Supplementary

Figure S1
Figure S2

HYDROCINNAMIC ACID-(18E0-0721) 1971 (12.657)

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**Fig. S1 Identification of AHL-degrading bacteria.** UPGMA phylogenetic derived based on 16S rDNA sequence against reference isolates with closest BLAST hits from NCBI database.

**Fig. S2 GC-MS analysis of QS-inhibitory fraction.** GC chromatogram and MS/MS analysis of the active fraction purified from *E. xiangfangensis* cell free extract. Peaks are a function of intensity measured in milli-absorption units over time in minutes.