

1 **SUPPORTING INFORMATION**

2 **This PDF file includes:**

3

4 Supporting Information Figures 1 to 13

5

6 Supporting Information Tables S1 to S4

7

8 Supporting Dataset S1 is uploaded separately as an excel spreadsheet)

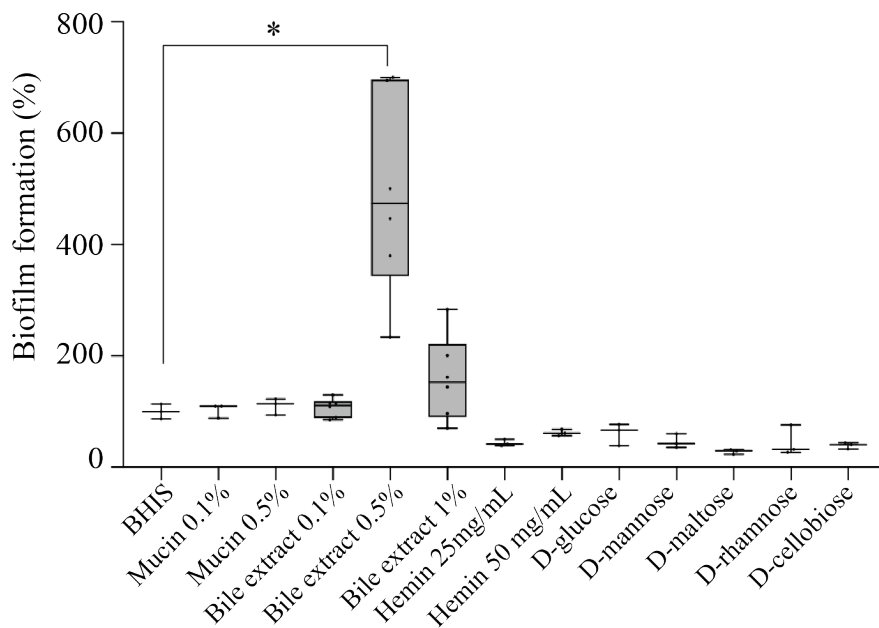
9

10 Supporting Information reference list

11

12 **SUPPORTING FIGURES**

13

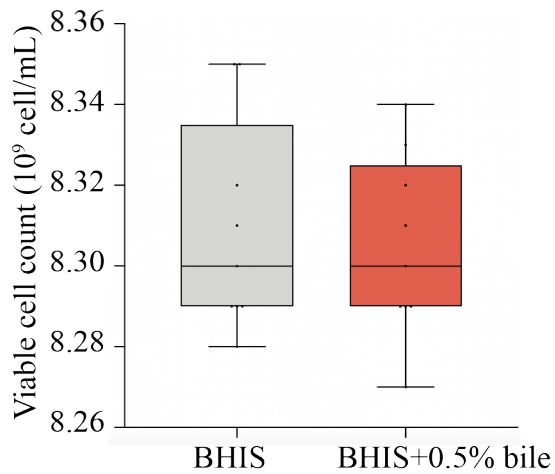


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15 Supporting Figure S1. **Bile is the only tested environment cue that induces biofilm**
16 **formation of *B. thetaiotaomicron* VPI-5482.** *B. thetaiotaomicron* VPI-5482 after 24h
17 growth in BHIS supplemented with 0.5% D-glucose, D-mannose, D-rhamnose, D-
18 cellobiose and D-maltose, 25 mg/L and 50 mg/L hemin, 0.1% and 0.5% mucin, and
19 0.1%, 0.5%, 1% bovine-ovine bile extract. Min-max boxplot of 3-6 biological replicates
20 for each strain. * p-value<0.05, ** p-value<0.005, Mann-Whitney test.

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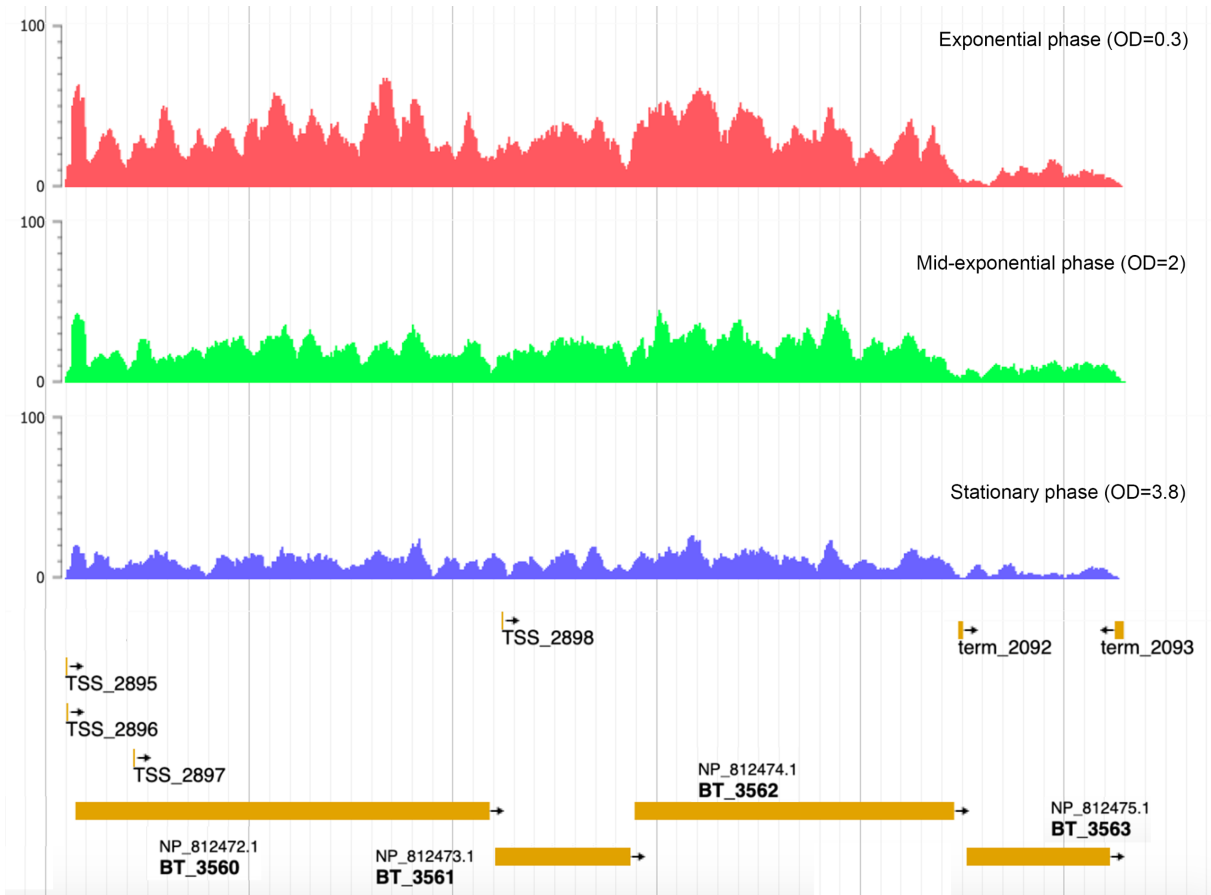
2

3 Supporting Figure S2. **0.5% bile extract concentration is non-toxic for *Bacteroides***
4 ***thetaiotaomicron***. **A.** Flow cytometry of *B. thetaiotaomicron* VPI-5482 cultures grown
5 in presence or absence of bile and dyed with propidium iodide to label live cells. The
6 viable cell count is shown as a min-max boxplot of 6 biological replicates.

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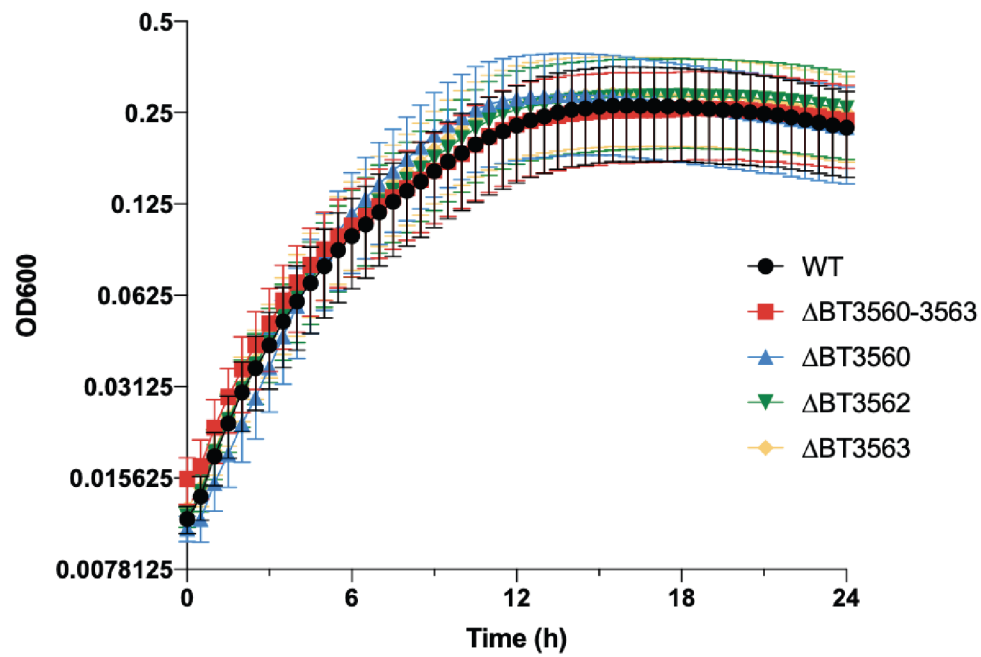
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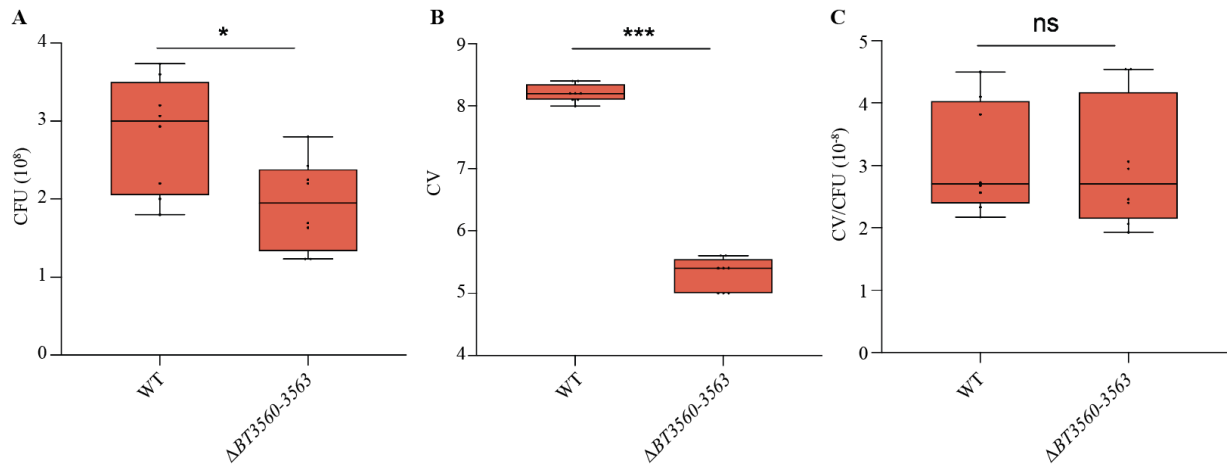
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4 Supporting Figure S3. **BT3560-BT3563 operon**. RNAseq reads from *B.*
5 *thetaitaomicron* VPI-5482 grown in TYG medium to exponential phase (OD=0.3) in
6 red, mid-exponential phase (OD=2) in green and stationary phase (OD=3.8) in blue
7 are mapped to the *BT3560-BT3563* genetic locus. Predicted transcriptional start sites
8 (TSS) and terminators (term) are depicted, showing the predicted operon structure of
9 *BT3560-BT3563*. Data and bioinformatics prediction from Theta-Base database (1)
10 (<https://bacteroides.helmholtz-hzi.de/>) plotted on JBrowse (2).

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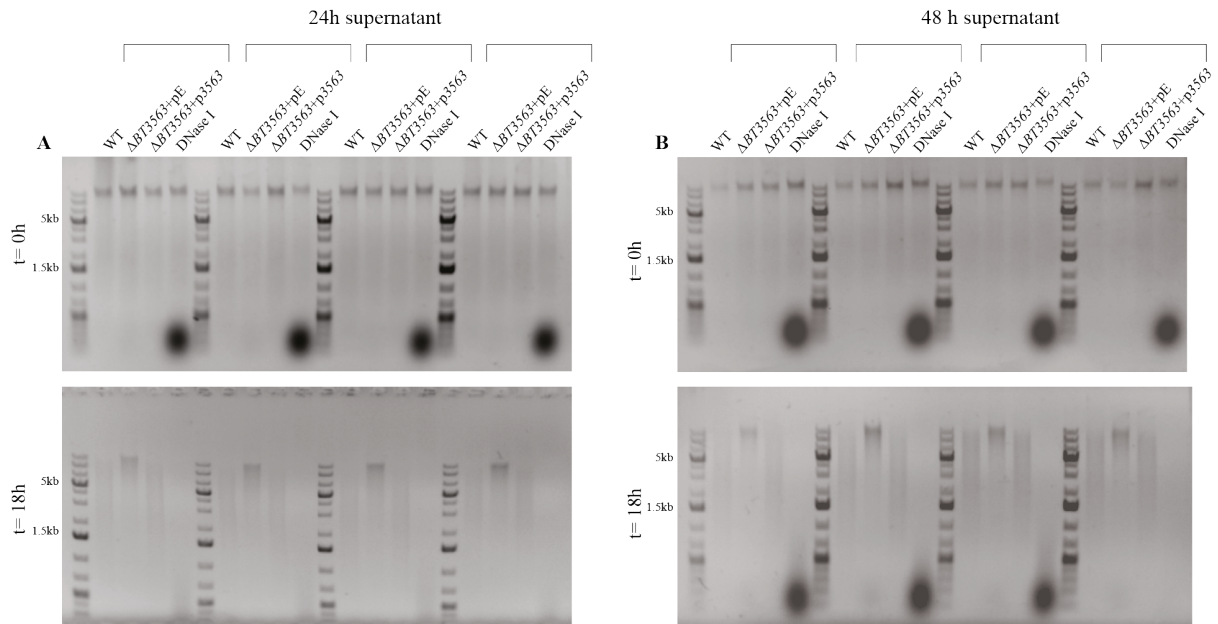


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 2 Supporting Figure S4. **Growth curve.** 24h growth curve of indicated strains in 96-well
 3 plate in BHIS+0.5% bile extract. Mean of 6 biological replicates, error bars represent
 4 standard error to the mean (SEM).
 5

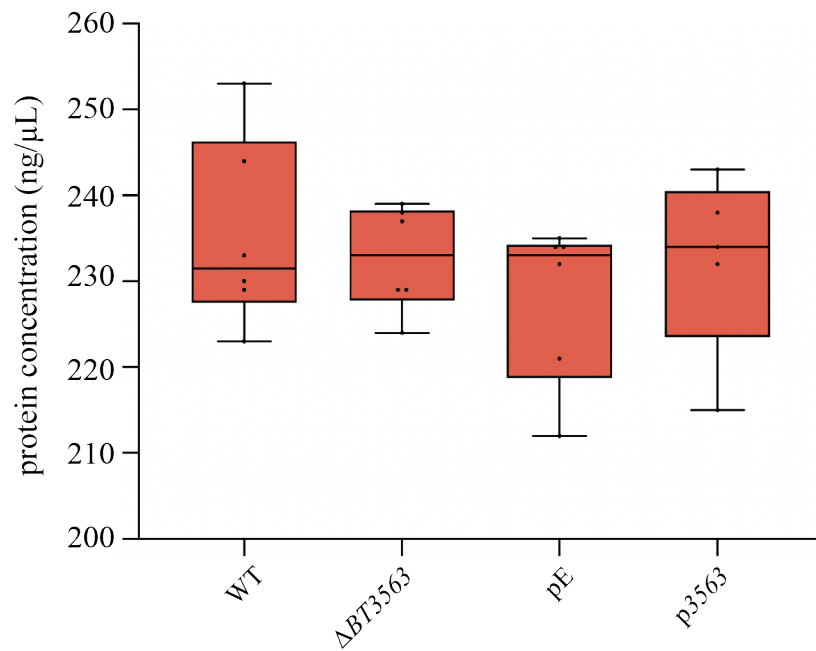


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Supporting Figure S5: **Quantification of cells in biofilm.** 96-well plate biofilm assay after 48h growth in BHIS+0.5% bile extract. Two plates were inoculated. One was used for **A.** resuspension of the biofilm and colony forming unit (CFU) count, the other was used for **B.** crystal violet (CV) staining. **C.** Ratio of CV over CFU count. Min-max boxplot of 8 biological replicates for each strain. * p-value<0.05, ***p-value<0.0005, Mann-Whitney test.



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 2 Supporting Figure S6. **BT3563 degrades DNA in culture supernatant.** Incubation of
 3 *B. thtaiotaomicron* genomic DNA (23ng/μL final concentration) with the supernatant
 4 of **A.** 24h and **B.** 48h bile-free cultures, as indicated, and loaded immediately on a 1 %
 5 agarose gel (t=0h) and after an overnight incubation at 37°C (t=18h). A control using
 6 DNase I rather than supernatant is shown in the last lane. pE: empty vector, p3563:
 7 vector constitutively expressing BT3563. One replicate of **B.** is shown in Figure 3A.
 8

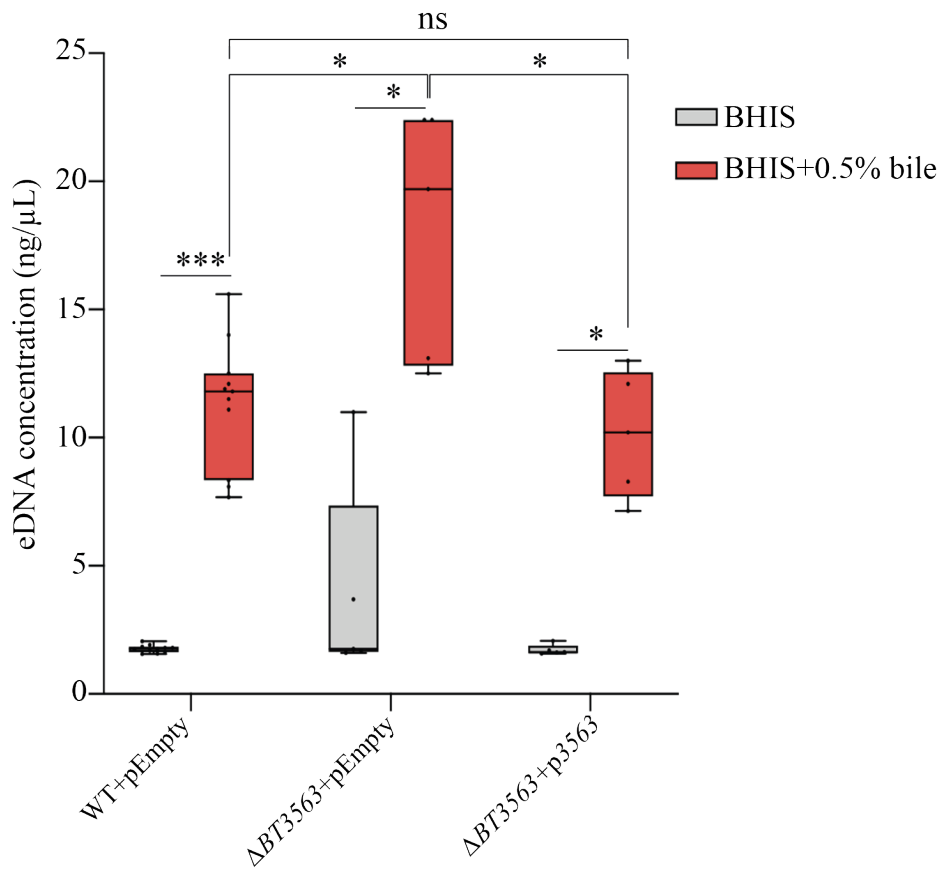


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2 Supporting Figure S7. **BT3563 does not impact protein concentration in the**
 3 **extracellular matrix.** Extracellular protein concentration (ng/ μ L) in the purified
 4 extracellular matrix of bile-dependent biofilms grown in BHIS+0.5% bile extract for 48h.
 5 Min-max boxplot of 6 biological replicates for each strain. * p-value<0.05, ** p-
 6 value<0.005, Mann-Whitney test.

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3 Supporting Figure S8. **Bile increases eDNA concentration in the supernatant.**

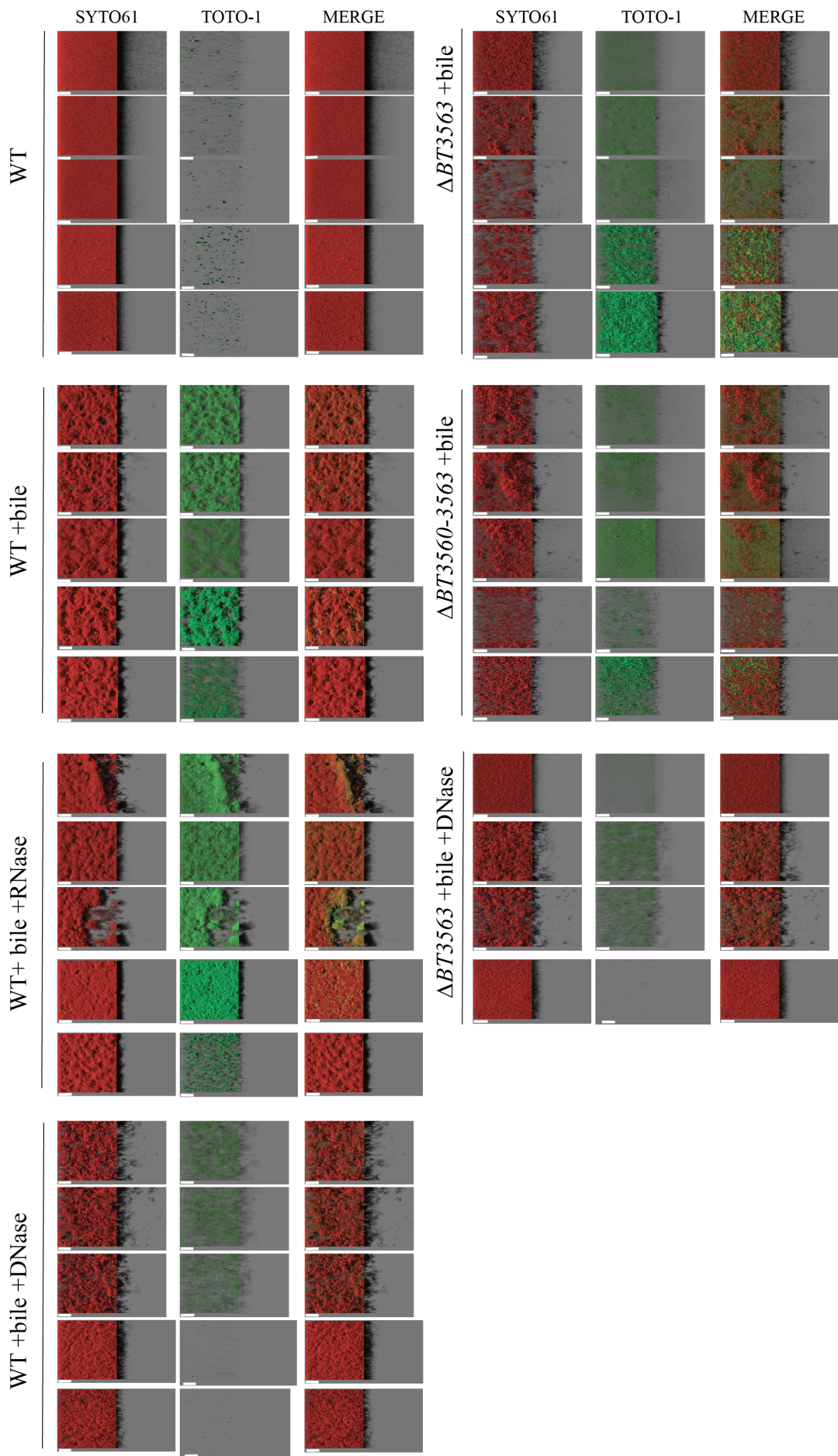
4 Extracellular DNA concentration (ng/μL) in the supernatant of overnight cultures of

5 indicated strains grown in BHIS or BHIS+0.5% bile extract. Min-max boxplot of 6-11

6 biological replicates for each strain. * p-value<0.05, *** p-value<0.0005, Mann-Whitney

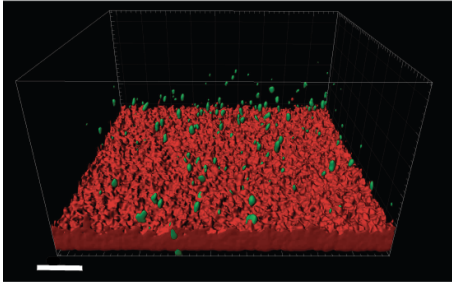
7 test.

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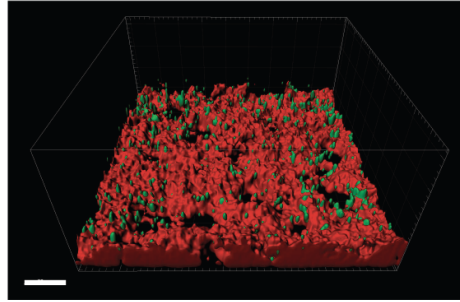


1 Supporting Figure S9. **Visualization of *B. thetaiotaomicron* biofilms.** IMARIS easy
2 3D projections from confocal laser scanning (CLSM) microscopy images of *B.*
3 *thetaiotaomicron* biofilms grown in plates in absence or presence of 0.5% bile extract
4 (“+bile”), RNase I (“+RNase”), or DNase I (“+DNase”). Cells are labelled with SYTO61
5 dye (left panel, in red). eDNA and dead cells are labelled with TOTO-1 (middle panel,
6 in green). The merged image is shown on the right. For each image, the virtual shadow
7 projection of the biofilm is shown on the right. Scale bars represent 40 µm.
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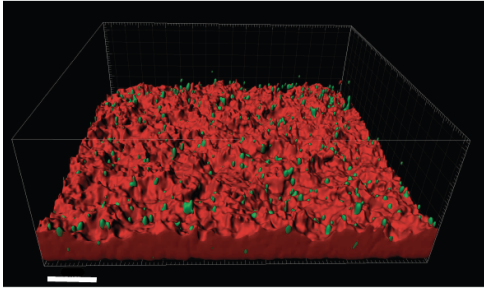
WT



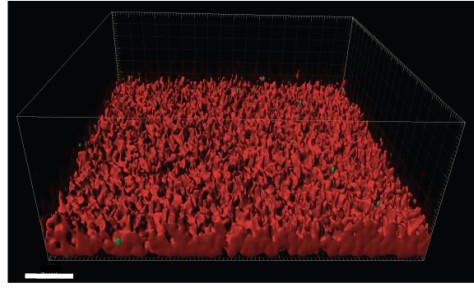
WT +bile



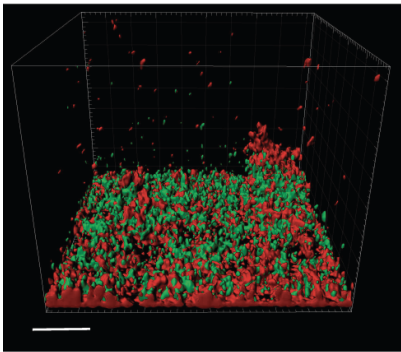
WT+ bile +RNase



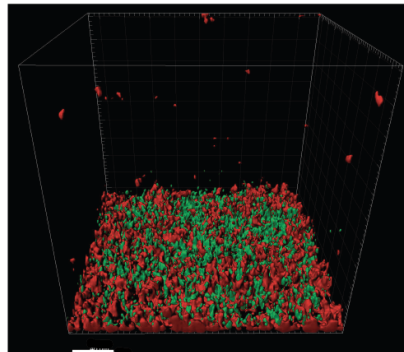
WT +bile +DNase



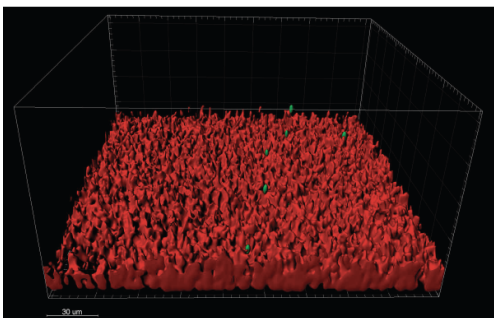
$\Delta BT3563$ +bile



$\Delta BT3560-3563$ +bile

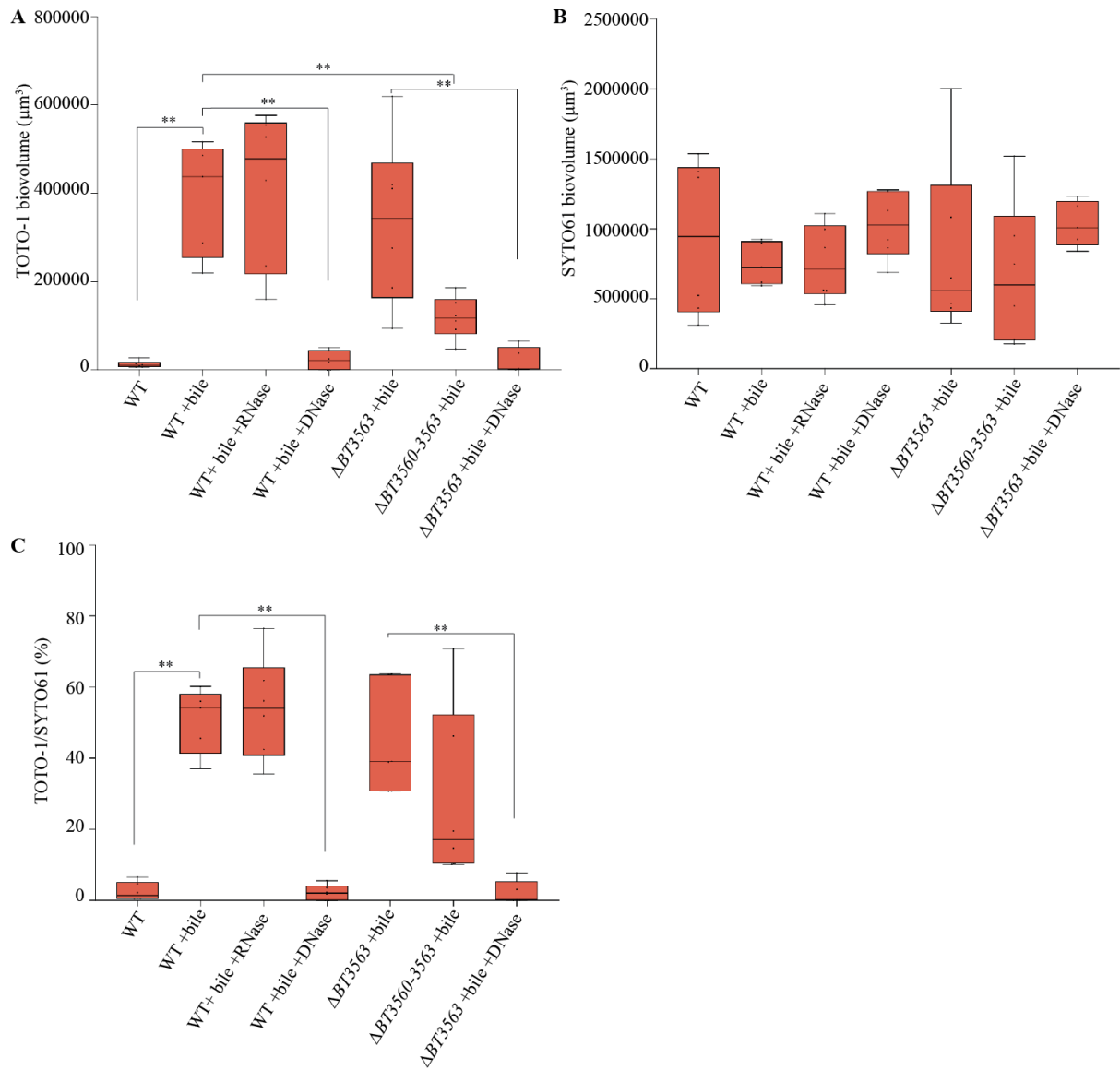


$\Delta BT3563$ +bile +DNase



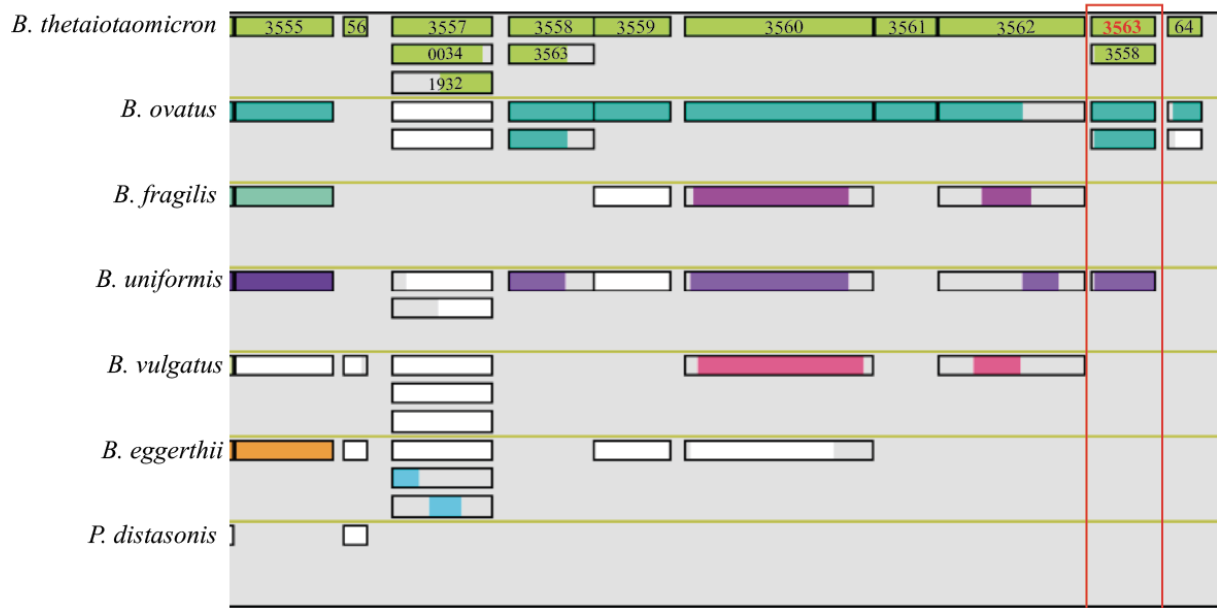
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Supporting Figure S10. **3D reconstruction of *B. thetaiotaomicron* biofilms.** 3D reconstruction of *B. thetaiotaomicron* biofilm grown in plates in absence or presence of 0.5% bile extract (“+bile”), RNase I (“+RNase”), or DNase I (“+DNase”). Merged images showing cells labelled with SYTO61 dye in red and extracellular DNA and dead cells labelled with TOTO-1 in green. Scale bar represent 30 μ m.



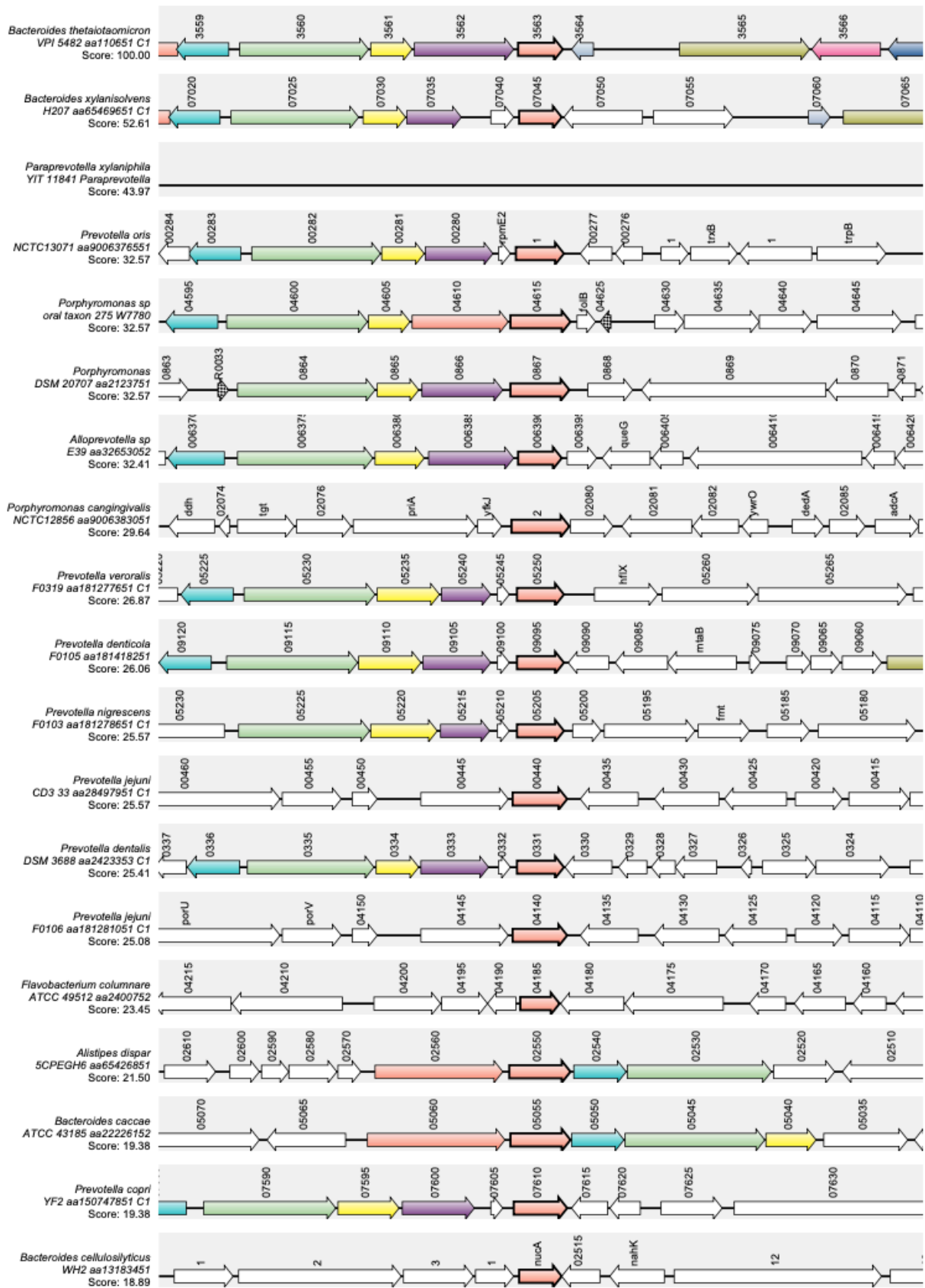
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 2 Supporting Figure S11. **Quantification of confocal microscopy images.** Min-Max
 3 boxplot of **A.** biovolumes of TOTO-1 (μm^3) and **B.** SYTO61 fluorescence (μm^3) and **C.**
 4 TOTO-1/SYTO61 fluorescence ratio (%). 5-6 biological replicates, each representing
 5 the mean of 2-3 technical replicates. ** p-value<0.005, Mann-Whitney test.

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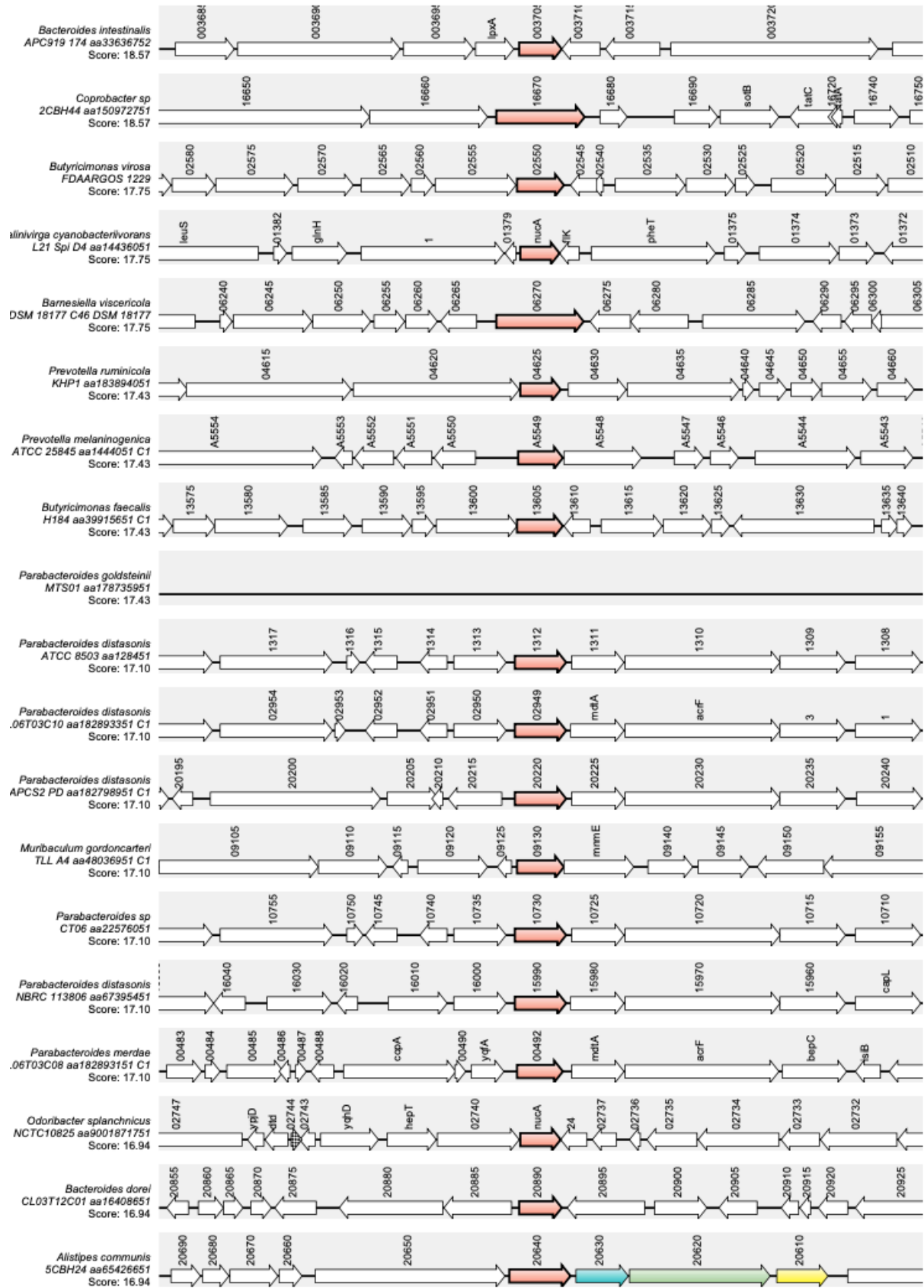


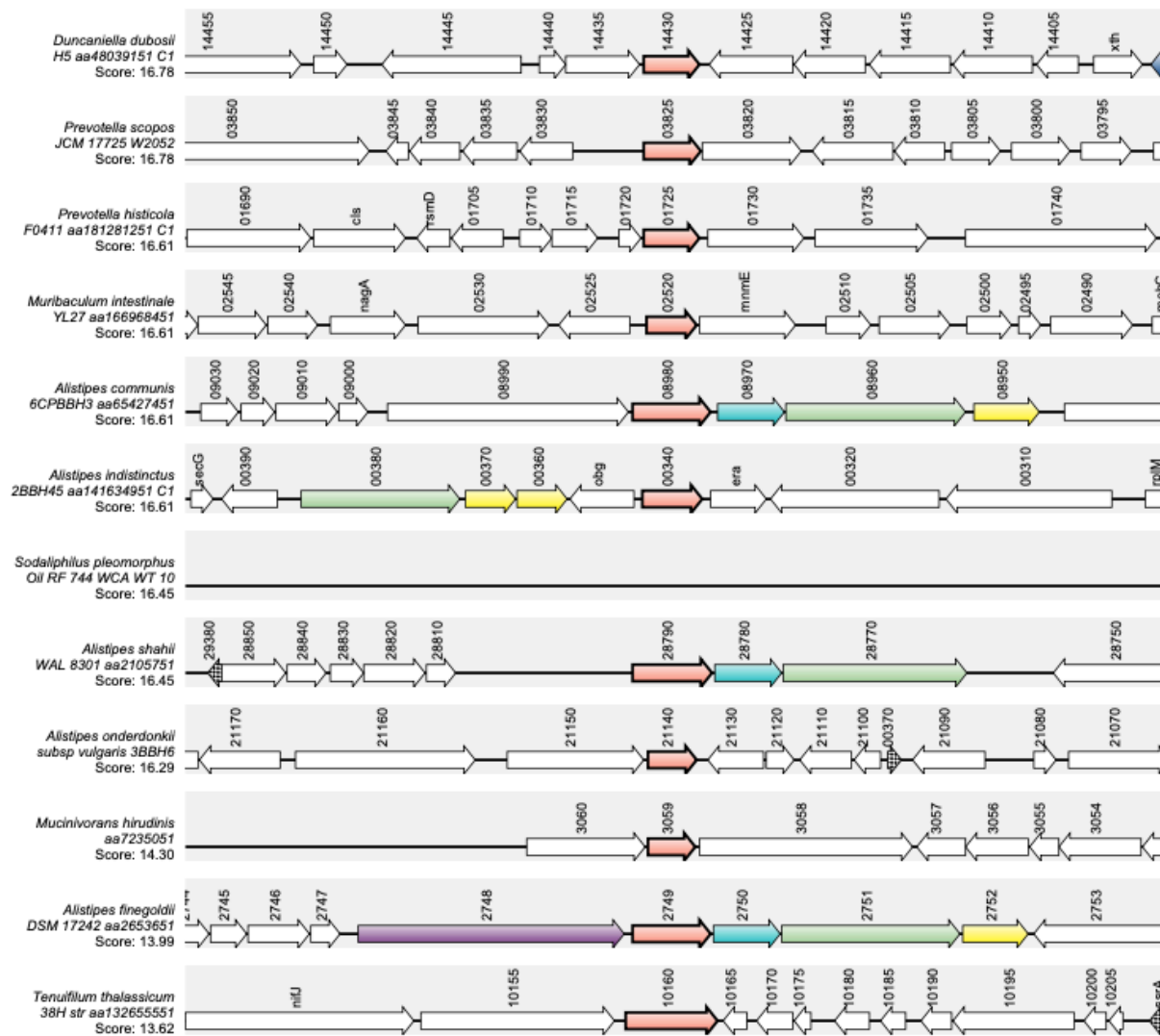
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2 Supporting Figure S12. **BT3555-3564 synteny among the tested Bacteroidales.**
3 Synteny analysis was performed using the Genome browser tool of the genome
4 analysis platform MicroScope,
5 (<https://mage.genoscope.cns.fr/microscope/mage/viewer.php?>) (3) For each genome,
6 the first line represents the genes on the chromosome, and the additional lines
7 represent homologs of the considered gene within the same genome, when applicable.
8 The colored bar represents the length of the homology. Locus tags are indicated for *B.*
9 *thetaitaomicron* VPI-5482 strain, and the homologs of *BT3563* are indicated in a red
10 square.

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Query protein sequence:

```

mrfnfrsvlllicctfflvscskddedenkeniafspielpalrngaddiflspstttfngqqvitysmey
dkskharwvafkyynvtgqtnwrrndwkqtewggdpwqsdpnipqadqrvsdfgkqgydrghicassd
rlyskdanegtffyymspnknyfngtkgiwndlegkvrtrwrsstfrdtlyvvkqgtdikenqwtiyg
gdkskpvkpyfmallckkgetykaigfwdqstvtvkpalsecaktideleeltgldffhnlpdnlenav
eskyaisawtqlq*

```

Genomes without synteny:

```

Dysgonomonas_sp_HDW5A_aa112995551
Proteiniphilum_saccharofermentans_M3_6_aa9000951351
Paludibacter_propionicigenes_WB4_aa1831351
Fermentimonas_caenicola_aa9535351
Petrimonas_mucosa_ING2_E5A_aa9000957951
Petrimonas_sp_IBARAKI_aa23564352
Porphyromonas_gingivalis_381_aa13142651
Porphyromonas_gingivalis_ATCC_33277_aa105051
Porphyromonas_gingivalis_KCOM_2796_aa27541151
Porphyromonas_gingivalis_LyG_2_aa181417451
Prevotella_denticola_KCOM_1525_aa35150451_C1
Prevotella_intermedia_ATCC_25611_DSM_20706_aa19539551_C1
Prevotella_multiformis_F0096_aa181279851_C1
Tannerella_forsythia_3313_aa15478751
Tannerella_sp_oral_taxon_HOT_286_W11666_aa30339251
Labilibaculum_antarcticum_SPP2_aa23562951
Alkalitalea_saponilacus_SC_BZ_SP2_aa22017951
Draconibacterium_orientale_FH5_aa6266351
Draconibacterium_sp_M1_aa104488351
Chryseobacterium_gallinarum_DSM_27622_aa10219751
Chryseobacterium_indoltheticum_ATCC_27950_aa38159151
Chryseobacterium_joostei_DSM_16927_aa38157751_C1
Chryseobacterium_indologenes_DSM_16777_aa160250551

```

3

4

1 Supporting Figure S13. **BT3563 synteny among diverse Bacteroidetes**. Synteny
2 analysis was performed using the web tool SyntTax (4). Homologs of the gene of
3 interest, *BT3563*, are marked in bold. Homologous genes are represented in the same
4 color. Locus tags are annotated on top of each gene. A list of all tested strains for which
5 no *BT3563* homologs was found is present at the bottom.

6

7

1 **SUPPORTING TABLES**

2

3 **Supporting Table S1. *Bacteroides thetaiotaomicron* strains used in this study**

Strain	Strain name 2	Origin	From	PATRIC ID	Genbank ID
jmh42	N03576	Perforated ulcer	CHU Limoges	818.1412	JAGURM000000000 0
jmh43	N03525	Blood	CHU Limoges	818.1456	JAGURL000000000
jmh44	N03594	Blood	CHU Limoges	818.1484	JAGWEU000000000 0
jmh47	N03736	Hepatic abscess	CHU Limoges	818.1421	JAGURK000000000
jmh50	Ana-1-p17	Ascitic fluid	CHU Limoges	818.1481	JAGWET000000000
jmh51	Ana2-p19	Blood	CHU Limoges	818.1411	JAGURJ000000000
jmh58	Ana4-p37	Blood	CHU Limoges	818.1450	JAGURI000000000
jmh60	os16-p16	Hip implant	CHU Limoges	818.1415	JAGURH000000000
jmh61	Ana4-p81	Continuous ambulatory peritoneal dialysis (CAPD)	CHU Limoges	818.1480	JAGWES000000000 0
jmh62	10018	Peritoneal fluid	CHU Lille	818.1419	JAGURG000000000
jmh63	10023	Blood	CHU Lille	818.1414	JAGURF000000000
jmh66	10254	Maxilar pus	CHU Lille	818.1416	JAGURE000000000
jmh68	10263	Blood	CHU Lille	818.1451	JAGURD000000000
jmh71	11276	Blood	CHU Lille	818.1482	JAGWER000000000 0
jmh72	11278	Anal abscess	CHU Lille	818.1449	JAGURC000000000
jmh76	11285	Fat tissue	CHU Lille	818.1483	JAGYXC000000000
jmh78	12309	Abdominal abscess	CHU Lille	818.1417	JAGURB000000000
jmh79	11314	Intestinal cyste	CHU Lille	818.1447	JAGURA000000000

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1 **Supporting Table S2. BT3563 homologs identified by blastp**

Genome	PATRIC ID	Length (AA)	ALN Length	Identity	Query cover	Subject cover	Hit from	Hit to	Score	E value
VPI-5482	fig 226186.12.peg.3626 (BT_3563)	293	293	100	100	100	1	293	614	0
jmh42	fig 818.1412.peg.329	296	296	87	99	99	4	296	532	0
jmh43	fig 818.1456.peg.161	396	396	34	81	60	149	385	119	8,00E-30
jmh44	fig 818.1484.peg.456	290	290	87	99	100	1	290	525	0
jmh47	fig 818.1421.peg.2384	290	290	87	99	100	1	290	525	0
jmh50	fig 818.1481.peg.2033	290	290	87	99	100	1	290	525	0
jmh51	fig 818.1411.peg.850	296	296	87	99	99	4	296	532	0
jmh58	fig 818.1450.peg.2100	223	223	97	77	100	1	223	457	1,00E-162
jmh60	fig 818.1415.peg.1161	399	399	34	81	59	152	388	119	1,00E-29
jmh61	fig 818.1480.peg.1186	291	291	87	100	100	1	291	527	0
jmh62	fig 818.1419.peg.360	399	399	34	81	59	152	388	119	9,00E-30
jmh63	fig 818.1414.peg.2874	396	396	34	81	60	149	385	119	9,00E-30
jmh66	fig 818.1416.peg.3454	291	291	87	100	100	1	291	527	0
jmh68	fig 818.1451.peg.696	399	399	34	81	59	152	388	119	1,00E-29
jmh71	fig 818.1482.peg.3309	399	399	34	81	59	152	388	119	1,00E-29
jmh72	fig 818.1449.peg.2960	396	396	34	81	60	149	385	119	8,00E-30
jmh76	fig 818.1483.peg.3838	296	296	85	93	92	26	296	478	1,00E-169
jmh78	fig 818.1417.peg.1663	293	293	100	100	100	1	293	613	0
jmh79	fig 818.1447.peg.3310	293	293	100	100	100	1	293	613	0

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1 **Supporting Table S3.** Bacterial strains and plasmids used in this study

Name in this paper	Genotype	Reference
<i>Bacteroides thetaiotaomicron</i>		
WT/VPI-5482	VPI-5482 <i>_Δtdk</i>	(5)
jmh42		(6)
jmh43		(6)
jmh44		(6)
jmh47		(6)
jmh50		(6)
jmh51		(6)
jmh58		(6)
jmh60		(6)
jmh61		(6)
jmh62		(6)
jmh63		(6)
jmh66		(6)
jmh68		(6)
jmh71		(6)
jmh72		(6)
jmh76		(6)
jmh78		(6)
jmh79		(6)
3H6	VPI 5482 <i>_Δtdk</i> - BT3560:: <i>Tn</i>	This study
26H1	VPI 5482 <i>_Δtdk</i> - BT3562:: <i>Tn</i>	This study
37G8	VPI 5482 <i>_Δtdk</i> - BT3560:: <i>Tn</i>	This study
46A4	VPI 5482 <i>_Δtdk</i> - BT3560:: <i>Tn</i>	This study
54A8	VPI 5482 <i>_Δtdk</i> - BT3560:: <i>Tn</i>	This study
55B7	VPI 5482 <i>_Δtdk</i> - BT3560:: <i>Tn</i>	This study
59E7	VPI 5482 <i>_Δtdk</i> - BT3560:: <i>Tn</i>	This study
62C12	VPI 5482 <i>_Δtdk</i> - BT3562:: <i>Tn</i>	This study
68H1	VPI 5482 <i>_Δtdk</i> - BT3560:: <i>Tn</i>	This study
<i>ΔBT3560-3563</i>	VPI 5482 <i>_Δtdk_ΔBT3560-3563</i>	This study
<i>ΔBT3560</i>	VPI 5482 <i>_Δtdk_ΔBT3560</i>	This study
<i>ΔBT3561</i>	VPI 5482 <i>_Δtdk_ΔBT3561</i>	This study
<i>ΔBT3562</i>	VPI 5482 <i>_Δtdk_ΔBT3562</i>	This study
<i>ΔBT3563</i>	VPI 5482 <i>_Δtdk_ΔBT3563</i>	This study
WT+pEmpty	VPI 5482 <i>_Δtdk</i> + pNBU2-bla-ery-p1311	This study
<i>ΔBT3560</i> +pEmpty	VPI 5482 <i>_Δtdk_ΔBT3560</i> + pNBU2-bla-erm-p1311	This study
<i>ΔBT3560</i> +p3560	VPI 5482 <i>_Δtdk_ΔBT3560</i> + pNBU2-bla-erm-p1311 <i>BT3560</i>	This study

Δ BT3562+pEmpty	VPI 5482 Δ tdk Δ BT3562 + pNBU2-bla-erm-p1311	This study
Δ BT3562+p3562	VPI 5482 Δ tdk Δ BT3560 + pNBU2-bla-erm-p1311 <i>BT3562</i>	This study
Δ BT3563+pEmpty	VPI 5482 Δ tdk Δ BT3563 + pNBU2-bla-tet-p1311	This study
Δ BT3563+p3563	VPI 5482 Δ tdk Δ BT3560 + pNBU2-bla-tet-p1311 <i>BT3563</i>	This study
Δ BT3560-3563+pEmpty	VPI 5482 Δ tdk Δ BT3560-3563 + pNBU2-bla-tet-p1311	This study
Δ BT3560-3563+p3563	VPI 5482 Δ tdk Δ BT3560 + pNBU2-bla-tet-p1311 <i>BT3563</i>	This study
jmh61 Δ 3563	jmh61_ Δ 3563 homolog	This study
jmh43 Δ 3563	jmh43_ Δ 3563 homolog	This study
Bacteroidales		
<i>Bacteroides fragilis</i> 638R		From Laurie Comstock
<i>Bacteroides ovatus</i> CIP 103756T/ATCC 8483		Institut Pasteur, collection
<i>Bacteroides eggerthii</i> CIP 104285T/DSM 20697		Institut Pasteur, collection
<i>Bacteroides vulgatus</i> CIP 103714T/ATCC 8482		Institut Pasteur, collection
<i>Bacteroides uniformis</i> CIP 103695T/ DSM 6597		Institut Pasteur, collection
<i>Parabacteroides distasonis</i> ATCC 8503		From Laurie Comstock
Escherichia coli		
S17 λ pir_pSAM-bt	S17 λ pir_pSAM-bt	(7)
S17 λ pir_pExchange-tdk	S17 λ pir_pExchange-tdk	(5)
S17 λ pir_pExchange-BT3560-3562	S17 λ pir_pExchange-BT3560-3562	This study
S17 λ pir_pExchange-BT3560-3563	S17 λ pir_pExchange-BT3560-3563	This study
S17 λ pir_pExchange-BT3560	S17 λ pir_pExchange-BT3560	This study
S17 λ pir_pExchange-BT3561	S17 λ pir_pExchange-BT3561	This study
S17 λ pir_pExchange-BT3562	S17 λ pir_pExchange-BT3562	This study
S17 λ pir_pExchange-BT3563	S17 λ pir_pExchange-BT3563	This study
S17 λ pir_pLGB13-jmh61_3563	S17 λ pir_pLGB13-BT3563 from jmh61	This study
S17 λ pir_pLGB13-jmh43_3563	S17 λ pir_pLGB13-BT3563 from jmh43	This study
S17 λ pir_pNBU2-bla-erm-p1311	S17 λ pir_pNBU2-bla-erm-p1311	This study
S17 λ pir_pNBU2-bla-erm-p1311-BT3560	S17 λ pir_pNBU2-bla-erm-p1311-BT3560	This study
S17 λ pir_pNBU2-bla-erm-p1311-BT3562	S17 λ pir_pNBU2-bla-erm-p1311-BT3562	This study
S17 λ pir_pNBU2-bla-tet-p1311	S17 λ pir_pNBU2-bla-tet-p1311	This study
S17 λ pir_pNBU2-bla-tet-p1311-BT3563	S17 λ pir_pNBU2-bla-tet-p1311-BT3563	This study
Plasmids		
Name	Description	Reference

pSAM-bt	Random transposon mutagenesis	(6)
pExchange-tdk	Site-directed unmarked gene deletion	(8)
pLGB13	Site-directed unmarked gene deletion in natural isolates	(9)
pExchange-BT3560-3562	Site-directed unmarked gene deletion	This study
pExchange-BT3560-3563	Site-directed unmarked gene deletion	This study
pExchange-BT3560	Site-directed unmarked gene deletion	This study
pExchange-BT3561	Site-directed unmarked gene deletion	This study
pExchange-BT3562	Site-directed unmarked gene deletion	This study
pExchange-BT3563	Site-directed unmarked gene deletion	This study
pLGB13-jmh61_3563	Site-directed unmarked gene deletion	This study
pLGB13-jmh43_3563	Site-directed unmarked gene deletion	This study
pNBU2-bla-erm-p1311	Site-directed unmarked gene deletion	(10)
pNBU2-bla-erm-p1311-BT3560	Complementation	This study
pNBU2-bla-erm-p1311-BT3562	Complementation	This study
pNBU2-bla-tet-p1311	Complementation	This study
pNBU2-bla-tet-p1311-BT3563	Complementation	This study

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Supporting Table S4: List of primers used in this study

Construct	Name	Sequence (5'-->3')	
pExchange	pEx-ch-F	TGGGAATCCCCTCCACCGC	
	pEx-ch-R	GGGGAGAGGACGGACAGAAGAT	
	pExchange R	CGTCGACTCGAATGTTATCTTC	
	pExchangeF	TCTAGAGCGGCCGCCACC	
pExchange-BT3560-3562	3560-5Fb	AGATAACATTCGAGTCGACGGTACTTTCCTTCTTTTTGGAAC	
	3560-5Rb	TACTTTAAAATATGCACCCAAATTTAAATTATTATTAGTGTTAATTTGTAGC	
	3562-3Fb	CACTAATAATAATTTAAATTTGGGTGCATATTTTAAAGTACCAGG	
	3562-3R	GCGGTGGCGGCCGCTCTAGATTGTGGATGAAGATCAGCAATAGAC	
pExchange-BT3560-3563	3560-5Fb	AGATAACATTCGAGTCGACGGTACTTTCCTTCTTTTTGGAAC	
	3560-5Rb	TATAACAAACAAGTTTTATTAATTTAAATTATTATTAGTGTTAATTTGTAGC	
	3563-3Fb	CACTAATAATAATTTAAATTAATAAAACTTGTTTGTATAGATATAATTAGACC	
	3563-3R	GCGGTGGCGGCCGCTCTAGAAACATATATCTTTGCTGTACAC	
	3560-extF	CGCTATACCCATTAAGCCATAC	
	3563-extR	GATATTAATGGCAACAACACC	
pExchange-BT3560	3560-3F	GATTAGGAATAGTGATTGCAATAAATGGGCAAATTAATACAAGGAAATG	
	3560-3R	GCGGTGGCGGCCGCTCTAGACAAGCTTCTGAGTTATCCTGTTTC	
	3560-5R	GTATTAATTTGCCATTTATTGCAATCACTATTCCTAATCTTTGTTTC	
	3560-5F	AGATAACATTCGAGTCGACGTTAGCGGATACAGAACAGATGG	
pExchange-BT3561	3561-3F	TAATACAAGGAAATGATATGCAAAGAAATAACTAATAAAAAATAATTTCAAC	
	3561-3R	GCGGTGGCGGCCGCTCTAGAAGAAGAGCTAGTACTTGTATATTTAAATC	
	3561-5R	TTTTATTAGTTATTTCTTTGCATATCATTTCTTGTATTAATTTGCC	
	3561-5F	AGATAACATTCGAGTCGACGTTATCAGGGTGATAACGATGGAC	
pExchange-BT3562	3562-3F	TGATGTTCTGCTCCTTATGTGGGTGCATATTTTAAAGTACCAGG	
	3562-3R	GCGGTGGCGGCCGCTCTAGATTGTGGATGAAGATCAGCAATAGAC	
	3562-5R	GTACTTTAAAATATGCACCCACATAAGGAGCAGGAACATCACTAC	
	3562-5F	AGATAACATTCGAGTCGACGTACGAACCTTGCCTACTGGCG	
	pExchange-BT3563	3563-3F	CTTTTTTAACAAAAATGAATTAATAAAACTTGTTTGTATAGATATAATTA GACC
		3563-3R	GCGGTGGCGGCCGCTCTAGAAACATATATCTTTGCTGTACAC
	3563-5R	CTATAACAAACAAGTTTTATTAATTCATTTTTGTTAAAAAAGGAG	
	3563-5F	GAAGATAACATTCGAGTCGACGGCAGATTTGAGTGCTCAAGC	
	3563-extF	GATAATACATGGGTATCATTGAC	
	3563-extR	GATATTAATGGCAACAACACC	
pLGB13	pLGB13-linR	TGATATCGAATTCCTGCAGC	
	pLGB13-linF	GCTTATCGATACCGTCGAC	
	pLGB13-chF	GGTGTAAGATTAGCATTATGAGTG	

	pLGB13- chR	CCATCACTGGAAGATAGGC
pLGB13- jmh61_3563	jmh61-3563- 5R	AACAAACAAGTTTTATTCTATATTGAAAATTAAGGGGAGTATATTAC
	jmh61-3563- 5F	GCTGCAGGAATTCGATATCAACTGAAACTCTTGGTGCG
	jmh61-3563- 3F	ACTCCCCTTAATTTTCAATATAGAATAAACTTGTGGTTATAGATATAA
	jmh61-3563- 3R	AGTCGACGGTATCGATAAGCGCGCATCAGCGAGATGTAATAAGC
pLGB13- jmh43_3563	jmh43-3563- 5R	TAAGCTAGCTTATTTAAGATATATATTTAGAGACAAGTAAC
	jmh43-3563- 5F	GAAGATAACATTCGAGTCGACGGCAGATTTGAGTGCTCAAGC
	jmh43-3563- 3F	CTCTAAATATATATCTTAAATAAGCTAGCTTATGAAAAACTGTTATTAG
	jmh43-3563- 3R	GATATTAATGGCAACAACACC
pNBU2-bla	pNBU-chR	GCCAATGCACAAATGCTGTTCC
	pNBU-chF	CAGGTGTATCCCATCCGG
	pNBU-F	CGACGTCGACTAATTGCC
	pNBU-R	ATGTTAAAAACAGATTTGGAGTGC
pNBU2-bla- erm-p1311- BT3560	NBU-3560-F	AATCTGTTTTTAACATATGAAACAAAGATTAGGAATAGTGATTGC
	NBU-3560- R	TAGGCAATTAGTCGACGTCGTTAGAATCTATATCCAATGTTCAAGAAAG C
pNBU2-bla- erm-p1311- BT3562	NBU-3562-F	AAATCTGTTTTTAACATATGAAAAAGATTCTAAATGCTTTATTCTTG
	NBU-3562- R	TAGGCAATTAGTCGACGTCGTTATTCACGAACCTTATATTCGGTAGG
pNBU2-bla-tet- p1311-BT3563	NBU-3563- R	TAGGCAATTAGTCGACGTCGCTATTGCAGTCCGGTCC
	NBU-3563-F	TCCAATCTGTTTTTAACATATGAGATTTTTTAATAGAAGTGTG

1 **Supporting Dataset S1** (excel spreadsheet). RNAseq analysis: table of A. all genes,
2 B. upregulated, C. downregulated genes in presence of 0.5% bile, D. COG functional
3 categories enrichment.
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Supplementary Information Reference list

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