

Table S1. The overall genome similarities (%) between *G. entanii* strains calculated by orthologous average nucleotide identity algorithm (OrthoANI).

	<i>G. entanii</i> AV429	<i>G. entanii</i> FXV2	<i>G. entanii</i> KS542	<i>G. entanii</i> KS544	<i>G. entanii</i> KS545	<i>G. entanii</i> SI2084
<i>G. entanii</i> AV429	/	98.60	98.34	98.31	98.32	98.33
<i>G. entanii</i> FXV2	98.60	/	98.50	98.51	98.52	98.48
<i>G. entanii</i> KS542	98.34	98.50	/	100.00	99.99	99.99
<i>G. entanii</i> KS544	98.31	98.51	100.00	/	99.99	99.98
<i>G. entanii</i> KS545	98.32	98.52	99.99	99.99	/	99.99
<i>G. entanii</i> SI2084	98.33	98.48	99.99	99.98	99.99	/

Table S2. *In silico* DNA-DNA hybridization analysis between genomes of *G. entanii* strains. The similarities were calculated by the Genome-to-Genome Distance Calculator 2.1.

	<i>G. entanii</i> AV429 (%)	<i>G. entanii</i> SI2084 (%)	<i>G. entanii</i> KS545 (%)	<i>G. entanii</i> KS544 (%)	<i>G. entanii</i> KS542 (%)	<i>G. entanii</i> FXV2 (%)
<i>G. entanii</i> AV429	100.0					
<i>G. entanii</i> SI2084	77.5	100.0				
<i>G. entanii</i> KS545	77.8	99.7	100.0			
<i>G. entanii</i> KS544	77.6	99.9	99.9	100.0		
<i>G. entanii</i> KS542	77.7	99.9	99.9	100.0	100.0	
<i>G. entanii</i> FXV2	88.4	78.9	78.3	79.2	79.2	100.0

Table S3. Distribution of different Rep proteins from *Novacetimonas*, *Komagataeibacter*, and *Acetobacter* plasmids in genomes of *Gluconacetobacter entanii* strains.

Plasmid (Acc. No.)	Rep protein (Acc. No.)	<i>G. entanii</i> LTH4560 ^T	<i>G. entanii</i> AV429	<i>G. entanii</i> SI2084	<i>G. entanii</i> FXV2
CP062148	QOF96883.1	+	+	+	-
AJ223503	CAA11421.1	+	+	-	-
AP012160	BAK85968.1	+	+	+	+
AP012161	BAK85224.1	+	+	+	-
AP012162	BAK85302.1	+	+	+	+
CP019877	AQU89268.1	+	+	+	-
CP019878	AQU89325.1	+	+	+	+
CP019879	AQU89344.1	+	+	+	+
CP023037	AXY23809.1	-	-	+	-
CP023038 (type 1)	AXY24020.1	-	-	+	-
CP023038 (type 2)	AXY24036.1	+	-	-	-
CP023039	AXY24109.1	+	-	-	-
CP023040	AXY24276.1	+	-	-	-
CM018731	KAB8122177.1	+	-	-	-
LT575494	SAY50089.1	-	-	+	-
CP004361	AHI27136.1	+	-	-	-
CP004362	AHI27138.1	+	+	-	-
CP004363	AHI27167.1	+	-	-	-
CP004364	AHI27256.1	+	+	+	+
CP039845	QHM90155.1	-	-	-	-
LN606601	CEF43042.1	+	+	+	+
CP043507 (type 1)	QEO18808.1	+	-	-	-
CP011123	ANA15375.1	+	+	+	+
LN609303 (type 1)	CEF57342.1	+	-	-	-
LN609304	CEF57494.1	+	+	+	+
AP018516 (type 1)	BBC81753.1	+	-	-	-
CP014688	AQT06463.1	+	-	-	-
CP030873	AXC27928.1	+	+	+	+
CP023190	AXN01876.1	+	-	-	-
AP023412	BCK77757.1	+	+	+	+

CP021925	ASC07527.1	+	+	+	+
CP015169 (type 1)	AOW50630.1	+	+	+	+
AP011122 (type 1)	BAI00816.1	+	-	-	-
AP011124	BAI01161.1	+	+	+	+
AP014882 (type 1)	BAU39745.1	+	-	-	-
AP014885	BAU39956.1	+	-	-	-
HF677572	CCT61022.1	+	+	+	-
HF677573	CCT61029.1	+	+	+	+
HF677576	CCT61057.1	+	-	-	-
Sum of Rep proteins		35	20	21	14

Table S4. KOs overrepresented in the *G. entanii* species group when compared to all other *Novacetimonas* species. Values in the table correspond to median gene/KO copy number values.

ID	<i>G. entanii</i> (n=9)	<i>Novacetimonas</i> spp. (n=15)	difference	Definition
K03496	6	2	4	parA, soj; chromosome partitioning protein
K00135	8	5	3	gabD; succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.79 1.2.1.20]
K03497	6	3	3	parB, spo0J; ParB family transcriptional regulator, chromosome partitioning protein
K03530	6	3	3	hupB; DNA-binding protein HU-beta
K01153	3	1	2	hsdR; type I restriction enzyme, R subunit [EC:3.1.21.3]
K04763	4	2	2	xerD; integrase/recombinase XerD
K18201	2	0	2	AGPHD1; hydroxylysine kinase [EC:2.7.1.81]
K22616	2	0	2	olsC; ornithine lipid ester-linked acyl 2-hydroxylase [EC:1.14.11.58]
K00064	1	0	1	E1.1.1.122; D-threo-aldose 1-dehydrogenase [EC:1.1.1.122]
K00077	2	1	1	panE, apbA; 2-dehydropantoate 2-reductase [EC:1.1.1.169]
K00111	2	1	1	glpA, glpD; glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]
K00146	1	0	1	feaB, tynC; phenylacetaldehyde dehydrogenase [EC:1.2.1.39]
K00151	1	0	1	hpaE, hpcC; 5-carboxymethyl-2-hydroxymuconic-semialdehyde dehydrogenase [EC:1.2.1.60]
K00154	1	0	1	E1.2.1.68; coniferyl-aldehyde dehydrogenase [EC:1.2.1.68]
K00156	1	0	1	poxB; pyruvate dehydrogenase (quinone) [EC:1.2.5.1]

K00330	2	1	1	nuoA; NADH-quinone oxidoreductase subunit A [EC:7.1.1.2]
K00331	2	1	1	nuoB; NADH-quinone oxidoreductase subunit B [EC:7.1.1.2]
K00334	2	1	1	nuoE; NADH-quinone oxidoreductase subunit E [EC:7.1.1.2]
K00335	2	1	1	nuoF; NADH-quinone oxidoreductase subunit F [EC:7.1.1.2]
K00336	2	1	1	nuoG; NADH-quinone oxidoreductase subunit G [EC:7.1.1.2]
K00337	2	1	1	nuoH; NADH-quinone oxidoreductase subunit H [EC:7.1.1.2]
K00339	2	1	1	nuoJ; NADH-quinone oxidoreductase subunit J [EC:7.1.1.2]
K00340	2	1	1	nuoK; NADH-quinone oxidoreductase subunit K [EC:7.1.1.2]
K00341	2	1	1	nuoL; NADH-quinone oxidoreductase subunit L [EC:7.1.1.2]
K00342	2	1	1	nuoM; NADH-quinone oxidoreductase subunit M [EC:7.1.1.2]
K00343	2	1	1	nuoN; NADH-quinone oxidoreductase subunit N [EC:7.1.1.2]
K00344	3	2	1	qor, CRYZ; NADPH:quinone reductase [EC:1.6.5.5]
K00433	1	0	1	cpo; non-heme chloroperoxidase [EC:1.11.1.10]
K00446	1	0	1	dmpB, xylE; catechol 2,3-dioxygenase [EC:1.13.11.2]
K00483	1	0	1	hpaB; 4-hydroxyphenylacetate 3-monooxygenase [EC:1.14.14.9]
K00549	2	1	1	metE; 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase [EC:2.1.1.14]
K00558	1	0	1	DNMT1, dcm; DNA (cytosine-5)-methyltransferase 1 [EC:2.1.1.37]
K00782	2	1	1	lIdG; L-lactate dehydrogenase complex protein lIdG
K00839	2	1	1	pucG; (S)-ureidoglycine---glyoxylate transaminase [EC:2.6.1.112]
K00864	2	1	1	glpK, GK; glycerol kinase [EC:2.7.1.30]
K01092	3	2	1	E3.1.3.25, IMPA, suhB; myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]
K01322	1	0	1	PREP; prolyl oligopeptidase [EC:3.4.21.26]
K01568	2	1	1	PDC, pdc; pyruvate decarboxylase [EC:4.1.1.1]
K01689	2	1	1	ENO, eno; enolase [EC:4.2.1.11]
K01703	2	1	1	leuC, IPMI-L; 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]
K01826	1	0	1	hpaF, hpcD; 5-carboxymethyl-2-hydroxymuconate isomerase [EC:5.3.3.10]
K01961	3	2	1	accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
K01971	1	0	1	ligD; bifunctional non-homologous end joining protein LigD [EC:6.5.1.1]
K02013	4	3	1	ABC.FEV.A; iron complex transport system ATP-binding protein [EC:7.2.2.-]
K02015	4	3	1	ABC.FEV.P; iron complex transport system permease protein
K02016	4	3	1	ABC.FEV.S; iron complex transport system substrate-binding protein
K02160	3	2	1	accB, bccP; acetyl-CoA carboxylase biotin carboxyl carrier protein

K02232	2	1	1	cobQ, cbiP; adenosylcobyrinic acid synthase [EC:6.3.5.10]
K02274	2	1	1	coxA, ctaD; cytochrome c oxidase subunit I [EC:7.1.1.9]
K02275	1	0	1	coxB, ctaC; cytochrome c oxidase subunit II [EC:7.1.1.9]
K02276	1	0	1	coxC, ctaE; cytochrome c oxidase subunit III [EC:7.1.1.9]
K02440	2	1	1	GLPF; glycerol uptake facilitator protein
K02509	1	0	1	hpaH; 2-oxo-hept-3-ene-1,7-dioate hydratase [EC:4.2.1.-]
K02510	1	0	1	hpaI, hpcH; 4-hydroxy-2-oxoheptanedioate aldolase [EC:4.1.2.52]
K03111	2	1	1	ssb; single-strand DNA-binding protein
K03299	5	4	1	TC.GNTP; gluconate:H ⁺ symporter, GntP family
K03442	1	0	1	mscS; small conductance mechanosensitive channel
K03559	3	2	1	exbD; biopolymer transport protein ExbD
K03561	3	2	1	exbB; biopolymer transport protein ExbB
K03762	1	0	1	proP; MFS transporter, MHS family, proline/betaine transporter
K03777	2	1	1	dld; D-lactate dehydrogenase (quinone) [EC:1.1.5.12]
K03832	3	2	1	tonB; periplasmic protein TonB
K04047	1	0	1	dps; starvation-inducible DNA-binding protein
K05343	1	0	1	treS; maltose alpha-D-glucosyltransferase / alpha-amylase [EC:5.4.99.16 3.2.1.1]
K05349	3	2	1	bgIX; beta-glucosidase [EC:3.2.1.21]
K05595	2	1	1	marC; multiple antibiotic resistance protein
K05896	3	2	1	scpA; segregation and condensation protein A
K06199	1	0	1	crcB, FEX; fluoride exporter
K07126	2	1	1	K07126; uncharacterized protein
K07152	3	2	1	SCO1; protein SCO1
K07160	2	1	1	pxpA; 5-oxoprolinase (ATP-hydrolysing) subunit A [EC:3.5.2.9]
K07221	2	1	1	oprO_P; phosphate-selective porin OprO and OprP
K07452	1	0	1	mcrB; 5-methylcytosine-specific restriction enzyme B [EC:3.1.21.-]
K07484	1	0	1	K07484; transposase
K07488	1	0	1	K07488; transposase
K07507	1	0	1	mgtC; putative Mg ²⁺ transporter-C (MgtC) family protein
K07789	3	2	1	mdtC; multidrug efflux pump
K08309	3	2	1	slt; soluble lytic murein transglycosylase [EC:4.2.2.-]
K08995	2	1	1	K08995; putative membrane protein

K09024	3	2	1	rutF; flavin reductase [EC:1.5.1.-]
K10680	2	1	1	nemA; N-ethylmaleimide reductase [EC:1.-.-.]
K10947	1	0	1	padR; PadR family transcriptional regulator, regulatory protein PadR
K12203	1	0	1	dotB, traJ; defect in organelle trafficking protein DotB [EC:7.2.4.8]
K12204	1	0	1	dotC, traI; defect in organelle trafficking protein DotC
K12217	1	0	1	icmO, trbC, dotL; intracellular multiplication protein IcmO [EC:7.2.4.8]
K12218	1	0	1	icmP, trbA; intracellular multiplication protein IcmP
K13993	1	0	1	HSP20; HSP20 family protein
K16092	2	1	1	btuB; vitamin B12 transporter
K16147	1	0	1	glgE; starch synthase (maltosyl-transferring) [EC:2.4.99.16]
K18843	1	0	1	hicB; antitoxin HicB
K18928	2	1	1	lldE; L-lactate dehydrogenase complex protein LldE
K18929	2	1	1	lldF; L-lactate dehydrogenase complex protein LldF
K18954	1	0	1	pobR; AraC family transcriptional regulator, transcriptional activator of pobA
K19147	1	0	1	mcrC; 5-methylcytosine-specific restriction enzyme subunit McrC
K19837	1	0	1	atzE; 1-carboxybiuret hydrolase [EC:3.5.1.131]
K21495	1	0	1	fitA; antitoxin FitA
K22473	2	1	1	adhA; alcohol dehydrogenase (quinone), dehydrogenase subunit [EC:1.1.5.5]
K22895	4	3	1	cruH; renierapurpurin 18,18'-hydroxylase
K23124	2	1	1	pxpC; 5-oxoprolinase (ATP-hydrolysing) subunit C [EC:3.5.2.9]

Table S5. KOs underrepresented in the *G. entanii* species when compared to all other *Novacetimonas* species. Values in the table correspond to median gene/KO copy number values.

ID	<i>G. entanii</i> (n=9)	<i>Novacetimonas</i> spp. (n=15)	Difference	Definition
K02014	24	29	-5	TC.FEV.OM; iron complex outermembrane receptor protein
K00059	3	5	-2	fabG, OAR1; 3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]
K02433	2	4	-2	gatA, QRSL1; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit A [EC:6.3.5.6 6.3.5.7]
K13771	3	5	-2	nsrR; Rrf2 family transcriptional regulator, nitric oxide-sensitive transcriptional repressor
K00027	1	2	-1	ME2, sfcA, maeA; malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]

K00117	2	3	-1	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
K00459	1	2	-1	ncd2, npd; nitronate monooxygenase [EC:1.13.12.16]
K00694	2	3	-1	bcsA; cellulose synthase (UDP-forming) [EC:2.4.1.12]
K00799	3	4	-1	GST, gst; glutathione S-transferase [EC:2.5.1.18]
K00820	1	2	-1	glms, GFPT; glutamine---fructose-6-phosphate transaminase (isomerizing) [EC:2.6.1.16]
K01114	1	2	-1	plc; phospholipase C [EC:3.1.4.3]
K01214	1	2	-1	ISA, treX; isoamylase [EC:3.2.1.68]
K01465	2	3	-1	URA4, pyrC; dihydroorotase [EC:3.5.2.3]
K01652	2	3	-1	E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
K01714	1	2	-1	dapA; 4-hydroxy-tetrahydrodipicolinate synthase [EC:4.3.3.7]
K01733	1	2	-1	thrC; threonine synthase [EC:4.2.3.1]
K02483	5	6	-1	K02483; two-component system, OmpR family, response regulator
K03307	2	3	-1	TC.SSS; solute:Na ⁺ symporter, SSS family
K03457	1	2	-1	TC.NCS1; nucleobase:cation symporter-1, NCS1 family
K03466	1	2	-1	ftsK, spoIIIE; DNA segregation ATPase FtsK/SpoIIIE, S-DNA-T family
K03566	1	2	-1	gcvA; LysR family transcriptional regulator, glycine cleavage system transcriptional activator
K03585	1	2	-1	acrA, mexA, adel, smeD, mtrC, cmeA; membrane fusion protein, multidrug efflux system
K04091	1	2	-1	ssuD, msuD; alkanesulfonate monooxygenase [EC:1.14.14.5 1.14.14.34]
K06221	1	2	-1	dkgA; 2,5-diketo-D-gluconate reductase A [EC:1.1.1.346]
K07552	2	3	-1	bcr, tcaB; MFS transporter, DHA1 family, multidrug resistance protein
K12373	2	3	-1	HEXA_B; hexosaminidase [EC:3.2.1.52]
K15553	2	3	-1	ssuA; sulfonate transport system substrate-binding protein
K15554	2	3	-1	ssuC; sulfonate transport system permease protein
K15555	2	3	-1	ssuB; sulfonate transport system ATP-binding protein [EC:7.6.2.14]
K18903	1	2	-1	oprC, opcM; outer membrane protein, multidrug efflux system
K22474	2	3	-1	adhB; alcohol dehydrogenase (quinone), cytochrome c subunit [EC:1.1.5.5]
K22736	1	2	-1	VIT; vacuolar iron transporter family protein

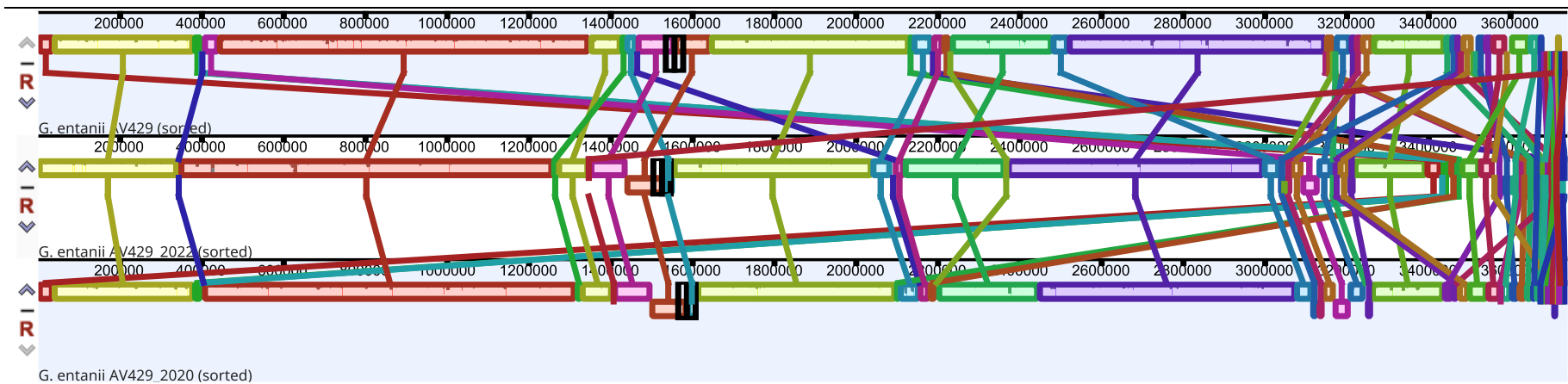


Figure S1. Aligned draft bacterial genomes of *G. entanii* AV429, *G. entanii* AV429-2020 and *G. entanii* AV429-2022 by Mauve. Each of the draft genome sequences was at the beginning aligned to a reference chromosome sequence *Novacetimonas hansenii* C110 (acc. no. CP062147). The matches are partitioned into a minimum set of collinear blocks. Each sequence of identically colored blocks represents a collinear set of matching regions. One connecting line is drawn per collinear block.