

Supplementary Materials

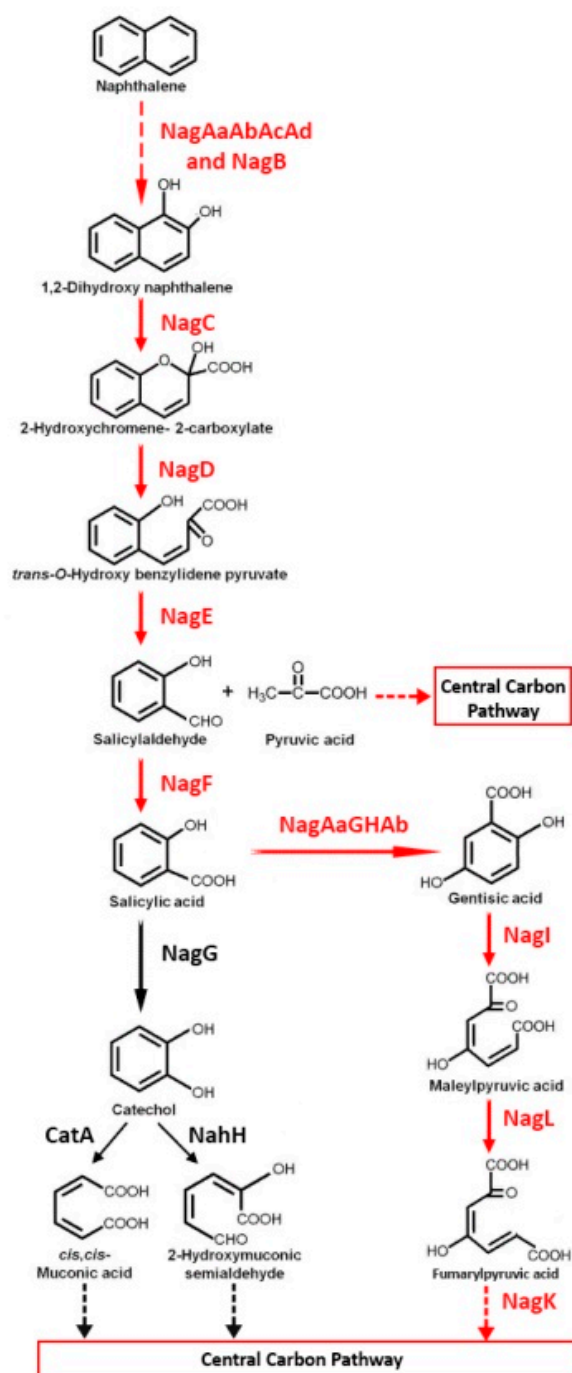


Figure S1. Scheme of naphthalene catabolic pathway via catechol (black arrows) and gentisic acid (red arrows). The enzymes involved in naphthalene catabolism are naphthalene 1,2-dioxygenase (NagAaAbAcAd), *cis*-naphthalene dihydrodiol dehydrogenase (NagB), 1,2-dihydroxynaphthalene dioxygenase (NagC), 2-hydroxy-2H-chromene-2-carboxylate isomerase (NagD), *trans*-o-hydroxybenzylidenepyruvate hydratase-aldolase (NagE), salicylaldehyde dehydrogenase (NagF), salicylate hydroxylase (NahG), catechol 2,3-dioxygenase (NahH), catechol 1,2-dioxygenase (catA), salicylate 5-hydroxylase (NagGHAAAb), gentisate 1,2-dioxygenase (NagI), maleylpyruvate isomerase (NagL), and fumarylpyruvate hydrolase (NagK). The red color indicates the naphthalene degradation pathway by the *Delftia tsuruhatensis* strain ULwDis3 and the enzymes involved in its catabolism.

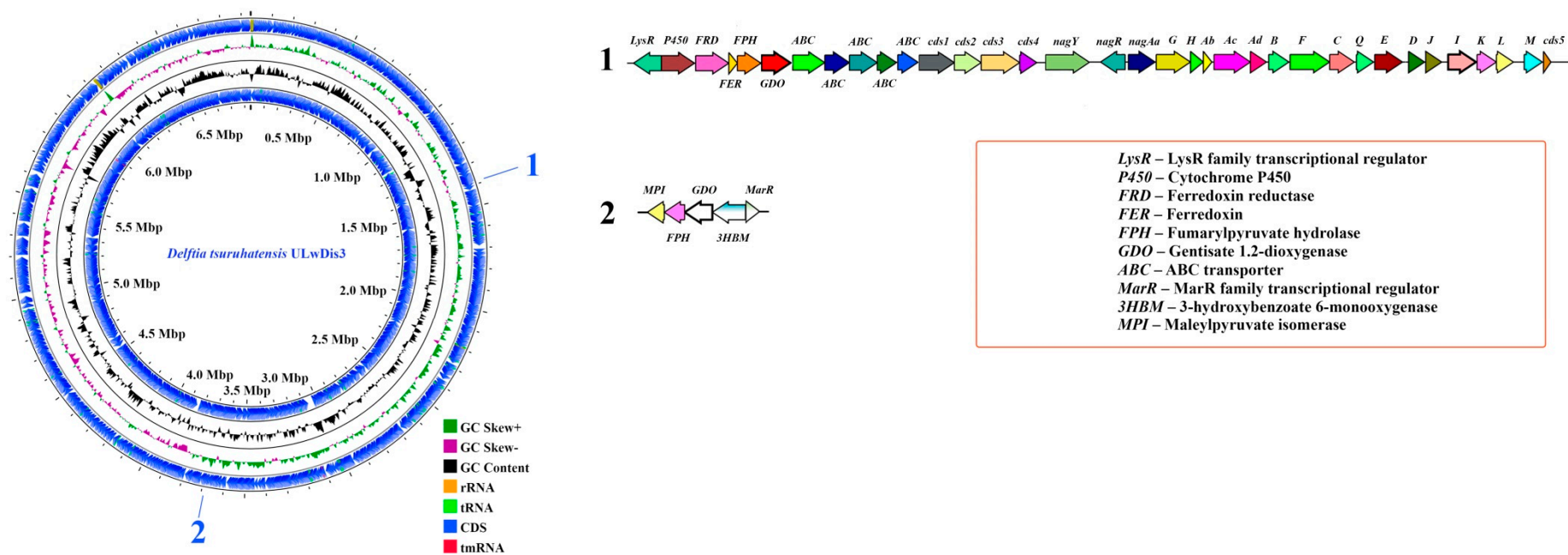


Figure S2. Circular map of the *Delftia tsuruhatensis* ULwDis 3 chromosome. From outside to the center: all CDS and RNA genes on forward strand, GC skew, GC content, and all CDS and RNA genes on reverse strand , .

1 - gene site with two gentisate dioxygenases, including the *nag* operon

2 - gene site with a third gentisate dioxygenase

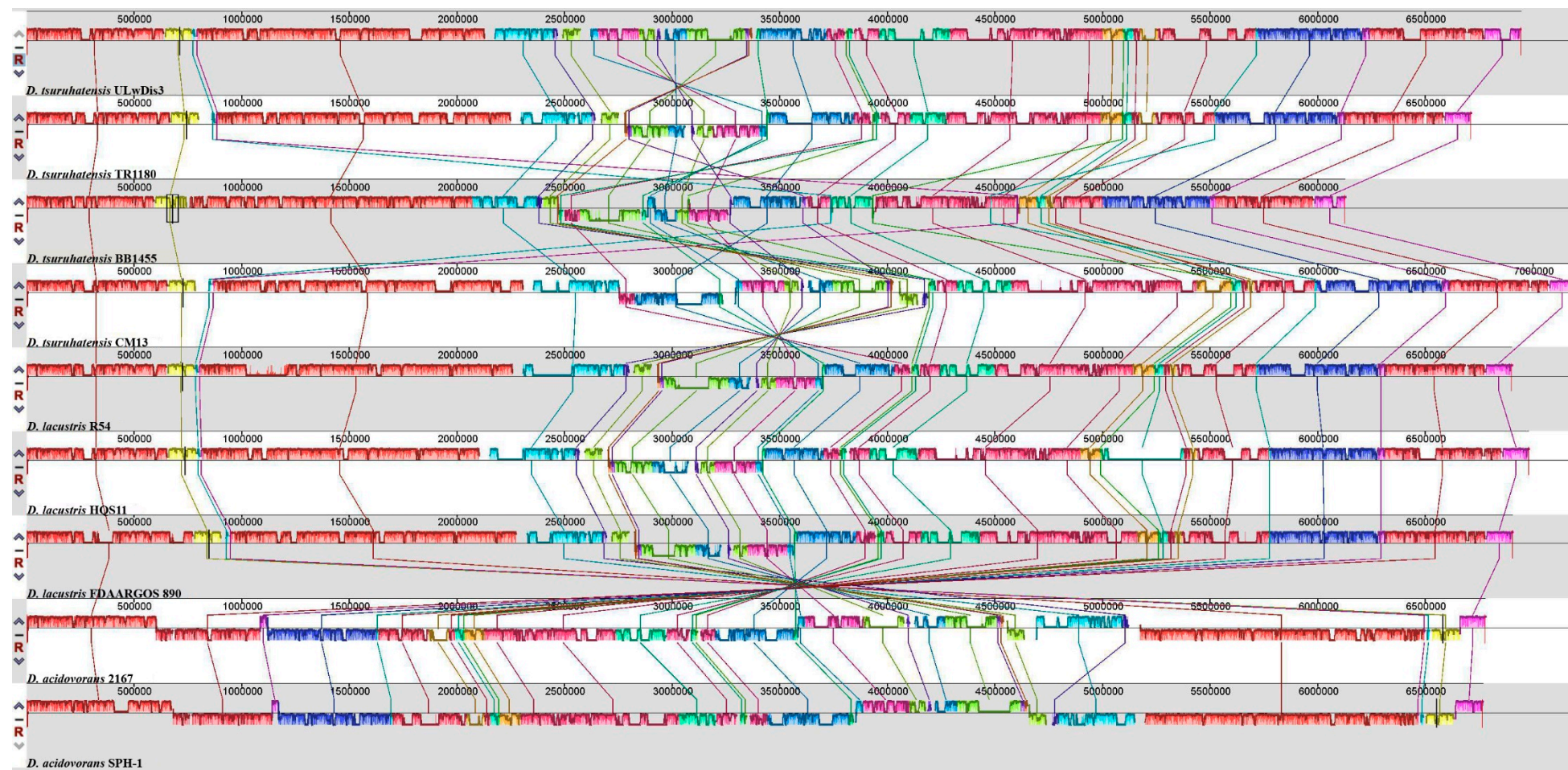


Figure S3. Whole genome comparative chromosomes Mauve alignment of different *Delftia* species strains.

*Colored blocks indicate genome regions aligned with parts of another genome. Each sequence of identically colored blocks represents a collinear set of matching. Homologous blocks in different genomes are connected with lines. Conservation level of genomic regions is shown by the height of the similarity profile.

Table S1. Similarity of predicted gene products from the *nag*-gene cluster of *D. tsuruhatensis* ULwDis3 to selected homologs.

Gene designation	Position (bp) ^a	GC%	Proposed function	No. of amino acids, ULwDis3/relative ^b	% Amino Acid identity	Source microorganism	GeneBank accession number ^c
<i>nagY</i>	1370733...	64.6	Chemotaxis protein	548/548	100	<i>Cupriavidus necator</i> U2	KAI3589261.1
	1372379d			548/429	100	<i>Burkholderia</i> sp. BC1	APP18104.1
<i>nagR</i>	1372346...	58.4	Transcriptional regulator, LysR family	301/301	100	<i>Cupriavidus necator</i> U2	KAI3589262.1
	1373251c			301/301	100	<i>Burkholderia</i> sp. BC1	APP18105
				301/318	83.1	<i>Polaromonas naphthalenivorans</i> CJ2	ABM37794.1
<i>nagAa</i>	1373368...	61.1	Ferredoxin reductase	328/328	100	<i>Cupriavidus necator</i> U2	KAI3589263.1
	1374354d			328/328	100	<i>Burkholderia</i> sp. BC1	APP18106.1
				328/328	75	<i>Polaromonas naphthalenivorans</i> CJ2	ABM37793.1
<i>nagG</i>	1374400...	61.8	Salicylate-5-hydroxylase, large oxygenase component	423/423	100	<i>Cupriavidus necator</i> U2	KAI3589264.1
	1375671d			423/423	99.1	<i>Burkholderia</i> sp. BC1	APP18107.1
				423/420	89.9	<i>Polaromonas naphthalenivorans</i> CJ2	ABM37792.1
<i>nagH</i>	1375674...	59.5	Salicylate-5-hydroxylase, small oxygenase component	161/161	100	<i>Cupriavidus necator</i> U2	KAI3589265.1
	1376159d			161/161	100	<i>Burkholderia</i> sp. BC1	APP18108.1
				161/161	86.3	<i>Polaromonas naphthalenivorans</i> CJ2	ABM37791.1
<i>nagAb</i>	1376170...	52.4	Ferredoxin	104/104	100	<i>Cupriavidus necator</i> U2	KAI3589266.1
	1376484d			104/104	100	<i>Burkholderia</i> sp. BC1	APP18109.1
				104/112	78.8	<i>Polaromonas naphthalenivorans</i> CJ2	ABM37790.1
<i>nagAc</i>	1376571...	53.2	Naphthalene dioxygenase, large oxygenase component	447/447	100	<i>Cupriavidus necator</i> U2	KAI3589267.1
	1377914d			447/447	98.4	<i>Burkholderia</i> sp. BC1	APP18110.1
				447/447	95.3	<i>Polaromonas naphthalenivorans</i> CJ2	ABM37789.1

<i>nagAd</i>	1377929... 1378513d	53.7	Naphthalene dioxygenase, small oxygenase component	194/194 194/194 194/194	99.8 94.3 89.7	<i>Cupriavidus necator</i> U2 <i>Burkholderia</i> sp. BC1 <i>Polaromonas naphthalenivorans</i> CJ2	KAI3589268.1 APP18111.1 ABM37788.1
<i>nagB</i>	1378523... 1379356d	55.9	<i>cis</i> -Naphthalene dihydrodiol dehydrogenase	277/273 277/259 277/259	99.6 94.2 93.1	<i>Cupriavidus necator</i> U2 <i>Burkholderia</i> sp. BC1 <i>Polaromonas naphthalenivorans</i> CJ2	KAI3589269.1 APP18112.1 ABM37789.1
<i>nagF</i>	1379405... 1380856d	59.9	Salicylaldehyde dehydrogenase	483/483 483/483 483/483	99.6 97.1 93.6	<i>Cupriavidus necator</i> U2 <i>Burkholderia</i> sp. BC1 <i>Polaromonas naphthalenivorans</i> CJ2	KAI3589270.1 APP18113.1 ABM37790.1
<i>nagC</i>	1380882... 1381790d	54.0	1,2- Dihydroxynaphtha lene dioxygenase	302/302 302/302 302/302	100 97.7 94.1	<i>Cupriavidus necator</i> U2 <i>Burkholderia</i> sp. BC1 <i>Polaromonas naphthalenivorans</i> CJ2	KAI3589271.1 APP18114.1 ABM37791.1
<i>nagQ</i>	1381863.. 1382498d	52.9	Outer membrane protein	211/211 211/180 211/211	100 93.2 91.5	<i>Cupriavidus necator</i> U2 <i>Burkholderia</i> sp. BC1 <i>Polaromonas naphthalenivorans</i> CJ2	KAI3589272.1 APP18115.1 ABM37792.1
<i>nagE</i>	1382556... 1383593d	57.2	<i>trans</i> -o- Hydroxybenzylide nepyruvate hydratase–aldolase	345/345 345/345 345/345	100 95.7 95.9	<i>Cupriavidus necator</i> U2 <i>Burkholderia</i> sp. BC1 <i>Polaromonas naphthalenivorans</i> CJ2	KAI3589273.1 APP18116.1 ABM37793.1
<i>nagD</i>	1383776... 1384375d	51.4	2- Hydroxychromene carboxylate isomerase	199/196 199/197 199/197	100 98.9 92.9	<i>Cupriavidus necator</i> U2 <i>Burkholderia</i> sp. BC1 <i>Polaromonas naphthalenivorans</i> CJ2	KAI3589274.1 APP18117.1 ABM37794.1
<i>nagJ</i>	1384434... 1385039d	55.4	Glutathione-S- transferase	201/201 201/201	99.5 99.5	<i>Cupriavidus necator</i> U2 <i>Burkholderia</i> sp. BC1	KAI3589275.1 APP18118.1

				201/201	93.5	<i>Polaromonas naphthalenivorans</i> CJ2	ABM37795.1
<i>nagI</i>	1385270... 1386310d	67.1	Gentisate 1,2- dioxygenase	346/346	100	<i>Cupriavidus necator</i> U2	KAI3589276.1
				346/355	100	<i>Burkholderia</i> sp. BC1	APP18119.1
				346/334	85.5	<i>Polaromonas naphthalenivorans</i> CJ2	ABM37796.1
<i>nagK</i>	1386344... 1387045d	64.0	Fumarylpyruvate hydrolase	233/233	100	<i>Cupriavidus necator</i> U2	KAI3589277.1
				233/192	100	<i>Burkholderia</i> sp. BC1	APP18120.1
				233/289	31.1	<i>Polaromonas naphthalenivorans</i> CJ2	ABM37797.1
<i>nagL</i>	1387057... 1387695d	67.3	Maleylpyruvate isomerase	212/212	100	<i>Cupriavidus necator</i> U2	KAI3589278.1
				212/212	100	<i>Burkholderia</i> sp. BC1	APP18121.1
<i>nagM</i>	1387791... 1388783d	59.2	Unknown	330/282	100	<i>Cupriavidus necator</i> U2	KAI3589279.1
				330/341	100	<i>Burkholderia</i> sp. BC1	APP18122.1

^a Letters indicate coding strand: c, complementary strand; d, direct strand.

^b Number of amino acids in ULwDis3 chromosome CDS/number in the closest relative.

^c GenBank accession number of the closest relative protein.

Table S2. Similarity of predicted gene products from *GDO2* and *GDO3* clusters of *D. tsuruhatensis* ULwDis3 to selected homologs.

Gene designation	Position (bp) ^a	GC%	Proposed function	No. of amino acids, ULwDis3/relative ^b	% Amino Acid identity	Source microorganism	GeneBank accession number ^c
GDO2 cluster							
LysR	1355489..	55.9	Transcriptional regulator, LysR family	305/305	100	Cupriavidus necator U2	KAI3589245.1
	1356406c			305/305	100	Comamonas testosteroni YAZ2	BCX54896.1
				305/339	100	Burkholderia multivorans BC00014	MBJ9658604.1
P450	1356541..	62.4	Biotin biosynthesis cytochrome P450	412/412	99.8	Cupriavidus necator U2	KAI3589246.1
	1357779d			412/412	100	Comamonas testosteroni YAZ2	BCX54897.1
				412/412	100	Burkholderia multivorans DDS 15A-1	AIO76613.1
FRD	1357787..	65.7	Ferredoxin reductase	412/412	100	Cupriavidus necator U2	KAI3589247.1
	1359025d			412/396	99.8	Xenophilus azovorans DSM 13620	WP_211260262.1
				412/412	100	Comamonas testosteroni YAZ2	BCX54898.1
FER	1359044..	58.9	Ferredoxin	105/106	100	Cupriavidus necator U2	KAI3589248.1
	1359364d			105/105	100	Comamonas testosteroni YAZ2	BCX54899.1
FPH2	1359375..	62.5	Fumarylpyruvate hydrolase	289/289	100	Cupriavidus necator U2	KAI3589249.1
	1360244d			289/286	75.1	Variovorax paradoxus	QFZ85153.1
				289/289	92.4	P. naphthalenivorans CJ2	ABM37779.1
GDO2	1360241..	62.5	Gentisate 1,2-dioxygenase	358/358	100	Cupriavidus necator U2	KAI3589250.1
	1361317d			358/328	99.7	Comamonas thiooxydans JC8	NZ_AWOS01000062
				358/351	78.5	Paraburkholderia phytofirmans OLGA172	ANB74996.1
GDO3 cluster							
MPI3	3685200..	70.7	Maleylpyruvate isomerase	213/213	99.5	Delftia sp. HK171	TQL81322.1
	3685841c			213/213	79.8	Variovorax sp. HW608	SCK13974.1

				213/214	87.7	<i>Comamonas</i> sp. AG1104	RDI10688.1
				213/212	72.3	<i>P. naphthalenivorans</i> CJ2	ABM38445.1
<i>FPH3</i>	3685861.. 3686568c	65.9	Fumarylpyru- vate hydrolase	235/235	89.7	<i>Acidovorax</i> sp. ST3	WP_110958765.1
				235/245	100	<i>Delftia lacustris</i> HQS1	BDE71824.1
				235/235	88.9	<i>Comamonas</i> sp. Tr-654	NIF82459.1
				235/235	82.1	<i>P. naphthalenivorans</i> CJ2	ABM38444.1
<i>GDO3</i>	3686607.. 3687644c	70.4	Gentisate 1,2- dioxygenase	345/345	84.1	<i>Acidovorax</i> sp. CCYZU-2555	MBS7781544.1
				345/345	99.1	<i>Delftia</i> sp. CH05	MXN31744.1
				345/351	73.9	<i>P. naphthalenivorans</i> CJ2	ABM38443.1
<i>3HBM</i>	3687661.. 3688869c	69.5	3- hydroxybenzoat e 6-hydroxylase	402/402	99.6	<i>Delftia</i> sp. CH05	MXN31745.1
				402/402	91.1	<i>Acidovorax</i> sp. KKS102	AFU46209.1
				402/402	99.5	<i>Delftia tsuruhatensis</i> TR1180	QFS65584.1
				402/400	78.6	<i>P. naphthalenivorans</i> CJ2	ABM38442.1
<i>marR</i>	3689074.. 3689610d	69.3	Transcriptional regulator, MarR family	178/178	97.1	<i>Delftia acidovorans</i> FDAARGOS_909	QPS09337.1
				178/182	80.3	<i>Comamonas</i> sp. AG1104	RDI10685.1
				178/178	98.9	<i>Delftia tsuruhatensis</i> TR1180	QFS65583.1
				178/161	50.4	<i>P. naphthalenivorans</i> CJ2	ABM38441.1

^a Letters indicate coding strand: c, complementary strand; d, direct strand.

^b Number of amino acids in ULwDis3 chromosome CDS/number in the closest relative.

^c GenBank accession number of the closest relative protein.

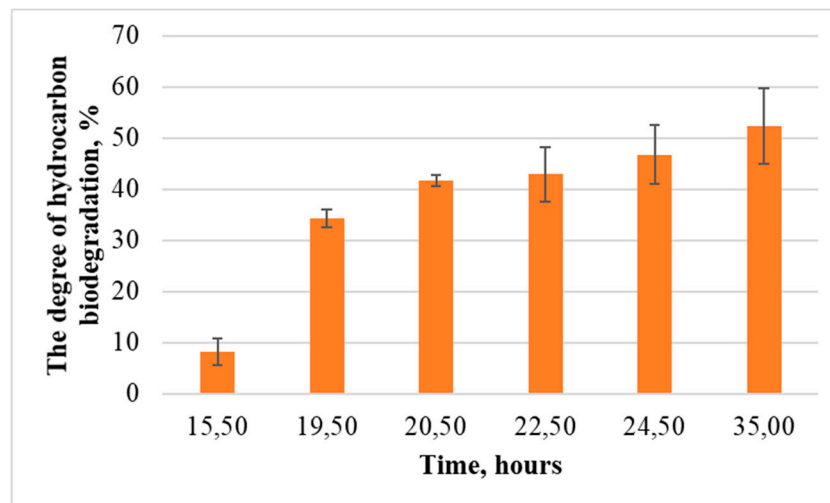


Figure S4. Dynamics of naphthalene degradation during cultivation of the strain during the experiment

Table S3. Growth adaptation phase of *Delftia tsuruhatensis* strain ULwDis 3 in liquid mineral medium with different concentrations of salicylate

Salicylate concentration, g/l	Adaptation growth phase, hours
0,3	23
0,4	40
0,5	55
0,6	80
0,8	174