**Table S1.** Sm18 significant up and down-regulated genes from 0 µM to 8 µM of Mn(II) in minimal medium MOPS with 10µM of Iron. Cutoff: adjusted pvalue (padj) < 0.01 and $Log_2$ fold change ($Log_2FC$) ≥ 1 or ≤ -1.

| Locus id | Gene name | $Log_2FC$ | DE | padj | Gene description |
|---|---|---|---|---|---|
| V8P27_004008 | mntP | 3.4 | Up | $4.2\ e^{-61}$ | Manganese efflux pump |
| V8P27_003797 | V8P27_003797 | 2.0 | Up | $1.4\ e^{-08}$ | Copper chaperone SCO1/SenC |
| V8P27_003805 | V8P27_003805 | 1.8 | UP | $1.4\ e^{-08}$ | HTH-type transcriptional regulator |
| V8P27_003804 | V8P27_003804 | 1.7 | UP | $6.0\ e^{-03}$ | DUF6436 domain-containing protein |
| V8P27_002360 | mntH | 1.0 | Down | $2.0\ e^{-05}$ | Mn2+/Fe2+ uptake protein |

**Table S2.** Sm18 significant up and down-regulated genes from 0 µM to 8 µM of Mn(II) in minimal medium MOPS without Iron. Cutoff: adjusted pvalue (padj) < 0.01 and $Log_2$ fold change ($Log_2FC$) ≥ 1 or ≤ -1.

| Locus id | Gene name | $Log_2FC$ | DE | padj | Gene description |
|---|---|---|---|---|---|
| V8P27_004008 | mntP | 4.0 | Up | $2.2\ e^{-131}$ | Manganese efflux pump |
| V8P27_001285 | V8P27_001285 | 2.2 | Up | $4.0\ e^{-04}$ | TonB-dependent receptor |
| V8P27_004004 | V8P27_004004 | 1.3 | Up | $1.8\ e^{-20}$ | Major Facilitator Superfamily transporter |
| V8P27_004005 | V8P27_004005 | 1.3 | Up | $4.8\ e^{-11}$ | DcaP outer membrane protein |
| V8P27_001286 | V8P27_001286 | 1.2 | Up | $3.7\ e^{-04}$ | MerC domain-containing protein |
| V8P27_000822 | prpE | 1.0 | Up | $1.3\ e^{-09}$ | propionate-CoA ligase |
| V8P27_002357 | V8P27_002357 | 4.6 | Down | $8.5e^{-122}$ | TonB-dependent receptor |
| V8P27_002358 | V8P27_002358 | 2.8 | Down | $5.3\ e^{-03}$ | Thioredoxin-fold protein |
| V8P27_003990 | V8P27_003990 | 2.0 | Down | $1.0\ e^{-05}$ | MFP of RND efflux pump |
| V8P27_001267 | V8P27_001267 | 1.8 | Down | $6.5\ e^{-03}$ | Cation Diffusion Facilitator transporter |
| V8P27_002373 | V8P27_002373 | 1.5 | Down | $8.4\ e^{-09}$ | Small Multidrug Resistance transporter |
| V8P27_003991 | V8P27_003991 | 1.5 | Down | $1.8\ e^{-14}$ | RND efflux pump |
| V8P27_002360 | mntH | 1.5 | Down | $8.2\ e^{-15}$ | Mn2+/Fe2+ uptake protein |
| V8P27_003989 | V8P27_003989 | 1.4 | Down | $4.0\ e^{-04}$ | OMF of RND efflux pump |
| V8P27_001268 | nfi | 1.3 | Down | $3.6\ e^{-08}$ | Endonuclease V |
| V8P27_001249 | V8P27_001249 | 1.3 | Down | $7.1\ e^{-07}$ | Uncharacterized protein |
| V8P27_001248 | map | 1.2 | Down | $1.7\ e^{-12}$ | Type I methionyl aminopeptidase |

**Table S3.** Strains used and constructed in this study.

| Strain name | Key strain | Reference/source |
|---|---|---|
| DH5α | Standard *Escherichia coli* cloning strain. F− endA1 glnV44 thi-1 recA1 relA1 gyrA96 deoR nupG purB20 | Laboratory strain collection |
| S17.1 | Standard *Escherichia coli* conjugative donor strain. recA, thiE1, pro-82, endA, hadR17. RP4-2(Km::Tn7, Tc::Mu1) | (1) |
| Sm18 | *Stenotrophomonas maltophilia* strain Sm18. Environmental isolate from Cuernavaca, Morelos, México. | (2) |
| Neff | *Acanthamoeba castellanii* strain Neff. Environmental isolate from USA | ATCC 30010 |
| Sm18Δ02357 | Deletion mutant of the ORF 02357 from *Stenotrophomonas maltophilia* Strain Sm18 | This work |
| Sm18Δ02358 | Deletion mutant of the ORF 02358 from *Stenotrophomonas maltophilia* Strain Sm18 | This work |
| Sm18ΔmntH | Deletion mutant of the ORF mntH from *Stenotrophomonas maltophilia* Strain Sm18 | This work |
| Sm18ΔmntP | Deletion mutant of the ORF mntP from *Stenotrophomonas maltophilia* Strain Sm18 | This work |
| Sm18ΔmntR | Deletion mutant of the ORF mntR from *Stenothophomonas maltophilia* Strain Sm18 | This work |
| Sm18/332 | *Stenotrophomonas maltophilia* strain Sm18 transformed with the empty vector pSEVA332 | This work |
| Sm18ΔmntH/332 | Sm18ΔmntH deletion mutant transformed with the empty vector pSEVA332 | This work |
| Sm18ΔmntH/332::*mntH* | Sm18ΔmntH deletion mutant transformed with the vector pSEVA332::mntH | This work |
| Sm18ΔmntP/332 | Sm18ΔmntP deletion mutant transformed with the empty vector pSEVA332 | This work |
| Sm18ΔmntP/332::*mntP* | Sm18ΔmntP deletion mutant transformed with the vector pSEVA332::mntP | This work |
| Sm18::mTn7TC1_Pc_mScarlet-I | *Stenotrophomonas maltophilia* strain Sm18 derivative tagged with mScarlet-I expressed from the strong constitutive Pc promoter. | (3) |
| Sm18Δ02357::mTn7TC1_Pc_mScarlet-I | Derivative of the Sm18Δ02357 deletion mutant, tagged with mScarlet-I and expressed under the strong constitutive Pc promoter | This work |
| Sm18Δ02358::mTn7TC1_Pc_mScarlet-I | Derivative of the Sm18Δ02358 deletion mutant, tagged with mScarlet-I and expressed under the strong constitutive Pc promoter | This work |
| Sm18ΔmntH::mTn7TC1_Pc_mScarlet-I | Derivative of the Sm18ΔmntH deletion mutant, tagged with mScarlet-I and expressed under the | This work |

| | | |
|---|---|---|
| | strong constitutive Pc promoter | |
| Sm18ΔmntP::mTn7TC1_Pc_mScarlet-I | Derivative of the Sm18ΔmntP deletion mutant, tagged with mScarlet-I and expressed under the strong constitutive Pc promoter | This work |
| Sm18ΔmntR::mTn7TC1_Pc_mScarlet-I | Derivative of the Sm18ΔmntR deletion mutant, tagged with mScarlet-I and expressed under the strong constitutive Pc promoter | This work |
| Sm18VIM02357 | Interrupted mutant of the ORF 02357 from *Stenotrophomonas maltophilia* Strain Sm18 | This work |
| Sm18VIMmntH | Interrupted mutant of the ORF mntH from *Stenotrophomonas maltophilia* Strain Sm18 | This work |
| Sm18VIMmntP | Interrupted mutant of the ORF mntP from *Stenotrophomonas maltophilia* Strain Sm18 | This work |
| Sm18VIMmntH::mTn7TC1_Pc_mScarlet-I | Derivative of the Sm18VIMmntH interrupted mutant, tagged with mScarlet-I and expressed under the strong constitutive Pc promoter | This work |
| Sm18/327 | *Stenotrophomonas maltophilia* strain Sm18 transformed with the empty expression vector pSEVA327 | This work |
| Sm18/327-pr_*02357-02358* | *Stenotrophomonas maltophilia* strain Sm18 transformed with the expression vector pSEVA327-pr_*02357-02358* | This work |
| Sm18/327-pr_*mntH* | *Stenotrophomonas maltophilia* strain Sm18 transformed with the expression vector pSEVA327-pr_*mntH* | This work |
| Sm18/327-pr_*mntP* | *Stenotrophomonas maltophilia* strain Sm18 transformed with the expression vector pSEVA327-pr_*mntP* | This work |
| Sm18/337R | *Stenotrophomonas maltophilia* strain Sm18 transformed with the empty expression vector pSEVA337R | This work |
| Sm18/337R-pr_*02357-02358* | *Stenotrophomonas maltophilia* strain Sm18 transformed with the expression vector pSEVA337R-pr_*02357-02358* | This work |
| Sm18/337R-pr_*mntH* | *Stenotrophomonas maltophilia* strain Sm18 transformed with the expression vector pSEVA337R-pr_*mntH* | This work |
| Sm18/337R-pr_*mntP* | *Stenotrophomonas maltophilia* strain Sm18 transformed with the expression vector pSEVA337R-pr_*mntP* | This work |
| Sm18ΔmntR/327 | Derivative of the Sm18ΔmntR deletion mutant transformed with the empty expression vector pSEVA327 | This work |
| Sm18ΔmntR/327-pr_*02357-02358* | Derivative of the Sm18ΔmntR deletion mutant transformed with the expression vector pSEVA327- | This work |

| | | |
|---|---|---|
| | pr_*02357-02358* | |
| Sm18ΔmntR/327-pr_*mntH* | Derivative of the Sm18ΔmntR deletion mutant transformed with the expression vector pSEVA327-pr_*mntH* | This work |
| Sm18ΔmntR/327-pr_*mntP* | Derivative of the Sm18ΔmntR deletion mutant transformed with the expression vector pSEVA327-pr_*mntP* | This work |

**Table S4:** Vectors used and constructed in this study,

| **Plasmid name** | **Plasmid features** | **Reference/source** |
|---|---|---|
| pUC18T_mTn7TC1_Pc_mScarlet-I | pUC18T_mTn7TC1_Pr_mScarlet-I derivative for chromosomal labeling of bacteria with constitutive mScarlet-I expression driven from the strong Pc promoter; 5,893 bp. | (3) |
| pTNS2 | R6K-based plasmid (ApR) encoding the TnsABCD Tn7 transposase expression genes; 9,615 bp. | AddGene #64968 |
| pEX18Tc | Transmisible plasmid containing OriT, for site-targeted mutagenesis in Gram negative bacteria; 6349 bp. | (4) |
| Sm18Δ02357_pEX18Tc | pEX18Tc derivative with homologous DNA genetic fragments flanking the ORF *02357* of Sm18; 7424 bp. | This work |
| Sm18Δ02358_pEX18Tc | pEX18Tc derivative with homologous DNA genetic fragments flanking the ORF *02358* of Sm18; 7343 bp. | This work |
| Sm18ΔmntH_pEX18Tc | pEX18Tc derivative with homologous DNA genetic fragments flanking the ORF *mntH* of Sm18; 7424 bp. | This work |
| Sm18ΔmntP_pEX18Tc | pEX18Tc derivative with homologous DNA genetic fragments flanking the ORF *mntP* of Sm18; 7375 bp. | This work |
| Sm18ΔmntR_pEX18Tc | pEX18Tc derivative with homologous DNA genetic fragments flanking the ORF *mntR* of Sm18; 7340 bp. | This work |
| pEX18TcΔSacB7_PEM7 | pEx18Tc derivative with expression of GFP under control of constitutive promoter PEM7 and deletion of the gen SacB; 6031 pb. | Laboratory constructions collection |
| Sm18VIM02357_pEX18TcΔSacB7_PEM7 | pEX18TcΔSacB7_PEM7 derivative with homologous fragment of the ORF *02357* of Sm18; 6404 bp. | This work |
| Sm18VIMmntH_pEX18TcΔSacB7_PEM7 | pEX18TcΔSacB7_PEM7 derivative with homologous fragment of the ORF *mntH* of Sm18; 6380 bp. | This work |
| Sm18VIMmntP_pEX18TcΔSacB7_PEM7 | pEX18TcΔSacB7_PEM7 derivative with homologous fragment of the ORF *mntP* of Sm18; 6360 bp. | This work |
| pSEVA332 | Empty vector (chloramphenicol resistance , ori pBBR1, cargo lacZα-pUC19); 3417 bp. | (5) |

| | | |
|---|---|---|
| pSEVA332::*mntH* | pSEVA332 digested with PacI and SpeI to remplace the lacZα-pUC19 cargo with mntH gene; 4452 bp. | This work |
| pSEVA332::*mntP* | pSEVA332 digested with PacI and SpeI to remplace the lacZα-pUC19 with mntP gene; 4077 bp. | This work |
| pSEVA327 | Empty expression vector (chloramphenicol resistance, ori RK2, cargo GFP); 4408 bp. | (5) |
| pSEVA327-pr_*02357-02358* | pSEVA327 containing the promoter region of the ORF 02357-02358; 4796 bp. | This work |
| pSEVA327-pr_*mntH* | pSEVA327 containing the promoter region of the ORF mntH; 4721 bp. | This work |
| pSEVA327-pr_*mntP* | pSEVA327 containing the promoter region of the ORF mntP; 4976 bp. | This work |
| pSEVA337R | Empty expression vector (chloramphenicol resistance, ori pBBR1, cargo mCherry); 3661 bp. | (5) |
| pSEVA337R-pr_*02357-02358* | pSEVA337R containing the promoter region of the ORF 02357-02358; 4049 bp. | This work |
| pSEVA337R-pr_*mntH* | pSEVA337R containing the promoter region of the ORF mntH; 3974 bp. | This work |
| pSEVA337R-pr_*mntP* | pSEVA337R containing the promoter region of the ORF mntP; 4229 bp. | This work |

**Table S5:** Primers synthesized in this study for constructing vectors.

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| **Primer name** | **Primer sequence (5’ to 3’)** | **Restriction sites** | **Reference/source** |
|---|---|---|---|
| Sm18_D02361_Fragment1.F | cgttgtaaaacgacggccagtgccatgtttggccagagc | None | This work |
| Sm18_D02361_Fragment1.R | tcgcagtgcttcacatgaaggcgtcgtcct | None | This work |
| Sm18_D02361_Fragment2.F | gacgccttcatgtgaagcactgcgagcgc | None | This work |
| Sm18_D02361_Fragment2.R | tctagagtcgacctgcaggcatgcatttcgcgcgaccc | None | This work |
| Sm18_D02362_Fragment1.F | tgtaaaacgacggccagtgccaaaaccaacctcggctgg | None | This work |
| Sm18_D02362_Fragment1.R | cgcgaccctaccaacagcgctcgcagt | None | This work |
| Sm18_D02362_Fragment2.F | gagcgctgttggtagggtcgcgcgaa | None | This work |
| Sm18_D02362_Fragment2.R | agagtcgacctgcaggcatgcatcgctgaaaagcacccccctt | None | This work |
| Sm18_DmntH_amp1. | taaaacgacggccagtgccagcgcacgaacgcttcgaaca | None | This work |

| | | | |
|---|---|---|---|
| FOR | agg | | |
| Sm18_DmntH_amp1.REV | gcatcaccccatggggccgaatatagctcc | None | This work |
| Sm18_DmntH_amp2.FOR | gccccatggggtgatgccagatccaggg | None | This work |
| Sm18_DmntH_amp2.REV | ggaaacagctatgaccatgattacgtacttccgcagcgactatccgcc | None | This work |
| Sm18DmntP_PCR1.FOR | cgttgtaaaacgacggccagtgccacgcttacgacctcaacgtct | None | This work |
| Sm18DmntP_PCR1.REV | cgcggaagcgttaaatgggggacatggacagc | None | This work |
| Sm18DmntP_PCR2.FOR | atgtcccccatttaacgcttccgcgattacgt | None | This work |
| Sm18DmntP_PCR2.REV | ggaaacagctatgaccatgattacgcgatgttctcgatcattctgccg | None | This work |
| Sm18_DmntR_Fragment1.F | tgtaaaacgacggccagtgccaaacagcgctcgctgcgaccga | None | This work |
| Sm18_DmntR_Fragment1.R | gcgcaggcgtgtagcggtggcgccgg | None | This work |
| Sm18_DmntR_Fragment2.F | cgccaccgctacacgcctgcgcctg | None | This work |
| Sm18_DmntR_Fragment2.R | agagtcgacctgcaggcatgcaatcacttcggccaggtcgcaggcgatgatcgc | None | This work |
| Sm18_VIM_02361.F | aaaaaGAATTCcacacccctcttccatcgg | EcoRI | This work |
| Sm18_VIM_02361.R | aaaAAGCTTcttgaccacttcgatgcgg | HindIII | This work |
| Sm18-VIM-mntH.F | aaaaAAGCTTctacatgatctcggtcggct | HindIII | This work |
| Sm18-VIM-mntH.R | aaaaGGATCCgaagatcaccatcagcagcg | BamHI | This work |
| Sm18-VIM-mntp.F1 | aaaaAAGCTTccccatttcgatcctcctga | HindIII | This work |
| Sm18-VIM-mntP.R1 | aaaaGGATCCcgccgatatgcacatccatg | BamHI | This work |
| Sm18_mntHcompl.f | aaaaTTAATTAAtagtcctccaccagctccatc | PacI | This work |
| Sm18_mntHcompl.R | aaaaACTAGTaaggcatccacgcatggcg | SpeI | This work |
| Sm18_mntPcompl.F1 | aaaaTTAATTAAgcttacgacctcaacgtc | PacI | This work |
| Sm18_mntPcompl.R | aaaaACTAGTatcgcgtgctgaccaagcc | SpeI | This work |
| Sm18_pr_02357.F | aaaaaGAATTCtaccgcaaccatggagcc | EcoRI | This work |
| Sm18_pr_02357.R | aaaAAGCTTctgactttcacctgcacgc | HindIII | This work |
| Sm18-pr-mntH-p3.f | atatGGATCCtagtcctccaccagctccatc | BamHI | This work |

| | | | |
|---|---|---|---|
| Sm18-pr-mntH-p3.R | atatAAGCTTaaccaccagtgacccttgtcg | HindIII | This work |
| Sm18-pr-mntP.F1 | atataGAATTCgcttacgacctcaacgtc | EcoRI | This work |
| Sm18-pr-mntP.R1 | atatGGATCCgatcaggaggatcgaaatg | BamHI | This work |

**TABLE S6:** Primers used and synthesized in this study for verifying constructions or mutants.

| Primer name | Primer sequence (5' to 3') | Mutant/Constructions | Reference /source |
|---|---|---|---|
| F24 | cgccagggttttcccagtcacgac | Forward primer for confirming constructs or merodiploids strains in plasmids pEXTc18 and constructs in pEXTc18ΔSacB7_PEM7 | (6) |
| R24 | agcggataacaatttcacacagga | Reverse primer for confirming constructs in plasmids pEXTc18, insertional mutations in pEXTc18ΔSacB7_PEM7 and Forward primer for confirming transcriptional fusions in pSEVA327 and pSEVA 337R | (6) |
| pBBR1_VER.F | cggccatcgtccacatatcc | Forward primer for confirming constructs in plasmid pSEVA332 | This work |
| Sm18_D02361_VER.F | atgttctgatcccgctttcg | Forward primer for confirming deletion mutant Sm18Δ02357 | This work |
| Sm18_D02361_VER.R | tgacgtacaccacttcggtatc | Reverse primer for confirming deletion mutant Sm18Δ02357 | This work |
| Sm18_D02362_VER.F | gctcgtggtacgtcaacctg | Forward primer for confirming deletion mutant Sm18Δ02358 | This work |
| Sm18_D02362_VER.R | gtcgagctgatctcggacct | Reverse primer for confirming deletion mutant Sm18Δ02358 | This work |
| Sm18_DmntH_VER.F | catagtcctccaccagctcc | Forward primer for confirming deletion mutant Sm18ΔmntH | This work |
| Sm18_DmntH_VER.R | tgaggcgttcttcagggag | Reverse primer for confirming deletion mutant Sm18ΔmntH | This work |
| Sm18_DmntP_VER.F | gctatacaaaccagccctgc | Forward primer for confirming deletion mutant Sm18ΔmntP | This work |
| Sm18_DmntP_VER.R | tggatcaggcgttggagaaa | Reverse primer for confirming deletion mutant Sm18ΔmntP | This work |
| Sm18_DmntR_VER.F | agcctggatgagagcgagag | Forward primer for confirming deletion mutant Sm18ΔmntR | This work |
| Sm18_DmntR_VER.R | ttcatggggccgaatatagc | Reverse primer for confirming deletion mutant Sm18ΔmntR | This work |
| Sm18_M02362_VER.R | tccaggctgacgtacaccac | Reverse primer for confirming | This work |

| | | | |
|---|---|---|---|
| | | merodiploids Sm18::pEX18Tc-02358 | |
| Sm18_MmntR_VER.R | agaccgtggagcgattcct | Reverse primer for confirming merodiploids Sm18::pEX18Tc-mntR | This work |
| Steno_glmS_down.F (Smal_glmS_down_1549F) | gacatgccggtggtggtgatcg | Forward primer for confirming insertion of pUC18T_mTn7TC1_Pc_mScarlet-I in Sm18 Strains | (3) |
| pTn7.R | cacagcataactggactgatttc | Reverse primer for confirming insertion of pUC18T_mTn7TC1_Pc_mScarlet-I in Sm18 Strains | (3) |

Note: Sm18::pEX18Tc-mntH merodiploid was confirm by F24 and Sm18_Pr_02361.R primers.

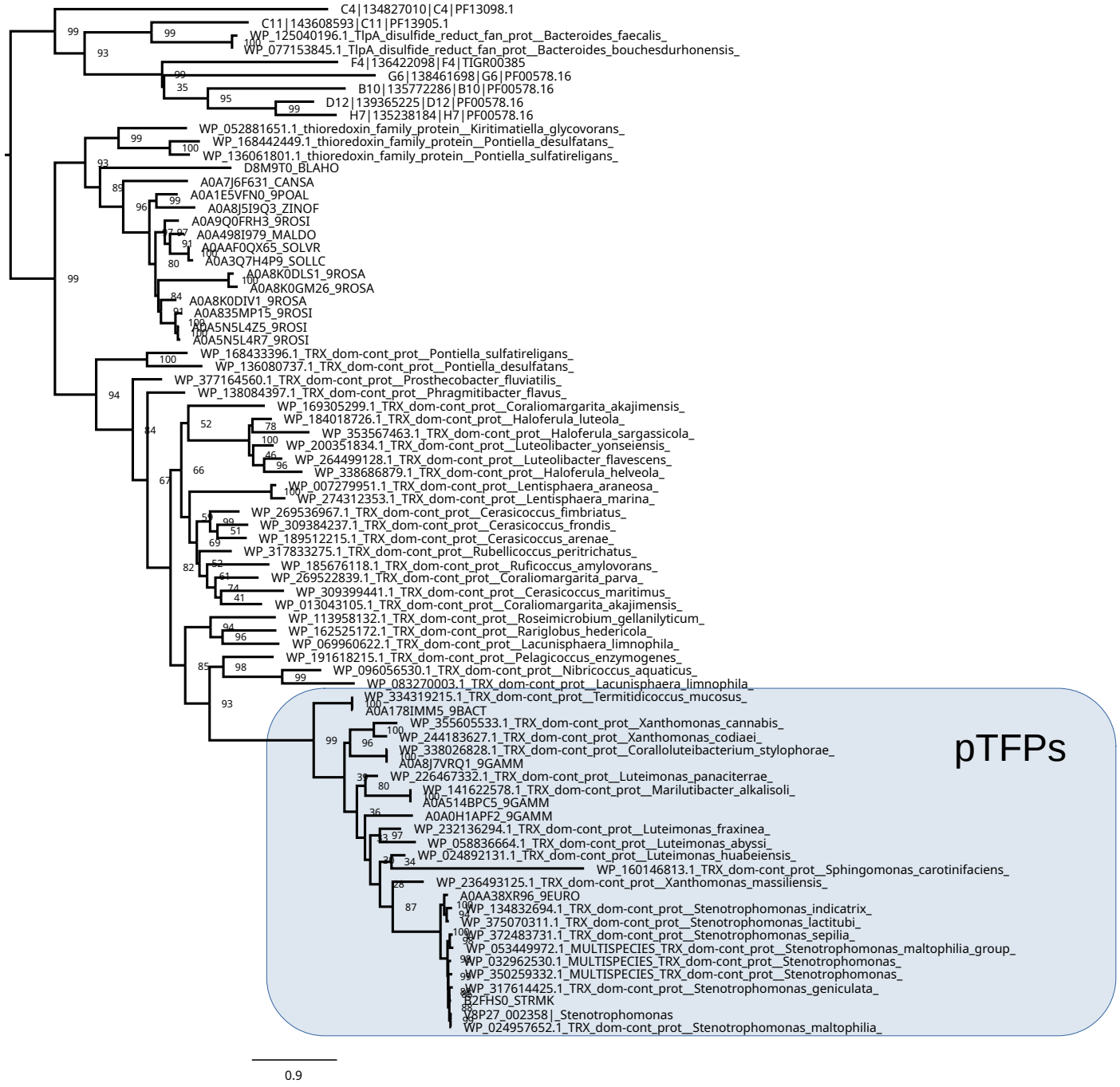


**FIG S1**. Maximum likelihood phylogeny estimated from 78 V8P27_002358 homologs collected from the NCBI RefSeq database (WP_ codes) via blastp, selected metagenomic sequences of thioredoxin superfamily proteins compiled by Nilewski et al. (7), and the UniProt Reference Proteomes v2025_01 identified by a hmmsearch through the HMMER portal using our pTFP.hmm profile HMM. A higly supported clade (box) groups V8P27_002358 with other bacterial sequences belonging to the orders Lysobacterales (Gammaproteobacteria), Sphingomonadales (Alphaproteobacteria), and Opitutales (Verrucomicrobiota; Opitutia). The scale bar represents the number of expected substitutions per site under the best-fitting Q.pfam+I+R4 model chosen according to the Bayesian Information criterion, as implemented in IQ-Tree. Internal nodes are labeled with bootstrap support values computed by IQ-Tree with UFBoot.

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