

Table S3. Example of genes sharing best similarities between the pan-chromosome, pan-plasmidome and/or closely or distantly related and unrelated lineages.

Network	Lineage	Gene	Sequence identity
<i>Rickettsia</i> pan-chromosome	α-proteobacteria:		
	<i>Orientia</i> sp., <i>Occidentia</i> spp., <i>Wolbachia</i> spp.	Transposases (<i>tnp</i>), integrases (<i>int</i>), integrative conjugative elements (<i>tra</i>)	34% - 93%
	<i>Ca. Arcanobacter</i>	Biotin synthase <i>bioB</i>	75%
	<i>Wolbachia</i> spp.	Protein phosphatase	66%
	<i>Ca. Odysella</i>	Hypothetical proteins	51% - 73%
	<i>Thalassospira</i> or <i>Maritalea</i>	Sugar kinases, ribokinase family	33%
	Pelagibacteraceae bacteria		
	<i>Rickettsia</i> pan-plasmidome	Transposases and integrases	33% - 100%
		Integrative conjugative elements	44% - 81%
		Small heat shock proteins	98.5%
		peptidase M50	59.7%
		Guanosine polyphosphate pyrophosphohydrolase/ synthetase	46% - 55%
		Thymidylate kinase	61.8%
		MFS-type sugar transporter	40% - 97%
		Proline/betaine transporter	50% - 60%
	Patatin-like phospholipase	62.3%	
	Distantly related or unrelated lineages		
	Several lineages	Transposases and integrases	35% - 80%,
	γ -proteobacteria: <i>Francisella</i> sp., <i>Caedibacter</i>	Proteins of unknown functions	53% - 74%
	Cytophagia: <i>Cardinium</i> sp.	Type I polyketide synthase	77%
	β -proteobacteria: <i>Chromobacterium</i> sp.	Phenylalanine-4-hydroxylase	55%
	δ -proteobacteria: <i>Ca. Magnetomorum</i> spp.	Archaeal ATPase family protein	62%
	Cyanobacteria: <i>Spirulina major</i>	Phage-related protein	62%
	Chlamydia: <i>Ca. Protochla. amoebophila</i>	Cell division protein Fic	66%
	Chlamydia: chlamydiales	Histidinol-phosphate aminotransferase family protein	60%
	Viruses, caudovirales	MFS-type sugar transporters	49% - 63%

<i>Rickettsia</i> pan-plasmidome			
<i>Rickettsia</i> pan-chromosome or other related/unrelated lineages			
α/γ -proteobacteria and actinobacteria: several species	Transposases and integrases		36% - 92%
α -proteobacteria, rickettsiales: <i>Wolbachia</i> spp.	Cluster of seven genes including the phytanoyl-CoA dioxygenase family protein and L-allo-threonine aldolase		47% - 79%
γ -proteobacteria: <i>Serratia marcescens</i>	Protein of unknown function		67%
Cytophagia: <i>Cardinium</i> spp.	HlyD family type I secretion periplasmic adaptor		64%
Actinobacteria: <i>Streptomyces</i> spp.	Tetratricopeptide repeat-containing protein		88.7%
<i>Rickettsia</i> pan-chromosome and other closer/distant relatives			
Several lineages	Transposases and integrases		31% - 100%
α -proteobacteria, rickettsiales: <i>Wolbachia</i> spp.	Clusters of biotin genes <i>bioA/B/C/D</i>		53% - 77%
δ -proteobacteria: <i>Lawsonia intracellularis</i>			
α -proteobacteria: <i>Orientia tsutsugamushi</i>	Cluster of conjugative elements		36% - 67%
γ -proteobacteria: <i>Legionella massiliensis</i>	Cluster of three genes including tyrosine-type recombinase/integrase, sodium/solute symporter family protein, GNAT family N-acetyltransferase		71% - 100%
γ -proteobacteria: <i>Pseudomonas</i> , Ca. <i>Hamiltonella</i> and/or <i>Berkiella</i>	Cluster of five genes encoding acetyltransferase, aromatic ring-hydroxylating dioxygenase subunit alpha, short chain dehydrogenase/reductase family protein, 3-oxoacyl-(acyl-carrier-protein) synthase III, acyl carrier protein and ABC multidrug transporter, permease/ATP-binding protein		63% - 98%