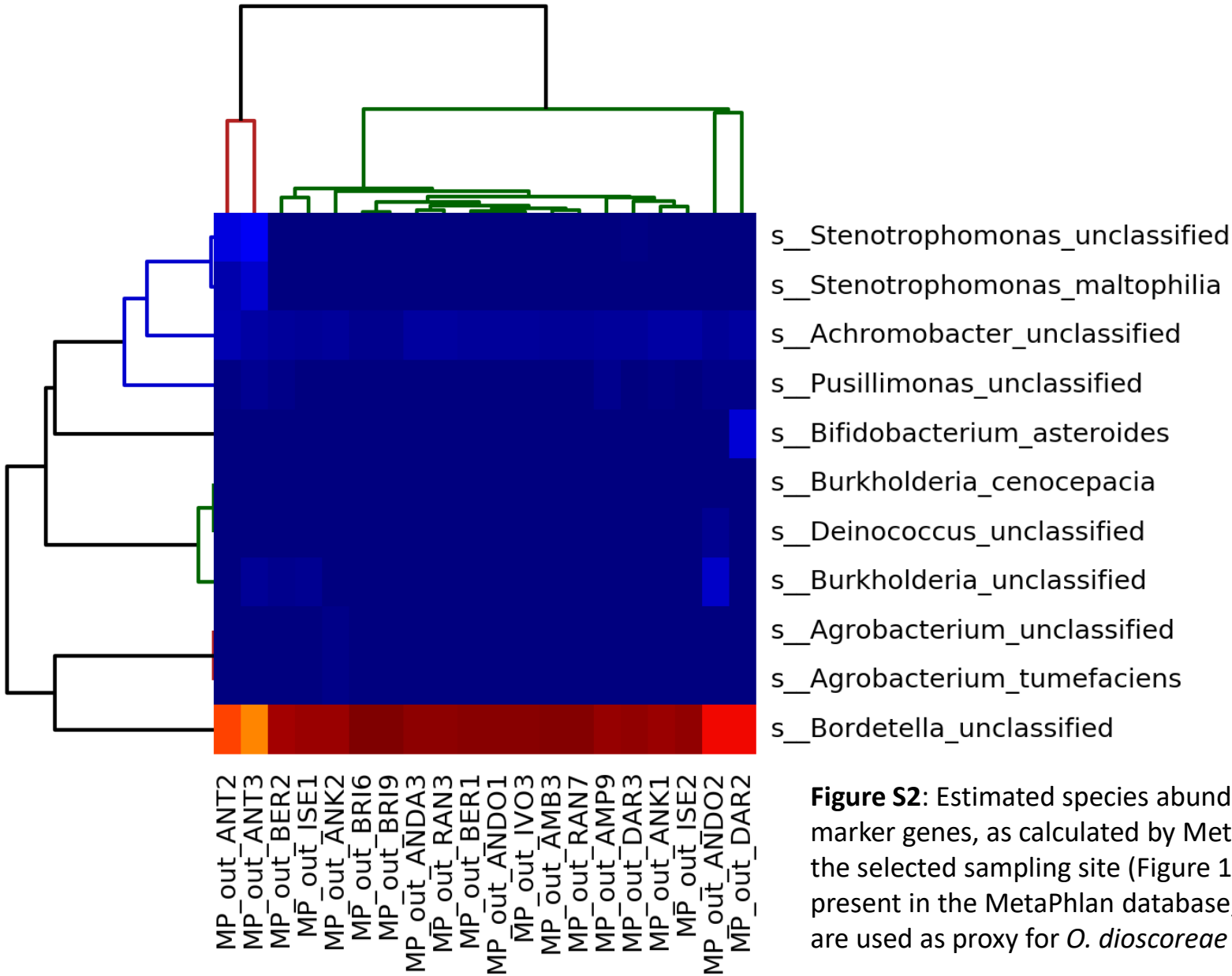
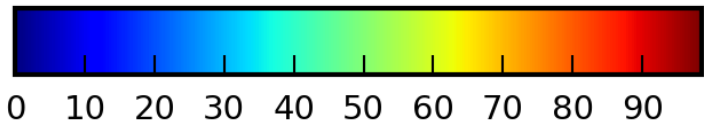
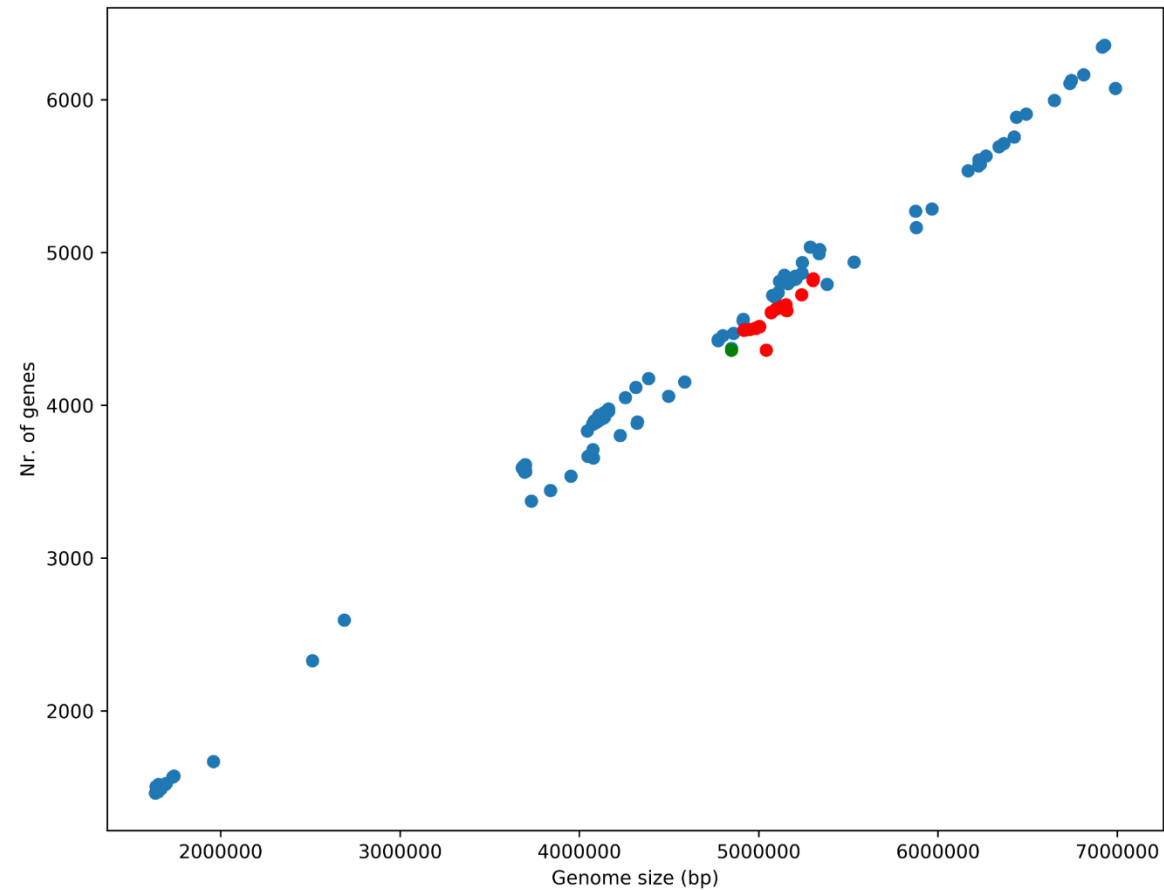


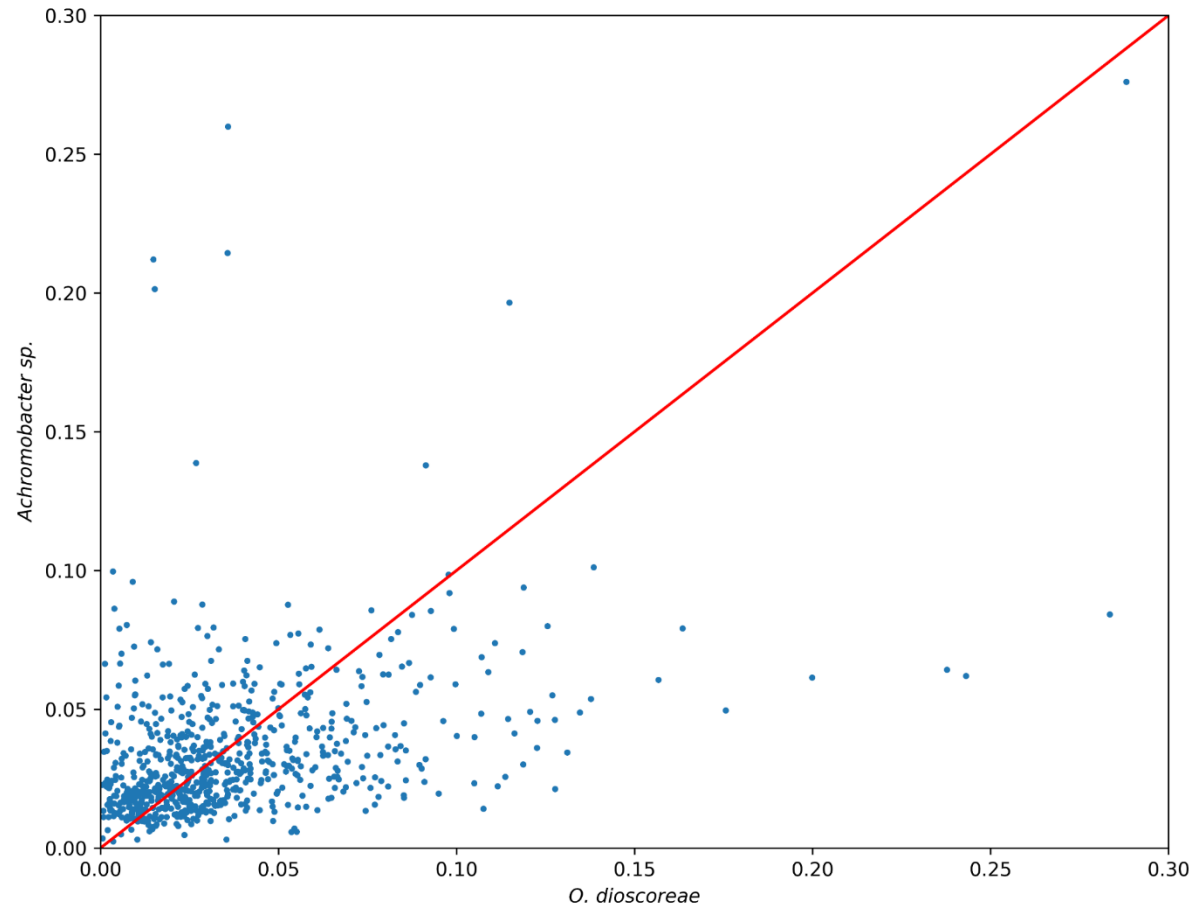
Figure S1: A. *nrdA* gene phylogeny with bootstrap values from wild-collected *O. dioscoreae*. Colored sample names represent samples sent for WGS. Red: samples from the east region; Blue: samples from the north region. B. Bootstrapped phylogeny of *O. dioscoreae* samples based on single copy core genes. Highlighted in red: samples collected in the Atsinanana region; highlighted in blue: samples collected in the Diana region; Black: Type strain LMG29303<sup>T</sup>.



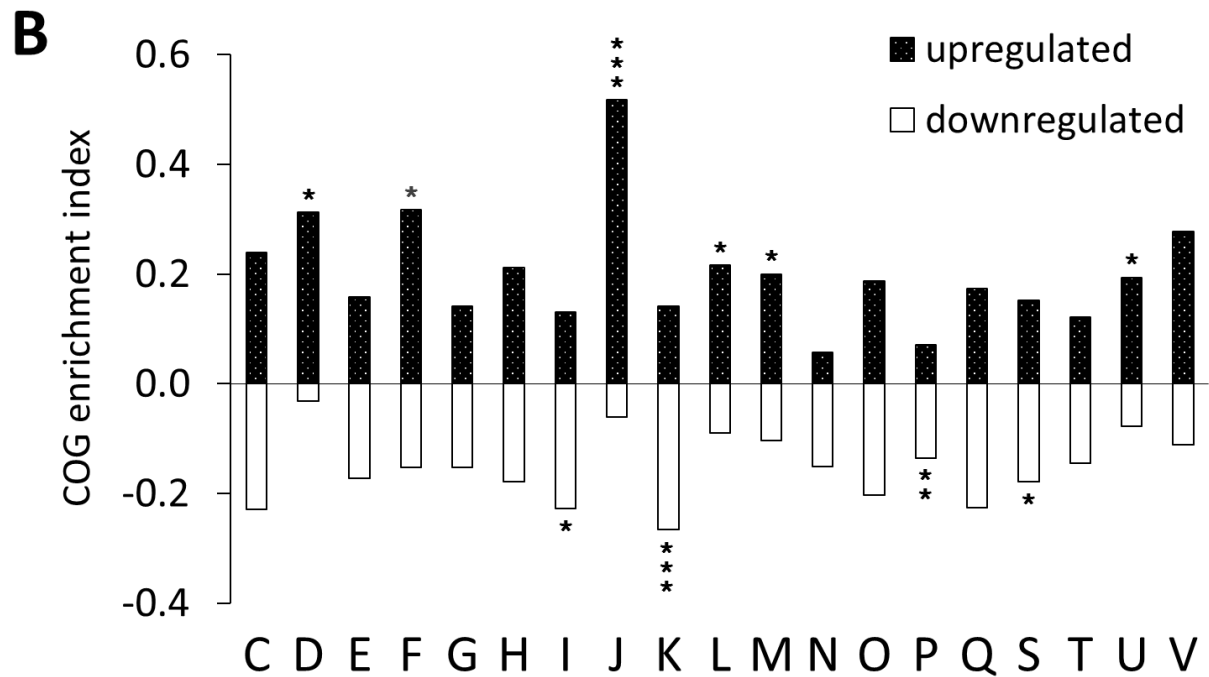
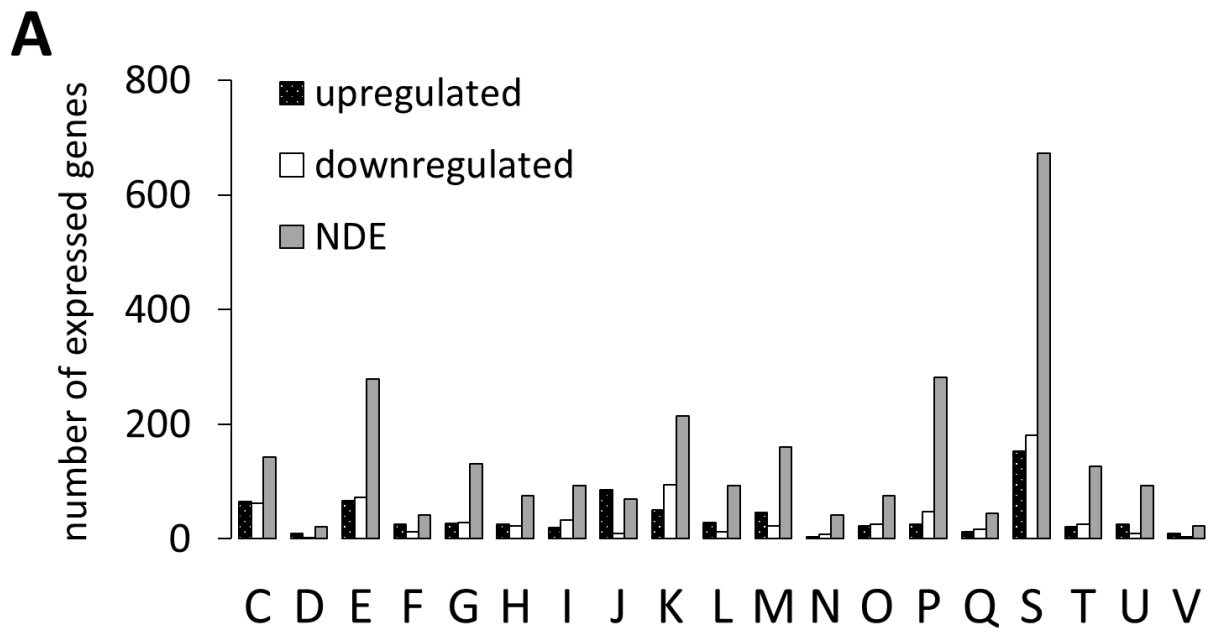
**Figure S2:** Estimated species abundance in the sequencing reads based on clade-specific marker genes, as calculated by MetaPhlan. Sample names (x-axis) correspond to reads from the selected sampling site (Figure 1). Since no clade-specific markers of *O. dioscoreae* are present in the MetaPhlan database, the closely related *Bordetella* and *Achromobacter* genera are used as proxy for *O. dioscoreae* abundance.



**Figure S3:** Genome size and number of genes of bacteria in the Alcaligenaceae family. RefSeq assemblies of all species belonging to the Alcaligenaceae family (taxonomy id 506, n=449) were downloaded from Genbank (accessed 13-11-2018) Green: *O. dioscoreae* typestrain (LMG29303<sup>T</sup>) Red: *O. dioscoreae* strains from Madagascar.



**Figure S4:** Comparison of the ratio of synonymous (dN) and nonsynonymous (dS) substitutions of the single-copy orthologs of several *Achromobacter* sp. (ENA accessions: ASM23678v2, ASM21974v1, GCS2v1, ASM118959v1, ASM163968v1, ASM16583v1, Achr\_xylo\_C54\_V2, ASM105105v1) and sampled *O. dioscoreae* genomes. Zero values were removed from the analysis. Mean *O. dioscoreae* dN/dS (0.0374) and mean *Achromobacter* sp. dN/dS (0.0339) did not differ significantly (Wilcoxon rank-sum p-value: 0.85)



**Figure S5: Functional profile of differentially expressed genes in the leaf nodule compared vs. Culture of *O. dioscoreae*.** A: Distribution of DEGs into functional COG categories. Black and white bars represent counts of up- and down-regulated genes, respectively. Grey bars indicate the total number of non-DEGs. B: COG enrichment for differentially regulated genes. The COG enrichment index is calculated by dividing the percentage of genes up- or down-regulated for each category by the percentage of genes in the genome belonging to the same category. Positive values represent upregulated genes in the *in planta* growth condition (when compared with axenic growth); negative values, to the downregulated genes. Enrichment index values that are significantly different from expected (two-tailed Fisher's exact test) are indicated by asterisks as follows: \*  $p \leq 0.05$ ; \*\*  $p \leq 0.01$ ; \*\*\*  $p \leq 0.001$ . COG categories: C – Energy production and conversion; D – Cell cycle control and mitosis; E – Amino acid metabolism and transport; F – Nucleotide metabolism and transport; G – Carbohydrate metabolism and transport; H – Coenzyme metabolism; I – Lipid metabolism; J – Translation; K – Transcription; L – Replication and repair; M – Cell wall/membrane/envelop biogenesis; N – Cell motility; O – Post-translational modification, protein turnover, chaperone functions; P – Inorganic ion transport and metabolism.; Q – Secondary structure; S – Function unknown; T – Signal transduction; U – Intracellular trafficking and secretion; V – Defence mechanisms.

Table S1: Strains and plasmids used in this study

| Strain                              | Genotype/Description   | Source/Reference          |
|-------------------------------------|--|---------------------------|
| <b><i>O. dioscoreae</i> strains</b> |  |                           |
| LMG 29303T                          | Leaf nodule isolate - Switzerland  | (Carlier et al., 2017)    |
| R67088                              | Leaf nodule isolate - Belgium  | (Carlier et al., 2017)    |
| R67584                              | Leaf nodule isolate - Congo  | This Study                |
| LF01                                | LMG 29303T, NaI <sup>R</sup>   | This Study                |
| FID1                                | LF01 $\Delta$ smpD, Km <sup>R</sup>                                      | This Study                |
| <b><i>E. coli</i> strains</b>       |  |                           |
| Top 10                              |  | Invitrogen                |
| S17-1                               | Donor, recA pro hsdR RP4-2-Tc::Mu-Km::Tn7 integrated into the chromosome | (Simon R et al., 1983)    |
| <b>Plasmids</b>                     |  |                           |
| pDONRpEX18                          | Gateway adapted donor vector; attP1 and attP2, sacB, Te <sup>R</sup>     | (Hmelo et al., 2000)      |
| pKD4                                | Km <sup>R</sup> -cassette  | (Datsenko & Wanner, 2015) |

Table S2. *Dioscorea sansibarensis* sampling locations in Madagascar.

| <b>Identifier</b> | <b>Locality</b> | <b>GPS coordinates</b> |               | <b>Date of sampling</b> |
|-------------------|-----------------|------------------------|---------------|-------------------------|
| ANDA              | Andranomanitra  | S12°25'10.3''          | E49°20'40.4'' | 05/2017                 |
| DAR               | Daraina         | S12°29'07.1''          | E49°23'46.4'' | 05/2017                 |
| ANT               | Antsakoabe      | S12°39'48.1''          | E49°17'42.7'' | 05/2017                 |
| ANDO              | Andranonakoko   | S12°55'36.8''          | E49°11'27.7'' | 05/2017                 |
| ISE               | Isesy           | S13°08'44.8''          | E49°04'49.1'' | 05/2017                 |
| BER               | Beramanja       | S13°22'14.0''          | E48°52'18.1'' | 05/2017                 |
| ANK               | Ankazomahity    | S13°28'56.8''          | E48°43'42.4'' | 05/2017                 |
| BRI               | Brickaville     | S18°49'19.1''          | E49°04'36.5'' | 11/2016                 |
| AMB               | Ambavaniasy     | S18°56'42.9''          | E48°30'48.0'' | 11/2016                 |
| RAN               | Ranomafana      | S18°58'35.7''          | E48°55'04.8'' | 11/2016                 |
| IVO               | Ivoala          | S19°02'21.3''          | E48°55'59.6'' | 11/2016                 |
| AMP               | Ampaho          | S19°26'56.1''          | E48°55'18.2'' | 11/2016                 |

Table S3. Oligonucleotide primers used in this study

| <b>Primer name</b>                               | <b>Sequence (5' - 3')</b>                           |
|--|---|
| <b>Primers used for phylogeny</b>                |   |
| Odio_nrdA_R                                      | GAGTCCTTCGCCTTCTTG                                  |
| Odio_nrdA_F                                      | ACTACTTCCCCACCTTCA                                  |
| matK-sans-R                                      | CTAGCACACGAAATCCGAA                                 |
| matK-sans-F                                      | AATACCCCATCCCATCCA                                  |
| rbcl-sans-R                                      | CGCGATGGATGTGAAGAA                                  |
| rbcl-sans-F                                      | TACGTGGTGGACTTGATTTT                                |
| rpl32-trnL-R                                     | ATTTGGAAGAAAAGGGGGT                                 |
| rpl32-trnL-F                                     | TTCCTAAGAGCAGCGTGT                                  |
| <b>Primers used for quantitative PCR</b>         |   |
| rpoD-06-R  | CACCATTTGGTCAGCTT                                   |
| rpoD-05-F  | GAACTCCCCCGCAAACAA                                  |
| galactonate_dehydratase-02-R                     | CTCCTTCACGTACTCCTC                                  |
| galactonate_dehydratase-01-F                     | CTACAACGCCTTCATCCA                                  |
| KASII-02-R                                       | AAGAACAGGCCATCGACA                                  |
| KASII-01-F                                       | GAGATCGCGGAAAACCAG                                  |
| PqqC-02-R  | TGAAGAACACCACCGCCT                                  |
| PqqC-01-F  | CTACCGCGACATGCTCAA                                  |
| ImpA-01-R  | TCACGCAGGGACAATTGG                                  |
| ImpA-02-F  | GCAGCAGTATTGGGAAGG                                  |
| nrp-02-R   | GCGAAGTTGAAGGTATAGGG                                |
| nrp-01-F   | GGTGTTTCGCTGCCTATTG                                 |
| <b>Primers used for smpD-mutant construction</b> |   |
| 00690-Dn-GW-03-F                                 | TACAAGAAAGCTGGGTAGACGGAATCCAGCCAGAC                 |
| 00690-Dn-kan-04-R                                | CGGAATAGGAACTAAGGAGGATATTCATATGGCAAGTCATGCAACACCAGA |
| 00690-Up-kan-05-R                                | GAACTTCGAAGCAGCTCCAGCCTATCGTGATAGACATGGGAGGA        |
| 00690-Up-GW-06-F                                 | TACAAAAAAGCAGGCTTCCGTGTTGCAAGAGGAGAT                |
| pKD4rev-2  | CATATGAATATCCTCCTTAGTTCCTATTCCG                     |
| pKD4fwd-2  | TAGGCTGGAGCTGCTTCGAAGTTC                            |



Table S5. Biolog PM1/PM2A read-out. Purple color development was scored at 24h and 48h.

| Substrate C-source                                 | Growth after |     |
|--|--------------|-----|
|  | 24h          | 48h |
| Succinic Acid                                      | x            |     |
| L-Proline  | x            |     |
| L-Lactic Acid                                      | x            |     |
| L-Glutamic Acid                                    |              | x   |
| D-Galactonic Acid- $\gamma$ -Lactone               |              | x   |
| D,L-Malic Acid                                     | x            |     |
| $\alpha$ -Keto-Glutamic Acid                       | x            |     |
| m-Tartaric Acid                                    | x            |     |
| $\alpha$ -Hydroxy Glutaric Acid- $\gamma$ -Lactone | x            |     |
| Citric Acid  | x            |     |
| Fumaric Acid                                       | x            |     |
| Propionic Acid                                     |              | x   |
| Mono Methyl Succinate                              |              | x   |
| Methyl Pyruvate                                    | x            |     |
| D-Malic Acid                                       | x            |     |
| L-Malic Acid                                       | x            |     |
| Pyruvic Acid                                       | x            |     |
| Citraconic Acid                                    |              | x   |
| $\beta$ -Hydroxy Butyric Acid                      | x            |     |
| Oxalomalic Acid                                    | x            |     |
| Succinamic Acid                                    | x            |     |
| D-Tartaric Acid                                    | x            |     |
| L-Pyroglutamic Acid                                | x            |     |

Table S6

Table S6. List of putative genes under positive selection

| Locus tag | Nr. of sites under positive selection | Average dN/dS | Log2FC | Gene Product   | Localization        |
|-----------|---------------------------------------|---------------|--------|--|---------------------|
| ODI_R0016 | 1                                     | 5.91          | 1.79   | Proteins containing SET domain   | Unknown             |
| ODI_R0030 | 1                                     | 5.76          | 0      | Acyl-CoA dehydrogenase   | Cytoplasmic         |
| ODI_R0039 | 1                                     | 3.82          | -1.71  | Methionine ABC transporter ATP-binding protein   | CytoplasmicMembrane |
| ODI_R0041 | 1                                     | 4.39          | 0      | Acyl-CoA dehydrogenase   | CytoplasmicMembrane |
| ODI_R0173 | 2                                     | 5.12          | -1.08  | Aspartyl-tRNA(Asn) amidotransferase subunit A @ Glutamyl-tRNA(Gln) amidotransferase subunit A        | Cytoplasmic         |
| ODI_R0183 | 1                                     | 6.04          | -2.15  | Bll5495 protein  | Unknown             |
| ODI_R0203 | 1                                     | 7.35          | -0.9   | FIG00431745: hypothetical protein<br>Predicted transcriptional regulator LiuR of leucine degradation | CytoplasmicMembrane |
| ODI_R0217 | 1                                     | 8.32          | -1.33  | pathway, MerR family   | Cytoplasmic         |
| ODI_R0262 | 1                                     | 5.12          | 0      | Outer membrane stress sensor protease DegS   | Periplasmic         |
| ODI_R0275 | 1                                     | 6.87          | -3.17  | Histidinol dehydrogenase   | Cytoplasmic         |
| ODI_R0292 | 1                                     | 5.95          | 0      | hypothetical protein   | CytoplasmicMembrane |
| ODI_R0308 | 1                                     | 6.89          | 2.16   | Cytochrome c oxidase polypeptide I   | CytoplasmicMembrane |
| ODI_R0328 | 1                                     | 6.17          | -1.09  | Transcriptional regulator, AsnC family   | Cytoplasmic         |
| ODI_R0387 | 1                                     | 6.54          | 0      | hypothetical protein   | Unknown             |
| ODI_R0475 | 1                                     | 4.13          | -0.93  | hypothetical protein   | Unknown             |
| ODI_R0484 | 1                                     | 3.66          | 0.46   | Spermidine synthase  | Unknown             |
| ODI_R0485 | 3                                     | 7.23          | -0.54  | Hypothetical oxidoreductase, YbiC homolog  | Cytoplasmic         |
| ODI_R0518 | 1                                     | 7.14          | -1.84  | CTP:molybdopterin cytidyltransferase   | Unknown             |
| ODI_R0533 | 1                                     | 5.74          | -3.74  | 3-polyprenyl-4-hydroxybenzoate carboxy-lyase UbiX  | Cytoplasmic         |
| ODI_R0537 | 1                                     | 5.29          | -1.96  | L-lactate dehydrogenase  | CytoplasmicMembrane |
| ODI_R0539 | 2                                     | 7.5           | 0      | probable membrane protein YPO3302  | CytoplasmicMembrane |
| ODI_R0541 | 3                                     | 9.39          | -2.11  | hypothetical protein   | Unknown             |
| ODI_R0556 | 2                                     | 7.45          | -1.89  | Phosphate regulon sensor protein PhoR (SphS)   | CytoplasmicMembrane |
| ODI_R0578 | 1                                     | 2.84          | 1.23   | 5-methyltetrahydrofolate--homocysteine methyltransferase   | Cytoplasmic         |
| ODI_R0584 | 1                                     | 5.09          | -3.13  | Tricarboxylate transport protein TctC  | Periplasmic         |
| ODI_R0643 | 1                                     | 4.33          | -1.9   | Xanthine and CO dehydrogenases maturation factor,<br>XdhC/CoxF family                                | Cytoplasmic         |
| ODI_R0647 | 13                                    | 8.89          | 2      | hypothetical protein   | Unknown             |

Table S6

|           |   |      |   |                     |
|-----------|---|------|---|---------------------|
| ODI_R0680 | 1 | 4.21 | 0 Shikimate 5-dehydrogenase I alpha                           | Cytoplasmic         |
| ODI_R0690 | 1 | 4.74 | 0.69 Probable transmembrane protein                           | CytoplasmicMembrane |
| ODI_R0698 | 6 | 8.99 | 2 hypothetical protein  | Unknown             |
| ODI_R0762 | 1 | 6.68 | 0 Membrane-fusion protein                                     | Unknown             |
|           |   |      | Type II/IV secretion system protein TadC, associated with Flp |                     |
| ODI_R0769 | 1 | 8.22 | -1.2 pilus assembly   | CytoplasmicMembrane |
| ODI_R0770 | 2 | 5.18 | -1.25 Flp pilus assembly protein TadB                         | CytoplasmicMembrane |
| ODI_R0813 | 1 | 6.86 | -1.22 hypothetical protein                                    | Unknown             |
| ODI_R0840 | 1 | 7.28 | 1.29 Uncharacterized protein YfiR precursor                   | Periplasmic         |
| ODI_R0862 | 3 | 7.31 | 1.54 Short chain dehydrogenase                                | Extracellular       |
| ODI_R0900 | 1 | 6.8  | 0.52 18K peptidoglycan-associated outer membrane lipoprotein  | OuterMembrane       |
| ODI_R0918 | 2 | 5.03 | 0 Tricarboxylate transport protein TctB                       | CytoplasmicMembrane |
| ODI_R0946 | 1 | 5.74 | 0 D-alanine--D-alanine ligase                                 | Cytoplasmic         |
| ODI_R0990 | 2 | 4.84 | 1.04 GGDEF domain protein                                     | Cytoplasmic         |
|           |   |      | TRAP-type C4-dicarboxylate transport system, large            |                     |
| ODI_R1014 | 1 | 5.02 | 0.95 permease component                                       | CytoplasmicMembrane |
| ODI_R1028 | 1 | 5.78 | -3.8 peptidase, M23/M37 family                                | CytoplasmicMembrane |
|           |   |      | Acetylornithine deacetylase/Succinyl-diaminopimelate          |                     |
| ODI_R1071 | 4 | 8.76 | -0.33 desuccinylase and related deacylases                    | Cytoplasmic         |
| ODI_R1111 | 1 | 3.58 | 0.64 Cytochrome c, mono-and diheme variants                   | CytoplasmicMembrane |
| ODI_R1118 | 2 | 8.46 | 2.51 4-hydroxy-tetrahydrodipicolinate reductase               | Cytoplasmic         |
|           |   |      | Outer membrane lipoprotein SmpA, a component of the           |                     |
| ODI_R1119 | 1 | 6.91 | 3.44 essential YaeT outer-membrane protein assembly complex   | OuterMembrane       |
| ODI_R1148 | 2 | 8.65 | 1.94 FIG152265: Sodium:solute symporter associated protein    | CytoplasmicMembrane |
| ODI_R1156 | 1 | 4.79 | -1.11 Methylglutaconyl-CoA hydratase                          | Cytoplasmic         |
| ODI_R1187 | 1 | 5.7  | 2.01 UPF0246 protein YaaA                                     | Cytoplasmic         |
| ODI_R1270 | 2 | 8.23 | 0 General secretion pathway protein L                         | Periplasmic         |
|           |   |      | RidA/YER057c/UK114 superfamily, group 2, YoaB-like            |                     |
| ODI_R1403 | 1 | 6.91 | 1.48 protein  | Cytoplasmic         |
| ODI_R1418 | 1 | 5.84 | 2.32 Tetrapyrrole methylase family protein                    | Unknown             |
| ODI_R1419 | 1 | 7.18 | 0 FIG146278: Maf/YceF/YhdE family protein                     | Cytoplasmic         |
| ODI_R1457 | 1 | 5.91 | -1.4 putative 4-hydroxybenzoyl-CoA thioesterase               | CytoplasmicMembrane |
| ODI_R1460 | 1 | 4.41 | 0 Tryptophan synthase alpha chain                             | Cytoplasmic         |
|           |   |      | Positive regulator of Tartrate                                |                     |
| ODI_R1465 | 1 | 7.11 | -3.45 dehydrogenase/decarboxylase/D-malic enzyme              | Unknown             |

Table S6

|           |   |      |   |                     |
|-----------|---|------|---|---------------------|
| ODI_R1472 | 1 | 6.58 | 0 putative periplasmic protein  | Unknown             |
| ODI_R1477 | 2 | 5.23 | 0 Probable transmembrane protein  | CytoplasmicMembrane |
| ODI_R1482 | 1 | 6.97 | 2.23 Protoporphyrinogen IX oxidase, novel form, HemJ  | CytoplasmicMembrane |
| ODI_R1484 | 1 | 6.45 | 0 putative membrane protein   | CytoplasmicMembrane |
| ODI_R1487 | 1 | 5.85 | 7.64 Thioesterase in siderophore biosynthesis gene cluster  | Cytoplasmic         |
| ODI_R1489 | 1 | 3.02 | 8.11 FIG00663483: hypothetical protein<br>Siderophore biosynthesis non-ribosomal peptide synthetase                   | Cytoplasmic         |
| ODI_R1490 | 2 | 3.95 | 8.14 modules  | CytoplasmicMembrane |
| ODI_R1498 | 1 | 8.21 | 8.16 Tricarboxylate transport protein TctC  | CytoplasmicMembrane |
| ODI_R1507 | 5 | 7.29 | 8.51 4'-phosphopantetheinyl transferase   | Unknown             |
| ODI_R1513 | 1 | 6.86 | 0.86 transcriptional regulator RhIR   | Cytoplasmic         |
| ODI_R1520 | 1 | 5.76 | 2.03 Cyclohexadienyl dehydrogenase  | Unknown             |
| ODI_R1522 | 1 | 7.61 | 3.47 Cytidylate kinase  | Cytoplasmic         |
| ODI_R1525 | 1 | 7.33 | 1.93 Probable transmembrane protein   | CytoplasmicMembrane |
| ODI_R1557 | 1 | 4.75 | Maleylacetoacetate isomerase @ Glutathione S-transferase,<br>1.25 zeta  | Cytoplasmic         |
| ODI_R1603 | 2 | 6.72 | 0 Nodulation protein J<br>4-carboxymuconolactone decarboxylase<br>domain/alkylhydroperoxidase AhpD family core domain | CytoplasmicMembrane |
| ODI_R1634 | 1 | 5.52 | -1.32 protein   | Unknown             |
| ODI_R1654 | 1 | 4.7  | -1.02 Allophanate hydrolase 2 subunit 2   | CytoplasmicMembrane |
| ODI_R1692 | 2 | 6.63 | 0 tRNA-specific 2-thiouridylase MnmA  | Cytoplasmic         |
| ODI_R1746 | 1 | 3.11 | 0 MFS transporter, DHA1 family<br>Ferric siderophore transport system, biopolymer transport                           | CytoplasmicMembrane |
| ODI_R1761 | 2 | 6.71 | 2.35 protein ExbB   | CytoplasmicMembrane |
| ODI_R1794 | 1 | 3.82 | 1.71 Membrane-bound metal-dependent hydrolase<br>Phosphopantothenoylcysteine decarboxylase /                          | CytoplasmicMembrane |
| ODI_R1795 | 1 | 5.54 | 1.48 Phosphopantothenoylcysteine synthetase   | Cytoplasmic         |
| ODI_R1796 | 2 | 8.19 | 1.73 Transcriptional regulator, IclR family   | Cytoplasmic         |
| ODI_R1803 | 1 | 4.56 | -1.32 Fumarylacetoacetate hydrolase family protein<br>Ribosome-associated heat shock protein implicated in the        | Cytoplasmic         |
| ODI_R1877 | 1 | 8.63 | -0.54 recycling of the 50S subunit (S4 paralog)   | Cytoplasmic         |
| ODI_R1904 | 1 | 6.36 | 1.74 FIG053235: Diacylglycerolamine hydrolase like  | Cytoplasmic         |
| ODI_R1905 | 2 | 5.67 | 2.06 Glutamate-ammonia-ligase adenyltransferase   | Cytoplasmic         |
| ODI_R1920 | 1 | 8.62 | -2.3 Transcriptional regulators   | Unknown             |

Table S6

|           |   |      |   |                     |
|-----------|---|------|---|---------------------|
| ODI_R1924 | 1 | 7.57 | -2.7 L-ectoine synthase   | Cytoplasmic         |
| ODI_R1968 | 1 | 5.31 | 0 transcriptional regulator<br>Type II/IV secretion system ATP hydrolase                                    | Unknown             |
| ODI_R2022 | 3 | 5.83 | 0 TadA/VirB11/CpaF, TadA subfamily  | Cytoplasmic         |
| ODI_R2027 | 2 | 5.96 | -2.03 Transcriptional regulator, LysR family  | Cytoplasmic         |
| ODI_R2031 | 1 | 5.07 | 0 FIGfam005179  | CytoplasmicMembrane |
| ODI_R2041 | 2 | 9.12 | -3.57 Iron compound ABC transporter, permease protein<br>Manganese ABC transporter, inner membrane permease | CytoplasmicMembrane |
| ODI_R2071 | 1 | 5.14 | -0.86 protein SitD<br>FIG000605: protein co-occurring with transport systems                                | CytoplasmicMembrane |
| ODI_R2077 | 1 | 5.97 | 0.45 (COG1739)  | Cytoplasmic         |
| ODI_R2086 | 1 | 6.08 | 0 hypothetical protein  | Unknown             |
| ODI_R2106 | 1 | 7.27 | -2.05 ABC transporter ATP-binding protein   | CytoplasmicMembrane |
| ODI_R2135 | 2 | 7.44 | -1.72 Flagellar basal-body P-ring formation protein FlgA  | Periplasmic         |
| ODI_R2214 | 1 | 5.98 | 1.06 UPF0125 protein yjF  | Unknown             |
| ODI_R2228 | 2 | 5.68 | 1.59 DNA polymerase III delta prime subunit   | Cytoplasmic         |
| ODI_R2287 | 2 | 6.96 | 2.38 Ferric iron ABC transporter, iron-binding protein  | Periplasmic         |
| ODI_R2295 | 1 | 5.05 | 0 Gluconokinase<br>TRAP-type C4-dicarboxylate transport system, small                                       | Periplasmic         |
| ODI_R2296 | 1 | 7.42 | 0 permease component<br>4-Hydroxy-2-oxoglutarate aldolase @ 2-dehydro-3-                                    | CytoplasmicMembrane |
| ODI_R2300 | 1 | 6.17 | -2.34 deoxyphosphogluconate aldolase  | Cytoplasmic         |
| ODI_R2303 | 1 | 5.68 | -2.55 Tiorf68 protein   | Unknown             |
| ODI_R2311 | 1 | 4.12 | 1.53 hypothetical protein   | Extracellular       |
| ODI_R2322 | 2 | 8.04 | 0 Cyanate ABC transporter, permease protein   | CytoplasmicMembrane |
| ODI_R2324 | 1 | 5.85 | -0.52 Anthranilate phosphoribosyltransferase like<br>Oligopeptide transport ATP-binding protein OppD (TC    | Cytoplasmic         |
| ODI_R2343 | 2 | 8.07 | 0 3.A.1.5.1)  | CytoplasmicMembrane |
| ODI_R2348 | 2 | 4.6  | -1.23<br>Transcriptional regulator, GntR family domain / Aspartate  | Cytoplasmic         |
| ODI_R2352 | 1 | 3.34 | -2.03 aminotransferase<br>FIG139991: Putative thiamine pyrophosphate-requiring                              | Cytoplasmic         |
| ODI_R2356 | 1 | 6.21 | 2.79 enzyme<br>ABC transporter in pyoverdin gene cluster, permease  | CytoplasmicMembrane |
| ODI_R2361 | 1 | 7.43 | 1.97 component  | CytoplasmicMembrane |

Table S6

|           |   |      |  |                     |
|-----------|---|------|--|---------------------|
| ODI_R2366 | 2 | 7.53 | 0 Nitrite reductase [NAD(P)H] small subunit  | Cytoplasmic         |
| ODI_R2368 | 1 | 6.47 | 0 Arginine/ornithine antiporter ArcD   | CytoplasmicMembrane |
| ODI_R2376 | 1 | 9.02 | -3.93 hypothetical protein   | Unknown             |
| ODI_R2386 | 3 | 9.85 | -0.76 Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3)  | Periplasmic         |
| ODI_R2388 | 2 | 7.03 | 0 UgpE (TC 3.A.1.1.3)  | CytoplasmicMembrane |
| ODI_R2432 | 1 | 8.47 | -0.82 putative membrane protein  | CytoplasmicMembrane |
| ODI_R2452 | 2 | 7.99 | -1.97 putative exported protein  | Periplasmic         |
| ODI_R2455 | 2 | 6.16 | 1.13 probable iron-sulfur binding protein YPO1417  | Unknown             |
| ODI_R2479 | 2 | 6.7  | 1.32 Iron-siderophore [Alcaligin-like] transport system, substrate-binding component @ Iron-siderophore transport system, Ferric enterobactin transport system permease protein FepG (TC 3.A.1.14.2) @ ABC-type Fe <sup>3+</sup> -siderophore transport system, permease 2 component | Unknown             |
| ODI_R2481 | 1 | 5.64 | 0.85 hypothetical protein  | CytoplasmicMembrane |
| ODI_R2511 | 1 | 5.51 | 2.33 TRAP transporter solute receptor, unknown substrate 7   | Extracellular       |
| ODI_R2535 | 1 | 6.15 | 0 Transcriptional regulator, ArsR family   | Unknown             |
| ODI_R2541 | 1 | 6.5  | -1.15 putative transmembrane efflux protein  | Unknown             |
| ODI_R2554 | 2 | 8.19 | 0 hypothetical protein   | CytoplasmicMembrane |
| ODI_R2585 | 1 | 4.21 | 2.73 N-acetylmannosaminyltransferase   | Unknown             |
| ODI_R2603 | 1 | 7.14 | -1.13 ABC transporter multidrug efflux pump, fused ATP-binding domains   | Cytoplasmic         |
| ODI_R2637 | 1 | 4.19 | -0.87 putative sigma-54-dependent transcriptional regulator  | Cytoplasmic         |
| ODI_R2647 | 2 | 3.9  | -1.69 Permease of the drug/metabolite transporter (DMT) superfamily  | CytoplasmicMembrane |
| ODI_R2650 | 1 | 6.87 | 0 diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)   | CytoplasmicMembrane |
| ODI_R2651 | 2 | 4.35 | -0.5 Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter, ATP-binding subunit SsuB  | CytoplasmicMembrane |
| ODI_R2657 | 2 | 5.46 | 0 Histone acetyltransferase HPA2 and related acetyltransferases  | Unknown             |
| ODI_R2667 | 2 | 7.83 | -2.31 Cyanophycin synthase   | Unknown             |
| ODI_R2844 | 1 | 3.37 | 0 putative lipoprotein   | Cytoplasmic         |
| ODI_R2907 | 1 | 4.9  | -2.23  | Unknown             |

Table S6

| Type II/IV secretion system protein TadC, associated with Flp |    |      |  |                     |
|---|----|------|--|---------------------|
| ODI_R2912   | 1  | 4.43 | 1.32 pilus assembly  | CytoplasmicMembrane |
| ODI_R2950   | 1  | 6.83 | -1.54 putative exported protein<br>Permease of the drug/metabolite transporter (DMT)                         | Unknown             |
| ODI_R2954   | 1  | 5.49 | 1.49 superfamily   | CytoplasmicMembrane |
| ODI_R2971   | 1  | 7.57 | 0 hypothetical protein   | CytoplasmicMembrane |
| ODI_R2987   | 1  | 5.86 | 0 Transketolase, N-terminal section  | Cytoplasmic         |
| ODI_R3000   | 2  | 6.2  | -1.03 Nitrilotriacetate monooxygenase component A  | Cytoplasmic         |
| ODI_R3008   | 1  | 5.6  | -0.54 Magnesium and cobalt efflux protein CorC   | CytoplasmicMembrane |
| ODI_R3011   | 2  | 7.35 | -1.43 hypothetical protein<br>Probable thiol oxidoreductase with 2 cytochrome c heme-                        | Unknown             |
| ODI_R3067   | 1  | 3.46 | 0.91 binding sites   | Unknown             |
| ODI_R3070   | 1  | 6.92 | -1.05 NADPH:quinone oxidoreductase   | Cytoplasmic         |
| ODI_R3085   | 2  | 7.52 | -1.44 FIG004556: membrane metalloprotease  | CytoplasmicMembrane |
| ODI_R3087   | 2  | 6.42 | 1.4 Tricarboxylate transport sensor protein TctE   | CytoplasmicMembrane |
| ODI_R3089   | 2  | 7.17 | 0 D-3-phosphoglycerate dehydrogenase   | Cytoplasmic         |
| ODI_R3117   | 1  | 6.42 | 0 Cytochrome B561<br>diguanylate cyclase/phosphodiesterase (GGDEF & EAL                                      | CytoplasmicMembrane |
| ODI_R3118   | 1  | 3.79 | 1.06 domains) with PAS/PAC sensor(s)   | CytoplasmicMembrane |
| ODI_R3122   | 1  | 5.69 | -2.64 hypothetical protein   | Unknown             |
| ODI_R3124   | 2  | 8.02 | 2.98 putative cytoplasmic protein  | Unknown             |
| ODI_R3137   | 10 | 9.61 | -1.77 N-ethylmaleimide reductase   | Cytoplasmic         |
| ODI_R3158   | 1  | 6.52 | 1.33 hypothetical protein<br>Survival protein SurA precursor (Peptidyl-prolyl cis-trans                      | Unknown             |
| ODI_R3173   | 2  | 6.42 | 0.61 isomerase SurA)   | CytoplasmicMembrane |
| ODI_R3287   | 1  | 7.38 | -0.38 Oxygen-insensitive NADPH nitroreductase  | Unknown             |
| ODI_R3296   | 1  | 4.76 | 2.54 Mannosyltransferase OCH1 and related enzymes  | Unknown             |
| ODI_R3303   | 1  | 5.27 | -1.78 Cyanate ABC transporter, ATP-binding protein   | CytoplasmicMembrane |
| ODI_R3358   | 1  | 3.91 | 0 Sensor protein PhoQ  | Unknown             |
| ODI_R3363   | 3  | 5.72 | 4.66 Catalase  | Periplasmic         |
| ODI_R3370   | 2  | 5.96 | -0.71 Acyl-CoA dehydrogenase, short-chain specific<br>Alkanesulfonates ABC transporter ATP-binding protein / | Cytoplasmic         |
| ODI_R3371   | 2  | 7.2  | -3 Sulfonate ABC transporter, ATP-binding subunit SsuB   | CytoplasmicMembrane |
| ODI_R3380   | 1  | 4.41 | 0 YbbL ABC transporter ATP-binding protein   | CytoplasmicMembrane |
| ODI_R3392   | 2  | 7.48 | 0.56 Molybdenum cofactor biosynthesis protein MoaC   | Cytoplasmic         |

Table S6

|           |   |      |   |                     |
|-----------|---|------|---|---------------------|
| ODI_R3397 | 1 | 5.62 | 1.25 Tricarboxylate transport protein TctC  | Periplasmic         |
| ODI_R3398 | 1 | 6.47 | -0.55 Demethylmenaquinone methyltransferase   | Cytoplasmic         |
| ODI_R3422 | 2 | 6.28 | 0 GCN5-related N-acetyltransferase  | Unknown             |
| ODI_R3436 | 1 | 6.73 | 2.28 hypothetical protein<br>Permease of the drug/metabolite transporter (DMT)  | CytoplasmicMembrane |
| ODI_R3443 | 1 | 6.31 | -1.32 superfamily   | CytoplasmicMembrane |
| ODI_R3479 | 2 | 5.79 | -1.56 Tricarboxylate transport protein TctC   | Unknown             |
| ODI_R3532 | 1 | 6.48 | -1.64 3-isopropylmalate dehydratase small subunit   | CytoplasmicMembrane |
| ODI_R3543 | 1 | 7.37 | 2.2 RNA polymerase sigma-70 factor, ECF subfamily   | Cytoplasmic         |
| ODI_R3551 | 1 | 5.33 | 1.94 ATP-dependent DNA ligase LigC  | Cytoplasmic         |
| ODI_R3577 | 1 | 5.26 | -1.32 Iron siderophore sensor protein   | CytoplasmicMembrane |
| ODI_R3585 | 2 | 5.92 | -0.67 NADH-ubiquinone oxidoreductase chain F  | Cytoplasmic         |
| ODI_R3591 | 1 | 4.58 | 1.33 Proline dehydrogenase<br>Branched-chain amino acid transport system permease                                       | Unknown             |
| ODI_R3594 | 1 | 5.16 | -1.07 protein LivM (TC 3.A.1.4.1)<br>Putative SigmaB asociated two-component system sensor                              | CytoplasmicMembrane |
| ODI_R3598 | 1 | 4.92 | 1.51 protein  | CytoplasmicMembrane |
| ODI_R3617 | 2 | 7.62 | 0 hypothetical protein  | Unknown             |
| ODI_R3652 | 1 | 5.29 | -2.58 ThiJ/Pfpl domain protein  | Unknown             |
| ODI_R3680 | 5 | 8.57 | -1.13 hypothetical protein  | Unknown             |
| ODI_R3683 | 4 | 7.42 | -2.19 FIG00858788: hypothetical protein   | Cytoplasmic         |
| ODI_R3692 | 1 | 6.24 | -2.06 Oxidoreductase, short-chain dehydrogenase/reductase family  | Cytoplasmic         |
| ODI_R3694 | 1 | 3.11 | -1.7 Capsule polysaccharide export protein  | Cytoplasmic         |
| ODI_R3717 | 1 | 7.46 | -1.12 Enoyl-[acyl-carrier-protein] reductase [NADH]   | CytoplasmicMembrane |
| ODI_R3741 | 1 | 7.25 | 0.83 putative membrane protein  | CytoplasmicMembrane |
| ODI_R3798 | 1 | 4.54 | 0 hypothetical protein  | Unknown             |
| ODI_R3799 | 1 | 6.07 | 0 Putative Heme-regulated two-component response regulator  | CytoplasmicMembrane |
| ODI_R3814 | 1 | 6.86 | 2.74 Phosphatidylethanolamine N-methyltransferase   | Unknown             |
| ODI_R3848 | 1 | 4.39 | 0 putative permease of ferrichrome ABC transporter<br>ABC-type Fe <sup>3+</sup> -siderophore transport system, permease | CytoplasmicMembrane |
| ODI_R3849 | 1 | 5.4  | 0 component   | CytoplasmicMembrane |
| ODI_R3850 | 1 | 7.38 | -1.09 transport   | CytoplasmicMembrane |
| ODI_R3853 | 5 | 3.96 | -3.26 Transcriptional regulator, LysR family  | Cytoplasmic         |
| ODI_R3858 | 1 | 7.31 | -2.64 Respiratory nitrate reductase delta chain   | Cytoplasmic         |



Table S6

|           |   |      |  |                     |
|-----------|---|------|--|---------------------|
| ODI_R3862 | 1 | 4.7  | -1.45 Nitrate/nitrite transporter  | CytoplasmicMembrane |
| ODI_R3870 | 1 | 4.11 | -1.34 Alkanesulfonate monooxygenase  | Cytoplasmic         |
| ODI_R3893 | 1 | 2.88 | -1.27 Putative diheme cytochrome c-553   | CytoplasmicMembrane |
| ODI_R3983 | 1 | 4.28 | 1.52 IcmF-related protein  | CytoplasmicMembrane |
| ODI_R4005 | 4 | 6.07 | 4.4 Uncharacterized protein ImpA   | Cytoplasmic         |
| ODI_R4009 | 1 | 6.41 | 3.24 Methylated-DNA--protein-cysteine methyltransferase  | Cytoplasmic         |
| ODI_R4017 | 1 | 2.37 | -0.45 RND multidrug efflux transporter   | CytoplasmicMembrane |
| ODI_R4021 | 3 | 6.97 | 1.18 Leader peptidase (Prepilin peptidase) / N-methyltransferase<br>TRAP dicarboxylate transporter, DctQ subunit, unknown      | CytoplasmicMembrane |
| ODI_R4034 | 1 | 6.05 | -1.3 substrate 5<br>Oligopeptide transport system permease protein OppB (TC  | CytoplasmicMembrane |
| ODI_R4056 | 1 | 4.49 | 0.67 3.A.1.5.1)  | CytoplasmicMembrane |
| ODI_R4138 | 1 | 5.12 | -1.07 Thioredoxin reductase<br>TRAP dicarboxylate transporter, DctM subunit, unknown   | Cytoplasmic         |
| ODI_R4142 | 1 | 4.73 | -0.69 substrate 3<br>TRAP-type C4-dicarboxylate transport system, small  | CytoplasmicMembrane |
| ODI_R4143 | 1 | 6.49 | 0 permease component   | CytoplasmicMembrane |
| ODI_R4182 | 2 | 7.57 | -4.74 Putative inner membrane protein<br>Histone acetyltransferase HPA2 and related  | Unknown             |
| ODI_R4236 | 2 | 9.21 | 0 acetyltransferases   | Cytoplasmic         |
| ODI_R4269 | 1 | 5.83 | 0 5-formyltetrahydrofolate cyclo-ligase  | Unknown             |
| ODI_R4282 | 2 | 5.68 | -2.03 Alpha-ketoglutarate-dependent taurine dioxygenase  | Cytoplasmic         |
| ODI_R4296 | 1 | 4.18 | -1.88 Zinc ABC transporter, periplasmic-binding protein ZnuA<br>Iron(III) dicitrate transport system, periplasmic iron-binding | Periplasmic         |
| ODI_R4315 | 2 | 7.8  | -1.26 protein FecB (TC 3.A.1.14.1)<br>Glutamate Aspartate transport system permease protein GltK                               | Unknown             |
| ODI_R4360 | 1 | 6.64 | 0 (TC 3.A.1.3.4)   | CytoplasmicMembrane |
| ODI_R4362 | 1 | 2.49 | 0 LysR-family transcriptional regulator  | Cytoplasmic         |
| ODI_R4382 | 2 | 8.8  | 0 A/G-specific adenine glycosylase   | CytoplasmicMembrane |