

H.sapMT1 MDCSCATGGSTCTGSCCKECKCTSCKKSCSSCCPMSCAKCAQGCICKGASEKCSCCA
 H.sapMT2 MDCSCAAGDSTCAGSCKCKECKCTSCKKSCSSCCPVGCAKCAQGCICKGASDKCSCCA
 H.sapMT3 MDCPCPSGGSTCADSCKCEGCKCTSCKKSCSSCCPAECEKCAKDCVCKGGEAKCSCCQ
 H.sapMT4 MDCVCMSSGGICMCGDNCKCTTCNCKTCRKSCCPCCPPGCAKCAQGCICKGGSDKCSCCP
 B.tauMT1 MDCSCPTGGSCSCAGSCTCKACRCPSCKKSCSSCCPVGCAKCAQGCVCKGASDKCSCCA
 B.tauMT2 MDCSCTAGESCTCAGSCKCKDKCASCKKSCSSCCPVGCAKCAQGCVCKGASDKCSCCA
 B.tauMT3 MDCPCPTGGSTCSDPCKCEGCTCASSKKSCSSCCPAECEKCAKDCVCKGGEGKCSCCQ
 B.tauMT4 MDCTCMSGGTCACGDNCKCTTCSCKTCRKSCCPCCPPGCAKCAQGCICKGASDKCSCCP
 C.lupMT2 MDCSCAAGGSTCAGSCKCKECKRCTSCKKSCSSCCPVGCAKCAQGCICKGASDKCSCCA
 C.lupMT1 MDCSCSTGGSTCAGSCKCKECKCTSCKKSCSSCCPVGCAKCAQGCICKGASDKCSCCA
 C.lupMT3 MDCPCPTGGSTCDGSCKCEGCKCTSCKKSCSSCCPAECEKCAKDCVCKGGEGKCSCCQ
 C.lupMT4 MDCTCMSGGICICGDNCKCTTCNCKTCRKSCCPCCPPGCAKCAQGCICKGGSDKCSCCA
 R.norMT1 MDCSCSTGGSTCSSSGCKNCKCTSCKKSCSSCCPVGCSKCAQGCVCKGASDKCTCCA
 R.norMT2 MDCSCATDGSCSCAGSCKCKQCKCTSCKKSCSSCCPVGCAKCSQGCICKEASDKCSCCA
 R.norMT3 MDCPCPTGGSTCSDKCKCKGCKCTNCKKSCSSCCPAGCEKCAKDCVCKGEEGKCSCCQ
 R.norMT4 MDCTCMSGGICICGDNCKCTTCSCKTCRKSCCPCCPPGCAKCAQGCICKGGSDKCSCCP
 G.galMT1 MDCPCATGGTCTCGDNCKCKNCKCTSCKKGCCSSCPAGCAKCAQGCVCKGPPSKCSCK
 G.galMT2 MDCTCAAGDSCSCAGSCKCKNCRCSRKSCSSCCPAGCENNAKGCVCKEPASKCSCH
 P.carMT1 MDCPCATGGTCTCGDNCKCKNCKCTSCKKGCCSSCPAGCAKCAQGCVCKGPPSKCSCK
 P.carMT2 MDCTCAAGDSCSCAGSCKCKNCRCSRKSCSSCCPASCSNAKGCVCKEPASKCSCH
 A.plaMT2 MDCTCAAGDSCSCAGSCKCKNCRCSRKSCSSCCPAGCENNAKGCVCKEPASKCSCH
 A.plaMT1 MDCPCATGGTCTCGDNCKCKNCKCTSCKKGCCSSCPAGCAKCAQGCVCKGPPSKCSCK
 C.chaMT MDCSCNTGGTCTCAGSCKCKNCKCTSCKKSCSSCCPAGCDNAKGCVCKEPLSKCSCH
 F.parMT MDCGCATGGSCSCAGSCKCKNCKCTSCKKTCCSSCPASCDNAKGCVCKEPSSKCSCH
 A.fraMT MDCTCAAGGSCSCAGSCKCKNCKCTSCKKSCSSCCPASCNHCAKGCICKEPSSKCSCH
 P.barMT MDCPCATGGTCTCAGSCKCKNCKCTSCQKSCSSCCPAGCTNAKGCVCKEPLSKCSCH
 E.quaMT MDCGCATGSSCSCNGSCKCKNCKCTSCKKSCSSCCPASCDNAKGCVCCKDPSLKCSCH
 P.sicMT MDCACATGGSTCAGSCKCKNCKCTSCKKSCSSCCPAGCAKCAKSCVCKEPLSKCSCH
 X.laeMT MDCKCETGASCSCGTTCSNSCKCTSCKKSCSSCCPAECSKCSQGHCEKGSKKCSCH
 X.troMT MDCNCETGASCSCANKCVCSNCKCTSCKKSCSSCCPAECSKCSKGCHCEKESKKCSCH
 A.mexMT MDCACATGGSCSCAGSCKCENCKCTSCKKSCSSCCPSECEKCGQGCVCKGGSSKCSCH
 T.carMT MDCGCASGGSCSCAGSCKCENCKCTSCKKSCSSCCPAGCDKCGQGCVCKGGSTKCSCH
 R.escMT MDCGCAAGGSCSCGDSCKCKDKCKGCKKSCSSCCPTDCTKCSQGCCEAKGSDTCSCH
 D.rerMT1 MDCECAKTGACNCGATCKCTNCQCTTCKKSCSSCCPSGCSKASGCVCKGNSCGTSCCQ
 D.rerMT2 MDCECAKTGTCNCGATCKCTNCQCTTCKKSCSSCCPSGCSKASGCVCKGNSCGSSCCQ
 C.hamMT1 MDCDCSKSGTCNCGGSTCTNCSCKSCKKSCCPCCPSGCTKASGCVCKGKTCDTSCCQ
 C.hamMT2 MDCDCSKSGTCNCGGSTCTNCSCTSCKKSCCPCCPSGCTKASGCVCKGKTCDTSCCQ
 T.berMT1 MDCQCSKSGTCNCGGSTCTNCSCKSCKKSCCPCCPSGCTKASGCVCKGKTCDTSCCQ
 T.berMT2 MDCECSKSGTCNCGGSTCTNCSCTSCKKSCCPCCPSGCTKASGCVCKGKTCDTSCCQ
 G.acuMT1 MDCDCSKSGTCNCGGSTCTNCSCKSCKKSCCPCCPSGCTKASGCVCKGKTCDTSCCQ
 G.acuMT2 MDCDCSKSGTCNCGGSTCTNCSCTSCKKSCCPCCPSGCTKASGCVCKGKTCDTSCCQ

Supplementary Figure 1. Alignment of the amino acid sequences of the vertebrates MTs used to infer the phylogenetic tree shown in Figure 1. The alignment was obtained using the program MUSCLE v3.8 and refined manually by the program Se-AL v20a11. Columns containing gaps were removed.