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1646                                                       AAA AAC TTA AAA AGA TTA ATT TTA TTA TTT AAT AGA
1682  ATG CAA CAG AAA CAA GTA AAT GTT ATT GAA TTT TTT AGT GGA ATT GGT GGA TTA CGT TCA AGT TAT GAA CGA TCT
   1  M   Q   Q   K   Q   V   N   V   I   E   F   F   S   G   I   G   G   L   R   S   S   Y   E   R   S
1757  TCA ATT AAT ATA AAT GCA ACA TTT ATA CCA TTT GAT ATA Agtttgaagataatataataaaaggaatatcaaaataaatattcaca
  26  S   I   N   I   N   A   T   F   I   P   F   D   I   N
1843  ataattatag   AT GAA ATT GCA AAT AAA ATA TAC TCA AAG AAT TTT AAA GAA GAA GTA CAA GTAgtttgtaatgattata
  40                  E   I   A   N   K   I   Y   S   K   N   F   K   E   E   V   Q   V
1922  tttattaaaaaagagtaatacataataaattatttatttaatagAAA AAT TTA GAT AGC ATT TCA ATA AAA CAA ATA GAA TCT TTA
  57                                              K   N   L   D   S   I   S   I   K   Q   I   E   S   L
2008  AAT TGT AAT ACA TGG TTT ATG AGT CCA CCT TGT CAA CCA TAT AAT AAT TCA ATA ATG TCT AAA CAT AAA GAT ATT
  71  N   C   N   T   W   F   M   S   P   P   C   Q   P   Y   N   N   S   I   M   S   K   H   K   D   I
2083  AAT GAT CCA AGA GCA AAA AGT GTA TTA CAT TTA TAT CGT GAT ATT CTT CCA TAT TTA ATA AAT AAA CCA AAA CAT
  96  N   D   P   R   A   K   S   V   L   H   L   Y   R   D   I   L   P   Y   L   I   N   K   P   K   H
2158  ATT TTT ATT GAA AAT GTT CCA TTA TTT AAA GAA TCA CTT GTT TTT AAA GAA ATT TAT AAT ATT CTT ATT AAA AAT
 121  I   F   I   E   N   V   P   L   F   K   E   S   L   V   F   K   E   I   Y   N   I   L   I   K   N
2233  CAA TAT TAT ATT AAA GAC ATT ATT TGT TCT CCT ATT GAT ATT GGA ATT CCA AAT AGT AGA ACT CGT TAT TAT GTT
 146  Q   Y   Y   I   K   D   I   I   C   S   P   I   D   I   G   I   P   N   S   R   T   R   Y   Y   V
2308  ATG GCA AGA TTA ACT CCT TTT AAA AAT GAA ATT CAA TTA CAT CAA GAA AAA GAG TCA ATG ATA TCA AAT TAT TTA
 171  M   A   R   L   T   P   F   K   N   E   I   Q   L   H   Q   E   K   E   S   M   I   S   N   Y   L
2383  GAT AAT AAT GTA AAT GAG TCT TAT TCT ATT CCT TCA GAT TTA ATT TTA AAG AAA GGA ATG TTA TTT Ggtttgtttt
 196  D   N   N   V   N   E   S   Y   S   I   P   S   D   L   I   L   K   K   G   M   L   F   D
2460  taatatattttaaataaaaacattgaaaatggatttaattgaaaag  AT  ATT GTT GGT AAA GAT GAT AAA AGG ACT TGT TGT TTT
 219                                                      I   V   G   K   D   D   K   R   T   C   C   F
2544  ACT AAG TCA TAT ACT AAA ATT GTT GAA GGA ACT GGT TCT ATT TAT TGT CCA ATA GAA CCT CAT TTT ATT CCA GTA
 231  T  K    S   Y   T   K   I   V   E   G   T   G   S   I    Y  C   P   I   E   P   H   F   I   P   V
2619  AAA AAG GCT GAA GAT TTA CTT ATA AAA ATT TAA GAT ATT TTA CTC CAA ATG AAA ATA AAA AAA ATT CAC GGA TTT
 256  K   K   A   E   D   L   L   N   K   N   L   R   Y   F   T   P   N   E   I   K   K   I   H   G   F
2694  TCT TCT AAT TTT ACA ACT CAA ATT GAT GGA TTA ACT GAT AAA CAA CAA TAT CAA TGT CTT GGT AAT AGC GTC TCT
 281  S   S   N   F   T   T   Q   I   D   G   L   T   D   K   Q   Q   Y   Q   C   L   G   N   S   V   S
2769  TGC TTT GTT ATA GCA CAA TTA ATG GAA TAT TTA TTC GAT GAC TTA AAA GAA TAA ATT ATT ATT TAT TTC AAC TTT
 306  C   F   V   I   A   Q   L   M   E   Y   L   F   D   D   L   K   E   *
2844  TGA ATT GAA TTA ATT TAT TTT TCA AGT TAA ATT GAA AAT TGT TTG TTT CAT TTT GGA TAT ACC AAA TAA AAA TAA
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**Supplementary Material Figure 1.** Nucleotide and deduced amino acid sequences of *Ehmeth*. The nucleotides that make up the introns are in lowercase letters. The DNA sequence encoding *Ehmeth* is included in the contigs (TIGR 316636 read in anti-paralel). The DNA polyadenylation starting site deduced from the analysis of *Ehmeth* cDNA is underlined (from nucleotide 2871).

```
Ehmeth          MQQKQVNVIEFFSGIGGLCSSYERSSININATFIPFDINEIANKIYSKNF-KEEVQVKNL 59
Dnmt2           --MEPLRVLELYSGVGGMHHALRESCIPA-QVVAAIDVNTVANEVYKYNFPHTQLLAKTI 57
                   : :.*:*::**:**:  : ..*.*    .. .:*:* :**::*. ** : :: .*.:

Ehmeth          DSISIKQIESLNCNTWFMSPPCQPYNNSIMSKHKDINDPRAKSVLHLYRDILPYLINKPK 119
Dnmt2           EGITLEEFDRLSFDMILMSPPCQPFTR--IGRQGDMTDSRTNSFLHIL-DILPRLQKLPK 114
                :.*:::::: *. :  :*******:..  :.:: *:.*.*::*.**:  **** * : **

Ehmeth          HIFIENVPLFKESLVFKEIYNILIKNQYYIKDIICSPIDIGIPNSRTRYYVMARLT---- 175
Dnmt2           YILLENVKGFEVSSTRDLLIQTIENCGFQYQEFILSPTSLGIPNSRLRYFLIAKLQSEPL 174
                :*::***  *: * . . : : : :  :  :::* ** .:****** **:::*:*

Ehmeth          PFKN-------------------------------------------------------- 179
Dnmt2           PFQAPGQVLMEFPKIESVHPQKYAMDVENKIQEKNVEPNISFDGSIQCSGKDAILFKLET 234
                **:

Ehmeth          --EIQLHQEKES-----MISNYLDNNVN-ESYSIPSDLILKKGMLFDIVGKDDKRTCCFT 231
Dnmt2           AEEIHRKNQQDSDLSVKMLKDFLEDDTDVNQYLLPPKSLLRYALLLDIVQPTCRRSVCFT 294
                  **: :::::*     *:.::*:::.: :.* :*.. :*: .:*:***    :*: ***

Ehmeth          KSYTKIVEGTGSIYCPIEPHFIP-----------VKKAEDLLNKNLRYFTPNEIKKIHGF 280
Dnmt2           KGYGSYIEGTGSVLQTAEDVQVENIYKSLTNLSQEEQITKLLILKLRYFTPKEIANLLGF 354
                *.* . :*****:  . *   :             ::  .**  :******:** :: **

Ehmeth          SSNFTTQIDGLTDKQQYQCLGNSVSCFVIAQLMEYLFDDLKE 322
Dnmt2           PPEFG-FPEKITVKQRYRLLGNSLNVHVVAKLIKILYE---- 391
                ..:*    : :* **:*: ****:. .*:*:*:: *::
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**Supplementary Material Figure 2.** Clustal W alignment (35) of Ehmeth and human Dnmt2 (accession no. AAC39764). Amino acids in the putative *S*-adenosyl methionine binding domain (from amino acid 5 to 22), the putative catalytic site (from amino acid 72 to 92), and the PROSITE signature to cytosine-specific DNA methyltransferases C-terminal (PS00095) (from amino acid 298 to 316) are in italics.