```
                1   •••••••••o••••••••••o••••••••••o••••••••••o••••••••••o   50
F_CAT               ---------------------------------MASAPTSKYNSHSLENE
H_SAP               ---------------------------------MASASTSKYNSHSLENE
M_MUS               ---------------------------------MASASASKYNSHSLENE
D_RER               MTFRRGSGFHLRLLRENSRLNAALESCRKVNAVMASAPIAPYNSSPLGNS

Conservation        0000000000000000000000000000000000****5586***66*6*7

               51   •••••••••o••••••••••o••••••••••o••••••••••o••••••••••o   100
F_CAT               SVKRTSRDGVNRDLSETVPRLPGETRITDKEVIYICPFNGPIKGRVYITN
H_SAP               SIKRTSRDGVNRDLTEAVPRLPGETLITDKEVIYICPFNGPIKGRVYITN
M_MUS               SIKKVSQDGVSQDVSETVPRLPGELLITEKEVIYICPFNGPIKGRVYITN
D_RER               SSQNASRESLKMEPLADVTLLPGEERVIDKDIIYICPYNAAVKGKVFITN

Conservation        *5755*78785584564*66****44968*89*****8*769**8*8***

              101   •••••••••o••••••••••o••••••••••o••••••••••o••••••••••o  150
F_CAT               YRLYLRSLETDSALILDVPLGVISRIEKMGGATSRGENSYGLDITCKDMR
H_SAP               YRLYLRSLETDSSLILDVPLGVISRIEKMGGATSRGENSYGLDITCKDMR
M_MUS               YRLYLRSLETDSALILDVPLGVISRIEKMGGATSRGENSYGLDITCKDLR
D_RER               YRLYFKNTDSETPVTLNIPLGVISRVEKMGGASSRGENSYGLEITCKDMR

Conservation        ****78768787586*79*******9******7*********8*****8*

              151   •••••••••o••••••••••o••••••••••o••••••••••o••••••••••o   200
F_CAT               NLRFALKQEGHSRRDMFDILTRYAFPLAHSLPIFAFLNEEKFNVDGWTVY
H_SAP               NLRFALKQEGHSRRDMFEILTRYAFPLAHSLPLFAFLNEEKFNVDGWTVY
M_MUS               NLRFALKQEGHSRRDMFEILVKHAFPLAHNLPLFAFVNEEKFNVDGWTVY
D_RER               NLRFALKQEGHSRRDIFEIIFKYAFPLSHGMQLFAFLSQEKYEENGWNVY

Conservation        ***************7*8*8477****8*5868***878**8767**7**

              201   •••••••••o••••••••••o••••••••••o••••••••••o••••••••••o   250
F_CAT               NPVEEYRRQGLPNHHWRITFINKCYELCDTYPALLVVPYRASDDDLRRVA
H_SAP               NPVEEYRRQGLPNHHWRITFINKCYELCDTYPALLVVPYRASDDDLRRVA
M_MUS               NPVEEYRRQGLPNHHWRISFINKCYELCETYPALLVVPYRTSDDDLRRIA
D_RER               EALEEYRRQGLPNNEWRVTFINKNYELCDTYPTILVVPYKATEDDLRKVA

Conservation        768**********76**97****5****8***78*****8778****89*


              251   •••••••••o••••••••••o••••••••••o••••••••••o••••••••••o   300
F_CAT               TFRSRNRIPVLSWIHPENKTVIVRCSQPLVGMSGKRNKDDEKYLDVIRET
H_SAP               TFRSRNRIPVLSWIHPENKTVIVRCSQPLVGMSGKRNKDDEKYLDVIRET
M_MUS               TFRSRNRLPVLSWIHPENKMVIMRCSQPLVGMSGKRNKDDEKYLDVIRET
D_RER               TFRSRCRIPVMSWFHKENHAVITRCSQPLVGMSGKRNKDDERYLDLIREA

Conservation        *****5*8**8**7*6**64**5*****************8***8***7

              301   •••••••••o••••••••••o••••••••••o••••••••••o••••••••••o   350
F_CAT               NRQISKLTIYDARPNVNAVANKATGGGYESDDAYHNAELFFLDIHNIHVM
H_SAP               NKQISKLTIYDARPSVNAVANKATGGGYESDDAYHNAELFFLDIHNIHVM
M_MUS               NKQTSKLMIYDARPSVNAVANKATGGGYESDDAYQNSELSFLDIHNIHVM
D_RER               N-GTTKLTIYDARPNVNAVANKATGGGYEGDDAYQNAELVFLDIHNIHVM

Conservation        *3657**6******7**************7****5*8**3**********
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             351  ·********o********o********o********o********o   400
F_CAT             RESLKKVKDIVYPNVEESHWLSSLESTHWLEHIKLVLTGAIQVADKVSSG
H_SAP             RESLKKVKDIVYPNVEESHWLSSLESTHWLEHIKLVLTGAIQVADKVSSG
M_MUS             RESLKKVKDIVYPNIEESHWLSSLESTHWLEHIKLVLTGAIQVADQVSSG
D_RER             RESLKKLKDIVYPNVEESHWLSSLESTHWLEHIKLVLSGAIQVADKVSSG

Conservation      ******8*******9*********************7*******7****

             401  ·********o********o********o********o********o   450
F_CAT             KSSVLVHCSDGWDRTAQLTSLAMLMLDSFYRSIEGFEILVQKEWISFGHK
H_SAP             KSSVLVHCSDGWDRTAQLTSLAMLMLDSFYRSIEGFEILVQKEWISFGHK
M_MUS             KSSVLVHCSDGWDRTAQLTSLAMLMLDSFYRTIEGFEILVQKEWISFGHK
D_RER             -SSVMVHCSDGWDRTAQLTSLSMLMLDSYYRTLRGFQVLMEKEWISFGHK

Conservation      5***8****************8******8**787**89*78*********

             451  ·********o********o********o********o********o   500
F_CAT             FASRIGHGDKNHADADRSPIFLQFIDCVWQMSKQFPTAFEFNERFLITIL
H_SAP             FASRIGHGDKNHTDADRSPIFLQFIDCVWQMSKQFPTAFEFNEQFLIIIL
M_MUS             FASRIGHGDKNHADADRSPIFLQFIDCVWQMSKQFPTAFEFNEGFLITVL
D_RER             FASRIGHGDKNHADQDRSPIFLQFIDCVWQMTKQFPTAFEFNERLLVVIL

Conservation      ************7*6****************7***********47*959*

             501  ·********o********o********o********o********o   550
F_CAT             DHLYSCRFGTFLYNCESARERQKVTERTVSLWSLINSNKDKFKNPFYTKE
H_SAP             DHLYSCRFGTFLFNCESARERQKVTERTVSLWSLINSNKEKFKNPFYTKE
M_MUS             DHLYSCRFGTFLFNCDSARERQKLTERTVSLWSLINSNKDKFKNPFYTKE
D_RER             DHLYSCRFGTFLYNCESVRDSNNVRTKTVSLWSYINSDTSLYINPFYTPE

Conservation      ************7**8*7*86778668******6***766685*****6*

             551  ·********o********o********o********o********o   600
F_CAT             INRVLYPVASMRHLELWVNYYIRWNPRIKQQQPNPVEQRYVELLALRDEY
H_SAP             INRVLYPVASMRHLELWVNYYIRWNPRIKQQQPNPVEQRYMELLALRDEY
M_MUS             INRVLYPVASMRHLELWVNYYIRWNPRVKQQQPNPVEQRYMELLALRDDY
D_RER             SSRVLYPVASMRHLELWVTYYIRWNPRIQHQQQSPVEQRYKELLALRDQY

Conservation      67****************7********976**67******5*******6*


             601  ·********o********o********o********o•   641
F_CAT             IQRLEELQLAGSA----KLAEPST-SPAGPSPMMPHVHTHF
H_SAP             IKRLEELQLANSA----KLSDPPT-SPSSPSQMMPHVQTHF
M_MUS             IKRLEELQLANSA----KLADAPA-STSSSSQMVPHVQTHF
D_RER             LKKLEELQLSDSAPSSTHLTNSSTPNAATPNQHITHLQTPF

Conservation      878******85**00006*6645707475676576*86*5*
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Supplementary Figure 2. Protein alignment of *MTM1* for diverse species. Domestic cat (FCAT, ENSFCAT00000024072.4, Refseq XM_023249466.1), human (HSA, ENST00000370396.7, Refseq NM_000252.3), mouse (MMU, ENMUST00000051970.12, Refseq NM_001164191.1), and zebrafish (DR, ENSDART00000149835.3, Refseq NM_001037684.2). Protein alignment produced using PRALINE[14]. The highlighted alanine at position 152 is conserved across diverse species indicating function importance and a high conservation score. The c.455C>T alteration causes a p.ala152val amino acid change.