

Supplementary Material

Table S1. Statistics of the obtained assembly and annotation.

Assembly		Annotation	
Number of contigs	3,589,453	Number of predicted genes	6,532,265
Total Bases	2,812,753,760	Number of KEGG categories	6,997
Min Length (bp)	200		
Median Length (bp)	461		
Mean Length (bp)	783		
Max Length (bp)	545,867		
N50	579,021		
N50 length	927		
N90	2,699,073		
N90 length	353		

Figure S1. Taxonomic composition of the bacterial communities at the family level. Only the families with abundance of 1%, or higher, in at least one sample have been reported.

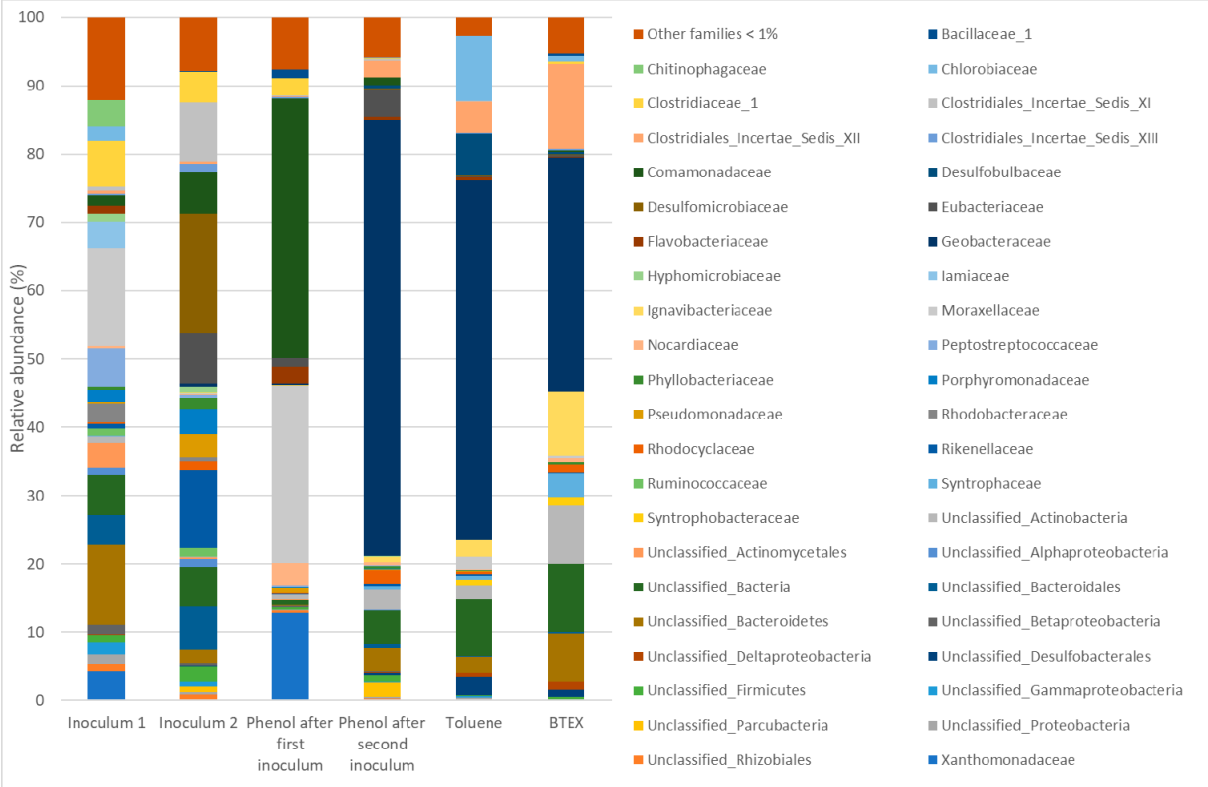


Figure S2. NMDS plot of Hellinger-transformed abundances of each ASV of anodes and inocula

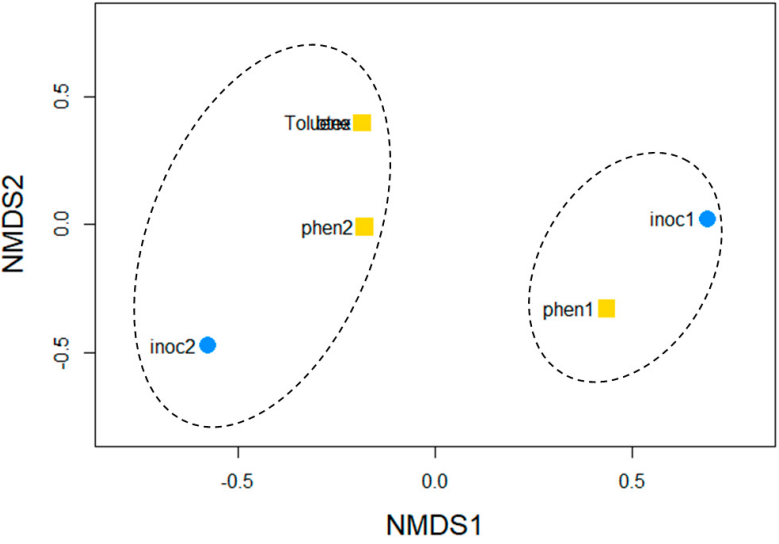


Table S2. Characteristics of reconstructed genomes.

Features									Taxonomy	
Reconstructed metagenome (bin)	inoculum 1	inoculum2	phenol	toluene	BTEX	Size (Mb)	Completeness (%)	Contamination (%)	MiGA	GTDB
	Coverage									
Bin 2			293	859	414	2.8	65%	1.8	Genus: <i>Geobacter</i> (p-value 0.0301***)	Genus: <i>Geobacter</i>
Bin 107			242	129	3	5.3	99%	1.8	Family: Geobacteraceae (p-value 0.0246***)	Order: Geobacterales; Family: Geobacteraceae
Bin 221		233				3.3	79%	1.8	Genus: <i>Desulfomicrobium</i> (p-value 0.022***)	Genus: <i>Desulfomicrobium</i>
Bin 277	151					5.1	90%	2.7	Class: Actinobacteria (p-value 0.000113****)	N/D

N/D: not determined

Figure S3. Anaerobic degradation pathways of ethylbenzene, toluene, xylenes and phenol. Adapted from (Von Netzer *et al.*, 2016) (Acosta-Gonzalez *et al.*, 2013) for toluene, ethylbenzene, xylenes through fumarate addition; (Y *et al.*, 1999) (Tschech and Fuchs, 1989) for oxidation of ethylbenzene to benzoyl-CoA; (Tschech and Fuchs, 1987) (Lack *et al.*, 1991) for phenol oxidation via 4-hydroxybenzoate

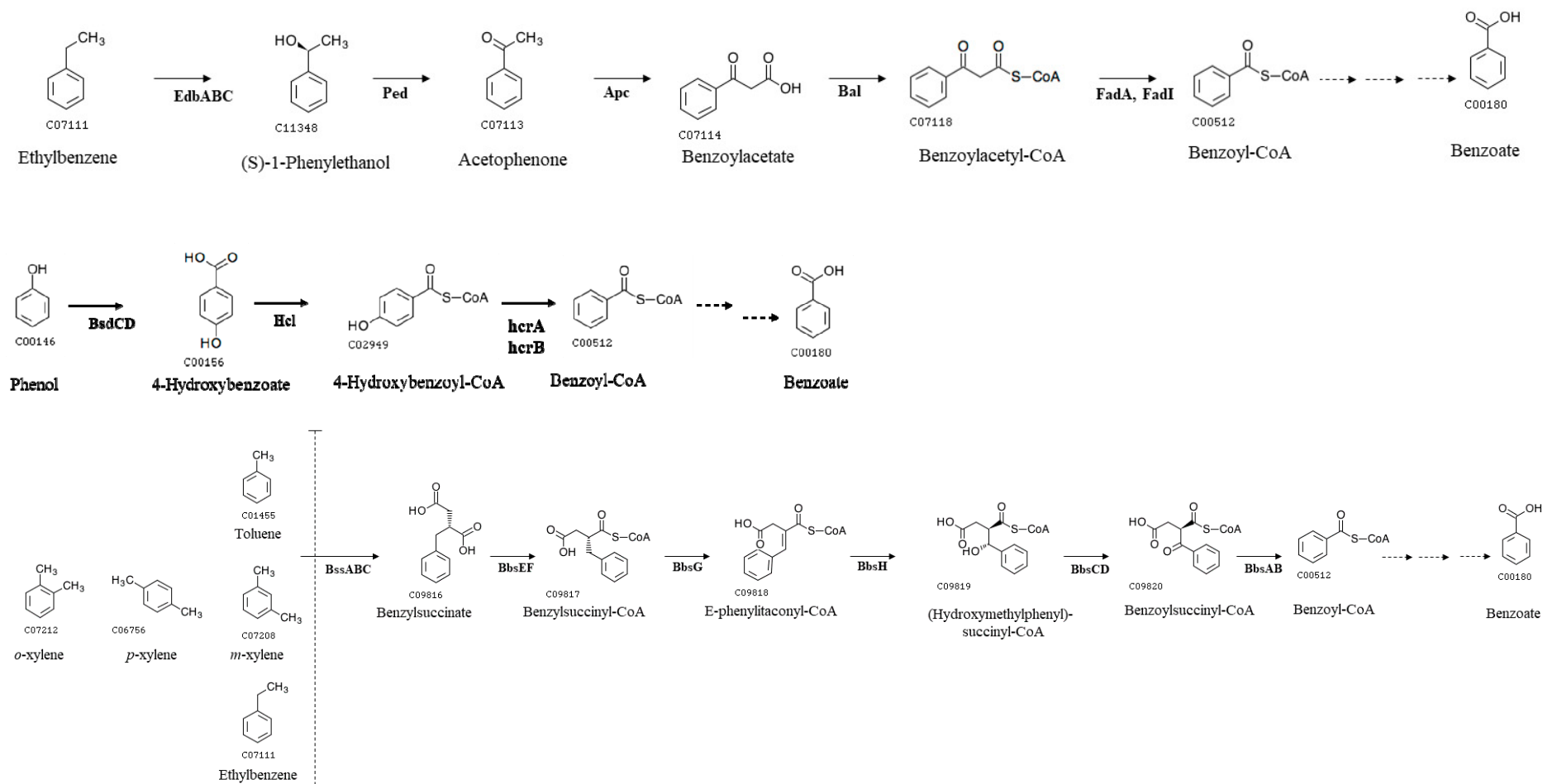
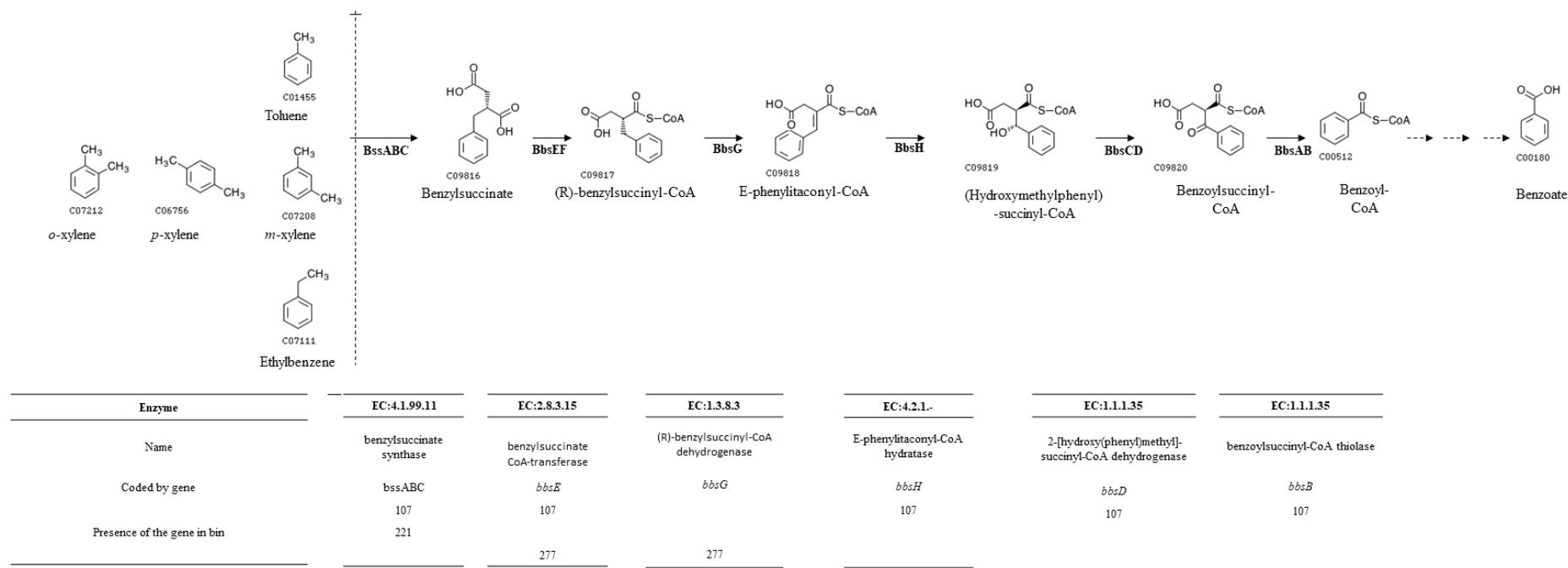
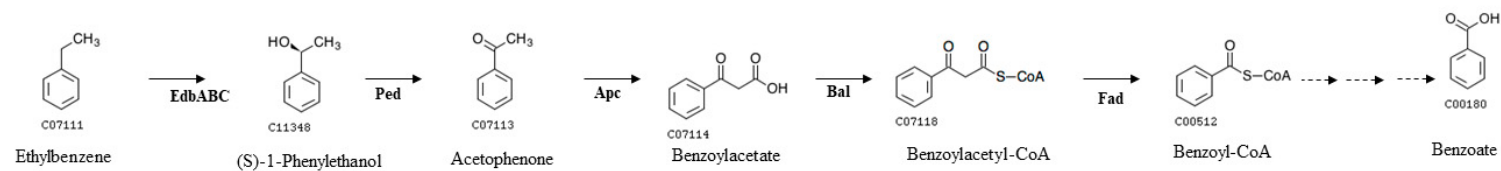
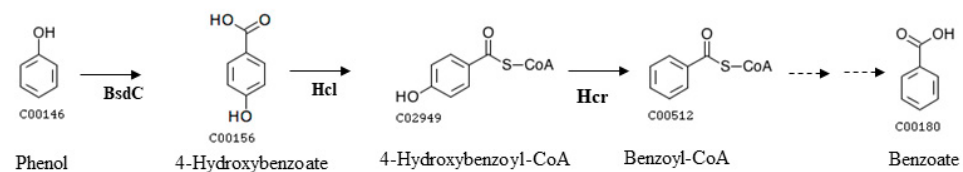


Figure S4. Presence of hydrocarbon genes in reconstructed genomes





Enzyme	EC:1.1.7.99.2	EC:1.1.1.311	EC:6.4.1.8	EC:6.2.1.-	[EC:2.3.1.16]
Name	ethylbenzene hydroxylase	(S)-1-Phenylethanol dehydrogenase	acetophenone carboxylase alpha beta gamma delta subunit	benzoylacetate-CoA ligase	acetyl-CoA acyltransferase
Coded by gene	<i>edbABC</i>	<i>ped</i>	<i>apc</i>	<i>bal</i>	
Presence of the gene in bin		107	107 221 (gamma subunit)		107
		277			277



Enzyme	EC:4.1.1.61	EC 6.2.1.27	EC:1.3.7.9
Name	4-hydroxybenzoate decarboxylase subunit C	4-hydroxybenzoate-CoA ligase	4-hydroxybenzoyl-CoA reductase subunit alpha beta gamma
Coded by gene	<i>bsdC</i>	<i>hcl</i>	<i>hcrABC</i>
Presence of the gene in bin	2 107		107
	221		221 (gamma subunit)

Databases

<https://gitlab.com/aespinoz/waterdata>

Bibliography

- Acosta-Gonzalez, A., Rossellò-Mòra, R., and Marques, S. (2013) Diversity of Benzylsuccinate Synthase-Like (bssA) Genes in Hydrocarbon-Polluted Marine Sediments Suggests Substrate- Dependent Clustering. *Appl Environ Microbiol* **79**: 3667–3676.
- Lack, A., Tommasi, I., Aresta, M., and Fuchs, G. (1991) Catalytic properties of phenol carboxylase. *Eur J Biochem* 473–479.
- Von Netzer, F., Kuntze, K., Vogt, C., Richnow, H.H., Boll, M., and Lueders, T. (2016) Functional gene markers for fumarate-adding and dearomatizing key enzymes in anaerobic aromatic hydrocarbon degradation in terrestrial environments. *J Mol Microbiol Biotechnol* **26**: 180–194.
- Tschech, A. and Fuchs, G. (1987) Anaerobic degradation of phenol by pure cultures of newly isolated denitrifying pseudomonads. *Arch Microbiol* **148**: 213–217.
- Tschech, A. and Fuchs, G. (1989) Anaerobic degradation of phenol via carboxylation to 4-hydroxybenzoate: in vitro study of isotope exchange between $^{14}\text{CO}_2$ and 4-hydroxybenzoate. *Arch Microbiol* **152**: 594–599.
- Y, J.H., Spormann, A.M., Beller, H.R., and Widdel, F. (1999) Anaerobic bacterial metabolism of hydrocarbons. *FEMS Microbiol Rev* **22**: 459–473.