Table S1. The 197 clade VI homologous proteins used in this study and classified into subfamilies. Characterized proteins are indicated in red whereas previously positioned clade VI proteins (1) also analyzed in this study are in blue.

| **Subfamily/Inferred substrate** | **Uniprot ID** | **Class** | **Organism** | **strain** |
|---|---|---|---|---|
| **Mn/Fe** | **EmfA/ Q2K5P7** | **Alphaproteobacteria** | ***Rhizobium etli*** | **CFN 42 / ATCC 51251** |
| **Mn/Fe** | A0NZQ3 | Alphaproteobacteria | *Labrenzia aggregata* | IAM 12614 |
| **Mn/Fe** | A1B4W1 | Alphaproteobacteria | *Paracoccus denitrificans* | Pd 1222 |
| **Mn/Fe** | A1UTI8 | Alphaproteobacteria | *Bartonella bacilliformis* | ATCC 35685 / KC583 |
| **Mn/Fe** | A3K9T2 | Alphaproteobacteria | *Sagittula stellata* | E-37 |
| **Mn/Fe** | A3W839 | Alphaproteobacteria | *Roseovarius sp* | 217 |
| **Mn/Fe** | A4WV59 | Alphaproteobacteria | *Rhodobacter sphaeroides* | ATCC 17025 / ATH 2.4.3 |
| **Mn/Fe** | A4YX26 | Alphaproteobacteria | *Bradyrhizobium sp* | ORS278 |
| **Mn/Fe** | A5EHC5 | Alphaproteobacteria | *Bradyrhizobium sp* | BTAi1 / ATCC BAA-1182 |
| **Mn/Fe** | A6E3R4 | Alphaproteobacteria | *Roseovarius sp* | TM1035 |
| **Mn/Fe** | A6UBU6 | Alphaproteobacteria | *Sinorhizobium medicae* | WSM419 |
| **Mn/Fe** | A6WZB0 | Alphaproteobacteria | *Ochrobactrum anthropi* | ATCC 49188 / DSM 6882 / NCTC 12168 |
| **Mn/Fe** | A7IBB6 | Alphaproteobacteria | *Xanthobacter autotrophicus* | ATCC BAA-1158 / Py2 |
| **Mn/Fe** | A8HZA2 (AZC_4559) | Alphaproteobacteria | *Azorhizobium caulinodans* | ATCC 43989 / DSM 5975 / ORS 571 |
| **Mn/Fe** | A9CI36 (Atu2274) | Alphaproteobacteria | *Agrobacterium tumefaciens* | C58 / ATCC 33970 |
| **Mn/Fe** | A9D260 | Alphaproteobacteria | *Hoeflea phototrophica* | DFL-43 |
| **Mn/Fe** | A9IWG7 | Alphaproteobacteria | *Bartonella tribocorum* | CIP 105476 / IBS 506 |
| **Mn/Fe** | A9VWZ9 | Alphaproteobacteria | *Methylobacterium extorquens* | PA1 |
| **Mn/Fe** | B0U9V3 | Alphaproteobacteria | *Methylobacterium sp* | Apr-46 |
| **Mn/Fe** | B1M587 | Alphaproteobacteria | *Methylobacterium radiotolerans* | ATCC 27329 / DSM 1819 / JCM 2831 |
| **Mn/Fe** | B1ZIK8 | Alphaproteobacteria | *Methylobacterium populi* | ATCC BAA-705 / NCIMB 13946 / BJ001 |
| **Mn/Fe** | B5ZY96 | Alphaproteobacteria | *Rhizobium leguminosarum* | WSM2304 |
| **Mn/Fe** | B6BDT9 | Alphaproteobacteria | *Rhodobacterales bacterium* | Y4I |
| **Mn/Fe** | B6JF82 | Alphaproteobacteria | *Oligotropha carboxidovorans* | ATCC 49405 / DSM 1227 / OM5 [Mississippi] |
| **Mn/Fe** | B6R6C6 | Alphaproteobacteria | *Pseudovibrio sp* | JE062 |
| **Mn/Fe** | B8IE75 | Alphaproteobacteria | *Methylobacterium nodulans* | ORS2060 / LMG 21967 |
| **Mn/Fe** | B9J7E1 | Alphaproteobacteria | *Agrobacterium radiobacter* | K84 / ATCC BAA-868 |
| **Mn/Fe** | B9JZM7 | Alphaproteobacteria | *Agrobacterium vitis* | S4 / ATCC BAA-846 |
| **Mn/Fe** | B9KKK8 | Alphaproteobacteria | *Rhodobacter sphaeroides* | KD131 / KCTC 12085 |
| **Mn/Fe** | B9QTI5 | Alphaproteobacteria | *Labrenzia alexandrii* | DFL-11 |
| **Mn/Fe** | C3MFQ2 | Alphaproteobacteria | *Rhizobium sp* | NGR234 |
| **Mn/Fe** | C4WFI7 | Alphaproteobacteria | *Ochrobactrum intermedium* | LMG 3301 |
| **Mn/Fe** | C6AEM9 | Alphaproteobacteria | *Bartonella grahamii* | as4aup |
| **Mn/Fe** | C6AT60 | Alphaproteobacteria | *Rhizobium leguminosarum* | WSM1325 |
| **Mn/Fe** | C6XHS3 | Alphaproteobacteria | *Liberibacter asiaticus* | psy62 |
| **Mn/Fe** | C7CB67 | Alphaproteobacteria | *Methylobacterium extorquens* | DSM 5838 / DM4 |

| | | | | |
|---|---|---|---|---|
| **Mn/Fe** | C7JV95 | Alphaproteobacteria | *Acetobacter pasteurianus* | IFO 3283 |
| **Mn/Fe** | D0CZP4 | Alphaproteobacteria | *Citreicella sp* | SE45 |
| **Mn/Fe** | D1FA77 | Alphaproteobacteria | *Brucella melitensis* | Ether |
| **Mn/Fe** | D5RLA9 | Alphaproteobacteria | *Roseomonas cervicalis* | ATCC 49957 |
| **Mn/Fe** | D6V6J0 | Alphaproteobacteria | *Afipia sp* | 1NLS2 |
| **Mn/Fe** | D7A6P8 | Alphaproteobacteria | *Starkeya novella* | ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB |
| **Mn/Fe** | D8JQY2 | Alphaproteobacteria | *Hyphomicrobium denitrificans* | ATCC 51888 / DSM 1869 / NCIB 11706 / TK 0415 |
| **Mn/Fe** | E2CGY7 | Alphaproteobacteria | *Roseibium sp* | TrichSKD4 |
| **Mn/Fe** | E3I587 | Alphaproteobacteria | *Rhodomicrobium vannielii* | ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299 |
| **Mn/Fe** | E4UCZ4 | Alphaproteobacteria | *Liberibacter solanacearum* | CLso-ZC1 |
| **Mn/Fe** | E6YKK1 | Alphaproteobacteria | *Bartonella rochalimae* | ATCC BAA-1498 |
| **Mn/Fe** | E6YUA6 | Alphaproteobacteria | *Bartonella sp* | 1-1C |
| **Mn/Fe** | E6Z0E2 | Alphaproteobacteria | *Bartonella schoenbuchensis* | R1 |
| **Mn/Fe** | E8THZ3 | Alphaproteobacteria | *Mesorhizobium ciceri* | HAMBI 2942 / LMG 23838 / WSM1271 |
| **Mn/Fe** | F1YVS4 | Alphaproteobacteria | *Acetobacter pomorum* | DM001 |
| **Mn/Fe** | F2A579 | Alphaproteobacteria | *Rhizobium etli* | CNPAF512 |
| **Mn/Fe** | F2J138 | Alphaproteobacteria | *Polymorphum gilvum* | LMG 25793 / CGMCC 1.9160 / SL003B-26A1 |
| **Mn/Fe** | F3SAH8 | Alphaproteobacteria | *Gluconacetobacter sp* | SXCC-1 |
| **Mn/Fe** | F5M3M6 | Alphaproteobacteria | *Rhodobacter sphaeroides* | WS8N |
| **Mn/Fe** | F6BML1 | Alphaproteobacteria | *Sinorhizobium meliloti* | BL225C |
| **Mn/Fe** | F7U7E2 | Alphaproteobacteria | *Agrobacterium tumefaciens* | F2 |
| **Mn/Fe** | F7VDX2 | Alphaproteobacteria | *Acetobacter tropicalis* | NBRC 101654 |
| **Mn/Fe** | F7YD96 | Alphaproteobacteria | *Mesorhizobium opportunistum* | LMG 24607 / HAMBI 3007 / WSM2075 |
| **Mn/Fe** | F8BR14 | Alphaproteobacteria | *Oligotropha carboxidovorans* | OM4 |
| **Mn/Fe** | F8JBF2 | Alphaproteobacteria | *Hyphomicrobium sp* | MC1 |
| **Mn/Fe** | G2I1N8 | Alphaproteobacteria | *Gluconacetobacter xylinus* | NBRC 3288 / BCRC 11682 / LMG 1693 |
| **Mn/Fe** | G4RA17 | Alphaproteobacteria | *Pelagibacterium halotolerans* | JCM 15775 / CGMCC 1.7692 / B2 |
| **Mn/Fe** | G6XFQ7 | Alphaproteobacteria | *Gluconobacter morbifer* | G707 |
| **Mn/Fe** | G6XR70 | Alphaproteobacteria | *Agrobacterium tumefaciens* | CCNWGS0286 |
| **Mn/Fe** | G6YDA7 | Alphaproteobacteria | *Mesorhizobium amorphae* | CCNWGS0123 |
| **Mn/Fe** | G8PIC9 | Alphaproteobacteria | *Pseudovibrio sp* | FO-BEG1 |
| **Mn/Fe** | G9A8Y6 | Alphaproteobacteria | *Rhizobium fredii* | HH103 |
| **Mn/Fe** | H0A3M0 | Alphaproteobacteria | *Acetobacteraceae bacterium* | |
| **Mn/Fe** | G4JXY2 | Alphaproteobacteria | *Mesorhizobium australicum* | WSM2073 |
| **Mn/Fe** | B5K1A4 | Alphaproteobacteria | *Octadecabacter arcticus* | 238 |
| **Mn/Fe** | H0G7M5 | Alphaproteobacteria | *Sinorhizobium meliloti* | CCNWSX0020 |
| **Mn/Fe** | H0H7S7 | Alphaproteobacteria | *Agrobacterium tumefaciens* | 5A |
| **Mn/Fe** | H0HP27 | Alphaproteobacteria | *Mesorhizobium alhagi* | CCNWXJ12-2 |
| **Mn/Fe** | H0RRQ5 | Alphaproteobacteria | *Bradyrhizobium sp* | ORS285 |
| **Mn/Fe** | H0SE15 | Alphaproteobacteria | *Bradyrhizobium sp* | ORS375 |

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|---|---|---|---|---|
| **Mn/Fe** | H0SXW1 | Alphaproteobacteria | *Bradyrhizobium sp* | STM 3809 |
| **Mn/Fe** | H1KMJ8 | Alphaproteobacteria | *Methylobacterium extorquens* | DSM 13060 |
| **Mn/Fe** | H1UCZ4 | Alphaproteobacteria | *Acetobacter pasteurianus* | NBRC 101655 |
| **Mn/Fe** | H3PKM5 | Alphaproteobacteria | *Brucella abortus* | NI474 |
| **Mn/Fe** | H4F9S2 | Alphaproteobacteria | *Rhizobium sp* | PDO-076 |
| **Mn/Fe** | I1AXE9 | Alphaproteobacteria | *Citreicella sp* | 357 |
| **Mn/Fe** | Q0FNJ5 | Alphaproteobacteria | *Pelagibaca bermudensis* | HTCC2601 |
| **Mn/Fe** | Q0G7C9 | Alphaproteobacteria | *Fulvimarina pelagi* | HTCC2506 |
| **Mn/Fe** | Q11G85 | Alphaproteobacteria | *Mesorhizobium sp* | BNC1 |
| **Mn/Fe** | Q1GDT8 | Alphaproteobacteria | *Ruegeria sp* | TM1040 |
| **Mn/Fe** | A9EH73 | Alphaproteobacteria | *Phaeobacter gallaeciensis* | |
| **Mn/Fe** | A9G8Z1 | Alphaproteobacteria | *Phaeobacter inhibens* | DSM 17395 |
| **Mn/Fe** | Q1MDH1 (RL3518) | Alphaproteobacteria | *Rhizobium leguminosarum* | 3841 |
| **Mn/Fe** | Q1YLU0 | Alphaproteobacteria | *Manganese-oxidizing bacterium* | SI85-9A1 |
| **Mn/Fe** | Q3J0P9 | Alphaproteobacteria | *Rhodobacter sphaeroides* | ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158 |
| **Mn/Fe** | Q5FQH9 | Alphaproteobacteria | *Gluconobacter oxydans* | 621H |
| **Mn/Fe** | Q6FZ47 | Alphaproteobacteria | *Bartonella quintana* | Toulouse |
| **Mn/Fe** | Q6G2K0 | Alphaproteobacteria | *Bartonella henselae* | ATCC 49882 / Houston 1 |
| **Mn/Fe** | Q98HP4 (Mlr2775) | Alphaproteobacteria | *Rhizobium loti* | MAFF303099 |
| **Mn** | C1CV15 | Deinococci | *Deinococcus deserti* | VCD115 / DSM 17065 / LMG 22923 |
| **Mn** | F0RP81 | Deinococci | *Deinococcus proteolyticus* | ATCC 35074 / DSM 20540 / JCM 6276 / NBRC 101906 / NCIMB 13154 / |
| **Mn** | H8GUD6 | Deinococci | *Deinococcus gobiensis* | DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0 |
| **Mn** | Q1J015 | Deinococci | *Deinococcus geothermalis* | DSM 11300 |
| **Mn** | **DR1236/ Q9RUZ4** | **Deinococci** | ***Deinococcus radiodurans*** | **ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 /** |
| **Fe** | A5GT73 | Oscillatoriophycideae | *Synechococcus sp* | RCC307 |
| **Fe** | A9AZ82 | Herpetosiphonales | *Herpetosiphon aurantiacus* | ATCC 23779 / DSM 785 |
| **Fe** | **Sll1263** | **Oscillatoriophycideae** | ***Synechocystis sp*** | **PCC6803** |
| **Fe** | B0C2E2 | Oscillatoriophycideae | *Acaryochloris marina* | MBIC 11017 |
| **Fe** | B2J8N9 (NpF2455) | Nostocales | *Nostoc punctiforme* | ATCC 29133 / PCC 73102 |
| **Fe** | B8HUU0 | Oscillatoriophycideae | *Cyanothece sp* | PCC 7425 / ATCC 29141 |
| **Fe** | D6TSV4 | Ktedonobacteria | *Ktedonobacter racemifer* | |
| **Fe** | E0U5V3 | Oscillatoriophycideae | *Cyanothece sp* | PCC 7822 |
| **Fe** | Q1AS44 | Rubrobacteridae | *Rubrobacter xylanophilus* | DSM 9941 / NBRC 16129 |
| **Fe** | Q7NKM3 | Gloeobacteria | *Gloeobacter violaceus* | PCC 7421 |
| **Zn/Cd** | B7AAA3 | Deinococci | *Thermus aquaticus* | Y51MC23 |
| **Zn/Cd** | E8PP06 | Deinococci | *Thermus scotoductus* | ATCC 700910 / SA-01 |
| **Zn/Cd** | F2NP50 | Deinococci | *Marinithermus hydrothermalis* | DSM 14884 / JCM 11576 / T1 |
| **Zn/Cd** | F6DGV3 | Deinococci | *Thermus thermophilus* | SG0.5JP17-16 |
| **Zn/Cd** | G8N817 | Deinococci | *Thermus sp* | CCB_US3_UF1 |

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|---|---|---|---|---|
| **Zn/Cd** | H7GGE1 | Deinococci | *Thermus sp* | RL |
| **Zn/Cd** | H9ZRF8 | Deinococci | *Thermus thermophilus* | JL-18 |
| **Zn/Cd** | **TtczrB/ Q5SJG8** | **Deinococci** | ***Thermus thermophilus*** | **HB8 / ATCC 27634 / DSM 579** |
| **A** | A2SKL0 | Betaproteobacteria | *Methylibium petroleiphilum* | PM1 |
| **A** | B0RL54 | Gammaproteobacteria | *Yersinia enterocolitica* | 29854 |
| **A** | B3QNW2 | Chlorobia | *Chlorobaculum parvum* | NCIB 8327 |
| **A** | C7LNE2 | Deltaproteobacteria | *Desulfomicrobium baculatum* | DSM 4028 / VKM B-1378 |
| **A** | C7RIT4 | Betaproteobacteria | *Accumulibacter phosphatis* | UW-1 |
| **A** | D9SHT4 | Betaproteobacteria | *Gallionella capsiferriformans* | ES-2 |
| **A** | E6VT11 | Deltaproteobacteria | *Desulfovibrio aespoeensis* | ATCC 700646 / DSM 10631 / Aspo-2 |
| **A** | E8XX38 | Gammaproteobacteria | *Rahnella sp* | Y9602 |
| **A** | F0JBH2 | Deltaproteobacteria | *Desulfovibrio desulfuricans* | ND132 |
| **A** | F3LT58 | Betaproteobacteria | *Rubrivivax benzoatilyticus* | JA2 |
| **A** | F3YZL7 | Deltaproteobacteria | *Desulfovibrio africanus* | Walvis Bay |
| **A** | G8QHR9 | Betaproteobacteria | *Azospira oryzae* | ATCC BAA-33 / DSM 13638 / PS |
| **A** | H5SQF8 | environmental samples. | *uncultured candidate* | |
| **A** | Q3B2Y3 | Chlorobia | *Pelodictyon luteolum* | DSM 273 |
| **A** | Q3SJT3 | Betaproteobacteria | *Thiobacillus denitrificans* | ATCC 25259 |
| **A** | Q47H82 | Betaproteobacteria | *Dechloromonas aromatica* | RCB |
| **B** | C0W5D2 | Actinobacteridae | *Actinomyces urogenitalis* | DSM 15434 |
| **B** | C7M9T6 | Actinobacteridae | *Brachybacterium faecium* | ATCC 43885 / DSM 4810 / NCIB 9860 |
| **B** | D0WR67 | Actinobacteridae | *Actinomyces sp* | F0332 |
| **B** | D1YFD7 | Actinobacteridae | *Propionibacterium acnes* | J139 |
| **B** | D7BN07 | Actinobacteridae | *Arcanobacterium haemolyticum* | ATCC 9345 / DSM 20595 / NBRC 15585 / NCTC 8452 / 11018 |
| **B** | D7GIW1 | Actinobacteridae | *Propionibacterium freudenreichii* | ATCC 9614 / CIP 103027 / CIRM-BIA1 |
| **B** | E4AF09 | Actinobacteridae | *Propionibacterium acnes* | HL037PA3 |
| **B** | E4FDS0 | Actinobacteridae | *Propionibacterium acnes* | HL037PA1 |
| **B** | E4GKU9 | Actinobacteridae | *Propionibacterium acnes* | HL005PA2 |
| **B** | E4GPP1 | Actinobacteridae | *Propionibacterium acnes* | HL005PA1 |
| **B** | E4GVF9 | Actinobacteridae | *Propionibacterium acnes* | HL082PA2 |
| **B** | E4HN55 | Actinobacteridae | *Propionibacterium acnes* | HL044PA1 |
| **B** | E4HRB0 | Actinobacteridae | *Propionibacterium acnes* | HL001PA1 |
| **B** | E6CK80 | Actinobacteridae | *Propionibacterium acnes* | HL050PA2 |
| **B** | E6DLA8 | Actinobacteridae | *Propionibacterium acnes* | HL027PA2 |
| **B** | E6SC04 | Actinobacteridae | *Intrasporangium calvum* | ATCC 23552 / DSM 43043 / JCM 3097 / NBRC 12989 / 7 KIP |
| **B** | E7N613 | Actinobacteridae | *Actinomyces sp* | F0337 |
| **B** | F1UAZ0 | Actinobacteridae | *Propionibacterium acnes* | HL097PA1 |
| **B** | F2UXR4 | Actinobacteridae | *Actinomyces viscosus* | C505 |
| **B** | F3CLN5 | Actinobacteridae | *Propionibacterium acnes* | HL087PA1 |
| **B** | F9EC55 | Actinobacteridae | *Actinomyces sp* | F0400 |

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|---|---|---|---|---|
| **B** | F9NPQ2 | Actinobacteridae | *Propionibacterium acnes* | SK182 |
| **B** | F9PH34 | Actinobacteridae | *Actinomyces sp* | F0384 |
| **B** | G4CVM1 | Actinobacteridae | *Propionibacterium avidum* | ATCC 25577 |
| **B** | G8VA47 | Actinobacteridae | *Propionibacterium acnes* | P.acn33 |
| **B** | G8VHW9 | Actinobacteridae | *Propionibacterium acnes* | P.acn17 |
| **B** | G8VNN5 | Actinobacteridae | *Propionibacterium acnes* | P.acn31 |
| **B** | G9PPY2 | Actinobacteridae | *Actinomyces sp* | F0330 |
| **B** | H5UPC8 | Actinobacteridae | *Mobilicoccus pelagius* | NBRC 104925 |
| **B** | H7GA50 | Actinobacteridae | *Propionibacterium acnes* | PRP-38 |
| **B** | Q6A6E4 | Actinobacteridae | *Propionibacterium acnes* | KPA171202 / DSM 16379 |
| **UNASSIGNED** | A1THH9 | Actinobacteridae | *Mycobacterium vanbaalenii* | DSM 7251 / PYR-1 |
| **UNASSIGNED** | A5UTC5 | Chloroflexales | *Roseiflexus sp* | RS-1 |
| **UNASSIGNED** | A7HB38 | Deltaproteobacteria | *Anaeromyxobacter sp* | Fw109-5 |
| **UNASSIGNED** | A7NKY9 | Chloroflexales | *Roseiflexus castenholzii* | DSM 13941 / HLO8 |
| **UNASSIGNED** | B4UMH8 | Deltaproteobacteria | *Anaeromyxobacter sp* | K |
| **UNASSIGNED** | B8GCX3 | Chloroflexales | *Chloroflexus aggregans* | MD-66 / DSM 9485 |
| **UNASSIGNED** | B8J6L1 | Deltaproteobacteria | *Anaeromyxobacter dehalogenans* | 2CP-1 / ATCC BAA-258 |
| **UNASSIGNED** | B9LDY2 | Chloroflexales | *Chloroflexus aurantiacus* | ATCC 29364 / DSM 637 / Y-400-fl |
| **UNASSIGNED** | C0XT98 | Actinobacteridae | *Corynebacterium lipophiloflavum* | DSM 44291 |
| **UNASSIGNED** | D3F1P0 | Rubrobacteridae | *Conexibacter woesei* | DSM 14684 / JCM 11494 / NBRC 100937 / ID131577 |
| **UNASSIGNED** | D3PR58 | Deinococci | *Meiothermus ruber* | ATCC 35948 / DSM 1279 / VKM B-1258 / 21 |
| **UNASSIGNED** | D7BID2 | Deinococci | *Meiothermus silvanus* | ATCC 700542 / DSM 9946 / VI-R2 |
| **UNASSIGNED** | D7WFC3 | Actinobacteridae | *Corynebacterium genitalium* | ATCC 33030 |
| **UNASSIGNED** | E1IG37 | Chloroflexales | *Oscillochloris trichoides* | DG6 |
| **UNASSIGNED** | E1YHW0 | Deltaproteobacteria | *uncultured Desulfobacterium* | |
| **UNASSIGNED** | E2MWT7 | Actinobacteridae | *Corynebacterium amycolatum* | SK46 |
| **UNASSIGNED** | E4U6A6 | Deinococci | *Oceanithermus profundus* | DSM 14977 / NBRC 100410 / VKM B-2274 / 506 |
| **UNASSIGNED** | E6JAL1 | Actinobacteridae | *Dietzia cinnamea* | P4 |
| **UNASSIGNED** | E8U342 | Deinococci | *Deinococcus maricopensis* | DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34 |
| **UNASSIGNED** | E8UAK8 | Deinococci | *Deinococcus maricopensis* | DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34 |
| **UNASSIGNED** | F1YN71 | Actinobacteridae | *Gordonia neofelifaecis* | NRRL B-59395 |
| **UNASSIGNED** | F9ZXP1 | Gammaproteobacteria | *Methylomonas methanica* | MC09 |
| **UNASSIGNED** | G4STS3 | Gammaproteobacteria | *Methylomicrobium alcaliphilum* | DSM 19304 / NCIMB 14124 / VKM B-2133 / 20Z |
| **UNASSIGNED** | G7HZN6 | Actinobacteridae | *Corynebacterium casei* | UCMA 3821 |
| **UNASSIGNED** | H0JS82 | Actinobacteridae | *Rhodococcus pyridinivorans* | AK37 |
| **UNASSIGNED** | H5UJW2 | Actinobacteridae | *Gordonia terrae* | NBRC 100016 |
| **UNASSIGNED** | I0I6L2 | Caldilineae | *Caldilinea aerophila* | DSM 14535 / JCM 11387 / NBRC 104270 / STL-6-O1 |
| **UNASSIGNED** | Q2IJP6 | Deltaproteobacteria | *Anaeromyxobacter dehalogenans* | 2CP-C |
| **UNASSIGNED** | Q607F9 | Gammaproteobacteria | *Methylococcus capsulatus* | ATCC 33009 / NCIMB 11132 / Bath |

Table S2. Strains and plasmids used in this study

| Strain | Relevant feature (s) | Reference |
|---|---|---|
| *Rhizobium etli* | | |
| CFN42 | Wild type strain. Nal$^{r}$, Sm$^{r}$. | (2) |
| *emfA-* | CFN42 derivative *RHE_CH03072*::pCACM*emfA*. Nal$^{r}$, Sm$^{r}$, Gm$^{r}$. | This work |
| *emfA-/emfA* | *EmfA*- derivative complemented with pCAC*emfA*. Nal$^{r}$, Sm$^{r}$, Tc$^{r}$, Gm$^{r}$. | This work |
| *Escherichia coli* | | |
| DH5α | Host for recombinant plasmids, Nal$^{r}$, Sm$^{s}$, Tc$^{s}$. | Stratagene |
| MC4100 | | (3) |
| GG48 | *E. coli* W3110 derivative *zntA*:Km, Δ*zitB*:Cm | (4) |
| CC48 | *E. coli* W3110 derivative *zntA*:Km, Δ*zitB* | This work |
| CC49 | *E. coli* GG48 derivative *zntA*:Km, Δ*zitB*, Δ*mntP*:Cm | This work |
| Plasmids | | |
| pCR 2.1-TOPO | Cloning vector, Km$^{r}$. | Invitrogen |
| pRK2013 | Conjugation helper, Km$^{r}$. | (5) |
| pBBR-MCS3 | Cloning vector, Tc$^{r}$ | (6) |
| pPDGm | pSK+ derivative, Gm$^{r}$, *mob*, promoterless *gusA*. | (7) |
| pCACM*emfA* | pPDGm derivative containing a 300 pb internal fragment of *emnA* gene, Gm$^{r}$. | This work |
| pCACT*emfA* | pCR 2.1-TOPO derivative carrying full *RHE_CH03072* gene, Cb$^{r}$, Km$^{r}$. | This work |
| pCAC*emfA* | pBBR-MCS3 derivative containing full-length *emnA* gene from pCACT*emfA* as a *KpnI-XbaI* fragment, Tc$^{r}$. | This work |

Table S3. Oligonucleotides used in this study. Restriction sites are indicated in bold.

| Name | Sequence 5'-3' | Use | Gene | Source |
|---|---|---|---|---|
| A | CC**GAATTC**ATCGCCTTCTTCGTCATCC | Mutation | *emfA* | This work |
| B | GCGG**AAGCTT**CCACATCGGACATGATATG | Mutation | *emfA* | This work |
| C | ACCGAAGCTTGACGATATGAGCGACAACG | Complementation | *emfA* | This work |
| D | GGGAATTCACATCGGTATTCGGCATCATG | Complementation | *emfA* | This work |
| E | CCCGGTCAGGACATTGTCATGAATATCACTGCTACTGTTCTTTGTAGGCTGGAGCTGCTTCG | Mutation *mntP* | *mntP* | This work |
| F | CCTCTGGCAGCGTTCTTATTAACCGTGGAAGTGCGTCCAGAGCATATGAATATCCTCCTTAG | Mutation *mntP* | *mntP* | This work |
| G | TCAAAATATGTTAAGGTTGCG | Sequencing *mntP* | *mntP* | This work |
| H | GACATTTGATGGAGCTGAAG | Sequencing *mntP* | *mntP* | This work |
| I | ATATATGCGACCGCCTTGAG | qRT-PCR | *emfA* | This work |
| N | GCCTCCTTGACGACTTTGAC | qRT-PCR | *emfA* | This work |
| Y | CGATGGCGAGACAGCTAAAT | qRT-PCR | *hisCd* | (8) |
| Z | ATCATCGCAACGCTATCTCC | qRT-PCR | *hisCd* | (8) |

## Supplementary references

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