

Supplementary table 1: SRA samples assembled and screened for *Wolbachia*. Highlighted by blue = positive screening resulting in new strains described in this study. Highlighted by grey = weak positive screening, not included into this study.

SRA sample	Source	Sub-order/Family	Vertebrate host	strain
SRR5308125	<i>Heterodoxus spiniger</i>	Amblycera/Boopidae	<i>Canis lupus</i>	
SRR5308130	<i>Macrogypus costalimai</i>	Amblycera/Gyropidae	<i>Cuniculus paca</i>	
SRR5308127	<i>Laemobothrion tinnunculi</i>	Amblycera/Laemobothriidae	<i>Falco longipennis</i>	
SRR5088470	<i>Osborniella crotophagae</i>	Amblycera/Menoponidae	<i>Crotophaga ani</i>	
SRR5308132	<i>Myrsidea</i> sp.	Amblycera/Menoponidae	<i>Myiothlypis luteoviridis</i>	
SRR8145978	<i>Menopon gallinae</i>	Amblycera/Menoponidae	<i>Gallus gallus</i>	
SRR8334265	<i>Meromenopon meropis</i>	Amblycera/Menoponidae	<i>Merops apiaster</i>	w Mmer
SRR5308140	<i>Ricinus</i> sp.	Amblycera/Ricinidae	<i>Myiothlypis luteoviridis</i>	
SRR5308146	<i>Cummingsia maculata</i>	Amblycera/Trimenoponidae	<i>Lestoros inca</i>	
SRR5088466	<i>Bothriometopus macrocnemis</i>	Ischnocera/Philopteridae	<i>Chauna torquata</i>	
SRR5308110	<i>Alcedoecus</i> sp.	Ischnocera/Philopteridae	<i>Halcyon badia</i>	w Alce
SRR5308111	<i>Anatoecus icterodes</i>	Ischnocera/Philopteridae	<i>Anas cyanoptera</i>	
SRR5308112	<i>Brueelia antiqua</i>	Ischnocera/Philopteridae	<i>Catharus ustulatus</i>	
SRR5308113	<i>Campanulotes compar</i>	Ischnocera/Philopteridae	<i>Columba livia</i>	
SRR5308114	<i>Chelopistes texanus</i>	Ischnocera/Philopteridae	<i>Ortalis vetula</i>	
SRR5308115	<i>Columbicola columbae</i>	Ischnocera/Philopteridae	<i>Columba livia</i>	
SRR5308116	<i>Craspedonirmus immer</i>	Ischnocera/Philopteridae	<i>Gavia immer</i>	
SRR5308117	<i>Docophoroides brevis</i>	Ischnocera/Philopteridae	<i>Diomedea exulans</i>	
SRR5308118	<i>Falcolipeurus marginalis</i>	Ischnocera/Philopteridae	<i>Cathartes aura</i>	
SRR5308119	<i>Fulicoffula longipila</i>	Ischnocera/Philopteridae	<i>Fulica americana</i>	
SRR5308120	<i>Goniodes ortygis</i>	Ischnocera/Philopteridae	<i>Colinus virginianus</i>	
SRR5308124	<i>Halipeurus diversus</i>	Ischnocera/Philopteridae	<i>Puffinus tenuirostris</i>	
SRR5308126	<i>Ibidoecus bisignatus</i>	Ischnocera/Philopteridae	<i>Plegadis chihi</i>	
SRR5308131	<i>Megaginus tataupensis</i>	Ischnocera/Philopteridae	<i>Crypturellus tataupa</i>	
SRR5308133	<i>Osculotes curta</i>	Ischnocera/Philopteridae	<i>Opisthocomus hoazin</i>	
SRR5308134	<i>Oxylipurus chiniri</i>	Ischnocera/Philopteridae	<i>Ortalis vetula</i>	
SRR5308135	<i>Pectinopygus varius</i>	Ischnocera/Philopteridae	<i>Phalacrocorax varius</i>	
SRR5308137	<i>Penenirmus auritus</i>	Ischnocera/Philopteridae	<i>Sphyrapicus varius</i>	w Paur
SRR5308139	<i>Quadriceps punctatus</i>	Ischnocera/Philopteridae	<i>Larus argentatus</i>	
SRR5308141	<i>Saemundssonina lari</i>	Ischnocera/Philopteridae	<i>Larus novaehollandiae</i>	
SRR5308142	<i>Strongylocotes lipogonus</i>	Ischnocera/Philopteridae	<i>Rhynchotus rufescens</i>	
SRR5308144	<i>Trichophlopterus babakotophilus</i>	Ischnocera/Philopteridae	<i>Propithecus verreauxi</i>	
SRR5308145	<i>Pessoaiella absita</i>	Ischnocera/Philopteridae	<i>Opisthocomus hoazin</i>	
SRR1821919	<i>Geomydoecus ewingi</i>	Ischnocera/Trichodectidae	not provided	
SRR5308121	<i>Geomydoecus aurei</i>	Ischnocera/Trichodectidae	<i>Thomomys bottae</i>	
SRR5308143	<i>Stachiella larseni</i>	Ischnocera/Trichodectidae	<i>Mustela vison</i>	

Supplementary Table 2: Busco evaluation of the genome's completeness; high level of duplication in wAlce highlighted by grey background.

Rickettsia database

wMeur1

C:85.7%[S:85.7%,D:0.0%],F:0.3%,M:14.0%,n:364

312 Complete BUSCOs (C)
312 Complete and single-copy BUSCOs (S)
0 Complete and duplicated BUSCOs (D)
1 Fragmented BUSCOs (F)
51 Missing BUSCOs (M)

364 Total BUSCO groups searched

wMmer

C:91.8%[S:91.8%,D:0.0%],F:0.3%,M:7.9%,n:364

334 Complete BUSCOs (C)
334 Complete and single-copy BUSCOs (S)
0 Complete and duplicated BUSCOs (D)
1 Fragmented BUSCOs (F)
29 Missing BUSCOs (M)

364 Total BUSCO groups searched

wMeur2

C:98.6%[S:98.6%,D:0.0%],F:0.3%,M:1.1%,n:364

359 Complete BUSCOs (C)
359 Complete and single-copy BUSCOs (S)
0 Complete and duplicated BUSCOs (D)
1 Fragmented BUSCOs (F)
4 Missing BUSCOs (M)

364 Total BUSCO groups searched

wPaur

C:97.0%[S:97.0%,D:0.0%],F:1.9%,M:1.1%,n:364

353 Complete BUSCOs (C)
353 Complete and single-copy BUSCOs (S)
0 Complete and duplicated BUSCOs (D)
7 Fragmented BUSCOs (F)
4 Missing BUSCOs (M)

364 Total BUSCO groups searched

wAlce

C:97.3%[S:61.0%,D:36.3%],F:2.2%,M:0.5%,n:364

354 Complete BUSCOs (C)
222 Complete and single-copy BUSCOs (S)
132 Complete and duplicated BUSCOs (D)
8 Fragmented BUSCOs (F)
2 Missing BUSCOs (M)

364 Total BUSCO groups searched

Proteobacteria database

wMeur1

C:68.5%[S:68.5%,D:0.0%],F:2.3%,M:29.2%,n:219

150 Complete BUSCOs (C)
150 Complete and single-copy BUSCOs (S)
0 Complete and duplicated BUSCOs (D)
5 Fragmented BUSCOs (F)
64 Missing BUSCOs (M)

219 Total BUSCO groups searched

wMmer

C:73.5%[S:73.5%,D:0.0%],F:2.3%,M:24.2%,n:219

161 Complete BUSCOs (C)
161 Complete and single-copy BUSCOs (S)
0 Complete and duplicated BUSCOs (D)
5 Fragmented BUSCOs (F)
53 Missing BUSCOs (M)

219 Total BUSCO groups searched

wMeur2

C:83.1%[S:83.1%,D:0.0%],F:1.8%,M:15.1%,n:219

182 Complete BUSCOs (C)
182 Complete and single-copy BUSCOs (S)
0 Complete and duplicated BUSCOs (D)
4 Fragmented BUSCOs (F)
33 Missing BUSCOs (M)

219 Total BUSCO groups searched

wPaur

C:82.2%[S:81.7%,D:0.5%],F:2.7%,M:15.1%,n:219

180 Complete BUSCOs (C)
179 Complete and single-copy BUSCOs (S)
1 Complete and duplicated BUSCOs (D)
6 Fragmented BUSCOs (F)
33 Missing BUSCOs (M)

219 Total BUSCO groups searched

wAlce

C:79.9%[S:51.1%,D:28.8%],F:4.6%,M:15.5%,n:219

175 Complete BUSCOs (C)
112 Complete and single-copy BUSCOs (S)
63 Complete and duplicated BUSCOs (D)
10 Fragmented BUSCOs (F)
34 Missing BUSCOs (M)

219 Total BUSCO groups searched

Supplementary table 3: Accession numbers of the sequences used in phylogenetic and comparative analyses. Blue background = new strains from chewing lice. Green background = taxa included into the phylogenetic analyses (2 gene = fbpA_coxA matrix, multigene = multigene matrix). SG = supergroup.
 * = assembly done in this study based on the SRA data. MLST = genes retrieved from pubMLST database (see methods).

						Accession number				
						NCBI			MLST	
2 gene	multi gene	Host species	Host taxon	Abbrev.	SG	SRA*/genome assembly	fbpA	coxA	fbpA	coxA
		Alcedoecus sp.	louse	w Alce	F	SRR5308110*/JAJEUA000000000	-	-	-	-
		Menacanthus eurysternus	louse	w Meur1	F	PRJNA768995*/CP085695	-	-	-	-
		Menacanthus eurysternus	louse	w Meur2	F	PRJNA768995*/JAJDJY000000000	-	-	-	-
		Meromenopon meropis	louse	w Mmer	F	SRR8334265*/JAJETZ000000000	-	-	-	-
		Penenirmus auritus	louse	w Paur	F	SRR5308137*/ JAJEUB000000000	-	-	-	-
		Acisoma panorpoides panorpoides	dragonfly		F		KC915265	KC915236	-	-
		Amblyomma americanum	tick		F		HM061163	HM061159	-	-
		Anax guttatus	dragonfly		F		KC915285	KC915256	-	-
		Apilitermes longiceps	termites		F		EF417907	EF417914	-	-
		Apoica sp.	wasp		F		EU126428	EU126210	-	-
		Armadillidium vulgare	carpenter bug	w VulC	B	ALWU000000000	-	-	-	-
		Atemnus politus	pseudoscorpion	w APoIK3	S	JAAXS000000000	-	-	-	-
		Atemnus politus	pseudoscorpion	w APoIK5	S	WQMQ000000000	-	-	-	-
		Brachythemis contaminata	dragonfly		F		KC915280	KC915250	-	-
		Brugia malayi	filarial nematode	w Bm	D	NC_006833	-	-	-	-
		Carposina sasakii	moth	w CauA	A	NZ_CP041215	-	-	-	-
		Cavitermes tuberosus	termites		F		MF953231	MF953228	-	-
		Chorthippus parallelus	grasshopper		F		JN698879	JN698878	-	-
		Chrysocoris stollis	jewel bugs		F		-	-	410	226
		Cimex hemipterus	bed bug	w Chem	T	NZ_CP061738	-	-	-	-
		Cimex lectularius	bed bug	w Cle	F	NZ_AP013028	-	-	-	-
		Cimex lectularius	bed bug	w Cle	F		DQ842349	DQ842275	-	-
		Cruorifilaria tubero cauda	filarial nematode	w Ctub	J	CP046579	-	-	-	-
		Ctenocephalides felis	flea	w CfeJ		NZ_CP051157	-	-	-	-
		Ctenocephalides felis	flea	w CfeT		NZ_CP051156	-	-	-	-
		Culex quinquefasciatus	mosquito	w Pip	B	NC_010981	-	-	-	-
		Dipetalonema caudispina	filarial nematode	w Dcau	J	CP046580	-	-	-	-
		Diplacodes trivialis	dragonfly		F		KC915276	KC915246	-	-
		Drosophila melanogaster	fly	w Mel	A	NC_002978	-	-	-	-
		Drosophila simulans	fly	w Ri	A	NC_012416	-	-	-	-
		Drosophila simulans	fly	w No	B	NC_021084	-	-	-	-
		Epophthalmia vittata	dragonfly		F		KC915284	KC915255	-	-
		Folsomia candida	springtail	w Fol	E	NZ_CP015510	-	-	-	-
		Icosta sp.	fly		F		MF461509	MF461499	-	-
		Ictinogomphus rapax	dragonfly		F		KC915282	KC915252	-	-
		Laodelphax striatellus	planthopper	w Stri	B	MUIX000000000	-	-	-	-
		Madathamugadia hiepei	filarial nematode	w Mhi	F	NZ_WQMP000000000	-	-	-	-
		Madathamugadia hiepei	filarial nematode	w Mhi	F		JQ888342	JQ888307	-	-
		Mansonella (Cutifilaria) perforata	filarial nematode		F		KU255337	KU255278	-	-
		Melophagus ovinus	fly	w Melo	F	CACREU02	-	-	-	-
		Mengenilla moldrzyki	Strepsiptera	w Men	F	SRX095325*				
		Nasutitermes ephratae	termites		F		KX036780	KX024837	-	-
		Nasutitermes itapocuensis	termites		F		KX036782	KX024839	-	-
		Nasutitermes jaraguae	termites		F		KX036784	KX024841	-	-
		Neotroponiscus carolii	Terrestrial isopods		F		KX036778	KX024835	-	-
		Neotroponiscus littoralis	Terrestrial isopods		F		KX036776	KX024833	-	-
		Nesobasis recava	damselflies		F		MH291053	MH290892	-	-
		Nesobasis telegastrum	damselflies		F		MH291048	MH290890	-	-
		Neurothemis tullia	dragonfly		F		KC915283	KC915254	-	-
		Nilaparvata lugens	planthopper	w Lug	B	MUIY010000000	-	-	-	-
		Nomada flava	bee	w Nfla	A	NZ_LYUW000000000	-	-	-	-
		Nycteribia kolenatii	fly		F		MF461503	MF461494	-	-
		Ocymyrmex picardi	ant		F		EU127822	EU127606	-	-
		Odontotermes horni	termites		F		GQ422843	GQ422835	-	-
		Odontotermes sp.	termites		F		GQ422844	GQ422836	-	-
		Onchocerca ochengi	filarial nematode	w Oo	C	NC_018267	-	-	-	-
		Onchocerca volvulus	filarial nematode	w Ov	C	NZ_HG810405	-	-	-	-
		Opisthophthalmus capensis	scorpions		F		-	-		31 30
		Opisthophthalmus granifrons	scorpions		F		-	-		33 31
		Opisthophthalmus litoralis	scorpions		F		-	-	57	56
		Orthetrum glaucum	dragonfly		F		KC915286	KC915257	-	-
		Osmia caerulescens	bee	w Oc	F	SRR1221705*	KP265901	-	-	-
		Paratrechina longicornis	ant		F		-	-	226	147
		Pratylenchus penetrans	lesion nematodes	w Ppe	L	MJMG010000000	-	-	-	-
		Procornitermes araujoi	termites		F		KX036785	KX024842	-	-
		Procornitermes lespesii	termites		F		KX036786	KX024843	-	-
		Pseudolynchia sp.	fly		F		MF461506	MF461497	-	-
		Supella longipalpa	cockroach		F		-	-		414 147
		Teratodes monticolis	grasshopper		F		-	-		125 147
		Trichogramma pretiosum	wasp	w Tpre	B	NZ_CM003641	-	-	-	-
		Trithemis pallidinervis	dragonfly		F		KC915267	KC915237	-	-
		Wuchereria bancrofti	filarial nematode	w Wb	D	NZ_NJBR000000000	-	-	-	-
		Zelotes sp.	spider		F		-	-	475	306

Supplementary table 4: Functional annotations of genes unique for a single genome. Highlighted by blue = new chewing lice strains. The three pantothenate related genes printed in bold blue.

wMeur1
3-methyl-2-oxobutanoate_hydroxymethyltransferase__EC_2.1.2.11
Ketopantoate_reductase_PanG__EC_1.1.1.169
Pantoate--beta-alanine_ligase__EC_6.3.2.1
34 hypothetical proteins
wMmer
Uroporphyrinogen_III_decarboxylase__EC_4.1.1.37
82 hypothetical proteins
wMeur2
Proton/glutamate_symport_protein_@_Sodium/glutamate_symport_protein
14 hypothetical proteins
wPaur
GTP-binding_protein_Era
LSU_ribosomal_protein_LSp_L11e
30 hypothetical proteins
wAlce
Zinc_ABC_transporter_periplasmic-binding_protein_ZnuA
zinc_protease
Arginyl-tRNA_synthetase__EC_6.1.1.19
Malate_dehydrogenase__EC_1.1.1.37
Phospholipase/carboxylesterase_family_protein__EC_3.1.-.-
tRNA_nucleotidyltransferase__EC_2.7.7.21__EC_2.7.7.25
Phosphoribosylformylglycinamide_cyclo-ligase__EC_6.3.3.1
35 hypothetical proteins
wCle
Hydroxyethylthiazole_kinase__EC_2.7.1.50
Hydroxymethylpyrimidine_phosphate_kinase_ThiD__EC_2.7.4.7
34 hypothetical protein
wMelo
acetyltransferase__GNAT_family
3-oxoacyl-[acyl-carrier_protein]_reductase__EC_1.1.1.100
ATP_synthase_delta_chain__EC_3.6.3.14
Thioredoxin_reductase__EC_1.8.1.9
2_3_4_5-tetrahydropyridine-2_6-dicarboxylate_N-succinyltransferase__EC_2.3.1.117
Phosphate_transport_system_permease_protein_PstC_TC_3.A.1.7.1
Ferric_iron_ABC_transporter__iron-binding_protein
wMelo_-_Lysyl-tRNA_synthetase_class_I__EC_6.1.1.6
D-alanine--D-alanine_ligase__EC_6.3.2.4
DNA_polymerase_III_delta_prime_subunit__EC_2.7.7.7
Uroporphyrinogen-III_synthase__EC_4.2.1.75
rRNA_small_subunit_methyltransferase_H
41 hypothetical proteins
wMhi
Xaa-Pro_aminopeptidase__EC_3.4.11.9
34 hypothetical proteins
wOc
Glycerol-3-phosphate_dehydrogenase_[NAD_P_+]__EC_1.1.1.94
Cytochrome_bd2_subunit_I
putative_Cytochrome_bd2_subunit_II
Osmotically_inducible_protein_Y_precursor
38 hypothetical proteins

Supplementary table 5: Overview of metabolic capacities - B vitamins and amino acids

			wMeur1	wMmer	wMeur2	wPaur	wAlce	wCle	wMhi	wMelo	wOC	wCfeT	sCol	
B vitamins	Thiamine	iscS												
		adk												
		tenA												
	Riboflavin	ribA												
		ribD												
		ribB												
		ribH												
		ribF												
		ribE												
	Pyridoxine	pdxJ												
		pdxH												
	Folate	folA/DHFR												
		folB												
		folKP												
		folC												
	Biotin	bioA												
		bioB												
		bioC												
		bioD												
		bioF												
		birA												
amino acids	Pantothenate	panB												
		panG												
		panC												
		panD												
	Asparagine, Aspartate	ansA												
	Arginine	argA												
		argB												
		argC												
		argD												
		argG												
		argF (argI, OTC)												
		argJ												
		argH												
	Phenylalanine	pheA												
		aspC												
	Tryptophan	trpD												
		trpG												
		trpC												
		trpA												
		trpF												
		trpB												
	Sulphate, cysteine	cysN												
		cysD												
		cysC												
		cysH												
		cysI												
		cysJ												
		cysQ												
		cysE												
		cysK												
	Methionine	metA												
		metB												
		metC												
		metE												
	Lysine	asd												
		dapA												
		dapB												
		dapD												
		dapE												
		dapF												
		lysA												
		thrA												
	Threonine	thrB												
		thrC												
	Leucine	leuA												
		leuC												
		leuD												
		leuB												
	Glycine	glyA												
	Histidine	hisA												
		hisB												
		hisC												
		hisD												
		hisF												
		hisG												
		hisH												
		hisI												
	Serine	serC												

present absent

Supplementary table 5: Overview of metabolic capacities - secretion systems and ABC transporters

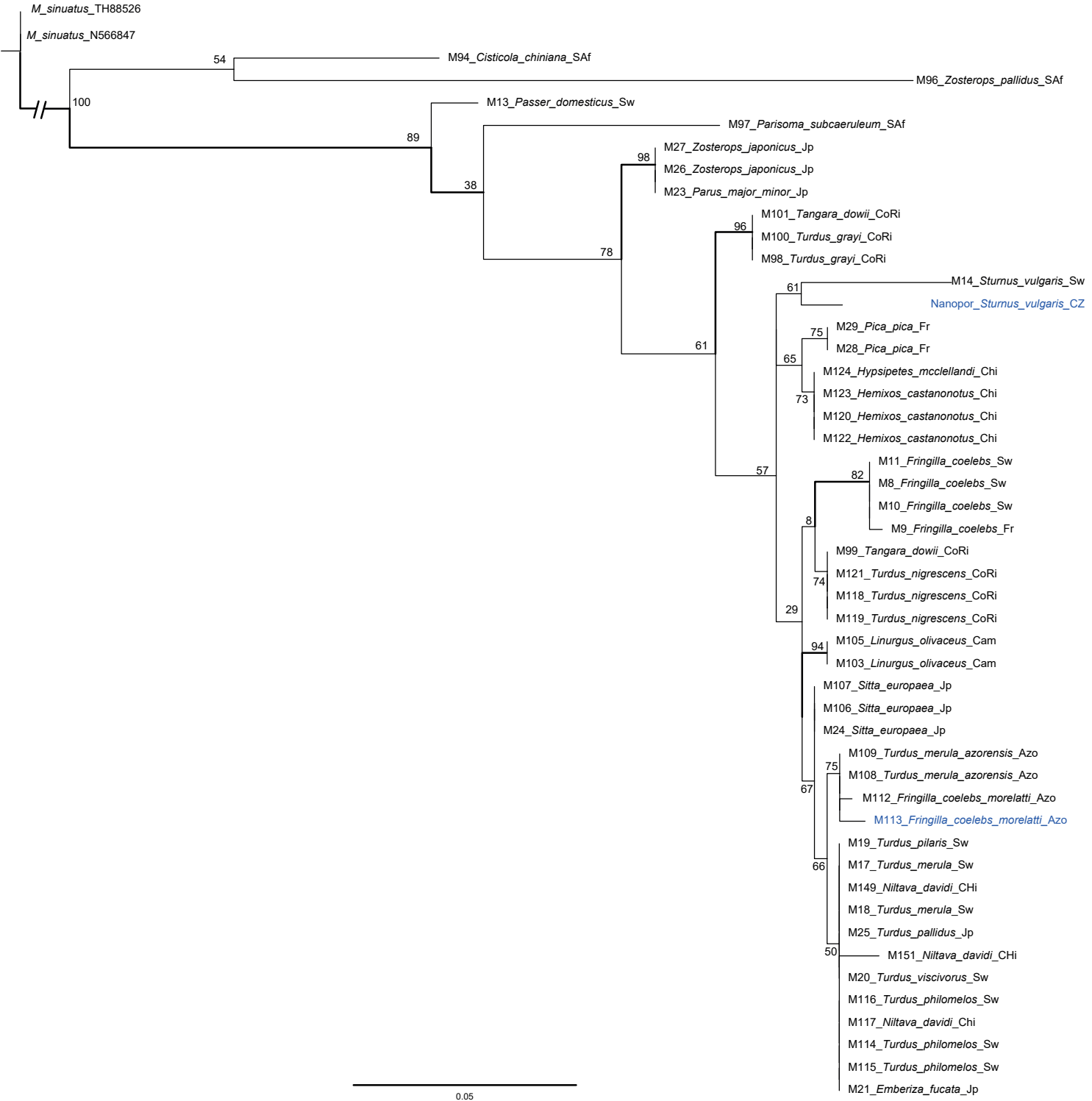
		wMeur1	wMmer	wMeur2	wPaur	wAlce	wCle	wMhi	wMelo	wOc	wCfeT	sCol
secretion system	Type I - tolC											
	Type II - gspD											
	Sec-SRP - secA											
	Sec-SRP - secB											
	Sec-SRP - secD											
	Sec-SRP - secF											
	Sec-SRP - secG											
	Sec-SRP - secY											
	Sec-SRP - YajC											
	Sec-SRP - YidC											
	Sec-SRP - ftsY											
	Sec-SRP - ffh											
	secE											
	Twin arginine targeting - Tata											
	Twin arginine targeting - TatC											
	Type IV - virB10											
	virB3											
	virB4											
	virB9											
	virB6											
	virB8											
	virB11											
	virD4											
ABC transporters	CcmA											
	CcmB											
	CcmC											
	haem exporter - PstA											
	haem exporter - PstB											
	haem exporter - PstC											
	haem exporter - PstS											
	phosphate trasport system - lolC_E											
	phosphate trasport system - lolD											
	lioprotein releasing systme - ZnuA											
	lioprotein releasing systme - ZnuB											
	lioprotein releasing systme - ZnuC											
	zinc transport system - BioY											
	biotin trasport system - AfuA											
	biotin trasport system - AfuB											
	biotin trasport system - AfuC											
	phospholipid trasport system - MlaC											
	phospholipid trasport system - MlaD											
	phospholipid trasport system - MlaE											
	phospholipid trasport system - MlaF											

present absent

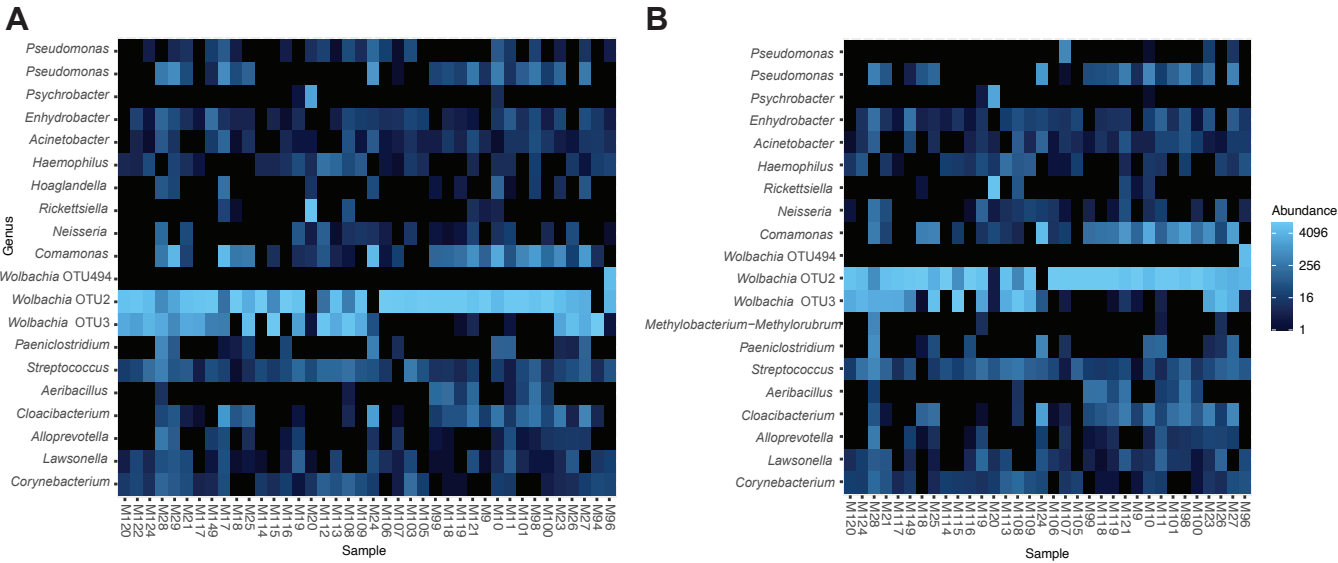
Supplementary table 5: Overview of metabolic capacities - cellular processes

[illegible]

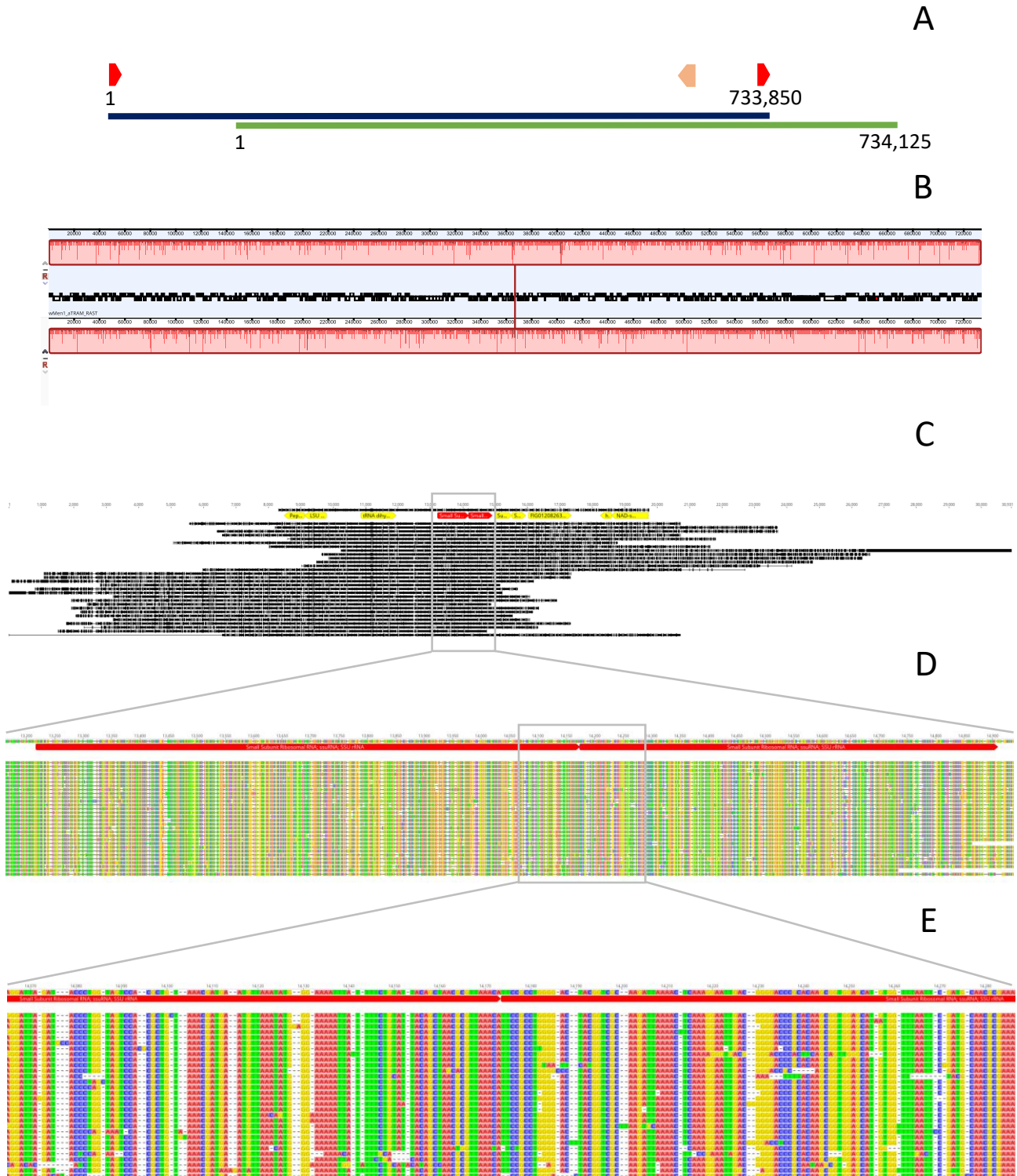
Supplementary figure 1: host phylogeny - relationships of *Menacanthus eurysternus* samples. The samples used in this study for the metagenomic assembly printed in blue.



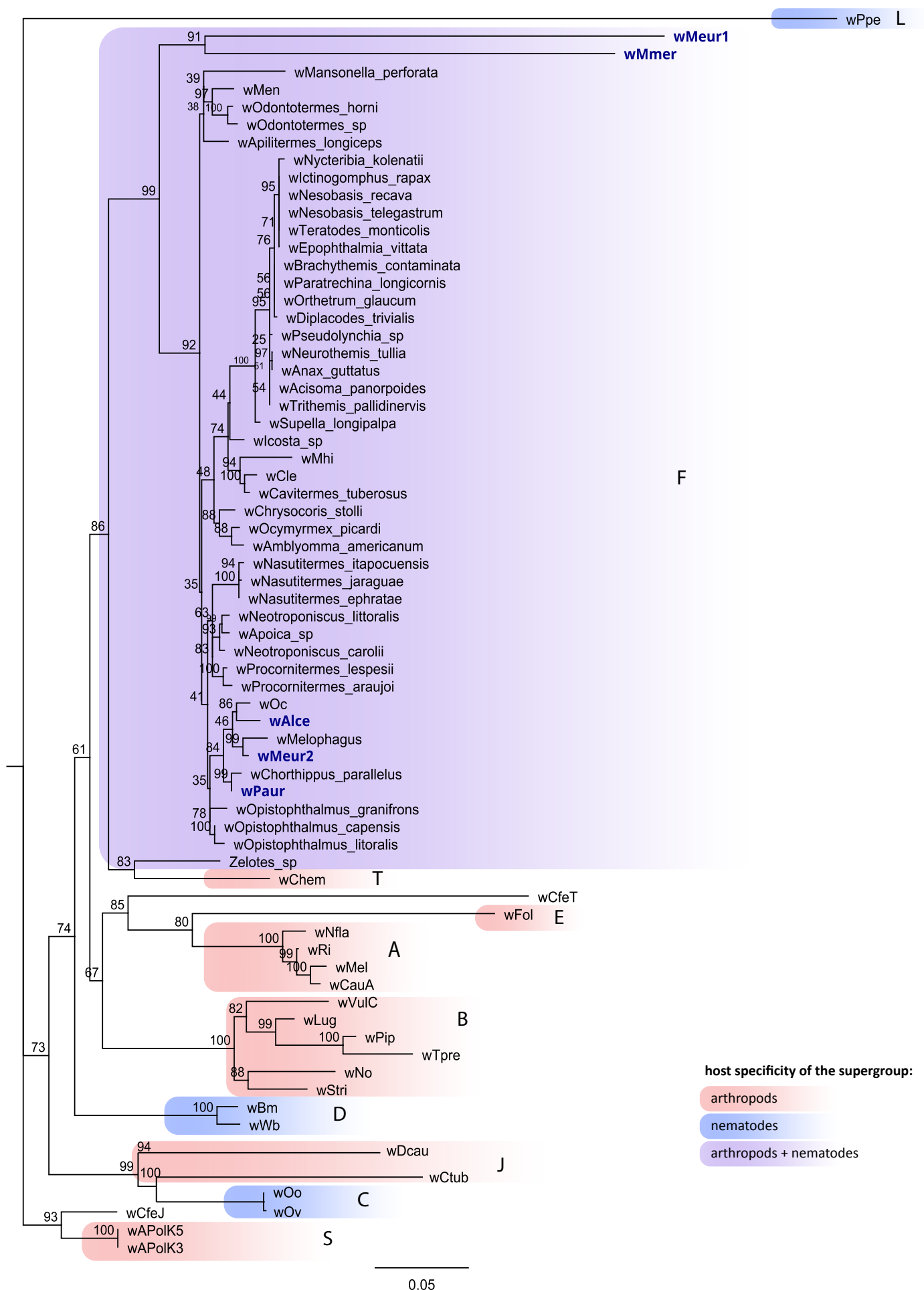
Supplementary figure 2: Compositional heat map for *M. eurysternus* microbiomes based on the strictly decontaminated 16S rRNA dataset (see Materials and Methods) rarefied at 1000 (A) and 2000 reads (B). The sample order reflects Figure 1 in the main manuscript. Additional information on the samples are found in Supplementary Data1.



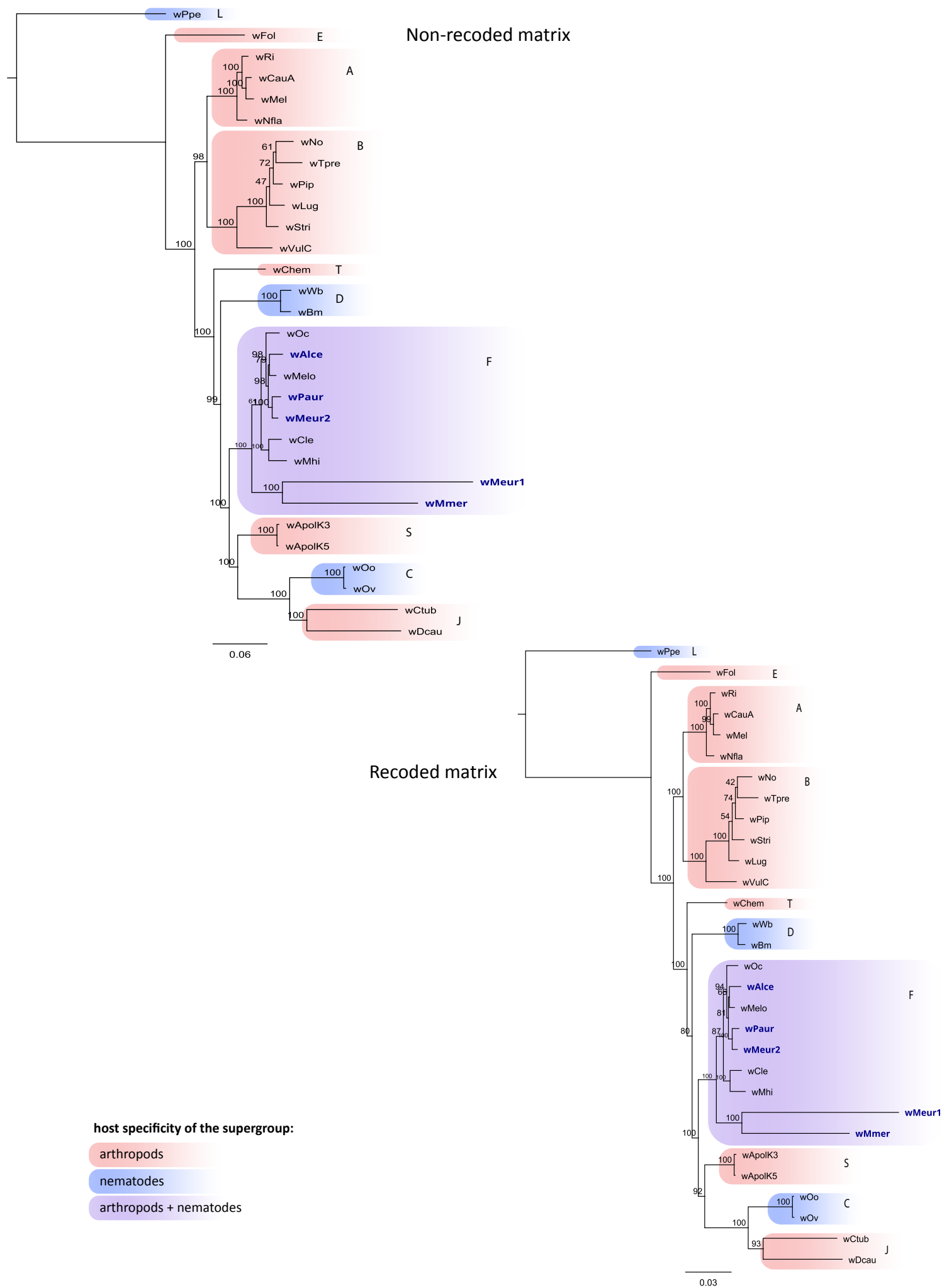
Supplementary figure 3: Genome size verification for the wMeur1 strain. A: Alignment of the genome obtained by extension of the Illumina contig with aTram/Sanger (blue) and the contig obtained by Nanopore read assembly (green). Arrowheads point to the positions of the 23S rRNA gene (pink) and two fragments of the split 16S rRNA gene (red). B: Mauve alignment of the two assemblies, Illumina-derived (top sequence) and Nanopore-derived (bottom sequence). C – E: Nanopore reads overlapping the ends of the Illumina-derived contig. The first sequence in the alignment shows concatenated 5' and 3' end of the Illumina-derived contig (10 Kb). The two fragments of 16S rRNA gene (red) correspond to the red arrowheads in A. Other 30 sequences are aligned Nanopore reads (10,988 - 19,122 bp long). Complete sequences (C) and the zoomed parts of the alignments (D,E) show that the Nanopore reads transverse the connection across several adjacent genes (yellow blocks).



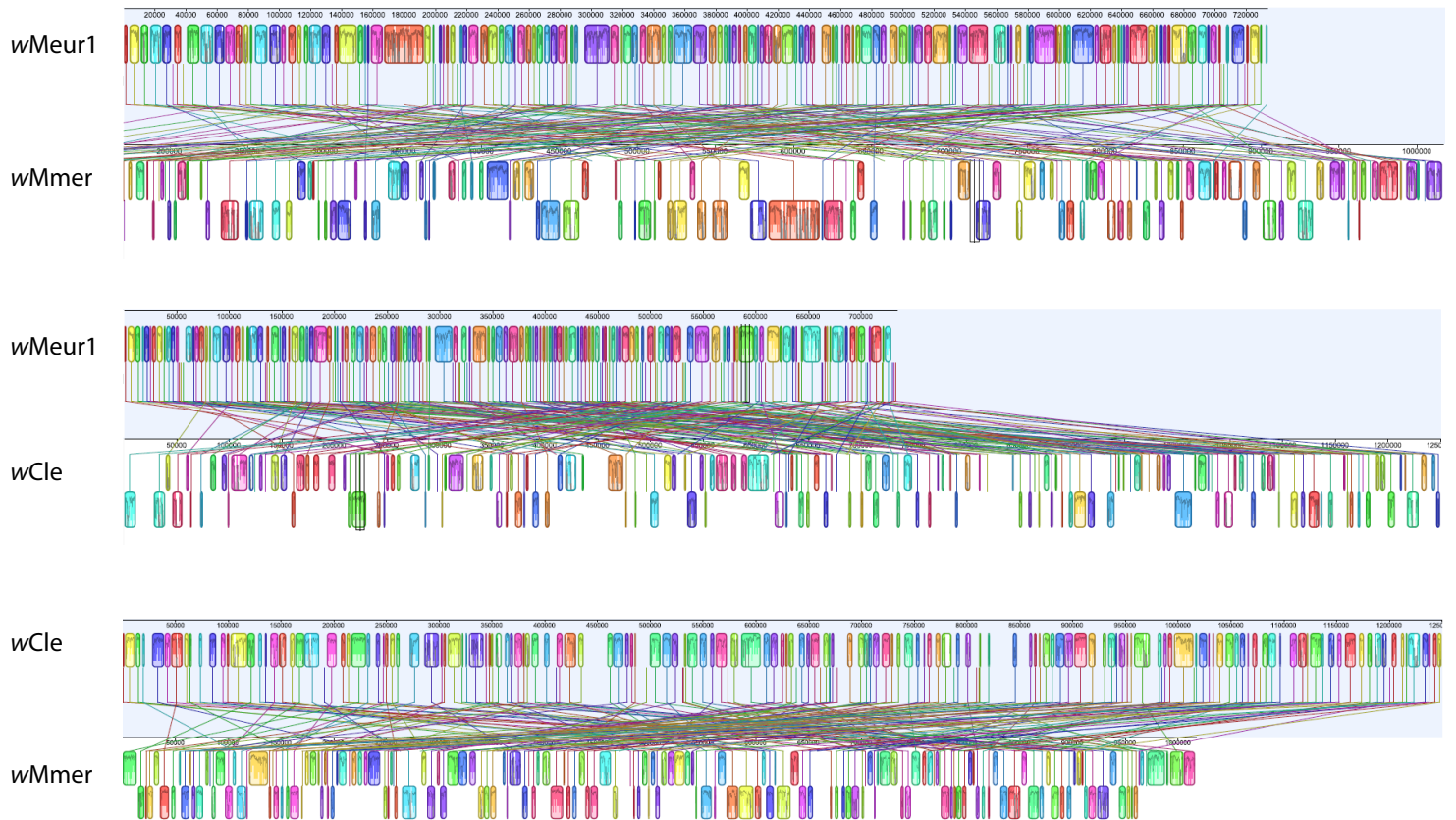
Supplementary figure 4: Phylogenetic tree derived from the two-gene matrix by IQ-TREE.
The genomes assembled in this study printed in bold blue.



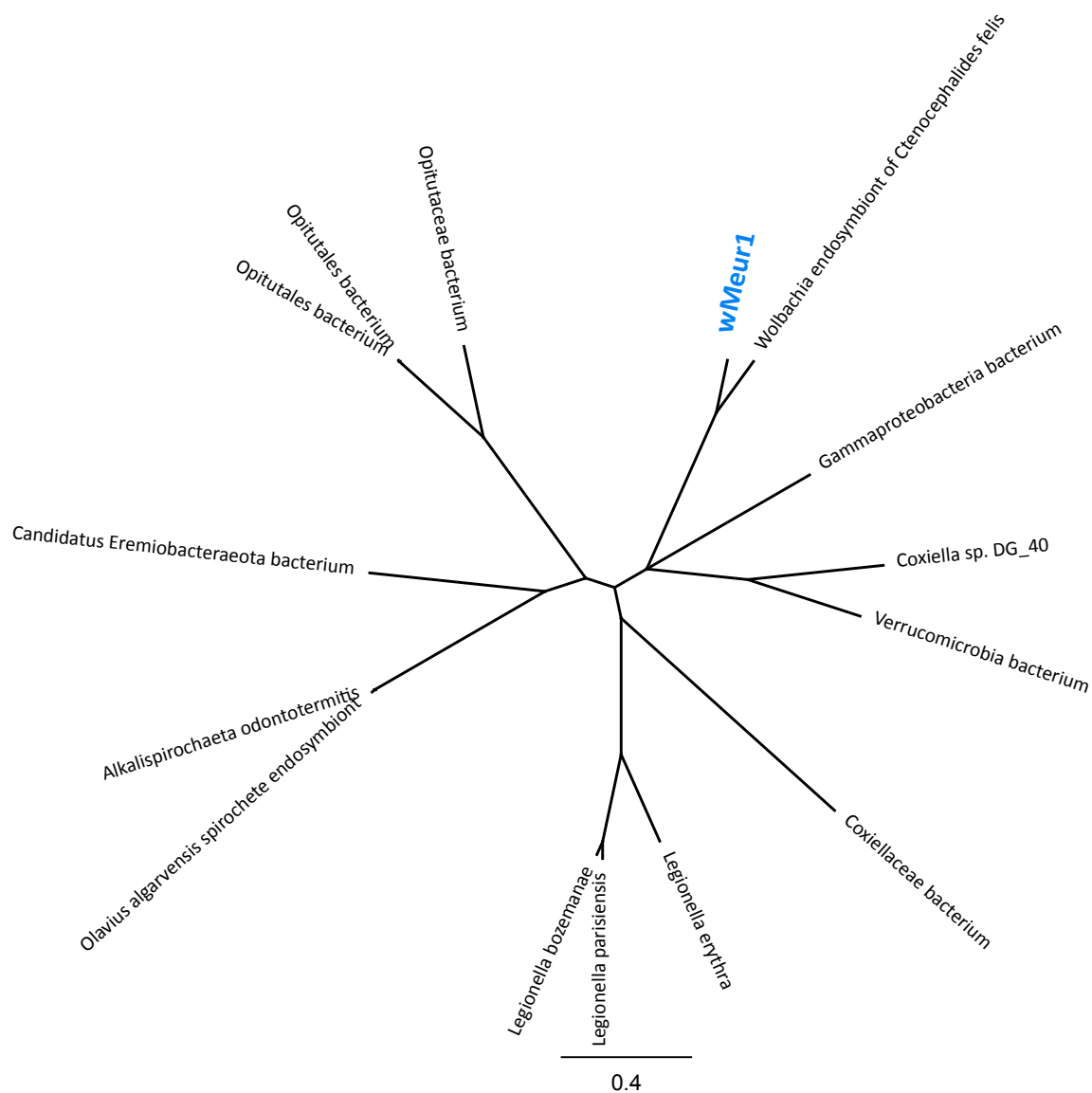
Supplementary figure 5: Phylogenetic trees derived from the multigene matrix by ML.
The genomes assembled in this study printed in bold blue.



Supplementary figure 6: Mauve synteny analysis.

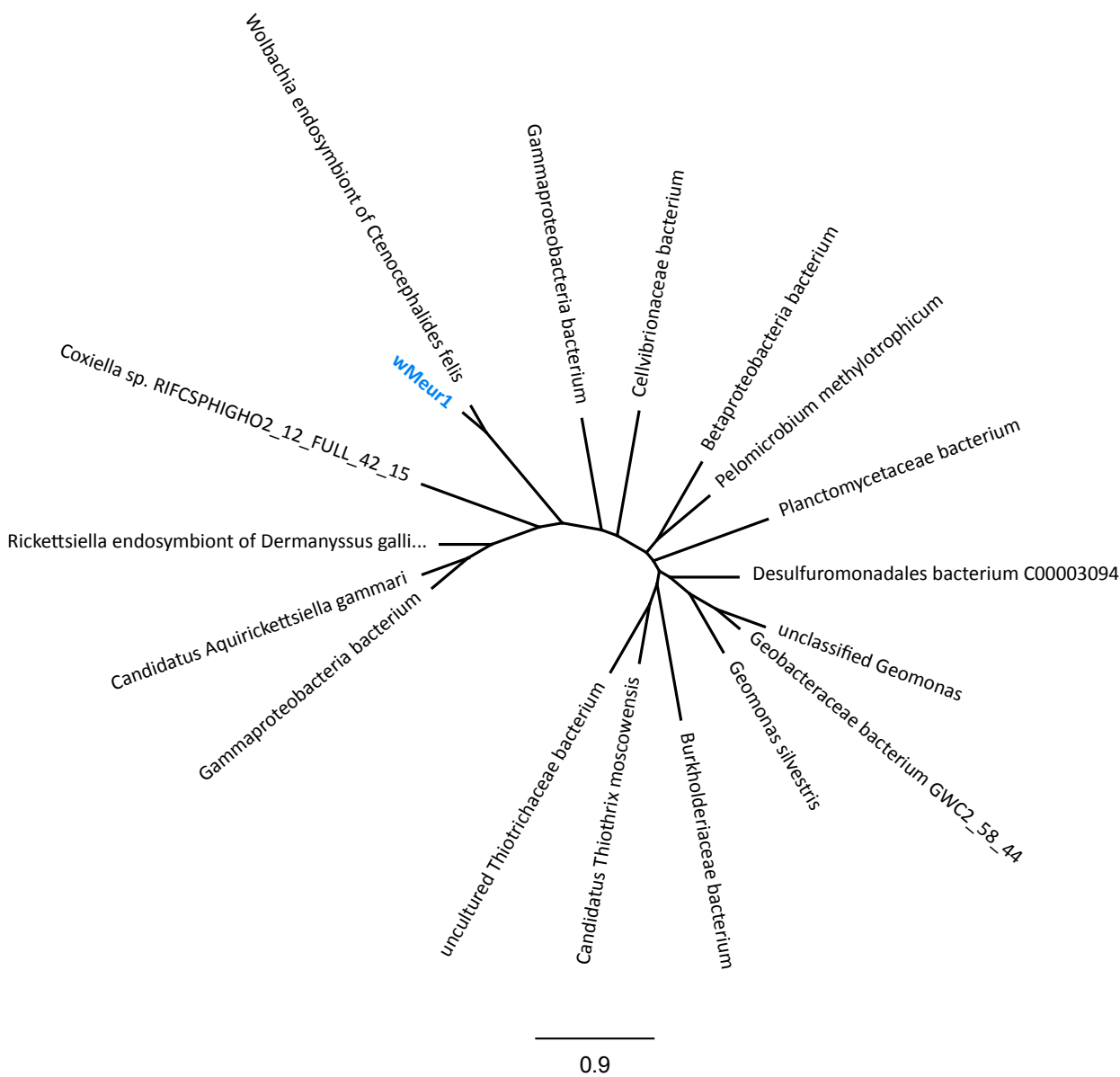


Supplementary figure 7A: Phylogenetic position of pantothenate synthesis related genes; Pantoate--beta-alanine ligase panC (EC 6.3.2.1)



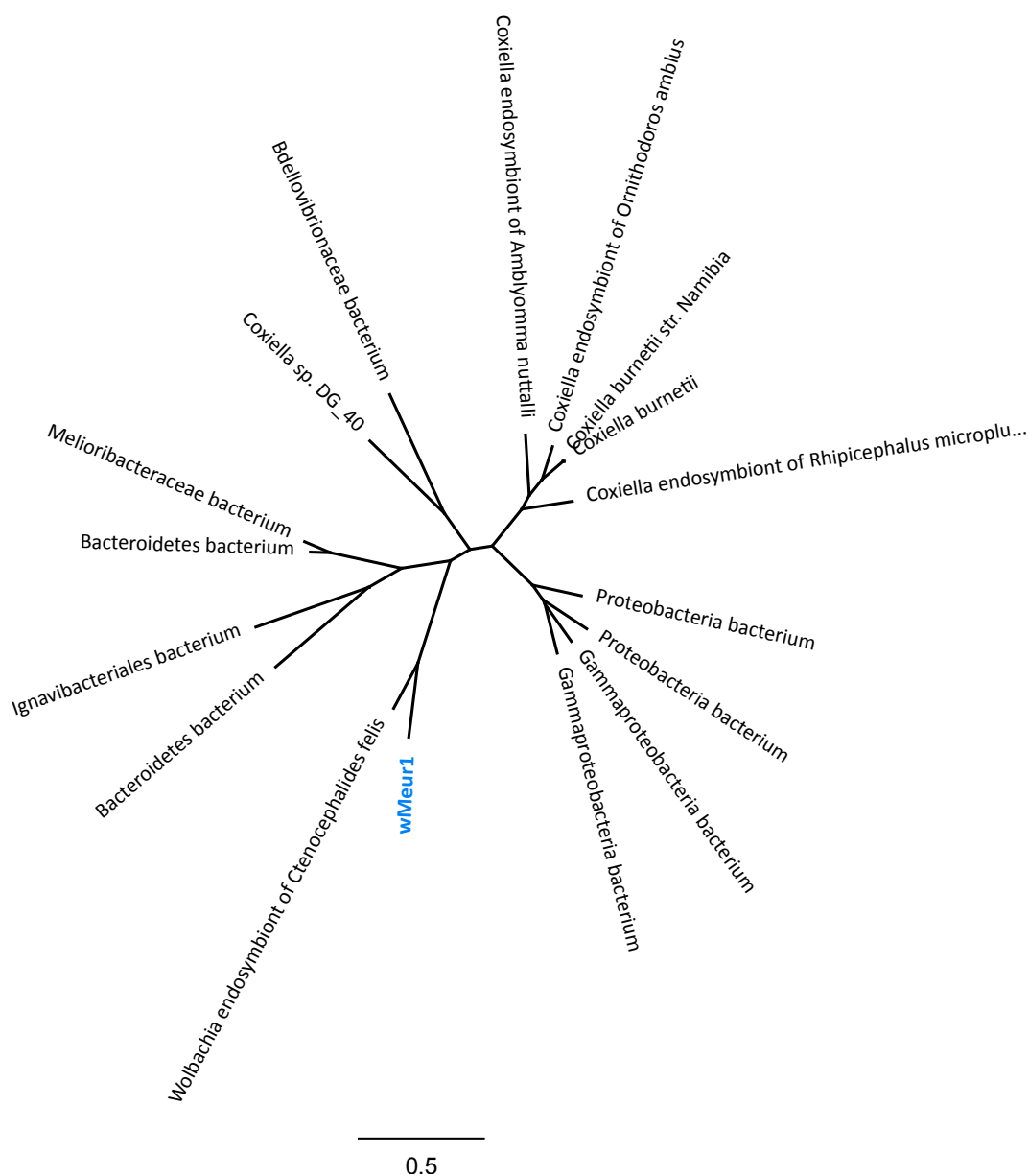
Organism	Name
Olavius algarvensis spirochete endosymbiont	WP_124032323
Alkalispirochaeta odontotermittis	WP_037564257
Candidatus Eremiobacteraeota bacterium	MBN9417370
Opitutaceae bacterium	MAM92216
Opitutales bacterium	MBT6769675
Opitutales bacterium	MBT3482533
Coxiellaceae bacterium	MBV53023
Legionella erythra	WP_058527648
Legionella parisiensis	WP_058516236
Legionella bozemaniae	WP_058458018
Wolbachia endosymbiont of Ctenocephalides felis wCfeT	WP_168464627
Gammaproteobacteria bacterium	MBI2790727
Coxiella sp. DG_40	KPJ67214
Verrucomicrobia bacterium	PWU05281

Supplementary figure 7B: Phylogenetic position of pantothenate synthesis related genes; Ketopantoate reductase PanG (EC 1.1.1.169)



Name	Accession
Gammaproteobacteria bacterium	TLY47062
Candidatus Aquirickettsiella gammari	RDH40168
Rickettsiella endosymbiont of Dermanyssus gallinae	WP_218814024
Wolbachia endosymbiont of Ctenocephalides felis wCfeT	WP_218938889
Gammaproteobacteria bacterium	HBA33227
Burkholderiaceae bacterium	MBV8634101
Cellvibrionaceae bacterium	MAZ88707
Planctomycetaceae bacterium	HID78016
Betaproteobacteria bacterium	MBI1965041
Pelomicrobium methylotrophicum	WP_147800823
Desulfuromonadales bacterium C00003094	OEU60518
uncultured Thiotrichaceae bacterium	CAA6822986
Candidatus Thiothrix moscowensis	MBJ6612093
Geomonas silvestris	WP_183355568
Geobacteraceae bacterium GWC2_58_44	OGU05969
unclassified Geomonas	WP_217289478
Coxiella sp. RIFCSPHIGHO2_12_FULL_42_15	OGO93865

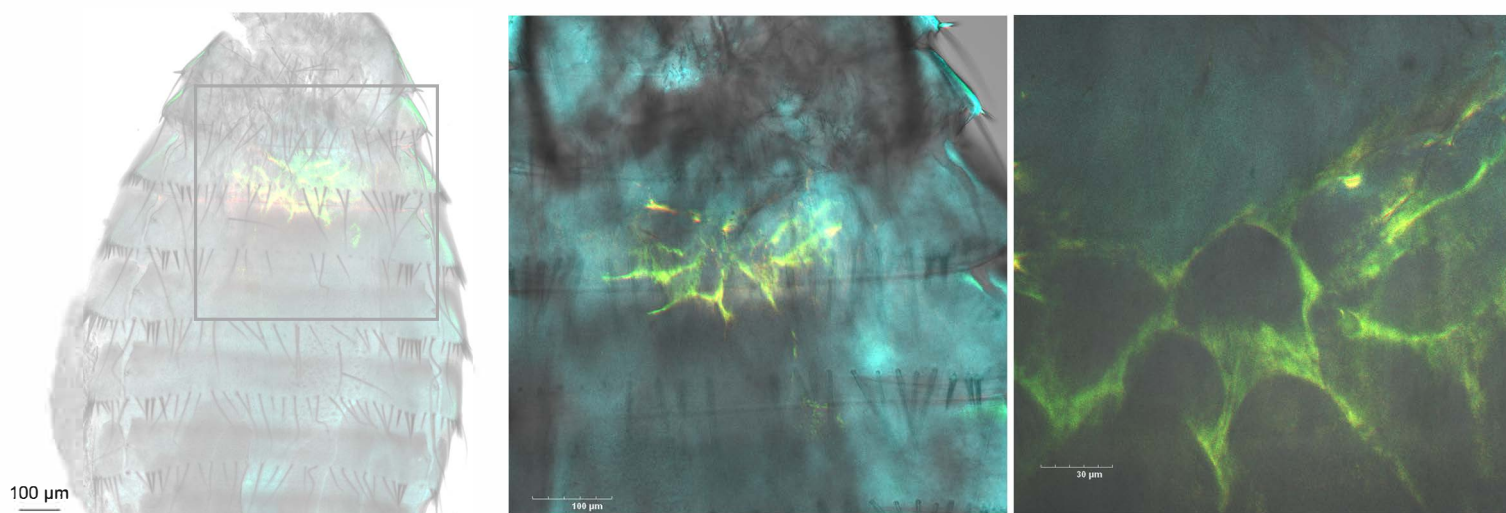
Supplementary figure 7C: Phylogenetic position of pantothenate synthesis related genes; 3-methyl-2-oxobutanoate hydroxymethyltransferase pan B (EC 2.1.2.11)



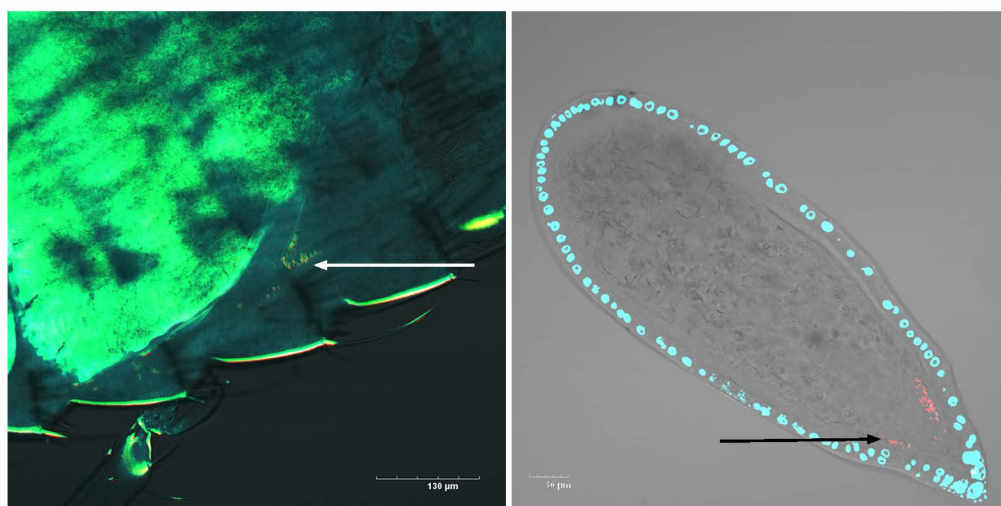
Name	Accession
Bacteroidetes bacterium	MBU0473530
Ignavibacteriales bacterium	MBN2571901
Melioribacteraceae bacterium	KAB2839543
Bacteroidetes bacterium	MBU2494347
Wolbachia endosymbiont of Ctenocephalides felis wCfeT	WP_168464630
Coxiella sp. DG_40	KPJ67213
Proteobacteria bacterium	MBS0288437
Proteobacteria bacterium	MBS0287918
Gammaproteobacteria bacterium	MBI2790726
Gammaproteobacteria bacterium	MBN9286951
Coxiella endosymbiont of Rhipicephalus microplus	WP_102157157
Coxiella endosymbiont of Amblyomma nuttalli	WP_211923626
Coxiella endosymbiont of Ornithodoros amblyus	MBW5802677
Coxiella burnetii str. Namibia	AIT63869
Coxiella burnetii	WP_080744740
Bdellovibrionaceae bacterium	MBT4762628

Supplementary figure 8: Localization of *Wolbachia* wMeur1 symbionts in female and male *M. eurysternus*. Whole mount FISH on a female individual with clusters of bacteriocytes located below the crop (A). *Wolbachia* wMeur1 symbionts located at the anterior pole of developing eggs within the female body cavity (left) and a dissected one (right). The arrows point to the *Wolbachia* wMeur1 cells (B). Whole mount FISH on a male individual with *Wolbachia* wMeur1 symbionts found in the reproductive tract (C).

A



B



C

