Synthetic routes for neutral hMOS

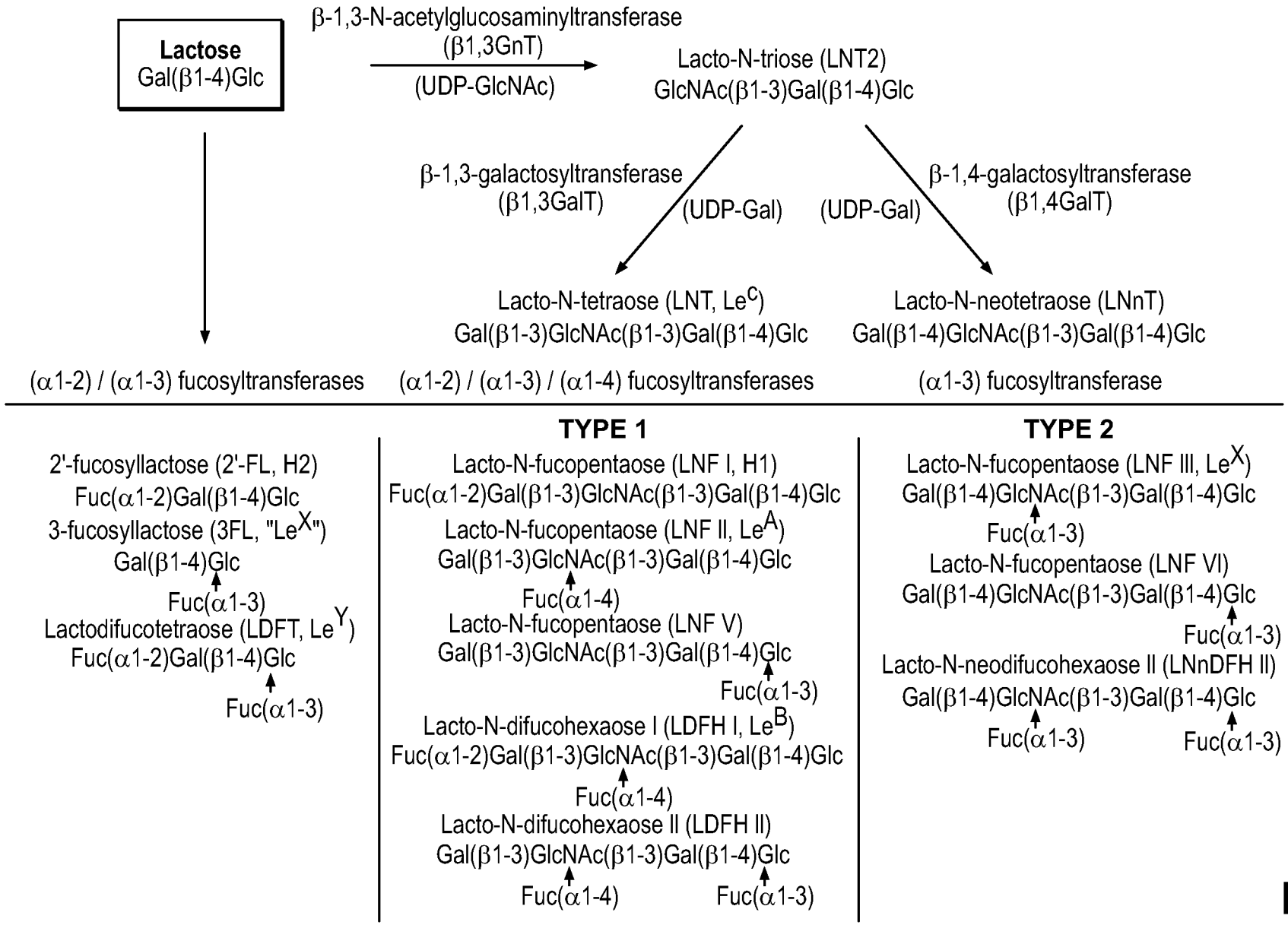


FIG. 1

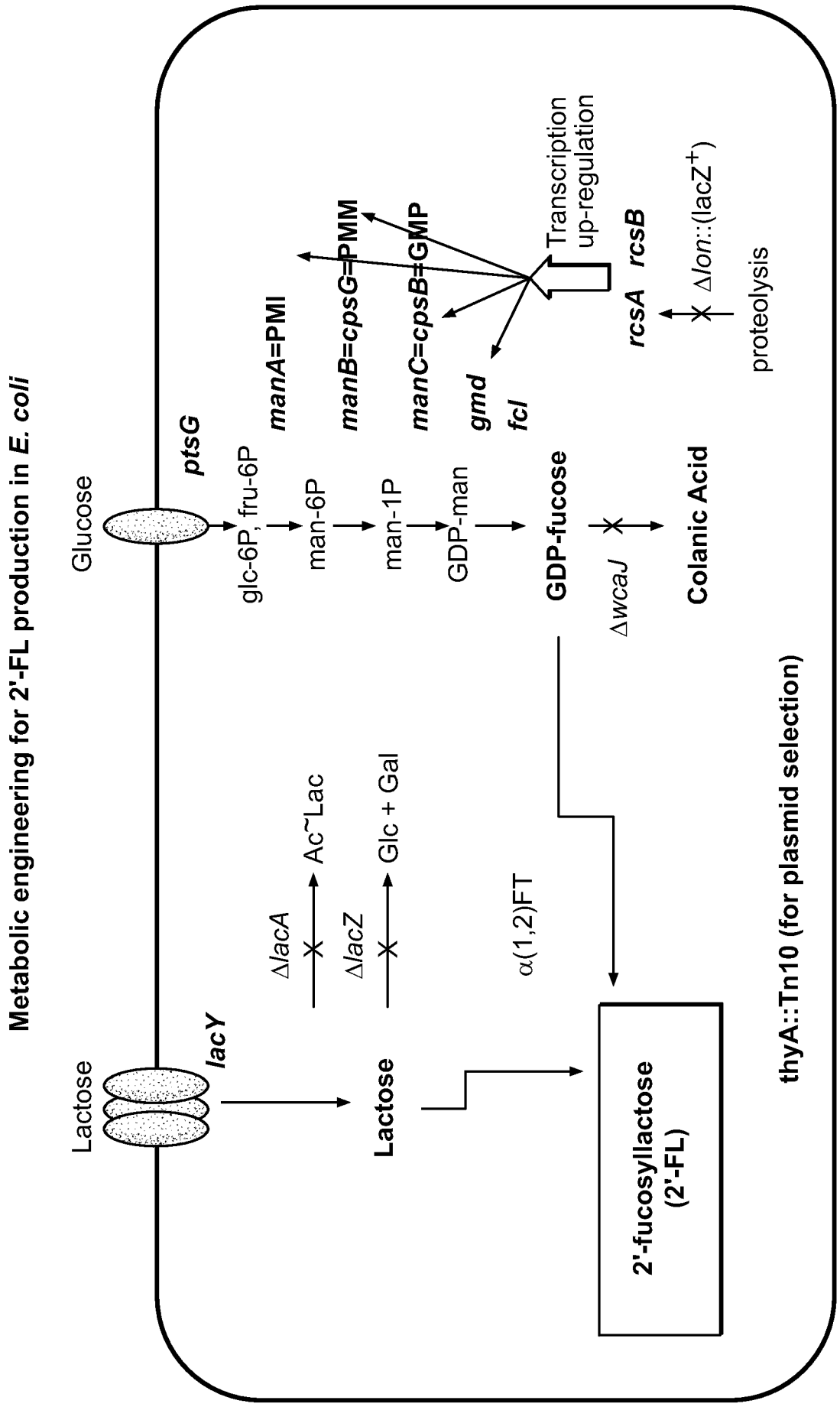

Metabolic engineering for 2'-FL production in E. coli
Glucose
ptsG
glc-6P, fru-6P
manA=PMI
man-6P
manB=cpsG=PMM
man-1P
manC=cpsB=GMP
GDP-man
gmd
fcl
GDP-fucose
Transcription up-regulation
rcsA rcsB
ΔlonΔ::(lacZ+)
proteolysis
ΔwcaJ
Colanic Acid
Lactose
lacY
ΔlacA
Ac~Lac
ΔlacZ
Glc + Gal
Lactose
α(1,2)FT
2'-fucosyllactose (2'-FL)
thyA::Tn10 (for plasmid selection)

FIG. 2

	1	2	3	4
H.pylori futC	1	70.10	23.97	22.57
H.mustelae futL	2	70.10	27.04	21.36
Bacteroides vulgatus futN	3	23.97	27.04	31.23
E. coli O126 wbgL	4	22.57	21.36	31.23

FIG. 3A

H.pylori futC MAFKVVQLCGGLGNQMFQYAFAKSLQKHSNTPVLLDITSFDWSDRKMQLE
H.mustelae futL MDFKIVQVHGGLGNQMFQYAFAKSLQTHLNIPVLLDTTWFDYGNRELGLH
Bacteroides vulgatus futN M- - RLIKVTGGLGNQMFIYAF- YRRMKKYYPKVRIDLSDMMHYKVHYGYE
E. coli 0126 wbgL M- - SIIRLQGGLGNQLFQFSFGYALSKINGTPLYFDISHYAENDDHGGYR
H.pylori futC LKPSRLTYFFGYFQDPRYFDAISPLIKQTFTLPPPPENNKNNKKEEEYQ
H.mustelae futL FEPSRIAYFHGYFQDPRYFEDISPLIKQTFTLPHPTEH- - - - - - - - AEQYS
Bacteroides vulgatus futN - - -WPLLYFKGFYQSERFFADIKDEVRESFTFDK- - - - - - - - - - NKANSRS
E. coli 0126 wbgL AQKWKSKKYIGYWQSEHFFHKHILDLKEFF- IPK- - - - - - - - - - NVSEQAN
H.pylori futC FVFCEDLEFT- QNLDLGYPFMDMTTRDKEEEAYWDMLLMQSCQHGIIANS
H.mustelae futL FLFCEDLEFV- QNLDLGYPFVDMTTRDGA- -AHWDMMLMQSCKHGIITNS
Bacteroides vulgatus futN YIFSDDIAWVKENLP- - LQNAVYIDWNTDELSWQDMMLMSHCKHHIICNS
E. coli 0126 wbgL FIFSDDIFWCKENIETLLSKKYNIYYSEDLSQEEDLWLMSLANHHIIANS
LFPIDLPYASAKEIAIAKMQHL- - - - - - - - PKLVRDALKCMGFDRVSQEIVFEYEPKL 100
LFPIDLQCASAQQIAAAHMQNL- - - - - - - - PRLVRGALRRMGLGRVSKEIVFEYMPEL 100
MHRVFNLPHTEFCINQP- LKKVIEFL- - - - - - FFKKIYERKQAPNSLRAF- - EKK- YF 95
LNNL- QIPEEYLQYTRKLNNIYKFLVRGSRLYPEIFLFLGFCNEFHAYGYDFE- YI 103
CKLSLILAA- KNSVFVHIRRGDYVG- - - - - - IGCQLGIDYQKKALEYMAKRVPNMEL 200
RKLSQILAA- KNSVFVHIRRGDYMR- - - - - - LGWQLDISYQLRAIAYMAKRVQNLEL 193
LNMLEILDKDENAVSLHIRRGDYLQPKHWATTGSVCQLPYYQNAIAEMSRRVASPSY 190
LLAAKILES- QSSLSIHIRRGDYTKNKTATLTHGVCSLEYYKKALNKIRDLAMIRDV 199
TYSWWAAYLIENPEKIII GPKHWLFGHENI- - - - - LCKEWVKIESHFEVKSQKYNA* 301
TYSWWAAYLIKNPEKIII GPSHWIYGNENI- - - - - LCKDWVKIESQFETKS* - - - - - 287
TFSWWGAWLNPNNDKTVIVPSRWFQHSEAPDIYP- - TGWIKVPVS* - - - - - - - - - 282
SFSWWGAYLGTSASQIVIYPTPWYDITPKNTYIPIVNHWINVDKHSSC* - - - - - - - - 298

FIG. 3B

FIG. 4A	FIG. 4B
FIG. 4C	FIG. 4D
FIG. 4E	FIG. 4F

FIG. 4

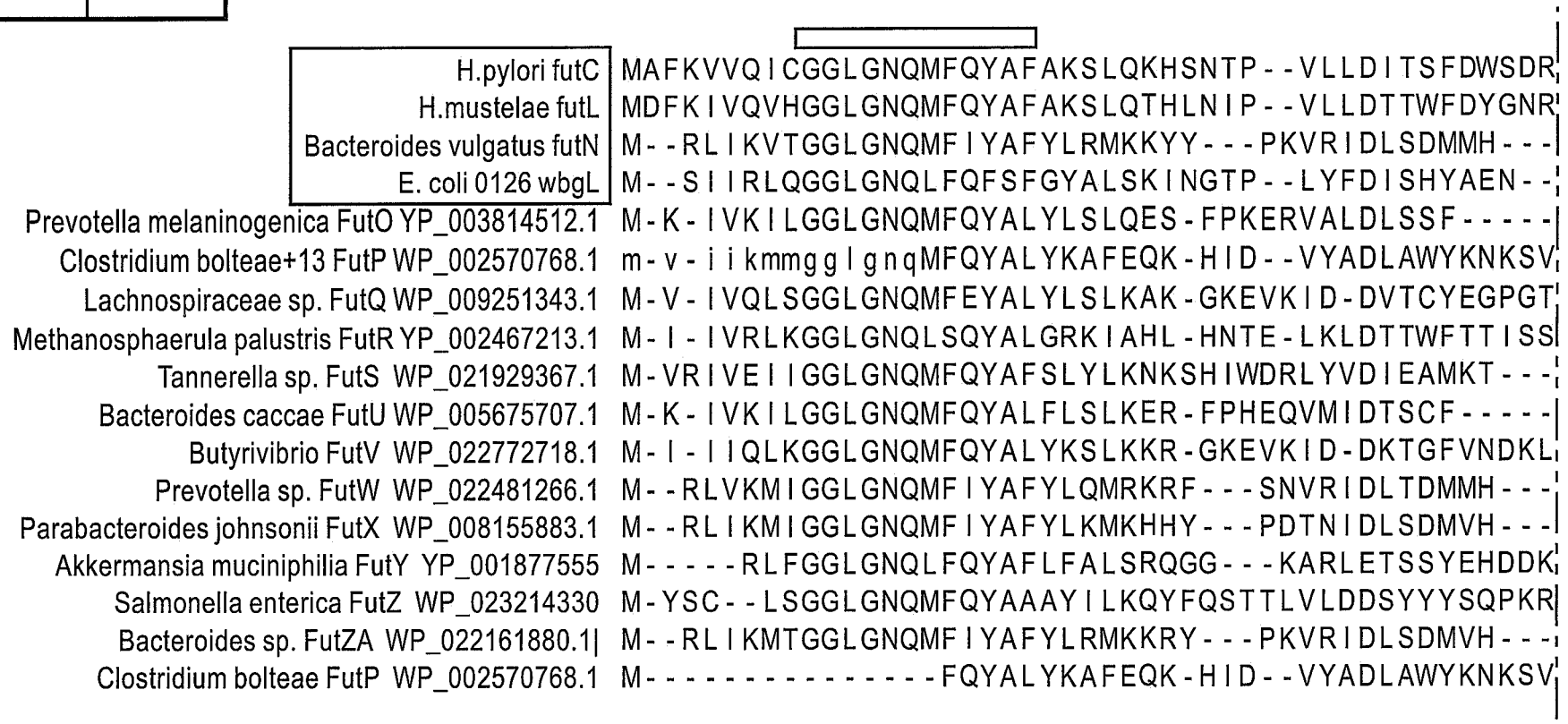


FIG. 4A

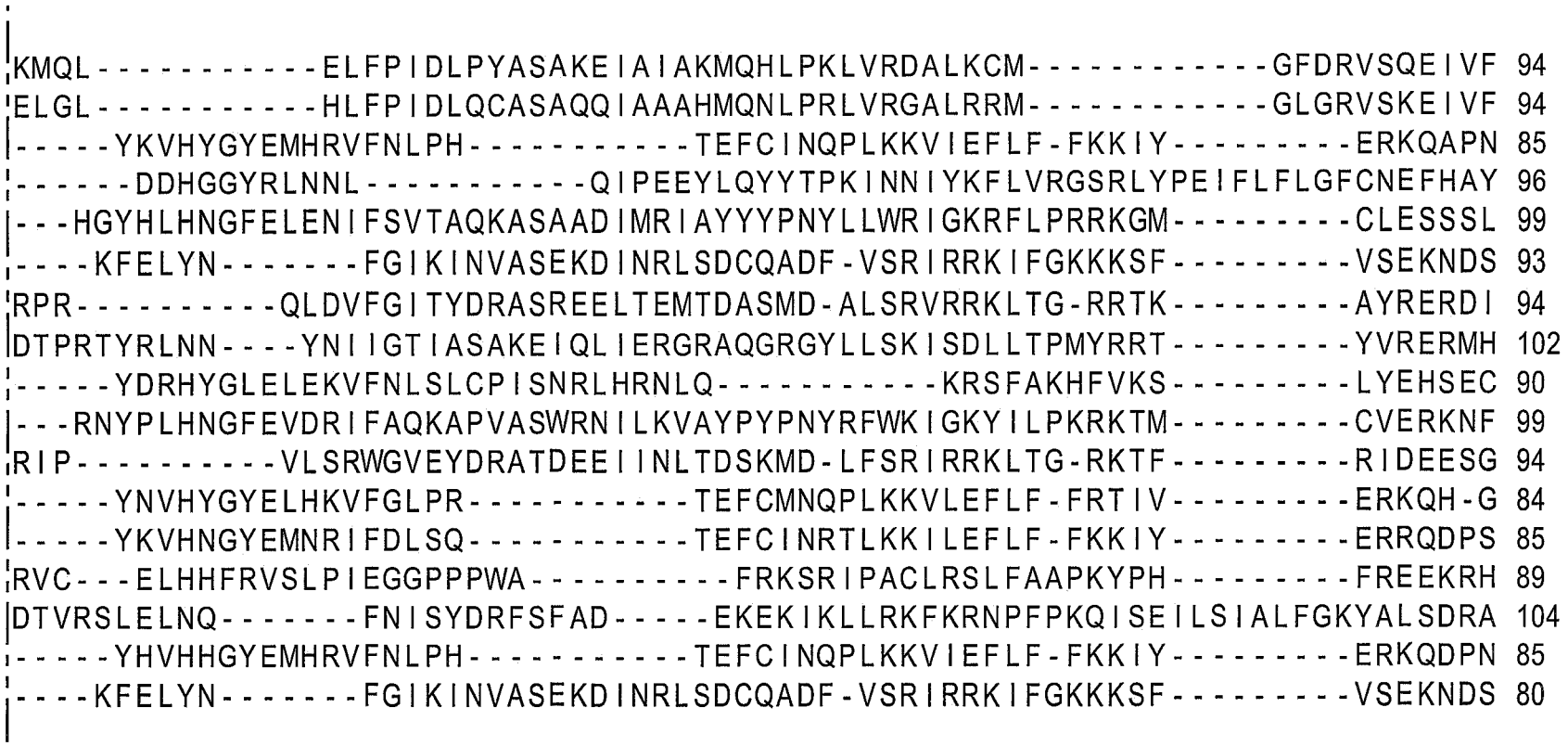

KMQL----------ELFPIDLPYASAKEIAIAKMQHLPKLVRDALKCM----------GFDRVSQEIVF 94
ELGL----------HLFPIDLQCASAQQIAAAHMQNLPRLVRGALRRM----------GLGRVSKEIVF 94
-----YKVHYGYEMHRVFNLPH----------TEFCINQPLKKVIEFLF-FKKIY---------ERKQAPN 85
------DDHGGYRLNNL----------QIPEEYLQYYTPKINNIYKFLVRGSRLYPEIFLFLGFCNEFHAY 96
---HGYHLHNGFELENIFSVTAQKASAADIMRIAYYYPNYLLWRIGKRFLPRRKGM---------CLESSSL 99
----KFELYN-------FGIKINVASEKDINRLSDCQADF-VSRIRRKIFGKKKSF---------VSEKNDS 93
RPR----------QLDVFGITYDRASREELTEMTDASMD-ALSRVRRKLTG-RRTK---------AYRERDI 94
DTPRTYRLNN----YNIIGTIASAKEIQLIERGRAQGRGYLLSKISDLLTPMYRRT---------YVRERMH 102
-----YDRHYGLELEKVFNLSLCPISNRLHRNLQ----------KRSFAKHFVKS---------LYEHSEC 90
---RNYPLHNGFEVDRIFAQKAPVASWRNILKVAYPYPNYRFWKIGKYILPKRKTM---------CVERKNF 99
RIP----------VLSRWGVEYDRATDEEIINLTDSKMD-LFSRIRRKLTG-RKTF---------RIDEESG 94
-----YNVHYGYELHKVFGLPR----------TEFCMNQPLKKVLEFLF-FRTIV---------ERKQH-G 84
-----YKVHNGYEMNRIFDLSQ----------TEFCINRTLKKILEFLF-FKKIY---------ERRQDPS 85
RVC---ELHHFRVSLPIEGGPPPWA---------FRKSRIPACLRSLFAAPKYPH---------FREEKRH 89
DTVRSLELNQ-------FNISYDRFSFAD-----EKEKIKLLRKFKRNPFPKQISEILSIALFGKYALSDRA 104
-----YHVHHGYEMHRVFNLPH----------TEFCINQPLKKVIEFLF-FKKIY---------ERKQDPN 85
----KFELYN-------FGIKINVASEKDINRLSDCQADF-VSRIRRKIFGKKKSF---------VSEKNDS 80

FIG. 4B


H.pylori futC EYEPKLLKPSR-LTYFFGYFQDPRYF--DAISPLIKQTFTLPPPPEN
H.mustelae futL EYMPELFEPSR-IAYFHGYFQDPRYF--EDISPLIKQTFTLPHPTEH
Bacteroides vulgatus futN SLRAFEKKYFWPLLYFKGFYQSERFF--ADIKDEVRESFTF----DK
E. coli 0126 wbgL GYDFEYIAQKWKSKKYIGYWQSEHFFHKHIL--DLKEFFI------P
Prevotella melaninogenica FutO YP_003814512.1 RFDESVLR-QEGNRYFDGYWQDERYF--AAYREKVLKAFTFPAFKRA
Clostridium bolteae+13 FutP WP_002570768.1 CYENDILR-M-DNVYLSGYWQTEKYF--SNTREKLLEDYSF-ALVNS
Lachnospiraceae sp. FutQ WP_009251343.1 NFDPLVME--KDPALLEGCFQSDKYF--RDCEGRVREAYRFRGIESG
Methanosphaerula palustris FutR YP_002467213.1 TFDKAILT-VPDNVYLDGYWQTEKYF--KDIEEILRREVTLKDEPDS
Tannerella sp. FutS WP_021929367.1 EFDEPVYRGLRPYRYYRGYWQNEGYFV--DIEPMIREAFQFNVNILS
Bacteroides caccae FutU WP_005675707.1 SFDAAVLT-RKGDCYYDGYWQHEEYF--CDMKETIWEAFSFPEPVDG
Butyrivibrio FutV WP_022772718.1 KFNPEILE--KENAYLVGYWQCDKYFDDKDVVREIREAFEKKPQE--
Prevotella sp. FutW WP_022481266.1 RMEPYTCQYVWPLVYFKGFYQSERYF--SEVKDEVRECFTF----NP
Parabacteroides johnsonii FutX WP_008155883.1 TLYPYEKRYFWPLLYFKGFYQSERFF--FDIKDDVRKAFSF----NL
Akkermansia muciniphilia FutY YP_001877555 GFDPGLAAPPRRHTYFKGYFQTEQYFL--HCREQLCREFRLKTPLTP
Salmonella enterica FutZ WP_023214330 FYTFETIKNIDKACLFSFYQDAD---LLNKYKQLILPLFELR---DD
Bacteroides sp. FutZA WP_022161880.1 SLRAFEKKYLWPLLYFKGFYQSERFF--ADIKDEVRKAFTF----DS
Clostridium bolteae FutP WP_002570768.1 CYENDILR-M-DNVYLSGYWQTEKYF--SNTREKLLEDYSF-ALVNS

FIG. 4C

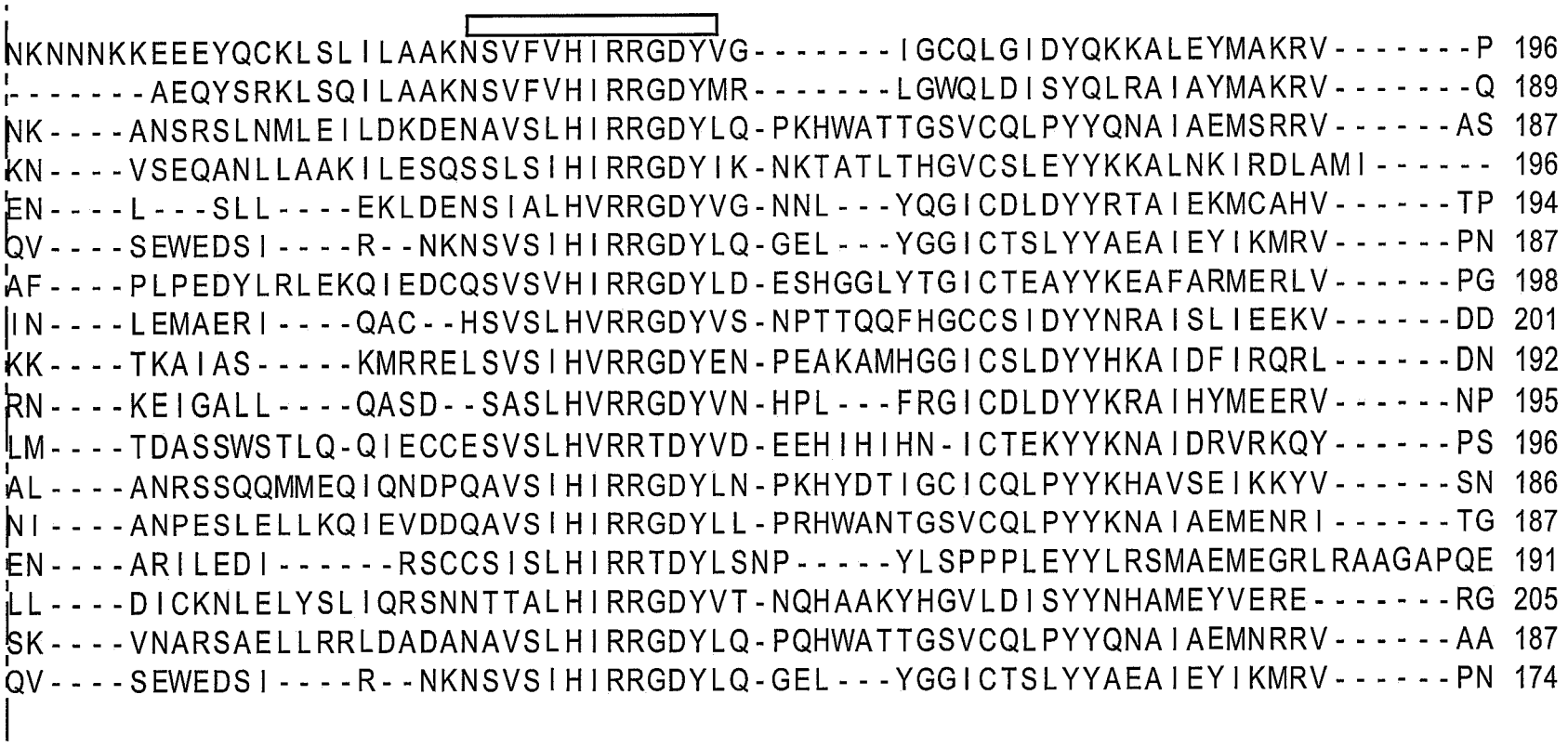

NKNNNKKEEEYQCKLSLILAAKNSVFVHIRRGDYVG-------IGCQLGIDYQKKALEYMAKRV-------P 196
-------AEQYSRKLSQILAAKNSVFVHIRRGDYMR-------LGWQLDISYQLRAIAYMAKRV-------Q 189
NK----ANSRSLNMLEILDKDENAVSLHIRRGDYLQ-PKHWATTGSVCQLPYYQNAIAEMSRRV------AS 187
KN----VSEQANLLAAKILESQSSLSIHIRRGDYIK-NKTATLTHGVCSLEYYKKALNKIRDLAMI------ 196
EN----L---SLL----EKLDENSIALHVRRGDYVG-NNL---YQGICDLDYYRTAIEKMCAHV------TP 194
QV----SEWEDSI----R--NKNSVSIHIRRGDYLQ-GEL---YGGICTSLYYAEAIEYIKMRV------PN 187
AF----PLPEDYLRLEKQIEDCQSVSVHIRRGDYLD-ESHGGLYTGICTEAYYKEAFARMERLV------PG 198
IN----LEMAERI----QAC--HSVSLHVRRGDYVS-NPTTQQFHGCCSIDYYNRAISLIEEKV------DD 201
KK----TKAIAS-----KMRRELSVSIHVRRGDYEN-PEAKAMHGGICSLDYYHKAIDFIRQRL------DN 192
RN----KEIGALL----QASD--SASLHVRRGDYVN-HPL---FRGICDLDYYKRAIHYMEERV------NP 195
LM----TDASSWSTLQ-QIECCESVSLHVRRTDYVD-EEHIHIHN-ICTEKYYKNAIDRVRKQY------PS 196
AL----ANRSSQQMMEQIQNDPQAVSIHIRRGDYLN-PKHYDTIGCICQLPYYKHAVSEIKKYV------SN 186
NI----ANPESLELLKQIEVDDQAVSIHIRRGDYLL-PRHWANTGSVCQLPYYKNAIAEMENRI------TG 187
EN----ARILEDI------RSCCSISLHIRRTDYLSNP-----YLSPPPLEYYLRSMAEMEGRLRAAGAPQE 191
LL----DICKNLELYSLIQRSNNTTALHIRRGDYVT-NQHAAKYHGVLDISYYNHAMEYVERE------RG 205
SK----VNARSAELLRRLDADANAVSLHIRRGDYLQ-PQHWATTGSVCQLPYYQNAIAEMNRRV------AA 187
QV----SEWEDSI----R--NKNSVSIHIRRGDYLQ-GEL---YGGICTSLYYAEAIEYIKMRV------PN 174

FIG. 4D


H.pylori futC NMELFVFCEDLEFT-QNLDLGYP---FMDMTTRDKEEEAYWDMLLMQ
H.mustelae futL NLELFLFCEDLEFV-QNLDLGYP---FVDMTTRDGA--AHWDMMLMQ
Bacteroides vulgatus futN PS-YYIFSDDIAWVKENL----PLQNAVYIDWNTDE-DSWQDMMLMS
E. coli 0126 wbgL -RDVFIFSDDIFWCKENIETLLSKKYNIYYSEDLSQEE---DLWLMS
Prevotella melaninogenica FutO YP_003814512.1 SL-FCIFSNDITWCQQHLQPYLKAP-VVYVTWNTGV-ESYRDMQLMS
Clostridium bolteae+13 FutP WP_002570768.1 AK-FFVFSDDVEWVKQQED----FKGFVIVDRNEYS-SALSDMYLMS
Lachnospiraceae sp. FutQ WP_009251343.1 AR-FFLFSNDPEWTREHFE----SKNCVLVEGSTED-TGYMDLYLMS
Methanosphaerula palustris FutR YP_002467213.1 PS-FFIFSDDLPWAKENLD--IPGEKT-FVAHNGPE-KEYCDLWLMS
Tannerella sp. FutS WP_021929367.1 NICFYLFSDDINWVEENLQL----ENRCIIDWNQGE-DSWQDMYLMS
Bacteroides caccae FutU WP_005675707.1 QL-YCVFSNDMAWCESHLRALLPGKEVVYVDWNKGA-ESYVDMRLMS
Butyrivibrio FutV WP_022772718.1 AV-FFIFTDDKEWCRDHFK----GPNFIVVELEEGDGTDIAEMTLMS
Prevotella sp. FutW WP_022481266.1 PH-FYVFSEDLDWVKANL----PLENAQYIDWNKGA-DSWQDMMLMS
Parabacteroides johnsonii FutX WP_008155883.1 PS-YYVFSDDISWVKENI----PLKKAVYVTWNKGE-DSWQDMMLMS
Akkermansia muciniphilia FutY YP_001877555 SLRYFIFSDDIEWARQNLRPALP---HVHVDINDG-GTGYFDLELMR
Salmonella enterica FutZ WP_023214330 KQNFIIFSDDVRWAQKAFLE----NDNCYVINNSDYDFSAIDMYLMS
Bacteroides sp. FutZA WP_022161880.1 PS-YYVFSDDIAWVKENI----PLQNAVYIDWNKGE-ESWQDMMLMS
Clostridium bolteae FutP WP_002570768.1 AK-FFVFSDDVEWVKQQED----FKGFVIVDRNEYS-SALSDMYLMS

FIG. 4E

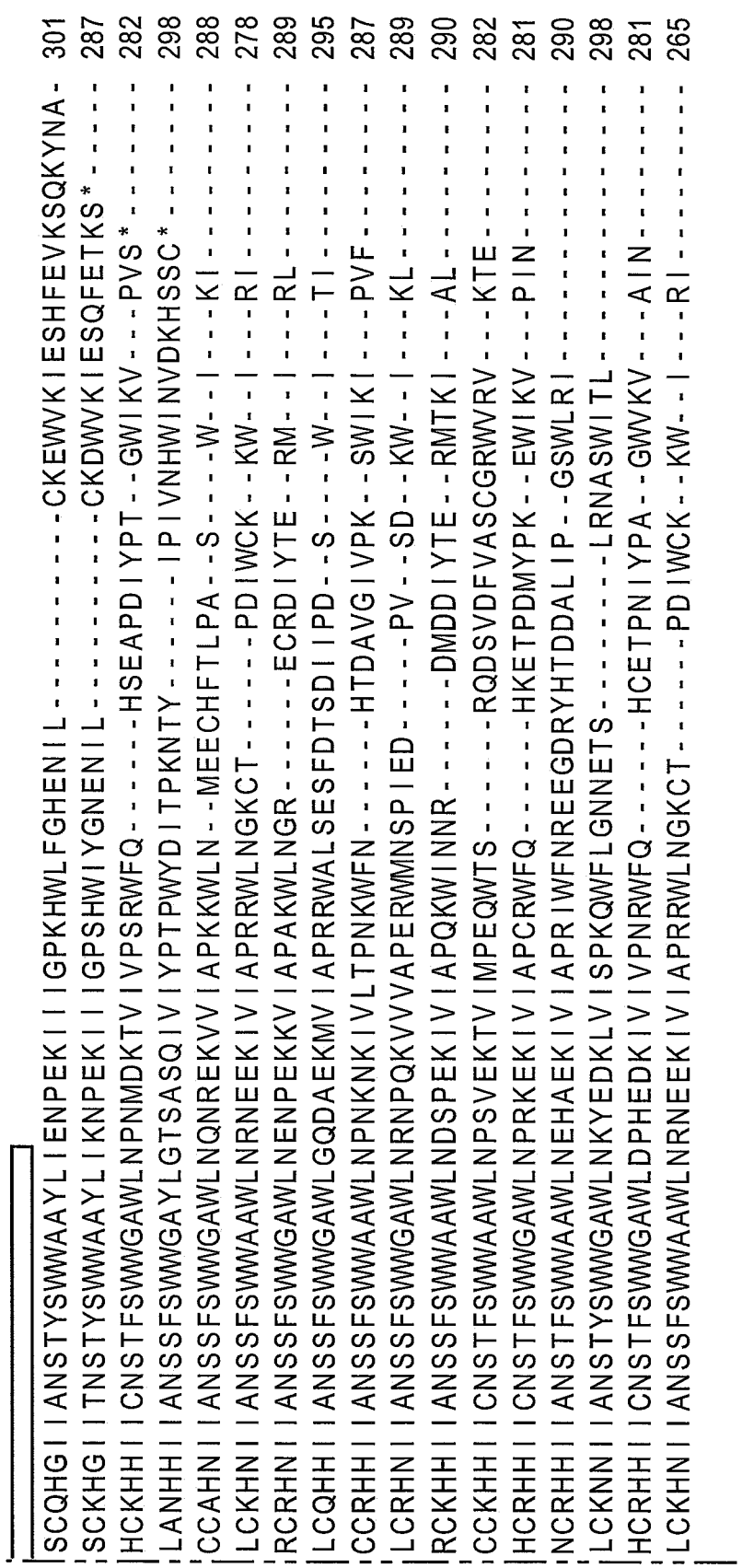

SCQHGIIANSTYSWWAAYLIENPEKIIIGPKHWLFGHENIL----------CKEWVKIESHFEVKSQKYNA- 301
SCKHGIITNSTYSWWAAYLIKNPEKIIIGPSHWIYGNENIL----------CKDWVKIESQFETKS*----- 287
HCKHHIICNSTFSWWGAWLNPNMDKTVIVPSRWFQ------HSEAPDIYPT--GWIKV---PVS*------ 282
LANHHIIANSSFSWWGAYLGTSASQIVIYPTPWYDITPKNTY------IPIVNHWINVDKHSSC*------ 298
CCAHNIIANSSFSWWGAWLNQNREKVVIAPKKWLN--MEECHFTLPA--S----W--I----KI---------- 288
LCKHNIIANSSFSWWAAWLNRNEEKIVIAPRRWLNGKCT------PDIWCK--KW--I----RI---------- 278
RCRHNIIANSSFSWWGAWLNENPEKKVIAPAKWLNGR------ECRDIYTE--RM--I----RL---------- 289
LCQHHIIANSSFSWWGAWLGQDAEKMVIAPRRWALSESFDTSDIIPD--S----W--I----TI---------- 295
CCRHHIIANSSFSWWAAWLNPNKNKIVLTPNKWFN------HTDAVGIVPK--SWIKI----PVF------- 287
LCRHNIIANSSFSWWGAWLNRNPQKVVVAPERWMNSPIED------PV--SD--KW--I----KL---------- 289
RCKHHIIANSSFSWWAAWLNDSPEKIVIAPQKWINNR------DMDDIYTE--RMTKI----AL---------- 290
CCKHHIICNSTFSWWAAWLNPSVEKTVIMPEQWTS------RQDSVDFVASCGRWVRV----KTE------- 282
HCRHHIICNSTFSWWGAWLNPRKEKIVIAPCRWFQ------HKETPDMYPK--EWIKV----PIN------- 281
NCRHHIIANSTFSWWAAWLNEHAEKIVIAPRIWFNREEGDRYHTDDALIP--GSWLRI---------------- 290
LCKNNIIANSTYSWWGAWLNKYEDKLVISPKQWFLGNNETS--------LRNASWITL---------------- 298
HCRHHIICNSTFSWWGAWLDPHEDKIVIVPNRWFQ------HCETPNIYPA--GWVKV----AIN------- 281
LCKHNIIANSSFSWWAAWLNRNEEKIVIAPRRWLNGKCT------PDIWCK--KW--I----RI---------- 265

FIG. 4F

FIG. 5A

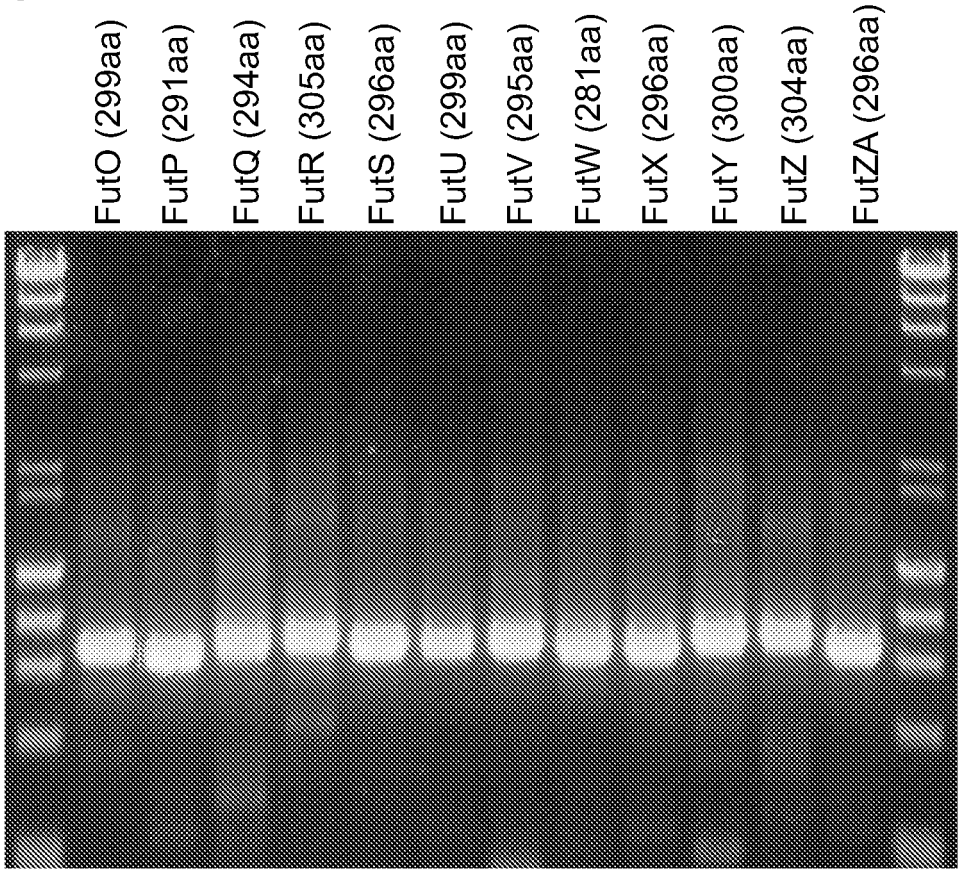
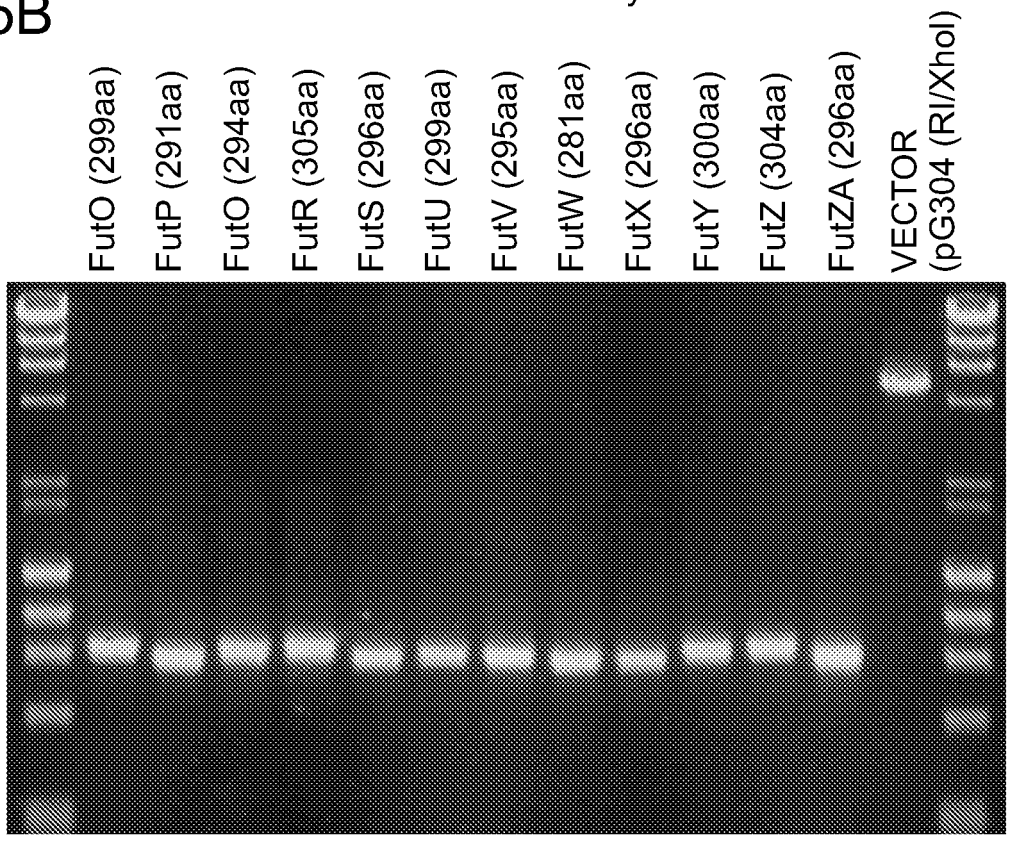

FutO (299aa)
FutP (291aa)
FutQ (294aa)
FutR (305aa)
FutS (296aa)
FutU (299aa)
FutV (295aa)
FutW (281aa)
FutX (296aa)
FutY (300aa)
FutZ (304aa)
FutZA (296aa)

FIG. 5B


Post-Gibson assembly PCR
FutO (299aa)
FutP (291aa)
FutO (294aa)
FutR (305aa)
FutS (296aa)
FutU (299aa)
FutV (295aa)
FutW (281aa)
FutX (296aa)
FutY (300aa)
FutZ (304aa)
FutZA (296aa)
VECTOR (pG304 (RI/XhoI)
Gel-purified RI/XhoI syngene fragment

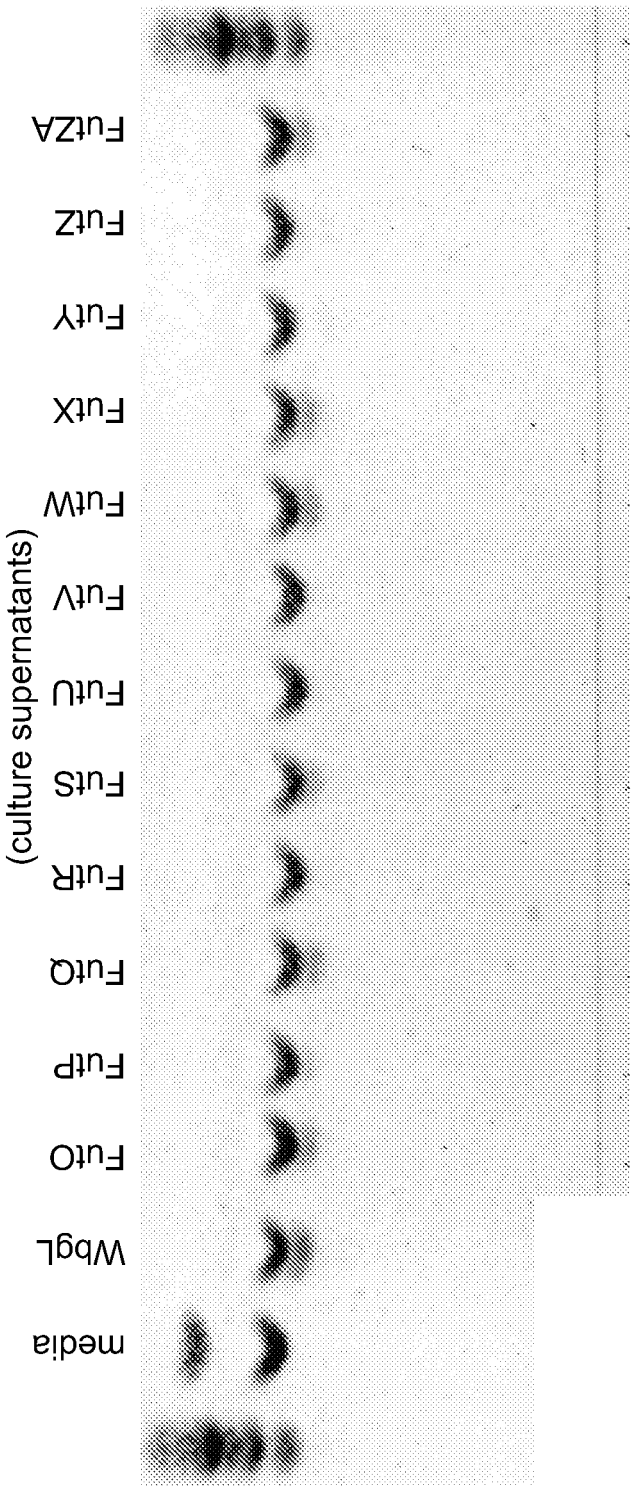

fuc
glc
gal
suc
tre
lac
2FL
(culture supernatants)
media
WbgL
FutO
FutP
FutQ
FutR
FutS
FutU
FutV
FutW
FutX
FutY
FutZ
FutZA

FIG. 6A

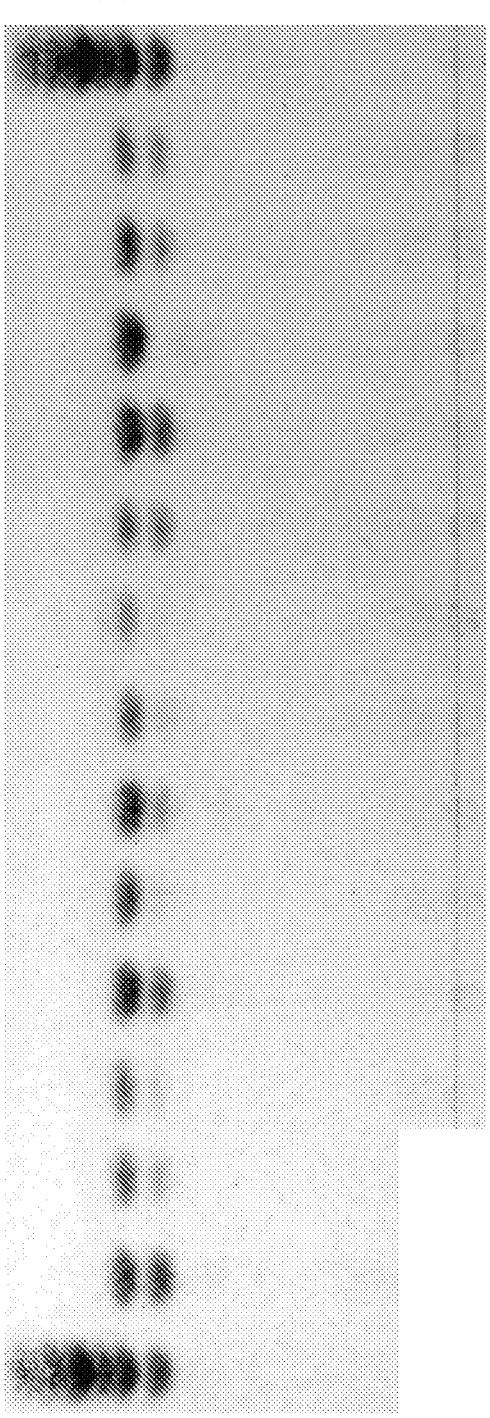

fuc
glc
gal
suc
tre
lac
2FL
(0.2 OD heat extracts)

FIG. 6B

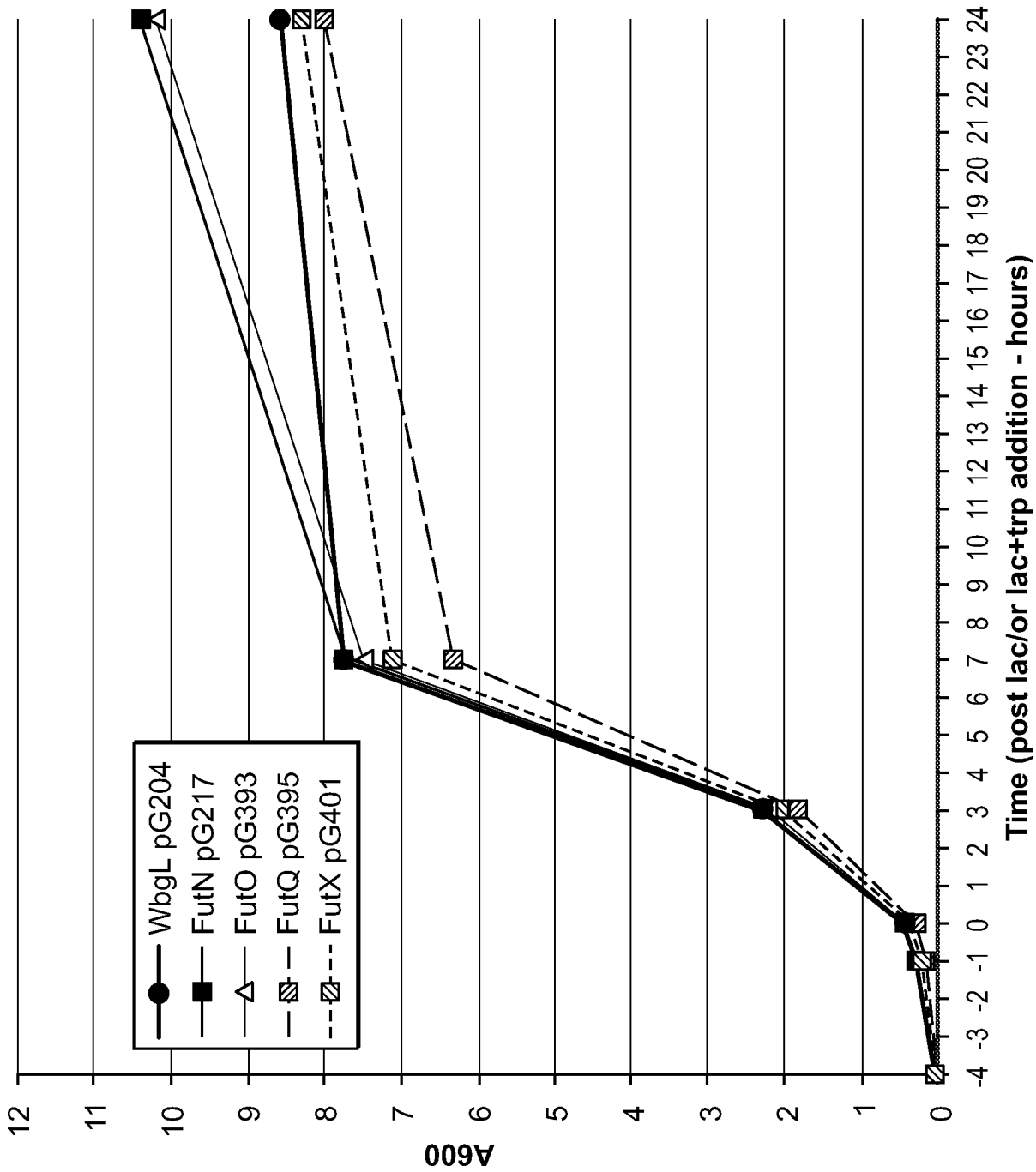

A600
Time (post lac/or lac+trp addition - hours)
WbgL pG204
FutN pG217
FutO pG393
FutQ pG395
FutX pG401

FIG. 7

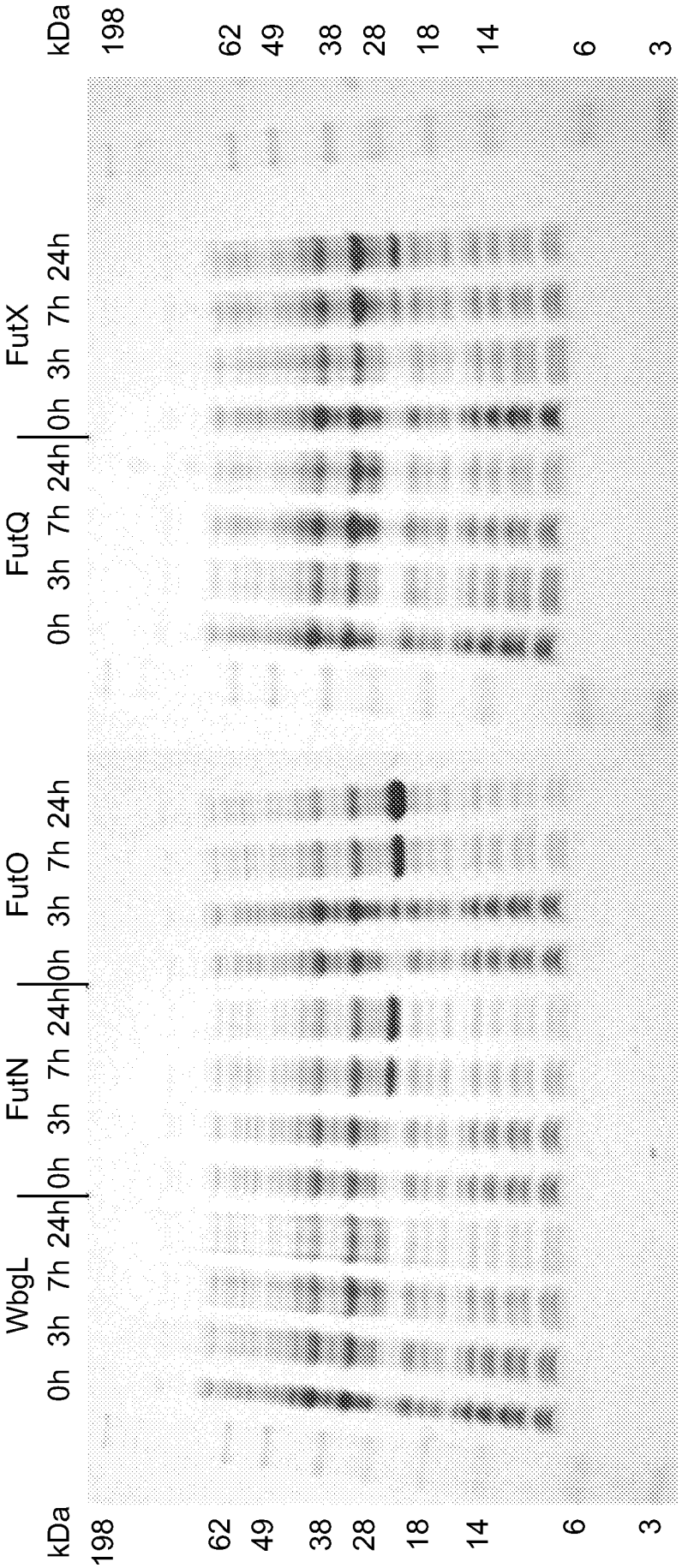

kDa
198
62
49
38
28
18
14
6
3
WbgL
0h 3h 7h 24h
FutN
0h 3h 7h 24h
FutO
0h 3h 7h 24h
FutQ
0h 3h 7h 24h
FutX
0h 3h 7h 24h

FIG. 8

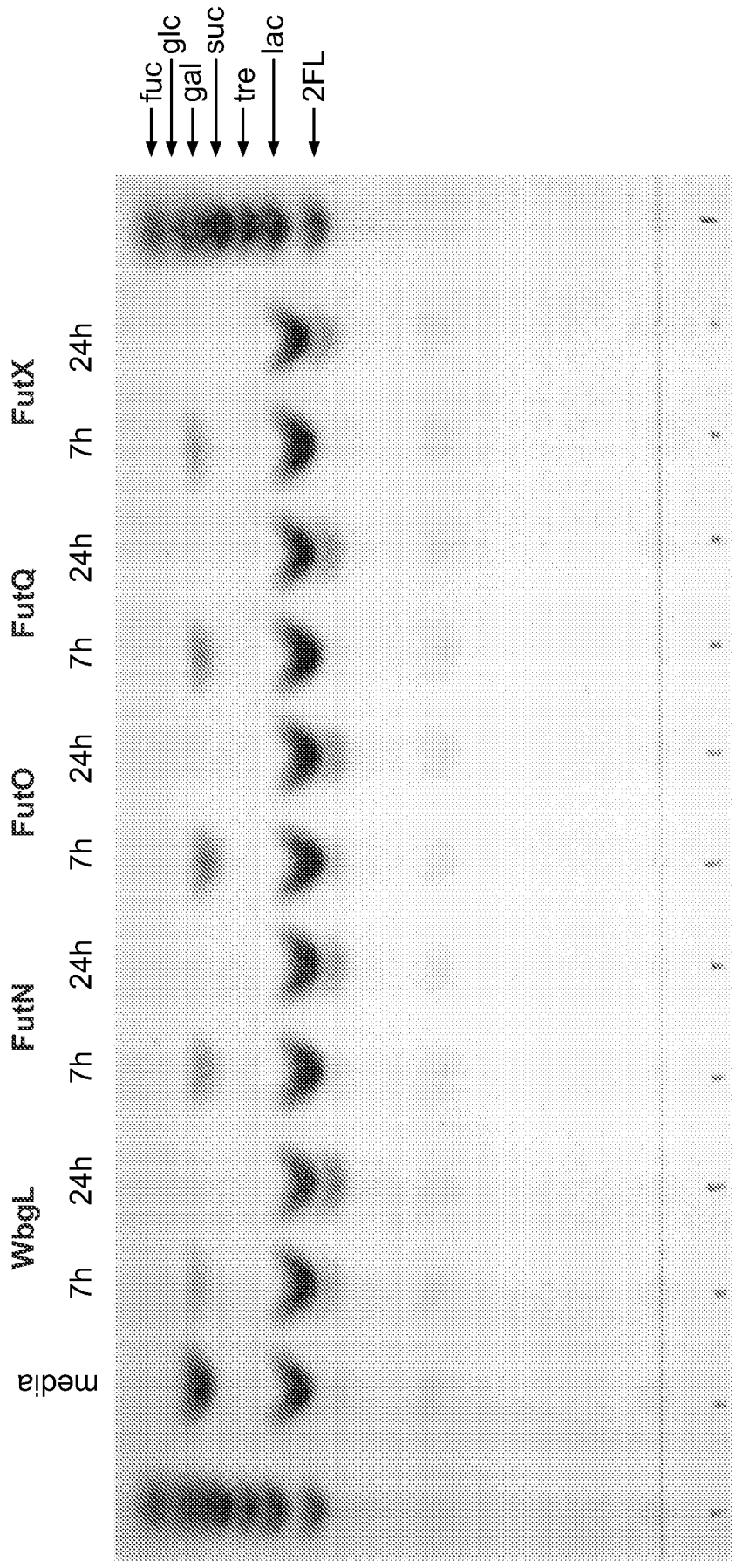
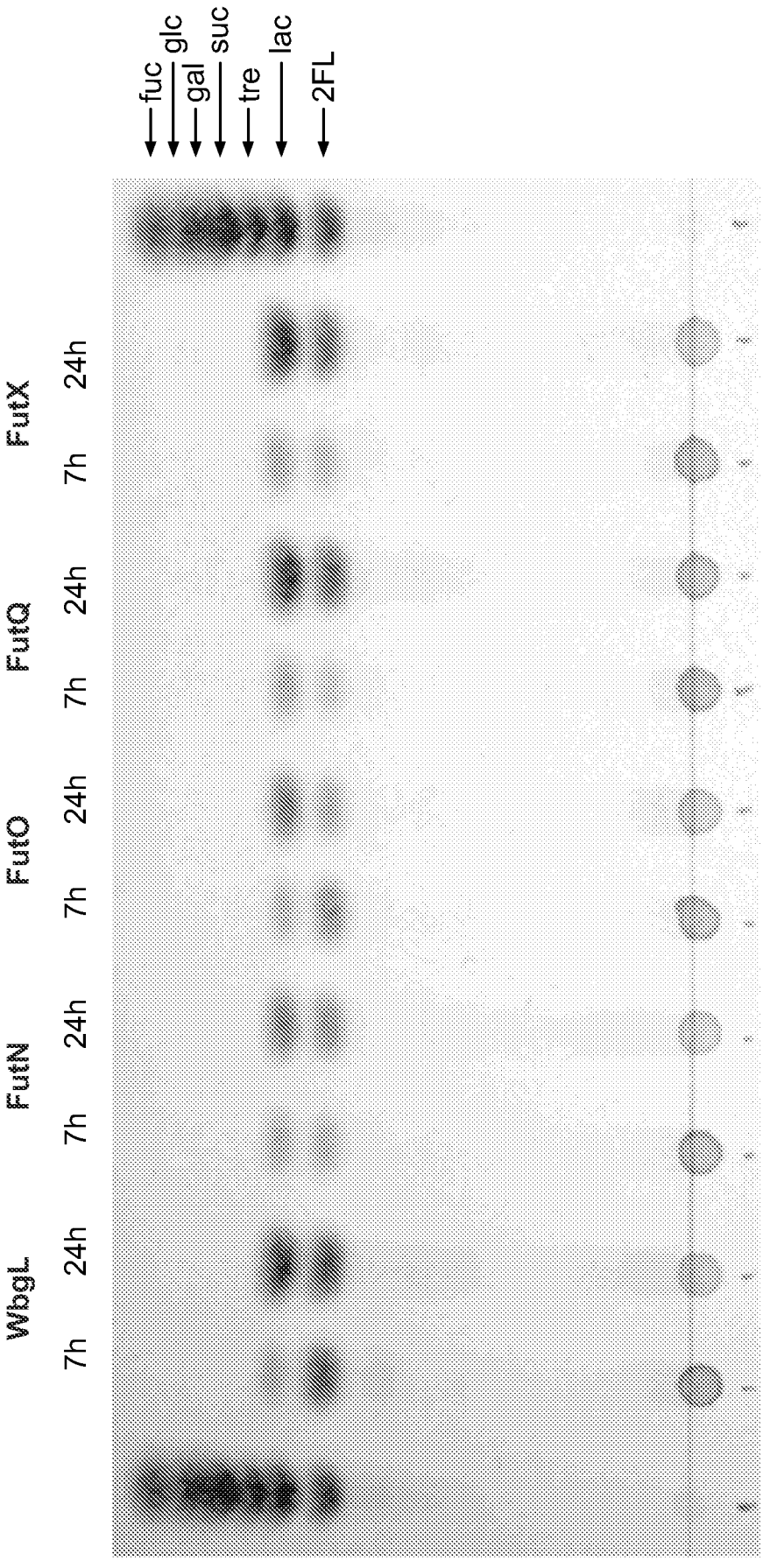

fuc
glc
gal
suc
tre
lac
2FL
media
7h
24h
WbgL
7h
24h
FutN
7h
24h
FutO
7h
24h
FutQ
7h
24h
FutX

FIG. 9A

FIG. 9B



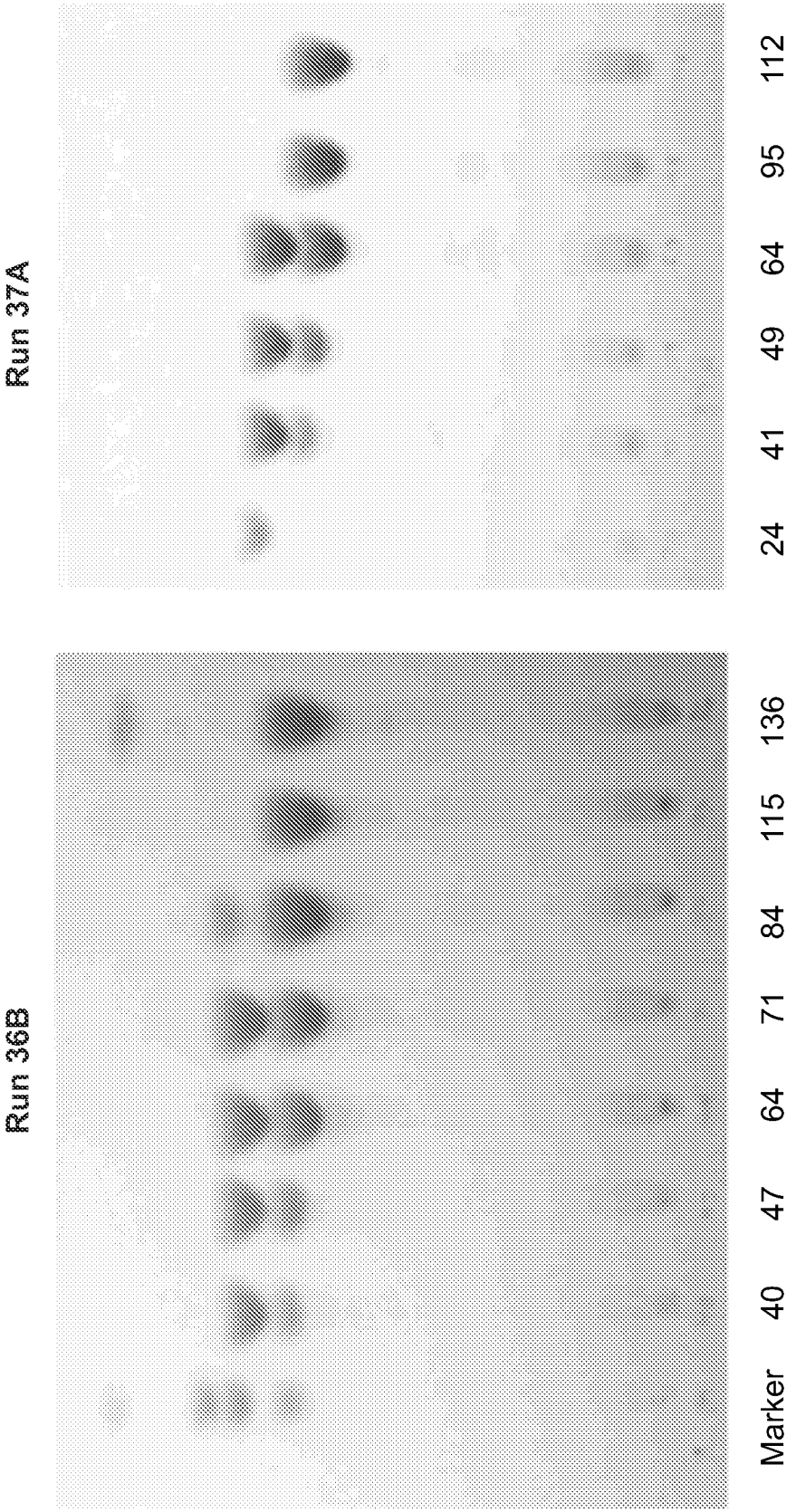


FIG. 10A

FIG. 10B

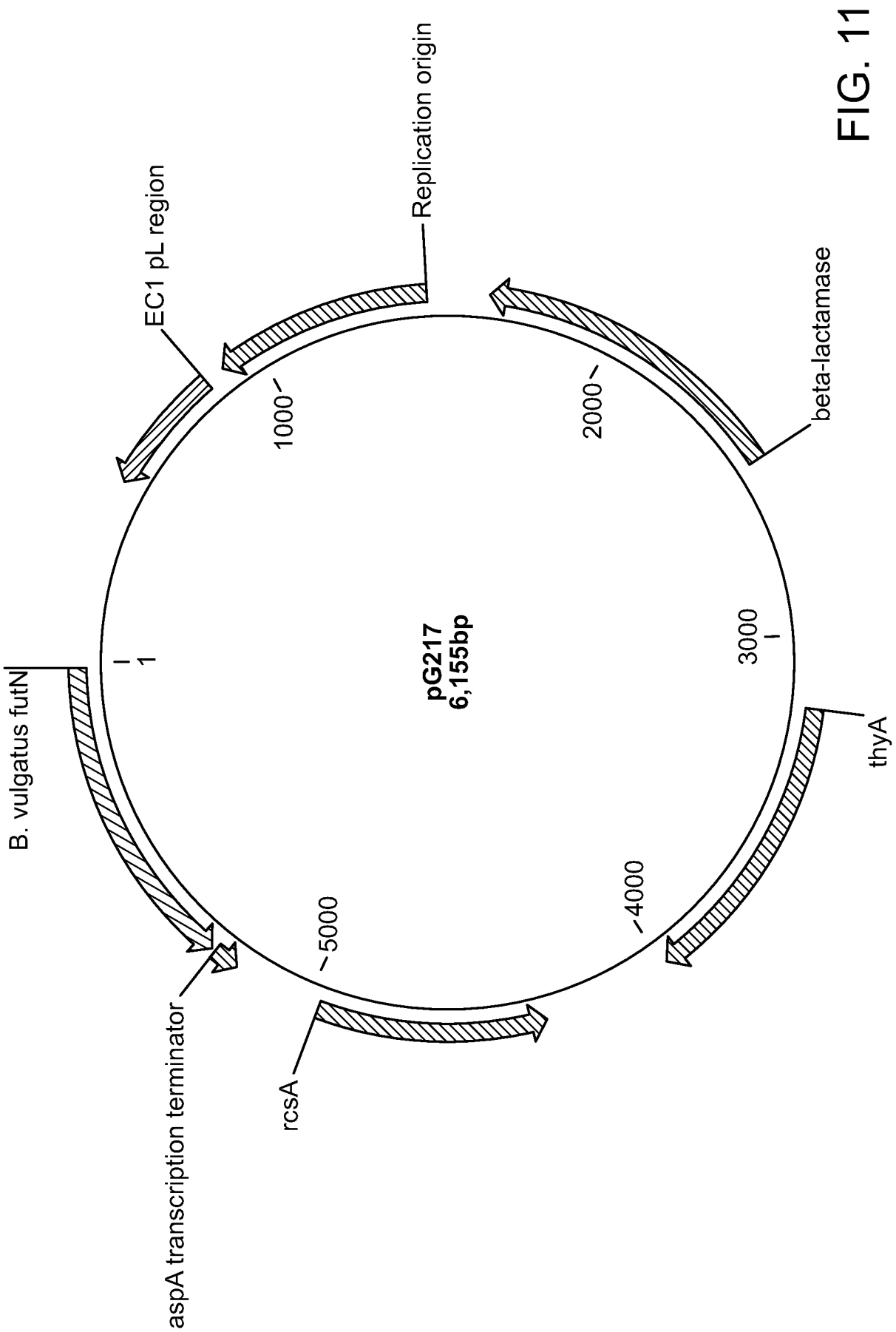

pG217
6,155bp
1
1000
2000
3000
4000
5000
Replication origin
beta-lactamase
thyA
rcsA
aspA transcription terminator
B. vulgatus futN
EC1 pL region

FIG. 11

FIG. 12

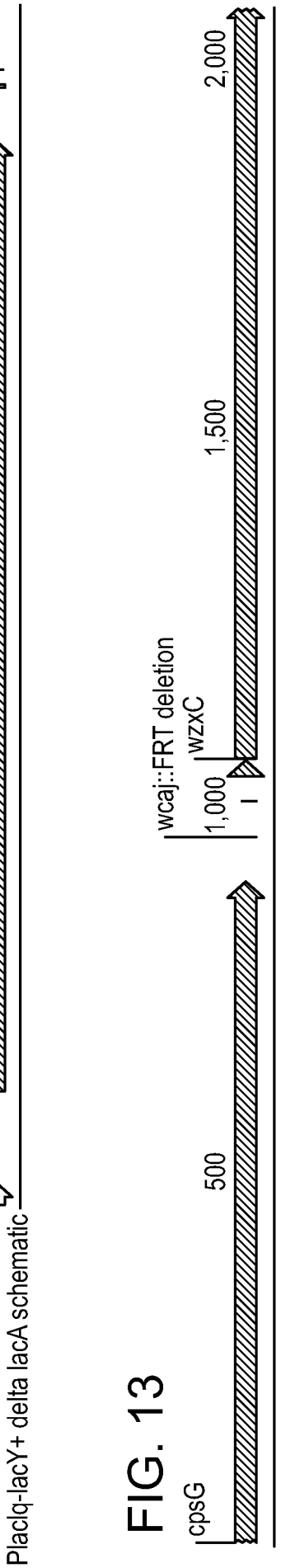


FIG. 13

FIG. 14

