

2 **Supplementary Tables**

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Table S1 Summary of genes with 2-fold or greater changes in mRNA expression under different PAHs treatment

<i>COG</i>		<i>All genes in the whole genome</i>		<i>Genes induced by one or more PAHs</i>		<i>Genes induced by all three PAHs</i>	
Category	Function	<i>Number</i>	<i>%</i>	<i>Number</i>	<i>%</i>	<i>Number</i>	<i>%</i>
A	RNA processing and modification	1	0.04	1	0.09	0	0.00
J	Translation, ribosomal structure and biogenesis	105	4.65	58	5.45	15	2.87
K	Transcription	32	1.42	15	1.41	5	0.96
L	Replication, recombination and repair	36	1.60	12	1.13	4	0.77
D	Cell cycle control, cell division, chromosome partitioning	12	0.53	5	0.47	4	0.77
M	Cell wall/membrane/envelope biogenesis	31	1.37	15	1.41	8	1.53
N	Cell motility	19	0.84	15	1.41	14	2.68
O	Posttranslational modification, protein turnover, chaperones	43	1.91	26	2.44	19	3.64
T	Signal transduction mechanisms	15	0.66	9	0.85	5	0.96

U	Intracellular trafficking, secretion, and vesicular transport	22	0.98	12	1.13	9	1.72
V	Defense mechanisms	16	0.71	6	0.56	3	0.57
C	Energy production and conversion	81	3.59	39	3.66	19	3.64
E	Amino acid transport and metabolism	98	4.34	36	3.38	20	3.83
F	Nucleotide transport and metabolism	34	1.51	17	1.60	10	1.92
G	Carbohydrate transport and metabolism	19	0.84	8	0.75	4	0.77
H	Coenzyme transport and metabolism	47	2.08	18	1.69	7	1.34
I	Lipid transport and metabolism	43	1.91	25	2.35	9	1.72
P	Inorganic ion transport and metabolism	63	2.79	31	2.91	16	3.07
Q	Secondary metabolites biosynthesis, transport and catabolism	24	1.06	13	1.22	3	0.57
R	General function prediction only	79	3.50	24	2.25	10	1.92
S	Function unknown	55	2.44	29	2.72	15	2.87
Not in COGs	Unclassified proteins	1381		651		323	
Total		2256		1065		522	

Table S2 PAHs degradation gene clusters in *Cycloclasticus* sp. P1

GenBank accession No.	Putative function	Protein similarity (%)	Organism
<i>Cluster A</i>			
Q91_0500	Ring hydroxylating dioxygenase, alpha subunit: Rieske (2Fe-2S) region protein (RHD-5 α subunit)	52.5	<i>Roseovarius</i> sp. 217
Q91_0501	Benzoate 1,2-dioxygenase small subunit (RHD-5 β subunit)	42.24	<i>Pseudomonas fulva</i> 12-X
Q91_0502	NADH:ubiquinone oxidoreductase, na translocating, f subunit	37.68	<i>Fervidobacterium nodosum</i> Rt17-B1
Q91_0503	ferredoxin-like protein	38.53	<i>Acidovorax</i> sp. JS42
Q91_0504	Metapyrocatechase (MPC) (CatO2ase) (Catechol 2,3-dioxygenase)	66.24	<i>Comamonas testosteroni</i> S44
Q91_0505	Catechol 2,3 dioxygenase, Xyle	57.24	<i>Marinobacter adhaerens</i> HP15
Q91_0506	Hypothetical CmpX-like protein	44.53	<i>Geobacillus</i> sp. Y4.1MC1
Q91_0507	2-hydroxymuconic semialdehyde dehydrogenase	69.96	<i>Marinobacter algicola</i> DG893
Q91_0508	2-hydroxypent-2,4-dienoate hydratase	68.85	<i>Cupriavidus metallidurans</i> CH34

Q91_0509	Acetaldehyde dehydrogenase 2/3	78.98	<i>Azoarcus</i> sp. BH72
Q91_0510	4-hydroxy-2-oxovalerate aldolase NahM	72.29	<i>Alkalilimnicola ehrlichii</i> MLHE-1
Q91_0511	4-oxalocrotonate decarboxylase NahK	73.85	<i>Acinetobacter</i> sp. YAA
Q91_0512	4-oxalocrotonate tautomerase family enzyme	69.84	<i>Azoarcus</i> sp. BH72
Q91_0513	hypothetical protein		
Q91_0514	bacterial luciferase-like oxidoreductase protein	45.07	<i>Marinomonas</i> sp. MWYL1
Q91_0515	Alpha/beta hydrolase fold protein	68.01	<i>Comamonas testosteroni</i> CNB-2
Cluster B			
Q91_0868	CRP/FNR family transcriptional regulator	29.82	<i>Thiocapsa roseopersicina</i>
Q91_0869	ABC transporter, permease protein	39.02	<i>Nitrosomonas</i> sp. AL212
Q91_0870	Aromatic-ring-hydroxylating dioxygenase, alpha subunit-like protein (RHD-4 α subunit)	39.77	<i>Novosphingobium</i> sp. PP1Y
Q91_0871	Biphenyl dioxygenase subunit beta (RHD-4 β subunit)	36.05	<i>Pandoraea pnomenusa</i>
Q91_0872	Fumarate reductase/succinate dehydrogenase flavoprotein domain protein	59.42	<i>Mycobacterium vanbaalenii</i> PYR-1

Q91_0873	4Fe-4S ferredoxin, iron-sulfur binding domain protein	68.83	<i>Mycobacterium</i> sp. KMS
Q91_0874	hypothetical protein	49.15	<i>Mycobacterium</i> sp. JLS
Q91_0875	ring-hydroxylating dioxygenase large subunit(RHD-1 α subunit)	64.42	<i>Mycobacterium</i> sp. S65
Q91_0876	Aromatic-ring-hydroxylating dioxygenase, beta subunit(RHD-1 β subunit)	52.63	<i>Mycobacterium</i> sp. KMS
Q91_0877	Alcohol dehydrogenase, zinc-binding domain protein	46.92	<i>Mycobacterium</i> sp. KMS
Q91_0878	hypothetical protein	26.67	<i>Marinobacter aquaeolei</i> VT8
Q91_0879	hypothetical protein	29.4	<i>Methylibium petroleiphilum</i> PM1
Q91_0880	Photosystem II stability/assembly factor-like protein	27.23	<i>Methylibium petroleiphilum</i> PM1
Q91_0881	Multidrug efflux transporter	33.11	marine gamma proteobacterium HTCC2080
Q91_0882	2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxononatrienedioate hydrolase 1	67.38	<i>Burkholderia</i> sp. H160
Q91_0883	Glutathione S-transferase	46.22	<i>Colwellia psychrerythraea</i> 34H
Q91_0884	Site-specific recombinase, phage integrase family protein	36.43	<i>Methylophaga thiooxidans</i> DMS010
Cluster C			

Q91_0959	Antibiotic biosynthesis monooxygenase subfamily	35.48	<i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB 382
Q91_0960	Efflux transporter, RND family, MFP subunit	34.12	<i>Thiobacillus denitrificans</i> ATCC 25259
Q91_0961	RND transporter, HAE1/HME family, permease protein	36.81	<i>Pseudomonas entomophila</i> L48
Q91_0962	Transcriptional regulator, TetR family	28.57	<i>Alcanivorax borkumensis</i> SK2
Q91_0963	Biphenyl-2,3-diol 1,2-dioxygenase (RHD-6 β subunit)	47.4	<i>Bacillus tusciae</i> DSM 2912
Q91_0964	Ring hydroxylating dioxygenase, alpha subunit/Rieske (2Fe-2S) protein(RHD-6 α subunit)	49.63	<i>Sphingobium japonicum</i> UT26
Q91_0965	Alpha/beta hydrolase fold protein	58.11	<i>Sphingomonas</i> sp. KA1
Q91_0966	Aromatic oxygenase small subunit	50.66	<i>Sphingomonas</i> sp. DN1
Q91_0967	Carbazole dioxygenase subunit	57.89	<i>Pseudomonas stutzeri</i>
Q91_0968	Toluate 1,2-dioxygenase subunit alpha	43.68	<i>Corynebacterium efficiens</i> YS-314
Q91_0969	Small subunit of terminal oxygenase component of anthranilate 1,2-dioxygenase	37.75	<i>Pseudomonas resinovorans</i>
Q91_0970	hypothetical protein		

Q91_0971	hypothetical protein	26.3	<i>Marinobacter aquaeolei</i> VT8
Q91_0972	hypothetical protein	29.61	marine gamma proteobacterium HTCC2080
Q91_0973	3-hydroxyisobutyrate dehydrogenase family protein	31.32	delta proteobacterium NaphS2
Q91_0974	Fnr-like transcriptional activator	45.37	<i>Beggiatoa</i> sp. PS
Q91_0975	hydroxylamine reductase	62.77	<i>Methylobacter tundripaludum</i> SV96
Q91_0976	Aromatic-ring-hydroxylating dioxygenase, alpha subunit-like protein (RHD-7 α subunit)	53.83	<i>Sphingomonas</i> sp. LH128
Q91_0977	PAH dioxygenase iron sulfur protein small subunit (RHD-7 β subunit)	39.31	<i>Cycloclasticus</i> sp. A5
Q91_0978	Transcriptional regulator, FNR-like	36.24	marine gamma proteobacterium HTCC2143
Cluster D			
Q91_2170	Aromatic ring-opening dioxygenase catalytic subunit LigB	50.6	<i>Acetobacter pasteurianus</i> IFO 3283-01
Q91_2171	Short-chain dehydrogenase/reductase SDR	48.48	delta proteobacterium NaphS2

Q91_2172	Short-chain dehydrogenase/reductase SDR	45.1	<i>Bordetella petrii</i> DSM 12804
Q91_2173	Aromatic-ring-hydroxylating dioxygenase, beta subunit(RHD-8 β subunit)	41.18	<i>Sphingobium chlorophenolicum</i> L-1
Q91_2174	Aromatic-ring-hydroxylating dioxygenase, alpha subunit-like protein (RHD-8 α subunit)	49.54	<i>Novosphingobium</i> sp. PP1Y
Q91_2175	Glutathione S-transferase domain	38.38	<i>Methylobacterium chloromethanicum</i> CM4
Q91_2176	Short-chain dehydrogenase/reductase SDR	46.12	<i>Caulobacter</i> sp. K31
Q91_2177	hypothetical protein	34.12	<i>Frankia</i> sp. EuI1c
Q91_2178	Rieske (2Fe-2S) iron-sulfur domain protein	35.26	<i>Oceanicola batsensis</i> HTCC2597
Q91_2179	NAD(P)H dehydrogenase	55.56	<i>Desulfotalea psychrophila</i> Lsv54
Q91_2180	Short-chain dehydrogenase/reductase SDR	62.84	<i>Ralstonia pickettii</i> 12D
Q91_2181	UbiA prenyltransferase family protein	46.84	<i>Colwellia psychrerythraea</i> 34H
Q91_2182	Disulfide bond formation protein	50	<i>Oceanospirillum</i> sp. MED92
Q91_2183	PhoH-like protein	50.23	<i>Methylobacterium nodulans</i> ORS 2060

Q91_2184	Nucleotide sugar dehydrogenase subfamily	70.26	<i>Thiomicrospira crunogena</i> XCL-2
Q91_2185	hypothetical protein	57.71	<i>Marinobacter</i> sp. ELB17
Q91_2186	phosphatidylserine decarboxylase	56.04	<i>Marinobacter</i> sp. ELB17
Q91_2187	hypothetical protein	60.41	<i>Marinobacter</i> sp. ELB17
Q91_2188	Aminotransferase class-III	57.22	<i>Marinobacter</i> sp. ELB17
Q91_2189	Ibuprofen CoA ligase	43.98	<i>Sphingomonas</i> sp. Ibu-2
Q91_2190	hypothetical protein	40	<i>Desulfarculus baarsii</i> DSM 2075
Q91_2191	thiolase/acyl transferase	45	<i>Sphingomonas</i> sp. Ibu-2
Q91_2192	Aromatic-ring-hydroxylating dioxygenase beta subunit	47.27	<i>Burkholderia</i> sp. Ch1-1
Q91_2193	ibuprofen CoA dioxygenase large subunit	53.19	<i>Sphingomonas</i> sp. Ibu-2
Q91_2194	transmembrane alkane 1-monooxygenase AlkB	33.89	<i>Conexibacter woesei</i> DSM 14684
Q91_2195	Alpha/beta hydrolase fold-containing protein	41.94	<i>Thermomicrobium roseum</i> DSM 5159
Q91_2196	Ring hydroxylating dioxygenase, alpha subunit/Rieske	53.75	<i>Methylocella silvestris</i> BL2

<i>Cluster E</i>			
Q91_2218	Isomerase	60.2	<i>Burkholderia</i> sp. DBT1
Q91_2219	PAH dioxygenase component ferredoxin	100	<i>Cycloclasticus</i> sp. A5
Q91_2220	PAH dioxygenase component ferredoxin reductase	100	<i>Cycloclasticus</i> sp. A5
Q91_2221	hypothetical protein	97.37	<i>Cycloclasticus</i> sp. A5
Q91_2222	Tryptophan synthase b subunit	98.72	<i>Cycloclasticus</i> sp. A5
Q91_2223	hypothetical protein	48.85	<i>Beggiatoa</i> sp. PS
Q91_2224	ring cleavage dioxygenase	100	<i>Cycloclasticus</i> sp. A5
Q91_2225	PAH dioxygenase iron sulfur protein small subunit(RHD-3 β subunit)	100	<i>Cycloclasticus</i> sp. A5
Q91_2226	PAH dioxygenase iron sulfur protein large subunit (RHD-3 α subunit)	99.78	<i>Cycloclasticus</i> sp. A5
Q91_2227	Aromatic dioxygenase large subunit	94.96	<i>Cycloclasticus</i> sp. A5
Q91_2228	4-hydroxythreonine-4-phosphate dehydrogenase	98.46	<i>Cycloclasticus</i> sp. A5
Q91_2229	hypothetical protein	54.33	<i>Novosphingobium</i> sp. PP1Y
Q91_2230	Aromatic-ring-hydroxylating dioxygenase beta subunit	51.28	<i>Methylocella silvestris</i> BL2

Q91_2231	Biphenyl dioxygenase large subunit	53.14	<i>Methylocella silvestris</i> BL2
Q91_2232	transcriptional regulator, Crp/Fnr family	34.18	<i>Marinobacter adhaerens</i> HP15
Q91_2233	Ring hydroxylating dioxygenase alpha subunit (RHD-9 α subunit)	57.11	<i>Sphingomonas</i> sp. P2
Q91_2234	Aromatic-ring-hydroxylating dioxygenase, beta subunit (RHD-9 β subunit)	34.21	<i>Mycobacterium</i> sp. JLS
Q91_2235	Short-chain dehydrogenase/reductase SDR	55.94	<i>Sphingobium xenophagum</i>
Q91_2236	Alcohol dehydrogenase large subunit	51.67	<i>Bradyrhizobium japonicum</i> USDA 110
Q91_2237	hypothetical protein	21.63	<i>Methylibium petroleiphilum</i> PM1
Q91_2238	hypothetical protein	24.02	uncultured <i>Desulfobacterium</i> sp.
Q91_2239	Multidrug efflux transporter	28.75	<i>Azoarcus</i> sp. BH72
Q91_2240	Glycosyl hydrolase, BNR repeat	38.24	<i>Candidatus Poribacteria</i> sp. WGA-A3
Q91_2241	Alcohol dehydrogenase, zinc-binding domain protein	48.28	<i>Rhodospirillum centenum</i> SW
Q91_2242	Permease, drug/metabolite transporter superfamily	27.52	<i>Bacillus</i> sp. 2_A_57_CT2
Q91_2243	Aromatic-ring-hydroxylating dioxygenase, beta subunit (RHD-2 β subunit)	48.31	<i>Novosphingobium aromaticivorans</i>

Q91_2244	Aromatic-ring-hydroxylating dioxygenase, alpha subunit-like protein (RHD-2 α subunit)	64.98	<i>Novosphingobium sp. PPIY</i>
Q91_2245	Toluate 1,2-dioxygenase electron transfer component	57.36	<i>Achromobacter piechaudii</i> ATCC 43553
Q91_2246	Glutathione s-transferase protein	42.23	<i>Burkholderia ubonensis</i> Bu
Q91_2247	hypothetical protein	38.41	<i>Methylomonas methanica</i> MC09
Q91_2248	Transglutaminase domain protein	35.8	<i>Sideroxydans lithotrophicus</i> ES-1
Q91_2249	Nitroreductase family protein	69.72	<i>Colwellia psychrerythraea</i> 34H
Q91_2250	FadL family outer membrane protein	33.71	<i>Oceanicaulis alexandrii</i> HTCC2633
Q91_2251	outer membrane protein transport protein	26.73	<i>Desulfovibrio sp.</i> ND132

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Table S3 Genes in the pyrene degradation pathway of *Cycloclasticus* sp. P1

GenBank accession No.	Putative function	Protein similarity (%)	Organism	Differential expression Ratio(Pyrene/CK)	P-value log2
Q91_0875	Pyrene ring-hydroxylating oxygenase, RHD-1 α subunit	64.42	<i>Mycobacterium</i> sp. S65	4.613	0.0000091
Q91_0876	Pyrene ring-hydroxylating oxygenase, RHD-1 β subunit	52.63	<i>Mycobacterium</i> sp. KMS	4.176	0.0000015
Q91_2219	PAH dioxygenase component ferredoxin	100	<i>Cycloclasticus</i> sp. A5	3.929	0.00004
Q91_2220	PAH dioxygenase component ferredoxin reductase	100	<i>Cycloclasticus</i> sp. A5	3.765	0.00013
Q91_0872	Dihydrodiol dehydrogenase	59.42	<i>Mycobacterium vanbaalenii</i> PYR-1	2.733	0.00005
Q91_2224	Ring cleavage dioxygenase	100	<i>Cycloclasticus</i> sp. A5	2.017	0.00072
Q91_1047	Decarboxylase	64.95	<i>Methylophaga thiooxidans</i> DMS010	2.583	0.000043
Q91_0870	dioxygenase, α -subunit	39.72	<i>Novosphingobium</i> sp. PP1Y	2.414	0.000058

Q91_0871	dioxygenase, β -subunit	36.05	<i>Pseudomonas extremaustralis</i> 14-3	1.369	0.000059
Q91_0872	Dihydrodiol dehydrogenase	59.42	<i>Mycobacterium vanbaalenii</i> PYR-1	2.733	0.000069
Q91_2218	isomerase	60.2	<i>Burkholderia</i> sp. DBT1	3.188	0.00038
Q91_1157	hydratase-aldolase	58.05	<i>Burkholderia</i> sp. Ch1-1	2.359	0.000052
Q91_0507	Aldehyde dehydrogenase	69.96	<i>Marinobacter algicola</i> DG893	1.183	0.000068
Q91_0344	hydroxylase	60.62	<i>Pseudoalteromonas atlantica</i> T6c	1.231	0.000065
Q91_0437	HBPA hydratase-aldolase	64.36	<i>Methylobacter tundripaludum</i> SV96	1.414	0.000062
Q91_0488	Salicylaldehyde dehydrogenase	56.48	<i>Novosphingobium</i> <i>aromaticivorans</i> DSM 12444	1.355	0.00015
Q91_1959	salicylaldehyde hydroxylase	44.61	<i>Methylobacter tundripaludum</i> SV96	1.066	0.00059

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Table S4 Genes in the phenanthrene degradation pathway of *Cycloclasticus* sp. P1

GenBank accession No.	Putative function	Protein similarity (%)	Organism	Differential expression	
				Log ₂ (Ratio Phe / CK)	P-value
Q91_2243	Phenanthrene ring-hydroxylating oxygenase, RHD-2 α subunit	48.31	<i>Novosphingobium aromaticivorans</i>	4.891	0.0000073
Q91_2244	Phenanthrene ring-hydroxylating oxygenase, RHD-2 β subunit	64.98	<i>Novosphingobium</i> sp. PP1Y	4.248	0.00000017
Q91_2219	PAH dioxygenase component ferredoxin	100	<i>Cycloclasticus</i> sp. A5	3.133	0.0000028
Q91_2220	PAH dioxygenase component ferredoxin reductase	100	<i>Cycloclasticus</i> sp. A5	3.400	0.000005
Q91_2235	Dihydrodiol dehydrogenase	55.94	<i>Sphingobium xenophagum</i>	1.623	0.000045
Q91_2224	Ring cleavage dioxygenase	100	<i>Cycloclasticus</i> sp. A5	2.348	0.000067
Q91_2218	isomerase	60.2	<i>Burkholderia</i> sp. DBT1	1.696	0.0000075
Q91_1157	hydratase-aldolase	58.05	<i>Burkholderia</i> sp. Ch1-1	2.099	0.0000337
Q91_0507	Aldehyde dehydrogenase	69.96	<i>Marinobacter algicola</i> DG893	2.360	0.000002
Q91_0344	hydroxylase	60.62	<i>Pseudoalteromonas</i>	1.613	0.000063

<i>atlantica</i> T6c						
Q91_2218	Hydroxy chromene-carboxylate isomerase	60.2	<i>Burkholderia</i> sp. DBT1	1.696	0.000007	
Q91_0437	HBPA hydratase-aldolase	64.36	<i>Methylobacter tundripaludum</i> SV96	2.142	0.000109	
Q91_0488	Salicylaldehyde dehydrogenase	56.48	<i>Novosphingobium aromaticivorans</i> DSM 12444	1.170	0.00007	
Q91_1959	salicylaldehyde hydroxylase	44.61	<i>Methylobacter tundripaludum</i> SV96	1.034	0.00001	

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TableS5 Genes in the naphthalene degradation pathway of *Cycloclasticus* sp. P1

GenBank accession No.	Putative function	Protein similarity (%)	Organism	Differential expression	
				Log ₂ (Ratio Nap/CK)	P-value
Q91_2225	Naphthalene ring-hydroxylating oxygenase, RHD-3 α subunit	100	<i>Cycloclasticus</i> sp. A5	3.71	0.0007
Q91_2226	Naphthalene ring-hydroxylating oxygenase, RHD-3 β subunit	99.78	<i>Cycloclasticus</i> sp. A5	3.522	0.0002
Q91_2219	PAH dioxygenase component ferredoxin	100	<i>Cycloclasticus</i> sp. A5	3.105	0.0001
Q91_2220	PAH dioxygenase component ferredoxin reductase	100	<i>Cycloclasticus</i> sp. A5	3.229	0.0002
Q91_2228	Dihydrodiol dehydrogenase	98.46	<i>Cycloclasticus</i> sp. A5	1.6 96	0.00005
Q91_2224	ring cleavage dioxygenase	100	<i>Cycloclasticus</i> sp. A5	1.458	0.231
Q91_2218	Hydroxy chromene-carboxylate isomerase	60.2	<i>Burkholderia</i> sp. DBT1	1.410	0.00003
Q91_0437	HBPA hydratase-aldolase	64.36	<i>Methylobacter tundripaludum</i> SV96	1.174	0.00045
Q91_0488	Salicylaldehyde dehydrogenase	56.48	<i>Novosphingobium aromaticivorans</i> DSM 12444	1.592	0.00004
Q91_1959	salicylaldehyde hydroxylase	44.61	<i>Methylobacter tundripaludum</i> SV96	1.235	0.00012

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TableS6 Genes in the benzoate degradation pathway of *Cycloclasticus* sp. P1.

GenBank No.	Putative function	Protein similarity(%)	Organism
Q91_0500	benzoate 1,2-dioxygenase subunit alpha	52.5	<i>Roseovarius</i> sp. 217
Q91_0501	benzoate/toluate 1,2-dioxygenase subunit beta	42.24	<i>Pseudomonas fulva</i> 12-X
Q91_1667	benzoate/toluate 1,2-dioxygenase electron transfer component	42.47	<i>Acidiphilium multivorum</i> AIU301
Q91_2245	dihydroxycyclohexadiene carboxylate dehydrogenase	57.36	<i>Achromobacter piechaudii</i> ATCC 43553
Q91_0505	catechol 2,3-dioxygenase	57.24	<i>Marinobacter adhaerens</i> HP15
Q91_0515	2-hydroxymuconate-semialdehyde hydrolase	68.01	<i>Comamonas testosteroni</i> CNB-2
Q91_0507	aminomuconate-semialdehyde dehydrogenase	69.96	<i>Marinobacter algicola</i> DG893
Q91_0512	4-oxalocrotonate tautomerase	69.84	<i>Azoarcus</i> sp. BH72
Q91_0511	4-oxalocrotonate decarboxylase	73.85	<i>Acinetobacter</i> sp. YAA

Q91_0508	2-keto-4-pentenoate hydratase	68.85	<i>Cupriavidus metallidurans</i> CH34
Q91_0510	4-hydroxy 2-oxovalerate aldolase	72.29	<i>Alkalilimnicola ehrlichii</i> MLHE-1
Q91_0509	acetaldehyde dehydrogenase	78.98	<i>Azoarcus</i> sp. BH72

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TableS7 Primers and vectors used or constructed in this study

<i>Primers /Plasmid</i>	<i>Relevant characteristics (Sequence)^a</i>	<i>Restriction enzyme</i>	<i>Reference or source</i>
primers			
Ferre_F	GAG <u>AGG ATC CTA</u> GAG AAG GAA ATT GAT GAG CAA TAT AGT ATT ATG TAA	<i>Bam</i> HI	This study
Ferre_R	TCT <u>CGA GCT CTT</u> ATT CAG CGG CTG GAA TAC AA	<i>Sac</i> I	This study
Reduc_F	GAG <u>AGA GCT CAG</u> AAG GAT CCT GAT TTA TGA CAA GTT ATA ACG TAA A AA	<i>Sac</i> I	This study
Reduc_R1	TCT <u>CAG ATC TTTA</u> ATA AAA ACG ATC GTA ATG A	<i>Bgl</i> II	This study
Reduc_R2	TCT <u>CCT GCA GTTA</u> ATA AAA ACG ATC GTA ATG A	<i>Pst</i> I	This study
RHD-1_F	GAG <u>AAG ATC TAG</u> AAG GAA GCC CTA TCAT GAC TGA TTT CGA AAA AAT TA	<i>Bgl</i> II	This study
RHD-1_R	TCT <u>CGA ATT CTT</u> ATA GTG GGT ACA CTA GAT AC	<i>Eco</i> RI	This study

RHD-2_F	GAG <u>AAG ATC TAG</u> AAG AAG GAG TTG ATA TGA GCA ATA GAA GAC TTG AGA	<i>Bgl</i> III	This study
RHD-2_R	TCT <u>CGA ATT CTT</u> AAA GGT AAA CGT TTA GAC TT	<i>Eco</i> RI	This study
RHD-3_F	GAG <u>AAG ATC TAG</u> AAG AAG AGA GTG AAA TGG TAG ATA TTA ATA AAC TGG	<i>Bgl</i> III	This study
RHD-3_R	TCT <u>CGA ATT CTC</u> AGA AGA ATA TAT ATA AAT TT	<i>Eco</i> RI	This study
RHD-4_F	GAG <u>AAG ATC TAG</u> AAG AAG GAG TTG GCA TGA TTG AGA TTG ATA AGC TGG	<i>Bgl</i> III	This study
RHD-4_R	TCT <u>CGA ATT CCT</u> ACA ACA AAC TAT TCA TAT TG	<i>Eco</i> RI	This study
RHD-5_F	GAG <u>ACT GCA GAG</u> AAG AAA GGT GAA TAA TGG GCA AAC AAA ATA AAA TCG	<i>Pst</i> I	This study
RHD-5_R	TCT <u>CGA ATT CCT</u> AAA CAC TAT AAA CAT CTA AT	<i>Eco</i> RI	This study
RHD-6_F	GAG <u>AAG ATC TAG</u> AAG AAG ATA CTG CAATGAATTTAG ATCAATTAAC TC	<i>Bgl</i> III	This study
RHD-6_R	TCT <u>CGA ATT CTT</u> ACT GAG TCA CAC CCA TAA TT	<i>Eco</i> RI	This study
RHD-7_F	GAG <u>AAG ATC TAG</u> AAG AAA TTA CAC ATA TGA AGC CAG TTA ATA AAT TAA	<i>Bgl</i> III	This study
RHD-7_R	TCT <u>CGA ATT CCT</u> AAAAGAAA CAGTGAATAT TT	<i>Eco</i> RI	This study
RHD-8_F	GAG <u>ACT GCA GAG</u> AAG AAA GGC GGT GCA TGA GTA AGT TTG ATT ACA A TA	<i>Pst</i> I	This study
RHD-8_R	TCT <u>CGA ATT CCT</u> AGCCATTG ACAGACTCCT TC	<i>Eco</i> RI	This study

RHD-9_F	GAG <u>ACT GCA GAG</u> AAG GAA GCC CTA TCA TGA CGC AAA TAC CTA A TAA CA	<i>Pst</i> I	This study
RHD-9_R	TCT <u>CGG TAC CTT</u> AG ATA GGG TAA GGA ACA TAA	<i>Kpn</i> I	This study
Plasmids			
pCR4-TOPO	Amp ^r Kan ^r ; cloning vector for sequencing		Invitrogen
pRSET-A	Amp ^r ; vector for gene expression		Invitrogen
pFR.1	pRSET-A vector with ferredoxin and reductase genes		This study
pFRR.1	pFR.1 containing α/β subunit genes of RHD-1		This study
pFRR.2	pFR.1 containing α/β subunit genes of RHD-2		This study
pFRR.3	pFR.1 containing α/β subunit genes of RHD-3		This study
pFRR.4	pFR.1 containing α/β subunit genes of RHD-4		This study
pFRR.5	pFR.1 containing α/β subunit genes of RHD-5		This study
pFRR.6	pFR.1 containing α/β subunit genes of RHD-6		This study
pFRR.7	pFR.1 containing α/β subunit genes of RHD-7		This study
pFRR.8	pFR.1 containing α/β subunit genes of RHD-8		This study

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pFRR.9	pFR.1 containing α/β subunit genes of RHD-9		This study
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