**Table S1.**

**Oligonucleotides used for Northern blot hybridization and FISH**

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| --- | --- | --- |
| **Name** | **Sequence 5’-3’** |  |
| tRNATyr -3 ́exon | GTGGTCCTTCCGGCCGGAATCGAA |  |
| tRNATyr- intron | TGTGATACCTGCAAACTCTACAG |  |
| snoRNA | CAACGTCCATCTGCGACGGCTTTA |  |
|  | **Sequence 5’-3’** | **Fluorophore** |
| TbtRNATyr-mature | AACCAGCGACCCTGTGATCTAC | 5 ́end Cy3 |
| TbtRNAGlu | TTCCGGTACCGGGAATCGAACCCGGATCTTC | 5 ́3 ́end AF488 |
|  |  |  |

**Oligonucleotides used for cloning and *in situ* tagging of Mtr2**

|  |  |
| --- | --- |
| **Name** | **Sequence 5’-3’** |
| Mtr2\_PetD1\_BamH1\_ Forward | GGGATAGGATCCAATGTCGGAATACGCAGATTGCACGGAA |
| Mtr2\_PetD1\_Hind III\_Reverse | GCGGCGAAGCTTCTCCTTTTCACTTAACCAGCGATAATAATCATTC |
| C-Ter-3XHAMtr2\_ Sam Dean\_ Forward | TTCAGAGGTTTGTTATTAGAAAGGTAGAAGAGCGGTATTACATAATGAATGATTATTATCGCTGGTTAAGTGAAAAGGAGGGTTCTGGTAGTGGTTCC |
| C-Ter-3XHAMtr2\_ Sam Dean\_ Reverse | TATGGACACAAAAAGAAATTGAGGAGCCAGATGGCCGCGATTTGCCACTTACACCACCAAATAGATGAACGTTGCAGTCTCCAATTTGAGAGACCTGTGC |

**Primers used for qRT-PCR analysis**

|  |  |
| --- | --- |
| **Transcripts** | **Sequences (5’-3’)** |
| 11.5090 | Forward: CAATCCCACAACACAGCG  Reverse: GCAATTCCTGTGACTGGG |
| 9.11740 | Forward: GCTTCCTTCAACTTTCTTGCCC  Reverse: CCTCCTTTTCCAGTTCCCG |
| 10.9450 | Forward: CAAAAGCCTATAAGGGAGGG  Reverse: TCGCCGACAGTGCCTACC |
| 10.1480 | Forwards: CCAAACTTGGGTTCCTTGAGG  Reverse: CGCAGAACATTTGACAGG |
| 2.220 | Forward: GGGCAAGTTTTCAGAAGTGTGG  Reverse: CCGCATAATCTTCCAGCAGC |
| 3.5660 | Forward: CGTTTCCACCAAAATTCCC  Reverse: CCGTCGCTCTTCATTATCTGG |
| 4.300 | Forward: GCAGCTCCACAAGGAAATAACG  Reverse: GCACCGTTCACCCAATCG |
| 11.3610 | Forward: GGAGTGTCCCTTCTAATGCC  Reverse: GGCTGCACGAGTTAGAACG |
| 7.2100 | Forward: GTCAGTTCAACAGGAGCCG  Reverse: GCACGCCATAACAAATACCC |
| 2.240 | Forward: AGAACGGCGGTAGTGTGG  Reverse: GGCACGACATCAACTTCC |
| 5.4590 | Forward: GTTCTATCTTGACCCCCACGG  Reverse: GCACTCGCTTCCATAAAGGG |
| 7.7400 | Forward: AGCCGTGTGTGGAGCTTAATGG  Reverse: GGAGGCCTTGTGACAGAATCC |