

Cucumber Metal Tolerance Protein 6 (CsMTP6) affects the mitochondrial Fe²⁺ and Mn²⁺ homeostasis

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Table S1

Yeast strains used in this work.

| Strain | Genotype | Source or reference |
|-----------------------|--|------------------------------|
| W303-1A | <i>MATa ade2-1 can1-100 his3-11,15 leu2-3,112 trp1-1 ura3-1</i> | Wallis <i>et al.</i> 1989 |
| W303-1A K667 | <i>CNB1::LEU2 PMC1::TRP1 VCX1Δ</i> | Cunningham and Fink 1996 |
| DY150 | <i>MATa ade2-1 can1-100 his3-11,15 leu2-3,112 trp1-1 ura3-52</i> | Li and Kaplan 2004 |
| DY150 mrs3mrs4 | <i>MRS3::KanMX MRS4::KanMX</i> | Li and Kaplan 2004 |
| DY150 mmt1mmt2 | <i>MMT1::KanMX MMT2::HIS3</i> | Li <i>et al.</i> 2014 |
| DY150 fet5smf3 | <i>FET5::HIS3 SMF3::KanMX</i> | Li <i>et al.</i> 2014 |
| BY4742 | <i>MATα his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0</i> | Brachmann <i>et al.</i> 1998 |
| BY4742 zrc1 | <i>ZRC1::KanMX4</i> | Euroscarf, Germany |
| BY4742 aft11 | <i>AFT1::KanMX4</i> | Euroscarf, Germany |
| BY4742 ccc1 | <i>CCC1::KanMX4</i> | Euroscarf, Germany |
| BY4742 smf1 | <i>SMF1::KanMX4</i> | Euroscarf, Germany |

Figure S1

Organ expression pattern of *CsMTP6* in cucumber. Real-time expression analyses of the level of *CsMTP6* transcript in the roots, hypocotyls, cotyledons, leaf petioles and leaves of 2-week-old cucumber seedlings growing in standard nutrition media. Bars represent average *CsMTP6* transcript levels relative to the constitutively expressed reference gene *CACS* calculated from the arithmetic means of ΔCp values obtained in three independent experiments. Asterisk indicates statistically significant difference ($*p<0.05$, $**p<0.01$; ANOVA with Tukey's correction) between the *CsMTP6* transcript levels measured in different cucumber organs.

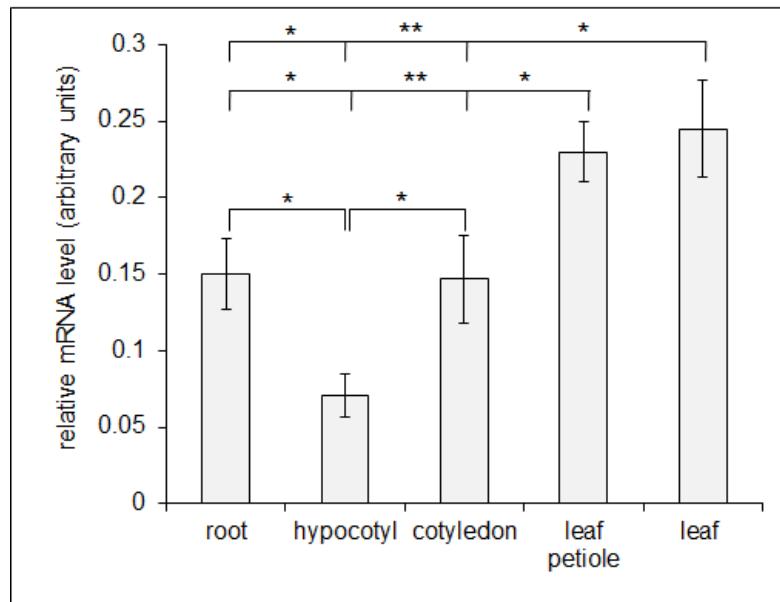


Figure S2

ClustalW alignment of the *CsMTP6* nucleic acid and CsMTP6 amino acid sequences. A-B, The alignment of *CsMTP6* nucleic acid (A) and CsMTP6 amino acid (B) sequences identified *ab initio* (FGENESH) in the genome of cucumber Chinese long and amplified on the cDNA of cucumber Krak (CsMTP6.Chin). C, The alignment of *CsMTP6* nucleic acid sequences amplified on the cDNA of cucumber Krak (GenBank acc. No. KX118275.1) and reconstructed from RNA-Seq reads from 10 cucumber Chinese long tissues (Csa7G395210.1). The identical nucleotides and amino acids are indicated by asterisks. The start and stop codons were marked in red.

A

| | |
|-------------|--|
| CsMTP6.Krak | ATGGGATAACAGATTCCACCGTCTCAATCCCATACTTCATCCTTCTATTCCAGGATTCC |
| CsMTP6.Chin | ATGGGATAACAGATTCCACCGTCTCAATCCCATACTTCATCCTTCTATTCCAGGATTCC |
| | ***** |
| CsMTP6.Krak | CCACCAACCCACAAAGAACATTCAATTCCCTCATTTCAATCTCCAGTCTTCATCCC |
| CsMTP6.Chin | CCACCAACCCACAAAGAACATTCAATTCCCTCATTTCAATCTCCAGTCTTCATCCC |
| | ***** |
| CsMTP6.Krak | CAATTACACATTCTAGGAATTATGATGATCCAAAGAGCAAATCTGCAGAAGGTGGCAT |
| CsMTP6.Chin | CAATTACACATTCTAGGAATTATGATGATCCAAAGAGCAAATCTGCAGAAGGTGGCAT |
| | ***** |
| CsMTP6.Krak | TTGGGTCACTCCCACCGCCATGACGATGATCATCGATTGGCCAAGAGGGTGAGAATATT |
| CsMTP6.Chin | TTGGGTCACTCCCACCGCCATGACGATGATCATCGATTGGCCAAGAGGGTGAGAATATT |
| | ***** |
| CsMTP6.Krak | TTCAAGTTGGGTCTTGGAGCTGACATTGGATTGGCTGTGGGAAGGCTGTGACGGGCTAT |
| CsMTP6.Chin | TTCAAGTTGGGTCTTGGAGCTGACATTGGATTGGCTGTGGGAAGGCTGTGACGGGCTAT |
| | ***** |
| CsMTP6.Krak | TTATCAGGAAGCACAGCTATTATAGCTGATGCGGCTCATTGGTTCTGATGTGGTCTT |
| CsMTP6.Chin | TTATCAGGAAGCACAGCTATTATAGCTGATGCGGCTCATTGGTTCTGATGTGGTCTT |
| | ***** |
| CsMTP6.Krak | AGTGGCATTGCTTATGGCATTAAAGCTGGAAAGCTCCAAAGACAAGGAGCATCCA |
| CsMTP6.Chin | AGTGGCATTGCTTATGGCATTAAAGCTGGAAAGCTCCAAAGACAAGGAGCATCCA |
| | ***** |
| CsMTP6.Krak | TATGGACATGGTAAATTGAAACTCTGGAGGCCCTGGAACTCTTCCATGCTTAGCA |
| CsMTP6.Chin | TATGGACATGGTAAATTGAAACTCTGGAGGCCCTGGAACTCTTCCATGCTTAGCA |
| | ***** |
| CsMTP6.Krak | ACTGCTGGTGGCATTGCTTGGCATGCTTCAGAACCTTACTG----- |
| CsMTP6.Chin | ACTGCTGGTGGCATTGCTTGGCATGCTTCAGAACCTTACTGAAACCTAGCTATTATACTT |
| | ***** |
| CsMTP6.Krak | ----- |
| CsMTP6.Chin | TCAGAATCCAATGTTCAAGGTTGAGGAATCTGCATGGCCTCTGTTCTTGC |
| | ----- |
| CsMTP6.Krak | -----GGCTTGTGTCAGCAGCTCCTGAAATAGTCATCAGCCTTGGACATGAAAGT |

CsMTP6.Chin AAGCAGGGCTTGTGTCAGCAGCTCCTGAAATAGTCATCAGCCTTGGACATGAAAGT*****

CsMTP6.Krak TTGCATAACCATAGCCATAGCATGGTGAAACATCATCATGGAATTGACATGGATCATCCT
CsMTP6.Chin TTGCATAACCATAGCCATAGCATGGTGAAACATCATCATGGAATTGACATGGATCATCCT*****

CsMTP6.Krak ATTCTAGCGTTGAATATGACTATTATATCAATATGTATCAAAGAAGGGCTTACTGGATA
CsMTP6.Chin ATTCTAGCGTTGAATATGACTATTATATCAATATGTATCAAAGAAGGGCTTACTGGATA*****

CsMTP6.Krak ACGAAACGAGCTGGGGAAAACGAGGAAGTGGACTCATGAAAGCAAATGCATGGCATCAT
CsMTP6.Chin ACGAAACGAGCTGGGGAAAACGAGGAAGTGGACTCATGAAAGCAAATGCATGGCATCAT*****

CsMTP6.Krak CGTGCATGCCATATCGTCTGTAGTTGCTCTCATGGTGTGGAGGTTCCATCCTGGG
CsMTP6.Chin CGTGCATGCCATATCGTCTGTAGTTGCTCTCATGGTGTGGAGGTTCCATCCTGGG*****

CsMTP6.Krak GTGAAGTTCTAGATCCCTAGCAGGACTCGTTGCTCTGGCATGATTCTAAAGGCCGGA
CsMTP6.Chin GTGAAGTTCTAGATCCCTAGCAGGACTCGTTGCTCTGGCATGATTCTAAAGGCCGGA*****

CsMTP6.Krak CTTCAAACGGACACCAGAGCATCTTGAATTAGTGGATGCTGCAATCCCTGCAGATCAA
CsMTP6.Chin CTTCAAACGGACACCAGAGCATCTTGAATTAGTGGATGCTGCAATCCCTGCAGATCAA*****

CsMTP6.Krak ATCGATCCTTCAAACAAACAATACTGCAAGTTGAGGGTGTCAAGGGTGCATCGGCTA
CsMTP6.Chin ATCGATCCTTCAAACAAACAATACTGCAAGTTGAGGGTGTCAAGGGTGCATCGGCTA*****

CsMTP6.Krak AGAGGAAGGAGAGCTGGCTCTTCTTGATCTCGATGTGCATATCGAGGTTGATCCATT
CsMTP6.Chin AGAGGAAGGAGAGCTGGCTCTTCTTGATCTCGATGTGCATATCGAGGTTGATCCATT*****

CsMTP6.Krak TTGAGTGTCACTGCCCTCATTCTATAGGTGAAATGTTGTCACGAGATTACATACGTCC
CsMTP6.Chin TTGAGTGTCACTGCCCTCATTCTATAGGTGAAATGTTGTCACGAGATTACATACGTCC*****

CsMTP6.Krak CATCCTGAAGTATCCGAAGTTTATACATATAGATCCCTCCATATCACATTTCCACCC
CsMTP6.Chin CATCCTGAAGTATCCGAAGTTTATACATATAGATCCCTCCATATCACATTTCCACCC*****

CsMTP6.Krak AAGCTATCGAACCGAACGCAAGCAGCTTCAGCAGGAACCTCAAATCAAAGTACAGACTCCCT
CsMTP6.Chin AAGCTATCGAACCGAACGCAAGCAGCTTCAGCAGGAACCTCAAATCAAAGTACAGACTCCCT*****

CsMTP6.Krak CTCACTGAGAACATTGAAGCAACCCTTCCGACATAGTCCAGTCAGGAAAC
CsMTP6.Chin CTCACTGAGAACATTGAAGCAACCCTTCCGACATAGTCCAGTCAGGAAAC*****

CsMTP6.Krak ATGATGGTTGAACGAATTACACCCACTTGTGCAAGGCAAGATCCTCCTCAAATCGAA
CsMTP6.Chin ATGATGGTTGAACGAATTACACCCACTTGTGCAAGGCAAGATCCTCCTCAAATCGAA*****

CsMTP6.Krak GTTTCAATGCCTCCCGACTTACTAATTGAAATGCGATGGATGTAGCAAACGAGCAGAA
CsMTP6.Chin GTTTCAATGCCTCCCGACTTACTAATTGAAATGCGATGGATGTAGCAAACGAGCAGAA*****

| | |
|-------------|--|
| CsMTP6.Krak | ATGGAAATCTGAAAGCAGATTCTAACATTGTTCATGTTAGCATTCAACTTCGTTGGGA |
| CsMTP6.Chin | ATGGAAATCTGAAAGCAGATTCTAACATTGTTCATGTTAGCATTCAACTTCGTTGGGA |
| | ***** |
| CsMTP6.Krak | CAACAAATTCCACAGCTCAGCCACTAA |
| CsMTP6.Chin | CAACAAATTCCACAGCTCAGCCACTAA |
| | ***** |

B

| | |
|-------------|---|
| CsMTP6.Krak | MGYRFHRLNPILQSFYSRISPPTHKEFHISIPSFQSPSLHPQFTFLGIYDDPKSKICRRWH |
| CsMTP6.Chin | MGYRFHRLNPILQSFYSRISPPTHKEFHISIPSFQSPSLHPQFTFLGIYDDPKSKICRRWH |
| | ***** |
| CsMTP6.Krak | LGHSHRHDDDHRFQEGENIFKLGADIGLAVGKAVTGYLSGSTAIIDAAHSVSDVVL |
| CsMTP6.Chin | LGHSHRHDDDHRFQEGENIFKLGADIGLAVGKAVTGYLSGSTAIIDAAHSVSDVVL |
| | ***** |
| CsMTP6.Krak | SGIALWSFKAGKAPKDKEHPYGHGFETLGALGISSMLATAGGIWAHASELLL----- |
| CsMTP6.Chin | SGIALWSFKAGKAPKDKEHPYGHGFETLGALGISSMLATAGGIWAHASELLNLAIIL |
| | ***** |
| CsMTP6.Krak | -----GLLSAAPEIVNQPGHESLHNHSHGEHHHGIDMDHP |
| CsMTP6.Chin | SESQCFQGSRNLAWSLFSCKQGLLSAAPEIVNQPGHESLHNHSHGEHHHGIDMDHP |
| | ***** |
| CsMTP6.Krak | IILALNMTIISICIKEGLYWITKRAGEKRGSGLMKANAWHHRADAISVVVALIGVGGSILG |
| CsMTP6.Chin | IILALNMTIISICIKEGLYWITKRAGEKRGSGLMKANAWHHRADAISVVVALIGVGGSILG |
| | ***** |
| CsMTP6.Krak | VKFLDPLAGLVSGMILKAGLQTGHQSILEVDAAPIPADQIDPFKQTILQVEGVKGCHRL |
| CsMTP6.Chin | VKFLDPLAGLVSGMILKAGLQTGHQSILEVDAAPIPADQIDPFKQTILQVEGVKGCHRL |
| | ***** |
| CsMTP6.Krak | RGRRAGSSLYLDVHIEVDPFLSVSAHSIGENVRHEIHTSHPEVSEVFIHIDPSISHFPP |
| CsMTP6.Chin | RGRRAGSSLYLDVHIEVDPFLSVSAHSIGENVRHEIHTSHPEVSEVFIHIDPSISHFPP |
| | ***** |
| CsMTP6.Krak | KLSNQQAASAGTSNQSTDFPLTENIEATVSDIVQSKFPENMMVERITPHLLQGKILLQIE |
| CsMTP6.Chin | KLSNQQAASAGTSNQSTDFPLTENIEATVSDIVQSKFPENMMVERITPHLLQGKILLQIE |
| | ***** |
| CsMTP6.Krak | VSMPPDPLLIRNAMDVAKRAEMEILKADSNIVHVS1QLRLGQQIPQLSH |
| CsMTP6.Chin | VSMPPDPLLIRNAMDVAKRAEMEILKADSNIVHVS1QLRLGQQIPQLSH |
| | ***** |

C

| | | |
|-----------------------------|--|----------|
| Csa7G395210.1 KX118275.1 | AGGAAACAGCATCGGTGGAGAGACGAAGGTTCTAACAGAGGAACAAGATTCCATT----- | 60 0 |
| Csa7G395210.1 KX118275.1 | TTCTCACAAATCTGTACAGAACATCGGTGCTTCACTCTGTTCTTTACTCTTGTTCAT----- | 120 0 |

| | | |
|-----------------------------|---|-------------|
| Csa7G395210.1 KX118275.1 | CTCTTCAACTCCATTCAACCAATTGTGAAATTAAACATCATTTCACAATCCTAAAG ----- | 180 0 |
| Csa7G395210.1 KX118275.1 | CTTCTGATCATCAAAATCCATCTCTCCCCACCAAAAACCTCCATTAAA ATG GGATACAGA ----- ATG GGATACAGA ***** | 240 12 |
| Csa7G395210.1 KX118275.1 | TTCCACCGTCTCAATCCCATACTCAATCCTCTATTCCAGGATTCCCCACCAACCCAC TTCCACCGTCTCAATCCCATACTCAATCCTCTATTCCAGGATTCCCCACCAACCCAC ***** | 300 72 |
| Csa7G395210.1 KX118275.1 | AAAGAATTTCATTCAATTCCCTCATTCAATCTCCAGTCTTCATCCCCAATTTCACATT AAAGAATTTCATTCAATTCCCTCATTCAATCTCCAGTCTTCATCCCCAATTTCACATT ***** | 360 132 |
| Csa7G395210.1 KX118275.1 | CTAGGAATTTATGATGATCCCAAGAGCAAAATCTGCAGAAGGTGGCATTGGGTCACTCC CTAGGAATTTATGATGATCCCAAGAGCAAAATCTGCAGAAGGTGGCATTGGGTCACTCC ***** | 420 192 |
| Csa7G395210.1 KX118275.1 | CACCGCCATGACGATGATCATCGATTGCCAAGAGGGTGAGAATATTTCAAGTTGGGT CACCGCCATGACGATGATCATCGATTGCCAAGAGGGTGAGAATATTTCAAGTTGGGT ***** | 480 252 |
| Csa7G395210.1 KX118275.1 | CTTGGAGCTGACATTGGATTGGCTGTGGGGAAAGGCTGTGACGGCTATTATCAGGAAGC CTTGGAGCTGACATTGGATTGGCTGTGGGGAAAGGCTGTGACGGCTATTATCAGGAAGC ***** | 540 312 |
| Csa7G395210.1 KX118275.1 | ACAGCTATTATAGCTGATGCGGCTCATTGGTTCTGATGTGGTTCTTAGTGGCATTGCT ACAGCTATTATAGCTGATGCGGCTCATTGGTTCTGATGTGGTTCTTAGTGGCATTGCT ***** | 600 372 |
| Csa7G395210.1 KX118275.1 | TTATGGTCATTTAACGCTGGAAAGCTCCAAAGACAAGGAGCATCCATATGGACATGGT TTATGGTCATTTAACGCTGGAAAGCTCCAAAGACAAGGAGCATCCATATGGACATGGT ***** | 660 432 |
| Csa7G395210.1 KX118275.1 | AAATTTGAAACTCTGGAGCCCTTGGAAACTCTTCCATGCTCTTAGCAACTGCTGGTGG AAATTTGAAACTCTGGAGCCCTTGGAAACTCTTCCATGCTCTTAGCAACTGCTGGTGG ***** | 720 492 |
| Csa7G395210.1 KX118275.1 | ATTGCTTGGCATGTTTCAGAACCTTTACTGGCTTGTGTCAGCAGCTCTGAAATAGTC ATTGCTTGGCATGTTTCAGAACCTTTACTGGCTTGTGTCAGCAGCTCTGAAATAGTC ***** | 780 552 |
| Csa7G395210.1 KX118275.1 | AATCAGCCTTTGGACATGAAAGTTGCATAACCATAGCCATAGCCATGGTAACATCAT AATCAGCCTTTGGACATGAAAGTTGCATAACCATAGCCATAGCCATGGTAACATCAT ***** | 840 612 |
| Csa7G395210.1 KX118275.1 | CATGGAATTGACATGGATCATCCTATTCTAGCGTTGAATATGACTATTATATCAATATGT CATGGAATTGACATGGATCATCCTATTCTAGCGTTGAATATGACTATTATATCAATATGT ***** | 900 672 |
| Csa7G395210.1 KX118275.1 | ATCAAAGAAGGGCTTACTGGATAACGAAACGAGCTGGGAAAACGAGGAAGTGGACTC ATCAAAGAAGGGCTTACTGGATAACGAAACGAGCTGGGAAAACGAGGAAGTGGACTC ***** | 960 732 |
| Csa7G395210.1 KX118275.1 | ATGAAAGCAAATGCATGGCATCATCGTGTGATGCCATATGCTGTAGTTGCTCTCATT ATGAAAGCAAATGCATGGCATCATCGTGTGATGCCATATGCTGTAGTTGCTCTCATT ***** | 1020 792 |
| Csa7G395210.1 KX118275.1 | GGTGTGGAGGTTCCATCTGGGTGAAGTTCTAGATCCCTAGCAGGACTCGTTGTC GGTGTGGAGGTTCCATCTGGGTGAAGTTCTAGATCCCTAGCAGGACTCGTTGTC ***** | 1080 852 |
| Csa7G395210.1 KX118275.1 | TCTGGCATGATTCTAAAGGCCGGACTTCAAACACTGGACACCAGAGCATCTTGGAAATTAGTG TCTGGCATGATTCTAAAGGCCGGACTTCAAACACTGGACACCAGAGCATCTTGGAAATTAGTG ***** | 1140 912 |

| | | |
|-----------------------------|---|--------------|
| Csa7G395210.1 KX118275.1 | GATGCTGCAATCCCTGCAGATCAAATCGATCCTTCAAACAAACAATACTGCAAGTTGAG GATGCTGCAATCCCTGCAGATCAAATCGATCCTTCAAACAAACAATACTGCAAGTTGAG ***** | 1200 972 |
| Csa7G395210.1 KX118275.1 | GGTGTCAGGGCTGCCATCGGCTAAGAGGAAGGAGAGCTGGCTCTTGTATCTCGAT GGTGTCAGGGCTGCCATCGGCTAAGAGGAAGGAGAGCTGGCTCTTGTATCTCGAT ***** | 1260 1032 |
| Csa7G395210.1 KX118275.1 | GTGCATATCGAGGGTGTGATCCATTGAGTGTCACTGCCGCTCATCTATAGGTGAAAAT GTGCATATCGAGGGTGTGATCCATTGAGTGTCACTGCCGCTCATCTATAGGTGAAAAT ***** | 1320 1092 |
| Csa7G395210.1 KX118275.1 | GTTCGTCACGAGATTCACTACGCCATCCTGAAGTATCCGAAGTGTGATCCATATAGAT GTTCGTCACGAGATTCACTACGCCATCCTGAAGTATCCGAAGTGTGATCCATATAGAT ***** | 1380 1152 |
| Csa7G395210.1 KX118275.1 | CCCTCCATATCACATTCCACCCAAGCTATCGAACCCAGCAAGCAGCTTCAGCAGGAAC CCCTCCATATCACATTCCACCCAAGCTATCGAACCCAGCAAGCAGCTTCAGCAGGAAC ***** | 1440 1212 |
| Csa7G395210.1 KX118275.1 | TCAAATCAAAGTACAGACTTCCCTCTCACTGAGAACATTGAAGCAACCGTTCCGACATA TCAAATCAAAGTACAGACTTCCCTCTCACTGAGAACATTGAAGCAACCGTTCCGACATA ***** | 1500 1272 |
| Csa7G395210.1 KX118275.1 | GTCCAGTCAAAATTCCAGAGAACATGATGGTTGAACGAATTACACCCACTTGTGCAA GTCCAGTCAAAATTCCAGAGAACATGATGGTTGAACGAATTACACCCACTTGTGCAA ***** | 1560 1332 |
| Csa7G395210.1 KX118275.1 | GGCAAGATCCTCCCAAATCGAAGTTCAATGCCCTCCGACTTACTAATTGAAATGCG GGCAAGATCCTCCCAAATCGAAGTTCAATGCCCTCCGACTTACTAATTGAAATGCG ***** | 1620 1392 |
| Csa7G395210.1 KX118275.1 | ATGGATGTAGCAAAACGAGCAGAAATGGAAATCTTGAAGCAGATTCTAACATTGTTCAT ATGGATGTAGCAAAACGAGCAGAAATGGAAATCTTGAAGCAGATTCTAACATTGTTCAT ***** | 1680 1452 |
| Csa7G395210.1 KX118275.1 | GTTAGCATTCAACTTCGTTGGGACAACAAATTCCACAGCTCAGCCAC TAA TTGACATAC GTTAGCATTCAACTTCGTTGGGACAACAAATTCCACAGCTCAGCCAC TAA ----- ***** | 1740 1503 |
| Csa7G395210.1 KX118275.1 | CAAAGGGATATATCGACACTTTCATATTACATCATATAACCAATATATTATTCCTACTC ----- | 1800 1503 |
| Csa7G395210.1 KX118275.1 | ATAATAAAATTTCGACTTAGATTAAGAGAACTTACCTTGCCAATGTTCAACCAA ----- | 1860 1503 |
| Csa7G395210.1 KX118275.1 | TAATATTCCCTCCAAATGGTTACAACCTTAACCTGTAAT ----- | 1900 1503 |

Figure S3

Western blot analysis of the mitochondria isolated from the WT or $\Delta mmt1\Delta mmt2$ yeast transformed with the pBT3-C-cGDO vector and the pUG35-GFP (v) or pUG35-CsMTP6-GFP vector (CsMTP6) using the antibodies against GFP.

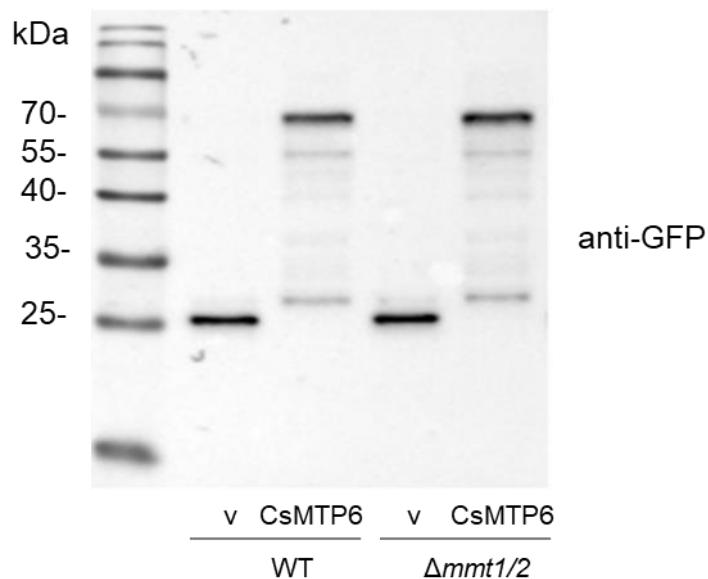


Figure S4

Localization of CsMTP6 in $\Delta zrc1$, K667 and $\Delta smf1$ cells. Yeast cultured overnight in control liquid SC/Glu-Ura media were diluted to OD₆₀₀ 0.1 and grown in liquid SC/Glu-Ura media supplemented with 5 mM ZnSO₄ ($\Delta zrc1$), 10 mM MnSO₄ (K667, $\Delta pmc1\Delta vcx1\Delta cnb$) or 20 mM EGTA ($\Delta smf1$) for 8-10 hours. 1 - transmission image of the cells expressing CsMTP6-GFP; 2 - GFP fluorescence; 3 - MitoTracker red fluorescence; 4 - merged image. Scale bars represent 5 μ m.

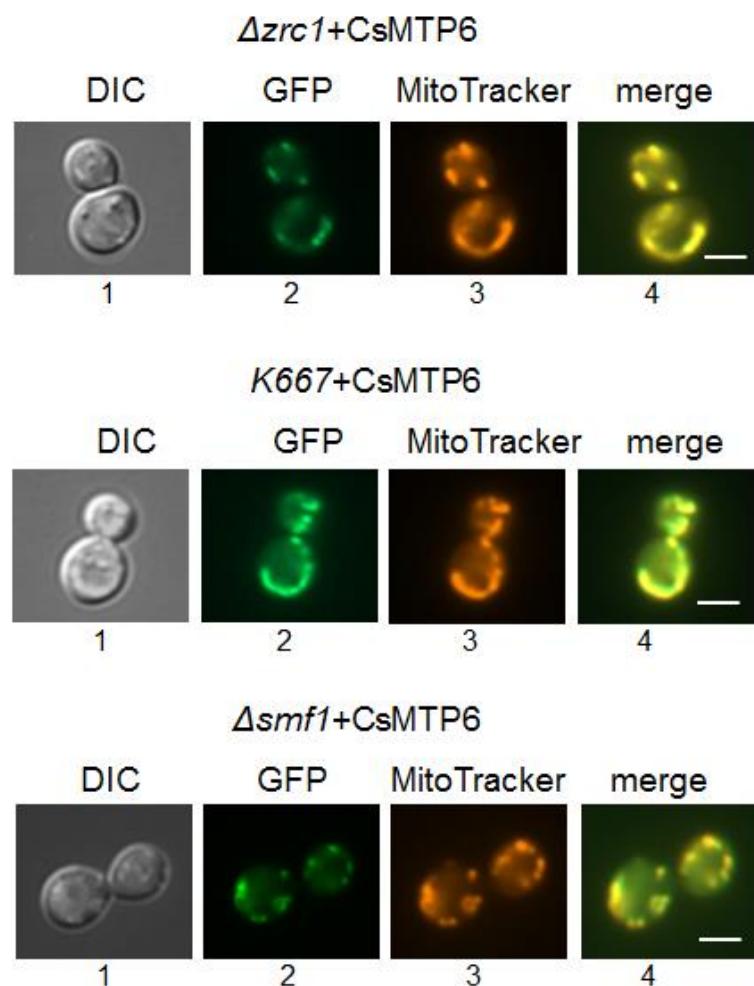


Figure S5

Effect of *CsMTP6* expression on yeast sensitivity to Zn, Ni and Cd. (A) Representative of serial dilutions of WT and mutants transformed with empty vector or *CsMTP6* placed onto SC/Glu-Ura medium supplemented with 5 mM ZnSO₄ ($\Delta zrc1$), 3 mM NiCl₂ or 0.01 mM CdCl₂ (K667) or control SC/Glu-Ura medium ($n=4$); (B) Mitochondrial content of Zn, Ni and Cd in yeast expressing *CsMTP6*. The data are expressed as the mean metal level (nmol/mg protein) \pm S.D. of three separate experiments.

