**Supplementary information**

Supplementary information contains 7 figures and 16 Tables.

**Supplementary Figure 1**. Assembled contigs with regions corresponding to biosynthetic gene clusters marked. Full description of BGC from each organism is provided in the Supplementary Table S13.

**Supplementary Figure 2**. Alignment of novel S-layer osidoreductases with their closest sequenctial homolog from *D. radiodurans* (WP\_027479552.1, red). Mma - *M. macarthurae* (magenta), Mme - *M. meiriae*, orange. **pLDDT** - predicted local-distance difference test, **pTM** - predicted template modelling, **TM** - template modelling, see [24, 25].

**Supplementary Figure 3**. **A)** Phenotypic assays of studied organisms with GNIII MicroPlate (Biolog). **B)** Biochemical assays of studied organisms Gram-positive identification card Vitek 2 GP ID (bioMérieux). Blue - absent, red - present. Assays were performed according to manufacturers' protocol.

**Supplementary Figure 4**. Phylogenetic tree based on alignment of MscS protein sequences from ISS organisms and their closest terrestrial relatives. Branch labels indicate substitutions per site. Ab - *A. burdickii* (blue), Asp - *A. agilis* 4041 (blue), Mma - *M. macarthurae* (burgundy), Msp - *Microbacterium* sp. ACCRU (burgundy), Lw - *L. williamsii* (yellow), Lsp - *Leifsonia* sp.ku-ls (yellow), Mme - *M. meiriae* (orange), Mp - *M. paraoxydans* LTR1 (orange), Pv - *P. vandeheii* (green), Psp - *Paenibacillus* sp. MAEPY (green).

**Supplementary Figure 5**. Alignment of DNA and amino acid sequence of aminopeptidases Mme\_001931 and WP\_268776344. Green boxes indicate sequence identity.

**Supplementary Figure 6**. Structure alignment of aminopeptidase Mme\_001931 (cyan) and WP\_0516188611 (red). **pLDDT** - predicted local-distance difference test, **pTM** - predicted template modelling, **TM** - template modelling, see [24, 25].

**Supplementary Figure 7**. Phylogenetic tree based on alignment of DNA-repair protein sequences from ISS organisms and *D. radiodurans* and *B. pumilus* SAFR-032. Branch labels indicate substitutions per site. Ab - *A. burdickii* (blue), Bp - *B. pumilus* (black), Dr - *D. radiodurans* (red), Mma - *M. macarthurae* (burgundy), Lw - *L. williamsii* (yellow), Mme - *M. meiriae* (orange), Pv - *P. vandeheii* (green).

**Supplementary Table 1**. ANI results for all ISS species.

**Supplementary Table 2**. Annotations of *M. macarthurae* genes.

**Supplementary Table 3**. Annotations of *A. burdickii* genes.

**Supplementary Table 4**. Annotations of *P. vandeheii* genes.

**Supplementary Table 5**. Annotations of *L. williamsii* genes.

**Supplementary Table 6**. Annotations of *M. meiriae* genes.

**Supplementary Table 7**. Annotations of *Microbacterium* sp. ACCRU genes.

**Supplementary Table 8**. Annotations of *A. agilis* 4041 genes.

**Supplementary Table 9**. Annotations of *Paenibacillus* sp. MAEPY2 genes.

**Supplementary Table 10**. Annotations of *Leifsonia* sp. ls-ku genes.

**Supplementary Table 11**. Annotations of *Microbacterium* sp. LTR1 genes.

**Supplementary Table 12**. Annotations of genes common in all ISS species.

**Supplementary Table 13**. Annotations of unique (not present in closest relative) genes shared by all ISS species.

**Supplementary Table 14**. DeepFRI annotations of unique (not present in closest relative) genes and antiSMASH predictions of BGCs.

**Supplementary Table 15**. Structure - based DeepFRI annotations of Mma\_002827 and Mme\_000934.

**Supplementary Table 16**. Predictions for plasmids and phage elements in the genomes of ISS species.