

Table S1. Sequencing and assembly statistics (QF: Quality Filtered)

	Illumina Mi-Seq PE reads		Pacbio P1 reads		Hybrid Assembly				
	Raw	QF	Raw	QF	Scaffolds	N50 (bp)	Median Coverage (X)	Connected components	Total Length (bp)
PMC627	8,853,009	8,406,837	41,220	35,296	278	399,971	24.27	108	18,049,162
PMC638	4,628,377	4,466,201	77,472	45,417	568	239,164	18.15	157	27,054,307
PMC644	2,892,901	2,841,124	55,143	36,786	294	3,057,515	26.18	59	13,855,426
PMC649	2,210,208	2,053,891	32,813	29,509	612	156,510	20.61	496	33,732,544

Table S2. KEGG functional modules displaying significant higher completeness in one taxon.

	Functional category	Sub-category	Module	Module Function
Alphaproteobacteria	Energy metabolism	Carbon fixation	M00169	CAM (Crassulacean acid metabolism), light
			M00173	Reductive citrate cycle (Arnon-Buchanan cycle)
			M00376	3-Hydroxypropionate bi-cycle
		ATP synthesis	M00143	NADH dehydrogenase (ubiquinone) Fe-S protein/flavoprotein complex, mitochondria
			M00149	Succinate dehydrogenase, prokaryotes
			M00152	Cytochrome bc1 complex
			M00154	Cytochrome c oxidase
			M00156	Cytochrome c oxidase, cbb3-type
	Lipid metabolism	Sterol biosynthesis	M00104	Bile acid biosynthesis, cholesterol => cholate/chenodeoxycholate
	Amino acid metabolism	Branched-chain amino acid metabolism	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA
	Metabolism of cofactors and vitamins	Cofactor and vitamin metabolism	M00622	Nicotinate degradation, nicotinate => fumarate
			M00128	Ubiquinone biosynthesis, eukaryotes, 4-hydroxybenzoate => ubiquinone
	Biosynthesis of terpenoids and polyketides	Enediynes biosynthesis	M00830	Neocarzinostatin naphthoate moiety biosynthesis, malonyl-CoA => ...=> 2-hydroxy-7-methoxy-5-methyl-1-naphthoyl-CoA
		Type II polyketide biosynthesis	M00778	Type II polyketide backbone biosynthesis, acyl-CoA + malonyl-CoA => polyketide
	Biosynthesis of other secondary metabolites	Biosynthesis of other secondary metabolites	M00789	Rebeccamycin biosynthesis, tryptophan => rebeccamycin
			M00837	Prodigiosin biosynthesis, L-proline => prodigiosin
	Xenobiotics biodegradation	Aromatics degradation	M00551	Benzoate degradation, benzoate => catechol / methylbenzoate => methylcatechol
	Gene set	Pathogenicity	M00542	EHEC/EPEC pathogenicity signature, T3SS and effectors
			M00564	Helicobacter pylori pathogenicity signature, cagA pathogenicity island
			M00651	Vancomycin resistance, D-Ala-D-Lac type
		Drug resistance	M00642	Multidrug resistance, efflux pump MexJK-OprM
			M00643	Multidrug resistance, efflux pump MexXY-OprM
Bacteroidetes	Carbohydrate metabolism	Central carbohydrate metabolism	M00010	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate
	Energy metabolism	Methane metabolism	M00358	Coenzyme M biosynthesis
	Metabolism of cofactors and vitamins	Cofactor and vitamin metabolism	M00126	Tetrahydrofolate biosynthesis, GTP => THF
Aphanizomenon	Energy metabolism	Carbon fixation	M00166	Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P
		Nitrogen metabolism	M00175	Nitrogen fixation, nitrogen => ammonia
		Photosynthesis	M00161	Photosystem II
			M00163	Photosystem I
		ATP synthesis	M00145	NAD(P)H quinone oxidoreductase, chloroplasts and cyanobacteria
			M00162	Cytochrome b6f complex
	Lipid metabolism	Fatty acid metabolism	M00873	Fatty acid biosynthesis in mitochondria, animals
	Metabolism of cofactors and vitamins	Cofactor and vitamin metabolism	M00117	Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone
			M00112	Tocopherol/tocotorienol biosynthesis
	Biosynthesis of terpenoids and polyketides	Other terpenoid biosynthesis	M00097	beta-Carotene biosynthesis, GGAP => beta-carotene
		Biosynthesis of other secondary metabolites	M00875	Staphyloferrin B biosynthesis, L-serine => staphyloferrin B
	Gene set	Drug resistance	M00652	Vancomycin resistance, D-Ala-D-Ser type
	Module set	Metabolic capacity	M00615	Nitrate assimilation

Table S3. Heterotrophic bacteria MAG coverages and sample Shannon indices.

MAG	Mean Coverage in PMC			
	627	638	644	649
Ac-Ac-01	2.50	3.62	1.73	15.32
Al-Ca-02	1.72	19.45	2.22	1.30
Al-Rb-03	1.80	26.89	1.43	2.12
Al-Rb-04	7.18	12.16	1.67	12.01
Al-Rb-05	10.10	11.05	2.04	10.49
Al-Rb-06	11.56	11.05	2.59	38.20
Al-Rs-07	3.59	45.81	2.42	2.02
Al-Sm-08	226.22	33.37	4.53	33.84
Al-Sm-09	22.54	1.88	1.63	1.83
Al-Sm-10	6.61	3.02	121.35	3.16
Al-Sm-11	3.27	1.49	1.21	9.35
Ba-Ch-12	4.60	2.32	84.84	1.26
Ba-Cy-13	3.72	75.13	1.45	1.30
Ba-Cy-14	15.55	92.23	81.61	11.29
Ba-Fb-15	9.91	1.35	2.01	9.93
Ba-Sa-16	60.76	5.66	10.27	6.61
Ba-Sb-17	1.67	19.71	3.29	3.45
Ba-Un-18	0	9.73	79.63	0
Be-Bu-19	1.73	2.16	3.14	28.52
Ge-Ge-20	1.52	2.96	2.37	9.43

Shannon index	1.19	1.66	0.90	2.11
---------------	------	------	------	------

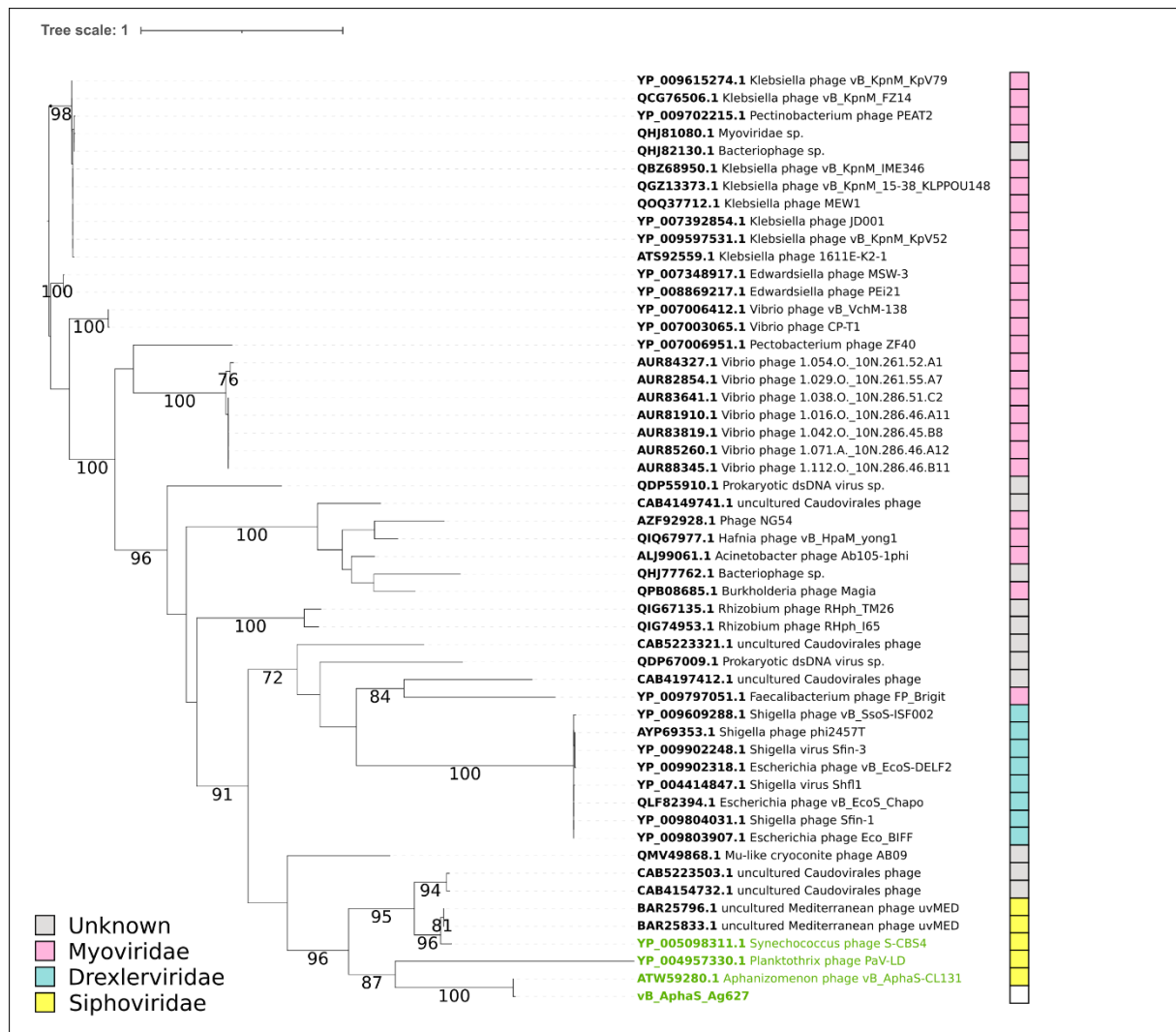


Figure S1. Phylogenetic tree based on portal protein sequences of 55 bacteriophages constructed using Maximum Likelihood method with 100 bootstraps (only values ≥ 60 are displayed). Green labels correspond to cyanophages. Multiple alignments were obtained using MAFFT and filtered by GBLOCKS. Phylogenetic inference was computed by PhyML with the best model determined by SMS (LG+G+F) on the AIC criterion.