Figure S4.

A)

```
HD2c       1 MEFWGLEVKPGSTVKCEPGYGFV--LHLSQAALGES----KK---SDNALMYVKI--DDQ
HD2a       1 MEFWGLEVKPGSTVKCEPGYGFV--LHLSQAALGES----KK---SDNALMYVKI--DDQ
HDT901     1 MEFWGLEVKPGSTVKCEPGHGFI--LHLSQAALGES----KK---SDNALMYVKV--DDQ
HD2b       1 MEFWGLEVKPGSTVKCEPGHGFI--LHVSQAALGES----KK---SDSALMYVKV--DDK
HDT701     1 MEFWGLEVKPGQTVKCEPEDERF--LHLSQAALGES----KKG--SDNAVMYVKT--DDQ
HDT801     1 MEFWGLEVKPNQSLKVSPDDDHF--LHLSQGALGEV----KK---DDKATMFVKI--GDQ
HDT802     1 MEFWGLEVKPNQSVKVSPDDEHF--LHLSQGALGEV----KK---DDKATMFVKI--GDQ
HDAT001    1 MEFWGLEVKPNQSIKVSPEDDHF--LHLSQAALGEV----KK---DDKTTLFVRVD-GGQ
HDT101     1 MEVGGQEVKPGATVSCKVGDGLV--IHLSQAALGES----KKA--SENAILSVNI--DDK
HDT1702    1 MEFWGAEVKVGETVKVDPSEFEAC-IHLSQAALGES----KKDK--EPVVLSLKV--GDQ
HDT1301    1 MEFWGAEVKVGETIKIDPYDLEA--IHISQVALGEA----KKDKPNESVVIYLKV--GEQ
HDT1202    1 MEFWGVEVKVGQTVTVDPMDPVDSYIHISQVALGEA----KKEKPNESVVLYLKV--GEQ
HDT1302    1 MEFWGVEVKAGQSVKVDPNDQCIGIIHISQVALGEG----KKGEASESVVLYLKV--ADM
HDT1401    1 MEFWGAEVKSGEPLTVQPGDGMV--LHLSQASLGEL----KKDK-SESVCLSVNI--DGK
HDT1102    1 MEFWGAEVKSGEPLTVQPGDGMV--LHLSQASLGEL----KKDK-SESACLSVNI--DGK
HDT1103    1 MEFWGAEVKSGQPLSVQPGDDMV--LHLSQASLGEV----KKDKASEPVCLSVTI--DGK
HDT1501    1 MEFWGIEVKAGQPIKTDPGASHV--IHLSQATLGES----K-NK-AESVPLYVNV--NGK
HDT1602    1 MQFWGVEVKAKEPSSVALEDGHI--IHLSQAALGEV----KKD--NEHVTLYVKV--EDK
HDT1       1 MEFWGIEVKSGKPVTVTPEEGIL--IHVSQASLGEC----KNKK-GEFVPLHVKV--GNQ
HDT2       1 MEFWGVAVTPKNATKVTPEEDSL--VHISQASL-DC----TV-KSGESVVLSVTV--GGA
HDT1402    1 MEFWGVEVKAGQTLKVKPELFKL--IHVSQAAIGEV----KDVKEAKYVPLRLTV--GDN
HDT1101    1 MEFWGVEVKAGQTLKVKPELFKL--IHISQAAIGEV----KDVKEAKYVPLRLTV--GDN
HDT1601    1 MQFWGVEVKNGSTLKVQPGEAKV--VHLSQACLGEV----KKDKGNESIRLYVQK--NSQ
HDT3       1 MEFWGVEVKNGKPLHLDPGLDRL--VHISQVALGES----KNNV-TEPIQLYVTV--GSD
HDT1502    1 MEFWGVEVKSGQNFEVELEDDGSRILHLSQVALGEGTGDNKKEKGKETICLY-------Q
HDT4       1 MEFWGIEIKPGKPFKVIQKDGFM--VHASQVTLGDVEKV-KK---DETFAVYVKIGDDEN
                                        **          ****  ***          **

HD2c      50 KLAIGTLSVDKNPHIQFDLIFDKEFELSHTSKTTSVFFTGYK
HD2a      50 KLAIGTLSVDKNPHIQFDLIFDKEFELSHTSKTTSVFFTGYK
HDT901    50 KLAIGTLSIDKFPQVQFDLVFDKEFELSHTSKTTSVFFSGYK
HD2b      50 KLAIGTLSIDKYPQIQFDLVFNKEFELSHTSKTTSVFFSGYK
HDT701    51 KLVIGTLSADKFPQIQFDLVFDKEFELSHTSKTASVFFSGYK
HDT801    50 KLAIGTLSTDKFPQIQFDLVFEKEFELSHNSKTSSVFFSGYK
HDT802    50 KLAIGTLSTDKFPQIQFDLVFEKEFELSHNSKTSSVFFSGYK
HDAT001   51 KLAIGTLSMDKFPQIQFDLVFEKEFELSHNSKTTSVFFSGYN
HDT101    51 KLVLGTLSVEKHPQISCDLVFDKDFELPHNSKTRSVFFRGYK
HDT1702   52 KFVLGTLNREKIPQVSLELVLDREFELSHNSKTASVHFCGYK
HDT1301   53 KLVLGTLTKDKIPQISLDIVLEKEFELSHNSKAASVHFCGYK
HDT1202   55 KIVLGTLSRDGIPHLSLDLVLDSDSELSHTSKSASVFFCGYR
HDT1302   55 KFVIGTLTKDSFPQTTLNINLNGETELSHNSKGTRVHFSGYK
HDT1401   52 KLVLGTLNSEKVPQQQFDLVFDRDFELSHNLKSGSVYFFGYK
HDT1102   52 KLVLGTLNSEKVPQQQFDLVFDKDFELSHNLKSGSVYFFGYK
HDT1103   53 KLVLGTLSLDKLPQQQFDLVFDRDFELSHNWKNGSVYFFGYK
HDT1501   51 KLVLGTLSHQNCPQLCFDLVFEQGFELSHNWKNGSVYFLGYM
HDT1602   51 KFVLGILS-QNNPQLSFDLVFDKDFEISHSAKNGSVHLLGYQ
HDT1      52 NLVLGTLSTENIPQLFCDLVFDKEFELSHTWGKGSVYFVGYK
HDT2      51 KLVIGTLSQDKFPQISFDLVFDKEFELSHSGTKANVHFIGYK
HDT1402   53 SYVIGTLSAEDRPQLMFDLVFEKEFELSHGWKNGSVHFIGYT
HDT1101   53 KYVIGTLSAEDRPQLMFDLVFEKEFELSHGWKNGSVHFMGYS
HDT1601   53 KFVIGILSLEKFPHINFDLVFEDEFELSHDWKHGSVHFAGYK
HDT3      52 KLLIGTLSHEKFPQLSTEIVLERNFALSHTWKNGSVFFSGYK
HDT1502   54 KFVVGTLSQEKCPQIALDLVLHDKFELFHTWKNGSVYVTGYY
HDT4      55 GFMIGNLSQ-KFPQFSIDLYLGHEFEISHN-STSSVYLIGYR
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Figure S4A

Multiple sequence alignment of histone deacetylase domain of the HD2 family proteins. The numbers listed in front of the sequences indicates the location in the histone deacetylase domain and not in the given protein sequence. * indicates the region edited out of the alignment for phylogenetic analysis.

B)

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HD2c       1 ATGGAGTTCTGGGGTCTCGAGGTCAAGCCTGGTTCCACTGTTAAGTGTGAGCCTGGATAT
Hd2a       1 ATGGAGTTCTGGGGTCTCGAGGTCAAGCCTGGTTCCACTGTTAAGTGTGAGCCTGGATAT
HDT1901    1 ATGGAGTTCTGGGGTCTTGAGGTCAAGCCTGGATCCACTGTTAAGTGTGAGCCTGGACAT
HD2b       1 ATGGAGTTCTGGGGTCTCGAGGTCAAACCTGGATCCACTGTCAAGTGTGAGCCTGGACAT
HDT701     1 ATGGAGTTCTGGGGTCTTGAAGTCAAGCCTGGACAGACTGTCAAATGTGAGCCTGAAGAT
HDT801     1 ATGGAGTTCTGGGGCCTTGAGGTTAAGCCTAACCAGTCCCTCAAGGTTTCACCTGATGAT
HDT802     1 ATGGAGTTCTGGGGCCTTGAGGTTAAGCCTAACCAGTCCGTCAAGGTTTCACCTGATGAC
HDT1001    1 ATGGAGTTCTGGGGCCTCGAGGTTAAGCCTAACCAGTCCATCAAGGTTTCTCCTGAAGAT
HDT101     1 ATGGAGGTCGGGGGTCAAGAAGTGAAGCCAGGAGCCACGGTTTCTTGCAAAGTTGGTGAT
HDT1202    1 ATGGAGTTTTGGGGTGTTGAGGTTAAGGTTGGTCAGACCGTGACAGTTGACCCAATGGAT
HDT1302    1 ATGGAGTTTTGGGGTGTTGAGGTTAAGGCTGGACAATCGGTTAAAGTTGATCCAAATGAT
HDT1702    1 ATGGAGTTTTGGGGTGCTGAGGTTAAGGTTGGGGAAACTGTTAAGGTCGACCCAAGCGAG
HDT1301    1 ATGGAGTTCTGGGGTGCTGAGGTTAAGGTTGGAGAAACTATCAAGATTGACCCATATGAC
HDT1401    1 ATGGAGTTTTGGGGTGCTGAGGTGAAAAGTGGAGAGCCCTTAACTGTACAGCCTGGAGAT
HDT1102    1 ATGGAGTTTTGGGGTGCTGAGGTGAAAAGTGGAGAGCCATTAACTGTACAGCCTGGAGAT
HDT1103    1 ATGGAATTTTGGGGTGCGGAGGTGAAAAGTGGACAACCTTTATCTGTACAGCCGGGAGAT
HDT1501    1 ATGGAGTTCTGGGGTATTGAAGTTAAAGCTGGACAGCCTATTAAAACGGACCCTGGTGCC
HDT1602    1 ATGCAATTCTGGGGTGTTGAGGTTAAAGCTAAAGAGCCTAGCTCTGTCGCTCTTGAAGAT
HDT1       1 ATGGAGTTCTGGGGAATTGAAGTTAAATCAGGAAAGCCAGTTACAGTGACTCCTGAAGAA
HDT2       1 ATGGAGTTCTGGGGAGTTGCGGTGACACCAAAAACGCTACTAAGGTGACTCCTGAAGAA
HDT1402    1 ATGGAGTTTTGGGGTGTTGAAGTGAAAGCAGGACAAACACTAAAGGTTAAGCCCGAGCTT
HDT1101    1 ATGGAGTTTTGGGGTGTTGAAGTGAAAGCAGGACAAACACTAAAGGTTAAGCCCGAGCTT
HDT1601    1 ATGCAATTNTGGGGTGTTGAGGTTAAGAATGGAAGTACTCTGAAGGTGCAACCTGGTGAA
HDT3       1 ATGGAGTTCTGGGGTGTTGAAGTTAAGAATGGCAAACCACTTCACCTAGATCCTGGGCTA
HDT1502    1 ATGGAGTTTTGGGGTGTTGAAGTTAAAAGTGGACAGAACTTTGAGGTTGAACTGGAGGAT
HDT4       1 ATGGAGTTTTGGGGTATCGAGATTAAGCCAGGGAAGCCATTTAAGGTGATACAAAAAGAT

HD2c      61 GGCTTTGTG------CTGCACCTTTCCCAGGCTGCTCTTGGGGAATCG------------
Hd2a      61 GGCTTTGTG------CTGCACCTTTCCCAGGCTGCTCTTGGGGAATCG------------
HDT1901   61 GGCTTTATC------CTGCACCTTTCGCAGGCTGCTCTCGGGGAATCA------------
HD2b      61 GGCTTTATC------CTGCACGTTTCCCAGGCTGCCCTTGGGGAATCA------------
HDT701    61 GAACGCTTT------TTGCACCTTTCTCAGGCTGCTCTTGGGGAATCA------------
HDT801    61 GACCACTTC------CTCCATCTCTCCCAGGGTGCCCTTGGTGAAGTC------------
HDT802    61 GAGCACTTC------CTCCATCTCTCCCAGGGTGCCCTTGGTGAAGTG------------
HDT1001   61 GACCACTTT------CTCCATCTCTCCCAGGCTGCCCTTGGTGAGGTC------------
HDT101    61 GGCTTGGTT------ATCCACCTTTCACAGGCTGCACTGGGGGAATCA------------
HDT1202   61 CCTGTGCATTCATACATACACATATCTCAGGTTGCGCTCGGAGAGGCG------------
HDT1302   61 CAATGTATCGGGATAATTCACATTTCTCAAGTTGCACTTGGGGAAGGG------------
HDT1702   61 TTTGAGGCATGC---ATTCACCTTTCCCAGGCTGCTCTTGGTGAGTCA------------
HDT1301   61 CTTGAAGCA------ATTCACATTTCTCAGGTTGCACTTGGTGAAGCA------------
HDT1401   61 GGGATGGTT------TTGCATCTTTCACAGGCATCTCTAGGTGAGTTG------------
HDT1102   61 GGGATGGTT------TTGCATCTTTCACAGGCATCTCTAGGTGAGTTG------------
HDT1103   61 GACATGGTT------TTGCATCTTTCACAGGCATCTCTTGGTGAGGTG------------
HDT1501   61 AGTCATGTC------ATCCATCTTTCCCAGGCAACACTTGGTGAGTCA------------
HDT1602   61 GGTCACATT------ATCCATCTTTCACAGGCTGCTCTTGGTGAGGTG------------
HDT1      61 GGCATTCTT------ATCCAGGTTTCTCAGGCATCGCTTGGAGAATGT------------
HDT2      61 GACAGCCTT------GTCCACATTTCTCAGGCTTCACTT---GACTGC------------
HDT1402   61 TTCAAGCTC------ATTCATGTTTCCCAGGCTGCCATCGGTGAAGTG------------
HDT1101   61 TTCAAGCTC------ATTCATATTTCTCAGGCTGCCATAGGTGAAGTG------------
HDT1601   61 GCGAAGGTT------GTGCACCTGTCACAGGCCTGTCTTGGGGAGGTC------------
HDT3      61 GACAGGCTC------GTGCACATCTCTCAGGTTGCTTTGGGAGAGAGT------------
HDT1502   61 GATGGCAGTAGGATCTTGCATCTTTCACAGGTTGCCCTTGGTGAGGGGACTGGTGATAAC
HDT4      61 GGATTCATG------GTCCATGCCTCTCAGGTTACCCTTGGTGACGTTGAGAAGGTT---

HD2c     103 AAGAAG---------AGTGATAATGCCTTGATGTATGTCAAAATT------GATGATCAG
Hd2a     103 AAGAAG---------AGTGATAATGCCTTGATGTATGTCAAAATT------GATGATCAG
HDT1901  103 AAGAAA---------AGTGACAATGCCTTGATGTACGTCAAAGTC------GACGATCAG
HD2b     103 AAGAAA---------AGTGACAGTGCCTTAATGTATGTCAAAGTT------GATGACAAG
HDT701   103 AAGAAAGGA------TCTGACAATGCAGTAATGTATGTTAAAACT------GATGATCAA
HDT801   103 AAGAAG---------GATGACAAGGCTACCATGTTCGTCAAGATT------GGCGACCAG
HDT802   103 AAGAAG---------GATGACAAGGCAACCATGTTCGTCAAGATT------GGCGACCAG
HDT1001  103 AAGAAG---------GATGACAAGACAACCTTGTTTGTCAGGGTCGAC---GGCGGCCAG
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HDT101   103 AAGAAAGCG------AGTGAGAATGCCATTTTGTCTGTTAATATT------GATGATAAG
HDT1202  109 AAAAAGGAGAAACCTAATGAGTCTGTGGTTTTGTATTTGAAAGTT------GGTGAACAG
HDT1302  109 AAGAAAGGCGAAGCAAGTGAATCTGTTGTTCTGTATTTGAAAGTT------GCTGATATG
HDT1702  106 AAGAAGGAC------AAAGAACCTGTGGTCCTTTCCCTGAAAGTT------GGTGACCAG
HDT1301  103 AAGAAAGACAAACCAAACGAGTCTGTGGTTATTTACCTCAAAGTT------GGTGAACAG
HDT1401  103 AAGAAGGATAAA---TCAGAAAGTGTCTGCTTGTCAGTGAATATT------GATGGCAAG
HDT1102  103 AAGAAGGATAAA---TCAGAAAGTGCCTGCTTGTCAGTGAATATT------GATGGCAAG
HDT1103  103 AAAAAGGATAAAGCATCAGAACCTGTATGCTTGTCTGTAACTATT------GATGGCAAG
HDT1501  103 AAGAAC---AAA---GCAGAGTCGGTTCCTCTCTATGTGAATGTT------AATGGGAAG
HDT1602  103 AAGAAGGAT------AATGAACATGTGACCTTGTATGTCAAGGTT------GAGGACAAG
HDT1     103 AAAAAC---AAGAAGGGAGAGTTTGTGCCTTTACATGTAAAGGTT------GGGAACCAG
HDT2     100 ACAGTG---AAATCTGGAGAATCTGTGGTTTTGAGTGTGACTGTT------GGTGGGGCT
HDT1402  103 AAGGATGTCAAAGAAGCCAAGTATGTTCCACTACGCCTAACTGTT------GGAGATAAC
HDT1101  103 AAGGATGTCAAAGAAGCCAAATATGTTCCACTACGCCTAACTGTT------GGAGATAAC
HDT1601  103 AAGAAGGACAAAGGAAATGAATCCATTCGTCTTTATGTCCAGAAG------AATTCCCAG
HDT3     103 AAGAAC---AATGTAACCGAACCAATCCAGCTTTACGTGACTGTT------GGATCGGAT
HDT1502  121 AAGAAAGAAAAAGGAAAGGAAACCATTTGTCTCTATCTCAAATTC------AAAAATCAG
HDT4     112 AAAAAA---------GATGAGACTTTTGCCGTTTATGTGAAGATTGGTGATGATGAGAAT

HD2c     148 AAACTTGCCATTGGAACCCTCTCTGTTGACAAGAACCCACACATACAATTTGATCTGATT
Hd2a     148 AAACTTGCCATTGGAACCCTCTCTGTTGACAAGAACCCACACATTCAATTTGATCTGATT
HDT1901  148 AAGCTTGCCATTGGAACCCTCTCTATTGACAAGTTTCCGCAAGTACAATTCGATTTGGTT
HD2b     148 AAGCTTGCCATTGGAACGCTCTCTATCGACAAATACCCACAGATACAATTCGATTTGGTT
HDT701   151 AAGCTAGTCATTGGAACCCTCTCAGCTGACAAGTTCCCTCAAATCCAGTTTGATTTGGTC
HDT801   148 AAGCTAGCCATCGGGACCCTCTCTACTGACAAGTTCCCTCAGATCCAGTTCGACCTCGTC
HDT802   148 AAGCTAGCCATCGGGACCCTCTCTACTGACAAGTTCCCTCAGATCCAGTTTGACCTCGTC
HDT1001  151 AAGCTAGCCATCGGGACCCTCTCTATGGACAAGTTCCCTCAGATCCAGTTCGACCTCGTC
HDT101   151 AAACTAGTGCTTGGAACCTTATCAGTTGAGAAGCATCCTCAGATCTCTTGTGATCTTGTA
HDT1202  163 AAGATTGTCTTGGGAACCCTTTCTAGGGATGGCATTCCTCATCTATCGTTGGATTTGGTT
HDT1302  163 AAGTTTGTTATAGGAACTCTTACTAAGGATTCCTTTCCTCAAACTACCTTGAATATCAAT
HDT1702  154 AAATTTGTTCTGGGAACCCTTAACAGGGAGAAGATTCCTCAAGTGTCTCTTGAATTAGTT
HDT1301  157 AAACTTGTTTTGGGAACCCTGACCAAGGACAAAATTCCTCAGATATCTCTTGATATTGTT
HDT1401  154 AAACTTGTTCTTGGGACACTCAACTCAGAGAAGGTGCCTCAACAGCAATTTGACCTGGTT
HDT1102  154 AAACTTGTTCTTGGGACACTCAACTCAGAGAAGGTGCCTCAACAGCAATTTGACCTGGTT
HDT1103  157 AAGCTTGTTCTTGGCACACTCAGCTTAGATAAGCTGCCTCAACAACAATTTGACCTGGTT
HDT1501  151 AAACTCGTTCTCGGAACACTTTCCCACCAGAATTGCCCGCAATTGTGTTTTGATTTAGTA
HDT1602  151 AAATTTGTTTTGGGTATATTGAGCCAGAACAAC---CCTCAGCTGTCTTTTGATTTGGTT
HDT1     154 AACTTGGTTCTGGGAACTCTATCGACTGAGAACATCCCTCAGCTTTTCTGTGATTTGGTA
HDT2     151 AAACTTGTTATTGGAACACTTTCACAAGACAAGTTCCCTCAGATTAGCTTTGATTTGGTT
HDT1402  157 AGTTATGTCATTGGAACTCTATCTGCTGAGGATAGACCTCAGTTGATGTTTGACTTGGTC
HDT1101  157 AAATATGTCATTGGAACTCTATCTGCTGAGGATAGACCTCAGTTGATGTTTGACTTGGTC
HDT1601  157 AAGTTTGTCATTGGAATTCTTTCCCTTGAAAAATTCCCTCATATAAATTTTGACCTTGTA
HDT3     154 AAGCTTCTCATTGGAACGCTATCTCATGAGAAGTTTCCTCAGCTGTCTACGGAGATTGTC
HDT1502  175 AAGTTTGTGGTTGGAACACTTTCCCAAGAGAAATGCCCCAGATAGCATTGGATTTGGTA
HDT4     163 GGGTTTATGATTGGAAATCTCTCAC---AGAAGTTTCCTCAATTTTCTATTGATCTCTAC

HD2c     208 TTCGATAAAGAGTTTGAGCTGTCGCACACATCAAAAACTACCAGCGTCTTCTTCACTGGC
Hd2a     208 TTCGATAAAGAGTTTGAGCTGTCGCACACATCAAAAACTACCAGCGTCTTCTTCACTGGC
HDT1901  208 TTCGATAAAGAGTTTGAGCTGTCGCACACATCAAAAACTACCAGTGTGTTCTTCTCTGGT
HD2b     208 TTCAATAAAGAGTTTGAGCTGTCACACACATCGAAAACTACCAGTGTATTTTTCTCTGGT
HDT701   211 TTTGACAAAGAGTTTGAGCTGTCACACACTTCAAAGACTGCTAGTGTGTTCTTTTCTGGC
HDT801   208 TTTGAGAAGGAGTTTGAGCTCTCACACAATTCCAAGACGTCCAGCGTCTTCTTCTCTGGC
HDT802   208 TTCGAGAAGGAGTTTGAGCTCTCACACAATTCCAAGACGTCCAGCGTCTTCTTCTCTGGC
HDT1001  211 TTCGAAAAGGAATTTGAGCTGTCACACAATTCCAAGACAACAAGCGTCTTCTTCTCTGGC
HDT101   211 TTTGATAAGGATTTTGAGCTACCACACAATTCAAAAACACGTAGCGTTTTCTTCCGTGGC
HDT1202  223 CTGGACTCCGATTCCGAGCTTTCCCACACTTCAAAAAGTGCCAGTGTCTTTTTCTGTGGG
HDT1302  223 CTAAACGGGGAGACTGAACTTTCTCACAATTCAAAGGGCACAAGAGTCCATTTCTCTGGA
HDT1702  214 CTTGACAGGGAGTTTGAGCTTTCTCACAACTCTAAAACTGCTAGTGTTCATTTCTGTGGA
HDT1301  217 CTTGAAAAGGAATTTGAGCTATCTCACAATTCCAAAGCTGCTAGTGTTCATTTCTGTGGA
HDT1401  214 TTTGATAGAGACTTTGAATTATCACACAACTTGAAAAGTGGCAGTGTCTACTTTTTTGGA
HDT1102  214 TTTGATAAAGACTTTGAATTATCTCACAACTTGAAAAGTGGCAGTGTCTACTTTTTTGGA
HDT1103  217 TTTGATAGAGACTTTGAACTATCACACAACTGGAAAAATGGTAGCGTCTACTTTTTTGGA
HDT1501  211 TTTGAGCAAGGCTTTGAGCTCTCTCACAACTGGAAAAATGGGAGCGTCTATTTCCTTGGT
HDT1602  208 TTTGACAAAGATTTTGAGATCTCACACAGTGCGAAGAACGGGAGCGTTCACCTCTTGGGA
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HDT1      214 TTCGACAAGGAGTTTGAGCTTTCTCACACTTGGGGAAAAGGAAGTGTTTACTTTGTTGGA
HDT2      211 TTTGATAAAGAGTTTGAGCTTTCACACAGCGGTACCAAAGCAAATGTTCATTTCATTGGC
HDT1402   217 TTTGAAAAGGAGTTTGAACTTTCACATGGATGGAAAAATGGGAGTGTGCACTTCATTGGA
HDT1101   217 TTTGAAAAGGAGTTTGAACTTTCACATGGATGGAAAAATGGGAGTGTGCACTTCATGGGA
HDT1601   217 TTTGAAGATGAGTTTGAGCTATCTCATGATTGGAAACATGGAAGTGTGCACTTTGCCGGA
HDT3      214 TTGGAAAGGAACTTTGCGCTGTCTCATACTTGGAAGAATGGGAGCGTTTTCTTCTCTGGT
HDT1502   235 TTGCATGACAAATTTGAGCTGTTCCATACGTGGAAGAATGGCAGCGTATATGTCACTGGC
HDT4      220 TTAGGGCACGAGTTTGAGATTTCTCACAACAGTACA---AGCAGTGTCTATCTTATTGGT

HD2c      268 TACAAG
Hd2a      268 TACAAG
HDT1901   268 TACAAG
HD2b      268 TACAAG
HDT701    271 TACAAA
HDT801    268 TACAAG
HDT802    268 TACAAG
HDT1001   271 TACAAT
HDT101    271 TACAAG
HDT1202   283 TACAGA
HDT1302   283 TACAAA
HDT1702   274 TACAAA
HDT1301   277 TACAAA
HDT1401   274 TACAAG
HDT1102   274 TACAAG
HDT1103   277 TACAAG
HDT1501   271 TACATG
HDT1602   268 TACCAG
HDT1      274 TACAAA
HDT2      271 TACAAA
HDT1402   277 TACACT
HDT1101   277 TACTCT
HDT1601   277 TATAAA
HDT3      274 TACAAA
HDT1502   295 TATTAT
HDT4      277 TACAGG
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Figure S4B

Multiple sequence alignment of nucleotides encoding the histone deacetylase domain of the HD2 family proteins. The codon alignment was matched to the amino acid alignment shown in Figure 4A and the regions edited out in the protein alignment were edited in DNA alignment too. The numbers listed in front of the sequences indicates the location in the histone deacetylase domain and not in the given coding sequence of the gene.