Supplementary figures

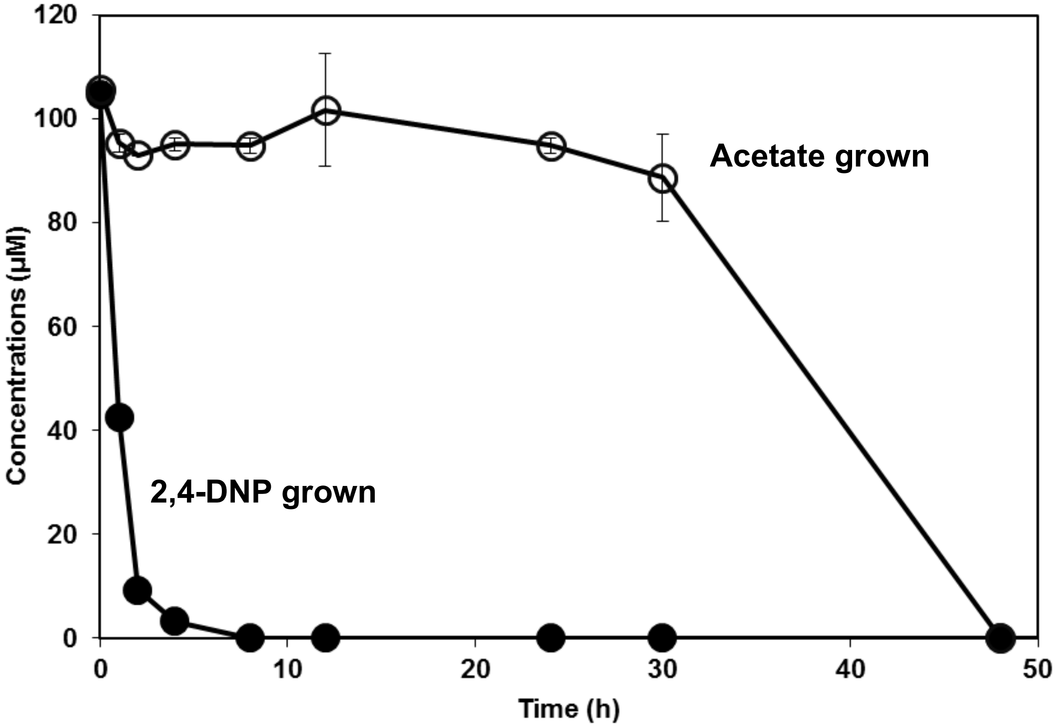

FIG. S1. Biodegradation of 2,4-DNP by *Nocardioides* sp. JS1661 pre-grown on acetate and 2,4-DNP.

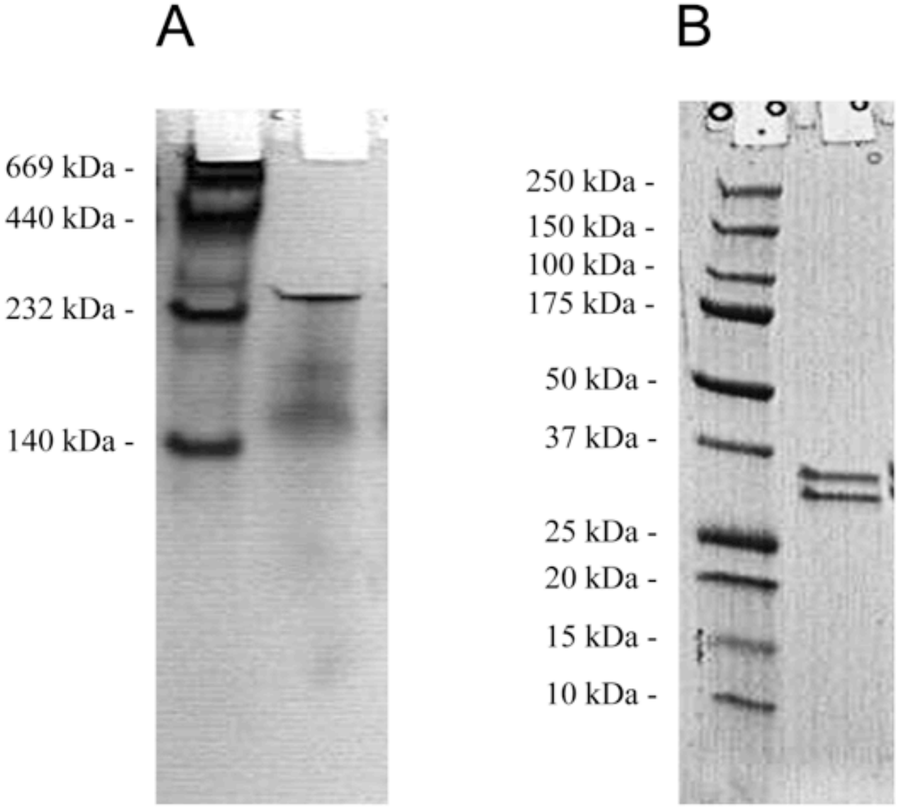

FIG. S2. Native gel (A) and denatured SDS-PAGE gel (B) of purified DNAN hydrolase from Source 15 PHE column. The upper band of the denatured SDS-PAGE (36 kDa) represent *dnH1* and the lower band (34 kDa) represent *dnH2*.

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                                                                                   rbs      M  S  V  T  S  Q  T  S  S ·
 701   GACACCGAGAACTGGACTCGTCGAGCGCGAGACATCGGCGCGGGCGCCCCAGGCTGTGCGATCAAAGGAGGCTGATGAGCGTGACGAGCCAGACGAGCTC

       · S  G  S  A  A  V  S  D  C  H  R  G  I  I  D  I  S  G  P  V  P  G  Y  E  W  E  P  S  M  T  T  E  P
 801   GAGTGGATCGGCAGCTGTATCCGACTGCCATCGCGGGATTATCGACATCTCTGGGCCGGTGCCGGGGTATGAGTGGGAGCCCTCCATGACGACCGAACCG

        V  R  G  R  V  W  T  I  T  D  G  V  F  R  T  L  A  I  E  G  D  T  G  V  I  A  V  D  T  F  W  S  P  G
       ·
 901   GTTCGCGGCCGGGTGTGGACGATCACCGACGGCGTCTTCCGAACGCTTGCGATCGAAGGCGACACCGGAGTCATCGCCGTCGACACCTTCTGGTCCCCGG

       ·  S  A  R  Q  Y  R  R  A  L  Q  S  H  F  P  R  K  P  V  H  T  I  I  Y  T  H  D  H  L  D  H  T  G  F ·
1001   GATCGGCCAGGCAGTACCGCAGAGCCCTCCAGAGTCACTTTCCGCGCAAGCCGGTGCACACGATCATCTACACCCACGACCACCTCGACCACACTGGCTT

       ·G  A  D  F  A  P  D  A  D  Q  I  L  A  H  E  L  T  A  E  V  I  A  R  R  S  S  D  G  Q  L  P  A  T
1101   TGGAGCCGACTTCGCTCCCGATGCCGATCAGATCCTTGCGCACGAGCTCACCGCCGAGGTGATCGCCCGCCGCAGCTCGGACGGTCAACTCCCCGCCACC

        R  T  W  S  G  E  R  L  E  V  S  I  D  G  A  E  F  E  L  I  Y  P  G  P  T  H  G  T  G  N  T  A  L  Y
       ·
1201   AGAACCTGGTCCGGCGAGCGACTCGAAGTTTCCATTGACGGCGCTGAGTTCGAGCTGATCTACCCCGGGCCGACCCACGGGACGGGGAACACCGCGTTGT

       ·  F  P  N  E  R  F  L  Y  M  A  D  T  V  F  T  G  P  T  Y  N  I  V  P  D  F  L  W  T  S  W  I  P  N ·
1301   ACTTTCCCAACGAGCGGTTCCTCTACATGGCCGACACCGTCTTCACCGGGCCGACCTACAACATCGTGCCTGACTTCCTGTGGACGAGCTGGATTCCTAA

       ·T  R  R  L  L  G  L  D  W  D  L  Y  V  P  G  H  F  W  R  L  S  R  R  E  F  E  A  D  F  E  L  W  D
1401   CACGCGACGTCTGCTCGGGCTCGACTGGGATCTCTACGTCCCGGGGCATTTCTGGCGGCTTTCGCGCCGAGAGTTCGAGGCCGACTTCGAGCTCTGGGAC

        A  T  A  A  C  A  L  D  A  L  R  A  G  V  D  I  D  N  F  A  D  V  K  K  F  T  Y  E  R  M  D  E  P  F
       ·
1501   GCAACAGCGGCTTGCGCCCTCGACGCGCTCCGTGCGGGGGTCGACATCGACAACTTCGCTGACGTCAAGAAGTTCACCTACGAACGAATGGATGAGCCGT

       ·  G  S  R  T  F  R  F  D  E  F  A  A  I  N  V  L  T  H  M  V  H  Y  Q  T  G  G  W  G  L  R  D  Y  E ·
1601   TCGGTAGCCGGACGTTCCGATTCGACGAGTTCGCCGCAATTAACGTGCTGACGCACATGGTGCACTACCAGACGGGGGGCTGGGGTCTGCGTGACTACGA

                                                                              M  T  G  R  Q  R  T  T  V  V  A  P  D  R  P
       ·P  Y  S  N  E  P  F  K  T  T  L  P  Q  R  L  G  S  P  L  *
1701   GCCGTACTCCAACGAGCCGTTCAAGACCACCCTCCCGCAGCGACTGGGATCGCCGCTGTGACCGGCCGGCAGCGCACGACGGTAGTCGCTCCTGACCGAC

       ·  V  Q  D  A  T  I  S  Q  L  T  T  R  V  W  T  V  A  I  D  G  Y  R  T  I  V  V  E  G  E  T  G  I  V ·
1801   CGGTTCAGGACGCCACGATCAGTCAGCTGACCACACGTGTCTGGACCGTCGCAATCGACGGGTATCGAACGATCGTCGTTGAGGGCGAGACGGGAATCGT

       ·A  I  N  S  F  G  T  P  S  A  Q  T  K  Y  R  E  L  I  T  Q  T  F  G  D  K  P  V  V  A  V  V  A  S
1901   CGCGATCAACTCGTTCGGAACGCCGTCAGCGCAGACCAAGTACCGTGAGCTGATCACTCAGACCTTCGGCGACAAGCCCGTCGTCGCTGTTGTCGCGTCC

        I  D  H  L  D  H  T  G  R  L  G  P  F  A  N  G  A  E  V  I  G  H  E  L  G  Q  A  I  A  F  G  R  G  L
2001   ATCGATCATCTCGACCACACCGGACGCCTCGGCCCCTTTGCTAACGGCGCGGAAGTGATCGGCCACGAGCTCGGACAGGCGATTGCTTTTGGTCGCGGAC

       ·  P  E  Q  K  L  A  D  T  V  V  T  G  P  V  T  E  I  E  R  A  G  V  R  L  V  L  R  Y  P  A  P  T  V ·
2101   TACCTGAGCAGAAGCTCGCCGACACTGTTGTGACGGGTCCGGTCACCGAGATCGAGCGTGCTGGTGTCAGACTCGTACTGCGGTACCCGGCGCCCACCGT

       ·G  T  G  N  L  A  V  D  L  P  D  D  D  V  V  F  M  V  G  L  Q  S  G  A  R  Y  G  I  F  P  D  F  H
2201   CGGCACCGGAAACCTGGCCGTTGACCTCCCCGACGACGACGTCGTCTTCATGGTCGGCCTCCAGTCCGGCGCTCGGTACGGCATCTTTCCAGACTTCCAC

        F  K  H  F  L  R  A  T  S  E  I  A  A  L  G  R  R  Y  F  V  P  G  R  S  E  V  M  D  A  G  Q  V  R  Q
2301   TTCAAGCACTTCCTGCGAGCAACCAGTGAGATCGCTGCGCTCGGGCGCCGGTACTTCGTGCCAGGTCGTTCCGAGGTCATGGATGCGGGCCAGGTGCGGC

       ·  A  L  E  Y  V  N  D  F  Q  N  A  C  Q  R  C  L  A  G  G  E  V  P  H  W  L  L  E  P  T  T  A  Y  L ·
2401   AGGCGCTGGAGTATGTGAACGACTTCCAGAACGCTTGTCAGCGCTGCCTCGCGGGTGGCGAGGTCCCGCACTGGCTGCTGGAGCCGACAACCGCCTACCT

       ·H  D  E  L  S  S  K  W  S  H  L  E  G  Y  D  P  V  A  V  G  L  G  G  L  R  V  V  C  H  Y  Y  M  G
2501   TCACGATGAGCTCTCCTCGAAGTGGTCCCATCTGGAGGGCTACGATCCGGTGGCCGTCGGACTGGGCGGGTTGCGGGTTGTGTGCCACTACTACATGGGT

        G  W  W  L  D  D  T  D  H  H  E  L  L  Y  D  H  L  T  V  R  T  Y  R  E  Y  R  E  R  L  A  T  A  G  T
2601   GGGTGGTGGCTCGACGACACTGACCATCACGAGCTGCTCTACGACCACCTCACCGTGCGGACCTACCGGGAGTACCGGGAACGCTTGGCAACTGCAGGCA

       ·  G  R  A  *
2701   CCGGCCGAGCCTGAGAAGGCCCTAAAGAAGGTCCGCGCGATCGGGAGGAGTTTCACCTGATGACGACCGTCGACGCCGTGGTCATCGGCGCGGGTCACCA
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FIG. S3. DNA sequence of the DNAN hydrolase genes indicating ribosomal binding site (RBS), putative start/stop codons and the positions of the N-terminal peptide sequences. The proteins designated “upper band” in the text corresponds to nucleotides 775-1762 and the “lower band” corresponds to 1759-2715. The matched peptides for the upper and lower bands cover 37% (122/329 AA's) and 55% (178/319 AA's) of the proteins, respectively. Covered amino acids (shown in red) include 113 from peptide sequencing and 6 from N-terminal sequencing (yellow highlighted) for the upper band and 172 from peptide sequencing and 6 from N-terminal sequencing for the lower band. Based on the N-terminal threonine, the first nine amino acids (marked in blue), seem to have been post-translationally removed by an unknown mechanism from the upper and the first amino acid (methionine, encoded by GTG: marked in blue), seems to have been post-translationally removed by the universal N-terminal methionine excision mechanism from the lower band.