

F_CAT	1	GGGGCGGGCCCTGGAGGGGGCGGAGCGGGGCCCGGGAGCGAAGCAGCCTGGCAACGGCGG	60
H_SAP	1	AGC-----CGA-GCAGCCTGGCAACGGCGG	24
F_CAT	61	TGGCGCCCGGAGCCCGAGAGTTTCCAGAATGGCTTCTGCACCAACTTCTAAATATAATTC	120
H_SAP	25	TGGCGCCCGGAGCCCGAGAGTTTCCAGGATGGCTTCTGCATCAACTTCTAAATATAATTC	84
F_CAT	121	ACACTCCTTGAGAAATGAATCTGTTAAGAGGACTTCTAGGGATGGAGTTAATCGAGACCT	180
H_SAP	85	ACACTCCTTGAGAAATGAGTCTATTAAGAGGACGTCTCGAGATGGAGTCAATCGAGATCT	144
F_CAT	181	CAGTGAGACTGTTTCTCGACTTCCAGGAGAACTCGCATCACTGACAAAGAAGTTATTTA	240
H_SAP	145	CACTGAGGCTGTTTCTCGACTTCCAGGAGAACTAATCACTGACAAAGAAGTTATTTA	204
F_CAT	241	CATATGTCCTTTCAATGGCCCATTAAGGGAAGAGTTTACATCACAAATTATCGTCTTTA	300
H_SAP	205	CATATGTCCTTTCAATGGCCCATTAAGGGAAGAGTTTACATCACAAATTATCGTCTTTA	264
F_CAT	301	TTTAAGAAGTTTGAAACGGATTCTGCTCTAATACTTGATGTTTCTCTGGGTGTGATCTC	360
H_SAP	265	TTTAAGAAGTTTGAAACGGATTCTTCTCTAATACTTGATGTTTCTCTGGGTGTGATCTC	324
F_CAT	361	CAGAATTGAAAAAATGGGAGGCGCGACAAGTAGAGGAGAAAATTCCTATGGTCTAGATAT	420
H_SAP	325	GAGAATTGAAAAAATGGGAGGCGCGACAAGTAGAGGAGAAAATTCCTATGGTCTAGATAT	384
F_CAT	421	TACTTGTAAGACATGAGGAACCTGAGGTTTTCGCTGAAACAGGAAGGCCACAGCAGAAG	480
H_SAP	385	TACTTGTAAGACATGAGGAACCTGAGGTTTCGCTTGTAAACAGGAAGGCCACAGCAGAAG	444

F_CAT	481	GGATATGTTTGACATTCTCACGAGATACGCCTTTCCCCTGGCACACAGTCTGCCAATATT	540
H_SAP	445	AGATATGTTTGAGATCCTCACGAGATACGCGTTTCCCCTGGCTCACAGTCTGCCATTATT	504
F_CAT	541	TGCATTTCTAAATGAAGAAAAGTTTAACTGGATGGATGGACAGTTTATAACCCAGTAGA	600
H_SAP	505	TGCATTTCTAAATGAAGAAAAGTTTAACTGGATGGATGGACAGTTTACAATCCAGTGGA	564
F_CAT	601	AGAATACAGAAGGCAGGGCTTGCCTAACCACCACTGGAGAATCACTTTTATCAATAAGTG	660
H_SAP	565	AGAATACAGGAGGCAGGGCTTGCCTAACCACCACTGGAGAATAACTTTTATTAATAAGTG	624
F_CAT	661	CTATGAACGTGTGACACCTACCCTGCTCTCTTGGTGGTTCATATCGTGCCTCAGATGA	720
H_SAP	625	CTATGAGCTCTGTGACACTTACCCTGCTCTTTTGGTGGTTCCTATCGTGCCTCAGATGA	684
F_CAT	721	TGATCTCAGGAGAGTCGCAACTTTTAGATCCAGAAACCGAATTCCAGTGCTGTCATGGAT	780
H_SAP	685	TGACCTCCGGAGAGTTGCAACTTTTAGGTCCCGAAATCGAATTCCAGTGCTGTCATGGAT	744
F_CAT	781	TCATCCAGAAAACAAGACCGTCATCGTGCCTTGCAGTCAGCCTCTTGTCGGTATGAGTGG	840
H_SAP	745	TCATCCAGAAAATAAGACGGTCATTGTGCGTTGCAGTCAGCCTCTTGTCGGTATGAGTGG	804
F_CAT	841	TAAACGGAATAAGGATGATGAGAAGTATCTCGATGTTATCAGGGAGACTAATAGACAAAT	900
H_SAP	805	GAAACGAAATAAAGATGATGAGAAATATCTCGATGTTATCAGGGAGACTAATAAACAAAT	864
F_CAT	901	TTCTAAACTCACAATCTATGATGCAAGACCCAATGTAAATGCAGTGGCGAACCAAGGCAAC	960
H_SAP	865	TTCTAAACTCACCATTTATGATGCAAGACCCAGCGTAAATGCAGTGGCCAACCAAGGCAAC	924

F_CAT	961	AGGAGGAGGATATGAAAGTGATGATGCATATCACAAACGCCGAACCTTTTCTTCTTAGACAT	1020
H_SAP	925	AGGAGGAGGATATGAAAGTGATGATGCATATCATAACGCCGAACCTTTTCTTCTTAGACAT	984
F_CAT	1021	TCATAACATTCATGTTATGAGGGAATCTTTAAAAAAGTCAAAGACATTGTTTATCCTAA	1080
H_SAP	985	TCATAATATTCATGTTATGCGGGAATCTTTAAAAAAGTGAAGGACATTGTTTATCCTAA	1044
F_CAT	1081	TGTGGAAGAATCTCACTGGTTGTCCAGTTTGGAGTCTACTCACTGGTTAGAACACATCAA	1140
H_SAP	1045	TGTAGAAGAATCTCATTGGTTGTCCAGTTTGGAGTCTACTCATTGGTTAGAACATATCAA	1104
F_CAT	1141	GCTTGTGTTTGACGGGAGCCATTCAGTAGCAGACAAAGTTTCTTCAGGGAAGAGCTCAGT	1200
H_SAP	1105	GCTCGTTTTGACAGGAGCCATTCAGTAGCAGACAAAGTTTCTTCAGGGAAGAGTTCAGT	1164
F_CAT	1201	GCTTGTGCACTGCAGTGATGGATGGGACAGAAGTCCCGCTGACGTCCCTGGCCATGCT	1260
H_SAP	1165	GCTTGTGCATTGCAGTGACGGATGGGACAGGACTGCTCAGCTGACATCCTTGCCATGCT	1224
F_CAT	1261	GATGTTGGACAGCTTCTACCGGAGCATCGAAGGGTTTGAAATACTGGTACAGAAAGAATG	1320
H_SAP	1225	GATGTTGGATAGCTTCTATAGGAGCATTGAAGGGTTCGAAATACTGGTACAAAAAGAATG	1284
F_CAT	1321	GATAAGTTTTGGACATAAATTTGCATCTAGAATAGGTCATGGTGACAAAAACCATGCCGA	1380
H_SAP	1285	GATAAGTTTTGGACATAAATTTGCATCTCGAATAGGTCATGGTGATAAAAACCACACCGA	1344
F_CAT	1381	TGCTGACCGATCTCCTATTTTCTCCAGTTTATTGATTGTGTATGGCAAATGTCAAACA	1440
H_SAP	1345	TGCTGACCGTTCTCCTATTTTCTCCAGTTTATTGATTGTGTGTGGCAAATGTCAAACA	1404

F_CAT	1441	GTTCCCTACAGCTTTTGAATTCAATGAACGGTTTTTTGATTACAATTTTGGATCATCTGTA	1500
H_SAP	1405	GTTCCCTACAGCTTTTGAATTCAATGAACAATTTTTGATTATAATTTTGGATCATCTGTA	1464
F_CAT	1501	TAGTTGCCGGTTTGGTACTTTCTTATACAACGTGAATCTGCTCGAGAAAGACAGAAAGT	1560
H_SAP	1465	TAGTTGCCGATTTGGTACTTTCTTATTCAACTGTGAATCTGCTCGAGAAAGACAGAAGGT	1524
F_CAT	1561	TACAGAAAGAACAGTATCTTTGTGGTCACTGATAAACAGTAATAAAGACAAATTCAAAAA	1620
H_SAP	1525	TACAGAAAGGACTGTTTCTTTATGGTCACTGATAAACAGTAATAAAGAAAAATTCAAAAA	1584
F_CAT	1621	CCCCTTCTATACTAAAGAAATCAATCGAGTTTATATCCAGTTGCCAGTATGCGTCACTT	1680
H_SAP	1585	CCCCTTCTATACTAAAGAAATCAATCGAGTTTATATCCAGTTGCCAGTATGCGTCACTT	1644
F_CAT	1681	GGAACCTTTGGGTGAATTACTACATTAGATGGAACCCAGATCAAGCAACAACAGCCCAA	1740
H_SAP	1645	GGAACCTCTGGGTGAATTACTACATTAGATGGAACCCAGGATCAAGCAACAACAGCCGAA	1704
F_CAT	1741	CCCGGTGGAACAGCGCTACGTGGAGCTCCTGGCCTTGCGTGACGAGTACATCCAGCGGCT	1800
H_SAP	1705	TCCAGTGGAGCAGCGTTACATGGAGCTCTTAGCCTTACGCGACGAATACATAAAGCGGCT	1764
F_CAT	1801	CGAGGAGTTGCAGCTCGCCGGCTCCGCCAAGCTCGCCGAGCCCTCCACCTCGCCGGCCGG	1860
H_SAP	1765	TGAGGAAGTGCAGCTCGCCAACTCTGCCAAGCTTTCTGATCCCCCAACTTCACCTTCCAG	1824
F_CAT	1861	CCCTTCGCCGATGATGCCCCATGTGCACACCCACTTCTGAGACGGGACCTGGGCGCCGCG	1920
H_SAP	1825	TCCTTCGCAAATGATGCCCCATGTGCAAACCTCACTTCTGAGGGGGACCTGGCACC GCA	1884

F_CAT	1921	GCGCAGCTCTGGGCAGAGGACGTCGTGGCCTTTCATCAGGGGCCTCTGTACAAAAGTAGAT	1980
H_SAP	1885	TTAGAGCTCGAAATAAAGGCGATAGCTGACTTTCATTTGGGGCATTGTAAAAAGTAGAT	1944
F_CAT	1981	TGAAATACTTGCCTCCATGTAGAACTGGAACCTAACACGATCTTAAACTCTTAAATATGTG	2040
H_SAP	1945	TAAAATATTTGCCTCCATGTAGAACTTGAACCTAACATAATCTTAAACTCTTGAATATGTG	2004
F_CAT	2041	CCTTCTAGAATACATATTACAAGAAAACCTAGCATCTACACGGCAATCAGAAGAAAGGA	2100
H_SAP	2005	CCTTCTAGAATACATATTACAAGAAAACCTACAGGGTCCACACGGCAATCAGAAGAAAGGA	2064
F_CAT	2101	GCCAAGATGAGGTTTTGGAAAATGCTAACACCTTTCAGAGCAGGTTTTGAGAGA-----	2155
H_SAP	2065	GCTGAGATGAGGTTTTGGAAAACCTGACACCTTAAAAAGCAGTTTTTGAAGACAAAA	2124
F_CAT	2156	-TTAAATTTAATTTACCTCTTTTGAATACTATGTATACAATATCTATTTGTGGGCTTA	2214
H_SAP	2125	TTTAGATTTAATTTACGTCTTGAGAAATACTATATATACAATATATATTTGTGGGCTTA	2184
F_CAT	2215	ATTGGAACGACGTGATTTTAAACT-AAAGTGAAAACCTGTGTTTGTGAAACGAATTTGCC	2273
H_SAP	2185	ATTGAAACAACATTATTTTAAAATCAAAGGGGATA--TATGTTTGTGGAATGGATTTTCC	2242
F_CAT	2274	TTAGGTTGCTCACGACAGTTGCTTTGGATTACCTAAAATGAATCCAAATGTGAAAGATG-	2332
H_SAP	2243	TGAAGCTGCTTA--ACAGTTGCTTTGGATTCTCTAAGATGAATCCAAATGTGAAAGATGC	2300
F_CAT	2333	---TTATTGCCAAAACCAAATGAGCTGTTCTTCTGAGGCATCATCCAAAAGCAAGGTGT	2389
H_SAP	2301	ATGTTACTGCCAAAACCAAATGAGCTCAGCTTCTTAGGCATTACCCAAAAGCAAGGTGT	2360

F_CAT	2390	TTAAATAATTGCCAAATTTTATACCATCGTCAAGTGGTACTTAAAGAGAAATAGCTGTG	2449
H_SAP	2361	TTAAGTAATTGCCAGCTTTTATACCATCATGA-GTGGTACTTAAGGAGAAATAGCTGTA	2419
F_CAT	2450	TAGATGAGTTTTTCATTAGTTTGAATTTTAGAATATGAAGTGTTCCTAATTTTCA	2509
H_SAP	2420	TAGATGAGTTTTTCATTATTTGAAATTTAGGGGTAGAAAATGTTTTCCCTAATTTTCC	2479
F_CAT	2510	AGAGGAGCGTATTTTTATATT-----ACACAGATGGGGCCAGTCAAATAGGATTTGAT	2563
H_SAP	2480	AGAGAAGCCTATTTTTATATTTTTAAAAAACTGACAGGGCCAGTTAAATATGATTTGCA	2539
F_CAT	2564	TTTTTTTTTAACGTTTTTGCCGTTCTATTTCTGAGTCTTCTATGAGCTTGCCATAAAT	2623
H_SAP	2540	TTTTTTA--AA---TTTGCCAGTTTTATTTCTAAATTCCTTCATGAGCTTGCCATAAAT	2594
F_CAT	2624	TCTGACCCACTTTCAGTTATGGAAAACCCCTCATATAGCACTGTTTGAGGATGGTGGG	2683
H_SAP	2595	TCGGAATGGTTTTTCGGGTTGTGGCAAACCCCAAAGAGAGCACTGTCCAAGGATGTCGGGA	2654
F_CAT	2684	GCGTTATGCTGCTGAGGTGACTGTTTTCGCAAACATCGCTCTAGTCAGACCAGCTTATCT	2743
H_SAP	2655	GCATCCTGCTGCTTAGGGGAATGTTTTCGCAAATGTTGCTCTAGTCAGTCCAGCTCATCT	2714
F_CAT	2744	GCCAAAGTGTAGGGTCGACCATCTCGGACGTATGAGCTGTTGCTAGAGCATCATTCTTTG	2803
H_SAP	2715	GCCAAAATGTAGGG-CTACCGTCTTGGATGCATGAGCTATTGCTAGAGCATCATCCTTAG	2773
F_CAT	2804	AAATAAAAGCTGCAGATGTACATTTGTTGAGCGTATT	2840
H_SAP	2774	AAATCAGTGCCCCAGATGTACATGTGTTGAGCGTATTCTTGAAAGTATTGTGTTTATGCA	2833

H_SAP 2834 TTTCAATTTCAATGGTGTGGCTTCCCCTCCCCACCCACGCGTGCATAAAAACTGGTTC 2893
H_SAP 2894 TACAAATTTTACTTGAAGTACCAGGCCGTTTGCTTTTTTCAGGTTGTTTTGTTTTATAGT 2953
H_SAP 2954 ATTAAGTGAAATTTTAAATGCACAGTTCATTTGCTATCTGAACTAATTCATTTATTAAG 3013
H_SAP 3014 TATATTTGTAAAAGCTAAGGCTCGAGTTAAAACAATGAAGTGTTCACATGATTTGTAA 3073
H_SAP 3074 AGGACTATTTATAACTAATATGGTTTTGTTTTCAATGAATTAAGAAAGATTAAATATATC 3133
H_SAP 3134 TTTGTAAATTATTTTATGTCATAGTTTAAATTGGTCTACCAAGTAAGACATCTCAAATACA 3193
H_SAP 3194 GTAGTATAATGTATGAATTTTGTAAAGTATAAGAAATTTTATTAGACATTCTCTTACTTTT 3253
H_SAP 3254 TGTAATGCTGTAAATATTTTCATAAATTAACAAAGTGTCACTCCATAAAAAAGAAAGCTAA 3313
H_SAP 3314 TACTAATAGCCTAAAAGATTTTGTGAAATTCATGAAAACTTTTTAATGGCAATAATGAC 3373
H_SAP 3374 TAAAGACCTGCTGTAATAAATGTATTAACCTGAAACCTAA 3412

Supplementary Figure 1. Coding sequencing alignment of *MTM1*. Alignment of domestic cat cDNA (Query: ENSFCAT00000024072.4, Refseq XM_023249466.1) and Homo sapiens cDNA (Subject: ENST00000370396.7, Refseq NM_000252.3) using the Needleman-Wunsch tool. Position of the cat *MTM1* cytosine to thymidine change highlighted.