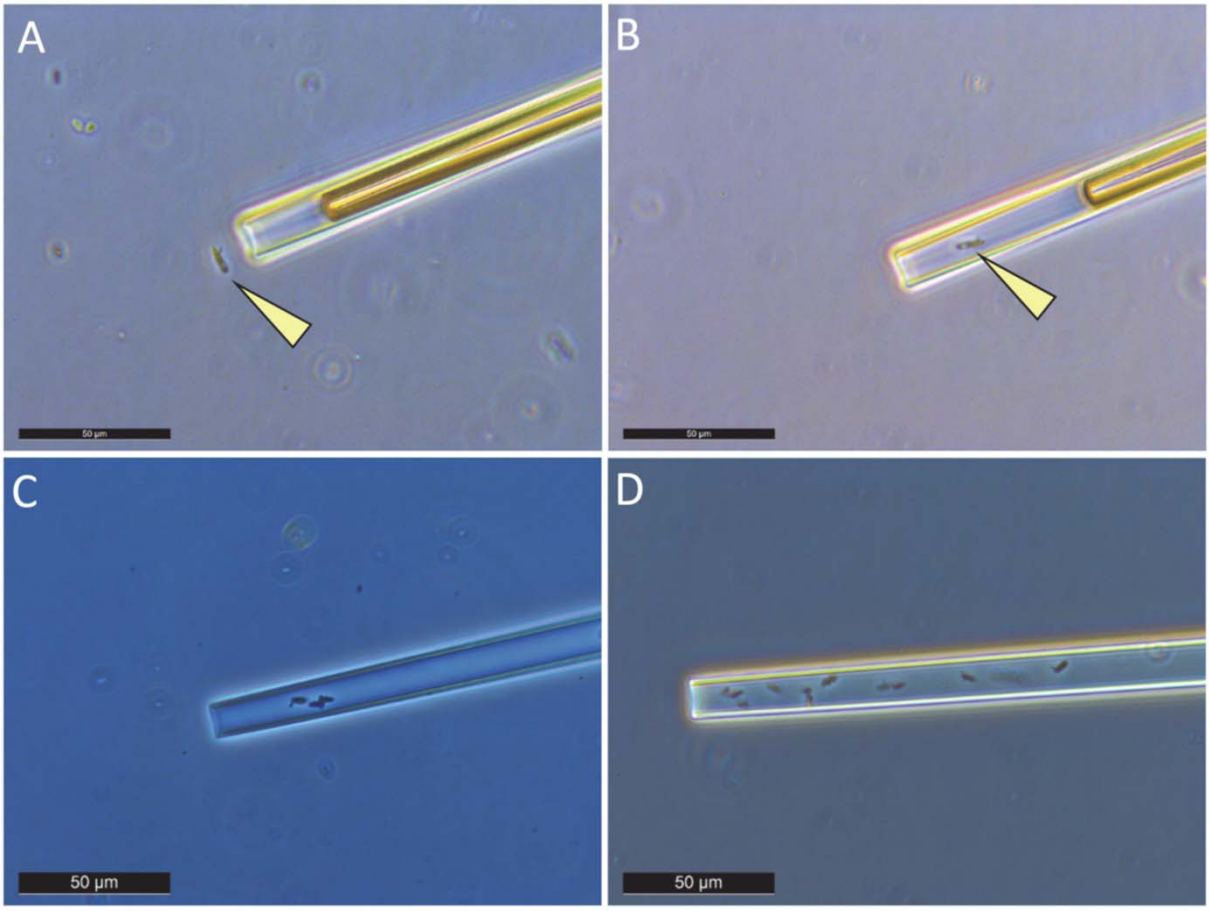
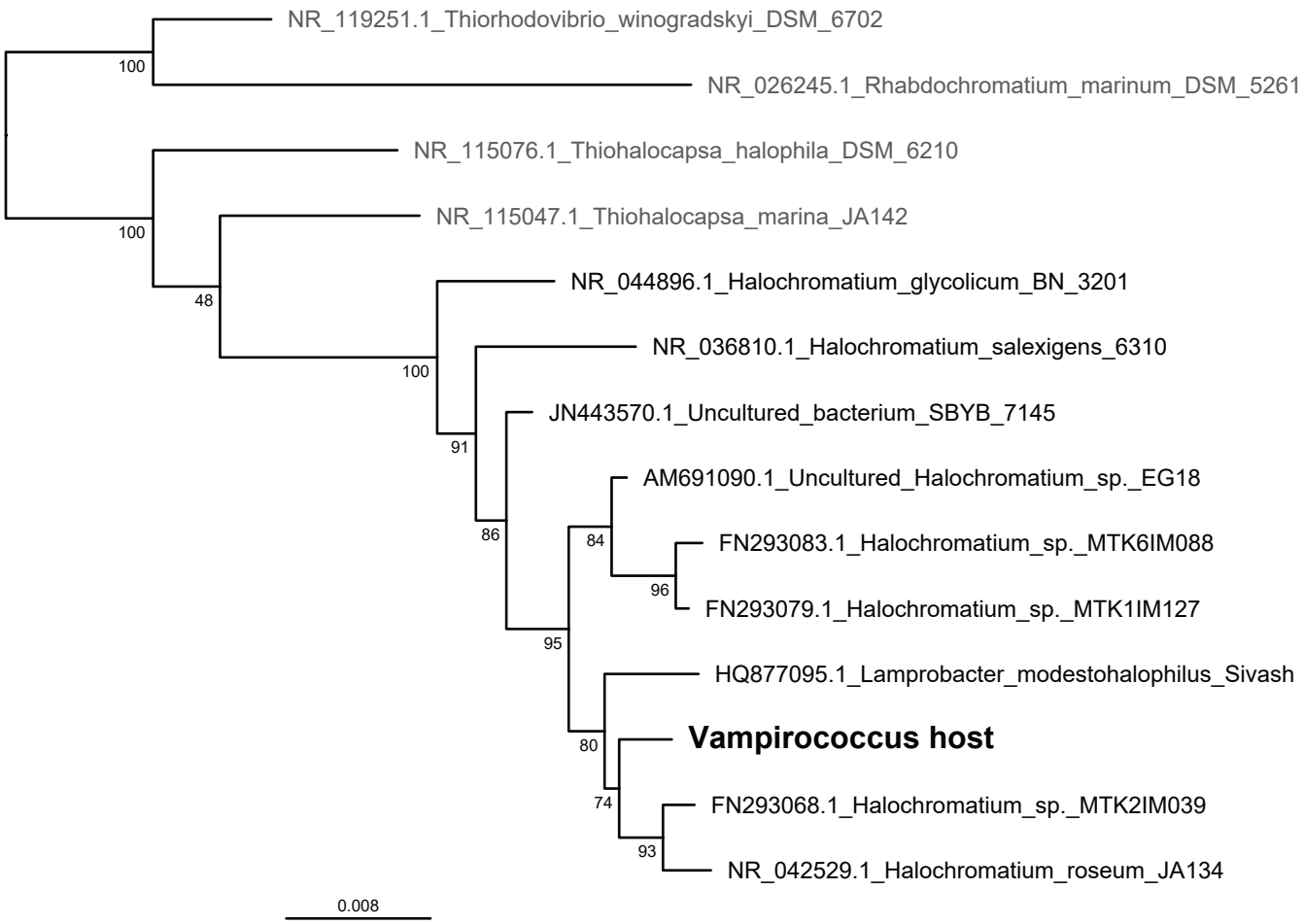
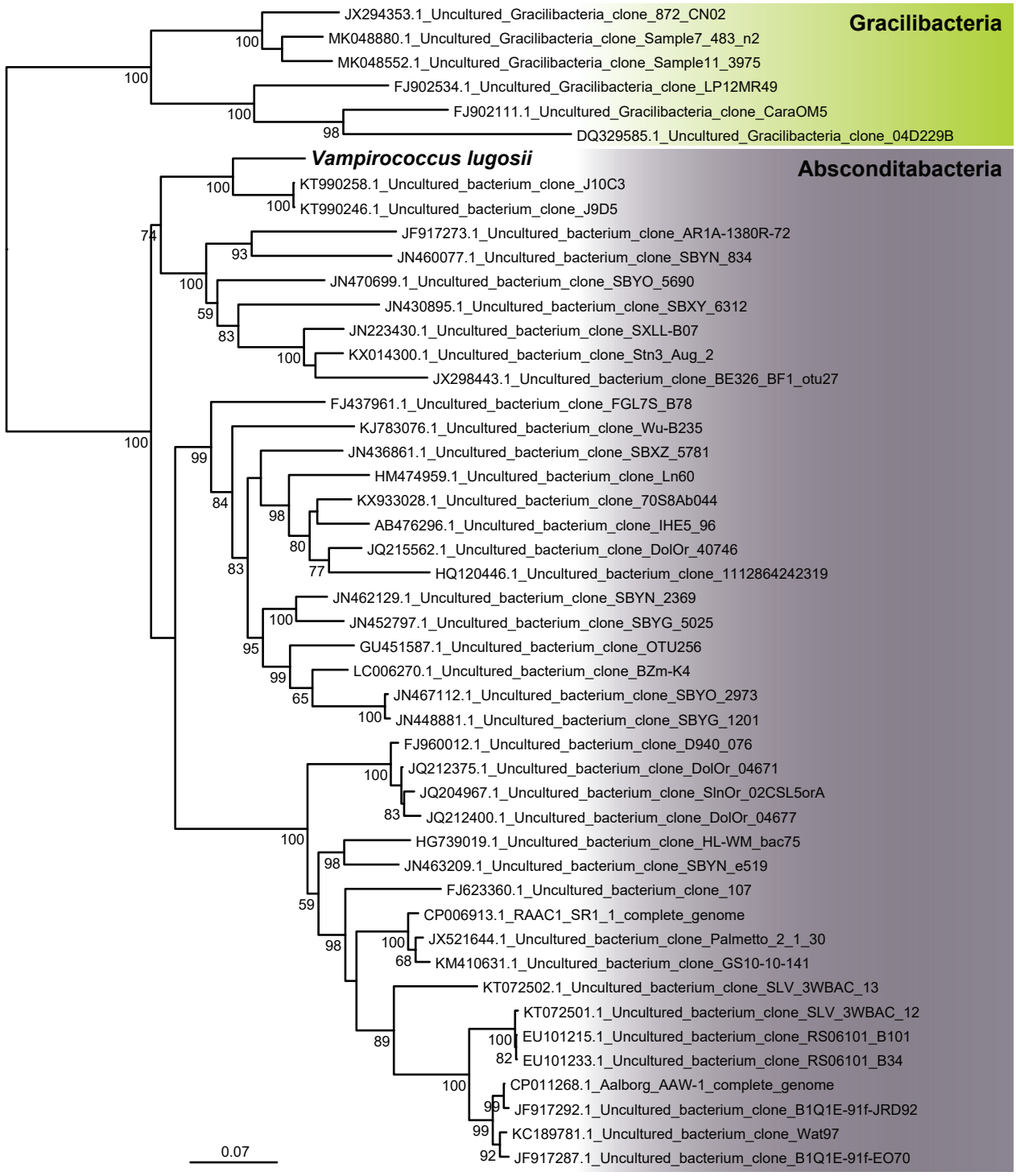


Extended Data Fig. 1 | Phase contrast microscopy images of micromanipulation of cells infected by *Vampirococcus* using a glass capillary. Yellow arrows in panels A and B indicate the same infected cells outside and inside the capillary. Panels C and D show capillaries containing several infected cells.



Extended Data Fig. 2 | 16S rRNA gene maximum likelihood phylogenetic tree of the *Vampirococcus* host. The tree is based on 1425 conserved aligned positions. Numbers at nodes are bootstrap support values (100 replicates).



Extended Data Fig. 3 | 16S rRNA gene maximum likelihood phylogenetic tree of *Vampirococcus*. The tree is based on 1282 conserved aligned positions. Numbers at nodes are bootstrap support values (100 replicates). The tree is rooted on several Gracilibacteria sequences.

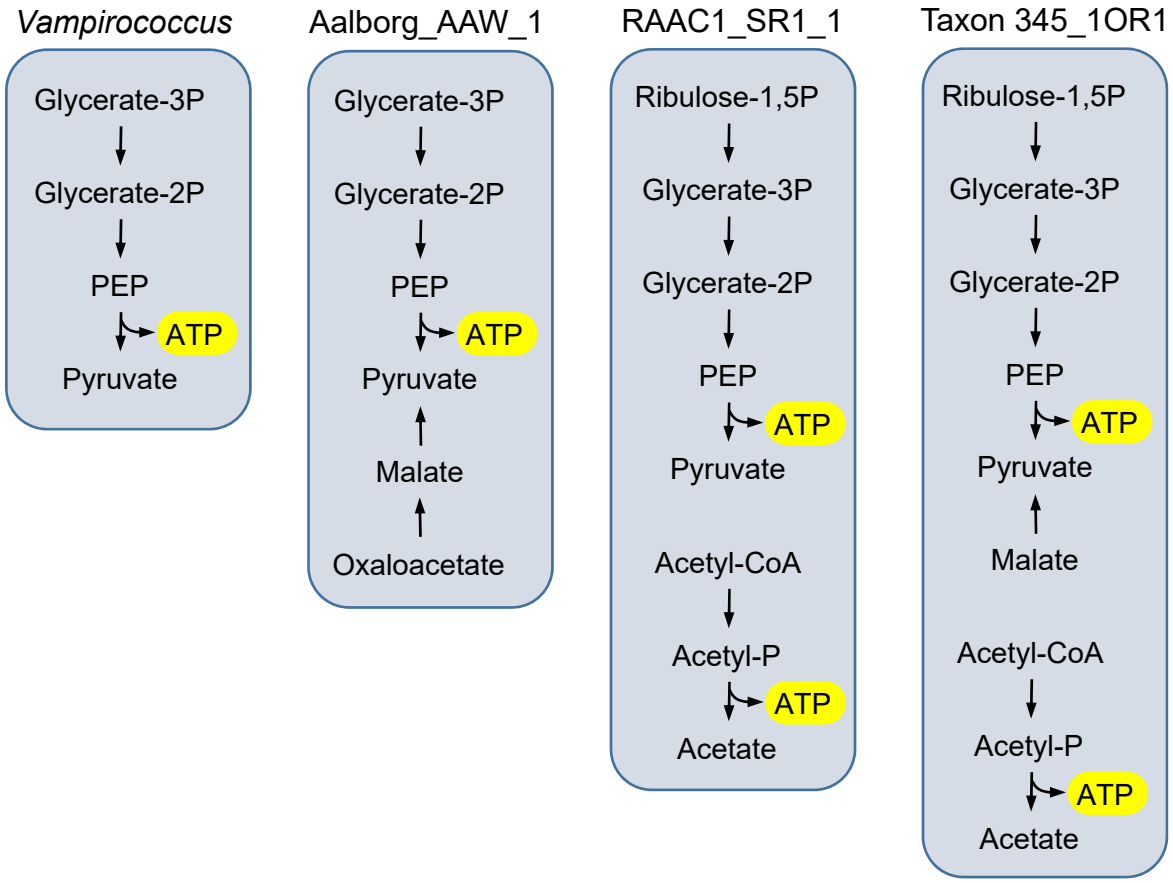
Extended Data Fig. 4. Maximum likelihood phylogenetic tree of 29 genotypes showing the position of Vietnamese/Lao. The tree is based on the concatenation of 16 genes (ribosomal protein S10, elongation factor Tu, ribosomal protein L4/L2, DNA-directed RNA polymerase subunits beta/beta', ribosomal protein L3, ribosomal protein S8, ribosomal protein L5, ribosomal protein S19, ribosomal protein L22, ribosomal protein S3, ribosomal protein L16, ribosomal protein L29, ribosomal protein S17, ribosomal protein L14, ribosomal protein L24, ribosomal protein L5). The tree is rooted at the concatenation of 16 genes of *Candidatus* Carsonella ruddii HT isolate Thiavenis, Hemiptera: aphids and scoloneids, support values > 95% displayed as black circles.

Protein	Function
VAMP_2_16	ATPase AAA
VAMP_2_102	uracil-DNA glycosylase
VAMP_2_126	amino acid kinase family protein
VAMP_2_142	acid phosphatase family membrane protein YuiD
VAMP_2_172	5'(3')-deoxyribonucleotidase, containing HAD-like domain
VAMP_2_376	coproporphyrinogen III oxidase
VAMP_2_652	spermidine synthase
VAMP_2_667	peptidase M50B family, putative
VAMP_2_731	hypothetical protein
VAMP_5_14	Asp-tRNAAsn/Glu-tRNAGln amidotransferase
VAMP_5_86	arginyl-tRNA synthetase
VAMP_5_322	sulfate permease
VAMP_5_352	hypothetical protein
VAMP_6_101	UDP-N-acetylenolpyruvoylglucosamine reductase
VAMP_7_1	group 1 glycosyl transferase
VAMP_7_38	glycosyltransferase
VAMP_7_63	sulfotransferase
VAMP_7_102	ATPase, AAA+ superfamily
VAMP_8_21	putative bacterial transferase
VAMP_8_278	zinc transporter ZupT
VAMP_11_1	type III restriction endonuclease
VAMP_11_32	death-on-curing protein
VAMP_11_87	membrane protein
VAMP_11_209	hypothetical protein
VAMP_12_204	hypothetical protein
VAMP_12_314	inosine 5'-monophosphate dehydrogenase
VAMP_12_407	membrane protein
VAMP_12_450	restriction endonuclease
VAMP_13_135	adenosylhomocysteinase
VAMP_13_214	lysophospholipase
VAMP_13_272	membrane protein
VAMP_13_309	ABC transporter
VAMP_13_360	superoxide dismutase
VAMP_16_4	hypothetical protein
VAMP_74-20_301	metal-dependent hydrolase
VAMP_74-20_334	type I site-specific deoxyribonuclease
VAMP_74-20_345	helix-turn-helix domain-containing protein
VAMP_74-20_352	hypothetical protein
VAMP_21_15	CRISPR-associated protein Csm3
VAMP_21_88	CRISPR/Cas system-associated protein
VAMP_21_151	CRISPR-associated protein Cas1
VAMP_21_166	CRISPR/Cas system-associated endoribonuclease
VAMP_22_222	HD superfamily hydrolase (HD-GYP...
VAMP_24_237	restriction endonuclease S subunit
VAMP_25_1	HD superfamily hydrolase
VAMP_25_65	putative diaminopimelate decarboxylase
VAMP_27_9	ATPase AAA, partial
VAMP_27_16	K+ transport system, NAD-binding
VAMP_27_59	hypothetical protein
VAMP_27_173	CDP-diglyceride synthetase
VAMP_31-433_4	putative transposase
VAMP_34_196	adenine specific DNA methylase
VAMP_34_248	putative DEAD/DEAH box helicase
VAMP_34_317	transposase
VAMP_36_45	predicted ATPase
VAMP_36_80	steroid 5-alpha reductase family
VAMP_36_96	CAAX protease, self-immunity related

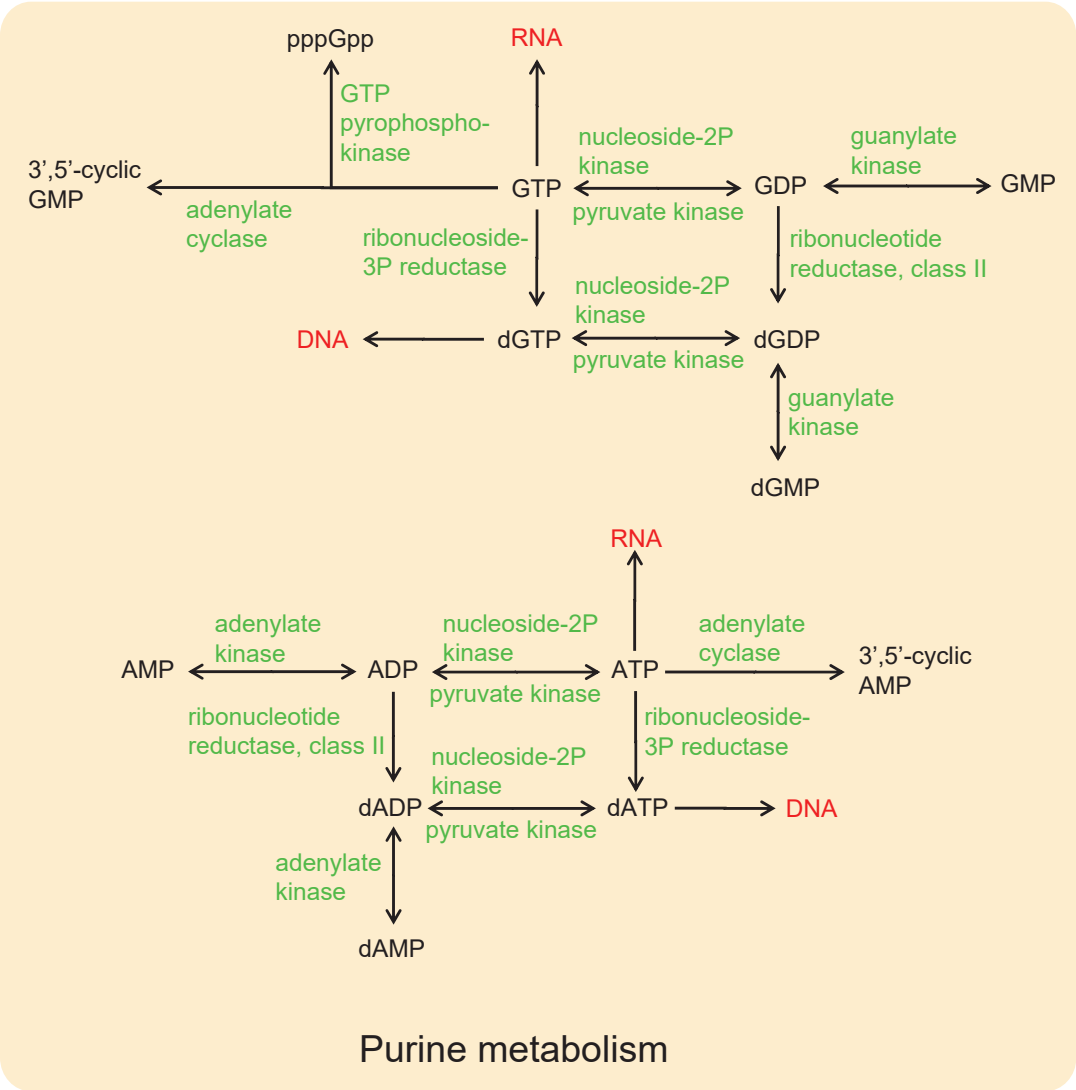
VAMP_40_134	surface antigen
VAMP_40_177	hAD phosphatase family IIIA
VAMP_41_97	C4-dicarboxylate ABC transporter
VAMP_44_14	thymidylate synthase
VAMP_44_34	ribosome-associated GTPase EngA
VAMP_44_51	helicase
VAMP_44_164	transposase, IS4 family
VAMP_46_8	ATPase AAA
VAMP_46_21	restriction endonuclease
VAMP_46_157	nitrous oxidase accessory protein
VAMP_48_7	ATPase AAA
VAMP_48_145	transposase
VAMP_48_161	Kazal-type serine protease inhibitor
VAMP_68-56_291	integrase
VAMP_59_23	hypothetical protein
VAMP_62_140	DNA methylase N-4
VAMP_63_143	hypothetical protein
VAMP_64_89	aspartate racemase
VAMP_64_127	integrase
VAMP_67_138	DNA binding protein, containing HHH motif
VAMP_68-56_2	hypothetical protein
VAMP_70_1	transposase
VAMP_74-20_92	hypothetical protein
VAMP_84_6	transposase, partial
VAMP_84_29	cell wall assembly/cell proliferation coordinating protein, KNR4
VAMP_84_167	transposase
VAMP_85_12	ATPase
VAMP_85_59	methyl-accepting chemotaxis protein (MCP)
VAMP_98_42	ATP-dependent endonuclease
VAMP_98_79	modification methylase HgaI-1
VAMP_98_91	type I restriction endonuclease subunit M
VAMP_98_96	DNA-binding beta-propeller fold protein YncE
VAMP_102_119	pectin lyase, putative
VAMP_106-108_174	metallo-beta-lactamase superfamily protein
VAMP_115_23	sialyltransferase, partial
VAMP_119_19	DNA-binding protein
VAMP_119_36	glycosyltransferase, GT2 family
VAMP_119_100	DNA binding protein, containing KilA-N domain
VAMP_125_114	hypothetical protein
VAMP_134_102	NAD(P)-dependent dehydrogenase
VAMP_134_122	AAA+ ATPase superfamily
VAMP_141_15	membrane protein
VAMP_144_15	nucleoside-triphosphatase
VAMP_152_39	DNA methyltransferase
VAMP_163_8	hypothetical protein
VAMP_163_14	hypothetical protein
VAMP_163_27	hypothetical protein
VAMP_163_38	transcription factor E (TFE)
VAMP_163_45	tRNA methyltransferase
VAMP_169_4	5-methylcytosine-specific restriction related enzyme
VAMP_197_9	AAA+ ATPase superfamily
VAMP_237_13	restriction endonuclease subunit S
VAMP_247_44	protease, CAAX family
VAMP_247_64	SPFH domain-containing protein
VAMP_283_8	ATPase AAA
VAMP_315_21	hypothetical protein
VAMP_325_1	outer membrane protein OmpA
VAMP_328_89	membrane protein

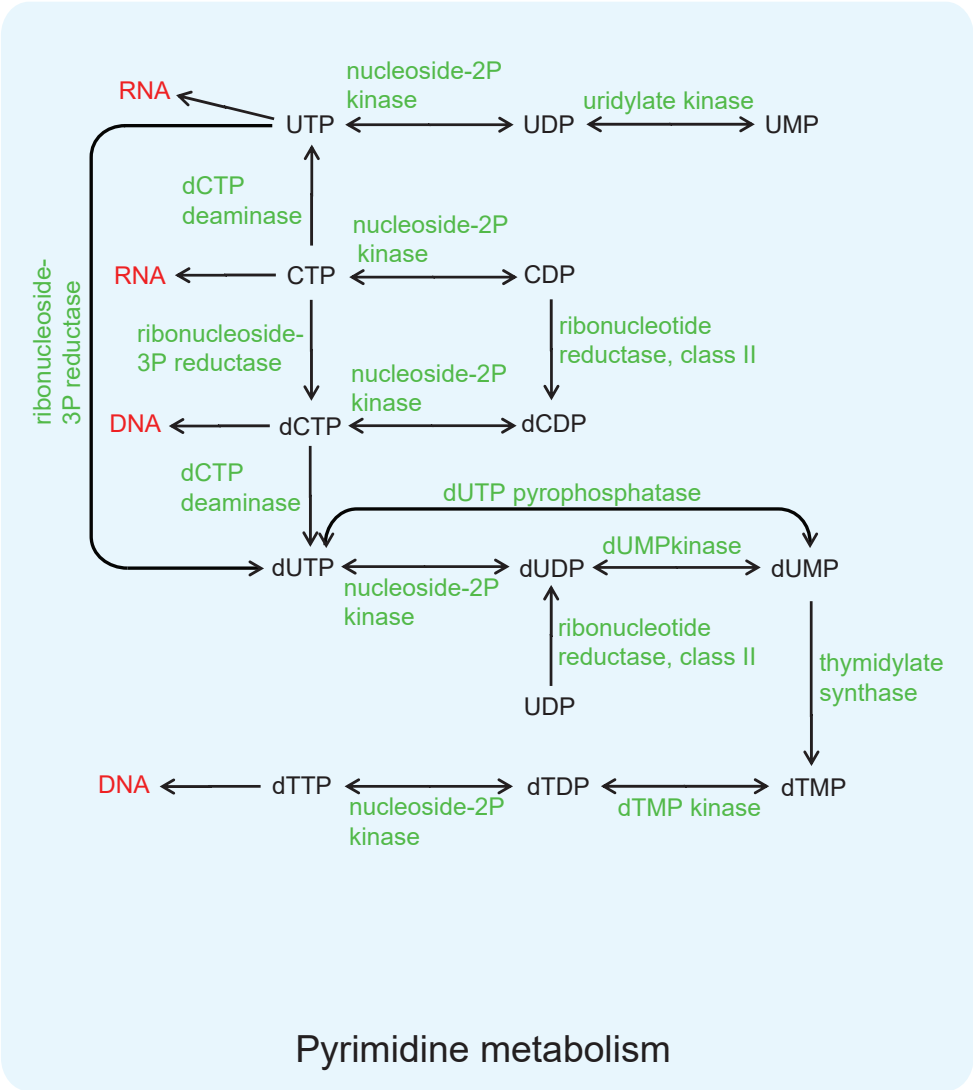
VAMP_368_47	protein of unknown function, DUF285
VAMP_379_21	cold-shock protein
VAMP_397_11	ribonuclease H
VAMP_405_17	ParB-like and HNH nuclease domains
VAMP_31-433_257	hypothetical protein
VAMP_472_45	hypothetical protein
VAMP_493_19	membrane protein
VAMP_525_55	5-methylcytosine-specific restriction endonuclease McrBC
VAMP_18_255	ATPase AAA
VAMP_18_221	chemotaxis protein
VAMP_18_122	hypothetical protein

Extended Data Fig. 5 | *Vampirococcus* genes acquired by horizontal gene transfer.



Extended Data Fig. 6 | ATP production pathways in *Vampirococcus* and three representative Absconditabacteria.



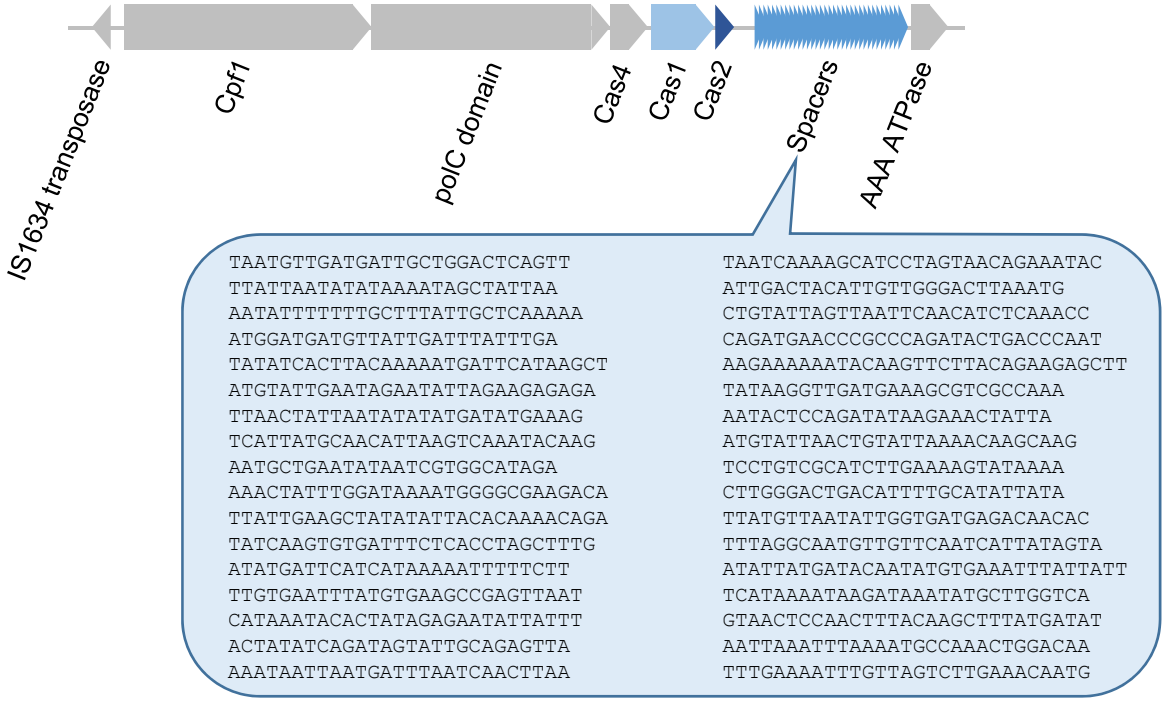


Extended Data Fig. 7 | Main pathways involved in purine and pyrimidine metabolism in *Vampirococcus*. Substrates are indicated in black, enzymes in green, and DNA and RNA in red.

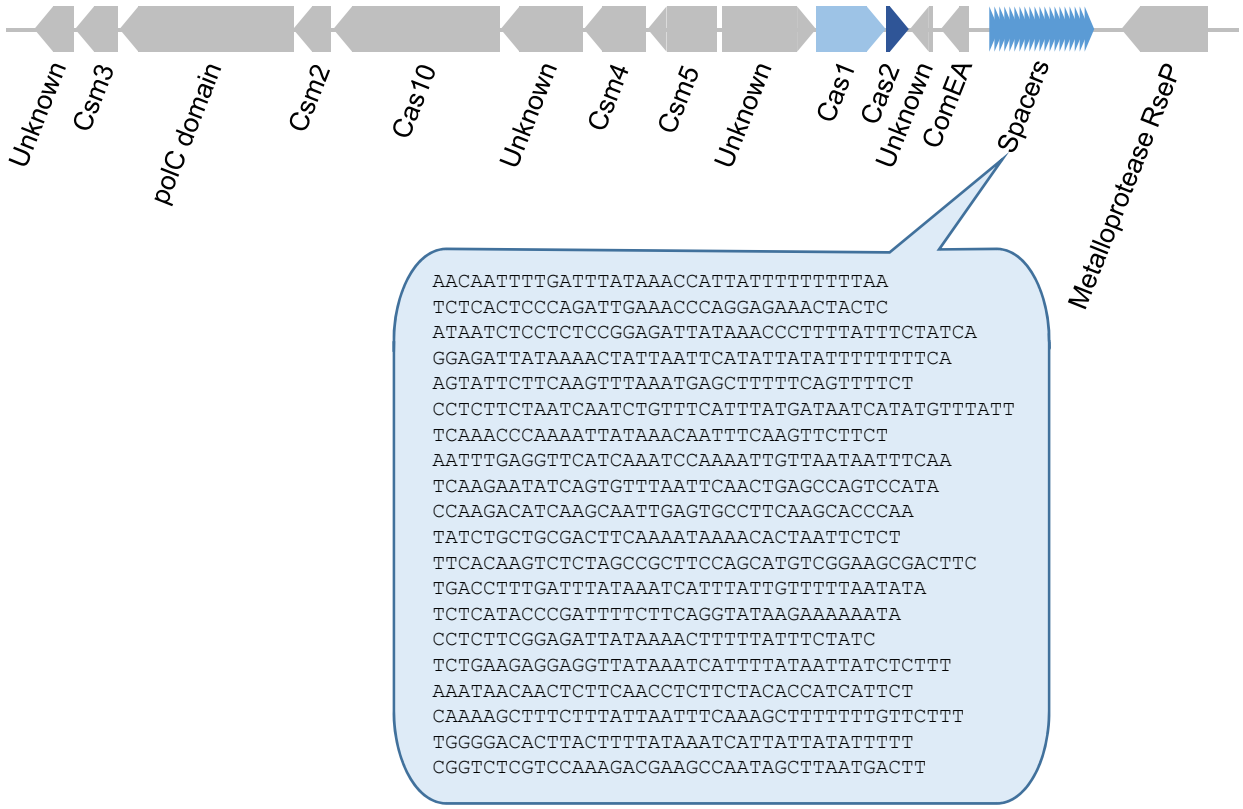
Protein	Function	Size
VAMP_16_20	hypothetical protein	4163
VAMP_134_102	NAD(P)-dependent dehydrogenase	2400
VAMP_6_203	alpha-2 macroglobulin	2368
VAMP_166_2	hypothetical protein	2284
VAMP_19_245	alpha-2 macroglobulin	1895
VAMP_328_89	membrane protein	1883
VAMP_95_65	YfaS, alpha-2 macroglobulin family	1871
VAMP_54_69	hypothetical protein	1723
VAMP_17-88-45_126	PKD repeat-containing protein	1396
VAMP_98_96	DNA-binding beta propeller protein YncE	1392

Extended Data Fig. 8 | Ten largest proteins encoded in the *Vampirococcus* genome.

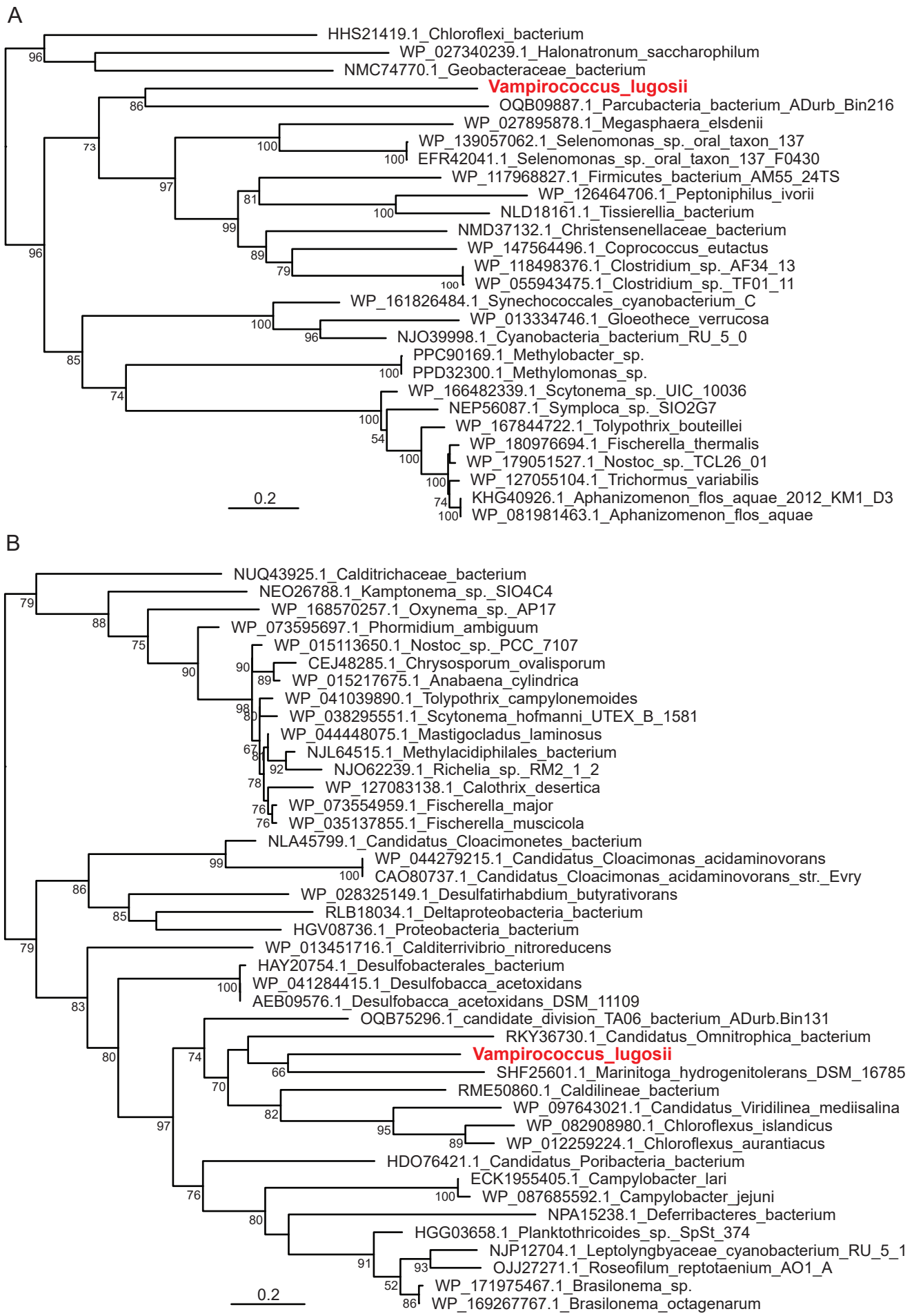
Class II type V



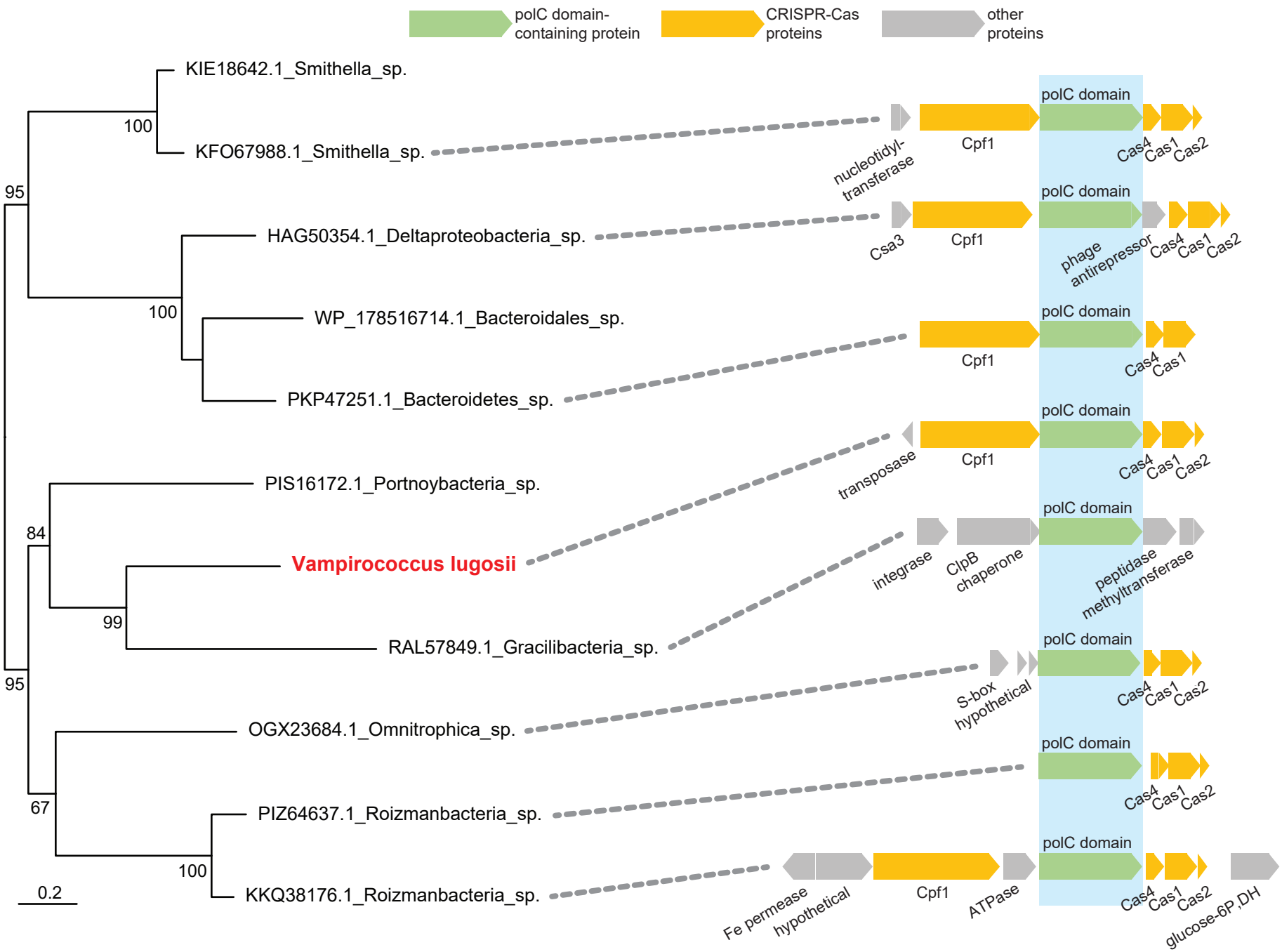
Class I type III



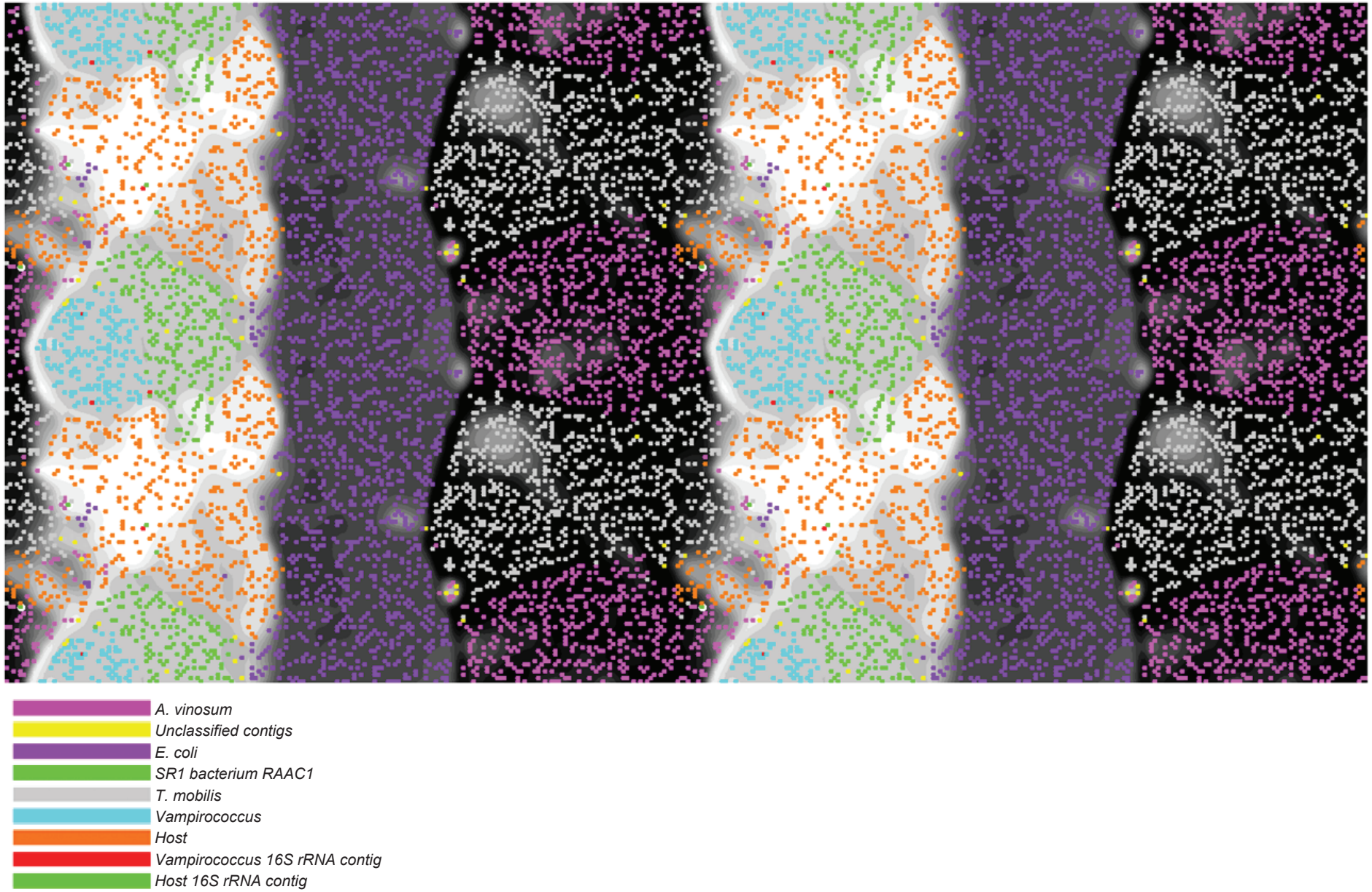
Extended Data Fig. 9 | The two CRISPR-Cas loci of *Vampirococcus* and their corresponding spacer sequences.



Extended Data Fig. 10 | Maximum likelihood phylogenetic trees of *Vampirococcus* type I class III CRISPR-Cas enzymes Cas1 'A) and Cas2 (B). The trees are based on 349 and 118 conserved aligned positions, respectively. Numbers at nodes are bootstrap support values (100 replicates, only values >50% are shown).



Extended Data Fig. 11 | Maximum likelihood phylogeny and genomic context of the *Vampirococcus* polC domain-containing protein associated to the class II type V CRISPR-Cas system. The genomic context is shown for the species for which genome sequence data are available. The polC domain-containing protein is shown in green and typical CRISPR-Cas proteins are shown in orange.



Extended Data Fig. 12 | Visualization of the ESOM map of the assembled DNA contigs of *Vampirococcus*, its host, and several reference genomes.