

Supplementary Table 1. Comparison of *Pseudomonas fluorescens* F113 ECM components outside *Pseudomonadales*

Name	Locus (PSF113_)	Protein predicted function	Protein homology	
<i>pgaA</i>	161	Poly-beta-1,6 N-acetyl-D-glucosamine export porin	<i>Paraburkholderia insulsa</i>	70%
			<i>Achromobacter</i> spp.	
<i>pgaB</i>	162	Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase	<i>Paraburkholderia insulsa</i>	63-77 %
			<i>Achromobacter</i> spp.	
			<i>Cupriavidus gilardii</i>	
<i>pgaC</i>	163	Poly-beta-1,6 N-acetyl-D-glucosamine synthase, catalytic subunit	<i>Paraburkholderia insulsa</i>	72-85 %
			<i>Achromobacter</i> spp.	
<i>pgaD</i>	164	Poly-beta-1,6-N-acetyl-D-glucosamine synthase, regulatory subunit; c-di-GMP-stimulated activity and dimerization	<i>Paraburkholderia insulsa</i>	36-46 %
			<i>Xenorhabdus beddingii</i>	
			<i>Citrobacter werkmanii</i>	
<i>papA</i>	1970	UDP-glucose/GDP-mannose dehydrogenase family protein	<i>Halomonas</i> sp. KM-1	61-62 %
			<i>Serratia</i> sp. M24T3	
			<i>Alishewanella aestuarii</i>	
			<i>Chelativorans</i> sp. BNC1	
<i>papB</i>	1969	Nucleoside-diphosphate-sugar epimerase	<i>Geobacillus</i> sp. WCH70	59-62 %
		NAD dependent epimerase/dehydratase	<i>Thermithiobacillus tepidarius</i>	
			<i>Balneatrix alpaca</i>	
			<i>Bacillus oceanisediminis</i>	
<i>papC</i>	1968	Undecaprenyl-phosphate galactose	<i>Zooshikella ganghwensis</i>	57-60 %
			<i>Desulfobulbus japonicus</i>	
			<i>Sphingomonas</i> sp. TZW2008	
<i>papD</i>	1967	Autophosphorylating protein tyrosine kinase	<i>Paraburkholderia insulsa</i>	71-72 %
			<i>Achromobacter</i> spp.	
			<i>Cupriavidus gilardii</i>	
<i>papE</i>	1966	Polysaccharide biosynthesis/export protein	<i>Zooshikella ganghwensis</i>	32-38 %
			<i>Gamma proteobacterium</i> HdN1	
			<i>Desulfobulbus japonicus</i>	
<i>papF</i>	1965	Uncharacterized protein involved in exopolysaccharide biosynthesis	<i>Zooshikella ganghwensis</i>	29-40 %
			<i>Gamma proteobacterium</i> HdN1	
			<i>Desulfobulbus japonicus</i>	
<i>papG</i>	1964	Glycosyl transferases group 1	<i>Zooshikella ganghwensis</i>	33-35 %
			<i>Gamma proteobacterium</i> HdN1	
			<i>Geobacter sulfurreducens</i>	
<i>papH</i>	1963	O-Antigen ligase	<i>Zooshikella ganghwensis</i>	38-43 %
			<i>Gamma proteobacterium</i> HdN1	

			<i>Desulfobulbus japonicus</i>	
<i>papI</i>	1962	Glycosyl transferases group 1	<i>Desulfobulbus japonicus</i>	40-43 %
			Gamma proteobacterium HdN1	
			<i>Zooshikella ganghwensis</i>	
<i>papJ</i>	1961	Glycosyl transferase, group 2 family protein	Gamma proteobacterium HdN1	40-47 %
			<i>Desulfobulbus japonicus</i>	
			<i>Zooshikella ganghwensis</i>	
<i>papK</i>	1960	Polysaccharide deacetylase	<i>Halomonas xinjiagensis</i>	38-41 %
			<i>Halomonas anticariensis</i>	
			<i>Halomonas xianhensis</i>	
<i>papL</i>	1959	Polysaccharide biosynthesis protein	Gamma proteobacterium HdN1	37-40 %
			<i>Zooshikella ganghwensis</i> <i>Desulfobulbus japonicus</i>	
<i>papM</i>	1958	Hypothetical protein (no putative conserved domains detected)	<i>Zooshikella ganghwensis</i> Gamma proteobacterium HdN1	35-42 %
			<i>Desulfobulbus japonicus</i>	
<i>papN</i>	1957	Hypothetical protein (no putative conserved domains detected)	<i>Zooshikella ganghwensis</i>	24-29 %
			<i>Desulfobulbus japonicus</i>	
<i>papO</i>	1956	Acetyltransferase (GNAT) domain	<i>Microvirga guangxiensis</i>	26-32 %
			Gamma proteobacterium HdN1	
			<i>Desulfobulbus japonicus</i>	
			<i>Zooshikella ganghwensis</i>	
<i>papP</i>	1955	YdjC-like protein	<i>Lachnospiraceae</i>	35-37 %
<i>lapA</i>	208	Protein LapA	<i>Stenotrophomonas rhizophila</i>	48-56%
			<i>Pantoea</i>	
<i>mapA</i>	1511	Putative hemagglutinin/hemolysin-like protein	<i>Pantoea</i>	40-56%
			<i>Aeromonas</i>	
<i>psmE</i>	3004	Protein PsmE	<i>Asticcaculis sp</i>	40-48%
			<i>Tanacetum cinerariifolium</i>	
			<i>Microvirga sp.</i> BSC39	
			<i>Methylobacter</i>	