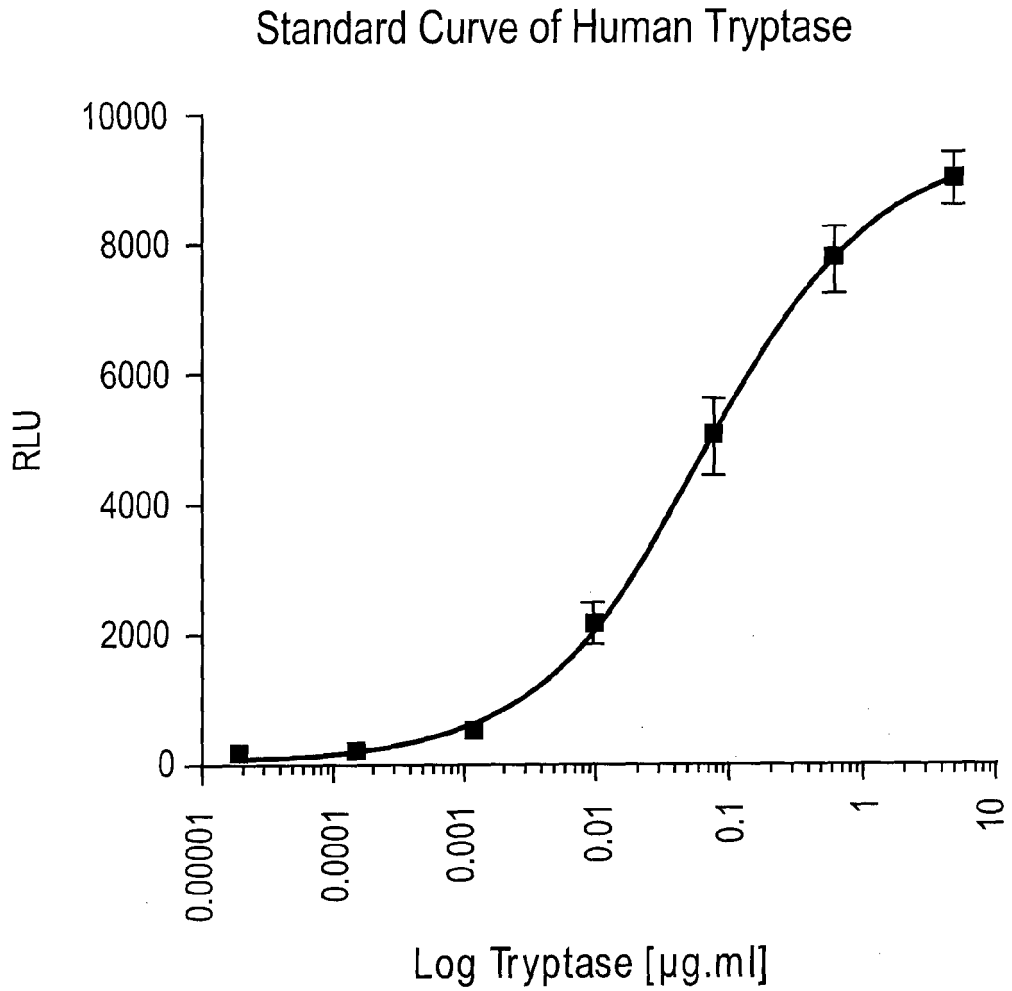

Standard Curve of Human Tryptase
10000
8000
6000
4000
2000
0
RLU
0.00001
0.0001
0.001
0.01
0.1
1
10
Log Tryptase [µg.ml]

FIG. 1

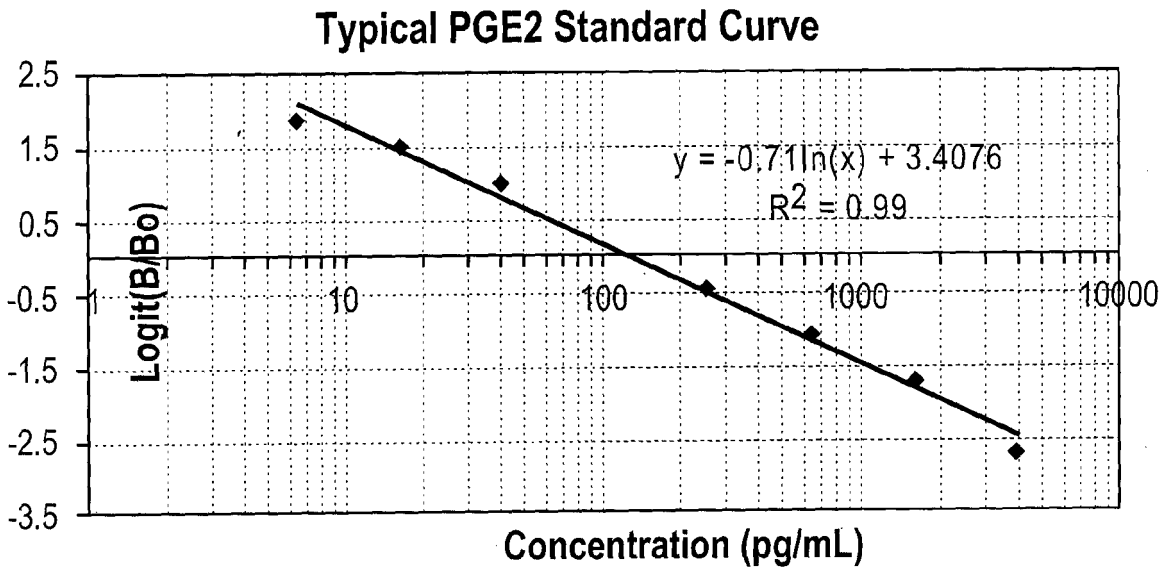

Typical PGE2 Standard Curve
2.5
1.5
0.5
-0.5
-1.5
-2.5
-3.5
Logit(B/Bo)
y = -0.71ln(x) + 3.4076
R2 = 0.99
1
10
100
1000
10000
Concentration (pg/mL)

FIG. 2

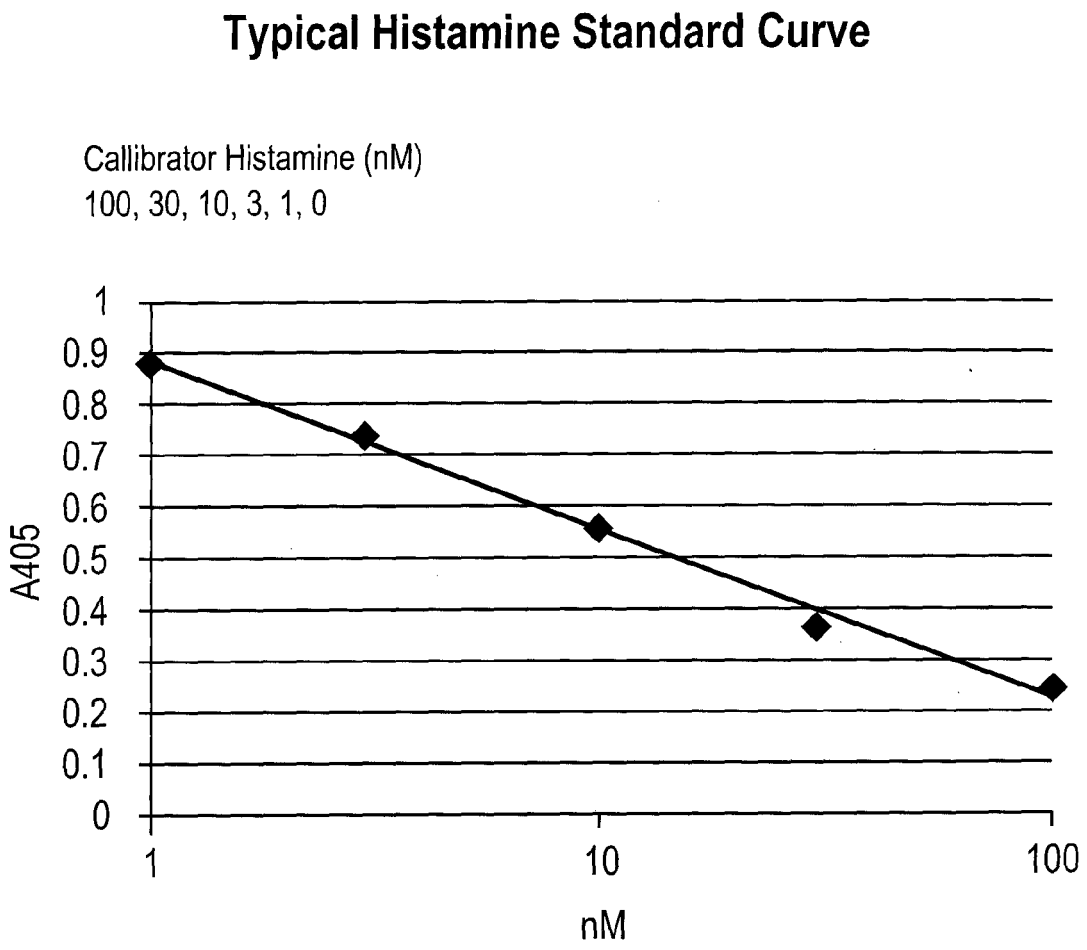
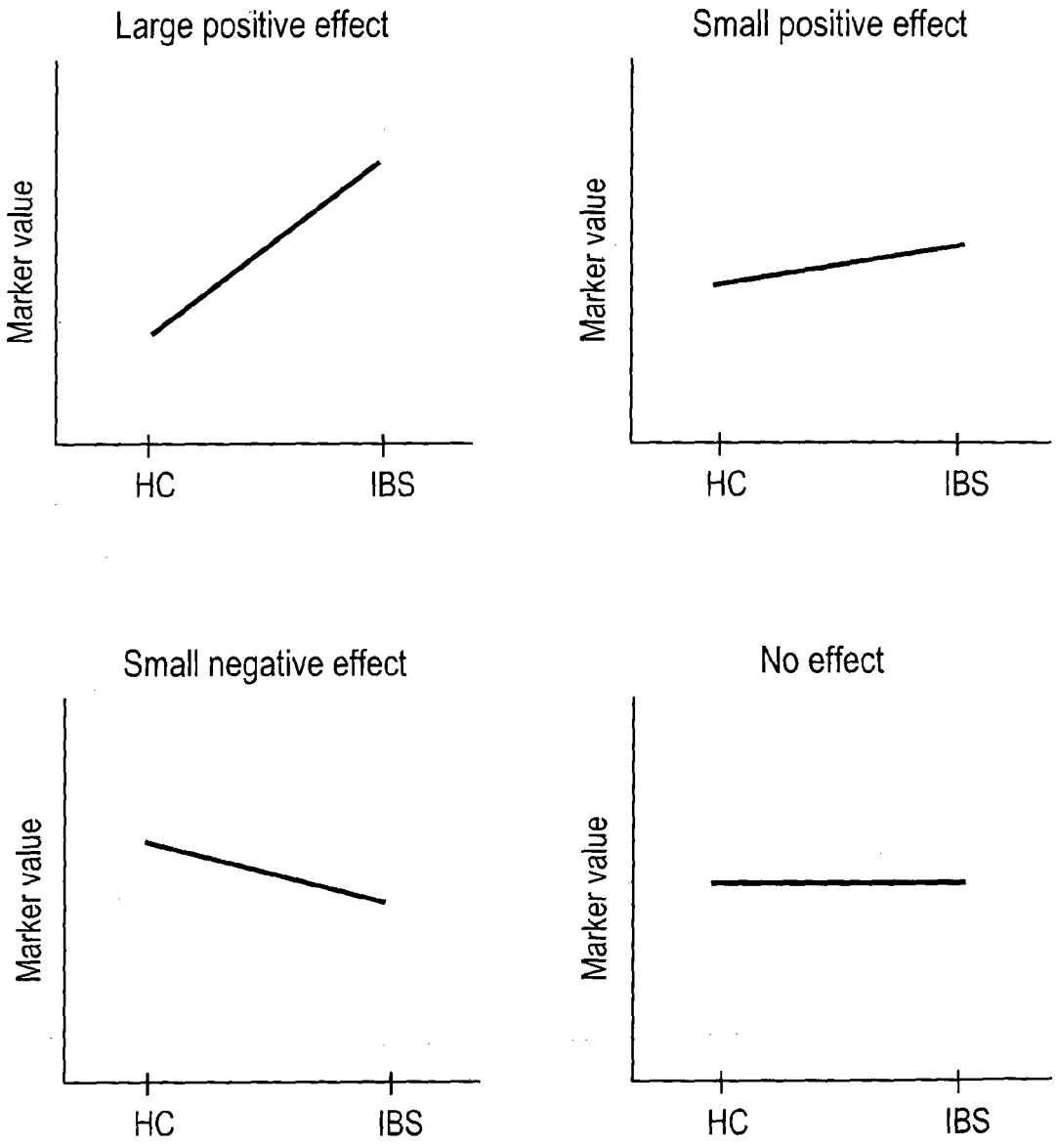

Typical Histamine Standard Curve
Callibrator Histamine (nM)
100, 30, 10, 3, 1, 0
A405
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
1
10
100
nM

FIG. 3



Estimate is the slope of the line.

FIG. 4

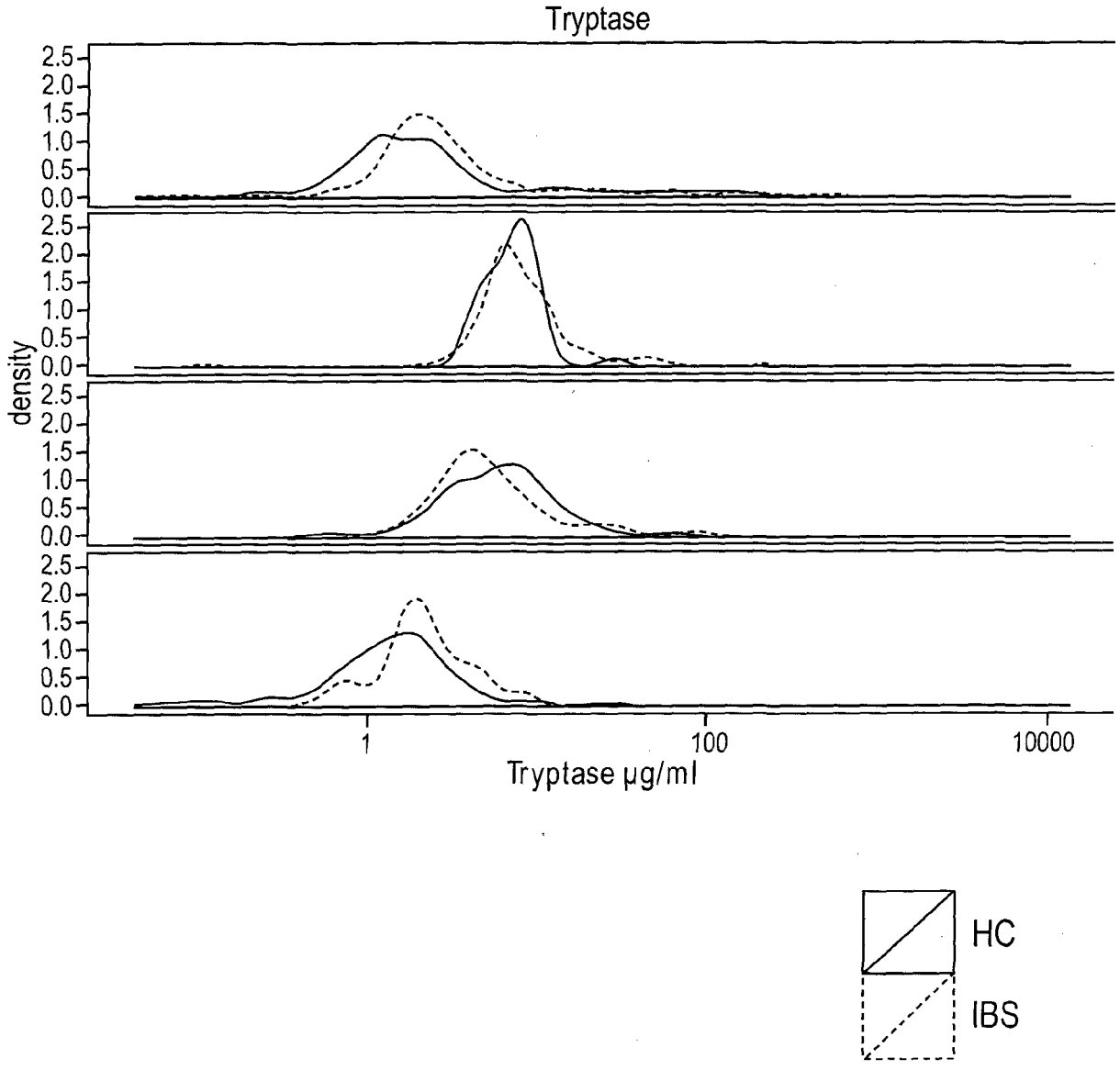

Tryptase
density
2.5
2.0
1.5
1.0
0.5
0.0
1
100
10000
Tryptase µg/ml
HC
IBS

FIG. 5

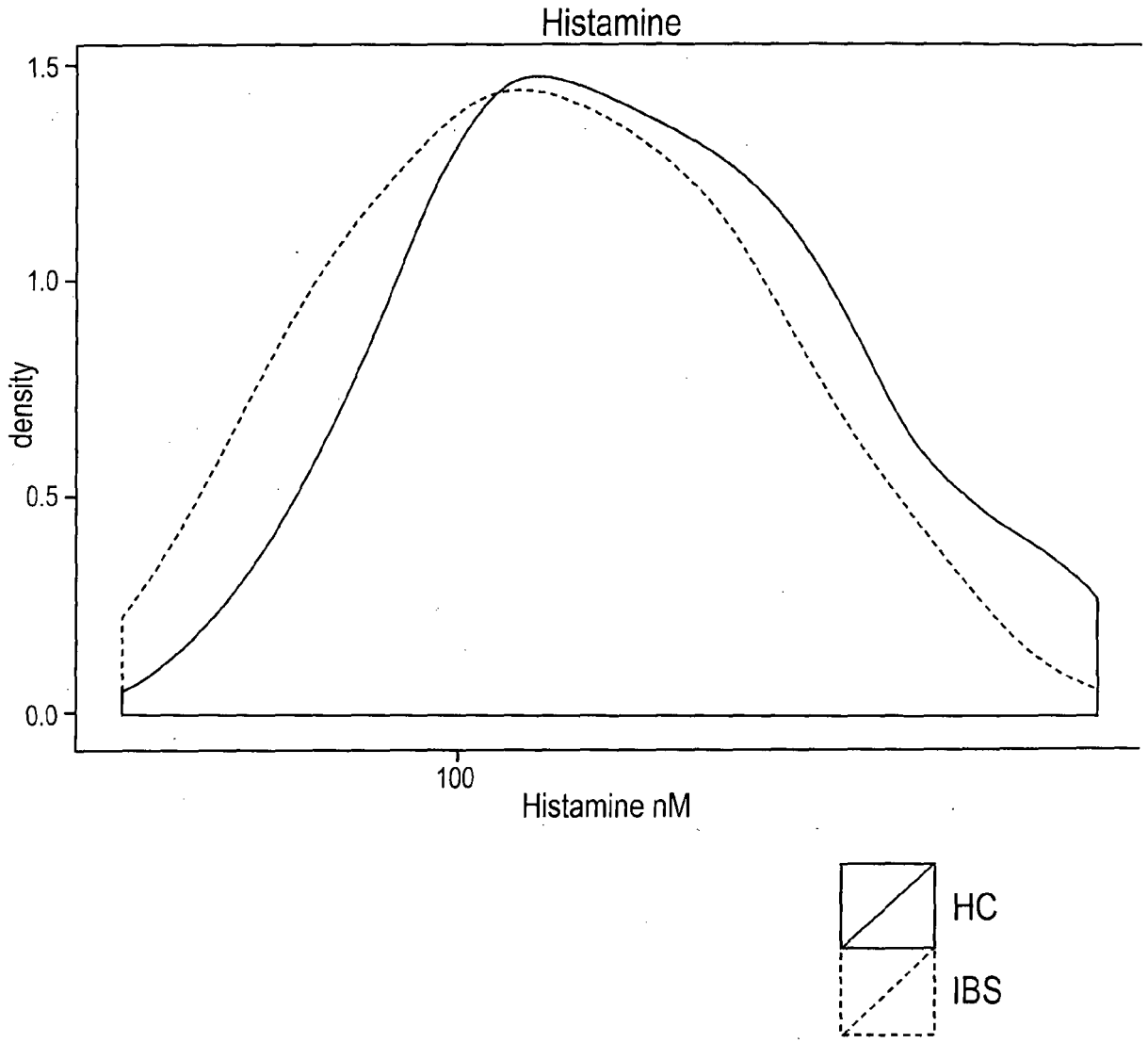


FIG. 6

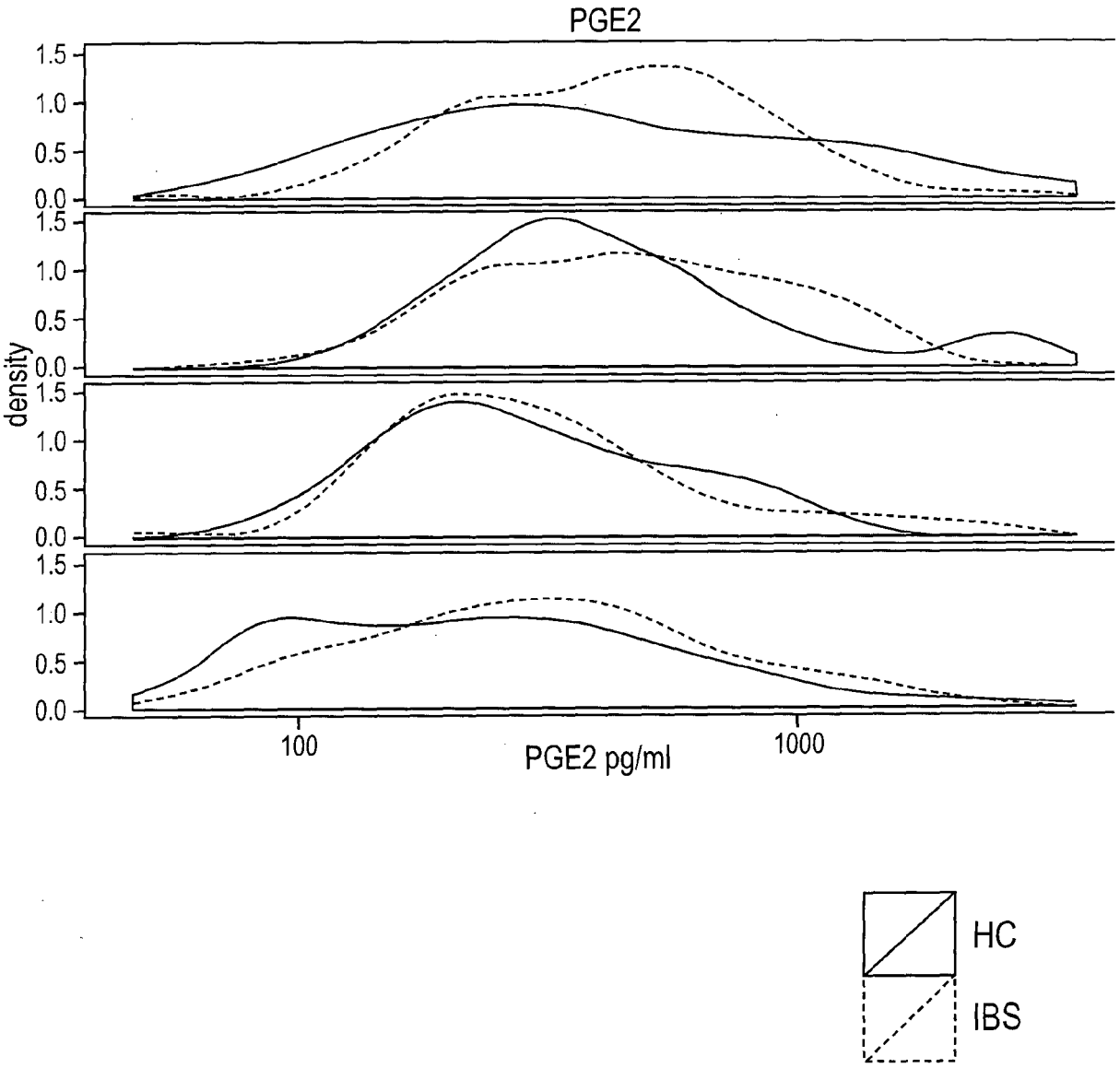


FIG. 7

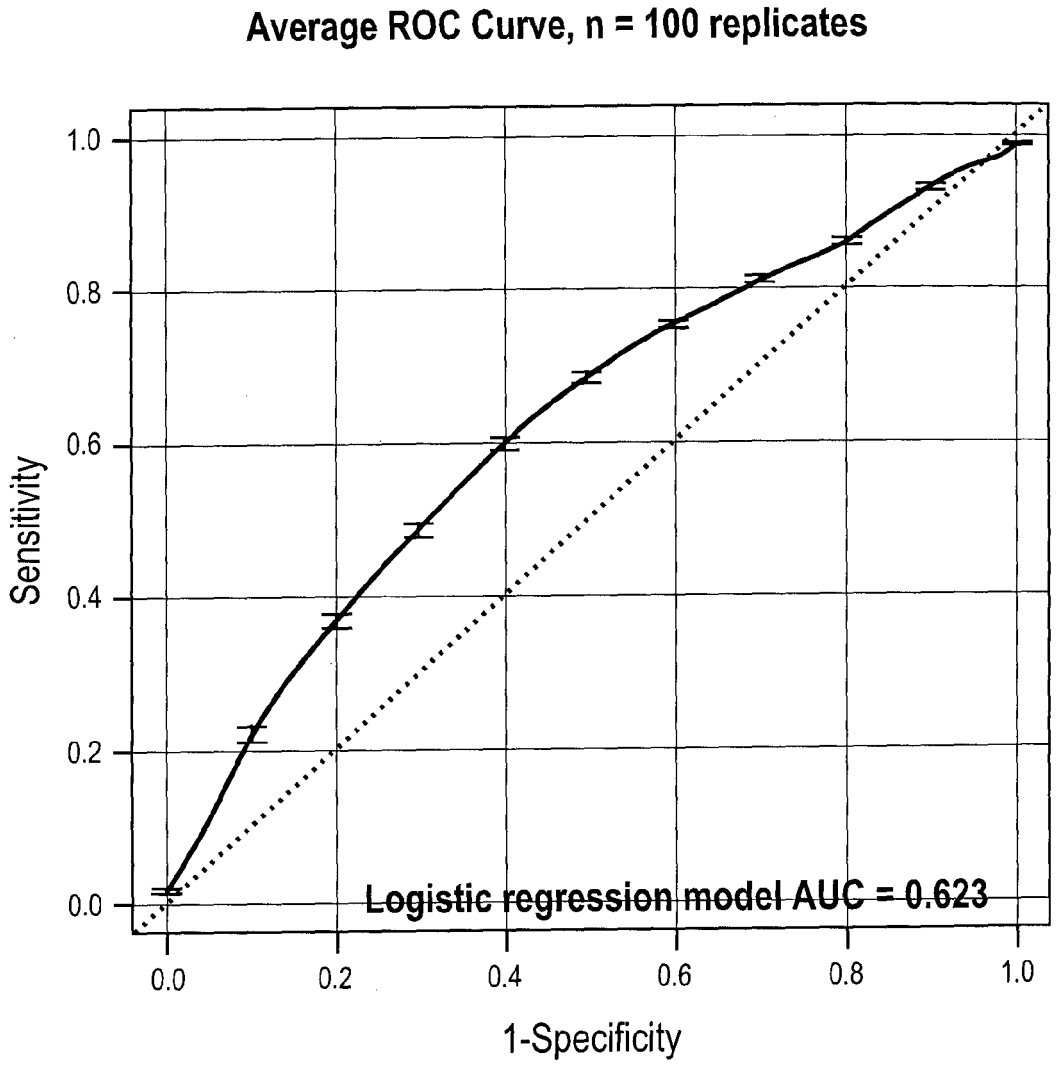

Average ROC Curve, n = 100 replicates
Sensitivity
1-Specificity
0.0
0.2
0.4
0.6
0.8
1.0
Logistic regression model AUC = 0.623

FIG. 8

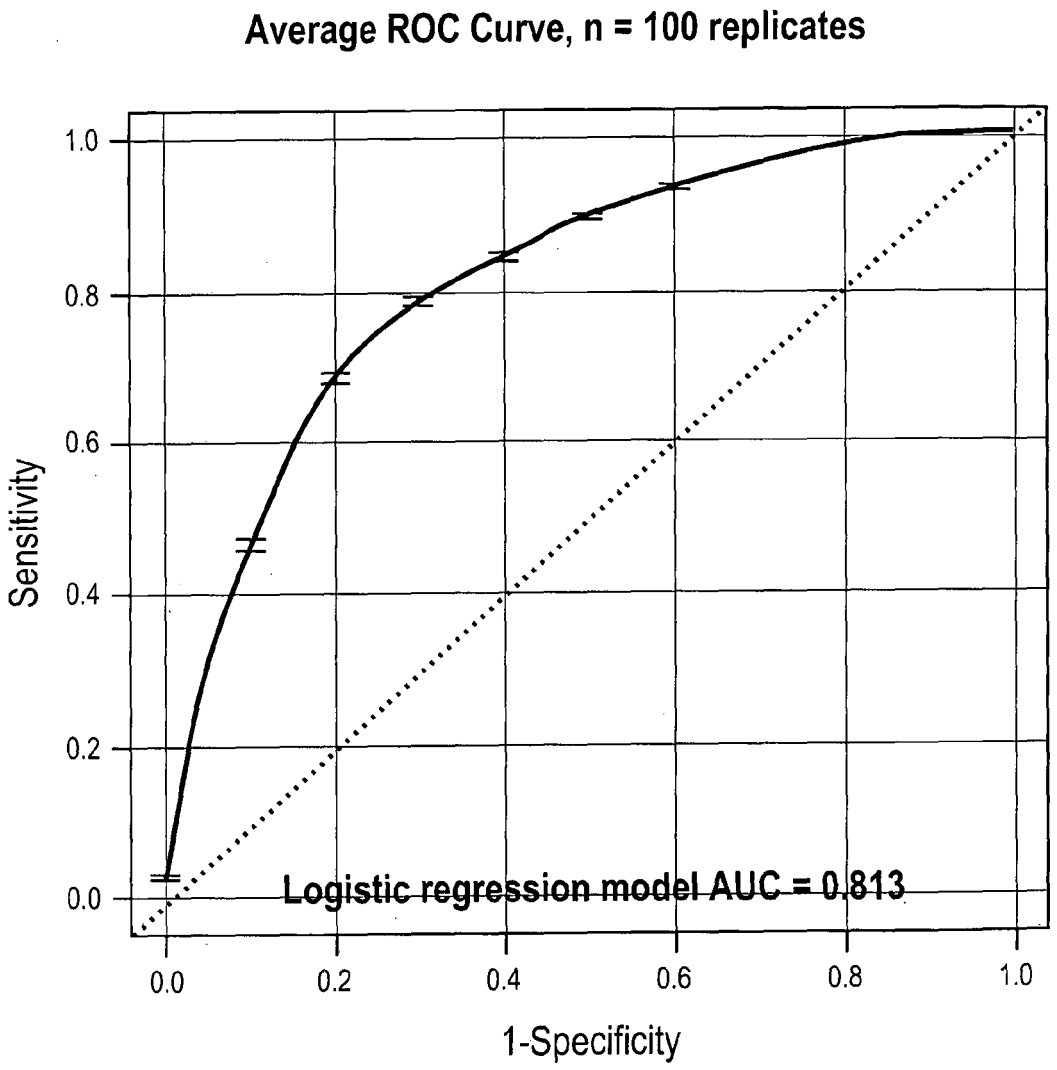

Average ROC Curve, n = 100 replicates
Sensitivity
1.0
0.8
0.6
0.4
0.2
0.0
Logistic regression model AUC = 0.813
0.0
0.2
0.4
0.6
0.8
1.0
1-Specificity

FIG. 9

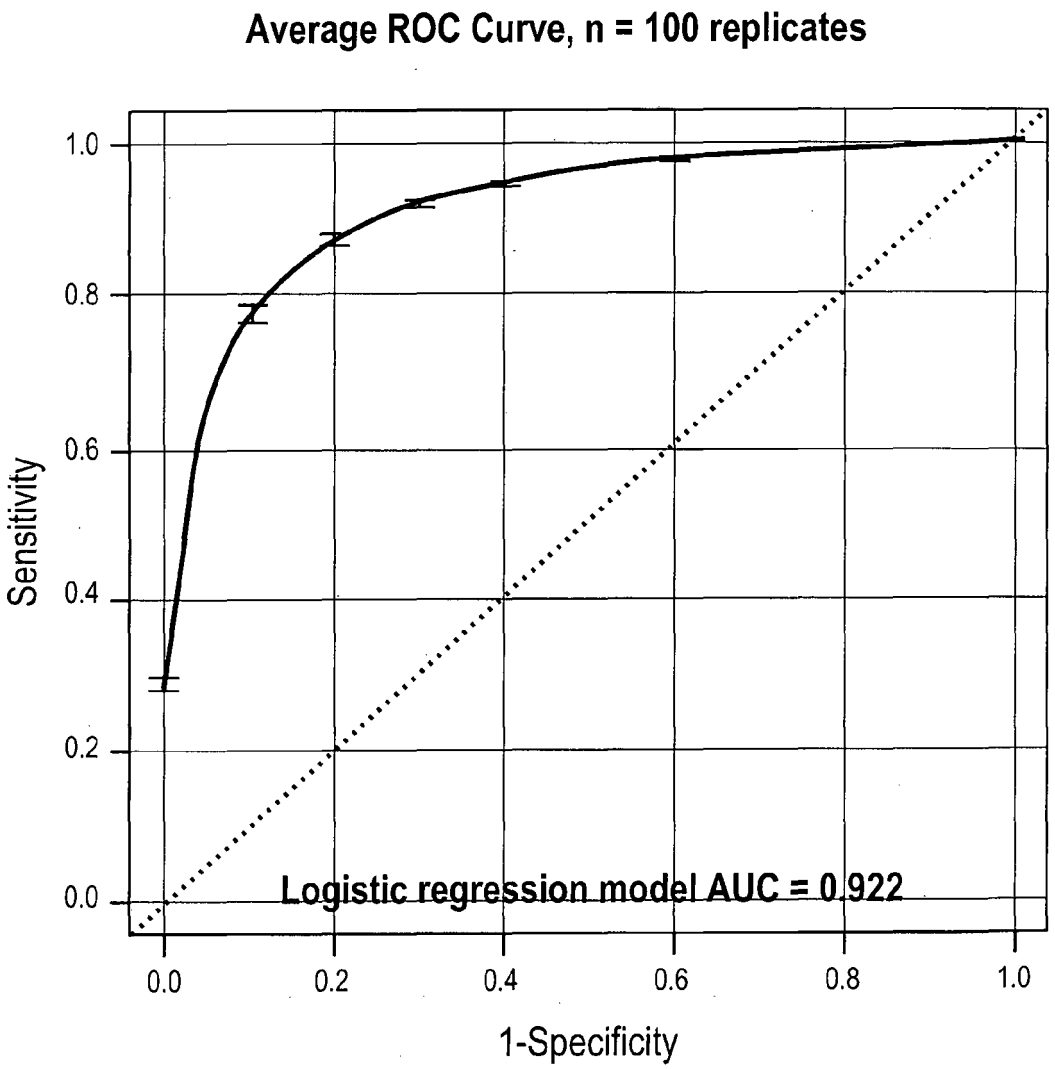

Average ROC Curve, n = 100 replicates
Sensitivity
1.0
0.8
0.6
0.4
0.2
0.0
Logistic regression model AUC = 0.922
0.0
0.2
0.4
0.6
0.8
1.0
1-Specificity

FIG. 10

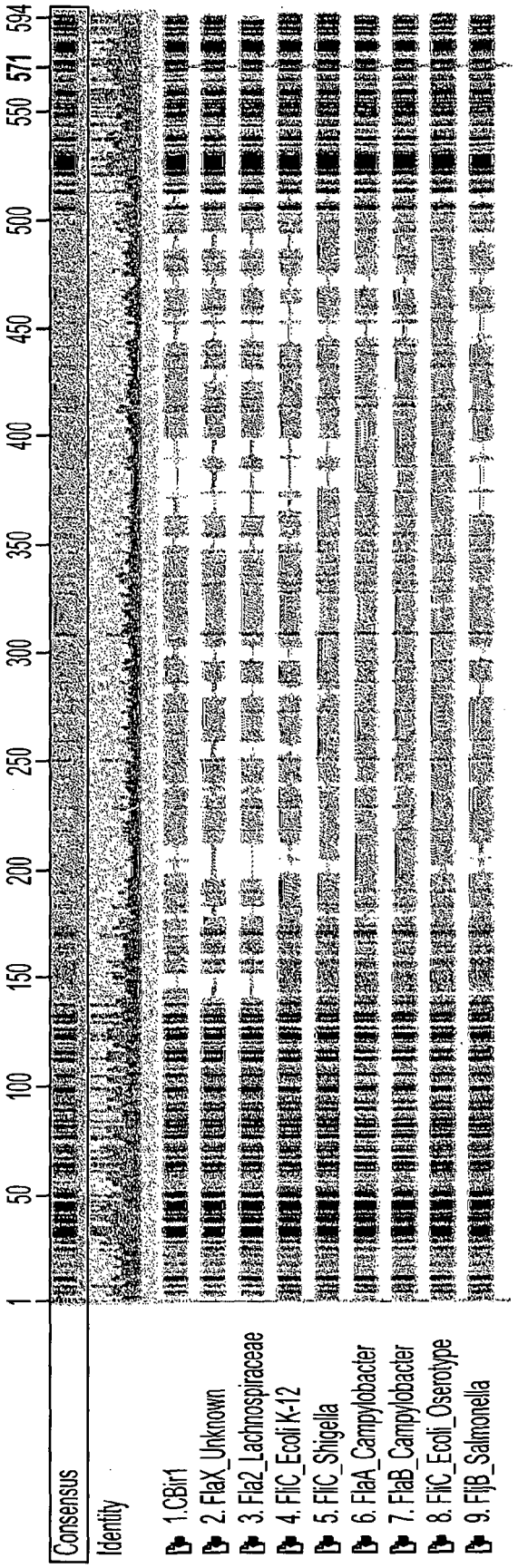

1
50
100
150
200
250
300
350
400
450
500
550
571
594
Consensus
Identity
1.CBir1
2.FlaX_Unknown
3.Fla2_Lachnospiraceae
4.FlC_Ecoli K-12
5.FlC_Shigella
6.FlaA_Campylobacter
7.FlaB_Campylobacter
8.FlC_Ecoli_Oserotype
9.FljB_Salmonella

FIG. 11

N-terminal

```
1                                                                   100
Consensus                    MAQVINTNSLALNTQNNLNKNQSSLSKSIERLSSGLRINSAADDAAGQAIANRFRSQIKGLTQASRNANDGISIAQTAEGALTEINNNLQRIRELAVQAA
Lachnospiraceae bacterium A4 clone  ..MVVQHNLRAMNSNRMLGITQGSLNKSTEKLSSGYKVNRAADDAAGLSISEKMRKQIRGLSQASLNAEDGISAVQTAEGALTEVHDMLQRMNELAVKAA
bacterium Fla-X              ..MVVQHNLRAMNSNRMLGITQGSLNKSTEKLSSGYKVNRAADDAAGLSISEKMRKQIRGLSQASLNAEDGISAVQTAEGALTEVHDMLQRMNELAVKAA
bacterium C8ir1              ..MVVQHNLQAMNSNRMLGITQKTASKSTEKLSSGYAINRAADNAAGLAISEKMRKQIRGLTQASTNAEDGISSVQTAEGALTEVHDMLQRMNELAIQAA
Shigella flexneri fliC       MAQVINTNSLSLITQNNINKNQSALSSSIERLSSGLRINSAKDDAAGQAIANRFTSNIKGLTQAARNANDGISVAQTTEGALSEINNNLQRIRELTVQAS
Escherichia coli fliC        MAQVINTNSLSLITQNNINKNQSALSSSIERLSSGLRINSAKDDAAGQAIANRFTSNIKGLTQAARNANDGISVAQTTEGALSEINNNLQRIRELTVQAT
Salmonella enteritidis fliC  .AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSSGLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQAT
Salmonella enteritidis PT4 fljB  MAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSSGLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQAT
Campylobacter jejuni flaA    MGFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAA
Campylobacter jejuni flaB    MGFRINTNIGALNAHANSVVNSNELDKSLSRLSSGLRINSAADDASGMAIADSLRSQAATLGQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAA

101                                                                 200
Consensus                    NGTNSDSDRDSIQDEIDQLLEEIDRVANTTQFNGVYVLSGNDTDMKIQVGANDGETITIDLTKIDSSKLGLTGFNVNGDGFISFKAATVIDLASAEANVK
Lachnospiraceae bacterium A4 clone  NGTNSTSDRQTIQDEVDQLLTEIDRVAETTKFNELYTLKG.DED..KVTRYLSAHDAGIEGTLTQG....ATNATFSMDQ.LKFGDT..IMIAGREYHIS
bacterium Fla-X              NGTNSTSDRQTIQDEVDQLLTEIDRVAETTKFNELYTLKG.DED..KVTRYLSAHDAGIEGTLTQG....ATNATFSMDQ.LKFGDT..IMIAGREYHIS
bacterium C8ir1              NGTNSEDDRSYIQDEIDQLTQEIDRVAETTKFNETYLLKG.DTKNVDAMDYTYSYKAVTTNTVARASVLAAENTATGMSVSISFASNSGKVTAADSNNLA
Shigella flexneri fliC       TGTNSDSDLDSIQDEIKSRLDEIDRVSGQTQFNGVNVLAK.DGSMKIQVGANDGQTITIDLKKIDSDTLGLNGFNVNGGGAVANTAASKADLVAANATVV
Escherichia coli fliC        TGTNSDSDLDSIQDEIKSRLDEIDRVSGQTQFNGVNVLAK.DGSMKIQVGANDGETITIDLKKIDSDTLGLNGFNVNGKGTITNKAATVSDLTSAGAKLN
Salmonella enteritidis fliC  NGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQ.DNQMKIQVGANDGETITIDLQKIDVKSLGLDGFNVNGP.....KEATVGDLKSSFKNVT
Salmonella enteritidis PT4 fljB  NGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQ.DNQMKIQVGANDGETITIDLQKIDVKSLGLDGFNVNGP.....KEATVGDLKSSFKNVT
Campylobacter jejuni flaA    QDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFK
Campylobacter jejuni flaB    QDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIEDFK
```

FIG. 12

Middle

```
                                 201                                                                                                 300
Consensus                        FDNVVISTSVGTGYDAKAEQILKSADKTGDIATADVKNGGVAVVTDGATDGKFAINAYTCSLTTSDAGDFEGALASAADSASKRDALKDTTGVIAGKDEN
Lachnospiraceae bacterium A4 clone .............GTQKQQ........GEIITSSVKIG..QQVT...IDG....IMYTCTATVSNADKFELT...............KDD..LIAKLDTS
bacterium Fla-X                  .............GTKAEQ........AAIITASVKIG..QQVT...IDG....IMYTCSS.VSNADKFELK...............SED..LIAKLDTS
bacterium CBir1                  .............KAIRDQ........GFTITTSTQNG..KVVYGLELNGSDAKANYTVSTVSMEAGTFKIL..............NSNKQVVASVTIS
Shigella flexneri fliC           GN....KYTVSAGYDAAKASDLLAGVSDGDTVQATINNG..FGTAASATNYKYDSASKSYSFDTTTAS........AAD.......VQKYLTPGVGDTAK
Escherichia coli fliC            ........TTTGLYDLKTENTLLT....TDAAFDKLGNG..DKVTVGGVDYTYAAKSDGFTTTKSTAGTGVDAAAQAADSASKRDALAATLHADVGKSVN
Salmonella enteritidis fliC      ...........GYDTYAAG........ADKYRVDINSG..AVVTDAAAPDKVYVNAANGQLTTDDAENN.....TAVD.......LFKTTKSTAGTAEA
Salmonella enteritidis PT4 fljB  ...........GYDTYAAG........ADKYRVDINSG..AVVTDAAAPDKVYVNAANGQLTTDDAENN.....TAVD.......LFKTTKSTAGTAEA
Campylobacter jejuni flaA        FDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQEFAINGVTIGKIEYKDGDGNGSLISAIN......AVKDTTGVQASKDEN
Campylobacter jejuni flaB        FDNVVISTSVGTGLGALAEEINKSADKTGVRATYDVKTTGVYAIKEGTTSQDFAINGVVIGQINYKDGDNNGQLVSAIN......AVKDTTGVQASKDEN

                                 301                                                                                                 400
Consensus                        GAIAGAIKDGMSGDGTDYIGAGTFDDGTKKSDDGAGKLIKNDGRDINGSAASLTAAGATTAAMISVNAASLGESKGVYSFTGADVFTFDDGKGGGKFVFT
Lachnospiraceae bacterium A4 clone S......LSIMSVNGKTYYGAGITDDRTVVSSIGAYKLIQKE....LGLASSIGADGSTQAS...VNAGVDGKTLKKPSFEGKWVFSIDKG........S
bacterium Fla-X                  S......LSIMSVNGKTYYGAGITDDRTVVSSIGAYKLIQKE....LGLASSIGADGATQAS...VNAGVDGKTLMKPSFEGKWVFSIDKG........S
bacterium CBir1                  TTASFKKVSGMSQIVTAYSVSAAYATGDVYSLYDADGNAISA....NKLDKYFTAGGATEAGGIATTLSANSGVPKVYDVLGKEVSAVSIA........S
Shigella flexneri fliC           GTIT..IDGSAQDVQISSDGKITASNGDKLYIDTTGRLTKN......GSGASLTEASLSTLAANNTKATTIDIGGTSISFTGNS.TTPDTI........T
Escherichia coli fliC            GSYT..TKDGTVSFETDSAGNITIG.GSQAYVDDAGNLTTNN....AGSAAKADMKALLKAASEGSDGASLTPNGTEYTIAKATPATTTPV........A
Salmonella enteritidis fliC      KAIAGAIKGGKEGDTFDYKG.VTFTIDTKTGDDGNGKVSTTI....NGEKVTLTVADIATGATD.VNAATLQSSKNVYTSVVNGQFTFDDK........T
Salmonella enteritidis PT4 fljB  KAIAGAIKGGKEGDTFDYKG.VTFTIDTKTGDDGNGKVSTTI....NGEKVTLTVADIATGATD.VNAATLQSSKNVYTSVVNGQFTFDDK........T
Campylobacter jejuni flaA        GKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFT
Campylobacter jejuni flaB        GKLVLTSADGRGIKITGDIGVGSGILANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFT

                                 401                                                                                                 500
Consensus                        KNVSAIKADLEAIDFGFHVGADKDDNNGAAYSIGSGVLSQGIAAGDAKTLGGNTLFDDDGSGFSSGTANGVSAALNTDAANVTNAGYASATDTNKDYAPA
Lachnospiraceae bacterium A4 clone VQVR......EDIDFSLHVGADADMNNKIAVKIG.........ALDTKGLGIQGLNVKD.........................................
bacterium Fla-X                  VQVR......EDIDFSLHVGADADMNNKIAVKIG.........ALDTKGLGIQGLNVKD.........................................
bacterium CBir1                  TLVTAVKDKTAALKMNFHVGADGTDNNKIKINIE.........AMTAKSLGVNGLKVSG.........................................
Shigella flexneri fliC           YSVTGAKVDQAAFDKAVSTSGNNVDFTTAGYSVN........GTTGAVTKGVDSVYVDNNEALT..TSDTVDFYLQ.DDGSVTNG...............
Escherichia coli fliC            PLIPGGITYQATVSKDVVLSETKAAAATSSITFNSGVLSKTIGFTAGESSDAAKSYVDDKGGITNVADYTVSYSVNKDNGSVTVAGYASATDTNKDYAPA
Salmonella enteritidis fliC      KNESAKLSDLEANN..AVKGESKITVNGAEYTAN........ATGDKITLAGKTMFIDK.......TASGVSTLIN.......................
Salmonella enteritidis PT4 fljB  KNESAKLSDLEANN..AVKGESKITVNGAEYTAN........ATGDKITLAGKTMFIDK.......TASGVSTLIN.......................
Campylobacter jejuni flaA        QNVSSISAFMSAQGSGFSRGSGFSVGSGKNLSVG...LSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAAN...................
Campylobacter jejuni flaB        QNVSSISAFMSAQGSGFSRGSGFSVGSGKNLSVG...LSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAAN...................
```

FIG. 13

C-Terminal

	501 … 600
Consensus	IGKAVNKDAAGKDETDAATTGKAATNPLDSIDDAISKIDAQRSSLGAVQNRLDSTINNLDNTVTNLTAAESRIRDADYATEVSNMSKANILAQAGQSVLA
Lachnospiraceae bacterium A4 clone	..................TTGAAATYAIDSIADAVARISAQRSLLGAVQNRLEHTINNLDNVVENTTAAESQIRDTDMATEMVKYSNNNVLAQAGQSMLA
bacterium Fla-X	..................TTGAAATYAIDSIADAVARISAQRSLLGAVQNRLEHTINNLDNVVENTTAAESQIRDTDMATEMVKYSNNNVLAQAGQSMLA
bacterium CBir1	..................SSGTNATNAIEIIAGAIKKVSTQRSALGAVQNRLEHTINNLDNIVENTTAAESGIRDTDMATEMVKYSNANILSQAGQSMLA
Shigella flexneri fliC	SGKAVYKDADGKLTTDAETKAATTADPLKALDEAISSIDKFRSSLGAVQNRLDSAVTNLNNTTTNLSEAQSRIQDADYATEVSNMSKAQIIQQAGNSVLA
Escherichia coli fliC	IGTAVNVNSAGKITTETTSAGSATTNPLAALDDAISSIDKFRSSLGAIQNRLDSAVTNLNNTTTNLSEAQSRIQDADYATEVSNMSKAQIIQQAGNSVLA
Salmonella enteritidis fliC	..............EDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLA
Salmonella enteritidis PT4 fljB	..............EDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLA
Campylobacter jejuni flaA	..........TTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGSYAMA
Campylobacter jejuni flaB	..........TTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFASESANFSKYNILAQSGSYAMS

	601 … 615
Consensus	QANQVPQNVLSLLQG
Lachnospiraceae bacterium A4 clone	QSNQANQGVLSLLG.
bacterium Fla-X	QSNQANQGVLQLLQ.
bacterium CBir1	QSNQSNQGVLQLLQ.
Shigella flexneri fliC	KANQVPQQVLSLLQG
Escherichia coli fliC	KANQVPQQVLSLLQG
Salmonella enteritidis fliC	QANQVPQNVLSLLR.
Salmonella enteritidis PT4 fljB	QANQVPQNVLSLLR.
Campylobacter jejuni flaA	QANSSQQNVLRLLQ.
Campylobacter jejuni flaB	QANAVQQNVLKLLQ.

FIG. 14

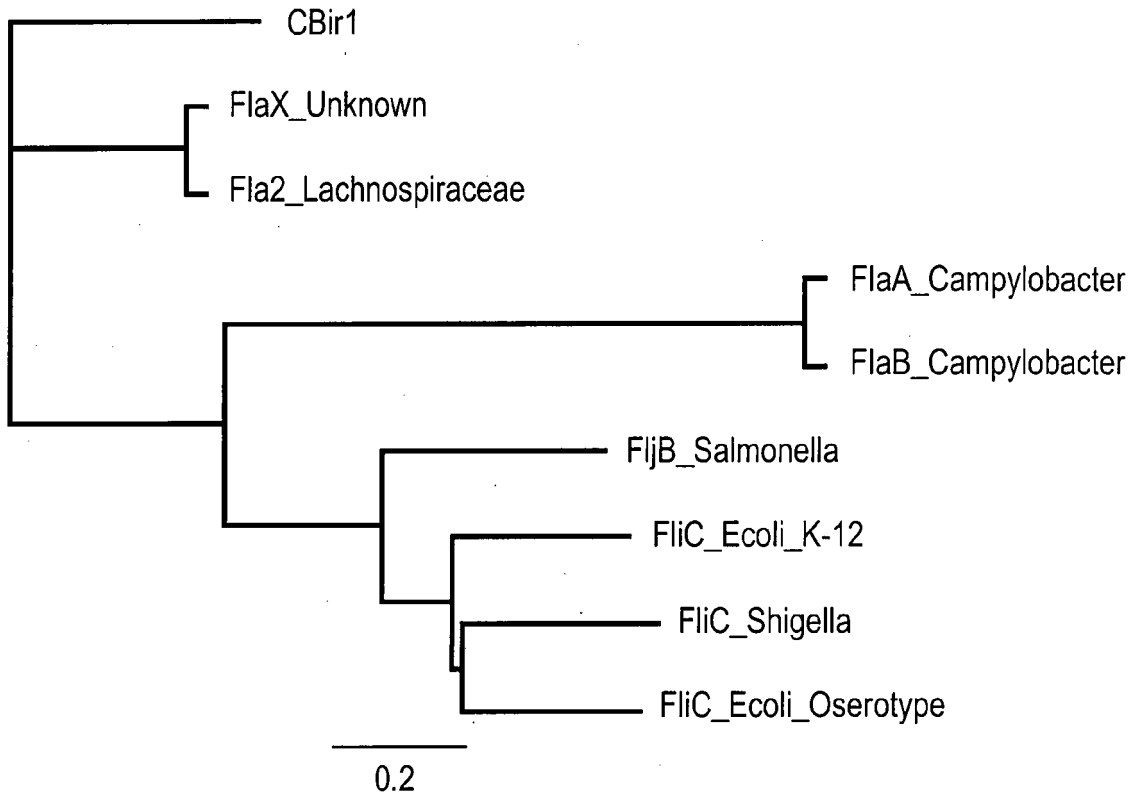

CBir1
FlaX_Unknown
Fla2_Lachnospiraceae
FlaA_Campylobacter
FlaB_Campylobacter
FljB_Salmonella
FliC_Ecoli_K-12
FliC_Shigella
FliC_Ecoli_Oserotype
0.2

FIG. 15

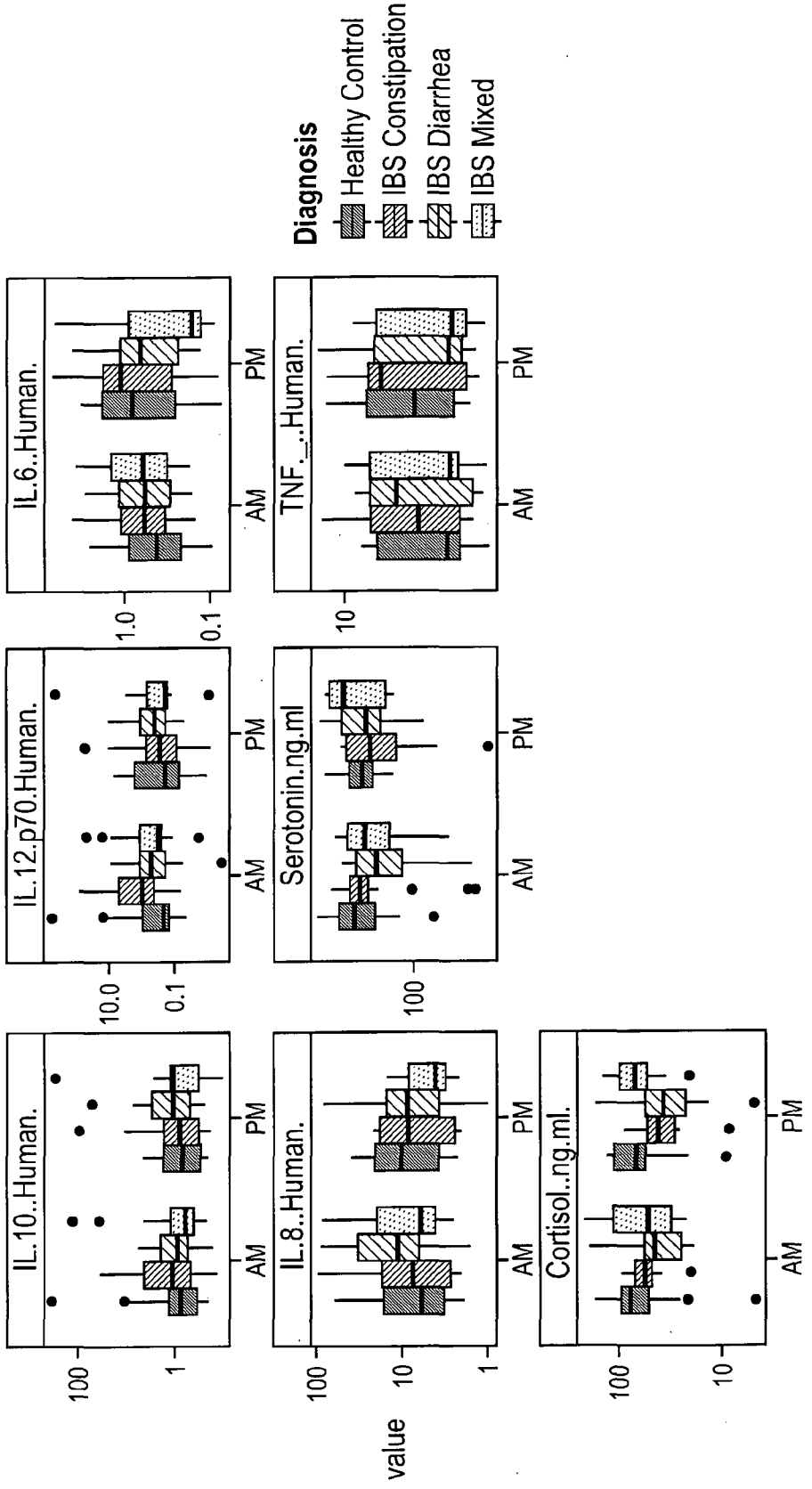

Diagnosis
Healthy Control
IBS Constipation
IBS Diarrhea
IBS Mixed
IL.10..Human.
IL.12.p70.Human.
IL.6..Human.
IL.8..Human.
Serotonin.ng.ml
TNF._..Human.
Cortisol..ng.ml.
value
AM
PM

FIG. 16

- **AM linear regression**
  - **Cortisol vs. Dx**

	Estimate	P
HC vs. IBS-C	-0.142	0.433
HC vs. IBS-D	-0.374	0.056
HC vs. IBS-M	-0.063	0.732

- **PM linear regression**
  - **Cortisol vs. Dx**

	Estimate	P
HC vs. IBS-C	-0.502	0.062
HC vs. IBS-D	**-0.636**	**0.012**
HC vs. IBS-M	0.022	0.942

FIG. 17

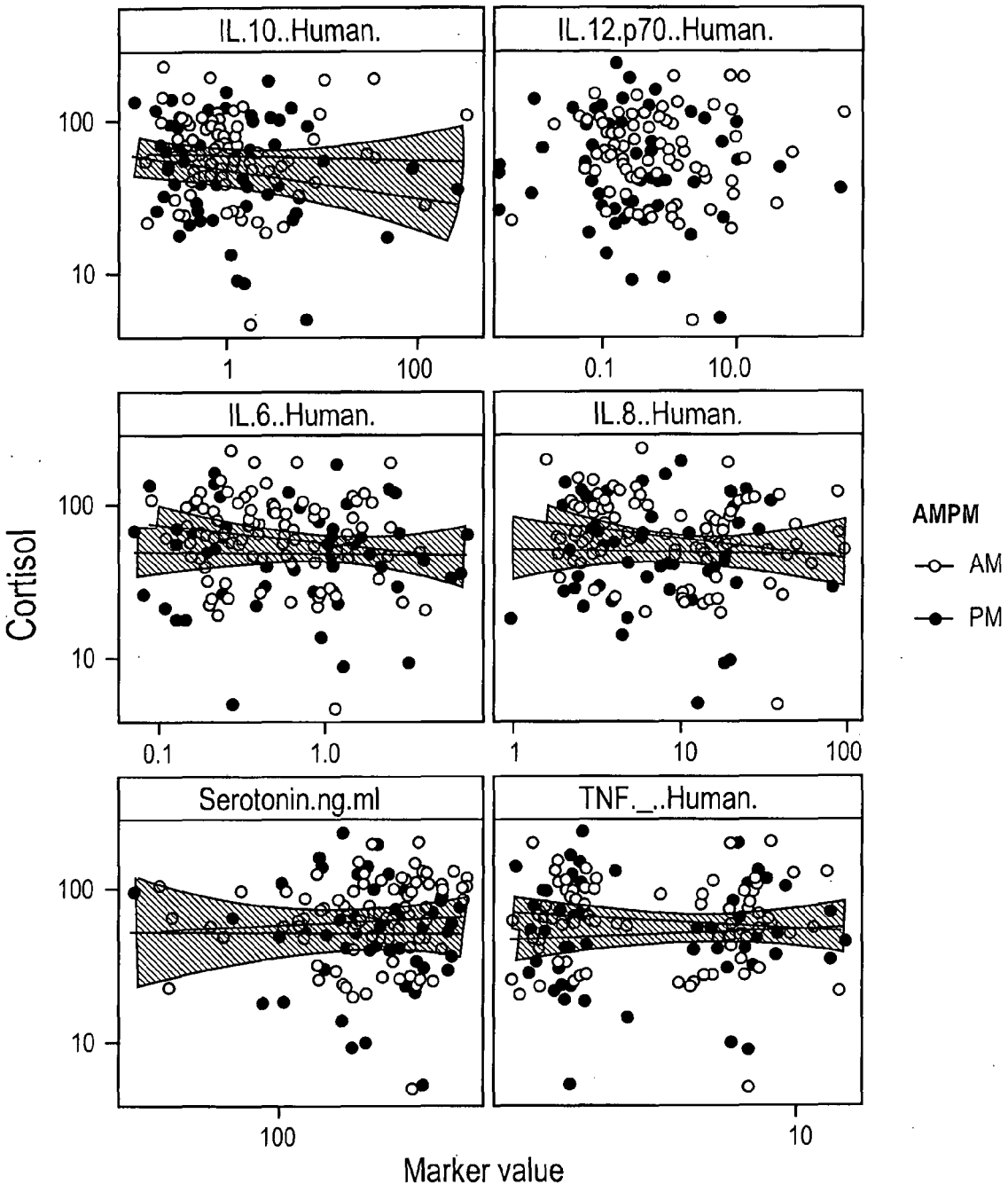
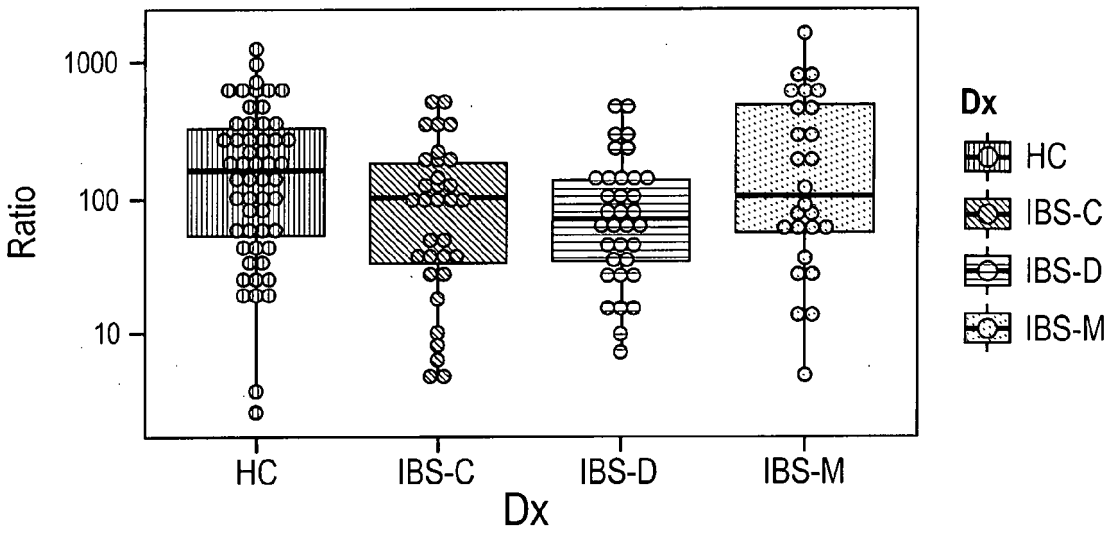

IL.10..Human.
IL.12.p70..Human.
IL.6..Human.
IL.8..Human.
Serotonin.ng.ml
TNF._..Human.
Cortisol
Marker value
AMPM
AM
PM

FIG. 18



- ANOVA
  - F = 2.678, p = 0.0494

FIG. 19

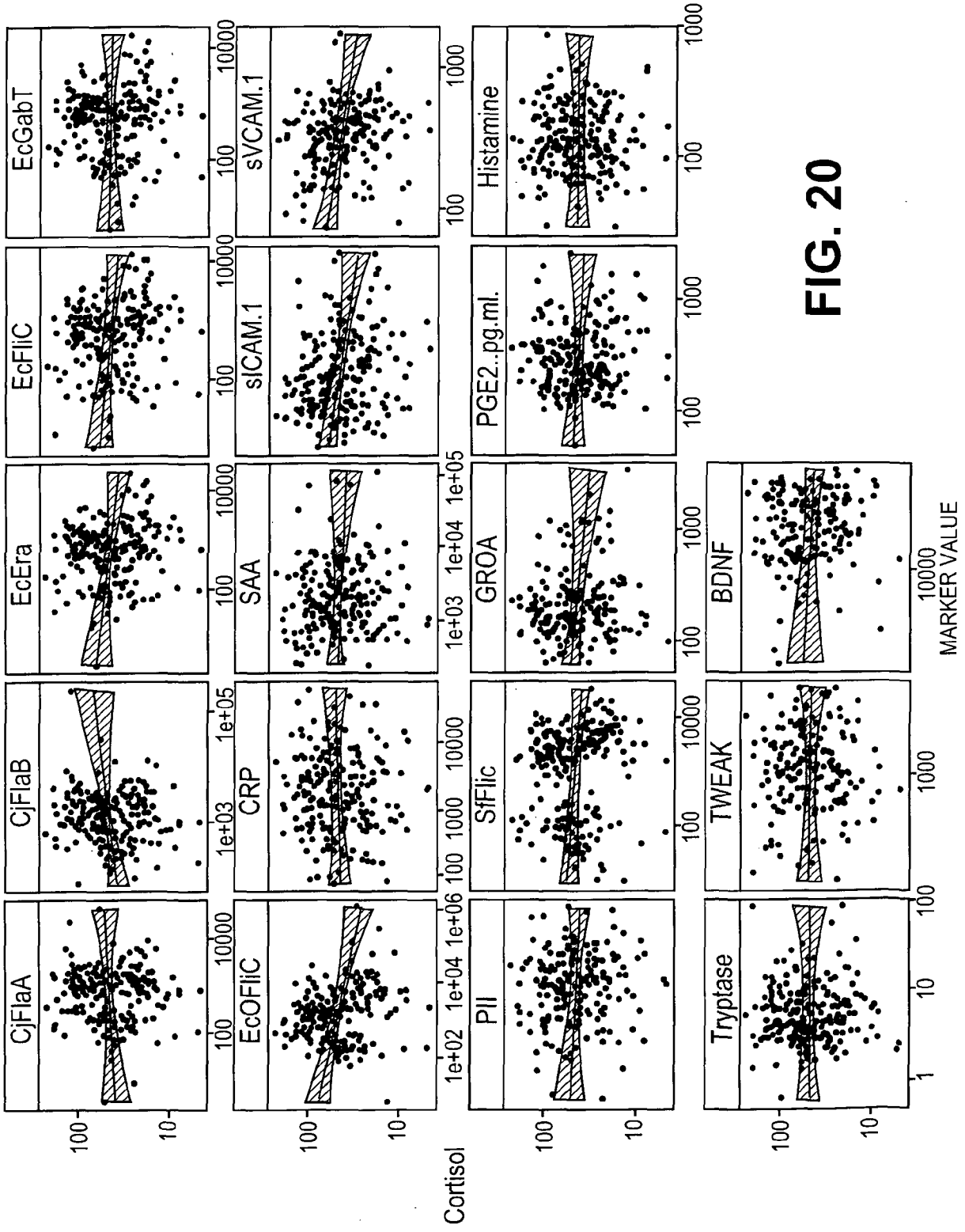
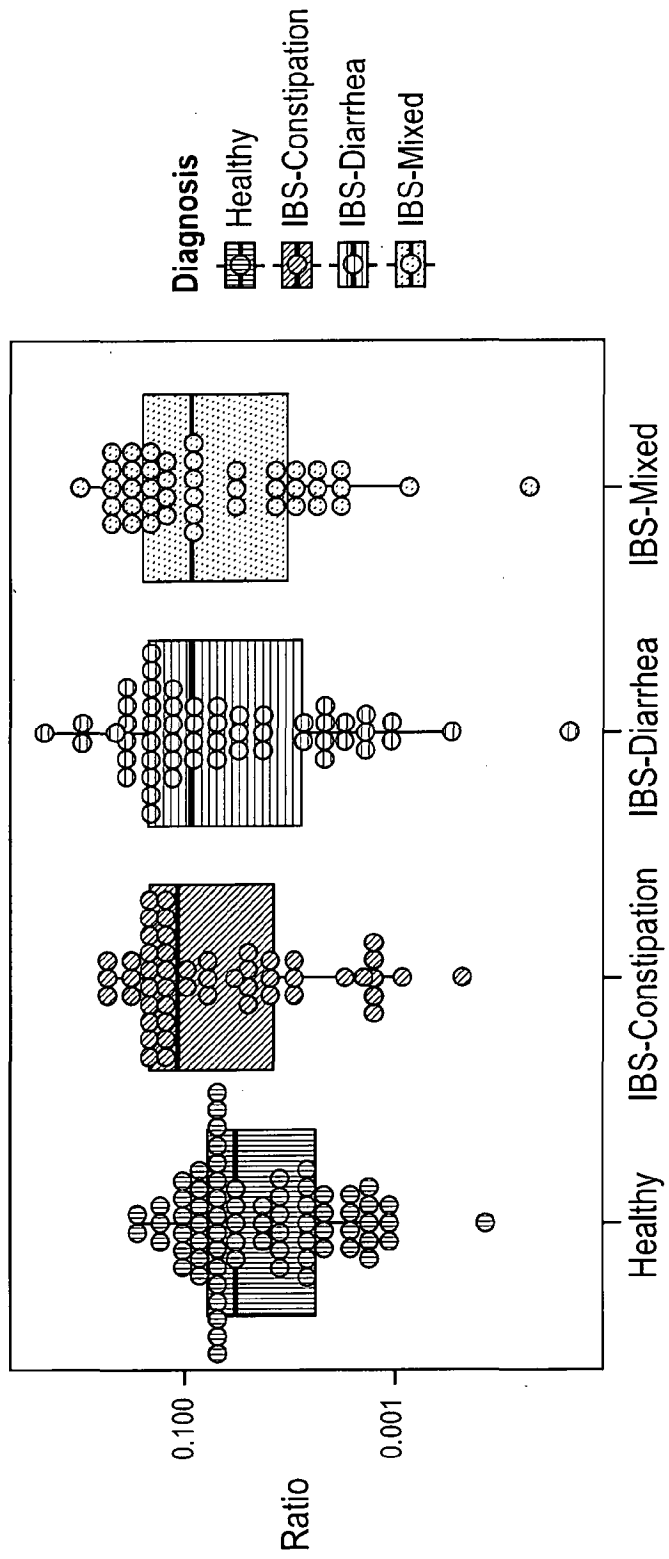

CjFlaA
CjFlaB
EcEra
EcFliC
EcGabT
EcOFliC
CRP
SAA
sICAM.1
sVCAM.1
PII
SfFlic
GROA
PGE2..pg.ml.
Histamine
Tryptase
TWEAK
BDNF
Cortisol
MARKER VALUE

FIG. 20

	Estimate	Std. Error	T-value	Pr(>|t|)	
(Intercept)	3.5361	3.3985	1.0400	0.3008	
CjFlaA	-0.0221	0.1907	-0.1160	0.9080	
CjFlaB	0.3847	0.2163	1.7780	0.0785	.
EcEra	0.0454	0.3785	0.1200	0.9047	
EcFliC	-0.2979	0.2812	-1.0600	0.2920	
EcGabT	0.4647	0.2355	1.9740	0.0513	.
EcOFliC	**-0.2110**	**0.0847**	**-2.4910**	**0.0145**	*
CRP	0.2027	0.1539	1.3170	0.1910	
SAA	0.0239	0.1402	0.1710	0.8650	
ICAM	-0.0734	0.3239	-0.2270	0.8211	
VCAM	0.0031	0.2316	0.0140	0.9892	
PII	-1.2749	1.0748	-1.1860	0.2385	
SfFlic	-0.1025	0.1007	-1.0180	0.3112	
GROA	0.0480	0.0991	0.4840	0.6293	
PGE2	-0.1335	0.1132	-1.1800	0.2411	
Histamine	-0.030	0.1335	-0.2470	0.8053	
Tryptase	-0.0764	0.0996	-0.7670	0.4449	
TWEAK	-0.0721	0.2193	-0.3290	0.7430	
BDNF	0.0361	0.1892	0.1910	0.8492	

FIG. 21



- ANOVA
  - F = 3.343, p = 0.020*
  - Significant difference in ratio among groups

FIG. 22

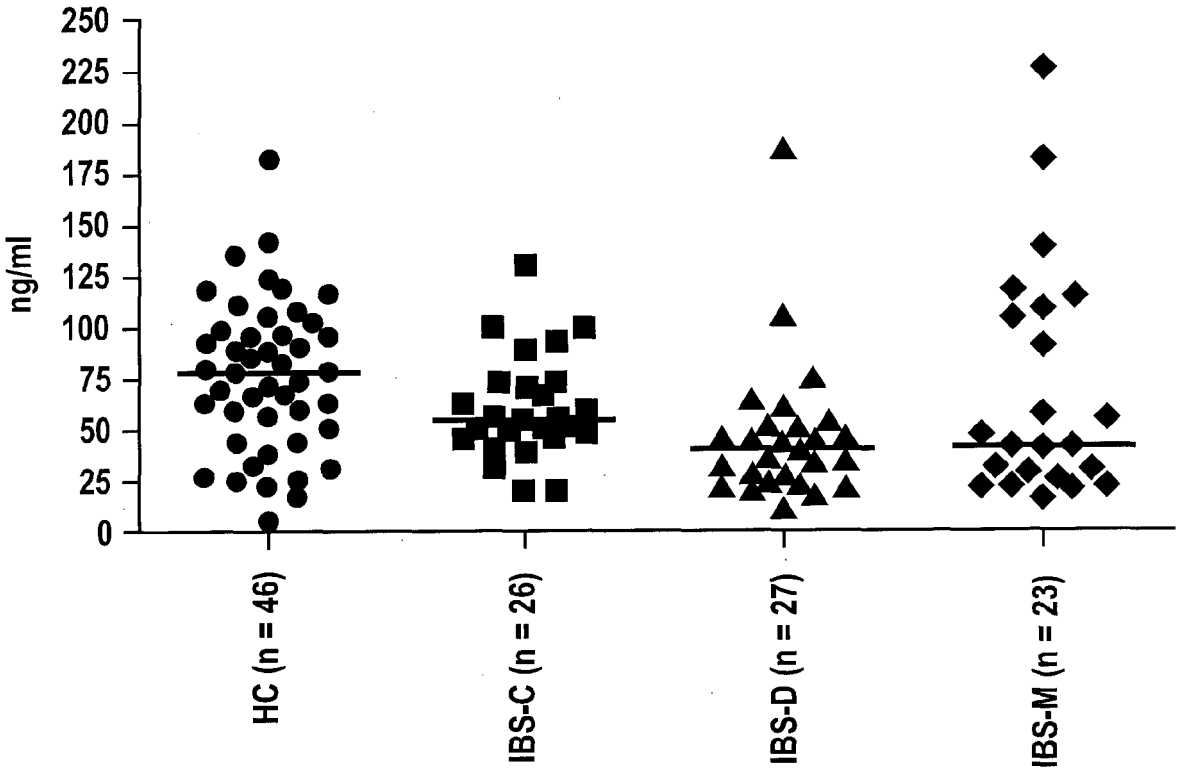

250
225
200
175
150
125
100
75
50
25
0
ng/ml
HC (n = 46)
IBS-C (n = 26)
IBS-D (n = 27)
IBS-M (n = 23)

FIG. 23

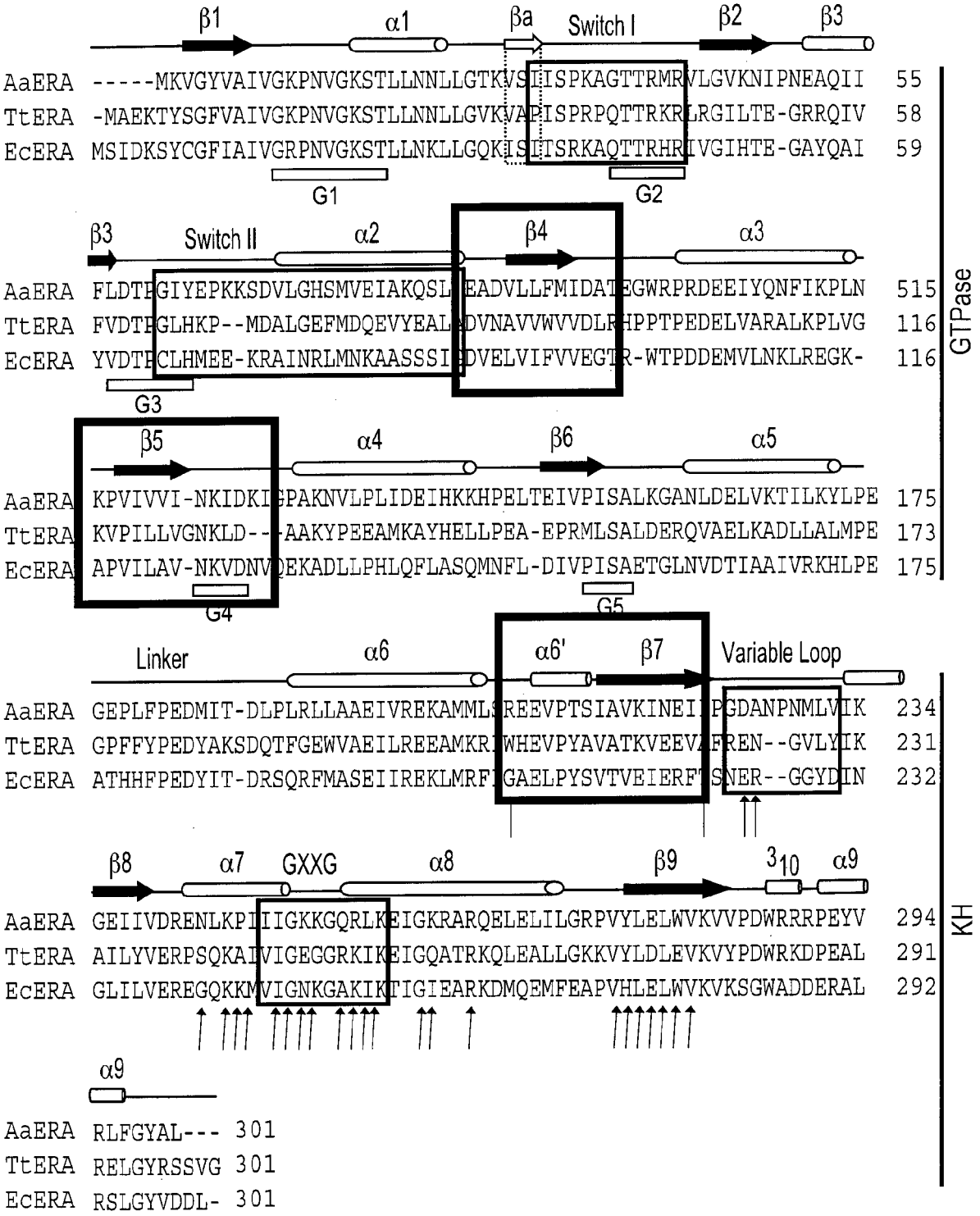

β1 α1 βa Switch I β2 β3
AaERA -----MKVGYVAIVGKPNVGKSTLLNNLLGTKVSIISPKAGTTRMRVLGVKNIPNEAQII 55
TtERA -MAEKTYSGFVAIVGKPNVGKSTLLNNLLGVKVAPISPRPQTTRKRLRGILTE-GRRQIV 58
EcERA MSIDKSYCGFIAIVGRPNVGKSTLLNKLLGQKISIISRKAQTTRHRIVGIHTE-GAYQAI 59
G1
G2
β3 Switch II α2 β4 α3
AaERA FLDTPGIYEPKKSDVLGHSMVEIAKQSLEEADVLLFMIDATEGWRPRDEEIYQNFIKPLN 515
TtERA FVDTPGLHKP--MDALGEFMDQEVYEALADVNAVVWVVDLRHPPTPEDELVARALKPLVG 116
EcERA YVDTPCLHMEE-KRAINRLMNKAASSSIGDVELVIFVVEGTR-WTPDDEMVLNKLREGK- 116
G3
β5 α4 β6 α5
AaERA KPVIVVI-NKIDKIGPAKNVLPLIDEIHKKHPELTEIVPISALKGANLDELVKTILKYLPE 175
TtERA KVPILLVGNKLD--AAKYPEEAMKAYHELLPEA-EPRMLSALDERQVAELKADLLALMPE 173
EcERA APVILAV-NKVDNVQEKADLLPHLQFLASQMNFL-DIVPISAETGLNVDTIAAIVRKHLPE 175
G4
G5
GTPase
Linker α6 α6' β7 Variable Loop
AaERA GEPLFPEDMIT-DLPLRLLAAEIVREKAMMLSREEVPTSIAVKINEIIPGDANPNMLVIK 234
TtERA GPFFYPEDYAKSDQTFGEWVAEILREEAMKRIWHEVPYAVATKVEEVAFREN--GVLYIK 231
EcERA ATHHFPEDYIT-DRSQRFMASEIIREKLMRFIGAELPYSVTVEIERFTSNER--GGYDIN 232
β8 α7 GXXG α8 β9 3₁₀ α9
AaERA GEIIVDRENLKPIIIGKKGQRLKEIGKRARQELELILGRPVYLELWVKVVPDWRRRPEYV 294
TtERA AILYVERPSQKAIVIGEGGRKIKEIGQATRKQLEALLGKKVYLDLEVKVYPDWRKDPEAL 291
EcERA GLILVEREGQKKMVIGNKGAKIKTIGIEARKDMQEMFEAPVHLELWVKVKSGWADDERAL 292
KH
α9
AaERA RLFGYAL--- 301
TtERA RELGYRSSVG 301
EcERA RSLGYVDDL- 301

FIG. 24

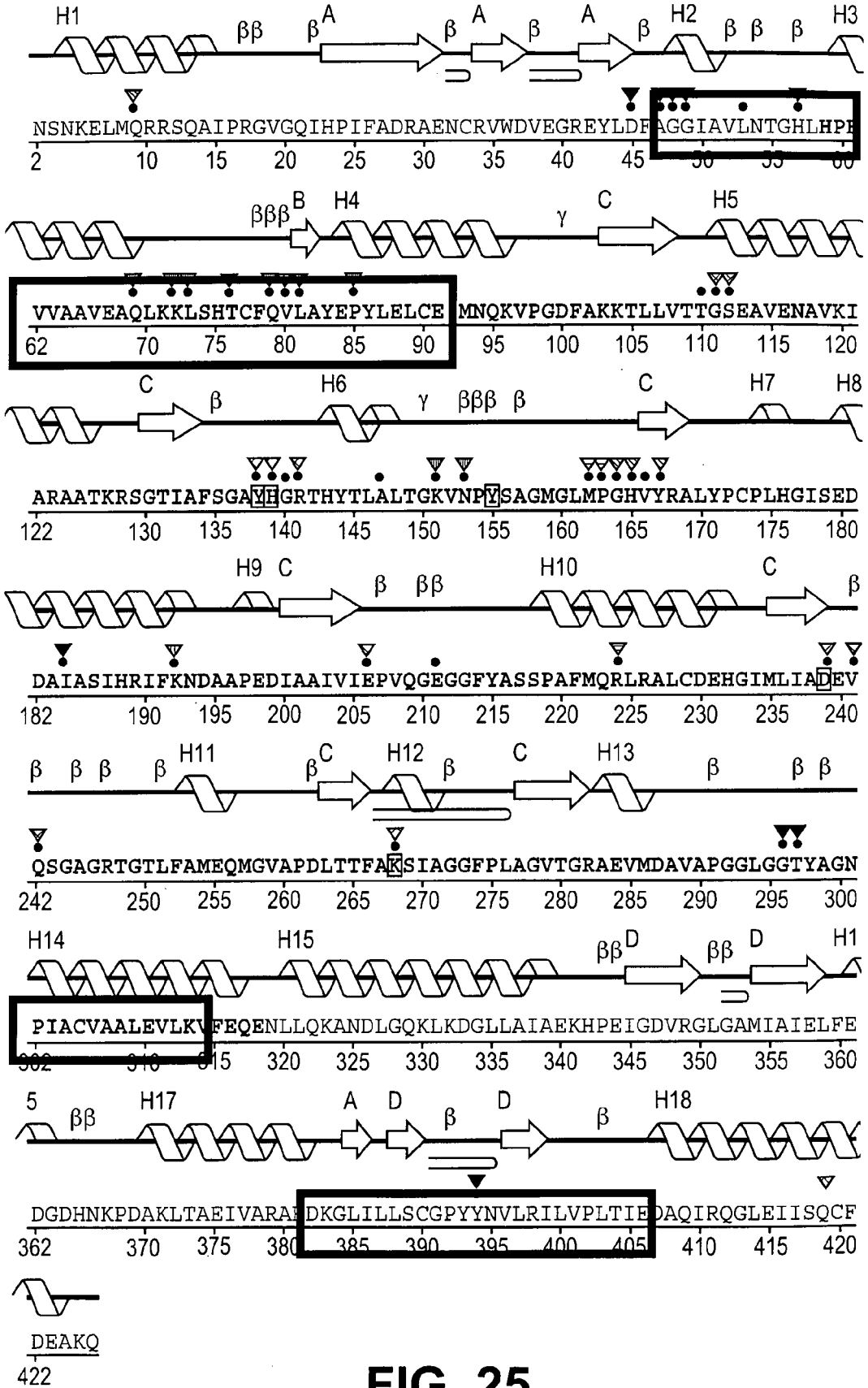

H1
ββ
β
A
β
A
β
A
β
H2
β β β
H3
NSNKELMQRRSQAIPRGVGQIHPIFADRAENCRVWDVEGREYLDFAGGIAVLNTGHLHPE
2 10 15 20 25 30 35 40 45 50 55 60
βββ
B
H4
γ
C
H5
VVAAVEAQLKKLSHTCFQVLAYEPYLELCE MNQKVPGDFAKKTLLVTTGSEAVENAVKI
62 70 75 80 85 90 95 100 105 110 115 120
C
β
H6
γ
βββ
β
C
H7
H8
ARAATKRSGTIAFSGAYHGRTHYTLALTGKVNPYSAGMGLMPGHVYRALYPCPLHGISED
122 130 135 140 145 150 155 160 165 170 175 180
H9
C
β
ββ
H10
C
β
DAIASIHRIFKNDAAPEDIAAIVIEPVQGEGGFYASSPAFMQRLRALCDEHGIMLIADEV
182 190 195 200 205 210 215 220 225 230 235 240
β β β β
H11
β
C
H12
β
C
H13
β
β β
QSGAGRTGTLFAMEQMGVAPDLTTFAKSIAGGFPLAGVTGRAEVMDAVAPGGLGGTYAGN
242 250 255 260 265 270 275 280 285 290 295 300
H14
H15
ββ
D
ββ
D
H1
PIACVAALEVLKVFEQENLLQKANDLGQKLKDGLLAIAEKHPEIGDVRGLGAMIAIELFE
302 310 315 320 325 330 335 340 345 350 355 360
5
ββ
H17
A
D
β
D
β
H18
DGDHNKPDAKLTAEIVARADKGLILLSCGPYYNVLRILVPLTIEDAQIRQGLEIISQCF
362 370 375 380 385 390 395 400 405 410 415 420
DEAKQ
422

FIG. 25

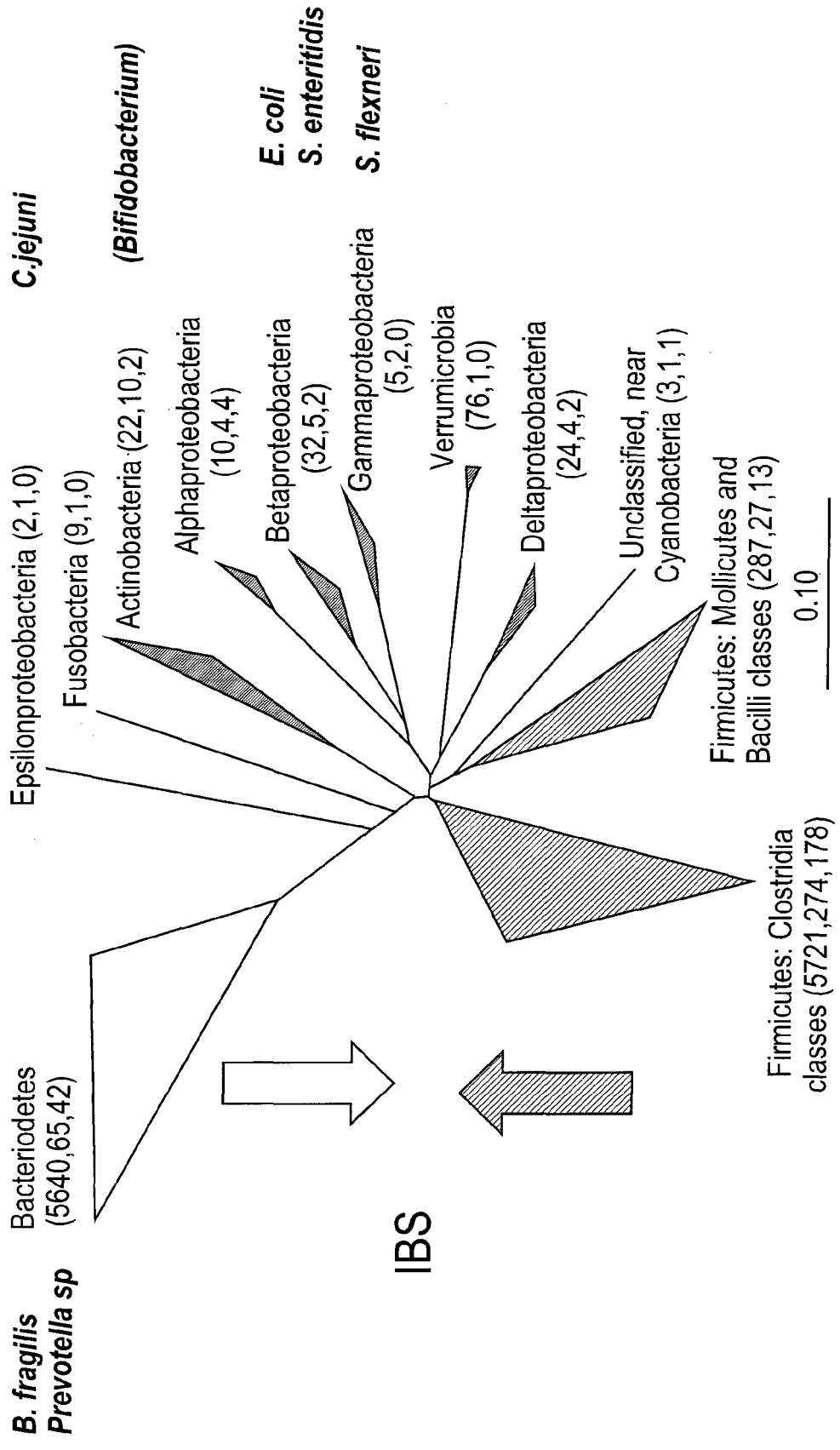

B. fragilis
Prevotella sp
Bacteriodetes (5640,65,42)
Epsilonproteobacteria (2,1,0)
Fusobacteria (9,1,0)
Actinobacteria (22,10,2)
C.jejuni
(Bifidobacterium)
Alphaproteobacteria (10,4,4)
Betaproteobacteria (32,5,2)
E. coli
S. enteritidis
Gammaproteobacteria (5,2,0)
S. flexneri
Verrumicrobia (76,1,0)
Deltaproteobacteria (24,4,2)
Unclassified, near Cyanobacteria (3,1,1)
Firmicutes: Mollicutes and Bacilli classes (287,27,13)
Firmicutes: Clostridia classes (5721,274,178)
0.10
IBS

FIG. 26

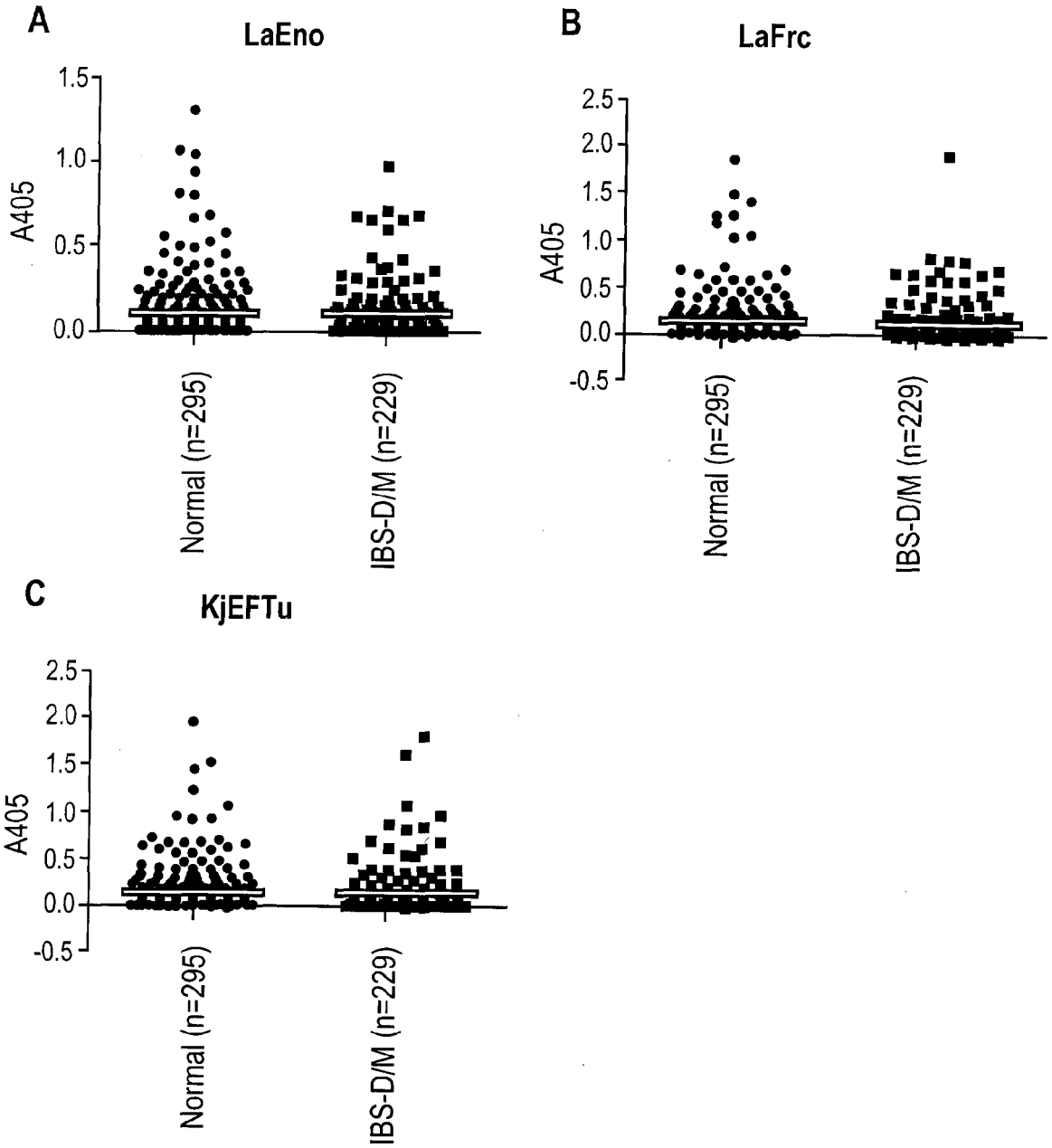

A
LaEno
A405
1.5
1.0
0.5
0.0
Normal (n=295)
IBS-D/M (n=229)
B
LaFrc
A405
2.5
2.0
1.5
1.0
0.5
0.0
-0.5
Normal (n=295)
IBS-D/M (n=229)
C
KjEFTu
A405
2.5
2.0
1.5
1.0
0.5
0.0
-0.5
Normal (n=295)
IBS-D/M (n=229)

FIG. 27

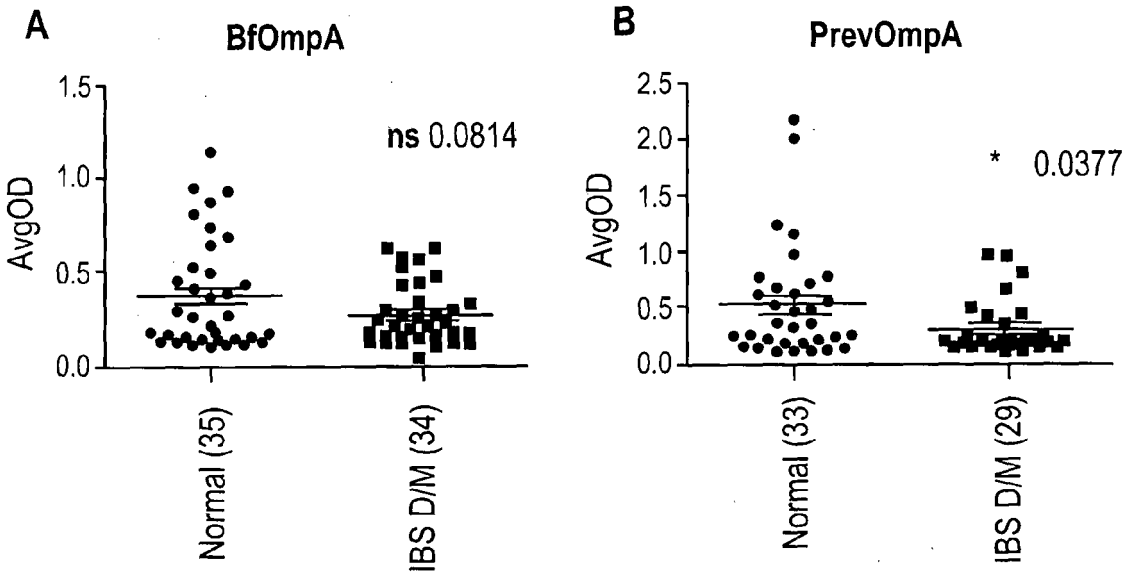

A
BfOmpA
AvgOD
1.5
1.0
0.5
0.0
ns 0.0814
Normal (35)
IBS D/M (34)
B
PrevOmpA
AvgOD
2.5
2.0
1.5
1.0
0.5
0.0
* 0.0377
Normal (33)
IBS D/M (29)

FIG. 28

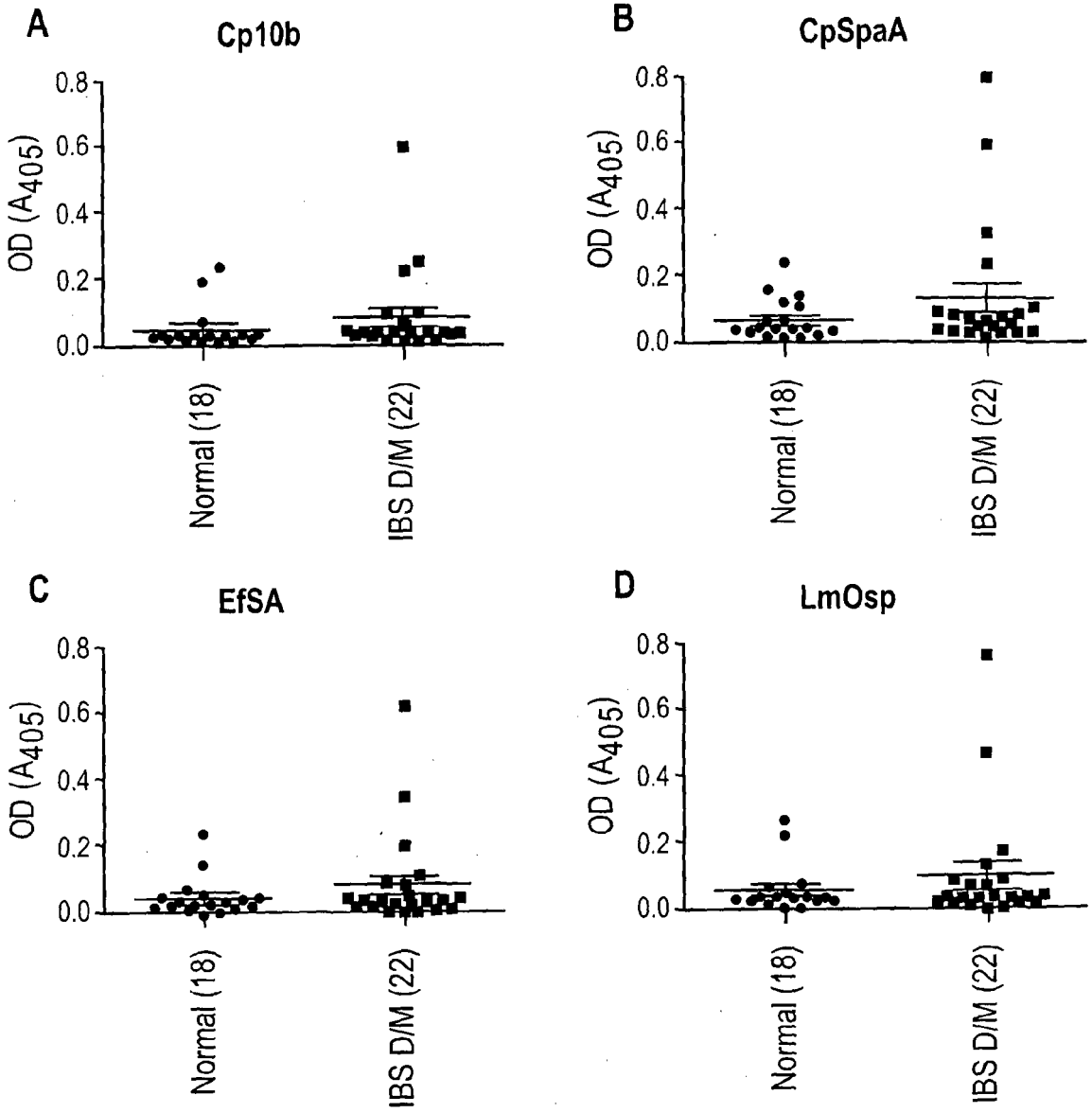

A
Cp10b
B
CpSpaA
C
EfSA
D
LmOsp
OD (A405)
0.0
0.2
0.4
0.6
0.8
Normal (18)
IBS D/M (22)

FIG. 29