Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:58:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094016.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_ERR2094016 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094016_1.fastq.gz ERR2094016_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:58:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,042
Mapped reads	1,765 / 9.27%
Unmapped reads	17,277 / 90.73%
Mapped paired reads	1,765 / 9.27%
Mapped reads, first in pair	839 / 4.41%
Mapped reads, second in pair	926 / 4.86%
Mapped reads, both in pair	1,614 / 8.48%
Mapped reads, singletons	151 / 0.79%
Secondary alignments	0
Supplementary alignments	24 / 0.13%
Read min/max/mean length	30 / 151 / 61.63
Duplicated reads (estimated)	1,057 / 5.55%
Duplication rate	20.49%
Clipped reads	834 / 4.38%

2.2. ACGT Content

Number/percentage of A's	56,193 / 26%
Number/percentage of C's	47,322 / 21.9%
Number/percentage of T's	55,116 / 25.5%
Number/percentage of G's	57,497 / 26.6%
Number/percentage of N's	0 / 0%

GC Percentage	48.5%

2.3. Coverage

Mean	0.0001
Standard Deviation	0.0815

2.4. Mapping Quality

Mean Mapping Quality	17.55

2.5. Insert size

Mean	200,315.05
Standard Deviation	5,628,158.77
P25/Median/P75	164 / 209 / 279

2.6. Mismatches and indels

General error rate	2.14%
Mismatches	4,360
Insertions	81
Mapped reads with at least one insertion	4.36%
Deletions	257
Mapped reads with at least one deletion	13.94%
Homopolymer indels	28.7%

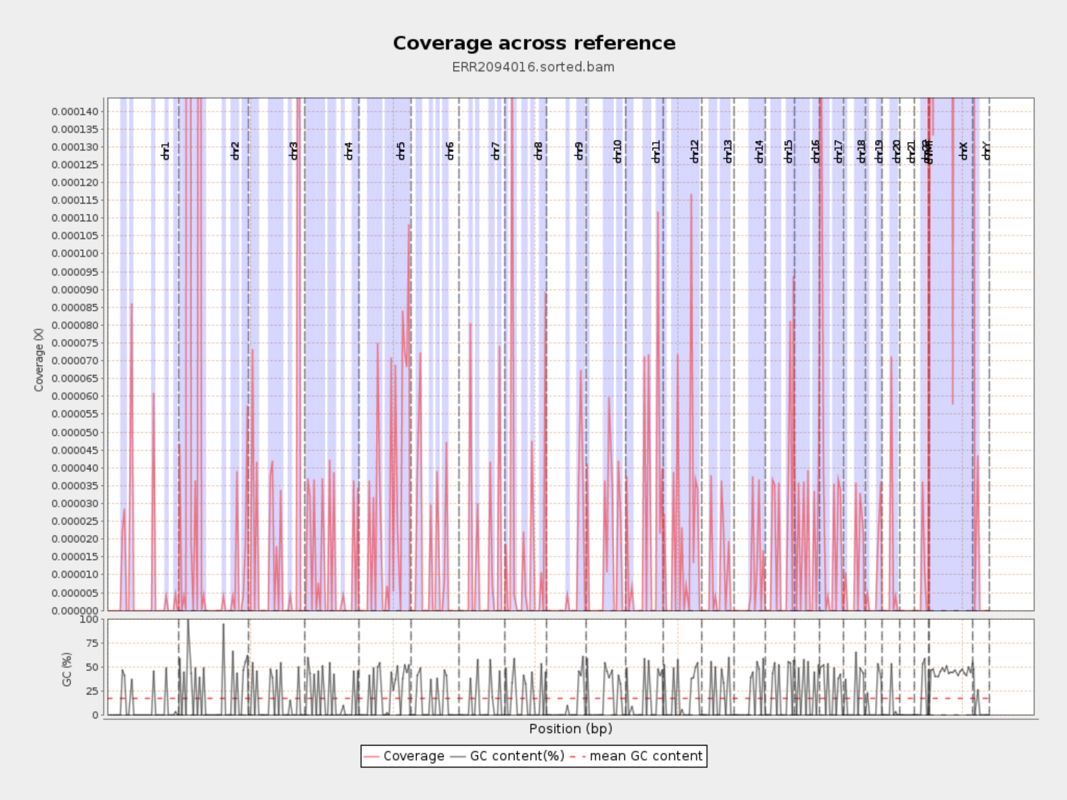
2.7. Chromosome stats

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

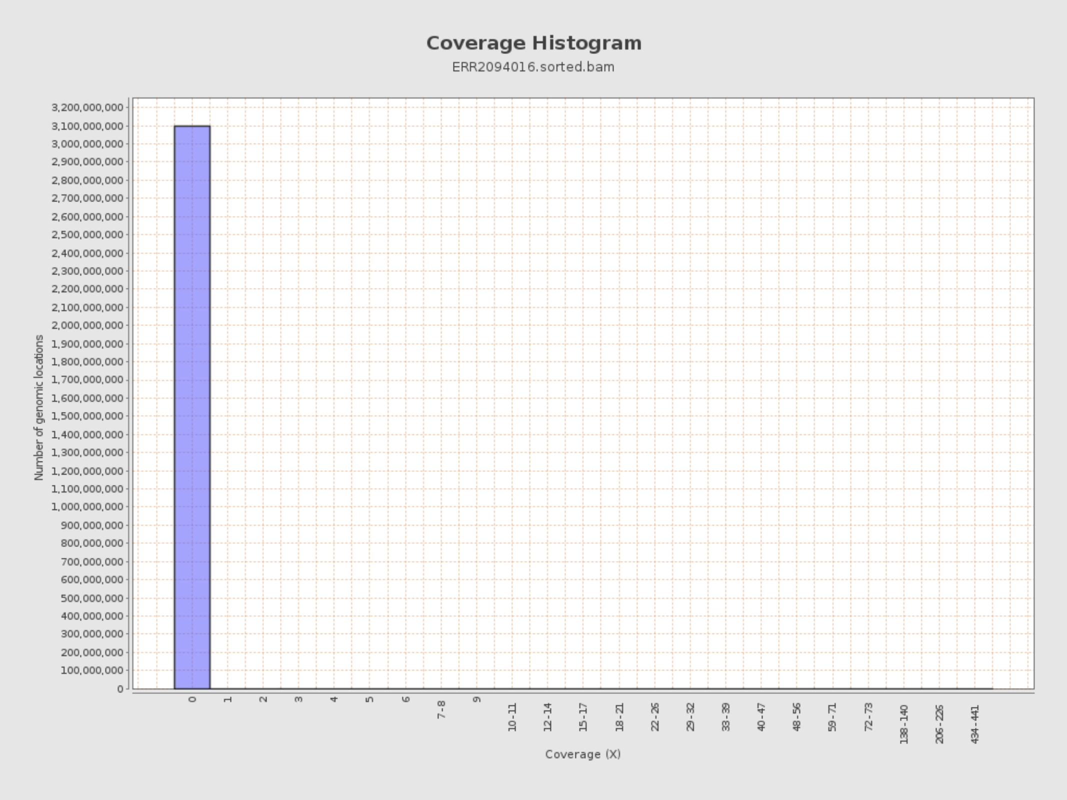
		bases	coverage	deviation
chr1	249250621	1599	0	0.0047
chr2	243199373	16254	0.0001	0.0444
chr3	198022430	4377	0	0.0127
chr4	191154276	2353	0	0.0043
chr5	180915260	5324	0	0.0082
chr6	171115067	1821	0	0.0049
chr7	159138663	1810	0	0.0046
chr8	146364022	2680	0	0.0081
chr9	141213431	1130	0	0.0042
chr10	135534747	1925	0	0.0049
chr11	135006516	2789	0	0.0076
chr12	133851895	2837	0	0.0076
chr13	115169878	932	0	0.0032
chr14	107349540	825	0	0.0035
chr15	102531392	2008	0	0.0057
chr16	90354753	1648	0	0.0049
chr17	81195210	2611	0	0.0114
chr18	78077248	784	0	0.0039
chr19	59128983	456	0	0.0031
chr20	63025520	580	0	0.004
chr21	48129895	0	0	0
chr22	51304566	362	0	0.0033
chrMT	16571	87849	5.3014	33.4664
chrX	155270560	72573	0.0005	0.0763

chrY	59373566	2125	0	0.018

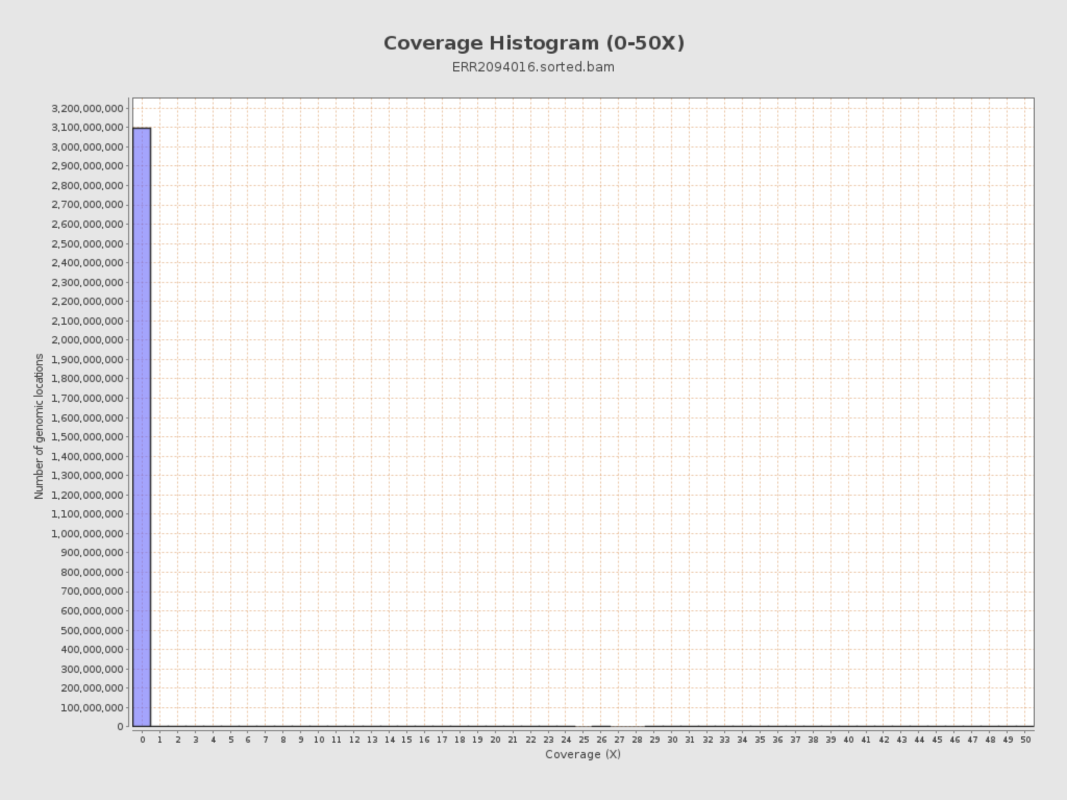
3. Results : Coverage across reference



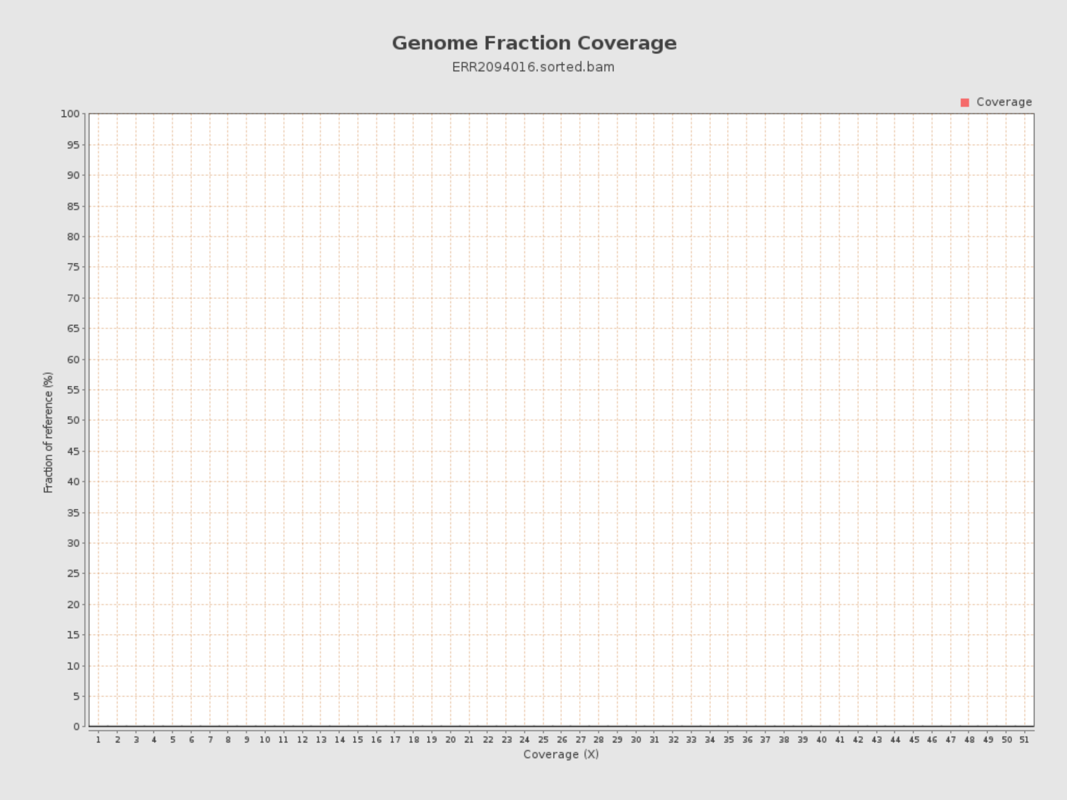
4. Results : Coverage Histogram



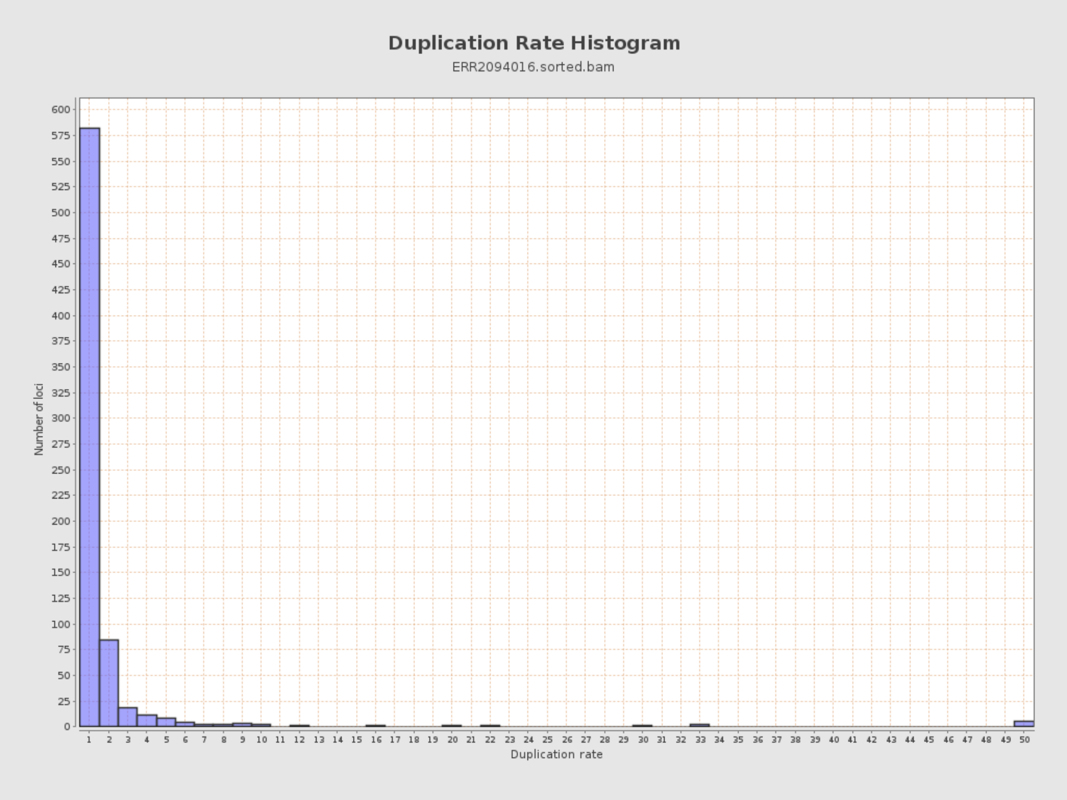
5. Results : Coverage Histogram (0-50X)



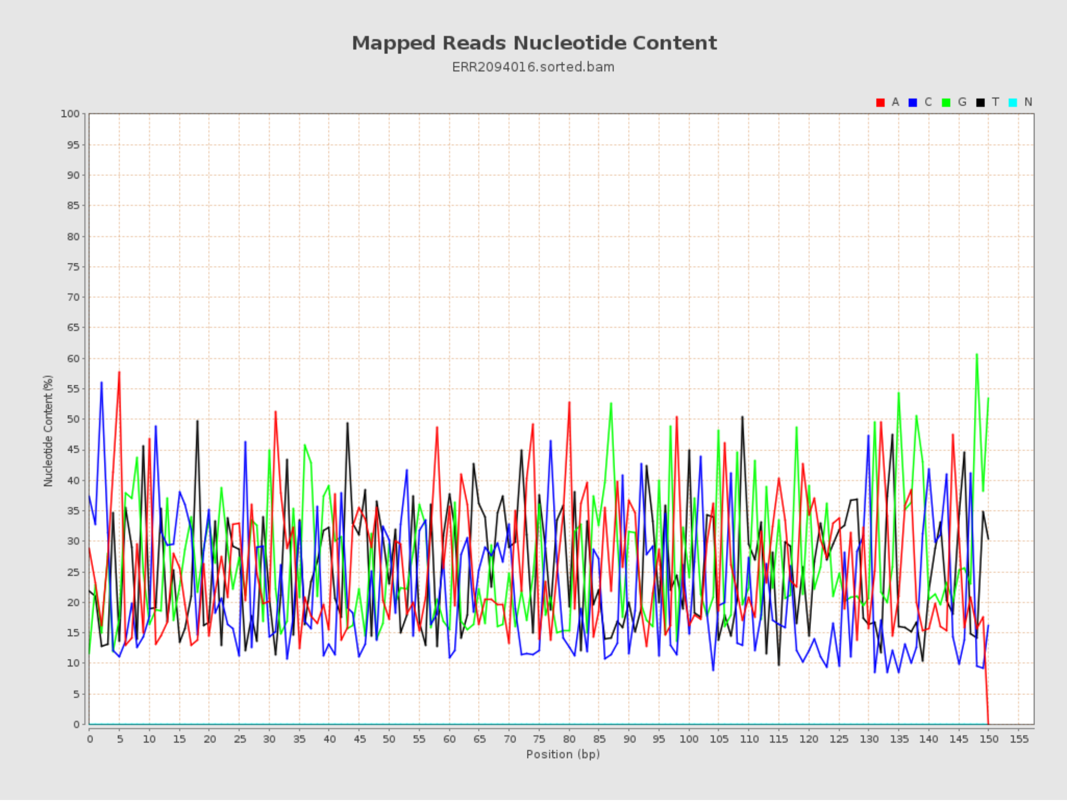
6. Results : Genome Fraction Coverage



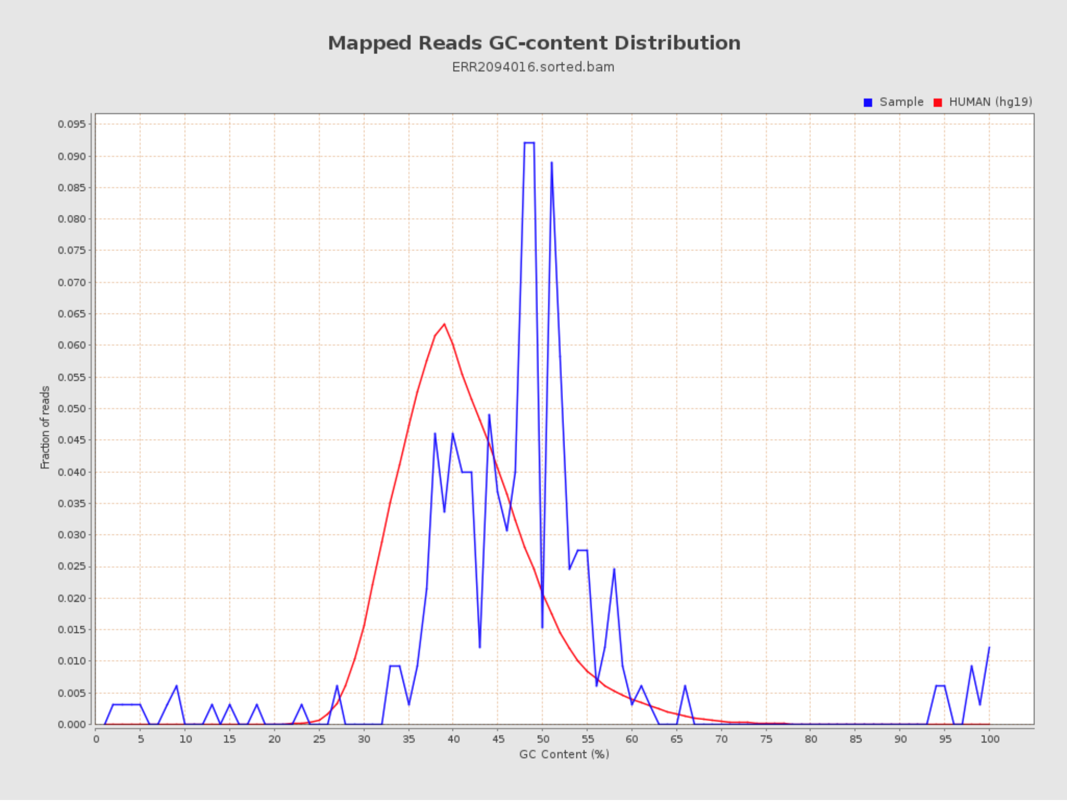
7. Results : Duplication Rate Histogram



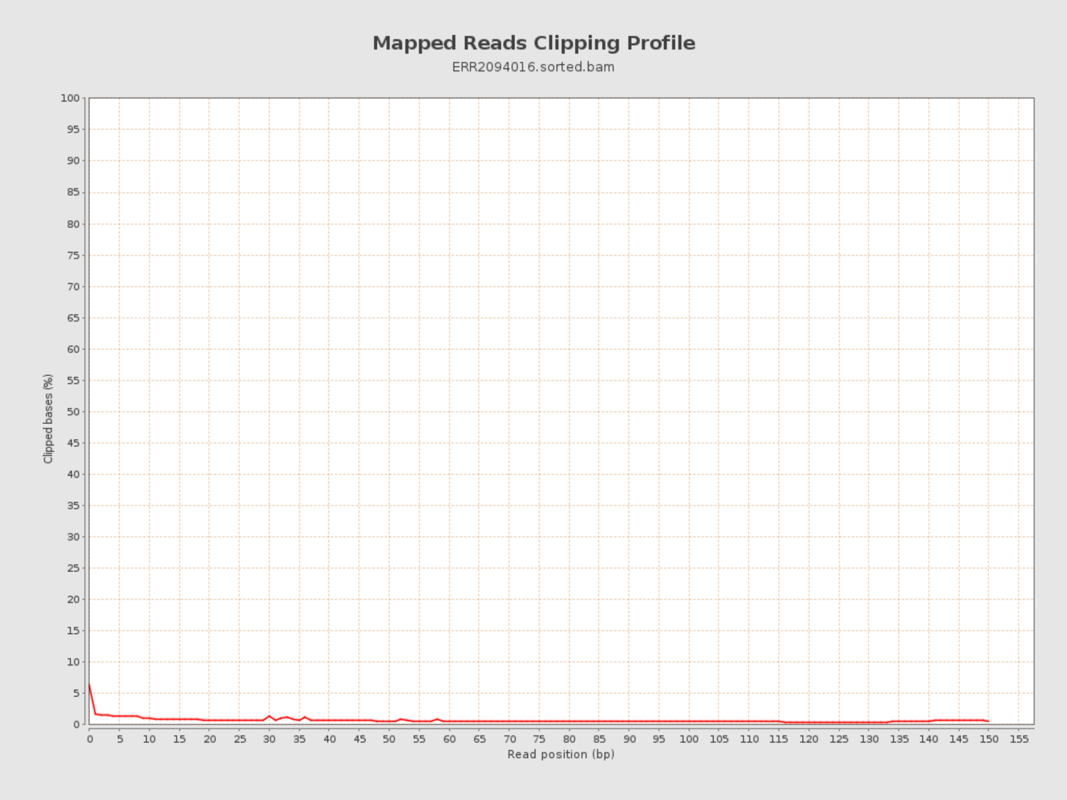
8. Results : Mapped Reads Nucleotide Content



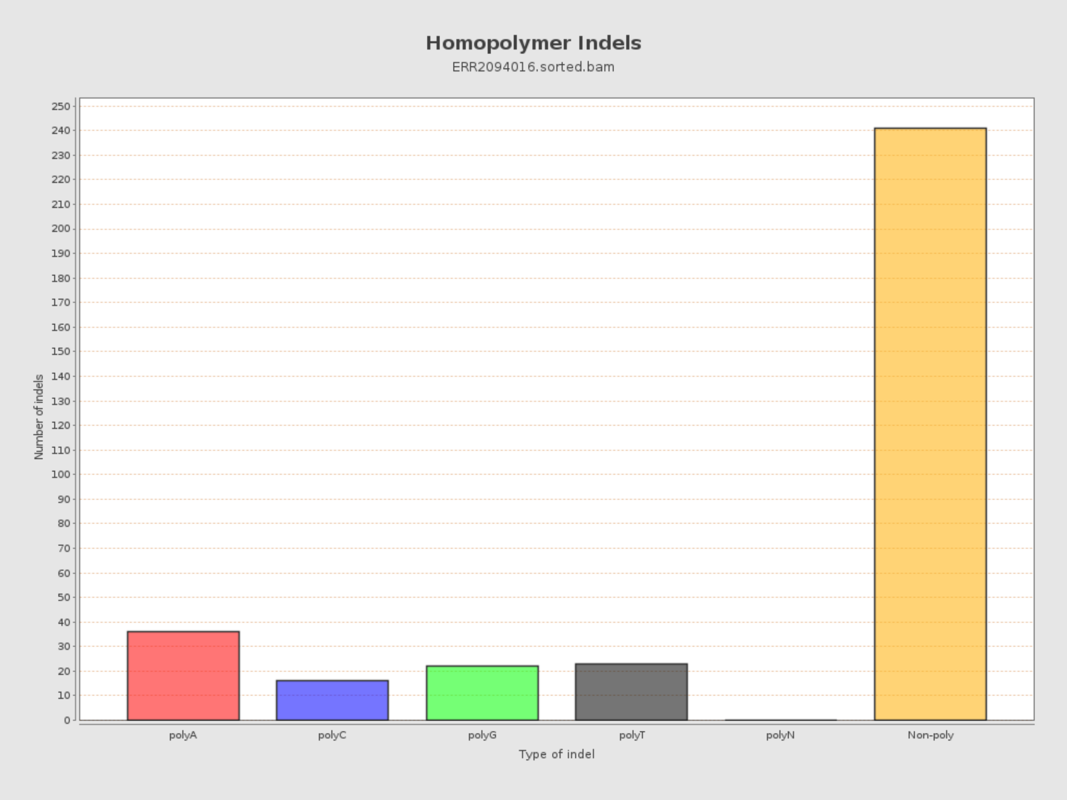
9. Results : Mapped Reads GC-content Distribution



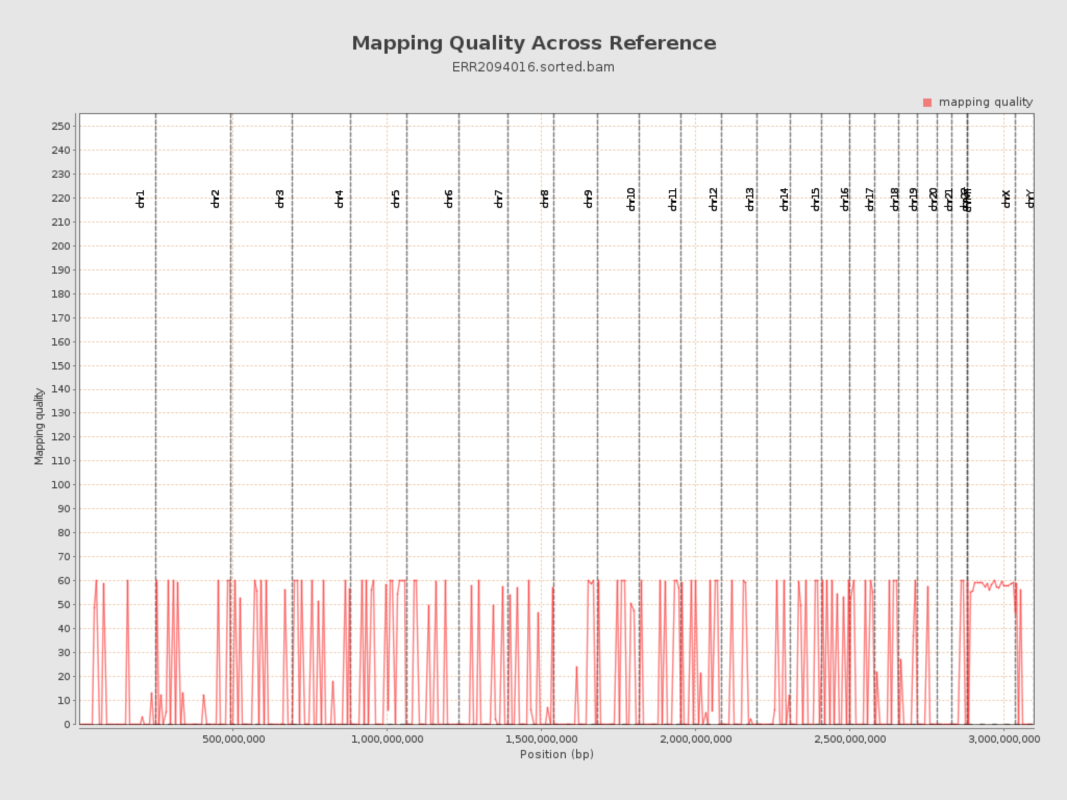
10. Results : Mapped Reads Clipping Profile



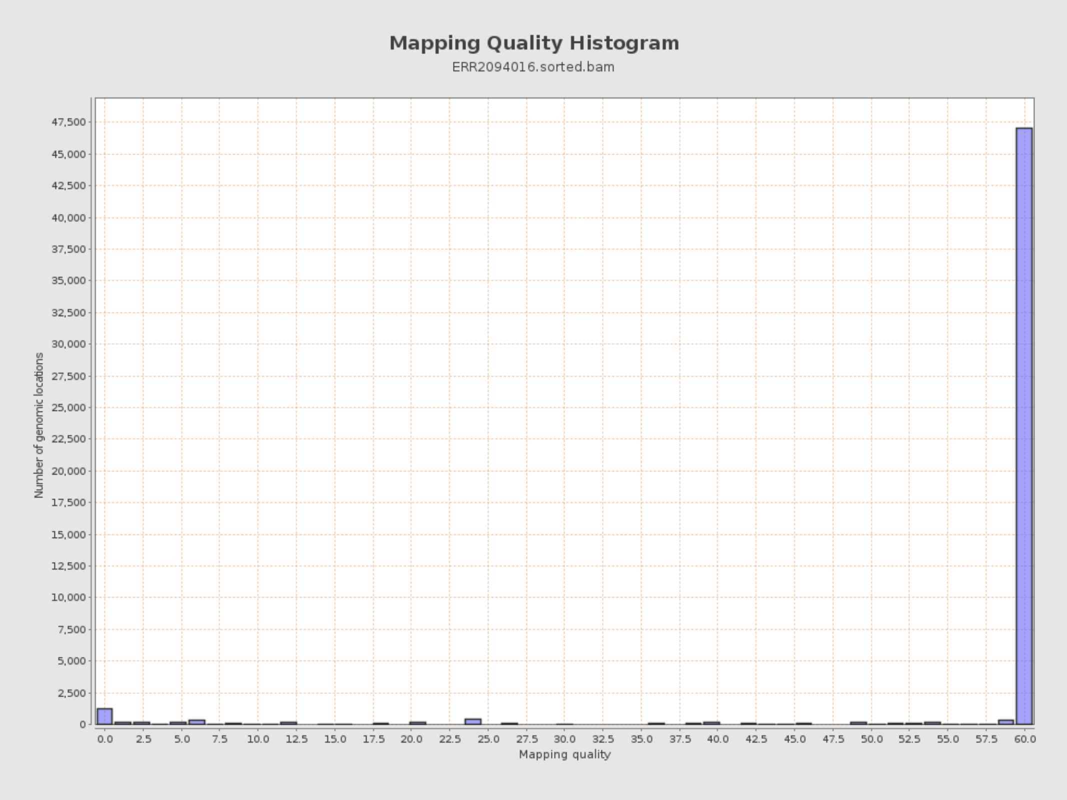
11. Results : Homopolymer Indels



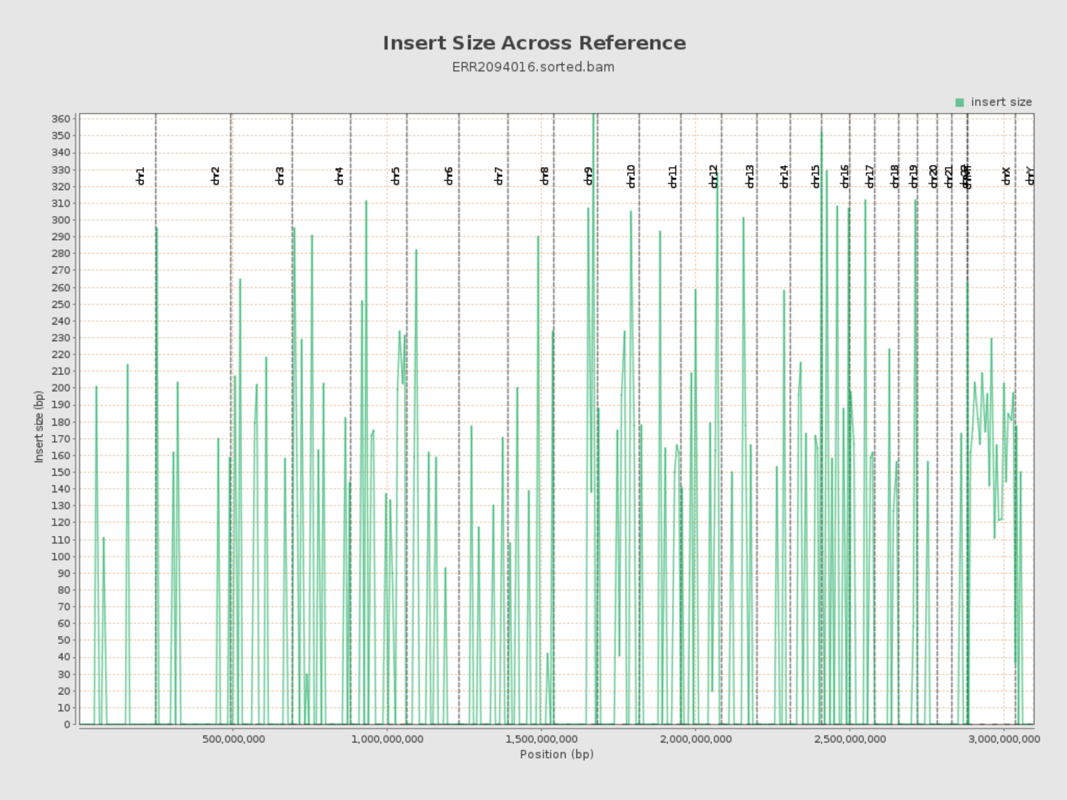
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram