SUPPORTING INFORMATION

Iron Acquisition Systems of Gram-negative Bacterial Pathogens Define TonB-Dependent Pathways to Novel Antibiotics

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Figure 5. Alignment of LGP sequences from Gram (-) bacterial pathogens. We used CLUSTALΩ (https://www.ebi.ac.uk/Tools/msa/clustalo/) to analyze the pair-wise identities of 79 LGP sequences (Table 2), and colored the conserved residues (>90% identity) blue. EcoFepA, the reference sequence, is outlined in red, and different elements of its tertiary structure are highlighted in its sequence, and displayed below the overall alignment: TonB-box, cyan; α-helices, pink; β -strands, green. The extent and quality of sequence conservation, and a consensus sequence are also shown beneath the alignment. This HD image may be magnified to view the relationships of the individual sequences.

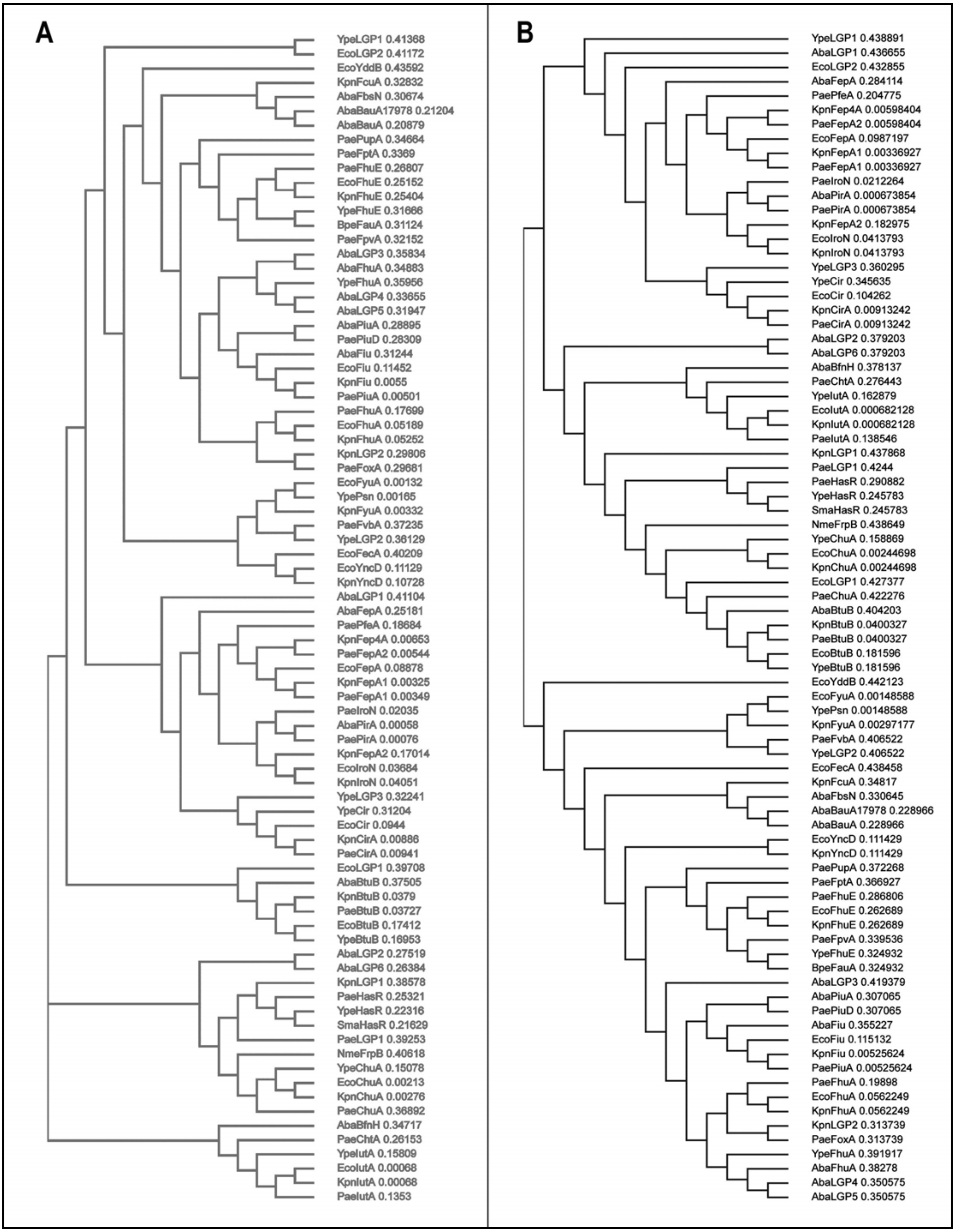

Figure S2. Relationships of LGPs from CRE/ESKAPE and other Gram (-) pathogens. We analyzed NCBI FASTA protein sequences (below; red residues designate signal sequences) by CLUSTALΩ using the BLOSUM62 matrix. **A. Cladogram.** The branching tree estimates the nearest-neighbor-joining patterns. **B. Phylogram.** The branching tree estimates phylogenetic relationships. The numerical scores estimate phylogenetic distance.

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>PaeFpvA
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>PaePupA
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>PaeFoxA
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>PaeChuA
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>PaeFepA1
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>PaePiuD
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>PaeFepA2
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>PaePfeA
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>PaePiuA
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>PaeChtA
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>PaeIutA
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>PaePirA
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>PaeFhuA
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>PaeIroN

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>PaeFptA
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>PaeFhuE
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>PaeFvbA
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>PaeCirA
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>PaeBtuB
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>PaeLGP1
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>YpeIutA
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