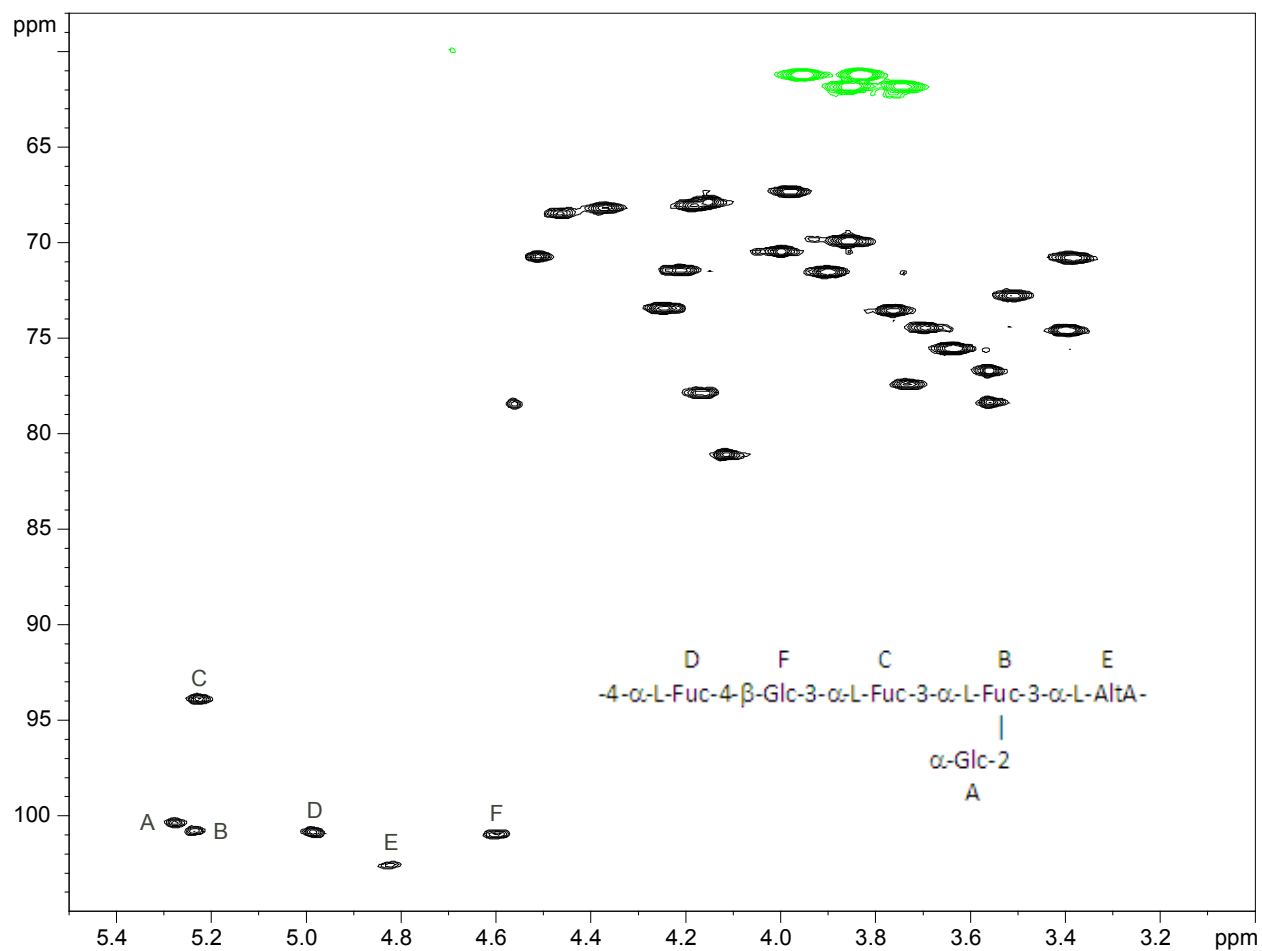
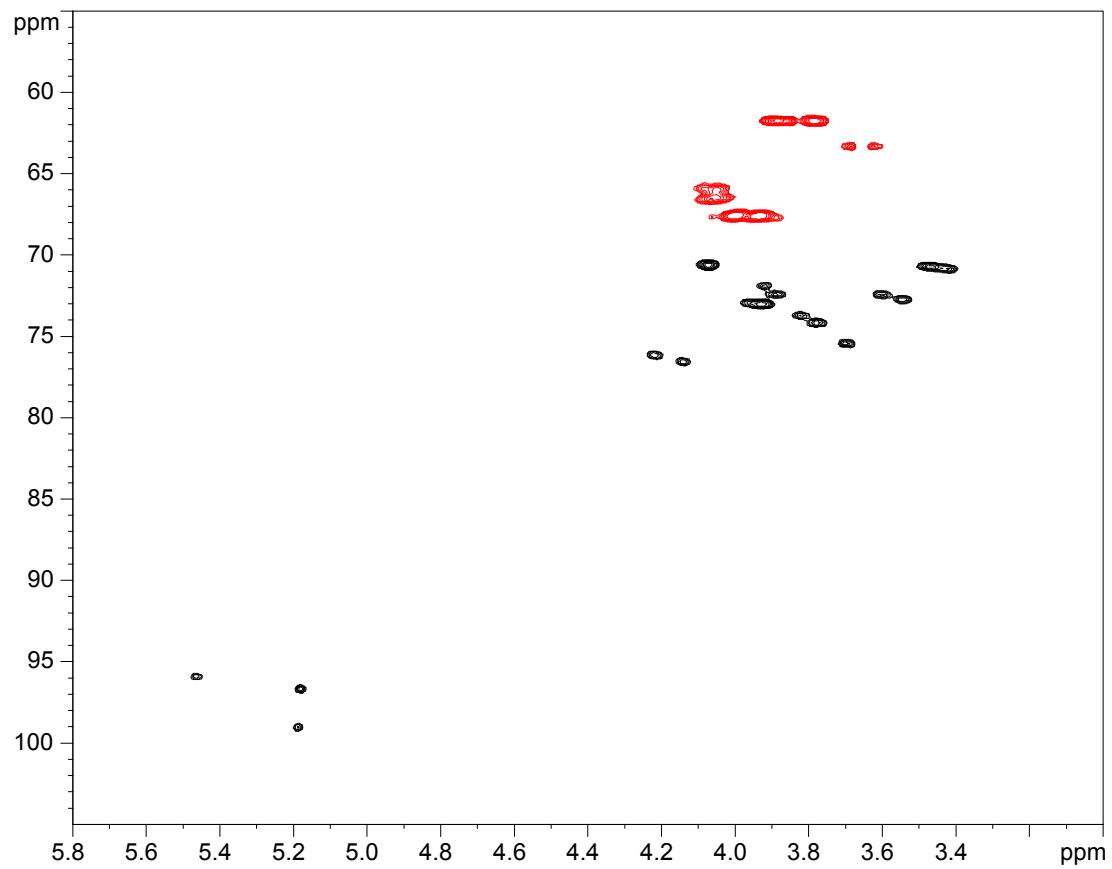


SUPPLEMENTAL FIGURE S1. <sup>1</sup>H-<sup>13</sup>C HSQC spectrum of the Pf1 (Levan) polysaccharide.

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**SUPPLEMENTAL FIGURE S2. Fragment of the  $^1\text{H}$ - $^{13}\text{C}$  HSQC spectrum of the Pf2 polysaccharide.**



SUPPLEMENTAL FIGURE S3.  $^1\text{H}$ - $^{13}\text{C}$  HSQC spectrum of PF3 (LTA).





SUPPLEMENTAL TABLE S2. **Annotation of the 17 genes associated with the putative *E. faecium* Tx16 legionaminic biosynthesis gene cluster.** Orthologues of Tx16 open reading frames (ORFs) were identified using TBLASTN queries of representative complete *C. jejuni*, *S. agalactiae* and *S. aureus* genomes (accessible via the NCBI Microbial nucleotide database).

<i>E. faecium</i> Tx16 gene <sup>1</sup> [gene ID]	Tx16 gene homologues (E values)		
	<i>Campylobacter jejuni</i> <sup>2</sup> [locus tag]	<i>Streptococcus agalactiae</i> <sup>3</sup> [gene ID]	<i>Staphylococcus aureus</i> <sup>4</sup> [gene ID]
<i>epaR</i> , Undecaprenyl-phosphate galactose-phosphotransferase [HMPREF0351_10907]	Undecaprenyl-phosphate diacetylBac PhosphoTransferase (10 <sup>-38</sup> ) <sup>†</sup> [Cj1124c]	Galactosyl transferase CpsE (10 <sup>-31</sup> ) <sup>†</sup> [1013978]	CPS biosynthesis protein Cap8M (10 <sup>-42</sup> ) <sup>†</sup> [3919835]
Family 2 glycosyl transferase [HMPREF0351_10908]	glucosyltransferase (10 <sup>-10</sup> ) <sup>†</sup> [Cj1146c]	Glycosyl transferase CpsO(V) (10 <sup>-14</sup> ) <sup>*</sup> [1013971]	Glycosyltransferase family 2 (10 <sup>-13</sup> ) <sup>†</sup> [446898095]
Group 1 glycosyl transferase [HMPREF0351_10909]	N'-diacetylBac-diphospho-undecaprenol-acetyl galactosaminyltransferase (10 <sup>-6</sup> ) <sup>†</sup> [Cj1125c]	Glycoside hydrolase (10 <sup>-7</sup> ) <sup>*</sup> [1013514]	Glycosyltransferase family 1 [446615158] (10 <sup>-10</sup> ) <sup>*</sup>
Family 14 glycosyl transferase [HMPREF0351_10910]	ND	ND	ND
Polysaccharide polymerase [HMPREF0351_10911]	ND	ND	ND
Hypothetical protein [HMPREF0351_10912]	ND	ND	ND
Hypothetical protein [HMPREF0351_10913]	ND	ND	ND
<i>cpsL</i> , CPS synthesis protein [HMPREF0351_10914]	ND	<i>cpsL</i> (10 <sup>-14</sup> ) <sup>†</sup> [1013969]	ND
<i>capD</i> , UDP-N-acetylglucosamine 4,6-dehydratase [HMPREF0351_10915]	UDP-N-acetylglucosamine 4,6-dehydratase (10 <sup>-76</sup> ) [Cj1293]	dTDP-glucose 4,6-dehydratase (10 <sup>-9</sup> ) <sup>*</sup> [1014005]	CPS biosynthesis protein Cap5D (10 <sup>-61</sup> ) <sup>*</sup> [3919826]
N-acetylneuraminatase synthase ( <i>legI</i> ) [HMPREF0351_10916]	<i>legI</i> <sup>5</sup> (10 <sup>-98</sup> ) <sup>*</sup> [Cj1327]	<i>neuB</i> (10 <sup>-87</sup> ) <sup>*</sup> [1013968]	ND

SUPPLEMENTAL TABLE S2 (Continued)

<i>E. faecium</i> Tx16 gene (Continued) <sup>1</sup> [gene ID]	Tx16 gene homologues (E values)		
	<i>Campylobacter jejuni</i> <sup>2</sup> [locus tag]	<i>Streptococcus agalactiae</i> <sup>3</sup> [gene ID]	<i>Staphylococcus aureus</i> <sup>4</sup> [gene ID]
UDP-N-acetylglucosamine 2-epimerase (legG) [HMPREF0351_10917]	legG <sup>5</sup> (10 <sup>-56</sup> )* [Cj1328]	neuC (10 <sup>-47</sup> )* [1013967]	UDP-N-acetylglucosamine 2-epimerase (10 <sup>-12</sup> )* [3919838]
IpsB, hexapeptide transferase [HMPREF0351_10918]	Unknown (10 <sup>-18</sup> ) [Cj1328]	neuD (10 <sup>-14</sup> )* [1013966]	Acetyl transferase (10 <sup>-5</sup> ) <sup>†</sup> [447147537]
Glutamine-scylo-inositol transaminase (legC) [HMPREF0351_10919]	legC <sup>5</sup> (10 <sup>-96</sup> )* [Cj1320]	ND	ND
Dehydrogenase [HMPREF0351_10920]	ND	ND	Unknown (10 <sup>-5</sup> ) <sup>†</sup> [3919494]
Dehydrogenase (PtmF) [HMPREF0351_10921]	PtmF <sup>5</sup> (10 <sup>-37</sup> )* [Cj1330]	ND	ND
N-acylneuraminate Cytidylyltransferase (LegF) [HMPREF0351_10922]	legF <sup>5</sup> (10 <sup>-33</sup> )* [Cj1331]	neuA (10 <sup>-13</sup> )* [1013965]	ND
UDP-glucose-4-epimerase [HMPREF0351_10923]	Epimerase/dehydratase (10 <sup>-41</sup> ) [Cj1319]	galE UDP-glucose 4-epimerase (10 <sup>-23</sup> )* [1014733]	NAD-dependent dehydratase (10 <sup>-81</sup> )* [3919466]

<sup>1</sup>Reference 22, Genbank NC\_017960; <sup>2</sup>strain NCTC11168, Genbank NC\_002163; <sup>3</sup>strain 2603V/R, Genbank NC\_004116; <sup>4</sup>strains NCTC8325 or N315, Genbank NC\_007795 or NC\_002745.

<sup>5</sup>Annotation based on biochemical activities described in reference 36.

“ND” – not detected (E value < 0.001)

\*E value reflects Tx16 ORF query coverage of >75% with BLAST orthologue.

<sup>†</sup>E value reflects Tx16 ORF query coverage of <75% with BLAST orthologue (partial or discontinuous).