Figure S1. Graphical representation of the best fitting curve for *L. neptuniae* viability as a function of the logarithm of IBP concentration.

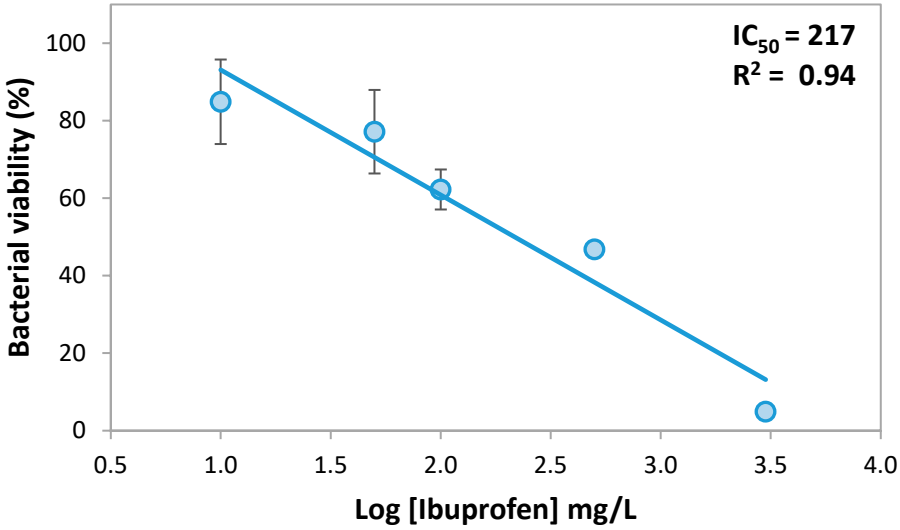
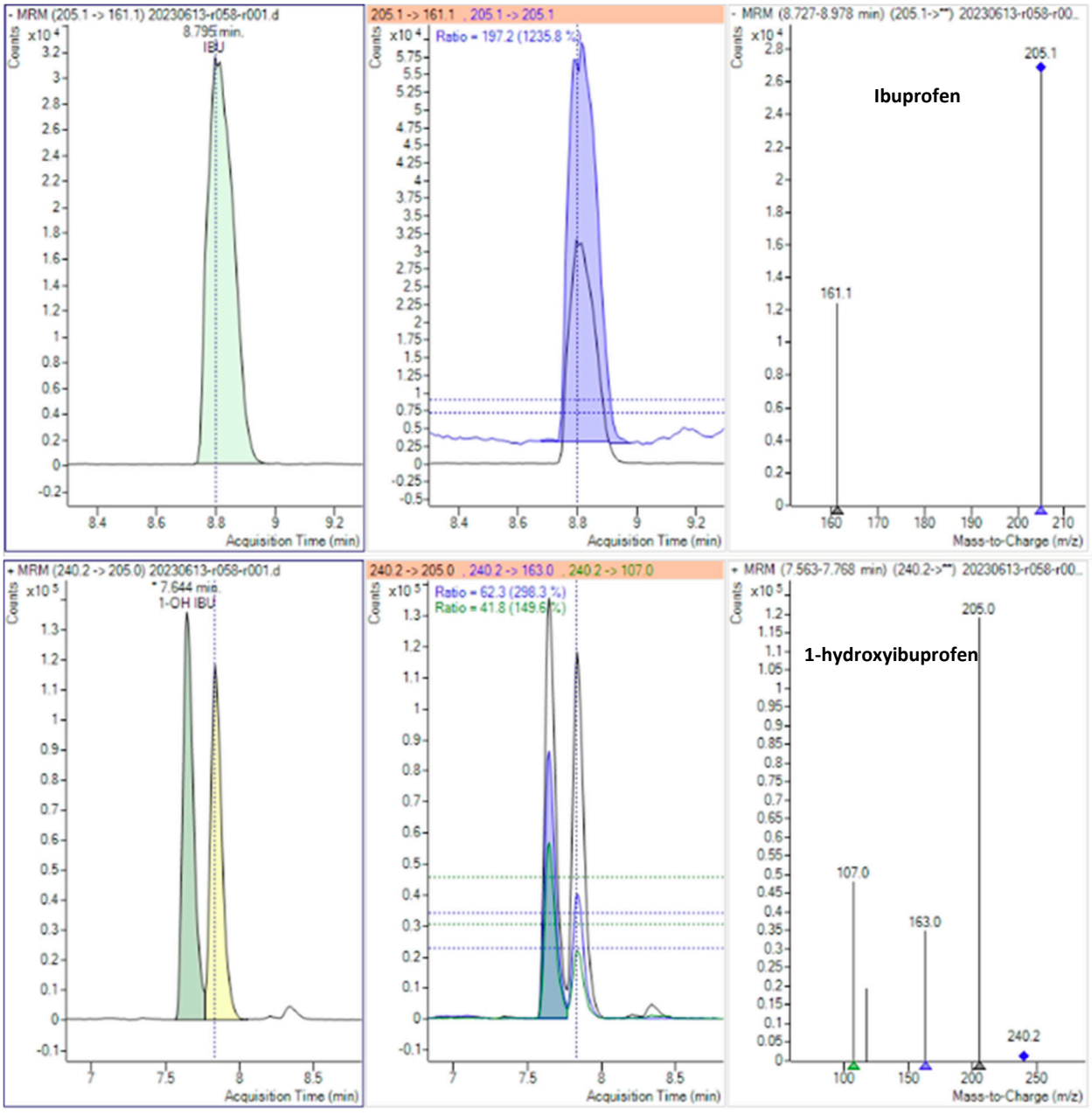


Figure S2. LC-MS/MS chromatograms and mass spectra of measured ibuprofen and metabolites in the sample extract after seven days of degradation in the absence of glucose.



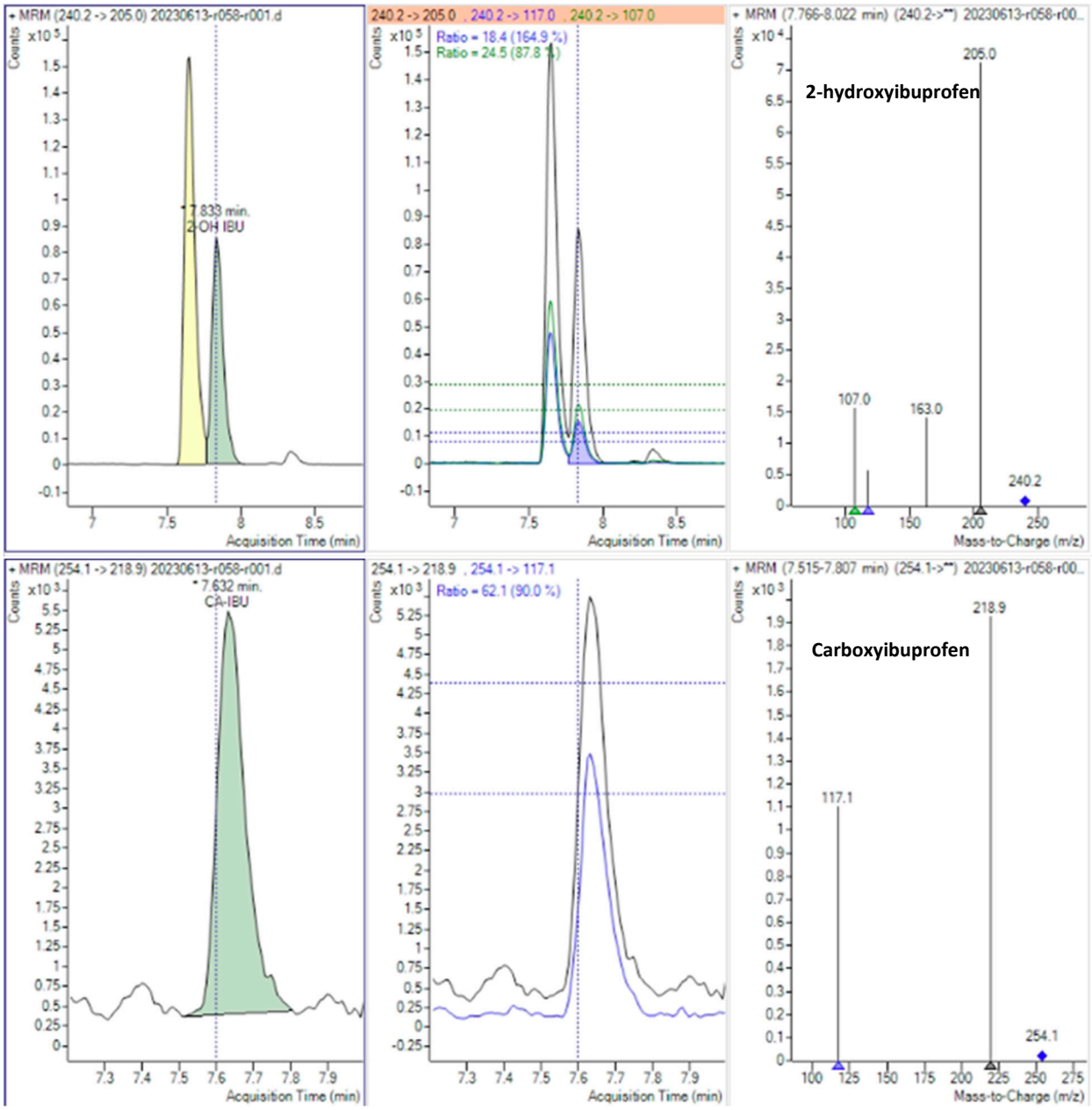

+ MRM (240.2 -> 205.0) 20230613-r058-r001.d
Counts
x10 5
7.833 min.
2-OH IBU
Acquisition Time (min)
240.2 -> 205.0 , 240.2 -> 117.0 , 240.2 -> 107.0
Ratio = 18.4 (164.9 %)
Ratio = 24.5 (87.8 %)
Acquisition Time (min)
+ MRM (7.766-8.022 min) (240.2->**) 20230613-r058-r00...
x10 4
205.0
2-hydroxyibuprofen
107.0
163.0
240.2
Mass-to-Charge (m/z)
+ MRM (254.1 -> 218.9) 20230613-r058-r001.d
x10 3
7.632 min.
CA-IBU
Acquisition Time (min)
254.1 -> 218.9 , 254.1 -> 117.1
Ratio = 62.1 (90.0 %)
Acquisition Time (min)
+ MRM (7.515-7.807 min) (254.1->**) 20230613-r058-r00...
x10 3
218.9
Carboxyibuprofen
117.1
254.1
Mass-to-Charge (m/z)

Figure S3. SEED diagram showing whole genome annotation and functional gene analysis of *Labrys neptuniae* CSW11.

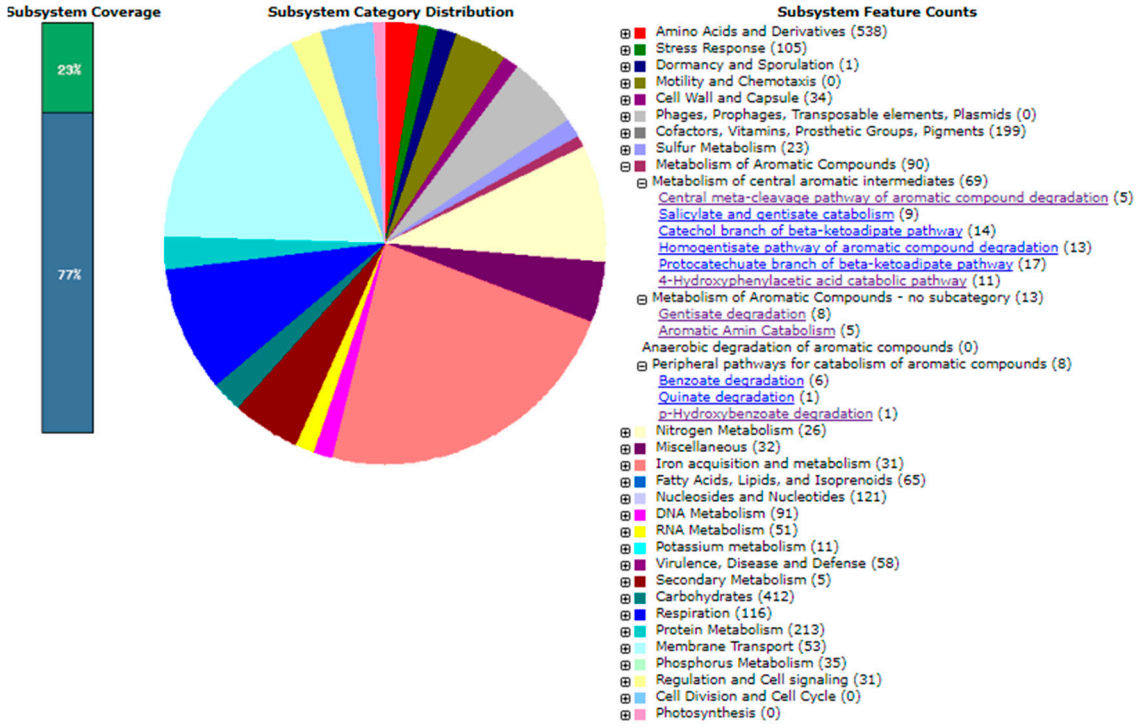


Table S1. Alignment of five-gene cluster *ipf*ABDEF and the *paa* genes encoding enzymes involved in the biodegradation pathway of ibuprofen and other phenylacetic acids, respectively, which are annotated proteins in the genome of *L. neptuniae* CSW11.

Gen	Organism	Enzyme	E-value	Identity (%)	Putative function
ipfA	Sphingomonas sp. Ibu-2	Ibuprofen CoA dioxygenase large subunit	2E-49	30	Benzoate 1,2-dioxygenase alpha subunit
ipfB	Sphingomonas sp. Ibu-2	Ibuprofen-CoA dioxygenase small subunit	7E-08	30	Benzoate 1,2-dioxygenase beta subunit
ipfD	Sphingomonas sp. Ibu-2	Thiolase/acyl transferase	0.65	24	3-ketoacyl-CoA thiolase @ Acetyl-CoA acetyltransferase
ipfE	Sphingomonas sp. Ibu-2	-	0.66	39	hypothetical protein
ipfF	Sphingomonas sp. Ibu-2	Ibuprofen CoA ligase	1E-52	31	Long-chain-fatty-acid--CoA ligase
paaA	E. coli K-12	-	-	-	-
paaB	E. coli K-12	phenylacetyl-CoA 1,2-epoxidase, subunit B	0.75	55	Hypotetical protein
paaC	E. coli K-12	phenylacetyl-CoA 1,2-epoxidase, structural subunit	0.80	36	aminoacid ABC transporter, ATP-binding protein
paaE	E. coli K-12	phenylacetyl-CoA 1,2-epoxidase, reductase subunit	2E-43	32	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1
paaF	E. coli K-12	putative 2,3-dehydroadipyl-CoA hydratase	2E-71	46	Enoyl-CoA hydratase
paaG	E. coli K-12	putative ring 1,2-epoxyphenylacetyl-CoA isomerase	2E-72	43	Enoyl-CoA hydratase

paaH	E. coli K-12	3-hydroxyadipyl-CoA dehydrogenase	1E-61	37	3-hydroxybutyryl-CoA dehydrogenase
paaI	E. coli K-12	phenylacetyl-CoA thioesterase	6E-04	30	cytosolic long-chain acyl-CoA thioester hydrolase family protein
paaJ	E. coli K-12	beta-ketoadipyl-CoA thiolase	1E-174	65	Acetyl-CoA acetyltransferase / 3-oxoadipyl-CoA thiolase
paaK	E. coli K-12	phenylacetate-CoA ligase	0.001	25	2,3-dihydroxybenzoate-AMP ligase of siderophore biosynthesis
paaL	E. coli K-12	-	-	-	-
paaM	E. coli K-12	-	-	-	-
paaX	E. coli K-12	DNA-binding transcriptional repressor PaaX	0.13	26	Dipeptide-binding ABC transporter, periplasmic substrate-binding component
paaY	E. coli K-12	2-hydroxycyclohepta-1,4,6-triene-1-carboxyl-CoA thioesterase	5E-38	39	Carbonic anhydrase-like protein MJ0304
paaZ	E. coli K-12	fused 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde dehydrogenase and oxepin-CoA hydrolase	2E-22	25	Succinate-semialdehyde dehydrogenase [NAD(P)+]