Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:53:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094039.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_ERR2094039 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094039_1.fastq.gz ERR2094039_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:53:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	392,588
Mapped reads	376,978 / 96.02%
Unmapped reads	15,610 / 3.98%
Mapped paired reads	376,978 / 96.02%
Mapped reads, first in pair	189,437 / 48.25%
Mapped reads, second in pair	187,541 / 47.77%
Mapped reads, both in pair	374,124 / 95.3%
Mapped reads, singletons	2,854 / 0.73%
Secondary alignments	0
Supplementary alignments	15,149 / 3.86%
Read min/max/mean length	30 / 151 / 141.49
Duplicated reads (estimated)	356,061 / 90.7%
Duplication rate	51.18%
Clipped reads	154,047 / 39.24%

2.2. ACGT Content

Number/percentage of A's	13,583,661 / 27.72%
Number/percentage of C's	10,889,580 / 22.22%
Number/percentage of T's	13,219,391 / 26.98%
Number/percentage of G's	11,308,642 / 23.08%
Number/percentage of N's	576 / 0%

GC Percentage	45.3%

2.3. Coverage

Mean	0.0162
Standard Deviation	4.069

2.4. Mapping Quality

Mean Mapping Quality	41.12

2.5. Insert size

Mean	648,277.69
Standard Deviation	7,030,288.66
P25/Median/P75	136 / 169 / 203

2.6. Mismatches and indels

General error rate	4.31%
Mismatches	2,074,354
Insertions	30,900
Mapped reads with at least one insertion	8.05%
Deletions	169,488
Mapped reads with at least one deletion	41.62%
Homopolymer indels	29.96%

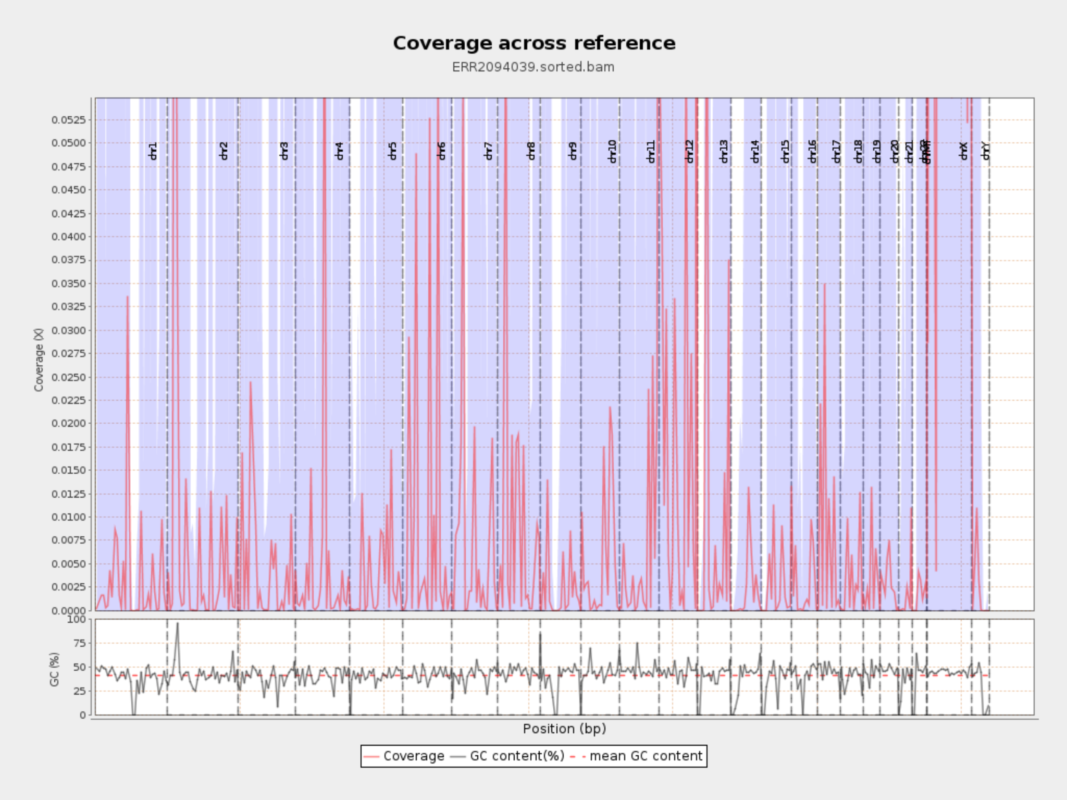
2.7. Chromosome stats

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

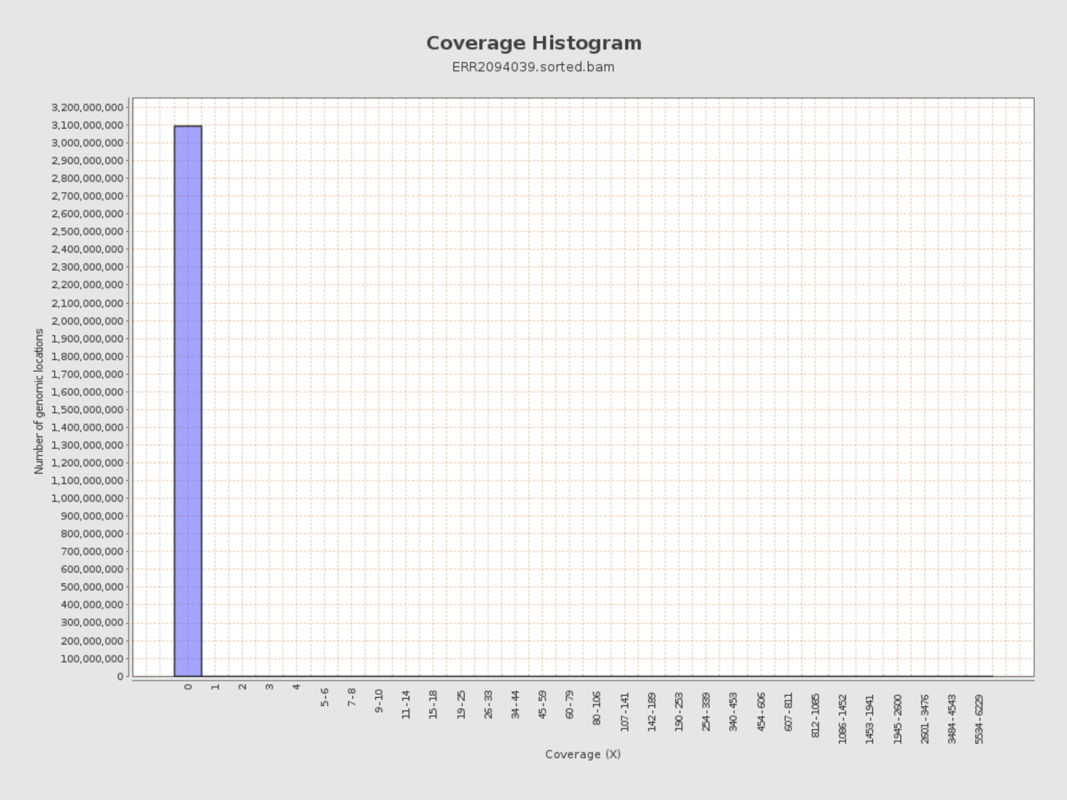
		bases	coverage	deviation
chr1	249250621	790657	0.0032	1.4357
chr2	243199373	1837014	0.0076	2.565
chr3	198022430	900422	0.0045	1.3192
chr4	191154276	1040011	0.0054	2.0779
chr5	180915260	647204	0.0036	1.1834
chr6	171115067	1795881	0.0105	4.3211
chr7	159138663	1217701	0.0077	2.4998
chr8	146364022	1336990	0.0091	3.2164
chr9	141213431	339278	0.0024	0.8123
chr10	135534747	713838	0.0053	1.7804
chr11	135006516	873725	0.0065	1.9392
chr12	133851895	2808879	0.021	5.4054
chr13	115169878	1100798	0.0096	2.9597
chr14	107349540	244096	0.0023	0.9193
chr15	102531392	244192	0.0024	0.7007
chr16	90354753	285675	0.0032	1.0081
chr17	81195210	668381	0.0082	2.1377
chr18	78077248	265790	0.0034	0.9432
chr19	59128983	197290	0.0033	0.9813
chr20	63025520	194466	0.0031	0.6264
chr21	48129895	77794	0.0016	0.3819
chr22	51304566	93402	0.0018	0.387
chrMT	16571	3212587	193.868	786.2358
chrX	155270560	29200719	0.1881	12.5327

chrY	59373566	150234	0.0025	0.7673

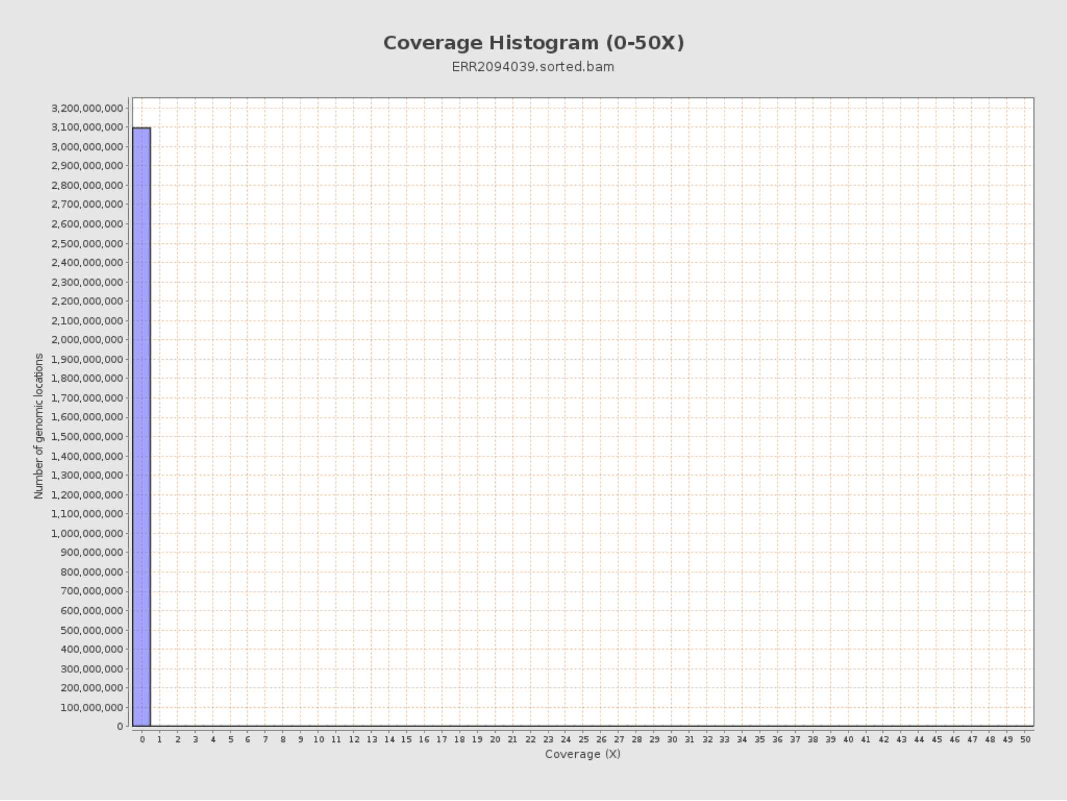
3. Results : Coverage across reference



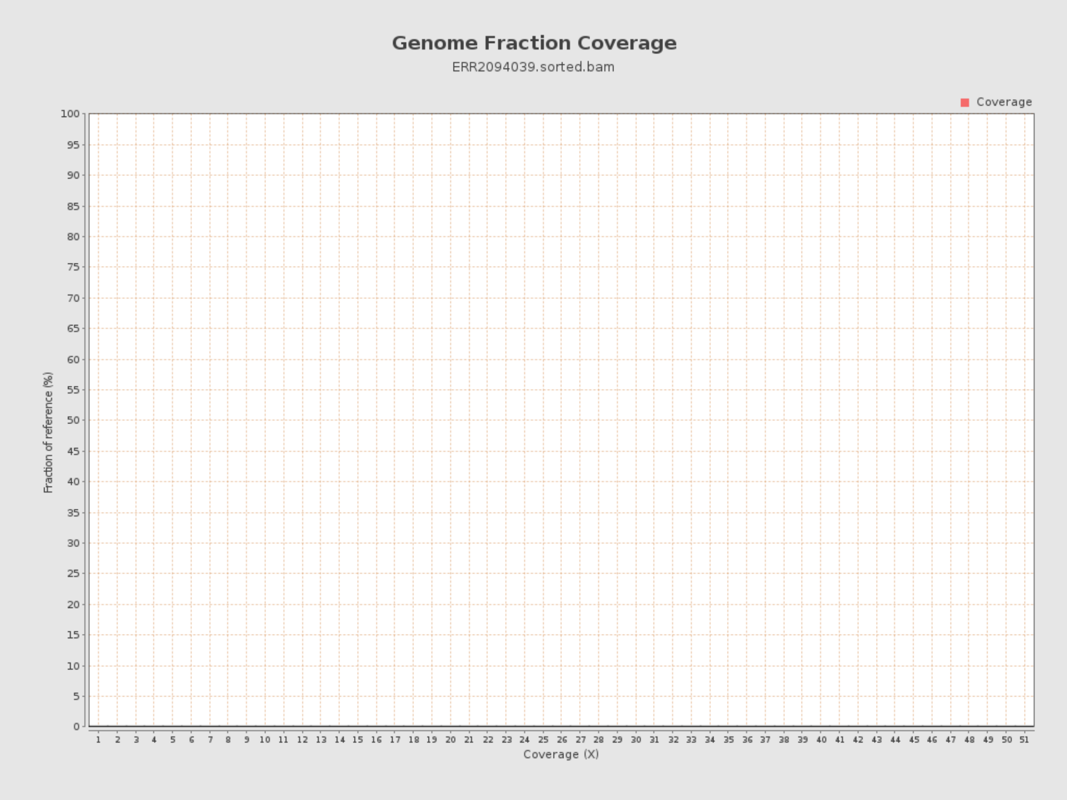
4. Results : Coverage Histogram



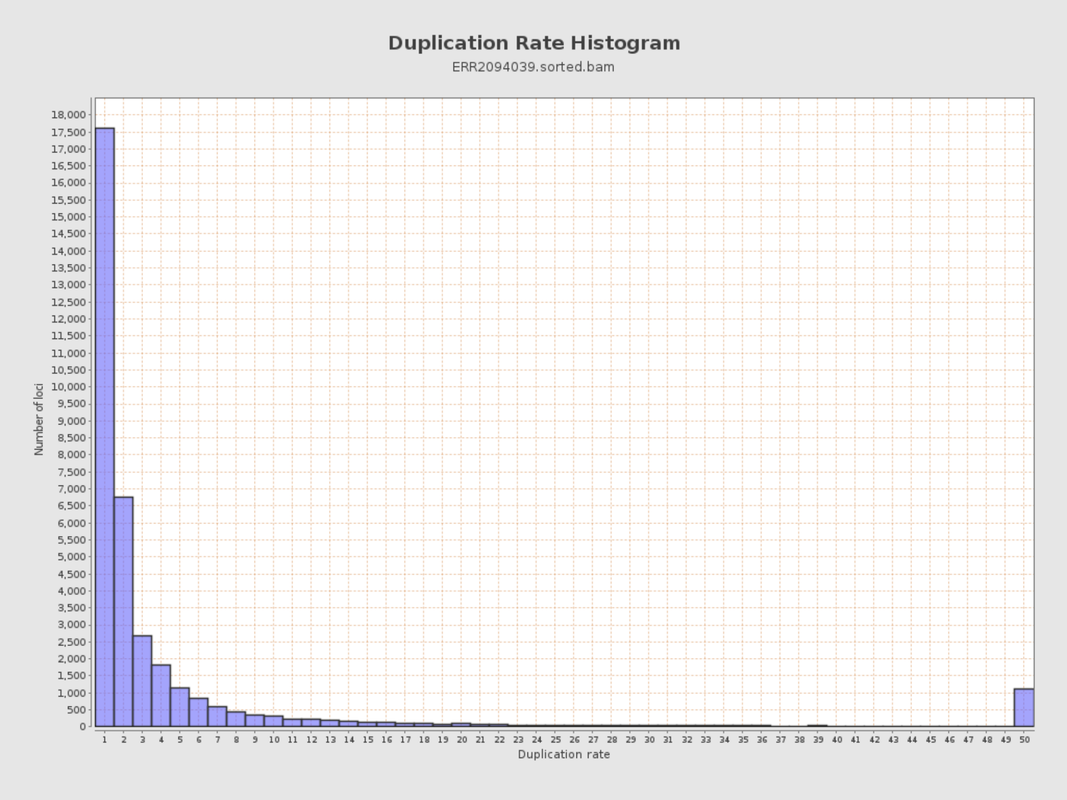
5. Results : Coverage Histogram (0-50X)



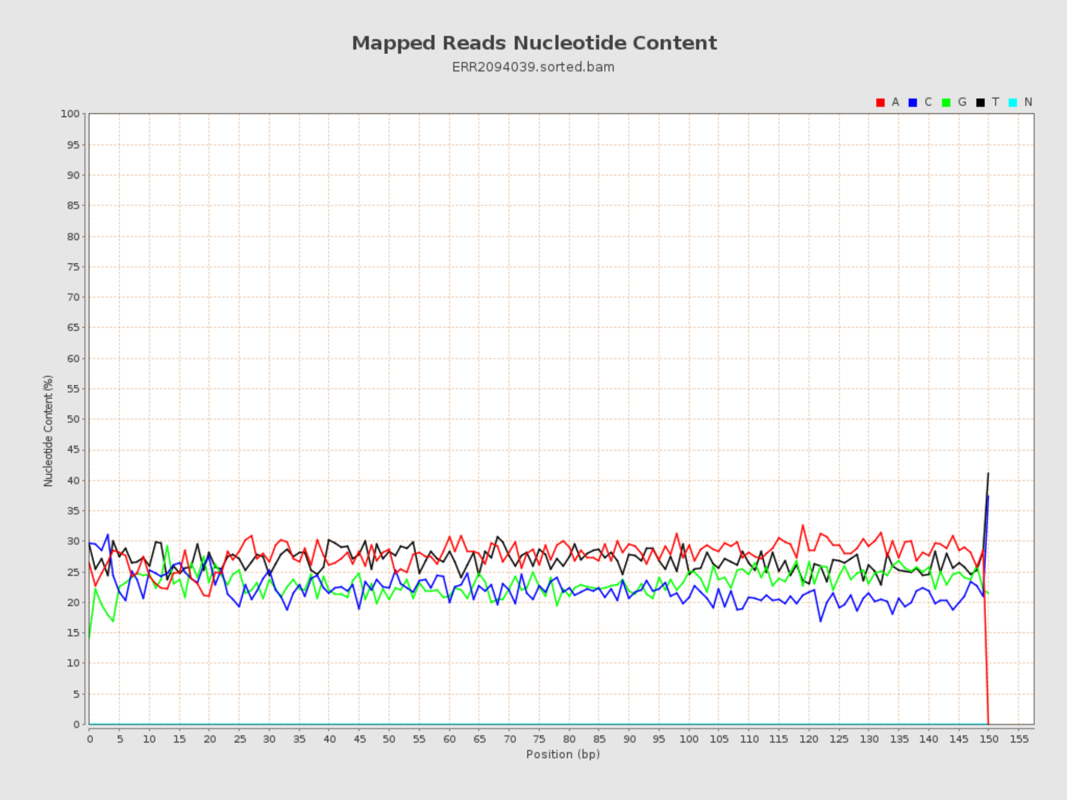
6. Results : Genome Fraction Coverage



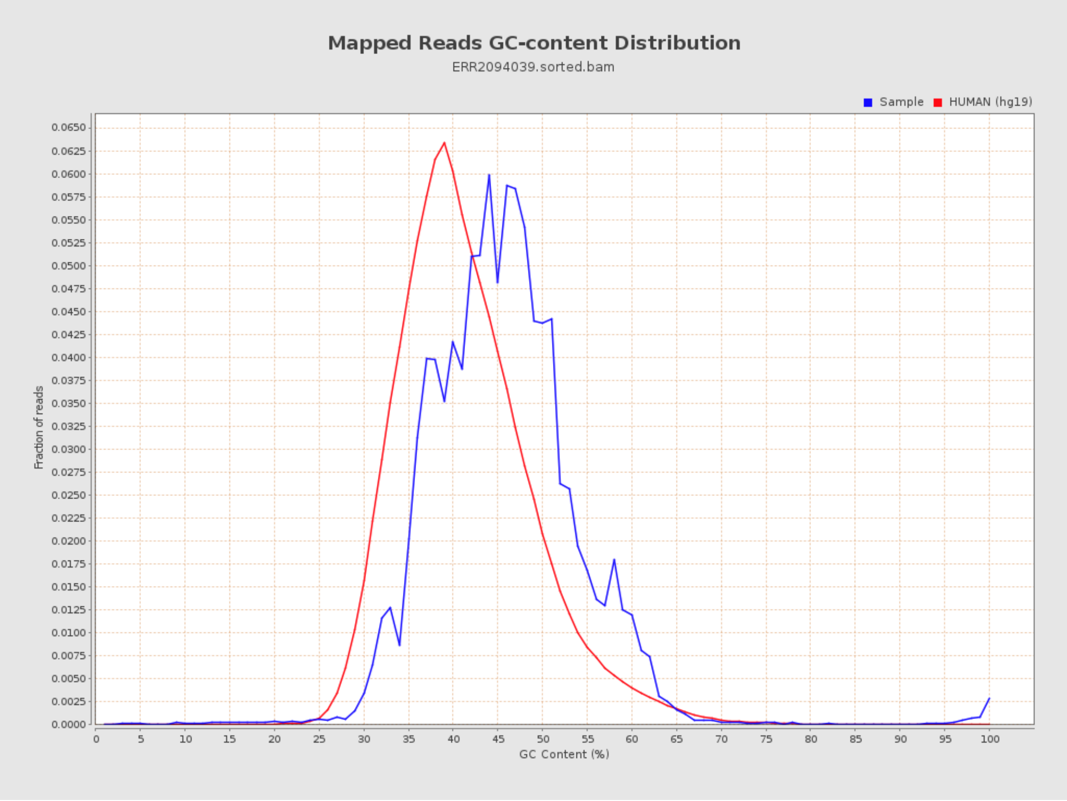
7. Results : Duplication Rate Histogram



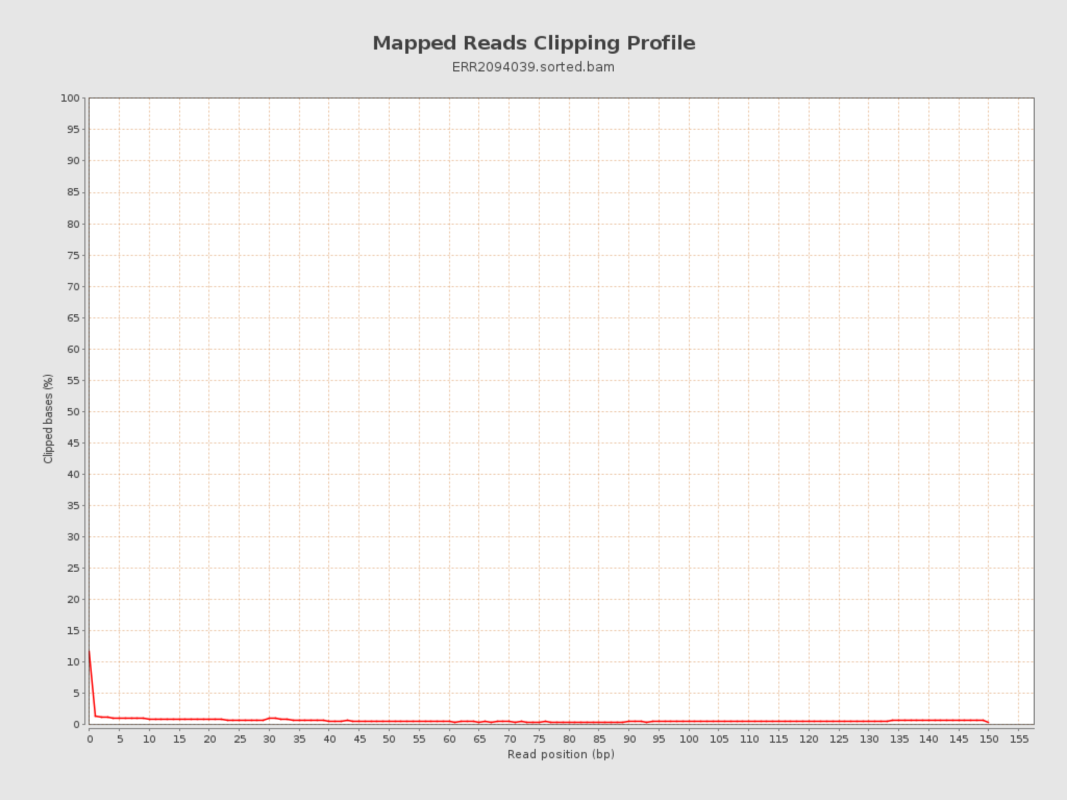
8. Results : Mapped Reads Nucleotide Content



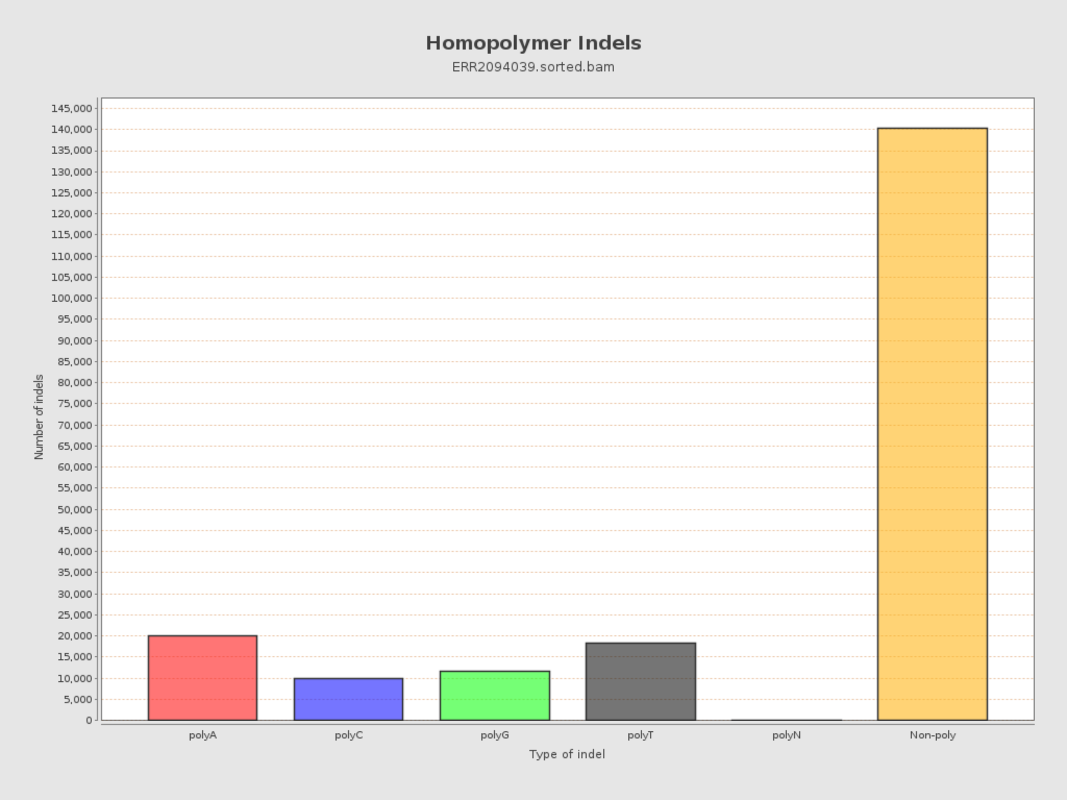
9. Results : Mapped Reads GC-content Distribution



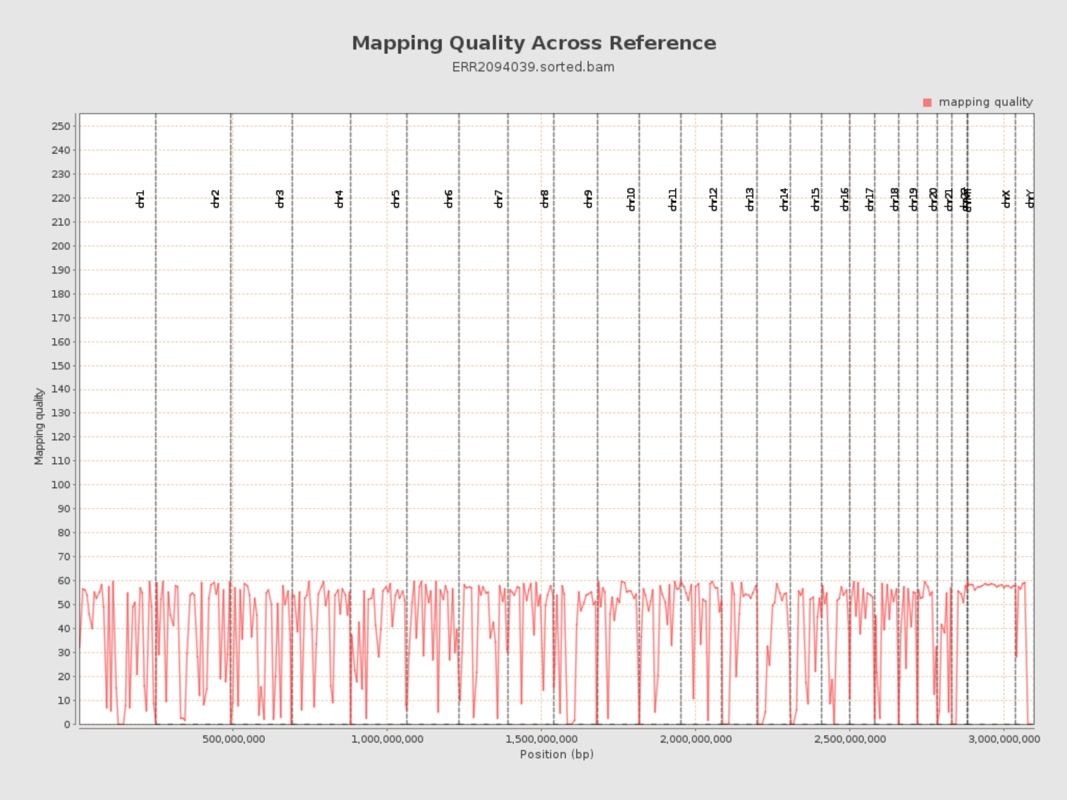
10. Results : Mapped Reads Clipping Profile



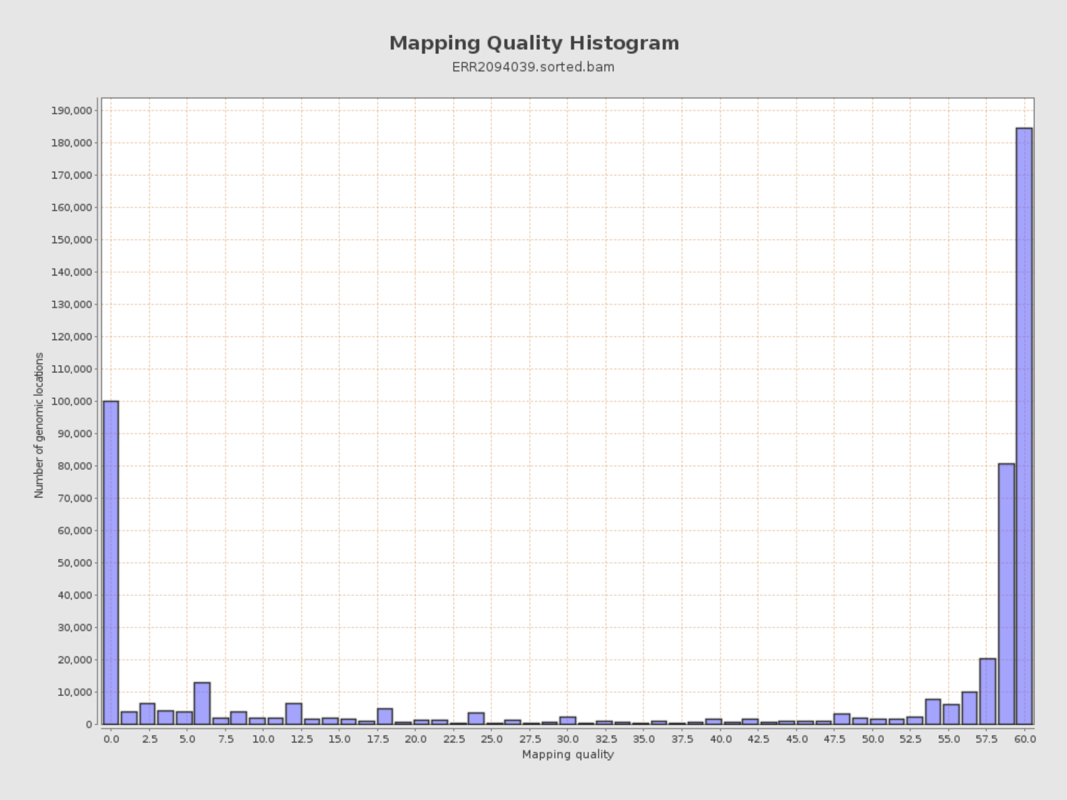
11. Results : Homopolymer Indels



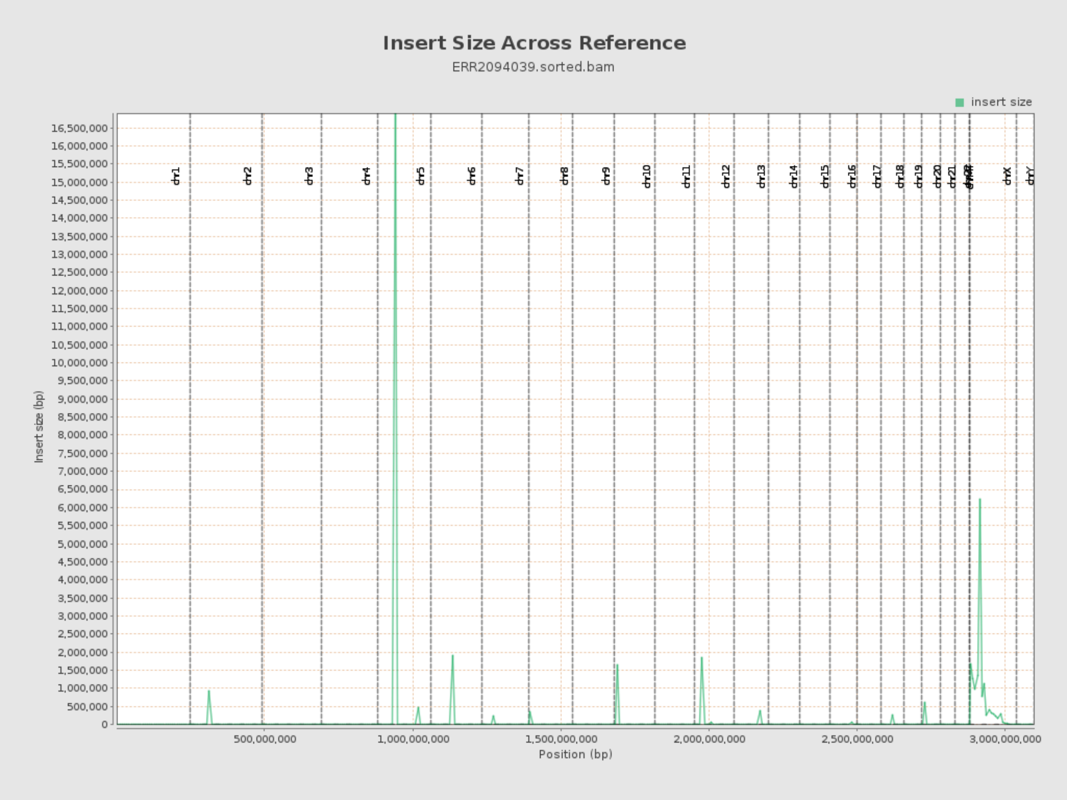
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram