

## Electronic supplementary information

### Efficient biodegradation of petroleum *n*-alkanes and polycyclic aromatic hydrocarbons by polyextremophilic *Pseudomonas aeruginosa* strain with multidegradative capacity

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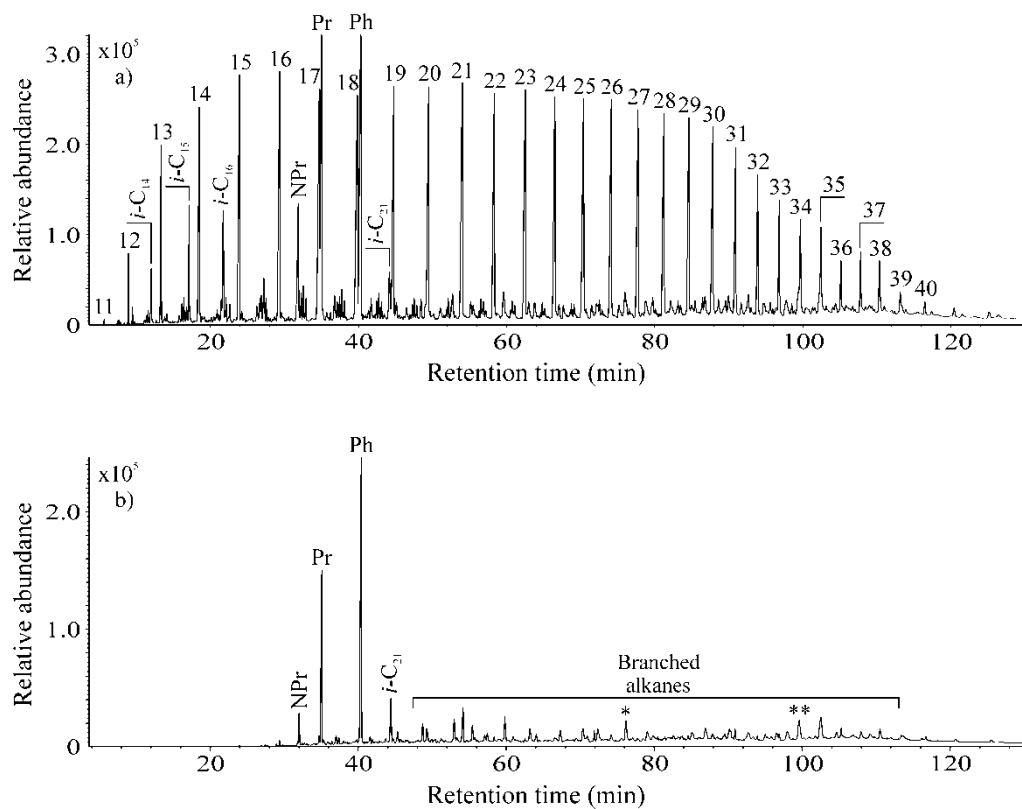
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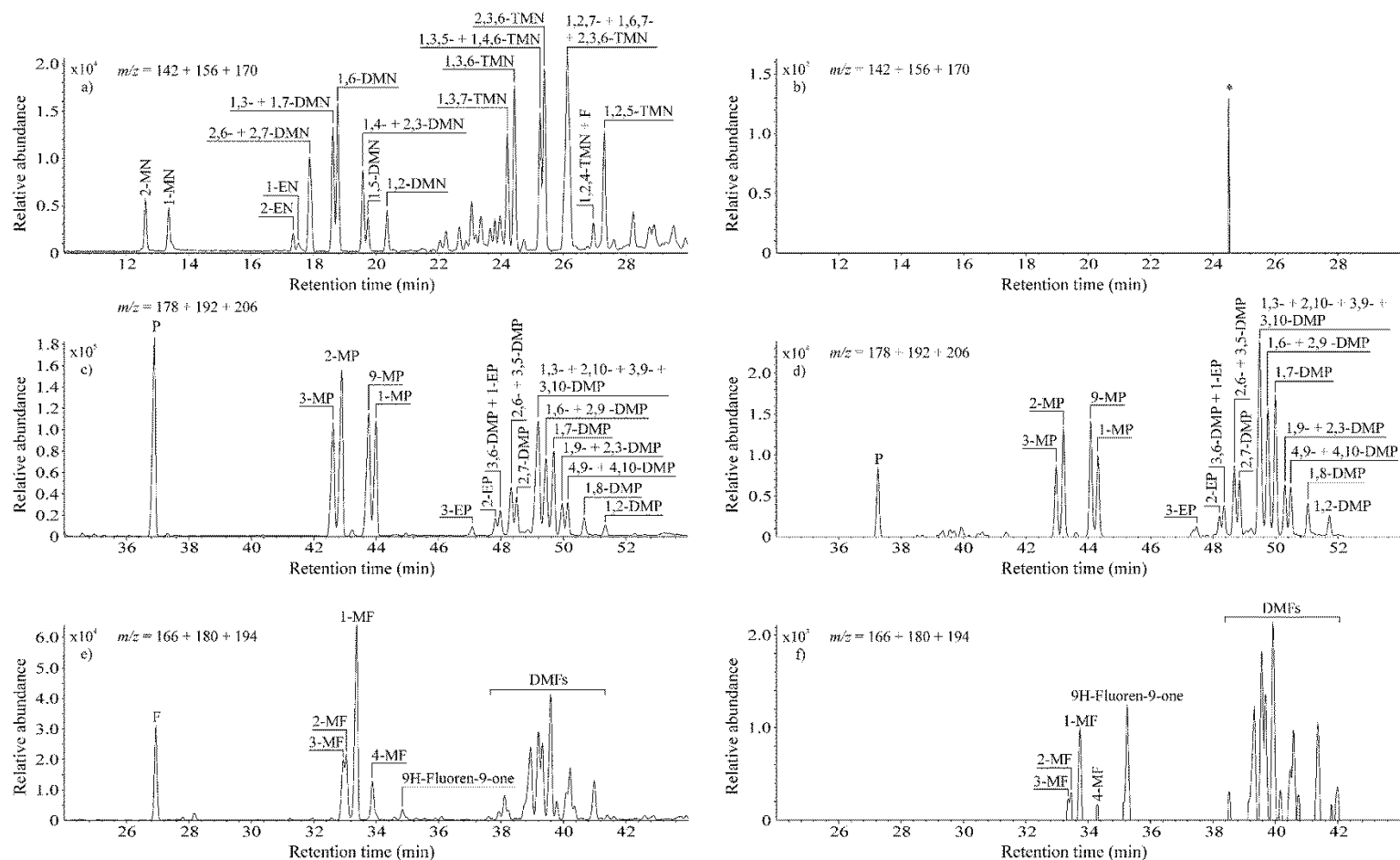
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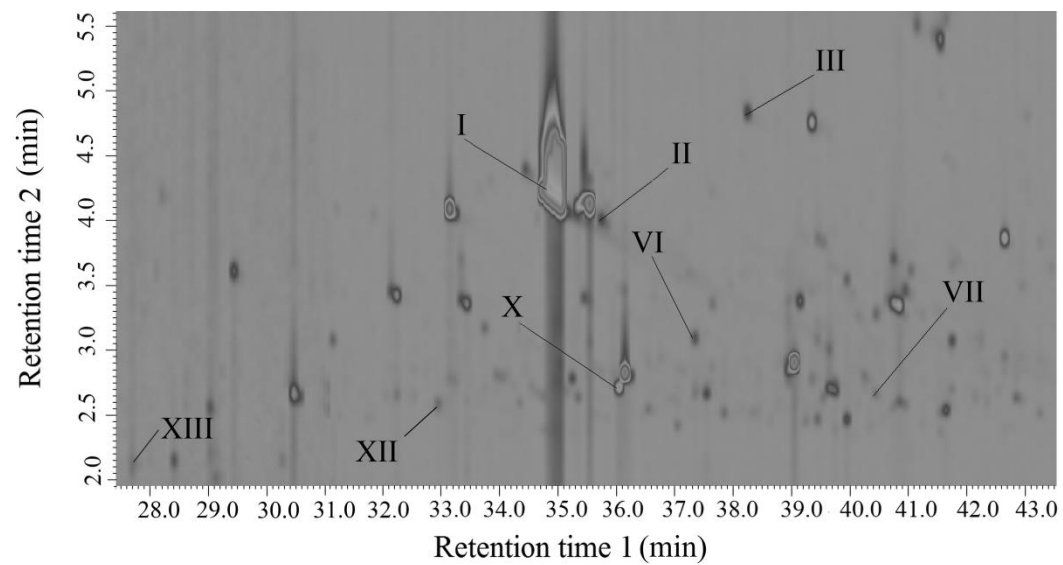
**Fig. S1** GC-MS ion fragmentograms of *n*-alkanes ( $m/z$  71) of control (a) and inoculated (b) aliphatic fraction from crude oil.

\* – Co-elution of C-ring monoaromatic sterane; \*\* – Co-elution of C<sub>34</sub>17 $\alpha$ (H)21 $\beta$ (H)(22R)-tetrakisohomohopane; For other peak assignments, see the legend of Fig. 2.



**Fig. S2** GC-MS ion fragmentograms of methylated naphthalenes ( $m/z$  142 + 156 + 170), phenanthrene and its methylated derivatives ( $m/z$  178 + 192 + 206), and fluorene and its methylated derivatives ( $m/z$  166 + 180 + 194) of control (a, c, e) and inoculated (b, d, f) aromatic fraction from crude oil.

MN – Methyl naphthalene; DMN – Dimethyl naphthalene; TMN – Trimethyl naphthalene; EN – Ethyl naphthalene; EP – Ethyl phenanthrene; \* – Impurity; For other peak assignments, see the legend of Fig. 2.



**Fig. S3** GCxGC-MS Total Ion Chromatogram of fluorene and its metabolites after 48 h of degradation. For assignments of compounds, see the legend of Fig. 3 and Table 1.

**Supplementary Table 1** Homology search analysis of the proteins involved in FLU biodegradation to phthalate

Protein of FLU biodegradation from <i>Terrabacter sp.</i> DBF63/ Accession	Homologous protein in <i>Pseudomonas aeruginosa</i> / Accession	Length	Identity, %
DbfA, Angular dioxygenase, large subunit/ Q93UV3	Dioxygenase, large subunit/ AGG56547.1	443/267	41
FlnB, 9-Fluorenyl dehydrogenase/ Q93UV4	SDR family oxidoreductase/ WP_134300711	357/ 266	36
FlnE, 2-hydroxy-6-oxo-6-(2'-carboxyphenyl)-hexa-2,4-dienoate hydrolase/ Q83ZF0	Alpha/beta hydrolase/ WP_148113522	328/ 182	35
FlnD, 2'-carboxy-2,3-dihydroxybiphenyl 1,2-dioxygenase/ Q83ZE9	Extradiol ring-cleavage dioxygenase/ WP_049955909	298/282	34
FlnC, Short-chain dehydrogenase/reductase/ Q83ZE7	SDR family oxidoreductase/WP_009685945	252/ 253	48