

SUPPLEMENTARY TABLES

Tab. S1. Primers sequences used for the characterization of the MTs mRNA sequences.

Primer	Sequence (5'-3')	T _m (°C)
Anchor-dT	CGGAGATCTCCAATGTGATGGGAATTC(T) ₁₇	61.9
5'RACE kit primer	GGCCACGCGTCGACTAGTACGGGIIGGGIIGGGIIG	79.2
TnewMTFW	AAGAGTGGGACCTGCAACTG	58.8
TnewMT1RE	TCTGAAGACATTCACAACAGCA	55.3
TnewMT2RE	AGACATTGGCAACAGGAATG	54.1
CmawMT1RE	TCTGAAGACATTCACAACAGCA	55.3
CmawMT2RE	AGACATTGGCAACAGGAATG	54.1
HvelMT1RE	AGGTCAGGCCTTTCACTGACAGC	63.5
HvelMT2RE	GGCTGAGGTCCTTCACTGACAGCAGC	68.0
3'RACEMT1TnewFW	ACACAAGCTGCTGTCACT	55.0
3'RACEMT2TnewFW	TGGAGCCTTTGTGAACTACT	54.6
3'RACEMT2ThanFW	GTGCAAAGGGAAGACTTGT	54.1
3'RACEMT1TeulFW	CTGCCCCGCTTCTGACTTT	57.0
3'RACEMT2TeulFW	CCGCTTCTGCTCTGGAAT	56.6
3'RACEMT1TpenFW	TTCTGCCTTTGGGATGGA	55.3
3'RACEMT1HvelFW	GCTGTCAGTGAAAGGCCTGACC	62.9
3'RACEMT2HvelFW	GCTGACAGTGAAGGACCTCAGC	62.3
5'RACEMT1TnewRE	TAAGGGCTCCATCCCAAAG	56.0
5'RACEMT2TnewRE	CAAAGGCTCCATTCCAGGAG	57.5
5'RACEMT2ThanRE	AGGTCTTCCCTTTGCACAC	56.7
5'RACEMT1TeulRE	AAGGGCTCCATCCCAAAG	56.5
5'RACEMT2TeulRE	CTCCTGGAATGGAGCCTTTGTG	60.0
5'RACEMT2TlepRE	GCTGGTGCAGGAGCAGTT	60.2
5'RACEHvelMT2RE	CAAAATTCACCATTTCTCTG	46.7
5'RACETberMT2RE	GAAGACATTCACAACAGCAA	51.8
5'RACEChamMT1RE	ATAAGGGCTCCATCCCAAAGG	56.0
5'RACEChamMT2RE	CAAAGGCTCCATTCCAAGAG	55.1
5'RACEGacutMT1RE	GCGGCTGAGGTCTTCACT	59.4

FW = forward primer, and RE =reverse primer; *oligo (dT)-adapter primer.

Tab. S2. GenBank accession number list of species which MT sequences were examined.

Species	Accession Number
<i>Anguilla anguilla</i>	DQ493910 (MT-1)
<i>Oncorhynchus mykiss</i>	M22487 (MT-2)
<i>Danio rerio</i>	BC049475 (MT-2)
<i>Gobio gobio</i>	AY953545 (MT-1), AY953546 (MT-2)
<i>Carassius carassius</i>	AY491048 (MT-1)
<i>Gadus morhua</i>	U08105
<i>Oryzias latipes</i>	AY466516
<i>Perca fluviatilis</i>	X97272
<i>Lithognathus mormyrus</i>	AF321007
<i>Pagrus major</i>	AB039668
<i>Sparus aurata</i>	U58774
<i>Notothenia coriiceps</i>	AJ006484 (MT-1), AJ006485 (MT-2)
<i>Pagothenia borchgrevinki</i>	AJ007562 (MT-1), AJ007563 (MT-2)
<i>Pleuragramma antarcticum</i> *	FJ870668 (MT-1)*, FJ870669 (MT-2)*
<i>Gobbionotothen gibberifrons</i> *	FJ870670 (MT-1)*, FJ870671 (MT-2)*
<i>Trematomus bernacchii</i> *	AJ011585 (MT-1), Z72485 (MT-2), FJ870672 (MT-2)*
<i>Trematomus hansonii</i> *	FJ870679 (MT-1)*, FJ870680 (MT-2)*
<i>Trematomus pennellii</i> *	FJ870685 (MT-1)*, FJ870686 (MT-2)*
<i>Trematomus newnesi</i> *	FJ870681 (MT-1)*, FJ870682 (MT-2)*
<i>Trematomus lepidorhinus</i> *	FJ870677 (MT-1)*, FJ870678 (MT-2)*
<i>Trematomus eulepidotus</i> *	FJ870683 (MT-1)*, FJ870684 (MT-2)*
<i>Histiodraco velifer</i> *	FJ870689 (MT-1)*, FJ870690 (MT-2)*
<i>Gymnodraco acuticeps</i> *	AJ007560 (MT-1), AJ007561 (MT-2), FJ870675 (MT-1)*, FJ870676 (MT-2)*
<i>Cygnodraco mawsoni</i> *	FJ870687 (MT-1)*, FJ870688 (MT-2)*
<i>Chionodraco rastrispinosus</i>	AJ011584 (MT-1), Z72484 (MT-2) Y12580 (MT-1), Y12581 (MT-2),
<i>Chionodraco hamatus</i> *	FJ870673 (MT-1)*, FJ870674 (MT-2)*
<i>Chaenocephalus aceratus</i>	AJ011583 (MT-1), Z72483 (MT-2)
<i>Parachaenichthys charcoti</i>	AJ007950 (MT-1), AJ007951 (MT-2)

The species names and the accession numbers which are indicated by symbol (*) correspond to the MT sequences characterized in our laboratory.