SUPPLEMENTARY INFORMATION

A conserved biosynthetic gene cluster is regulated by quorum sensing in a shipworm symbiont

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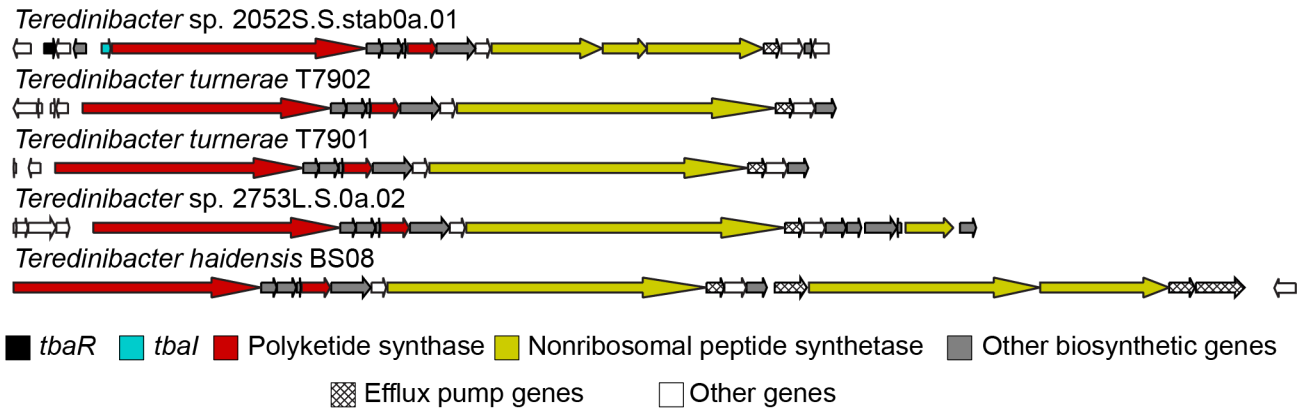

Figure S1. GCF_3 is conserved in cellulolytic shipworm symbionts. Representative shipworm symbionts and their biosynthetic gene clusters belonging to GCF_3. Amino acid identity of core biosynthetic genes is at least 65% in all cases. Genes are colored according to predicted function in antiSMASH 6.0 (1).

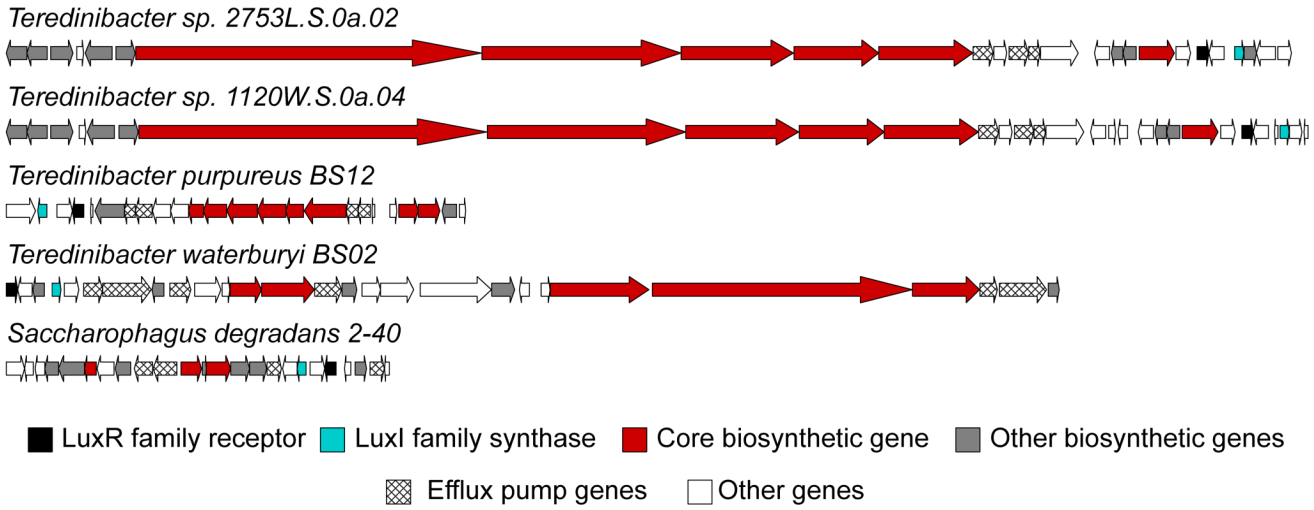

Figure S2. Biosynthetic gene clusters co-located with quorum sensing genes in other shipworm symbiont genomes. Genes are colored according to predicted function in antiSMASH 6.0 (1).

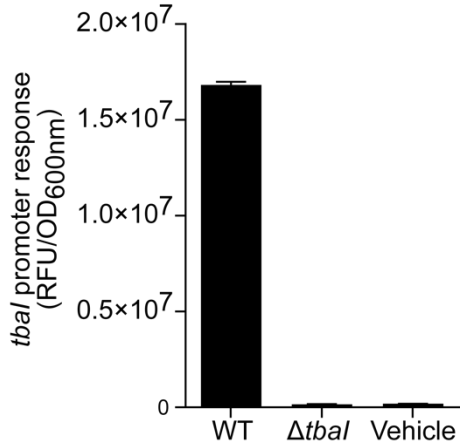

Figure S3. Response of P_{tbaI}-*gfp E. coli* reporter strain EAWP128 to crude supernatant extracts of the 2052S and Δ*tbaI* mutant strains. Vehicle: ethyl acetate.

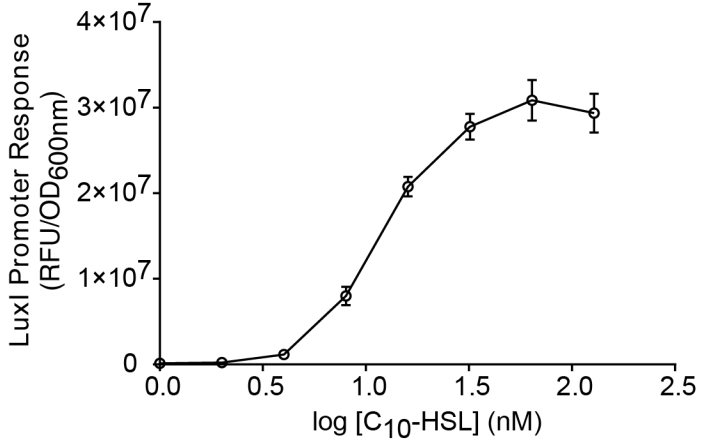

Figure S4. Response of P_{tbaI}-*gfp E. coli* reporter strain EAWP128 to a commercial standard of C_{10}-HSL.

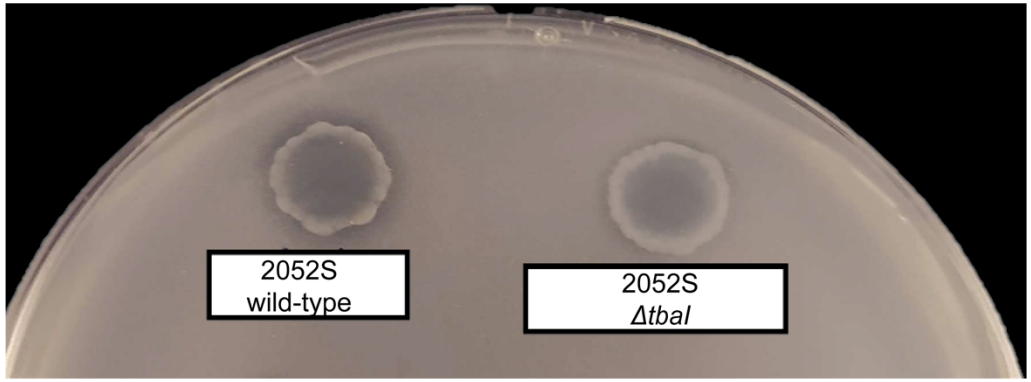

Figure S5. The Δ*tbaI* strain retains its cellulolytic ability. Small halo around the spotted colony on the shipworm basal medium (SBM) cellulose plate indicates cellulolysis.

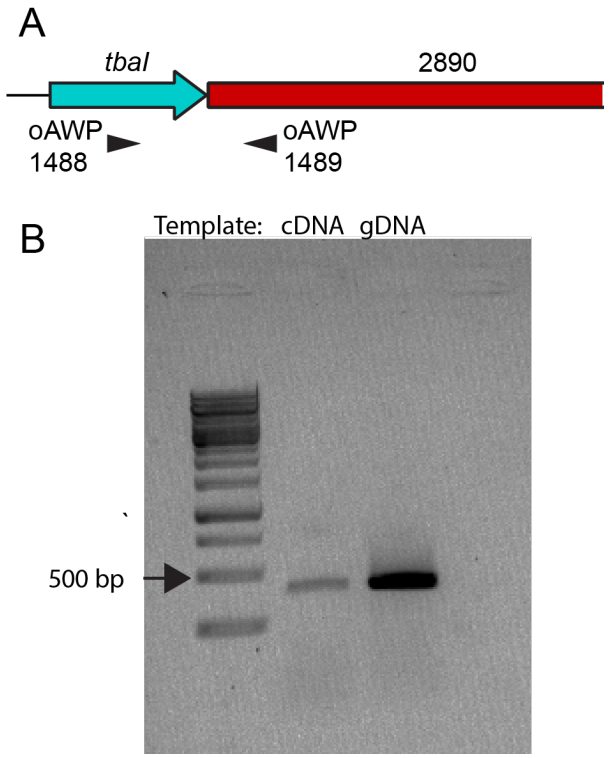

Figure S6. The predicted PKS gene K256DRAFT_2890 is co-transcribed with *tbaI*. (A) Locations of primers designed to span open reading frames of *tbaI* and K256DRAFT_2890. (B) Amplification of the region in A. The PCR template was either genomic DNA (gDNA) or cDNA from 2052S. Expected product size: 427 bp.

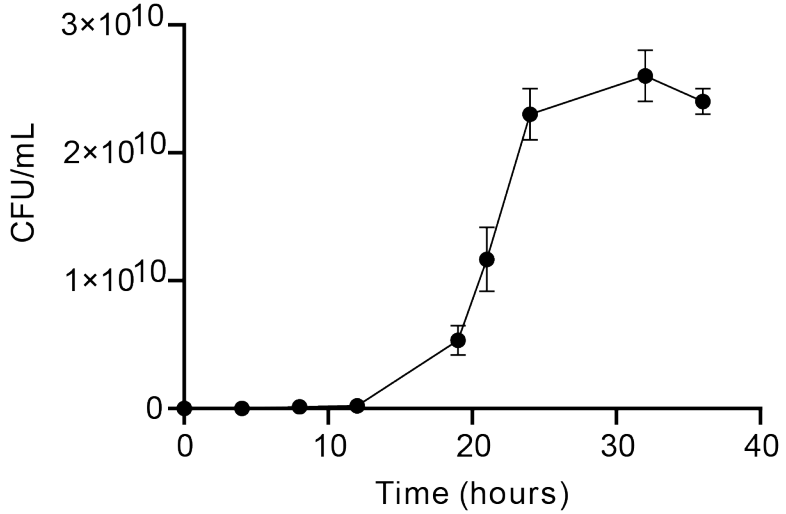

Figure S7. Growth curve of 2052S in SBM cellulose.

Table S1. Shipworm isolate strain information.

Isolate name	Metabolic type	Host shipworm	Collection site	Sequencing center	Estimated genome size (bp)	% GC	IMG Genome ID	Reference
Teredinibacter sp. PMS-2052S.S.stab0a.01	Cellulolytic	PMS-1959H *Bactronophorus* cf. *thoracites*	Butuan, Agusan del Norte, Philippines	JGI-DOE	5,635,926	54.68	2541046951	(2)
Teredinibacter turnerae T7901	Cellulolytic	*Bankia gouldi*	Beaufort, North Carolina, USA	J. Craig Venter Institute	5,193,164	50.89	2541046951	
Teredinibacter turnerae T7902	Cellulolytic	*Lyrodus pedicellatus*	Long Beach, California, USA	JGI-DOE	5,387,817	50.81	2513237099	
Teredinibacter sp. PMS-2753L.S.0a.02	Cellulolytic	PMS-2749X *Bactronophorus thoracites*	Infanta, Quezon, Philippines	JGI-DOE	6,056,039	47.96	2579779156	
Teredinibacter haidensis Bs08	Cellulolytic	*Bankia setacea*	Puget Sound, Washington, USA	JGI-DOE	4,814,259	47.18	2767802764	
Teredinibacter sp. 1120W.S.0a.04	Cellulolytic	PMS-1114L *Teredo fulleri*	Panglao, Bohol, Philippines	JGI-DOE	5,699,307	50.39	2558309032	
Teredinibacter purpureus BS12	Cellulolytic	*Bankia setacea*	Puget Sound, Washington, USA	JGI-DOE	4,921,245	45.72	2878457929	
Teredinibacter waterburyi BS02	Cellulolytic	*Bankia setacea*	Puget Sound, Washington, USA	JGI-DOE	3,886,134	47.76	2781125611	

Table S2. HR-MS/MS peak list for C_{10}-HSL ($[M+H]^+$) produced by 2052s compared to commercial standard. The 10 most intense signals are shown for each sample.

2052S		**Standard**	
m/z	Intensity	*m/z*	Intensity
102.0563	6.50E+03	102.0565	2.90E+04
256.1914	6.30E+03	256.1915	2.90E+04
155.1430	6.10E+03	155.1431	2.10E+04
238.1810	1.20E+03	238.1813	9.20E+03
95.0874	9.40E+02	95.0871	8.80E+03
81.0723	8.70E+02	81.0718	8.60E+03
74.0631	8.60E+02	74.0629	8.30E+03
228.1940	8.10E+02	156.1468	8.10E+03
156.1456	7.60E+02	137.1328	8.00E+03
137.1326	7.32E+02	228.1968	7.90E+03

REFERENCES

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2. Altamia MA, Lin Z, Trindade-Silva AE, Uy ID, Shipway JR, Wilke DV, Concepcion GP, Distel DL, Schmidt EW, Haygood MG. 2020. Secondary Metabolism in the Gill Microbiota of Shipworms (Teredinidae) as Revealed by Comparison of Metagenomes and Nearly Complete Symbiont Genomes. mSystems https://doi.org/10.1128/mSystems.00261-20