US 20110065598A1

(19) **United States**

(12) **Patent Application Publication**

(10) **Pub. No.: US 2011/0065598 A1**

(43) **Pub. Date: Mar. 17, 2011**

Labrie et al.

(54) **METHODS AND DEVICES FOR DETECTING DIABETIC NEPHROPATHY AND ASSOCIATED DISORDERS**

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(73) Assignee: **Rules-Based Medicine, Inc.**, Austin, TX (US)

(21) Appl. No.: **12/852,282**

(22) Filed: **Aug. 6, 2010**

Related U.S. Application Data

(60) Provisional application No. 61/327,389, filed on Apr. 23, 2010, provisional application No. 61/232,091, filed on Aug. 7, 2009.

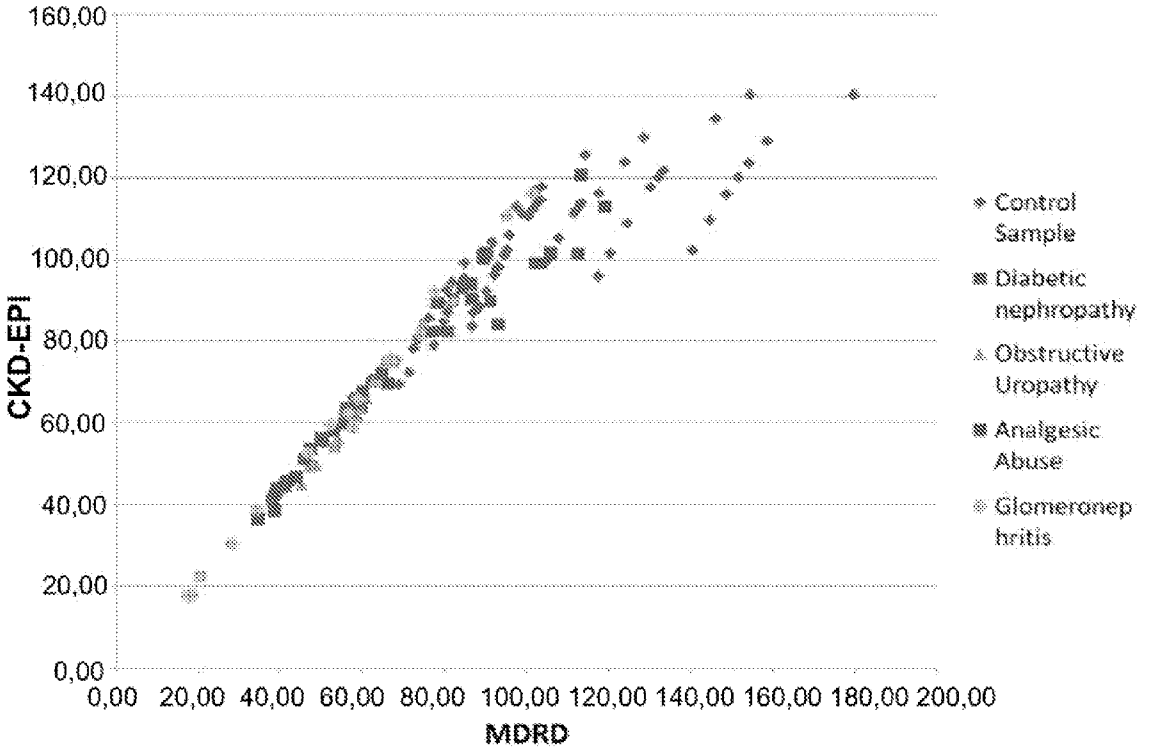
Publication Classification

(51) **Int. Cl.**
C40B 30/04 (2006.01)

(52) **U.S. Cl.** **506/9**

(57) **ABSTRACT**

Methods and devices for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal are described. In particular, methods and devices for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder using measured concentrations of a combination of three or more analytes in a test sample taken from the mammal are described.


160,00
140,00
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100,00
80,00
60,00
40,00
20,00
0,00
CKD-EPI
0,00 20,00 40,00 60,00 80,00 100,00 120,00 140,00 160,00 180,00 200,00
MDRD
Control Sample
Diabetic nephropathy
Obstructive Uropathy
Analgesic Abuse
Glomeronephritis

FIG. 1

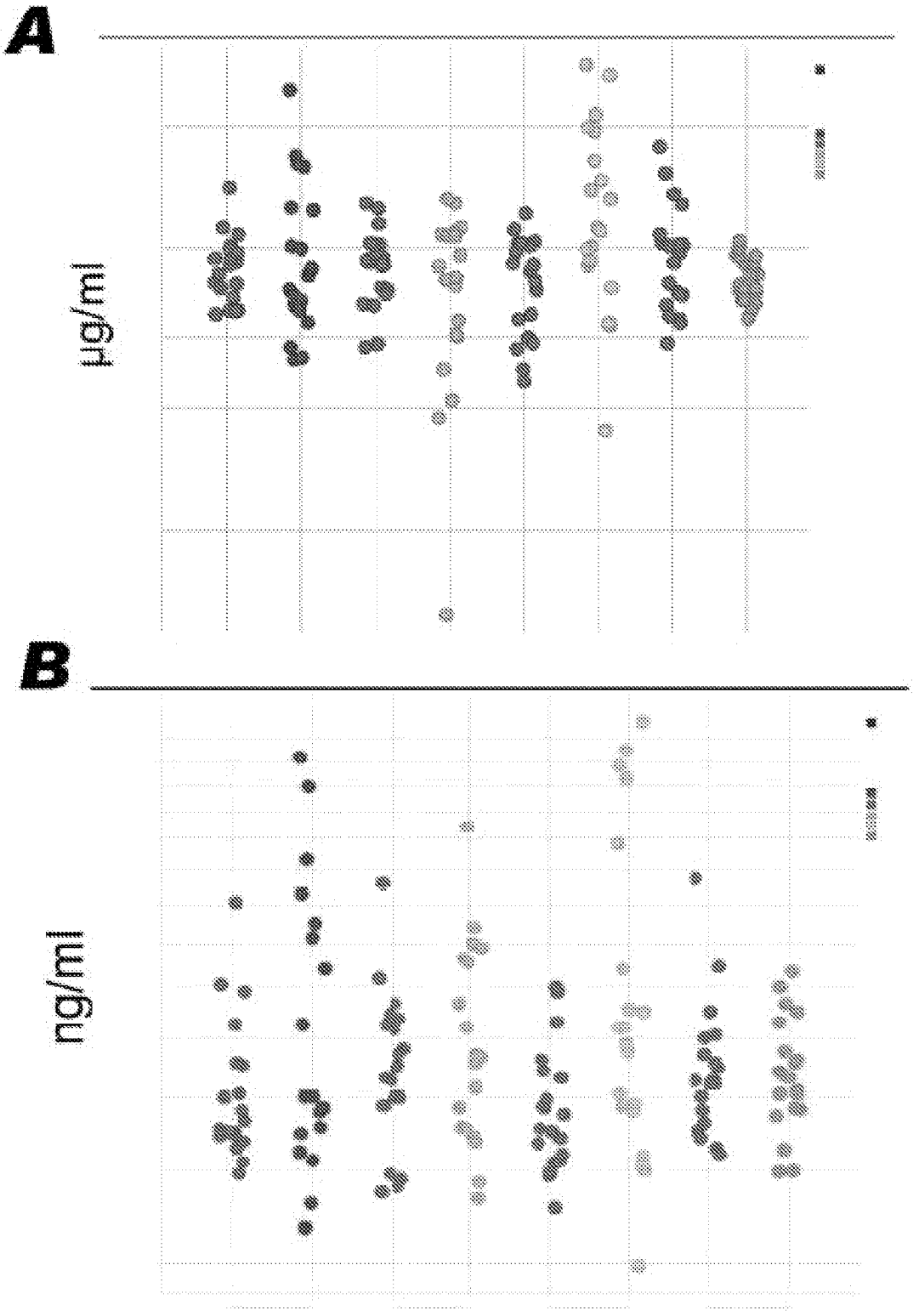

FIG. 2

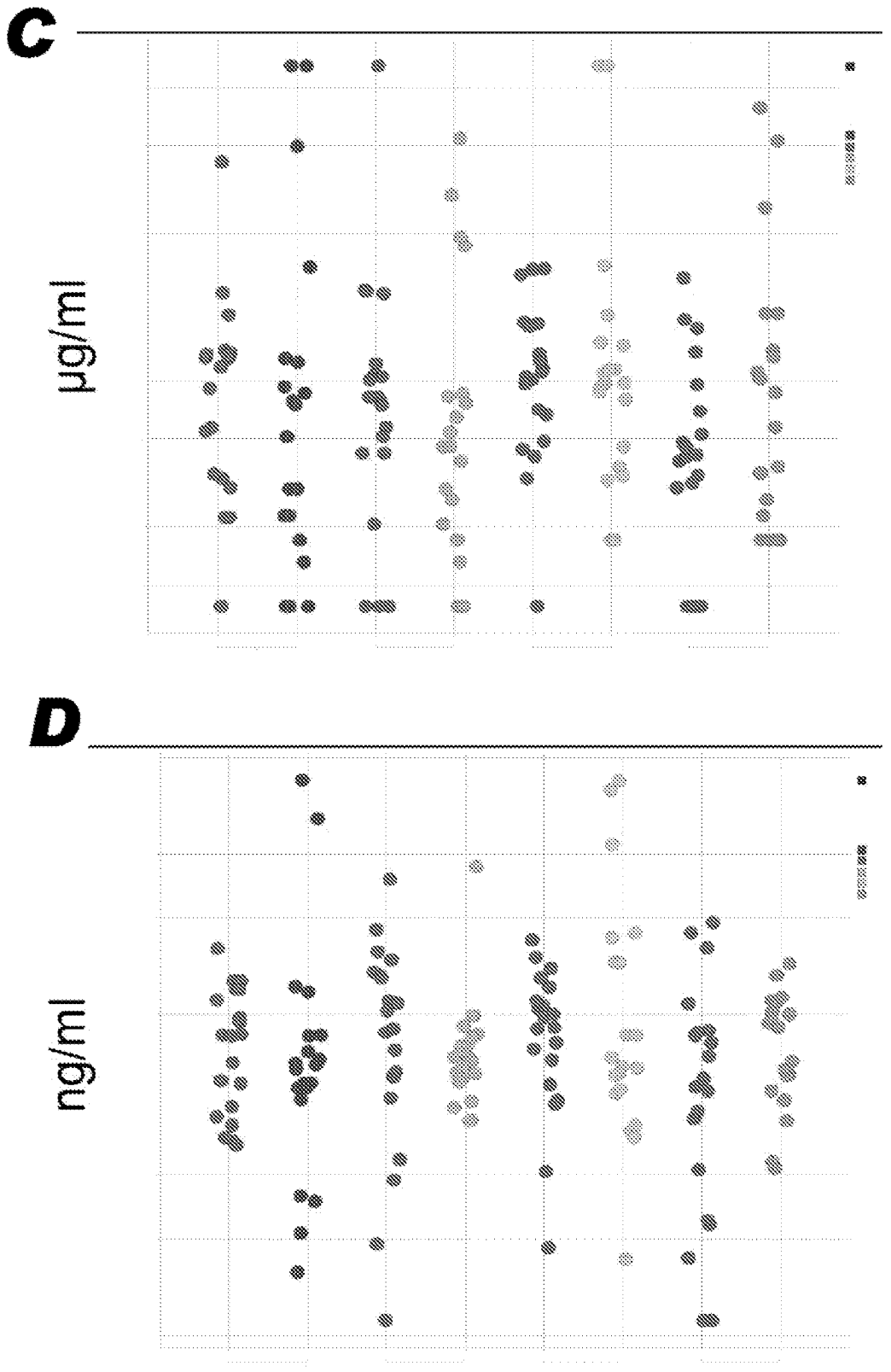

FIG. 2

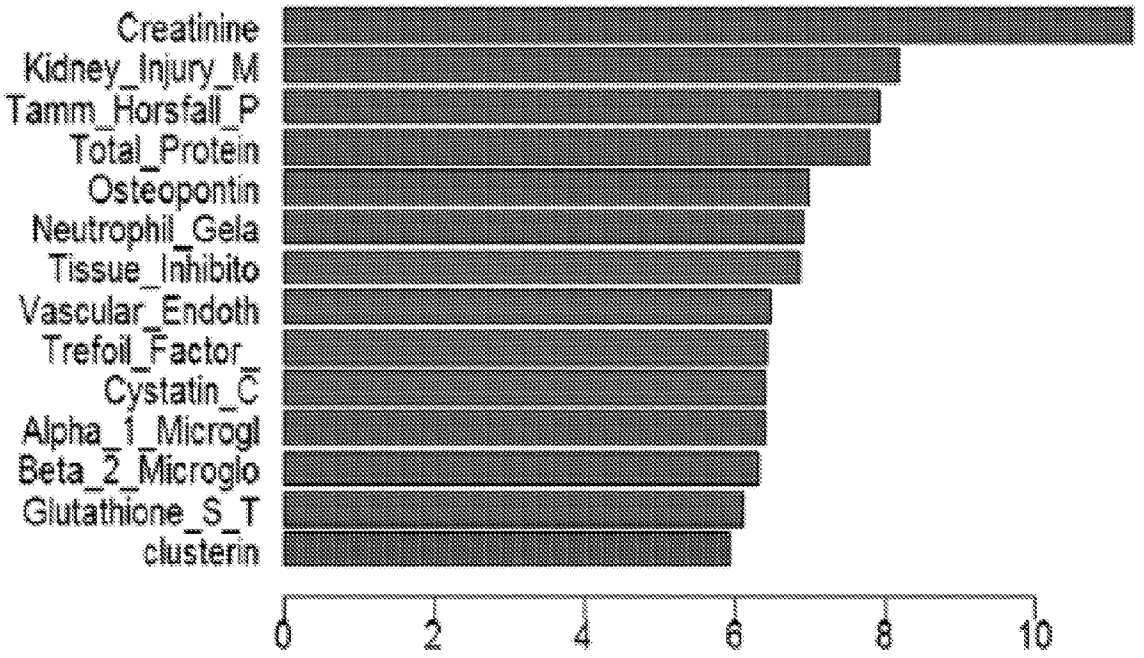
Creatinine
Kidney_Injury_M
Tamm_Horsfall_P
Total_Protein
Osteopontin
Neutrophil_Gela
Tissue_Inhibito
Vascular_Endoth
Trefoil_Factor_
Cystatin_C
Alpha_1_Microgl
Beta_2_Microglo
Glutathione_S_T
clusterin
0
2
4
6
8
10

FIG. 3

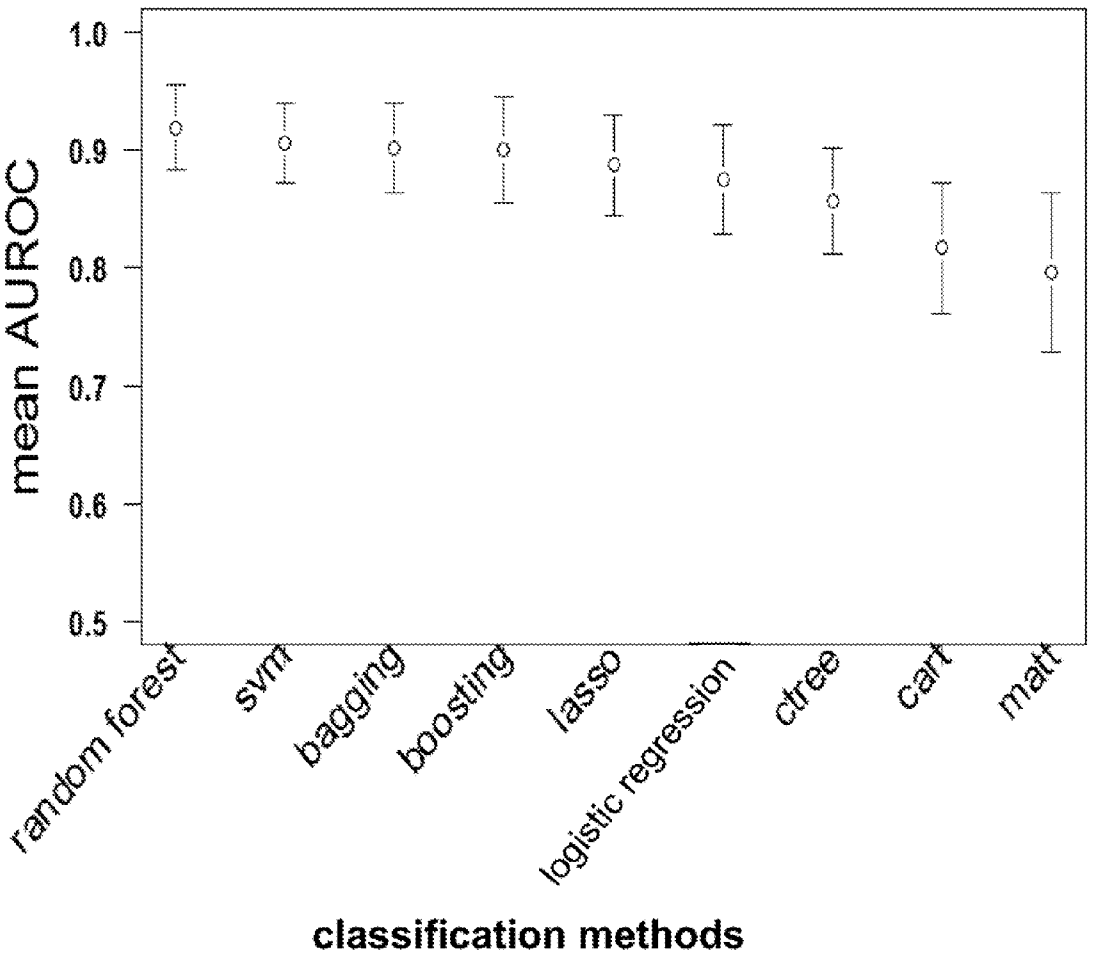
mean AUROC
1.0
0.9
0.8
0.7
0.6
0.5
random forest
svm
bagging
boosting
lasso
logistic regression
ctree
cart
matt
classification methods

FIG. 4A

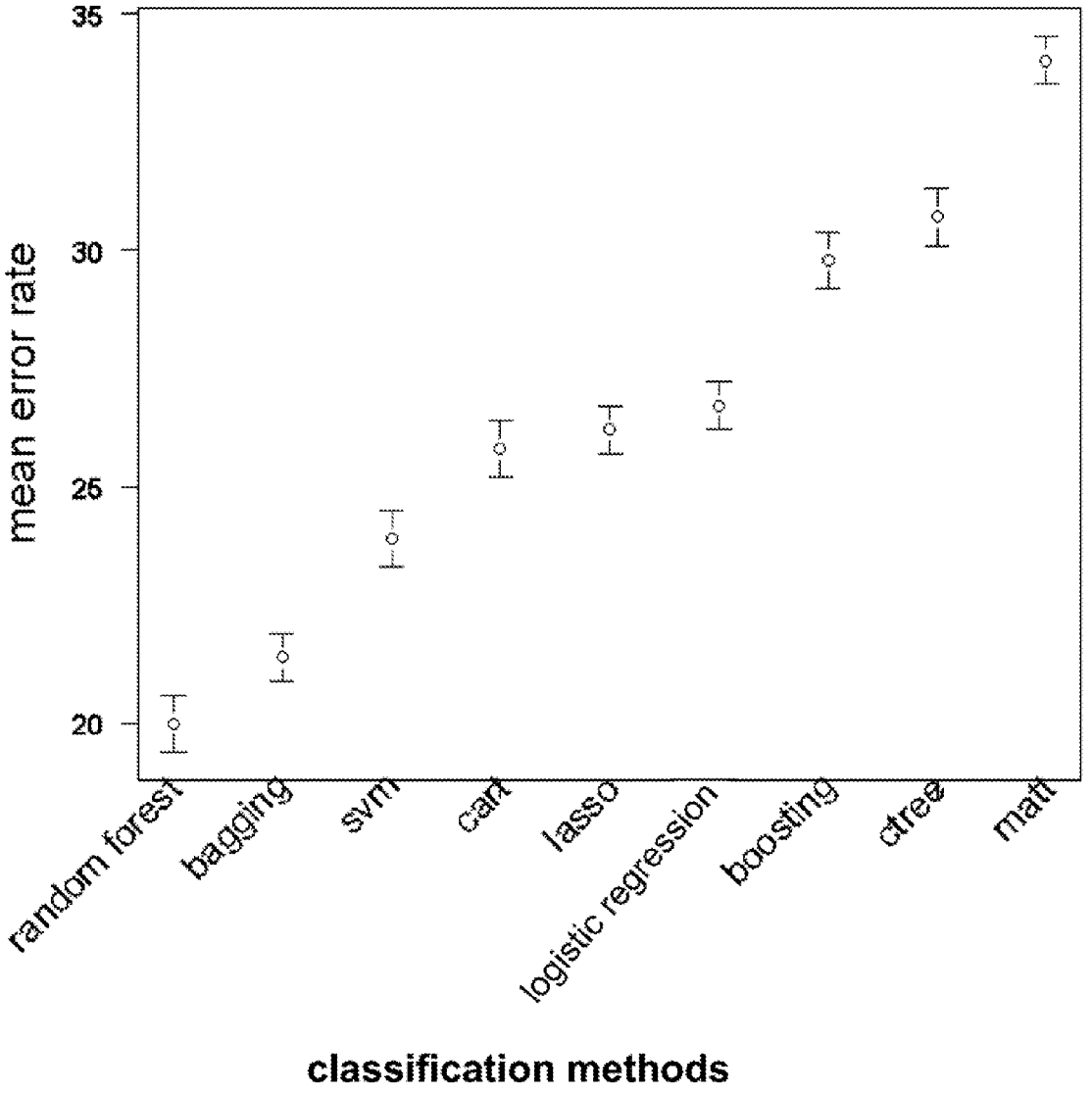
35
30
25
20
mean error rate
random forest
bagging
svm
cart
lasso
logistic regression
boosting
ctree
matl
classification methods

FIG. 4B

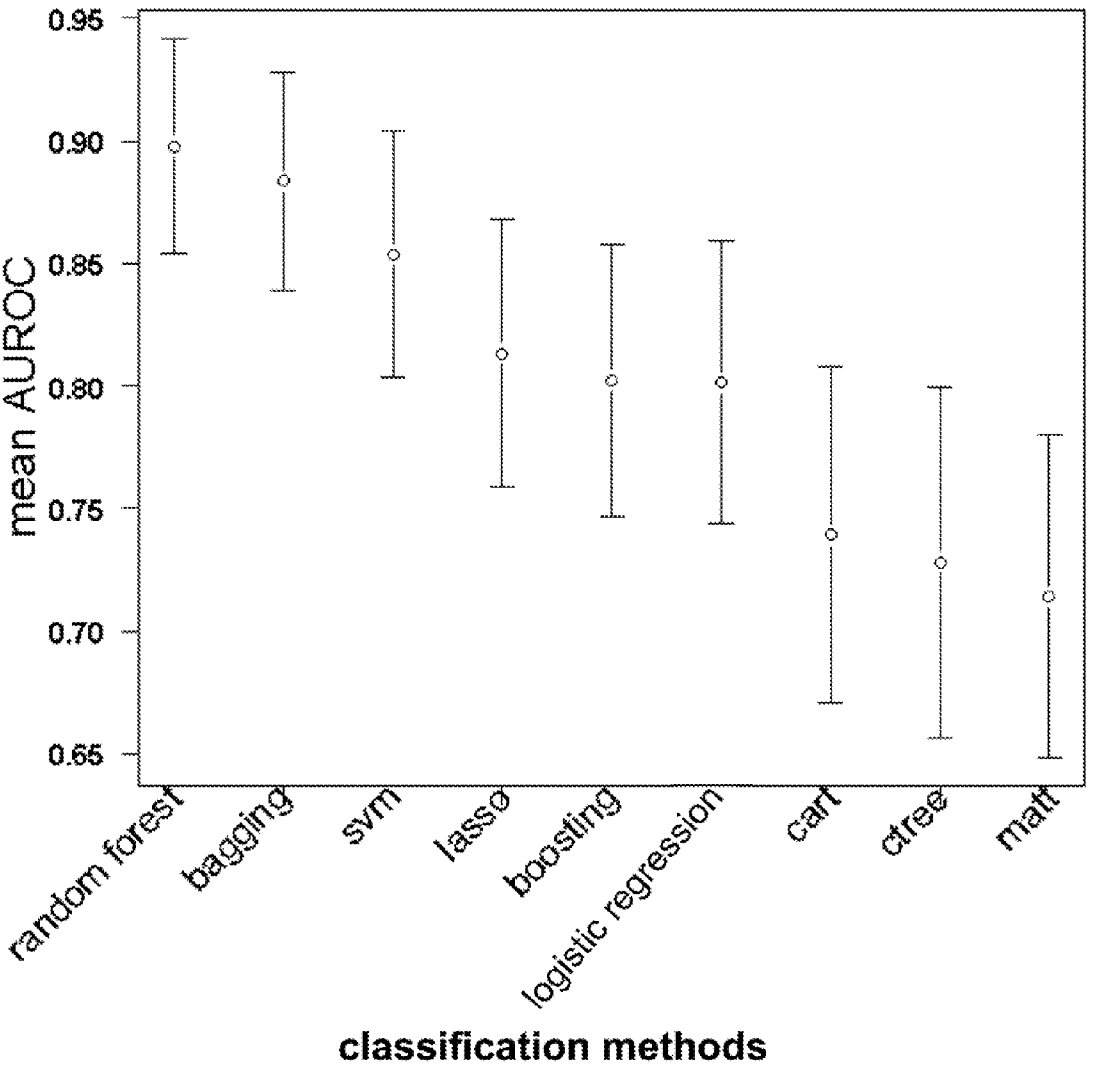
0.95
0.90
0.85
0.80
0.75
0.70
0.65
mean AUROC
random forest
bagging
svm
lasso
boosting
logistic regression
cart
ctree
matt
classification methods

FIG. 4C

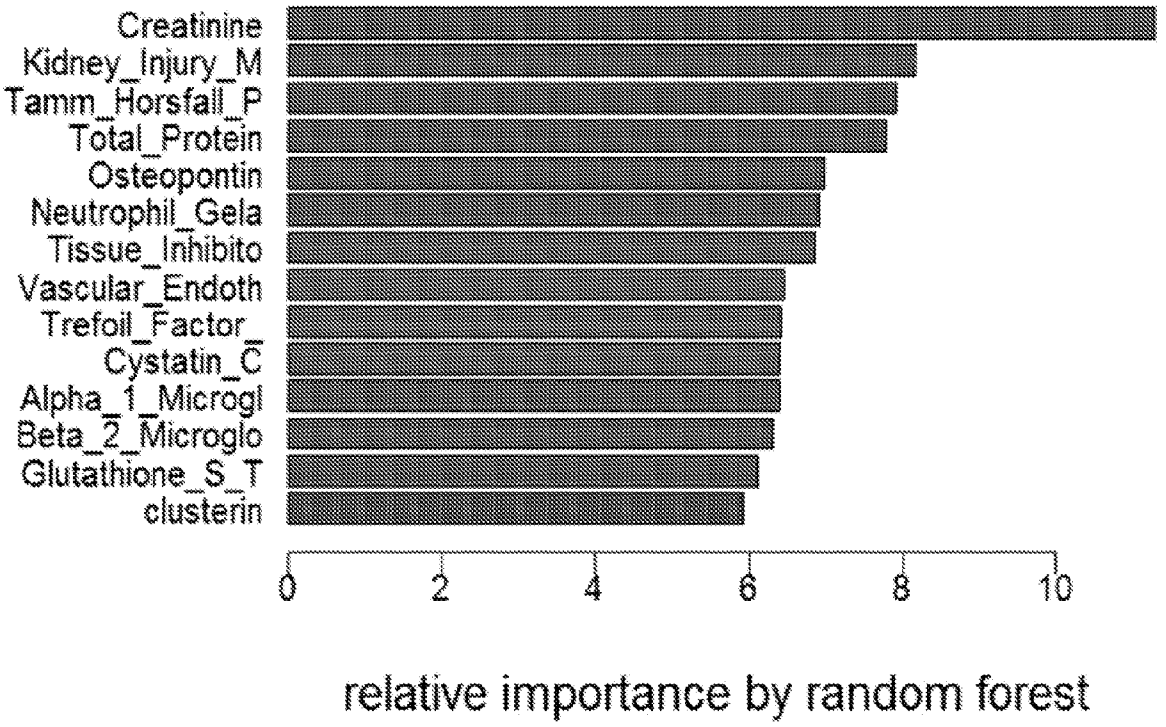
Creatinine
Kidney_Injury_M
Tamm_Horsfall_P
Total_Protein
Osteopontin
Neutrophil_Gela
Tissue_Inhibito
Vascular_Endoth
Trefoil_Factor_
Cystatin_C
Alpha_1_Microgl
Beta_2_Microglo
Glutathione_S_T
clusterin
0
2
4
6
8
10
relative importance by random forest

FIG. 5A

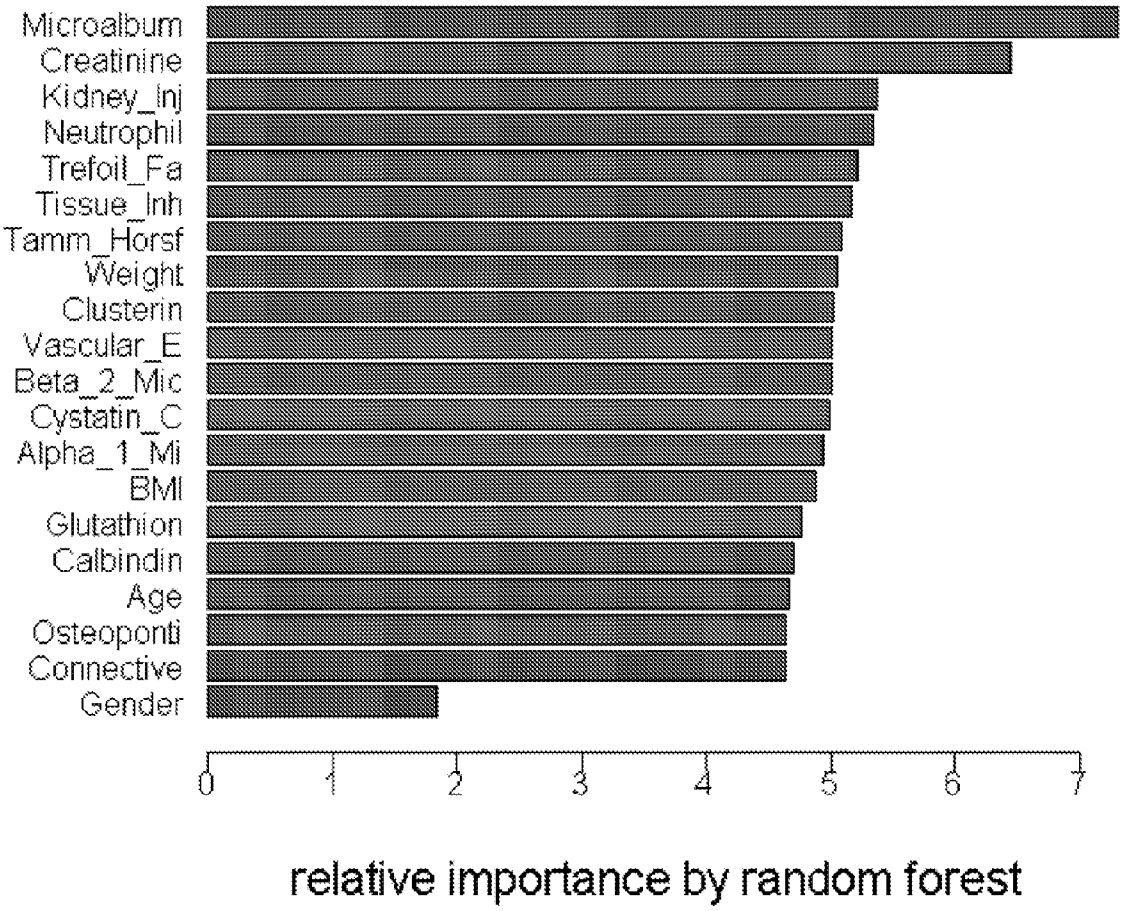
Microalbum
Creatinine
Kidney_Inj
Neutrophil
Trefoil_Fa
Tissue_Inh
Tamm_Horsf
Weight
Clusterin
Vascular_E
Beta_2_Mic
Cystatin_C
Alpha_1_Mi
BMI
Glutathion
Calbindin
Age
Osteoponti
Connective
Gender
0
1
2
3
4
5
6
7
relative importance by random forest

FIG. 5B

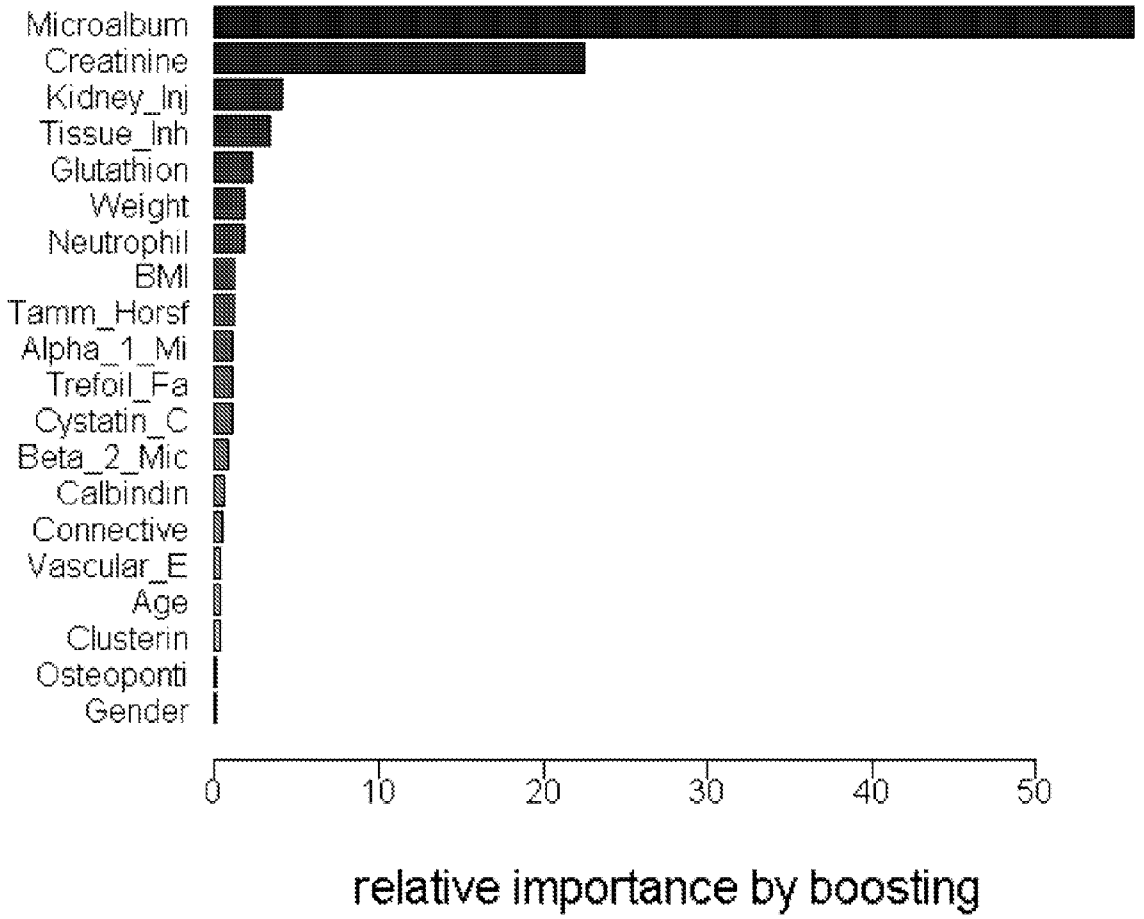
Microalbum
Creatinine
Kidney_Inj
Tissue_Inh
Glutathion
Weight
Neutrophil
BMI
Tamm_Horsf
Alpha_1_Mi
Trefoil_Fa
Cystatin_C
Beta_2_Mic
Calbindin
Connective
Vascular_E
Age
Clusterin
Osteoponti
Gender
0
10
20
30
40
50
relative importance by boosting

FIG. 5C

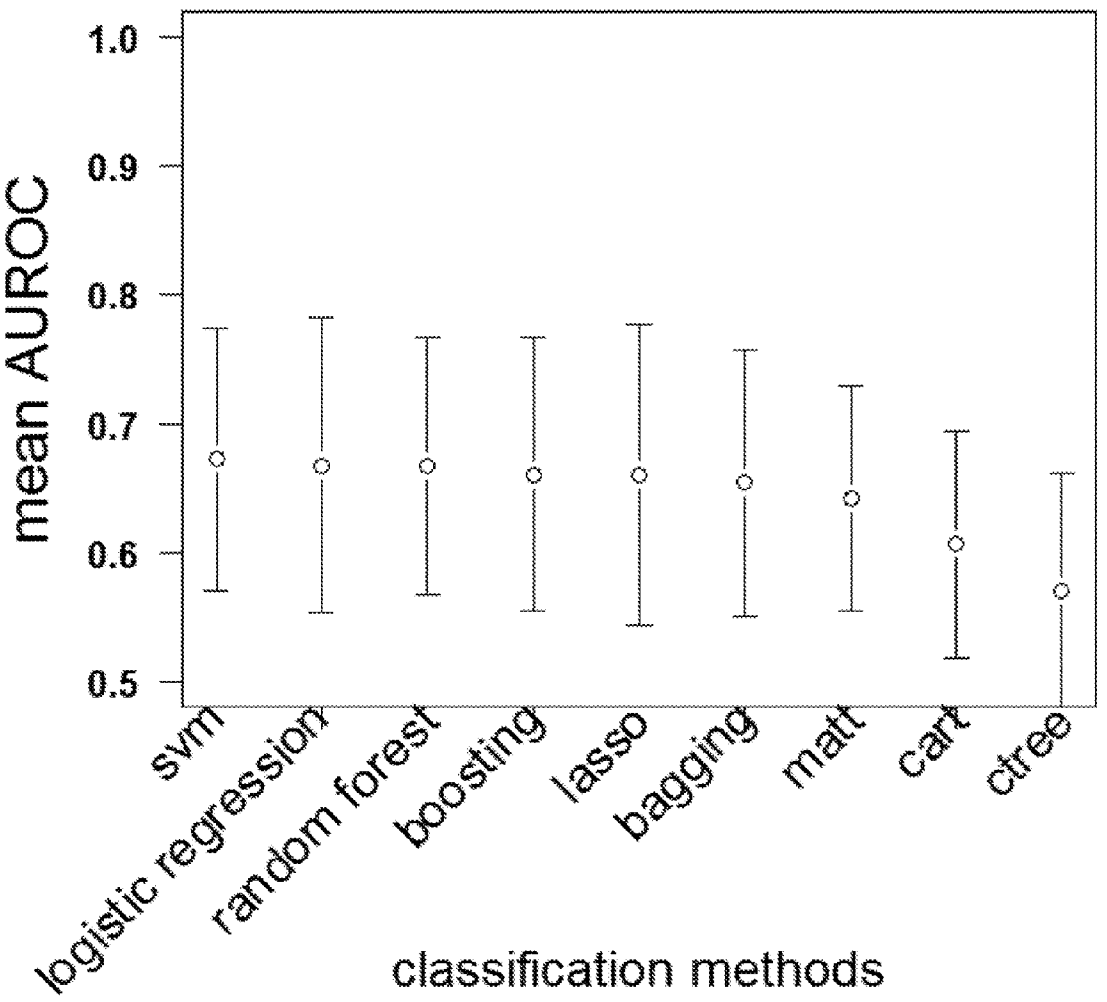
1.0
0.9
0.8
0.7
0.6
0.5
mean AUROC
svm
logistic regression
random forest
boosting
lasso
bagging
matt
cart
ctree
classification methods

FIG. 6A

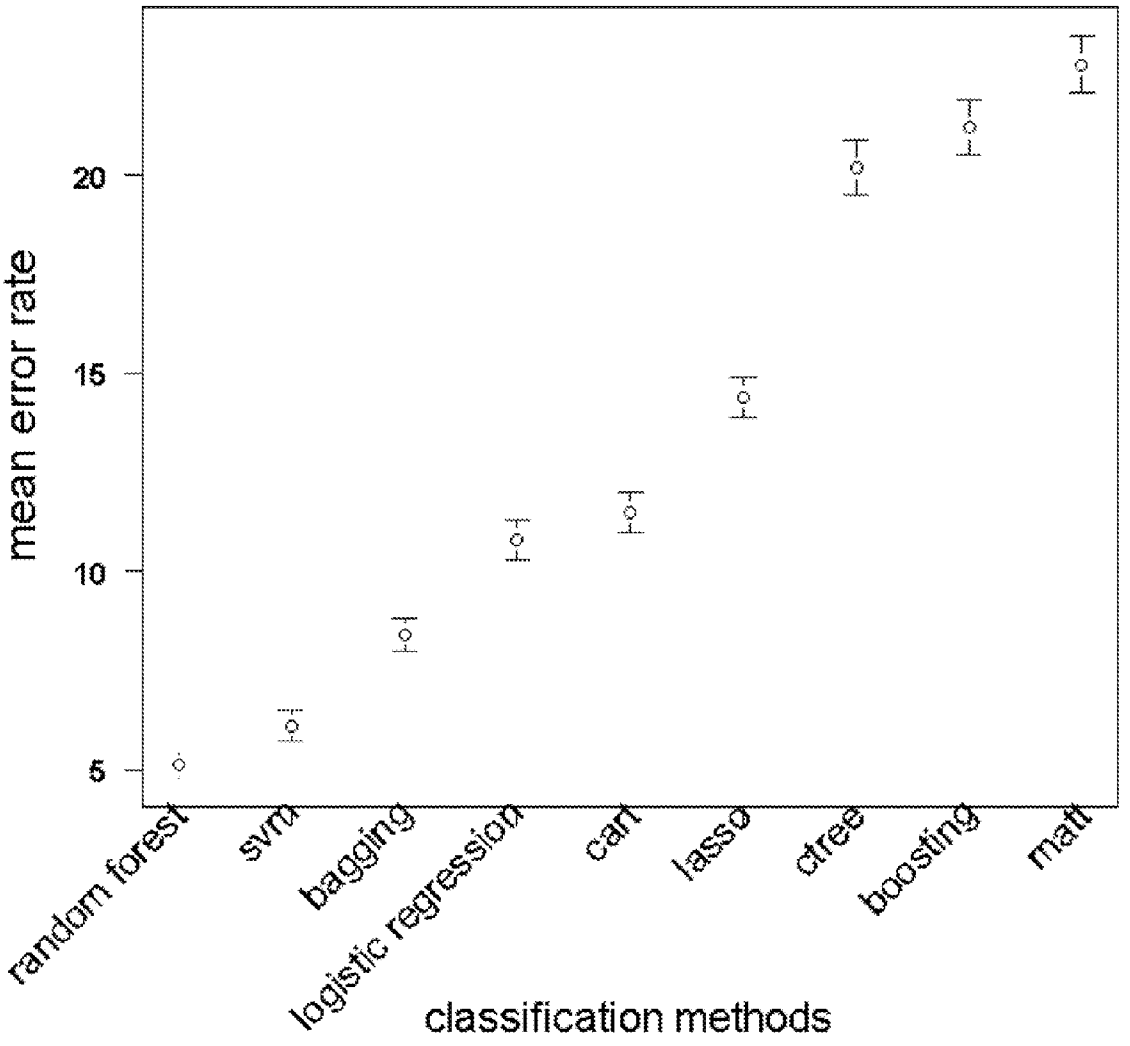
mean error rate
5
10
15
20
random forest
svm
bagging
logistic regression
cart
lasso
ctree
boosting
matl
classification methods

FIG. 6B

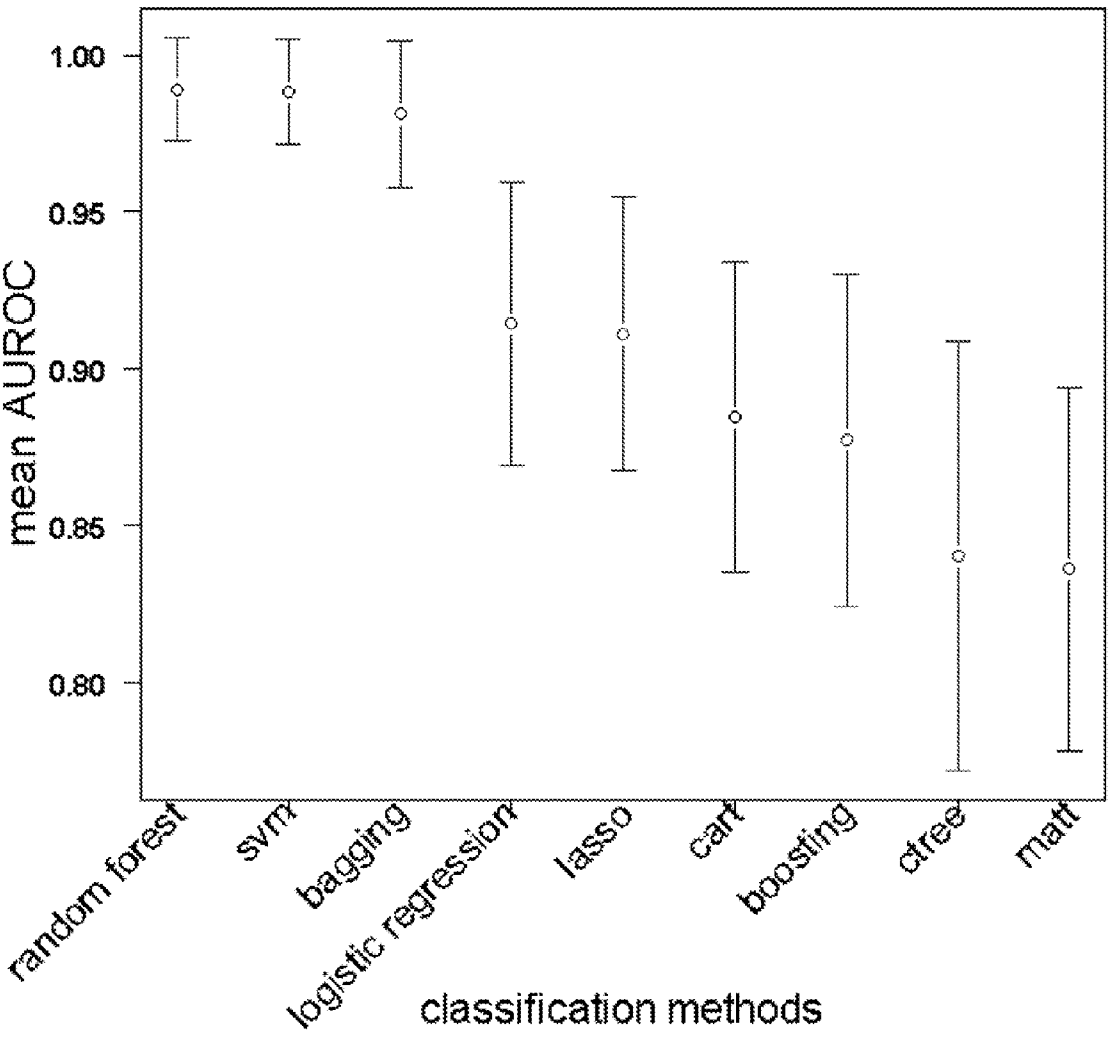
1.00
0.95
0.90
0.85
0.80
mean AUROC
random forest
svm
bagging
logistic regression
lasso
cart
boosting
ctree
matt
classification methods

FIG. 6C

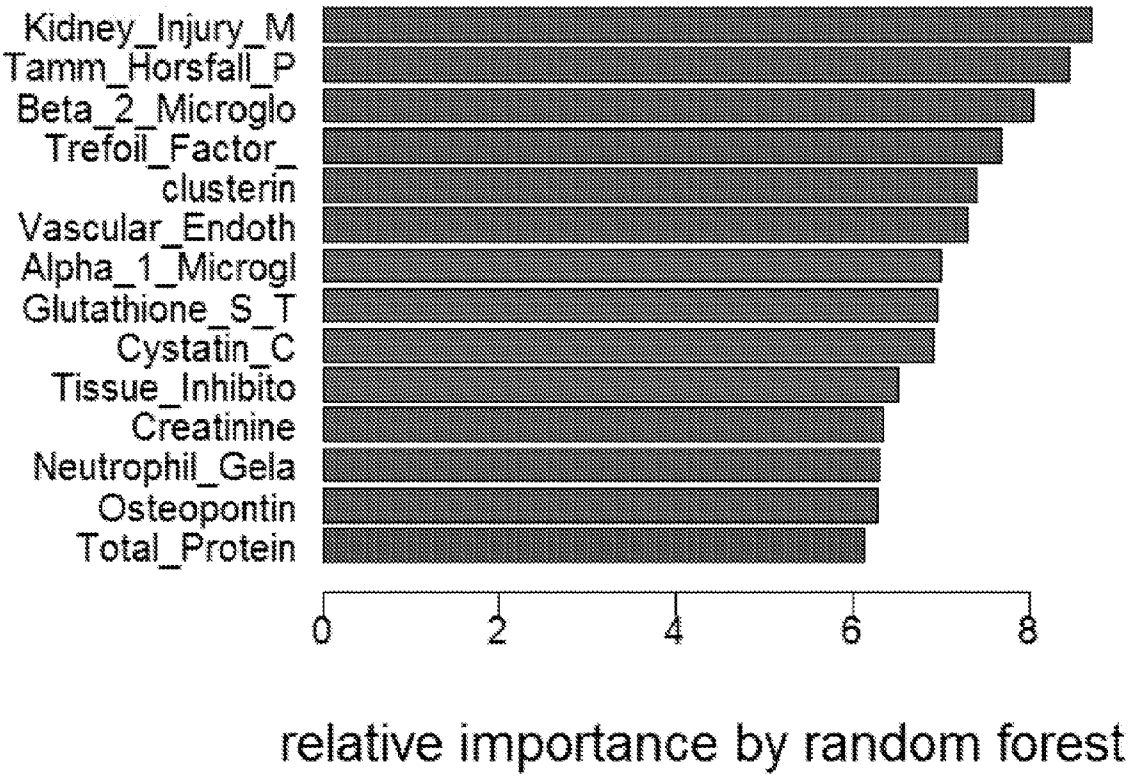
Kidney_Injury_M
Tamm_Horsfall_P
Beta_2_Microglo
Trefoil_Factor_
clusterin
Vascular_Endoth
Alpha_1_Microgl
Glutathione_S_T
Cystatin_C
Tissue_Inhibito
Creatinine
Neutrophil_Gela
Osteopontin
Total_Protein
0
2
4
6
8
relative importance by random forest

FIG. 7A

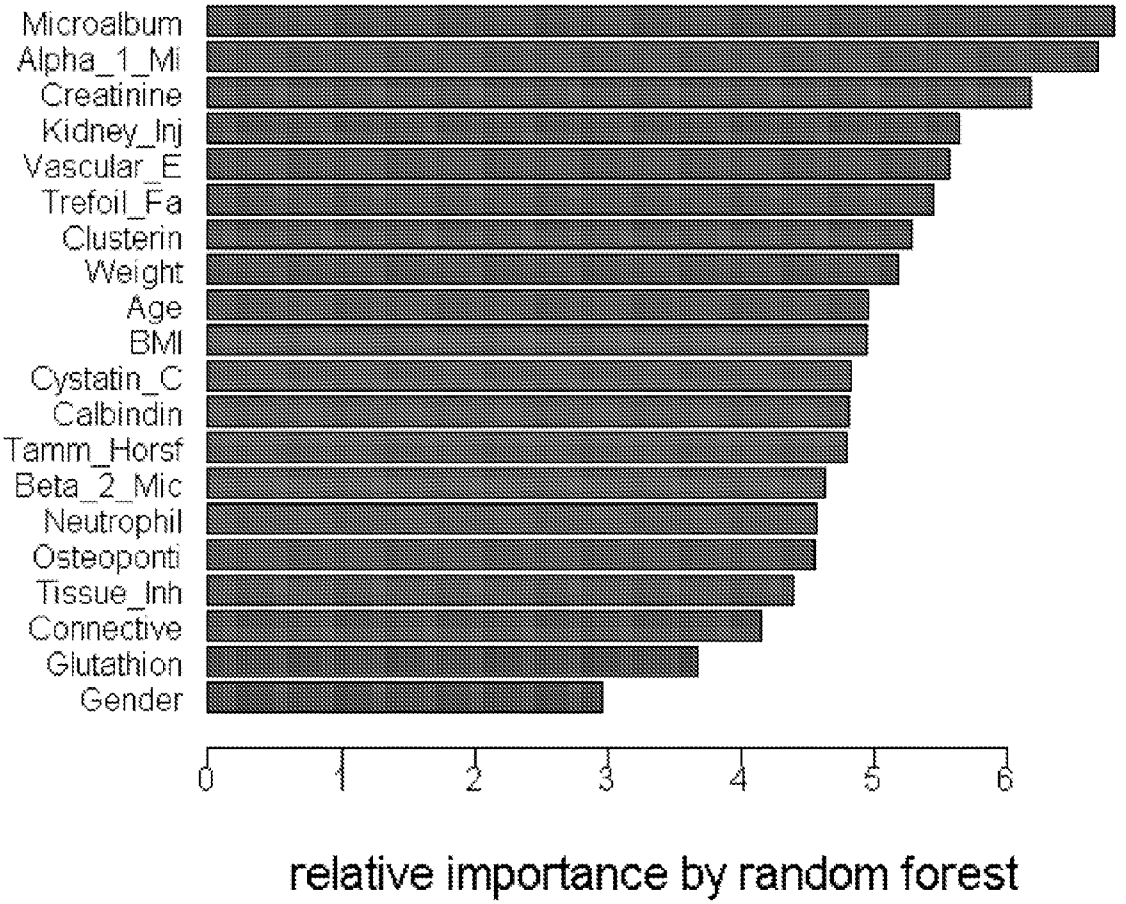
Microalbum
Alpha_1_Mi
Creatinine
Kidney_Inj
Vascular_E
Trefoil_Fa
Clusterin
Weight
Age
BMI
Cystatin_C
Calbindin
Tamm_Horsf
Beta_2_Mic
Neutrophil
Osteoponti
Tissue_Inh
Connective
Glutathion
Gender
0
1
2
3
4
5
6
relative importance by random forest

FIG. 7B

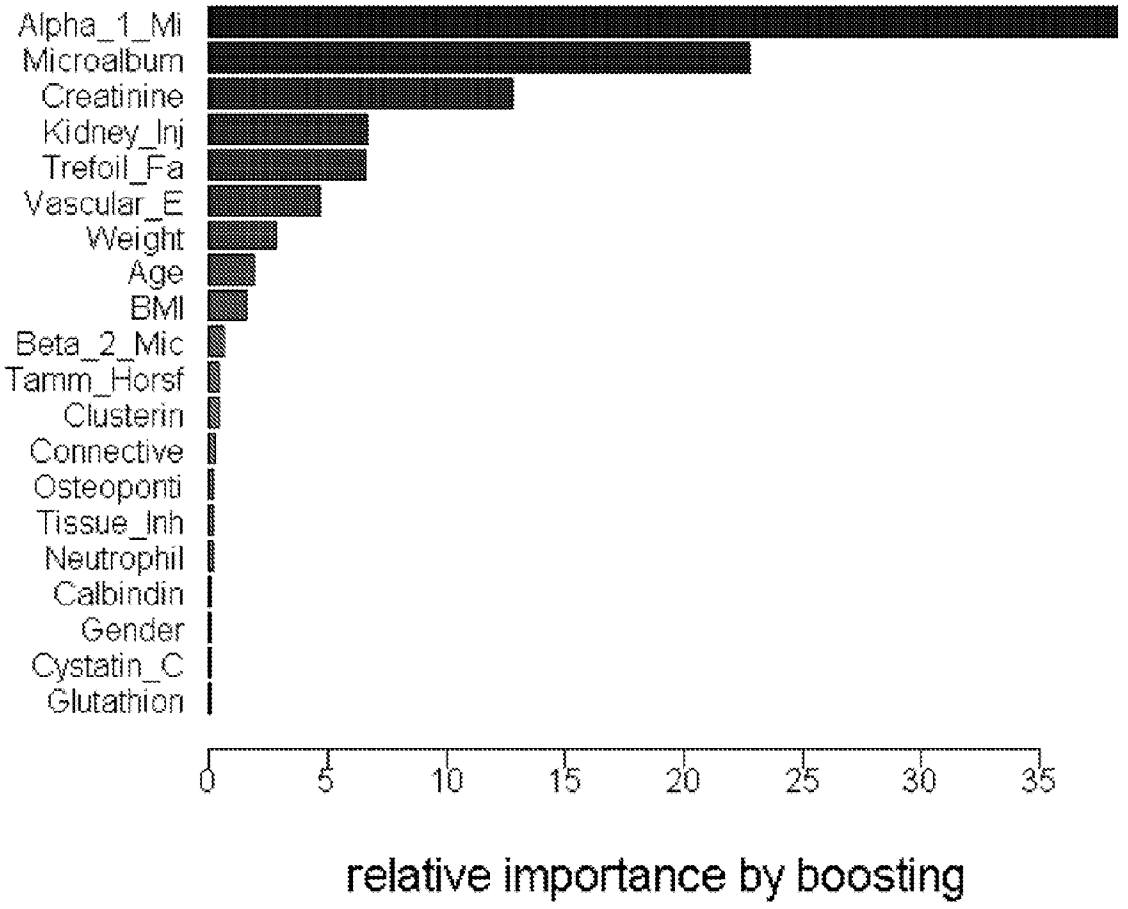
Alpha_1_Mi
Microalbum
Creatinine
Kidney_Inj
Trefoil_Fa
Vascular_E
Weight
Age
BMI
Beta_2_Mic
Tamm_Horsf
Clusterin
Connective
Osteoponti
Tissue_Inh
Neutrophil
Calbindin
Gender
Cystatin_C
Glutathion
0
5
10
15
20
25
30
35
relative importance by boosting

FIG. 7C

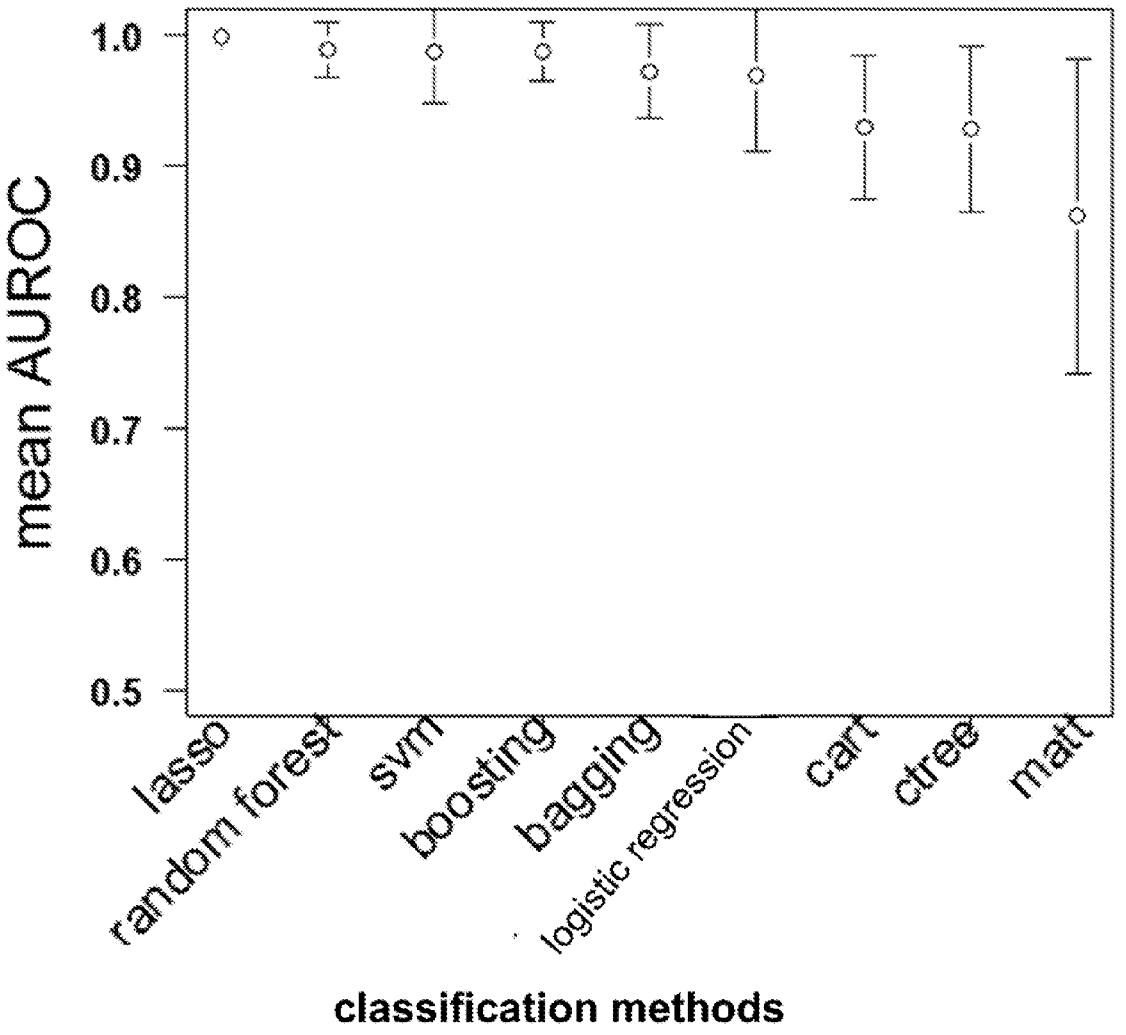
mean AUROC
1.0
0.9
0.8
0.7
0.6
0.5
lasso
random forest
svm
boosting
bagging
logistic regression
cart
ctree
matt
classification methods

FIG. 8A

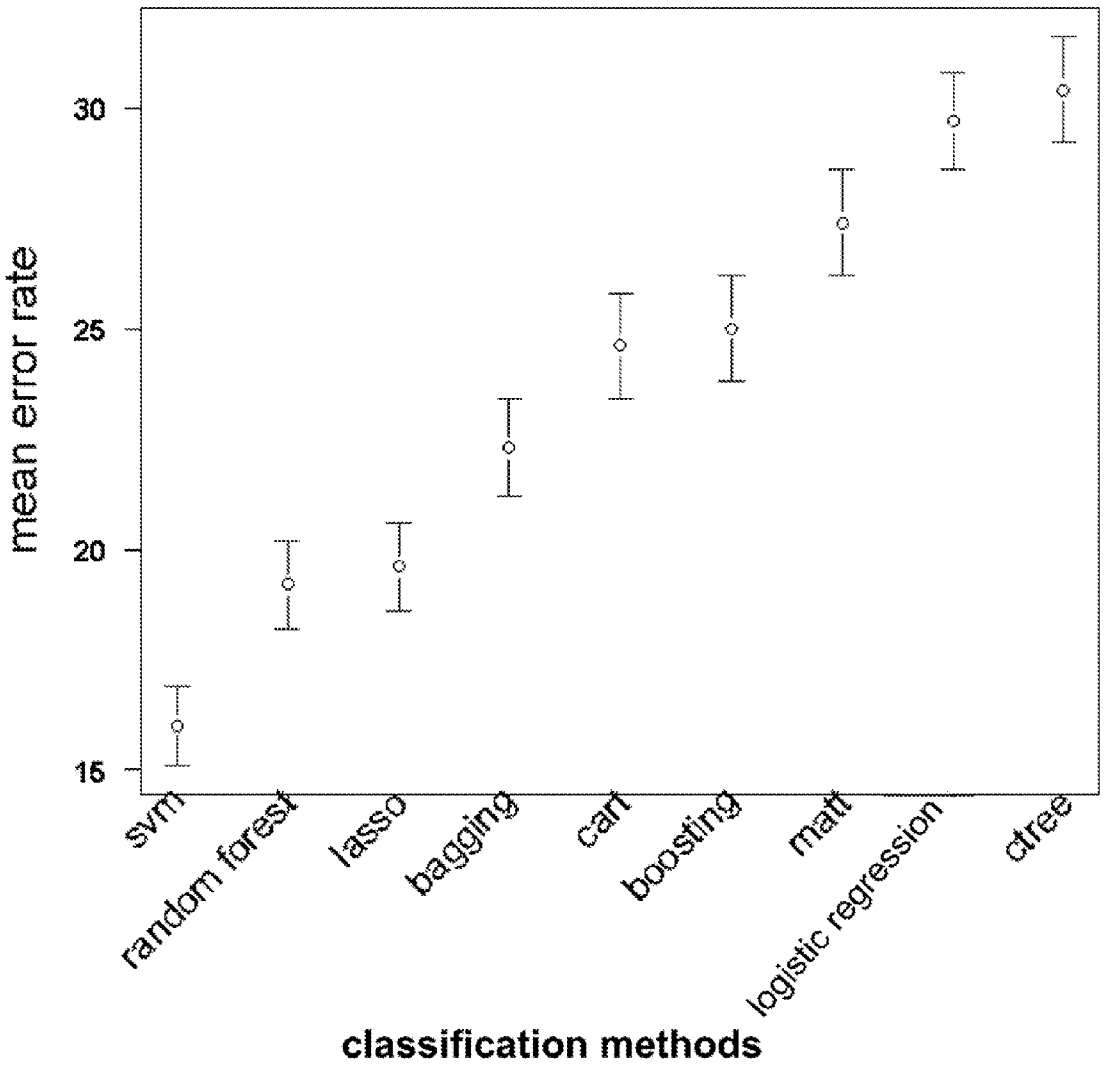
mean error rate
30
25
20
15
svm
random forest
lasso
bagging
cart
boosting
matt
logistic regression
ctree
classification methods

FIG. 8B

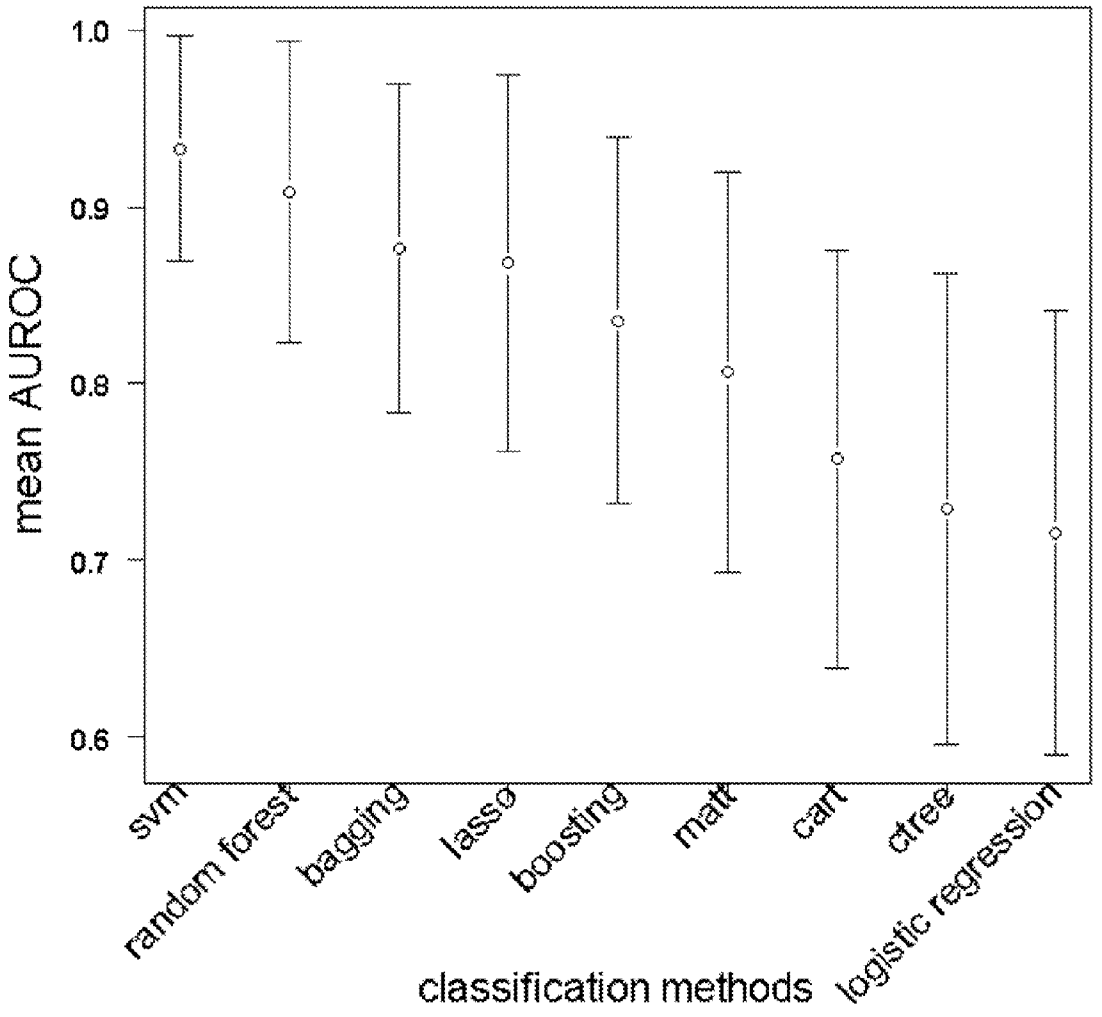
1.0
0.9
0.8
0.7
0.6
mean AUROC
svm
random forest
bagging
lasso
boosting
nnet
cart
ctree
logistic regression
classification methods

FIG. 8C

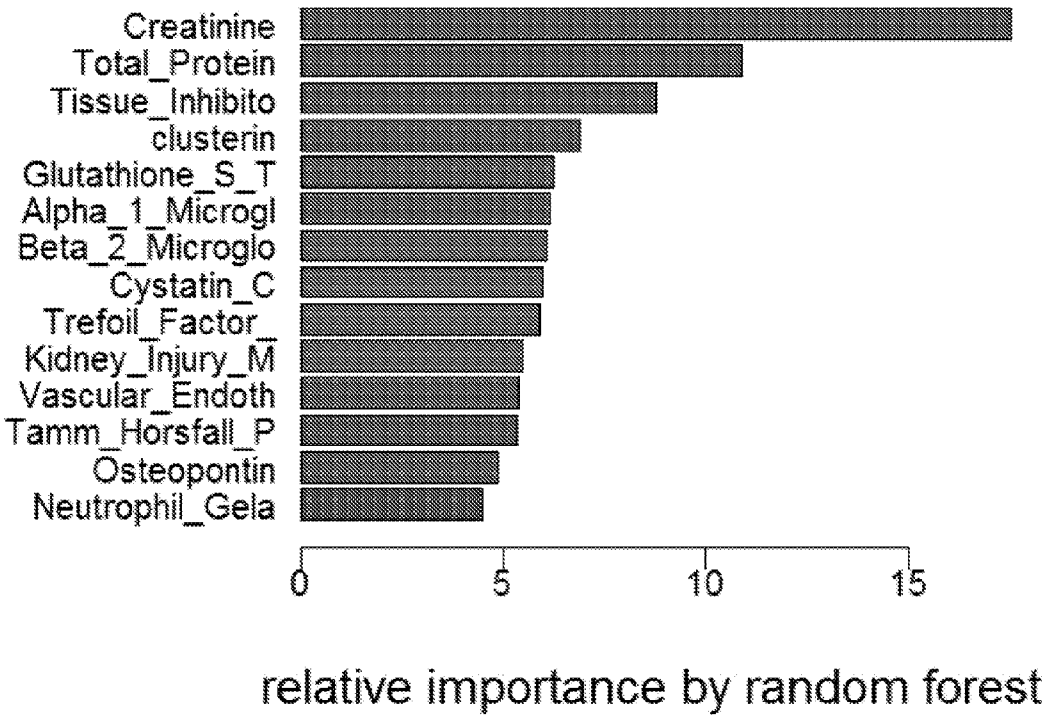
Creatinine
Total_Protein
Tissue_Inhibito
clusterin
Glutathione_S_T
Alpha_1_Microgl
Beta_2_Microglo
Cystatin_C
Trefoil_Factor_
Kidney_Injury_M
Vascular_Endoth
Tamm_Horsfall_P
Osteopontin
Neutrophil_Gela
0
5
10
15
relative importance by random forest

FIG. 9A

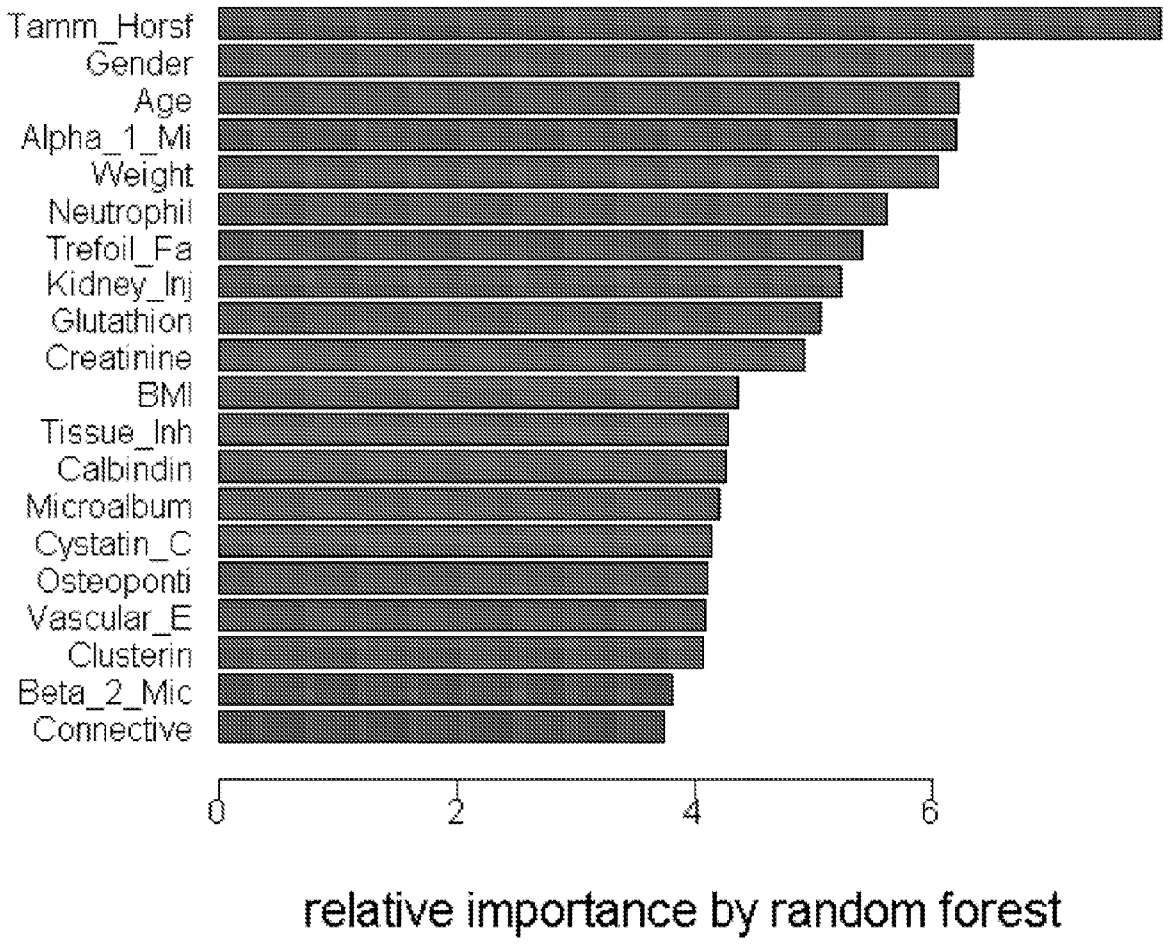
Tamm_Horsf
Gender
Age
Alpha_1_Mi
Weight
Neutrophil
Trefoil_Fa
Kidney_Inj
Glutathion
Creatinine
BMI
Tissue_Inh
Calbindin
Microalbum
Cystatin_C
Osteoponti
Vascular_E
Clusterin
Beta_2_Mic
Connective
0
2
4
6
relative importance by random forest

FIG. 9B

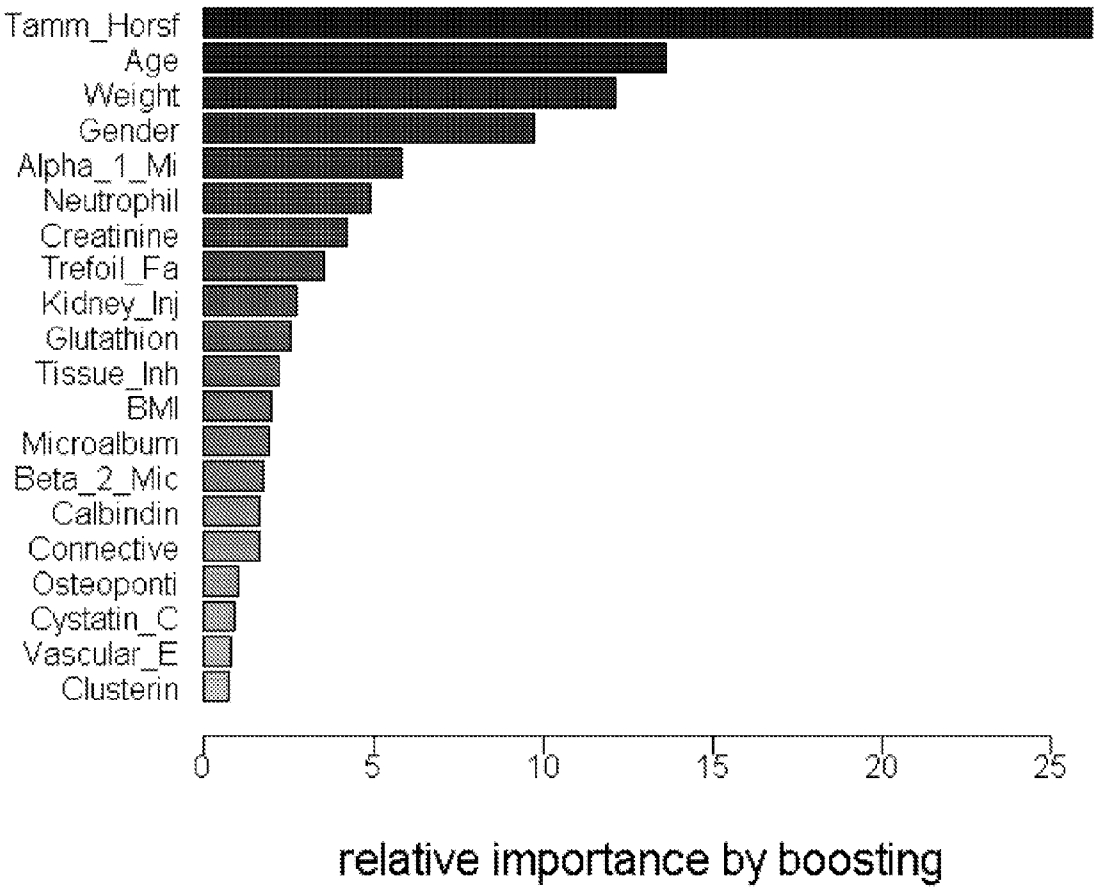
Tamm_Horsf
Age
Weight
Gender
Alpha_1_Mi
Neutrophil
Creatinine
Trefoil_Fa
Kidney_Inj
Glutathion
Tissue_Inh
BMI
Microalbum
Beta_2_Mic
Calbindin
Connective
Osteoponti
Cystatin_C
Vascular_E
Clusterin
0
5
10
15
20
25
relative importance by boosting

FIG. 9C

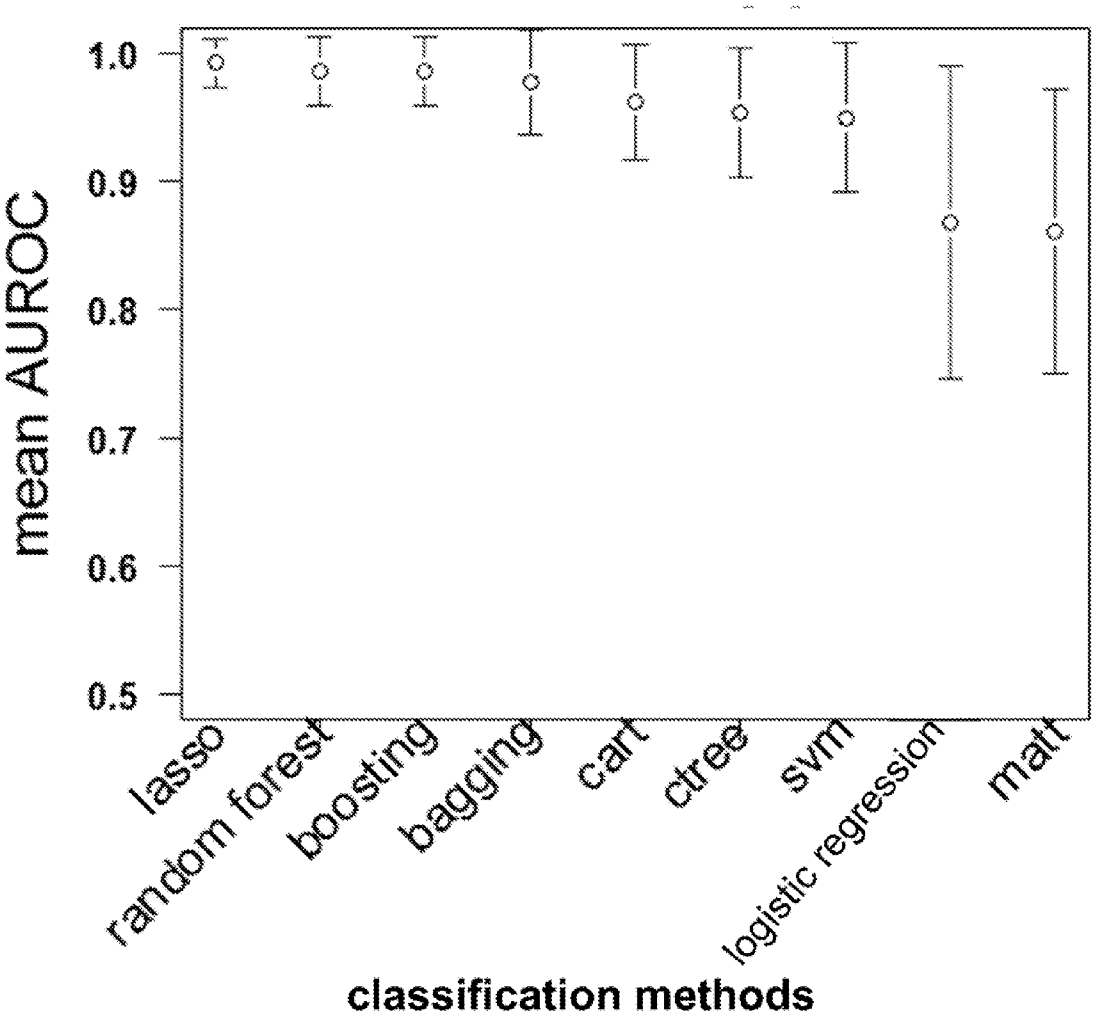
mean AUROC
1.0
0.9
0.8
0.7
0.6
0.5
lasso
random forest
boosting
bagging
cart
ctree
svm
logistic regression
matt
classification methods

FIG. 10A

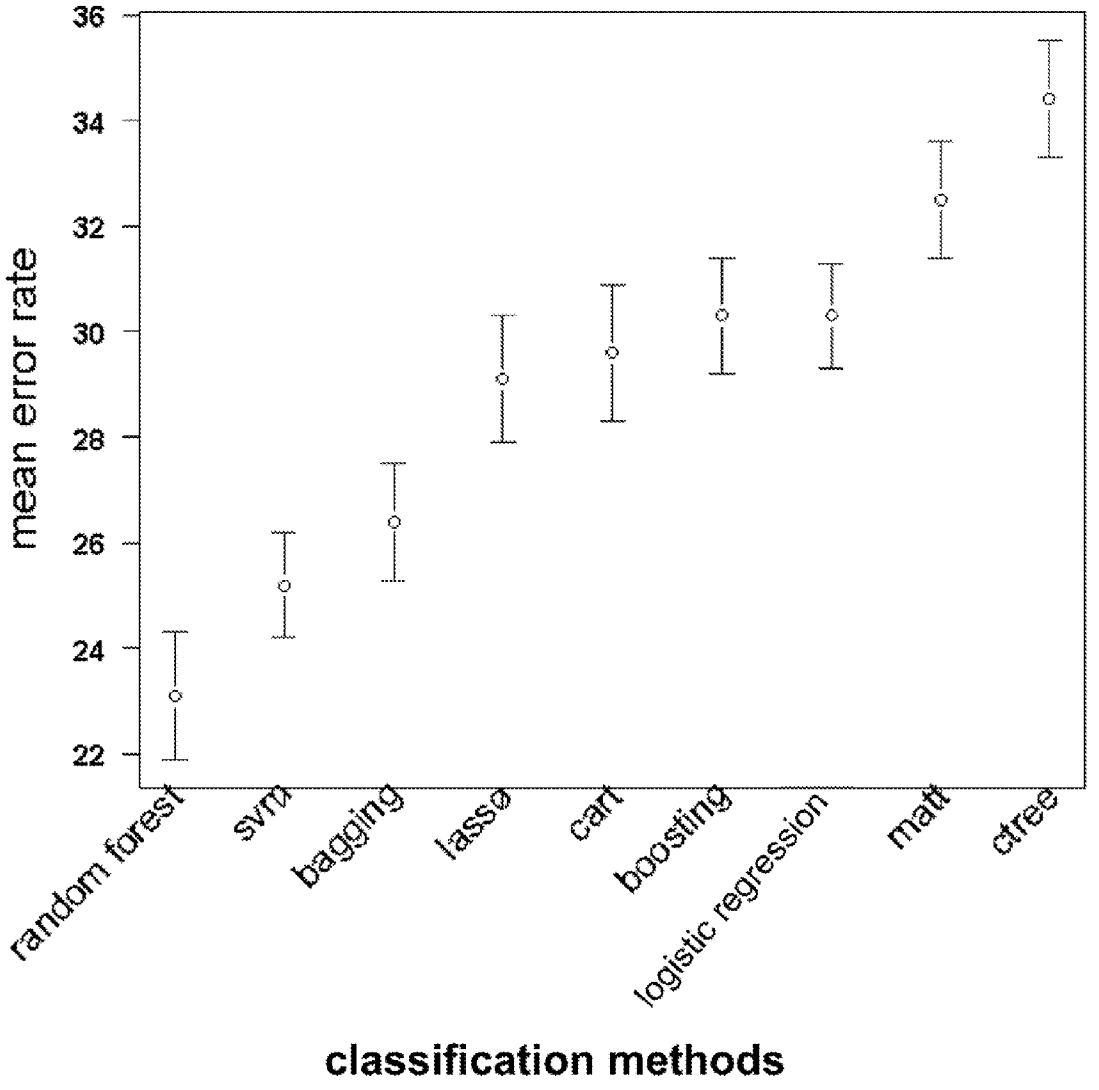
36
34
32
30
28
26
24
22
mean error rate
random forest
svm
bagging
lasso
cart
boosting
logistic regression
matt
ctree
classification methods

FIG. 10B

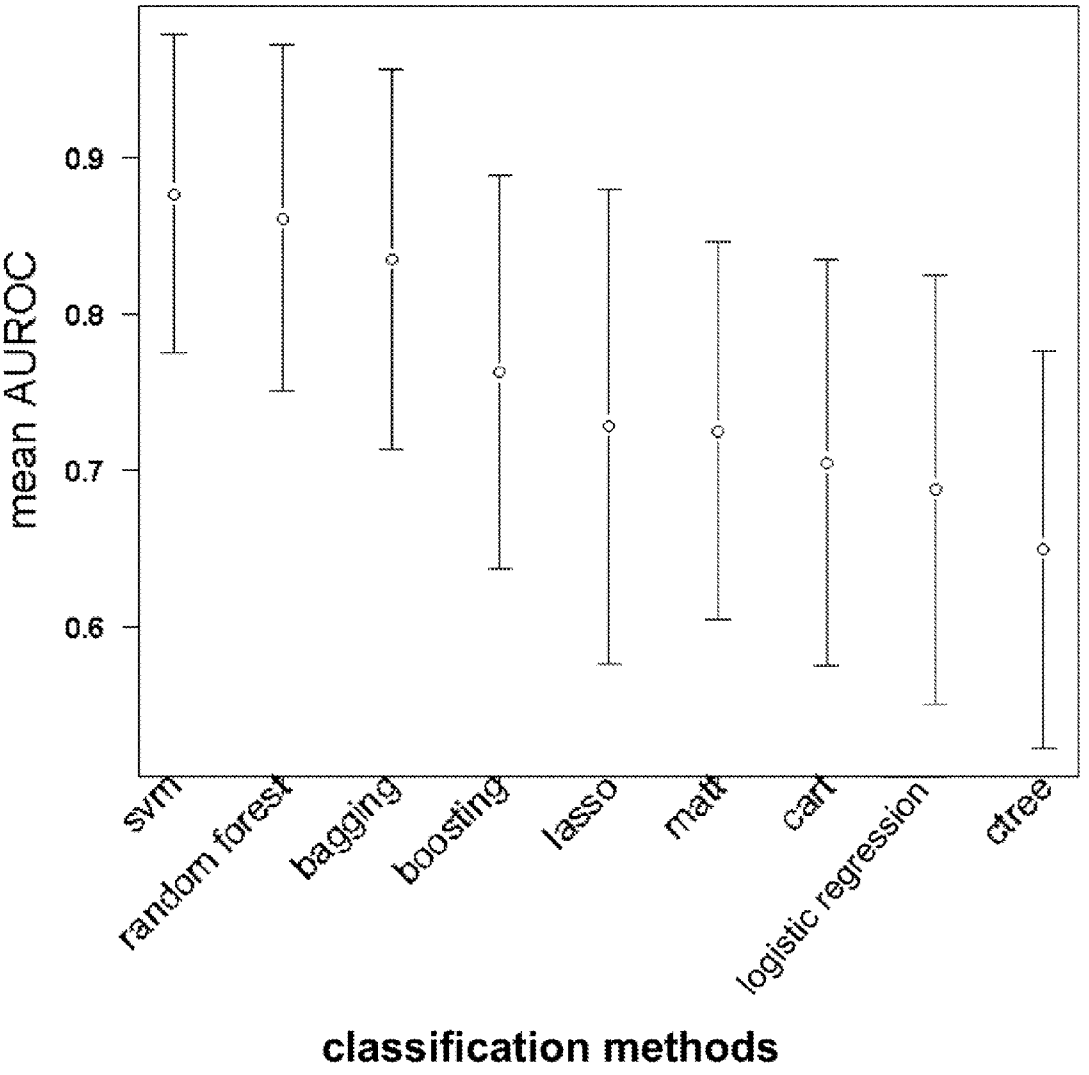
mean AUROC
0.9
0.8
0.7
0.6
svm
random forest
bagging
boosting
lasso
nnet
cart
logistic regression
ctree
classification methods

FIG. 10C

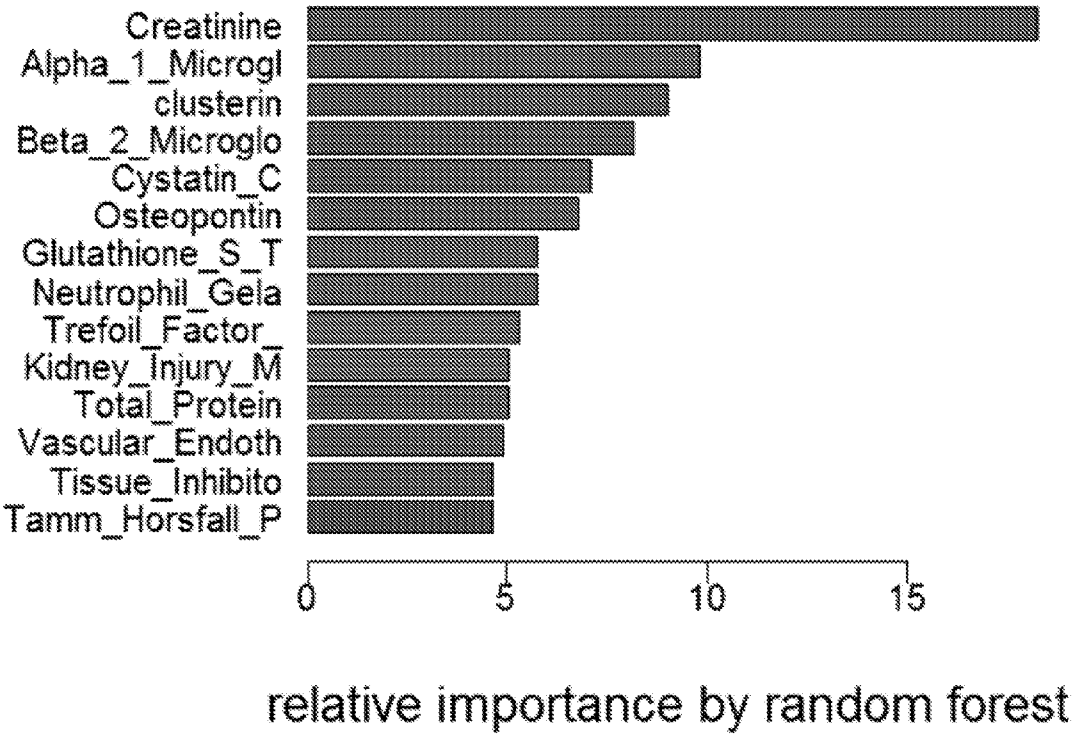
Creatinine
Alpha_1_Microgl
clusterin
Beta_2_Microglo
Cystatin_C
Osteopontin
Glutathione_S_T
Neutrophil_Gela
Trefoil_Factor_
Kidney_Injury_M
Total_Protein
Vascular_Endoth
Tissue_Inhibito
Tamm_Horsfall_P
0
5
10
15
relative importance by random forest

FIG. 11A

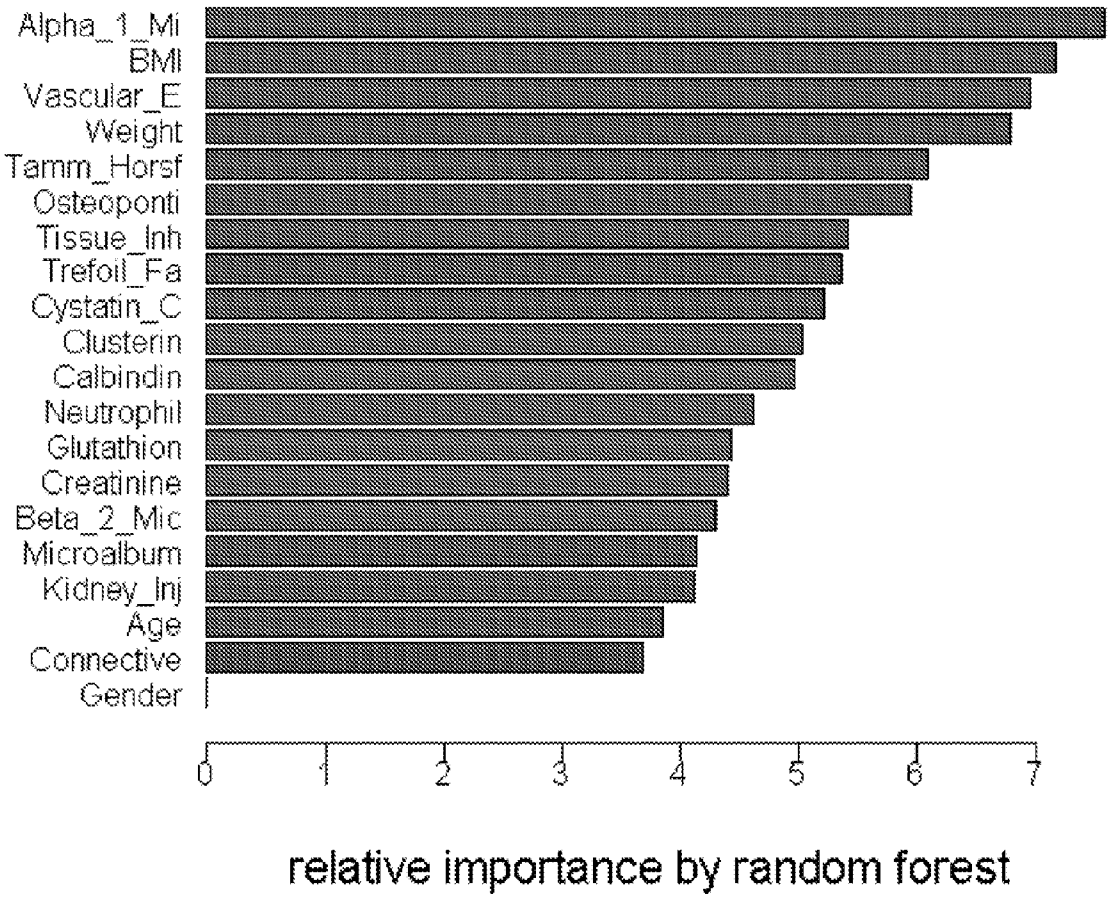
Alpha_1_Mi
BMI
Vascular_E
Weight
Tamm_Horsf
Osteoponti
Tissue_Inh
Trefoil_Fa
Cystatin_C
Clusterin
Calbindin
Neutrophil
Glutathion
Creatinine
Beta_2_Mic
Microalbum
Kidney_Inj
Age
Connective
Gender
0
1
2
3
4
5
6
7
relative importance by random forest

FIG. 11B

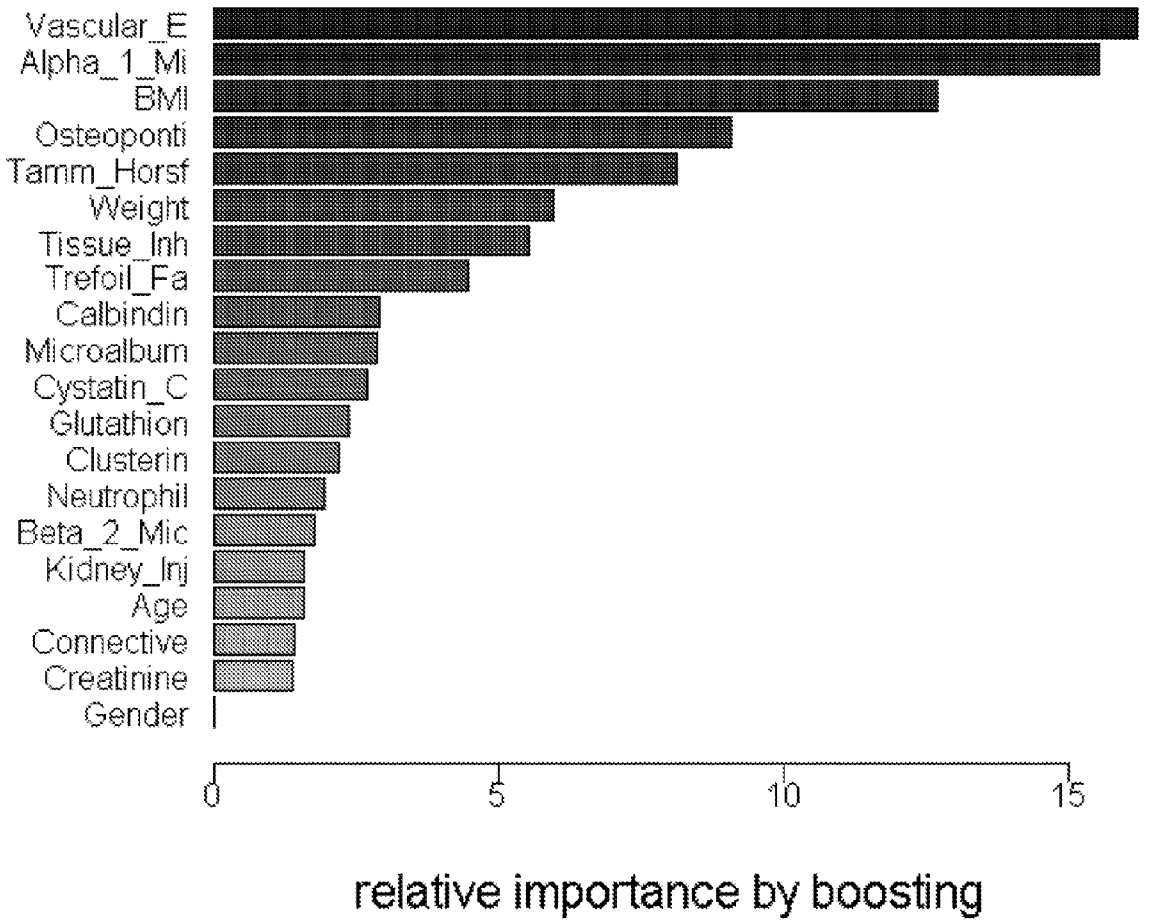
Vascular_E
Alpha_1_Mi
BMI
Osteoponti
Tamm_Horsf
Weight
Tissue_Inh
Trefoil_Fa
Calbindin
Microalbum
Cystatin_C
Glutathion
Clusterin
Neutrophil
Beta_2_Mic
Kidney_Inj
Age
Connective
Creatinine
Gender
0
5
10
15
relative importance by boosting

FIG. 11C

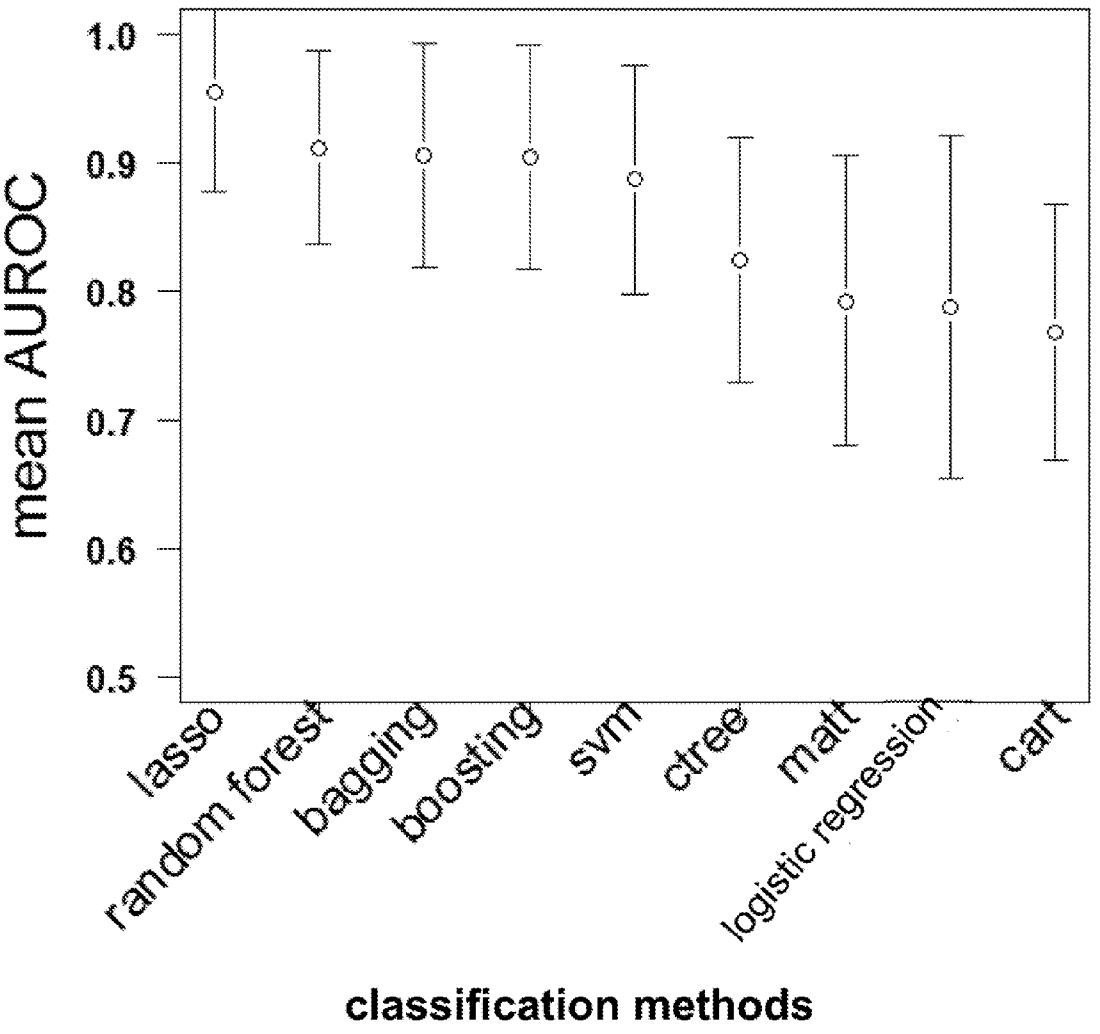
mean AUROC
1.0
0.9
0.8
0.7
0.6
0.5
lasso
random forest
bagging
boosting
svm
ctree
matt
logistic regression
cart
classification methods

FIG. 12A

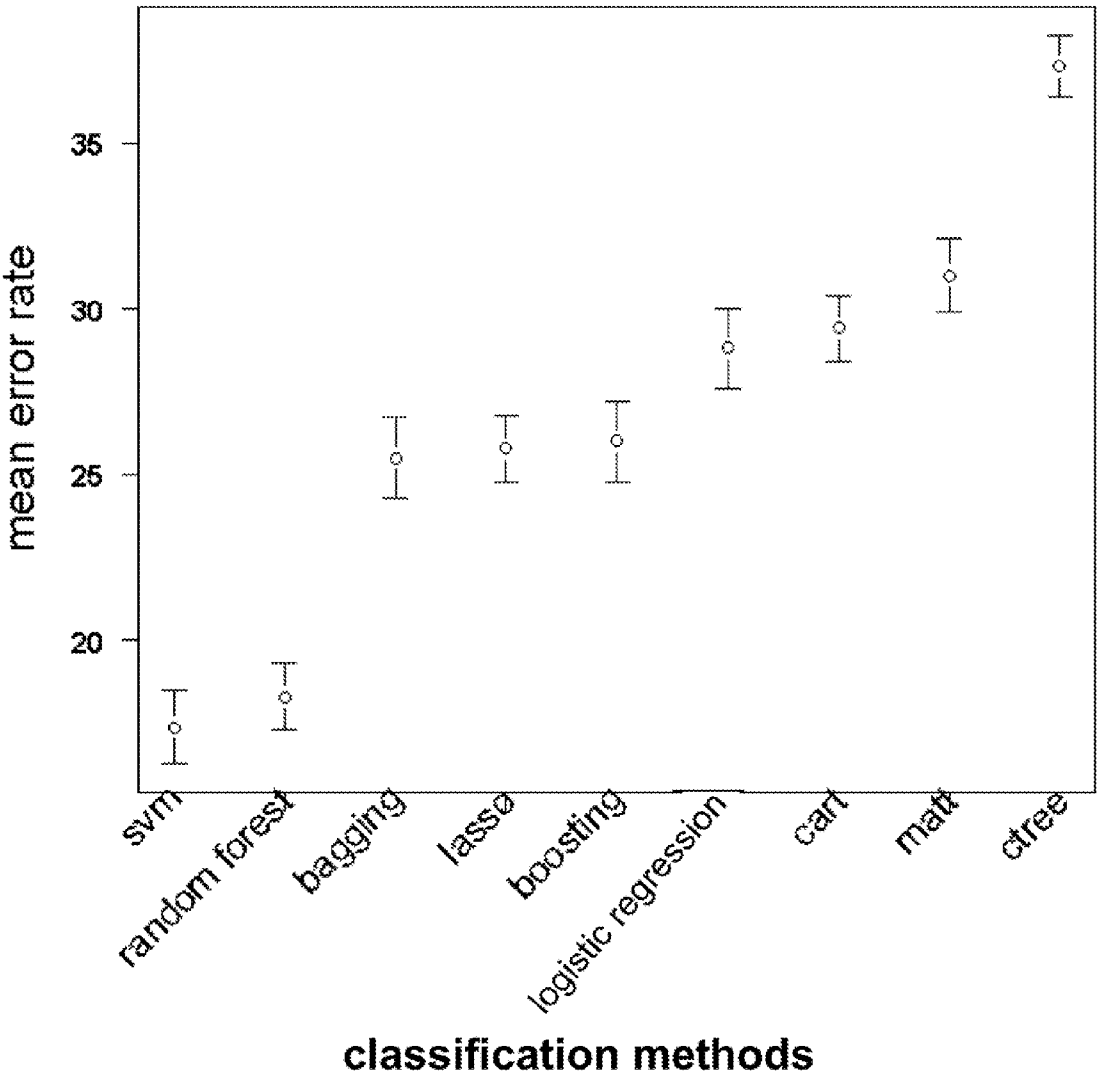
mean error rate
35
30
25
20
svm
random forest
bagging
lasso
boosting
logistic regression
cart
mart
ctree
classification methods

FIG. 12B

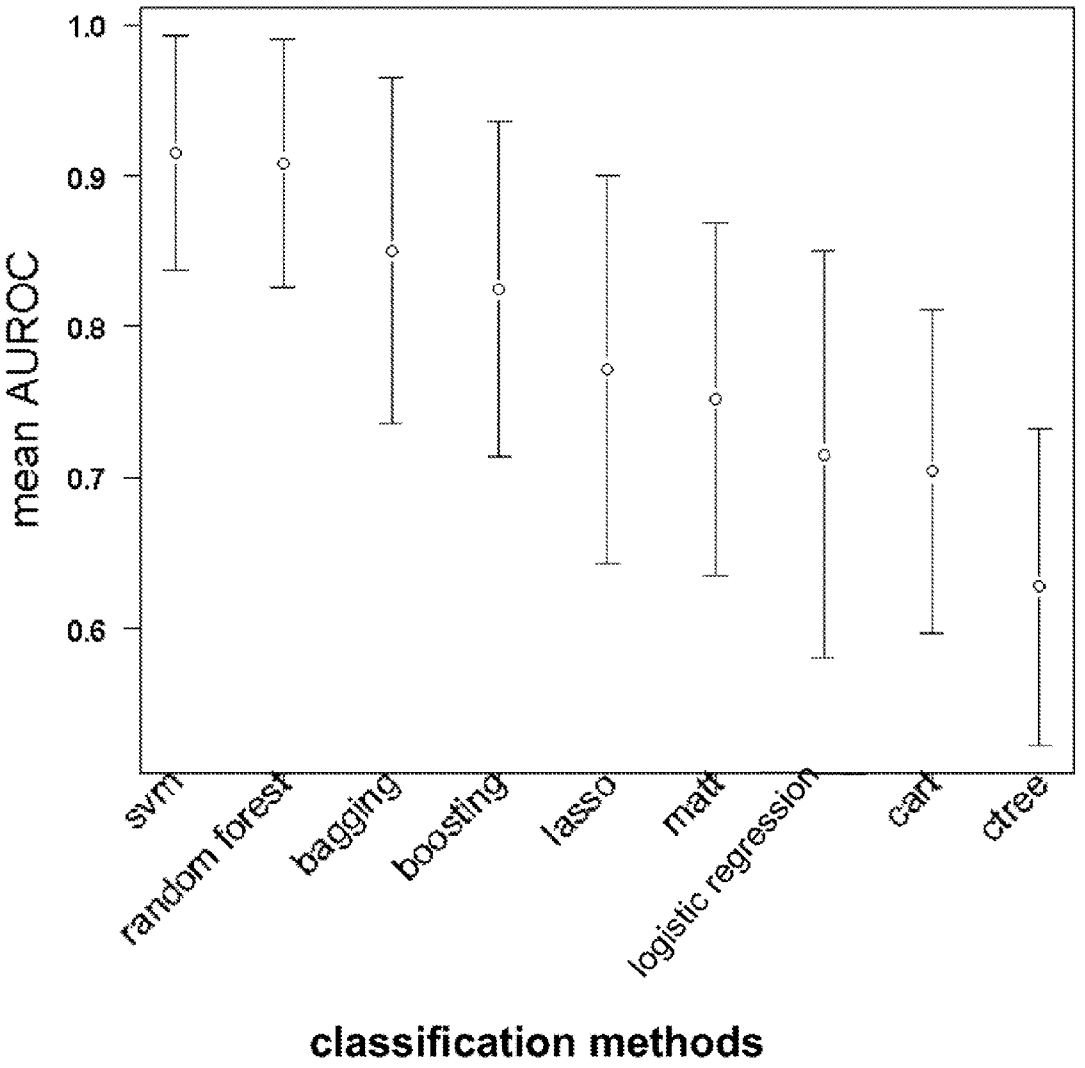
1.0
0.9
0.8
0.7
0.6
mean AUROC
svm
random forest
bagging
boosting
lasso
matt
logistic regression
cart
ctree
classification methods

FIG. 12C

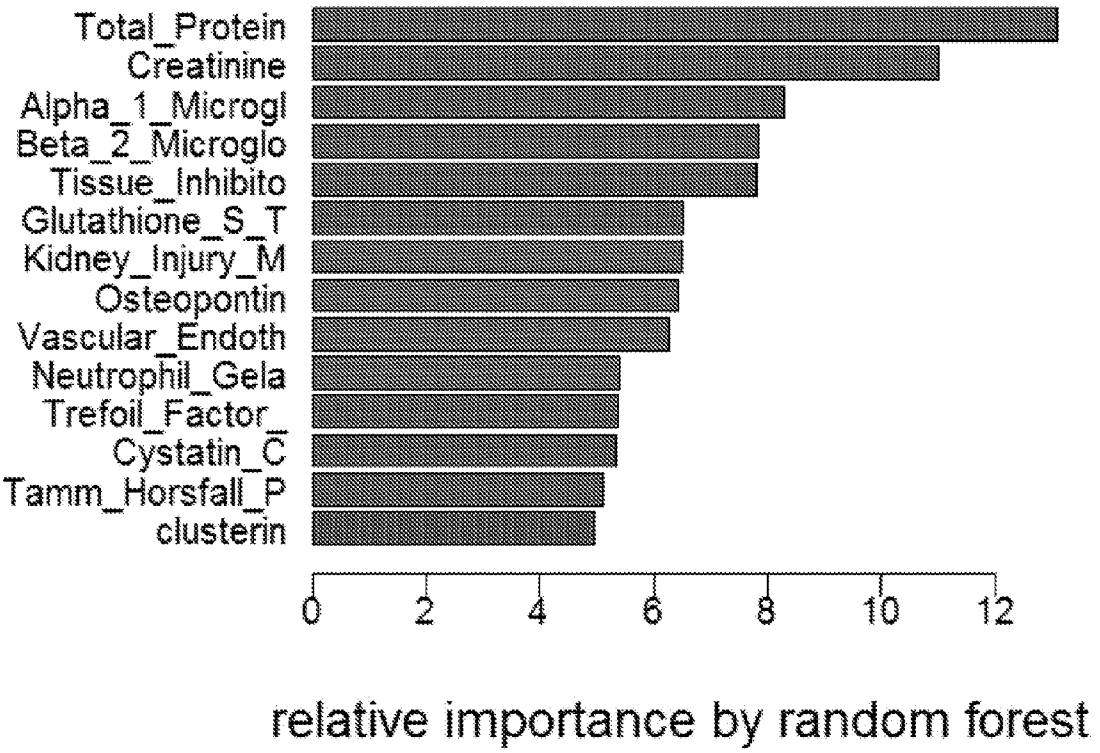
Total_Protein
Creatinine
Alpha_1_Microgl
Beta_2_Microglo
Tissue_Inhibito
Glutathione_S_T
Kidney_Injury_M
Osteopontin
Vascular_Endoth
Neutrophil_Gela
Trefoil_Factor_
Cystatin_C
Tamm_Horsfall_P
clusterin
0
2
4
6
8
10
12
relative importance by random forest

FIG. 13A

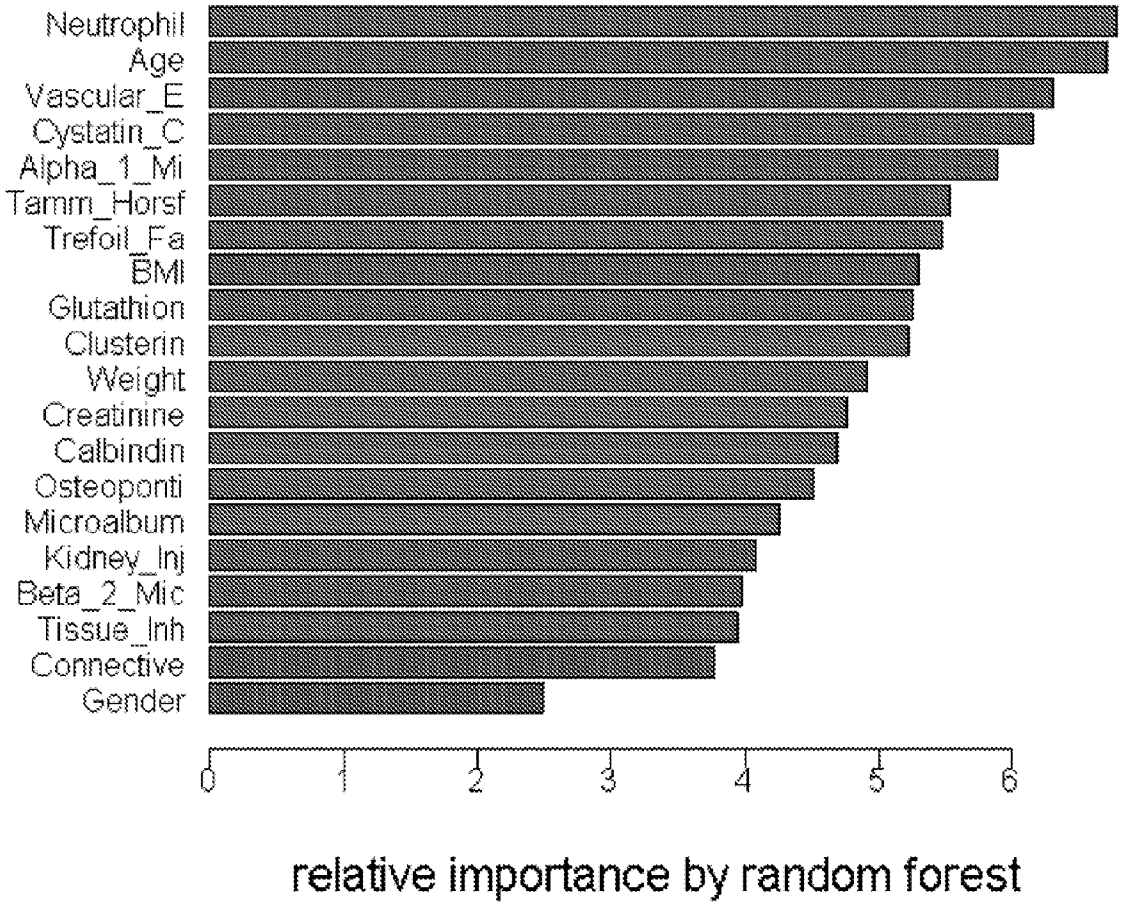
Neutrophil
Age
Vascular_E
Cystatin_C
Alpha_1_Mi
Tamm_Horsf
Trefoil_Fa
BMI
Glutathion
Clusterin
Weight
Creatinine
Calbindin
Osteoponti
Microalbum
Kidney_Inj
Beta_2_Mic
Tissue_Inh
Connective
Gender
0
1
2
3
4
5
6
relative importance by random forest

FIG. 13B

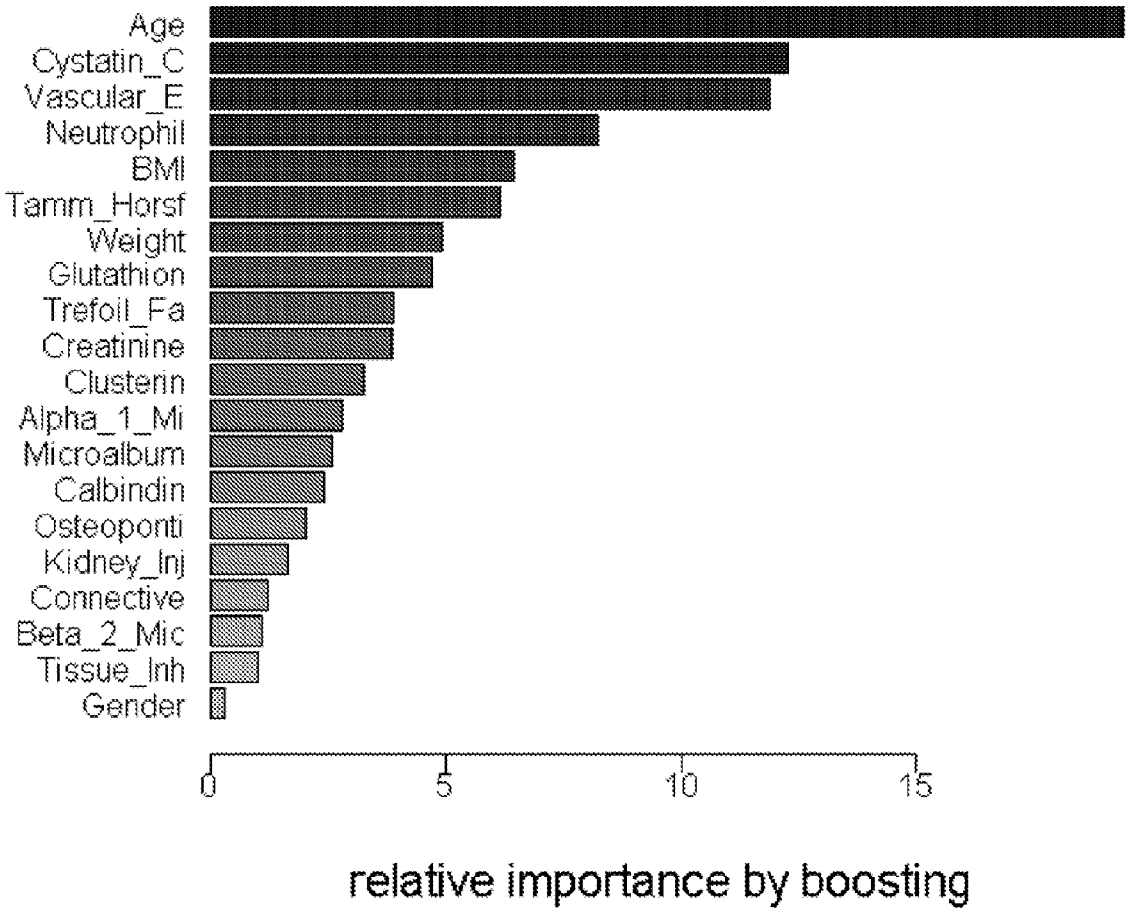
Age
Cystatin_C
Vascular_E
Neutrophil
BMI
Tamm_Horsf
Weight
Glutathion
Trefoil_Fa
Creatinine
Clusterin
Alpha_1_Mi
Microalbum
Calbindin
Osteoponti
Kidney_Inj
Connective
Beta_2_Mic
Tissue_Inh
Gender
0
5
10
15
relative importance by boosting

FIG. 13C

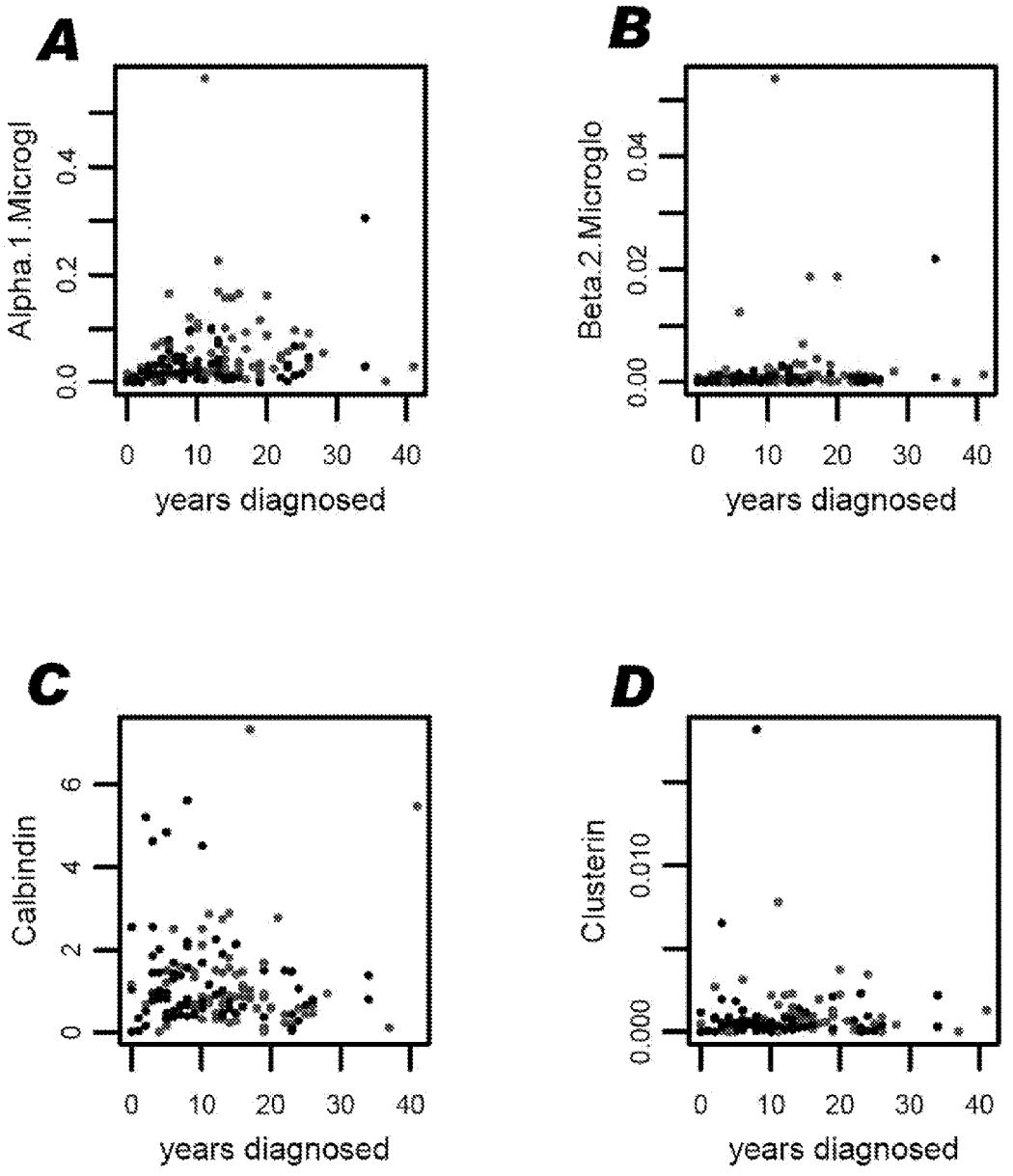
A
Alpha.1.Microgl
0.0
0.2
0.4
0
10
20
30
40
years diagnosed
B
Beta.2.Microglo
0.00
0.02
0.04
0
10
20
30
40
years diagnosed
C
Calbindin
0
2
4
6
0
10
20
30
40
years diagnosed
D
Clusterin
0.000
0.010
0
10
20
30
40
years diagnosed

FIG. 14

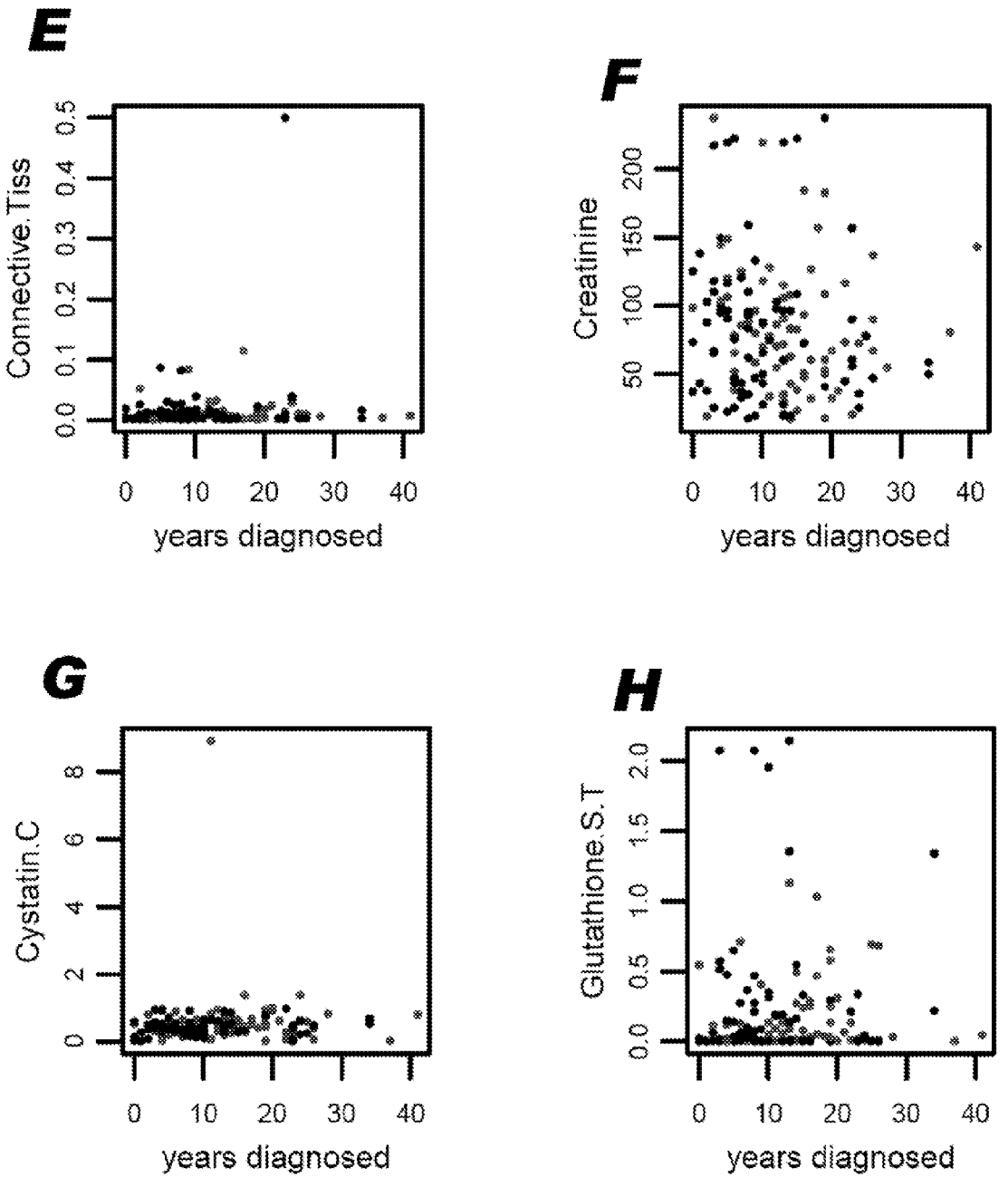
E
Connective.Tiss
0.0
0.1
0.2
0.3
0.4
0.5
0
10
20
30
40
years diagnosed
F
Creatinine
50
100
150
200
0
10
20
30
40
years diagnosed
G
Cystatin.C
0
2
4
6
8
0
10
20
30
40
years diagnosed
H
Glutathione.S.T
0.0
0.5
1.0
1.5
2.0
0
10
20
30
40
years diagnosed

FIG. 14

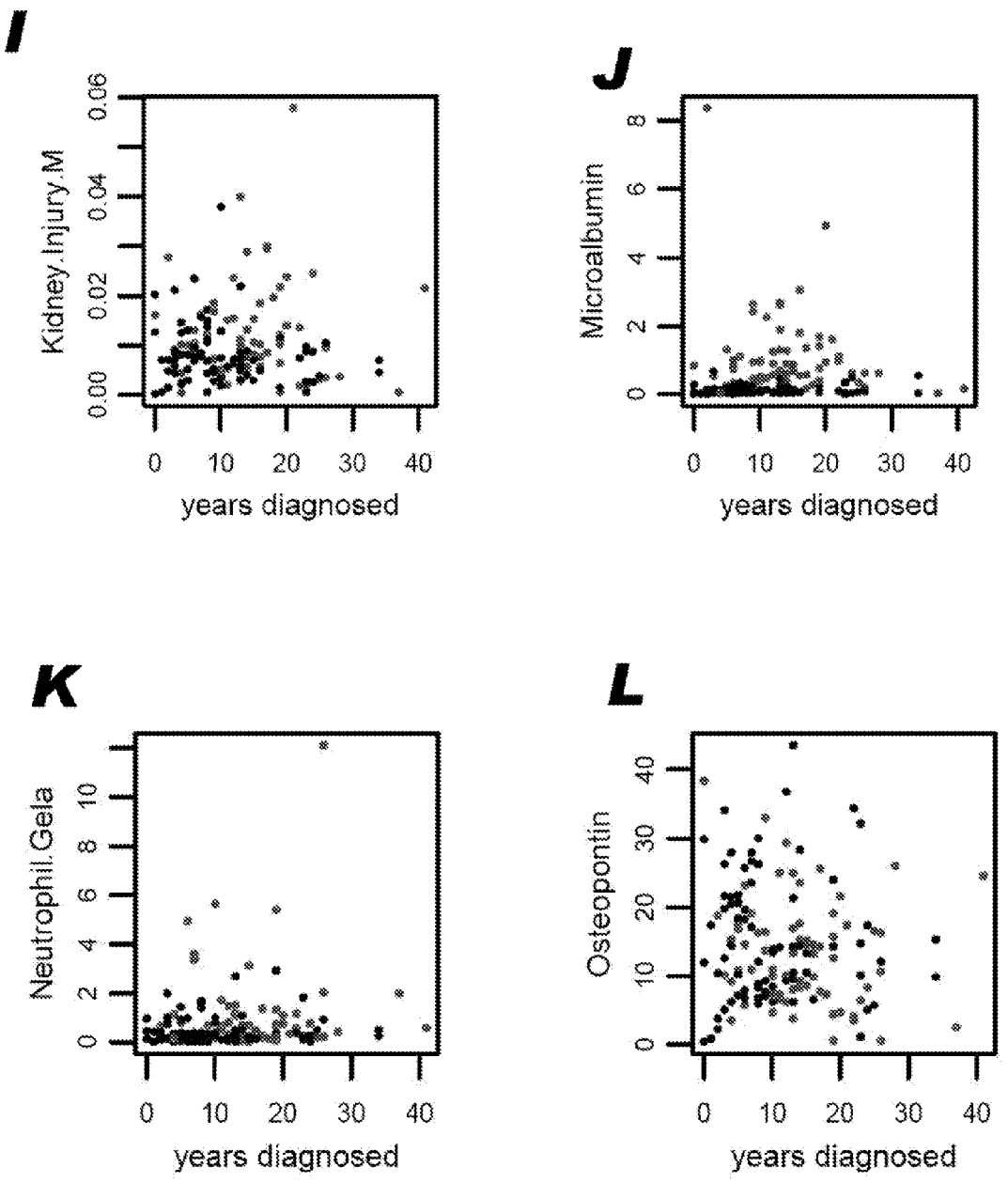
I
Kidney.Injury.M
0.00
0.02
0.04
0.06
0
10
20
30
40
years diagnosed
J
Microalbumin
0
2
4
6
8
0
10
20
30
40
years diagnosed
K
Neutrophil.Gela
0
2
4
6
8
10
0
10
20
30
40
years diagnosed
L
Osteopontin
0
10
20
30
40
0
10
20
30
40
years diagnosed

FIG. 14

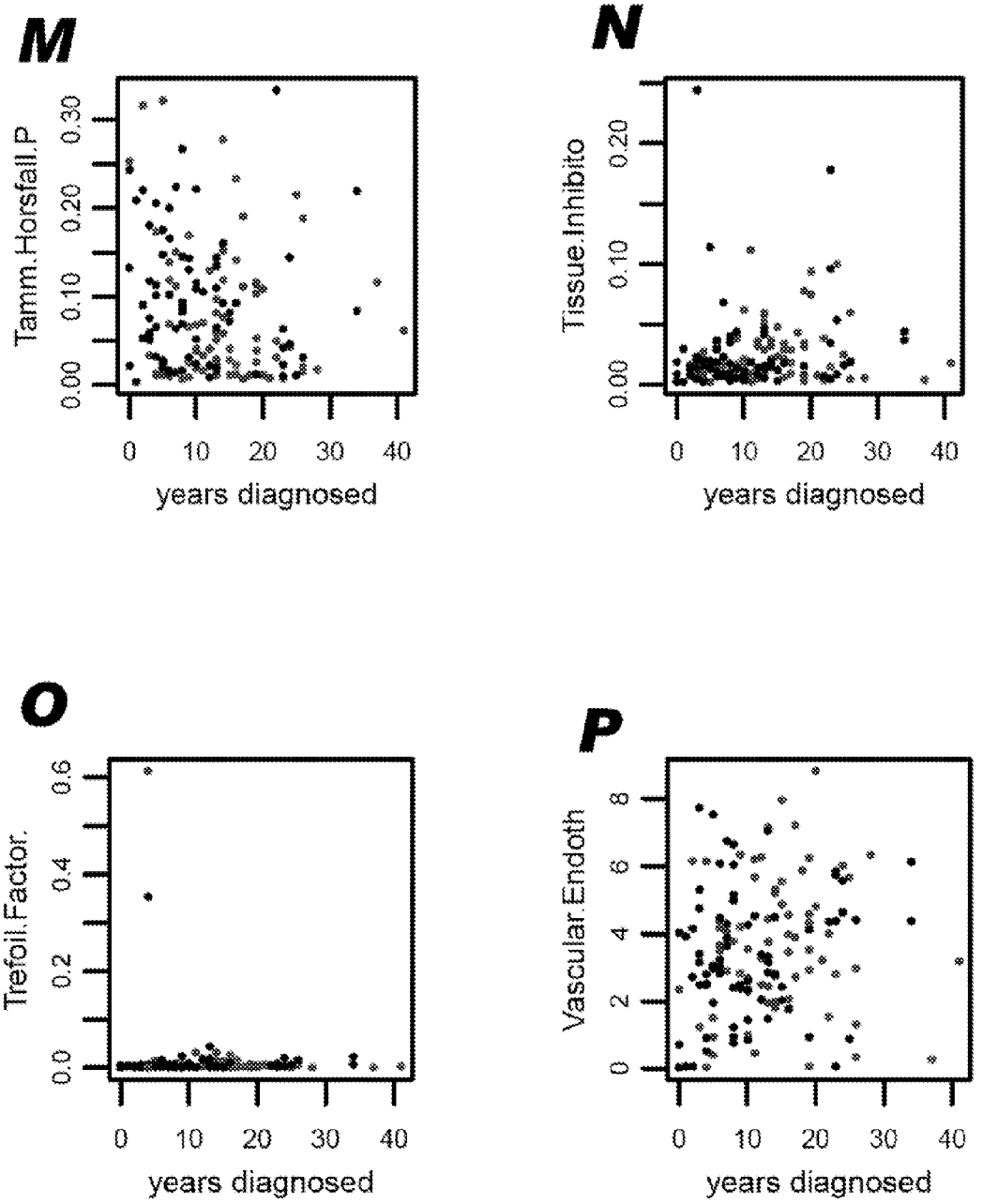
M
Tamm.Horsfall.P
0.00
0.10
0.20
0.30
0
10
20
30
40
years diagnosed
N
Tissue.Inhibito
0.00
0.10
0.20
0
10
20
30
40
years diagnosed
O
Trefoil.Factor.
0.0
0.2
0.4
0.6
0
10
20
30
40
years diagnosed
P
Vascular.Endoth
0
2
4
6
8
0
10
20
30
40
years diagnosed

FIG. 14

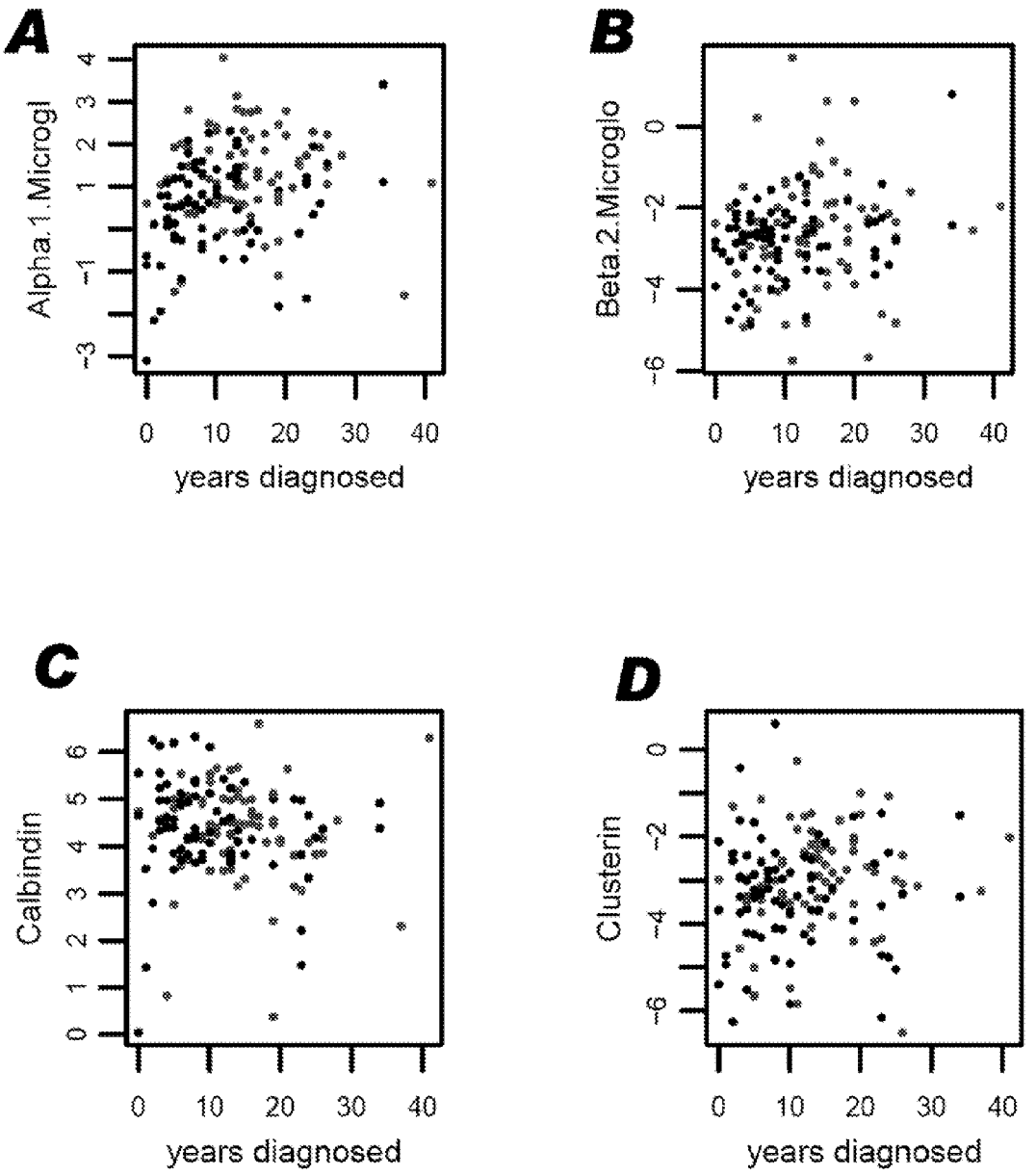
A
Alpha.1.Microgl
-3
-1
1
2
3
4
0
10
20
30
40
years diagnosed
B
Beta.2.Microglo
-6
-4
-2
0
0
10
20
30
40
years diagnosed
C
Calbindin
0
1
2
3
4
5
6
0
10
20
30
40
years diagnosed
D
Clusterin
-6
-4
-2
0
0
10
20
30
40
years diagnosed

FIG. 15

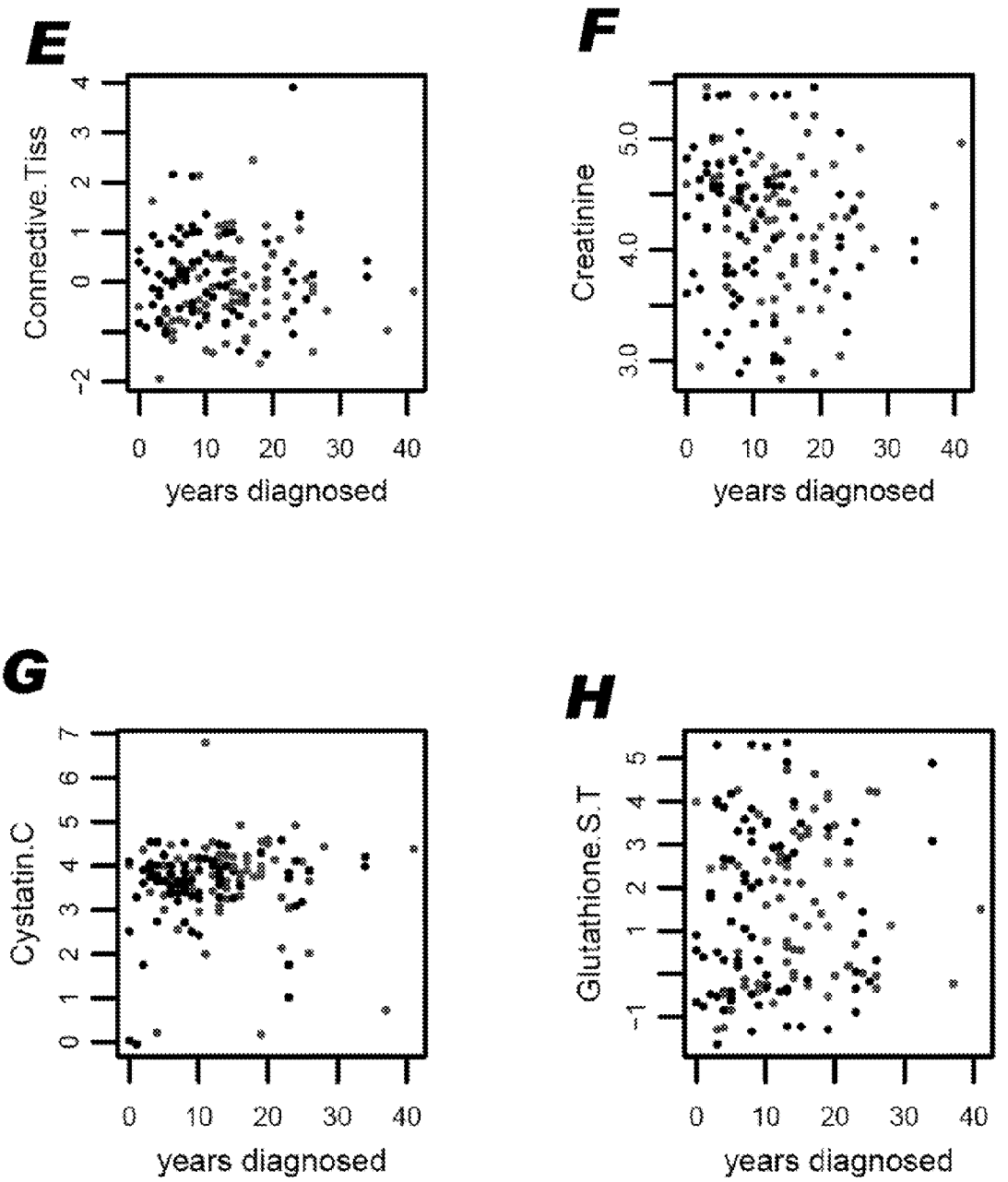
E
Connective.Tiss
-2
0
1
2
3
4
0
10
20
30
40
years diagnosed
F
Creatinine
3.0
4.0
5.0
0
10
20
30
40
years diagnosed
G
Cystatin.C
0
1
2
3
4
5
6
7
0
10
20
30
40
years diagnosed
H
Glutathione.S.T
-1
1
2
3
4
5
0
10
20
30
40
years diagnosed

FIG. 15

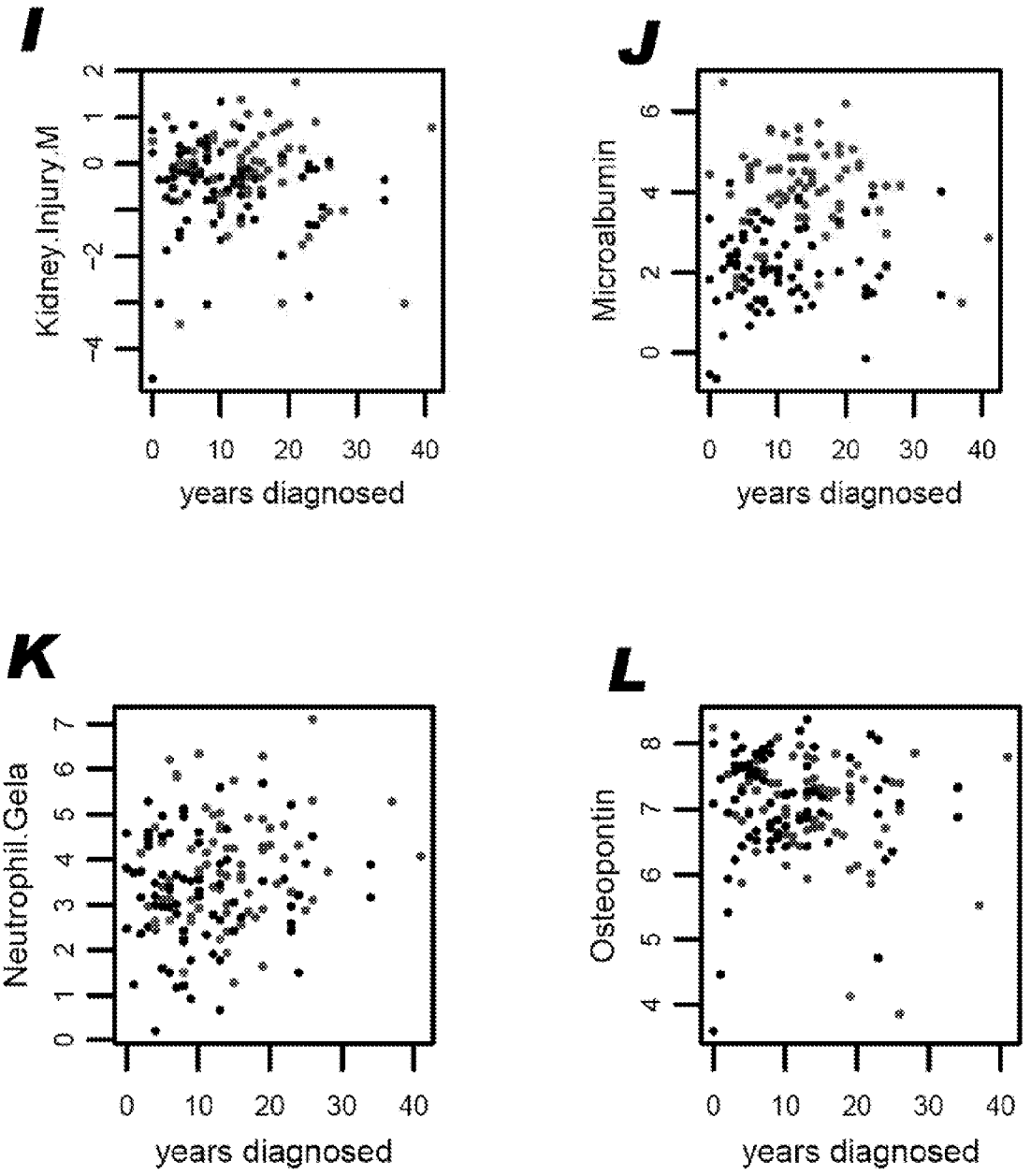
I
Kidney.Injury.M
years diagnosed
J
Microalbumin
years diagnosed
K
Neutrophil.Gela
years diagnosed
L
Osteopontin
years diagnosed

FIG. 15

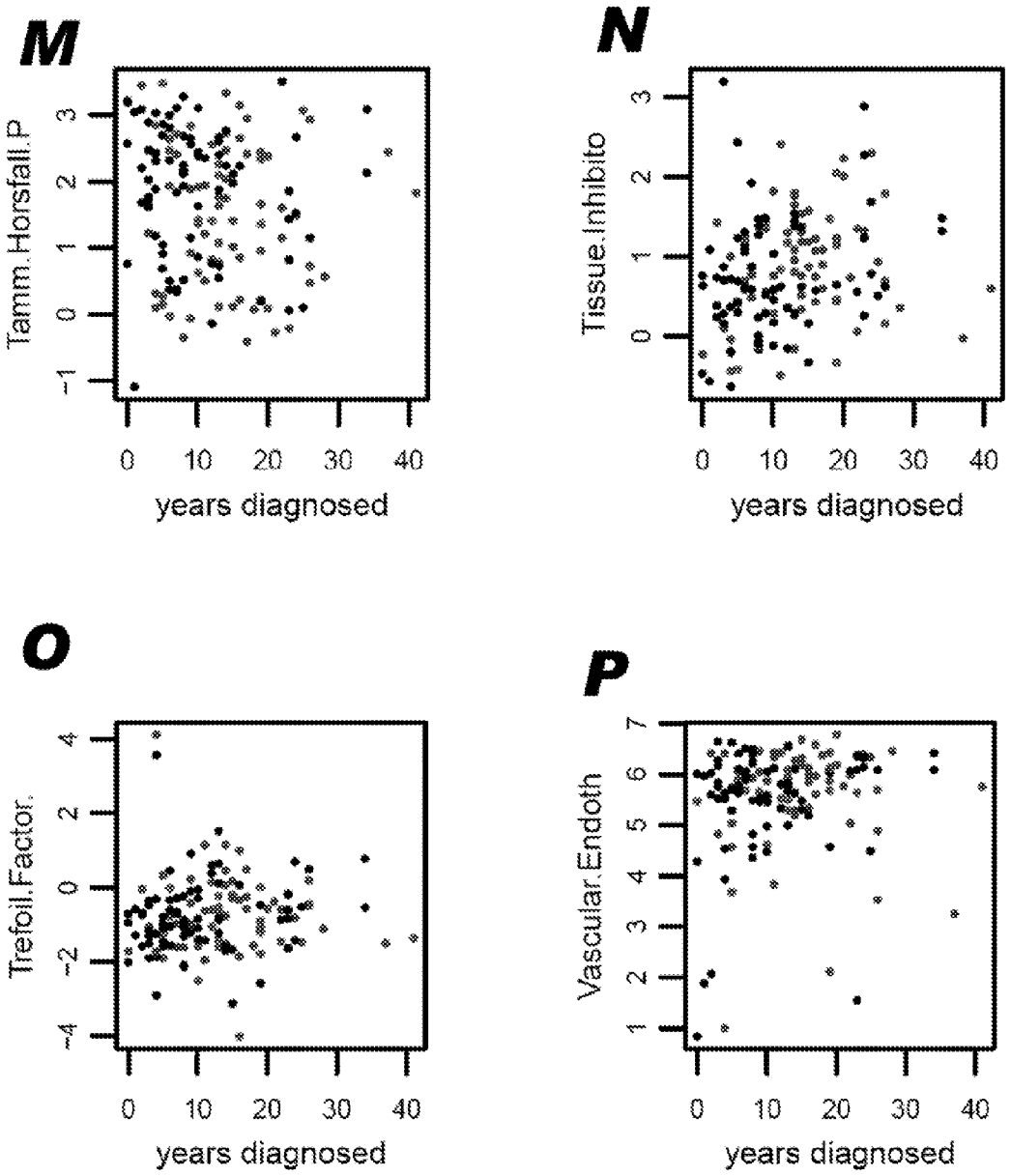
M
Tamm.Horsfall.P
−1
0
1
2
3
0
10
20
30
40
years diagnosed
N
Tissue.Inhibito
0
1
2
3
0
10
20
30
40
years diagnosed
O
Trefoil.Factor.
−4
−2
0
2
4
0
10
20
30
40
years diagnosed
P
Vascular.Endoth
1
2
3
4
5
6
7
0
10
20
30
40
years diagnosed

FIG. 15

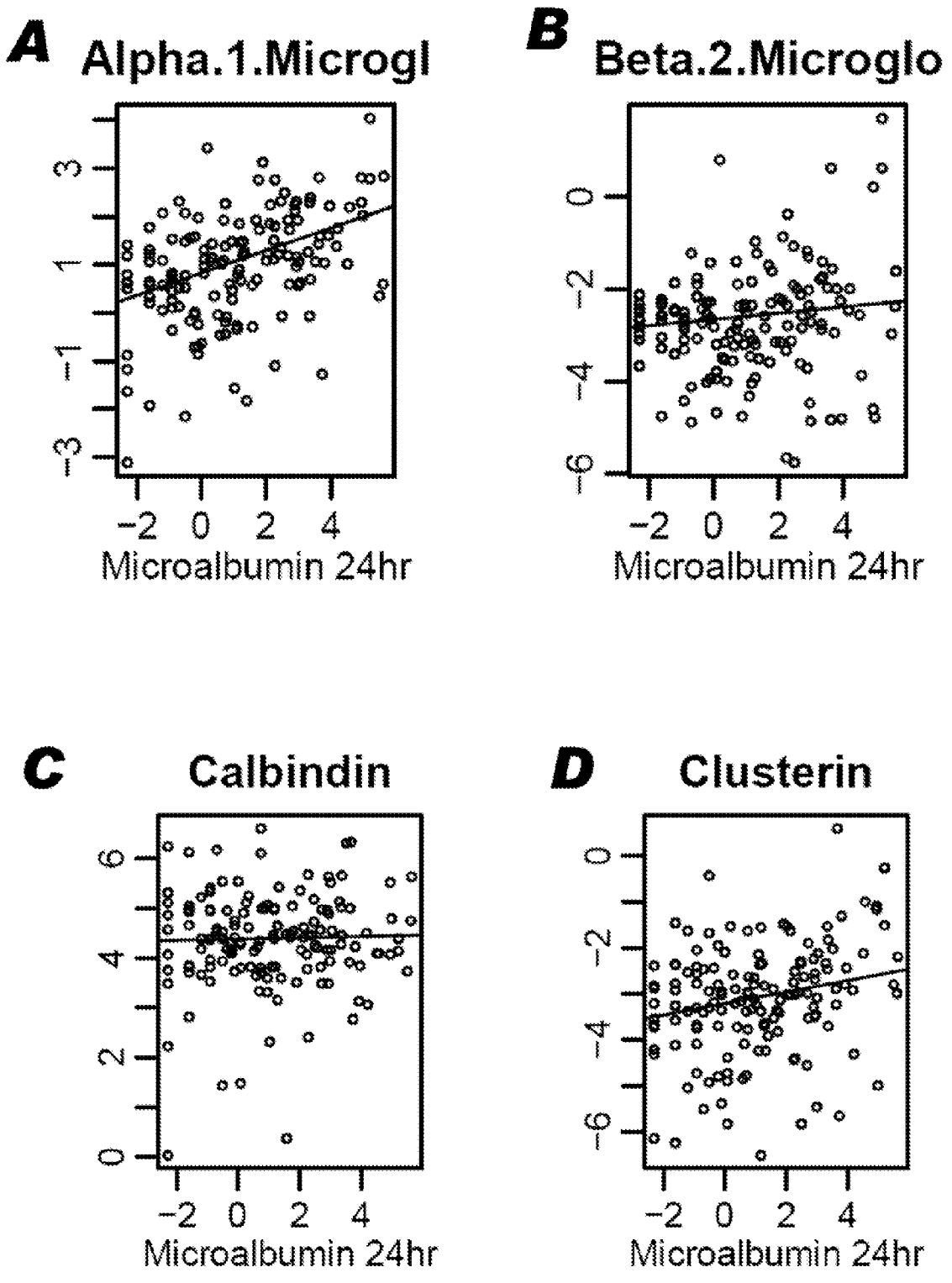
A
Alpha.1.Microgl
3
1
-1
-3
-2 0 2 4
Microalbumin 24hr
B
Beta.2.Microglo
0
-2
-4
-6
-2 0 2 4
Microalbumin 24hr
C
Calbindin
6
4
2
0
-2 0 2 4
Microalbumin 24hr
D
Clusterin
0
-2
-4
-6
-2 0 2 4
Microalbumin 24hr

FIG. 16

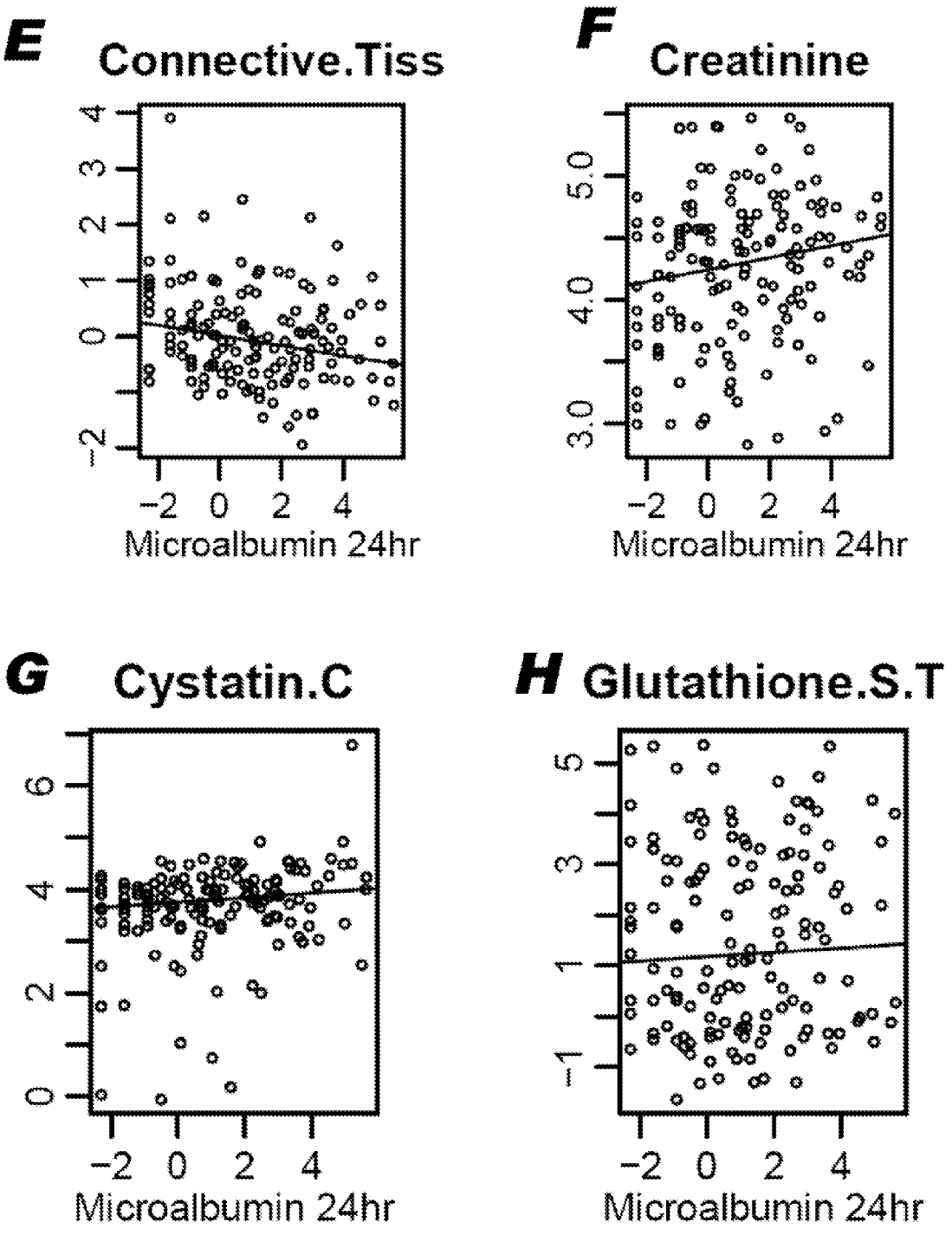
E
Connective.Tiss
−2 0 1 2 3 4
−2 0 2 4
Microalbumin 24hr
F
Creatinine
3.0 4.0 5.0
−2 0 2 4
Microalbumin 24hr
G
Cystatin.C
0 2 4 6
−2 0 2 4
Microalbumin 24hr
H
Glutathione.S.T
−1 1 3 5
−2 0 2 4
Microalbumin 24hr

FIG. 16

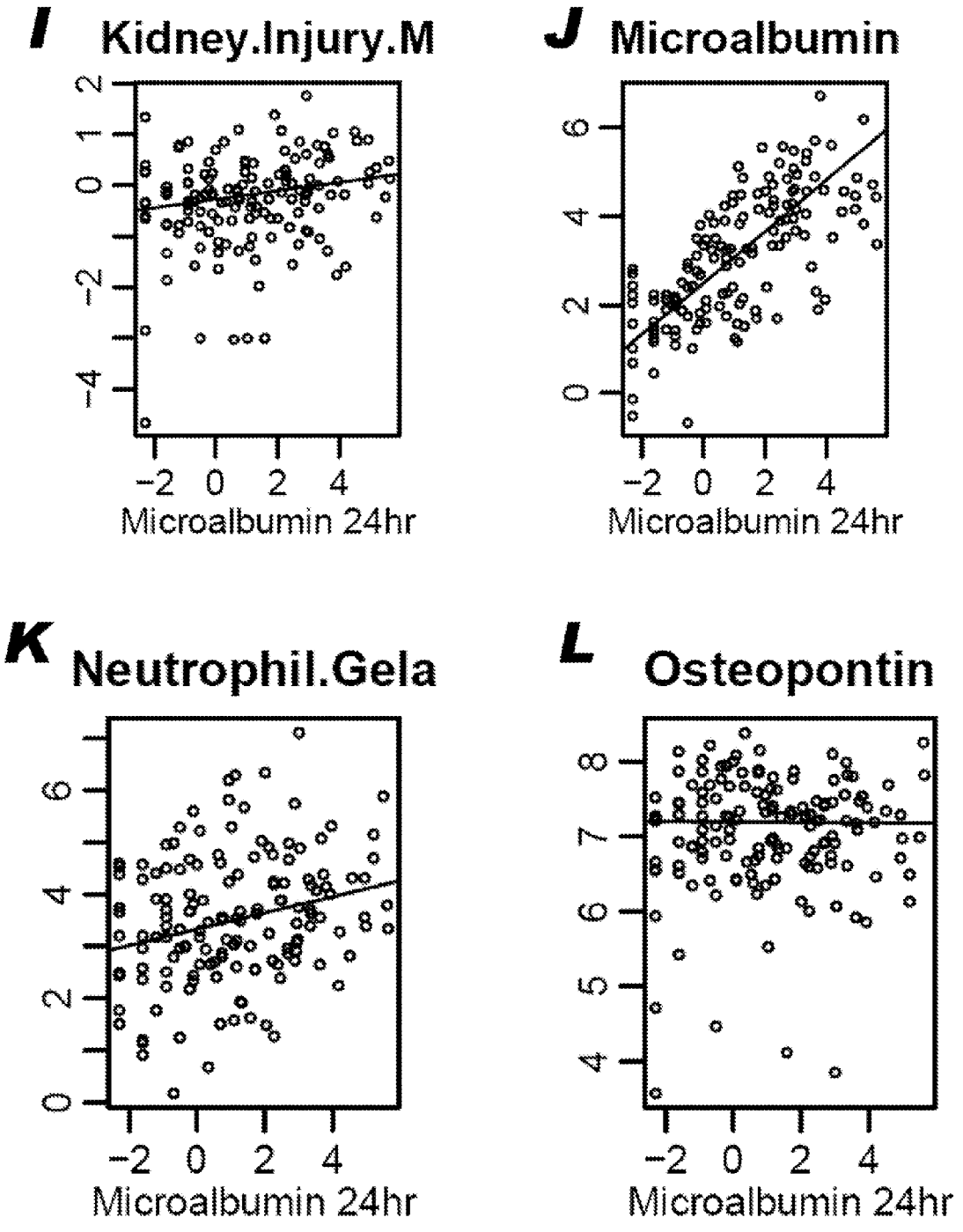
I
Kidney.Injury.M
Microalbumin 24hr
J
Microalbumin
Microalbumin 24hr
K
Neutrophil.Gela
Microalbumin 24hr
L
Osteopontin
Microalbumin 24hr

FIG. 16

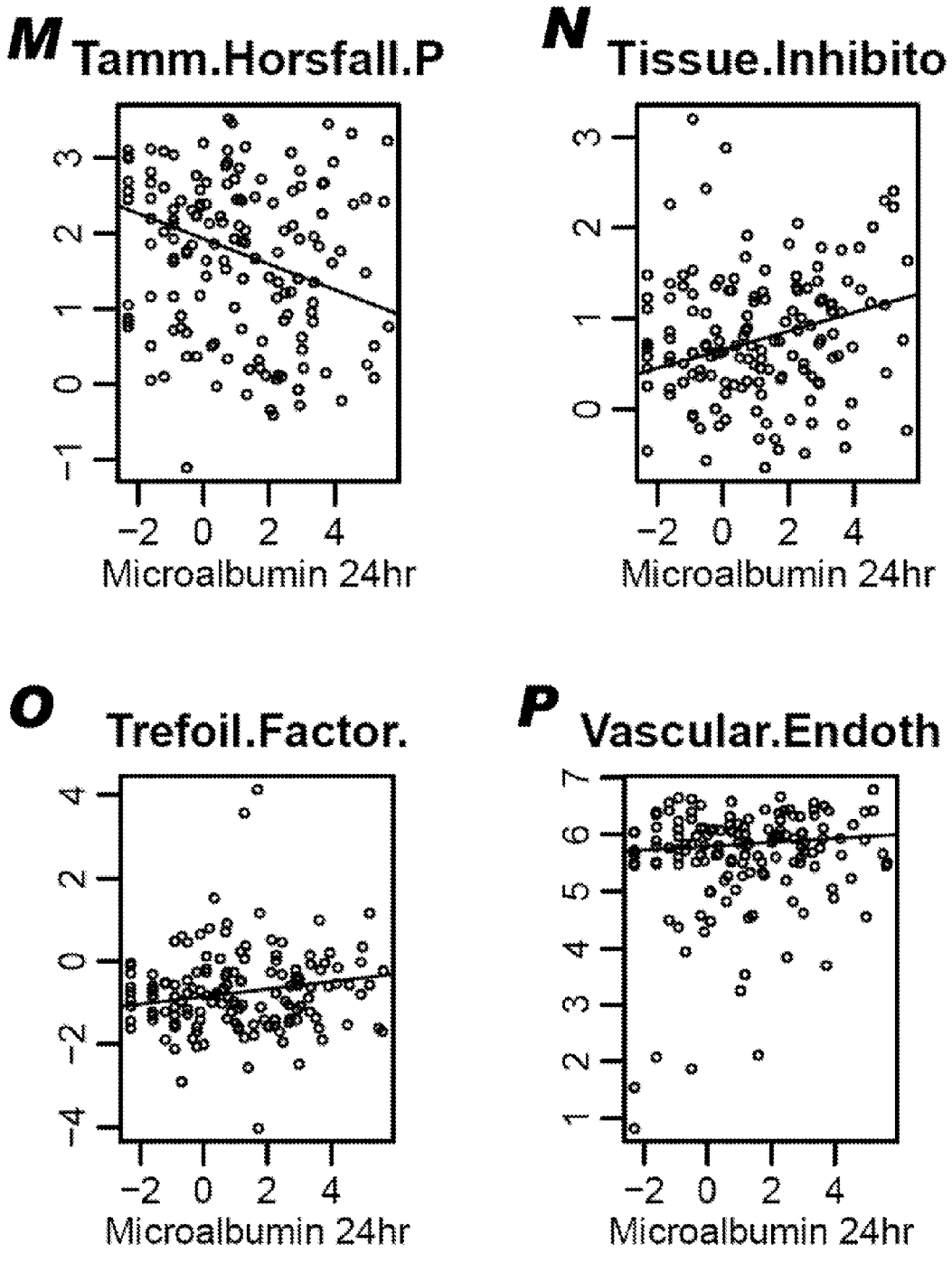
M
Tamm.Horsfall.P
−1 0 1 2 3
−2 0 2 4
Microalbumin 24hr
N
Tissue.Inhibito
0 1 2 3
−2 0 2 4
Microalbumin 24hr
O
Trefoil.Factor.
−4 −2 0 2 4
−2 0 2 4
Microalbumin 24hr
P
Vascular.Endoth
1 2 3 4 5 6 7
−2 0 2 4
Microalbumin 24hr

FIG. 16

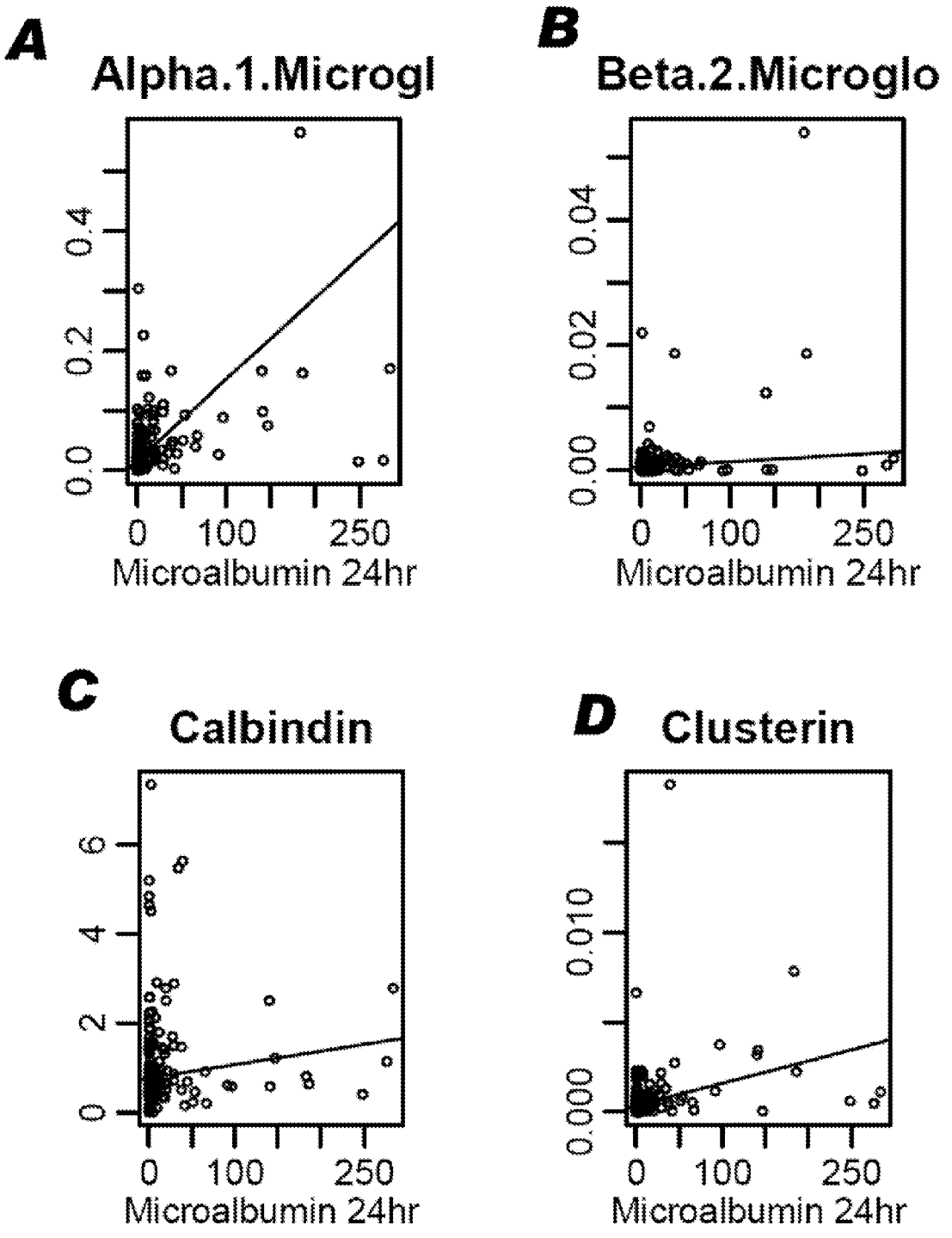
A
Alpha.1.Microgl
0.0
0.2
0.4
0
100
250
Microalbumin 24hr
B
Beta.2.Microglo
0.00
0.02
0.04
0
100
250
Microalbumin 24hr
C
Calbindin
0
2
4
6
0
100
250
Microalbumin 24hr
D
Clusterin
0.000
0.010
0
100
250
Microalbumin 24hr

FIG. 17

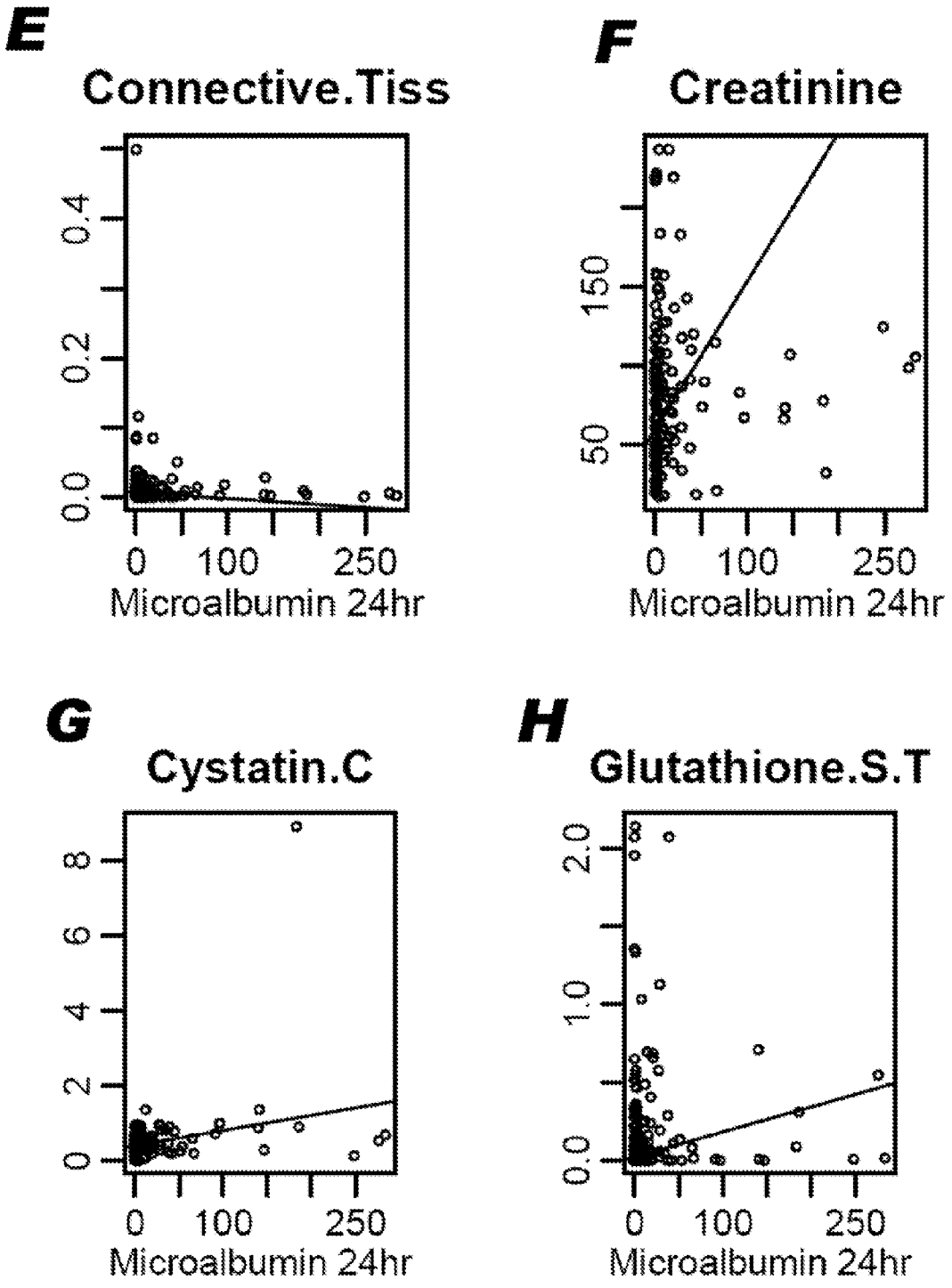
E
Connective.Tiss
0.0
0.2
0.4
0
100
250
Microalbumin 24hr
F
Creatinine
50
150
0
100
250
Microalbumin 24hr
G
Cystatin.C
0
2
4
6
8
0
100
250
Microalbumin 24hr
H
Glutathione.S.T
0.0
1.0
2.0
0
100
250
Microalbumin 24hr

FIG. 17

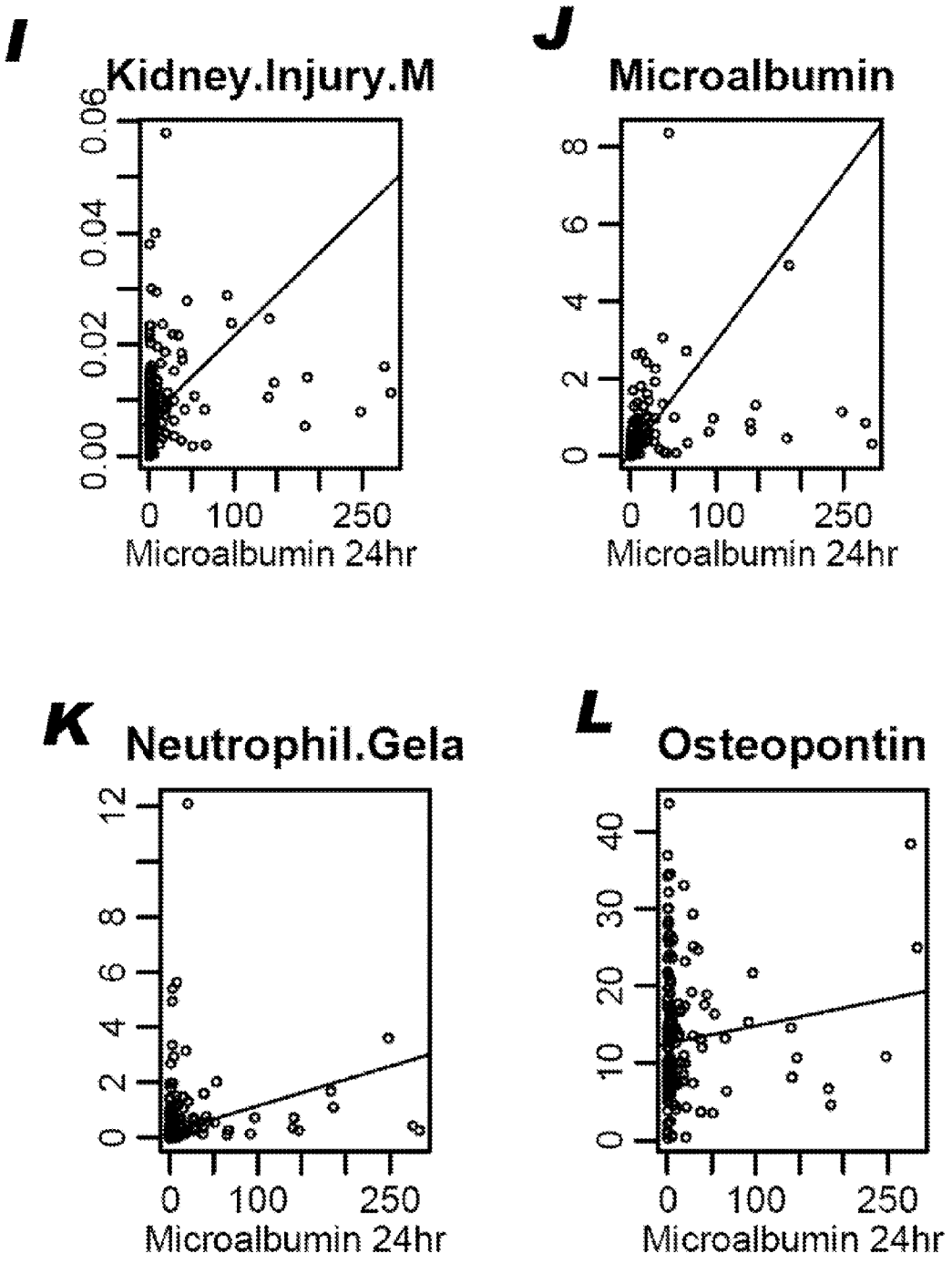
I
Kidney.Injury.M
0.00
0.02
0.04
0.06
0
100
250
Microalbumin 24hr
J
Microalbumin
0
2
4
6
8
0
100
250
Microalbumin 24hr
K
Neutrophil.Gela
0
2
4
6
8
12
0
100
250
Microalbumin 24hr
L
Osteopontin
0
10
20
30
40
0
100
250
Microalbumin 24hr

FIG. 17

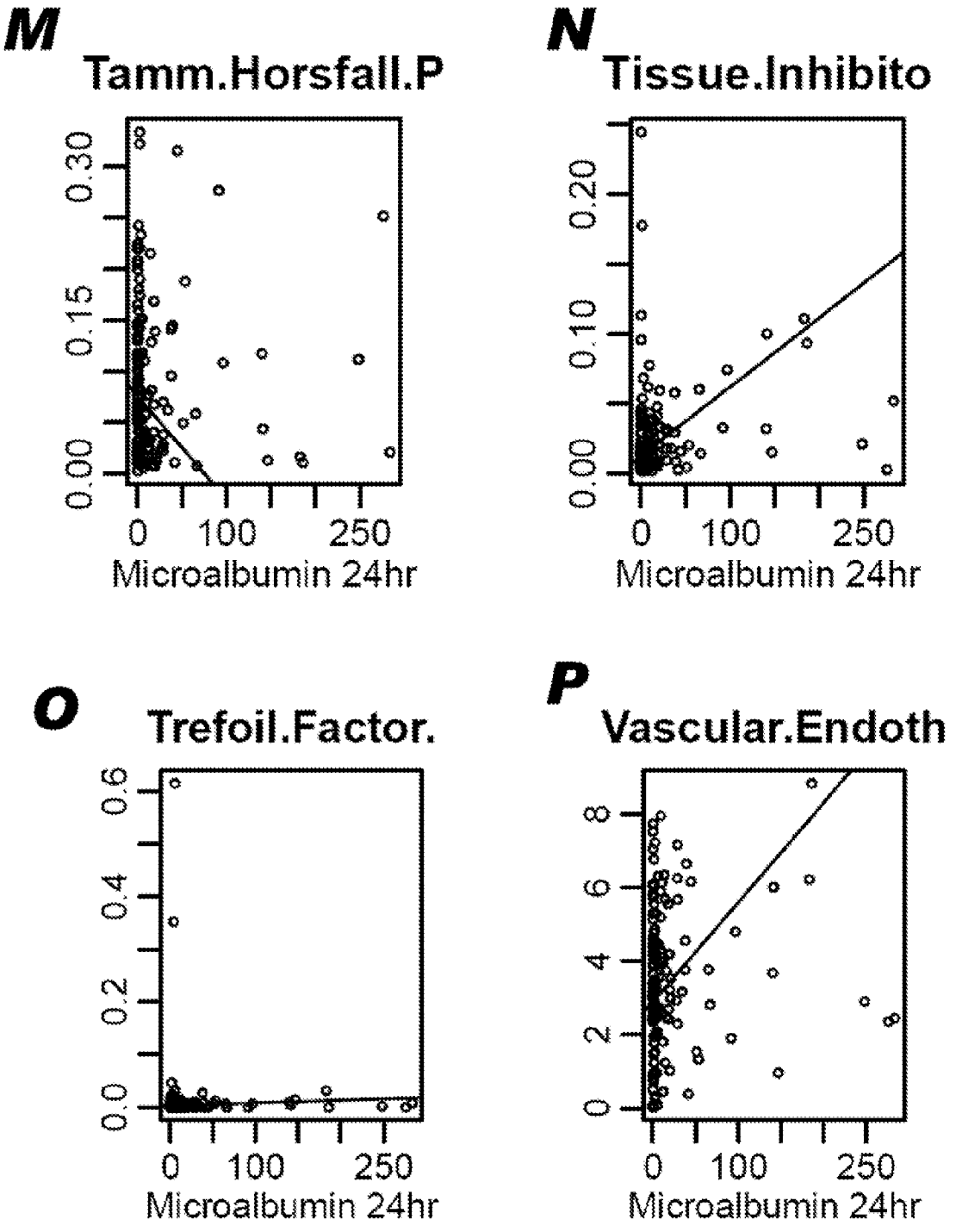
M
Tamm.Horsfall.P
0.00
0.15
0.30
0
100
250
Microalbumin 24hr
N
Tissue.Inhibito
0.00
0.10
0.20
0
100
250
Microalbumin 24hr
O
Trefoil.Factor.
0.0
0.2
0.4
0.6
0
100
250
Microalbumin 24hr
P
Vascular.Endoth
0
2
4
6
8
0
100
250
Microalbumin 24hr

FIG. 17

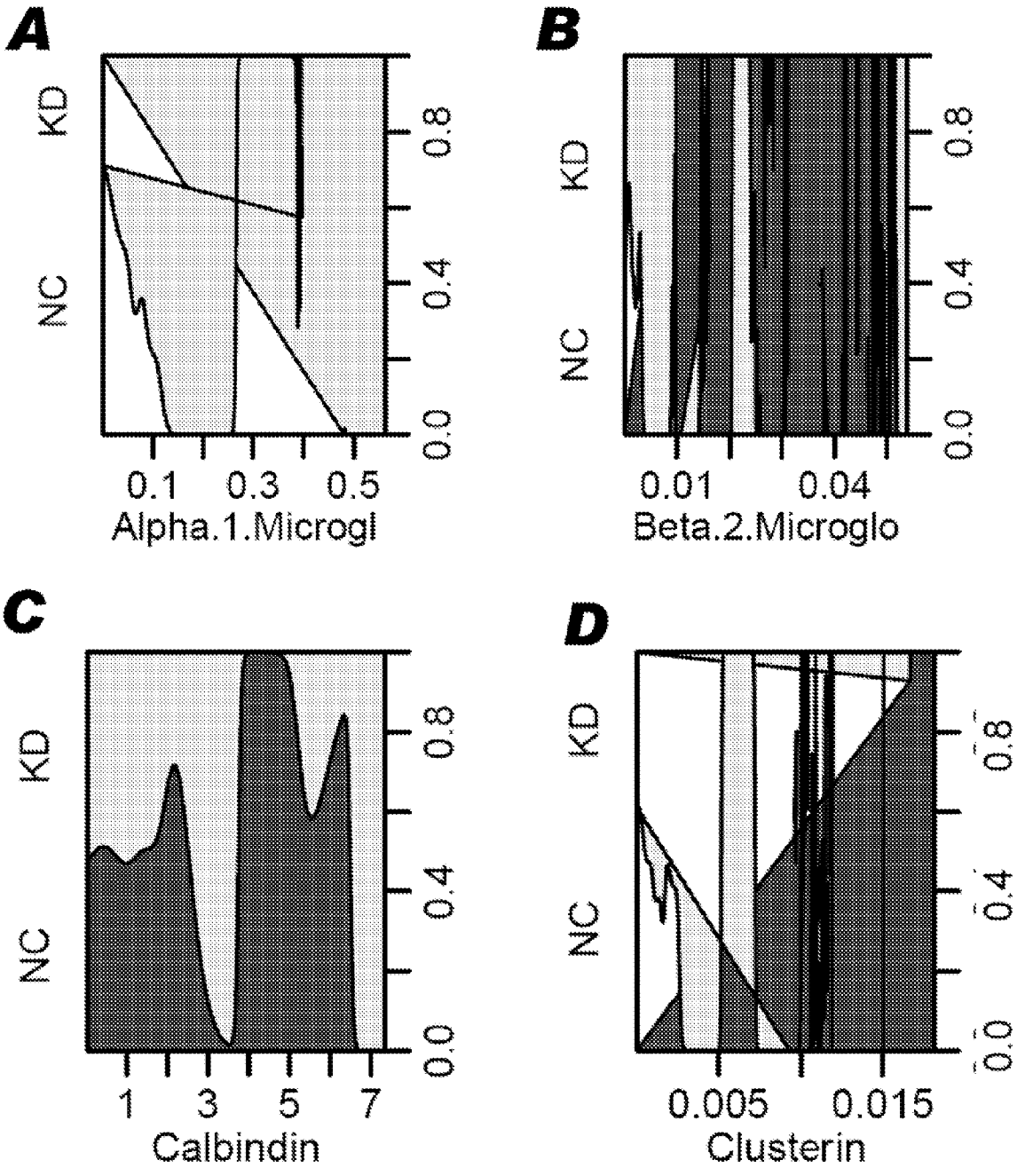
A
KD
NC
0.0
0.4
0.8
0.1
0.3
0.5
Alpha.1.Microgl
B
KD
NC
0.0
0.4
0.8
0.01
0.04
Beta.2.Microglo
C
KD
NC
0.0
0.4
0.8
1
3
5
7
Calbindin
D
KD
NC
0.0
0.4
0.8
0.005
0.015
Clusterin

FIG. 18

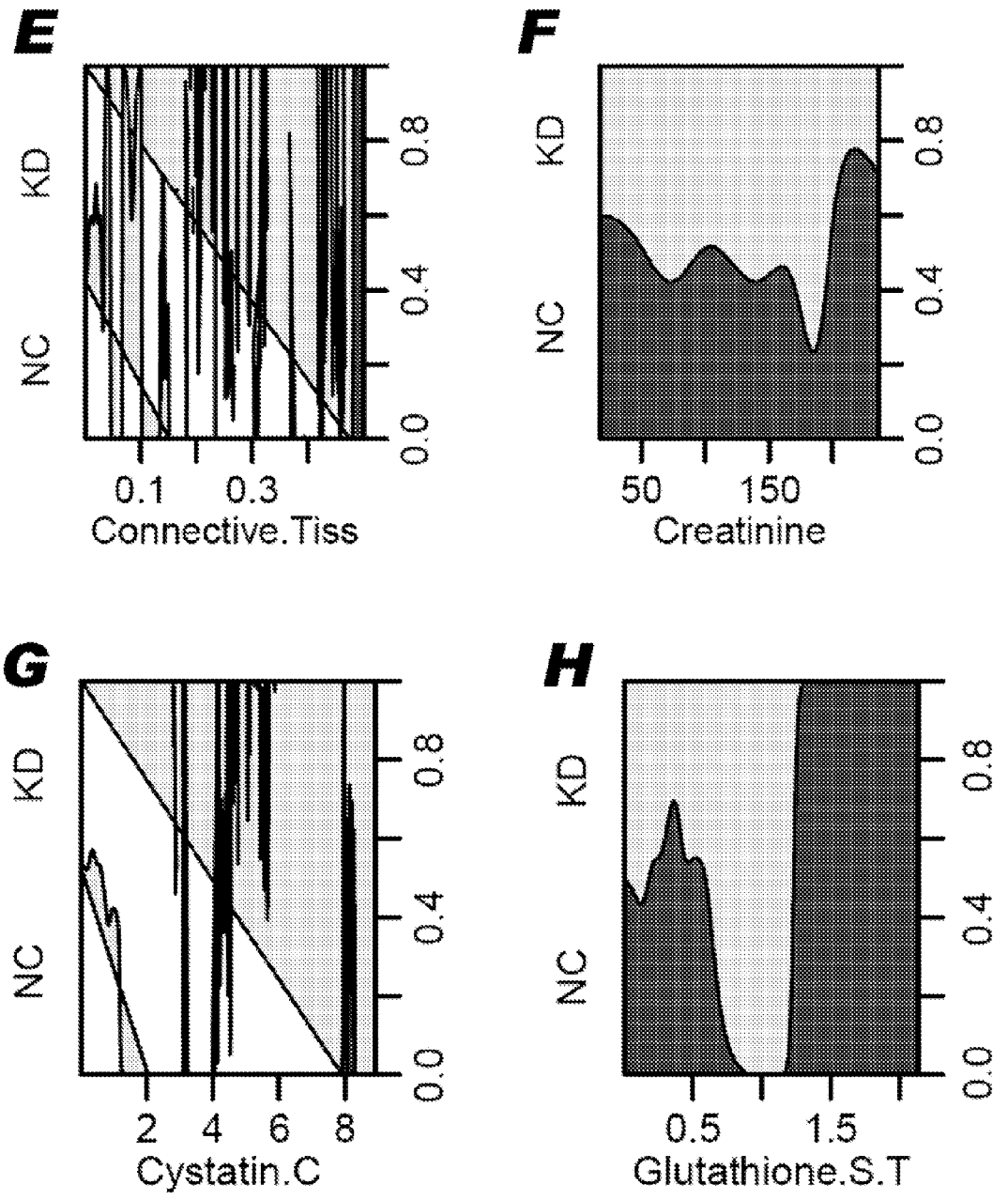
E
KD
NC
0.0
0.4
0.8
0.1
0.3
Connective.Tiss
F
KD
NC
0.0
0.4
0.8
50
150
Creatinine
G
KD
NC
0.0
0.4
0.8
2
4
6
8
Cystatin.C
H
KD
NC
0.0
0.4
0.8
0.5
1.5
Glutathione.S.T

FIG. 18

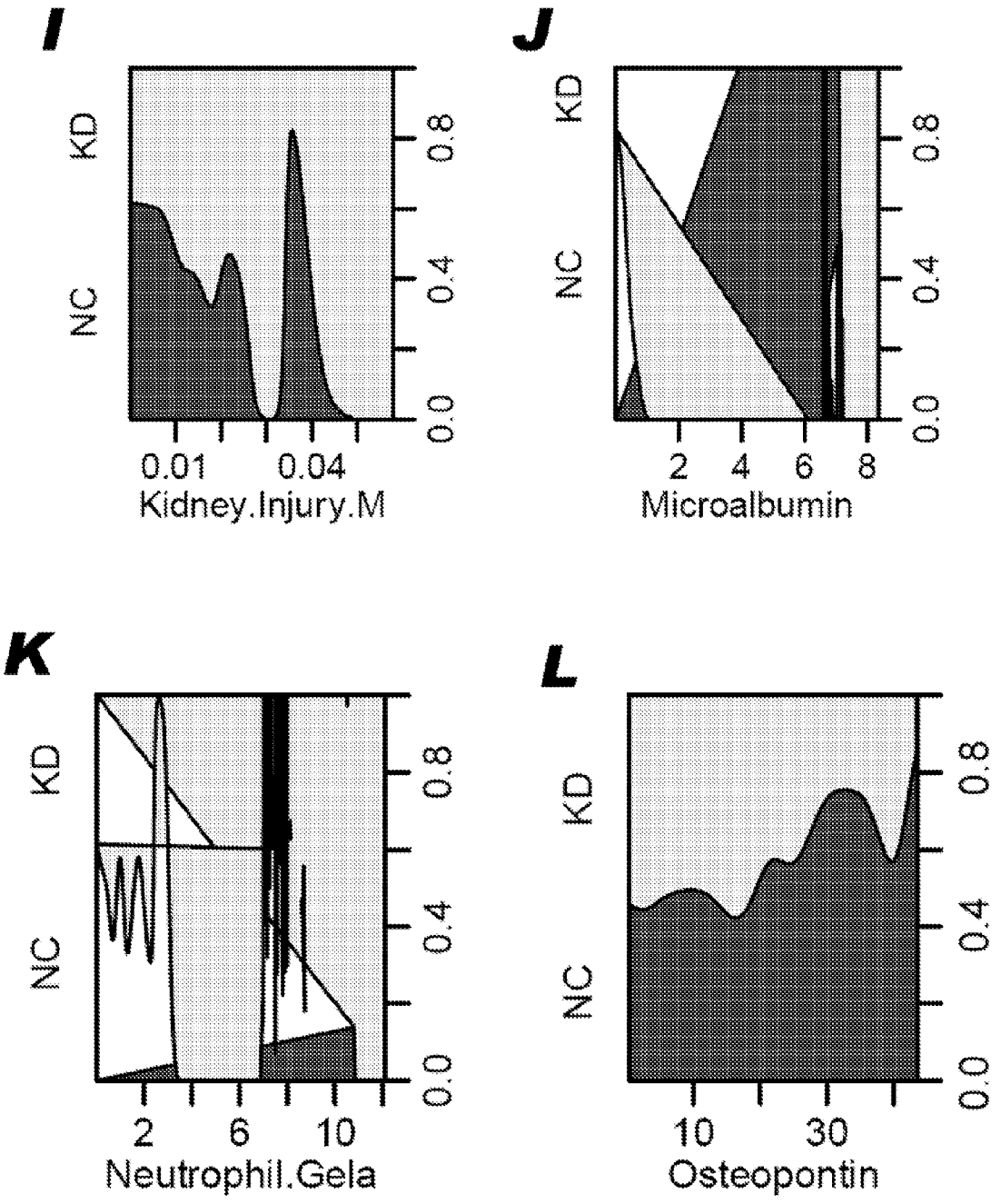
I
KD
NC
0.0
0.4
0.8
0.01
0.04
Kidney.Injury.M
J
KD
NC
0.0
0.4
0.8
2
4
6
8
Microalbumin
K
KD
NC
0.0
0.4
0.8
2
6
10
Neutrophil.Gela
L
KD
NC
0.0
0.4
0.8
10
30
Osteopontin

FIG. 18

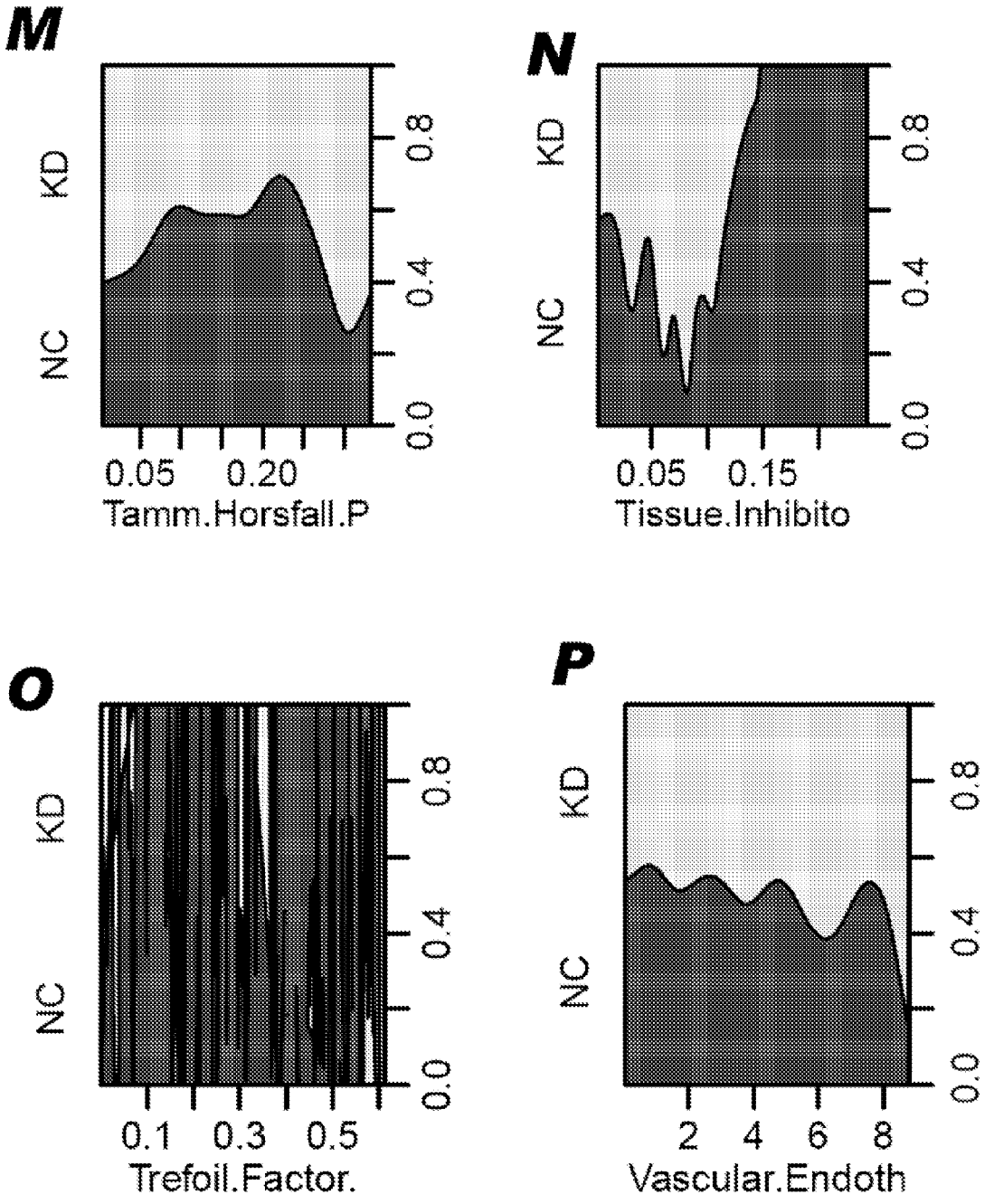
M
KD
NC
0.0
0.4
0.8
0.05
0.20
Tamm.Horsfall.P
N
KD
NC
0.0
0.4
0.8
0.05
0.15
Tissue.Inhibito
O
KD
NC
0.0
0.4
0.8
0.1
0.3
0.5
Trefoil.Factor.
P
KD
NC
0.0
0.4
0.8
2
4
6
8
Vascular.Endoth

FIG. 18

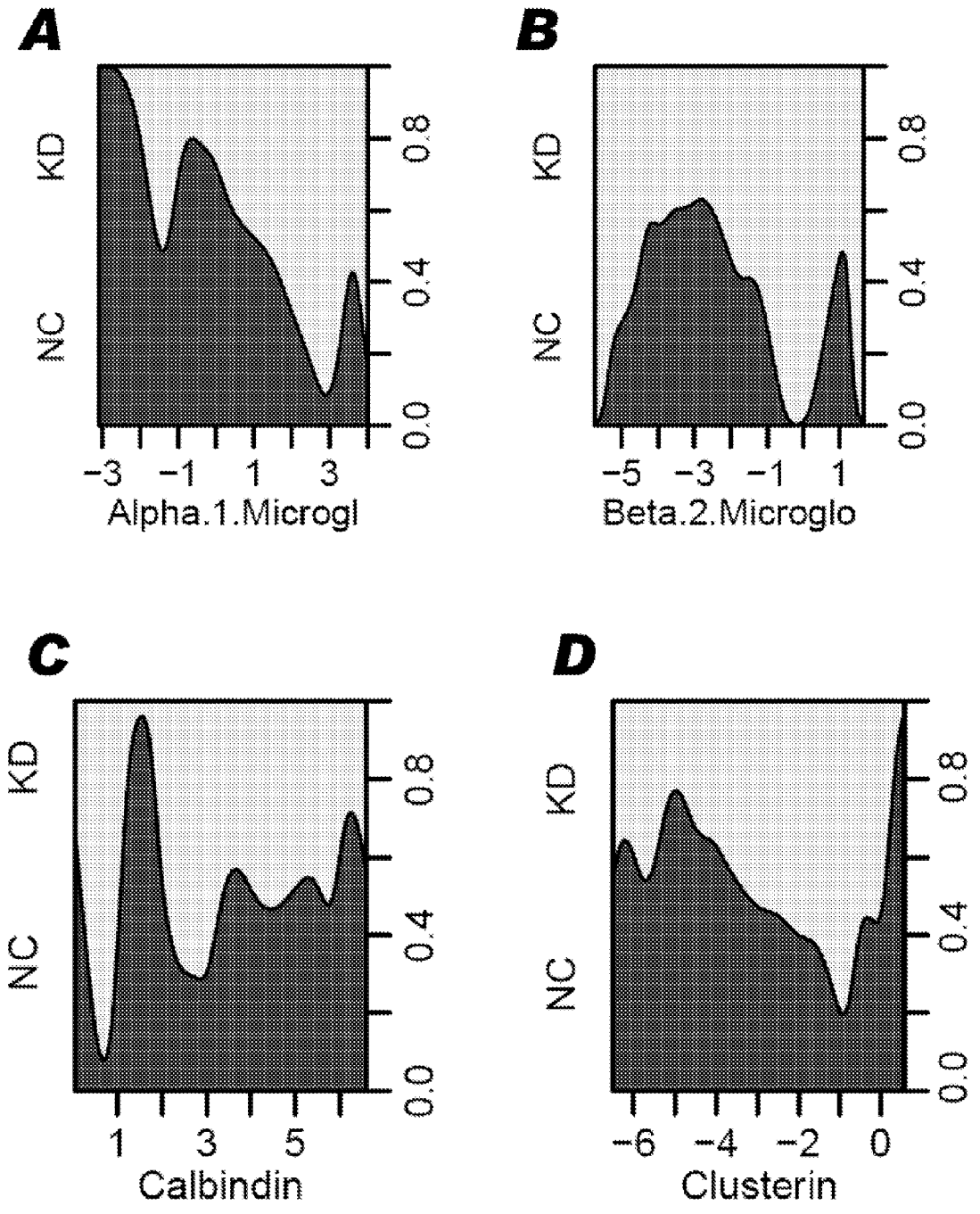
A
KD
NC
0.0
0.4
0.8
−3 −1 1 3
Alpha.1.Microgl
B
KD
NC
0.0
0.4
0.8
−5 −3 −1 1
Beta.2.Microglo
C
KD
NC
0.0
0.4
0.8
1 3 5
Calbindin
D
KD
NC
0.0
0.4
0.8
−6 −4 −2 0
Clusterin

FIG. 19

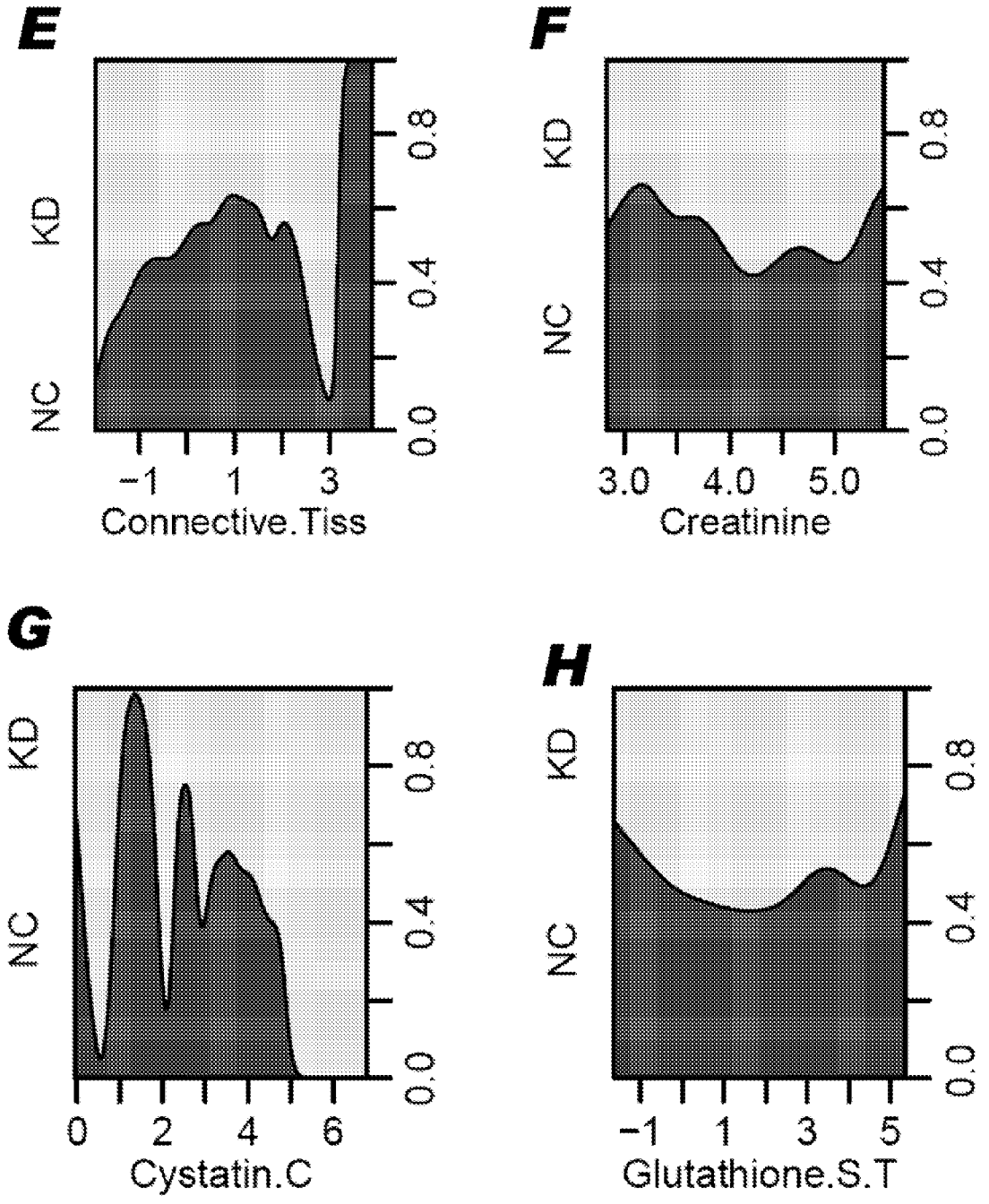
E
KD
NC
0.0
0.4
0.8
−1
1
3
Connective.Tiss
F
KD
NC
0.0
0.4
0.8
3.0
4.0
5.0
Creatinine
G
KD
NC
0.0
0.4
0.8
0
2
4
6
Cystatin.C
H
KD
NC
0.0
0.4
0.8
−1
1
3
5
Glutathione.S.T

FIG. 19

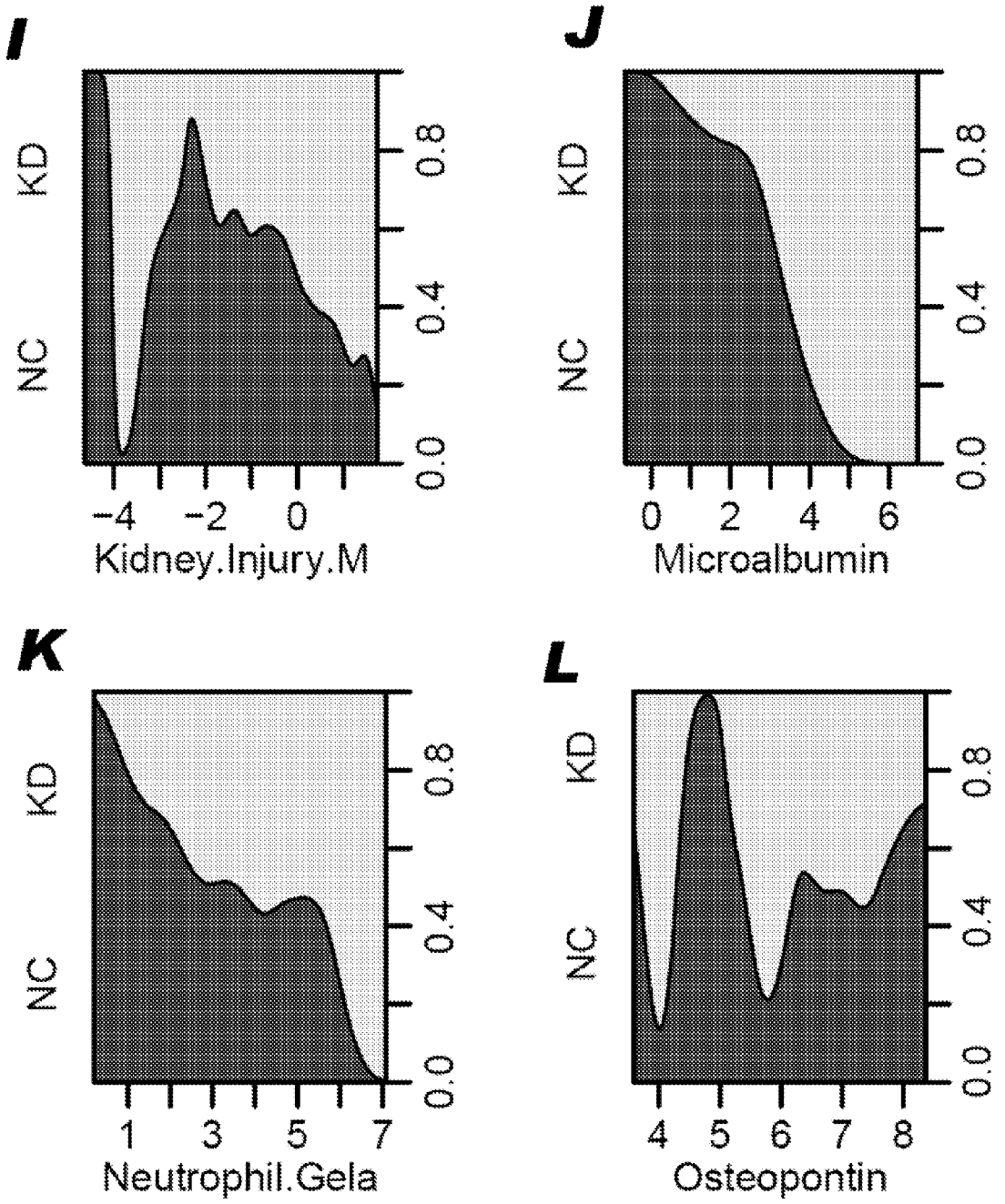
I
KD
NC
0.0
0.4
0.8
−4
−2
0
Kidney.Injury.M
J
KD
NC
0.0
0.4
0.8
0
2
4
6
Microalbumin
K
KD
NC
0.0
0.4
0.8
1
3
5
7
Neutrophil.Gela
L
KD
NC
0.0
0.4
0.8
4
5
6
7
8
Osteopontin

FIG. 19

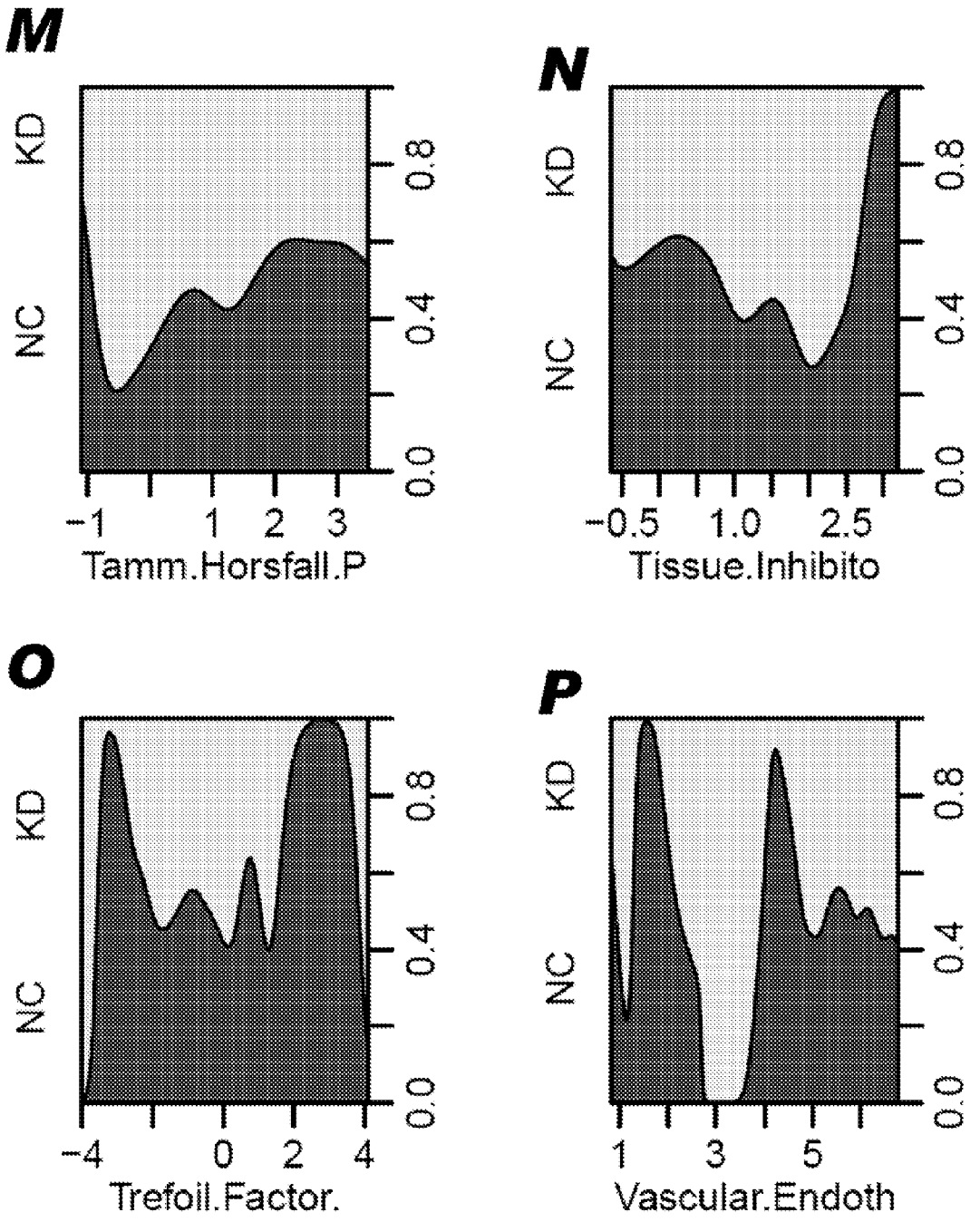
M
KD
NC
0.0
0.4
0.8
−1
1
2
3
Tamm.Horsfall.P
N
KD
NC
0.0
0.4
0.8
−0.5
1.0
2.5
Tissue.Inhibito
O
KD
NC
0.0
0.4
0.8
−4
0
2
4
Trefoil.Factor.
P
KD
NC
0.0
0.4
0.8
1
3
5
Vascular.Endoth

FIG. 19

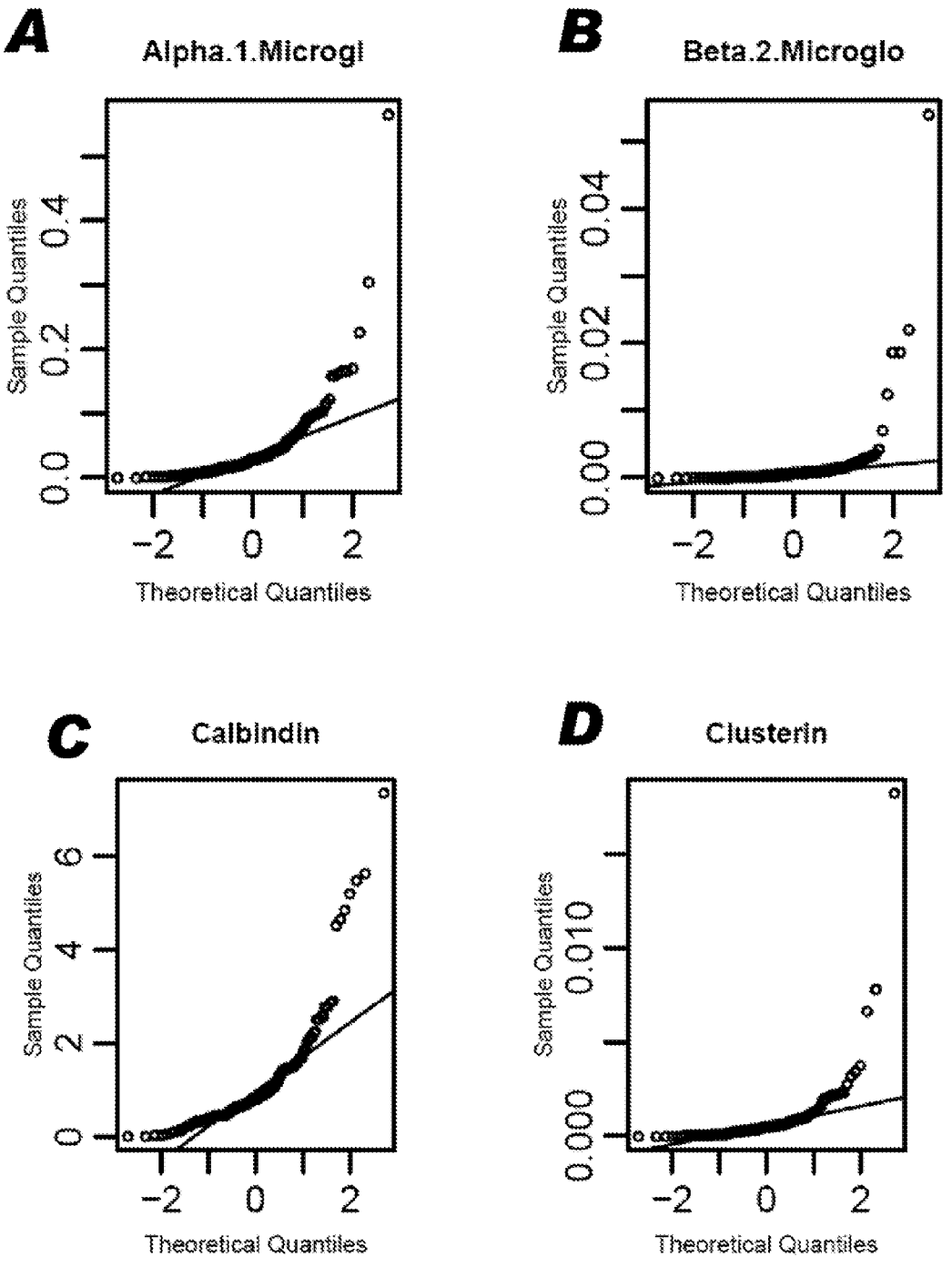
A
Alpha.1.Microgl
Sample Quantiles
0.0
0.2
0.4
−2
0
2
Theoretical Quantiles
B
Beta.2.Microglo
Sample Quantiles
0.00
0.02
0.04
−2
0
2
Theoretical Quantiles
C
Calbindin
Sample Quantiles
0
2
4
6
−2
0
2
Theoretical Quantiles
D
Clusterin
Sample Quantiles
0.000
0.010
−2
0
2
Theoretical Quantiles

FIG. 20

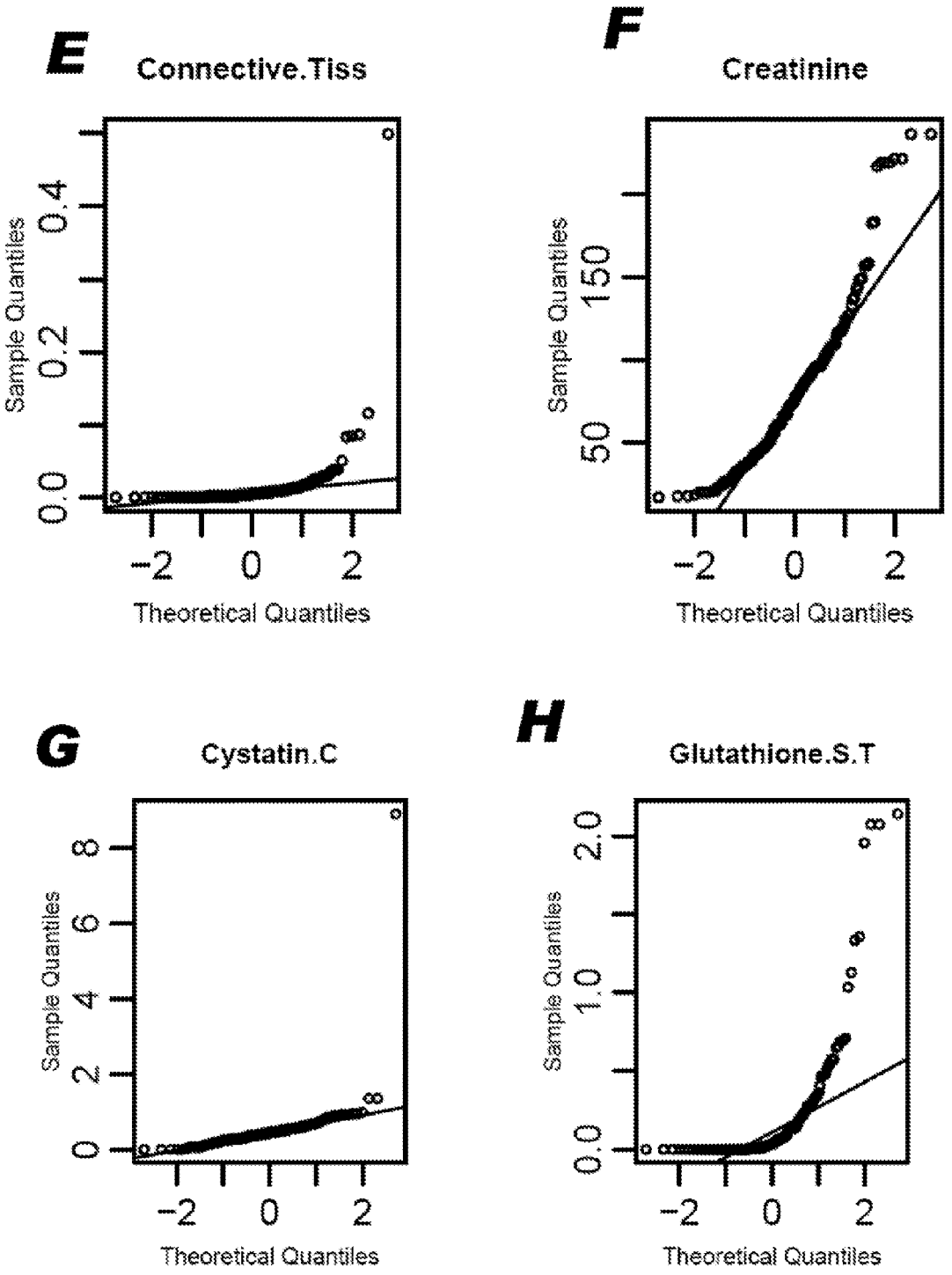
E
Connective.Tiss
Sample Quantiles
0.0
0.2
0.4
−2
0
2
Theoretical Quantiles
F
Creatinine
Sample Quantiles
50
150
−2
0
2
Theoretical Quantiles
G
Cystatin.C
Sample Quantiles
0
2
4
6
8
−2
0
2
Theoretical Quantiles
H
Glutathione.S.T
Sample Quantiles
0.0
1.0
2.0
−2
0
2
Theoretical Quantiles

FIG. 20

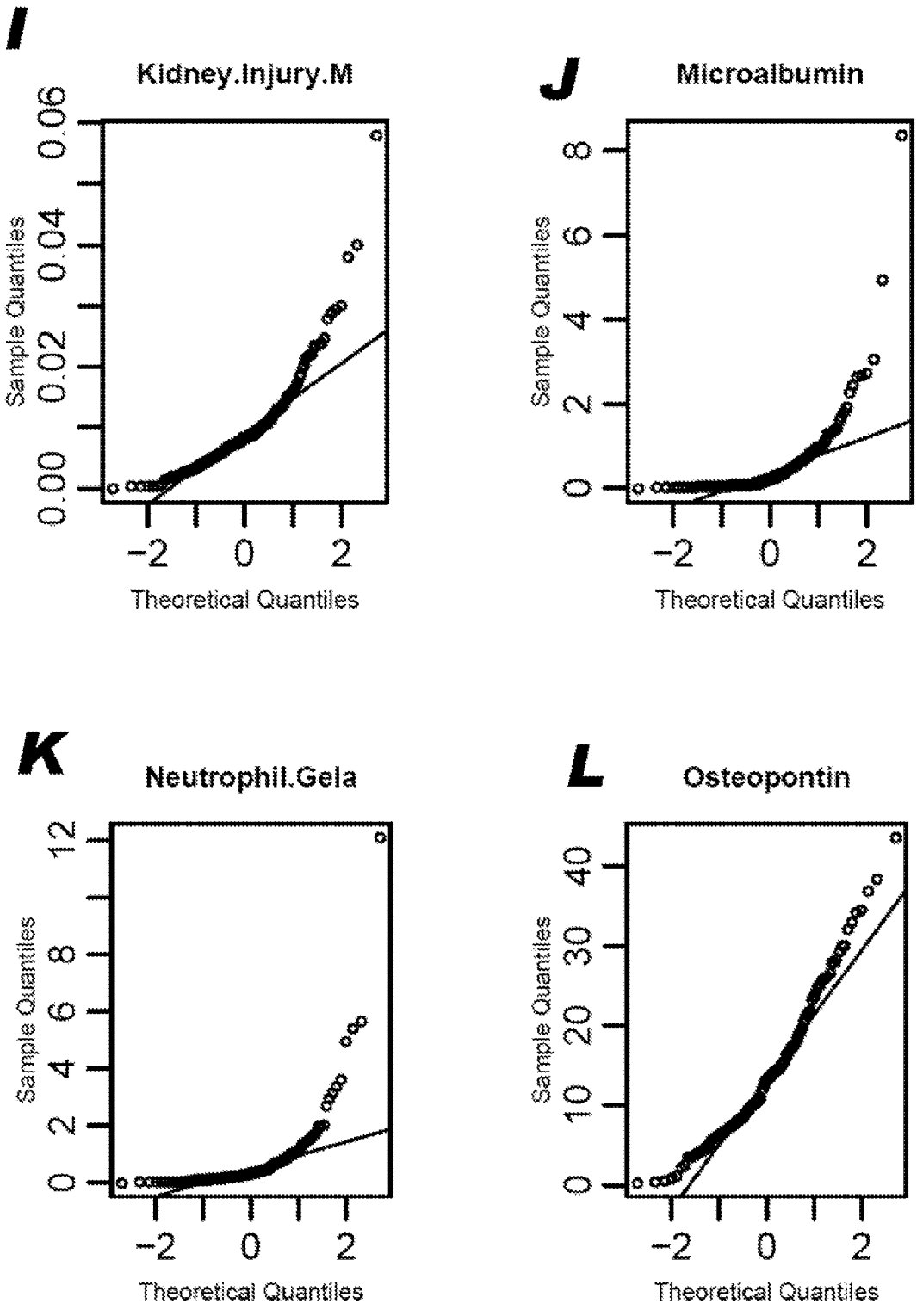
I
Kidney.Injury.M
Sample Quantiles
0.00
0.02
0.04
0.06
−2
0
2
Theoretical Quantiles
J
Microalbumin
Sample Quantiles
0
2
4
6
8
−2
0
2
Theoretical Quantiles
K
Neutrophil.Gela
Sample Quantiles
0
2
4
6
8
12
−2
0
2
Theoretical Quantiles
L
Osteopontin
Sample Quantiles
0
10
20
30
40
−2
0
2
Theoretical Quantiles

FIG. 20

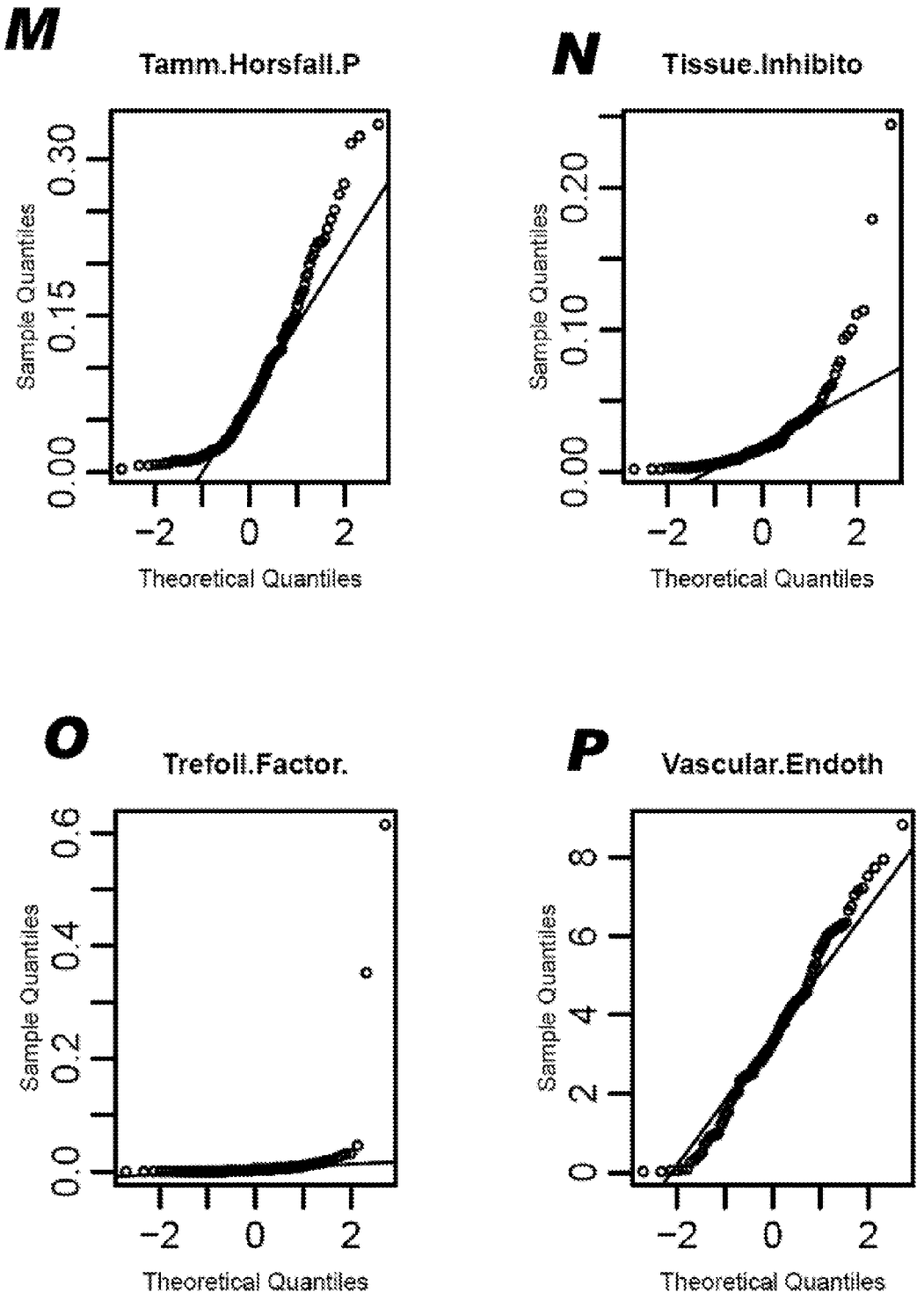
M
Tamm.Horsfall.P
Sample Quantiles
0.00
0.15
0.30
−2
0
2
Theoretical Quantiles
N
Tissue.Inhibito
Sample Quantiles
0.00
0.10
0.20
−2
0
2
Theoretical Quantiles
O
Trefoil.Factor.
Sample Quantiles
0.0
0.2
0.4
0.6
−2
0
2
Theoretical Quantiles
P
Vascular.Endoth
Sample Quantiles
0
2
4
6
8
−2
0
2
Theoretical Quantiles

FIG. 20

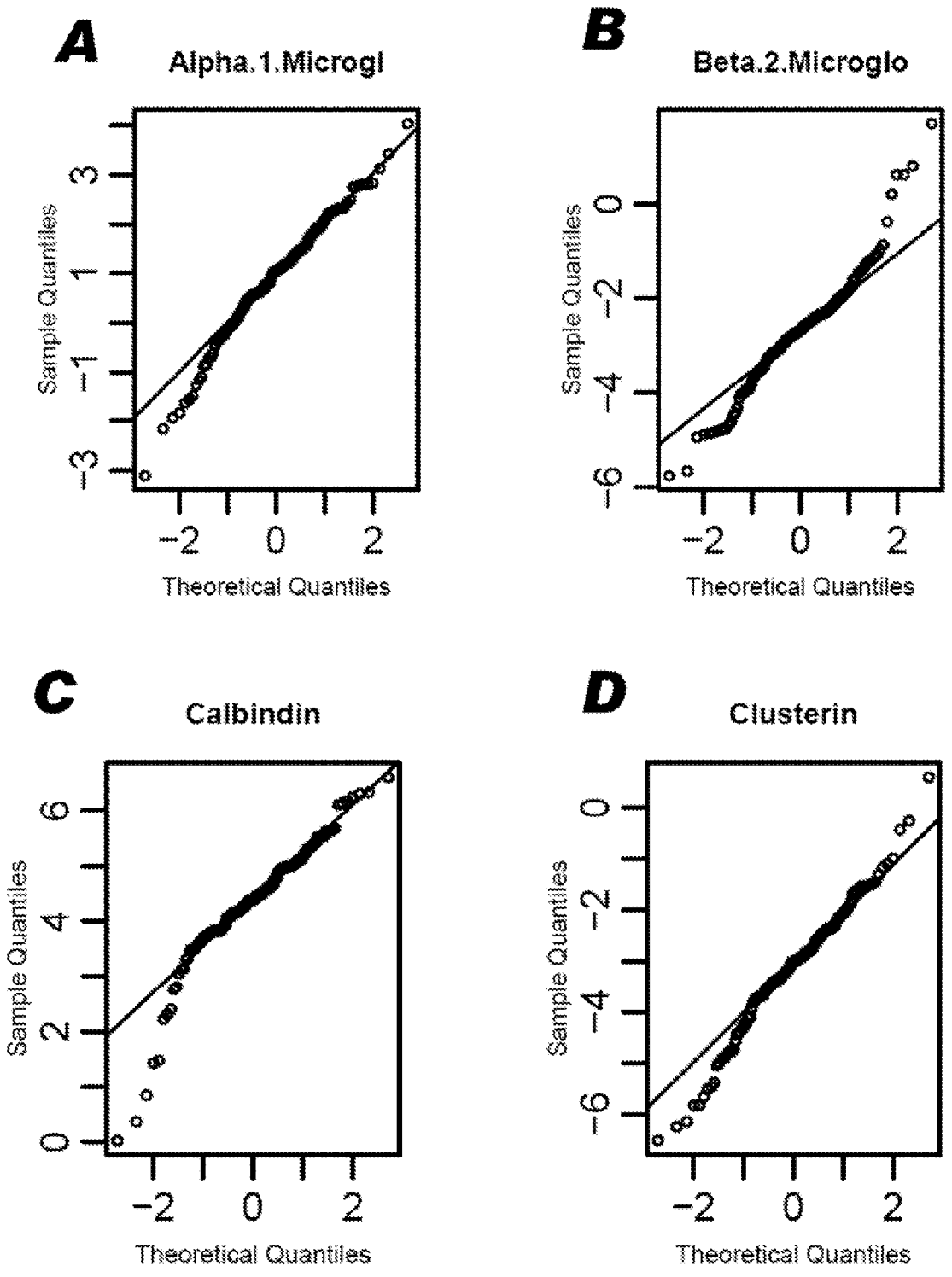
A
Alpha.1.Microgl
Sample Quantiles
Theoretical Quantiles
B
Beta.2.Microglo
Sample Quantiles
Theoretical Quantiles
C
Calbindin
Sample Quantiles
Theoretical Quantiles
D
Clusterin
Sample Quantiles
Theoretical Quantiles

FIG. 21

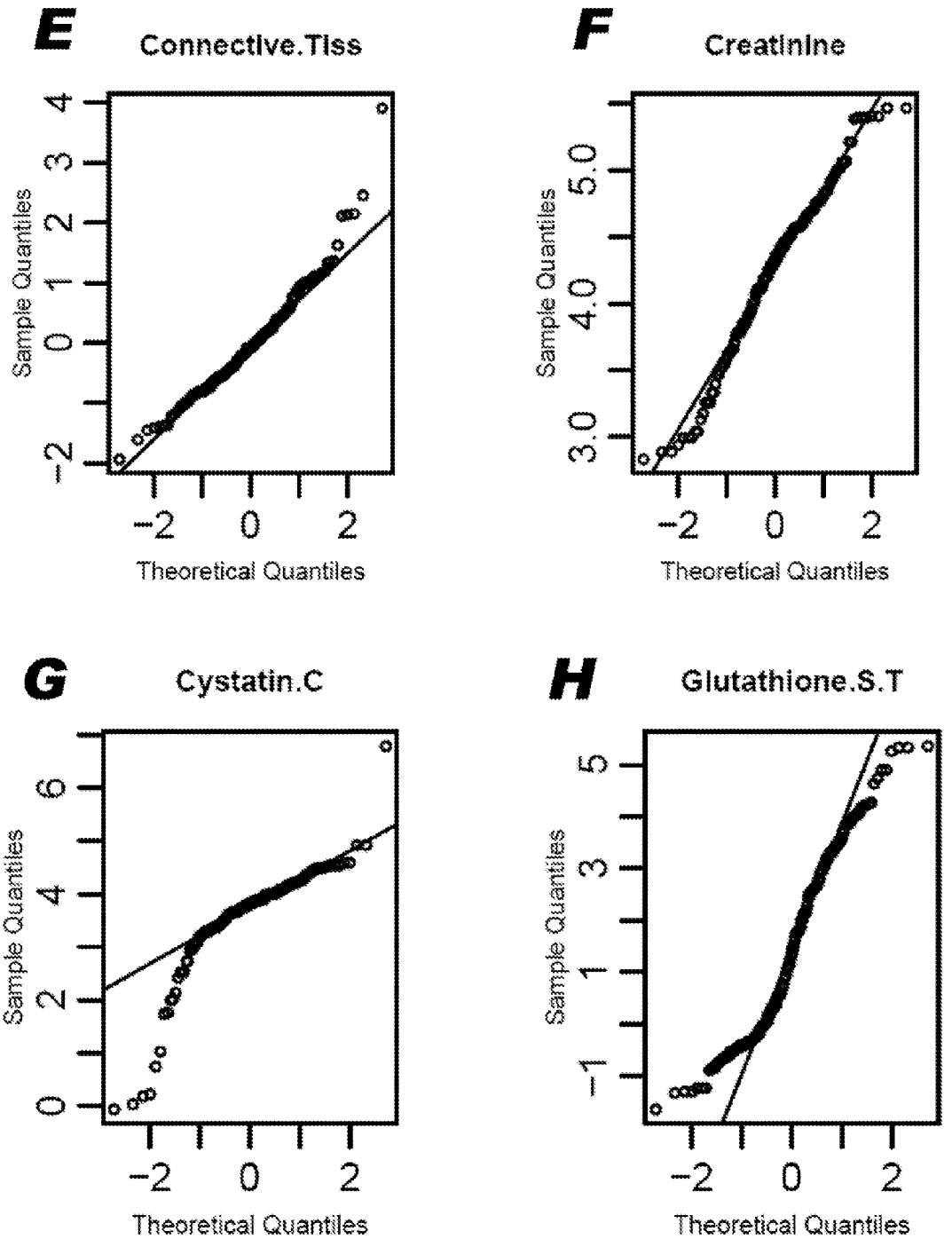
E
Connective.Tiss
Sample Quantiles
Theoretical Quantiles
F
Creatinine
Sample Quantiles
Theoretical Quantiles
G
Cystatin.C
Sample Quantiles
Theoretical Quantiles
H
Glutathione.S.T
Sample Quantiles
Theoretical Quantiles

FIG. 21

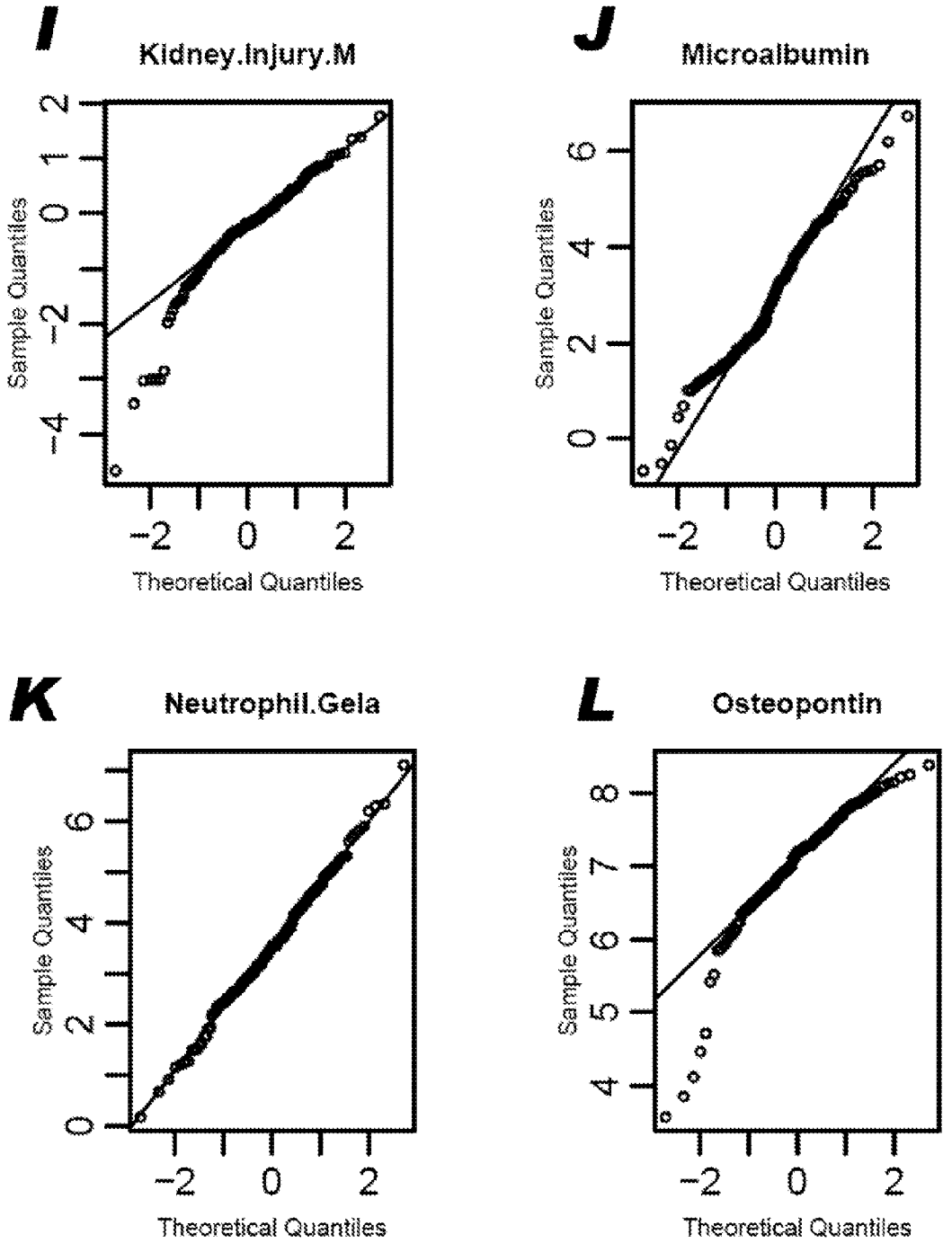
I
Kidney.Injury.M
Sample Quantiles
Theoretical Quantiles
J
Microalbumin
Sample Quantiles
Theoretical Quantiles
K
Neutrophil.Gela
Sample Quantiles
Theoretical Quantiles
L
Osteopontin
Sample Quantiles
Theoretical Quantiles

FIG. 21

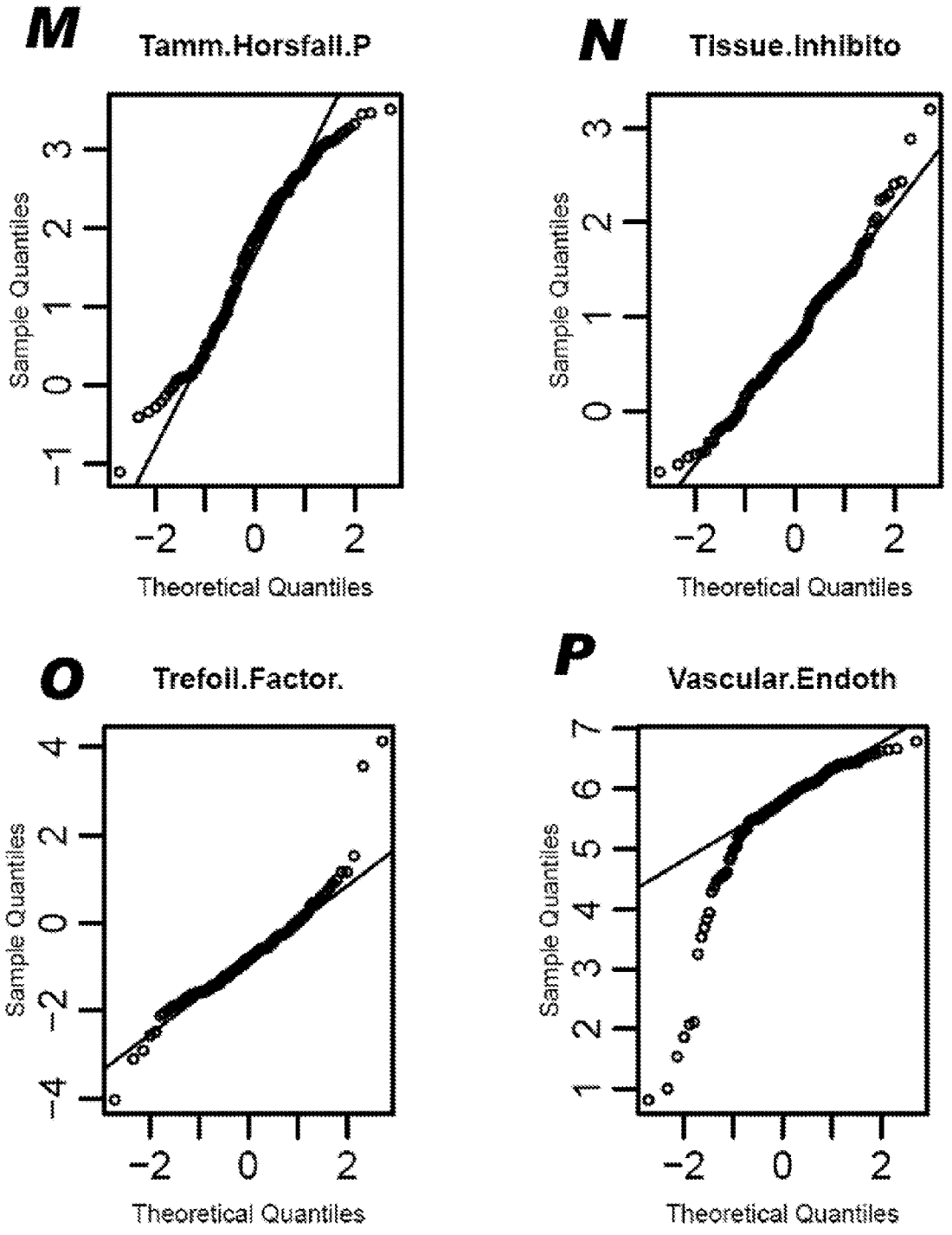
M
Tamm.Horsfall.P
Sample Quantiles
Theoretical Quantiles
N
Tissue.Inhibito
Sample Quantiles
Theoretical Quantiles
O
Trefoil.Factor.
Sample Quantiles
Theoretical Quantiles
P
Vascular.Endoth
Sample Quantiles
Theoretical Quantiles

FIG. 21

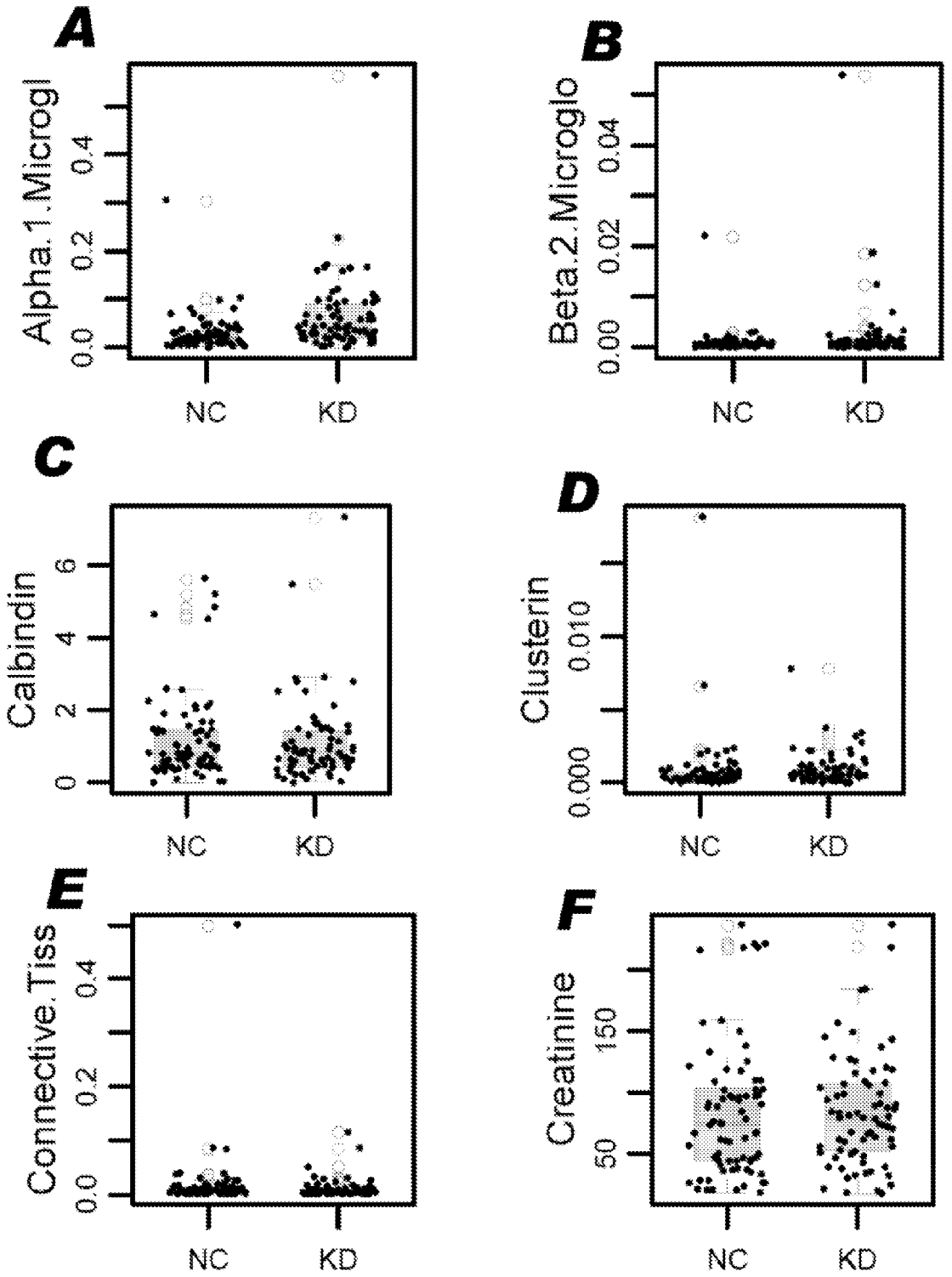
A
Alpha.1.Microgl
0.0
0.2
0.4
NC
KD
B
Beta.2.Microglo
0.00
0.02
0.04
NC
KD
C
Calbindin
0
2
4
6
NC
KD
D
Clusterin
0.000
0.010
NC
KD
E
Connective.Tiss
0.0
0.2
0.4
NC
KD
F
Creatinine
50
150
NC
KD

FIG. 22

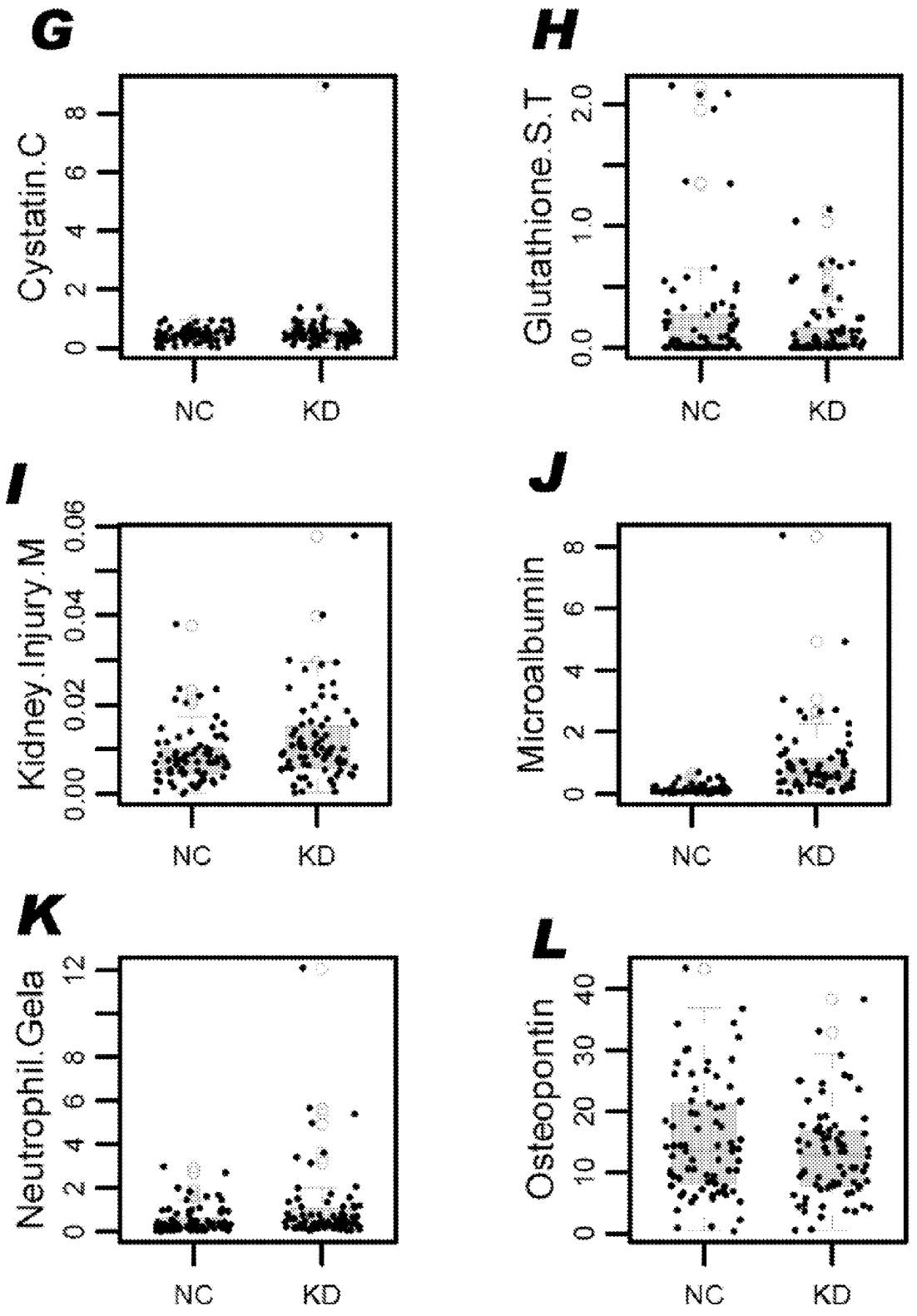
G
Cystatin.C
0
2
4
6
8
NC
KD
H
Glutathione.S.T
0.0
1.0
2.0
NC
KD
I
Kidney.Injury.M
0.00
0.02
0.04
0.06
NC
KD
J
Microalbumin
0
2
4
6
8
NC
KD
K
Neutrophil.Gela
0
2
4
6
8
12
NC
KD
L
Osteopontin
0
10
20
30
40
NC
KD

FIG. 22

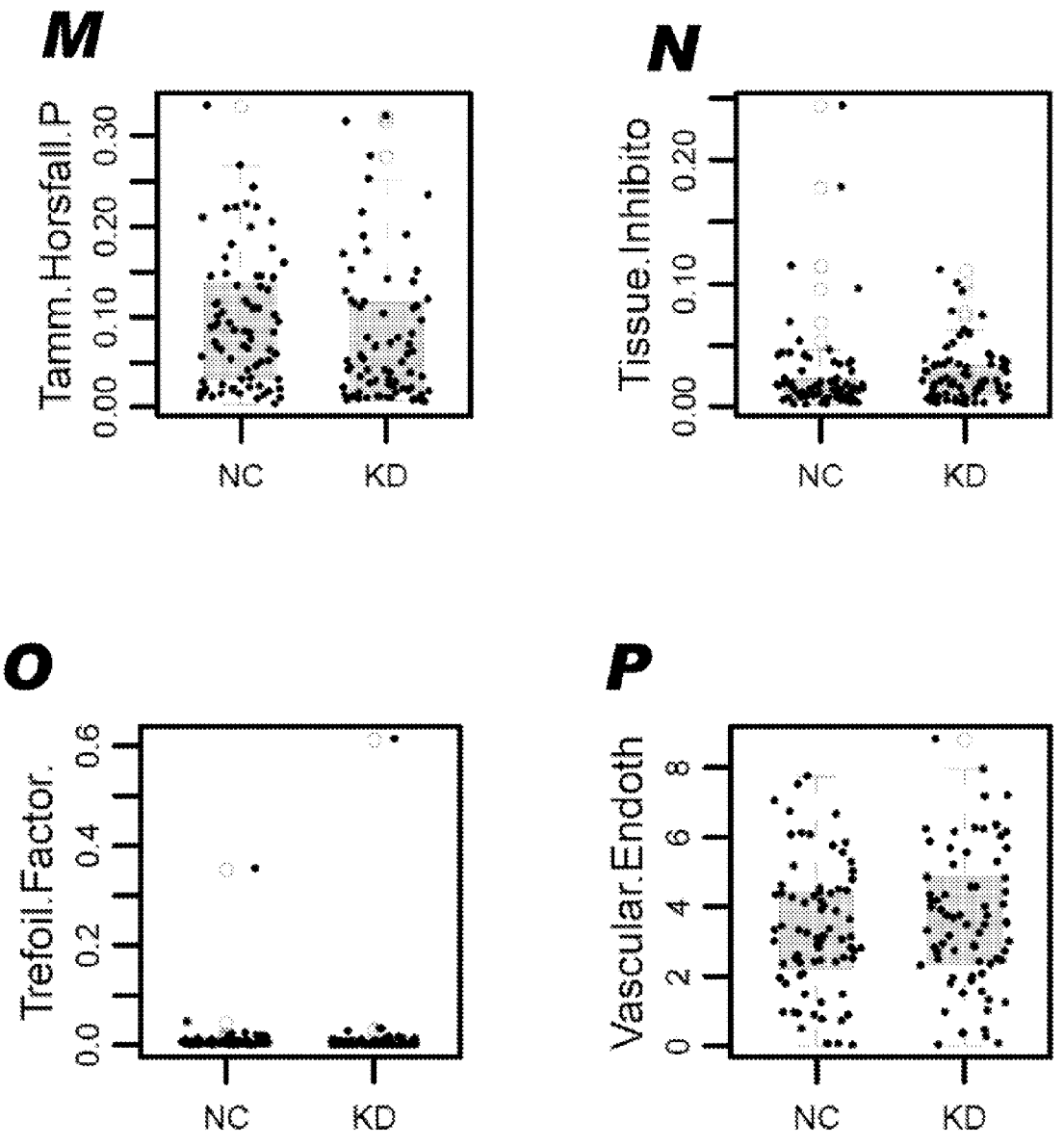
M
Tamm.Horsfall.P
0.00
0.10
0.20
0.30
NC
KD
N
Tissue.Inhibito
0.00
0.10
0.20
NC
KD
O
Trefoil.Factor.
0.0
0.2
0.4
0.6
NC
KD
P
Vascular.Endoth
0
2
4
6
8
NC
KD

FIG. 22

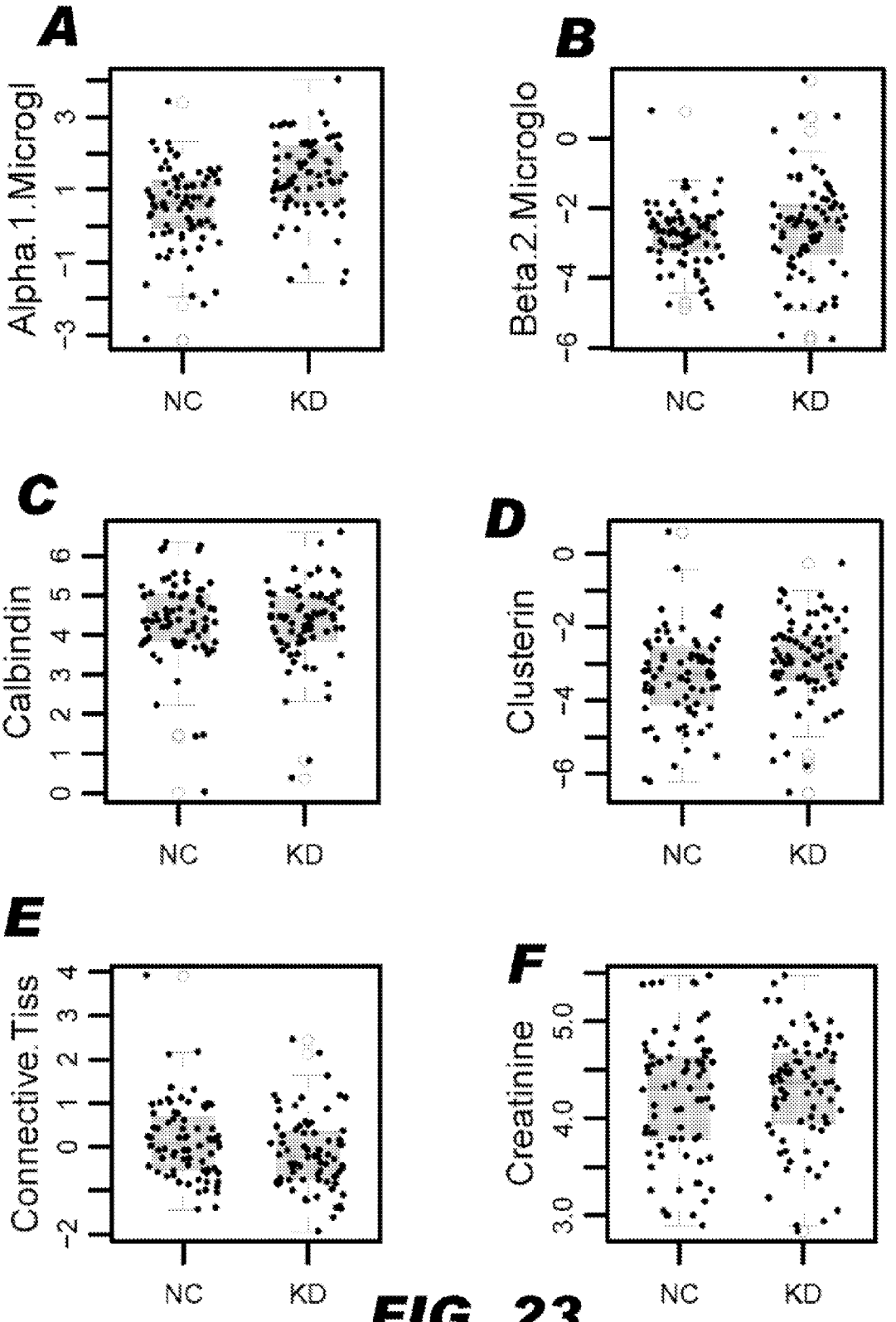
A
Alpha.1.Microgl
−3
−1
1
3
NC
KD
B
Beta.2.Microglo
−6
−4
−2
0
NC
KD
C
Calbindin
0
1
2
3
4
5
6
NC
KD
D
Clusterin
−6
−4
−2
0
NC
KD
E
Connective.Tiss
−2
0
1
2
3
4
NC
KD
F
Creatinine
3.0
4.0
5.0
NC
KD

FIG. 23

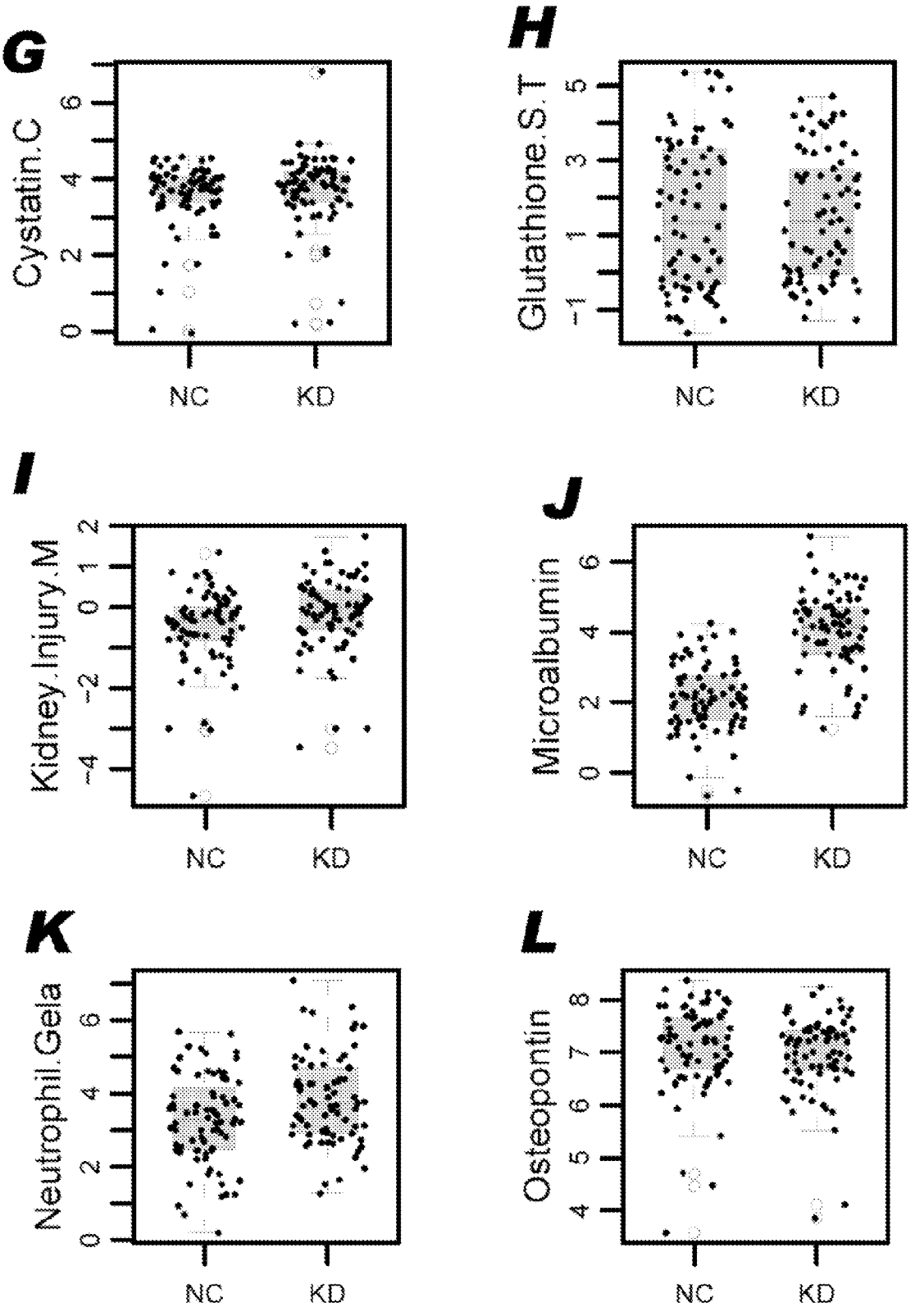
G
Cystatin.C
0
2
4
6
NC
KD
H
Glutathione.S.T
−1
1
3
5
NC
KD
I
Kidney.Injury.M
−4
−2
0
1
2
NC
KD
J
Microalbumin
0
2
4
6
NC
KD
K
Neutrophil.Gela
0
2
4
6
NC
KD
L
Osteopontin
4
5
6
7
8
NC
KD

FIG. 23

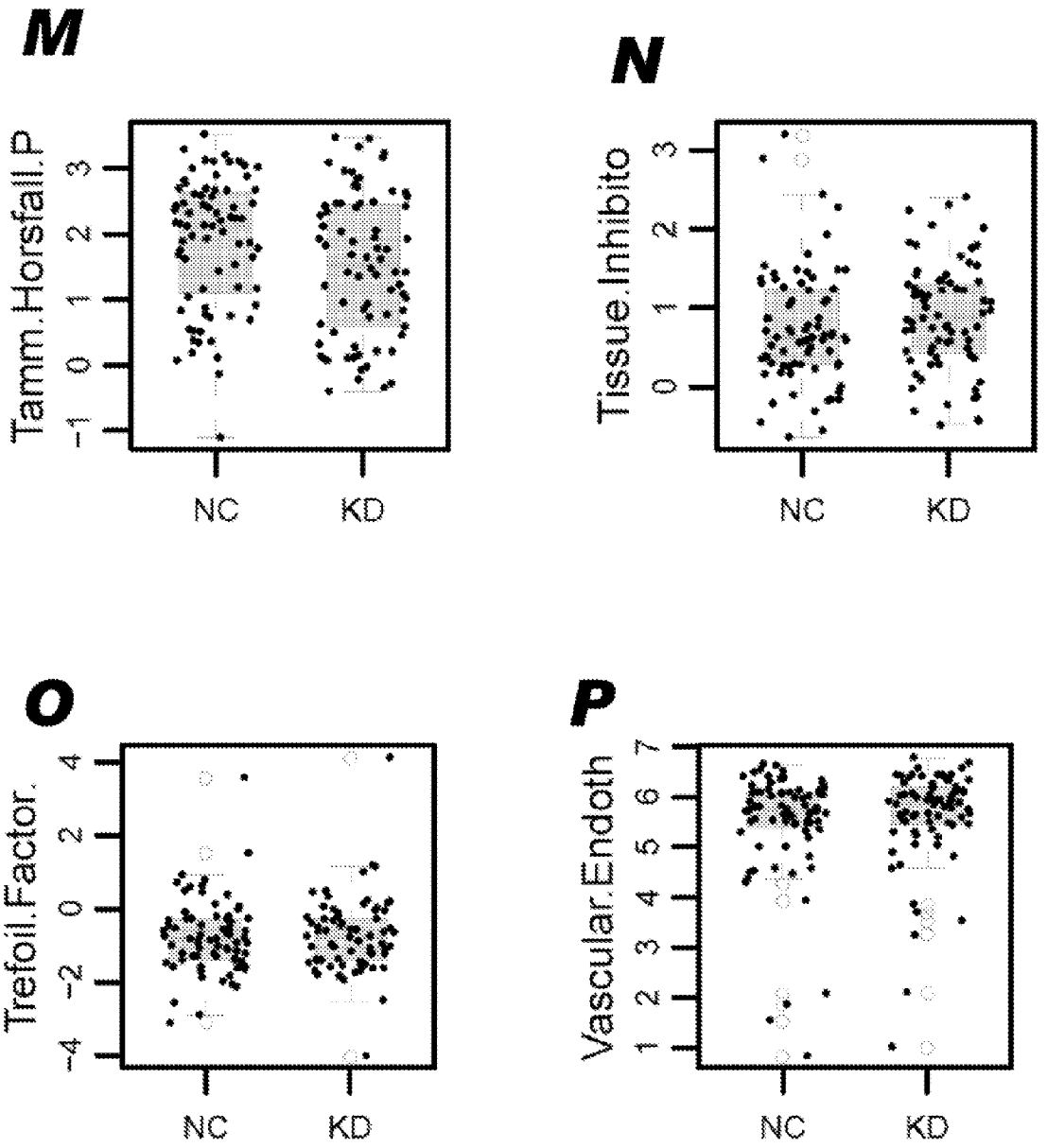
M
Tamm.Horsfall.P
−1 0 1 2 3
NC
KD
N
Tissue.Inhibito
0 1 2 3
NC
KD
O
Trefoil.Factor.
−4 −2 0 2 4
NC
KD
P
Vascular.Endoth
1 2 3 4 5 6 7
NC
KD

FIG. 23

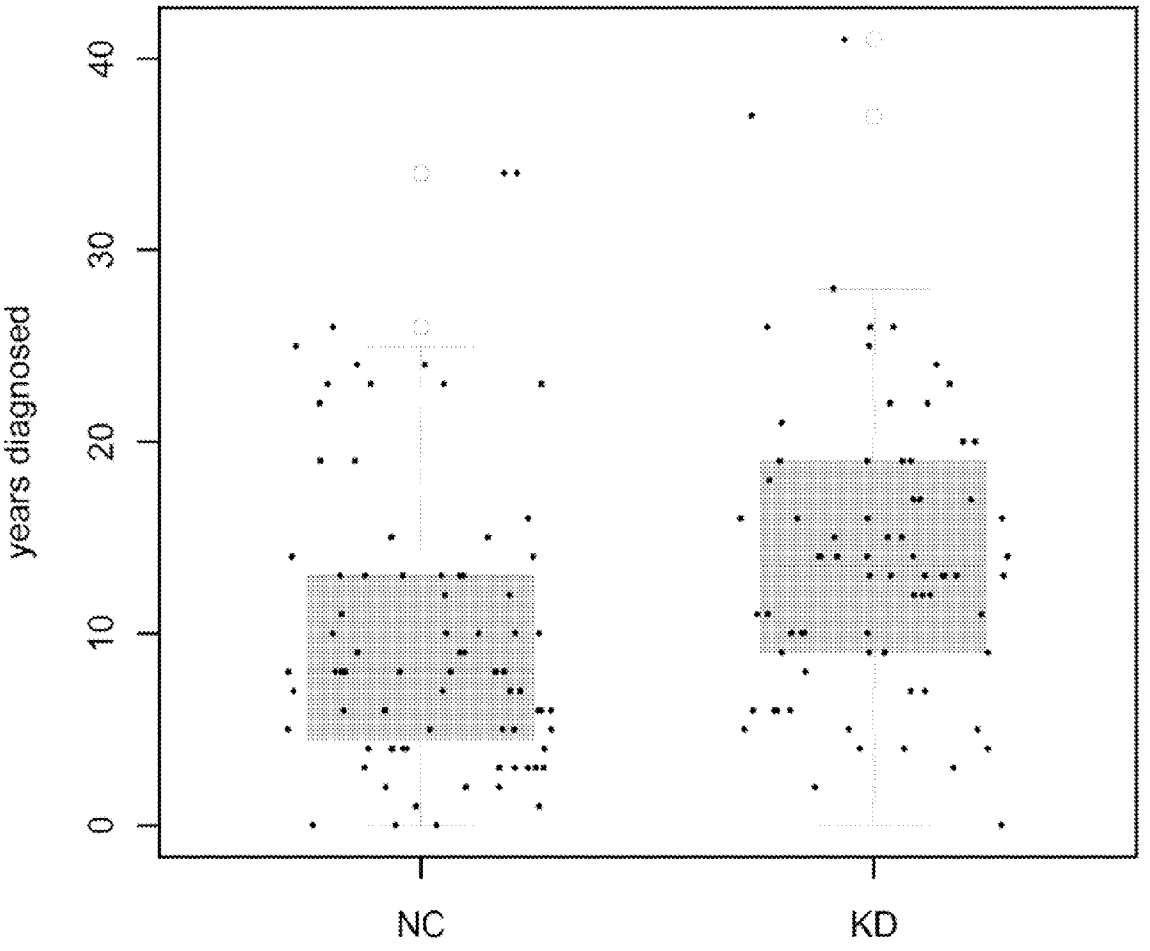

FIG. 24

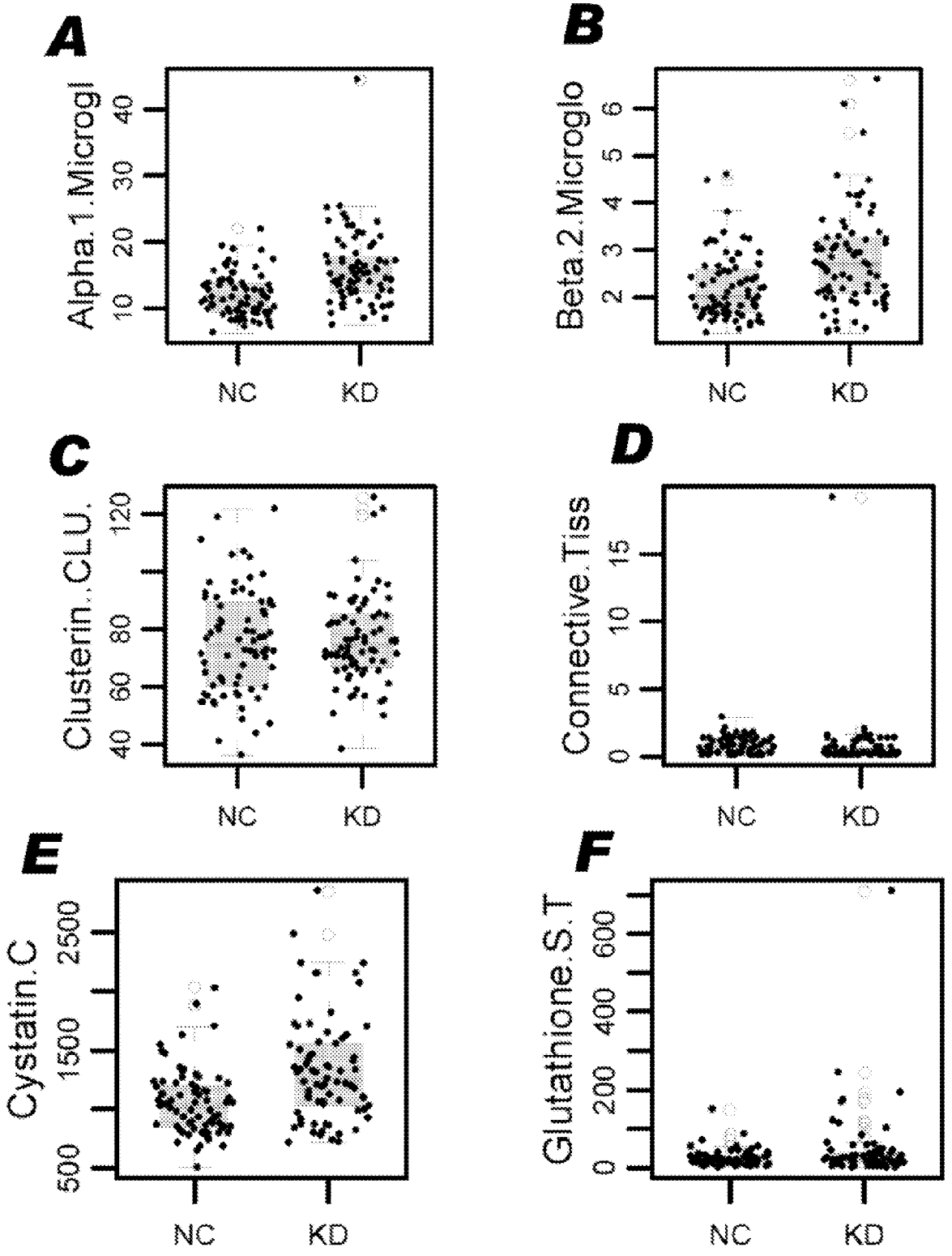
A
Alpha.1.Microgl
10
20
30
40
NC
KD
B
Beta.2.Microglo
2
3
4
5
6
NC
KD
C
Clusterin..CLU.
40
60
80
120
NC
KD
D
Connective.Tiss
0
5
10
15
NC
KD
E
Cystatin.C
500
1500
2500
NC
KD
F
Glutathione.S.T
0
200
400
600
NC
KD

FIG. 25

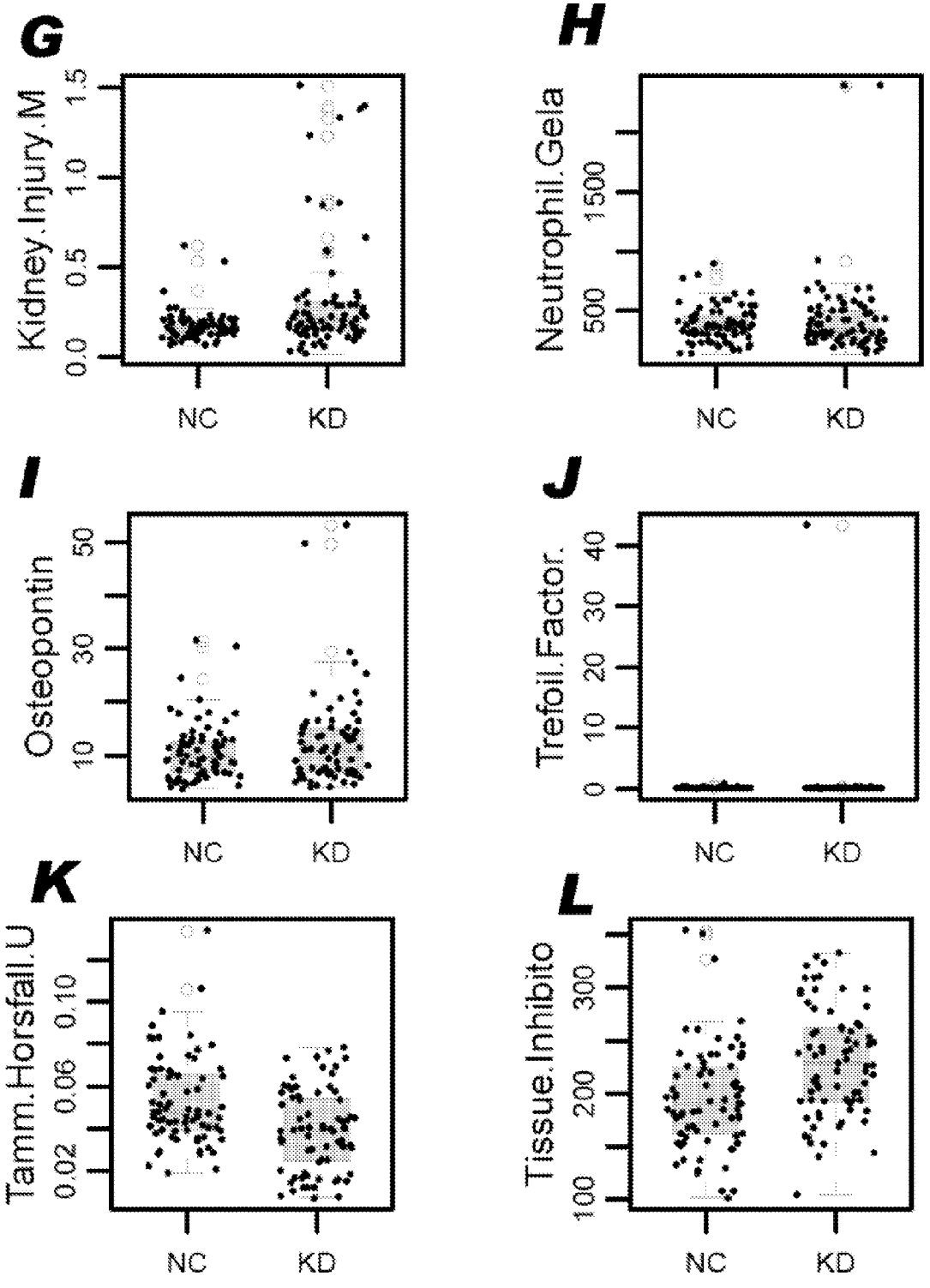
G
Kidney.Injury.M
0.0
0.5
1.0
1.5
NC
KD
H
Neutrophil.Gela
500
1500
NC
KD
I
Osteopontin
10
30
50
NC
KD
J
Trefoil.Factor.
0
10
20
30
40
NC
KD
K
Tamm.Horsfall.U
0.02
0.06
0.10
NC
KD
L
Tissue.Inhibito
100
200
300
NC
KD

FIG. 25

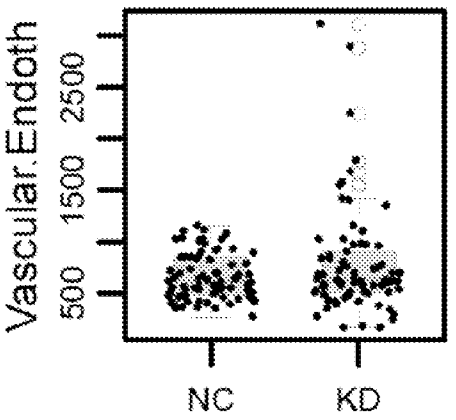

FIG. 25M

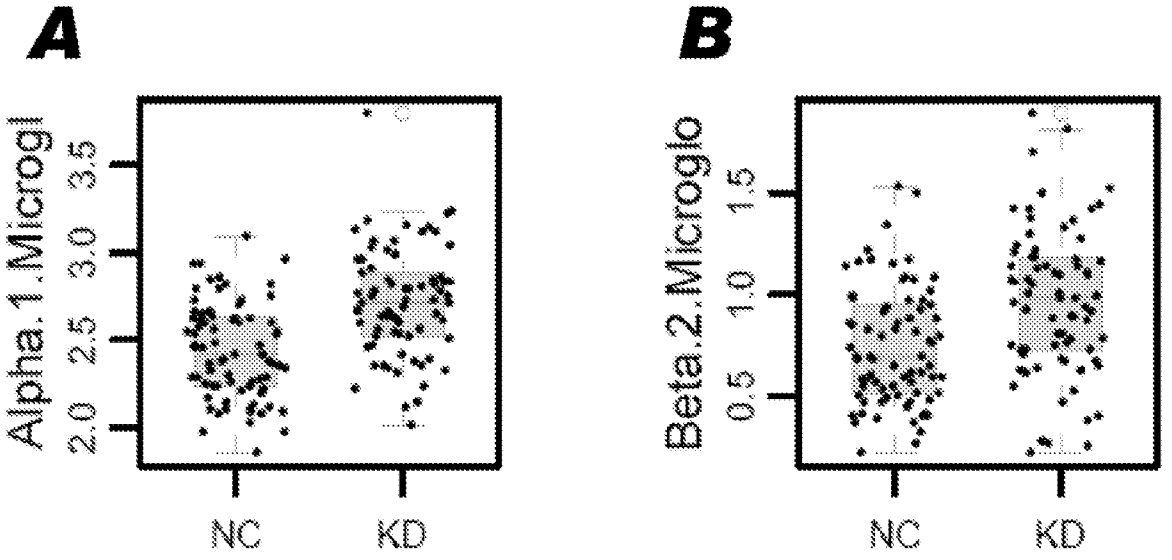

FIG. 26

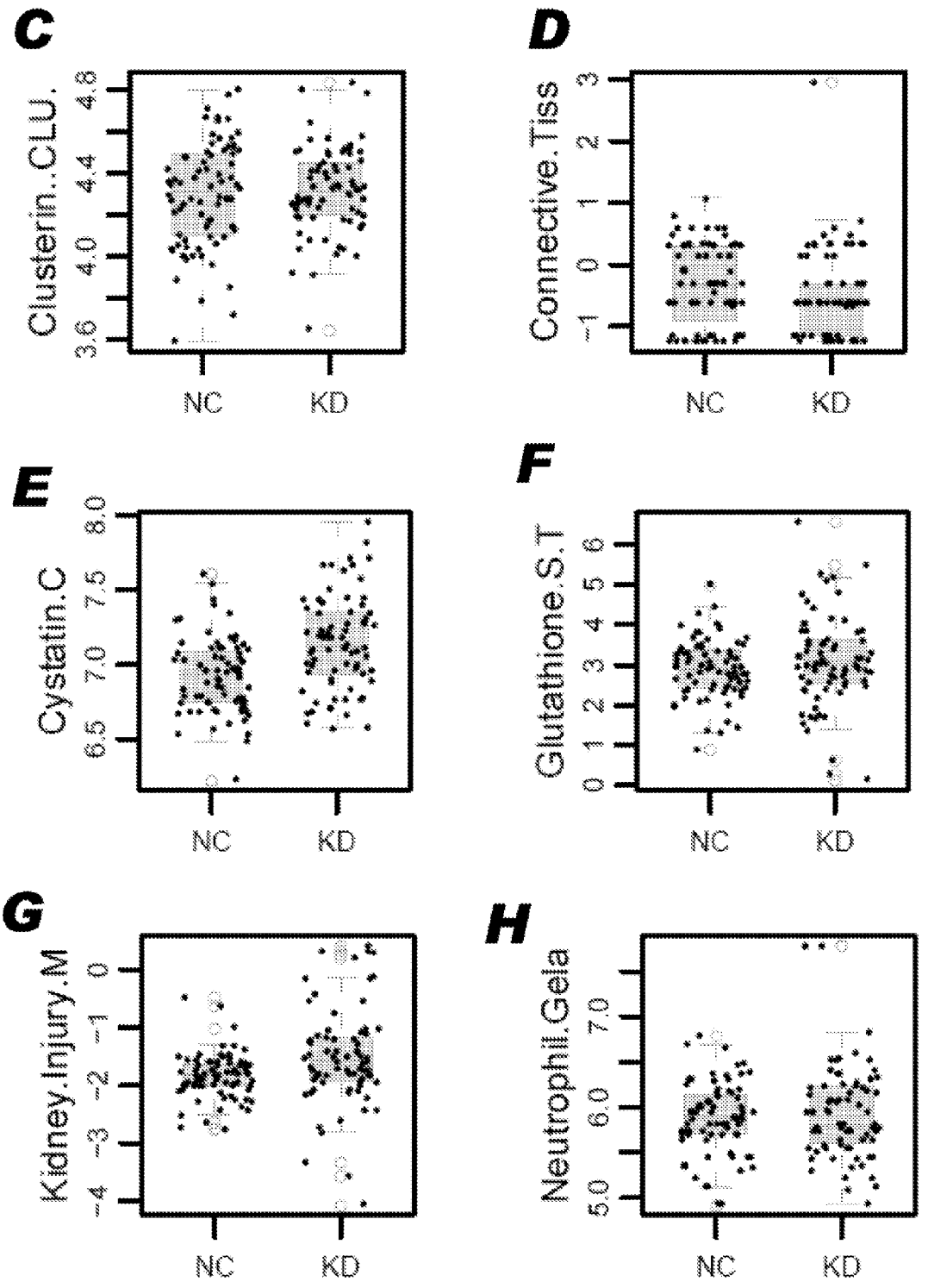
C
Clusterin..CLU.
3.6
4.0
4.4
4.8
NC
KD
D
Connective.Tiss
−1
0
1
2
3
NC
KD
E
Cystatin.C
6.5
7.0
7.5
8.0
NC
KD
F
Glutathione.S.T
0
1
2
3
4
5
6
NC
KD
G
Kidney.Injury.M
−4
−3
−2
−1
0
NC
KD
H
Neutrophil.Gela
5.0
6.0
7.0
NC
KD

FIG. 26

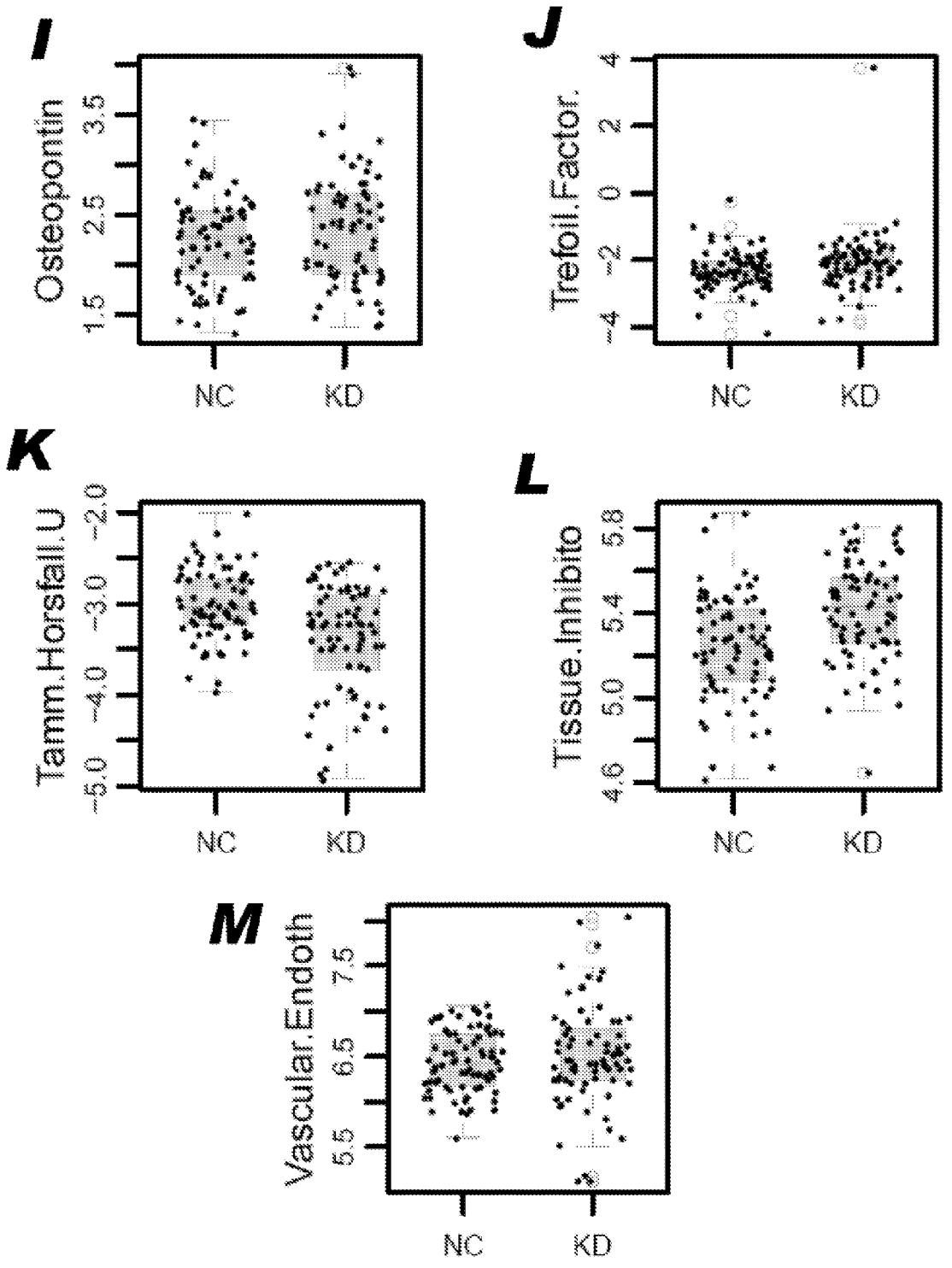
I
Osteopontin
1.5
2.5
3.5
NC
KD
J
Trefoil.Factor.
−4
−2
0
2
4
NC
KD
K
Tamm.Horsfall.U
−5.0
−4.0
−3.0
−2.0
NC
KD
L
Tissue.Inhibito
4.6
5.0
5.4
5.8
NC
KD
M
Vascular.Endoth
5.5
6.5
7.5
NC
KD

FIG. 26

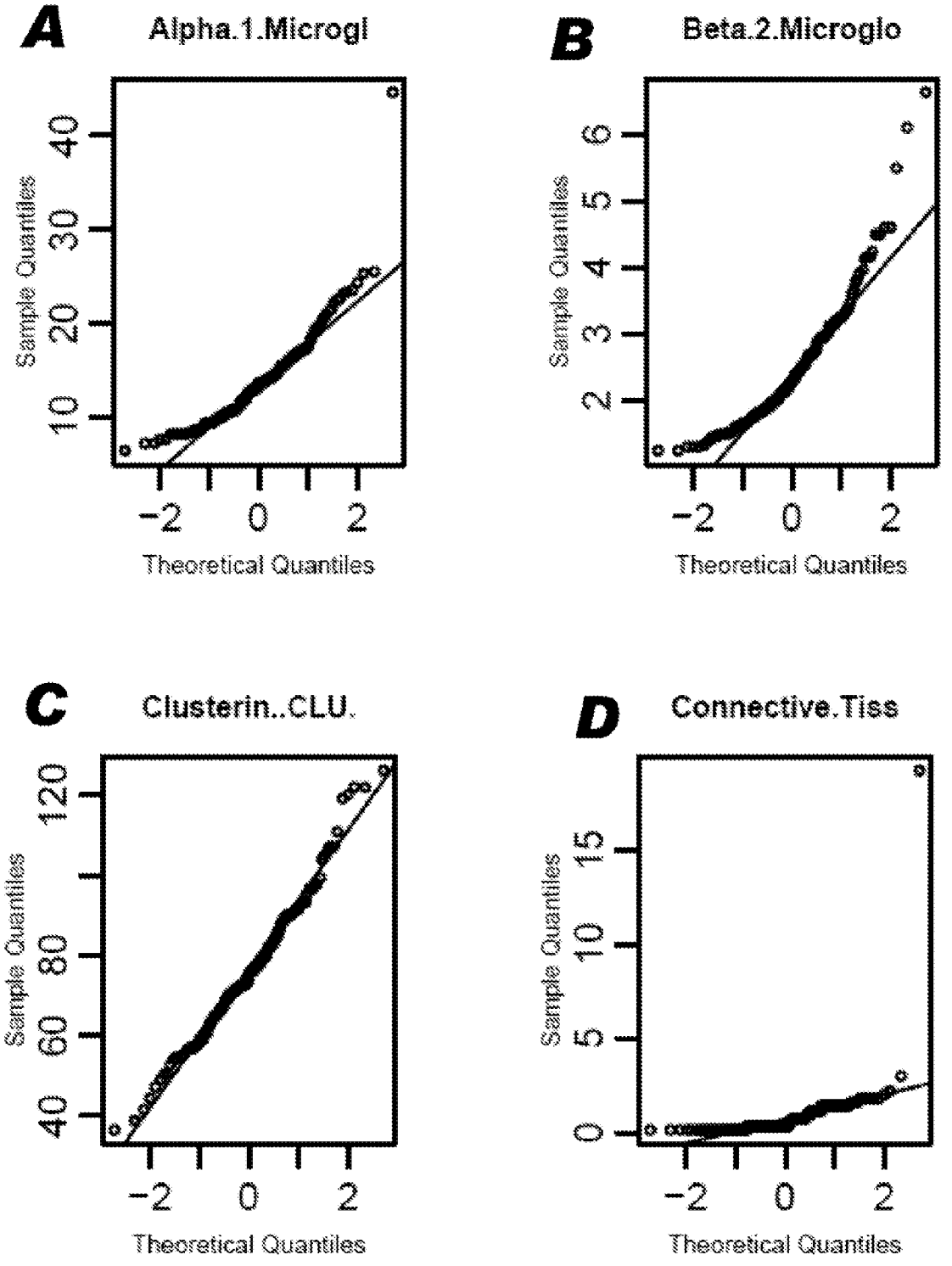
A
Alpha.1.Microgl
Sample Quantiles
10
20
30
40
−2
0
2
Theoretical Quantiles
B
Beta.2.Microglo
Sample Quantiles
2
3
4
5
6
−2
0
2
Theoretical Quantiles
C
Clusterin..CLU.
Sample Quantiles
40
60
80
120
−2
0
2
Theoretical Quantiles
D
Connective.Tiss
Sample Quantiles
0
5
10
15
−2
0
2
Theoretical Quantiles

FIG. 27

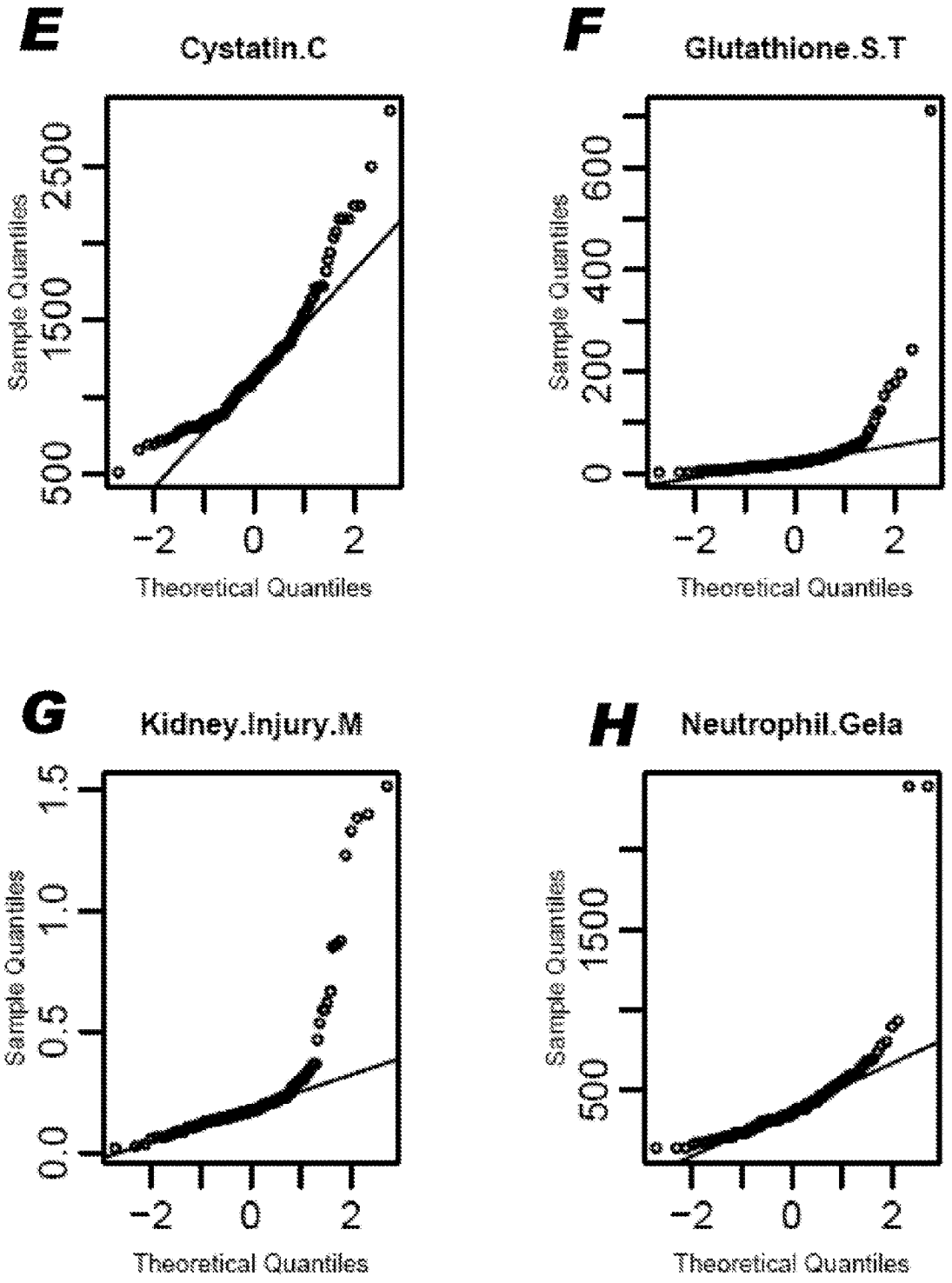
E
Cystatin.C
Sample Quantiles
500
1500
2500
−2
0
2
Theoretical Quantiles
F
Glutathione.S.T
Sample Quantiles
0
200
400
600
−2
0
2
Theoretical Quantiles
G
Kidney.Injury.M
Sample Quantiles
0.0
0.5
1.0
1.5
−2
0
2
Theoretical Quantiles
H
Neutrophil.Gela
Sample Quantiles
500
1500
−2
0
2
Theoretical Quantiles

FIG. 27

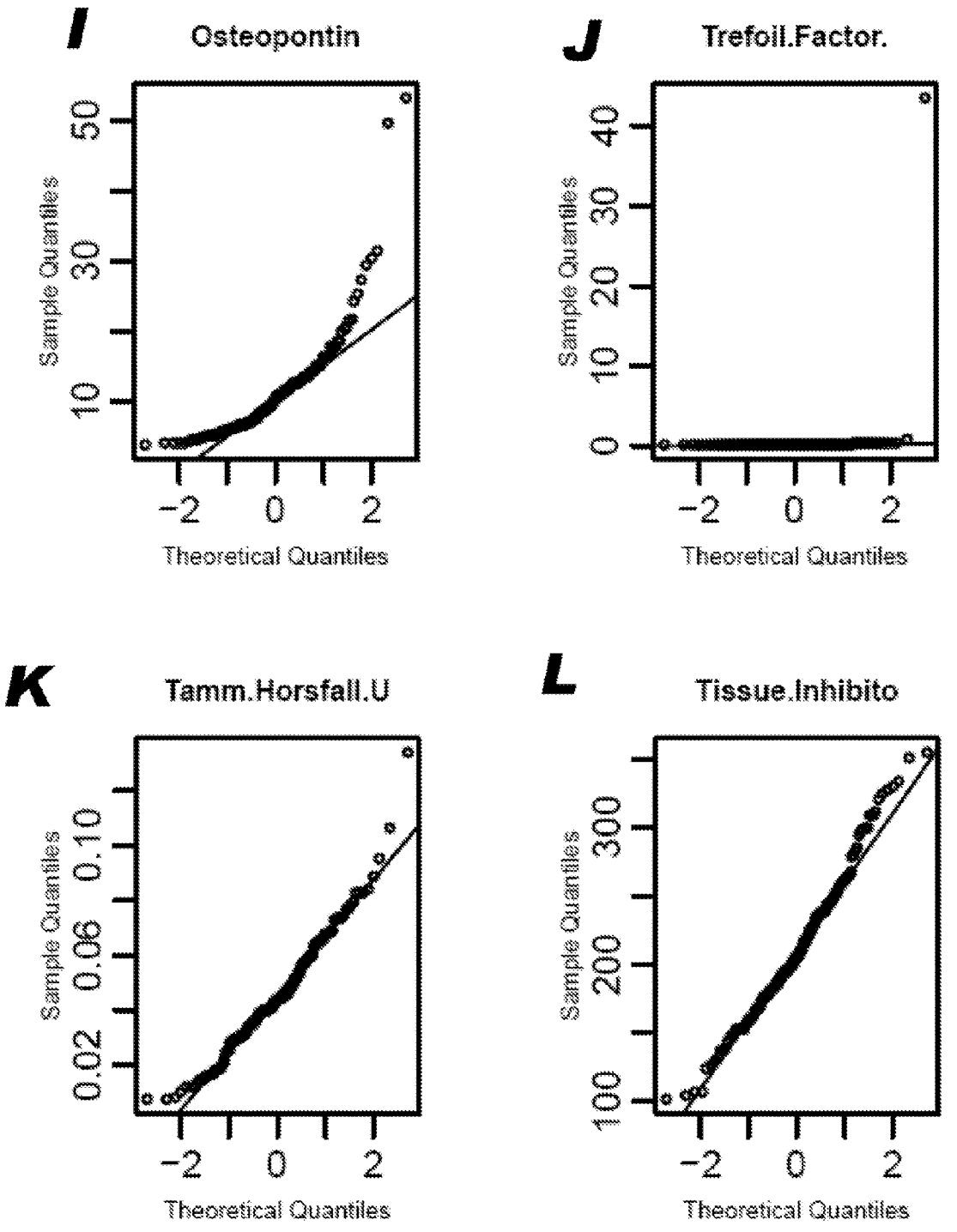
I
Osteopontin
Sample Quantiles
10
30
50
−2
0
2
Theoretical Quantiles
J
Trefoil.Factor.
Sample Quantiles
0
10
20
30
40
−2
0
2
Theoretical Quantiles
K
Tamm.Horsfall.U
Sample Quantiles
0.02
0.06
0.10
−2
0
2
Theoretical Quantiles
L
Tissue.Inhibito
Sample Quantiles
100
200
300
−2
0
2
Theoretical Quantiles

FIG. 27

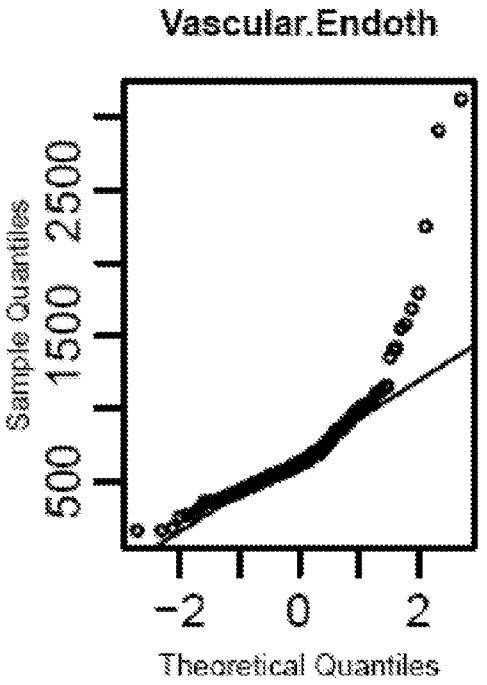

FIG. 27M

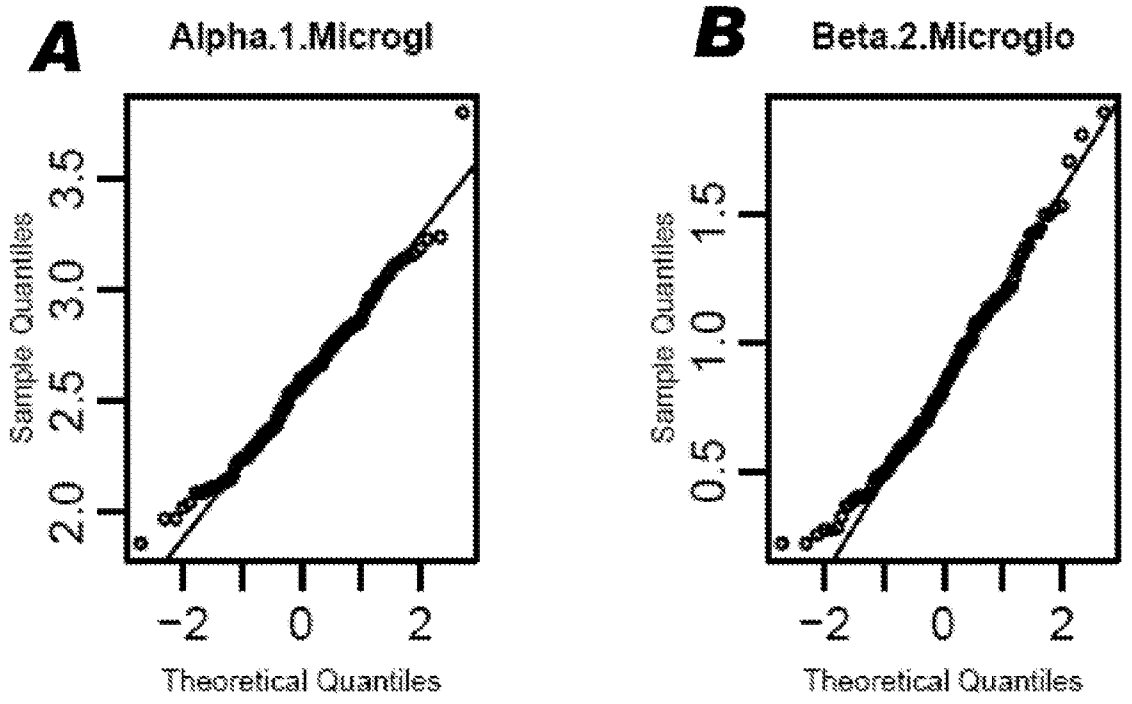

FIG. 28

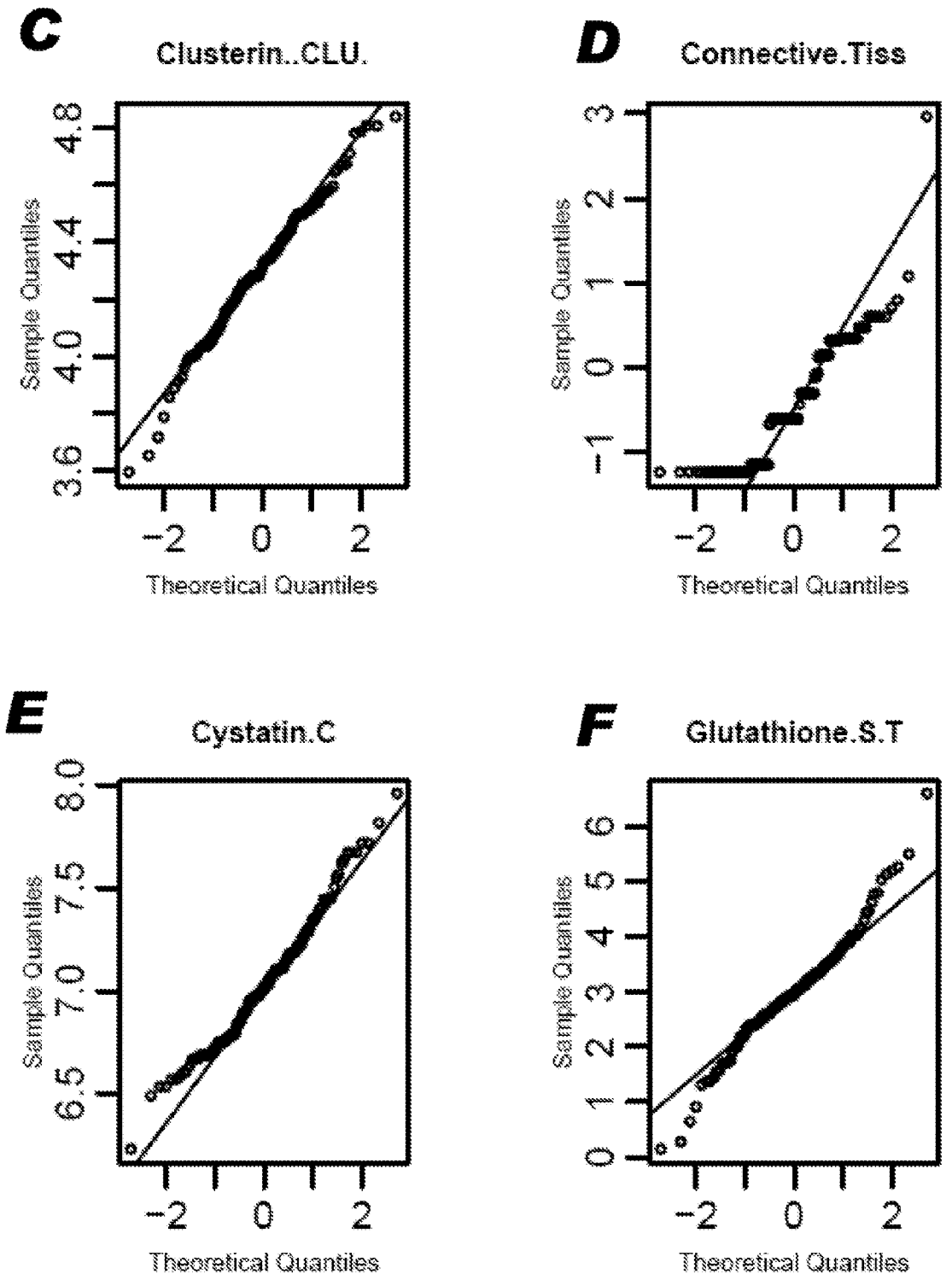
C
Clusterin..CLU.
Sample Quantiles
Theoretical Quantiles
D
Connective.Tiss
Sample Quantiles
Theoretical Quantiles
E
Cystatin.C
Sample Quantiles
Theoretical Quantiles
F
Glutathione.S.T
Sample Quantiles
Theoretical Quantiles

FIG. 28

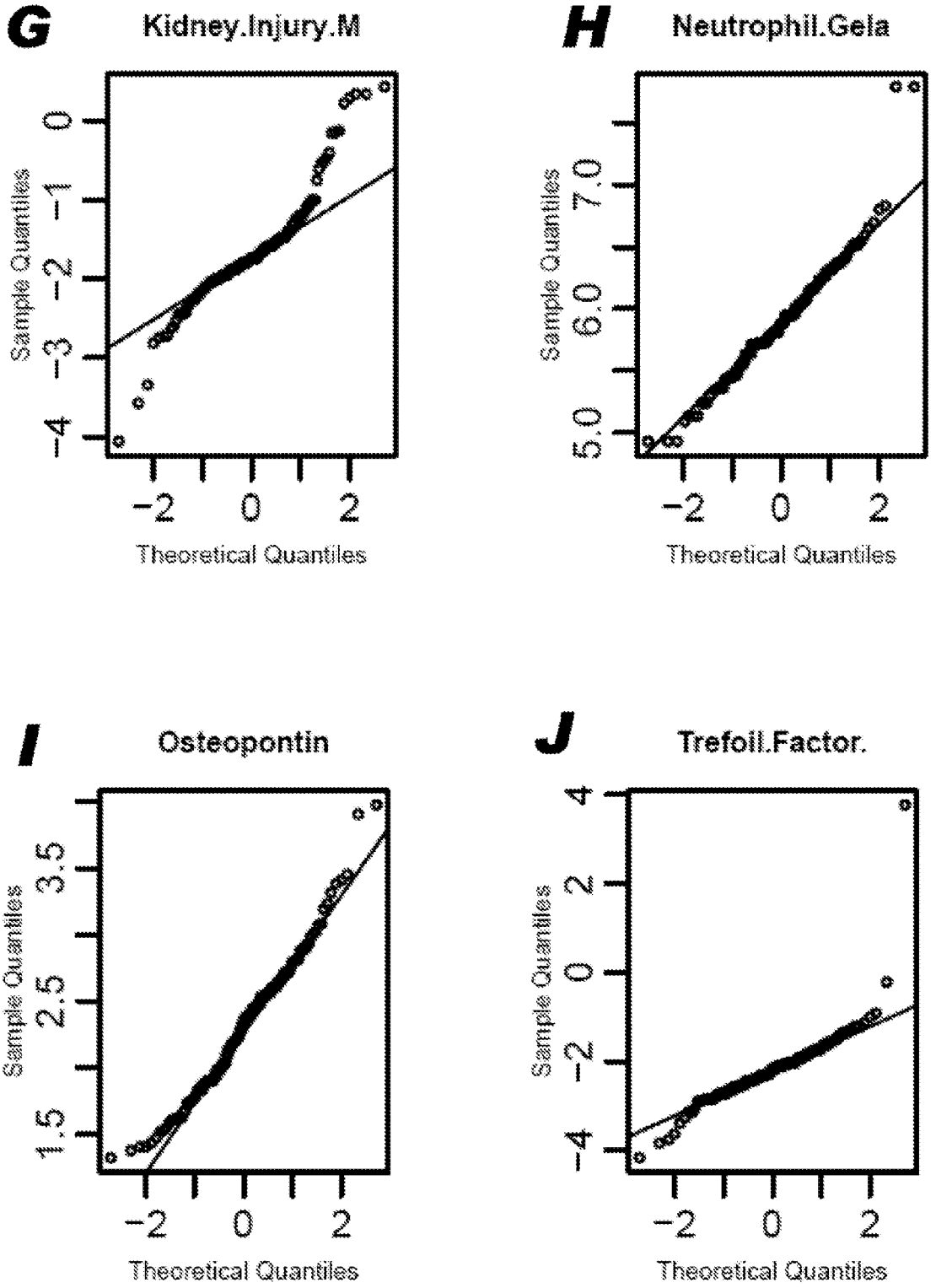
G
Kidney.Injury.M
Sample Quantiles
Theoretical Quantiles
H
Neutrophil.Gela
Sample Quantiles
Theoretical Quantiles
I
Osteopontin
Sample Quantiles
Theoretical Quantiles
J
Trefoil.Factor.
Sample Quantiles
Theoretical Quantiles

FIG. 28

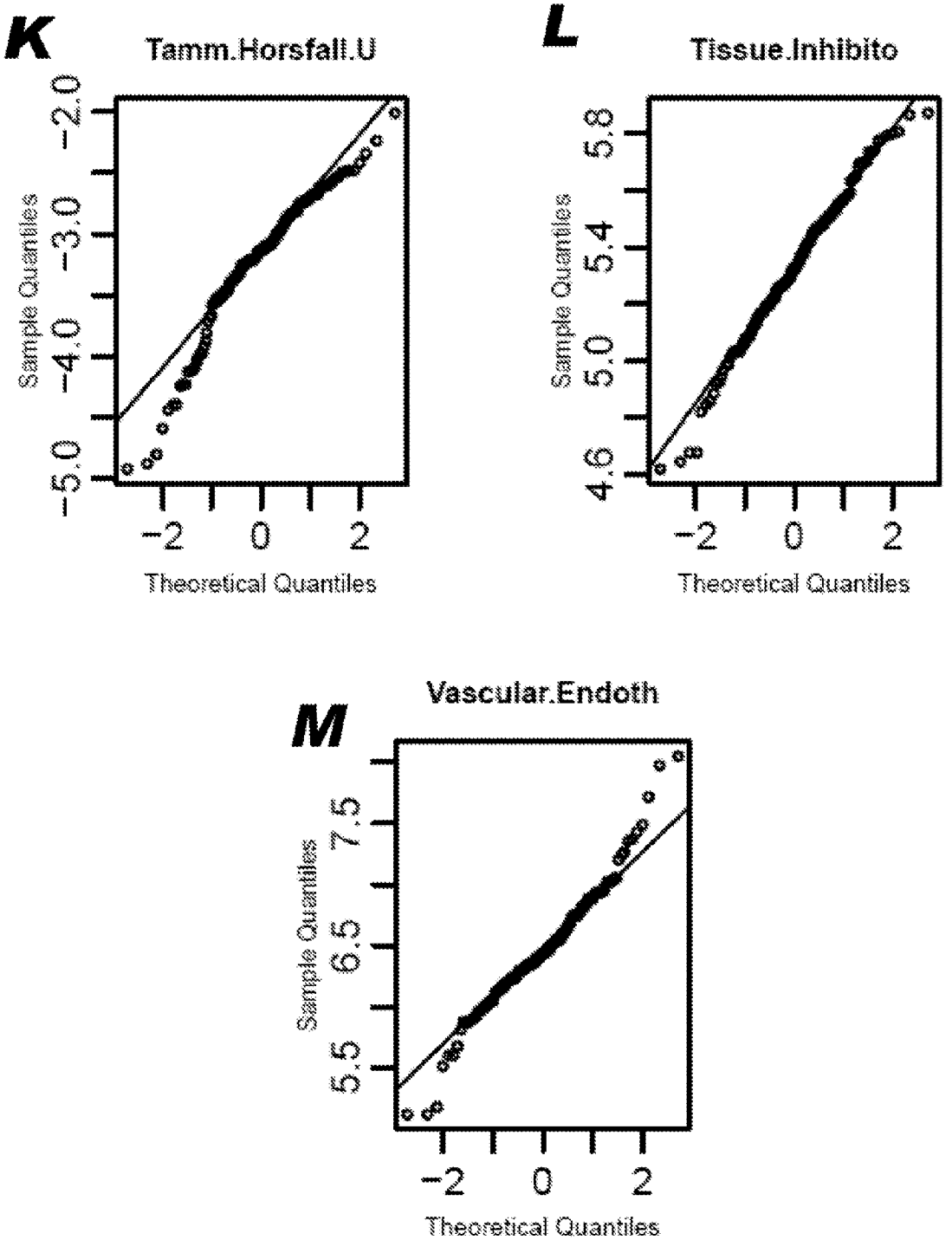
K
Tamm.Horsfall.U
Sample Quantiles
−5.0
−4.0
−3.0
−2.0
−2
0
2
Theoretical Quantiles
L
Tissue.Inhibito
Sample Quantiles
4.6
5.0
5.4
5.8
−2
0
2
Theoretical Quantiles
M
Vascular.Endoth
Sample Quantiles
5.5
6.5
7.5
−2
0
2
Theoretical Quantiles

FIG. 28

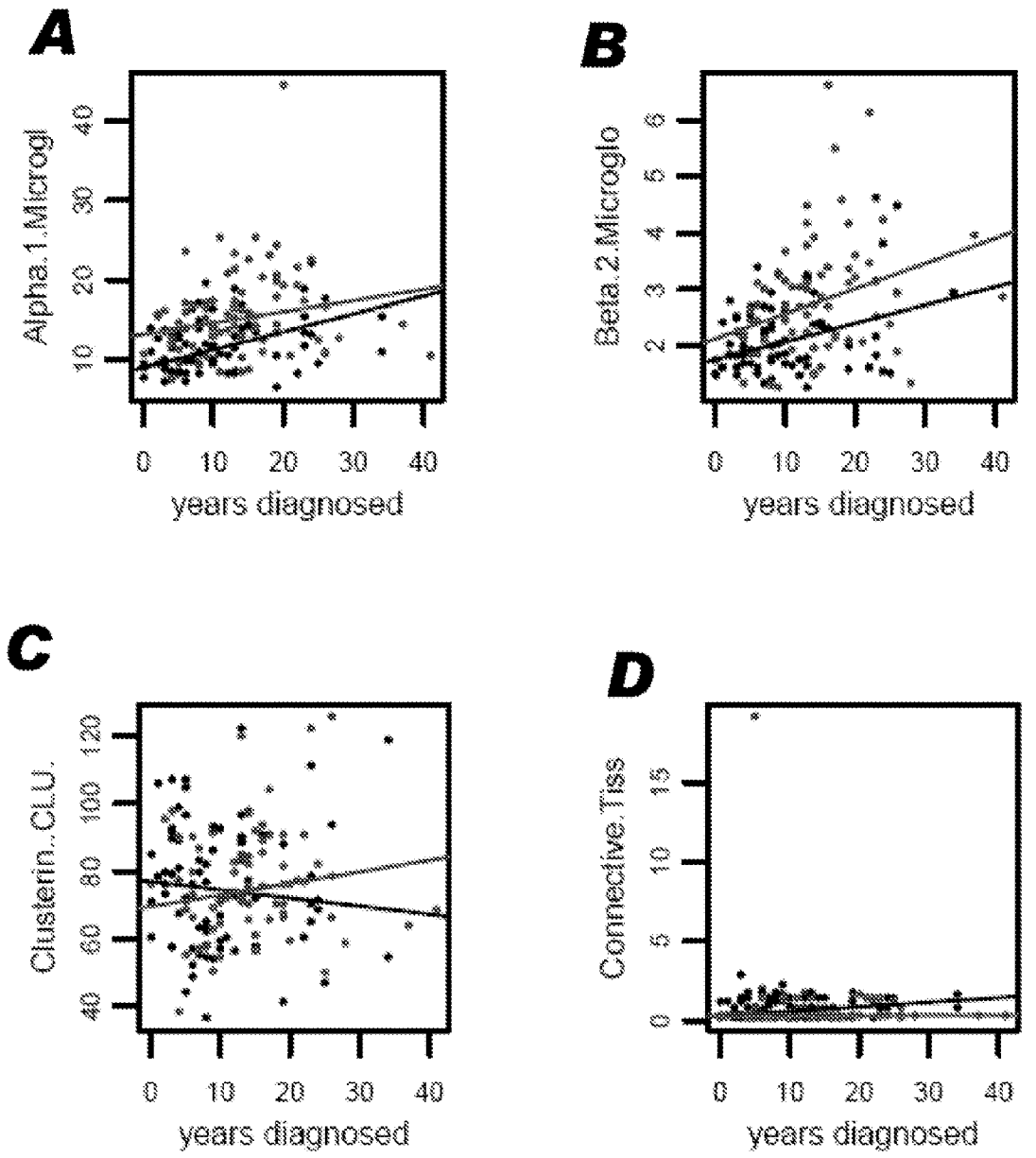
A
Alpha.1.Microgl
10
20
30
40
0
10
20
30
40
years diagnosed
B
Beta.2.Microglo
2
3
4
5
6
0
10
20
30
40
years diagnosed
C
Clusterin..CLU.
40
60
80
100
120
0
10
20
30
40
years diagnosed
D
Connective.Tiss
0
5
10
15
0
10
20
30
40
years diagnosed

FIG. 29

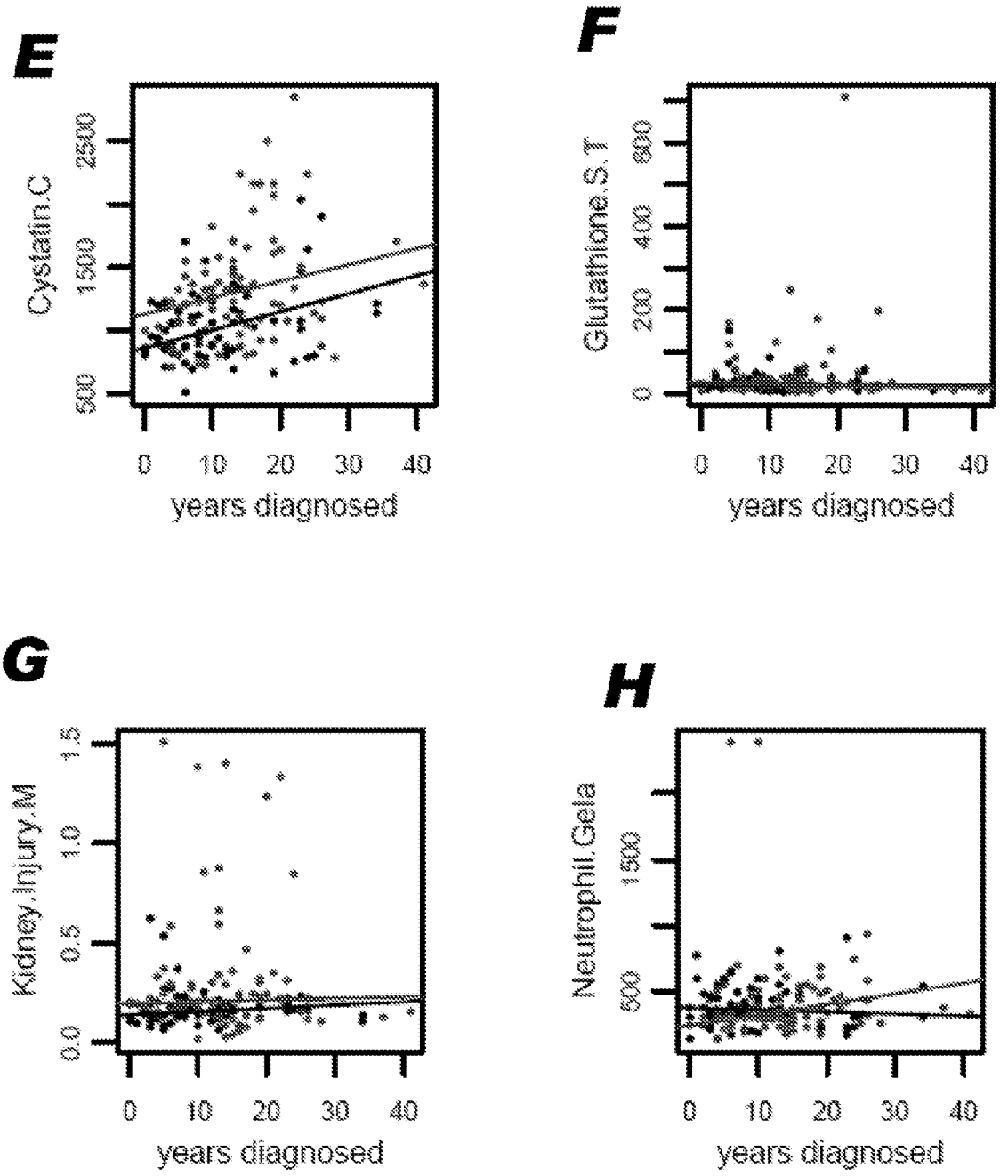
E
Cystatin.C
500
1500
2500
0
10
20
30
40
years diagnosed
F
Glutathione.S.T
0
200
400
600
0
10
20
30
40
years diagnosed
G
Kidney.Injury.M
0.0
0.5
1.0
1.5
0
10
20
30
40
years diagnosed
H
Neutrophil.Gela
500
1500
0
10
20
30
40
years diagnosed

FIG. 29

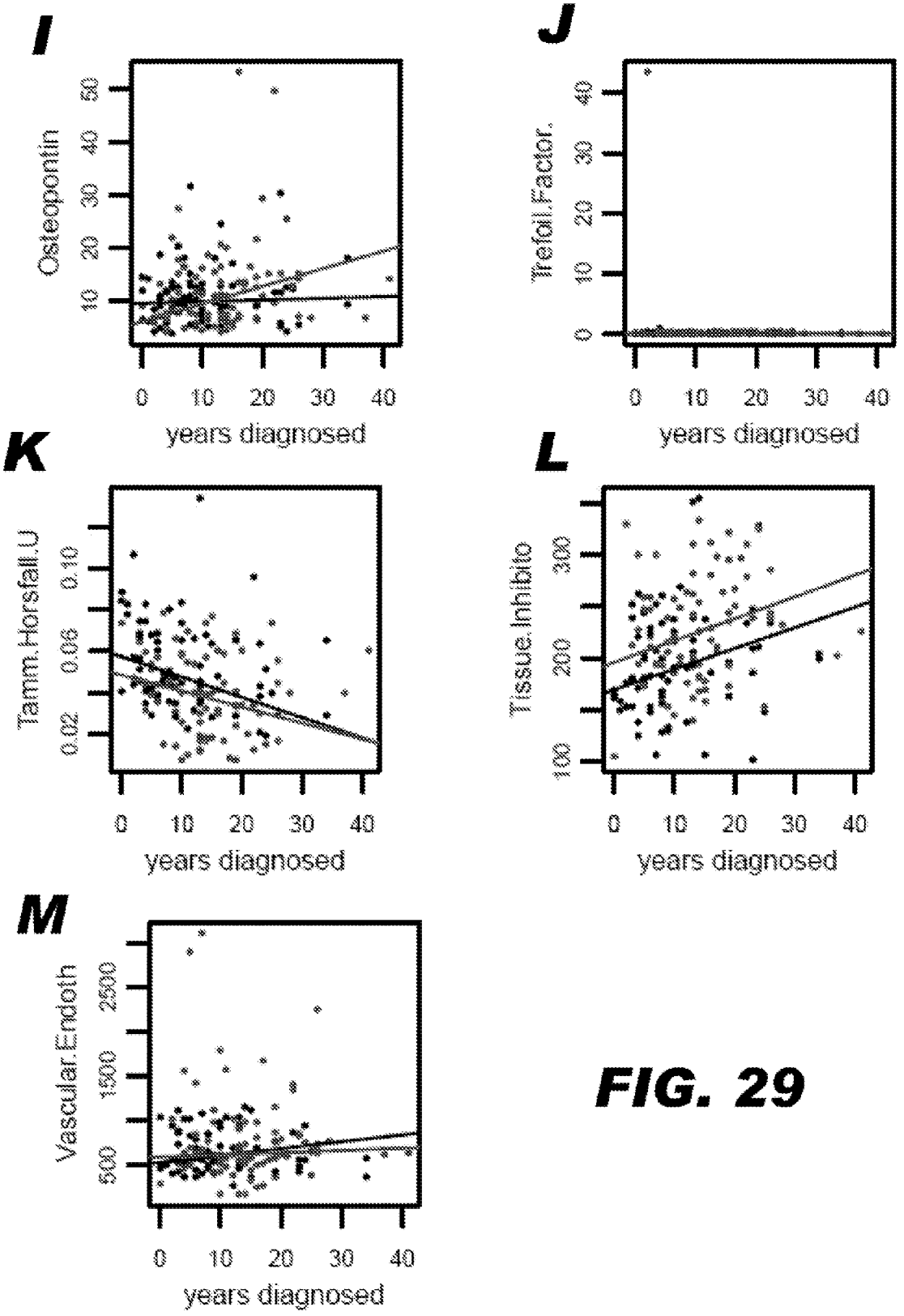
I
Osteopontin
10
20
30
40
50
0
10
20
30
40
years diagnosed
J
Trefoil.Factor.
0
10
20
30
40
0
10
20
30
40
years diagnosed
K
Tamm.Horsfall.U
0.02
0.06
0.10
0
10
20
30
40
years diagnosed
L
Tissue.Inhibito
100
200
300
0
10
20
30
40
years diagnosed
M
Vascular.Endoth
500
1500
2500
0
10
20
30
40
years diagnosed

FIG. 29

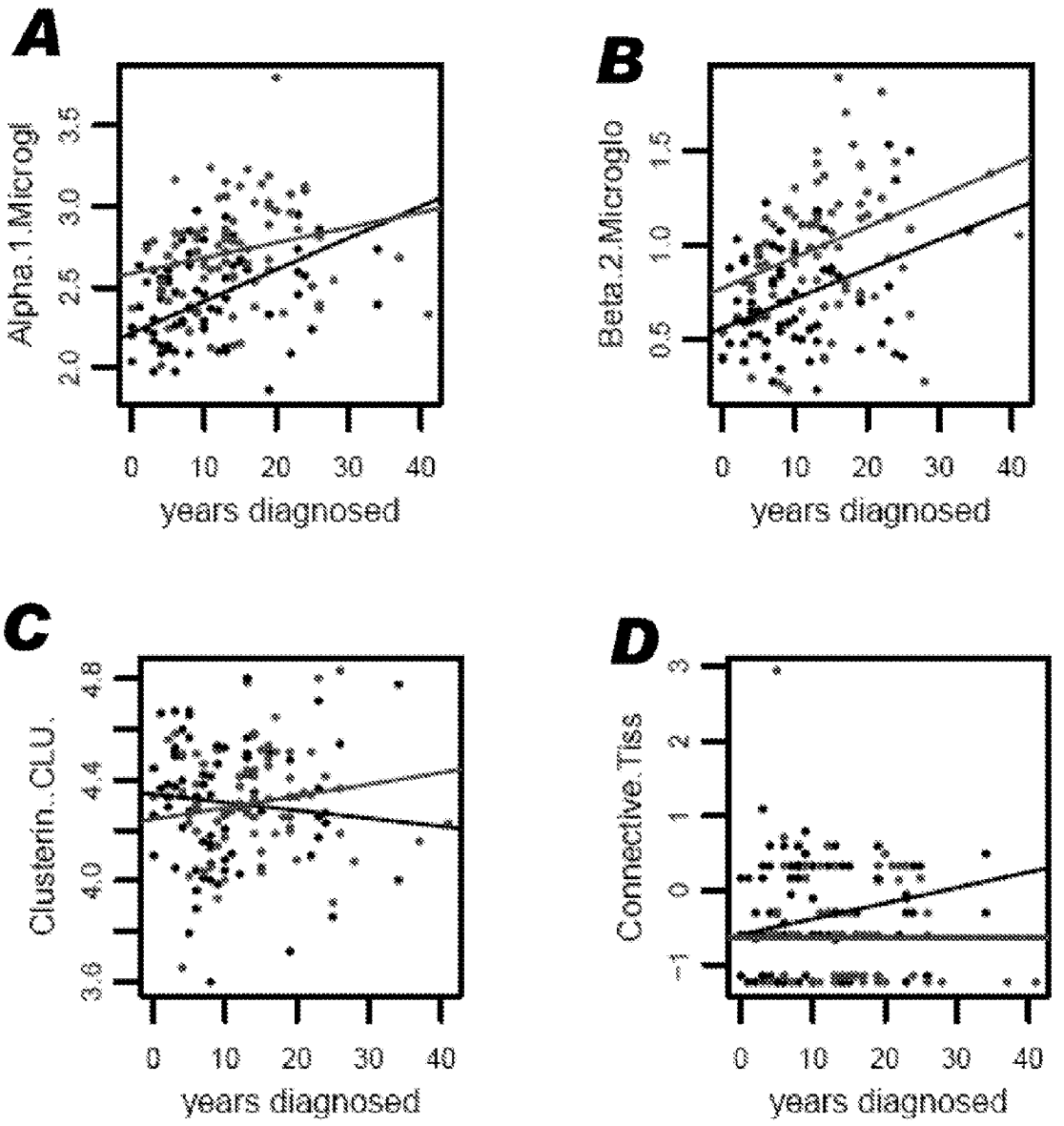
A
Alpha.1.Microgl
2.0
2.5
3.0
3.5
0
10
20
30
40
years diagnosed
B
Beta.2.Microglo
0.5
1.0
1.5
0
10
20
30
40
years diagnosed
C
Clusterin..CLU.
3.8
4.0
4.4
4.8
0
10
20
30
40
years diagnosed
D
Connective.Tiss
−1
0
1
2
3
0
10
20
30
40
years diagnosed

FIG. 30

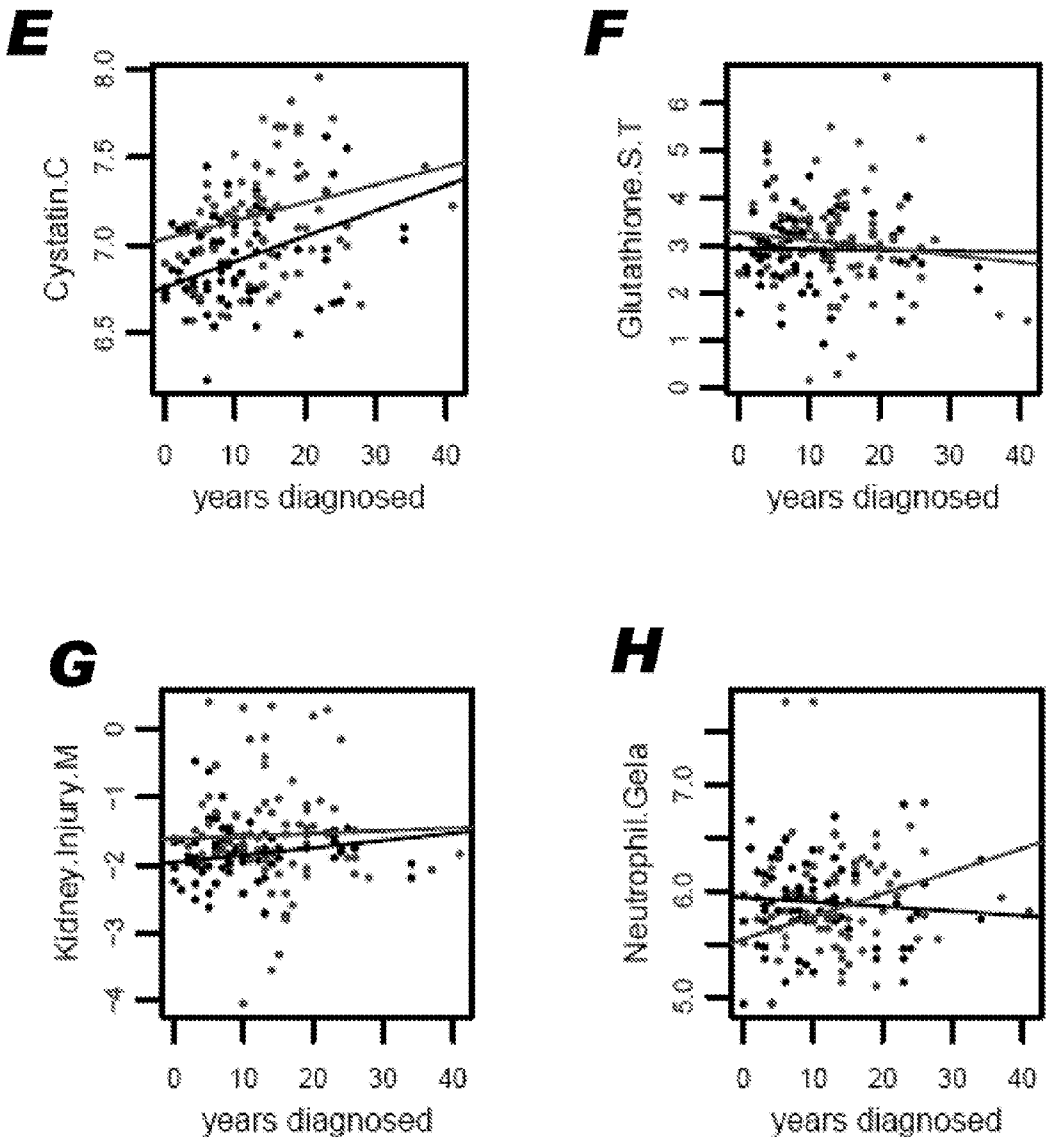
E
Cystatin.C
8.0
7.5
7.0
6.5
0
10
20
30
40
years diagnosed
F
Glutathione.S.T
6
5
4
3
2
1
0
0
10
20
30
40
years diagnosed
G
Kidney.Injury.M
0
-1
-2
-3
-4
0
10
20
30
40
years diagnosed
H
Neutrophil.Gela
7.0
6.0
5.0
0
10
20
30
40
years diagnosed

FIG. 30

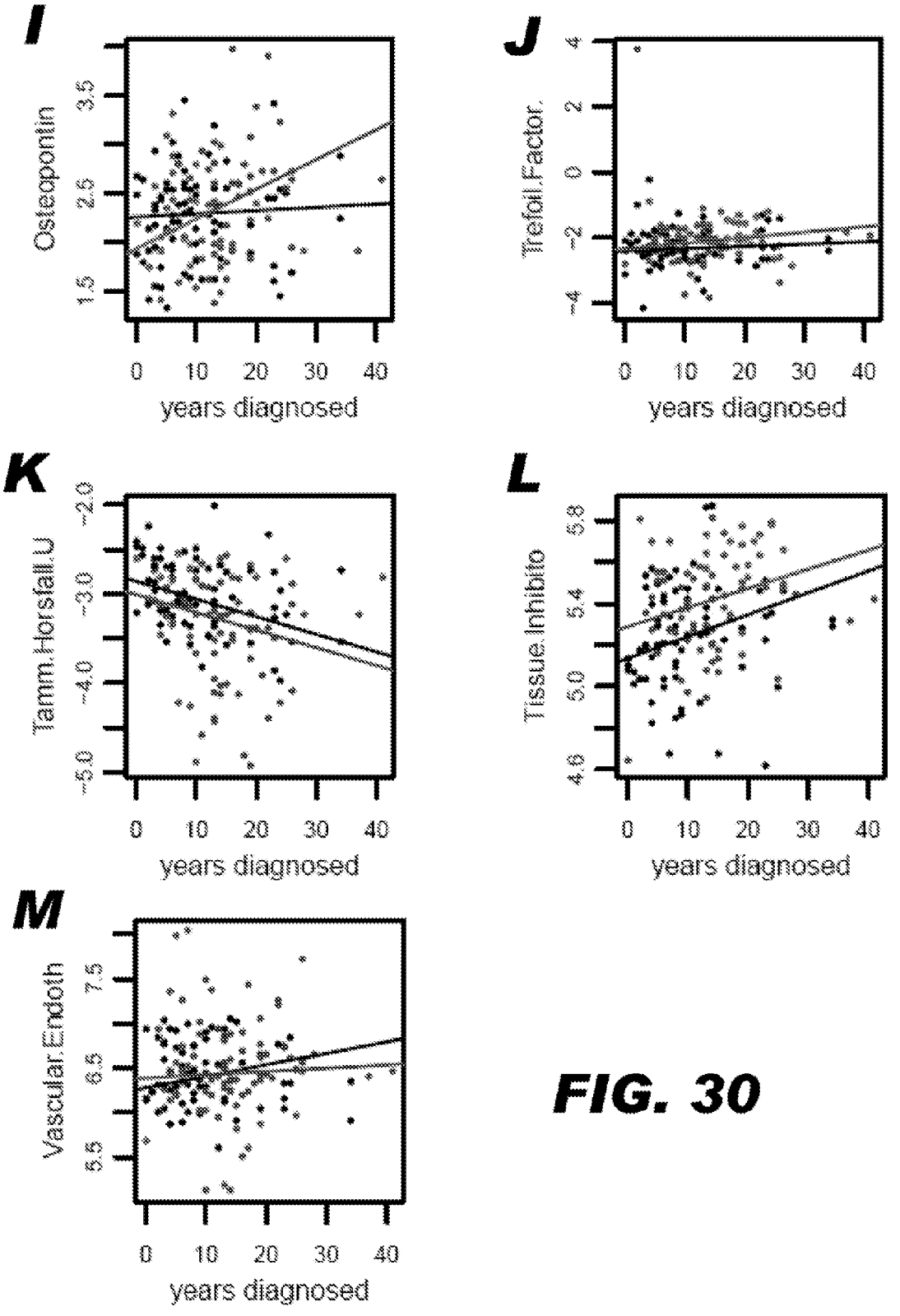
I
Osteopontin
1.5
2.5
3.5
0
10
20
30
40
years diagnosed
J
Trefoil.Factor.
-4
-2
0
2
4
0
10
20
30
40
years diagnosed
K
Tamm.Horsfall.U
-5.0
-4.0
-3.0
-2.0
0
10
20
30
40
years diagnosed
L
Tissue.Inhibito
4.6
5.0
5.4
5.8
0
10
20
30
40
years diagnosed
M
Vascular.Endoth
5.5
6.5
7.5
0
10
20
30
40
years diagnosed

FIG. 30

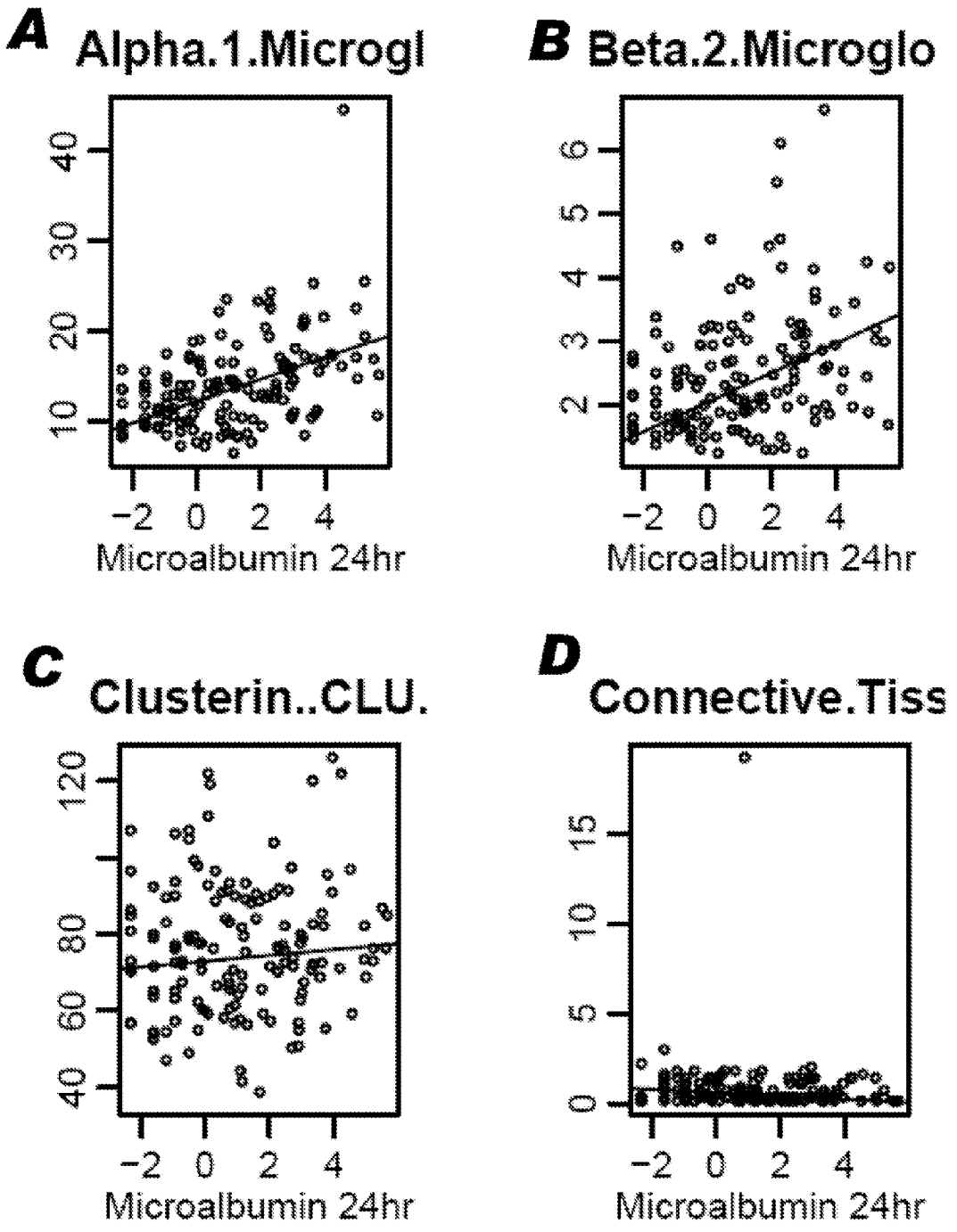
A
Alpha.1.Microgl
10
20
30
40
−2
0
2
4
Microalbumin 24hr
B
Beta.2.Microglo
2
3
4
5
6
−2
0
2
4
Microalbumin 24hr
C
Clusterin..CLU.
40
60
80
120
−2
0
2
4
Microalbumin 24hr
D
Connective.Tiss
0
5
10
15
−2
0
2
4
Microalbumin 24hr

FIG. 31

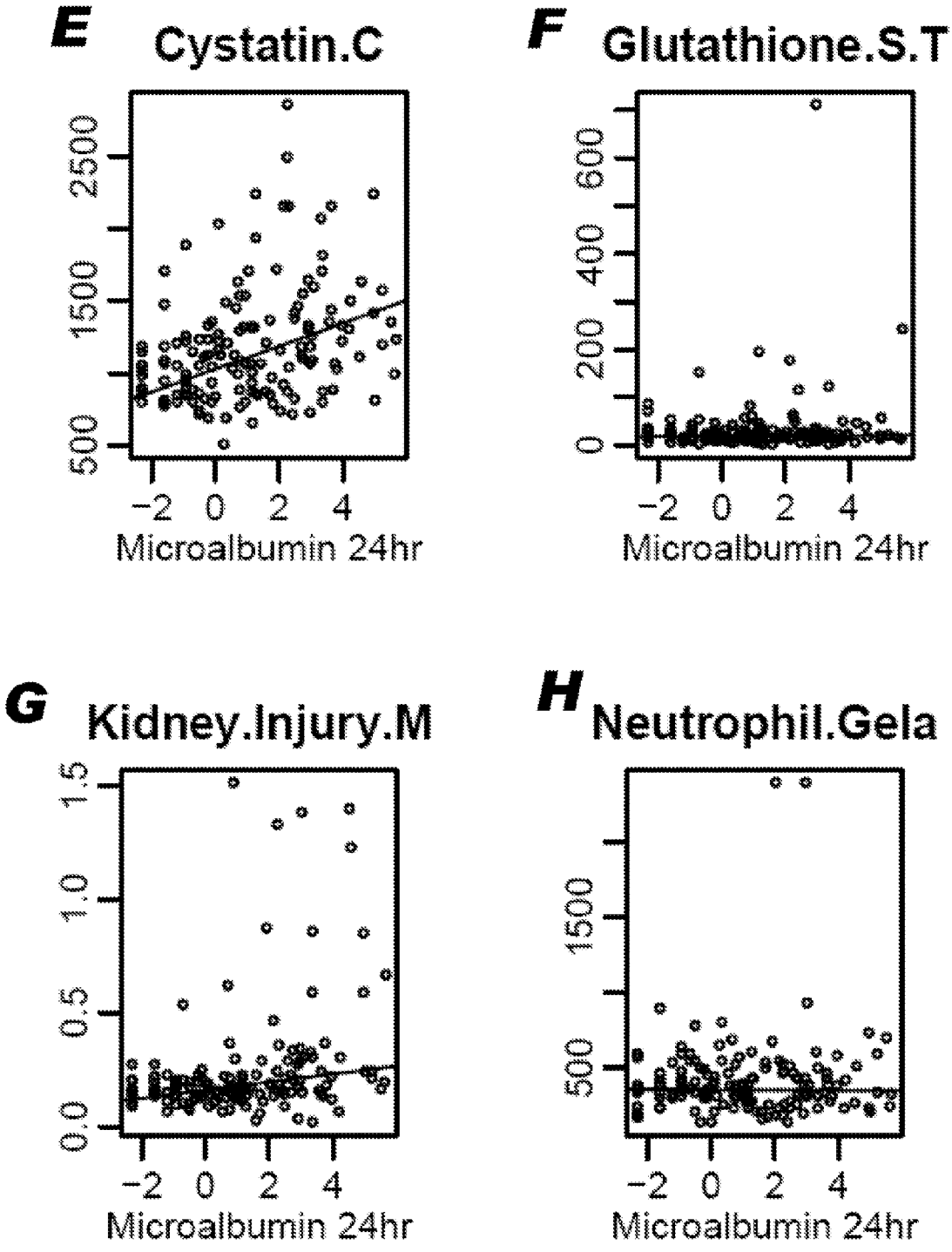
E
Cystatin.C
500
1500
2500
−2 0 2 4
Microalbumin 24hr
F
Glutathione.S.T
0
200
400
600
−2 0 2 4
Microalbumin 24hr
G
Kidney.Injury.M
0.0
0.5
1.0
1.5
−2 0 2 4
Microalbumin 24hr
H
Neutrophil.Gela
500
1500
−2 0 2 4
Microalbumin 24hr

FIG. 31

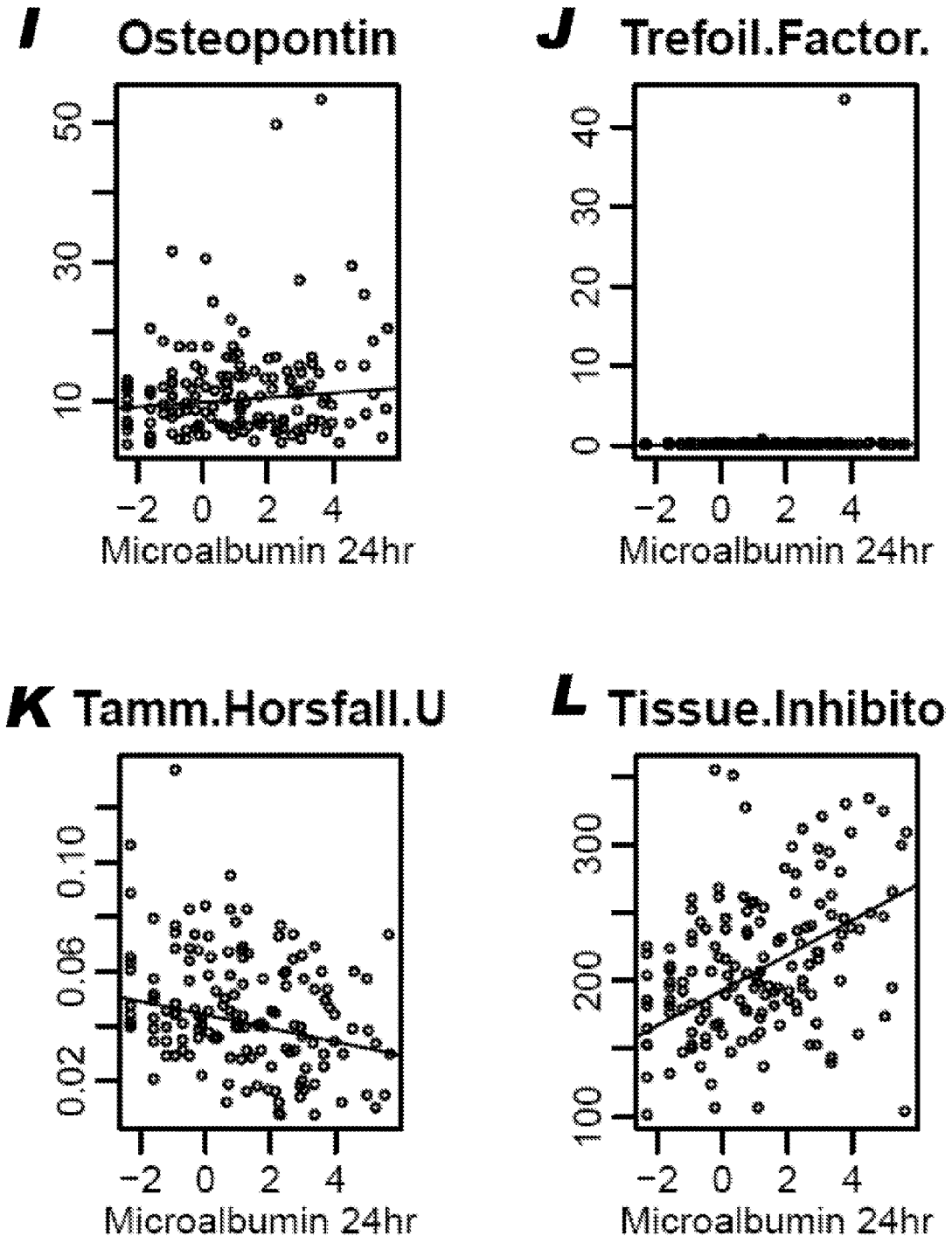
I
Osteopontin
50
30
10
−2 0 2 4
Microalbumin 24hr
J
Trefoil.Factor.
40
30
20
10
0
−2 0 2 4
Microalbumin 24hr
K
Tamm.Horsfall.U
0.10
0.06
0.02
−2 0 2 4
Microalbumin 24hr
L
Tissue.Inhibito
300
200
100
−2 0 2 4
Microalbumin 24hr

FIG. 31

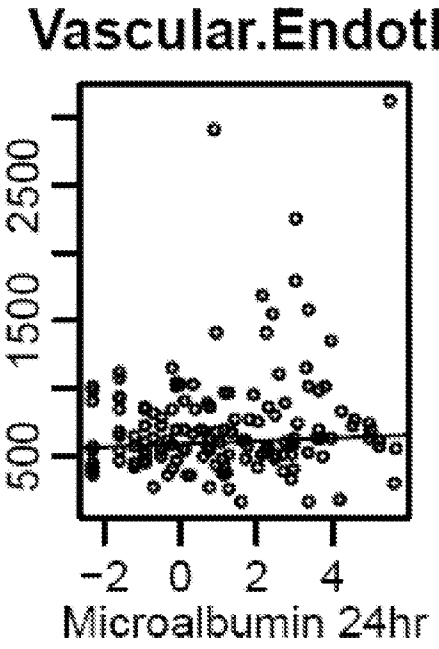

FIG. 31M

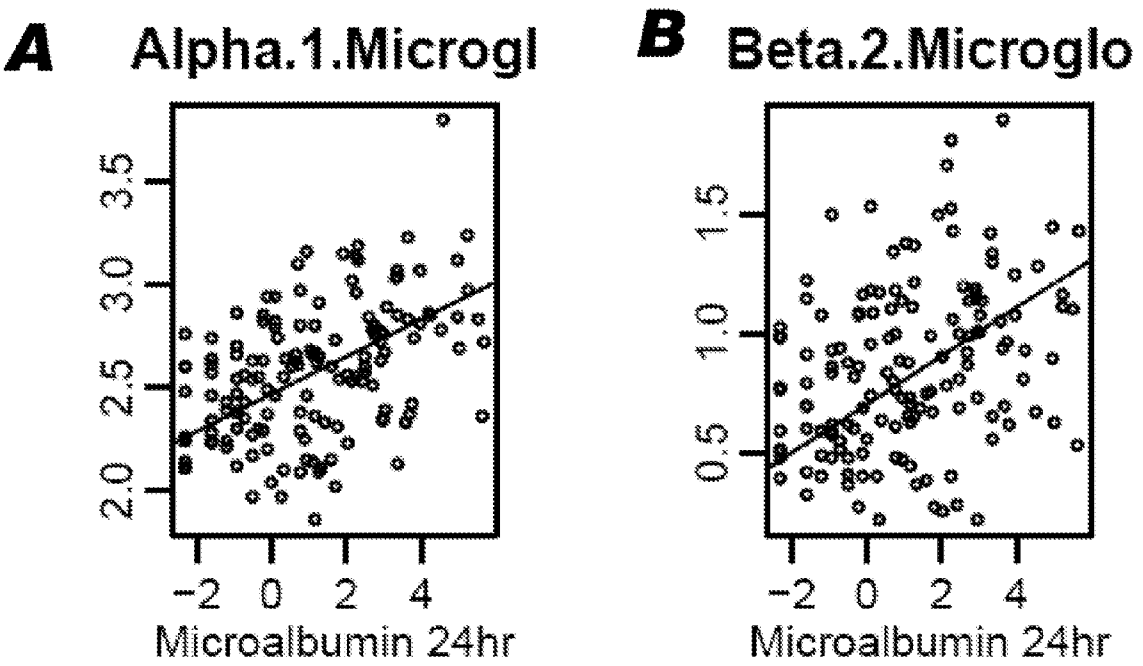

FIG. 32

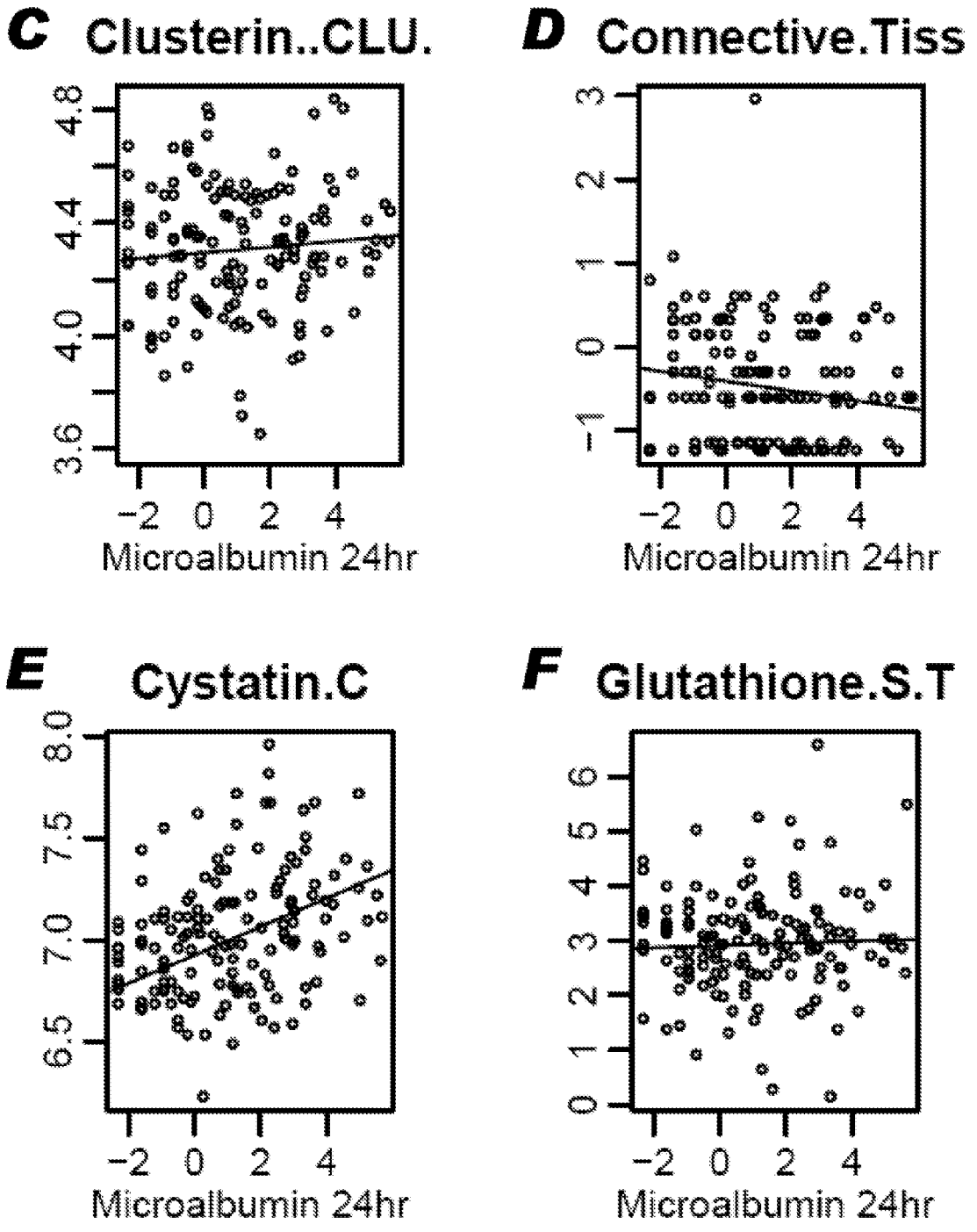
C Clusterin..CLU.
4.8
4.4
4.0
3.6
−2 0 2 4
Microalbumin 24hr
D Connective.Tiss
3
2
1
0
−1
−2 0 2 4
Microalbumin 24hr
E Cystatin.C
8.0
7.5
7.0
6.5
−2 0 2 4
Microalbumin 24hr
F Glutathione.S.T
6
5
4
3
2
1
0
−2 0 2 4
Microalbumin 24hr

FIG. 32

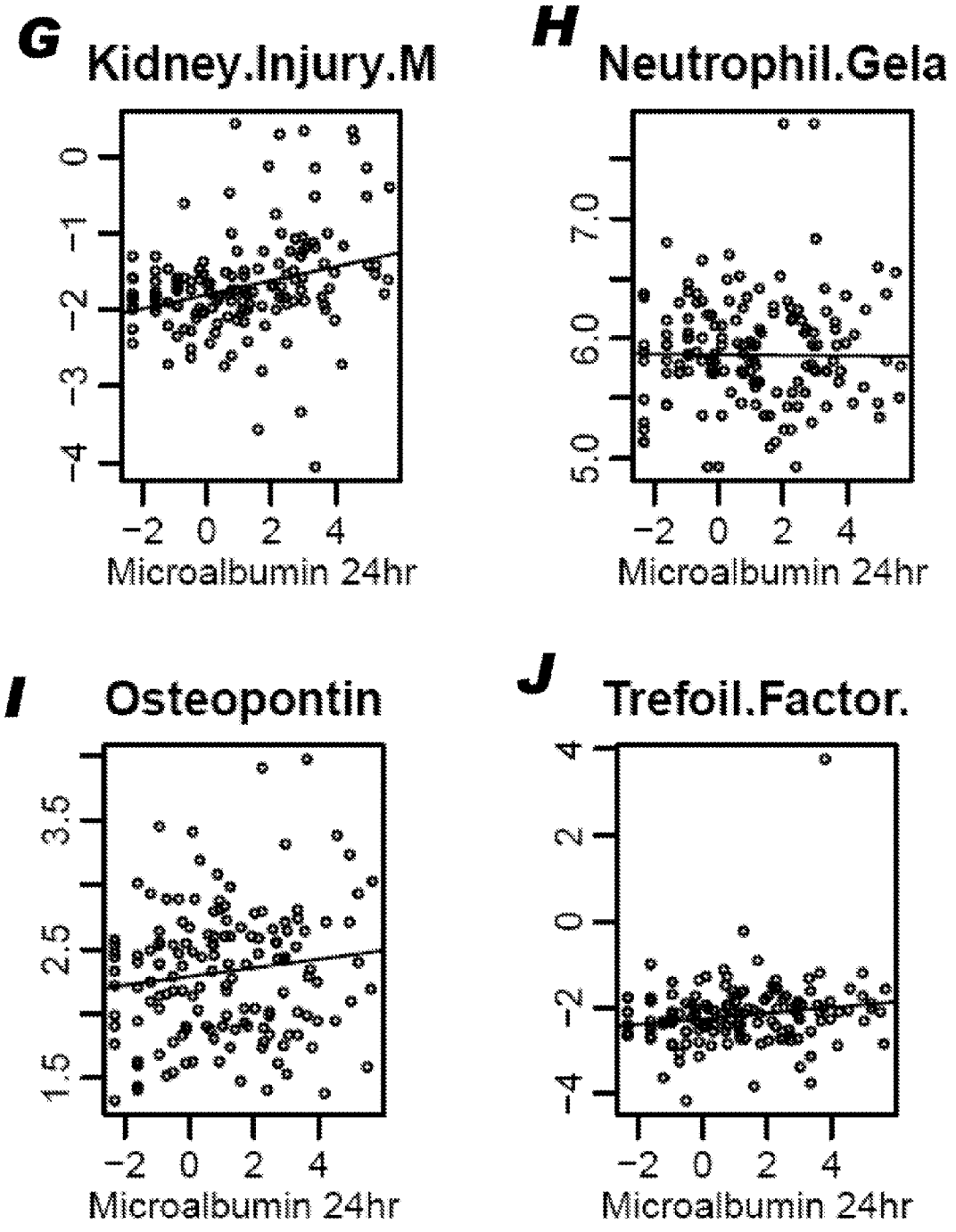
G
Kidney.Injury.M
0
−1
−2
−3
−4
−2 0 2 4
Microalbumin 24hr
H
Neutrophil.Gela
7.0
6.0
5.0
−2 0 2 4
Microalbumin 24hr
I
Osteopontin
3.5
2.5
1.5
−2 0 2 4
Microalbumin 24hr
J
Trefoil.Factor.
4
2
0
−2
−4
−2 0 2 4
Microalbumin 24hr

FIG. 32

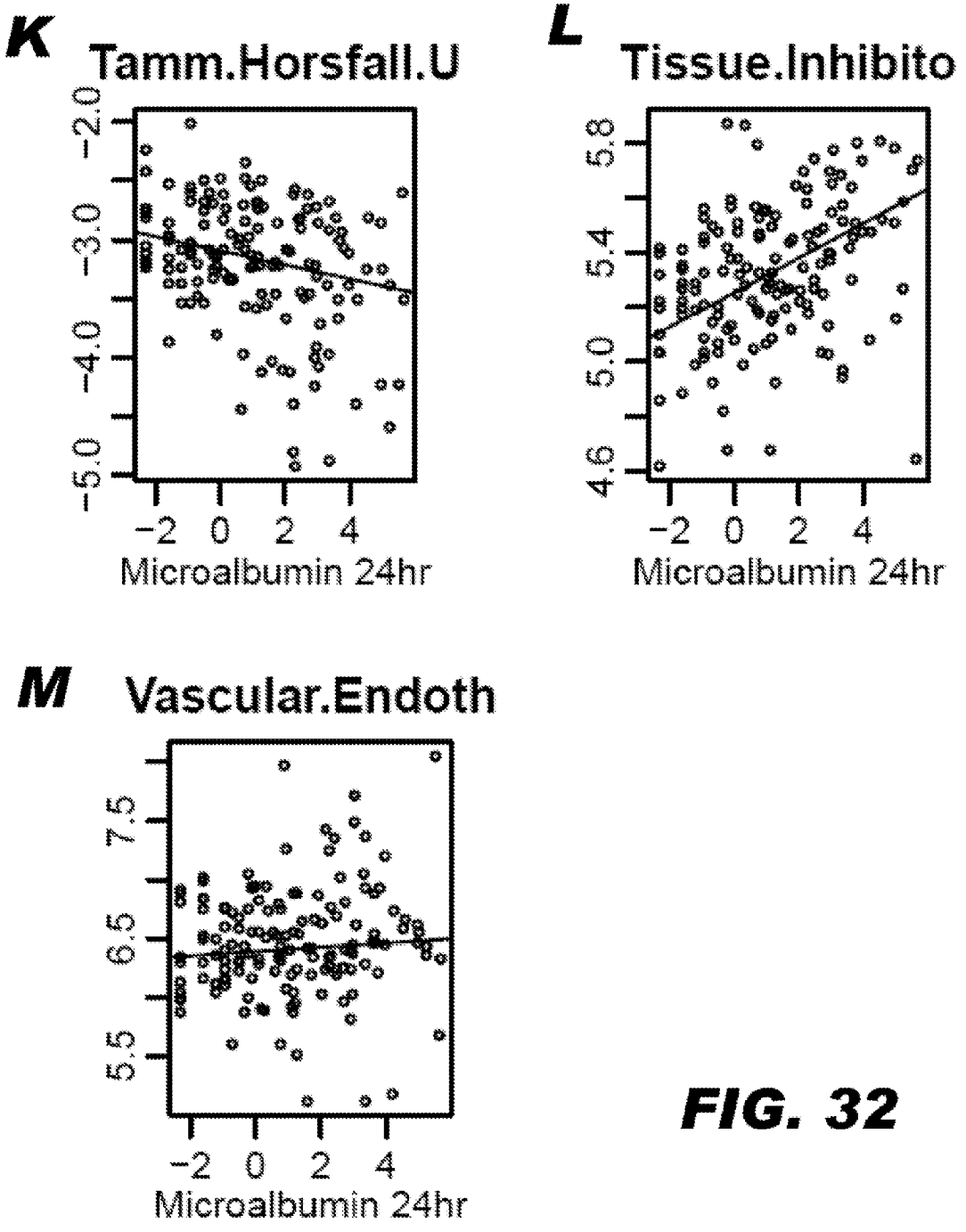
K
Tamm.Horsfall.U
−2.0
−3.0
−4.0
−5.0
−2 0 2 4
Microalbumin 24hr
L
Tissue.Inhibito
5.8
5.4
5.0
4.6
−2 0 2 4
Microalbumin 24hr
M
Vascular.Endoth
7.5
6.5
5.5
−2 0 2 4
Microalbumin 24hr

FIG. 32

METHODS AND DEVICES FOR DETECTING DIABETIC NEPHROPATHY AND ASSOCIATED DISORDERS

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the priority of U.S. provisional application Ser. No. 61/327,389, filed Apr. 23, 2010, and U.S. provisional application Ser. No. 61/232,091, filed Aug. 7, 2009, each of which is hereby incorporated by reference in its entirety and is related to U.S. patent application Ser. No. [Not Yet Assigned], entitled Methods and Devices for Detecting Obstructive Uropathy and Associated Disorders, Computer Methods and Devices for Detecting Kidney Damage, Methods and Devices for Detecting Kidney Damage, Devices for Detecting Renal Disorders, Methods and Devices for Detecting Kidney Transplant Rejection, and Methods and Devices for Detecting Glomerulonephritis and Associated Disorders, Attorney Docket Nos. 060075-, filed on the same date as this application, the entire contents of which are incorporated herein by reference.

FIELD OF THE INVENTION

[0002] The invention encompasses methods and devices for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal. In particular, the present invention provides methods and devices for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder using measured concentrations of a combination of three or more analytes in a test sample taken from the mammal.

BACKGROUND OF THE INVENTION

[0003] The urinary system, in particular the kidneys, perform several critical functions such as maintaining electrolyte balance and eliminating toxins from the bloodstream. In the human body, the pair of kidneys together process roughly 20% of the total cardiac output, amounting to about 1 L/min in a 70-kg adult male. Because compounds in circulation are concentrated in the kidney up to 1000-fold relative to the plasma concentration, the kidney is especially vulnerable to injury due to exposure to toxic compounds.

[0004] Diabetic nephropathy is the most common cause of chronic kidney failure and end-stage kidney disease in the United States. People with both type 1 and type 2 diabetes are at risk. Existing diagnostic tests such as BUN and serum creatine tests typically detect only advanced stages of kidney damage. Other diagnostic tests such as kidney tissue biopsies or CAT scans have the advantage of enhanced sensitivity to earlier stages of kidney damage, but these tests are also generally costly, slow, and/or invasive.

[0005] A need exists in the art for a fast, simple, reliable, and sensitive method of detecting diabetic nephropathy or an associated disorder. In a clinical setting, the early detection of kidney damage would help medical practitioners to diagnose and treat kidney damage more quickly and effectively.

SUMMARY OF THE INVENTION

[0006] The present invention provides methods and devices for diagnosing, monitoring, or determining a renal disorder in a mammal. In particular, the present invention provides methods and devices for diagnosing, monitoring, or determining a renal disorder using measured concentrations of a combination of three or more analytes in a test sample taken from the mammal.

[0007] One aspect of the invention encompasses a method for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal. The method typically comprises providing a test sample comprising a sample of bodily fluid taken from the mammal. Then, the method comprises determining a combination of sample concentrations for three or more sample analytes in the test sample, wherein the sample analytes are selected from the group consisting of alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF. The combination of sample concentrations may be compared to a data set comprising at least one entry, wherein each entry of the data set comprises a list comprising three or more minimum diagnostic concentrations indicative of diabetic nephropathy or an associated disorder. Each minimum diagnostic concentration comprises a maximum of a range of analyte concentrations for a healthy mammal. Next, the method comprises determining a matching entry of the dataset in which all minimum diagnostic concentrations are less than the corresponding sample concentrations and identifying an indicated disorder comprising the particular disorder of the matching entry.

[0008] Another aspect of the invention encompasses a method for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal. The method generally comprises providing a test sample comprising a sample of bodily fluid taken from the mammal. Then the method comprises determining the concentrations of three or more sample analytes in a panel of biomarkers in the test sample, wherein the sample analytes are selected from the group consisting of alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF. Diagnostic analytes are identified in the test sample, wherein the diagnostic analytes are the sample analytes whose concentrations are statistically different from concentrations found in a control group of humans who do not suffer from diabetic nephropathy or an associated disorder. The combination of diagnostic analytes is compared to a dataset comprising at least one entry, wherein each entry of the dataset comprises a combination of three or more diagnostic analytes reflective of diabetic nephropathy or an associated disorder. The particular disorder having the combination of diagnostic analytes that essentially match the combination of sample analytes is then identified.

[0009] An additional aspect of the invention encompasses a method for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal. The method usually comprises providing an analyte concentration measurement device comprising three or more detection antibodies. Each detection antibody comprises an antibody coupled to an indicator, wherein the antigenic determinants of the antibodies are sample analytes associated with diabetic nephropathy or an associated disorder. The sample analytes are generally selected from the group consisting of alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF. The method next comprises providing a test sample comprising three or more sample analytes and a bodily fluid taken

from the mammal. The test sample is contacted with the detection antibodies and the detection antibodies are allowed to bind to the sample analytes. The concentrations of the sample analytes are determined by detecting the indicators of the detection antibodies bound to the sample analytes in the test sample. The concentrations of each sample analyte correspond to a corresponding minimum diagnostic concentration reflective of diabetic nephropathy or an associated disorder.

[0010] Other aspects and iterations of the invention are described in more detail below.

DESCRIPTION OF FIGURES

[0011] FIG. **1** shows the four different disease groups from which samples were analyzed, and a plot of two different estimations on eGFR outlining the distribution within each group.

[0012] FIG. **2** is a number of scatter plots of results on selected proteins in urine and plasma. The various groups are indicated as follows—control: blue, AA: red, DN: green, GN: yellow, OU: orange. (A) A1M in plasma, (B) cystatin C in plasma, (C) B2M in urine, (D) cystatin C in urine.

[0013] FIG. **3** depicts the multivariate analysis of the disease groups and their respective matched controls using plasma results. Relative importance shown using the random forest model.

[0014] FIG. **4** depicts three graphs showing the mean AUROC and its standard deviation (A) for plasma samples, and mean error rates (B) and mean AUROC (C) from urine samples for each classification method used to distinguish disease samples vs. normal samples. Disease encompasses analgesic abuse (AA), glomerulonephritis (GN), obstructive uropathy (OU), and diabetic nephropathy (DN). Normal=NL.

[0015] FIG. **5** depicts three graphs showing the average importance of analytes and clinical variables from 100 bootstrap runs measured by random forest (A and B) or boosting (C) to distinguish disease (AA+GN+ON+DN) samples vs. normal samples from plasma (A) and urine (B and C).

[0016] FIG. **6** depicts three graphs showing the mean AUROC and its standard deviation (A) for plasma samples, and mean error rates (B) and mean AUROC (C) from urine samples for each classification method used to distinguish diabetic nephropathy samples vs. normal samples. Abbreviations as in FIG. **4**.

[0017] FIG. **7** depicts three graphs showing the average importance of analytes and clinical variables from 100 bootstrap runs measured by random forest (A and B) or boosting (C) to distinguish diabetic nephropathy samples vs. normal samples from plasma (A) and urine (B and C).

[0018] FIG. **8** depicts three graphs showing the mean AUROC and its standard deviation (A) for plasma samples, and mean error rates (B) and mean AUROC (C) from urine samples for each classification method used to distinguish analgesic abuse samples vs. diabetic nephropathy samples. Abbreviations as in FIG. **4**.

[0019] FIG. **9** depicts three graphs showing the average importance of analytes and clinical variables from 100 bootstrap runs measured by random forest (A and B) or boosting (C) to distinguish analgesic abuse samples vs. diabetic nephropathy samples from plasma (A) and urine (B and C).

[0020] FIG. **10** depicts three graphs showing the mean AUROC and its standard deviation (A) for plasma samples, and mean error rates (B) and mean AUROC (C) from urine samples for each classification method used to distinguish obstructive uropathy samples vs. diabetic nephropathy samples. Abbreviations as in FIG. **4**.

[0021] FIG. **11** depicts three graphs showing the average importance of analytes and clinical variables from 100 bootstrap runs measured by random forest (A and B) or boosting (C) to distinguish obstructive uropathy samples vs. diabetic nephropathy samples from plasma (A) and urine (B and C).

[0022] FIG. **12** depicts three graphs showing the mean AUROC and its standard deviation (A) for plasma samples, and mean error rates (B) and mean AUROC (C) from urine samples for each classification method used to distinguish diabetic nephropathy samples vs. glomerulonephritis samples. Abbreviations as in FIG. **4**.

[0023] FIG. **13** depicts three graphs showing the average importance of analytes and clinical variables from 100 bootstrap runs measured by random forest (A and B) or boosting (C) to distinguish diabetic nephropathy samples vs. glomerulonephritis samples from plasma (A) and urine (B and C).

[0024] FIG. **14** depicts several graphs illustrating the linear correlation between an analyte and years diagnosed with diabetes. Red=cases; Black=controls. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cystatin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0025] FIG. **15** depicts several graphs illustrating the log correlation between an analyte and years diagnosed with diabetes. Red=cases; Black=controls. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cystatin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0026] FIG. **16** depicts several graphs illustrating the log correlation between an analyte and clinical 24 hr microalbumin. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cystatin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0027] FIG. **17** depicts several graphs illustrating the linear correlation between an analyte and clinical 24 hr microalbumin. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cystatin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0028] FIG. **18** depicts several graphs illustrating linear cdplots of urine analytes compared to diabetic disease. Levels were normalized to urine creatinine. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cystatin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0029] FIG. **19** depicts several graphs illustrating log cdplots of urine analytes compared to diabetic disease. Levels were normalized to urine creatinine. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cystatin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0030] FIG. **20** depicts several graphs illustrating linear qqplots of urine analytes compared to diabetic disease. Levels were normalized to urine creatinine. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cysta-

tin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0031] FIG. **21** depicts several graphs illustrating log qqplots of urine analytes compared to diabetic disease. Levels were normalized to urine creatinine. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cystatin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0032] FIG. **22** depicts several graphs illustrating linear stripcharts of urine analytes compared to diabetic kidney disease (KD) or diabetic patients with out kidney disease controls (NC). Levels were normalized to urine creatinine. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cystatin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0033] FIG. **23** depicts several graphs illustrating log stripcharts of urine analytes compared to diabetic kidney disease (KD) or diabetic patients with out kidney disease controls (NC). Levels were normalized to urine creatinine. (A) A1M, (B) B2M, (C) calbindin, (D) clusterin, (E) CTGF, (F) creatinine, (G) cystatin C, (H) GST α, (I) KIM-1, (J) microalbumin, (K) NGAL, (L) osteopontin, (M) THP, (N) TIMP-1, (O) TFF-3, and (P) VEGF.

[0034] FIG. **24** depicts a graph illustrating years diagnosed v. disease.

[0035] FIG. **25** depicts several graphs illustrating linear stripcharts of serum analytes compared to diabetic kidney disease (KD) or diabetic patients with out kidney disease controls (NC). (A) A1M, (B) B2M, (C) clusterin, (D) CTGF, (E) cystatin C, (F) GST α, (G) KIM-1, (H) NGAL, (I) osteopontin, (J) TFF-3, (K) THP, (L) TIMP-1, and (M) VEGF.

[0036] FIG. **26** depicts several graphs illustrating log stripcharts of serum analytes compared to diabetic kidney disease. (A) A1M, (B) B2M, (C) clusterin, (D) CTGF, (E) cystatin C, (F) GST α, (G) KIM-1, (H) NGAL, (I) osteopontin, (J) TFF-3, (K) THP, (L) TIMP-1, and (M) VEGF.

[0037] FIG. **27** depicts several graphs illustrating linear qqplots of serum analytes compared to diabetic kidney disease. (A) A1M, (B) B2M, (C) clusterin, (D) CTGF, (E) cystatin C, (F) GST α, (G) KIM-1, (H) NGAL, (I) osteopontin, (J) TFF-3, (K) THP, (L) TIMP-1, and (M) VEGF.

[0038] FIG. **28** depicts several graphs illustrating log qqplots of serum analytes compared to diabetic kidney disease. (A) A1M, (B) B2M, (C) clusterin, (D) CTGF, (E) cystatin C, (F) GST α, (G) KIM-1, (H) NGAL, (I) osteopontin, (J) TFF-3, (K) THP, (L) TIMP-1, and (M) VEGF.

[0039] FIG. **29** depicts several graphs illustrating a linear comparison of analytes v. years diagnosed. Red=cases; Black=controls. (A) A1M, (B) B2M, (C) clusterin, (D) CTGF, (E) cystatin C, (F) GST α, (G) KIM-1, (H) NGAL, (I) osteopontin, (J) TFF-3, (K) THP, (L) TIMP-1, and (M) VEGF.

[0040] FIG. **30** depicts several graphs illustrating a log comparison of analytes v. years diagnosed. Red=cases; Black=controls. (A) A1M, (B) B2M, (C) clusterin, (D) CTGF, (E) cystatin C, (F) GST α, (G) KIM-1, (H) NGAL, (I) osteopontin, (J) TFF-3, (K) THP, (L) TIMP-1, and (M) VEGF.

[0041] FIG. **31** depicts several graphs illustrating a linear comparison of serum analytes v. clinical microalbumin. (A) A1M, (B) B2M, (C) clusterin, (D) CTGF, (E) cystatin C, (F) GST α, (G) KIM-1, (H) NGAL, (I) osteopontin, (J) TFF-3, (K) THP, (L) TIMP-1, and (M) VEGF.

[0042] FIG. **32** depicts several graphs illustrating a log comparison of serum analytes v. clinical microalbumin. (A) A1M, (B) B2M, (C) clusterin, (D) CTGF, (E) cystatin C, (F) GST α, (G) KIM-1, (H) NGAL, (I) osteopontin, (J) TFF-3, (K) THP, (L) TIMP-1, and (M) VEGF.

DETAILED DESCRIPTION OF THE INVENTION

[0043] It has been discovered that a multiplexed panel of at least three, six, or preferably 16 biomarkers may be used to detect diabetic nephropathy and associated disorders. As used herein, the term "diabetic nephropathy" refers to a disorder characterized by angiopathy of capillaries in the kidney glomeruli. The term encompasses Kimmelstiel-Wilson syndrome, or nodular diabetic glomerulosclerosis and intercapillary glomerulonephritis. Additionally, the present invention encompasses biomarkers that may be used to detect a disorder associated with diabetic nephropathy. As used herein, the phrase "a disorder associated with diabetic nephropathy" refers to a disorder that stems from angiopathy of capillaries in the kidney glomeruli. For instance, non-limiting examples of associated disorders may include nephritic syndrome, chronic kidney failure, and end-stage kidney disease.

[0044] The biomarkers included in a multiplexed panel of the invention are analytes known in the art that may be detected in the urine, serum, plasma and other bodily fluids of mammals. As such, the analytes of the multiplexed panel may be readily extracted from the mammal in a test sample of bodily fluid. The concentrations of the analytes within the test sample may be measured using known analytical techniques such as a multiplexed antibody-based immunological assay. The combination of concentrations of the analytes in the test sample may be compared to empirically determined combinations of minimum diagnostic concentrations and combinations of diagnostic concentration ranges associated with healthy kidney function or diabetic nephropathy or an associated disorder to determine whether diabetic nephropathy or an associated disorder is indicated in the mammal.

[0045] One embodiment of the present invention provides a method for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal that includes determining the presence or concentration of a combination of three or more sample analytes in a test sample containing the bodily fluid of the mammal. The measured concentrations of the combination of sample analytes is compared to the entries of a dataset in which each entry contains the minimum diagnostic concentrations of a combination of three of more analytes reflective of diabetic nephropathy or an associated disorder. Other embodiments provide computer-readable media encoded with applications containing executable modules, systems that include databases and processing devices containing executable modules configured to diagnose, monitor, or determine a renal disorder in a mammal. Still other embodiments provide antibody-based devices for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal.

[0046] The analytes used as biomarkers in the multiplexed assay, methods of diagnosing, monitoring, or determining a renal disorder using measurements of the analytes, systems and applications used to analyze the multiplexed assay measurements, and antibody-based devices used to measure the analytes are described in detail below.

I. Analytes in Multiplexed Assay

[0047] One embodiment of the invention measures the concentrations of three, six, or preferable sixteen biomarker ana-

lytes within a test sample taken from a mammal and compares the measured analyte concentrations to minimum diagnostic concentrations to diagnose, monitor, or determine diabetic nephropathy or an associated disorder in a mammal. In this aspect, the biomarker analytes are known in the art to occur in the urine, plasma, serum and other bodily fluids of mammals. The biomarker analytes are proteins that have known and documented associations with early renal damage in humans. As defined herein, the biomarker analytes include but are not limited to alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF. A description of each biomarker analyte is given below.

(a) Alpha-1 Microglobulin (A1M)

[0048] Alpha-1 microglobulin (A1M, Swiss-Prot Accession Number P02760) is a 26 kDa glycoprotein synthesized by the liver and reabsorbed in the proximal tubules. Elevated levels of A1M in human urine are indicative of glomerulotubular dysfunction. A1M is a member of the lipocalin super family and is found in all tissues. Alpha-1-microglobulin exists in blood in both a free form and complexed with immunoglobulin A (IgA) and heme. Half of plasma A1M exists in a free form, and the remainder exists in complexes with other molecules including prothrombin, albumin, immunoglobulin A and heme. Nearly all of the free A1M in human urine is reabsorbed by the megalin receptor in proximal tubular cells, where it is then catabolized. Small amounts of A1M are excreted in the urine of healthy humans. Increased A1M concentrations in human urine may be an early indicator of renal damage, primarily in the proximal tubule.

(b) Beta-2 Microglobulin (B2M)

[0049] Beta-2 microglobulin (B2M, Swiss-Prot Accession Number P61769) is a protein found on the surfaces of all nucleated cells and is shed into the blood, particularly by tumor cells and lymphocytes. Due to its small size, B2M passes through the glomerular membrane, but normally less than 1% is excreted due to reabsorption of B2M in the proximal tubules of the kidney. Therefore, high plasma levels of B2M occur as a result of renal failure, inflammation, and neoplasms, especially those associated with B-lymphocytes.

(c) Calbindin

[0050] Calbindin (Calbindin D-28K, Swiss-Prot Accession Number P05937) is a Ca-binding protein belonging to the troponin C superfamily. It is expressed in the kidney, pancreatic islets, and brain. Calbindin is found predominantly in subpopulations of central and peripheral nervous system neurons, in certain epithelial cells involved in Ca2+ transport such as distal tubular cells and cortical collecting tubules of the kidney, and in enteric neuroendocrine cells.

(d) Clusterin

[0051] Clusterin (Swiss-Prot Accession Number P10909) is a highly conserved protein that has been identified independently by many different laboratories and named SGP2, S35-S45, apolipoprotein J, SP-40, 40, ADHC-9, gp80, GPIII, and testosterone-repressed prostate message (TRPM-2). An increase in clusterin levels has been consistently detected in apoptotic heart, brain, lung, liver, kidney, pancreas, and retinal tissue both in vivo and in vitro, establishing clusterin as a ubiquitous marker of apoptotic cell loss. However, clusterin protein has also been implicated in physiological processes that do not involve apoptosis, including the control of complement-mediated cell lysis, transport of beta-amyloid precursor protein, shuttling of aberrant beta-amyloid across the blood-brain barrier, lipid scavenging, membrane remodeling, cell aggregation, and protection from immune detection and tumor necrosis factor induced cell death.

(e) Connective Tissue Growth Factor (CTGF)

[0052] Connective tissue growth factor (CTGF, Swiss-Prot Accession Number P29279) is a 349—amino acid cysteine-rich polypeptide belonging to the CCN family. In vitro studies have shown that CTGF is mainly involved in extracellular matrix synthesis and fibrosis. Up-regulation of CTGF mRNA and increased CTGF levels have been observed in various diseases, including diabetic nephropathy and cardiomyopathy, fibrotic skin disorders, systemic sclerosis, biliary atresia, liver fibrosis and idiopathic pulmonary fibrosis, and nondiabetic acute and progressive glomerular and tubulointerstitial lesions of the kidney. A recent cross-sectional study found that urinary CTGF may act as a progression promoter in diabetic nephropathy.

(f) Creatinine

[0053] Creatinine is a metabolite of creatine phosphate in muscle tissue, and is typically produced at a relatively constant rate by the body. Creatinine is chiefly filtered out of the blood by the kidneys, though a small amount is actively secreted by the kidneys into the urine. Creatinine levels in blood and urine may be used to estimate the creatinine clearance, which is representative of the overall glomerular filtration rate (GFR), a standard measure of renal function. Variations in creatinine concentrations in the blood and urine, as well as variations in the ratio of urea to creatinine concentration in the blood, are common diagnostic measurements used to assess renal function.

(g) Cystatin C (Cyst C)

[0054] Cystatin C (Cyst C, Swiss-Prot Accession Number P01034) is a 13 kDa protein that is a potent inhibitor of the C1 family of cysteine proteases. It is the most abundant extracellular inhibitor of cysteine proteases in testis, epididymis, prostate, seminal vesicles and many other tissues. Cystatin C, which is normally expressed in vascular wall smooth muscle cells, is severely reduced in both atherosclerotic and aneurismal aortic lesions.

(h) Glutathione S-Transferase Alpha (GST-Alpha)

[0055] Glutathione S-transferase alpha (GST-alpha, Swiss-Prot Accession Number P08263) belongs to a family of enzymes that utilize glutathione in reactions contributing to the transformation of a wide range of compounds, including carcinogens, therapeutic drugs, and products of oxidative stress. These enzymes play a key role in the detoxification of such substances.

(i) Kidney Injury Molecule-1 (KIM-1)

[0056] Kidney injury molecule-1 (KIM-1, Swiss-Prot Accession Number Q96D42) is an immunoglobulin superfamily cell-surface protein highly upregulated on the surface of injured kidney epithelial cells. It is also known as TIM-1

(T-cell immunoglobulin mucin domain-1), as it is expressed at low levels by subpopulations of activated T-cells and hepatitis A virus cellular receptor-1 (HAVCR-1). KIM-1 is increased in expression more than any other protein in the injured kidney and is localized predominantly to the apical membrane of the surviving proximal epithelial cells.

(j) Microalbumin

[0057] Albumin is the most abundant plasma protein in humans and other mammals. Albumin is essential for maintaining the osmotic pressure needed for proper distribution of body fluids between intravascular compartments and body tissues. Healthy, normal kidneys typically filter out albumin from the urine. The presence of albumin in the urine may indicate damage to the kidneys. Albumin in the urine may also occur in patients with long-standing diabetes, especially type 1 diabetes. The amount of albumin eliminated in the urine has been used to differentially diagnose various renal disorders. For example, nephrotic syndrome usually results in the excretion of about 3.0 to 3.5 grams of albumin in human urine every 24 hours. Microalbuminuria, in which less than 300 mg of albumin is eliminated in the urine every 24 hours, may indicate the early stages of diabetic nephropathy.

(k) Neutrophil Gelatinase-Associated Lipocalin (NGAL)

[0058] Neutrophil gelatinase-associated lipocalin (NGAL, Swiss-Prot Accession Number P80188) forms a disulfide bond-linked heterodimer with MMP-9. It mediates an innate immune response to bacterial infection by sequestrating iron. Lipocalins interact with many different molecules such as cell surface receptors and proteases, and play a role in a variety of processes such as the progression of cancer and allergic reactions.

(l) Osteopontin (OPN)

[0059] Osteopontin (OPN, Swiss-Prot Accession Number P10451) is a cytokine involved in enhancing production of interferon-gamma and IL-12, and inhibiting the production of IL-10. OPN is essential in the pathway that leads to type I immunity. OPN appears to form an integral part of the mineralized matrix. OPN is synthesized within the kidney and has been detected in human urine at levels that may effectively inhibit calcium oxalate crystallization. Decreased concentrations of OPN have been documented in urine from patients with renal stone disease compared with normal individuals.

(m) Tamm-Horsfall Protein (THP)

[0060] Tamm-Horsfall protein (THP, Swiss-Prot Accession Number P07911), also known as uromodulin, is the most abundant protein present in the urine of healthy subjects and has been shown to decrease in individuals with kidney stones. THP is secreted by the thick ascending limb of the loop of Henley. THP is a monomeric glycoprotein of ~85 kDa with ~30% carbohydrate moiety that is heavily glycosylated. THP may act as a constitutive inhibitor of calcium crystallization in renal fluids.

(n) Tissue Inhibitor of Metalloproteinase-1 (TIMP-1)

[0061] Tissue inhibitor of metalloproteinase-1 (TIMP-1, Swiss-Prot Accession Number P01033) is a major regulator of extracellular matrix synthesis and degradation. A certain balance of MMPs and TIMPs is essential for tumor growth and health. Fibrosis results from an imbalance of fibrogenesis and fibrolysis, highlighting the importance of the role of the inhibition of matrix degradation role in renal disease.

(o) Trefoil Factor 3 (TFF3)

[0062] Trefoil factor 3 (TFF3, Swiss-Prot Accession Number Q07654), also known as intestinal trefoil factor, belongs to a small family of mucin-associated peptides that include TFF1, TFF2, and TFF3. TFF3 exists in a 60-amino acid monomeric form and a 118-amino acid dimeric form. Under normal conditions TFF3 is expressed by goblet cells of the intestine and the colon. TFF3 expression has also been observed in the human respiratory tract, in human goblet cells and in the human salivary gland. In addition, TFF3 has been detected in the human hypothalamus.

(p) Vascular Endothelial Growth Factor (VEGF)

[0063] Vascular endothelial growth factor (VEGF, Swiss-Prot Accession Number P15692) is an important factor in the pathophysiology of neuronal and other tumors, most likely functioning as a potent promoter of angiogenesis. VEGF may also be involved in regulating blood-brain-barrier functions under normal and pathological conditions. VEGF secreted from the stromal cells may be responsible for the endothelial cell proliferation observed in capillary hemangioblastomas, which are typically composed of abundant microvasculature and primitive angiogenic elements represented by stromal cells.

II. Combinations of Analytes Measured by Multiplexed Assay

[0064] The method for diagnosing, monitoring, or determining a renal disorder involves determining the presence or concentrations of a combination of sample analytes in a test sample. The combinations of sample analytes, as defined herein, are any group of three or more analytes selected from the biomarker analytes, including but not limited to alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF. In one embodiment, the combination of analytes may be selected to provide a group of analytes associated with diabetic nephropathy or an associated disorder.

[0065] In one embodiment, the combination of sample analytes may be any three of the biomarker analytes. In other embodiments, the combination of sample analytes may be any four, any five, any six, any seven, any eight, any nine, any ten, any eleven, any twelve, any thirteen, any fourteen, any fifteen, or all sixteen of the sixteen biomarker analytes. In some embodiments, the combination of sample analytes comprises alpha-1 microglobulin, beta-2 microglobulin, cystatin C, KIM-1, THP, and TIMP-1. In another embodiment, the combination of sample analytes may be a combination listed in Table A.

TABLE A

alpha-1 microglobulin	beta-2 microglobulin	calbindin
alpha-1 microglobulin	beta-2 microglobulin	clusterin
alpha-1 microglobulin	beta-2 microglobulin	CTGF
alpha-1 microglobulin	beta-2 microglobulin	creatinine
alpha-1 microglobulin	beta-2 microglobulin	cystatin C
alpha-1 microglobulin	beta-2 microglobulin	GST-alpha
alpha-1 microglobulin	beta-2 microglobulin	KIM-1

TABLE A-continued

alpha-1 microglobulin	beta-2 microglobulin	microalbumin
alpha-1 microglobulin	beta-2 microglobulin	NGAL
alpha-1 microglobulin	beta-2 microglobulin	osteopontin
alpha-1 microglobulin	beta-2 microglobulin	THP
alpha-1 microglobulin	beta-2 microglobulin	TIMP-1
alpha-1 microglobulin	beta-2 microglobulin	TFF-3
alpha-1 microglobulin	beta-2 microglobulin	VEGF
alpha-1 microglobulin	calbindin	clusterin
alpha-1 microglobulin	calbindin	CTGF
alpha-1 microglobulin	calbindin	creatinine
alpha-1 microglobulin	calbindin	cystatin C
alpha-1 microglobulin	calbindin	GST-alpha
alpha-1 microglobulin	calbindin	KIM-1
alpha-1 microglobulin	calbindin	microalbumin
alpha-1 microglobulin	calbindin	NGAL
alpha-1 microglobulin	calbindin	osteopontin
alpha-1 microglobulin	calbindin	THP
alpha-1 microglobulin	calbindin	TIMP-1
alpha-1 microglobulin	calbindin	TFF-3
alpha-1 microglobulin	calbindin	VEGF
alpha-1 microglobulin	clusterin	CTGF
alpha-1 microglobulin	clusterin	creatinine
alpha-1 microglobulin	clusterin	cystatin C
alpha-1 microglobulin	clusterin	GST-alpha
alpha-1 microglobulin	clusterin	KIM-1
alpha-1 microglobulin	clusterin	microalbumin
alpha-1 microglobulin	clusterin	NGAL
alpha-1 microglobulin	clusterin	osteopontin
alpha-1 microglobulin	clusterin	THP
alpha-1 microglobulin	clusterin	TIMP-1
alpha-1 microglobulin	clusterin	TFF-3
alpha-1 microglobulin	clusterin	VEGF
alpha-1 microglobulin	CTGF	creatinine
alpha-1 microglobulin	CTGF	cystatin C
alpha-1 microglobulin	CTGF	GST-alpha
alpha-1 microglobulin	CTGF	KIM-1
alpha-1 microglobulin	CTGF	microalbumin
alpha-1 microglobulin	CTGF	NGAL
alpha-1 microglobulin	CTGF	osteopontin
alpha-1 microglobulin	CTGF	THP
alpha-1 microglobulin	CTGF	TIMP-1
alpha-1 microglobulin	CTGF	TFF-3
alpha-1 microglobulin	CTGF	VEGF
alpha-1 microglobulin	creatinine	cystatin C
alpha-1 microglobulin	creatinine	GST-alpha
alpha-1 microglobulin	creatinine	KIM-1
alpha-1 microglobulin	creatinine	microalbumin
alpha-1 microglobulin	creatinine	NGAL
alpha-1 microglobulin	creatinine	osteopontin
alpha-1 microglobulin	creatinine	THP
alpha-1 microglobulin	creatinine	TIMP-1
alpha-1 microglobulin	creatinine	TFF-3
alpha-1 microglobulin	creatinine	VEGF
alpha-1 microglobulin	cystatin C	GST-alpha
alpha-1 microglobulin	cystatin C	KIM-1
alpha-1 microglobulin	cystatin C	microalbumin
alpha-1 microglobulin	cystatin C	NGAL
alpha-1 microglobulin	cystatin C	osteopontin
alpha-1 microglobulin	cystatin C	THP
alpha-1 microglobulin	cystatin C	TIMP-1
alpha-1 microglobulin	cystatin C	TFF-3
alpha-1 microglobulin	cystatin C	VEGF
alpha-1 microglobulin	GST-alpha	KIM-1
alpha-1 microglobulin	GST-alpha	microalbumin
alpha-1 microglobulin	GST-alpha	NGAL
alpha-1 microglobulin	GST-alpha	osteopontin
alpha-1 microglobulin	GST-alpha	THP
alpha-1 microglobulin	GST-alpha	TIMP-1
alpha-1 microglobulin	GST-alpha	TFF-3
alpha-1 microglobulin	GST-alpha	VEGF
alpha-1 microglobulin	KIM-1	microalbumin
alpha-1 microglobulin	KIM-1	NGAL
alpha-1 microglobulin	KIM-1	osteopontin
alpha-1 microglobulin	KIM-1	THP
alpha-1 microglobulin	KIM-1	TIMP-1
alpha-1 microglobulin	KIM-1	TFF-3

TABLE A-continued

alpha-1 microglobulin	KIM-1	VEGF
alpha-1 microglobulin	microalbumin	NGAL
alpha-1 microglobulin	microalbumin	osteopontin
alpha-1 microglobulin	microalbumin	THP
alpha-1 microglobulin	microalbumin	TIMP-1
alpha-1 microglobulin	microalbumin	TFF-3
alpha-1 microglobulin	microalbumin	VEGF
alpha-1 microglobulin	NGAL	osteopontin
alpha-1 microglobulin	NGAL	THP
alpha-1 microglobulin	NGAL	TIMP-1
alpha-1 microglobulin	NGAL	TFF-3
alpha-1 microglobulin	NGAL	VEGF
alpha-1 microglobulin	osteopontin	THP
alpha-1 microglobulin	osteopontin	TIMP-1
alpha-1 microglobulin	osteopontin	TFF-3
alpha-1 microglobulin	osteopontin	VEGF
alpha-1 microglobulin	THP	TIMP-1
alpha-1 microglobulin	THP	TFF-3
alpha-1 microglobulin	THP	VEGF
alpha-1 microglobulin	TIMP-1	TFF-3
alpha-1 microglobulin	TIMP-1	VEGF
alpha-1 microglobulin	TFF-3	VEGF
beta-2 microglobulin	calbindin	clusterin
beta-2 microglobulin	calbindin	CTGF
beta-2 microglobulin	calbindin	creatinine
beta-2 microglobulin	calbindin	cystatin C
beta-2 microglobulin	calbindin	GST-alpha
beta-2 microglobulin	calbindin	KIM-1
beta-2 microglobulin	calbindin	microalbumin
beta-2 microglobulin	calbindin	NGAL
beta-2 microglobulin	calbindin	osteopontin
beta-2 microglobulin	calbindin	THP
beta-2 microglobulin	calbindin	TIMP-1
beta-2 microglobulin	calbindin	TFF-3
beta-2 microglobulin	calbindin	VEGF
beta-2 microglobulin	clusterin	CTGF
beta-2 microglobulin	clusterin	creatinine
beta-2 microglobulin	clusterin	cystatin C
beta-2 microglobulin	clusterin	GST-alpha
beta-2 microglobulin	clusterin	KIM-1
beta-2 microglobulin	clusterin	microalbumin
beta-2 microglobulin	clusterin	NGAL
beta-2 microglobulin	clusterin	osteopontin
beta-2 microglobulin	clusterin	THP
beta-2 microglobulin	clusterin	TIMP-1
beta-2 microglobulin	clusterin	TFF-3
beta-2 microglobulin	clusterin	VEGF
beta-2 microglobulin	CTGF	creatinine
beta-2 microglobulin	CTGF	cystatin C
beta-2 microglobulin	CTGF	GST-alpha
beta-2 microglobulin	CTGF	KIM-1
beta-2 microglobulin	CTGF	microalbumin
beta-2 microglobulin	CTGF	NGAL
beta-2 microglobulin	CTGF	osteopontin
beta-2 microglobulin	CTGF	THP
beta-2 microglobulin	CTGF	TIMP-1
beta-2 microglobulin	CTGF	TFF-3
beta-2 microglobulin	CTGF	VEGF
beta-2 microglobulin	creatinine	cystatin C
beta-2 microglobulin	creatinine	GST-alpha
beta-2 microglobulin	creatinine	KIM-1
beta-2 microglobulin	creatinine	microalbumin
beta-2 microglobulin	creatinine	NGAL
beta-2 microglobulin	creatinine	osteopontin
beta-2 microglobulin	creatinine	THP
beta-2 microglobulin	creatinine	TIMP-1
beta-2 microglobulin	creatinine	TFF-3
beta-2 microglobulin	creatinine	VEGF
beta-2 microglobulin	cystatin C	GST-alpha
beta-2 microglobulin	cystatin C	KIM-1
beta-2 microglobulin	cystatin C	microalbumin
beta-2 microglobulin	cystatin C	NGAL
beta-2 microglobulin	cystatin C	osteopontin
beta-2 microglobulin	cystatin C	THP
beta-2 microglobulin	cystatin C	TIMP-1
beta-2 microglobulin	cystatin C	TFF-3

TABLE A-continued

beta-2 microglobulin	cystatin C	VEGF
beta-2 microglobulin	GST-alpha	KIM-1
beta-2 microglobulin	GST-alpha	microalbumin
beta-2 microglobulin	GST-alpha	NGAL
beta-2 microglobulin	GST-alpha	osteopontin
beta-2 microglobulin	GST-alpha	THP
beta-2 microglobulin	GST-alpha	TIMP-1
beta-2 microglobulin	GST-alpha	TFF-3
beta-2 microglobulin	GST-alpha	VEGF
beta-2 microglobulin	KIM-1	microalbumin
beta-2 microglobulin	KIM-1	NGAL
beta-2 microglobulin	KIM-1	osteopontin
beta-2 microglobulin	KIM-1	THP
beta-2 microglobulin	KIM-1	TIMP-1
beta-2 microglobulin	KIM-1	TFF-3
beta-2 microglobulin	KIM-1	VEGF
beta-2 microglobulin	microalbumin	NGAL
beta-2 microglobulin	microalbumin	osteopontin
beta-2 microglobulin	microalbumin	THP
beta-2 microglobulin	microalbumin	TIMP-1
beta-2 microglobulin	microalbumin	TFF-3
beta-2 microglobulin	microalbumin	VEGF
beta-2 microglobulin	NGAL	osteopontin
beta-2 microglobulin	NGAL	THP
beta-2 microglobulin	NGAL	TIMP-1
beta-2 microglobulin	NGAL	TFF-3
beta-2 microglobulin	NGAL	VEGF
beta-2 microglobulin	osteopontin	THP
beta-2 microglobulin	osteopontin	TIMP-1
beta-2 microglobulin	osteopontin	TFF-3
beta-2 microglobulin	osteopontin	VEGF
beta-2 microglobulin	THP	TIMP-1
beta-2 microglobulin	THP	TFF-3
beta-2 microglobulin	THP	VEGF
beta-2 microglobulin	TIMP-1	TFF-3
beta-2 microglobulin	TIMP-2	VEGF
beta-2 microglobulin	TFF-3	VEGF
calbindin	clusterin	CTGF
calbindin	clusterin	creatinine
calbindin	clusterin	cystatin C
calbindin	clusterin	GST-alpha
calbindin	clusterin	KIM-1
calbindin	clusterin	microalbumin
calbindin	clusterin	NGAL
calbindin	clusterin	osteopontin
calbindin	clusterin	THP
calbindin	clusterin	TIMP-1
calbindin	clusterin	TFF-3
calbindin	clusterin	VEGF
calbindin	CTGF	creatinine
calbindin	CTGF	cystatin C
calbindin	CTGF	GST-alpha
calbindin	CTGF	KIM-1
calbindin	CTGF	microalbumin
calbindin	CTGF	NGAL
calbindin	CTGF	osteopontin
calbindin	CTGF	THP
calbindin	CTGF	TIMP-1
calbindin	CTGF	TFF-3
calbindin	CTGF	VEGF
calbindin	creatinine	cystatin C
calbindin	creatinine	GST-alpha
calbindin	creatinine	KIM-1
calbindin	creatinine	microalbumin
calbindin	creatinine	NGAL
calbindin	creatinine	osteopontin
calbindin	creatinine	THP
calbindin	creatinine	TIMP-1
calbindin	creatinine	TFF-3
calbindin	creatinine	VEGF
calbindin	cystatin C	GST-alpha
calbindin	cystatin C	KIM-1
calbindin	cystatin C	microalbumin
calbindin	cystatin C	NGAL
calbindin	cystatin C	osteopontin
calbindin	cystatin C	THP

TABLE A-continued

calbindin	cystatin C	TIMP-1
calbindin	cystatin C	TFF-3
calbindin	cystatin C	VEGF
calbindin	GST-alpha	KIM-1
calbindin	GST-alpha	microalbumin
calbindin	GST-alpha	NGAL
calbindin	GST-alpha	osteopontin
calbindin	GST-alpha	THP
calbindin	GST-alpha	TIMP-1
calbindin	GST-alpha	TFF-3
calbindin	GST-alpha	VEGF
calbindin	KIM-1	microalbumin
calbindin	KIM-1	NGAL
calbindin	KIM-1	osteopontin
calbindin	KIM-1	THP
calbindin	KIM-1	TIMP-1
calbindin	KIM-1	TFF-3
calbindin	KIM-1	VEGF
calbindin	microalbumin	NGAL
calbindin	microalbumin	osteopontin
calbindin	microalbumin	THP
calbindin	microalbumin	TIMP-1
calbindin	microalbumin	TFF-3
calbindin	microalbumin	VEGF
calbindin	NGAL	osteopontin
calbindin	NGAL	THP
calbindin	NGAL	TIMP-1
calbindin	NGAL	TFF-3
calbindin	NGAL	VEGF
calbindin	osteopontin	THP
calbindin	osteopontin	TIMP-1
calbindin	osteopontin	TFF-3
calbindin	osteopontin	VEGF
calbindin	THP	TIMP-1
calbindin	THP	TFF-3
calbindin	THP	VEGF
calbindin	TIMP-1	TFF-3
calbindin	TIMP-1	VEGF
calbindin	TFF-3	VEGF
clusterin	CTGF	creatinine
clusterin	CTGF	cystatin C
clusterin	CTGF	GST-alpha
clusterin	CTGF	KIM-1
clusterin	CTGF	microalbumin
clusterin	CTGF	NGAL
clusterin	CTGF	osteopontin
clusterin	CTGF	THP
clusterin	CTGF	TIMP-1
clusterin	CTGF	TFF-3
clusterin	CTGF	VEGF
clusterin	creatinine	cystatin C
clusterin	creatinine	GST-alpha
clusterin	creatinine	KIM-1
clusterin	creatinine	microalbumin
clusterin	creatinine	NGAL
clusterin	creatinine	osteopontin
clusterin	creatinine	THP
clusterin	creatinine	TIMP-1
clusterin	creatinine	TFF-3
clusterin	creatinine	VEGF
clusterin	cystatin C	GST-alpha
clusterin	cystatin C	KIM-1
clusterin	cystatin C	microalbumin
clusterin	cystatin C	NGAL
clusterin	cystatin C	osteopontin
clusterin	cystatin C	THP
clusterin	cystatin C	TIMP-1
clusterin	cystatin C	TFF-3
clusterin	cystatin C	VEGF
clusterin	GST-alpha	KIM-1
clusterin	GST-alpha	microalbumin
clusterin	GST-alpha	NGAL
clusterin	GST-alpha	osteopontin
clusterin	GST-alpha	THP
clusterin	GST-alpha	TIMP-1
clusterin	GST-alpha	TFF-3

TABLE A-continued

clusterin	GST-alpha	VEGF
clusterin	KIM-1	microalbumin
clusterin	KIM-1	NGAL
clusterin	KIM-1	osteopontin
clusterin	KIM-1	THP
clusterin	KIM-1	TIMP-1
clusterin	KIM-1	TFF-3
clusterin	KIM-1	VEGF
clusterin	microalbumin	NGAL
clusterin	microalbumin	osteopontin
clusterin	microalbumin	THP
clusterin	microalbumin	TIMP-1
clusterin	microalbumin	TFF-3
clusterin	microalbumin	VEGF
clusterin	NGAL	osteopontin
clusterin	NGAL	THP
clusterin	NGAL	TIMP-1
clusterin	NGAL	TFF-3
clusterin	NGAL	VEGF
clusterin	osteopontin	THP
clusterin	osteopontin	TIMP-1
clusterin	osteopontin	TFF-3
clusterin	osteopontin	VEGF
clusterin	THP	TIMP-1
clusterin	THP	TFF-3
clusterin	THP	VEGF
clusterin	TIMP-1	TFF-3
clusterin	TIMP-1	VEGF
clusterin	TFF-3	VEGF
CTGF	creatinine	cystatin C
CTGF	creatinine	GST-alpha
CTGF	creatinine	KIM-1
CTGF	creatinine	microalbumin
CTGF	creatinine	NGAL
CTGF	creatinine	osteopontin
CTGF	creatinine	THP
CTGF	creatinine	TIMP-1
CTGF	creatinine	TFF-3
CTGF	creatinine	VEGF
CTGF	cystatin C	GST-alpha
CTGF	cystatin C	KIM-1
CTGF	cystatin C	microalbumin
CTGF	cystatin C	NGAL
CTGF	cystatin C	osteopontin
CTGF	cystatin C	THP
CTGF	cystatin C	TIMP-1
CTGF	cystatin C	TFF-3
CTGF	cystatin C	VEGF
CTGF	GST-alpha	KIM-1
CTGF	GST-alpha	microalbumin
CTGF	GST-alpha	NGAL
CTGF	GST-alpha	osteopontin
CTGF	GST-alpha	THP
CTGF	GST-alpha	TIMP-1
CTGF	GST-alpha	TFF-3
CTGF	GST-alpha	VEGF
CTGF	KIM-1	microalbumin
CTGF	KIM-1	NGAL
CTGF	KIM-1	osteopontin
CTGF	KIM-1	THP
CTGF	KIM-1	TIMP-1
CTGF	KIM-1	TFF-3
CTGF	KIM-1	VEGF
CTGF	microalbumin	NGAL
CTGF	microalbumin	osteopontin
CTGF	microalbumin	THP
CTGF	microalbumin	TIMP-1
CTGF	microalbumin	TFF-3
CTGF	microalbumin	VEGF
CTGF	NGAL	osteopontin
CTGF	NGAL	THP
CTGF	NGAL	TIMP-1
CTGF	NGAL	TFF-3
CTGF	NGAL	VEGF
CTGF	osteopontin	THP
CTGF	osteopontin	TIMP-1

TABLE A-continued

CTGF	osteopontin	TFF-3
CTGF	osteopontin	VEGF
CTGF	THP	TIMP-1
CTGF	THP	TFF-3
CTGF	THP	VEGF
CTGF	TIMP-1	TFF-3
CTGF	TIMP-1	VEGF
CTGF	TFF-3	VEGF
creatinine	cystatin C	GST-alpha
creatinine	cystatin C	KIM-1
creatinine	cystatin C	microalbumin
creatinine	cystatin C	NGAL
creatinine	cystatin C	osteopontin
creatinine	cystatin C	THP
creatinine	cystatin C	TIMP-1
creatinine	cystatin C	TFF-3
creatinine	cystatin C	VEGF
creatinine	GST-alpha	KIM-1
creatinine	GST-alpha	microalbumin
creatinine	GST-alpha	NGAL
creatinine	GST-alpha	osteopontin
creatinine	GST-alpha	THP
creatinine	GST-alpha	TIMP-1
creatinine	GST-alpha	TFF-3
creatinine	GST-alpha	VEGF
creatinine	KIM-1	microalbumin
creatinine	KIM-1	NGAL
creatinine	KIM-1	osteopontin
creatinine	KIM-1	THP
creatinine	KIM-1	TIMP-1
creatinine	KIM-1	TFF-3
creatinine	KIM-1	VEGF
creatinine	microalbumin	NGAL
creatinine	microalbumin	osteopontin
creatinine	microalbumin	THP
creatinine	microalbumin	TIMP-1
creatinine	microalbumin	TFF-3
creatinine	microalbumin	VEGF
creatinine	NGAL	osteopontin
creatinine	NGAL	THP
creatinine	NGAL	TIMP-1
creatinine	NGAL	TFF-3
creatinine	NGAL	VEGF
creatinine	osteopontin	THP
creatinine	osteopontin	TIMP-1
creatinine	osteopontin	TFF-3
creatinine	osteopontin	VEGF
creatinine	THP	TIMP-1
creatinine	THP	TFF-3
creatinine	THP	VEGF
creatinine	TIMP-1	TFF-3
creatinine	TIMP-1	VEGF
creatinine	TFF-3	VEGF
cystatin C	GST-alpha	KIM-1
cystatin C	GST-alpha	microalbumin
cystatin C	GST-alpha	NGAL
cystatin C	GST-alpha	osteopontin
cystatin C	GST-alpha	THP
cystatin C	GST-alpha	TIMP-1
cystatin C	GST-alpha	TFF-3
cystatin C	GST-alpha	VEGF
cystatin C	KIM-1	microalbumin
cystatin C	KIM-1	NGAL
cystatin C	KIM-1	osteopontin
cystatin C	KIM-1	THP
cystatin C	KIM-1	TIMP-1
cystatin C	KIM-1	TFF-3
cystatin C	KIM-1	VEGF
cystatin C	microalbumin	NGAL
cystatin C	microalbumin	osteopontin
cystatin C	microalbumin	THP
cystatin C	microalbumin	TIMP-1
cystatin C	microalbumin	TFF-3
cystatin C	microalbumin	VEGF
cystatin C	NGAL	osteopontin
cystatin C	NGAL	THP

TABLE A-continued

cystatin C	NGAL	TIMP-1
cystatin C	NGAL	TFF-3
cystatin C	NGAL	VEGF
cystatin C	osteopontin	THP
cystatin C	osteopontin	TIMP-1
cystatin C	osteopontin	TFF-3
cystatin C	osteopontin	VEGF
cystatin C	THP	TIMP-1
cystatin C	THP	TFF-3
cystatin C	THP	VEGF
cystatin C	TIMP-1	TFF-3
cystatin C	TIMP-1	VEGF
cystatin C	TFF-3	VEGF
GST-alpha	KIM-1	microalbumin
GST-alpha	KIM-1	NGAL
GST-alpha	KIM-1	osteopontin
GST-alpha	KIM-1	THP
GST-alpha	KIM-1	TIMP-1
GST-alpha	KIM-1	TFF-3
GST-alpha	KIM-1	VEGF
GST-alpha	microalbumin	NGAL
GST-alpha	microalbumin	osteopontin
GST-alpha	microalbumin	THP
GST-alpha	microalbumin	TIMP-1
GST-alpha	microalbumin	TFF-3
GST-alpha	microalbumin	VEGF
GST-alpha	NGAL	osteopontin
GST-alpha	NGAL	THP
GST-alpha	NGAL	TIMP-1
GST-alpha	NGAL	TFF-3
GST-alpha	NGAL	VEGF
GST-alpha	osteopontin	THP
GST-alpha	osteopontin	TIMP-1
GST-alpha	osteopontin	TFF-3
GST-alpha	osteopontin	VEGF
GST-alpha	THP	TIMP-1
GST-alpha	THP	TFF-3
GST-alpha	THP	VEGF
GST-alpha	TIMP-1	TFF-3
GST-alpha	TIMP-1	VEGF
GST-alpha	TFF-3	VEGF
KIM-1	microalbumin	NGAL
KIM-1	microalbumin	osteopontin
KIM-1	microalbumin	THP
KIM-1	microalbumin	TIMP-1
KIM-1	microalbumin	TFF-3
KIM-1	microalbumin	VEGF
KIM-1	NGAL	osteopontin
KIM-1	NGAL	THP
KIM-1	NGAL	TIMP-1
KIM-1	NGAL	TFF-3
KIM-1	NGAL	VEGF
KIM-1	osteopontin	THP
KIM-1	osteopontin	TIMP-1
KIM-1	osteopontin	TFF-3
KIM-1	osteopontin	VEGF
KIM-1	THP	TIMP-1
KIM-1	THP	TFF-3
KIM-1	THP	VEGF
KIM-1	TIMP-1	TFF-3
KIM-1	TIMP-1	VEGF
KIM-1	TFF-3	VEGF
microalbumin	NGAL	osteopontin
microalbumin	NGAL	THP
microalbumin	NGAL	TIMP-1
microalbumin	NGAL	TFF-3
microalbumin	NGAL	VEGF
microalbumin	osteopontin	THP
microalbumin	osteopontin	TIMP-1
microalbumin	osteopontin	TFF-3
microalbumin	osteopontin	VEGF
microalbumin	THP	TIMP-1
microalbumin	THP	TFF-3
microalbumin	THP	VEGF
microalbumin	TIMP-1	TFF-3
microalbumin	TIMP-1	VEGF

TABLE A-continued

microalbumin	TFF-3	VEGF
NGAL	osteopontin	THP
NGAL	osteopontin	TIMP-1
NGAL	osteopontin	TFF-3
NGAL	osteopontin	VEGF
NGAL	THP	TIMP-1
NGAL	THP	TFF-3
NGAL	THP	VEGF
NGAL	TIMP-1	TFF-3
NGAL	TIMP-1	VEGF
NGAL	TFF-3	VEGF
osteopontin	THP	TIMP-1
osteopontin	THP	TFF-3
osteopontin	THP	VEGF
osteopontin	TIMP-1	TFF-3
osteopontin	TIMP-1	VEGF
osteopontin	TFF-3	VEGF
THP	TIMP-1	TFF-3
THP	TIMP-1	VEGF
THP	TFF-3	VEGF
TIMP-1	TFF-3	VEGF

[0066] In one exemplary embodiment, the combination of sample analytes may include creatinine, KIM-1, and THP. In another exemplary embodiment, the combination of sample analytes may include microalbumin, creatinine, and KIM-1. In yet another exemplary embodiment, the combination of sample analytes may include KIM-1, THP, and B2M. In still another exemplary embodiment, the combination of sample analytes may include microalbumin, A1M, and creatinine. In an alternative exemplary embodiment, the sample is a urine sample, and the combination of sample analytes may include microalbumin, alpha-1 microglobulin, NGAL, KIM-1, THP, and clusterin. In another alternative exemplary embodiment, the sample is a plasma sample, and the combination of sample analytes may include alpha-1 microglobulin, cystatin C, THP, beta-2 microglobulin, TIMP-1, and KIM-1.

III. Test Sample

[0067] The method for diagnosing, monitoring, or determining a renal disorder involves determining the presence of sample analytes in a test sample. A test sample, as defined herein, is an amount of bodily fluid taken from a mammal. Non-limiting examples of bodily fluids include urine, blood, plasma, serum, saliva, semen, perspiration, tears, mucus, and tissue lysates. In an exemplary embodiment, the bodily fluid contained in the test sample is urine, plasma, or serum.

(a) Mammals

[0068] A mammal, as defined herein, is any organism that is a member of the class Mammalia. Non-limiting examples of mammals appropriate for the various embodiments may include humans, apes, monkeys, rats, mice, dogs, cats, pigs, and livestock including cattle and oxen. In an exemplary embodiment, the mammal is a human.

(b) Devices and Methods of Taking Bodily Fluids from Mammals

[0069] The bodily fluids of the test sample may be taken from the mammal using any known device or method so long as the analytes to be measured by the multiplexed assay are not rendered undetectable by the multiplexed assay. Non-limiting examples of devices or methods suitable for taking bodily fluid from a mammal include urine sample cups, ure-

thral catheters, swabs, hypodermic needles, thin needle biopsies, hollow needle biopsies, punch biopsies, metabolic cages, and aspiration.

[0070] In order to adjust the expected concentrations of the sample analytes in the test sample to fall within the dynamic range of the multiplexed assay, the test sample may be diluted to reduce the concentration of the sample analytes prior to analysis. The degree of dilution may depend on a variety of factors including but not limited to the type of multiplexed assay used to measure the analytes, the reagents utilized in the multiplexed assay, and the type of bodily fluid contained in the test sample. In one embodiment, the test sample is diluted by adding a volume of diluent ranging from about ½ of the original test sample volume to about 50,000 times the original test sample volume.

[0071] In one exemplary embodiment, if the test sample is human urine and the multiplexed assay is an antibody-based capture-sandwich assay, the test sample is diluted by adding a volume of diluent that is about 100 times the original test sample volume prior to analysis. In another exemplary embodiment, if the test sample is human serum and the multiplexed assay is an antibody-based capture-sandwich assay, the test sample is diluted by adding a volume of diluent that is about 5 times the original test sample volume prior to analysis. In yet another exemplary embodiment, if the test sample is human plasma and the multiplexed assay is an antibody-based capture-sandwich assay, the test sample is diluted by adding a volume of diluent that is about 2,000 times the original test sample volume prior to analysis.

[0072] The diluent may be any fluid that does not interfere with the function of the multiplexed assay used to measure the concentration of the analytes in the test sample. Non-limiting examples of suitable diluents include deionized water, distilled water, saline solution, Ringer's solution, phosphate buffered saline solution, TRIS-buffered saline solution, standard saline citrate, and HEPES-buffered saline.

IV. Multiplexed Assay Device

[0073] In one embodiment, the concentration of a combination of sample analytes is measured using a multiplexed assay device capable of measuring the concentrations of up to sixteen of the biomarker analytes. A multiplexed assay device, as defined herein, is an assay capable of simultaneously determining the concentration of three or more different sample analytes using a single device and/or method. Any known method of measuring the concentration of the biomarker analytes may be used for the multiplexed assay device. Non-limiting examples of measurement methods suitable for the multiplexed assay device may include electrophoresis, mass spectrometry, protein microarrays, surface plasmon resonance and immunoassays including but not limited to western blot, immunohistochemical staining, enzyme-linked immunosorbent assay (ELISA) methods, and particle-based capture-sandwich immunoassays.

(a) Multiplexed Immunoassay Device

[0074] In one embodiment, the concentrations of the analytes in the test sample are measured using a multiplexed immunoassay device that utilizes capture antibodies marked with indicators to determine the concentration of the sample analytes.

(i) Capture Antibodies

[0075] In the same embodiment, the multiplexed immunoassay device includes three or more capture antibodies. Capture antibodies, as defined herein, are antibodies in which the antigenic determinant is one of the biomarker analytes. Each of the at least three capture antibodies has a unique antigenic determinant that is one of the biomarker analytes. When contacted with the test sample, the capture antibodies form antigen-antibody complexes in which the analytes serve as antigens.

[0076] The term "antibody," as used herein, encompasses a monoclonal ab, an antibody fragment, a chimeric antibody, and a single-chain antibody.

[0077] In some embodiments, the capture antibodies may be attached to a substrate in order to immobilize any analytes captured by the capture antibodies. Non-limiting examples of suitable substrates include paper, cellulose, glass, or plastic strips, beads, or surfaces, such as the inner surface of the well of a microtitration tray. Suitable beads may include polystyrene or latex microspheres.

(ii) Indicators

[0078] In one embodiment of the multiplexed immunoassay device, an indicator is attached to each of the three or more capture antibodies. The indicator, as defined herein, is any compound that registers a measurable change to indicate the presence of one of the sample analytes when bound to one of the capture antibodies. Non-limiting examples of indicators include visual indicators and electrochemical indicators.

[0079] Visual indicators, as defined herein, are compounds that register a change by reflecting a limited subset of the wavelengths of light illuminating the indicator, by fluorescing light after being illuminated, or by emitting light via chemiluminescence. The change registered by visual indicators may be in the visible light spectrum, in the infrared spectrum, or in the ultraviolet spectrum. Non-limiting examples of visual indicators suitable for the multiplexed immunoassay device include nanoparticulate gold, organic particles such as polyurethane or latex microspheres loaded with dye compounds, carbon black, fluorophores, phycoerythrin, radioactive isotopes, nanoparticles, quantum dots, and enzymes such as horseradish peroxidase or alkaline phosphatase that react with a chemical substrate to form a colored or chemiluminescent product.

[0080] Electrochemical indicators, as defined herein, are compounds that register a change by altering an electrical property. The changes registered by electrochemical indicators may be an alteration in conductivity, resistance, capacitance, current conducted in response to an applied voltage, or voltage required to achieve a desired current. Non-limiting examples of electrochemical indicators include redox species such as ascorbate (vitamin C), vitamin E, glutathione, polyphenols, catechols, quercetin, phytoestrogens, penicillin, carbazole, murranes, phenols, carbonyls, benzoates, and trace metal ions such as nickel, copper, cadmium, iron and mercury.

[0081] In this same embodiment, the test sample containing a combination of three or more sample analytes is contacted with the capture antibodies and allowed to form antigen-antibody complexes in which the sample analytes serve as the antigens. After removing any uncomplexed capture antibodies, the concentrations of the three or more analytes are determined by measuring the change registered by the indicators attached to the capture antibodies.

[0082] In one exemplary embodiment, the indicators are polyurethane or latex microspheres loaded with dye compounds and phycoerythrin.

(b) Multiplexed Sandwich Immunoassay Device

[0083] In another embodiment, the multiplexed immunoassay device has a sandwich assay format. In this embodiment, the multiplexed sandwich immunoassay device includes three or more capture antibodies as previously described. However, in this embodiment, each of the capture antibodies is attached to a capture agent that includes an antigenic moiety. The antigenic moiety serves as the antigenic determinant of a detection antibody, also included in the multiplexed immunoassay device of this embodiment. In addition, an indicator is attached to the detection antibody.

[0084] In this same embodiment, the test sample is contacted with the capture antibodies and allowed to form antigen-antibody complexes in which the sample analytes serve as antigens. The detection antibodies are then contacted with the test sample and allowed to form antigen-antibody complexes in which the capture agent serves as the antigen for the detection antibody. After removing any uncomplexed detection antibodies the concentration of the analytes are determined by measuring the changes registered by the indicators attached to the detection antibodies.

(c) Multiplexing Approaches

[0085] In the various embodiments of the multiplexed immunoassay devices, the concentrations of each of the sample analytes may be determined using any approach known in the art. In one embodiment, a single indicator compound is attached to each of the three or more antibodies. In addition, each of the capture antibodies having one of the sample analytes as an antigenic determinant is physically separated into a distinct region so that the concentration of each of the sample analytes may be determined by measuring the changes registered by the indicators in each physically separate region corresponding to each of the sample analytes.

[0086] In another embodiment, each antibody having one of the sample analytes as an antigenic determinant is marked with a unique indicator. In this manner, a unique indicator is attached to each antibody having a single sample analyte as its antigenic determinant. In this embodiment, all antibodies may occupy the same physical space. The concentration of each sample analyte is determined by measuring the change registered by the unique indicator attached to the antibody having the sample analyte as an antigenic determinant.

(d) Microsphere-Based Capture-Sandwich Immunoassay Device

[0087] In an exemplary embodiment, the multiplexed immunoassay device is a microsphere-based capture-sandwich immunoassay device. In this embodiment, the device includes a mixture of three or more capture-antibody microspheres, in which each capture-antibody microsphere corresponds to one of the biomarker analytes. Each capture-antibody microsphere includes a plurality of capture antibodies attached to the outer surface of the microsphere. In this same embodiment, the antigenic determinant of all of the capture antibodies attached to one microsphere is the same biomarker analyte.

[0088] In this embodiment of the device, the microsphere is a small polystyrene or latex sphere that is loaded with an indicator that is a dye compound. The microsphere may be between about 3 μm and about 5 μm in diameter. Each capture-antibody microsphere corresponding to one of the biomarker analytes is loaded with the same indicator. In this manner, each capture-antibody microsphere corresponding to a biomarker analyte is uniquely color-coded.

[0089] In this same exemplary embodiment, the multiplexed immunoassay device further includes three or more biotinylated detection antibodies in which the antigenic determinant of each biotinylated detection antibody is one of the biomarker analytes. The device further includes a plurality of streptaviden proteins complexed with a reporter compound. A reporter compound, as defined herein, is an indicator selected to register a change that is distinguishable from the indicators used to mark the capture-antibody microspheres.

[0090] The concentrations of the sample analytes may be determined by contacting the test sample with a mixture of capture-antigen microspheres corresponding to each sample analyte to be measured. The sample analytes are allowed to form antigen-antibody complexes in which a sample analyte serves as an antigen and a capture antibody attached to the microsphere serves as an antibody. In this manner, the sample analytes are immobilized onto the capture-antigen microspheres. The biotinylated detection antibodies are then added to the test sample and allowed to form antigen-antibody complexes in which the analyte serves as the antigen and the biotinylated detection antibody serves as the antibody. The streptaviden-reporter complex is then added to the test sample and allowed to bind to the biotin moieties of the biotinylated detection antibodies. The antigen-capture microspheres may then be rinsed and filtered.

[0091] In this embodiment, the concentration of each analyte is determined by first measuring the change registered by the indicator compound embedded in the capture-antigen microsphere in order to identify the particular analyte. For each microsphere corresponding to one of the biomarker analytes, the quantity of analyte immobilized on the microsphere is determined by measuring the change registered by the reporter compound attached to the microsphere.

[0092] For example, the indicator embedded in the microspheres associated with one sample analyte may register an emission of orange light, and the reporter may register an emission of green light. In this example, a detector device may measure the intensity of orange light and green light separately. The measured intensity of the green light would determine the concentration of the analyte captured on the microsphere, and the intensity of the orange light would determine the specific analyte captured on the microsphere.

[0093] Any sensor device may be used to detect the changes registered by the indicators embedded in the microspheres and the changes registered by the reporter compound, so long as the sensor device is sufficiently sensitive to the changes registered by both indicator and reporter compound. Non-limiting examples of suitable sensor devices include spectrophotometers, photosensors, colorimeters, cyclic coulometry devices, and flow cytometers. In an exemplary embodiment, the sensor device is a flow cytometer.

V. Method for Diagnosing, Monitoring, or Determining a Renal Disorder

[0094] In one embodiment, a method is provided for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder that includes providing a test sample,

determining the concentration of a combination of three or more sample analytes, comparing the measured concentrations of the combination of sample analytes to the entries of a dataset, and identifying diabetic nephropathy or an associated disorder based on the comparison between the concentrations of the sample analytes and the minimum diagnostic concentrations contained within each entry of the dataset.

(a) Diagnostic Dataset

[0095] In an embodiment, the concentrations of the sample analytes are compared to the entries of a dataset. In this embodiment, each entry of the dataset includes a combination of three or more minimum diagnostic concentrations indicative of a particular renal disorder. A minimum diagnostic concentration, as defined herein, is the concentration of an analyte that defines the limit between the concentration range corresponding to normal, healthy renal function and the concentration reflective of a particular renal disorder. In one embodiment, each minimum diagnostic concentration is the maximum concentration of the range of analyte concentrations for a healthy, normal individual. The minimum diagnostic concentration of an analyte depends on a number of factors including but not limited to the particular analyte and the type of bodily fluid contained in the test sample. As an illustrative example, Table 1 lists the expected normal ranges of the biomarker analytes in human plasma, serum, and urine.

TABLE 1

Normal Concentration Ranges In Human Plasma, Serum, and Urine Samples

		Plasma		Sera		Urine	
Analyte	Units	low	high	low	high	low	high
Calbindin	ng/ml	—	<5.0	—	<2.6	4.2	233
Clusterin	μg/ml	86	134	37	152	—	<0.089
CTGF	ng/ml	2.8	7.5	—	<8.2	—	<0.90
GST-alpha	ng/ml	6.7	62	1.2	52	—	<26
KIM-1	ng/ml	0.053	0.57	—	<0.35	0.023	0.67
VEGF	pg/ml	222	855	219	1630	69	517
B2M	μg/ml	0.68	2.2	1.00	2.6		<0.17
Cyst C	ng/ml	608	1170	476	1250	3.9	79
NGAL	ng/ml	89	375	102	822	2.9	81
OPN	ng/ml	4.1	25	0.49	12	291	6130
TIMP-1	ng/ml	50	131	100	246	—	<3.9
A1M	μg/ml	6.2	16	5.7	17	—	<4.2
THP	μg/ml	0.0084	0.052	0.0079	0.053	0.39	2.6
TFF3	μg/ml	0.040	0.49	0.021	0.17	—	<21
Creatinine	mg/dL	—	—	—	—	13	212
Microalbumin	μg/ml	—	—	—	—	—	>16

[0096] In one embodiment, the high values shown for each of the biomarker analytes in Table 1 for the analytic concentrations in human plasma, sera and urine are the minimum diagnostics values for the analytes in human plasma, sera, and urine, respectively. In one exemplary embodiment, the minimum diagnostic concentration in human plasma of alpha-1 microglobulin is about 16 μg/ml, beta-2 microglobulin is about 2.2 μg/ml, calbindin is greater than about 5 ng/ml, clusterin is about 134 μg/ml, CTGF is about 16 ng/ml, cystatin C is about 1170 ng/ml, GST-alpha is about 62 ng/ml, KIM-1 is about 0.57 ng/ml, NGAL is about 375 ng/ml, osteopontin is about 25 ng/ml, THP is about 0.052 μg/ml, TIMP-1 is about 131 ng/ml, TFF-3 is about 0.49 μg/ml, and VEGF is about 855 pg/ml.

[0097] In another exemplary embodiment, the minimum diagnostic concentration in human sera of alpha-1 microglobulin is about 17 μg/ml, beta-2 microglobulin is about 2.6 μg/ml, calbindin is greater than about 2.6 ng/ml, clusterin is about 152 μg/ml, CTGF is greater than about 8.2 ng/ml, cystatin C is about 1250 ng/ml, GST-alpha is about 52 ng/ml, KIM-1 is greater than about 0.35 ng/ml, NGAL is about 822 ng/ml, osteopontin is about 12 ng/ml, THP is about 0.053 μg/ml, TIMP-1 is about 246 ng/ml, TFF-3 is about 0.17 μg/ml, and VEGF is about 1630 pg/ml.

[0098] In yet another exemplary embodiment, the minimum diagnostic concentration in human urine of alpha-1 microglobulin is about 233 μg/ml, beta-2 microglobulin is greater than about 0.17 μg/ml, calbindin is about 233 ng/ml, clusterin is greater than about 0.089 μg/ml, CTGF is greater than about 0.90 ng/ml, cystatin C is about 1170 ng/ml, GST-alpha is greater than about 26 ng/ml, KIM-1 is about 0.67 ng/ml, NGAL is about 81 ng/ml, osteopontin is about 6130 ng/ml, THP is about 2.6 μg/ml, TIMP-1 is greater than about 3.9 ng/ml, TFF-3 is greater than about 21 μg/ml, and VEGF is about 517 pg/ml.

[0099] In one embodiment, the minimum diagnostic concentrations represent the maximum level of analyte concentrations falling within an expected normal range. Diabetic nephropathy or an associated disorder may be indicated if the concentration of an analyte is higher than the minimum diagnostic concentration for the analyte.

[0100] If diminished concentrations of a particular analyte are known to be associated with diabetic nephropathy or an associated disorder, the minimum diagnostic concentration may not be an appropriate diagnostic criterion for identifying diabetic nephropathy or an associated disorder indicated by the sample analyte concentrations. In these cases, a maximum diagnostic concentration may define the limit between the expected normal concentration range for the analyte and a sample concentration reflective of diabetic nephropathy or an associated disorder. In those cases in which a maximum diagnostic concentration is the appropriate diagnostic criterion,

sample concentrations that fall below a maximum diagnostic concentration may indicate diabetic nephropathy or an associated disorder.

[0101] A critical feature of the method of the multiplexed analyte panel is that a combination of sample analyte concentrations may be used to diagnose diabetic nephropathy or an associated disorder. In addition to comparing subsets of the biomarker analyte concentrations to diagnostic criteria, the analytes may be algebraically combined and compared to corresponding diagnostic criteria. In one embodiment, two or more sample analyte concentrations may be added and/or subtracted to determine a combined analyte concentration. In another embodiment, two or more sample analyte concentrations may be multiplied and/or divided to determine a combined analyte concentration. To identify diabetic nephropathy or an associated disorder, the combined analyte concentration may be compared to a diagnostic criterion in which the corresponding minimum or maximum diagnostic concentrations are combined using the same algebraic operations used to determine the combined analyte concentration.

[0102] In yet another embodiment, the analyte concentration measured from a test sample containing one type of body fluid may be algebraically combined with an analyte concentration measured from a second test sample containing a second type of body fluid to determine a combined analyte concentration. For example, the ratio of urine calbindin to plasma calbindin may be determined and compared to a corresponding minimum diagnostic urine:plasma calbindin ratio to identify a particular renal disorder.

[0103] A variety of methods known in the art may be used to define the diagnostic criteria used to identify diabetic nephropathy or an associated disorder. In one embodiment, any sample concentration falling outside the expected normal range indicates diabetic nephropathy or an associated disorder. In another embodiment, the multiplexed analyte panel may be used to evaluate the analyte concentrations in test samples taken from a population of patients having diabetic nephropathy or an associated disorder and compared to the normal expected analyte concentration ranges. In this same embodiment, any sample analyte concentrations that are significantly higher or lower than the expected normal concentration range may be used to define a minimum or maximum diagnostic concentration, respectively. A number of studies comparing the biomarker concentration ranges of a population of patients having a renal disorder to the corresponding analyte concentrations from a population of normal healthy subjects are described in the examples section below.

[0104] In an exemplary embodiment, an analyte value in a test sample higher than the minimum diagnostic value for the top 3 analytes of the particular sample type (e.g. plasma, urine, etc.), wherein the top 3 are determined by the random forest classification method may result in a diagnosis of diabetic nephropathy.

VI. Automated Method for Diagnosing, Monitoring, or Determining a Renal Disorder

[0105] In one embodiment, a system for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal is provided that includes a database to store a plurality of renal disorder database entries, and a processing device that includes the modules of a renal disorder determining application. In this embodiment, the modules are executable by the processing device, and include an analyte input module, a comparison module, and an analysis module.

[0106] The analyte input module receives three or more sample analyte concentrations that include the biomarker analytes. In one embodiment, the sample analyte concentrations are entered as input by a user of the application. In another embodiment, the sample analyte concentrations are transmitted directly to the analyte input module by the sensor device used to measure the sample analyte concentration via a data cable, infrared signal, wireless connection or other methods of data transmission known in the art.

[0107] The comparison module compares each sample analyte concentration to an entry of a renal disorder database. Each entry of the renal disorder database includes a list of minimum diagnostic concentrations reflective of a particular renal disorder. The entries of the renal disorder database may further contain additional minimum diagnostic concentrations to further define diagnostic criteria including but not limited to minimum diagnostic concentrations for additional types of bodily fluids, additional types of mammals, and severities of a particular disorder.

[0108] The analysis module determines a most likely renal disorder by combining the particular renal disorders identified by the comparison module for all of the sample analyte concentrations. In one embodiment, the most likely renal disorder is the particular renal disorder from the database entry having the most minimum diagnostic concentrations that are less than the corresponding sample analyte concentrations. In another embodiment, the most likely renal disorder is the particular renal disorder from the database entry having minimum diagnostic concentrations that are all less than the corresponding sample analyte concentrations. In yet other embodiments, the analysis module combines the sample analyte concentrations algebraically to calculate a combined sample analyte concentration that is compared to a combined minimum diagnostic concentration calculated from the corresponding minimum diagnostic criteria using the same algebraic operations. Other combinations of sample analyte concentrations from within the same test sample, or combinations of sample analyte concentrations from two or more different test samples containing two or more different bodily fluids may be used to determine a particular renal disorder in still other embodiments.

[0109] The system includes one or more processors and volatile and/or nonvolatile memory and can be embodied by or in one or more distributed or integrated components or systems. The system may include computer readable media (CRM) on which one or more algorithms, software, modules, data, and/or firmware is loaded and/or operates and/or which operates on the one or more processors to implement the systems and methods identified herein. The computer readable media may include volatile media, nonvolatile media, removable media, non-removable media, and/or other media or mediums that can be accessed by a general purpose or special purpose computing device. For example, computer readable media may include computer storage media and communication media, including but not limited to computer readable media. Computer storage media further may include volatile, nonvolatile, removable, and/or non-removable media implemented in a method or technology for storage of information, such as computer readable instructions, data structures, program modules, and/or other data. Communication media may, for example, embody computer readable

instructions, data structures, program modules, algorithms, and/or other data, including but not limited to as or in a modulated data signal. The communication media may be embodied in a carrier wave or other transport mechanism and may include an information delivery method. The communication media may include wired and wireless connections and technologies and may be used to transmit and/or receive wired or wireless communications. Combinations and/or sub-combinations of the above and systems, components, modules, and methods and processes described herein may be made.

[0110] The following examples are included to demonstrate preferred embodiments of the invention.

EXAMPLES

[0111] The following examples illustrate various iterations of the invention.

Example 1

Least Detectable Dose and Lower Limit of Quantitation of Assay for Analytes Associated with Renal Disorders

[0112] To assess the least detectable doses (LDD) and lower limits of quantitation (LLOQ) of a variety of analytes associated with renal disorders, the following experiment was conducted. The analytes measured were alpha-1 microglobulin (A1M), beta-2 microglobulin (B2M), calbindin, clusterin, CTGF, cystatin C, GST-alpha, KIM-1, NGAL, osteopontin (OPN), THP, TIMP-1, TFF-3, and VEGF.

[0113] The concentrations of the analytes were measured using a capture-sandwich assay using antigen-specific antibodies. For each analyte, a range of standard sample dilutions ranging over about four orders of magnitude of analyte concentration were measured using the assay in order to obtain data used to construct a standard dose response curve. The dynamic range for each of the analytes, defined herein as the range of analyte concentrations measured to determine its dose response curve, is presented below.

[0114] To perform the assay, 5 μL of a diluted mixture of capture-antibody microspheres were mixed with 5 μL of blocker and 10 μL of pre-diluted standard sample in each of the wells of a hard-bottom microtiter plate. After incubating the hard-bottom plate for 1 hour, 10 μL of biotinylated detection antibody was added to each well, and then the hard-bottom plate was incubated for an additional hour. 10 μL of diluted streptavidin-phycoerythrin was added to each well and then the hard-bottom plate was incubated for another 60 minutes.

[0115] A filter-membrane microtiter plate was pre-wetted by adding 100 μL wash buffer, and then aspirated using a vacuum manifold device. The contents of the wells of the hard-bottom plate were then transferred to the corresponding wells of the filter-membrane plate. All wells of the hard-bottom plate were vacuum-aspirated and the contents were washed twice with 100 μL of wash buffer. After the second wash, 100 μL of wash buffer was added to each well, and then the washed microspheres were resuspended with thorough mixing. The plate was then analyzed using a Luminex 100 Analyzer (Luminex Corporation, Austin, Tex., USA). Dose response curves were constructed for each analyte by curve-fitting the median fluorescence intensity (MFI) measured from the assays of diluted standard samples containing a range of analyte concentrations.

[0116] The least detectable dose (LDD) was determined by adding three standard deviations to the average of the MFI signal measured for 20 replicate samples of blank standard solution (i.e. standard solution containing no analyte). The MFI signal was converted to an LDD concentration using the dose response curve and multiplied by a dilution factor of 2.

[0117] The lower limit of quantification (LLOQ), defined herein as the point at which the coefficient of variation (CV) for the analyte measured in the standard samples was 30%, was determined by the analysis of the measurements of increasingly diluted standard samples. For each analyte, the standard solution was diluted by 2 fold for 8 dilutions. At each stage of dilution, samples were assayed in triplicate, and the CV of the analyte concentration at each dilution was calculated and plotted as a function of analyte concentration. The LLOQ was interpolated from this plot and multiplied by a dilution factor of 2.

[0118] The LDD and LLOQ results for each analyte are summarized in Table 2:

TABLE 2

LDD, LLOQ, and Dynamic Range of Analyte Assay

				Dynamic Range	
Analyte	Units	LDD	LLOQ	minimum	maximum
Calbindin	ng/mL	1.1	3.1	0.516	2580
Clusterin	ng/mL	2.4	2.3	0.676	3378
CTGF	ng/mL	1.3	3.8	0.0794	400
GST-alpha	ng/mL	1.4	3.6	0.24	1,200
KIM-1	ng/mL	0.016	0.028	0.00478	24
VEGF	pg/mL	4.4	20	8.76	44,000
β-2M	μg/mL	0.012	0.018	0.0030	15
Cystatin C	ng/mL	2.8	3.7	0.60	3,000
NGAL	ng/mL	4.1	7.8	1.2	6,000
Osteopontin	ng/mL	29	52	3.9	19,500
TIMP-1	ng/mL	0.71	1.1	0.073	365
A-1M	μg/mL	0.059	0.29	0.042	210
THP	μg/mL	0.46	0.30	0.16	800
TFF-3	μg/mL	0.06	0.097	0.060	300

[0119] The results of this experiment characterized the least detectable dose and the lower limit of quantification for fourteen analytes associated with various renal disorders using a capture-sandwich assay.

Example 2

Precision of Assay for Analytes Associated with Renal Disorders

[0120] To assess the precision of an assay used to measure the concentration of analytes associated with renal disorders, the following experiment was conducted. The analytes measured were alpha-1 microglobulin (A1M), beta-2 microglobulin (B2M), calbindin, clusterin, CTGF, cystatin C, GST-alpha, KIM-1, NGAL, osteopontin (OPN), THP, TIMP-1, TFF-3, and VEGF. For each analyte, three concentration levels of standard solution were measured in triplicate during three runs using the methods described in Example 1. The

percent errors for each run at each concentration are presented in Table 3 for all of the analytes tested:

TABLE 3

Precision of Analyte Assay

Analyte	Average concentration (ng/mL)	Run 1 Error (%)	Run 2 Error (%)	Run 2 Error (%)	Interrun Error (%)
Calbindin	4.0	6	2	6	13
	36	5	3	2	7
	281	1	6	0	3
Clusterin	4.4	4	9	2	6
	39	5	1	6	8
	229	1	3	0	2
CTGF	1.2	10	17	4	14
	2.5	19	19	14	14
	18	7	5	13	9
GST-alpha	3.9	14	7	5	10
	16	13	7	10	11
	42	1	16	6	8
KIM-1	0.035	2	0	5	13
	0.32	4	5	2	8
	2.9	0	5	7	4
VEGF	65	10	1	6	14
	534	9	2	12	7
	5,397	1	13	14	9
β-2M	0.040	6	1	8	5
	0.43	2	2	0	10
	6.7	6	5	11	6
Cystatin C	10.5	4	1	7	13
	49	0	0	3	9
	424	2	6	2	5
NGAL	18.1	11	3	6	13
	147	0	0	6	5
	1,070	5	1	2	5
Osteopontin	44	1	10	2	11
	523	9	9	9	7
	8,930	4	10	1	10
TIMP-1	2.2	13	6	3	13
	26	1	1	4	14
	130	1	3	1	4
A-1M	1.7	11	7	7	14
	19	4	1	8	9
	45	3	5	2	4
THP	9.4	3	10	11	11
	15	3	7	8	6
	37	4	5	0	5
TFF-3	0.3	13	3	11	12
	4.2	5	8	5	7
	1.2	3	7	0	13

[0121] The results of this experiment characterized the precision of a capture-sandwich assay for fourteen analytes associated with various renal disorders over a wide range of analyte concentrations. The precision of the assay varied between about 1% and about 15% error within a given run, and between about 5% and about 15% error between different runs. The percent errors summarized in Table 2 provide information concerning random error to be expected in an assay measurement caused by variations in technicians, measuring instruments, and times of measurement.

Example 3

Linearity of Assay for Analytes Associated with Renal Disorders

[0122] To assess the linearity of an assay used to measure the concentration of analytes associated with renal disorders, the following experiment was conducted. The analytes measured were alpha-1 microglobulin (A1M), beta-2 microglobulin (B2M), calbindin, clusterin, CTGF, cystatin C, GST-alpha, KIM-1, NGAL, osteopontin (OPN), THP, TIMP-1, TFF-3, and VEGF. For each analyte, three concentration levels of standard solution were measured in triplicate during three runs using the methods described in Example 1. Linearity of the assay used to measure each analyte was determined by measuring the concentrations of standard samples that were serially-diluted throughout the assay range. The % recovery was calculated as observed vs. expected concentration based on the dose-response curve. The results of the linearity analysis are summarized in Table 4.

TABLE 4

Linearity of Analyte Assay

Analyte	Dilution	Expected concentration	Observed concentration	Recovery (%)
Calbindin	1:2	61	61	100
(ng/mL)	1:4	30	32	106
	1:8	15	17	110
Clusterin	1:2	41	41	100
(ng/mL)	1:4	21	24	116
	1:8	10	11	111
CTGF	1:2	1.7	1.7	100
(ng/mL)	1:4	0.84	1.0	124
	1:8	0.42	0.51	122
GST-alpha	1:2	25	25	100
(ng/mL)	1:4	12	14	115
	1:8	6.2	8.0	129
KIM-1	1:2	0.87	0.87	100
(ng/mL)	1:4	0.41	0.41	101
	1:8	0.21	0.19	93
VEGF	1:2	2,525	2,525	100
(pg/mL)	1:4	1,263	1,340	106
	1:8	631	686	109
β-2M	1:100	0.63	0.63	100
(μg/mL)	1:200	0.31	0.34	106
	1:400	0.16	0.17	107
Cystatin C	1:100	249	249	100
(ng/mL)	1:200	125	122	102
	1:400	62	56	110
NGAL	1:100	1,435	1,435	100
(ng/mL)	1:200	718	775	108
	1:400	359	369	103
Osteopontin	1:100	6,415	6,415	100
(ng/mL)	1:200	3,208	3,275	102
	1:400	1,604	1,525	95
TIMP-1	1:100	35	35	100
(ng/mL)	1:200	18	18	100
	1:400	8.8	8.8	100
A-1M	1:2000	37	37	100
(μg/mL)	1:4000	18	18	99
	1:8000	9.1	9.2	99
THP	1:2000	28	28	100
(μg/mL)	1:4000	14	14	96
	1:8000	6.7	7.1	94
TFF-3	1:2000	8.8	8.8	100
(μg/mL)	1:4000	3.8	4.4	86
	1:8000	1.9	2.2	86

[0123] The results of this experiment demonstrated reasonably linear responses of the sandwich-capture assay to variations in the concentrations of the analytes in the tested samples.

Example 4

Spike Recovery of Analytes Associated with Renal Disorders

[0124] To assess the recovery of analytes spiked into urine, serum, and plasma samples by an assay used to measure the concentration of analytes associated with renal disorders, the

following experiment was conducted. The analytes measured were alpha-1 microglobulin (A1M), beta-2 microglobulin (B2M), calbindin, clusterin, CTGF, cystatin C, GST-alpha, KIM-1, NGAL, osteopontin (OPN), THP, TIMP-1, TFF-3, and VEGF. For each analyte, three concentration levels of standard solution were spiked into known urine, serum, and plasma samples. Prior to analysis, all urine samples were diluted 1:2000 (sample: diluent), all plasma samples were diluted 1:5 (sample: diluent), and all serum samples were diluted 1:2000 (sample: diluent).

[0125] The concentrations of the analytes in the samples were measured using the methods described in Example 1. The average % recovery was calculated as the proportion of the measurement of analyte spiked into the urine, serum, or plasma sample (observed) to the measurement of analyte spiked into the standard solution (expected). The results of the spike recovery analysis are summarized in Table 5.

TABLE 5

Spike Recovery of Analyte Assay in Urine, Serum, and Plasma Samples

Analyte	Spike Concentration	Recovery in Urine Sample (%)	Recovery in Serum Sample (%)	Recovery in Plasma Sample (%)
Calbindin	66	76	82	83
(ng/mL)	35	91	77	71
	18	80	82	73
	average	82	80	76
Clusterin	80	72	73	75
(ng/mL)	37	70	66	72
	20	90	73	70
	average	77	70	72
CTGF	8.4	91	80	79
(ng/mL)	4.6	114	69	78
	2.4	76	80	69
	average	94	77	75
GST-alpha	27	75	84	80
(ng/mL)	15	90	75	81
	7.1	82	84	72
	average	83	81	78
KIM-1	0.63	87	80	83
(ng/mL)	.029	119	74	80
	0.14	117	80	78
	average	107	78	80
VEGF	584	88	84	82
(pg/mL)	287	101	77	86
	123	107	84	77
	average	99	82	82
β-2M	0.97	117	98	98
(μg/mL)	0.50	124	119	119
	0.24	104	107	107
	average	115	108	105
Cystatin C	183	138	80	103
(ng/mL)	90	136	97	103
	40	120	97	118
	average	131	91	108
NGAL	426	120	105	111
(ng/mL)	213	124	114	112
	103	90	99	113
	average	111	106	112
Osteopontin	1,245	204	124	68
(ng/mL)	636	153	112	69
	302	66	103	67
	average	108	113	68
TIMP-1	25	98	97	113
(ng/mL)	12	114	89	103
	5.7	94	99	113
	average	102	95	110
A-1M	0.0028	100	101	79
(μg/mL)	0.0012	125	80	81
	0.00060	118	101	82
	average	114	94	81

TABLE 5-continued

Spike Recovery of Analyte Assay in Urine, Serum, and Plasma Samples

Analyte	Spike Concentration	Recovery in Urine Sample (%)	Recovery in Serum Sample (%)	Recovery in Plasma Sample (%)
THP	0.0096	126	108	90
(μg/mL)	0.0047	131	93	91
	0.0026	112	114	83
	average	123	105	88
TFF-3	0.0038	105	114	97
(μg/mL)	0.0019	109	104	95
	0.0010	102	118	93
	average	105	112	95

[0126] The results of this experiment demonstrated that the sandwich-type assay is reasonably sensitive to the presence of all analytes measured, whether the analytes were measured in standard samples, urine samples, plasma samples, or serum samples.

Example 5

Matrix Interferences of Analytes Associated with Renal Disorders

[0127] To assess the matrix interference of hemoglobin, bilirubin, and triglycerides spiked into standard samples, the following experiment was conducted. The analytes measured were alpha-1 microglobulin (A1M), beta-2 microglobulin (B2M), calbindin, clusterin, CTGF, cystatin C, GST-alpha, KIM-1, NGAL, osteopontin (OPN), THP, TIMP-1, TFF-3, and VEGF. For each analyte, three concentration levels of standard solution were spiked into known urine, serum, and plasma samples. Matrix interference was assessed by spiking hemoglobin, bilirubin, and triglyceride into standard analyte samples and measuring analyte concentrations using the methods described in Example 1. A % recovery was determined by calculating the ratio of the analyte concentration measured from the spiked sample (observed) divided by the analyte concentration measured form the standard sample (expected). The results of the matrix interference analysis are summarized in Table 6.

TABLE 6

Matrix Interference of Hemoglobin, Bilirubin, and Triglyceride on the Measurement of Analytes

Analyte	Matrix Compound Spiked into Sample	Maximum Spike Concentration	Overall Recovery (%)
Calbindin	Hemoglobin	500	110
(mg/mL)	Bilirubin	20	98
	Triglyceride	500	117
Clusterin	Hemoglobin	500	125
(mg/mL)	Bilirubin	20	110
	Triglyceride	500	85
CTGF	Hemoglobin	500	91
(mg/mL)	Bilirubin	20	88
	Triglyceride	500	84
GST-alpha	Hemoglobin	500	100
(mg/mL)	Bilirubin	20	96
	Triglyceride	500	96
KIM-1	Hemoglobin	500	108
(mg/mL)	Bilirubin	20	117
	Triglyceride	500	84

TABLE 6-continued

Matrix Interference of Hemoglobin, Bilirubin, and Triglyceride on the Measurement of Analytes

Analyte	Matrix Compound Spiked into Sample	Maximum Spike Concentration	Overall Recovery (%)
VEGF	Hemoglobin	500	112
(mg/mL)	Bilirubin	20	85
	Triglyceride	500	114
β-2M	Hemoglobin	500	84
(μg/mL)	Bilirubin	20	75
	Triglyceride	500	104
Cystatin C	Hemoglobin	500	91
(ng/mL)	Bilirubin	20	102
	Triglyceride	500	124
NGAL	Hemoglobin	500	99
(ng/mL)	Bilirubin	20	92
	Triglyceride	500	106
Osteopontin	Hemoglobin	500	83
(ng/mL)	Bilirubin	20	86
	Triglyceride	500	106
TIMP-1	Hemoglobin	500	87
(ng/mL)	Bilirubin	20	86
	Triglyceride	500	93
A-1M	Hemoglobin	500	103
(μg/mL)	Bilirubin	20	110
	Triglyceride	500	112
THP	Hemoglobin	500	108
(μg/mL)	Bilirubin	20	101
	Triglyceride	500	121
TFF-3	Hemoglobin	500	101
(μg/mL)	Bilirubin	20	101
	Triglyceride	500	110

[0128] The results of this experiment demonstrated that hemoglobin, bilirubin, and triglycerides, three common compounds found in urine, plasma, and serum samples, did not significantly degrade the ability of the sandwich-capture assay to detect any of the analytes tested.

Example 6

Sample Stability of Analytes Associated with Renal Disorders

[0129] To assess the ability of analytes spiked into urine, serum, and plasma samples to tolerate freeze-thaw cycles, the following experiment was conducted. The analytes measured were alpha-1 microglobulin (A1M), beta-2 microglobulin (B2M), calbindin, clusterin, CTGF, cystatin C, GST-alpha, KIM-1, NGAL, osteopontin (OPN), THP, TIMP-1, TFF-3, and VEGF. Each analyte was spiked into known urine, serum, and plasma samples at a known analyte concentration. The concentrations of the analytes in the samples were measured using the methods described in Example 1 after the initial addition of the analyte, and after one, two and three cycles of freezing and thawing. In addition, analyte concentrations in urine, serum and plasma samples were measured immediately after the addition of the analyte to the samples as well as after storage at room temperature for two hours and four hours, and after storage at 4° C. for 2 hours, four hours, and 24 hours.

[0130] The results of the freeze-thaw stability analysis are summarized in Table 7. The % recovery of each analyte was calculated as a percentage of the analyte measured in the sample prior to any freeze-thaw cycles.

TABLE 7

Freeze-Thaw Stability of the Analytes in Urine, Serum, and Plasma

	Period	Urine Sample		Serum Sample		Plasma Sample	
Analyte	and Temp	Concentration	Recovery (%)	Concentration	Recovery (%)	Concentration	Recovery (%)
Calbindin	Control	212	100	31	100	43	100
(ng/mL)	1X	221	104	30	96	41	94
	2X	203	96	30	99	39	92
	3X	234	110	30	97	40	93
Clusterin	0	315	100	232	100	187	100
(ng/mL)	1X	329	104	227	98	177	95
	2X	341	108	240	103	175	94
	3X	379	120	248	107	183	98
CTGF	0	6.7	100	1.5	100	1.2	100
(ng/mL)	1X	7.5	112	1.3	82	1.2	94
	2X	6.8	101	1.4	90	1.2	100
	3X	7.7	115	1.2	73	1.3	107
GST-	0	12	100	23	100	11	100
alpha	1X	13	104	24	105	11	101
(ng/mL)	2X	14	116	21	92	11	97
	3X	14	111	23	100	12	108
KIM-1	0	1.7	100	0.24	100	0.24	100
(ng/mL)	1X	1.7	99	0.24	102	0.22	91
	2X	1.7	99	0.22	94	0.19	78
	3X	1.8	107	0.23	97	0.22	93
VEGF	0	1,530	100	1,245	100	674	100
(pg/mL)	1X	1,575	103	1,205	97	652	97
	2X	1,570	103	1,140	92	612	91
	3X	1,700	111	1,185	95	670	99

TABLE 7-continued

Freeze-Thaw Stability of the Analytes in Urine, Serum, and Plasma

Analyte	Period and Temp	Urine Sample Concentration	Urine Sample Recovery (%)	Serum Sample Concentration	Serum Sample Recovery (%)	Plasma Sample Concentration	Plasma Sample Recovery (%)
β-2M	0	0.0070	100	1.2	100	15	100
(μg/mL)	1X	0.0073	104	1.1	93	14	109
	2X	0.0076	108	1.2	103	15	104
	3X	0.0076	108	1.1	97	13	116
Cystatin C	0	1,240	100	1,330	100	519	100
(ng/mL)	1X	1,280	103	1,470	111	584	113
	2X	1,410	114	1,370	103	730	141
	3X	1,420	115	1,380	104	589	113
NGAL	0	45	100	245	100	84	100
(ng/mL)	1X	46	102	179	114	94	112
	2X	47	104	276	113	91	108
	3X	47	104	278	113	91	109
Osteopontin	0	38	100	1.7	100	5.0	100
(ng/mL)	1X	42	110	1.8	102	5.5	110
	2X	42	108	1.5	87	5.5	109
	3X	42	110	1.3	77	5.4	107
TIMP-1	0	266	100	220	100	70	100
(ng/mL)	1X	265	100	220	10	75	108
	2X	255	96	215	98	77	110
	3X	295	111	228	104	76	109
A-1M	0	14	100	26	100	4.5	100
(μg/mL)	1X	13	92	25	96	4.2	94
	2X	15	107	25	96	4.3	97
	3X	16	116	23	88	4.0	90
THP	0	4.6	100	31	100	9.2	100
(μg/mL)	1X	4.4	96	31	98	8.8	95
	2X	5.0	110	31	100	9.2	100
	3X	5.2	114	27	85	9.1	99
TFF-3	0	4.6	100	24	100	22	100
(μg/mL)	1X	4.4	96	23	98	22	103
	2X	5.0	110	24	103	22	101
	3X	5.2	114	19	82	22	102

[0131] The results of the short-term stability assessment are summarized in Table 8. The % recovery of each analyte was calculated as a percentage of the analyte measured in the sample prior to any short-term storage.

TABLE 8

Short-Term Stability of Analytes in Urine, Serum, and Plasma

Analyte	Storage Time/ Temp	Urine Sample Sample Conc.	Urine Sample Recovery (%)	Serum Sample Sample Conc.	Serum Sample Recovery (%)	Plasma Sample Sample Conc.	Plasma Sample Recovery (%)
Calbindin	Control	226	100	33	100	7	100
(ng/mL)	2 hr/ room temp	242	107	30	90	6.3	90
	2 hr. @ 4° C.	228	101	29	89	6.5	93
	4 hr @ room temp	240	106	28	84	5.6	79
	4 hr. @ 4° C.	202	89	29	86	5.5	79
	24 hr. @ 4° C.	199	88	26	78	7.1	101
Clusterin	Control	185	100	224	100	171	100
(ng/mL)	2 hr @ room temp	173	94	237	106	180	105
	2 hr. @ 4° C.	146	79	225	100	171	100

TABLE 8-continued

Short-Term Stability of Analytes in Urine, Serum, and Plasma

Analyte	Storage Time/ Temp	Urine Sample Sample Conc.	Urine Sample Recovery (%)	Serum Sample Sample Conc.	Serum Sample Recovery (%)	Plasma Sample Sample Conc.	Plasma Sample Recovery (%)
	4 hr @ room temp	166	89	214	96	160	94
	4 hr. @ 4° C.	157	85	198	88	143	84
	24 hr. @ 4° C.	185	100	207	92	162	94
CTGF	Control	1.9	100	8.8	100	1.2	100
(ng/mL)	2 hr @ room temp	1.9	99	6.7	76	1	83
	2 hr. @ 4° C.	1.8	96	8.1	92	1.1	89
	4 hr @ room temp	2.1	113	5.6	64	1	84
	4 hr. @ 4° C.	1.7	91	6.4	74	0.9	78
	24 hr. @ 4° C.	2.2	116	5.9	68	1.1	89
GST-	Control	14	100	21	100	11	100
alpha	2 hr @ room temp	11	75	23	107	11	103
(ng/mL)	2 hr. @ 4° C.	13	93	22	104	9.4	90
	4 hr @ room temp	11	79	21	100	11	109
	4 hr. @ 4° C.	12	89	21	98	11	100
	24 hr. @ 4° C.	13	90	22	103	14	129
KIM-1	Control	1.5	100	0.23	100	0.24	100
(ng/mL)	2 hr @ room temp	1.2	78	0.2	86	0.22	90
	2 hr. @ 4° C.	1.6	106	0.23	98	0.21	85
	4 hr @ room temp	1.3	84	0.19	82	0.2	81
	4 hr. @ 4° C.	1.4	90	0.22	93	0.19	80
	24 hr. @ 4° C.	1.1	76	0.18	76	0.23	94
VEGF	Control	851	100	1215	100	670	100
(pg/mL)	2 hr @ room temp	793	93	1055	87	622	93
	2 hr. @ 4° C.	700	82	1065	88	629	94
	4 hr @ room temp	704	83	1007	83	566	84
	4 hr. @ 4° C.	618	73	1135	93	544	81
	24 hr. @ 4° C.	653	77	1130	93	589	88
β-2M	Control	0.064	100	2.6	100	1.2	100
(μg/mL)	2 hr @ room temp	0.062	97	2.4	92	1.1	93
	2 hr. @ 4° C.	0.058	91	2.2	85	1.2	94
	4 hr @ room temp	0.064	101	2.2	83	1.2	94

TABLE 8-continued

Short-Term Stability of Analytes in Urine, Serum, and Plasma

Analyte	Storage Time/ Temp	Urine Sample Sample Conc.	Urine Sample Recovery (%)	Serum Sample Sample Conc.	Serum Sample Recovery (%)	Plasma Sample Sample Conc.	Plasma Sample Recovery (%)
	4 hr. @ 4° C.	0.057	90	2.2	85	1.2	98
	24 hr. @ 4° C.	0.06	94	2.5	97	1.3	103
Cystatin C (ng/mL)	Control	52	100	819	100	476	100
	2 hr @ room temp	50	96	837	102	466	98
	2 hr. @ 4° C.	44	84	884	108	547	115
	4 hr @ room temp	49	93	829	101	498	105
	4 hr. @ 4° C.	46	88	883	108	513	108
	24 hr. @ 4° C.	51	97	767	94	471	99
NGAL (ng/mL)	Control	857	100	302	100	93	100
	2 hr @ room temp	888	104	287	95	96	104
	2 hr. @ 4° C.	923	108	275	91	92	100
	4 hr @ room temp	861	101	269	89	88	95
	4 hr. @ 4° C.	842	98	283	94	94	101
	24 hr. @ 4° C.	960	112	245	81	88	95
Osteopontin (ng/mL)	Control	2243	100	6.4	100	5.2	100
	2 hr @ room temp	2240	100	6.8	107	5.9	114
	2 hr. @ 4° C.	2140	95	6.4	101	6.2	120
	4 hr @ room temp	2227	99	6.9	108	5.8	111
	4 hr. @ 4° C.	2120	95	7.7	120	5.2	101
	24 hr. @ 4° C.	2253	100	6.5	101	6	116
TIMP-1 (ng/mL)	Control	17	100	349	100	72	100
	2 hr @ room temp	17	98	311	89	70	98
	2 hr. @ 4° C.	16	94	311	89	68	95
	4 hr @ room temp	17	97	306	88	68	95
	4 hr. @ 4° C.	16	93	329	94	74	103
	24 hr. @ 4° C.	18	105	349	100	72	100
A-1M (μg/mL)	Control	3.6	100	2.2	100	1	100
	2 hr @ room temp	3.5	95	2	92	1	105
	2 hr. @ 4° C.	3.4	92	2.1	97	0.99	99

TABLE 8-continued

Short-Term Stability of Analytes in Urine, Serum, and Plasma

Analyte	Storage Time/ Temp	Urine Sample Sample Conc.	Urine Sample Recovery (%)	Serum Sample Sample Conc.	Serum Sample Recovery (%)	Plasma Sample Sample Conc.	Plasma Sample Recovery (%)
	4 hr @ room temp	3.2	88	2.2	101	0.99	96
	4 hr. @ 4° C.	3	82	2.2	99	0.97	98
	24 hr. @ 4° C.	3	83	2.2	100	1	101
THP	Control	1.2	100	34	100	2.1	100
(μg/mL)	2 hr @ room temp	1.2	99	34	99	2	99
	2 hr. @ 4° C.	1.1	90	34	100	2	98
	4 hr @ room temp	1.1	88	27	80	2	99
	4 hr. @ 4° C.	0.95	79	33	97	2	95
	24 hr. @ 4° C.	0.91	76	33	98	2.4	116
TFF-3	Control	1230	100	188	100	2240	100
(μg/mL)	2 hr @ room temp	1215	99	179	95	2200	98
	2 hr. @ 4° C.	1200	98	195	104	2263	101
	4 hr @ room temp	1160	94	224	119	2097	94
	4 hr. @ 4° C.	1020	83	199	106	2317	103
	24 hr. @ 4° C.	1030	84	229	122	1940	87

[0132] The results of this experiment demonstrated that the analytes associated with renal disorders tested were suitably stable over several freeze/thaw cycles, and up to 24 hrs of storage at a temperature of 4° C.

Example 8

Analysis of Kidney Biomarkers in Plasma and Urine from Patients with Renal Injury

[0133] A screen for potential protein biomarkers in relation to kidney toxicity/damage was performed using a panel of biomarkers, in a set of urine and plasma samples from patients with documented renal damage. The investigated patient groups included diabetic nephropathy (DN), obstructive uropathy (OU), analgesic abuse (AA) and glomerulonephritis (GN) along with age, gender and BMI matched control groups. Multiplexed immunoassays were applied in order to quantify the following protein analytes: Alpha-1 Microglobulin (α1M), KIM-1, Microalbumin, Beta-2-Microglobulin (β2M), Calbindin, Clusterin, CystatinC, TreFoilFactor-3 (TFF-3), CTGF, GST-alpha, VEGF, Calbindin, Osteopontin, Tamm-HorsfallProtein (THP), TIMP-1 and NGAL.

[0134] Li-Heparin plasma and mid-stream spot urine samples were collected from four different patient groups. Samples were also collected from age, gender and BMI matched control subjects. 20 subjects were included in each group resulting in a total number of 160 urine and plasma samples. All samples were stored at −80° C. before use. Glomerular filtration rate for all samples was estimated using two different estimations (Modification of Diet in Renal Disease or MDRD, and the Chronic Kidney Disease Epidemiology Collaboration or CKD-EPI) to outline the eGFR (estimated glomerular filtration rate) distribution within each patient group (FIG. **1**). Protein analytes were quantified in human plasma and urine using multiplexed immunoassays in the Luminex xMAP™ platform. The microsphere-based multiplex immunoassays consist of antigen-specific antibodies and optimized reagents in a capture-sandwich format. Output data was given as g/ml calculated from internal standard curves. Because urine creatinine (uCr) correlates with renal filtration rate, data analysis was performed without correction for uCr. Univariate and multivariate data analysis was performed comparing all case vs. control samples as well as cases vs. control samples for the various disease groups.

[0135] The majority of the measured proteins showed a correlation to eGFR. Measured variables were correlated to eGFR using Pearson's correlations coefficient, and samples from healthy controls and all disease groups were included in the analysis. 11 and 7 proteins displayed P-values below 0.05 for plasma and urine (Table 9) respectively.

TABLE 9

Correlation analysis of eGFR and variables for all case samples

URINE			PLASMA		
Variable	Pearson's r	P-Value	Variable	Pearson's r	P-Value
Alpha-1-Microglobulin	−0.08	0.3	Alpha-1-Microglobulin	−0.33	***<0.0001***
Beta-2-Microglobulin	−0.23	*0.003*	Beta-2-Microglobulin	−0.39	***<0.0001***
Calbindin	−0.16	0.04	Calbindin	−0.18	**<0.02**
Clusterin	−0.07	**0.4**	Clusterin	−0.51	***<0.0001***
CTGF	−0.08	0.3	CTGF	−0.05	0.5
Creatinine	−0.32	***<0.0001***	Cystatin-C	−0.42	<0.0001
Cystatin-C	−0.24	*0.002*	GST-alpha	−0.12	0.1
GST-alpha	−0.11	0.2	KIM-1	−0.17	**0.03**
KIM-1	−0.08	0.3	NGAL	−0.28	*<0.001*
Microalbumin_UR	−0.17	**0.03**	Osteopontin	−0.33	***<0.0001***
NGAL	−0.15	0.07	THP	−0.31	***<0.0001***
Osteopontin	−0.19	**0.02**	TIMP-1	−0.28	*<0.001*
THP	−0.05	0.6	TFF3	−0.38	***<0.0001***
TIMP-1	−0.19	**0.01**	VEGF	−0.14	0.08
TFF2	−0.09	0.3			
VEGF	−0.07	0.4			

P values <0.0001 are shown in bold italics
P values <0.005 are shown in bold
P values <0.05 are shown in italics

[0136] For the various disease groups, univariate statistical analysis revealed that in a direct comparison (T-test) between cases and controls, a number of proteins were differentially expressed in both urine and plasma (Table 10 and FIG. **2**). In particular, clusterin showed a marked differential pattern in plasma.

TABLE 10

Differentially regulated proteins by univariate statistical analysis

Group	Matrix	Protein	p-value
AA	Urine	Calbindin	0.016
AA	Urine	NGAL	0.04
AA	Urine	Osteopontin	0.005
AA	Urine	Creatinine	0.001
AA	Plasma	Calbindin	0.05
AA	Plasma	Clusterin	0.003
AA	Plasma	KIM-1	0.03
AA	Plasma	THP	0.001
AA	Plasma	TIMP-1	0.02
DN	Urine	Creatinine	0.04
DN	Plasma	Clusterin	0.006
DN	Plasma	KIM-1	0.01
GN	Urine	Creatinine	0.004
GN	Urine	Microalbumin	0.0003
GN	Urine	NGAL	0.05
GN	Urine	Osteopontin	0.05
GN	Urine	TFF3	0.03
GN	Plasma	Alpha 1 Microglobulin	0.002
GN	Plasma	Beta 2 Microglobulin	0.03
GN	Plasma	Clusterin	0.00
GN	Plasma	Cystatin C	0.01
GN	Plasma	KIM-1	0.003
GN	Plasma	NGAL	0.03
GN	Plasma	THP	0.001
GN	Plasma	TIMP-1	0.003
GN	Plasma	TFF3	0.01
GN	Plasma	VEGF	0.02
OU	Urine	Clusterin	0.02

TABLE 10-continued

Differentially regulated proteins by univariate statistical analysis

Group	Matrix	Protein	p-value
OU	Urine	Microalbumin	0.007
OU	Plasma	Clusterin	0.00

[0137] Application of multivariate analysis yielded statistical models that predicted disease from control samples (plasma results are shown in FIG. **3**)

[0138] In conclusion, these results form a valuable base for further studies on these biomarkers in urine and plasma both regarding baseline levels in normal populations and regarding the differential expression of the analytes in various disease groups. Using this panel of analytes, error rates from ada-boosting and/or random forest were low enough (<10%) to allow a prediction model to differentiate between control and disease patient samples. Several of the analytes showed a greater correlation to eGFR in plasma than in urine.

Example 9

Statistical Analysis of Kidney Biomarkers in Plasma and Urine from Patients with Renal Injury

[0139] Urine and plasma samples were taken from 80 normal control group subjects and 20 subjects from each of four disorders: analgesic abuse, diabetic nephropathy, glomerulonephritis, and obstructive uropathy. The samples were analyzed for the quantity and presence of 16 different proteins (alpha-1 microglobulin (α1M), beta-2 microglobulin (β2M), calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF) as described in Example 1 above. The goal was to determine the analytes that distinguish

between a normal sample and a diseased sample, a normal sample and a diabetic nephropathy (DN) sample, and finally, an diabetic nephropathy sample from the other disease samples (obstructive uropathy (DN), analgesic abuse (AA), and glomerulonephritis (GN)).

[0140] From the above protein analysis data, bootstrap analysis was used to estimate the future performance of several classification algorithms. For each bootstrap run, training data and testing data was randomly generated. Then, the following algorithms were applied on the training data to generate models and then apply the models to the testing data to make predictions: automated Matthew's classification algorithm, classification and regression tree (CART), conditional inference tree, bagging, random forest, boosting, logistic regression, SVM, and Lasso. The accuracy rate and ROC areas were recorded for each method on the prediction of the testing data. The above was repeated 100 times. The mean and the standard deviation of the accuracy rates and of the ROC areas were calculated.

[0141] The mean error rates and AUROC were calculated from urine and AUROC was calculated from plasma for 100 runs of the above method for each of the following comparisons: disease (AA+GN+OU+DN) vs. normal (FIG. **4**, Table 11), DN vs. normal (FIG. **6**, Table 13), DN vs. AA (FIG. **8**, Table 15), OU vs. DN (FIG. **10**, Table 17), and GN vs. DN (FIG. **12**, Table 19).

[0142] The average relative importance of 16 different analytes (alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF) and 4 different clinical variables (weight, BMI, age, and gender) from 100 runs were analyzed with two different statistical methods—random forest (plasma and urine samples) and boosting (urine samples)—for each of the following comparisons: disease (AA+GN+OU+DN) vs. normal (FIG. **5**, Table 12), DN vs. normal (FIG. **7**, Table 14), DN vs. AA (FIG. **9**, Table 16), OU vs. DN (FIG. **11**, Table 18), and GN vs. DN (FIG. **13**, Table 20).

TABLE 11

Disease v. Normal

method	Mean AUROC	Standard deviation AUROC
random forest	0.931	0.039
bagging	0.919	0.045
svm	0.915	0.032
boosting	0.911	0.06
lasso	0.897	0.044
logistic regression	0.891	0.041
ctree	0.847	0.046
cart	0.842	0.032
matt	0.83	0.023

TABLE 12

Disease v. Normal

analyte	relative importance
Creatinine	11.606
Kidney_Injury_M	8.486
Tamm_Horsfall_P	8.191

TABLE 12-continued

Disease v. Normal

analyte	relative importance
Total_Protein	6.928
Osteopontin	6.798
Neutrophil_Gela	6.784
Tissue_Inhibito	6.765
Vascular_Endoth	6.716
Trefoil_Factor_	6.703
Cystatin_C	6.482
Alpha_1_Microgl	6.418
Beta_2_Microglo	6.228
Glutathione_S_T	6.053
clusterin	5.842

TABLE 13

DN v. NL

method	Mean AUROC	Standard deviation AUROC
svm	0.672	0.102
logistic regression	0.668	0.114
random forest	0.668	0.1
boosting	0.661	0.107
lasso	0.66	0.117
bagging	0.654	0.103
matt	0.642	0.087
cart	0.606	0.088
ctree	0.569	0.091

TABLE 14

DN v. NL

analyte	Relative importance
Kidney_Injury_M	8.713
Tamm_Horsfall_P	8.448
Beta_2_Microglo	8.037
Trefoil_Factor_	7.685
clusterin	7.394
Vascular_Endoth	7.298
Alpha_1_Microgl	6.987
Glutathione_S_T	6.959
Cystatin_C	6.920
Tissue_Inhibito	6.511
Creatinine	6.344
Neutrophil_Gela	6.305
Osteopontin	6.265
Total_Protein	6.133

TABLE 15

DN v. AA

method	Mean AUROC	Standard deviation AUROC
lasso	0.999	0.008
random forest	0.989	0.021
svm	0.988	0.039
boosting	0.988	0.022
bagging	0.972	0.036
logistic regression	0.969	0.057
cart	0.93	0.055
ctree	0.929	0.063
matt	0.862	0.12

TABLE 16

DN v. AA

analyte	Relative importance
Creatinine	17.57
Total_Protein	10.90
Tissue_Inhibito	8.77
clusterin	6.89
Glutathione_S_T	6.24
Alpha_1_Microgl	6.15
Beta_2_Microglo	6.06
Cystatin_C	5.99
Trefoil_Factor_	5.88
Kidney_Injury_M	5.49
Vascular_Endoth	5.38
Tamm_Horsfall_P	5.33
Osteopontin	4.86
Neutrophil_Gela	4.47

TABLE 17

OU v. DN

method	mean_AUROC	std_AUROC
lasso	0.993	0.019
random forest	0.986	0.027
boosting	0.986	0.027
bagging	0.977	0.04
cart	0.962	0.045
ctree	0.954	0.05
svm	0.95	0.059
logistic regression	0.868	0.122
matt	0.862	0.111

TABLE 18

OU v. DN

analyte	Relative importance
Creatinine	18.278
Alpha_1_Microgl	9.808
clusterin	9.002
Beta_2_Microglo	8.140

TABLE 18-continued

OU v. DN

analyte	Relative importance
Cystatin_C	7.101
Osteopontin	6.775
Glutathione_S_T	5.731
Neutrophil_Gela	5.720
Trefoil_Factor_	5.290
Kidney_Injury_M	5.031
Total_Protein	5.030
Vascular_Endoth	4.868
Tissue_Inhibito	4.615
Tamm_Horsfall_P	4.611

TABLE 19

GN v. DN

method	Mean AUROC	Standard deviation of AUROC
lasso	0.955	0.077
random forest	0.912	0.076
bagging	0.906	0.087
boosting	0.904	0.087
svm	0.887	0.089
ctree	0.824	0.095
matt	0.793	0.114
logistic regression	0.788	0.134
cart	0.768	0.1

TABLE 20

GN v. DN

analyte	Relative importance
Total_Protein	13.122
Creatinine	11.028
Alpha_1_Microgl	8.291
Beta_2_Microglo	7.856
Tissue_Inhibito	7.799
Glutathione_S_T	6.532
Kidney_Injury_M	6.489
Osteopontin	6.424
Vascular_Endoth	6.262
Neutrophil_Gela	5.418
Trefoil_Factor_	5.382
Cystatin_C	5.339
Tamm_Horsfall_P	5.117
clusterin	4.940

Example 10

Diabetic Kidney Disease Urine Analyte Analyses

[0143] Collaborators from Texas Diabetes and Endocrinology (H1) provided urine samples for 150 patients with diabetes, of which 75 patients had kidney disease and 75 did not. The samples were analyzed using the sixteen analytes detailed in section I above. The goals of the analyses were as follows: 1) Determine if there are analytes (alone or in com-

bination) that can separate patients with kidney disease from patients without kidney disease (controls); 2) Determine the relationships of analytes and kidney disease category to years since diagnosis, age, gender, and BMI.

[0144] Values of <LOW> were replaced by half of the minimum value for each variable. Variables with more than 50% missing values were not analyzed. Values given as '>nnn' were taken as the "nnn" value following the ">" sign.

[0145] Analyte values were normalized to the urine creatinine value in the panel for each patient. Normalized value=100*the original analyte value divided by the creatinine value.

[0146] The distribution of values for most analytes was skewed, so the original values were log transformed. Analyses were performed using both the original values and the log transformed values.

[0147] In the graphs and statistical output, patients without kidney disease are labeled "NC" (normal control). Patients with kidney disease are labeled "KD" (kidney disease).

[0148] Graphs of the analyte values versus disease category (NC vs. KD) on original scale and log scale are shown in FIG. **22** and FIG. **23**. Normal distribution qqplots are shown in FIG. **20** and FIG. **21**. Scatterplots of each analyte versus the 24-hour microalbumin (from the clinical data) are shown FIG. **16** and FIG. **17**. A graph of the kidney disease category versus years since diagnosis and of analyte values versus years since diagnosis are in FIG. **14**, FIG. **15**, and FIG. **24**. In these graphs, red are patients with kidney disease, black are controls. It is evident that the presence of kidney disease is a function of years since diagnosis. Thus, models to predict kidney disease may perform better if the number of years since diagnosis is included as a covariate.

[0149] We performed t-tests of the values of each analyte versus disease category (NC vs. KD). Linear models of analyte versus disease category and covariates gave similar results.

TABLE 21

T-test p-values for each analyte versus disease category (NC vs. KD) using log scale.

Analytes	t-test p-value
Microalbumin	2.68E−21
Alpha.1.Microglobulin	1.29E−05
Neutrophil.Gelatinase.Associated.Lipocalin..NGAL.	0.004
Kidney.Injury.Molecule.1..KIM.1.	0.024
Clusterin	0.037
Tamm.Horsfall.Protein..THP.	0.041
Connective.Tissue.Growth.Factor..CTGF.	0.044
Tissue.Inhibitor.of.Metalloproteinase.1..TIMP.1.	0.180
Beta.2.Microglobulin	0.334
Cystatin.C	0.348
Osteopontin	0.352
Vascular.Endothelial.Growth.Factor..VEGF.	0.426
Creatinine	0.567
Calbindin	0.707
Glutathione.S.Transferase.alpha..GST.alpha.	0.863
Trefoil.Factor.3..TFF3.	0.878

TABLE 22

T-test p-values for each analyte versus disease category (NC vs. KD) using original scale.

Analytes	t-test p-value
Microalbumin	1.11E−08
Alpha.1.Microglobulin	0.0007
Kidney.Injury.Molecule.1..KIM.1.	0.0072
Neutrophil.Gelatinase.Associated.Lipocalin..NGAL.	0.0190
Osteopontin	0.1191
Glutathione.S.Transferase.alpha..GST.alpha.	0.1250
Beta.2.Microglobulin	0.1331
Tamm.Horsfall.Protein..THP.	0.1461
Cystatin.C	0.1489
Connective.Tissue.Growth.Factor..CTGF.	0.2746
Vascular.Endothelial.Growth.Factor..VEGF.	0.3114
Calbindin	0.6189
Tissue.Inhibitor.of.Metalloproteinase.1..TIMP.1.	0.6944
Clusterin	0.7901
Trefoil.Factor.3..TFF3.	0.7918
Creatinine	0.9710

[0150] We calculated the area under the ROC curve (AUROC) for classification of disease (NC vs. KD) for the following analytes and covariates: AUROC for each analyte individually (Table 23) and AUROC for individual analytes in logistic regression models that included the covariates year diagnosed, age, gender, and BMI (Table 24).

TABLE 23

AUROC for each analyte individually for classification of disease (NC vs. KD) using log scale

Analytes	AUROC
Microalbumin	0.90
Alpha.1.Microglobulin	0.71
Kidney.Injury.Molecule.1..KIM.1.	0.63
Neutrophil.Gelatinase.Associated.Lipocalin..NGAL.	0.62
Clusterin	0.61
Tamm.Horsfall.Protein..THP.	0.60
Connective.Tissue.Growth.Factor..CTGF.	0.60
Tissue.Inhibitor.of.Metalloproteinase.1..TIMP.1.	0.58
Cystatin.C	0.56
Osteopontin	0.56
Beta.2.Microglobulin	0.56
Vascular.Endothelial.Growth.Factor..VEGF.	0.55
Creatinine	0.52
Calbindin	0.51
Trefoil.Factor.3..TFF3.	0.51
Glutathione.S.Transferase.alpha..GST.alpha.	0.50

TABLE 24

AUROC for individual analytes in logistic regression models that included the covariates year since diagnosis, age, gender, and BMI.

Analytes	AUROC
Microalbumin	0.90
Alpha.1.Microglobulin	0.74
Connective.Tissue.Growth.Factor..CTGF.	0.71
Neutrophil.Gelatinase.Associated.Lipocalin..NGAL.	0.69
Kidney.Injury.Molecule.1..KIM.1.	0.69
Tamm.Horsfall.Protein..THP.	0.69
Creatinine	0.69
Tissue.Inhibitor.of.Metalloproteinase.1..TIMP.1.	0.68
Clusterin	0.68

TABLE 24-continued

AUROC for individual analytes in logistic regression models that included the covariates year since diagnosis, age, gender, and BMI.

Analytes	AUROC
Glutathione.S.Transferase.alpha..GST.alpha.	0.68
Osteopontin	0.68
Calbindin	0.68
Trefoil.Factor.3..TFF3.	0.68
Cystatin.C	0.67
Vascular.Endothelial.Growth.Factor..VEGF.	0.67
Beta.2.Microglobulin	0.67

[0151] We calculated the area under the ROC curve (AUROC) for classification of disease (NC vs. KD) for the following combinations of analytes and covariates. For the combination of all analytes in a logistic regression model (without covariates), the AUROC=0.94. For the combination of all analytes in a logistic regression model (including covariates), the AUROC=0.95. For the combination of all analytes, excluding microalbumin, in a logistic regression model (without covariates), the AUROC=0.85. For the combination of all analytes, excluding microalbumin, in a logistic regression model (including covariates), the AUROC=0.87. Finally, we calculated the area under the ROC curve (AUROC) for classification of disease (NC vs. KD) for 24-hour clinical microalbumin from the patient record, which gave AUROC=0.97.

Example 11

Diabetic Kidney Disease Serum Analyte Analyses

[0152] This report presents the statistical analysis of the serum data for the patients detailed in Example 10 above. The samples were analyzed using fourteen of the analytes detailed in section I above. The goals of the analyses were as follows: 1) Determine if there are analytes (alone or in combination) that can separate patients with kidney disease from patients without kidney disease (controls); 2) Determine the relationships of analytes and kidney disease category to years since diagnosis, age, gender, and BMI.

[0153] Values of <LOW> were replaced by half of the minimum value for each variable. Variables with more than 50% missing values were not analyzed. The only such analyte in this data set was Calbindin. Values given as '>nnn' were taken as the "nnn" value following the ">" sign.

[0154] The distribution of values for most analytes was skewed, so we log transformed the original values. We performed analyses using both the original values and the log transformed values.

[0155] In the graphs and statistical output, patients without kidney disease are labeled "NC" (normal control). Patients with kidney disease are labeled "KD" (kidney disease).

[0156] Graphs of the analyte values versus disease category (NC vs. KD) on original scale and log scale are shown in FIG. **25** and FIG. **26**. Normal distribution qqplots are shown in FIG. **27** and FIG. **28**. Scatterplots of each analyte versus the 24-hour microalbumin (from the clinical data) are shown in FIG. **31** and FIG. **32**. Graphs of analyte values versus years since diagnosis are shown in FIG. **29** and FIG. **30**. In these graphs, red are patients with kidney disease, black are controls. It is evident that analyte values and the presence of kidney disease is a function of years since diagnosis. Thus, models to predict kidney disease may perform better if the number of years since diagnosis is included as a covariate.

[0157] We performed t-tests of the values of each analyte versus disease category (NC vs. KD). Linear models of analyte versus disease category and covariates gave similar results.

TABLE 25

T-test p-values for each analyte versus disease category (NC vs. KD) using log scale.

Analytes	t-test p-value
Alpha.1.Microglobulin..A1Micro.	8.03E−08
Cystatin.C	4.51E−06
Tamm.Horsfall.Urinary.Glycoprotein..THP.	5.35E−06
Beta.2.Microglobulin..B2M.	3.88E−05
Tissue.Inhibitor.of.Metalloproteinases.1..TIMP.1.	4.20E−05
Kidney.Injury.Molecule.1...KIM.1.	0.00343048
Trefoil.Factor.3..TFF3.	0.05044019
Connective.Tissue.Growth.Factor..CTGF.	0.06501133
Glutathione.S.Transferase.alpha..GST.alpha.	0.27177709
Osteopontin	0.2762483
Vascular.Endothelial.Growth.Factor..VEGF.	0.33297341
Neutrophil.Gelatinase.Associated.Lipocalin..NGAL.	0.5043943
Clusterin..CLU.	0.5730406

TABLE 26

T-test p-values for each analyte versus disease category (NC vs. KD) using original scale.

Analytes	t-test p-value
Alpha.1.Microglobulin..A1Micro.	4.29E−07
Cystatin.C	5.52E−06
Tamm.Horsfall.Urinary.Glycoprotein..THP.	3.19E−05
Beta.2.Microglobulin..B2M.	4.56E−05
Tissue.Inhibitor.of.Metalloproteinases.1..TIMP.1.	5.02E−05
Kidney.Injury.Molecule.1...KIM.1.	0.000343
Vascular.Endothelial.Growth.Factor..VEGF.	0.044555
Glutathione.S.Transferase.alpha..GST.alpha.	0.052145
Osteopontin	0.146316
Neutrophil.Gelatinase.Associated.Lipocalin..NGAL.	0.21544
Trefoil.Factor.3..TFF3.	0.300221
Clusterin..CLU.	0.756401
Connective.Tissue.Growth.Factor..CTGF.	0.985909

[0158] We calculated the area under the ROC curve (AUROC) for classification of disease (NC vs. KD) for the following analytes and covariates using log scale. AUROC for each analyte individually (Table 27) and AUROC for individual analytes in logistic regression models that included the covariates year diagnosed, age, gender, and BMI (Table 28).

TABLE 27

AUROC for each analyte individually for classification of disease (NC vs. KD)

Analytes	AUROC
Alpha.1.Microglobulin..A1Micro.	0.743154
Cystatin.C	0.705548
Tissue.Inhibitor.of.Metalloproteinases.1..TIMP.1.	0.695857
Beta.2.Microglobulin..B2M.	0.693901
Tamm.Horsfall.Urinary.Glycoprotein..THP.	0.684566
Kidney.Injury.Molecule.1...KIM.1.	0.654783
Trefoil.Factor.3..TFF3.	0.617977

TABLE 27-continued

AUROC for each analyte individually for classification of disease (NC vs. KD)

Analytes	AUROC
Connective.Tissue.Growth.Factor..CTGF.	0.60144
Glutathione.S.Transferase.alpha..GST.alpha.	0.549698
Osteopontin	0.546497
Vascular.Endothelial.Growth.Factor..VEGF.	0.541874
Clusterin..CLU.	0.512002
Neutrophil.Gelatinase.Associated.Lipocalin..NGAL.	0.506312

TABLE 28

AUROC for individual analytes in logistic regression models that included the covariates year since diagnosis, age, gender, and BMI.

Analytes	AUROC
Alpha.1.Microglobulin..A1Micro.	0.760846
Cystatin.C	0.731863
Tissue.Inhibitor.of.Metalloproteinases.1..TIMP.1.	0.728841
Tamm.Horsfall.Urinary.Glycoprotein..THP.	0.725818
Beta.2.Microglobulin..B2M.	0.718706
Kidney.Injury.Molecule.1...KIM.1.	0.697724
Trefoil.Factor.3..TFF3.	0.689189
Connective.Tissue.Growth.Factor..CTGF.	0.682877
Glutathione.S.Transferase.alpha..GST.alpha.	0.678165
Clusterin..CLU.	0.676565
Vascular.Endothelial.Growth.Factor..VEGF.	0.674431
Osteopontin	0.673898
Neutrophil.Gelatinase.Associated.Lipocalin..NGAL.	0.672653

[0159] We calculated the area under the ROC curve (AUROC) for classification of disease (NC vs. KD) for the following combinations of analytes and covariates. For the combination of all analytes in a logistic regression model (without covariates), the AUROC=0.85. For the combination of all analytes in a logistic regression model (including covariates), the AUROC=0.86.

[0160] It should be appreciated by those of skill in the art that the techniques disclosed in the examples above represent techniques discovered by the inventors to function well in the practice of the invention. Those of skill in the art should, however, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments that are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention, therefore all matter set forth or shown in the accompanying drawings is to be interpreted as illustrative and not in a limiting sense.

What is claimed is:

1. A method for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal, the method comprising:

a. providing a test sample comprising a sample of bodily fluid taken from the mammal;

b. determining sample concentrations for sample analytes in the test sample, wherein the sample analytes are alpha-1 microglobulin, beta-2 microglobulin, cystatin C, KIM-1, THP and TIMP-1 or microalbumin, alpha-1 microglobulin, NGAL, KIM-1, THP, and clusterin;

c. comparing the combination of sample concentrations to a data set comprising at least one entry, wherein each entry of the data set comprises a list comprising three or more minimum diagnostic concentrations indicative of diabetic nephropathy or an associated disorder, wherein each minimum diagnostic concentration comprises a maximum of a range of analyte concentrations for a healthy mammal;

d. determining a matching entry of the dataset in which all minimum diagnostic concentrations are less than the corresponding sample concentrations; and,

e. identifying an indicated disorder comprising the particular disorder of the matching entry.

2. A method for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal, the method comprising:

a. providing a test sample comprising a sample of bodily fluid taken from the mammal;

b. determining a combination of sample concentrations for three or more sample analytes in the test sample, wherein the sample analytes are selected from the group consisting of alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF;

c. comparing the combination of sample concentrations to a data set comprising at least one entry, wherein each entry of the data set comprises a list comprising three or more minimum diagnostic concentrations indicative of diabetic nephropathy or an associated disorder, wherein each minimum diagnostic concentration comprises a maximum of a range of analyte concentrations for a healthy mammal;

d. determining a matching entry of the dataset in which all minimum diagnostic concentrations are less than the corresponding sample concentrations; and,

e. identifying an indicated disorder comprising the particular disorder of the matching entry.

3. The method of claim **2**, wherein the mammal is selected from the group consisting of humans, apes, monkeys, rats, mice, dogs, cats, pigs, and livestock including cattle and oxen.

4. The method of claim **2**, wherein the bodily fluid is selected from the group consisting of urine, blood, plasma, serum, saliva, semen, and tissue lysates.

5. The method of claim **2**, wherein the minimum diagnostic concentration in human plasma of alpha-1 microglobulin is about 16 μg/ml, beta-2 microglobulin is about 2.2 μg/ml, calbindin is greater than about 5 ng/ml, clusterin is about 134 μg/ml, CTGF is about 16 ng/ml, cystatin C is about 1170 ng/ml, GST-alpha is about 62 ng/ml, KIM-1 is about 0.57 ng/ml, NGAL is about 375 ng/ml, osteopontin is about 25 ng/ml, THP is about 0.052 μg/ml, TIMP-1 is about 131 ng/ml, TFF-3 is about 0.49 μg/ml, and VEGF is about 855 pg/ml.

6. The method of claim **2**, wherein the minimum diagnostic concentration in human sera of alpha-1 microglobulin is about 17 μg/ml, beta-2 microglobulin is about 2.6 μg/ml, calbindin is greater than about 2.6 ng/ml, clusterin is about 152 μg/ml, CTGF is greater than about 8.2 ng/ml, cystatin C is about 1250 ng/ml, GST-alpha is about 52 ng/ml, KIM-1 is greater than about 0.35 ng/ml, NGAL is about 822 ng/ml, osteopontin is about 12 ng/ml, THP is about 0.053 μg/ml, TIMP-1 is about 246 ng/ml, TFF-3 is about 0.17 μg/ml, and VEGF is about 1630 pg/ml.

7. The method of claim **2**, wherein the minimum diagnostic concentration in human urine of alpha-1 microglobulin is about 233 μg/ml, beta-2 microglobulin is greater than about 0.17 μg/ml, calbindin is about 233 ng/ml, clusterin is greater than about 0.089 μg/ml, CTGF is greater than about 0.90 ng/ml, cystatin C is about 1170 ng/ml, GST-alpha is greater

than about 26 ng/ml, KIM-1 is about 0.67 ng/ml, NGAL is about 81 ng/ml, osteopontin is about 6130 ng/ml, THP is about 2.6 μg/ml, TIMP-1 is greater than about 3.9 ng/ml, TFF-3 is greater than about 21 μg/ml, and VEGF is about 517 pg/ml.

8. The method of claim **2**, wherein a combination of sample concentrations for six or more sample analytes in the test sample are determined.

9. The method of claim **8**, wherein sample concentrations are determined for the analytes selected from the group consisting of alpha-1 microglobulin, beta-2 microglobulin, cystatin C, KIM-1, THP, and TIMP-1.

10. The method of claim **2**, wherein a combination of sample concentrations for sixteen sample analytes in the test sample are determined.

11. A method for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal, the method comprising:

a. providing a test sample comprising a sample of bodily fluid taken from the mammal;

b. determining the concentrations of three or more sample analytes in a panel of biomarkers in the test sample, wherein the sample analytes are selected from the group consisting of alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF;

c. identifying diagnostic analytes in the test sample, wherein the diagnostic analytes are the sample analytes whose concentrations are statistically different from concentrations found in a control group of humans who do not suffer from diabetic nephropathy or an associated disorder;

d. comparing the combination of diagnostic analytes to a dataset comprising at least one entry, wherein each entry of the dataset comprises a combination of three or more diagnostic analytes reflective of diabetic nephropathy or an associated disorder; and,

e. identifying the particular disorder having the combination of diagnostic analytes that essentially match the combination of sample analytes.

12. The method of claim **11**, wherein the mammal is selected from the group consisting of humans, apes, monkeys, rats, mice, dogs, cats, pigs, and livestock including cattle and oxen.

13. The method of claim **11**, wherein the bodily fluid is selected from the group consisting of urine, blood, plasma, serum, saliva, semen, and tissue lysates.

14. The method of claim **11**, wherein the test sample is plasma and the diagnostic analytes comprise creatinine, KIM-1 and THP or creatinine, KIM-1, and TIMP-1.

15. The method of claim **11**, wherein the test sample is urine and the diagnostic analytes comprise microalbumin, creatinine, and KIM-1 or microalbumin, cystatin C, and creatinine.

16. A method for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal, the method comprising:

a. providing an analyte concentration measurement device comprising three or more detection antibodies, wherein each detection antibody comprises an antibody coupled to an indicator, wherein the antigenic determinants of the antibodies are sample analytes associated with diabetic nephropathy or an associated disorder, and wherein the sample analytes are selected from the group consisting of alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF;

b. providing a test sample comprising three or more sample analytes and a bodily fluid taken from the mammal;

c. contacting the test sample with the detection antibodies and allowing the detection antibodies to bind to the sample analytes;

d. determining the concentrations of the sample analytes by detecting the indicators of the detection antibodies bound to the sample analytes in the test sample; and,

e. comparing the concentrations of each sample analyte to a corresponding minimum diagnostic concentration reflective of diabetic nephropathy or an associated disorder.

17. The method of claim **16**, wherein the bodily fluid is selected from the group consisting of urine, blood, plasma, serum, saliva, semen, and tissue lysates.

18. The method of claim **16**, wherein the analyte concentration measurement device comprises six or more detection antibodies.

19. The method claim **16**, wherein the analyte concentration measurement device comprises sixteen detection antibodies.

20. The method of claim **16**, wherein the sample analytes are selected from the group consisting of microalbumin, alpha-1 microglobulin, NGAL, KIM-1, THP, and clusterin.

21. The method of claim **16**, wherein the sample analytes are selected from the group consisting of A1M, cystatin C, THP, B2M, TIMP-1, and KIM-1.

22. A method for diagnosing, monitoring, or determining diabetic nephropathy or an associated disorder in a mammal, the method comprising:

a. providing a test sample comprising a sample of bodily fluid taken from the mammal;

b. determining sample concentrations for sample analytes in the test sample, wherein the sample analytes are alpha-1 microglobulin, beta-2 microglobulin, calbindin, clusterin, CTGF, creatinine, cystatin C, GST-alpha, KIM-1, microalbumin, NGAL, osteopontin, THP, TIMP-1, TFF-3, and VEGF;

c. comparing the combination of sample concentrations to a data set comprising at least one entry, wherein each entry of the data set comprises a list comprising three or more minimum diagnostic concentrations indicative of diabetic nephropathy or an associated disorder, wherein each minimum diagnostic concentration comprises a maximum of a range of analyte concentrations for a healthy mammal;

d. determining a matching entry of the dataset in which all minimum diagnostic concentrations are less than the corresponding sample concentrations; and,

e. identifying an indicated disorder comprising the particular disorder of the matching entry.

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