

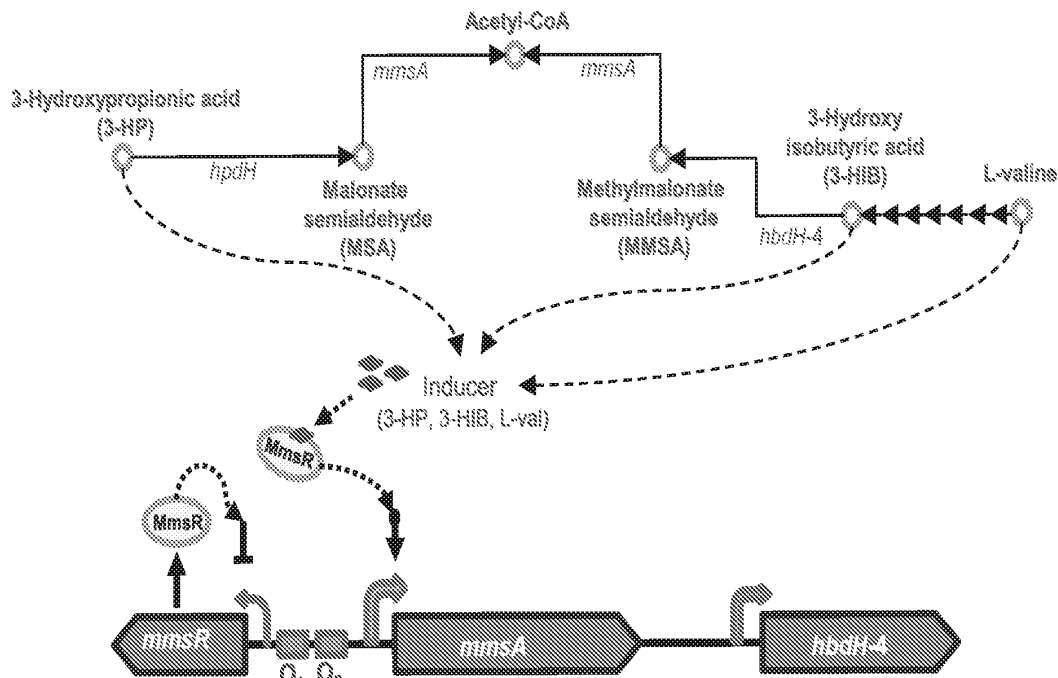


FIG. 1A

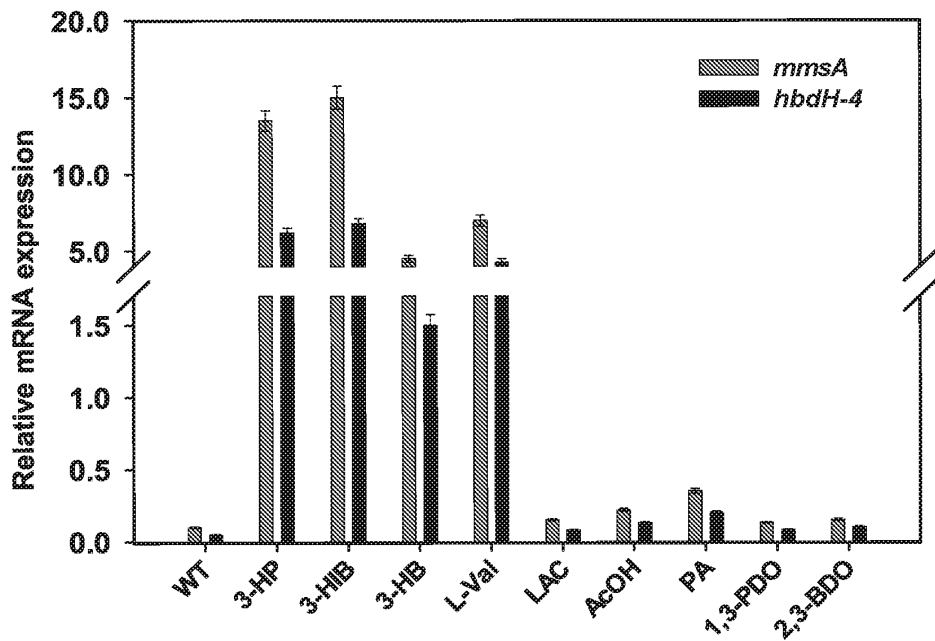


FIG. 1B

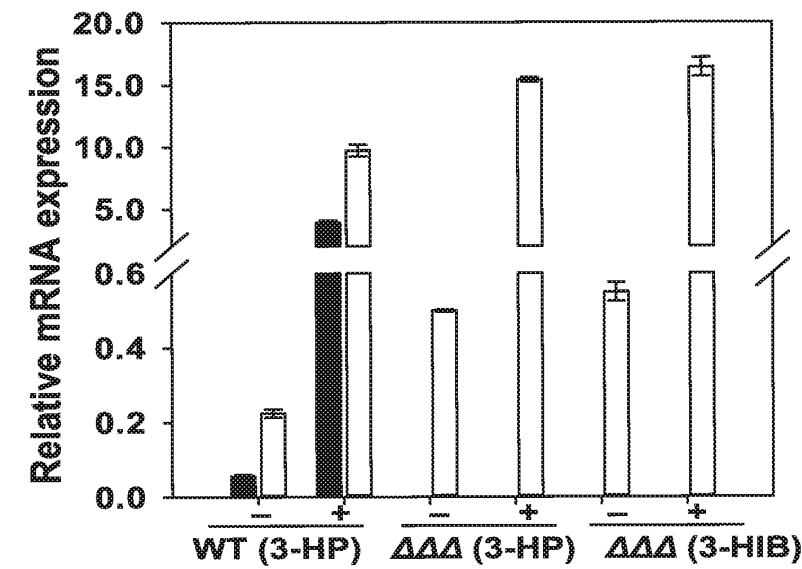


FIG. 2A

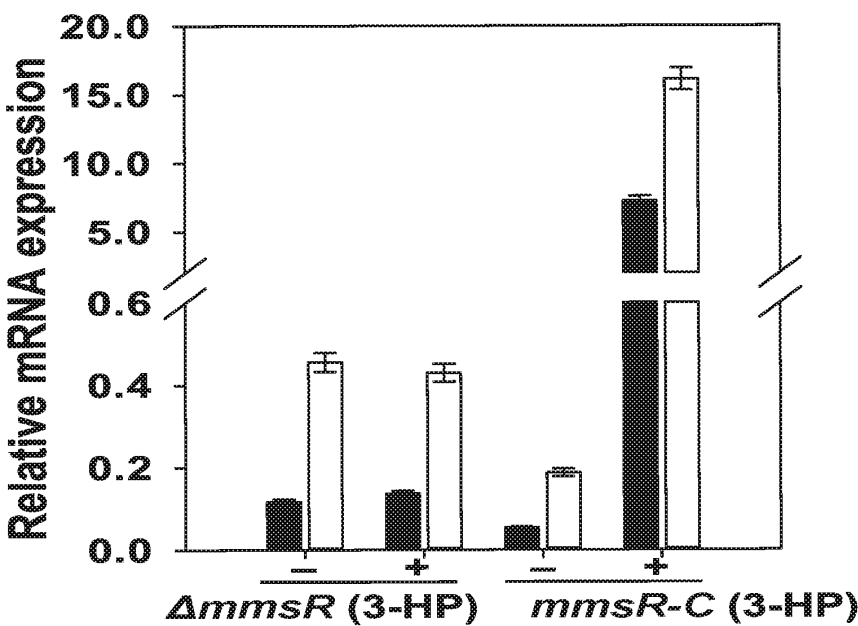


FIG. 2B

Figure 6

Detailed description: This figure shows a DNA sequence alignment between the mmsA gene from Pseudomonas fluorescens Pf-0 (top) and several mutants (bottom). The top sequence is labeled 'mmsA' and has a scale bar above it indicating positions -117, -60, -37, -27, -14, and +1. Below the top sequence are six mutant sequences, each preceded by a label: P_{mmsA}-wt, P_{mmsA}-Δ1, P_{mmsA}-Δ2, P_{mmsA}-Δ3, P_{mmsA}-Δ4, and P_{mmsA}-Δ3-Δ4. Vertical dashed lines connect corresponding nucleotide positions across all sequences. Horizontal arrows indicate deletions: Δ1 (from -60 to -37), Δ2 (from -37 to -27), Δ3 (from -27 to -14), and Δ4 (from -14 to +1). The bottom-most sequence, P_{mmsA}-Δ3-Δ4, shows a combined deletion from -60 to +1.

Sequence	Position	Nucleotide
P _{mmsA} -wt	-117	G
	-116	A
	-115	T
	-114	C
	-113	T
	-112	C
	-111	C
	-110	C
	-109	A
	-108	C
	-107	C
	-106	G
	-105	C
	-104	C
	-103	A
	-102	G
	-101	C
	P _{mmsA} -Δ1	-117
-116		A
-115		T
-114		C
-113		T
-112		C
-111		C
-110		C
-109		A
-108		C
-107		C
-106		G
-105		C
-104		C
-103		A
-102		G
-101		C
-60		G
P _{mmsA} -Δ2	-117	G
	-116	A
	-115	T
	-114	C
	-113	T
	-112	C
	-111	C
	-110	C
	-109	A
	-108	C
	-107	C
	-106	G
	-105	C
	-104	C
	-103	A
	-102	G
	-101	C
	-37	G
P _{mmsA} -Δ3	-117	G
	-116	A
	-115	T
	-114	C
	-113	T
	-112	C
	-111	C
	-110	C
	-109	A
	-108	C
	-107	C
	-106	G
	-105	C
	-104	C
	-103	A
	-102	G
	-101	C
	-27	G
P _{mmsA} -Δ4	-117	G
	-116	A
	-115	T
	-114	C
	-113	T
	-112	C
	-111	C
	-110	C
	-109	A
	-108	C
	-107	C
	-106	G
	-105	C
	-104	C
	-103	A
	-102	G
	-101	C
	-14	G
P _{mmsA} -Δ3-Δ4	-117	G
	-116	A
	-115	T
	-114	C
	-113	T
	-112	C
	-111	C
	-110	C
	-109	A
	-108	C
	-107	C
	-106	G
	-105	C
	-104	C
	-103	A
	-102	G
	-101	C
	+1	G

[illegible]

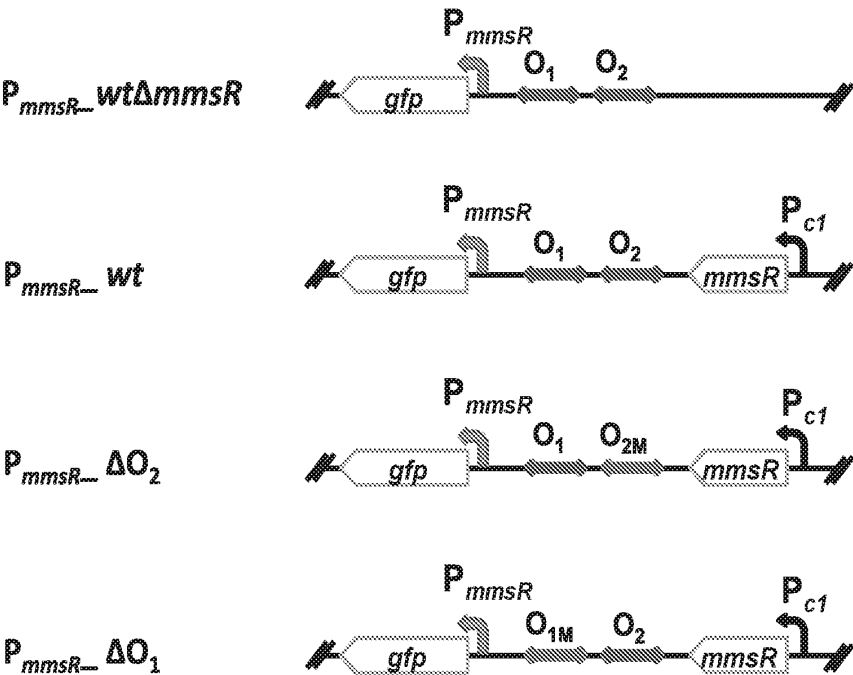


FIG. 4A

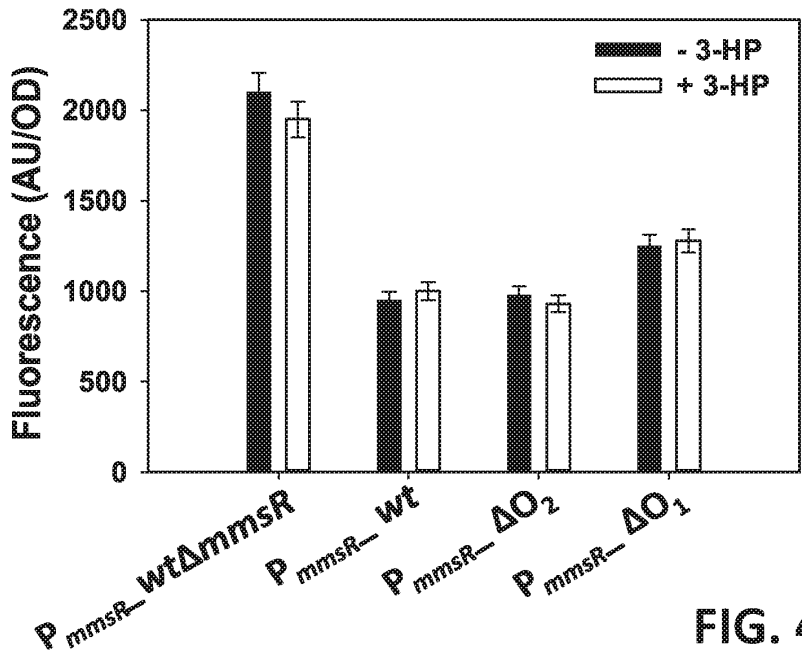
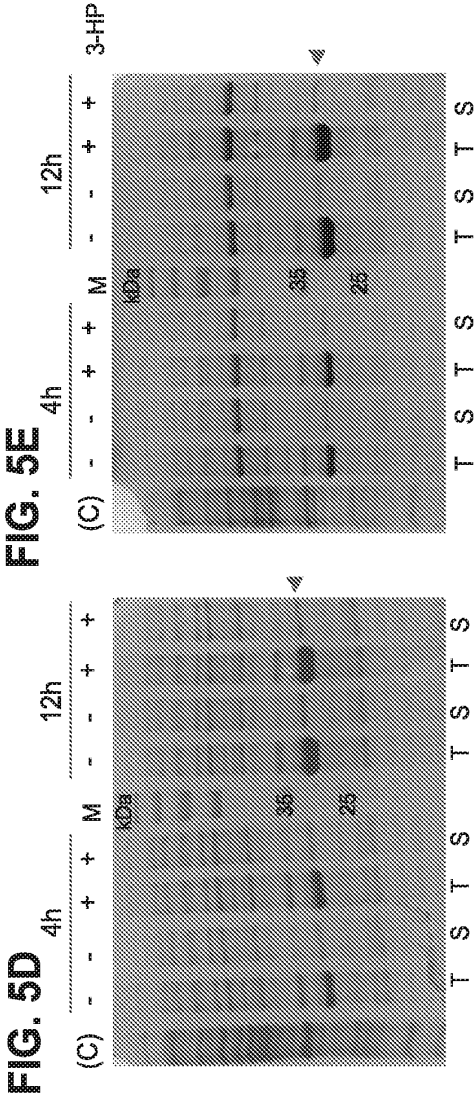
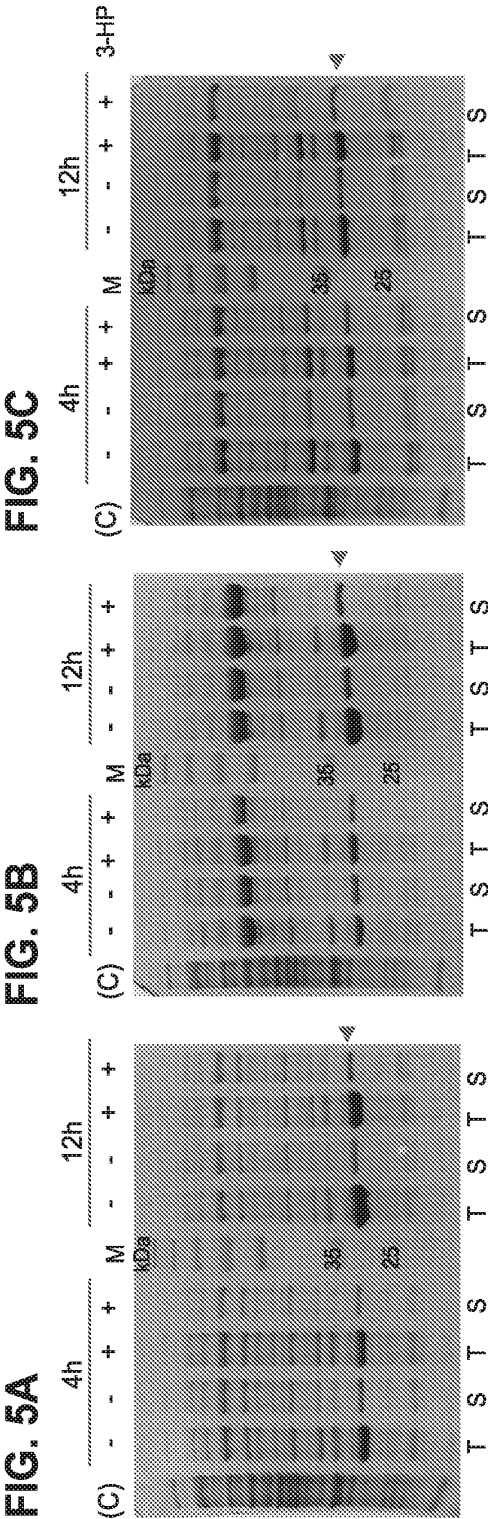


FIG. 4B



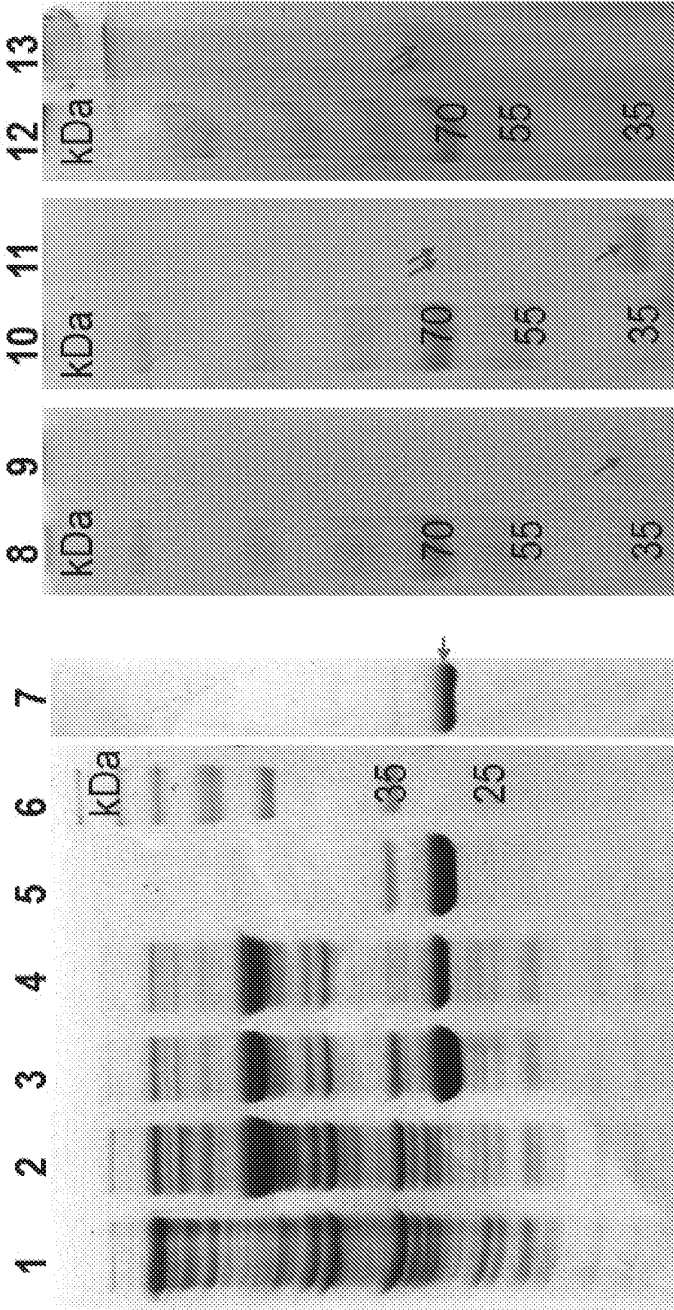


FIG. 6B

FIG. 6A

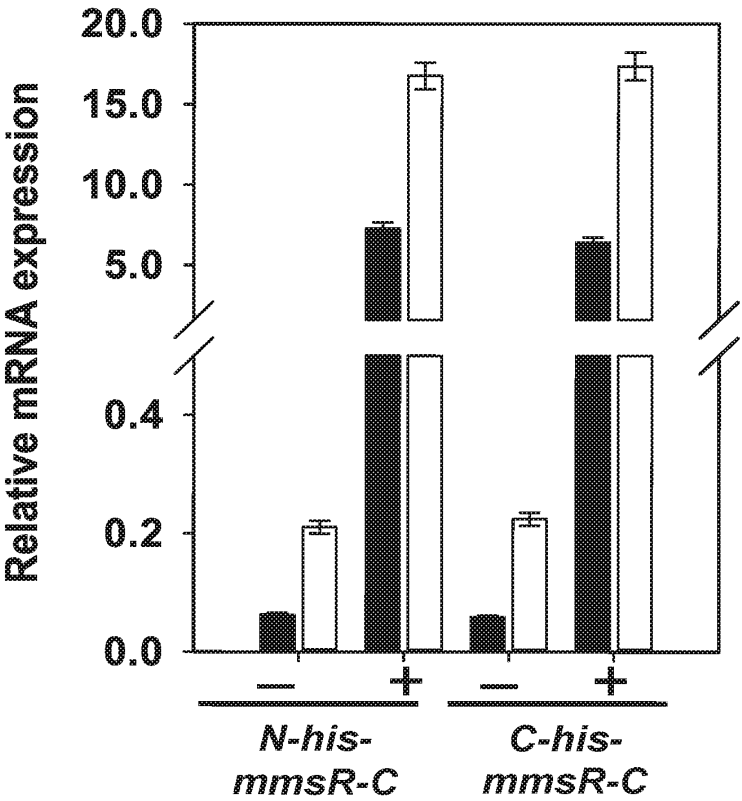


FIG. 6C

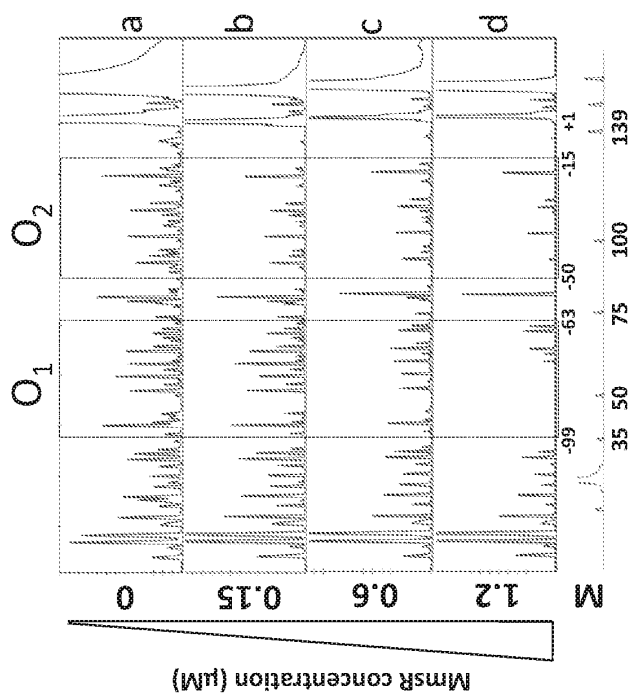


FIG. 7B

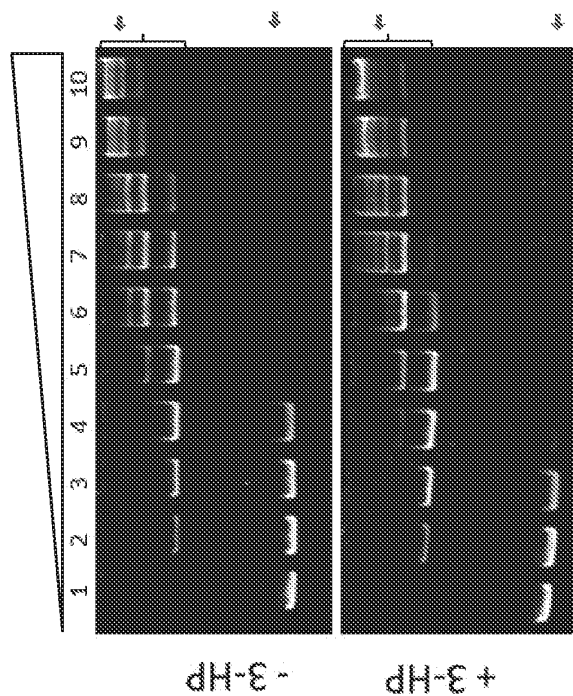


FIG. 7A

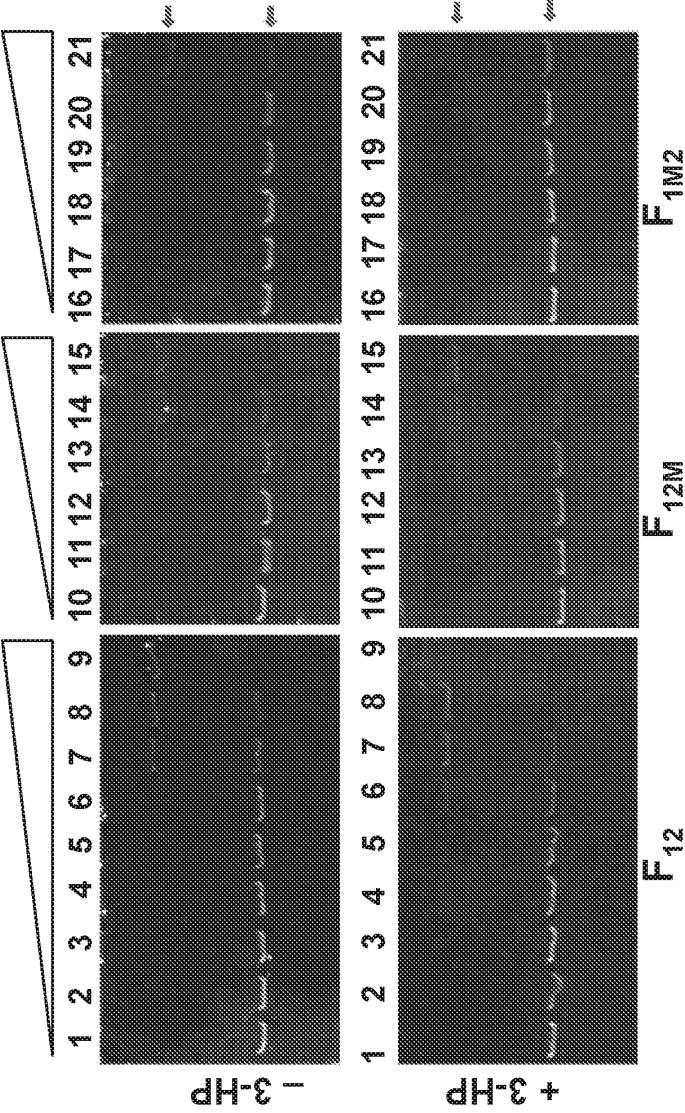


FIG. 8

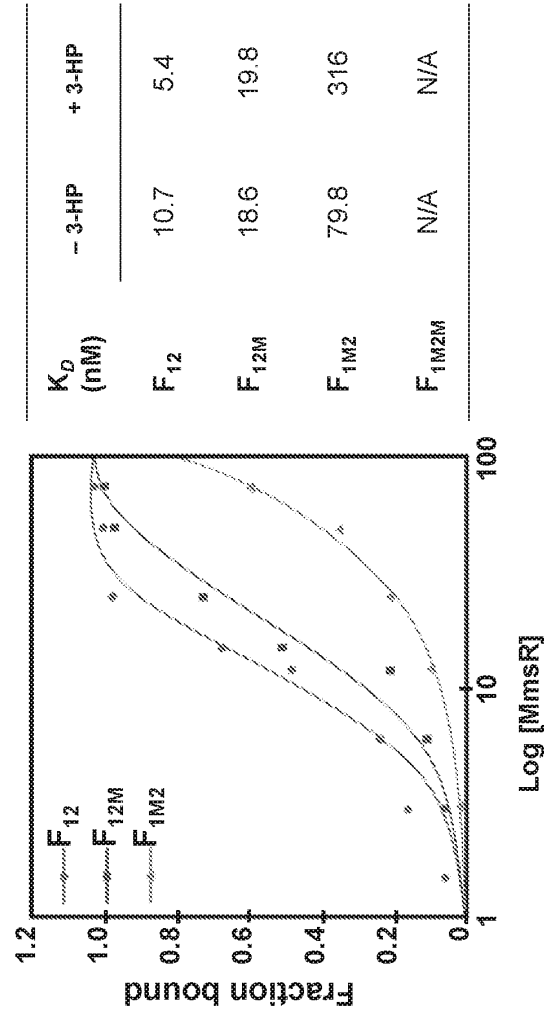


FIG. 9

FIG. 10A

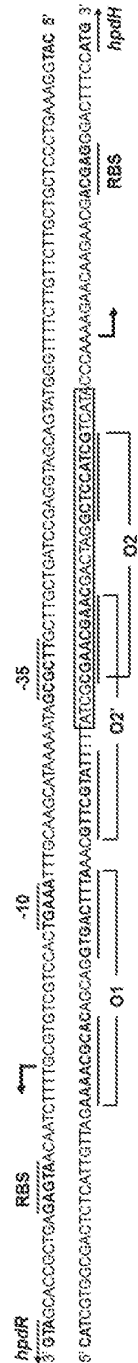


FIG. 10B

01	AAAACGCAC TAAAGTCAC	6/9
02'	GTTTCGTATT GTTTCGTTCCG	6/9
02	CGAACGAAC CGATGGAGC	6/9
NN AAGTAAC Consensus		

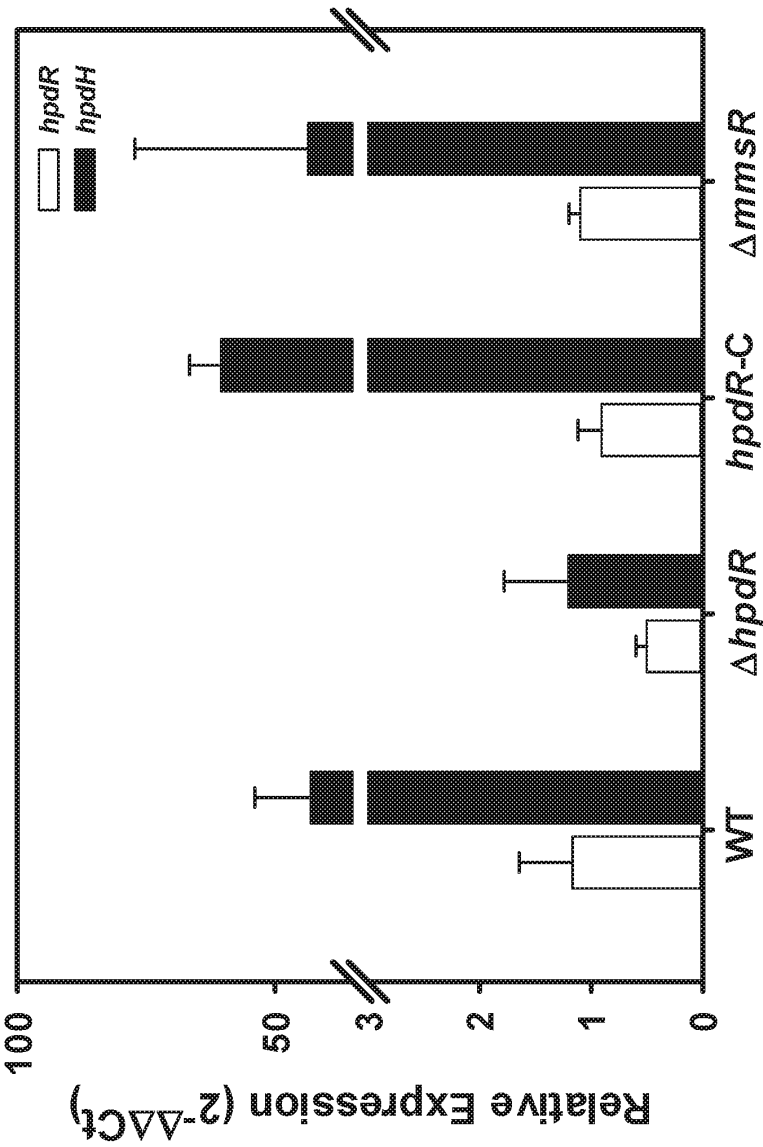


FIG. 11A

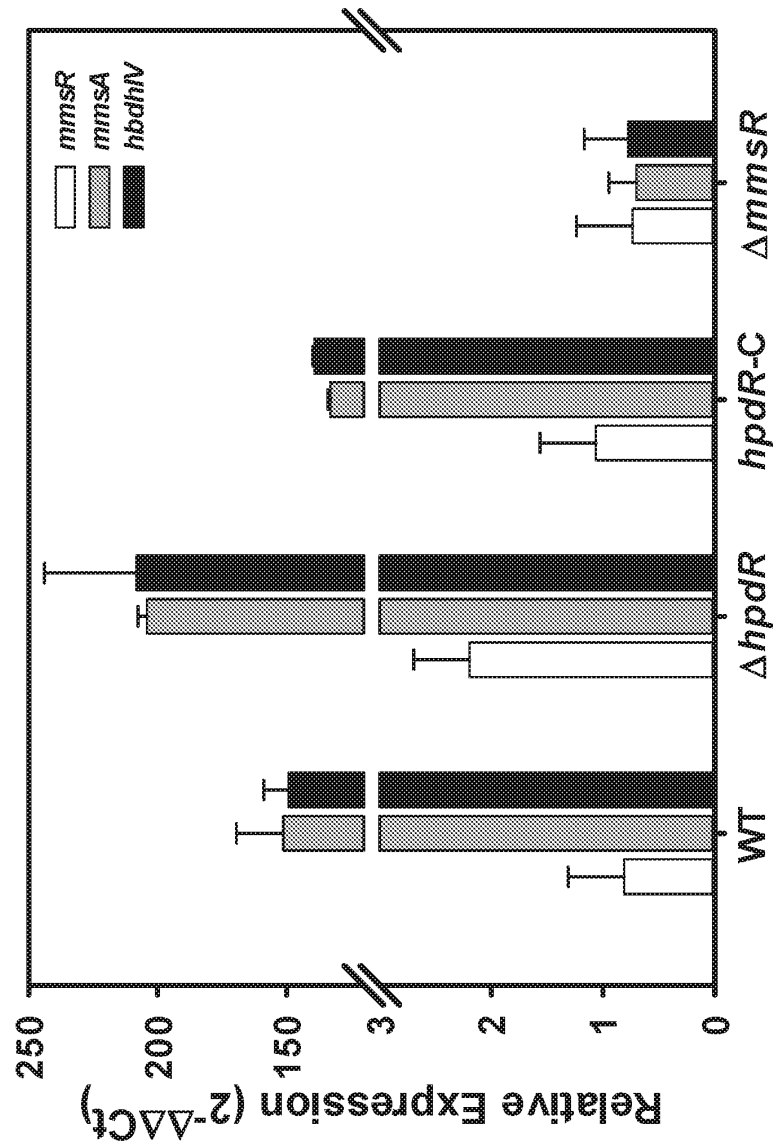


FIG. 11B

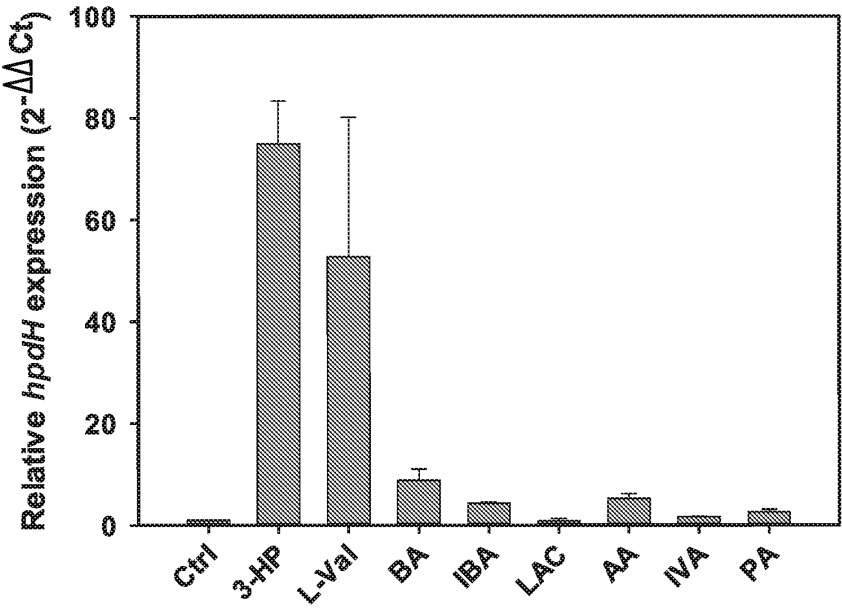


FIG. 12A

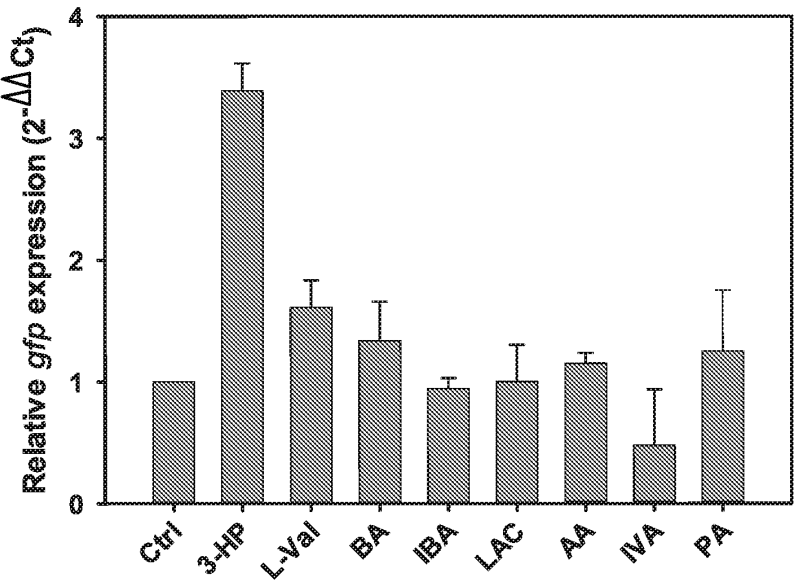


FIG. 12B

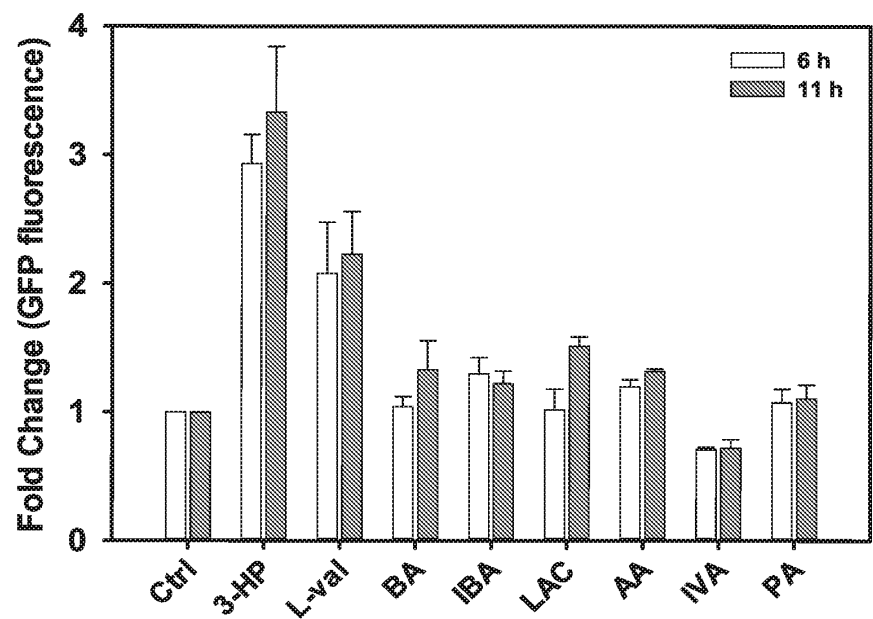


FIG. 12C

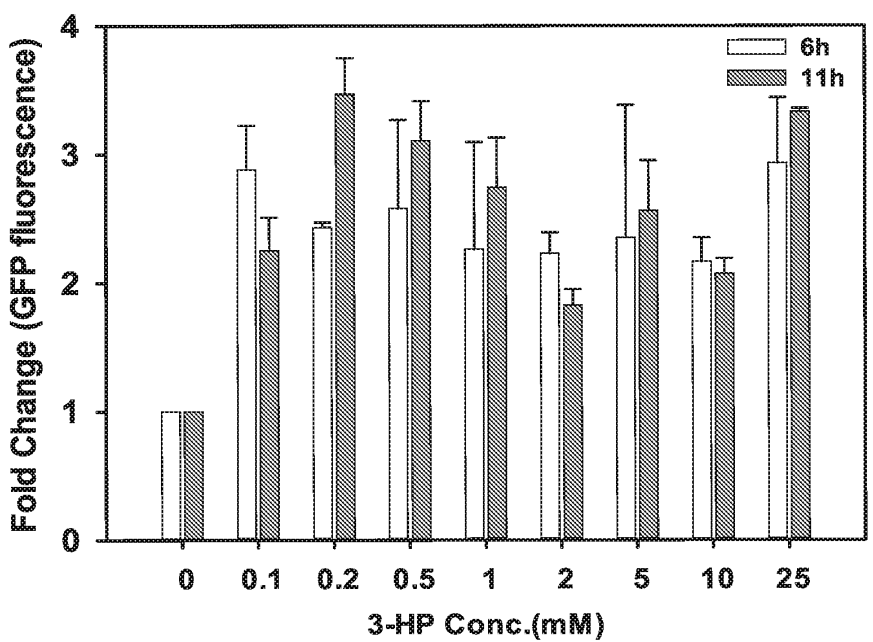


FIG. 12D

P_{hpdH(wt)} 5' CGTATTTTATCGCGAAACGAACGACTAGGCTCCATCGTCATACCCCAAAAGAACAAAGAAACGACGAGGGGACTTTTCC 3'

P_{hpdH(p1)} 5' CGTATTTTATCGCGAAACGAACGACTAGGCTCCATCGTCATACCCCAAAAGAACAAAGAAACGACGAGGGGACTTTTCC 3'

P_{hpdH(p2)} 5' CGTATTTTATCGCGAAACGAACGACTAGGCTCCATCGTCATACCCCAAAAGAACAAAGAAACGACGAGGGGACTTTTCC 3'

P_{hpdH(p3)} 5' CGTATTTTATCGCGAAACGAACGACTAGGCTCCATCGTCATACCCCAAAAGAACAAAGAAACGACGAGGGGACTTTTCC 3'

P_{hpdH(p4)} 5' CGTATTTTATCGCGAAACGAACGACTAGGCTCCATCGTCATACCCCAAAAGAACAAAGAAACGACGAGGGGACTTTTCC 3'

P_{hpdH(p5)} 5' CGTATTTTATCGCGAAACGAACGACTAGGCTCCATCGTCATACCCCAAAAGAACAAAGAAACGACGAGGGGACTTTTCC 3'

P_{hpdH(p6)} 5' CGTATTTTATCGCGAAACGAACGACTAGGCTCCATCGTCATACCCCAAAAGAACAAAGAAACGACGAGGGGACTTTTCC 3'

P_{hpdH(p7)} 5' CGTATTTTATCGCGAAACGAACGACTAGGCTCCATCGTCATACCCCAAAAGAACAAAGAAACGACGAGGGGACTTTTCC 3'

FIG. 13A

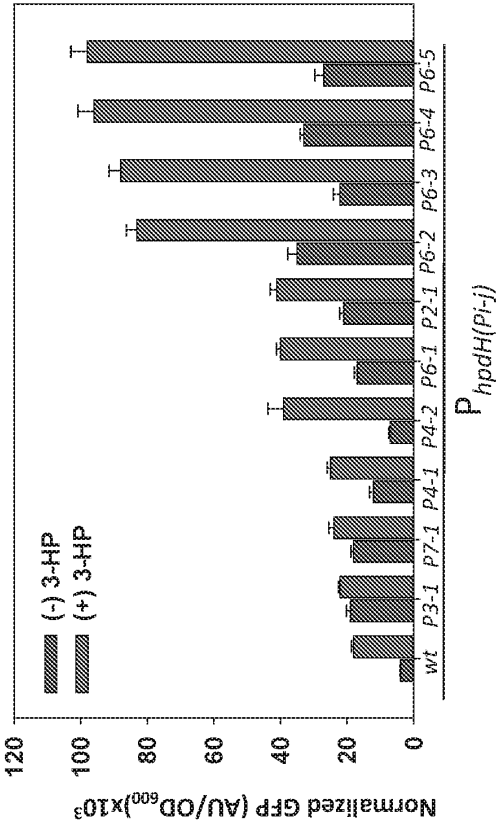


FIG. 13B

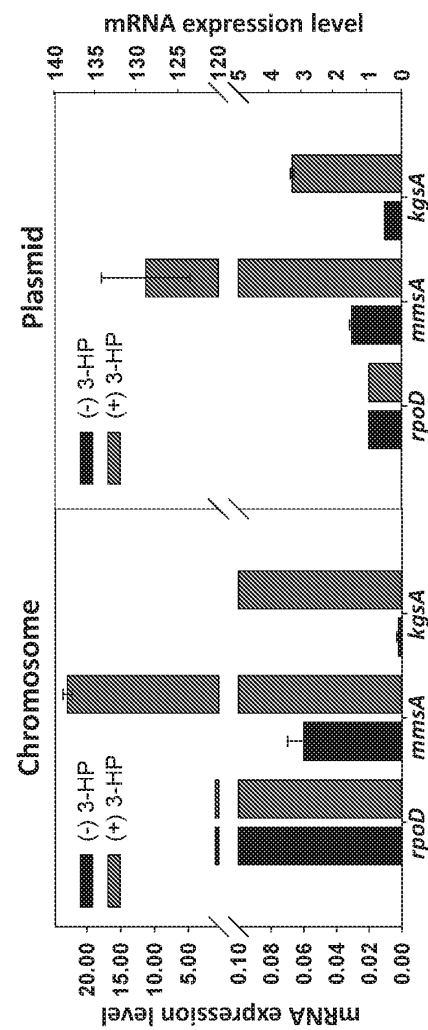


FIG. 14A

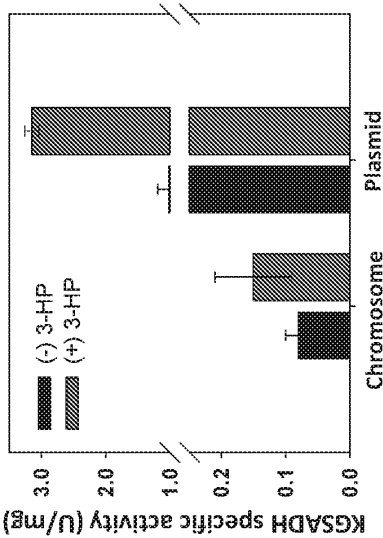


FIG. 14B

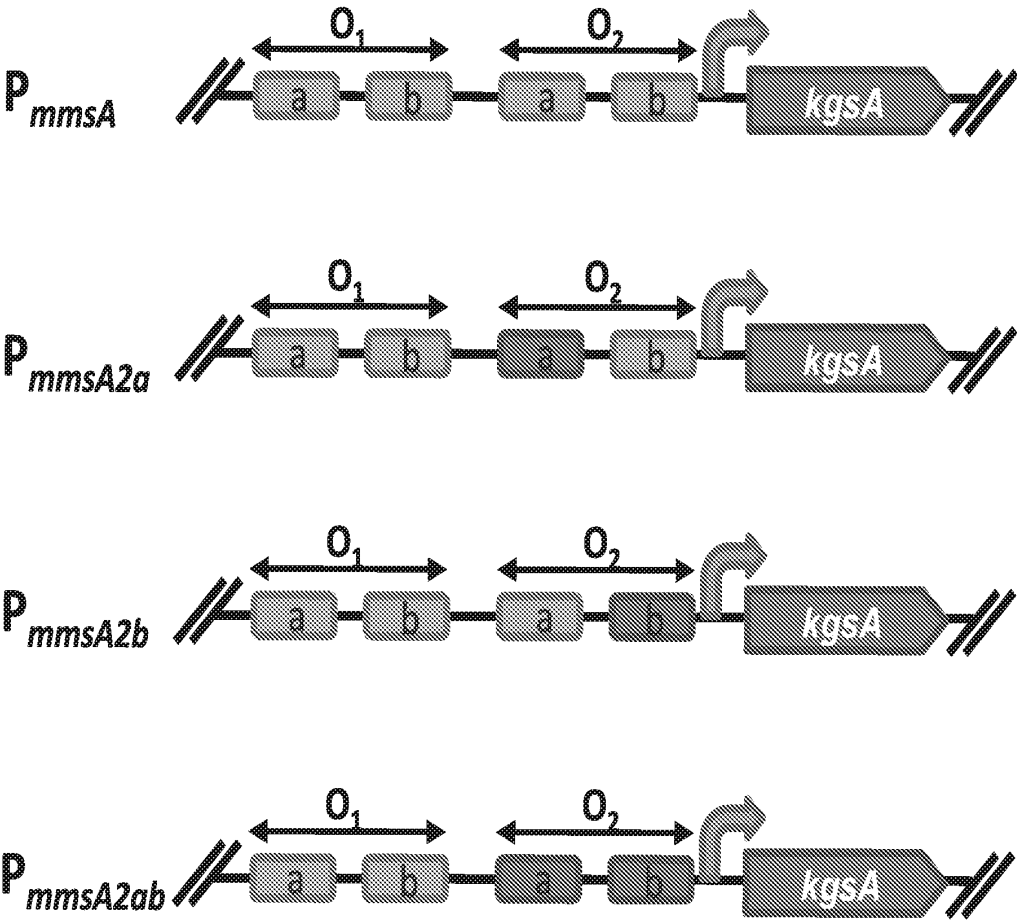


FIG. 15A

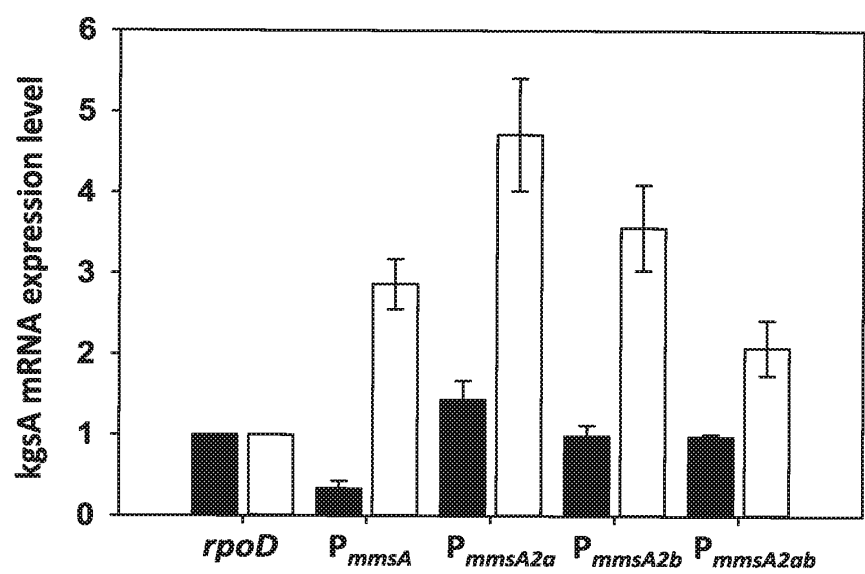


FIG. 15B

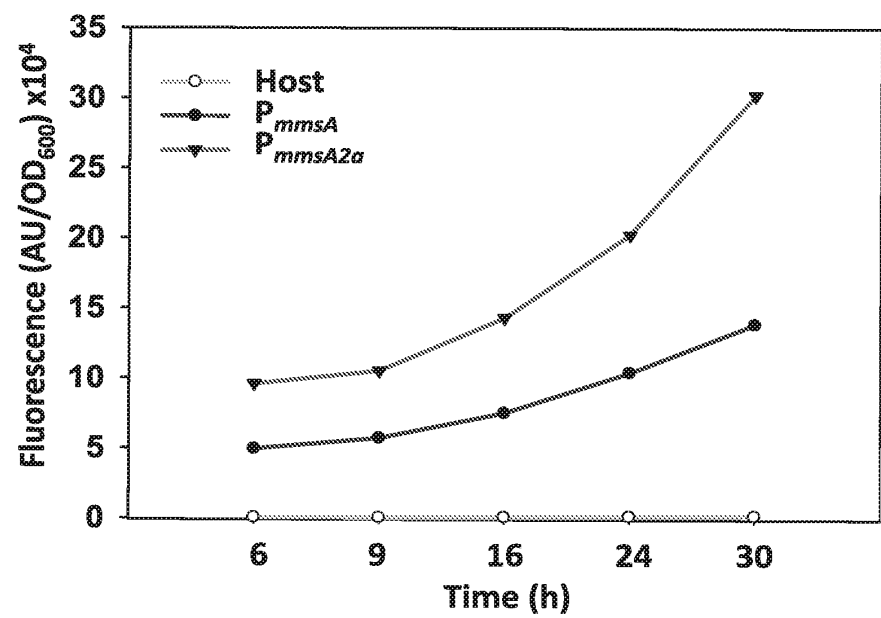


FIG. 15C

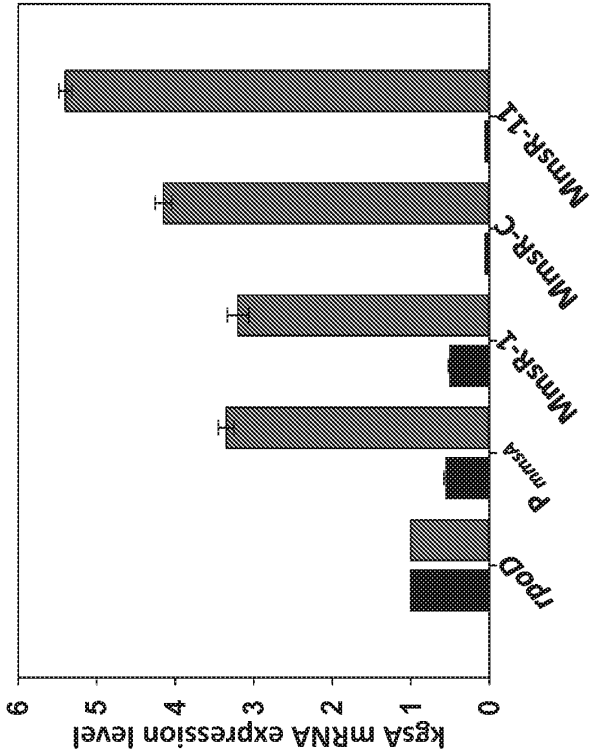


FIG. 16B

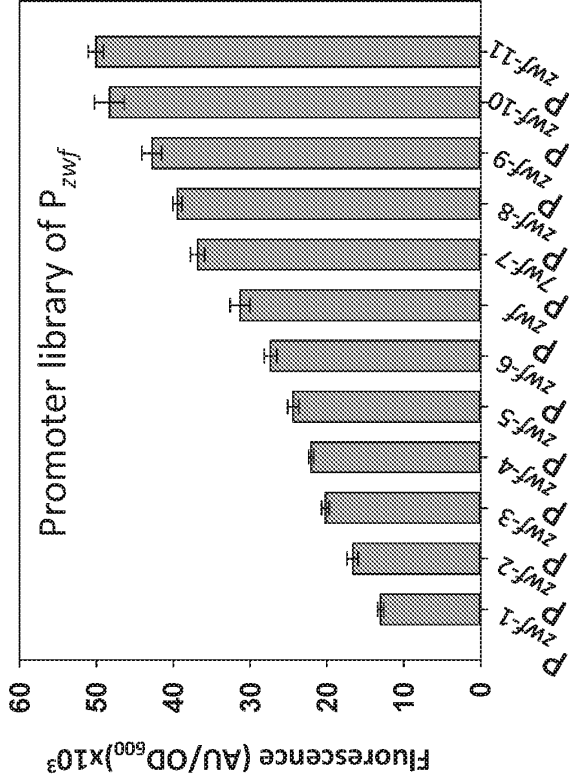


FIG. 16A

FIG. 17 A

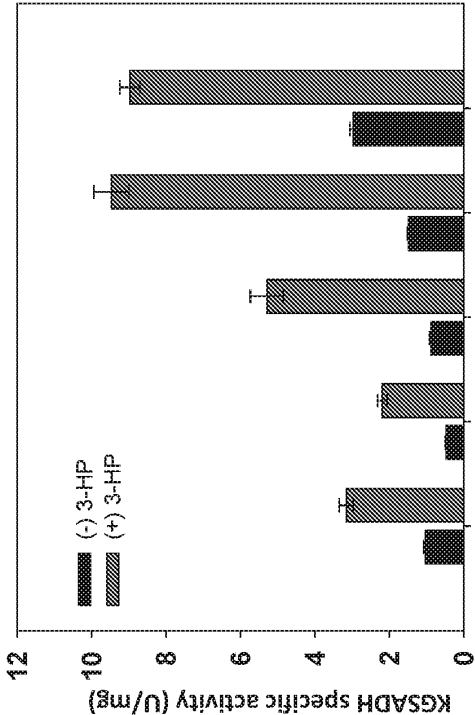


FIG. 17 B

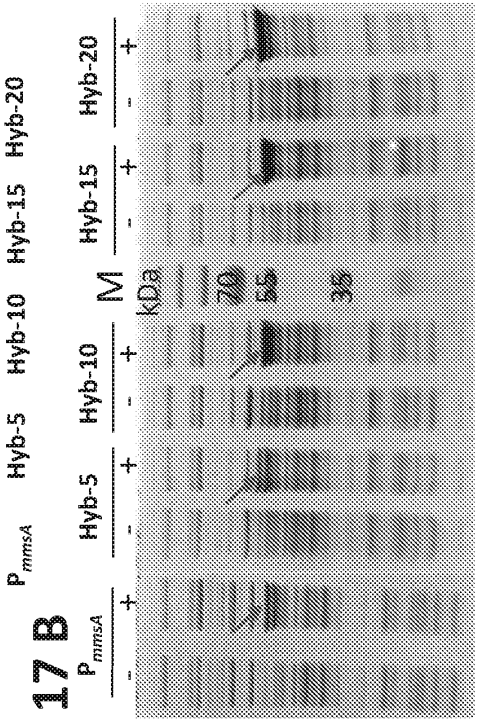


FIG. 17 C

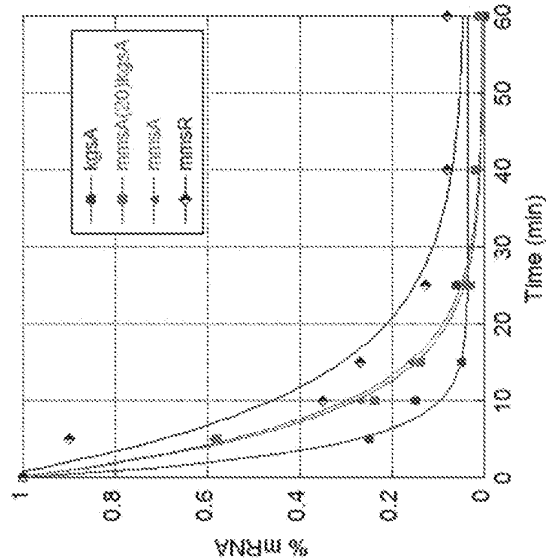


FIG. 17 D

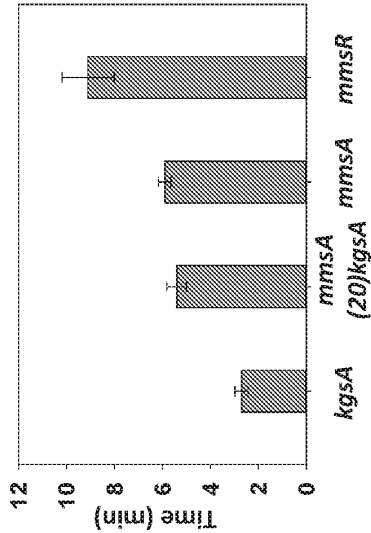


FIG. 18 A

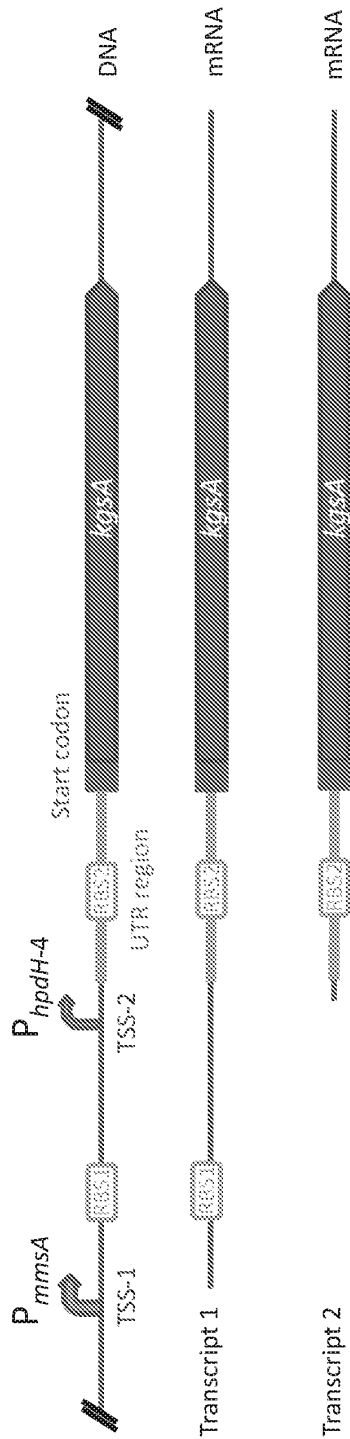


FIG. 18 B

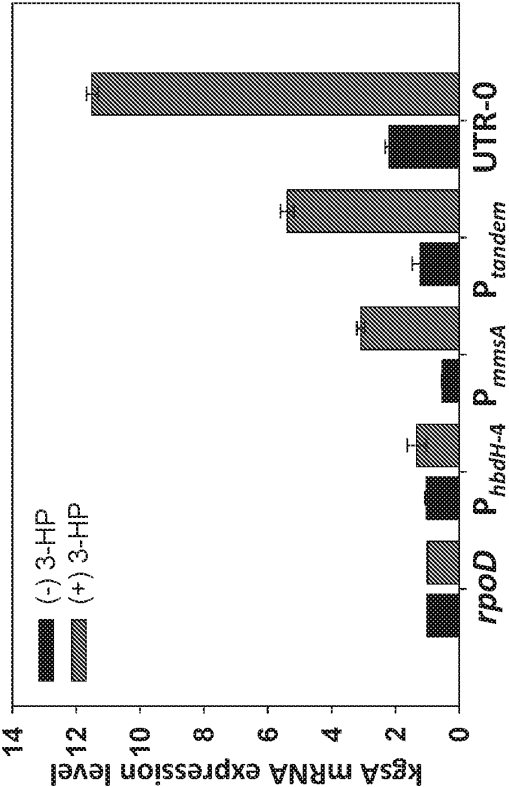


FIG. 18 C

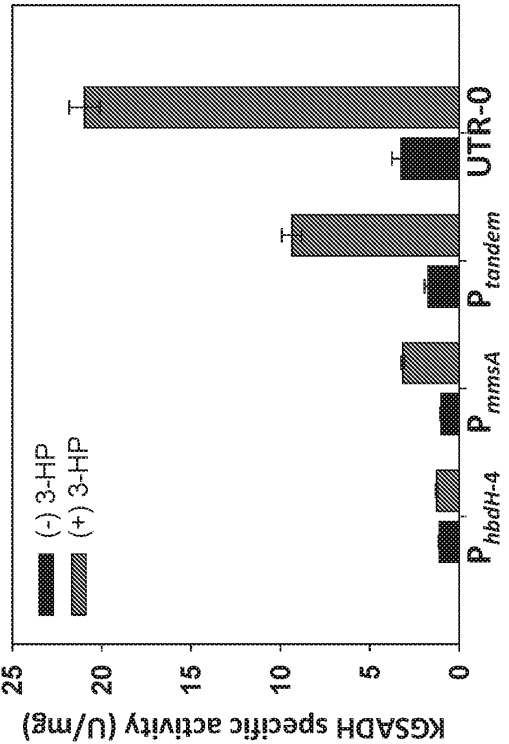


FIG. 19A

Strain	Prediction (a.u.)	Fold
<i>P_{mmsA}</i>	26884	0.09
UTR-0	302528	1.00
UTR-1	66824	0.22
UTR-2	319930	1.06
UTR-3	625945	2.07
UTR-4	1168900	3.90
UTR-5	2025947	6.70
UTR-6	3748169	12.39

FIG. 19C

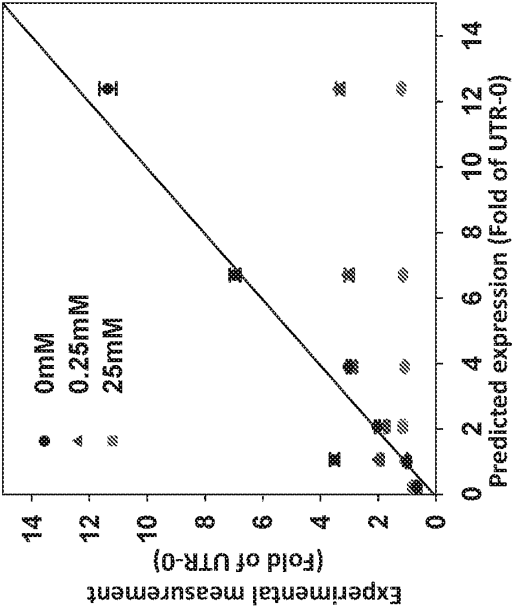
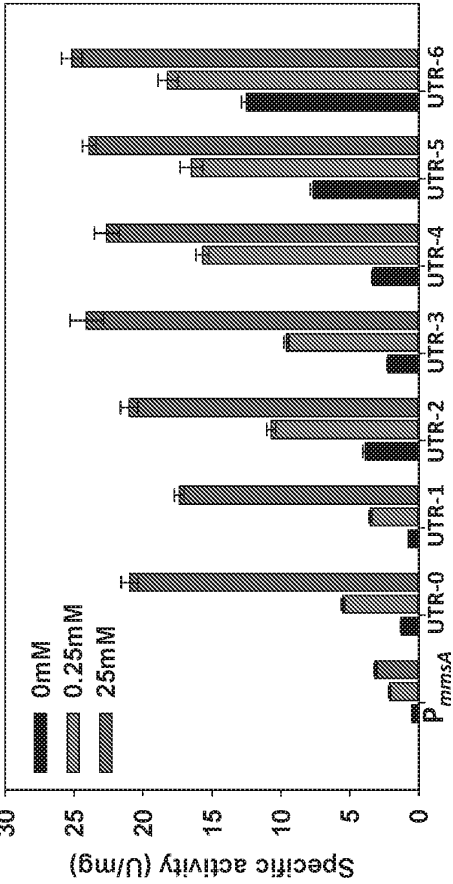


FIG. 19B



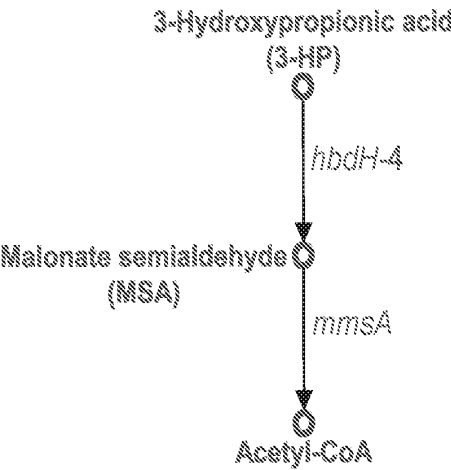


FIG. 20 A

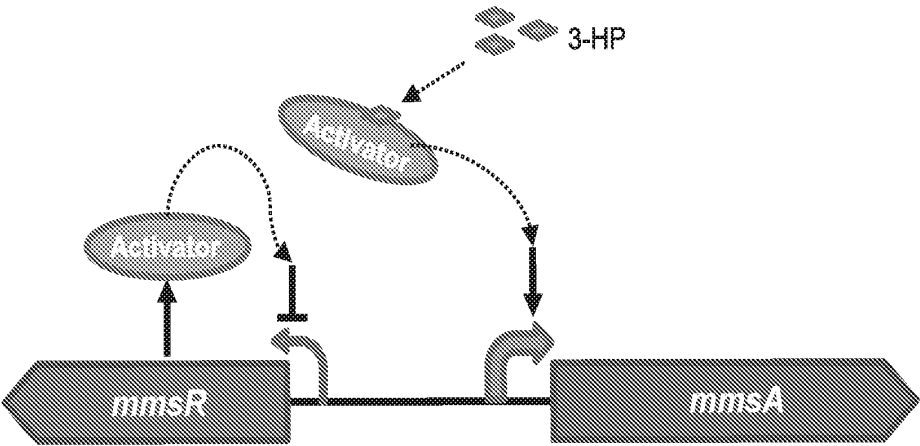


FIG. 20 B

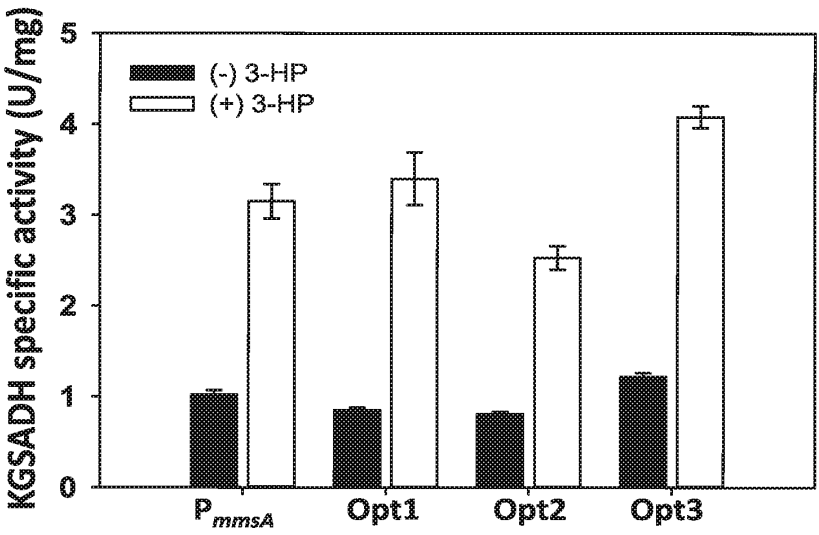


FIG. 21A

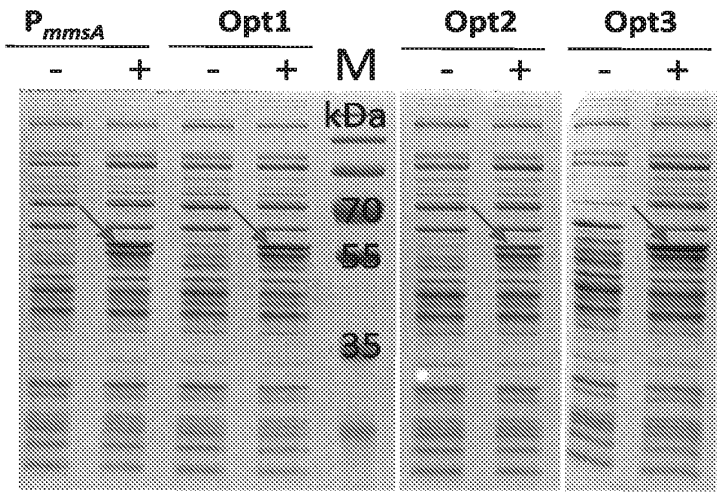


FIG. 21B

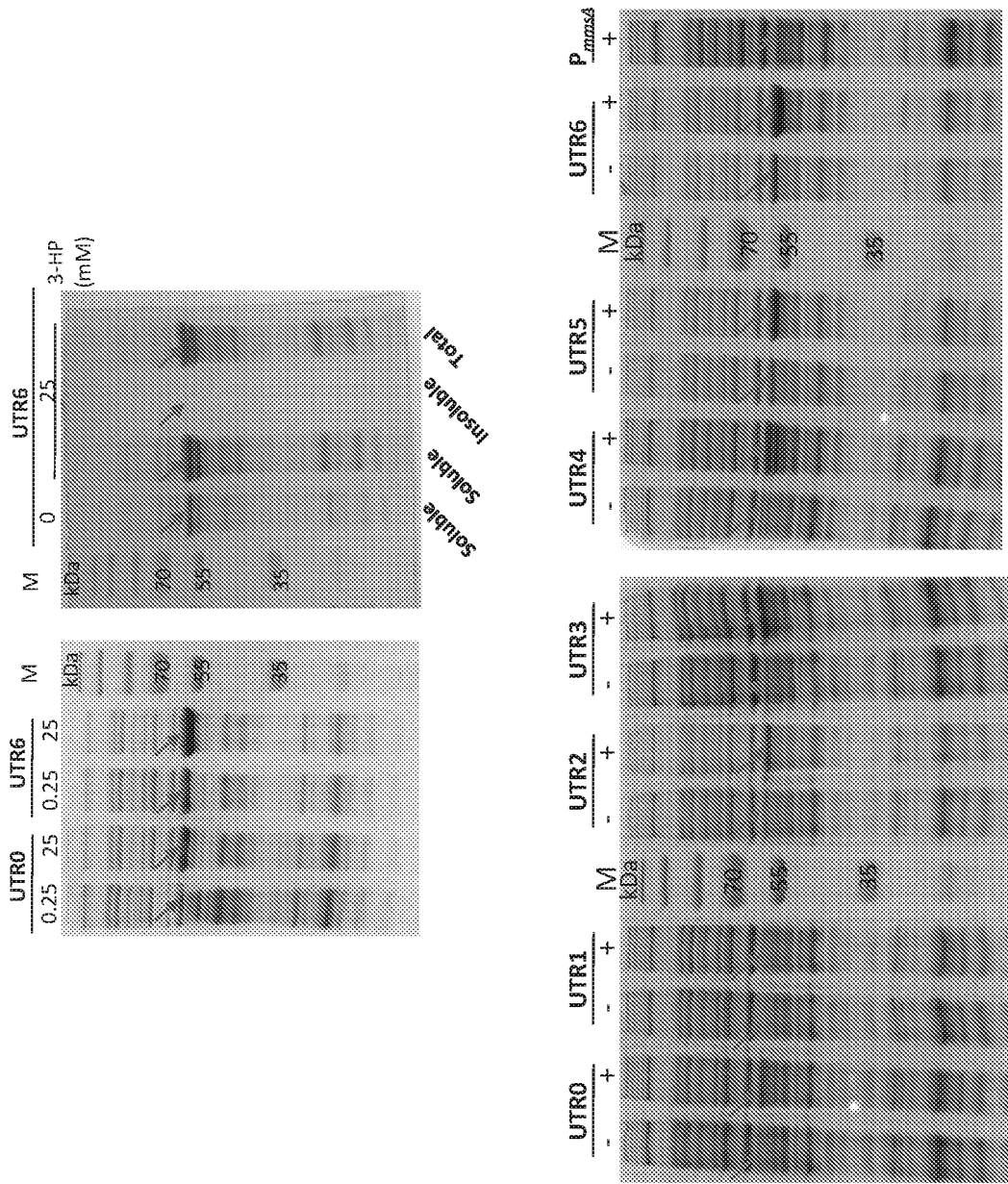
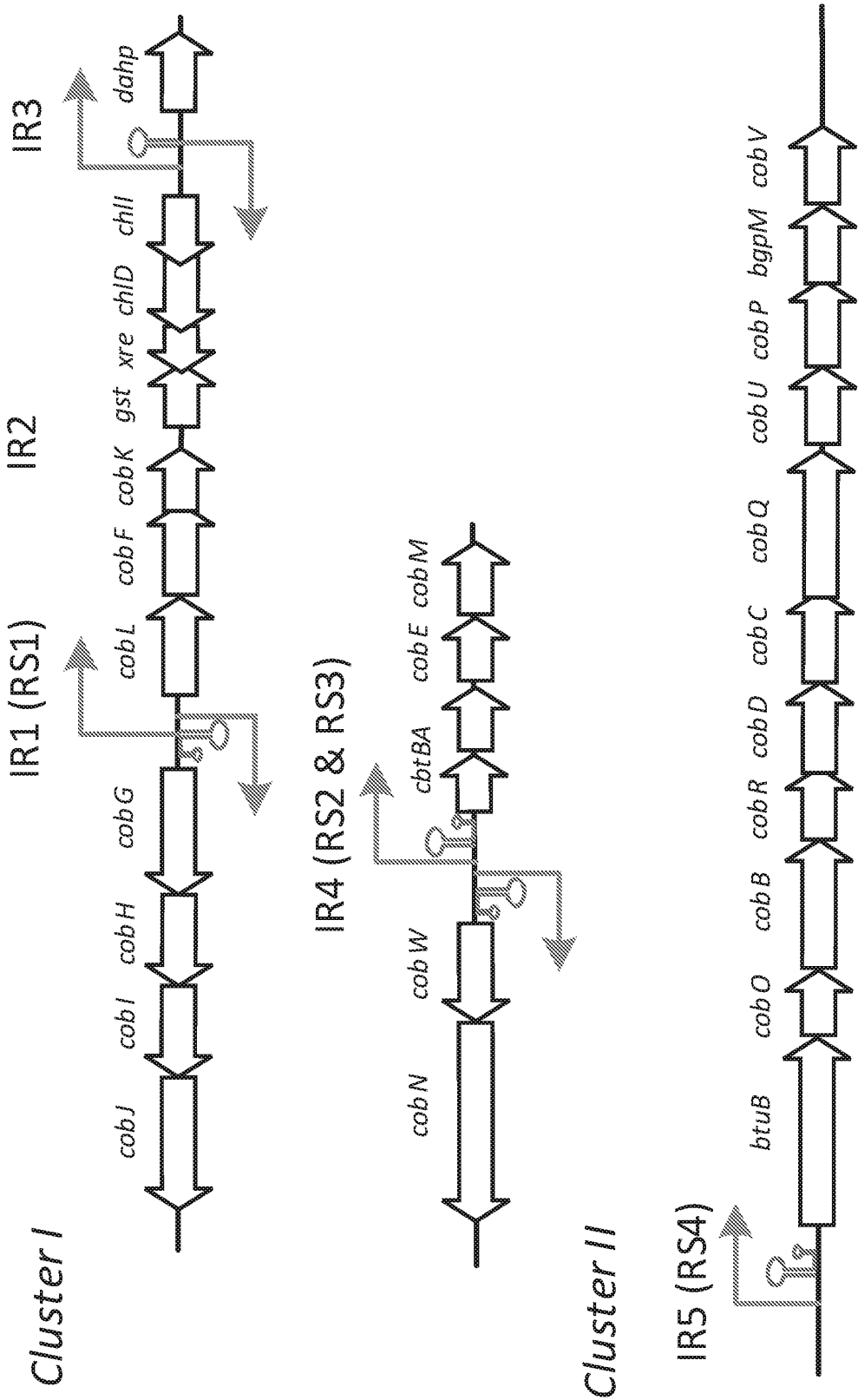
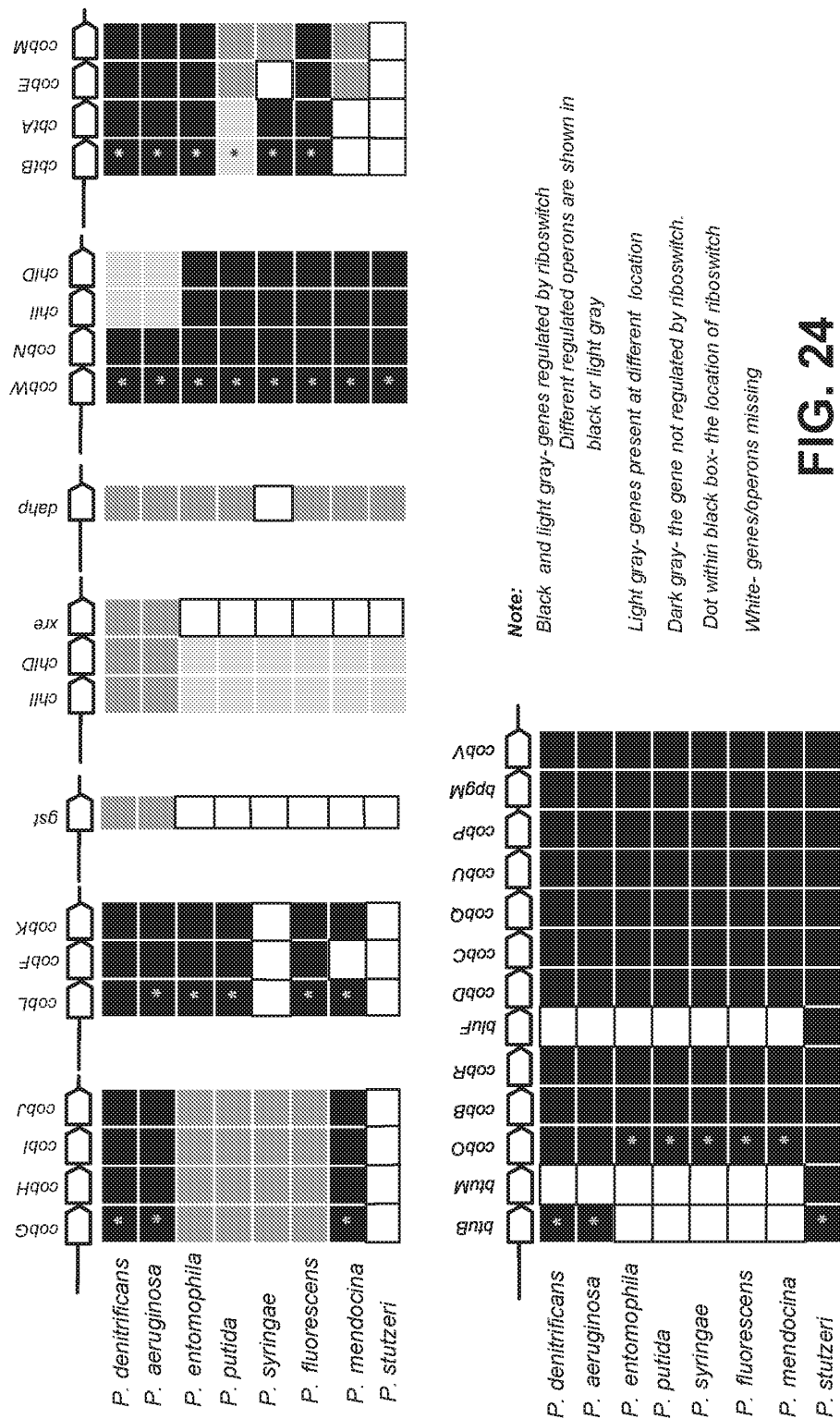


FIG. 22

FIG. 23





A. RS1 before cobG

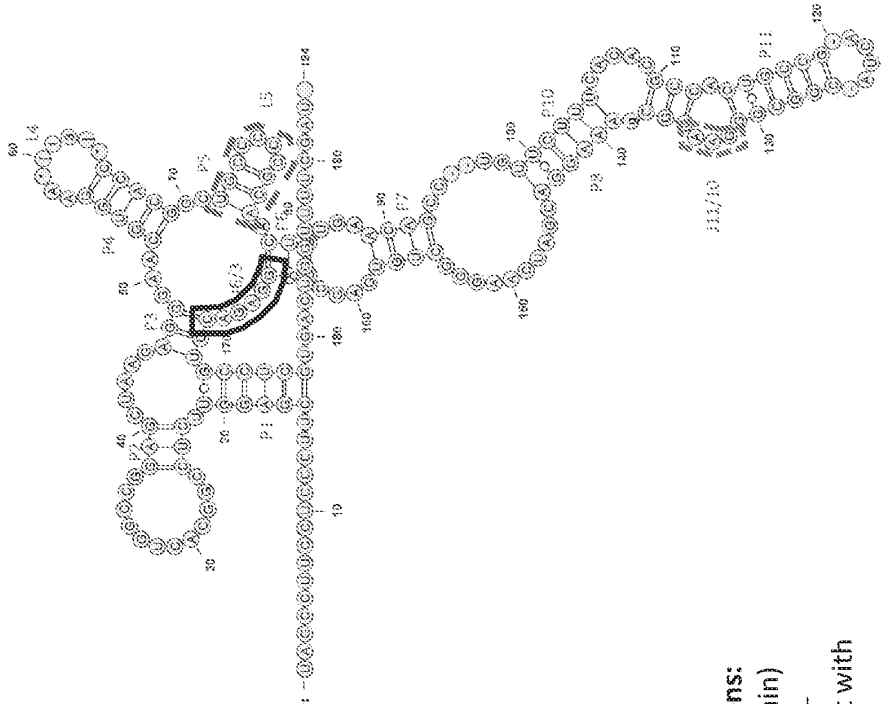


FIG. 25A

Highly conserved regions:
P5-15 (regulatory domain)
J6/3 (receptor domain)-
GAA of J11/10 (interact with
regulatory domain)

C. RS3 in front of cbtB

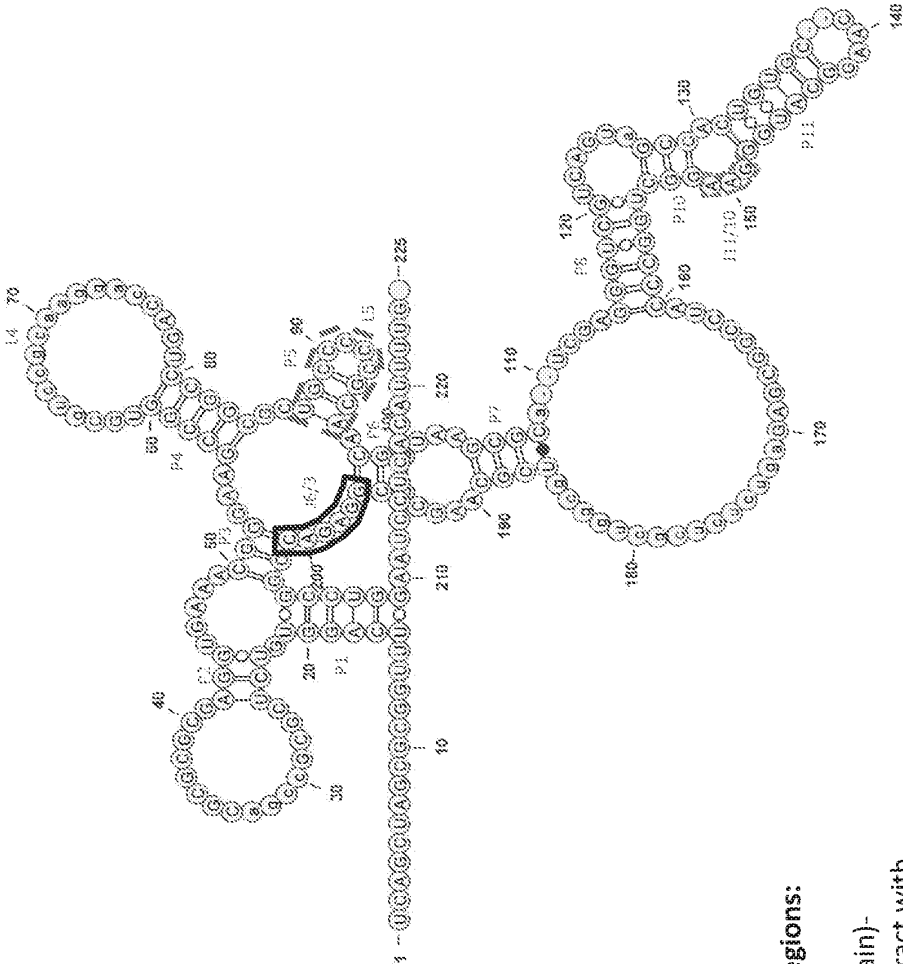
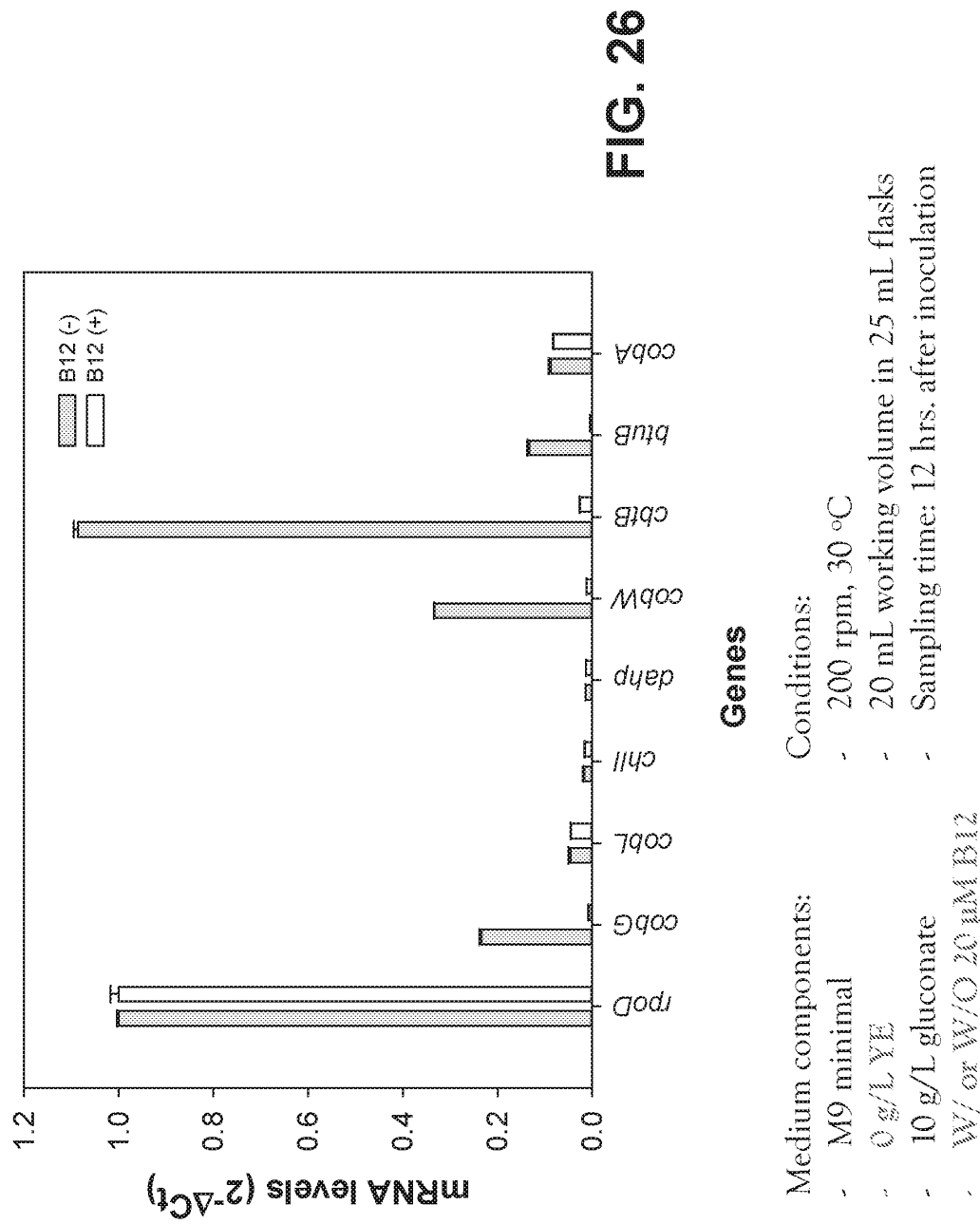


FIG. 25C

Highly conserved regions:
(regulatory domain)
j6/3 (receptor domain)-
GAA of 111/10 (interact with
regulatory domain)



Medium components:

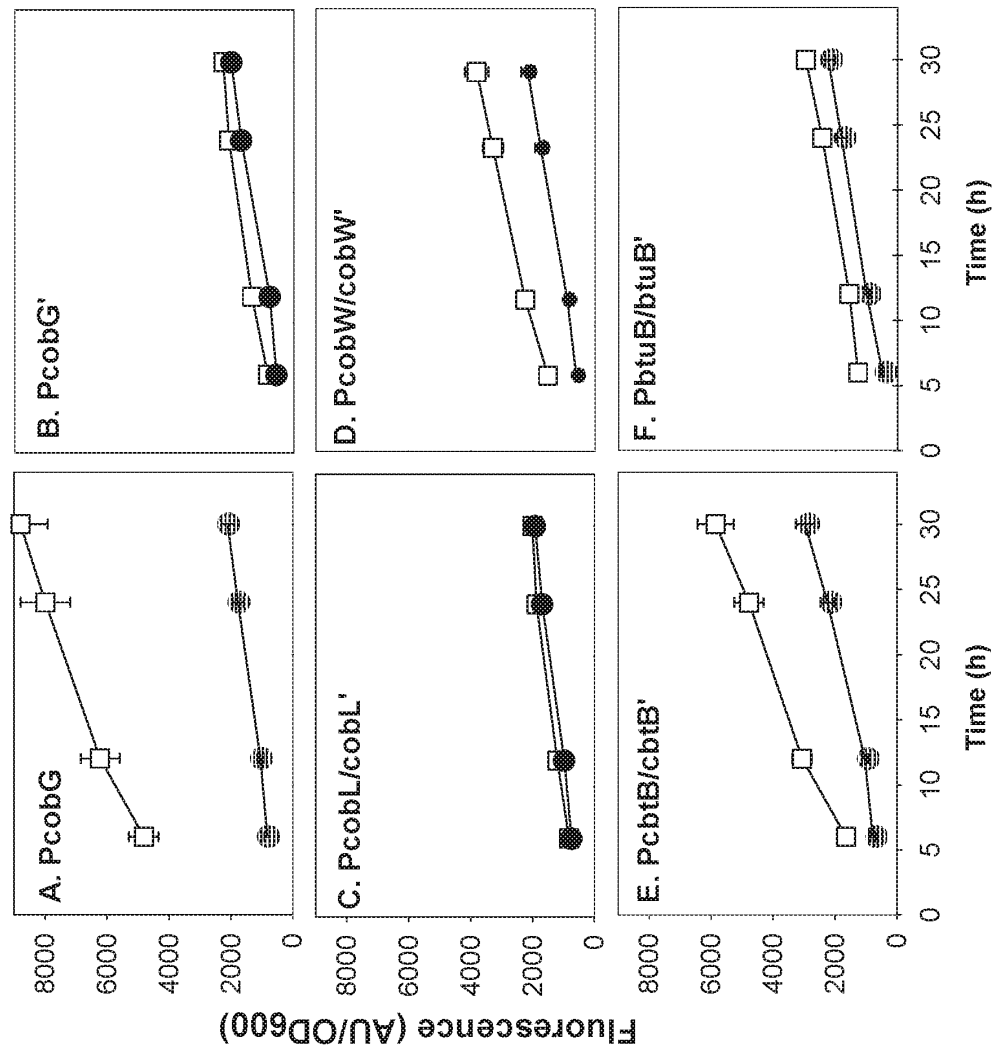
- M9 minimal
- 0 g/L YE
- 10 g/L gluconate
- ± 20 μ M CoB12

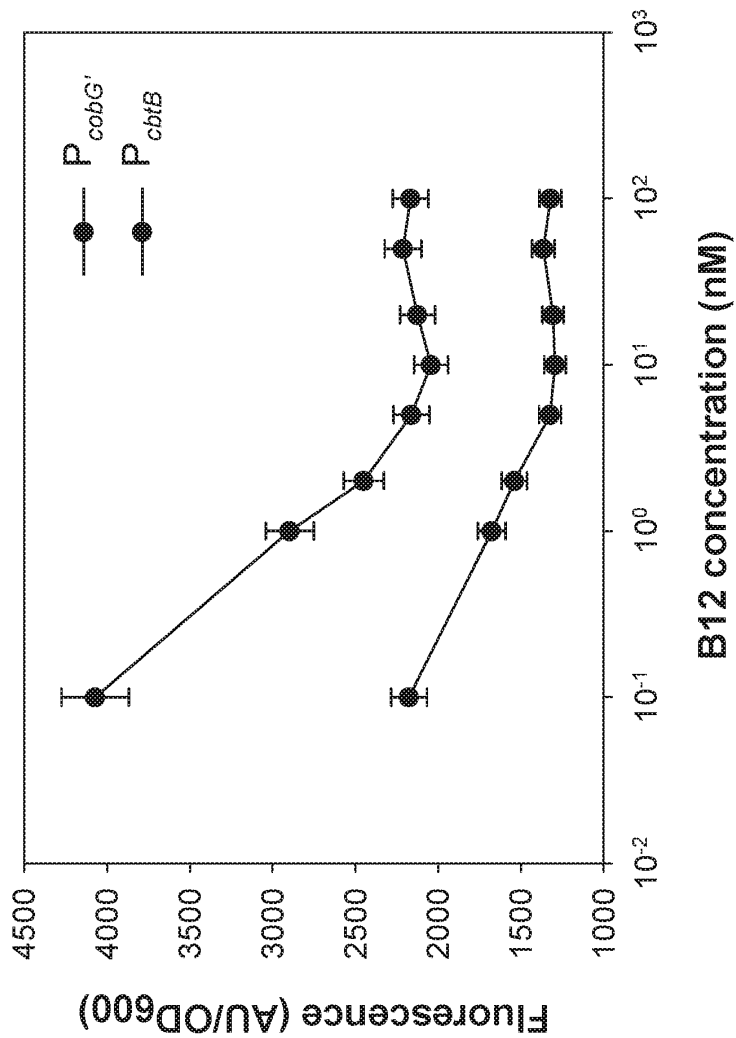
Conditions:

- 200 rpm, 30 °C
- 20 mL working volume in 250 mL Erlenmeyer flask

A: P_{cobG'} (IR1)
B: P_{cobW'} (IR3)
C: P_{cobB'} (IR3)
D: P_{btuB'} (IR4)
E: no plasmid containing

FIG. 27





Medium components:

- M9 minimal
- 0 g/L YE
- 10 g/L gluconate
- 0.1 ~ 100 nM CoB12

Conditions:

- 200 rpm, 30 °C
- 1.2 mL working volume in 2 mL well (using 96 wells block)
- Sampling time: 12h after inoculation

FIG. 28

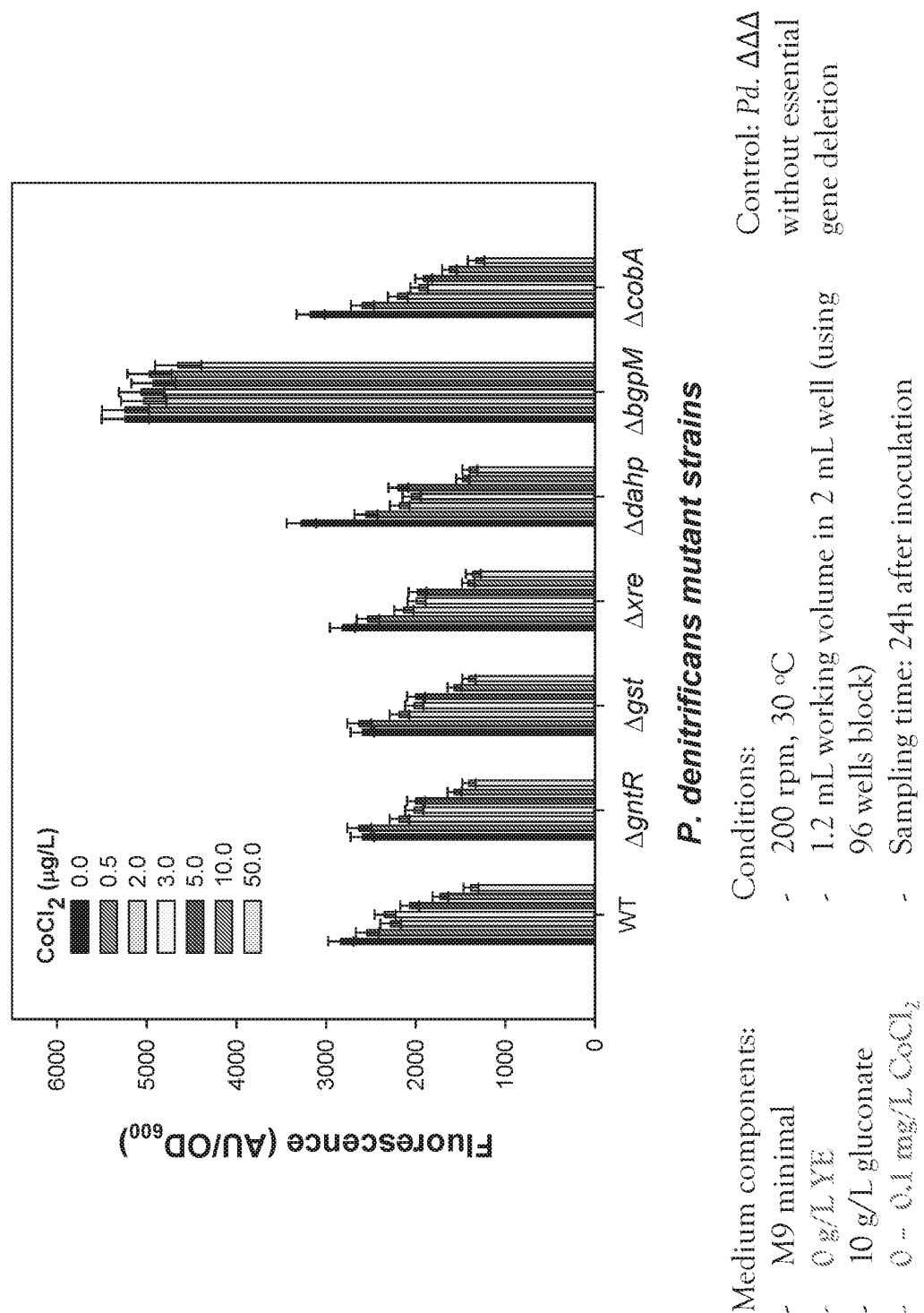


FIG. 29A

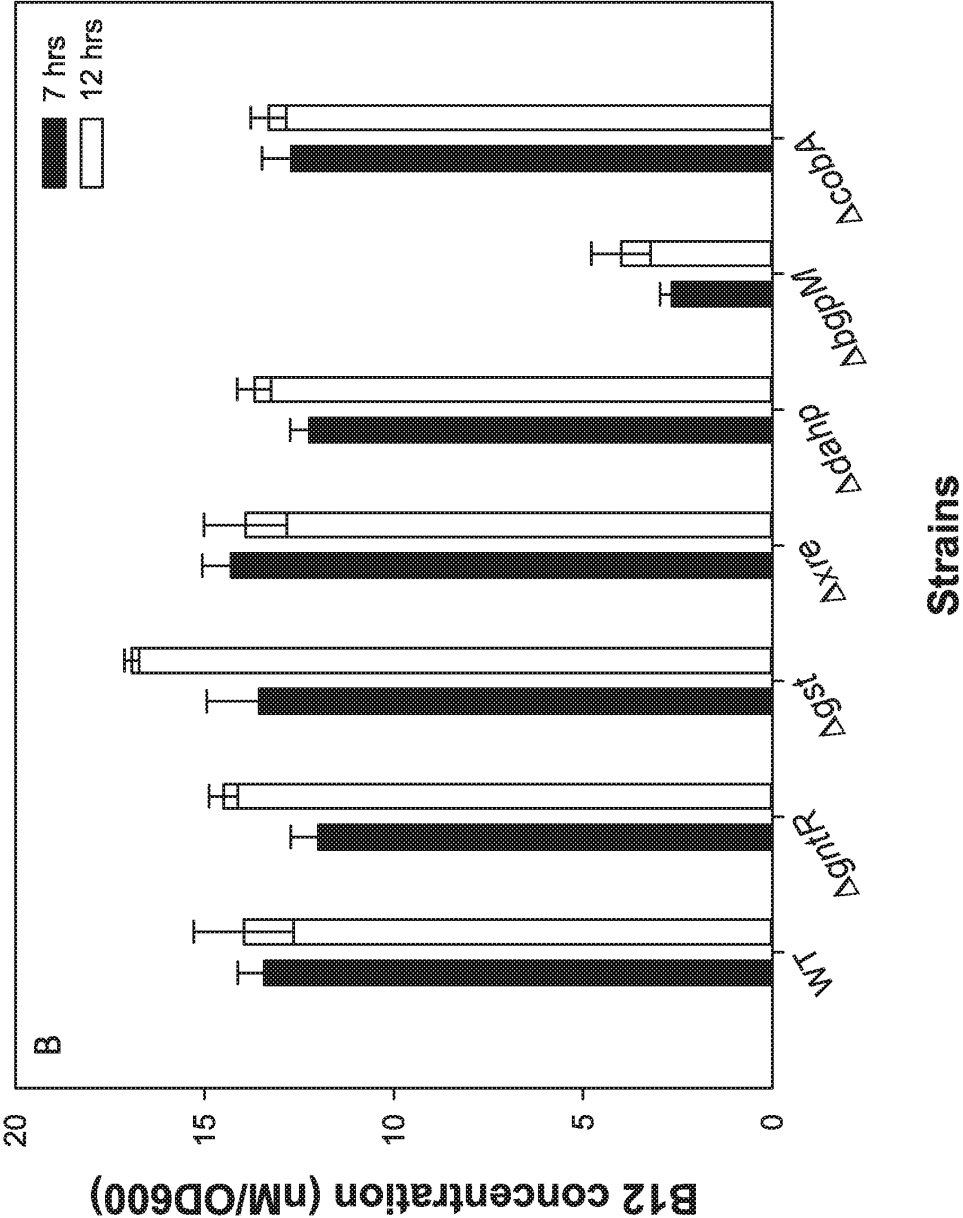


FIG. 29B

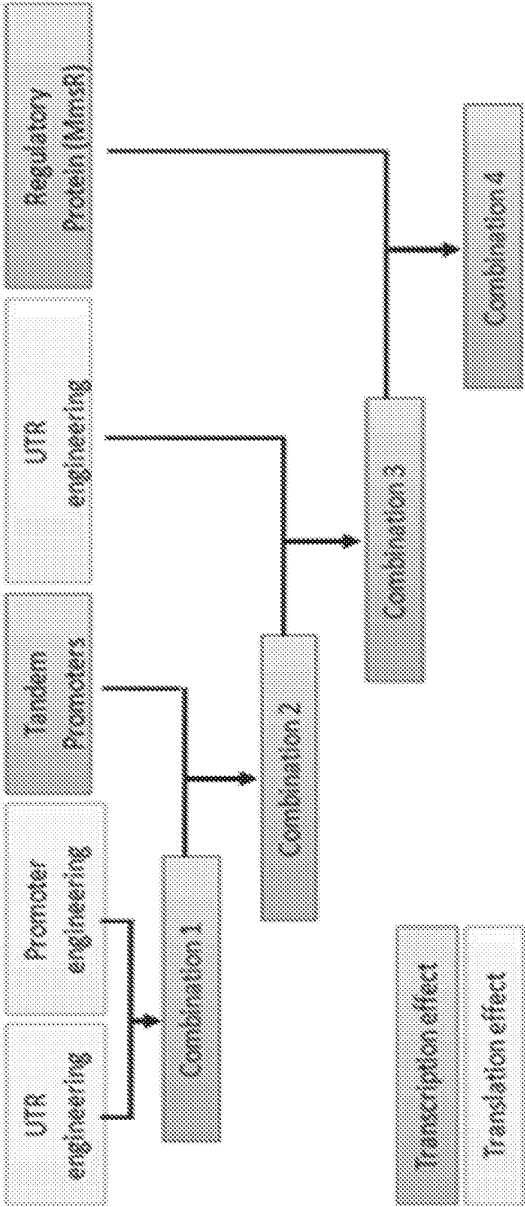


FIG. 30A

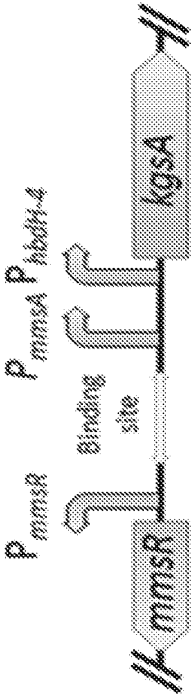


FIG. 30B

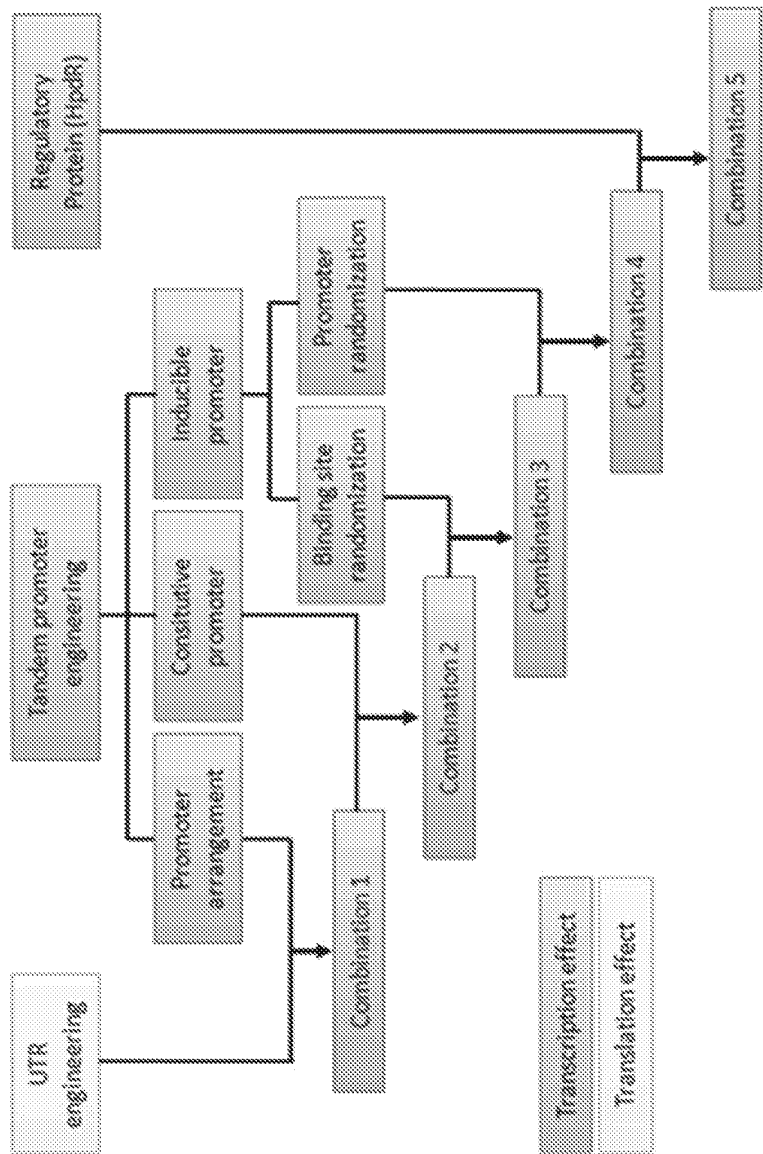


FIG. 31A

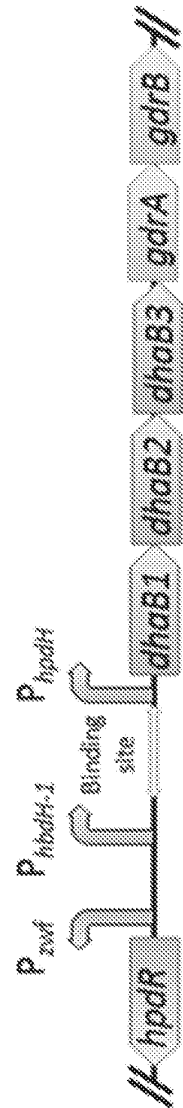


FIG. 31B

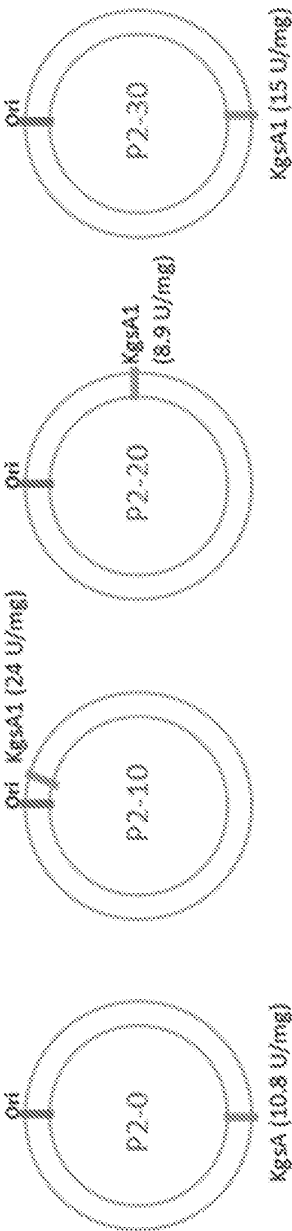


FIG. 32

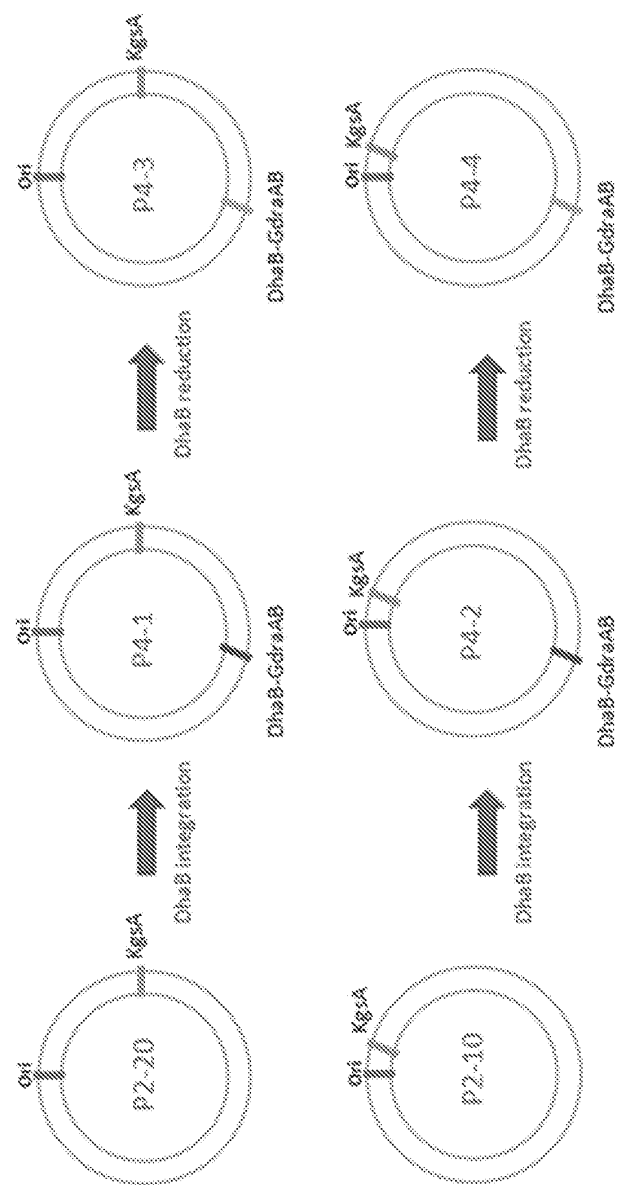


FIG. 33

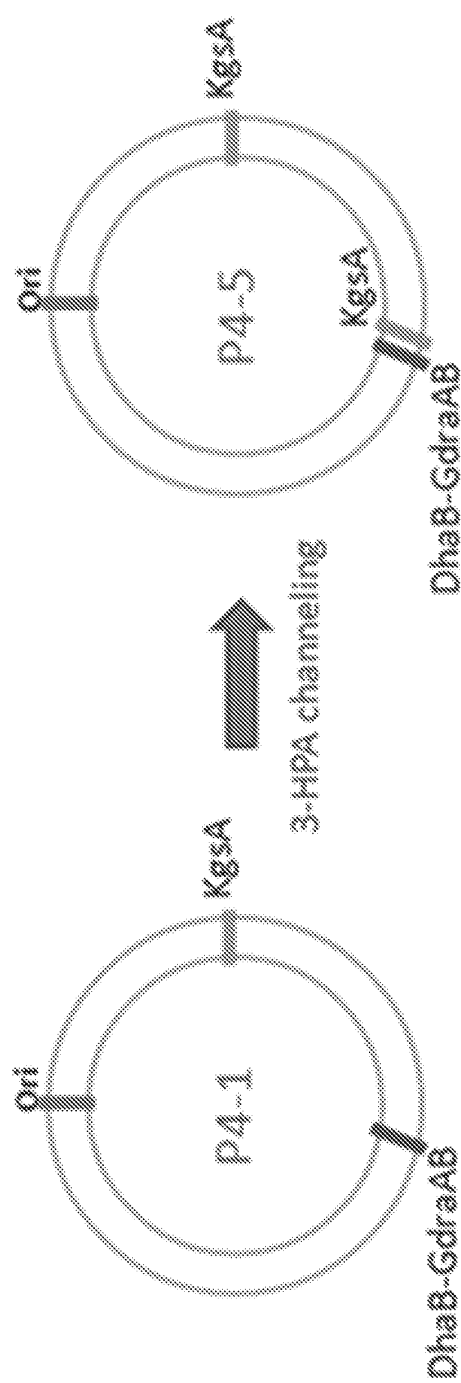


FIG. 34

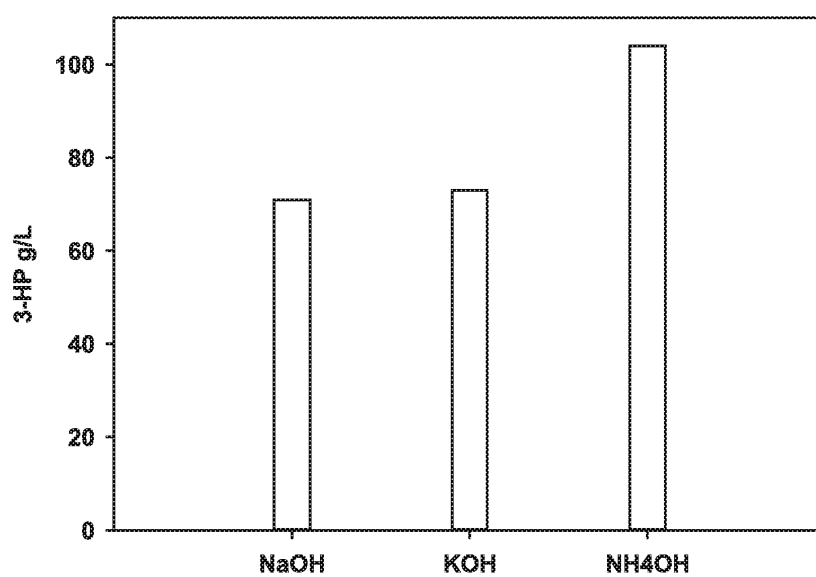


FIG. 35

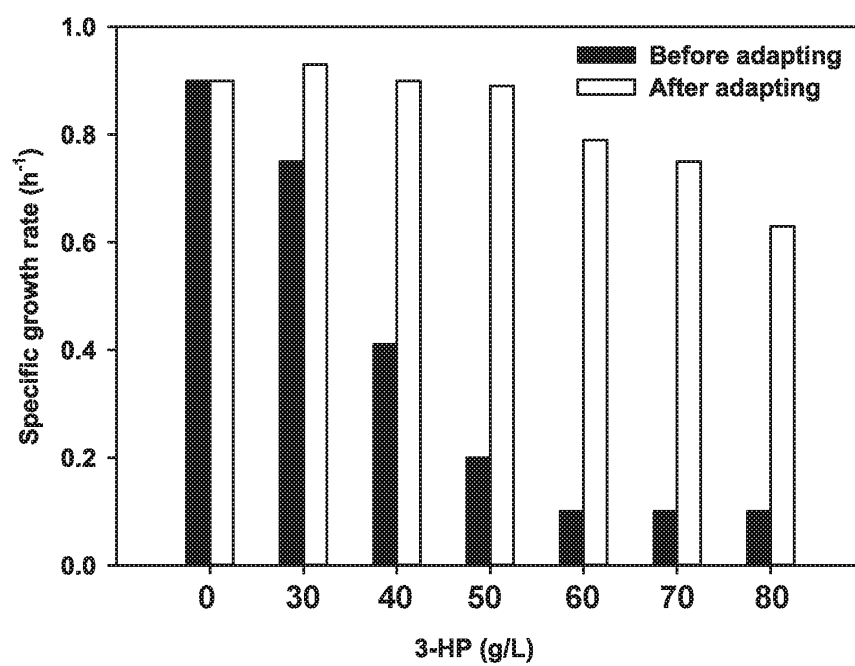
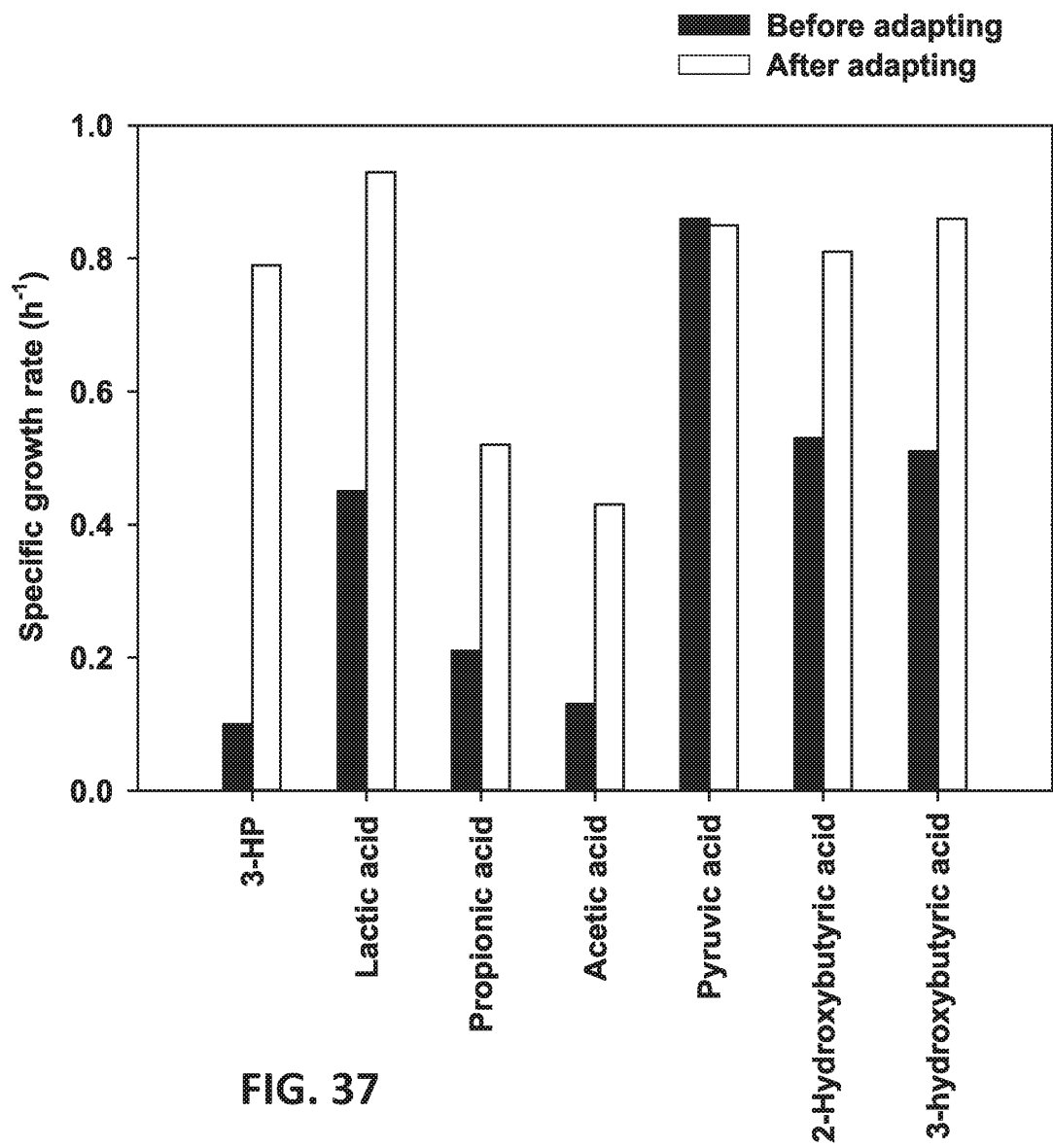


FIG. 36



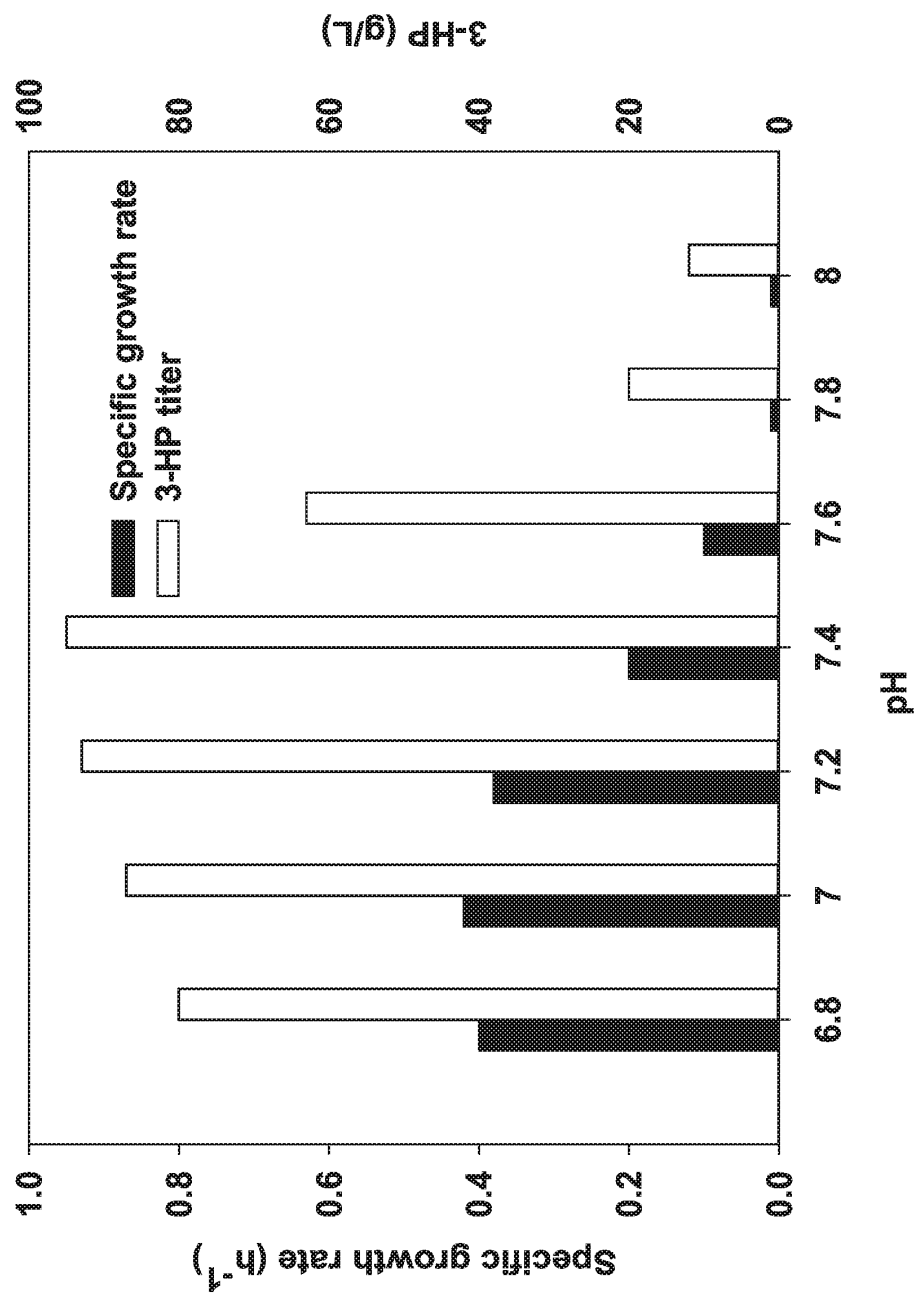


FIG. 38

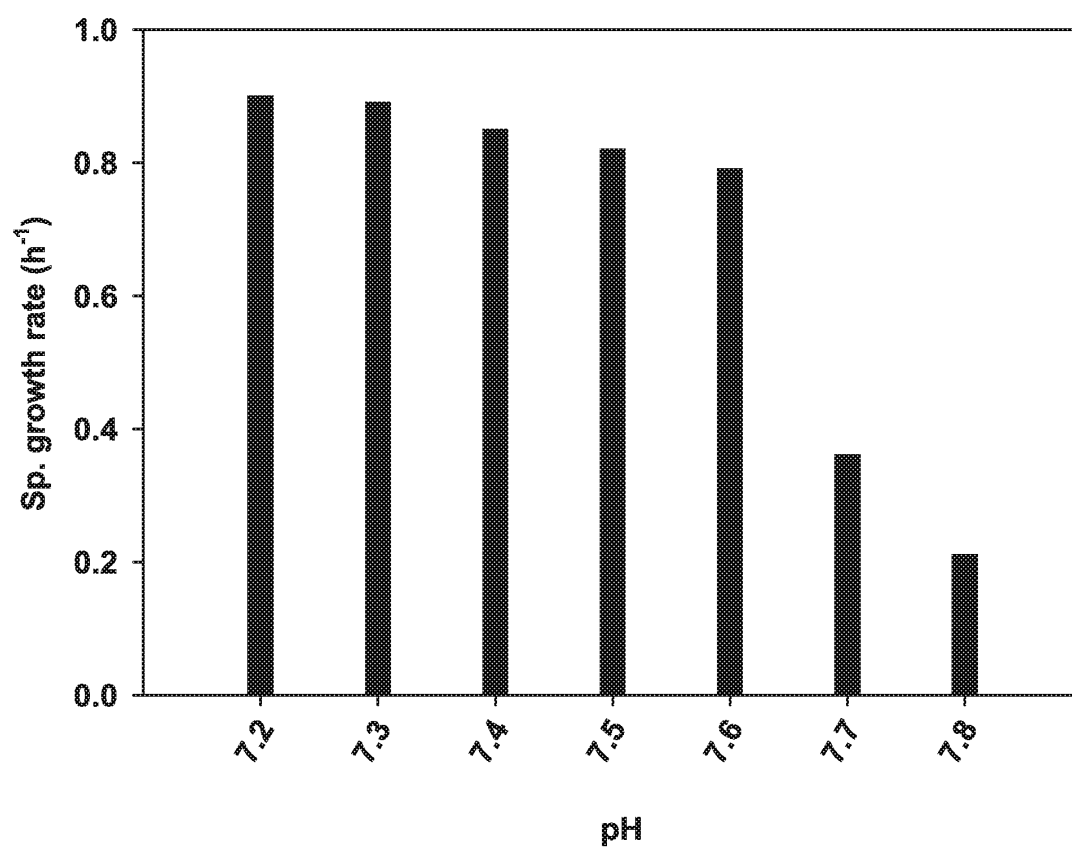


FIG. 39

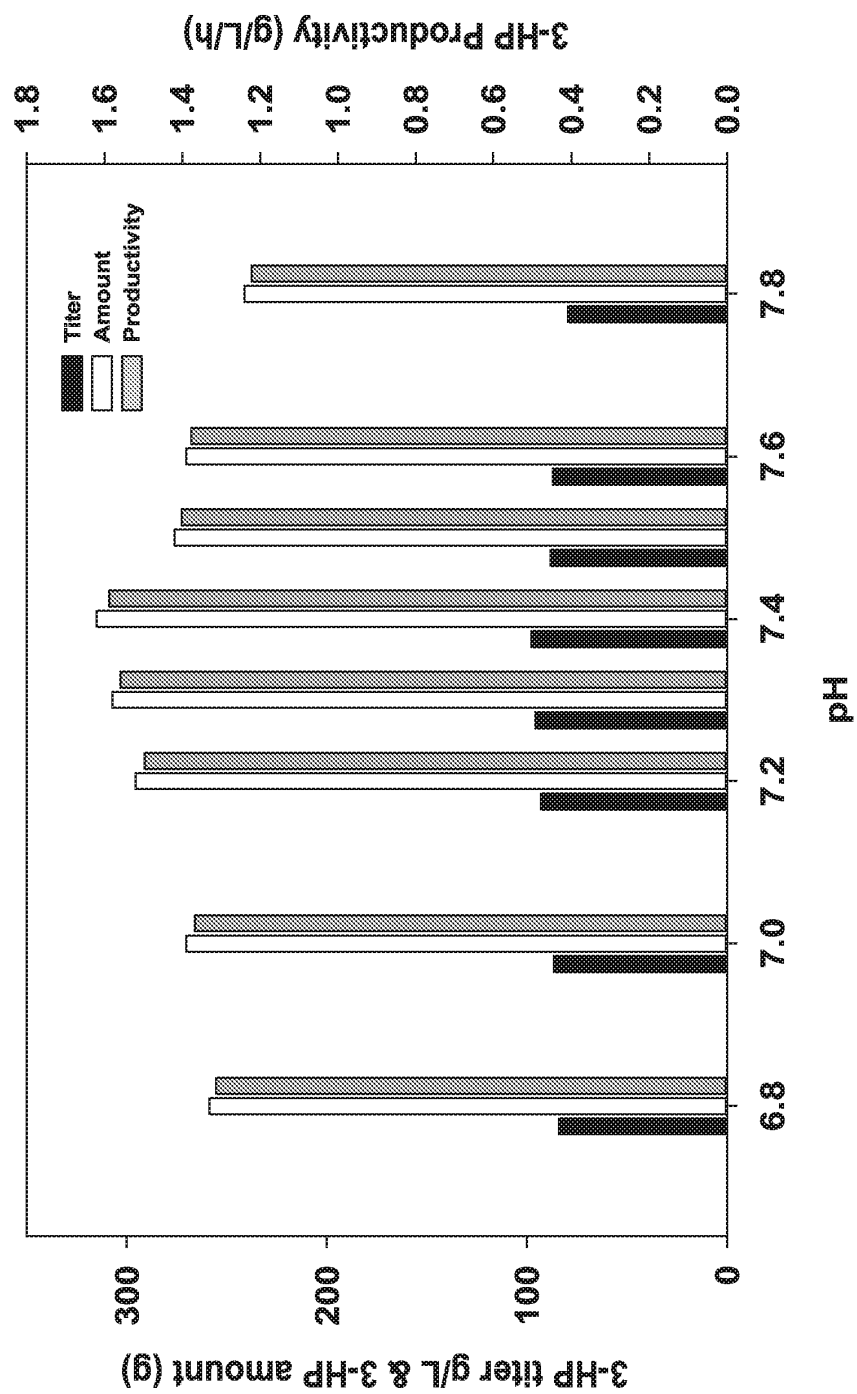


FIG. 40

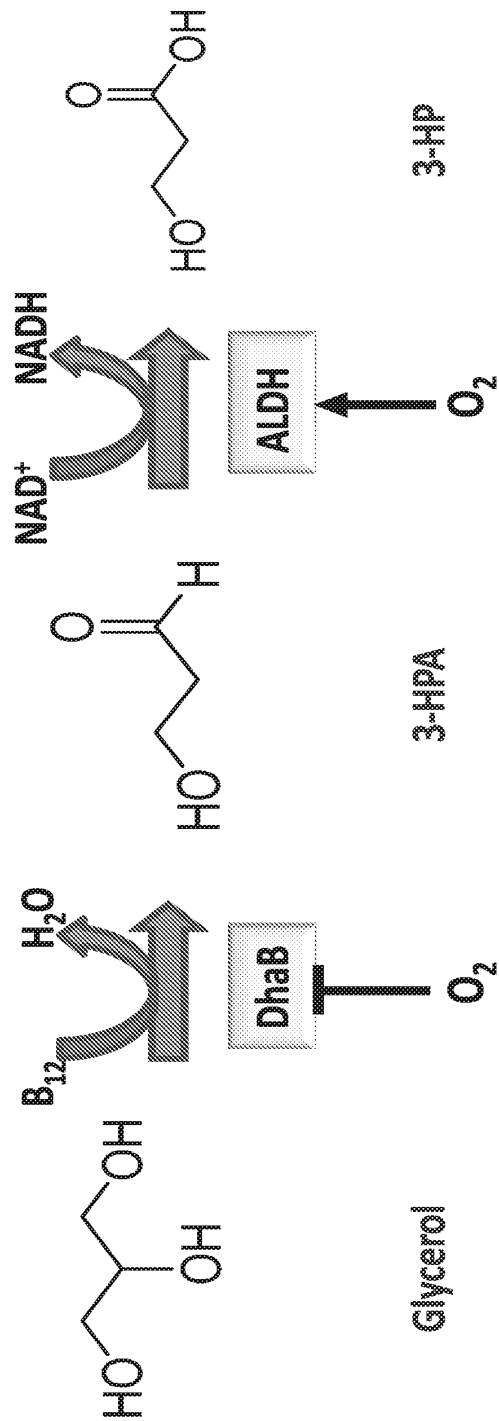
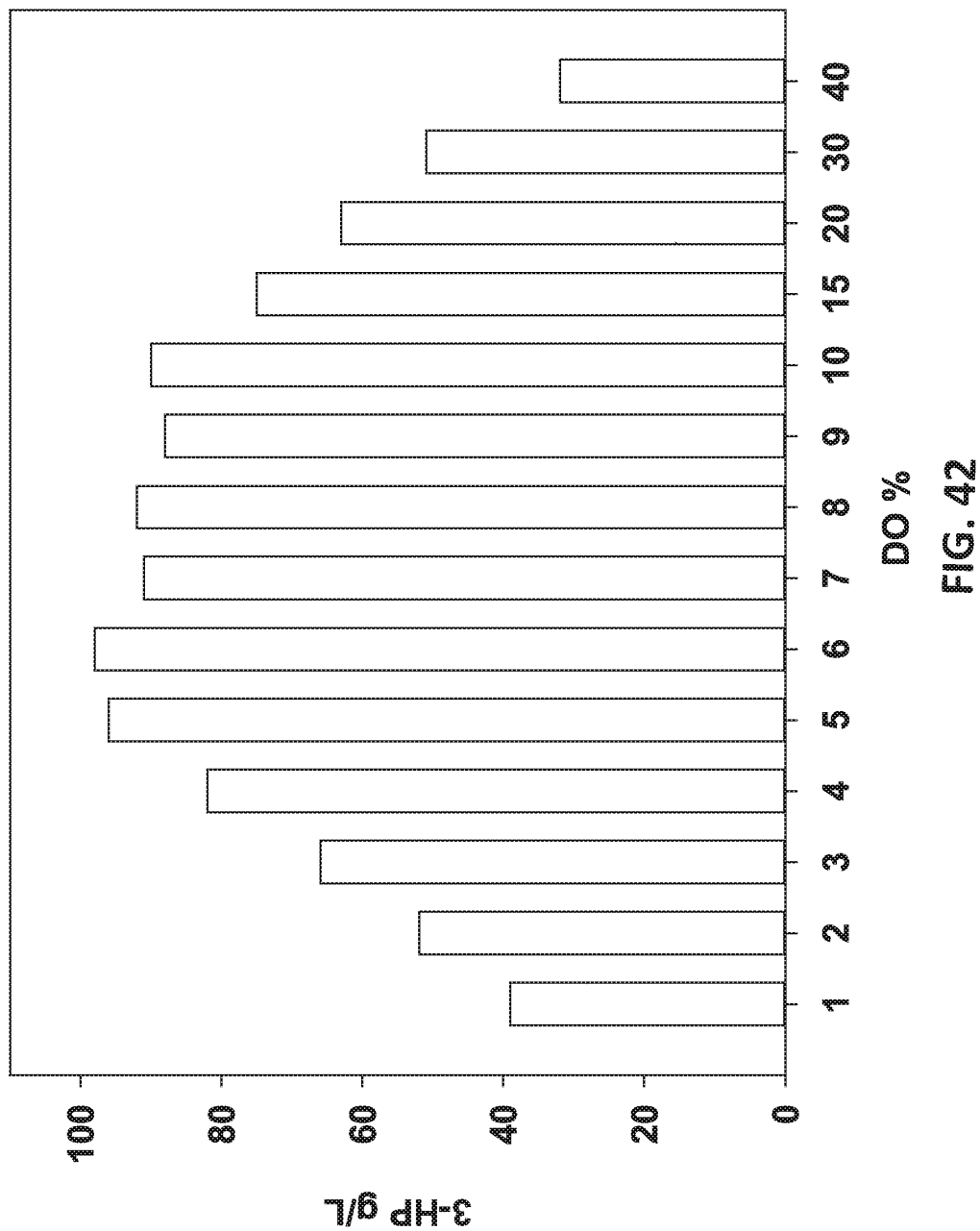


FIG. 41



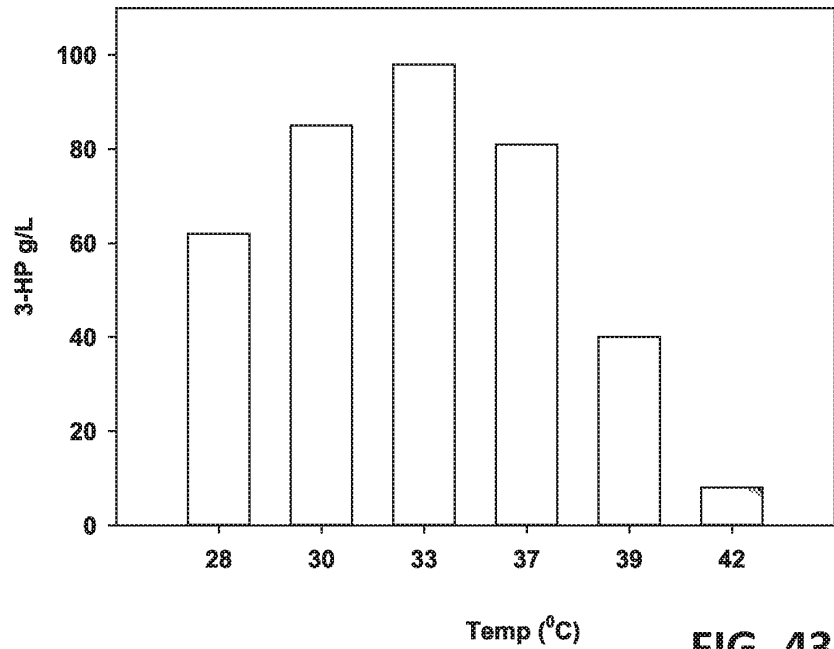


FIG. 43

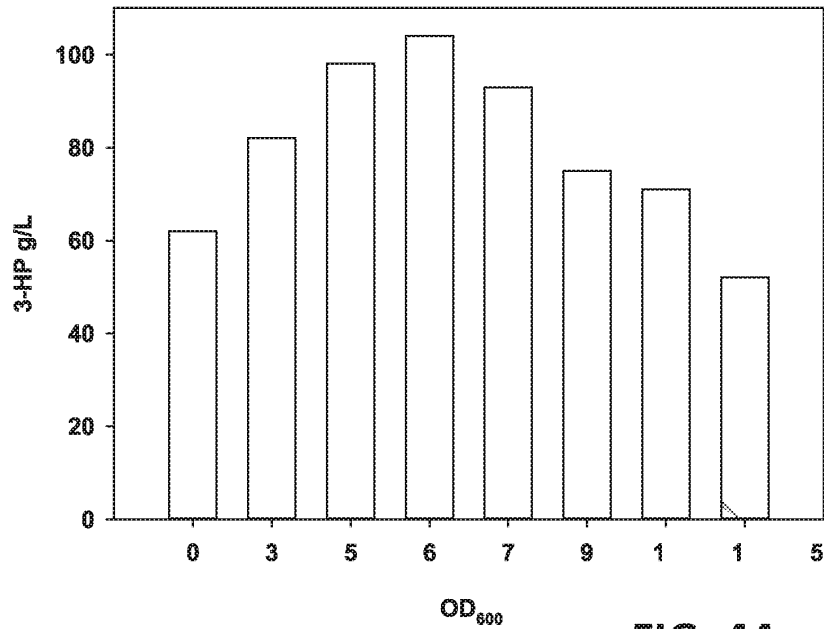


FIG. 44

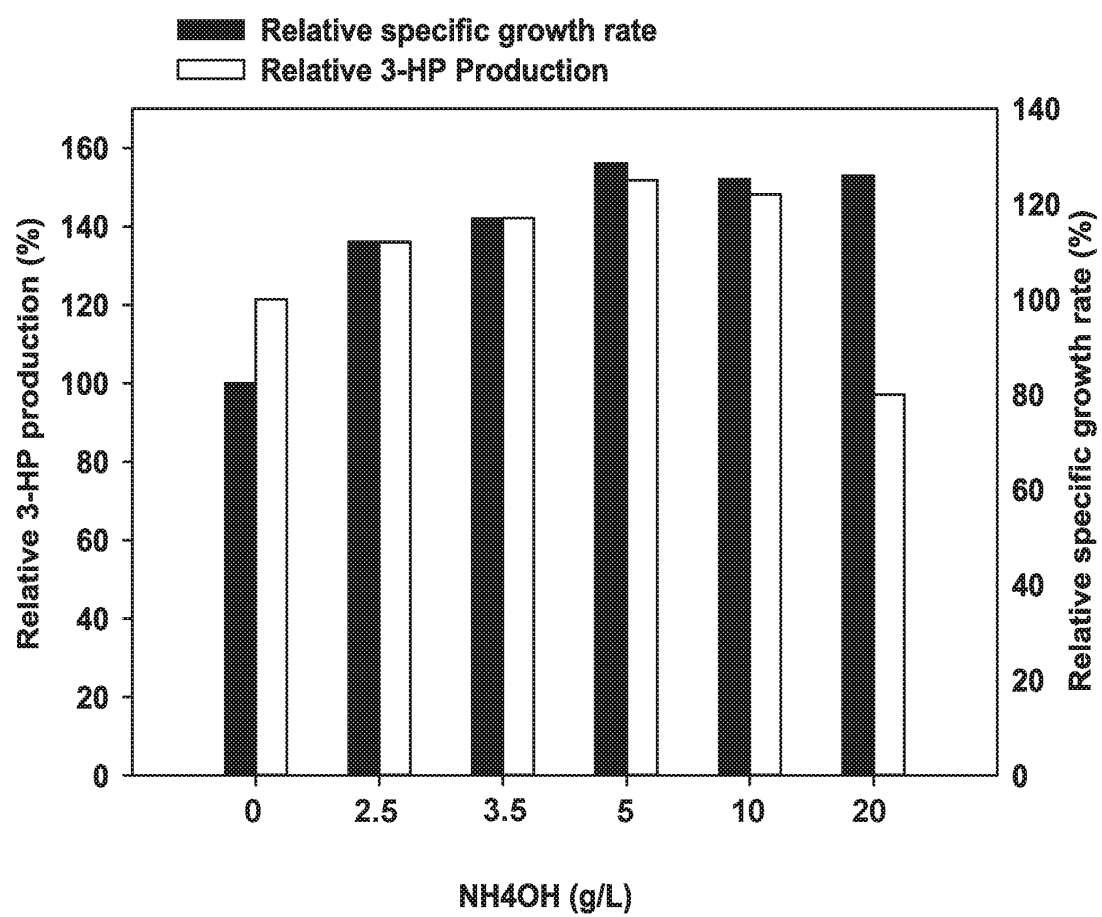


FIG. 45

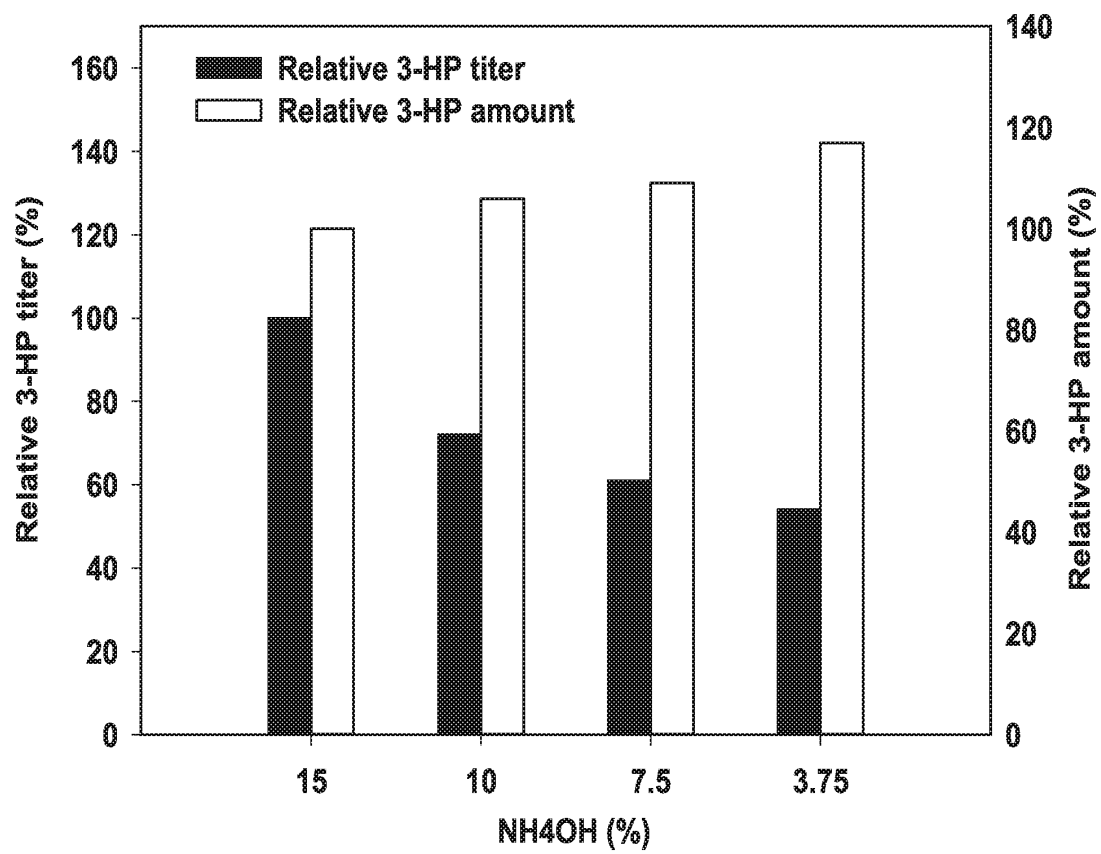


FIG. 46

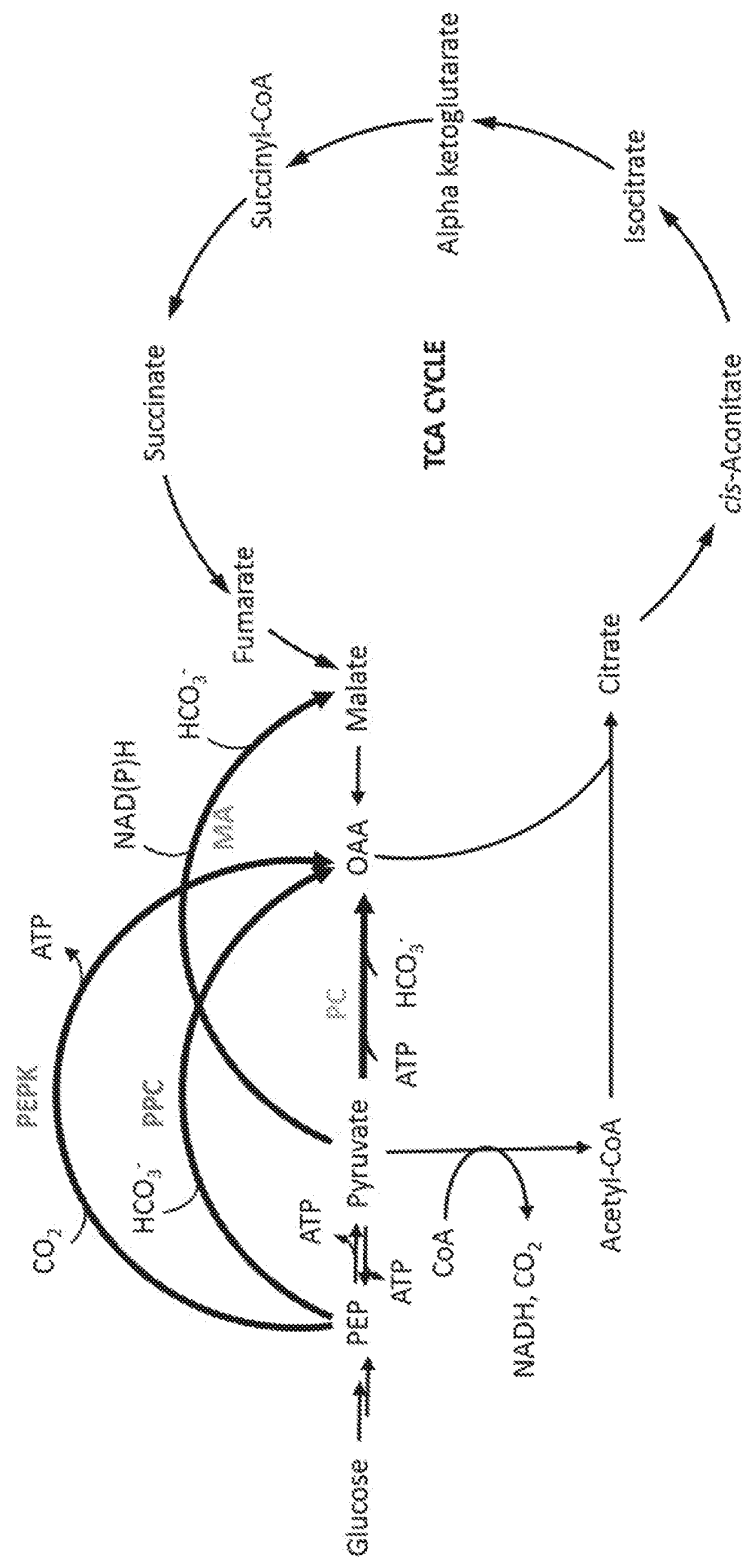


FIG. 47

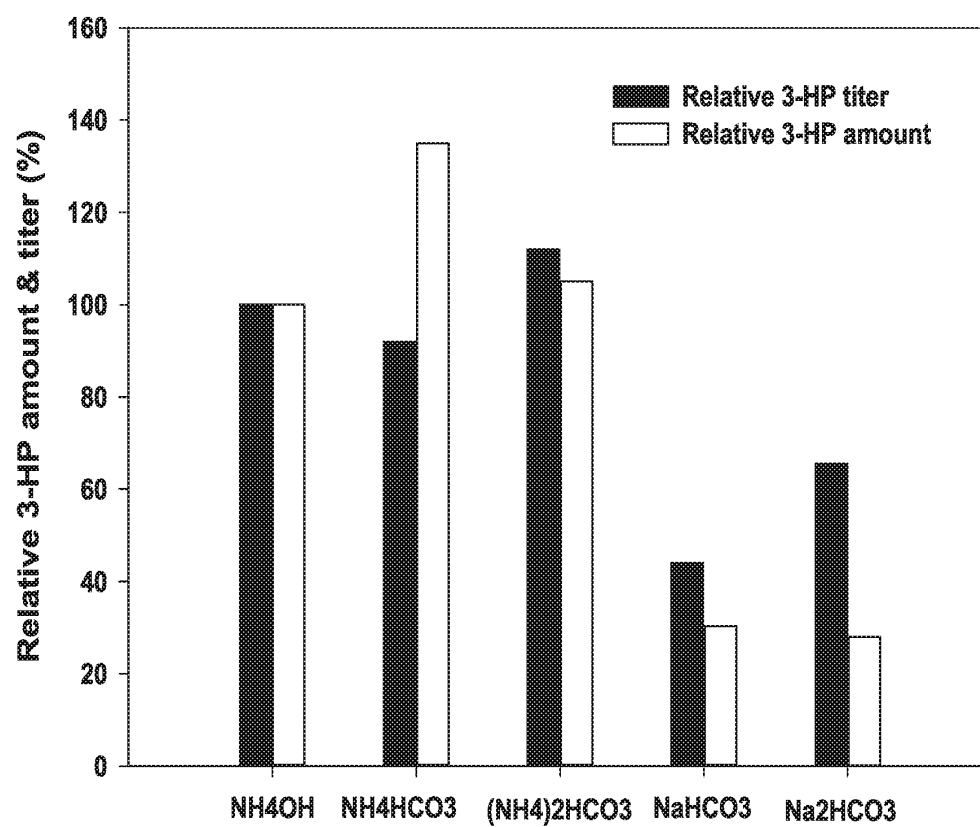


FIG. 48

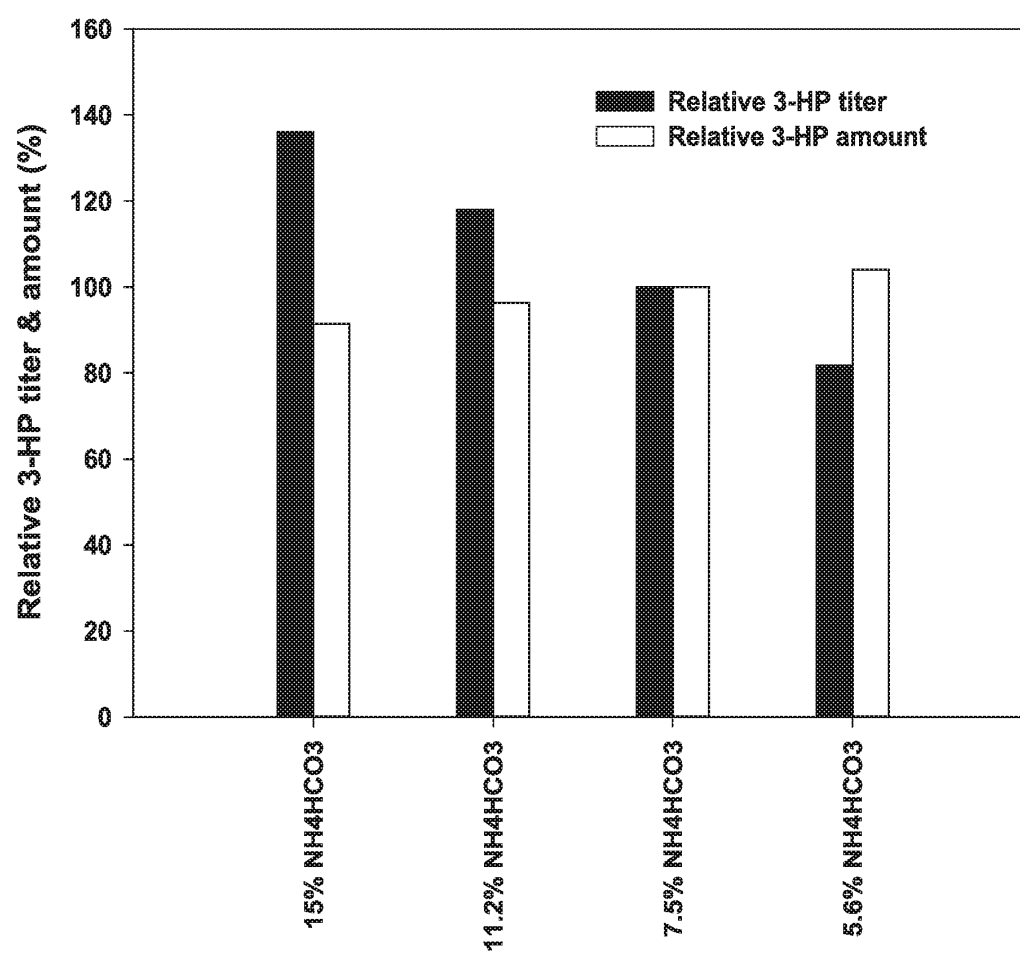


FIG. 49

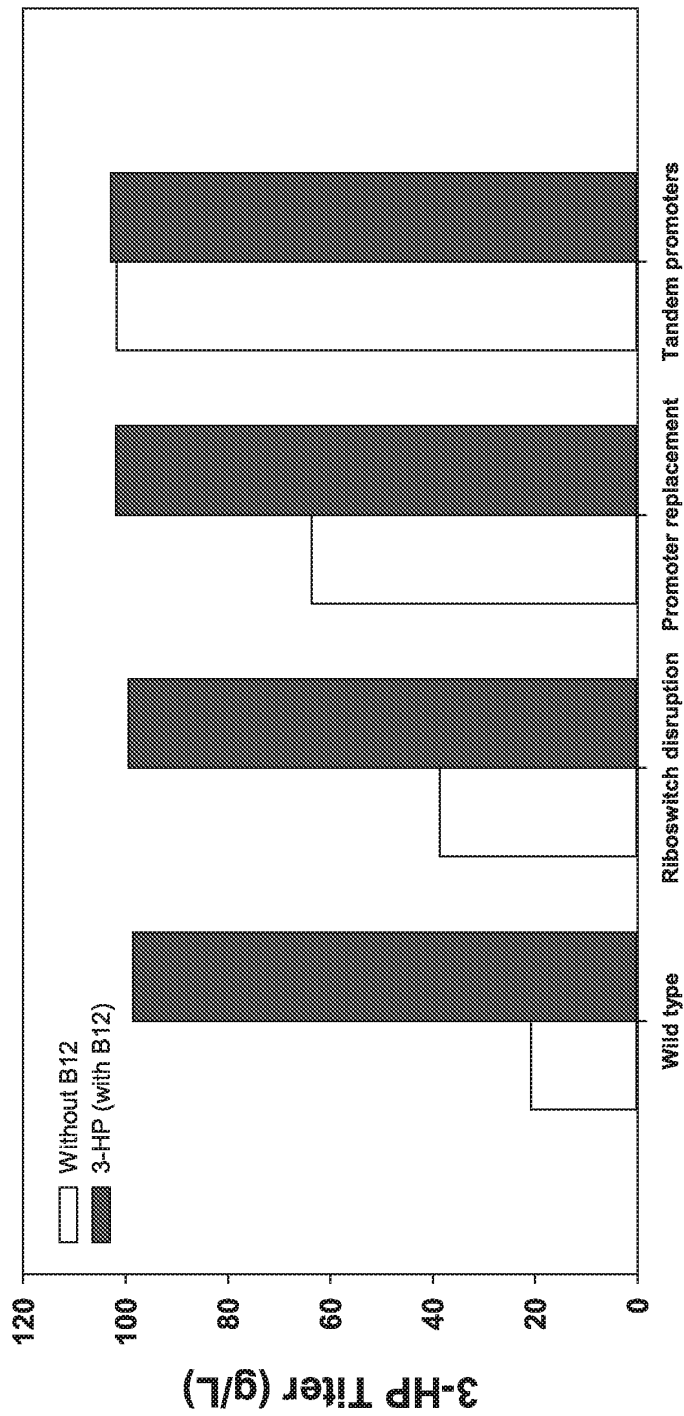


FIG. 50

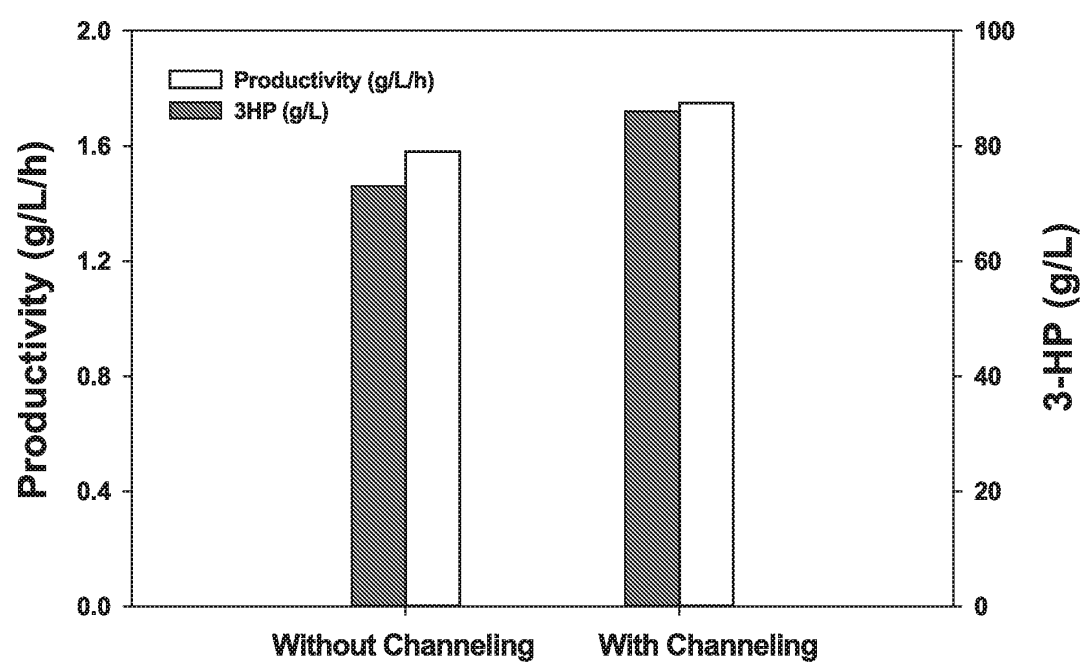


FIG. 51

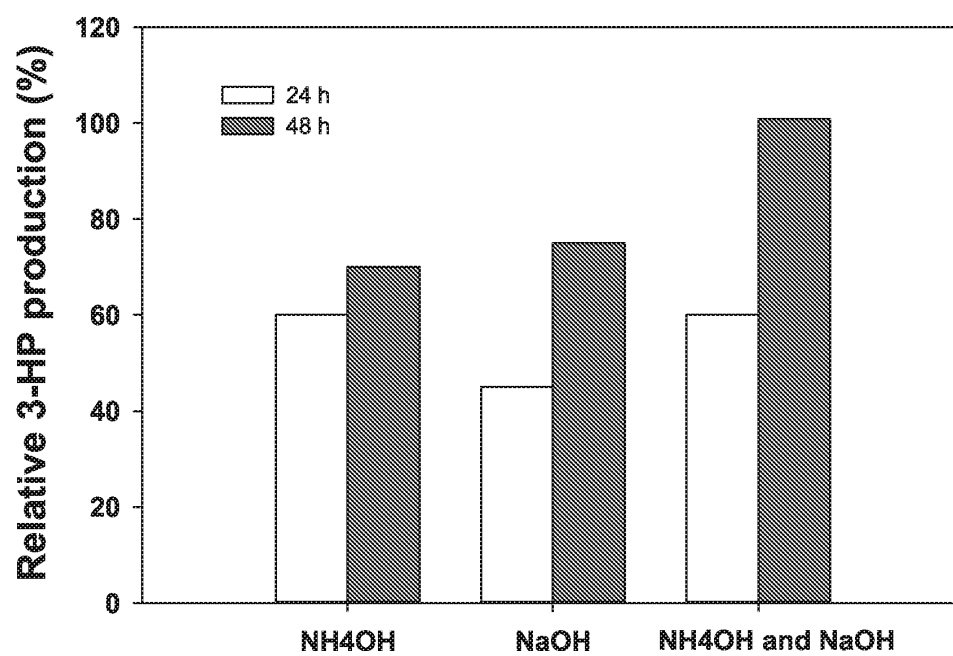


FIG. 52

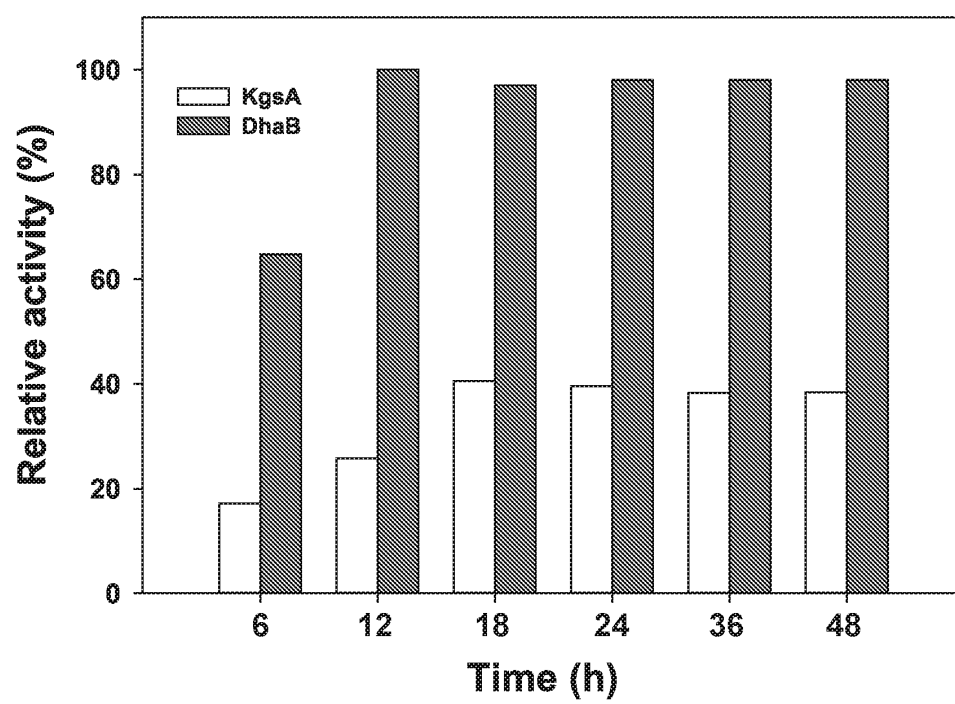


FIG. 53

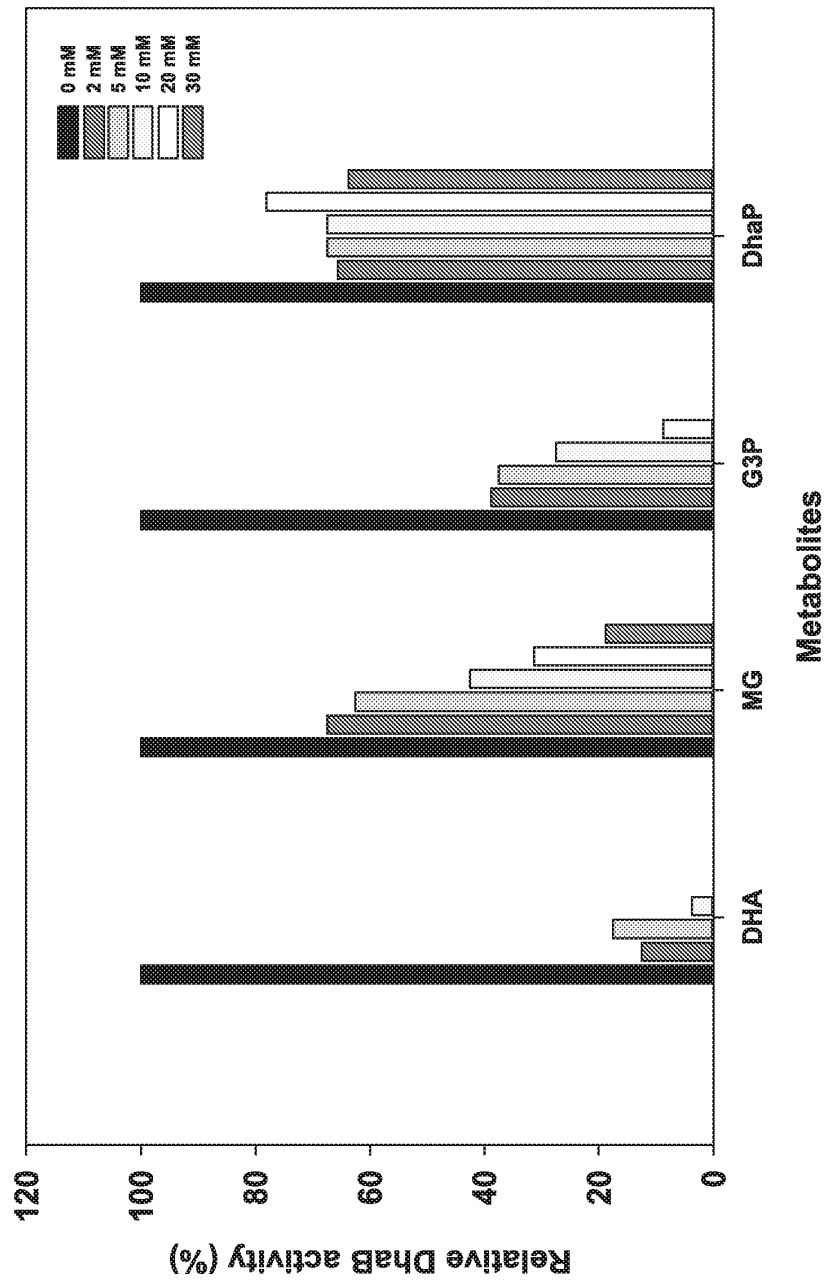


FIG. 54

FIG. 55A

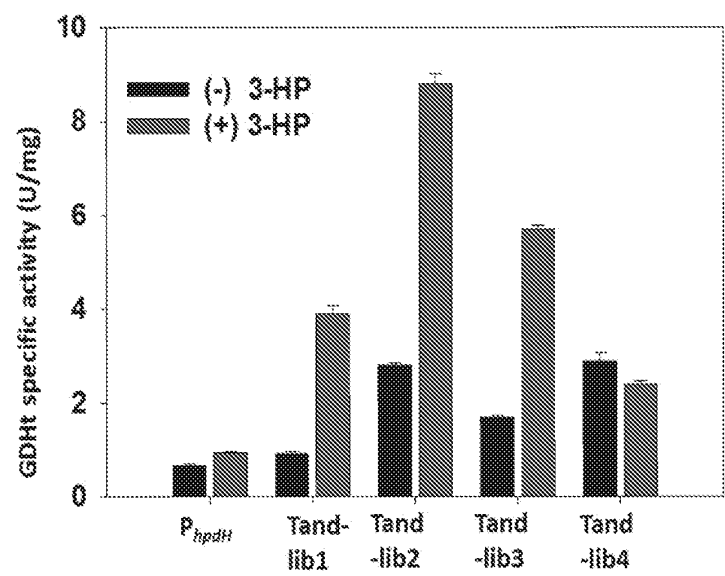
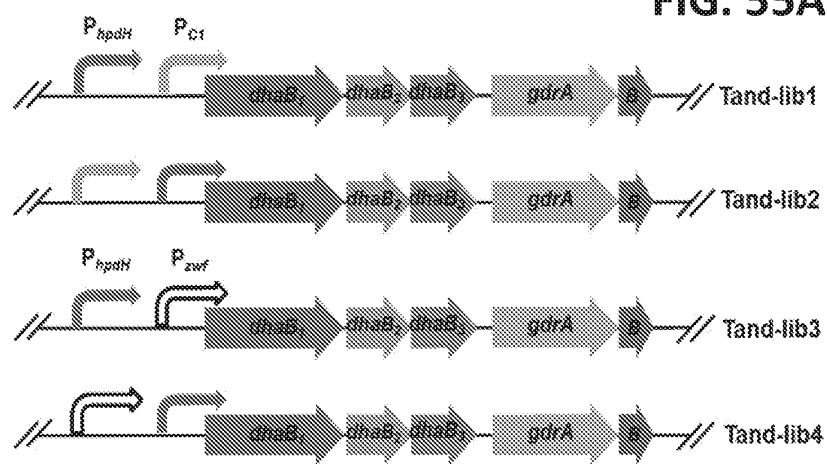


FIG. 55B

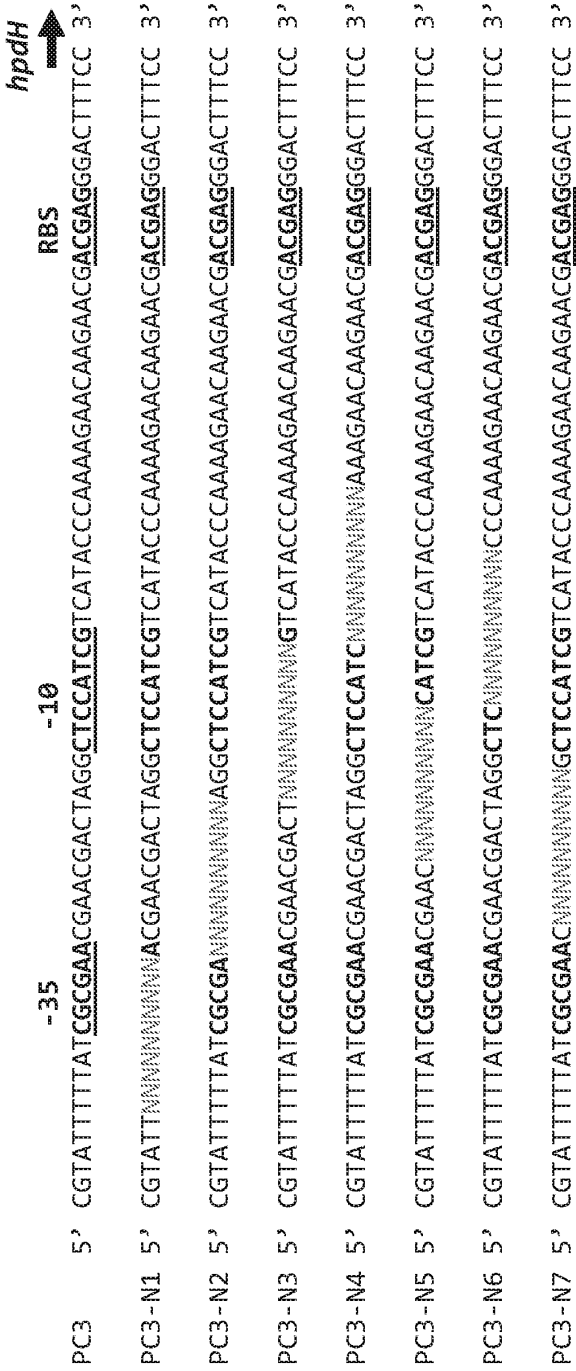


FIG. 56

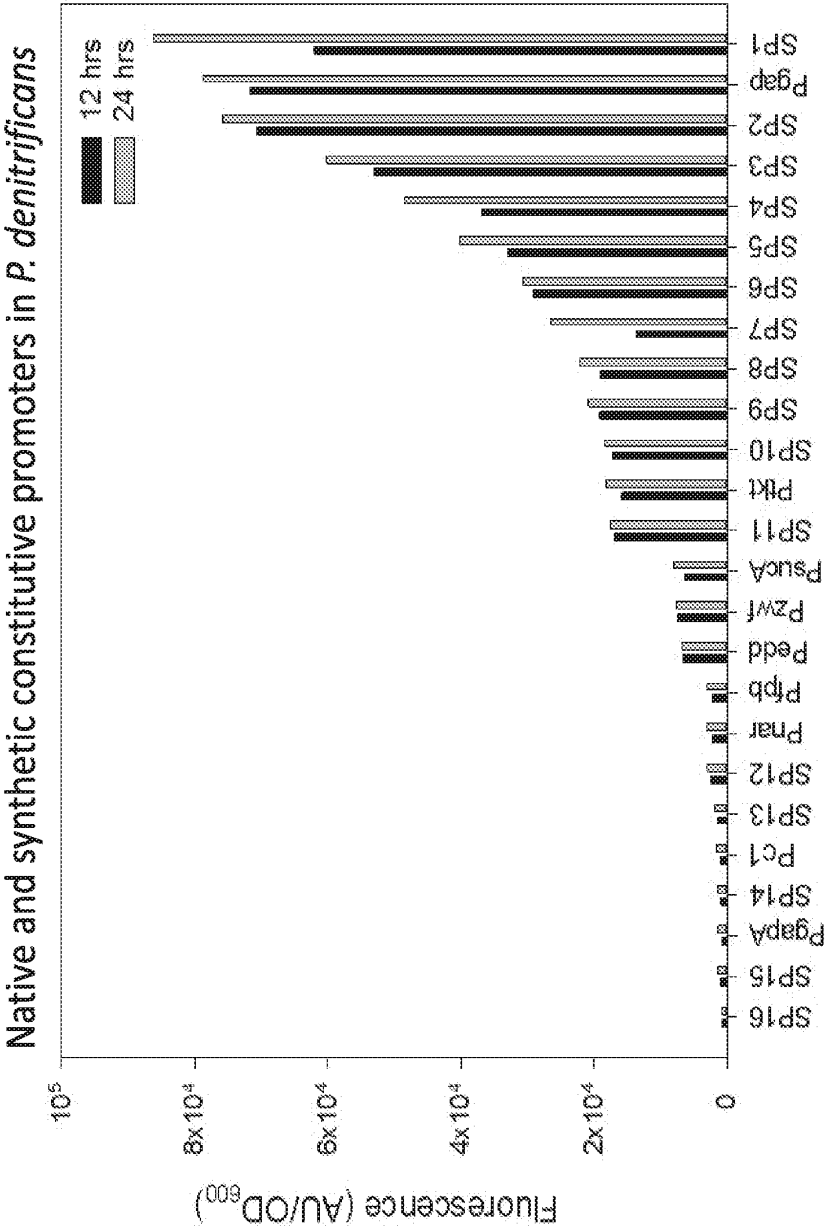
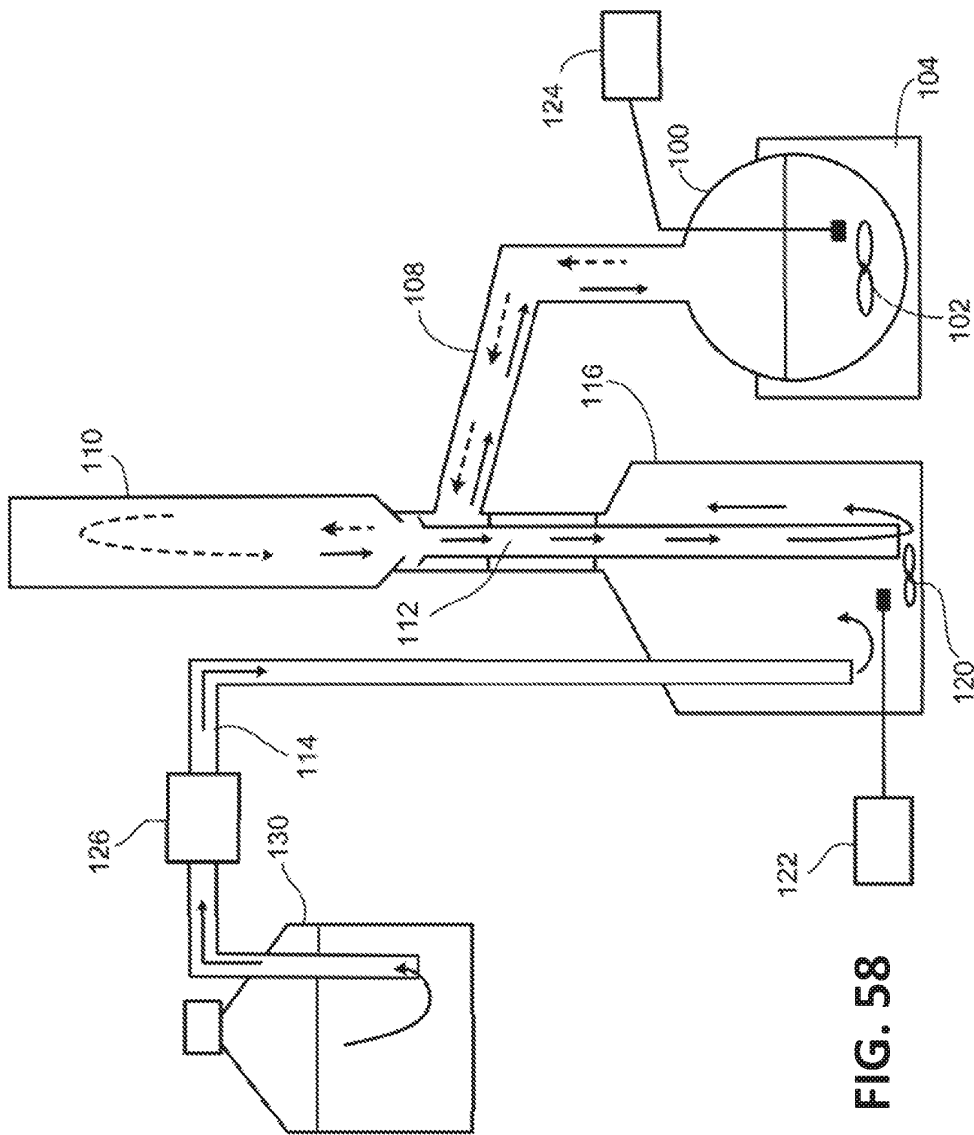
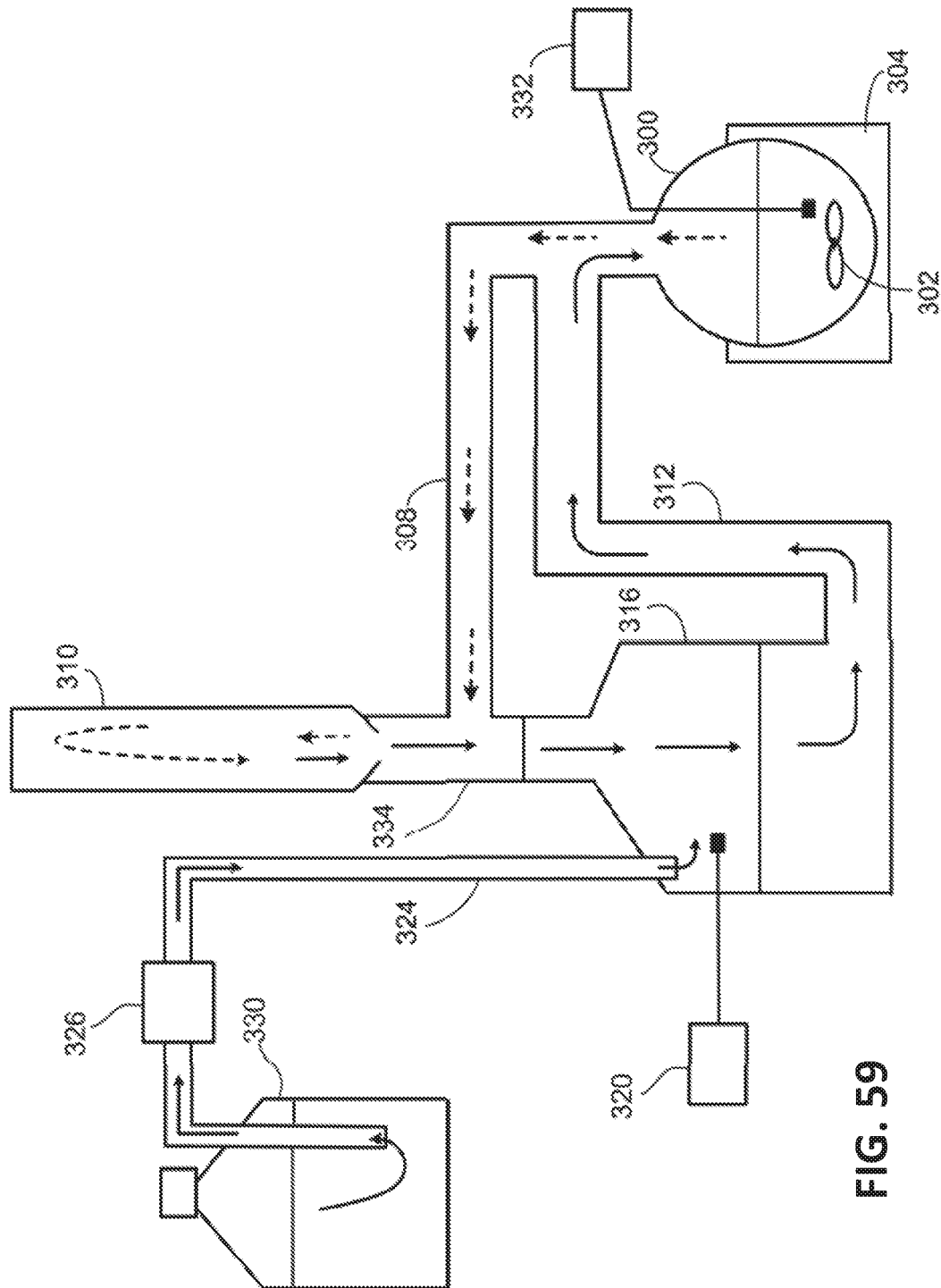
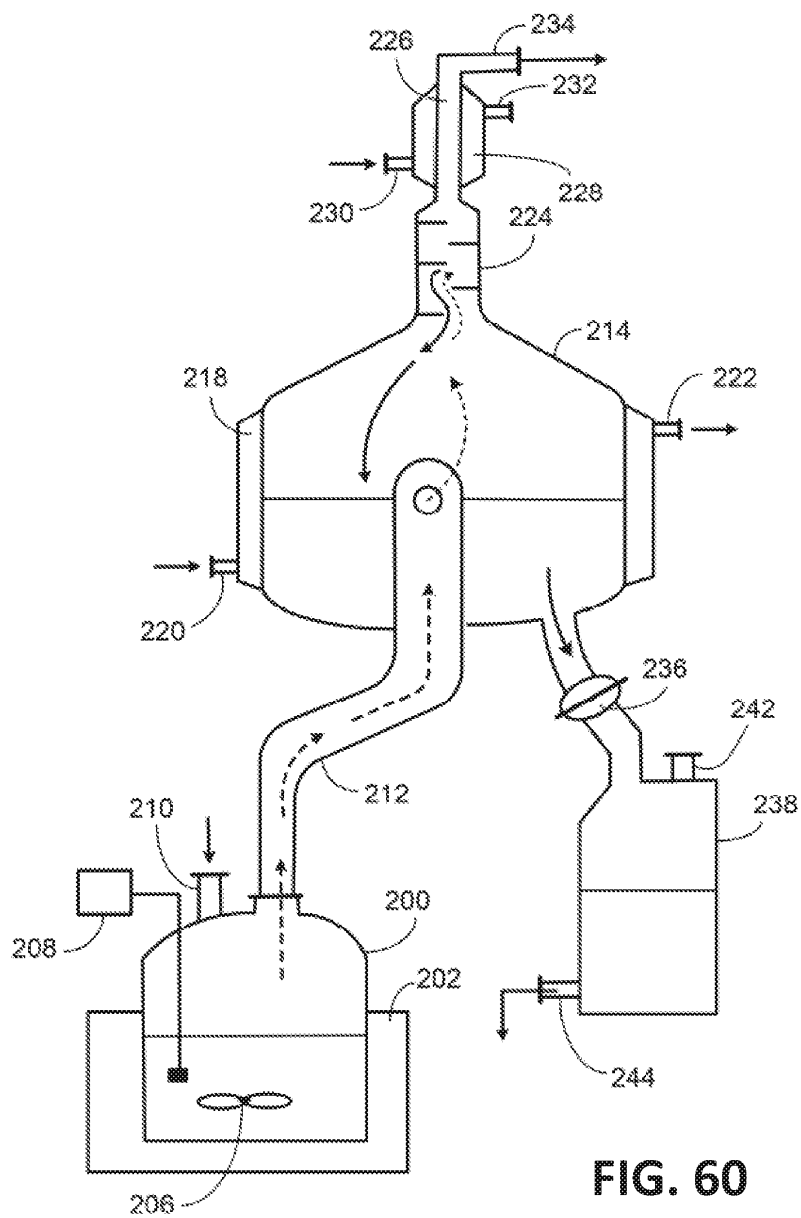


FIG. 57





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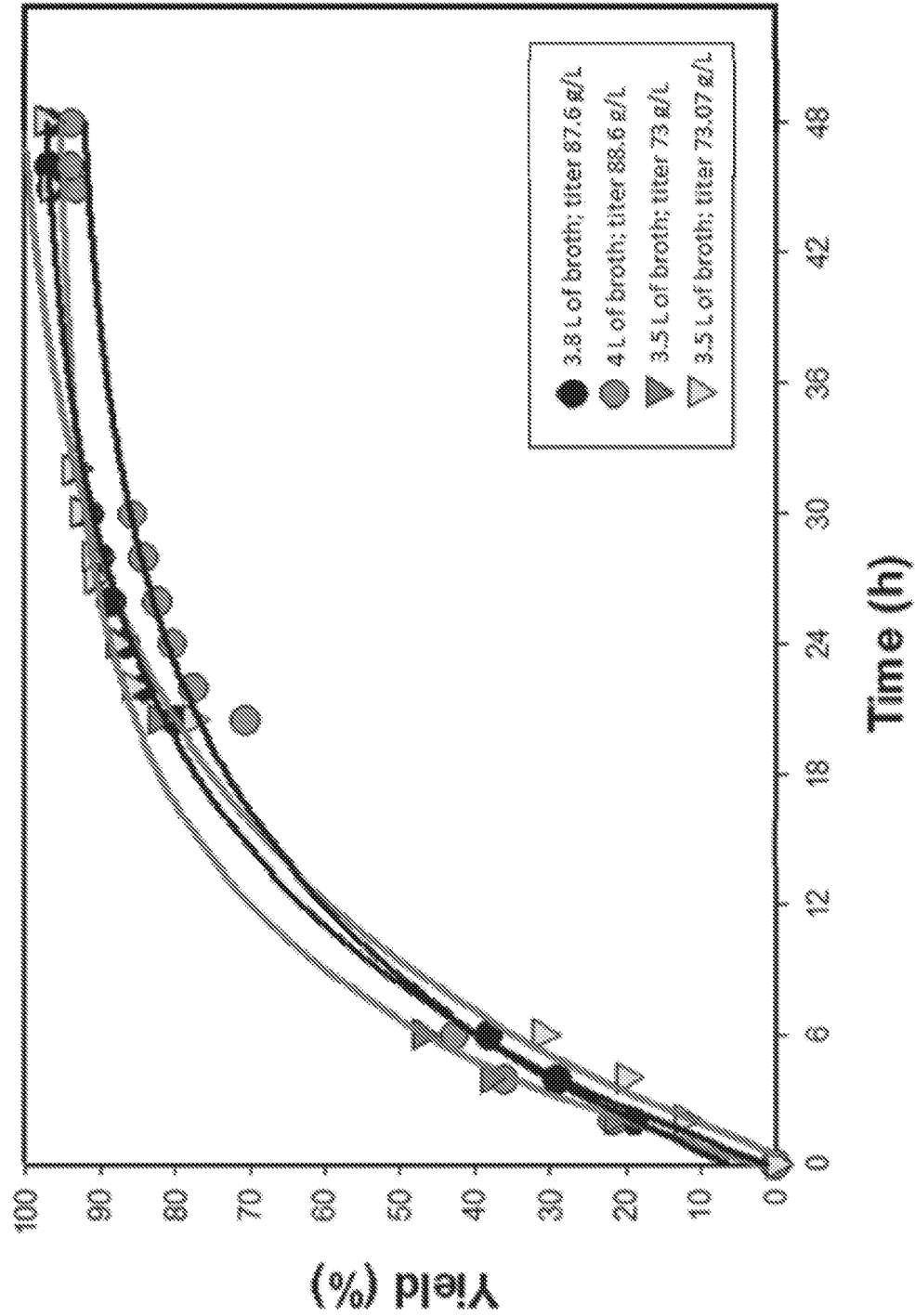


FIG. 61