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2 **Fig. S1.** Phylogenetic affiliation of the almost entire (1241 positions) 16S rRNA gene sequence

3 of *Paenibacillus* sp. strain UY79 relative to *Paenibacillus* spp., isolated from soil, rhizosphere

4 or different plant compartments (root nodule, root, leaf, seed). Sequences of *P. larvae* ATCC

5 9545 (a pathogen of *Apis mellifera*) and *P. lautus* NBRC15380 (a human pathogen) were also

6 included in the analysis. The tree was constructed using MEGA X program. The evolutionary

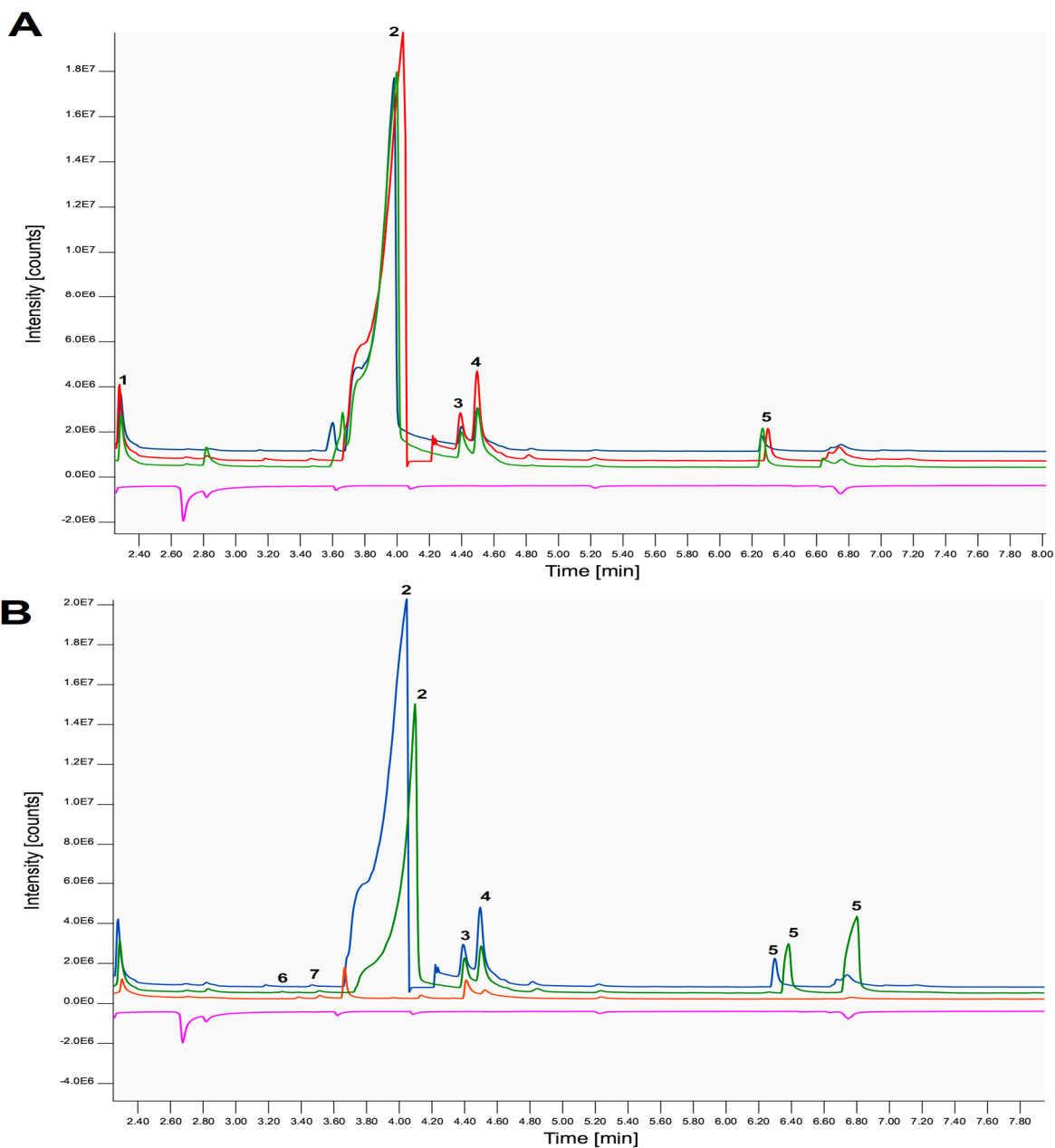
7 history was inferred by using the Maximum Likelihood method and Kimura 2-parameter

8 model (1). Numbers at each node represent percentage of bootstrap replications calculated

9 from 1,000 replicate trees (2). Branches corresponding to partitions reproduced in less than

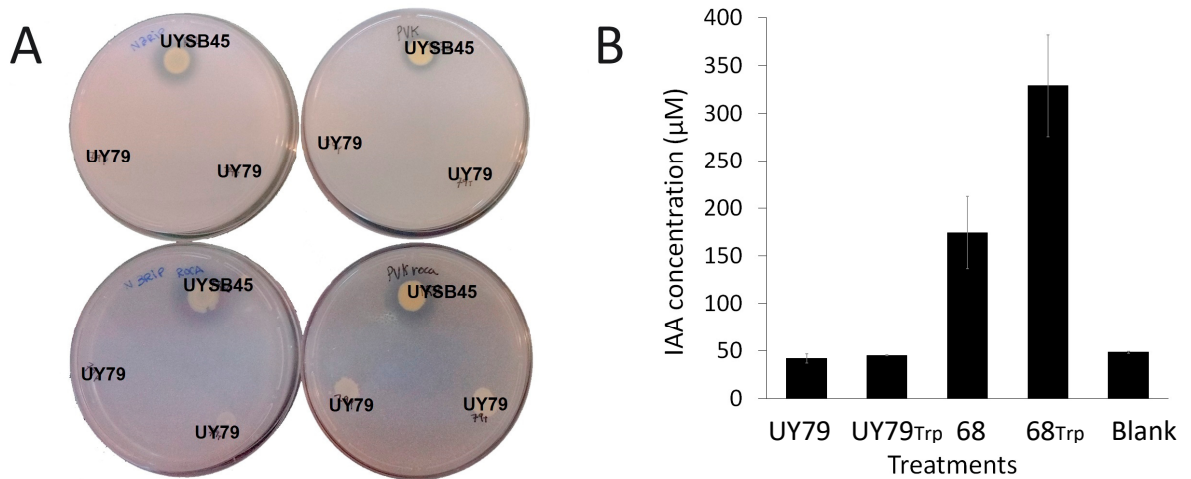
10 60% bootstrap replicates were collapsed. Strain UY79 is shown in red, type strains are

11 indicated with a superscript T and NCBI accession numbers are shown in parentheses.



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13 **Fig. S2.** SPME-GC-MS chromatograms. (A) Chromatograms of VCs produced by a 7-day culture
 14 of UY79, collected by 30 min exposure to SPEM (red) or 10 min exposure to SPEM (blue); by a
 15 36h culture of UY79 and 30min exposure to SPEM (green); and by PDA medium after 7 days
 16 of incubation and 30 min exposure to SPEM (fuchsia). (B) Chromatograms of VCs produced at
 17 7 days and 30-min exposure to SPEM by UY79 (blue), *S. rolfsii* 1948 (red), UY79 faced to *S.*
 18 *rolfsii* 1948 (green) and PDA medium (fuchsia). Identification of peaks depicted in the figure
 19 correspond to: (1) 2-methyl-1-propanol, (2) 3-hydroxy-2-butanone, (3) 3-methyl-1-butanol,
 20 (4) 2-methyl-1-butanol, (5) 2,3-butanediol, (6) 2-ethylfuran and (7) 2,5-dimethylfuran.



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22 **Fig. S3.** *In vitro* evaluation of plant-growth promotion traits of *Paenibacillus* sp. strain UY79.

23 **A)** Phosphate solubilization was visualized as a clear halo around colonies grown in NBRIP (left)
 24 or PVK (right) medium. Phosphate was supplied as $(\text{PO}_4)_2\text{Ca}_3$ (upper plates) or as rock
 25 phosphate (bottom plates). *Pantoea* sp. strain UYSB45 was used as positive control. **B)** IAA
 26 production was assessed colorimetrically using the Salkowski reagent. *Microbacterium* sp.
 27 strain UYFA68 (abbreviated as 68) was used as a positive control. Strain UY79 is abbreviated
 28 as 79. Conditions with the addition of tryptophan are indicated as Trp. Medium without
 29 bacteria was used as a negative control (Blank)

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| | | Strain | Phenotype | |
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| | | | TY medium | TSA medium |
| | | <i>B. elkanii</i> U-1301 | I | nd |
| | Coexistence (Co) | <i>B. elkanii</i> U-1302 | I | nd |
| | | <i>E. meliloti</i> 1021 | Co | nd |
| | Inhibition (I) | <i>R. tropici</i> CIAT 899 | Co | nd |
| | | <i>C. necator</i> . UYPR2.512 | Co | II |
| | | <i>Paraburkholderia</i> sp. UYPR4.13 | nd | Co |
| | Inhibition (II) | <i>P. protegenes</i> Pf-5 | NG | NG |
| | | <i>P. fluorescens</i> UP61 | nd | NG |
| | Inhibition (I) | <i>P. fluorescens</i> U148 | nd | NG |
| | | <i>A. brasilense</i> SP7 | III | III |
| | | <i>Streptomyces</i> sp. UYFA 156 | nd | III |
| | Inhibition (IV) | <i>E. caratovora</i> SCC3193 | Co | nd |
| | | <i>B. subtilis</i> ATCC 6633 | IV | Co |

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Fig. S4. Evaluation of antibiosis by UY79 strain against different soil bacteria. Antibiosis was analyzed by using the soft-agar overlay assay. The assay was performed twice. Different types of bacterial interactions were observed. Examples of the interaction exerted and their classification are depicted in the pictures: coexistence (Co), growth of both strains was observed and no halo of inhibition was visualized; inhibition I (I), inhibition halo around the drop of UY79 culture and moderate growth of UY79; inhibition (II), inhibition halo around the drop of UY79 and poor growth of UY79; inhibition (III) good growth of UY79 and inhibition halo in the drop; inhibition (IV), good growth of UY79 and inhibition halo around the drop of UY79 culture. NG, no visible growth of UY79; nd, not done.

59 **Table S1.** Genome statistics for *Paenibacillus* sp. strain UY79

| Attribute | Value | Bioinformatic tool used |
|-----------------------------------|-----------------|--------------------------------|
| Genome size (bp) | 4970505 | Quast v5.0.2 |
| N° of clean reads | 12720648 | FastQC |
| N° of contigs | 167 | Quast v5.0.2 |
| N ₅₀ (bp) | 281104 | Quast v5.0.2 |
| L ₅₀ (bp) | 5 | Quast v5.0.2 |
| Maximum contig length (bp) | 1146979 | Quast v5.0.2 |
| Minimum contig length (bp) | 71 | Quast v5.0.2 |
| Avg genome coverage (X) | 235.7 | Bowtie2, Samtools, Bedtools |
| G+C content (%) | 46.4 | Quast v5.0.2 |
| No. of predicted coding sequences | 5353 | RAST 2.0 |
| RNA genes | 109 | RAST 2.0 |
| Plasmid | 1 | PlasFlow |
| Plasmid size (bp) | 42743 | RAST 2.0 |
| GenBank accession n° | JAFFQR010000000 | |
| SRA accession n° | PRJNA697992 | |

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62 **Table S2.** Relevant VCs produced by *Paenibacillus* sp. strain UY79 grown alone. VCs were
 63 collected from bacterial cultures grown for 36 h or for 7 days and extracted for 10 minutes
 64 or 30 minutes sorption to SPEM fibers

| Compound ^a | RT ^b | | | Area (%) | | |
|-----------------------|----------------------|---------|---------|----------|---------|---------|
| | 36 h | 7 d | 7 d | 36 h | 7 d | 7 d |
| | (30min) ^c | (10min) | (30min) | (30min) | (10min) | (30min) |
| 2-methyl-1-propanol | 2.283 | 2.281 | 2.274 | 1.77 | 2.51 | 1.70 |
| 3-hydroxy-2-butanone | 3.995 | 3.752 | 4.043 | 70.38 | 76.25 | >65 |
| 3-methyl-1-butanol | 4.399 | 4.398 | 4.391 | 1.11 | 0.90 | 2.66 |
| 2-methyl-1-butanol | 4.501 | 4.497 | 4.495 | 4.40 | 4.33 | 5.31 |
| 2,3-butanediol | 6.268 | 6.262 | 6.301 | 1.71 | 1.06 | 1.14 |

65 ^a Compounds were identified by comparison of the mass spectra against reference libraries
 66 (NIST 08, Wiley 139)

67 ^b RT: Retention time

68 ^c VCs were collected from bacterial cultures grown for 36 h or 7 days and extracted for 10 or
 69 30 minutes with SPEM fibers

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71 **Table S3.** Proteins or genes of interest for this work mined in the genome of *Paenibacillus* sp.
 72 strain UY79

| Putative activity | Predicted function | RAST ID | Tool used for mining |
|---------------------------|---|-----------|----------------------|
| Cellulase activity | | | |
| | Cellulose 1,4-beta-cellobiosidase (reducing end) (EC 3.2.1.176) | UY79_2001 | RAST |
| | Cellulose 1,4-beta-cellobiosidase (reducing end) (EC 3.2.1.176) | UY79_4217 | RAST |
| | Endo-1,4-beta-glucanase (cellulase) (EC 3.2.1.4) | UY79_2748 | RAST |
| | Endo-1,4-beta-glucanase E1precursor (EC 3.2.1.4) | UY79_2705 | RAST |
| | Endo-1,4-beta-glucanase B precursor (EC 3.2.1.4) | UY79_948 | RAST |
| | Endoglucanase | UY79_2712 | RAST |
| | Endo-beta-1,3-1,4 glucanase (licheninase) (EC 3.2.1.73) | UY79_916 | RAST |
| Beta-glucosidase activity | | | |
| | Beta-glucosidase (EC 3.2.1.21) | UY79_4825 | RAST |
| | Beta-glucosidase (EC 3.2.1.21) | UY79_1789 | RAST |
| | Beta-glucosidase (EC 3.2.1.21) | UY79_1150 | RAST |

Chitinase activity

| | | |
|-------------------------|-----------|------|
| Chitinase (EC 3.2.1.14) | UY79_3954 | RAST |
|-------------------------|-----------|------|

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| Chitin binding protein | UY79_1619 | RAST |
|------------------------|-----------|------|

Xylanase activity

| | | |
|---|-----------|------|
| Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | UY79_5258 | RAST |
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| Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | UY79_5194 | RAST |
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| Endo-1,4-beta-xylanase (EC 3.2.1.8) | UY79_5111 | RAST |
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| Endo-1,4-beta-xylanase (EC 3.2.1.8) | UY79_3919 | RAST |
|-------------------------------------|-----------|------|

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| Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | UY79_3218 | RAST |
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| Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | UY79_3217 | RAST |
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| Endo-1,4-beta-xylanase (EC 3.2.1.8) | UY79_3987 | RAST |
|-------------------------------------|-----------|------|

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| Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | UY79_2728 | RAST |
|---|-----------|------|

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| Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | UY79_2727 | RAST |
|---|-----------|------|

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| Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | UY79_2726 | RAST |
|---|-----------|------|

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| Endo-1,4-beta-xylanase (EC 3.2.1.8) | UY79_203 | RAST |
| Endo-1,4-beta-xylanase (EC 3.2.1.8) | UY79_178 | RAST |
| Endo-1,4-beta-xylanase (EC 3.2.1.8) | UY79_907 | RAST |
| Xylan 1,4-beta-xylosidase (EC 3.2.1.37) | UY79_1887 | RAST |
| Xylan 1,4-beta-xylosidase (EC 3.2.1.37) | UY79_135 | RAST |
| Xylan alpha-1,2-glucuronosidase (EC 3.2.1.131) | UY79_134 | RAST |
| Protease | | |
| Bacillopeptidase F | UY79_2733 | RAST |
| HCN production | NOT FOUND | |
| NRPS | | |
| NRPS: Tridecaptin | UY79_5164 | RAST, antiSMASH |
| | UY79_5163 | RAST, antiSMASH |
| NRPS-like | UY79_3034 | RAST, antiSMASH |
| NRPS | UY79_2567 | RAST, antiSMASH |
| | UY79_2566 | RAST, antiSMASH |

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| NRPS: Fusaricidin B | UY79_2178 | RAST, antiSMASH |
| | UY79_2177 | RAST, antiSMASH |
| NRPS: Tridecaptin | UY79_2096 | RAST, antiSMASH |
| | UY79_2094 | RAST, antiSMASH |
| | UY79_2093 | RAST, antiSMASH |
| NRPS | UY79_1857 | RAST, antiSMASH |
| Lasso peptide Paeninodin | UY79_3797 | antiSMASH |
| Nitrogen fixation | | |
| Nitrogenase iron protein, NifH | NOT FOUND | |
| Auxin production | | |
| Indole acetic acid synthesis | NOT FOUND | |
| Phosphate solubilization | | |
| Alkaline phosphatase (EC 3.1.3.1) | UY79_2289 | RAST |
| Siderophore biosynthesis and iron/ siderophore transport | | |

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| ABC transporter (iron/B12/siderophore/hemin), PBP | UY79_5210 | RAST |
| Siderophore biosynthesis diaminobutyrate-- 2-oxoglutarate aminotransferase (EC 2.6.1.76) | UY79_5202 | RAST, antiSMASH |
| PF06276.12 (Ferric iron reductase FhuF-like transporter) | UY79_5200 | antiSMASH |
| Achromobactin biosynthesis protein, AcsC- like | UY79_5199 | RAST, antiSMASH |
| Achromobactin biosynthesis protein AcsB | UY79_5198 | RAST, antiSMASH |
| Diaminopimelate decarboxylase (EC 4.1.1.20) | UY79_5197 | RAST, antiSMASH |
| Achromobactin biosynthesis protein AcsA @ Siderophore synthetase superfamily, group B | UY79_5196 | RAST, antiSMASH |
| ABC-type Fe ³⁺ -siderophore transport system, PBP | UY79_5186 | RAST |
| Fe-bacillibactin uptake system FeuB | UY79_5185 | RAST |
| ABC-type Fe ³⁺ -siderophore transport system, permease | UY79_5184 | RAST |
| ABC-type Fe ³⁺ -siderophore transport system | UY79_5183 | RAST |

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| Ferrichrome transport ATP-binding protein FhuC | UY79_4883 | RAST |
| Ferric uptake regulation protein Fur | UY79_4700 | RAST |
| Fe-bacillibactin uptake system FeuC | UY79_3500 | RAST |
| Siderophore transport protein | UY79_3038 | RAST |
| Ferrichrome transport system permease protein FhuB | UY79_4121 | RAST |
| Ferrichrome transport system permease protein FhuG | UY79_4120 | RAST |
| ABC-type Fe ³⁺ -siderophore transport system, permease | UY79_2524 | RAST |
| ABC-type Fe ³⁺ -siderophore transport system, permease | UY79_2038 | RAST |
| Ferrous iron transport periplasmic protein EfeO, | UY79_1725 | RAST |
| Ferrous iron transporter FeoB | UY79_1175 | RAST |
| Ferrichrome-binding periplasmic protein precursor (TC 3.A.1.14.3) | UY79_825 | RAST |

Motility

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|-----------------------|---------------------------------------|------|
| <i>fla/che</i> operon | UY79_2937- UY79_2983, UY79_3019 | RAST |
|-----------------------|---------------------------------------|------|

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| Large flagellar gene cluster | UY79_4992- | RAST |
|------------------------------|------------|------|

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| | UY79_5014 | |
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| Stator operon <i>motAB</i> | UY79_5051- | RAST |
|----------------------------|------------|------|

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| | UY79_5052, | |
|--|------------|--|

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| | UY79_4227- | |
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| | UY79_4228 | |
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Putative genes involved in volatile compound production

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|--------------------------------------|------------|------|
| Acetolactate synthase (E.C. 2.2.1.6) | UY79_3438, | RAST |
|--------------------------------------|------------|------|

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| | UY79_3439, | |
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| | UY79_5281 | |
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| Acetoin biosynthesis (E.C. 1.1.1.304) | UY79_4819 | BLASTP, HMMER, PFAM, HHPRED, MODELLER |
|---------------------------------------|-----------|--|

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| 2,3-butanediol biosynthesis (E.C. 1.1.1.4) | UY79_2598 | BLASTP, HMMER, PFAM, HHPRED, MODELLER |
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| 2-methyl-1-butanol biosynthesis (Amino acid aminotransferase E.C 2.6.1.42) | UY79_1834 | RAST, BLASTP, HMMER, PFAM, |
|---|-----------|-------------------------------|

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| 2-methyl-1-butanol biosynthesis (2-ketoacid decarboxylase) | UY79_2174 | BLASTP, HMMER, PFAM, HHPRED, MODELLER |
|---|-----------|--|

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| 2-methyl-1-butanol biosynthesis (Alcohol dehydrogenase EC 1.1.1.1) | UY79_273, UY79_705, UY79_1349, UY79_2626, UY79_4296 | RAST |
|---|---|------|

CRISPR/Cas system^a

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|---|---|
| CRISPR-associated protein Cas1, Cas2, Cas3, Cas4, Cas5, Csd1(Cas8c), Csd2/Csh2(Cas7) | UY79_5312, UY79_1015, UY79_5311, UY79_5313 to UY79_5317 |
|---|---|

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|--|---|
| CRISPR-associated RAMP Cmr1, Cmr2; Cmr3, Cmr4, Cmr5, Cmr6 | UY79_1469 to UY79_1464, UY79_1471, UY79_1472, UY79_1534 |
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Phages

| | | |
|--|---------------------------|---|
| <i>Tenacibaculum</i> phage pT24 (<i>Myoviridae</i> family) | UY79_2931 to UY79_2972 | Prophage hunter (A ^b) |
| <i>Vibrio</i> phage phi2 (<i>Myoviridae</i> family) | UY79_383 to UY79_469 | Prophage hunter (A) Phaster (I ^c) |
| <i>Brevibacillus</i> phage Jimmer2 (<i>Myoviridae</i> family) | UY79_3611 to UY79_3691 | Prophage hunter (A) Phaster (I) |
| <i>Bacillus</i> phage vB BtS BMBtp14 (<i>Siphoviridae</i> family) | UY79_1908 to UY79_1998 | Prophage hunter (A) Phaster (IN ^d) |
| <i>Paenibacillus</i> phage Shelly (<i>Siphoviridae</i> family) | UY79_2361 to UY79_2429 | Prophage hunter (AM ^e) Phaster (IN) |
| <i>Lactococcus</i> phage bIL312 (<i>Siphoviridae</i> family) | UY79_4988 to UY79_5025 | Prophage hunter (A) |
| <i>Paenibacillus</i> phage PG1 (<i>Siphoviridae</i> family) | UY79_3855 to UY79_3385 | Prophage hunter (AM) Phaster(IN) |
| <i>Moraxella</i> phage mcat7 (<i>Siphoviridae</i> family) | UY79_4609 to UY79_4645 | Prophage hunter (AM) |

73 ^a Several CRISPR related regions were detected: eighty-four CRISPR repeats and seventy-six
74 CRISPR spacers, distributed among eight CRISPR arrays, and two CRISPR/CAS systems with

75 the following protein arrangement: Cas3-Cas5-Csd1(Cas8c)-Csd2/Csh2(Cas7)-Cas4-Cas1-
76 Cas2, corresponding for putative Type I-C system and fCmr6-Cmr1-Cmr2-Cmr3-Cmr4-Cmr5-
77 Cmr6, corresponding for putative Type III-B system (Table S3). Similar systems have also
78 been described in *P. polymyxa* A18 (Type I-C and III-B), *Bacillus halodurans* (Type I-C) and
79 *Pyrococcus furiosus* (Type III-B) (3, 4).

80 ^bA: active

81 ^cI: intact

82 ^dIN: incomplete

83 ^eAM: ambiguous

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