



**Figure S1.** Expanded phylogenetic tree of *intI* genes from the *Shewanella* spp.. Tree construction was done using the maximum-likelihood method with model LG+I+G4 and a bootstrap of 1000 replicates. IntI1 to IntI10 integron integrases were identified in red. Classification of each group was based on a matrix constructed with MatGAT software (Table S2).