Figure S1. A. Additional information on the identified *B. theta* TonB proteins. B and C. Sequence similarity via pairwise sequence alignment of full TonB protein (B) or C-terminal TonB domain as defined in Table 1 (C). The number of matches of the total alignment length is shown in parentheses.

A

Protein Name	Locus Tag	# of Predicted TMH	Location of Helices (residue #s)	Notes
TonB1	BT0813	5	4-26, 38-57, 93-155, 188-207, 274-296	
TonB2	BT1056	1 (low confidence prediction)	60-85	• Potential miscalled start due to overlap with BT1055
TonB3	BT1668	0		• SPI cleavage site between residues 19 and 20
TonB4	BT2059	1	15-37	
TonB5	BT2665	1	38-57	
TonB6	BT2762	1	16-38	
TonB7	BT3192	0		• Often annotated as TBDT due to PF13715
TonB8	BT3673	0		• At end of RG-II PUL3 (Ndeh 2017) • SPI cleavage site between residues 20 and 21
TonB9	BT3896	0		• Potential miscalled start due to overlap with BT3897
TonB10	BT3898	4	5-27, 39-93, 94-116, 275-297	
TonB11	BT4460	1	65-87	• Potential miscalled start due to overlap with BT4461 • Often annotated as TBDT due to PF13715

B

	BT1056 TonB2	BT1668 TonB3	BT2059 TonB4	BT2665 TonB5	BT2762 TonB6	BT3192 TonB7	BT3673 TonB8	BT3896 TonB9	BT3898 TonB10	BT4460 TonB11	*E. coli*
BT0813 TonB1	26.5% (131/494)	33.3% (166/499)	26.6% (131/492)	26.5% (132/498)	27.0% (126/467)	27.0% (126/467)	15.8% (93/589)	17.1% (96/563)	46.1% (289/627)	28.5% (160/562)	18.1% (91/504)
BT1056 TonB2		28.2% (113/400)	41.9% (125/298)	44.6% (137/307)	44.3% (132/298)	38.8% (119/307)	20.1% (86/427)	4.07% (134/329)	20.6% (133/646)	21.7% (107/492)	29.7% (89/300)
BT1668 TonB3			28.7% (107/373)	26.4% (107/406)	21.8% (89/409)	28.7% (108/376)	14.3% (71/495)	16.8% (82/489)	20.1% (135/671)	19.6% (112/572)	10.5% (50/474)
BT2059 TonB4				50.7% (144/284)	73.1% (166/227)	41.2% (117/284)	24.2% (93/384)	40.9% (122/298)	18.7% (122/652)	17.6% (87/494)	36.8% (100/272)
BT2665 TonB5					51.6% (141/273)	37.3% (116/311)	20.0% (85/425)	25.3% (99/392)	20.6% (140/681)	21.7% (108/497)	34.1% (101/296)
BT2762 TonB6						30.2% (97/321)	24.9% (94/378)	28.4% (101/356)	19.6% (124/632)	20.1% (94/468)	36.8% (95/258)
BT3192 TonB7							19.9% (80/402)	37.3% (116/311)	21.6% (133/616)	25.5% (121/474)	33.8% (95/281)
BT3673 TonB8								39.7% (129/325)	17.7% (122/689)	9.2% (56/609)	12.9% (54/420)
BT3896 TonB9									26.7% (165/618)	27.3% (131/479)	28.9% (98/339)
BT3898 TonB10										26.1% (182/698)	18.4% (114/618)
BT4460 TonB11											16.5% (85/514)

C

	BT1056 TonB2	BT1668 TonB3	BT2059 TonB4	BT2665 TonB5	BT2762 TonB6	BT3192 TonB7	BT3673 TonB8	BT3896 TonB9 TonB_C1	BT3896 TonB9 TonB_C2	BT3898 TonB10 TonB_C1	BT3898 TonB10 TonB_C2	BT4460 TonB11	*E. coli*
BT0813 TonB1	73.4% (58/79)	58.4% (45/77)	88.5% (69/78)	75.6% (59/78)	78.2% (61/78)	67.9% (55/81)	76.9% (60/78)	70.1% (54/77)	74.4% (58/78)	74.4% (58/78)	70.5% (55/78)	45.5% (35/77)	49.4% (39/79)
BT1056 TonB2		53.8% (42/78)	78.5% (62/79)	74.7% (59/79)	79.7% (63/79)	57.8% (48/83)	72.2% (57/79)	58.2% (46/79)	67.1% (53/79)	68.4% (54/79)	68.4% (54/79)	36.7% (29/79)	40.2% (33/82)
BT1668 TonB3			53.8% (42/78)	85.9% (67/78)	87.2% (68/78)	65.4% (53/81)	74.4% (58/78)	67.9% (53/78)	69.2% (54/78)	80.8% (63/78)	78.2% (61/78)	42.3% (33/78)	41.2% (33/80)
BT2059 TonB4				85.9% (67/78)	88.5% (69/78)	70.4% (57/81)	79.5% (62/78)	65.4% (51/78)	73.1% (57/78)	76.9% (60/78)	74.4% (58/78)	42.3% (33/78)	45.1% (37/82)
BT2665 TonB5					87.2% (68/78)	65.4% (53/81)	74.4% (58/78)	67.9% (53/78)	69.2% (54/78)	80.8% (63/78)	78.2% (61/78)	42.3% (33/78)	41.2% (33/80)
BT2762 TonB6						66.7% (54/81)	75.6% (59/78)	67.9% (53/78)	69.2% (54/78)	75.6% (59/78)	78.2% (61/78)	41.0% (32/78)	39.5% (34/86)
BT3192 TonB7							61.7% (50/81)	58.0% (47/81)	66.7% (54/81)	61.7% (50/81)	61.7% (50/81)	45.7% (37/81)	46.9% (38/81)
BT3673 TonB8								65.4% (51/78)	66.7% (52/78)	70.5% (55/78)	65.4% (51/78)	39.7% (31/78)	40.0% (32/80)
BT3896 TonB9 TonB_C1									62.8% (49/78)	64.1% (50/78)	60.3% (47/78)	41.6% (32/77)	43.8% (35/80)
BT3896 TonB9 TonB_C2										70.5% (55/78)	70.5% (55/78)	46.2% (36/78)	43.9% (36/82)
BT3898 TonB10 TonB_C1											73.1% (57/78)	41.0% (32/78)	41.0% (34/83)
BT3898 TonB10 TonB_C2												42.3% (33/78)	43.8% (35/80)
BT4460 TonB11													37.8% (28/74)

Figure S2. Multiple sequence alignment of the eleven identified TonB proteins from *B. thetaiotaomicron* with *E. coli* TonB and *Pseudomonas aeruginosa* TonB1. Highly conserved residues discussed in the text are highlighted in yellow, deviations from this conservation are highlighted in green.

```
Pseudomonas_aeruginosa_TonB1        ------------------------------------------------------------      0
Escherichia_coli_TonB               ------------------------------------------------------------      0
BT4460                              ------------------------------------------------------------      0
BT1668                              -------MKKIVISLLLLTLSFRLSAQ-----------------IDYLEPVKPFTTYT--      34
BT3896_Nterm_plus_TonB_Domain1      ------------------------------------------------------------      0
BT3192                              ------------------------------------------------------------      0
BT1056                              ------------------------------------------------------------      0
BT3673                              ------------------------------------------------------------      0
BT2059                              ------------------------------------------------------------      0
BT0813                              MESFAIYLIKVNIALIVLYAFYKLSFSKDTFFRLRRIMLLLICVTSLIYPLIDFSGWTDE      60
BT3896_TonB_Domain2                 ------------------------------------------------------------      0
BT3898_Nterm_plus_TonB_Domain1      MTPELAYFLKINVAIALFYAFYRLFFHKDTFFHWRRTALLCFFGISLLYPLLNIQEWIKE      60
BT2665                              ------------------------------------------------------------      0
BT2762                              ------------------------------------------------------------      0
BT3898_TonB_Domain2                 ------------------------------------------------------------      0

Pseudomonas_aeruginosa_TonB1        ------------------------------------------------------------      0
Escherichia_coli_TonB               ------------------------------------------------------------      0
BT4460                              ------------------------------------------------------------      0
BT1668                              ---------------------------------------------------G--------      35
BT3896_Nterm_plus_TonB_Domain1      ------------------------------------------------------------      0
BT3192                              ------------------------------------------------------------      0
BT1056                              ------------------------------------------------------------      0
BT3673                              ------------------------------------------------------------      0
BT2059                              ------------------------------------------------------------      0
BT0813                              YAIGETFTTVYNKL-LPEVLVTTALPVATTEVEVTTWQAG--TWLWIIYGLGIGMLLLRN      117
BT3896_TonB_Domain2                 ------------------------------------------------------------      0
BT3898_Nterm_plus_TonB_Domain1      QEPMVAMADLYATIILPEQIIEAP------QETTANWQELIPQILGFIYWTGVLLLALRF      114
BT2665                              ------------------------------------------------------------      0
BT2762                              ------------------------------------------------------------      0
BT3898_TonB_Domain2                 ------------------------------------------------------------      0
```

```
Pseudomonas_aeruginosa_TonB1        ------------------------------------------------------------      0
Escherichia_coli_TonB               ------------------------------------------------------------      0
BT4460                              -MKLLDYIRG-------LRKGKEAHRLEKESMKDPFLADAMDGYHQVEGDHEEQINKLRM      52
BT1668                              --ELGEYYRNVFSL------------LNTGFQQRPYARFVAIP---S--FSPEYA-----      71
BT3896_Nterm_plus_TonB_Domain1      ------------------------------------------------------------      0
BT3192                              ------------------------------------------------------------      0
BT1056                              --------------------------MKRGKQTCKILKDIR-------------------      15
BT3673                              ------------------------------------------------------------      0
BT2059                              -------------------------------------------------------MEVKK      5
BT0813                              LLEVSKIHRSLVCSQRYSLKGVPVYQSEDVGEPCSFFHWIFIN---PMQYSDKEINEILI      174
BT3896_TonB_Domain2                 ------------------------------------------------------------      0
BT3898_Nterm_plus_TonB_Domain1      LIQLGSIIRLHFLCPKSTIQGSRVHILKKGTGPFSFFHWIFIH---PESHTESEISEIIT      171
BT2665                              ------------------------------------------------------------      0
BT2762                              ------------------------------------------------------------      0
BT3898_TonB_Domain2                 ------------------------------------------------------------      0

Pseudomonas_aeruginosa_TonB1        ------------------------------------------------------------      0
Escherichia_coli_TonB               ------------------------------------------------------------      0
BT4460                              KVNAHSAKKRNTYAVTWSIAACLIIGIGISSYFLFLK-----Q--NVGEDVFIAKEQPAA      105
BT1668                              ---MSVEK---------KNGRCLLIANTLSRTYWQAEK---------GTV------KVET      104
BT3896_Nterm_plus_TonB_Domain1      ------------------------------------------------------------      0
BT3192                              -----------------MKRLSFILSFIV---CICV------------------------      16
BT1056                              ---RQIAE---------ANDIE-----FITSEC---------------------------      31
BT3673                              ------------------------------------------------------------      0
BT2059                              SPKADLEG---------KKSTWLLIGYVVVLAFMFVAFEWTQRDVKIDTSQAVA------      50
BT0813                              HEQTHVRE---------LHSLDIILVQLVILLCWFNPFSWLIRSEIRMNHEYLADKQVVT      225
BT3896_TonB_Domain2                 ------------------------------------------------------------      0
BT3898_Nterm_plus_TonB_Domain1      HEETHARQ---------YHSADVLVSEIMCTFCWFNPFVWLMKREVRGNLEYMADHRVLE      222
BT2665                              -----------------------MAKLDLASSEWCQ-LIF--------------------      16
BT2762                              ---------------------------------------M--------------------      1
BT3898_TonB_Domain2                 ------------------------------------------------------------      0

Pseudomonas_aeruginosa_TonB1        -----------------MSPQPSR---SPDRFSLAALAEDHPTAPAQGDE----SESLPC      36
Escherichia_coli_TonB               ------------------------------------------------------------      0
BT4460                              TATVPAHKEDTSLSAPKMEPDSGRPSATKETVGKDIIAKTRQDSPSQSTPSGAPSATVPK      165
BT1668                              K-------------------------------SVE-------ISQSLYQS----------      116
BT3896_Nterm_plus_TonB_Domain1      ------------------------------------------------------------      0
BT3192                              ------------------------------------------------------------      16
BT1056                              --------------------------------------------QYQGDC----------      37
BT3673                              ------------------------------------------------------------      0
BT2059                              ------------------------------------------------------------      50
BT0813                              S-------------------------------GYD-------KKSYQYHL----------      237
BT3896_TonB_Domain2                 ------------------------------------------------------------      0
BT3898_Nterm_plus_TonB_Domain1      T-------------------------------GHD-------SKSYQYHL----------      234
BT2665                              E-------------------------------GKN-------QAYGAYR-----------      27
BT2762                              E-------------------------------AKK-------SKKAA-------------      10
BT3898_TonB_Domain2                 ------------------------------------------------------------      0
```

```
Pseudomonas_aeruginosa_TonB1        VN---------AQRGEPNLRVV------------------DCSGARRDE----EVAVEEV      65
Escherichia_coli_TonB               ------------------------------------------------------------      0
BT4460                              AVASKAATPQATPAGTPIMEEMVAPAEELEEAAITTVTDTSFLDANRKKMKAAQ------      219
BT1668                              ------------------------------------------LGAIARL-----------      123
BT3896_Nterm_plus_TonB_Domain1      ------------------------------------------------------------      0
BT3192                              ----------------------------------------------------AN---TND      21
BT1056                              ------------------------------------------LGTCPKCE--AEVR----      49
BT3673                              ------------------------------------------------------------      0
BT2059                              -----------------------------------------------------DVVFEEE      57
BT0813                              ------------------------------------------LGIKHTSLAAANFYNNFS      255
BT3896_TonB_Domain2                 ------------------------------------------------------------      0
BT3898_Nterm_plus_TonB_Domain1      ------------------------------------------LGLAHHKA-AANLSNSFN      251
BT2665                              ------------------------------------------------------------      27
BT2762                              ------------------------------------------------------------      10
BT3898_TonB_Domain2                 ------------------------------------------------------------      0


Pseudomonas_aeruginosa_TonB1        LIPYA--HGSDPEDVPGEPPKSRWWLSSGAAVAMHVAIIGALVWVMPTP-----------      112
Escherichia_coli_TonB               --------------MTLDLPRRFPWPT-LLSVCIHGAVVAGLLYTSVHQ-----------      34
BT4460                              ---LTTQMNNMIKGKVTDD--RG------E------PLVGANVTY-----------KGAT      251
BT1668                              ---VTSQI-QDLDGSTAGL-------------------DGVVYYF---SS----------      147
BT3896_Nterm_plus_TonB_Domain1      -----MKH-QQL--SRANGTKRPFLLA-LI-------------AF-SLGFC---------      28
BT3192                              VFSQKREL-QQFKGKVTNL-------Q-GE------PVRAVSIYI-PGTGRYT-------      58
BT1056                              --YLE----QQLERKRM----AGKAIT-IL------GISAGLVAMAPMTSCSSSPNKGTN      92
BT3673                              ------------------------------------------------------------      0
BT2059                              IIPITETP-EQATPPPPEA----------P------KVAE-LLEI--VDDQ---------      88
BT0813                              VLPLKKRI-KMLNRKRTHNIMVGKYLM-FI------PVAA-LLLL--FSNCAN--KKA--      300
BT3896_TonB_Domain2                 ------------------------------------------------------------      0
BT3898_Nterm_plus_TonB_Domain1      VLPLKNRI-KMMNKRRTKEIGRTKYLM-FL------PLAA-LLMI--ISN----------      290
BT2665                              --------------MRANSPRRHTIAM-LI------VVAI---AI--VGFTIP--TL---      56
BT2762                              ----------------IENQRGSWLLM-GL------VVAL-AFMF--VSFEWT--QHD--      40
BT3898_TonB_Domain2                 ------------------------------------------------------------      0

                                                                            Proline-rich linker
Pseudomonas_aeruginosa_TonB1        --------AELNLGHGELPKTMQVNFVQL-EKKAEP----TPQPPAAAP-EPTPPKIEEP      158
Escherichia_coli_TonB               ---------VIELPAPA--QPISVTMVTP-ADLEPPQAVQPPPEPVVEP-EPE----PEP      77
BT4460                              YGAITDINGEFSLPKKEGNEILTAHYIGY-----NP--VSIP-ADTSKNMLIA---MSEN      300
BT1668                              ----TDAKG------KEMMGRKWSPMKGTLMERLVL--VCQSTYMFSQGENISEQALAEE      195
BT3896_Nterm_plus_TonB_Domain1      ------------------------HYA---------------------------------      31
BT3192                              ---SSDMNGDFSVEAKHKETLRFSHIG---M-----------------------------      83
BT1056                              QETISDSTN---------ASVMFGEI-------------CPTPVE------DTIP-MVEK      123
BT3673                              ------------------------------------------------------------      0
BT2059                              ----ADIEEST-------------------------------------T-----------      96
BT0813                              DKVQSDTEKAD-------------------------------------T-----------      312
BT3896_TonB_Domain2                 ------------------------------------------------------------      0
BT3898_Nterm_plus_TonB_Domain1      IEVVARTTK---------------EFAKEMM-------AAPEEQGVSQTELANGP-----      323
BT2665                              LKLATPEQKEVMTEVTTLSKLAEPEIKQEEMKRVEP--VAPPPPALKSSIKFTAP-VIKK      113
BT2762                              VRVAAVSSDDESIFVTELVPITFPE------EKLE----PPPPPETKVTELFE---IVDD      87
BT3898_TonB_Domain2                 ------------------------------------------------------------      0
```

```
                                      Proline-rich linker
Pseudomonas_aeruginosa_TonB1        KPEPPKPKP--VEKPKPKPKPKPK--------PVENAIPKAKPKPEPKPKPEPEPSTEAS      208
Escherichia_coli_TonB               IPEPPKEAPVVIEKPKPKPKPKPK--------PVKKVQEQPKR--DVKPV------ES--      119
BT4460                              KT-TLDEVVVTG---YGA-QKKVAVTGAISAVSIKDLKKASG-------A--LQKSDT--      344
BT1668                              ATALLKELE-HRTKEQPDAHKKPMYVGIYSVGPKL-------------------KT----      231
BT3896_Nterm_plus_TonB_Domain1      ------EAKVQPTEAFTSN--------------V--------------DSLIINDNNK--      55
BT3192                              -----KDVLIQLDKDFPSELLVRMKPDTFQINNI---FIQKK-------QIIKVKPED--      126
BT1056                              DTVNKQE-----LPELPQ-E-----MGLIEITPISGDIITVK----------DSLSEK--      160
BT3673                              ---------------MNTK--------------LFGLFIALLV--CLPSLAQQKPVEK--      27
BT2059                              ---------------------------------ILNEDNTPKV--EVKYVPVQVVEEE--      119
BT0813                              ---------------------------------IELTA-EPE---KTAEPQVDITITE--      333
BT3896_TonB_Domain2                 ------------------------------------------------------------      0
BT3898_Nterm_plus_TonB_Domain1      --------------ELPDGM-----TGVATLQDKKGMQKTKEV--APPPPPAPVKSAT--      360
BT2665                              DEEVHEDDEIKSQEELTSTK-----V-AISIADVKGNDEANGA--DIADLK-QVVTQA--      162
BT2762                              TEEVTDNVSVVPD-------------------NV--N---EPY--KVVWVPPVVETKE--      119
BT3898_TonB_Domain2                 ------------------------------------------------------------      0

                                                                                     C-term domain begins
Pseudomonas_aeruginosa_TonB1        SQPSPSSAAPPPAPTVGQSTPGAQTAPSGSQGPAGLPSGSLNDSDIKPLRMDPPVYPRMA      268
Escherichia_coli_TonB               RPASPFENTAPARPTSS-------TATAAT----SKPVT-SVASGPRALSRNQPQYPARA      167
BT4460                              ----------LKDAVISQK--------ADSLQGPVVPEPVTGMKQYKKYLKKNLAYPADD      386
BT1668                              ----------HS-----------------GKQIEELPCL--ADVCVREYVAGQMIYPAEL      262
BT3896_Nterm_plus_TonB_Domain1      ----------DKDETI-------------YEAVDEMPKFPGGTQALFKYLGENIQYPEEV      92
BT3192                              ----------MPEQTM-------------INFIINGPDFPGGLSGFDEFIKKNIQYPEEA      163
BT1056                              ----------DSLTDV-------------LEVAAVMPEFPGGARELMKFISANIRYPSMS      197
BT3673                              ----------VDSDGV-------------YLMPDQMPEFPGGMQAMMKFLTTNIKYPVEA      64
BT2059                              ----------PEEQTI-------------FEVVENMPDFPGGQAALMQYLAKNIKYPTIA      156
BT0813                              ----------TKGDSI-------------YSVVETMPDFPGGQKELLSFLSRNIKYPTKA      370
BT3896_TonB_Domain2                 ----------------------------------------------------HITYWKNA      8
BT3898_Nterm_plus_TonB_Domain1      ----------VNDSVV-------------FEVVEEMPDFPGGQSALMEYLAKNIKYPATA      397
BT2665                              ----------AEPEKV-------------FDMVEQMPTFPGGQQELMSYLGKNIKYPTIA      199
BT2762                              ----------VEEDVI-------------HVSVEVMPEFPGGSAELLKYLSTHIKYPTMS      156
BT3898_TonB_Domain2                 ----------------------------------------------------NIKYPTMA      8
                                                                                           *
```

```
Pseudomonas_aeruginosa_TonB1        QARRIEGRVKVLFTITSDGRIDDIQVLESVPSRMFDREV--RQAMAKWRFEPRVSGGKIV      326
Escherichia_coli_TonB               QALRIEGQVKVKFDVTPDGRVDNVQILSAKPANMFEREV--KNAMRRWRYEPGKPGSGIV      225
BT4460                              ACAEVKGKVTLTFFVNKEGRPFDIKVKESLCKSLDKEAIRLIQEGPDWTYGN--QS-AEI      443
BT1668                              LKDNVSGYALCEFTIDKEGVILRPHILKSTHPEFAEEALRIVKEMPNWTPAL--VGGKAV      320
BT3896_Nterm_plus_TonB_Domain1      QKLGIAGRVITQFVISKKGEITSVAVVRSLHPELDKQAIQAITAMPTWTPGK--KDGKVV      150
BT3192                              FQAGEEGQVTVEFTIDVNGYVSDAKVTKSVSASLDKEALRIIESMPRWKSGM--QLGRPV      221
BT1056                              QGGVCQGRAIVQFIVDKEGNIVQPKVVRGVDPYLDKEALRVVGLMPKWKPGEL-DDGTKV      256
BT3673                              QKKGVSGRVIVQFVIMEDGTLDQAKVVRGVDPLLDEEALRVVKLMPKWKPGM--DRGEAV      122
BT2059                              QENGTQGRVIVQFVVNKDGSIVDAKVVRSVDPYLDKEALRVINTMPKWKPGM--QRGKPV      214
BT0813                              IENKIQGRVIVQFVVNKDGSIFGAKVVRSVDPDLDKEALRVINSMPKWKPGM--QKGEPV      428
BT3896_TonB_Domain2                 AKQKEEGRVIVTFIVRKDGQITDARVVRSVSPTLDAEALRIISNMPKWEPGE--NNGVPV      66
BT3898_Nterm_plus_TonB_Domain1      HENGKQGRVIVMFVVKKDGSISDVKTVRGVDPYLDKEAERVIAAMPNWKPGK--QRGQAV      455
BT2665                              QENGTQGRVIIQFVVERDGTITDVHVARGVDPYLDKEAVRVVQSMPKWIPGK--QNGKAV      257
BT2762                              QEMGSQGRVIVQFVVDKDGSITNPTVVRGVDAYLDKEAIRVISGMPKWKPGV--QNGKKV      214
BT3898_TonB_Domain2                 QQNKEQGKVLVQIVIGKDGNVSNIKILEGASAWLDAEAIRVVRGMPKWEPGK--QNGQAV      66
                                          * .   : :  .*         .    :  .          *           :
```

3rd β-sheet for paring with TonBox

```
Pseudomonas_aeruginosa_TonB1        ARQATKMFFFKIEKRR--------------------------------------------      342
Escherichia_coli_TonB               VNI-----LFKINGTTEIQ-----------------------------------------      239
BT4460                              TVKFHK------------------------------------------------------      449
BT1668                              ESDYTLYVPFRPQLYKEQLQIRERELSKKH------------------------------      350
BT3896_Nterm_plus_TonB_Domain1      NVKFTLPINFHPTPAATTKATGEQ--------QPDST--------------------TDK      182
BT3192                              AVRMSVPINFVIEQDYQVIDSLQV---KTNT-----------------------------      249
BT1056                              AVRFTIPVMFRLQ-----------------------------------------------      269
BT3673                              KVRFTAPIMFNLSRSEAQRPTFPELVVPIGQEVENRSLQGVWQSCVVQPGEHGYKILLLP      182
BT2059                              RVKFTVPVMFRLQ-----------------------------------------------      227
BT0813                              SVKFTVPIVFRNQLN---------------------------------------------      443
BT3896_TonB_Domain2                 SVKYTIPIMFRLR-----------------------------------------------      79
BT3898_Nterm_plus_TonB_Domain1      NVRFTVPVTFRLSGPEPAKPAETPEAVAIEKFEE-V--------VVVGYGPKEATPNNEP      506
BT2665                              RVKFTVPVMFRLQ-----------------------------------------------      270
BT2762                              RVKYTVPVVFRLQ-----------------------------------------------      227
BT3898_TonB_Domain2                 AVEYTFPITFRLQ-----------------------------------------------      79

Pseudomonas_aeruginosa_TonB1        ------------------------------------------------------------      342
Escherichia_coli_TonB               ------------------------------------------------------------      239
BT4460                              ------------------------------------------------------------      449
BT1668                              ------------------------------------------------------------      350
BT3896_Nterm_plus_TonB_Domain1      VFMTAQKMPRFPK----E---QGELDQYLKQ-----------------------------      206
BT3192                              ------------------------------------------------------------      249
BT1056                              ------------------------------------------------------------      269
BT3673                              VLKIVSPDQTFMNIMTAGMNGRSNAIIYCQGEYSLPSDGTYVEMVEKSVDPVFIQGVKNE      242
BT2059                              ------------------------------------------------------------      227
BT0813                              ------------------------------------------------------------      443
BT3896_TonB_Domain2                 ------------------------------------------------------------      79
BT3898_Nterm_plus_TonB_Domain1      TFKVVDEMPKF----PGG---QEGLMRYLAK-----------------------------      530
BT2665                              ------------------------------------------------------------      270
BT2762                              ------------------------------------------------------------      227
BT3898_TonB_Domain2                 ------------------------------------------------------------      79
```

```
Pseudomonas_aeruginosa_TonB1        -----------------------------------------        342
Escherichia_coli_TonB               -----------------------------------------        239
BT4460                              -----------------------------------------        449
BT1668                              -----------------------------------------        350
BT3896_Nterm_plus_TonB_Domain1      -----------------------------------------        206
BT3192                              -----------------------------------------        249
BT1056                              -----------------------------------------        269
BT3673                              ISVERLHDNLIKLSFTVPGQGRKVTEYWFRAPSPDVKIMAD        283
BT2059                              -----------------------------------------        227
BT0813                              -----------------------------------------        443
BT3896_TonB_Domain2                 -----------------------------------------        79
BT3898_Nterm_plus_TonB_Domain1      -----------------------------------------        530
BT2665                              -----------------------------------------        270
BT2762                              -----------------------------------------        227
BT3898_TonB_Domain2                 -----------------------------------------        79
```

Figure S3. Multiple sequence alignment of the TonB-dependent transporters SusC, BT0364, BT1763, BT2264, BT3332, and BT4671 from *B. theta,* RagA from *Porphyromonas gingivalis*, HasR from *Serratia marcecens*, FecA and FhuE from *E. coli*, and FoxA and Fpva from *Pseudomonas aeruginosa*. The predicted Tonbox for *B. theta* TBDT are highlighted in yellow, characterized Tonboxes for the additional TBDT are highlighted in green.

```
BT2264                             ------------------------------------------------------------    0
Porphyromonas_gingivalis_RagA      ------------------------MKRMTLFFLCLLTSIGWA--------------MAQN    22
BT3332                             ----------------------------MLSILGMLLL--SVPF---------V-LA--Q    18
BT0364                             -------------------------MKNFILILCLATFSQWV--------------YAQN    21
BT1763                             --------MPGI---------M--KNKKLLCSVCFLFA--FMSA---------L-WGQ-N    28
SusC                               -------MKKGN---------F--MFKVLLMLIAGIFL--SIDA---------F-AQQ--    28
BT4671                             -------MNCNI---------LNLRHLTVLLILCTAFLGGAIPA---------F-AQQGG    34
Smarcescens_HasR                   -----MFIHKGT------TPAGRLATAVRAALAAMMLTQPAVALAAQAEASSAQAAQQKN    49
Ecoli_FecA                         -----------MTPLRVFRKTTPLVNTIRLSLLPLAGL--------------SFSAFAAQ    35
Pseudomonas_aeruginosa_FoxA        MTATAVVLRNAPSSLD-FPRASRLSRSVRAALLSLAMAAGAAPL--CASAAEAAAEQARP    57
Ecoli_FhuE                         ------------------------------------------------------------    0
Paeruginosa_FpvA                   --------MPAPHGLSPLSKAFLMRRAFQRRILPHSLA---MAL--SLPLAGYVQAQEVE    47


BT2264                             ------------------------------------------------------------    0
Porphyromonas_gingivalis_RagA      RTVKGTVISSEDNEPLIGANVVVV---GNTTIGAATDLDGNFTLSVPA----NAKMLRVS    75
BT3332                             VLVKGTV-KDNLGEGVPGASVQV----KGTSQGTITDLDGKFTLNIPQ----KNATLVIS    69
BT0364                             KQITGRV-VDTKGEAAIGASILE----KGTTNGTITDFDGNFKLTVGP-----KAVLQIS    71
BT1763                             ITVKGNVTSKTDGQPIIGASVVET---TATTNGTITDFDGNFTLSVPV-----NSTLKIT    80
SusC                               ITVKGIV-KDTTGEPVIGANVVV----KGTTTGTITDFDGNFQLSAKQ-----GDIIVVS    78
BT4671                             KKMTGQV-IDENKEPMIGVSILI----VGTSTGTVTDFDGNYTLNVPK----DSKELQFS    85
Smarcescens_HasR                   FNIAAQPLQSAMLRFAEQAGMQVFFDEVKLDGMQAAALNGSMSVEQGLRRLIGGNPVAFR    109
Ecoli_FecA                         VNIAPGSLDKALNQYAAHSGFTLSVDASLTRGKQSNGLHGDYDVESGLQQLLDGSGLQVK    95
Pseudomonas_aeruginosa_FoxA        YAIPAGQLGDVLNRFAREAGITLSATPAQTGGYSSQGLRGSFTVQQGLARLLADTPLEAE    117
Ecoli_FhuE                         ---------MLSTQFNRDNQYQAITKPSL----------------------LAGC-----    24
Paeruginosa_FpvA                   FDIPPQALGSALQEFGRQADIQVLYRPEEVRNKRSSAIKGKLEPNQAITELLRGTGASVD    107
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BT2264                             ---MQTQEVAIKP---NLKVVLRSDAQQI--DEVVVTAMGI------------------    33
Porphyromonas_gingivalis_RagA      YSGMTTKEVAIAN---VMKIVLDPDSKVL--EQVVVLGYGT------------------    111
BT3332                             FIGYVTVEQKADS-QKPMVITLKEDTKTL--DEVVVVGYQE------------------    107
BT0364                             YIGYKTQEIPVAN-KTKLNITMEEDTEVL--DEVVVVGYGA------------------    109
BT1763                             YIGYKPVTVKAAA---IVNVLLEEDTQMV--DEVVVTGYTT------------------    116
SusC                               FIGYQPQELPVAA---QMNVILKDDTEIL--DEVVVIGYGQ------------------    114
BT4671                             YVGYETKVITIPVNSNVLNVQMKSDSQVL--SDVVIIGYGT------------------    124
Smarcescens_HasR                   LQPQGQIVLSRLP-------TANGDGGALALDSLTVLGAGG----------------NNA    146
Ecoli_FecA                         PLGNNSWTLEPAP-------APKEDALT-----VVGDWLGD-----------------AR    126
Pseudomonas_aeruginosa_FoxA        DQGDGSFVLREAP-------A--KDGDVLNMQAVEVFALGNNLGSTDGYLATHSQIATKT    168
Ecoli_FhuE                         -----IAL-ALLP-------SAAFAAPATEETVIVEGSATAPDDGENDYSVTSTSAGTKM    71
Paeruginosa_FpvA                   FQGNAITI-SVAE-------A-ADSSVDLGATMITSNQLGTITEDSGSYTPGTIATATRL    158
                                                                    :
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Plug Domain Begins

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BT2264                             KRSEKALGYAATSVGGEKIAESRTSDVMSSLAGKIAGVQISSTSSDPGAS--NSVIIRGV    91
Porphyromonas_gingivalis_RagA      GQKLSTVSGSVAKVSSEKLAEKPVANIMDALQGQVAGMQVMTTSGDPTAV--ASVEIHGT    169
BT3332                             VRR-RDLTGSVAKANMADVLTAPVASFDQALGGRIAGVNVTSGEGMPGGN--MSIVIRGN    164
BT0364                             QKK-ESVVGAISQVSSKELLKSPAANISQAIAGKISGVITSQTSGAPGAD-DMKIYIRGR    167
BT1763                             QRK-ADLTGAVSVVKVDEIQKQGENNPVKALQGRVPGMNIT-ADGNPSGS--ATVRIRGI    172
SusC                               VKK-NDMTGSVMAIKPDELSKGITTNAQDMLSGKIAGVSVISNDGTPGGG--AQIRIRGG    171
BT4671                             QRK-SDLTGSVASVGTKDFNKGMVSSPEELVNGKIAGVQIVNGGGSPTSV--STIRIRGG    181
Smarcescens_HasR                   NDWVYDEPRSVSVISREQMDNRPARHAADIL-EQTTGAYSSVSQQDP----ALSVNIRGI    201
Ecoli_FecA                         ENDVFEHAGARDVIRREDFAKTGATTMREVL-NRIPGVSAPENNGTGSHDLAMNFGIRGL    185
Pseudomonas_aeruginosa_FoxA        SKPLLETSQTVSVITREQIDDTASKTVQQAM-RYTPGIFTGQVGASNRYDYVV---MRGF    224
Ecoli_FhuE                         QMTQRDIPQSVTIVSQQRMEDQQLQTLGEVM-ENTLGISKSQADSDRALYY-----SRGF    125
Paeruginosa_FpvA                   VLTPRETPQSITVVTRQNMDDFGLNNIDDVM-RHTPGITVSAYDTDRNNYY-----ARGF    212
                                            :        .         . :     *                    :*

BT2264                             SSLSGTNQPLYVVDGVPLNNSTVYSTDGLNSGYDFGNGANAINPDDVANMTILKGAAATA    151
Porphyromonas_gingivalis_RagA      GSLGASSAPLYIVDGMQTSLDV----------------VATMNPNDFESMSVLKDASATS    213
BT3332                             NSLTQENSPLFVIDGFPIEDSS---------------AASTLNPSDIESLDFLKDASATA    209
BT0364                             ASFAGDNQPLILVDGVERE-------------------FSQIAPDDIESISTLKDASATA    208
BT1763                             GTLN-NNDPLYIIDGVPTKAG-----------------MHELNGNDIESIQVLKDAASAS    214
SusC                               SSLNASNDPLIVIDGLAIDNEG-IK--------GMANGLSMVNPADIETLTVLKDASATA    222
BT4671                             ASLNASNDPLIVLDGVPMEVGGSIS--------GGGNFLSLINPNDIESMTVLKDASSTA    233
Smarcescens_HasR                   QD--Y-GRVNMNIDGMRQNFQK--------SGHGQRNGTMYIDSELLSGVTIDKGTTG-G    249
Ecoli_FecA                         NPRLA-SRSTVLMDGIPVPFAP--------YGQ-PQLSLAPVSLGNMDAIDVVRGGGA-V    234
Pseudomonas_aeruginosa_FoxA        AD--N-SVDNIYLDGLKAMGDS--------GT--F--SSMQVDPYFLERIDVLKGPSS-V    268
Ecoli_FhuE                         Q------IDNYMVDGIPTYF-E--------SR--WNLGDALSDMALFERVEVVRGATG-L    167
Paeruginosa_FpvA                   S------INNFQYDGIPSTARN--------VG--YSAGNTLSDMAIYDRVEVLKGATG-L    255
                                                **.                                 :   :.  .
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BT2264                             LYGSRAANGVVMITTKSGRKEKGVGIEYNGGVQWSTVLRLPE------------FQNEFG     199
Porphyromonas_gingivalis_RagA      IYGARAANGVVFIQTKKGKMSERGRITFNASYGISQILNTKPLDNMMTGDELLDFQVKAG     273
BT3332                             IYGARGANGVVIITTKKGKVGR-AQLSYDGSFGVQHVTRTI---PMMDAYEFVKLQNEM-     264
BT0364                             VYGVRGANGVMLITTKRGKEQK-PTVSLTANWQIQSPTRQD---TYLDSYNSVVLLEEA-     263
BT1763                             IYGSRAANGVIIITTKQGKKGQ-IKINFDASVSASMYQSKM---NVLNTEQYGRAMWQA-     269
SusC                               IYGSRASNGVIIITTKKGKNGQAPSVSYNGSVSFSKTQKRY---DVLSGDEYRAYANQL-     278
BT4671                             IYGSRASNGVIIITTKKGSGSD-IKVSFQTTNSIATKTKTS---DMLNTDEFINIVNQY-     288
Smarcescens_HasR                   MGSAGTLGGIATFNTVSASDFLAPGKELGGKLHASTGD----------------------     287
Ecoli_FecA                         RYGPQSVGGVVNFVTRAI------PQDFG----IEAGV----------------------     262
Pseudomonas_aeruginosa_FoxA        LYGRSLPGGLVALTSKKPL-----YEDYRQ-ITGSIGN----------------------     300
Ecoli_FhuE                         MTGTGNPSAAINMVRKHAT-----SREFKGDVSAEYGS----------------------     200
Paeruginosa_FpvA                   LTGAGSLGATINLIRKKP------THEFKGHVELGAGS----------------------     287
                                     .    ..   :

BT2264                             MGWNGNHTELE-------NGSWGPRFDGSMQLWGNVY------NNSQKLKPYVAMPDNIK     246
Porphyromonas_gingivalis_RagA      F--WGNNQTVQKVKDM--------ILAGAEDLYGNYDSLKDEYGKT--LFPV--DFNHDA     319
BT3332                             ---YPTVVAGS------YLMN--Y------------------EGKQWTLDDY--KNIPQY     293
BT0364                             ---LANDGLPSQY-----------S-ASDIEMYKRA------SAGQLSGIDA--LLYPNV     300
BT1763                             ---YVNDGENPNGNALGYAYNWGYNADGNPVLYGMT------LSKYLDSKNT--MPVADT     318
SusC                               ---WG---------------------DK--------------------LPAD--LGTANT     292
BT4671                             ---GT---------------------EH--------------------QKSL--LGDYRT     302
Smarcescens_HasR                   ---NGTHFIG---------------------------------------SGILALGNETG     305
Ecoli_FecA                         ---EGQLSPTSSQN--------NPKETHNLMVGGTA------DNGF--GTALLYSGTRGS     303
Pseudomonas_aeruginosa_FoxA        ---MGQKEMGFDFS--------GPLDEEK---------------RI--AYRLIGLGKGSD     332
Ecoli_FhuE                         ---WNKERYVADLQ--------SPLTEDG---------------KI--RARIVGGYQNND     232
Paeruginosa_FpvA                   ---WDNYRSELDVS--------GPLTESG---------------NV--RGRAVAAYQDKH     319


BT2264                             D-FFDAGFRY-----SNSLSFNGA-TDKSDYYVSFSQISDDGMIPTDAD---------SY     290
Porphyromonas_gingivalis_RagA      D-WLKALFKTAP-TSQGDISFSGG-SQGTSYYASIGYFDQEGMAREPA----------NF     366
BT3332                             N-WQDEIFKTAW-QQNHTVRLAGG-TEGVRYNASLSYFDQDGTLIETG-----------Y     339
BT0364                             D-WYDTVLRNSAPAQRYNVNIQGG-TKRMRYFTSAEYYNQQGLFKEFSQDEYGNKSNSSF     358
BT1763                             D-WFDEITRTGV-IQQYNLSVSNGS-EKGSSFFSLGYYKNLGVIKDTD-----------F     364
SusC                               D-WQDQIFRTAV-STDHHVSING-GFKNLPYRVSLGYTDDNGIVKTSN-----------F     338
BT4671                             N-WNDEIYQTAF-GTDNNLSVSGLALPWLPFRVSTGMYYQDGILKTDN-----------T     349
Smarcescens_HasR                   DILLAASERHLG-----------------DYW--PGNKGDIGNIRINN-------DTGNY     339
Ecoli_FecA                         D-WREHSATRID------------------------------------------------     314
Pseudomonas_aeruginosa_FoxA        T-QFDHVKEERY-----------------AI-----------------------------     345
Ecoli_FhuE                         S-WLDRYNSEKT-----------------FF-----------------------------     245
Paeruginosa_FpvA                   S-FMDHYERKTS-----------------VY-----------------------------     332
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BT2264                             DKYTFSARGSHKAGA----LTF-------------SSSLNYAYQKN--NFATTGQGLSML    331
Porphyromonas_gingivalis_RagA      KRYSGRLNFESRINEW-LKVGA-------------NLSGAIANRRSA----DYFGKYYMG    408
BT3332                             KRMQGRMNTVVRRGKLNMSLTT-------------NYSRSIQTGSTP-SSTSYSGMNN--    383
BT0364                             KRFAFRANLDFLMTKD-LTLSV-------------NFGTRFEERRGPNSNESRDGTYS--    402
BT1763                             DRFSARMNSDYKLIDD-I-LTI-------------G--QHFTLNRTS-EVQAPGGIIE--    404
SusC                               RRFTASVNLAPSFFED-H-LKF-------------NINAKFMN-GKN-RYADTGAAIG--    379
BT4671                             KRFTGNVNLTPSFFHN-E-LRF-------------NIGLKGTY-SKN-RFADTDAIWA--    390
Smarcescens_HasR                   DRYAESIKNNKIPDTH---YRMHSRLAKVGWNLPANQRLQLSYLQTQ----TASPIAG--    390
Ecoli_FecA                         ---DLMLKSKYAPDEV---HTF-----------------NSLLQYYD----GEADMPG--    345
Pseudomonas_aeruginosa_FoxA        ---APTLAIDFSDDTT---LTL-----------------QG-YLQHD----PNGGYHG--    375
Ecoli_FhuE                         ---SGIVDADLGDLTT---LSA-----------------GYEYQRID----VNSPTWG--    276
Paeruginosa_FpvA                   ---YGILEFDLNPDTM---LTV-----------------GADYQDND----PKGSGWS--    363


BT2264                             NSLYQTPRD-------ISIIGLEDQNDPFNTPGYYYTPYGVMN-----------------    367
Porphyromonas_gingivalis_RagA      SGTFGVL----------TM-P------------RYYNPFDVNGDLADVYYMYGATRPSMT    445
BT3332                             -LFYSVW----------GYRPVTSPDTPLSFLM----DSSTDNAV-------DSSNDYRF    421
BT0364                             -QAF----------------YEMNHTPGWLFPVSYTVGEGEDQ-----KTLYSGSSQYQN    440
BT1763                             -TALDIP----------SAIPVYASDGSWGGPVGGWPD--------------RRN-----    434
SusC                               -GALAID----------PTRPVYSNEDPYQFTGGYWQNINSTTGFSNPDWKYTSNPNSPQ    428
BT4671                             -G-STLN----------PTIPVYSGNDTF---GGYNEAIDANG-VP--------VTGALA    426
Smarcescens_HasR                   -T-LTNLGT----------RPPY--ELGWKRTGYTDV-MA--------------------    415
Ecoli_FecA                         -G---------------LSRADY-DADRWQSTRPYDRFWGRR------------------    370
Pseudomonas_aeruginosa_FoxA        -G-VPADGTLSHHNGRHISREFFDGEPSKDDFDRTQRMFG--------------------    413
Ecoli_FhuE                         -G-LPRWNTDGSS--NSYDRARS-TAPDWAYNDKEINKVF--------------------    311
Paeruginosa_FpvA                   -GSFPLFDSQGNR--NDVSRSFN-NGAKWSSWEQYTRTVF--------------------    399


BT2264                             -PYYILN---NY--LNEYESERFYGKFQLDYEFL---KYFKFTYRMGLDTTTGQSDKGKP    418
Porphyromonas_gingivalis_RagA      EPY--FAKMRPF----SSESHQANVNGFA--QITPI-KGLTLKAQAGVDITNTRTSSKRM    496
BT3332                             NPIKSQKN--EYRKSY-TNNLQ--MNGFAE--YE-VLKGLKLKVSAGYTYDSRKQDQFNN    473
BT0364                             NIVARFAKAGFYRSTNTINE----TNFIVDYKMNWLTKGLAAKGMLSFDYDAYYRRAFNA    496
BT1763                             -PRAVLE---YN-KDNRYTYWRMFGDAYV--NLTPFK-GFNLRSTFGLDYANKQARYFTY    486
SusC                               NPLAALE---LK--NDKANSNDFVGNVDVDYKFHFLP-DLRLHASIGGEYAEGTQTTIVS    482
BT4671                             NAVGRLN---QY--DSTSDVYRFIGSASVDWNVRWVK-GLRLHTTGGYDWSKGKGHIYVP    480
Smarcescens_HasR                   -RNAAFD-------YSLAPE-------DV----DWL--DFQAKLYYVDTQDD--SDTYST    452
Ecoli_FecA                         -KLASLG-------YQFQP----DSQHKF----NIQ--GF-----YTQ------------    395
Pseudomonas_aeruginosa_FoxA        ---YQLE-------HRIDDVWSARQNFRY----LDS--DVDLSQVYAY------------    445
Ecoli_FhuE                         ---MTLK-------QQFADTWQATLNATH----SEV--EFDSKMMYVDAYVN--K----A    349
Paeruginosa_FpvA                   ---ANLE-------HNFANGWVGKVQLDH----KIN--GYHAPL----------------    427
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BT2264                             -NLYALYYEGTPNGEGQ--GSSSPFSGETGQYSE---------QITRRREINQDIMVNFN    466
Porphyromonas_gingivalis_RagA      -PN--NPYDSTPLGERR-------------------ERA------YRDVSKSFTNTAEYK    528
BT3332                             -SN----TR---YGGPT--STDKVN----AQVTR-----------QERLTWLNENTLTYQ    508
BT0364                             -DF--ATYE---LNDRT---NYNSID-AYTQFNTDTELAYLGNDQTTTYKLYMEFQLNWA    546
BT1763                             ------PYQ---EGTQT--NNGKSAV-EAKQ--------------EHWTKWMWNAIATYQ    520
SusC                               ------PYS---FGNNY--YGWNGD---VTQ--------------YKY-NLSYNIYVQYI    513
BT4671                             -KEAVSYYT---TGGRD--YTYGP------Q--------------KNY-NKLLTIYANYH    513
Smarcescens_HasR                   SSLLDNGYA---TRTR-------------------------------LRTYGAQAQNTSR    478
Ecoli_FecA                         --TLRSGYL---EQGKR--ITLSPR----NYWVR-----------GIEPR------YSQI    427
Pseudomonas_aeruginosa_FoxA        ------GWS---ASEPNKLNRYFSG----AREH--------------LQAYIVDNMLQAE    478
Ecoli_FhuE                         DGMLVGPYS---NYGPG--FDYVGG----TGWNS-----------GKRKVDALDLFADGS    389
Paeruginosa_FpvA                   -GAIMGDWP---APDNS--AKIV------AQKYT-----------GETKSNSLDIYLTGP    464


BT2264                             MPVN-DFNINALVGFNGNERK--------VSYQYSEVNDLTIPTWFN---LKNSGKTPIV    514
Porphyromonas_gingivalis_RagA      FSIDEKHDLTALMGHEYIEYEGDVIGASSKGFESDKL--------MLLSQGKTGNSLSLP    580
BT3332                             TNIK-KKHFLNVLGGITFQNS---------DYEIYSFRTTHIPNESLGMAGMSEGQAGTT    558
BT0364                             RKFG-KHDITAMALYNQN---------------------------------------DYR    566
BT1763                             LEVG-KHRGDVMIGMELNRED----DSHFSGYKED--FSILTPDYMW---PDAGSGTAQA    570
SusC                               KSLG-ANDFDIMVGGEEQ-------HFHRNGFEEGQGWDSYT----Q---EPHDAKLREQ    558
BT4671                             N------DFDAIHSGIDV-------TV---GY-DYQFWKYTTPFYAI--LSADGVQQSTS    554
Smarcescens_HasR                   FS--------LAPGHDFRA-----------NYGLEFYYDKATSDSSRQGME---GVTP--    514
Ecoli_FecA                         FMIG-PSAHEVGVGYRYLNEST---------HEMRYYTATS------SGQLPS-GSSPYD    470
Pseudomonas_aeruginosa_FoxA        FATG-AARHTLLTGLDYQRRRTVVDWRSGSASALDAFNPVY-------GDDAISYF--PD    528
Ecoli_FhuE                         YELF-GRQHNLMFGGSYSK----QNNRYFSSWA-NIFPDEIGSFYNFNGNFPQTDWSPQS    443
Paeruginosa_FpvA                   FQFL-GREHELVVGTSASF----SHWEGKSYWNLRNYDNTTDDFINWDGDIGKPDWGTPS    519


BT2264                             EQHMELRRLMGVFGQFEGSWKNMLYLTVTARNDWSSTLPKENRSFFYPGITG-SFIFSEL    573
Porphyromonas_gingivalis_RagA      EHRVAEYAYLSFFSRFNYGFDKWMYIDFSVRNDQSSRFGSNNRSAWFYSVGG-MFDIYNK    639
BT3332                             TSAKSSWAMLSYLGRVTYNYMSKYYATVSFRADGSSKFNKDNRYGYFPSGSL-AWSFSEE    617
BT0364                             YQADLAERYQGLVGRATYGYDDRYLAEVNFGYNGSENFMRGRRFGFFPSFSV-GWRISNE    625
BT1763                             YGAGEGYSLVSFFGKMNYSYADRYLLSLTLRRDGSSRFGKNHRYATFPSVSL-GWRITQE    629
SusC                               TAYATRNTLVSYFGRLNYSLLNRYLFTFTMRWDGSSRFSKDNRWGTFPSLAL-GWKIKEE    617
BT4671                             AATDQRHSLMSYYGRLNYTFMDRYLLMATMRRDGSSRFASDNRWGTFPSVAL-AWRVSQE    613
Smarcescens_HasR                   ---AGNRSVASLFANLTYDYDGWLTLEGGLRYDRYRLRGQTGL--SYPDLAKDGQRYTID    569
Ecoli_FecA                         RDTRSGTEAHAWYLDDKID-IGNWTITPGMRFEHIESYQNNAI--T--------------    513
Pseudomonas_aeruginosa_FoxA        DNHTRRLEQTGVYLQDLID-IDQWRFSLGLRQDWVSVTDKNRS--T--------------    571
Ecoli_FhuE                         LAQDDTTHMKSLYAATRVTLADPLHLILGARYTNWRVDTLTY------------------    485
Paeruginosa_FpvA                   QYIDDKTRQLGSYMTARFNVTDDLNLFLGGRVVDYRVTGLNP------------------    561
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BT2264                              -LNDNLQDVITFGK------IRASWGKTGNDADVY-------MVNPVYAQSSNRIP----    615
Porphyromonas_gingivalis_RagA       -FIQE-SNWLSDLR------LKMSYGTTGNSEIGNY------NHQALVTVN---------    676
BT3332                              EFMKPLKSVLSSGK------VRLSWGLTGNNRIGEY------DYYALLAVLKSRVGSYTS    665
BT0364                              AFMKGTEEWLNNLK------IRASYGEVGNDVYKVNGVKQRFLYQAVWTQ----------    669
BT1763                              NFMKEL-TWLDDLK------LRASWGQTGNQEISNL-----A-RYTIYAPN---------    667
SusC                                NFLKDV-NVLSDLK------LRLGWGITGQQNIGDD-----FAYLPLYVVN---------    656
BT4671                              HFFEPLRTVMNDVK------LRVSYGITGQQDGITN-----YGYIPVYTPG---------    653
Smarcescens_HasR                    NPCKALRLTGCSTTTREDWDVDRDQGKLSPTLAVAVRPGV--EWLELYTTY---------    618
Ecoli_FecA                          ---------GT--------HEEVSYNAPLPALNVLYHLTD--S-WNLYANT---------    544
Pseudomonas_aeruginosa_FoxA         ---------GS--------KADDDWEKFTGRIGALYLFDN--G-LAPYVSY---------    602
Ecoli_FhuE                          --------------------SM-EKNHTTPYAGLVFDIND--N-WSTYASY---------    512
Paeruginosa_FpvA                    --------------------TIRESGRFIPYVGAVYDLND--T-YSVYASY---------    589
                                                                                    .

BT2264                              ---FGSLTFPLGGVN-----------------AYSAGNVLGSNTLSPEMTTESEVGLNMA    655
Porphyromonas_gingivalis_RagA       -------N--YTEDAM-----------------GLSISTAGNPDLSWEKQSQFNFGLAAG    710
BT3332                              TNSLPSGVYPFDNDA---------------TNAGVVPTSLPNKDLKWETTEQWNAGLDLG    710
BT0364                              ----IANDYHFGTTGYT----------------GIYESQYPNYAVTWERAHKYNLGLEFG    709
BT1763                              ---YGT-TDSFGGQSYGTAYDITGSNGGGVLPSGFKRNQIGNDNIKWETTTQTNVGIDFS    723
SusC                                ---NEYAQYPFGDTYY-----------------STSRPKAFNENLKWEKTTTWNAGLDFG    696
BT4671                              ---LDGAQYLFGGNPI-----------------YTYRPEAYNPELKWETTKSWNYGIDLA    693
Smarcescens_HasR                    -------GKSWRPPAITETLT----N----GSAHSSSTQYPNPFLQPERSRAWEVGFNVQ    663
Ecoli_FecA                          -------EGSFGTVQYSQI-----------------GKAVQSGNVEPEKARTWELGTRYD    580
Pseudomonas_aeruginosa_FoxA         -------SESFNPNA---------------------YSDASGTPLAPTEGKQWELGLKFQ    634
Ecoli_FhuE                          -------TSIFQPQND---------------------RDSSGKYLAPITGNNYELGLKSD    544
Paeruginosa_FpvA                    -------TDIFMPQDS--W-----------------YRDSSNKLLEPDEGQNYEIGIKGE    623
                                                                             .  :        : *

BT2264                              FF-----KNRLSFDVSYYNRNTDKQIFSLAMDPASGY-------TAQNMNLGKIRNRGIE    703
Porphyromonas_gingivalis_RagA       AF-----NNRLSAEVDFYVRTTNDMLIDVPMPYISGF-------FSQYQNVGSMKNTGVD    758
BT3332                              FF-----DERIGITMDIYRKTTRDLLLDASLPFSSG-------YYSATKNIGKVRNDGLE    758
BT0364                              LW-----NGLLNGNIDVFYEKRNDILTPYLTRPQWVG------VNMAAGNLGETNNKGFE    758
BT1763                              LF-----KQSLYGSLEYYYKKATDILTEMAGVGVLGE------GGSRWINSGAMKNQGFE    772
SusC                                FL-----NGRITGGIDGYFRKTDDLLNSVKIPVGTNF------NAQMTQNIGSLENYGME    745
BT4671                              FL-----ENRFTFSADFYTRKTENLLATVPMPAGTNF------DKLMLQNVGNVDSKGLE    742
Smarcescens_HasR                    QPDLWFEGDRLVAKVGYFDTKVDNYINLAIDRNKPGLVQPSIGNAAYVNNLSKTRFRGLE    723
Ecoli_FecA                          -------DGALTAEMGLFLINFNNQYDSNQ-------------TNDTVTARGKTRHTGLE    620
Pseudomonas_aeruginosa_FoxA         AP-----GSNSFYTASLFHITQENVASKEP-------------QDNFYTSVGEVRSQGLE    676
Ecoli_FhuE                          WM-----NSRLTTTLAIFRIEQDNVAQSTGT-PIPGSN-----GETAYKAVDGTVSKGVE    593
Paeruginosa_FpvA                    YL-----DGRLNTSLAYFEIHEENRAEEDAL-YNSKPTNPA--ITYAYKGI-KAKTKGYE    674
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BT2264                              LLISGTPIRTK----DFSWELTWNFTKNWSKVISLPEELGGITTIYGL----NGGTSMYA    755
Porphyromonas_gingivalis_RagA       LSLKGTIYQNK----DWNVYASANFNYNRQEITKLFFGLNKYMLPNT------GT---I-    804
BT3332                              LSLNTVNFQTR----AFKWTTNFNISFNKNKVLALSENQTALLTAAQFDQNYNGQSSYIA    814
BT0364                              IELKHANHIGK----DFTYNASLTFSHARNEIRNMDEPATKTAYRKQE-----GH---P-    805
BT1763                              FNLGYRNKTAF----GLTYDLNGNISTYRNEILELPETVAANGKFGGN-----GV---KS    820
SusC                                FSINAKPIVTK----DFTWDLSYNITWNHNEITKLTGGDDSDY-YVEA-----GD---KI    792
BT4671                              LSVTGHIINTK----NWSWTASANAAWQKVRIKNLTLTPGAPSPDTEV-----GP---W-    789
Smarcescens_HasR                    YQLNYDAGVFYADLTYTHMIGKNEFCSNK----AWLGGRLR-------------------    760
Ecoli_FecA                          TQARYDLGTLTPTLDNVSIYASYAYVNAE---------IRE-------------------    652
Pseudomonas_aeruginosa_FoxA         LEAH------TQLSDNLKLLGSYTYTDIT---------YTK-------------------    702
Ecoli_FhuE                          FELN------GAITDNWQLTFGATRYIAE-------------------------------    616
Paeruginosa_FpvA                    AEIS------GELAPGWQVQAGYTHKIIR-------------------------------    697


BT2264                              ITGMP------------VGVFKAQVAERDP-Q---------------------GRIVVNS    781
Porphyromonas_gingivalis_RagA       ----------WEIGYP-NSFYMAEYAGIDKKTGKQLWY----------------VPGQVD    837
BT3332                              KVGLPMG---LMYGYVYEGTYKYD--DFNK-SGNSYSLKPGVPHYSTETNTQPGMPKYAD    868
BT0364                              -----IN---QYFGLVCDGFVTQA--DLNN-PD--------FP-VSTFGNVQVGDLKYRD    845
BT1763                              VVGHTYG---AQVGYIADGIFKSQ--DEVD-N------------HATQEGAAVGRIRYRD    862
SusC                                SRGNNTKVQAHKVGYAANSFYVYQ--QVYD--------------E----NGKPIENMFVD    832
BT4671                              --IDAYQMQVFSTDYAPYSFYLYK--QLYD-A------------E----TGQPIEGLYAD    828
Smarcescens_HasR                    -YGDGSR---------RGNFYVEPDAASND----------FVT-----------------    783
Ecoli_FecA                          -KGDTY----------GN---------LVP----------FSP-----------------    665
Pseudomonas_aeruginosa_FoxA         -SLDGNQ---------GH---------TPN----------QAP-----------------    716
Ecoli_FhuE                          ---DNEG---------NA---------VNP----------NLP-----------------    628
Paeruginosa_FpvA                    ---DDSG---------KK---------VST----------WEP-----------------    709


BT2264                              S--TGLPVE----ASEFGICGDMNNKYQMGVSTNLKYKGI--------SLGIDFDIRQGG    827
Porphyromonas_gingivalis_RagA       ADGNKVTTSQYSADLETRIDKSVTPPITGGFSLGASWKGL--------SLDADFAYIVGK    889
BT3332                              LNGDGVVDS----NDRTI-IGRGLPIHTGGFTNNFEYKGI--------DLSIFFQWSYGN    915
BT0364                              MNGDGFIDS----RDETFIGYSDVPENTYALSLGCEYKGI--------GFSIMFQGVDHV    893
BT1763                              IDHNGVIDE----RDQNW-IYDPTPSFSYGLNIYLEYKNF--------DLTMFWQGVQGV    909
SusC                                RNGNGTIDS----GDKYI-YKKPAGDVLMGLTSKMQYKNF--------DFSFSLRASLNN    879
BT4671                              LDGDGEITN----KDRYH-HHSPAPDWILGFSTSLRYKKW--------TLSTSLRANIGG    875
Smarcescens_HasR                    CD-----------GGTQFGSAAYLPGDRGSVTLGGRAFDRKLDAGVTVRFAPGYQDSSVP    832
Ecoli_FecA                          KH-----------KGTLGVDYKPG-----NWTFNL---------------NSDFQSSQFA    694
Pseudomonas_aeruginosa_FoxA         KH-----------MASLWADYAFDAGPLSGLSIGG---------------GARYVGETWA    750
Ecoli_FhuE                          RT-----------TVKMFTSYRLP--VMPELTVGG---------------GVNWQNRVYT    660
Paeruginosa_FpvA                    QD-----------QLSLYTSYKFK-GALDKLTVGG---------------GARWQGKSWQ    742
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BT2264                             VMYSRTKDI-NYFTGNAIQTAYNDRNPLIVPNSVNKIVNGENVTYVENTTPITSSNIYKY    886
Porphyromonas_gingivalis_RagA      WMINNDRY----FTENGGGLMQLNKDKML----LNAWTEDNKETD-------VPK-----    929
BT3332                             DIMNANRL---FFESSNNRSRELNQFASY----ANRWTPENPTSD-------IPA---AT    958
BT0364                             SRYYDAEAMYAFVNGGKV-------KEHH----LNRWNPNQSEAY-NLTHASYPLLHYDS    941
BT1763                             DIISDVKKKSDFWSASNV--GFLNKGTRL----LNAWSPTNPNSD-------IPA-LTRS    955
SusC                               YVYYDFLSNKANVSTSGL---------FS----NNAYSNTSA-----------EA-VALG    914
BT4671                             YIFNGMAMNTGAWETM------------S----YNDYQLNNLN----------RS-FLDT    908
Smarcescens_HasR                   SN----------------------------------------------------------    834
Ecoli_FecA                         DNANTVKE-----------------------------------------S------    703
Pseudomonas_aeruginosa_FoxA        DKENTLRV----------------------------------------------------    758
Ecoli_FhuE                         DT----VT-----------------------------------------P------    665
Paeruginosa_FpvA                   MVYNNPRS-----------------------------------------R------    751


BT2264                             WGDGGSDMGSCFLVDKSYVKLRSVVLGWDLPKRWLAKT-PFQAVKVSAYGNNLFVWTPSS    945
Porphyromonas_gingivalis_RagA      -LGQSPQFDTHLLENASFLRLKNLKLTYVLPNSLFAGQNVIGGARVYLMARNLLTVT--K    986
BT3332                             NSSSNRVISSRIIEDGSYLRLKNVTVGYTFPAKLVKKW-KIDKARVYVAAQNLWTCT--G    1015
BT0364                             YGDHNQRKNSFFLKNGNFLRLKNIELSYSLPARWIRKV-AMNECRVYVNANNLITWD--K    998
BT1763                             DTNNEQRVSTYFVENGSFLKLRNIQLGYTVPAVISKKM-RMDRLRFYCSAQNLLTIKSKN    1014
SusC                               LSGQGDYMSDYFIHNASFLRCDNITLGYSFQNLWKTQTYKGVGGRVYATVQNPFIIS--K    972
BT4671                             RFTKRQFLSDHYLENASFLKMDNLQLSYDFGRIYKT-----IGLHASAMVQNVFTVT--K    961
Smarcescens_HasR                   -YPYLADWPKYT--------LFDLYASYKLT----------DSLTLRGSVENLTNRAYVV    875
Ecoli_FecA                         ADGSTGRIPGFM--------LWGARVAYDFGP-------QMADLNLAFGVKNIFDQDYFI    748
Pseudomonas_aeruginosa_FoxA        --------PDYT--------LVDARIGYDLGKL------GLKGLDVSLNANNLLDKDYVA    796
Ecoli_FhuE                         YGTFRAEQGSYA--------LVDLFTRYQVT----------KNFSLQGNVNNLFDKTYDT    707
Paeruginosa_FpvA                   WEK--FSQEDYW--------LVDLMARYQIT----------DKLSASVNVNNVFDKTYYT    791
                                                         .    : .                    .*


BT2264                             NTFIDPEMTSFGNDLEGNYGEYTANPSSRRFGFNLMVKF  984
Porphyromonas_gingivalis_RagA      YKGFDPEAG-------GNVG-KNQYPNSKQYVAGIQLSF  1017
BT3332                             YSGYDPEVSVRNSALTPGLD-YSSYPRAYSISFGVSLGF  1053
BT0364                             LDGLCDPE---------SEG-SNRYPIMKTVNFGVNIKF  1027
BT1763                             FTGEDPENP-------N-----FSYPIPVNITFGLNIGF  1041
SusC                               YKGLDPEVK-------SGID-ANPYPRAMTFLLGLSLQF  1003
BT4671                             YKGVDPETA-------NGVD-TSVYPRPRTYSITIGLNF  992
Smarcescens_HasR                   SYGET---------------LANTLGRGRTVQGGVEYRF  899
Ecoli_FecA                         RSYDDNN-------------KGIYAGQPRTLYMQGSLKF  774
Pseudomonas_aeruginosa_FoxA        SCYSL---------------DFCYFGEKRNVTATVNYQF  820
Ecoli_FhuE                         NVE-----------------GSIVYGTPRNFSITGTYQF  729
Paeruginosa_FpvA                   NIGFY---------------TSASYGDPRNLMFSTRWDF  815
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Figure S4. Average growth curves of wild-type (WT) and TonBox deletion (ΔTonBox) *B. thetaiotaomicron* cultured in 2.5 mg ml^{-1} maltose (A) and maltoheptaose (B).

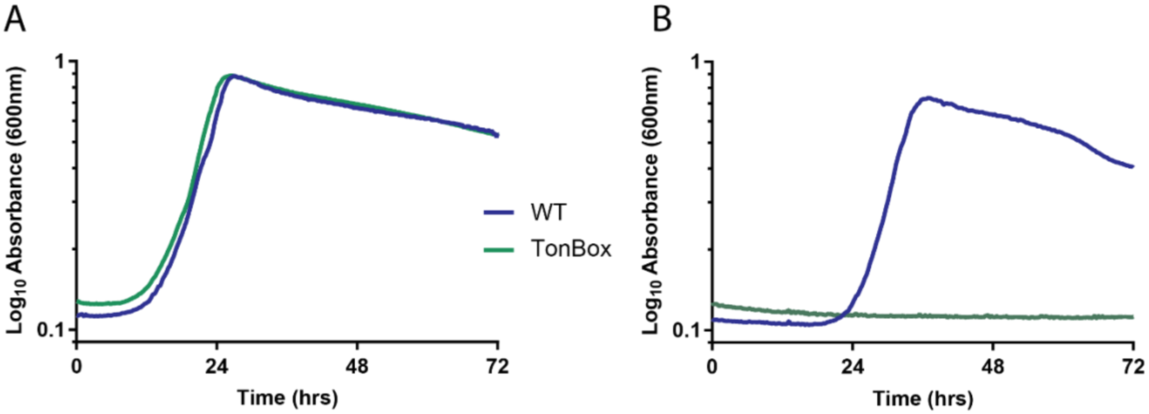
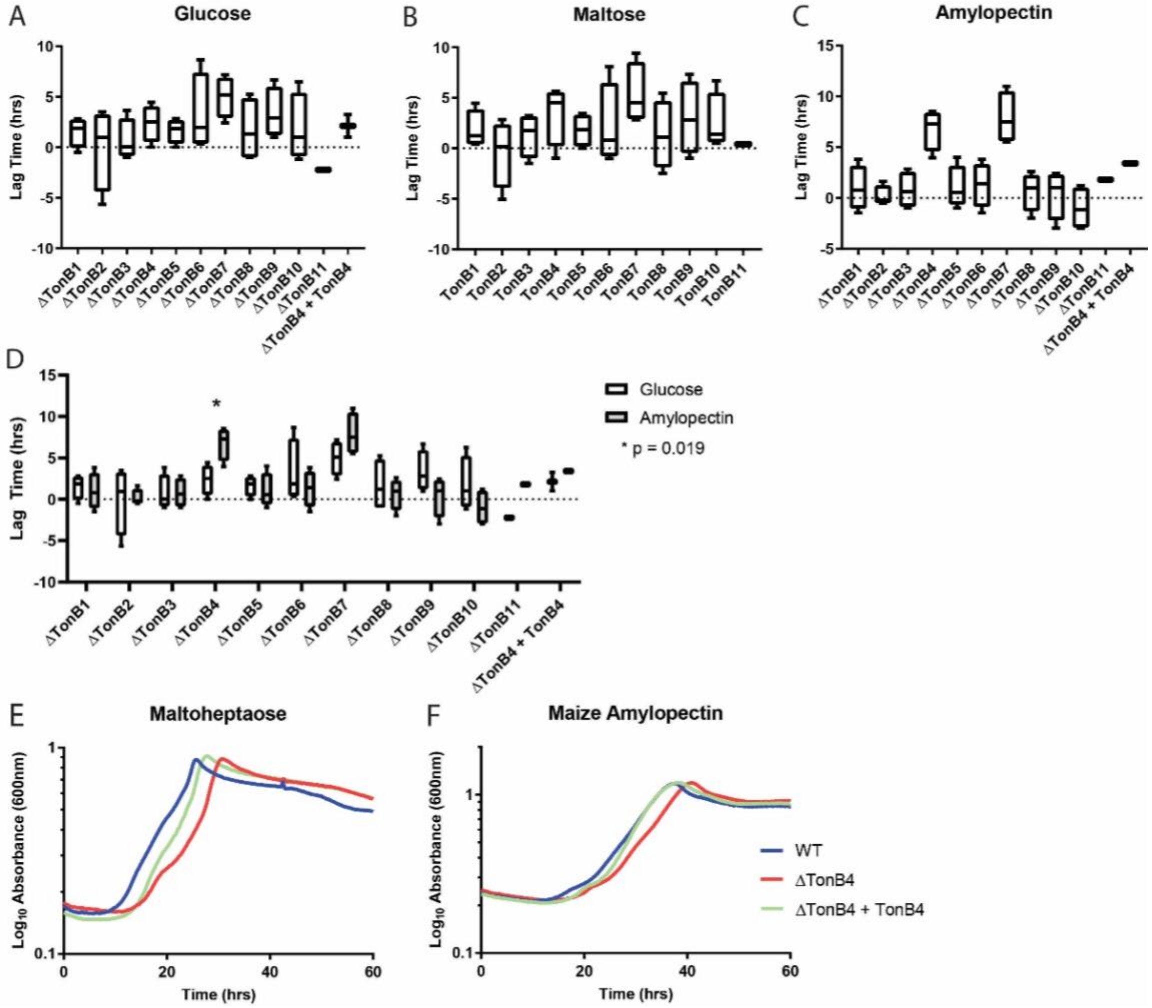


Figure S5. A-C. Lag times (time for absorbance to reach or surpass 0.3) were measured for four independent experiments and normalized to the corresponding growth of the wild-type strain for each experiment. Each box shows the 25-75% percentile, the whiskers show minimum to maximal values, the line in the middle of the box shows the median of the data. Each strain was grown on 5 mg ml^{-1} glucose (A), 5 mg ml^{-1} maltose (B), or 2.5 mg ml^{-1} potato amylopectin (C) as the sole carbon source. **D**. Lag times for growth on glucose and potato amylopectin (as also shown in A and C) are presented to allow for comparison across TonB deletion strains. P-value determined by unpaired T-test. **E-F**. Representative average growth curves of wild-type (WT), TonB4 deletion strain, and the TonB4 deletion strain with the TonB4 gene complemented in another location on the genome cultured on 2.5 mg ml^{-1} maltoheptaose (E) or 5 mg ml^{-1} maize amylopectin (F).


A
Glucose
Lag Time (hrs)
10
5
0
-5
-10
ΔTonB1
ΔTonB2
ΔTonB3
ΔTonB4
ΔTonB5
ΔTonB6
ΔTonB7
ΔTonB8
ΔTonB9
ΔTonB10
ΔTonB11
ΔTonB4 + TonB4
B
Maltose
Lag Time (hrs)
10
5
0
-5
-10
TonB1
TonB2
TonB3
TonB4
TonB5
TonB6
TonB7
TonB8
TonB9
TonB10
TonB11
C
Amylopectin
Lag Time (hrs)
15
10
5
0
-5
ΔTonB1
ΔTonB2
ΔTonB3
ΔTonB4
ΔTonB5
ΔTonB6
ΔTonB7
ΔTonB8
ΔTonB9
ΔTonB10
ΔTonB11
ΔTonB4 + TonB4
D
Lag Time (hrs)
15
10
5
0
-5
-10
*
Glucose
Amylopectin
* p = 0.019
ΔTonB1
ΔTonB2
ΔTonB3
ΔTonB4
ΔTonB5
ΔTonB6
ΔTonB7
ΔTonB8
ΔTonB9
ΔTonB10
ΔTonB11
ΔTonB4 + TonB4
E
Maltoheptaose
Log10 Absorbance (600nm)
1
0.1
0
20
40
60
Time (hrs)
F
Maize Amylopectin
Log10 Absorbance (600nm)
1
0.1
0
20
40
60
Time (hrs)
WT
ΔTonB4
ΔTonB4 + TonB4