Supplementary Figure S1: Alignment of the synthetic stabilized mouse *Atp7a* cDNA sequence (Synth_mAtp7a) with the native *Atp7a* cDNA sequence (mAtp7a). Only the altered bases in the synthetic sequence are shown. Alignments were generated using MUltiple Sequence Comparison by Log Expectation software (http://www.ebi.ac.uk/Tools/msa/muscle/) with output using Boxshade software (http://embnet.vital-it.ch/software/BOX_form.html).

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mATP7A          1 ATGGAGCCAAGTGTGGATGCAAATTCAATTACTATCACTGTTGAGGGAATGACATGTATT
Synth_mAtp7a    1 .....A..TTCA..C..C..T..CAGC..C..C.....C..C..A..G.....C..C..C

mATP7A         61 TCCTGTGTCCGGACCATTGAACAGCAGATTGGGAAAGTGAATGGTGTCCATCACATTAAA
Synth_mAtp7a   61 AGT..C...A.A.....C..G..A.....C..A..G..C..C..G..T..C.....C..G

mATP7A        121 GTTTCACTAGAAGAAAAGAGTGCAACCATTATTTATGACCCTAAACTTCAGACTCCAAAG
Synth_mAtp7a  121 ..CAGTT.G..G..G..A..C..T..G..C..C..C..T..C..GT.A..A..C..G...

mATP7A        181 ACCCTCCAAGAAGCTATCGATGACATGGGCTTTGATGCTCTTCTCCACAATGCTAACCCC
Synth_mAtp7a  181 ..TT.A..G..G..C..T..C........A..C..C..C..A..G.....C..C..T..T

mATP7A        241 CTCCCTGTCTTAACCAATACCGTGTTCCTGACTGTTACTGCTCCACTGACTCTGCCTTGG
Synth_mAtp7a  241 ..A..C..TC.C..T..C..T..C........C..C..C.....TT....CT....A...

mATP7A        301 GACCATATCCAAAGTACATTGCTCAAGACCAAGGGTGTGACTGGTGTTAAGATTTCCCCT
Synth_mAtp7a  301 ..T..C.....G..C..GC..T.G.....G..A..C..C..C..C..C.....CAGT..A

mATP7A        361 CAGCAAAGAAGTGCAGTAGTCACCATAATTCCATCTGTGGTGAGTGCCAGTCAGATTGTG
Synth_mAtp7a  361 ..A..GC.TTC...T..C..G..G..C..C..TAG...T..CTC...TTC......C..T

mATP7A        421 GAGCTGGTCCCAGACCTCAGTTTAGACATGGGAACTCAGGAGAAAAAGTCAGGAGCTTGT
Synth_mAtp7a  421 ...T....T..T.....GTC.C.T........C..A..A.....G..AAGT..C..C..C

mATP7A        481 GAAGAGCACAGCACGCCTCAGGCAGGGGAAGTCATGCTGAAGATGAAAGTGGAAGGGATG
Synth_mAtp7a  481 ..G..A........A..A..A..T..C..G........C........G..T..G..C...

mATP7A        541 ACCTGCCATTCATGTACTAGCACCATTGAAGGAAAAGTTGGAAAGCTGCAAGGTGTTCAG
Synth_mAtp7a  541 ..T..T..CAGT..C..CTCT.....C..G..C..G..C..G..A.....G.....C..A

mATP7A        601 CGCATTAAAGTGTCCCTAGACAACCAAGAAGCTACTATTGTTTTTCAACCTCATCTCATC
Synth_mAtp7a  601 .....C..G..CAGT..T.....T..G..G..A..C..C..C..C..G.....C..G...

mATP7A        661 ACAGCAGAGGAAATAAAGAAGCAGATTGAAGCCGTGGGTTTCCCAGCCTTCATAAAAAAG
Synth_mAtp7a  661 ..T..T..A..G..C.....A.....C..G..T..T..C..T..T..T.....C..G...

mATP7A        721 CAGCCGAAGTACCTCAAATTGGGAGCCATTGATGTTGAGCGCCTGAAGAACACACCGGTC
Synth_mAtp7a  721 ..A..C......T.G..GC.A........C..C..C..AA.A...........T..T...

mATP7A        781 AAATCTTCAGAAGGATCTCAGCAAAAGAGCCCATCATATCCCAGTGACTCCACAACCATG
Synth_mAtp7a  781 ..GAG.AGT..G..TAG...A..G...TCT..TAGC..C..TTCC..TAG...T......
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mATP7A          841 TTCACCATAGAGGGCATGCATTGTAAATCGTGTGTGTCCAATATTGAAAGTGCTTTATCT
Synth_mAtp7a  841 ........C..A..G.....C..C..GAGT..C..CAG...C..C..GTC...C..GAG.

mATP7A          901 ACACTCCAGTATGTAAGCAGTATAGTAGTTTCTTTAGAGAATAGGTCAGCCATTGTAAAG
Synth_mAtp7a  901 ..TT.G.....C..TTCT..C..C..T..CAG.C.T.....CC.TAGT.....C..G...

mATP7A          961 TACAATGCAAGCTTAGTCACTCCAGAAATGCTGAGAAAGGCAATAGAGGCCATTTCACCG
Synth_mAtp7a  961 .....C..TTCTC.G.....C..T..G...T.AC.G..A..C..C..A..G..CAGT..T

mATP7A         1021 GGGCAATACAGAGTTAGTATTGCAAGTGAAGTTGAAAGTACCG---CCAGCTCTCCCTCC
Synth_mAtp7a 1021 ..C..G...C.T..CTCC..C..TTC...G..C..GTC...T.CTT.T..TC..AG....

mATP7A         1078 AGCTCATCTCTTCAGAAGATGCCTTTGAACATAGTTAGCCAGCCTCTGACCCAAGAAGCT
Synth_mAtp7a 1081 ..--..G..-.A..A........C........C..CTCT..A..CT.A..T..G..G..C

mATP7A         1138 GTGATAAACATAAATGGCATGACTTGTAATTCTTGTGTGCAGTCTATAGAGGGTGTAATA
Synth_mAtp7a 1138 ..C........C..C..G.....C..C..CAG...C..C..A..C..C..A..C..C..C

mATP7A         1198 TCAAAAAAGCCAGGTGTAAAATCCATCCACGTGTCCCTCGCAAACAGCACAGGGACTATT
Synth_mAtp7a 1198 AGT..G..A..T..C..G..GAG......T..CAGTT.G..G...TCT..T..C..C..C

mATP7A         1258 GAATTTGATCCTCTACTAACCTCTCCAGAAACCTTGCGAGAAGCAATTGAAGACATGGGA
Synth_mAtp7a 1258 ..G..C..C..A..G..G...AG...T..G..TC.AA.......T..C..G..T.....C

mATP7A         1318 TTTGATGCTGCCTTGCCAGCAGACATGAAAGAGCCACTGGTAGTGATAGCTCAGCCCTCA
Synth_mAtp7a 1318 ..C..C..C..TC.T..T..T........G..A..CT....T..C..C..A..A..TAGC

mATP7A         1378 CTGGAAACACCTCTTTTGCCCTCAAGT---AATGAGCTAGAAAATGTGATGACGTCAGTT
Synth_mAtp7a 1378 T....G.---...CC....TAC.T...TCC..C...T....G..C..C.....TAGT..C

mATP7A         1435 CAGAACAAGTGTTACATACAGGTCTCTGGGATGACCTGTGCTTCTTGTGTAGCAAACATT
Synth_mAtp7a 1435 ..A........C.....C..A..TAG...C.....T..C..CAG...C..T..G.....C

mATP7A         1495 GAACGCAATTTAAGACGAGAAGAAGGAATATATTCTGTACTTGTTGCCCTAATGGCTGGC
Synth_mAtp7a 1495 ..GA.A..CC..C.TA....G..G..C..C..CAG...TT.A..C..T..C.....C..A

mATP7A         1555 AAGGCAGAAGTAAGATATAACCCAGCTGTTATCCAACCCCGAGTGATAGCAGAGTTTATT
Synth_mAtp7a 1555 .....T..G..TC.C..C.....T..C..C.....G..TA....C..C..T.....C..C

mATP7A         1615 CGAGAGCTTGGATTTGGAGCTATGGTGATGGAAAACGCTGGGGAAGGCAACGGCATCTTG
Synth_mAtp7a 1615 A.......G..C..C.....C.....C.....G..T..C..C..G..A..T..A..TC.T

mATP7A         1675 GAACTTGTTGTGAGAGGAATGACGTGTGCTTCCTGTGTCCATAAAATTGAATCAACACTC
Synth_mAtp7a 1675 ..GT.A..C..CC.T..C.....T..C..CAGT..C..G..C..G..C..GAGC..CT.G

mATP7A         1735 ACAAAACACAAAGGGATCTTCTACTGCTCTGTGGCCCTGGCAACTAACAAAGCACATATT
Synth_mAtp7a 1735 ..C..G.....G..A............AGC..T..AT....C..C..T..G..C..C..C

mATP7A         1795 AAATATGATCCAGAAATTATTGGTCCCAGAGATATTATCCATACCATCGGAAGCTTAGGC
Synth_mAtp7a 1795 ..G..C..C..T..G..C..C..A..TC.T..C..C.....C........GTCA..G..T

mATP7A         1855 TTTGAAGCTTCTTTGGTCAAGAAAGATCGATCAGCCAACCACTTAGATCATAAACGAGAA
Synth_mAtp7a 1855 ..C..G..CAGC..A........G..CA..AGC..G.....TC....C..C..GA....G
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mATP7A       1915 ATAAAACAATGGAGAGGGTCTTTCCTTGTGAGCCTGTTTTTCTGTATCCCTGTAATGGGA
Synth_mAtp7a 1915 ..C..G..G...C.C..AAGC..TT.G..TTCAT....C..T..C.....A..G.....G

mATP7A       1975 CTGATGGTCTATATGATGGTTATGGATCACCACCTTGCAACTCTTCACCATAATCAGAAC
Synth_mAtp7a 1975 T.......G..C........A.....C..T..TT.G..G..CT.G..T..C..C..A..T

mATP7A       2035 ATGAGTAATGAAGAAATGATCAACATGCATTCTGCTATGTTTCTGGAGCGTCAGATCCTG
Synth_mAtp7a 2035 ...TCA..C..G..G.....T..T.....CAG...A.....CT....AA.A..A..AT..

mATP7A       2095 CCAGGACTGTCCATTATGAATTTGTTGTCCCTTTTATTGTGTCTACCTGTACAGTTTTGT
Synth_mAtp7a 2095 ..T..GT..AGT..C.....CC.AC.AAGTT.GC.TC.T..CT.G..A..C..A..C...

mATP7A       2155 GGCGGCTGGTACTTCTACATTCAGGCTTACAAAGCACTGAAGCATAAGACAGCAAACATG
Synth_mAtp7a 2155 ..G..G.....T..T..T..C..A..A..T..G..TT....A..C..A..C..G..T...

mATP7A       2215 GATGTGCTGATTGTGCTGGCAACCACCATCGCATTTGCCTACTCTCTGGTTATTCTTCTG
Synth_mAtp7a 2215 ..C..AT....C..CT....T..T..T..T..T..C..T..TAG.T....C..CT.GT..

mATP7A       2275 GTTGCAATGTTTGAGAGAGCCAAAGTGAACCCCATTACCTTCTTTGATACACCTCCTATG
Synth_mAtp7a 2275 ..A..T.....C..AC....A..G..C..T..T..C..A..T..C..C..T..C..C...

mATP7A       2335 CTGTTTGTGTTTATTGCACTAGGACGATGGCTGGAACATATAGCGAAGGGCAAAACCTCC
Synth_mAtp7a 2335 T.A..C..A..C..C..CT....GA.....T....G..C..C..T..A..G..G..TAGT

mATP7A       2395 GAGGCTCTTGCAAAGCTAATTTCATTACAAGCAACTGAAGCCACTATTGTAACTCTGAAC
Synth_mAtp7a 2395 ..A..CT.G..T..AT.G..CAGTC....G..T..C..G..T..C..C..T..CT....T

mATP7A       2455 TCTGAAAATCTCCTCCTGAGTGAAGAACAAGTGGATGTGGAACTTGTACAACGTGGAGAT
Synth_mAtp7a 2455 AG...G..CT.GT.GT..TCA..G..G..G..T..C..T..GT.G..T..GA.A..G..C

mATP7A       2515 ATCATTAAGGTTGTTCCAGGAGGCAAATTTCCAGTGGATGGCCGTGTTATTGAAGGACAT
Synth_mAtp7a 2515 ..T..C..A..C..C..T..G..G..G..C..T..T..C..GA.A..A..C..G..G..C

mATP7A       2575 TCTATGGTGGACGAGTCCCTCATCACAGGGGAGGCAATGCCTGTGGCTAAGAAACCTGGC
Synth_mAtp7a 2575 AG......T..T..AAGTT.G..T..T..A..A..T.....C..T..C..A..G..C..G

mATP7A       2635 AGCACGGTGATTGCAGGTTCCATTAACCAGAATGGATCTCTCCTCATCCGAGCAACACAT
Synth_mAtp7a 2635 TCA..C..T..C..T..GAGT..C..T..A..C..GAG.T.GT.G..TA....T..T..C

mATP7A       2695 GTGGGAGCAGATACAACCCTTTCTCAGATCGTCAAACTTGTGGAGGAGGCACAGACATCA
Synth_mAtp7a 2695 ..T..G..T..C..C..AT.GAG...A..T..T..GT.G..T..A..A..T..A..CAGT

mATP7A       2755 AAGGCTCCTATCCAGCAGTTTGCAGACAAACTCAGTGGCTACTTTGTTCCTTTCATCGTC
Synth_mAtp7a 2755 ..A..C..C..T..A..A..C..T..T..GT.GTCA..G..T..C..C..C..T..T..T

mATP7A       2815 TTGGTTTCCATTGTTACCCTCTTGGTGTGGATTATAATTGGATTTCAAAATTTTGAAATT
Synth_mAtp7a 2815 C.A..CAGT..C..C..TT.GC.C..T.....C..T..A..G..C..G..C..C..G..C

mATP7A       2875 GTGGAAACCTACTTTCCCGGCTATAATAGAAGCATCTCCCGAACAGAAACCATAATACGC
Synth_mAtp7a 2875 ..T..G......................................................

mATP7A       2935 TTTGCTTTCCAAGCCTCTATCACGGTTCTGTGTATCGCATGTCCCTGTTCACTGGGACTA
Synth_mAtp7a 2935 ............................................................
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mATP7A        2995 GCCACTCCAACTGCTGTGATGGTGGGCACAGGAGTAGGTGCTCAGAATGGCATACTTATC
Synth_mAtp7a 2995 ............................................................

mATP7A        3055 AAAGGTGGGGAGCCACTGGAAATGGCTCATAAGGTAAAGGTAGTGGTATTTGATAAGACT
Synth_mAtp7a 3055 .................C..G.......................................

mATP7A        3115 GGAACCATCACCCATGGAACCCCAGTAGTGAATCAAGTGAAGGTTCTCGTGGAAAGTAAC
Synth_mAtp7a 3115 ............................................................

mATP7A        3175 AAGATATCACGCAATAAGATCCTGGCCATTGTGGGGACTGCAGAAAGTAACAGTGAACAT
Synth_mAtp7a 3175 ............................................................

mATP7A        3235 CCTTTAGGAGCAGCTGTAACCAAATATTGCAAAAAGGAGCTGGACACTGAAACCCTGGGT
Synth_mAtp7a 3235 ............................................................

mATP7A        3295 ACCTGTACAGATTTCCAGGTTGTACCAGGCTGTGGTATTAGCTGTAAAGTCACCAATATT
Synth_mAtp7a 3295 ............................................................

mATP7A        3355 GAAGGTTTGCTACATAAGAGTAACTTGAAGATAGAAGAAAATAACATTAAAAATGCATCC
Synth_mAtp7a 3355 ............................................................

mATP7A        3415 CTGGTTCAAATTGATGCAATTAATGAACAGTCATCAACTTCATCTTCTATGATTATTGAT
Synth_mAtp7a 3415 ............................................................

mATP7A        3475 GCTCATCTCTCAAATGCTGTTAATACTCAGCAGTACAAAGTCCTCATTGGTAACCGGGAA
Synth_mAtp7a 3475 ............................................................

mATP7A        3535 TGGATGATTAGAAATGGTCTTGTCATAAGTAATGATGTAGATGAATCTATGATTGAACAT
Synth_mAtp7a 3535 ............................................................

mATP7A        3595 GAAAGAAGAGGTCGGACTGCTGTCTTGGTGACAATCGATGATGAGCTGTGTGGCTTGATT
Synth_mAtp7a 3595 ............................................................

mATP7A        3655 GCTATTGCTGATACTGTGAAACCTGAGGCCGAGTTGGCTGTACACATTCTGAAATCTATG
Synth_mAtp7a 3655 ............................................................

mATP7A        3715 GGTTTAGAAGTAGTTCTGATGACTGGAGACAACAGTAAAACTGCTCGGTCTATTGCTTCT
Synth_mAtp7a 3715 ............................................................

mATP7A        3775 CAGGTTGGCATTACTAAGGTGTTTGCTGAAGTTCTACCTTCCCACAAAGTTGCTAAGGTG
Synth_mAtp7a 3775 ............................................................

mATP7A        3835 AAGCAGCTCCAAGAGGAGGGCAAACGTGTAGCAATGGTAGGAGATGGAATCAATGACTCC
Synth_mAtp7a 3835 ............................................................

mATP7A        3895 CCAGCTCTGGCAATGGCAAACGTTGGAATTGCCATAGGCACAGGCACAGATGTAGCCATT
Synth_mAtp7a 3895 ............................................................

mATP7A        3955 GAAGCAGCTGATGTGGTTTTGATAAGGAATGACCTTCTGGATGTTGTGGCAAGTATTGAC
Synth_mAtp7a 3955 ............................................................

mATP7A        4015 TTGTCAAGGAAAACAGTCAAGAGGATTCGAATCAATTTTGTCTTTGCTCTAATTTATAAT
Synth_mAtp7a 4015 ............................................................
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mATP7A        4075 CTGGTTGGAATTCCCATCGCTGCTGGAGTTTTCCTGCCCATCGGTTTGGTTTTACAACCC
Synth_mAtp7a 4075 ............................................................

mATP7A        4135 TGGATGGGATCCGCAGCAATGGCCGCTTCATCTGTCTCTGTAGTCCTTTCTTCCCTTTTC
Synth_mAtp7a 4135 ............................................................

mATP7A        4195 CTCAAGCTTTACAGGAAACCTACGTATGACAATTATGAGTTGCATCCCCGGAGCCACACA
Synth_mAtp7a 4195 ............................................................

mATP7A        4255 GGACAGAGGAGTCCTTCAGAAATCAGTGTTCACGTTGGAATAGATGACACCTCAAGAAAT
Synth_mAtp7a 4255 ............................................................

mATP7A        4315 TCTCCAAGGCTGGGTTTGCTGGACCGGATTGTCAACTATAGCAGAGCCTCCATAAATTCA
Synth_mAtp7a 4315 ............................................................

mATP7A        4375 CTGCTGTCTGACAAGCGCTCCCTGAACAGCGTTGTTACTAGTGAACCTGACAAGCACTCG
Synth_mAtp7a 4375 ............................................................

mATP7A        4435 CTTCTGGTGGGCGACTTCCGGGAAGATGATGACACCACACTGTAA
Synth_mAtp7a 4435 .............................................
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