Supplemental Information

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                    10        20        30        40        50        60
                    |         |         |         |         |         |
H. sapiens     MADFG-----ISAGQFVAVVWDKSSPVEALKGLVDKLQALTG---NEGRVSVEN-----I
M. musculus    MEEFG-----ISPGQLVAVFWDKSSPEEALKKLVARLQELTG---SEGQVFMEN-----V
X. laevis      MDDLAN--LVFPGQQVAVTWDGSSSTEALKEFVSKLQEVVA---LRGKVSVEN-----I
S. cerevisiae  MSQYKTGLLLIHPAVTTTPELVENTKAQAASKKVKFVDQFLINKLNDGSITLENAKYETV
                *  :       :  ..  .:       .:  :*  .  * ::  .    * :  :** :

Prim.cons.     M4DFG2GLLLISPGQ4VAV4WDKSSP4EALKKLV4KLQELTGNKLNEG4VSVENAKYET2


                    70        80        90        100       110       120
                    |         |         |         |         |         |
H. sapiens     KQLLQSAHKESSFDIILSGLVPGSTTLHSAEI-LAEIARILRPG-GCLFLKEPVETAVDN
M. musculus    TQLLQSSHKESSFDVILSGVVPGSTSLHSAEV-LAEMARILRPG-GCLFLKEPVETAEVN
X. laevis      ERLLLSAHADSSFDAILLGMVQGTQCIHSSEV-LAEVARILKPG-GALIIQEPVAAGAG-
S. cerevisiae  HYLTPEAQTDIKFPKKLISVLADSLKPNGSLIGLSDIYKVDALINGFEIINEPDYCWIKM
                *  .::: .* * .::.:  :.: *:::  ::    *  :::**

Prim.cons.     4QLLQSAHK2SSFD4ILSGVVPGST4LHS2E2GLAEIARILRPGNGCL22KEPVETA44N


                    130       140       150       160       170       180
                    |         |         |         |         |         |
H. sapiens     N-SKVKTASKLCSALTLSGLVEVKELQREPLTPEEVQSVREHLGHESDNLLFVQITGKKP
M. musculus    N-DKMKTASKLCSALTLSGLVEIKELQREALSPEEVQSVQEHLGYHSDSLRSVRVTGKKP
X. laevis      --AQLRTPEHLSSVLKLSGLTEVTQLLQEPLNPEQKQGVVELLGYNGNDVSTIRIRAKKP
S. cerevisiae  DSSKLNQTVSIPLKKKKTNNTKIQSGSKLPTFKKASSSTSNLPSFKKADHSRQPIVKETD
                  ::. . :  . :. .:: .  :.      :  ... :  ...  . : :.

Prim.cons.     NSSKLKTASKLCSAL2LSGL2EVKELQREPL4PEEVQSV4E2LGY4SDDLS4VRITGKKP


                    190       200       210       220       230       240
                    |         |         |         |         |         |
H. sapiens     NFEVGSSRQLKLSITKKSSP--SVKPAVDPAAAKLWTLSANDMEDDSMDLIDSDELLDPE
M. musculus    NFEVGSSSQLKLPN-KKSS--SVKPVVDPAAAKLWTLSANDMEDDSVDLIDSDELLDPE
X. laevis      NYEVGSSRQLSLPKRKTAE-----KPSVDPAAAKLWTLSASDMNDDDVDILDSDELLDQE
S. cerevisiae  SFKPPSFKMTTEPKVYRVVDDLIEDSDDDDFSSDSSKAQYFDQVDTSDDSIEEEELIDED
                .:: *   . .           .. *  ::. * * . * ::.:**:* :

Prim.cons.     NFEVGSSRQLKLPK3KKSS2DLSVKP4VDPAAAKLWTLSANDMEDDSVDLIDSDELLDPE


                    250       260       270       280       290       300
                    |         |         |         |         |         |
H. sapiens     DLKKPDPASLRAASCGEG--KKRKACKNCTCGLAEELEKEKSREQM--------------
M. musculus    DLKRPDPASLKAPSCGEG--KKRKACKNCTCGLAEELEREQSKAQ---------------
X. laevis      DLKKPAPSSLLASGCGEGSEKKRKACKNCTCGLAEELEAEKTPSTV--------------
S. cerevisiae  GSGK---SMITMITCGKSKTKKKKACKDCTCGMKEQEENEINDIRSQQDKVVKFTEDELT
                .  :   :: :    **:.   **;****;****; *;: * * .

Prim.cons.     DLKKPDP2SL4A4SCGEG22KKRKACKNCTCGLAEELE4EKS44Q3QQDKVVKFTEDELT


                    310       320       330       340       350
                    |         |         |         |         |
H. sapiens     ------SSQPKSACGNCYLGDAFRCASCPYLGMPAFKPGEKVLLSDSNLHDA
M. musculus    ------SSQPKSACGNCYLGDAFRCANCPYLGMPAFKPGEQVLLSNSNLQDA
X. laevis      ------PKAAPSACGNCYLGDAFRCASCPYLGMPAFKPGEKVLLNPTKLQDA
S. cerevisiae  EIDFTIDGKKVGGCGSCSLGDAFRCSGCPYLGLPAFKPGQPINLDSISDDL-
                       .**.* *******;.*****;******; : *. . .

Prim.cons.     EIDFTISSQPKSACGNCYLGDAFRCASCPYLGMPAFKPGEKVLLS4SNLQDA
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Cysteine residues that were
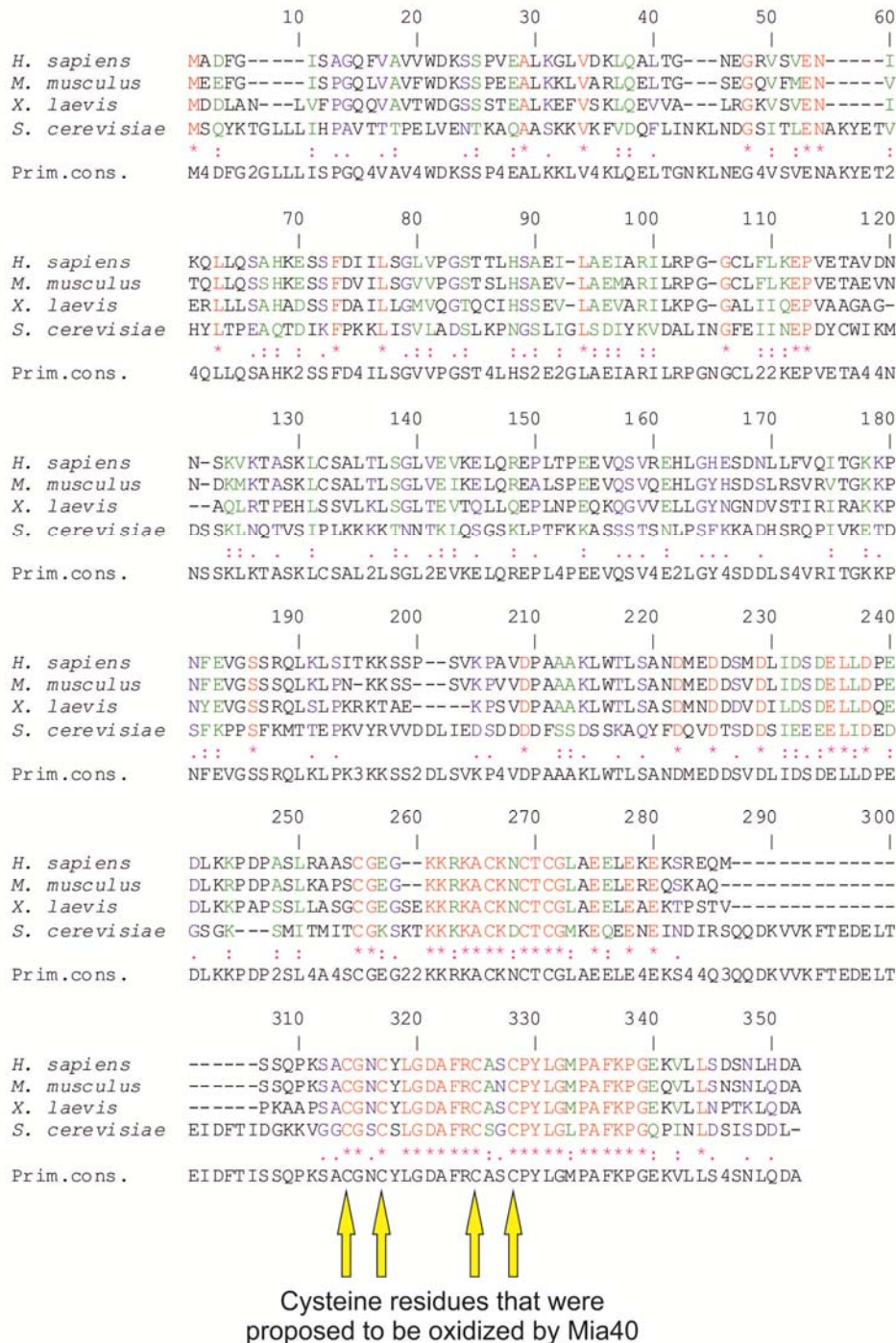proposed to be oxidized by Mia40

Fig. S1: Sequence alignment of members of the anamorsin/Dre2 family. The following sequences were aligned by use of the CLUSTAL W algorithm [1]: *Homo sapiens* NP_064709.2, *Mus musculus* NP_598902.1, *Xenopus laevis* NP_001164545.1, *Saccharomyces cerevisiae* P36152.1. The cysteine residues that were proposed to be oxidized by Mia40 in the conserved C-terminal region are indicated by arrowheads.

1. Thompson JD, Higgins DG, and Gibson TJ (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. **Nucleic Acids Res.** 22, 4673-4680.