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(54) **HARNESSING GUT MICROBES FOR GLYCAN DETECTION AND QUANTIFICATION**

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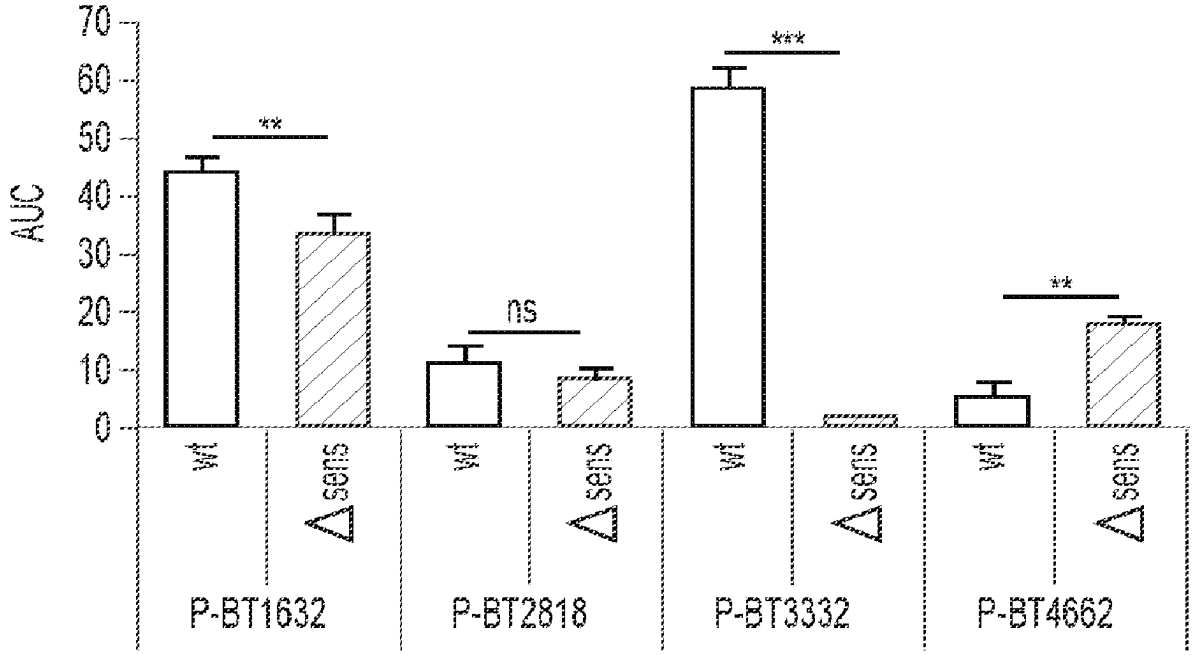
(52) **U.S. Cl.**

CPC ***C12Q 1/02*** (2013.01); ***C12N 9/0071*** (2013.01); ***C12N 15/74*** (2013.01); ***C12Q 1/66*** (2013.01); ***C12Y 114/14003*** (2013.01); *G01N 2400/10* (2013.01)

(57) **ABSTRACT**

The present disclosure relates compositions and methods of engineering microbial strains to detect and quantify glycan molecules.

Specification includes a Sequence Listing.



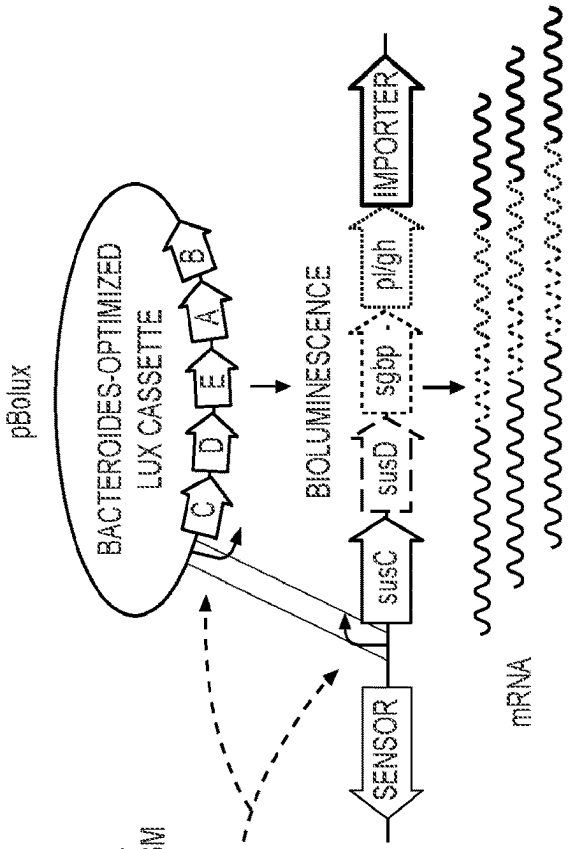

pBolux
BACTEROIDES-OPTIMIZED
LUX CASSETTE
C
D
E
A
B
BIOLUMINESCENCE
susC
susD
sgbp
pl/gh
IMPORTER
SENSOR
mRNA

FIG. 1B

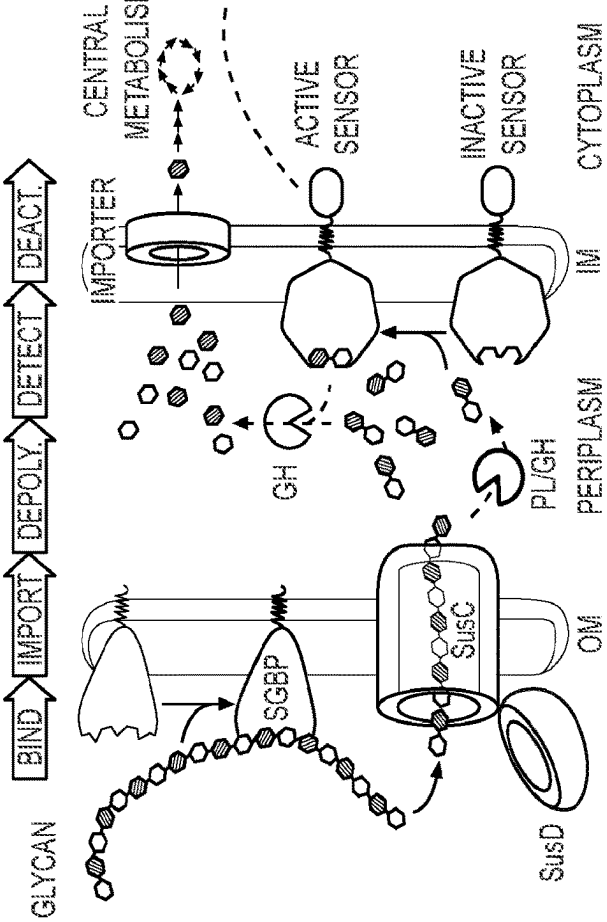

GLYCAN
BIND
IMPORT
DEPOLY
DETECT
DEACT
SGBP
SusC
SusD
OM
GH
PL/GH
PERIPLASM
IM
IMPORTER
CENTRAL
METABOLISM
ACTIVE
SENSOR
INACTIVE
SENSOR
CYTOPLASM

FIG. 1A

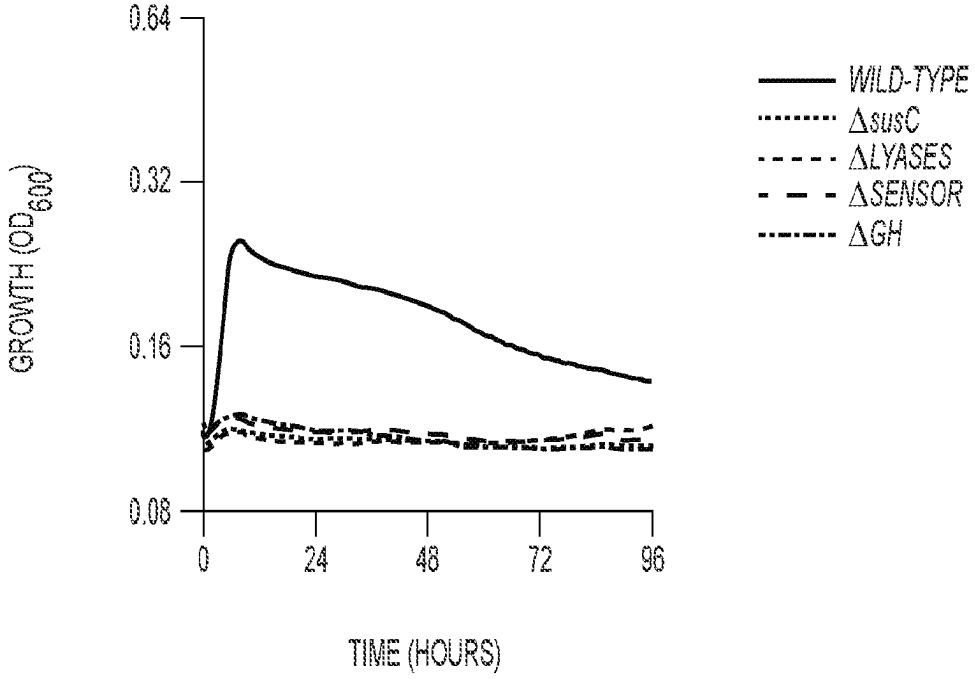

0.64
0.32
0.16
0.08
GROWTH (OD_{600})
0
24
48
72
96
TIME (HOURS)
WILD-TYPE
ΔsusC
ΔLYASES
ΔSENSOR
ΔGH

FIG. 1C

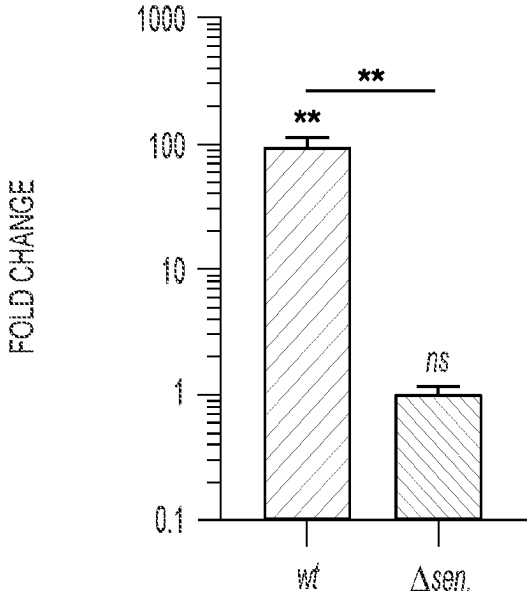

1000
100
10
1
0.1
FOLD CHANGE
**
**
ns
wt
Δsen.

FIG. 1D

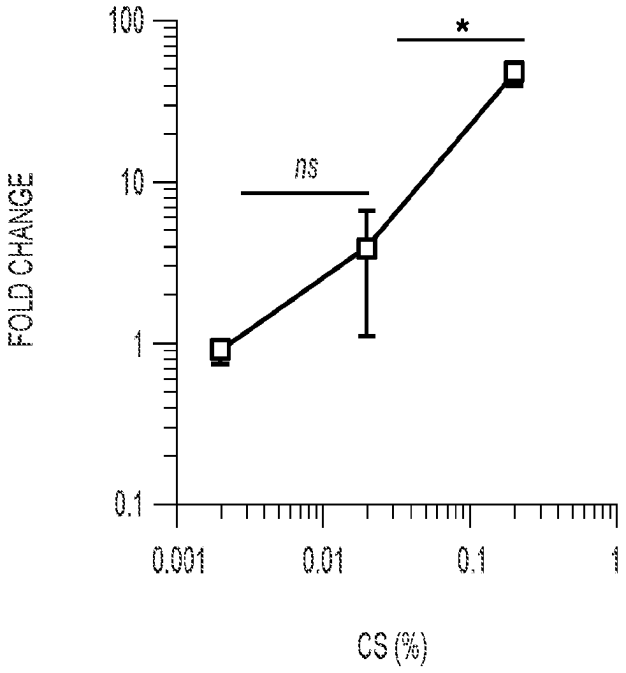

100
10
1
0.1
FOLD CHANGE
ns
*
0.001
0.01
0.1
1
CS (%)

FIG. 1E

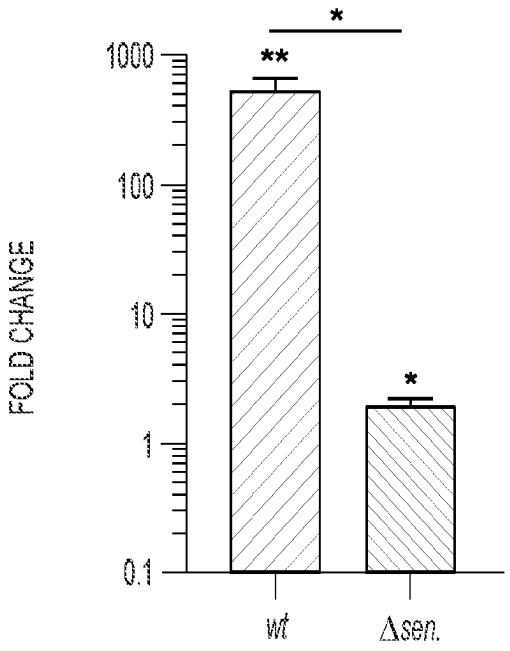

1000
100
10
1
0.1
FOLD CHANGE
*
**
*
wt
Δsen.

FIG. 1F

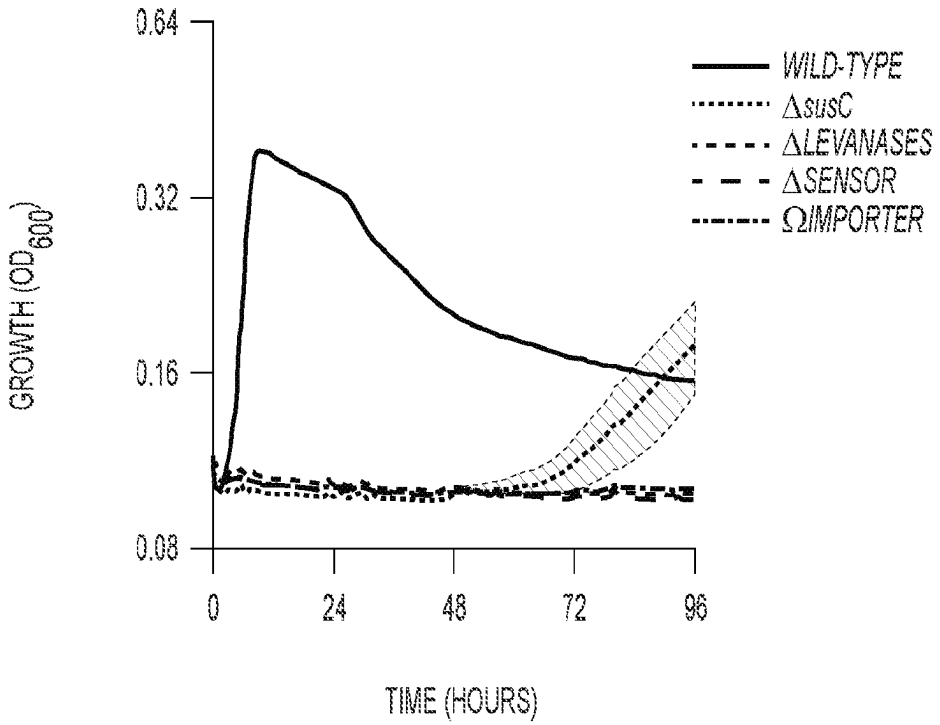

0.64
0.32
0.16
0.08
GROWTH (OD_{600})
0
24
48
72
96
TIME (HOURS)
WILD-TYPE
ΔsusC
ΔLEVANASES
ΔSENSOR
ΩIMPORTER

FIG. 1G

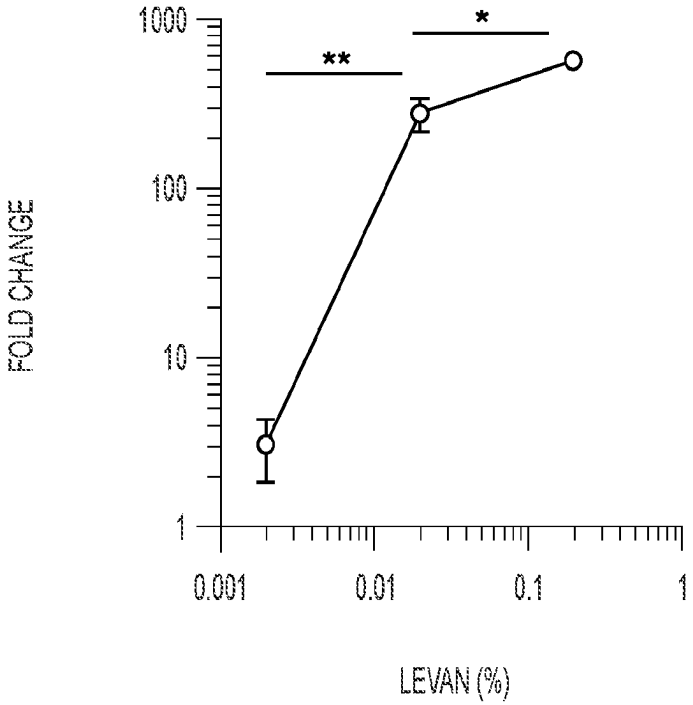

1000
100
10
1
FOLD CHANGE
**
*
0.001
0.01
0.1
1
LEVAN (%)

FIG. 1H

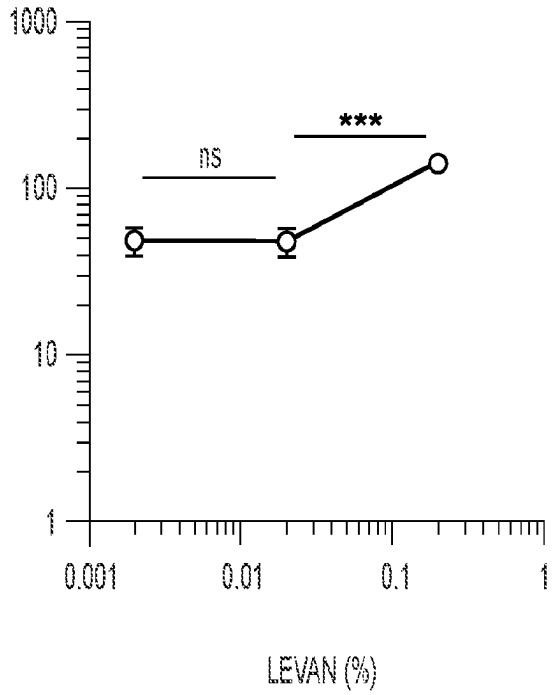

1000
100
10
1
ns
***
0.001
0.01
0.1
1
LEVAN (%)

FIG. 1I

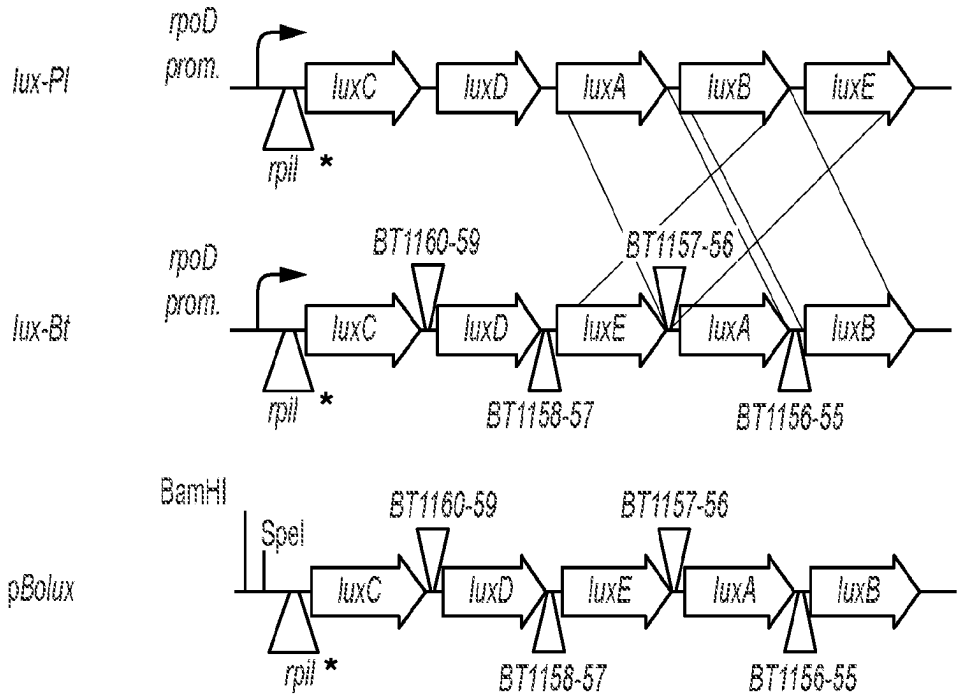

lux-PI
rpoD prom.
luxC
luxD
luxA
luxB
luxE
rpiI *
lux-Bt
rpoD prom.
BT1160-59
BT1157-56
luxC
luxD
luxE
luxA
luxB
rpiI *
BT1158-57
BT1156-55
pBolux
BamHI
SpeI
BT1160-59
BT1157-56
luxC
luxD
luxE
luxA
luxB
rpiI *
BT1158-57
BT1156-55

FIG. 2A

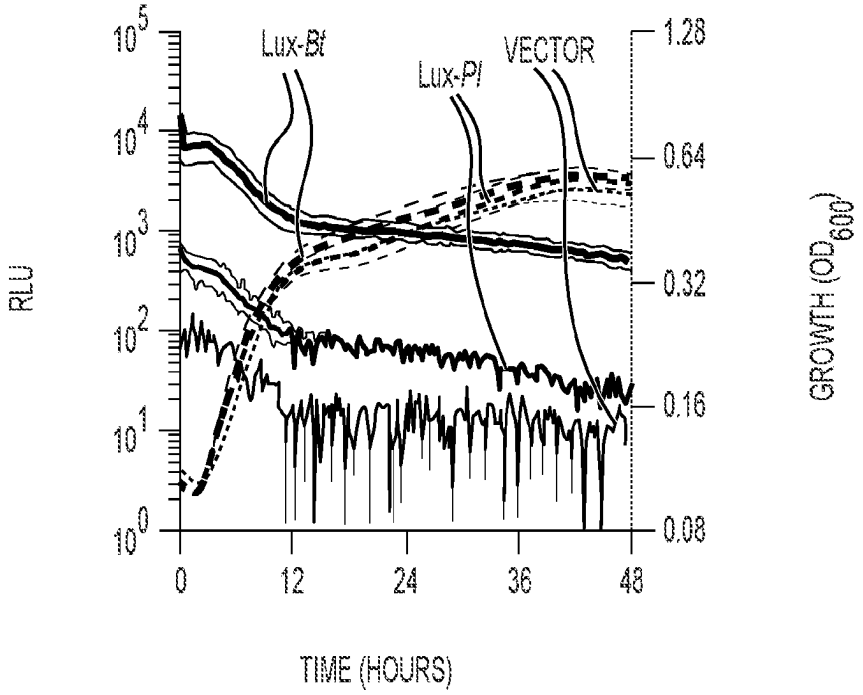

Lux-Bt
Lux-Pl
VECTOR
RLU
GROWTH (OD600)
TIME (HOURS)
10^5
10^4
10^3
10^2
10^1
10^0
1.28
0.64
0.32
0.16
0.08
0
12
24
36
48

FIG. 2B

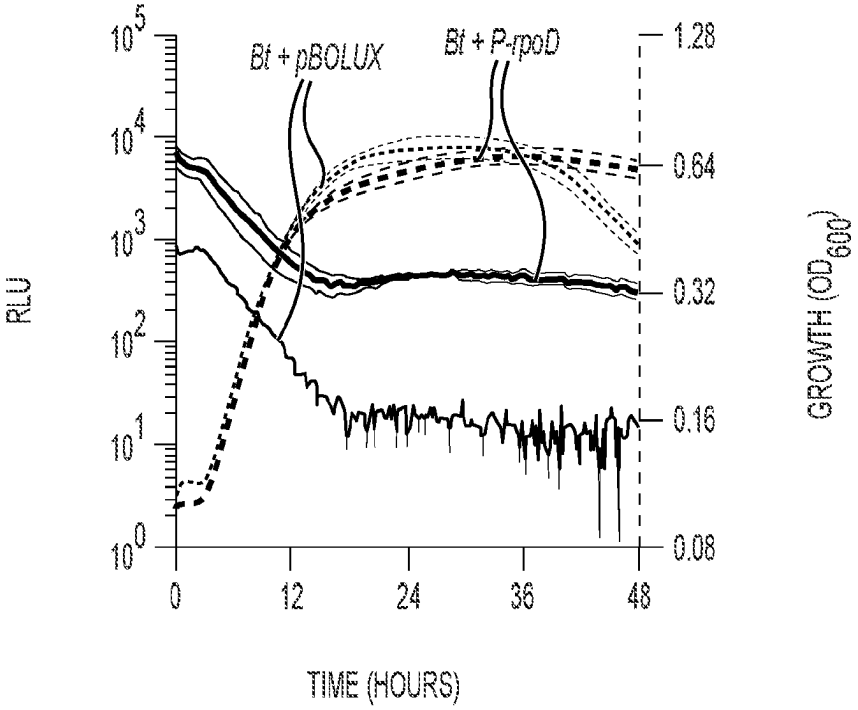

Bt + pBOLUX
Bt + P-rpoD
RLU
GROWTH (OD600)
TIME (HOURS)
10^5
10^4
10^3
10^2
10^1
10^0
1.28
0.64
0.32
0.16
0.08
0
12
24
36
48

FIG. 2C

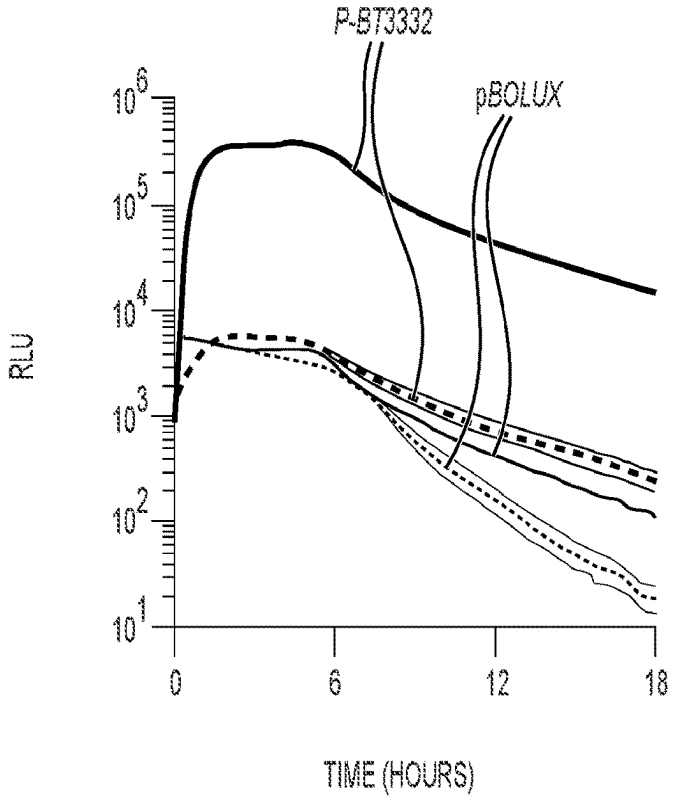

P-BT3332
pBOLUX
RLU
10^6
10^5
10^4
10^3
10^2
10^1
0
6
12
18
TIME (HOURS)

FIG. 3A

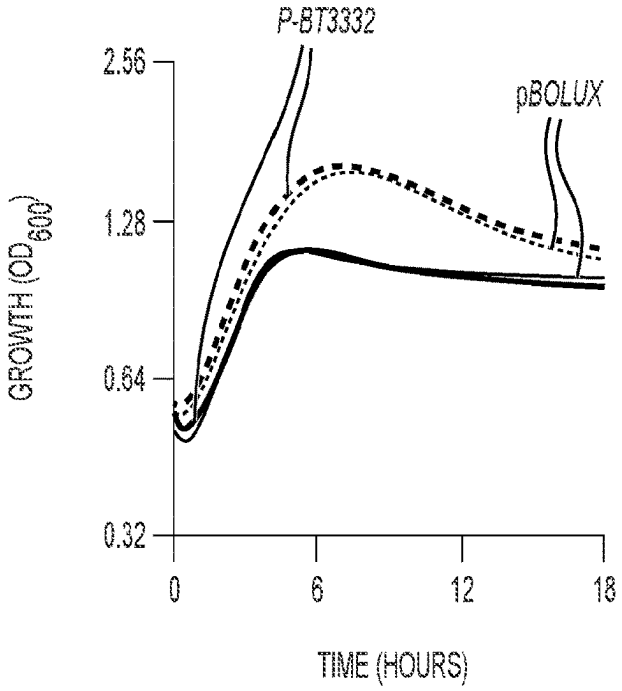

P-BT3332
pBOLUX
GROWTH (OD_{600})
2.56
1.28
0.64
0.32
0
6
12
18
TIME (HOURS)

FIG. 3B

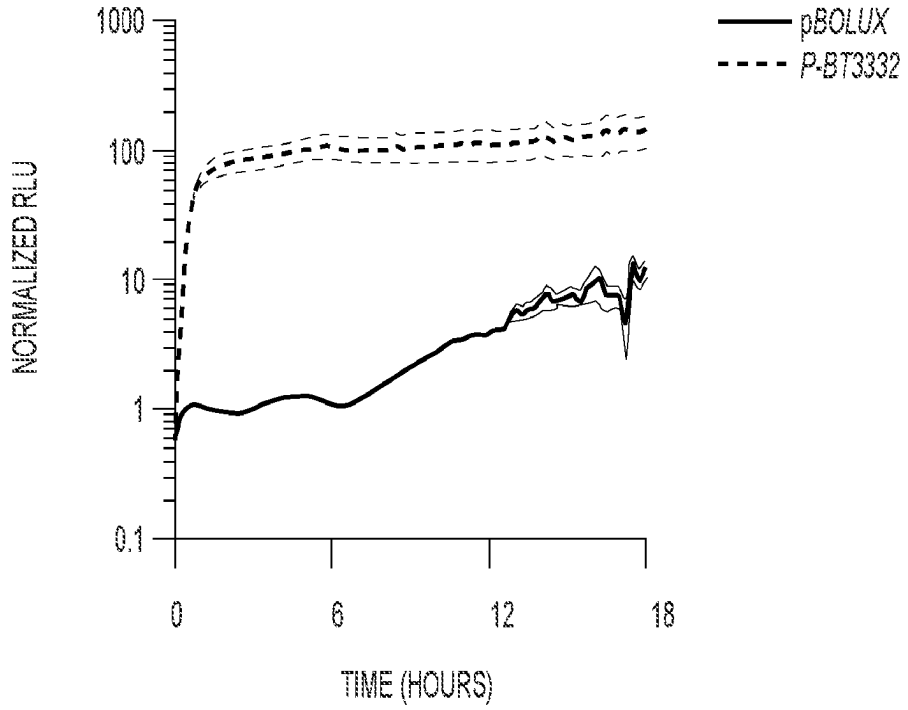

1000
100
10
1
0.1
NORMALIZED RLU
0
6
12
18
TIME (HOURS)
pBOLUX
P-BT3332

FIG. 3C

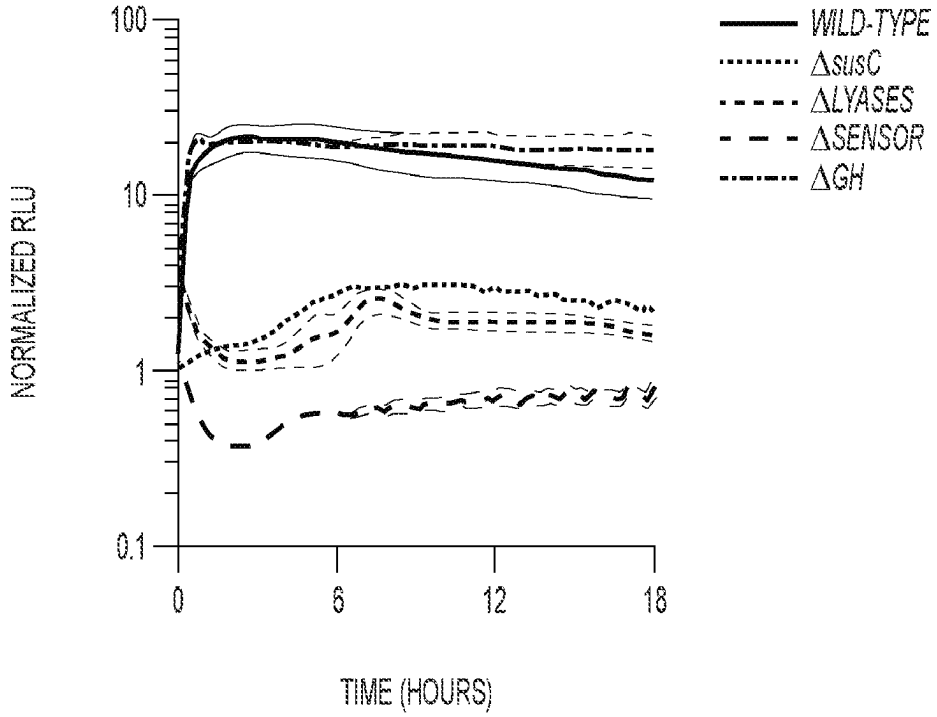

100
10
1
0.1
NORMALIZED RLU
0
6
12
18
TIME (HOURS)
WILD-TYPE
ΔsusC
ΔLYASES
ΔSENSOR
ΔGH

FIG. 3D

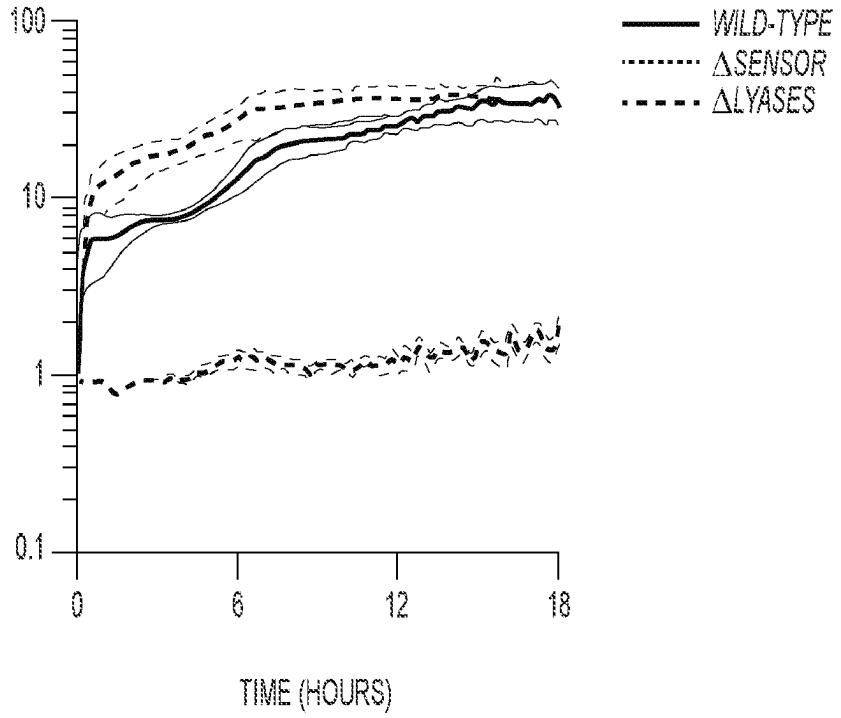

100
10
1
0.1
0
6
12
18
TIME (HOURS)
WILD-TYPE
ΔSENSOR
ΔLYASES

FIG. 3E

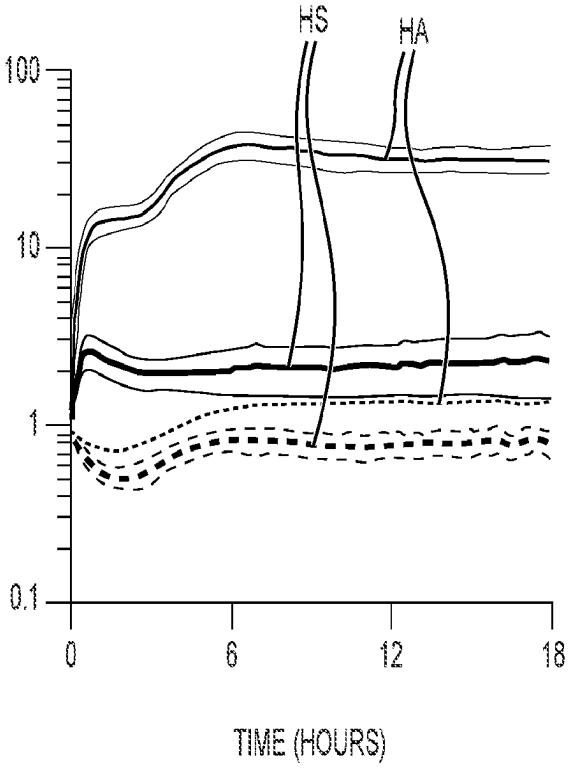

HS
HA
100
10
1
0.1
0
6
12
18
TIME (HOURS)

FIG. 3F

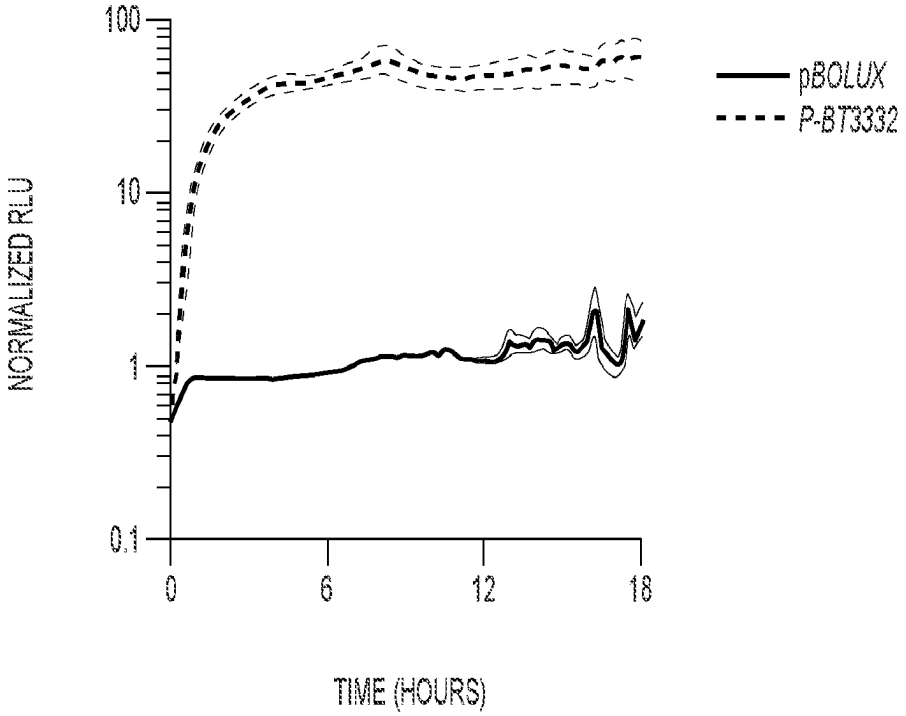

100
10
1
0.1
NORMALIZED RLU
0
6
12
18
TIME (HOURS)
pBOLUX
P-BT3332

FIG. 4A

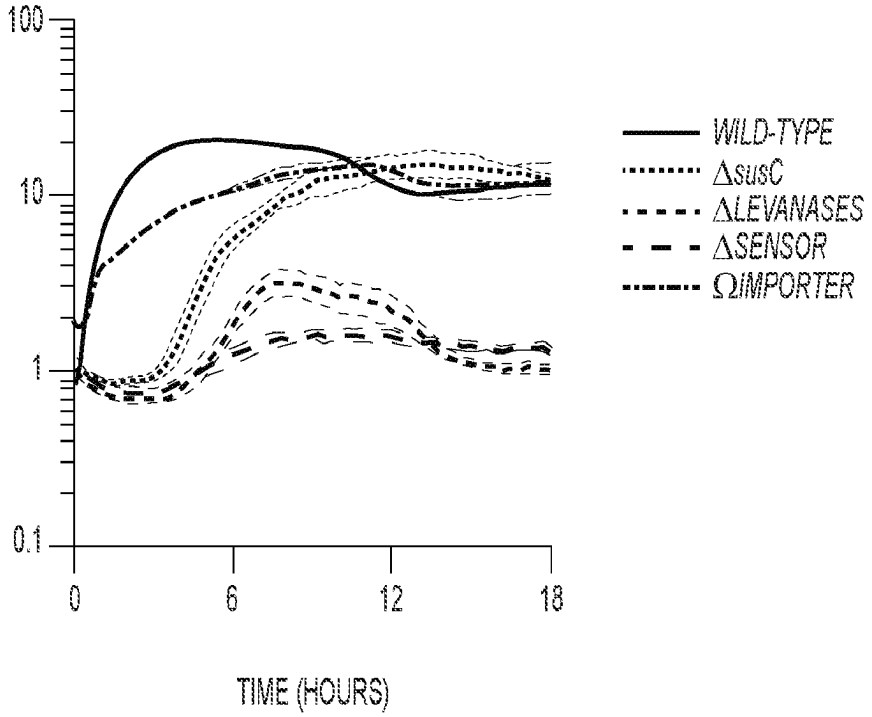

100
10
1
0.1
0
6
12
18
TIME (HOURS)
WILD-TYPE
ΔsusC
ΔLEVANASES
ΔSENSOR
ΩIMPORTER

FIG. 4B

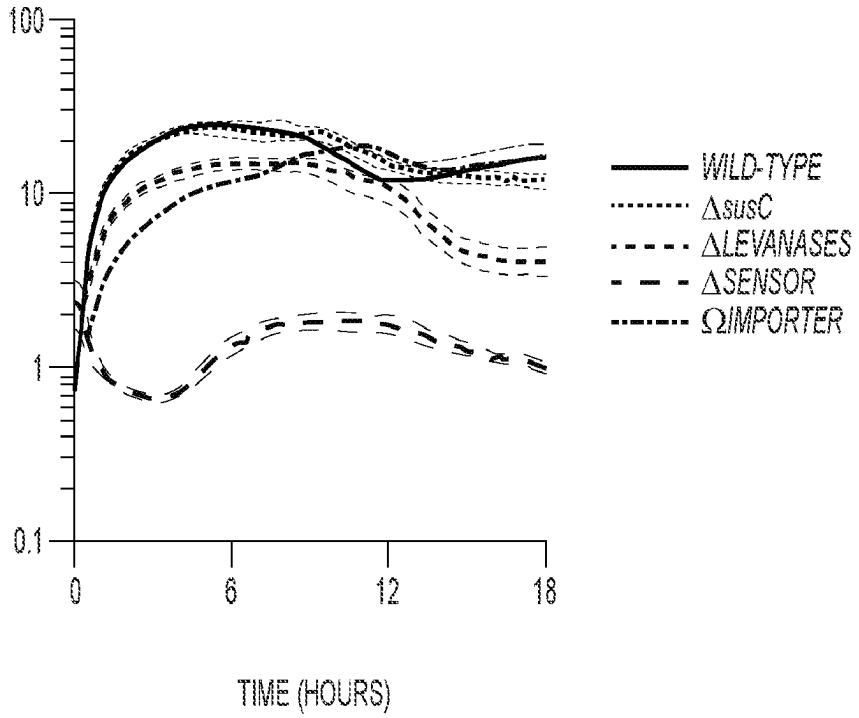

100
10
1
0.1
0
6
12
18
TIME (HOURS)
WILD-TYPE
ΔsusC
ΔLEVANASES
ΔSENSOR
ΩIMPORTER

FIG. 4C

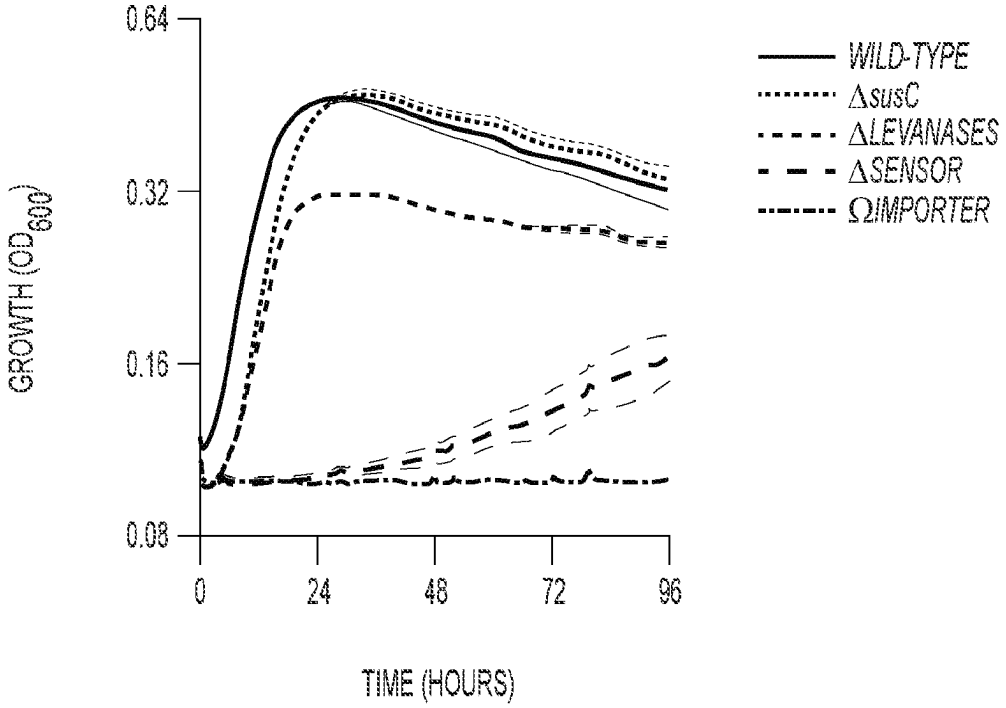

0.64
0.32
0.16
0.08
GROWTH (OD600)
0
24
48
72
96
TIME (HOURS)
WILD-TYPE
ΔsusC
ΔLEVANASES
ΔSENSOR
ΩIMPORTER

FIG. 4D

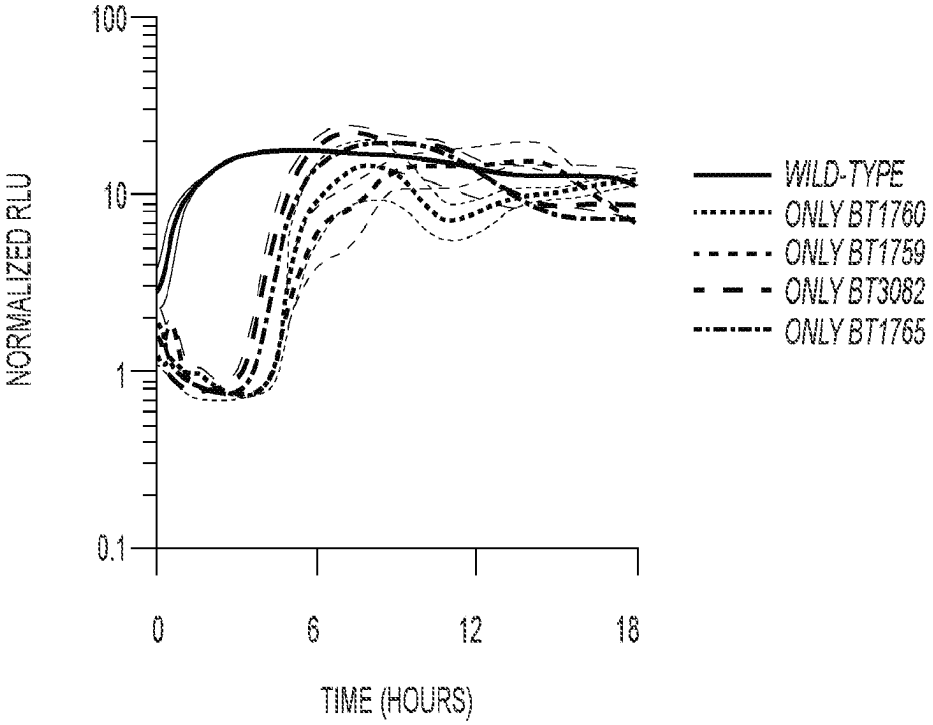

100
10
1
0.1
NORMALIZED RLU
0
6
12
18
TIME (HOURS)
WILD-TYPE
ONLY BT1760
ONLY BT1759
ONLY BT3082
ONLY BT1765

FIG. 4E

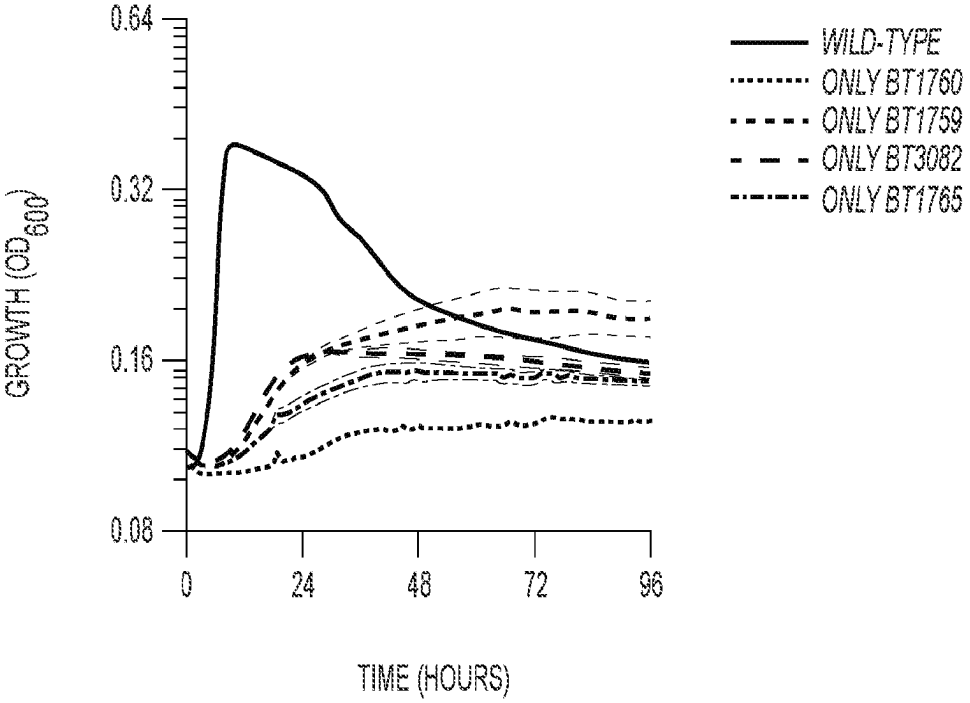

0.64
0.32
0.16
0.08
GROWTH (OD_{600})
0
24
48
72
96
TIME (HOURS)
WILD-TYPE
ONLY BT1760
ONLY BT1759
ONLY BT3082
ONLY BT1765

FIG. 4F

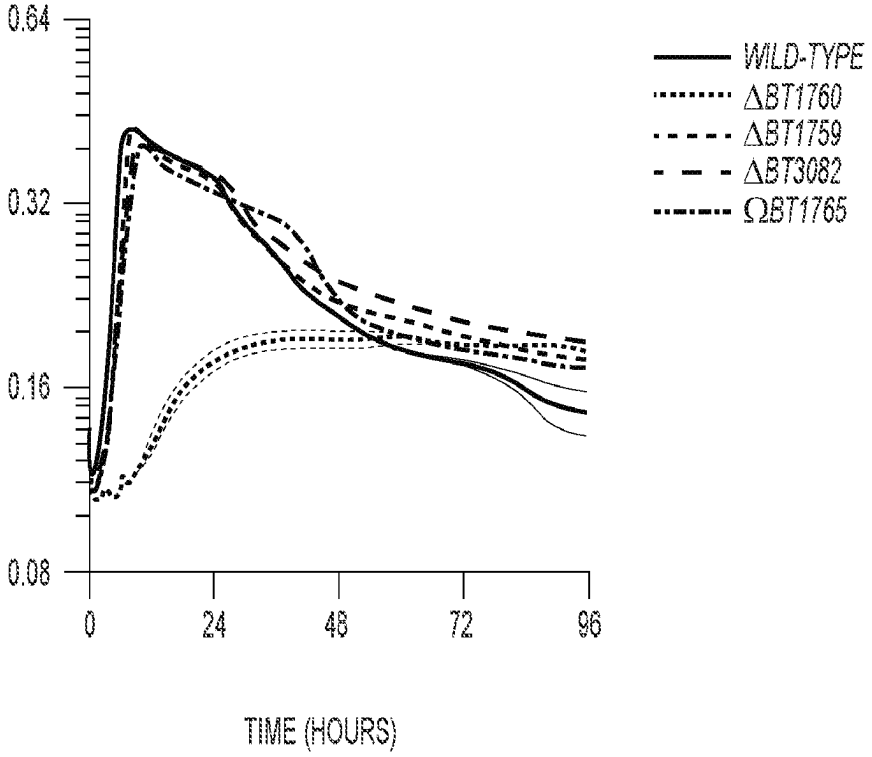

0.64
0.32
0.16
0.08
0
24
48
72
96
TIME (HOURS)
WILD-TYPE
ΔBT1760
ΔBT1759
ΔBT3082
ΩBT1765

FIG. 4G

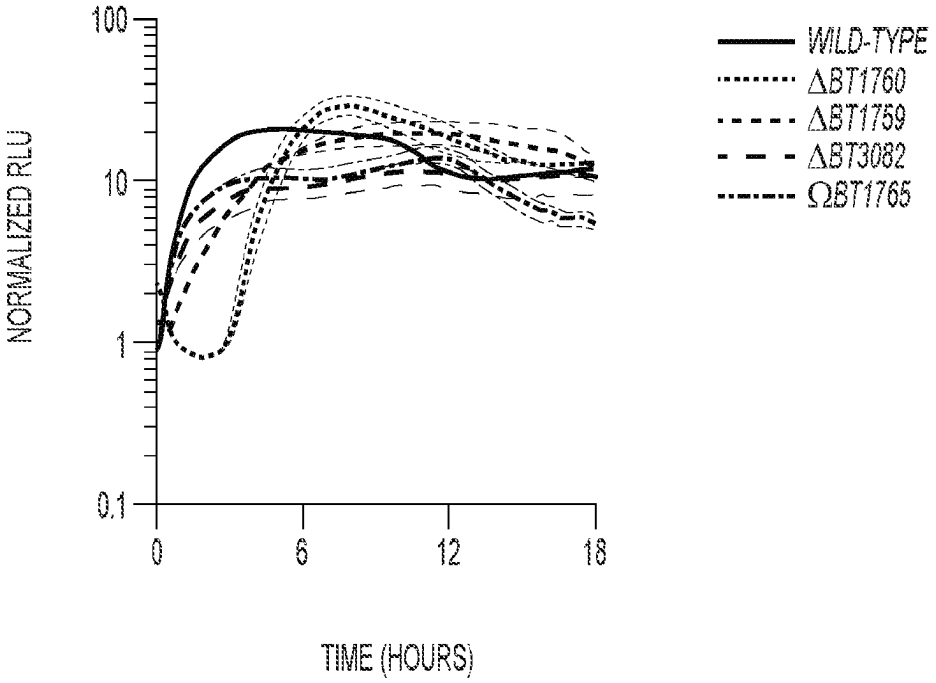

100
10
1
0.1
NORMALIZED RLU
0
6
12
18
TIME (HOURS)
WILD-TYPE
ΔBT1760
ΔBT1759
ΔBT3082
ΩBT1765

FIG. 4D

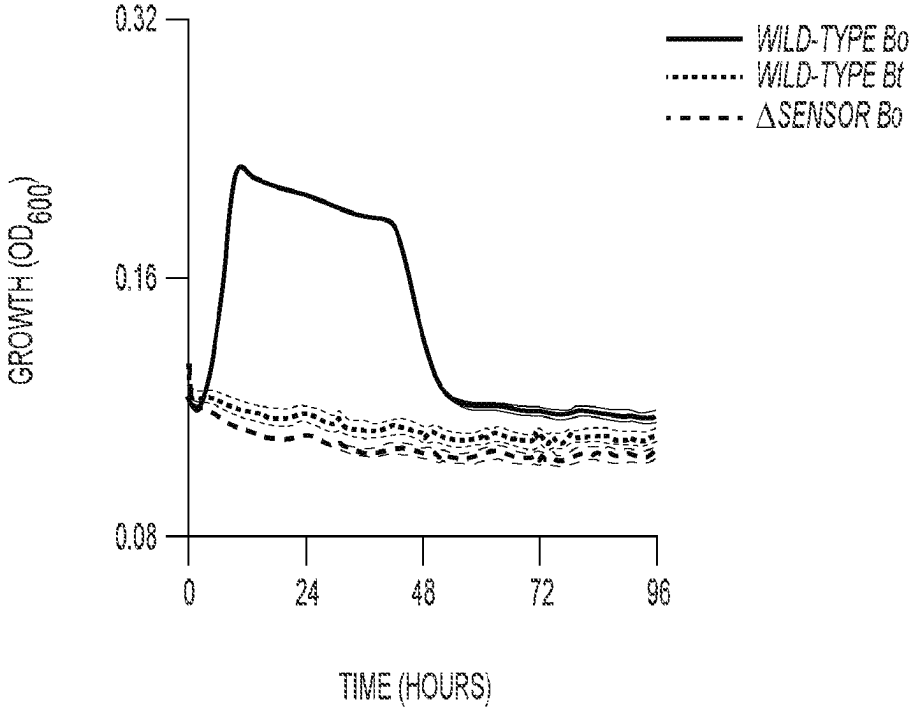

0.32
0.16
0.08
GROWTH (OD_{600})
0
24
48
72
96
TIME (HOURS)
WILD-TYPE Bo
WILD-TYPE Bt
ΔSENSOR Bo

FIG. 5A

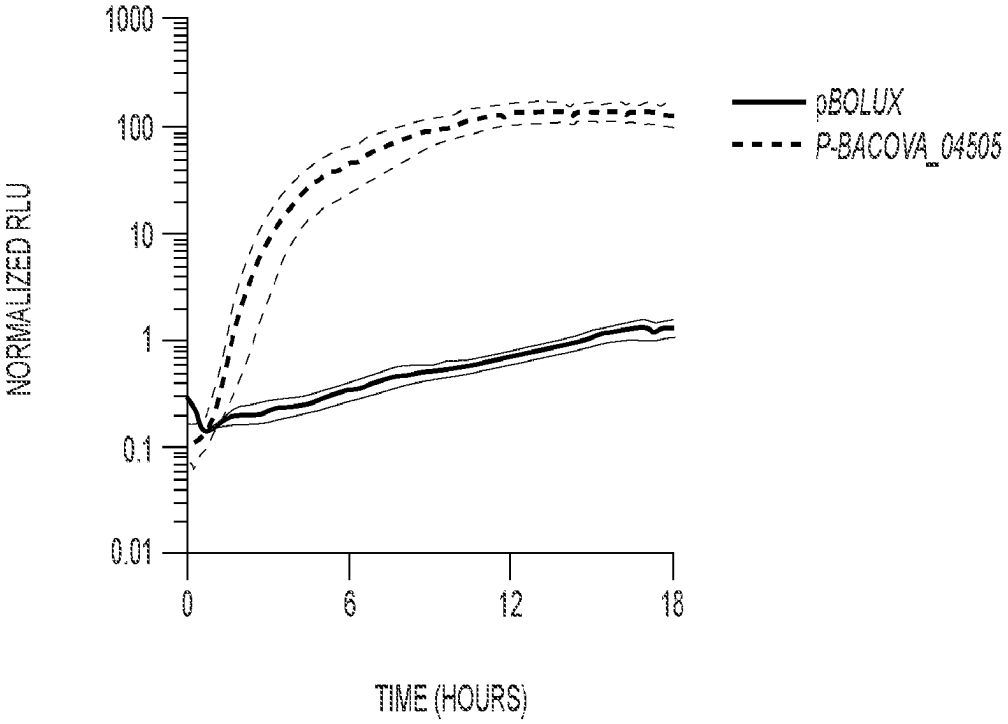

1000
100
10
1
0.1
0.01
NORMALIZED RLU
0
6
12
18
TIME (HOURS)
pBOLUX
P-BACOVA_04505

FIG. 5B

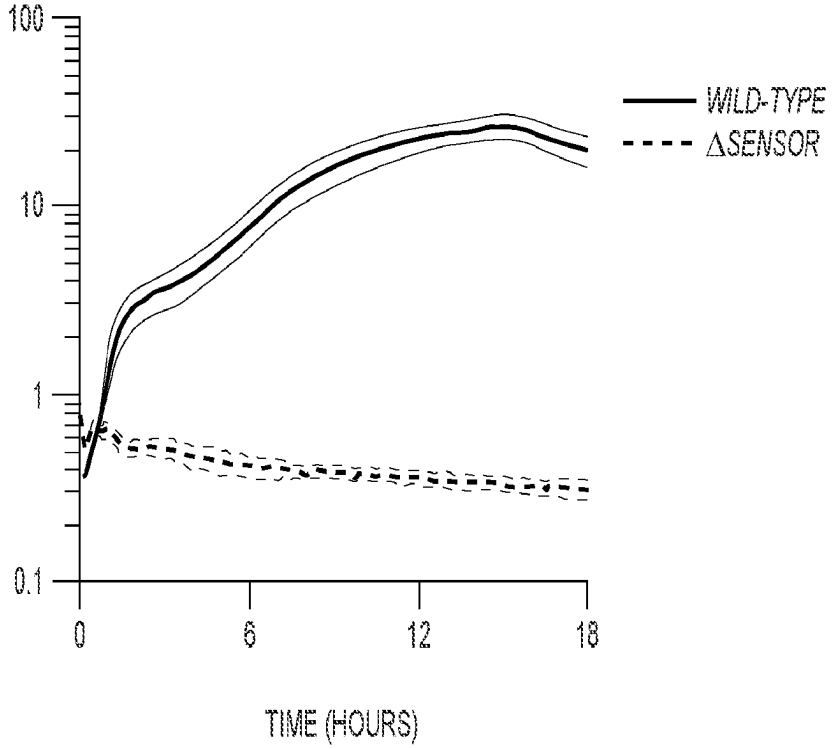

100
10
1
0.1
0
6
12
18
TIME (HOURS)
WILD-TYPE
ΔSENSOR

FIG. 5C

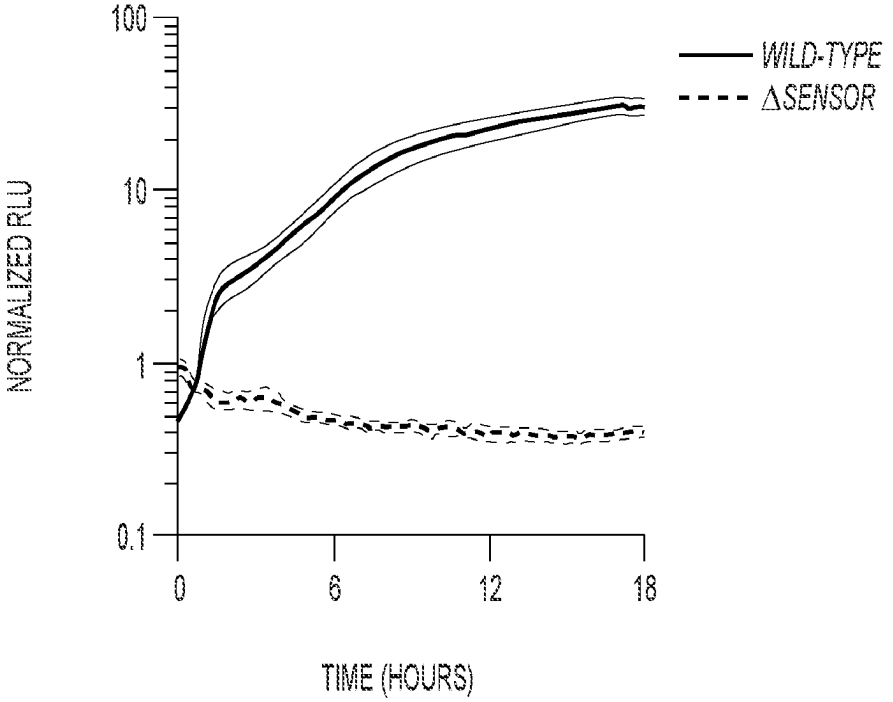

100
10
1
0.1
NORMALIZED RLU
0
6
12
18
TIME (HOURS)
WILD-TYPE
ΔSENSOR

FIG. 5D

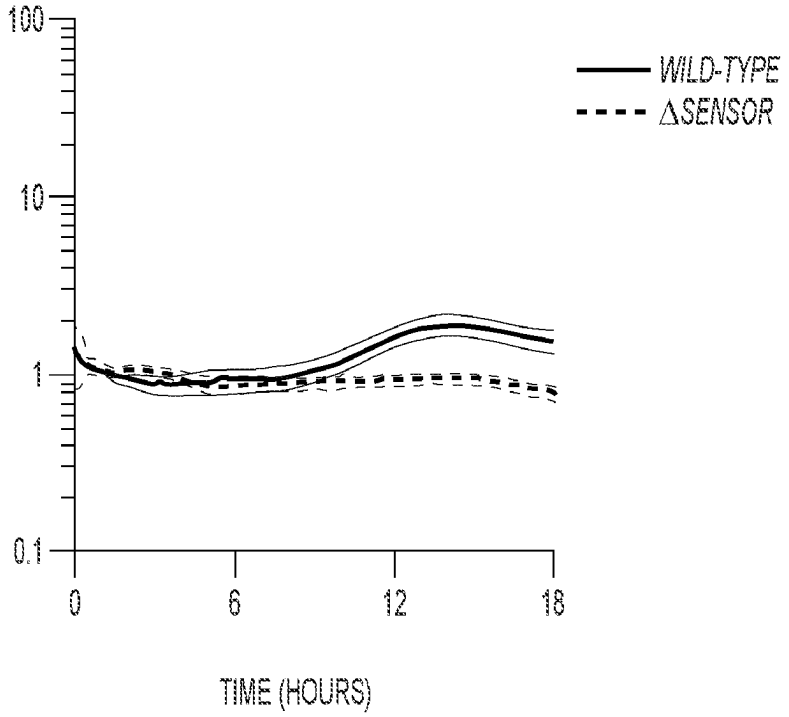

100
10
1
0.1
0
6
12
18
TIME (HOURS)
WILD-TYPE
ΔSENSOR

FIG. 5E

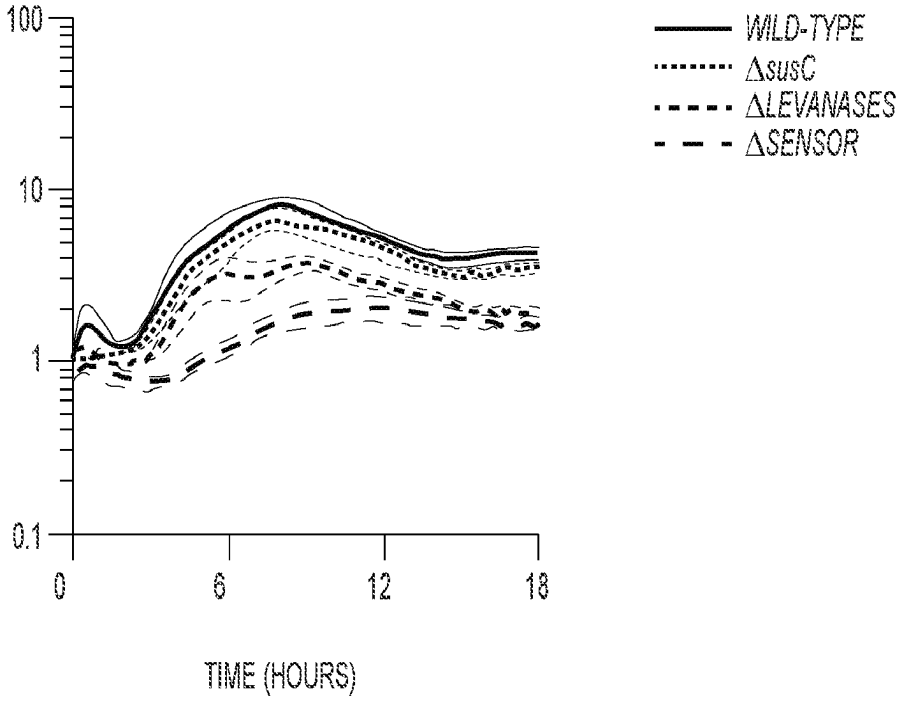

100
10
1
0.1
0
6
12
18
TIME (HOURS)
WILD-TYPE
ΔsusC
ΔLEVANASES
ΔSENSOR

FIG. 5F

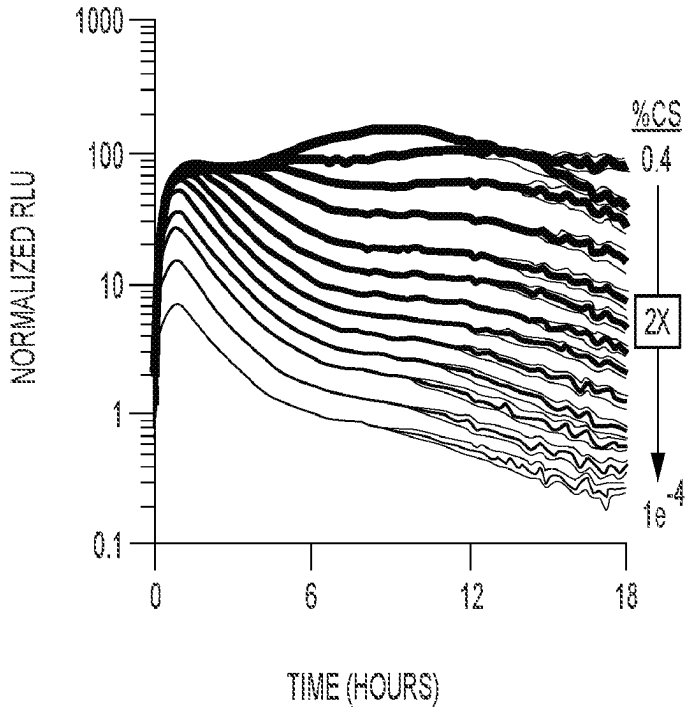

1000
100
10
1
0.1
NORMALIZED RLU
%CS
0.4
2X
1e-4
0
6
12
18
TIME (HOURS)

FIG. 6A

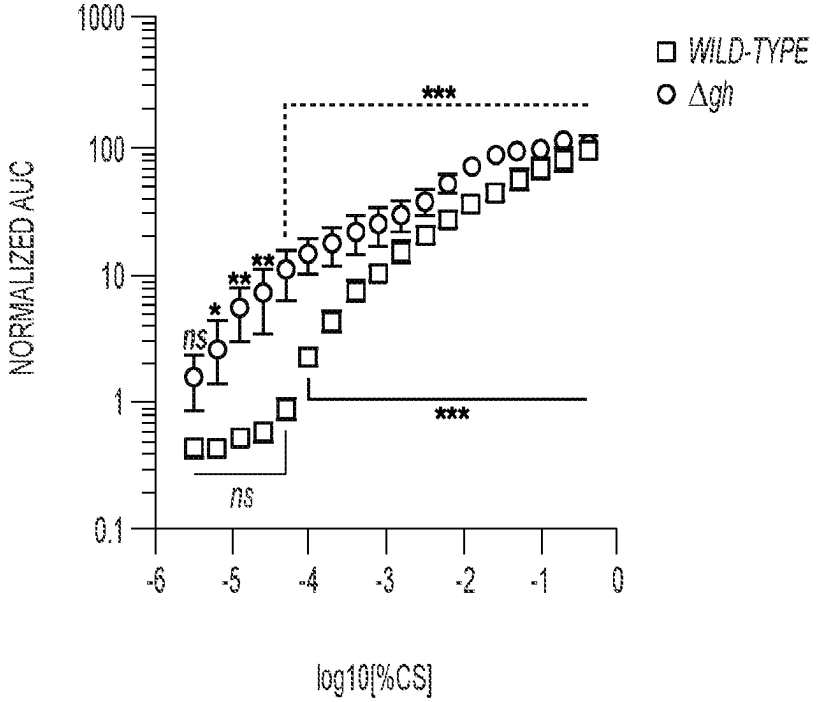

1000
100
10
1
0.1
NORMALIZED AUC
WILD-TYPE
Δgh
***
**
*
ns
***
ns
-6
-5
-4
-3
-2
-1
0
log10[%CS]

FIG. 6B

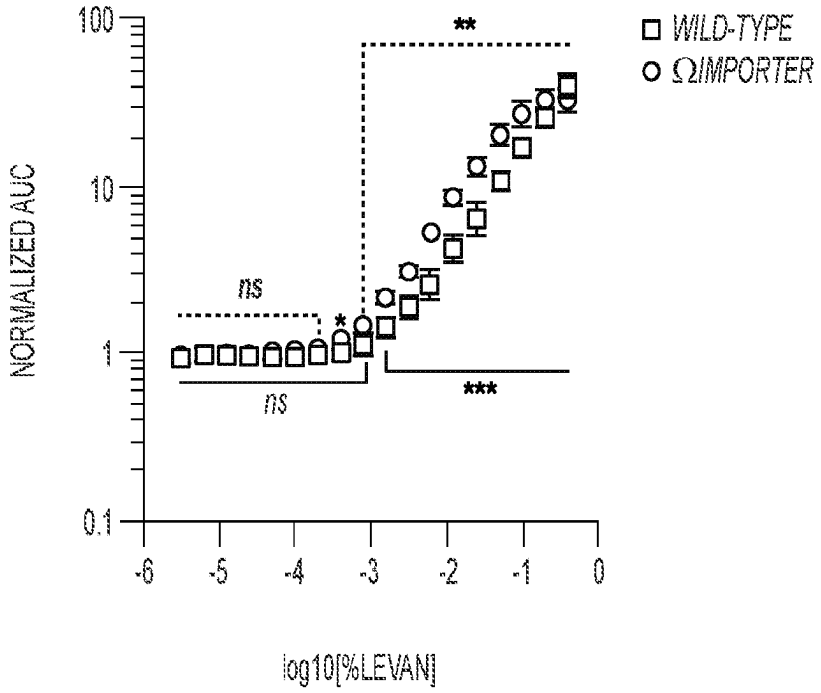

100
10
1
0.1
NORMALIZED AUC
-6
-5
-4
-3
-2
-1
0
log10[%LEVAN]
ns
*
**
ns
***
WILD-TYPE
ΩIMPORTER

FIG. 6C

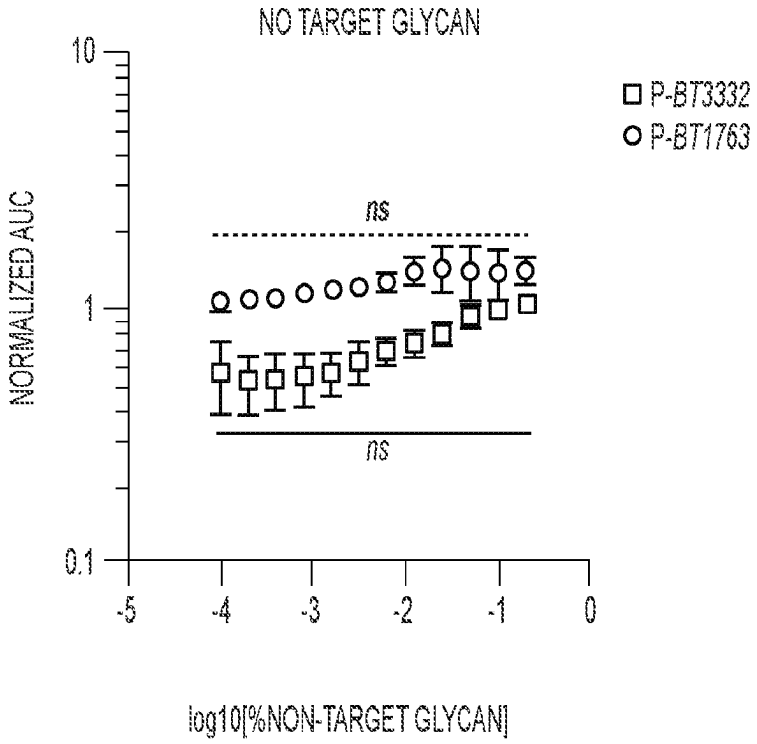

NO TARGET GLYCAN
10
1
0.1
NORMALIZED AUC
-5
-4
-3
-2
-1
0
log10[%NON-TARGET GLYCAN]
ns
ns
P-BT3332
P-BT1763

FIG. 6D

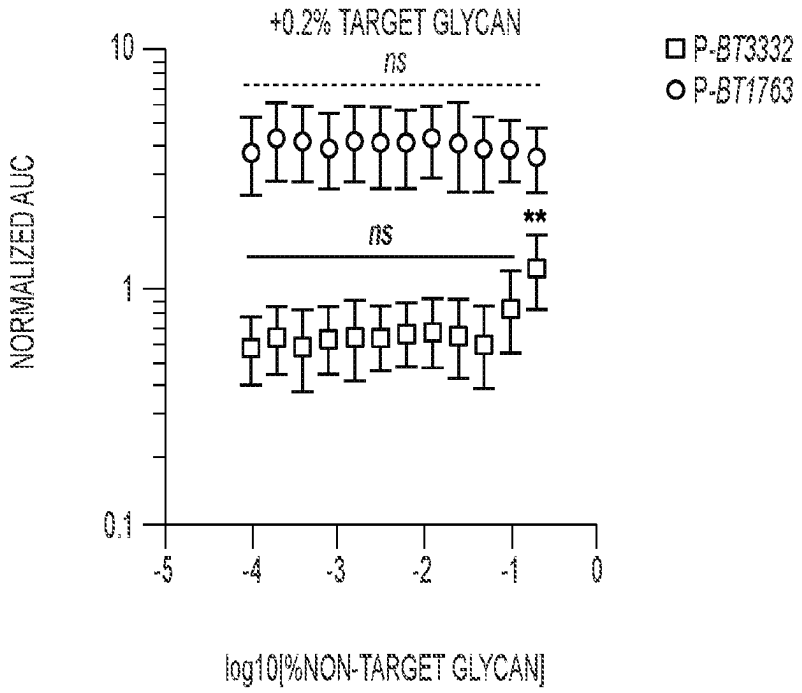

+0.2% TARGET GLYCAN
ns
ns
**
P-BT3332
P-BT1763
NORMALIZED AUC
10
1
0.1
-5
-4
-3
-2
-1
0
log10[%NON-TARGET GLYCAN]

FIG. 6E

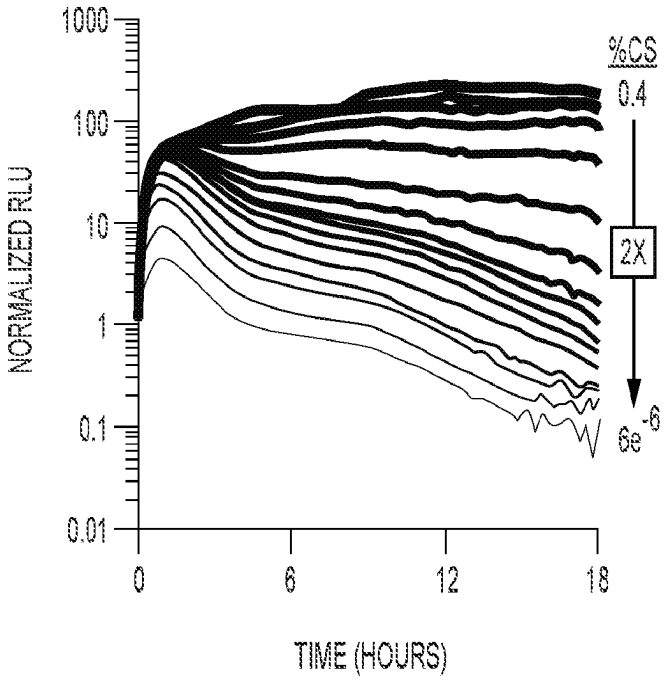

%CS
0.4
2X
6e-6
NORMALIZED RLU
1000
100
10
1
0.1
0.01
0
6
12
18
TIME (HOURS)

FIG. 6F

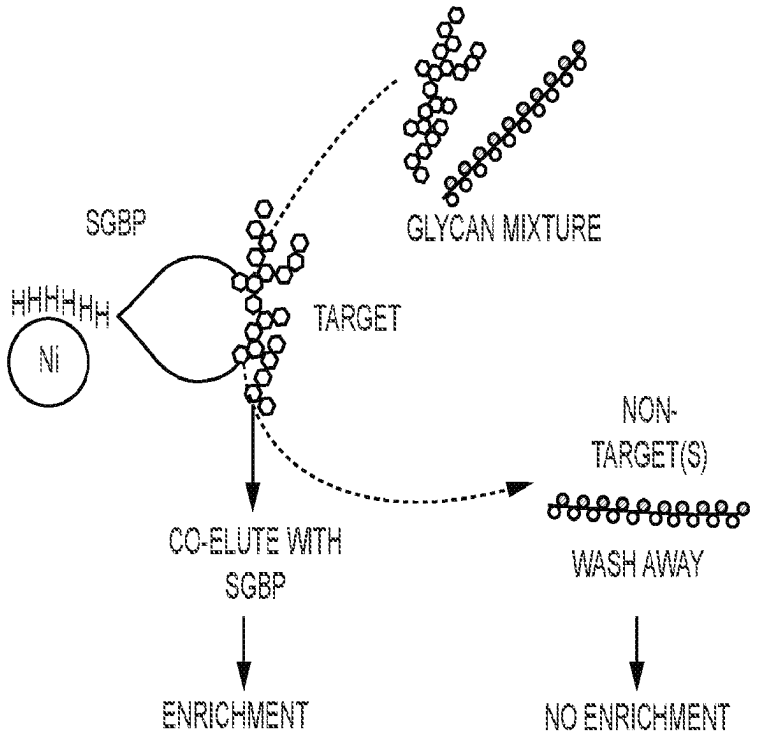


FIG. 7A

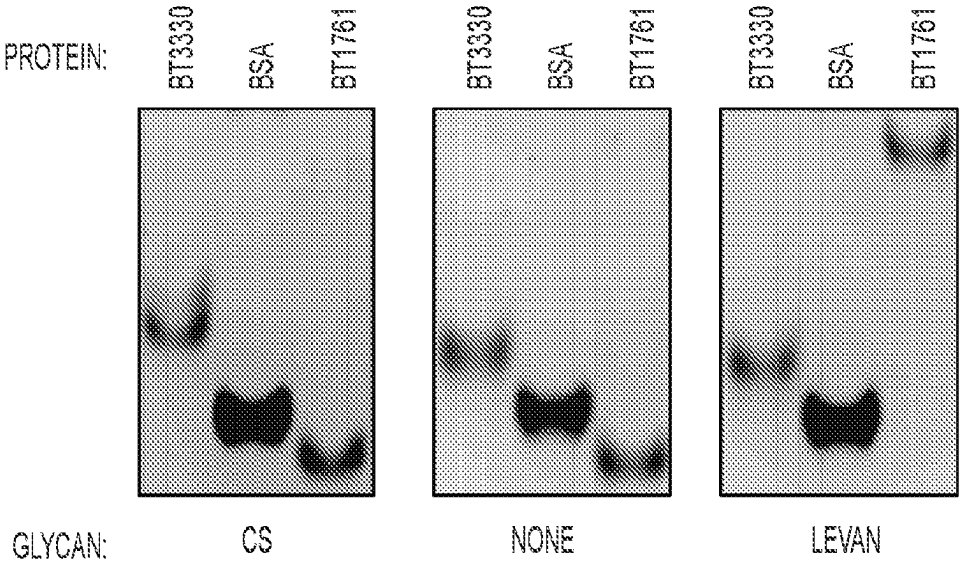


FIG. 7B FIG. 7C FIG. 7D

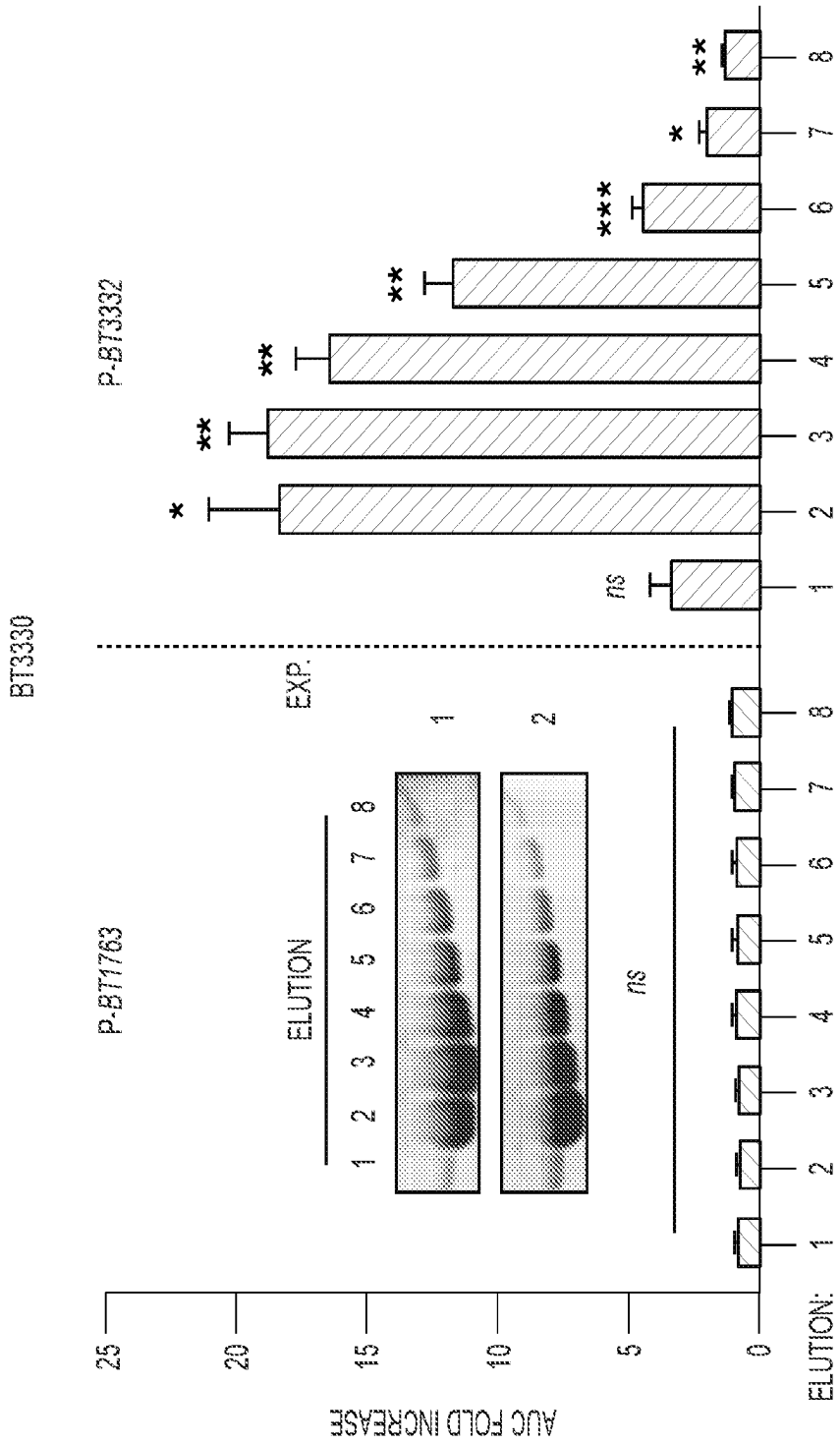

P-BT1763
BT3330
P-BT3332
EXP.
ELUTION
1 2 3 4 5 6 7 8
1
2
ns
ns
*
**
**
**
***
*
**
AUC FOLD INCREASE
25
20
15
10
5
0
ELUTION:
1 2 3 4 5 6 7 8

FIG. 7E

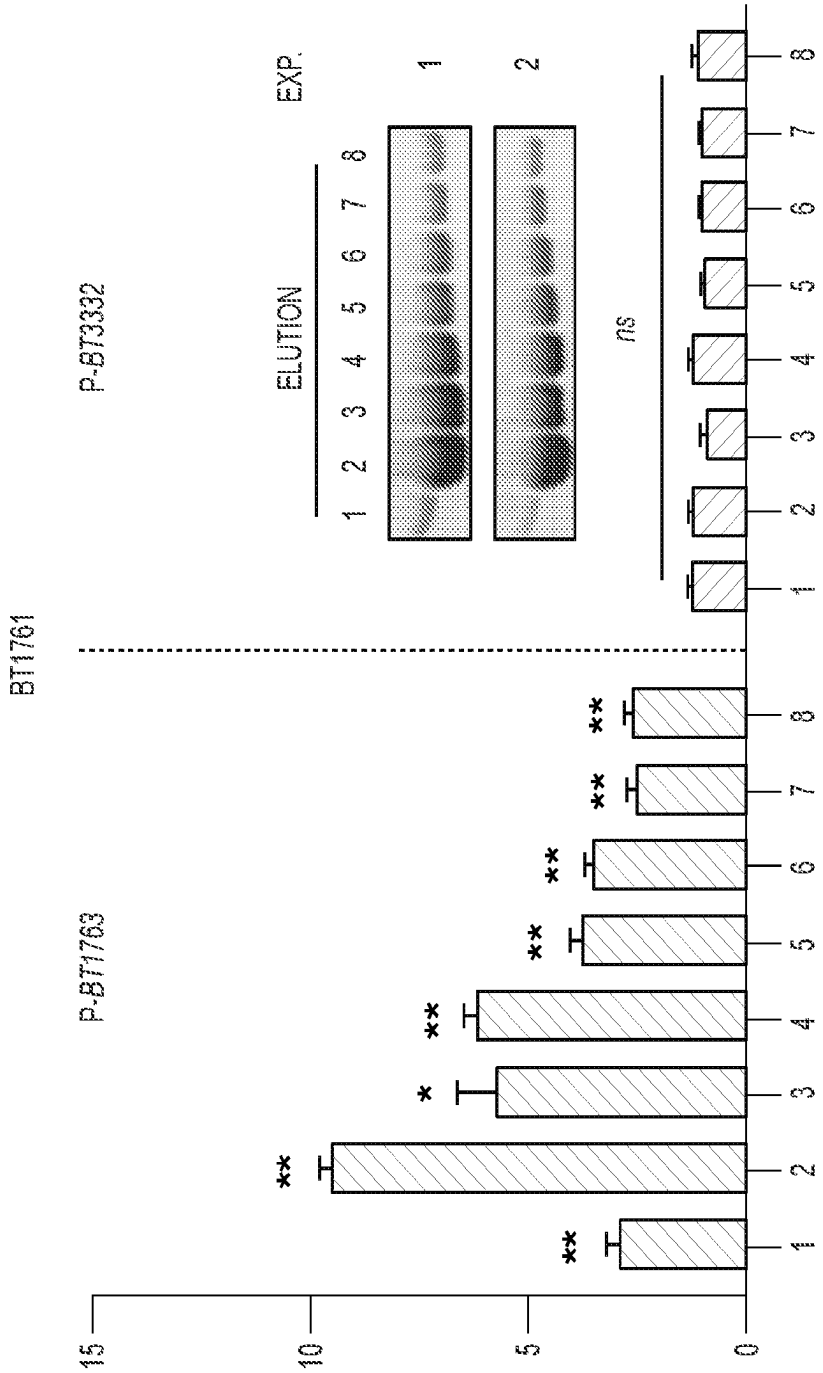


FIG. 7F

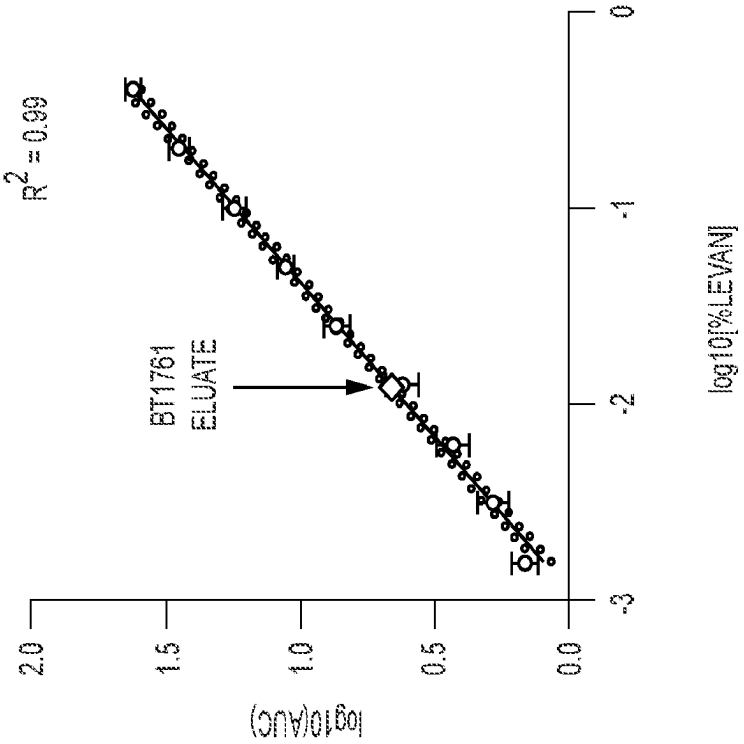

$R^2 = 0.99$
BT1761
ELUATE
log10(AUC)
2.0
1.5
1.0
0.5
0.0
-3
-2
-1
0
log10[%LEVAN]

FIG. 7H

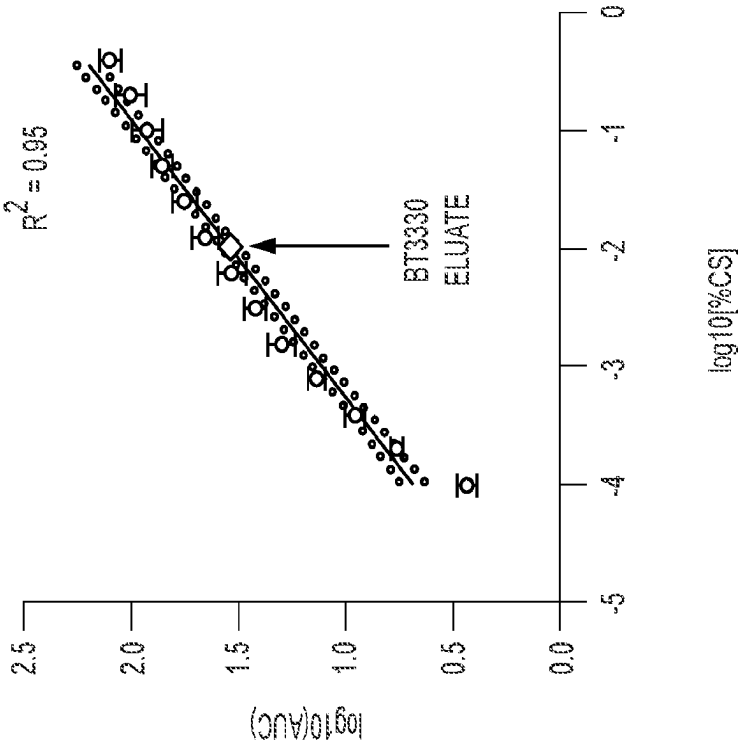

$R^2 = 0.95$
BT3330
ELUATE
log10(AUC)
2.5
2.0
1.5
1.0
0.5
0.0
-5
-4
-3
-2
-1
0
log10[%CS]

FIG. 7G

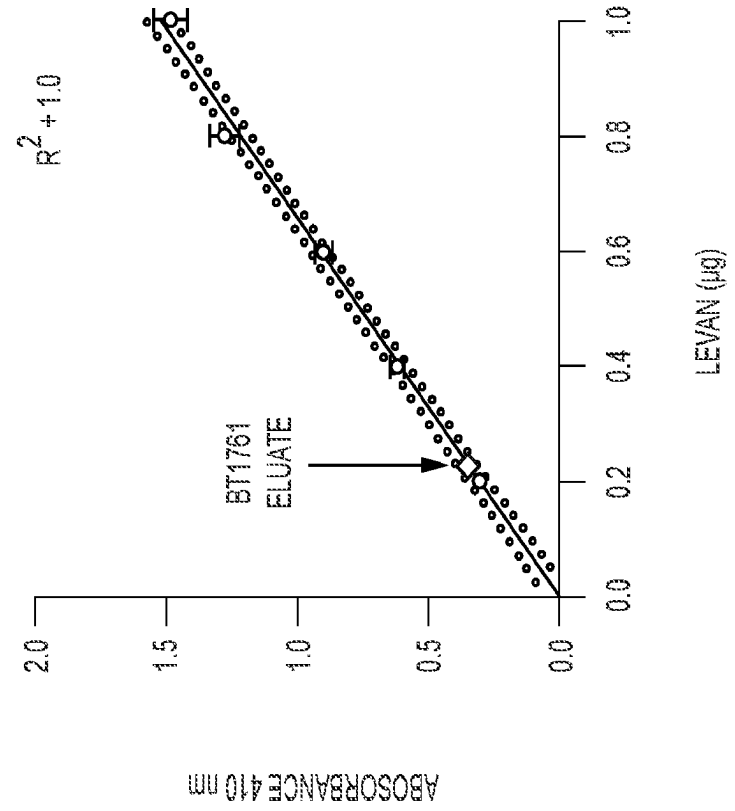

R^2 + 1.0
BT1761
ELUATE
ABSORBANCE 410 nm
LEVAN (µg)
0.0
0.5
1.0
1.5
2.0
0.0
0.2
0.4
0.6
0.8
1.0

FIG. 7J

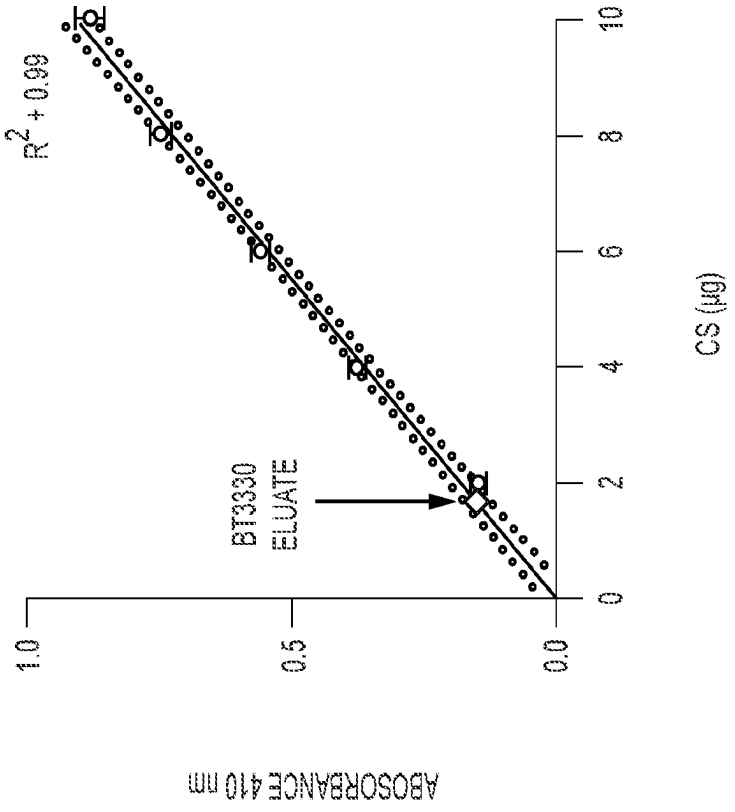

R^2 + 0.99
BT3330
ELUATE
ABSORBANCE 410 nm
CS (µg)
0.0
0.5
1.0
0
2
4
6
8
10

FIG. 7I

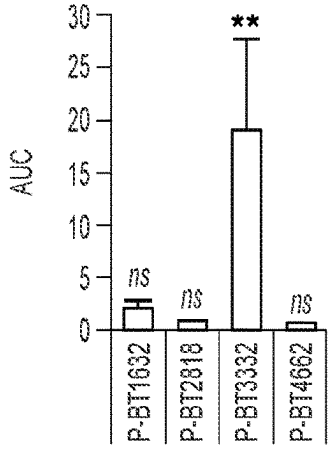


FIG. 7K

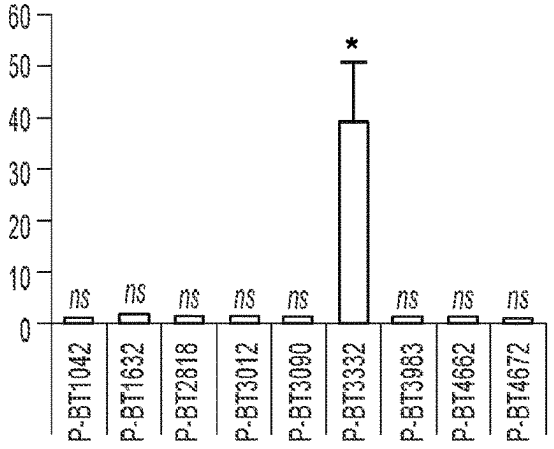


FIG. 7L

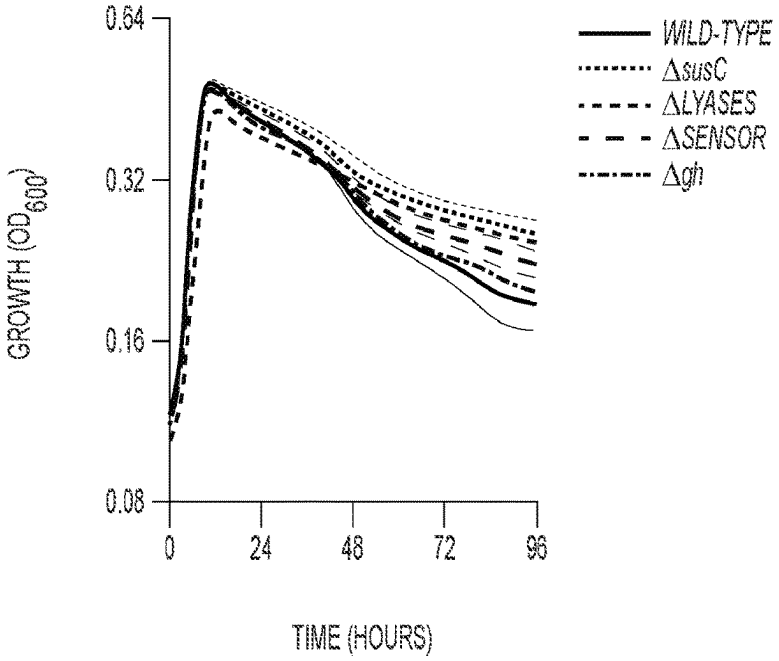


FIG. 8A

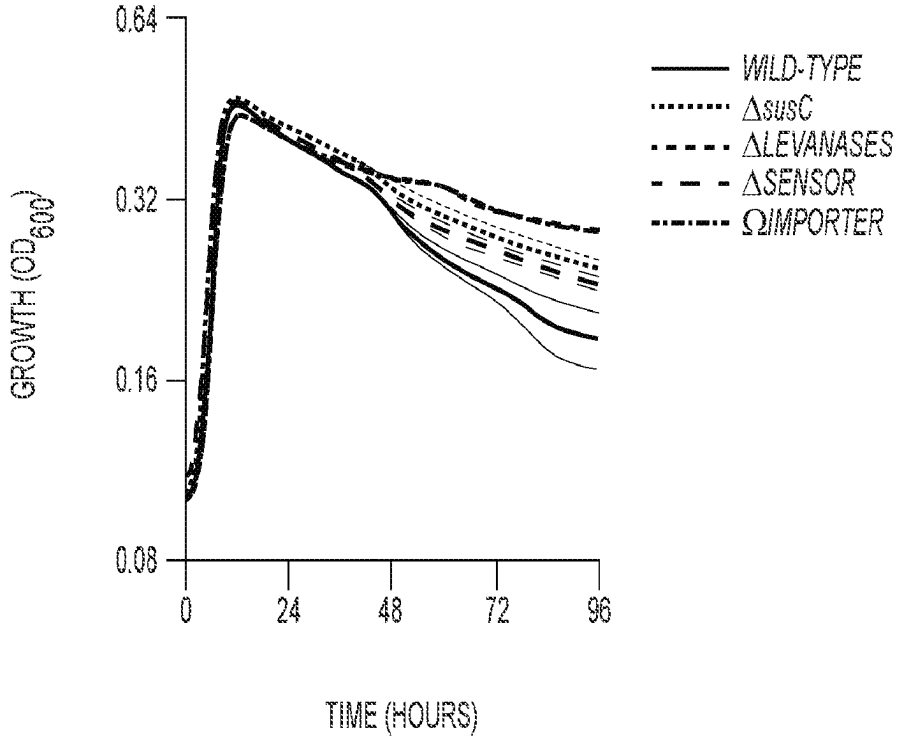

0.64
0.32
0.16
0.08
GROWTH (OD_{600})
0
24
48
72
96
TIME (HOURS)
WILD-TYPE
ΔsusC
ΔLEVANASES
ΔSENSOR
ΩIMPORTER

FIG. 8B

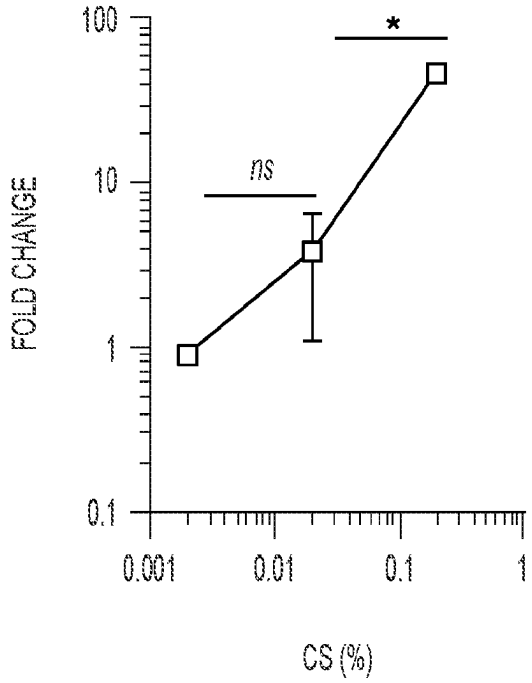

100
10
1
0.1
FOLD CHANGE
ns
*
0.001
0.01
0.1
1
CS (%)

FIG. 8C

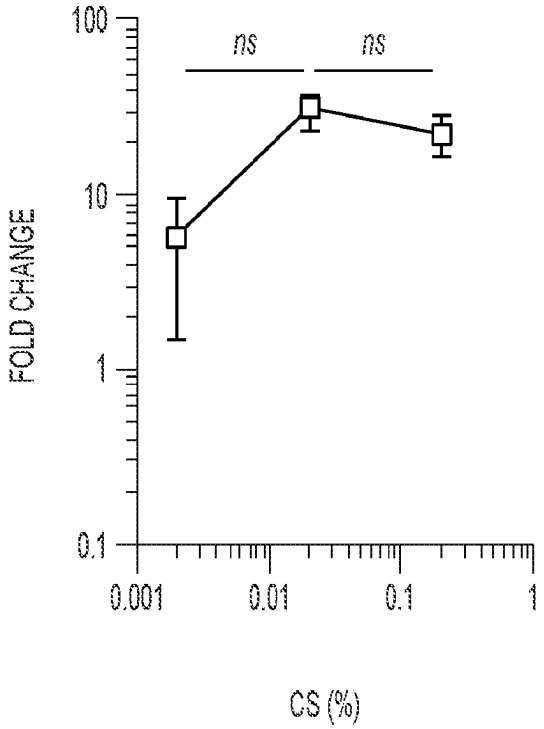

100
10
1
0.1
FOLD CHANGE
ns
ns
0.001
0.01
0.1
1
CS (%)

FIG. 8D

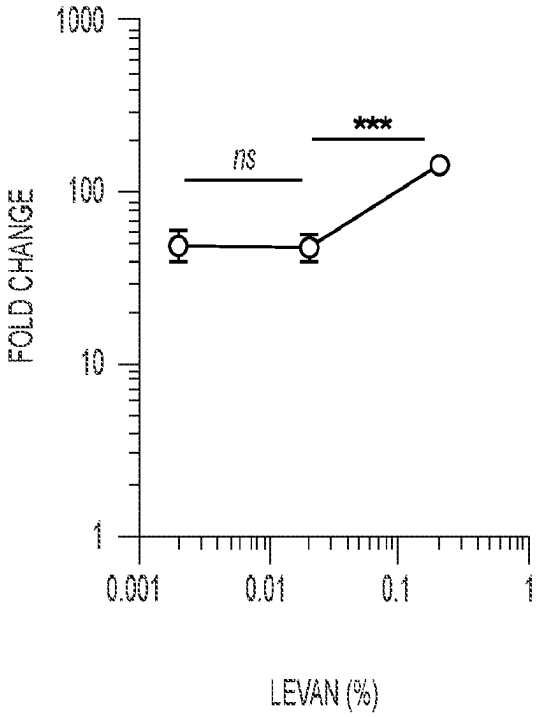

1000
100
10
1
FOLD CHANGE
ns
***
0.001
0.01
0.1
1
LEVAN (%)

FIG. 8E

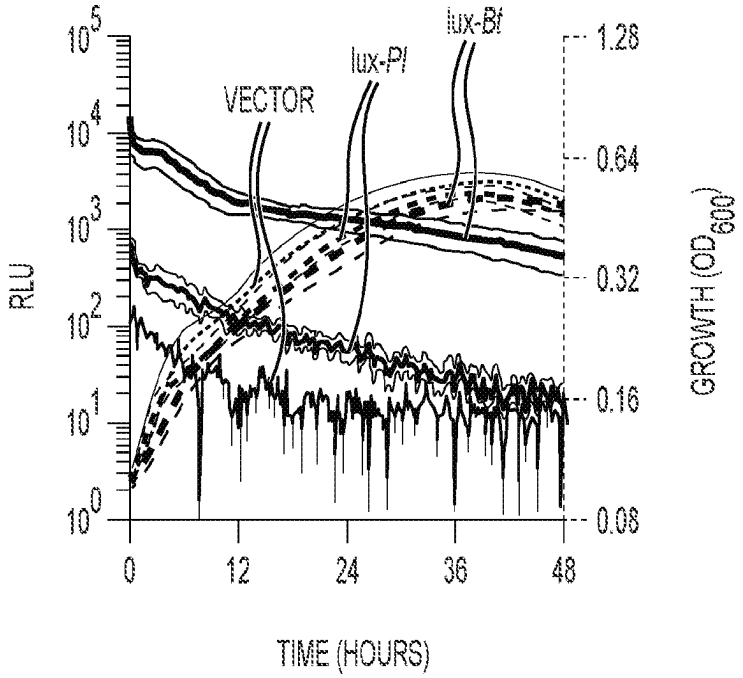

VECTOR
lux-Pl
lux-Bf
RLU
GROWTH (OD600)
TIME (HOURS)
1.28
0.64
0.32
0.16
0.08
0
12
24
36
48

FIG. 9A

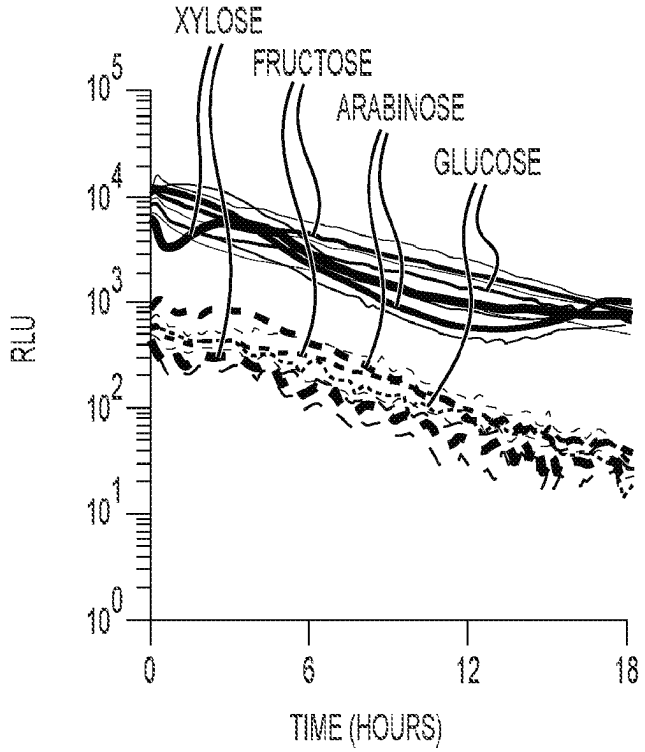

XYLOSE
FRUCTOSE
ARABINOSE
GLUCOSE
RLU
TIME (HOURS)
0
6
12
18

FIG. 9B

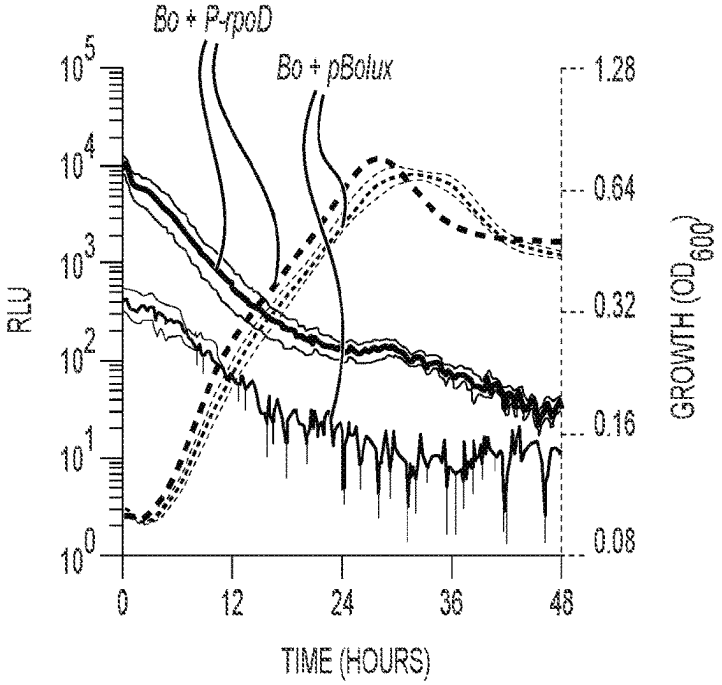

Bo + P-rpoD
Bo + pBolux
RLU
GROWTH (OD600)
TIME (HOURS)
1.28
0.64
0.32
0.16
0.08
0
12
24
36
48

FIG. 9C

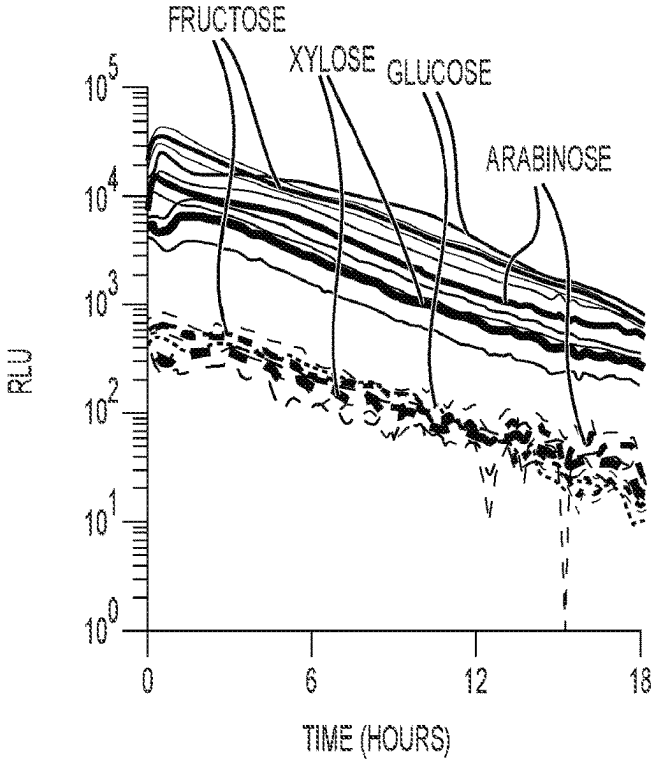

FRUCTOSE
XYLOSE
GLUCOSE
ARABINOSE
RLU
TIME (HOURS)
0
6
12
18

FIG. 9D

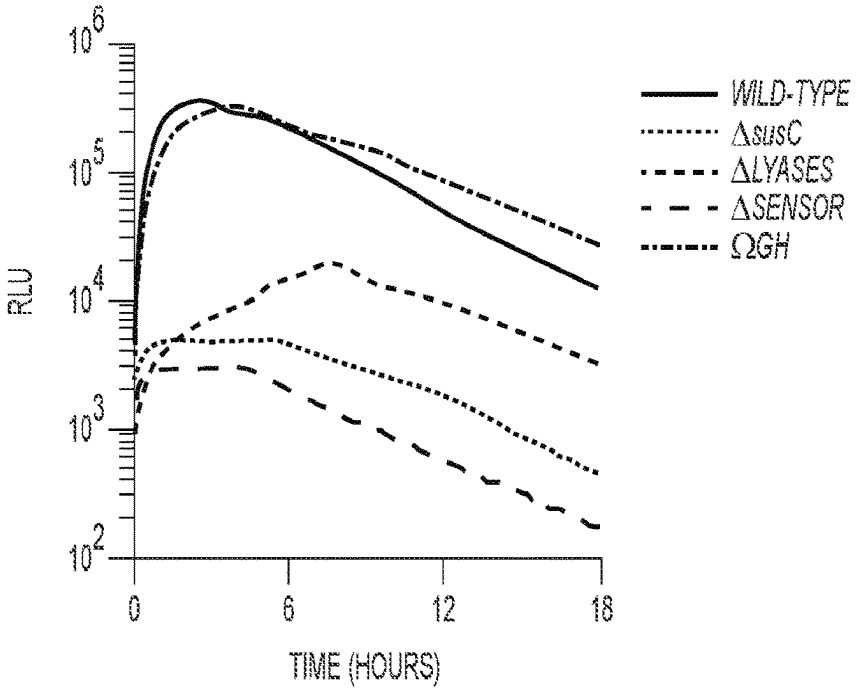


FIG. 10A

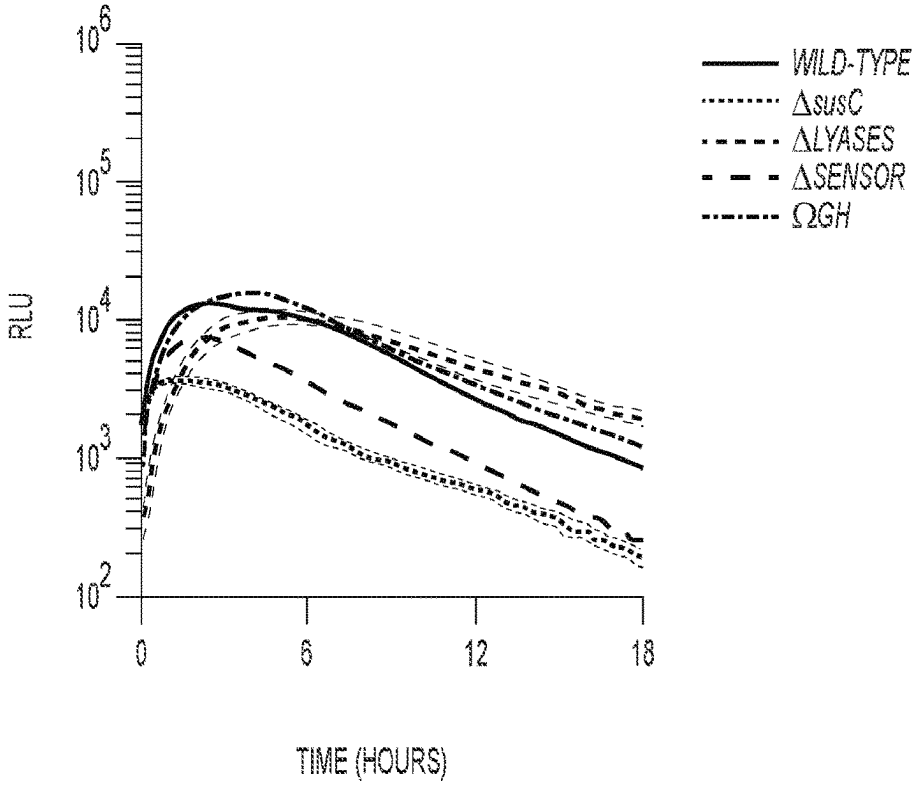


FIG. 10B

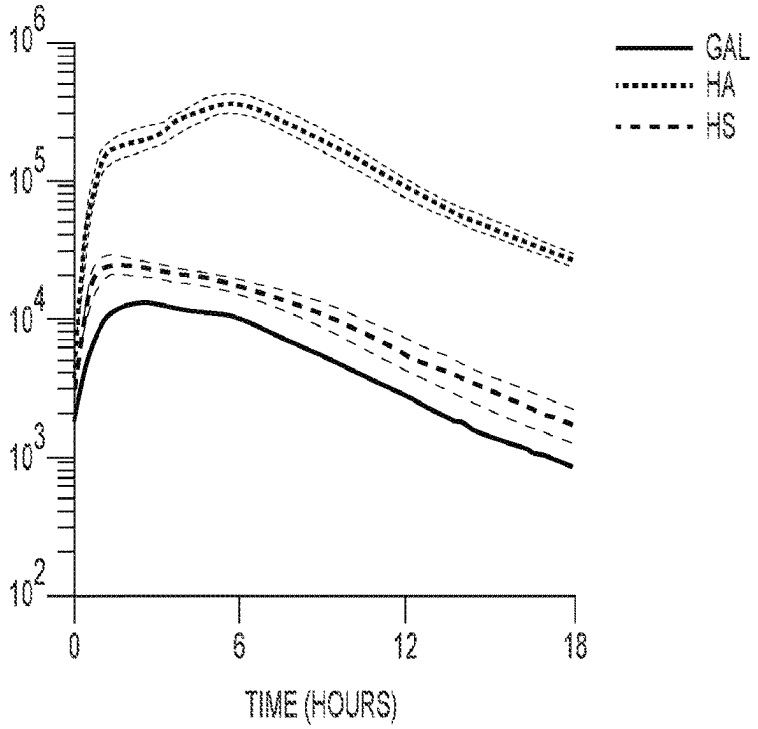


FIG. 10C

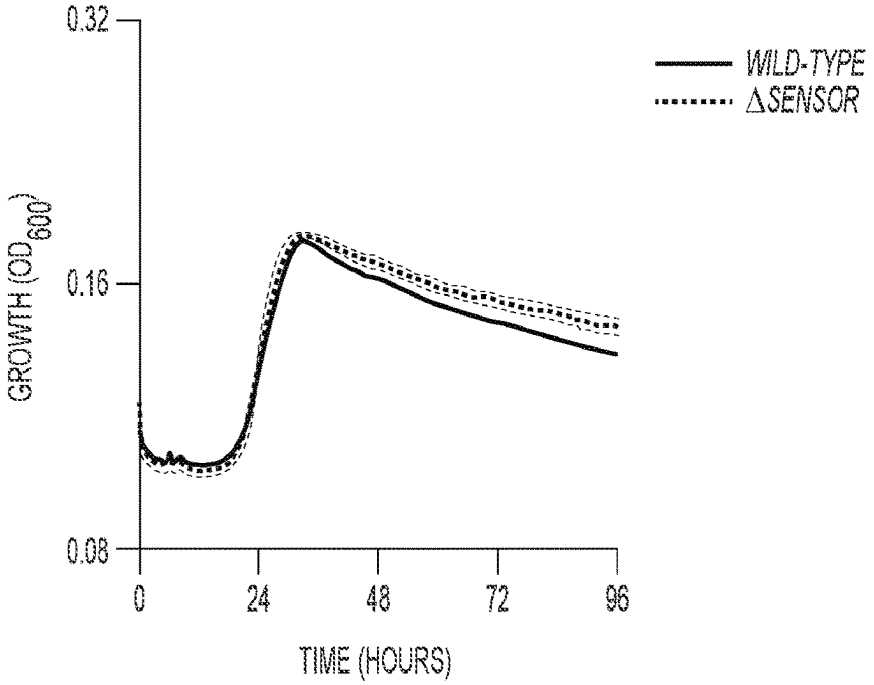


FIG. 10D

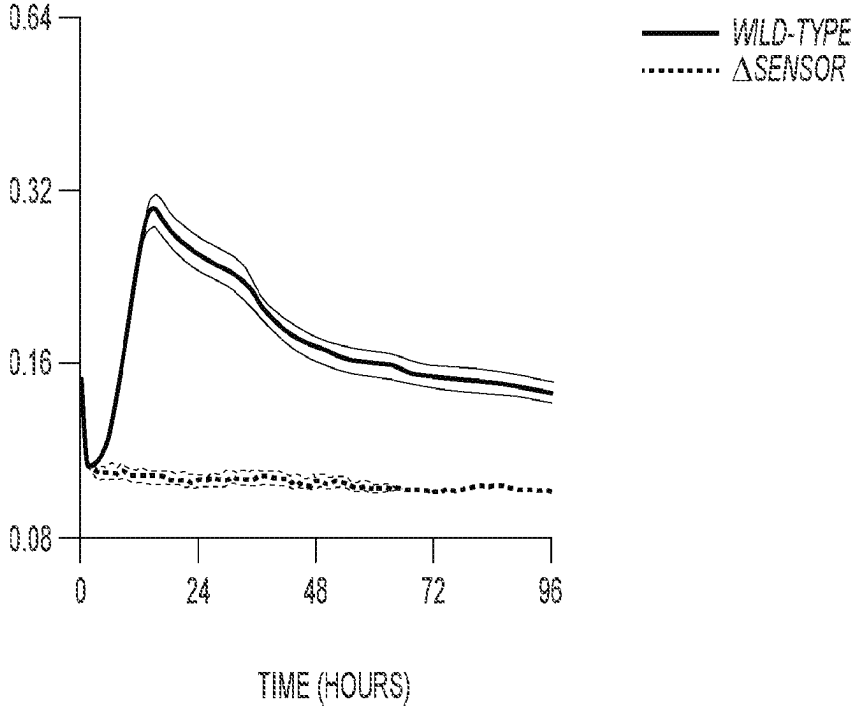


FIG. 10E

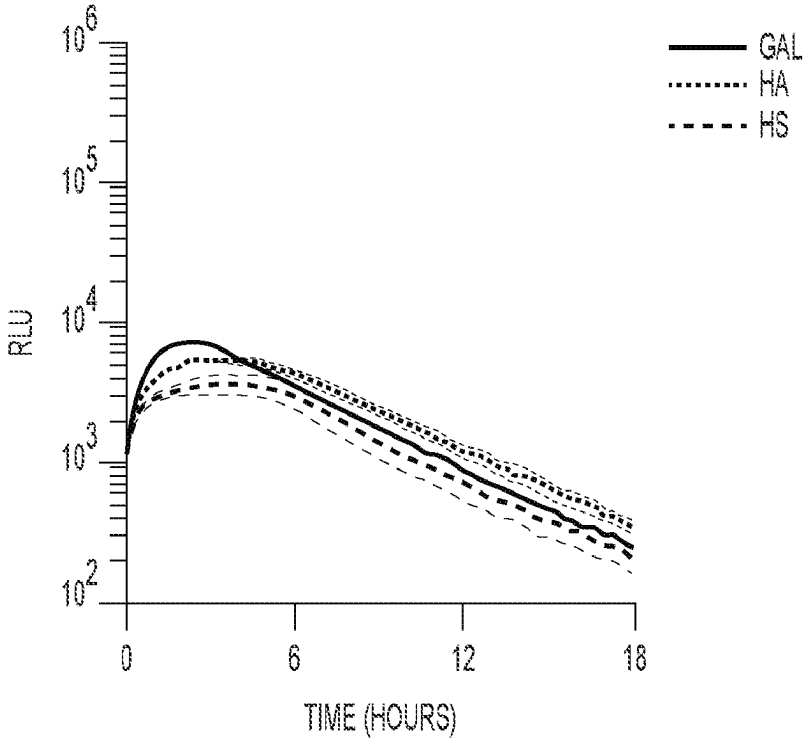


FIG. 10F

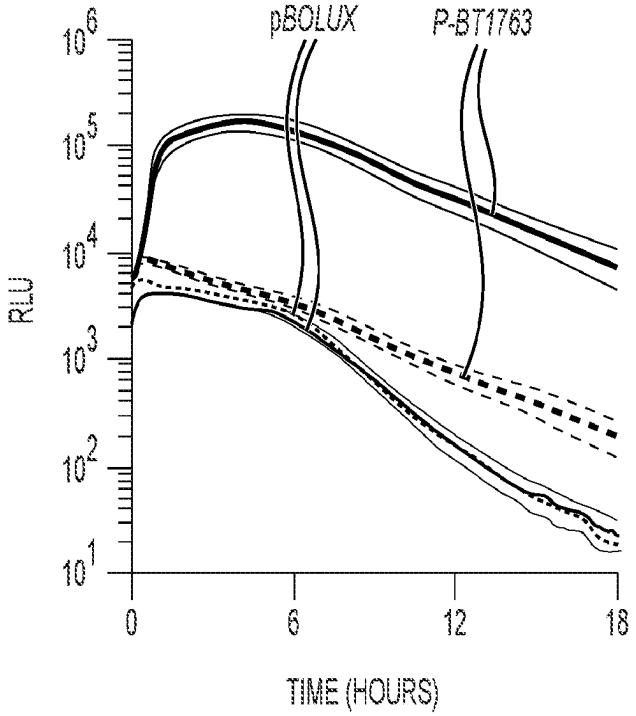


FIG. 11A

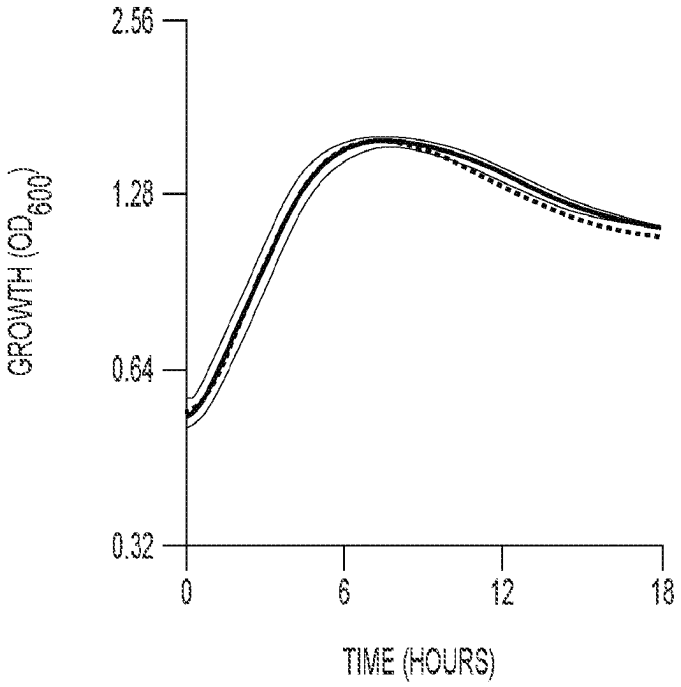


FIG. 11B

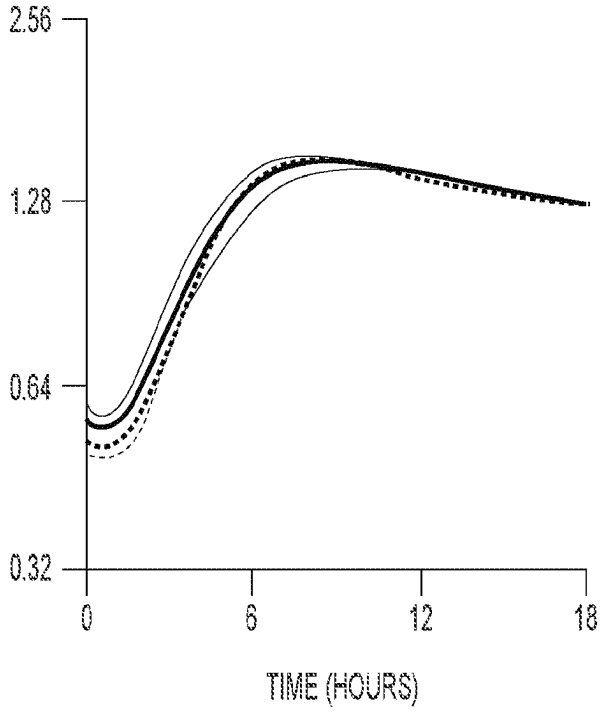


FIG. 11C

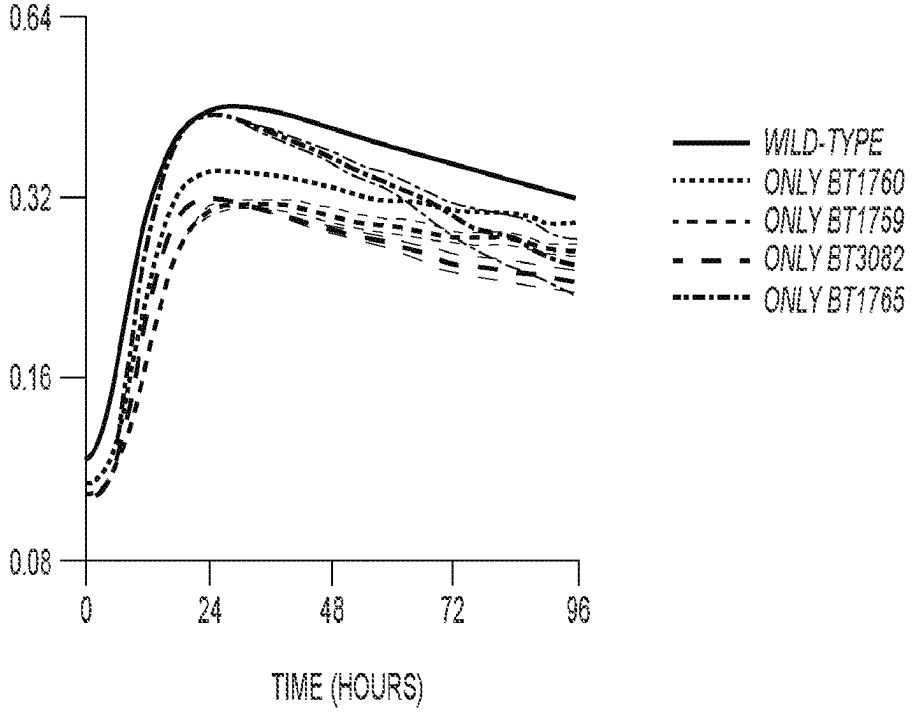


FIG. 11D

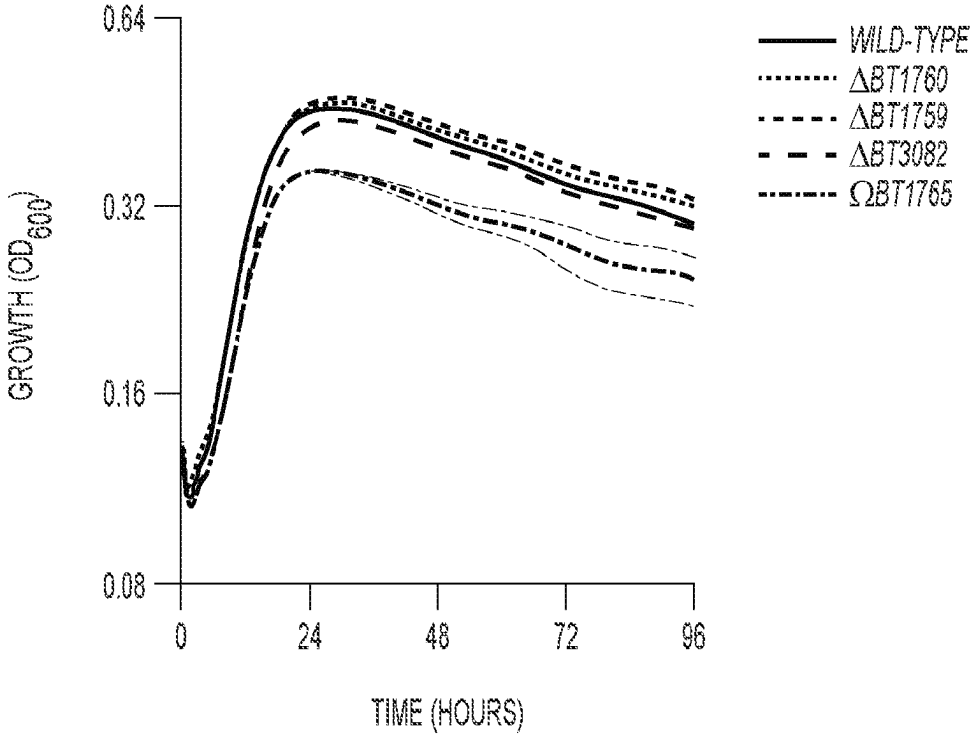


FIG. 11E

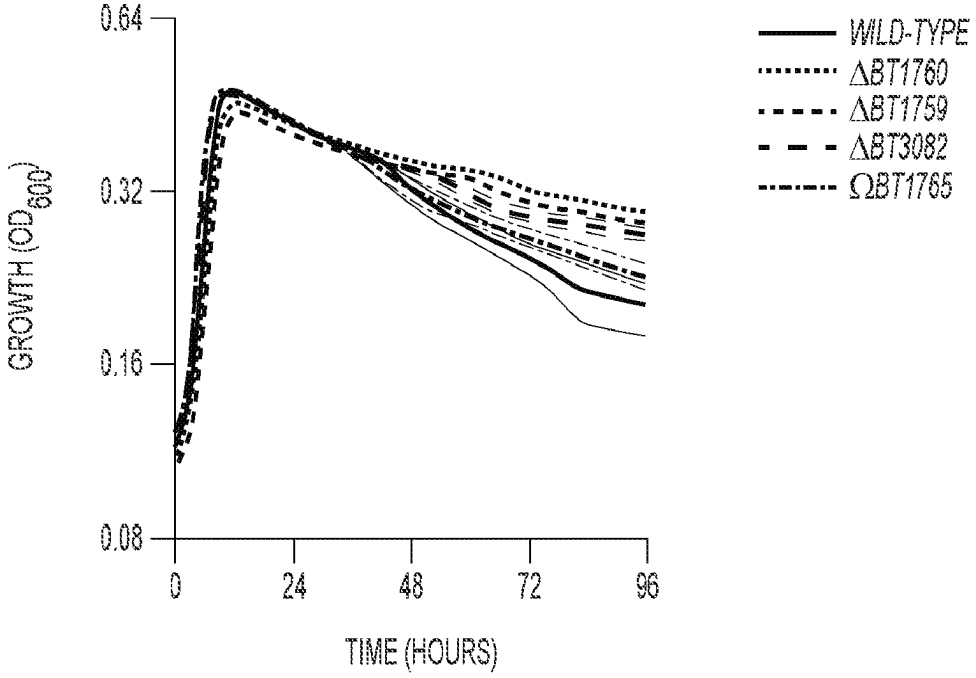


FIG. 11F

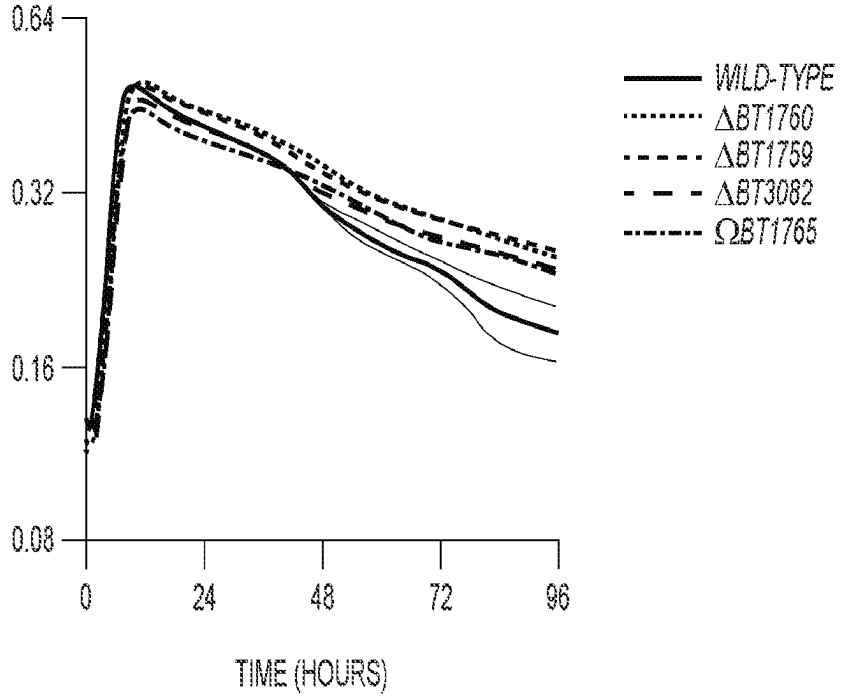


FIG. 11G

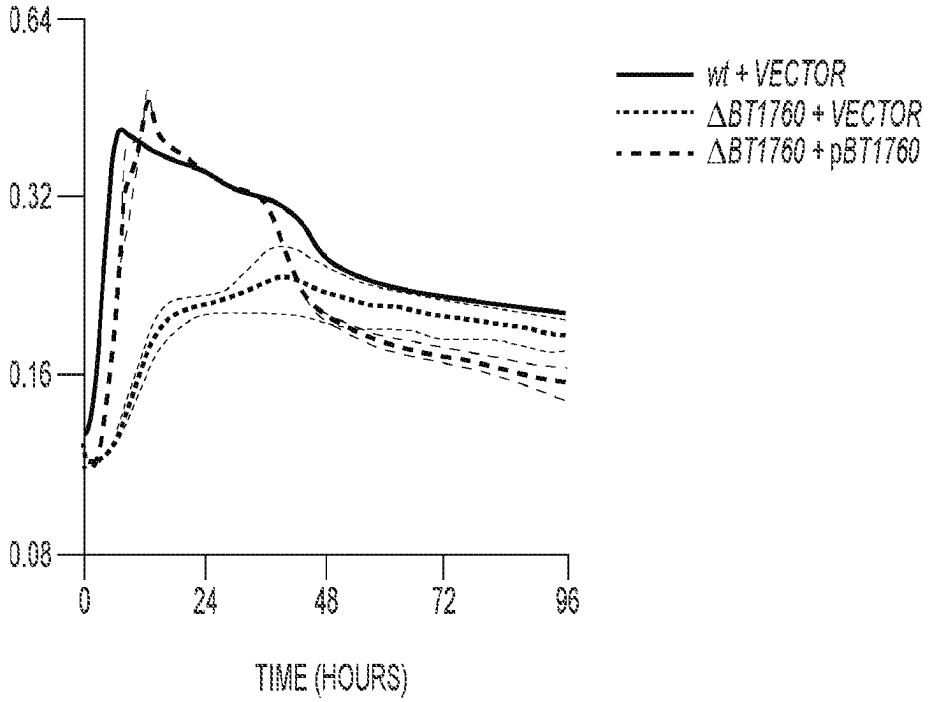


FIG. 11H

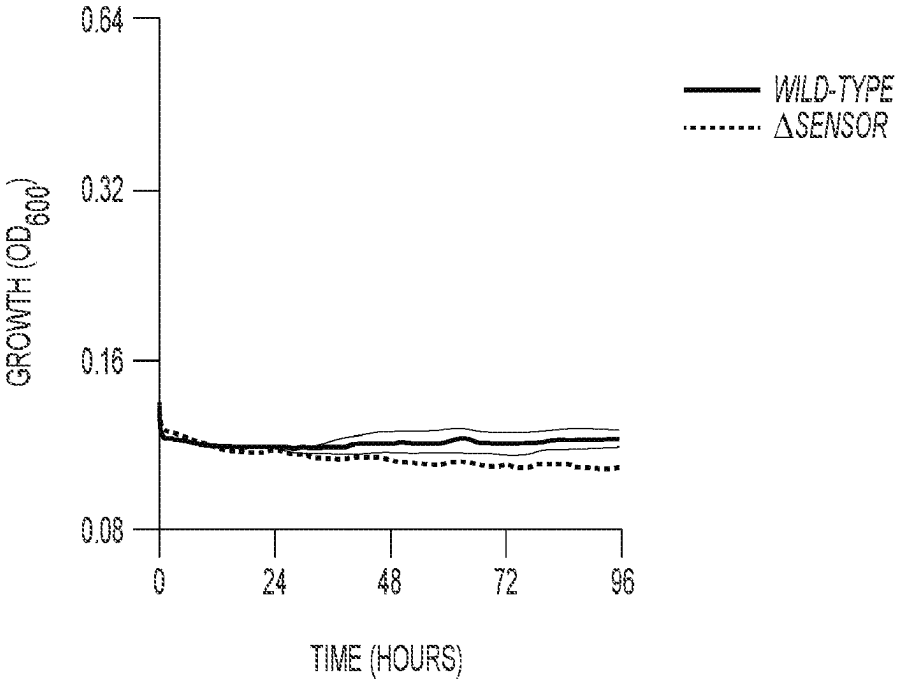


FIG. 12A

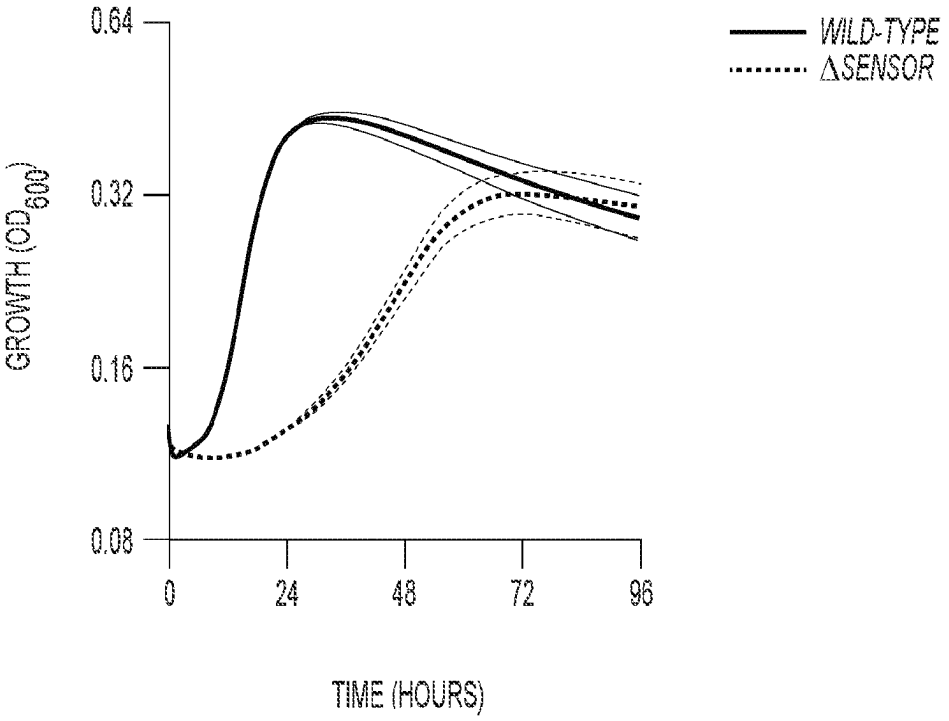


FIG. 12B

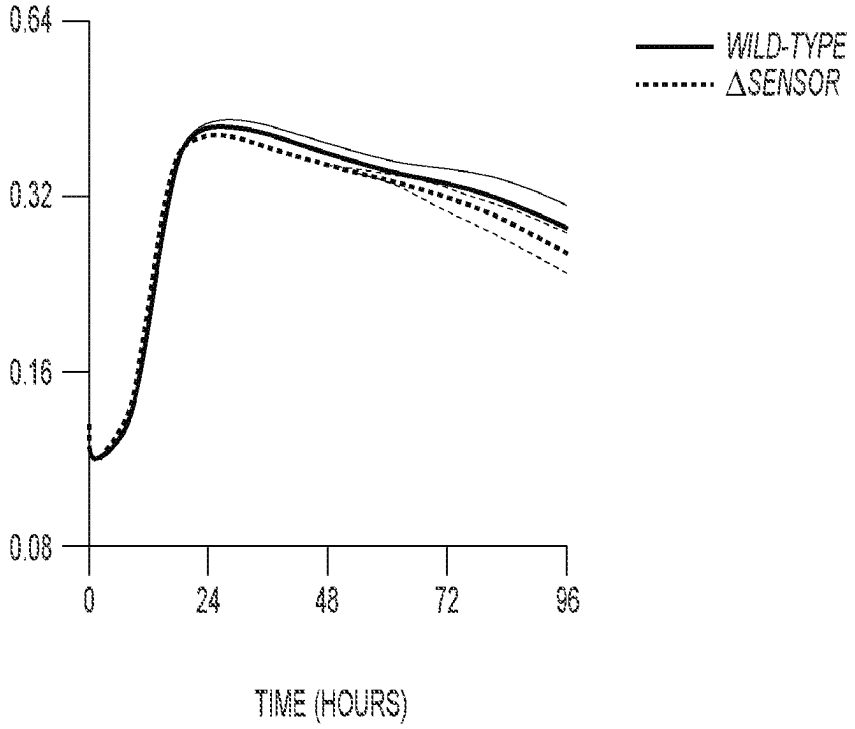


FIG. 12C

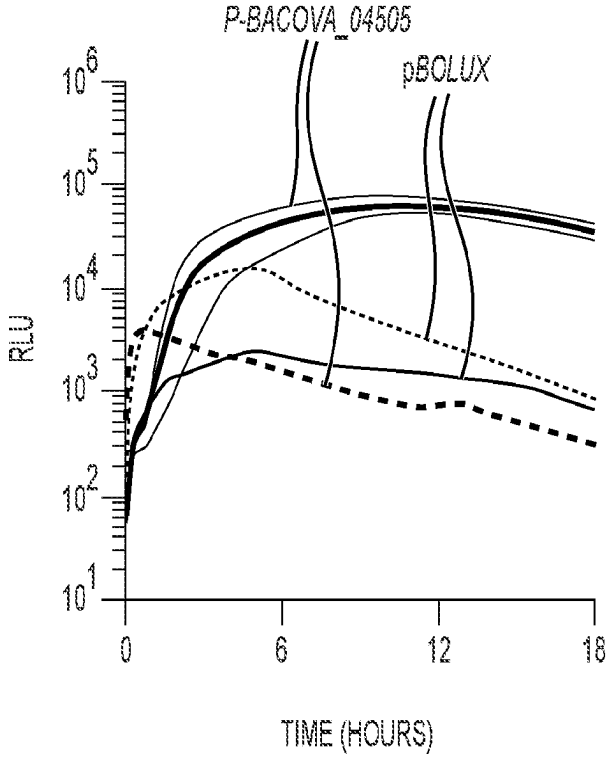


FIG. 12D

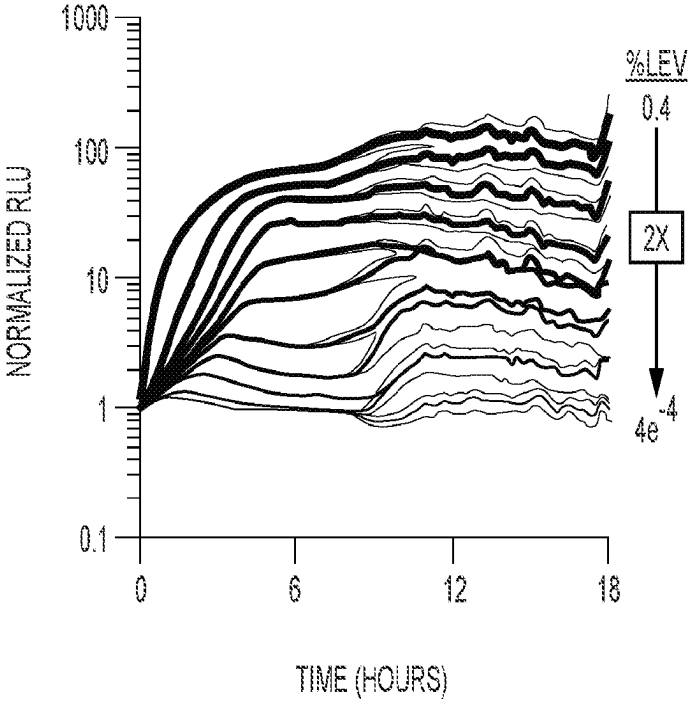


FIG. 13A

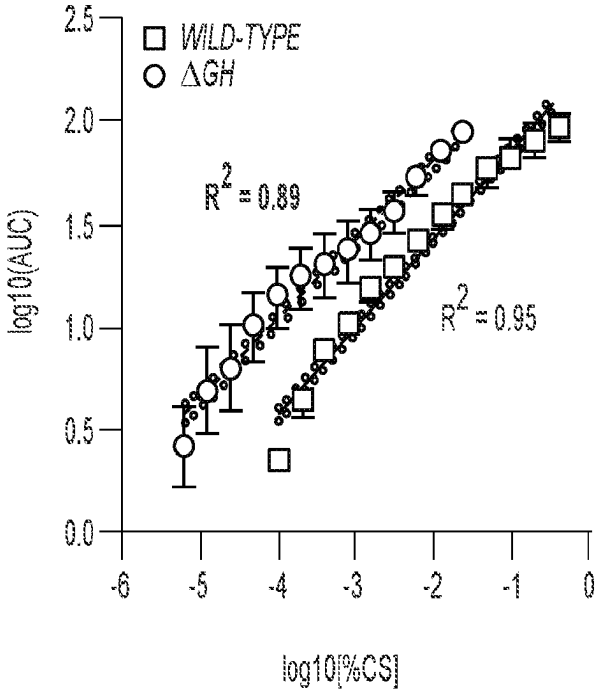


FIG. 13B

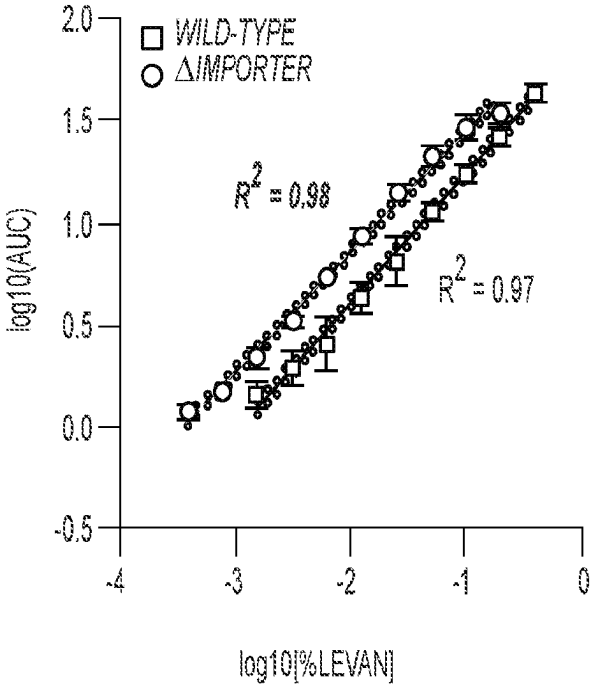


FIG. 13D

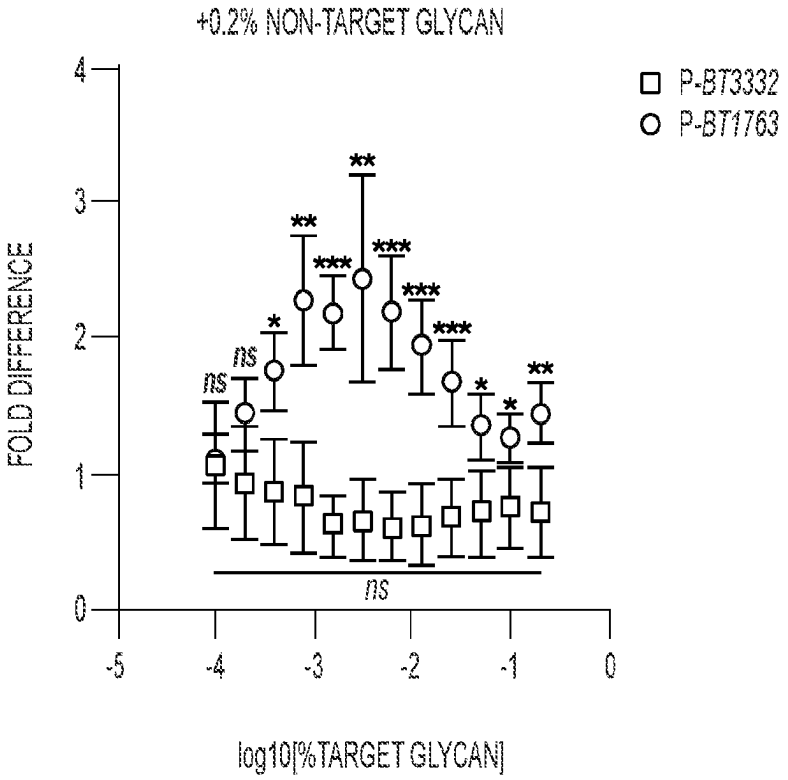


FIG. 13D

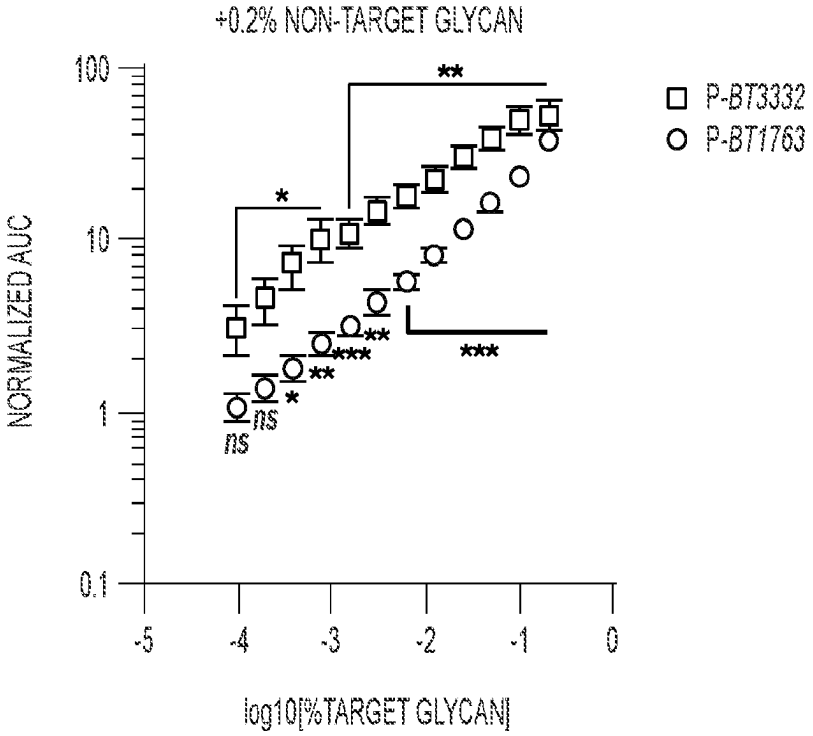


FIG. 13E

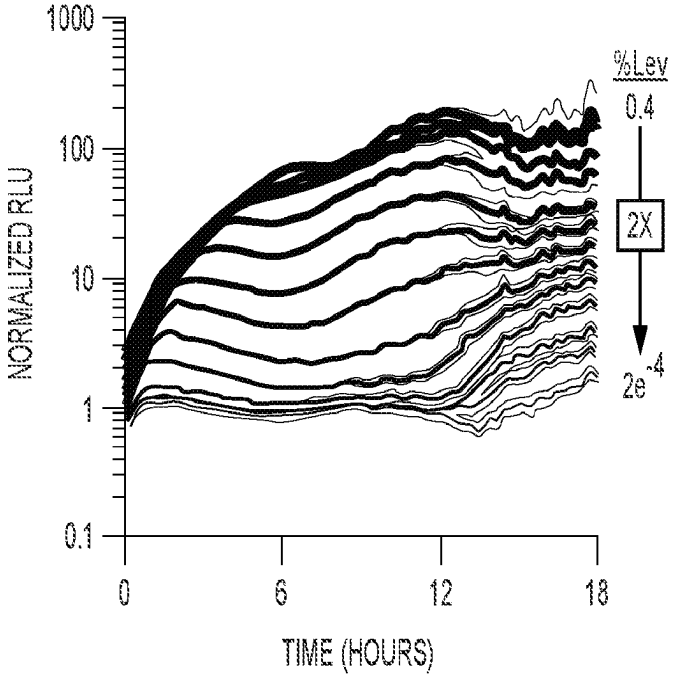


FIG. 13F

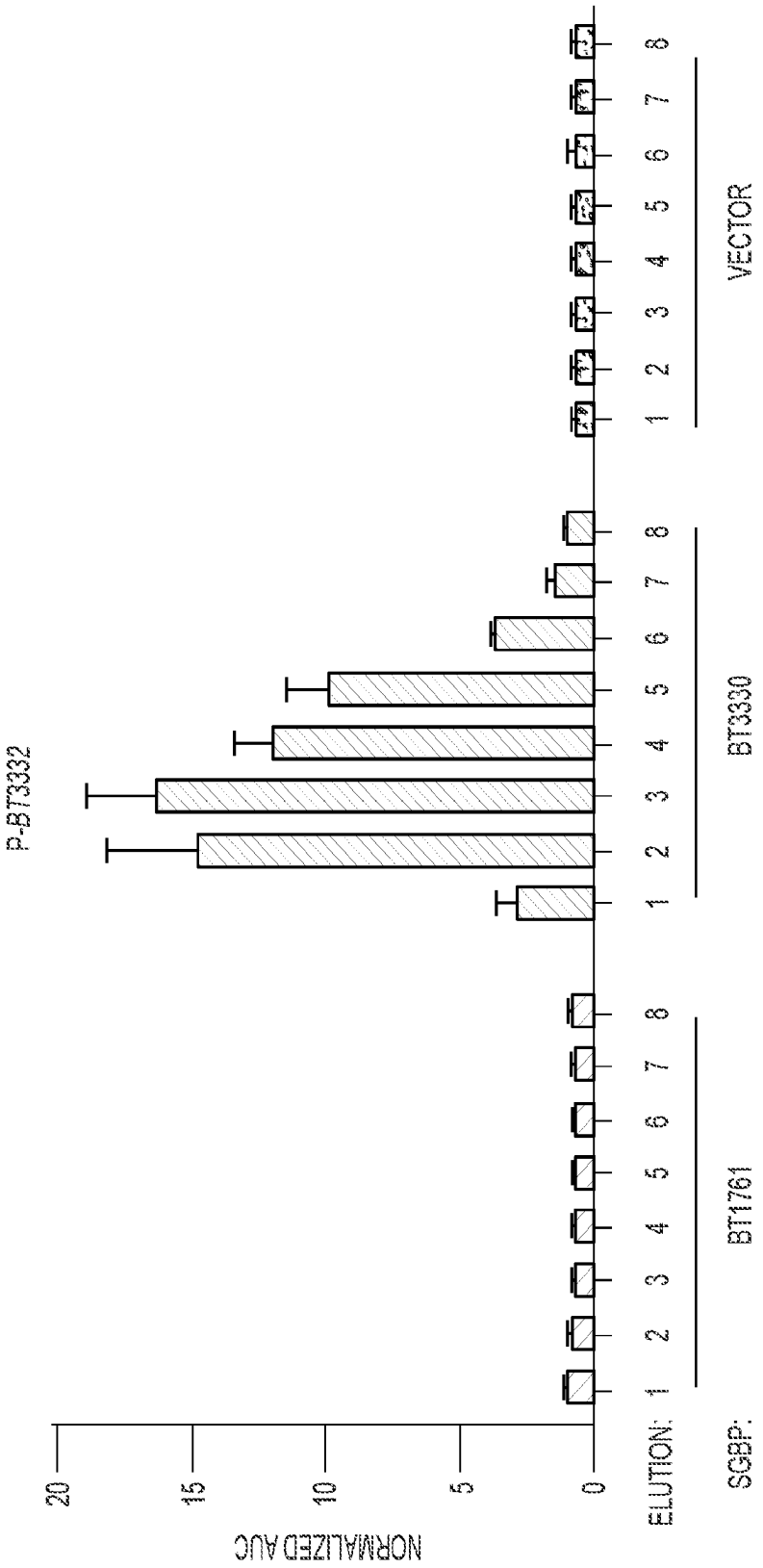

P-BT3332
NORMALIZED AUC
20
15
10
5
0
ELUTION: 1 2 3 4 5 6 7 8 1 2 3 4 5 6 7 8 1 2 3 4 5 6 7 8
SGBP: BT1761 BT3330 VECTOR

FIG. 14A

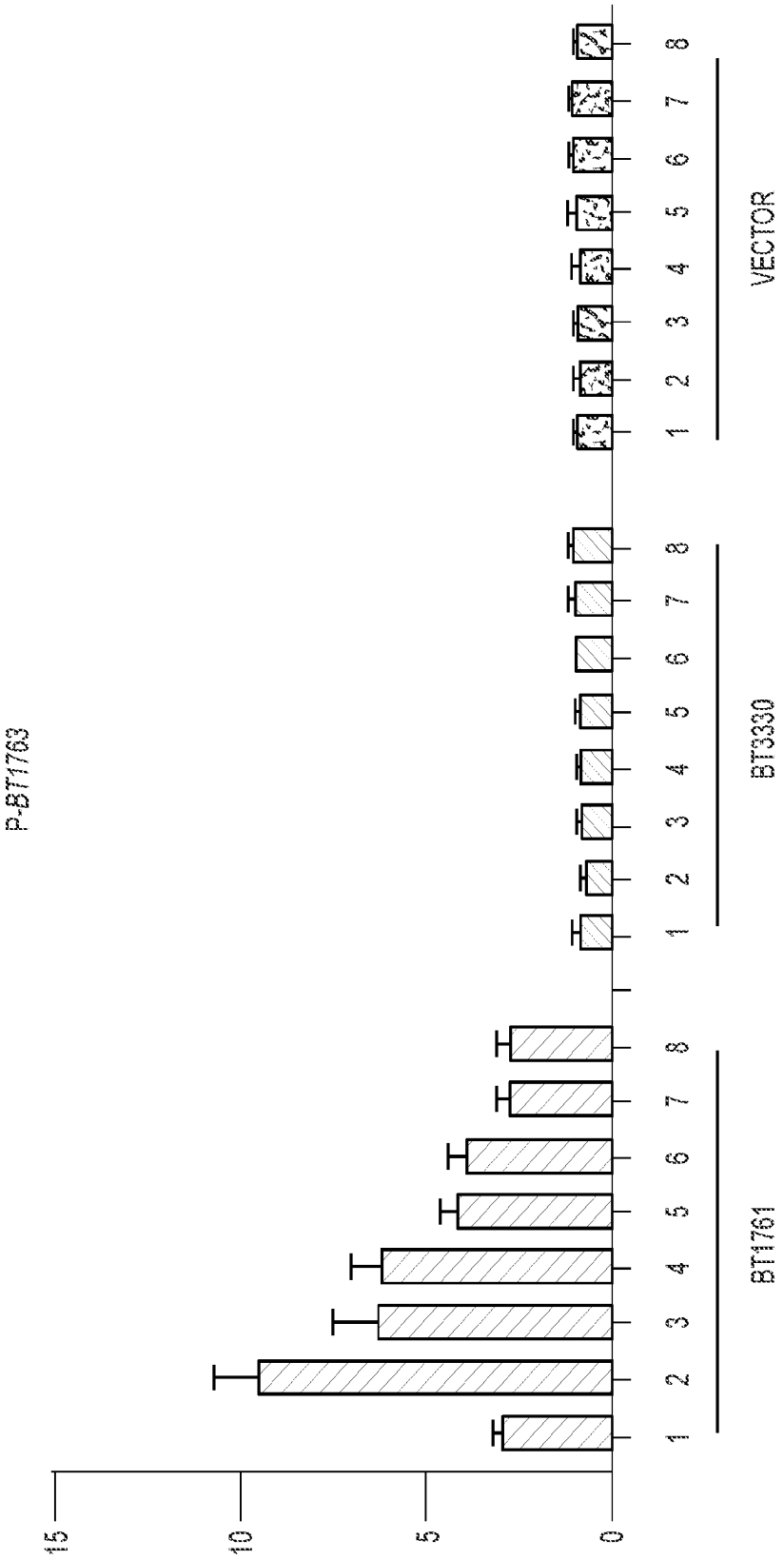

P-BT1763
15
10
5
0
1 2 3 4 5 6 7 8
BT1761
1 2 3 4 5 6 7 8
BT3330
1 2 3 4 5 6 7 8
VECTOR

FIG. 14B

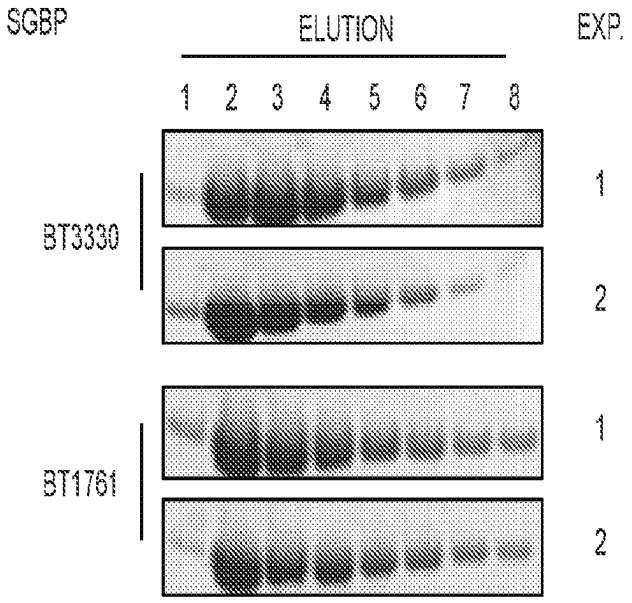


FIG. 14C

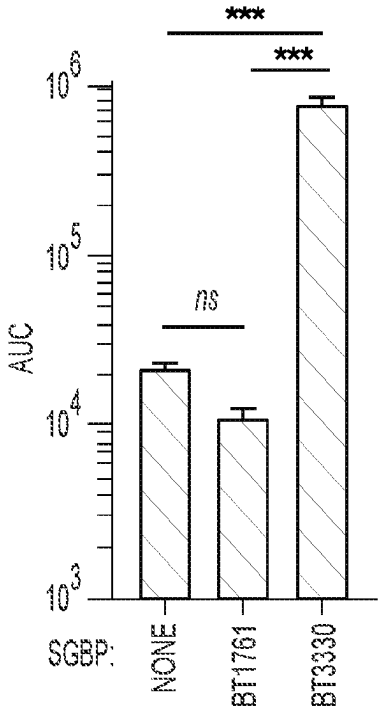


FIG. 14D

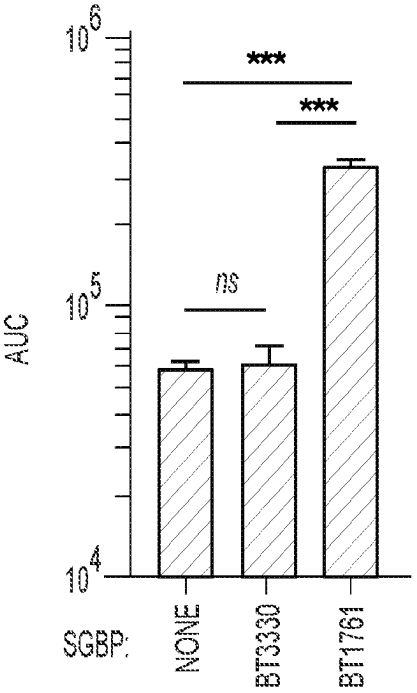


FIG. 14E

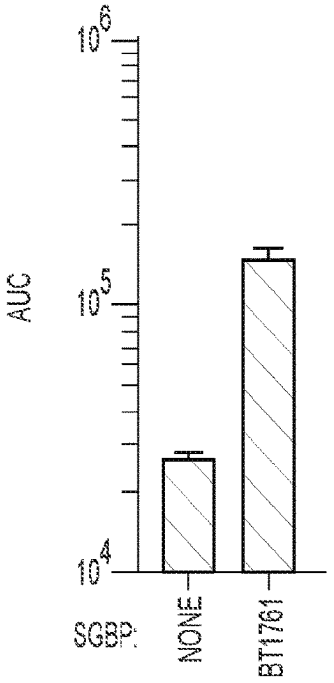


FIG. 14F

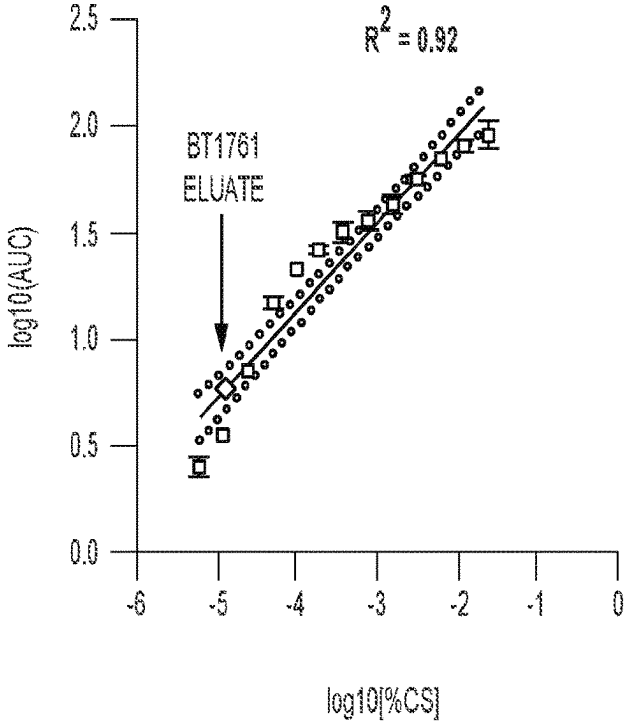


FIG. 14G

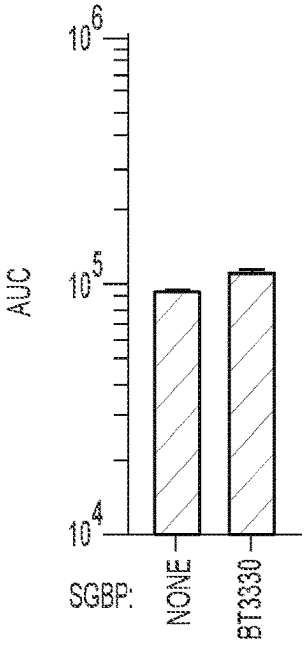


FIG. 14H

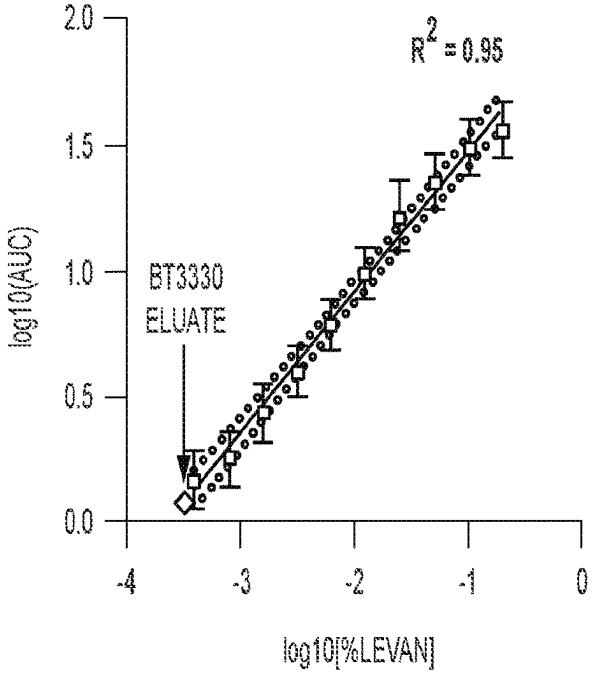


FIG. 14I

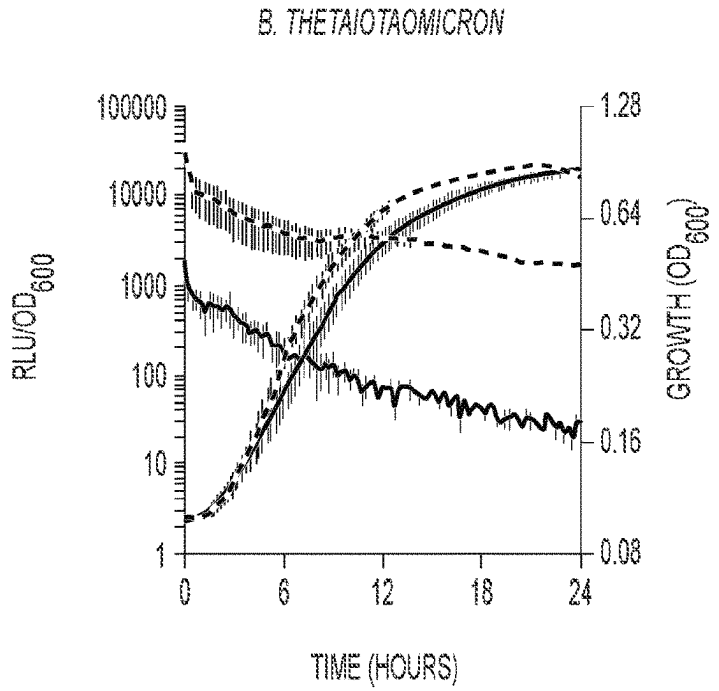


FIG. 15A

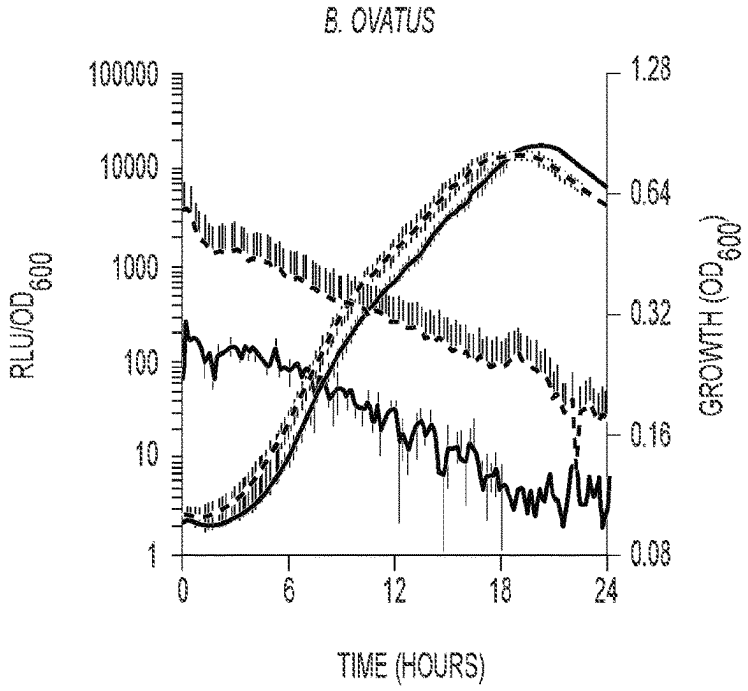


FIG. 15B

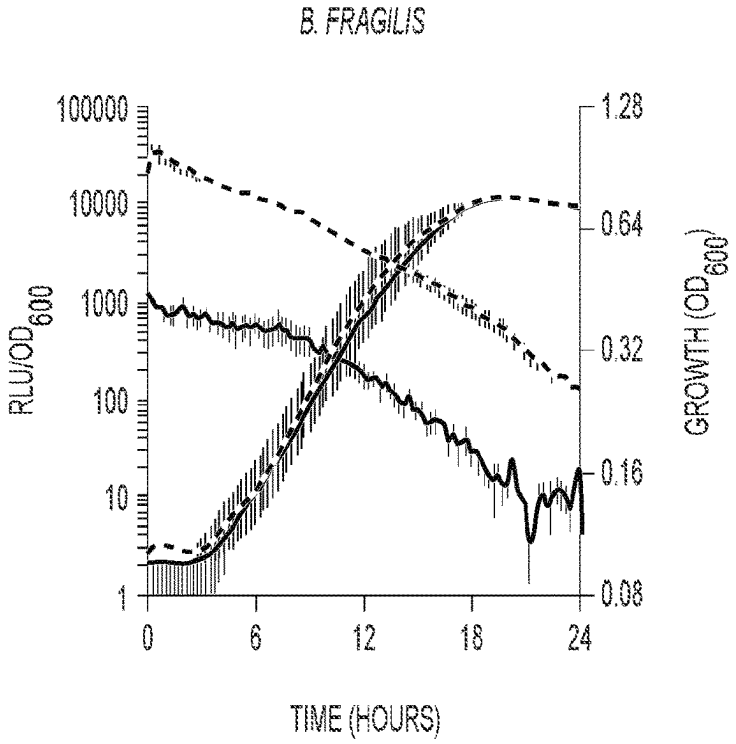


FIG. 15C

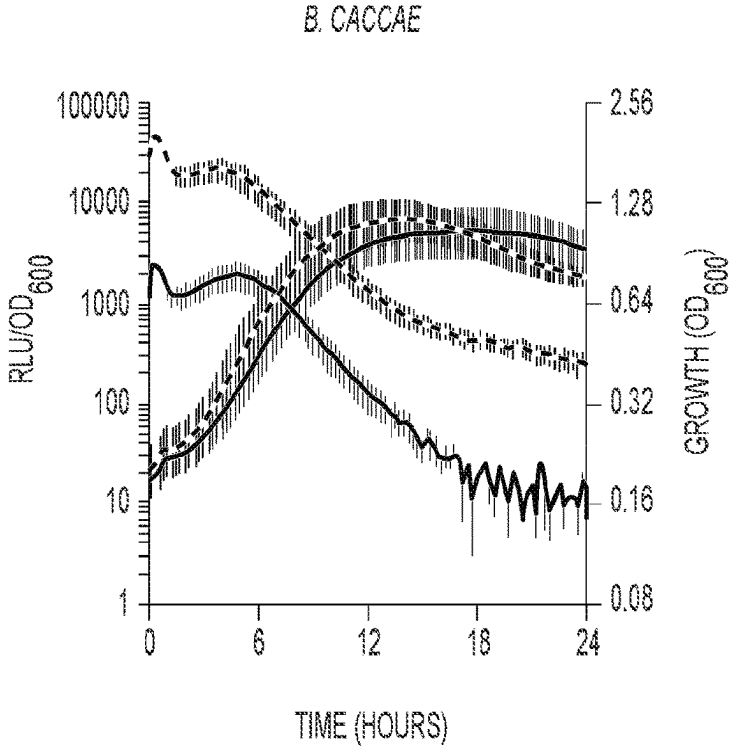


FIG. 15D

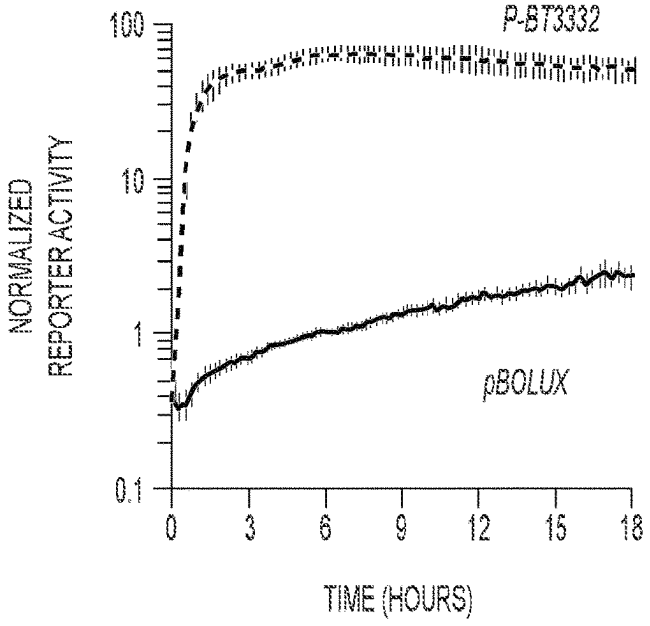


FIG. 16A

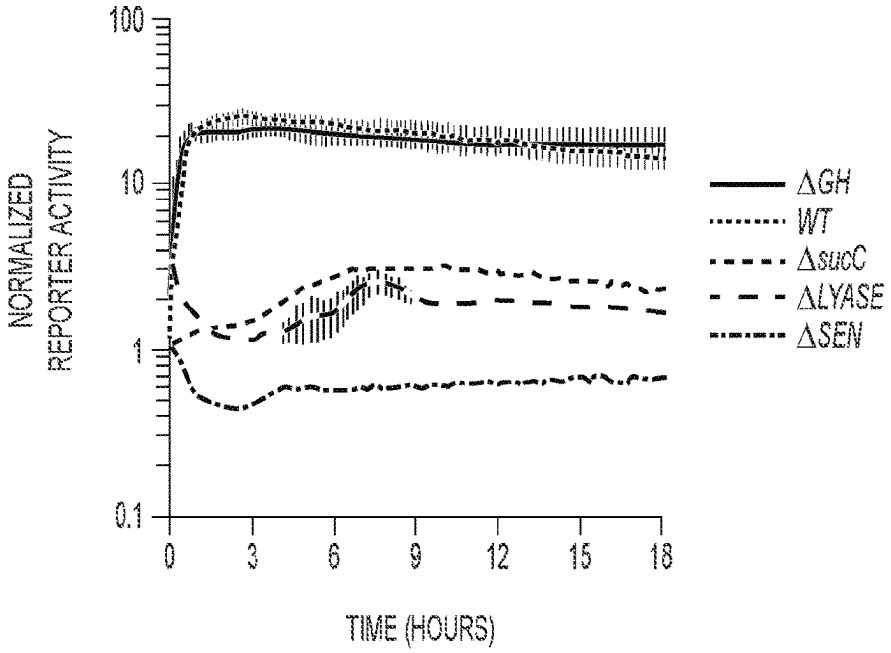


FIG. 16B

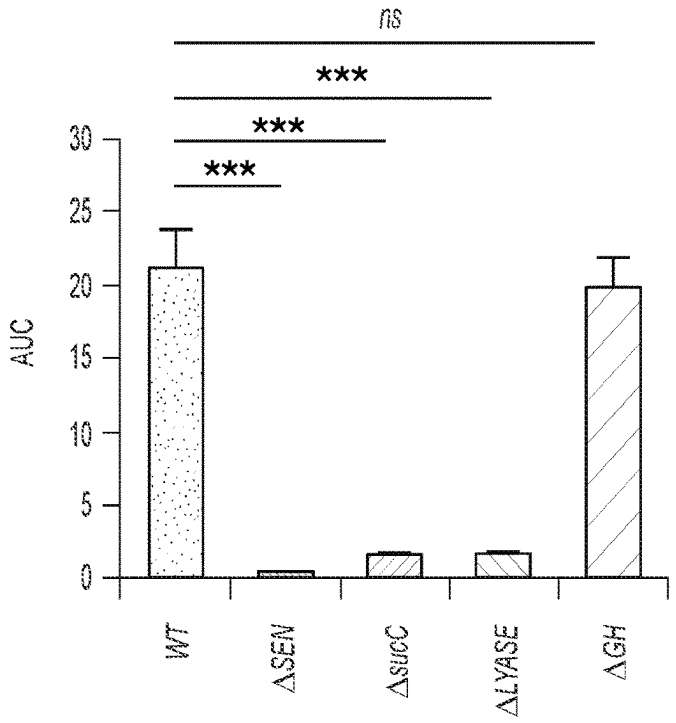


FIG. 16C

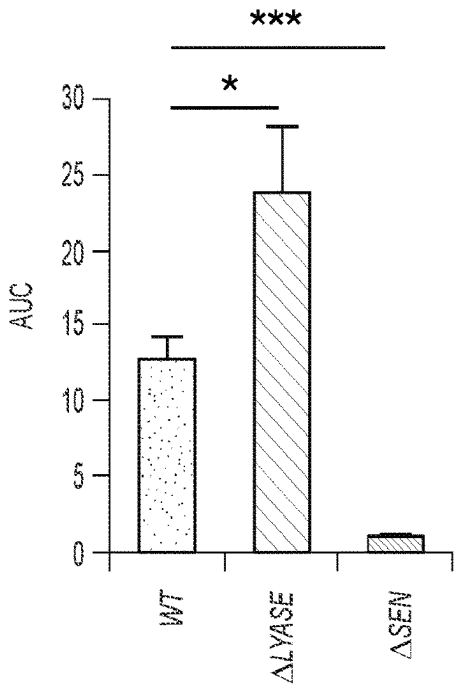


FIG. 16D

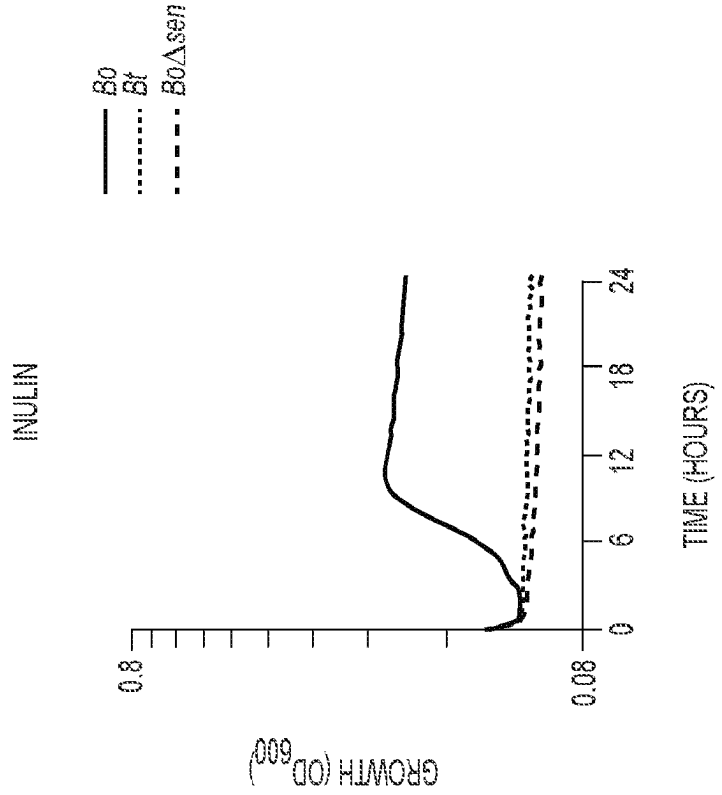


FIG. 17B

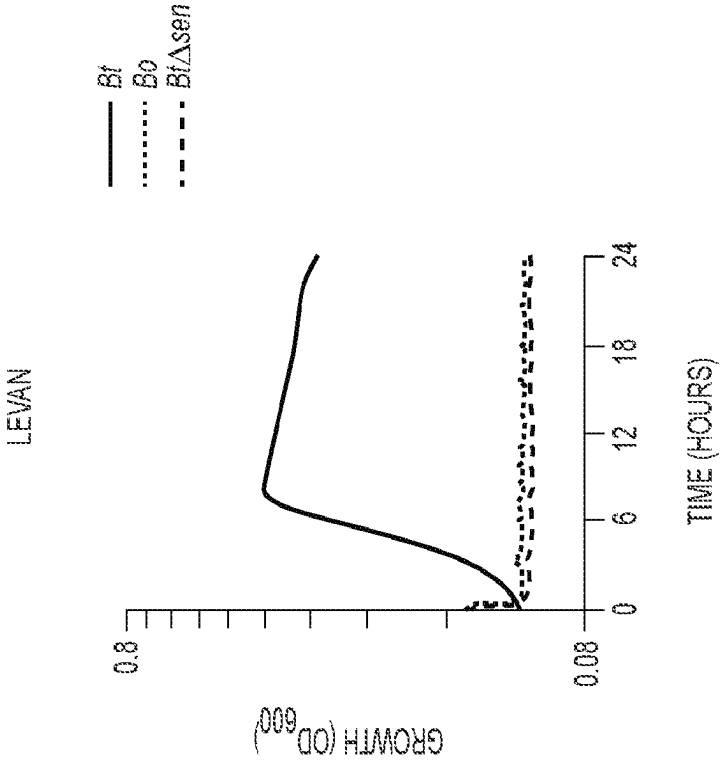


FIG. 17C

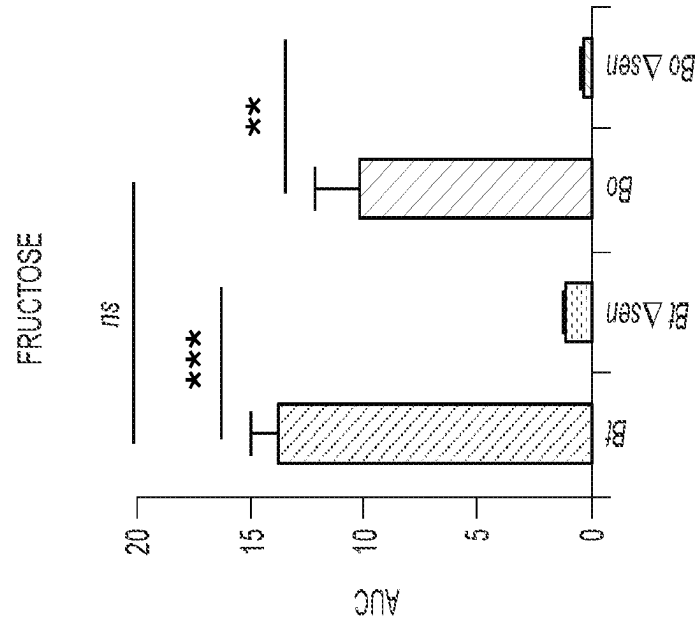


FIG. 17D

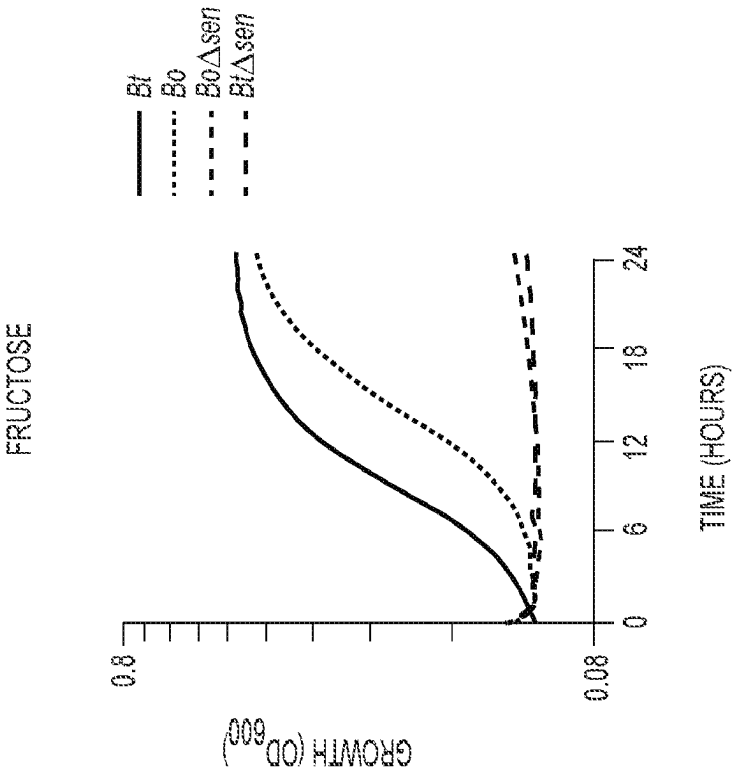


FIG. 17C

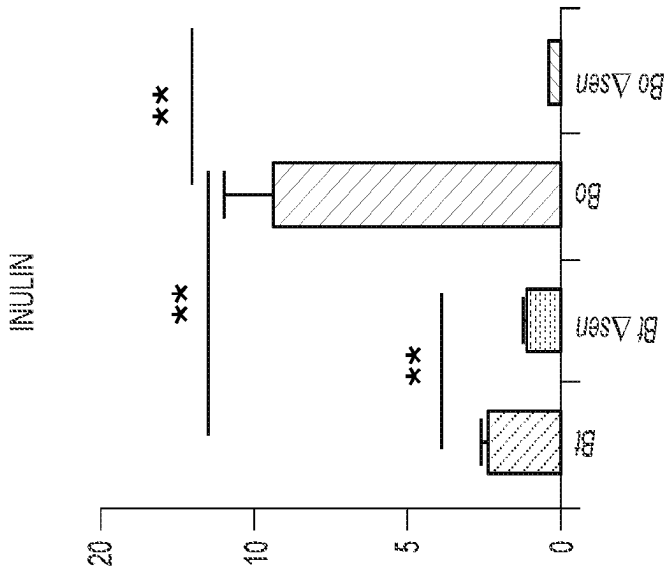


FIG. 17F

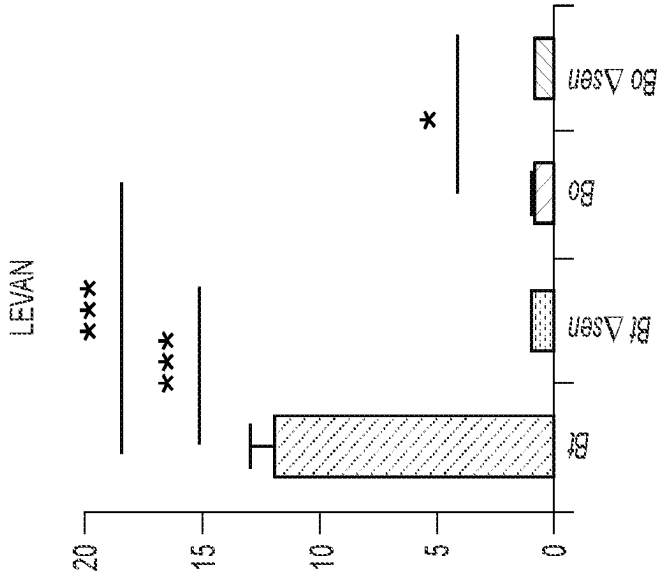


FIG. 17E

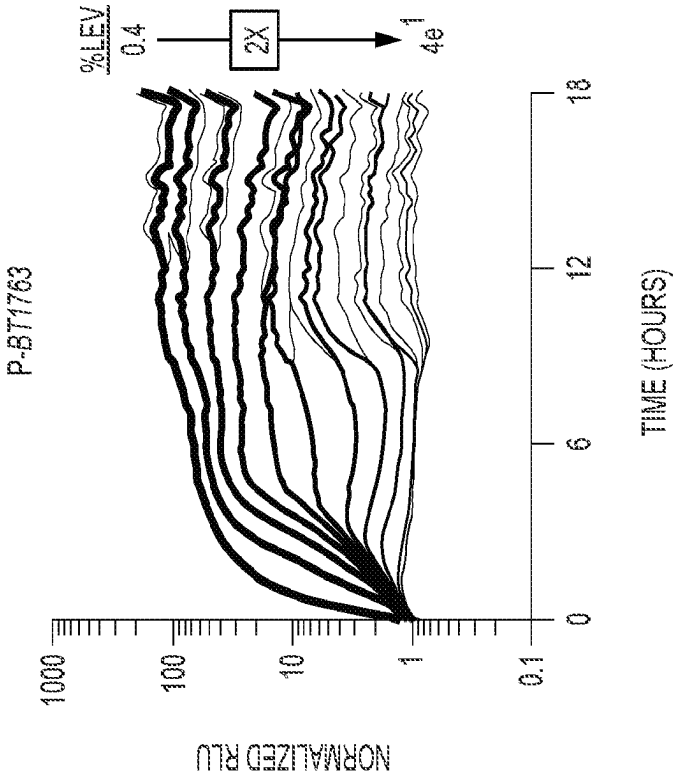


FIG. 18B

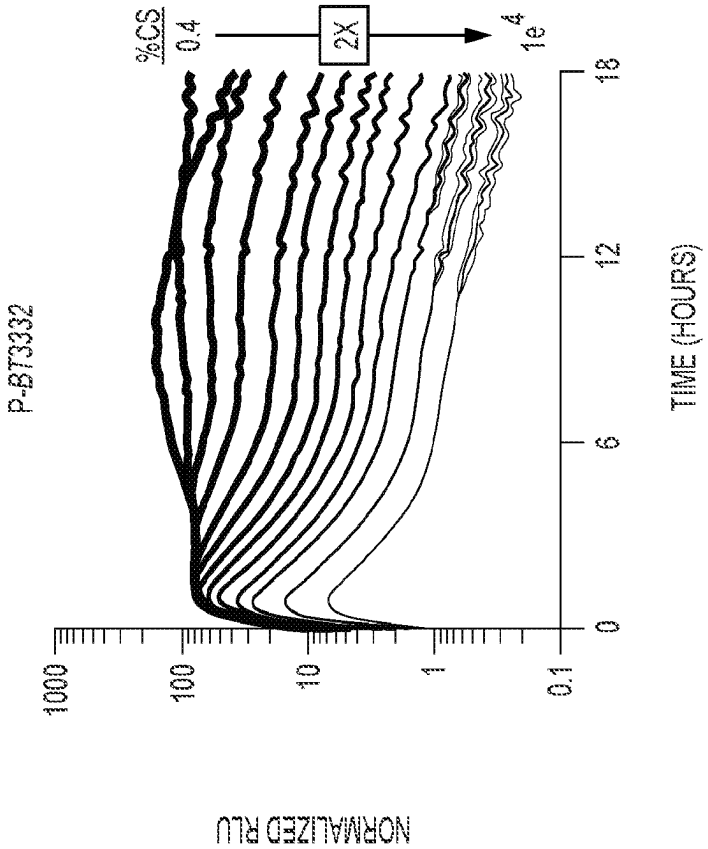


FIG. 18A

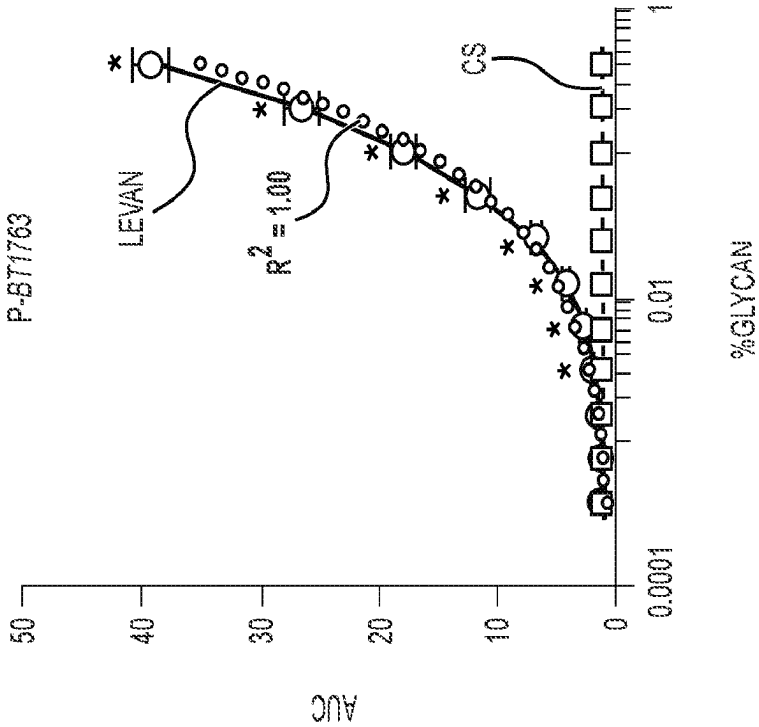


FIG. 18D

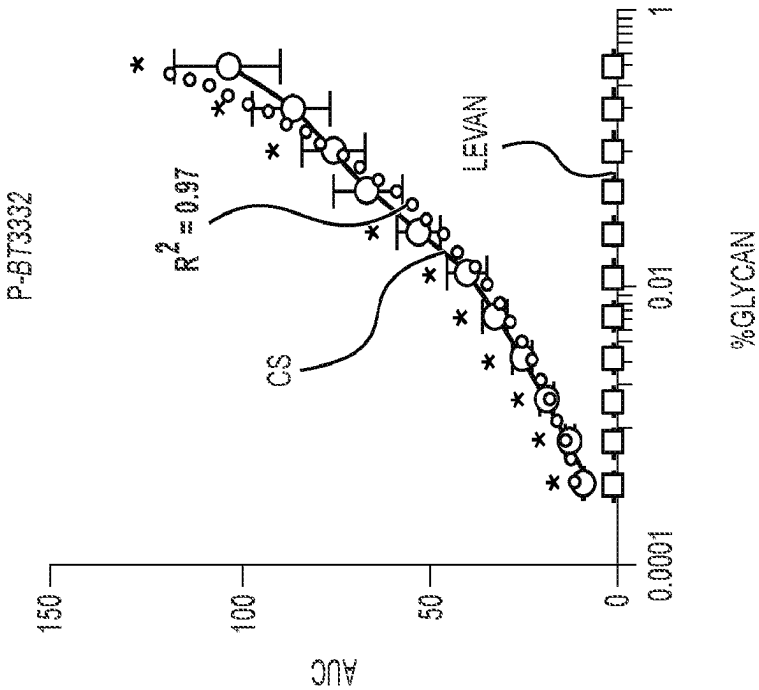


FIG. 18C

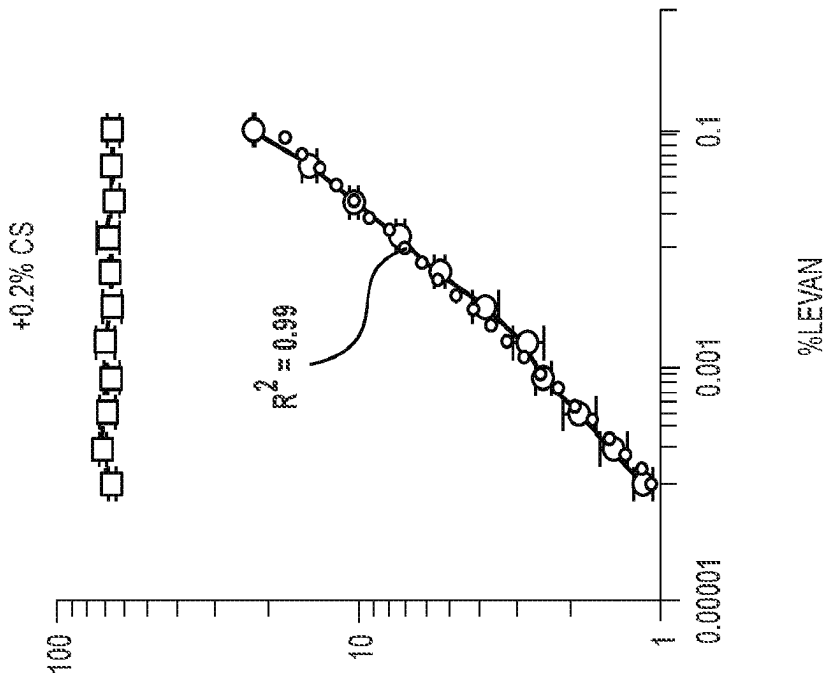


FIG. 18F

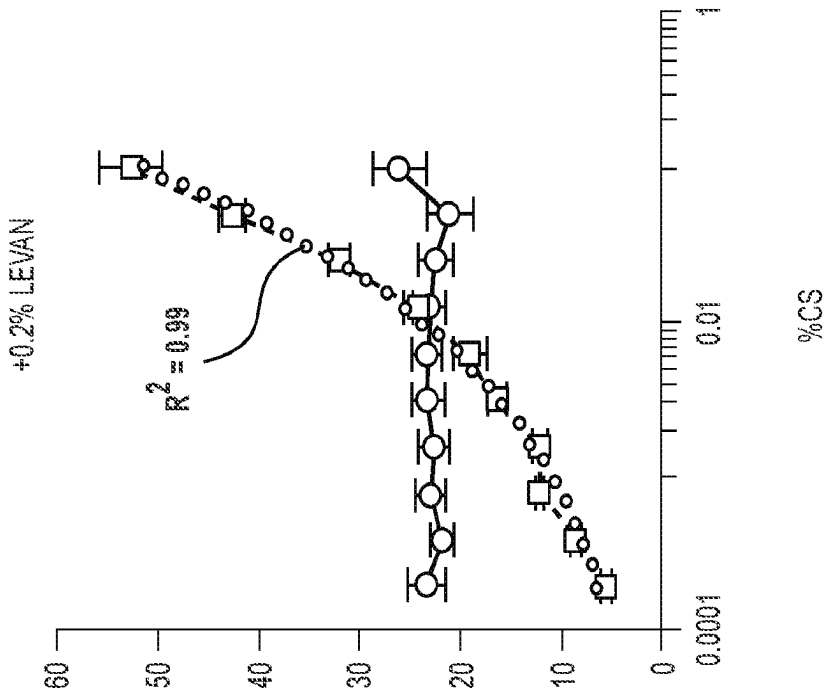


FIG. 18E

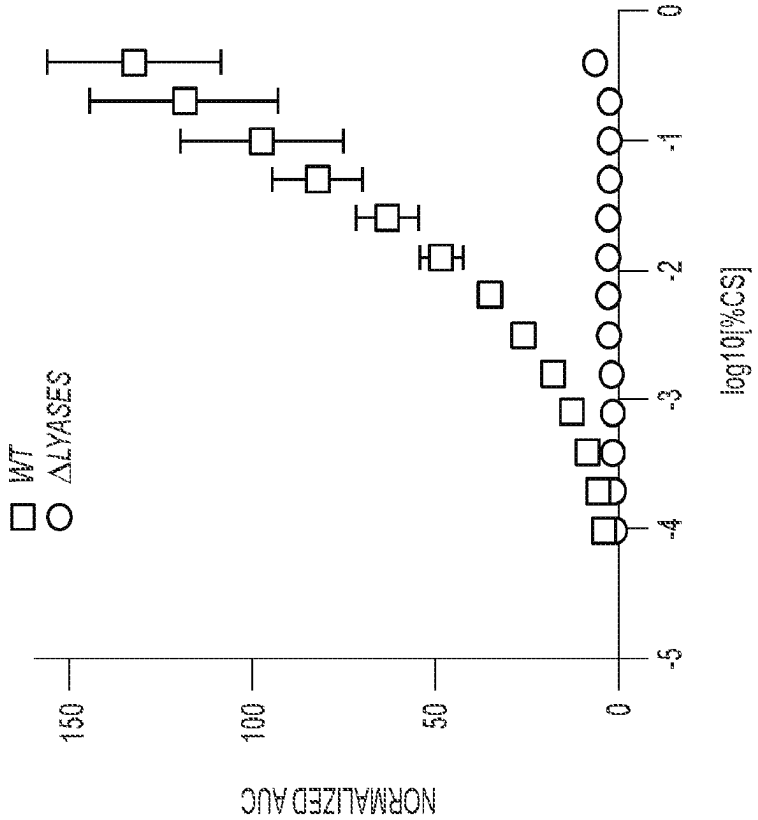


FIG. 19B

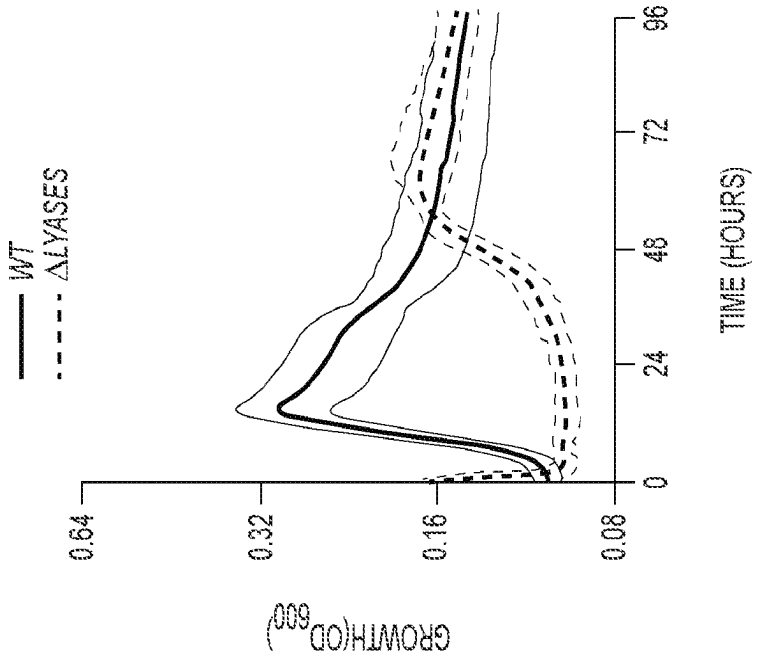


FIG. 19A

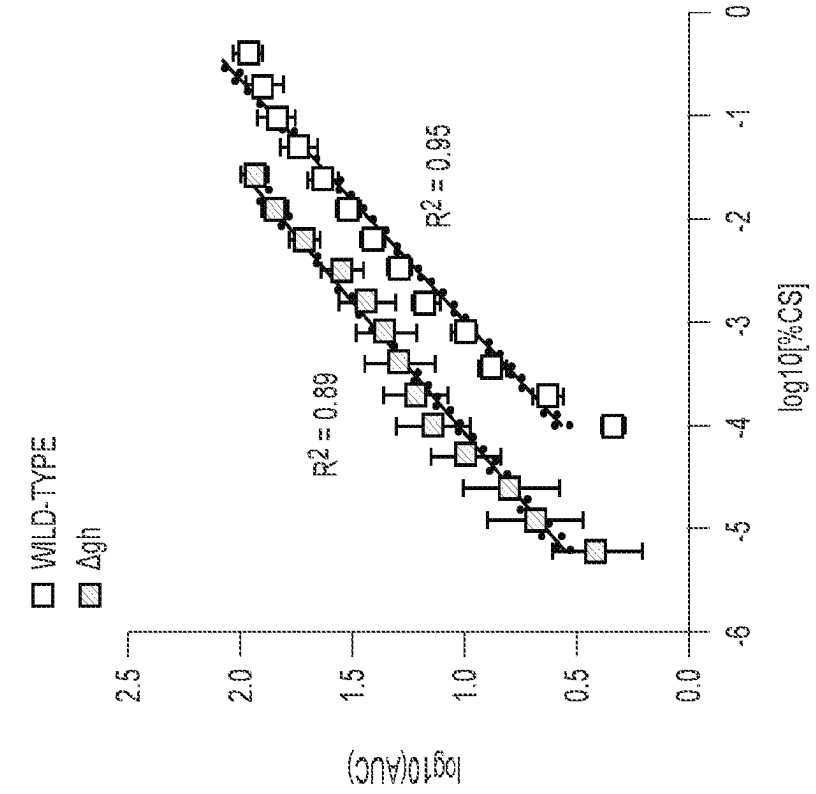


FIG. 19D

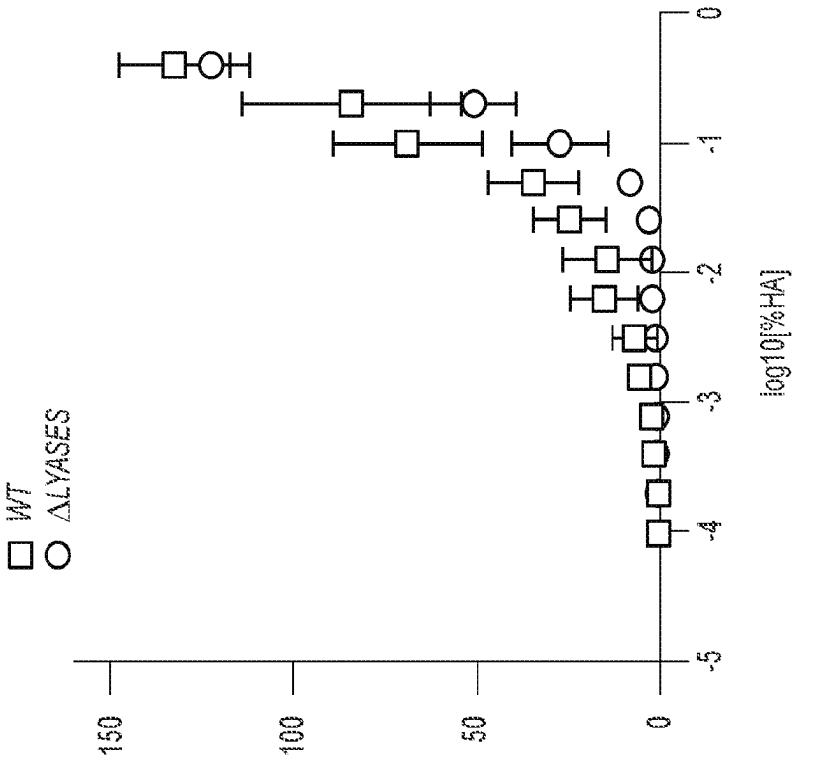


FIG. 19C

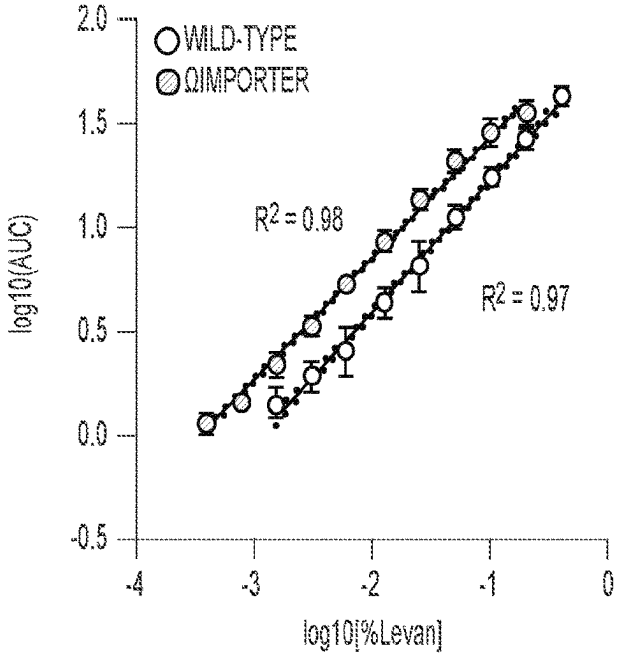


FIG. 19E

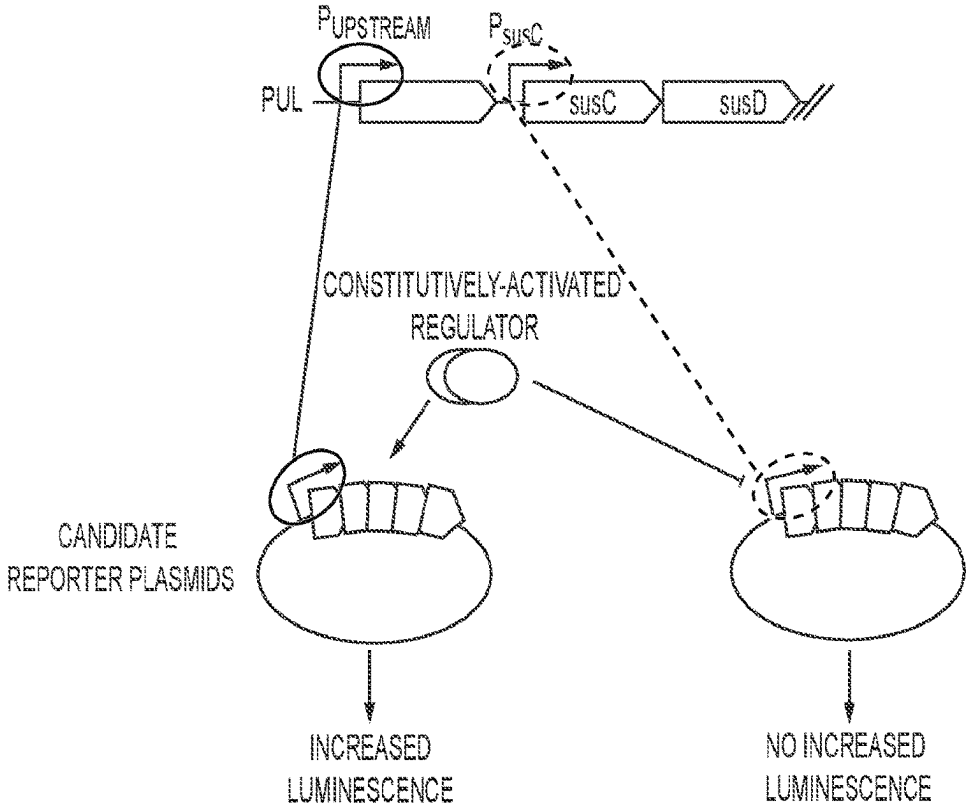


FIG. 20A

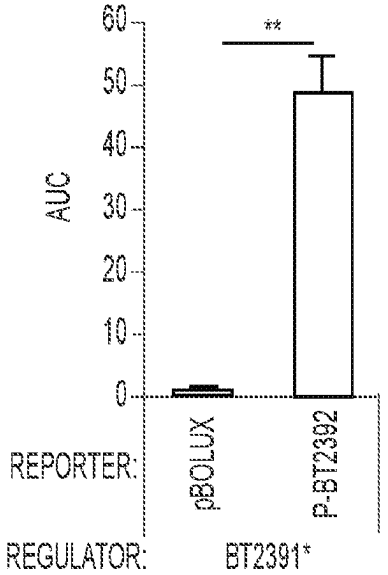


FIG. 20B

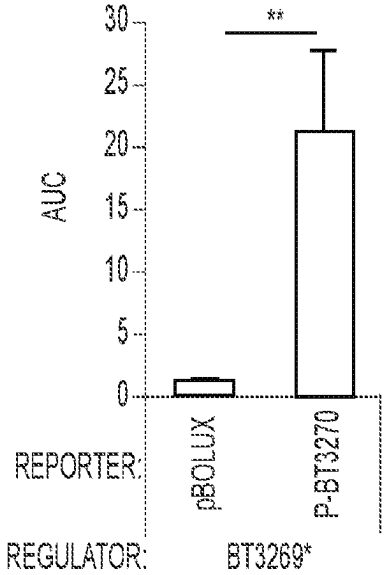


FIG. 20C

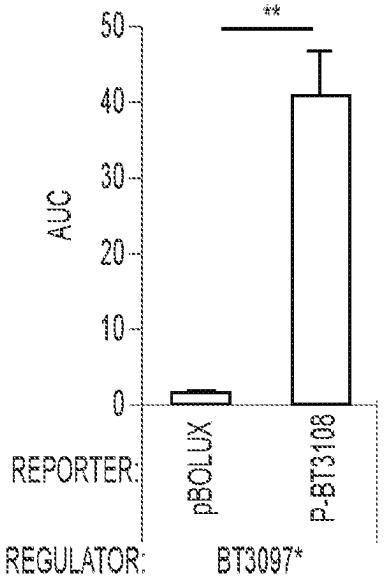


FIG. 20D

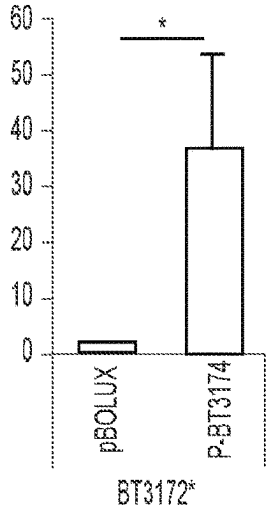


FIG. 20E

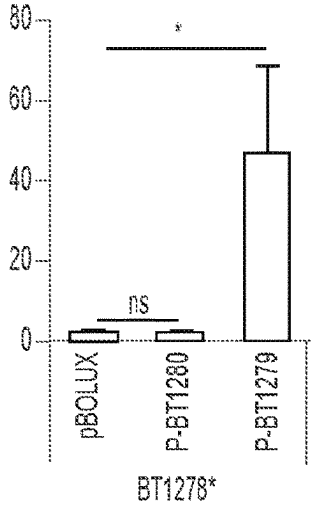


FIG. 20F

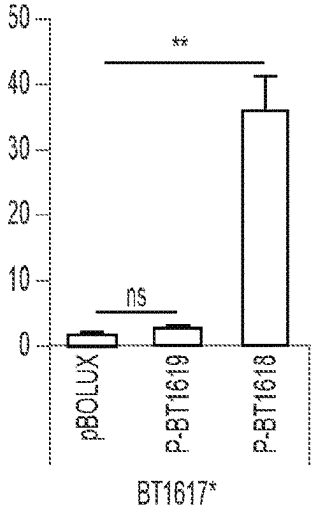


FIG. 20G

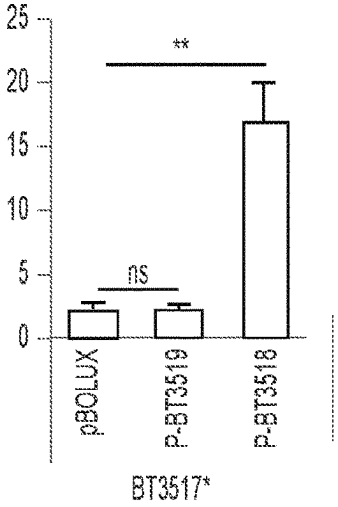


FIG. 20H

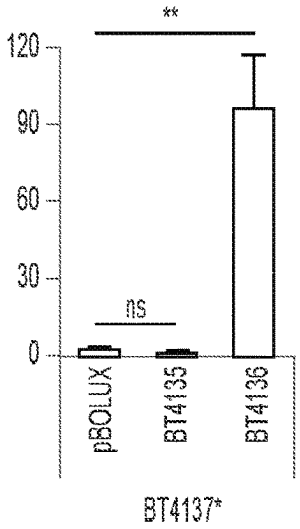


FIG. 20I

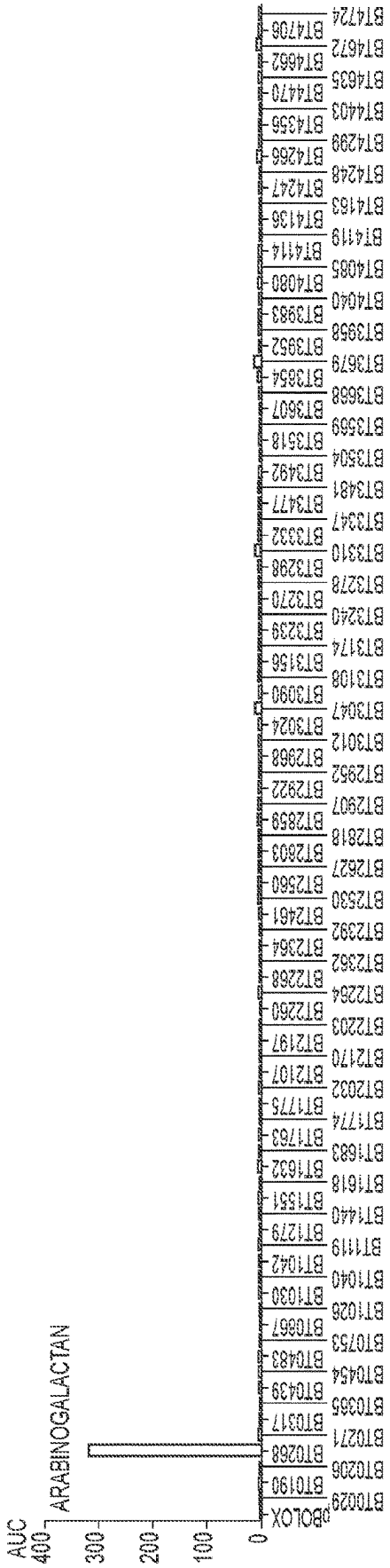


FIG. 21A

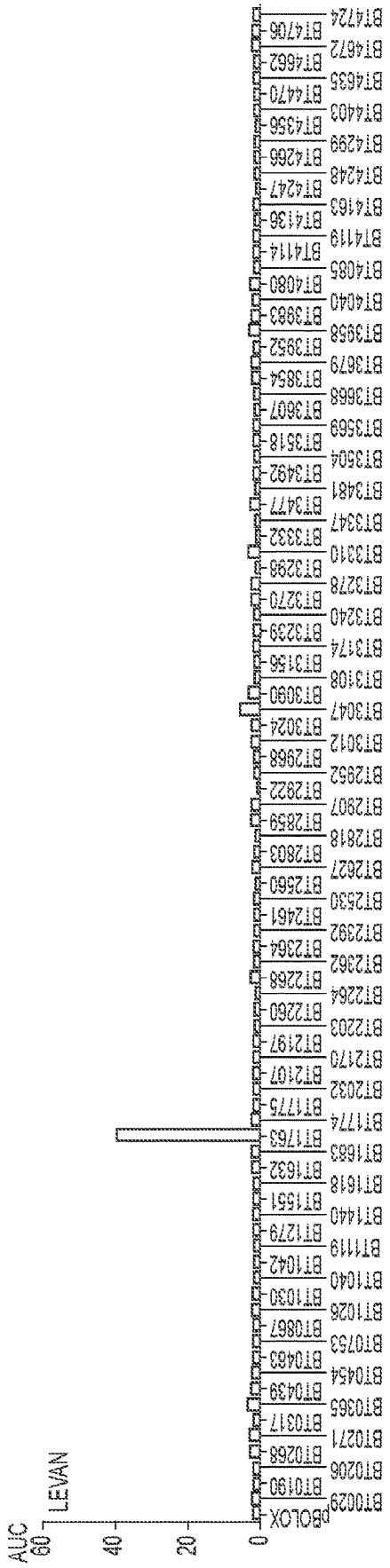


FIG. 21B

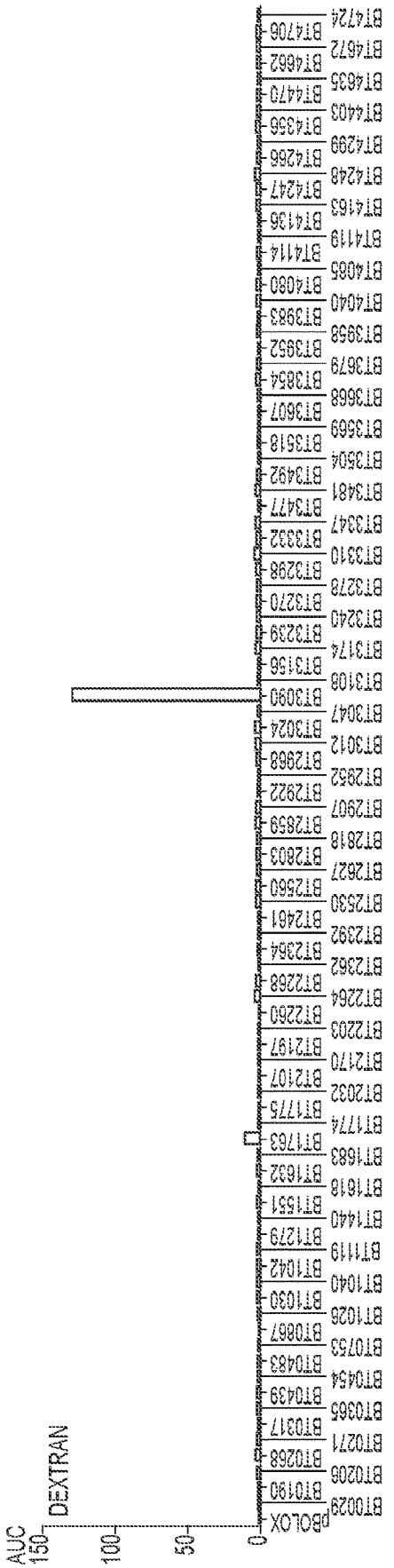


FIG. 21C

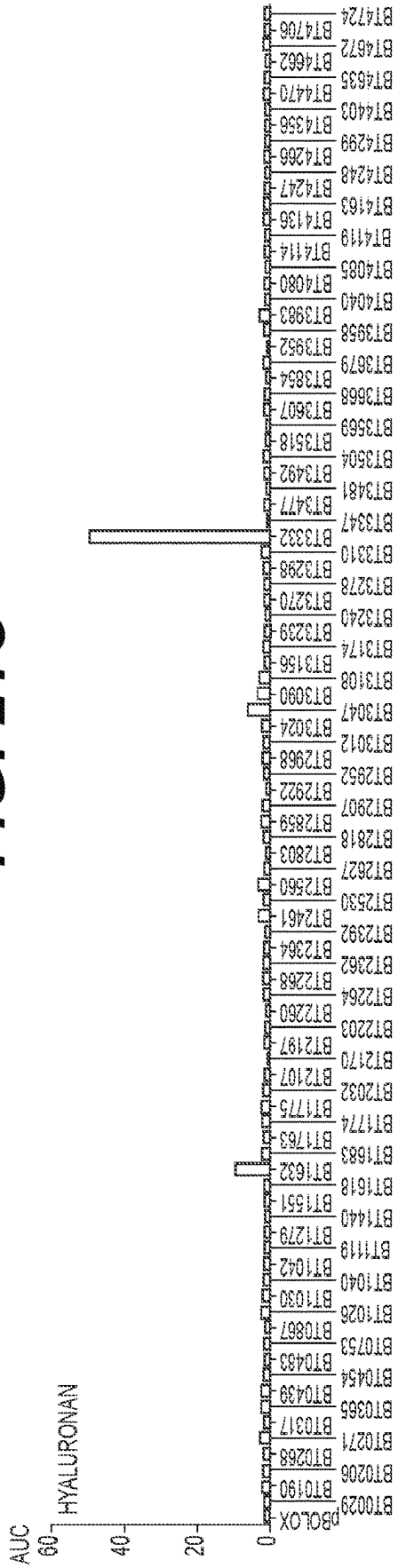


FIG. 21D

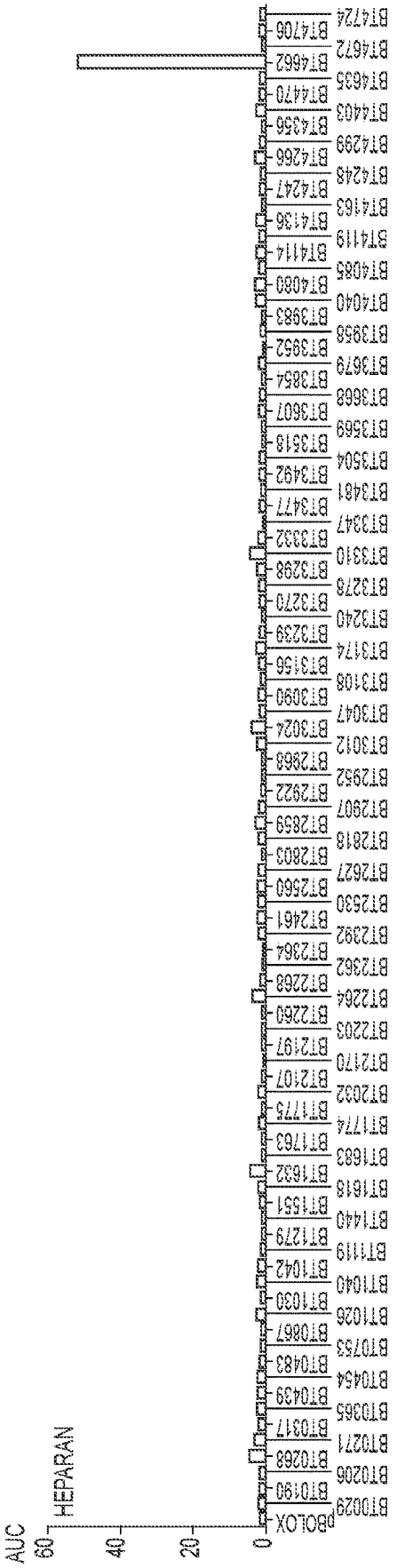


FIG. 21E

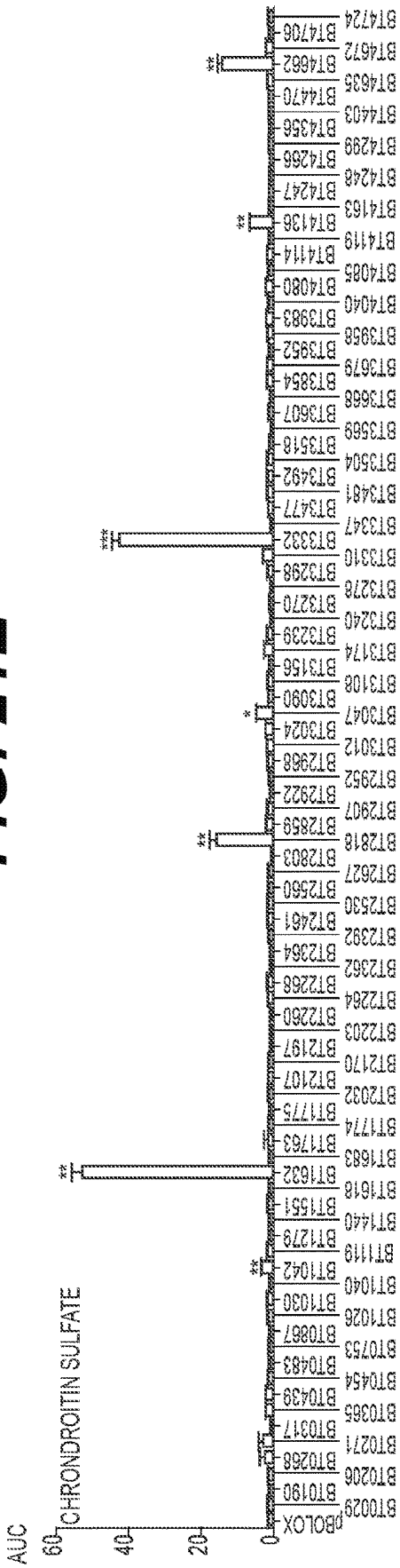


FIG. 21F

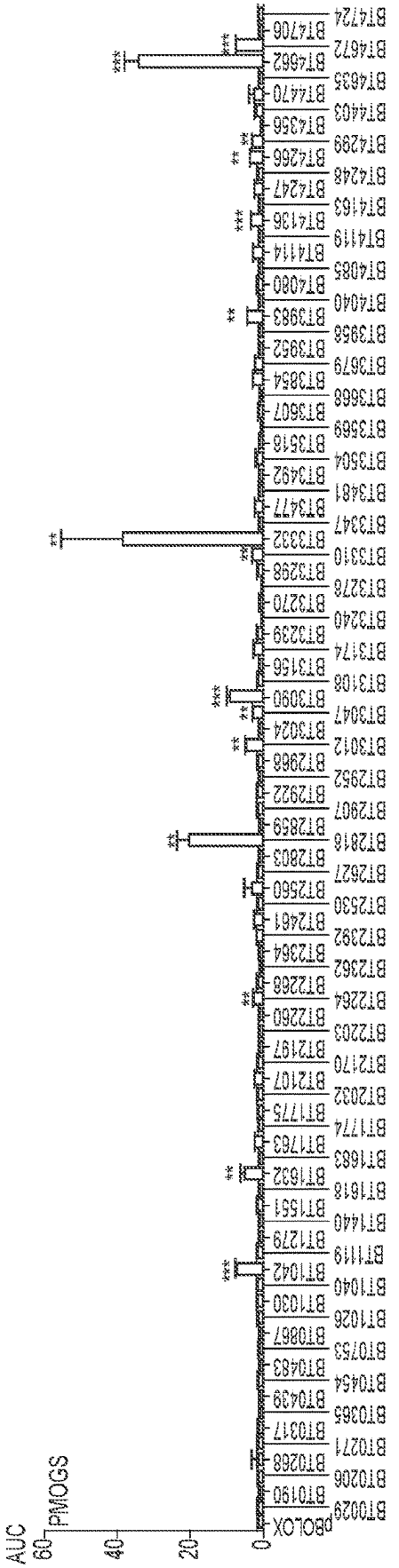


FIG. 21G

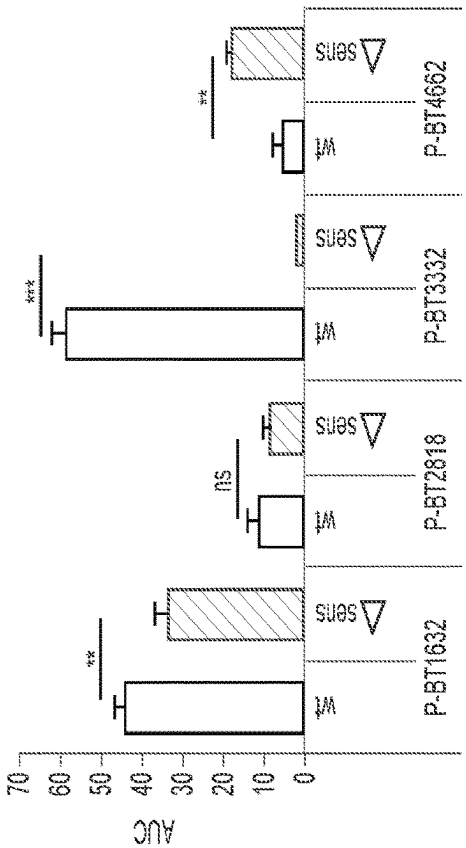


FIG. 22A

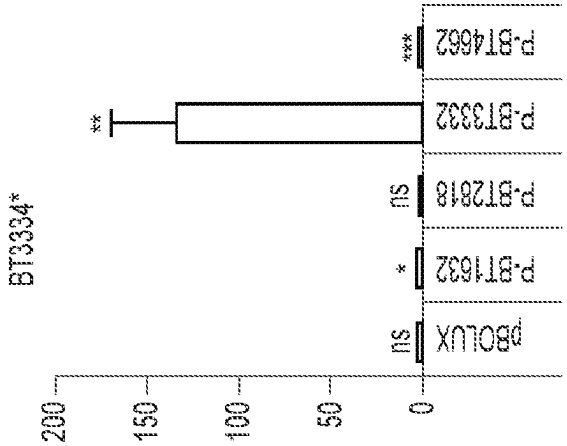


FIG. 22C

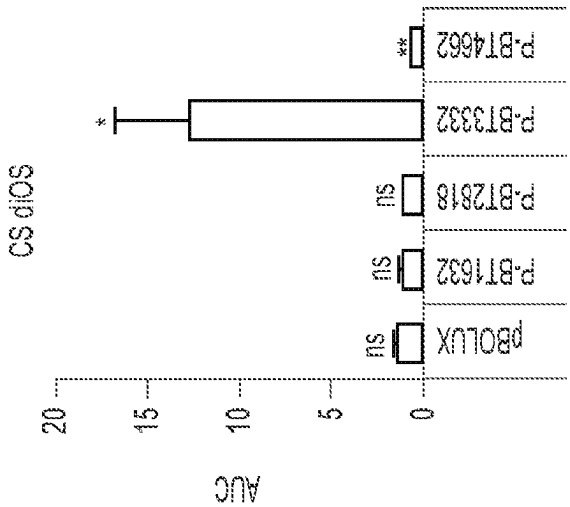


FIG. 22B

HARNESSING GUT MICROBES FOR GLYCAN DETECTION AND QUANTIFICATION

RELATED APPLICATION

[0001] This PCT application claims priority to, and the benefit of, U.S. Provisional Patent Application No. 63/328,555, filed Apr. 7, 2022, entitled "HARNESSING GUT MICROBES FOR GLYCAN DETECTION AND QUANTIFICATION," which is incorporated by reference herein in its entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under Grant No. AI149319 awarded by the National Institutes of Health/NIAID. The Government has certain rights in the invention.

REFERENCE TO SEQUENCE LISTING

[0003] The sequence listing submitted on Apr. 7, 2023, as an .XML file entitled "11196-101WO1_Sequence_Listing.xml" created on Apr. 7, 2023, and having a file size of 360,902 bytes is hereby incorporated by reference pursuant to 37 C.F.R. § 1.52 (e) (5).

FIELD

[0004] The present disclosure relates compositions and methods of engineering microbial strains to detect and quantify glycan molecules.

BACKGROUND

[0005] Characterization of glycan molecules present in heterogenous mixtures has generally been performed using lectins, nuclear magnetic resonance, or liquid or gas chromatography (LC or GC, respectively) followed by mass spectrometry methods. Using these methods are proven to be expensive and requires tremendous investments in expertise, instrumentation, and consumable products. Furthermore, these approaches require glycan separation and derivatization prior to implementation, which can result in non-uniform detection and often necessitate tandem parallel approaches to achieve high-confidence results. Detection of glycan molecules in heterogenous mixtures allows for profiling microbes present in a patient, specifically in the gastrointestinal tract of the patient. Further, glycan detection can allow for early detection, treatment, and/or prevention of pathogenic microbes within a patient.

[0006] Given the limitations described above, there is a need to effectively and efficiently detect and quantify glycans in heterogenous mixtures using improved and optimized methods.

[0007] The compositions and methods disclosed herein address these needs.

SUMMARY

[0008] The present disclosure provides a system for sensing and detecting glycan molecules using a bacterial reporter plasmid.

[0009] In one aspect, one aspect, disclosed herein are reporter plasmids comprising a luciferase reporter cassette, a first polysaccharide utilization locus (PUL), and a first glycan-specific promoter.

[0010] Also disclosed herein are reporter plasmids of any preceding aspect, wherein the first PUL encodes any combination of proteins comprising a surface glycan binding protein (SGBP), an outer membrane channel, a digestive enzyme, a glycan importer, or a glycan sensor.

[0011] In one aspect disclosed herein are reporter plasmids of any preceding aspect, wherein the first PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan (OG)-specific PUL, or variants thereof.

[0012] Also disclosed herein are reporter plasmids of any preceding aspect, wherein the first glycan specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof including, but not limited to glycan specific promoters comprising the nucleic acids sequence as set forth in SEQ ID NOs 74-76, or SEQ ID NOs: 262-354.

[0013] In one aspect disclosed herein are reporter plasmids of any preceding aspect, wherein the reporter plasmid further comprises a second PUL. In some embodiments, the second PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof. In some embodiments, the first PUL is interchangeable with the second PUL.

[0014] Also disclosed herein are reporter plasmids of any preceding aspect, wherein the reporter plasmid further comprises a second glycan-specific promoter. In some embodiments, the first glycan-specific promoter is interchangeable with the second glycan-specific promoter. In some embodiments, the second glycan-specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

[0015] In one aspect, disclosed herein are reporter plasmids of any preceding aspect, wherein the second glycan-specific promoter comprises the nucleic acids sequence as set forth in SEQ ID NOs 74-76, or SEQ ID NOs: 262-354.

[0016] Also disclosed herein are reporter plasmids of any preceding aspect, wherein the reporter plasmid comprises a *Bacteroides*-optimized lux (Bolux) plasmid.

[0017] Also disclosed herein are engineered bacteria comprising the reporter plasmid of any preceding aspect. For example, disclosed herein are engineered bacteria harboring a reporter plasmid wherein the reporter plasmid comprises a luciferase reporter cassette, a first polysaccharide utilization locus (PUL), and a first glycan-specific promoter. In some aspects, the first PUL encodes any combination of proteins comprising a surface glycan binding protein (SGBP), an outer membrane channel, a digestive enzyme, a glycan importer, or a glycan sensor. In some embodiments, the first

PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof. In some aspects, the first glycan specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

[0018] In one aspect, disclosed herein are engineered bacteria of any preceding aspect, wherein the first glycan-specific promoter comprises the nucleic acids sequence as set forth in SEQ ID NOs 74-76, or SEQ ID NOs: 262-354.

[0019] Also disclosed herein are engineered bacteria of any preceding aspect, further comprising a second PUL. In some aspects, the second PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof. In some aspects, the first PUL is interchangeable with the second PUL.

[0020] In one aspect, disclosed herein are engineered bacteria of any preceding aspect, further comprising a second glycan-specific promoter. In some embodiments, the first glycan-specific promoter is interchangeable with the second glycan-specific promoter. In some aspects, the second glycan-specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

[0021] Also disclosed herein are engineered bacteria of any preceding aspect, wherein the second glycan-specific promoter comprises the nucleic acids sequence as set forth in SEQ ID NOs 74-76, or SEQ ID NOs: 262-354.

[0022] In some aspects, disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria originates from a gastrointestinal bacterium. In some aspects, the engineered bacteria originates from a *Bacteroides* bacterium including, but not limited to *Bacteroides thetaiotaomicron* (Bt), *Bacteroides ovatus* (Bo), *Bacteroides fragilis* (Bf), *Bacteroides* caccae (Bc) or a variant strain thereof.

[0023] Also disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria overexpresses the chondroitin sulfate (CS)-specific PUL when exposed to a CS glycan, or derivatives thereof.

[0024] In some aspects, disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria overexpresses the levan-specific PUL when exposed to a levan glycan, or derivatives thereof.

[0025] Also disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria overexpresses the inulin-specific PUL when exposed to an inulin glycan, or derivatives thereof.

[0026] In some aspects, disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria overexpresses the arabinogalactan-specific PUL when exposed to an arabinogalactan, or derivatives thereof.

[0027] Also disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria overexpresses the dextran-specific PUL when exposed to a dextran glycan, or derivatives thereof.

[0028] In some aspects, disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria overexpresses the hyaluronan (HA)-specific PUL when the engineered bacteria is exposed to a HA glycan, or derivatives thereof.

[0029] Also disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria overexpresses the heparan sulfate (HS)-specific PUL when exposed to a HS glycan, or derivatives thereof.

[0030] In some aspects, disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria overexpresses the O-glycan(OG)-specific PUL when exposed to an OG glycan mixture, or derivatives thereof.

[0031] Also disclosed herein are engineered bacteria of any preceding aspect, wherein the engineered bacteria emits a light signal when overexpressing any PUL of any preceding aspect. In some aspects, the light signal is decreased when the glycan molecule is broken down into a monosaccharide molecule.

[0032] In one aspect, disclosed herein are glycan-sensing systems comprising the engineered bacteria or reporter plasmid of any preceding aspect. For example, disclosed herein is a glycan-sensing system comprising an engineered bacteria harboring a reporter plasmid, wherein the reporter plasmid comprises a luciferase reporter cassette, a first polysaccharide utilization locus (PUL), and a first glycan-specific promoter, wherein the glycan-sensing system detects and quantifies a glycan molecule.

[0033] In some embodiments, the glycan molecule comprises chondroitin sulfate, arabinan, heparan sulfate, hyaluronan, fructan, levan, mannan, or derivatives thereof. In some embodiments, the glycan molecule is located in the gastrointestinal tract of a mammal.

[0034] In some embodiments, the first PUL encodes any combination of proteins comprising a surface glycan binding protein (SGBP), an outer membrane channel, a digestive enzyme, a glycan importer, or a glycan sensor.

[0035] In some embodiments, the first PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan (OG)-specific PUL, or variants thereof.

[0036] In some embodiments, the first glycan specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

[0037] In some embodiments, the system further comprises a second PUL. In some embodiments, the second PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof. In some embodiments, the first PUL is interchangeable with the second PUL.

[0038] In some embodiments, the system further comprises a second glycan-specific promoter. In some embodiments, the first glycan-specific promoter is interchangeable with the second glycan-specific promoter. In some embodiments, the second glycan-specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan (OG)-specific promoter, or variants thereof.

[0039] In some embodiments, the first or second glycan-specific promoter comprises the nucleic acids sequence as set forth in SEQ ID NOs 74-76, or SEQ ID NOs: 262-354.

[0040] In some embodiments, the reporter plasmid comprises a *Bacteroides*-optimized lux (Bolux) plasmid.

[0041] In some embodiments, the engineered bacteria originates from a gastrointestinal bacterium. In some embodiments, the engineered bacteria originates from a *Bacteroides* bacterium. In some embodiments, the engineered bacteria originates from a *Bacteroides thetaiotaomicron* (Bt), *Bacteroides ovatus* (Bo), *Bacteroides fragilis* (Bf), *Bacteroides caccae* (Bc) or a variant strain thereof.

[0042] In some embodiments, the engineered bacteria are grown in an anaerobic environment. In some embodiments, the engineered bacteria are grown in a 96-well, a 384-well, or a 1536-well microplate.

[0043] In some embodiments, the engineered bacteria overexpresses the chondroitin sulfate (CS)-specific PUL when exposed to a CS glycan, or derivatives thereof.

[0044] In some embodiments, the engineered bacteria overexpresses the levan-specific PUL when exposed to a levan glycan, or derivatives thereof.

[0045] In some embodiments, the engineered bacteria overexpresses the inulin-specific PUL when exposed to an inulin glycan, or derivatives thereof.

[0046] In some embodiments, the engineered bacteria overexpresses the arabinogalactan-specific PUL when exposed to an arabinogalactan, or derivatives thereof.

[0047] In some embodiments, the engineered bacteria overexpresses the dextran-specific PUL when exposed to a dextran glycan, or derivatives thereof.

[0048] In some embodiments, the engineered bacteria overexpresses the hyaluronan (HA)-specific PUL when the engineered bacteria is exposed to a HA glycan, or derivatives thereof.

[0049] In some embodiments, the engineered bacteria overexpresses the heparan sulfate (HS)-specific PUL when exposed to a HS glycan, or derivatives thereof.

[0050] In some embodiments, the engineered bacteria overexpresses the O-glycan(OG)-specific PUL when exposed to an OG glycan mixture, or derivatives thereof.

[0051] In some embodiments, the engineered bacteria emits a light signal when overexpressing any PUL of any preceding aspect.

[0052] In some embodiments, the light signal is decreased when the glycan molecule is broken down into a monosaccharide molecule.

[0053] In one aspect, disclosed herein is a method of detecting a glycan, the method comprising isolating and preserving a tissue sample from a subject, preparing, and culturing the glycan-sensing system of any preceding aspect in a microplate in an anaerobic environment, adding the tissue sample into the microplate, and detecting and quantifying a light signal emitted from the system of any preceding aspect.

[0054] In some embodiments, the tissue sample comprises at least one glycan. In some embodiments, the light signal is detected and quantified using a microplate reader, a spectrophotometer, or an instrument capable of measuring the light signal. In some embodiments, the tissue sample comprises a tissue biopsy, a blood sample, or a saliva sample.

[0055] In some embodiments, the method prevents, treats, or reduces a gastrointestinal disease or disorder in the subject.

[0056] In one aspect, disclosed herein is a method of treating or preventing a gastrointestinal disease or disorder in a subject in need thereof, the method comprising isolating and preserving a tissue sample from a subject, preparing and culturing the glycan-sensing system of any preceding aspect in a microplate in an anaerobic environment, adding the tissue sample into the microplate, detecting and quantifying a light signal emitted from the system, and performing or administering a therapeutic procedure to the subject comprising pathological amounts of a glycan relative to a control tissue comprising normal amounts of the glycan.

[0057] In some embodiments, the tissue sample comprises at least one glycan. In some embodiments, the light signal is detected and quantified using a microplate reader, a spectrophotometer, or an instrument capable of measuring the light signal. In some embodiments, the tissue sample comprises a tissue biopsy, a blood sample, or a saliva sample.

[0058] In some embodiments, the therapeutic procedure comprises a surgical procedure, a therapeutic agent, a lifestyle change, or a combination thereof.

[0059] In some embodiments, the surgical procedure comprises bariatric surgery, esophageal surgery, foregut surgery, hernia surgery, gastroesophageal reflux disease surgery, surgical nutrition, colorectal surgery, gallbladder surgery, liver surgery, bile duct surgery, pancreatic surgery, tumor excision, or combinations thereof. In some embodiments, the therapeutic agent comprises a laxative, an antacid, a proton pump inhibitor, a histamine blocker, an anti-inflammatory agent, a steroid, a vitamin, an intravenous fluid, an antibiotic, a probiotic, or combinations thereof. In some embodiments, the lifestyle change comprises a dietary alteration, an exercise program, a sedentary lifestyle, or combinations thereof.

[0060] In some embodiments, the gastrointestinal disease or disorder comprises heartburn, irritable bowel syndrome, lactose intolerance, gallstones, cholecystitis, cholangitis, anal fissure, hemorrhoids, proctitis, colon polyps, infective colitis, ulcerative colitis, ischemic colitis, Crohn's disease, radiation colitis, celiac disease, diarrhea (chronic or acute), constipation (chronic or acute), diverticulosis, diverticulitis, acid reflux (gastroesophageal reflux (GER) or gastroesophageal reflux disease (GERD)), Hirschsprung disease, abdominal adhesions, achalasia, acute hepatic porphyria (AHP), anal fistulas, bowel incontinence, centrally mediated abdominal pain syndrome (CAPS), clostridioides difficile infection, cyclic vomiting syndrome (CVS), dyspepsia, eosinophilic gastroenteritis, globus, inflammatory bowel disease, malabsorption, scleroderma, or volvulus.

[0061] In some embodiments, the subject is a human.

[0062] In one aspect, disclosed herein is a kit for detecting or purifying a glycan molecule, the kit comprising an apparatus comprising a binding medium and a surface

glycan binding protein (SGBP), wherein the binding medium comprises a matrix of biomolecules, the SGBP comprises a peptide label, and the SGBP is attached to the matrix; a container comprising an equilibration buffer, a container comprising a releasing buffer, and a container comprising a washing buffer.

[0063] In some embodiments, the glycan molecule comprises chondroitin sulfate, arabinan, heparan sulfate, hyaluronan, fructan, levan, mannan, or derivatives thereof.

[0064] In some embodiments, the SGBP comprises a chondroitin sulfate (CS)-specific SGBP, a levan-specific SGBP, an inulin-specific SGBP, an arabinogalactan-specific SGBP, a dextran-specific SGBP, a hyaluronan (HA)-specific SGBP, a heparan sulfate (HS)-specific SGBP, an O-glycan (OG)-specific SGBP, or variants thereof.

[0065] In some embodiments, the matrix comprises a nickel-conjugated agarose polymer. In some embodiments, the peptide label comprises a hexa-histidine label. In some embodiments, the releasing buffer comprises a histidine solution. In some embodiments, the washing buffer comprises a buffered solution comprising water, phosphate buffered saline solution, a tris-buffered saline solution, or variants thereof.

[0066] In some embodiments, the kit is combined with the glycan-sensing system of any preceding aspect to detect the glycan molecule.

BRIEF DESCRIPTION OF FIGURES

[0067] The accompanying figures, which are incorporated in and constitute a part of this specification, illustrate several aspects described below.

[0068] FIGS. **1**A, **1**B, **1**C, **1**D, **1**E, **1**F, **1**G, **1**H, and **1**I show the (FIG. **1**A) PUL-encoded surface glycan binding proteins (SGBPs) sequester target glycans prior to their translocation across the outer membrane by the corresponding SusC channel. Once in the periplasm, the glycan is depolymerized into mono, di-, or oligo-saccharide signatures that bind their cognate sensor, which subsequently activates PUL transcription in the cytoplasm. The sensor ligand is subsequently further degraded into monosaccharide components and transported across the inner membrane, where they enter central metabolism, thereby deactivating the sensor. FIG. **1**B shows a cartoon depicting the strategy employed in this proposal to harness the PUL-encoded glycan detection machinery to report the presence of distinct glycans. FIG. **1**C shows the growth of wild-type (wt, black) or mutant Bt strains deficient for the PUL-encoded susC transporter (ΔBT3332, blue), lyases (ΔBT3324 ΔBT3350 ΩBT4410, purple), sensor (ΔBT3334, red) or glycosyl hydrolase (gh, ΔBT3348, orange) supplied CS as the sole carbon source. n=8, error bars are SEM. FIG. **1**D shows the fold increase in susC transcript levels were measured by qPCR 120 minutes following the introduction of 0.2% CS to cultures of wild-type Bt or a strain deficient for the corresponding PUL sensor, BT3334. FIG. **1**E shows the fold change in susC transcript levels were measured by qPCR 120 minutes following the introduction of 0.2, 0.02, or 0.002% CS prepared with galactose to a final carbohydrate content of 0.5%. FIG. **1**F shows the fold increase in susC transcript levels were measured by qPCR 120 minutes following the introduction of 0.2% levan to cultures of wild-type Bt or a strain deficient for the corresponding PUL sensor, BT1754. FIG. **1**G shows the growth of wild-type (wt, black) or mutant Bt strains deficient for the PUL-encoded susC transporter (ΔBT1763, blue), levanases (ΔBT1760-59 ΔBT3082 ΩBT1765, purple), sensor (ΔBT1754, orange) or fructose importer (ΩBT1758, purple) supplied levan as the sole carbon source. n=8, error bars are SEM. FIGS. **1**H and **1**I show the fold change in susC transcript levels were measured by qPCR after (FIG. **1**H) 120 or (FIG. **1**I) 60 minutes following the introduction of 0.2, 0.02, or 0.002% levan prepared with galactose to a final carbohydrate content of 0.5%. For FIGS. **1**D-**1**G, n=6, error bars are SEM, p-values were calculated by paired two-tailed Student's t-test, and R2 values were computed by Microsoft Excel power trendline functions. ns indicates values <0.05, *<0.05, **<0.01, and ***<0.001.

[0069] FIGS. **2**A, **2**B, and **2**C show the construction of a *Bacteroides*-optimized bioluminescent reporter. FIG. **2**A shows the schematic depicting the construction of a bioluminescent reporter that encodes the entire Pl lux cassette under control of the Bt rpoD promoter and rpiL* RBS (top); a *Bacteroides* optimized lux cassette with rearranged luxA-E (indicated by the shaded regions) and Bt intergenic regions from a constitutively expressed Bt operon (BT1160-1155; middle); or pBolux which has BamHI and SpeI sites positioned upstream of the *Bacteroides* optimized lux cassette (bottom) in the multi-copy plasmid pLYL01. FIG. **2**B shows the relative luminescence (solid lines) or growth (dashed lines) from Bt strains harboring an empty vector (black) or plasmids containing either the lux operon from Pl (blue) or the *Bacteroides*-optimized lux cassette (red) expressed from the Bt rpoD promoter and rpiL* RBS were measured during growth in minimal media containing 0.5% galactose as the sole carbon source. FIG. **2**C shows the relative luminescence (solid lines) or growth (dashed lines) of Bt strains harboring empty pBolux (black) or a plasmid with the Bt rpoD promoter cloned into the BamHI and SpeI sites (red) during growth in galactose as the sole carbon source. All values in FIGS. **2**B and **2**C are the mean of 8 biological replicates and error bars are SEM in color-matched shading. Source data are provided as a Source Data file.

[0070] FIGS. **3**A, **3**B, **3**C, **3**D, **3**E, and **3**F show the construction of a glycan-responsive reporter in Bt. FIG. **3**A shows the relative luminescence from wild-type Bt strains harboring pBolux (black) or a plasmid including the promoter region preceding the CS-inducible susC gene (P-BT3332, pink lines) following the introduction of CS as the sole carbon source normalized by the relative luminescence of identical cultures supplied galactose. Values are the mean of 12 biological replicates and error is SEM in color-matched shading. FIG. **3**B shows the relative luminescence from wild-type Bt (black) or strains lacking a CS-inducible susC (ΔBT3332, blue), 3 CS-specific lyases (ΔBT3324 ΔBT3350 ΩBT4410, purple), CS-sensor (ΔBT3334, red), or a glucuronyl hydrolase (ΔBT3348, orange) harboring P-BT3332 following the introduction of an equal mixture of CS and galactose normalized to measurements from identical strains supplied galactose alone. FIG. **3**C shows the relative luminescence from wild-type Bt (black) or strains lacking 3 CS-specific lyases (ΔBT3324 ΔBT3350 ΩBT4410, purple) or the CS-sensor (ΔBT3334, red) harboring P-BT3332 following the introduction of a mixture of unsulfated CS disaccharide (di0S) and galactose normalized to measurements from identical strains supplied galactose alone. Values are the mean of 6 biological replicates and error is SEM in color-matched shading. FIGS. **3**D-**3**F shows the relative luminescence from wild-type Bt

(solid lines) or strains lacking the CS-sensor (ΔBT3334, dashed lines) harboring P-BT3332 following the introduction of a mixture of galactose and either hyaluronic acid (HA, green) or heparin (blue) and galactose normalized to measurements from identical strains supplied galactose alone. For FIGS. **3**B and **3**D, values are the mean of 8 biological replicates and error is SEM in color-matched shading. Source data are provided as a Source Data file.

[0071] FIGS. **4**A, **4**B, **4**C, **4**D, **4**E, **4**F, **4**G, and **4**H show the levan-responsive reporter reveals multiple levanases coordinate fructan utilization in Bt. FIG. **4**A shows the relative luminescence from wild-type Bt harboring pBolux (black) or a plasmid including the promoter region preceding the levan inducible susC gene (P-BT1763, pink) following the introduction of levan as the sole carbon source and normalized by the relative luminescence of identical cultures supplied galactose. Values are the mean of 12 biological replicates and error is SEM in color-matched shading. FIGS. **4**B and **4**C show the relative luminescence from wild-type Bt (black) or strains lacking the levan-inducible susC (ΔBT1763, blue), 4 levan-specific hydrolases (ΔBT1760-1759 ΔBT3082 ΩBT1765, purple), fructan sensor (ΔBT1754, red), or a putative inner membrane fructose transporter (ΩBT1758, orange) harboring P-BT1763 were measured following the introduction of an equal mixture of galactose and (FIG. **4**B) levan or (FIG. **4**C) fructose and normalized by the relative luminescence of identical cultures supplied galactose alone. FIG. **4**D shows the growth of wild-type Bt (black) or strains lacking the levan-inducible susC (ΔBT1763, blue), 4 levan-specific hydrolases (ΔBT1760-1759 ΔBT3082 ΩBT1765, purple), fructan sensor (ΔBT1754, red), or a putative inner membrane fructose transporter (ΩBT1758, orange) were measured during anaerobic culture in minimal media containing fructose as a sole carbon source. FIG. **4**E shows the relative luminescence of wild-type Bt or strains lacking all other levanases except BT1760 (ΔBT1759 ΔBT3082 ΩBT1765, pink), BT1759 (ΔBT1760 ΔBT3082 ΩBT1765, teal), BT3082 (ΔBT1760-59 ΩBT1765, lavender), or BT1765 (ΔBT1760-59 ΔBT3082, purple) harboring the levan-responsive reporter following the introduction of a mixture of levan and galactose normalized with measurements from identical cultures supplied galactose alone. FIG. **4**F-**4**H show the relative luminescence of wild-type Bt or strains lacking BT1760 (pink), BT1759 (teal), BT3082 (lavender), or BT1765 (purple) harboring P-BT1763 following the introduction of a mixture of levan and galactose normalized with measurements from identical cultures supplied galactose alone. For FIGS. **4**B-**4**F, values are the mean of 8 biological replicates and error is SEM in color-matched shading. Source data are provided as a Source Data file.

[0072] FIGS. **5**A, **5**B, **5**C, **5**D, **5**E, and **5**F show the species-specific responses that enable PUL reporters to distinguish between compositionally identical yet structurally distinct glycans. FIG. **5**A shows the growth of wild-type Bt (gray) and Bo (black) or a strain lacking the Bo inulin sensor (ΔBACOVA_04496, red) were measured during anaerobic culture in minimal media containing inulin as a sole carbon source. FIG. **5**B shows the relative luminescence from wild-type Bo harboring pBolux (black) or a plasmid including the promoter region preceding the inulin-inducible susC gene (P-BACOVA_04505, pink) were measured following the introduction of inulin as the sole carbon source and normalized by the relative luminescence from identical cultures supplied galactose. Values are the mean of 12 biological replicates and error is SEM in color-matched shading. FIGS. **4**C-**4**F show the relative luminescence from wild-type Bo harboring P-BACOVA_04505 (black) or an isogenic strain lacking the Bo inulin sensor (ΔBACOVA_04496, red) were measured following the introduction of an equal mixture of galactose and (FIG. **4**C) inulin or (FIG. **4**D) fructose and normalized by the relative luminescence of identical cultures supplied galactose alone. For FIGS. **4**A, **4**C, and **4**D, values are the mean of 8 biological replicates and error is SEM in color-matched shading. Source data are provided as a Source Data file.

[0073] FIGS. **6**A, **6**B, **6**C, **6**D, **6**E, and **6**F show the PUL-reporters reflect dose-dependent transcription. FIG. **6**A shows the relative luminescence from a wild-type Bt strain harboring P-BT3332 following the introduction of 2-fold serial dilutions of 0.4% CS containing galactose to a total carbohydrate content of 0.5% and normalized to identical cultures supplied galactose alone. FIG. **6**B shows the relative luminescence from a wild-type Bt strain harboring P-BT1763 following the introduction of 2-fold serial dilutions of 0.4% levan containing galactose to a total carbohydrate content of 0.5% and normalized to identical cultures supplied galactose alone. For FIGS. **6**A-**6**B, values are the mean of 12 biological replicates and error is SEM in color-matched shading. FIG. **6**C shows the AUC of response curves measured from wild-type Bt (black, see panel a) or a mutant lacking the glucuronyl hydrolase (Δgh, orange, see panel f) harboring P-BT3332 supplied 2-fold dilutions of CS to each strain and normalized by identical cultures supplied galactose alone. FIG. **6**D shows the AUC of response curves measured from wild-type Bt (black, see panel b) or a mutant lacking a putative inner membrane transporter harboring P-BT1763 supplied 2-fold dilutions of levan to each strain and normalized by identical cultures supplied galactose alone. For FIGS. **6**C-**6**D, values are the mean of 12 biological replicates, error bars are standard deviation, and P-values were computed by 2-way ANOVA with Dunnett correction and *** indicates values <0.001, **<0.01, *<0.05, and ns >0.05. FIG. **6**E The AUC of response curves measured from wild-type Bt strains harboring either P-BT3332 (open blue squares) supplied mixtures containing 2-fold serial dilutions of levan or P-BT1763 (open red circles) supplied 2-fold serial dilutions of CS with galactose to a total carbohydrate content of 0.5% and normalized by identical cultures supplied galactose alone. Values are the mean of 6 biological replicates, error bars represent standard deviation, and P-values were computed using 2-way ANOVA with Tukey's honest significance test and ns indicates values >0.05.

[0074] FIG. **6**F shows the relative luminescence from a gh-deficient Bt strain harboring P-BT3332 following the introduction of 2-fold serial dilutions of 0.4% CS containing galactose to a final carbohydrate content of 0.5% and normalized to identical cultures supplied galactose alone. Values are the mean of 12 biological replicates and error is SEM in color-matched shading. Source data are provided as a Source Data file.

[0075] FIGS. **7**A, **7**B, **7**C, **7**D, **7**E, **7**F, **7**G, **7**H, **7**I, **7**J, **7**K, and **7**L show the development of a glycan affinity isolation strategy using PUL-reporters. FIG. **7**A shows a cartoon depicting an affinity isolation strategy whereby recombinant, PUL-encoded SGBP is immobilized using metal affinity chromatography and binds its target when incubated with heterogenous glycan mixtures, which subsequently

co-elutes following the addition of excess histidine. FIGS. **7**B-**7**D show the migration of purified recombinant his-tagged BT3330 and BT1761 proteins were examined by affinity-PAGE using acrylamide gels containing (FIG. **7**B) CS, (FIG. **7**C) no glycan, or (FIG. **7**D) levan. FIGS. **7**E-**7**F show the fold increases in reporter activity (AUC) from Bt strains harboring either a levan-specific reporter (P-BT1763, black bars) or a CS-specific reporter (P-BT3332, black bars) supplied 8 step-wise eluates from (FIG. **7**E) BT3330 or (FIG. **7**F) BT1761 pre-incubated with an equal mixture of CS and levan normalized by reporter strains supplied eluates from identical reactions containing *E. coli* lysates harboring an empty vector. Inset: SDS-PAGE analysis of E1-E8 demonstrating the amount of (FIG. **7**E) BT3330 or (FIG. **7**F) BT1761 present in each fraction. FIGS. **7**G-**7**J show the pooled, concentrated eluates from (FIG. **7**G & FIG. **7**I) BT3330 or (FIG. **7**H & FIG. **7**J) BT1761 pre-incubated with a CS and levan mixture were supplied Bt strains harboring (FIG. **7**G) P-BT3332 or (FIG. **7**H) P-BT1763 and compared to standard curves of identical strains supplied 2-fold diluted CS or levan, respectively. Alternatively, the material was analyzed for total glycosaminoglycans (FIG. **7**I) or fructans (FIG. **7**J) using commercially available colorimetric assays according to the manufacturer's instructions. n=4, error bars are standard deviation; p-values were computed using a paired, two-tailed, Student's t-test; R2 values were computed using simple linear regression analysis in Prism and the 95% confidence interval is displayed as a dashed line. FIGS. **7**K-**7**L show the pooled, concentrated BT3330 eluates pre-incubated with either (FIG. **7**K) a CS and levan mixture or (FIG. **7**L) a 0.1% PMOG solution were supplied to reporter strains differentially activated by CS or PMOGs (see FIGS. **8**F&G, respectively). For all panels n=4, error bars are standard deviation, p-values were computed using a two-tailed student's t-test and ns indicates p-values >0.05, *<0.05, **, 0.01, ***<0.001.

[0076] FIGS. **8**A, **8**B, **8**C, **8**D, and **8**E show the PULs are required for glycan-specific growth conditions and transcriptional responses. FIG. **8**A shows growth of wild-type Bt (GT23; black) or strains lacking a CS-inducible susC (ΔBT3332; GT2926; blue), 3 CS-specific lyases (ΔBT3324 ΔBT3350 ΩBY4410; GT3086; purple), CS-sensor (ΔBT3334; GT150; red), or a glucuronyl hydrolyase (ΔBT3348; VR69; orange were measured during anaerobic culture in minimal media containing galactose as a sole carbon source. FIG. **8**B shows the growth of wild-type Bt (GT231 black) or strains lacking a levan-inducible susC (ΔBT1763; GT3196; blue), 4 levanases (ΔBT1760-1759 ΔBT3082 ΩBT1765; GT3348; purple), fructan-sensor (ΔBT1754; GT16S; red), or a putative inner membrane fructose importer (ΩBT1758; GT3379; orange) were measured during anaerobic culture in minimal media containing galactose as a sole carbon source. For FIGS. **8**A and **8**B, values are the mean of 8 biological replicates and error bars are SEM in color-matched shading. FIGS. **8**C-**8**E show the fold increase of (FIGS. **8**C and **8**D) BT3332 or (FIG. **8**E) BT1763 mRNA levels in wildtype Bt following the introduction of mixtures containing either 0.2%, 0.02%, or 0.02% CS or levan supplemented with galactose to 0.5% total carbohydrate. The fold increase was calculated as the change in transcript levels between cultures before and after 2 hours or 1 hour following induction of glycan mixtures. Values are average of 6 independent measurements, error bars represent SEM, and P-values were calculated by 2-way ANOVA with Tukey's honest significance test and *** represents values <0.001, *<0.05, and ns indicates values >0.05.

[0077] FIGS. **9**A, **9**B, **9**C, and **9**D show the bioluminescence during anaerobic growth across *Bacteroides* species and growth conditions. FIG. **9**A shows the relative luminescence (solid lines) or growth (dashed lines) from Bt strains harboring an empty vector (GT1866; black) or plasmids containing either the lux operon from *P. luminescens* (GT3137; blue) or the *Bacteroides*-optimized lux cassette (GT1541; red) expressed from the Bt rpoD promoter and rpiL* RBS was measured during growth in minimal media containing 0.5% glucose. FIG. **9**B shows the relative luminescence of Bt strains harboring empty pBolux (GT1867; dashed lines) or a plasmid with the corresponding rpoD promoter cloned into the BamHI and SpeI sites (GT1868; solid lines) during growth in glucose (black), fructose (red), arabinose (purple), or xylose (green) as the sole carbon source. FIG. **9**C shows the relative luminescence (solid lines) or growth (dashed lines) of Bo strains harboring empty pBolux (GT3489; black) or a plasmid with the Bo rpoD promoter cloned into the BamHI and SpeI sites (GT3490; red) during growth in galactose as the sole carbon source. FIG. **9**D shows the relative luminescence of Bo strains harboring empty pBolux (GT3489; dashed lines) or a plasmid with the corresponding rpoD promoter cloned into BamHI and SpeI sites (GT3490; solid lines) during growth in glucose (black), fructose (red), arabinose (purple), or xylose (green) as the sole carbon source. For all figures, values are the mean of 8 biological replicates and error is SEM in color-matched shading.

[0078] FIGS. **10**A, **10**B, **10**C, **10**D, **10**E, and **10**F show that the BT3332 promoter confers CS and HA-inducible bioluminescence in pBolux. FIGS. **10**A and **10**B show the relative luminescence from wild-type Bt (GT1934, black lines) or strains lacking the CS-inducible susC (ΔBT3334; GT2939; blue), 3 CS-specific lyases (ΔBT3324 ΔBT3350 ΩBT4410; GT3117; purple), CS-sensor (ΔBT3334; BT2618; red), or a glucuronyl hydrolyase (ΔBT3348; GT3102; orange) harboring pBolux including the promoter region preceding BT3332 (P-BT3332) following the introduction of an equal mixture of CS and galactose or galactose alone. FIG. **10**C shows the relative luminescence from wild-type Bt (GT1934) harboring P-BT3332 following the introduction of galactose alone (black lines) or an equal mixture of galactose and HA (green lines) or HS (blue lines). FIGS. **10**D AND **10**E show the growth of wild-type Bt (GT23; black) or a strain lacking the CS-sensor (ΔBT3334; GT150; red) were measured during anaerobic culture in minimal media containing HS or HA as a sole carbon source. FIG. **10**F the relative luminescence from a CS-sensor deficient strain (ΔBT3334; GT2618) harboring P-BT3332 following the introduction of galactose alone (black lines) or an equal mixture of galactose and HA (green lines) or HS (blue lines). For all figures, values are the mean of 8 biological replicates, error bars are SEM in color-matched shading.

[0079] FIGS. **11**A, **11**B, **11**C, **11**D, **11**E, **11**F, **11**G, and **11**H show a fructan-responsive reporter reveal new insights into Bt levan utilization. FIG. **11**A shows the relative luminescence from wild-type Bt harboring empty pBolux (black) or a plasmid including the region upstream of the levan-inducible susC (P-BT1763, pink) following the introduction of 0.5% levan (solid lines) or 0.5% galactose (dashed lines). Values are the mean of 12 biological replicates, error is SEM

in color-matched shading. FIGS. **11**B and **11**C show the growth of wild-type Bt harboring empty pBolux (black) or P-BT1763 (pink) following the introduction of 0.5% galactose or 0.5% levan. For FIGS. **11**A, **11**B, and **11**C, values are the mean of 12 biological replicates, error is SEM in color-matched shading. FIGS. **11**D and **11**F show the growth of wild-type Bt or strains lacking all other levanases except BT1760 (ΔBT1759 ΔBT3082 ΩBT1765; GT3347; pink), BT1759 (ΔBT1760 ΔBT3082 Ω1765; GT3346; teal), BT3082 (ΔBT1760-59 ΩBT1765; gt3401; lavender), or BT1765 (ΔBT1760-59 Δ3082; GT3308; purple) in 0.1% fructose or galactose as a sole carbon source. FIGS. **11**E and **11**G show the growth wild-type Bt (GT23, black) or strains lacking either BT1760 (GT3181; pink), BT1759 (GT3226; teal), BT3082 (GT3303; lavender), or BT1765 (GT; purple) 0.1% fructose or galactose as a sole carbon source. FIG. **11**H shows the growth of wild-type Bt (GT2111. Black) or BT1760-deficient strains (GT3215; pink) harboring empty pNBU2 or a plasmid encoding BT1760 (GT3216, green) in 0.1% levan as the sole carbon source.

[0080] FIGS. **12**A, **12**B, **12**C, and **12**D show a fructan-responsive PUL in Bo exhibits inulin-inducible activity. FIGS. **12**A, **12**B, and **12**C show the growth of wild-type Bo (ATCC 8483; black) or a strain lacking the Bo inulin sensor (ΔBACOVA_04496; GT3183; red) were measured during anerobic culture in minimal media containing levan, fructose, or galactose as the sole carbon source. Values are the mean of 8 biological replicates and errors bars are SEM in color-matched shading.

[0081] FIG. **12**D shows the relative luminescence from wild-type Bo harboring empty pBolux (black) or a plasmid that includes the region preceding an inulin-inducible susC (P-BACOVA_04505; pink) were measured following the introduction of 0.5% inulin (solid lines) or 0.5% galactose (dashed lines). Values are the mean of 12 biological replicates and error is SEM in color-matched shading.

[0082] FIGS. **13**A, **13**B, **13**C, **13**D, **13**E, and **13**F show that PUL reporters display concentration dependent responses to target glycans. FIG. **13**A shows the relative luminescence from a wild-type Bt strain harboring a P-BT1763 (GT1893) following the introduction of mixtures containing 2-fold serial dilutions of 0.4% levan balanced with galactose to a final carbohydrate content of 0.5% and normalized to identical cultures supplied galactose alone. Values are the mean of 12 biological replicates and error bars are SEM in color-matched shading. FIGS. **13**B and **13**C show the log 10 AUC responses within the linear range from wild-type Bt (black; FIG. **13**B: GT1934; FIG. **13**C: GT1893) or mutants defective for PUL-sensor deactivation (orange; FIG. **13**B: GT3102; FIG. **13**C: GT3393) harboring P-BT3332 or P-BT1763 and supplied 2× serial dilutions of 0.4% CS or levan balanced with galactose to 0.5% total carbohydrate content and normalized to response from identical cultures supplied galactose alone. Values are the mean of 12 biological replicates and error is standard deviation. Solid lines represent the simple linear regression models corresponding to responses from each strain and color-matched dashed lines represents the 95% confidence intervals computed in Prism. FIGS. **13**D and **13**E show the fold difference between the AUC of response from wild-type Bt strains harboring either P-BT3332 (blue squares) or P-BT1763 (red circles) supplied glycan mixtures containing 2-fold serial dilutions of 0.2% CS or levan, respectively, in the presence or absence of constant 0.2% levan or CS, respectively, and balanced with galactose to 0.5% total carbohydrate normalized by the AUC of responses from identical cultures supplied alone. FIG. **13**E shows the AUC of responses from wild-type Bt strains harboring either P-BT3332 (GT1934; blue squares) or P-BT1763 (GT1893; red circles) supplied glycan mixtures containing 2-fold serial dilutions of 0.2% CS or levan, respectively, in the presence of constant 0.2% levan or CS, respectively, and balanced with galactose to 0.5% total carbohydrate normalized by the AUC of responses from identical cultures supplied galactose alone. Values represent the average of 6 biological replicates and error bars are standard deviation. P-values were calculated with 2-way ANOVA with Tukey's honest significance test and *** represents values <0.001, **<0.01, *<0.05, and ns >0.05. FIG. **13**F shows the relative luminescence from a BT1758-deficient Bt strain harboring P-BT1763 (GT3393) following the introduction of 2-fold serial dilutions of 0.4% levan containing galactose to a final carbohydrate content of 0.5% and normalized to identical cultures supplied galactose alone. Values are the mean of 12 biological replicates and error bars are SEM in color-matched shading.

[0083] FIGS. **14**A, **14**B, **14**C, **14**D, **14**E, **14**F, **14**G, **14**H, and **14**I show the glycan-responsive reporter strains can indicate target glycan abundance. FIGS. **14**A and **14**B show the AUC of responses from wild-type Bt strains harboring either a P-BT3332 (GT1934; open bars) or P-BT1763 (GT1893, filled bars) supplied elution fractions from nickel-NTA agarose incubated with *E. Coli* whole cell lysates from strains containing empty pT7-7 vector, or plasmids engineered to overexpress BT1761 or BT3330 and pre0incubated with a mixture of 0.1% of both levan and CS. All elution fractions were supplemented with 0.4% galactose. Values represent an average of 4 total replicates from two independent experiments and error bars are SEM. FIG. **14**C shows the Coomassie stained SDS-PAGE gels showing the corresponding protein levels for BT3330 (top 2 gels) or BT1761 (bottom 2 gels) in each elution fraction. FIGS. **14**D and **14**E show the AUC responses from wild-type Bt strains harboring either P-BT3332 (GT1934; open bars) or P-BT1763 (GT1893, filled bars) supplied galactose alone or concentrated material co-purifying with BT3330 or BT1761 supplemented with 0.4% galactose. Values are the average of 4 measurements from 2 independent experiments, error is standard deviation and P-values were computed using 1-way ANOVA with Tukey's honest significance test and *** represents values <0.001 and ns indicates values >0.05. FIG. **14**F shows the AUC of responses from a BT3348-deficient Bt strain harboring P-BT3332 supplied galactose alone (none) or concentrated material co-purifying BT1761 supplemented with 0.4% galactose. FIG. **14**G shows identical cultures to those described in FIG. **14**F were supplied 2-fold serial dilutions of CS containing galactose to 0.5% total carbohydrate content and all measurements were normalized to responses from cultures supplied galactose alone. FIG. **14**H shows the AUC of responses from a BT1758-deficient Bt strain harboring P-BT1763 supplied galactose alone or concentrated material co-purifying with BT3330 and supplemented with 0.4% galactose. FIG. **14**I shows identical cultures to those described in FIG. **14**H were supplied 2-fold dilutions of levan containing galactose to 0.5% total carbohydrate content and all measurements were normalized to responses from cultures supplied galactose alone. For FIGS. **14**F-**14**I, values represent the average of 2 measurements from a single experiment and error bars are

standard deviation. For FIGS. **14**G-**14**H, solid lines represent simple linear regression models and color-matched dashed lines are the 95% confidence intervals computed in Prism.

[0084] FIGS. **15**A, **15**B, **15**C, and **15**D show a *Bacteroides* transcriptional reporter functions across many species. Relative luminescence (left axis) and growth (right axis) detected from 4 different wild-type *Bacteroides* species, (FIG. **15**A) Bt, (FIG. **15**B) Bo, (FIG. **15**C) Bf, or (FIG. **15**D) Bc harboring a promoter-less *Bacteroides*-optimized lux cassette control plasmid (pBolux, black lines) or one encoding the constitutively active rpoD promoter (red lines) cultured in minimal media containing 0.5% galactose as the sole carbon source. n=4, error bars are SEM.

[0085] FIGS. **16**A, **16**B, **16**C, and **16**D show how PUL-reporters respond to target glycans. FIG. **16**A shows the reporter activity over 18 hours in wild-type Bt harboring a promoter-less reporter plasmid (pBolux, gray) or one with the promoter preceding the CS-specific susC gene (P-BT3332, black) in 0.5% CS normalized to identical strains supplied 0.5% galactose. n=6. FIG. **16**B shows the normalized reporter activity over time harboring the CS-responsive PUL reporter in wild-type Bt (wt, black) or mutants lacking either the CS-sensor (Δsen, red), CS-specific susC gene (ΔsusC, blue), 3 CS-specific lyases (Δlyase, purple), or a CS-disaccharide specific glucuronyl hydrolase (Δgh, orange) supplied a mixture of 0.2% CS and 0.2% galactose and normalized to identical strains supplied 0.4% galactose. FIG. **16**C shows the AUC for all strains in (B) were computed for 18 hours following the introduction of CS. n=8. FIG. **16**D shows the AUC computed from normalized reporter activity from wild-type Bt (wt, black) or strains lacking 3 CS-specific lyases (Δlyase, purple) or the CS-specific sensor (Δsen, red) harboring the P-BT3332 reporter plasmid and supplied CS-disaccharide. n=6. For all panels, error bars are SEM. For (C-D) p-values were calculated using paired, two-tailed student's t-tests. ns indicates values >0.05, *<0.05, **<0.01, and ***<0.001.

[0086] FIGS. **17**A, **17**B, **17**C, **17**D, **17**E, and **17**F show the species-specific PUL-reporters differentially detect compositionally identical but structurally distinct glycans. FIGS. **17**A-**17**C show the growth of wild-type Bt (black) or Bo (gray) strains or mutants lacking the corresponding fructan PUL-sensor genes, BT1754 (BtΔsen, red) or BACOVA_04496 (BoΔsen, yellow), respectively, cultured in (FIG. **17**A) levan, (FIG. **17**B) inulin, or (FIG. **17**C) fructose as the sole carbon source. FIGS. **17**D-**17**F show the fructan-responsive reporter activity of the strains described for (FIGS. **17**A-**17**C) following the introduction of galactose supplemented with equal amounts and (FIG. **17**D) fructose, (FIG. **17**E) levan, or (FIG. **17**F) inulin and normalized to the non-inducing condition (galactose alone). The area under each curve was computed for 18 hours following the introduction of each glycan mixture. For all panels: n=8, error bars are SEM, P-values were calculated by paired, two-tailed Student's t-test. ns indicates values <0.05, *<0.05, **<0.01, and ***<0.001.

[0087] FIGS. **18**A, **18**B, **18**C, **18**D, and **18**E show that PUL-reporters elicit specific dose-dependent responses to target glycans. FIG. **18**A shows the reporter activity from wild-type Bt harboring the levan-reporters supplied 2× dilutions of the corresponding glycan in galactose to a final carbohydrate content of 0.5% and normalized to identical strains supplied galactose alone. FIG. **18**B shows the quantified CS-reporter activity normalized to a non-inducing condition (0.5% galactose) following the introduction of 2× serial dilutions of CS (filled circles) or levan (open circles) in galactose to a final glycan concentration of 0.5%. FIG. **18**C shows the quantified levan-dependent reporter activity normalized to a non-inducing condition (0.5% galactose) following the introduction of 2× serial dilutions of levan (open circles) or CS (filled circles) in galactose to a final glycan concentration of 0.5%. FIG. **18**D shows the quantified CS-reporter (P-BT3332; filled circles) or levan-reporter (P-BT1763; open circles) activity from strains supplied mixtures containing 2× serial dilutions of CS in constant 0.2% levan and galactose to final carbohydrate content of 0.5%. FIG. **18**E shows the quantified CS-reporter (P-BT3332; filled circles) or levan-reporter (P-BT1763; open circles) activity from strains supplied mixtures containing 2× serial dilutions of CS in constant 0.2% levan and galactose to final carbohydrate content of 0.5%. For all panels: n=4, error bars are SEM, p-values were calculated using a paired, two-tailed Student's t-test. * indicates p-values below 0.05 compared to strains supplied galactose. R2 values were computed by MS Excel power trendline function.

[0088] FIGS. **19**A, **19**B, **19**C, **19**D, and **19**E show the mutations disrupting PUL-encoding activities can narrow target specificity or increase reporter sensitivity. FIG. **19**A shows the growth of wild-type Bt (black) or a strain lacking 3 CS-specific lyases (purple) in 0.1% HA as a sole carbon source. n=4, error is standard deviation. FIGS. **19**B-**19**C shows the AUC from wild-type Bt (black) or a lyase-deficient mutant (purple) harboring the CS/HA-reporter (P-BT3332) following the introduction of 2-fold titrations of (FIG. **19**B) CS or (FIG. **19**C) HA and normalized to a non-inducing condition (0.5% galactose). n=4, error bars are standard deviation. FIG. **19**D shows the reporter activity (AUC) was measured from wild-type Bt (black line) or the gh-deficient strain (orange) harboring the CS-reporter (P-BT3332) following the introduction of 2× serial dilutions of CS in galactose to a final glycan concentration of 0.5% and normalized to an identical strain supplied galactose alone. FIG. **19**E shows the reporter activity (AUC) was measured from wild-type Bt (black line) or a fructose importer-deficient strain (orange) harboring the levan-reporter (P-BT1763) following the introduction of 2× serial dilutions of levan in galactose to a final glycan concentration of 0.5% and normalized to an identical strain supplied galactose alone. n=6 and error bars are standard deviation.

[0089] FIGS. **20**A, **20**B, **20**C, **20**D, **20**E, **20**F, **20**G, **20**H, and **20**I show the glycan-independent validation of reporter plasmids. FIG. **20**A shows a schematic depicting our approach to validate PUL reporters in the absence of known glycan ligands and identify optimal promoters for sensor/regulator-dependent glycan-induced transcription activation. FIGS. **20**B-**20**I show the fold increase (AUC) in reporter activity in strains over-expressing a constitutively activated form of the PUL regulators: (FIG. **20**B) BT2391, (FIG. **20**C) BT3269, (FIG. **20**D) BT3097, (FIG. **20**E) BT3172, (FIG. **20**F) BT1278, (FIG. **20**G) BT1617, (FIG. **20**H) BT3517, or (FIG. **20**I) BT4137 and harboring promoter-less pBolux or a plasmid containing putative promoter regions from the corresponding PUL. The fold increase in reporter activity was calculated as the AUC from strains harboring each reporter plasmids and over-expressing the indicated regulator normalized by a strain harboring

identical reporter plasmids and an empty over-expression vector. n=4, error bars are standard deviation, p-values were calculated using paired, two-tailed student's t-tests, ns indicates p-values >0.05, *, <0.05, and **<0.01.

[0090] FIGS. **21**A, **21**B, **21**C, **21**D, **21**E, **21**F, and **21**G show a high-throughput Bt PUL-reporter array specifically detects target glycans individually and in biologically derived mixtures. FIG. **21**A-**21**G show the fold increase in reporter activity (AUC) of strains harboring 95-distinct PUL reporter plasmids (labeled on the x-axis by the corresponding PUL-encoded susC gene) or the promoter-less pBolux plasmid (1st bar) following the introduction of a mixture of 0.1% galactose and 0.4% (FIG. **21**A) arabinogalactan, (FIG. **21**B) levan, (FIG. **21**C) dextran, (FIG. **21**D) hyaluronan, (FIG. **21**E) heparan sulfate, (FIG. **21**F) chondroitin sulfate, or (FIG. **21**G) PMOGs. FIGS. **21**A-**21**E are from a single experiment, FIG. **21**F and FIG. **21**G are the average of 3 or 5 independent replicates, respectively. Error bars are standard deviation, p-values were calculated using a paired, two-tailed student's t-test and * indicates p-values <0.05, **<0.01, and ***<0.001.

[0091] FIGS. **22**A, **22**B, and **22**C show that PUL-sensors specifically activate target PULs. FIGS. **22**A-**22**B show the bioluminescence from wild-type or BT3334-deficient Bt strains harboring P-BT1632, P-BT2818, P-BT3332, or P-BT4662 were measured in response to a mixture of galactose and (FIG. **22**A) CS or (FIG. **22**B) CS-disaccharide (di0S) and normalized by identical strains supplied galactose. FIG. **22**C shows the bioluminescence from Bt strains harboring the reporters described in panels A&B and over-expressing a constitutively active BT3334 protein (BT3334*). Measurements were normalized by values from a strain harboring identical reporters and an empty over-expression vector. n=4, error bars are standard deviation, and p-values were calculated by two-tailed student's t-test. ns indicates p-values <0.05, *<0.05, **<0.01, and ***<0.001.

DETAILED DESCRIPTION

[0092] The following description of the disclosure is provided as an enabling teaching of the disclosure in its best, currently known embodiment(s). To this end, those skilled in the relevant art will recognize and appreciate that many changes can be made to the various embodiments of the invention described herein, while still obtaining the beneficial results of the present disclosure. It will also be apparent that some of the desired benefits of the present disclosure can be obtained by selecting some of the features of the present disclosure without utilizing other features. Accordingly, those who work in the art will recognize that many modifications and adaptations to the present disclosure are possible and can even be desirable in certain circumstances and are a part of the present disclosure. Thus, the following description is provided as illustrative of the principles of the present disclosure and not in limitation thereof.

[0093] Reference will now be made in detail to the embodiments of the invention, examples of which are illustrated in the drawings and the examples. This invention may, however, be embodied in many different forms and should not be construed as limited to the embodiments set forth herein.

Terminology

[0094] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. The term "comprising" and variations thereof as used herein is used synonymously with the term "including" and variations thereof and are open, non-limiting terms. Although the terms "comprising" and "including" have been used herein to describe various embodiments, the terms "consisting essentially of" and "consisting of" can be used in place of "comprising" and "including" to provide for more specific embodiments and are also disclosed. As used in this disclosure and in the appended claims, the singular forms "a", "an", "the", include plural referents unless the context clearly dictates otherwise.

[0095] The following definitions are provided for the full understanding of terms used in this specification.

[0096] The terms "about" and "approximately" are defined as being "close to" as understood by one of ordinary skill in the art. In one non-limiting embodiment the terms are defined to be within 10%. In another non-limiting embodiment, the terms are defined to be within 5%. In still another non-limiting embodiment, the terms are defined to be within 1%.

[0097] As used herein, the terms "may," "optionally," and "may optionally" are used interchangeably and are meant to include cases in which the condition occurs as well as cases in which the condition does not occur. Thus, for example, the statement that a formulation "may include an excipient" is meant to include cases in which the formulation includes an excipient as well as cases in which the formulation does not include an excipient.

[0098] "Composition" refers to any agent that has a beneficial biological effect. Beneficial biological effects include both therapeutic effects, e.g., treatment of a disorder or other undesirable physiological condition, and prophylactic effects, e.g., prevention of a disorder or other undesirable physiological condition. The terms also encompass pharmaceutically acceptable, pharmacologically active derivatives of beneficial agents specifically mentioned herein, including, but not limited to, a vector, polynucleotide, cells, salts, esters, amides, proagents, active metabolites, isomers, fragments, analogs, and the like. When the term "composition" is used, then, or when a particular composition is specifically identified, it is to be understood that the term includes the composition per se as well as pharmaceutically acceptable, pharmacologically active vector, polynucleotide, salts, esters, amides, proagents, conjugates, active metabolites, isomers, fragments, analogs, etc.

[0099] "Comprising" is intended to mean that the compositions, methods, etc. include the recited elements, but do not exclude others. "Consisting essentially of" when used to define compositions and methods, shall mean including the recited elements, but excluding other elements of any essential significance to the combination. Thus, a composition consisting essentially of the elements as defined herein would not exclude trace contaminants from the isolation and purification method and pharmaceutically acceptable carriers, such as phosphate buffered saline, preservatives, and the like. "Consisting of" shall mean excluding more than trace elements of other ingredients and substantial method steps for administering the compositions provided and/or claimed in this disclosure. Embodiments defined by each of these transition terms are within the scope of this disclosure.

[0100] By "reduce" or other forms of the word, such as "reducing" or "reduction," means lowering of an event or characteristic (e.g., tumor growth). It is understood that this

is typically in relation to some standard or expected value, in other words it is relative, but that it is not always necessary for the standard or relative value to be referred to. For example, "reduces tumor growth" means reducing the rate of growth of a tumor relative to a standard or a control.

[0101] By "prevent" or other forms of the word, such as "preventing" or "prevention," is meant to stop a particular event or characteristic, to stabilize or delay the development or progression of a particular event or characteristic, or to minimize the chances that a particular event or characteristic will occur. Prevent does not require comparison to a control as it is typically more absolute than, for example, reduce. As used herein, something could be reduced but not prevented, but something that is reduced could also be prevented. Likewise, something could be prevented but not reduced, but something that is prevented could also be reduced. It is understood that where reduce or prevent are used, unless specifically indicated otherwise, the use of the other word is also expressly disclosed.

[0102] The term "subject" refers to any individual who is the target of administration or treatment. The subject can be a vertebrate, for example, a mammal. In one aspect, the subject can be human, non-human primate, bovine, equine, porcine, canine, or feline. The subject can also be a guinea pig, rat, hamster, rabbit, mouse, or mole. Thus, the subject can be a human or veterinary patient. The term "patient" refers to a subject under the treatment of a clinician, e.g., physician.

[0103] A "control" is an alternative subject or sample used in an experiment for comparison purposes. A control can be "positive" or "negative."

[0104] The term "treatment" refers to the medical management of a patient with the intent to cure, ameliorate, stabilize, or prevent a disease, pathological condition, or disorder. This term includes active treatment, that is, treatment directed specifically toward the improvement of a disease, pathological condition, or disorder, and also includes causal treatment, that is, treatment directed toward removal of the cause of the associated disease, pathological condition, or disorder. In addition, this term includes palliative treatment, that is, treatment designed for the relief of symptoms rather than the curing of the disease, pathological condition, or disorder; preventative treatment, that is, treatment directed to minimizing or partially or completely inhibiting the development of the associated disease, pathological condition, or disorder; and supportive treatment, that is, treatment employed to supplement another specific therapy directed toward the improvement of the associated disease, pathological condition, or disorder.

[0105] A "promoter," as used herein, refers to a sequence in DNA that mediates the initiation of transcription by an RNA polymerase. Transcriptional promoters may comprise one or more of a number of different sequence elements as follows: 1) sequence elements present at the site of transcription initiation; 2) sequence elements present upstream of the transcription initiation site and; 3) sequence elements down-stream of the transcription initiation site. The individual sequence elements function as sites on the DNA, where RNA polymerases and transcription factors facilitate positioning of RNA polymerases on the DNA bind.

[0106] As used herein, the term "buffer" refers to a solution consisting of a mixture of acid and its conjugate base, or vice versa. The solution is used as a means of keeping the pH at a nearly constant range to be used in a wide variety of chemical and biological applications.

[0107] "Culture" or "cell culture" is the process by which cells, including bacterial cells, are grown under controlled conditions, generally outside their natural environment. These conditions vary for each cell type, but generally consist of a suitable vessel with a substrate or medium that supplies the essential nutrients (amino acids, carbohydrates, vitamins, minerals), growth factors, hormones, and gases (CO_2, O_2), and regulates the physio-chemical environment (pH buffer, osmotic pressure, temperature). Most cells require a surface or an artificial substrate to form an adherent culture as a monolayer (one single-cell thick), whereas others can be grown free floating in a medium as a suspension culture.

[0108] The term "administer," "administering", or derivatives thereof refer to delivering a composition, substance, inhibitor, or medication to a subject or object by one or more the following routes: oral, topical, intravenous, subcutaneous, transcutaneous, transdermal, intramuscular, intra-joint, parenteral, intra-arteriole, intradermal, intraventricular, intracranial, intraperitoneal, intralesional, intranasal, rectal, vaginal, by inhalation or via an implanted reservoir. The term "parenteral" includes subcutaneous, intravenous, intramuscular, intra-articular, intra-synovial, intrasternal, intrathecal, intrahepatic, intralesional, and intracranial injections or infusion techniques.

[0109] The term "detect" or "detecting" refers to an output signal released for the purpose of sensing of physical phenomenon. An event or change in environment is sensed and signal output released in the form of light.

[0110] A "primer" is a short polynucleotide, generally with a free 3'-OH group that binds to a target or "template" potentially present in a sample of interest by hybridizing with the target, and thereafter promoting polymerization of a polynucleotide complementary to the target. A "polymerase chain reaction" ("PCR") is a reaction in which replicate copies are made of a target polynucleotide using a "pair of primers" or a "set of primers" consisting of an "upstream" and a "downstream" primer, and a catalyst of polymerization, such as a DNA polymerase, and typically a thermally-stable polymerase enzyme. Methods for PCR are well known in the art, and taught, for example in "PCR: A PRACTICAL APPROACH" (M. MacPherson et al., IRL Press at Oxford University Press (1991)). All processes of producing replicate copies of a polynucleotide, such as PCR or gene cloning, are collectively referred to herein as "replication." A primer can also be used as a probe in hybridization reactions, such as Southern or Northern blot analyses. Sambrook et al., supra.

[0111] "Transformation" of a cellular organism with DNA means introducing DNA into an organism so that at least a portion of the DNA is replicable, either as an extrachromosomal element or by chromosomal integration. The cell is termed "host cell" and it may be either prokaryotic or eukaryotic. Typical prokaryotic host cells include various strains of *E. coli* or *Bacteroides*. The introduced DNA sequence may be from the same species as the host cell of a different species from the host cell, or it may be a hybrid DNA sequence, containing some foreign and some homologous DNA.

[0112] The terms "treat," "treating," and grammatical variations thereof as used herein, include partially or completely delaying, alleviating, mitigating, or reducing the

intensity of one or more attendant symptoms of a disorder or condition and/or alleviating, mitigating, or impeding one or more causes of a disorder or condition. Treatments according to the disclosure may be applied preventively, prophylactically, palliatively, or remedially. Treatments are administered to a subject prior to onset (e.g., before obvious signs of disease]), during early onset (e.g., upon initial signs and symptoms of disease), or after an established development of disease.

[0113] The term "antibiotics" refers to a type of antimicrobial substance active against bacteria. These are the most important type of antimicrobial agent for fighting bacterial infections, and antibiotics medications are widely used in the treatment and prevention of such infections. They may either kill or inhibit the growth of bacteria.

[0114] Used herein, the term "probiotics" refers to live microorganisms promoted with claims that they provide health benefits when consumed, generally by improving or restoring the gut flora.

[0115] As used herein, "normal" refers to a standard of health where no disease, disorder, abnormal condition, mutation, or dysfunction exists within a particular subject or patient. "Normal" can also refer to an average or typical state or condition.

[0116] As used herein, "wild-type" refers to the genetic and physical characteristics of the typical form of a species as it occurs in nature. A wild-type or wild type characteristic is conceptualized as a product of the standard "normal" allele at a gene locus, in contrast to that produced by a non-standard "mutant" allele.

[0117] As used herein, "preserve," "preserved," "preservation," "preserving" and any grammatical variations thereof as used herein, refers to the act of keeping any object, composition, or compound intact, alive, or free from decomposition/decay.

[0118] Reference also is made herein to peptides, polypeptides, proteins, and compositions comprising peptides, polypeptides, and proteins. As used herein, a polypeptide and/or protein is defined as a polymer of amino acids, typically of length≥100 amino acids (Garrett & Grisham, Biochemistry, 2nd edition, 1999, Brooks/Cole, 110). A peptide is defined as a short polymer of amino acids, of a length typically of 20 or less amino acids, and more typically of a length of 12 or less amino acids (Garrett & Grisham, Biochemistry, 2nd edition, 1999, Brooks/Cole, 110).

[0119] As used herein, "harbor", "harboring", and any grammatical variations thereof refers to a subject, including, but not limited to a cell, vector, bacteria, virus, fungi, tissue, or any other organism containing or being the host to another organism, molecule, compound, nucleic acid, protein, or any other composition.

[0120] A "cassette" or "gene cassette" refers to a mobile genetic element that generally contains a gene and a recombination site. Gene cassettes can move around within an organism's genome or can be transferred to another organism in the environment.

[0121] "Quantify", "quantifying", "quantification", and any other grammatical variations thereof refer to the process of acquiring numerical values to determine, express, or measure an amount of a substance or signal.

[0122] "Anaerobic" refers to living, active, occurring, or existing in the absence of oxygen.

[0123] As used herein, the term "apparatus" refers to a technical equipment or machinery needed for a particular activity or purpose. Herein, the apparatus is used to separate biomolecules from one another for further purification and collection. The apparatus can comprise one or multiple components to form a complex structure needed to perform a particular function.

[0124] As used herein, a "container" refers to a receptacle or enclosure for holding a product, substance, or composition used in storage, packaging, and transportation, including shipping. The product, substance, or composition are kept inside of the container to protect and prevent contamination from the outside environment. A container is also meant to partially or completely enclose the product, substance, or composition.

Reporter Plasmids

[0125] As used herein, a "reporter plasmid" refers to a type of expression vector containing a reporter gene, also called "reporter vector", that can be used to identify and characterize promoter and/or enhancer element functions relative to gene expression. Expression of the reporter gene corresponds to the transcriptional activity of the reporter gene. In general, reporter genes are nucleic acid sequences whose products, or proteins, can be readily assayed, measured, or quantified following transformation or transfection into a host cell. Reporter genes include, but are not limited to luciferase reporter genes (lux or luc), beta-galactosidase reporter gene (lacZ), chloramphenicol acetyltransferase (cat), green fluorescent protein reporter gene (gfp), red fluorescent protein reporter gene (rfp), and derivatives thereof. It should be noted that luciferase reporter gene are the preferred reporter gene because luciferase reporter genes are readily expressed in an anaerobic environment.

[0126] The reporter plasmid can comprise any combination of gene elements to allow for transcription including, but not limited to promoter sequences, activator and/or enhanced elements (including, but not limited to transcription factor binding sites and polymerase binding sites), and operator and/or silenced elements (including, but not limited to repressor protein binding sites).

[0127] Thus in one aspect, disclosed herein are reporter plasmids comprising a luciferase reporter cassette, a first polysaccharide utilization locus (PUL), and a first glycan-specific promoter.

[0128] Also disclosed herein are reporter plasmids, wherein the first PUL encodes any combination of proteins comprising a surface glycan binding protein (SGBP), an outer membrane channel, a digestive enzyme, a glycan importer, or a glycan sensor.

[0129] In one aspect disclosed herein are reporter plasmids, wherein the first PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof.

[0130] Also disclosed herein are reporter plasmids, wherein the first glycan specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof including, but not limited to glycan specific promoters comprising the nucleic acids sequence as set forth in SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ

ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 266, SEQ ID NO: 267, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, SEQ ID NO: 323, SEQ ID NO: 324, SEQ ID NO: 325, SEQ ID NO: 326, SEQ ID NO: 327, SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 331, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 338, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 343, SEQ ID NO: 344, SEQ ID NO: 345, SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, SEQ ID NO: 349, SEQ ID NO: 350, SEQ ID NO: 351, SEQ ID NO: 352, SEQ ID NO: 353, or SEQ ID NO: 354.

[0131] In one aspect disclosed herein are reporter plasmids, wherein the reporter plasmid further comprises a second PUL. In some embodiments, the second PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan (OG)-specific PUL, or variants thereof. In some embodiments, the first PUL is interchangeable with the second PUL.

[0132] Also disclosed herein are reporter plasmids, wherein the reporter plasmid further comprises a second glycan-specific promoter. In some embodiments, the first glycan-specific promoter is interchangeable with the second glycan-specific promoter. In some embodiments, the second glycan-specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

[0133] In one aspect, disclosed herein are reporter plasmids, wherein the second glycan-specific promoter comprises the nucleic acids sequence as set forth in SEQ ID NOs 74-76, or SEQ ID NOS: 262-354.

[0134] Also disclosed herein are reporter plasmids, wherein the reporter plasmid comprises a *Bacteroides*-optimized lux (Bolux) plasmid.

Engineered Bacteria

[0135] An engineered bacteria, or a genetically engineered bacteria, are bacteria harboring additional genetic material, usually in the form of a plasmid vector, that allows said bacteria the ability to efficiently express native or foreign proteins for a specific purpose. It should be noted that more than one gene and other genetic material can be inserted into a plasmid, which can then be further integrated into bacteria.

[0136] Generating engineered bacteria in the gastrointestinal (GI) microbiome serves as an option for treating multiple diseases by genetically altering the bacteria residing in the GI tract. Genetically altering the GI microbiome allows for molecular profiling of the GI tract, altering gut bacteria to destroy pathogenic bacteria, or using genetically engineered bacteria to modify deficient enzymes or proteins. Specifically, molecular profiling of the GI tract includes detecting and quantifying the presence of glycans, oligosaccharides, monosaccharides, and other biomolecules in the GI tract. Such an approach also indicates the presence of pathogenic microorganisms or deficient enzymes and/or proteins.

[0137] Also disclosed herein are engineered bacteria comprising any of the reporter plasmid disclosed herein. For example, disclosed herein are engineered bacteria harboring a reporter plasmid wherein the reporter plasmid comprises a luciferase reporter cassette, a first polysaccharide utilization locus (PUL), and a first glycan-specific promoter. In some aspects, the first PUL encodes any combination of proteins comprising a surface glycan binding protein (SGBP), an outer membrane channel, a digestive enzyme, a glycan importer, or a glycan sensor. In some embodiments, the first PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof. In some aspects, the first glycan specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

[0138] In one aspect, disclosed herein are engineered bacteria, wherein the first glycan-specific promoter comprises the nucleic acids sequence as set forth in SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 266, SEQ ID NO: 267, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, SEQ ID NO: 323, SEQ ID NO: 324, SEQ ID NO: 325, SEQ ID NO: 326, SEQ ID NO: 327, SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 331, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 338, SEQ ID NO: 339, SEQ ID NO: 340, SEQ

ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 343, SEQ ID NO: 344, SEQ ID NO: 345, SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, SEQ ID NO: 349, SEQ ID NO: 350, SEQ ID NO: 351, SEQ ID NO: 352, SEQ ID NO: 353, or SEQ ID NO: 354.

[0139] Also disclosed herein are engineered bacteria, further comprising a second PUL. In some aspects, the second PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof. In some aspects, the first PUL is interchangeable with the second PUL.

[0140] In one aspect, disclosed herein are engineered bacteria, further comprising a second glycan-specific promoter. In some embodiments, the first glycan-specific promoter is interchangeable with the second glycan-specific promoter. In some aspects, the second glycan-specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

[0141] Also disclosed herein are engineered bacteria, wherein the second glycan-specific promoter comprises the nucleic acids sequence as set forth in SEQ ID NOs 74-76, or SEQ ID NOs: 262-354.

[0142] In some aspects, disclosed herein are engineered bacteria, wherein the engineered bacteria originates from a gastrointestinal bacterium. In some aspects, the engineered bacteria originates from a *Bacteroides* bacterium including, but not limited to *Bacteroides thetaiotaomicron* (Bt), *Bacteroides ovatus* (Bo), *Bacteroides fragilis* (Bf), *Bacteroides* caccae (Bc) or a variant strain thereof.

[0143] Also disclosed herein are engineered bacteria, wherein the engineered bacteria overexpresses the chondroitin sulfate (CS)-specific PUL when exposed to a CS glycan, or derivatives thereof.

[0144] In some aspects, disclosed herein are engineered bacteria, wherein the engineered bacteria overexpresses the levan-specific PUL when exposed to a levan glycan, or derivatives thereof.

[0145] Also disclosed herein are engineered bacteria, wherein the engineered bacteria overexpresses the inulin-specific PUL when exposed to an inulin glycan, or derivatives thereof.

[0146] In some aspects, disclosed herein are engineered bacteria, wherein the engineered bacteria overexpresses the arabinogalactan-specific PUL when exposed to an arabinogalactan, or derivatives thereof.

[0147] Also disclosed herein are engineered bacteria, wherein the engineered bacteria overexpresses the dextran-specific PUL when exposed to a dextran glycan, or derivatives thereof.

[0148] In some aspects, disclosed herein are engineered bacteria, wherein the engineered bacteria overexpresses the hyaluronan (HA)-specific PUL when the engineered bacteria is exposed to a HA glycan, or derivatives thereof.

[0149] Also disclosed herein are engineered bacteria, wherein the engineered bacteria overexpresses the heparan sulfate (HS)-specific PUL when exposed to a HS glycan, or derivatives thereof.

[0150] In some aspects, disclosed herein are engineered bacteria, wherein the engineered bacteria overexpresses the O-glycan(OG)-specific PUL when exposed to an OG glycan mixture, or derivatives thereof.

[0151] Also disclosed herein are engineered bacteria, wherein the engineered bacteria emits a light signal when overexpressing any PUL. In some aspects, the light signal is decreased when the glycan molecule is broken down into a monosaccharide molecule.

Glycan-Sensing Systems and Compositions

[0152] Glycans are polymer compounds comprising several smaller monosaccharide molecules usually linked together by glycosidic bonds. Glycan can also exist as homopolymers or heteropolymer, wherein the monosaccharide units can also be linked in a linear or branched formation. Common types of glycans include, but are not limited to O-linked glycans, N-linked glycans, and glycosaminoglycans. Glycans are substantive components of the gastrointestinal (GI) tract system of eukaryotic organisms. Microorganisms that reside in the GI tract are adept at consuming glycans and other polysaccharide molecules establishing a symbiotic relationship between gut microorganisms and the host. Fluctuations in the abundance of glycans create a diverse and heterogeneous environment in which the gut microorganisms can strive and proliferate. Thus, glycans shape and influence the composition and abundance of gut microbiome. Further, abnormalities in the gut microbiome glycan composition can also implicate presence of diseases and/or disorder. Given the influence of glycans in the GI tract, there is a need to develop compositions, systems, and methods of detecting homogenous or heterogenous mixtures of glycans for profiling, treating, preventing, reducing, and/or decreasing GI diseases and/or disorders in a subject.

[0153] In one aspect, disclosed herein is a glycan-sensing system comprising any of the reporter plasmids disclosed herein and/or any of the engineered bacteria disclosed herein.

[0154] In one aspect, disclosed herein is a glycan-sensing system comprising an engineered bacteria harboring a reporter plasmid, wherein the reporter plasmid comprises a luciferase reporter cassette, a first polysaccharide utilization locus (PUL), and a first glycan-specific promoter, wherein the glycan-sensing system detects and quantifies a glycan molecule.

[0155] As used herein, a "PUL" refers to a co-regulated group of genes that sense the presence of surrounding nutrients and enable digestion of glycans and other polysaccharides molecules. The GI microbiome comprises numerous PULs that enable bacterial species to recognize and consume glycan molecules. It should be noted that a PUL can be glycan specific.

[0156] In some embodiments, the glycan molecule comprises chondroitin sulfate, arabinan, heparan sulfate, hyaluronan, fructan, levan, mannan, or derivatives thereof. In some embodiments, the glycan is an N-linked glycan. In some embodiments, the glycan is an O-linked glycan. In some embodiments, the glycan is a branched glycan. In some embodiments, the glycan is a linear glycan. In some embodiments, the glycan molecule comprises pectic galactan, starch, glucan, galactomannan, glucomannan, homogalacturonan, xyloglucan, dermatan, xylan, rhamnogalac-

turonan, or derivative thereof. In some embodiments, the glycan molecule is located in the gastrointestinal tract of a mammal.

[0157] The genes within a PUL can encode a glycan utilization system, including, but not limited to a starch utilization system (Sus system). The gene products of the glycan utilization system generally localize to the outer membrane or periplasm of a bacterium, and function to sequentially bind to the glycan on the bacterial surface, degrade it into oligosaccharides, and transport the oligosaccharides into the periplasmic space for further degradation into monosaccharides. In some embodiments, the first PUL encodes any combination of proteins comprising a surface glycan binding protein (SGBP), an outer membrane channel, a digestive enzyme, a glycan importer, or a glycan sensor. In some embodiments, the SGBP comprises a SusD, SusG, SusE, or Sus F protein. In some embodiments, the outer membrane channel comprises a Sus C channel protein. In some embodiments, the digestive enzyme comprises a lyase, an amylase, or an enzyme capable or degrade glycans, carbohydrates, or polysaccharides. In some embodiments, the digestive enzyme comprises a Sus A or SusB enzyme. In some embodiments, glycan importer is located on the inner membrane of a bacterial cell. In some embodiments, glycan sensor comprises a SusR protein.

[0158] In some embodiments, the first PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan (OG)-specific PUL, or variants thereof.

[0159] In some embodiments, the first glycan specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

[0160] In some embodiments, the system further comprises a second PUL. In some embodiments, the second PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof. In some embodiments, the first PUL is interchangeable with the second PUL.

[0161] In some embodiments, the system further comprises a second glycan-specific promoter. In some embodiments, the first glycan-specific promoter is interchangeable with the second glycan-specific promoter. In some embodiments, the second glycan-specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan (OG)-specific promoter, or variants thereof.

[0162] In some embodiments, the first or second glycan-specific promoter comprises SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 266, SEQ ID NO: 267, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, SEQ ID NO: 323, SEQ ID NO: 324, SEQ ID NO: 325, SEQ ID NO: 326, SEQ ID NO: 327, SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 331, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 338, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 343, SEQ ID NO: 344, SEQ ID NO: 345, SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, SEQ ID NO: 349, SEQ ID NO: 350, SEQ ID NO: 351, SEQ ID NO: 352, SEQ ID NO: 353, or SEQ ID NO: 354.

[0163] In some embodiments, the luciferase reporter cassette comprises one or more genes selected from lux C, lux D, lux E, lux A, and lux B. In some embodiments, the luciferase reporter cassette originates from a *Photorhabdus* bacteria. In some embodiments, the luciferase reporter cassette originates from a *Photorhabdus luminescens* (PI) bacteria. In some embodiments, the gene products of the luciferase reporter cassette emit a light signal.

[0164] In some embodiments, the reporter plasmid comprises a *Bacteroides*-optimized lux (Bolux) plasmid.

[0165] In some embodiments, the engineered bacteria originates from a gastrointestinal bacterium. In some embodiments, the engineered bacteria originates from a *Bacteroides* bacterium. In some embodiments, the engineered bacteria originates from a *Bacteroides thetaiotaomicron* (Bt), *Bacteroides ovatus* (Bo), *Bacteroides fragilis* (Bf), *Bacteroides* caccae (Bc) or a variant strain thereof. In some embodiments, the engineered bacteria originates from a *Bacteroides acidifaciens* (Ba), *Bacteroides barnesiaes* (Bb), *Bacteroides caecicola, Bacteroides caecigallinarum, Bacteroides cellulosilyticus, Bacteroides cellulosolvens, Bacteroides ciarus, Bacteroides coagulans, Bacteroides coprocola, Bacteroides coprophilus, Bacteroides coprosuis, Bacteroides dorei, Bacteroides eggerthii, Bacteroidesgracilis, Bacteroides faecichinchillae, Bacteroides faecis, Bacteroides finegoldii, Bacteroides fluxus, Bacteroides galacturonicus, Bacteroides gallinaceum, Bacteroides gallinarum, Bacteroides goldsteinii, Bacteroides graminisolvens, Bacteroides helcogene, Bacteroides intestinalis, Bacteroides luti, Bacteroides massiliensis, Bacteroides nordii, Bacteroides oris, Bacteroides paurosaccharolyticus, Bacteroides plebeius, Bacteroides polypragmatus, Bacteroides proprionicifaciens, Bacteroides putredinis, Bacteroides pyogenes, Bacteroides reticulotermitis, Bacteroides rodentium, Bacteroides salanitronis, Bacteroides salyersiae, Bacteroides sartorii, Bacteroides sedmenti, Bacteroides stercoris, Bacteroides suis, Bacteroides tectus, Bacteroides uniformis, Bacteroides vulgatus*, or *Bacteroides xylanisolvens.*

[0166] In some embodiments, the engineered bacteria are grown in an anaerobic environment. In some embodiments, the engineered bacteria are grown in a 96-well, a 384-well, or a 1536-well microplate.

[0167] In some embodiments, the engineered bacteria overexpresses the chondroitin sulfate (CS)-specific PUL when exposed to a CS glycan, or derivatives thereof.

[0168] In some embodiments, the engineered bacteria overexpresses the levan-specific PUL when exposed to a levan glycan, or derivatives thereof.

[0169] In some embodiments, the engineered bacteria overexpresses the inulin-specific PUL when exposed to an inulin glycan, or derivatives thereof.

[0170] In some embodiments, the engineered bacteria overexpresses the arabinogalactan-specific PUL when exposed to an arabinogalactan, or derivatives thereof.

[0171] In some embodiments, the engineered bacteria overexpresses the dextran-specific PUL when exposed to a dextran glycan, or derivatives thereof.

[0172] In some embodiments, the engineered bacteria overexpresses the hyaluronan (HA)-specific PUL when the engineered bacteria is exposed to a HA glycan, or derivatives thereof.

[0173] In some embodiments, the engineered bacteria overexpresses the heparan sulfate (HS)-specific PUL when exposed to a HS glycan, or derivatives thereof.

[0174] In some embodiments, the engineered bacteria overexpresses the O-glycan(OG)-specific PUL when exposed to an OG glycan mixture, or derivatives thereof.

[0175] In some embodiments, the engineered bacteria emits a light signal when overexpressing any PUL disclosed herein.

[0176] In some embodiments, the light signal is decreased when the glycan molecule is broken down into a monosaccharide molecule.

Methods of Detecting Glycan Molecules

[0177] In one aspect, disclosed herein is a method of detecting a glycan, the method comprising isolating and preserving a tissue sample from a subject, preparing, and culturing the glycan-sensing system disclosed herein in a microplate in an anaerobic environment, adding the tissue sample into the microplate, and detecting and quantifying a light signal emitted from the system.

[0178] In one aspect, disclosed herein is a method of detecting a glycan, the method comprising isolating and preserving a tissue sample from a subject, preparing, and culturing any of the engineered bacteria disclosed herein in a microplate in an anaerobic environment, adding the tissue sample into the microplate, and detecting and quantifying a light signal emitted from the engineered bacteria.

[0179] In one aspect, disclosed herein is a method of detecting a glycan, the method comprising isolating and preserving a tissue sample from a subject, preparing any of the reporter plasmids disclosed herein in a microplate in an anaerobic environment, adding the tissue sample into the microplate, and detecting and quantifying a light signal emitted from the reporter plasmid.

[0180] In some embodiments, the tissue sample comprises at least one glycan. In some embodiments, the light signal is detected and quantified using a microplate reader, a spectrophotometer, or an instrument capable of measuring the light signal. In some embodiments, the tissue sample comprises a tissue biopsy, a blood sample, or a saliva sample. In some embodiments, the tissue sample comprises a tissue biopsy from the GI tract, including, but not limited to a tongue scraping, buccal swab, an esophageal tissue, a stomach tissue, an intestinal tissue (including the small intestines and/or the large intestines), a liver tissue, a gallbladder tissue, a pancreatic tissue, a colorectal tissue,

[0181] In some embodiments, the method prevents, treats, or reduces a gastrointestinal disease or disorder in the subject. In some embodiments, the gastrointestinal disease or disorder comprises heartburn, irritable bowel syndrome, lactose intolerance, gallstones, cholecystitis, cholangitis, anal fissure, hemorrhoids, proctitis, colon polyps, infective colitis, ulcerative colitis, ischemic colitis, Crohn's disease, radiation colitis, celiac disease, diarrhea (chronic or acute), constipation (chronic or acute), diverticulosis, diverticulitis, acid reflux (gastroesophageal reflux (GER) or gastroesophageal reflux disease (GERD)), Hirschsprung disease, abdominal adhesions, achalasia, acute hepatic porphyria (AHP), anal fistulas, bowel incontinence, centrally mediated abdominal pain syndrome (CAPS), clostridioides difficile infection, cyclic vomiting syndrome (CVS), dyspepsia, eosinophilic gastroenteritis, globus, inflammatory bowel disease, malabsorption, scleroderma, or volvulus.

Methods of Treating or Preventing Gastrointestinal Diseases or Disorders

[0182] In one aspect, disclosed herein is a method of treating or preventing a gastrointestinal disease or disorder in a subject in need thereof, the method comprising isolating and preserving a tissue sample from a subject, preparing and culturing any of the glycan-sensing systems disclosed herein in a microplate in an anaerobic environment, adding the tissue sample into the microplate, detecting and quantifying a light signal emitted from the system, and performing or administering a therapeutic procedure to the subject comprising pathological amounts of a glycan relative to a control tissue comprising normal amounts of the glycan.

[0183] In one aspect, disclosed herein is a method of treating or preventing a gastrointestinal disease or disorder in a subject in need thereof, the method comprising isolating and preserving a tissue sample from a subject, preparing and culturing any of the engineered bacteria disclosed herein in a microplate in an anaerobic environment, adding the tissue sample into the microplate, detecting and quantifying a light signal emitted from the engineered bacteria, and performing or administering a therapeutic procedure to the subject comprising pathological amounts of a glycan relative to a control tissue comprising normal amounts of the glycan.

[0184] In one aspect, disclosed herein is a method of treating or preventing a gastrointestinal disease or disorder in a subject in need thereof, the method comprising isolating and preserving a tissue sample from a subject, preparing any of the reporter plasmids disclosed herein in a microplate in an anaerobic environment, adding the tissue sample into the microplate, detecting and quantifying a light signal emitted from the reporter plasmid, and performing or administering a therapeutic procedure to the subject comprising pathological amounts of a glycan relative to a control tissue comprising normal amounts of the glycan.

[0185] In some embodiments, the tissue sample comprises at least one glycan. In some embodiments, the tissue sample comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48,

49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, or more glycans. In some embodiments, the tissue sample comprises N-linked glycans, O-linked glycans, or combinations thereof. In some embodiments, the tissue sample comprises branched glycans or linear glycans, or combinations thereof. In some embodiments, the tissue sample comprises one or any combination of glycans comprising chondroitin sulfate, arabinan, heparan sulfate, hyaluronan, fructan, levan, mannan, pectic galactan, starch, glucan, galactomannan, glucomannan, homogalacturonan, xyloglucan, dermatan, xylan, rhamnogalacturonan, or derivatives thereof.

[0186] In some embodiments, the light signal is detected and quantified using a microplate reader, a spectrophotometer, or an instrument capable of measuring the light signal. In some embodiments, the tissue sample comprises a tissue biopsy, a blood sample, or a saliva sample. In some embodiments, the tissue sample comprises a tissue biopsy, a blood sample, or a saliva sample. In some embodiments, the tissue sample comprises a tissue biopsy from the GI tract, including, but not limited to a tongue scraping, buccal swab, an esophageal tissue, a stomach tissue, an intestinal tissue (including the small intestines and/or the large intestines), a liver tissue, a gallbladder tissue, a pancreatic tissue, a colorectal tissue,

[0187] In some embodiments, the therapeutic procedure comprises a surgical procedure, a therapeutic agent, a lifestyle change, or a combination thereof.

[0188] In some embodiments, the surgical procedure comprises bariatric surgery, esophageal surgery, foregut surgery, hernia surgery, gastroesophageal reflux disease surgery, surgical nutrition, colorectal surgery, gallbladder surgery, liver surgery, bile duct surgery, pancreatic surgery, tumor excision, or combinations thereof. In some embodiments, the therapeutic agent comprises a laxative, an antacid, a proton pump inhibitor, a histamine blocker, an anti-inflammatory agent, a steroid, a vitamin, an intravenous fluid, an antibiotic, a probiotic, or combinations thereof. In some embodiments, the lifestyle change comprises a dietary alteration, an exercise program, a sedentary lifestyle, or combinations thereof.

[0189] In some embodiments, the gastrointestinal disease or disorder comprises heartburn, irritable bowel syndrome, lactose intolerance, gallstones, cholecystitis, cholangitis, anal fissure, hemorrhoids, proctitis, colon polyps, infective colitis, ulcerative colitis, ischemic colitis, Crohn's disease, radiation colitis, celiac disease, diarrhea (chronic or acute), constipation (chronic or acute), diverticulosis, diverticulitis, acid reflux (gastroesophageal reflux (GER) or gastroesophageal reflux disease (GERD)), Hirschsprung disease, abdominal adhesions, achalasia, acute hepatic porphyria (AHP),

anal fistulas, bowel incontinence, centrally mediated abdominal pain syndrome (CAPS), clostridioides difficile infection, cyclic vomiting syndrome (CVS), dyspepsia, eosinophilic gastroenteritis, globus, inflammatory bowel disease, malabsorption, scleroderma, or volvulus.

[0190] In some embodiments, the subject is a human.

Kits of Detecting a Glycan Molecule

[0191] In one aspect, disclosed herein is a kit for detecting or purifying a glycan molecule, the kit comprising an apparatus comprising a binding medium and a surface glycan binding protein (SGBP), wherein the binding medium comprises a matrix of biomolecules, the SGBP comprises a peptide label, and the SGBP is attached to the matrix; a container comprising an equilibration buffer, a container comprising a releasing buffer, and a container comprising a washing buffer.

[0192] In some embodiments, the glycan molecule comprises chondroitin sulfate, arabinan, heparan sulfate, hyaluronan, fructan, levan, mannan, or derivatives thereof.

[0193] In some embodiments, the SGBP comprises a chondroitin sulfate (CS)-specific SGBP, a levan-specific SGBP, an inulin-specific SGBP, an arabinogalactan-specific SGBP, a dextran-specific SGBP, a hyaluronan (HA)-specific SGBP, a heparan sulfate (HS)-specific SGBP, an O-glycan (OG)-specific SGBP, or variants thereof.

[0194] In some embodiments, the matrix comprises a nickel-conjugated agarose polymer. In some embodiments, the matrix comprises a stationary or porous composition of biomolecules, including, but not limited to a metal ion (including, but not limited to cobalt, nickel, and copper), an antibody, a protein, a nucleic acid, a hormone, and metabolite capable of reversibly binding a target composition, compound, or molecule.

[0195] In some embodiments, the SGBP is directly conjugated to a peptide label or the SGBP is conjugated to the peptide label by a linker. It is contemplated that the location and placement of the peptide label on the SGBP is not limited. In some embodiments, the peptide label comprises a hexa-histidine label. In some embodiments, the releasing buffer comprises a histidine solution. In some embodiments, the releasing buffer comprises a buffer with a high salt concentration. In some embodiments, the releasing buffer comprises a buffer with a low salt concentration. In some embodiments the releasing buffer comprises a buffer with a low pH. In some embodiments, the releasing buffer comprises a buffer with a high pH. In some embodiments, the releasing buffer is a buffer comprising an ionic charge. In some embodiments, the releasing buffer comprises a buffer with a neutral ionic charge. In some embodiments, the releasing buffer comprises a buffer with a neutral pH. In some embodiments, the washing buffer comprises a buffered solution comprising water, phosphate buffered saline solution, a tris-buffered saline solution, or variants thereof.

[0196] In some embodiments, the kit is combined with any of the glycan-sensing systems disclosed herein to detect the glycan molecule.

[0197] In some embodiments, the kit is combined with any of the engineered bacteria disclosed herein the glycan molecule.

[0198] In some embodiments, the kit is combined with any of the reporter plasmids disclosed herein to detect the glycan molecule.

EXAMPLES

[0199] The following examples are set forth below to illustrate the compositions, devices, methods, and results according to the disclosed subject matter. These examples are not intended to be inclusive of all aspects of the subject matter disclosed herein, but rather to illustrate representative methods and results. These examples are not intended to exclude equivalents and variations of the present invention which are apparent to one skilled in the art.

Example 1: Harnessing Gut Microbes for Glycan Detection and Quantification

[0200] The mammalian gut microbiota is a critical human health factor and a premier target for therapeutic modulation. The gut microbiota composition is influenced by the host diet, intestinal mucosa, and co-resident microbes, which all contribute to the availability of complex oligo- and poly-saccharides, collectively referred to herein as glycans. Glycans are highly abundant macromolecules found in every domain of life, mediate critical cellular processes, and exhibit extraordinary structural diversity conferred by unique non-linear arrangements, glycosidic linkages, and monosaccharide components. Altering glycan availability in the intestine modulates the gut microbiota by favoring the expansion of microbial populations that can consume individual glycan structures, which typically requires differentially available enzymatic activities. The mammalian intestine can exhibit disease-associated alterations in mucosal glycosylation influencing the abundance of gut microbial populations. Thus, evaluating glycans associated with intestinal diseases reveal disease biomarkers, therapeutic targets, or prebiotic compounds. However, unlike nucleic acids and proteins, glycan structural complexity limits high-throughput examinations of heterogenous glycan mixtures using individual methodologies frequently requiring parallel tandem approaches to comprehensively examine complex heterogenous glycan mixtures. Therefore, new tools and approaches are necessary to efficiently survey mixtures for unique glycan structures that could modulate microbial abundance and activity in the gut.

[0201] Microbes have evolved systems dedicated to glycan recognition and consumption from a myriad of biological sources. Members of the gut microbiota encode vast repertoires of glycan utilization machinery conferring unparalleled access to the diverse substrates present in the intestinal lumen and facilitate gut colonization. For example, a dominant and abundant bacterial group present in the mammalian gut, called the *Bacteroides*, encode discreet, tightly linked, coordinately regulated gene clusters called polysaccharide utilization loci (PULs) that mediate the consumption of structurally distinct glycans. Many *Bacteroides* species encode vast PUL libraries endowing these organisms with the ability to consume structurally diverse complex polysaccharides derived from the host diet, co-resident microbes, and the intestinal mucosa to successfully thrive in the mammalian gut. Most PULs are transcriptionally regulated such that individual genes are expressed at low constitutive levels until encountering their target glycans (FIG. **1**A), resulting in rapid and dramatic increases in corresponding PUL transcripts (FIG. **1**B). These responses are directed by sensor proteins that recognize mono-, di-, or oligo-saccharide signatures of their corresponding target glycan(s) and subsequently increase PUL transcript levels in a rapid and

dramatic fashion (FIGS. **1**A and **1**B). The ability of PUL sensors to direct PUL transcription changes in response to glycan availability demonstrates their use as biosensors to be employed to surveille heterogenous mixtures.

[0202] Additionally, PULs encode proteins possessing glycan binding, transport, and depolymerization activities that exhibit substrate specificity and confer species-specific access to discreet glycan subsets (FIG. **1**A). For example, *B. thetaiotaomicron* (Bt) and a closely related species, *B. ovatus* (Bo) both encode similar polyfructan-specific PULs that confer discreet target glycan specificities. The Bt fructan PUL facilitates the consumption of the β-2,6-linked polyfructan, levan, which is inaccessible to Bo, while the Bo fructan PUL facilitates utilization of the β-2,1-linked polyfructan, inulin, which is inaccessible to Bt. Species specific poly-fructan utilization is mediated independently of the fructan PUL-sensor, which activates PUL transcription in both Bt and Bo following detection of monomeric fructose. Thus, species-specific differences in target glycan utilization can rely on PUL-encoded factors that distinguish between compositionally similar yet structurally distinct glycans. Moreover, the specificity exhibited by SGBPs (FIG. **1**A) demonstrates their use as affinity purification reagents to isolate PUL-target glycans from complex heterogenous mixtures aiding in their structural characterization However, the paucity of specific, sensitive, and cost-effective glycan detection methods has hindered the development of such approaches.

[0203] *Bacteroides* PUL sensors are described to be harnessed as tools to detect their corresponding target glycans by examining changes in PUL transcription following the introduction of various biological samples. However, examining PUL transcription in response to glycan mixtures has relied on molecular approaches such a qPCR, microarrays, and RNAseq to detect transcriptional changes in *Bacteroides* species. Furthermore, the anaerobic growth requirements of *Bacteroides* species have previously limited the implementation of traditional transcriptional reporters such as GFP and luciferase to ex vivo measurements at discreet times. Herein, a *Bacteroides*-optimized luciferase reporter is generated to accurately reflect transcription during growth in anaerobic culture and is readily quantifiable. Reporter plasmids containing PUL promoters can sensitively and specifically indicate the presence of target glycans and these responses require PUL-encoded transport, degradation, and detection machinery in multiple *Bacteroides* species. Moreover, it was determined that target glycans elicit dose-dependent responses from their corresponding PUL reporters that can be used to quantify glycan abundance as accurately as commercially available kits. Finally, an affinity purification strategy was developed using PUL-encoded SGBPs to isolate individual target glycans from heterogenous mixtures by employing PUL-reporters as glycan detection and quantification tools. This microbial glycomics toolkit is readily scalable and will enable efficient characterization of unknown PUL ligands, identify previously concealed genetic determinants governing microbial glycan utilization, and ultimately reveal the glycomic interface between mammals and their gut microbiotas.

Results

[0204] *Bacteroides* PUL sensors promote dose-dependent transcriptional responses to target glycans. *Bacteroides* species frequently encode many PULs (Bt and Bo encode 88 and 112, respectively, each putatively dedicated to the utilization of distinct glycan substrates. PULs include a susCD-encoded complex necessary for the translocation of a target glycans across the outer membrane (FIG. **1**A) and the levels of susCD-containing transcripts increase rapidly and dramatically following exposure to their cognate target glycan (FIG. **1**B). For example, transcripts corresponding to the susC gene, BT3332, located within a Bt PUL required for chondroitin sulfate (CS) utilization (FIG. **1**C) increase 92-fold after 120 minutes following the addition of CS to the media (FIG. **1**D). Similarly, transcripts corresponding to another susC gene, BT1763, located within the Bt PUL necessary for levan utilization (FIG. **1**E), increase 530-fold following the addition of levan (FIG. **1**F). These increases in susC transcript levels require sensor proteins that often bind target glycan-derived ligands in the periplasm and subsequently direct transcriptional responses in the cytoplasm (FIG. **1**A). Accordingly, Bt mutants lacking either the CS or levan PUL sensors, are unable to grow on their corresponding target glycans as sole carbon sources (FIGS. **1**C and **1**E, respectively) or increase PUL transcription (FIGS. **1**D and **1**F, respectively), but exhibit no growth defects on galactose (FIGS. **8**A and **8**B, respectively).

[0205] Interestingly, BT1763 and BT3332 transcript levels exhibited corresponding decreases when Bt was supplied 10-fold dilutions of levan or CS (FIGS. **1**G and **8**C, respectively) indicating that *Bacteroides* PUL transcriptional responses are concentration-dependent. However, the relationship between susC-transcript and glycan concentrations detected at 120 minutes was not apparent after 60 minutes following glycan addition (FIGS. **8**D and **8**E), demonstrating the dynamic nature of PUL transcription. These results show that PUL sensors promote dose-dependent transcriptional responses over time, which are harnessed to report unknown target glycan abundances by measuring changes in corresponding susC-transcript levels.

[0206] Construction of a *Bacteroides*-optimized bioluminescent transcriptional reporter. Quantifying susC transcription by qPCR or transcriptomics is expensive and inefficient, requiring kinetic sampling to accommodate variations in PUL transcriptional responses. Therefore, a transcriptional reporter was engineered that accurately reflects transcript levels in *Bacteroides* species over time during anaerobic growth without additional oxygenation. Previously constructed transcriptional reporters in Bt require terminal measurements following cell lysis limiting their applications for kinetic measurements and fluorophores such as GFP require exposure to oxygen for proper maturation or exhibit high background fluorescence. In contrast, the production of bacterial LuxCDABE proteins and biosynthesis of the luciferase long-chain aldehyde substrate can be achieved anaerobically although luciferase activity is oxygen dependent. It was contemplated that lux-mediated bioluminescence could function in *Bacteroides* species during growth under anaerobic conditions when expressed from *Bacteroides* promoters and ribosomal binding sites, which differ from those typically found in Firmicutes and Proteobacteria. Therefore, the *Photorhabdus luminescens* (Pl) luxCDABE cassette was engineered in the multi-copy plasmid, pLYL01, preceded by the Bt rpoD promoter (BT1311) and an optimized *Bacteroides* ribosome binding site, rpiL*, that facilitates high levels of gene expression (FIG. **2**A). A wild-type Bt strain harboring the Pl lux cassette exhibited detectable luminescence during anaerobic growth in minimal media

containing galactose (FIG. **2**B) or glucose (FIG. **9**A) and grew similarly to a strain harboring the empty vector under identical conditions (FIGS. **2**B and **9**A, respectively).

[0207] To further optimize luciferase activity, the lux operon was re-organized to luxCDEAB and exchanged the Pl intergenic regions for the Bt intergenic regions from BT1160-1155 (FIG. **2**A), which increased luminescence output approximately 10-fold over the Pl cassette without altering growth kinetics (FIGS. **2**B and **9**A). A Bt strain harboring the *Bacteroides*-optimized lux cassette exhibited consistently higher relative luminescence than a strain expressing the Pl cassette during logarithmic growth (FIGS. **2**B and **9**A) and remained readily detectable even in late stationary phase over 48 hours (FIG. **2**B). A plasmid containing tandem BamHI and SpeI restriction sites upstream of rpiL*-luxCDEAB (pBolux, FIG. **2**A) were constructed for efficient cloning of promoters. A Bt strain harboring pBolux exhibited similar sustained luminescence over 18 hours in galactose (FIG. **2**C), glucose, fructose, arabinose, or xylose as sole carbon sources (FIG. **9**B). Introduction of the Bt rpoD promoter into the BamHI and SpeI sites increased activity 10-fold independently of carbon source (FIGS. **2**C and **9**B). Introduction of pBolux into Bo produced similar results across all conditions and a plasmid preceded by the region upstream of the Bo rpoD gene (BACOVA_00615) increased luminescence approximately 10-fold (FIGS. **9**C and **9**D). These data indicate that pBolux can reflect promoter-dependent transcription in multiple *Bacteroides* species during anaerobic culture with minimal cost to bacterial growth.

[0208] Engineering a glycan responsive PUL reporter. To determine if pBolux can accurately indicate changes in PUL transcription in response to target glycans, the 300 bp region was introduced immediately upstream of the susC gene from the CS PUL (P-BT3332). Luminescence (FIG. **3**A) and growth (FIG. **3**B) was measured in a wild-type Bt strain harboring P-BT3332 or promoter-less pBolux for 18 hours following the introduction of CS or galactose as the sole carbon source. After only 2 hours, the relative luminescence from a strain harboring P-BT3332 was 46-fold greater and reached a peak activity of 65-fold by 7 hours following the introduction of CS compared to cultures supplied galactose alone (FIGS. **3**A and **3**C). Conversely, a strain harboring pBolux exhibited identical luminescence in CS relative to galactose until 6 hours where it increased 7-fold over 18 hours (FIG. **3**C). P-BT3332-driven reporter increases imposed no detectable growth alterations indicating that increased luminescence carries minimal fitness cost (FIG. **3**B).

[0209] To examine whether genes encoded within the CS PUL (BT3328-BT3334 & BT4410-BT4411) are required for the observed P-BT3332-specific luminescence increases in CS, reporter activity in mutant Bt strains deficient for CS transport, depolymerization, and detection activities necessary for growth on CS (FIG. **1**C) were compared following the introduction of a mixture of 0.2% CS and 0.2% galactose (FIG. **10**A) (galactose was added as a supplemental carbon source to support growth and luciferase activity) or galactose alone (FIG. **10**B). A mutant lacking the CS-sensor, BT3334, exhibited no increased luminescence over 18 hours following the introduction of CS (FIG. **3**D). The reduced bioluminescence exhibited by this strain was not the consequence of disabling growth on CS because a mutant lacking a glucuronyl hydrolase, BT3348 (gh), is unable to utilize CS (FIG. **1**C), but exhibits sensor-dependent PUL transcription and increased reporter activity similar to wild-type Bt (FIG. **3**D). These data show that disabling genes necessary to generate the PUL-sensor ligand, the 6- or un-sulfated CS-derived disaccharide (di0S), in the periplasm prevent sensor-dependent reporter activity increases. Consistent with this notion, a mutant lacking the CS PUL-encoded susC transporter, BT3332, exhibited a dramatic reduction in reporter activity with a peak activity of 3.1-fold increase at 10 hours putatively by reducing CS importation from the extracellular environment (FIG. **3**D). Furthermore, disabling 3 CS-specific polysaccharide lyases necessary for the conversion of CS-polymers into di0S (BT3324, BT3350, and BT4410) also dramatically reduced reporter activity in response to CS relative to wild-type Bt, peaking at 3.3-fold after 1 hour following the introduction of CS (FIG. **3**D). However, supplying di0S increased luminescence 39.6-fold by 16 hours in the lyase-deficient but not the sensor-deficient mutant (FIG. **3**E). Collectively, these data indicate that a strain harboring P-BT3332 can indicate the presence of CS in a manner dependent on PUL-encoded glycan importation, depolymerization, and detection activities.

[0210] To determine whether increased activity from a strain containing P-BT3332 were limited to CS-PUL substrates, luminescence was examined following the addition of a structurally similar but compositionally distinct glycosaminoglycan, heparin sulfate (HS, FIG. **10**C), which is consumed by Bt independently of the CS-PUL (FIG. **10**D). A strain harboring the CS-reporter exhibited a dramatically lower activity following the addition of HS compared to the addition of CS (FIG. **3**F), peaking at 2.6-fold after an hour. Conversely, the addition of hyaluronic acid (HA), which also activates sensor-dependent CS-PUL gene expression required for HA utilization (FIG. **10**E), increased reporter activity similarly to CS in wild-type Bt but not the sensor-deficient mutant (FIGS. **3**F and **10**F). Thus, the *Bacteroides*-optimized lux reporter can specifically indicate the presence of target glycans by reflecting PUL sensor-dependent responses to glycan-derived ligands.

[0211] A fructan-responsive reporter reveals new insights into Bt levan utilization. Bt consumption of the polyfructan, levan, requires a distinct PUL encoded by BT1754-BT1765 and includes an unlinked but co-regulated exo-levanase, BT3082. A Bt strain harboring pBolux containing the region preceding the corresponding susC gene (P-BT1763) exhibits 35-fold increased activity 5.5 hours after the introduction of levan compared to galactose (FIGS. **4**A and **11**A). Levan-dependent reporter activity requires the BT1763 promoter region because a strain harboring the promoter-less control plasmid, pBolux, exhibits no change after 18 hours following the introduction of levan (FIGS. **4**A and **11**A). Differences in reporter-activity cannot be attributed to plasmid-dependent growth effects because both strains exhibit identical growth kinetics in either galactose (FIG. **11**B) or levan (FIG. **11**C). Reporter activation requires levan-derived fructose detection by the PUL sensor protein, BT1754, because a mutant lacking BT1754 displays only 1.4- or 1.7-fold increased reporter activity following the introduction of either levan (FIG. **4**B) or fructose (FIG. **4**C), respectively. Moreover, a strain lacking the corresponding susC gene exhibited a 3-hour delay before reporter activity increased following the addition of levan (FIG. **4**B) and 60-hour lag before detectable growth on levan as the sole carbon source (FIG. **1**E). Conversely, identical strains

exhibit reporter activity (FIG. **3**C) and growth kinetics (FIG. **3**D) resembling wild-type Bt when supplied fructose, confirming that the fructan-specific SusC is dispensable for transport of monomeric fructose and internalizes levan-derived fructo-oligosaccharides. Consistent with this notion, it was determined that inactivation of 4 levanases (BT1760, BT1759, BT1765 and BT3083) reduced levan-dependent reporter activity to levels similar to the BT1754-deificient strain (FIG. **4**B) and abolished utilization of levan as the sole carbon source (FIG. **1**E). Strains harboring only a single levanase, generated by disabling various combinations of all other 3 levanases, exhibited reporter activity increases in levan after a 4-hour delay (FIG. **4**E) and grow on levan as the sole carbon source (FIG. **4**F) albeit at dramatically reduced rates and maximum cell densities compared to wild-type Bt. Unexpectedly, all strains lacking the exo-levanase, BT1765, exhibited reduced maximum cell densities during growth in fructose as the sole carbon source (FIGS. **11**D and **11**E), and this was specific because BT1765-deficient strains grew similarly to wild-type Bt in galactose (FIGS. **11**F and **11**G). Finally, reduced levan-dependent reporter activity in any mutant is not due to diminished growth because a mutant deficient for the inner membrane fructose importer, BT1758, cannot grow on levan (FIG. **1**E) or fructose (FIG. **4**D) as sole carbon sources but exhibit reporter activity resembling wild-type Bt in response to either carbohydrate (FIGS. **4**B and **4**C, respectively). Collectively, these data demonstrate that P-BT1763 containing strains indicate the presence of levan-derived fructose in a manner requiring PUL-encoded transport, depolymerization and detection proteins independently of its utilization.

[0212] These results reveal that Bt employs multiple levanases to consume levan and demonstrate that three distinct exo-levanases can function independently of the endo-levanase, BT1760, contrasting previous conflicting reports asserting this gene was either essential or dispensable for growth on levan. To examine the role of BT1760 in levan utilization, a BT1760-deficient strain was constructed, which exhibited reduced growth on levan as the sole carbon source (FIG. **4**G) and delayed reporter activation in response to levan compared to wild-type Bt (FIG. **4**H). This mutant exhibited growth and reporter activity resembling wild-type Bt when complemented in trans (FIG. **11**H) indicating that this BT1760 mutation did not disrupt expression of downstream genes required for levan utilization (FIG. **1**E). Furthermore, a mutant encoding only BT1760 and lacking all known exo-levanases (ΔBT1759, ΔBT3082 ΩBT1765), exhibited the greatest delay in reporter activity increases (FIG. **4**E) and achieved the lowest maximum growth on levan as the sole carbon source (FIG. **4**F) compared to any other combination of levanase mutations. Collectively, these data demonstrate that exo-levanases function independently of BT1760 to liberate fructose from levan highlighting that Bt levan utilization is not completely understood. Finally, these results illustrate how the pBolux reporter plasmid can be implemented to genetically dissect the contributions of individual PUL-encoded activities to target glycan consumption.

[0213] Species-specific reporter responses distinguish between compositionally identical glycans. *Bacteroides* species can differentially consume structurally distinct glycans comprised of identical monosaccharide components. This is exemplified by the fructan PUL, which is conserved across several species and confers Bt the ability to consume the β (2,6)-linked polyfructan, levan (FIG. **1**E), but not the β (2,1)-linked polyfructan, inulin (FIG. **5**A). Conversely, a similar PUL in Bo (BACOVA_04496-BACOVA_04507) confers inulin (FIG. **5**A) but not levan utilization (FIG. **12**A). Bo inulin utilization requires the PUL-sensor protein, BACOVA_04496, because a mutant lacking the corresponding gene is unable to grow on inulin as a sole carbon source (FIG. **5**A) and exhibits reduced growth rates on fructose (FIG. **12**B) but not galactose (FIG. **12**C), showing that the Bo fructan PUL sensor detects monomeric fructose similarly to the Bt fructan PUL sensor. To examine how similar PULs encoded by closely related species can confer access to compositionally identical yet structurally distinct glycans, a Bo strain was generated harboring a reporter plasmid containing the region upstream of the corresponding susC gene (P-BACOVA_04505). This strain exhibits dramatically increased activity following the addition of inulin compared to galactose, in contrast to a promoter-less control plasmid (FIGS. **5**B and **12**D). Inulin-dependent reporter activity increases in Bo requiring the fructan PUL sensor because no change in reporter activity was observed when the sensor mutant was supplied inulin (FIG. **5**C) or fructose (FIG. **5**D). Collectively, these results indicate that the Bo fructan PUL sensor responds to monomeric fructose in a manner similar to the Bt sensor although each PUL confers access to structurally distinct glycans. Thus, identical PUL sensor specificities are employed to mediate utilization of distinct fructans showing that other PUL-encoded products facilitate species-specific growth on inulin and levan.

[0214] Interestingly, the addition of levan elicits detectable reporter activity increases in wild-type Bo harboring P-BACOVA_04505 compared to a strain lacking the corresponding PUL-sensor (FIG. **5**E) although Bo is unable to grow on levan as a sole carbon source (FIG. **12**A). Similarly, wild-type Bt harboring P-BT1763 exhibited detectable reporter activity increases when supplied inulin compared to a sensor-deficient strain (FIG. **5**F), showing that Bo and Bt can derive fructose from levan and inulin, respectively, in quantities insufficient to support growth. It is contemplated that these responses reflect slow, non-specific, and extracellular liberation of fructose from non-target fructans because a Bt strain lacking the fructan-PUL encoded susC gene, BT1763, exhibits identical reporter activity relative to the wild-type strain following the addition of fructose (FIG. **4**C) or inulin (FIG. **5**F). Although inulin-dependent reporter activity was substantially reduced in a strain lacking 4 levanases, luminescence levels were greater than a sensor-deficient mutant suggesting Bt possesses unknown inulin-degrading activities that can likely liberate fructose monomers slowly and non-specifically compared to Bo (FIG. **5**F). Collectively, these results demonstrate how PUL reporters exhibit highly sensitive responses in distinct gut *Bacteroides* species and can detect the presence of compositionally identical but structurally distinct glycans independently of their utilization.

[0215] PUL reporters exhibit linear dose-dependent responses. To determine if dose-dependent PUL transcriptional responses elicited by target glycans (FIGS. **1**G and **8**C) are reflected by the corresponding PUL-reporter activity, 2-fold serial dilutions of either CS or levan were supplied to Bt strains harboring either the CS- or fructan-responsive reporter plasmids described above. A wild-type Bt strain containing P-BT3332 exhibited increased reporter activity when supplied between 0.0001% (1 μg/mL) and

0.4% (4 mg/mL) CS relative to identical cultures supplied only galactose (FIG. **6**A). Similarly, a wild-type Bt strain containing P-BT1763 displayed concentration-dependent reporter activity increases when supplied between 0.0016% (16 μg/mL) and 0.4% levan (FIG. **13**A). Quantifying the area under each curve (AUC) revealed that the CS- and levan-reporter responses increase linearly within these ranges (FIGS. **6**B and **6**C) and the logarithm of corresponding AUC values follows a linear regression model with an R2 of 0.95 and 0.97, respectively, when supplied their target ligands (FIGS. **13**B and **13**C). Reporter strains respond specifically to their corresponding target glycan because neither the CS- or levan-responsive strains exhibited significantly increased luminescence when supplied with any concentration of levan or CS, respectively (FIG. **6**D). These data show that the linear, concentration-dependent reporter activity increases exhibited by engineered Bt strains in response to their target glycans could be used to estimate target glycan abundance in an unknown sample concentration. However, bacterial species including Bt exhibit hierarchical glycan utilization, facilitating the prioritized expression of genes necessary for the consumption of more-over less-preferred substrates, hindering target-glycan detection in PUL-reporter strains. However, the CS-reporter strain produced similar dose-dependent responses in the presence of levan (FIG. **13**D) and exhibited an identical linear range of detection relative to those collected in the absence of levan (FIG. **13**E). Interestingly, the levan-responsive strain exhibited greater reporter activity responses to levan in the presence of 0.2% CS (FIG. **13**D) expanding the lower range of responsiveness down to 0.0004% (4 μg/mL) levan and suggesting that the presence of CS may enhance luciferase activity. Consistent with this notion, the addition of 0.2% CS significantly increased the levan-responsive reporter activity when supplied with 0.2% levan (FIGS. **6**E and **13**D) but did not significantly change fructan-reporter activity in the absence of levan (FIG. **6**D). Taken together, these data show that PUL reporters can indicate the presence of target substrates in glycan mixtures.

[0216] Sensor-dependent PUL transcription by target glycans is typically resolved by negative feedback mechanisms whereby PUL-encoded activities remove the glycan-derived, PUL-sensor ligand from the periplasm, thereby reducing PUL sensor activation (FIG. **1**A). For example, the CS-responsive PUL relies on a glucuronyl hydrolase (gh) to hydrolyze di0S into its monosaccharide components N-acetyl galactosamine and 5-keto 4-deoxyuronate, thereby removing the sensor ligand and reducing transcription activation. Therefore, a mutant lacking BT3348 exhibits increased PUL-transcription relative to wild-type Bt as the CS-sensor is deactivated by this activity. Accordingly, a gh-deficient strain harboring P-BT3332 exhibits detectable responses between 0.000006% (6 ng/ml) and 0.4% CS (FIG. **6**F) but the linearity of these responses reached a maximum at 0.0125% (125 μg/mL) (FIGS. **6**B and **13**B). Similarly, a strain lacking the inner-membrane fructose importer, BT1758, harboring P-BT1763 exhibited increased luminescence at levan concentrations as low as 0.0004% and this response achieved its maximum at 0.2% levan (FIG. **6**C) limiting the upper range of its linear responsiveness (FIG. **13**C). Thus, PUL-reporter activity can be genetically tuned to extend target glycan sensitivity by preventing PUL-sensor deactivation, which horizontally shifts the linear ranges of glycan detection. Collectively, this data show PUL-reporters offer new specific and highly sensitive glycan detection reagents that estimate glycan abundances across wide linear ranges spanning more than 3 orders of magnitude.

[0217] PUL-reporters facilitate target glycan isolation using SGBPs. PULs often encode SGBPs that facilitate glycan sequestration along the outer membrane (FIG. **1**A). SGBPs specifically bind their cognate glycan ligands and can discriminate between compositionally similar, structurally distinct glycans. For example, BT1761, an SGBP encoded in the Bt levan utilization PUL, binds to levan but not inulin and BT3330, an SGBP encoded in the Bt CS utilization PUL differentially binds CS polymers greater than 20 disaccharide units in size. Consistent with these findings, recombinant BT3330 protein exhibited a reduced migration following affinity-PAGE in the presence of CS (FIG. **7**A) but not in its absence (FIG. **7**B). Conversely, BT1761 protein exhibited a decreased relative migration following affinity-PAGE in the presence of levan (FIG. **7**C) but not in its absence (FIG. **7**B). Furthermore, the altered migration of both proteins was specific to the presence of target glycans because BT3330 migration was similar in the presence of levan (FIG. **7**C) relative to gels lacking glycan (FIG. **7**B) and BT1761 migration in CS-containing gels (FIG. **7**A) was similar in the absence of glycan (FIG. **7**B). These results indicate that each PUL-encoded SGBP can distinguish between target and non-target glycans in vitro and putatively facilitate target glycan isolation from a heterogenous mixture. PUL-reporter strains were thought to exhibit sensitive (FIGS. **6**B and **6**C) and specific (FIG. **6**D) detection of target glycans even in the presence of non-target molecules (FIGS. **13**D and **13**E), they could serve as glycan detection reagents to identify fractions enriched for glycans of interest using immobilized, recombinant SGBPs. Thus, cell lysates were combined and prepared from *E. coli* strains engineered to over-express either N-terminally his-tagged BT1761 or BT3330 with an equal mixture of levan and CS. After incubation, SGBPs were captured using Ni-agarose, washed extensively, and subsequently eluted with free histidine so that each fraction could be supplied directly to Bt cultures harboring either P-BT3332 or P-BT1763. Elutions 2 through 8 from columns containing BT3330 elicited significantly increased CS-responsive reporter activity compared to control reactions incubated with lysates prepared from *E. coli* strains harboring an empty vector (FIGS. **7**D and **14**A). Conversely, identical fractions supplied to the fructan-responsive reporter strain resulted in activity that was indistinguishable from those eluted from vector control containing lysates (FIGS. **7**D and **14**B) indicating that BT3330-containing fractions (FIG. **14**C) were enriched for CS over levan. Conversely, fractions co-eluting with BT1761 (FIG. **14**C) elicited increased activity from the levan-(FIGS. **7**E and **14**B) but not the CS-responsive reporter strain relative to elutions from a vector control (FIGS. **7**E and **14**A), indicating BT1761 enriched levan over CS.

[0218] To measure SGBP-mediated target glycan enrichment, pooled fractions co-eluting with either BT3330 or BT1761 that elicited significantly increased reporter activity compared to control fractions were concentrated (FIGS. **7**D and **7**E). The concentrated material was supplied to Bt strains harboring CS- or levan-reporter plasmids and compared to a standard curve of 2-fold dilutions of either CS- or levan (FIGS. **7**F and **7**G, respectively). Glycans co-eluting with BT3330 elicited increased activity from a wild-type Bt

strain harboring P-BT3332 (FIGS. **7**F and **14**D) but not P-BT1763 (FIG. **14**E). Conversely, glycans co-eluting with BT1761 stimulated levan-(FIGS. **7**G and **14**E) but not CS-responsive reporter activity (FIG. **14**D). The BT3330 eluate contained 205.6 μg/mL CS and the BT1761 eluate contained 244.4 μg/mL levan using a simple linear regression of log 10 reduced AUC values from corresponding standard curves (FIGS. **7**F and **7**G, respectively). To verify these results with reporter-independent methods, total fructan or glycosaminoglycan content was measured from identical samples using colorimetric assays (Biovision and Megazyme, respectively), which indicated that concentrated eluates co-purifying with BT3330 containing 168.2 μg/mL CS (FIG. **7**H) but no detectable levan and material co-purifying with BT1761 contained 229.7 μg/mL levan (FIG. **7**I) but no detectable CS. To estimate the concentration of non-target glycans co-purifying with each SGBP, the concentrated eluate was supplied to hyper-sensitive strains defective for sensor deactivation, which exhibit extended target glycan detection ranges (FIGS. **13**B and **13**C). The concentrated eluates from BT1761 increased CS-responsive reporter activity in the gh-deficient strain harboring P-BT3332 (FIG. **14**F) within the linear range of detection (FIG. **14**G) indicating that 0.0000086% (86.7 ng/ml) CS co-purified with BT1761, representing a 939.7-fold enrichment for levan over CS. However, an estimate of the SGBP-mediated enrichment of CS over levan was not obtained because the concentrated BT3330 eluate stimulated 1.2-fold increased levan-responsive reporter activity in the fructose importer-deficient strain harboring P-BT1763 (FIG. **14**H) but this was outside of the linear range of quantification (FIG. **14**I). Collectively, these data demonstrate that PUL reporters are powerful detection tools that can facilitate target glycan isolation from heterogenous mixtures and measurement beyond the limits of commercially available solutions.

Discussion

[0219] This disclosure provides a new reporter system that kinetically monitors transcription during anaerobic growth in prominent human gut commensal bacteria. Here, introduction of pBolux plasmids containing PUL promoters generates glycan-sensitive bacterial strains that require PUL-encoded transport, depolymerization, and detection activities (FIGS. **3**-**5**). It is demonstrated that *Bacteroides* PUL sensors elicit concentration-dependent transcriptional responses (FIGS. **1**G and **8**C) that are recapitulated by corresponding reporter strains (FIGS. **6** and **13**) and can indicate the presence of corresponding target molecules at concentrations below the limits of detection of commercially available kits (FIGS. **7**F-**7**I). Moreover, it is demonstrated that reporter sensitivity can be genetically tuned to respond by glycan degree of polymerization by disabling glycan depolymerization machinery (FIGS. **3**-**4**) or achieve lower limits of detection disabling PUL-encoded genes necessary for PUL deactivation (FIGS. **6**F, **13**B, and **13**C-**13**F). It is also demonstrated that reporter responses are readily quantifiable and can estimate unknown target glycan concentrations (FIGS. **7**F and **7**G) similar to reporter-independent methods (FIGS. **7**H and **7**I). Thus, this example establishes a new glycomics toolset that employs *Bacteroides* PULs to facilitate simple, rapid, and high-throughput detection and quantification of gut microbial substrates in heterogeneous mixtures.

[0220] Examining bacterial glycan utilization has previously relied on detectable growth on commercially purified glycans or steady-state transcriptional changes following introduction of undefined glycan mixtures. It is demonstrated that PUL reporters can indicate bacterial transcriptional responses to target glycans in dramatically smaller volumes (as low as 30 μL) (FIGS. **6** and **7**) and require substantially less material than similar measurements using ex vivo approaches such as qPCR, transcriptomics, or NanoLuc. Furthermore, pBolux-derived reporter strains overcome the need for kinetic sampling of bacterial cultures because changes in gene expression can be measured over time into late stationary phase (FIGS. **1**I-**1**J) and can indicate target glycans independently of their utilization (FIGS. **1**C, **1**E, **3**D, and **4**B). Finally, because these strains can be cultured ad infinitum and do not require harvesting mRNA or cDNA synthesis, they offer a high-throughput, cost-effective tool to measure changes in gene transcription during growth. These advantages render pBolux a powerful, efficient, and relatively inexpensive tool to examine *Bacteroides* gene transcription in various conditions including in response to glycans.

[0221] To demonstrate the advantages of pBolux-derived plasmids, two PUL-reporters were leveraged to devise an affinity isolation approach whereby recombinant PUL-encoded SGBPs isolate target glycans from a mixture (FIG. **7**). Because the corresponding reporter strains can specifically and sensitively detect target glycans even in the presence of non-targets (FIGS. **6**D, **6**E, **13**D, and **13**E), fractions containing two distinct SGBPs copurifying with miniscule amounts of their corresponding glycan ligands were identified (FIGS. **7**A and **7**B). Furthermore, using a strain with extended limits of target glycan detection, contaminating non-target glycan abundance demonstrated that this approach achieved 940-fold enrichment of target from non-target molecules (FIGS. **14**F and **14**G). It is contemplated that similar approaches could be implemented to isolate and characterize unknown PUL-targets such as those derived from the mammalian mucosa, which can exert prebiotic effects when administered in aggregate, for downstream structural characterization. In total, the dedicated glycan utilization machinery possessed by gut microbes has been harnessed to develop tools that enable simple, efficient, and inexpensive glycan detection, isolation and quantification tools that are readily scalable and distributable.

[0222] It is demonstrated how glycan-responsive reporters can harness species-specific glycan preferences to detect structurally distinct yet compositionally identical glycans (FIG. **4**-**5**). With some *Bacteroides* species encoding over one hundred different PULs, many with unknown glycan targets, the accessible glycome of intestinal microbes is vast and largely uncharacterized. Moreover, some annotated PULs putatively facilitate utilization of unknown glycan substrates that confer species-specific gut colonization advantages, which represent attractive therapeutic targets and be identified by implementing analogous approaches to those described here. Because PUL reporters can indicate the presence of target glycans at extremely low abundances (FIGS. **6**B&C,S**6**B&C FIGS. **6**B, **6**C, **13**B, and **13**C), without serving as growth substrates (FIGS. **3**D,**4**B&C,**5**E&F FIGS. **3**D, **4**B, **4**C, **5**E, and **5**F), and even in the presence of other glycans (FIGS. **6**D&E,S**6**D&E FIGS. **6**D, **6**E, **13**D, and **13**E), PUL reporters used to efficiently screen various mixtures for the presence of target glycans. Thus, construct-

ing pBolux plasmids containing promoters from PULs with unknown targets could be used to examine differential glycan abundances across low-yield biological samples in high-throughput applications enabling new glycan surveillance approaches.

Methods

[0223] Bacterial culture. All *E. coli* strains were cultured on LB agar (BD) aerobically at 37° C. and inoculated from single colonies into LB media (BD) with agitation at 275 rpm. All *Bacteroides* strains were cultured on brain-heart infusion agar (BHI, Sigma) containing 5% horse blood (Hardy) anaerobically and inoculated from single colonies into TYG incubated under identical conditions. *Bacteroides* strains were sub-cultured at the indicated dilutions from stationary phase growth in TYG into minimal media containing the indicated carbon sources described in the corresponding figure legends. All strains were cultured in the presence of antibiotic selection where appropriate at the following concentrations: 100 μg/mL ampicillin, 2 μg/mL tetracycline, 25 μg/mL erythromycin.

[0224] Growth Measurements. *Bacteroides* strains were cultured anaerobically to stationary phase in TYG and diluted 1:200 into pre-reduced minimal media containing the indicated carbon sources [glucose, galactose, fructose arabinose, xylose, and chondroitin sulfate (Sigma); levan and inulin (Megazyme)] in pre-reduced 96-well or 384-well clear microplates (Corning). To remove free fructose from inulin, a 1% inulin solution was passed over a ZebaSpin de-salting column (ThermoFisher) prior to the addition of cultures. Kinetic absorbance measurements were taken at 600 nm every 15 minutes for 96 hours using a Tecan Infinite M-plex maintained at 37° C. in a Coy anaerobic chamber with a 2.5% hydrogen atmosphere.

[0225] Strain construction. A plasmid encoding the *Psuedorhabdus luminescens* lux cassette under control of the *B. thetaiotaomicon* rpoD promoter (BT1311) was generated by amplifying products from pmini-Tn5 luxCDABE Tc using primers W3115 and W3124 and PBT1311-rpiL* from strain NS340 with primers W2952 and W2905. The resulting amplicons were assembled with pNBU2-tetQ digested with BamHI-HF and SalI-HF (NEB) using the NEBuilder Assembly Master Mix (NEB). The resulting plasmid (pNBU2-lux-Pl) was verified by Sanger sequencing before its introduction into *B. thetaiotaomicron* by di-parental mating to generate strain GT962, and the insert was sub-cloned into pLYL01 using BamHI-HF and SalI-HF to generate plux-Pl.

[0226] To generate a *B. thetaiotaomicron* optimized lux cassette, luxC (primers W2952 and W3265), luxD (primers W3266 and W3267), luxE (primers W3268 and W3269), luxA (primers W3270 and W3271) and luxB (primers W3272 and W3273) were amplified from GT962 genomic DNA and assembled with pNBU2-tetQb digested with BamHI-HF and SalI-HF (NEB) using the NEBuilder Assembly Master Mix (NEB). The resulting plasmid (pNBU2-lux-Bt) was verified by Sanger sequencing before being sub-cloned into pLYL01 using BamHI-HF and SalI-HF to generate plux-Bt. A promoter-less *Bacteroides* optimized lux cassette was generated by assembling the lux cassette from plux-Bt, amplified with primers 1080 and 1011, with pLYL01 digested with BamHI (NEB) and SalI-HF (NEB) using the NEBuilder Assembly Master Mix (NEB). The resulting plasmid, pBolux, contains tandem BamHI and SpeI restriction sites for cloning and was used for all experiments as a negative control. To construct chondroitin sulfate, levan, and inulin-responsive reporters, the 300 bp region upstream of BT3332 (primers 1232 and 1373), BT1763 (primers 1150 and 1304), or (primers 1943 and 1944) were amplified and combined with pBolux digested with BamHI-HF and SpeI-HF (NEB) using the NEBuilder Assembly Master Mix (NEB).

[0227] Generating loss-of-function mutations in Bt were performed using pEXCHANGE-tdk or pKNOCK-ermGb. A Bo strain lacking BACOVA_04496 was constructed using a similar allelic exchange method with pSIE1. All mutations were verified by Sanger sequencing across the chromosomal region of interest. All strains, plasmids and primers are listed in Tables 1-4, 5a, and 5b, respectively.

TABLE 1

Strains used.

Name	Genotype	Plasmid
	E. coli	
S17-1	λpir	—
BL21 (DE3)	*E. coli* B dcm ompT hsdS(rB-mB-) gal λDE3	—
	B. thetaiotaomicron	
GT23	Δtdk	—
VR69	Δtdk ΔBT3348	—
GT150	Δtdk ΔBT3334	—
GT165	Δtdk ΔBT1754	—
GT962	Δtdk	pNBU2-lux-Pl
GT1059	Δtdk	pNBU2-lux-Bt
GT3137	Δtdk	p-lux-Pl
GT1541	Δtdk	p-lux-Bo
GT1866	Δtdk	pLYL01
GT1867	Δtdk	pBolux
GT1893	Δtdk	P-BT1763
GT1934	Δtdk	P-BT3332
GT2111	Δtdk att-1:pNBU2-ermR	—
GT2618	Δtdk ΔBT3334	P-BT3332
GT2620	Δtdk ΔBT1754	P-BT1763
GT2926	Δtdk ΔBT3332	—
GT2939	Δtdk ΔBT3332	P-BT3332

TABLE 1-continued

Strains used.		
Name	Genotype	Plasmid
GT3086	Δtdk ΔBT3324 ΔBT3350 BT4410::pKNOCK-ermGb	—
GT3102	Δtdk ΔBT3348	P-BT3332
GT3117	Δtdk ΔBT3324 ΔBT3350 BT4410::pKNOCK-ermGb	P-BT3332
GT3181	Δtdk ΔBT1760	—
GT3192	Δtdk ΔBT1760	P-BT1763
GT3196	Δtdk ΔBT1763	—
GT3199	Δtdk ΔBT1763	P-BT1763
GT3215	Δtdk ΔBT1760 att-1::pNBU2-ermGb	—
GT3216	Δtdk ΔBT1760 att-1::pNBU2-ermGb::P_{BT1763}-BT1760	—
GT3226	Δtdk ΔBT1759	—
GT3246	Δtdk ΔBT1759	P-BT1763
GT3282	Δtdk BT1765::pKNOCK-ermGb	—
GT3299	Δtdk BT1765::pKNOCK-ermGb	P-BT1763
GT3303	Δtdk ΔBT3082	—
GT3308	Δtdk ΔBT1760-59 ΔBT3082	—
GT3346	Δtdk ΔBT1760 ΔBT3082 BT1765::pKNOCK-ermGb	—
GT3347	Δtdk ΔBT1759 ΔBT3082 BT1765::pKNOCK-ermGb	—
GT3348	Δtdk ΔBT1760-59 ΔBT3082 BT1765::pKNOCK-ermG	—
GT3358	Δtdk ΔBT1759 ΔBT3082 BT1765::pKNOCK-ermGb	P-BT1763
GT3356	Δtdk ΔBT1760 ΔBT3082 BT1765::pKNOCK-ermGb	P-BT1763
GT3360	Δtdk ΔBT1760-59 ΔBT3082 BT1765::pKNOCK-ermG	P-BT1763
GT3379	Δtdk BT1758:pKNOCK-ermGb	—
GT3393	Δtdk BT1758:pKNOCK-ermGb	P-BT1763
GT3534	Δtdk ΔBT3082	P-BT1763
	Bacteroides ovatus (ATCC 8483)	
ATCC 8483	—	—
GT3173	—	P-BACOVA 04505
GT3179	BACOVA_04495::pSIE1::ΔBACOVA_04496	—
GT3180	—	pBolux
GT3183	ΔBACOVA_04496	—
GT3189	ΔBACOVA_04496	P-BACOVA_04505
GT3190	ΔBACOVA 04496	pBolux
GT3489	—	P-BACOVA 04505
GT3490	—	pBolux

TABLE 2

Primers used.			
identifier	name	sequence (5' → 3')	purpose
		qPCR	
1044	qBT16s_f	ggtagtccacacagtaaacgatgaa (SEQ ID NO: 1)	measure 16s rRNA levels using
1045	qBT16s_r	cccgtcaaattcctttgagtttc (SEQ ID NO: 2)	qPCR
1060	qBT3332_f	tggttgtcggctatcaggaagt (SEQ ID NO: 3)	measure BT3332 mRNA levels
1061	qBT3332_r	acatctgccatgttggctttc (SEQ ID NO: 4)	using qPCR
1056	qBT1763_f	agcgtaaagccgacctgaca (SEQ ID NO: 5)	measure BT1763 mRNA levels
1057	qBT1763_r	tcaccttgcttctggatttcg (SEQ ID NO: 6)	using qPCR
		lux reporter construction	
w2952	pNBU-P-BT1311_f	gctctagaactagtggatcctgatctggaagaagcaatg aaagct (SEQ ID NO: 7)	clone the Bt rpoD promoter preceding the_rpiL* RBS
w2905	rpiL*_r	catattcgtttaattaaataaataatttattttattttaaa (SEQ ID NO: 8)	
w3115	rpiL *-luxC_f	atttatttaattaaacgaatatgactaaaaaaatttcattcat tattaacgg (SEQ ID NO: 9)	clone the P. luminescens lux cassette preceded by the rpiL* RBS into pNBU2
w3124	luxE-nbu_r	aagataggcaattagtcgactcaactattaaatgcttggt ttaagcttaa (SEQ ID NO: 10)	
w3265	luxC_r	tttacaatttgccatgcggattacgggacaaatacaagg aacttatc (SEQ ID NO: 11)	clone the Bacteroides-optimized lux cassette preceded by the rpiL* RBS into pNBU2
w3266	luxD_f	tccgcatggcaaattgtaaattgtaaatcgtaaaatagta atatattaatggaaaataaatccaaatataaaaccatc (SEQ ID NO: 12)	

TABLE 2-continued

identifier	name	sequence (5' → 3')	purpose
		Primers used.	
w3267	luxD_r	attctttatcctcctccttattaagacagcgaaatcgcttga (SEQ ID NO: 13)	
w3268	luxE_f	taaggaggaggataaagaatatgacttcatatgttgata aacaagagatc (SEQ ID NO: 14)	
w3269	luxE_r	agtgttaccttcattcatccttcttcacccttcatttatatca actattaaatgcttggtttaagctt (SEQ ID NO: 15)	
w3270	luxA_f	ggatgaatgaaggtaacactcataaactcgaaattcttc attcttaatttttaattaaaatatatgaaatttggaaacttttt gcttac (SEQ ID NO: 16)	
w3271	luxA_r	ccattgtcttattcctttctttataatagcgaacgttgtttttct ttaag (SEQ ID NO: 17)	
w3272	luxB_f	agaaaggaataagacaatggatatgaaatttggattgtt cttccttaac (SEQ ID NO: 18)	
w3273	luxB_r	aagataggcaattagtcgacttacatgtggtactttttaat attatcatcaacaa (SEQ ID NO: 19)	
1080	pLYL-SpeI-rpil*_f	gctcggtacccggggatccactagtcactcccgcatttt aaaataaaataaattatttatttaattaaacg (SEQ ID NO: 20)	clone the Bacteroides-optimized lux cassette into pLYL01 and introduce a SpeI site
1011	PLYL luxB_r	tgcatgcctgcaggtcgacttacatgtggtactttttaata ttatcatcaacaatattg (SEQ ID NO: 21)	
1081	pBolux-P-BT1311_f	gctcggtacccggggatcctgatctggaagaagcaatg aaagct (SEQ ID NO: 22)	clone the Bt rpoD promoter into pBolux
1082	pBolux-P-BT1311_r	aaatgcgggagtgactagtcaaagttacgacaaataatt tgttaacatacatatttaggc (SEQ ID NO: 23)	
2109	pBolux-Bo-PrpoD_f	gctcggtacccggggatccatctggaagaagtaatgaa agctgc (SEQ ID NO: 24)	clone the Bo_rpoD promoter into pBolux
2110	pBolux-Bo-PrpoD_r	aaatgcgggagtgactagtcaaagttacgacaaataatt tgttaacatacaaaa (SEQ ID NO: 25)	
1150	pBolux-pBT1763_f	gctcggtacccggggatcctatcattcagttttctgttggt tactttgagiga (SEQ ID NO: 26)	clone the BT1763 promoter into pBolux
1304	pBolux-pBT1763_r	aaatgcgggagtgactagttagtttaatgttattaatttaa aagtacgaattttctcttttcgatg (SEQ ID NO: 27)	
1232	pBolux-pBT3332_f	gctcggtacccggggatccaaaatggaactgggcaat gacagg (SEQ ID NO: 28)	clone the BT3332 promoter into pBolux
1373	pBolux-pBT3332_r	aaatgcgggagtgactagtcctttttcttgtctggttggat agatgtttttt (SEQ ID NO: 29)	
1943	pBolux-pBACOVA_04505_f	gctcggtacccggggatccttgtttgttggagattgttttc atatcgttg (SEQ ID NO: 30)	clone the BACOVA 04505 promoter into pBolux
1944	pBolux-pBACOVA_04505_r	aaatgcgggagtgactagttagtttgatgttattaaattaa aagtacgaattttac (SEQ ID NO: 31)	
		Engineering mutations	
1846	pEXC-ΔBT3332_5f	gctctagaactagtggatccgacagcctccagctgacg g (SEQ ID NO: 32)	engineer a chromosomal deletion of BT3332
1535	pEXC-ΔBT3332_5r	catccttttttcttgtctggttggat (SEQ ID NO: 33)	
1847	pEXC-ΔBT3332_3f	accagacaagaaaaaggatgaaagcattaaaaataac aatcatagctctattggca (SEQ ID NO: 34)	
1848	pEXC-ΔBT3332_3r	aagataacattcgagtcgacatagaagctggctctttcg aaatagtc (SEQ ID NO: 35)	
11492	pEXC-ΔBT1754_5f	cgggatccgtggactattttgctgaaagcgga (SEQ ID NO: 36)	engineer a chromosomal deletion of BT1754
11493	pEXC-ΔBT1754_5r	tccccccgggttcatagttctttctgtaatccaattaaga (SEQ ID NO: 37)	

TABLE 2-continued

Primers used.

identifier	name	sequence (5' → 3')	purpose
11494	pEXC-ΔBT1754_3f	tccccccgggtttcattgatatcgtaaagagggat (SEQ ID NO: 38)	
11495	pEXC-ΔBT1754_3r	acgcgtcgactgccacacttccgtgcactt (SEQ ID NO: 39)	
1880	pEXC-ΔBT1763_5f	gctctagaactagtggatcccagtaatgaagagacatta cgg (SEQ ID NO: 40)	engineer a chromosomal deletion of BT1763
1819	pEXC-ΔBT1763_5r	tagtttaatgttattaatttaaaagtacgaattttctcttttcg atg (SEQ ID NO: 41)	
1839	pEXC-ΔBT1763_3f	aaattaataacattaaactaatgaaaaagataatatatata gcaacaatcggaattacc (SEQ ID NO: 42)	
1840	pEXC-ΔBT1763_3r	aagataacattcgagtcgacctgtttcaggtcttcttcgtt gattcc (SEQ ID NO: 43)	
1972	pEXC-ΔBT1760_5f	gctctagaactagtggatccgcttcttccgtcagtcttct (SEQ ID NO: 44)	engineer a chromosomal deletion of BT1760
1973	pEXC-ΔBT1760_5r	ttatttacacaagtagttgattgcattgagag (SEQ ID NO: 45)	
1974	pEXC-ΔBT1760_3f	tcaactacttgtgtaaataatgaaaactacaccggcaagt aacatc (SEQ ID NO: 46)	
1975	pEXC-ΔBT1760_3r	aagataacattcgagtcgactatcgcaacggggcggtg t (SEQ ID NO: 47)	
2011	pEXC-ΔBT1759_5f	gctctagaactagtggatccctggaagatttgaaagcaa ctac (SEQ ID NO: 48)	engineer a chromosomal deletion of BT1759
2012	pEXC-ΔBT1759_5r	tcaataagtgcttacctgaacgtctg (SEQ ID NO: 49)	
2013	pEXC-ΔBT1759_3f	ttcaggtaagcacttattgaaaaacgactttcttctccctg c (SEQ ID NO: 50)	
2014	pEXC-ΔBT1759_3r	aagataacattcgagtcgactgctccccacatggcaatg t (SEQ ID NO: 51)	
2015	pEXC-ΔBT1760-59_3f	tcaactacttgtgtaaataaaaaacgactttcttctccctg c (SEQ ID NO: 52)	engineer a chromosomal deletion of BT1760-59
2052	pEXC-ΔBT3082_5f	gctctagaactagtggatccccctctcaattggcgaaag aaaatc (SEQ ID NO: 53)	engineer a chromosomal deletion of BT3082
2053	pEXC-ΔBT3082_5r	agctattttatttattagtttgtaaaatcggagt (SEQ ID NO: 54)	
2054	pEXC-ΔBT3082_3f	cgattttacaaactaataaataaaatagctacggaaatca aaagctatctttgttttcag (SEQ ID NO: 55)	
2055	pEXC-ΔBT3082_3r	aagataacattcgagtcgacttccactggtaggctcgat g (SEQ ID NO: 56)	
2058	pKO-BT1765_f	gctctagaactagtggatcctgggaacatttggctcctg c (SEQ ID NO: 57)	engineer a chromosomal knock-out of BT1765
2059	pKO-BT1765_r	ggcccccccctcgaggtcgacatcattgtcctgtgtatag agtccc (SEQ ID NO: 58)	
2077	pKO-BT1758_f	cgctctagaactagtggatccagaaaaccgtgttactca gtttgatcg (SEQ ID NO: 59)	engineer a chromosomal knock-out of BT1758
2078	pKO-BT1758_r	gggcccccccctcgaggtcgacaaataacagagaacac attcgagttacc (SEQ ID NO: 60)	

TABLE 2-continued

identifier	name	sequence (5' → 3')	purpose
		Primers used.	
1978	pSIE1_ΔBACOVA_04496_5f	gattagcattatgaggatcctttggctatcccggcatcga (SEQ ID NO: 61)	engineer a chromosomal deletion of BACOVA 04496
1979	ΔBACOVA_04496_5r	tgacgtgaatagttttgatttctcatttttttcgtatttctttcta tgacc (SEQ ID NO: 62)	
1980	ΔBACOVA_04496_3f	aatcaaaactattcacgtcagaatacaataaatc (SEQ ID NO: 63)	
1981	ASIE1_dBACOVA_04496_3r	tccaccgcggtggcggccgcgcagtatatacaaatag ggttacgtct (SEQ ID NO: 64)	
		BT1760 complementation	
1818	pNBU2-pBT1763_f	gctctagaactagtggatcctatcattcagttttctgttggt tactttgag (SEQ ID NO: 65)	Complement the BT1760 deletion strain in trans
2007	P-BT1763-BT1760_f	cgtacttttaaattaataacattaaactaatgatgaaaaat atgatcttacctatagcat (SEQ ID NO: 66)	
2008	pNBU2-BT1760_r	aagataggcaattagtcgactcaataagtgcttacctga acgtc (SEQ ID NO: 67)	
		SGBP over-expression	
1723	pT7-7-H6-BT1761_f	agaaggagatatacatatgcatcaccatcaccatcaca gtgatgacttcaaatccggcc (SEQ ID NO: 68)	BT1761 overexpression in BL21 (DE3)
1724	pT7-7-BT1761_r	gcttatcatcgataagcttttatttacacaagtagttgattg cattgagag (SEQ ID NO: 69)	
2087	pT7-6H-4G-BT3330_f	agaaggagatatacatatgcatcaccatcaccatcacg gaggtggaggtgacgggctggacgaagcggtaggt (SEQ ID NO: 70)	BT3330 overexpression in BL21 (DE3)
2088	pT7-7-BT3330_r	agcttatcatcgataagcttattccactacgtttaccacca t (SEQ ID NO: 71)	

TABLE 3

Name	Description
	Plasmids used
pLYL01	empty multi-copy vector
pNBU2-erm	empty single-copy vector conferring erythromycin resistance
pNBU2-tet	empty single-copy vector conferring tetracycline resistance
pNBU-lux-Pl	The *Psuedorhabdus luminescens* lux cassette cloned into pNBU2-tetR
pNBU-lux-Bt	The *Bacteroides* optimized lux cassette cloned into pNBU2-tetR
p-lux-Pl	The *Psuedorhabdus luminescens* lux cassette sub-cloned into pLYL01
p-lux-Bt	The *Bacteroides* optimized lux cassette sub-cloned into pLYL01
pBolux	pLYL01 harboring BamHI and SpeI sites upstream of the *Bacteroides* optimized lux cassette
P-Bt-rpoD	277 bp upstream of BT1311 were cloned into the BamHI and SpeI sites in pBolux
P-Bo-rpoD	278 bp upstream of BACOVA_00615 were cloned into the BamHI and SpeI sites in pBolux
P-BT3332	300 bp upstream of BT3332 were cloned into pBolux
P-BT1763	300 bp upstream of BT1763 were cloned into pBolux
pBolux::P-BACOVA_04496	300 bp upstream of BACOVA_04496 were cloned into pBolux
pEXCHANGE-tdk	empty plasmid used to generate chromosomal deletions in Bt
pEXCHANGE-ΔBT3332	plasmid used to generate a chromosomal deletion of BT3332
pEXCHANGE-ΔBT1763	plasmid used to generate a chromosomal deletion of BT1763
pEXCHANGE-ΔBT1760	plasmid used to generate a chromosomal deletion of BT1760
pEXCHANGE-ΔBT1759	plasmid used to generate a chromosomal deletion of BT1759
pEXCHANGE-ΔBT1760-59	plasmid used to generate a chromosomal deletion of BT1760-59
pEXCHANGE-ΔBT1754	plasmid used to generate a chromosomal deletion of BT1754

TABLE 3-continued

Plasmids used	
Name	Description
pEXCHANGE-ΔBT3082	plasmid used to generate a chromosomal deletion of BT3082
pKNOCK-ermG	plasmid to generate chromosomal insertions in Bt
pKNOCK-ermG-BT1765KO	plasmid used to inactivate BT1765
pKNOCK-ermG-BT1758KO	plasmid used to inactivate BT1758
pKNOCK-ermG-BT4410KO	plasmid used to inactivate BT4410
pSIE1	empty plasmid to generate chromosomal deletions in Bo
pSIE1::ΔBACOVA_04495	plasmid to delete BACOVA_04495 in Bo
pT7-7	empty vector for protein over-expression
pT7-7::H6-4G-BT3330	pT7-7 construct for over-expression of BT3330 [D21-E347] with an N-terminal hexahistidine tag
pT7-7::H6-BT1761	pT7-7 construct for over-expression of BT1761 [S25-K461] with an N-terminal hexahistidine tag

[0228] Transcript quantification. mRNA was prepared from 1.0 mL of pelleted Bt cell culture treated with RNA protect (Qiagen) using the RNeasy kit (Qiagen) according to the manufacturer's directions. cDNA was subsequently synthesized from 1.0 μg of isolated RNA using Superscript VILO IV master mix (ThermoFisher) according to the manufacturer's directions. Transcript levels were measured by qPCR using Fast SYBR Green PCR Master Mix (Applied Biosystems) and primers 1060 and 1061 (BT3332) or 1056 and 1057 (BT1763) and monitored using a QuantStudio 12K Flex instrument (Applied Biosystems). All mRNA transcripts were normalized to 16s IRNA measured from 1,000-fold diluted cDNA using primers 1044 and 1045.

[0229] Measuring bioluminescence during growth in various monosaccharides. Bt and Bo strains were cultured in TYG containing 2 μg/mL tetracycline overnight before being diluted 200-fold into minimal media containing 0.5% carbon source in a sterile 96-well white, clear-bottomed microplate (Corning 3610). Absorbance at 600 nm and luminescence were measured every 15 minutes for 48 hours using a Tecan Infinite M-plex. RLU were calculated as luminescence values divided by absorbance at 600 nm.

[0230] Measuring bioluminescence in response to glycans. Bt and Bo strains were cultured in TYG containing 2 μg/mL tetracycline overnight before being diluted 50-fold into minimal media containing 0.5% galactose anaerobically grown to mid-exponential phase at 37° C. (approximately 4 hours). Cultured cells were pelleted by centrifugation before the supernatant was removed, and cells were resuspended in 2× minimal media lacking a carbon source. Equal volumes of each cell suspension were transferred to a pre-reduced, white, clear bottom 384-well microplate (Corning 3765) containing equal volume of the indicated carbon source. Absorbance at 600 nm and luminescence were measured every 15 minutes for 18 hours using a Tecan Infinite M-Plex instrument anaerobically at 37° C. temperature. RLU were calculated as luminescence values divided by absorbance at 600 nm and normalized to identical measurements from each strain supplied only galactose.

[0231] Protein overexpression and purification. *E. coli* BL21 (DE3) cells were transformed with pT7-7 plasmids encoding SGBPs. Fresh transformants were cultured overnight in LB supplemented with 100 μg/mL ampicillin at 37° C. with agitation. The following day, cultures were diluted 50-fold in LB supplemented with 100 μg/mL ampicillin and incubated for approximately 2 hours at 37° C. with agitation to mid-exponential phase (OD_{600}~0.45-0.6). Cultures were cooled on ice before isopropyl β-thiogalactopyranoside (IPTG) was added to a final concentration of 50 μM and incubated at 30° C. with agitation for 4 hours. Cells were pelleted by centrifugation at 7197×g for 10 min at 4° C. before the supernatant was decanted and cell pellets were frozen on dry ice and stored at −80° C. Pellets were thawed on ice, resuspended in 20 mM Tris/HCl buffer, pH 8.0, containing 100 mM NaCl and lysed in 2.0 mL tubes containing 250 μL volumes of 0.1 mm silica beads placed in a pre-chilled aluminum block using a Bead beater-96 (BioSpec) for 5 cycles of 40 second beating at 2400 rpm and 5 minutes resting at 4° C. Lysates were centrifuged at 20,000×g for 10 minutes at 4° C. and the supernatant was combined with 0.2 mL pre-equilibrated Ni-NTA sepharose and 10 mL of 20 mM Tris/HCl buffer, pH 8.0, containing 100 mM NaCl for 1 hour at room temperature with rocking. The slurry was packed into a 2 mL purification column (Pierce) and the liquid phase removed by gravity flow before washing with 3 mL of wash buffer (20 mM Tris/HCl buffer, pH 8.0, containing 100 mM NaCl). SGBPs were eluted from the column with 3 mL of elution buffer (20 mM Tris/HCl buffer, pH 8.0, containing 100 mM NaCl and 25 mM histidine), concentrated and buffer exchanged using centrifugal concentrators (Millipore) and 6 successive additions of storage buffer (10 mM Tris/HCl buffer containing 10% glycerol). Protein concentrations were estimated by BCA assay (Pierce) and stored at −80° C.

[0232] Affinity PAGE. 100 pmol of protein was combined with native PAGE loading buffer and electrophoresed in a 10% polyacrylamide matrix containing 10% (w/v) acrylamide in Tris, glycine buffer, pH 8.8. at 20 mA for 3.5 hours at room temperature. Gels contained 0.1% CS or levan and BSA was used as a negative control. Proteins were visualized by Coomassie Blue staining.

[0233] SGBP target glycan isolation. 500 μL of clarified protein lysate was pre-incubated with 1.0 mL of a mixture containing 0.1% levan and 0.1% CS overnight at 4° C. with rocking before combination with 200 μL pre-equilibrated Ni-NTA agarose (Sigma) in 9 mL of 20 mM Tris/HCl buffer,

pH 8.0, containing 100 mM NaCl, for 1 hour at RT with rocking. The slurry was packed into a 2 mL purification column (Pierce) and the liquid phase removed by gravity flow before washing 4 times with 1 mL of 20 mM Tris/HCl buffer, pH 8.0, containing 100 mM NaCl. SGBPs were eluted from the column in a total of 4 mL elution buffer (20 mM Tris/HCl buffer, pH 8.0, 100 mM NaCl and 25 mM histidine). Glycan content was measured as described above whereby mid-exponential cells were pelleted by centrifugation and re-suspended into 2× minimal media containing 0.4% galactose. Each cell suspension was transferred to a pre-reduced, white, clear bottom 384-well microplate (Corning 3765) containing equal volumes of column fractions. Absorbance and luminescence were measured kinetically under anaerobic conditions as described above. Target glycan containing elution fractions were combined and treated with 0.1 mg/mL Proteinase K in 10 mM Tris, pH 7.5 containing 20 mM calcium chloride for 2 hours at 65° C. Total glycans were combined with 3 volumes of 200 proof ethanol, incubated overnight with rocking at 4° C., pelleted by centrifugation, and resuspended in one tenth the original volume of water.

[0234] Reporter-independent glycan measurements. Total levan content was assayed using the Fructan Assay Kit (K-Fruc, Megazyme), modified to include the hydrolysis and absorbance measurement at 410 nm against a standard curve of 0.2-1 mg levan. CS abundance was estimated using the Total Glycosaminoglycan Assay Kit (K2085, BioVision), according to the manufacturer's directions against a standard curve of 0.2-10 μg CS.

[0235] Statistical analysis. Repeated measurements were analyzed by paired, two-tailed Student's t-test, 1-way, or 2-way ANOVA using Graphpad Prism where appropriate as indicated in each figure legend.

Example 2: Applications for Harnessing Gut Microbes

[0236] Glycans facilitate critical biological functions and control the mammalian gut microbiota composition by supplying differentially accessible nutrients to distinct microbial subsets. Therefore, identifying unique glycan substrates that support defined microbial populations will inform new therapeutic avenues to treat diseases via modulation of the gut microbiota composition and metabolism. However, examining heterogenous glycan mixtures for individual microbial substrates is hindered by glycan structural complexity and diversity, which presents substantial challenges to glycomics approaches. Fortuitously, gut microbes encode specialized sensor proteins that recognize unique glycan structures and in-turn activate predictable, specific, and dynamic transcriptional responses. Herein, the microbial machinery is harnessed to indicate the presence and abundance of compositionally similar, yet structurally distinct glycans, using a developed transcriptional reporter. It demonstrated how these tools can be implemented to examine glycan mixtures, isolate target molecules for downstream characterization, and quantify the recovered products. Thus, a toolkit will dramatically enhance the understanding of the mammalian intestinal environment and identify host-microbial interactions critical for human health.

Example 3: Development of Methods for Detecting and Quantifying Glycans

[0237] Modern glycomics approaches face technical and biophysical limitations that hinder comprehensive characterization of heterogeneous glycan mixtures typically derived from biological samples. For example, glycomic analyses by mass spectrometry requires sample derivatization and ionization that bias detection due to the non-uniform labeling of individual monosaccharides, covalent decorations, and branched structures exhibited by many glycans. Conversely, nuclear magnetic resonance (NMR) precisely determines composition, sequence, and structural arrangements but requires isolation of individual glycan species to achieve optimal resolution. Isolation of individual target glycans from a complex mixture requires subsequent rounds of fractionation using sequential high-performance liquid chromatographic (HPLC) approaches to sort compositionally similar but structurally distinct molecules. Glycan binding aptamers and proteins, such as lectins, can directly indicate the presence of distinct targets but their narrow specificity paired with high-cost limits their accessibility as high-throughput glycan surveillance tools. Consequently, glycomics strategies often require the application of multiple, tandem methodologies to comprehensively examine the complex mixtures typically extracted from eukaryotic, prokaryotic, and plant materials. Therefore, new, accessible, and inexpensive technologies are imperative to facilitate simple, rapid surveillance of crude glycan preparations that indicate the presence and abundance of distinct structures.

[0238] Collectively, the challenges facing their characterization have limited the understanding of the glycans present in various ecological niches, referred to as the glycome, and has lagged behind the understanding of the abundance and dynamics of the organisms occupying those niches. This is exemplified by the mammalian intestinal environment, where the gut microbiome and its transcriptome have been extensively examined by NGS methodologies that take advantage of the linear, uniform compositions of nucleic acids. Thus, the microbial populations and their transcriptional fluctuations have been well-defined, revealing incredible inter-individual compositional variation and uncovering their contributions to human health and disease. This work has revealed how the intestinal glycome influences gut microbial fitness and metabolism, thereby driving the microbiome composition and the synthesis of clinically important metabolites. Thus, the intestinal glycome is an untapped reservoir of molecules that could be employed to modulate gut microbial abundance and metabolism for clinically beneficial outcomes. New glycomic approaches have been developed to interface with existing technologies to detect glycans that serve as gut microbial signals and growth substrates, and subsequently isolate relevant molecules from biologically-derived mixtures for downstream structural characterization using conventional approaches. Bacterial taxa that dominate in the intestinal environment have evolved specialized glycan detection and utilization machinery to identify available substrates that can serve as nutrient sources and respond by producing enzymes that facilitate substrate sequestration, importation, and consumption. Many of these bacteria employ a panoply of different glycan sensor proteins that recognize structurally distinct glycans and facilitate transcription activation of the appropriate enzymatic repertoire to efficiently utilize target glycans. The glycan detection machinery possessed by gut bacteria has been harnessed to indicate the presence and abundance of distinct glycans in vitro using a new transcriptional reporter system. Furthermore, we implemented this reporter in a high-throughput capacity to define the glycome of a bio-

logically derived heterogenous glycan mixture through the prism of gut microbes. Moreover, this reporter-mediated detection is utilized to facilitate isolation of target glycans of interest using affinity purification strategies for downstream structural and functional characterization. Finally, it is demonstrated that these microbial responses can be readily quantified to estimate the relative abundance of recovered glycans similarly to commercially available products. Therefore, a new suite of glycomics tools have been established that can overcome many of the current challenges facing glycomics and have developed an inexpensive, readily distributable glycan surveillance platform to examine crude glycan preparations in a high-throughput manner and affinity purification tools to isolate target molecules for downstream characterization.

[0239] Moreover, because the glycans found in the intestinal environment are derived from a myriad of environmental sources including plant and animal tissue, the tools that result from this example extend far beyond the gut microbiota to enhance existing glycomics workflows. Finally, genetic tuning can modulate the responsiveness of these systems to narrow glycan structural specificity and extend the limits of detection indicating their modularity.

Results

[0240] *Bacteroides* PUL sensors elicit dose-dependent transcriptional responses to cognate glycan ligands. Species of the bacterial genus, *Bacteroides*, are predominantly found in the mammalian intestinal tract and encode genetically linked, coordinately regulated gene clusters called polysaccharide utilization loci (PULs). Most *Bacteroides* species encode many different PULs, each conferring the ability to consume one or a small subset of structurally distinct glycans. PULs encode genes that facilitate the sequestration, importation, depolymerization, and detection of a target glycan (FIG. **1**A). PUL transcripts are typically expressed constitutively at low levels until the target glycan is encountered in the environment, at which time PUL transcripts are rapidly and dramatically increased (FIG. **1**B). These increases in PUL transcription are mediated by unique sensor proteins that bind mono-, di-, or oligo-saccharide signatures derived from the target glycan in the periplasm directly facilitating transcription of PUL genes in the cytoplasm, an activity necessary for efficient utilization of the target glycan (FIG. **1**C). For example, introduction of the glycosaminoglycan, chondroitin sulfate (CS), results in a 92-fold increase in the transcript level of the *Bacteroides thetaiotaomicron* (Bt) CS-specific PUL, which requires the CS sensor gene, BT3334, because a mutant deficiency for the CS-sensor is unable to increase CS-PUL expression (FIG. **1**D) and is unable to grow on CS as a sole carbon source (FIG. **1**C). Interestingly, CS-dependent changes in PUL gene transcription are dose-dependent, such that adding increasing amounts of CS to the media results in corresponding increases in PUL-encoded susC (BT3332) transcript levels (FIG. **1**E). Similarly, introduction of the common dietary fiber, levan, increases transcription of the corresponding susC gene, BT1763, 530-fold, which requires the levan sensor, BT1754 (FIG. **1**F) and is necessary for levan utilization (FIG. **1**G) (35). Increasing amounts of levan elicit concentration-dependent increases in the corresponding susC transcript levels (FIG. **1**H), However, these responses are kinetic, and require sampling at discreet times following glycan addition (FIGS. **1**H and **1**I).

[0241] *Bacteroides* PUL reporters indicate the presence of target glycans. The data show that the rapid, dramatic, and predictable increases in PUL transcript levels can indicate the relative abundance of PUL-specific glycans and therefore be harnessed as glycan biosensors. However, measuring PUL transcription by qPCR or high-throughput sequencing is cumbersome, expensive, and requires kinetic sampling (FIGS. **1**E, **1**H, and **1**I). Thus, the first transcriptional reporter plasmid (named pBolux, for *Bacteroides*-optimized lux) was developed that can quantify gene transcription during anaerobic growth across *Bacteroides* species. Because this reporter encodes a complete bacterial luciferase cassette, measuring activity is achieved kinetically, without the addition of exogenous reagents, and exhibits extremely low background as *Bacteroides* species do not natively produce bioluminescence. Reporter plasmids harboring the region upstream of the constitutively active rpoD gene, exhibited dramatically increased reporter activity compared to the promoter-less pBolux plasmid in Bt (FIG. **15**A), *Bacteroides ovatus* (Bo; FIG. **15**B), *Bacteroides fragilis* (Bf; FIG. **15**C), or *Bacteroides* caccae (Bc, FIG. **15**D) without an obvious fitness cost as strains harboring these constructs grew identically to those harboring a promoter-less control plasmid (FIG. **15**A-**15**D, respectively).

[0242] Bt PUL-promoters were cloned preceding the plasmid-encoded lux cassette and measured reporter activity in the presence or absence of known target glycans. For example, a strain harboring a reporter plasmid that included the CS-PUL promoter (i.e., region upstream of the corresponding susC gene, BT3332) resulted in a dramatically increased reporter activity following the introduction of CS compared to a control strain harboring the promoter-less plasmid (FIG. **16**A The PUL-encoded activities (depicted in FIG. **1**A) were responsible for these CS-induced reporter activity increases by culturing the mutants unable to grow in CS (FIG. **1**C) in galactose prior to the introduction of a mixture of CS and galactose. The reporter activity was subsequently measured over 18 hours (FIG. **16**B) and the area under each curve (AUC) was calculated for simple statistical comparisons (FIG. **16**C). For example, CS-induced reporter activity requires the PUL-encoded outer membrane transporter SusC, because a mutant lacking the corresponding gene, BT3332, was unable to transport CS into the bacterial periplasm and exhibits dramatically reduced activity compared to wild-type Bt in the presence of CS (FIGS. **16**B and **16**C). Reporter activation requires the depolymerization of CS into disaccharides that bind the sensor in the bacterial periplasm (FIG. **1**A) because a mutant deficient in 3 PUL-encoded CS-specific lyases (Alyase) is unable to increase reporter activity in response to CS (FIGS. **16**B and **16**C) but this can be overcome by the addition of pre-digested chondroitin disaccharides (FIG. **16**D). In all cases, increased reporter activity requires the corresponding PUL-sensor as a mutant lacking the CS-sensor gene, BT3334, exhibited no increase in the presence of either chondroitin sulfate (FIGS. **16**B and **16**C) or chondroitin disaccharide (FIG. **16**D). The reduced reporter activity observed in all of these mutants was due to the inability to activate the CS-sensor rather than a consequence of impairing CS utilization because a mutant lacking the CS-specific glucuronyl hydrolase, BT3348, which is necessary to hydrolyze the CS-sensor ligand and grow in CS (FIG. **1**C), elicits reporter activation similar to wild-type Bt (FIGS. **16**B and **16**C). Thus, these engineered strains can specifically indi-

cate the presence of target glycans in the environment by defined mechanisms possessed by PUL-encoded gene products.

[0243] Species-specific responses distinguish between compositionally identical, structurally distinct glycans. Differentiating between compositionally identical glycans requires specialized LC/MS protocols due to the generation of molecules with identical masses following derivatization and ionization. However, different *Bacteroides* species encode similar PULs that confer distinct substrate specificities for compositionally identical yet structurally distinct glycans. For example, the Bt fructan PUL facilitates consumption of the β2,6-linked polyfructan, levan (FIG. **17**A), but not the β2,1-linked polyfructan, inulin (FIG. **17**B). Conversely, Bo encodes a highly similar PUL to the one in Bt but facilitates utilization of inulin (FIG. **17**B) and is unable to mediate the consumption of levan (FIG. **17**A). Bt and Bo exhibit disparate fructan specificities despite both PULs encoding nearly identical sensor proteins that bind the monosaccharide fructose, which is the sole degradation product of both inulin and levan, in-turn activating PUL transcription in the cytoplasm and facilitating growth (FIG. **17**C). PUL-reporter plasmids were generated in Bt and Bo containing regions upstream of their respective fructan PUL susC genes and determined that both Bt and Bo reporter strains exhibit similar sensor-dependent reporter activity increases when supplied fructose (FIG. **17**D). As expected, the Bt fructan PUL-reporter exhibited 12-fold increased activity in levan (FIG. **17**E) but only 2-fold increased activity in response to inulin (FIG. **17**F). Conversely, the Bo PUL-reporter exhibited a 9.3-fold increase in reporter activity following the introduction of inulin (FIG. **17**F) but no increase in levan (FIG. **17**E). These results demonstrate that PULs exhibit substrate specificity even when the PUL-sensor responds to identical ligands, indicating that growth substrate specificity can be mediated by additional-PUL encoded activities. Finally, these results highlight that these reporters can detect very low levels of substrates because statistically significant differences between wild-type and sensor-deficient Bt strains were detected (FIG. **17**F), indicating that Bt can liberate monomeric fructose from inulin at comparatively low rates insufficient for growth (FIG. **17**B). Thus, by uncoupling PUL signaling from growth, microbial responses to glycans can be examined independently of substrate utilization, facilitating detection of structurally distinct but compositionally identical glycans.

[0244] *Bacteroides* PUL reporters elicit linear dose-dependent responses to target glycans. PUL-sensors elicit dose-dependent increases in PUL transcript levels (FIGS. **1**E and **1**G) indicating that these responses could be used to quantify glycan abundance relative to a standard curve. Accordingly, PUL-reporters also exhibit dose-dependent responses to target glycans over a linear range greater than three orders of magnitude (FIGS. **18**A and **18**B). Quantifying the AUC following 18 hours after the introduction of two-fold serial dilutions of either CS or levan revealed a linear response from a wild-type Bt strain harboring the CS-reporter supplied between 0.4 to 0.0004% (4.0 to 0.004 mg/mL) CS but no response from any amount of levan (FIG. **18**C). Conversely, strains harboring the levan-reporter plasmid exhibited similar linear dose-dependent responses between two-fold serial dilutions of levan but not CS (FIG. **18**D). Furthermore, both the CS and levan-reporters retained linear responsiveness even when 0.2% of the other glycan was present (FIGS. **18**E and **18**F). These data indicate that the dose-dependent responses of PUL-reporters could be used as standard curves to quantify target glycan abundances present in complex heterogenous mixtures.

[0245] Mutations can narrow glycan specificity and enhance reporter sensitivity. PUL-sensor mediated transcription activation requires enzymatic conversion of target glycans into mono-, di-, or oligosaccharide signatures mediated by PUL-encoded polysaccharide lyases or glycosyl hydrolases that cleave the glycosidic bonds tethering distinct repeating disaccharides. The CS-PUL encodes 3-discreet CS-specific lyases that are collectively required for growth on CS (FIG. **1**C) and increased PUL-reporter activity in response to CS (FIGS. **16**B and **16**C). These lyases also depolymerize a similar glycosaminoglycan, hyaluronan (HA), into disaccharides detected by the same PUL-sensor. However, HA depolymerization is also mediated by an additional unknown enzymatic activity that is unable to act on CS and therefore, a lyase-deficient mutant can grow on HA (FIG. **19**A) but not CS (FIG. **1**C). Consequently, a lyase-deficient mutant is no longer able to elicit dose-dependent responses in CS compared to wild-type Bt (FIG. **19**B) but retains this ability in HA (FIG. **19**C). These data demonstrate how directed mutations can further enhance glycan detection specificity by differentiating between two structurally similar, yet compositionally distinct glycans, which cannot be achieved using commercially available kits.

[0246] Following activation by binding glycan-derived ligands, PUL-sensors are deactivated and returned to steady state by the processive removal of their cognate glycan-derived ligands (FIG. **1**A). Deactivation of the CS-reporter requires hydrolysis of glycan-derived disaccharides into their monosaccharide components by a glucuronyl hydrolase (gh), encoded by BT3348 in Bt. Thus, a gh-deficient mutant accumulates CS-derived disaccharides, prevents PUL-sensor deactivation, which promotes increased PUL transcription relative to wild-type Bt. Consequently, it was determined that the gh-deficient strain exhibited significant CS-reporter activity increases when supplied CS amounts as low as 0.000006% (60 ng/mL), which were undetectable by wild-type Bt harboring the same CS-reporter construct (FIG. **19**D). Therefore, by successfully uncoupling PUL transcription from bacterial growth, mutations that prevent PUL-sensor deactivation can be employed, extending the lower limits of detection and quantification well below those of commercially available solutions.

Conclusions

[0247] PUL transcription activation is directly facilitated by PUL sensor proteins that detect mono-, di-, or oligosaccharide signatures derived from their corresponding target glycan. These glycan signatures are generated by progressive and compartmentalized enzymatic activities that facilitate glycan sequestration outside of the cell, followed by target glycan importation and subsequent depolymerization (FIG. **1**A). PUL reporters can capture these events and elicit dose-dependent luminescence increases following the introduction of target glycans into cultured *Bacteroides* reporter strains. These properties are harnessed to reveal the presence and abundance of previously undetectable glycans and dramatically enhance understanding of the interactions between gut microbes and their mammalian hosts.

A High-Throughput Glycan Detection Platform.

[0248] A bioluminescent reporter is demonstrated to be coupled to PUL promoters from different *Bacteroides* species (FIG. **15**) to distinguish between compositionally identical, but structurally distinct glycans (FIG. **17**). It has been contemplated to develop libraries of reporter strains representing every predicted PUL across 4 different species. It is further contemplated to develop a high-throughput detection platform that harnesses arrayed reporter strains to simply, accurately, and inexpensively detect the abundance of all glycans that are recognized by these PULs. Thus, leading to the building of a comprehensive resource that can aid in identifying the presence of distinct glycans from a myriad of biological sources including plant, animal, and microbial products.

[0249] Reporter plasmids are generated representing every annotated PUL present in *B. thetaiotaomicron* (strain VPI-5482; 96 predicted PULs), *B. ovatus* (ATCC 8483; 107 predicted PULs), *B. fragilis* (NCTC 9343, 55 predicted PULs), and *B. caccae* (ATCC 43185; 60 predicted PULs). These species were chosen because they encode PUL subsets with distinct glycan specificities and biological niches. PULs are identified using computational methods that examine the genomic sequence for susCD gene pairs, which are the minimum PUL components, and various arrangements of genes whose products encode glycan binding, hydrolysis, and lyase activities. PULs are often polycistronic transcripts initiated from one or a small set of promoters upstream of the corresponding susC gene. Publicly available RNAseq datasets from each organism are used to identify putative transcription start sites to guide putative PUL promoter selection prior to cloning. Plasmids are introduced into their corresponding *Bacteroides* species, and the resulting strains validated by glycan-dependent and -independent approaches described below. Validated reporter strains are cultured in rich media, combined with glycerol to a final concentration of 10%, and all strains will be dispensed into 50×96-well plates for storage at −80° C. using a Tecan Evo Freedom 200 instrument located at the Penn State Cancer Institute.

[0250] Glycan-dependent validation is achieved when significant increases in bioluminescence are detected following the addition of glycan mixtures to strains harboring putative reporter plasmids that are greater than identical cultures supplied galactose alone. Additionally, glycan-responsive reporters are introduced into mutant strains lacking corresponding PUL-sensors when available and examined for reduced PUL-reporter activation in response to identical glycan mixtures (as demonstrated for CS in FIG. **16**). Glycan-independent validation are achieved using strains engineered to express constitutively active forms of the putative PUL regulator that can increase corresponding PUL transcription in the absence of target glycan, an approach we previously developed. Candidate reporter plasmids containing putative PUL promoters are introduced into strains engineered to express the corresponding constitutively active PUL regulator (cartooned in FIG. **20**A). To demonstrate the feasibility of this approach, a draft array was generated including reporter constructs representing 95 predicted and experimentally established Bt PULs and validated all possible reporters using glycan-dependent or -independent approaches. Over half of the initially constructed reporters were experimentally validated (FIGS. **20**B-**20**E). When PUL-reporters exhibited no glycan-responsive increases in engineered strains, alternative plasmids were constructed using promoter regions from upstream genes, which generated PUL-regulator-dependent bioluminescence increases (FIGS. **20**E-**20**I). Furthermore, to determine whether constitutively active PUL-regulators elicited specific activation of target PULs, RNAseq analysis was performed comparing genome-wide transcription in strains harboring an empty vector or over-expressing BT3172*, which increased luminescence from P-BT3174 (FIG. **20**E) and is a constitutively-active form of a PUL regulator important for Bt intestinal colonization and putatively senses an unknown host-derived glycan. A strain expressing BT3172* exhibited between 8 and 120-fold increases in the corresponding PUL genes, BT3171-BT3180, but no other PUL transcripts were differentially expressed, indicating specific regulation of target genes by these engineered regulatory proteins. Therefore, this strategy can be used to specifically validate each reporter in lieu of known sources containing target glycans and additional PUL reporter constructs in Bo, Bf, and Bc can be validated in this manner or by measuring reporter activity increases in conditions known to activate the corresponding PUL or using glycan-dependent approaches described above.

[0251] To examine the ability of individual reporters to elicit target-glycan dependent increases in reporter activity, the activity of every Bt reporter is measured following the introduction of commercially purified glycans derived from plants: arabinogalactan and levan; microbes: dextran and HA, or animal tissue: HS and CS. Because genome wide Bt transcriptional responses to these glycans have been previously characterized, bioluminescence from the corresponding reporter strain is observed to be increased. Accordingly, the addition of each glycan to the array elicited the PUL-reporter activity increases. For example, arabinogalactan increased activity from P-BT0268 315-fold (FIG. **21**A), levan increased activity from P-BT1763 39-fold FIG. **21**B), dextran increased P-BT3090 activity 130-fold (FIG. **21**C), HA increased P-BT3332 activity 50-fold (FIG. **21**D), HS increased P-BT4662 activity 50-fold (FIG. **21**E) and CS increased P-BT3332 activity 42-fold (FIG. **21**F). While the addition of arabinogalactan, levan, dextran, HA, and HS elicited a dominant response from the corresponding PUL reporters, CS elicited 6 additional significant responses including 3 that increased greater than 10-fold compared to the galactose treated control, P-BT1632, P-BT2818, and P-BT4662 (FIG. **21**F). It was determined that the activation of these reporters was due to the presence of contaminating glycans present in the CS mixture (which is estimated at ~70% purity by Sigma) rather than the results of promiscuous, non-specific activation by CS or the CS-sensor in the following ways: 1.) A mutant lacking the CS-sensor reduced the activation of P-BT3332 45-fold but only reduced P-BT1632 reporter 1.3-fold (FIG. **22**A), 2.) The addition of purified CS disaccharide, which serves as the ligand for the CS-sensor, only activates P-BT3332 (FIG. **22**B), and 3.) The overexpression of a constitutively active form of BT3334 (BT3334*) increased luminescence from P-BT3332 greater than 100-fold while the other examined reporters were less that 2-fold different (FIG. **22**C). Thus, the activation of additional reporters by CS is due to the presence of additional glycans targeted by distinct Bt PULs indicating that the array can effectively detect distinct molecules present in biologically derived glycan mixtures. Consistent with this notion, 15 PUL-reporters were significantly increased following addition of a biologically-derived glycan mixture,

porcine mucosal O-glycans, (PMOGs), consistent with the characterized Bt transcriptional responses. Thus, this approach can detect multiple PUL-specific ligands in biological mixtures.

[0252] Validated, arrayed reporter libraries are generated representing a total of 318 predicted PULs across 4 distinct *Bacteroides* species. Including all PUL-reporters in a single array requires increased array capacity such that all strains can be cultured in 384-well plates prior to the introduction of samples, which is done in 1536-well plates to accommodate 3 distinct samples per reporter strain and a negative control condition (galactose). Increasing capacity using 1536-well plates enables glycan screening to be achieved with reporters from all species simultaneously, thereby increasing the likelihood of detecting molecules of interest with smaller volumes of material than those required for screening in 384-well plates. Arrays containing all strains are manufactured by a Tecan Freedom Evo 200 that can repeatedly dispense into 384-well plates prior to long-term cryogenic storage. Cultured strains are anaerobically transferred using a semi-automated, repeating pipetting instrument. Reporter activity is measured in a Tecan Spark instrument housed in a Coy flexible anaerobic chamber over 18 hours.

[0253] An arrayed library of PUL reporters are generated that can detect small quantities of distinct glycan ligands present in crude biological extracts. Based on results with microbial and mammalian glycans, each strain exhibits accurate and sensitive reporter activity increases in response to specific glycan ligands. This offers users a rapid and inexpensive survey of known and unknown glycans as observed though the lens of the gut microbiota. Finally, tailored arrays, containing PUL-reporter subsets of interest in wild-type or mutant backgrounds that exhibit altered target glycan specificities or sensitivities (FIG. **19**) are generated in 96- or 384-well microplates.

A Glycan Isolation Platform.

[0254] Determining which PULs are activated via increased reporter activity indicates the presence of a distinct target glycan in samples with unknown glycan content. However, the identity of these molecule(s) may be unknown as only a small fraction of PULs have experimentally determined glycan targets. This is in part due to the challenges facing modern glycomics, which limit structural characterizations of heterogenous glycans mixtures. To overcome these challenges, PUL-reporters are employed as detection agents following glycan fractionation to isolate individual structures from heterogenous mixtures for downstream structural characterization. Moreover, affinity purification approaches are developed using PUL encoded surface glycan binding proteins (SGBPs) to facilitate simple, low-cost isolation of target molecules. Thus, glycans of interest can be identified in a biological sample using the arrays described previously and subsequently isolate individual glycans from these mixtures for downstream compositional and structural analysis. This stepwise approach helps circumvent challenges facing current glycomics strategies which are hindered by a paucity of simple and effective glycan separation strategies.

[0255] *Bacteroides* PULs frequently encode SGBPs that localize the bacterial outer membrane to aid in substrate sequestration prior to importation via the corresponding SusC transporter (FIG. **1**A). SGBPs display specificity for target glycan structures and are capable of distinguishing between compositionally identical but structurally distinct glycans. Herein, SGBPs are encoded by PULs with unknown target specificities to isolate the corresponding glycan of interest from heterogenous mixtures (FIGS. **21**F and **21**G) that can activate distinct reporters (FIG. **7**A). SGBPs fused to hexa-histidine tags are expressed in *E. coli* strain BL21 (DE3) for purification with nickel-conjugated agarose reagents as previously described. Immobilized recombinant protein are incubated with mixtures containing the putative glycan ligands, extensively washed to remove unbound material, and finally eluted with any bound glycans using free histidine. Histidine is used rather than imidazole because it is non-toxic to all *Bacteroides* cultures tested to date, allowing elution fractions to be added directly to cultured PUL-reporter strains. Corresponding PUL-reporter activity is measured following the addition of the resulting wash and elution fractions against all reporter strains that were activated by the initial glycan mixture. If elutions elicit increased reporter activity corresponding to target glycans but not non-target glycans, then these fractions are considered enriched for target glycans and analyzed by NMR.

[0256] To develop this approach, PULs with experimentally defined target specificities are chosen that encode conserved SGBPs. For example, the CS-PUL encodes BT3330 and the levan-PUL encodes BT1761, each exhibiting previously determined in vitro binding affinities for CS and levan, respectively. Accordingly. purified, recombinant over-expressed BT3330 and BT1761 specifically bind to CS and levan, respectively, using affinity-PAGE (FIGS. **7**B-**7**D). Cell lysates prepared from *E. coli* strains over-expressing either BT3330 or BT1761 were individual combined with an equal mixture of CS and levan, incubated, packed into a column, washed extensively, and eluted with histidine. Eluates from both reactions contained the over-expressed SGBP (FIGS. **7**E and **7**F) and were supplied to either the CS- or levan reporter strains. Eluates containing BT3330 elicited significant luminescence increases in P-BT3332 but not P-BT1763 containing strains (FIG. **7**E), and eluates containing BT1761 increased reporter activity from strains harboring P-BT1763 but not P-BT3332 (FIG. **7**F). The elutions were pooled, concentrated, and measured using standard curves from each reporter, which indicated that material recovered from BT3330 contained 205.6 μg/mL CS (FIG. **7**G) but no detectable levan. Conversely, BT1761 eluates contained 244.4 μg/mL of levan (FIG. **7**H) with no detectable CS. These measurements were validated using a total glycosaminoglycans assay kit (Biovision) or fructan assay kit (Megazyme), which indicated we recovered 228.5 μg/mL CS but no levan from BT3330 and 271.5 μg/mL levan but no CS from BT1761 (FIGS. **7**I and **7**J, respectively). Finally, reporters that were differentially activated in response to CS (FIG. **21**F) were no longer significantly increased following the addition of material co-purifying with BT3330 (FIG. **7**K). Collectively, the viability of this approach is demonstrated built upon an incredibly sensitive and specific glycan-detection platform with the ability to rapidly expand the identity of PUL-target glycans.

[0257] This method is optimized by identifying stepwise changes in pH, salt concentrations, incubations times, and flow rates that improve target glycan retention. Finally, common parameters that can facilitate target glycan enrichment from SGBPs from the CS, levan, or heparan PULs are applied to PULs with unknown target glycans present in

PMOGs, a more complex, commercially available biologically-derived glycan mixture (FIG. **21**G) that can be used as a source of PUL-target glycans as demonstrated with BT3330 (FIG. **7**L). First, a glycan isolation assay is implemented with the BT4135-PUL reporter using the validated BT4136-promoted PUL-reporter plasmid (FIG. **20**I). This PUL contains the putative SGBP encoded by BT4133, which will be over-expressed, purified and incubated with a 0.1% PMOG solution. The unbound material (flow-through), wash, and elution fractions are examined using all PUL-reporters significantly activated by PMOGs (FIG. **21**G). Elution fractions that elicit BT4135 PUL-reporter activation, but not non-target reporters are considered enriched for the P-BT4136 activating glycan and are structurally characterized using compositional and NMR analyses of recovered material.

[0258] Concomitant with the development of affinity approaches, sequential UHPLC protocols are implemented to fractionate PMOGs by anion exchange chromatography using DEAE over a step-wise sodium chloride gradient as previously described and subsequently fractionated using reverse phase C-18 as previously described. The resulting material is dialyzed and dried by rotary evaporator, resuspended in water, and supplied to cultured strains harboring selected PUL-reporters that exhibited increased activation upon screening with a complete array.

Affinity purification protocols are developed to simply isolate glycans that activate distinct PUL reporters using SGBPs cloned, over-expressed, and purified from the corresponding PUL. Successful implementation of this approach is demonstrated using SGBPs with known binding affinities (FIG. **7**) and have contemplated implementing similar approaches with unknown glycans present in PMOGs. Therefore, a universal strategy is developed to isolate target glycans of interest from a heterogenous mixture that increases activity from a corresponding PUL-reporter.

A Tunable Glycan Measurement System Using PUL Reporters.

[0259] Measuring the abundance of individual glycans requires expensive, non-renewable reagents that can fail to distinguish between compositionally similar molecules. It has been demonstrated that PUL-sensors elicit dose-dependent increases in target gene transcription in response to their cognate glycan ligands (FIGS. **1**E and **1**G), and this is recapitulated with the corresponding PUL-reporters (FIGS. **18**A-**18**D) even in the presence of additional non-target glycans (FIG. **18**E) across wide linear ranges. Therefore, glycan measurement methods are developed using standard curves derived from the AUC of PUL reporter dose-dependent responses. Additionally, mutant strains are identified and characterized that enhance PUL-reporter sensitivity and narrow target glycan specificity by taking advantage of these system's abilities to distinguish between structurally distinct glycans (FIG. **19**). This example generates a simple and inexpensive approach to measuring unknown target glycan quantities present in heterogenous mixtures.

[0260] Dose-dependent reporter responses to known glycan ligands are examined to define the limits of detection and quantification for each system. A standard set of measurement conditions are optimized that generate consistent results across Bt PUL-reporters specific for 1.) CS/HA, 2.) levan, 3.) arabinan, 4.) α-mannan and 5.) heparan sulfate by measuring the corresponding reporter activity against a standard curve of purified ligand. The supporting monosaccharide identity and abundance, supplement bacterial cultures with additional macronutrients, and determine time for computing AUC is varied to identify conditions that generate the optimal linear range across all 5 reporters. Subsequently, PUL-reporter measurements are compared against lab-generated or biologically derived glycan mixtures using each of the 5 reporters and validate these measurements using commercially available kits designed to measure the corresponding glycans (CS/HA and heparan sulfate: Biovision; levan and arabinan: Megazyme; mannan: Bio-rad). In many cases, measurements may be lower than the limits of detection or quantification of commercial kits.

[0261] It has been demonstrated that a mutation preventing CS-specific PUL-sensor deactivation generates detectable PUL-reporter responses at CS levels below the limits of detection in wild-type Bt (FIG. **19**D). This indicates that blocking the consumption of the PUL-ligand leads to PUL-sensor hyperactivation and increasing the sensitivity of PUL-reporters to their target glycan. The linear range for the CS PUL-reporter had dramatically shifted to linear responsiveness to CS in a Bt mutant defective for PUL-deactivation, reaching as low as 0.000006% CS compared to 0.0001% observed in wild-type Bt (FIG. **19**A). Additional mutants are generated that block PUL-reporters with known glycan specificities and determine 1.) whether the corresponding PUL-reporters exhibit expanded limits of detection, 2.) the increased sensitivity elicits dose-dependent responses, and 3.) these responses can accurately measure unknown target glycan concentrations present in biological mixtures. This is determined using PULs with known target glycans that have commercially available kits to validate measurements: CS using the BT3348-deficient mutant, levan using a mutant defective for the inner membrane fructose transporter encoded by BT1758, and arabinan using a mutant lacking the inner membrane oligo-arabinose transporter, araP.

[0262] PUL-reporters produce glycan measurements resembling those generated using commercially available kits or MS/MS. Furthermore, genetically disrupting PUL-sensor deactivation increases the sensitivity of additional PUL-reporters, reducing their limits of detection and quantification without reducing specificity. Finally, disabling specific enzymatic activities "blinds" *Bacteroides* PUL-sensors to glycan subsets enabling narrower detection specificities relative to wild-type strains while retaining wide linear ranges of quantification.

Outlook

[0263] The fruits of this example are the development and production of a high-throughput tool, that can rapidly surveille samples for a diverse collection of glycans derived from plant, animal, or microbial sources. The detection of an activated PUL-reporter indicates the presence of a known or unknown glycan ligand corresponding to a microbial signal or growth substrate that corresponds to a locus containing glycan binding protein(s). Therefore, activation of PUL-reporters that respond to unknown glycan structures reveals gene products that can aid in glycan isolation using the methods described herein, for downstream functional and structural analyses using existing methodologies. Finally, these PUL-reporters can perform as robust glycan measurement tools that circumvent limitations associated with mea-

suring some glycans using mass spec, NMR, or lectins and that by harnessing defined PUL mutations, further enhancing target sensitivity and refining specificity. The products herein represent an end-to-end pipeline from crudely extracted cellular material to isolating molecules of interest that differentially activated microbial gene expression.

TABLE 4

GT1893, GT1934, and GT3173 Primers and Promoters

strain	plasmid	susC	primer ID	primer sequence	promoter sequence	regu-lator	regu-lator classglycan
GT1893	P-BT1763	BT1763	1150	gctcggtacccggggat cctatcattcagttttctgt tggttactttgagtga (SEQ ID NO: 26)	tatcattcagttttctgttggtt actttgagtgattatatgcttg ttatatgaataatatccctttttt acaaggacttaaattactata caaaggtagtattttctatga ttgagagagaatataatccc gactttcttatgatggagaat tattcttataaaaccctataaa atagcgttctatgcaacatat cttacagcatttgaaacatttt tttcagtcggttgacttaaat caaccgtaatttgcatcatc gaaaagagaaaattcgtact tttaaattaataacattaaact a (SEQ ID NO: 74)	BT1754	HTCS levan
			1304	AAATGCGGGA GTGACTAGTTA GTTTAATGTTA TTAATTTAAAA GTACGAATTTT CTCTTTTCGAT G (SEQ ID NO: 27)			
GT1934	P-BT3332	BT3332	1232	GCTCGGTACCC GGGGATCCAA AATGGAACTG GGCAATGACA GG (SEQ ID NO: 28)	aaaatggaactgggcaatg acaggcatccccagctgta cgatttatccgccgatccat cggagaaaaacaatgtagc gaaacagcatccggaagtt gtcagggagctgtccgaac tgcttgaatcggtaaagaca agataaccaatgagaatag cagatttgtattattttgtatca atcttgaataattctatccata tgagaacaatcaatgcgtat atctttgccatcgtaaattca acaaaatcacttaatttttaat atatgaaaaaacatctatcc aaccagacaagaaaaagg (SEQ ID NO: 75)	BT3334	HTCS chondroitin sulfate / hyaluronan
			1373	AAATGCGGGA GTGACTAGTCC TTTTTCTTGTC TGGTTGGATA GATGTTTTTT (SEQ ID NO: 29)			
GT3173	P-BACOVA_04505	BACOVA_04505	1943	GCTCGGTACCC GGGGATCCttgttt gttggagattgttttcata tcgttg (SEQ ID NO: 72)	ttgtttgttggagattgttttca tatcgttgatttttcagttgac tacaaccagtagttaactcta tttttaagttcttatcacctgc aaaggtaatattttccatactt actggagaatagatattctat aattcttctatttcgaagaata atgtataaaaccctataaaat agcgttctatgcaacaaatg ttatagcctttgaaacatttttt tcagtcgtttgatataaatca accgtaatttgcatcatcgat atagtaaaattcgtacttttaa tttaataacatcaaacta (SEQ ID NO: 76)	BACOVA_04496	HTCS inulin
			1944	AAATGCGGGA GTGACTAGTtag tttgatgttattaaattaaa agtacgaattttac (SEQ ID NO: 73)			

TABLE 5A

Bt Reporter Array Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
1	GT1867	—			empty vector
2	GT4079	BT0029	2445	pBolux-P-BT0028-500-f	AGCTCGGTACCCGGGGATCCaggacgaaaatgtaa ctttgcca (SEQ ID NO: 77)
			2446	pBolux-P-BT0028-500-r	ATGCGGGAGTGACTAGTacttactatttttctcgctgca aaattcca (SEQ ID NO: 78)

TABLE 5A-continued

Bt Reporter Array Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
3	GT4080	BT0140	1106	pLYL-PBT0140_fwd	GCTCGGTACCCGGGGATCCCTTCCAATGATACTGAAGAGAAAATCATTGCTG (SEQ ID NO: 79)
			2447	pBolux-P-BT0140-363-r	ATGCGGGAGTGACTAGTaacattaaatttgaggtttaaaatagtattaaattc (SEQ ID NO: 80)
4	GT3787	BT0190	1108	pLYL-PBT0190_fwd	GCTCGGTACCCGGGGATCCTCTGGAGTCCGTACTTAAATCCATCGA (SEQ ID NO: 81)
			1311	rpiL-PBT0190_rev_new	AAATGCGGGAGTGACTAGTAAATTTGTGCGTTTTAGTAATTGACTAAAGTTATTAAAAACAAG(SEQ ID NO: 82)
5	GT4081	BT0206	2448	pBolux-P-BT0206-700-f	AGCTCGGTACCCGGGGATCCcgtgtggcacggctgcagct (SEQ ID NO: 83)
			1312	rpiL-PBT0206_rev_new	AAATGCGGGAGTGACTAGTCTTTGATACTTGAATTTAAATTAATGAATTGATTTATTTTTACAGATTTATCTAC(SEQ ID NO: 84)
6	GT1873	BT0268	1112	pLYL-PBT0268_fwd	GCTCGGTACCCGGGGATCCGTCTAAGTCTTCTCTTTATAGGAAAATGAAATTAGC (SEQ ID NO: 85)
			1313	rpiL-PBT0268_rev_new	AAATGCGGGAGTGACTAGTACTATTAGATTTATAAAGTTATTTAGACCAAATAAGTATTAGTTGTGC (SEQ ID NO: 86)
7	GT1875	BT0317	1116	pLYL-PBT0317_fwd	GCTCGGTACCCGGGGATCCTTCAATTTCAATAATAACTTTTGTGTGTTAGAGTCCCT (SEQ ID NO: 87)
			1315	rpiL-PBT0317_rev_new	AAATGCGGGAGTGACTAGTAATACTGCTCTTTTAAGGTTAATAAAAATTGTCTGTGTG (SEQ ID NO: 88)
8	GT1876	BT0364	1012	pLYL-PBT0365_fwd	GCTCGGTACCCGGGGATCCTCAATGTGACACCAAGCGCACTG (SEQ ID NO: 89)
			1084	PBT0365-ATGr-SpeI	AAATGCGGGAGTGACTAGTAAGTAGTAACGGCCATTTCCTTGTCTTC (SEQ ID NO: 90)
9	GT4117	BT0439	2449	pBolux-P-BT0439-500-f	AGCTCGGTACCCGGGGATCCaagtggattgacgatgcacg (SEQ ID NO: 91)
			2253	rpiL-BT0439-381-r	ATGCGGGAGTGACTAGTgtttactagtgataataaacagaatgtcgt (SEQ ID NO: 92)
10	GT1878	BT0452	1120	pLYL-PBT0454_fwd	GCTCGGTACCCGGGGATCCAAAATAGGAATTTGCGTCTGATGTACAAAAACG (SEQ ID NO: 93)
			1317	rpiL-PBT0454_rev_new	AAATGCGGGAGTGACTAGTCCCCGAAACTCCGTAATAGACCA (SEQ ID NO: 94)
11	GT1879	BT0483	1122	pLYL-PBT0483_fwd	GCTCGGTACCCGGGGATCCGCTATGGCTACGGATACGGTTACG (SEQ ID NO: 95)
			1318	rpiL-PBT0483_rev_new	AAATGCGGGAGTGACTAGTAATTATCATTTTTTAAGGGATAATACAAATATAACAAAAAAAACGGG (SEQ ID NO: 96)
12	GT3779	BT0754	1124	pLYL-PBT0754_fwd	GCTCGGTACCCGGGGATCCTATTGCCCATCGTCTGGAACGT (SEQ ID NO: 97)
			1319	rpiL-PBT0754_rev_new	AAATGCGGGAGTGACTAGTTTTTATCACTATTAAAGGTTAACATATAGTTATTTATCGTAGCTGC (SEQ ID NO: 98)
13	GT4083	BT0867	2450	pBolux-P-BT0867-700-f	AGCTCGGTACCCGGGGATCCgaatattgcaaaggtaatttttaaaattgtttttccc (SEQ ID NO: 99)
			1320	rpiL-PBT0867_rev_new	AAATGCGGGAGTGACTAGTAATTTTGATTTTAAAATAATAACTAGTTTACCGGTTTTGTTTGT (SEQ ID NO: 100)

TABLE 5A-continued

Bt Reporter Array Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
14	GT3972	BT1029	2394	pLYL-PBT1030_fwd	GCTCGGTACCCGGGGATCCGGTGGATTAC AATGATCTTATCCATTCGTCC (SEQ ID NO: 101)
			1322	rpiL-PBT1030_rev_new	AAATGCGGGAGTGACTAGTAGATTAAATT TTAATTTATATAAAATGATATATTACATCA TCAGACATCTATTCACAT (SEQ ID NO: 102)
15	GT1884	BT1040	1132	pLYL-PBT1040_fwd	GCTCGGTACCCGGGGATCCTGGTGTTTCCT TTAAAACCAAAATGCC (SEQ ID NO: 103)
			1323	rpiL-PBT1040_rev_new	AAATGCGGGAGTGACTAGTTGTGACTTTTA GGGGTTGGGC (SEQ ID NO: 104)
16	GT1885	BT1042	1134	pLYL-PBT1042_fwd	GCTCGGTACCCGGGGATCCTAGTTTTTCAG AACTACTTAATGCTCTATTTATCAAATGAT TATG (SEQ ID NO: 105)
			1324	rpiL-PBT1042_rev_new	AAATGCGGGAGTGACTAGTCTTATTCTTTT TAATTAGAAATAGTTTTTAGGTAGTTAACA AACATGTG (SEQ ID NO: 106)
17	GT4131	BT1119	2455	pBolux-P-BT1119-700f	AGCTCGGTACCCGGGGATCCattaagggggggcta tgctg (SEQ ID NO: 107)
			1325	rpiL-PBT1119_rev_new	AAATGCGGGAGTGACTAGTCTTGATTCGTT AAATCTCTGTAGATTCCCCAG (SEQ ID NO: 108)
18	GT3780	BT1280	1138	pLYL-PBT1280_fwd	GCTCGGTACCCGGGGATCCAGACCAGGCA CCACTATCTGAG (SEQ ID NO: 109)
			1326	rpiL-PBT1280_rev_new	AAATGCGGGAGTGACTAGTTTTCTTAGTAT TAGGTTATTAACTAAATTATTTCACGGTAA TTGAATAG (SEQ ID NO: 110)
19	GT1888	BT1440	1140	pLYL-PBT1440_fwd	GCTCGGTACCCGGGGATCCTCTTAAAAGCG CTTGGTTTGGCC (SEQ ID NO: 111)
			1327	rpiL-PBT1440_rev_new	AAATGCGGGAGTGACTAGTAATTTTGTGGC TTAGGATTTATTTGCTTGTTCTAAC (SEQ ID NO: 112)
20	GT1889	BT1552	1142	pLYL-PBT1551_fwd	GCTCGGTACCCGGGGATCCAAGGGGAAAG TCGAAAGGTGG (SEQ ID NO: 113)
			1328	rpiL-PBT1551_rev_new	AAATGCGGGAGTGACTAGTTAAGTCCTTTT ACTTTTAATTATTATTAAAAACAGCCGCA (114)
21	GT3781	BT1619	1144	pLYL-PBT1619_fwd	GCTCGGTACCCGGGGATCCCATACACATCA TCGTCCCTCCGC (SEQ ID NO: 115)
			1329	rpiL-PBT1619_rev_new	AAATGCGGGAGTGACTAGTACTTTTGTGAG TTAATCATTAATACTAATTTAAGTGTACAC AAC (SEQ ID NO: 116)
22	GT1891	BT1631	1146	pLYL-PBT1632_fwd	GCTCGGTACCCGGGGATCCGGGCGGAAGA GTTTTTAAGAGAGAATATAG (SEQ ID NO: 117)
			1330	rpiL-PBT1632_rev_ncw	AAATGCGGGAGTGACTAGTAAGTTTATTA ATTAAGATTACCTTTTATATAAGTAGCGAA GTCTTTCC (SEQ ID NO: 118)
23	GT4118	BT1683	2456	pBolux-P-BT1683-700f	AGCTCGGTACCCGGGGATCCgtactatgcagagagt tacg (SEQ ID NO: 119)
			1331	rpiL-PBT1683_rev_new	AAATGCGGGAGTGACTAGTTCGTTTTAATT TAAAGTTAATATTAATTTTCCTTTGTTTAGT AAAATACAATT (SEQ ID NO: 120)
24	GT1893	BT1763	1150	pLYL-PBT1763_fwd	Gctcggtacccggggatcctatcattcagttttctgttggttactttgagt ga (SEQ ID NO: 26)
			1304	rpiL-PBT1763_rev_new	AAATGCGGGAGTGACTAGTTAGTTTAATGT TATTAATTTAAAAGTACGAATTTTCTCTTTT CGATG (SEQ ID NO: 27)

TABLE 5A-continued

Bt Reporter Array Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
25	GT4119	BT1774	2457	pBolux-P-BT1775-700f	AGCTCGGTACCCGGGGATCCgcttaattttcgcttaattgattattaa (SEQ ID NO: 121)
			1334	rpiL-PBT1775_rev_new	AAATGCGGGAGTGACTAGTCGTGATTTTCAAATAATTTTTCACGGTCTCTTTTTTATATTATAC (SEQ ID NO: 122)
26	GT3908	BT1875	2346	pBolux-BT1876-300-f	AGCTCGGTACCCGGGGATCCtggaacgtgaacttgaaaac (SEQ ID NO: 123)
			2347	rpiL-BT1876-300-r	ATGCGGGAGTGACTAGTatttatgctttctataaaggagac (SEQ ID NO: 124)
27	GT1898	BT2107	1160	pLYL-PBT2107_fwd	GCTCGGTACCCGGGGATCCTGTAATCTATCTAATTTTATGTTCGTTTCATAAATTTAAAACCATACA (SEQ ID NO: 125)
			1337	rpiL-PBT2107_rev_new	AAATGCGGGAGTGACTAGTACTCTGTGATTTTAAAAAGTAAGTCATAAGGGTTTTATATTAGA (SEQ ID NO: 126)
28	GT3783	BT2172	2262	pBolux-BT2170-300-f	AGCTCGGTACCCGGGGATCCcgaccggcttccggaacgtt (SEQ ID NO: 127)
			2263	rpiL-BT2170-300-r	ATGCGGGAGTGACTAGTcattcaatctttttagtgattaatcggt (SEQ ID NO: 128)
29	GT3782	BT2196	2260	pBolux-BT2197-300-f	AGCTCGGTACCCGGGGATCCttgcttataaatctattcgtctgacag (SEQ ID NO: 129)
			2261	rpiL-BT2197-300-r	ATGCGGGAGTGACTAGTattgcgcgcttttaataagaagacac (SEQ ID NO: 130)
30	GT3878	BT2202	2266	pBolux-BT2203-M-37-f	AGCTCGGTACCCGGGGATCCgctggcactggcctatggta (SEQ ID NO: 131)
			2267	rpiL-BT2203-M-37-r	ATGCGGGAGTGACTAGTacglattaggititttaaataaaacaataagtaaataac (SEQ ID NO: 132)
31	GT1901	BT2260	1166	pLYL-PBT2260_fwd	GCTCGGTACCCGGGGATCCAATAAAAGCGCCTCTTATAGCATGATACTATTTTTTGT (SEQ ID NO: 133)
			1340	rpiL-PBT2260_rev_new	AAATGCGGGAGTGACTAGTACCAATATACGAAATCTGCAAAGTCTTTGC (SEQ ID NO: 134)
32	GT1902	BT2264	1168	pLYL-PBT2264_fwd	GCTCGGTACCCGGGGATCCGGTGGTGAGAAATATTCGGGAAATATAAAAATAGTATCC (SEQ ID NO: 135)
			1341	rpiL-PBT2264_rev_new	AAATGCGGGAGTGACTAGTACCGATGTACGAAATTTGCAAAGTCTTTG (SEQ ID NO: 136)
33	GT1904	BT2362	1172	pLYL-PBT2362_fwd	GCTCGGTACCCGGGGATCCAAAGATAGTAAAAATCAACCCATTCCGATTCAAAG (SEQ ID NO: 137)
			1343	rpiL-PBT2362_rev_new	AAATGCGGGAGTGACTAGTGTTTTTTGTTTAATTGTATGTTCACTAATTGGTTTTTGAATAGT (SEQ ID NO: 138)
34	GT1905	BT2364	1174	pLYL-PBT2364_fwd	GCTCGGTACCCGGGGATCCCTACGACCTTTACCGCTACCATTATCAAC (SEQ ID NO: 139)
			1344	rpiL-PBT2364_rev_new	AAATGCGGGAGTGACTAGTACTTTTATATTTAAAAATACATTTGCTATAAAGTCGATACAAAGGA (SEQ ID NO: 140)
35	GT1906	BT2393	1176	pLYL-PBT2392_fwd	GCTCGGTACCCGGGGATCCGCAAATGATAAAAAAGCAATTTTGAATGAAAAGATATACATG (SEQ ID NO: 141)
			1345	rpiL-PBT2392_rev_new	AAATGCGGGAGTGACTAGTGTTTTTCTATAAGATTTTATTAGTTTGAAAAAAGGTCTTTTAGGC (SEQ ID NO: 142)

TABLE 5A-continued

Bt Reporter Array Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
36	GT3911	BT2461	2348	pBolux-BT2462-300-f	AGCTCGGTACCCGGGGATCCttgcaatcattacctga acaaacct (SEQ ID NO: 143)
			2349	rpiL-BT2462-300-r	ATGCGGGAGTGACTAGTctttttatcgttttcatttatataa cgattc (SEQ ID NO: 144)
37	GT4137	BT2531	2458	pBolux-P-BT2529-700f	AGCTCGGTACCCGGGGATCCgaaacgccagacga atcagg (SEQ ID NO: 145)
			2351	rpiL-BT2529-300-r	ATGCGGGAGTGACTAGTcaatactttttaattttcatttct tttgc (SEQ ID NO: 146)
38	GT2372	BT2560	1638	pLYL-PBT2561_fwd	GCTCGGTACCCGGGGATCCAAGTGCAGGA GCATGAGCT (SEQ ID NO: 147)
			1639	rpiL-PBT2561_rev_	AAATGCGGGAGTGACTAGTAGTATTAAAA ATTAAGACTATGCAAATGAAAGCAA (SEQ ID NO: 148)
39	GT1910	BT2626	1184	pLYL-PBT2627_fwd	GCTCGGTACCCGGGGATCCAGATAGATATT GGGAGTGCATATGTTTGTTTTTAC (SEQ ID NO: 149)
			1349	rpiL-PBT2627_rev_new	AAATGCGGGAGTGACTAGTTTCTATATTCT TTATATTTGATTAGTTTCTATTATATGATTA AACAGCGGATATC (SEQ ID NO: 150)
40	GT2375	BT2805	1642	pLYL-PBT2803_fwd	GCTCGGTACCCGGGGATCCTATGAAAGTC AGCTTTTACGCCTCTTTG (SEQ ID NO: 151)
			1643	rpiL-PBT2803_rev_new	AAATGCGGGAGTGACTAGTGCATAGTTTTC TACATTAATAATTGGTTTATATAATCTCAA AAATGATATCTTATA (SEQ ID NO: 152)
41	GT1912	BT2818, BT2820	1188	pLYL-PBT2818_fwd	GCTCGGTACCCGGGGATCCTGTTCCTTACA AAGCCTCCTTTTCCA (SEQ ID NO: 153)
			1351	rpiL-PBT2818_rev_new	AAATGCGGGAGTGACTAGTACTGTTTAATT TGATAGGTTAATAATATATTTAGTTTATAG TTAGGTCAAC (SEQ ID NO: 154)
42	GT4138	BT2859	2459	pBolux-P-BT2859-700f	AGCTCGGTACCCGGGGATCCactacctcaaaacgc agatc (SEQ ID NO: 155)
			1352	rpiL-PBT2859_rev_new	AAATGCGGGAGTGACTAGTGTATCAGAAT TTTAAATTAGTATTAGAGTTCACATTTAAG GATAAATCA (SEQ ID NO: 156)
43	GT4122	BT2894	2460	pBolux-P-BT2896-700f	AGCTCGGTACCCGGGGATCCgttctaacttttaccgc aaac (SEQ ID NO: 157)
			1353	rpiL-PBT2896_rev_new	AAATGCGGGAGTGACTAGTTTTCTTTATTA TTTTGGTTAAACATTTATATCATGATCCTTA TAAAAGG (SEQ ID NO: 158)
44	GT1915	BT2905	1194	pLYL-PBT2907_fwd	GCTCGGTACCCGGGGATCCTGTGGACATTG GTACGGACG (SEQ ID NO: 159)
			1354	rpiL-PBT2907_rev_new	AAATGCGGGAGTGACTAGTAATATTATAG TATTTAGTTATCACTTAAAAATTTAGTTATT ATCTTATTGTTGATTATTC (SEQ ID NO: 160)
45	BT4123	BT2906	2461	pBolux-P-BT2909-700f	AGCTCGGTACCCGGGGATCCccgggcgaatggca caccta (SEQ ID NO: 161)
			2462	pBolux-P-BT2909r	ATGCGGGAGTGACTAGTagcattattcatttttaattatg atac (SEQ ID NO: 162)
46	GT1917	BT2920	1411	pLYL-PBT2922_fwd_new	GCTCGGTACCCGGGGATCCGTACATGCAG GATCTATATCCCCG (SEQ ID NO: 163)
			1356	rpiL-PBT2922_rev_new	AAATGCGGGAGTGACTAGTATATAATTAG ATTATTGTTTCGACTGATTGACGCAGA (SEQ ID NO: 164)
47	GT1918	BT2952	1200	pLYL-PBT2952_fwd	GCTCGGTACCCGGGGATCCCTTCGGAATTG CTAACACCTACG (SEQ ID NO: 165)
			1357	rpiL-PBT2952_rev_new	AAATGCGGGAGTGACTAGTAAGTTAGACT TTTTGAATAACATAATAATTAAGTCAATAT AAATAGTTAAGTATAGT (SEQ ID NO: 166)

TABLE 5A-continued

Bt Reporter Array Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
48	GT3975	BT2952	2399	pBolux-BT2956-300-f	AGCTCGGTACCCGGGGATCCaatgtaaggacaagt cctgagaagag (SEQ ID NO: 167)
			2400	rpiL-BT2956-300-r	ATGCGGGAGTGACTAGTgatatgattcttttagtattagc tgatggg (SEQ ID NO: 168)
49	GT1919	BT2968	1202	pLYL-PBT2968_fwd	GCTCGGTACCCGGGGATCCGATGTGCACTA TGTCTTGGCTGATG (SEQ ID NO: 169)
			1358	rpiL-PBT2968_rev_new	AAATGCGGGAGTGACTAGTAAATTATTAG ATTAGTTAATGATAAATACTTGTTTTCCAT TTAAAAGAGATTC (SEQ ID NO: 170)
50	GT2365	BT3012	1629	pLYL-PBT3011_fwd	GCTCGGTACCCGGGGATCCACAATCGGCT AAAGTCATAAACCTGAC (SEQ ID NO: 171)
			1630	rpiL-PBT3011_rev_	AAATGCGGGAGTGACTAGTCTTTTTTATAA TATTAATGAGTTCTATTGAATTCACGTC (SEQ ID NO: 172)
51	GT4124	BT3024	2463	pBolux-P-BT3024-700f	AGCTCGGTACCCGGGGATCCaaaaacaatgcaaga aatggaaac (SEQ ID NO: 173)
			1360	rpiL-PBT3024_rev_new	AAATGCGGGAGTGACTAGTAATTTATTGTA TTAGATTATAAACTCTATTCAATTGTTGAT TGATCCA (SEQ ID NO: 174)
52	GT1922	BT3046	1208	pLYL-PBT3047_fwd	GCTCGGTACCCGGGGATCCAGTTGTGTTTC TTGCAGCCAAC (SEQ ID NO: 175)
			1361	rpiL.PBT3047_rev_new	AAATGCGGGAGTGACTAGTAACGTTTTTCT TTTTACATATTAAATTATTGGTTCACTAAA AATTC (SEQ ID NO: 176)
53	GT1923	BT3090	1210	pLYL-PBT3090_fwd	GCTCGGTACCCGGGGATCCGCTACTCTGTG ACCACTATTTATAATTACCGG (SEQ ID NO: 177)
			1362	rpiL-PBT3090_rev_new	AAATGCGGGAGTGACTAGTGTACATCAAT TTAAAGTTAATATTAGGATTACTTTTTGTTT TCACTG (SEQ ID NO: 178)
54	GT1924	BT3103	1212	pLYL-PBT3108_fwd	GCTCGGTACCCGGGGATCCTAATGTAGCTG GCAGACATCCG (SEQ ID NO: 179)
			1363	rpiL-PBT3108_rev_new	AAATGCGGGAGTGACTAGTATGATTCTAA AAAGTTAAACGTTATTTATGTATGATTGTG ATGC (SEQ ID NO: 180)
55	GT1925	BT3156	1214	pLYL-PBT3156_fwd	GCTCGGTACCCGGGGATCCACAAAAAAAC ATTCATTCCTAAAATAAAGGATGATGGAC (SEQ ID NO: 181)
			1364	rpiL PBT3156_rev_new	AAATGCGGGAGTGACTAGTGGATAATTTA AAATTAATATTAGGTTAATACATTTCAGGC AACTAGATC (SEQ ID NO: 182)
56	GT1926	BT3174	1216	pLYL-PBT3174_fwd	GCTCGGTACCCGGGGATCCCTGCAAAACG TCCTGTTTCTAAAAAATG (SEQ ID NO: 183)
			1365	rpiL-PBT3174_rev_new	AAATGCGGGAGTGACTAGTCTGTTTCCTTT TTTTCATAATACTACATTTAATAATAAAGA TTCATACT (SEQ ID NO: 184)
57	GT1927	BT3239	1412	pLYL-PBT3239_fwd_new	GCTCGGTACCCGGGGATCCAAGGAAGTGT TTAGATGACATAATGATTATTTGAACAG (SEQ ID NO: 185)
			1413	pLYL-PBT3239_rev_new	AAATGCGGGAGTGACTAGTCGTTGTACCTT TCACTAATACGGATGC (SEQ ID NO: 186)
58	GT1928	BT3240	1220	pLYL-PBT3240_fwd	GCTCGGTACCCGGGGATCCCCTGTCACCTT TTTAGGTGTTTGG (SEQ ID NO: 187)
			1414	pLYL-PBT3240_rev_new	AAATGCGGGAGTGACTAGTATTCTCCTATA ACCTATTTTCATACTAATTATTTATATCTAA TAT (SEQ ID NO: 188)

TABLE 5A-continued

Bt Reporter Array Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
59	GT1929	BT3271	1222	pLYL-PBT3270_fwd	GCTCGGTACCCGGGGATCCTCCTTGCTTTT GTGGGGGTG (SEQ ID NO: 189)
			1368	rpiL-PBT3270_rev_new	AAATGCGGGAGTGACTAGTAATTTTATCTA TTTCTAATGAGGATTTTATCTTTGCTTTACT ATAATTATAC (SEQ ID NO: 190)
60	GT1930	BT3279	1224	pLYL-PBT3278_fwd	GCTCGGTACCCGGGGATCCTCTCTTGAAAC TGTGAAGACTCAAAAGAAG (SEQ ID NO: 191)
			1369	rpiL-PBT3278_rev_new	AAATGCGGGAGTGACTAGTATTATTTCAGG TTATTTATAGCAAAGACGACTAAGAAG (SEQ ID NO: 192)
61	GT3977	BT3297	2403	pBolux-BT3299-300-f	AGCTCGGTACCCGGGGATCCatattcctgaaagccg gagaatcc (SEQ ID NO: 193)
			2404	rpiL-BT3299-300-r	ATGCGGGAGTGACTAGTgacgctatgtgtaatttttacct tgtgtg (SEQ ID NO: 194)
62	GT1933	BT3310	1230	pLYL-PBT3310_fwd	GCTCGGTACCCGGGGATCCGAATACAATTT ATAATTATCGGGCGAAAGTAAAAAACAAA GC (SEQ ID NO: 195)
			1372	rpiL-PBT3310_rev_new	AAATGCGGGAGTGACTAGTGCGTATTAATT TTAAAGTTTATAATTAAGGTATGTGCTTGA CAG (SEQ ID NO: 196)
63	GT1934	BT3332	1232	pLYL-PBT3332_fwd	GCTCGGTACCCGGGGATCCAAAATGGAAC TGGGCAATGACAGG (SEQ ID NO: 28)
			1373	rpiL-PBT3332_rev_new	AAATGCGGGAGTGACTAGTCCTTTTTCTTG TCTGGTTGGATAGATGTTTTTT (SEQ ID NO: 29)
64	GT1935	BT3346	1234	pLYL-PBT3347_fwd	GCTCGGTACCCGGGGATCCACATTTCTCCC TTGAAGGGC (SEQ ID NO: 197)
			1374	rpiL-PBT3347_rev_new	AAATGCGGGAGTGACTAGTAAATATAAAT AATAAAATGGTTAAAGTGCATCCGAACAA TAAATATTATTGC (SEQ ID NO: 198)
65	GT1936	BT3475	1236	pLYL-PBT3477_fwd	GCTCGGTACCCGGGGATCCAAAGTTAGAA GTCATCAATTAATAGACCTTCATTTTGG (SEQ ID NO: 199)
			1377	rpiL-PBT3492_rev_new	AAATGCGGGAGTGACTAGTGATTTTGTTTT TTTTCATACGTAAAAAATTAATGATTAATA AAATATTATATTGTTGG (SEQ ID NO: 201)
66	GT1938	BT3494	1240	pLYL-PBT3492_fwd	GCTCGGTACCCGGGGATCCGTTTGTAGATC CTCTTTATAAATACATCAATGAAACT (SEQ ID NO: 200)
			1377	rpiL-PBT3492_rev_new	AAATGCGGGAGTGACTAGTGATTTTGTTTT TTTTCATACGTAAAAAATTAATGATTAATA AAATATTATATTGTTGG (SEQ ID NO: 201)
67	GT1939	BT3505	1242	pLYL-PBT3504_fwd	GCTCGGTACCCGGGGATCCCCATTGGACTC CCGCAAAGA (SEQ ID NO: 202)
			1378	rpiL-PBT3504_rev_new	AAATGCGGGAGTGACTAGTTTTACATTTCA TGTTTTTCATTCTAGTTAATAATAAATGTAT AGTTAATTAAAC (SEQ ID NO: 203)
68	GT3784	BT3519	1254	pLYL-PBT3519_fwd	GCTCGGTACCCGGGGATCCGAATAAATGT CGAATTTGACTCAGCGCTAAG (SEQ ID NO: 204)
			1384	rpiL PBT3519_rev_new	AAATGCGGGAGTGACTAGTAATATTATTAT TTTATAACTTAATACTTACAGGCATATGAG CCCC (SEQ ID NO: 205)
69	GT1940	BT3569	1244	pLYL-PBT3569_fwd	GCTCGGTACCCGGGGATCCGTCTGCCTGAT GTAAAAGAGTAGTTGCA (SEQ ID NO: 206)
			1379	rpiL-PBT3569_rev_new	AAATGCGGGAGTGACTAGTTCGTTACTATT TAGGTTGAAGTTTATTCTGCCG (SEQ ID NO: 207)

TABLE 5A-continued

Bt Reporter Array Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
70	GT1941	BT3604	1246	pLYL-PBT3607_fwd	GCTCGGTACCCGGGGATCCAATGTCGCGAT GAGCAACAG (SEQ ID NO: 208)
			1380	rpiL-PBT3607_rev_new	AAATGCGGGAGTGACTAGTAGTTTACTTTT TTTAGTTTCTACTCTTTTTAGTATATATTTA ACCTATTG (SEQ ID NO: 209)
71	GT1946	BT3680	1256	pLYL-PBT3679_fwd	GCTCGGTACCCGGGGATCCCGTAAAGGGA ACTATAGTGCATCTTGC (SEQ ID NO: 210)
			1385	rpiL-PBT3679_rev_new	AAATGCGGGAGTGACTAGTAGCAAAAATA TTTAAGATATTAGTAAATAAAAAATTAACC GTTCATTAATTGA (SEQ ID NO: 211)
72	GT1942	BT3670	1248	pLYL-PBT3668_fwd	GCTCGGTACCCGGGGATCCATTTTTCCAGT TCCAATCGGCATTATG (SEQ ID NO: 212)
			1381	rpiL-PBT3668_rev_new	AAATGCGGGAGTGACTAGTAAATATTCCT ATTAGATTATATACCGCAAATGTAACAAC (SEQ ID NO: 213)
73	GT4084	BT3702	2451	pBolux-P-BT3703-300-f	AGCTCGGTACCCGGGGATCCtacttcctgcctcatct gctttc (SEQ ID NO: 214
			2452	pBolux-P-BT3703-300-r	ATGCGGGAGTGACTAGTctatttatggtattaaattataa gctaac (SEQ ID NO: 215)
74	GT3970	BT3750	2392	pBolux-BT3749-300-f	AGCTCGGTACCCGGGGATCCatcgtctggatggaaa atctcataaag (SEQ ID NO: 216)
			2387	rpiL-BT3749-300-r	ATGCGGGAGTGACTAGTattataagttgagttactttata agtaataaacag (SEQ ID NO: 217)
75	GT1944	BT3854	1252	pLYL-PBT3854_fwd	GCTCGGTACCCGGGGATCCATCGGTGGCG GAGCCTGTCC (SEQ ID NO: 218)
			1383	rpiL-PBT3854_rev_new	AAATGCGGGAGTGACTAGTAACAGAATCC AAAGAAAGGATGCTCCC (SEQ ID NO: 219)
76	GT4140	BT3952	2467	pBolux-P-BT3952-700f	AGCTCGGTACCCGGGGATCCttatatggaagacctg gaagg (SEQ ID NO: 220)
			1386	rpiL-PBT3952_rev_new	AAATGCGGGAGTGACTAGTACTACTTGTTT TTAATTAATAATAATAAGGTTACCAAATAC GTTTAATACG (SEQ ID NO: 221)
77	GT3971	BT3958	2393	pBolux-BT3958-500-f	GCTCGGTACCCGGGGATCCagaggaactatagtgctt cttgcg (SEQ ID NO: 222)
			1387	rpiL-PBT3958_rev_new	AAATGCGGGAGTGACTAGTGTTACTTTGTT TTTTTTAATTAATACTAAGGTTATCAATCG CCT (SEQ ID NO: 223)
78	GT1949	BT3983	1262	pLYL-PBT3983_fwd	GCTCGGTACCCGGGGATCCATATTTGACTC CGGATTATTTTCGCTGGT (SEQ ID NO: 224)
			1388	rpiL-PBT3983_rev_new	AAATGCGGGAGTGACTAGTTAGTTTTTATA TAAATATTAGAATCGATATTCCATTTATTA TTTTCGATTCACA (SEQ ID NO: 225)
79	GT4128	BT4039	2468	pBolux-P-BT4040-700f	AGCTCGGTACCCGGGGATCCagaatataacaaccttt atcacg (SEQ ID NO: 226)
			1389	rpiL-PBT4040_rev_new	AAATGCGGGAGTGACTAGTAAATTAATAT TAGTTTTATTAAAGGTAAAAAGGGTAAAA ACAAGTTGAAG (SEQ ID NO: 227)
80	GT4141	BT4081	2469	pBolux-P-BT4080-700f	AGCTCGGTACCCGGGGATCCctattatcagaagalg gagtga (SEQ ID NO: 228)
			1390	rpiL-PBT4080_rev_new	AAATGCGGGAGTGACTAGTAGAAAATACC GTTTTTAAGAATTTATATAATAATAATGAT CATAATTTTACTTTCG (SEQ ID NO: 229)

TABLE 5A-continued

Bt Reporter Array Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
81	GT1952	BT4088 & 90	1268	pLYL-PBT4085_fwd	GCTCGGTACCCGGGGATCCATTTTCCGGGT AGTGCTGACTTT (SEQ ID NO: 230)
			1391	rpiL-PBT4085_rev_new	AAATGCGGGAGTGACTAGTTATTATTAGTT CTTTTTAATATGTGTACTATTTTATTGTTAT TTATCTAATGACGA (SEQ ID NO: 231)
82	GT1953	BT4114	1270	pLYL-PBT4114_fwd	GCTCGGTACCCGGGGATCCTTGAGTAAAG AATACACCAATCTGGAGGTATATCT (SEQ ID NO: 232)
			1392	rpiL-PBT4114_rev_new	AAATGCGGGAGTGACTAGTCTTTTGTTCTT TTATATTAGATTATTAATATTCGAGTGTGT CCAC (SEQ ID NO: 233)
83	GT1954	BT4121	1272	pLYL-PBT4119_fwd	GCTCGGTACCCGGGGATCCAATTGAGTGTC CATCAGGCG (SEQ ID NO: 234)
			1393	rpiL-PBT4119_rev_new	AAATGCGGGAGTGACTAGTCATTTCAATTT AAAGTTAATACATATTACTATCTAATCAAT ACTTATGTTACATGC (SEQ ID NO: 235)
84	GT2134	BT4135	1274	pLYL-PBT4135_fwd	GCTCGGTACCCGGGGATCCAGTACCTACCA ATGGAGAATTCAGC (SEQ ID NO: 236)
			1394	rpiL-PBT4135_rev_new	AAATGCGGGAGTGACTAGTACCATACAAA CAAAACAGGATTAATATTTGTAGTATTCTT C (SEQ ID NO: 237)
85	GT1956	BT4164	1276	pLYL-PBT4163_fwd	GCTCGGTACCCGGGGATCCACAATTATATT TGAAAAGTTTGCCATATTGCTTTTATATAT GG (SEQ ID NO: 238)
			1395	rpiL-PBT4163_rev_new	AAATGCGGGAGTGACTAGTCTTGTCCTCAC AAGAGAGAAAAAAAGG (SEQ ID NO: 239)
86	GT1957	BT4247	1278	pLYL-PBT4247_fwd	GCTCGGTACCCGGGGATCCGAATGTTATGG ATATCAATTGGAAGGACGGA (SEQ ID NO: 240)
			1396	rpiL-PBT4247_rev_new	AAATGCGGGAGTGACTAGTGATTTAACTTG TTGTGAGGTTAAATATTGGGTTAATTATTA GA (SEQ ID NO: 241)
87	GT1959	BT4267	1282	pLYL-PBT4266_fwd	GCTCGGTACCCGGGGATCCCTGGAATTTTT TTTATGTAATATACCCTTTACTTCTTATTAC GG (SEQ ID NO: 242)
			1398	rpiL-PBT4266_rev_new	AAATGCGGGAGTGACTAGTTGTTTTTCTGT GATTAAAGGTTAATAATTAGTTGGGTTAAT ATG (SEQ ID NO: 243)
88	GT1960	BT4298	1284	pLYL-PBT4299_fwd	GCTCGGTACCCGGGGATCCTGGAGAGCAA TAGAGACCTTATGC (SEQ ID NO: 244)
			1399	rpiL-PBT4299_rev_new	AAATGCGGGAGTGACTAGTTGTTTTTCTGT GATAAAAGGTTAATAATTAGATTGGTTAA AAAAAAGTG (SEQ ID NO: 245)
89	GT3785	BT4357	2274	pBolux-BT4356-300-f	AGCTCGGTACCCGGGGATCCagaagggagtcttgc actatttc (SEQ ID NO: 246)
			2275	rpiL-BT4356-300-r	ATGCGGGAGTGACTAGTcccttattccaccttttttattata tgacaag (SEQ ID NO: 247)
90	GT2850	BT4404	1751	pLYL-PBT4403_f500	GCTCGGTACCCGGGGATCCGGAAGTTGAT GCTGAAGATGTT (SEQ ID NO: 248)
			1752	pLYL-PBT4403_r	AAATGCGGGAGTGACTAGTCATTAATTTCT TCCTTTATACACTAAATAC (SEQ ID NO: 249)
91	GT1963	BT4470	1290	pLYL-PBT4470_fwd	GCTCGGTACCCGGGGATCCTCTTTGTCTCC GAAAAACAAGAGTCCG (SEQ ID NO: 250)
			1402	rpiL-PBT4470_rev_new	AAATGCGGGAGTGACTAGTTTCAATAAGTT GTTTTTCACCATCTCCGTGC (SEQ ID NO: 251)

TABLE 5A-continued

Bt Reporter Array_Primers

Construct	Bt strain	SusC	Primer number	Primer name	Sequence
92	GT2367	BT4634	1631	pLYL-PBT4635_fwd	GCTCGGTACCCGGGGATCCTAAAGCCAAA AAGAAACTTACTGTACCTC (SEQ ID NO: 252)
			1632	rpiL-PBT4635_rev_	AAATGCGGGAGTGACTAGTTTTCAATGTTG ATTTATCTTAGGACAATCTCAA (SEQ ID NO: 253)
93	GT1965	BT4660	1294	pLYL-PBT4662_fwd	GCTCGGTACCCGGGGATCCTTTTTTTCTTCT TTTATTGAATGATGACGGATTTTAAAATCA TC (SEQ ID NO: 254)
			1404	rpiL-PBT4662_rev_new	AAATGCGGGAGTGACTAGTACTTTATTAGG TTTTATAATTATTAAAAGTGTTATTTTACTG TTGC (SEQ ID NO: 255)
94	GT1966	BT4671	1296	pLYL-PBT4672_fwd	GCTCGGTACCCGGGGATCCTGTCTCCCGTG GAATATATCAAGTCC (SEQ ID NO: 256)
			1405	rpiL-PBT4672_rev_new	AAATGCGGGAGTGACTAGTGCTATCAAAT TTAGTGGTTTGTTGATAGCG (SEQ ID NO: 257)
95	GT3786	BT4707	1298	pLYL-PBT4707_fwd	GCTCGGTACCCGGGGATCCCAGGCAGATG ATACATTCACAAAGAAAAAGAT (SEQ ID NO: 258)
			1406	rpiL-PBT4707_rev_new	AAATGCGGGAGTGACTAGTAACTAAAGGT AGTTTTAGATTTAAAGCATATTTAGGATAT AATGCA (SEQ ID NO: 259)
96	GT3879	BT4724	1300	pLYL-PBT4724_fwd	GCTCGGTACCCGGGGATCCACTTCCTAAAG AATACTTTACGGGAACGATTC (SEQ ID NO: 260)
			1407	rpiL-PBT4724_rev_new	AAATGCGGGAGTGACTAGTATATCAAAAC TTTTAAGTTGTTTGACAGGTATACCGA (SEQ ID NO: 261)

TABLE 5B

Bt Reporter Array_Promoters

Construct	Promoter	Promoter sequence	Linked Regulator
1	—	—	
2	BT0028	Aggacgaaaatgtaactttgccataacaaaaaactttatgtctaa agatatagaaactttggataataacaaagcccgggcttgcgaagt ctgggctttgcgcataaaaaagggtgtgccaacgttgaagtgcac ctcaaaagttagataaaaaactttggggtcatttcacatttgac acaatctctttcttttcaactttcttatacttttatgaccaaaga gaaagaaaaagattatgtgcgtttgaatatgttaaaatatgaccc gatttgtcacgtttaggtggtatttctttttgtcgaactaggaa ttttgtttttgcgacctacagattttccatttcctgttttcagac tgcaaatttacgaataatccatattttatttctatatatgtaat aataacaaattaaagaatttaataattccttaatattcccgaaag aaatgtgaaataaaatatatggaattttgcagcgagaaaaaatag taagt (SEQ ID NO: 280)	no linked regulator
3	BT0140	Cttccaatgatactgaagagaaaatcattgctgatgatttgatgg cgatggaacggacacggttggcagccatgcccgaacagcgacggc tgatctatacgttaaatcgttttgaggataaatcttctccggaga tagcctccgaattagaattgagttgccgtacagtggaaaaccatc tttttctcggacgccgtgatatgcgtgacttcttccgaaactgta tataaaattattcatataataaacaacctttggtgcttatggaaa aggaatcaatactgagtgagaggtatctttatgcctcaacaaatt ttagagaacaagaatttaatactatttttaaacctcaaatttaat gtt (SEQ ID NO: 281)	BT0139

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
4	BT0189 (300)	Tctggagtccgtacttaaatccatcgaatttatcagtgatatcaa ttataagaaagaaggcaggaatatacttctttataaaaaatgaga attaaaaaatagatcaatgtttaacccgttaataaggacagaatg aaagcatcaccctcatagaaactccctaaaaagatagaagcactc ctaaggaatgcttctatccgcaacccggacggatattcattcgct tcgacccaaatgaataacgtatcgcacgttgcttgtttttaataa ctttagtcaattactaaaacgcacaaattt (SEQ ID NO: 282)	BT0188_89
5	BT0206	Cgtgtggcacggctgcagctacttttacgaatccgtagttcatct tgtacctttttatatatagtgggtacaaaaataggaaatagtttt ggatttttgccctttttgactctgaatcctcaaaatgaggtgtctt atgtcgttttaatgactattgcataagcaactaataagaatgtca aatggaaagtaatatggtcttatttttgacggtttatatgggata tatctatttgtttattaatattttgttaattatgcaataaaaaga catttgaggaaatttggtataaaaaatgagactttttgtttttc tatttaactattataattatatttgtagccaaattaaagaatttt ataggcaatttacacctaaacaaacgataagcacttattaatatc tataattttagagagatggacatacactttattagtattgcagcg acacaagacatttatttagacatatggcgtaatattaaaaatcag ccaagctaatttccctattctatatattgtatagactatttgata gtctgtcctggaacgatgataaaagtatacttttcaaagtcgctc caaggggagaagtatattactgtttcatgcgtgaagcgtaatatg ctaagttttcgttttgtagataaatctgtaaaaataaatcaattc attaatttaaattcaagtatcaaag (SEQ ID NO: 283)	no linked regulator
6	BT0268	Gtctaagtcttctctttataggaaaatgaaattagcaacaggact gtcacccattgagtttattcgaaatataagattaaaacatggaag tcaattattgaaggataaatcaatatccgtagcagaggtagctta tgaatgcggattttctaatcctaaatattttgcaacctgttttaa agaagaatttggcgtaactccaaaggaatatcaaaaatcttgtta ggataaaaataatatgaacttaaaatacacaagtacgcgtcttaa tggaagatgcgtacttttccatatatcaatgatctatcccatttg aatgattcctgaacttatattgaacgatttttagacctgttatag ttaatagcgattatggtccaattttggaagtttttgaatgattag agaacttctttctactggataactcgcacttttgtgacgcatttg atgcacaactaatacttatttggtctaaataactttataaatcta atagt (SEQ ID NO: 284)	BT_0267
7	BT0317	Ttcaatttcaataataacttttgtgtgttagagtccctggaatgc tgagtgtctacagcagttccagggatttctttattatcttttcat ttaatgccaaagaaggttcattctgttttgaatattgtaattttg ttagccgatataattattctttttgtttaaagaaaaaaaactact tattttcttgttatttaaaataaattcatatttttgtaatcgtag tcagaaccaaactatgaaatattgacgtcctctctacacacagac aatttttattaaccttaaaagagcagtatt (SEQ ID NO: 285)	BT0326? BT4338 binds upstream of BT0317 in No C
8	BT0365	Tcaatgtgacaccaagcgcactgctgaataacgaagaataactga tataagggttgctattatgaaacaatgatagcagcccttcgtctt aaaatgagctcattttaagagacatccgtccaagattatactcaa agtgtaaaaaagacacttatataaccgtttatccacctcgaaaat tcatttgtccacctttaatatactcatcggttgtatttttgcgac actacaacgagtagaattattgttgaaccattaatatcaatatct atgaagacaaggaaatggccgttactactt (SEQ ID NO: 286)	BT0366
9	BT0439	Ttcattatccggccagaagtttgatgaaaaacaattttatcaatc aattactgacttcgaatatgagtggacattatccaaagagcacca tcctataatttctggagagaacccgatattgttggccaagacatt atctgagaaatatatgcaatatttttattaagtacatacctcaaa ataattataaattataaaacaaaacagcctatgaatataataccg aacttataattaaggaaattatcaaatctaaagaagaaaaaaata cagaattacttaactttaaattattaatgt (SEQ ID NO: 287)	BT0433?
10	BT0454	Aaaataggaatttgcgtctgatgtacaaaaacggtgtctgaagct ttcacaaagatagagcaccctaacaagagaataagggtaaataaa taatgatttcttttcataaatgggggtattagttaatttaacgaa ggcaaagataagattttctctgcatatatttaacagtcaaagcga	no linked regulator

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
		caaacttgcgtttttttaccaagttctcgtaggactagtcaacact ctgaccaccgttcttgctcttgtgatcattgacagggtcggccgc aagcaactggtctattacggagtttcgggg (SEQ ID NO: 288)	
11	BT0483	Gctatggctacggatacggttacggacaggaaaaaggtgctaaat cgtaatccggttctaagaataaacctgagaataaacgatagcccg tttcaatctgattgaccacagtatatcccccaagatatagtcagt cagatatagccgaccgcttgattttccccaatcaagcggtttgtt gtattcatctacgttgacaatataatttttatatcccatatcaaa gaaaagcgggtatccggacaaccagatgcccgtttttttttgttat atttgtattatcccttaaaaaatgataatt (SEQ ID NO: 289)	no linked regulator
12	BT0753	Tattgcccatcgtctggaacgtaaattccaggtgaagatcagcat agaaagcgaacgtctgaaggccgaacacttctccggttctttcga cagcaatcagaatatttatgatatattacacgaaatcaacgttga gaaacaatacacgtggaaagtcagtggtgacaccatctttattac cgataaaagaaagggggtaagataaaaggaaggagaaagaaaatg gacacagccgatagatataccggcagtccgcagctacgataaata actatatgttaacctttaatagtgataaaa (SEQ ID NO: 290)	BT0752/ 53
13	BT0867	Ttgatgctttttttaaaagttatttcttcgtttaccctatctttt ccttttataattctgataaagtaatatttcaggaggtatttgaaa ttaatatgtactcataatactcatcccaccaagttctccatgaac ttataccgccttagagtttactaaattctatatttcacaacctaa tttttaatcaaaaatcaacacacaatcaatgcctatggaaatatt acagtattatgatttaccatccctatcgtttacaaacaaaaccgg taaactagttattattttaaaatcaaaatt (SEQ ID NO: 291)	no linked regulator
14	BT1030 (700)	Ggtggattacaatgatcttatccattcgtcctttatatgaatcgg ttaaagtggaagttaaaacgatgtgaagatgtggagaagaacgat gattggaatataaaatatttaaaagaaaattttcaacaataatgg ggaggggaattatgatatagtttaataaaactaagagaaaaaact tcagattctattttttattctttttaagagattacgattctttta gttgtatctttttatttatgtgaatagatgtctgatgatgtaata tatcattttatataaattaaaatttaatct (SEQ ID NO: 292)	no linked regulator
15	BT1040	Tggtgtttcctttaaaaccaaaatgccgttccttttaaaccaacg actgctccgttcgtatattttaaagctctttcatagaattgaaga tggcatttttatgcactaagcaattgttttatgcaaacacatcgc ataatcttgcaataaattatacatttttttgctatttattagatt tcatagactttgactacctggctattcttaaaaatagaacataaa gaagtatgaaaacagctataaattcattactcccaatcaatcacg cttgccaacgcccaacccctaaaagtcaca (SEQ ID NO: 293)	no linked regulator
16	BT1042	Tagtttttcagaactacttaatgctctatttatcaaatgattatg tatttatttttcaaaaaaatgcttagtctaaccatttttttacgaa aaaaaatcttattttcgtttagtatggttgcagtatcaaatgtat tactgatgaataagcgcttatgaaaaatcatttttagtgtaacct ttaaatttataaatatgagaaacagagatacatagatcctttgta tgagtggcggttatatttattacccgcacatgtttgttaactacc taaaaactatttctaattaaaaagaataag (SEQ ID NO: 294)	no linked regulator
17	BT1119	Acaaaaggagataaatgaccagatatataacagtagtattacatt aaggtaaagaacaaccatggtatagtattattgcaatttaactat ttaaagtttgtttataatcaaatcatttaaagatttttgtccttc tatgatttttttgtgtttgataaatgtcgtaattaaataaaaaata tcacgcataatgactttttctttttttctaaatttcttcaaatgac aaattattgttacctttgtaatgtaatgtagttaatggttgcgct tataaagtccttggaaaggatttatgtataaaagaggtagatgtt tactctgttcttgtttggattatcagcatcactgatatgaaataa caaaaaaaatatacaatggctaagcggacggacaggcagggaaat agtacagattcccaatccccctctttataatacattgcgtataag atttattaactgtctggtctggggaatctacagagatttaacgaa tcaag (SEQ ID NO: 295)	no linked regulator

TABLE 5B-continued

Bt_Reporter_Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
18	BT1279	Agaccaggcaccactatctgaggtaatggatgtgatagtaaatgt agtaggtcaaatgaactataagataaaaggagaccgctgctactt aatcccaaagtaatgggtatcatcccaaaagaaaaacagtaaaaa aacaacaatataataacctttttaaccactaaagattcatgcaaa aaagtatccggaacggagccctaactctatcccggatatgaaatc aagattctcaatattagagttttactctattcaattaccgtgaaa taatttagttaataacctaatactaagaaa (SEQ ID NO: 296)	BT1278/ 79
19	BT1440	Tcttaaaagcgcttggtttggccggtatcacagaatcagtttgca gactatcgctcataagggtatctctcctttcagcctgggcctgta aggagagtgacagaaacagaaaaagagatagaacaatttgcttca tcctgtgatttttcgttgttatgattgatgctgttcgtttcacga atgtactacctttcgttgatttatactaataatcgtctaaaaaaa tgtttcgtttcctaaacaaatgagatatgtattctgttagttaga acaagcaaataaatcctaagccacaaaatt (SEQ ID NO: 297)	no linked regulator
20	BT1551	Aaggggaaagtcgaaaggtggcacaaaggcagcctgctttttttc ctgtgcataccccctccacgcaacaggccaataataaagcagcaat atatcttttcattatcttcttcactttttactcctgcaaatgta cattattccaactagattacgaaatatccgggaagaatgatagca gatgaacctagttaataattccttttattattatattcgcaacta aactgtaatcattatattattaatattattacttttgcggctgtt tttaataataattaaaagtaaaaggactta (SEQ ID NO: 298)	no linked regulator
21	BT1618	Catacacatcatcgtccctccgcatctggctaccaccgatgtata taccatcaagttcaaacaaaaagcccctatcaaggagatcatgaa tatcgtgaccaaaaccataggaaacatagactataaagtcgaaga cgagaacattctcttaatttattcacccctaaataagaaaggagg ccgatagacagaaaaaagggagtcgatatttcgcggataccaact cccccaaatcaaaattacttcatttaaattagttgtgtacactta aattagtattaatgattaactcacaaaagt (SEQ ID NO: 299)	BT1617/ 18
22	BT1632	Gggcggaagagtttttaagagagaatatagtatcatgagtatatt cgggtaattagagttaatgaaaggcggagatattcggaaacggat attgccgcctttctttttttgtctcgaaagttgtctgataatgtc tgttgacctcgaaaaatgcgataaaatggactattttagacattt ttggaagaatcatagccaaaatcgaacatcttaaatcttagatat aacctaaatttgtggcagtgaatgtcaggaaagacttcgctactt atataaaaggtaatcttaattaataaactt (SEQ ID NO: 300)	BT1635
23	BT1683	Gtactatgcagagagttacggacacgcagccagttgaccggaaaa aagtcgttctttcggaagaaacggtaaccgaacatggaattatcc agattgcggaattcaataagaatgcaggtgcgtgatgcttcttgt gtgagatgctccagcatttcaccgaaaatttcttcctccttctct ttacttgccggtagagaagtgtccagaaattcacctgcaccatat accacacattgtttgacaagagaggagggaagccacttttttggtc ttgcgtatggcggcaagcaggcgtgctacaggtctgccttcttct gttgccactatcagtagcggggtatatcccggagtcgattcatag atctgaaacaactccttggaatgaaaagtattggttcccggtaaa tcaggaatgtcttttccgcgataatatgttgttagtttaagtggc atccaaatacaaatttacactttttattcttcattcaacaataaa aaagagaatttgttggcttagcctaaaatttgtctttttatcctt tgcatatatttgaggaaaaaaaggcttggaaaagcgaatttttgt attattgtcgtcctttgtgagtacagaagtaaaatggaaacgtct atataaaagattatgctaattgtattttactaaacaaaggaaaat taatattaactttaaattaaaacga (SEQ ID NO: 301)	no linked regulator
24	BT1763	Tatcattcagttttctgttggttactttgagtgattatatgcttg ttatatgaataatatccctttttacaaggacttaaattactatac aaaggtagtattttctatgattgagagagaatataatcccgactt tcttatgatggagaattattcttataaaaccctataaaatagcgt tctatgcaacatatcttacagcatttgaaacatttttttcagtcg gttgacttaaatcaaccgtaatttgcatcatcgaaaagagaaaat tcgtacttttaaattaataacattaaacta (SEQ ID NO: 74)	BT1754

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
25	BT1775	Gcttaattttcgcttaattgattattaaatatcccttaaatgtag aatttatgcaaataagtatgctgaagaggggataaaagttagctg tagttataaatattcctgttattccttattatataggaaacttat attatatgagaaatagggaatagtacaacttaaagcttatatcat ggggagcgctttgaaaatctatcaggaataacgccattgtaatac taaaaatccacatcttatataatcggataagtcactaattggata tctcctaatttgtgttatgtttgtatagtatttgccttatttacc tttttagcctttctacttgaaatattcttctttttgcaggaagtg aatactcatttagataaagaaatagggtgtggacagcatactaca ggatataaaacttcccccttttcctgaaattaatacctaagattg cgaaaaattataagaagatagtattagttttaaaattaattagaa attaatcagagtttaatcgtattttataaaaaatcttaagcaggc tcttgttactttgcatcagaactcaaaaataaccttaaatattaa gtttgttcagtcgacgctttcttaaataatagataaaaagggtgt tttcgaggtgtaacaaatagcaaatgtataatataaaaaagagac cgtgaaaaattatttgaaaatcacg (SEQ ID NO: 302)	no linked regulator
26	BT1876	Tggaacgtgaacttgaaaacgaaatatataaggctatcgataaat tgccggacgaatgccgtcgggtttttgctaaaagtcgctttgaag gaaaatcatacgaagaaatttccggtgaactgggaatatctatta atacagttaagtatcatataaagaatgctttagcttctttacacg ctcatttgagtaagtacctgatttctctattactattttttttca ggtaaagcgaaaaaaaatcattttctgactacccttaattaaaaa acaactgtctcctttatagaaagcataaat (SEQ ID NO: 303)	BT1877/ 76
27	BT2107	Tgtaatctatctaattttatgttcgtttcataaatttaaaaccat acacacaaagccgcattaacatttattctcaaaacaaccattcat atataaatttatattaaataaataaatctttctagttttcctgct ttaaatatatatatttgcaatatgtatatacatatagacattata taatacatatatcataagcaattaatactatgtagattaaaatat acagcctttatatacaagaaatcacattaaatctaatataaaacc cttatgacttacttttttaaaatcacagagt (SEQ ID NO: 304)	BT2103 or BT2104
28	BT2170	Cgaccggcttccggaacgttgccgggaaatattcatccgtatccg tgaagaaaaacaaagttatgcccaagtagcagaagaattggatat cagcataaagacagttgatgcccagctacagaaagctgtctcccg actgaaagagatgatttcgtccagcggataaccggagatcacccg aaccgttcagcacttctttttatattaacttttatttgcacaaa aggcgtagggagtttctgtcaatctccggtctttatcagcaaata aaccgattaatcactaaaaaagattgaatg (SEQ ID NO: 305)	BT2169/ 71
29	BT2197	Ttgcttataaatctattcgtctgacagttgttgaactttcgtctg acagttgttgaactttcgtctaacaactgtcagacgaaagttcaa caactgtcagacgattaaatttaagtataatgaatactaaatctg tgtacatcaagaattaaatcttagagtaaatccgaacagattagt tcgtttcaaaacagttcttagcttaaacttattggattttacttc ccttccttgatttttttcattttcctttggtggtaaatgtaagt tgctgtgtcttcttattaaaagcgcgcaat (SEQ ID NO: 306)	BT2198/ 2197
30	BT2203	Gctggcactggcctatggtatgcatgcccttaaccatacaggttc gtcacaagaagcaattctgcaatattccctgtttgtgcgtgagta caagcaaatgatgaatgaagaatattctacttcttatgcagagct gatgagcaaaaatcctccttttcatcgataaaaacatatcggtta atgatatttattcgcttattaatccgttattaacccatcactaat aagttgtttaaccttgctacattatgtttgcagcgatgttattta cttattgttttatttaaaaacctaatacgt (SEQ ID NO: 307)	BT2204
31	BT2260	Aataaaagcgcctcttatagcatgatactatttttgtttataat agctccttgttttatagatataatattgattataagataaatagt tttcatttcggtagagaagtggtattacataaaagagagtaaaac attagctgaattagggtaattaactgtcaaatagatatataagct atttctgcttgataaaatatcgactggtgttactgatttatcccc tatatacctaactgattatcagttatatataaatccattagttct gcaaagactttgcagatttcgtatattggt (SEQ ID NO: 308)	no linked regulator

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
32	BT2264	Ggtggtgagaaatattcgggaaatataaaaatagtatccaataat aatacctcatataaataaaataaagacataactttcttataatga atgaactaaatgattgaaatggatagaaacagggtatcattcgtt aaagaaaagggtagttataatgctgataaataattgattatcacg tttatatatggatacaataacatatatgacgattaggtttatatt tctcattattataataatcaacactttatataaagaattagttct gcaaagactttgcaaatttcgtacatcggt (SEQ ID NO: 309)	no linked regulator
33	BT2362	Aaagatagtaaaaatcaacccattccgattcaaagtcaactttat ttttttcaatccacaacgctctatgcctatttttgtccaatcag tctaaataaactgatattgatagtggcgccacatcaaatacatac actcagagattgaccgtcaattcacggtacaatcgcagttttaac caataaaatctaatagcctatggagtaaatcaaatcggtataatc ggaacatagatttaaatcattcagagatttaactattcaaaaacc aattagtgaacatacaattaaacaaaaaac (SEQ ID NO: 310)	unknown
34	BT2364	Ctacgacctttaccgctaccattatcaacggcagtgagtatcaga atccgggatattaaattgtaagacctatatacccaatcattatcg gtacgataatccatatagccacgctatttatcgtaccaatgattg gggatattttccacacctttccacatttttccacacctccccaat aatatcgtttttttcaactctgctgttaatctgtatcttatcctt tcagcatttctttatatcctattggtatatcctttgtatcgactt tatagcaaatgtatttttaaatataaaagt (SEQ ID NO: 311)	unknown
35	BT2392	Gcaaatgataaaaaaagcaattttgaatgaaaagatatacatgga tgaataaaagcatatgctcctgattccttgaaataccctaagttt gtatcctgaaaaccgaacggaaagtgtgcttcacaattatatata gccatttacacctttgaatctataatatttaaaacaattaatcac atgagagaaaaagccaaaagcccttaagtcaaattgaaatcaatt agaatctattaaaccttatttaaatagaaagcctaaaagaccttt tttcaaactaataaaatcttatagaaaaac (SEQ ID NO: 312)	BT2391
36	BT2462	Ttgcaatcattacctgaacaaacctcccgtatatttactctcagc cgatttggaaataaaacaaatcgggaaattgcctgcgaattaaat atttcaatcaaagatgtggaatatcatatatccaaatcacttaag gctcttagaaaaacgctaaaagattacctgcctttattttatttc tttttttaccatatgtaacaccgattactacgcacgttcctttat cttttgaaaaaaatattctttttcgtttagggtaaaccgaagatg aatcgttatataaatgaaaacgataaaaag (SEQ ID NO: 313)	BT2463/ 2462
37	BT2529	Gaaacgccagacgaatcaggactttaccgaaaagcaatacgagca catccacttcatgatgaagctgaccgatgatgccctcgcacaaat gattgtggtggtagagaaaccggaacaccaaagcattgatatcaa caagtctttcaacatcgaaaacgaaatcaataactaccgtaacca actgaaaaatcagaatattctggatgtcaacaacaaggaatatga ttatcagatgggagtctattatatggatattatcgccgaatgtga gaaactgggcgactatgtagtgaatgtggtagaagccagcagtga tgtaaaagagaagaaagcctcttaaataaagaggaactcaatcaa agaaatggatagccaatttatgcgttgcagcataaaattgactat ccatttctttttatttccacacagacaaaacaactcatgtccgt ttacaaggacactcacactttacaaagacgttacatttttttacag acgttacgattacatttcttttccgtgaagttcccgttaagcttt tactgcgcctattgcaggtctttttttgcatatacatttgcgcc aaaatacacaggggcctatgtttagtaccattttccaatgaccgg acaaaggcattccaaaagaaaaccaaatctctaatttaaagcaaa agaaatgaaaattaaaaaagtattg (SEQ ID NO: 314)	no linked regulator
38	BT2561	Aagtgcaggagcatgagctaatccagtatgaatcccgttccatca cccgaagtctatcttcgcccaaagagcagacttttaaaacagaac gtatcattttatggtttctgaataaaagaaatattcccatcctga aaaaagacagagaagcattttgggaaaagttgtctcctgagattc atgaattatataataataaatatgaaagtcagcttttacgcctct ttgactttacggcgtggatggaatccaaaattcggaaagaaaaac tgtctgaagtcctcagagcacgtgctagcgcaaaagaatgttaaa gagtaaggtgtttgattcgtatttcagacgataaaaacactcttt	BT2561/ 62

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
		tcaaatctccattttctctttgtaattatataaattcgcttcaca ttacctctatattctctcctctatacaaggaaaatccaatataag atatcatttttgagattatataaaccaattattaatgtagaaaac tatgcatgattattgctttcatttgcatagtcttaatttttaata ct (SEQ ID NO: 315)	
39	BT2627	Agatagatattgggagtgcatatgtttgtttttacaagatgataa agtgtattatagcgacaatatagtaaatatttgtgccaagagaaa gagactgattaaatattctgagggaatggaagtttgaaaacttac atttgcatataattgacttgtgatttttattattagaatagttat tatttgttatacttttaaattaaaatgcttatgaatattatagaa agacatccaccatgattaatgatatccgctgtttaatcatataat agaaactaatcaaatataaagaatatagaa (SEQ ID NO: 316)	BT2628/ BT3786
40	BT2803	Tatgaaagtcagcttttacgcctctttgactttacggcgtggatg gaatccaaaattcggaaagaaaaactgtctgaagtcctcagagca cgtgctagcgcaaaagaatgttaaagagtaaggtgtttgattcgt atttcagacgataaaaacactcttttcaaatctccattttctctt tgtaattatataaattcgcttcacattacctctatattctctcct ctatacaaggaaaatccaatataagatatcatttttgagattata taaaccaattattaatgtagaaaactatgc (SEQ ID NO: 317)	BT2802 (rusR)
41	BT2818	Tgttccttacaaagcctccttttccattccgtctataattttgta tcaaggtctacccatttgttacagatagtgtttctagctatttgt gcacctaatttggtgaatattgcacgtccatttttcacatcaccc ctaattttgcatcatcattaaaagataaatgaagttaaccttatt gcacataagcaaaggatatatttagaaactgaagagagaataaag agaataaaagtcacccccaacccggttgacctaactataaactaa atatattattaacctatcaaattaaacagt (SEQ ID NO: 318)	BT2826
42	BT2859	Actacctcaaaacgcagatcgtatccttgctgtataaccgtcaga aagaacgcgaagcattctccaagcgtccgttcttcccgacgaata agatgcagatgaataaggtggatgaagagtttatgaataaagtga ttcgtaccatcgaggaaaatatcatagataccaatctgaacgtag agcatcttgccgagattctgggcatgagtcgttccagtctgctgc ggaaaataaagatgctttccaatctgtctcctgggacttcatccg tttaatccgattgaggaaggctgccgaactgattcatgaaggtaa atacctgattggagatatctgctttatggtaggtatcaactcacc gtcctatttcagcaagcttttcctgaaacagtttggcatgacacc taaagatttcgagaaacaaagtcaggcagacaaagaaaagataga catgccttcgtgaccgtccgggtgcactataacaaatgatgcaca aaaatgaaacatctgcggaaaatatgcttcagatgtagtctggtg ctgcaaaaatggtatttttgcagtgattttattataccgccta tatatatactcctacttttgccatcgttccggataaggaaagata accccttcggtgaacggattgatttatccttaaatgtgaactct aatactaatttaaaattctgatac (SEQ ID NO: 319)	BT2860
43	BT2896	Gttctaacttttaccgcaaactgaaaggagtattggatatgagtc cgaatgagtatcttcgtttgatacgtttaaagaaagctgcccagc ttctgaaagatggaagatatgggattgtagaaatttcttatatgg taggattcaattcaccttcttatttctcaaactgttttaagaaac aatttggagtgttaccaaaagatttcatgcaatgaacaaattctt ataaaattgctctaaaactgattctgactatctctgcactgtttt ttggatagaatttaataatatcaggttaatttcttatatccttttt caggtaggttccgataactttgcgaatgtctcgaaggtaggaact tattttctgaccagtctatttggttgggaaaaaactttcttctag atcaattaatatagaagtaacggataaataccagattagaaactg gctttataagctattaattattattaatcaatatctaatttttcg cgcgaatatgattttgtatgtattgtttggtagatagggagaaga gttgatacataaataaggaattggcaggtattagtttttttataa aactcttcttccacttttcttcgctgaagtatataatccttaaat aatacgatttatgaacaaattccttttataaggatcatgatataa atgtttaaccaaaataataaagaaa (SEQ ID NO: 320)	BT2897

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
44	BT2907	Tgtggacattggtacggacgagcgttatccagttatggcttactt caaggattgacaggagtccgatatgatgctgtagataaaacactg tatattaattcaaaaataggagactttattagctttatcagtacg gagtctggatttggtaatatagaacttcgttccggaaaacctttt gtaaaagtagtatccggtcatatagaggttgacagatttgtcgta tcggggaaagtagttgaataatcaacaataagataataactaaat ttttaagtgataactaaatactataatatt (SEQ ID NO: 321)	BT2910
45	BT2909	Ccgggcgaatggcacacctattatcctaattatcaaacaggttgg agtcattattggatcggcttttgcggtccggaagttgatagctgg atgacgaatgagtattgttcgaaagaaagtcctgtatttaaggtc ggtatcaatgatgagatcgtttctttattcagaaaagctattgat gttgctaacgaagaacctactttatatcaacgcgtattgagtgga ttggtgacctatctggtagcactaatgtgtagtatcgataagaac cttcaggtagagaatgatgatttctcttctaaaatagattatgct tgtgtgctcatgaaggaattgatagatcaaccagtttctatgcaa gagattgccaaaaaagcaggtatgggatattctctttttcgaaag ttgtttaaggaacagaagaattatgcacctgtgcaatatttccag aatctgaaaatacagaaagccatagagttgttgactactactact attccggtaaaagagatagcatataggctcgattttgaatccccg gcttatttctctgcccggttcaagaaacaaacaggaaaatcacct atagaatatcgagaagaatttcgtatcaaataatgatagtgttct ggcaattatcgaaagtctttctcttttaagatgactaagtttgta tcataattaaaaaatgaataatgct (SEQ ID NO: 322)	BT2910
46	BT2922	Gtacatgcaggatctatatccccgttgcattgcgcatatatacac aatgtacagggcatatagatcctgcatattgcatatatatagctt atctgcctctttttattgcaatattttatgtgcttttatgtggt atatgaaacaattatctcattcctgtttcatttggtatagatttg ctattctttcttctatttgagacattattgcgatttattgggata tttatattacccaaaaactatctcatccgctaattttgtctgcgt caatcagtcgaaacaataatctaattatat (SEQ ID NO: 323)	BT2923
47	BT2952	Cttcggaattgctaacacctacgggactaaagttacttacaggta cagtaattattcttgccggaatcattttctttgcgatagcagggc acaacagagatagcaaaagccgccagacgcactctgaaacaccta ttaagaaaaatttcaggaaagggttaattatctgtttgcttgcag gaatattcggacctatgattaactttgctttcgtttatggggcac ccttacaagaaaaggctgtagcaacgggagcatcttctctttatg cagccaacgtgatatggagtatcgctttgagtgccggatttatta ttaatctccttgaatgtatccgtttgttcggcaagaatcaatctt ggaaaacttaccgacatcgtacaaccggaggcctgataatggctt ctctggcaggggtattatggtatctgagcattatgttctatggta tgggaggcagttttatgggagttttaggagcttctgtgggctggg ctaccatgcaatcgacagctattattgcaggtaatgtggccggac ttgcttccggcgagtggaaaggagctacccgctatgccatccgga tgatggtgataggattggtatgtctcatcggaggagtggtggtga ttgccctctaacgactatacttaactatttatattgacttaatta ttatgttattcaaaaagtctaactt (SEQ ID NO: 324)	no linked regulator (BT2957 maybe?)
48	BT2956	Aatgtaaggacaagtcctgagaagaggttatattcactcttgcaa tatgaaacttttcatttgcactcagaaaataggatagcttaaaaa cggaatctctcatattctttttgatttgattgcaatattaagag ttagccttcacaaacacaacccgtgaagactctttttatatgtc aaagcataaaaagtcggaatagcgtaaaaaaactaccgctatgaa taatttctatcggaaaaacgtatatggacaacctctacctttgtc cccatcagctaatactaaaagaatcatatc (SEQ ID NO: 325)	no linked regulator (BT2957 maybe?)
49	BT2968	Gatgtgcactatgtcttggctgatgtaaccttggaacaaggtaag aatacaattaaaaccgttgcaacatataatggaaaagaatacact gacgagattgaatggaactataccggcgaaaagaagcgaagtgcc gattggagtgaaaacaaagaagagcacgcaggttggtaatcggag acgtttctgtatgtaatctgaaaaatgttgaatctaaaatataaa agcctatgaatgaaatgagaaagaatctcttttaaatggaaaaca agtatttatcattaactaatctaataattt (SEQ ID NO: 326)	BT2971

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
50	BT3011	Atcaacgagtatgactggcgctcaagtaaatatcgctttaccaac aagccattacaggaattcatcgattttatcaaccgttcataccat gtaaacatcataattaaagaagaaaagctcaaagagctgaagttt aacggaactatacgtaaagacgagccgcttaccaatatcatcgaa aagatatgtatcagcctcgatttaaaagaaaaacaagaaaataac aacatcatattatattaatacataagaatcaattatcaatatatt cactattaacctttagaaacatgaaaaac (SEQ ID NO: 327)	BT3012/ 11
51	BT3024	Aaaaacaatgcaagaaatggaaactgctttcatcatatccggcaa gaatattaagaaaggactccggtttgacgatgtaagcatgatgca atacgatgtggcgtccactatcgcccgcatctttcatttagaaca accacaagtttggataggtagacccatggagattgttttcaaata atcattcaggatgattaataggatgggaaaaggagaagctaaaat aactggcttctcctttttatttatctatccacgctcataagata ggagattataaatactatttcttataagtaacaaaatgagcagtc ataatagttttatttcctataagtaatagaaatcacacctccaca gctgttaattaccgaataatacttgcatcaacatacatatcctta taccttttgtcccccggtaacacaacataatataacttcaatcata aaatgtactcttttgacattcttaataagcaatccaactgattaa agcagcattcaaacattctgataggacatcttatcttttgtttat tcaaattaaaatacaatacgatagaattgtattagtaaatgataa aatactacttgtctgacggagcattatcgcctacttttgcatcat cagttattggttgaagtttccatggatcaatcaacaattgaatag agtttataatctaatacaataaatt (SEQ ID NO: 328)	no linked regulator
52	BT3047	Agttgtgtttcttgcagccaacgtgtgtaaatcgtttatgaatga ttctctacgtttttgaatgatttttataatgtaaaatctacact cattcgtatctttgctgtagataacaacgaaataaactaatatta tgaaaatgaaaactaatataatctttaaaaaactaaagtcattcg tcaatcgatgtctttttcctgattatatgtgctgttttatcttcc tgcgtttataacgctgatatgccaataaagaatttttagtgaacc aataatttaatatgtaaaaagaaaaacgtt (SEQ ID NO: 329)	maybe BT3048?
53	BT3090	Gctactctgtgaccactatttataattaccggacacgtgtccgca acaaggcactcggcgaacgggatgagtttgaggctaaagtaatga aaatagggaaggtggaagagtaagaaatccactactttttagca cggtcgctattctataatattcttattattagtgttttatgctgt tttgtactgtataaaccactatatttttgctatctggcaaaagaa gcgcatttaattgtggatacttttgtttcagtgaaaacaaaaagt aatcctaatattaactttaaattgatgtac (SEQ ID NO: 330)	BT3091
54	BT3108	Taatgtagctggcagacatccggaactgcttgagcggttaaagca ggaatttttgtgcaaacagatggattttatcgtagtgaggtgga agaagaaccattaaaataagcccgataaccccttctggaaagcat ttgattgattaggtattagattgttttgcaggaattggtgtagaa ggatagtttctgaacatgtgtgctcataataaaacatattttcta tcgtctacacctttttctttactttgctgcatcacaatcata cataaataacgtttaactttttagaatcat (SEQ ID NO: 331)	BT3097?
55	BT3156	Acaaaaaaacattcattcctaaaataaaggatgatggactaattt atatatccatgaataaaggagataatcttaccataatcatcccctt aataacaattttgcagtaaatgcgttatttttgctgcgtttata cactattaaaataacacatttacctaattttgactcgttgaattt agaaaattatcacattaaatctaataatatatgaaacgaattcga gatttccccaccactgacaagacaacgatctagttgcctgaaatg tattaacctaatattaattttaaattatcc (SEQ ID NO: 332)	BT3154
56	BT3174	Ctgcaaaacgtcctgtttctaaaaaatgcgggtttttgcctaaaa aacagtttgtttgtcactgcacgggaagtgaatcaccatctattg gcatttgtttttgatcacttctctatcaataatgatcatttagcg gattgcacagggttcttttgatcattattgaattttaattgatga tttttgaatgtttccttttatgctgtggttgtatttttgtcgaag attgaaacttattgttagctagtgaaagtatgaatctttattatt aaatgtagtattatgaaaaaaaggaaacag (SEQ ID NO: 333)	BT3172

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
57	BT3239	AAGGAAGTGTTTAGATGACATAATGATTATTTGAACAGGGCTAAA TTTGCACATACTGACATAAATGTGACATTATGATAGTTTGATGAT ATATATTTATCTTCATAACTATCATAATGTATTTACAATAGTTTT CAAATTTATTTTGAATAATTGTTTTGTATTTATAAATATGTGCTT ATATTTGCAAAATAGCACTAAGCGAAAATAAGCGACTTACTAATT CTTATAATAATAAAGAGTGTTTATGAAAAGAAAATTAATGCTGTT ATTGGCCTGCTTGCTGGCAAGCATAGGTCTAGTGATTGCCCAAAC ACCTAAAAAGGTGACAGGTGTCGTCATTTCTGAGGAAGATGATCA GCCTGTTGTGGGAGCATCCGTATTAGTGAAAGGTACAACG (SEQ ID NO: 334)	no linked regulator
58	BT3240	CCTGTCACCTTTTTAGGTGTTTGGGCAATCACTAGACCTATGCTT GCCAGCAAGCAGGCCAATAACAGCATTAATTTTCTTTTCATAAAC ACTCTTTATTATTATAAGAATTAGTAAGTCGCTTATTTTCGCTTA GTGCTATTTTGCAAATATAAGCACATATTTATAAATACAAAACAA TTATTCAAAATAAATTTGAAAACTATTGTAAATACATTATGATAG TTATGAAGATAAATATATATCATCAAACTATCATAATGTCACATT TATGTCAGTATGTGCAAATTTAGCCCTGTTCAAATAATCATTATG TCATCTAAACACTTCCTTTTTATCTTTAACTAAGCCTTGAATAAT ATAAAAATTATATTAGATATAAATAATTAGTATGAAAATAGGTTA TAGGAGAAT (SEQ ID NO: 335)	no linked regulator
59	BT3270	Tccttgcttttgtgggggtgaagtgactgtgatgtggcttattta agtggatgagccgttatgtttaacaggtaaacaaagcttggttag catttttagtaagctatatgtgttcgttccatgtctgtgtcttat tgcattgtatatcaattagctaagtccgaaagtgacggatgatga taaaatatgagtttcaaactccttagtaaaagctaaaaaatacat cattttaatagcggcaacgaaaaaaaacaaatatttttaagatg cctaattgtcatttattgatggctgaattttgattctgaaaaggg aatgatttgttaaatatgtcatttttgttgctgaataatgtcata atgatagtttttcattcttttccgttttcgtacggagagtatctc ataaaaaaataatcatctttttgtcacccatttatggacgttatgt ataattatagtaaagcaaagataaaatcctcattagaaatagata aaatt (SEQ ID NO: 336)	BT3269/ 3270
60	BT3278	Tctcttgaaactgtgaagactcaaaagaagagagcaatgtccttc cttagaaaaaaattaggctcctatcattttctattattacaaatg ttacttccctaaaaagaagcataacactcaatccgctttacttgt taacacctgtttgcaatgaacaaaatgttcgttgtttttcttgat tattgtacaaaaagaacggtcttctaaataaataaagtatctttt gaataaaaaaacttcagaatcctgtccctcatttttcttcttag tcgtctttgctataaataacctgaaataat (SEQ ID NO: 337)	BT3277/ 3278
61	BT3299	Atattcctgaaagccggagaatccacaactgtcaagatgacatta cctaaagaatcatttatgtattttgatgtcaacagaactcagttc gtcactgatccgggtatttacaatataatgcttggcttctcctct agagatattaaagcacaaaaaaatattcaatatacactatagatt gcataatcaataagtaacatgaaatatatttgtatcaaaactgta gcaatttacttgctcgcaaccttacctttattggcgaacgcctca acacacaaggtaaaaattacacatagcgtc (SEQ ID NO: 338)	BT3302
62	BT3310	Gaatacaatttataattatcgggcgaaagtaaaaaacaaagctcg tggttccagagaagatttcgaagatttagttcggaaaatacgttg atcgatgttgtaacctatccactttttaggcctctttggttgata ttaacttgctgtttattagtggtttgtatgtttgtataatccact tattataccctcattgtcaaatcacttcagtttctttatactttt gacctgtgcttctgaaatagtggcgaaagtcctgtcaagcacata ccttaattataaactttaaaattaatacgc (SEQ ID NO: 339)	BT3309
63	BT3332	Aaaatggaactgggcaatgacaggcatccccagctgtacgattta tccgccgatccatcggagaaaaacaatgtagcgaaacagcatccg gaagttgtcagggagctgtccgaactgcttgaatcggtaaagaca agataaccaatgagaatagcagatttgtattattttgtatcaatc ttgaataattctatccatatgagaacaatcaatgcgtatatcttt gccatcgtaaattcaacaaaatcacttaatttttaatatatgaaa	BT3334

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
		aaacatctatccaaccagacaagaaaaagg (SEQ ID NO: 75)	
64	BT3347	Acatttctcccttgaagggcatatttgcacagatattccccaaaa gcctgcttaattatttaatgtaattgaaaatgtaattataataat ctgactaatatataatatattctggtcatttcaaaaaaaaggcat tctaactcttctacatttttattatatttatttgtaattaaccga ttgattgttaattataattatcatcatcacacctacataaagtta tgcaaactaaataagaaattacttatttagttagctttgccatgt cttttctcagtcaaactcttcgttgatgagaatcagacatatata gatatttgtacttaaatctacaacatattatgagcacaacatgcc aacatcaacaaggtgaaggatacctaaaactcctaaagatttaga tacatattatgcttataataagaaagataggcaaacgttgtaagc aataatatttattgttcggatgcactttaaccattttattattta tattt (SEQ ID NO: 340)	no linked regulator
65	BT3477	Aaagttagaagtcatcaattaatagaccttcattttgggttggta aggataaaatctgctcaaaaaaggataaatactgctcaaacaacg tcagagcccctattccgtatgttaaaagaacgtttgaaatccaaa aaagaatagattttgtcctttcttgaacacagatttccttgttt cttttattaattccattattttgtgtcatcaagatgagatactat ggaaaataaagagtttgttaaagctcgatatttgctagaaataca cgatttgttagccgcttctccataacatttcatcctaaatatgac agtactgatattatatattaaaggtataggaaaacgggtataaag attgcaattattcaaaggtgagatagtattaaggtaaaaagtgga tttaaaagaatacttagggcttgtttttttatgaggtaaataaga ttgatggatggataaccttggatttgaagattaatttaaagcaaa tattt (SEQ ID NO: 341)	BT3465??
66	BT3492	Gtttgtagatcctctttataaatacatcaatgaaactacttcacg tgtgcctatcagtgactggcatgataccaaaactggcagaatgac cggatttaaggcacgttccgtaattggaggatattggatacaagt gttaatggataagatgaatcattaaaaatatggacaataagttga aagaatactttttcgcatggatgaatcatttcagcataatacaac aagagataagtaatgaaccaacaatataatattttattaatcatt aatttttacgtatgaaaaaaaacaaaatc (SEQ ID NO: 342)	no linked regulator
67	BT3504	Ccattggactcccgcaaagagtatacaaagtctgactggattatg tggacagctgctatgtcttcagatttagaaactttcaagaaattc atagatccactctataaatatatcaatgaaactacttcgcgggta cctatcagtgattggcatcacacagacagtggtgaatgggttggg tttaaagcgcgttcggttattggaggatactggatgcaagtgtta atggacaaaactcgatgaaatgtttaattaactatacatttatta ttaactagaatgaaaaacatgaaatgtaaa (SEQ ID NO: 343)	no linked regulator
68	BT3518	Gaataaatgtcgaatttgactcagcgctaagtaagataaaatgtt ccggaaaaattgatttgaaagacaactttgagacagtaattaatg gattaacctttgtagcaccaatatcttatgcctatgatggacagt ataaaacttatcgggtcgtgaaaaaatagacacagaaaaatatag taattaataaaataaatctcaagaatttatggcgatttttataaa gagtggataatactgctgtattatccagatggggctcatatgcct gtaagtattaagttataaaataataatatt (SEQ ID NO: 344)	BT3517/ 3518
69	BT3569	Gtctgcctgatgtaaaagagtagttgcattacctccatcatgaca agcagagagagacaaaatcaggaacaaccctataatataagaaag aagtagcttcatagttcgtttcgttttacaaatgtaaatagaata aaacaaacaagcaacaaaaagacaaataattttttcacacatcat aattacaatgttaaaattgccctttctctctctttccctaatctt ttttgcctttcatttgttcactttgttactttcgccggaagacgg cagaataaacttcaacctaaatagtaacga (SEQ ID NO: 345)	no linked regulator
70	BT3607	Aatgtcgcgatgagcaacagagtcaatcatgacccaacccctgaa tcaaacgaaattatatatgatttttttaaatggtacttgcattca gcaaataaatctaccaaagagtagaaagatgcgtttttttgaatac actttttcgtttttttgcgcaaaaaatcaactctggatgcctaac tttgttctatcaattcatccaagtaacctaaattacttgactaaa	BT3609?

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
		atgattagcctatgaaaaatatacactagaaaacataaaatgccc catctgcgaatggggcaatattaatgccatattaataaaactaat cataaattatcgcccaattaataaataacacaataataaattcat aattaataaattaaaagtgctagctcaaaggaattaataaagcta gcagatgattccgagttagtaataaatattaaactattaaaaatt caataggttaaatatatactaaaaagagtagaaactaaaaaaagt aaact (SEQ ID NO: 346)	
71	BT3679	Cgtaaagggaactatagtgcatcttgcgtaccactatagtggcac gaactaatatgactaacaaaaaacttaattgttcgtagctaagga cttaagaatgtgagcgataacctgcaaggagtgaactgatttcat taacggtttaccatataacaaattattgttttattgatgttatgt tatatgtggtttttattttacagatcagattatccttattccttg gtcgaattatagtttaaaaaggaggaatatctataattcgacctc agataactcatattggacctcatctggagtgacttaacttacatt tgcacttgttaattggtcgttgaaatcataaatcaattaatgaac ggttaatttttatttactaatatcttaaatatttttgct (SEQ ID NO: 347)	BT3678
72	BT3668	Atttttccagttccaatcggcattatgaatagccaaacctatgtt caaaacaagcgggtgcaatttatcaacaaatgaagccatagcata tagggtttattaatgtgaagataaagatatataaaaaataaatat aactcttttgatgtcgataattttaaataatatatcgatattgtt ttataataaatcctgctatagtcgttcatgtcgatattgtattac tctaaatcgtattagtcctacaatgtggactgccgagttgttaca tttgcggtatataatctaataggaatattt (SEQ ID NO: 348)	BT3667?
73	BT3703	Tacttcctgcctcatctgctttcgatttattgacagagaaaaagg ttgaattaagaaatgaattaacacttccaagtcgtgaaatatacc ttttatccttttaataagttcacttcaacttatatttatcagaat acagaaaagaaataaactactgtaaaacaaaacattaacattaat acaaacttgtatttttattctagacaacccaaagtctcaagatgg ttgctatatttgcaatatccggaacagagcggagtaaaaatatta gttagcttataatttaataccataaataga (SEQ ID NO: 349)	BT3705
74	BT3749	Atcgtctggatggaaaatctcataaagaaatagctgaagaattgg gtatcagtgtcaaaggagtggagtatcatataagcaaagctgtga agctgctgcgtgataatctgaaagagtatgctcctttcctgatat tttttatttgatgatcttgaaaatatctttttctcctctttttt aataacagcaaaaaaagttgtatttctcactagggattattttta gtgagtggtattctatatgaaagggggagcaaatatactcctgtt tattacttataaagtaactcaacttataat (SEQ ID NO: 350)	BT3748/ BT3749
75	BT3854	Atcggtggcggagcctgtcctcatcggtgccggaaataggtctca tcggtacccgaaataaatccttgcggagtaaggcactcattatac catcaaataataattgtttttttttatcatgaaaacattattgat aactagatacttatgcgaaaagaatgaaattctttatcgctatta atctaaaattaatatggcattaaggactggaattctatatttgct tcagaaacggacgggatatcctccactatgtttctgatgacttga gcggatcgaactataaccttataaaatgatggaaatatgaaaaac gacacttcttaactactgcttggacttacttgtcagagaaagttt tcttgagatgaaaacggtttgaatcaattaatgttaatctataaa ttatgaaaacaggaaagagcaaagatcatttgcaaagagtttttt taaggttcctttatttgataatggggagcatcctttctttggatt ctgtt (SEQ ID NO: 351)	BT3853
76	BT3952	Ttatatggaagacctggaaggctgggcagattctattgtttgtac cactacggaacaggcggattttgtcaggaagttcttgcaggtcgt ggagcagaatctggatcgtgaagatttgggctccacgtttgtggc agaacaaatgttgatgagttcccgtcagttctaccggaggtttaa ggagatttcgggtatgtcacccagcgatttgattaaagattaccg gatggagaaggccgcccgtttgttgcagaacgaggaactgtctat tcaggatgtaatttccgatgtaggtatatccagtcgtgcttactt ctacaaagagtttacccgtaagtttggcgtaactcctaaggtata tagagagaagcttttagggaatgacactcataaaaatcaggagtg aacagccaggaagcggtctggtattagttgccaagaaataaattc ccatgctgatctgtgctgctttttaaggttggtctcctttgtact	BT3951

TABLE 5B-continued

Bt_Reporter_Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
		ctcttttgttttccattatttattattctgatatatagggtatta tccagtactctattttaccatctgtactttaaacagacatttttt ctcttctctgtttttttggcgcacaggagtatctcatttctttggc tattcctttaatttgcgtcaacgtattaaacgtatttggtaacct tattattattaattaaaaacaagtagt (SEQ ID NO: 352)	
77	BT3958	Agaggaactatagtgcttcttgcgtccaactatagtggaacgaaa gggaaactacagtagaacgaatgaatttggactgataagaaatta gtttttcaaagtctttcggttaatgattcgggattccttcattcc ttctgttctttggtcgtttggggtgacagatatatttgaattcat gtctgtatagattttatttattactgcttacgaataaactttttta ataaaagtggcgaaaaggcggctattataacttgatacaatgtgc gcaaacttgtgctctgtttgtacgtgaatgaatgctatgtgttga tatatagatgtttataatgtgctttatttctcctttctgttctat aaatgagcattttcattttgacataattttgtcacttctgcggaa tattcttaatattaaaagtttttaatttgcttccgcttataagaa ttatataggcgattgataaccttagtattaattaaaaaaaacaaa gtaac (SEQ ID NO: 353)	BT3957
78	BT3983	Atatttgactccggattattttcgctggttgtatacggcatttac tcgcgccacgaagacattgtatctggtgaattatcccaaagaaca aattttataaaagatttctttttttcttcgtaaataattgattc ccagtctagatgaatggggagatactcgttgtgaaaaaataaata tgagattatatttattttttttcaaaaacctctaagtgtttttca aggtatgggttgttatataaatgtgaatcgaaaataataaatgga atatcgattctaatatttatataaaaacta (SEQ ID NO: 354)	unknown (possibly BT3994/93
79	BT4040	Agaatataacaacctttatcacgctgtgtactatccaaatagcaa ttaaatagtttctcccttacacccgtaattaaacgactgccaaaa tgctttatatttaagaagtgagttttcgcccggtctgaccgaaa caatcaaccaattaaaaaggaatagaggaataattaaactaagtt cttgtagaacttagcacaaaaaacagtctgttaatccatttgtat ctaaactaacgcatctaactaagcaatagatttaccatctttttt gctaaaaatcaacgattcgtgcgcaaatatactaattagtttgaa aaagtcatactatttttcaataatatttcatatttaaattacaaa taagtttttcaattattctcatttaatcaatcaacgggtagaaac agagtgagtatttcactattacacgtttacagcccccaatacttc ccattgattatcaacaacatgcattctattccatcttatcatcta ctatattatagttctacaagaactaagacatagaacctattattt ttctgactttaaatcagcatagttcagcacacaaataaaagtttt aacttctaattttaatgcctatgagaaagaaataagtattccaaa tccaagagtacccacaagtacttcaacttgtttttaccctttta cctttaataaaactaatattaattt (SEQ ID NO: 262)	no linked regulator
80	BT4080	Ctattatcagaagatggagtgataaaagggcaatatagtactatg ggagatacttatgttaattggacacgtgatgacaccataacggga gatgtatatcaaaagagttattttgatcgtatgattgaaagaaat caagtaaatgcttatctgaaagaaaaggaagaagctgttcgtatt tggaaggaaatagaactgatatctcaaaaactacattttccctca gaagaattgaatcattttattcgtatttcctgttcgtatggacgc attaaatatgagctttttgctgtttcgtggcagattatgctatgc ggttatgtggcagatacaacaaaaaagtcttttaaccggatagag atggataaatatattactgcatttgatgatttgtggaaagaatgg aacgacttatctctagaaaacgataattgcccttcaatgtataag atttcttctaactttttttggttttcctgtaggtatacaagagacc attgataaatacaggaaatagttttcatttttttcttcttatatgt tatagaatataaaaaaataaatgaatattacttagtggttagtat tagtctagtcgtcttactattaatagtagcaaaaagtatgagaaa gaaacataaaataacgaaagtaaaattatgatcattattattata taaattcttaaaaacggtattttct (SEQ ID NO: 263)	BT4069? BT4070?
81	BT4085	Attttccgggtagtgctgacttttgtcgtccttatttttatcgta ttttcaattgggaaagcatatatgatgaagatgattgatagctac tgacggattcatcttggtaaattgatttagaaagtcatttcttca taaaagggagaaatgactttctttttaatatgttctgagctttc ctgcatacaagtaaatttattaataaaaaacatgtaattgtttta gtggtatatcatttttaaatcgtcattagataaataacaataaaa	?

TABLE 5B-continued

Bt_Reporter_Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
		tagtacacatattaaaaagaactaataata (SEQ ID NO: 264)	
82	BT4114	Ttgagtaaagaatacaccaatctggaggtatatctgaatgagcta gtgaatcatctgtatcctgcggattctaaaaaaaaaactaaaagc ccgaataaacagttataaaagattaagacgagagtacatttcccc ataaatcctcgtctttattcattttatgccggaaaaacaaaaaat actatcgtaaaaacaaatattacacatcccacaagccccaaaaac ataattttgcaccagtgagaactctaagagtggacacactcgaat attaataatctaatataaaagaacaaaag (SEQ ID NO: 265)	BT4111
83	BT4119	Aattgagtgtccatcaggcggctagcatttagagtatgatgaatg ctagccgcctgatggacacttttattctaatccaagcaaatactg aaaatgactagtagaaattactatgtaaagtaaaatatggaattt ttggtattttaatcccaaaatctcgtatctgatattttagtgata aaatagtgcacctaaacgctcaaaaagtcccctctctttatgttt tatataacttcttttgcacatatgaaacaaaaaataagaactata aatcaggaatattaatgaataaacatgagatgattcctgtttcaa ttttccccatgttttcaacgattgatttgcatgtaacataagtat tgattagatagtaatatgtattaactttaaattgaaatga (SEQ ID NO: 266)	BT4124
84	BT4136	Agtacctaccaatggagaattcagcaacattatgcacaacccatt gcctcaaacggtctatttcaatcaaaaagttcaggcacgctttat caaactggaagccaccactcccactgatacagccgcaaaagttga accaaatgaaatcggagtaacaatagccccttgattttacattca tcacaagtactaactaaaagcaaaaatcagaatagaaaagacgcc atctattttgatttttacactatataaatcttcttattatcaaat taactccaatgaaggcaaagaaagagaaattagtcttaatgaaga taacagatctttaatatataaggactgtctatccaaacttatcga aaaatttaattaaccacaagattcatgcttattgaaaacacaaga atgaattgttaacacttttaatttctatgattaatgaaaaacaaa atagtggtggaagaatactacaaatattaatcctgttttgtttgt atggt (SEQ ID NO: 267)	BT4137
85	BT4163	Acaattatatttgaaaagtttgccatattgcttttatatatggtt attcttgtttcaagaaaaaccggaataaattgtattatctacact ctttcttatttaaaaaacgcgttcagagcatgtattttcgttcaa aaggcggtattttccatgtttatgtacgattcttcattgctattt cttatataagtcgttaagtttgcaacagtttttcacaggtattat gataaagtgcccgaagaaaaacagaatctaacttttgtttaatta aaaaatagataaaatagatttatattgttacttaacagattttaa tattatgagaaatgtgatgaatcgtaagcggcattggctgctatt attgctcctctcaccttttttctctcttgtgaggacaag (SEQ ID NO: 268)	BT4178?
86	BT4247	Gaatgttatggatatcaattggaaggacggaagatacaacttcaa agaaaccccattatcccagctcatttcgattataaatcaaatata ccaatcaaatataattctagaaggaaagtttactaaacagccttc attcacaggcagcatccgttatgatgaaacattggatgacgtgat agataaactctgtttcagccttaaccttacatacaaaaaacagaa tagaaaaatagtaatatataattaaccatatttctaataattaac ccaatatttaacctcacaacaagttaaatc (SEQ ID NO: 269)	BT4250/ BT4248
87	BT4266	Ctggaattttttttatgtaatatacccttttacttcttattacggc ctattcgccagagattgttggtgaaggagaaaatattattatata tggtagaaattaaggtgtgcattttatttcttatgcatttattct tttggggatctactacctttttttatttagtatatttgaaaataaa tagttgtgcttggctgttatgattcatttttatatttaacagatt gggataagttgctctagaacttggtagttttataccaataagtgt atttttcctgttttcataggctattcaaaggttattaagtttgt gtgctacttaagacggtgtaaagttattaataaaattggtgaacg caatgtttttttatttttaattatcggcaaacgatgtttttttta atttttcattctactactcagatcgtaataagatagatataatct tttaattattgtatattgttgattattagtattttatcgctttgg ataccaagttctagagcgacttattccaatcggtcaattacgact atatttcttaataattatttatgataatgcgaaattataggccgc ctccgggctgtgattaaatttttattatcgtttcttcagcataga tcagaacagtgctgaagagagattgaattcattaaaaatttcaat	

TABLE 5B-continued

Bt_Reporter_Array_Promoters

Construct	Promoter	Promoter sequence	Linked Regulator
		acccccaagaaaaacaaatgaatgataacagtcaaacacaactat atatattccaaaacttactaaatattaagataaagcatacacacc caaaaacaaacgtattagagtaaaaatgcacatcttatttctacc acattatcataatgctagatatagaatagtaagttttctacttat ccatattaacccaactaattattaacctttaatcacagaaaaaca (SEQ ID NO: 270)	
88	BT4299	Tggagagcaatagagaccttatgccaaattgaataattttgaaga agtcgtaataggacttggtatgtatgtgtataagtgtcttatata taattgattaattggttgatggatgcttgggatgacaatttatga actatatagtagaattgagattctaaaaaaatggtgtttgttgat aattaaaataaaaaagatattgtatttttcgatttattaataac tttacaccgtcttagaatagtacatgcacttaataacctttgaat agcctatggaaacagtagaaaatatactttggggtataaaaatac caagtcctattacgacttagccccaattaatcaatatgattataa ccttaaattaacatttatgaaaactcttagcaacagccctccgcc tttcaaaatcggagaattcgatctcatttttttactttatttca gcacagatcagaataggtatgatatgtattctgagttcattatca acttcaataccccaatttaagaagatgaataatagcagtcaaac acacccatatattttcaaacttactcatacatacaaaaacaaacg tatacccttgtatgcataccctagttctacccacatagtagaca cacaagagtaggtttccctatcactttttttaaccaatctaatt attaacctttatcacagaaaaaca (SEQ ID NO: 271)	BT4300?
89	BT4356	Cgttcacgggaacctttacaaatcaacgtttggaaaagattctgg aatattttaaagtatcctccaaaatacgctggaaacatatcaatg atgacaaggatggaagtgacagaaaaaaagagataatagagattt attgattaacctttaacaatttagtagtatgaaagcaaaacccac ttagaaaaaagtatgggaagattttggcagatctccccatactaa aatgaatcaattgaaaatgcttgtttggcagacaagcatagttaa ctcattttcaacttaaatcaatacaaaatt (SEQ ID NO: 272)	BT4355/ 56
90	BT4403	Ggaagttgatgctgaagatgttgctcaagatattttctgtaagct ttggttacaaccggaaatatggcttgacaatgaaaatgaattaga taactacctctttataatgaccagaaacattattctgaatatctt caagcatcagcaaatcgaacgggaatatcaggaaggataccttga gaaaacagtacttcatgaattgatagaaggggaagatgcccttaa taatatatattatgaagaaatgttgctggttgttcgcctgacttt ggaaaaaatgcctgaacggcgaaggttaatattcgagctgagtcg ttttaagggattaagttataaagaaatcgcagaaaagcttaatgt ttccatccgtacggtagagcaccaggtgtatttagcactgataga actaaaaaaagtgcttctatttttattttttctatttcctttaa gtagtgtttttcttttagttgtatttagtgtataaaggaagaaat ta (SEQ ID NO: 273)	BT4402/ 03
91	BT4470	Tctttgtctccgaaaaacaagagtccgacaatgcgccacatatca ttgttcaggttcggataataaaaatccatcgaccaccgttttctt tgtggcggaaaacttcccagcatcagcaactttgcttttggtggg agaaagggttttaaaggatgtttttcgatttcaatctccatattg atgtaatttcctacaaaaataacgaatctattcttttccttcaaa atagttgcggaaaaaaacaaatttaaaaatatttggctatttttg cacggagatggtgaaaaacaacttattgaa (SEQ ID NO: 274)	?
92	BT4635	Ctcccaataacttattaagttataatgaacaggaaggcatccata tccaatcggtagacgtacaaaaatatatcgcctggaaagatggtt tttacctcttccaaacagaaaaactaaaagacattgctacaaaac tcagcgattactatggcaaaaagatcatgatagacagtccattga agaccattacctgcagtggtaaactagatttgaaagaagatcttg acgaagttcttcagacactaatacggactgtcccggcaagaatag aaaaatcagatggaattatccatatttatgtaaaacattaattaa aatcgaaagcctatgaataaacattatccttaaaaaaataaggcc gaataataccccttaatatcatccggcctttgattaaattacttac acgttaatattaattaatctaatcattacaaatgtatgaaaaagc accgattatttagtcaccaaaggactaaagataaacaactattac taatc (SEQ ID NO: 275)	BT4636/ 35

TABLE 5B-continued

Bt Reporter Array_Promoters			
Construct	Promoter	Promoter sequence	Linked Regulator
93	BT4662	Ttttttcttcttttattgaatgatgacggattttaaaatcatcc atccaaacaacctaaattgtacagaacctattccatatcatatta caatgtcataacattatgacacataaaaaactaggatacaggaga taaacagctttttaaacaaaaacaacatatgtctcaacaaattt gatatcaaaaaaatcatttttgaacaaagtatgaacaacctaaat taaagaatctaattaatgaggttacatttgcaacagtaaaataac acttttaataattataaaacctaataaagt (SEQ ID NO: 276)	BT4663
94	BT4672	Tgtctcccgtggaatatatcaagtccatccgcatgaagaaagctg ccatgttattgcaacaaaagaaattcaccgttgccgaagtgatgt atatggtaggattttccaatcattcttatttctccaaatgctttc aggcagagtttggaaaaacaccgcgccaatacttgaatgacgggc tgtagaggcattttagggcttttcgtcctatttttatccttatat gtccaatctgtgcttttatgaaaatgccaggcagtctatctttgc cgctatcaacaaaccactaaatttgatagc (SEQ ID NO: 277)	BT4673
95	BT4706	caggcagatgatacattcacaaagaaaaagataatagtagattta tattagtaaccataaaaatgagaatagcctatgagataacacaaa gatcgtaaaaaaaggaagaaagctgctaccaacagctgtcttccc ccaatttttcagattcgcggtaaggagtcttgcaaacgctaaccg gaatcaaaccacagttcattatagtaataaactttagttaaccgc aaatgtatgaaaaaaaatcattcatttattgcattatatcctaaa tatgctttaaatctaaaactacctttagtt (SEQ ID NO: 278)	BT4705/ 06
96	BT4723	Acttcctaaagaatactttacgggaacgattcctagtggcggcat acagaacgccttgaatattctcatgcttacttcgccttttatta tgaaatggatggctcggtcattgtcttgaaagagaagtagataag catctttatcatgaaattagatatagccattcctgagttttcccc cggaatggctttttaatttatgaagaaccgttagttaacaagagt taaagatagatagccgattggacgaaaggggagagcagtcggtat acctgtcaaacaacttaaaagttttgatat (SEQ ID NO: 279)	BT4722/ 23

[0264] It will be apparent to those skilled in the art that various modifications and variations can be made in the present disclosure without departing from the scope or spirit of the invention. Other embodiments of the disclosure will be apparent to those skilled in the art from consideration of the specification and practice of the methods disclosed herein. It is intended that the specification and examples be considered as exemplary only, with a true scope and spirit of the invention being indicated by the following claims.

SEQUENCE LISTING

```
Sequence total quantity: 354
SEQ ID NO: 1            moltype = DNA  length = 25
FEATURE                 Location/Qualifiers
source                  1..25
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 1
ggtagtccac acagtaaacg atgaa                                          25

SEQ ID NO: 2            moltype = DNA  length = 23
FEATURE                 Location/Qualifiers
source                  1..23
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 2
cccgtcaaat tcctttgagt ttc                                            23

SEQ ID NO: 3            moltype = DNA  length = 22
FEATURE                 Location/Qualifiers
source                  1..22
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
```

-continued

```
SEQUENCE: 3
tggttgtcgg ctatcaggaa gt                                              22

SEQ ID NO: 4            moltype = DNA  length = 21
FEATURE                 Location/Qualifiers
source                  1..21
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 4
acatctgcca tgttggcttt c                                               21

SEQ ID NO: 5            moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
source                  1..20
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 5
agcgtaaagc cgacctgaca                                                 20

SEQ ID NO: 6            moltype = DNA  length = 21
FEATURE                 Location/Qualifiers
source                  1..21
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 6
tcaccttgct tctggatttc g                                               21

SEQ ID NO: 7            moltype = DNA  length = 45
FEATURE                 Location/Qualifiers
source                  1..45
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 7
gctctagaac tagtggatcc tgatctggaa gaagcaatga aagct                     45

SEQ ID NO: 8            moltype = DNA  length = 41
FEATURE                 Location/Qualifiers
source                  1..41
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 8
catattcgtt taattaaata aataatttat tttattttaa a                         41

SEQ ID NO: 9            moltype = DNA  length = 52
FEATURE                 Location/Qualifiers
source                  1..52
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 9
atttatttaa ttaaacgaat atgactaaaa aaatttcatt cattattaac gg             52

SEQ ID NO: 10           moltype = DNA  length = 50
FEATURE                 Location/Qualifiers
source                  1..50
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 10
aagataggca attagtcgac tcaactatta aatgcttggt ttaagcttaa                50

SEQ ID NO: 11           moltype = DNA  length = 47
FEATURE                 Location/Qualifiers
source                  1..47
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 11
tttacaattt gccatgcgga ttacgggaca aatacaagga acttatc                   47

SEQ ID NO: 12           moltype = DNA  length = 78
FEATURE                 Location/Qualifiers
source                  1..78
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 12
tccgcatggc aaattgtaaa ttgtaaatcg taaaatagta atatattaat ggaaaataaa  60
tccaaatata aaaccatc                                                   78
```

-continued

```
SEQ ID NO: 13          moltype = DNA  length = 42
FEATURE                Location/Qualifiers
source                 1..42
                       mol_type = genomic DNA
                       organism = Pseudorhabdus luminescens
SEQUENCE: 13
attctttatc ctcctcctta ttaagacagc gaaatcgctt ga                    42

SEQ ID NO: 14          moltype = DNA  length = 50
FEATURE                Location/Qualifiers
source                 1..50
                       mol_type = genomic DNA
                       organism = Pseudorhabdus luminescens
SEQUENCE: 14
taaggaggag gataaagaat atgacttcat atgttgataa acaagagatc            50

SEQ ID NO: 15          moltype = DNA  length = 68
FEATURE                Location/Qualifiers
source                 1..68
                       mol_type = genomic DNA
                       organism = Pseudorhabdus luminescens
SEQUENCE: 15
agtgttacct tcattcatcc ttcttcaccc ttcatttata tcaactatta aatgcttggt  60
ttaagctt                                                          68

SEQ ID NO: 16          moltype = DNA  length = 89
FEATURE                Location/Qualifiers
source                 1..89
                       mol_type = genomic DNA
                       organism = Pseudorhabdus luminescens
SEQUENCE: 16
ggatgaatga aggtaacact cataaactcg aaattcttca ttcttaattt ttaattaaaa  60
tatatgaaat ttggaaactt tttgcttac                                   89

SEQ ID NO: 17          moltype = DNA  length = 50
FEATURE                Location/Qualifiers
source                 1..50
                       mol_type = genomic DNA
                       organism = Pseudorhabdus luminescens
SEQUENCE: 17
ccattgtctt attcctttct ttataatagc gaacgttgtt tttctttaag            50

SEQ ID NO: 18          moltype = DNA  length = 49
FEATURE                Location/Qualifiers
source                 1..49
                       mol_type = genomic DNA
                       organism = Pseudorhabdus luminescens
SEQUENCE: 18
agaaaggaat aagacaatgg atatgaaatt tggattgttc ttccttaac             49

SEQ ID NO: 19          moltype = DNA  length = 55
FEATURE                Location/Qualifiers
source                 1..55
                       mol_type = genomic DNA
                       organism = Pseudorhabdus luminescens
SEQUENCE: 19
aagataggca attagtcgac ttacatgtgg tactttttaa tattatcatc aacaa      55

SEQ ID NO: 20          moltype = DNA  length = 71
FEATURE                Location/Qualifiers
source                 1..71
                       mol_type = genomic DNA
                       organism = Pseudorhabdus luminescens
SEQUENCE: 20
gctcggtacc cggggatcca ctagtcactc ccgcatttta aaataaaata aattatttat  60
ttaattaaac g                                                      71

SEQ ID NO: 21          moltype = DNA  length = 59
FEATURE                Location/Qualifiers
source                 1..59
                       mol_type = genomic DNA
                       organism = Pseudorhabdus luminescens
SEQUENCE: 21
tgcatgcctg caggtcgact tacatgtggt actttttaat attatcatca acaatattg  59

SEQ ID NO: 22          moltype = DNA  length = 44
```

-continued

```
FEATURE                 Location/Qualifiers
source                  1..44
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 22
gctcggtacc cggggatcct gatctggaag aagcaatgaa agct                    44

SEQ ID NO: 23           moltype = DNA  length = 60
FEATURE                 Location/Qualifiers
source                  1..60
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 23
aaatgcggga gtgactagtc aaagttacga caaataattt gttaacatac atatttaggc  60

SEQ ID NO: 24           moltype = DNA  length = 44
FEATURE                 Location/Qualifiers
source                  1..44
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 24
gctcggtacc cggggatcca tctggaagaa gtaatgaaag ctgc                    44

SEQ ID NO: 25           moltype = DNA  length = 54
FEATURE                 Location/Qualifiers
source                  1..54
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 25
aaatgcggga gtgactagtc aaagttacga caaataattt gttaacatac aaaa        54

SEQ ID NO: 26           moltype = DNA  length = 53
FEATURE                 Location/Qualifiers
source                  1..53
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 26
gctcggtacc cggggatcct atcattcagt tttctgttgg ttactttgag tga         53

SEQ ID NO: 27           moltype = DNA  length = 66
FEATURE                 Location/Qualifiers
source                  1..66
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 27
aaatgcggga gtgactagtt agtttaatgt tattaattta aaagtacgaa ttttctcttt  60
tcgatg                                                              66

SEQ ID NO: 28           moltype = DNA  length = 43
FEATURE                 Location/Qualifiers
source                  1..43
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 28
gctcggtacc cggggatcca aaatggaact gggcaatgac agg                     43

SEQ ID NO: 29           moltype = DNA  length = 52
FEATURE                 Location/Qualifiers
source                  1..52
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 29
aaatgcggga gtgactagtc ctttttcttg tctggttgga tagatgtttt tt           52

SEQ ID NO: 30           moltype = DNA  length = 50
FEATURE                 Location/Qualifiers
source                  1..50
                        mol_type = genomic DNA
                        organism = Pseudorhabdus luminescens
SEQUENCE: 30
gctcggtacc cggggatcct tgtttgttgg agattgtttt catatcgttg              50

SEQ ID NO: 31           moltype = DNA  length = 56
FEATURE                 Location/Qualifiers
source                  1..56
                        mol_type = genomic DNA
```

-continued

```
                        organism = Pseudorhabdus luminescens
SEQUENCE: 31
aaatgcggga gtgactagtt agtttgatgt tattaaatta aaagtacgaa ttttac      56

SEQ ID NO: 32           moltype = DNA  length = 39
FEATURE                 Location/Qualifiers
source                  1..39
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 32
gctctagaac tagtggatcc gacagcctcc agctgacgg                         39

SEQ ID NO: 33           moltype = DNA  length = 25
FEATURE                 Location/Qualifiers
source                  1..25
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 33
catccttttt cttgtctggt tggat                                        25

SEQ ID NO: 34           moltype = DNA  length = 56
FEATURE                 Location/Qualifiers
source                  1..56
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 34
accagacaag aaaaaggatg aaagcattaa aaataacaat catagctcta ttggca      56

SEQ ID NO: 35           moltype = DNA  length = 47
FEATURE                 Location/Qualifiers
source                  1..47
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 35
aagataacat tcgagtcgac atagaagctg gctctttcga aatagtc                47

SEQ ID NO: 36           moltype = DNA  length = 33
FEATURE                 Location/Qualifiers
source                  1..33
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 36
cgggatccgt ggactacttt tgctgaaagc gga                               33

SEQ ID NO: 37           moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 37
tccccccggg ttcatagttc tttctgtaat ccaattaaga                        40

SEQ ID NO: 38           moltype = DNA  length = 35
FEATURE                 Location/Qualifiers
source                  1..35
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 38
tccccccggg tttcattgat atcgtaaaga gggat                             35

SEQ ID NO: 39           moltype = DNA  length = 30
FEATURE                 Location/Qualifiers
source                  1..30
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 39
acgcgtcgac tgccacactt ccgtgcactt                                   30

SEQ ID NO: 40           moltype = DNA  length = 42
FEATURE                 Location/Qualifiers
source                  1..42
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 40
gctctagaac tagtggatcc cagtaatgaa gagacattac gg                     42
```

-continued

```
SEQ ID NO: 41          moltype = DNA  length = 47
FEATURE                Location/Qualifiers
source                 1..47
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 41
tagtttaatg ttattaattt aaaagtacga attttctctt ttcgatg                47

SEQ ID NO: 42          moltype = DNA  length = 59
FEATURE                Location/Qualifiers
source                 1..59
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 42
aaattaataa cattaaacta atgaaaaaga taatatatat agcaacaatc ggaattacc   59

SEQ ID NO: 43          moltype = DNA  length = 47
FEATURE                Location/Qualifiers
source                 1..47
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 43
aagataacat tcgagtcgac ctgtttcagg tcttcttcgt tgattcc                47

SEQ ID NO: 44          moltype = DNA  length = 40
FEATURE                Location/Qualifiers
source                 1..40
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 44
gctctagaac tagtggatcc gcttcttccg tcagtcttct                        40

SEQ ID NO: 45          moltype = DNA  length = 32
FEATURE                Location/Qualifiers
source                 1..32
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 45
ttatttacac aagtagttga ttgcattgag ag                                32

SEQ ID NO: 46          moltype = DNA  length = 46
FEATURE                Location/Qualifiers
source                 1..46
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 46
tcaactactt gtgtaaataa tgaaaactac accggcaagt aacatc                 46

SEQ ID NO: 47          moltype = DNA  length = 39
FEATURE                Location/Qualifiers
source                 1..39
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 47
aagataacat tcgagtcgac tatcgcaacg gggcggtgt                         39

SEQ ID NO: 48          moltype = DNA  length = 43
FEATURE                Location/Qualifiers
source                 1..43
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 48
gctctagaac tagtggatcc ctggaagatt tgaaagcaac tac                    43

SEQ ID NO: 49          moltype = DNA  length = 26
FEATURE                Location/Qualifiers
source                 1..26
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 49
tcaataagtg cttacctgaa cgtctg                                       26

SEQ ID NO: 50          moltype = DNA  length = 42
FEATURE                Location/Qualifiers
source                 1..42
                       mol_type = genomic DNA
```

-continued

```
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 50
ttcaggtaag cacttattga aaaacgactt tcttctccct gc                    42

SEQ ID NO: 51           moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 51
aagataacat tcgagtcgac tgctccccac atggcaatgt                       40

SEQ ID NO: 52           moltype = DNA  length = 42
FEATURE                 Location/Qualifiers
source                  1..42
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 52
tcaactactt gtgtaaataa aaaacgactt tcttctccct gc                    42

SEQ ID NO: 53           moltype = DNA  length = 45
FEATURE                 Location/Qualifiers
source                  1..45
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 53
gctctagaac tagtggatcc ccctctcaat tggcgaaaga aaatc                 45

SEQ ID NO: 54           moltype = DNA  length = 34
FEATURE                 Location/Qualifiers
source                  1..34
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 54
agctatttta tttattagtt tgtaaaatcg gagt                             34

SEQ ID NO: 55           moltype = DNA  length = 60
FEATURE                 Location/Qualifiers
source                  1..60
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 55
cgattttaca aactaataaa taaaatagct acggaaatca aaagctatct ttgttttcag  60

SEQ ID NO: 56           moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 56
aagataacat tcgagtcgac ttccactggt aggctcgatg                       40

SEQ ID NO: 57           moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 57
gctctagaac tagtggatcc tgggaacatt tggctcctgc                       40

SEQ ID NO: 58           moltype = DNA  length = 45
FEATURE                 Location/Qualifiers
source                  1..45
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 58
ggcccccccct cgaggtcgac atcattgtcc tgtgtataga gtccc                45

SEQ ID NO: 59           moltype = DNA  length = 48
FEATURE                 Location/Qualifiers
source                  1..48
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 59
cgctctagaa ctagtggatc cagaaaaccg tgttactcag tttgatcg              48
```

-continued

```
SEQ ID NO: 60          moltype = DNA  length = 49
FEATURE                Location/Qualifiers
source                 1..49
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 60
gggccccccc tcgaggtcga caaataacag agaacacatt cgagttacc              49

SEQ ID NO: 61          moltype = DNA  length = 40
FEATURE                Location/Qualifiers
source                 1..40
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 61
gattagcatt atgaggatcc tttggctatc ccggcatcga                        40

SEQ ID NO: 62          moltype = DNA  length = 51
FEATURE                Location/Qualifiers
source                 1..51
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 62
tgacgtgaat agttttgatt tctcattttt ttcgtatttc tttctatgac c           51

SEQ ID NO: 63          moltype = DNA  length = 34
FEATURE                Location/Qualifiers
source                 1..34
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 63
aatcaaaact attcacgtca gaatacaata aatc                              34

SEQ ID NO: 64          moltype = DNA  length = 47
FEATURE                Location/Qualifiers
source                 1..47
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 64
tccaccgcgg tggcggccgc gcagtatata caaatagggt tacgtct                47

SEQ ID NO: 65          moltype = DNA  length = 51
FEATURE                Location/Qualifiers
source                 1..51
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 65
gctctagaac tagtggatcc tatcattcag ttttctgttg gttactttga g           51

SEQ ID NO: 66          moltype = DNA  length = 60
FEATURE                Location/Qualifiers
source                 1..60
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 66
cgtactttta aattaataac attaaactaa tgatgaaaaa tatgatctta cctatagcat  60

SEQ ID NO: 67          moltype = DNA  length = 44
FEATURE                Location/Qualifiers
source                 1..44
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 67
aagataggca attagtcgac tcaataagtg cttacctgaa cgtc                   44

SEQ ID NO: 68          moltype = DNA  length = 59
FEATURE                Location/Qualifiers
source                 1..59
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 68
agaaggagat atacatatgc atcaccatca ccatcacagt gatgacttca aatccggcc   59

SEQ ID NO: 69          moltype = DNA  length = 51
FEATURE                Location/Qualifiers
source                 1..51
                       mol_type = genomic DNA
```

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                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 69
gcttatcatc gataagcttt tatttacaca agtagttgat tgcattgaga g          51

SEQ ID NO: 70           moltype = DNA  length = 73
FEATURE                 Location/Qualifiers
source                  1..73
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 70
agaaggagat atacatatgc atcaccatca ccatcacgga ggtggaggtg acgggctgga  60
cgaagcggta ggt                                                     73

SEQ ID NO: 71           moltype = DNA  length = 42
FEATURE                 Location/Qualifiers
source                  1..42
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 71
agcttatcat cgataagctt attccactac gtttaccacc at                     42

SEQ ID NO: 72           moltype = DNA  length = 50
FEATURE                 Location/Qualifiers
source                  1..50
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 72
gctcggtacc cggggatcct tgtttgttgg agattgtttt catatcgttg             50

SEQ ID NO: 73           moltype = DNA  length = 56
FEATURE                 Location/Qualifiers
source                  1..56
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 73
aaatgcggga gtgactagtt agtttgatgt tattaaatta aaagtacgaa ttttac      56

SEQ ID NO: 74           moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 74
tatcattcag ttttctgttg gttactttga gtgattatat gcttgttata tgaataatat  60
cccttttac aaggacttaa attactatac aaaggtagta ttttctatga ttgagagaga  120
atataatccc gactttctta tgatggagaa ttattcttat aaaaccctat aaaatagcgt  180
tctatgcaac atatcttaca gcatttgaaa catttttttc agtcggttga cttaaatcaa  240
ccgtaatttg catcatcgaa aagagaaaat tcgtactttt aaattaataa cattaaacta  300

SEQ ID NO: 75           moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 75
aaaatggaac tgggcaatga caggcatccc cagctgtacg atttatccgc cgatccatcg  60
gagaaaaaca atgtagcgaa acagcatccg gaagttgtca gggagctgtc cgaactgctt  120
gaatcggtaa agacaagata accaatgaga atagcagatt tgtattattt tgtatcaatc  180
ttgaataatt ctatccatat gagaacaatc aatgcgtata tctttgccat cgtaaattca  240
acaaaatcac ttaattttta atatatgaaa aaacatctat ccaaccagac aagaaaaagg  300

SEQ ID NO: 76           moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 76
ttgtttgttg gagattgttt tcatatcgtt gatttttttca gttgactaca accagtagtt  60
aactctattt ttaagttctt atcacctgca aaggtaatat tttccatact tactggagaa  120
tagatattct ataattcttc tatttcgaag aataatgtat aaaaccctat aaaatagcgt  180
tctatgcaac aaatgttata gcctttgaaa catttttttc agtcgtttga tataaatcaa  240
ccgtaatttg catcatcgat atagtaaaat tcgtactttt aatttaataa catcaaacta  300

SEQ ID NO: 77           moltype = DNA  length = 43
FEATURE                 Location/Qualifiers
source                  1..43
```

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                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 77
agctcggtac ccggggatcc aggacgaaaa tgtaactttg cca                    43

SEQ ID NO: 78         moltype = DNA  length = 48
FEATURE               Location/Qualifiers
source                1..48
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 78
atgcgggagt gactagtact tactattttt tctcgctgca aaattcca               48

SEQ ID NO: 79         moltype = DNA  length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 79
gctcggtacc cggggatccc ttccaatgat actgaagaga aaatcattgc tg          52

SEQ ID NO: 80         moltype = DNA  length = 54
FEATURE               Location/Qualifiers
source                1..54
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 80
atgcgggagt gactagtaac attaaatttg aggtttaaaa atagtattaa attc        54

SEQ ID NO: 81         moltype = DNA  length = 46
FEATURE               Location/Qualifiers
source                1..46
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 81
gctcggtacc cggggatcct ctggagtccg tacttaaatc catcga                 46

SEQ ID NO: 82         moltype = DNA  length = 63
FEATURE               Location/Qualifiers
source                1..63
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 82
aaatgcggga gtgactagta aatttgtgcg ttttagtaat tgactaaagt tattaaaaac  60
aag                                                                63

SEQ ID NO: 83         moltype = DNA  length = 40
FEATURE               Location/Qualifiers
source                1..40
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 83
agctcggtac ccggggatcc cgtgtggcac ggctgcagct                        40

SEQ ID NO: 84         moltype = DNA  length = 74
FEATURE               Location/Qualifiers
source                1..74
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 84
aaatgcggga gtgactagtc tttgatactt gaatttaaat taatgaattg atttattttt  60
acagatttat ctac                                                    74

SEQ ID NO: 85         moltype = DNA  length = 55
FEATURE               Location/Qualifiers
source                1..55
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 85
gctcggtacc cggggatccg tctaagtctt ctctttatag gaaaatgaaa ttagc       55

SEQ ID NO: 86         moltype = DNA  length = 67
FEATURE               Location/Qualifiers
source                1..67
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
```

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SEQUENCE: 86
aaatgcggga gtgactagta ctattagatt tataaagtta tttagaccaa ataagtatta  60
gttgtgc                                                            67

SEQ ID NO: 87          moltype = DNA  length = 57
FEATURE                Location/Qualifiers
source                 1..57
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 87
gctcggtacc cggggatcct tcaatttcaa taataacttt tgtgtgttag agtccct     57

SEQ ID NO: 88          moltype = DNA  length = 58
FEATURE                Location/Qualifiers
source                 1..58
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 88
aaatgcggga gtgactagta atactgctct tttaaggtta ataaaaattg tctgtgtg    58

SEQ ID NO: 89          moltype = DNA  length = 42
FEATURE                Location/Qualifiers
source                 1..42
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 89
gctcggtacc cggggatcct caatgtgaca ccaagcgcac tg                     42

SEQ ID NO: 90          moltype = DNA  length = 47
FEATURE                Location/Qualifiers
source                 1..47
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 90
aaatgcggga gtgactagta agtagtaacg gccatttcct tgtcttc                47

SEQ ID NO: 91          moltype = DNA  length = 40
FEATURE                Location/Qualifiers
source                 1..40
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 91
agctcggtac ccggggatcc aagtggattg acgatgcacg                        40

SEQ ID NO: 92          moltype = DNA  length = 47
FEATURE                Location/Qualifiers
source                 1..47
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 92
atgcgggagt gactagtgtt tactagtgat aataaacaga atgtcgt                47

SEQ ID NO: 93          moltype = DNA  length = 52
FEATURE                Location/Qualifiers
source                 1..52
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 93
gctcggtacc cggggatcca aaataggaat ttgcgtctga tgtacaaaaa cg          52

SEQ ID NO: 94          moltype = DNA  length = 42
FEATURE                Location/Qualifiers
source                 1..42
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 94
aaatgcggga gtgactagtc cccgaaactc cgtaatagac ca                     42

SEQ ID NO: 95          moltype = DNA  length = 43
FEATURE                Location/Qualifiers
source                 1..43
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 95
gctcggtacc cggggatccg ctatggctac ggatacggtt acg                    43
```

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SEQ ID NO: 96          moltype = DNA  length = 66
FEATURE                Location/Qualifiers
source                 1..66
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 96
aaatgcggga gtgactagta attatcattt tttaagggat aatacaaata taacaaaaaa  60
aacggg                                                             66

SEQ ID NO: 97          moltype = DNA  length = 41
FEATURE                Location/Qualifiers
source                 1..41
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 97
gctcggtacc cggggatcct attgcccatc gtctggaacg t                      41

SEQ ID NO: 98          moltype = DNA  length = 65
FEATURE                Location/Qualifiers
source                 1..65
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 98
aaatgcggga gtgactagtt tttatcacta ttaaaggtta acatatagtt atttatcgta  60
gctgc                                                              65

SEQ ID NO: 99          moltype = DNA  length = 57
FEATURE                Location/Qualifiers
source                 1..57
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 99
agctcggtac ccggggatcc gaatattgca aaggtaattt ttaaaattgt ttttccc     57

SEQ ID NO: 100         moltype = DNA  length = 63
FEATURE                Location/Qualifiers
source                 1..63
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 100
aaatgcggga gtgactagta attttgattt taaaataata actagtttac cggttttgtt  60
tgt                                                                63

SEQ ID NO: 101         moltype = DNA  length = 50
FEATURE                Location/Qualifiers
source                 1..50
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 101
gctcggtacc cggggatccg gtggattaca atgatcttat ccattcgtcc             50

SEQ ID NO: 102         moltype = DNA  length = 77
FEATURE                Location/Qualifiers
source                 1..77
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 102
aaatgcggga gtgactagta gattaaattt taatttatat aaaatgatat attacatcat  60
cagacatcta ttcacat                                                 77

SEQ ID NO: 103         moltype = DNA  length = 46
FEATURE                Location/Qualifiers
source                 1..46
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 103
gctcggtacc cggggatcct ggtgtttcct ttaaaaccaa aatgcc                 46

SEQ ID NO: 104         moltype = DNA  length = 40
FEATURE                Location/Qualifiers
source                 1..40
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 104
aaatgcggga gtgactagtt gtgactttta ggggttgggc                        40
```

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SEQ ID NO: 105          moltype = DNA  length = 64
FEATURE                 Location/Qualifiers
source                  1..64
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 105
gctcggtacc cggggatcct agtttttcag aactacttaa tgctctattt atcaaatgat  60
tatg                                                               64

SEQ ID NO: 106          moltype = DNA  length = 68
FEATURE                 Location/Qualifiers
source                  1..68
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 106
aaatgcggga gtgactagtc ttattctttt taattagaaa tagtttttag gtagttaaca  60
aacatgtg                                                           68

SEQ ID NO: 107          moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 107
agctcggtac ccggggatcc attaaggggg ggctatgctg                        40

SEQ ID NO: 108          moltype = DNA  length = 51
FEATURE                 Location/Qualifiers
source                  1..51
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 108
aaatgcggga gtgactagtc ttgattcgtt aaatctctgt agattcccca g           51

SEQ ID NO: 109          moltype = DNA  length = 41
FEATURE                 Location/Qualifiers
source                  1..41
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 109
gctcggtacc cggggatcca gaccaggcac cactatctga g                      41

SEQ ID NO: 110          moltype = DNA  length = 68
FEATURE                 Location/Qualifiers
source                  1..68
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 110
aaatgcggga gtgactagtt ttcttagtat taggttatta actaaattat ttcacggtaa  60
ttgaatag                                                           68

SEQ ID NO: 111          moltype = DNA  length = 42
FEATURE                 Location/Qualifiers
source                  1..42
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 111
gctcggtacc cggggatcct cttaaaagcg cttggtttgg cc                     42

SEQ ID NO: 112          moltype = DNA  length = 55
FEATURE                 Location/Qualifiers
source                  1..55
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 112
aaatgcggga gtgactagta attttgtggc ttaggattta tttgcttgtt ctaac       55

SEQ ID NO: 113          moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 113
gctcggtacc cggggatcca aggggaaagt cgaaaggtgg                        40

SEQ ID NO: 114          moltype = DNA  length = 59
```

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```
FEATURE                 Location/Qualifiers
source                  1..59
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 114
aaatgcggga gtgactagtt aagtcctttt acttttaatt attattaaaa acagccgca   59

SEQ ID NO: 115          moltype = DNA  length = 42
FEATURE                 Location/Qualifiers
source                  1..42
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 115
gctcggtacc cggggatccc atacacatca tcgtccctcc gc                     42

SEQ ID NO: 116          moltype = DNA  length = 63
FEATURE                 Location/Qualifiers
source                  1..63
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 116
aaatgcggga gtgactagta cttttgtgag ttaatcatta atactaattt aagtgtacac  60
aac                                                                63

SEQ ID NO: 117          moltype = DNA  length = 49
FEATURE                 Location/Qualifiers
source                  1..49
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 117
gctcggtacc cggggatccg ggcggaagag tttttaagag agaatatag              49

SEQ ID NO: 118          moltype = DNA  length = 67
FEATURE                 Location/Qualifiers
source                  1..67
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 118
aaatgcggga gtgactagta agtttattaa ttaagattac cttttatata agtagcgaag  60
tctttcc                                                            67

SEQ ID NO: 119          moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 119
agctcggtac ccggggatcc gtactatgca gagagttacg                        40

SEQ ID NO: 120          moltype = DNA  length = 72
FEATURE                 Location/Qualifiers
source                  1..72
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 120
aaatgcggga gtgactagtt cgttttaatt taaagttaat attaattttc ctttgtttag  60
taaaatacaa tt                                                      72

SEQ ID NO: 121          moltype = DNA  length = 48
FEATURE                 Location/Qualifiers
source                  1..48
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 121
agctcggtac ccggggatcc gcttaatttt cgcttaattg attattaa               48

SEQ ID NO: 122          moltype = DNA  length = 64
FEATURE                 Location/Qualifiers
source                  1..64
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 122
aaatgcggga gtgactagtc gtgattttca aataattttt cacggtctct tttttatatt  60
atac                                                               64

SEQ ID NO: 123          moltype = DNA  length = 40
```

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```
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 123
agctcggtac ccggggatcc tggaacgtga acttgaaaac                        40

SEQ ID NO: 124          moltype = DNA  length = 41
FEATURE                 Location/Qualifiers
source                  1..41
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 124
atgcgggagt gactagtatt tatgctttct ataaaggaga c                      41

SEQ ID NO: 125          moltype = DNA  length = 67
FEATURE                 Location/Qualifiers
source                  1..67
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 125
gctcggtacc cggggatcct gtaatctatc taattttatg ttcgtttcat aaatttaaaa  60
ccataca                                                            67

SEQ ID NO: 126          moltype = DNA  length = 63
FEATURE                 Location/Qualifiers
source                  1..63
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 126
aaatgcggga gtgactagta ctctgtgatt ttaaaaagta agtcataagg gttttatatt  60
aga                                                                63

SEQ ID NO: 127          moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 127
agctcggtac ccggggatcc cgaccggctt ccggaacgtt                        40

SEQ ID NO: 128          moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
source                  1..46
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 128
atgcgggagt gactagtcat tcaatctttt ttagtgatta atcggt                 46

SEQ ID NO: 129          moltype = DNA  length = 47
FEATURE                 Location/Qualifiers
source                  1..47
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 129
agctcggtac ccggggatcc ttgcttataa atctattcgt ctgacag                47

SEQ ID NO: 130          moltype = DNA  length = 43
FEATURE                 Location/Qualifiers
source                  1..43
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 130
atgcgggagt gactagtatt gcgcgctttt aataagaaga cac                    43

SEQ ID NO: 131          moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 131
agctcggtac ccggggatcc gctggcactg gcctatggta                        40

SEQ ID NO: 132          moltype = DNA  length = 55
FEATURE                 Location/Qualifiers
source                  1..55
```

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```
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 132
atgcgggagt gactagtacg tattaggttt ttaaataaaa caataagtaa ataac       55

SEQ ID NO: 133        moltype = DNA  length = 57
FEATURE               Location/Qualifiers
source                1..57
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 133
gctcggtacc cggggatcca ataaaagcgc ctcttatagc atgatactat tttttgt     57

SEQ ID NO: 134        moltype = DNA  length = 49
FEATURE               Location/Qualifiers
source                1..49
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 134
aaatgcggga gtgactagta ccaatatacg aaatctgcaa agtctttgc              49

SEQ ID NO: 135        moltype = DNA  length = 58
FEATURE               Location/Qualifiers
source                1..58
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 135
gctcggtacc cggggatccg gtggtgagaa atattcggga aatataaaaa tagtatcc    58

SEQ ID NO: 136        moltype = DNA  length = 48
FEATURE               Location/Qualifiers
source                1..48
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 136
aaatgcggga gtgactagta ccgatgtacg aaatttgcaa agtctttg               48

SEQ ID NO: 137        moltype = DNA  length = 54
FEATURE               Location/Qualifiers
source                1..54
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 137
gctcggtacc cggggatcca aagatagtaa aaatcaaccc attccgattc aaag        54

SEQ ID NO: 138        moltype = DNA  length = 63
FEATURE               Location/Qualifiers
source                1..63
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 138
aaatgcggga gtgactagtg ttttttgttt aattgtatgt tcactaattg gtttttgaat  60
agt                                                                63

SEQ ID NO: 139        moltype = DNA  length = 48
FEATURE               Location/Qualifiers
source                1..48
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 139
gctcggtacc cggggatccc tacgaccttt accgctacca ttatcaac               48

SEQ ID NO: 140        moltype = DNA  length = 65
FEATURE               Location/Qualifiers
source                1..65
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 140
aaatgcggga gtgactagta cttttatatt taaaaataca tttgctataa agtcgataca  60
aagga                                                              65

SEQ ID NO: 141        moltype = DNA  length = 62
FEATURE               Location/Qualifiers
source                1..62
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
```

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```
SEQUENCE: 141
gctcggtacc cggggatccg caaatgataa aaaaagcaat tttgaatgaa aagatataca  60
tg                                                                 62

SEQ ID NO: 142          moltype = DNA  length = 64
FEATURE                 Location/Qualifiers
source                  1..64
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 142
aaatgcggga gtgactagtg tttttctata agattttatt agtttgaaaa aaggtctttt  60
aggc                                                               64

SEQ ID NO: 143          moltype = DNA  length = 45
FEATURE                 Location/Qualifiers
source                  1..45
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 143
agctcggtac ccggggatcc ttgcaatcat tacctgaaca aacct                  45

SEQ ID NO: 144          moltype = DNA  length = 48
FEATURE                 Location/Qualifiers
source                  1..48
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 144
atgcgggagt gactagtctt tttatcgttt tcatttatat aacgattc               48

SEQ ID NO: 145          moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 145
agctcggtac ccggggatcc gaaacgccag acgaatcagg                        40

SEQ ID NO: 146          moltype = DNA  length = 47
FEATURE                 Location/Qualifiers
source                  1..47
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 146
atgcgggagt gactagtcaa tactttttta attttcattt cttttgc                47

SEQ ID NO: 147          moltype = DNA  length = 38
FEATURE                 Location/Qualifiers
source                  1..38
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 147
gctcggtacc cggggatcca agtgcaggag catgagct                          38

SEQ ID NO: 148          moltype = DNA  length = 54
FEATURE                 Location/Qualifiers
source                  1..54
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 148
aaatgcggga gtgactagta gtattaaaaa ttaagactat gcaaatgaaa gcaa        54

SEQ ID NO: 149          moltype = DNA  length = 54
FEATURE                 Location/Qualifiers
source                  1..54
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 149
gctcggtacc cggggatcca gatagatatt gggagtgcat atgtttgttt ttac        54

SEQ ID NO: 150          moltype = DNA  length = 74
FEATURE                 Location/Qualifiers
source                  1..74
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 150
aaatgcggga gtgactagtt tctatattct ttatatttga ttagtttcta ttatatgatt  60
```

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```
aaacagcgga tatc                                                    74

SEQ ID NO: 151          moltype = DNA  length = 47
FEATURE                 Location/Qualifiers
source                  1..47
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 151
gctcggtacc cggggatcct atgaaagtca gcttttacgc ctctttg                47

SEQ ID NO: 152          moltype = DNA  length = 75
FEATURE                 Location/Qualifiers
source                  1..75
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 152
aaatgcggga gtgactagtg catagttttc tacattaata attggtttat ataatctcaa  60
aaatgatatc ttata                                                   75

SEQ ID NO: 153          moltype = DNA  length = 45
FEATURE                 Location/Qualifiers
source                  1..45
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 153
gctcggtacc cggggatcct gttccttaca aagcctcctt ttcca                  45

SEQ ID NO: 154          moltype = DNA  length = 70
FEATURE                 Location/Qualifiers
source                  1..70
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 154
aaatgcggga gtgactagta ctgtttaatt tgataggtta ataatatatt tagtttatag  60
ttaggtcaac                                                         70

SEQ ID NO: 155          moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 155
agctcggtac ccggggatcc actacctcaa aacgcagatc                        40

SEQ ID NO: 156          moltype = DNA  length = 68
FEATURE                 Location/Qualifiers
source                  1..68
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 156
aaatgcggga gtgactagtg tatcagaatt ttaaattagt attagagttc acatttaagg  60
ataaatca                                                           68

SEQ ID NO: 157          moltype = DNA  length = 41
FEATURE                 Location/Qualifiers
source                  1..41
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 157
agctcggtac ccggggatcc gttctaactt ttaccgcaaa c                      41

SEQ ID NO: 158          moltype = DNA  length = 68
FEATURE                 Location/Qualifiers
source                  1..68
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 158
aaatgcggga gtgactagtt ttctttatta ttttggttaa acatttatat catgatcctt  60
ataaaagg                                                           68

SEQ ID NO: 159          moltype = DNA  length = 39
FEATURE                 Location/Qualifiers
source                  1..39
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 159
```

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```
gctcggtacc cggggatcct gtggacattg gtacggacg                          39

SEQ ID NO: 160          moltype = DNA  length = 79
FEATURE                 Location/Qualifiers
source                  1..79
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 160
aaatgcggga gtgactagta atattatagt atttagttat cacttaaaaa tttagttatt  60
atcttattgt tgattattc                                                79

SEQ ID NO: 161          moltype = DNA  length = 40
FEATURE                 Location/Qualifiers
source                  1..40
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 161
agctcggtac ccggggatcc ccgggcgaat ggcacaccta                         40

SEQ ID NO: 162          moltype = DNA  length = 45
FEATURE                 Location/Qualifiers
source                  1..45
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 162
atgcgggagt gactagtagc attattcatt ttttaattat gatac                   45

SEQ ID NO: 163          moltype = DNA  length = 43
FEATURE                 Location/Qualifiers
source                  1..43
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 163
gctcggtacc cggggatccg tacatgcagg atctatatcc ccg                     43

SEQ ID NO: 164          moltype = DNA  length = 56
FEATURE                 Location/Qualifiers
source                  1..56
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 164
aaatgcggga gtgactagta tataattaga ttattgtttc gactgattga cgcaga       56

SEQ ID NO: 165          moltype = DNA  length = 42
FEATURE                 Location/Qualifiers
source                  1..42
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 165
gctcggtacc cggggatccc ttcggaattg ctaacaccta cg                      42

SEQ ID NO: 166          moltype = DNA  length = 76
FEATURE                 Location/Qualifiers
source                  1..76
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 166
aaatgcggga gtgactagta agttagactt tttgaataac ataataatta agtcaatata  60
aatagttaag tatagt                                                   76

SEQ ID NO: 167          moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
source                  1..46
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 167
agctcggtac ccggggatcc aatgtaagga caagtcctga gaagag                  46

SEQ ID NO: 168          moltype = DNA  length = 47
FEATURE                 Location/Qualifiers
source                  1..47
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 168
atgcgggagt gactagtgat atgattcttt tagtattagc tgatggg                 47
```

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```
SEQ ID NO: 169          moltype = DNA  length = 44
FEATURE                 Location/Qualifiers
source                  1..44
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 169
gctcggtacc cggggatccg atgtgcacta tgtcttggct gatg                    44

SEQ ID NO: 170          moltype = DNA  length = 72
FEATURE                 Location/Qualifiers
source                  1..72
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 170
aaatgcggga gtgactagta aattattaga ttagttaatg ataaatactt gttttccatt  60
taaaagagat tc                                                       72

SEQ ID NO: 171          moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
source                  1..46
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 171
gctcggtacc cggggatcca caatcggcta aagtcataaa cctgac                  46

SEQ ID NO: 172          moltype = DNA  length = 58
FEATURE                 Location/Qualifiers
source                  1..58
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 172
aaatgcggga gtgactagtc ttttttataa tattaatgag ttctattgaa ttcacgtc    58

SEQ ID NO: 173          moltype = DNA  length = 44
FEATURE                 Location/Qualifiers
source                  1..44
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 173
agctcggtac ccggggatcc aaaaacaatg caagaaatgg aaac                    44

SEQ ID NO: 174          moltype = DNA  length = 67
FEATURE                 Location/Qualifiers
source                  1..67
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 174
aaatgcggga gtgactagta atttattgta ttagattata aactctattc aattgttgat  60
tgatcca                                                             67

SEQ ID NO: 175          moltype = DNA  length = 41
FEATURE                 Location/Qualifiers
source                  1..41
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 175
gctcggtacc cggggatcca gttgtgtttc ttgcagccaa c                       41

SEQ ID NO: 176          moltype = DNA  length = 65
FEATURE                 Location/Qualifiers
source                  1..65
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 176
aaatgcggga gtgactagta acgtttttct ttttacatat taaattattg gttcactaaa  60
aattc                                                               65

SEQ ID NO: 177          moltype = DNA  length = 51
FEATURE                 Location/Qualifiers
source                  1..51
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 177
gctcggtacc cggggatccg ctactctgtg accactattt ataattaccg g            51

SEQ ID NO: 178          moltype = DNA  length = 66
```

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```
FEATURE                 Location/Qualifiers
source                  1..66
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 178
aaatgcggga gtgactagtg tacatcaatt taaagttaat attaggatta ctttttgttt  60
tcactg                                                              66

SEQ ID NO: 179          moltype = DNA  length = 41
FEATURE                 Location/Qualifiers
source                  1..41
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 179
gctcggtacc cggggatcct aatgtagctg gcagacatcc g                       41

SEQ ID NO: 180          moltype = DNA  length = 63
FEATURE                 Location/Qualifiers
source                  1..63
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 180
aaatgcggga gtgactagta tgattctaaa aagttaaacg ttatttatgt atgattgtga  60
tgc                                                                 63

SEQ ID NO: 181          moltype = DNA  length = 58
FEATURE                 Location/Qualifiers
source                  1..58
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 181
gctcggtacc cggggatcca caaaaaaaca ttcattccta aaataaagga tgatggac    58

SEQ ID NO: 182          moltype = DNA  length = 68
FEATURE                 Location/Qualifiers
source                  1..68
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 182
aaatgcggga gtgactagtg gataatttaa aattaatatt aggttaatac atttcaggca  60
actagatc                                                            68

SEQ ID NO: 183          moltype = DNA  length = 47
FEATURE                 Location/Qualifiers
source                  1..47
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 183
gctcggtacc cggggatccc tgcaaaacgt cctgtttcta aaaaatg                 47

SEQ ID NO: 184          moltype = DNA  length = 68
FEATURE                 Location/Qualifiers
source                  1..68
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 184
aaatgcggga gtgactagtc tgtttccttt ttttcataat actacattta ataataaaga  60
ttcatact                                                            68

SEQ ID NO: 185          moltype = DNA  length = 57
FEATURE                 Location/Qualifiers
source                  1..57
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 185
gctcggtacc cggggatcca aggaagtgtt tagatgacat aatgattatt tgaacag      57

SEQ ID NO: 186          moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
source                  1..46
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 186
aaatgcggga gtgactagtc gttgtacctt tcactaatac ggatgc                  46

SEQ ID NO: 187          moltype = DNA  length = 43
```

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```
FEATURE                 Location/Qualifiers
source                  1..43
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 187
gctcggtacc cggggatccc ctgtcacctt tttaggtgtt tgg                    43

SEQ ID NO: 188          moltype = DNA  length = 64
FEATURE                 Location/Qualifiers
source                  1..64
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 188
aaatgcggga gtgactagta ttctcctata acctattttc atactaatta tttatatcta  60
atat                                                               64

SEQ ID NO: 189          moltype = DNA  length = 39
FEATURE                 Location/Qualifiers
source                  1..39
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 189
gctcggtacc cggggatcct ccttgctttt gtgggggtg                         39

SEQ ID NO: 190          moltype = DNA  length = 71
FEATURE                 Location/Qualifiers
source                  1..71
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 190
aaatgcggga gtgactagta attttatcta tttctaatga ggattttatc tttgctttac  60
tataattata c                                                       71

SEQ ID NO: 191          moltype = DNA  length = 49
FEATURE                 Location/Qualifiers
source                  1..49
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 191
gctcggtacc cggggatcct ctcttgaaac tgtgaagact caaaagaag              49

SEQ ID NO: 192          moltype = DNA  length = 57
FEATURE                 Location/Qualifiers
source                  1..57
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 192
aaatgcggga gtgactagta ttatttcagg ttatttatag caaagacgac taagaag     57

SEQ ID NO: 193          moltype = DNA  length = 44
FEATURE                 Location/Qualifiers
source                  1..44
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 193
agctcggtac ccggggatcc atattcctga aagccggaga atcc                   44

SEQ ID NO: 194          moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
source                  1..46
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 194
atgcgggagt gactagtgac gctatgtgta atttttacct tgtgtg                 46

SEQ ID NO: 195          moltype = DNA  length = 61
FEATURE                 Location/Qualifiers
source                  1..61
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 195
gctcggtacc cggggatccg aatacaattt ataattatcg ggcgaaagta aaaaacaaag  60
c                                                                  61

SEQ ID NO: 196          moltype = DNA  length = 63
FEATURE                 Location/Qualifiers
```

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```
source                  1..63
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 196
aaatgcggga gtgactagtg cgtattaatt ttaaagttta taattaaggt atgtgcttga  60
cag                                                                63

SEQ ID NO: 197          moltype = DNA  length = 39
FEATURE                 Location/Qualifiers
source                  1..39
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 197
gctcggtacc cggggatcca catttctccc ttgaagggc                         39

SEQ ID NO: 198          moltype = DNA  length = 71
FEATURE                 Location/Qualifiers
source                  1..71
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 198
aaatgcggga gtgactagta aatataaata ataaaatggt taaagtgcat ccgaacaata  60
aatattattg c                                                       71

SEQ ID NO: 199          moltype = DNA  length = 57
FEATURE                 Location/Qualifiers
source                  1..57
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 199
gctcggtacc cggggatcca aagttagaag tcatcaatta atagaccttc attttgg     57

SEQ ID NO: 200          moltype = DNA  length = 56
FEATURE                 Location/Qualifiers
source                  1..56
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 200
gctcggtacc cggggatccg tttgtagatc ctctttataa atacatcaat gaaact      56

SEQ ID NO: 201          moltype = DNA  length = 77
FEATURE                 Location/Qualifiers
source                  1..77
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 201
aaatgcggga gtgactagtg attttgtttt ttttcatacg taaaaaatta atgattaata  60
aaatattata ttgttgg                                                 77

SEQ ID NO: 202          moltype = DNA  length = 39
FEATURE                 Location/Qualifiers
source                  1..39
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 202
gctcggtacc cggggatccc cattggactc ccgcaaaga                         39

SEQ ID NO: 203          moltype = DNA  length = 73
FEATURE                 Location/Qualifiers
source                  1..73
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 203
aaatgcggga gtgactagtt ttacatttca tgtttttcat tctagttaat aataaatgta  60
tagttaatta aac                                                     73

SEQ ID NO: 204          moltype = DNA  length = 50
FEATURE                 Location/Qualifiers
source                  1..50
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 204
gctcggtacc cggggatccg aataaatgtc gaatttgact cagcgctaag             50

SEQ ID NO: 205          moltype = DNA  length = 64
FEATURE                 Location/Qualifiers
```

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```
source                  1..64
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 205
aaatgcggga gtgactagta atattattat tttataactt aatacttaca ggcatatgag  60
cccc                                                               64

SEQ ID NO: 206          moltype = DNA  length = 47
FEATURE                 Location/Qualifiers
source                  1..47
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 206
gctcggtacc cggggatccg tctgcctgat gtaaaagagt agttgca                47

SEQ ID NO: 207          moltype = DNA  length = 52
FEATURE                 Location/Qualifiers
source                  1..52
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 207
aaatgcggga gtgactagtt cgttactatt taggttgaag tttattctgc cg          52

SEQ ID NO: 208          moltype = DNA  length = 39
FEATURE                 Location/Qualifiers
source                  1..39
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 208
gctcggtacc cggggatcca atgtcgcgat gagcaacag                         39

SEQ ID NO: 209          moltype = DNA  length = 69
FEATURE                 Location/Qualifiers
source                  1..69
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 209
aaatgcggga gtgactagta gtttactttt tttagtttct actcttttta gtatatattt  60
aacctattg                                                          69

SEQ ID NO: 210          moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
source                  1..46
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 210
gctcggtacc cggggatccc gtaaagggaa ctatagtgca tcttgc                 46

SEQ ID NO: 211          moltype = DNA  length = 72
FEATURE                 Location/Qualifiers
source                  1..72
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 211
aaatgcggga gtgactagta gcaaaaatat ttaagatatt agtaaataaa aaattaaccg  60
ttcattaatt ga                                                      72

SEQ ID NO: 212          moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
source                  1..46
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 212
gctcggtacc cggggatcca tttttccagt tccaatcggc attatg                 46

SEQ ID NO: 213          moltype = DNA  length = 58
FEATURE                 Location/Qualifiers
source                  1..58
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 213
aaatgcggga gtgactagta aatattccta ttagattata taccgcaaat gtaacaac    58

SEQ ID NO: 214          moltype = DNA  length = 43
FEATURE                 Location/Qualifiers
source                  1..43
```

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```
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 214
agctcggtac ccggggatcc tacttcctgc ctcatctgct ttc                    43

SEQ ID NO: 215        moltype = DNA  length = 47
FEATURE               Location/Qualifiers
source                1..47
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 215
atgcgggagt gactagttct atttatggta ttaaattata agctaac                47

SEQ ID NO: 216        moltype = DNA  length = 47
FEATURE               Location/Qualifiers
source                1..47
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 216
agctcggtac ccggggatcc atcgtctgga tggaaaatct cataaag                47

SEQ ID NO: 217        moltype = DNA  length = 52
FEATURE               Location/Qualifiers
source                1..52
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 217
atgcgggagt gactagtatt ataagttgag ttactttata agtaataaac ag          52

SEQ ID NO: 218        moltype = DNA  length = 39
FEATURE               Location/Qualifiers
source                1..39
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 218
gctcggtacc cggggatcca tcggtggcgg agcctgtcc                         39

SEQ ID NO: 219        moltype = DNA  length = 46
FEATURE               Location/Qualifiers
source                1..46
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 219
aaatgcggga gtgactagta acagaatcca aagaaaggat gctccc                 46

SEQ ID NO: 220        moltype = DNA  length = 41
FEATURE               Location/Qualifiers
source                1..41
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 220
agctcggtac ccggggatcc ttatatggaa gacctggaag g                      41

SEQ ID NO: 221        moltype = DNA  length = 70
FEATURE               Location/Qualifiers
source                1..70
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 221
aaatgcggga gtgactagta ctacttgttt ttaattaata ataataaggt taccaaatac  60
gtttaatacg                                                         70

SEQ ID NO: 222        moltype = DNA  length = 43
FEATURE               Location/Qualifiers
source                1..43
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 222
gctcggtacc cggggatcca gaggaactat agtgcttctt gcg                    43

SEQ ID NO: 223        moltype = DNA  length = 63
FEATURE               Location/Qualifiers
source                1..63
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 223
```

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```
aaatgcggga gtgactagtg ttactttgtt ttttttaatt aatactaagg ttatcaatcg  60
cct                                                                63

SEQ ID NO: 224          moltype = DNA  length = 48
FEATURE                 Location/Qualifiers
source                  1..48
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 224
gctcggtacc cggggatcca tatttgactc cggattattt tcgctggt               48

SEQ ID NO: 225          moltype = DNA  length = 73
FEATURE                 Location/Qualifiers
source                  1..73
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 225
aaatgcggga gtgactagtt agtttttata taaatattag aatcgatatt ccatttatta  60
ttttcgattc aca                                                     73

SEQ ID NO: 226          moltype = DNA  length = 43
FEATURE                 Location/Qualifiers
source                  1..43
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 226
agctcggtac ccggggatcc agaatataac aacctttatc acg                    43

SEQ ID NO: 227          moltype = DNA  length = 69
FEATURE                 Location/Qualifiers
source                  1..69
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 227
aaatgcggga gtgactagta aattaatatt agttttatta aaggtaaaaa gggtaaaaac  60
aagttgaag                                                          69

SEQ ID NO: 228          moltype = DNA  length = 42
FEATURE                 Location/Qualifiers
source                  1..42
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 228
agctcggtac ccggggatcc ctattatcag aagatggagt ga                     42

SEQ ID NO: 229          moltype = DNA  length = 75
FEATURE                 Location/Qualifiers
source                  1..75
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 229
aaatgcggga gtgactagta gaaaataccg tttttaagaa tttatataat aataatgatc  60
ataattttac tttcg                                                   75

SEQ ID NO: 230          moltype = DNA  length = 42
FEATURE                 Location/Qualifiers
source                  1..42
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 230
gctcggtacc cggggatcca ttttccgggt agtgctgact tt                     42

SEQ ID NO: 231          moltype = DNA  length = 75
FEATURE                 Location/Qualifiers
source                  1..75
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 231
aaatgcggga gtgactagtt attattagtt ctttttaata tgtgtactat tttattgtta  60
tttatctaat gacga                                                   75

SEQ ID NO: 232          moltype = DNA  length = 54
FEATURE                 Location/Qualifiers
source                  1..54
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
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SEQUENCE: 232
gctcggtacc cggggatcct tgagtaaaga atacaccaat ctggaggtat atct        54

SEQ ID NO: 233          moltype = DNA  length = 64
FEATURE                 Location/Qualifiers
source                  1..64
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 233
aaatgcggga gtgactagtc ttttgttctt ttatattaga ttattaatat tcgagtgtgt  60
ccac                                                               64

SEQ ID NO: 234          moltype = DNA  length = 39
FEATURE                 Location/Qualifiers
source                  1..39
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 234
gctcggtacc cggggatcca attgagtgtc catcaggcg                         39

SEQ ID NO: 235          moltype = DNA  length = 75
FEATURE                 Location/Qualifiers
source                  1..75
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 235
aaatgcggga gtgactagtc atttcaattt aaagttaata catattacta tctaatcaat  60
acttatgtta catgc                                                   75

SEQ ID NO: 236          moltype = DNA  length = 44
FEATURE                 Location/Qualifiers
source                  1..44
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 236
gctcggtacc cggggatcca gtacctacca atggagaatt cagc                   44

SEQ ID NO: 237          moltype = DNA  length = 60
FEATURE                 Location/Qualifiers
source                  1..60
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 237
aaatgcggga gtgactagta ccatacaaac aaaacaggat taatatttgt agtattcttc  60

SEQ ID NO: 238          moltype = DNA  length = 62
FEATURE                 Location/Qualifiers
source                  1..62
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 238
gctcggtacc cggggatcca caattatatt tgaaaagttt gccatattgc ttttatatat  60
gg                                                                 62

SEQ ID NO: 239          moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
source                  1..46
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 239
aaatgcggga gtgactagtc ttgtcctcac aagagagaaa aaaagg                 46

SEQ ID NO: 240          moltype = DNA  length = 50
FEATURE                 Location/Qualifiers
source                  1..50
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 240
gctcggtacc cggggatccg aatgttatgg atatcaattg gaaggacgga             50

SEQ ID NO: 241          moltype = DNA  length = 62
FEATURE                 Location/Qualifiers
source                  1..62
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 241
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aaatgcggga gtgactagtg atttaacttg ttgtgaggtt aaatattggg ttaattatta  60
ga                                                                 62

SEQ ID NO: 242          moltype = DNA  length = 63
FEATURE                 Location/Qualifiers
source                  1..63
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 242
gctcggtacc cggggatccc tggaattttt tttatgtaat ataccccttta cttcttatta  60
cgg                                                                63

SEQ ID NO: 243          moltype = DNA  length = 63
FEATURE                 Location/Qualifiers
source                  1..63
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 243
aaatgcggga gtgactagtt gtttttctgt gattaaaggt taataattag ttgggttaat  60
atg                                                                63

SEQ ID NO: 244          moltype = DNA  length = 43
FEATURE                 Location/Qualifiers
source                  1..43
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 244
gctcggtacc cggggatcct ggagagcaat agagacctta tgc                    43

SEQ ID NO: 245          moltype = DNA  length = 68
FEATURE                 Location/Qualifiers
source                  1..68
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 245
aaatgcggga gtgactagtt gtttttctgt gataaaaggt taataattag attggttaaa  60
aaaaagtg                                                           68

SEQ ID NO: 246          moltype = DNA  length = 43
FEATURE                 Location/Qualifiers
source                  1..43
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 246
agctcggtac ccggggatcc agaagggagt cttgcactat ttc                    43

SEQ ID NO: 247          moltype = DNA  length = 48
FEATURE                 Location/Qualifiers
source                  1..48
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 247
atgcgggagt gactagtccc ttattccacc tttttattat atgacaag               48

SEQ ID NO: 248          moltype = DNA  length = 41
FEATURE                 Location/Qualifiers
source                  1..41
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 248
gctcggtacc cggggatccg gaagttgatg ctgaagatgt t                      41

SEQ ID NO: 249          moltype = DNA  length = 49
FEATURE                 Location/Qualifiers
source                  1..49
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 249
aaatgcggga gtgactagtc attaatttct tcctttatac actaaatac              49

SEQ ID NO: 250          moltype = DNA  length = 46
FEATURE                 Location/Qualifiers
source                  1..46
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 250
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gctcggtacc cggggatcct ctttgtctcc gaaaaacaag agtccg                46

SEQ ID NO: 251          moltype = DNA  length = 50
FEATURE                 Location/Qualifiers
source                  1..50
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 251
aaatgcggga gtgactagtt tcaataagtt gtttttcacc atctccgtgc            50

SEQ ID NO: 252          moltype = DNA  length = 48
FEATURE                 Location/Qualifiers
source                  1..48
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 252
gctcggtacc cggggatcct aaagccaaaa agaaacttac tgtacctc              48

SEQ ID NO: 253          moltype = DNA  length = 52
FEATURE                 Location/Qualifiers
source                  1..52
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 253
aaatgcggga gtgactagtt ttcaatgttg atttatctta ggacaatctc aa         52

SEQ ID NO: 254          moltype = DNA  length = 63
FEATURE                 Location/Qualifiers
source                  1..63
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 254
gctcggtacc cggggatcct ttttttcttc ttttattgaa tgatgacgga ttttaaaatc  60
atc                                                               63

SEQ ID NO: 255          moltype = DNA  length = 65
FEATURE                 Location/Qualifiers
source                  1..65
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 255
aaatgcggga gtgactagta ctttattagg ttttataatt attaaaagtg ttattttact  60
gttgc                                                             65

SEQ ID NO: 256          moltype = DNA  length = 45
FEATURE                 Location/Qualifiers
source                  1..45
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 256
gctcggtacc cggggatcct gtctcccgtg gaatatatca agtcc                 45

SEQ ID NO: 257          moltype = DNA  length = 49
FEATURE                 Location/Qualifiers
source                  1..49
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 257
aaatgcggga gtgactagtg ctatcaaatt tagtggtttg ttgatagcg             49

SEQ ID NO: 258          moltype = DNA  length = 51
FEATURE                 Location/Qualifiers
source                  1..51
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 258
gctcggtacc cggggatccc aggcagatga tacattcaca aagaaaaaga t          51

SEQ ID NO: 259          moltype = DNA  length = 65
FEATURE                 Location/Qualifiers
source                  1..65
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 259
aaatgcggga gtgactagta actaaaggta gttttagatt taaagcatat ttaggatata  60
atgca                                                             65
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SEQ ID NO: 260          moltype = DNA  length = 51
FEATURE                 Location/Qualifiers
source                  1..51
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 260
gctcggtacc cggggatcca cttcctaaag aatactttac gggaacgatt c           51

SEQ ID NO: 261          moltype = DNA  length = 56
FEATURE                 Location/Qualifiers
source                  1..56
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 261
aaatgcggga gtgactagta tatcaaaact tttaagttgt ttgacaggta taccga      56

SEQ ID NO: 262          moltype = DNA  length = 700
FEATURE                 Location/Qualifiers
source                  1..700
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 262
agaatataac aacctttatc acgctgtgta ctatccaaat agcaattaaa tagtttctcc  60
cttacacccg taattaaacg actgccaaaa tgctttatat ttaagaagtg agtttttcgc  120
ccggtctgac cgaaacaatc aaccaattaa aaaggaatag aggaataatt aaactaagtt  180
cttgtagaac ttagcacaaa aaacagtctg ttaatccatt tgtatctaaa ctaacgcatc  240
taactaagca atagatttac catctttttt gctaaaaatc aacgattcgt gcgcaaatat  300
actaattagt ttgaaaaagt catactattt ttcaataata tttcatattt aaattacaaa  360
taagtttttc aattattctc atttaatcaa tcaacgggta gaaacagagt gagtatttca  420
ctattacacg tttacagccc ccaatacttc ccattgatta tcaacaacat gcattctatt  480
ccatcttatc atctactata ttatagttct acaagaacta agacatagaa cctattattt  540
ttctgacttt aaatcagcat agttcagcac acaaataaaa gttttaactt ctaattttaa  600
tgcctatgag aaagaaataa gtattccaaa tccaagagta cccacaagta cttcaacttg  660
tttttaccct ttttaccttt aataaaacta atattaattt                        700

SEQ ID NO: 263          moltype = DNA  length = 700
FEATURE                 Location/Qualifiers
source                  1..700
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 263
ctattatcag aagatggagt gataaaaggg caatatagta ctatgggaga tacttatgtt  60
aattggacac gtgatgacac cataacggga gatgtatatc aaaagagtta ttttgatcgt  120
atgattgaaa gaaatcaagt aaatgcttat ctgaaagaaa aggaagaagc tgttcgtatt  180
tggaaggaaa tagaactgat atctcaaaaa ctacattttc cctcagaaga attgaatcat  240
tttattcgta tttcctgttc gtatggacgc attaaatatg agctttttgc tgtttcgtgg  300
cagattatgc tatgcggtta tgtggcagat acaacaaaaa agtcttttaa ccggatagag  360
atggataaat atattactgc atttgatgat ttgtggaaag aatggaacga cttatctcta  420
gaaaacgata attgcccttc aatgtataag atttcttcta actttttttgg ttttcctgta  480
ggtatacaag agaccattga taaatacagg aaatagtttt catttttttct tcttatatgt  540
tatagaatat aaaaaaataa atgaatatta cttagtggtt agtattagtc tagtcgtctt  600
actattaata gtagcaaaaa gtatgagaaa gaaacataaa ataacgaaag taaaattatg  660
atcattatta ttatataaat tcttaaaaac ggtattttct                        700

SEQ ID NO: 264          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 264
attttccggg tagtgctgac ttttgtcgtc cttattttta tcgtattttc aattgggaaa  60
gcatatatga tgaagatgat tgatagctac tgacggattc atcttggtaa attgatttag  120
aaagtcattt cttcataaaa gggagaaatg actttctttt ttaatatgtt ctgagctttc  180
ctgcatacaa gtaaatttat taataaaaaa catgtaattg ttttagtggt atatcatttt  240
taaatcgtca ttagataaat aacaataaaa tagtacacat attaaaaaga actaataata  300

SEQ ID NO: 265          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 265
ttgagtaaag aatacaccaa tctggaggta tatctgaatg agctagtgaa tcatctgtat  60
cctgcggatt ctaaaaaata aaactaaaag cccgaataaa cagttataaa agattaagac  120
gagagtacat ttccccataa atcctcgtct ttattcattt tatgccggaa aaacaaaaaa  180
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tactatcgta aaaacaaata ttacacatcc cacaagcccc aaaaacataa ttttgcacca  240
gtgagaactc taagagtgga cacactcgaa tattaataat ctaatataaa agaacaaaag  300

SEQ ID NO: 266          moltype = DNA  length = 400
FEATURE                 Location/Qualifiers
source                  1..400
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 266
aattgagtgt ccatcaggcg gctagcattt agagtatgat gaatgctagc cgcctgatgg  60
acacttttat tctaatccaa gcaaatactg aaaatgacta gtagaaatta ctatgtaaag  120
taaaatatgg aatttttggt attttaatcc caaaatctcg tatctgatat tttagtgata  180
aaatagtgca cctaaacgct caaaaagtcc cctctcttta tgttttatat aacttctttt  240
gcacatatga aacaaaaaat aagaactata aatcaggaat attaatgaat aaacatgaga  300
tgattcctgt ttcaattttc cccatgtttt caacgattga tttgcatgta acataagtat  360
tgattagata gtaatatgta ttaactttaa attgaaatga                        400

SEQ ID NO: 267          moltype = DNA  length = 500
FEATURE                 Location/Qualifiers
source                  1..500
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 267
agtacctacc aatggagaat tcagcaacat tatgcacaac ccattgcctc aaacggtcta  60
tttcaatcaa aaagttcagg cacgctttat caaactggaa gccaccactc ccactgatac  120
agccgcaaaa gttgaaccaa atgaaatcgg agtaacaata gccccttgat tttacattca  180
tcacaagtac taactaaaag caaaaatcag aatagaaaag acgccatcta ttttgatttt  240
tacactatat aaatcttctt attatcaaat taactccaat gaaggcaaag aaagagaaat  300
tagtcttaat gaagataaca gatctttaat atataaggac tgtctatcca aacttatcga  360
aaaatttaat taaccacaag attcatgctt attgaaaaca caagaatgaa ttgttaacac  420
ttttaatttc tatgattaat gaaaaacaaa atagtggtgg aagaatacta caaatattaa  480
tcctgttttg tttgtatggt                                              500

SEQ ID NO: 268          moltype = DNA  length = 400
FEATURE                 Location/Qualifiers
source                  1..400
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 268
acaattatat ttgaaaagtt tgccatattg cttttatata tggttattct tgtttcaaga  60
aaaaccggaa taaattgtat tatctacact ctttcttatt taaaaaacgc gttcagagca  120
tgtattttcg ttcaaaaggc ggtattttcc atgtttatgt acgattcttc attgctattt  180
cttatataag tcgttaagtt tgcaacagtt tttcacaggt attatgataa agtgcccgaa  240
gaaaaacaga atctaacttt tgtttaatta aaaaatagat aaaatagatt tatattgtta  300
cttaacagat tttaatatta tgagaaatgt gatgaatcgt aagcggcatt ggctgctatt  360
attgctcctc tcacctttt ttctctcttg tgaggacaag                         400

SEQ ID NO: 269          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 269
gaatgttatg gatatcaatt ggaaggacgg aagatacaac ttcaaagaaa ccccattatc  60
ccagctcatt tcgattataa atcaaatata ccaatcaaat ataattctag aaggaaagtt  120
tactaaacag ccttcattca caggcagcat ccgttatgat gaaacattgg atgacgtgat  180
agataaactc tgtttcagcc ttaaccttac atacaaaaaa cagaatagaa aaatagtaat  240
atataattaa ccatatttct aataattaac ccaatattta acctcacaac aagttaaatc  300

SEQ ID NO: 270          moltype = DNA  length = 900
FEATURE                 Location/Qualifiers
source                  1..900
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 270
ctggaatttt ttttatgtaa tataccctttt acttcttatt acggcctatt cgccagagat  60
tgttggtgaa ggagaaaata ttattatata tggtagaaat taaggtgtgc attttatttc  120
ttatgcattt attcttttgg ggatctacta cctttttat ttagtatatt tgaaaataaa  180
tagttgtgct tggctgttat gattcatttt tatatttaac agattgggat aagttgctct  240
agaacttggt agttttatac caataagtgt atttttcct gttttcatag gctattcaaa  300
ggttattaag tttgtgtgct acttaagacg gtgtaaagtt attaataaaa ttggtgaacg  360
caatgttttt tttattttaa ttatcggcaa acgatgtttt ttttaatttt tcattctact  420
actcagatcg taataagata gatataatct tttaattatt gtatattgtt gattattagt  480
attttatcgc tttggatacc aagttctaga gcgacttatt ccaatcggtc aattacgact  540
atatttctta ataattattt atgataatgc gaaattatag gccgcctccg ggctgtgatt  600
aaatttttat tatcgtttct tcagcataga tcagaacagt gctgaagaga gattgaattc  660
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attaaaaatt tcaatacccc caagaaaaac aaatgaatga taacagtcaa acacaactat  720
atatattcca aaacttacta aatattaaga taaagcatac acacccaaaa acaaacgtat  780
tagagtaaaa atgcacatct tatttctacc acattatcat aatgctagat atagaatagt  840
aagttttcta cttatccata ttaacccaac taattattaa cctttaatca cagaaaaaca  900

SEQ ID NO: 271          moltype = DNA  length = 700
FEATURE                 Location/Qualifiers
source                  1..700
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 271
tggagagcaa tagagacctt atgccaaatt gaataatttt gaagaagtcg taataggact  60
tggtatgtat gtgtataagt gtcttatata taattgatta attggttgat ggatgcttgg  120
gatgacaatt tatgaactat atagtagaat tgagattcta aaaaaatggt gtttgttgat  180
aattaaaata aaaaagatat tgtatttttc gattttatta ataactttac accgtcttag  240
aatagtacat gcacttaata acctttgaat agcctatgga aacagtagaa aatatacttt  300
ggggtataaa aataccaagt cctattacga cttagcccca attaatcaat atgattataa  360
ccttaaatta acatttatga aaactcttag caacagccct ccgcctttca aaatcggaga  420
attcgatctc atttttttac ttttatttca gcacagatca gaataggtat gatatgtatt  480
ctgagttcat tatcaacttc aatacccccca atttaagaag atgaataata gcagtcaaac  540
acacccatat attttcaaac ttactcatac atacaaaaac aaacgtatac cccttgtatg  600
catacccctag ttctacccac atagtagaca cacaagagta ggtttcccta tcactttttt  660
ttaaccaatc taattattaa ccttttatca cagaaaaaca                         700

SEQ ID NO: 272          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 272
cgttcacggg aacctttaca aatcaacgtt tggaaaagat tctggaatat tttaaagtat  60
cctccaaaat acgctggaaa catatcaatg atgacaagga tggaagtgac agaaaaaaag  120
agataataga gatttattga ttaaccttta acaatttagt agtatgaaag caaaacccac  180
ttagaaaaaa gtatgggaag attttggcag atctccccat actaaaatga atcaattgaa  240
aatgcttgtt tggcagacaa gcatagttaa ctcattttca acttaaatca atacaaaatt  300

SEQ ID NO: 273          moltype = DNA  length = 497
FEATURE                 Location/Qualifiers
source                  1..497
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 273
ggaagttgat gctgaagatg ttgctcaaga tattttctgt aagctttggt tacaaccgga  60
aatatggctt gacaatgaaa atgaattaga taactacctc tttataatga ccagaaacat  120
tattctgaat atcttcaagc atcagcaaat cgaacgggaa tatcaggaag gataccttga  180
gaaaacagta cttcatgaat tgatagaagg ggaagatgcc cttaataata tatattatga  240
agaaatgttg ctggttgttc gcctgacttt ggaaaaaatg cctgaacggc gaaggttaat  300
attcgagctg agtcgtttta agggattaag ttataaagaa atcgcagaaa agcttaatgt  360
ttccatccgt acggtagagc accaggtgta tttagcactg atagaactaa aaaaagtgct  420
tctattttta ttttttctat tttcctttaa gtagtgtttt tcttttagtt gtatttagtg  480
tataaaggaa gaaatta                                                  497

SEQ ID NO: 274          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 274
tctttgtctc cgaaaaacaa gagtccgaca atgcgccaca tatcattgtt caggttcgga  60
taataaaaat ccatcgacca ccgttttctt tgtggcggaa aacttcccag catcagcaac  120
tttgcttttg gtgggagaaa gggttttaaa ggatgttttt cgatttcaat ctccatattg  180
atgtaatttc ctacaaaaat aacgaatcta ttcttttcct tcaaaatagt tgcggaaaaa  240
aacaaattta aaaatatttg gctatttttg cacggagatg gtgaaaaaca acttattgaa  300

SEQ ID NO: 275          moltype = DNA  length = 500
FEATURE                 Location/Qualifiers
source                  1..500
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 275
ctcccaataa cttattaagt tataatgaac aggaaggcat ccatatccaa tcggtagacg  60
tacaaaaata tatcgcctgg aaagatggtt tttacctctt ccaaacagaa aaactaaaag  120
acattgctac aaaactcagc gattactatg gcaaaaagat catgatagac agtccattga  180
agaccattac ctgcagtggt aaactagatt tgaaagaaga tcttgacgaa gttcttcaga  240
cactaatacg gactgtcccg gcaagaatag aaaaatcaga tggaattatc catatttatg  300
taaaacatta attaaaatcg aaagcctatg aataaacatt atccttaaaa aaataaggcc  360
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gaataatacc cttaatatca tccggccttt gattaaatta cttacacgtt aatattaatt  420
aatctaatca ttacaaatgt atgaaaaagc accgattatt tagtcaccaa aggactaaag  480
ataaacaact attactaatc                                              500

SEQ ID NO: 276          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 276
ttttttctt cttttattga atgatgacgg attttaaaat catccatcca aacaacctaa  60
attgtacaga acctattcca tatcatatta caatgtcata acattatgac acataaaaaa  120
ctaggataca ggagataaac agctttttta aacaaaaaca acatatgtct caacaaattt  180
gatatcaaaa aaatcatttt tgaacaaagt atgaacaacc taaattaaag aatctaatta  240
atgaggttac atttgcaaca gtaaaataac acttttaata attataaaac ctaataaagt  300

SEQ ID NO: 277          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 277
tgtctcccgt ggaatatatc aagtccatcc gcatgaagaa agctgccatg ttattgcaac  60
aaaagaaatt caccgttgcc gaagtgatgt atatggtagg attttccaat cattcttatt  120
tctccaaatg ctttcaggca gagtttggaa aaacaccgcg ccaatacttg aatgacgggc  180
tgtagaggca ttttagggct tttcgtccta tttttatcct tatatgtcca atctgtgctt  240
ttatgaaaat gccaggcagt ctatctttgc cgctatcaac aaaccactaa atttgatagc  300

SEQ ID NO: 278          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 278
caggcagatg atacattcac aaagaaaaag ataatagtag atttatatta gtaaccataa  60
aaatgagaat agcctatgag ataacacaaa gatcgtaaaa aaaggaagaa agctgctacc  120
aacagctgtc ttcccccaat ttttcagatt cgcggtaagg agtcttgcaa acgctaaccg  180
gaatcaaacc acagttcatt atagtaataa actttagtta accgcaaatg tatgaaaaaa  240
aatcattcat ttattgcatt atatcctaaa tatgctttaa atctaaaact acctttagtt  300

SEQ ID NO: 279          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 279
acttcctaaa gaatacttta cgggaacgat tcctagtggc ggcatacaga acgccttgaa  60
tattctcatg cttacttcgc ctttttatta tgaaatggat ggctcggtca ttgtcttgaa  120
agagaagtag ataagcatct ttatcatgaa attagatata gccattcctg agttttcccc  180
cggaatggct ttttaattta tgaagaaccg ttagttaaca agagttaaag atagatagcc  240
gattggacga aaggggagag cagtcggtat acctgtcaaa caacttaaaa gttttgatat  300

SEQ ID NO: 280          moltype = DNA  length = 500
FEATURE                 Location/Qualifiers
source                  1..500
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 280
aggacgaaaa tgtaactttg ccataacaaa aaactttatg tctaaagata tagaaacttt  60
ggataataac aaagcccggg cttgcgaagt ctgggctttg cgcataaaaa agggtgtgcc  120
aacgttgaag tgcacctcaa aagttagata aaaaactttt ggggtcattt cacatttgac  180
acaatctctt tcttttcaac tttcttatac ttttatgacc aaagagaaag aaaaagatta  240
tgtgcgtttg aatatgttaa aatatgaccc gatttgtcac gtttaggtgg tatttctttt  300
ttgtcgaact aggaattttg tttttgcgac ctacagattt tccatttcct gttttcagac  360
tgcaaattta cgaataatcc atatttttat ttctatatat gtaataataa caaattaaag  420
aatttaataa ttccttaata ttcccgaaag aaatgtgaaa taaaatatat ggaattttgc  480
agcgagaaaa aatagtaagt                                              500

SEQ ID NO: 281          moltype = DNA  length = 363
FEATURE                 Location/Qualifiers
source                  1..363
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 281
cttccaatga tactgaagag aaaatcattg ctgatgattt gatggcgatg gaacggacac  60
ggttggcagc catgcccgaa cagcgacggc tgatctatac gttaaatcgt tttgaggata  120
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aatcttctcc ggagatagcc tccgaattag aattgagttg ccgtacagtg gaaaaccatc  180
tttttctcgg acgccgtgat atgcgtgact tcttccgaaa ctgtatataa aattattcat  240
ataataaaca acctttggtg cttatggaaa aggaatcaat actgagtgag aggtatcttt  300
atgcctcaac aaattttaga gaacaagaat ttaatactat ttttaaacct caaatttaat  360
gtt                                                                363

SEQ ID NO: 282          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 282
tctggagtcc gtacttaaat ccatcgaatt tatcagtgat atcaattata agaaagaagg  60
caggaatata cttctttata aaaaatgaga attaaaaaat agatcaatgt ttaacccgtt  120
aataaggaca gaatgaaagc atcaccctca tagaaactcc ctaaaaagat agaagcactc  180
ctaaggaatg cttctatccg caacccggac ggatattcat tcgcttcgac ccaaatgaat  240
aacgtatcgc acgttgcttg tttttaataa ctttagtcaa ttactaaaac gcacaaattt  300

SEQ ID NO: 283          moltype = DNA  length = 700
FEATURE                 Location/Qualifiers
source                  1..700
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 283
cgtgtggcac ggctgcagct acttttacga atccgtagtt catcttgtac ctttttatat  60
atagtgggta caaaaatagg aaatagtttt ggatttttgc ccttttgact ctgaatcctc  120
aaaatgaggt gtcttatgtc gttttaatga ctattgcata agcaactaat aagaatgtca  180
aatggaaagt aatatggtct tatttttgac ggtttatatg ggatatatct atttgtttat  240
taatattttg ttaattatgc aataaaaaga catttgagga aatttggtat aaaaaatgag  300
actttttgtt ttttctattt aactattata attatatttg tagccaaatt aaagaatttt  360
ataggcaatt tacacctaaa caaacgataa gcacttatta atatctataa ttttagagag  420
atggacatac actttattag tattgcagcg acacaagaca tttatttaga catatggcgt  480
aatattaaaa atcagccaag ctaatttccc tattctatat attgtataga ctatttgata  540
gtctgtcctg gaacgatgat aaaagtatac ttttcaaagt cgctccaagg ggagaagtat  600
attactgttt catgcgtgaa gcgtaatatg ctaagttttc gttttgtaga taaatctgta  660
aaaataaatc aattcattaa tttaaattca agtatcaaag                        700

SEQ ID NO: 284          moltype = DNA  length = 500
FEATURE                 Location/Qualifiers
source                  1..500
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 284
gtctaagtct tctctttata ggaaaatgaa attagcaaca ggactgtcac ccattgagtt  60
tattcgaaat ataagattaa aacatggaag tcaattattg aaggataaat caatatccgt  120
agcagaggta gcttatgaat gcggattttc taatcctaaa tattttgcaa cctgttttaa  180
agaagaattt ggcgtaactc caaaggaata tcaaaaatct tgttaggata aaaataatat  240
gaacttaaaa tacacaagta cgcgtcttaa tggaagatgc gtacttttcc atatatcaat  300
gatctatccc atttgaatga ttcctgaact tatattgaac gatttttaga cctgttatag  360
ttaatagcga ttatggtcca attttggaag tttttgaatg attagagaac ttctttctac  420
tggataactc gcacttttgt gacgcatttg atgcacaact aatacttatt tggtctaaat  480
aactttataa atctaatagt                                              500

SEQ ID NO: 285          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 285
ttcaatttca ataataactt ttgtgtgtta gagtccctgg aatgctgagt gtctacagca  60
gttccaggga tttctttatt atcttttcat ttaatgccaa agaaggttca ttctgttttg  120
aatattgtaa ttttgttagc cgatataatt attctttttg tttaaagaaa aaaaactact  180
tattttcttg ttatttaaaa taaattcata tttttgtaat cgtagtcaga accaaactat  240
gaaatattga cgtcctctct acacacagac aatttttatt aaccttaaaa gagcagtatt  300

SEQ ID NO: 286          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 286
tcaatgtgac accaagcgca ctgctgaata acgaagaata actgatataa gggttgctat  60
tatgaaacaa tgatagcagc ccttcgtctt aaaatgagct cattttaaga gacatccgtc  120
caagattata ctcaaagtgt aaaaaagaca cttatataac cgtttatcca cctcgaaaat  180
tcatttgtcc acctttaata tactcatcgg ttgtattttt gcgacactac aacgagtaga  240
attattgttg aaccattaat atcaatatct atgaagacaa ggaaatggcc gttactactt  300
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SEQ ID NO: 287          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 287
ttcattatcc ggccagaagt ttgatgaaaa acaattttat caatcaatta ctgacttcga  60
atatgagtgg acattatcca aagagcacca tcctataatt tctggagaga acccgatatt  120
gttggccaag acattatctg agaaatatat gcaatatttt tattaagtac atacctcaaa  180
ataattataa attataaaac aaaacagcct atgaatataa taccgaactt ataattaagg  240
aaattatcaa atctaaagaa gaaaaaaata cagaattact taactttaaa ttattaatgt  300

SEQ ID NO: 288          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 288
aaaataggaa tttgcgtctg atgtacaaaa acggtgtctg aagctttcac aaagatagag  60
caccctaaca agagaataag ggtaaataaa taatgatttc ttttcataaa tgggggtatt  120
agttaattta acgaaggcaa agataagatt ttctctgcat atatttaaca gtcaaagcga  180
caaacttgcg ttttttacca agttctcgta ggactagtca acactctgac caccgttctt  240
gctcttgtga tcattgacag ggtcggccgc aagcaactgg tctattacgg agtttcgggg  300

SEQ ID NO: 289          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 289
gctatggcta cggatacggt tacggacagg aaaaaggtgc taaatcgtaa tccggttcta  60
agaataaacc tgagaataaa cgatagcccg tttcaatctg attgaccaca gtatatcccc  120
caagatatag tcagtcagat atagccgacc gcttgatttt ccccaatcaa gcggtttgtt  180
gtattcatct acgttgacaa tataattttt atatcccata tcaaagaaaa gcgggtatcc  240
ggacaaccag atgcccgttt tttttgttat atttgtatta tcccttaaaa aatgataatt  300

SEQ ID NO: 290          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 290
tattgcccat cgtctggaac gtaaattcca ggtgaagatc agcatagaaa gcgaacgtct  60
gaaggccgaa cacttctccg gttctttcga cagcaatcag aatatttatg atatattaca  120
cgaaatcaac gttgagaaac aatacacgtg gaaagtcagt ggtgacacca tctttattac  180
cgataaaaga aagggggtaa gataaaagga aggagaaaga aaatggacac agccgataga  240
tataccggca gtccgcagct acgataaata actatatgtt aacctttaat agtgataaaa  300

SEQ ID NO: 291          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 291
ttgatgcttt ttttaaaagt tatttcttcg tttaccctat cttttccttt tataattctg  60
ataaagtaat atttcaggag gtatttgaaa ttaatatgta ctcataatac tcatcccacc  120
aagttctcca tgaacttata ccgccttaga gtttactaaa ttctatattt cacaacctaa  180
tttttaatca aaaatcaaca cacaatcaat gcctatggaa atattacagt attatgattt  240
accatcccta tcgtttacaa acaaaaccgg taaactagtt attattttaa aatcaaaatt  300

SEQ ID NO: 292          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 292
ggtggattac aatgatctta tccattcgtc ctttatatga atcggttaaa gtggaagtta  60
aaacgatgtg aagatgtgga gaagaacgat gattggaata taaaatattt aaaagaaaat  120
tttcaacaat aatggggagg ggaattatga tatagtttaa taaaactaag agaaaaaact  180
tcagattcta ttttttattc tttttaagag attacgattc ttttagttgt atctttttat  240
ttatgtgaat agatgtctga tgatgtaata tatcatttta tataaattaa aatttaatct  300

SEQ ID NO: 293          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
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                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 293
tggtgtttcc tttaaaacca aaatgccgtt ccttttaaac caacgactgc tccgttcgta  60
tattttaaag ctctttcata gaattgaaga tggcattttt atgcactaag caattgtttt  120
atgcaaacac atcgcataat cttgcaataa attatacatt tttttgctat ttattagatt  180
tcatagactt tgactacctg gctattctta aaaatagaac ataaagaagt atgaaaacag  240
ctataaattc attactccca atcaatcacg cttgccaacg cccaacccct aaaagtcaca  300

SEQ ID NO: 294         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 294
tagtttttca gaactactta atgctctatt tatcaaatga ttatgtattt atttttcaaa  60
aaaatgctta gtctaaccat tttttacgaa aaaaaatctt attttcgttt agtatggttg  120
cagtatcaaa tgtattactg atgaataagc gcttatgaaa aatcattttt agtgtaacct  180
ttaaatttat aaatatgaga aacagagata catagatcct ttgtatgagt ggcggttata  240
tttattaccc gcacatgttt gttaactacc taaaaactat ttctaattaa aaagaataag  300

SEQ ID NO: 295         moltype = DNA  length = 500
FEATURE                Location/Qualifiers
source                 1..500
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 295
acaaaaggag ataaatgacc agatatataa cagtagtatt acattaaggt aaagaacaac  60
catggtatag tattattgca atttaactat ttaaagtttg tttataatca aatcatttaa  120
agatttttgt ccttctatga ttttttgtgt ttgataaatg tcgtaattaa ataaaaaata  180
tcacgcataa tgactttttc ttttttctaa atttcttcaa atgacaaatt attgttacct  240
ttgtaatgta atgtagttaa tggttgcgct tataaagtcc ttggaaagga tttatgtata  300
aaagaggtag atgtttactc tgttcttgtt tggattatca gcatcactga tatgaaataa  360
caaaaaaaat atacaatggc taagcggacg gacaggcagg gaaatagtac agattcccaa  420
tccccctctt tataatacat tgcgtataag atttattaac tgtctggtct ggggaatcta  480
cagagattta acgaatcaag                                              500

SEQ ID NO: 296         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 296
agaccaggca ccactatctg aggtaatgga tgtgatagta aatgtagtag gtcaaatgaa  60
ctataagata aaaggagacc gctgctactt aatcccaaag taatgggtat catcccaaaa  120
gaaaaacagt aaaaaaacaa caatataata accttttaa ccactaaaga ttcatgcaaa  180
aaagtatccg gaacggagcc ctaactctat cccggatatg aaatcaagat tctcaatatt  240
agagttttac tctattcaat taccgtgaaa taatttagtt aataacctaa tactaagaaa  300

SEQ ID NO: 297         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 297
tcttaaaagc gcttggtttg gccggtatca cagaatcagt ttgcagacta tcgctcataa  60
gggtatctct cctttcagcc tgggcctgta aggagagtga cagaaacaga aaaagagata  120
gaacaatttg cttcatcctg tgatttttcg ttgttatgat tgatgctgtt cgtttcacga  180
atgtactacc tttcgttgat ttatactaat aatcgtctaa aaaaatgttt cgtttcctaa  240
acaaatgaga tatgtattct gttagttaga acaagcaaat aaatcctaag ccacaaaatt  300

SEQ ID NO: 298         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 298
aaggggaaag tcgaaaggtg gcacaaaggc agcctgcttt ttttcctgtg catacccctc  60
cacgcaacag gccaataata aagcagcaat atatcttttc attatcttct tcactttttt  120
actcctgcaa atgtacatta ttccaactag attacgaaat atccgggaag aatgatagca  180
gatgaaccta gttaataatt ccttttatta ttatattcgc aactaaactg taatcattat  240
attattaata ttattacttt tgcggctgtt tttaataata attaaaagta aaaggactta  300

SEQ ID NO: 299         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
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                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 299
catacacatc atcgtccctc cgcatctggc taccaccgat gtatatacca tcaagttcaa  60
acaaaaagcc cctatcaagg agatcatgaa tatcgtgacc aaaaccatag gaaacataga  120
ctataaagtc gaagacgaga acattctctt aatttattca cccctaaata agaaaggagg  180
ccgatagaca gaaaaaaggg agtcgatatt tcgcggatac caactccccc aaatcaaaat  240
tacttcattt aaattagttg tgtacactta aattagtatt aatgattaac tcacaaaagt  300

SEQ ID NO: 300        moltype = DNA  length = 300
FEATURE               Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 300
gggcggaaga gtttttaaga gagaatatag tatcatgagt atattcgggt aattagagtt  60
aatgaaaggc ggagatattc ggaaacggat attgccgcct ttctttttt gtctcgaaag  120
ttgtctgata atgtctgttg acctcgaaaa atgcgataaa atggactatt ttagacattt  180
ttggaagaat catagccaaa atcgaacatc ttaaatctta gatataacct aaatttgtgg  240
cagtgaatgt caggaaagac ttcgctactt atataaaagg taatcttaat taataaactt  300

SEQ ID NO: 301        moltype = DNA  length = 700
FEATURE               Location/Qualifiers
source                1..700
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 301
gtactatgca gagagttacg gacacgcagc cagttgaccg gaaaaaagtc gttctttcgg  60
aagaaacggt aaccgaacat ggaattatcc agattgcgga attcaataag aatgcaggtg  120
cgtgatgctt cttgtgtgag atgctccagc atttcaccga aaatttcttc ctccttctct  180
ttacttgccg gtagagaagt gtccagaaat tcacctgcac catataccac acattgtttg  240
acaagagagg agggaagcca ctttttggtc ttgcgtatgg cggcaagcag gcgtgctaca  300
ggtctgcctt cttctgttgc cactatcagt agcggggtat atcccggagt cgattcatag  360
atctgaaaca actccttgga atgaaaagta ttggttcccg gtaaatcagg aatgtctttt  420
ccgcgataat atgttgttag tttaagtggc atccaaatac aaatttacac tttttattct  480
tcattcaaca ataaaaaaga gaatttgttg gcttagccta aaatttgtct ttttatcctt  540
tgcatatatt tgaggaaaaa aaggcttgga aaagcgaatt tttgtattat tgtcgtcctt  600
tgtgagtaca gaagtaaaat ggaaacgtct atataaaaga ttatgctaat tgtattttac  660
taaacaaagg aaaattaata ttaactttaa attaaaacga                        700

SEQ ID NO: 302        moltype = DNA  length = 700
FEATURE               Location/Qualifiers
source                1..700
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 302
gcttaatttt cgcttaattg attattaaat atcccttaaa tgtagaattt atgcaaataa  60
gtatgctgaa gaggggataa aagttagctg tagttataaa tattcctgtt attccttatt  120
atataggaaa cttatattat atgagaaata gggaatagta caacttaaag cttatatcat  180
ggggagcgct ttgaaaatct atcaggaata acgccattgt aatactaaaa atccacatct  240
tatataatcg gataagtcac taattggata tctcctaatt tgtgttatgt ttgtatagta  300
tttgccttat ttaccttttt agcctttcta cttgaaatat tcttcttttt gcaggaagtg  360
aatactcatt tagataaaga aatagggtgt ggacagcata ctacaggata taaaacttcc  420
ccctttcct gaaattaata cctaagattg cgaaaaatta taagaagata gtattagttt  480
taaaattaat tagaaattaa tcagagttta atcgtatttt ataaaaaatc ttaagcaggc  540
tcttgttact ttgcatcaga actcaaaaat aaccttaaat attaagtttg ttcagtcgac  600
gctttcttaa ataatagata aaaagggtgt tttcgaggtg taacaaatag caaatgtata  660
atataaaaaa gagaccgtga aaaattattt gaaaatcacg                        700

SEQ ID NO: 303        moltype = DNA  length = 300
FEATURE               Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 303
tggaacgtga acttgaaaac gaaatatata aggctatcga taaattgccg gacgaatgcc  60
gtcgggtttt tgctaaaagt cgctttgaag gaaaatcata cgaagaaatt tccggtgaac  120
tgggaatatc tattaataca gttaagtatc atataaagaa tgctttagct tctttacacg  180
ctcatttgag taagtacctg atttctctat tactattttt tttcaggtaa agcgaaaaaa  240
aatcattttc tgactaccct taattaaaaa acaactgtct cctttataga aagcataaat  300

SEQ ID NO: 304        moltype = DNA  length = 300
FEATURE               Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
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SEQUENCE: 304
tgtaatctat ctaattttat gttcgtttca taaatttaaa accatacaca caaagccgca  60
ttaacattta ttctcaaaac aaccattcat atataaattt atattaaata aataaatctt  120
tctagttttc ctgctttaaa tatatatatt tgcaatatgt atatacatat agacattata  180
taatacatat atcataagca attaatacta tgtagattaa aatatacagc ctttatatac  240
aagaaatcac attaaatcta atataaaacc cttatgactt actttttaaa atcacagagt  300

SEQ ID NO: 305         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 305
cgaccggctt ccggaacgtt gccgggaaat attcatccgt atccgtgaag aaaaacaaag  60
ttatgcccaa gtagcagaag aattggatat cagcataaag acagttgatg cccagctaca  120
gaaagctgtc tcccgactga aagagatgat ttcgtccagc ggataaccgg agatcacccg  180
aaccgttcag cacttctttt ttatattaac ttttatttgc acaaaaggcg tagggagttt  240
ctgtcaatct ccggtcttta tcagcaaata aaccgattaa tcactaaaaa agattgaatg  300

SEQ ID NO: 306         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 306
ttgcttataa atctattcgt ctgacagttg ttgaactttc gtctgacagt tgttgaactt  60
tcgtctaaca actgtcagac gaaagttcaa caactgtcag acgattaaat ttaagtataa  120
tgaatactaa atctgtgtac atcaagaatt aaatcttaga gtaaatccga acagattagt  180
tcgtttcaaa acagttctta gcttaaactt attggatttt acttcccttc cttgattttt  240
tttcattttc ctttggtggt aaatgtaagt tgctgtgtct tcttattaaa agcgcgcaat  300

SEQ ID NO: 307         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 307
gctggcactg gcctatggta tgcatgccct taaccataca ggttcgtcac aagaagcaat  60
tctgcaatat tccctgtttg tgcgtgagta caagcaaatg atgaatgaag aatattctac  120
ttcttatgca gagctgatga gcaaaaatcc tccttttcat cgataaaaac atatcggtta  180
atgatattta ttcgcttatt aatccgttat taacccatca ctaataagtt gtttaacctt  240
gctacattat gtttgcagcg atgttattta cttattgttt tatttaaaaa cctaatacgt  300

SEQ ID NO: 308         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 308
aataaaagcg cctcttatag catgatacta ttttttgttt ataatagctc cttgttttat  60
agatataata ttgattataa gataaatagt tttcatttcg gtagagaagt ggtattacat  120
aaaagagagt aaaacattag ctgaattagg gtaattaact gtcaaataga tatataagct  180
atttctgctt gataaaatat cgactggtgt tactgattta tcccctatat acctaactga  240
ttatcagtta tatataaatc cattagttct gcaaagactt tgcagatttc gtatattggt  300

SEQ ID NO: 309         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 309
ggtggtgaga aatattcggg aaatataaaa atagtatcca ataataatac ctcatataaa  60
taaaataaag acataacttt cttataatga atgaactaaa tgattgaaat ggatagaaac  120
agggtatcat tcgttaaaga aaagggtagt tataatgctg ataaataatt gattatcacg  180
tttatatatg gatacaataa catatatgac gattaggttt atatttctca ttattataat  240
aatcaacact ttatataaag aattagttct gcaaagactt tgcaaatttc gtacatcggt  300

SEQ ID NO: 310         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 310
aaagatagta aaaatcaacc cattccgatt caaagtcaac tttatttttt ttcaatccac  60
aacgctctat gcctattttt gtccaatcag tctaaataaa ctgatattga tagtggcgcc  120
acatcaaata catacactca gagattgacc gtcaattcac ggtacaatcg cagttttaac  180
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caataaaatc taatagccta tggagtaaat caaatcggta taatcggaac atagatttaa  240
atcattcaga gatttaacta ttcaaaaacc aattagtgaa catacaatta aacaaaaaac  300

SEQ ID NO: 311          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 311
ctacgacctt taccgctacc attatcaacg gcagtgagta tcagaatccg ggatattaaa  60
ttgtaagacc tatataccca atcattatcg gtacgataat ccatatagcc acgctattta  120
tcgtaccaat gattggggat attttccaca cctttccaca tttttccaca cctccccaat  180
aatatcgttt ttttcaactc tgctgttaat ctgtatctta tcctttcagc atttctttat  240
atcctattgg tatatccttt gtatcgactt tatagcaaat gtatttttaa atataaaagt  300

SEQ ID NO: 312          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 312
gcaaatgata aaaaaagcaa ttttgaatga aaagatatac atggatgaat aaaagcatat  60
gctcctgatt ccttgaaata ccctaagttt gtatcctgaa aaccgaacgg aaagtgtgct  120
tcacaattat atatagccat ttacaccttt gaatctataa tatttaaaac aattaatcac  180
atgagagaaa aagccaaaag cccttaagtc aaattgaaat caattagaat ctattaaacc  240
ttatttaaat agaaagccta aaagaccttt tttcaaacta ataaaatctt atagaaaaac  300

SEQ ID NO: 313          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 313
ttgcaatcat tacctgaaca aacctcccgt atatttactc tcagccgatt tggaaataaa  60
acaaatcggg aaattgcctg cgaattaaat atttcaatca aagatgtgga atatcatata  120
tccaaatcac ttaaggctct tagaaaaacg ctaaaagatt acctgccttt attttatttc  180
ttttttacc atatgtaaca ccgattacta cgcacgttcc tttatctttt gaaaaaaata  240
ttctttttcg tttagggtaa accgaagatg aatcgttata taaatgaaaa cgataaaaag  300

SEQ ID NO: 314          moltype = DNA  length = 700
FEATURE                 Location/Qualifiers
source                  1..700
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 314
gaaacgccag acgaatcagg actttaccga aaagcaatac gagcacatcc acttcatgat  60
gaagctgacc gatgatgccc tcgcacaaat gattgtggtg gtagagaaac cggaacacca  120
aagcattgat atcaacaagt ctttcaacat cgaaaacgaa atcaataact accgtaacca  180
actgaaaaat cagaatattc tggatgtcaa caacaaggaa tatgattatc agatgggagt  240
ctattatatg gatattatcg ccgaatgtga gaaactgggc gactatgtag tgaatgtggt  300
agaagccagc agtgatgtaa aagagaagaa agcctcttaa ataaagagga actcaatcaa  360
agaaatggat agccaattta tgcgttgcag cataaaattg actatccatt tctttttat  420
ttccacacag acaaaacaac tcatgtccgt ttacaaggac actcacactt tacaaagacg  480
ttacattttt tacagacgtt acgattacat ttcttttccg tgaagttccc gttaagcttt  540
tactgcgcct attgcaggtc tttttttgc atatacattt gcgccaaaat acacaggggc  600
ctatgtttag taccattttc caatgaccgg acaaaggcat tccaaaagaa aaccaaatct  660
ctaatttaaa gcaaaagaaa tgaaaattaa aaaagtattg                        700

SEQ ID NO: 315          moltype = DNA  length = 542
FEATURE                 Location/Qualifiers
source                  1..542
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 315
aagtgcagga gcatgagcta atccagtatg aatcccgttc catcacccga agtctatctt  60
cgcccaaaga gcagactttt aaaacagaac gtatcatttt atggtttctg aataaaagaa  120
atattcccat cctgaaaaaa gacagagaag cattttggga aaagttgtct cctgagattc  180
atgaattata taataataaa tatgaaagtc agcttttacg cctctttgac tttacggcgt  240
ggatggaatc caaaattcgg aaagaaaaac tgtctgaagt cctcagagca cgtgctagcg  300
caaaagaatg ttaaagagta aggtgtttga ttcgtatttc agacgataaa aacactcttt  360
tcaaatctcc attttctctt tgtaattata taaattcgct tcacattacc tctatattct  420
ctcctctata caaggaaaat ccaatataag atatcatttt tgagattata taaaccaatt  480
attaatgtag aaaactatgc atgattattg ctttcatttg catagtctta atttttaata  540
ct                                                                 542

SEQ ID NO: 316          moltype = DNA  length = 300
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FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 316
agatagatat tgggagtgca tatgtttgtt tttacaagat gataaagtgt attatagcga  60
caatatagta aatatttgtg ccaagagaaa gagactgatt aaatattctg agggaatgga  120
agtttgaaaa cttacatttg catataattg acttgtgatt tttattatta gaatagttat  180
tatttgttat acttttaaat taaaatgctt atgaatatta tagaaagaca tccaccatga  240
ttaatgatat ccgctgttta atcatataat agaaactaat caaatataaa gaatatagaa  300

SEQ ID NO: 317          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 317
tatgaaagtc agcttttacg cctctttgac tttacggcgt ggatggaatc caaaattcgg  60
aaagaaaaac tgtctgaagt cctcagagca cgtgctagcg caaaagaatg ttaaagagta  120
aggtgtttga ttcgtatttc agacgataaa aacactcttt tcaaatctcc attttctctt  180
tgtaattata taaattcgct tcacattacc tctatattct ctcctctata caaggaaaat  240
ccaatataag atatcatttt tgagattata taaaccaatt attaatgtag aaaactatgc  300

SEQ ID NO: 318          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 318
tgttccttac aaagcctcct tttccattcc gtctataatt ttgtatcaag gtctacccat  60
ttgttacaga tagtgtttct agctatttgt gcacctaatt tggtgaatat tgcacgtcca  120
tttttcacat cacccctaat tttgcatcat cattaaaaga taaatgaagt taaccttatt  180
gcacataagc aaaggatata tttagaaact gaagagagaa taaagagaat aaaagtcacc  240
cccaacccgg ttgacctaac tataaactaa atatattatt aacctatcaa attaaacagt  300

SEQ ID NO: 319          moltype = DNA  length = 700
FEATURE                 Location/Qualifiers
source                  1..700
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 319
actacctcaa aacgcagatc gtatccttgc tgtataaccg tcagaaagaa cgcgaagcat  60
tctccaagcg tccgttcttc ccgacgaata agatgcagat gaataaggtg gatgaagagt  120
ttatgaataa agtgattcgt accatcgagg aaaatatcat agataccaat ctgaacgtag  180
agcatcttgc cgagattctg ggcatgagtc gttccagtct gctgcggaaa ataaagatgc  240
tttccaatct gtctcctgtg gacttcatcc gtttaatccg attgaggaag gctgccgaac  300
tgattcatga aggtaaatac ctgattggag atatctgctt tatggtaggt atcaactcac  360
cgtcctattt cagcaagctt ttcctgaaac agtttggcat gacacctaaa gatttcgaga  420
aacaaagtca ggcagacaaa gaaaagatag acatgccttc gtgaccgtcc gggtgcacta  480
taacaaatga tgcacaaaaa tgaaacatct gcggaaaata tgcttcagat gtagtctggt  540
gctgcaaaaa tggtattttt tgcagtgatt tttattatac cgcctatata tatactccta  600
cttttgccat cgttccggat aaggaaagat aaccccttc ggtgaacgga ttgatttatc  660
cttaaatgtg aactctaata ctaatttaaa attctgatac                        700

SEQ ID NO: 320          moltype = DNA  length = 700
FEATURE                 Location/Qualifiers
source                  1..700
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 320
gttctaactt ttaccgcaaa ctgaaaggag tattggatat gagtccgaat gagtatcttc  60
gtttgatacg tttaaagaaa gctgcccagc ttctgaaaga tggaagatat gggattgtag  120
aaatttctta tatggtagga ttcaattcac cttcttattt ctcaaactgt tttaagaaac  180
aatttggagt gttaccaaaa gatttcatgc aatgaacaaa ttcttataaa attgctctaa  240
aactgattct gactatctct gcactgtttt ttggatagaa tttaataata tcaggttaat  300
ttcttatatc cttttcaggt aggttccgat aactttgcga atgtctcgaa ggtaggaact  360
tattttctga ccagtctatt tggttgggaa aaaactttct tctagatcaa ttaatataga  420
agtaacggat aaataccaga ttagaaactg gctttataag ctattaatta ttattaatca  480
atatctaatt tttcgcgcga atatgatttt gtatgtattg tttggtagat agggagaaga  540
gttgatacat aaataaggaa ttggcaggta ttagtttttt tataaaactc ttcttccact  600
tttcttcgct gaagtatata atccttaaat aatacgattt atgaacaaat tccttttata  660
aggatcatga tataaatgtt taaccaaaat aataaagaaa                        700

SEQ ID NO: 321          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
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                      mol_type = genomic DNA
                      organism = Bacteroides thetaiotaomicron
SEQUENCE: 321
tgtggacatt ggtacggacg agcgttatcc agttatggct tacttcaagg attgacagga  60
gtccgatatg atgctgtaga taaaacactg tatattaatt caaaaatagg agactttatt  120
agctttatca gtacggagtc tggatttggt aatatagaac ttcgttccgg aaaacctttt  180
gtaaaagtag tatccggtca tatagaggtt gacagatttg tcgtatcggg gaaagtagtt  240
gaataatcaa caataagata ataactaaat ttttaagtga taactaaata ctataatatt  300

SEQ ID NO: 322         moltype = DNA  length = 700
FEATURE                Location/Qualifiers
source                 1..700
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 322
ccgggcgaat ggcacaccta ttatcctaat tatcaaacag gttggagtca ttattggatc  60
ggcttttgcg gtccggaagt tgatagctgg atgacgaatg agtattgttc gaaagaaagt  120
cctgtattta aggtcggtat caatgatgag atcgtttctt tattcagaaa agctattgat  180
gttgctaacg aagaacctac tttatatcaa cgcgtattga gtggattggt gacctatctg  240
gtagcactaa tgtgtagtat cgataagaac cttcaggtag agaatgatga tttctcttct  300
aaaatagatt atgcttgtgt gctcatgaag gaattgatag atcaaccagt ttctatgcaa  360
gagattgcca aaaaagcagg tatgggatat tctctttttc gaaagttgtt taaggaacag  420
aagaattatg cacctgtgca atatttccag aatctgaaaa tacagaaagc catagagttg  480
ttgactacta ctactattcc ggtaaaagag atagcatata ggctcgattt tgaatccccg  540
gcttatttct ctgcccggtt caagaaacaa acaggaaaat cacctataga atatcgagaa  600
gaatttcgta tcaaataatg atagtgttct ggcaattatc gaaagtcttt ctcttttaag  660
atgactaagt ttgtatcata attaaaaaat gaataatgct                        700

SEQ ID NO: 323         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 323
gtacatgcag gatctatatc cccgttgcat tgcgcatata tacacaatgt acagggcata  60
tagatcctgc atattgcata tatatagctt atctgcctct tttttattgc aatattttat  120
gtgcttttat gtggtatatg aaacaattat ctcattcctg tttcatttgg tatagatttg  180
ctattctttc ttctatttga gacattattg cgatttattg ggatatttat attacccaaa  240
aactatctca tccgctaatt ttgtctgcgt caatcagtcg aaacaataat ctaattatat  300

SEQ ID NO: 324         moltype = DNA  length = 700
FEATURE                Location/Qualifiers
source                 1..700
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 324
cttcggaatt gctaacacct acgggactaa agttacttac aggtacagta attattcttg  60
ccggaatcat tttctttgcg atagcagggc acaacagaga tagcaaaagc cgccagacgc  120
actctgaaac acctattaag aaaaatttca ggaaagggtt aattatctgt ttgcttgcag  180
gaatattcgg acctatgatt aactttgctt tcgtttatgg ggcaccctta caagaaaagg  240
ctgtagcaac gggagcatct tctctttatg cagccaacgt gatatggagt atcgctttga  300
gtgccggatt tattattaat ctccttgaat gtatccgttt gttcggcaag aatcaatctt  360
ggaaaactta ccgacatcgt acaaccggag gcctgataat ggcttctctg gcaggggtat  420
tatggtatct gagcattatg ttctatggta tgggaggcag ttttatggga gttttaggag  480
cttctgtggg ctgggctacc atgcaatcga cagctattat tgcaggtaat gtggccggac  540
ttgcttccgg cgagtggaaa ggagctaccc gctatgccat ccggatgatg gtgataggat  600
tggtatgtct catcggagga gtggtggtga ttgccctcta acgactatac ttaactattt  660
atattgactt aattattatg ttattcaaaa agtctaactt                        700

SEQ ID NO: 325         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
SEQUENCE: 325
aatgtaagga caagtcctga gaagaggtta tattcactct tgcaatatga aacttttcat  60
ttgcactcag aaaataggat agcttaaaaa cggaatctct catattcttt tttgatttga  120
ttgcaatatt aagagttagc cttcacaaac acaacccgtg aagactcttt tttatatgtc  180
aaagcataaa aagtcggaat agcgtaaaaa aactaccgct atgaataatt tctatcggaa  240
aaacgtatat ggacaacctc tacctttgtc cccatcagct aatactaaaa gaatcatatc  300

SEQ ID NO: 326         moltype = DNA  length = 300
FEATURE                Location/Qualifiers
source                 1..300
                       mol_type = genomic DNA
                       organism = Bacteroides thetaiotaomicron
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SEQUENCE: 326
gatgtgcact atgtcttggc tgatgtaacc ttggaacaag gtaagaatac aattaaaacc  60
gttgcaacat ataatggaaa agaatacact gacgagattg aatggaacta taccggcgaa  120
aagaagcgaa gtgccgattg gagtgaaaac aaagaagagc acgcaggttg gtaatcggag  180
acgtttctgt atgtaatctg aaaaatgttg aatctaaaat ataaaagcct atgaatgaaa  240
tgagaaagaa tctcttttaa atggaaaaca agtatttatc attaactaat ctaataattt  300

SEQ ID NO: 327          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 327
atcaacgagt atgactggcg ctcaagtaaa tatcgcttta ccaacaagcc attacaggaa  60
ttcatcgatt ttatcaaccg ttcataccat gtaaacatca taattaaaga agaaaagctc  120
aaagagctga agtttaacgg aactatacgt aaagacgagc cgcttaccaa tatcatcgaa  180
aagatatgta tcagcctcga tttaaaagaa aaacaagaaa ataacaacat catattatat  240
taatacataa gaatcaatta tcaatatatt cactattaac cttttagaaa catgaaaaac  300

SEQ ID NO: 328          moltype = DNA  length = 700
FEATURE                 Location/Qualifiers
source                  1..700
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 328
aaaaacaatg caagaaatgg aaactgcttt catcatatcc ggcaagaata ttaagaaagg  60
actccggttt gacgatgtaa gcatgatgca atacgatgtg gcgtccacta tcgcccgcat  120
ctttcattta gaacaaccac aagtttggat aggtagaccc atggagattg ttttcaaata  180
atcattcagg atgattaata ggatgggaaa aggagaagct aaaataactg gcttctcctt  240
ttttatttat ctatccacgc tcataagata ggagattata aatactattt cttataagta  300
acaaaatgag cagtcataat agttttattt cctataagta atagaaatca cacctccaca  360
gctgttaatt accgaataat acttgcatca acatacatat ccttatacct ttgtcccccg  420
gtaacacaac ataatataac ttcaatcata aaatgtactc ttttgacatt cttaataagc  480
aatccaactg attaaagcag cattcaaaca ttctgatagg acatcttatc ttttgtttat  540
tcaaattaaa atacaatacg atagaattgt attagtaaat gataaaatac tacttgtctg  600
acggagcatt atcgcctact tttgcatcat cagttattgg ttgaagtttc catggatcaa  660
tcaacaattg aatagagttt ataatctaat acaataaatt                        700

SEQ ID NO: 329          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 329
agttgtgttt cttgcagcca acgtgtgtaa atcgtttatg aatgattctc tacgtttttt  60
gaatgatttt tataatgtaa aatctacact cattcgtatc tttgctgtag ataacaacga  120
aataaactaa tattatgaaa atgaaaacta atataatctt taaaaaacta aagtcattcg  180
tcaatcgatg tctttttcct gattatatgt gctgttttat cttcctgcgt ttataacgct  240
gatatgccaa taaagaattt ttagtgaacc aataatttaa tatgtaaaaa gaaaaacgtt  300

SEQ ID NO: 330          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 330
gctactctgt gaccactatt tataattacc ggacacgtgt ccgcaacaag gcactcggcg  60
aacgggatga gtttgaggct aaagtaatga aaatagggaa ggtggaagag taagaaatcc  120
actacttttt tagcacggtc gctattctat aatattctta ttattagtgt tttatgctgt  180
tttgtactgt ataaaccact atatttttgc tatctggcaa aagaagcgca tttaattgtg  240
gatacttttg tttcagtgaa aacaaaaagt aatcctaata ttaactttaa attgatgtac  300

SEQ ID NO: 331          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 331
taatgtagct ggcagacatc cggaactgct tgagcggtta aagcaggaat tttttgtgca  60
aacagatgga ttttatcgta gtgaggtgga agaagaacca ttaaaataag cccgataacc  120
ccttctggaa agcatttgat tgattaggta ttagattgtt ttgcaggaat tggtgtagaa  180
ggatagtttc tgaacatgtg tgctcataat aaaacatatt ttctatcgtc tacacctttt  240
ttcttttact tttgctgcat cacaatcata cataaataac gtttaacttt ttagaatcat  300

SEQ ID NO: 332          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
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source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 332
acaaaaaaac attcattcct aaaataaagg atgatggact aatttatata tccatgaata  60
aaggagataa tcttaccata atcatccctt aataacaatt ttgcagtaaa tgcgttattt  120
tttgctgcgt ttatacacta ttaaaataac acatttacct aattttgact cgttgaattt  180
agaaaattat cacattaaat ctaataatat atgaaacgaa ttcgagattt ccccaccact  240
gacaagacaa cgatctagtt gcctgaaatg tattaaccta atattaattt taaattatcc  300

SEQ ID NO: 333          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 333
ctgcaaaacg tcctgtttct aaaaaatgcg ggtttttgcc taaaaaacag tttgtttgtc  60
actgcacggg aagtgaatca ccatctattg gcatttgttt ttgatcactt ctctatcaat  120
aatgatcatt tagcggattg cacagggttc ttttgatcat tattgaattt taattgatga  180
tttttgaatg tttcctttta tgctgtggtt gtatttttgt cgaagattga aacttattgt  240
tagctagtga aagtatgaat ctttattatt aaatgtagta ttatgaaaaa aaggaaacag  300

SEQ ID NO: 334          moltype = DNA  length = 400
FEATURE                 Location/Qualifiers
source                  1..400
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 334
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atttacaata gttttcaaat ttattttgaa taattgtttt gtatttataa atatgtgctt  180
atatttgcaa aatagcacta agcgaaaata agcgacttac taattcttat aataataaag  240
agtgtttatg aaaagaaaat taatgctgtt attggcctgc ttgctggcaa gcataggtct  300
agtgattgcc caaacaccta aaaaggtgac aggtgtcgtc atttctgagg aagatgatca  360
gcctgttgtg ggagcatccg tattagtgaa aggtacaacg                        400

SEQ ID NO: 335          moltype = DNA  length = 414
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source                  1..414
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 335
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aataacagca ttaattttct tttcataaac actctttatt attataagaa ttagtaagtc  120
gcttattttc gcttagtgct attttgcaaa tataagcaca tatttataaa tacaaaacaa  180
ttattcaaaa taaatttgaa aactattgta aatacattat gatagttatg aagataaata  240
tatatcatca aactatcata atgtcacatt tatgtcagta tgtgcaaatt tagccctgtt  300
caaataatca ttatgtcatc taaacacttc ctttttatct ttaactaagc cttgaataat  360
ataaaaatta tattagatat aaataattag tatgaaaata ggttatagga gaat        414

SEQ ID NO: 336          moltype = DNA  length = 500
FEATURE                 Location/Qualifiers
source                  1..500
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 336
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atgtctgtgt cttattgcat tgtatatcaa ttagctaagt ccgaaagtga cggatgatga  180
taaaatatga gtttcaaact ccttagtaaa agctaaaaaa tacatcattt taatagcggc  240
aacgaaaaaa aacaaatatt ttttaagatg cctaattgtc atttattgat ggctgaattt  300
tgattctgaa aagggaatga tttgttaaat atgtcatttt tgttgctgaa taatgtcata  360
atgatagttt ttcattcttt tccgttttcg tacggagagt atctcataaa aaataatcat  420
ctttttgtca cccatttatg gacgttatgt ataattatag taaagcaaag ataaaatcct  480
cattagaaat agataaaatt                                              500

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source                  1..300
                        mol_type = genomic DNA
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ggctcctatc attttctatt attacaaatg ttacttccct aaaaagaagc ataacactca  120
atccgcttta cttgttaaca cctgtttgca atgaacaaaa tgttcgttgt ttttcttgat  180
tattgtacaa aaagaacggt cttctaaata aataaagtat cttttgaata aaaaaacttc  240
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SEQ ID NO: 338          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
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SEQUENCE: 338
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atgtattttg atgtcaacag aactcagttc gtcactgatc cgggtattta caatataatg  120
cttggcttct cctctagaga tattaaagca caaaaaaata ttcaatatac actatagatt  180
gcataatcaa taagtaacat gaaatatatt tgtatcaaaa ctgtagcaat ttacttgctc  240
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SEQ ID NO: 339          moltype = DNA  length = 300
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source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 339
gaatacaatt tataattatc gggcgaaagt aaaaaacaaa gctcgtggtt ccagagaaga  60
tttcgaagat ttagttcgga aaatacgttg atcgatgttg taacctatcc actttttagg  120
cctctttggt tgatattaac ttgctgttta ttagtggttt gtatgtttgt ataatccact  180
tattataccc tcattgtcaa atcacttcag tttctttata cttttgacct gtgcttctga  240
aatagtggcg aaagtcctgt caagcacata ccttaattat aaactttaaa attaatacgc  300

SEQ ID NO: 340          moltype = DNA  length = 500
FEATURE                 Location/Qualifiers
source                  1..500
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 340
acatttctcc cttgaagggc atatttgcac agatattccc caaaagcctg cttaattatt  60
taatgtaatt gaaaatgtaa ttataataat ctgactaata tataatatat tctggtcatt  120
tcaaaaaaaa ggcattctaa ctcttctaca tttttattat atttatttgt aattaaccga  180
ttgattgtta attataatta tcatcatcac acctacataa agttatgcaa actaaataag  240
aaattactta tttagttagc tttgccatgt cttttctcag tcaaactctt cgttgatgag  300
aatcagacat atatagatat ttgtacttaa atctacaaca tattatgagc acaacatgcc  360
aacatcaaca aggtgaagga tacctaaaac tcctaaagat ttagatacat attatgctta  420
taataagaaa gataggcaaa cgttgtaagc aataatattt attgttcgga tgcactttaa  480
ccattttatt atttatattt                                              500

SEQ ID NO: 341          moltype = DNA  length = 500
FEATURE                 Location/Qualifiers
source                  1..500
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 341
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cttttattaa ttccattatt ttgtgtcatc aagatgagat actatggaaa ataaagagtt  240
tgttaaagct cgatatttgc tagaaataca cgatttgtta gccgcttctc cataacattt  300
catcctaaat atgacagtac tgatattata tattaaaggt ataggaaaac gggtataaag  360
attgcaatta ttcaaaggtg agatagtatt aaggtaaaaa gtggatttaa aagaatactt  420
agggcttgtt tttttatgag gtaaataaga ttgatggatg gataaccttg gatttgaaga  480
ttaatttaaa gcaaatattt                                              500

SEQ ID NO: 342          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 342
gtttgtagat cctctttata aatacatcaa tgaaactact tcacgtgtgc ctatcagtga  60
ctggcatgat accaaaactg gcagaatgac cggatttaag gcacgttccg taattggagg  120
atattggata caagtgttaa tggataagat gaatcattaa aaatatggac aataagttga  180
aagaatactt tttcgcatgg atgaatcatt tcagcataat acaacaagag ataagtaatg  240
aaccaacaat ataatatttt attaatcatt aatttttac gtatgaaaaa aaacaaaatc  300

SEQ ID NO: 343          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 343
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tttaaagcgc gttcggttat tggaggatac tggatgcaag tgttaatgga caaaactcga  240
tgaaatgttt aattaactat acatttatta ttaactagaa tgaaaaacat gaaatgtaaa  300

SEQ ID NO: 344          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
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                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 344
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cctatgatgg acagtataaa acttatcggg tcgtgaaaaa atagacacag aaaaatatag  180
taattaataa aataaatctc aagaatttat ggcgattttt ataaagagtg gataatactg  240
ctgtattatc cagatggggc tcatatgcct gtaagtatta agttataaaa taataatatt  300

SEQ ID NO: 345          moltype = DNA  length = 300
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SEQUENCE: 345
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aatgtaaata gaataaaaca aacaagcaac aaaaagacaa ataatttttt cacacatcat  180
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gttcactttg ttactttcgc cggaagacgg cagaataaac ttcaacctaa atagtaacga  300

SEQ ID NO: 346          moltype = DNA  length = 500
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source                  1..500
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SEQUENCE: 346
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ttagtaataa atattaaact attaaaaatt caataggtta aatatatact aaaaagagta  480
gaaactaaaa aaagtaaact                                              500

SEQ ID NO: 347          moltype = DNA  length = 400
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source                  1..400
                        mol_type = genomic DNA
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SEQUENCE: 347
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tatatgtggt ttttatttta cagatcagat tatccttatt ccttggtcga attatagttt  240
aaaaaggagg aatatctata attcgacctc agataactca tattggacct catctggagt  300
gacttaactt acatttgcac ttgttaattg gtcgttgaaa tcataaatca attaatgaac  360
ggttaatttt ttatttacta atatcttaaa tatttttgct                        400

SEQ ID NO: 348          moltype = DNA  length = 300
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source                  1..300
                        mol_type = genomic DNA
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SEQUENCE: 348
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caatttatca acaaatgaag ccatagcata tagggtttat taatgtgaag ataaagatat  120
ataaaaaata aatataactc ttttgatgtc gataatttta aataatatat cgatattgtt  180
ttataataaa tcctgctata gtcgttcatg tcgatattgt attactctaa atcgtattag  240
tcctacaatg tggactgccg agttgttaca tttgcggtat ataatctaat aggaatattt  300

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acaaacttgt atttttattc tagacaaccc aaagtctcaa gatggttgct atatttgcaa  240
tatccggaac agagcggagt aaaaatatta gttagcttat aatttaatac cataaataga  300

SEQ ID NO: 350          moltype = DNA  length = 300
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source                  1..300
                        mol_type = genomic DNA
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ctcctttcct gatatttttt atttgatgat cttgaaaata tctttttctc ctctttttt  180
aataacagca aaaaaagttg tatttctcac tagggattat ttttagtgag tggtattcta  240
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SEQ ID NO: 351          moltype = DNA  length = 500
FEATURE                 Location/Qualifiers
source                  1..500
                        mol_type = genomic DNA
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SEQUENCE: 351
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gaaaacatta ttgataacta gatacttatg cgaaaagaat gaaattcttt atcgctatta  180
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ggaaatatga aaaacgacac ttcttaacta ctgcttggac ttacttgtca gagaaagttt  360
tcttgagatg aaaacggttt gaatcaatta atgttaatct ataaattatg aaaacaggaa  420
agagcaaaga tcatttgcaa agagtttttt taaggttcct ttatttgata atggggagca  480
tcctttcttt ggattctgtt                                              500

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SEQUENCE: 352
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ctccacgttt gtggcagaac aaatgttgat gagttcccgt cagttctacc ggaggtttaa  180
ggagatttcg ggtatgtcac ccagcgattt gattaaagat taccggatgg agaaggccgc  240
ccgtttgttg cagaacgagg aactgtctat tcaggatgta atttccgatg taggtatatc  300
cagtcgtgct tacttctaca aagagtttac ccgtaagttt ggcgtaactc ctaaggtata  360
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gtctggtatt agttgccaag aaataaattc ccatgctgat ctgtgctgct ttttaaggtt  480
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tccagtactc tattttacca tctgtacttt aaacagacat tttttctctt ctctgttttt  600
tggcgcacag gagtatctca tttctttggc tattccttta atttgcgtca acgtattaaa  660
cgtatttggt aaccttatta ttattaatta aaaacaagta gt                     702

SEQ ID NO: 353          moltype = DNA  length = 500
FEATURE                 Location/Qualifiers
source                  1..500
                        mol_type = genomic DNA
                        organism = Bacteroides thetaiotaomicron
SEQUENCE: 353
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gtctgtatag attttattta ttactgctta cgaataaact ttttaataaa agtggcgaaa  240
aggcggctat tataacttga tacaatgtgc gcaaacttgt gctctgtttg tacgtgaatg  300
aatgctatgt gttgatatat agatgtttat aatgtgcttt atttctcctt tctgttctat  360
aaatgagcat tttcattttg acataatttt gtcacttctg cggaatattc ttaatattaa  420
aagtttttaa tttgcttccg cttataagaa ttatataggc gattgataac cttagtatta  480
attaaaaaaa acaaagtaac                                              500

SEQ ID NO: 354          moltype = DNA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
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                        organism = Bacteroides thetaiotaomicron
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SEQUENCE: 354
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tgagattata tttatttttt ttcaaaaacc tctaagtgtt tttcaaggta tgggttgtta  240
tataaatgtg aatcgaaaat aataaatgga atatcgattc taatatttat ataaaaacta  300
```

1. A glycan-sensing system comprising an engineered bacteria harboring a reporter plasmid, wherein the reporter plasmid comprises a luciferase reporter cassette, a first polysaccharide utilization locus (PUL), and a first glycan-specific promoter, wherein the glycan-sensing system detects and quantifies a glycan molecule.

2. The system of claim **1**, wherein the glycan molecule comprises chondroitin sulfate, arabinan, heparan sulfate, hyaluronan, fructan, levan, mannan, or derivatives thereof.

3. (canceled)

4. The system of claim **1**, wherein the first PUL encodes any combination of proteins comprising a surface glycan binding protein (SGBP), an outer membrane channel, a digestive enzyme, a glycan importer, or a glycan sensor.

5. The system of claim **1**, wherein the first PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan (OG)-specific PUL, or variants thereof.

6. The system of claim **1**, wherein the first glycan specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

7. The system of claim **1**, further comprising a second PUL.

8. The system of any one of claim **7**, wherein the second PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof.

9. The system of claim **7**, wherein the first PUL is interchangeable with the second PUL.

10. The system of claim **1**, further comprising a second glycan-specific promoter.

11. The system of claim **10**, wherein the first glycan-specific promoter is interchangeable with the second glycan-specific promoter.

12. The system of claim **10**, wherein the second glycan-specific promoter comprises a CS-specific promoter, a levan-specific promoter, an inulin-specific promoter, an arabinogalactan-specific promoter, a dextran-specific promoter, a HA-specific promoter, a HS-specific promoter, an O-glycan(OG)-specific promoter, or variants thereof.

13. The system of claim **1**, wherein the first or second glycan-specific promoter comprises SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 266, SEQ ID NO: 267, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, SEQ ID NO: 323, SEQ ID NO: 324, SEQ ID NO: 325, SEQ ID NO: 326, SEQ ID NO: 327, SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 331, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 338, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 343, SEQ ID NO: 344, SEQ ID NO: 345, SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, SEQ ID NO: 349, SEQ ID NO: 350, SEQ ID NO: 351, SEQ ID NO: 352, SEQ ID NO: 353, or SEQ ID NO: 354.

14. The system of claim **1**, wherein the reporter plasmid comprises a *Bacteroides*-optimized lux (Bolux) plasmid.

15. (canceled)

16. The system of claim **1**, wherein the engineered bacteria originates from a *Bacteroides* bacterium.

17-29. (canceled)

30. A method of detecting a glycan, the method comprising:

isolating and preserving a tissue sample from a subject,

preparing and culturing the glycan-sensing system of claim **1** in a microplate in an anaerobic environment,

adding the tissue sample into the microplate, and

detecting and quantifying a light signal emitted from the system.

31-34. (canceled)

35. A method of treating or preventing a gastrointestinal disease or disorder in a subject in need thereof, the method comprising:

isolating and preserving a tissue sample from a subject,

preparing and culturing the glycan-sensing system of claim **1** in a microplate in an anaerobic environment,

adding the tissue sample into the microplate,

detecting and quantifying a light signal emitted from the system, and

performing or administering a therapeutic procedure to the subject comprising pathological amounts of a glycan relative to a control tissue comprising normal amounts of the glycan.

36-44. (canceled)

45. A kit for detecting or purifying a glycan molecule, the kit comprising:

an apparatus comprising a binding medium and a surface glycan binding protein (SGBP), wherein the binding medium comprises a matrix of biomolecules, the SGBP comprises a peptide label, and the SGBP is attached to the matrix,

a container comprising an equilibration buffer,

a container comprising a releasing buffer, and

a container comprising a washing buffer.

46-52. (canceled)

53. A reporter plasmid comprising a luciferase reporter cassette, a first polysaccharide utilization locus (PUL), and a first glycan-specific promoter.

54-56. (canceled)

57. The reporter plasmid of claim **53**, wherein the first PUL encodes any combination of proteins comprising a surface glycan binding protein (SGBP), an outer membrane channel, a digestive enzyme, a glycan importer, or a glycan sensor.

58. The reporter plasmid of claim **53**, wherein the first PUL comprises a chondroitin sulfate (CS)-specific PUL, a levan-specific PUL, an inulin-specific PUL, an arabinogalactan-specific PUL, a dextran-specific PUL, a hyaluronan (HA)-specific PUL, a heparan sulfate (HS)-specific PUL, an O-glycan(OG)-specific PUL, or variants thereof.

59-66. (canceled)

67. An engineered bacteria comprising the reporter plasmid of claim **53**.

68-92. (canceled)

* * * * *