## His-MaAPX1 GST-MaMsrB2



Figure S1 SDS-PAGE of expressed recombinant His-APX1 protein and GSTMaMsrB2 from E. coli BL21. "Before" and "After" referred to before and after protein purification.


Figure S2 Expression of MaAPX1 and MaMsrB2 genes of banana fruit stored under air (control) or $60 \%$ oxygen at $25^{\circ} \mathrm{C}$. (A, C) control fruit. (B, D) fruit stored under $60 \%$ oxygen. The expression levels were expressed as a ratio relative to that of 0 d for control fruit, which was set as 1 . Each value represents the mean $\pm \mathrm{SE}$ of three biological replicates. Different letters indicated statistically significant differences between the samples (Student's t test; $\mathrm{P}<0.05$ ).


Figure S3 Multiple alignment of MaAPX1 with AtAPX1 (Arabidopsis thaliana, NP_001030991.2), SIAPX2 (Solanum lycopersicum, NP_001318094.1), OsAPX2 (Oryza sativa, XP_015646556.1), AcAPX (Ananas comosus, XP_020108209.1), ZaAPX (Zantedeschia aethiopica, AAC08576.1). \#: heme binding site; *: substrate
binding site; $\bullet: \mathrm{K}^{+}$binding site).


Figure S4 Phylogenetic alignment of MaMsrB1 and MaMsrB2 with MsrBs from Arabidopsis thaliana, Capsicum annuum, Carica papaya, Medicago truncatula, Oropetium thomaeum, Oryza sativa, Populus trichocarpa, Ricinus communis and Zea mays.

| AtMsrB1 | NASSTR. .LTIIQSSEVSAR. . . . TRINYVSKINHSGEACRSLSKPRNLSLSVYSMGSS | 53 |
| :---: | :---: | :---: |
| AtMsrB2 | MAFNIITPGRVYSATSLTEVSTIKAAFVKPPIASPSRRNLLRESSSPLSE | 50 |
| RcMsrb |  | 0 |
| ZmMsrB | NAARCSIAASVVRTGSRDLSPSFSFIAAALPSARLRFVGAKVRGGGYTCRLRAVCAMGSA | 60 |
| NtmsrB2 | MGSQILKISPFASSSIENATPFLRFC्रAKTVVTISKTQFRSNSIVSSSGEVPL | 52 |
| CaMsrB2 | MIFHQCXAPET . .IIFSSTSLLRFHAKRNCG . . . . QFRHLGEVCSS . | 39 |
| MaMsrb1 |  | 0 |
| MaMsrB2 | MISRWK. . . . ILRISR. . . . . . . . . AVKFGSHRRRR. . . . . . . . . . . . . . SSAFAMGSS | 31 |
| AtMsrB1 | . SSSPKPD . . . NVQEAEKNEEASLSENEWKKRITEECYYITRCKGTERAFTGEYWNSKT | 108 |
| AtMsrB2 | PSLRRGFHGGRIVAMGSSAPESUNKPEEEDFAIISEECFRILRCKGTEYPGIGEYNKVFD | 110 |
| RcMsrb | MAAA . GSIQKSEGEWRAILSEECFHILEEKGTERKFTGEYDKFFG | 44 |
| ZmMsrB | PSSSQSPSPHTPSGQTQGKADYKSLSEDEWKKRITEECYYVTEQKGTERAFTGEYWNTKT | 120 |
| NtmsrB2 | SNNKRGLSGG.VVAMASATGGSVQKSEDEDRRAILSEECRRILRCKGTEYPGTGEYDKFYG | 111 |
| CaMsrb2 | .KRRFRGG. IIANATP . .GSVHKSEDEWRAILSEECFRILEQKGMEYPGTGEYDKESG | 93 |
| MaMsrB1 | NASS . . GFVQKSEEDWWCAILSEECRFILESKGTEYPGTGCYDKFEA | 44 |
| MaMsrB2 | .SSSQRPD. . . .CQVQEFANVNFASLSDEERKKQITEECYYITEQKGTERAFIGEYWNTKT | 86 |
| AtMsrb1 |  | 168 |
| AtMsrB2 | DGIYCOAGCGTPIYKSTIKEDSGCGWEAFFDGLPGAITRTRDP. . DGREIEIITAACGG | 167 |
| Remsrb | EGIYNCAGOETPLYKSTTKEDSGCGWEAFFEGLPGAINRSEDP . . DGEETEITCVACGG | 101 |
| ZmMsrB | FGIYCQVCODTPLFCSSTKEDSGTGWESYYKPIGEENVKSKLDMSIIFMEETEVICATCDA | 180 |
| NtmsrB2 | EGIYCOAGCGTPIYKSTTKENSGCGWEAFFEGLPGAINRTADP. . DGEEIEITCAACGG | 168 |
| CaMsrb2 | YCOAGOGTPIYNSTTKENSCCGWEAFFEGLPGAINRTPDP . . . DGREISITTCAPCGG | 150 |
| MaMsrB1 | DGIYEOAGCGTPIYKSTTKENSGCGWEAFFEGLPGAINRTPDP. . DGREISIITCAACGG | 1 |
| MaMsrib2 | FGTYHCICODTPIFESNTKEDSGTGWESYYEPIGNNVKSKLDMSIIFMEETEVICAACDA | 146 |
| AtMsrB1 | HLGEVEDDG . PRFTIGKEYCLNSAALKINALEKTRD | 202 |
| AtMsrb2 | GLGEVEKGEGFPTPTDEEHCVNSISLKFTPENPTL | 202 |
| RcMsrb | ELGEVEKGEGHKTPIDESHCYNSVSIKSIGEINCXVREMAEN | 142 |
| ZmMsrB | GLGEVEDDG. . PEPTGKEYCINSASLKLKPQ | 209 |
| NtmsrB2 | GLGEVEKGEGFPTPIDESHCVNSISLKEAFANS | 201 |
| CaMsrB2 | ELGEVEKGEGFENPTNEEHCYNSISLKETEANS | 183 |
| MaMsrB1 | ELGEVEKGEGENTPTDEER WNSISLKEVEASQS | 134 |
| MaMsrib2 | GLGEVEDDG. .PEPTGKEYCHNSASLKLKPK | 175 |

Figure S5 Multiple alignment of MaMsrB1 and MaMsrB2 with AtMsrB1, AtMsrB2, RcMsrB, ZmMsrB, NtMsrB2 and CaMsrB2. The conserved recycling motifs (B), conserved catalytic domain (D) and the zinc fixation motifs (A and C) are indicated by black lines.

Table S1 Summary of primers used in this study.

| Gene | Forward(5'-3') | Reverse( $\mathbf{5}^{\prime}-3^{\prime}$ ) |
| :---: | :---: | :---: |
| For full length cloning |  |  |
| MaAPX1 | ATGGCGAAGTCGTATCCGACGG | TTAAGCCTCAGCAAATCCGAGTT |
|  | TGAGTG | CTGA |
| MaMsrB2 | ATGATCAGTCGATGGAAAATCC | CTACTTCGGCTTCAGCTTTAGGG |
|  | TCCGC | ATGC |
| For qRT-PCR in banana |  |  |
| MaAPX1 | GGGCTCAACATCGCTGTCAGGC | GGCACCTTCCCAGTGTGTGTCCA |
|  | TCTT | CCA |
| MaMsrB2 | TCTTTGTGCTGCCTGCGAT | CAGATGTCCGATAGATTTTGTC |
| MaActin | TGGTATGGAAGCCGCTGGTA | TCTGCTGGAATGTGCTGAGG |
| For qRT-PCR in Arabidopsis |  |  |
| MaAPXI | TCTTGTGGAGAAATATGCTGCC | TTGGGACAACTCCAGTGAAA |
| $A t U B Q$ | GATCTTTGCCGGAAAACAATTG | CGACTTGTCATTAGAAAGAAAG |
|  | GAGGATGG | AGATAACA |
| For overexpression in Arabidopsis |  |  |
| MaAPX1- | GGACTCTTGACCATGGTAATGG | GTCAGATCTACCATGGTAGCCTC |
| 1302 | CGAAGTCGTATCCGACGGTGA | AGCAAATCCGAGTTCT |
| For subcellular localization |  |  |
| MaAPX1- | GGACTCTTGACCATGGTAATGG | GTCAGATCTACCATGGTAGCCTC |
| GFP | CGAAGTCGTATCCGACGGTGA | AGCAAATCCGAGTTCT |
| MaMsrB2- | GGACTCTTGACCATGGTAATGA | GTCAGATCTACCATGGTCTACTT |
| GFP | TCAGTCGATGGAAAATCCTCCG | CGGCTTCAGCTTTAGGGATGC |
|  | C |  |
| For site-directed mutagenesis of Met residues to glutamine and valine |  |  |
| MaAPXIM | AACTGTGCCCCGTTGCAGCTCC | GAGCCGGAGCTGCAACGGGGCA |
| $36 Q$ | GGCTC | CAGTT |


| MaAPXIM | AACTGTGCCCCGTTGGTGCTCC | GAGCCGGAGCACCAACGGGGCA |
| :---: | :---: | :---: |
| 36 V | GGCTC | CAGTT |
| For BiFC |  |  |
| MaAPXI- | CGCGCCACTAGTGGATCCATGG | GGGAGCGGTACCCTCGAGAGCC |
| YC | CGAAGTCGTATCCGACGGTGAG | TCAGCAAATCCGAGTTCTGA |
|  | TG |  |
| MaAPXI- | CGCGCCACTAGTGGATCCATGG | GGGAGCGGTACCCTCGAGAGCC |
| $Y N$ | CGAAGTGGACTTGAAGAAGTCG | TCAGCAAATCCGAGTTCTGA |
|  | TG |  |
| MaMsrB2- | CGCGCCACTAGTGGATCCATGA | GGGAGCGGTACCCTCGAGCTTC |
| YC | TCAGTCGATGGAAAATCCTCCG | GGCTTCAGCTTTAGGGATGC |
|  | C |  |
| For Y2H |  |  |
| MaAPX1- | GAGGAGGACCTGCATATGGCGA | ACGGATCCCCGGGAATTCTTAA |
| $B D$ | AGTCGTATCCGACGGTGAGTG | GCCTCAGCAAATCCGAGTTCT |
| MaAPXI- | CCAGATTACGCTCATATGGCGA | CCCACCCGGGTGGAATTCTTAA |
| $A D$ | AGTCGTATCCGACGGTGAGTG | GCCTCAGCAAATCCGAGTTCT |
| MaMsrB2- | CCAGATTACGCTCATATGATGA | CCCACCCGGGTGGAATTCCTACT |
| $A D$ | TCAGTCGATGGAAAATCCTCCG | TCGGCTTCAGCTTTAGGGATGC |
|  | C |  |
| MaMsrB2- | GAGGAGGACCTGCATATGATGA | ACGGATCCCCGGGAATTCCTACT |
| BD | TCAGTCGATGGAAAATCCTCCG | TCGGCTTCAGCTTTAGGGATGC |
|  | C |  |
| For protein expression |  |  |
| MaAPXI- | CCGCGCGGCAGCCATATGGCGA | AGTCATGCTAGCCATATGTTAAG |
| His | AGTCGTATCCGACGGTGA | CCTCAGCAAATCCGAGTTCT |
| MaMsrB2- | CTGGTTCCGCGTGGATCCATGA | CCGGGAATTCGGGGATCCCTAC |
| GST | TCAGTCGATGGAAAATCCTCCG | TTCGGCTTCAGCTTTAGGGATGC |
|  | C |  |

