



Figure S1. The growth status of the bacteria that transformed pGEX-6p-1-MT and pGEX-6p-1: (A) the 0.6 mM Zn stress group; (B) 0.9 mM Zn stress group. All data are presented as the mean  $\pm$  SD ( $n = 3$ ). “\*”:  $p < 0.05$ ; “\*\*”:  $p < 0.01$ .

**Table S1. The primers and their sequences**

Primer	Sequence(5'-3')	Purpose
<i>MT</i> -F1	CCTTCAGTCTGCTGGTCTCT	PCR
<i>MT</i> -R1	TCTCGTTTTAGTGGCAGTCG	PCR
<i>MTF1</i> -F1	TAACTGTGATGAGAGCGGG	PCR
<i>MTF1</i> -R1	GCTGAAGTATCCACAAGACC	PCR
5' <i>MT</i> -R1	ATGCACTTCCCCGCTTTGGC	5'RACE
5' <i>MT</i> -R2	CCTTTGGTCCTCTGGGACTTCTGG	5'RACE
5' <i>MTF1</i> -R1	GTGTAACCTCTGGTGGGCTCGAA	5'RACE
5' <i>MTF1</i> -R2	CACATCCCTGCACATCACACTCAAA	5'RACE
3' <i>MT</i> -F1	AAAGCGGGGAAGTGCAT	3'RACE
3' <i>MT</i> -F2	GTACCAAAGCTGGAAAATGC	3'RACE
3' <i>MTF1</i> -F1	GAGGCAGGTCGGGGCAGTGGTAG	3'RACE
3' <i>MTF1</i> -F2	CCTGTGATACAAACCGTGATTCCTGG	3'RACE
q <i>MT</i> -F	TGCTTTGAGACAAGATGCC	RT-PCR&RT-qPCR
q <i>MT</i> -R	ACTTCCCCGCTTTGACAC	RT-PCR&RT-qPCR
q <i>MTF1</i> -F	CAGTCTCAAGACTCACACAT	RT-PCR&RT-qPCR
q <i>MTF1</i> -R	TTGCTATGGCCATCTCTAAG	RT-PCR&RT-qPCR
$\beta$ - <i>actin</i> -F	CACGGAATCGTCACCAACT	Reference gene
$\beta$ - <i>actin</i> -R	AGAAGCATACAGGGACAGCA	Reference gene
yh- <i>MT</i> -F	CGCGGATCCATGCCGGCAACTGACTGC	Prokaryotic expression
yh- <i>MT</i> -R	CCGCTCGAGCTTGCATTTGCAGCCCTC	Prokaryotic expression
si <i>MT</i> -sense	CCAGCUGUAAAUGCAGCAATT	RNA inference
si <i>MT</i> -antisense	UUGCUGCAUUUACAGCUGGTT	RNA inference
si <i>MTF1</i> -sense	GCCAGAUGGAGAGAAGUAUTT	RNA inference
si <i>MTF1</i> -antisense	AUACUUCUCUCCAUCUGGCTT	RNA inference
siNC-sense	UUCUCCGAACGUGUCACGUTT	RNA inference
siNC-antisense	ACGUGACACGUUCGGAGAATT	RNA inference

**Table S2. The GenBank accession numbers and isoforms of the MT homologs**

Specie	GenBank accession number	Isoform
<i>Sinohyriopsis cumingii</i>	ACZ06027.1	MT
<i>Alectryonella plicatula</i>	ALA14799.1	MT
<i>Magallana gigas</i>	CAB64869.1	MT
<i>Perinereis nuntia</i>	AFE61618.1	MT
<i>Pomacea canaliculata</i>	XP_025111375.1	MT 20-III-like X3
<i>Cerastoderma edule</i>	CDF59687.1	MT
<i>Perna viridis</i>	AEX60795.1	MT1D
<i>Danio rerio</i>	NP_571150.1	MT1
<i>Carassius auratus</i>	AAB32777.1	MT
<i>Oryzias latipes</i>	NP_001098255.1	MT
<i>Gallus gallus</i>	BAF51974.1	MT
<i>Homo sapiens</i>	AAP97267.1	MT1M
<i>Mus musculus</i>	AAQ24163.1	MT1K
<i>Zootoca vivipara</i>	CAJ32319.1	MT

Note: For *Homo sapiens*, *Mus musculus* and other species with multiple isoforms, we compared their similarities and finally chose MT or MT1 for comparison.

**Table S3. The GenBank accession numbers and isoforms of the MTF1 homologs**

Specie	GenBank accession number	Isoform
<i>Chaetura pelagica</i>	XM_009996683.1	MTF1
<i>Crotalus tigris</i>	XM_039329224.1	MTF1
<i>Lacerta agilis</i>	XM_033157482.1	MTF1
<i>Mus musculus</i>	NP_032662.3	MTF1
<i>Rattus norvegicus</i>	NP_001102147.1	MTF1
<i>Homo sapiens</i>	NP_005946.2	MTF1
<i>Gallus gallus</i>	NP_001026666.1	MTF1
<i>Xenopus tropicalis</i>	XP_031752770.1	MTF1
<i>Rana temporaria</i>	XP_040193139.1	MTF1
<i>Danio rerio</i>	NP_694513.1	MTF1
<i>Oryzias melastigma</i>	XP_036071630.1	MTF1
<i>Strongylocentrotus purpuratus</i>	XP_030850345.1	MTF1
<i>Mytilus edulis</i>	CAG2198514.1	MTF1
<i>Mytilus coruscus</i>	CAC5383271.1	MTF1
<i>Chionoecetes opilio</i>	KAG0726832.1	MTF1