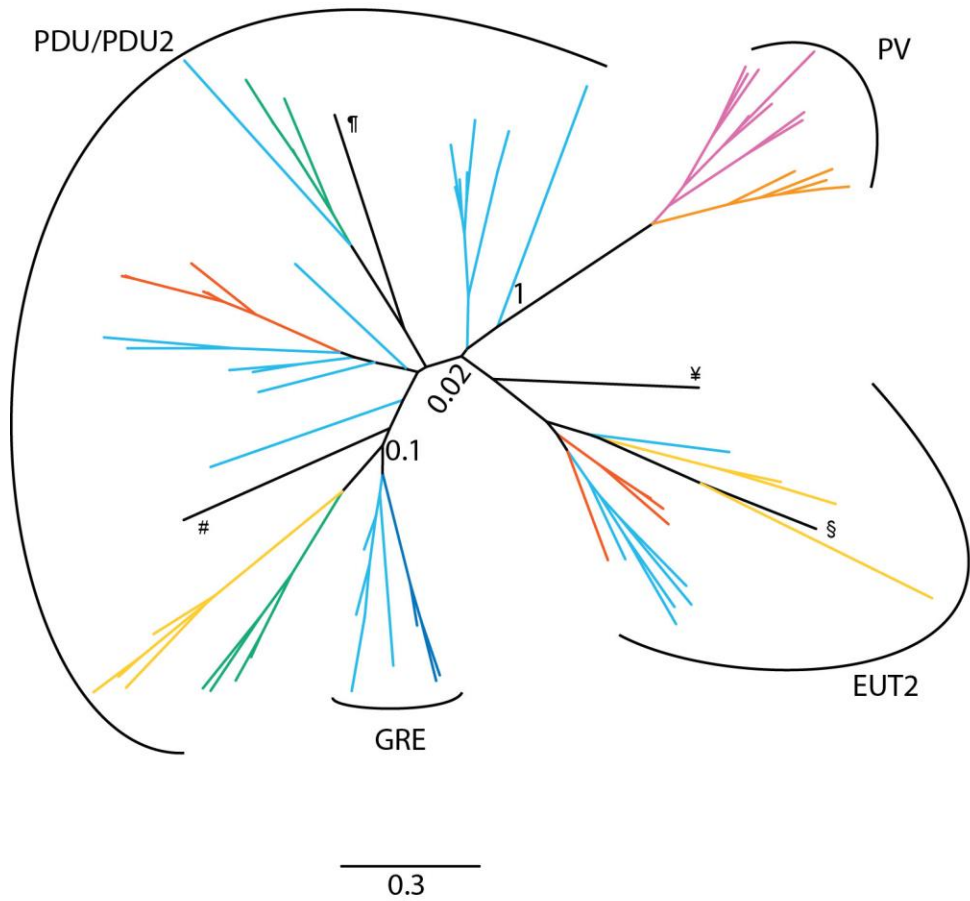
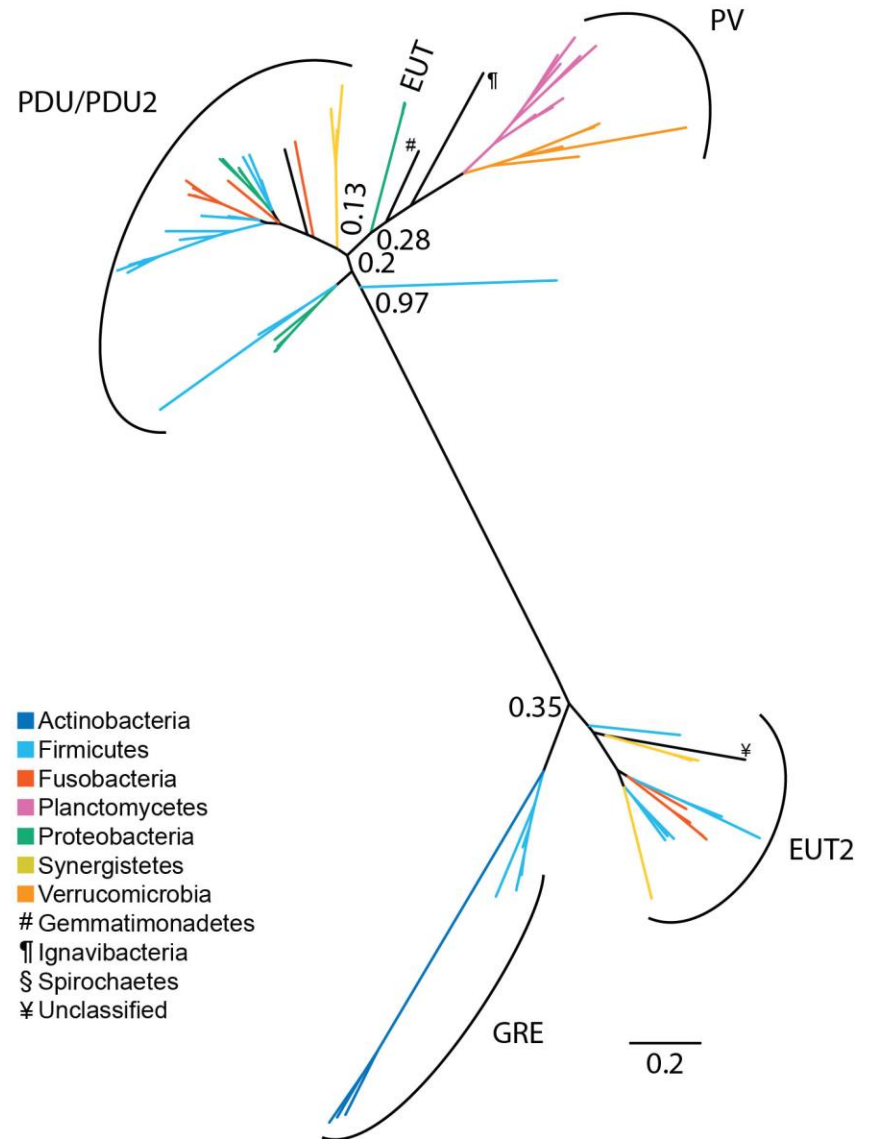


**A** Phosphotransacylase (*pduL* homologs) tree

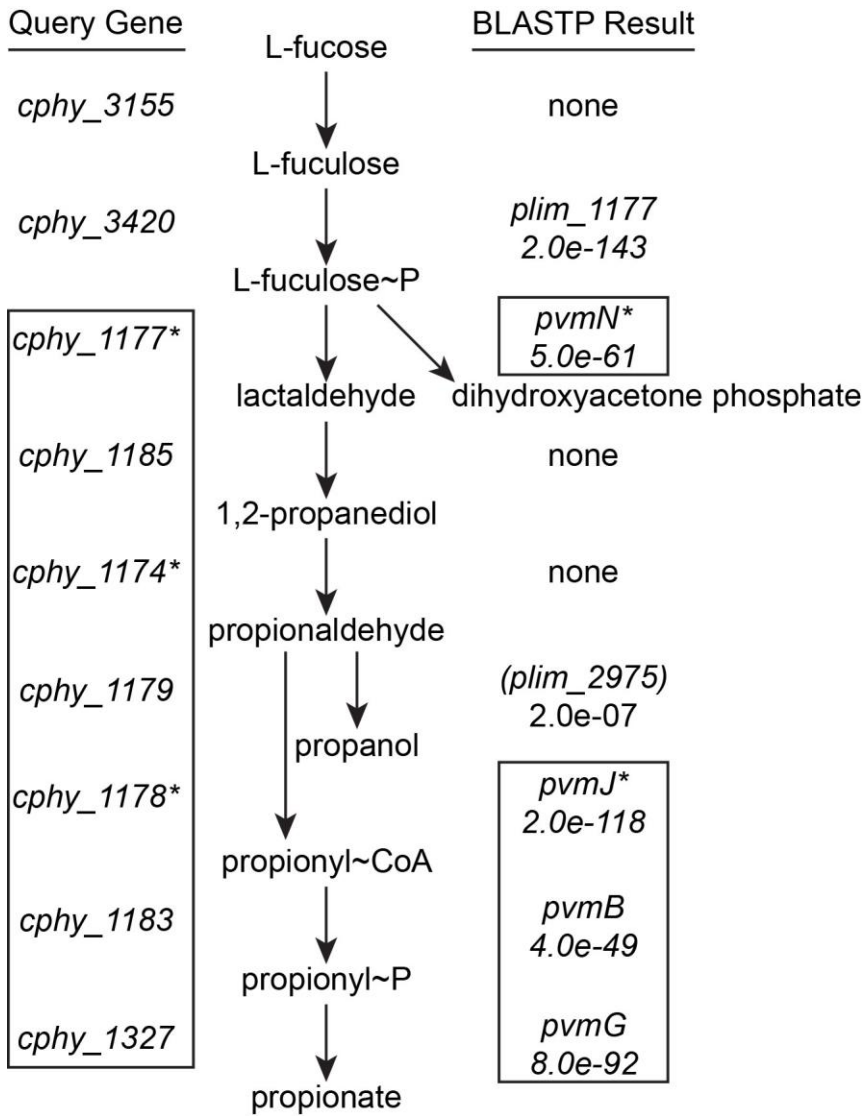


**B** Aldehyde Dehydrogenase (*pduP* homologs) tree

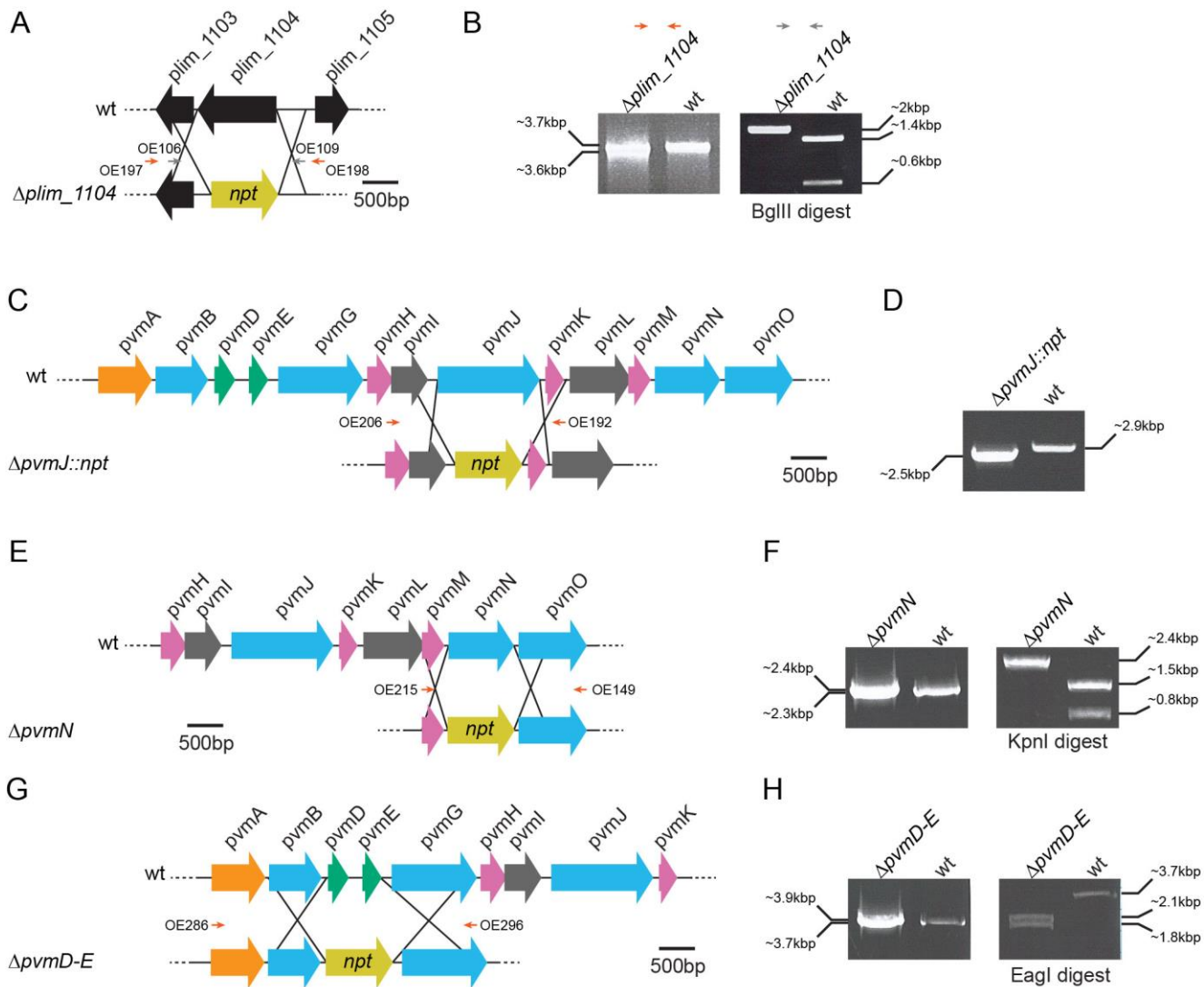


- Actinobacteria
- Firmicutes
- Fusobacteria
- Planctomycetes
- Proteobacteria
- Synergistetes
- Verrucomicrobia
- # Gemmatimonadetes
- †† Ignavibacteria
- § Spirochaetes
- ≠ Unclassified

**Figure S1.** Individual gene trees for (A) PduL homologs and (B) PduP homologs. Bootstrap values of nodes separated clades of differing function of the associated metabolosomes. Scale bars indicate number of substitutions per amino acid position.



**Figure S2.** Results of pairwise comparisons of BMC-related enzymes from *P. limnophilus* and *C. phytofermentans*. The proposed degradation pathway of L-fucose in *C. phytofermentans* is shown in the center, flanked by *C. phytofermentans* (left) and *P. limnophilus* (right) genes identified by their locus tags; *C. phytofermentans* genes predicted to catalyze each reaction shown were used as queries to search the *P. limnophilus* genome for homologs using BLASTP. Genes shown in parentheses did not yield best bidirectional hits. Genes marked with an asterisk contain a predicted BMC targeting peptide sequence. Boxes are drawn around genes that are within a BMC locus.



**Figure S3.** Description of mutants used in this study. A) Homologous recombination to make the  $\Delta plim_{1104}$  mutant, with primer pair OE197, 198 shown in orange arrows, and primer pair OE106, 109 shown in gray arrows. B) PCR genotyping to confirm the mutant. A BglIII restriction site in the *plim\_{1104}* gene was used to differentiate between the two genotypes. C)  $\Delta pvmJ$  mutant, with primer pair OE206, 192 depicted with orange arrows used for D) PCR genotyping. E)  $\Delta pvmN$  mutant, with primer pair OE149, 215 shown in orange arrows, used for F) PCR genotyping, with a KpnI restriction site in the *pvmN* gene used to differentiate genotypes. G)  $\Delta pvmDE$  mutant, with primer pair OE286, 296 shown in orange arrows, used for H) PCR genotyping, with the EagI restriction site in the *npt* gene used to differentiate genotypes.

$$\frac{A_{\text{mutant}} - A_{\text{wt}}}{A_{\text{wt}}} \times (A_{\text{mutant}} - A_{\text{wt}}) = \text{negative} \quad \text{positive}$$

PM1	1	2	3	4	5	6
A	Negative Control	L-Arabinose	N-Acetyl-D-Glucosamine	D-Saccharic acid	Succinic acid	D-Galactose
B	D-Serine	D-Sorbitol	Glycerol	<b>L-Fucose</b>	D-Glucuronic acid	D-Gluconic acid
C	D-Glucose-6-Phosphate	D-Galactonic acid-g-Lactone	DL-Malic acid	D-Ribose	Tween 20	L-Rhamnose
D	L-Asparagine	D-Aspartic acid	D-Glucosaminic acid	1,2-Propanediol	Tween 40	a-Ketoglutaric acid
E	L-Glutamine	m-Tartaric acid	D-Glucose-1-Phosphate	D-Fructose-6-Phosphate	Tween 80	a-Hydroxyglutaric acid-g-Lactone
F	Gly-Asp	Citric acid	m-Inositol	D-Threonine	Fumaric acid	<b>Bromosuccinic acid</b>
G	Gly-Glu	Tricarballic acid	L-Serine	L-Threonine	L-Alanine	Ala-Gly
H	Gly-Pro	p-Hydroxyphenyl Acetic acid	m-Hydroxyphenyl Acetic acid	Tyramine	D-Psicose	L-Lyxose
PM1	7	8	9	10	11	12
A	L-Aspartic acid	L-Proline	D-Alanine	D-Trehalose	D-Mannose	Dulcitol
B	DL-a-Glycerol Phosphate	D-Xylose	L-Lactic acid	Formic acid	D-Mannitol	L-Glutamic acid
C	D-Fructose	<b>Acetic acid</b>	a-D-Glucose	Maltose	D-Melibiose	Thymidine
D	a-Ketobutyric acid	a-Methyl-D-Galactoside	a-D-Lactose	Lactulose	Sucrose	Uridine
E	a-Hydroxybutyric acid	b-Methyl-D-Glucoside	Adonitol	Maltotriose	2'-Deoxyadenosine	Adenosine
F	Propionic acid	Mucic acid	Glycolic acid	Glyoxylic acid	D-Cellobiose	Inosine
G	Acetoacetic acid	N-Acetyl-D-Mannosamine	Mono-Methylsuccinate	Methylpyruvate	D-Malic acid	L-Malic acid
H	Glucuronamide	Pyruvic acid	L-Galactonic acid-g-Lactone	D-Galacturonic acid	Phenylethylamine	2-Aminoethanol
PM2	1	2	3	4	5	6
A	Negative Control	Chondroitin Sulfate C	a-Cyclodextrin	b-Cyclodextrin	g-Cyclodextrin	Dextrin
B	N-Acetyl-D-Galactosamine	N-Acetyl-Neuraminic acid	b-D-Allose	Amygdalin	<b>D-Arabinose</b>	D-Arabitol
C	Gentiobiose	L-Glucose	D-Lactitol	<b>D-Melezitose</b>	Maltitol	a-Methyl-D-Glucoside
D	<b>D-Raffinose</b>	Salicin	Sedoheptulosan	L-Sorbose	Stachyose	D-Tagatose
E	Capric acid	Caproic acid	Citraconic acid	Citramalic acid	<b>D-Glucosamine</b>	2-Hydroxybenzoic acid
F	D-Lactic acid Methyl Ester	Malonic acid	<b>Melibionic acid</b>	Oxalic acid	Oxalomalic acid	Quinic acid
G	Acetamide	L-Alaninamide	N-Acetyl-L-Glutamic acid	L-Arginine	Glycine	L-Histidine
H	L-Omithine	L-Phenylalanine	L-Pyroglytamic acid	L-Valine	D,L-Carnitine	sec-Butylamine
PM2	7	8	9	10	11	12
A	Gelatin	Glycogen	Inulin	Laminarin	Mannan	<b>Pectin</b>
B	L-Arabitol	Arbutin	2-Deoxy-D-Ribose	i-Erythritol	D-Fucose	3-O-b-D-Galactopyranosyl-D-Arabinose
C	b-Methyl-D-Galactoside	3-Methylglucose	b-Methyl-D-Glucuronic acid	<b>a-Methyl-D-Mannoside</b>	b-Methyl-D-Xyloside	Palatinose
D	Turanose	Xylitol	N-Acetyl-D-Glucosaminitol	g-Amino-N-Butyric acid	d-Amino Valeric acid	Butyric acid
E	4-Hydroxybenzoic acid	b-Hydroxybutyric acid	g-Hydroxybutyric acid	a-Keto-Valeric acid	Itaconic acid	5-Keto-D-Gluconic acid
F	D-Ribono-1,4-Lactone	Sebacic acid	Sorbic acid	Succinamic acid	D-Tartaric acid	L-Tartaric acid
G	L-Homoserine	Hydroxy-L-Proline	L-Isoleucine	L-Leucine	L-Lysine	L-Methionine
H	D,L-Octopamine	Putrescine	Dihydroxyacetone	2,3-Butanediol	2,3-Butanedione	3-Hydroxy-2-butanone

**Figure S4.** Analysis of Biolog Phenotypic Microarray data.  $A_{\text{mutant}}$  refers to the absorbance value of  $\Delta pvmJ::IN(npt)$ -inoculated plates, and  $A_{\text{wt}}$  refers to  $\Delta plim_{1104}$ . The five carbon sources with the lowest values are bolded. In decreasing order:  $\alpha$ -methyl-D-mannoside, D-melezitose, L-fucose, D-raffinose, Pectin.

$\Delta\text{plim}_{1104}$ , PM1 plate

	1	2	3	4	5	6	7	8	9	10	11	12
A	0	-0.007	0.102	-0.018	-0.011	0.145	0.027	0.091	0.049	0.131	0.136	-0.001
B	-0.002	-0.017	-0.006	0.069	0.172	0.031	0.012	0.081	0.042	-0.076	0.029	0.029
C	-0.004	-0.077	-0.021	0.043	-0.076	0.026	0.012	0.006	0.179	0.191	0.093	-0.08
D	0.022	-0.091	0.018	0.025	-0.065	0.016	-0.087	0.168	0.116	0.12	0.187	-0.079
E	0.072	-0.058	-0.029	0.006	-0.061	-0.013	-0.082	0.245	-0.007	0.127	-0.094	-0.096
F	0.035	-0.074	0.026	-0.039	0.013	0.001	-0.08	-0.052	-0.094	-0.075	0.141	-0.096
G	0.059	-0.083	0.035	0.04	-0.031	-0.013	-0.045	0.107	0.031	-0.003	-0.029	-0.023
H	-0.037	-0.089	-0.09	-0.094	-0.025	0.068	0.158	0.1	-0.077	-0.09	-0.066	-0.076

$\Delta\text{pvmJ}::\text{IN}(npt)$ , PM1 plate

	1	2	3	4	5	6	7	8	9	10	11	12
A	0	0.06	0.112	0.007	0.025	0.152	0.033	0.079	0.052	0.107	0.065	-0.003
B	0.008	0.028	0.015	-0.012	0.119	0.04	0.04	0.154	0.037	-0.007	0.037	0.022
C	0.006	-0.004	0.011	0.129	-0.003	0.007	0.025	0.058	0.134	0.126	0.094	-0.008
D	0.037	-0.01	0.025	0.036	0.002	0.031	-0.008	0.142	0.115	0.11	0.134	-0.002
E	0.043	-0.002	0.01	0.02	0.003	0.014	-0.008	0.17	0.027	0.06	-0.019	-0.022
F	0.027	-0.005	0.046	0.005	0.012	0.029	-0.003	0.006	-0.018	0.004	0.106	-0.02
G	0.021	-0.014	0.048	0.044	-0.001	0.008	0.022	0.084	0.028	0.016	0.001	0
H	0.026	-0.013	-0.012	-0.017	0.013	0.164	0.103	0.053	-0.013	-0.012	0.037	-0.008

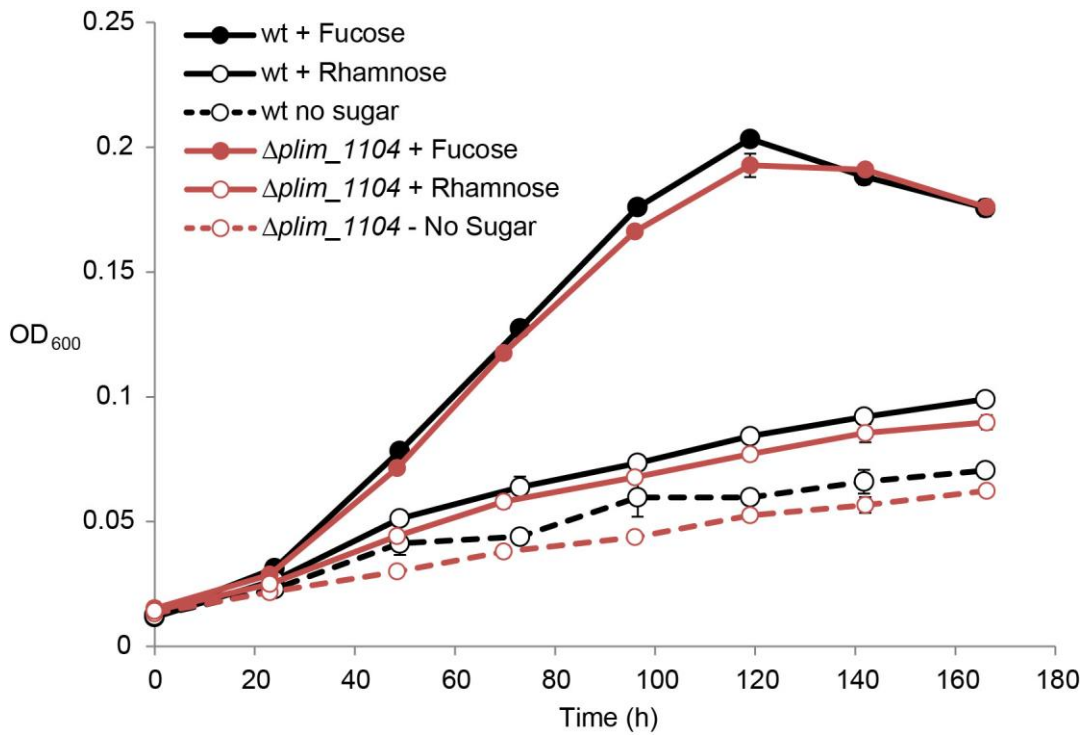
$\Delta\text{plim}_{1104}$ , PM2 plate

	1	2	3	4	5	6	7	8	9	10	11	12
A	0	0	-0.045	-0.018	-0.026	-0.067	0.011	-0.011	0.007	0.009	0.053	0.204
B	0.255	0.002	-0.063	-0.002	0.014	-0.059	0.031	-0.001	0.104	0.011	0.034	-0.042
C	0.18	0.118	0.218	0.178	0.171	0.241	0.167	0.002	0.053	0.262	0.035	0.129
D	0.164	0.07	-0.004	-0.04	0.052	0.051	0.194	0.005	0.017	-0.062	-0.071	-0.058
E	-0.073	-0.076	-0.07	-0.056	0.017	-0.074	-0.074	-0.054	0.016	-0.071	-0.076	-0.023
F	-0.011	-0.017	0.11	-0.044	-0.037	0.009	-0.061	-0.058	-0.012	-0.01	-0.022	-0.068
G	0.009	-0.027	0.013	-0.049	-0.006	0	-0.027	0.071	-0.055	-0.051	-0.018	-0.067
H	-0.017	-0.069	-0.024	-0.05	-0.002	-0.048	-0.069	-0.001	0.109	0.014	-0.048	-0.019

$\Delta\text{pvmJ}::\text{IN}(npt)$ , PM2 plate

	1	2	3	4	5	6	7	8	9	10	11	12
A	0	0.01	-0.007	0	0.002	-0.011	0.014	0.014	0.007	-0.013	0.015	0.041
B	0.192	0.003	0.009	0.049	0.082	-0.007	0.025	0.053	0.171	0.015	0.021	0.013
C	0.134	0.058	0.124	0.068	0.12	0.186	0.151	0.007	0.048	0.144	0.038	0.076
D	0.056	0.096	0.001	0.005	0.033	0.035	0.126	0.012	0.016	-0.008	-0.011	-0.008
E	-0.014	-0.011	-0.011	-0.007	0.076	-0.011	-0.016	-0.013	0.015	-0.01	-0.022	0.086
F	-0.002	0.002	0.044	0.017	0.027	0.011	-0.011	-0.012	0.054	-0.002	-0.004	-0.011
G	0.002	-0.002	0.01	0.009	0.01	0.016	0.001	0.052	-0.011	-0.005	-0.007	0.006
H	0.003	-0.014	-0.009	-0.011	-0.004	0.001	-0.015	0.001	0.193	-0.001	0.006	0.009

**Figure S5.** Raw Biolog Phenotypic Microarray data for *Δplim\_1104* and *ΔpvmJ::IN(npt)* inoculated into plates PM1 and PM2, and incubated for five days. Values are absorbance at 590nm, well A1 (no carbon source) was used to blank each plate. Carbon source identity key is available in Figure S4.



**Figure S6.** Growth profile comparison between wild-type (black) and  $\Delta plim_{1104}$  (red), on L-fucose (solid circles), L-rhamnose (open circles), and no sugar added (open circles with dashed line). Data points are an average of three independently grown liquid cultures (n=3), and error bars depict one standard deviation.

**Table S1.** New nomenclature of BMC-related genes of the PVM BMC gene cluster

<b>Gene Name</b>	<b>Representative Accession Number</b>	<b>Updated Annotation</b>	<b>Note</b>
<i>pvmA</i>	YP_003629787	Transcriptional regulator	Not present in <i>O. TAV</i> species or <i>O. terrae</i> . Inverted in the <i>Verrucomicrobia</i> species SCGC AAA164-E04 and DG1235
<i>pvmB</i>	YP_003629786	Phosphotransacylase	
<i>pvmC</i>	NP_865042	Hypothetical Protein	No function prediction, only present in <i>R. baltica</i>
<i>pvmD</i>	YP_003629785	BMC-H shell protein	
<i>pvmE</i>	YP_003629784	BMC-H shell protein	
<i>pvmF</i>	YP_004178760	BMC-H shell protein	Only present in <i>S. acidiphila</i> and <i>I. pallida</i>
<i>pvmG</i>	YP_003629783	Lactate Kinase	
<i>pvmH</i>	YP_003629782	BMC-P shell protein	
<i>pvmI</i>	YP_003629781	Hypothetical Protein	No function prediction, only present in the Planctomyces genus
<i>pvmJ</i>	YP_003629780	Lactaldehyde Dehydrogenase	Contains BMC targeting peptide
<i>pvmK</i>	YP_003629779	BMC-P shell protein	
<i>pvmL</i>	YP_003629778	Hypothetical Protein	No function prediction, not present in <i>I. pallida</i> or the <i>Verrucomicrobia</i>
<i>pvmM</i>	YP_003629777	BMC-P shell protein	
<i>pvmN</i>	YP_003629776	Aldolase	Contains BMC targeting peptide
<i>pvmO</i>	YP_003629775	1,2-propanediol dehydrogenase	Not present in <i>P. brasiliensis</i>



**Table S2.** List of Oligonucleotides used in this study

<b>Primer Name</b>	<b>Description</b>	<b>Sequence</b>
OE053	<i>npt</i> promoter forward primer	TATAGAATTCAGATCTCGGAATTGCCAGCT
OE054	<i>npt</i> reverse primer	TATAGGATCCTCAGAAGAACTCGTC
OE106	<i>plim_1104</i> upstream region forward primer	TATAGAATTCATGAGATCTGCCACAACCTTTTGTTCAGTCG
OE107	<i>plim_1104</i> upstream region reverse primer	TATAGGATCCTCGAAAAGCTTATCGCCAAT
OE108	<i>plim_1104</i> downstream region forward primer	TATAGAATTCATGAGATCTGCCACTTCAAGATCCAGTTCC
OE109	<i>plim_1104</i> downstream region reverse primer	TATAGGATCCGCCCGCCTACATGCTTATTA
OE149	<i>pvmO</i> reverse primer	TATATCTAGACTAGAGCACCTTTTCGATGGTC
OE189	<i>pvmJ</i> upstream region forward primer	TATAGAATTCATGAGATCTCATGGGTTGTAGTGCATTG
OE190	<i>pvmJ</i> upstream region reverse primer	TATAGGATCCCGATTCCGGTCTTTTCATCTGGCT
OE191	<i>pvmJ</i> downstream region forward primer	TATAGAATTCATGAGATCTTTTCACACGCAGCCGCC
OE192	<i>pvmJ</i> downstream region reverse primer	TATAGGATCCGGGACTTTGTCTGGTCGTTTA
OE193	<i>pvmN</i> upstream region forward primer	TATAGAATTCATGAGATCTAGGAGTGGCACCATGAGATT
OE194	<i>pvmN</i> upstream region reverse primer	TATAGGATCCATGATCGTTGTGGGTTGTGA
OE195	<i>pvmN</i> downstream region forward primer	TATAGAATTCATGAGATCTGCTGGTGAAGATGATCACCGAGC
OE196	<i>pvmN</i> downstream region reverse primer	TATAGGATCCATGACATCGCTATTGGCACA
OE206	<i>pvmH</i> forward primer	TATACATATGTTCTTCGCACGCGTC
OE215	<i>pvmM</i> forward primer	TATACATATGAGATTAGCCGAAGTGATTGGCC
OE255	<i>pvmD</i> upstream region forward primer	TATAGAATTCATGAGATCTATGTCTCTGATTCTGTGGTTGC
OE284	<i>pvmD</i> upstream region reverse primer	TATAGGATCCGAAAACCTTCTCTCAAGAAATGGAAC
OE285	<i>pvmE</i> downstream region forward primer	TATAGAATTCATGAGATCTGGTTGTCTTGGGTGGGATCG
OE286	<i>pvmG</i> reverse primer	TATAGGATCCCTAGGACTTTGAAAGAAGTTCGGC
OE288	<i>pvmE</i> downstream region reverse primer	TATAGGATCCGGCTACTGTTCTCGCCAATT

**Table S3.** Genomes and accession numbers of genes used in phylogenetic analysis for Figure 1B and

Supplementary Figures S1A and S1B.

Phylum	Species	<i>pduL</i> homolog accession(s)		<i>pduP</i> homolog accession(s)	
		GenBank	IMG	GenBank	IMG
Actinobacteria	<i>Atopobium fossor</i> DSM 15642		2512382991		2523432309
Actinobacteria	<i>Collinsella tanakaei</i> YIT 12063		2514564925		2514564922
Actinobacteria	<i>Olsenella uli</i> VPI, DSM 7084	YP_003800316		YP_003800320	
Firmicutes	<i>Acetobacterium woodii</i> WB1, DSM 1030		2512382991		2512382985
Firmicutes	<i>Alkaliphilus metalliredigens</i> QYMF	YP_001318154 YP_001321599		YP_001318151 YP_001321600	
Firmicutes	<i>Bacillus azotoformans</i> LMG 9581		2524346580		2524346575
Firmicutes	<i>Clostridium botulinum</i> Bf	ZP_02618436		ZP_02618437	
Firmicutes	<i>Clostridium carboxidivorans</i> P7, DSM 15243	ZP_06853152 ZP_06856827		ZP_06853151 ZP_06855343	
Firmicutes	<i>Clostridium difficile</i> VPI 10463, ATCC 43255		2512433896		2512433893
Firmicutes	<i>Clostridium ljungdahlii</i> PETC, DSM 13528	YP_003782098		YP_003779366	
Firmicutes	<i>Clostridium methylpentosum</i> R2, DSM 5476	ZP_03705299		ZP_03705305	
Firmicutes	<i>Clostridium phytofermentans</i> ISDg	YP_001559739 YP_001558300 YP_001558543		YP_001559742 YP_001558295 YP_001558542	
Firmicutes	<i>Clostridium sporogenes</i> ATCC 15579	ZP_02995752		ZP_02995751	
Firmicutes	<i>Enterococcus faecalis</i> AR01/DG	ZP_05593144		ZP_05593147	
Firmicutes	<i>Eubacterium limosum</i> KIST612	YP_003961982		YP_003961977	
Firmicutes	<i>Geobacillus</i> <i>thermoglucosidasius</i> C56-YS93	YP_004587975		YP_004587980	
Firmicutes	<i>Lactobacillus reuteri</i> SD2112, ATCC 55730	YP_004649427		YP_004649422	
Firmicutes	<i>Listeria monocytogenes</i> M7	AEH92193		AEH92176	
Firmicutes	<i>Ruminococcus gnavus</i> ATCC 29149	ZP_02040264		ZP_02040258	

<i>Firmicutes</i>	<i>Ruminococcus obeum</i> ATCC 29174	ZP_01962375	ZP_01962381	
<i>Firmicutes</i>	<i>Shuttleworthia satelles</i> DSM 14600	ZP_04454648	ZP_04454656	
<i>Firmicutes</i>	<i>Streptococcus merionis</i> DSM 19192		2515206018	2515206798
<i>Firmicutes</i>	<i>Thermoanaerobacterium saccharolyticum</i> JW/SL-YS485, DSM 8691		2519480168	2519480174
<i>Firmicutes</i>	<i>Thermoanaerobacterium xylanolyticum</i> LX-11, DSM 7097	YP_004471771	YP_004471777	
<i>Fusobacteria</i>	<i>Fusobacterium</i> sp. 1_1_41FAA	ZP_08600040	ZP_08600044	
<i>Fusobacteria</i>	<i>Fusobacterium</i> sp. 11_3_2		2514694583	2514694579
<i>Fusobacteria</i>	<i>Fusobacterium</i> sp. 12_1B	ZP_06748804	ZP_06748808	
<i>Fusobacteria</i>	<i>Fusobacterium</i> sp. 3_1_33	ZP_05815059	ZP_05815063	
<i>Fusobacteria</i>	<i>Fusobacterium ulcerans</i> ATCC 49185	ZP_05632380	ZP_05632384	
<i>Fusobacteria</i>	<i>Fusobacterium varium</i> ATCC 27725	ZP_04860876 ZP_04860159	ZP_04860880 ZP_04860157	
<i>Fusobacteria</i>	<i>Ilyobacter polytropus</i> CuHBu1, DSM 2926	YP_003968462	YP_003968466	
<i>Fusobacteria</i>	<i>Leptotrichia buccalis</i> C-1013-b, DSM 1135	YP_003162997	YP_003162999	
<i>Fusobacteria</i>	<i>Leptotrichia hofstadii</i> F0254	ZP_05902074	ZP_05902076	
<i>Fusobacteria</i>	<i>Sebaldella termitidis</i> ATCC 33386	YP_003307845	YP_003307836	
<i>Gemmatimonadetes</i>	<i>Gemmatimonadetes bacterium</i> JGI 0000112-M07		2517735326	2517733962
<i>Ignavibacteria</i>	<i>Melioribacter roseus</i> P3M		2517204486	2517204481
<i>Planctomycetes</i>	<i>Blastopirellula marina</i> SH 106T, DSM 3645	ZP_01094341	ZP_01094335	
<i>Planctomycetes</i>	<i>Isosphaera pallida</i> IS1B, ATCC 43644	YP_004178757	YP_004178763	
<i>Planctomycetes</i>	<i>Pirellula staleyi</i> DSM 6068	YP_003371803	YP_003371808	
<i>Planctomycetes</i>	<i>Planctomyces brasiliensis</i> IFAM 1448, DSM 5305	YP_004271671	YP_004271677	
<i>Planctomycetes</i>	<i>Planctomyces limnophilus</i> Mu 290, DSM 3776	YP_003629786	YP_003629780	

<i>Planctomycetes</i>	<i>Planctomyces maris DSM</i> 8797	ZP_01855342	ZP_01855336
<i>Planctomycetes</i>	<i>Rhodopirellula baltica SH 1</i>	NP_865043	NP_865037
<i>Planctomycetes</i>	<i>Singulisphaera acidiphila</i> MOB10, DSM 18658		2509618795
<i>Proteobacteria</i>	<i>Citrobacter freundii ATCC</i> 8090		2520192262
<i>Proteobacteria</i>	<i>Escherichia coli MS 116-1</i>	ZP_07163384	ZP_07163393
<i>Proteobacteria</i>	<i>Klebsiella pneumoniae 342</i>	YP_002236775	YP_002236771
<i>Proteobacteria</i>	<i>Pectobacterium wasabiae</i> WPP163	YP_003261437	YP_003261430
<i>Proteobacteria</i>	<i>Rhodobacter sphaeroides</i> WS8N	ZP_08415799	ZP_08415804
<i>Proteobacteria</i>	<i>Rhodopseudomonas palustris</i> BisB18	YP_531051	YP_531056
<i>Proteobacteria</i>	<i>Salmonella enterica enterica sv</i> <i>Typhimurium LT2</i>	NP_460992	NP_460996
<i>Proteobacteria</i>	<i>Shewanella putrefaciens CN-32</i>		2524134173
<i>Spirochaetes</i>	<i>Brachyspira intermedia</i> PWS/A		2511986595
<i>Synergistetes</i>	<i>Anaerobaculum</i> <i>hydrogeniformans ATCC</i> BAA-1850	ZP_06440568	ZP_06440562
<i>Synergistetes</i>	<i>Anaerobaculum mobile NGA,</i> DSM 13181	AFM20793	AFM20799
<i>Synergistetes</i>	<i>Cloacibacillus eoryensis 158,</i> DSM 19522		2510278482
<i>Synergistetes</i>	<i>Dethiosulfovibrio</i> <i>peptidovorans SEBR 4207,</i> DSM 11002		2501566260
<i>Synergistetes</i>	<i>Thermanaerovibrio</i> <i>acidaminovorans Su883, DSM</i> 6589	YP_003316598	YP_003316596
<i>Synergistetes</i>	<i>Thermanaerovibrio velox Z-</i> 9701, DSM 12556		2508842204
<i>Synergistetes</i>	<i>Thermovirga lienii Cas60314,</i> DSM 17291		2505285803
<i>Unclassified</i>	<i>Bacillus sp. URHB0009</i>		2523076465
<i>Verrucomicrobia</i>	<i>Opitutaceae bacterium sp.</i> TAV1		2508839157

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<i>Verrucomicrobia</i>	<i>Opitutaceae sp. TAV2</i>		2517755627	2517755621
<i>Verrucomicrobia</i>	<i>Opitutaceae sp. TAV5</i>		2510264820	2510264826
<i>Verrucomicrobia</i>	<i>Opitutus terrae PB90-1</i>	YP_001818174		YP_001818180
<i>Verrucomicrobia</i>	<i>Verrucomicrobia bacterium</i> SCGC AAA164-E04		2236429775	2236429769
<i>Verrucomicrobia</i>	<i>Verrucomicrobiales sp.</i> DG1235	ZP_05056059		ZP_05055688

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**Table S4.** Accession numbers and references for genes in Table 2.

<b>Gene Name</b>	<b>Accession</b>	<b>Reference(s) for (Predicted) Function</b>
<i>PduA</i>	NP_460983	(1)
<i>PduB</i>	NP_460984	(2–4)
<i>PduC</i>	NP_460985	(5)
<i>PduD</i>	NP_460986	(5)
<i>PduE</i>	NP_460987	(5)
<i>PduJ</i>	NP_460990	(2-4)
<i>PduK</i>	NP_460991	(2-4)
<i>PduL</i>	NP_460992	(6)
<i>PduN</i>	NP_460994	(2-4)
<i>PduP</i>	NP_460996	(7)
<i>PduQ</i>	NP_460997	(8)
<i>PduT</i>	NP_460999	(2-4)
<i>PduU</i>	NP_461000	(2-4)
<i>PduW</i>	NP_461002	(9)
<i>Ack</i>	NP_461279	(10)
<i>EutB</i>	NP_461393	(11, 12)
<i>EutC</i>	NP_461392	(10, 11)
<i>EutD</i>	NP_461401	(13)
<i>EutE</i>	NP_461398	(14)
<i>EutG</i>	NP_461396	(15, 16)
<i>EutK</i>	NP_461390	(17)
<i>EutL</i>	NP_461391	(17)
<i>EutM</i>	NP_461400	(17)
<i>EutN</i>	NP_461399	(17)
<i>EutS</i>	NP_461405	(17)
<i>Cphy_1174</i>	YP_001558291	(18)
<i>Cphy_1176</i>	YP_001558293	(18)
<i>Cphy_1177</i>	YP_001558294	(18)
<i>Cphy_1178</i>	YP_001558295	(18)
<i>Cphy_1179</i>	YP_001558296	(18)
<i>Cphy_1180</i>	YP_001558297	(18)
<i>Cphy_1181</i>	YP_001558298	(18)
<i>Cphy_1182</i>	YP_001558299	(18)
<i>Cphy_1183</i>	YP_001558300	(18)
<i>Cphy_1184</i>	YP_001558301	(18)
<i>Cphy_1185</i>	YP_001558302	(18)
<i>Cphy_1186</i>	YP_001558303	(18)



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