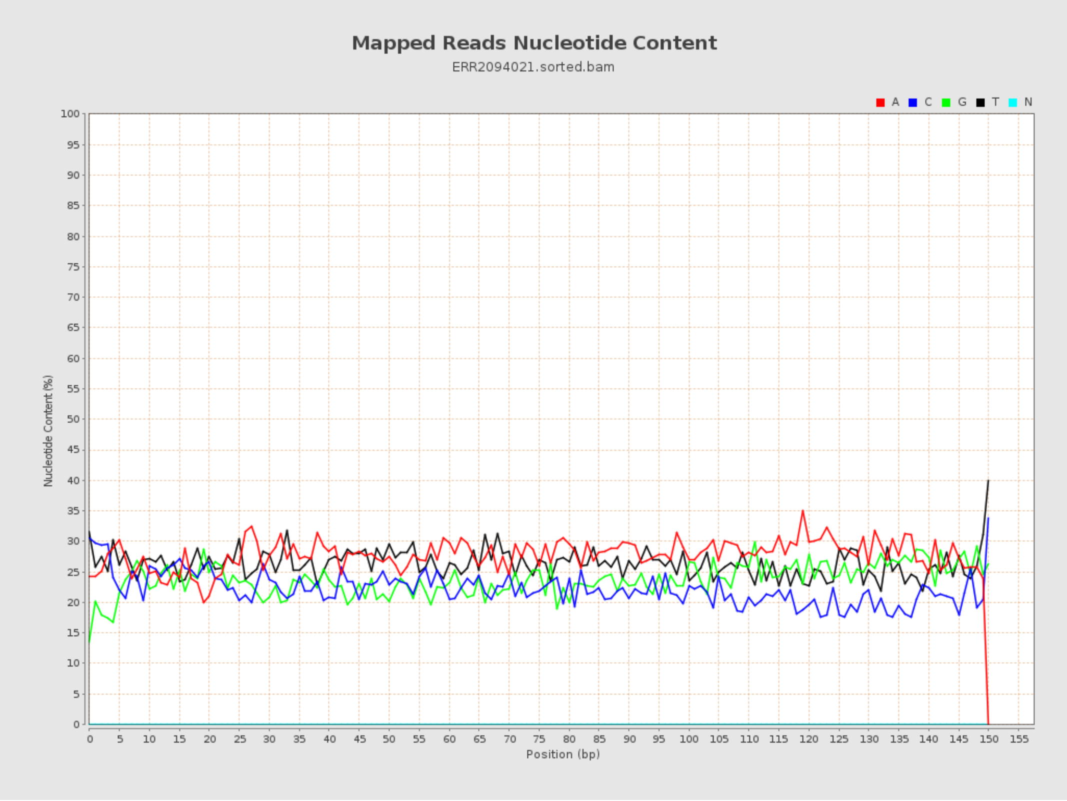
6. Results : Genome Fraction Coverage



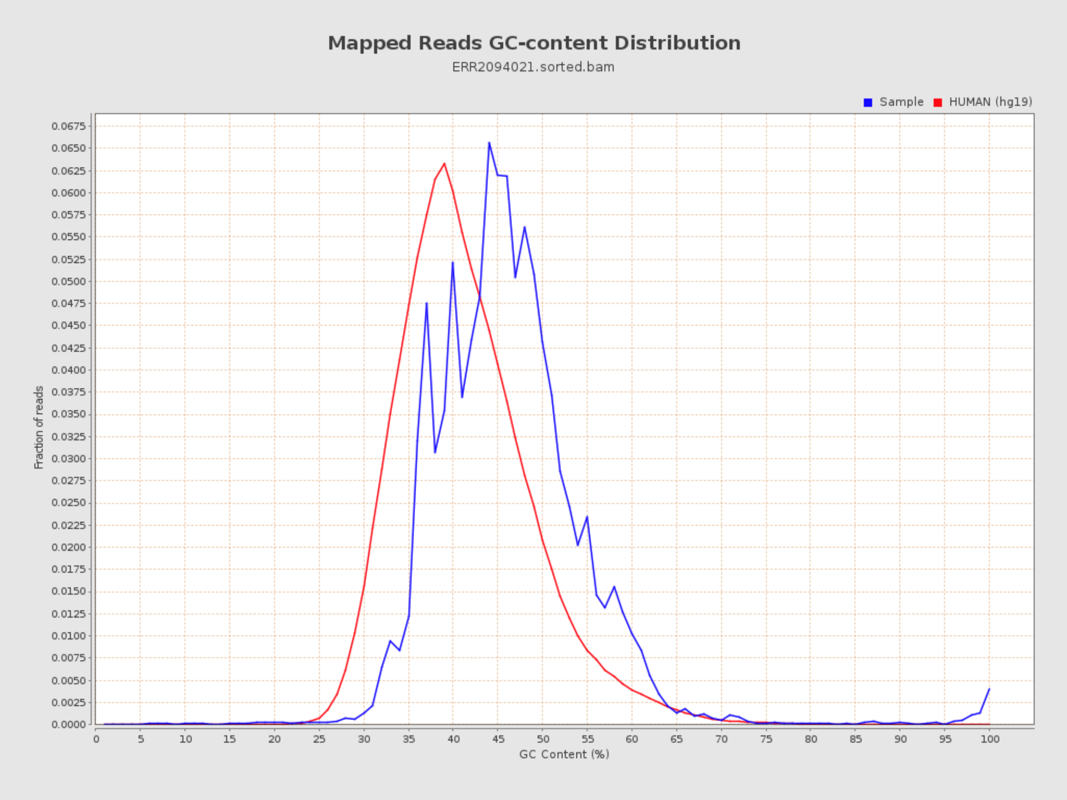
7. Results : Duplication Rate Histogram



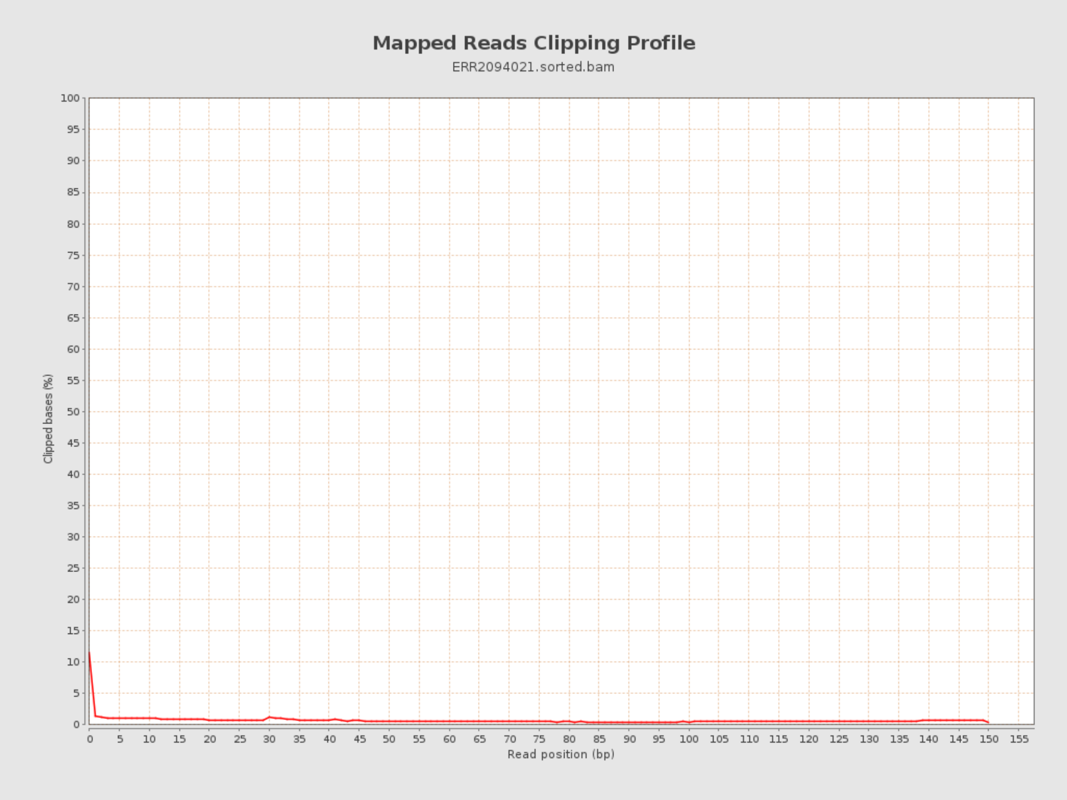
8. Results : Mapped Reads Nucleotide Content



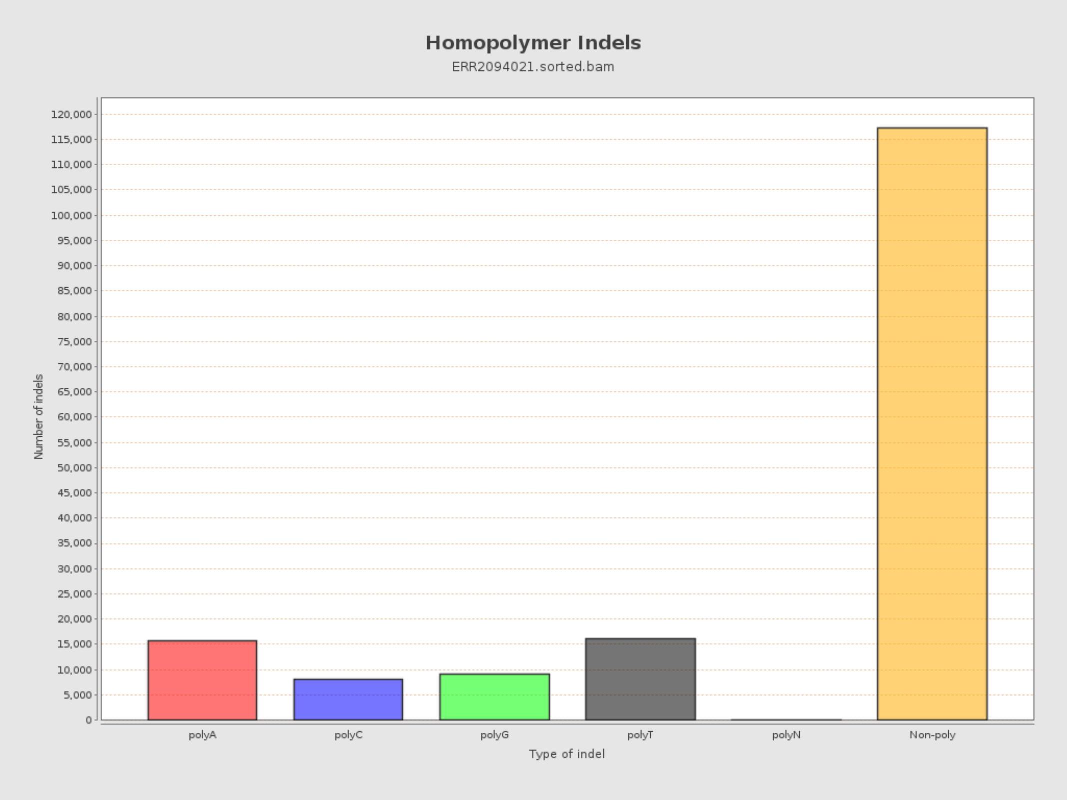
9. Results : Mapped Reads GC-content Distribution



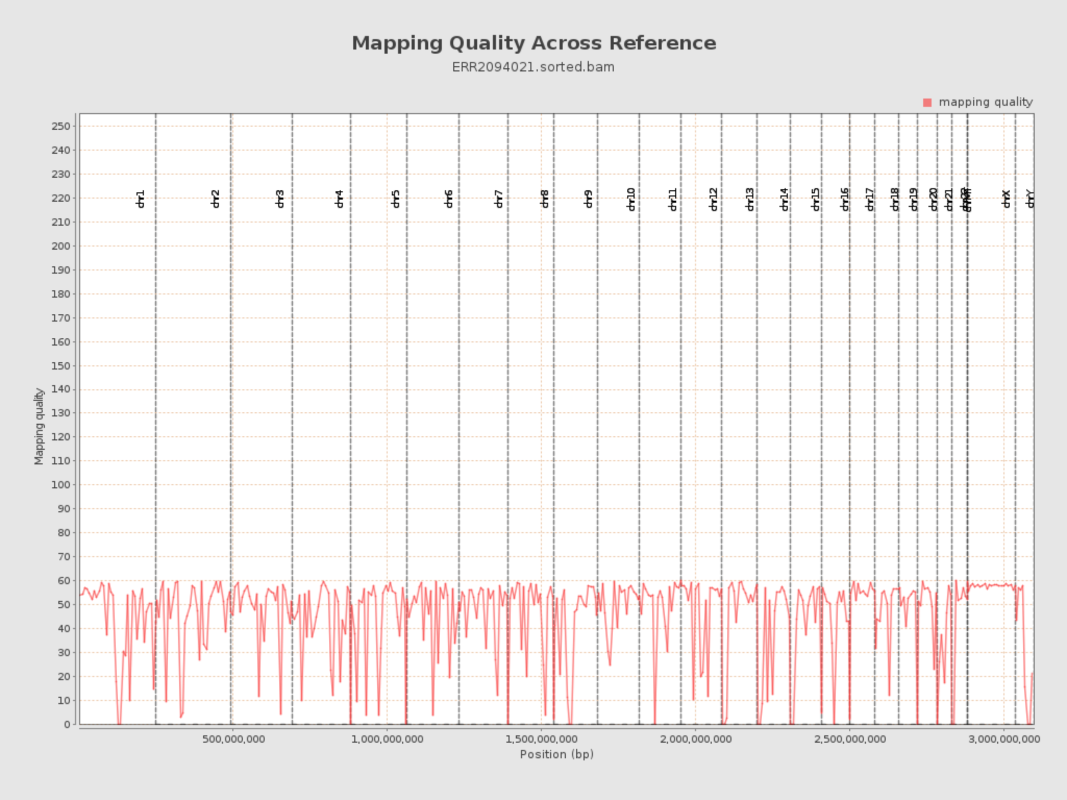
10. Results : Mapped Reads Clipping Profile



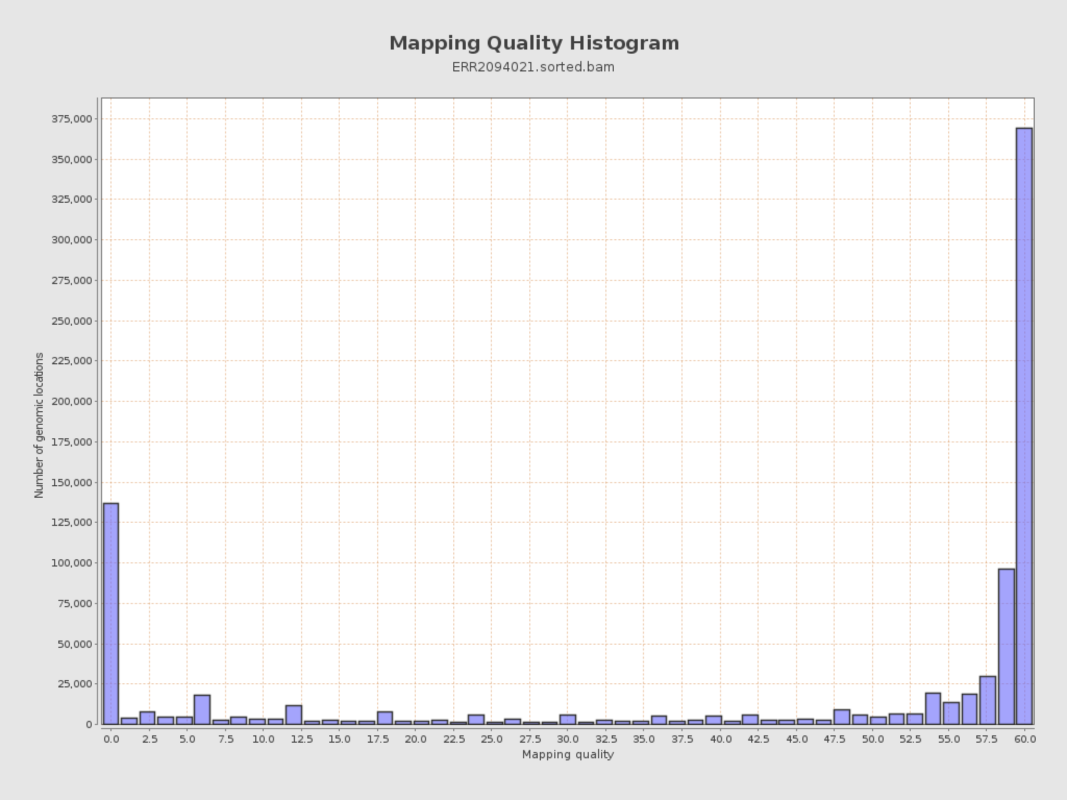
11. Results : Homopolymer Indels



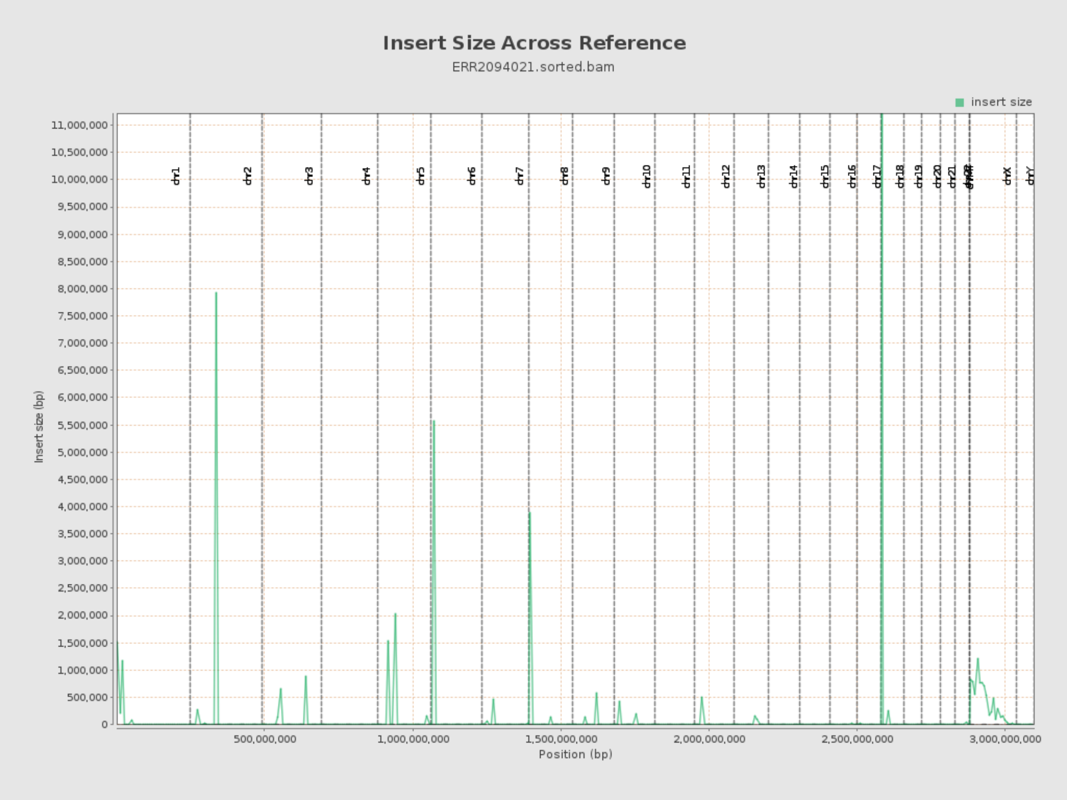
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram