

Supplementary material

Table S1. Primers used in this work. To allow assembly of the PCR fragments, primers B and C contain sequences overlapping each other.

Gene	Primer name	Sequence (5'-3')	Template
Deletion mutants			
NVH-1387 (<i>Ynd operon</i>)	A 1586 <i>yndDSLICA</i>	GCTTGAGCAGACATTGCTTG	NVH-1378
	B 1799 <i>YndD-E₁SLIC _B</i>	GAACCTCTACATGCCACTCACTCATCC	
	C 1800 <i>YndD-E₁SLIC _C</i>	AGTGGCATGTAGAGGTTGAGCC	
	D 1669 <i>YndE₁_D</i>	TATGATCGTCGTCGGCTTGG	
NVH-1412 (<i>gerKACB</i>)	A 1549 <i>gerKoppf</i>	ACGAGGTTATCGGCAATACG	NVH-1387
	B 1952 <i>gerKBslicB</i>	CGGGAAGGATCACATATTTTTCCTTG	
	C 1953 <i>gerKBslicC</i>	AGGAAAAATATGTGATCCTTCCCGCT	
	D 1954 <i>gerKBslicD</i>	CGAGTCCCATAAAAACAAG	
NVH-1404 (1387Δ <i>gerKA-C</i>)	A 1549 <i>gerKoppf</i>	ACGAGGTTATCGGCAATACG	NVH-1387
	B 1562 <i>gerKslicB</i>	TCTTTTCATTACATATTTTTCCTTGCCGAAGC	
	C 1563 <i>gerKslicC</i>	AAGGAAAAATATGTGAATGAAAGAGAGAGGAGG	
	D 1564 <i>gerKD2rev</i>	TTTCCAAGAATGGGCAAAAG	
NVH-1389 (<i>gerAB</i>)	A 1807 <i>gerAB-A</i>	AGCGTGATTATGGAAGTGACGAT	MW3
	B 1808 <i>gerAB-B</i>	CTTTTTTTTCATGAAGAACTACATGCGCCGAGCATTGTGCTGG	
	C 1809 <i>gerAB-C</i>	CAATGCTCGGCGCATGTAGTTCTTCATGAAAAAAGGGAAT	
	D 1810 <i>gerAB-D</i>	GCTCCTCTGAGAAAATCAGGACTTGC	
NVH-1369 (<i>yndE₃</i>)	A 1658 <i>YndE₃_A</i>	GCGCTCATTATGGAAGTGGC	MW3
	B 1659 <i>YndE₃_B</i>	CAAGCGTCACATAAGCGTTTCCCT	
	C 1660 <i>YndE₃_C</i>	AACGCTTATGTGACGCTTAAAAAGA	
	D 1661 <i>YndE₃_D</i>	GGCTTGATCCCTTCCCGAG	
NVH-1378 (<i>yndE₃E₂</i>)	A 1658 <i>YndE₃_A</i>	GCGCTCATTATGGAAGTGGC	NVH-1369
	B 1841 <i>Ynd_E₃-E₂_B</i>	TTCCTCCTCACTTACATAAAGCGTTCCCT	
	C 1842 <i>YndE₃-E₂_C</i>	AGGAAAACGCTTATGTAAGTGAGGAGGAAAAAGT	
	D 1665 <i>YndE₂_D</i>	CATTTTCAACGATTTTAAGC	
NVH-1405 (<i>yndE₃E₂E₁</i>)	A 1666 <i>YndE₁_A</i>	CATCGAAAGGGGATTGGGG	NVH-1378
	B 1667 <i>YndE₁_B</i>	GAACCTCTACATTGCGCGTTTCTC	
	C 1668 <i>YndE₁_C</i>	CGCGCAATGTAGAGGTTGAGCC	
	D 1669 <i>YndE₁_D</i>	TATGATCGTCGTCGGCTTGG	
NVH-1371 (<i>yndF₂</i>)	A 1628 <i>YndF₂-A</i>	GCCGTCACCGTGAATAAGGA	MW3
	B 1630 <i>YndF₂-B</i>	GATTAAGCTACATGATCCCC	
	C 1631 <i>YndF₂-C</i>	GGGATCATGTAGCTTAATCATGA	
	D 1629 <i>YndF₂-D</i>	TGCCTTTCAGATGACCTTTTACC	
RT-PCR	<i>rpoBf/rpoBr</i>	ACCTTCTTATCAGTGGTTTCTTGAT / CCTCAATTGGCGATATGTCTTG	MW3
	<i>yndD</i> 1697/1698	GCGGTCGGCTTTACAGA / CCGTGTGCTCAAAAAGG	
	<i>yndE₃</i> 1695/1696	CGAAGAGCGCATCACCATT / TGTCCCAAGCAGGAAATTGG	
	<i>yndE₂</i> 1693/1694	CCCCGACAAAACGCTATATCA / AAAGTCTCCCGGCCACTT	
	<i>yndF₁</i> 1699/1700	ATTGCTGTGCGAACTGCTAGA / TACTGCTCGGCTGATTCA	
	<i>yndE₁</i> 1691/1692	TGCCAAGAACCCTGTAGAAG / GCCTAATAGGACGGAAATCCATAC	
	<i>yndF₂</i> 1701/1702	GCCATGTCAGTCGATCACCTT / TGAGAGCGGTTTCTTTGA	
Trans complementation (pHT315)			
NVH-1473 (1412 pHT315- <i>yndD</i>)	1948 <i>yndpromF</i>	ATAGCGGCCGCACGCCTCAAGATCCGAAATA	NVH-1378
	1946 <i>YndDR</i>	ATAGCGGCCGCTTCGTGCCTGACCATCATAA	
NVH-1438 (1412 pHT315- <i>yndF₁</i>)	1948 <i>yndpromF</i>	ATAGCGGCCGCACGCCTCAAGATCCGAAATA	NVH-1378
	1945 <i>YndF₁R</i>	AATTGCGGCCGCTTCTTCTGTTACTGATCCC	

Gene fusions for cis-complementing (pMAD)			
SLIC 1	A 1948 yndpromF	ATAGCGGCCGCACGCCTCAAGATCCGAAATA	MW3
	B 1838 YndE3_compl_SLIC_B	TTCGTGCCTGACCATCATGCCACTCACTCATCCCCTGC	
	C 1839 yndE3_compl_SLIC_C	AGGGGATGAGTGAGTGGCATGATGGTCAGGCACGAAGAG	
	D 1700 YndF1RT-PCR R	TACTGCTCGGCCTGATTCA	
promE₃E₂E₁*	A 1948 yndpromF	ATAGCGGCCGCACGCCTCAAGATCCGAAATA	SLIC 1
	B 1959 nyE2E1 slicB	ATTAGAAGTTCTTTAAATAACGGATGGTG	MW3
	1960 nyE2E1 slicC	TCCGTTATTTAAAGAAGTCTAATCACG	
	1951 E1 slicD	CTAGCTTTGCACTGCCTTCTTT	
NVH-1421 (1369::yndE₃)	1948 yndpromF	ATAGCGGCCGCACGCCTCAAGATCCGAAATA	promE ₃ E ₂ E ₁
	1963 E ₃ R NotI	TTATGCGGCCGCTCAGCTGATCCCTGT	
NVH-1416 (1405::yndE₃E₂)	1948 yndpromF	ATAGCGGCCGCACGCCTCAAGATCCGAAATA	promE ₃ E ₂ E ₁
	1962 E ₂ R NotI	ATATGCGGCCGCTTAGTTTTTTTCAAAC	
NVH-1417 1405::yndE₃E₂E₁	1948 yndpromF	ATAGCGGCCGCACGCCTCAAGATCCGAAATA	promE ₃ E ₂ E ₁
	1961 E ₁ R NotI	AATTGCGGCCGCCTAGCTTTGCACTGCCTTCTTT	
NVH-1413 (1404::yndDE₂F₁)	1948 yndpromF	ATAGCGGCCGCACGCCTCAAGATCCGAAATA	NVH-1369
	1945 F ₁ R NotI	AATTGCGGCCGCGTTCTTCTGTACTGATCCC	
NVH-1427 (1412::yndDF₁)	1948 yndpromF	ATAGCGGCCGCACGCCTCAAGATCCGAAATA	NVH-1378
	1945 F ₁ R NotI	AATTGCGGCCGCGTTCTTCTGTACTGATCCC	

*prom is the 362 bp region upstream of *yndD*

Table S2. Percentages of amino acid sequence identity and similarity of Ynd subunits in *B. licheniformis* ATCC15480/DSM13.

Amino acid sequence alignments		Identity (%) ^a	Similarity (%) ^a
YndE₁	YndE₂	52	75
YndE₁	YndE₃	54	75
YndE₂	YndE₃	64	83
YndF₁ (aa 215-398)	YndF₂	60	79

^aCalculated over the full length of the protein