FIGURE 1

Table 1. Efflux-mediated resistance to non-fluoroquinolone antimicrobials

Antimicrobial	Efflux system	Pump family	Gene location	Organism(s)	Reference[a]
Chloramphenicol & florfenicol Chloramphenicol	Cml, CmlA, CmlB	MF	mostly plasmid; some chromosome	P. aeruginosa, E. aerogenes, K. pneumonia, S. enterica serovar Typhimurium	48
	Cml, Cmlv, Cmr, Cmx, CmrA	?	plasmid & chromosome	Streptomyces spp., Corynebacterium spp., Rhodococcus spp.	48
	MdfA[b]	MF	chromosome	E. coli	74
	MexEF-OprN[c], variety of three-component RND pumps[d]	RND	chromosome	P. aeruginosa, several Gram-negative bacteria	74, 79
	OqxAB	RND	plasmid	E. coli	84
Chloramphenicol, florfenicol	Flo, FloR, pp-Flo	MF	plasmid & chromosome	E. coli, K. pneumoniae, V. cholerae, S. enterica serovar Typhimurium	48
	FexA	?	plasmid	S. lentus	70
Macrolides, lincosamides, streptogramins & ketolides Macrolides	Mef(A)	MF	chromosome	Streptococcus spp., Corynebacterium spp., Enterococcus spp., Micrococcus spp., Staphylococcus spp., Acinetobacter spp., Bacteroides spp., Neisseria spp., several Enterobacteriaceae and Pseudomonadaceae commensals	146, 176
Macrolides, type B streptogramins	Msr(A)	ABC	plasmid	Staphylococcus spp.	173, 175
	Msr(C)	ABC	chromosome	E. faecium	146, 180
Macrolides, ketolides	Msr(D)	ABC	chromosome	S. pneumoniae	149
Macrolides, lincosamides, type A streptogramins	MdeA	MF	chromosome	S. aureus, S. hemolyticus, B. cereus, B. subtilis	192
Type A streptogramins	Vga(A/B)	ABC	plasmid	S. aureus	173
Lincosamides, streptogramins	Lsa	ABC	chromosome	E. faecalis	173, 186
Clindamycin	Lsa(B)	ABC	plasmid	S. sciuri	187
Lincosamides	LmrB	MF	chromosome?	B. subtilis	189, 190
Lincosamides	LmrB	MF	chromosome	C. glutamicum	191
Erythromycin	Cme	MF	chromosome	C. difficile	172
Macrolides, lincosamides, type B streptogramins	?[e]	?	[f]	S. pyogenes	188
Macrolides	MacAB-TolC	ABC	chromosome	E. coli	521
Macrolides	MtrCDE	RND	chromosome	N. gonorrhoeae	168, 197, 198
Macrolides, lincosamides, ketolides	AcrAB-TolC, Mex[g]; RND pumps in several Gram-negative bacteria[h]	RND	chromosome	E. coli, E. aerogenes, P. aeruginosa; other Gram-negative bacteria	74, 195, 196
Erythromycin	MdfA[i]	MF	chromosome	E. coli	74
Erythromycin	?	?	?	Campylobacter spp.	202, 480
Erythromycin, roxythromycin	MexCD-OprJ	RND	plasmid	Pseudomonas spp.	201
Tetracyclines & glycylcyclines Tetracyclines	Tet(A), Tet(B), Tet(C), Tet(D), Tet(E), Tet(G), Tet(H), Tet(J), Tet(Y), Tet(Z), Tet(30), Tet(39)	MF	Plasmid	Gram-negative bacteria	47, 96, 522
	Tet(K), Tet(L)	MF	plasmid	Gram-positive bacteria	47, 522
	Tet38	MF	chromosome	S. aureus	94
	Tet(V)	MF	chromosome	M. tuberculosis, M. fortuitum	95
	Rv1258/Tap	MF	chromosome	M. tuberculosis, M. fortuitum	129, 130

Table 1. (continued)

	P55/Rv1410	MF	chromosome	M. tuberculosis, M. bovis	131
	MdfA[m]	MF	chromosome	E. coli	74
	MexAB-OprM[f], several three-component pumps of the RND family				74
Glycylcyclines	AcrAB-TolC, MexXY-OprM, MexAB-OprM, MexCD-OprJ	RND	chromosome	P. mirabilis, E. coli, K. pneumoniae, M. morganii P. aeruginosa	460–464a
	MepA	MATE	chromosome	S. aureus	464a
β-Lactams					
	AcrAB-TolC[j]	RND	chromosome	H. influenzae	331
	MexAB-OprM[k]; several three-component pumps of RND family[l]	RND	chromosome	P. aeruginosa; several Gram-negative bacteria	74, 250
	LmrA[m]	ABC	chromosome	L. lactis	85
Aminoglycosides					
	AcrAD-TolC	RND	chromosome	E. coli	74, 523
	BpeAB-OprB	RND	chromosome	B. pseudomallei	292
	AmrAB-OprA	RND	chromosome	B. pseudomallei	524
	MexXY-OprM	RND	chromosome	P. aeruginosa	74, 306, 307
	MexAB-OprM[n]	RND	chromosome	P. aeruginosa	74
	EmrE[n]	RND	chromosome	P. aeruginosa	74
	MdfA[m]	MF	chromosome	E. coli	74
	LmrA[m]	ABC	chromosome	L. lactis	85
Oxazolidinones					
	AcrAB-TolC, AcrEF-TolC	RND	chromosome	E. coli	196

[a]Where efflux systems have been described in earlier review articles, these are highlighted here, otherwise original articles are cited.
[b]This multidrug efflux system was originally identified as the Cmr/CmlA chloramphenicol exporter.
[c]Mutant strains of P. aeruginosa overexpressing MexEF-OprN are readily selected in vitro using chloramphenicol.78–80
[d]Where tested, RND-type efflux systems that promote resistance to chloramphenicol also promote florfenicol resistance (e.g. AcrAB-TolC75 and AcrEF-TolC86 in S. enterica serovar Typhimurium).
[e]Efflux has been demonstrated although an efflux system has not been identified.
[f]The efflux gene(s) has not been identified though its mobility has been confirmed.
[g]Mutant strains of P. aeruginosa overexpressing MexCD-OprJ can be selected in vitro using erythromycin (Poole, unpublished results).
[h]Export of macrolides, lincosamides and streptogramins by three-component RND type multidrug efflux systems may explain the insusceptibility of many Gram-negative bacteria to these agents.
[i]Mutant strains of P. aeruginosa overproducing MexAB-OprM can be selected in vitro using tetracycline.78,132,133
[j]Associated with resistance to ampicillin in clinical strains.331
[k]Implicated in resistance to meropenem322 and ticarcillin323,324 in clinical isolates.
[l]While man RNDtype multidrug efflux systems accommodate b-lactams (see text), few are implicated as primary determinants of resistance, in laboratory or clinical isolates.
[m]Cloned gene promotes very modest increases in MICs to the indicated antimicrobial.
[n]Show a modest contribution to intrinsic aminoglycoside resistance but only seen in low ionic strength media.

Table 2. Efflux-mediated resistance to fluoroquinolones[a]

Efflux system	Pump family	Antimicrobial[b]	Organism(s)	Reference
Gram-positive				
NorA	MF	NOR, CIP	S. aureus	209, 525
NorB	MF	NOR, CIP, MOX, SPR	S. aureus	94
?[c]	?	NOR, CIP, MOX, GAT, SPR	S. aureus	212
PmrA	MF	NOR, CIP	S. pneumoniae	209, 526
?[d]	?	NOR, CIP, MOX	S. pneumoniae	213
EmeA	MF	NOR, CIP	E. faecalis	235, 235a
Lde	MF	NOR, CIP	L. monocytogenes	233
EfrAB	ABC	NOR, CIP	E. faecalis	352
?[e]	?	FQ	B. anthracis	237, 527
Bmr	MF	FQ	B. subtilis	209
Blt	MF	FQ	B. subtilis	209
Bmr3	MF	FQ	B. subtilis	528
MD1, MD2[f]	ABC	CIP	M. hominis	240
LfrA	MF	FQ (CIP, NOR?)	M. smegmatis	242, 529
EfpA	MF	CIP, NOR	M. smegmatis	242
Rv1634	MF	FQ	M. tuberculosis	129
Rv1258c	MF	OFL	M. tuberculosis	245
Rv2686c-Rv2687c-Rv2688c[g]	ABC	FQ	M. tuberculosis	243
LmrA	ABC	CIP, OFL	L. lactis	85
Mmr	SMR	CIP, NOR	M. smegmatis	242
Gram-negative				
AcrAB-TolC, AcrEF-TolC	RND	FQ	E. coli	74
MexAB-OprM, MexCD-OprJ,	RND	FQ	P. aeruginosa	74, 250
MexEF-OprN, MexXY-OprM[h]				
AcrAB-TolC	RND	FQ	Enterobacter spp.	74, 258, 530
AcrAB-TolC	RND	FQ	Klebsiella spp.	74, 76, 263, 531
AcrAB-TolC	RND	FQ	S. enterica (Typhimurium, Enteritidis)	75, 270–272, 532
AcrEF-TolC	RND	FQ	S. enterica serovar Typhimurium	86
SmeABC, SmeDEF	RND	FQ	S. maltophilia	74, 277, 289, 533, 534
CmeABC, CmeDEF	RND	FQ	C. jejuni	74, 256, 257, 535
SdeAB	RND	FQ	S. marcescens	194, 276, 535a
SdeXY	RND	NOR	S. marcescens	74
MtrCDE	RND	FQ	N. gonorrhoeae	210, 280
CeoAB-OpcM	RND	FQ	B. cepacia (cenocepacia)	82
AcrAB	RND	CIP	P. mirabilis	74
AdeABC	RND	FQ	A. baumannii	74
VcaM	ABC	CIP, NOR	V. cholerae	290
Orf12-Orf11-Orf10 (plasmid)[i]	ABC	NAL, NOR	Pseudomonas spp.	193
MdfA	MF	FQ	E. coli	210, 291
?	?	FQ	A. salmonicida	255
?	?	FQ	C. freundii	536, 537
?	?	OFL	P. vulgaris	538
?	?	CIP, NOR	B. fragilis	209, 539

[a]Excluding MATE family multidrug exporters.
[b]NOR, norfloxacin; CIP, ciprofloxacin; MOX, moxifloxacin; GAT, gatifloxacin; SPR, sparfloxacin; OFL, ofloxacin; NAL, nalidixic acid; FQ, fluoroquinolones.
[c]Efflux-mediated resistance observed but the specific determinant has not been identified; not NorA.
[d]Efflux-mediated resistance observed but the specific determinant has not been identified; not PmrA.
[e]Efflux-mediated resistance observed but the specific determinant not identified.
[f]Cytoplasmic membrane-associated ABC type efflux system assembled from 2 subunits.
[g]Cytoplasmic membrane-associated ABC type efflux system assembled from 3 subunits.
[h]Accommodates fluoroquinolones although no reports of fluoroquinolones selecting for MexXY-overproducing mutants in vitro or in vivo.
[i]Encodes an ABC-MFP component of a probable ABC-MFP-OMF multidrug export system.

Figure 2

Transfection experiments

Decoy targets

Bacterium	ATCC/Strain	Classification	Indication	Target	Description
Mycobacterium smegmatis	MC2 155	Gram-positive/ Actinobacteria/ Lipid-rich cell wall	Considered non-pathogenic model for TB	WhiB7 consensus (**396**)	Transcriptional regulator of antibiotic resistance genes
				sigma-54 (**601**)	Major controller of adaptive response
Staphylococcus aureus	6538NA (FDA test strain)	Gram-positive/ Firmicutes/ coccus- golden balls	Many: TSS/ pneumonia/ scepticemia	WalR consensus (**448**)	2CS regulating antibiotic sensitivity, particularly wall structure. Also known as YYcG consensus
				GISA consensus	Genes upregulated in glycopeptide-intermediate strains, candidate TFDs identified by bioinformatics
				AgrA consensus	Regulator of virulence, candidate sequence identified by bioniformatics
Clostridium diffcile	BAA-1382	Gram-positive/ Firmicutes/ commensal gut bacterium	Diarrhoea to toxic PMC	TcdR consesnus (**506**)	Alternative sigma factor that is autoregulated and drives expression of two exotoxins
Pseudomonas aeruginosa	-	Gram-negative/ Proteobacteria/ faculative anearobe	Lung infection in CF patients/ Model for biofilm formation	Vfr consensus (**508**)	Global regulator of virulence factors
				sigma-54 (**601**)	Major controller of adaptive response
Escherichia coli	K12	Gram-negative/ Proteobacteria/ faculative anearobe	Many: pneumonia/ septicemia	fadR consensus (**511**)	Regulator of essential enzymes required for fatty acid synthesis
				fur (**600**)	Regulator of iron uptake
Streptococcus pneumoniae	-	Gram-positive/ Firmicutes/ in nasopharynx	Several: menigitis Now vaccinated against	not determined	
				sigma-54 (**601**)	Major controller of adaptive response
Klebsiella pneumonia	GG4	Gram-negative/opportunistic pathogen	Scepticemia/Crohns /?Ankylosing spondilitis	NtrC (**556**)	Down regulates an essential gene, glnA
				sigma-54 (**601**)	Major controller of adaptive response

Figure 3

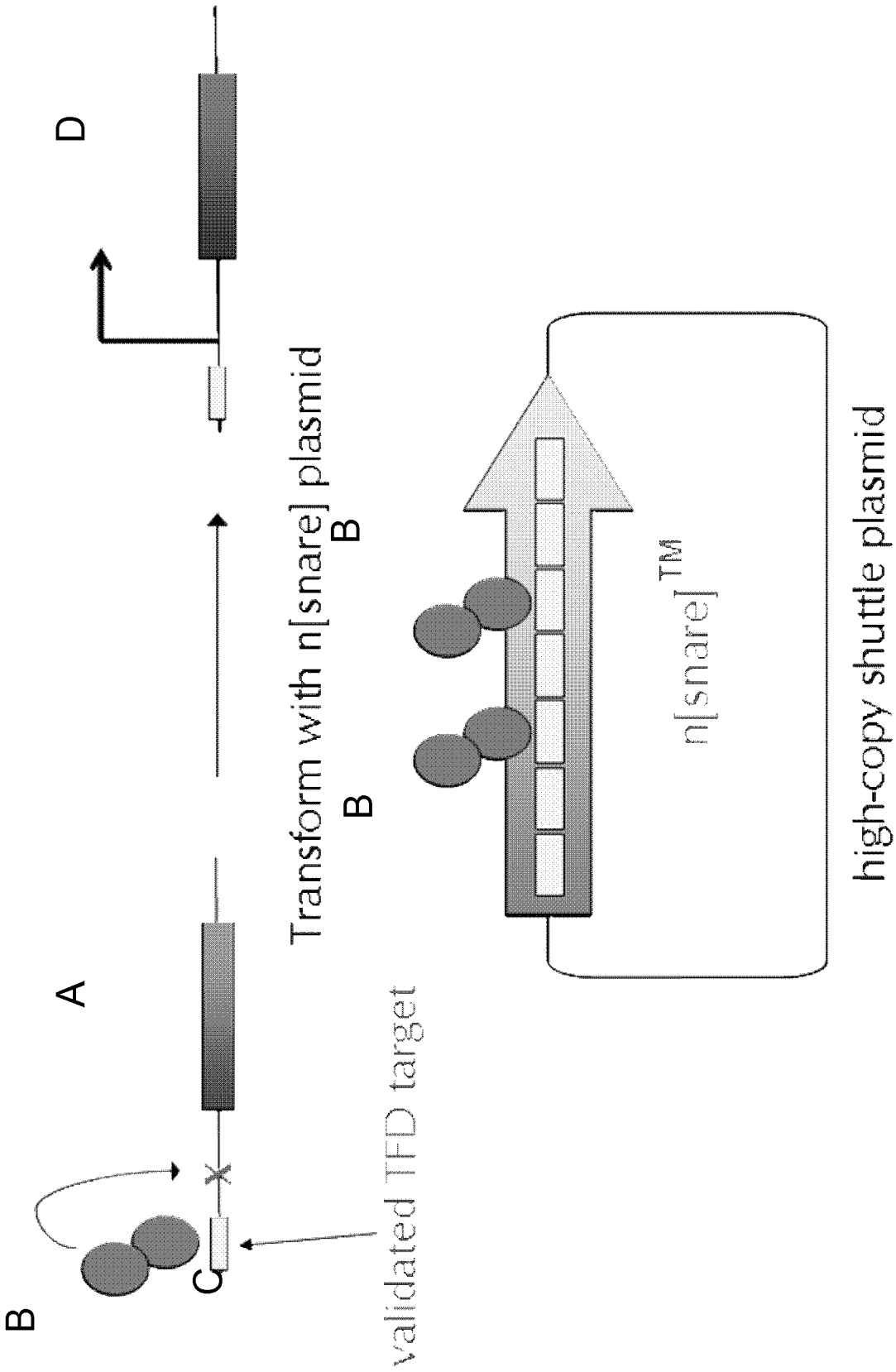

B
C
A
validated TFD target
Transform with n[snare] plasmid
B
D
n[snare]TM
high-copy shuttle plasmid

Figure 4

```
CTTGG TTTTT CCAAG AGAAGAGC ccg cca tgg cgg ccg cgg gaa ttc NNN NNN TCA CTA GTG AAT TCG CGG CCG CCT GCTCTTCG CCG TCA AAA AGA CGG a
GAACC AAAAA GGTTC TCTTCTCG ggc ggt acc gcc ggc gcc ctt aag NNN NNN AGT GAT CAC TTA AGC GCC GGC GGA CGTGAAGC GGC AGT TTT TCT GCC

T WITH Nt.BspQI (NEB: R0644L)

CTTGG TTTTT CCAAG AGAAGAGC ccg cca tgg cgg ccg cgg gaa ttc NNN NNN TCA CTA GTG AAT TCG CGG CCG CCT GCTCTTCG
                TCTTCTCG ggc ggt acc gcc ggc gcc ctt aag NNN NNN AGT GAT CAC TTA AGC GCC GGC GGA CGTGAAGC GGC AGT TTT TCT GCC

E WITH T4 DNA POLYMERASE
```

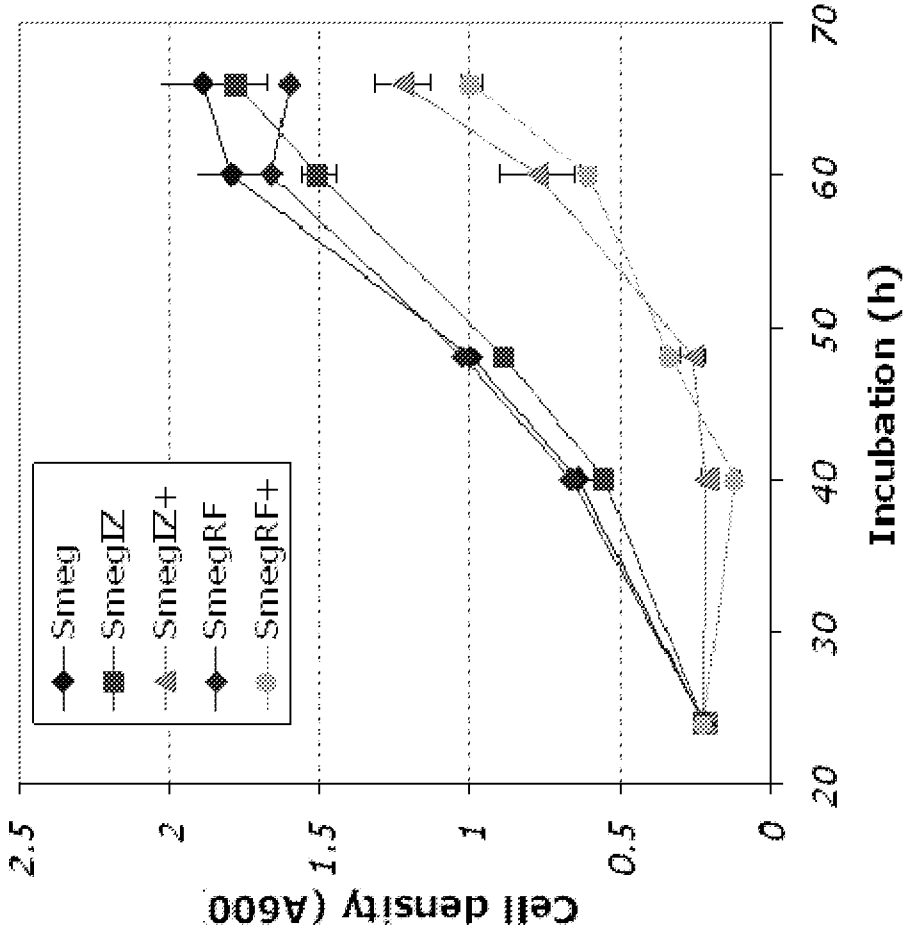

Cell density (A600)
2.5
2
1.5
1
0.5
0
20
30
40
50
60
70
Incubation (h)
Smeg
SmegIZ
SmegIZ+
SmegRF
SmegRF+

Figure 5

Figure 6

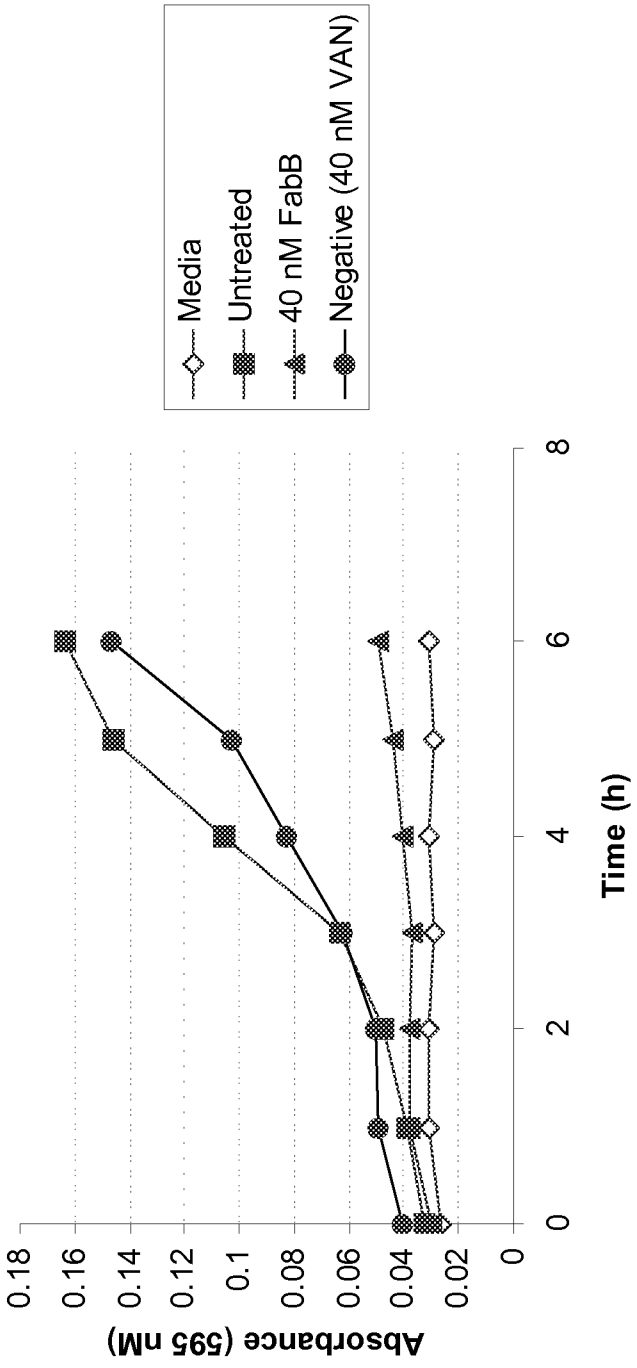

Media
Untreated
40 nM FabB
Negative (40 nM VAN)
Absorbance (595 nM)
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0
2
4
6
8
Time (h)

Figure 7

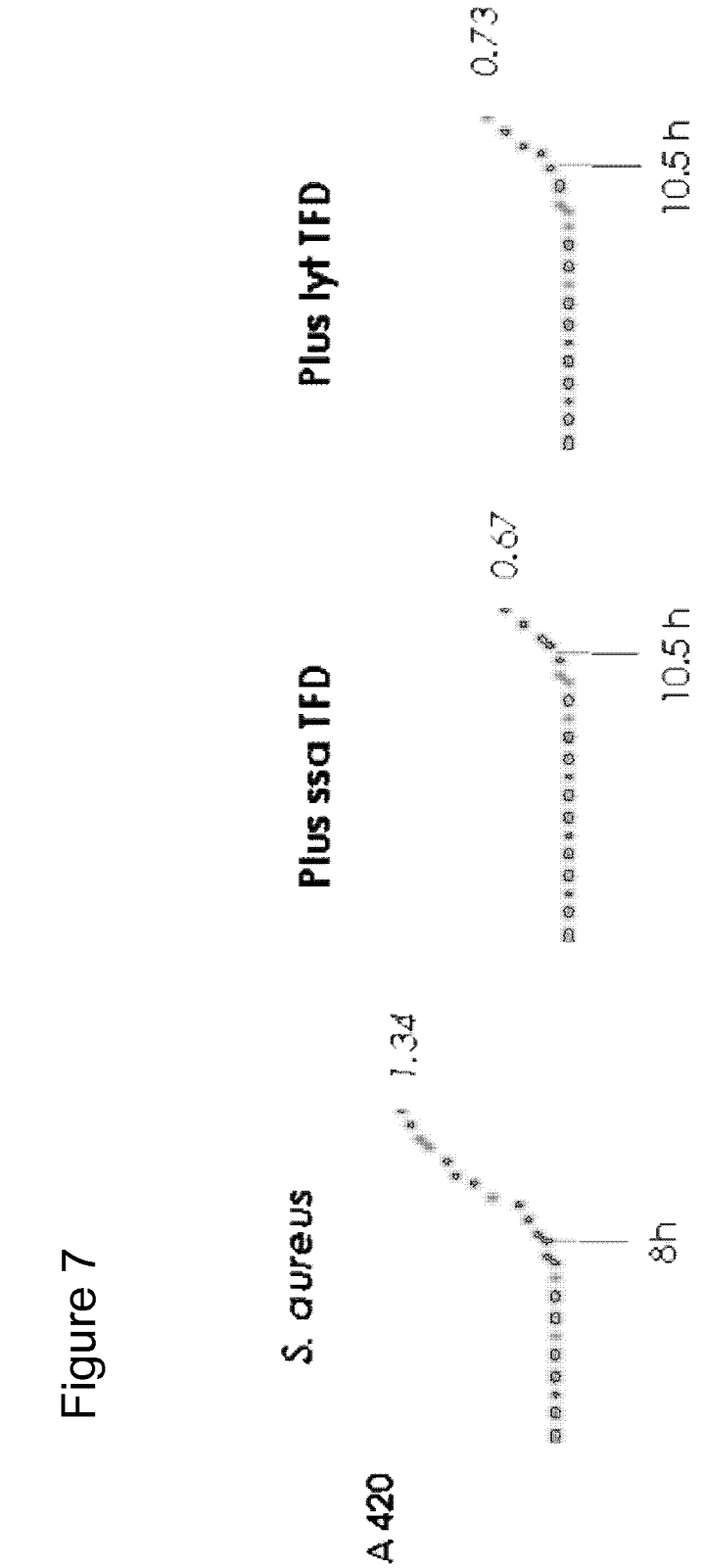

A 420
S. aureus
1.34
8h
Plus ssa TFD
0.67
10.5 h
Plus lyt TFD
0.73
10.5 h

Figure 8

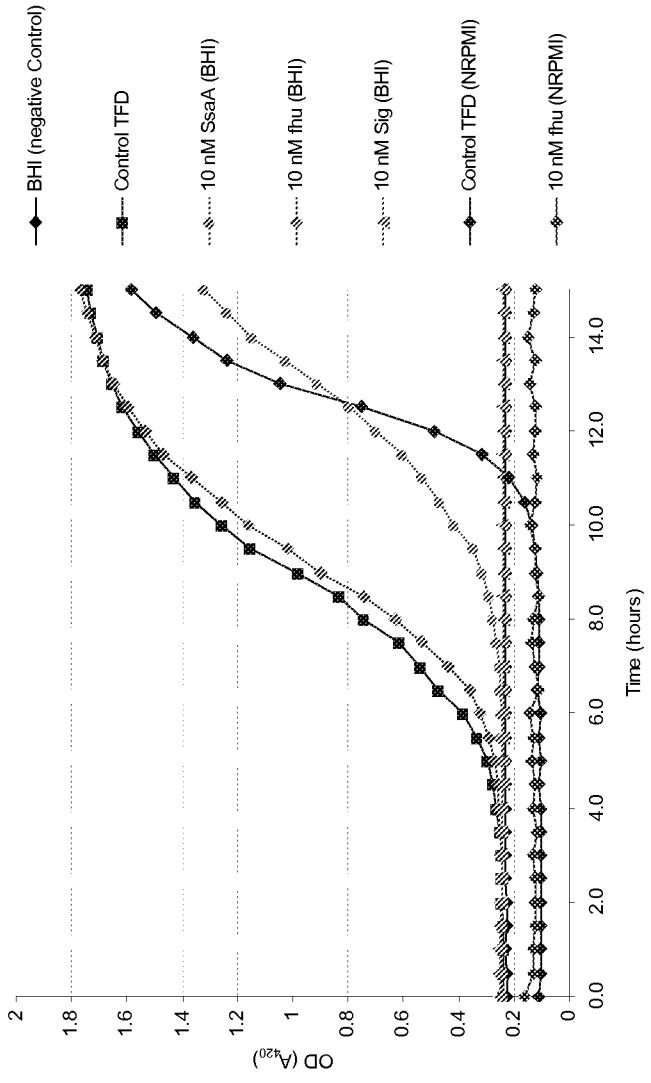
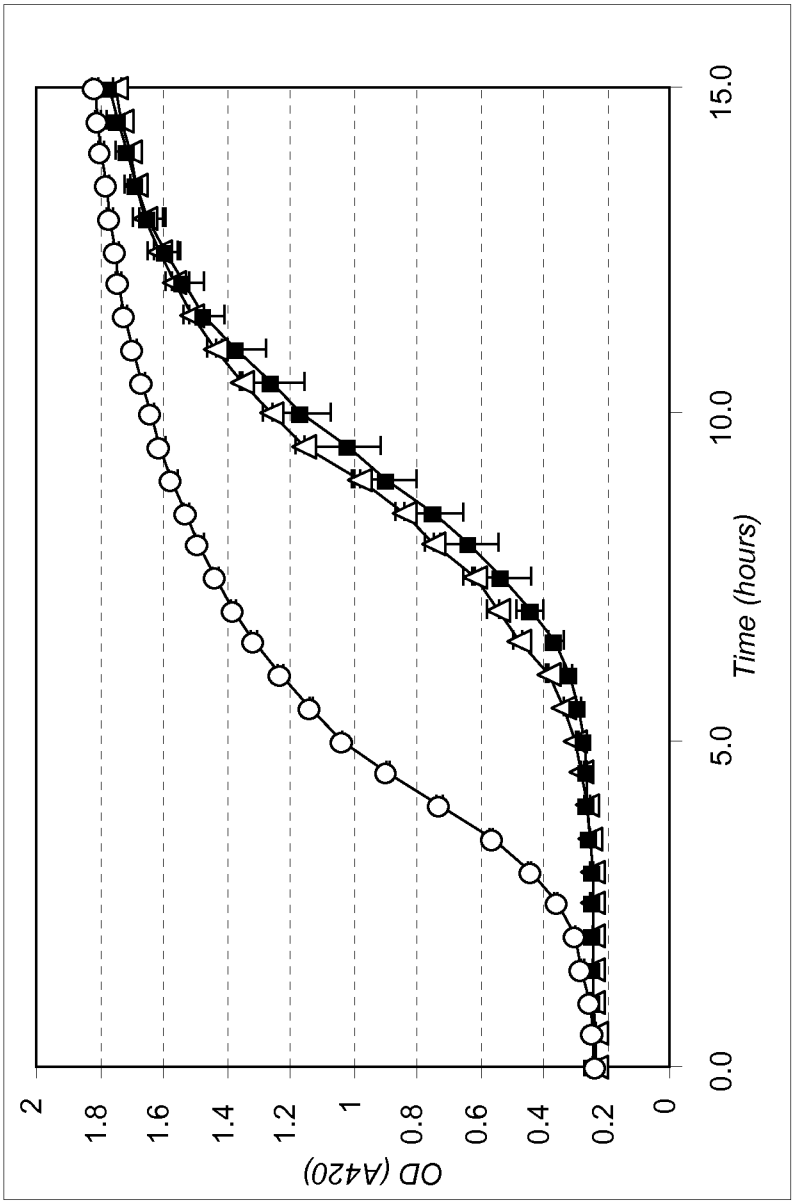

BHI (negative Control)
Control TFD
10 nM SsaA (BHI)
10 nM fhu (BHI)
10 nM Sig (BHI)
Control TFD (NRPMI)
10 nM fhu (NRPMI)
OD (A420)
Time (hours)
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8
2
0.0
2.0
4.0
6.0
8.0
10.0
12.0
14.0

Figure 9



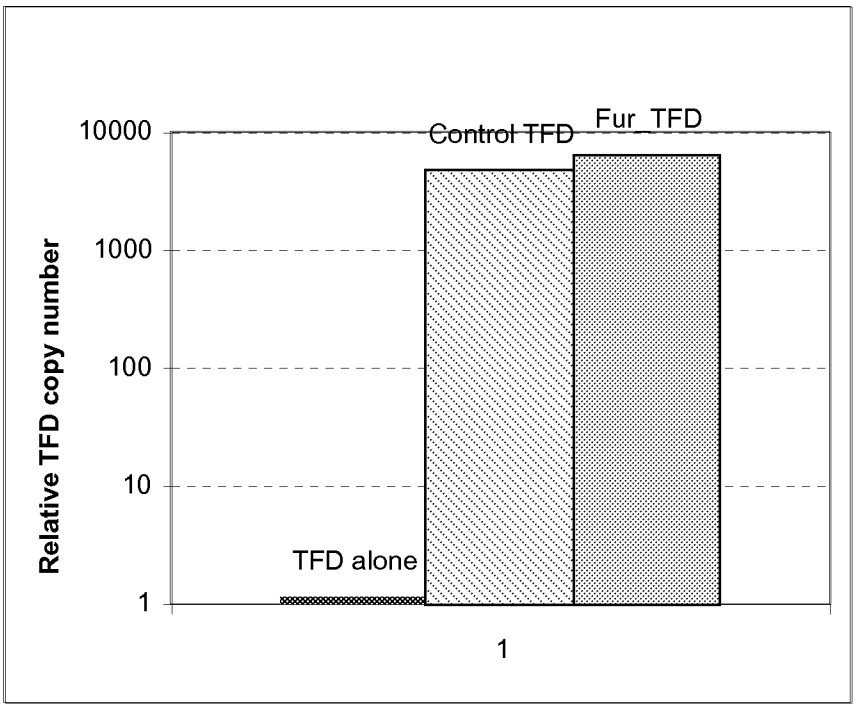


Figure 10A

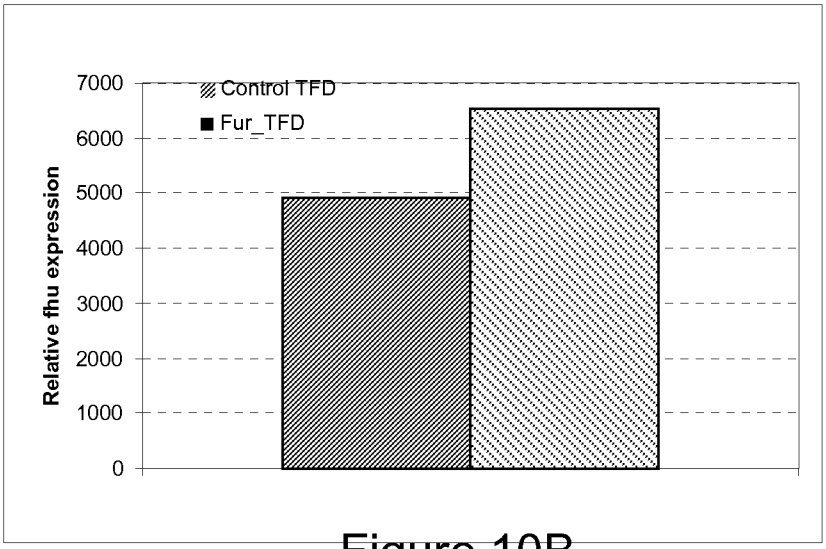


Figure 10B

Figure 11

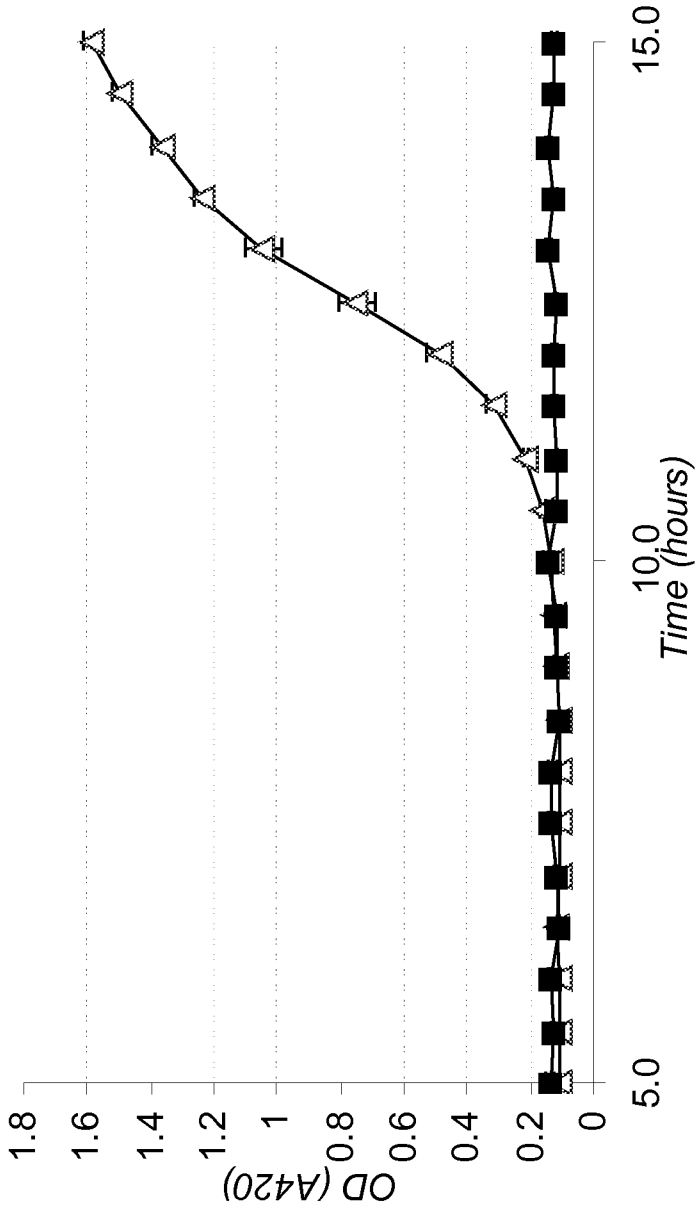
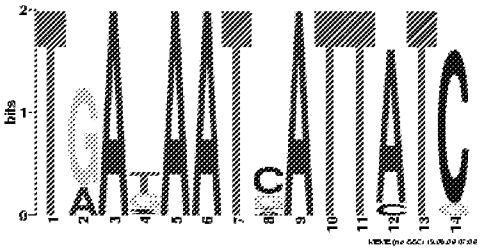


Figure 12




```
                                SAfur_consensus    (1)  TGAGAATCATTATC-
                                  Banthacis_GBAA1093   (1)  TGAGAATCATTATC-
                                   Banthracis_BA4651   (1)  TGAGAATCATTATC-
                                   Banthracis_BAS1021  (1)  TGAGAATCATTATC-
                                  Banthracis_GBAA4651  (1)  TGAGAATCATTATC-
                                  Bcereus_BCAH820_1177 (1)  TGAGAATCATTATC-
                                  Bcereus_BCAH820_4500 (1)  TGAGAATCATTATC-
                                  Bcereus_BCB4264_A4540 (1)  TGAGAATCATTATC-
                                  Bcereus_BCG9842_B0695 (1)  TGAGAATCATTATC-
                                    Bcereus_BCZK4165   (1)  TGAGAATCATTATC-
                                  Saureus_SAOUHSC_00329 (1)  TGAGAATCATTATC-
                                   Banthracis_BAS4317  (1)  -GAGAATGATTATC-
                                    Bcereus_BCZK4166   (1)  -GAGAATGATTATCA
                                  Banthracis_GBAA4652  (1)  -GAGAATGATTATCA
                              Lmonocytogenes_LMHCC_1523 (1)  -GAGAATGATTCTCA
                             Lmonocytogenes_LMOf2365_1136 (1)  -GAGAATGATTCTCA
                                    Saureus_MW0088_A   (1)  -GAGAATGATTCTCA
                                  Saureus_NWMN_0059_A  (1)  -GAGAATGATTCTCA
                                   Saureus_SA0111_A    (1)  -GAGAATGATTCTCA
                                  Saureus_SAB0054c_A   (1)  -GAGAATGATTCTCA
                                  Saureus_SACOL0099_A  (1)  -GAGAATGATTCTCA
                                  Saureus_SAHV_0114_A  (1)  -GAGAATGATTCTCA
                                   Saureus_SAR0118_A   (1)  -GAGAATGATTCTCA
                                   Saureus_SAS0089_A   (1)  -GAGAATGATTCTCA
                                  Saureus_SaurJH1_0106_A (1)  -GAGAATGATTCTCA
                                  Saureus_SAUSA300_0117_A (1)  -GAGAATGATTCTCA
                                   Saureus_SAV0115_A   (1)  -GAGAATGATTCTCA
                                 Saureus_USA300HOU_0126_A (1)  -GAGAATGATTCTCA
                                   Bcereus_BCG9842_B3605 (1)  -GAGAATGATTATCA
                                    Bcereus_BCQ_4208   (1)  -GAGAATGATTATCA
                                   Saureus_SAB0685_A   (1)  -GAGAATGATTATCA
                                  Saureus_SAOUHSC_00746_A (1)  -GAGAATGATTATCA
                              Lmonocytogenes_LMHCC_0596_A (1)  TGAGAATGATTATC-
                                   Saureus_MW0323_A   (1)  TGAGGTTGATTATC-
                                  Saureus_SaurJH9_0395_A (1)  TGAGGTTGATTATC-
                             Lmonocytogenes_LMOf2365_1990_A (1)  TGAGAATGATTATC-
                                 Lmopnocytogenes_lmo1960_A (1)  TGAGAATGATTATC-
                                  Banthracis_BAS5233_A  (1)  -GAGAATAAATTTCA
                                    Bcereus_BC5383_A    (1)  -GAGAATAAATTTCA
                                  Bcereus_BCAH187_A5561_A (1)  -GAGAATAAATTTCA
                                  Bcereus_BCB4264_A5506_A (1)  -GAGAATAAATTTCA
                                    Bcereus_BCE_5512_A  (1)  -GAGAATAAATTTCA
                                  Bcereus_BCG9842_B5445_A (1)  -GAGAATAAATTTCA
                                    Bcereus_BCQ_5223_A  (1)  -GAGAATAAATTTCA
                                Lmonocytogenes_LMHCC_1524_A (1)  -GAGAATAAATTTCA
                                Lmonocytogenes_LMHCC_0597_A (1)  TGAGAATTATTATC-
                                 Lmonocytogenes_lmo1959_A (1)  TGAGAATTATTATC-
                             Lmonocytogenes_LMOf2365_1989_A (1)  TGAGAATTATTATC-
                                 Lmonocytogenes_lmo0484  (1)  TGAGAATCATTATC-
                                 Lmonocytogenes_lmo1131  (1)  TGAGAATCATTATC-
                                   Saureus_MW0089_A   (1)  TGAGAATCATTATC-
                                  Saureus_NWMN_0060_A  (1)  TGAGAATCATTATC-
                                   Saureus_SA0112_A    (1)  TGAGAATCATTATC-
                                  Saureus_SACOL0100_A  (1)  TGAGAATCATTATC-
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                                   Saureus_SAR0119_A   (1)  TGAGAATCATTATC-
                                   Saureus_SAS0090_A   (1)  TGAGAATCATTATC-
                                  Saureus_SaurJH1_0107_A (1)  TGAGAATCATTATC-
                                  Saureus_SaurJH9_0103_A (1)  TGAGAATCATTATC-
                                  Saureus_SAUSA300_0118_A (1)  TGAGAATCATTATC-
                                   Saureus_SAV0116_A   (1)  TGAGAATCATTATC-
                                 Saureus_USA300HOU_0127_A (1)  TGAGAATCATTATC-
                                          Consensus    (1)  TGATAAT ATTATC
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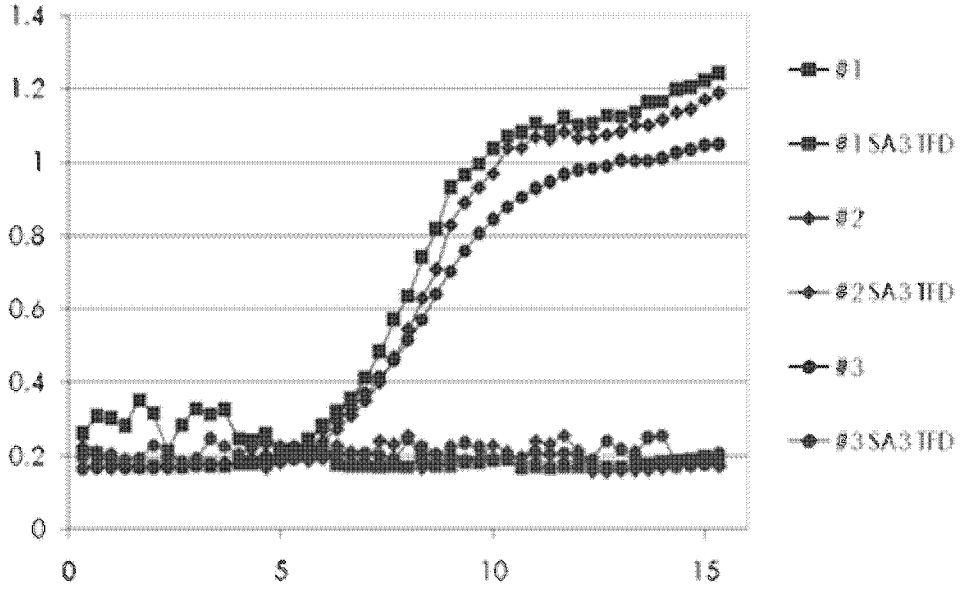


Figure 13

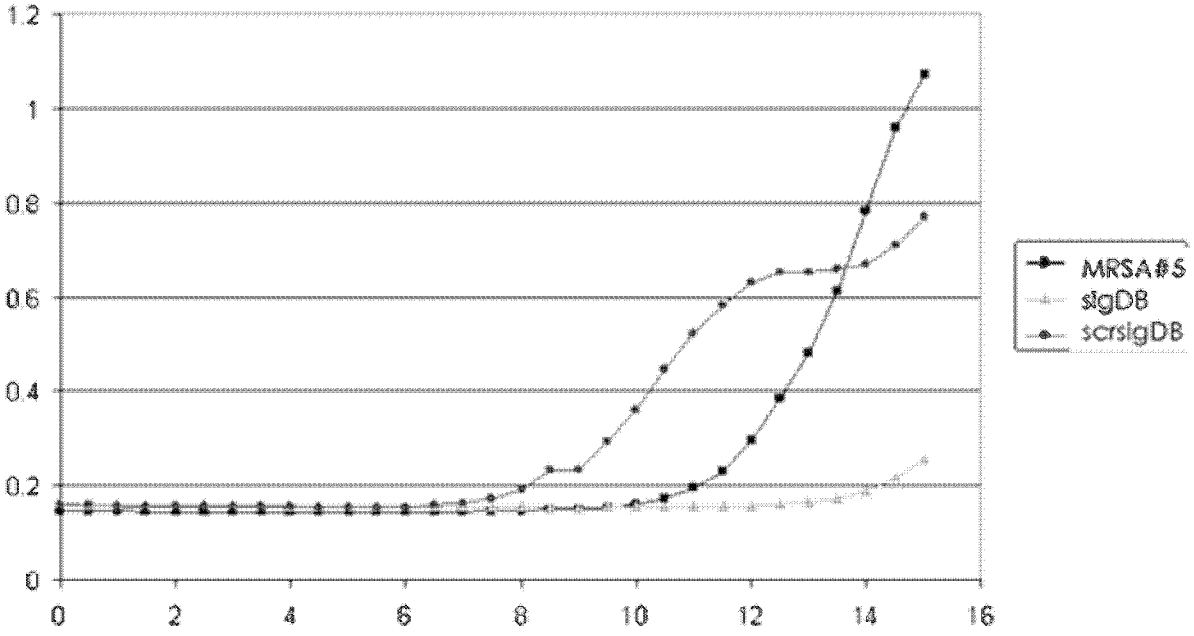


Figure 14

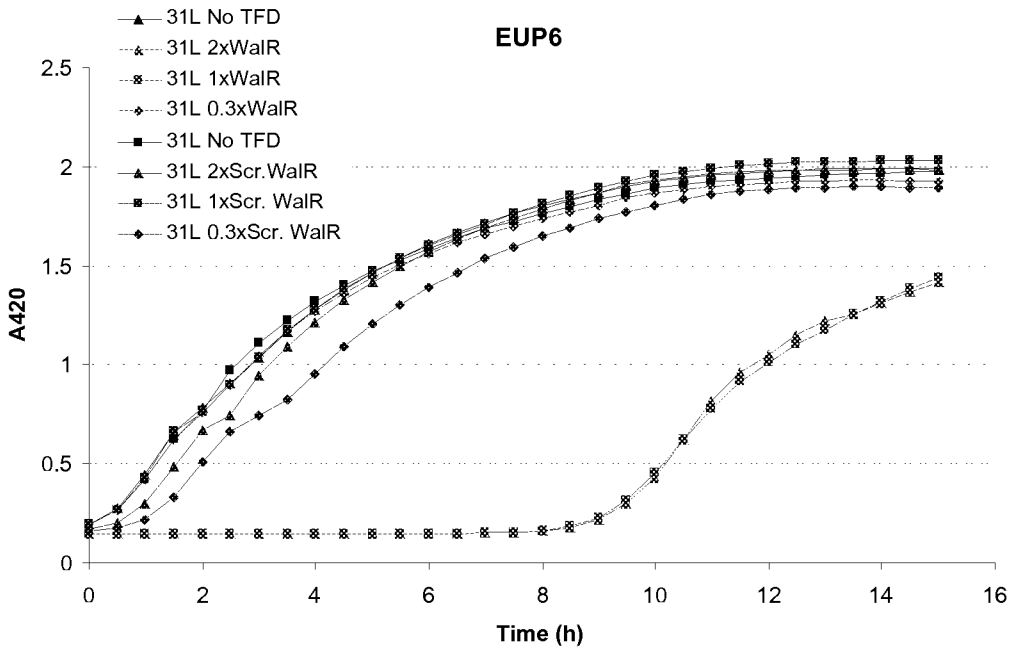


Figure 15

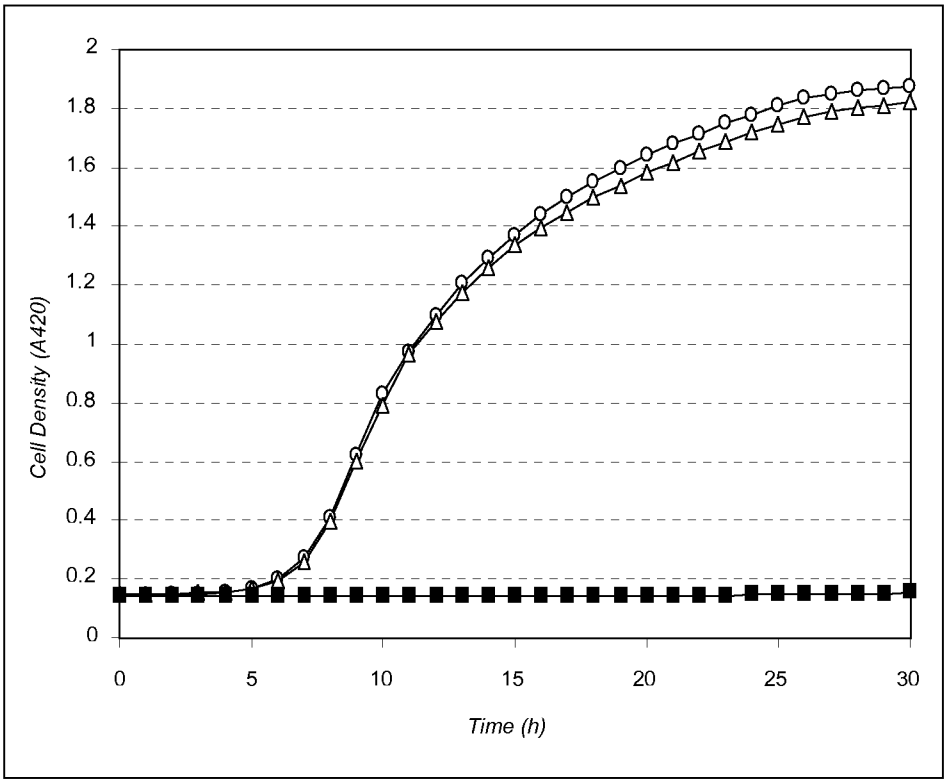


Figure 16

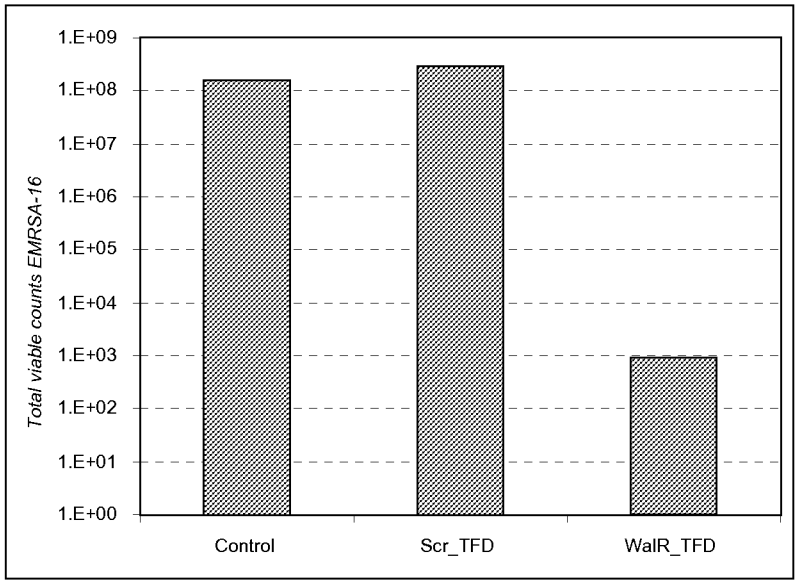


Figure 17A

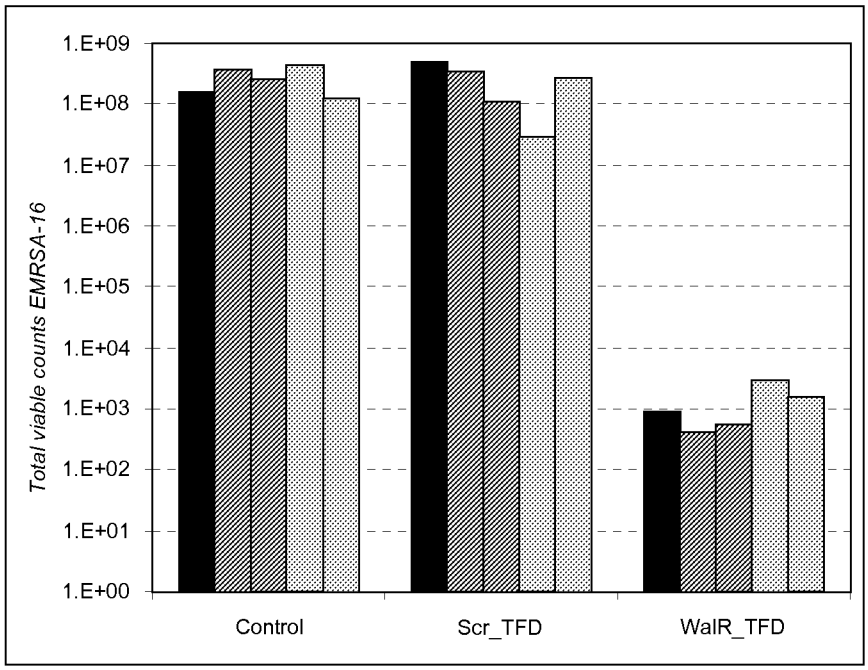
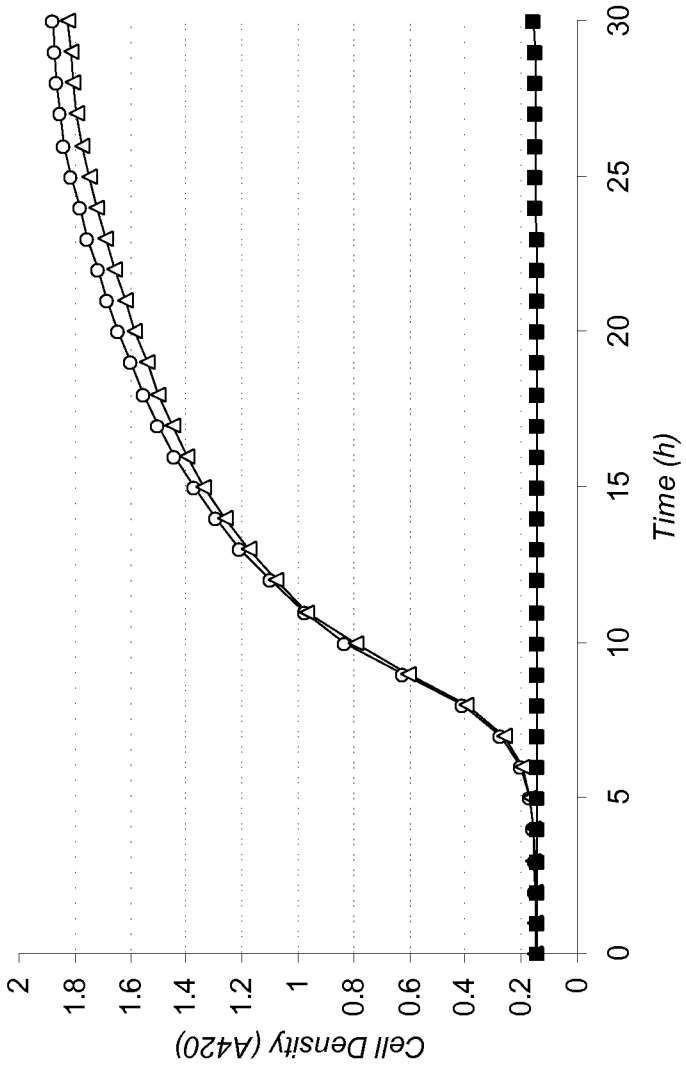


Figure 17B

Figure 17C


Cell Density (A420)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
5
10
15
20
25
30
Time (h)

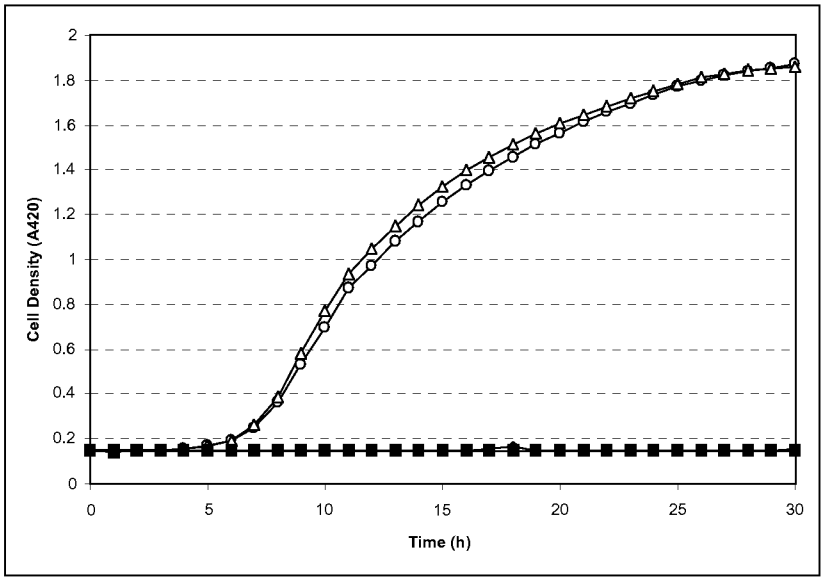


Figure 18

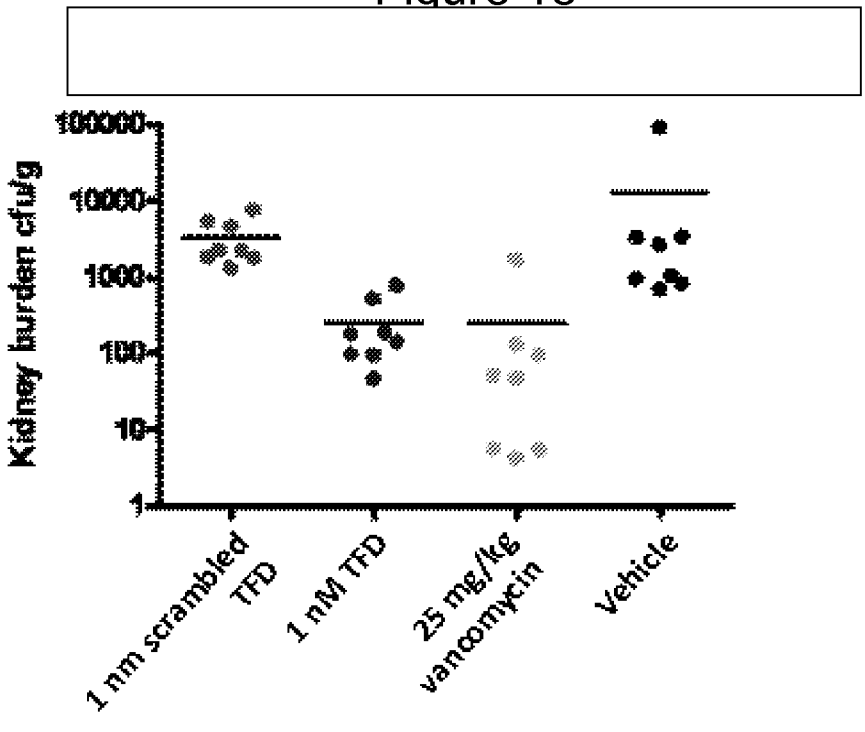


Figure 19

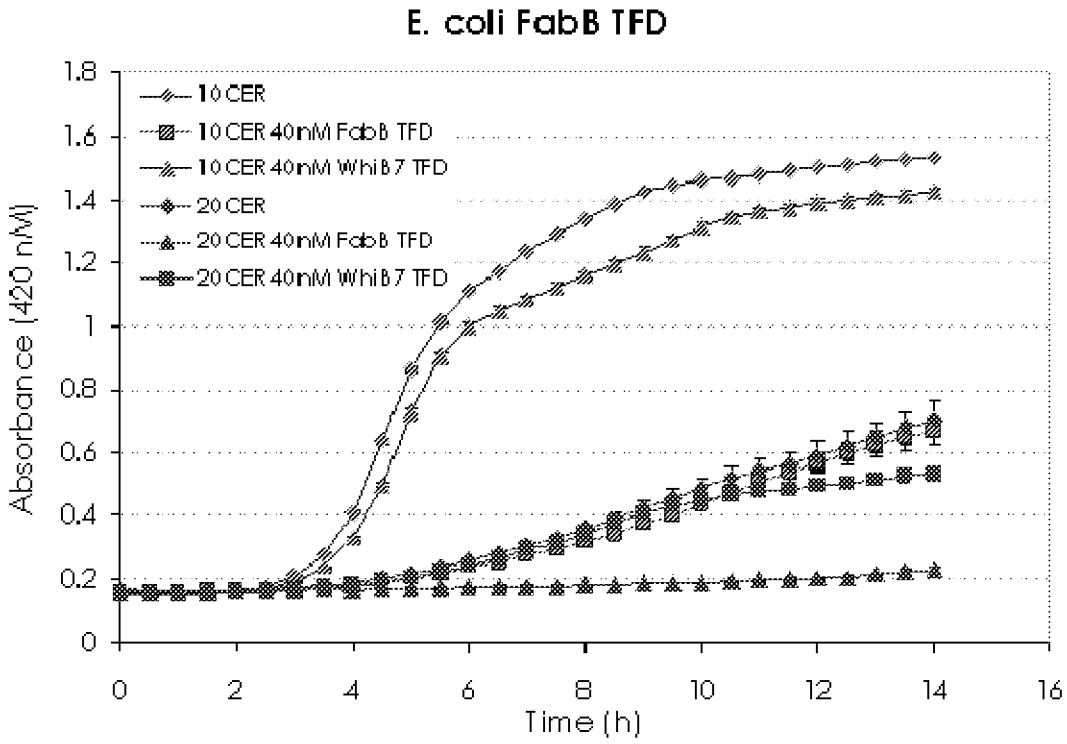


Figure 20

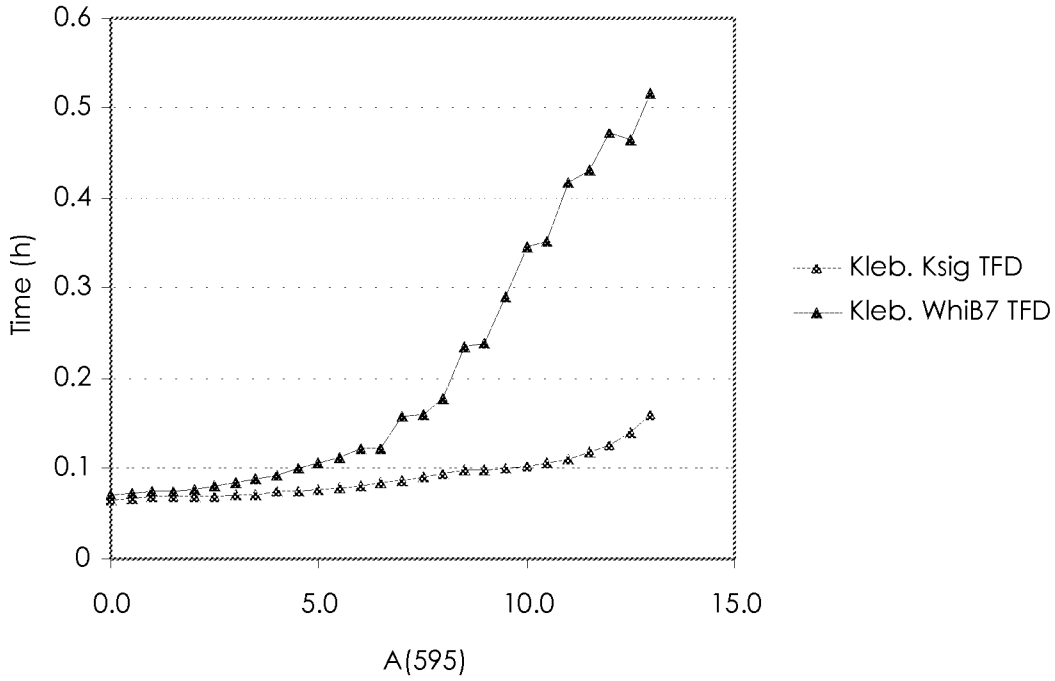


Figure 21

Figure 22

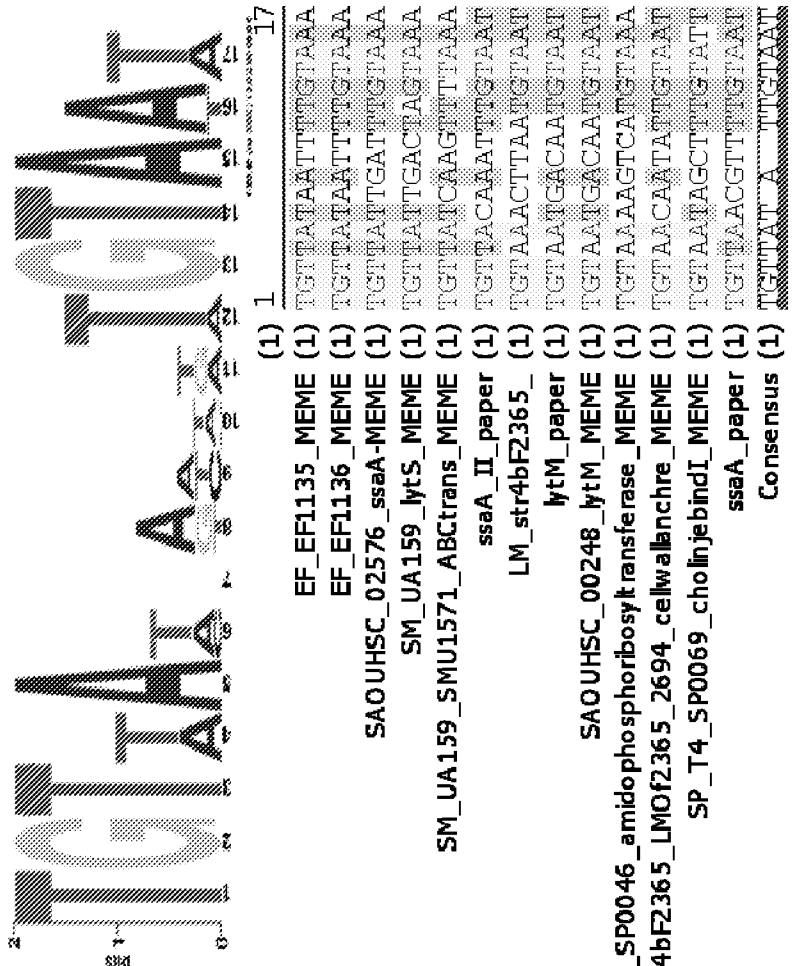
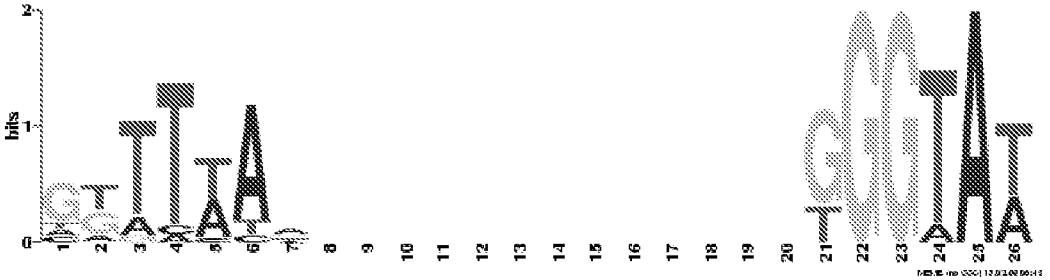

bits
1
2
(1) 1 17
EF_EF1135_MEME (1) TGTTATAATTTTGTAAA
EF_EF1136_MEME (1) TGTTATAATTTTGTAAA
SAOUHSC_02576_ssaA-MEME (1) TGTTATTGATTTTGTAAA
SM_UA159_lytS_MEME (1) TGTTATTGACTAGTAAA
SM_UA159_SMU1571_ABCtrans_MEME (1) TGTTATCAAGTTTTAAA
ssaA_II_paper (1) TGTTACAAATTTTGTAAT
LM_str4bF2365_ (1) TGTAAACTTAATGTAAT
lytM_paper (1) TGTAATGACAATGTAAT
SAOUHSC_00248_lytM_MEME (1) TGTAATGACAATGTAAT
SP_T4_SP0046_amidophosphoribosyltransferase_MEME (1) TGTAAAAGTCATGTAAA
LM_str4bF2365_LMOf2365_2694_cellwallanchre_MEME (1) TGTAACAATATTGTAAT
SP_T4_SP0069_cholinjebindI_MEME (1) TGTAATAGCTTTTGTATT
ssaA_paper (1) TGTTAACGTTTTTGTAAT
Consensus (1) TGTTATTAA TTTGTAAT

Figure 23

A.



B.

Sequence Name	Description	E-value	Length
NC_010079_USA300HOU_0495	1 5723	1.9	5724
NC_006582_ABC3117	-1 18	5.1	121
NC_006322_BLi03319	-1 202	7.9	203
NC_006270_BL02593	-1 202	7.9	203
NC_007530_GBAA1815	1 4	10	121
NC_005945_BAS1680	1 4	10	121
NC_003997_BA1815	1 4	10	121
NC_010079_USA300HOU_0701	1 136	11	137
NC_009782_SAHV_0675	1 136	11	137
NC_009641_NWMN_0647	1 136	11	137
NC_009632_SaurJH1_0718	1 136	11	137
NC_009487_SaurJH9_0702	1 136	11	137
NC_007795_SAOUHSC_00686	1 136	11	137
NC_007793_SAUSA300_0664	1 136	11	137
NC_007622_SAB0627	1 136	11	137
NC_003923_MW0640	1 136	11	137
NC_002953_SAS0643	1 136	11	137
NC_002952_SAR0731	1 136	11	137
NC_002951_SACOL0738	1 136	11	137
NC_002758_SAV0678	1 136	11	137
NC_002745_SA0633	1 136	11	137
NC_011969_BCQ_1823	1 4	20	121
NC_011773_BCAH820_1860	1 4	20	121
NC_011658_BCAH187_A1936	1 4	20	121
NC_008600_BALH_1592	1 4	20	121
NC_006274_BCZK1626	1 4	20	121
NC_003210_lmo1940	-1 79	34	121
NC_009004_llmg_1109	-1 -5	37	121
NC_011773_BCAH820_1667	1 71	41	121
NC_011773_BCAH820_1666	-1 71	41	121
NC_011725_BCB4264_A1632	1 71	41	121
NC_011725_BCB4264_A1631	-1 71	41	121
NC_011658_BCAH187_A1743	1 71	41	121
NC_011658_BCAH187_A1742	-1 71	41	121

Sequence Name	Description	E-value	Length
NC_007530_GBAA1597	1 71	41	121
NC_007530_GBAA1596	-1 71	41	121
NC_006274_BCZK1453	1 71	41	121
NC_006274_BCZK1452	-1 71	41	121
NC_005957_BT9727_1453	1 71	41	121
NC_005957_BT9727_1452	-1 71	41	121
NC_005945_BAS1480	1 71	41	121
NC_005945_BAS1481	-1 71	41	121
NC_004722_BC1574	1 71	41	121
NC_004722_BC1573	-1 71	41	121
NC_003997_BA1597	1 71	41	121
NC_003997_BA1596	-1 71	41	121
NC_003909_BCE_1703	1 71	41	121
NC_003909_BCE_1702	-1 71	41	121
NC_003923_MW2356	1 256	44	257
NC_003923_MW2355	-1 256	44	257
NC_002953_SAS2324	1 256	44	257
NC_002953_SAS2323	-1 256	44	257
NC_009004_llmg_2123	-1 -5	48	121
NC_008527_LACR_1793	-1 -5	48	121
NC_002662_L44970	1 -5	48	121
NC_010999_LCABL_28620	1 33	48	121
NC_008526_LSEI_2672	1 33	48	121
NC_009725_RBAM_029740	1 135	49	136
NC_002570_BH4025	-1 -5	49	121
NC_010382_Bsph_rRNA055S	1 191	52	192
NC_002570_BH1834	1 -33	53	121
NC_009782_SAHV_2416	1 266	53	267
NC_009782_SAHV_2415	-1 266	53	267
NC_009632_SaurJH1_2507	1 266	53	267
NC_009632_SaurJH1_2506	-1 266	53	267
NC_009487_SaurJH9_2458	1 266	53	267
NC_009487_SaurJH9_2457	-1 266	53	267
NC_002758_SAV2432	1 266	53	267

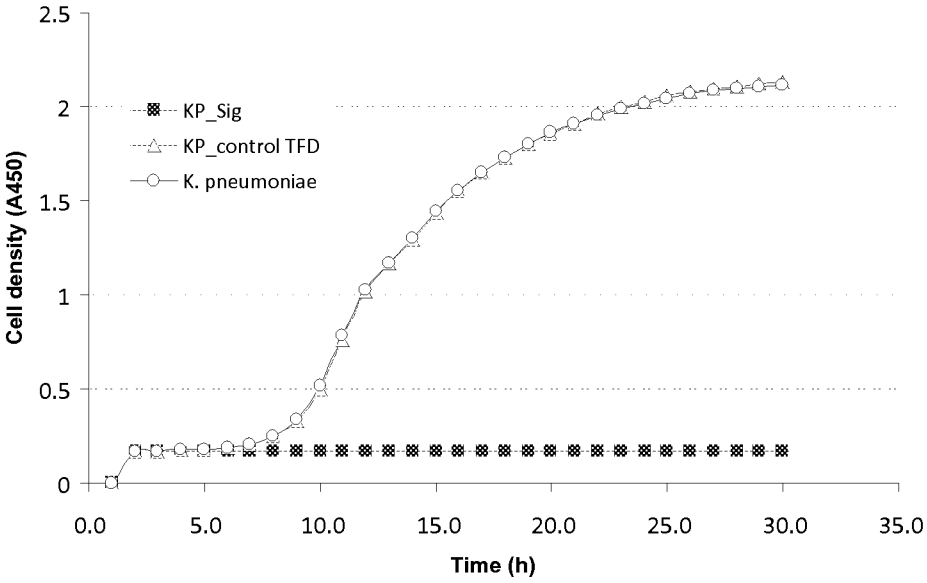


Figure 24A

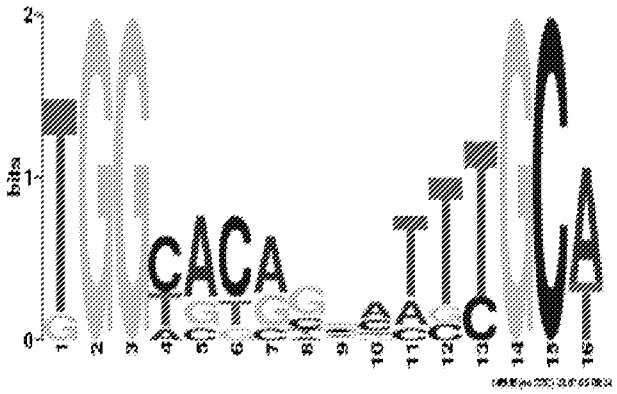


Figure 24B