Title	Genome-wide analytical approaches using semi-quantitative expression proteomics for aromatic hydrocarbon metabolism in <i>Pseudomonas putida</i> F1
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Fig. S1. The metabolic pathway of toluene, ethylbenzene, benzene, and *p*-cymene in *P. putida* F1. The number in parentheses indicates a reaction step and a key enzyme: (1) toluene dioxygenase (EC:1.14.12.11), (2) *cis*-benzene glycol dehydrogenase (EC:1.3.1.19), (3) catechol 2,3-dioxygenase (EC:1.13.11.2), (4) 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase (EC:3.7.1.9), (5) 2-keto-4-pentenoate hydratase (EC:4.2.1.80), (6) 4-hydroxy 2-oxovalerate aldolase (EC:4.1.3.39), (7) acetaldehyde dehydrogenase (EC:1.2.1.10), (8) catechol 1,2-dioxygenase (EC:1.13.11.1), (9) muconate cycloisomerase (EC:5.5.1.1), (10) muconolactone isomerase (EC:5.3.3.4), (11) 3-oxoadipate enol-lactonase (EC:3.1.1.24), (12) 3-oxoacid CoA-transferase (EC:2.8.3.6), (13) β -ketoadipyl CoA thiolase (EC:2.3.1.174, EC:2.3.1.16), (14) acetyl-CoA synthetase (EC:6.2.1.1), (15) propionyl-CoA synthetase (EC:6.2.1.17), (16) methylcitrate synthase (EC:2.3.3.5), (17) 2-methylcitrate dehydratase (EC:4.2.1.79), (18) 2-methylisocitrate dehydratase (EC:4.2.1.99), (19) 2-methylisocitrate lyase (EC:4.1.3.30), (20) *p*-cymene monooxygenase (EC:1.14.13.-), (21) *p*-cumin alcohol dehydrogenase (EC:1.1.1.90), (22) *p*-cumin aldehyde dehydrogenase (EC:1.2.1.29), (23) *p*-cumate 2,3-dioxygenase (EC:1.13.11.-), (24) 2,3-dihydroxy-2,3-dihydro-*p*-cumate dehydrogenase (EC:1.3.1.58), (25) 2,3-dihydroxy-*p*-cumate-3,4-dioxygenase (EC:1.13.11.-), (26) HCOMODA decarboxylase (EC:4.1.1.-), and (27) HOMODA hydrolase (EC:3.7.1.-).

Fig. S2. SDS-PAGE of proteins of *P. putida* F1 cells grown with glucose (G), toluene (T), ethylbenzene (E), benzene (B), *p*-cymene (Cy), and *p*-cumate (Cu). Gels were cut into 60 strips for in-gel digestion.