**Supplementary Table S1**

**Table S1.** Bacterial strains and plasmids used in this study

|  |  |  |
| --- | --- | --- |
| **Strain/plasmid** | **Genotype/description** | **Source/reference** |
| *E. asburiae* strainL1 | Lettuce isolate. QS strain with the formation of purple violacein pigment in the presence of short chain exogenous AHL molecules. | (Lau et al., 2013) |
| ***E. coli*** |  |  |
| DH5αTOP10 | Host without presence of plasmid that yield high quality and concentration of inserted plasmid. dl*ac*Z∆M15 ∆(*lacZYA-argF*)U169 *rec*A1 *end*A1 hsdR17(*rK-mK+*) *supE*44 *thi-1 gyrA96 relA1*.Host without presence of plasmid that yield high quality and concentration of inserted plasmid. F- *mcrA* ∆(*mrr-hsd*RMS-*mcr*BC) ф80*lac*Z∆M15 ∆l*ac*X74 *rec*A1 *ara*D139 ∆(*ara*A-leu)7697 *gal*U *gal*K *rps*L (StrR) *end*A1 *nup*G | Invitrogen, USAInvitrogen, USA |
| **Plasmids** |  |  |
| pGEM®-T | Toxin-antitoxin (TA) cloning vector, AmpR. | Promega, USA |
| pGEM®-T-*easR* | pGEMT containing 693 bp of *easR* with NdeI-BglII sites | This study |
| pMULTIAHLPROM | pMP220-derived Broad-host-range plasmid containing 8-*luxI* type promoters *(luxI*, *cviI*, *ahlI*, *rhlI*, *cepI*, *phzI*, *traI and ppuI)* fused to a promoterless *lacZ* gene, TetR.  | (Steindler et al., 2008) |
| pLNBADpLNBAD-*easR*TOP10-pMULTI-pLNBAD-*easR*  | Multiple cloning site; contains PBAD promoter; CmR.pLNBAD containing 693 bp of *easR* with NdeI-BglII sites; CmRpMULTIAHLPROM containing pLNBAD cloned with 693 bp of *easR*; TetR and CmR | (Lemonnier et al., 2003)This studyThis study |

aAmpR, CmR and TetR indicate resistance to ampicillin, chloramphenicol, and tetracycline, respectively

**Supplementary Table S2**

**Table S2.** Functional motifs in EasR predicted by MOTIF software

|  |  |  |  |
| --- | --- | --- | --- |
| Pfam | Motif | Position/(Independent E-value)\* | Recognition sequence |
| Autoind\_bind | Autoinducer bindingdomain | 19…152/ (6×10-18) | LDAFFEDFKGIVFAYAIMNKKDPSQMRIINNSPEWFDIYLDRKYQFIDPVIIRALRCVEDFFWESDVILSDGYNLTRIFNESVQYDIYQGQTFPLHDYLNNLVVLSVISPKHSGIDIEKYRPQFLSFLVQLHQK |
| GerE | Bacterial regulatoryproteins, *luxR* family | 168…220/ (1.1×10-20) | LSPRERQILKWVSAGKTYAEISVILSIAERTVKFHMGNVMKKLGVNNARHAIK |
| Sigma-70\_r4\_2 | Sigma-70, region 4 | 168…210/ (5.4×10-6) | LSPRERQILKWVSAGKTYAEISVILSIAERTVKFHMGNVMKKL |
| Sigma-70\_r4 | Sigma-70, region 4 | 168…210/ (0.00033) | LSPRERQILKWVSAGKTYAEISVILSIAERTVKFHMGNVMKKL |
| HTH\_23 | Homeodomain-likedomain | 174…199/ (0.09) | QILKWVSAGKTYAEISVILSIAERTV |
| HTH\_38 | Helix-turn-helixdomain | 168…199/ (0.11) | LSPRERQILKWVSAGKTYAEISVILSIAERTV |

\*E-value represent the probability that a sequence could arise randomly by chance, values below 0.01 could be

 of random appearance.