

Supplemental material

The biocontrol agent and insect pathogen *Photorhabdus luminescens* interacts with plant roots

Alice Regaiolo^{1,*}, Nazzareno Dominelli^{1,*}, Karsten Andresen, Ralf Heermann*

¹Johannes-Gutenberg-University Mainz, Institute of Molecular Physiology (imP), Microbiology and Wine Research, Johann-Joachim-Becher-Weg 13, 55128 Mainz, Germany

* the authors contributed equally to the manuscript

*corresponding author (heermann@uni-mainz.de)

Keywords: Entomopathogenic bacteria, entomopathogenic nematodes, bacteria-plant interaction, phenotypic heterogeneity

Table S1: List of Differentially Expressed Genes in *P. luminescens* 2° cells in the presence of pea root exudates obtained from RNAseq analysis.

| Gene Name | log2 Fold Change | p value | Function |
|---------------------|------------------|----------|---|
| <i>PluDJC_11885</i> | 6.87628 | 0.0206 | chitinase |
| <i>PluDJC_24115</i> | 6.3953 | 0.0021 | periplasmic heavy metal sensor |
| <i>PluDJC_23505</i> | 5.81879 | 5.00E-04 | bacterioferritin-associated ferredoxin |
| <i>PluDJC_12430</i> | 5.76817 | 0.00645 | DUF805 domain-containing protein |
| <i>PluDJC_15505</i> | 5.61564 | 0.0019 | DUF3277 family protein |
| <i>PluDJC_12460</i> | 5.36275 | 0.0092 | chitin-binding protein |
| <i>PluDJC_11345</i> | 5.31142 | 0.02365 | hypothetical protein |
| <i>PluDJC_10990</i> | 5.2556 | 0.00385 | hypothetical protein |
| <i>PluDJC_15690</i> | 5.25491 | 5.00E-05 | catalase |
| <i>PluDJC_03740</i> | 5.2489 | 0.01665 | membrane protein |
| <i>PluDJC_03960</i> | 5.18849 | 0.00955 | XRE family transcriptional regulator. MrfJ Protein. repressor |
| <i>PluDJC_21620</i> | 5.17417 | 0.01265 | tail fiber assembly protein |
| <i>PluDJC_10985</i> | 5.11816 | 5.00E-05 | inverse autotransporter beta-barrel domain-containing protein |
| <i>PluDJC_12425</i> | 5.09951 | 0.00045 | FAD-dependent oxidoreductase |
| <i>PluDJC_13800</i> | 4.88762 | 0.0077 | hemin uptake protein HemP |
| <i>PluDJC_12440</i> | 4.80771 | 5.00E-05 | polyketide cyclase |
| <i>PluDJC_12435</i> | 4.71877 | 5.00E-05 | 4-aminobutyrate--2-oxoglutarate transaminase |
| <i>PluDJC_15515</i> | 4.64699 | 0.0119 | bacteriophage protein |
| <i>PluDJC_15015</i> | 4.57809 | 0.00845 | hypothetical protein |
| <i>PluDJC_15510</i> | 4.56877 | 5.00E-05 | DUF3383 domain-containing protein |
| <i>PluDJC_02160</i> | 4.47625 | 0.00015 | hypothetical protein |
| <i>PluDJC_00675</i> | 4.47415 | 0.0188 | universal stress protein UspB |
| <i>PluDJC_12445</i> | 4.35122 | 5.00E-05 | gamma-aminobutyraldehyde dehydrogenase |
| <i>PluDJC_00280</i> | 4.28976 | 0.02455 | D-ribose pyranase |
| <i>PluDJC_13625</i> | 4.23568 | 0.0431 | DUF1289 domain-containing protein. oxidoreductase |
| <i>PluDJC_07845</i> | 4.22692 | 0.00695 | cold shock-like protein CspD |
| <i>PluDJC_11030</i> | 4.20947 | 5.00E-05 | stress response protein YchH |
| <i>smpB</i> | 4.02402 | 5.00E-05 | SsrA-binding protein. smpB |
| <i>PluDJC_12275</i> | 4.01263 | 5.00E-05 | hypothetical protein. polyurethanase |
| <i>PluDJC_13620</i> | 4.00864 | 5.00E-05 | transcriptional regulator SlyA |
| <i>PluDJC_23060</i> | 3.96129 | 0.00825 | tRNA |
| <i>PluDJC_15445</i> | 3.80448 | 0.01645 | tail fiber assembly protein |
| <i>PluDJC_05330</i> | 3.78353 | 5.00E-05 | single-stranded DNA-binding protein |
| <i>PluDJC_11440</i> | 3.76167 | 0.01685 | hypothetical protein |
| <i>PluDJC_10375</i> | 3.60964 | 5.00E-05 | PRD domain-containing protein |
| <i>PluDJC_05625</i> | 3.59259 | 0.01425 | PilT/PilU family type 4a pilus ATPase |
| <i>PluDJC_05655</i> | 3.58648 | 0.0442 | DsbA family protein |
| <i>PluDJC_10370</i> | 3.56927 | 5.00E-05 | hypothetical protein |
| <i>PluDJC_14550</i> | 3.45793 | 5.00E-05 | DUF1508 domain-containing protein |

| | | | |
|---------------------|---------|----------|--|
| <i>PluDJC_06205</i> | 3.45331 | 5.00E-05 | transcription antiterminator/RNA stability regulator CspE |
| <i>PluDJC_05350</i> | 3.43194 | 0.0118 | hypothetical protein |
| <i>PluDJC_21720</i> | 3.35034 | 0.0036 | hypothetical protein. VImB like protein |
| <i>PluDJC_10380</i> | 3.34207 | 5.00E-05 | YhfX family PLP-dependent enzyme |
| <i>PluDJC_22225</i> | 3.32812 | 1.00E-04 | ornithine carbamoyltransferase |
| <i>PluDJC_17480</i> | 3.32431 | 5.00E-05 | hypothetical protein |
| <i>PluDJC_14040</i> | 3.32314 | 0.00545 | metal ABC transporter permease |
| <i>PluDJC_14580</i> | 3.32114 | 5.00E-05 | class I fructose-bisphosphate aldolase |
| <i>PluDJC_13845</i> | 3.29206 | 0.00045 | hypothetical protein |
| <i>PluDJC_03315</i> | 3.26786 | 5.00E-05 | matrixin family metalloprotease. serralyisin |
| <i>PluDJC_23500</i> | 3.23158 | 5.00E-05 | bacterioferritin |
| <i>PluDJC_21145</i> | 3.20286 | 5.00E-05 | APC family permease |
| <i>PluDJC_10255</i> | 3.20245 | 0.0021 | D-serine transporter DsdX |
| <i>PluDJC_22230</i> | 3.1211 | 0.02115 | hypothetical protein |
| <i>PluDJC_14950</i> | 3.10185 | 5.00E-05 | iron ABC transporter permease |
| <i>PluDJC_05520</i> | 3.09809 | 0.02425 | DUF3085 domain-containing protein |
| <i>PluDJC_02265</i> | 3.08015 | 0.001 | VRR-NUC domain-containing protein |
| <i>PluDJC_00270</i> | 3.05975 | 0.00105 | ATPase RavA stimulator ViaA |
| <i>PluDJC_21140</i> | 3.05353 | 0.0041 | DUF3156 family protein |
| <i>PluDJC_10865</i> | 3.03807 | 0.006 | tail assembly protein |
| <i>PluDJC_20090</i> | 2.99454 | 0.0268 | hypothetical protein |
| <i>PluDJC_12930</i> | 2.9624 | 5.00E-05 | cob(I)alamin adenosyltransferase |
| <i>PluDJC_03495</i> | 2.95802 | 0.0208 | Rho-binding antiterminator |
| <i>PluDJC_16740</i> | 2.94935 | 0.00155 | iron-sulfur cluster assembly protein IscA |
| <i>PluDJC_19160</i> | 2.88271 | 0.00155 | transcriptional regulator BofA |
| <i>PluDJC_09110</i> | 2.84985 | 0.0227 | ribosome modulation factor |
| <i>PluDJC_06705</i> | 2.7834 | 0.0014 | hypothetical protein |
| <i>PluDJC_19815</i> | 2.72432 | 0.02195 | pirin family protein |
| <i>PluDJC_03822</i> | 2.71407 | 7.00E-04 | hypothetical protein |
| <i>PluDJC_10280</i> | 2.69455 | 0.00185 | type II toxin-antitoxin system RelE/ParE family toxin. addiction module toxin RelE |
| <i>PluDJC_21035</i> | 2.67326 | 0.0393 | DUF1435 family protein |
| <i>PluDJC_04230</i> | 2.65053 | 5.00E-05 | type VI secretion system tip protein VgrG |
| <i>PluDJC_06425</i> | 2.64932 | 5.00E-05 | ferric iron uptake transcriptional regulator |
| <i>PluDJC_16170</i> | 2.63146 | 5.00E-05 | TIGR01777 family protein |
| <i>PluDJC_24585</i> | 2.62299 | 0.0057 | formate dehydrogenase cytochrome b556 subunit |
| <i>PluDJC_12480</i> | 2.56253 | 0.00105 | TIGR02293 family toxin-antitoxin system antitoxin component |
| <i>PluDJC_10855</i> | 2.54253 | 5.00E-05 | aquaporin Z |
| <i>PluDJC_19360</i> | 2.52862 | 0.0021 | phosphate regulon transcriptional regulatory protein PhoB |
| <i>PluDJC_19615</i> | 2.48874 | 5.00E-05 | 3,4-dihydroxy-2-butanone-4-phosphate synthase |
| <i>PluDJC_15335</i> | 2.45739 | 0.00325 | addiction module antidote protein. HigA family. XRE transcriptional regulator |
| <i>PluDJC_07425</i> | 2.45194 | 0.0019 | molybdopterin synthase catalytic subunit MoaE |
| <i>PluDJC_05975</i> | 2.42781 | 5.00E-05 | carbon storage regulator |

| | | | |
|---------------------|---------|----------|---|
| <i>PluDJC_11960</i> | 2.42218 | 0.0059 | type II toxin-antitoxin system ParD family antitoxin |
| <i>PluDJC_12890</i> | 2.40357 | 5.00E-05 | hypothetical protein |
| <i>PluDJC_00425</i> | 2.36509 | 0.0049 | DUF2282 domain-containing protein |
| <i>PluDJC_13835</i> | 2.34191 | 0.00035 | helix-turn-helix domain-containing protein. AraC transcriptor regulator |
| <i>PluDJC_19790</i> | 2.34134 | 5.00E-05 | DUF883 domain-containing protein. membrane protein |
| <i>PluDJC_02070</i> | 2.3336 | 0.0094 | protein SlyX |
| <i>PluDJC_14480</i> | 2.30292 | 0.0363 | phosphoribosylglycinamide formyltransferase |
| <i>PluDJC_13815</i> | 2.2889 | 0.00015 | hemin ABC transporter substrate-binding protein |
| <i>PluDJC_10275</i> | 2.27857 | 0.02465 | hypothetical protein |
| <i>PluDJC_06710</i> | 2.27206 | 0.00245 | peptidase M4 family protein |
| <i>PluDJC_06415</i> | 2.25413 | 0.00235 | type II toxin-antitoxin system YafQ family toxin |
| <i>PluDJC_13505</i> | 2.25023 | 0.00025 | Zinc transport protein ZntB |
| <i>PluDJC_09560</i> | 2.24855 | 0.00085 | biofilm formation regulator BssS |
| <i>PluDJC_12215</i> | 2.24528 | 0.0035 | hypothetical protein. Arc family DNAbindprotein. toxic-antitoxic system HicB Nitrosomonas |
| <i>PluDJC_14210</i> | 2.23683 | 0.00075 | hypothetical protein |
| <i>PluDJC_14215</i> | 2.20892 | 0.0032 | type II restriction endonuclease PaeR7I |
| <i>PluDJC_05660</i> | 2.20764 | 0.0077 | MBL fold metallo-hydrolase. beta lactamase |
| <i>PluDJC_11000</i> | 2.20329 | 5.00E-05 | hypothetical protein |
| <i>PluDJC_23725</i> | 2.20201 | 5.00E-05 | 1,4-dihydroxy-2-naphthoate polyprenyltransferase |
| <i>PluDJC_22505</i> | 2.19933 | 0.00245 | putative DNA-binding transcriptional regulator |
| <i>PluDJC_20235</i> | 2.1914 | 5.00E-05 | DNA-binding transcriptional regulator Fis |
| <i>PluDJC_10995</i> | 2.18196 | 2.00E-04 | hypothetical protein |
| <i>PluDJC_12485</i> | 2.17299 | 0.0024 | RES domain-containing protein |
| <i>PluDJC_11445</i> | 2.16917 | 1.00E-04 | heat shock protein HslJ |
| <i>PluDJC_06415</i> | 2.14987 | 0.0025 | type II toxin-antitoxin system RelB/DinJ family antitoxin. XRE transcription reg. |
| <i>PluDJC_11575</i> | 2.14 | 0.04645 | type II toxin-antitoxin system RelE/ParE family toxin |
| <i>PluDJC_07760</i> | 2.11571 | 0.0155 | hypothetical protein |
| <i>PluDJC_01825</i> | 2.10368 | 5.00E-05 | Hcp family type VI secretion system effector |
| <i>PluDJC_01280</i> | 2.08546 | 5.00E-05 | disulfide bond formation protein B |
| <i>PluDJC_12855</i> | 2.07901 | 0.0061 | alpha/beta hydrolase |
| <i>PluDJC_08510</i> | 2.07629 | 5.00E-05 | Rpn family recombination-promoting nuclease/putative transposase |
| <i>PluDJC_17325</i> | 2.07437 | 5.00E-05 | autotransporter domain-containing esterase. lipase |
| <i>PluDJC_09110</i> | 2.0739 | 0.0109 | acylphosphatase |
| <i>PluDJC_11430</i> | 2.07134 | 5.00E-05 | YcgN family cysteine cluster protein |
| <i>PluDJC_16735</i> | 2.02714 | 5.00E-05 | co-chaperone HscB |
| <i>PluDJC_12100</i> | 2.01634 | 0.0033 | cytotoxin |
| <i>PluDJC_21835</i> | 2.00046 | 0.01005 | transcription/translation regulatory transformer protein RfaH |
| <i>PluDJC_17215</i> | 1.98906 | 5.00E-05 | SsrA-binding protein SmpB |
| <i>PluDJC_21205</i> | 1.98172 | 5.00E-05 | FAD-binding oxidoreductase |
| <i>PluDJC_12235</i> | 1.95376 | 0.01195 | type II toxin-antitoxin system RelE/ParE family toxin. plasmid stabilization |

| | | | |
|---------------------|---------|----------|--|
| <i>PluDJC_16745</i> | 1.93679 | 5.00E-05 | Fe-S cluster assembly scaffold IscU |
| <i>PluDJC_14955</i> | 1.9312 | 5.00E-05 | iron ABC transporter substrate-binding protein |
| <i>PluDJC_05675</i> | 1.91638 | 5.00E-05 | diaminopimelate decarboxylase |
| <i>PluDJC_20230</i> | 1.91563 | 5.00E-05 | tRNA dihydrouridine synthase DusB |
| <i>PluDJC_15955</i> | 1.91108 | 5.00E-05 | hypothetical protein. RhS like core protein |
| <i>PluDJC_13400</i> | 1.91107 | 0.00235 | peptide-methionine (R)-S-oxide reductase |
| <i>PluDJC_20020</i> | 1.89217 | 5.00E-05 | ribosome hibernation promoting factor |
| <i>PluDJC_21845</i> | 1.87584 | 5.00E-05 | Sec-independent protein translocase subunit TatC |
| <i>PluDJC_17730</i> | 1.87298 | 5.00E-05 | oxidative stress defense protein |
| <i>PluDJC_10820</i> | 1.85825 | 0.00075 | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase |
| <i>PluDJC_03675</i> | 1.85577 | 5.00E-05 | murein hydrolase activator NlpD. peptidase M23 |
| <i>PluDJC_10165</i> | 1.84506 | 5.00E-05 | flagellar regulatory protein FlIZ |
| <i>PluDJC_12565</i> | 1.83847 | 0.04995 | electron transport complex subunit RsxA |
| <i>PluDJC_14965</i> | 1.82471 | 0.0043 | LysR family transcriptional regulator |
| <i>PluDJC_13395</i> | 1.79979 | 0.00365 | DUF1315 family protein |
| <i>PluDJC_20450</i> | 1.7985 | 5.00E-05 | Rpn family recombination-promoting nuclease/putative transposase |
| <i>PluDJC_17205</i> | 1.79667 | 0.00985 | RnfH family protein |
| <i>PluDJC_23730</i> | 1.79095 | 5.00E-05 | ribonuclease E activity regulator RraA |
| <i>PluDJC_22695</i> | 1.7892 | 1.00E-04 | HTH-type transcriptional repressor. nsrR |
| <i>PluDJC_14225</i> | 1.78843 | 5.00E-05 | modification methylase PaeR7I |
| <i>PluDJC_18465</i> | 1.78439 | 5.00E-05 | aldehyde dehydrogenase family protein |
| <i>PluDJC_21200</i> | 1.77666 | 1.00E-04 | DUF861 domain-containing protein |
| <i>PluDJC_23835</i> | 1.76404 | 0.02815 | type II toxin-antitoxin system RelE/ParE family toxin |
| <i>PluDJC_15330</i> | 1.75186 | 0.0191 | hypothetical protein |
| <i>PluDJC_21135</i> | 1.74492 | 0.01235 | hypothetical protein |
| <i>PluDJC_14230</i> | 1.74194 | 5.00E-05 | glutamine-hydrolyzing GMP synthase |
| <i>PluDJC_12355</i> | 1.73682 | 0.00845 | antitoxin |
| <i>PluDJC_03420</i> | 1.72425 | 3.00E-04 | Ribosome-recycling factor |
| <i>PluDJC_13055</i> | 1.71168 | 0.00255 | acyl-CoA thioester hydrolase YciA |
| <i>PluDJC_16275</i> | 1.70755 | 6.00E-04 | tripartite tricarboxylate transporter permease |
| <i>PluDJC_13055</i> | 1.70033 | 0.00155 | TonB system transport protein TonB |
| <i>PluDJC_07415</i> | 1.69656 | 0.0028 | cyclic pyranopterin monophosphate synthase MoaC |
| <i>PluDJC_05175</i> | 1.68868 | 0.001 | hypothetical protein |
| <i>PluDJC_22575</i> | 1.68068 | 0.0019 | YtfJ family protein |
| <i>PluDJC_16000</i> | 1.67868 | 5.00E-05 | Rpn family recombination-promoting nuclease/putative transposase |
| <i>PluDJC_20450</i> | 1.67621 | 0.00235 | LysR family transcriptional regulator |
| <i>PluDJC_10030</i> | 1.65666 | 0.0126 | XRE family transcriptional regulator. 2-hydroxyacid dehydrogenase |
| <i>PluDJC_12230</i> | 1.64065 | 0.00335 | ribbon-helix-helix protein. CopG family |
| <i>PluDJC_07315</i> | 1.63698 | 0.0021 | pyridoxal phosphatase |
| <i>PluDJC_22560</i> | 1.63545 | 0.0021 | peptide-methionine (S)-S-oxide reductase MsrA |

| | | | |
|---------------------|---------|----------|--|
| <i>PluDJC_20270</i> | 1.62865 | 0.0055 | high-affinity branched-chain amino acid ABC transporter permease LivM |
| <i>PluDJC_05975</i> | 1.60914 | 0.02175 | inner membrane protein YpjD |
| <i>PluDJC_18840</i> | 1.60126 | 5.00E-05 | Rpn family recombination-promoting nuclease/putative transposase |
| <i>PluDJC_01480</i> | 1.59558 | 5.00E-05 | hypothetical protein |
| <i>PluDJC_01370</i> | 1.59286 | 0.00445 | hypothetical protein |
| <i>PluDJC_00420</i> | 1.58851 | 0.01285 | DUF692 domain-containing protein |
| <i>PluDJC_14235</i> | 1.57953 | 5.00E-05 | IMP dehydrogenase |
| <i>PluDJC_16750</i> | 1.56049 | 1.00E-04 | IscS subfamily cysteine desulfurase |
| <i>PluDJC_24585</i> | 1.53773 | 0.0027 | Ribonuclease P protein component. rpnA |
| <i>PluDJC_17855</i> | 1.52983 | 0.0082 | beta-lactamase regulator AmpE |
| <i>PluDJC_03065</i> | 1.52406 | 0.0024 | co-chaperone DjIA |
| <i>PluDJC_13055</i> | 1.51748 | 0.02755 | DUF440 family protein. dsDNA-mimic protein |
| <i>PluDJC_00265</i> | 1.47121 | 0.00405 | aspartate--ammonia ligase |
| <i>PluDJC_21130</i> | 1.46246 | 0.0283 | nucleotidyl transferase AbiEii/AbiGii toxin family protein |
| <i>PluDJC_21175</i> | 1.45249 | 0.00055 | DUF1795 domain-containing protein |
| <i>PluDJC_19505</i> | 1.45004 | 0.00035 | ImmA/IrrE family metallo-endopeptidase |
| <i>PluDJC_19015</i> | 1.44936 | 0.00195 | hypothetical protein |
| <i>PluDJC_24570</i> | 1.44852 | 0.00265 | sulfate ABC transporter substrate-binding protein |
| <i>PluDJC_03680</i> | 1.44391 | 5.00E-04 | RNA polymerase sigma factor RpoS |
| <i>PluDJC_01485</i> | 1.44165 | 0.00035 | hypothetical protein |
| <i>PluDJC_12355</i> | 1.42461 | 0.00245 | SDR family oxidoreductase. 3-ketoacyl-ACP reductase |
| <i>PluDJC_16730</i> | 1.42423 | 2.00E-04 | Fe-S protein assembly chaperone HscA |
| <i>PluDJC_21905</i> | 1.4122 | 0.0036 | 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase |
| <i>PluDJC_16905</i> | 1.40851 | 0.0351 | hypothetical protein. plasmid stabilization protein |
| <i>PluDJC_13785</i> | 1.40537 | 5.00E-05 | phosphoenolpyruvate synthase |
| <i>PluDJC_04730</i> | 1.39957 | 0.0219 | helix-turn-helix transcriptional regulator |
| <i>PluDJC_13425</i> | 1.39599 | 0.00015 | fatty acid metabolism transcriptional regulator FadR |
| <i>PluDJC_12095</i> | 1.39504 | 0.04055 | antitoxin |
| <i>PluDJC_08625</i> | 1.3869 | 0.00055 | Rpn family recombination-promoting nuclease/putative transposase |
| <i>PluDJC_24405</i> | 1.37401 | 0.0012 | 3-deoxy-D-manno-octulosonic acid transferase |
| <i>PluDJC_10415</i> | 1.37326 | 0.00475 | LuxR family transcriptional regulator |
| <i>PluDJC_15625</i> | 1.37283 | 0.0149 | type II toxin-antitoxin system VapC family toxin. plasmid stability protein StbB |
| <i>PluDJC_07410</i> | 1.36905 | 0.001 | GTP 3'\.8-cyclase MoaA |
| <i>PluDJC_20380</i> | 1.36375 | 0.00195 | DUF29 domain-containing protein |
| <i>PluDJC_19735</i> | 1.35608 | 0.01355 | helix-turn-helix domain-containing protein. XRE family transcriptional regulator |
| <i>PluDJC_07405</i> | 1.34536 | 0.00675 | uridine diphosphate-N-acetylglucosamine-binding protein YvckK |
| <i>PluDJC_01395</i> | 1.33651 | 0.00035 | molecular chaperone |
| <i>PluDJC_10395</i> | 1.3361 | 0.0048 | membrane protein |
| <i>PluDJC_20265</i> | 1.33303 | 0.0424 | ABC transporter ATP-binding protein |
| <i>PluDJC_21195</i> | 1.32154 | 0.00245 | aldehyde dehydrogenase family protein |

| | | | |
|---------------------|----------|----------|---|
| <i>PluDJC_12740</i> | 1.29411 | 0.0268 | glycosyltransferase family 2 protein |
| <i>PluDJC_17240</i> | 1.28963 | 0.00235 | type II toxin-antitoxin system HicB family antitoxin |
| <i>PluDJC_17245</i> | 1.27696 | 0.04085 | type II toxin-antitoxin system HicA family toxin |
| <i>PluDJC_16725</i> | 1.27329 | 0.0146 | ISC system 2Fe-2S type ferredoxin |
| <i>PluDJC_16415</i> | 1.26898 | 0.00115 | Rpn family recombination-promoting nuclease/putative transposase |
| <i>PluDJC_13975</i> | 1.26798 | 4.00E-04 | integration host factor subunit alpha |
| <i>PluDJC_19435</i> | 1.24997 | 0.036 | DUF1062 domain-containing protein |
| <i>PluDJC_01735</i> | 1.2353 | 0.0382 | hypothetical protein |
| <i>PluDJC_14415</i> | 1.23365 | 0.00835 | AI-2E family transporter |
| <i>PluDJC_19730</i> | 1.23284 | 0.0116 | toxin RelE |
| <i>PluDJC_11450</i> | 1.21704 | 0.02515 | 2-hydroxyacid dehydrogenase. D-lactate dehydrogenase |
| <i>PluDJC_11395</i> | 1.2035 | 0.00085 | long-chain-fatty-acid--CoA ligase FadD |
| <i>PluDJC_17480</i> | 1.20171 | 0.002 | propionate catabolism operon regulatory protein PrpR |
| <i>PluDJC_23690</i> | 1.19478 | 0.0023 | met regulon transcriptional regulator MetJ |
| <i>PluDJC_16265</i> | 1.19449 | 0.02545 | tripartite tricarboxylate transporter substrate binding protein |
| <i>PluDJC_22740</i> | 1.18887 | 0.00305 | LysR family transcriptional regulator |
| <i>PluDJC_16185</i> | 1.18467 | 0.00535 | colicin V production protein |
| <i>PluDJC_22525</i> | 1.16278 | 0.03965 | transcriptional regulator ArgR. arginine repressor |
| <i>PluDJC_14475</i> | 1.16265 | 0.02605 | phosphoribosylformylglycinamide cyclo-ligase |
| <i>PluDJC_05665</i> | 1.13742 | 0.01895 | LysR family transcriptional regulator |
| <i>PluDJC_12900</i> | 1.1341 | 0.00695 | hypothetical protein |
| <i>PluDJC_19695</i> | 1.12832 | 0.00445 | tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD |
| <i>PluDJC_19360</i> | 1.12401 | 0.00205 | Rpn family recombination-promoting nuclease/putative transposase |
| <i>PluDJC_11425</i> | 1.11948 | 0.00545 | fumarylacetoacetate hydrolase family protein |
| <i>PluDJC_16910</i> | 1.11796 | 0.00235 | phosphoribosylformylglycinamide synthase |
| <i>PluDJC_13095</i> | 1.10895 | 0.01135 | oligopeptide ABC transporter permease OppB |
| <i>PluDJC_06975</i> | 1.08714 | 0.0117 | Nif3-like dinuclear metal center hexameric protein |
| <i>PluDJC_21840</i> | 1.07155 | 0.0026 | porphobilinogen synthase |
| <i>PluDJC_06075</i> | 1.04972 | 0.005 | outer membrane protein assembly factor BamD |
| <i>PluDJC_19500</i> | 1.02164 | 0.01975 | hypothetical protein |
| <i>PluDJC_11435</i> | 1.01839 | 0.007 | hypothetical protein |
| <i>PluDJC_10415</i> | 1.00322 | 0.0086 | helix-turn-helix transcriptional regulator. LuxR family transcriptional regulator |
| <i>PluDJC_20195</i> | -6.75812 | 0.0127 | Bcr/CflA family efflux MFS transporter |
| <i>PluDJC_02900</i> | -5.97221 | 5.00E-05 | molecular chaperone DnaJ |
| <i>PluDJC_18970</i> | -5.89903 | 5.00E-05 | molecular chaperone HtpG |
| <i>PluDJC_20460</i> | -5.87562 | 5.00E-05 | co-chaperone GroES |
| <i>PluDJC_15900</i> | -5.76873 | 0.0338 | aspartate aminotransferase family protein |
| <i>PluDJC_20195</i> | -5.63593 | 1.00E-04 | isocitrate/isopropylmalate dehydrogenase family protein |
| <i>PluDJC_02895</i> | -5.59007 | 5.00E-05 | molecular chaperone DnaK |
| <i>PluDJC_15400</i> | -5.50578 | 0.01655 | hypothetical protein |
| <i>PluDJC_03235</i> | -5.47929 | 0.0127 | hypothetical protein |

| | | | |
|---------------------|----------|----------|--|
| <i>PluDJC_23720</i> | -5.46407 | 5.00E-05 | HslU--HslV peptidase ATPase subunit |
| <i>PluDJC_23490</i> | -5.25005 | 5.00E-05 | 50S ribosomal protein L3 |
| <i>PluDJC_00990</i> | -5.24041 | 0.01015 | asparagine synthase |
| <i>PluDJC_20885</i> | -5.20137 | 0.00905 | OmpA family protein |
| <i>PluDJC_18730</i> | -5.1898 | 0.0127 | cold-shock protein |
| <i>PluDJC_20795</i> | -5.15252 | 0.009 | Hcp family type VI secretion system effector |
| <i>PluDJC_23400</i> | -5.07539 | 0.0127 | 50S ribosomal protein L30 |
| <i>PluDJC_22830</i> | -5.05348 | 0.01655 | hypothetical protein |
| <i>PluDJC_20455</i> | -5.04552 | 5.00E-05 | chaperonin GroEL |
| <i>PluDJC_23460</i> | -5.03935 | 5.00E-05 | 50S ribosomal protein L22 |
| <i>PluDJC_15035</i> | -4.93148 | 0.01655 | 50S ribosomal protein L25 |
| <i>PluDJC_20620</i> | -4.92246 | 0.0127 | hypothetical protein |
| <i>PluDJC_19475</i> | -4.87518 | 0.0127 | DUF29 domain-containing protein |
| <i>PluDJC_19620</i> | -4.76388 | 0.01655 | accessory factor UbiK family protein |
| <i>PluDJC_14110</i> | -4.73338 | 5.00E-05 | non-heme ferritin |
| <i>PluDJC_05070</i> | -4.72299 | 5.00E-05 | 5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase |
| <i>PluDJC_22270</i> | -4.66768 | 5.00E-04 | anaerobic ribonucleoside-triphosphate reductase |
| <i>PluDJC_03630</i> | -4.64818 | 0.0057 | sulfate adenylyltransferase subunit CysD |
| <i>PluDJC_05075</i> | -4.6352 | 0.0173 | 2-hydroxyhepta-2.4-diene-1.7-dioate isomerase |
| <i>PluDJC_02595</i> | -4.56917 | 0.0011 | PLP-dependent transferase |
| <i>PluDJC_06090</i> | -4.56117 | 5.00E-05 | ATP-dependent chaperone ClpB |
| <i>PluDJC_14895</i> | -4.5512 | 0.0127 | NAD(P)-dependent oxidoreductase |
| <i>PluDJC_15080</i> | -4.54606 | 0.0127 | DUF4431 domain-containing protein |
| <i>PluDJC_23465</i> | -4.5234 | 5.00E-05 | 50S ribosomal protein L22 |
| <i>PluDJC_09075</i> | -4.51146 | 0.0034 | N-glycosyltransferase |
| <i>PluDJC_23715</i> | -4.51042 | 0.0039 | ATP-dependent protease subunit HslV |
| <i>PluDJC_03240</i> | -4.48918 | 5.00E-05 | serine protease |
| <i>PluDJC_13405</i> | -4.45225 | 5.00E-05 | glyceraldehyde-3-phosphate dehydrogenase |
| <i>PluDJC_23375</i> | -4.43112 | 5.00E-05 | 30S ribosomal protein S11 |
| <i>PluDJC_05065</i> | -4.42829 | 5.00E-05 | 3.4-dihydroxyphenylacetate 2.3-dioxygenase |
| <i>PluDJC_20190</i> | -4.40881 | 0.027 | RraA family protein |
| <i>PluDJC_23510</i> | -4.40336 | 7.00E-04 | elongation factor Tu |
| <i>PluDJC_23160</i> | -4.40151 | 7.00E-04 | ketol-acid reductoisomerase |
| <i>PluDJC_18810</i> | -4.37768 | 0.0484 | peptidylprolyl isomerase B |
| <i>PluDJC_23475</i> | -4.37201 | 5.00E-05 | 50S ribosomal protein L2 |
| <i>PluDJC_15890</i> | -4.33825 | 5.00E-05 | succinylglutamate-semialdehyde dehydrogenase |
| <i>PluDJC_22415</i> | -4.3382 | 0.0443 | 30S ribosome-binding factor RbfA |
| <i>PluDJC_20185</i> | -4.32084 | 0.02335 | hypothetical protein |
| <i>PluDJC_22425</i> | -4.30021 | 5.00E-05 | transcription termination/antitermination protein NusA |
| <i>PluDJC_20435</i> | -4.28931 | 0.03255 | elongation factor P |
| <i>PluDJC_24455</i> | -4.27371 | 0.0483 | 50S ribosomal protein L28 |
| <i>PluDJC_14980</i> | -4.23319 | 0.00115 | 1-phosphofructokinase |

| | | | |
|---------------------|----------|----------|---|
| <i>PluDJC_06065</i> | -4.22895 | 0.0272 | bifunctional chorismate mutase/prephenate dehydratase |
| <i>PluDJC_17660</i> | -4.20563 | 5.00E-05 | aminomethyl-transferring glycine dehydrogenase |
| <i>PluDJC_23395</i> | -4.19595 | 5.00E-05 | 50S ribosomal protein L15 |
| <i>PluDJC_15895</i> | -4.17214 | 0.00035 | arginine N-succinyltransferase |
| <i>PluDJC_23440</i> | -4.14683 | 5.00E-05 | 50S ribosomal protein L14 |
| <i>PluDJC_05925</i> | -4.08762 | 0.0127 | xanthine phosphoribosyltransferase |
| <i>PluDJC_03410</i> | -4.02548 | 5.00E-05 | elongation factor Ts |
| <i>PluDJC_23420</i> | -4.01003 | 5.00E-05 | 30S ribosomal protein S8 |
| <i>PluDJC_19135</i> | -4.00171 | 5.00E-05 | endopeptidase La |
| <i>PluDJC_14155</i> | -3.96761 | 4.00E-04 | PTS mannose/fructose/sorbose transporter subunit IIC |
| <i>PluDJC_10155</i> | -3.95257 | 5.00E-05 | flagellin FliC |
| <i>PluDJC_23405</i> | -3.94488 | 5.00E-05 | 30S ribosomal protein S5 |
| <i>PluDJC_14125</i> | -3.93415 | 0.00085 | Protein yebF precursor |
| <i>PluDJC_07585</i> | -3.898 | 0.00395 | ABC-F family ATPase |
| <i>PluDJC_04775</i> | -3.89699 | 0.00715 | hypothetical protein |
| <i>PluDJC_23370</i> | -3.88934 | 5.00E-05 | 30S ribosomal protein S4 |
| <i>PluDJC_22835</i> | -3.88769 | 0.0065 | hypothetical protein |
| <i>PluDJC_23380</i> | -3.87673 | 5.00E-05 | 30S ribosomal protein S13 |
| <i>PluDJC_17670</i> | -3.87083 | 5.00E-05 | glycine cleavage system aminomethyltransferase GcvT |
| <i>PluDJC_00210</i> | -3.8684 | 5.00E-05 | F0F1 ATP synthase subunit gamma |
| <i>PluDJC_10365</i> | -3.85439 | 5.00E-05 | PTS fructose transporter subunit IIBC |
| <i>PluDJC_20410</i> | -3.83925 | 0.0209 | fumarate reductase (quinol) flavoprotein subunit |
| <i>PluDJC_05050</i> | -3.829 | 0.00205 | NAD-dependent succinate-semialdehyde dehydrogenase |
| <i>PluDJC_19150</i> | -3.81257 | 5.00E-05 | trigger factor |
| <i>PluDJC_05080</i> | -3.79826 | 0.02955 | hpaG1 |
| <i>PluDJC_23430</i> | -3.7865 | 5.00E-05 | 50S ribosomal protein L5 |
| <i>PluDJC_03405</i> | -3.78376 | 5.00E-05 | 30S ribosomal protein S2 |
| <i>PluDJC_03505</i> | -3.74437 | 5.00E-05 | proline--tRNA ligase |
| <i>PluDJC_17665</i> | -3.74065 | 0.00025 | glycine cleavage system protein GcvH |
| <i>PluDJC_22430</i> | -3.70907 | 0.00505 | ribosome maturation factor RimP |
| <i>PluDJC_23360</i> | -3.69971 | 5.00E-05 | 50S ribosomal protein L17 |
| <i>PluDJC_15410</i> | -3.69637 | 0.00175 | glycosyltransferase family 2 protein |
| <i>PluDJC_22820</i> | -3.68195 | 0.0215 | type VI secretion system tip protein VgrG |
| <i>PluDJC_04680</i> | -3.66691 | 0.00025 | hypothetical protein |
| <i>PluDJC_00220</i> | -3.66295 | 5.00E-05 | F0F1 ATP synthase subunit delta |
| <i>PluDJC_14160</i> | -3.65908 | 1.00E-04 | PTS mannose transporter subunit IID |
| <i>PluDJC_23365</i> | -3.63227 | 5.00E-05 | DNA-directed RNA polymerase subunit alpha |
| <i>PluDJC_07685</i> | -3.5685 | 5.00E-05 | NADP-dependent phosphogluconate dehydrogenase |
| <i>PluDJC_23435</i> | -3.56649 | 5.00E-05 | 50S ribosomal protein L24 |
| <i>PluDJC_23470</i> | -3.56254 | 0.00025 | 30S ribosomal protein S19 |
| <i>PluDJC_01585</i> | -3.55806 | 5.00E-05 | ABC transporter substrate-binding protein |
| <i>PluDJC_22420</i> | -3.54059 | 5.00E-05 | translation initiation factor IF-2 |

| | | | |
|---------------------|----------|----------|---|
| <i>PluDJC_06980</i> | -3.52694 | 5.00E-05 | citrate synthase |
| <i>PluDJC_22520</i> | -3.51176 | 5.00E-05 | malate dehydrogenase |
| <i>PluDJC_02800</i> | -3.49904 | 5.00E-05 | bifunctional aspartate kinase/homoserine dehydrogenase I |
| <i>PluDJC_23455</i> | -3.49402 | 5.00E-05 | 50S ribosomal protein L16 |
| <i>PluDJC_10360</i> | -3.48217 | 5.00E-05 | fused PTS fructose transporter subunit IIA/HPr protein |
| <i>PluDJC_12500</i> | -3.47764 | 5.00E-05 | DUF945 domain-containing protein |
| <i>PluDJC_00225</i> | -3.47403 | 5.00E-05 | F0F1 ATP synthase subunit B |
| <i>PluDJC_14150</i> | -3.47368 | 5.00E-05 | PTS mannose transporter subunit IIAB |
| <i>PluDJC_23410</i> | -3.45524 | 4.00E-04 | 50S ribosomal protein L18 |
| <i>PluDJC_01000</i> | -3.44739 | 0.0107 | spore coat protein CotH |
| <i>PluDJC_05045</i> | -3.43519 | 5.00E-05 | 2-oxo-hepta-3-ene-1,7-dioic acid hydratase |
| <i>PluDJC_03195</i> | -3.42765 | 5.00E-05 | type I secretion system permease/ATPase |
| <i>PluDJC_22380</i> | -3.40744 | 5.00E-05 | DEAD/DEAH family ATP-dependent RNA helicase |
| <i>PluDJC_24665</i> | -3.40342 | 0.00135 | membrane protein insertase YidC |
| <i>PluDJC_15885</i> | -3.3805 | 6.00E-04 | N-succinylarginine dihydrolase |
| <i>PluDJC_01185</i> | -3.36459 | 0.0188 | amino acid ABC transporter permease |
| <i>PluDJC_02135</i> | -3.34239 | 5.00E-05 | 50S ribosomal protein L1 |
| <i>PluDJC_21340</i> | -3.34119 | 0.0014 | DUF2170 family protein |
| <i>PluDJC_23350</i> | -3.34103 | 0.0139 | alternative ribosome-rescue factor A |
| <i>PluDJC_09965</i> | -3.33637 | 0.0081 | flagellar hook protein FlgE |
| <i>PluDJC_04850</i> | -3.31278 | 0.0117 | LuxR family transcriptional regulator |
| <i>PluDJC_12820</i> | -3.30834 | 0.01905 | LapA family protein |
| <i>PluDJC_05040</i> | -3.3004 | 0.00035 | 4-hydroxy-2-oxoheptanedioate aldolase |
| <i>PluDJC_00215</i> | -3.24946 | 5.00E-05 | F0F1 ATP synthase subunit alpha |
| <i>PluDJC_05605</i> | -3.2397 | 0.04805 | XTP/dITP diphosphatase |
| <i>PluDJC_16645</i> | -3.22894 | 0.04875 | hypothetical protein |
| <i>PluDJC_09035</i> | -3.20613 | 0.00015 | porin |
| <i>PluDJC_02810</i> | -3.20074 | 1.00E-04 | threonine synthase |
| <i>PluDJC_04670</i> | -3.19587 | 5.00E-05 | phosphopyruvate hydratase |
| <i>PluDJC_23415</i> | -3.18905 | 5.00E-05 | 50S ribosomal protein L6 |
| <i>PluDJC_07560</i> | -3.18581 | 0.0192 | alkylphosphonate utilization protein |
| <i>PluDJC_01815</i> | -3.16993 | 1.00E-04 | type VI secretion system contractile sheath large subunit |
| <i>PluDJC_00205</i> | -3.16294 | 5.00E-05 | F0F1 ATP synthase subunit beta |
| <i>PluDJC_12505</i> | -3.12825 | 0.00265 | adenosine deaminase |
| <i>PluDJC_23770</i> | -3.12396 | 5.00E-05 | 6-phosphofructokinase |
| <i>PluDJC_23390</i> | -3.11666 | 5.00E-05 | preprotein translocase subunit SecY |
| <i>PluDJC_21890</i> | -3.0847 | 0.01225 | uridine phosphorylase |
| <i>PluDJC_18050</i> | -3.07707 | 0.0015 | 3-isopropylmalate dehydratase large subunit |
| <i>PluDJC_22660</i> | -3.07559 | 1.00E-04 | primosomal replication protein N |
| <i>PluDJC_14625</i> | -3.06769 | 0.0117 | N-acetylmuramoyl-L-alanine amidase |
| <i>PluDJC_21810</i> | -3.04963 | 0.0448 | Xaa-Pro dipeptidase |
| <i>PluDJC_23425</i> | -3.04647 | 5.00E-05 | 30S ribosomal protein S14 |

| | | | |
|---------------------|----------|----------|--|
| <i>PluDJC_22650</i> | -3.03198 | 5.00E-05 | 50S ribosomal protein L9 |
| <i>PluDJC_22400</i> | -3.02897 | 5.00E-05 | polyribonucleotide nucleotidyltransferase |
| <i>PluDJC_02805</i> | -3.02659 | 1.00E-04 | homoserine kinase |
| <i>PluDJC_21585</i> | -3.02403 | 0.0107 | acetyltransferase |
| <i>PluDJC_18965</i> | -3.02032 | 0.00135 | adenylate kinase |
| <i>PluDJC_03500</i> | -3.01953 | 0.00305 | envelope stress response activation lipoprotein NlpE |
| <i>PluDJC_07780</i> | -2.99674 | 5.00E-05 | HAAAP family serine/threonine permease |
| <i>PluDJC_05060</i> | -2.99649 | 0.01615 | 5-carboxymethyl-2-hydroxymuconate Delta-isomerase |
| <i>PluDJC_07020</i> | -2.99549 | 5.00E-05 | succinate--CoA ligase subunit alpha |
| <i>PluDJC_02145</i> | -2.97868 | 5.00E-05 | 50S ribosomal protein L7/L12 |
| <i>PluDJC_23445</i> | -2.96957 | 0.00175 | 30S ribosomal protein S17 |
| <i>PluDJC_20635</i> | -2.95889 | 5.00E-05 | hypothetical protein |
| <i>PluDJC_00700</i> | -2.95275 | 5.00E-05 | oligopeptidase A |
| <i>PluDJC_15590</i> | -2.94675 | 5.00E-05 | DNA topoisomerase (ATP-hydrolyzing) subunit A |
| <i>PluDJC_16640</i> | -2.92786 | 5.00E-05 | Hcp family type VI secretion system effector |
| <i>PluDJC_02140</i> | -2.92019 | 5.00E-05 | 50S ribosomal protein L10 |
| <i>PluDJC_16085</i> | -2.91525 | 0.0121 | 3-hydroxy-5-phosphonooxypentane-2,4-dione thiolase |
| <i>PluDJC_22815</i> | -2.90286 | 5.00E-05 | type VI secretion system baseplate subunit TssF |
| <i>PluDJC_11870</i> | -2.85078 | 0.00595 | DUF1283 family protein |
| <i>PluDJC_08355</i> | -2.8247 | 5.00E-05 | formate C-acetyltransferase |
| <i>PluDJC_06725</i> | -2.82382 | 0.01575 | YgiW/Ydel family stress tolerance OB fold protein |
| <i>PluDJC_18005</i> | -2.81416 | 0.0063 | acetolactate synthase 3 large subunit |
| <i>PluDJC_06035</i> | -2.78523 | 5.00E-05 | tRNA (guanosine(37)-N1)-methyltransferase TrmD |
| <i>PluDJC_04665</i> | -2.78487 | 5.00E-05 | CTP synthase (glutamine hydrolyzing) |
| <i>PluDJC_02600</i> | -2.74841 | 5.00E-05 | pyridoxal-phosphate dependent enzyme |
| <i>PluDJC_02540</i> | -2.73765 | 5.00E-04 | hypothetical protein |
| <i>PluDJC_00230</i> | -2.72186 | 0.00095 | F0F1 ATP synthase subunit C |
| <i>PluDJC_04455</i> | -2.71373 | 0.0155 | 3-methyl-2-oxobutanoate hydroxymethyltransferase |
| <i>PluDJC_02130</i> | -2.7045 | 5.00E-05 | 50S ribosomal protein L11 |
| <i>PluDJC_05700</i> | -2.7007 | 0.0035 | Na(+)-translocating NADH-quinone reductase subunit A |
| <i>PluDJC_01180</i> | -2.70032 | 0.0131 | amino acid ABC transporter permease |
| <i>PluDJC_16790</i> | -2.6995 | 5.00E-05 | serine hydroxymethyltransferase |
| <i>PluDJC_21330</i> | -2.69473 | 1.00E-04 | DUF2491 family protein |
| <i>PluDJC_03635</i> | -2.67841 | 1.00E-04 | sulfate adenylyltransferase subunit CysN |
| <i>PluDJC_14390</i> | -2.62635 | 5.00E-05 | outer membrane protein assembly factor BamC |
| <i>PluDJC_13420</i> | -2.61606 | 5.00E-05 | D-amino acid dehydrogenase |
| <i>PluDJC_21500</i> | -2.60064 | 0.00605 | MBL fold metallo-hydrolase |
| <i>PluDJC_01600</i> | -2.59507 | 0.0159 | dipeptide ABC transporter ATP-binding protein |
| <i>PluDJC_11590</i> | -2.5853 | 0.0361 | urease subunit gamma |
| <i>PluDJC_22665</i> | -2.58386 | 0.00075 | 30S ribosomal protein S6 |
| <i>PluDJC_21670</i> | -2.55542 | 2.00E-04 | glucose-6-phosphate isomerase |
| <i>PluDJC_02940</i> | -2.55256 | 0.00155 | transcriptional activator NhaR |

| | | | |
|---------------------|----------|----------|---|
| <i>PluDJC_19635</i> | -2.53173 | 5.00E-05 | membrane protein |
| <i>PluDJC_01590</i> | -2.52541 | 5.00E-05 | dipeptide ABC transporter permease DppB |
| <i>PluDJC_04685</i> | -2.5212 | 5.00E-05 | cysteine desulfurase |
| <i>PluDJC_01175</i> | -2.51885 | 5.00E-05 | transporter substrate-binding domain-containing protein |
| <i>PluDJC_09930</i> | -2.51319 | 5.00E-05 | hypothetical protein |
| <i>PluDJC_06040</i> | -2.50252 | 0.00025 | 50S ribosomal protein L19 |
| <i>PluDJC_22410</i> | -2.49472 | 5.00E-05 | tRNA pseudouridine(55) synthase TruB |
| <i>PluDJC_00515</i> | -2.49396 | 5.00E-05 | phosphoenolpyruvate carboxykinase (ATP) |
| <i>PluDJC_02155</i> | -2.49393 | 5.00E-05 | DNA-directed RNA polymerase subunit beta' |
| <i>PluDJC_12060</i> | -2.4783 | 0.0045 | PhzF family phenazine biosynthesis protein |
| <i>PluDJC_00025</i> | -2.47395 | 0.01785 | Hcp family type VI secretion system effector |
| <i>PluDJC_22065</i> | -2.47289 | 1.00E-04 | S8 family peptidase |
| <i>PluDJC_07270</i> | -2.46512 | 5.00E-05 | 2.3-diphosphoglycerate-dependent phosphoglycerate mutase |
| <i>PluDJC_22060</i> | -2.45832 | 5.00E-05 | AAA family ATPase |
| <i>PluDJC_21290</i> | -2.41888 | 0.0232 | LamB/YcsF family protein |
| <i>PluDJC_02320</i> | -2.41804 | 0.00305 | zinc-binding dehydrogenase |
| <i>PluDJC_09970</i> | -2.41371 | 0.00905 | flagellar basal body rod protein FlgF |
| <i>PluDJC_02115</i> | -2.41195 | 5.00E-05 | elongation factor Tu |
| <i>PluDJC_07015</i> | -2.41088 | 5.00E-05 | ADP-forming succinate--CoA ligase subunit beta |
| <i>PluDJC_14900</i> | -2.4104 | 0.0046 | DUF496 family protein |
| <i>PluDJC_14630</i> | -2.40512 | 5.00E-05 | alanine:cation symporter family protein |
| <i>PluDJC_06790</i> | -2.40334 | 5.00E-05 | hypothetical protein |
| <i>PluDJC_22485</i> | -2.40143 | 0.00015 | GTPase ObgE |
| <i>PluDJC_17515</i> | -2.39825 | 5.00E-05 | lysine--tRNA ligase |
| <i>PluDJC_09505</i> | -2.37938 | 0.0117 | MurR/RpiR family transcriptional regulator. iron-sulfur cluster assembly protein HesB |
| <i>PluDJC_03445</i> | -2.37141 | 5.00E-05 | outer membrane protein assembly factor BamA |
| <i>PluDJC_19700</i> | -2.36717 | 5.00E-05 | 30S ribosomal protein S21 |
| <i>PluDJC_18960</i> | -2.35838 | 0.0144 | ferrochelatase |
| <i>PluDJC_13040</i> | -2.34874 | 0.00035 | attachment protein |
| <i>PluDJC_13025</i> | -2.33488 | 0.01145 | outer membrane protein OmpW |
| <i>PluDJC_01820</i> | -2.29714 | 0.0174 | type VI secretion system contractile sheath small subunit |
| <i>PluDJC_13610</i> | -2.28238 | 5.00E-05 | anhydro-N-acetylmuramic acid kinase |
| <i>PluDJC_02110</i> | -2.27966 | 5.00E-05 | elongation factor G |
| <i>PluDJC_03785</i> | -2.26604 | 0.0368 | dihydrofolate reductase |
| <i>PluDJC_14395</i> | -2.26105 | 0.00025 | 4-hydroxy-tetrahydrodipicolinate synthase |
| <i>PluDJC_05000</i> | -2.26049 | 5.00E-05 | 4-hydroxyphenylacetate 3-monooxygenase. Pyoverdin chromophore biosynthetic protein pvcC |
| <i>PluDJC_02395</i> | -2.25982 | 5.00E-05 | uroporphyrinogen decarboxylase |
| <i>PluDJC_22540</i> | -2.25019 | 5.00E-05 | inorganic diphosphatase |
| <i>PluDJC_21060</i> | -2.24603 | 0.0023 | 4-hydroxyphenylacetate 3-monooxygenase |
| <i>PluDJC_14100</i> | -2.24169 | 0.00165 | copper homeostasis membrane protein CopD |
| <i>PluDJC_20365</i> | -2.23922 | 5.00E-05 | glycerol dehydrogenase |
| <i>PluDJC_05715</i> | -2.23588 | 0.04415 | NADH:ubiquinone reductase (Na(+)-transporting) subunit D |

| | | | |
|---------------------|----------|----------|--|
| <i>PluDJC_03640</i> | -2.22971 | 0.03285 | adenylyl-sulfate kinase |
| <i>PluDJC_17760</i> | -2.22447 | 0.03335 | UPF0231 family protein |
| <i>PluDJC_00025</i> | -2.22382 | 5.00E-05 | aspartate-semialdehyde dehydrogenase |
| <i>PluDJC_04855</i> | -2.22364 | 5.00E-05 | transketolase |
| <i>PluDJC_04320</i> | -2.21559 | 0.0369 | hypoxanthine phosphoribosyltransferase |
| <i>PluDJC_03450</i> | -2.21189 | 5.00E-05 | molecular chaperone Skp |
| <i>PluDJC_05965</i> | -2.20463 | 5.00E-05 | recombinase RecA |
| <i>PluDJC_21555</i> | -2.20139 | 0.00025 | alanine racemase |
| <i>PluDJC_19125</i> | -2.20003 | 5.00E-05 | peptidylprolyl isomerase. chaperone |
| <i>PluDJC_18470</i> | -2.19177 | 5.00E-05 | sodium:alanine symporter family protein |
| <i>PluDJC_02150</i> | -2.19033 | 5.00E-05 | DNA-directed RNA polymerase subunit beta. rpoB |
| <i>PluDJC_13115</i> | -2.19009 | 5.00E-05 | bifunctional acetaldehyde-CoA/alcohol dehydrogenase |
| <i>PluDJC_16345</i> | -2.18851 | 0.00185 | imidazolonepropionase |
| <i>PluDJC_09690</i> | -2.18289 | 0.01635 | flagellar transcriptional regulator FlhC. AraC family transcriptional regulator |
| <i>PluDJC_17755</i> | -2.18231 | 0.005 | small-conductance mechanosensitive channel MscS |
| <i>PluDJC_12555</i> | -2.18222 | 0.01005 | oxidoreductase |
| <i>PluDJC_01605</i> | -2.17215 | 0.0019 | ABC transporter ATP-binding protein |
| <i>PluDJC_11470</i> | -2.16784 | 0.0141 | FMN-dependent NADH-azoreductase |
| <i>PluDJC_01130</i> | -2.16347 | 5.00E-05 | RNA-binding transcriptional accessory protein |
| <i>PluDJC_06175</i> | -2.16231 | 3.00E-04 | proline/glycine betaine ABC transporter ATP-binding protein ProV |
| <i>PluDJC_02840</i> | -2.15639 | 0.04315 | molybdopterin adenylyltransferase |
| <i>PluDJC_23135</i> | -2.13294 | 5.00E-05 | transcription termination factor Rho |
| <i>PluDJC_09030</i> | -2.13125 | 7.00E-04 | porin. outer membrane porin protein C |
| <i>PluDJC_19175</i> | -2.11998 | 5.00E-05 | ion channel protein Tsx |
| <i>PluDJC_04900</i> | -2.11783 | 5.00E-05 | erythrose-4-phosphate dehydrogenase |
| <i>PluDJC_19040</i> | -2.11655 | 5.00E-05 | efflux RND transporter periplasmic adaptor subunit |
| <i>PluDJC_06815</i> | -2.10384 | 1.00E-04 | glutamate--tRNA ligase |
| <i>PluDJC_06770</i> | -2.10345 | 0.0421 | phosphocarrier protein Hpr |
| <i>PluDJC_24225</i> | -2.09372 | 0.0061 | IS630 family transposase |
| <i>PluDJC_02945</i> | -2.08527 | 0.0058 | 30S ribosomal protein S20 |
| <i>PluDJC_07060</i> | -2.08325 | 0.00065 | ATP-grasp domain-containing protein |
| <i>PluDJC_02065</i> | -2.08284 | 5.00E-05 | peptidylprolyl isomerase |
| <i>PluDJC_00235</i> | -2.0816 | 0.00025 | F0F1 ATP synthase subunit A |
| <i>PluDJC_06380</i> | -2.07112 | 5.00E-05 | glutamine--tRNA ligase |
| <i>PluDJC_07630</i> | -2.05821 | 0.0057 | cytidine deaminase |
| <i>PluDJC_03625</i> | -2.04555 | 0.0022 | uroporphyrinogen-III C-methyltransferase |
| <i>PluDJC_12405</i> | -2.04434 | 5.00E-05 | decarboxylase |
| <i>PluDJC_13035</i> | -2.04276 | 0.02015 | attachment protein |
| <i>PluDJC_03415</i> | -2.03474 | 0.00755 | UMP kinase |
| <i>PluDJC_05035</i> | -2.03319 | 0.00045 | 4-hydroxyphenylacetate permease |
| <i>PluDJC_23540</i> | -2.02595 | 0.0459 | bifunctional biotin-. bifunctional biotin--[acetyl-CoA-carboxylase] synthetase/biotin operon repressor |

| | | | |
|---------------------|----------|----------|---|
| <i>PluDJC_07460</i> | -2.02269 | 0.00375 | secretion protein HlyD |
| <i>PluDJC_09975</i> | -2.01749 | 0.00475 | flagellar basal-body rod protein FlgG |
| <i>PluDJC_07885</i> | -2.01739 | 5.00E-05 | leucine-responsive transcriptional regulator Lrp |
| <i>PluDJC_22455</i> | -2.00954 | 0.02365 | dihydropteroate synthase |
| <i>PluDJC_14385</i> | -1.9954 | 5.00E-05 | phosphoribosylaminoimidazolesuccinocarboxamide synthase |
| <i>PluDJC_13980</i> | -1.99125 | 5.00E-05 | phenylalanine--tRNA ligase subunit beta |
| <i>PluDJC_15790</i> | -1.98091 | 5.00E-04 | NADH-quinone oxidoreductase subunit B |
| <i>PluDJC_07610</i> | -1.97439 | 0.0372 | GTP cyclohydrolase I FoIE |
| <i>PluDJC_07655</i> | -1.97013 | 5.00E-05 | methionine--tRNA ligase |
| <i>PluDJC_00190</i> | -1.9657 | 5.00E-05 | glutamine--fructose-6-phosphate transaminase (isomerizing) |
| <i>PluDJC_21335</i> | -1.96152 | 5.00E-05 | PspA/IM30 family protein |
| <i>PluDJC_02585</i> | -1.94774 | 5.00E-05 | phosphopentomutase |
| <i>PluDJC_17185</i> | -1.94748 | 5.00E-05 | nucleotide exchange factor GrpE |
| <i>PluDJC_20170</i> | -1.94651 | 5.00E-05 | acetyl-CoA carboxylase biotin carboxylase subunit |
| <i>PluDJC_01270</i> | -1.9434 | 7.00E-04 | glutamate--ammonia ligase |
| <i>PluDJC_05085</i> | -1.93293 | 0.01385 | homoprotocatechuate degradation operon regulator HpaR |
| <i>PluDJC_15545</i> | -1.92022 | 0.0255 | branched-chain amino acid transaminase |
| <i>PluDJC_17045</i> | -1.91791 | 0.00015 | elongation factor 4 |
| <i>PluDJC_22450</i> | -1.91638 | 2.00E-04 | phosphoglucosamine mutase |
| <i>PluDJC_05425</i> | -1.91607 | 0.0128 | putative addiction module antidote protein |
| <i>PluDJC_09455</i> | -1.91506 | 4.00E-04 | type I-F CRISPR-associated protein Csy3. CRISPR-associated protein Cas5 |
| <i>PluDJC_16340</i> | -1.90758 | 0.0045 | formimidoylglutamase |
| <i>PluDJC_03455</i> | -1.90729 | 5.00E-05 | UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase |
| <i>PluDJC_19310</i> | -1.90442 | 5.00E-05 | protein translocase subunit SecD |
| <i>PluDJC_23225</i> | -1.90105 | 5.00E-04 | threonine ammonia-lyase. biosynthetic |
| <i>PluDJC_02955</i> | -1.89762 | 5.00E-05 | isoleucine--tRNA ligase |
| <i>PluDJC_04515</i> | -1.88872 | 3.00E-04 | similar to killer protein pyocin s3 hypothetical protein |
| <i>PluDJC_03020</i> | -1.88426 | 5.00E-05 | hypothetical protein |
| <i>PluDJC_06730</i> | -1.87588 | 0.02915 | RpoE-regulated lipoprotein |
| <i>PluDJC_06025</i> | -1.87082 | 0.0129 | 30S ribosomal protein S16 |
| <i>PluDJC_00200</i> | -1.86972 | 0.00015 | F0F1 ATP synthase subunit epsilon |
| <i>PluDJC_00195</i> | -1.85512 | 0.00015 | bifunctional UDP-N-acetylglucosamine diphosphorylase |
| <i>PluDJC_21245</i> | -1.8451 | 0.02295 | type II toxin-antitoxin system antitoxin CcdA. pirin |
| <i>PluDJC_01450</i> | -1.83564 | 0.02495 | DNA-directed RNA polymerase subunit omega. rpoZ |
| <i>PluDJC_15540</i> | -1.83056 | 0.0016 | phenylacetate--CoA ligase family protein |
| <i>PluDJC_00690</i> | -1.81119 | 5.00E-05 | NADP-specific glutamate dehydrogenase |
| <i>PluDJC_15740</i> | -1.80172 | 0.00065 | NADH-quinone oxidoreductase subunit M |
| <i>PluDJC_02075</i> | -1.79299 | 5.00E-05 | FKBP-type peptidyl-prolyl cis-trans isomerase |
| <i>PluDJC_06030</i> | -1.79014 | 5.00E-05 | ribosome maturation factor RimM |
| <i>PluDJC_21550</i> | -1.78714 | 1.00E-04 | aspartate/tyrosine/aromatic aminotransferase |
| <i>PluDJC_02105</i> | -1.78284 | 5.00E-05 | 30S ribosomal protein S7 |
| <i>PluDJC_17785</i> | -1.77294 | 5.00E-05 | dihydrolipoyl dehydrogenase |

| | | | |
|---------------------|----------|----------|---|
| <i>PluDJC_07100</i> | -1.77234 | 5.00E-05 | cytochrome bd-I ubiquinol oxidase subunit CydA |
| <i>PluDJC_22460</i> | -1.77129 | 5.00E-05 | ATP-dependent zinc metalloprotease FtsH |
| <i>PluDJC_06700</i> | -1.76373 | 5.00E-05 | ribosome biogenesis GTPase Der |
| <i>PluDJC_04435</i> | -1.74831 | 0.0034 | ABC transporter ATP-binding protein |
| <i>PluDJC_19185</i> | -1.74013 | 1.00E-04 | cytochrome o ubiquinol oxidase subunit I |
| <i>PluDJC_04905</i> | -1.73751 | 5.00E-05 | phosphoglycerate kinase |
| <i>PluDJC_05770</i> | -1.73579 | 0.00035 | NADH:ubiquinone reductase (Na ⁺)-transporting) subunit F |
| <i>PluDJC_15600</i> | -1.73274 | 5.00E-05 | ribonucleoside-diphosphate reductase subunit alpha |
| <i>PluDJC_14085</i> | -1.73172 | 0.00315 | GAF domain-containing protein |
| <i>PluDJC_07475</i> | -1.70536 | 0.00265 | ATP-dependent RNA helicase RhlE |
| <i>PluDJC_01595</i> | -1.69647 | 0.00065 | dipeptide ABC transporter permease DppC |
| <i>PluDJC_09665</i> | -1.68886 | 0.00015 | transcription antiterminator/RNA stability regulator CspE. cold-shock protein |
| <i>PluDJC_08385</i> | -1.68799 | 5.00E-05 | 3-phosphoserine/phosphohydroxythreonine transaminase |
| <i>PluDJC_19655</i> | -1.67724 | 0.00185 | bifunctional D-glycero-beta-D-manno-heptose-7-phosphate kinase |
| <i>PluDJC_08365</i> | -1.67445 | 0.00015 | 30S ribosomal protein S12 methylthiotransferase accessory factor YcaO |
| <i>PluDJC_22185</i> | -1.66975 | 5.00E-05 | valine--tRNA ligase |
| <i>PluDJC_11035</i> | -1.66524 | 4.00E-04 | ribose-phosphate pyrophosphokinase |
| <i>PluDJC_16055</i> | -1.65552 | 4.00E-04 | autoinducer-2 kinase |
| <i>PluDJC_06690</i> | -1.65304 | 0.00025 | tetratricopeptide repeat protein |
| <i>PluDJC_20470</i> | -1.64978 | 5.00E-05 | aspartate ammonia-lyase |
| <i>PluDJC_20465</i> | -1.64196 | 0.02475 | FxsA family protein |
| <i>PluDJC_14680</i> | -1.63983 | 5.00E-05 | NADP-dependent isocitrate dehydrogenase |
| <i>PluDJC_22445</i> | -1.63361 | 3.00E-04 | preprotein translocase subunit SecE |
| <i>PluDJC_06685</i> | -1.63022 | 5.00E-05 | histidine--tRNA ligase |
| <i>PluDJC_09550</i> | -1.62979 | 3.00E-04 | sulfurtransferase |
| <i>PluDJC_14105</i> | -1.61236 | 0.00185 | CopC domain-containing protein YobA |
| <i>PluDJC_24495</i> | -1.60239 | 0.0032 | YicC family protein |
| <i>PluDJC_20165</i> | -1.60056 | 0.00325 | acetyl-CoA carboxylase biotin carboxyl carrier protein |
| <i>PluDJC_02240</i> | -1.59238 | 0.0013 | maltose/maltodextrin ABC transporter substrate-binding protein MalE |
| <i>PluDJC_01875</i> | -1.58493 | 6.00E-04 | histidinol-phosphatase |
| <i>PluDJC_19950</i> | -1.58131 | 0.00025 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase |
| <i>PluDJC_23605</i> | -1.58115 | 0.0047 | Si-specific NAD(P)(+) transhydrogenase soluble pyridine nucleotide transhydrogenase |
| <i>PluDJC_04100</i> | -1.5766 | 0.0064 | threo-3-hydroxy-L-aspartate ammonia-lyase |
| <i>PluDJC_15775</i> | -1.56986 | 8.00E-04 | NADH-quinone oxidoreductase subunit NuoF |
| <i>PluDJC_24435</i> | -1.56836 | 0.04195 | glycosyltransferase family 1 protein |
| <i>PluDJC_14005</i> | -1.56123 | 2.00E-04 | threonine--tRNA ligase |
| <i>PluDJC_03390</i> | -1.55381 | 0.0034 | 2.3.4.5-tetrahydropyridine-2.6-dicarboxylate N-succinyltransferase |
| <i>PluDJC_04690</i> | -1.55329 | 5.00E-04 | MFS transporter |
| <i>PluDJC_11570</i> | -1.55221 | 0.00025 | Re/Si-specific NAD(P)(+) transhydrogenase subunit beta |
| <i>PluDJC_08490</i> | -1.54967 | 2.00E-04 | chromosome partition protein MukB |

| | | | |
|---------------------|----------|----------|---|
| <i>PluDJC_22695</i> | -1.54525 | 5.00E-05 | FtsH protease activity modulator HflK |
| <i>PluDJC_16880</i> | -1.5421 | 5.00E-05 | NAD+ synthase |
| <i>PluDJC_02090</i> | -1.54198 | 0.008 | sulfurtransferase complex subunit TusC |
| <i>PluDJC_02100</i> | -1.53206 | 0.00135 | 30S ribosomal protein S12 |
| <i>PluDJC_11050</i> | -1.52388 | 0.0041 | glutamyl-tRNA reductase. hemA |
| <i>PluDJC_22465</i> | -1.5224 | 2.00E-04 | 23S rRNA (uridine(2552)-2'-O)-methyltransferase RlmE |
| <i>PluDJC_01070</i> | -1.52026 | 0.0075 | cluster biogenesis protein NfuA |
| <i>PluDJC_13705</i> | -1.51988 | 5.00E-05 | major outer membrane lipoprotein |
| <i>PluDJC_24370</i> | -1.51166 | 0.00635 | ADP-glyceromanno-heptose 6-epimerase |
| <i>PluDJC_01545</i> | -1.51148 | 0.00285 | glycine--tRNA ligase subunit alpha |
| <i>PluDJC_23235</i> | -1.51042 | 0.00095 | branched-chain amino acid transaminase |
| <i>PluDJC_19130</i> | -1.50037 | 4.00E-04 | DNA-binding protein HU-beta |
| <i>PluDJC_17995</i> | -1.48714 | 0.00095 | catabolite repressor/activator |
| <i>PluDJC_06080</i> | -1.4744 | 0.00195 | 23S rRNA pseudouridine(1911/1915/1917) synthase RluD |
| <i>PluDJC_16320</i> | -1.47412 | 8.00E-04 | histidine ammonia-lyase |
| <i>PluDJC_04515</i> | -1.47319 | 0.0014 | hypothetical protein |
| <i>PluDJC_03055</i> | -1.4626 | 0.03105 | peptidylprolyl isomerase SurA |
| <i>PluDJC_19580</i> | -1.45783 | 0.00015 | outer membrane channel protein TolC |
| <i>PluDJC_16325</i> | -1.45737 | 0.00795 | urocanate hydratase |
| <i>PluDJC_19290</i> | -1.43939 | 0.0169 | 6.7-dimethyl-8-ribityllumazine synthase |
| <i>PluDJC_07905</i> | -1.4309 | 1.00E-04 | serine--tRNA ligase |
| <i>PluDJC_14080</i> | -1.42201 | 0.0011 | RNA chaperone ProQ |
| <i>PluDJC_22800</i> | -1.41572 | 0.00535 | phosphatidylserine decarboxylase |
| <i>PluDJC_12400</i> | -1.41284 | 0.00905 | tyrosine transporter TyrP |
| <i>PluDJC_15075</i> | -1.4087 | 0.00765 | hypothetical protein |
| <i>PluDJC_02870</i> | -1.40337 | 0.00695 | UDP-glucose--hexose-1-phosphate uridylyltransferase |
| <i>PluDJC_07895</i> | -1.40043 | 0.00445 | outer membrane lipoprotein chaperone LolA |
| <i>PluDJC_01885</i> | -1.39553 | 1.00E-04 | DNA polymerase I |
| <i>PluDJC_14815</i> | -1.39015 | 0.00845 | metal-dependent hydrolase |
| <i>PluDJC_23005</i> | -1.38284 | 0.0022 | diaminopimelate epimerase |
| <i>PluDJC_11530</i> | -1.3785 | 0.0017 | alpha/beta hydrolase |
| <i>PluDJC_17520</i> | -1.37555 | 0.0025 | peptide chain release factor 2 |
| <i>PluDJC_19540</i> | -1.37545 | 0.01595 | 2.5-didehydrogluconate reductase DkgA |
| <i>PluDJC_24365</i> | -1.36845 | 4.00E-04 | glycine C-acetyltransferase |
| <i>PluDJC_01275</i> | -1.36589 | 0.0017 | ribosome-dependent GTPase TypA |
| <i>PluDJC_19885</i> | -1.36537 | 0.00235 | stringent starvation protein A |
| <i>PluDJC_19895</i> | -1.35979 | 0.0035 | 50S ribosomal protein L13 |
| <i>PluDJC_23230</i> | -1.35898 | 0.00095 | dihydroxy-acid dehydratase |
| <i>PluDJC_06765</i> | -1.3513 | 1.00E-04 | phosphoenolpyruvate-protein phosphotransferase PtsI |
| <i>PluDJC_14120</i> | -1.34918 | 0.0022 | prolyl aminopeptidase |
| <i>PluDJC_02590</i> | -1.34907 | 0.00365 | purine-nucleoside phosphorylase. DeoD |
| <i>PluDJC_11380</i> | -1.34889 | 0.0088 | tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB |

| | | | |
|---------------------|----------|----------|--|
| <i>PluDJC_17390</i> | -1.3425 | 0.01975 | hypothetical protein |
| <i>PluDJC_05685</i> | -1.33905 | 0.0063 | D-sedoheptulose 7-phosphate isomerase. gmhA |
| <i>PluDJC_21005</i> | -1.33591 | 0.0062 | peptide chain release factor 3 |
| <i>PluDJC_07010</i> | -1.33196 | 3.00E-04 | 2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase |
| <i>PluDJC_21215</i> | -1.33185 | 0.01165 | nucleoside hydrolase |
| <i>PluDJC_13415</i> | -1.33146 | 0.00175 | alanine racemase |
| <i>PluDJC_11155</i> | -1.32724 | 0.00655 | molecular chaperone |
| <i>PluDJC_04475</i> | -1.32127 | 0.00345 | RNA polymerase-binding protein DksA |
| <i>PluDJC_00020</i> | -1.32037 | 1.00E-04 | DNA topoisomerase (ATP-hydrolyzing) subunit B |
| <i>PluDJC_17900</i> | -1.31993 | 0.00065 | preprotein translocase subunit SecA |
| <i>PluDJC_14730</i> | -1.31955 | 0.0043 | peptidase T |
| <i>PluDJC_19670</i> | -1.30385 | 0.0324 | SH3 domain-containing protein |
| <i>PluDJC_07145</i> | -1.30035 | 7.00E-04 | peptidoglycan-associated lipoprotein Pal |
| <i>PluDJC_07140</i> | -1.29562 | 0.00095 | Tol-Pal system protein TolB |
| <i>PluDJC_20150</i> | -1.29392 | 0.0012 | rod shape-determining protein |
| <i>PluDJC_21320</i> | -1.29349 | 0.00435 | DUF1190 domain-containing protein |
| <i>PluDJC_19045</i> | -1.28778 | 4.00E-04 | multidrug efflux RND transporter permease subunit |
| <i>PluDJC_22585</i> | -1.28618 | 0.0036 | peptidyl-prolyl cis-trans isomerase |
| <i>PluDJC_11565</i> | -1.2833 | 0.002 | Re/Si-specific NAD(P)(+) transhydrogenase subunit alpha |
| <i>PluDJC_19315</i> | -1.27983 | 0.0398 | preprotein translocase subunit YajC |
| <i>PluDJC_14065</i> | -1.27463 | 0.01055 | L-cystine transporter |
| <i>PluDJC_13595</i> | -1.27279 | 0.00945 | pyridoxal kinase PdxY |
| <i>PluDJC_10045</i> | -1.27148 | 0.0349 | hypothetical protein |
| <i>PluDJC_22580</i> | -1.25208 | 0.0081 | 3'-(2')-5'-bisphosphate nucleotidase CysQ |
| <i>PluDJC_14265</i> | -1.23321 | 7.00E-04 | NADP-dependent oxaloacetate-decarboxylating malate dehydrogenase |
| <i>PluDJC_02455</i> | -1.231 | 0.0173 | HTH-type transcriptional regulator GntR |
| <i>PluDJC_10850</i> | -1.226 | 0.00535 | universal stress protein |
| <i>PluDJC_21565</i> | -1.22567 | 0.00535 | quinone oxidoreductase |
| <i>PluDJC_15735</i> | -1.22506 | 0.0046 | NADH-quinone oxidoreductase subunit NuoN |
| <i>PluDJC_15745</i> | -1.22358 | 0.00825 | NADH-quinone oxidoreductase subunit L |
| <i>PluDJC_20040</i> | -1.22302 | 0.00855 | nucleoside diphosphate kinase regulator |
| <i>PluDJC_07880</i> | -1.21716 | 0.00255 | thioredoxin-disulfide reductase |
| <i>PluDJC_02410</i> | -1.21046 | 0.00205 | DNA-binding protein HU-alpha |
| <i>PluDJC_14810</i> | -1.20792 | 0.02345 | purine nucleoside phosphoramidase |
| <i>PluDJC_23765</i> | -1.20742 | 0.0054 | triose-phosphate isomerase |
| <i>PluDJC_21325</i> | -1.20519 | 0.02765 | DUF350 domain-containing protein |
| <i>PluDJC_16310</i> | -1.19537 | 0.00795 | 50S ribosomal protein L3 N(5)-glutamine methyltransferase |
| <i>PluDJC_18860</i> | -1.19305 | 0.011 | Luciferase |
| <i>PluDJC_04320</i> | -1.19029 | 0.0165 | multicopper oxidase CueO |
| <i>PluDJC_01615</i> | -1.18696 | 0.014 | insulinase family protein |
| <i>PluDJC_19320</i> | -1.18407 | 0.0093 | tRNA guanosine(34) transglycosylase Tgt |
| <i>PluDJC_22475</i> | -1.18031 | 0.00235 | transcription elongation factor GreA |

| | | | |
|---------------------|----------|---------|---|
| <i>PluDJC_07265</i> | -1.17839 | 0.0013 | 3-deoxy-7-phosphoheptulonate synthase |
| <i>PluDJC_07855</i> | -1.17606 | 0.0021 | ATP-dependent Clp protease ATP-binding subunit ClpA |
| <i>PluDJC_06775</i> | -1.17523 | 0.00155 | cysteine synthase A |
| <i>PluDJC_04660</i> | -1.17208 | 0.01 | nucleoside triphosphate pyrophosphohydrolase |
| <i>PluDJC_00695</i> | -1.16217 | 0.0275 | 16S rRNA (guanine(1516)-N(2))-methyltransferase RsmJ |
| <i>PluDJC_23320</i> | -1.16051 | 0.027 | hypothetical protein |
| <i>PluDJC_01550</i> | -1.14224 | 0.0049 | glycine--tRNA ligase subunit beta |
| <i>PluDJC_21560</i> | -1.13805 | 0.00595 | replicative DNA helicase DnaB |
| <i>PluDJC_03385</i> | -1.13471 | 0.0046 | DUF3461 family protein |
| <i>PluDJC_14075</i> | -1.13449 | 0.00265 | carboxy terminal-processing peptidase |
| <i>PluDJC_04665</i> | -1.13399 | 0.0029 | RES domain-containing protein |
| <i>PluDJC_19145</i> | -1.13265 | 0.0034 | ATP-dependent Clp protease proteolytic subunit |
| <i>PluDJC_03430</i> | -1.12539 | 0.03775 | (2E.6E)-farnesyl-diphosphate-specific ditrans.polycis-undecaprenyl-diphosphate synthase |
| <i>PluDJC_19300</i> | -1.12535 | 0.03595 | transcriptional regulator NrdR |
| <i>PluDJC_06750</i> | -1.12185 | 0.0083 | sulfate/thiosulfate ABC transporter ATP-binding protein CysA |
| <i>PluDJC_02970</i> | -1.11681 | 0.018 | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase |
| <i>PluDJC_05940</i> | -1.11331 | 0.00675 | glutamate-5-semialdehyde dehydrogenase |
| <i>PluDJC_17180</i> | -1.10669 | 0.0339 | uracil-DNA glycosylase |
| <i>PluDJC_22690</i> | -1.10395 | 0.00295 | protease modulator HflC |
| <i>PluDJC_13600</i> | -1.10187 | 0.0034 | tyrosine--tRNA ligase |
| <i>PluDJC_21830</i> | -1.10187 | 0.01215 | 4-hydroxy-3-polyprenylbenzoate decarboxylase |
| <i>PluDJC_14885</i> | -1.10071 | 0.01535 | 23S rRNA pseudouridine(955/2504/2580) synthase RluC |
| <i>PluDJC_19235</i> | -1.09653 | 0.0452 | (2E.6E)-farnesyl diphosphate synthase. geranyltranstransferase |
| <i>PluDJC_17920</i> | -1.09396 | 0.00465 | cell division protein FtsZ |
| <i>PluDJC_02795</i> | -1.09312 | 0.0019 | two-component system response regulator ArcA |
| <i>PluDJC_04995</i> | -1.08617 | 0.0409 | 4-hydroxyphenylacetate 3-monooxygenase. reductase component |
| <i>PluDJC_19210</i> | -1.08434 | 0.01135 | YajQ family cyclic di-GMP-binding protein |
| <i>PluDJC_03400</i> | -1.08179 | 0.02315 | type I methionyl aminopeptidase |
| <i>PluDJC_21240</i> | -1.0801 | 0.04215 | transcriptional regulator |
| <i>PluDJC_15870</i> | -1.07616 | 0.00855 | hypothetical protein |
| <i>PluDJC_09040</i> | -1.07518 | 0.0066 | asparagine--tRNA ligase |
| <i>PluDJC_13375</i> | -1.07391 | 0.03725 | NAD(P)H nitroreductase |
| <i>PluDJC_17780</i> | -1.07129 | 0.0081 | bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase |
| <i>PluDJC_01475</i> | -1.06353 | 0.00425 | hypothetical protein |
| <i>PluDJC_09445</i> | -1.06073 | 0.02225 | type I-F CRISPR-associated protein Csy1 |
| <i>PluDJC_15785</i> | -1.05225 | 0.00205 | NADH-quinone oxidoreductase subunit C/D |
| <i>PluDJC_02760</i> | -1.04836 | 0.00235 | energy-dependent translational throttle protein EttA |
| <i>PluDJC_07545</i> | -1.04661 | 0.0369 | dihydrodipicolinate synthase family protein |
| <i>PluDJC_09090</i> | -1.04657 | 0.00635 | ABC transporter ATP-binding protein. heme transporter |
| <i>PluDJC_09015</i> | -1.04391 | 0.0083 | MBL fold metallo-hydrolase |
| <i>PluDJC_15865</i> | -1.04243 | 0.0106 | cysteine desulfurase |

| | | | |
|---------------------|-----------|---------|--|
| <i>PluDJC_03440</i> | -1.02667 | 0.0121 | sigma E protease regulator RseP |
| <i>PluDJC_16885</i> | -1.02294 | 0.03025 | two-component system response regulator GlrR |
| <i>PluDJC_14585</i> | -1.02046 | 0.0417 | bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase |
| <i>PluDJC_01405</i> | -1.01899 | 0.0083 | type 1 fimbrial protein |
| <i>PluDJC_21315</i> | -1.01865 | 0.01655 | glutathionylspermidine synthase family protein |
| <i>PluDJC_23620</i> | -1.01661 | 0.0196 | argininosuccinate synthase |
| <i>PluDJC_07105</i> | -1.01609 | 0.0057 | cytochrome d ubiquinol oxidase subunit II |
| <i>PluDJC_12490</i> | -1.00471 | 0.0069 | class II fumarate hydratase |
| <i>PluDJC_19910</i> | -1.00216 | 0.0459 | DUF1043 family protein |
| <i>PluDJC_04615</i> | -0.983999 | 0.01815 | glutamate-1-semialdehyde 2.1-aminomutase |
| <i>PluDJC_16810</i> | -0.976948 | 0.0142 | recombinase family protein |
| <i>PluDJC_00010</i> | -0.973209 | 0.0151 | DNA polymerase III subunit beta |
| <i>PluDJC_16220</i> | -0.967192 | 0.02785 | 4-phosphoerythronate dehydrogenase PdxB |
| <i>PluDJC_11560</i> | -0.960898 | 0.0282 | DUF1471 domain-containing protein |
| <i>PluDJC_04910</i> | -0.955236 | 0.0092 | class II fructose-bisphosphate aldolase |
| <i>PluDJC_18930</i> | -0.954552 | 0.0169 | bifunctional UDP-sugar hydrolase/5'-nucleotidase |
| <i>PluDJC_19890</i> | -0.951499 | 0.02685 | 30S ribosomal protein S9 |
| <i>PluDJC_02095</i> | -0.945779 | 0.04495 | sulfurtransferase complex subunit TusB |
| <i>PluDJC_07150</i> | -0.945015 | 0.0399 | cell division protein CpoB |
| <i>PluDJC_21645</i> | -0.943788 | 0.01595 | repressor LexA |
| <i>PluDJC_23335</i> | -0.937009 | 0.01425 | methionyl-tRNA formyltransferase |
| <i>PluDJC_19555</i> | -0.891898 | 0.026 | DNA topoisomerase IV subunit A |
| <i>PluDJC_00385</i> | -0.876923 | 0.0282 | acetate--CoA ligase |
| <i>PluDJC_04465</i> | -0.875604 | 0.0275 | polynucleotide adenylyltransferase PcnB |
| <i>PluDJC_04310</i> | -0.873257 | 0.03825 | polyamine aminopropyltransferase |
| <i>PluDJC_11410</i> | -0.841721 | 0.0315 | septum site-determining protein MinD |
| <i>PluDJC_12845</i> | -0.837123 | 0.01315 | type I DNA topoisomerase |
| <i>PluDJC_06995</i> | -0.834874 | 0.033 | succinate dehydrogenase flavoprotein subunit |
| <i>PluDJC_13640</i> | -0.832057 | 0.0422 | Grx4 family monothiol glutaredoxin |
| <i>PluDJC_03485</i> | -0.829846 | 0.0361 | acetyl-CoA carboxylase carboxyl transferase subunit alpha |
| <i>PluDJC_22390</i> | -0.821941 | 0.02615 | lipoprotein Nlpl |
| <i>PluDJC_06695</i> | -0.820083 | 0.02445 | outer membrane protein assembly factor BamB |
| <i>PluDJC_10270</i> | -0.817147 | 0.04315 | phospholipase D |
| <i>PluDJC_17040</i> | -0.816615 | 0.0348 | signal peptidase I |
| <i>PluDJC_01415</i> | -0.803801 | 0.02055 | molecular chaperone. pilus protein assembly |
| <i>PluDJC_15860</i> | -0.795186 | 0.03495 | class I SAM-dependent methyltransferase |
| <i>PluDJC_11275</i> | -0.791935 | 0.047 | Holliday junction branch migration protein RuvA |
| <i>PluDJC_06305</i> | -0.785998 | 0.04015 | magnesium/cobalt transporter CorC |
| <i>PluDJC_02835</i> | -0.777254 | 0.03235 | transaldolase |
| <i>PluDJC_18885</i> | -0.738176 | 0.04805 | co-chaperone YbbN |
| <i>PluDJC_17710</i> | -0.712913 | 0.0452 | phosphoglycerate dehydrogenase |

Table S2: HPLC analysis of pea root exudates

| H ₂ O portion | | | |
|--------------------------|--------|----------|---|
| Number | R time | Area | Name |
| 1 | 5.246 | 3.49E+08 | O-Ethylhydroxylamine, 2TMS derivative |
| 2 | 9.792 | 2.58E+06 | Phosphoric acid, 2 TMS monometil |
| 3 | 9.951 | 2.02E+06 | Oxalic acid, 2TMS derivative |
| 4 | 10.29 | 4.41E+05 | Propanedioic acid, 2TMS derivative |
| 5 | 11.18 | 1.52E+06 | L-Serine, 2TMS derivative |
| 6 | 11.29 | 1.20E+06 | Ethanolamine, 3TMS derivative |
| 7 | 11.4 | 9.70E+06 | Silanol, trimethyl-, phosphate (3:1) |
| 8 | 11.46 | 1.51E+07 | Glycerol, 3TMS derivative |
| 9 | 11.76 | 2.09E+06 | L-Threonine, 2TMS derivative |
| 10 | 11.91 | 6.61E+05 | Glycine. 3TMS derivative |
| 11 | 12.73 | 6.45E+07 | L-Homoserine, 2TMS derivative |
| 12 | 13.47 | 3.11E+06 | Butanoic acid, 2,4-bis[(trimethylsilyl)oxy]-, TMS ester |
| 13 | 13.99 | 2.13E+07 | Homoserine, 3TMS derivative |
| 14 | 14.48 | 1.38E+07 | Malic acid, 3TMS derivative |
| 15 | 14.54 | 2.01E+06 | (({3,4-Bis[(trimethylsilyl)oxy]phenyl)methyl |
| 16 | 14.94 | 1.90E+06 | L-Asparagine |
| 17 | 15 | 1.63E+06 | 4-Aminobutanoic acid, 3TMS derivative |
| 18 | 15.07 | 1.80E+06 | Pyroglutamic acid, TMS derivative |
| 19 | 15.27 | 1.59E+06 | DL-Phenylalanine, TMS derivative |
| 20 | 15.38 | 6.82E+08 | Trihydroxybutyric acid, 4TMS |
| 21 | 16.29 | 1.34E+06 | L-(+)- Tartaric acid, 4TMS derivative |
| 22 | 17.08 | 1.07E+06 | D-(+)-Xylose, 4TMS ether |
| 23 | 17.23 | 4.53E+05 | Arabinitol, 5TMS derivative |
| 24 | 18.32 | 1.94E+06 | Methyl galactoside, 4TMS derivative |
| 25 | 18.9 | 1.03E+06 | Ribonic acid, 2,3,4,5-tetrakis-O-(TMS) -, TMS ester |
| 26 | 19.12 | 1.89E+07 | Methyl galactoside (15,2R,3S,4R,5R)-, 4TM |
| 27 | 19.27 | 7.55E+06 | D-Psicose, pentakis(trimethylsilyl) ether |

| | | | |
|--------------------------|--------|----------|--|
| 28 | 19.5 | 2.64E+06 | Ethyl alpha-D-glucopyranoside, 4TMS |
| 29 | 19.59 | 2.29E+07 | D-Allose, 5TMS ether |
| 30 | 19.68 | 1.11E+06 | D-Pinitol, 5TMS ether |
| 31 | 19.85 | 6.54E+06 | D-(+)-Talose, 5TMS ether |
| 32 | 19.94 | 4.97E+06 | Glucopyranose, 5TMS derivative |
| 33 | 20.61 | 8.60E+05 | Palmitic Acid, TMS derivative |
| 34 | 21 | 7.81E+06 | Myo-Inositol, 6TMS derivative |
| 35 | 21.78 | 7.18E+05 | Phytol, TMS derivative |
| 36 | 21.84 | 5.35E+05 | D-Glucose, STMS derivative |
| 37 | 24.57 | 6.34E+05 | D-(+)- Turanose, 8TMS ether |
| 38 | 24.67 | 1.04E+06 | D-(+)-Turanose, 8TMS ether |
| 39 | 25.56 | 1.09E+07 | Sucrose, 8 TMS derivative |
| 40 | 25.63 | 4.71E+05 | D-(+)-Turanose, 8TMS ether |
| | | | |
| MetOH portion | | | |
| 1 | 4.575 | 3.55E+07 | Hydroxy acetonitrile |
| 2 | 4.767 | 6.49E+06 | - |
| 3 | 4.835 | 1.89E+07 | - |
| 4 | 5.237 | 3.42E+08 | O-Ethylhydroxylamine, 2TMS derivative |
| 5 | 5.492 | 1.51E+05 | Boric acid, 3TMS derivative |
| 6 | 5.572 | 2.67E+05 | Tetramethylsilane |
| 7 | 7.381 | 3.12E+05 | Lactic acid, 2TMS derivative |
| 8 | 8.302 | 1.82E+05 | 6-Ethyl-2-methyloctane |
| 9 | 10.452 | 1.56E+05 | Diethyl 2-aminomalonate |
| 10 | 11.448 | 4.80E+05 | Glycerol, 3TMS derivative |
| 11 | 18.814 | 7.29E+05 | 1,2-Benzenedicarboxylic acid, bis (2-methlypropyl) ester |
| 12 | 20.194 | 1.36E+05 | 3,8-Dimethylundecane |
| 13 | 20.608 | 5.78E+05 | Palmitic acid, TMS derivative |
| 14 | 22.390 | 4.39E+05 | Stearic acid, TMS derivative |
| 15 | 24.559 | 1.21E+05 | 3,8-Dimethylundecane |
| 16 | 24.822 | 1.27E+06 | Di- <i>n</i> -octyl phtalate |

| | | | |
|----|--------|----------|---------------------------------|
| 17 | 25.715 | 2.14E+05 | 2,6,10,14-Tetramethylhexadecane |
| 18 | 26.083 | 1.77E+5 | 7-Methylhexadecane |
| 19 | 26.800 | 1.25E+05 | 1-Iodoeicosane |
| 20 | 26.910 | 4.09E+05 | Squalene |

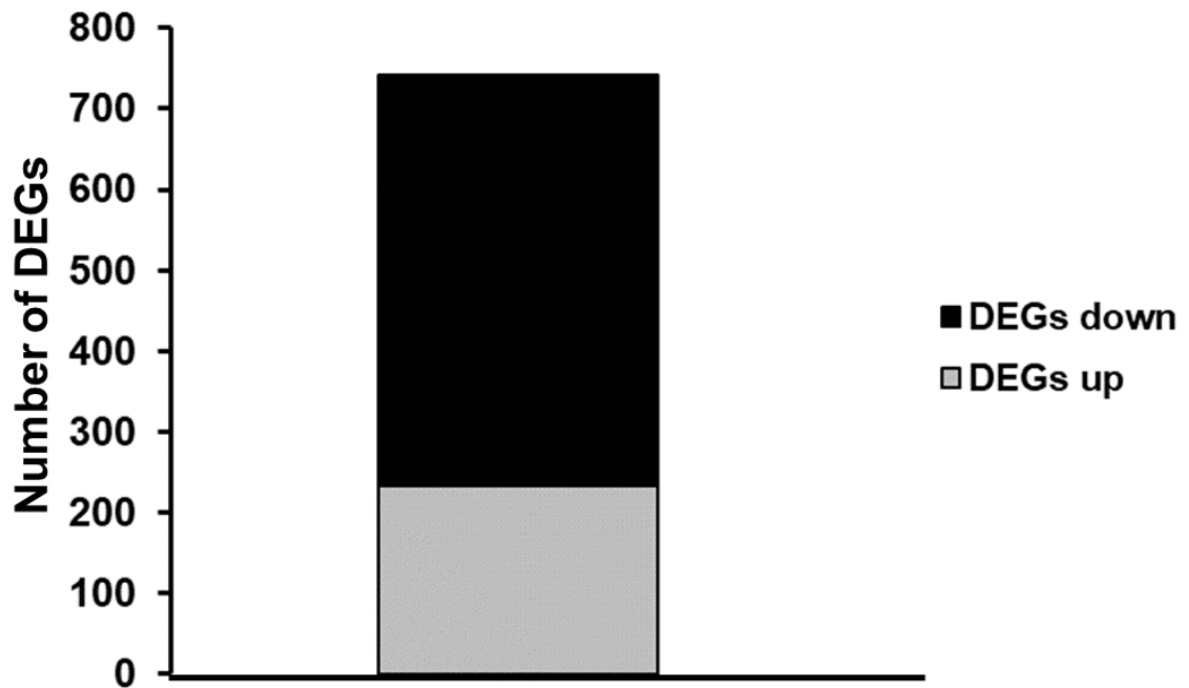


Figure S1: Number of differential expressed genes (DEGs). DEGs between *P. luminescens* 2° cultivated in LB with 3% root exudates from *Pisum sativum* var *Arvica* and its control (*P. luminescens* 2° in LB) resulting from the RNAseq analysis. 233 DEGs were upregulated (light grey) whereas 508 showed downregulation (black).

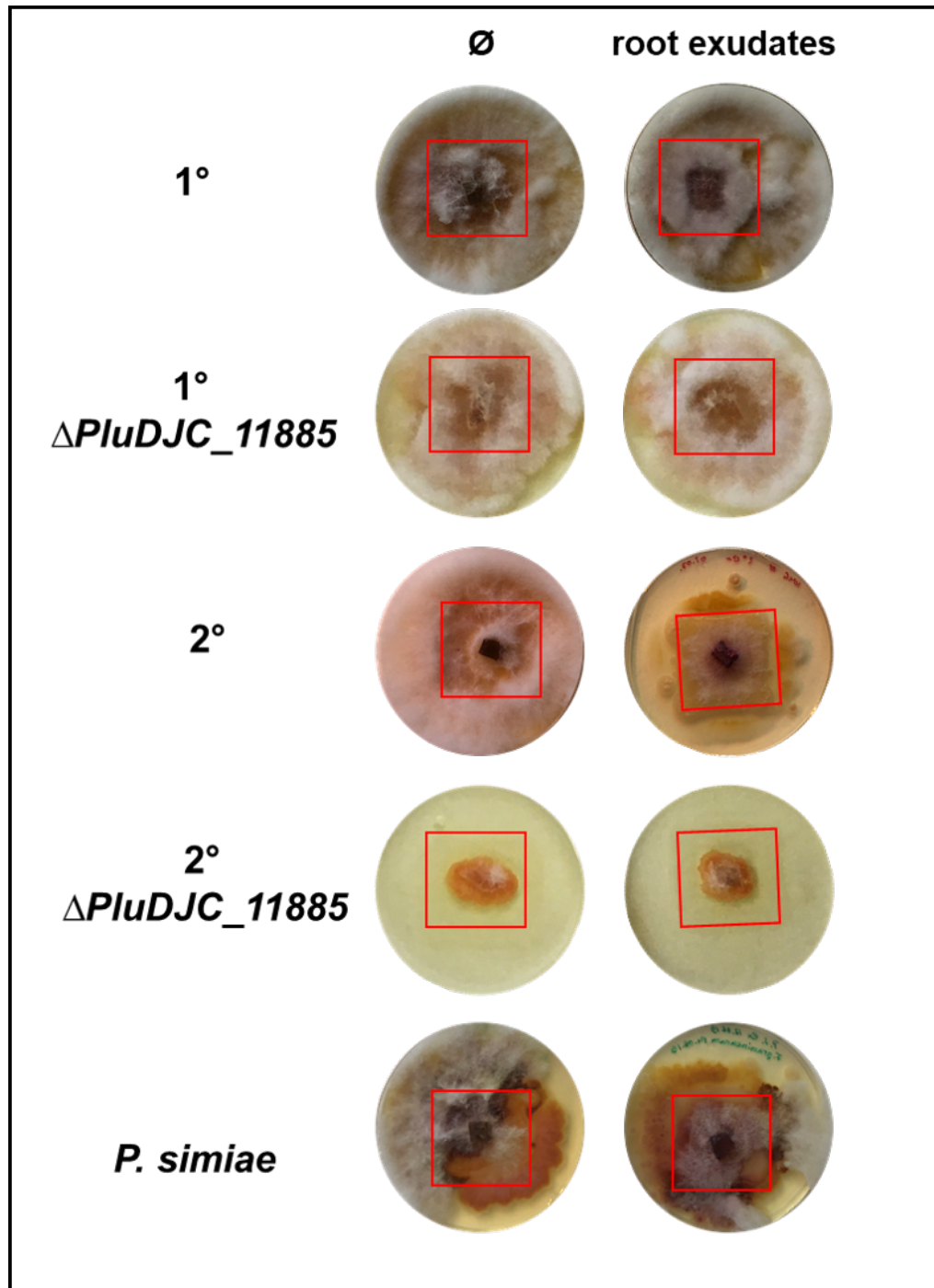


Figure S2: Plant root exudates induced fungal growth inhibition activity in *P. luminescens* 2°. Fungal growth inhibition assay with plant pathogenic *Fusarium graminearum* HM6PIS performed on YMG agar plates. *P. luminescens* 1°, *P. luminescens* 2°, wild type and their respective *chitinase* knockout mutants, and *P. simiae* WCS417; cultivated O/N in LB with and without plant root exudates, were placed around HM6PIS (red square) and incubated for 14d at 26°C. *P. luminescens* 2° cultivated in LB with plant root exudates inhibited the growth of *F. graminearum*, activity visible also for *P. simiae*. *P. luminescens* 2° chitinase knockout mutant showed a stronger growth inhibition capacity compared to its wild type. *P. luminescens* 1° and its knockout mutant do not show fungal growth inhibition. Three biological replicates were considered for each experiment.