Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:45:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093984.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_ERR2093984 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093984_1.fastq.gz ERR2093984_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:45:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	353,152
Mapped reads	332,608 / 94.18%
Unmapped reads	20,544 / 5.82%
Mapped paired reads	332,608 / 94.18%
Mapped reads, first in pair	167,230 / 47.35%
Mapped reads, second in pair	165,378 / 46.83%
Mapped reads, both in pair	329,402 / 93.27%
Mapped reads, singletons	3,206 / 0.91%
Secondary alignments	0
Supplementary alignments	20,477 / 5.8%
Read min/max/mean length	30 / 151 / 138.79
Duplicated reads (estimated)	311,171 / 88.11%
Duplication rate	49.61%
Clipped reads	168,377 / 47.68%

2.2. ACGT Content

Number/percentage of A's	10,948,413 / 26.58%
Number/percentage of C's	9,613,250 / 23.34%
Number/percentage of T's	10,283,468 / 24.97%
Number/percentage of G's	10,343,206 / 25.11%
Number/percentage of N's	411 / 0%

GC Percentage	48.45%

2.3. Coverage

Mean	0.0136
Standard Deviation	2.484

2.4. Mapping Quality

Mean Mapping Quality	41.71

2.5. Insert size

Mean	1,092,531.51
Standard Deviation	9,520,003.21
P25/Median/P75	122 / 159 / 194

2.6. Mismatches and indels

General error rate	3.7%
Mismatches	1,474,713
Insertions	23,914
Mapped reads with at least one insertion	7.06%
Deletions	118,619
Mapped reads with at least one deletion	34.24%
Homopolymer indels	28.26%

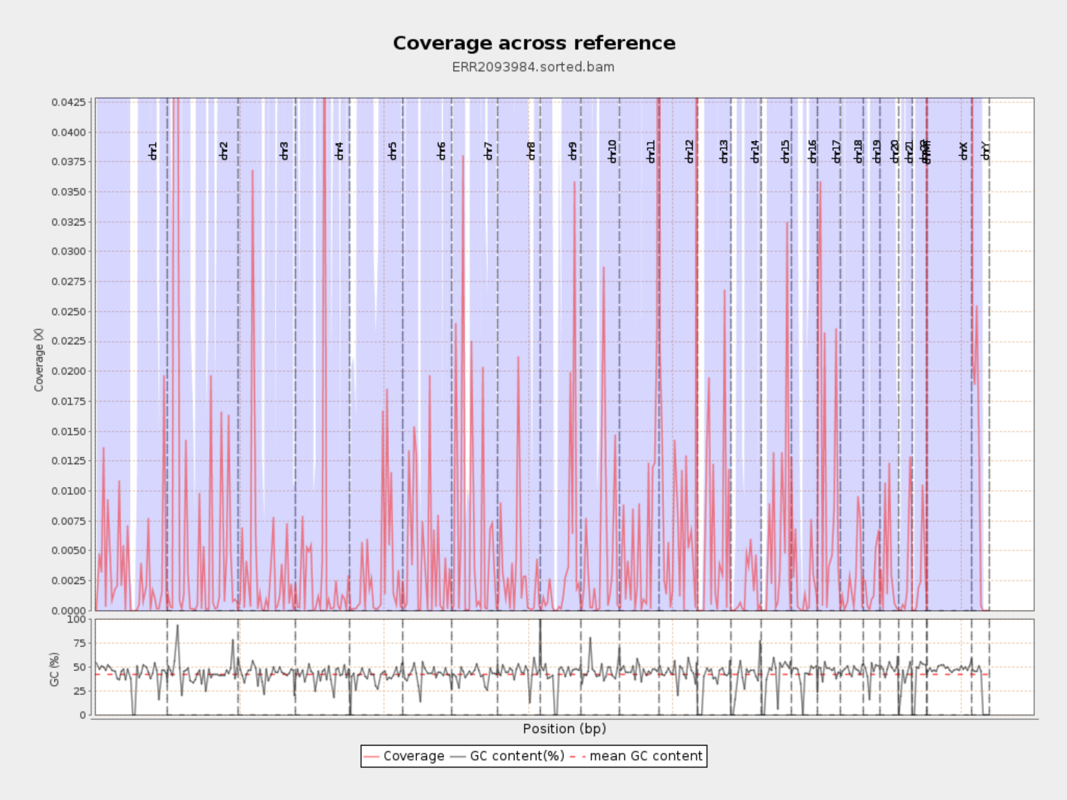
2.7. Chromosome stats

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

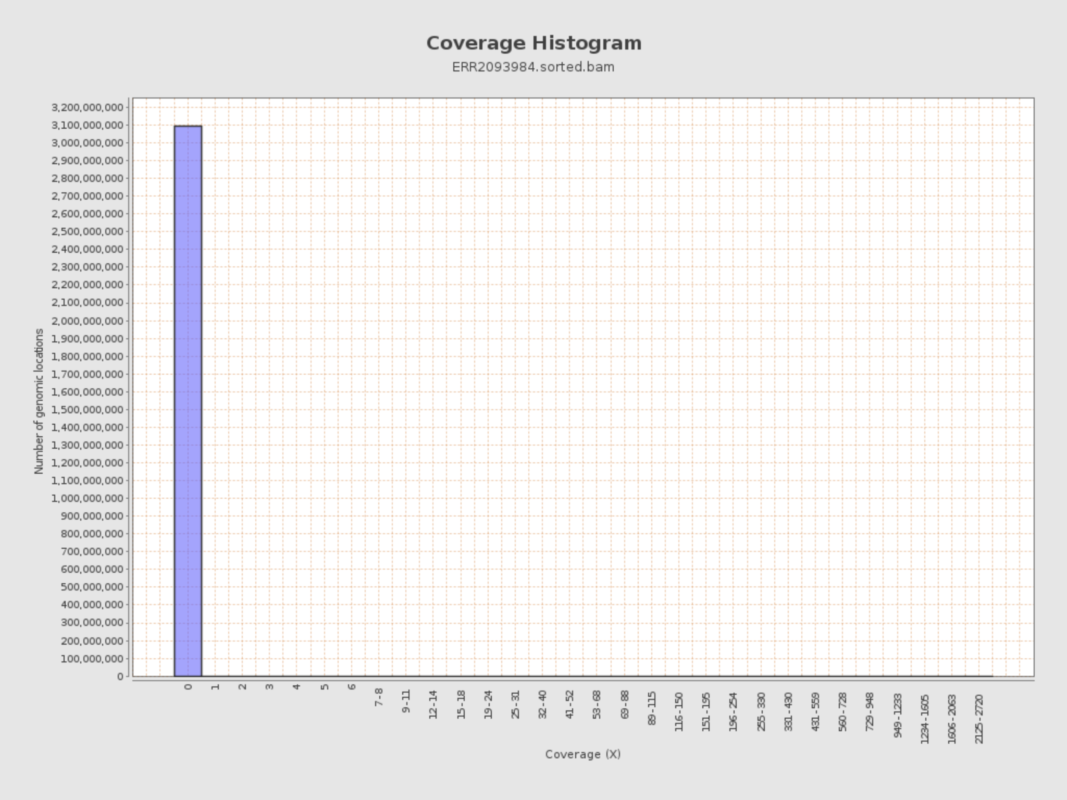
		bases	coverage	deviation
chr1	249250621	833757	0.0033	1.1238
chr2	243199373	1872636	0.0077	2.4106
chr3	198022430	685787	0.0035	1.0057
chr4	191154276	760310	0.004	1.1537
chr5	180915260	604548	0.0033	1.418
chr6	171115067	805424	0.0047	1.2817
chr7	159138663	1043541	0.0066	1.9607
chr8	146364022	455030	0.0031	0.97
chr9	141213431	615305	0.0044	1.3659
chr10	135534747	696527	0.0051	1.5149
chr11	135006516	838308	0.0062	1.5141
chr12	133851895	1034640	0.0077	1.8753
chr13	115169878	732734	0.0064	1.6959
chr14	107349540	175195	0.0016	0.5277
chr15	102531392	632268	0.0062	1.6922
chr16	90354753	246410	0.0027	0.8005
chr17	81195210	1003515	0.0124	2.8668
chr18	78077248	210872	0.0027	0.7523
chr19	59128983	140416	0.0024	0.6554
chr20	63025520	238436	0.0038	1.1233
chr21	48129895	169615	0.0035	0.8554
chr22	51304566	133732	0.0026	0.599
chrMT	16571	528570	31.8973	129.7083
chrX	155270560	26977904	0.1737	8.8571

chrY	59373566	569258	0.0096	1.3348

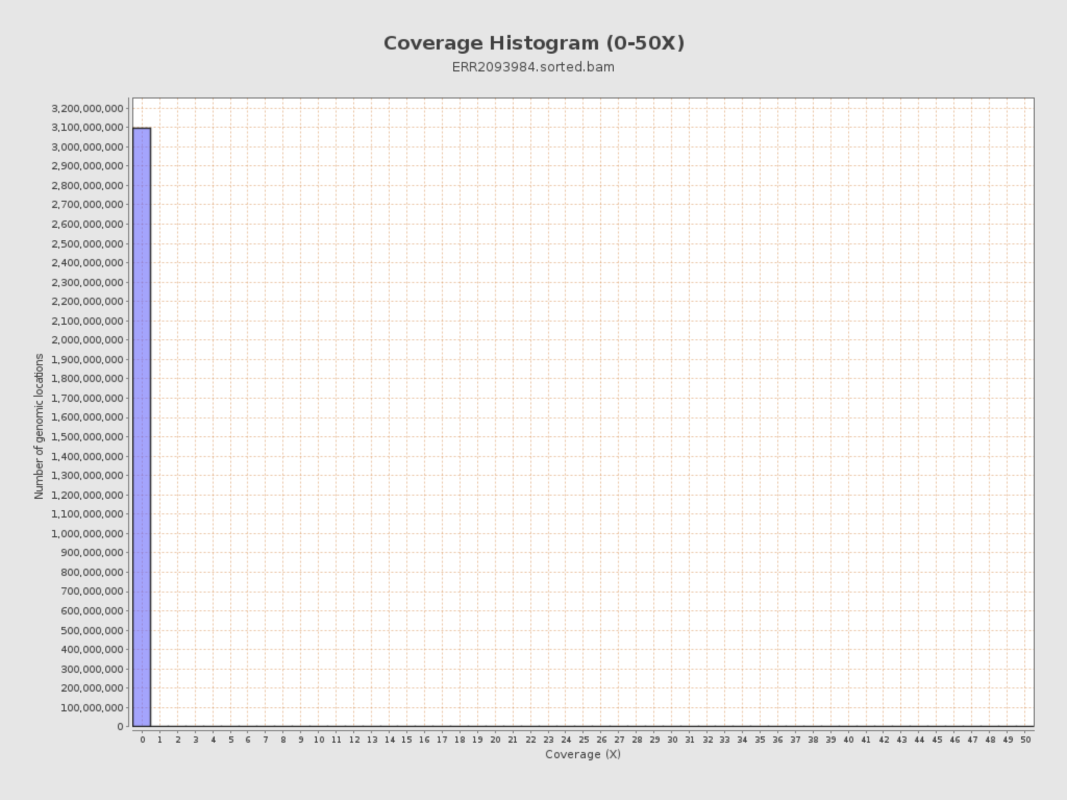
3. Results : Coverage across reference



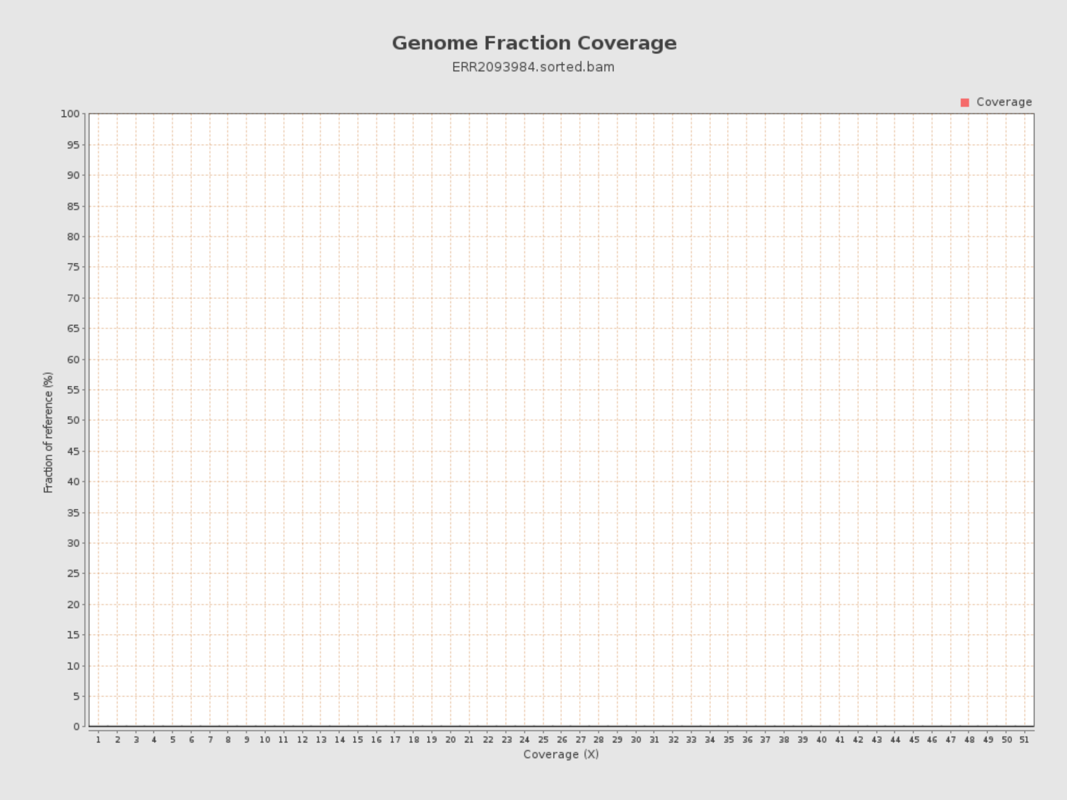
4. Results : Coverage Histogram



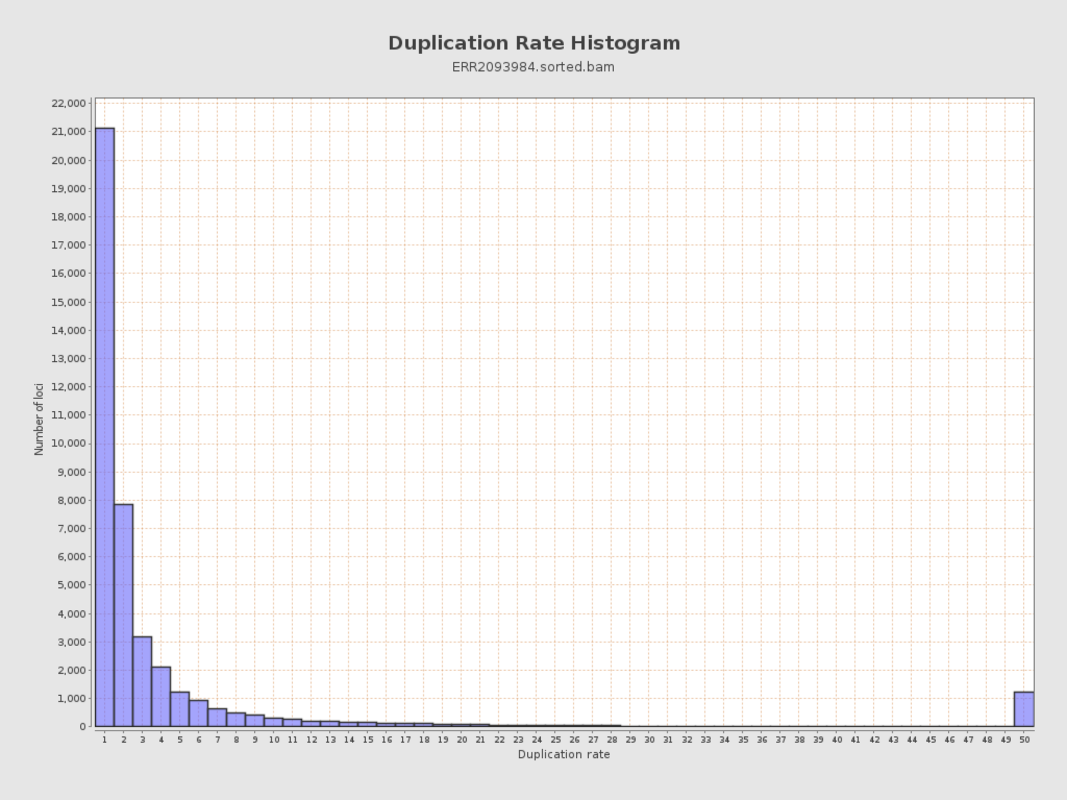
5. Results : Coverage Histogram (0-50X)



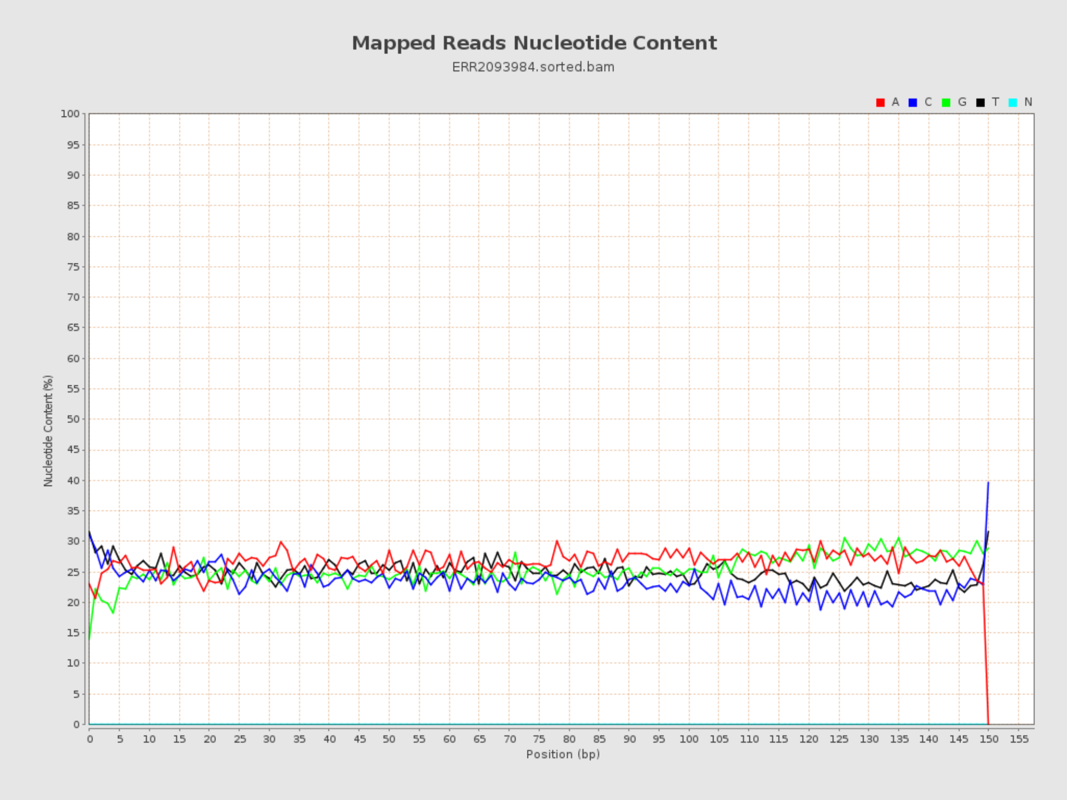
6. Results : Genome Fraction Coverage



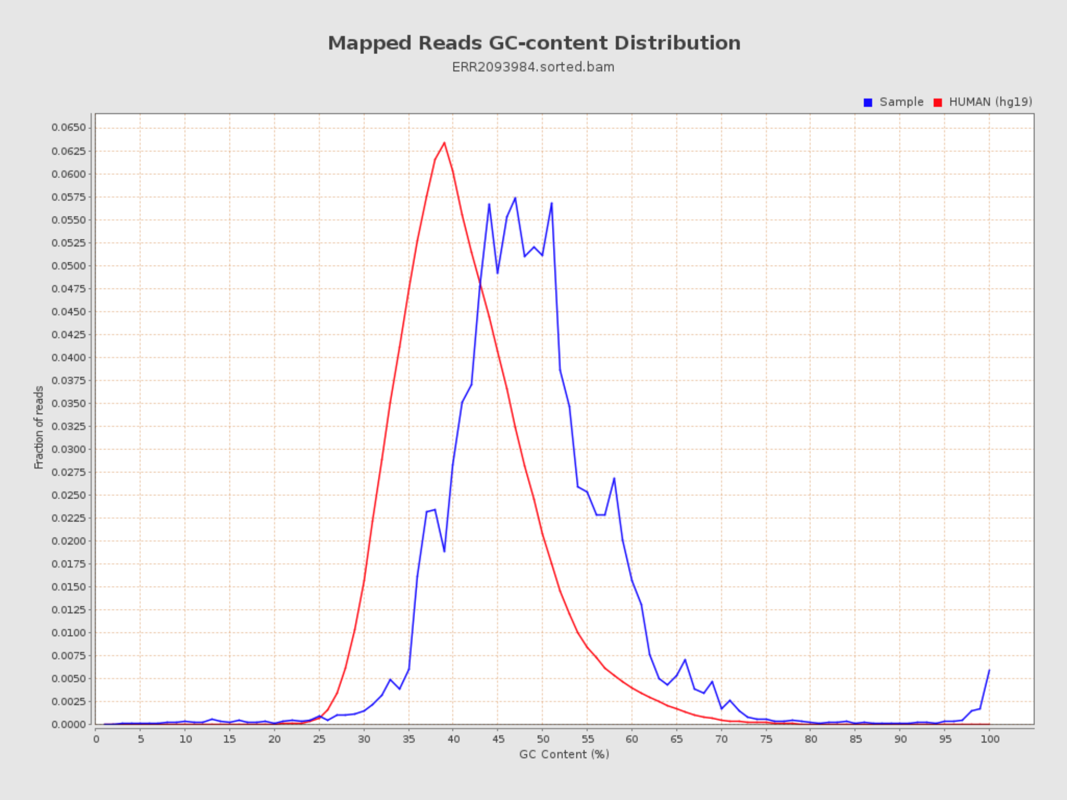
7. Results : Duplication Rate Histogram



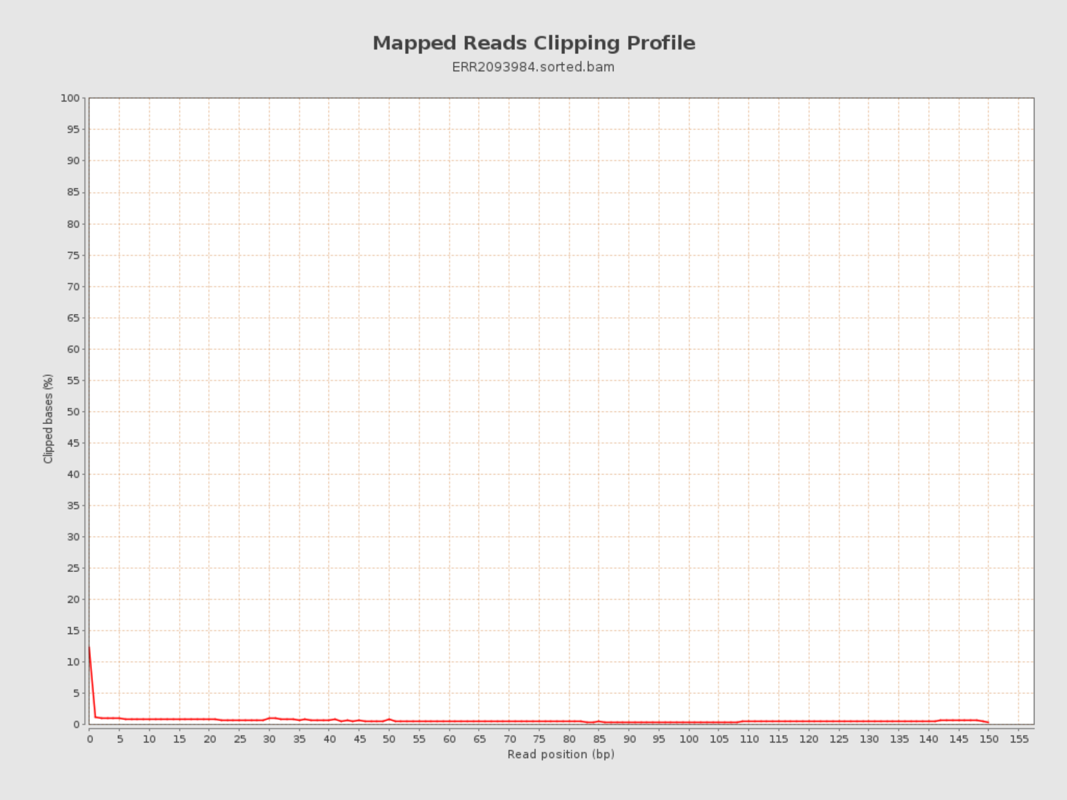
8. Results : Mapped Reads Nucleotide Content



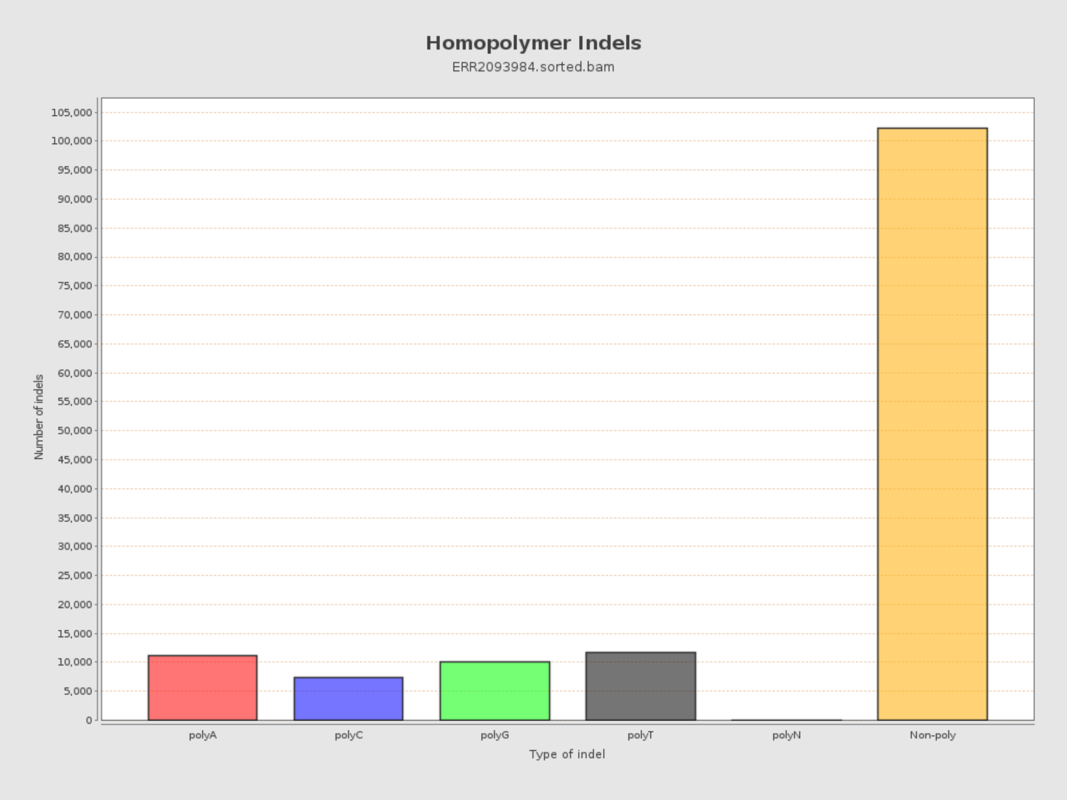
9. Results : Mapped Reads GC-content Distribution



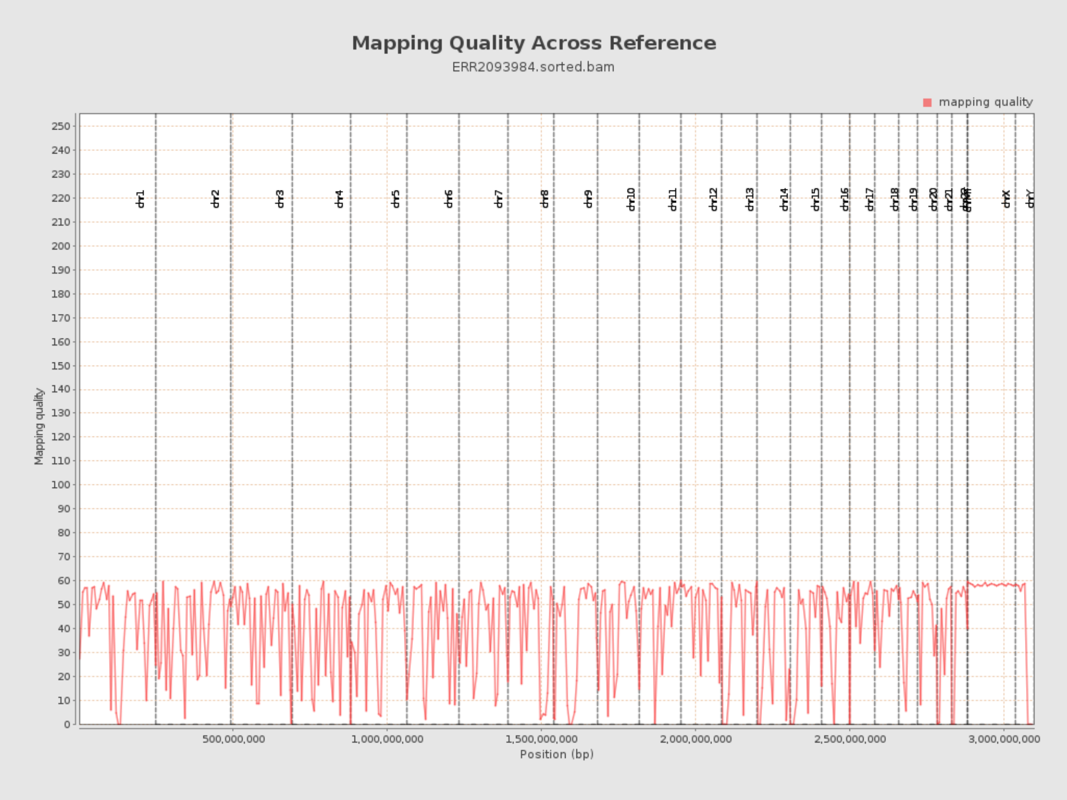
10. Results : Mapped Reads Clipping Profile



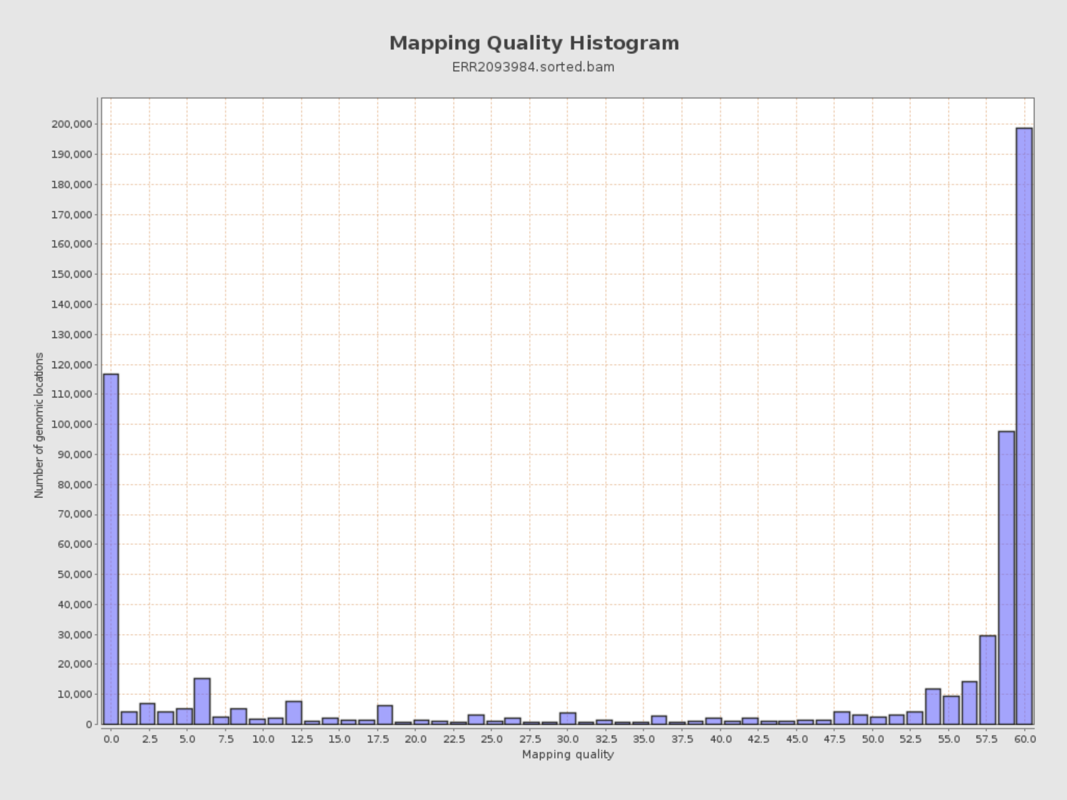
11. Results : Homopolymer Indels



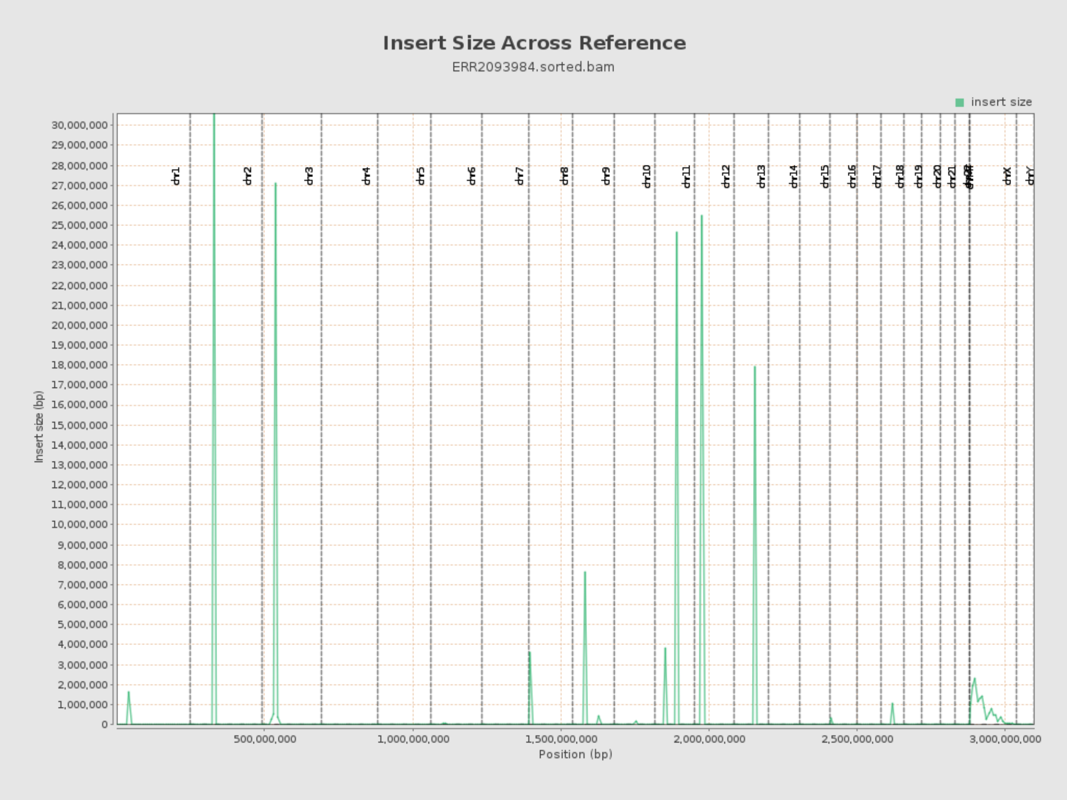
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram