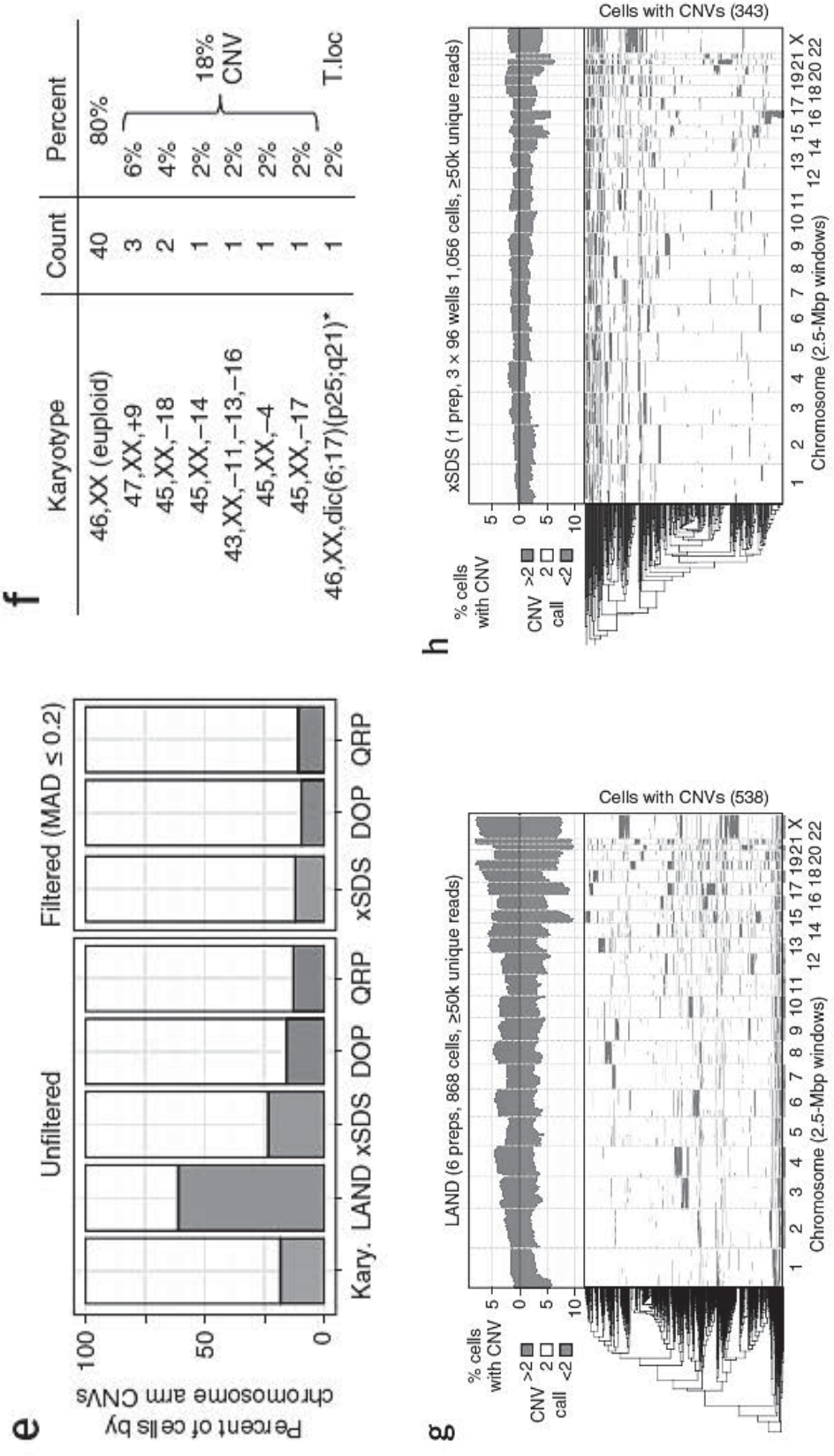
e
Unfiltered
Filtered (MAD ≤ 0.2)
Percent of cells by chromosome arm CNVs
100
50
0
Kary.
LAND
xSDS
DOP
QRP
xSDS
DOP
QRP
f
Karyotype
Count
Percent
46,XX (euploid)
40
80%
47,XX,+9
3
6%
45,XX,−18
2
4%
45,XX,−14
1
2%
18% CNV
43,XX,−11,−13,−16
1
2%
45,XX,−4
1
2%
45,XX,−17
1
2%
46,XX,dic(6;17)(p25;q21)*
1
2%
T.loc
g
LAND (6 preps, 868 cells, ≥50k unique reads)
Cells with CNVs (538)
% cells with CNV
CNV call
>2
2
<2
Chromosome (2.5-Mbp windows)
h
xSDS (1 prep, 3 × 96 wells 1,056 cells, ≥50k unique reads)
Cells with CNVs (343)
% cells with CNV
CNV call
>2
2
<2
Chromosome (2.5-Mbp windows)

FIG. 7

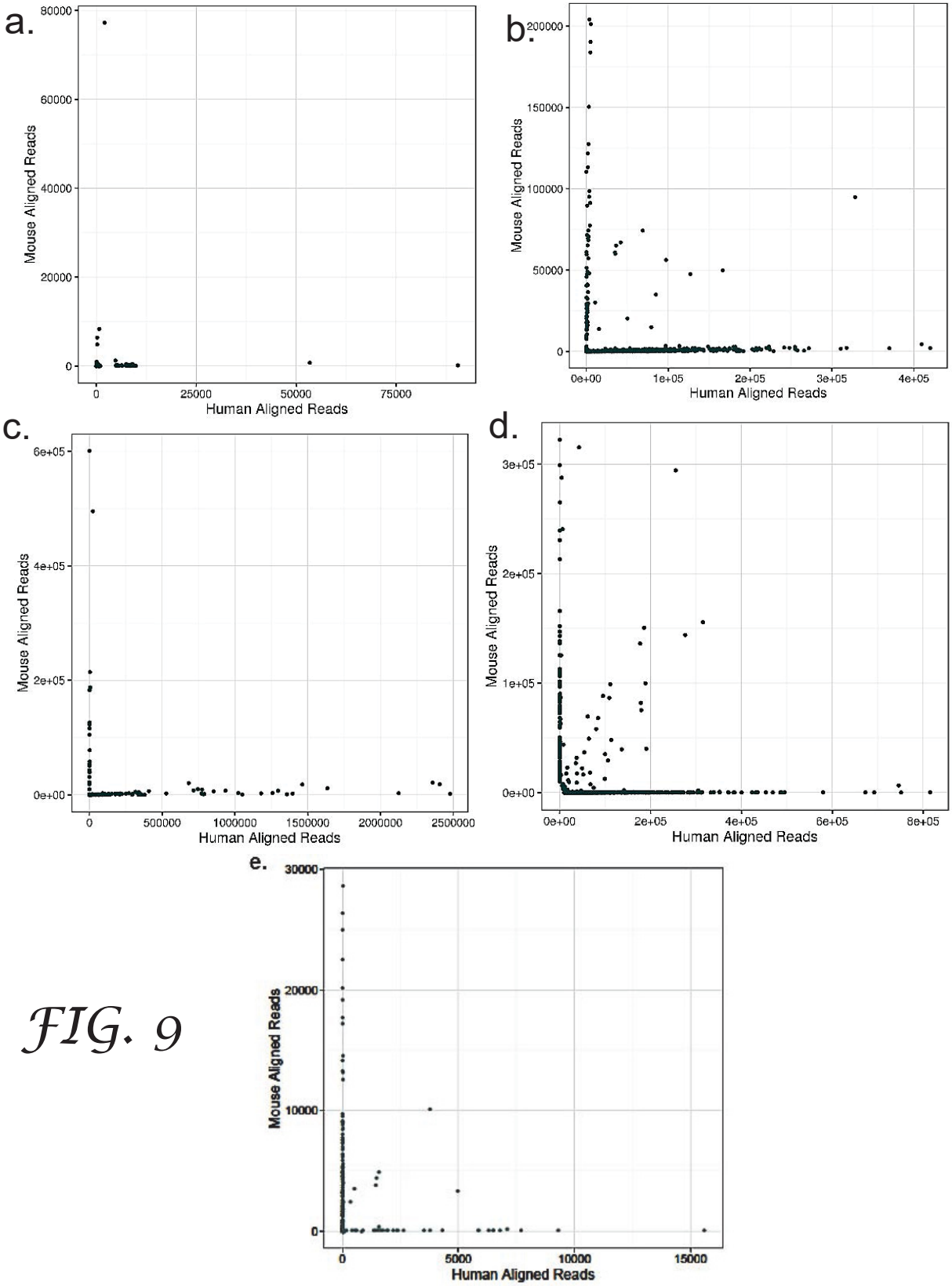
a.
Mouse Aligned Reads
Human Aligned Reads
b.
Mouse Aligned Reads
Human Aligned Reads
c.
Mouse Aligned Reads
Human Aligned Reads
d.
Mouse Aligned Reads
Human Aligned Reads
e.
Mouse Aligned Reads
Human Aligned Reads

FIG. 9

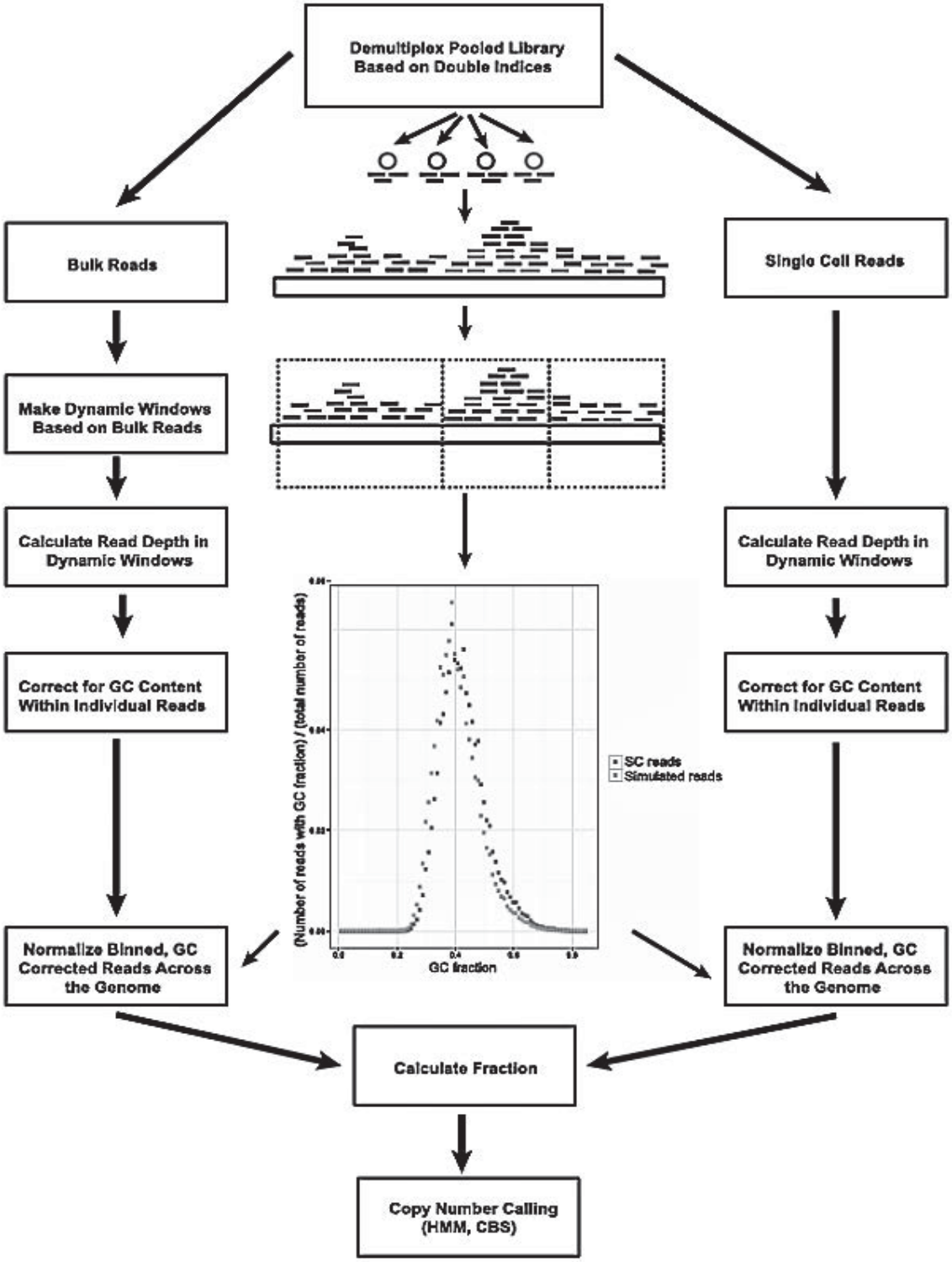
Demultiplex Pooled Library Based on Double Indices
Bulk Reads
Single Cell Reads
Make Dynamic Windows Based on Bulk Reads
Calculate Read Depth in Dynamic Windows
Calculate Read Depth in Dynamic Windows
Correct for GC Content Within Individual Reads
Correct for GC Content Within Individual Reads
(Number of reads with GC fraction) / (total number of reads)
GC fraction
SC reads
Simulated reads
Normalize Binned, GC Corrected Reads Across the Genome
Normalize Binned, GC Corrected Reads Across the Genome
Calculate Fraction
Copy Number Calling (HMM, CBS)

FIG. 12

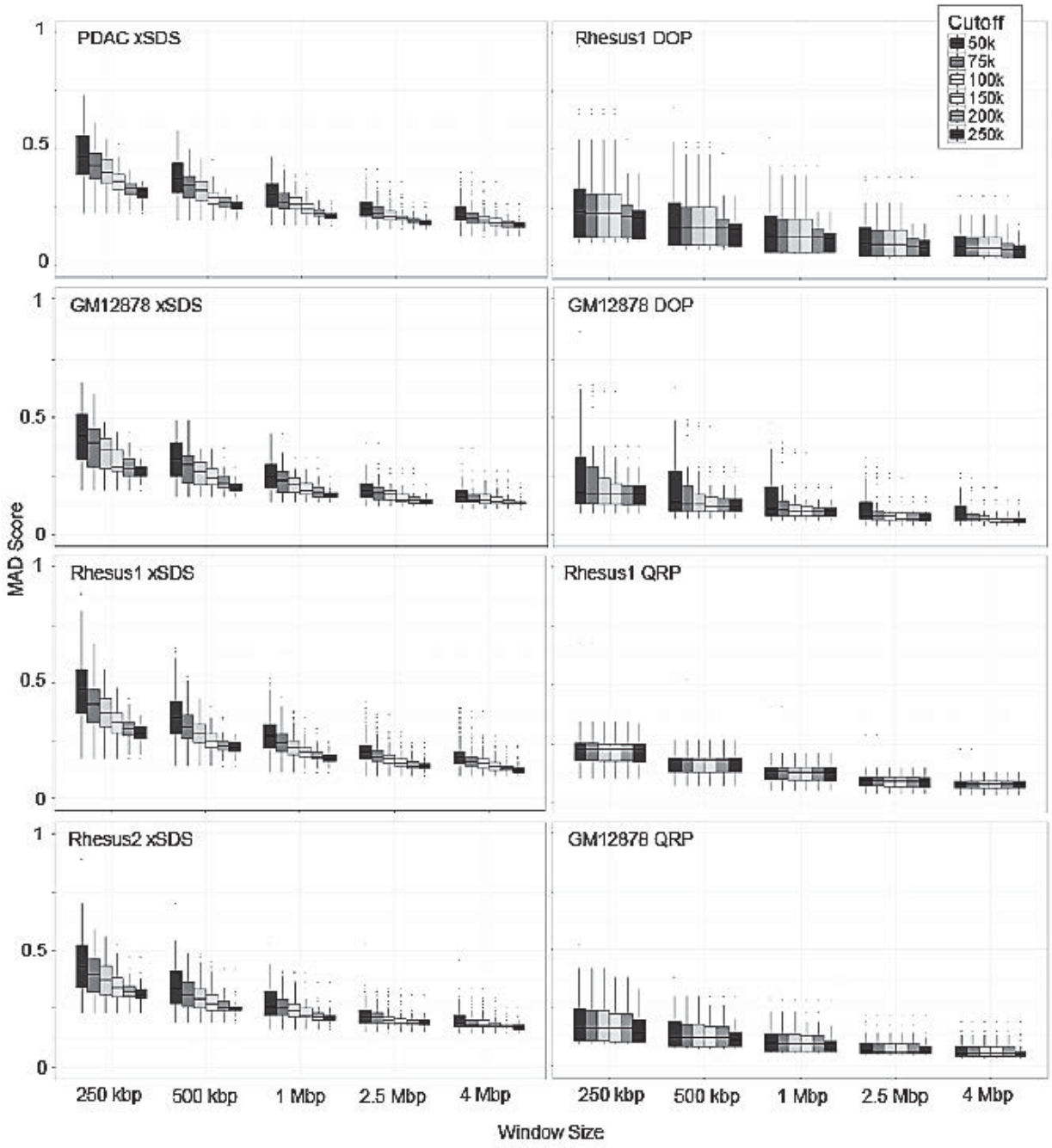
PDAC xSDS
Rhesus1 DOP
GM12878 xSDS
GM12878 DOP
Rhesus1 xSDS
Rhesus1 QRP
Rhesus2 xSDS
GM12878 QRP
Cutoff
50k
75k
100k
150k
200k
250k
MAD Score
1
0.5
0
250 kbp
500 kbp
1 Mbp
2.5 Mbp
4 Mbp
Window Size

FIG. 14-1

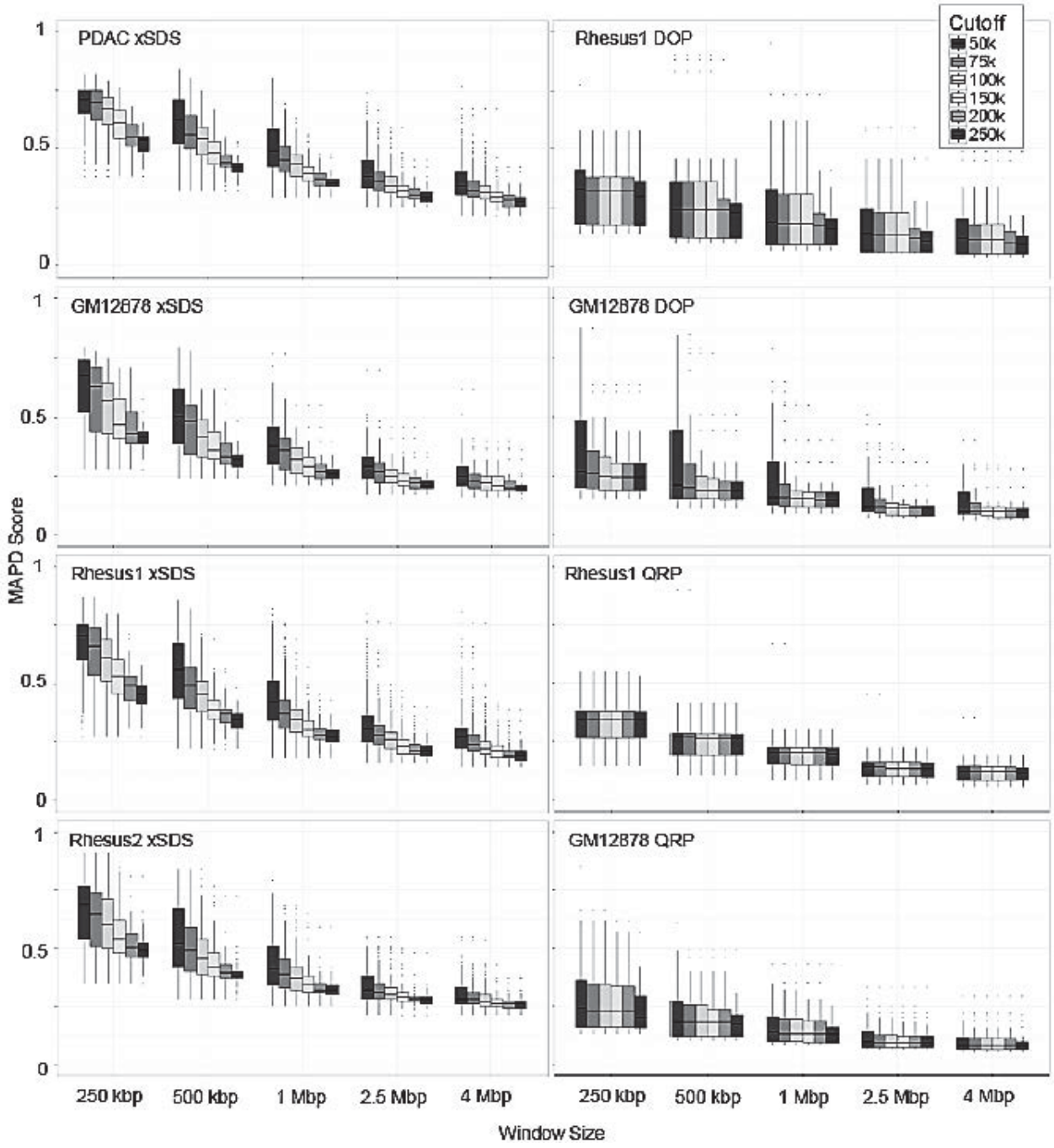
PDAC xSDS
Rhesus1 DOP
GM12878 xSDS
GM12878 DOP
Rhesus1 xSDS
Rhesus1 QRP
Rhesus2 xSDS
GM12878 QRP
Cutoff
50k
75k
100k
150k
200k
250k
MAPD Score
1
0.5
0
250 kbp
500 kbp
1 Mbp
2.5 Mbp
4 Mbp
Window Size

FIG. 14-2

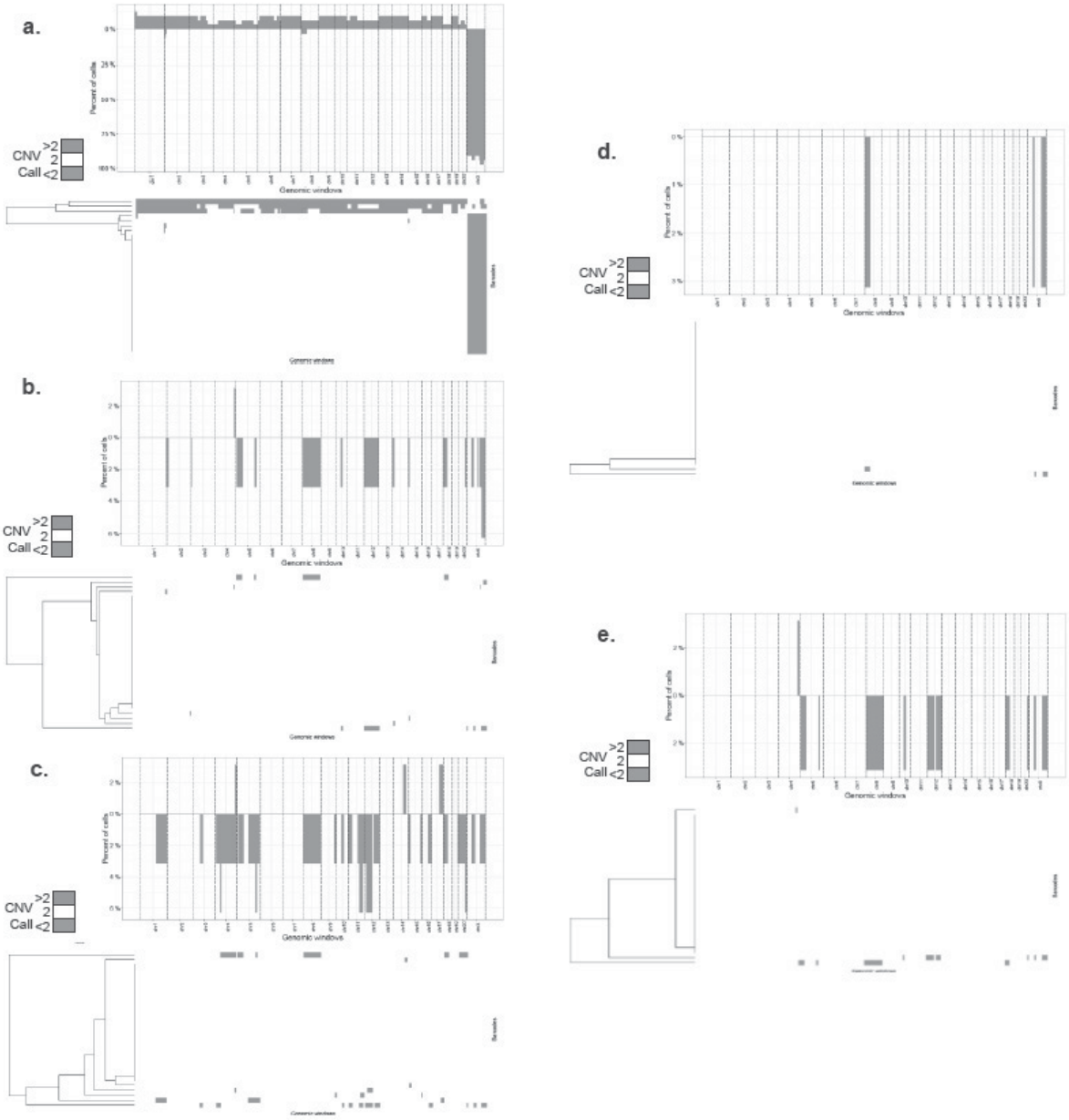
a.
b.
c.
d.
e.
CNV
Call
>2
2
<2
Percent of cells
Genomic windows
Barcodes

FIG. 16

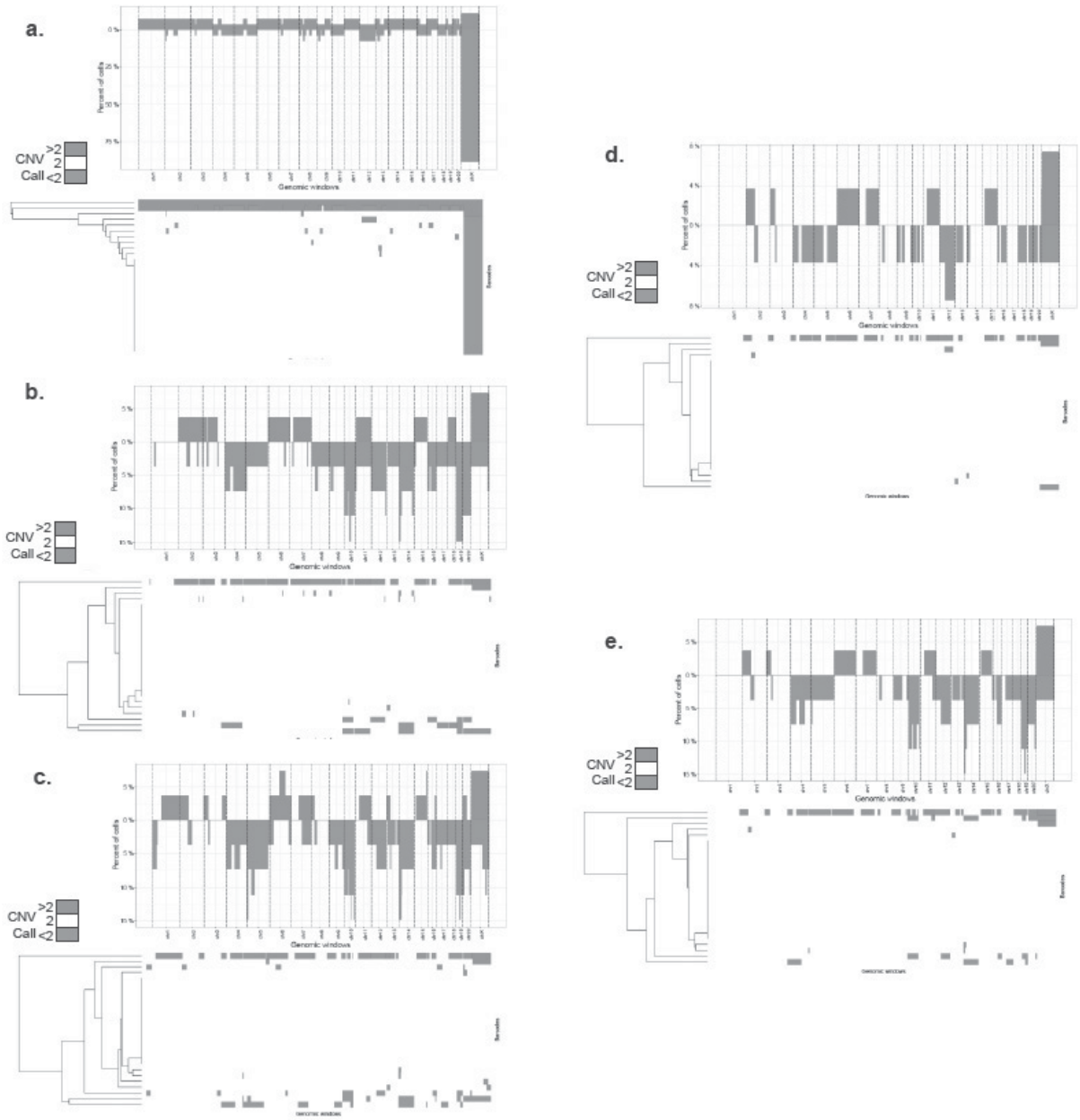
a.
b.
c.
d.
e.
CNV
Call
>2
2
<2
Genomic windows
Percent of cells
Barcodes

FIG. 17

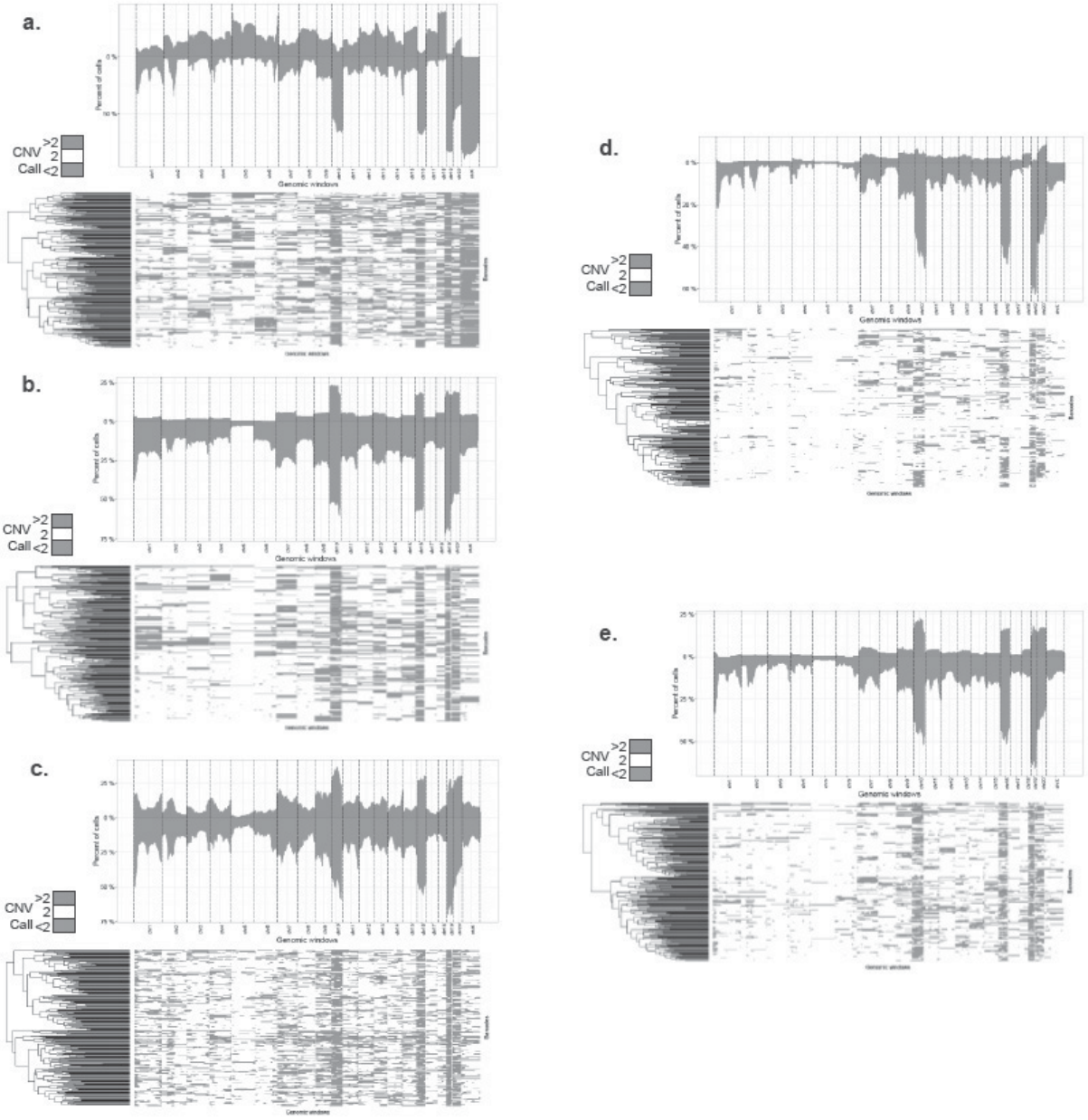
a.
b.
c.
d.
e.
CNV Call
>2
2
<2
Percent of cells
Genomic windows
Barcodes

FIG. 18

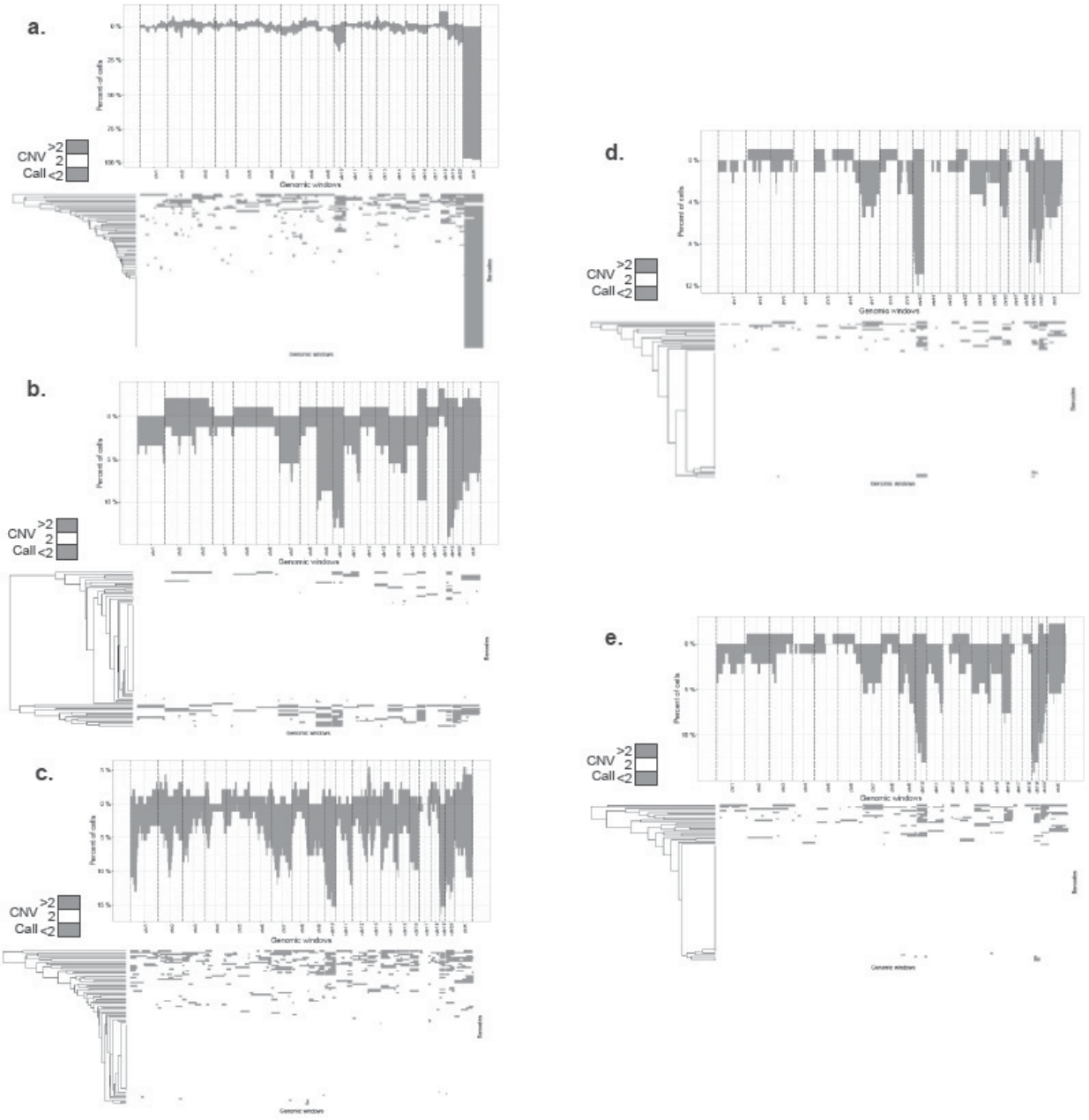
a.
b.
c.
d.
e.
CNV
Call
>2
2
<2
Genomic windows
Percent of cells
Barcodes

FIG. 19

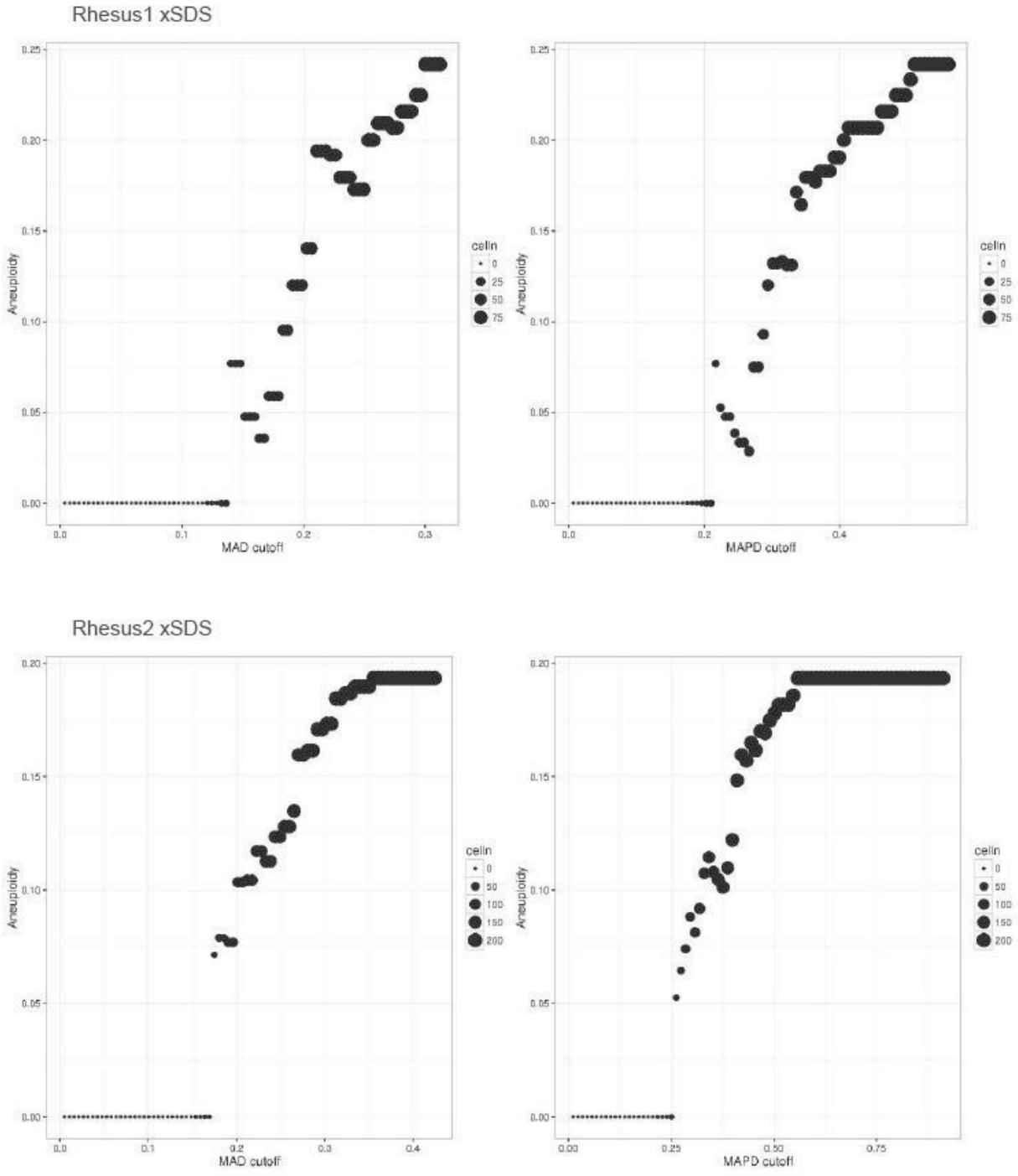
Rhesus1 xSDS
Aneuploidy
MAD cutoff
MAPD cutoff
cells
0
25
50
75
Rhesus2 xSDS
Aneuploidy
MAD cutoff
MAPD cutoff
cells
0
50
100
150
200

FIG. 22-1

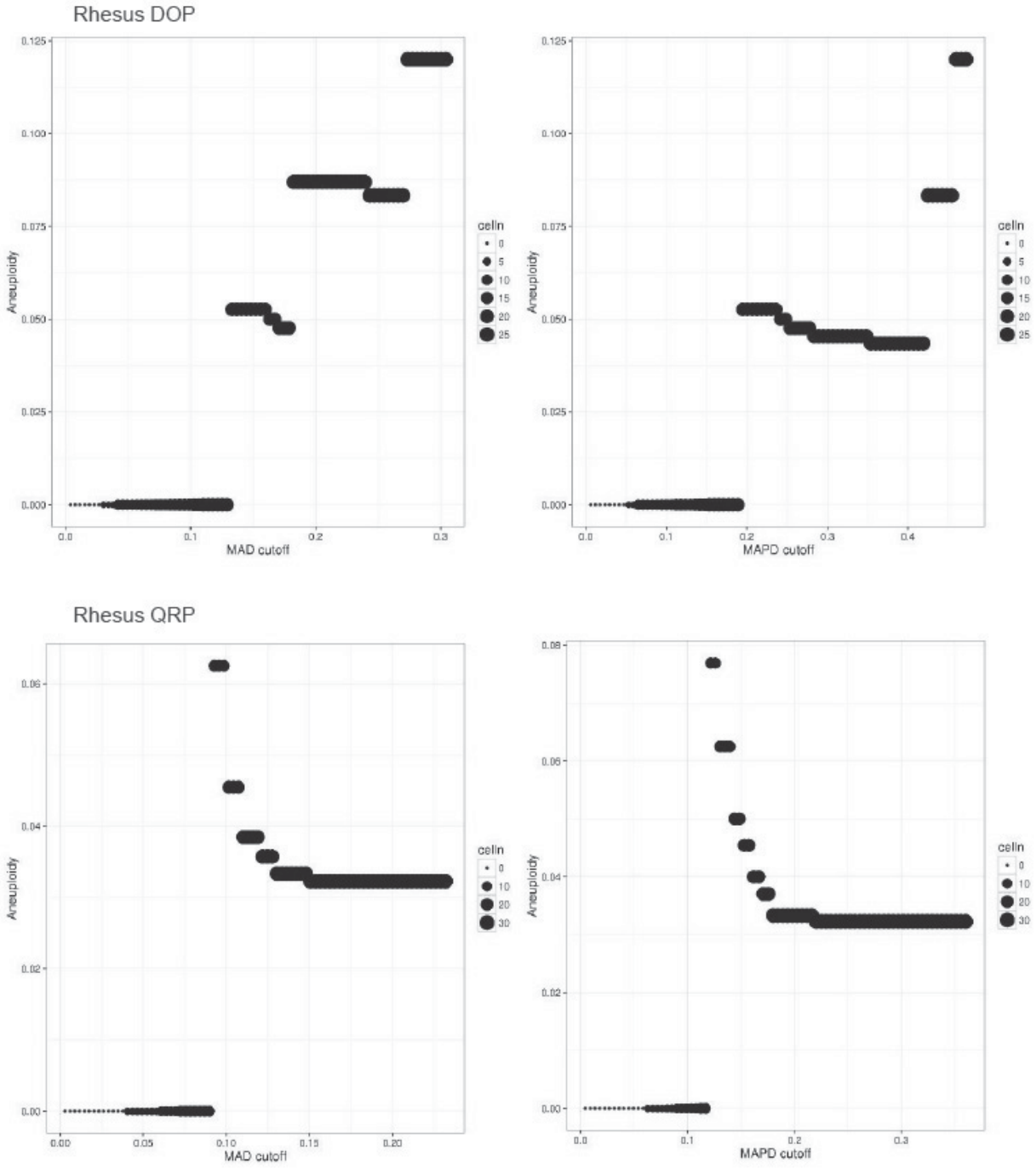
Rhesus DOP
Aneuploidy
MAD cutoff
MAPD cutoff
cells
Rhesus QRP

FIG. 22-2

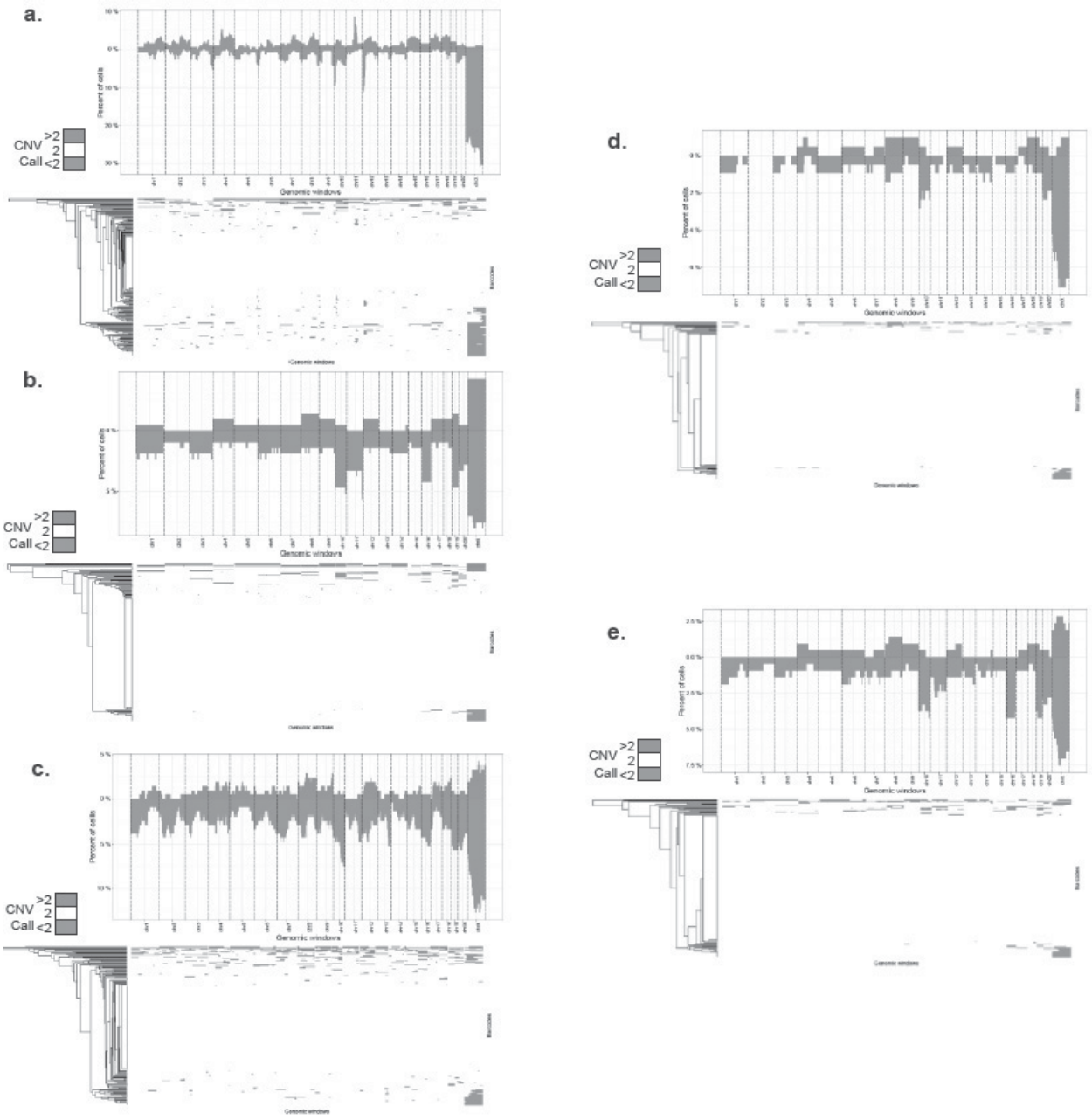
a.
b.
c.
d.
e.
CNV >2
2
Call <2
Percent of cells
Genomic windows
Barcodes

FIG. 23

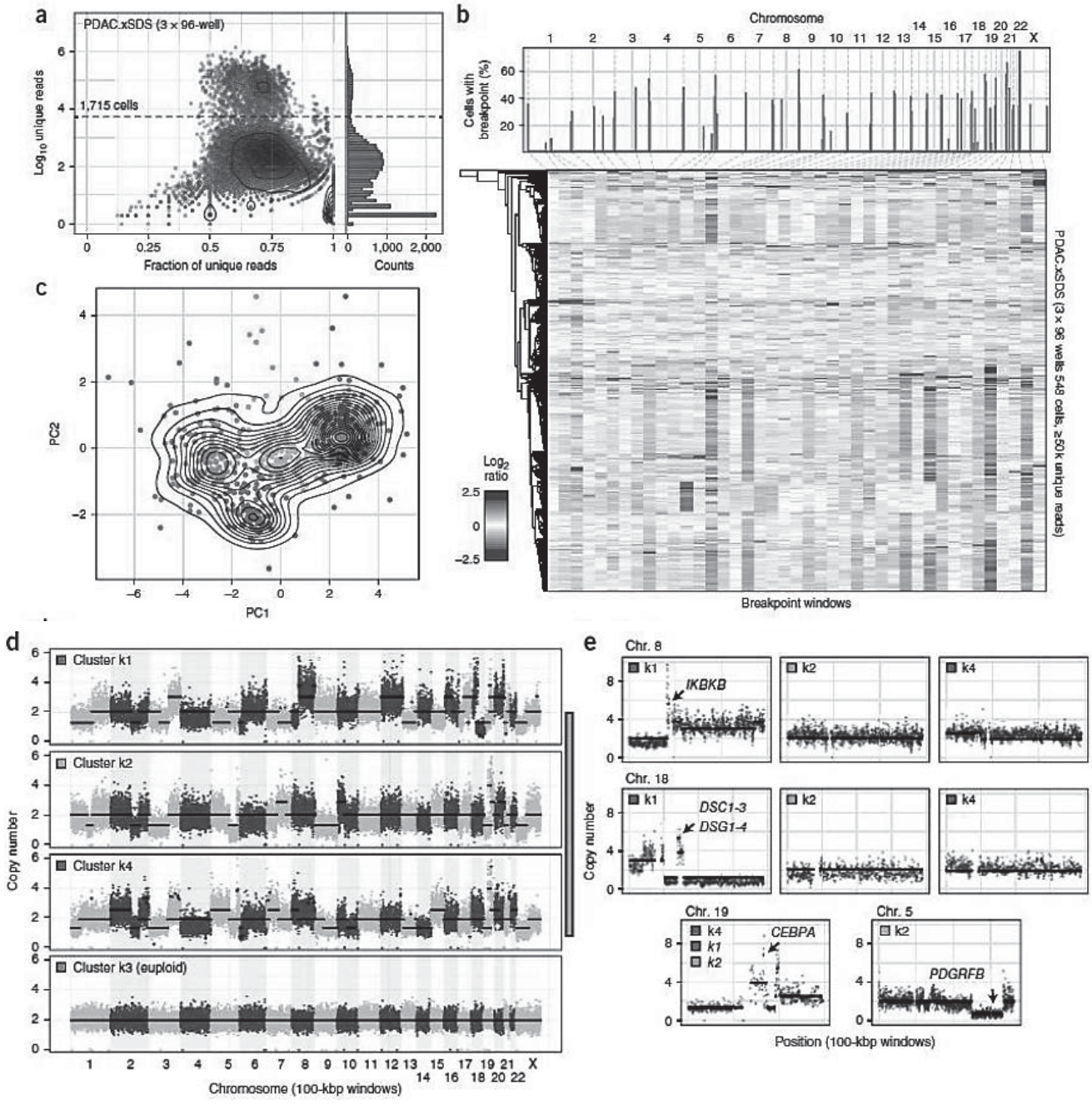
a
PDAC xSDS (3 × 96-well)
1,715 cells
Log10 unique reads
Fraction of unique reads
Counts
b
Chromosome
Cells with breakpoint (%)
Log2 ratio
PDAC xSDS (3 × 96 wells 548 cells ≥ 50k unique reads)
Breakpoint windows
c
PC2
PC1
d
Cluster k1
Cluster k2
Cluster k4
Cluster k3 (euploid)
Copy number
Chromosome (100-kbp windows)
e
Chr. 8
IKBKB
Chr. 18
DSC1-3
DSG1-4
Chr. 19
CEBPA
Chr. 5
PDGRFB
Copy number
Position (100-kbp windows)

FIG. 24

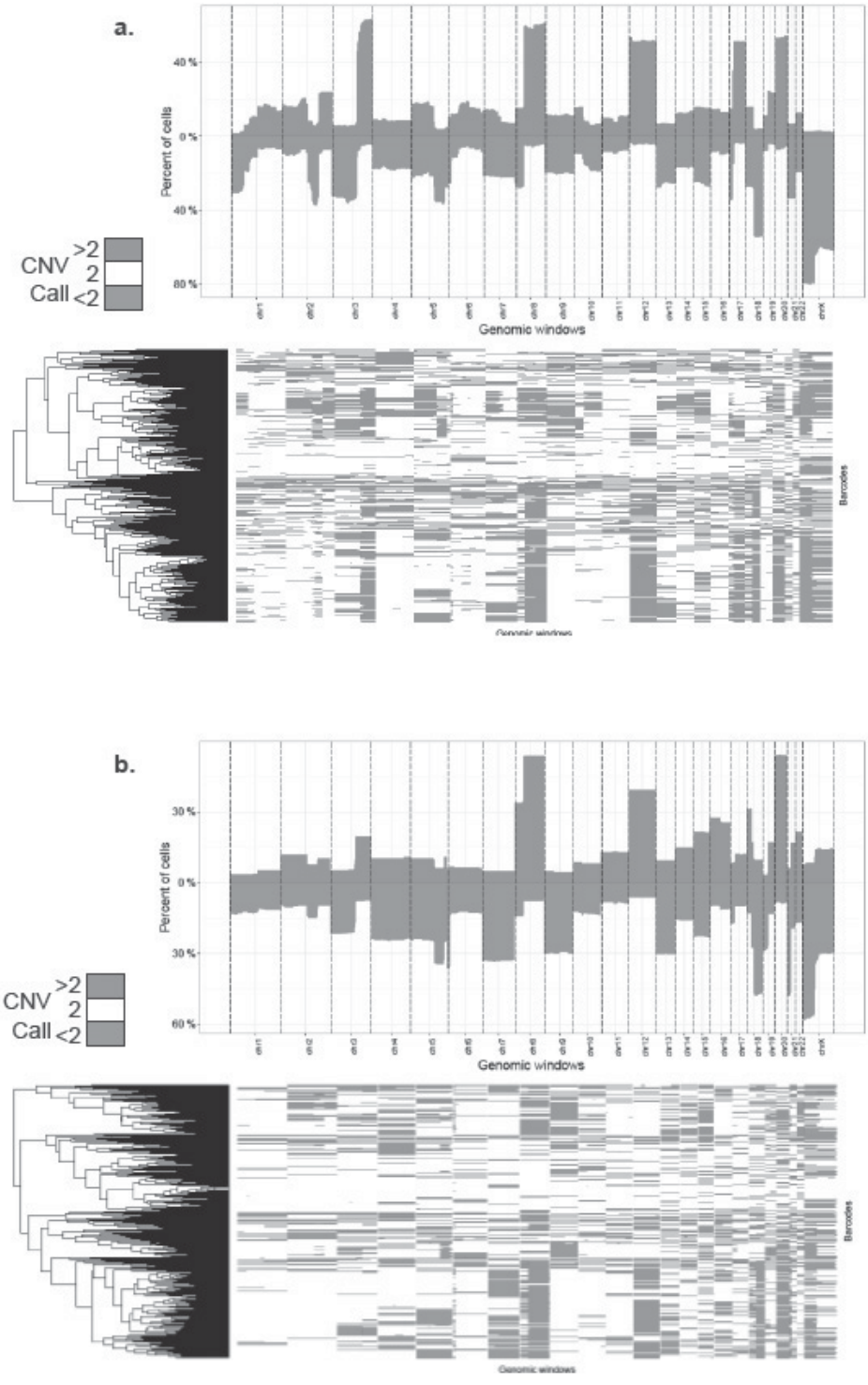
a.
Percent of cells
40 %
0 %
40 %
80 %
CNV
Call
>2
2
<2
Genomic windows
Barcodes
b.
Percent of cells
30 %
0 %
30 %
60 %
CNV
Call
>2
2
<2
Genomic windows
Barcodes

FIG. 25-1

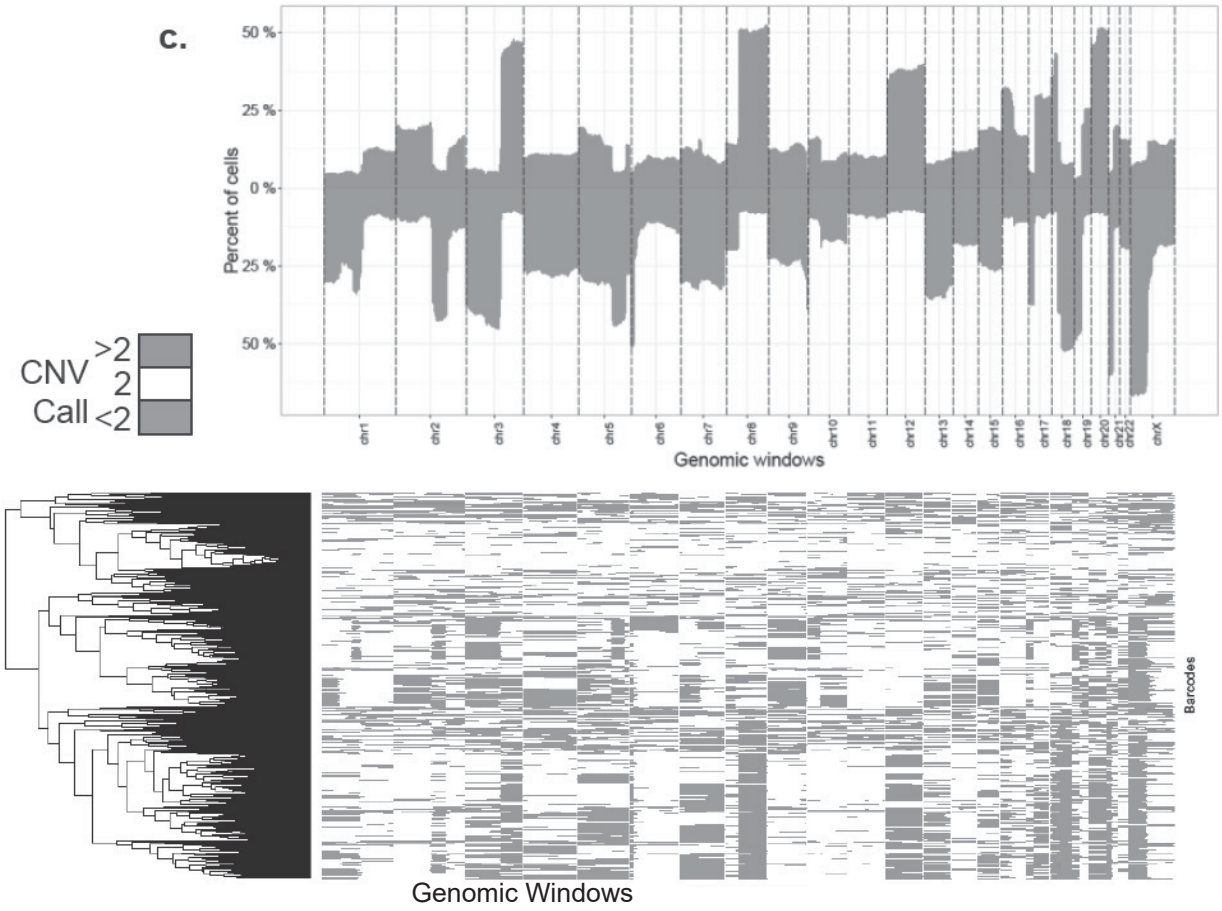
c.
50 %
25 %
0 %
25 %
50 %
Percent of cells
CNV Call
>2
2
<2
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
Genomic windows
Barcodes
Genomic Windows

FIG. 25-2

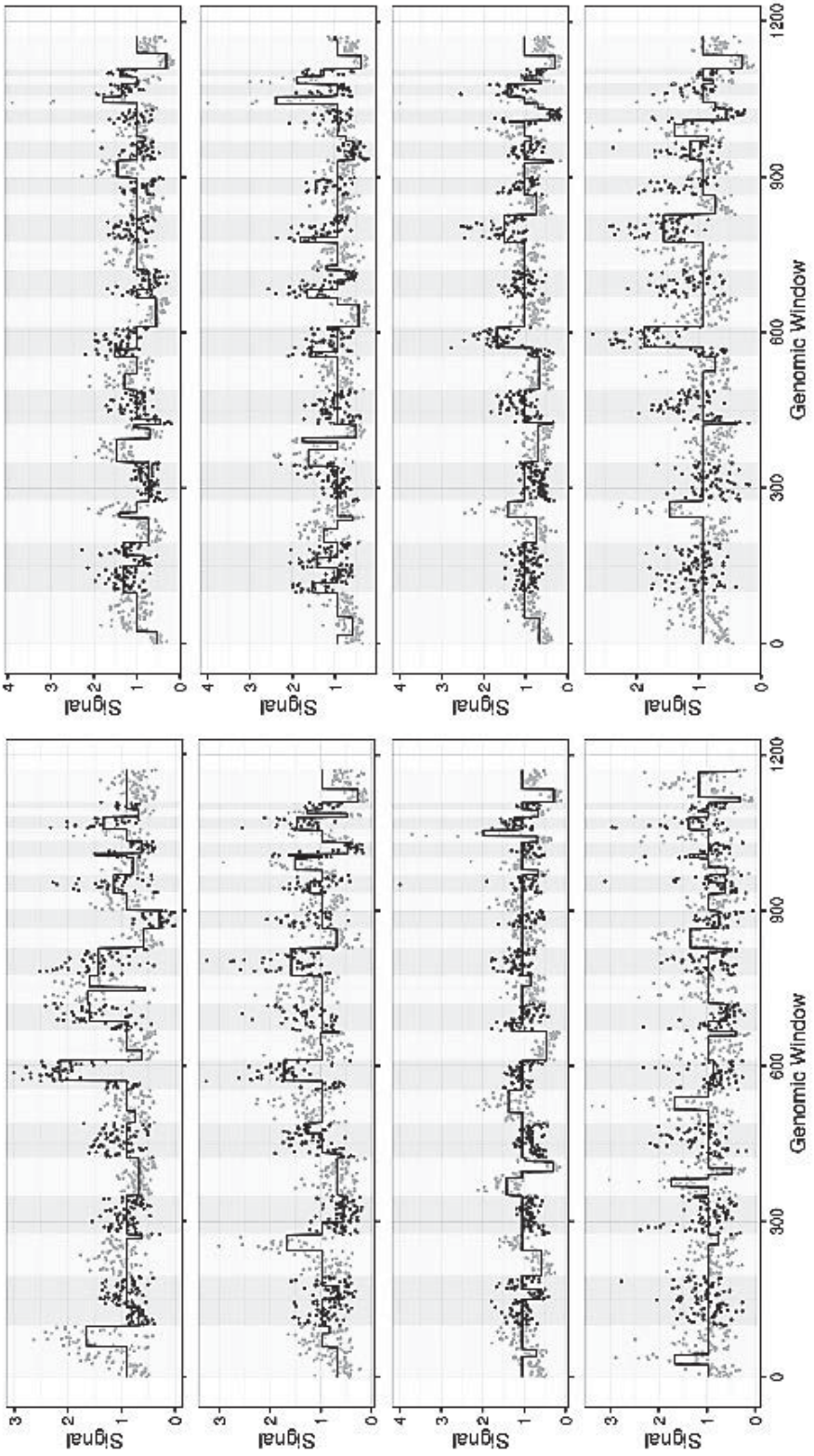

FIG. 26

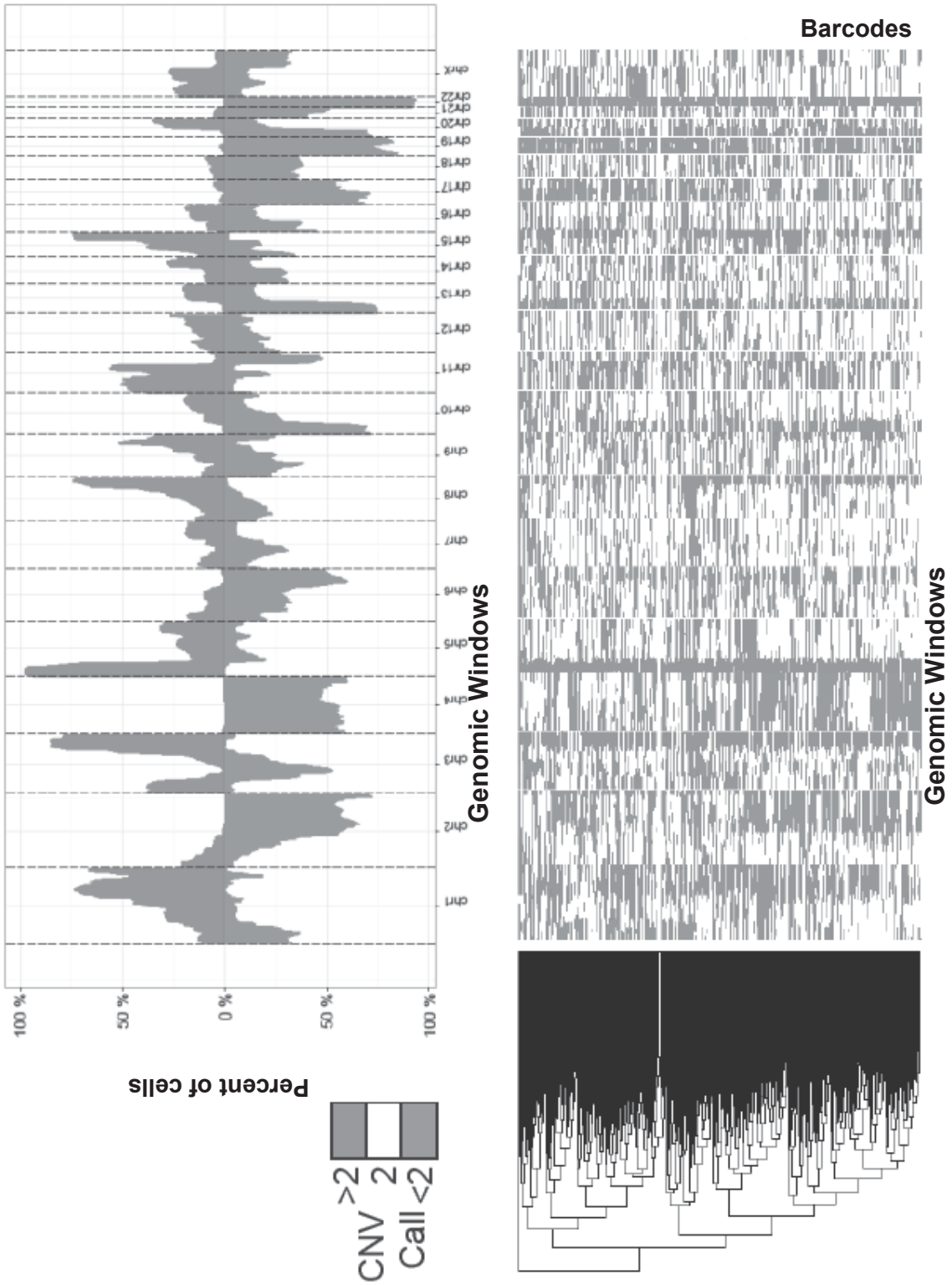
Barcodes
Genomic Windows
Genomic Windows
Percent of cells
100 %
50 %
0 %
50 %
100 %
CNV Call
>2
2
<2

FIG. 28

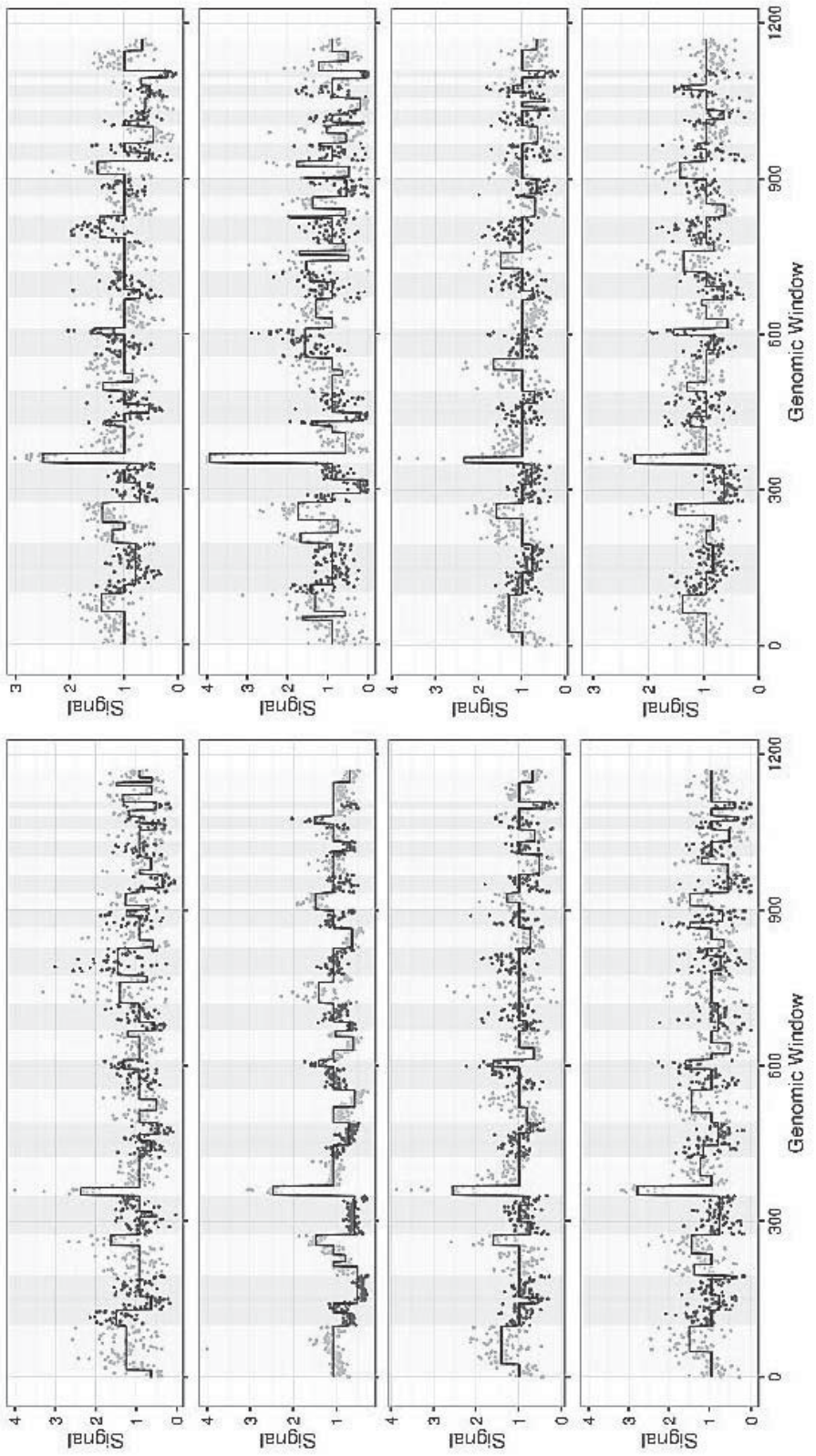

FIG. 29

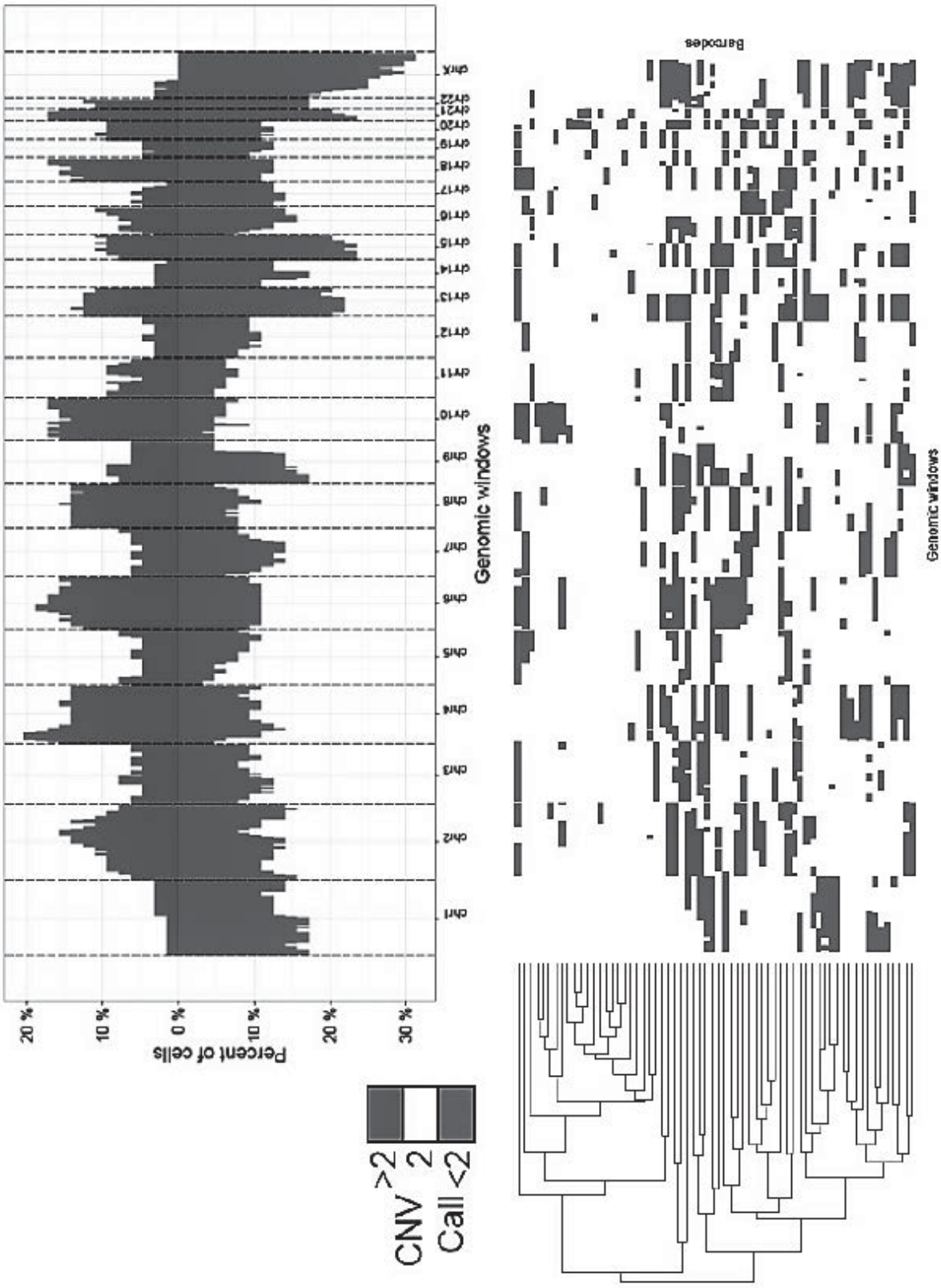
Barcodes
Genomic windows
Genomic windows
Percent of cells
20 %
10 %
0 %
10 %
20 %
30 %
CNV >2
2
Call <2

FIG. 32

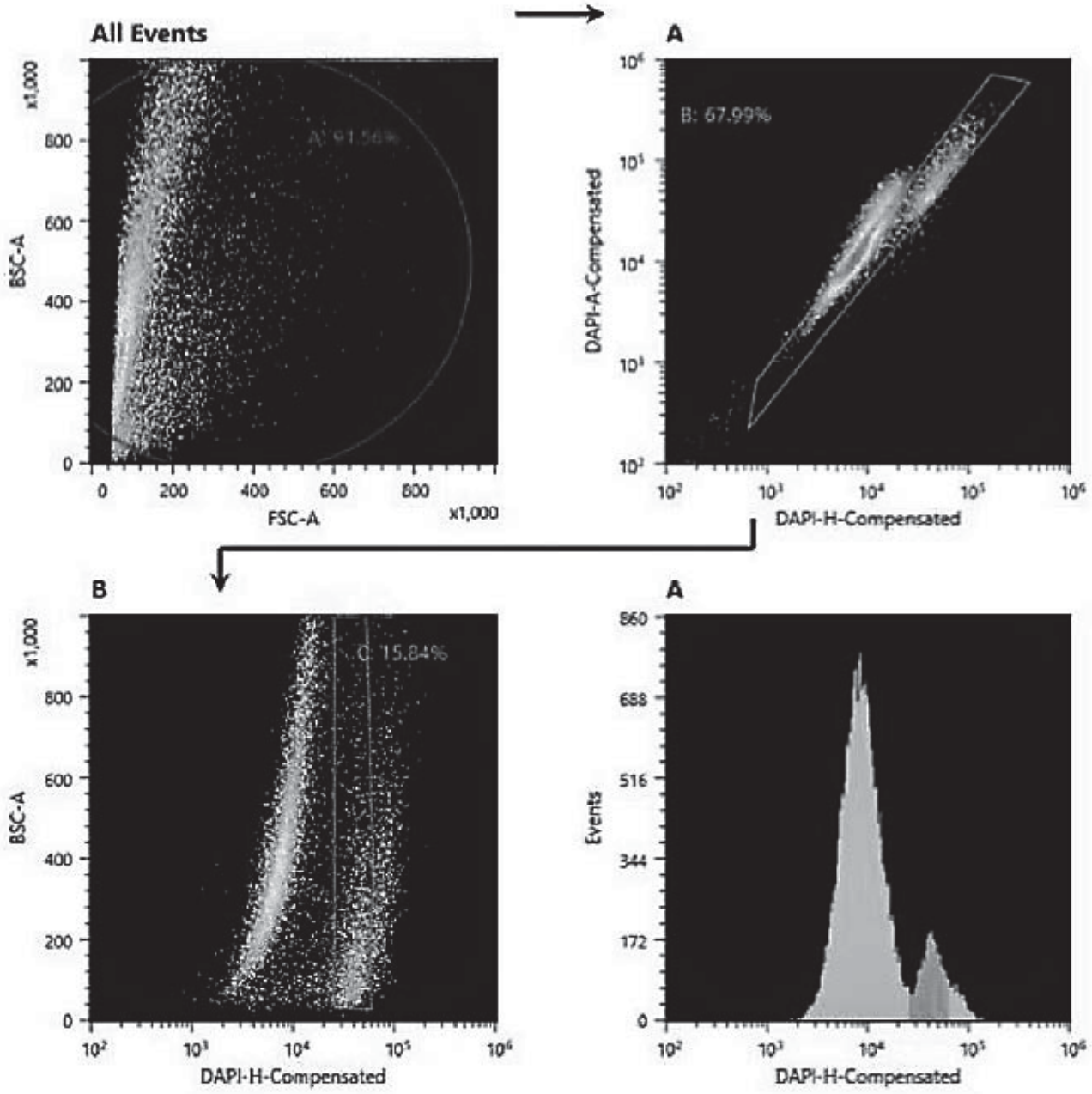
All Events
x1,000
800
600
400
200
0
BSC-A
0
200
400
600
800
FSC-A
x1,000
A
B: 67.99%
DAPI-A-Compensated
DAPI-H-Compensated
B
C: 15.84%
BSC-A
DAPI-H-Compensated
A
860
688
516
344
172
0
Events
DAPI-H-Compensated

FIG. 33