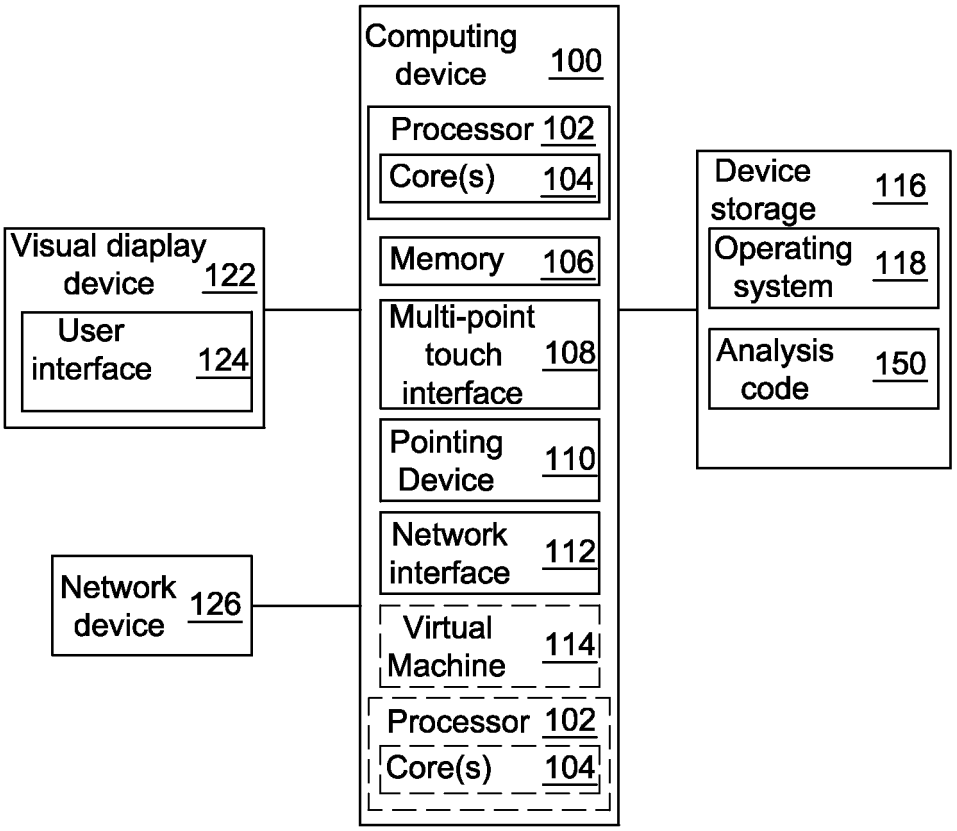

Computing device 100
Processor 102
Core(s) 104
Memory 106
Multi-point touch interface 108
Pointing Device 110
Network interface 112
Virtual Machine 114
Processor 102
Core(s) 104
Visual diaplay device 122
User interface 124
Network device 126
Device storage 116
Operating system 118
Analysis code 150

FIG. 1

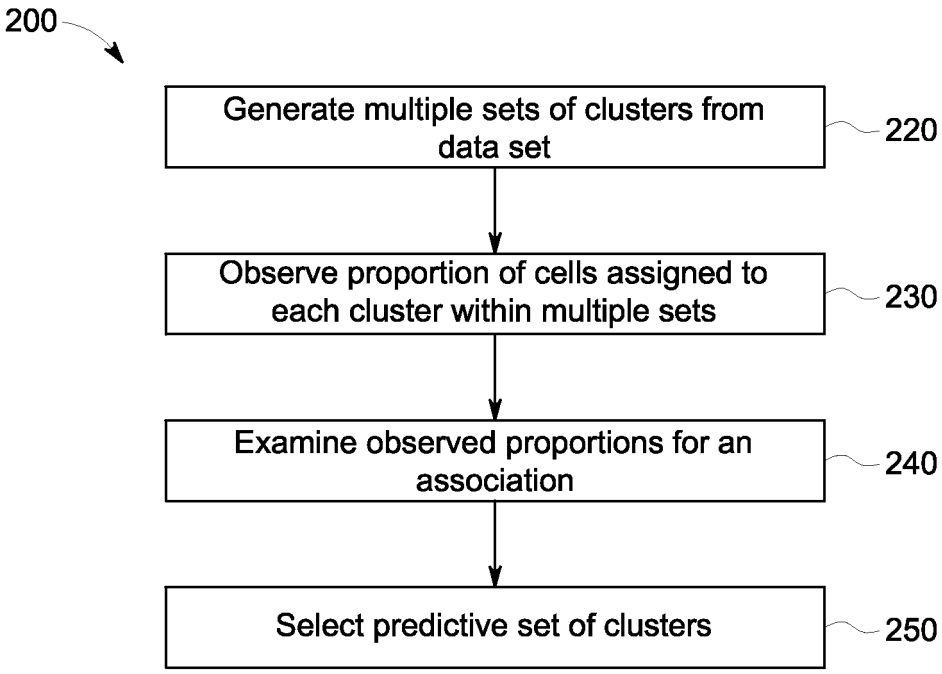

200
Generate multiple sets of clusters from data set
220
Observe proportion of cells assigned to each cluster within multiple sets
230
Examine observed proportions for an association
240
Select predictive set of clusters
250

FIG. 2

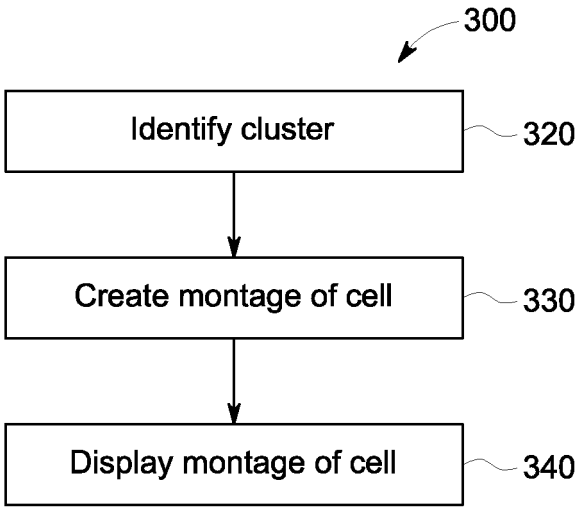

300
Identify cluster
320
Create montage of cell
330
Display montage of cell
340

FIG. 3

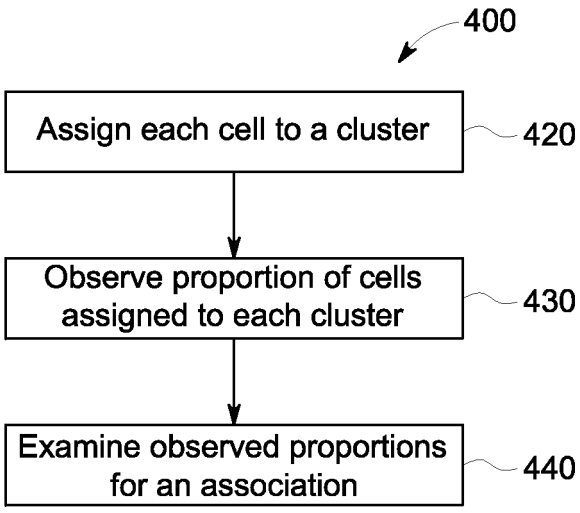

400
Assign each cell to a cluster
420
Observe proportion of cells assigned to each cluster
430
Examine observed proportions for an association
440

FIG. 4

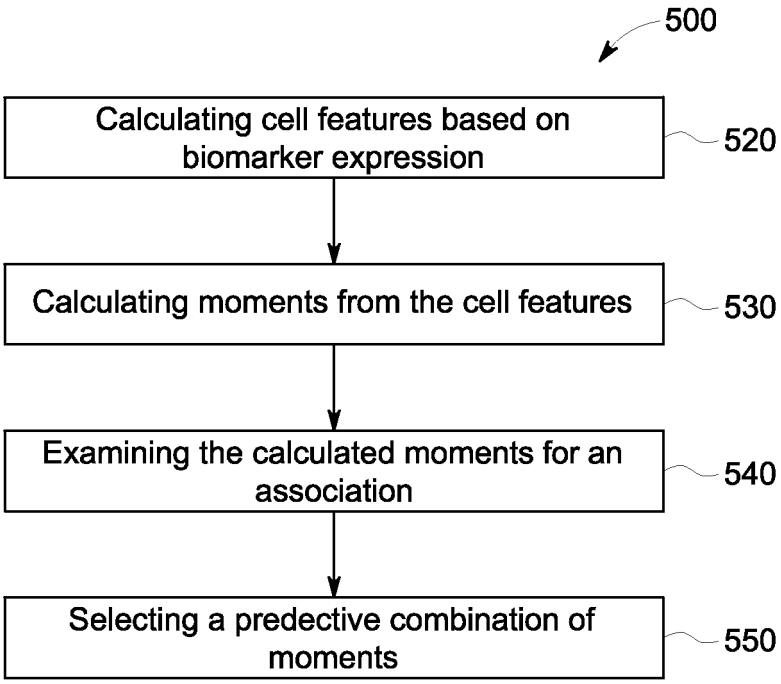

500
Calculating cell features based on biomarker expression
520
Calculating moments from the cell features
530
Examining the calculated moments for an association
540
Selecting a predective combination of moments
550

FIG. 5

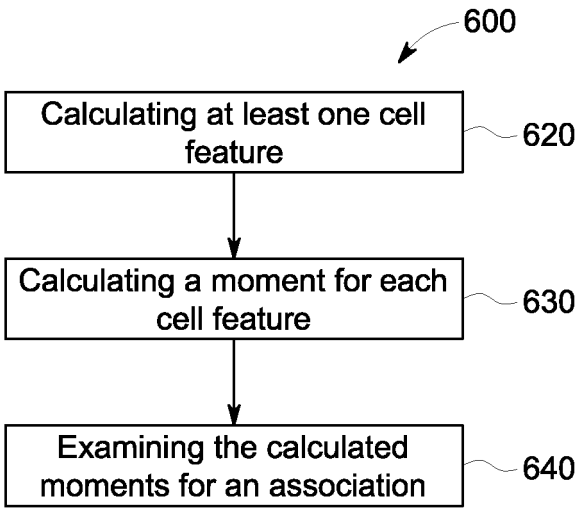

600
Calculating at least one cell feature
620
Calculating a moment for each cell feature
630
Examining the calculated moments for an association
640

FIG. 6

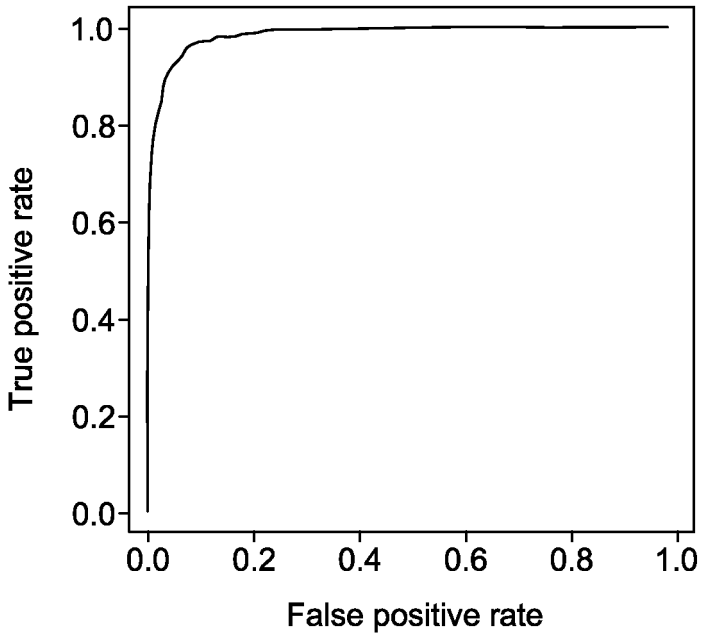

1.0
0.8
0.6
0.4
0.2
0.0
True positive rate
0.0
0.2
0.4
0.6
0.8
1.0
False positive rate

FIG. 7

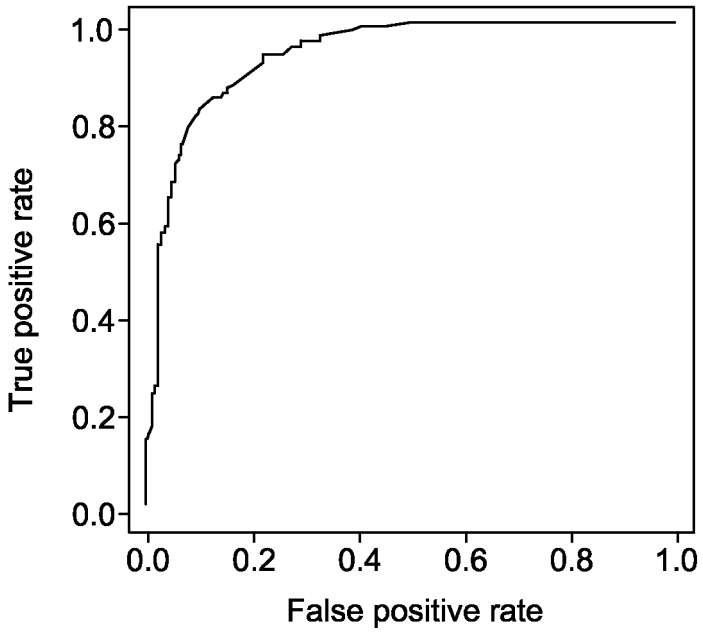

1.0
0.8
0.6
0.4
0.2
0.0
True positive rate
0.0
0.2
0.4
0.6
0.8
1.0
False positive rate

FIG. 8

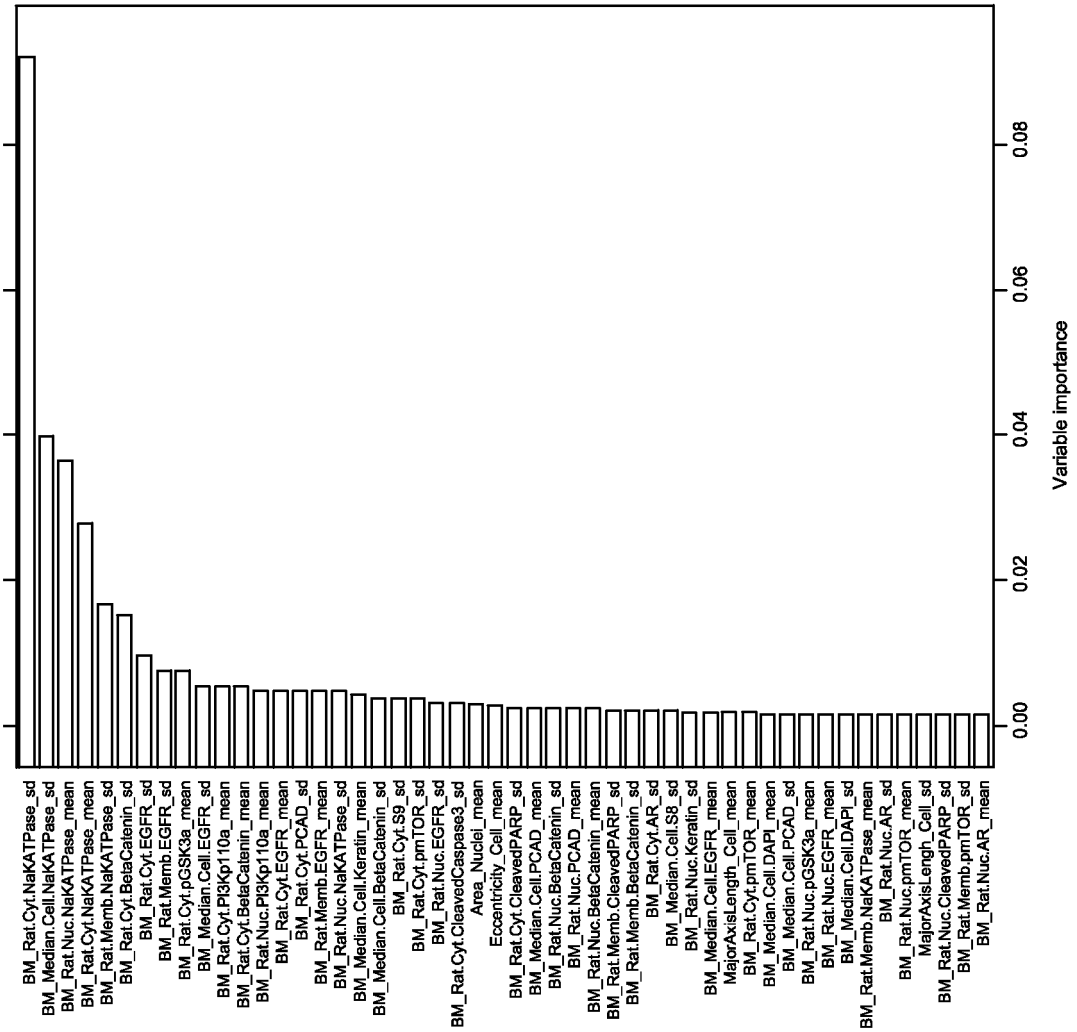

BM_Rat.Cyt.NaKATPase_sd
BM_Median.Cell.NaKATPase_sd
BM_Rat.Nuc.NaKATPase_mean
BM_Rat.Cyt.NaKATPase_mean
BM_Rat.Memb.NaKATPase_sd
BM_Rat.Cyt.BetaCatenin_sd
BM_Rat.Cyt.EGFR_sd
BM_Rat.Memb.EGFR_sd
BM_Rat.Cyt.pGSK3a_mean
BM_Median.Cell.EGFR_sd
BM_Rat.Cyt.Pi3Kp110a_mean
BM_Rat.Cyt.BetaCatenin_mean
BM_Rat.Nuc.Pi3Kp110a_mean
BM_Rat.Cyt.EGFR_mean
BM_Rat.Cyt.PCAD_sd
BM_Rat.Memb.EGFR_mean
BM_Rat.Nuc.NaKATPase_sd
BM_Median.Cell.Keratin_mean
BM_Median.Cell.BetaCatenin_sd
BM_Rat.Cyt.S9_sd
BM_Rat.Cyt.pmTOR_sd
BM_Rat.Nuc.EGFR_sd
BM_Rat.Cyt.CleavedCaspase3_sd
Area_Nuclei_mean
Eccentricity_Cell_mean
BM_Rat.Cyt.CleavedPARP_sd
BM_Median.Cell.PCAD_mean
BM_Rat.Nuc.BetaCatenin_sd
BM_Rat.Nuc.PCAD_mean
BM_Rat.Nuc.BetaCatenin_mean
BM_Rat.Memb.CleavedPARP_sd
BM_Rat.Memb.BetaCatenin_sd
BM_Rat.Cyt.AR_sd
BM_Median.Cell.S6_sd
BM_Rat.Nuc.Keratin_sd
BM_Median.Cell.EGFR_mean
MajorAxisLength_Cell_mean
BM_Rat.Cyt.pmTOR_mean
BM_Median.Cell.DAPI_mean
BM_Median.Cell.PCAD_sd
BM_Rat.Nuc.pGSK3a_mean
BM_Rat.Nuc.EGFR_mean
BM_Median.Cell.DAPI_sd
BM_Rat.Memb.NaKATPase_mean
BM_Rat.Nuc.AR_sd
BM_Rat.Nuc.pmTOR_mean
MajorAxisLength_Cell_sd
BM_Rat.Nuc.CleavedPARP_sd
BM_Rat.Memb.pmTOR_sd
BM_Rat.Nuc.AR_mean
0.00
0.02
0.04
0.06
0.08
Variable importance

FIG. 9

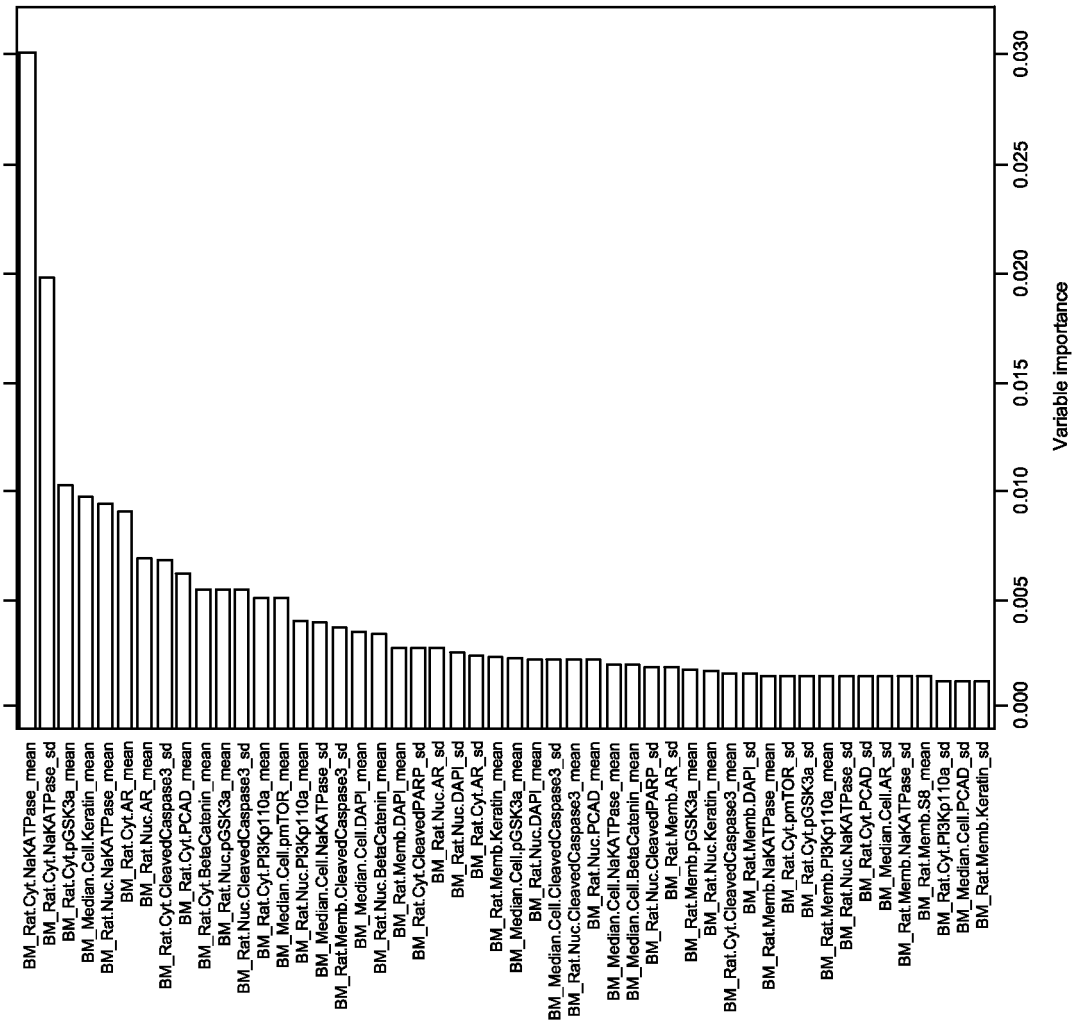

BM_Rat.Cyt.NaKATPase_mean
BM_Rat.Cyt.NaKATPase_sd
BM_Rat.Cyt.pGSK3a_mean
BM_Median.Cell.Keratin_mean
BM_Rat.Nuc.NaKATPase_mean
BM_Rat.Cyt.AR_mean
BM_Rat.Nuc.AR_mean
BM_Rat.Cyt.CleavedCaspase3_sd
BM_Rat.Cyt.PCAD_mean
BM_Rat.Cyt.BetaCatenin_mean
BM_Rat.Nuc.pGSK3a_mean
BM_Rat.Nuc.CleavedCaspase3_sd
BM_Rat.Cyt.PI3Kp110a_mean
BM_Median.Cell.pmTOR_mean
BM_Rat.Nuc.PI3Kp110a_mean
BM_Median.Cell.NaKATPase_sd
BM_Rat.Memb.CleavedCaspase3_sd
BM_Median.Cell.DAPI_mean
BM_Rat.Nuc.BetaCatenin_mean
BM_Rat.Memb.DAPI_mean
BM_Rat.Cyt.CleavedPARP_sd
BM_Rat.Nuc.AR_sd
BM_Rat.Nuc.DAPI_sd
BM_Rat.Cyt.AR_sd
BM_Rat.Memb.Keratin_mean
BM_Median.Cell.pGSK3a_mean
BM_Rat.Nuc.DAPI_mean
BM_Median.Cell.CleavedCaspase3_sd
BM_Rat.Nuc.CleavedCaspase3_mean
BM_Rat.Nuc.PCAD_mean
BM_Median.Cell.NaKATPase_mean
BM_Median.Cell.BetaCatenin_mean
BM_Rat.Nuc.CleavedPARP_sd
BM_Rat.Memb.AR_sd
BM_Rat.Memb.pGSK3a_mean
BM_Rat.Nuc.Keratin_mean
BM_Rat.Cyt.CleavedCaspase3_mean
BM_Rat.Memb.DAPI_sd
BM_Rat.Memb.NaKATPase_mean
BM_Rat.Cyt.pmTOR_sd
BM_Rat.Cyt.pGSK3a_sd
BM_Rat.Memb.PI3Kp110a_mean
BM_Rat.Nuc.NaKATPase_sd
BM_Rat.Cyt.PCAD_sd
BM_Median.Cell.AR_sd
BM_Rat.Memb.NaKATPase_sd
BM_Rat.Memb.S8_mean
BM_Rat.Cyt.PI3Kp110a_sd
BM_Median.Cell.PCAD_sd
BM_Rat.Memb.Keratin_sd
0.000
0.005
0.010
0.015
0.020
0.025
0.030
Variable importance

FIG. 10

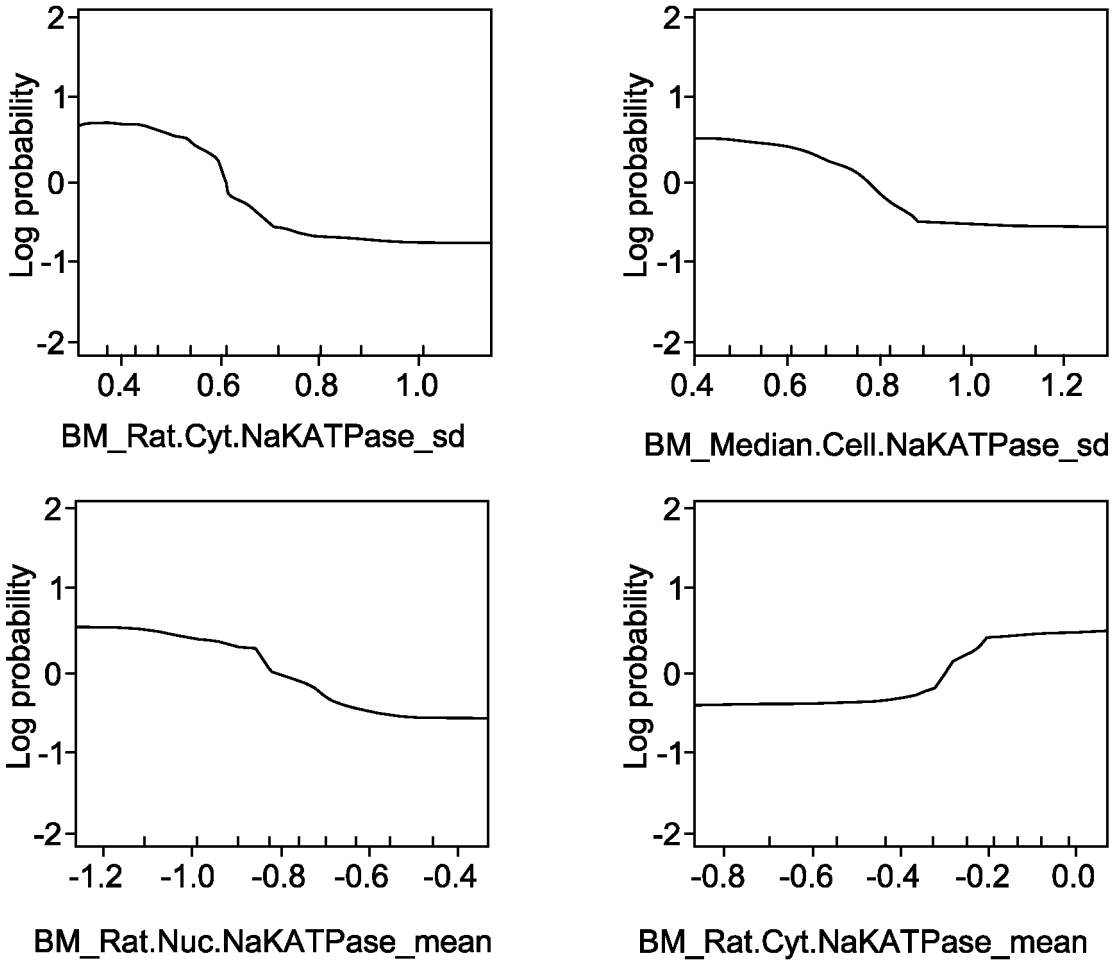

Log probability
2
1
0
-1
-2
0.4
0.6
0.8
1.0
BM_Rat.Cyt.NaKATPase_sd
Log probability
2
1
0
-1
-2
0.4
0.6
0.8
1.0
1.2
BM_Median.Cell.NaKATPase_sd
Log probability
2
1
0
-1
-2
-1.2
-1.0
-0.8
-0.6
-0.4
BM_Rat.Nuc.NaKATPase_mean
Log probability
2
1
0
-1
-2
-0.8
-0.6
-0.4
-0.2
0.0
BM_Rat.Cyt.NaKATPase_mean

FIG. 11

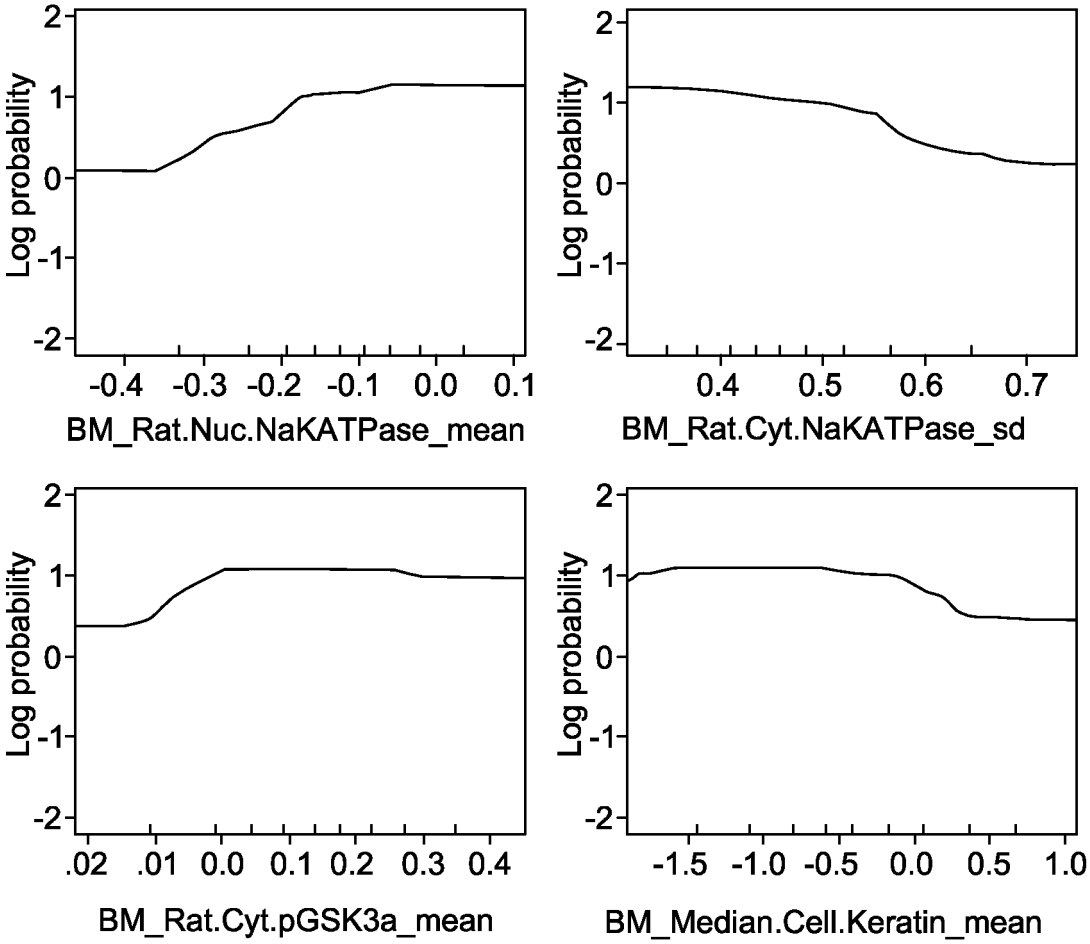

Log probability
2
1
0
-1
-2
-0.4 -0.3 -0.2 -0.1 0.0 0.1
BM_Rat.Nuc.NaKATPase_mean
Log probability
2
1
0
-1
-2
0.4 0.5 0.6 0.7
BM_Rat.Cyt.NaKATPase_sd
Log probability
2
1
0
-1
-2
.02 .01 0.0 0.1 0.2 0.3 0.4
BM_Rat.Cyt.pGSK3a_mean
Log probability
2
1
0
-1
-2
-1.5 -1.0 -0.5 0.0 0.5 1.0
BM_Median.Cell.Keratin_mean

FIG. 12

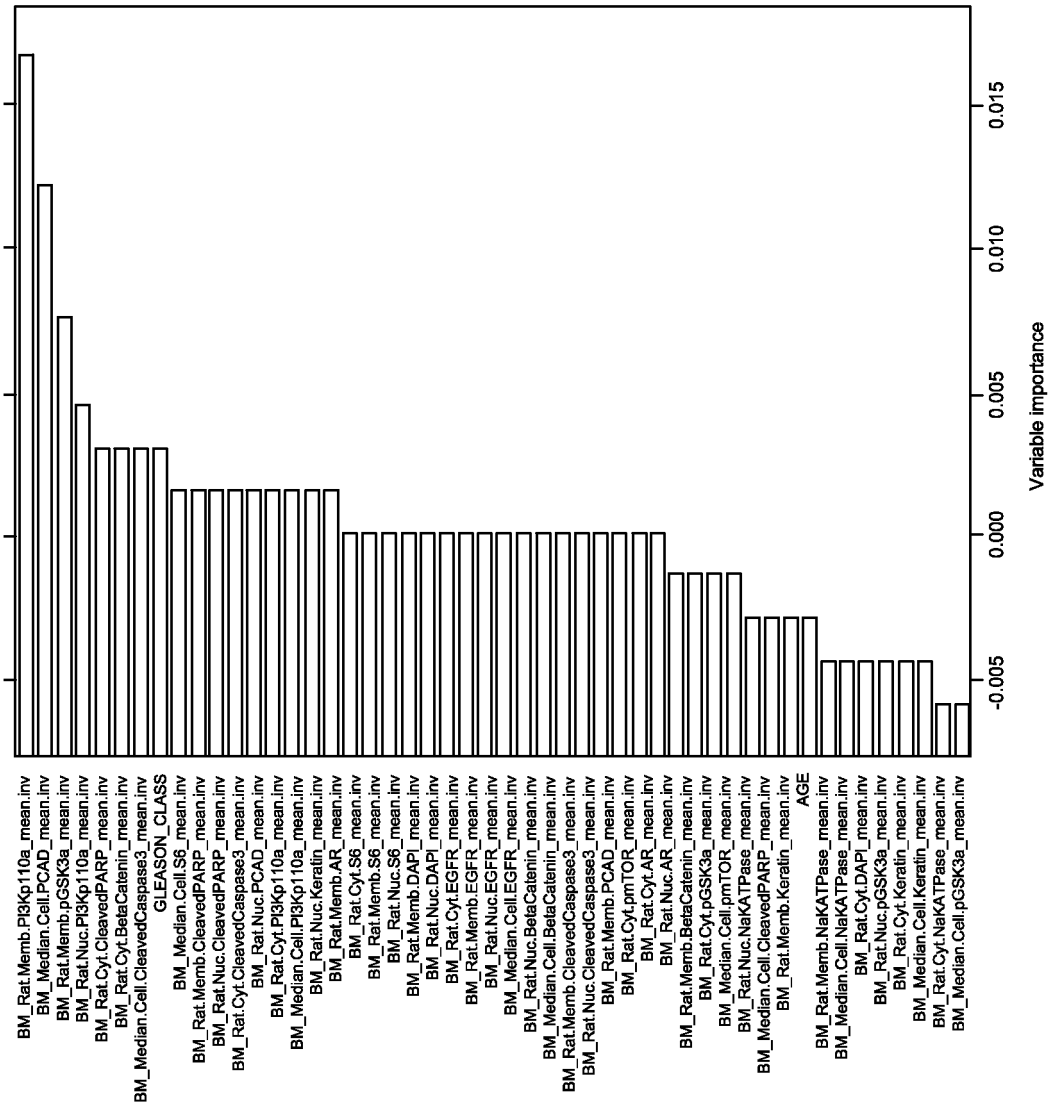

BM_Rat.Memb.PI3Kp110a_mean.inv
BM_Median.Cell.PCAD_mean.inv
BM_Rat.Memb.pGSK3a_mean.inv
BM_Rat.Nuc.PI3Kp110a_mean.inv
BM_Rat.Cyt.CleavedPARP_mean.inv
BM_Rat.Cyt.BetaCatenin_mean.inv
BM_Median.Cell.CleavedCaspase3_mean.inv
GLEASON_CLASS
BM_Median.Cell.S6_mean.inv
BM_Rat.Memb.CleavedPARP_mean.inv
BM_Rat.Nuc.CleavedPARP_mean.inv
BM_Rat.Cyt.CleavedCaspase3_mean.inv
BM_Rat.Nuc.PCAD_mean.inv
BM_Rat.Cyt.PI3Kp110a_mean.inv
BM_Median.Cell.PI3Kp110a_mean.inv
BM_Rat.Nuc.Keratin_mean.inv
BM_Rat.Memb.AR_mean.inv
BM_Rat.Cyt.S6_mean.inv
BM_Rat.Memb.S6_mean.inv
BM_Rat.Nuc.S6_mean.inv
BM_Rat.Memb.DAPI_mean.inv
BM_Rat.Nuc.DAPI_mean.inv
BM_Rat.Cyt.EGFR_mean.inv
BM_Rat.Memb.EGFR_mean.inv
BM_Rat.Nuc.EGFR_mean.inv
BM_Median.Cell.EGFR_mean.inv
BM_Rat.Nuc.BetaCatenin_mean.inv
BM_Median.Cell.BetaCatenin_mean.inv
BM_Rat.Memb.CleavedCaspase3_mean.inv
BM_Rat.Nuc.CleavedCaspase3_mean.inv
BM_Rat.Memb.PCAD_mean.inv
BM_Rat.Cyt.pmTOR_mean.inv
BM_Rat.Cyt.AR_mean.inv
BM_Rat.Nuc.AR_mean.inv
BM_Rat.Memb.BetaCatenin_mean.inv
BM_Rat.Cyt.pGSK3a_mean.inv
BM_Median.Cell.pmTOR_mean.inv
BM_Rat.Nuc.NaKATPase_mean.inv
BM_Median.Cell.CleavedPARP_mean.inv
BM_Rat.Memb.Keratin_mean.inv
AGE
BM_Rat.Memb.NaKATPase_mean.inv
BM_Median.Cell.NaKATPase_mean.inv
BM_Rat.Cyt.DAPI_mean.inv
BM_Rat.Nuc.pGSK3a_mean.inv
BM_Rat.Cyt.Keratin_mean.inv
BM_Median.Cell.Keratin_mean.inv
BM_Rat.Cyt.NaKATPase_mean.inv
BM_Median.Cell.pGSK3a_mean.inv
-0.005
0.000
0.005
0.010
0.015
Variable importance

FIG. 13

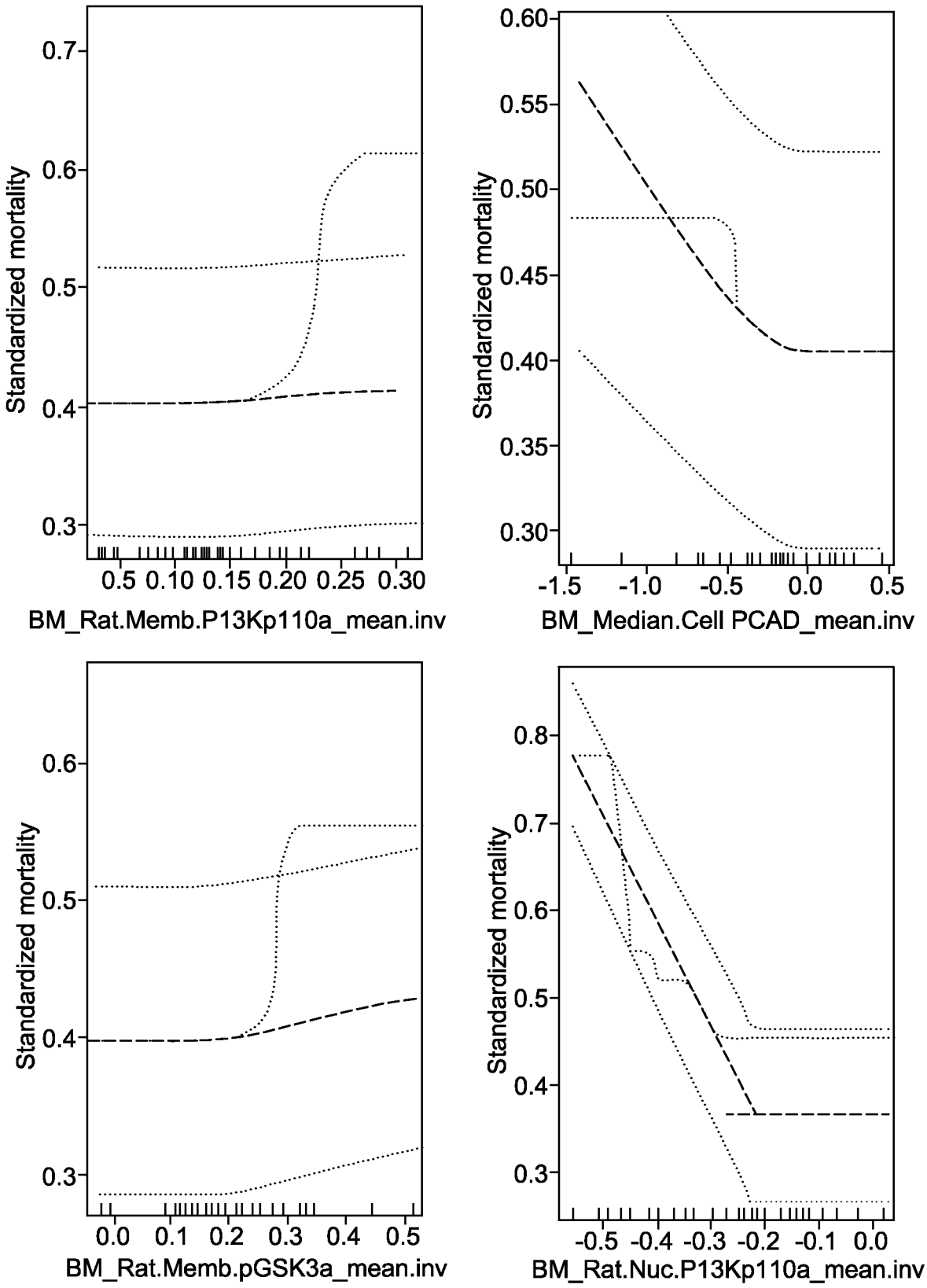

Standardized mortality
0.7
0.6
0.5
0.4
0.3
0.5 0.10 0.15 0.20 0.25 0.30
BM_Rat.Memb.P13Kp110a_mean.inv
Standardized mortality
0.60
0.55
0.50
0.45
0.40
0.35
0.30
-1.5 -1.0 -0.5 0.0 0.5
BM_Median.Cell PCAD_mean.inv
Standardized mortality
0.6
0.5
0.4
0.3
0.0 0.1 0.2 0.3 0.4 0.5
BM_Rat.Memb.pGSK3a_mean.inv
Standardized mortality
0.8
0.7
0.6
0.5
0.4
0.3
-0.5 -0.4 -0.3 -0.2 -0.1 0.0
BM_Rat.Nuc.P13Kp110a_mean.inv

FIG. 14

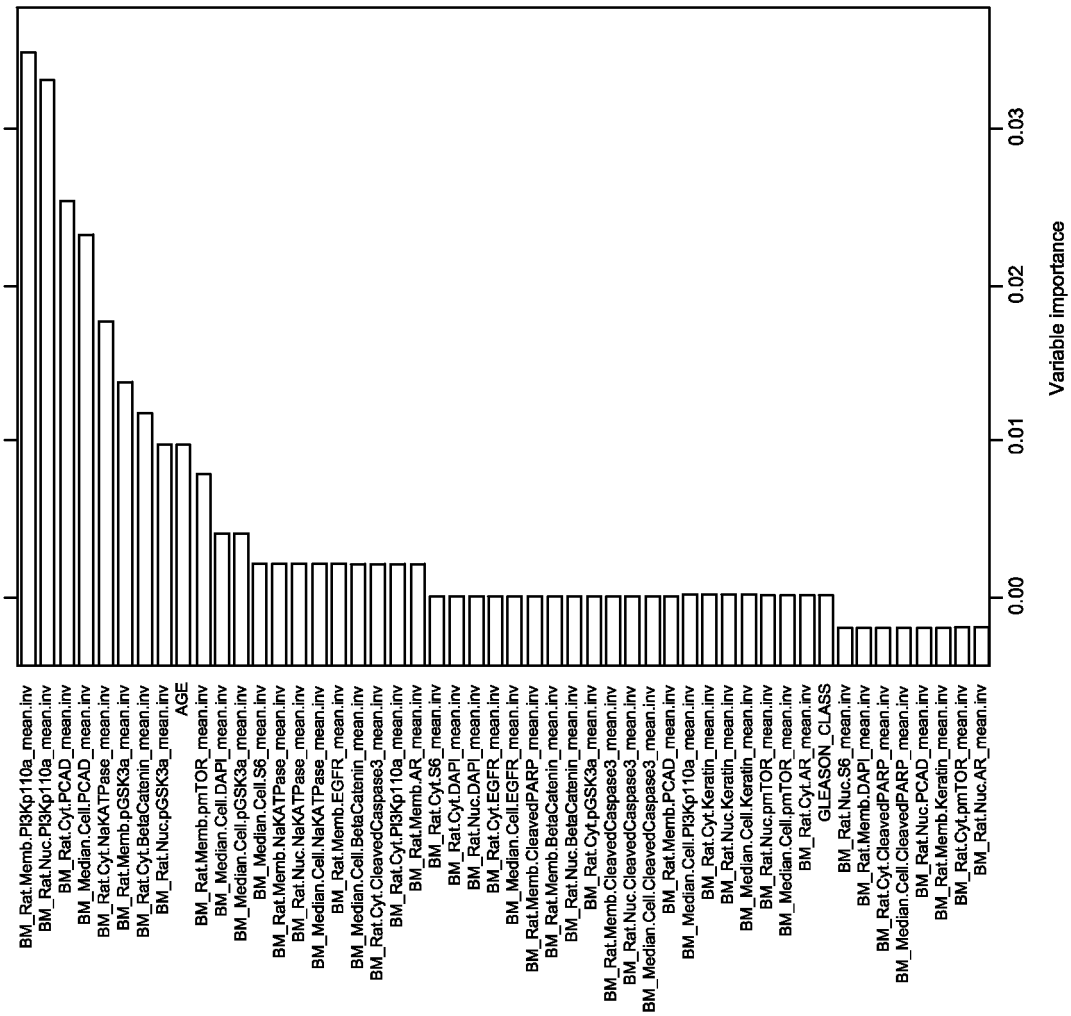

BM_Rat.Memb.PI3Kp110a_mean.inv
BM_Rat.Nuc.PI3Kp110a_mean.inv
BM_Rat.Cyt.PCAD_mean.inv
BM_Median.Cell.PCAD_mean.inv
BM_Rat.Cyt.NaKATPase_mean.inv
BM_Rat.Memb.pGSK3a_mean.inv
BM_Rat.Cyt.BetaCatenin_mean.inv
BM_Rat.Nuc.pGSK3a_mean.inv
AGE
BM_Rat.Memb.pmTOR_mean.inv
BM_Median.Cell.DAPI_mean.inv
BM_Median.Cell.pGSK3a_mean.inv
BM_Median.Cell.S6_mean.inv
BM_Rat.Memb.NaKATPase_mean.inv
BM_Rat.Nuc.NaKATPase_mean.inv
BM_Median.Cell.NaKATPase_mean.inv
BM_Rat.Memb.EGFR_mean.inv
BM_Median.Cell.BetaCatenin_mean.inv
BM_Rat.Cyt.CleavedCaspase3_mean.inv
BM_Rat.Cyt.PI3Kp110a_mean.inv
BM_Rat.Memb.AR_mean.inv
BM_Rat.Cyt.S6_mean.inv
BM_Rat.Cyt.DAPI_mean.inv
BM_Rat.Nuc.DAPI_mean.inv
BM_Rat.Cyt.EGFR_mean.inv
BM_Median.Cell.EGFR_mean.inv
BM_Rat.Memb.CleavedPARP_mean.inv
BM_Rat.Memb.BetaCatenin_mean.inv
BM_Rat.Nuc.BetaCatenin_mean.inv
BM_Rat.Cyt.pGSK3a_mean.inv
BM_Rat.Memb.CleavedCaspase3_mean.inv
BM_Rat.Nuc.CleavedCaspase3_mean.inv
BM_Median.Cell.CleavedCaspase3_mean.inv
BM_Rat.Memb.PCAD_mean.inv
BM_Median.Cell.PI3Kp110a_mean.inv
BM_Rat.Cyt.Keratin_mean.inv
BM_Rat.Nuc.Keratin_mean.inv
BM_Median.Cell.Keratin_mean.inv
BM_Rat.Nuc.pmTOR_mean.inv
BM_Median.Cell.pmTOR_mean.inv
BM_Rat.Cyt.AR_mean.inv
GLEASON_CLASS
BM_Rat.Nuc.S6_mean.inv
BM_Rat.Memb.DAPI_mean.inv
BM_Rat.Cyt.CleavedPARP_mean.inv
BM_Median.Cell.CleavedPARP_mean.inv
BM_Rat.Nuc.PCAD_mean.inv
BM_Rat.Memb.Keratin_mean.inv
BM_Rat.Cyt.pmTOR_mean.inv
BM_Rat.Nuc.AR_mean.inv
0.00
0.01
0.02
0.03
Variable importance

FIG. 15

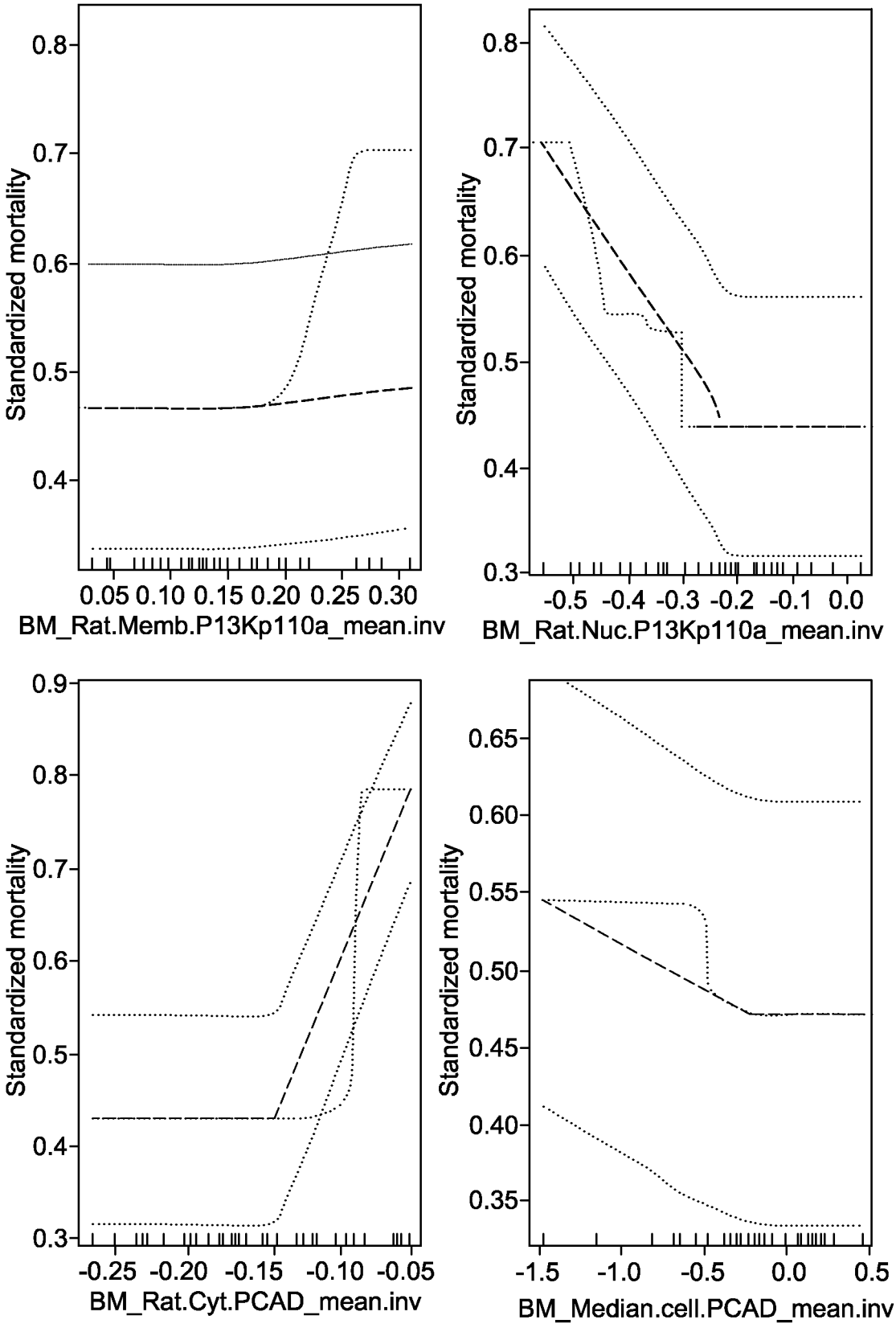

Standardized mortality
0.8
0.7
0.6
0.5
0.4
0.05 0.10 0.15 0.20 0.25 0.30
BM_Rat.Memb.P13Kp110a_mean.inv
Standardized mortality
0.8
0.7
0.6
0.5
0.4
0.3
-0.5 -0.4 -0.3 -0.2 -0.1 0.0
BM_Rat.Nuc.P13Kp110a_mean.inv
Standardized mortality
0.9
0.8
0.7
0.6
0.5
0.4
0.3
-0.25 -0.20 -0.15 -0.10 -0.05
BM_Rat.Cyt.PCAD_mean.inv
Standardized mortality
0.65
0.60
0.55
0.50
0.45
0.40
0.35
-1.5 -1.0 -0.5 0.0 0.5
BM_Median.cell.PCAD_mean.inv

FIG. 16

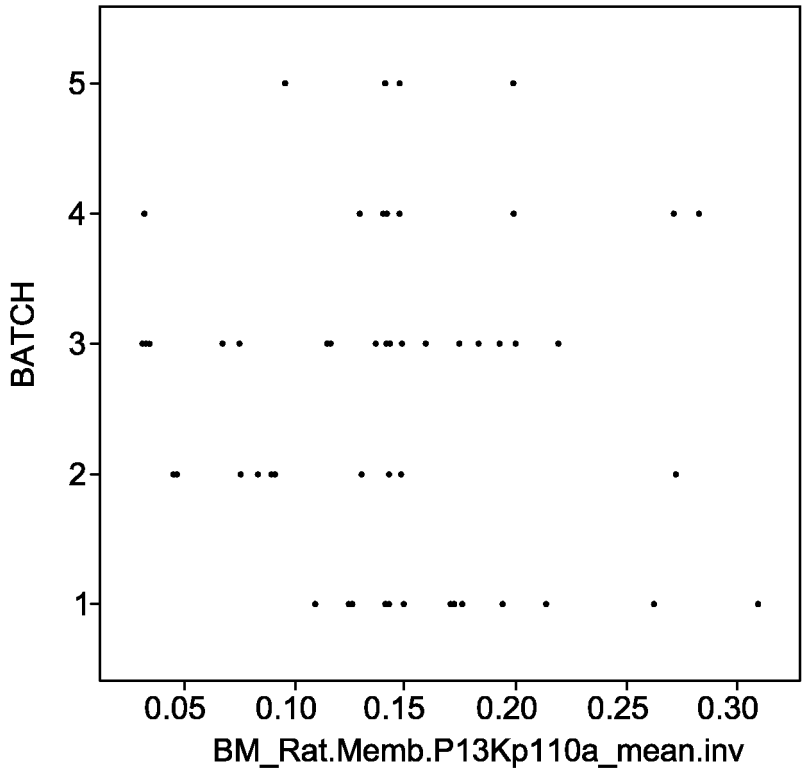

BATCH
5
4
3
2
1
0.05
0.10
0.15
0.20
0.25
0.30
BM_Rat.Memb.P13Kp110a_mean.inv

FIG. 17

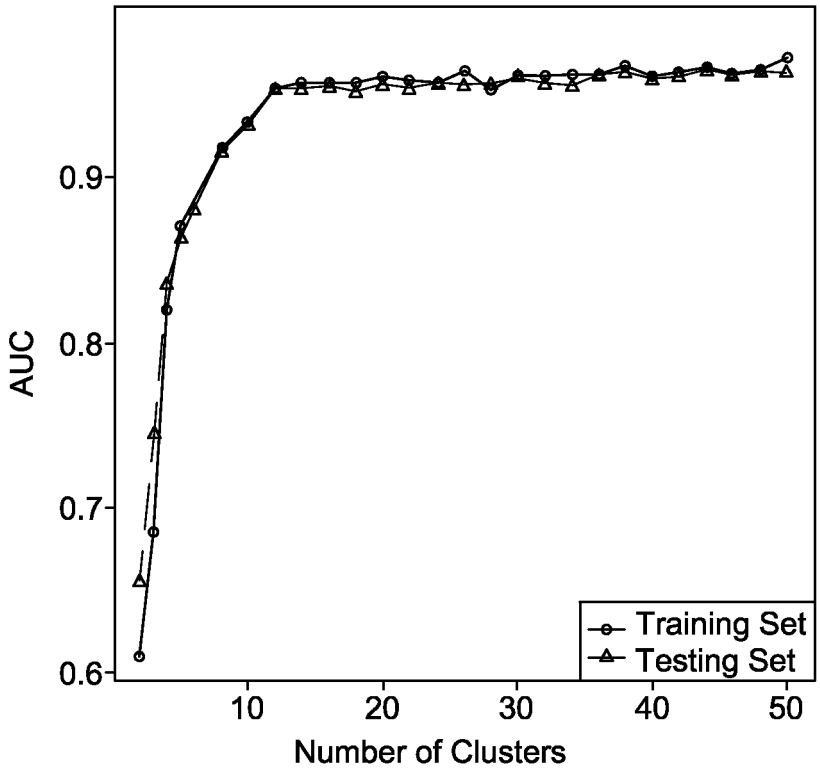

AUC
0.9
0.8
0.7
0.6
10
20
30
40
50
Number of Clusters
Training Set
Testing Set

FIG. 18

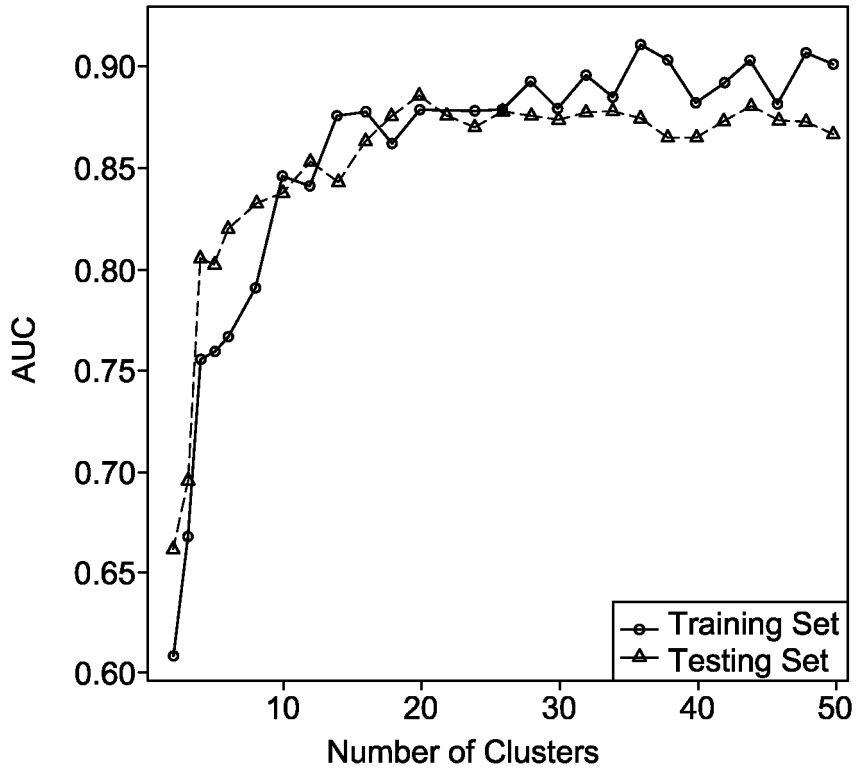

AUC
0.90
0.85
0.80
0.75
0.70
0.65
0.60
10
20
30
40
50
Number of Clusters
Training Set
Testing Set

FIG. 19

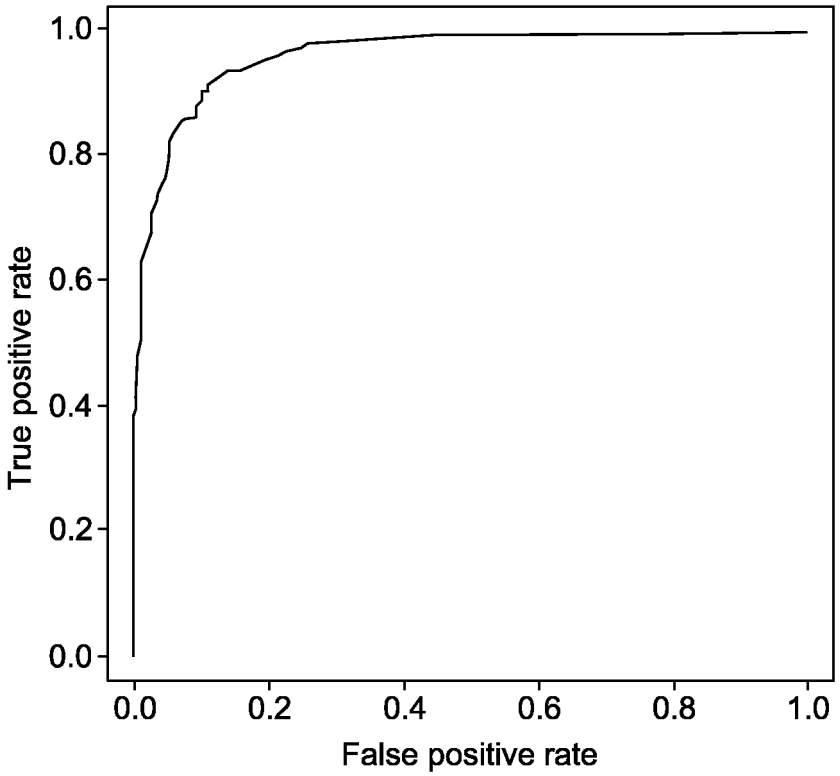

1.0
0.8
0.6
0.4
0.2
0.0
True positive rate
0.0
0.2
0.4
0.6
0.8
1.0
False positive rate

FIG. 20

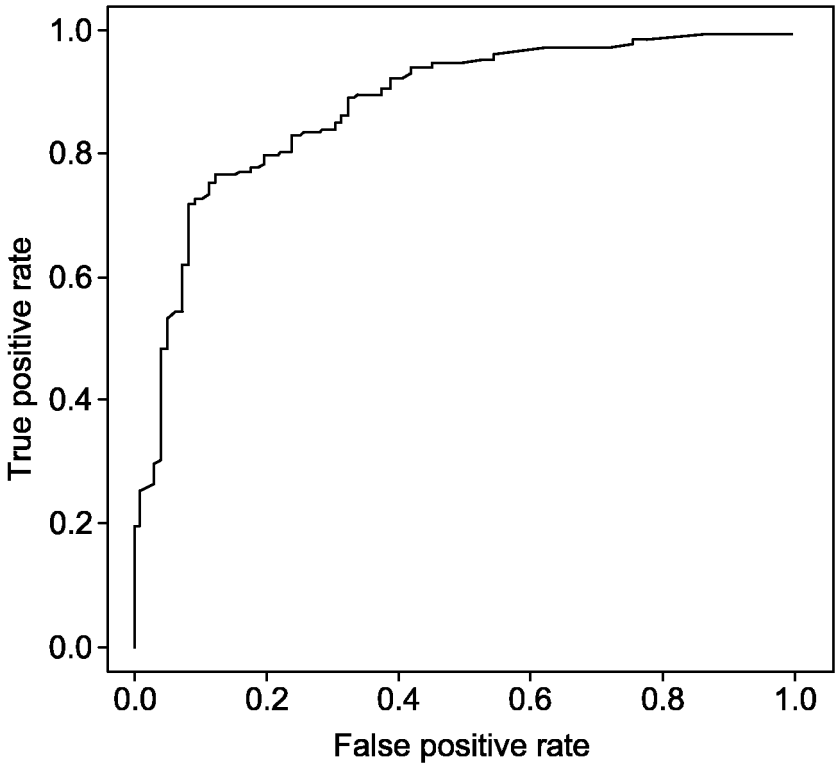

1.0
0.8
0.6
0.4
0.2
0.0
True positive rate
0.0
0.2
0.4
0.6
0.8
1.0
False positive rate

FIG. 21

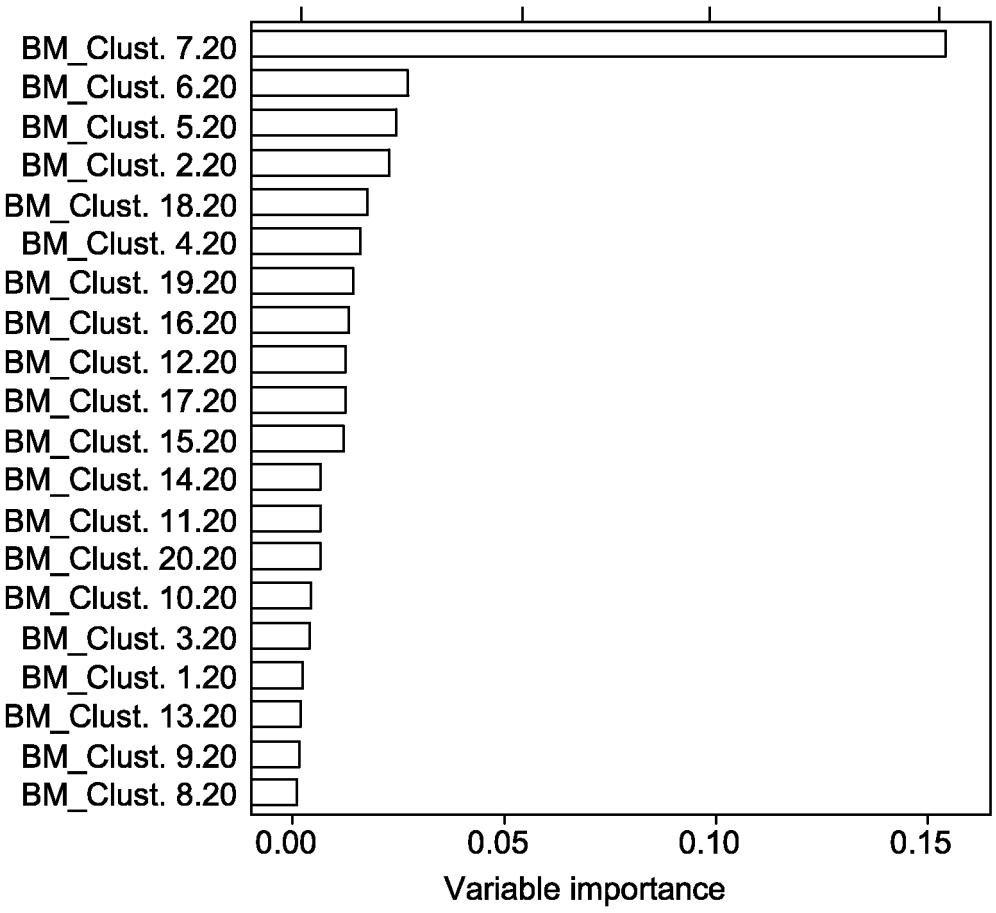

BM_Clust. 7.20
BM_Clust. 6.20
BM_Clust. 5.20
BM_Clust. 2.20
BM_Clust. 18.20
BM_Clust. 4.20
BM_Clust. 19.20
BM_Clust. 16.20
BM_Clust. 12.20
BM_Clust. 17.20
BM_Clust. 15.20
BM_Clust. 14.20
BM_Clust. 11.20
BM_Clust. 20.20
BM_Clust. 10.20
BM_Clust. 3.20
BM_Clust. 1.20
BM_Clust. 13.20
BM_Clust. 9.20
BM_Clust. 8.20
0.00
0.05
0.10
0.15
Variable importance

FIG. 22

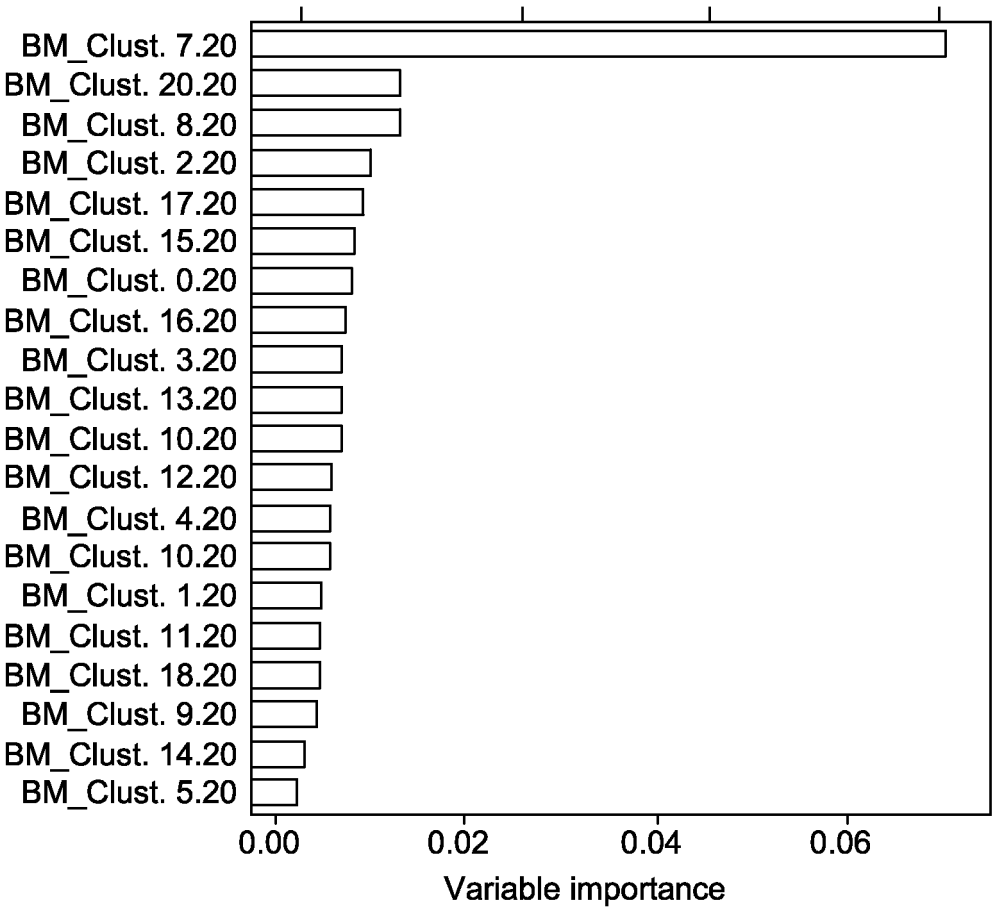

BM_Clust. 7.20
BM_Clust. 20.20
BM_Clust. 8.20
BM_Clust. 2.20
BM_Clust. 17.20
BM_Clust. 15.20
BM_Clust. 0.20
BM_Clust. 16.20
BM_Clust. 3.20
BM_Clust. 13.20
BM_Clust. 10.20
BM_Clust. 12.20
BM_Clust. 4.20
BM_Clust. 10.20
BM_Clust. 1.20
BM_Clust. 11.20
BM_Clust. 18.20
BM_Clust. 9.20
BM_Clust. 14.20
BM_Clust. 5.20
0.00
0.02
0.04
0.06
Variable importance

FIG. 23

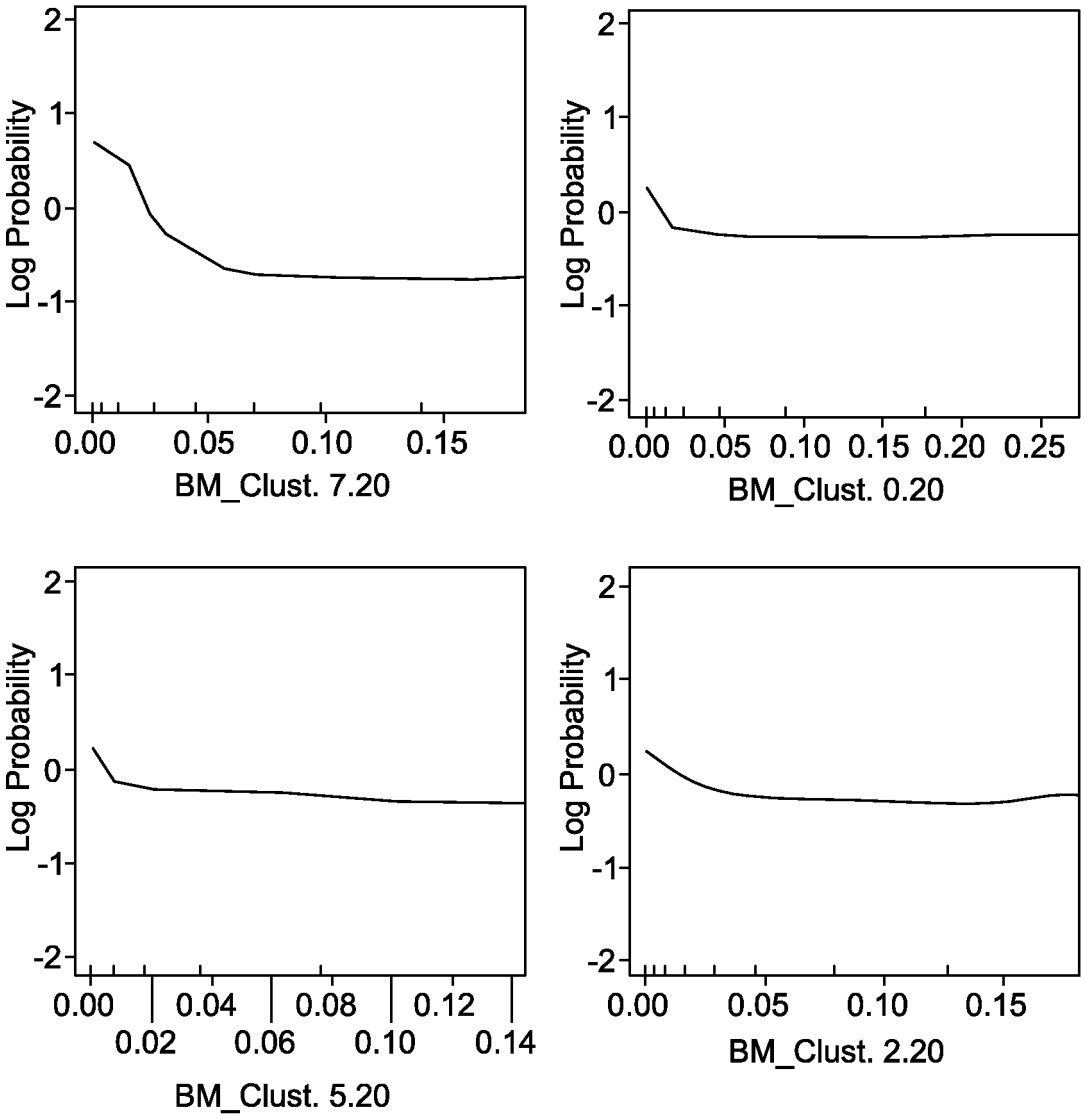

Log Probability
2
1
0
-1
-2
0.00
0.05
0.10
0.15
BM_Clust. 7.20
Log Probability
2
1
0
-1
-2
0.00
0.05
0.10
0.15
0.20
0.25
BM_Clust. 0.20
Log Probability
2
1
0
-1
-2
0.00
0.04
0.08
0.12
0.02
0.06
0.10
0.14
BM_Clust. 5.20
Log Probability
2
1
0
-1
-2
0.00
0.05
0.10
0.15
BM_Clust. 2.20

FIG. 24

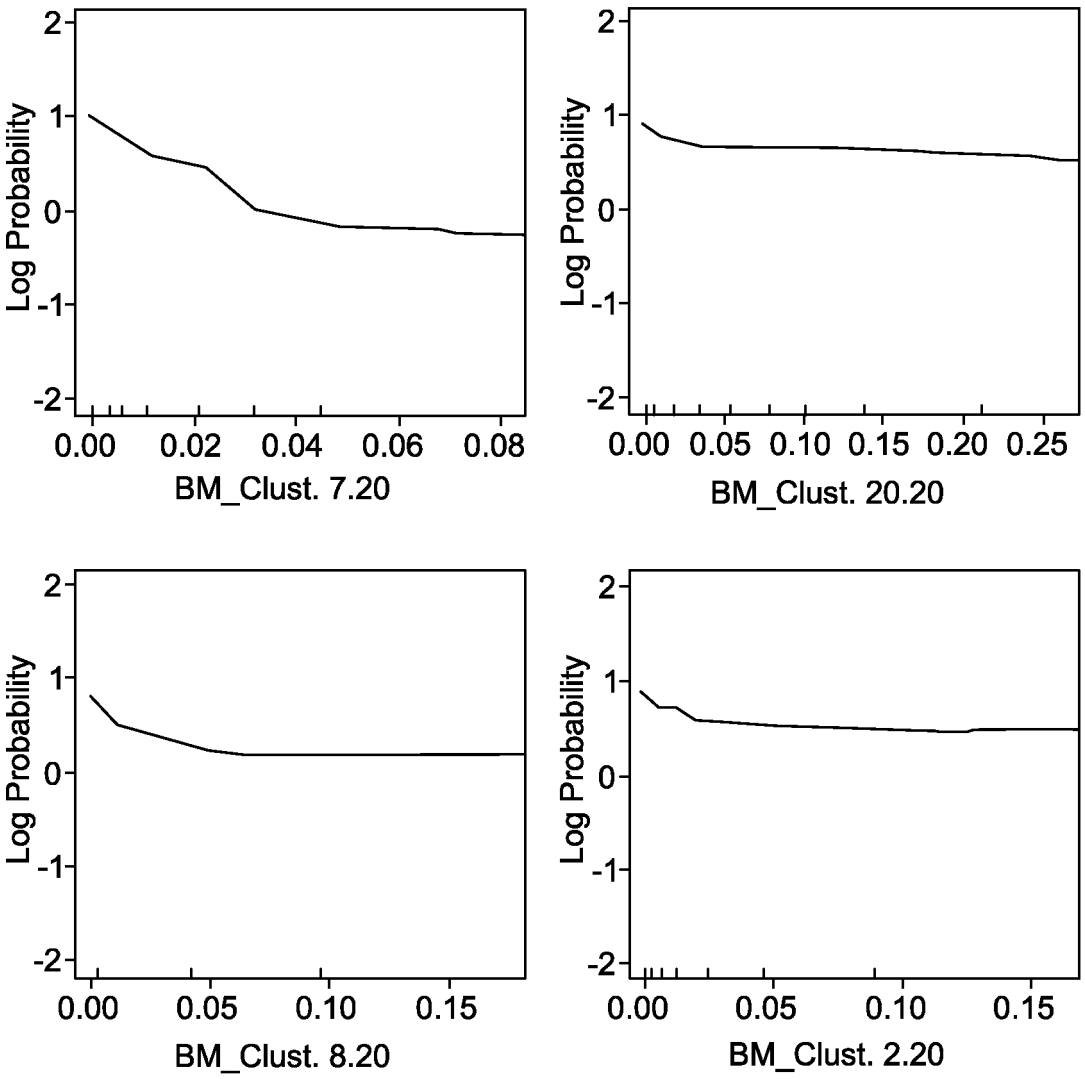

Log Probability
2
1
0
-1
-2
0.00
0.02
0.04
0.06
0.08
BM_Clust. 7.20
Log Probability
2
1
0
-1
-2
0.00
0.05
0.10
0.15
0.20
0.25
BM_Clust. 20.20
Log Probability
2
1
0
-1
-2
0.00
0.05
0.10
0.15
BM_Clust. 8.20
Log Probability
2
1
0
-1
-2
0.00
0.05
0.10
0.15
BM_Clust. 2.20

FIG. 25

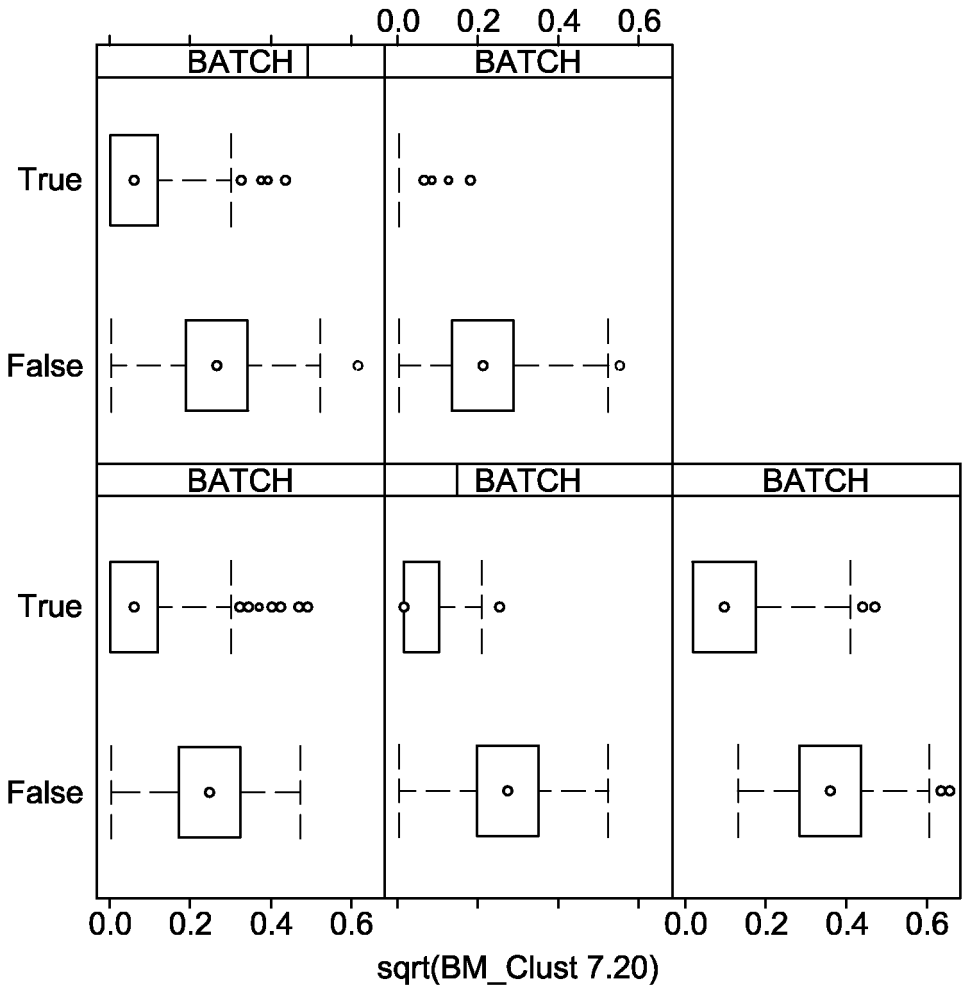

0.0
0.2
0.4
0.6
BATCH
BATCH
True
False
BATCH
BATCH
BATCH
True
False
0.0
0.2
0.4
0.6
0.0
0.2
0.4
0.6
sqrt(BM_Clust 7.20)

FIG. 26

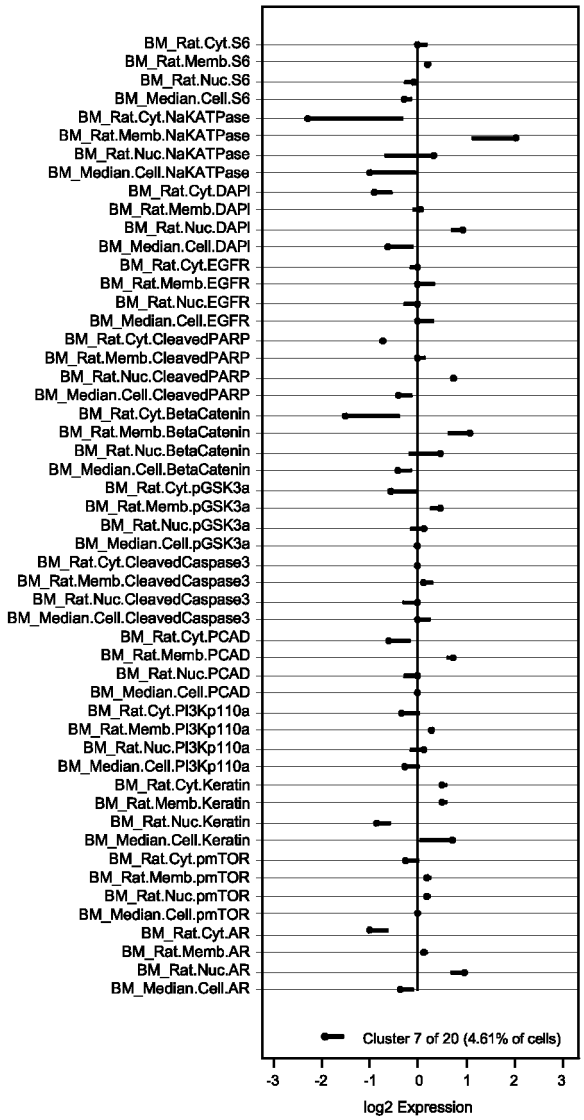

BM_Rat.Cyt.S6
BM_Rat.Memb.S6
BM_Rat.Nuc.S6
BM_Median.Cell.S6
BM_Rat.Cyt.NaKATPase
BM_Rat.Memb.NaKATPase
BM_Rat.Nuc.NaKATPase
BM_Median.Cell.NaKATPase
BM_Rat.Cyt.DAPI
BM_Rat.Memb.DAPI
BM_Rat.Nuc.DAPI
BM_Median.Cell.DAPI
BM_Rat.Cyt.EGFR
BM_Rat.Memb.EGFR
BM_Rat.Nuc.EGFR
BM_Median.Cell.EGFR
BM_Rat.Cyt.CleavedPARP
BM_Rat.Memb.CleavedPARP
BM_Rat.Nuc.CleavedPARP
BM_Median.Cell.CleavedPARP
BM_Rat.Cyt.BetaCatenin
BM_Rat.Memb.BetaCatenin
BM_Rat.Nuc.BetaCatenin
BM_Median.Cell.BetaCatenin
BM_Rat.Cyt.pGSK3a
BM_Rat.Memb.pGSK3a
BM_Rat.Nuc.pGSK3a
BM_Median.Cell.pGSK3a
BM_Rat.Cyt.CleavedCaspase3
BM_Rat.Memb.CleavedCaspase3
BM_Rat.Nuc.CleavedCaspase3
BM_Median.Cell.CleavedCaspase3
BM_Rat.Cyt.PCAD
BM_Rat.Memb.PCAD
BM_Rat.Nuc.PCAD
BM_Median.Cell.PCAD
BM_Rat.Cyt.PI3Kp110a
BM_Rat.Memb.PI3Kp110a
BM_Rat.Nuc.PI3Kp110a
BM_Median.Cell.PI3Kp110a
BM_Rat.Cyt.Keratin
BM_Rat.Memb.Keratin
BM_Rat.Nuc.Keratin
BM_Median.Cell.Keratin
BM_Rat.Cyt.pmTOR
BM_Rat.Memb.pmTOR
BM_Rat.Nuc.pmTOR
BM_Median.Cell.pmTOR
BM_Rat.Cyt.AR
BM_Rat.Memb.AR
BM_Rat.Nuc.AR
BM_Median.Cell.AR
Cluster 7 of 20 (4.61% of cells)
-3
-2
-1
0
1
2
3
log2 Expression

FIG. 27

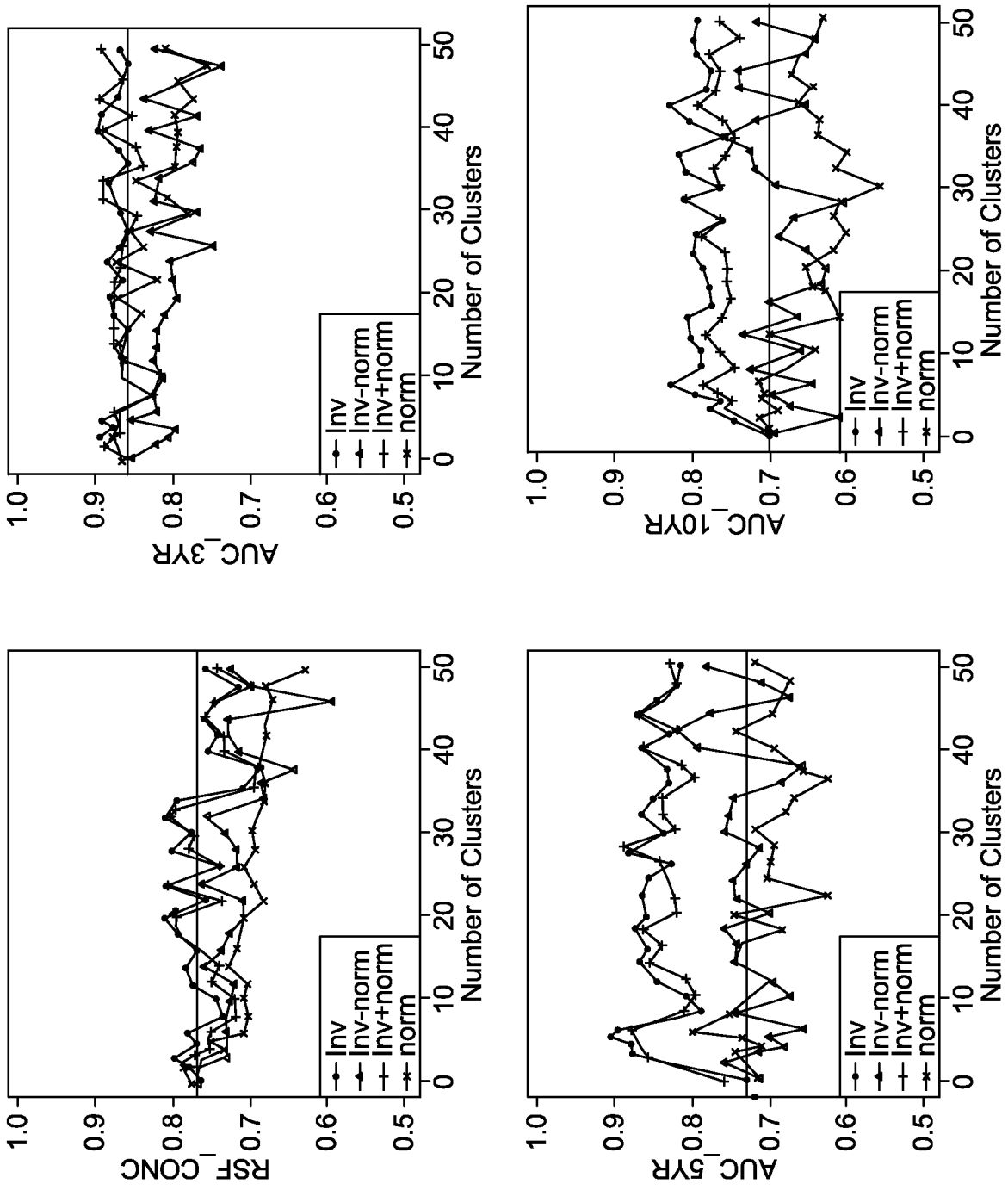

AUC_3YR
AUC_10YR
RSF_CONC
AUC_5YR
1.0
0.9
0.8
0.7
0.6
0.5
0
10
20
30
40
50
Number of Clusters
Inv
Inv-norm
Inv+norm
norm

FIG. 28

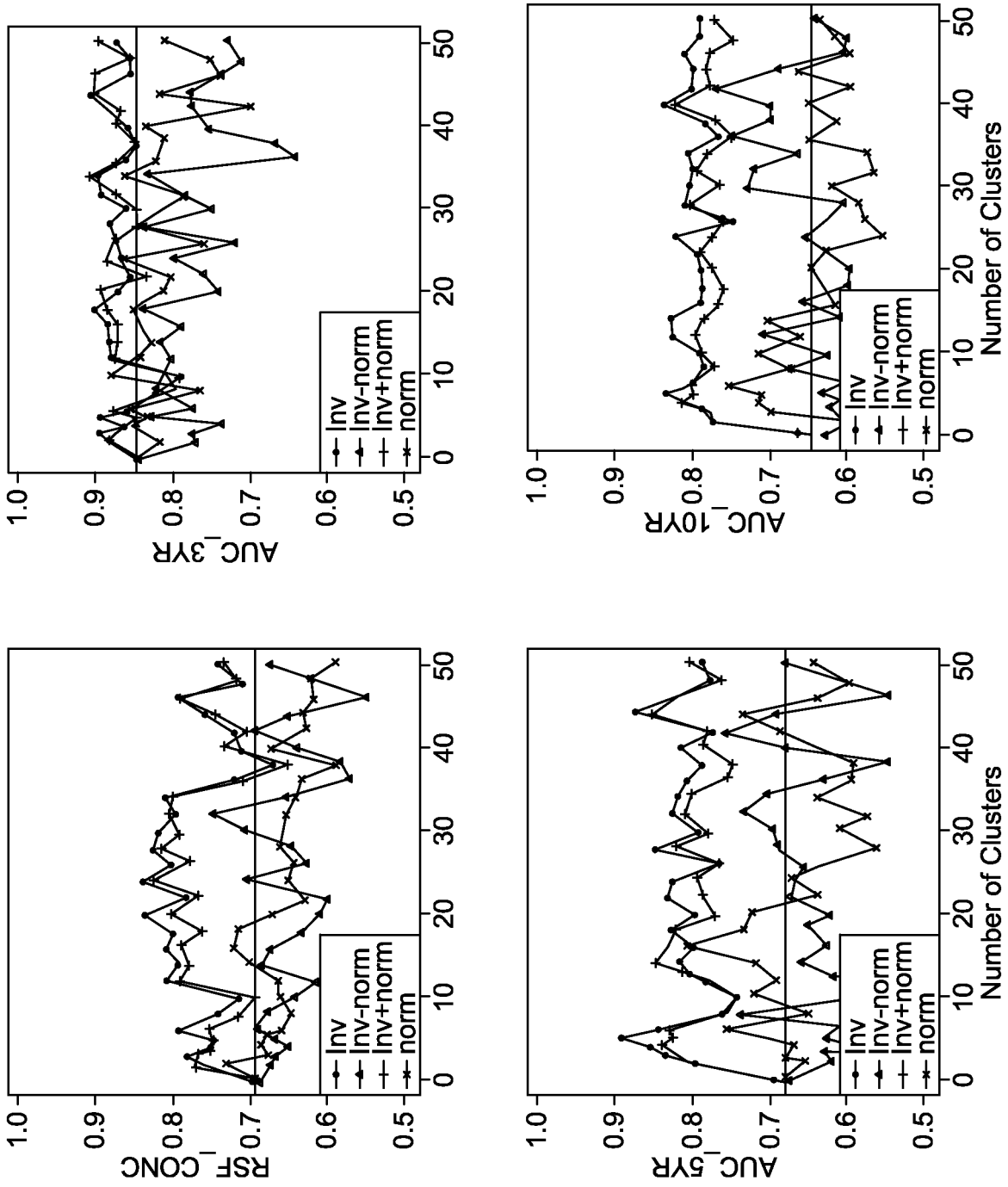

AUC_3YR
AUC_10YR
RSF_CONC
AUC_5YR
Number of Clusters
Number of Clusters
Inv
Inv-norm
Inv+norm
norm

FIG. 29

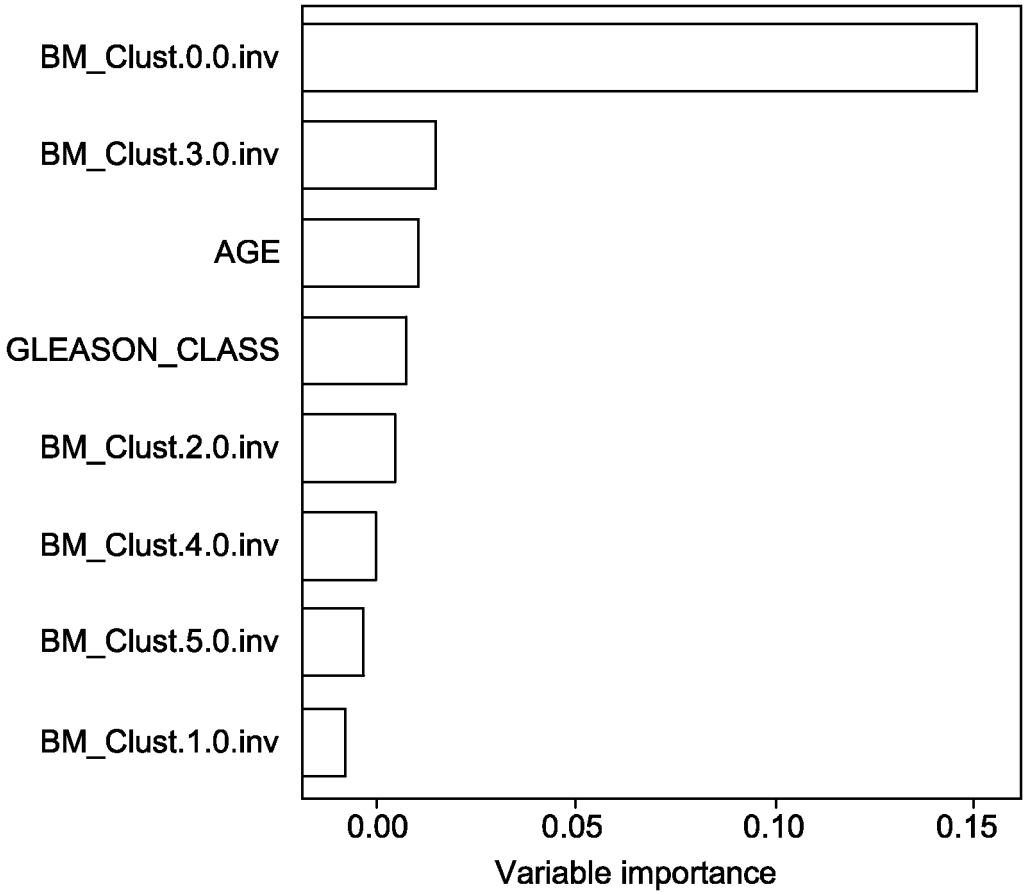

BM_Clust.0.0.inv
BM_Clust.3.0.inv
AGE
GLEASON_CLASS
BM_Clust.2.0.inv
BM_Clust.4.0.inv
BM_Clust.5.0.inv
BM_Clust.1.0.inv
0.00
0.05
0.10
0.15
Variable importance

FIG. 30

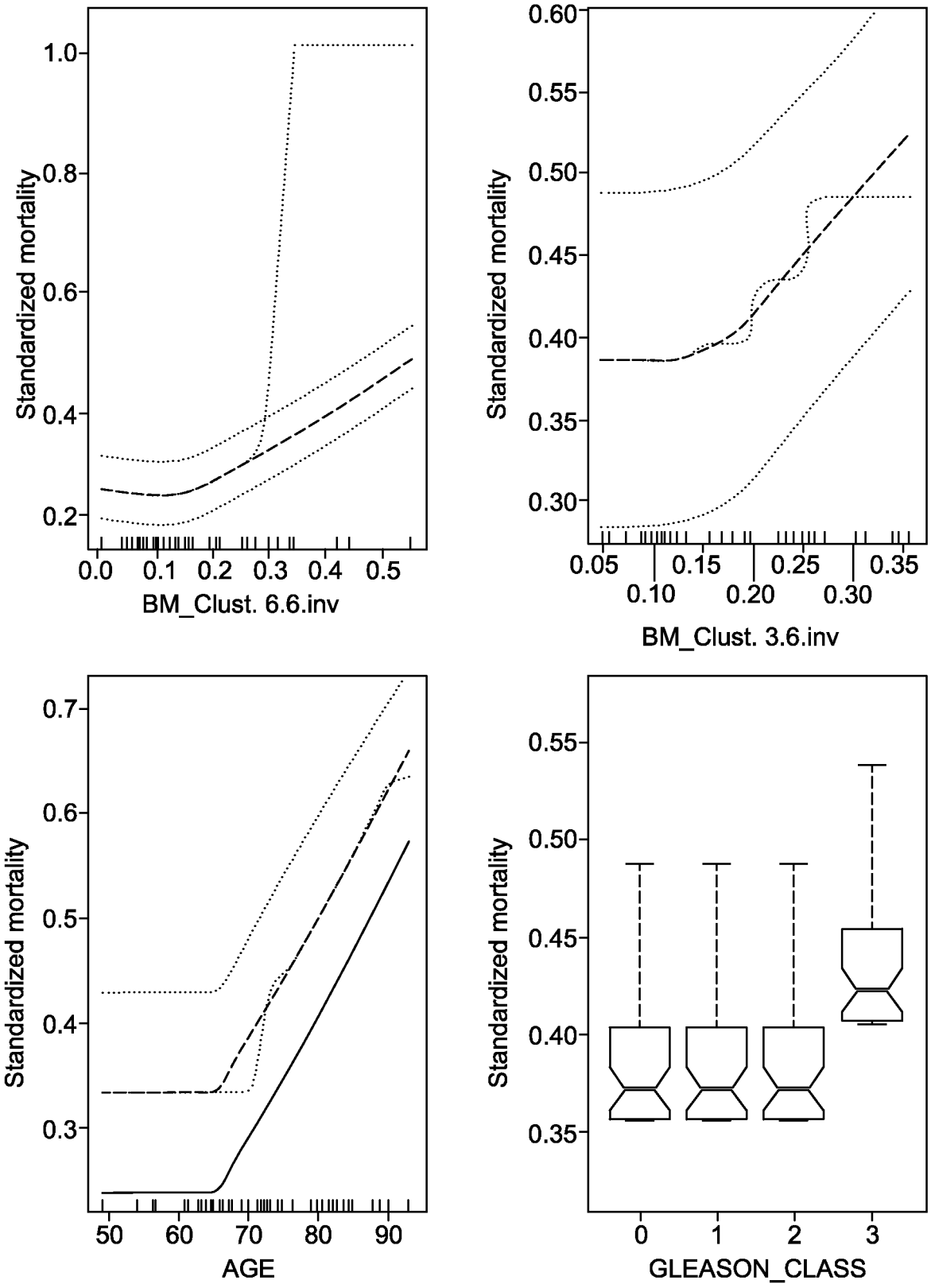

Standardized mortality
1.0
0.8
0.6
0.4
0.2
0.0 0.1 0.2 0.3 0.4 0.5
BM_Clust. 6.6.inv
Standardized mortality
0.60
0.55
0.50
0.45
0.40
0.35
0.30
0.05 0.15 0.25 0.35
0.10 0.20 0.30
BM_Clust. 3.6.inv
Standardized mortality
0.7
0.6
0.5
0.4
0.3
50 60 70 80 90
AGE
Standardized mortality
0.55
0.50
0.45
0.40
0.35
0 1 2 3
GLEASON_CLASS

FIG. 31

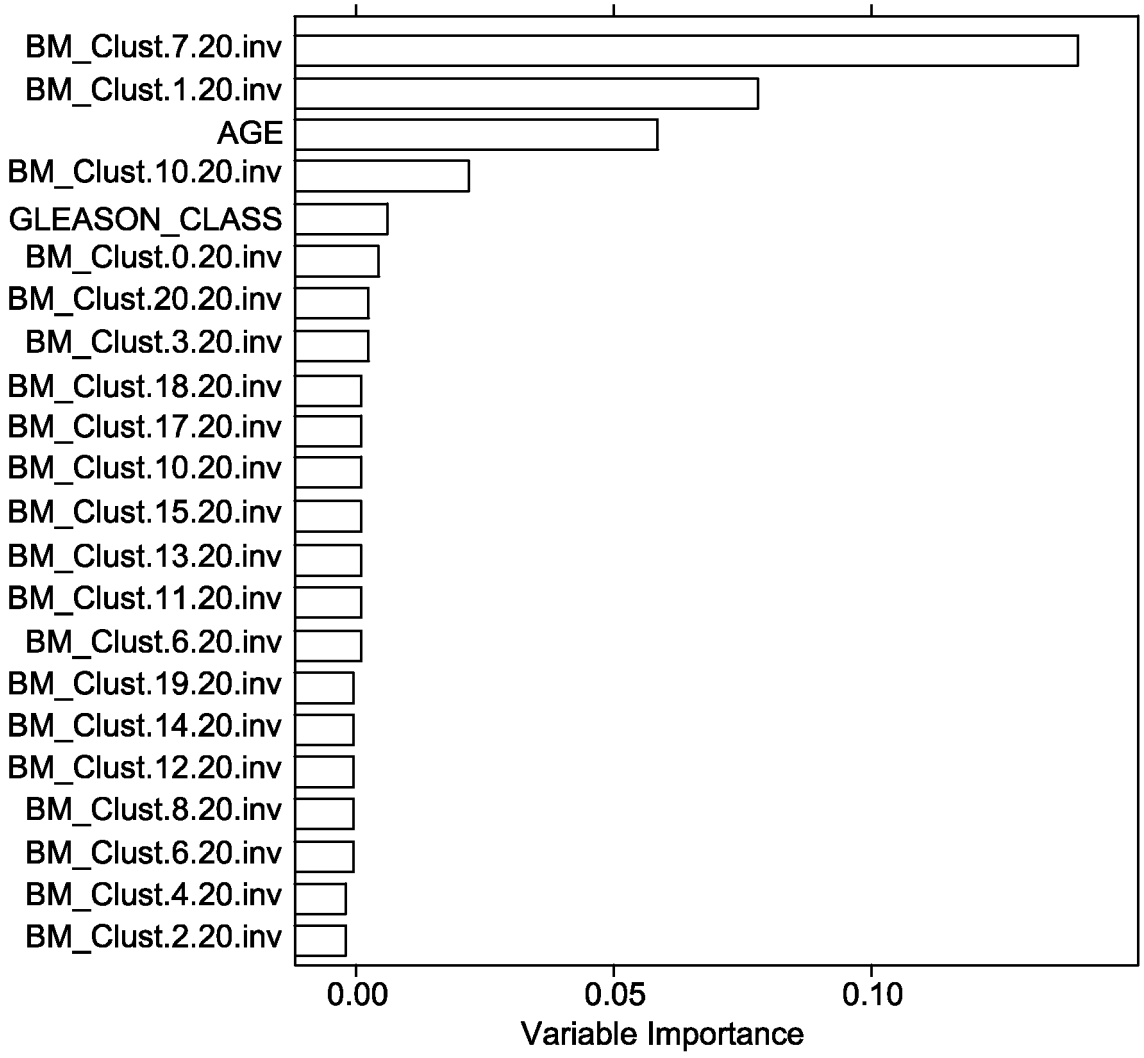

BM_Clust.7.20.inv
BM_Clust.1.20.inv
AGE
BM_Clust.10.20.inv
GLEASON_CLASS
BM_Clust.0.20.inv
BM_Clust.20.20.inv
BM_Clust.3.20.inv
BM_Clust.18.20.inv
BM_Clust.17.20.inv
BM_Clust.10.20.inv
BM_Clust.15.20.inv
BM_Clust.13.20.inv
BM_Clust.11.20.inv
BM_Clust.6.20.inv
BM_Clust.19.20.inv
BM_Clust.14.20.inv
BM_Clust.12.20.inv
BM_Clust.8.20.inv
BM_Clust.6.20.inv
BM_Clust.4.20.inv
BM_Clust.2.20.inv
0.00
0.05
0.10
Variable Importance

FIG. 32

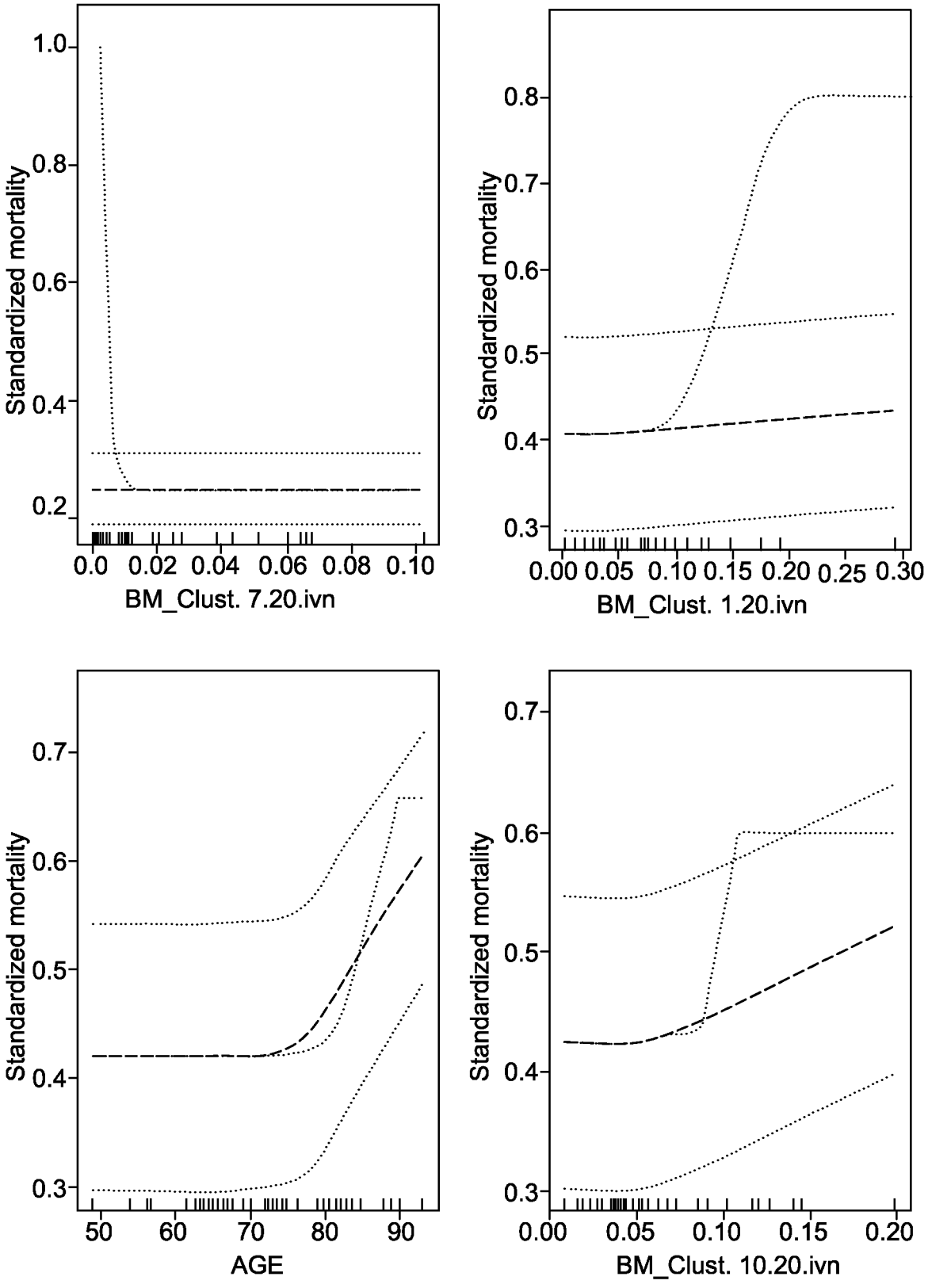

Standardized mortality
1.0
0.8
0.6
0.4
0.2
0.0 0.02 0.04 0.06 0.08 0.10
BM_Clust. 7.20.ivn
Standardized mortality
0.8
0.7
0.6
0.5
0.4
0.3
0.00 0.05 0.10 0.15 0.20 0.25 0.30
BM_Clust. 1.20.ivn
Standardized mortality
0.7
0.6
0.5
0.4
0.3
50 60 70 80 90
AGE
Standardized mortality
0.7
0.6
0.5
0.4
0.3
0.00 0.05 0.10 0.15 0.20
BM_Clust. 10.20.ivn

FIG. 33

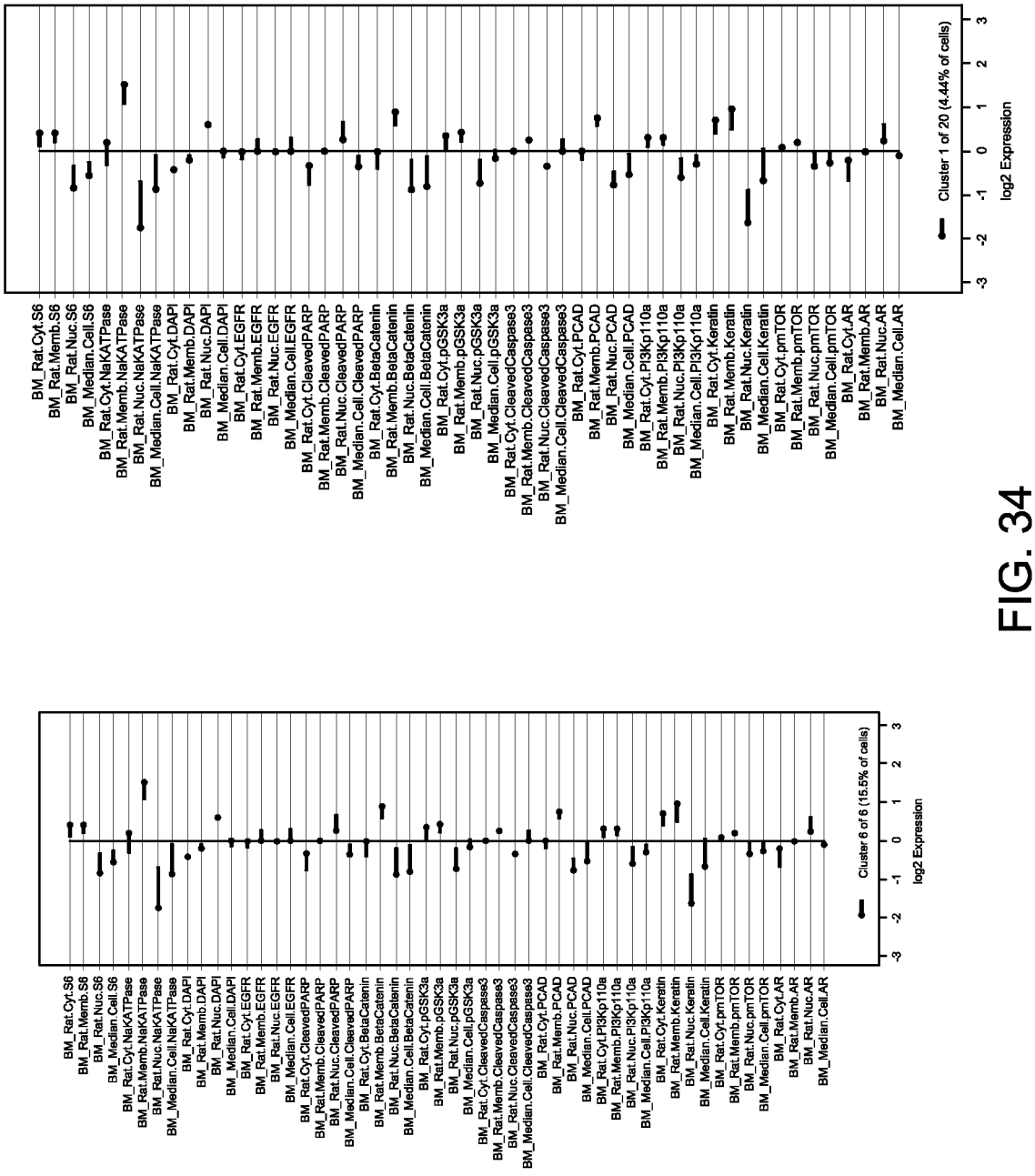

BM_Rat.Cyt.S6
BM_Rat.Memb.S6
BM_Rat.Nuc.S6
BM_Median.Cell.S6
BM_Rat.Cyt.NaKATPase
BM_Rat.Memb.NaKATPase
BM_Rat.Nuc.NaKATPase
BM_Median.Cell.NaKATPase
BM_Rat.Cyt.DAPI
BM_Rat.Memb.DAPI
BM_Rat.Nuc.DAPI
BM_Median.Cell.DAPI
BM_Rat.Cyt.EGFR
BM_Rat.Memb.EGFR
BM_Rat.Nuc.EGFR
BM_Median.Cell.EGFR
BM_Rat.Cyt.CleavedPARP
BM_Rat.Memb.CleavedPARP
BM_Rat.Nuc.CleavedPARP
BM_Median.Cell.CleavedPARP
BM_Rat.Cyt.BetaCatenin
BM_Rat.Memb.BetaCatenin
BM_Rat.Nuc.BetaCatenin
BM_Median.Cell.BetaCatenin
BM_Rat.Cyt.pGSK3a
BM_Rat.Memb.pGSK3a
BM_Rat.Nuc.pGSK3a
BM_Median.Cell.pGSK3a
BM_Rat.Cyt.CleavedCaspase3
BM_Rat.Memb.CleavedCaspase3
BM_Rat.Nuc.CleavedCaspase3
BM_Median.Cell.CleavedCaspase3
BM_Rat.Cyt.PCAD
BM_Rat.Memb.PCAD
BM_Rat.Nuc.PCAD
BM_Median.Cell.PCAD
BM_Rat.Cyt.PI3Kp110a
BM_Rat.Memb.PI3Kp110a
BM_Rat.Nuc.PI3Kp110a
BM_Median.Cell.PI3Kp110a
BM_Rat.Cyt.Keratin
BM_Rat.Memb.Keratin
BM_Rat.Nuc.Keratin
BM_Median.Cell.Keratin
BM_Rat.Cyt.pmTOR
BM_Rat.Memb.pmTOR
BM_Rat.Nuc.pmTOR
BM_Median.Cell.pmTOR
BM_Rat.Cyt.AR
BM_Rat.Memb.AR
BM_Rat.Nuc.AR
BM_Median.Cell.AR
-3
-2
-1
0
1
2
3
log2 Expression
Cluster 1 of 20 (4.44% of cells)
Cluster 6 of 6 (15.5% of cells)

FIG. 34

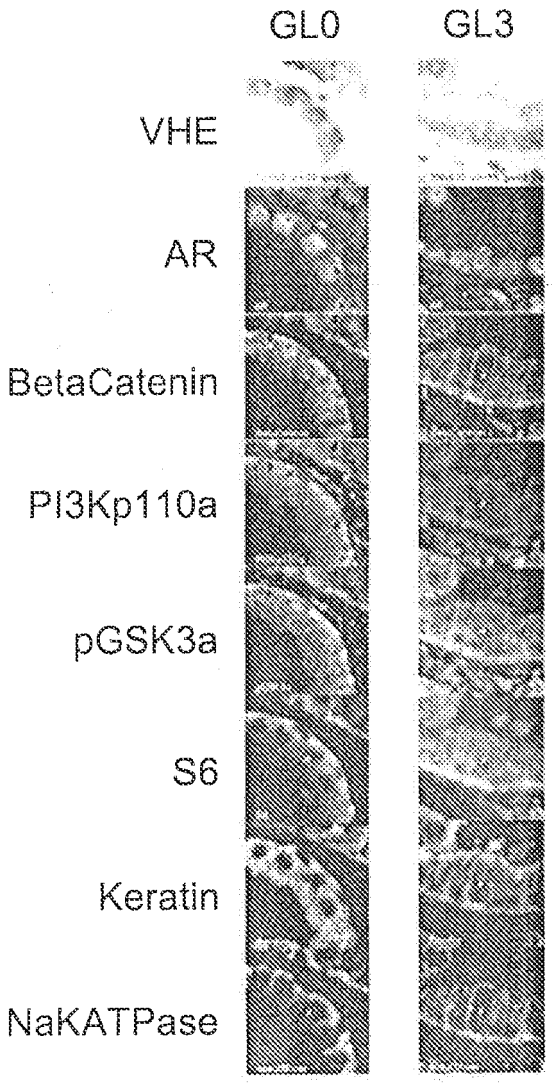

GL0
GL3
VHE
AR
BetaCatenin
PI3Kp110a
pGSK3a
S6
Keratin
NaKATPase

FIG. 35