

**Figure S1.** Annotation of *OdMT1* and *OdMT2* genes were supported by EST and SRA sequences. (**A**) *OdMT1* gene was annotated as 'GSOIDP00013076001-unnamed product' in the Oikobase, scaffold\_50 from 61,593 nt to 61,997 nt (plus strand). Comparison of the genomic sequence (top line) with the EST FP794470.1 (bottom line) supported the annotated 3 exons / 2 introns structure. (**B**) *OdMT2* gene was not annotated in the Oikobase, scaffold\_16: from 829,667 nt to 831,025 nt (minus strand). *OdMT2* gene structure was deduced by comparison of the genomic sequences (short lines; **Table S1**) covering 75% of the gene, from position 335 (exon 2) to 1359 (exon 4). Exon 1 and the 5' end of exon 2 were deduced by comparison with *OdMT1* and manual inspection of the ORFs.

A. 1	RXXXPPAR GCTGTTTCGATAAGCAGT <mark>CGGTGAACTTTGATAAGGCAAAAA</mark> ACGCTTGACAGGAAAAGCCATAAAAACCGTCAAAAACAAAATTGCCTTTTTTACTGTTAA	100
101	RXR/PPAR HSF MREF TTTCTGACTTGTTCCAAGCAAAAGCTCAAGCCCTTTTTAGAAACGTCTCAAATTGAGCCTTATCCTCATCCCTTTTCAGCATAAATTGTGGAAGCTTGAGT	200
201	bZIP RXR/PPAR HSF RXR/PPAR HSF HSF ATTGCAGCTTGCTTTTCCATGGTCAAAATCGGGTTTAGAGCTTCAAGCTTCTTGAACCTCGGGAGTTTTGAGTTTTGAGTTTGGAT	300
301	<u>bzip</u> GCCGGCACCTCATTTGGAGACGAAAAATACAG <mark>TCAATTACCAACTCGGCCAGG</mark> TCCTTAAGCTCAATCCATTGCGCAAGGGTAATATTCTGCTTATTCAC	400
401	HSF GTTCCGAAAAATTCACAAAACAATTTAAGGACCGCCAAAAACAATAATTCTATCTTTTCAAGAGCAGTTTCAAAAAACAGACATTGAAAGACTTGCAGAA	500
501	RXR/PPAR TAAGGTTCAACACGGAATTTGCGCAAGAATAGCGCAAATTCGAAAAAGTCAAAAAACCGGCA <mark>AAAAAGCTCAAAAAAGTGGAATTTC</mark> IAAATCTATTTAGT	600
601	KSF CGTCAAAAAACGATGATAAGTTTGACAGAGCAGAATTCAAAAACAAGCTTGTCTTCATTCA	700
701	HSF	800
801	ATTTGGGCACCTGTTTGTTTTATTCAGAATAAAATTTAACGTGTTACGGAQACAAGTGGCTCAAGAACTTTTCTTCCCACGAAAAAATATGCAAAAAATGGAA	900
901	CACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1000
1001	ATGGATCCGGTTTGCTCTTTCCGCTGCGCAGGTAAAAAGGGCCATAAATGAAAATTCTAGCGCGTTTTTAGAAAACTGCGCAGGATGCGTCGATTGC M D P V C S F R C C E E N C A G C V D C	1100
1101	CCAGCTGGCTGTGATCCCTGCAAATGCACGTTGGAAGTCTGCAAGAAAGTTTGCGAAGGTAAAAACTTTCTGGAAATCTTTCTAAAAAGTCGCGGTTTTA P A G C D P C K C T L E V C K K V C E	1200
1201	TAATCTATAÀATTCAGGTTĠCAAAGATTGĊCCTCCCGGATGCGAGCCGTĠCAAATGCGAÀAAATGCTCCÀCCAAGAAATGCAAAAGCAATTGCTGCCCCGA G C K D C P P G C E P C K C E K C S T K K C K S N C C P T	1300
1301	<u>CCAGCACAGCGGAATAA</u> AGTCGGATTCCAGCTTTGGAAACAACCATTTAACGTCTGACACAAATTCTTTTCTAACATTTTTTTT	1400
<b>B.</b> 1	bzip	100
101	TTTCGTTTTGTTTTTTTCGCTTTGCCAGCTTTTGCTTTCATGCTATTCAGCTTTTTTGCAACACTTTTAGATGGCTTCTTTACTTTTTGAATGCTCTC	200
201	MREF <u>bzip</u> HSF AGAATTTTTCATTTTCAAATTTTCACTCTTTG <mark>TGACA</mark> GCCAGATTATTATTTAATCTTGT <mark>TCAAGCTTTGAAGTTCTAGAAAAATTGCAAGCAGAGCAT</mark>	300
301	KXK/PPAR Image: Comparison of the comp	400
401	AGCGOTCGAAGCAGTTCTCGCAGAATCGGGCCTATAAAAAACTTTTTAAAAGTTTCAGATTTCGTAGGTTTGCTTTATGAATCATAAAAATAACAAGAATC	500
501	AGGTTATAAAAAAAACTAAGATGCTTAGGAATAATATTTAAAATAAAGTCTGTACTTCTGCTTTTT <mark>GGAAATCTGCTAAATGGTCAACATCTCC</mark> AAGAATG	600
601	GTTTTAGCAATGATTTGGTGAAGTTTATTCCCCGAATCGAGTTCCAGCAGCTTTTGTGAAAGATTCCAGTGGTGCTTTACAGAGAAATCCGCGCCAAGAA	700
701	CACCCTCCATCAGATTCTGAATTTAATAAATTAACTTGTTATGGATAAAACTGTATAAATAA	800
801	AAATTATTGATCTAAGTTGAATTCTTCGGTTCTTCGTTTACATAGAATGTT	900
901	CGTAAATAATAGAATAACAAATAACTCCCCATATATATTCAACGCAAATTATTTCTTTC	1000
1001	ATGGAAGTAAAACGACCAAACAACTGCTGCCCGGCTAAGTGCCTAGGTTGCAAGGGATGCCCACCAGGTGAGAACTAATAAACTCTTATAAATTCAAGTA MEVKRPNNCCPAKCLGCKGCPPG	1100
1101	TATTAAATTGAAATTCTTTCACCCGCTAACTGTAACCTAAGGGTGTGAACCTTGTATTTGCAACATGGATACCTGCAAAAATATCTGCAACAAATGTAAA C E P C I C N M D T C K N I C N K C K	1200
1201	GAGTGCCCGAAAAACGAGTTCGGCTGCGACCCTTGCAAGTGTCCTAAGTGCTCCAAGCTTGGATGCACATGCGATTGCTGCCACAAAAAATGTTGTGTTA E C P K N E F G C D P C K C P K C S K L G C T C D C C H K K C C V	1300
1301	CCGATTGCGATGGATGTAAGACTTGCCCCCGGGCTGTGAACCATGCAAGTGCTCAATGAATG	1400
1401	AAAATCTGAATCCGGTTGCGACCCCTGCGAATGCTCCAAATGCGCTTTAAAGGGATGCAAGTGCGACTGCTGTCCCAAGGACACCTGCTGTGAAGCTTCC R K S E S G C D P C E C S K C A L K G C K C D C C P K D T C C E A S	1500
1501	TGCGAAGGCTGCAAGAACTGTCCTCCAGGCTGTGAGCCCTGCAAGTGTACCTTGAATTGCTGCATGAAAATCTGTGACGACTGCCAAGGACTGCCCAAAAT C E G C K N C P P G C E P C K C T L N C C M K I C D D C K D C P K	1600
1601	CCGAAAACGGCTGCGACCCATGCAACTGCCGTAAGTGCTCCAGAAAAGGATGCAATTGCGACTGCTGCCAAGTGACGACTGCTGTAAAGCTTCCTGCGA S E N G C D P C N C R K C S R K G C N C D C C P S D D C C K A S C	1700
1701	GGGATGTATCAATTGTCCTCCAGGATGTGACCCATGCGAGTGCTCAATGGACGAATGCAAGAAAATATGCAAAAAATGCAACAACTGCCGAAAGGGCGAG EGCINCPPGCDPCECS <mark>MDECKKICKKCNNCRKGE</mark>	1800
1801	TCCGGGTGTGACCCATGTGAGTGTCGAAAGTGCTCCCGAAACGGCTGTGACTGTGATGCTGCCCGAAGGACTCCTGTTGCGAGGCATCTTGTGAAGGAT S G C D P C E C R K C S R N G C D C D C C P K D S C C E A S C E G	1900
1901	GCACGGACTGTCCTCAAGGCTGTAAGCCTTGCAAGTGCACCATGAATAGCTGCATGAAAACTTGTGACAAGTGCAAGGACTGTCCCAAATCAGCCTCAGG C T D C P Q G C K P C K C T M N S C M K T C D K C K D C P K S A S	2000
2001	CTGTGACCCTTGCGAGTGCCTAAAATGTTCCCGAAAGGGCTGCGAGTGTGATTGCTGCCCCCAAAAAAATGACTGCTGCGAAGGTAAAAAATTATGAACA G C D P C E C L K C S R K G C E C D C C P Q K N D C C E A	2100
2101	ATTTTGTCACTAACTAAAATATTAGCGTTCTGTCAAGGATGTAAGAATTGCCCACCTGGATGTAACCCATGCAAGTGTACCTTGAACTTCTGTGCCAAAA FCQGCKNCPPGCNPCKCTLNFCAKI	2200
2201	TTTGCAACGGTAACTTCAAAAAAACAGAACGGAGAATGATAAGATAAGATAAGTAAG	2300
2301	GCGTCAAATGCTCTGCCAAAGGATGCAAATGCGATTGCTGCCCCAAAAAATGCTGTTAAA 2360	

**Figure S2.** *OdMTs* genomic regions. (**A**) Genomic region of *OdMT1* gene along with 1 Kb of the 5' flanking promoter region and *in silico* translation of CDS. Deduced OdMT1 protein is made of a single repeat unit (RU) with an internal repeat –C7a (green background) and C7b (orange background)– and a C-terminal tail (blue background). (**B**) Genomic region of *OdMT2* gene along with 1 Kb of the 5' flanking promoter region and *in silico* translation of CDS. Deduced OdMT2 protein is made of 6 RUs, each one with the same C7a/C7b/C-tail structure (green, blue and orange backgrounds, respectively). Putative binding sites for transcription factors in the promoter regions of both genes are depicted with the same colour code than in Figure 2: MREF (orange boxes), bZIP transcription factors (purple boxes), RXR/PPAR (blue boxes) and animal or yeast HSF (green and yellow boxes, respectively). Notice that some boxes overlap (see **Table S3** for additional details).



**Figure S3.** FPLC elution profiles at 254 nm of recombinant metal-OdMT1 (top panels) and metal-OdMT2 (low panels) complexes with Zn, Cd and Cu. Notice that whereas metal-OdMT1 complexes were obtained from *E. coli* cultures grown in medium supplemented with Zn, Cd or Cu, metal-OdMT2 complexes were only obtained from cultures grown in Cd-enriched media (central low panel). The intensity range was kept at the same values for better comparison among the chromatograms.