Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:09:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094123.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_ERR2094123 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094123_1.fastq.gz ERR2094123_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:09:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	522,048
Mapped reads	484,946 / 92.89%
Unmapped reads	37,102 / 7.11%
Mapped paired reads	484,946 / 92.89%
Mapped reads, first in pair	243,105 / 46.57%
Mapped reads, second in pair	241,841 / 46.33%
Mapped reads, both in pair	482,220 / 92.37%
Mapped reads, singletons	2,726 / 0.52%
Secondary alignments	0
Supplementary alignments	1,941 / 0.37%
Read min/max/mean length	30 / 151 / 143.72
Duplicated reads (estimated)	482,569 / 92.44%
Duplication rate	39.65%
Clipped reads	50,722 / 9.72%

2.2. ACGT Content

Number/percentage of A's	19,935,259 / 27.8%
Number/percentage of C's	15,280,120 / 21.31%
Number/percentage of T's	20,602,532 / 28.73%
Number/percentage of G's	15,887,892 / 22.16%
Number/percentage of N's	987 / 0%

GC Percentage	43.47%

2.3. Coverage

Mean	0.0232
Standard Deviation	42.4103

2.4. Mapping Quality

Mean Mapping Quality	21.1

2.5. Insert size

Mean	10,110.24
Standard Deviation	989,995.41
P25/Median/P75	217 / 237 / 266

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	1,140,663
Insertions	20,635
Mapped reads with at least one insertion	4.2%
Deletions	48,954
Mapped reads with at least one deletion	9.88%
Homopolymer indels	65.24%

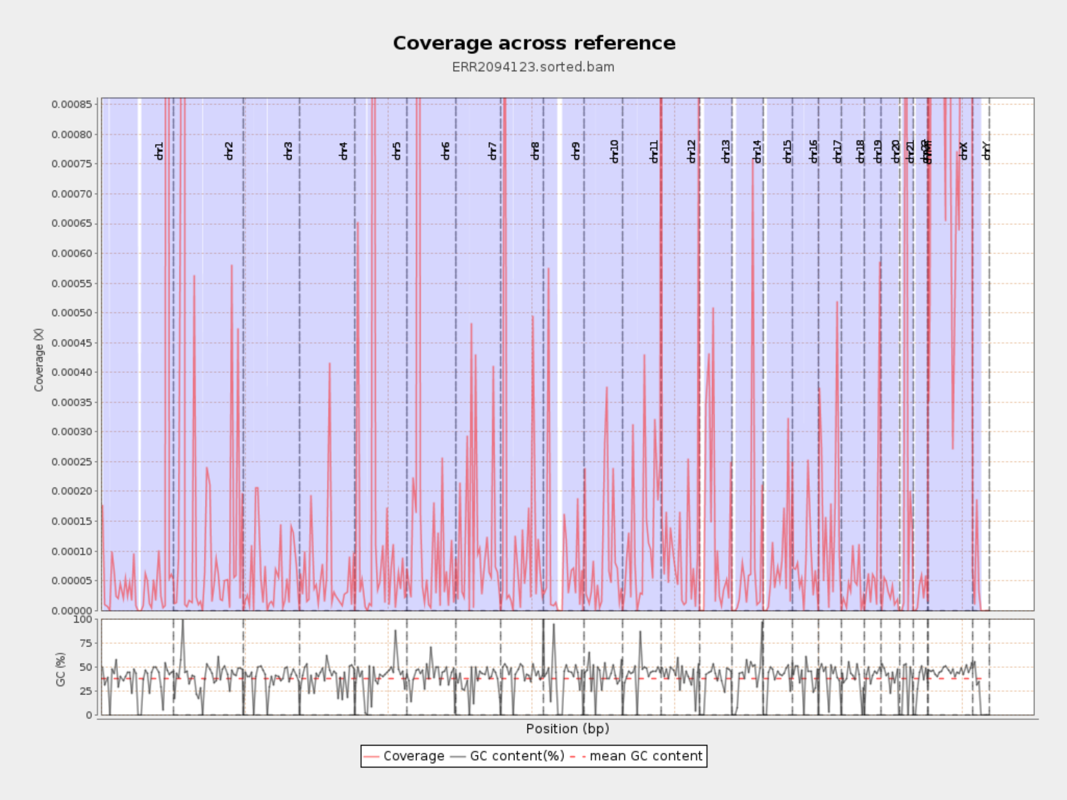
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

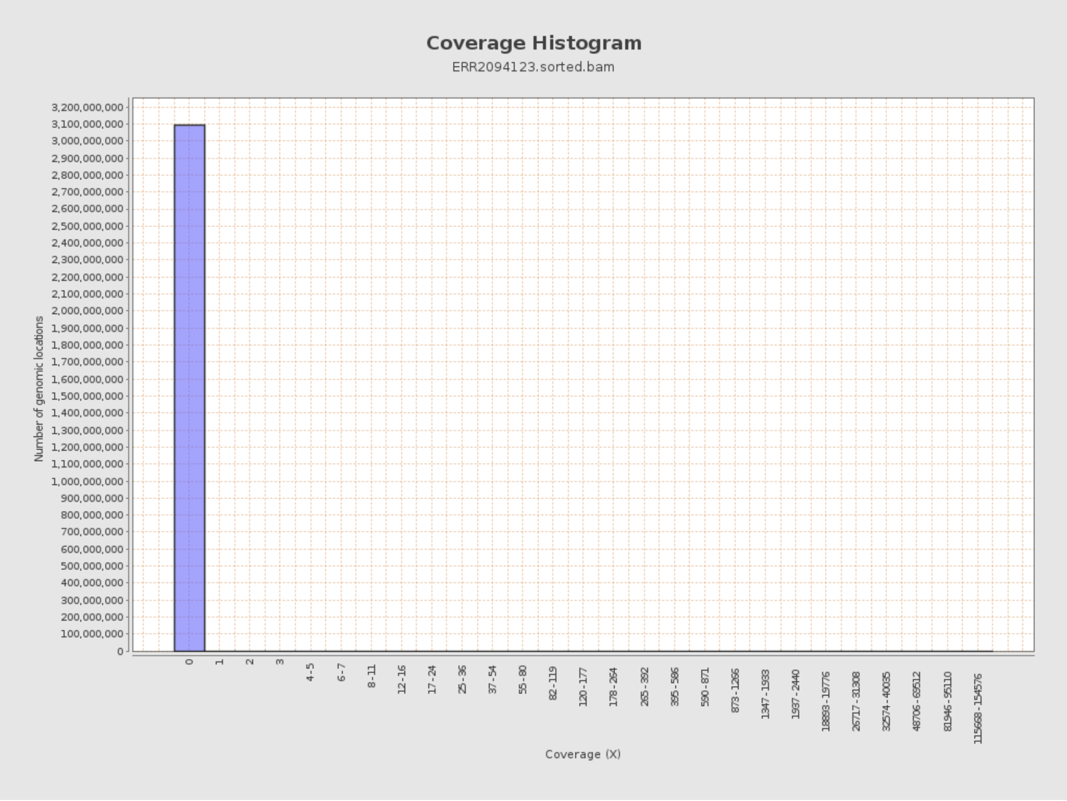
		bases	coverage	deviation
chr1	249250621	45097	0.0002	0.2178
chr2	243199373	228894	0.0009	0.8296
chr3	198022430	11424	0.0001	0.014
chr4	191154276	11327	0.0001	0.0171
chr5	180915260	34028	0.0002	0.1145
chr6	171115067	37483	0.0002	0.1608
chr7	159138663	20730	0.0001	0.0319
chr8	146364022	21686	0.0001	0.0699
chr9	141213431	11022	0.0001	0.0234
chr10	135534747	12595	0.0001	0.023
chr11	135006516	19174	0.0001	0.0277
chr12	133851895	13336	0.0001	0.0269
chr13	115169878	15035	0.0001	0.046
chr14	107349540	10465	0.0001	0.0431
chr15	102531392	8143	0.0001	0.0192
chr16	90354753	6505	0.0001	0.0178
chr17	81195210	14293	0.0002	0.0411
chr18	78077248	3395	0	0.0125
chr19	59128983	6350	0.0001	0.0952
chr20	63025520	1769	0	0.0063
chr21	48129895	14527	0.0003	0.1372
chr22	51304566	1476	0	0.0068
chrMT	16571	70268990	4,240.4798	17,832.2714
chrX	155270560	963121	0.0062	2.3817

chrY	59373566	2120	0	0.0101

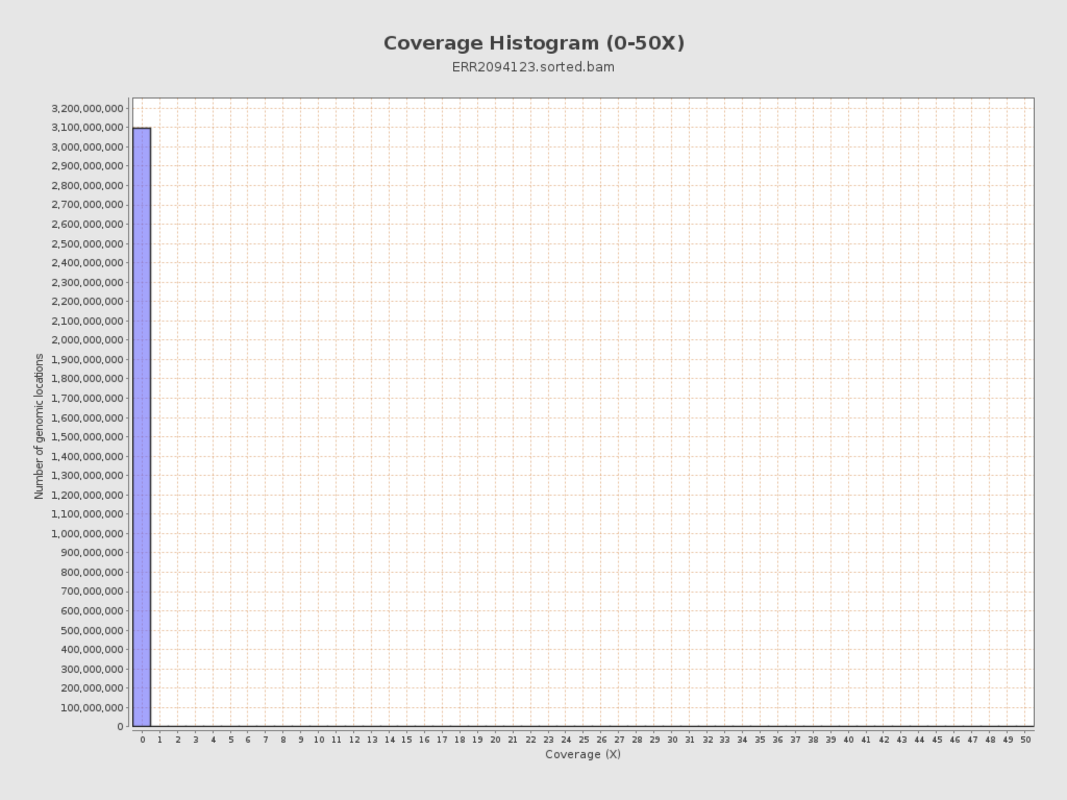
3. Results : Coverage across reference



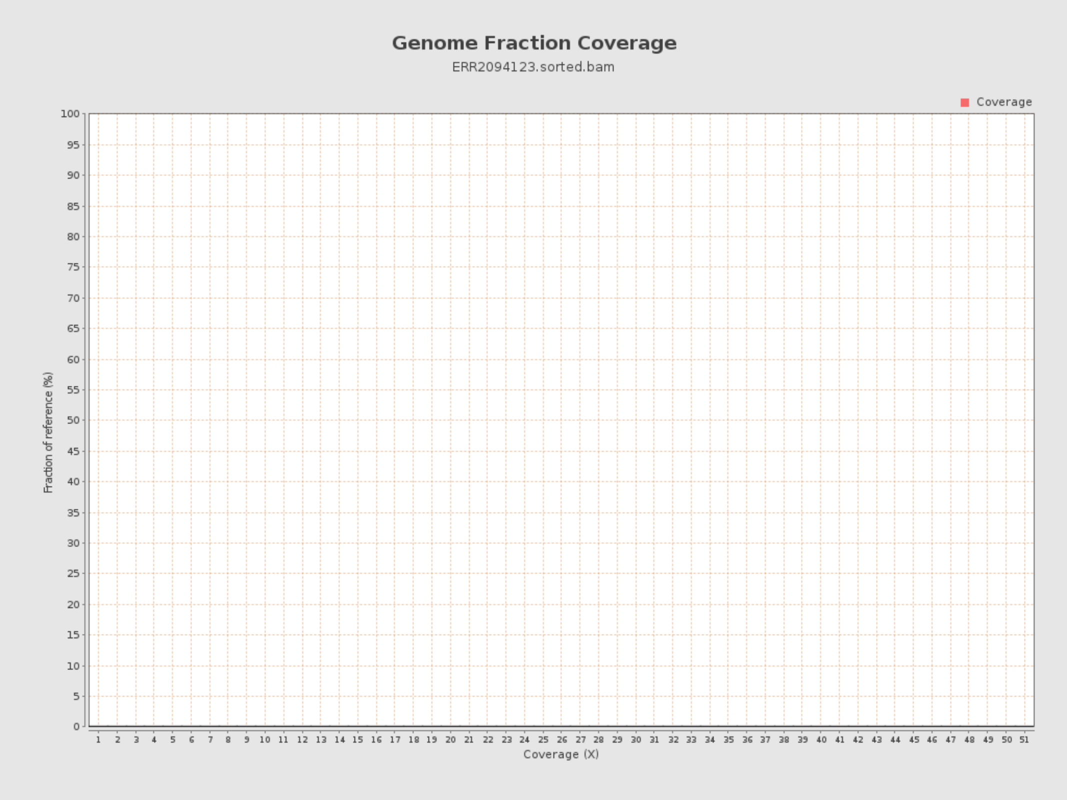
4. Results : Coverage Histogram



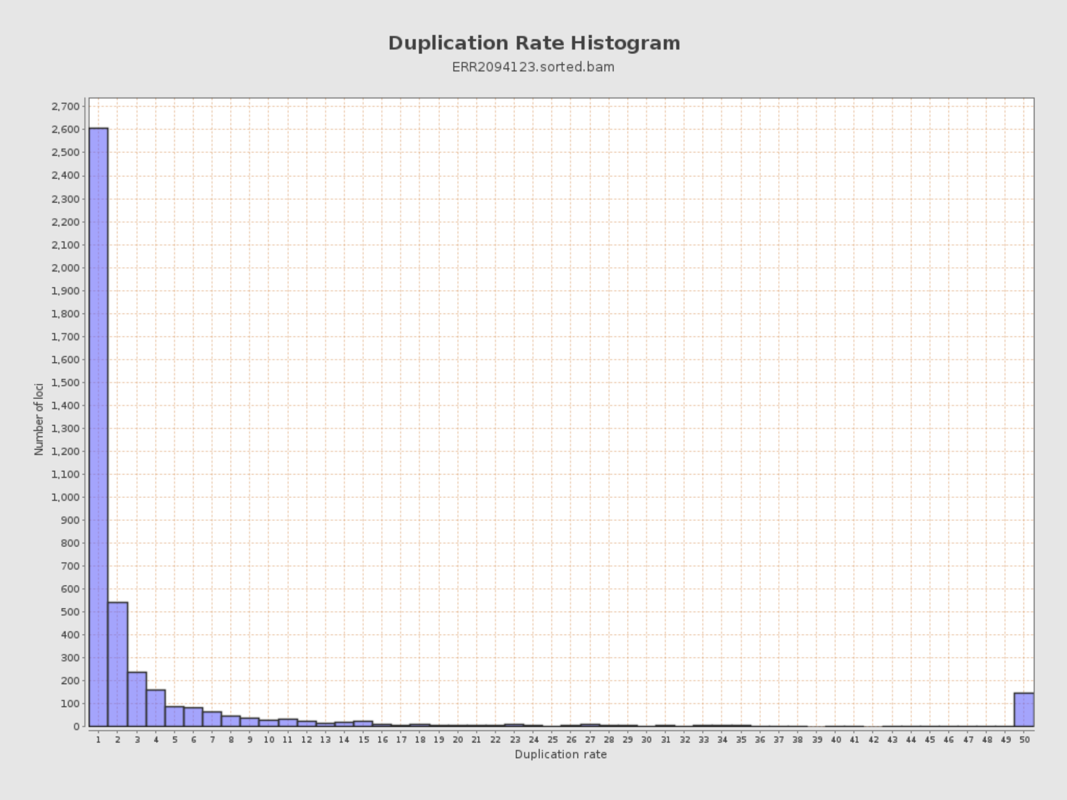
5. Results : Coverage Histogram (0-50X)



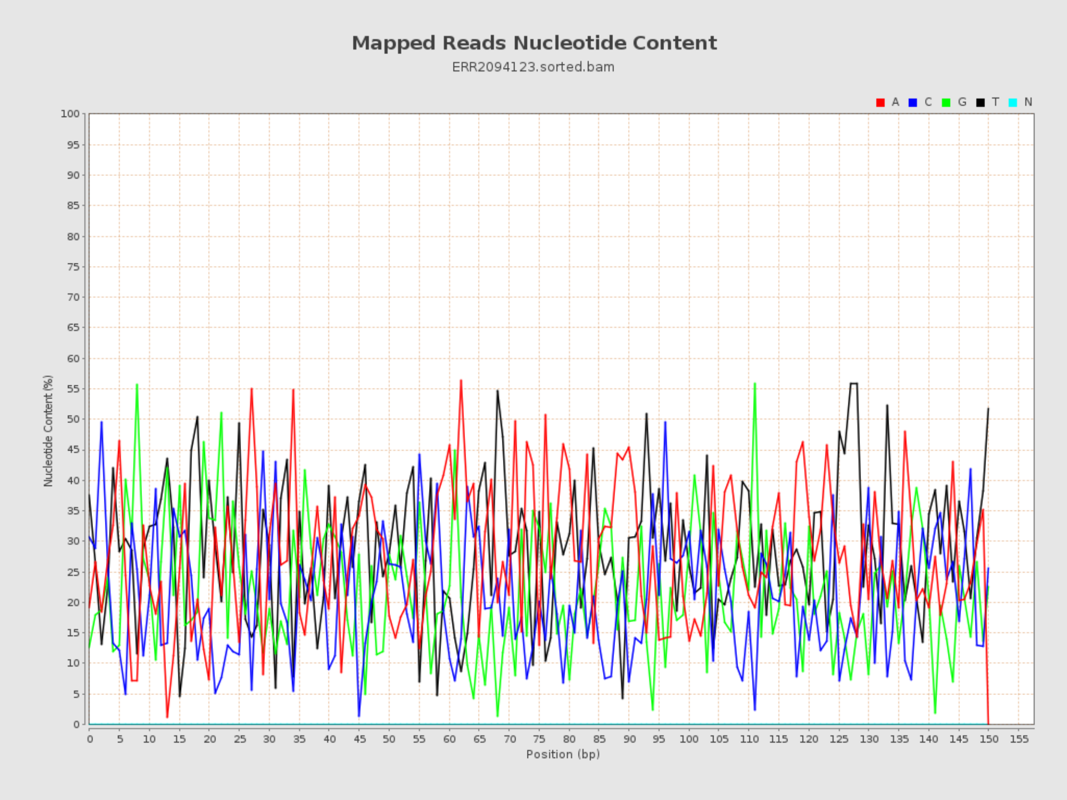
6. Results : Genome Fraction Coverage



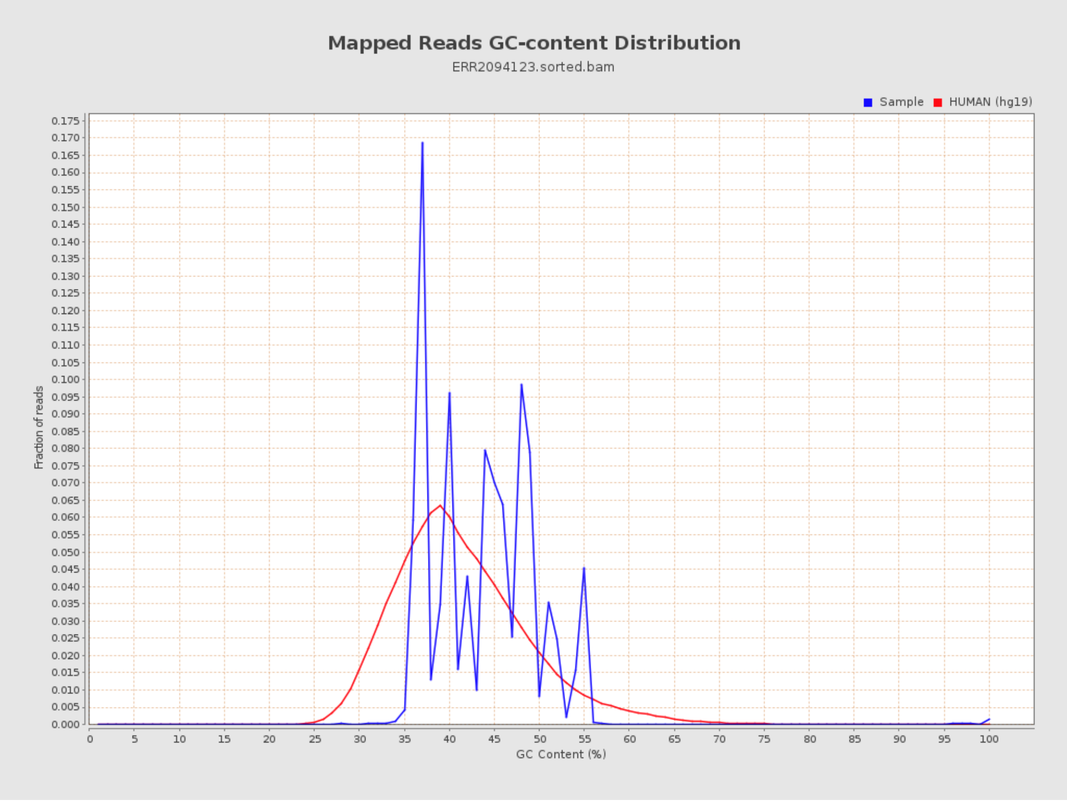
7. Results : Duplication Rate Histogram



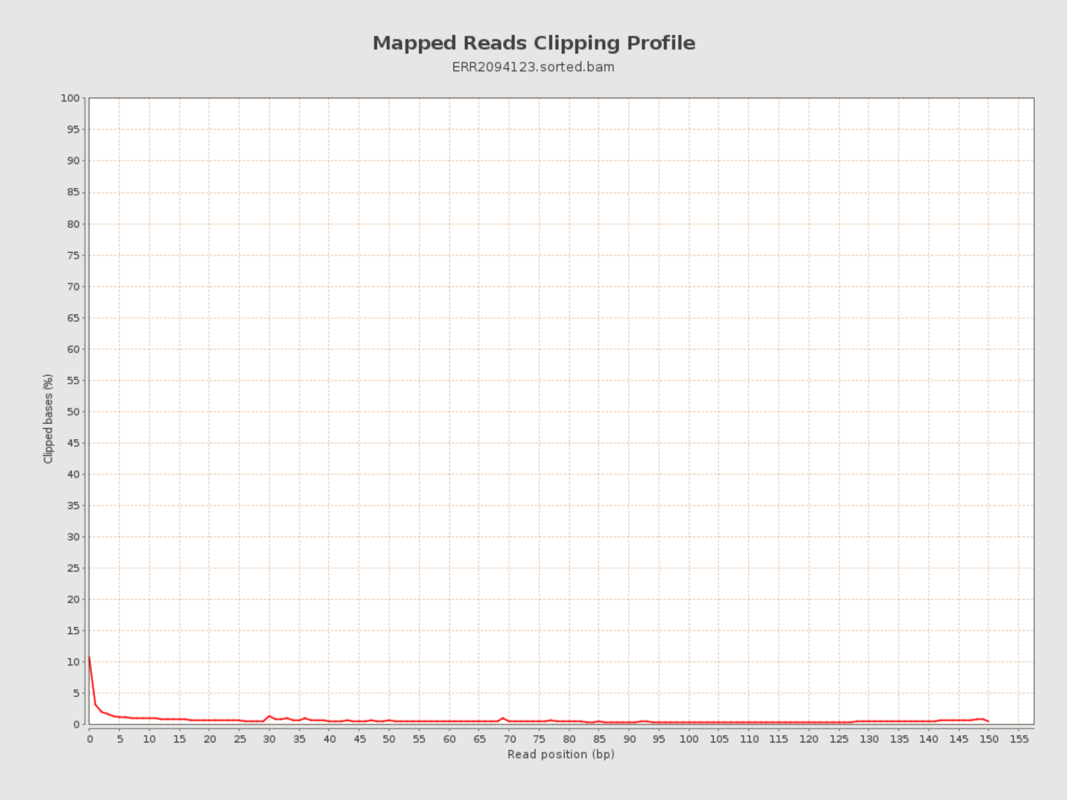
8. Results : Mapped Reads Nucleotide Content



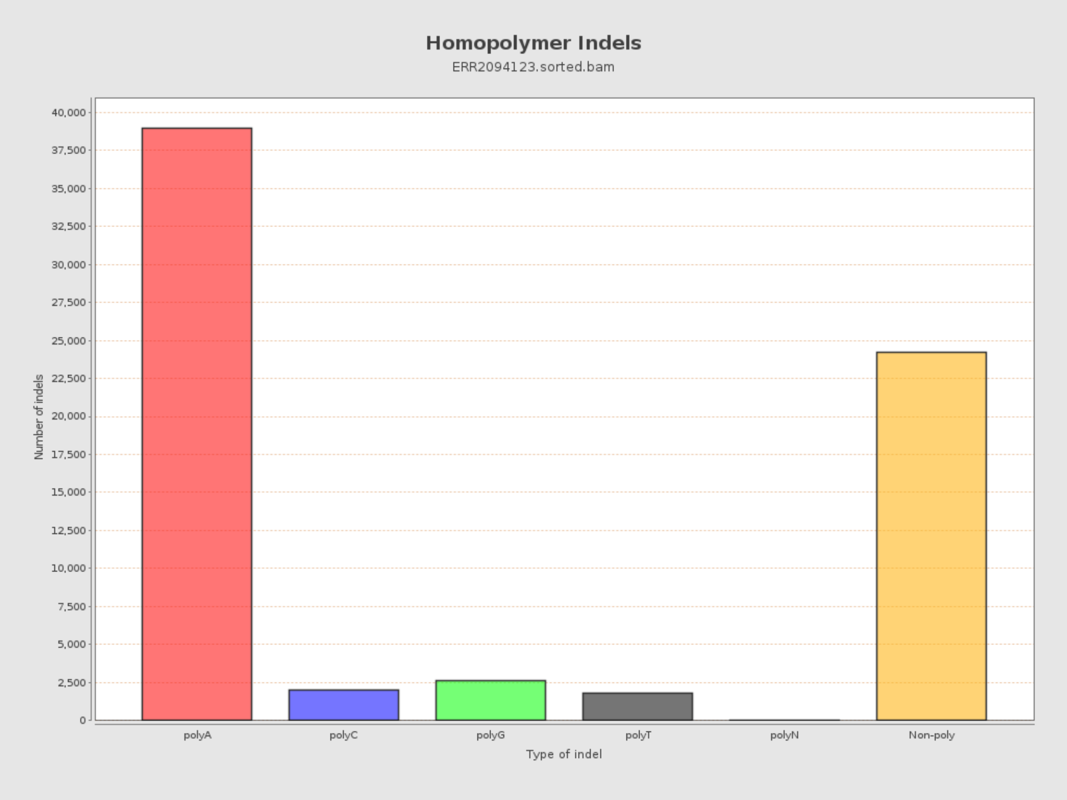
9. Results : Mapped Reads GC-content Distribution



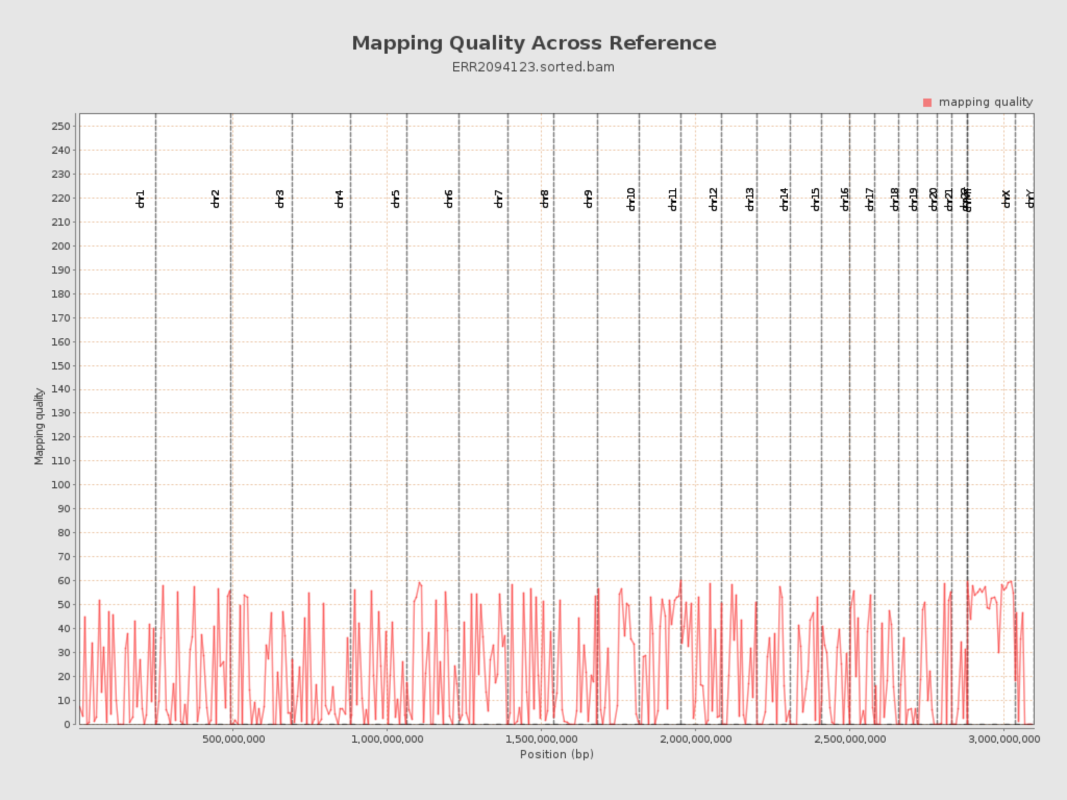
10. Results : Mapped Reads Clipping Profile



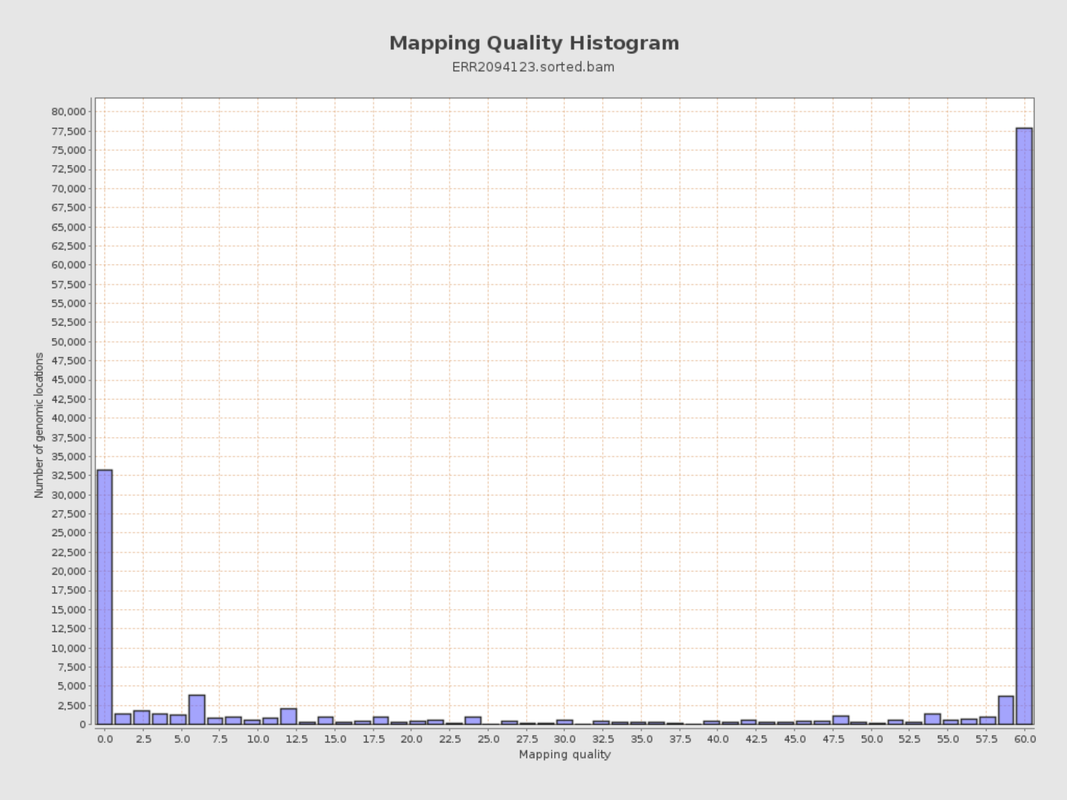
11. Results : Homopolymer Indels



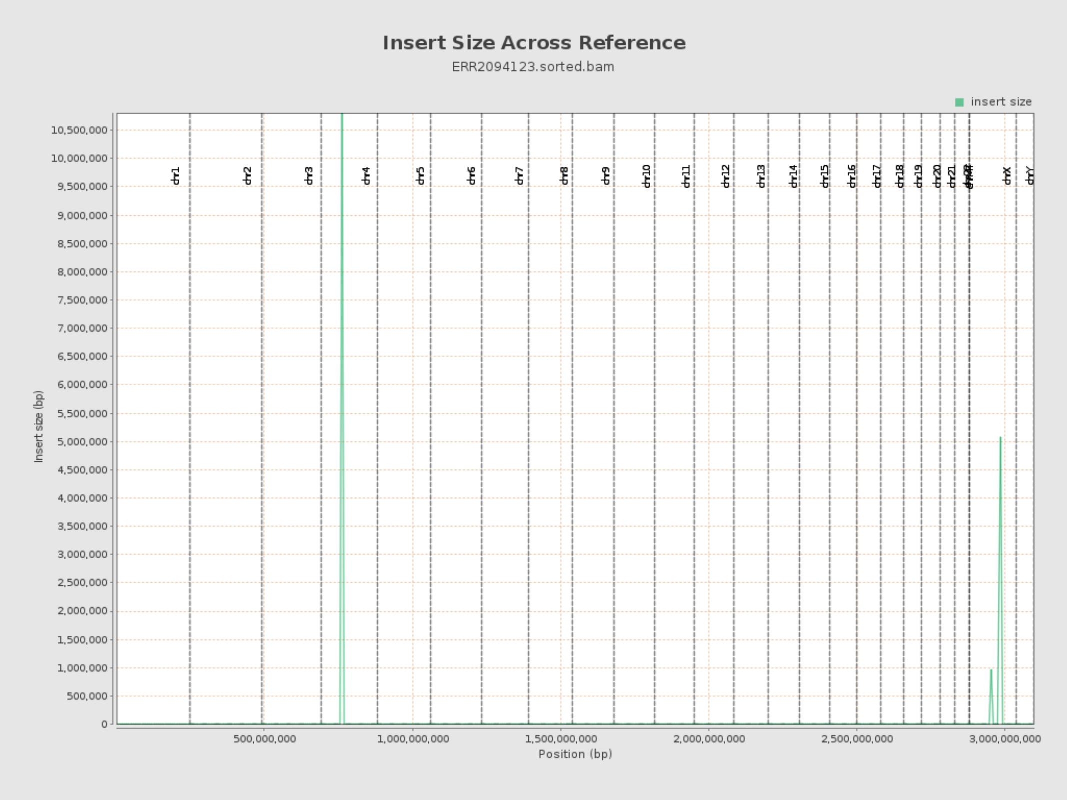
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram