

Table S1. Oligonucleotide primers used in this study. K, R, W, and Y are based on the IUPAC code, where K stands for T/G, R stands for A/G, W stands for A/T, and Y stands for C/T.

Primer name	Sequence (5'–3')
1pr2ie	CTTATACTTCGGCTCGATGCGTGGTGTATGCACC
1pr2yk	CGCTGATTTGCTCTTATAGCGTGGTGTATGCACC
1Pr3IE	GGTGCATCACCACGCATCGAGCCGAAGTATAAG
1Pr3YK	GGTGCATCACCACGCTATAAGAGCAAATCAGCG
4Pr3	GGTGCATCACCACGCATTACAAGTCAACACTC
1Pr4	ATTCATGACTCCGTATTCTTTATTATTTAC
3PrA2162c	TGCTCTCGGAACCAAGTC
4pr2	GAGTGTTGACTTGTAATGCGTGGTGTATGCACC
5PrA2162280	GTTGAATGATGGTGAACGTG
a13AleI	TTTTCCACCGTAGTGTATTATTACCTGTG
a15pTG	CGAAATCATCAAATTTTCCCATTTTGAGTGCCTCC
a25pTG	CGAAATCATCAAATTTTGCCATTTTGAGTGCCTCC
a43AleI	TGTACACTAAAGTGGATTTATTGACCCTTTAAT
i5pTG	CTTTTTATTAATACTACTATTCTTCATTTTGAGTGCCTCC
iAleIb	TTTCACTTTTGTGACCCATACTAATC
lanA14	GTATTCTAGATTATTTACCTGTGATATGGC
lanA44	CTAATCTAGATTTATTGACCCTTTAATTTACATGTG
lanC340	GWRWKGSWTGGTGTATG
NisA-BspHF	CACTCATCATGAGTACAAAAGATTTTAAC
NisA-BspHR	ACTATCTCATGATTTGGTTATTTGCT
nzrevcpJAZZ	AAATGGTCAGTTAATCAGTTCT
p181	GCGAAGATAACAGTGACTCTA
p54	CGGCTCTGATTAATTCTGAAG
pIL253F	CGACAATGATTGTATTTGC
pIL253R	TAGTTCTTGTGGTTACGTGG
pJAZZf	TGATTACATTTGCGGCCTAAC
pr1	ATTCATGAGTACAAAAGATTTTAACTTGG
pTG262-F	GGTCGACTCTAGAGGATCC
pTG262-R	GCCGGAAAGAGCGAAAATG
pTGA13	GGAGGCACTCAAATGGGAAAATTTGATGATTTCCG
pTGA23	GGAGGCACTCAAATGGCAAATTTGATGATTTCCG
pTGI3	GGAGGCACTCAAATGGGAAAATTTGATGATTTCCG
reverse	AGCGGATAACAATTTACACAGGA
rlanC460	WDYWCCWBNWARWADWCC
spI5	GCACTCAAATGAGAAGATATTTAATAC
splA1	CGTTATCTAATACTGATCTATGG
splA2	GATTTATTGACCCTTGCCCTCTTTCTTTTTG
splA3	AAAAGAAAGGAGGCAAGGGTCAATAAATCT
splA4	ATAATCATCTGCTCCACTC
splI3AleI	ATTCACTTTTGTGCACTCTAGTTTCC
universal	GTTTTCCCAGTCACGACGTTGT

Table S2 *B. obeum* A2-162 putative lantibiotic cluster analysis

Gene	Predicted function	GC %	Size (aa [†])	Top BlastP match (E value)	% Identity	Top conserved domain/superfamily (E value)
<i>orf1</i>	Partial transcriptional regulator	38.3	127	WP_005421656 transcriptional regulator, <i>B. obeum</i> (3e-78)	94 over 126 aa	No conserved domains
<i>nsoF</i>	Immunity	34.7	238	WP_044912948 multispecies lantibiotic ABC transporter ATP-binding protein, Clostridiales (9e-118)	169 over 233 aa	TIGR03740, gallidermin-class lantibiotic protection ABC transporter, ATP-binding subunit (9,71e-131)
<i>nsoE</i>	Immunity	32.2	239	WP_065541939 lantibiotic ABC transporter permease, <i>Blautia</i> sp YL58 (7e-51)	92 over 238 aa	TIGR03732, lantibiotic protection ABC transporter permease subunit, MutE/EpiE family (3.51e-40))
<i>nsoG</i>	Immunity	31.6	309	WP_029471090 hypothetical protein, Clostridiales bacterium VE202-06 (2e-42)	95 over 247 aa	TIGR03733, lantibiotic protection ABC transporter permease subunit, MutG family (4.39e-30)
<i>nsoI</i>	Immunity	30.2	297	WP_040329118 hypothetical protein, <i>Clostridium ihumii</i> (2e-50)	98 over 260 aa	No conserved domains
<i>nsoR1</i>	Response regulator	34.5	221	SCH54198 <i>Staphylococcus</i> exoprotein expression protein R, uncultured <i>Blautia</i> sp (3e-82)	120 over 185 aa	COG0745, DNA binding response regulator, OmpR family (1.37e-62)
<i>nsoK1</i>	Signal transduction histidine kinase	30.1	452	CBL21418 signal transduction histidine kinase, <i>Ruminococcus</i> sp. SR1/5 (2e-125)	201 over 451 aa	COG0642, Signal transduction histidine kinase (5.07e-39)
<i>nsoA1</i>	Lantibiotic prepeptide	46.2	56	WP_069329679 lantibiotic nisin A, <i>Paenibacillus</i> sp TI45-13ar (9e-17)	60 over 55 aa	TIGR03731, lantibiotic, gallidermin/nisin family (1.15e-07)
<i>nsoA2</i>	Lantibiotic prepeptide	45.6	56	WP_06932967 lantibiotic nisin A, <i>Paenibacillus</i> sp TI45-13ar (9e-17)	62 over 55 aa	TIGR03731, lantibiotic, gallidermin/nisin family (7.39e-08)
<i>nsoA3</i>	Lantibiotic prepeptide	45.0	56	WP_069329679 lantibiotic nisin A, <i>Paenibacillus</i> sp TI45-13ar (9e-17)	62 over 55 aa	TIGR03731, lantibiotic, gallidermin/nisin family (7.39e-08)

<i>nsoA4</i>	Lantibiotic prepeptide	32.8	57	YP_001124394 lantibiotic antimicrobial precursor peptide, <i>Geobacillus thermodenitrificans</i> NG80-2 (7e-06)	59 over 41 aa	cl03420, Gallidermin super family (4.59e-04)
<i>nsoR2</i>	Response regulator	29.4	234	WP_065541933 DNA-binding response regulator, <i>Blautia</i> sp YL58 (3e-108)	157 over 220 aa	COG0745, DNA binding response regulator, OmpR family (4.47e-65)
<i>nsoK2</i>	Signal transduction histidine kinase	28.8	452	WP_065541932 sensor histidine kinase, <i>Blautia</i> sp YL58 (1e-153)	221 over 451 aa	COG0642, Signal transduction histidine kinase (1.84e-24)
<i>nsoB</i>	Lantibiotic dehydratase	31.0	1019	WP_069329682 subtilin biosynthesis protein SpaB, <i>Paenibacillus</i> sp TI45-13ar (e0.0)	414 over 1023 aa	pfam04738, Lantibiotic dehydratase, C terminus (8.94e-116)
<i>nsoT</i>	Lantibiotic transporter	30.2	603	WP_065541930 ABC transporter ATP-binding protein, <i>Blautia</i> sp YL58 (e0.0)	390 over 600 aa	COG1132, ABC-type multidrug transport system, ATPase and permease components [Defense mechanisms] (1.06e-83)
<i>nsoC</i>	Lantibiotic cyclase	32.8	448	WP_065541929 Hypothetical protein, <i>Blautia</i> sp YL58 (1e-177)	236 over 412 aa	cd04793, cyclases involved in the biosynthesis of lantibiotics (3.26e-116)
<i>orf2</i>	Putative transposase	37.4	128	SCH51517 Uncharacterised protein, uncultured <i>Eubacterium</i> sp. (1e-77)	92 over 121 aa	No conserved domains
<i>orf3</i>	Partial transposase	37.7	46	CUO47820 transposase, <i>Doria longicatena</i> (4e-14)	80 over 44 aa	No conserved domains
<i>orf4</i>	Partial transposase	42.0	69	CUP17848 transposase, <i>Blautia wexlerae</i> (2e-21)	95 over 44 aa	No conserved domains
<i>orf5</i>	Partial DNA binding protein	36.1	71	WP_065547559 transcriptional regulator, <i>Lachnoclostridium</i> sp. YL32 (7e-40)	96 over 71 aa	cd00093, HTH-XRE helix turn helix XRE-family like proteins (9.61e-14)
<i>orf6</i>	Partial DNA binding	30.8	52	WP_065547559 transcriptional regulator,	85 over	No conserved domains

	protein			<i>Lachnospirillum</i> sp. YL32 (3e-21)	52 aa	
<i>orf7</i>	DNA binding response regulator	32.4	242	WP_065547558 DNA binding response regulator, <i>Lachnospirillum</i> sp. YL32 (1e-163)	91 over 241 aa	COG3279, DNA-binding response regulator, LytR/AlgR family (9.14e-36)
<i>orf8</i>	sensory histidine kinase	34.6	130	SCH93137 sensory histidine kinase, uncultured <i>Ruminococcus</i> sp. (5e-45)	67 over 129 aa	No conserved domains

† aa, amino acids