

Query

Listeria Genomic Island 1



Blastn results

Clostridium saccharolyticum WM1
E-value 0.0, Query coverage 61%



Desulfotomaculum acetoxidans DSM 771
E-value 0.0, Query coverage 46%



Clostridium kluyveri NBRC 12016
E-value 0.0, Query coverage 57%



Clostridium kluyveri DSM 555
E-value 0.0, Query coverage 57%



Desulfitobacterium hafniense Y51
E-value 0.0, Query coverage 50%



Eubacterium rectale DSM 17629
E-value 0.0, Query coverage 33%



10kbp

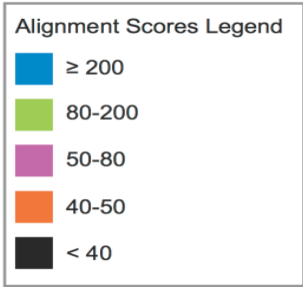


FIG S1. The blastn nucleotide sequence homology of LGI1 to the other publically available genomes in the NCBI database.

Listeria monocytogenes 08-5578 (CP001602)
Listeria monocytogenes 08-5923 (CP001604)
Desulfitobacterium dehalogenans ATCC 51507 (CP003348)
 E-value 2x10⁻⁴⁹, Query coverage 100%, Identity 74%
Desulfitobacterium hafniense DCB-2 (CP001336)
 E-value 1x10⁻³⁸, Query coverage 100%, Identity 72%
Desulfitobacterium hafniense Y51 (AP008230)
 E-value 6x10⁻³⁶, Query coverage 100%, Identity 71%
Desulfitobacterium hafniense PCS-E (LK996017)
 E-value 6x10⁻³⁶, Query coverage 100%, Identity 71%
Clostridium scatologenes ATCC 25775 (CP009933)
 E-value 7x10⁻²⁹, Query coverage 96%, Identity 70%
Clostridium ljungdahlii DSM 13528 (CP001666)
 E-value 1x10⁻²⁴, Query coverage 99%, Identity 68%
Clostridium autoethanogenum DSM 10061 (CP006763)
 E-value 1x10⁻²⁴, Query coverage 99%, Identity 68%

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1      10      20      30      40      50      60
|      |      |      |      |      |
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ATGGAATGGATTTTATTAGCAGTCGCTATCGTACTTGAACCTGTTGGAACAACATTGATG
ATGCAATGGGTTTATTAGCCCTGGCTATTTACTTGAATTTTGGGACAACACTAATG
ATGCAATGGATTTATTAGCCCTGGCTATTTACTGAAATTTTGGGACAACACTGATG
ATGCAATGGGTTTACTTAGCCCTGGCTATTTACTGAAATTTTGGGACAACACTGATG
ATGCAATGGGTTTACTTAGCCCTGGCTATTTACTGAAATTTTGGGACAACACTGATG
ATGGAATGGATTTACCTTATTCTTGGCATTTTATTGAAATTGCAAGGAACAACATTAATG
-TGGAATGGATTTATCTAATTGGAGCTATTATACTTGAAACAATAAGGAACAACTTGTATG
-TGGAATGGATTTATCTAATTGGAGCTATTATACTTGAAACAATAAGGAACAACTTGTATG
  
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Clostridium ljungdahlii DSM 13528 (CP001666)
Clostridium autoethanogenum DSM 10061 (CP006763)

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61      70      80      90      100     110     120
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AAGATGTCTGTATGGATTTACAAAATTACTGCCAGCTTTAGGAACAATTCCTAACGTATGGC
  
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Clostridium autoethanogenum DSM 10061 (CP006763)

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121     130     140     150     160     170     180
|      |      |      |      |      |
CTATGTTTCGGTTCCTTAGCATTAGCATTAAAAAAAATACCGGTTAGTGCAGCATATGCTT
CTATGTTTCGGTTCCTTAGCATTAGCATTAAAAAAAATACCGGTTAGTGCAGCATATGCTT
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TTATGTTTCGGTTCCTTAGCATTAGCATTAAAAAAAATACCGGTTAGTGCAGCATATGCTT
TTATGTTTCGGTTCCTTAGCATTAGCATTAAAAAAAATACCGGTTAGTGCAGCATATGCTT
TTATGTTTCGGTTCCTTAGCATTAGCATTAAAAAAAATACCGGTTAGTGCAGCATATGCTT
ATATGCTTTATTTGTTTATCTATGGCGTTGAAAAAAAATAGATAAAGTGTGGCATATGCTT
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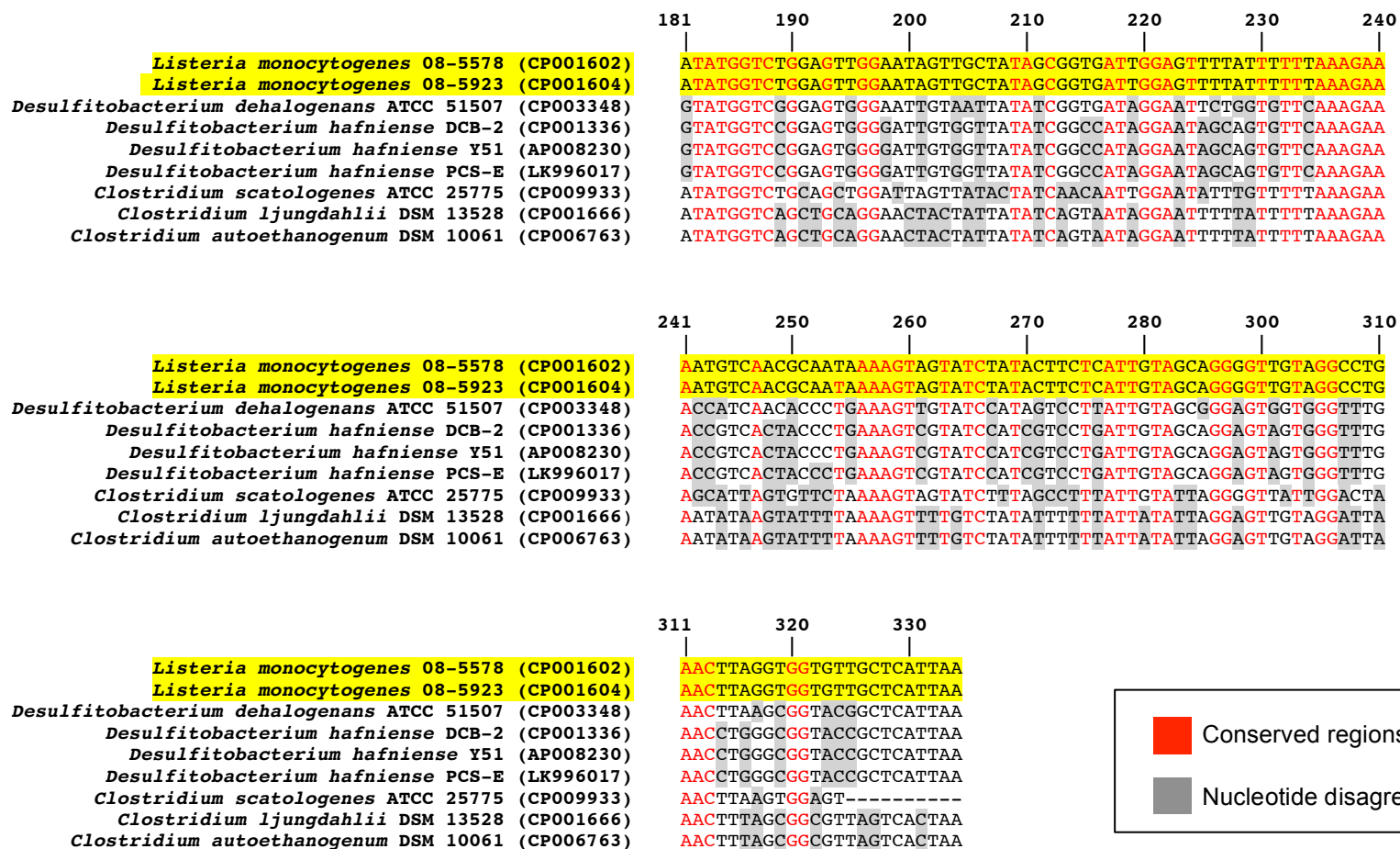


FIG S2. The blastn nucleotide sequence homology of *emrE_{Lm}* (highlighted in yellow) to the other publicly available genomes in the NCBI database.

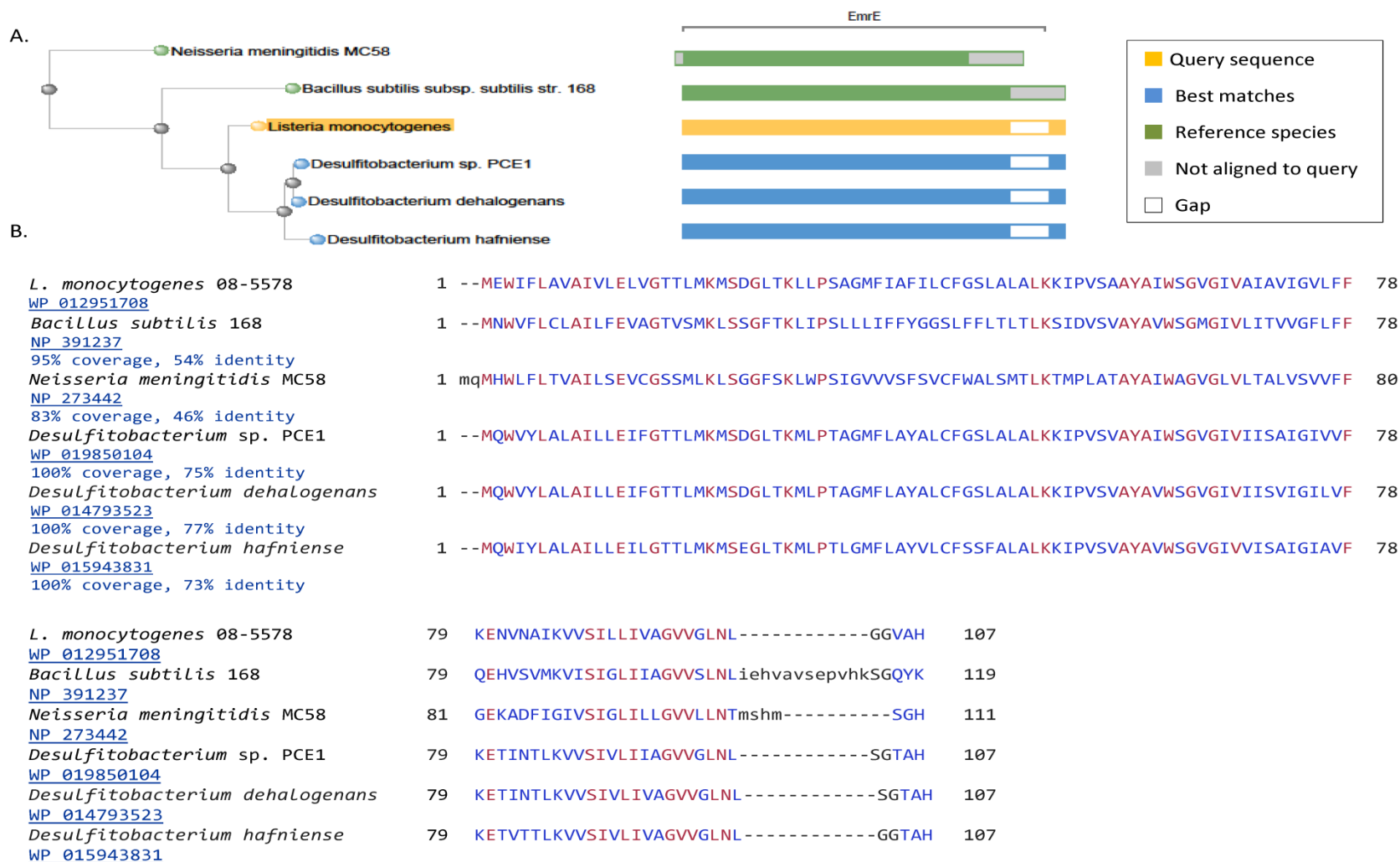


FIG S3. The graphic representation (A) and blastp protein sequence homology (B) of *emrE_{Lm}* to the other publicly available proteins in the NCBI database obtained using SmartBlast. Reference species represent matches from well-studied species.