Table S3. KEGG pathway analysis of differentially expressed ON proteins in MOB-513-pdgcB in the absence (-Mn) or the presence (+Mn) of manganese.

| Locus Tag | Protein | ON | Kegg Pathway name |
|-----------|---------|----|------------------|
| fig|286.1388.|pag.1099| Signal transduction histidine kinase CheA | MOB-513-pdgcB | B, ST |
| fig|286.1388.|pag.1617| Pyruvate dehydrogenase E1 component (EC 1.2.4.1) | MOB-513-pdgcB | CM, BSM, MMDE |
| fig|286.1388.|pag.1725| Multidrug efflux system, outer membrane factor lipoprotein => OprM of MexEF-OprN system | MOB-513-pdgcB | T |
| fig|286.1388.|pag.2770| Transcriptional regulator, AraC family | MOB-513-pdgcB | GIP |
| fig|286.1388.|pag.2130| D-amino acid dehydrogenase (EC 1.4.99.6) | MOB-513-pdgcB | AM |
| fig|286.1388.|pag.2619| Transcriptional regulator, ArcA family | MOB-513-pdgcB | GIP |
| fig|286.1388.|pag.3505| Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GKE | MOB-513-pdgcB | CM, BSM, MMDE |
| fig|286.1388.|pag.3637| Exoelectrogenic monoculture V beta chain (EC 3.1.11.5) | MOB-513-pdgcB | GIP |
| fig|286.1388.|pag.5226| Spermidine/spermine imprimase/ABC transporter substrate-binding protein PotD (EC 3.1.11.12) | MOB-513-pdgcB | GIP |
| fig|286.1388.|pag.5632| Similar to citrate lyase beta chain, 3 | MOB-513-pdgcB | NA |
| fig|286.1388.|pag.11| DNA-binding response regulator KdpE | MOB-513-pBdgc | QS |
| fig|286.1388.|pag.879| Nitrate ABC transporter, substrate-binding protein | MOB-513-pBdgc | T |
| fig|286.1388.|pag.2698| TonB-dependent ferric citrate/leukobactin receptor protein | MOB-513-pBdgc | T |
| fig|286.1388.|pag.3549| hypothetical protein | MOB-513-pBdgc | NA |
| fig|286.1388.|pag.4447| Universal stress protein UspA and related nucleotide-binding proteins | MOB-513-pBdgc | NA |
| fig|286.1388.|pag.4659| serine/threonine protein kinase | MOB-513-pBdgc | NA |
| fig|286.1388.|pag.5040| Transcriptional regulator, GntR family | MOB-513-pBdgc | GIP |
| fig|286.1388.|pag.6854| Exonuclease SssC | MOB-513-pBdgc | NA |
| fig|286.1388.|pag.7013| RTX toxins and related C2t+b-binding proteins | MOB-513-pBdgc | NA |
| fig|286.1388.|pag.7014| RTX toxins and related C2t+b-binding proteins | MOB-513-pBdgc | NA |

| Locus Tag | Protein | ON | Kegg Pathway name |
|-----------|---------|----|------------------|
| fig|286.1388.|pag.11| DNA-binding response regulator KdpE | MOB-513-pdEmty | QS, ST |
| fig|286.1388.|pag.71| CBS domain protein | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.775| Lipo polysaccharide export system protein LptC | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.1186| hypothetical protein | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.1725| Multidrug efflux system MdABC-Taor, membrane fusion component MdA | MOB-513-pdEmty | ST |
| fig|286.1388.|pag.1719| Glutathione S-transferase (EC 2.5.1.18) | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.1725| Multidrug efflux system, outer membrane factor lipoprotein => OprM of MexEF-OprN system | MOB-513-pdEmty | T |
| fig|286.1388.|pag.1726| Multidrug efflux system, inner membrane factor lipoprotein => OprN of MexEF-OprN system | MOB-513-pdEmty | T |
| fig|286.1388.|pag.1800| Cytochrome c oxidase (EC 3.5.5.4) | MOB-513-pdEmty | XBM, AM, EM, MMDE |
| fig|286.1388.|pag.2118| h-oxacyl[acyl-carrier protein] reductase (EC 1.1.1.100) | MOB-513-pdEmty | GIP |
| fig|286.1388.|pag.2130| D-amino acid dehydrogenase (EC 1.4.99.6) | MOB-513-pdEmty | AM |
| fig|286.1388.|pag.2382| Transcriptional regulator, LysR family | MOB-513-pdEmty | GIP |
| fig|286.1388.|pag.2552| Transcriptional regulator, AraC family | MOB-513-pdEmty | GIP |
| fig|286.1388.|pag.2969| Methyl-accepting chemotaxis sensor/transducer protein | MOB-513-pdEmty | BC, ST |
| fig|286.1388.|pag.3230| YID protein, required for LPS synthesis | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.3903| Cation transport ATPase | MOB-513-pdEmty | T |
| fig|286.1388.|pag.4541| GDDF domain/porA domain protein | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.4658| Protein phosphaetase 2C-like | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.5377| DOPA-4,5-dioxygenase (EC 1.14.99.99) | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.6972| Cytochrome c heme lyase subunit CcmF | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.7063| 3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.3.4.11) | MOB-513-pdEmty | MCV, BSM, BoC |
| fig|286.1388.|pag.7194| Uncharacterized amino acid permease, Gbg family | MOB-513-pdEmty | NA |
| fig|286.1388.|pag.141| Catalase KatE (EC 1.11.1.6) | MOB-513-pBdgc | ST, AM, CM, BSM |
| fig|286.1388.|pag.320| hypothetical protein | MOB-513-pBdgc | P |
| fig|286.1388.|pag.875| Nitrate ABC transporter, substrate-binding protein | MOB-513-pBdgc | T, EM |
| fig|286.1388.|pag.4774| hypothetical protein | MOB-513-pBdgc | NA |
| fig|286.1388.|pag.7013| RTX toxins and related C2t+b-binding proteins | MOB-513-pBdgc | NA |
| fig|286.1388.|pag.7014| RTX toxins and related C2t+b-binding proteins | MOB-513-pBdgc | NA |

**Kegg Pathway Name**

- **BC**: Bacterial chemotaxis
- **B**: Biofilm
- **QS**: Quorum sensing
- **P**: Peroxisome
- **T**: transporters
- **ST**: Signal transduction
- **GIP**: Genetic Information Processing
- **XBM**: Xenobiotics biodegradation and metabolism
- **M**: Metabolism of cofactors and vitamins
- **A**: Amino acid metabolism
- **N**: Nucleotide metabolism
- **E**: Energy metabolism
- **C**: Carbohydrate metabolism
- **B**: Biosynthesis of secondary metabolites
- **MMDE**: Microbial metabolism in diverse environments
- **BoC**: Biosynthesis of cofactors
- **NA**: Not Assigned