Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:29:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093979.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_ERR2093979 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093979_1.fastq.gz ERR2093979_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:29:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093979.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	348,438
Mapped reads	323,976 / 92.98%
Unmapped reads	24,462 / 7.02%
Mapped paired reads	323,976 / 92.98%
Mapped reads, first in pair	162,836 / 46.73%
Mapped reads, second in pair	161,140 / 46.25%
Mapped reads, both in pair	320,774 / 92.06%
Mapped reads, singletons	3,202 / 0.92%
Secondary alignments	0
Supplementary alignments	20,916 / 6%
Read min/max/mean length	30 / 151 / 138.18
Duplicated reads (estimated)	303,707 / 87.16%
Duplication rate	49.64%
Clipped reads	168,853 / 48.46%

2.2. ACGT Content

Number/percentage of A's	10,680,491 / 26.66%
Number/percentage of C's	9,308,060 / 23.23%
Number/percentage of T's	10,013,605 / 24.99%
Number/percentage of G's	10,064,470 / 25.12%
Number/percentage of N's	359 / 0%

GC Percentage	48.35%

2.3. Coverage

Mean	0.0132
Standard Deviation	2.4435

2.4. Mapping Quality

Mean Mapping Quality	41.65

2.5. Insert size

Mean	1,095,028.69
Standard Deviation	9,570,462.82
P25/Median/P75	124 / 162 / 195

2.6. Mismatches and indels

General error rate	3.66%
Mismatches	1,421,408
Insertions	23,877
Mapped reads with at least one insertion	7.23%
Deletions	112,444
Mapped reads with at least one deletion	33.27%
Homopolymer indels	28.65%

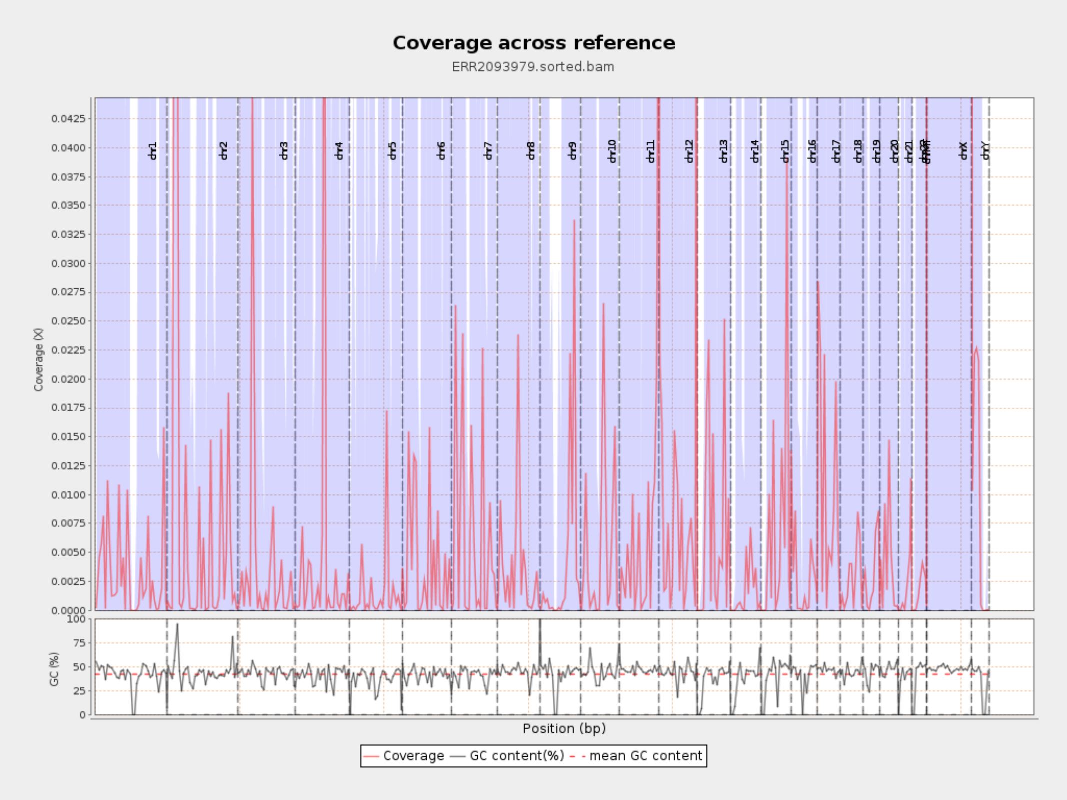
2.7. Chromosome stats

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

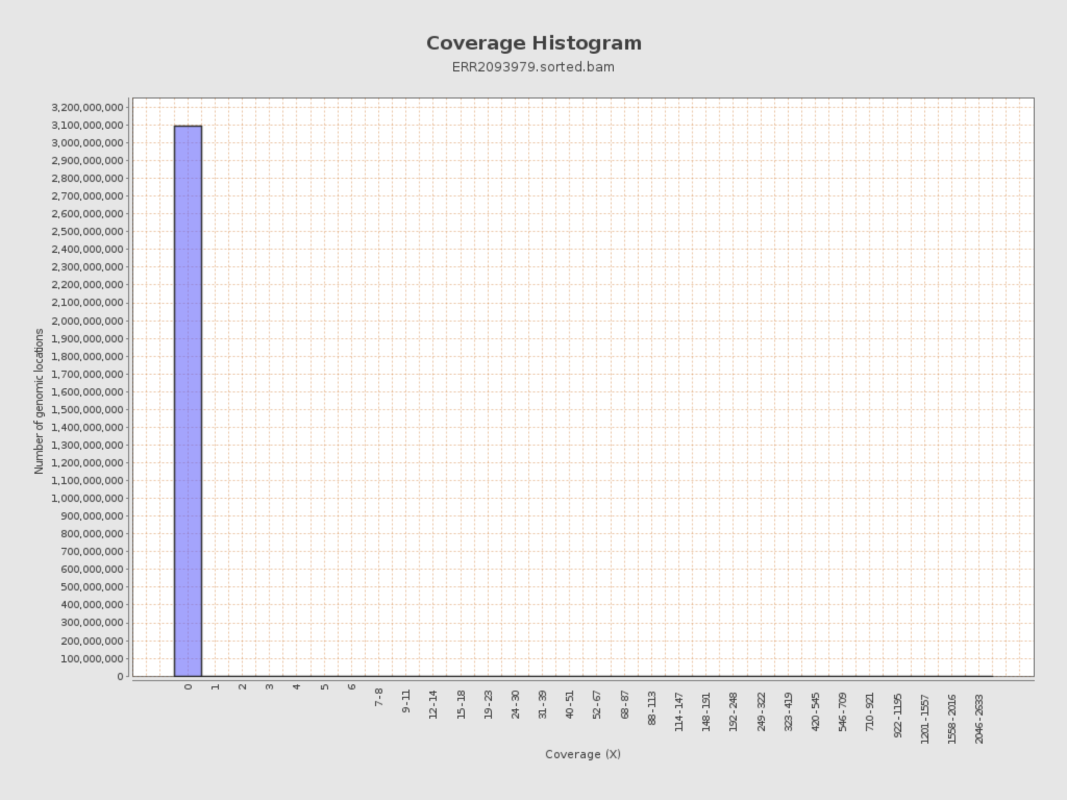
		bases	coverage	deviation
chr1	249250621	825543	0.0033	1.023
chr2	243199373	1797577	0.0074	2.3049
chr3	198022430	711128	0.0036	1.1292
chr4	191154276	865428	0.0045	1.3632
chr5	180915260	287833	0.0016	0.8822
chr6	171115067	723905	0.0042	1.241
chr7	159138663	970687	0.0061	1.7912
chr8	146364022	548268	0.0037	1.1267
chr9	141213431	625157	0.0044	1.3377
chr10	135534747	729884	0.0054	1.4947
chr11	135006516	731810	0.0054	1.3861
chr12	133851895	1020135	0.0076	1.8956
chr13	115169878	802966	0.007	1.8792
chr14	107349540	169729	0.0016	0.5559
chr15	102531392	718538	0.007	1.9402
chr16	90354753	269989	0.003	0.8603
chr17	81195210	913101	0.0112	2.5667
chr18	78077248	230100	0.0029	0.7451
chr19	59128983	177186	0.003	0.8524
chr20	63025520	270345	0.0043	1.226
chr21	48129895	114365	0.0024	0.4329
chr22	51304566	85820	0.0017	0.3854
chrMT	16571	693602	41.8564	170.1486
chrX	155270560	25995096	0.1674	8.6745

chrY	59373566	571970	0.0096	1.3296

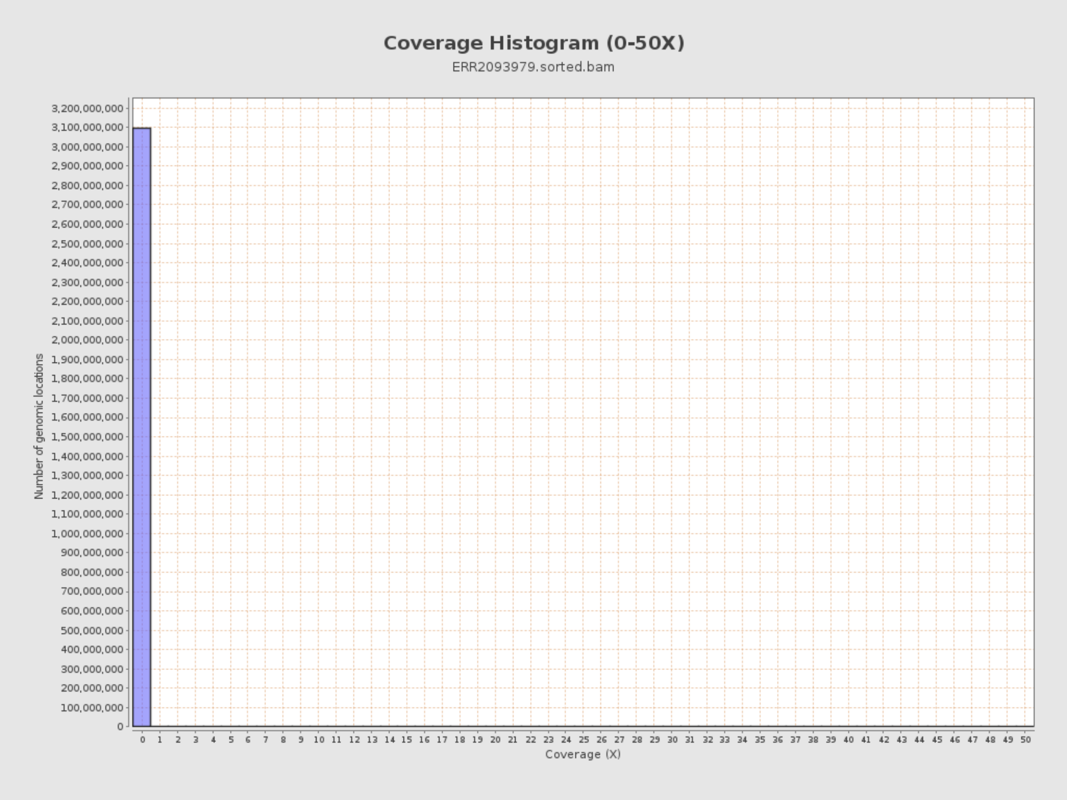
3. Results : Coverage across reference



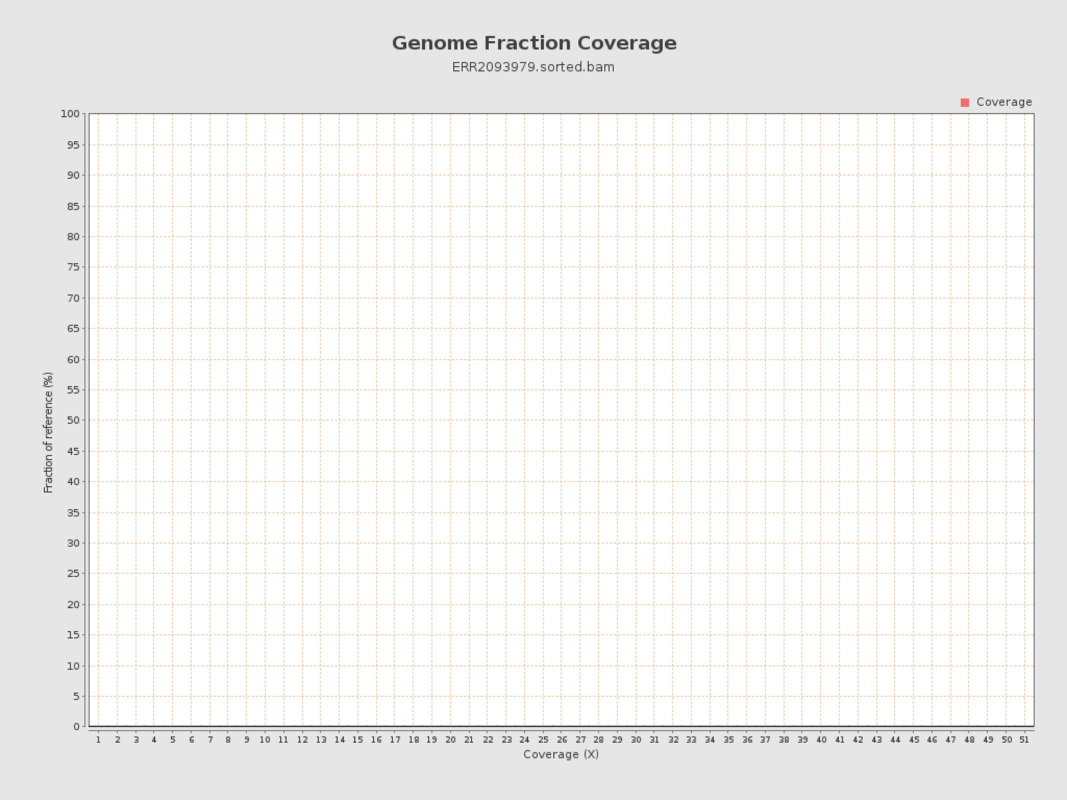
4. Results : Coverage Histogram



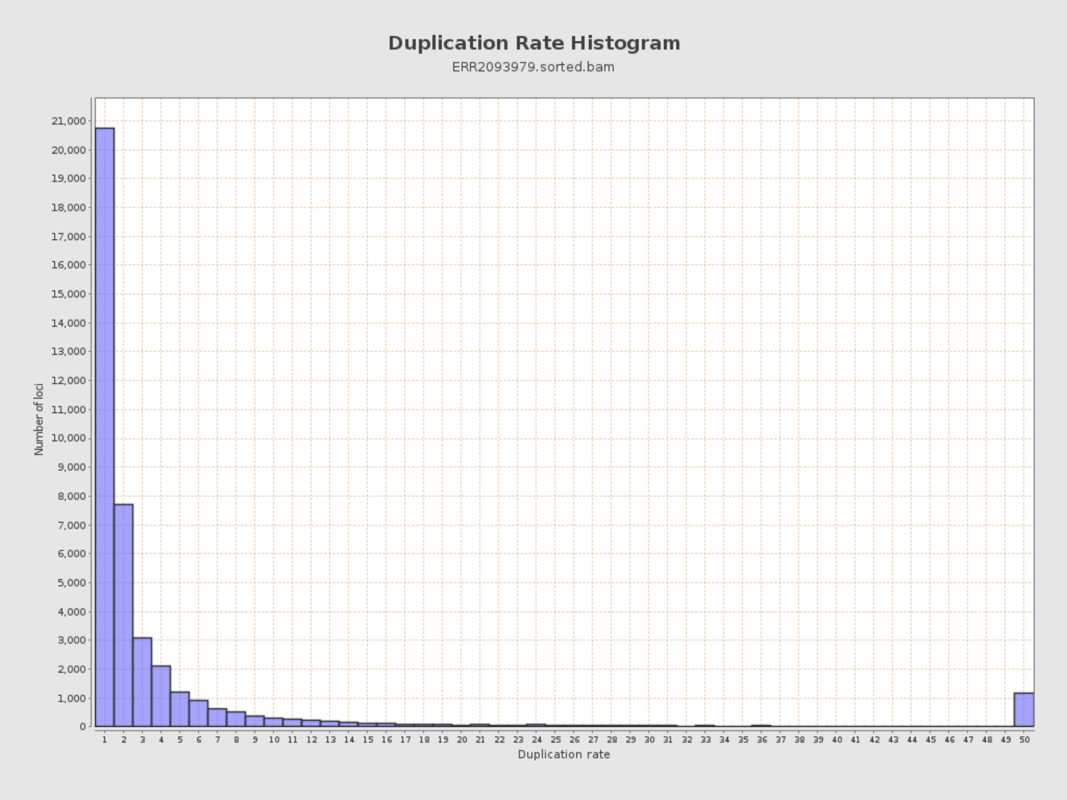
5. Results : Coverage Histogram (0-50X)



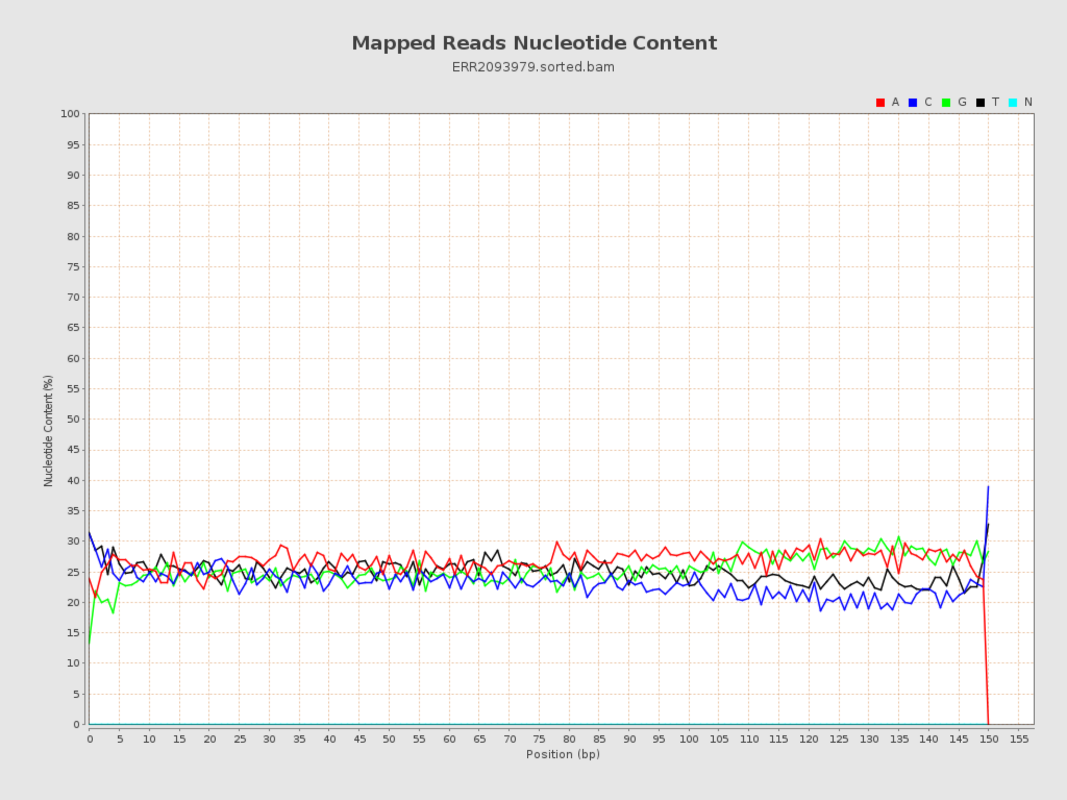
6. Results : Genome Fraction Coverage



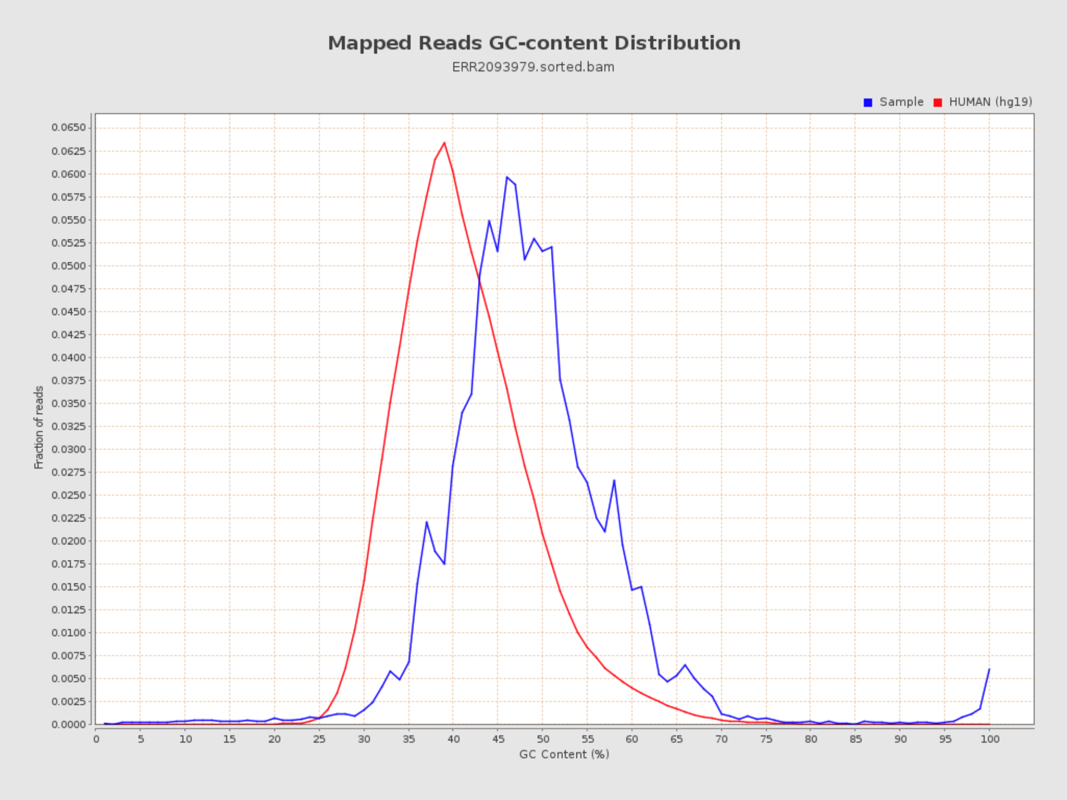
7. Results : Duplication Rate Histogram



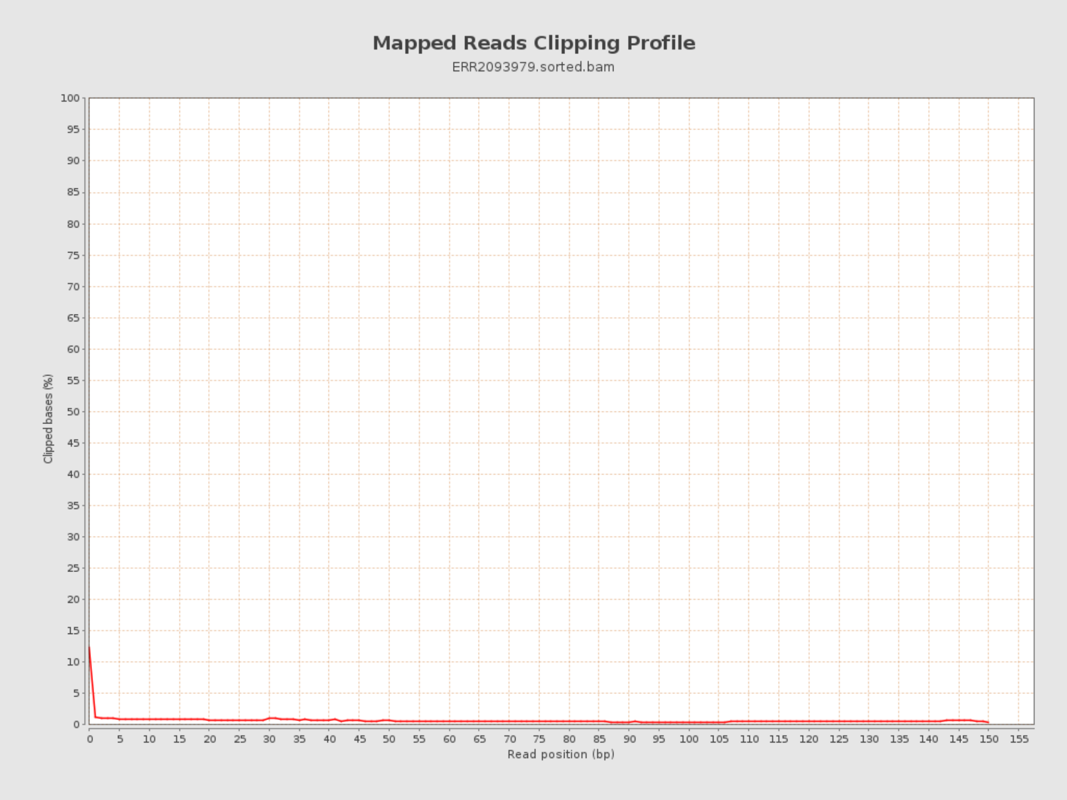
8. Results : Mapped Reads Nucleotide Content



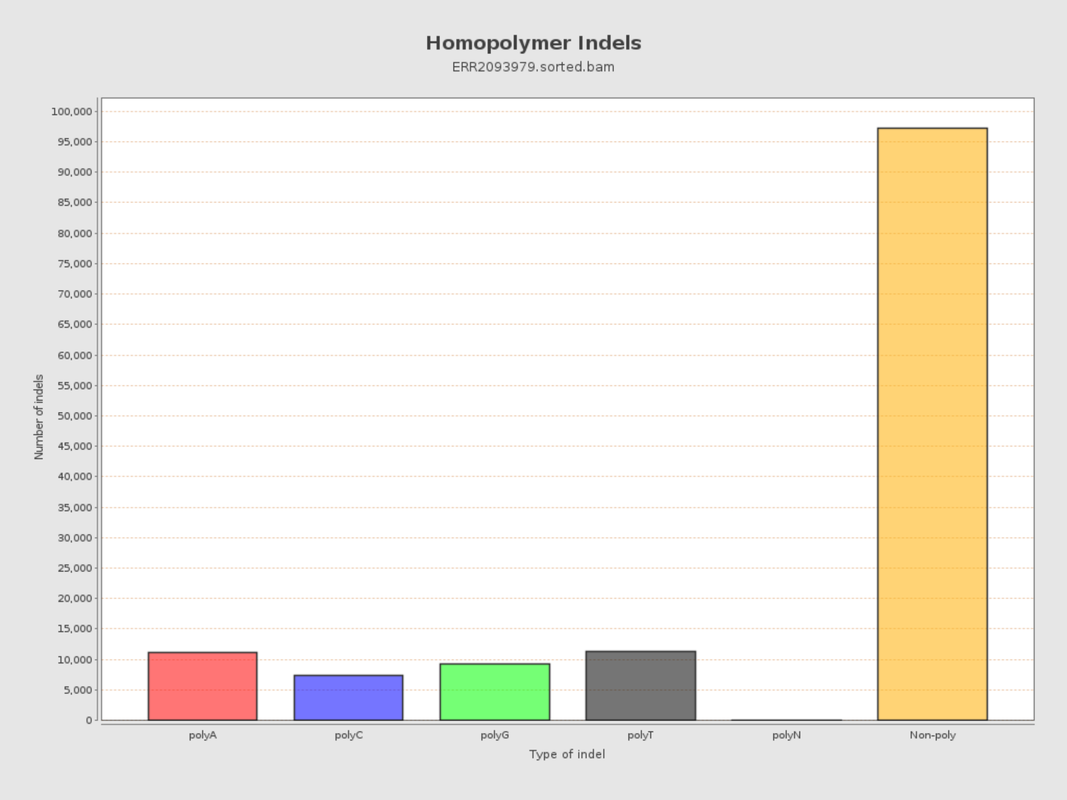
9. Results : Mapped Reads GC-content Distribution



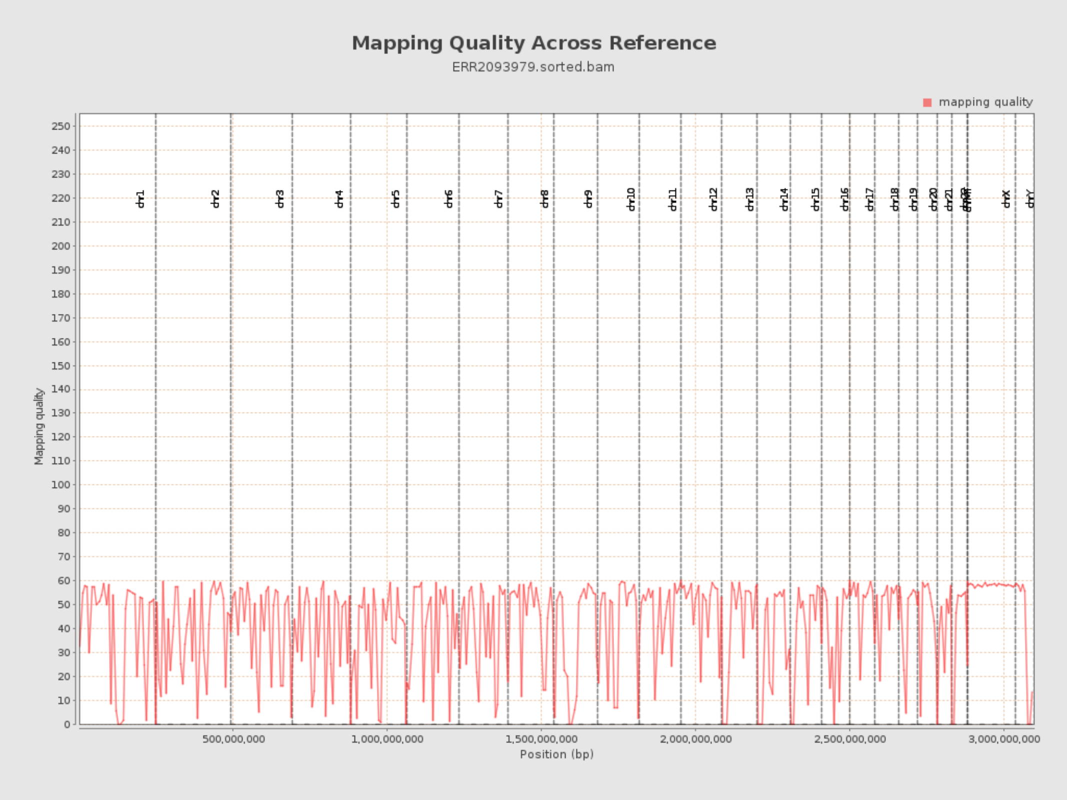
10. Results : Mapped Reads Clipping Profile



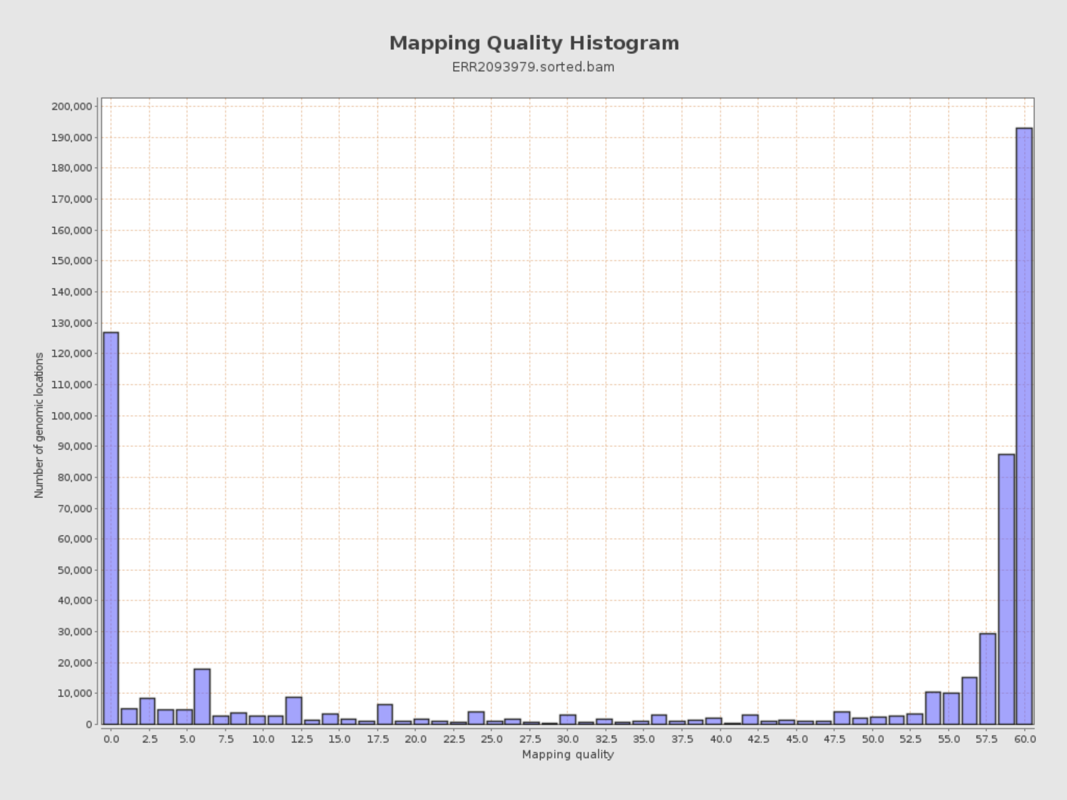
11. Results : Homopolymer Indels



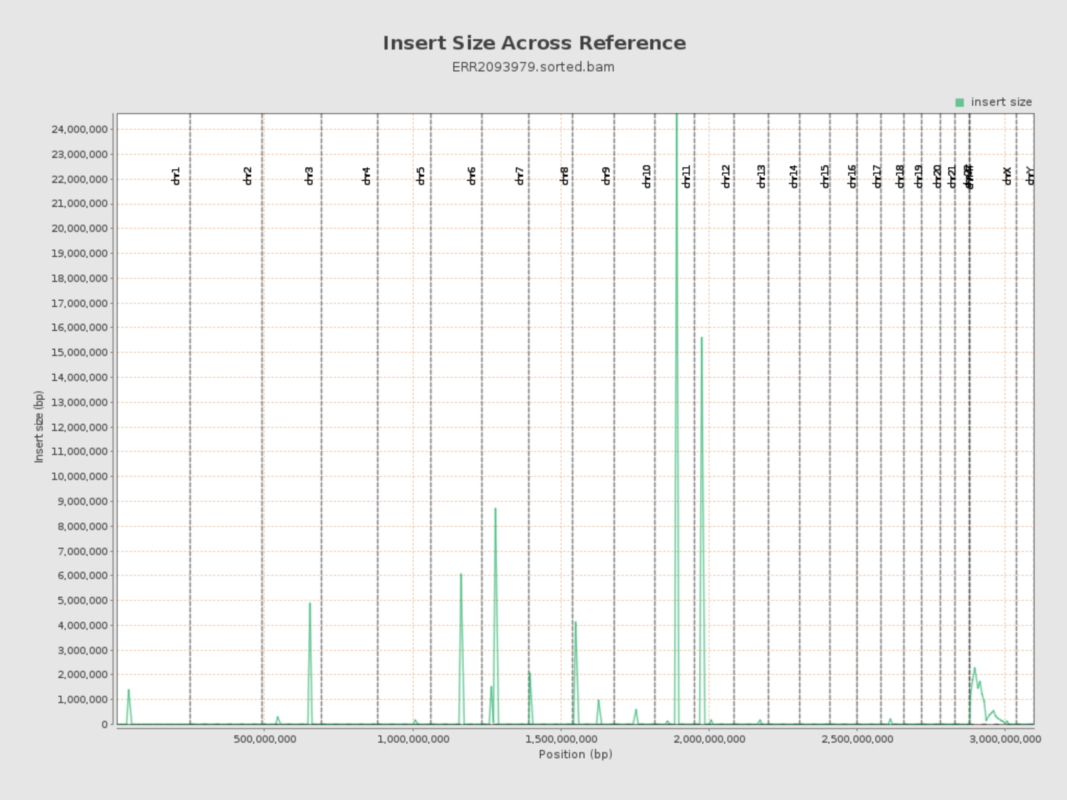
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram