

Journal Name: AMB Express

Manuscript Title: Potential of *Variovorax paradoxus* isolate BFB1_13 for bioremediation of BTEX contaminated sites

Tibor BENEDEK^{a*}, Flóra SZENTGYÖRGYI^a, Veronika GERGÓCS^b, Ofir MENASHE^{c,d},
Perla Abigail FIGUEROA GONZALEZ^e, Alexander J. PROBST^e, Balázs KRISZT^f, András
TÁNCICS^a

^a*Hungarian University of Agriculture and Life Sciences, Institute of Aquaculture and Environmental Safety, Department of Molecular Ecology, Gödöllő, H-2100, Páter K. u. 1, Hungary;*

^b*Institute for Soil Sciences, Budapest, H-1022, Herman Ottó út 15, Hungary*

^c*Water Industry Engineering Department, Achi Racov School of Engineering, Kinneret Academic College on the Sea of Galilee, D.N. Emek Ha'Yarden 15132, Israel*

^d*BioCastle Water Technologies Ltd., Tzemah, Israel*

^e*Group for Aquatic Microbial Ecology, Environmental Microbiology and Biotechnology, Faculty of Chemistry, University of Duisburg-Essen, Essen, Universitätsstr. 5, 45141 Essen, Germany*

^JHungarian University of Agriculture and Life Sciences, Institute of Aquaculture and Environmental Safety, Department of Environmental Safety, Gödöllő, H-2100, Páter K. u. 1, Hungary;

*Corresponding author: Tel.: +36-(28)-522-000 ext. 1611

E-mail: benedek.tibor@uni-mate.hu

Number of figures: 3

Number of tables: 6

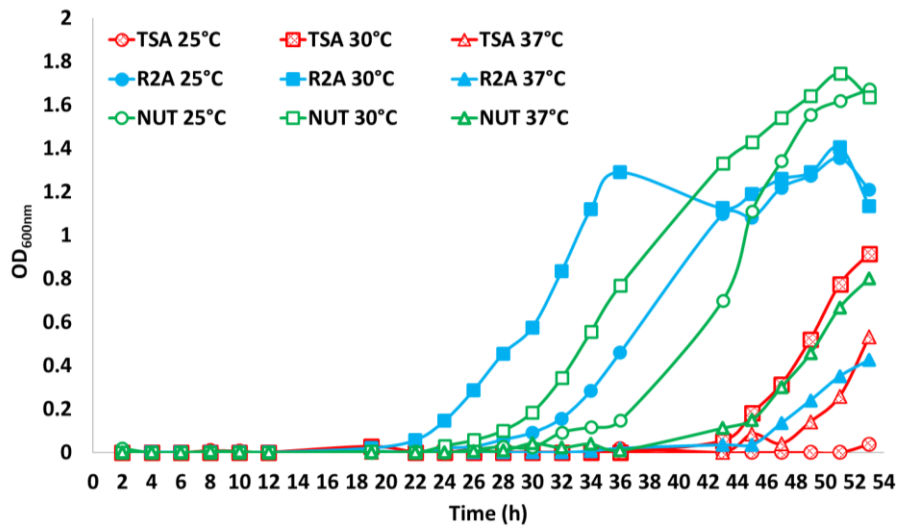


Fig. S1 Optimal growth media and temperature for the cultivation of *V. paradoxus* strain BFB1_13 assessed at pH 7

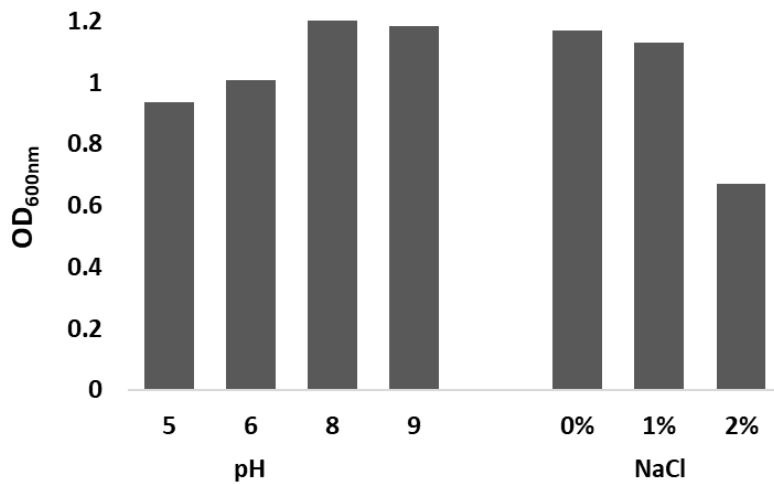


Fig. S2 pH and NaCl tolerance of *V. paradoxus* strain BFB1_13 assessed after 48 hours of incubation in nutrient-broth at 30 °C.

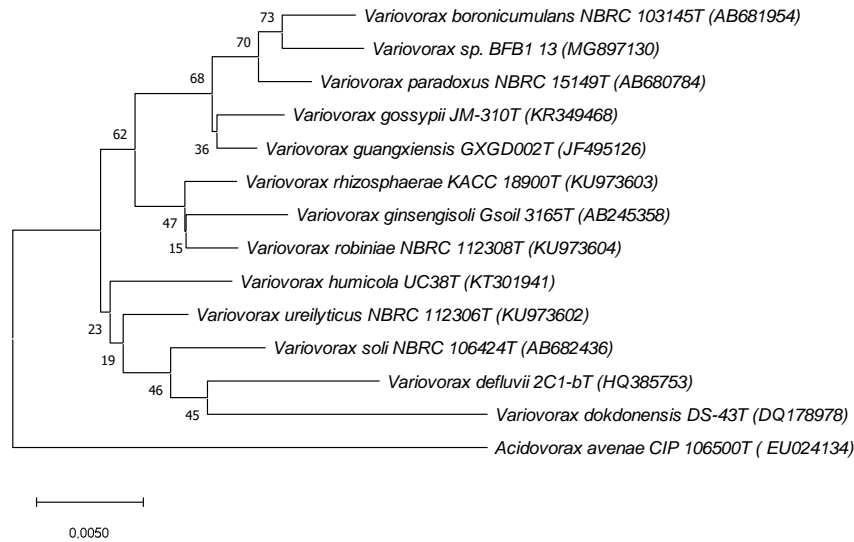


Fig. S3 Evolutionary relationships of *Variovorax* type species

The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tree with the sum of branch length = 0.10070672 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (10000 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. This analysis involved 14 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 1401 positions in the final dataset.

Evolutionary analyses were conducted in MEGA X [4].

1. Saitou N. and Nei M. (1987). The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4:406-425.
2. Felsenstein J. (1985). Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39:783-791.
3. Tamura K., Nei M., and Kumar S. (2004). Prospects for inferring very large phylogenies by using the neighbor-joining method. *Proceedings of the National Academy of Sciences (USA)* 101:11030-11035.
4. Kumar S., Stecher G., Li M., Knyaz C., and Tamura K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* 35:1547-1549.

Table S1: Composition of the used growth media

Component (g)	Growth Media		
	Nutrient	R2A	TSA
NaCl	5	-	5
Yeast Extract	2	0.5	-
Meat Extract	1	-	-
Tryptone	-	-	15
Casein Peptone	5	0.5	-
Soy Peptone	-	-	5
Soluble Starch	-	0.5	-
K₂HPO₄	-	0.3	-
MgSO₄ · 7 H₂O	-	0.05	-
Sodium-Pyruvate	-	0.3	-
D-Glucose	-	0.5	-
Casamino Acids	-	0.5	-
H₂O	1000	1000	1000

Table S2:

Three types of models could be fitted to degradation processes of the six molecules. The table contains the name of the curve type and the coefficient estimates of the fitted models (\pm standard error). T-tests compared the coefficients between the two systems and p-values are displayed.

The explanation of the parameters are the following:

Logistic function : $Y = p_1 + p_2/(1 + \exp(-p_3 * (X - p_4)))$

Saturation function: $Y = p_1 + p_2 * (1 - \exp(-p_3 * X))$

Linear function: $Y = \text{intercept} + \text{slope} * X$

Compounds	Systems	Models	Parameters:			
			p ₁	p ₂	p ₃	p ₄
Benzene	Aerob	logistic	0.66±0.37	7.25±0.85	0.56±0.16	9.69±0.53
	Micro	curve	0.45±0.41	7.11±0.82	0.55±0.15	9.01±0.53
	t-test	p-value	0.709	0.904	0.954	0.367
Toluene	Aerob	logistic	0.37±0.61	8.12±1.16	0.39±0.11	8.37±0.60
	Micro	curve	0.51±0.52	7.64±0.92	0.44±0.11	8.07±0.53
	t-test	p-value	0.86	0.746	0.738	0.711
Ethyl-benzene	Aerob	saturation	0.61±0.29	7.56±1.55	0.07±0.03	-
	Micro	curve	0.62±0.28	10.46±3.04	0.05±0.02	-
	t-test	p-value	0.972	0.398	0.587	-
<i>p</i> -xylene	Aerob	saturation	0.41±0.31	5.64±0.55	0.13±0.03	-
	Micro	curve	0.76±0.29	8.40±2.00	0.07±0.03	-
	t-test	p-value	0.408	0.188	0.161	-
<i>m</i> -xylene	Aerob	saturation	0.38±0.31	8.59±2.23	0.06±0.03	-
	Micro	curve	0.75±0.31	8.80±1.80	0.07±0.03	-
	t-test	p-value	0.397	0.94	0.861	-
<i>o</i> -xylene	Aerob	linear	slope			
	Micro	function	0.77±0.48			
	t-test	p-value	0.76±0.48			
			0.986			

Table S3:

Results from the Kruskal-Wallis tests comparing the concentration reduction values at the 168th hour for the first and second investigation (microcosm experiment N° 2 vs. 3).

	Chi-squared value	p-value
Benzene	4.64	0.200
Toluene	3.00	0.392
Ethylbenzene	2.59	0.459
<i>o</i> -xylene	3.00	0.392
<i>p</i> -xylene	6.44	0.092
<i>m</i> -xylene	2.59	0.459

Table S4: Monooxygenase and dioxygenase genes encoded by *Variovorax paradoxus* strain BFB1_13

Monooxygenases encoded by <i>V. paradoxus</i> strain BFB1_13			
Locus tag (MaGe)	Gene	Length (aa)	Putative function
VPARBFB13_v1_5500013	<i>oxyS</i>	510	Anhydrotetracycline 6-monooxygenase
VPARBFB13_v1_2430008	–	545	4-hydroxyphenylacetate 3-monooxygenase
VPARBFB13_v1_3890036	<i>nphA</i>	528	4-nitrophenol 2-monooxygenase, oxygenase component
VPARBFB13_v1_2180002	<i>phzS</i>	417	5-methylphenazine-1-carboxylate 1-monooxygenase
VPARBFB13_v1_3360002	<i>phzS</i>	432	5-methylphenazine-1-carboxylate 1-monooxygenase
VPARBFB13_v1_6040005	<i>nicC</i>	381	6-hydroxynicotinate 3-monooxygenase
VPARBFB13_v1_2080059	–	375	Alkanesulfonate monooxygenase
VPARBFB13_v1_5810015	–	358	Alkanesulfonate monooxygenase
VPARBFB13_v1_3810102	<i>ssuD</i>	390	Alkanesulfonate monooxygenase, FMNH(2)-dependent
VPARBFB13_v1_5170002	<i>ssuD</i>	388	Alkanesulfonate monooxygenase, FMNH(2)-dependent
VPARBFB13_v1_790010	<i>petC</i>	263	Ammonia monooxygenase gamma subunit
VPARBFB13_v1_4400034	–	792	Anthraniloyl-CoA monooxygenase
VPARBFB13_v1_330012	–	95	Antibiotic biosynthesis monooxygenase
VPARBFB13_v1_1620036	–	116	Antibiotic biosynthesis monooxygenase
VPARBFB13_v1_2040006	–	107	Antibiotic biosynthesis monooxygenase
VPARBFB13_v1_2960008	–	100	Antibiotic biosynthesis monooxygenase
VPARBFB13_v1_5520003	–	112	Antibiotic biosynthesis monooxygenase
VPARBFB13_v1_2640009	–	395	Sulfonate monooxygenase
VPARBFB13_v1_1040001	<i>dmoA</i>	486	Dimethyl-sulfide monooxygenase
VPARBFB13_v1_2070004	<i>dmoA</i>	461	Dimethyl-sulfide monooxygenase
VPARBFB13_v1_3740029	<i>dmoA</i>	502	Dimethyl-sulfide monooxygenase
VPARBFB13_v1_3740039	<i>dmoA</i>	469	Dimethyl-sulfide monooxygenase
VPARBFB13_v1_3740043	<i>dmoA</i>	458	Dimethyl-sulfide monooxygenase
VPARBFB13_v1_5010008	<i>dmoA</i>	484	Dimethyl-sulfide monooxygenase
VPARBFB13_v1_5010010	<i>sfnG</i>	376	FMNH(2)-dependent dimethylsulfone monooxygenase
VPARBFB13_v1_370009	<i>limB</i>	390	Limonene 1,2-monooxygenase
VPARBFB13_v1_1280009	<i>pvdA</i>	437	L-ornithine N(5)-monooxygenase
VPARBFB13_v1_3050015	–	389	Luciferase-like monooxygenase
VPARBFB13_v1_3970001	–	519	Monooxygenase
VPARBFB13_v1_1840048	<i>rutA</i>	371	Monooxygenase of the alternative pyrimidine degradation
VPARBFB13_v1_370007	<i>scmK</i>	451	N-acetyl-S-(2-succino)cysteine monooxygenase
VPARBFB13_v1_5610004	<i>scmK</i>	444	N-acetyl-S-(2-succino)cysteine monooxygenase

VPARBFB13_v1_5810014	<i>scmK</i>	456	N-acetyl-S-(2-succino)cysteine monooxygenase
VPARBFB13_v1_3300031	_	170	Nitrotriacetate monooxygenase component B
VPARBFB13_v1_350002	_	321	Nitronate monooxygenase
VPARBFB13_v1_5060008	_	373	Nitronate monooxygenase
VPARBFB13_v1_5640002	_	320	Nitronate monooxygenase
VPARBFB13_v1_60032	_	93	Phenol 2-monooxygenase P0 subunit
VPARBFB13_v1_1220004	<i>sfnC</i>	440	putative FMNH2-dependent monooxygenase SfnC
VPARBFB13_v1_3740042	<i>sfnC</i>	394	putative FMNH2-dependent monooxygenase SfnC
VPARBFB13_v1_110011	<i>ygiN</i>	103	putative quinol monooxygenase YgiN
VPARBFB13_v1_720003	_	485	putative Unspecific monooxygenase
VPARBFB13_v1_2930007	_	104	Quinol monooxygenase YgiN
VPARBFB13_v1_420067	<i>tmoD</i>	103	Toluene-4-monooxygenase, effector component
VPARBFB13_v1_420068	<i>tmoC</i>	112	Toluene-4-monooxygenase, ferredoxin component
VPARBFB13_v1_420070	<i>tmoA</i>	497	Toluene-4-monooxygenase, hydroxylase component subunit α
VPARBFB13_v1_420066	<i>tmoE</i>	329	Toluene-4-monooxygenase, hydroxylase component subunit β
VPARBFB13_v1_420069	<i>tmoB</i>	91	Toluene-4-monooxygenase, hydroxylase component subunit γ
VPARBFB13_v1_4490014	<i>tsaM</i>	357	Toluene-4-sulfonate monooxygenase, iron-sulfur subunit TsaM1
VPARBFB13_v1_3570073	_	176	Ubiquinone biosynthesis monooxygenase Coq7

Dioxygenases encoded by *V. paradoxus* BFB1_13

Locus tag (MaGe)	Gene	Length (aa)	Putative function
VPARBFB13_v1_420099	_	304	2,3-dihydroxy-p-cumate-3,4-dioxygenase (CmtC)
VPARBFB13_v1_1740011	_	276	2,3-dihydroxyphenylpropionate 1,2-dioxygenase
VPARBFB13_v1_3050062	<i>nicX</i>	348	2,5-dihydroxypyridine 5,6-dioxygenase
VPARBFB13_v1_2080056	_	211	3-mercaptopropionate dioxygenase
VPARBFB13_v1_4840024	_	197	Cinnamic acid dioxygenase, small subunit
VPARBFB13_v1_250002	_	408	Trans-cinnamate dioxygenase ferredoxin reductase subunit
VPARBFB13_v1_1510004	<i>ygiD</i>	309	4,5-DOPA dioxygenase extradiol
VPARBFB13_v1_4490055	<i>hpd</i>	376	4-hydroxyphenylpyruvate dioxygenase
VPARBFB13_v1_6000006	_	262	4-hydroxyphenylpyruvate dioxygenase
VPARBFB13_v1_4780024	_	219	Alkylated DNA repair dioxygenase AlkB
VPARBFB13_v1_890004	<i>tfdA</i>	298	2,4-dichlorophenoxyacetate dioxygenase
VPARBFB13_v1_6140039	<i>tfdA</i>	293	2,4-dichlorophenoxyacetate dioxygenase
VPARBFB13_v1_5800007	<i>atsK</i>	322	Sulfate ester dioxygenase
VPARBFB13_v1_2120016	<i>tauD</i>	283	Alpha-ketoglutarate-dependent taurine dioxygenase
VPARBFB13_v1_3050001	_	349	Alpha-ketoglutarate-dependent taurine dioxygenase
VPARBFB13_v1_1010042	<i>andAa</i>	411	Anthranilate 1,2-dioxygenase, reductase component
VPARBFB13_v1_3050066	_	366	Anthranilate dioxygenase reductase

VPARBFB13_v1_380052	_	352	Aromatic ring-hydroxylating dioxygenase subunit alpha
VPARBFB13_v1_640013	_	377	Aromatic ring-hydroxylating dioxygenase subunit alpha
VPARBFB13_v1_1740012	_	112	Aromatic ring-opening dioxygenase subunit LigA
VPARBFB13_v1_620005	_	277	Aromatic ring-opening dioxygenase, catalytic subunit,
VPARBFB13_v1_5890034	_	155	Aromatic-ring-hydroxylating dioxygenase
VPARBFB13_v1_420107	_	161	Aromatic-ring-hydroxylating dioxygenase subunit beta
VPARBFB13_v1_420091	<i>benB</i>	165	Benzoate 1,2-dioxygenase subunit beta
VPARBFB13_v1_170032	_	435	Benzoate/toluate 1,2-dioxygenase alpha subunit
VPARBFB13_v1_170031	_	165	Benzoate/toluate 1,2-dioxygenase beta subunit
VPARBFB13_v1_3300008	<i>bphC</i>	200	Biphenyl-2,3-diol 1,2-dioxygenase 3
VPARBFB13_v1_1850032	_	148	Catechol 2,3-dioxygenase
VPARBFB13_v1_4780048	_	134	Catechol 2,3-dioxygenase
VPARBFB13_v1_4840035	_	126	Catechol 2,3-dioxygenase
VPARBFB13_v1_590022	<i>linE</i>	317	Chlorohydroquinone/hydroquinone 1,2-dioxygenase
VPARBFB13_v1_2990001	_	212	Cysteine dioxygenase
VPARBFB13_v1_590050	_	515	Dioxygenase
VPARBFB13_v1_4780082	_	490	Dioxygenase
VPARBFB13_v1_3410048	_	116	DOPA 4,5-dioxygenase
VPARBFB13_v1_4900006	_	299	Fe(2+)/alpha-ketoglutarate-dependent dioxygenase LpxO
VPARBFB13_v1_2200015	_	359	Gentisate 1,2-dioxygenase
VPARBFB13_v1_2360015	<i>hmgA</i>	437	Homogentisate 1,2-dioxygenase
VPARBFB13_v1_1820005	<i>chqB</i>	292	Hydroxyquinol 1,2-dioxygenase
VPARBFB13_v1_2150040	_	177	Hydroxyquinol 1,2-dioxygenase
VPARBFB13_v1_4480016	<i>ndoR</i>	331	Napht. 1,2-dioxygenase, reductase component
VPARBFB13_v1_3050067	<i>ndoA</i>	106	Napht. 1,2-dioxygenase system, ferredoxin component
VPARBFB13_v1_4480011	<i>nagAb</i>	107	Naphth. 1,2-dioxygenase/salicylate 5-hydroxylase, ferredoxin
VPARBFB13_v1_3050064	_	172	Ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA
VPARBFB13_v1_420101	<i>cmtAb</i>	425	p-cumate 2,3-dioxygenase system, large oxygenase component
VPARBFB13_v1_420100	<i>cmtAc</i>	162	p-cumate 2,3-dioxygenase system, small oxygenase component
VPARBFB13_v1_1430030	<i>pobA</i>	410	Phenoxybenzoate dioxygenase subunit alpha
VPARBFB13_v1_40044	<i>pobB</i>	324	Phenoxybenzoate dioxygenase subunit beta
VPARBFB13_v1_380051	<i>pobB</i>	323	Phenoxybenzoate dioxygenase subunit beta
VPARBFB13_v1_1430024	<i>pobB</i>	329	Phenoxybenzoate dioxygenase subunit beta
VPARBFB13_v1_5890025	_	162	Phenylpropionate dioxygenase
VPARBFB13_v1_5890024	_	439	Phenylpropionate dioxygenase, large terminal subunit
VPARBFB13_v1_5800001	_	278	Phytanoyl-CoA dioxygenase
VPARBFB13_v1_1910004	_	181	Predicted 2-oxoglutarate-and Fe(II)-dependent dioxygenase YbiX
VPARBFB13_v1_2150009	<i>pcaG</i>	205	Protocatechuate 3,4-dioxygenase alpha chain
VPARBFB13_v1_2150010	<i>pcaH</i>	239	Protocatechuate 3,4-dioxygenase beta chain
VPARBFB13_v1_1010030	_	450	Phenylpropionate dioxygenase, large terminal subunit

VPARBFB13_v1_1010031	_	179	Putative 3-phenylpropanoate dioxygenase
VPARBFB13_v1_5010018	_	298	putative 2,4-dichlorophenoxyacetate dioxygenase
VPARBFB13_v1_3890057	_	393	Putative dioxygenase VC_1345
VPARBFB13_v1_570062	_	420	Putative Hydroxyquinol 1,2-dioxygenase
VPARBFB13_v1_170033	_	192	Putative Phthalate 4,5-dioxygenase
VPARBFB13_v1_2830009	_	676	Putative Phthalate 4,5-dioxygenase
VPARBFB13_v1_3720018	_	234	Quercetin 2,3-dioxygenase
VPARBFB13_v1_2070005	_	304	Taurine dioxygenase
VPARBFB13_v1_3740030	<i>tauD</i>	285	Taurine dioxygenase, 2-oxoglutarate-dependent
VPARBFB13_v1_3740031	<i>tauD</i>	279	Taurine dioxygenase, 2-oxoglutarate-dependent
VPARBFB13_v1_4350010	<i>tphAIII</i>	344	Terephthalate 1,2-dioxygenase, reductase component 2
VPARBFB13_v1_4350007	<i>tphA2I</i>	418	Terephthalate 1,2-dioxygenase, subunit alpha 1
VPARBFB13_v1_4350008	<i>tphA3I</i>	155	Terephthalate 1,2-dioxygenase, subunit beta 1
VPARBFB13_v1_420092	<i>xylX</i>	445	Toluate 1,2-dioxygenase subunit alpha
VPARBFB13_v1_4840026	_	455	Biphenyl-2,3-dioxygenase subunit alpha
VPARBFB13_v1_590019	_	293	Tryptophan 2,3-dioxygenase
VPARBFB13_v1_1620042	<i>kynA</i>	317	Tryptophan 2,3-dioxygenase
VPARBFB13_v1_2900001	<i>kynA</i>	283	Tryptophan 2,3-dioxygenase

Table S5: Annotation and predicted function of the proposed BTEX catabolic genes detected in the genome of *V. paradoxus* strain BFB1_13

Locus tag (MaGe)	Gene	Length (aa)*	Putative function	EC number
VPARBFB13_v1_420070	<i>tmoA</i>	496	Toluene-4-monooxygenase, hydroxylase component subunit α	
VPARBFB13_v1_420069	<i>tmoB</i>	90	Toluene-4-monooxygenase, hydroxylase component subunit γ	
VPARBFB13_v1_420068	<i>tmoC</i>	111	Toluene-4-monooxygenase, ferredoxin component	1.14.13.236
VPARBFB13_v1_420067	<i>tmoD</i>	102	Toluene-4-monooxygenase, effector component	
VPARBFB13_v1_420066	<i>tmoE</i>	328	Toluene-4-monooxygenase, hydroxylase component subunit β	
VPARBFB13_v1_420065	<i>tmoF</i>	338	Toluene-4-monooxygenase, electron transfer component	1.18.1.3
VPARBFB13_v1_420086	<i>dmpK</i>	72	Phenol hydroxylase P0 protein	
VPARBFB13_v1_60032		92		
VPARBFB13_v1_420085	<i>dmpL</i>	330	Phenol hydroxylase P1 protein	
VPARBFB13_v1_60031		305		
VPARBFB13_v1_420084	<i>dmpM</i>	89	Phenol hydroxylase P2 protein	
VPARBFB13_v1_420123		89		
VPARBFB13_v1_60029		98		
VPARBFB13_v1_420083	<i>dmpN</i>	519	Phenol hydroxylase P3 protein	1.14.13.7
VPARBFB13_v1_420122		519		
VPARBFB13_v1_60027		531		
VPARBFB13_v1_420082	<i>dmpO</i>	118	Phenol hydroxylase P4 protein	
VPARBFB13_v1_420121		118		
VPARBFB13_v1_60026		120		
VPARBFB13_v1_420081	<i>dmpP</i>	354	Phenol hydroxylase P5 protein	
VPARBFB13_v1_420120		354		
VPARBFB13_v1_60025		352		
VPARBFB13_v1_60023		310		
VPARBFB13_v1_420080		314		
VPARBFB13_v1_420119	<i>xylE</i>	314	Catechol 2,3-dioxygenase	1.13.11.2
VPARBFB13_v1_1010044		314		
VPARBFB13_v1_3270059		314		

VPARBFB13_v1_60022		484		
VPARBFB13_v1_420078	<i>dmpC</i>	484	2-hydroxymuconate-6-	1.2.1.85
VPARBFB13_v1_420117		484	semialdehyde	
VPARBFB13_v1_1010045		484	dehydrogenase	
VPARBFB13_v1_60016		63		
VPARBFB13_v1_420071	<i>praC, xylH</i>	63	2-hydroxy-muconate	5.3.2.6
VPARBFB13_v1_1010050		63	tautomerase	
VPARBFB13_v1_60021	<i>dmpD</i>	274	2-hydroxy-muconate	3.7.1.9
VPARBFB13_v1_1010051		276	semialdehyde hydrolase	
VPARBFB13_v1_3270057	<i>todF</i>	280	2-hydroxy-6-oxohepta-2,4-	3.7.1.25
			dienoate hydrolase	
VPARBFB13_v1_60017		262		
VPARBFB13_v1_420072	<i>dmpH, xylI</i>	262	4-oxalocrotonate	4.1.1.77
VPARBFB13_v1_420112		262	decarboxylase	
VPARBFB13_v1_1010049		263		
VPARBFB13_v1_60020		260		
VPARBFB13_v1_420077	<i>mhpD, xylJ</i>	264	2-keto-4-pentenoate/2-	4.2.1.80/4.2.1.132
VPARBFB13_v1_420116		264	hydroxyhexa-2,4-dienoate	
VPARBFB13_v1_1010046		262	hydratase	
VPARBFB13_v1_60018		358		
VPARBFB13_v1_420073	<i>bphI, xylK</i>	347	4-hydroxy-2-oxovalerate/4-	4.1.3.39/4.1.3.43
VPARBFB13_v1_420113		347	hydroxy-2-oxohexanoate	
VPARBFB13_v1_1010048		342	aldolase	
VPARBFB13_v1_420063	<i>xylM</i>	211	Xylene monooxygenase	1.14.15.26
VPARBFB13_v1_4840055	<i>xylB</i>	367	Aryl-alcohol dehydrogenase	1.1.1.90
VPARBFB13_v1_4890002	<i>xylC</i>	400	Salicylaldehyde /vanillin/benzaldehyde dehydrogenase	1.2.1.7/1.2.1.28
VPARBFB13_v1_170032	<i>benA-xylX</i>	434	Benzoate/toluate 1,2-	1.14.12.10/1.14.12.-
VPARBFB13_v1_420092		444	dioxygenase α subunit	
VPARBFB13_v1_170031	<i>benB-xylY</i>	164	Benzoate/toluate 1,2-	1.14.12.10/1.14.12.-
VPARBFB13_v1_420091		164	dioxygenase β subunit	
VPARBFB13_v1_420090	<i>benD-xylL</i>	273	Dihydroxy cyclohexadiene carboxylate dehydrogenase	1.3.1.25
VPARBFB13_v1_1010030	<i>ndoB</i>	449	Naphthalene 1,2- dioxygenase system, large oxygenase component	1.14.12.12

VPAFBFB13_v1_3050067	<i>ndoA</i>	105	Naphthalene 1,2-dioxygenase/ferredoxin component	1.18.1.7
VPAFBFB13_v1_4480011	<i>nagAb</i>	106		
VPAFBFB13_v1_4480016	<i>nagAa, ndoR</i>	330	Naphthalene 1,2-dioxygenase, reductase component	1.18.1.7
VPAFBFB13_v1_1730008	<i>styA</i>	424	Styrene monooxygenase	1.14.14.11
VPAFBFB13_v1_600002	<i>styD</i>	443	Phenylacetaldehyde dehydrogenase	1.2.1.39
VPAFBFB13_v1_3890017		476		
VPAFBFB13_v1_2360015	<i>hmgA</i>	436	Homogentisate 1,2-dioxygenase	1.13.11.5
VPAFBFB13_v1_2140079	<i>maiA</i>	222	Maleylacetoacetate isomerase	5.2.1.2
VPAFBFB13_v1_5970002		224		
VPAFBFB13_v1_1430037	<i>fah</i>	448	Fumarylacetoacetase	3.7.1.2
VPAFBFB13_v1_2360013		422		

*-aa, amino acids

Table S6: The number and closest affiliation of toluene 4-monooxygenase, phenol-2-hydroxylase and catechol 2,3-dioxygenase encoding genes detected in the genome of *V. paradoxus* strain BFB1_13

Locus Tag (MaGe)	Gene	Best match according to the UniProt BLAST search / Amino acid sequence similarities are shown (%)			
		UniProtKB/TrEMBL (Unreviewed)		UniProtKB/Swiss-Prot (Reviewed)	
VPARBFB13_v1_420070	<i>tmoA</i>	<i>Methylibium petroleiphilum</i> LMG 22953	86	<i>Pseudomonas mendocina</i> ATCC 25411	64
VPARBFB13_v1_420069	<i>tmoB</i>	<i>Rugosibacter aromaticivorans</i> Ca6	79	<i>Pseudomonas mendocina</i> ATCC 25411	49
VPARBFB13_v1_420068	<i>tmoC</i>	<i>Thiomonas delicata</i> DSM 5494	81	<i>Pseudomonas mendocina</i> ATCC 25411	49
VPARBFB13_v1_420067	<i>tmoD</i>	<i>Methylibium petroleiphilum</i> LMG 22953	70	<i>Pseudomonas mendocina</i> ATCC 25411	52
VPARBFB13_v1_420066	<i>tmoE</i>	<i>Methylibium petroleiphilum</i> LMG 22953	84	<i>Pseudomonas mendocina</i> ATCC 25411	61
VPARBFB13_v1_420065	<i>tmoF</i>	<i>Pseudoxanthomonas spadix</i> Bda-59	66	<i>Pseudomonas resinovorans</i> ATCC 14235	44
VPARBFB13_v1_420086	<i>dmpK</i>	<i>Burkholderiales bacterium</i> PBB5	65	<i>Pseudomonas</i> sp. strain CF600	44
VPARBFB13_v1_60032		<i>Variovorax</i> sp. PDC80	100	<i>Pseudomonas</i> sp. strain CF600	46
VPARBFB13_v1_420085	<i>dmpL</i>	<i>Hydrogenophaga</i> sp. T4	75	<i>Pseudomonas</i> sp. strain CF600	48
VPARBFB13_v1_60031		<i>Variovorax</i> sp. PDC80	99	<i>Pseudomonas</i> sp. strain CF600	53
VPARBFB13_v1_420084	<i>dmpM</i>	<i>Hydrogenophaga</i> sp. T4	79	<i>Pseudomonas</i> sp. strain CF600	42
VPARBFB13_v1_420123		<i>Hydrogenophaga</i> sp. T4	79	<i>Pseudomonas</i> sp. strain CF600	42
VPARBFB13_v1_60029		<i>Variovorax</i> sp. PDC80	99	<i>Pseudomonas</i> sp. strain CF600	50
VPARBFB13_v1_420083	<i>dmpN</i>	<i>Leptothrix cholodnii</i> ATCC 51168	88	<i>Pseudomonas</i> sp. strain CF600	66
VPARBFB13_v1_420122		<i>Leptothrix cholodnii</i> ATCC 51168	88	<i>Pseudomonas</i> sp. strain CF600	66
VPARBFB13_v1_60027		<i>Variovorax</i> sp. PDC80	100	<i>Pseudomonas</i> sp. strain CF600	66
VPARBFB13_v1_420082	<i>dmpO</i>	<i>Hydrogenophaga</i> sp. T4	87	<i>Pseudomonas</i> sp. strain CF600	44
VPARBFB13_v1_420121		<i>Hydrogenophaga</i> sp. T4	87	<i>Pseudomonas</i> sp. strain CF600	44
VPARBFB13_v1_60026		<i>Variovorax</i> sp. PDC80	100	<i>Pseudomonas</i> sp. strain CF600	47
VPARBFB13_v1_420081	<i>dmpP</i>	<i>Pseudoxanthomonas spadix</i> BDa-59	81	<i>Pseudomonas</i> sp. strain CF600	58
VPARBFB13_v1_420120		<i>Pseudoxanthomonas spadix</i> BDa-59	81	<i>Pseudomonas</i> sp. strain CF600	58
VPARBFB13_v1_60025		<i>Variovorax</i> sp. PDC80	98	<i>Pseudomonas</i> sp. strain CF600	58
VPARBFB13_v1_3270059	<i>xylE</i>	<i>Caenimonas</i> sp. HX-9-20	92	<i>Pseudomonas putida</i> DSM 291	44
VPARBFB13_v1_1010044		<i>Noviherbaspirillum</i> sp. Root189	86	<i>Pseudomonas putida</i> DSM 291	44
VPARBFB13_v1_420080		<i>Caenimonas</i> sp. HX-9-20	92	<i>Pseudomonas putida</i> DSM 291	43
VPARBFB13_v1_420119		<i>Caenimonas</i> sp. HX-9-20	92	<i>Pseudomonas putida</i> DSM 291	43
VPARBFB13_v1_60023		<i>Variovorax</i> sp. PDC80	100	<i>Pseudomonas putida</i> DSM 291	62

