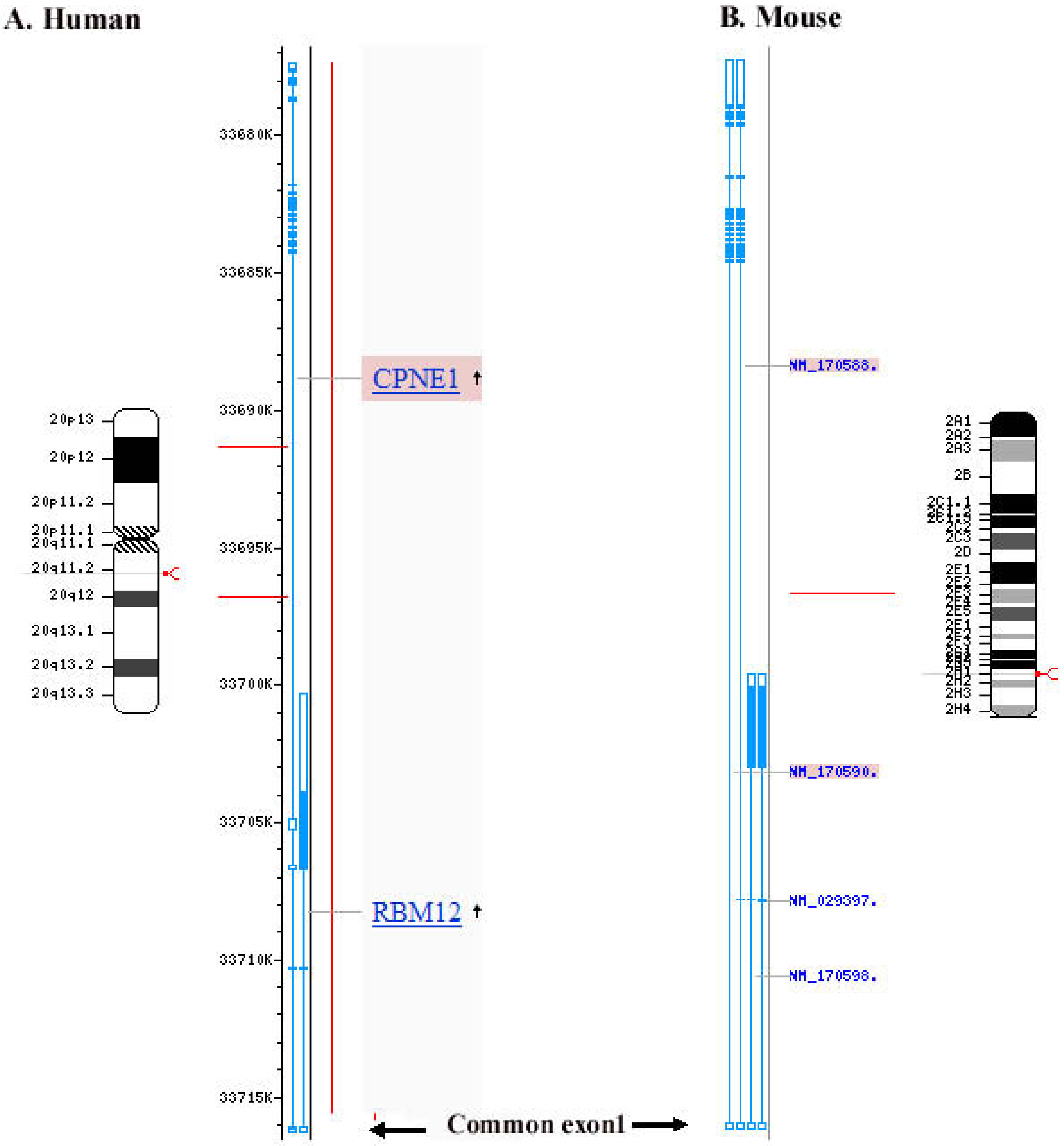
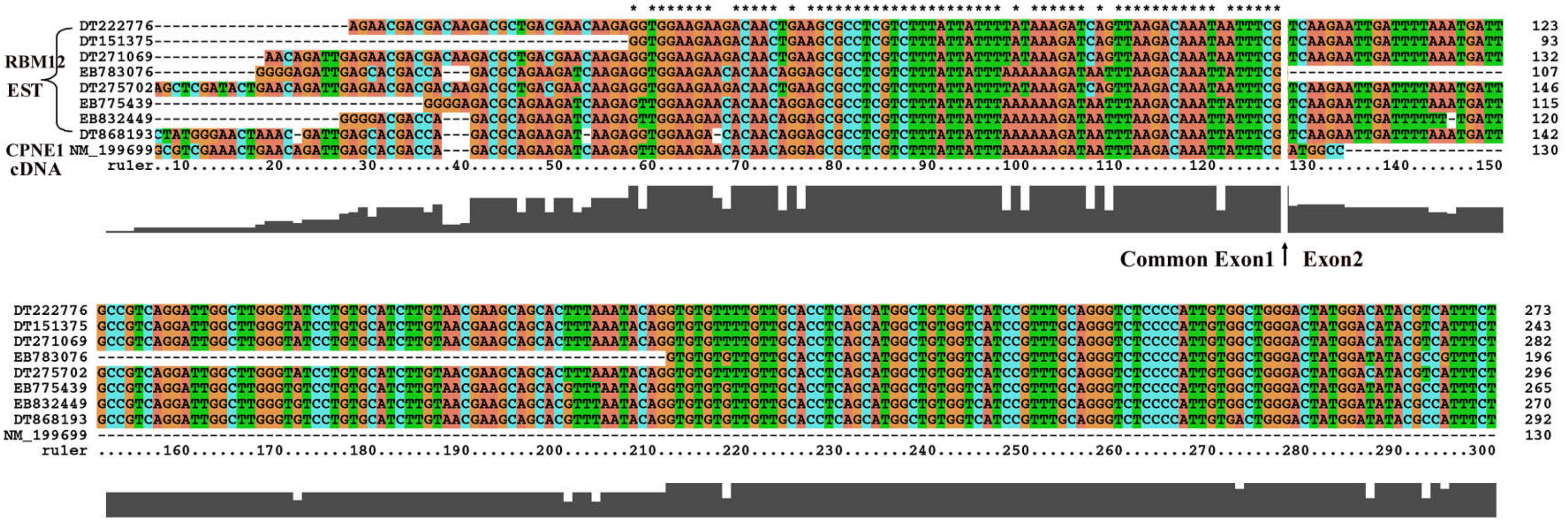
Supplementary Figure 1. Mapviewer display of CPNE1 and RBM12 in human and mouse genome



Supplementary Figure 2.

Zebrafish RBM12 EST sequences aligning with Zebrafish CPNE1 cDNA, NM_199699

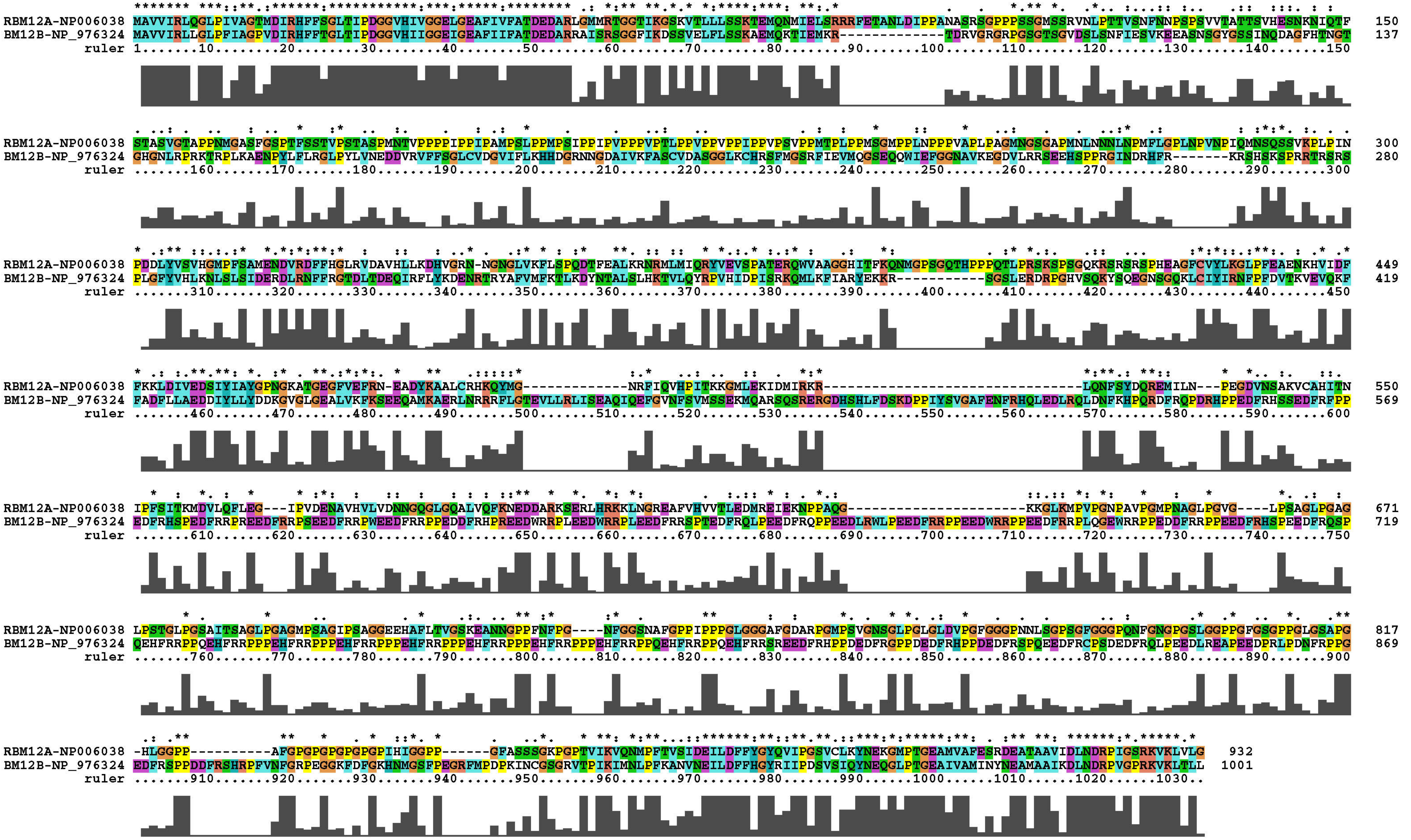
--Evidence of sharing most 5' exon and therefore promoter between the two genes in zebrafish



```
                                                            * ******* ***** * ********************* * ****** * *********** ******
 DT222776---------------------AGAACGACGACAAGACGCTGACGAACAAGAGGTGGAAGAAGACAACTGAAGCGCCTCGTCTTTATTATTTTATAAAGATCAGTTAAGACAAATAATTTCG TCAAGAATTGATTTTAAATGATT  123
 DT151375---------------------------------------------------GGTGGAAGAAGACAACTGAAGCGCCTCGTCTTTATTATTTTATAAAGATCAGTTAAGACAAATAATTTCG TCAAGAATTGATTTTAAATGATT   93
 DT271069------------AACAGATTGAGAACGACGACAAGACGCTGACGAACAAGAGGTGGAAGAAGACAACTGAAGCGCCTCGTCTTTATTATTTTATAAAGATCAGTTAAGACAAATAATTTCG TCAAGAATTGATTTTAAATGATT  132
 EB783076-----------GGGGAGATTGAGCACGACCA---GACGCAGAAGATCAAGAGGTGGAAGAACACAACAGGAGCGCCTCGTCTTTATTATTTAAAAAAGATAATTTAAGACAAATTATTTCG -----------------------  107
 DT275702AGCTCGATACTGAACAGATTGAGAACGACGACAAGACGCTGACGAACAAGAGGTGGAAGAAGACAACTGAAGCGCCTCGTCTTTATTATTTTATAAAGATCAGTTAAGACAAATAATTTCG TCAAGAATTGATTTTAAATGATT  146
 EB775439-----------------------------GGGGAGACGCAGAAGATCAAGAGTTGGAAGAACACAACAGGAGCGCCTCGTCTTTATTATTTAAAAAAGATAATTTAAGACAAATTATTTCG TCAAGAATTGATTTTAAATGATT  115
 EB832449--------------------GGGGACGACCA---GACGCAGAAGATCAAGAGTTGGAAGAACACAACAGGAGCGCCTCGTCTTTATTATTTAAAAAAGATAATTTAAGACAAATTATTTCG TCAAGAATTGATTTTTT-TGATT  120
 DT868193CTATGGGAACTAAAC-GATTGAGCACGACCA---GACGCAGAAGAT-AAGAGGTGGAAGA-CACAACAGGAGCGCCTCGTCTTTATTATTTAAAAAAGATAATTTAAGACAAATTATTTCG TCAAGAATTGATTTTAAATGATT  142
NM_199699GCGTCGAAACTGAACAGATTGAGCACGACCA---GACGCAGAAGATCAAGAGTTGGAAGAACACAACAGGAGCGCCTCGTCTTTATTATTTAAAAAAGATAATTTAAGACAAATTATTTCG ATGGCC-----------------  130
    ruler..10........20........30........40........50........60........70........80........90.......100.......110.......120....... 130.......140.......150
```

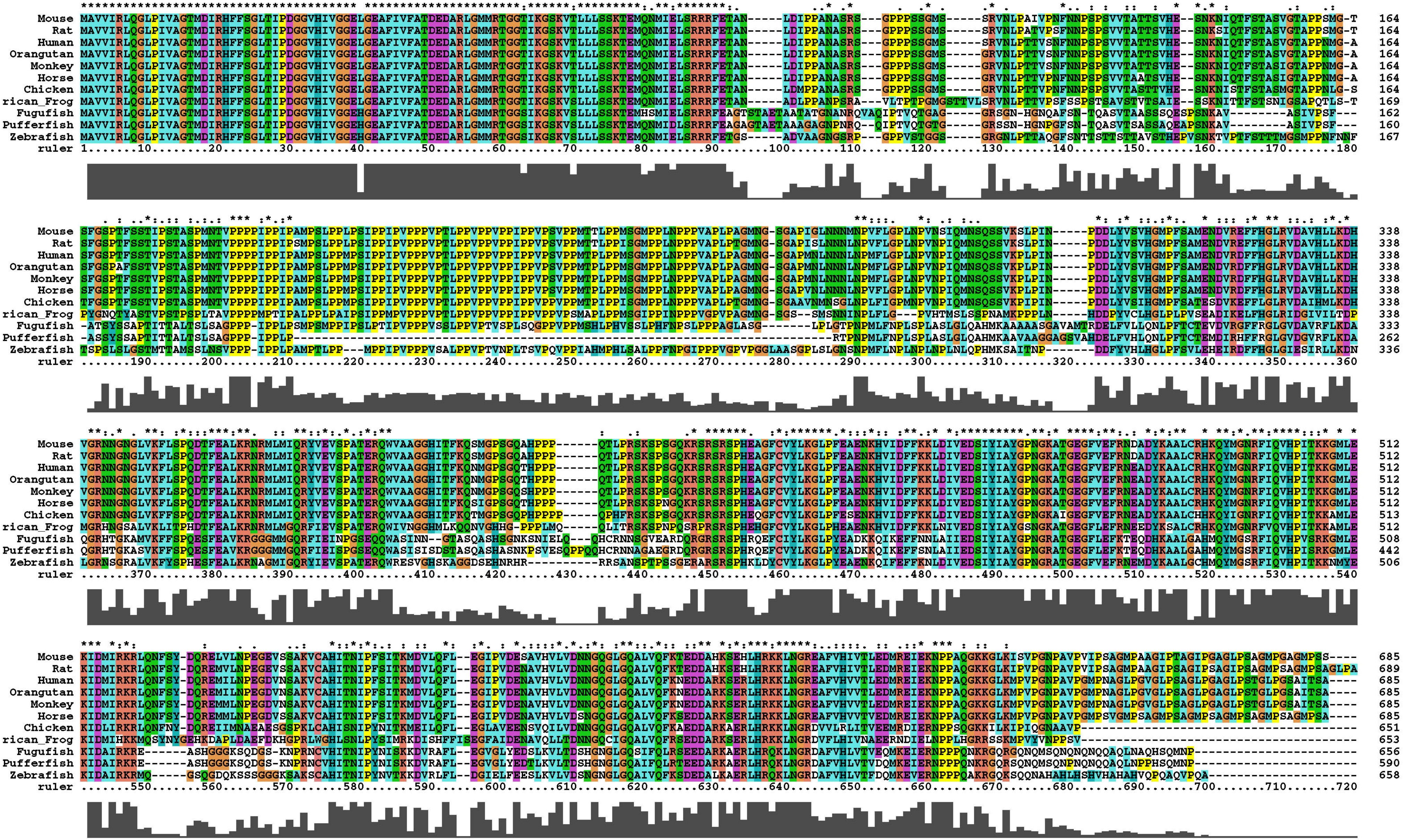
```
 DT222776GCCGTCAGGATTGGCTTGGGTATCCTGTGCATCTTGTAACGAAGCAGCACTTTAAATACAGGTGTGTTTTGTTGCACCTCAGCATGGCTGTGGTCATCCGTTTGCAGGGTCTCCCCATTGTGGCTGGGACTATGGACATACGTCATTTCT  273
 DT151375GCCGTCAGGATTGGCTTGGGTATCCTGTGCATCTTGTAACGAAGCAGCACTTTAAATACAGGTGTGTTTTGTTGCACCTCAGCATGGCTGTGGTCATCCGTTTGCAGGGTCTCCCCATTGTGGCTGGGACTATGGACATACGTCATTTCT  243
 DT271069GCCGTCAGGATTGGCTTGGGTATCCTGTGCATCTTGTAACGAAGCAGCACTTTAAATACAGGTGTGTTTTGTTGCACCTCAGCATGGCTGTGGTCATCCGTTTGCAGGGTCTCCCCATTGTGGCTGGGACTATGGACATACGTCATTTCT  282
 EB783076-------------------------------------------------------------GTGTGTGTTGTTGCACCTCAGCATGGCTGTGGTCATCCGTTTGCAGGGTCTCCCCATTGTGGCTGGGACTATGGATATACGCCGTTTCT  196
 DT275702GCCGTCAGGATTGGCTTGGGTATCCTGTGCATCTTGTAACGAAGCAGCACTTTAAATACAGGTGTGTTTTGTTGCACCTCAGCATGGCTGTGGTCATCCGTTTGCAGGGTCTCCCCATTGTGGCTGGGACTATGGACATACGTCATTTCT  296
 EB775439GCCGTCAGGATTGGCTTGGGTGTCCTGTGCATCTTGTAACGAAGCAGCACGTTTAATACAGGTGTGTGTTGTTGCACCTCAGCATGGCTGTGGTCATCCGTTTGCAGGGTCTCCCCATTGTGGCTGGGACTATGGATATACGCCATTTCT  265
 EB832449GCCGTCAGGATTGGCTTGGGTGTCCTGTGCATCTTGTAACGAAGCAGCACGTTTAATACAGGTGTGTGTTGTTGCACCTCAGCATGGCTGTGGTCATCCGTTTGCAGGGTCTCCCCATTGTGGCTGGGACTATGGATATACGCCATTTCT  270
 DT868193GCCGTCAGGATTGGCTTGGGTGTCCTGTGCATCTTGTAACGAAGCAGCACGTTTAATACAGGTGTGTGTTGTTGCACCTCAGCATGGCTGTGGTCATCCGTTTGCAGGGTCTCCCCATTGTGACTGGGACTATGGATATACGCCATTTCT  292
NM_199699------------------------------------------------------------------------------------------------------------------------------------------------------  130
    ruler.......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
```

Supple. Fig3A. alignment of Human RBM12 and RBM12B: Better conservation on the N- and C- terminus



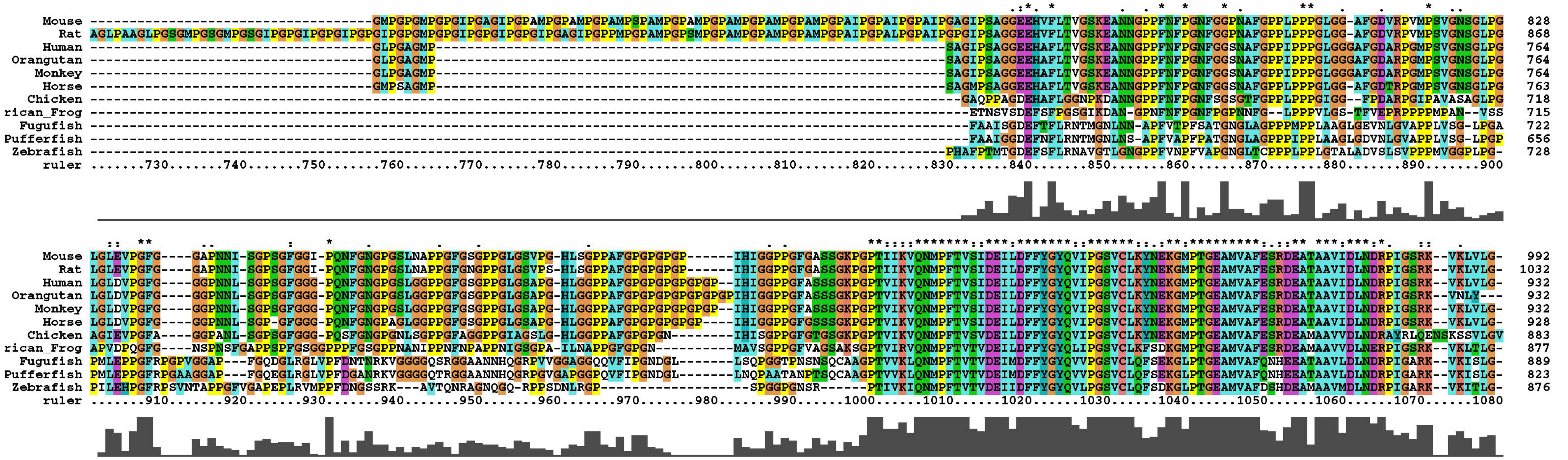
```
                ******* ***::**.:******:***********:***:*****:******** .: *:** **.*.* *:****:***: **:.*              .   .   *.** *.  .*.. :...:: :..   .:: :::.  : :
RBM12A-NP006038 MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGELGEAFIVFATDEDARLGMMRTGGTIKGSKVTLLLSSKTEMQNMIELSRRRFETANLDIPPANASRSGPPPSSGMSSRVNLPTTVSNFNNPSPSVVTATTSVHESNKNIQTF   150
BM12B-NP_976324 MAVVIRLLGLPFIAGPVDIRHFFTGLTIPDGGVHIIGGEIGEAFIIFATDEDARRAISRSGGFIKDSSVELFLSSKAEMQKTIEMKR-------------TDRVGRGRPGSGTSGVDSLSNFIESVKEEASNSGYGSSINQDAGFHTNGT   137
          ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                . ..: .  ..   : ..  *   :*  ..  :.    .   : .:  *    .     .   ..:   ..           . :  :   *    ::    *   ..:   .   .  ..:*  .:         : :*:*. :. . .
RBM12A-NP006038 STASVGTAPPNMGASFGSPTFSSTVPSTASPMNTVPPPPIPPIPAMPSLPPMPSIPPIPVPPPVPTLPPVPPVPPIPPVPSVPPMTPLPPMSGMPPLNPPPVAPLPAGMNGSGAPMNLNNNLNPMFLGPLNPVNPIQMNSQSSVKPLPIN   300
BM12B-NP_976324 GHGNLRPRKTRPLKAENPYLFLRGLPYLVNEDDVRVFFSGLCVDGVIFLKHHDGRNNGDAIVKFASCVDASGGLKCHRSFMGSRFIEVMQGSEQQWIEFGGNAVKEGDVLRRSEEHSPPRGINDRHFR-------KRSHSKSPRRTRSRS   280
          ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                * .:** ::.:.:*  *.*:*:**:*  :   ::   : ..* .  .:* * : :*   **. :: ::  * *.:.* :.:* :   .:   *:           . :* *.:.   .::  ...     :*:*::.:**:. : .* .*
RBM12A-NP006038 PDDLYVSVHGMPFSAMENDVRDFFHGLRVDAVHLLKDHVGRN-NGNGLVKFLSPQDTFEALKRNRMLMIQRYVEVSPATERQWVAAGGHITFKQNMGPSGQTHPPPQTLPRSKSPSGQKRSRSRSPHEAGFCVYLKGLPFEAENKHVIDF   449
BM12B-NP_976324 PLGFYVHLKNLSLSIDERDLRNFFRGTDLTDEQIRFLYKDENRTRYAFVMFKTLKDYNTALSLHKTVLQYRPVHIDPISRKQMLKFIARYEKKR-----------SGSLERDRPGHVSQKYSQEGNSGQKLCIYIRNFPFDVTKVEVQKF   419
          ruler .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                * .: :.**.**: *. :* . **.:*:*:. *   **   .:::::*             :.*   ..: ..  ::  .  *:*                                *:**.: **::      *  *.. :.   ::.
RBM12A-NP006038 FKKLDIVEDSIYIAYGPNGKATGEGFVEFRN-EADYKAALCRHKQYMG-------------NRFIQVHPITKKGMLEKIDMIRKR--------------------------------LQNFSYDQREMILN---PEGDVNSAKVCAHITN   550
BM12B-NP_976324 FADFLLAEDDIYLLYDDKGVGLGEALVKFKSEEQAMKAERLNRRRFLGTEVLLRLISEAQIQEFGVNFSVMSSEKMQARSQSRERGDHSHLFDSKDPPIYSVGAFENFRHQLEDLRQLDNFKHPQRDFRQPDRHPPEDFRHSSEDFRFPP   569
          ruler .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

                  *  :  *. :  *     * :*:  :   ::  :   : : : ::**  *  *.  *: *:       .  :.:: * : . *.:                       ::.:: *: *:   *   :   *         *. .:  :
RBM12A-NP006038 IPFSITKMDVLQFLEG---IPVDENAVHVLVDNNGQGLGQALVQFKNEDDARKSERLHRKKLNGREAFVHVVTLEDMREIEKNPPAQG----------------------KKGLKMPVPGNPAVPGMPNAGLPGVG----LPSAGLPGAG   671
BM12B-NP_976324 EDFRHSPEDFRRPREEDFRRPSEEDFRRPWEEDFRRPPEDDFRHPREEDWRRPLEEDWRRPLEEDFRRSPTEDFRQLPEEDFRQPPEEDLRWLPEEDFRRPPEEDWRRPPEEDFRRPLQGEWRRPPEDDFRRPPEEDFRHSPEEDFRQSP   719
          ruler .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750

                      * .       *       ..         . *    .:. .. ** :*      :*  .       **      :  :     *. .  * *. .:  *   .  .  .      ..  :       .*  .*  ..  *.   .**
RBM12A-NP006038 LPSTGLPGSAITSAGLPGAGMPSAGIPSAGGEEHAFLTVGSKEANNGPPFNFPG----NFGGSNAFGPPIPPPGLGGGAFGDARPGMPSVGNSGLPGLGLDVPGFGGGPNNLSGPSGFGGGPQNFGNGPGSLGGPPGFGSGPPGLGSAPG   817
BM12B-NP_976324 QEHFRRPPQEHFRRPPPEHFRRPPPEHFRRPPPEHFRRPPPEHFRRPPPEHFRRPPPEHFRRPPQEHFRRPPQEHFRRSREEDFRHPPDEDFRGPPDEDFRHPPDEDFRSPQEEDFRCPSDEDFRQLPEEDLREAPEEDPRLPDNFRPPG   869
          ruler .......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900

                 .: .**           **   *   . *  ::*. *      .   ..*.   * **: *:**...::******:**::**.**.::***:*:*****:**: . :** **: ******:*.*****.*
RBM12A-NP006038 -HLGGPP----------AFGPGPGPGPGPGPIHIGGPP------GFASSSGKPGPTVIKVQNMPFTVSIDEILDFFYGYQVIPGSVCLKYNEKGMPTGEAMVAFESRDEATAAVIDLNDRPIGSRKVKLVLG   932
BM12B-NP_976324 EDFRSPPDDFRSHRPFVNFGRPEGGKFDFGKHNMGSFPEGRFMPDPKINCGSGRVTPIKIMNLPFKANVNEILDFFHGYRIIPDSVSIQYNEQGLPTGEAIVAMINYNEAMAAIKDLNDRPVGPRKVKLTLL  1001
          ruler .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030..
```

Supplementary Figure 3B. Alignment of RBM12 Orthologs and high conservation on the N-terminus



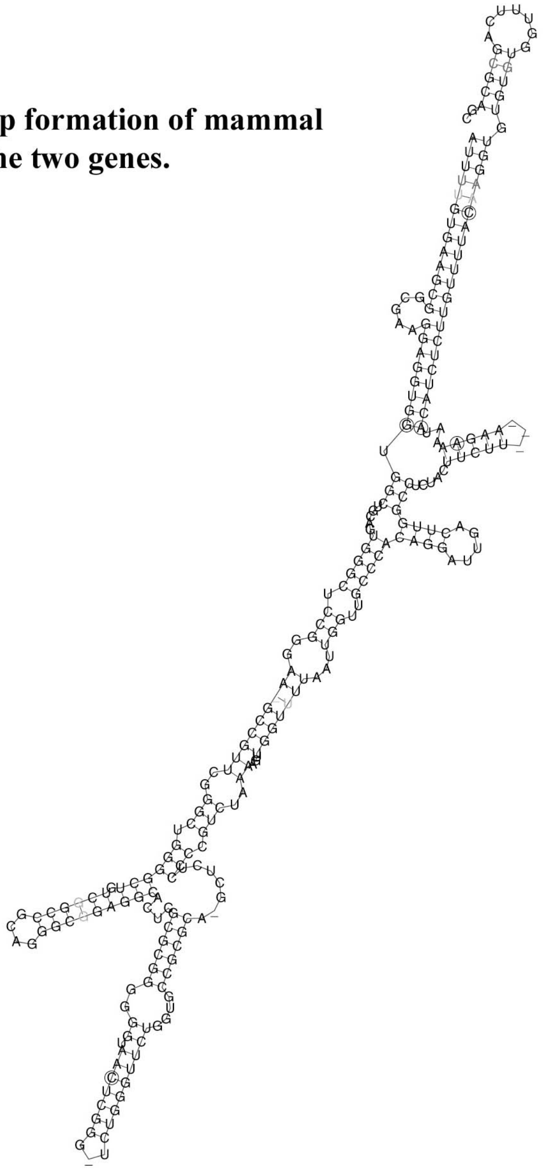
```
           *************************************** **********************:******:*********:.**:*******:.          ..* .*      .  .* .     .* .       *.. : :  ::  :  *  *.* :        .:  .:
     Mouse MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGELGEAFIVFATDEDARLGMMRTGGTIKGSKVTLLLSSKTEMQNMIELSRRRFETAN-----LDIPPANASRS---GPPPSSGMS-----SRVNLPAIVPNFNNPSPSVVTATTSVHE--SNKNIQTFSTASVGTAPPSMG-T   164
       Rat MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGELGEAFIVFATDEDARLGMMRTGGTIKGSKVTLLLSSKTEMQNMIELSRRRFETAN-----LDIPPANASRS---GPPPSSGMS-----SRVNLPATVPSFNNPSPSVVTATTSVHE--SNKSIQTFSTASVGTAPPSMG-T   164
     Human MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGELGEAFIVFATDEDARLGMMRTGGTIKGSKVTLLLSSKTEMQNMIELSRRRFETAN-----LDIPPANASRS---GPPPSSGMS-----SRVNLPTTVSNFNNPSPSVVTATTSVHE--SNKNIQTFSTASVGTAPPNMG-A   164
 Orangutan MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGELGEAFIVFATDEDARLGMMRTGGTIKGSKVTLLLSSKTEMQNMIELSRRRFETAN-----LDIPPANASRS---GPPPSSGMS-----GRVNLPTTVSNFNNPSPSVVTATTSVHE--SNKNIQTFSTASVGTAPPNMG-A   164
    Monkey MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGELGEAFIVFATDEDARLGMMRTGGTIKGSKVTLLLSSKTEMQNMIELSRRRFETAN-----LDIPPANASRS---GPPPSSGMS-----GRVNLPTTVSNFNNPSPSVVTATTSVHE--SNKNIQTFSTASIGTAPPNMG-A   164
     Horse MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGELGEAFIVFATDEDARLGMMRTGGTIKGSKVTLLLSSKTEMQNMIELSRRRFETAN-----LDIPPANASRS---GPPPSSGMS-----GRVNLPTTVPNFNNPSPSVVTAATSVHE--SNKNIQTFSTASIGTAPPNMG-A   164
   Chicken MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGELGEAFIVFATDEDARLGMMRTGGTIKGSKVTLLLSSKTEMQNMIELSRRRFETAN-----LDMPPANASRS---GPPPSSGMS-----GRVNLPTTVPNFNNPSPSVVTASTTVHE--SNKNISTFSTASMGTAPPNLG-S   164
rican_Frog MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGELGEAFIVFATDEDARLGMMRTGGTIKGSKVSLLLSSKTEMQNMIELSRRRFETAN-----ADLPPANPSRA---VLTPTPGMGSTTVLSRVNLPTTVPSFSSPSTSAVSTVTSAIE--SSKNITTFSTSNIGSAPQTLS-T   169
  Fugufish MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGEHGEAFIVFATDEDARLGMMRTGGSIKGSKVSLLLSSKTEMHSMIELSRRRFEAGTSTAETAATATGNANRQVAQIPTVQTGAG-----GRSGN-HGNQAFSN-TQASVTAASSSQESPSNKAV--------ASIVPSF---   162
Pufferfish MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGEHGEAFIVFATDEDARLGMMRTGGSIKGSKVSLLLSSKTEMQNMIDLSRRRFEAGAGTAETAAAGAGNPNRQ--QIPTVQTGTG-----GRSSN-HGNPGFSN-TQASVTSASSAQEAPSNKAV--------ASIVPSF---   160
 Zebrafish MAVVIRLQGLPIVAGTMDIRHFFSGLTIPDGGVHIVGGEHGEAFIVFATDEDARLGMMRTGGSIKGSKVSLLLSSKTEMQNMIELSRRRFETGS-----ADVAAGNGSRP---GPPVSTGGS-----GRGNLPTTAQGFSNTTSTTSTTAVSTHEPVSNKTVPTFSTTTMGSMPPNFNNF   167
     ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150.......160.......170.......180

              . : ..*:.:: :.:.: *** :*.:*                                                                               **:::.   *: .: :..                *: :* ::.:*:.  * ::: :* ** ::.: :*.*
     Mouse SFGSPTFSSTIPSTASPMNTVPPPPIPPIPAMPSLPPLPSIPPIPVPPPVPTLPPVPPVPPIPPVPSVPPMTTLPPMSGMPPLNPPPVAPLPAGMNG-SGAPIGLNNNMNPVFLGPLNPVNSIQMNSQSSVKSLPIN-----PDDLYVSVHGMPFSAMENDVREFFHGLRVDAVHLLKDH   338
       Rat SFGSPTFSSTIPSTASPMNTVPPPPIPPIPSMPSLPPLPSIPPIPVPPPVPTLPPVPPVPPIPPVPSVPPMTTLPPISGMPPLNPPPVAPLPTGMNG-SGAPISLNNNLNPVFLGPLNPVNPIQMNSQSSVKSLPIN-----PDDLYVSVHGMPFSAMENDVREFFHGLRVDAVHLLKDH   338
     Human SFGSPTFSSTVPSTASPMNTVPPPPIPPIPAMPSLPPMPSIPPIPVPPPVPTLPPVPPVPPIPPVPSVPPMTPLPPMSGMPPLNPPPVAPLPAGMNG-SGAPMNLNNNLNPMFLGPLNPVNPIQMNSQSSVKPLPIN-----PDDLYVSVHGMPFSAMENDVRDFFHGLRVDAVHLLKDH   338
 Orangutan SFGSPAFSSTVPSTASPMNTVPPPPIPPIPAMPSLPPMPSIPPIPVPPPVPTLPPVPPVPPIPPVPSVPPMTPLPPMSGMPPLNPPPVAPLPAGMNG-SGAPMNLNNNLNPMFLGPLNPVNPIQMNSQSSVKPLPIN-----PDDLYVSVHGMPFSAMENDVRDFFHGLRVDAVHLLKDH   338
    Monkey SFGSPTFSSTVPSTASPMNTVPPPPIPPIPAMPSLPPMPSIPPIPVPPPVPTLPPVPPVPPIPPVPSVPPMTPLPPMSGMPPLNPPPVAPLPAGMNG-SGAPMNLNNNLNPMFLGPLNPVNPIQMNSQSSVKPLPIN-----PDDLYVSVHGMPFSAMENDVRDFFHGLRVDAVHLLKDH   338
     Horse SFGSPTFSSTIPSTASPMNTVPPPPIPPIPAMPSLPPMPSIPPIPVPPPVPTLPPVPPVPPIPPVPSVPPMTPLPPMSGMPPLNPPPVAPLPAGMNG-SGAPVNLNNNLNPVFLGPLNPVNPIQMNSQSSVKPLPIN-----PDDLYVSVHGMPFSAMENDVRDFFHGLRVDAVHLLKDH   338
   Chicken TFGSPTFSSTVPSTASPMNTVPPPPIPPIPAMPSLPPMPSIPPIPVPPPVPTLPPVPPVPPIPPVPPVPPMTPIPPISGMPPLNPPPVAPLPTGMNG-SGAAVNMNSGLNPLFIGPMNPVNPIQMNSQSSVKPIPIN-----PDDLYVSIHGMPFSATESDVKEFFLGLRVDAIHMLKDH   338
rican_Frog PYGNQTYASTVPSTPSPLTAVPPPPMPTIPALPPLPAIPSIPPMPVPPPVPTLPPVPPVPPIPPVPPVPSMAPLPPMSGIPPINPPPVGPVPAGMNG-SGS--SMSNNINPLFLG---PVHTMSLSSPNAMKPPPLN-----HDDPYVCLHGLPLPVSEADIKELFHGLRIDGIVILTDP   338
  Fugufish -ATSYSSAPTITTALTSLSAGPPP-IPPLPSMPSMPPIPSLPTIPVPPPVSSLPPVPTVSPLSQGPPVPPMSHLPHVSSLPHFNPSLPPPAGLASG-------LPLGTPNPMLFNPLSPLASLGLQAHMKAAAAASGAVAMTRDELFVLLQNLPFTCTEVDVRGFFRGLGVDAVRFLKDA   333
Pufferfish -ASSYSSAPTITTALTSLSAGPPP-IPPLP----------------------------------------------------------------------------RTPNPMLFNPLSPLASLGLQAHMKAAVAAGGAGSVAHDELFVHLQNLPFTCTEMDIRHFFRGLGVDGVRFLKDA   262
 Zebrafish TSPSLSLGSTMTTAMSSLNSVPPP-IPPLPAMPTLPP---MPPIPVPPPVSALPPVPTVNPLTSVPQVPPIAHMPHLSALPPFNPGIPPPVGPVPGGLAASGPLSLGNSNPMFLNPLNPLNPLNLQPHMKSAITNP-------DDFYVHLHGLPFSVLEHEIRDFFHGLGIESIRLLKDN   336
     ruler .......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300.......310.......320.......330.......340.......350.......360

            **:.* . **: :*:::***:**.  :: **::*:.*.:*:**                             :   .:      .* ******.  :*:******.*:::*:: :**.:* *:*********.**:* ****:**:.: *:*:**  * **:*.**:****:::* * *
     Mouse VGRNNGNGLVKFLSPQDTFEALKRNRMLMIQRYVEVSPATERQWVAAGGHITFKQSMGPSGQAHPPP------QTLPRSKSPSGQKRSRSRSPHEAGFCVYLKGLPFEAENKHVIDFFKKLDIVEDSIYIAYGPNGKATGEGFVEFRNDADYKAALCRHKQYMGNRFIQVHPITKKGMLE   512
       Rat VGRNNGNGLVKFLSPQDTFEALKRNRMLMIQRYVEVSPATERQWVAAGGHITFKQSMGPSGQAHPPP------QTLPRSKSPSGQKRSRSRSPHEAGFCVYLKGLPFEAENKHVIDFFKKLDIVEDSIYIAYGPNGKATGEGFVEFRNDADYKAALCRHKQYMGNRFIQVHPITKKGMLE   512
     Human VGRNNGNGLVKFLSPQDTFEALKRNRMLMIQRYVEVSPATERQWVAAGGHITFKQNMGPSGQTHPPP------QTLPRSKSPSGQKRSRSRSPHEAGFCVYLKGLPFEAENKHVIDFFKKLDIVEDSIYIAYGPNGKATGEGFVEFRNEADYKAALCRHKQYMGNRFIQVHPITKKGMLE   512
 Orangutan VGRNNGNGLVKFLSPQDTFEALKRNRMLMIQRYVEVSPATERQWVAAGGHITFKQNMGPSGQTHPPP------QTLPRSKSPSGQKRSRSRSPHEAGFCVYLKGLPFEAENKHVIDFFKKLDIVEDSIYIAYGPNGKATGEGFVEFRNEADYKAALCRHKQYMGNRFIQVHPITKKGMLE   512
    Monkey VGRNNGNGLVKFLSPQDTFEALKRNRMLMIQRYVEVSPATERQWVAAGGHITFKQNMGPSGQSHPPP------QTLPRSKSPSGQKRSRSRSPHEAGFCVYLKGLPFEAENKHVIDFFKKLDIVEDSIYIAYGPNGKATGEGFVEFRNEADYKAALCRHKQYMGNRFIQVHPITKKGMLE   512
     Horse VGRNNGNGLVKFLSPQDTFEALKRNRMLMIQRYVEVSPATERQWVAAGGHITFKQSIGPSGQTHPPP------QTLPRSKSPNGQKRSRSRSPHEAGFCVYLKGLPFEAENKHVIDFFKKLDIVEDSIYIAYGPNGKATGEGFVEFRNEADYKAALCRHKQYMGNRFIQVHPITKKGMLE   512
   Chicken VGRNNGNGLVKFFSPQDTFEALKRNRMLMIQRYVEVSPATERQWVAAGGHITFKQTMGPSGQPHPPPP-----QPHFRSKSPSGQKRSRSRSPHEQGFCVYLKGLPFESENKHVIDFFKKLDIVEDSIYIAYGPNGKAIGEGFVEFRNEADYKAALCHHKQYIGNRFIQVHPITKKAMLE   513
rican_Frog MGRHNGSALVKLITPHDTFEALKRNRMLMGQRFIEVSPATERQWIVNGGHMLKQQNVGHHG-PPPLMQ-----QLITRSKSPNPQSRPRSRSPHEHGFCVYLKGLPHEAENKHVIDFFKKLNIVEDSIYIAYGSNGKATGEGFLEFRNEEDYKSALCRHKQYMGNRFVQVHPITKKAMLE   512
  Fugufish QGRHTGKAMVKFFSPQESFEAVKRGGGMMGQRFIEINPGSEQQWASINN--GTASQASHSGNKSNIELQ---QHCRNNSGVEARDQRGRSRSPHRQEFCIYLKGLPYEADKKQIKEFFNNLAIIEDSIYIAYGPNGRATGEGFLEFKTEQDHKAALGAHMQYMGSRFIQVHPVSRKGMLE   508
Pufferfish QGRHTGKASVKFFSPQESFEAVKRGGGMMGQRFIEISPGSEQQWASISISDSTASQASHASNKPSVESQPPQQHCRNNAGAEGRDQRGRSRSPHRQEFCVYLKGLPYEADKKQIKEFFSNLAIIEDSIYIAYGPNGRATGEGFLEFKTEQDHKAALGAHMQYMGSRFIQVHPISRKGMLE   442
 Zebrafish LGRNSGRALVKFYSPHESFEALKRNAGMIGQRYIEVSPATERQWRESVGHSKAGGDSEHNRHR----------RRSANSPTPSSGERARSRSPHKLDYCVYLKGLPYEAENKQIFEFFKNLDIVEDSIYIAYGPNGRATGEGFVEFRNEMDYKAALGCHMQYMGSRFIQVHPITKKNMYE   506
     ruler .......370.......380.......390.......400.......410.......420.......430.......440.......450.......460.......470.......480.......490.......500.......510.......520.......530.......540

           *** *:*:         :    . .    ..:   *::*:*:.: : ::  *:  :*. : *.::::*.*.:*: :**::.*::  ::** *:*:***:*****:..::::. :: .::* *** : ::  :
     Mouse KIDMIRKRLQNFSY-DQRELVLNPEGEVSSAKVCAHITNIPFSITKMDVLQFL--EGIPVDESAVHVLVDNNGQGLGQALVQFKTEDDAHKSEHLHRKKLNGREAFVHIVTLEDMREIEKNPPAQGKKGLKISVPGNPAVPVIPSAGMPAAGIPTAGIPGAGLPSAGMPGAGMPSS----   685
       Rat KIDMIRKRLQNFSY-DQREMVLNPEGEVSSAKVCAHITNIPFSITKMDVLQFL--EGIPVDENAVHVLVDNNGQGLGQALVQFKTEDDAHKSEHLHRKKLNGREAFVHIVTLEDMREIEKNPPAQGKKGLKIPVPGNPAVPVIPSAGMPAAGIPSAGIPSAGIPSAGMPSAGMPSAGLPA   689
     Human KIDMIRKRLQNFSY-DQREMILNPEGDVNSAKVCAHITNIPFSITKMDVLQFL--EGIPVDENAVHVLVDNNGQGLGQALVQFKNEDDARKSERLHRKKLNGREAFVHVVTLEDMREIEKNPPAQGKKGLKMPVPGNPAVPGMPNAGLPGVGLPSAGLPGAGLPSTGLPGSAITSA----   685
 Orangutan KIDMIRKRLQNFSY-DQREMILNPEGDVNSAKVCAHITNIPFSITKMDVLQFL--EGIPVDENAVHVLVDNNGQGLGQALVQFKNEDDARKSERLHRKKLNGREAFVHVVTLEDMREIEKNPPAQGKKGLKMPVPGNPAVPGMPNAGLPGVGLPSAGLPGAGLPSTGLPGSAITSA----   685
    Monkey KIDMIRKRLQNFSY-DQREMMLNPEGDVNSAKVCAHITNIPFSITKMDVLQFL--EGIPVDENAVHVLVDNNGQGLGQALVQFKNEDDARKSERLHRKKLNGREAFVHVVTLEDMREIEKNPPAQGKKGLKMPVPGNPAVPGMPNAGLPGVGLPSAGLPGAGLPSTGLPGSAITSA----   685
     Horse KIDMIRKRLQNFSY-DQREMMLNPEGDVSSAKVCAHITNIPFSITKMDVLQFL--EGIPVDENAVHVLVDSNGQGLGQALVQFKSEDDARKSERLHRKKLNGREAFVHVVTVEDMREIEKNPPAQGKKGLKMPVPGNPAVPGMPSVGMPSAGMPSAGMPSAGMPSAGMPSAGMPSA----   685
   Chicken KIDLIRKRLQNFNY-DQREIIMNAEAESGSPKLCAHISNIPYNITKMEILQFL--EGLAVEENSVQILVDNNGQGLGQALVQFKAEDDARKAERLHRKKLNGRDVVLRLITVEEMRDIERNPPSQGKKILKIPIQGNAAVP---------------------------------------   651
rican_Frog KIDMIHKKMQSYNYGEHKDAPLDAEFDKHGPRLWGHLSNLPYSIMRKDISHFFISEGFAIDENAVQLLTDNNGQCIGQALVQFRSEDDARKSERLHRKKLNGRDVFLHIVNAEERNDIELNPPLHGRRSSKMPVYVNPPSV---------------------------------------   653
  Fugufish KIDAIRKRE------ASHGGGKSQDGS-KNPRNCVHITNIPYNISKKDVRAFL--EGVGLYEDSLKVLTDSHGNGLGQSIFQLRSEEDARKAERLHRQKLNGRDAFVHLVTVEQMKEIERNPPPQNKRGQRGQNQMSQNQNQNQQAQLNAQHSQMNP-----------------------   656
Pufferfish KIDAIRKRE------ASHGGGKSQDGS-KNPRNCVHITNIPYNISKKDVRAFL--EGVGLYEDTLKVLTDSHGNGLGQAIFQLRTEEDARKAERLHRQKLNGRDAFVHLVTVDQMKEIERNPPPQNKRGQRSQNQMSQNPNQNQQAQLNPPHSQMNP-----------------------   590
 Zebrafish KIDAIRKRMQ-----GSQGDQKSSSGGGKSAKSCAHITNIPYNVTKKDVRLFL--DGIELFEESLKVLVDSNGNGLGQAIVQFKSDEDALKAERLHRQKLNGRDAFVHLVTFDQMKEVERNPPPQAKRGQKSQQNAHAHLHSHVHAHAHVQPQAQVPQA---------------------   658
     ruler .......550.......560.......570.......580.......590.......600.......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720
```

Supple. Fig 3B-continued: Better conservation on the c-terminus for RBM12 Orthologs



```
                                                                                                                                .:*. *        .  . *  *    * .       **   .    .     *  ..
     Mouse ------------------------------------GMPGPGMPGPGIPGAGIPGPAMPGPAMPGPAMPSPAMPGPAMPGPAMPGPAMPGPAMPGPAIPGPAIPGPAIPGAGIPSAGGEEHVFLTVGSKEANNGPPFNFPGNFGGPNAFGPPLPPPGLGG-AFGDVRPVMPSVGNSGLPG   828
       Rat AGLPAAGLPGSGMPGSGMPGSGIPGPGIPGPGIPGPGIPGPGMPGPGIPGPGIPGPGIPGAGIPGPPMPGPAMPGPSMPGPAMPGPAMPGPAMPGPAIPGPALPGPAIPGPGIPSAGGEEHVFLTVGSKEANNGPPFNFPGNFGGPNAFGPPLPPPGLGG-AFGDVRPVMPSVGNSGLPG   868
     Human ------------------------------------GLPGAGMP-----------------------------------------------------------------SAGIPSAGGEEHAFLTVGSKEANNGPPFNFPGNFGGSNAFGPPIPPPGLGGGAFGDARPGMPSVGNSGLPG   764
 Orangutan ------------------------------------GLPGAGMP-----------------------------------------------------------------SAGIPSAGGEEHAFLTVGSKEANNGPPFNFPGNFGGSNAFGPPIPPPGLGGGAFGDARPGMPSVGNSGLPG   764
    Monkey ------------------------------------GLPGAGMP-----------------------------------------------------------------SAGIPSAGGEEHAFLTVGSKEANNGPPFNFPGNFGGSNAFGPPIPPPGLGGGAFGDARPGMPSVGNSGLPG   764
     Horse ------------------------------------GMPSAGMP-----------------------------------------------------------------SAGMPSAGGEEHAFLTVGSKEANNGPPFNFPGNFGGSNAFGPPLPPPGLGG-AFGDTRPGMPSVGNSGLPG   763
   Chicken ---------------------------------------------------------------------------------------------------------------GAQPPAGDEHAFLGGNPKDANNGPPFNFPGNFSGSGTFGPPLPPPGIGG--FPDARPGIPAVASAGLPG   718
rican_Frog ----------------------------------------------------------------------------------------------------------------ETNSVSDEFSFPGSGIKDAN-GPNFNFPGNFPGPNNFG--LPPPVLGS-TFVEPRPPPPMPAN--VSS   715
  Fugufish ----------------------------------------------------------------------------------------------------------------FAAISGDEFTFLRNTMGNLNN-APFVTPFSATGNGLAGPPPMPPLAAGLGEVNLGVAPPLVSG-LPGA   722
Pufferfish ----------------------------------------------------------------------------------------------------------------FAAIGGDEFNFLRNTMGNLNS-APFVAPFPATGNGLAGPPPIPPLAAGLGDVNLGVAPPLVSG-LPGP   656
 Zebrafish -------------------------------------------------------------------------------------------------------------PHAFPTMTGDEFSFLRNAVGTLGNGPPFVNPFVAPGNGLTCPPPLPPLGTALADVSLSVPPPMVGGPLPG-   728
     ruler .......730.......740.......750.......760.......770.......780.......790.......800.......810.......820.......830.......840.......850.......860.......870.......880.......890.......900

             ::  **      ..         :    *    .        .    .             .                      . .          **::::*******::***:*******::******::.:**:*********:.::** ***:***:*.   ::   .
     Mouse LGLEVPGFG----GAPNNI-SGPSGFGGI-PQNFGNGPGSLNAPPGFGSGPPGLGSVPG-HLSGPPAFGPGPGPGP------IHIGGPPGFGASSGKPGPTIIKVQNMPFTVSIDEILDFFYGYQVIPGSVCLKYNEKGMPTGEAMVAFESRDEATAAVIDLNDRPIGSRK--VKLVLG-   992
       Rat LGLEVPGFG----GAPNNI-SGPSGFGGI-PQNFGNGPGSLNAPPGFGNGPPGLGSVPS-HLSGPPAFGPGPGPGP------IHIGGPPGFGASSGKPGPTIIKVQNMPFTVSIDEILDFFYGYQVIPGSVCLKYNEKGMPTGEAMVAFESRDEATAAVIDLNDRPIGSRK--VKLVLG-  1032
     Human LGLDVPGFG----GGPNNL-SGPSGFGGG-PQNFGNGPGSLGGPPGFGSGPPGLGSAPG-HLGGPPAFGPGPGPGPGPGP--IHIGGPPGFASSSGKPGPTVIKVQNMPFTVSIDEILDFFYGYQVIPGSVCLKYNEKGMPTGEAMVAFESRDEATAAVIDLNDRPIGSRK--VKLVLG-   932
 Orangutan LGLDVPGFG----GGPNNL-SGPSGFGGG-PQNFGNGPGSLGGPPGFGSGPPGLGSAPG-HLGGPPAFGPGPGPGPGPGPGPIHIGGPPGFASSSGKPGPTVIKVQNMPFTVSIDEILDFFYGYQVIPGSVCLKYNEKGMPTGEAMVAFESRDEATAAVIDLNDRPIGSRK--VNLY---   932
    Monkey LGLDVPGFG----GGPNNL-SGPSGFGGG-PQNFGNGPGSLGGPPGFGSGPPGLGSAPG-HLGGPPAFGPGPGPGPGPGP--IHIGGPPGFASSSGKPGPTVIKVQNMPFTVSIDEILDFFYGYQVIPGSVCLKYNEKGMPTGEAMVAFESRDEATAAVIDLNDRPIGSRK--VKLVLG-   932
     Horse LGLDVPGFG----GGPNNL-SGP-GFGGG-PQNFGNGPAGLGGPPGFGSGPPGLGSAPG-HLGGPPAFGPGPGPGPGP----IHIGGPPGFGSSSGKPGPTVIKVQNMPFTVSIDEILDFFYGYQVIPGSVCLKYNEKGMPTGEAMVAFESRDEATAAVIDLNDRPIGSRK--VKLVLG-   928
   Chicken AGIEVPGFA----GGPANL-SGPSGFGGG-PQSFGNGPGNLSGPPGFAGGPPGIAGSLG-HLGGPPAFGPGPGN--------IHISGPPGFGTGSGKPGPTVIKVQNMPFTVSVDEILDFFYGYQVIPGSVCLKYNEKGMPTGEAMVAFESRDEAMAAVVDLNDRAYRLQENSKSSVLGV   883
rican_Frog APVDPQGFG----NSPNSFGAPPSPFGSGGPPPFGSGPPNANIPPNFNPAPPNIGSGPA-ILNAPPGFGPGN----------MAVSGPPGFVAGSAKSGPTVIRVQNMPFTVTVDEILDFFYGYQLIPGSVCLKFSDKGMPTGEAMVAFESRDEAMAAVVDLNERPIGSRK--VKLTLG-   877
  Fugufish PMLEPPGFRPGPVGGAP---FGQDGLRGLVPFDNTNRKVGGGGQSRGGAANNHQGRPVVGGAGGQQVFIPGNDGL-------LSQPGGTPNSNSQCAAGPTVVKLQNMPFTVTVDEIMDFFYGYQVVPGSVCLQFSEKGLPTGEAMVAFQNHEEATAAVLDLNDRPIGARK--VKISLG-   889
Pufferfish PMLEPPGFRPGAAGGAP---FGQEGLRGLVPFDGANRKVGGGGQTRGGAANNHQGRPGVGAPGGPQVFIPGNDGL-------LNQPAATANPTSQCAAGPTVVKLQNMPFTVTVDEIMDFFYGYQVVPGSVCLQFSEKGLPTGEAMVAFQNHEEATAAVLDLNDRPIGARK--VKISLG-   823
 Zebrafish PILEHPGFRPSVNTAPPGFVGAPEPLRVMPPFDNGSSRK---AVTQNRAGNQGQ-RPPSDNLRGP-------------------SPGGPGNSR------PTIVKIQNMPFTVTVDEIIDFFYGYQVLPGSVCLQFSDKGLPTGEAMVAFDSHDEAMAAVMDLNDRPIGARK--VKITLG-   876
     ruler .......910.......920.......930.......940.......950.......960.......970.......980.......990......1000......1010......1020......1030......1040......1050......1060......1070......1080
```

Supple. Fig4: Stem-loop formation of mammal 5'UTR sequences for the two genes.



5'UTR sequences from several mammals were aligned using ClustalX and a consensus secondary RNA structure formation was predicted using Alifold program. The sequences used include sequences from exon 1, exon2 and non-coding part of exon3, which represent the longest 5'UTR sequences in RBM12 gene.

Supplementary Figure 5.

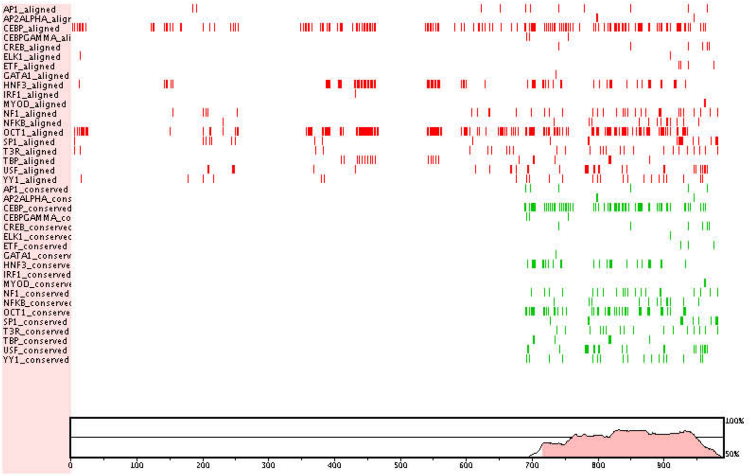
Sequence alignment for the region upstream of CPNE1/RBM12 gene pair cDNA (1000 bp) from human, mouse, rat and chicken using MAVID program (http://baboon.math.berkeley.edu/mavid/)

Bray N and Pachter L, MAVID: Constrained ancestral alignment of multiple sequences,, *Genome Research*, 14:693-699 (2004).

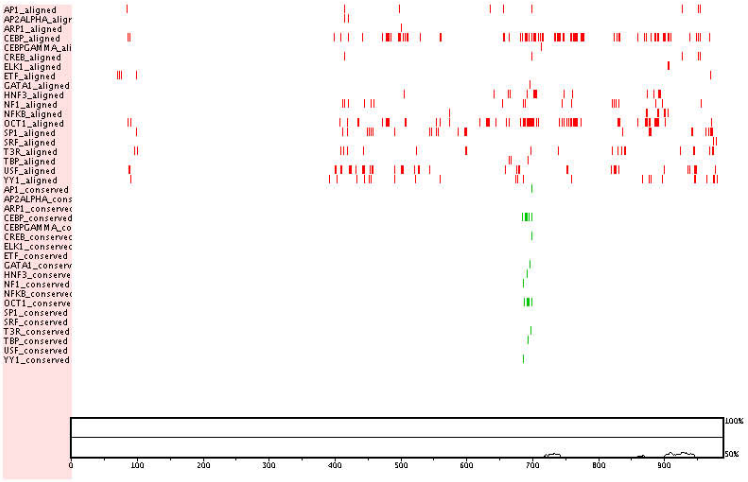
```
Mouse    CTTCC-----------TTCCTTTCTTCCT-----------TTCTCTCTCTCTCTCT---C
Human    TTTCTGAGACGAAGTTTCGCTTTTGTCATCCAGGGTGGAGTGCAATGGCGCCATCTGGGC
Rat      CCTCCCCAATCACCCCCTTCCT---CCTGCACAGGCGGCATAGTCTG----------G--
chicken  CCCCTGGGAGCTTCCATTGGCTGTGCCTGGAGTGCATGCATGTGCTGACTTTGTTGGG--
         1........10........20........30........40........50.........

Mouse    TCTCT-----CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT------
Human    TCACTGCAACCTCCACCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGC
Rat      ----TGCAGCCT------------------------------------------------
chicken  ----TGCCACTTGT--------------------------------------------GA
         61.......70........80........90........100.......110........

Mouse    ---------------------CTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT
Human    TGGGACCACAAGCACCGCCACCACACCCAGCTAGTT------------------------
Rat      -AGGACTTCAGGTATAATCAGATACCAGGGATTAT--------------ATGGGCGGCCA
chicken  TAAGAACAAATGAATGACAAGATACCAGGG-TGCT--------------ACAGGGTGCAA
         121......130.......140.......150.......160.......170........

Mouse    TCTTTCTTTCTTTCTTTCTGTGTGTGTTTAAGACAGGGTTTCTCTGTGTAGTGCTGGCTG
Human    --------------TTTGTATTTTTAGTAGAGGCTGGGTTTTGCCTTGTTGGCCAGACCG
Rat      GGAGAGATTAAAAGACATTTTCCGGGCTGGAGAGATGGCTCAGCGGTTAAGAGCA-----
chicken  ACAGGGA---------GCTGCGTGTGGTGCACAGAGGGCCCAAC---TTGGCCCT-----
         181......190.......200.......210.......220.......230........

Mouse    GTCTCAAACTCAGAA-------ATCTGCCTGCCTCTGCCTCCCAA-GTGCGGGGATTAGA
Human    GTCTCGAACTCCTGACCTCATGATCCGCCCTTCTCGGACTCCCAAAGTGCTGGGATTATA
Rat      ---------------------------CCCGACTACTCTTCCAGAGGTCCTGAGTTCAGT
chicken  ---------------------------CTTGGCTAAGGAGACAAAAGGGAGGGGTTCACT
         241......250.......260.......270.......280.......290........

Mouse    GGCTTGTGCCACCACTGCCAAGCAGGATTATTTTCTCTTTCTTTCTTTCT----------
Human    GGCGTGAGCCACCGCGCTCGGCCTGTATAA---------ACTTTTTTTTT----------
Rat      TCCC--AGCAACCACATGGTGGCTCA-CAACCATCT---------------------GTA
chicken  TGAC--AGAAGGGATACATTTTCAGAGCAACCTTATCAGAAATAAAGTCTAAAAGCAGTA
         301......310.......320.......330.......340.......350........

Mouse    -----------------------------------TTCTTTCTTTCTTTCTTTCTTTCTT
Human    -----------------------------------TTTTTTTTTTTTTTTTGAGATGGAG
Rat      AAG---------------AGATCCGATGCCGGGGGTTGGGGATTTAGCTCAGTGGTAGAG
chicken  AAGCCAGGGTTACCAAGGAGATGAGCAGGTGGGGGCTGTTTATT---GGAAGGGGTTGAG
         361......370.......380.......390.......400.......410........

Mouse    -------------------------TCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT
Human    -------------------------TCTTGC--TCTTTCGCCCAGGCCGGAGTGCAGTGG
Rat      CGCTTGCCTAGCAAGC---ACAAGGCCCTGGGTTCGGTCCCCAGCTCCGAAAAAAAGAAA
chicken  AG--TGGTGAGGAAGAGTAAGAAGGGGCTCTGTGAACATCCCAGCGCC------------
         421......430.......440.......450.......460.......470........

Mouse    TTCTTTCTTTCTTTCTTTCTTTCTCTTCCTTCCTTCCTTCCTTTTTCTTTCTTTCTTTCT
Human    CGCAATCTCGGCTCACTGCAAGCTCCGCCTCCCAGGTTCACGCTAT--------------
Rat      AAAAAAAGAGATTCGATGCC--CTCTTC--------------------------------
chicken  ----------------TGCCAGCACTGC--------------------------------
         481......490.......500.......510.......520.......530........

Mouse    TTCTTTTCTTTCTCTCTCTTTCTTTCTCTTTCTTTCTTTCT-----------TTCTTTCT
Human    --------------TCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGTGCCCGCC
Rat      ---------------------------------TGGTGTATCTGAAGACAGCTACAGTGT
chicken  ---------------------------------TGGTTGGTGCTGAG-CAGCAGCCGAGC
         541......550.......560.......570.......580.......590........

Mouse    TTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT
Human    ACCACGC-----------------------------------------------------
Rat      ACTTATAT---------------ATAAAAAATGAATAAAT---CTTTAAAAAAAGACATT
chicken  TGTCACAATCCTGGCTTTGCTGGATAAAAA-------------GTTTGCTGTATGACTGT
         601......610.......620.......630.......640.......650........

Mouse    TTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTTT
Human    --------------------------------------CCGGCTAATTTTTTGTATTTTT
Rat      TTCCTTCTTTTTATA---TTTGTTCTTTATATTTATATCTATTTTCATTTTAATTTTATT
chicken  GTGCTCCGTGCAGCAGACTGTGCTGGTTGTGTTT---TCTATTGGAAGTGAGA-------
         661......670.......680.......690.......700.......710........
```

```
Mouse   TGGTTTTTCGAGACAGGGTTTCTCTGTATAGTCCTGGCTGTCCTG--------------G
Human   TAG----AAGAGACGGGGTTTCACCGTGTTAGCCAGGATGGTCTC--------------G
Rat     AATGTCTCTGTGTAAGAGTTTGTGCACATGAGTGAAGATGTCTTCAGAGGCCAGAGGAGG
chicken --------GCTGGCACAGTCTGTTCCATGGAGGCACAGTGCTGGCGGAGGTGCCTCGCTG
        721......730.......740.......750.......760.......770........

Mouse   AACTCACTCTGTAGCCCAGGCTGGCCTCGAACTCAGAATTCGCCTGCCTCTGCCTCCCA-
Human   ATCT---------------------CCCGACCTCGTGATCCGCCCGCCTCGGCCTCCCAA
Rat     GCGTCAGATTTGAGGCCCGAGTTACTTGAGGTT--------------GTGAGCAGCTCAA
chicken TGCTCCCAT-------CAGGGTGAGCTCTGGTT--------------GTGTGCA------
        781......790.......800.......810.......820.......830........

Mouse   ---------------------------------------------T----------TTTT
Human   AGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCCCCGGCCT----------GTAT
Rat     GACTTCGTGAAGAGCAGTATGAGCTTTTATCCTTTGAGCCTTTTCTCCACCCCAAGGCAA
chicken --------------CAGCAAGAACGTTTAAC---TGAG-------------CGAAGGGTG
        841......850.......860.......870.......880.......890........

Mouse   TTTTTTTTCAATAGTCAAAAAAAGGTTCAAGCTTTTGCTTCTT-----------------
Human   AAACTCTTAAATGG--GAAAAAAGAATCAGGTTTTGGCTGTTTTGTCAGGATATAATAAC
Rat     AATATTTTCAATAGCCAAAAAAAAACAAAA----------------------CAAAACAG
chicken AAT-------GCAGCAAAGGGGACTTACAA----------------------CAAAAAGG
        901......910.......920.......930.......940.......950........

Mouse   ---------------GGTGCG-------TTTAATCCTCAAGACAGTTCTGCAGTGAAGGC
Human   TAGCCACCACGTTGTGGTCCA-------TTTAATCCTCAAAAAACTT------AGAGGTA
Rat     GACCTTTTGCTTGGTGGTGCG-------TTTAATCCTGAAGACAGTTCTGCAGTGTAGGC
chicken GCACTGACTCGGGGTAGTGTGGCACAGCTCTAATTCT---GCCACCTTCTAAGTGAAGAA
        961......970.......980.......990.......1000......1010.......

Mouse   ATTGTTTTTCTC-CCTTCACGGGGGTCTCCAAG----------------AGCCAAAGGAG
Human   AGCACAATTCGCTCCTTCCGCGGAAACTGGAAG----------------ACGTGAAGCA-
Rat     ACAC-----------TTTCACGGGGGCTCTAA----------------AAGCCAAAGGAA
chicken GCAGCA----GCTTGTTGCCTCAGGGCTCTACGTTCGTTGCCAATCTGATGCCTCTGGTT
        1021.....1030......1040......1050......1060......1070.......

Mouse   CCTGTACTTTAAAAGCTCTGCAAGGAA---------------------------------
Human   -----ATTTGCACAGTCTTGCAGTGAA----------------GGGCCAAGCTAGACACT
Rat     CCTGTAC---AAAAGCTCTGCAGCGAACCT------------------------------
chicken ACTCAGC---AGTAACCCTTCCGCTCACTTGTACCACCGTTAATTTCCAGAAAACTCAAC
        1081.....1090......1100......1110......1120......1130.......

Mouse   -----------------CCTTGGACAATAGC--------------------TTCAGGTCT
Human   CATACCCAGCCCACCCGCCAGGGCCACTAGC--------------------CCAAGGTCG
Rat     --------------------TGGACAATAGC--------------------TTCAGGCCG
chicken ATATCATCGATGTATACTATTGTACGAGAGGCAACGATACGTATCGTGCGATACAGGTCT
        1141.....1150......1160......1170......1180......1190.......

Mouse   GACTTT-------------GCAAACAGCTACTAAA-ATACCGGGTTCACCA-----CAAA
Human   GTCCTGTGCGCCAACAGTCGCAAGCAGGGACTGAATATCCCCCTCTTAGCA-----CAAA
Rat     GACTCTGCA--------------AACAGCAATTAAAAGCCGGGTTTA-------GCCAAA
chicken GACGGTGCTCTGTTCAGCCCCTAACTGGACATCAAACCCCGCTGTGGTACCGGCGCGGCA
        1201.....1210......1220......1230......1240......1250.......

Mouse   TACCTGCAACTTCCGAGCTTTTGCCCCCACCCCA-----AATCCTCAGCGCGCCTGCGTC
Human   ACCCAGTAACTTCCGGGAGAT------CGCCCGA-----GACCGTCAGCGCGCTTGCGCG
Rat     TACCTGCAACTTCCAAAGTTTCCCCCT--CCCCACTCCGAAACCTCAGCGCGCCTGCGTC
chicken CAGCCCCACCTCACACACACACCCCCTGACGCGAGGCGCGAACCGCGCTGCGCATGCGCC
        1261.....1270......1280......1290......1300......1310.......

Mouse   TCCCATCAG---------------------------GTGACGTCGGCAGCGGCGCCCCGC
Human   GCCCCT-------------------------------TGACGTCAACCACGCCGTTCCTC
Rat     TCCCACCAG---------------------------GTGACGTCGGTAGCGGCGCTCCGC
chicken ATCCACCACTGCGCGCAGCCCCACCCCGGGCAGGGAGAGACGGCCGTAGGGGGGCGCTGC
        1321.....1330......1340......1350......1360......1370.......

Mouse   C-----------------------------------------------------------
Human   CCCCTTCTGGAA------------------------------------------------
Rat     ---------------------------------------------------CCACTCTGG
chicken GCGCGCGGCGGAGCCCCGCCCTCCTCCTTCCGCCGGGCCCTCAGCCCCGCCCCTCCCTGG
        1381.....1390......1400......1410......1420......1430.......
```

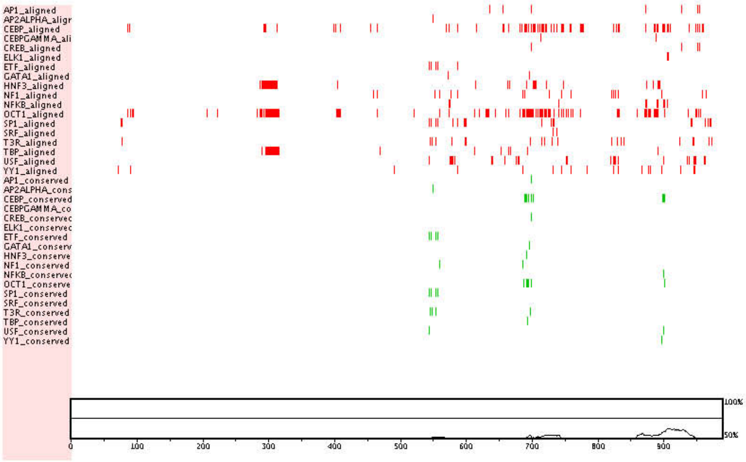
```
Mouse    ------------------------------T
Human    -----------------------------CG
Rat      GAACGCGGAGCGG-------GCG-GGCGGCC
chicken  CGGCGGGTGGCGGCGCCGCAGCGAGGCGGCC
         1441.....1450......1460........
```



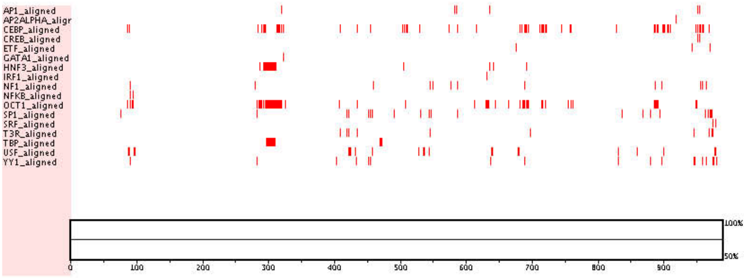
A. Mouse-rat pair



C. Human-rat pair



B. Human-mouse pair



D. Human-chicken pair

Supplementary Figure 6.
Transcription factor binding sites detection in the promoter regions of CPNE1/RBM12 in human, mouse, rat, and chicken.

1,000 bp DNA sequences upstream CPNE1/RBM12 cDNA were used in transcription factor binding sites analysis using rVISTA (http://genome.lbl.gov/vista/index.shtml). rVISTA combines searching the major transcription binding site database TRANSFAC from Biobase with a comparative sequence analysis. The program first identifies potential transcription factor binding sites in each of the two aligned sequences, and determines which of the predicted sites are aligned and conserved between the species in the alignment.

X-axis is the nucleotide sequence in the first sequence, with 1000 the nucleotide immediately 5' to the first nucleotide of CPNE1/RBM12 cDNA.
In each figure, the lower panel is the sequence alignment index between the sequence pairs, while the upper panel is the identified transcription factor binding sites, with the red color for aligned TF binding sites and the green color conserved TF binding sites.

Aligned binding sites: all the binding sites in the two sequences were identified independently, but only those with core binding site positions corresponded in the alignment of the two sequences were selected as aligned binding sites.

Conserved binding sites: predicted binding sites located in the sequence fragments conserved between two species at the level of over 80% over 24 bp window were selected as conserved binding sites.

Supplementary Fig 7. cDNA sequences that align with human RBM12 cDNA, NM_006047 These cDNA sequences all have very close 5' transcription initiation sites, usually within 40bp of each other. This indicates that the sharing of most 5' exon probably reflects the sharing of the same promoter. (The ones with longer 5' sequences on the display are mostly aligned genomic sequences).