

Table S3. Summary of model output for the default and bacteria response models. Pearson correlations and p values between experimental and model data for metabolites and corresponding genes are shown. n.a., not applicable.

Metabolite or gene name/locus tag		Pattern category	Default model		Recognition model	
			r	p	r	p
Metabolites						
	Leucine	M-1	-0.412	0.033	0.701	0.000
	Glycerol 3-phosphate	M-1	-0.181	0.365	0.554	0.003
	DHPS	M-1	-0.104	0.605	0.725	0.000
	DMSP	M-1	-0.246	0.217	0.824	0.000
	Acetate	M-2	0.580	0.002	n.a.	n.a.
	Glucose	M-3	0.807	0.000	0.913	0.000
	Uridine	M-3	0.887	0.000	n.a.	n.a.
	Proline	M-4	0.567	0.002	n.a.	n.a.
Genes						
	<i>Leucine</i> ivD	G-2	0.22	< 0.05	0.17	< 0.05
	mccA	G-2	0.30	< 0.01	0.21	< 0.05
	SPO0390	G-2	0.01	0.73	0.07	0.18
<i>Glycerol 3-phosphate</i>	SPO0731	G-1	0.34	< 0.01	0.26	< 0.05
	ugpE	G-1	0.32	< 0.01	0.25	< 0.05
	SPO0369	G-1	0.44	< 0.001	0.35	< 0.01
<i>DHPS</i>	hpsK	G-1	0.42	< 0.001	0.33	< 0.01
	hpsN	G-1	0.42	< 0.001	0.34	< 0.01
<i>DMSP</i>	dmdA	G-1	0.42	< 0.001	0.34	< 0.01
	dddW	G-1	0.45	< 0.001	0.36	< 0.01
	dddD	G-1	0.42	< 0.001	0.34	< 0.01
	dddP	G-1	0.44	< 0.001	0.36	< 0.01
<i>Acetate</i>	SPO0325	G-2	0.26	< 0.05	n.a.	n.a.
	SPO0326	G-2	0.29	< 0.01	n.a.	n.a.
<i>Glucose</i>	galM	G-1	0.32	< 0.01	0.31	< 0.01
	xyfF	G-1	0.19	< 0.05	0.17	< 0.05
<i>Uridine</i>	iunH	G-1	0.28	< 0.05	n.a.	n.a.
<i>Proline</i>	SPO1031	G-1	0.25	< 0.05	n.a.	n.a.
	SPO2441	G-1	0.24	< 0.05	n.a.	n.a.
	SPOA0231	G-1	0.27	< 0.05	n.a.	n.a.