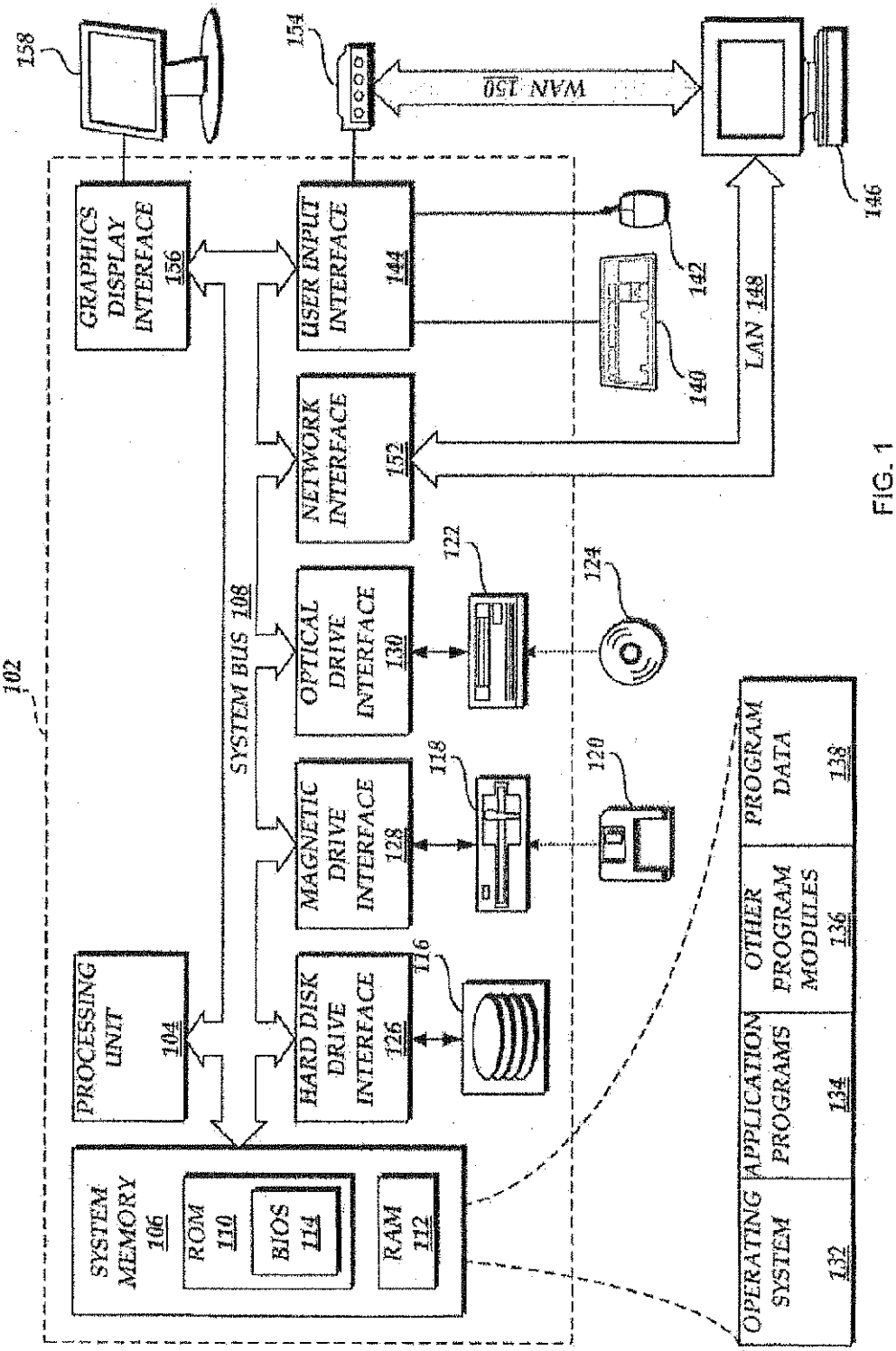

158
154
WAN 150
146
GRAPHICS DISPLAY INTERFACE 156
USER INPUT INTERFACE 144
142
140
LAN 148
NETWORK INTERFACE 152
122
124
OPTICAL DRIVE INTERFACE 130
SYSTEM BUS 108
102
118
120
MAGNETIC DRIVE INTERFACE 128
PROCESSING UNIT 104
116
HARD DISK DRIVE INTERFACE 126
SYSTEM MEMORY 106
ROM 110
BIOS 114
RAM 112
OPERATING SYSTEM 132
APPLICATION PROGRAMS 134
OTHER PROGRAM MODULES 136
PROGRAM DATA 138

FIG. 1

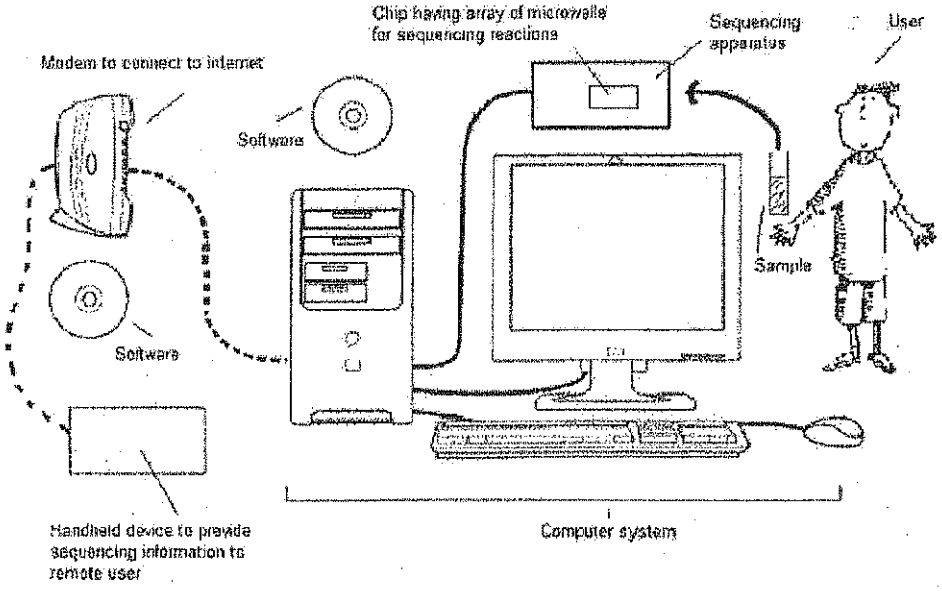

Chip having array of microwells for sequencing reactions
Sequencing apparatus
User
Modem to connect to internet
Software
Sample
Software
Handheld device to provide sequencing information to remote user
Computer system

FIG. 2

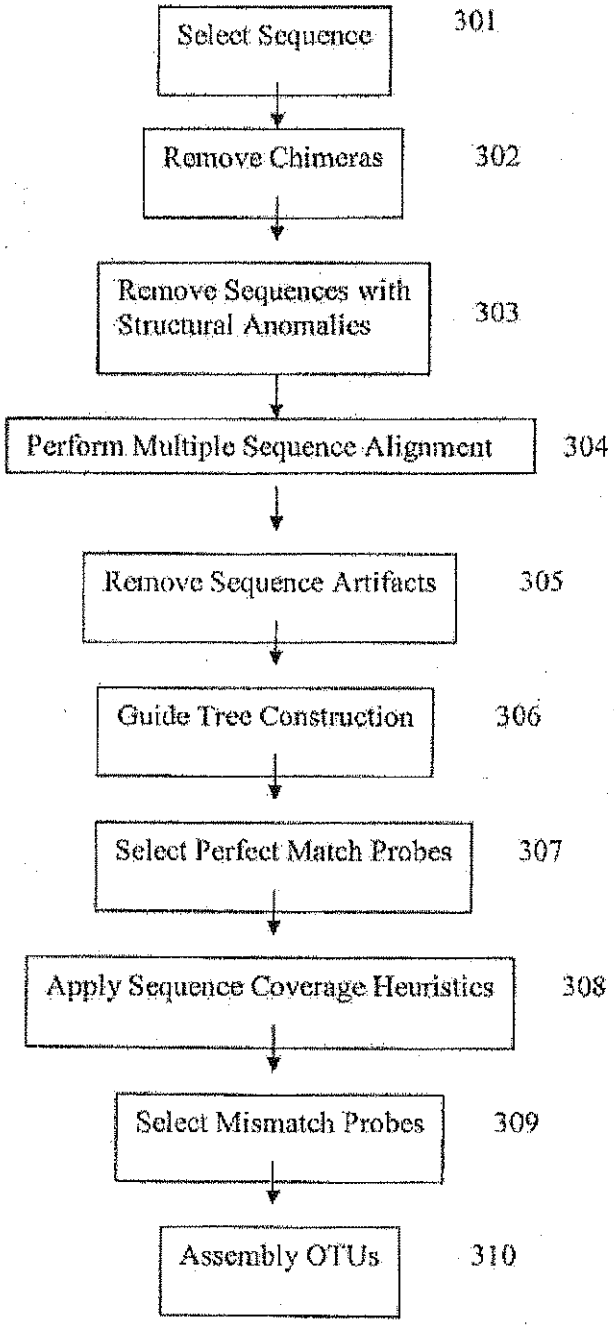

Select Sequence
301
Remove Chimeras
302
Remove Sequences with Structural Anomalies
303
Perform Multiple Sequence Alignment
304
Remove Sequence Artifacts
305
Guide Tree Construction
306
Select Perfect Match Probes
307
Apply Sequence Coverage Heuristics
308
Select Mismatch Probes
309
Assembly OTUs
310

Fig. 3

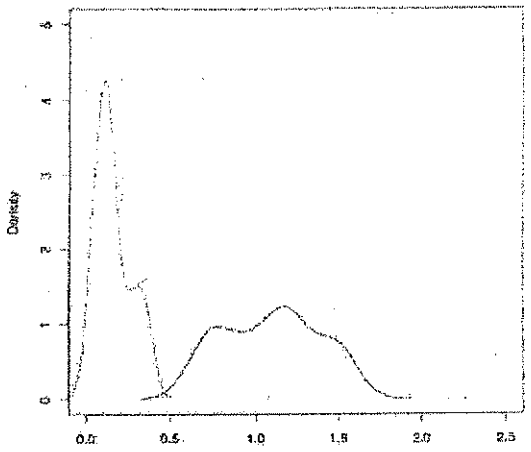


Fig. 4A

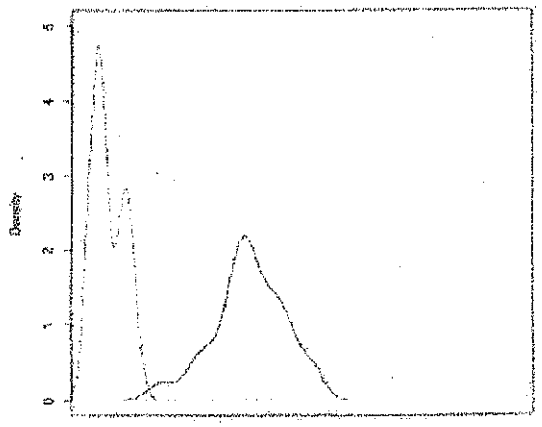


Fig. 4B

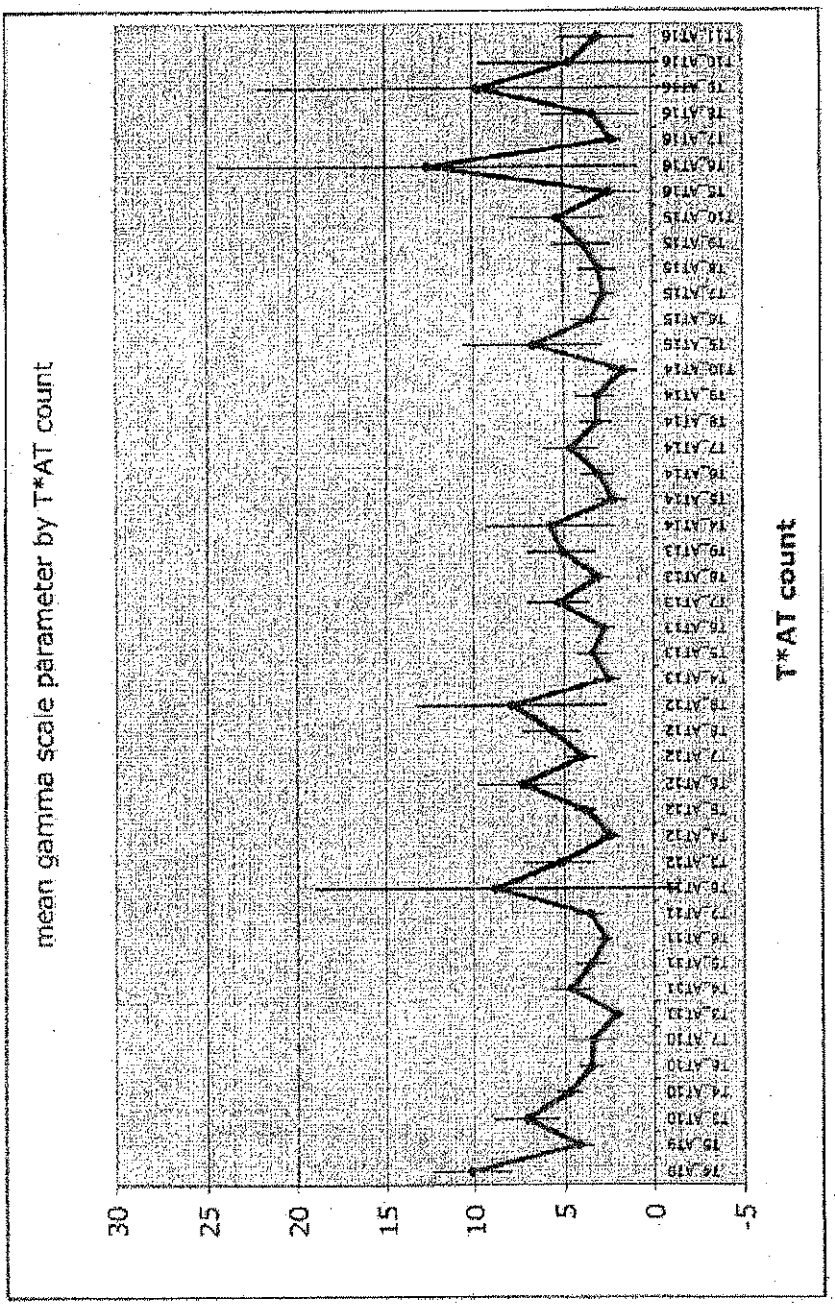

mean gamma scale parameter by T*AT count
T*AT count
30
25
20
15
10
5
0
-5

Fig. 5

Fig. 6

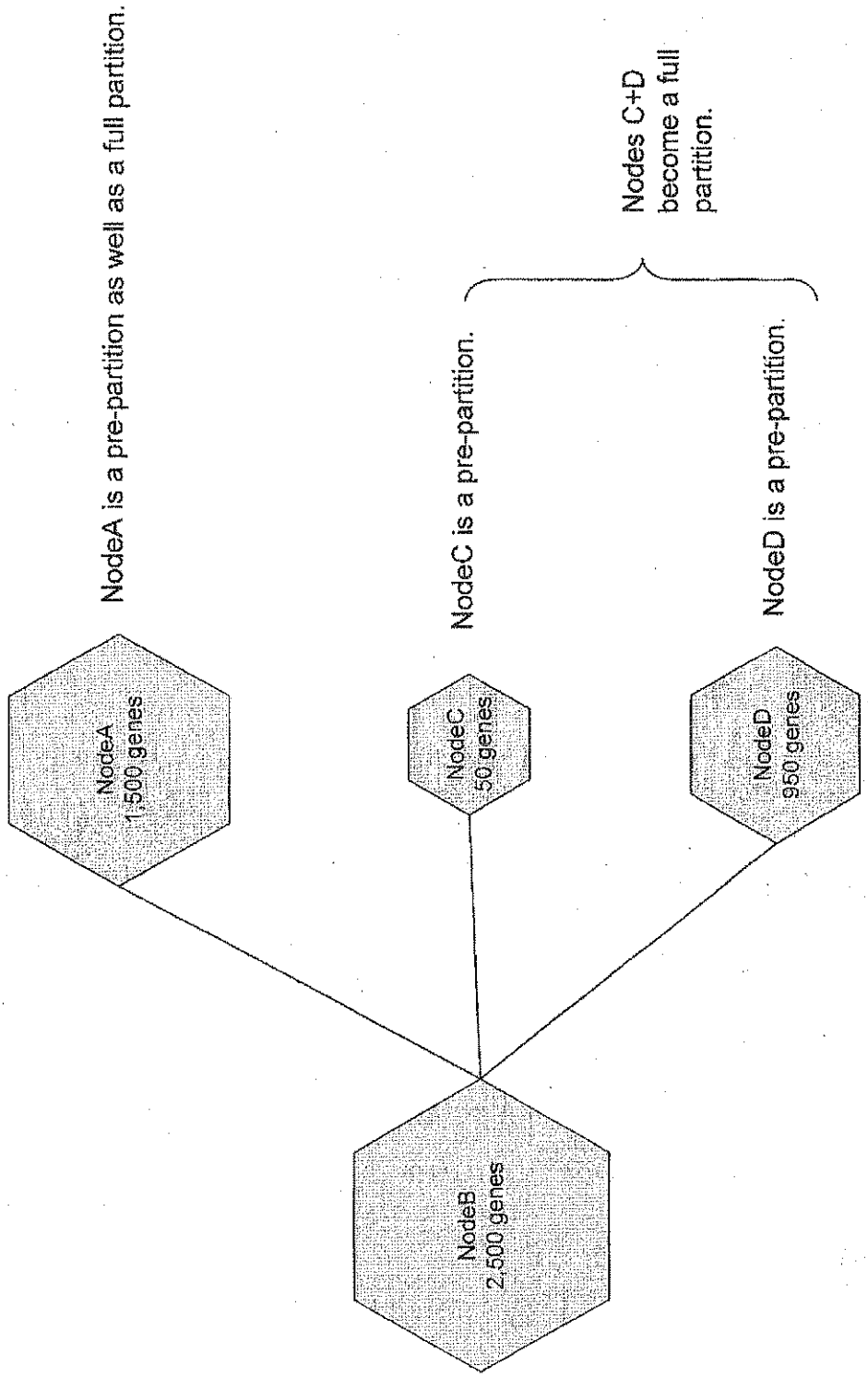

NodeA is a pre-partition as well as a full partition.
NodeA
1,500 genes
NodeC is a pre-partition.
NodeC
50 genes
Nodes C+D
become a full
partition.
NodeD is a pre-partition.
NodeD
950 genes
NodeB
2,500 genes

Fig. 7

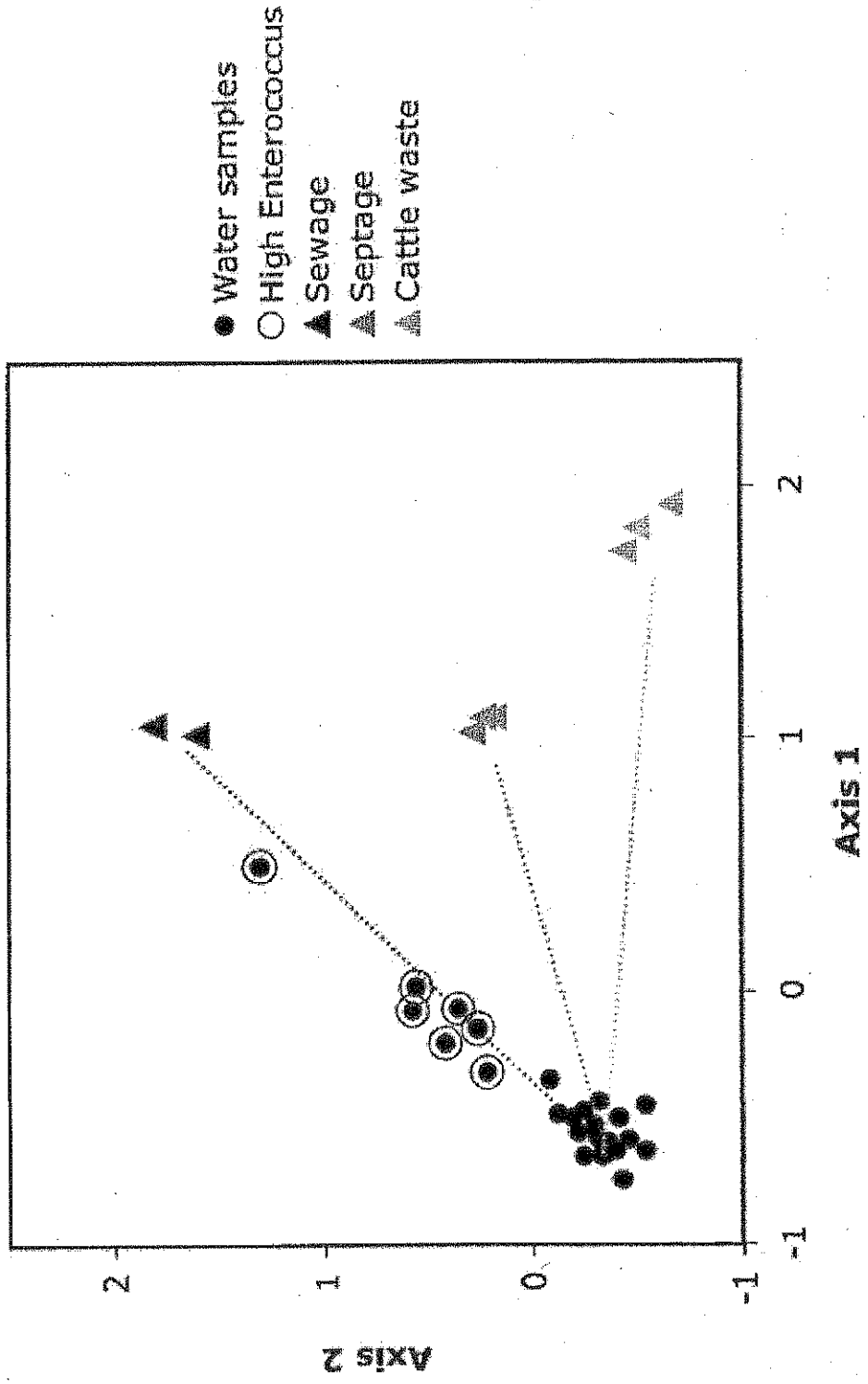
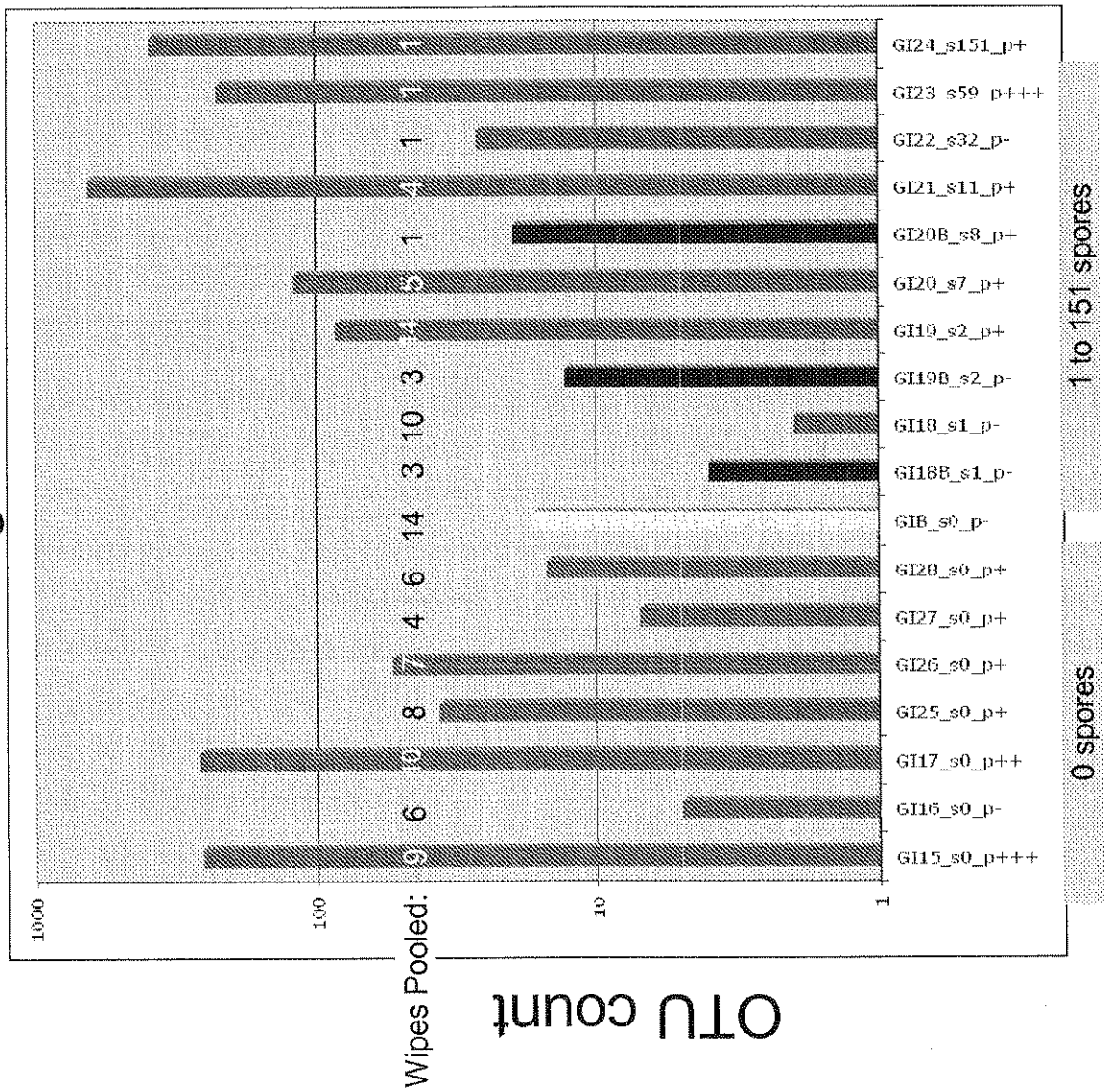

Water samples
High Enterococcus
Sewage
Septage
Cattle waste
Axis 2
Axis 1
2
1
0
-1
2
1
0
-1

Fig. 8


GI24_s151_p+
GI23_s59_p+++
GI22_s32_p-
GI21_s11_p+
GI20B_s8_p+
GI20_s7_p+
GI19_s2_p+
GI19B_s2_p-
GI18_s1_p-
GI18B_s1_p-
GIB_s0_p-
GI28_s0_p+
GI27_s0_p+
GI26_s0_p+
GI25_s0_p+
GI17_s0_p++
GI16_s0_p-
GI15_s0_p+++
1 to 151 spores
0 spores
1000
100
10
1
OTU count
Wipes Pooled:

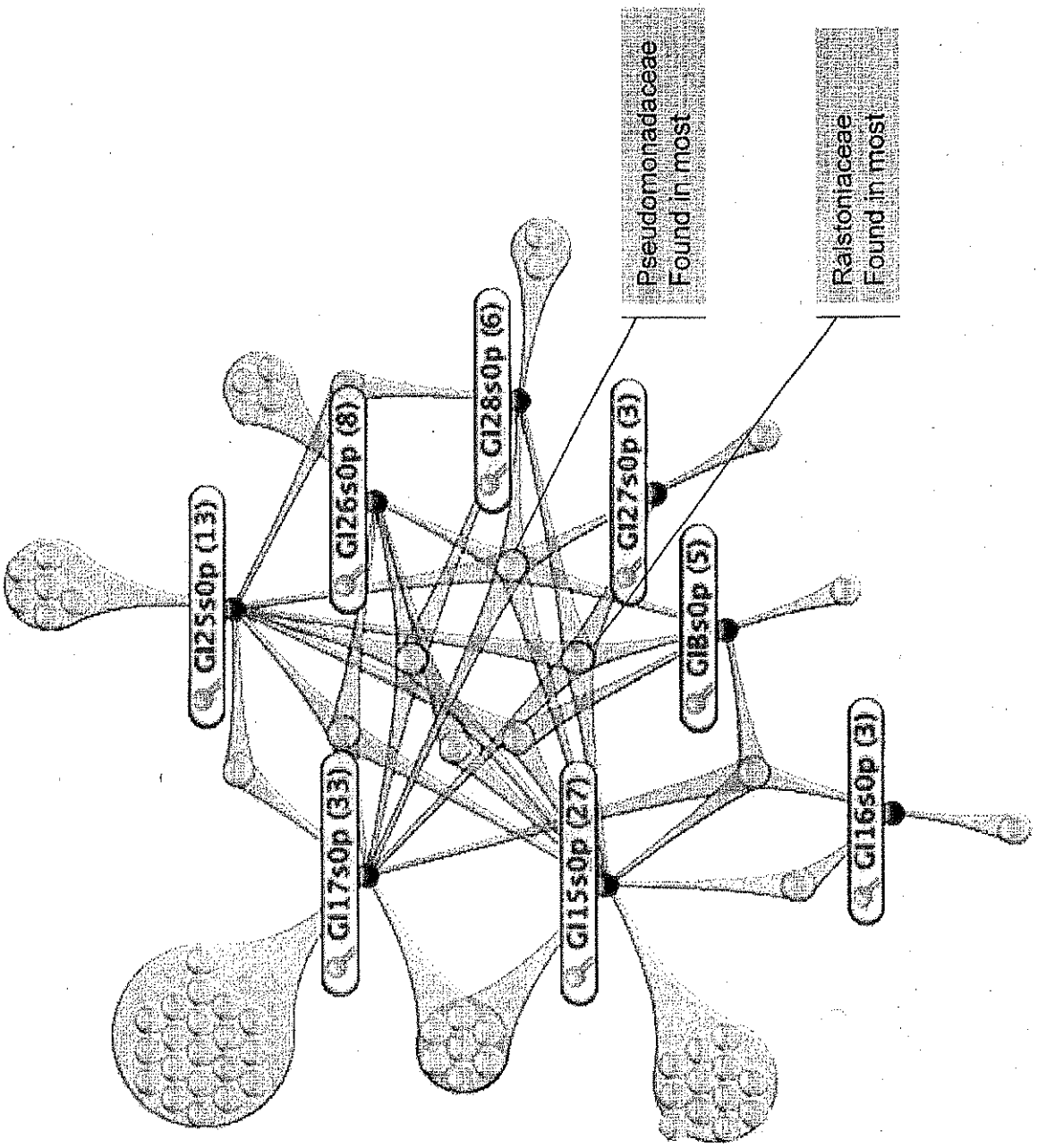

Pseudomonadaceae
Found in most
Ralstoniaceae
Found in most
Gl28s0p (6)
Gl26s0p (8)
Gl27s0p (3)
Gl25s0p (13)
Gl8s0p (5)
Gl17s0p (33)
Gl15s0p (27)
Gl16s0p (3)

Fig. 9

Fig10A

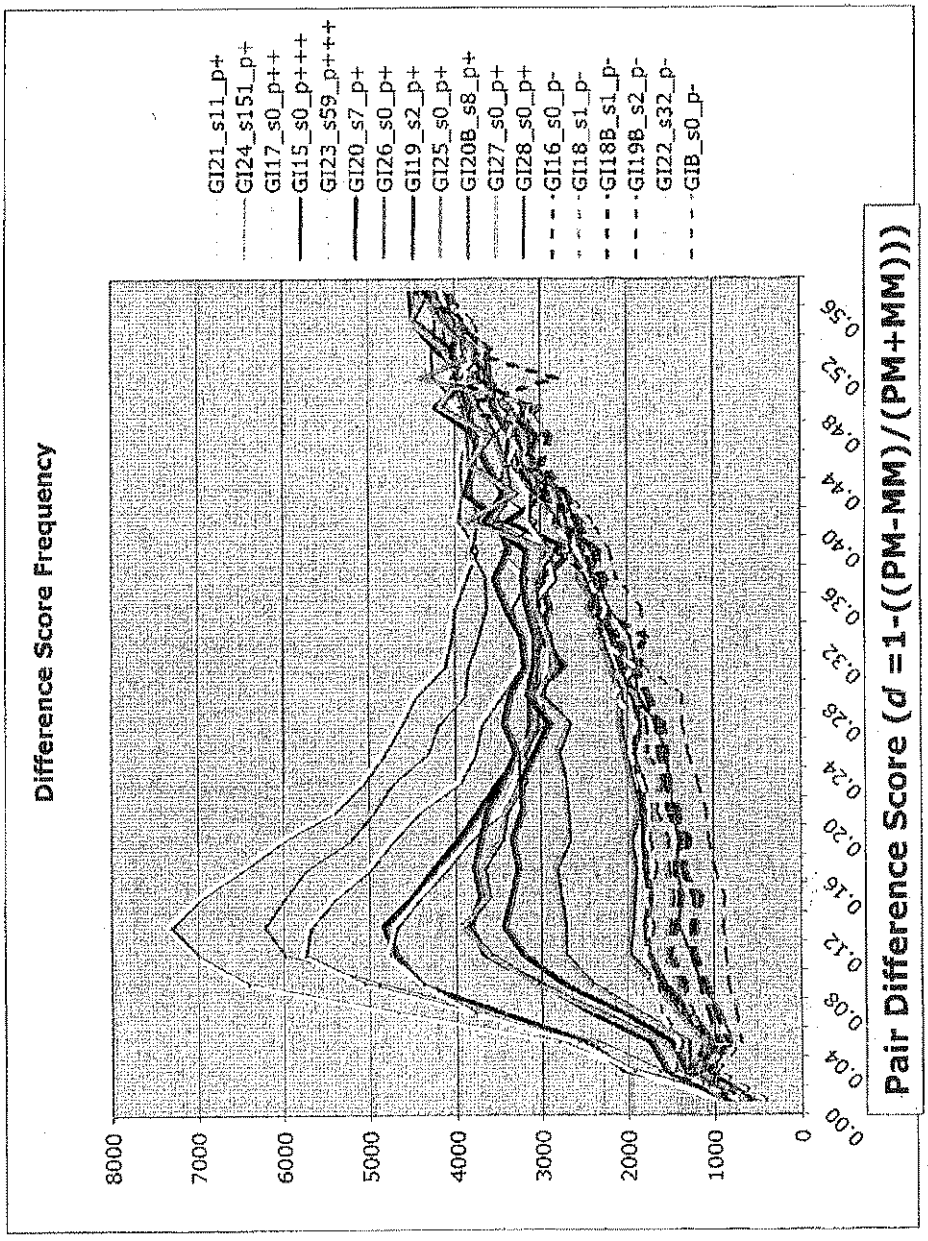

Difference Score Frequency
8000
7000
6000
5000
4000
3000
2000
1000
0
0.00
0.04
0.08
0.12
0.16
0.20
0.24
0.28
0.32
0.36
0.40
0.44
0.48
0.52
0.56
Pair Difference Score (d =1-((PM-MM)/(PM+MM)))
GI21_s11_p+
GI24_s151_p+
GI17_s0_p++
GI15_s0_p+++
GI23_s59_p+++
GI20_s7_p+
GI26_s0_p+
GI19_s2_p+
GI25_s0_p+
GI20B_s8_p+
GI27_s0_p+
GI28_s0_p+
GI16_s0_p-
GI18_s1_p-
GI18B_s1_p-
GI19B_s2_p-
GI22_s32_p-
GIB_s0_p-

Fig. 10B

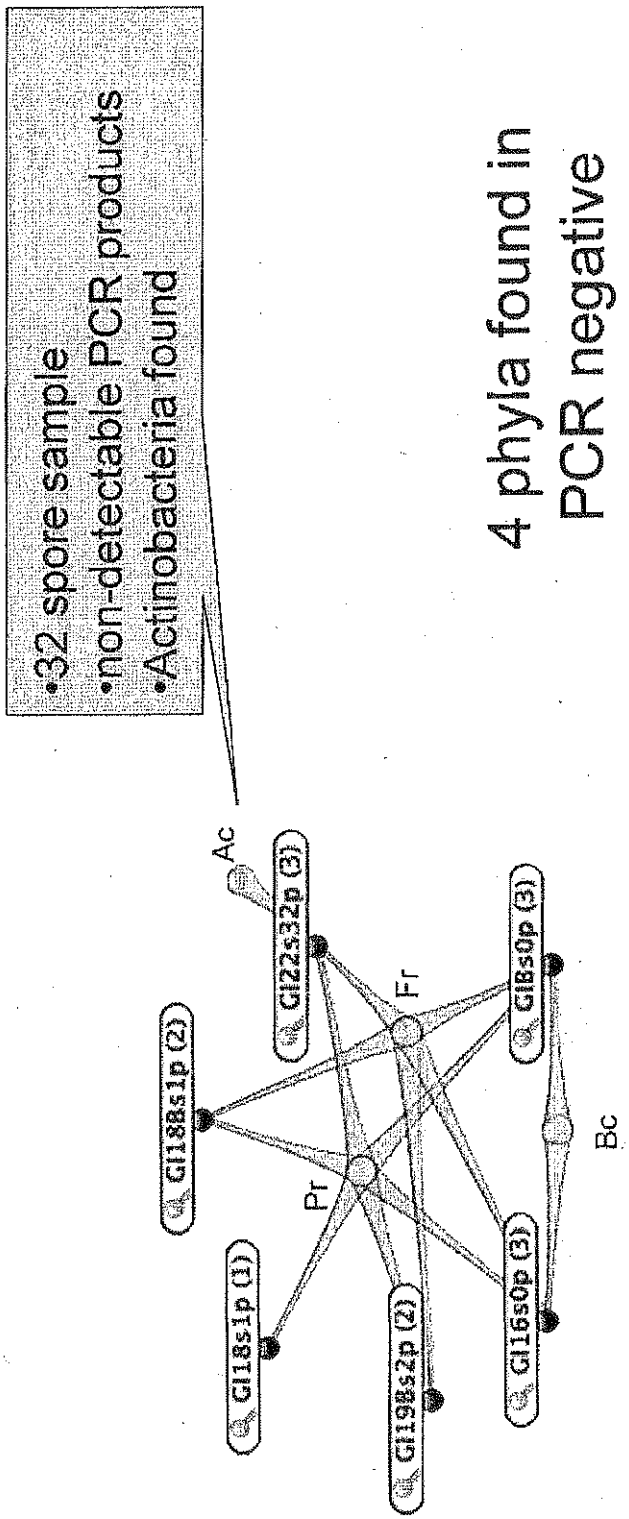

•32 spore sample
•non-defectable PCR products
•Actinobacteria found
4 phyla found in PCR negative samples
Gl18s1p (2)
Gl22s32p (3)
Gl18s1p (1)
Gl198s2p (2)
Gl16s0p (3)
Gl8s0p (3)
Ac
Fr
Pr
Bc
Pr: Proteobacteria Fr: Firmicutes Bc: Bacteroidetes AO: ABY1_OD1 Ac: Actinobacteria CyL Cyanobacteria Pl: Planctomycetes 49:49S1_2B_6

Figure 11 Faecalibacterium OTU 36742

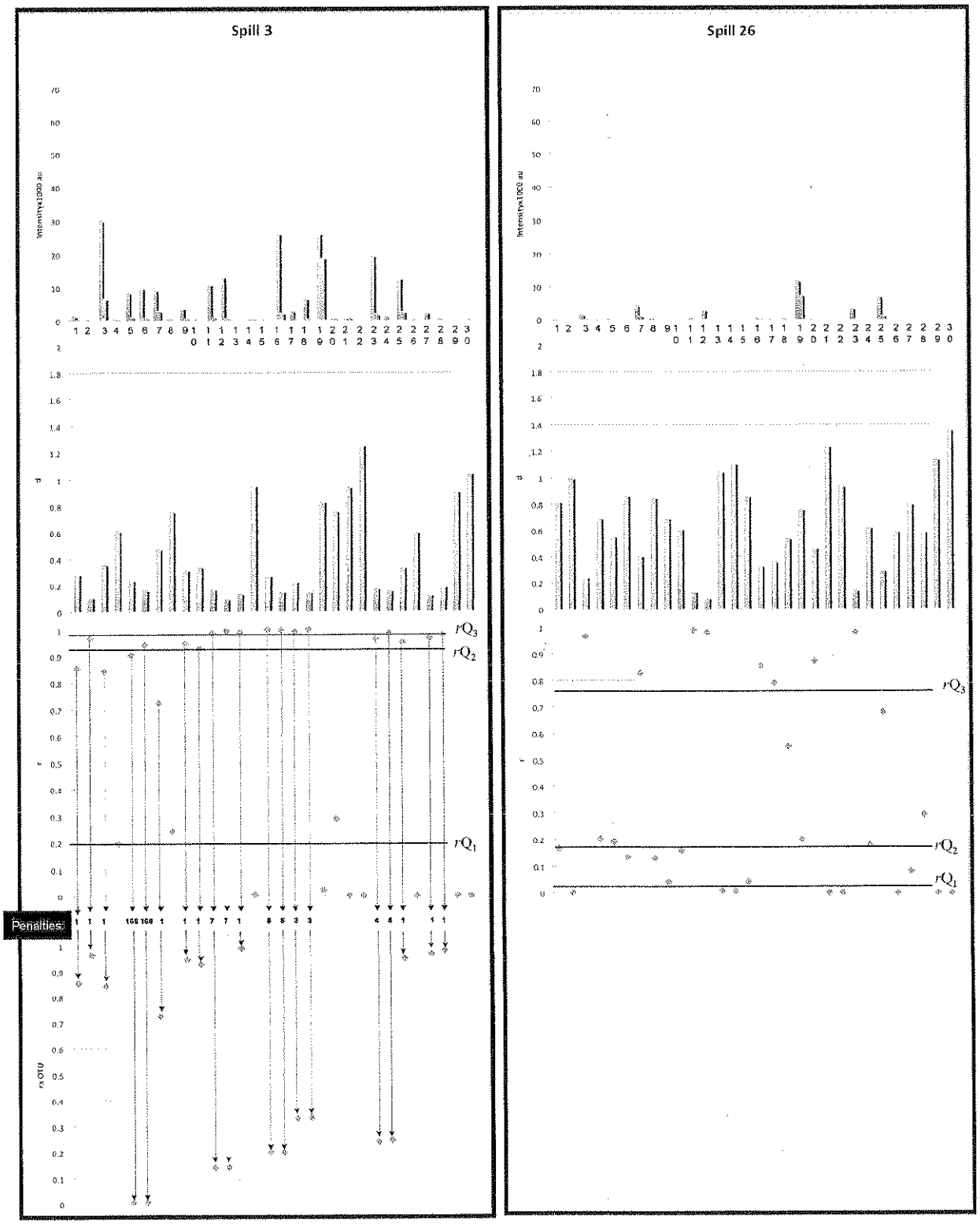


Figure 12 Ruminococcus OTU 38712

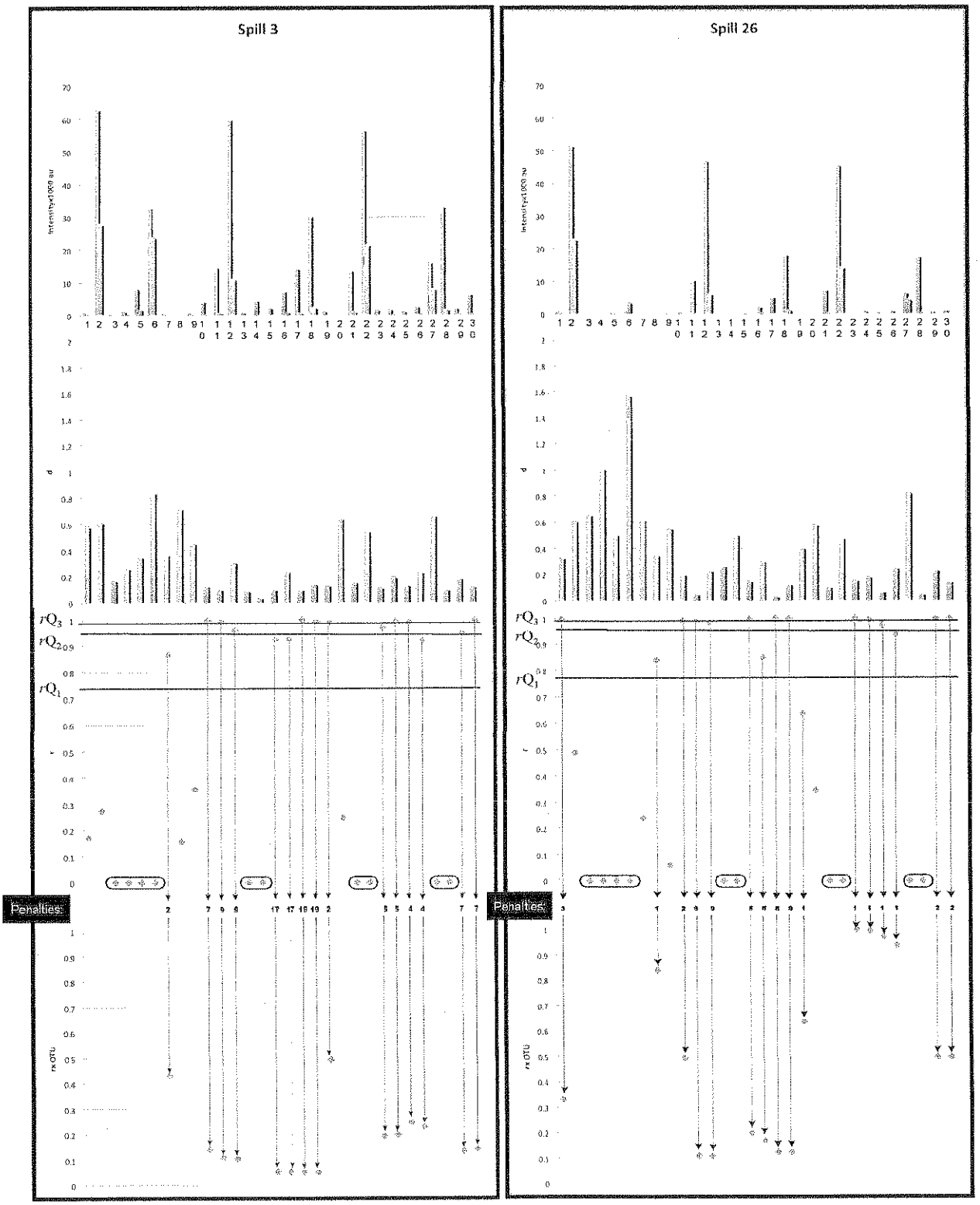


Fig. 13

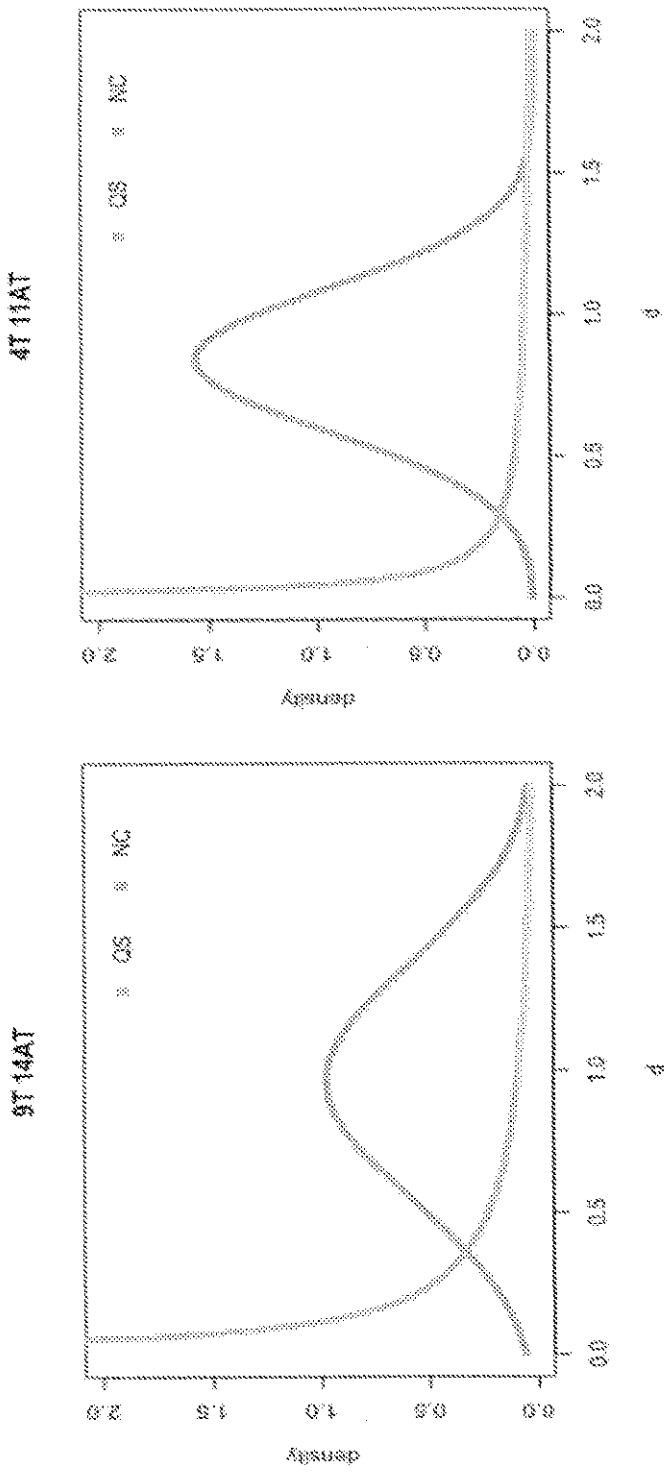


Fig. 14

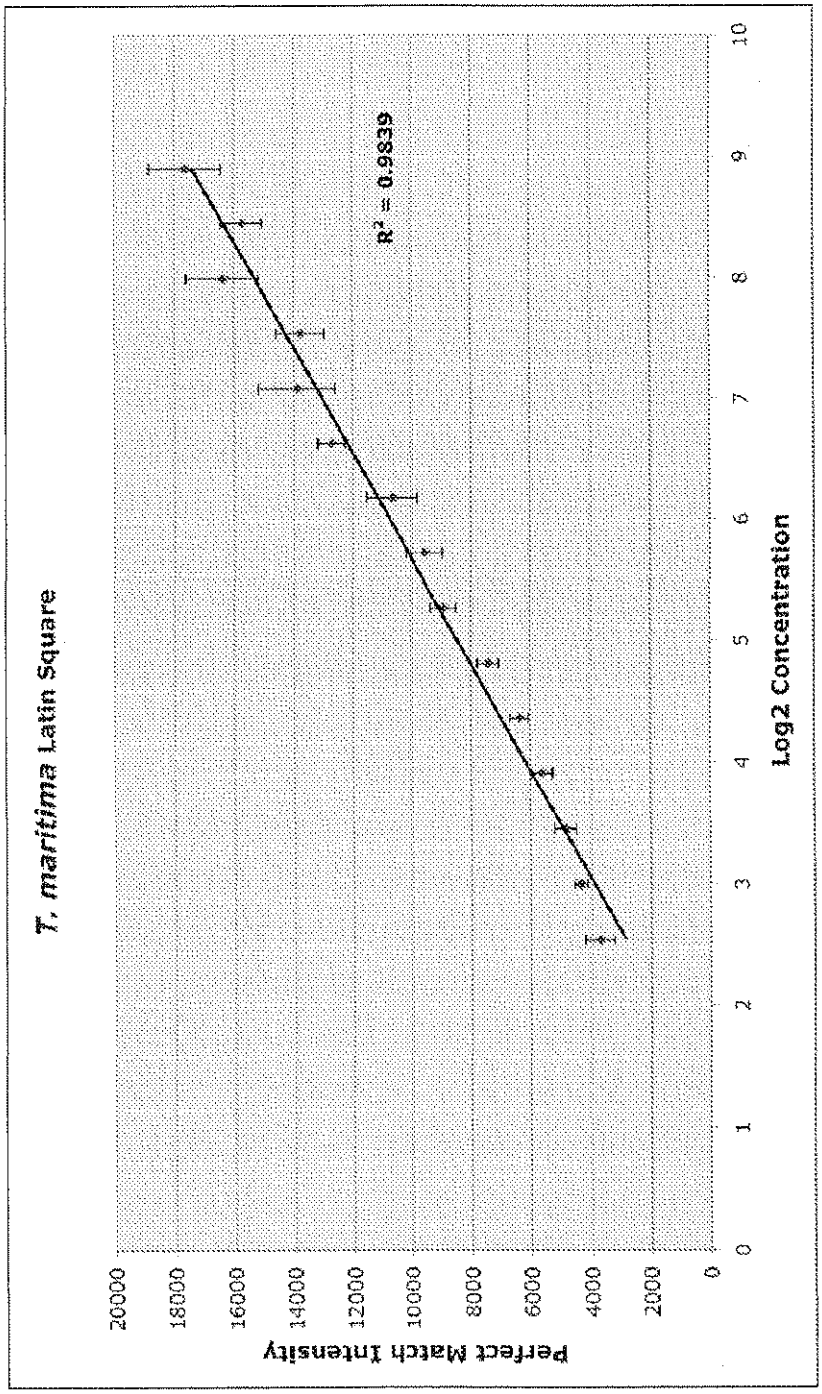

T. maritima Latin Square
R² = 0.9839
Perfect Match Intensity
Log2 Concentration
0
2000
4000
6000
8000
10000
12000
14000
16000
18000
20000
0
1
2
3
4
5
6
7
8
9
10

Fig. 15

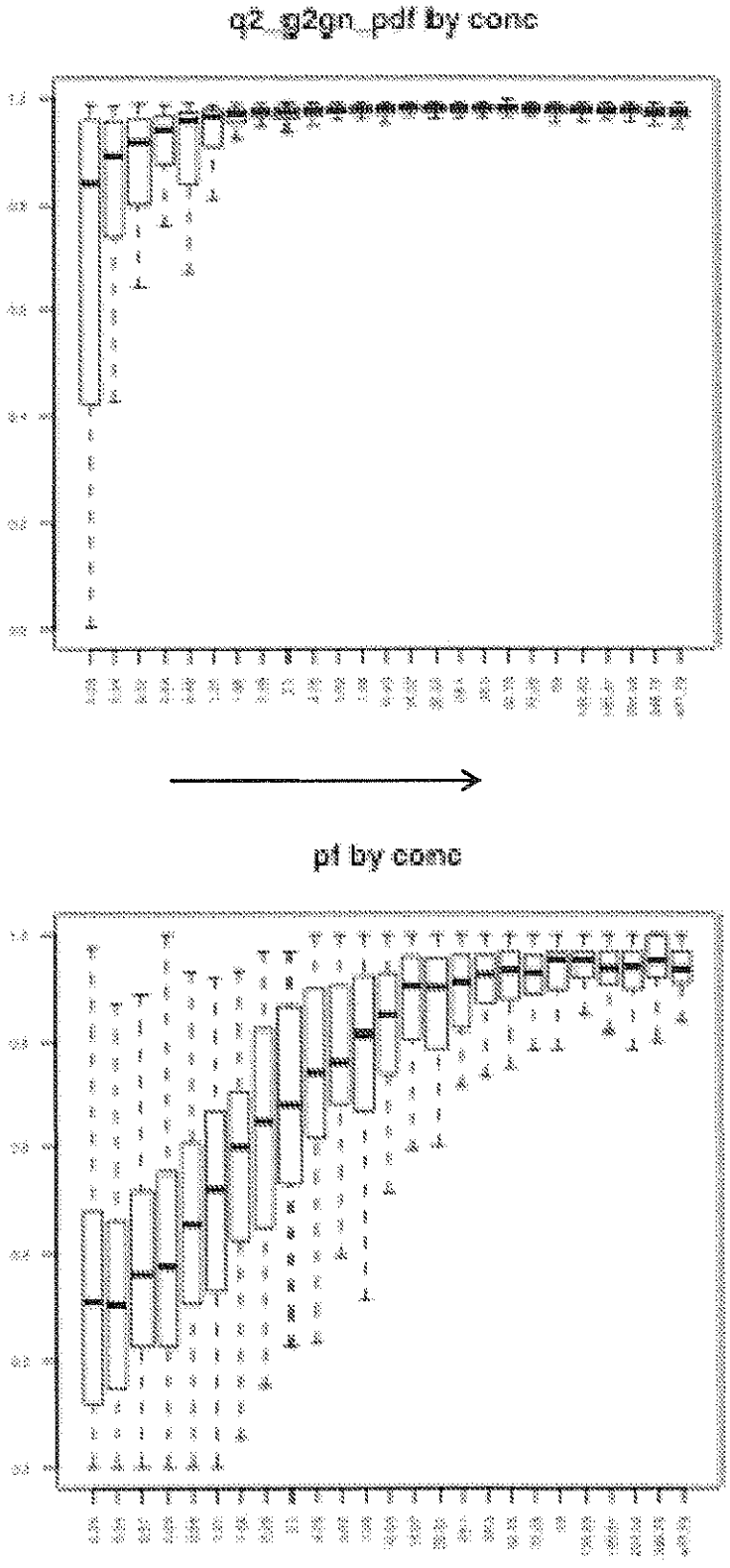


Fig. 16

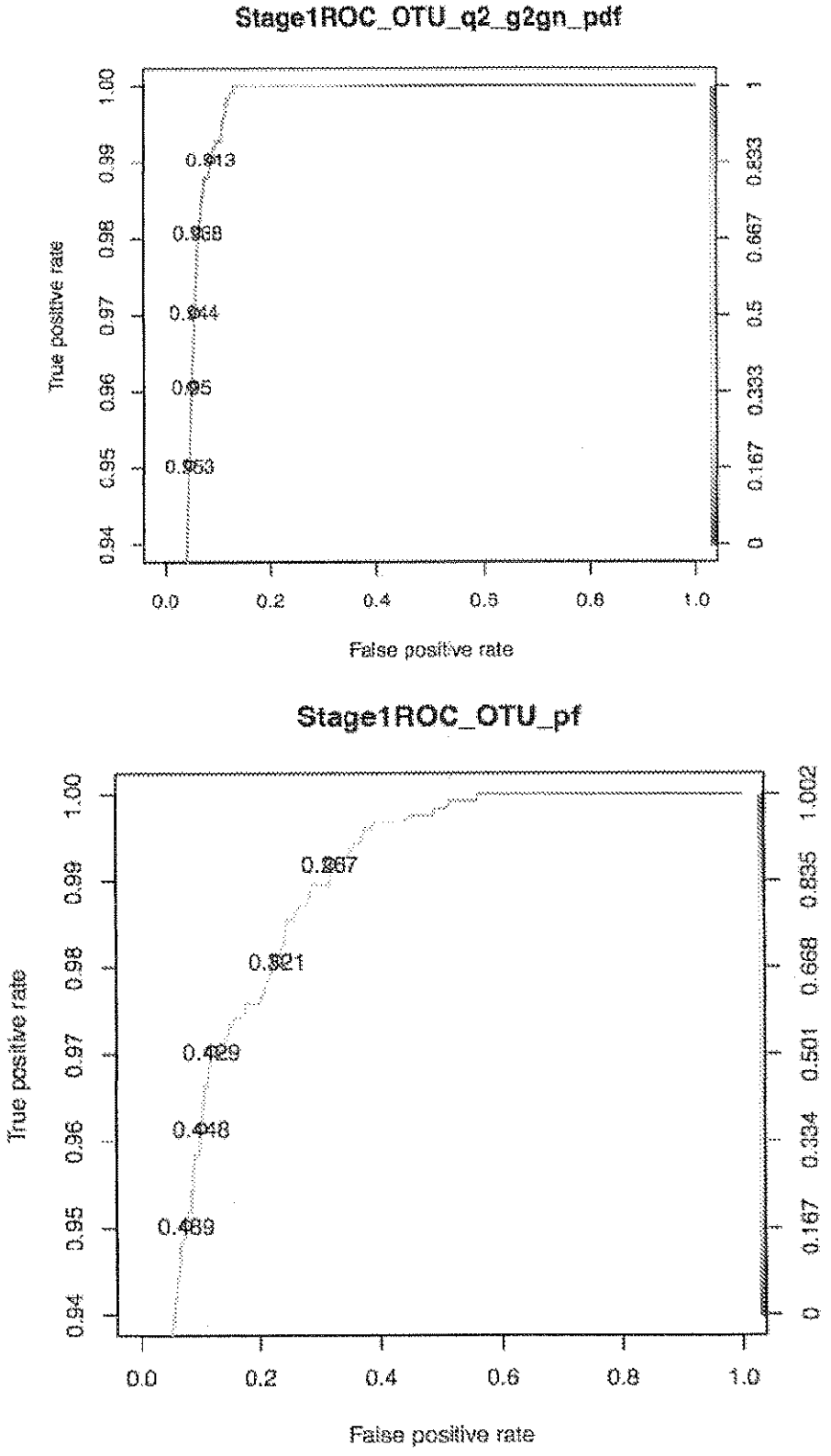

Stage1ROC_OTU_q2_g2gn_pdf
True positive rate
False positive rate
0.94
0.95
0.96
0.97
0.98
0.99
1.00
0.0
0.2
0.4
0.6
0.8
1.0
0.167
0.333
0.5
0.667
0.833
1
0.913
0.963
Stage1ROC_OTU_pf
True positive rate
False positive rate
0.94
0.95
0.96
0.97
0.98
0.99
1.00
0.0
0.2
0.4
0.6
0.8
1.0
0
0.167
0.334
0.501
0.668
0.835
1.002
0.429
0.469

Fig. 17

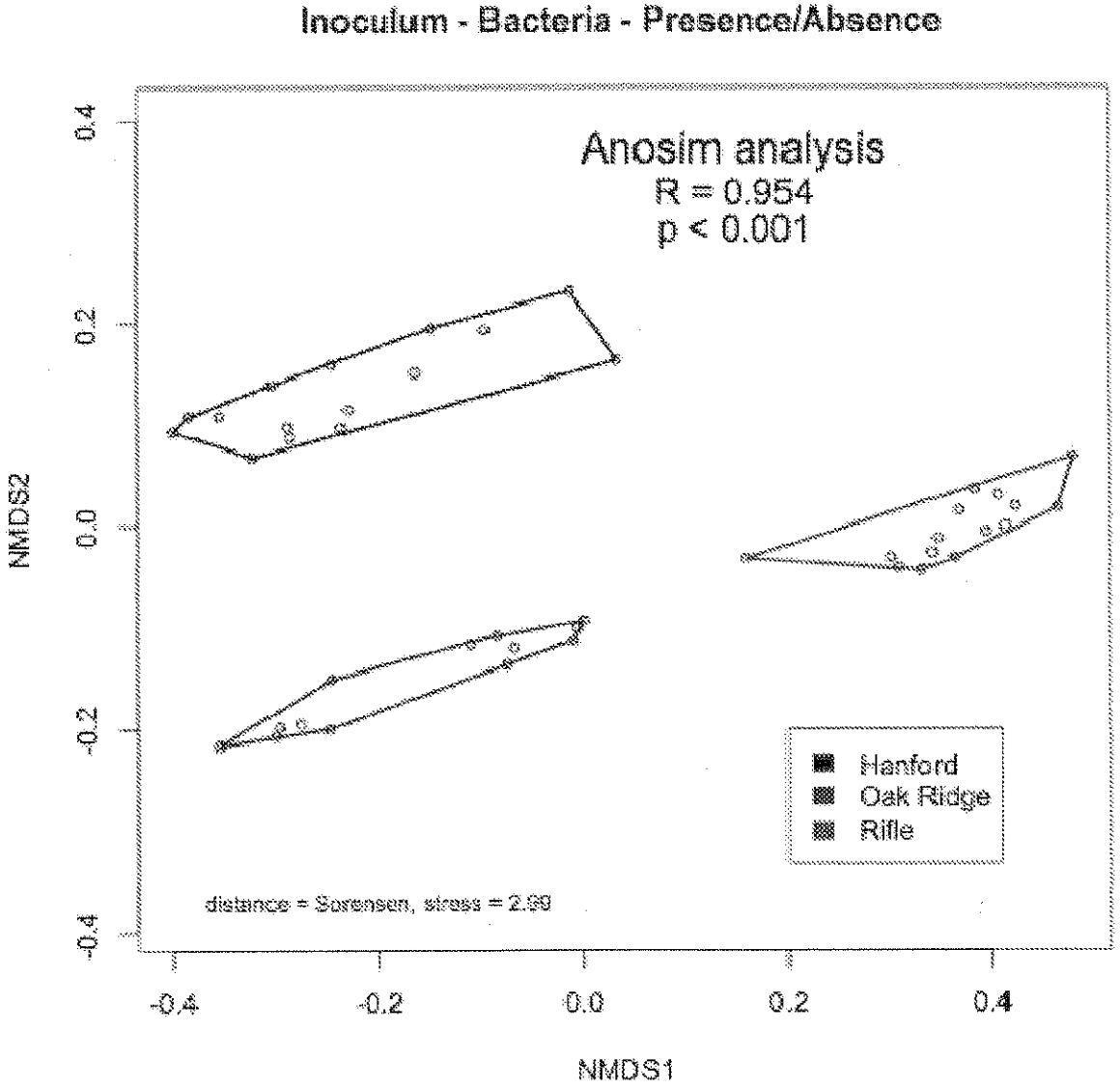

Inoculum - Bacteria - Presence/Absence
Anosim analysis
R = 0.954
p < 0.001
Hanford
Oak Ridge
Rifle
distance = Sorensen, stress = 2.99
NMDS1
NMDS2
-0.4
-0.2
0.0
0.2
0.4

Fig. 18

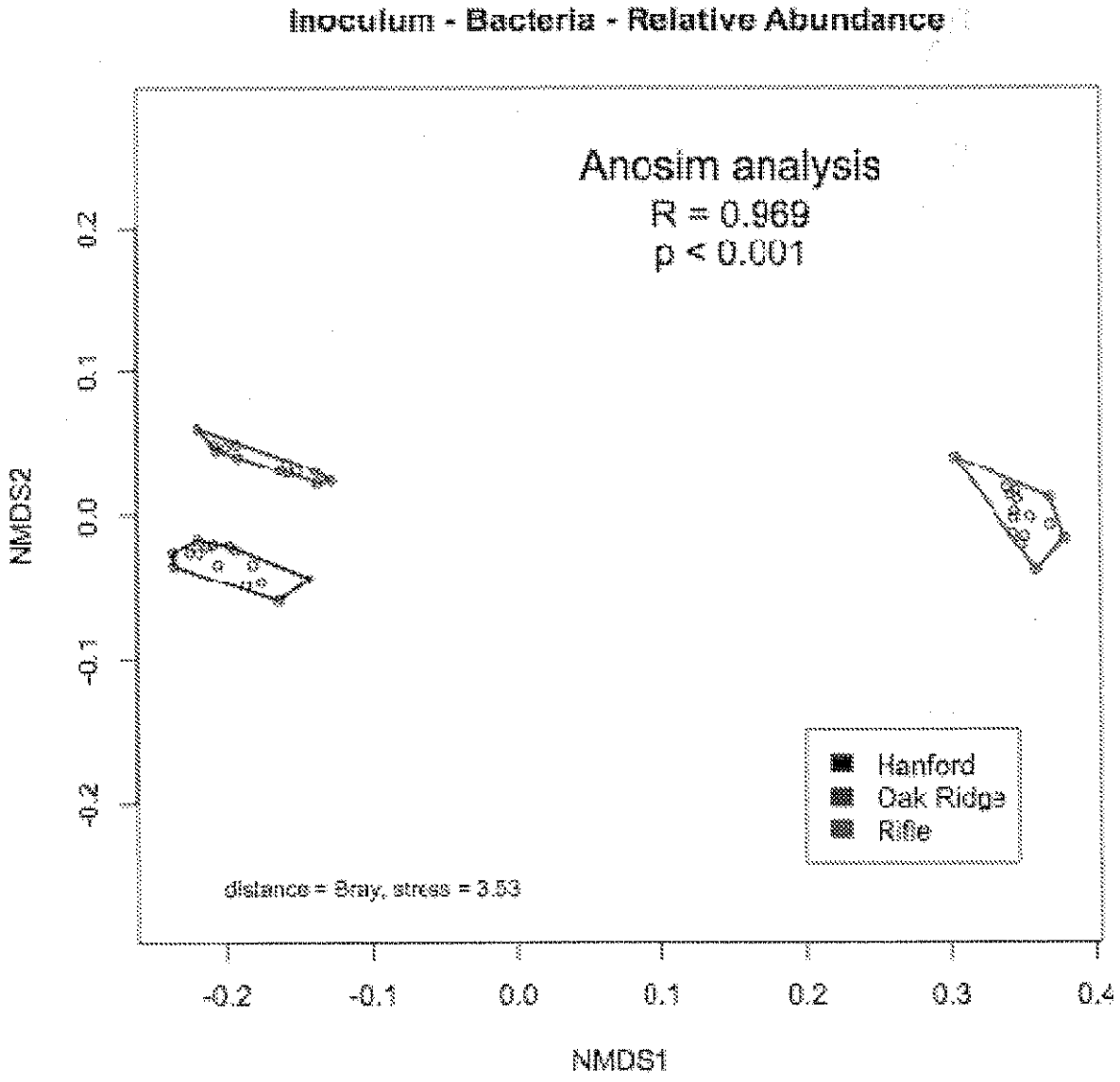

Inoculum - Bacteria - Relative Abundance
Anosim analysis
R = 0.969
p < 0.001
Hanford
Oak Ridge
Rifle
distance = Bray, stress = 3.53
NMDS1
NMDS2
-0.2
-0.1
0.0
0.1
0.2
0.3
0.4

Figure 19

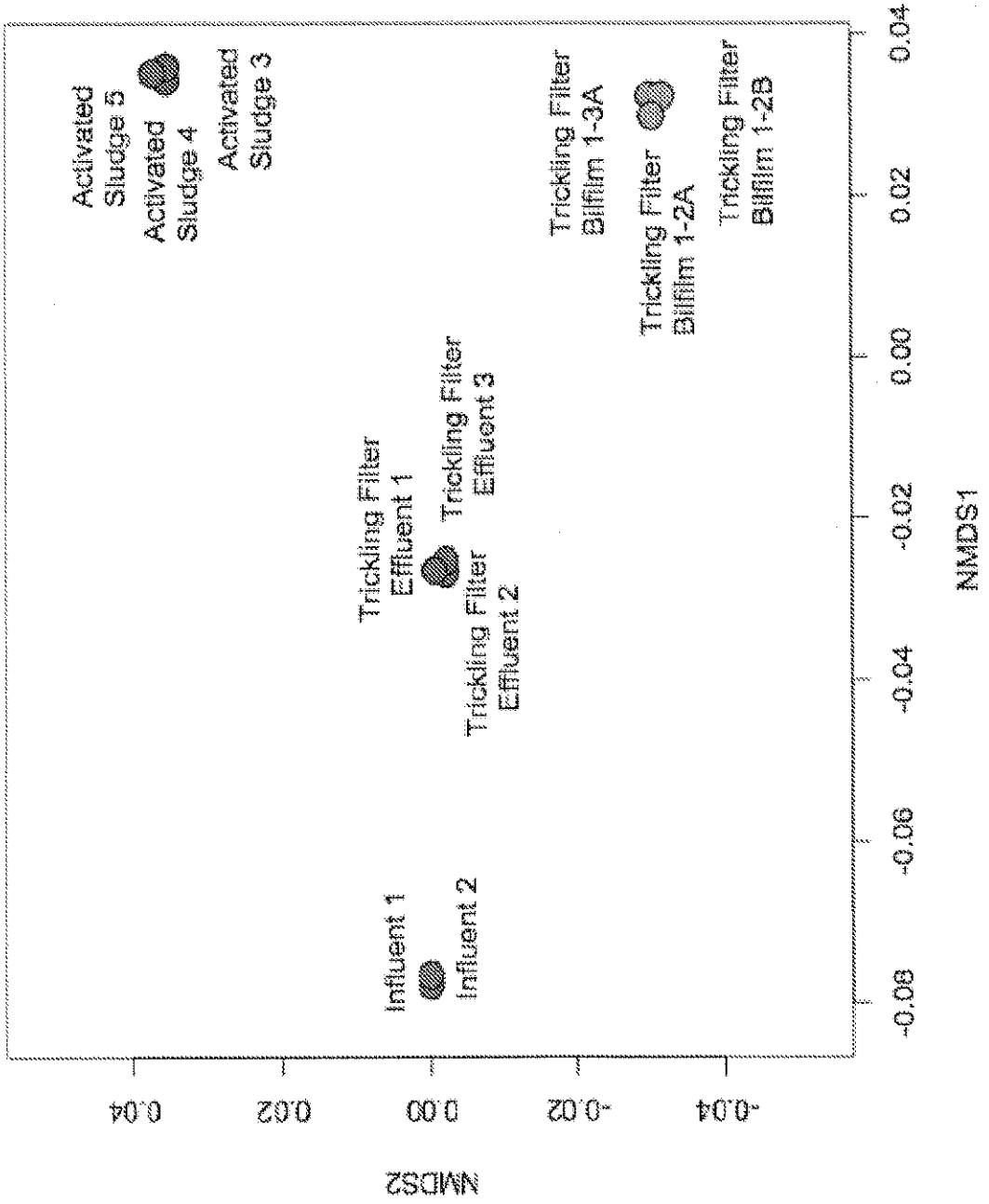

Activated Sludge 5
Activated Sludge 4
Activated Sludge 3
Trickling Filter Biffilm 1-3A
Trickling Filter Biffilm 1-2A
Trickling Filter Biffilm 1-2B
Trickling Filter Effluent 1
Trickling Filter Effluent 3
Trickling Filter Effluent 2
Influent 1
Influent 2
NMDS1
NMDS2
-0.08
-0.06
-0.04
-0.02
0.00
0.02
0.04

Figure 20

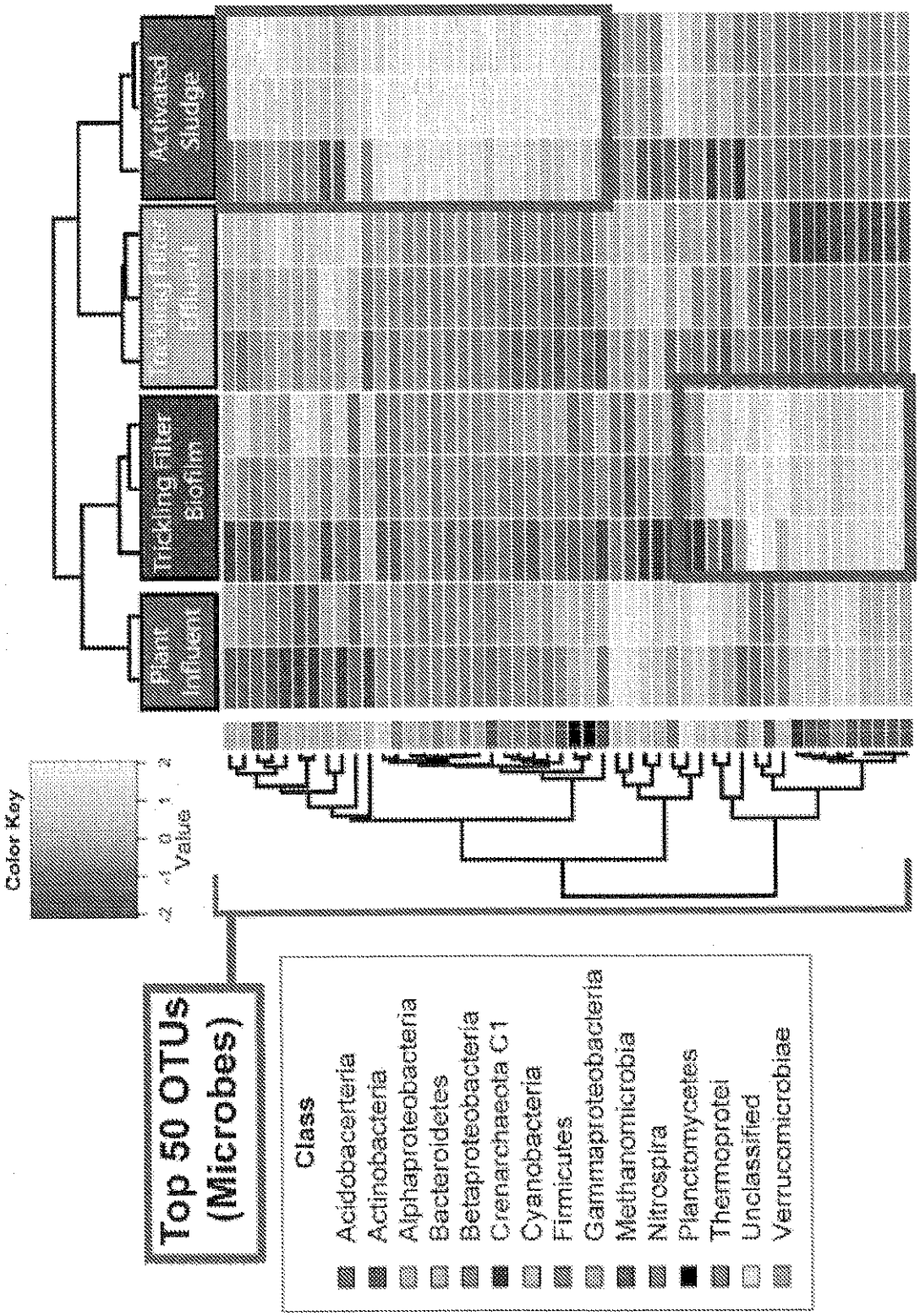

Top 50 OTUs (Microbes)
Color Key
Value
Plant Influent
Trickling Filter Biofilm
Activated Sludge
Class
Acidobacteriia
Actinobacteria
Alphaproteobacteria
Bacteroidetes
Betaproteobacteria
Crenarchaeota C1
Cyanobacteria
Firmicutes
Gammaproteobacteria
Methanomicrobia
Nitrospira
Planctomycetes
Thermoprotei
Unclassified
Verrucomicrobiae

Figure 21

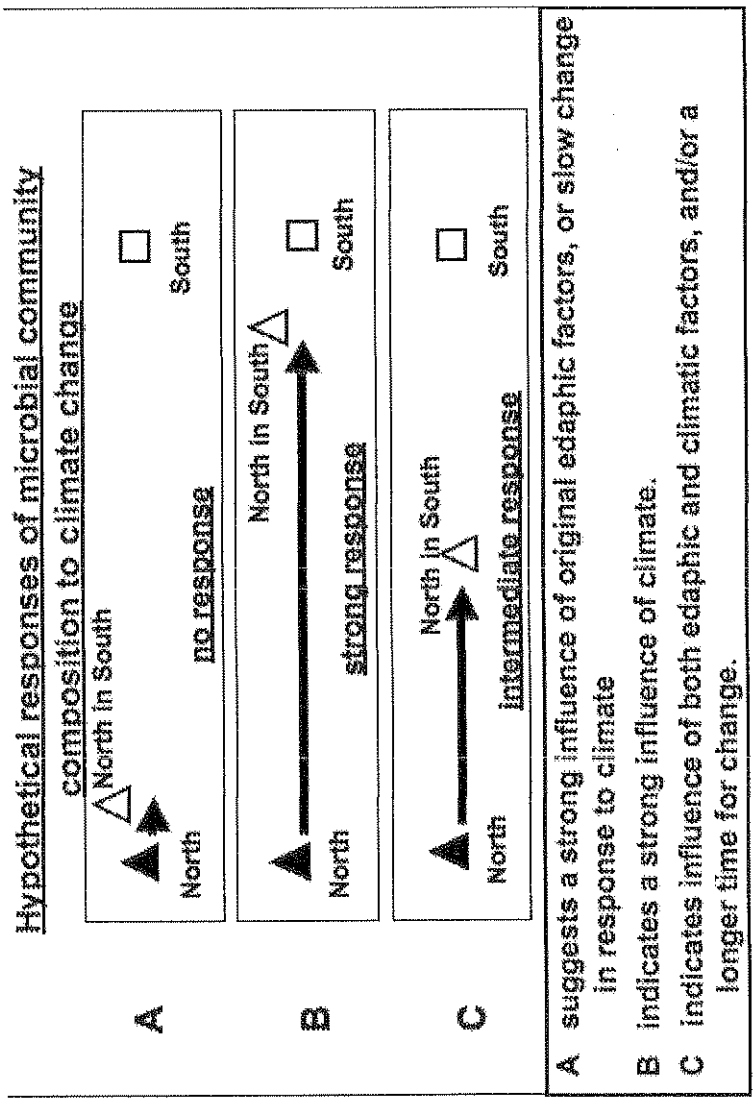

Hypothetical responses of microbial community composition to climate change
A
North in South
North
South
no response
B
North in South
North
South
strong response
C
North in South
North
South
intermediate response
A suggests a strong influence of original edaphic factors, or slow change in response to climate
B indicates a strong influence of climate.
C indicates influence of both edaphic and climatic factors, and/or a longer time for change.

Figure 22

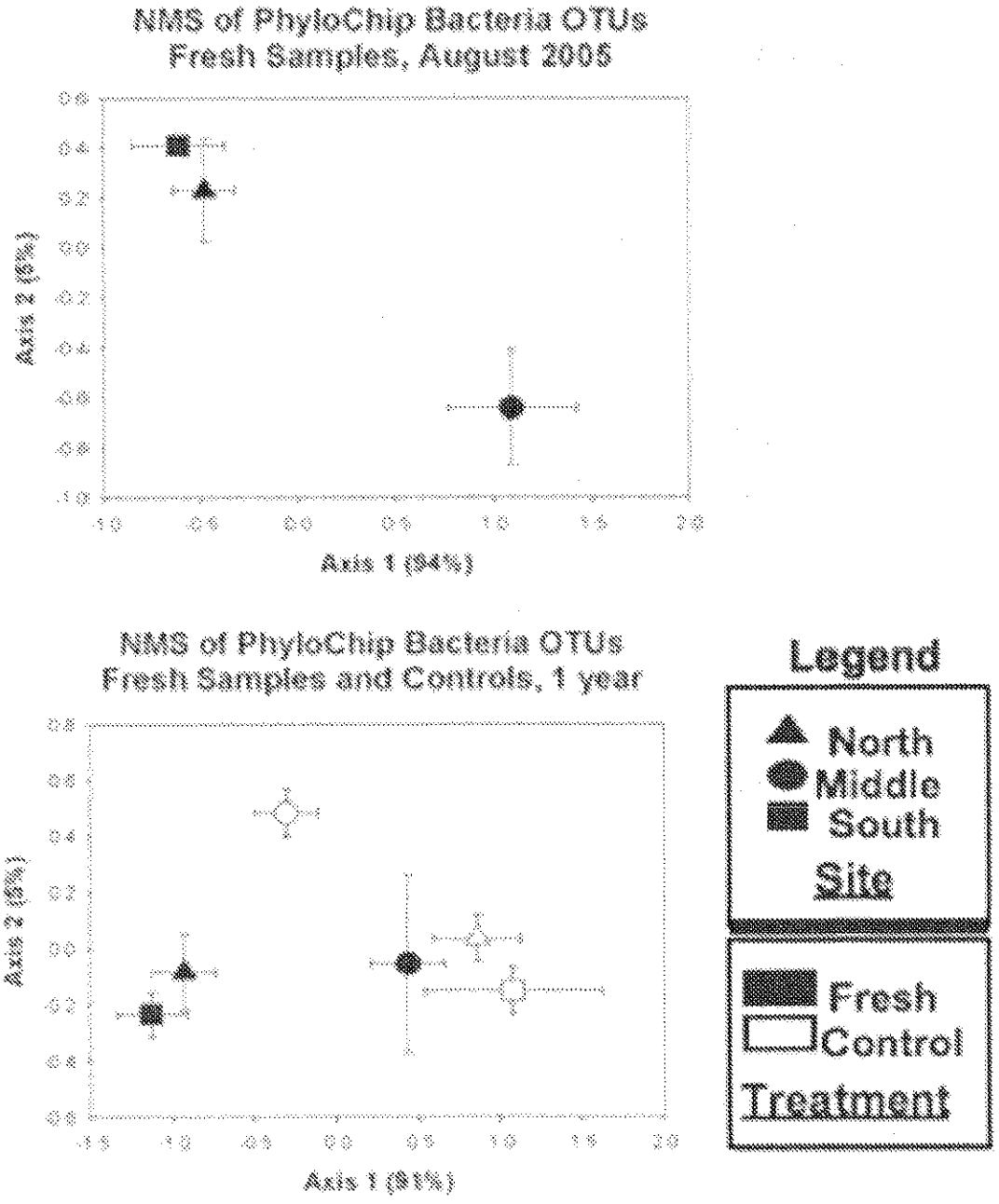

NMS of PhyloChip Bacteria OTUs
Fresh Samples, August 2005
Axis 2 (6%)
Axis 1 (94%)
NMS of PhyloChip Bacteria OTUs
Fresh Samples and Controls, 1 year
Axis 2 (6%)
Axis 1 (91%)
Legend
North
Middle
South
Site
Fresh
Control
Treatment

Figure 23

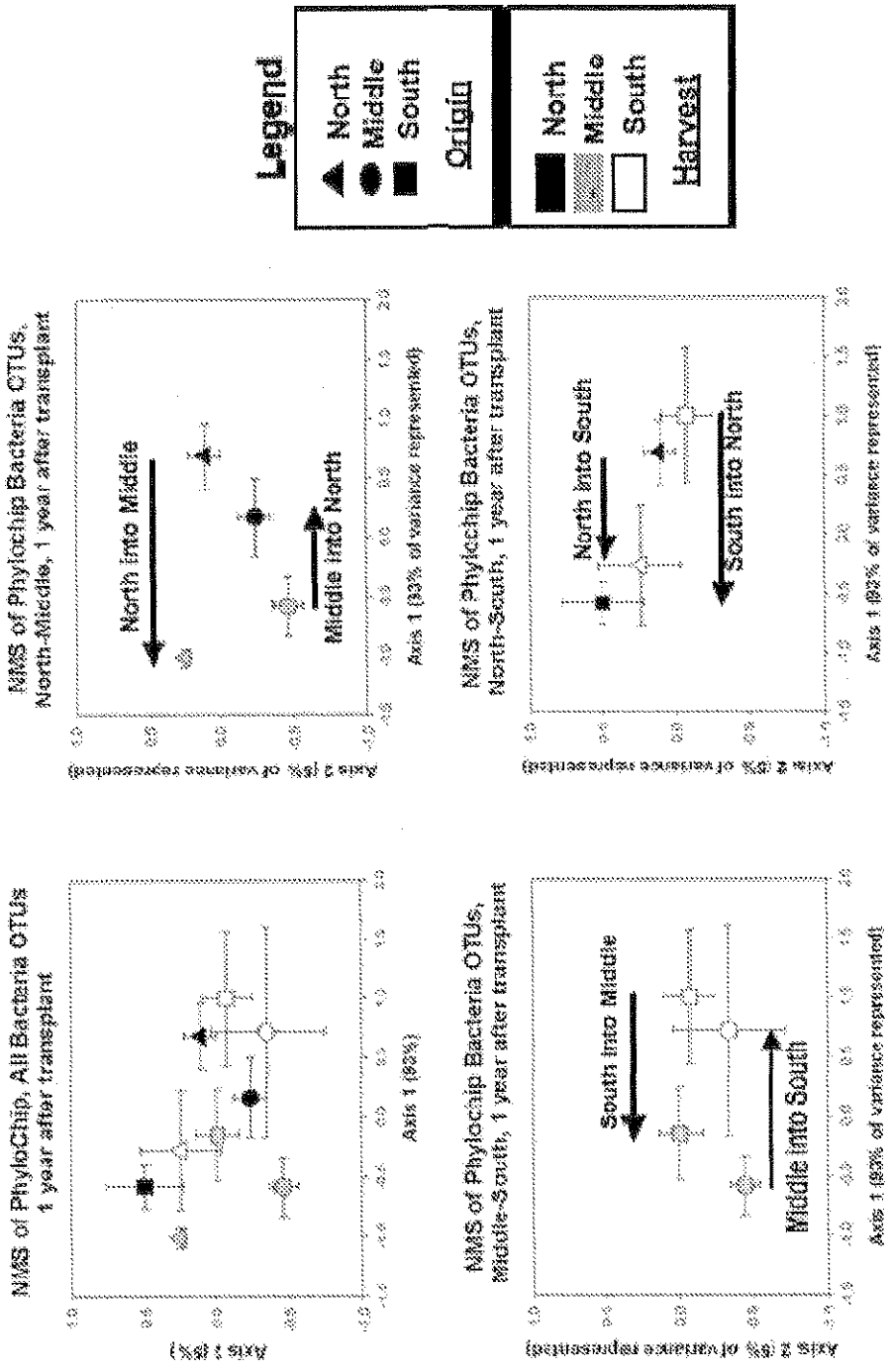

Legend
North
Middle
South
Origin
North
Middle
South
Harvest
NMS of PhyloChip, All Bacteria OTUs
1 year after transplant
Axis 1 (82%)
Axis 2 (8%)
MMS of Phylochip Bacteria OTUs,
North-Middle, 1 year after transplant
North into Middle
Middle into North
Axis 1 (83% of variance represented)
Axis 2 (8% of variance represented)
MMS of Phylochip Bacteria OTUs,
North-South, 1 year after transplant
North into South
South into North
Axis 1 (82% of variance represented)
Axis 2 (8% of variance represented)
MMS of Phylochip Bacteria OTUs,
Middle-South, 1 year after transplant
South into Middle
Middle into South
Axis 1 (83% of variance represented)
Axis 2 (8% of variance represented)

Figure 24

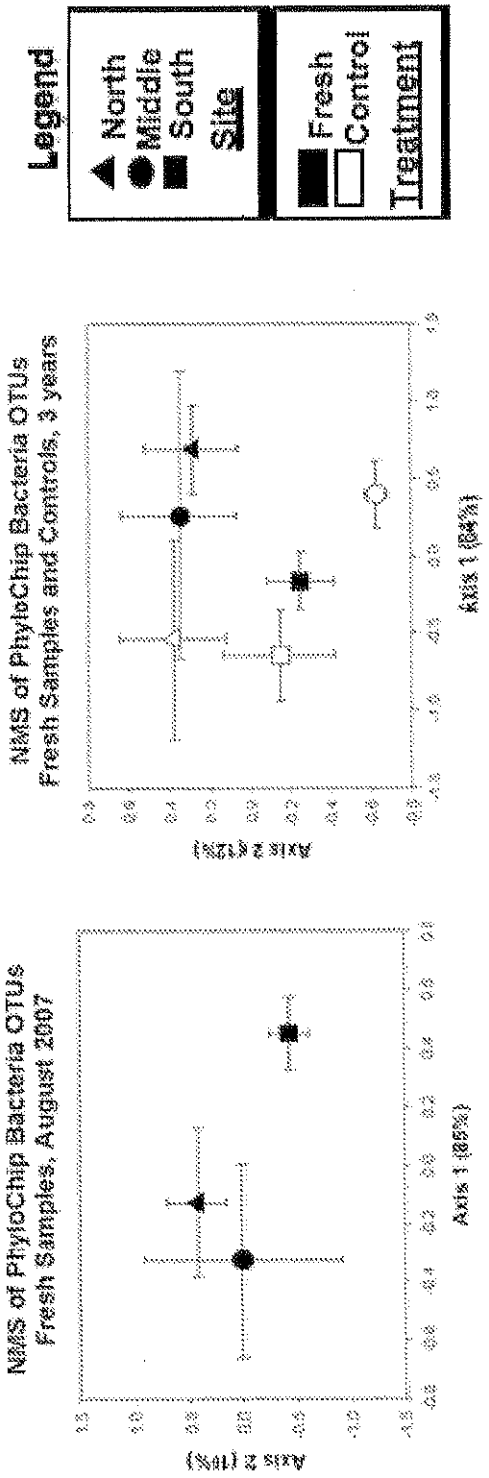

NMS of PhyloChip Bacteria OTUs
Fresh Samples, August 2007
Axis 2 (11%)
Axis 1 (85%)
NMS of PhyloChip Bacteria OTUs
Fresh Samples and Controls, 3 years
Axis 2 (12%)
Axis 1 (84%)
Legend
North
Middle
South
Site
Fresh
Control
Treatment

Figure 25

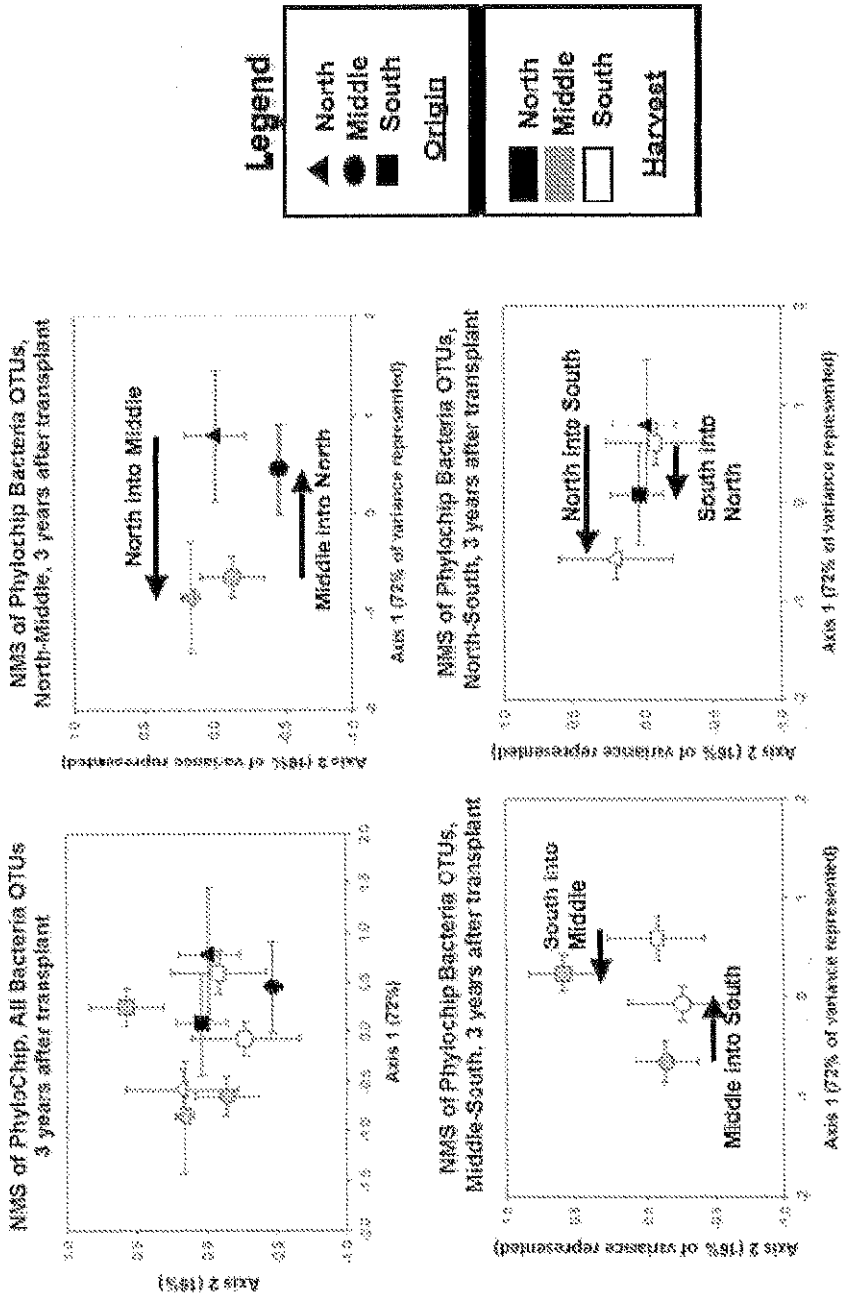

Legend
North
Middle
South
Origin
North
Middle
South
Harvest
MMS of PhyloChip, All Bacteria OTUs
3 years after transplant
Axis 2 (18%)
Axis 1 (72%)
MMS of Phylochip Bacteria OTUs,
North-Middle, 3 years after transplant
North into Middle
Middle into North
Axis 2 (18% of variance represented)
Axis 1 (72% of variance represented)
MMS of Phylochip Bacteria OTUs,
North-South, 3 years after transplant
North into South
South into North
Axis 2 (18% of variance represented)
Axis 1 (72% of variance represented)
MMS of Phylochip Bacteria OTUs,
Middle-South, 2 years after transplant
South into Middle
Middle into South
Axis 2 (18% of variance represented)
Axis 1 (72% of variance represented)

Figure 26

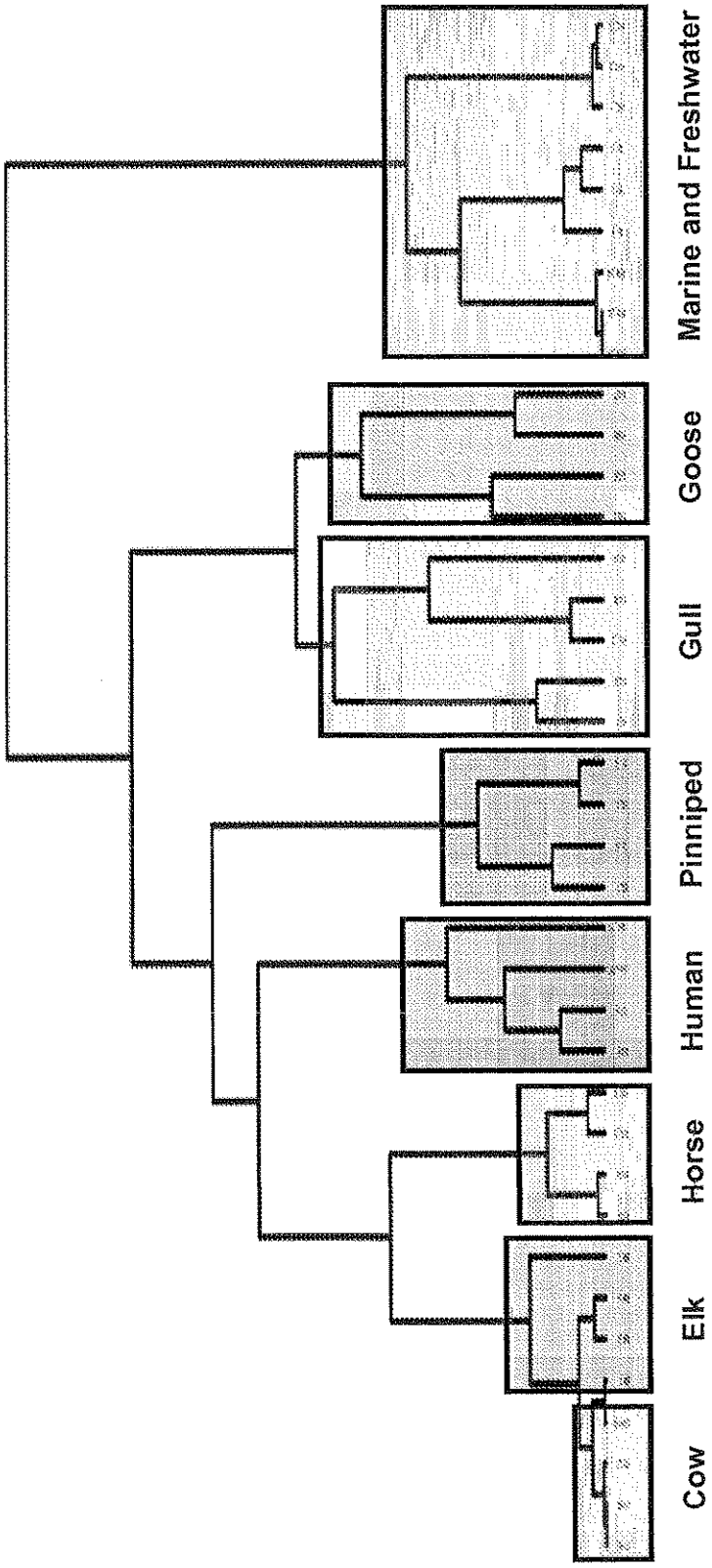

Marine and Freshwater
Goose
Gull
Pinniped
Human
Horse
Elk
Cow

Figure 27

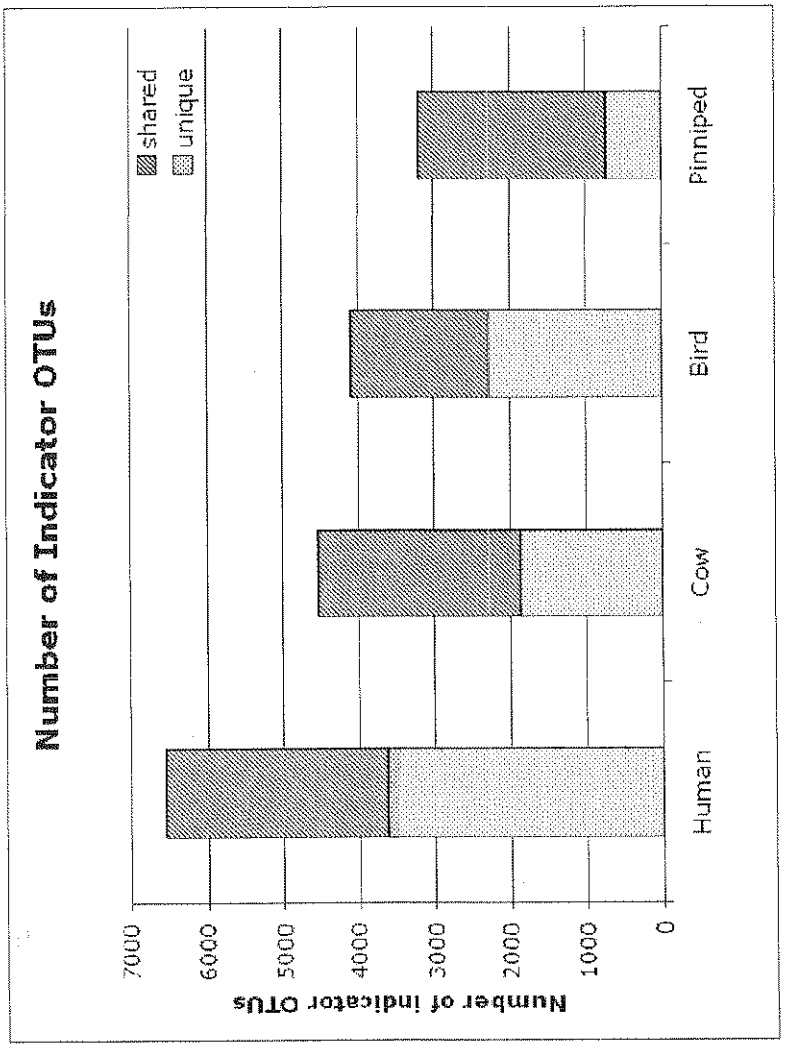

Number of Indicator OTUs
shared
unique
Number of indicator OTUs
7000
6000
5000
4000
3000
2000
1000
0
Human
Cow
Bird
Pinniped

Figure 28

Compare indicator communities with elevated OTUs from each sample

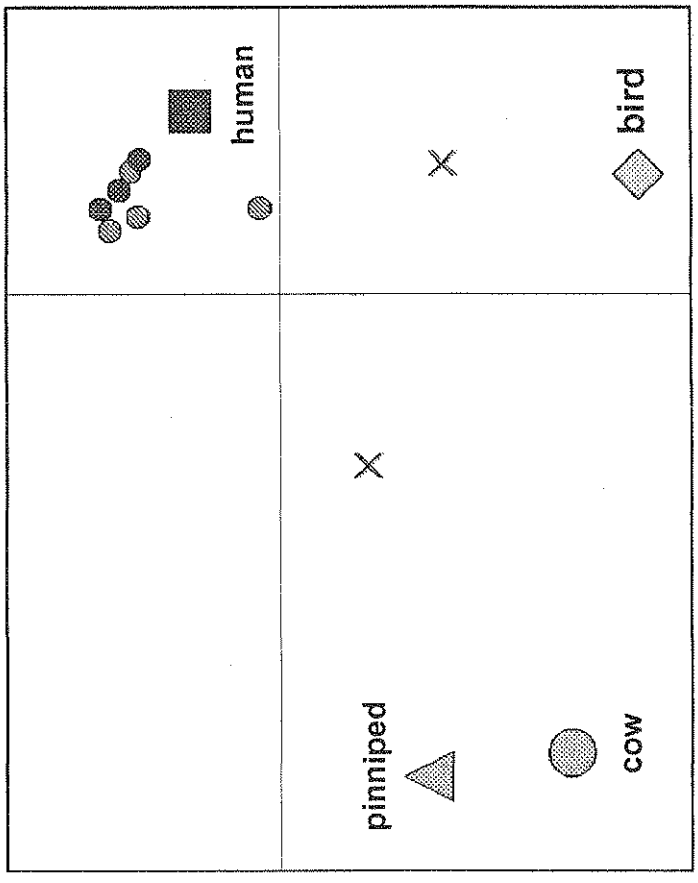


Figure 29

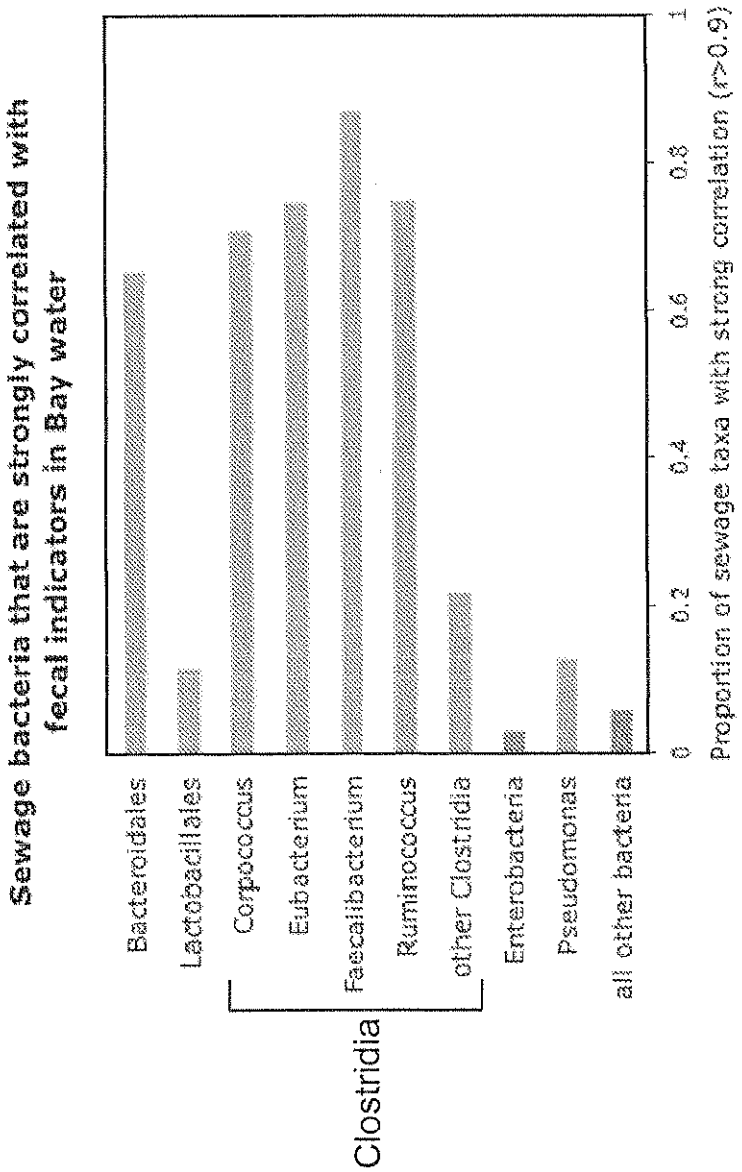
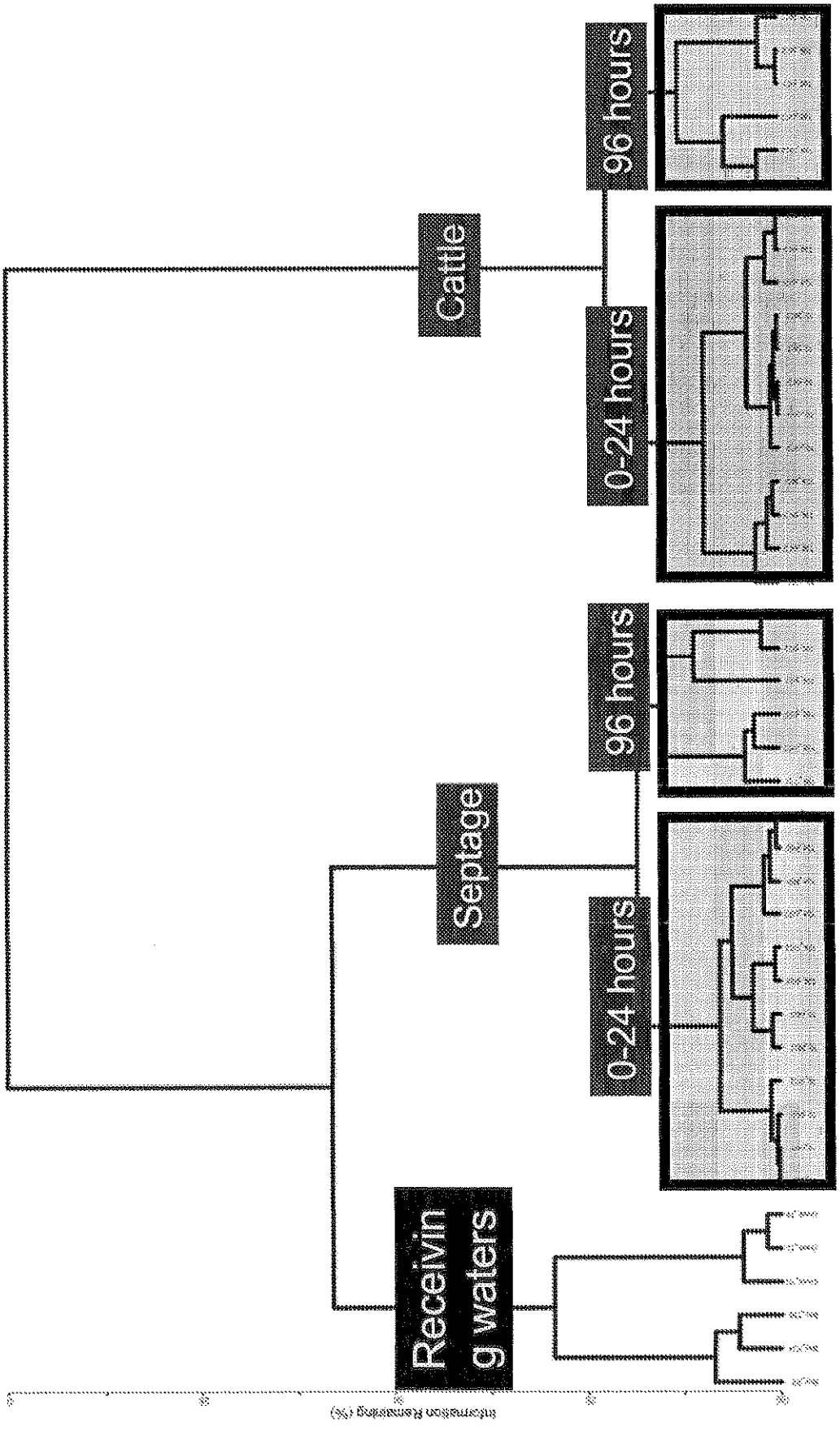

Sewage bacteria that are strongly correlated with fecal indicators in Bay water
Bacteroidales
Lactobacillales
Clostridia
Corpococcus
Eubacterium
Fascalibacterium
Ruminococcus
other Clostridia
Enterobacteria
Pseudomonas
all other bacteria
0
0.2
0.4
0.6
0.8
1
Proportion of sewage taxa with strong correlation (r>0.9)

Figure 30


Cattle
96 hours
0-24 hours
Septage
96 hours
0-24 hours
Receiving waters
Information Remaining (%)

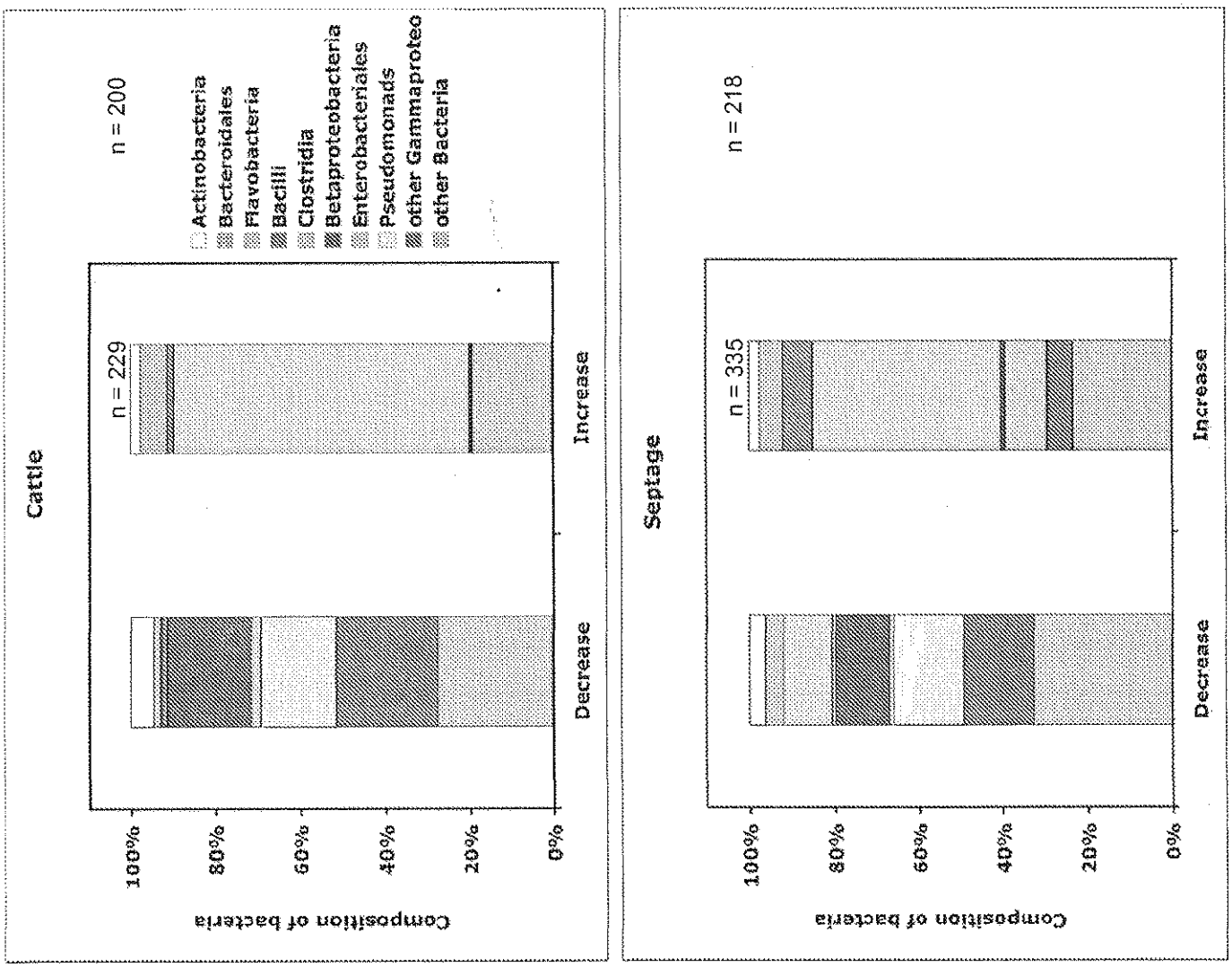

Cattle
n = 200
n = 229
Actinobacteria
Bacteroidales
Flavobacteria
Bacilli
Clostridia
Betaproteobacteria
Enterobacteriales
Pseudomonads
other Gammaproteo
other Bacteria
Composition of bacteria
100%
80%
60%
40%
20%
0%
Decrease
Increase
Septage
n = 218
n = 335
Composition of bacteria
100%
80%
60%
40%
20%
0%
Decrease
Increase

FIGURE 31

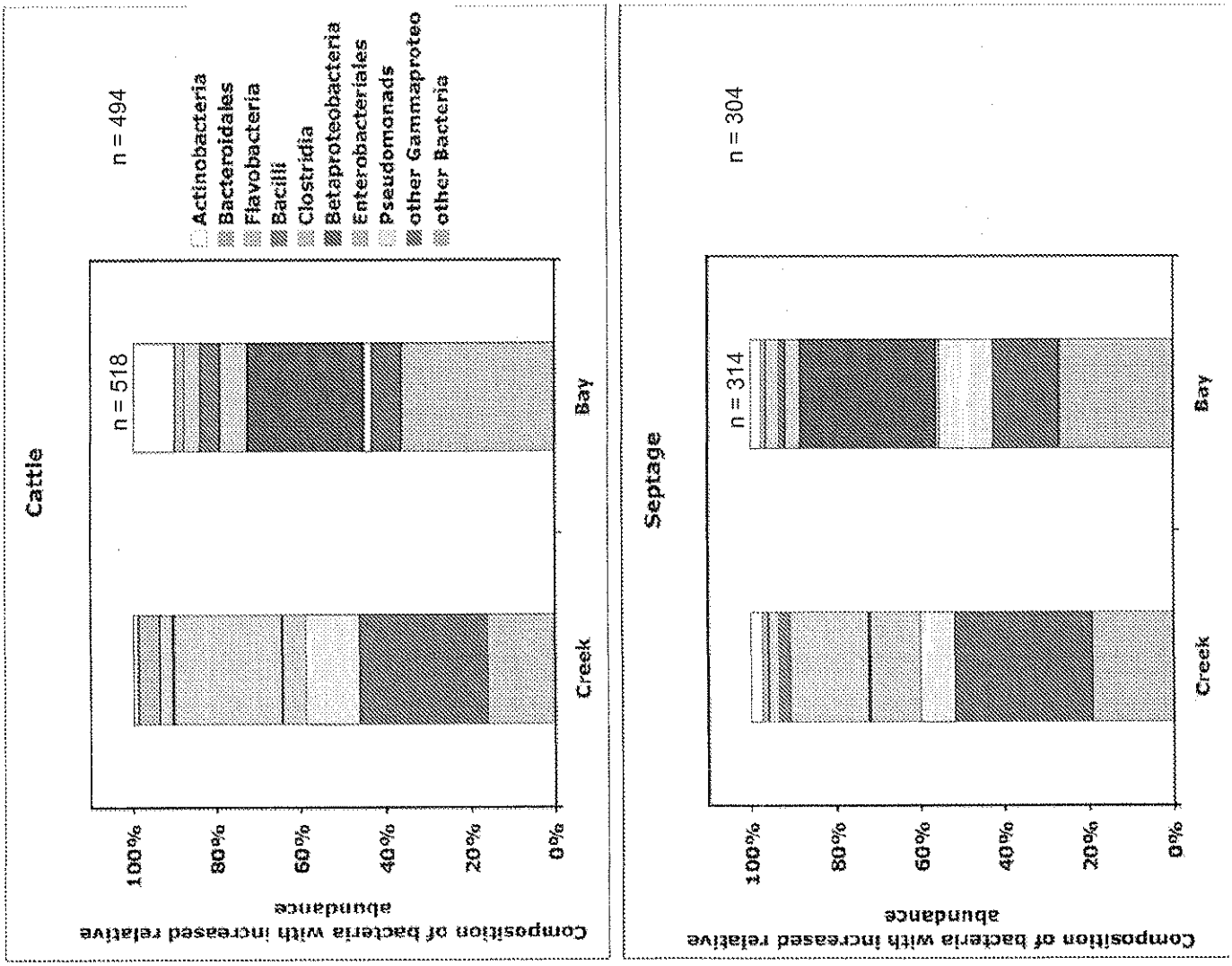
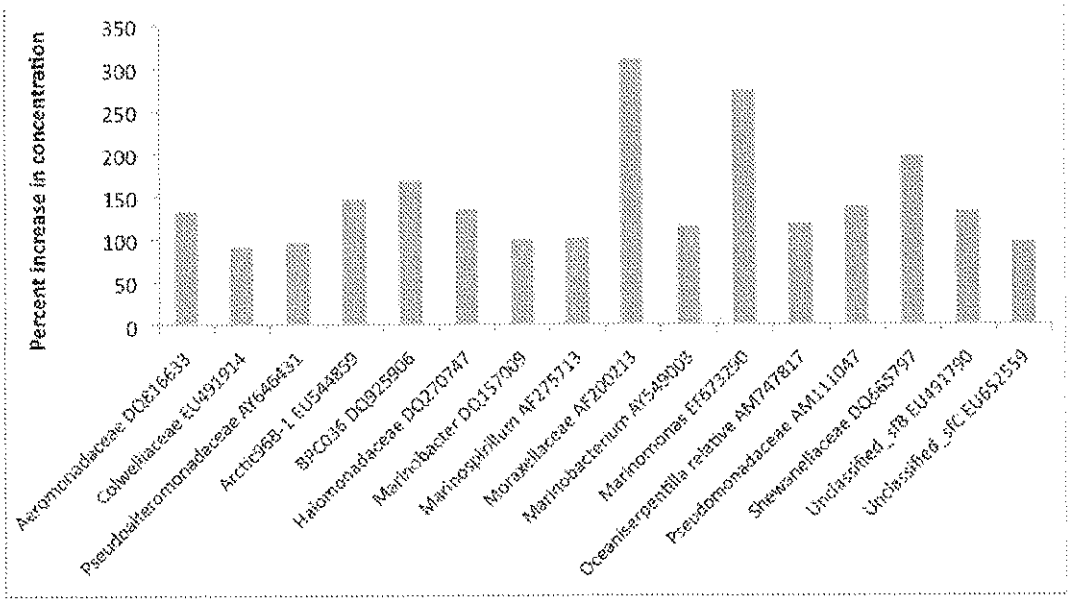

Cattle
n = 494
n = 518
Actinobacteria
Bacteroidales
Flavobacteria
Bacilli
Clostridia
Betaproteobacteria
Enterobacteriales
Pseudomonads
other Gammaproteo
other Bacteria
100%
80%
60%
40%
20%
0%
Creek
Bay
Composition of bacteria with increased relative abundance
Septage
n = 304
n = 314
100%
80%
60%
40%
20%
0%
Creek
Bay
Composition of bacteria with increased relative abundance

FIGURE 32

Figure 33


Percent increase in concentration
350
300
250
200
150
100
50
0
Aeromonadaceae DQ816633
Colwelliaceae EU491914
Pseudoalteromonadaceae AY646431
Arctic96B-1 EU544859
BPC035 DQ925906
Haliomonadaceae DQ270747
Marinobacter DQ157709
Marinospirillum AF275713
Moraxellaceae AF200213
Marinobacterium AY549005
Marinomonas EF672250
Oceaniserpentilla relative AM747817
Pseudomonadaceae AM111047
Shewanellaceae DQ685797
Unclassified_sf8 EU491790
Unclassified_sfC EU652559