### ADDITIONAL FILE 1

**Table S1. Taxonomic Distribution of Organisms Possessing AHL Lactonase and AHL Acylase with Respect to the Amino Acid Sequences of the Enzyme Present in the Reference Organisms:** *Bacillus* sp. SB4 (GenBank AAR85482.1), *Ralstonia* sp. XJ12B (GenBank AAO41113.1)

|                   | **AHL-Lactonase** | **AHL-Acylase** |
|-------------------|-------------------|-----------------|
| **Reference Organism** | **Bacillus** sp. SB4 (GenBank AAR85482.1) | **Ralstonia** sp. XJ12B (GenBank AAO41113.1) |

**Actinobacteria**

- *Arthrobacter chlorophenolicus* A6
- *Frankia* sp. EAN1pec
- *Mycobacterium* sp. MCS
- *Mycobacterium smegmatis* str. MC2 155
- *M. marinum* M
- *Streptomyces clavuligerus* ATCC 27064
- *Rubrobacter xylanophilus* DSM 9941
- *Rhodococcus* sp. RHA1
- *S. ambofaciens* ATCC 23877
- *S. griseus* subsp. *griseus* NBRC 13350
- *S. lavendulae* subsp. *lavendulae*
- *S. moharaensis*
- *S. sviceus* ATCC 29083
- *Symbio bacterium thermophilum* IAM 14863

**Acidobacteria**

- *Candidatus Koribacter versatilis* Ellin345
- *Solibacter usitatus* Ellin6076
- *Uncultured Acidobacteria bacterium*

**Cyanobacteria**

- *Cyanothece* sp. ATCC 51142
- *Cyanothece* sp. CCY0110
- *Cyanothece* sp. PCC 7424
- *Cyanothece* sp. PCC 7822
- *Cyanothece* sp. PCC 8801
- *Cyanothece* sp. PCC 8802
- *Gloeobacter violaceus* PCC 7421
- *Microcoleus chthonoplastes* PCC 7420
- *Nostoc punctiforme* PCC 73102
- *Synechocystis* sp. PCC 6803

**Bacteroidetes**

- *Cellulophaga* sp. MED134
- *Algoriphagus* sp. PR1
- *Croceibacter atlanticus* HTCC2559
- *Microscilla marina* ATCC 23134
- *Flavobacteria* Pedobacter sp. BAL39
- *Polaribacter ursensis* 23-P
- *Robiginitalea biformata* HTCC2501
- *Salinibacter ruber* DSM 13855
### Table S1. Contd....

| AHL-Lactonase | AHL-Acylase |
|---------------|-------------|
| **Reference Organism** | **Bacillus sp. SB4** (GenBank AAR85482.1) | **Ralstonia sp. XJ12B** (GenBank AA041113.1) |
| Chloroflexi |  |
| Dehalococcoides sp. VS | Chloroflexus aggregans DSM 9485 |
| C. aurantiacus J-10-fl |  |
| Herpetosiphon aurantiacus ATCC 23779 |  |
| Roseiflexus sp. RS-1 |  |
| Roseiflexus castenholzi DSM 13941 |  |
| Deinococcus-Thermus |  |
| Deinococcus radiodurans R1 | Deinococcus radiodurans R1 |
| D. geothermalis DSM 11300 | Thermus aquaticus Y51MC23 |
| Firmicutes |  |
| Bacillus sp. | Bacillus sp. B14905 |
| Bacillus sp. 240B1 | Bacillus anthracis str. A0488 |
| Bacillus sp. 42 | B. badis |
| Bacillus sp. 91 | B. cereus B4264 |
| Bacillus sp. A24 | B. coahulensis m4-4 |
| Bacillus sp. B14905 | B. thuringiensis serovar konkukian str. 97-27 |
| Bacillus sp. COT1 | Oceanobacillus iheyensis HTE831 |
| Bacillus sp. CSX-1 |  |
| Bacillus sp. SB4 |  |
| Bacillus anthracis str. Ames |  |
| B. cereus |  |
| B. cereus 03BB108 |  |
| B. cereus AH1134 |  |
| B. cereus AH187 |  |
| B. cereus AH820 |  |
| B. cereus AH820 |  |
| B. cereus ATCC 10987 |  |
| B. cereus ATCC 14579 |  |
| B. cereus B4264 |  |
| B. cereus E33L |  |
| B. cereus G9241 |  |
| B. cereus G9842 |  |
| B. cereus NVH0597-99 |  |
| B. cereus W |  |
| B. licheniformis ATCC 14580 |  |
| B. subtilis |  |
| B. thuringiensis serovar galleriae |  |
| B. thuringiensis serovar kim |  |
| B. thuringiensis serovar konkukian str. 97-27 |  |
| AHL-Lactonase | AHL-Acylase |
|---------------|------------|
| **Reference Organism** | **Firmicutes** |
| **Bacillus sp. SB4** (GenBank AAB5582.1) | Ralstonia sp. XJ12B (GenBank AAO4113.1) |
| *B. thuringiensis* serovar kurstaki |  |
| *B. thuringiensis* serovar ostrinia |  |
| *B. thuringiensis* |  |
| *B. thuringiensis* serovar alesti |  |
| *B. thuringiensis* serovar canadensis |  |
| *B. thuringiensis* serovar israelensis ATCC 35646 |  |
| *B. thuringiensis* serovar japonensis |  |
| *B. thuringiensis* serovar jinhongiensis |  |
| *B. thuringiensis* serovar kyushuensis |  |
| *B. thuringiensis* serovar oswaldocruz |  |
| *B. thuringiensis* serovar pakistani |  |
| *B. thuringiensis* serovar toumanoffi |  |
| *B. thuringiensis* str. Al Hakam |  |
| *B. weihenstephanensis* KBAB4 |  |
| *Caldicellulosiruptor saccharolyticus* DSM 8903 |  |
| *Clostridium beijerinckii* NCIMB 8052 |  |
| *C. bolteae* ATCC BAA-613 |  |
| *C. kluyveri* DSM 555 |  |
| *C. scindens* ATCC 35704 |  |
| *Dorea longicatena* DSM 13814 |  |
| *Geobacillus* sp. WCH70 |  |
| *Lysinibacillus sphaericus* C3-41 |  |
| *Moorella thermoacetica* ATCC 39073 |  |
| *Pelotomaculum thermopropionicum* SI |  |
| *Staphylococcus aureus* RF122 |  |
| *S. aureus* subsp. *aureus* MW2 |  |
| *S. aureus* subsp. *aureus* MSSA476 |  |
| *S. aureus* subsp. *aureus* Mu50 |  |
| *S. saprophyticus* subsp. *saprophyticus* ATCC 15305 |  |
| *Thermosinus carboxydivorans* Nor1 |  |
| **Alpha-Proteobacteria** |  |
| *Acidiphilium cryptum* JF-5 | *Brevundimonas diminuta* |
| *Agrobacterium tumefaciens* | *Caulobacter crescentus* CB15 |
| *A. tumefaciens* str. CS8 | *Caulobacter* sp. K31 |
| *Bradyrhizobium* sp. ORS278 | *Erythrobacter* sp. NAP1 |
| *Bradyrhizobium japonicum* USDA 110 | *Erythrobacter* sp. SD-21 |
| Reference Organism                                      | AHL-Lactonase | AHL-Acylase |
|---------------------------------------------------------|---------------|-------------|
| **Bacillus sp. SB4 (GenBank AAB85482_1)**               |               |             |
| **Ralstonia sp. XJ12B (GenBank AAC041113_1)**           |               |             |
| **Alpha-Proteobacteria**                                |               |             |
| Granulibacter bethesdensis CGDNIH1                      |               |             |
| Hyphomonas neptunium ATCC 15444                         |               |             |
| Jannaschia sp. CCS1                                    |               |             |
| Oceanicola granulosus HTCC2516                          |               |             |
| Mesorhizobium sp. BNC1                                  |               |             |
| Paracoccus denitrificans PD1222                         |               |             |
| Phenylodobacterium zucineum HLK1                        |               |             |
| Rhizobium etli CN 42                                    |               |             |
| R. leguminosarum bv. trifolii WSM2304                   |               |             |
| Rhodobacterales bacterium HTCC2083                      |               |             |
| Rhodopseudomonas palustris TIE-1                        |               |             |
| Roseobacter sp. CCS2                                    |               |             |
| Roseobacter litoralis Och 149                           |               |             |
| R. denitrificans OCh 114                                |               |             |
| Sagittula stellata E-37                                 |               |             |
| Sphingomonas wittichii RW1                              |               |             |
| Stappia aggregata IAM 12614                             |               |             |
| **Beta-Proteobacteria**                                 |               |             |
| Burkholderia cenocepacia J2315                          |               |             |
| B. graminis C4D1M                                       |               |             |
| B. xenovorans LB400                                      |               |             |
| Ralstonia solanacearum GMI1000                          |               |             |
| Ralstonia eutropha JMP134                                |               |             |
|                        |               |             |
|                        |               |             |
|                        |               |             |
| Reference Organism | AHL-Lactonase | AHL-Acylase |
|--------------------|--------------|-------------|
| *Bacillus* sp. SB4 (GenBank AAB54821.1) |  |  |
| *Ralstonia* sp. XJ12B (GenBank AAOM1113.1) |  |  |

**Beta-Proteobacteria**
- *Ralstonia eutropha* H16
- *R. eutropha* JMP134
- *R. metallidurans* CH34
- *R. pickettii* 12J
- *R. solanacearum* GMI1000

**Gamma-Proteobacteria**
- *Acinetobacter sp. ADP1*
- *A. baumannii* AB0057
- *A. baumannii* ACICU
- *A. baumannii* AYE
- *A. baumannii* AYE
- *Alteromonas macleodii* 'Deep ecotype'
- *Marinomonas* sp. MWYL1
- *Cellvibrio japonicus* Ueda107
- *Photorhabdus luminescens* subsp. *laumondii* TTO1
- *Escherichia coli* KT 71
- *Pseudomonas stutzeri* A1501
- *Gamma proteobacterium* KT 71
- *Xanthomonas axonopodis* pv. *citri* str. 306
- *Hahella chejuensis* KCTC 2396
- *X. campestris pv. campestris* str. 8004
- *Idiomarina baltica* OS145
- *X. campestris pv. campestris* str. ATCC 33913
- *marine Gamma proteobacterium* HTCC2143
- *X. campestris pv. campestris* str. B100
- *marine Gamma proteobacterium* HTCC2207
- *X. campestris pv. vesicatoria* str. 85-10
- *Marinobacter algicola* DG893
- *Xylella fastidiosa* 9a5c
- *Mycococcus xanthus* DK 1622
- *X. fastidiosa* Ann-1
- *Nitrococcus mobilis* Nb-231
- *X. fastidiosa* M12
- *Oceanobacter* sp. RED65
- *Photorhabdus luminescens* subsp. *laumondii* TTO1
- *Providencia rettgeri*
- *P. stuartii* ATCC 25827
- *Pseudomonas* sp. 130
- *Pseudomonas* sp. GK16
- *Pseudomonas* sp. SY-77-1
- *Pseudomonas* sp. THA1
- *Pseudomonas* sp. THA2
- *Pseudomonas* sp. THA3
- *Pseudomonas* sp.
- *Pseudomonas aeruginosa* 2192
- *P. aeruginosa* C3719
- *P. aeruginosa* PA7
| Reference Organism                  | AHL-Lactonase  | AHL-Acylase          |
|-----------------------------------|----------------|---------------------|
| **Bacillus sp. SB4**              |                |                     |
| (GenBank AAR85482.1)              |                |                     |
| **Ralstonia sp. XJ12B**           |                |                     |
| (GenBank AA041113.1)              |                |                     |
| **Gamma-Proteobacteria**          |                |                     |
| *P. aeruginosa* PACS2             |                |                     |
| *P. aeruginosa* PAO1              |                |                     |
| *P. aeruginosa* UCBPP-PA14        |                |                     |
| *P. entomophila* L48              |                |                     |
| *P. fluorescens* Pf0-1            |                |                     |
| *P. fluorescens* Pf-5             |                |                     |
| *P. putida* F1                    |                |                     |
| *P. putida* GB-1                  |                |                     |
| *P. putida* KT2440                |                |                     |
| *P. putida* W619                  |                |                     |
| *P. syringae* pv. phaseolicola 1448A |            |                     |
| *P. syringae* pv. syringae B728a |                |                     |
| *P. syringae* pv. tomato str. DC3000 |            |                     |
| *Psychrobacter cryohalolentis* K5 |                |                     |
| *Serratia proteamaculans* 568     |                |                     |
| *Shewanella* sp. ANA-3            |                |                     |
| *Shewanella* sp. MIB015           |                |                     |
| *Shewanella* sp. MR-4             |                |                     |
| *Shewanella* sp. MR-7             |                |                     |
| *Shewanella* sp. W3-18-1          |                |                     |
| *Shewanella amazonensis* SB2B     |                |                     |
| *S. baltica* OS155                |                |                     |
| *S. baltica* OS185                |                |                     |
| *S. frigidimarina* NCIMB 400      |                |                     |
| *S. oneidensis* MR-1              |                |                     |
| *S. putrefaciens* 200             |                |                     |
| *S. putrefaciens* CN-32           |                |                     |
| *S. woodyi* ATCC 51908            |                |                     |
| **Delta-Proteobacteria**          |                |                     |
| *Desulfatibacillum* alkenivorans AK-01 |            |                     |
| *D. alkenivorans* AK-01           |                |                     |
| *Desulfovibrio* desulfuricans subsp. desulfuricans* str. G20 | |                     |
| *Plesiocystis pacifica* SIR-1     |                |                     |
| *D. vulgaris* subsp. vulgaris str. Hildenborough | |                     |
| *Stigmatella aurantiaca* DW4/3-1  |                |                     |
| *Desulfococcus* oleovorans Hxd3   |                |                     |
| *Sorangium cellulosum* ‘So ce 56’ |                |                     |
| Reference Organism | AHL-Lactonase | AHL-Acylase |
|--------------------|---------------|-------------|
| Bacillus sp. SB4  | (GenBank AAB85482.1) | Ralstonia sp. XJ12B |
| (GenBank AAO41113.1) |               |             |
| Euryarchaeota      |               |             |
| Archaeoglobus fulgidus DSM 4304 | A. fulgidus DSM 4304 |
| Halocarcula marismortui ATCC 43049 |             |
| Halobacterium salinarum R1 |             |
| Halorobium lacusprofundi ATCC 49239 |             |
| Natromonas pharaonis DSM 2160 |             |
| Thermoplasma acidophilum DSM 1728 |             |
| T. volcanium GSS1 |             |
| Crenarchaeota      |               |             |
| Sulfolobus solfataricus P2 | Pyrobaculum calidifontis JCM 11548 |
| Tenacibaculum sp. MED152 |             |
| Sphingobacteria    |               |             |
| Microscilla marina ATCC 23134 |             |
| Spirochaetales     |               |             |
| Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130 |             |
| L. interrogans serovar Lai str. 56601 |             |
| Nitrospirales      |               |             |
| Thermodesulfovibrio yellowstonii DSM 11347 |             |
| Planctomycetes (Ascomycota) |             |
| Aspergillus clavatus NRRL 1 |             |
| A. oryzae RIB40 |             |
| Aspergillus nidulans FGSC A4 |             |
| Coccioides immitis RS |             |
| Penicillium chrysogenum Wisconsin 54-1255 |             |
| Phaeosphaeria nodorum SN15 |             |
Fig. (S1). Regular expression diagrama of signatures (nucleotides) of Actinobacterial gene (aaiA) for AHL lactonase obtained with respect to Bacillus sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (http://meme.edu/meme.html)

Fig. (S2). Regular expression diagrama of signatures (nucleotides) of Firmicutes gene (aaiA) for AHL lactonase obtained with respect to Bacillus sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (http://meme.edu/meme.html)
Fig. (S3). Regular expression diagram of signatures (nucleotides) of Alpha-Proteobacterial gene ($aiiA$) for AHL lactonase obtained with respect to Bacillus sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (http://meme.edu/meme.html)

Fig. (S4). Regular expression diagram of signatures (nucleotides) of Beta-Proteobacterial gene ($aiiA$) for AHL lactonase obtained with respect to Bacillus sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (http://meme.edu/meme.html)
Fig. (S5). Regular expression diagram of signatures (nucleotides) of Gamma-Proteobacterial gene (aiiA) for AHL lactonase obtained with respect to Bacillus sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (http://meme.edu/meme.html)

Fig. (S6). Regular expression diagram of signatures (nucleotides) of Delta-Proteobacterial gene (aiiA) for AHL lactonase obtained with respect to Bacillus sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (http://meme.edu/meme.html)

Fig. (S7). Regular expression diagram of signatures (nucleotides) of Euryarchaeota gene (aiiA) for AHL lactonase obtained with respect to Bacillus sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (http://meme.edu/meme.html)
Fig. (S8). Regular expression diagram of signatures (nucleotides) of Ascomycota gene (aiiA) for AHL lactonase obtained with respect to Bacillus sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (http://meme.edu/meme.html)

Fig. (S9). Regular expression diagram of signatures (nucleotides) of Actinobacterial gene (aiiA) for AHL acylase obtained with respect to Ralstonia sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (http://meme.edu/meme.html)

Fig. (S10). Regular expression diagram of signatures (nucleotides) of Bacteroidetes gene (aiiA) for AHL acylase obtained with respect to Ralstonia sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (http://meme.edu/meme.html)
**Fig. (S11).** Regular expression diagram of signatures (nucleotides) of Cyanobacteria gene (aiiA) for AHL acylase obtained with respect to *Ralstonia* sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (http://meme.edu/meme.html)

**Fig. (S12).** Regular expression diagram of signatures (nucleotides) of Alpha-Proteobacterial gene (aiiA) for AHL acylase obtained with respect to *Ralstonia* sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (http://meme.edu/meme.html)

**Fig. (S13).** Regular expression diagram of signatures (nucleotides) of Beta-Proteobacteria gene (aiiA) for AHL acylase obtained with respect to *Ralstonia* sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (http://meme.edu/meme.html)
**Fig. (S14).** Regular expression diagram of signatures (nucleotides) Gamma-Proteobacterial member- *Pseudomonas* gene (*aiiA*) for AHL acylase obtained with respect to *Ralstonia* sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (http://meme.edu/meme.html)

**Fig. (S15).** Regular expression diagram of signatures (nucleotides) of Gamma-Proteobacterial member- *Shewanella* sp. gene (*aiiA*) for AHL acylase obtained with respect to *Ralstonia* sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (http://meme.edu/meme.html)
Fig. (S16). Regular expression diagram of signatures (nucleotides) of other sequences of Gamma-Proteobacterial gene (aiiA) for AHL acylase obtained with respect to Ralstonia sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (http://meme.edu/meme.html)
### Table S2. Representation of motifs obtained for Actinobacteria through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (aiiA) of Bacillus sp. SB4 GenBank AAR85482.1)

| Organism                     | Signatures (Nucleotides) | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|------------------------------|--------------------------|----|----|----|----|----|----|----|----|----|-----|
| Actinobacteria               |                          |    |    |    |    |    |    |    |    |    |     |
| Arthrobacter chlorophenolicus A6 |                          | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
| Candidatus koribacter versatilis Ellin345 |                    | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
| Frankia sp. EAN1pec           |                          | +  | +  | +  | +  | +  | +  | +  | +  | +  | -   |
| Mycobacterium marinum M       |                          | +  | ++ | +  | +  | +  | +  | +  | +  | +  | -   |
| M. smegmatis str. MC2 155     |                          | +  | +  | ++ | +  | +  | +  | +  | +  | +  | ++  |
| Mycobacterium sp. MCS         |                          | +  | ++ | +  | ++ | +  | +  | -  | -  | +  | +   |
| Rhodococcus sp. RHA1          |                          | +  | +  | +  | +  | ++ | +  | +  | +  | +  | +   |
| Streptomyces clavuligerus ATCC 27064 |                    | +  | +  | +  | +  | +  | +  | +  | -  | -  | +   |
| Deinococcus clavuligerus ATCC 27064 |                    | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Firmicutes                    |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0   |
| Alpha-Proteobacteria          |                          | 0  | 1  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0   |
| Beta-Proteobacteria           |                          | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 1  | 0  | 0   |
| Gamma-Proteobacteria          |                          | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 2  | 0  | 0   |
| Delta-Proteobacteria          |                          | 0  | 2  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0   |
| Euryarchaeota                 |                          | 0  | 0  | 0  | 0  | 0  | 0  | 2  | 1  | 0  | 0   |
| Crenarchaeota                 |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Ascomycota                    |                          | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0   |
| Frequency of occurrence within Actinobacteria |                  | 8/8 | 8/8 | 8/8 | 8/8 | 8/8 | 8/8 | 8/8 | 6/8 | 5/8 | 7/8  |
| Total frequency of occurrence |                          | 8/110 | 12/110 | 8/110 | 8/110 | 8/110 | 8/110 | 14/110 | 12/110 | 5/110 | 7/110 |

### Table S3. Representation of motifs obtained for Firmicutes through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (aiiA) of Bacillus sp. SB4 GenBank AAR85482.1)

| Organism                    | Signatures (Nucleotides) | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|-----------------------------|--------------------------|----|----|----|----|----|----|----|----|----|-----|
| Firmicutes                  |                          |    |    |    |    |    |    |    |    |    |     |
| Bacillus sp. 91             |                          | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
| Bacillus sp. A24            |                          | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
| Bacillus sp. B14905         |                          | +  | +  | -  | -  | -  | -  | -  | +  | -  | -   |
| Bacillus sp. SB4            |                          | +  | +  | +  | ++ | +  | +  | +  | +  | +  | +   |
| Bacillus anthracis str. Ames|                          | +  | -  | -  | +  | -  | -  | -  | -  | -  | +   |
| B. cereus                   |                          | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
### Table 3S. contd....

| Organism                                      | Signatures (Nucleotides) |
|-----------------------------------------------|--------------------------|
|                                               | M1  | M2  | M3  | M4  | M5  | M6  | M7  | M8  | M9  | M10 |
| **Firmicutes**                                |     |     |     |     |     |     |     |     |     |     |
| *B. cereus* W                                 | -   | -   | +   | +   | -   | -   | -   | -   | -   | +   |
| *B. licheniformis ATCC 14580*                 | +   | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| *B. subtilis* strain BSI                      | +   | +   | +   | +   | ++  | +   | +   | +   | +   | +   |
| *B. thuringiensis str. BCR-ZYR25*             | +   | +   | +   | +   | ++  | +   | +   | +   | +   | +   |
| *B. thuringiensis serovar israelensis ATCC 35646* | +   | +   | -   | +   | -   | -   | -   | +   | -   | -   |
| *B. thuringiensis str. Al Hakam*              | +   | +   | -   | +   | -   | -   | -   | -   | +   | -   |
| *B. weihenstephanensis* KBAB4                 | +   | -   | -   | -   | -   | -   | -   | -   | -   | +   |
| Caldicellulosiruptor saccharolyticus DSM 8903 | +   | -   | -   | -   | -   | -   | -   | -   | -   | +   |
| *Clostridium beijerinckii* NCIMB 8052         | -   | +   | +   | -   | -   | -   | -   | -   | -   | -   |
| *C. bolteae* ATCC BAA-613                     | +   | -   | -   | -   | -   | -   | -   | -   | -   | +   |
| *C. kluyveri* DSM 555                         | +   | -   | -   | -   | -   | -   | +   | -   | -   | ++  |
| *C. scindens* ATCC 35704                      | +   | -   | -   | -   | -   | -   | +   | -   | -   | -   |
| *Dorea longicatena* DSM 13814                 | -   | -   | +   | -   | -   | -   | -   | -   | -   | +   |
| Geobacillus sp. WCH70                         | +   | -   | -   | -   | -   | -   | -   | -   | -   | -   |
| Lysinibacillus sphaericus C3-41               | +   | -   | -   | +   | -   | -   | +   | -   | -   | +   |
| *Moorella thermoacetica* ATCC 39073           | +   | +   | -   | -   | -   | -   | -   | -   | -   | +   |
| Pelotomaculum thermopropionicum SI             | +   | -   | -   | -   | -   | -   | -   | -   | -   | +++ |
| Staphylococcus aureus RF122                    | +   | +   | +   | +   | +   | +   | +   | -   | -   | +   |
| *S. aureus* subsp. aureus MSSA476             | +   | +   | +   | +   | +   | +   | +   | +   | +   | +   |
| *S. aureus* subsp. aureus Mu50                | +   | +   | +   | +   | +   | +   | +   | +   | +   | +   |
| *S. aureus* subsp. aureus MW2                 | +   | +   | +   | +   | +   | +   | +   | +   | +   | +   |
| *S. saprophyticus* subsp. saprophyticus ATCC 15305 | -   | +   | -   | -   | -   | -   | -   | -   | -   | -   |
| *Thermosinus carboxydivorans* Nor1             | -   | -   | -   | -   | -   | -   | -   | +   | -   | -   |
| Actinobacteria                                | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| Deinococcus-Thermus                           | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| Alpha-Proteobacteria                          | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| Beta-Proteobacteria                           | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| Gamma-Proteobacteria                          | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| Delta-Proteobacteria                          | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| Euryarchaeota                                 | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| Crenarchaeota                                 | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| Ascomycota                                    | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   |
| Frequency of occurrence within Firmicutes     | 25/30| 16/30| 13/30| 15/30| 10/30| 10/30| 14/30| 12/30| 14/30| 21/30|
| Total frequency of occurrence                 | 25/110| 16/110| 13/110| 15/110| 10/110| 10/110| 14/110| 12/110| 14/110| 21/110|
Table S4. Representation of motifs obtained for Alpha-Proteobacteria through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (\(\textit{aaiA}\)) of \(\textit{Bacillus}\) sp. SB4 GenBank AAR85482.1)

| Organism | Signatures (Nucleotides) | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|----------|--------------------------|----|----|----|----|----|----|----|----|----|-----|
| Alpha-Proteobacteria | | | | | | | | | | | |
| Acidiphilium cryptum JF-5 | | | | | | | | | | | |
| Agrobacterium tumefaciens | | | | | | | | | | | |
| Bradyrhizobium japonicum USDA 110 | | | | | | | | | | | |
| Bradyrhizobium sp. ORS278 | | | | | | | | | | | |
| Granulibacterium CGDN1H1 | | | | | | | | | | | |
| Hyphomonas neptunium ATCC 15444 | | | | | | | | | | | |
| Jannaschia sp. CCS1 | | | | | | | | | | | |
| Jannaschia sp. CCS1 | | | | | | | | | | | |
| Labrenzia aggregata IAM 12614 | | | | | | | | | | | |
| Mesorhizobium sp. BNC1 | | | | | | | | | | | |
| Oceanicola granulosus HTCC2516 | | | | | | | | | | | |
| Paracoccus denitrificans PD1222 | | | | | | | | | | | |
| Phenylbacterium zuccineum HLK1 | | | | | | | | | | | |
| Rhizobium etli CFN 42 | | | | | | | | | | | |
| R. leguminosarum bv. trifolii WSM2304 | | | | | | | | | | | |
| Rhodobacterales bacterium HTCC2083 | | | | | | | | | | | |
| Rhodopseudomonas palustris TIE-1 | | | | | | | | | | | |
| Roseobacter denitrificans OCh 114 | | | | | | | | | | | |
| Roseobacter literatus Och 149 | | | | | | | | | | | |
| Roseobacter sp. CCS2 | | | | | | | | | | | |
| Sagittula stellata E-37 | | | | | | | | | | | |
| Sphingomonas wittichii RW1 | | | | | | | | | | | |
| Actinobacteria | | | | | | | | | | | |
| Deinococcus-Thermus | | | | | | | | | | | |
| Firmicutes | | | | | | | | | | | |
| Beta-Proteobacteria | | | | | | | | | | | |
| Gamma-Proteobacteria | | | | | | | | | | | |
| Delta-Proteobacteria | | | | | | | | | | | |
| Euryarchaeota | | | | | | | | | | | |
| Crenarchaeota | | | | | | | | | | | |
| Ascomycota | | | | | | | | | | | |

Frequency of occurrence within Alpha-Proteobacteria: 22/22 15/22 19/22 21/22 13/22 21/22 19/22 10/22 10/22 12/22

Total frequency of occurrence: 22/110 15/110 19/110 21/110 13/110 21/110 21/110 10/110 10/110 12/110
Table S5. Representation of motifs obtained for Beta-Proteobacteria through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (aiiA) of Bacillus sp. SB4 GenBank AAR85482.1)

| Organism                             | Signatures (Nucleotides) |
|--------------------------------------|--------------------------|
|                                      | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
| Beta-Proteobacteria                  |    |    |    |    |    |    |    |    |    |     |
| Burkholderia cenocepacia J2315       | +++|    |    |    |    |    |    |    |    |     |
| B. graminis C4DM                     | +  | +  | +  | +  | +  | +  | +  | +  | +  | +    |
| B. xenovorans LB400                  | +  | +  | +  | +  | +  | +  | +  | +  | +  | +    |
| Ralstonia eutropha JMP34             | +  | +  | +  | +  | +  | +  | +  | +  | +  | +    |
| R. solanacearum GMI1000              | +  | +  | +  | +  | +  | +  | +  | +  | +  | +    |
| Actinobacteria                       | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Deinococcus-Thermus                  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Firmicutes                           | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Alpha-Proteobacteria                 | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Gamma-Proteobacteria                 | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 4  | 0  | 0    |
| Delta-Proteobacteria                 | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Euryarchaeota                        | 0  | 0  | 0  | 0  | 0  | 0  | 2  | 1  | 0  | 0    |
| Crenarchaeota                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Ascomycota                           | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Frequency of occurrence within Beta-Proteobacteria | 5/5| 5/5| 5/5| 5/5| 5/5| 5/5| 5/5| 5/5| 5/5| 5/5  |
| Total frequency of occurrence        | 5/110 | 7/110 | 5/110 | 5/110 | 5/110 | 5/110 | 11/110 | 6/110 | 5/110 |
Table S6. Representation of motifs obtained for Gamma-Proteobacteria through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (aiiA) of Bacillus sp. SB4 GenBank AAR85482.1)

| Organism                                      | Signatures (Nucleotides) | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|-----------------------------------------------|-------------------------|----|----|----|----|----|----|----|----|----|-----|
| Gamma-Proteobacteria                          |                         |    |    |    |    |    |    |    |    |    |     |
| Acinetobacter sp. ADP1                        |                         | +  | +  | +  | +  | +  | -  | +  | +  | +  | +   |
| Acinetobacter baumannii AB0057                |                         | -  | +  | +  | +  | +  | -  | +  | +  | +  | +   |
| A. baumannii ACICU                            |                         | -  | +  | ++ | +  | +  | -  | +  | +  | +  | +   |
| A. baumannii AYE                              |                         | +  | +  | +  | +  | +  | -  | +  | -  | +  | +   |
| Marine gamma proteobacterium HTCC2080         |                         | -  | +  | -  | -  | -  | -  | -  | -  | -  | -   |
| Marinomonas sp. MWYL1                         |                         | +  | +  | +  | +  | +  | -  | -  | -  | +  | +   |
| Photorhabdus luminescens subsp. laumondii TTO1 |                         | +  | -  | -  | -  | -  | -  | -  | +  | -  | -   |
| Pseudomonas stutzeri A1501                    |                         | +  | +  | +  | -  | -  | +  | +  | +  | +  | +   |
| Xanthomonas axonopodis pv. citri str. 306     |                         | +  | +  | +  | +  | +++| +  | +  | +  | +  | +   |
| X. campestris pv. campestris str. 8004        |                         | -  | +  | +  | -  | -  | -  | -  | -  | -  | +   |
| X. campestris pv. campestris str. ATCC 33913  |                         | +  | +  | +  | ++ | +  | +  | +  | +  | +  | +   |
| X. campestris pv. campestris str. B100       |                         | -  | +  | +  | +  | +  | -  | -  | -  | +  | -   |
| X. campestris pv. vesicatoria str. 85-10     |                         | +  | +  | +  | +  | ++ | +  | +  | +  | +  | +   |
| Xylella fastidiosa 9°5c                       |                         | +  | +  | +  | +  | ++ | +  | +  | +  | +  | +   |
| X. fastidiosa Ann-1                          |                         | +  | +  | +  | +  | ++ | +  | +  | +  | +  | +   |
| X. fastidiosa M12                            |                         | +  | +  | +  | +  | ++ | +  | +  | +  | +  | +   |
| Actinobacteria                                |                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Deinococcus-Thermus                           |                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Firmicutes                                    |                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Alpha-Proteobacteria                          |                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Beta-Proteobacteria                           |                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Delta-Proteobacteria                          |                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Euryarchaeota                                 |                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Crenarchaeota                                 |                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Ascomycota                                    |                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Frequency of occurrence within Gamma-proteobacteria |                     | 11/16 | 15/16 | 14/16 | 14/16 | 10/16 | 9/16 | 11/16 | 12/16 | 12/16 | 14/16 |
| Total frequency of occurrence                 |                         | 11/110 | 15/110 | 14/110 | 14/110 | 10/110 | 9/110 | 11/110 | 12/110 | 12/110 | 14/110 |
Table S7. Representation of motifs obtained for Delta-Proteobacteria through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (aIIA) of Bacillus sp. SB4 GenBank AAR85482.1)

| Signatures (Nucleotides) | Organism                          | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|--------------------------|-----------------------------------|----|----|----|----|----|----|----|----|----|-----|
|                          | Delta-Proteobacteria              |    |    |    |    |    |    |    |    |    |     |
|                          | Desulfobacillus akkenivorus AK-01  | +  | +  | +  | ++ | +  | ++ | +  | +  | +  |     |
|                          | Desulfococcus oleovorans Htx3     | +  | +  | +  | +  | +  | +  | +  | +  | +  |     |
|                          | Desulfovibrio desulfuricans str. G20 | +  | +  | +  | +  | +  | +  | +  | +  | +  |     |
|                          | D. vulgaris subsp. vulgaris str. Hildenborough | ++ | +  | +  | +  | +  | +  | +  | +  | +  |     |
|                          | Sorangium cellulosum 'So ce 56'   | +  | +  | +  | -  | +  | ++ | +  | +  | +  |     |
|                          | Actinobacteria                    | 0  | 0  | 0  | 2  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Deinococcus-thermus                | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Firmicutes                         | 0  | 0  | 0  | 3  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Alpha-Proteobacteria               | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Beta-Proteobacteria                | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Gamma-Proteobacteria               | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Euryarchaeota                      | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Crenarchaeota                      | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Ascomycota                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Frequency of occurrence within Delta-Proteobacteria | 5/5 | 5/5 | 5/5 | 4/5 | 5/5 | 5/5 | 5/5 | 5/5 | 5/5 | 5/5 |
|                          | Total frequency of occurrence      | 5/110 | 5/110 | 5/110 | 11/110 | 5/110 | 5/110 | 5/110 | 5/110 | 5/110 | 5/110 |

Table S8. Representation of motifs obtained for Euryarchaeota through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (aIIA) of Bacillus sp. SB4 GenBank AAR85482.1)

| Signatures (Nucleotides) | Organism                           | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|--------------------------|------------------------------------|----|----|----|----|----|----|----|----|----|-----|
|                          | Euryarchaeota                      |    |    |    |    |    |    |    |    |    |     |
|                          | Archaeoglobus fulgidus DSM 4304    | -  | +  | +  | +  | +  | +  | +  | +  | +  |     |
|                          | Halocarcina marismortui ATCC 43049  | ++ | +  | -  | -  | -  | -  | -  | +  | -  | +   |
|                          | Halobalobus lacusprofundi ATCC 49239 | +  | +  | -  | +  | +++ | -  | -  | +  | -  | +   |
|                          | Natronomonas pharaonis DSM 2160     | +  | +  | -  | +  | +  | +  | ++ | -  | -  | -   |
|                          | Thermoplasma acidophilum DSM 1728   | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
|                          | Thermoplasma volcanium GSS1        | +  | +  | +  | +  | ++ | +  | +  | +  | +  | +   |
|                          | T. volcanium GSS1                  | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
|                          | T. volcanium GSS1                  | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
|                          | Actinobacteria                     | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Deinococcus-Thermus                | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Firmicutes                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Alpha-Proteobacteria               | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Beta-Proteobacteria                | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Gamma-Proteobacteria               | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Delta-Proteobacteria               | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Crenarchaeota                      | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Ascomycota                         | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
|                          | Frequency of occurrence within Euryarchaeota | 7/8 | 8/8 | 5/8 | 7/8 | 7/8 | 6/8 | 6/8 | 8/8 | 5/8 | 6/8 |
|                          | Total frequency of occurrence      | 7/110 | 8/110 | 5/110 | 7/110 | 7/110 | 6/110 | 6/110 | 8/110 | 5/110 | 6/110 |
### Table S9. Representation of motifs obtained for Ascomycota through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (aiiA) of *Bacillus* sp. SB4 GenBank AAR85482.1)

| Organism                    | Signatures (Nucleotides) | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|-----------------------------|--------------------------|----|----|----|----|----|----|----|----|----|-----|
| Ascomycota                  |                          |    |    |    |    |    |    |    |    |    |     |
| *Aspergillus clavatus* NRRL 1|                          | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
| *A. oryzae* RIB40           |                          | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
| *Coccidioides immitis* RS   |                          | ++ | +  | ++ | +  | +  | +  | +  | +  | +  | +   |
| *Phaeosphaeria nodorum* SN15|                          | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
| Actinobacteria              |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Deinococcus-Thermus         |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Firmicutes                  |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Beta-Proteobacteria         |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Gamma-Proteobacteria        |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Delta-Proteobacteria        |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Euryarchaeota               |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Crenarchaeota               |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Frequency of occurrence     |                          | 4/4| 4/4| 4/4| 4/4| 4/4| 4/4| 4/4| 4/4| 4/4| 4/4 |
| Total frequency of occurrence|                          | 4/110| 4/110| 4/110| 4/110| 4/110| 4/110| 4/110| 4/110| 4/110| 4/110|

### Table S10. Representation of motifs obtained for Actinobacteria through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (aiiD) of *Ralstonia* sp. XJ12B GenBank AAC41113.1)

| Organism                    | Signatures (Nucleotides) | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|-----------------------------|--------------------------|----|----|----|----|----|----|----|----|----|-----|
| Actinobacteria              |                          |    |    |    |    |    |    |    |    |    |     |
| *Nocardioioides* sp. JS614  |                          | +++| ++ | +  | ++ | +  | +++| -  | +++| +  | -   |
| *Salinispora arenicola* CNS-205|                          | +++| ++ | +  | -  | -  | -  | +  | -  | +++| +   |
| *S. tropica* CNB-440        |                          | +  | +  | ++ | -  | ++ | -  | ++ | +  | -  | -   |
| *Streptomyces* sp. FERM BP-5809|                          | +  | +  | +  | +++| ++ | ++ | +  | +  | +   |
| *Streptomyces* sp. M664     |                          | ++ | +  | ++ | +++| ++ | ++ | +  | +  | +   |
| *Streptomyces* sp. Mg1      |                          | ++ | +  | +++| +  | +  | +  | +  | ++ | +++|
| *Streptomyces griseus* subsp. griseus NBRC 13350|                          | +  | +  | ++ | +  | ++ | +  | +++| +  | +   |
| *Rhodopirellula baltica* SH 1|                          | +++| +  | ++ | +  | +  | -  | +  | ++ | -   |
| Cyanobacteria               |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Alpha-Proteobacteria        |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Beta-Proteobacteria         |                          | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Gamma-Proteobacteria        |                          | 5  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Deinococcus-Thermus         |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Bacteroidetes               |                          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  |     |
| Frequency of occurrence     |                          | 9  | 9  | 9  | 6  | 7  | 8  | 7  | 9  | 9  | 7   |
| Total frequency of occurrence|                          | 15/94| 9/94| 9/94| 6/94| 7/94| 8/94| 7/94| 9/94| 9/94| 7/94|
Table S11: Representation of motifs obtained for Bacteroidetes through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (aiiD) of *Ralstonia* sp. XJ12B GenBank AAO41113.1)

| Organisms            | Signatures (Nucleotides) | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|----------------------|--------------------------|----|----|----|----|----|----|----|----|----|-----|
| **Bacteroidetes**    |                          |    |    |    |    |    |    |    |    |    |     |
| Algoriphagus sp. PR1 | ++                       | +  | +  | +  | +  | +++ | +  | +  | +  | +  | +   |
| Microscilla marina ATCC 23134 | + | +  | +  | +  | -  | +  | +  | +  | +  | ++ | +   |
| Pedobacter sp. BAL39 | +                        | -  | ++ | +  | +  | +  | ++ | +  | +  | +  | +   |
| Polaribacter irgensii 23-P | + | +  | +  | +  | ++ | +  | +  | +  | +  | +  | +   |
| Robiginitalea bifurcata HTCC2501 | ++ | ++ | +  | +  | +  | ++ | +  | +  | +  | +  | +   |
| R. bifurcata HTCC2501 | -                        | +  | +  | -  | +  | +  | +  | +  | -  | +  | +   |
| Salinibacter ruber DSM 13855 | - | -  | -  | -  | -  | -  | +  | +  | -  | -  | -   |
| **Actinobacteria**   |                          |    |    |    |    |    |    |    |    |    |     |
| Actinobacteria       | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| Alpha-Proteobacteria | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| Beta-Proteobacteria  | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| Gamma-Proteobacteria | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| Deinococcus-Thermus  | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| **Frequency of occurrence within Bacteroidetes** | 5 | 5  | 7  | 5  | 5  | 5  | 7  | 7  | 5  | 6   |
| **Total Frequency of occurrence** | 6/94 | 5/94 | 7/94 | 5/94 | 5/94 | 5/94 | 7/94 | 7/94 | 5/94 | 6/94 |

Table S12. Representation of motifs obtained for Cyanobacteria through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (aiiD) of *Ralstonia* sp. XJ12B GenBank AAO41113.1)

| Organisms            | Signatures (Nucleotides) | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|----------------------|--------------------------|----|----|----|----|----|----|----|----|----|-----|
| **Cyanobacteria**    |                          |    |    |    |    |    |    |    |    |    |     |
| Cyanothece sp. CCY 0110 | + | +  | +  | +  | +  | +  | ++ | +  | +  | +  | ++  |
| Cyanothece sp. ATCC 51142 | + | +  | +  | +  | +  | +  | +  | +  | +  | +  | ++  |
| Cyanothece sp. PCC 8802 | +                        | +  | +  | +  | +  | +  | ++ | +  | +  | +  | +   |
| Cyanothece sp. PCC 7424 | +                        | +  | +  | +  | +  | +  | +  | +  | +  | +  | +   |
| Cyanothece sp. PCC 7822 | +                        | +  | +  | +  | +  | +  | +++ | +  | +  | +  | +   |
| Synechocystis sp. PCC 6803 | +                     | ++ | +  | +  | +  | +  | +  | +  | +  | +  | ++  |
| Cyanothece sp. PCC 8801 | +                        | +  | +  | ++ | +  | +  | +  | +  | -  | -   | -   |
| *Nostoc punctiforme* PCC 73102 (Nostoc punctiforme ATCC 29133) | - | +  | +  | ++ | +  | +  | +  | -  | -   | -   | -   |
| Microcoleus chthonoplastes PCC 7420 | - | +  | +  | +  | ++ | +  | -  | -  | -   | -   | -   |
| **Actinobacteria**   |                          |    |    |    |    |    |    |    |    |    |     |
| Actinobacteria       | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| **Bacteroidetes**    |                          |    |    |    |    |    |    |    |    |    |     |
| Alpha-Proteobacteria | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| Beta-Proteobacteria  | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| Gamma-Proteobacteria | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| Deinococcus-Thermus  | 0                        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   | 0   |
| **Frequency of occurrence within Cyanobacteria** | 7 | 9  | 9  | 9  | 9  | 9  | 5  | 6  | 6   |
| **Total Frequency of occurrence** | 7/94 | 9/94 | 9/94 | 9/94 | 9/94 | 9/94 | 9/94 | 5/94 | 6/94 | 6/94 |
Table S13. Representation of motifs obtained for Alpha-Proteobacteria through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene \((a\text{ii}D)\) of \textit{Ralstonia} sp. XJ12B GenBank AAO41113.1)

| Organisms                      | Signatures (Nucleotides) | M1   | M2   | M3   | M4   | M5   | M6   | M7   | M8   | M9   | M10  |
|--------------------------------|--------------------------|------|------|------|------|------|------|------|------|------|------|
|                                |                          |      |      |      |      |      |      |      |      |      |      |
| **Alphaproteobacteria**        |                          |      |      |      |      |      |      |      |      |      |      |
| \textit{Bermanella marisrubri} | strain RED65             | +    | +    | -    | -    | -    | -    | ++   | -    | ++   | +    |
| \textit{Caulobacter} sp. K31   |                          | +    | ++   | ++   | +    | ++   | +    | +++  | ++   | +    | +    |
| \textit{Erythrobacter} litoralis HTCC2594 |                   | +    | +    | ++   | +    | ++   | +    | ++   | +    | +    | ++++ |
| \textit{Erythrobacter} sp. NAP1 |                          | +    | -    | -    | +    | +    | -    | -    | ++   | +++  | +    |
| \textit{Erythrobacter} sp. SD-21 |                          | +    | -    | -    | +    | +    | -    | -    | +    | +    | ++++ |
| \textit{Hyphomonas} neptunium ATCC 15444 |                     | -    | -    | -    | -    | -    | +    | +    | -    | +    | ++   |
| \textit{Parvibaculum} lavamentivorans DS-1 |                  | +++  | +    | +    | ++   | ++   | +    | +    | +    | +    | ++   |
| \textit{Sphingopyxis} alaskensis RB2256 |                       | ++   | +    | +    | +    | +    | +    | +    | +    | +    | +    |
| Actinobacteria                 |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Cyanobacteria                  |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Beta-Proteobacteria            |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Gamma-Proteobacteria           |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Deinococcus-Thermus            |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Bacteroidetes                  |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Frequency of occurrence within Alpha-Proteobacteria |               | 7    | 6    | 5    | 6    | 6    | 7    | 6    | 8    | 8    |      |
| Total frequency of occurrence  |                          | 7/94 | 6/94 | 5/94 | 6/94 | 6/94 | 6/94 | 7/94 | 6/94 | 8/94 | 8/94 |

Table S14. Representation of motifs obtained for Beta-Proteobacteria through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene \((a\text{ii}D)\) of \textit{Ralstonia} sp. XJ12B GenBank AAO41113.1)

| Organism                      | Signatures (Nucleotides) | M1   | M2   | M3   | M4   | M5   | M6   | M7   | M8   | M9   | M10  |
|--------------------------------|--------------------------|------|------|------|------|------|------|------|------|------|------|
|                                |                          |      |      |      |      |      |      |      |      |      |      |
| **Beta-Proteobacteria**        |                          |      |      |      |      |      |      |      |      |      |      |
| \textit{Acidovorax} avenae subsp. citrulli AAC00-1 |                  | +    | +    | +    | +    | +    | +    | +++  | +++  | ++   | +    |
| \textit{Delfia} acidovorans    |                          | ++   | +    | ++   | +    | +    | +    | +++  | ++   | ++   | +    |
| \textit{Limnobacter} sp. MED105 |                          | +    | ++   | ++   | +    | +    | +    | +    | +    | +    | +    |
| \textit{Ralstonia} sp. XJ12B   |                          | +++  | -    | +    | ++   | +++  | +    | -    | -    | +    | ++   |
| \textit{Ralstonia} aestropha H16 |                         | +    | ++   | -    | ++   | +++  | -    | +    | +    | +    | ++   |
| \textit{R. metallicarum} CH34  |                          | -    | ++   | -    | +    | -    | ++   | +    | +    | +    | +    |
| \textit{R. pickettii} 12J      |                          | +++  | +    | +    | +    | ++   | +++  | +    | +    | +    | +    |
| \textit{R. solanacearum} GMI1000 |                         | ++   | +    | +    | +++  | +++  | +    | ++   | +    | +    | +    |
| Actinobacteria                 |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Cyanobacteria                  |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Alpha-Proteobacteria           |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Gamma-Proteobacteria           |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Deinococcus-Thermus            |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Bacteroidetes                  |                          | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 0    |
| Frequency of occurrence within Beta-Proteobacteria |                | 7    | 7    | 7    | 6    | 7    | 7    | 6    | 8    | 7    |      |
| Total frequency of occurrence  |                          | 7/94 | 7/94 | 7/94 | 6/94 | 8/94 | 7/94 | 7/94 | 6/94 | 8/94 | 7/94 |
Table S15. Representation of motifs obtained for *Pseudomonas* sp. through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (*aaiD*) of *Ralstonia* sp. XJ12B GenBank AAO41113.1)

| Organisms                     | Signatures (Nucleotides) |
|-------------------------------|--------------------------|
|                               | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
| **Gamma-Proteobacteria - *Pseudomonas* spp.** |     |    |    |    |    |    |    |    |    |     |
| *Pseudomonas* sp. GK16        | +++| +  | +  | +  | +  | +++| +  | +  | +  | +++ |
| *Pseudomonas* sp. THA3        | +++| +  | +  | +  | +  | +++| +  | +  | +  | +++ |
| *Pseudomonas* sp. THA1        | +++| +  | +  | +  | +  | +++| +  | +  | +  | +++ |
| *Pseudomonas* sp. THA2        | +++| +  | +  | +  | +  | ++ | +  | +  | +  | +++ |
| *Pseudomonas* syringae pv. tomato str. DC3000 | +  | +  | ++ | +  | +  | +  | +  | +  | ++ | +  |
| *P.* syringae pv. phaseolicola 1448" | ++ | +  | ++ | +  | +  | +  | +  | +  | +  | ++ |
| *P.* syringae pv. syringae B728a | +  | +  | +  | +  | +  | +  | +  | +  | ++ | +  |
| *Pseudomonas* sp. 130         | +++| +  | +  | +  | +  | +++| +  | +  | +  | +++ |
| *P. aeruginosa* 2192          | ++ | ++ | +  | +  | +  | +  | +  | +  | +  | ++ |
| *P. aeruginosa* C3719         | ++ | ++ | +  | +  | +  | +  | +  | +  | +  | ++ |
| *P. aeruginosa* PACS2         | ++ | ++ | +  | +  | +  | +  | ++ | ++ | ++ | ++ |
| *P. aeruginosa* UCBPP-PA14    | +  | ++ | +  | +  | +  | +  | ++ | ++ | ++ | ++ |
| *P. aeruginosa* PA01          | ++ | ++ | +  | +  | +  | +  | ++ | +  | +  | ++ |
| *P. aeruginosa* PA7           | +  | +  | +  | +  | ++ | ++ | +++| +  | +  | ++ |
| *P. fluorescens* Pf-5         | ++ | +  | +++| +  | +  | +  | ++ | +  | +  | ++ |
| *P. fluorescens* Pf0-1        | +  | +  | +++| +  | +  | +  | +  | +  | +  | +  |
| *P. putida* F1                | -  | +  | ++ | +  | +  | +  | +  | +  | +  | ++ |
| *P. putida* KT2440            | ++ | +  | +  | ++ | ++ | +  | +  | ++ | ++ | +++ |
| *P. putida* W619              | +  | +  | +  | +  | +  | +  | ++ | ++ | ++ | ++ |
| *P. putida* GB-1              | -  | +  | +++| +  | +  | +  | +  | +  | +  | ++ |
| *P. entomophila* L48          | +  | +  | +  | +  | +  | ++ | +  | +  | ++ | +  |
| *Shewanella* sp. ANA-3        | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* sp. MR-4         | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* sp. MIB015       | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* sp. MR-7         | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* sp. W3-18-1      | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Stigmatella* aurantiaca DW4/3-1 | -  | -  | -  | -  | +  | -  | -  | -  | -  | -  |
| *Shewanella* woodii ATCC 51908 | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. balitca* OS185             | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. baltica* OS155             | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. oneidensis* MR-1           | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. putrefaciens* CN-32        | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. frigidimarina* NCIMB 400   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. amazonensis* SB2B          | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Alteromonas* macleodii 'Deep ecotype' | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Azotobacter* vinelandii AvOP  | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Cellvibrio* japonicus Ueda107 | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| Gamma proteobacterium KT 71    | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
### Table S15. contd....

| Organisms                          | Signatures (Nucleotides) |
|------------------------------------|--------------------------|
|                                    | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
| **Gamma-Proteobacteria - Pseudomonas spp.** |    |    |    |    |    |    |    |    |    |     |
| **Hahella chejuensis KCTC 2396**   |    |    |    |    |    |    |    |    |    |     |
| **Idiomarina baltica OS145**       |    |    |    |    |    |    |    |    |    |     |
| Marine Gamma proteobacterium HTCC2143 |    |    |    |    |    |    |    |    |    |     |
| Marine Gamma proteobacterium HTCC2207 |    |    |    |    |    |    |    |    |    |     |
| Marinobacter algicola DG893         |    |    |    |    |    |    |    |    |    |     |
| Myxococcus xanthus DK 1622          |    |    |    |    |    |    |    |    |    |     |
| Photobacterium damselae subsp. laumondii TTO1 |    |    |    |    |    |    |    |    |    |     |
| Psychrobacter cryohalolentis K5     |    |    |    |    |    |    |    |    |    |     |
| S. putrefaciens 200                 |    |    |    |    |    |    |    |    |    |     |
| **Actinobacteria**                  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Bacteroidetes                       | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| **Cyanobacteria**                   | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| Deinococcus-Thermus                 | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| **Alpha-Proteobacteria**            | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| **Beta-Proteobacteria**             | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| **Frequency of occurrence within Gamma-Proteobacteria** | 18 | 20 | 20 | 21 | 20 | 20 | 20 | 20 | 21 | 20 |
| **Total frequency of occurrence**   | 19/94 | 21/94 | 21/94 | 22/94 | 21/94 | 21/94 | 21/94 | 20/94 | 21/94 | 21/94 |

Table S16. Representation of motifs obtained for Shewanella sp. through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (aiiD) of Ralstonia sp. XJ12B GenBank AAO41113.1)

### Table S16.

| Organisms                          | Signatures (Nucleotides) |
|------------------------------------|--------------------------|
|                                    | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
| **Gamma-Proteobacteria - Shewanella spp.** |    |    |    |    |    |    |    |    |    |     |
| **Pseudomonas sp. GK16**            |    |    |    |    |    |    |    |    |    |     |
| **Pseudomonas sp. THA3**            |    |    |    |    |    |    |    |    |    |     |
| **Pseudomonas sp. THA1**            |    |    |    |    |    |    |    |    |    |     |
| **Pseudomonas sp. THA2**            |    |    |    |    |    |    |    |    |    |     |
| **Pseudomonas syringae** pv. tomato str. DC3000 |    |    |    |    |    |    |    |    |    |     |
| **P. syringae** pv. phaseolicola str.1448A |    |    |    |    |    |    |    |    |    |     |
| **P. syringae** pv. syringae B728a |    |    |    |    |    |    |    |    |    |     |
| **P. syringae**                     |    |    |    |    |    |    |    |    |    |     |
| **P. aeruginosa** 2192              |    |    |    |    |    |    |    |    |    |     |
| **P. aeruginosa** C3719             |    |    |    |    |    |    |    |    |    |     |
| **P. aeruginosa** PACS2             |    |    |    |    |    |    |    |    |    |     |
| **P. aeruginosa** UCBPP-PA14        |    |    |    |    |    |    |    |    |    |     |
| **P. aeruginosa** PAO1              |    |    |    |    |    |    |    |    |    |     |
| **P. aeruginosa** PA7               |    |    |    |    |    |    |    |    |    |     |
| **P. fluorescens** Pf-5             |    |    |    |    |    |    |    |    |    |     |
Table S16. contd….

| Organisms                     | Signatures (Nucleotides) |
|-------------------------------|--------------------------|
|                               | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
| Gamma-Proteobacteria - Shewanella spp. |    |    |    |    |    |    |    |    |    |     |
| P. fluorescens Pf0-1         | -  | -  | -  | -  | -  | -  | -  | -  | -  | -   |
| P. putida F1                  | -  | -  | -  | -  | -  | -  | -  | -  | -  | -   |
| P. putida KT2440              | -  | -  | -  | -  | -  | -  | -  | -  | -  | -   |
| P. putida W619                | -  | -  | -  | -  | -  | -  | -  | -  | -  | -   |
| P. putida GB-1                | -  | -  | -  | -  | -  | -  | -  | -  | -  | -   |
| P. entomophila L48           | -  | -  | -  | -  | -  | -  | -  | -  | -  | -   |
| Shewanella sp. MR-4           | +  | +  | +  | +  | +  | +  | +  | +  | ++ | +   |
| Shewanella sp. MIB015         | +  | +  | ++ | +  | +  | +  | +  | +  | ++ | +   |
| Shewanella sp. MR-7           | ++ | +  | +  | +  | ++ | +  | +  | +  | ++ | +   |
| Shewanella sp. ANA-3          | ++ | +  | +  | +  | +  | +  | +  | +  | ++ | +   |
| Shewanella sp. W3-18-1        | ++ | +  | ++ | +  | +  | +  | +  | +  | ++ | +   |
| Shewanella woodyi ATCC 51908  | ++ | +  | ++ | -  | -  | +  | +  | -  | -  | +++++ |
| S. baltica OS185              | +  | +  | +  | +  | +  | +  | ++ | +  | +  | ++   |
| S. baltica OS155              | +  | +  | +  | +  | +  | +  | +  | +  | +  | +++  |
| S. oneidensis MR-1            | ++ | +  | ++ | +  | +  | +  | +  | +  | ++ | +   |
| S. putrefaciens CN-32         | ++ | +  | +  | +  | +  | +  | +  | +  | +  | +    |
| S. frigidimarina NCIMB 400    | ++ | +++| +  | +  | +  | +  | +  | +  | +  | +    |
| S. amazonensis SB2B           | ++ | +++| +  | +  | +  | +  | +  | +  | +  | +    |
| S. putrefaciens 200           | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Alteromonas macleodii 'Deep ecotype' | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Azotobacter vinelandii AvOP   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Cellvibrio japonicus Ueda107  | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Gamma proteobacterium KT 71   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Halhaella chejuensis KCTC 2396 | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Idiomarina baltica OS145      | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Marine Gamma proteobacterium HTCC2143 | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Marine Gamma proteobacterium HTCC2207 | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Marinobacter aligcola DG893   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Myxococcus xanthus DK 1622    | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Photobacterium luminescens subsp. Laeomondii TTO1 | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Plesiocystis pacifica SIR-1   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Psychrobacter cryohalolentis K5 | -  | -  | -  | -  | -  | -  | -  | -  | -  | -    |
| Actinobacteria                | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Bacteroidetes                 | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Cyanobacteria                 | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Deinococcus-Thermus           | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Alpha-Proteobacteria          | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |
| Beta-Proteobacteria           | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0    |

Frequency of occurrence within Gamma-Proteobacteria

| Frequency of occurrence | 12/94 | 12/94 | 12/94 | 11/94 | 11/94 | 12/94 | 12/94 | 11/94 | 12/94 | 12/94 |
|-------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|

Total frequency of occurrence = 1294
Table S17. Representation of motifs obtained for Gamma-Proteobacterial members other than *Pseudomonas* spp. and *Shewanella* spp. through MEME (http://meme.edu/meme.html) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (*aiiD*) of *Ralstonia* sp. XJ12B GenBank AAO41113.1)

| Organisms                                | Signatures (Nucleotides) |
|------------------------------------------|--------------------------|
|                                          | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10|
| **Gamma-Proteobacteria**                |    |    |    |    |    |    |    |    |    |    |
| *Pseudomonas* sp. GK16                   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Pseudomonas* sp. THA3                   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Pseudomonas* sp. THA1                   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Pseudomonas* sp. THA2                   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Pseudomonas* syringae pv. tomato str. DC3000 | -  | -  | +  | -  | -  | -  | -  | -  | -  | -  |
| *P. syringae* pv. phaseolicola 1448°     | -  | -  | +  | -  | -  | -  | -  | -  | -  | -  |
| *P. syringae* pv. syringae B728a        | -  | -  | +  | -  | -  | -  | -  | -  | -  | -  |
| *P. syringae*                           | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *P. aeruginosa* 2192                     | -  | -  | -  | -  | -  | -  | -  | +  | -  | -  |
| *P. aeruginosa* C3719                    | -  | -  | -  | -  | -  | -  | -  | +  | -  | -  |
| *P. aeruginosa* PACS2                    | -  | -  | -  | -  | -  | -  | -  | +  | -  | -  |
| *P. aeruginosa* UCBPP-PA14               | -  | -  | -  | -  | -  | -  | -  | +  | -  | -  |
| *P. aeruginosa* PAO1                     | -  | -  | -  | -  | -  | -  | -  | +  | -  | -  |
| *P. aeruginosa* PA7                      | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *P. fluorescens* Pf-5                    | -  | +  | -  | -  | -  | -  | -  | -  | -  | -  |
| *P. fluorescens* Pf0-1                   | -  | +  | +  | -  | -  | -  | -  | -  | -  | -  |
| *P. putida* F1                           | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *P. putida* KT2440                       | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *P. putida* W619                         | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *P. putida* GB-1                         | -  | -  | -  | +  | -  | -  | -  | -  | -  | -  |
| *P. entomophila* L48                     | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* sp. ANA-3                   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* sp. MR-4                    | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* sp. MIB015                   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* sp. MR-7                    | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* sp. W3-18-1                 | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Shewanella* woodyi ATCC 51908           | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. baltica* OS185                        | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. baltica* OS155                        | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. oneidensis* MR-1                      | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. putrefaciens* CN-32                   | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. frigidimarina* NCIMB 400              | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. putrefaciens* 200                     | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *S. amazonensis* SB2B                    | -  | -  | -  | -  | -  | -  | -  | -  | -  | -  |
| *Alteromonas* macleodii 'Deep ecotype'    | -  | -  | -  | -  | -  | -  | -  | +  | -  | -  |
| *Azotobacter* vinelandii AvOP             | +  | +  | +  | + + | +  | +  | +  | +  | +  | +  |
| *Cellvibrio* japonicus Ueda107            | +++| ++ | ++ | ++ | +  | +  | +  | +  | +  | +  |
Table S17. contd....

| Organisms                          | M1 | M2 | M3 | M4 | M5 | M6 | M7 | M8 | M9 | M10 |
|------------------------------------|----|----|----|----|----|----|----|----|----|-----|
| **Gamma-Proteobacteria**           |    |    |    |    |    |    |    |    |    |     |
| Congregibacter litoralis KT71      | -  | +  | -  | -  | +  | -  | -  | +  | +  |     |
| Hahella chejuensis KCTC 2396       | +  | ++ | +  | +  | ++ | +  | +  | ++ | +  |     |
| Idiomarina baltica OS145           | +  | +  | +  | +  | +  | +  | ++ | +  | +  |     |
| Marine Gamma proteobacterium HTCC2143 | +  | +  | ++ | -  | -  | +  | -  | -  | +  |     |
| Marine Gamma proteobacterium HTCC2207 | -  | +  | -  | +  | ++ | +  | +++ | ++ | +  |     |
| Marinobacter algicola DG893        | ++ | +  | ++ | +++ | +  | +  | +  | +  | +  |     |
| Photorhabdus luminescens subsp. laumondii TTO1 | +  | +++ | +  | +  | ++ | +  | +  | +  | +  |     |
| Psychrobacter cryohalolentis K5    | +  | -  | -  | -  | +  | -  | +  | +  | +++ | +  |
| **Actinobacteria**                 | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| **Bacteroidetes**                  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| **Cyanobacteria**                  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| **Deinococcus-Thermus**            | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| **Alpha-Proteobacteria**           | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0   |
| **Beta-Proteobacteria**            | 0  | 0  | 0  | 0  | 0  | 2  | 0  | 0  | 0  | 0   |
| Total frequency of occurrence      | 8/94 | 11/94 | 12/94 | 8/94 | 11/94 | 8/94 | 9/94 | 8/94 | 14/94 | 11/94 | 10/94 |

**ADDITIONAL FILE 4**

**SIGNATURE ANALYSIS – FREQUENCY AND DISTRIBUTION PATTERN**

**AHL-lactonase and -acylase specific signature:** The sequences of 4 to 30 data sets submitted groupwise to MEME program (http://meme.nbcr.net/meme/meme.html) revealed ten signatures (25-30 nucleotides, nts in length) for each species. Regular expression diagram of signatures (nucleotides) (Additional files) and the frequency of occurrence of motifs obtained through MEME for different taxonomic groups (Additional files) have been presented with reference to:

**i) AHL-lactonase gene (aiiA) of Bacillus sp. SB4 GenBank AAR85482.1 (Additional files 2-3):**

a) Actinobacteria: Data (Figure S1 and Table S2) reveal that seven out of 10 signatures designated as M1, M3 to M6, M9 and M10 were observed to be present at high frequency among actinobacterial members. These can be considered as unique as they were absent from all other taxonomic groups. Incidentally, the order of occurrence of these signatures within the gene aiiA didn’t follow any unique pattern.

b) Firmicutes: Data (Figure S2 and Table S3) reveal two signatures – M1 and M10 among Firmicutes to occur with highest frequencies of 25/30 and 21/30. These signatures can be considered as unique on the basis of their absence from all other taxonomic groups. The order of distribution of all the 10 signatures was almost similar (M5)-M4-M7-M1-M2-M3-M10-M4-M8-M9-M5 in the cases of Bacillus sp. SB4, Bacillus sp. 91, Bacillus sp. A24, B. cereus, B. subtilis strain BS1 and B. thuringiensis strain BCR-ZYR25. Two other B. thuringiensis str. Al Hakam and B. thuringiensis serovar israelensis ATCC 35646 have only 4/10 signatures ordered as M9-M4-M1-M2. Another distinct group possessing primarily two signatures oriented as M10-M1 was constituted of Bacillus anthracis str. Ames, Bacillus weihenstephanensis KBAB4, Clostridium bolteae ATCC BAA-613, Clostridium kluyveri DSM 555, Geobacillus sp. WCH70 M. thermoacetica ATCC 39073. Signs in similar orientation: M9-M3-M4-M7-M10-M6-M1-M8-M2-M5 were observed in all the strains of S. aureus: RF122, MW2, MSSA476 and Mu50.

c) _-Proteobacteria: Data (Figure S3 and Table S4) reveals that five signatures – M1, M3, M4, M6 and M7 in genes (aiiA) from organisms belonging to _-Proteobacteria occurred with a high frequency of 19/22 to 22/22. These signatures can be considered as unique on the basis of their absence from all other taxonomic groups. A screening of the regular expression diagram (Additional file 6) however, didn’t reveal any pattern of occurrence of the signatures within the gene to be unique to any genera. A. tumefaciens and Sagittula stellata E-37 showed repetitiveness for M3 and M4, and Jannaschia sp. CCS1 had many signatures in duplicate – M1, M3, M7 and M10.
d) _ß-Proteobacteria: Data (Figure S4 and Table S5) reveals that all the 10 signatures were present in *Burkholderia* spp. and *Ralstonia* spp. Except the signatures – M2, M8 and M10, all other signatures were present exclusively among these 5 organisms of _ß-Proteobacterial group. Incidentally no correlation between the genera and the order of distribution of the signatures - M1, M3, M4, M5, M6, M7 and M9 could be established.

e) _ß-Proteobacteria: Data (Figure S5 and Table S6) reveals that signatures M2, M3, M4 and M10 were found to occur with higher frequency of 14/16 to 15/16. All the signatures were exclusive to this _ß-Proteobacterial group, since these were absent from all other taxonomic groups. High similarity in the order of occurrence of the signatures was observed largely within the genera such as *Acinetobacter*, *Xanthomonas* and *Xylella*.

f) _ß-Proteobacteria: Data (Figure S6 and Table S7) reveals that all the signatures except M4 were present in all the members of this taxonomic group and were unique, since they were not observed in any other taxonomic group. The order of occurrence of these signatures was different in all the organisms of this group.

g) Euryarchaeota: Data (Figure S7 and Table S8) reveals that all the signatures except M3 and M9 were present with a high frequency among the different members of Euryarchaeota. These can be considered as unique to this group as these could not be observed among other taxonomic groups.

h) Ascomycota: Data (Figure S8 and Table S9) reveals that all the 10 signatures were present with equal frequency and were unique to this taxonomic group. The order of occurrence of these signatures within the gene for AHL-lactonase of these organisms was almost identical except *Aspergillus oryzae* RIB40, which had signatures M1 and M3 in duplicate.

**ii) AHL-acylase gene (aiiD) of Ralstonia sp. XJ12B GenBank AA041113.1** (Additional files 2-3):

a) Actinobacteria: Data (Figure S9 and Table S10) show that signatures M1 to M3, M8 and M9 were present with a high frequency of 9/9. All signatures except M1 can be considered as unique to Actinobacteria on the basis of their absence from all other taxonomic groups where as M1 was also present in organisms belonging to _ß-Proteobacteria and _ß-Proteobacteria. Visual observation of Figure (Additional file 18) reveals that there is a lot of variation in the order of occurrence of the 10 signatures. However, it can be recorded that all the signatures showed multiplicity of occurrence in the range of 2 to 4.

b) Bacteroidetes: Data (Figure S10 and Table S11) revealed that signatures – M3, M7 and M8 were present in all the organisms under consideration. Duplication of signatures was observed in 5 out of 7 organisms. No characteristic order of occurrence of signatures or their location at a give position within the gene sequence was evident. However, all the signatures can be considered as unique except M1, which was found to occur among cyanobacterial members as well.

c) Cyanobacteria: Data (Figure S11 and Table S12) revealed that signatures – M2 to M7 were present in all the organisms under consideration with a frequency of 9/9. Duplication of signatures was observed in 7 out of 9 organisms. Characteristic order of occurrence of signatures or their location at a give position within the gene sequence was evident among *Cyanothece* spp. as M4-M7-M2-(M10)-M5-M8-M1-M6-M3-M9-M10. On the other hand, similarities in order of signatures were also evident among *Nostoc*, *Microcoleus* and some *Cyanothece* strains as M6-M5-M2-M7-(M4)-M3-(M1)-M4. However, signatures can be considered as unique as these were found to occur exclusively among cyanobacteria.

d) _ß-Proteobacteria: Data (Figure S12 and Table S13) show that signatures – M1, M7, M9 and M10 occurred with high frequency of 7/8 to 8/8. All the signatures were found to be present only with the members of _ß-Proteobacteria, hence may be considered as unique. There was no unique order of occurrence of signatures which could be correlated to any genera or species. All the signatures were present as repeats in at least one of the organisms and each organism had at least one of the signatures as duplicated.

e) _ß-Proteobacteria: Data (Figure S13 and Table S14) show that almost all the signatures were present at high frequency of 6/8 to 7/8. Due to their absence from other taxonomic groups, we may consider them as unique to _ß-Proteobacterial members. Out of the 10 signatures, at least one of them was found to be present as multiple repeats and each of the organisms had at least one of the signatures in repeat form. We could not draw any co-relation between the order of occurrence of the signatures and the organisms possessing them, primarily because of their high repetition with the gene.

f) _ß-Proteobacteria: As this group of organisms was quite large we have presented the organisms in three categories (to suit to the criteria of MEME procedures - See Methods for justifications): i) *Pseudomonas* spp. (Figure S14 and Table S15) show, ii) *Shewanella* spp. (Additional files 30,31) show and iii) others members of _ß-Proteobacterial group (Figure S15 and Table S16).

i) For *Pseudomonas* spp. (Figure S14 and Table S15) signatures M1 to M10 occurred with a high frequency of 19/21 to 20/21. Except signature M4, none of the signatures were found in any other member of _ß-Proteobacteria or any other taxonomical group, which may thus be called as unique to *Pseudomonas* spp. Signatures M1 and M8 were found to be absent only from the two strains of *Pseudomonas putida* - F1 and GB-1.

ii) For *Shewanella* spp. (Figure S15 and Table S16), signatures M1 to M10 occurred with a high frequency of 11/12 to 12/12. *Shewanella woodyi* ATCC 51908 was the only organism which lacked signatures M4, M5, M8 and M9. The signatures observed here were absent among all other members of _ß-Proteobacteria or any other taxonomical group, which may thus be called as unique to *Shewanella* spp. No clear cut co-relation could be drawn between the order of occurrence of the signatures and the organisms possessing them.
iii) For _-Proteobacterial members other than *Pseudomonas* spp. and *Shewanella* spp. The information on the occurrence of signature (Figure S16 and Table S17) shows that the overall frequency of signatures was low which may be because of high diversity of organisms in this “category”. Signatures M3 and M8 occurred with a relatively high frequency of 12/16 to 14/16. Signatures M1, M6, M7, M9 and M10 were found to be present only among the organisms under consideration. We could not draw any clear cut co-relation between the order of occurrence of the signatures and the organisms possessing them. *Alteromonas macleodii* 'Deep ecotype' was unique as it possessed only three signatures – M8, M9 and M10.

### ADDITIONAL FILE 5

| Organism                     | Gi Number | Signature (Nucleotide) No. |
|------------------------------|-----------|---------------------------|
| *Pseudomonas* sp. THA1       | gi|316991|72|gi|AY311407.3| |
| *Pseudomonas* sp. THA2       | gi|316991|74|gi|AY311408.1| |
| *Pseudomonas* sp. THA3       | gi|316991|76|gi|AY311409.1| |
| *Pseudomonas* sp. 130        | gi|1386616|104|2266 |
| *Pseudomonas* sp. GE16       | gi|14526438|101|2263 |
| *Pseudomonas* aeruginosa PA04 | gi|11064330|16|65617-2638005 | |
| *Pseudomonas* aeruginosa C519 | gi|19454515|11|435593-437881 | |
| *Pseudomonas* aeruginosa PAC52 | gi|10759893|32|15673-3215961 | |
| *Pseudomonas* aeruginosa 2152 | gi|19455037|16|44376-1646664 | |
| *Pseudomonas* aeruginosa UCSF | gi|11604852|20|06922-30007276 | |
| *Pseudomonas* aeruginosa PA7  | gi|13298346|29|55521-2957803 | |

**Fig. (S17). Signatures of AHL-acylase gene in Pseudomonas spp.** Figure showing Similarity of signatures of gene (aaiD) for AHL-acylase of Pseudomonas spp.
Fig. (S18a). Phylogenetic tree based on AHL-acylase gene. Figure showing Phylogenetic trees based on full length sequences of gene (aiiD) for AHL-acylase of Pseudomonas spp.
Fig. (S18b). Phylogenetic tree based on regular expressions of AHL-acylase gene: Figure showing Phylogenetic trees based on regular expressions of signatures of gene (aiiD) for AHL-acylase of Pseudomonas spp.