Supplementary

Figure S1

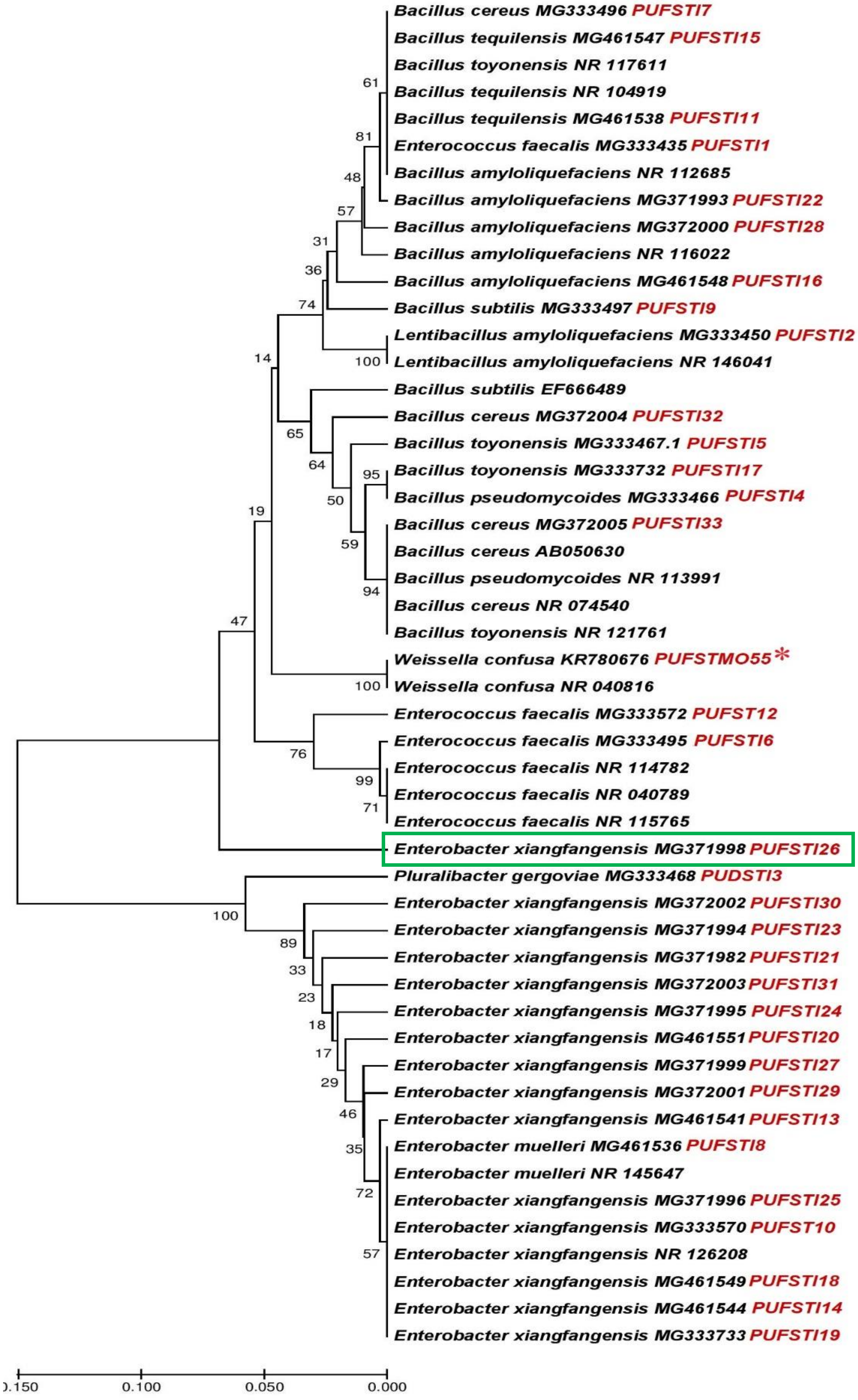

Figure S2

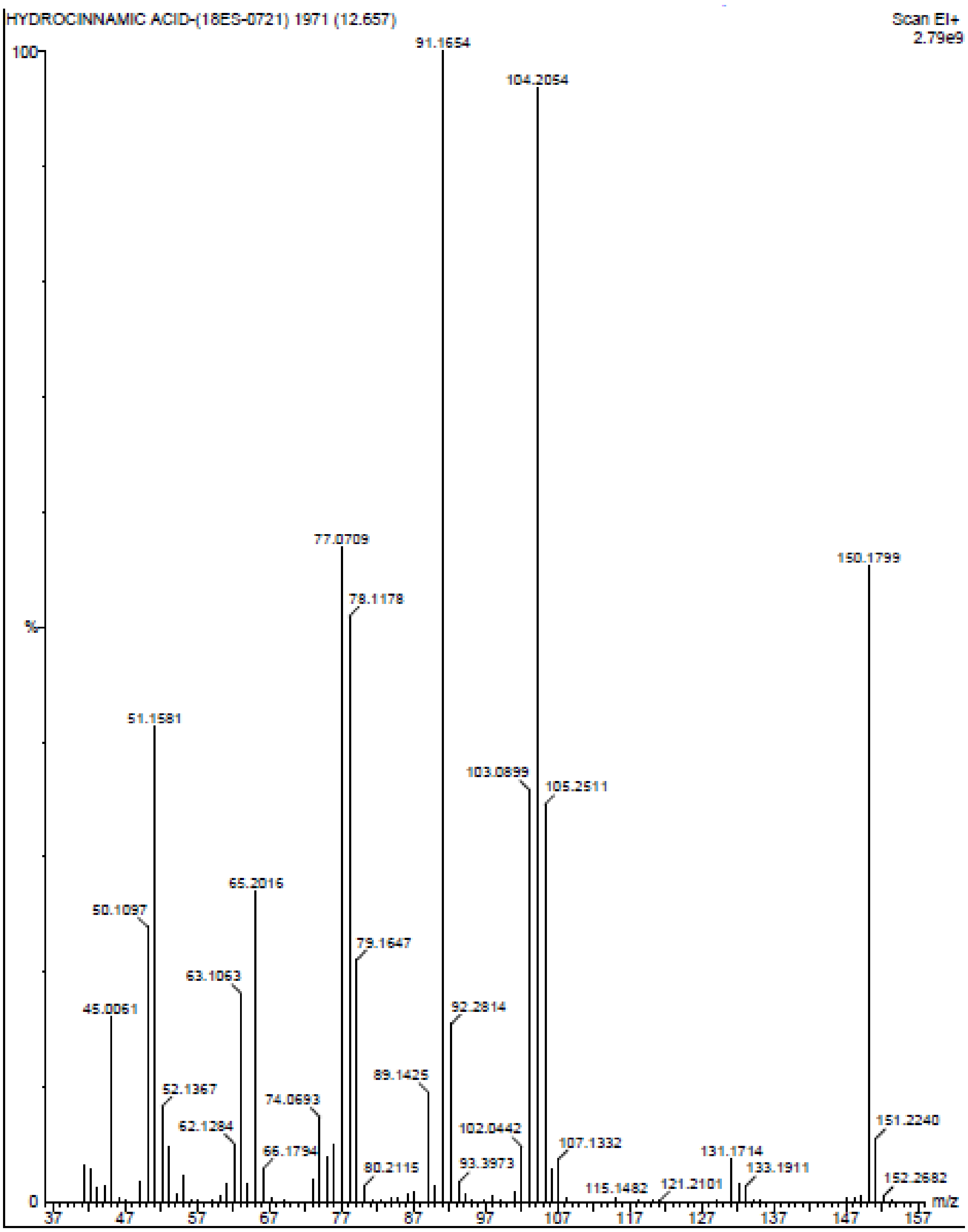
HYDROCINNAMIC ACID-(18ES-0721) 1971 (12.657)
Scan EI+
2.79e9
100
%
0
91.1654
104.2054
77.0709
150.1799
78.1178
51.1581
103.0899
105.2511
65.2016
50.1097
79.1647
63.1063
45.0061
92.2814
89.1425
52.1367
74.0693
62.1284
102.0442
151.2240
107.1332
66.1794
131.1714
93.3973
80.2115
133.1911
152.2682
115.1482
121.2101
m/z
37
47
57
67
77
87
97
107
117
127
137
147
157

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.