

## Supporting figure legends

**SI\_Figure 1.** Fluorescence images showing the effect of different formamide concentrations on hybridization specificity of community genome arrays. The locations of individual probes on the pilot arrays are listed in SM\_Table 1. Whole genomic DNA from *A. tolulyticus* Td-21 was randomly labeled with the fluorescent dye Cy5 (red pseudocolor) and hybridized with the CGA at 55°C for 12–15 h in the presence of 0, 10, 20, 30, 40, 50, 60, or 70% (v/v) formamide. The hybridization signal for the targeted Td-21 genome is circled.

**SI\_Figure 2.** Detection sensitivity of CGA hybridization using labeled pure genomic DNA. Genomic DNA from a pure culture of *P. stutzeri* B2-2 was labeled with Cy3 using the random primer labeling method. Labeled target DNA was hybridized to the community genome array at total concentrations of 0.2, 0.5, 1, 2, and 5 ng in a total hybridization solution volume of 3 µl. The arrays were scanned with 100% laser power and 100% PMT gain. The scanned image display of the hybridization reaction is presented, with the arrow indicating the hybridization signal for the B2-2 genome probe. Other fluorescent spots indicate cross-hybridization of the labeled target DNA with genomes from other *P. stutzeri* strains.

## Supporting Table

S1\_Table 1. Locations of reference strains on the community genome array

Rows	Column s <sup>+</sup>	Column Groups	Species#	Strains/genes	G+C Content
1	a	γ-proteobacteria	<i>Shewanella algae</i>	BrY	52-55
2	a	γ-proteobacteria	<i>Shewanella pealeana</i>	ANG-SQ1	45
3	a	γ-proteobacteria	<i>Shewanella algae</i>	OK-1	52-55

4	a	$\gamma$ -proteobacteria	<i>Shewanella amazonensis</i>	SB2B	52
5	a	$\gamma$ -proteobacteria	<i>Shewanella woodyi</i>	MS32	39
6	a	$\gamma$ -proteobacteria	<i>Shewanella oneidensis</i>	MR-1	45
7	a	$\gamma$ -proteobacteria	<i>S. oneidensis</i>	MR-4	45
8	a	$\beta$ -proteobacteria	<i>Azoarcus tolulyticus</i>	Td-1	69.3
9	a	$\beta$ -proteobacteria	<i>A. tolulyticus</i>	Td-2	67.8
10	a	$\beta$ -proteobacteria	<i>A. tolulyticus</i>	Td-3	68.5
11	a	$\beta$ -proteobacteria	<i>A. tolulyticus</i>	Td-15	68.0*
12	a	$\beta$ -proteobacteria	<i>A. tolulyticus</i>	Td-17	66.9
13	a	$\beta$ -proteobacteria	<i>A. tolulyticus</i>	Td-19	67.3
14	a	$\beta$ -proteobacteria	<i>A. tolulyticus</i>	Td-21	68.6
15	a	$\beta$ -proteobacteria	<i>Azoarcus</i> sp.	BL-11	67.4
1	b	$\beta$ -proteobacteria	<i>A. indigens</i>	VB22 <sup>T</sup>	68.0*
2	b	$\gamma$ -proteobacteria	<i>Shewanella</i> sp.	A8-3	49*
3	b	$\gamma$ -proteobacteria	<i>Pseudomonas stutzeri</i>	B2-2	63.0*
4	b	$\gamma$ -proteobacteria	<i>Halomonas variabilis</i>	B9-12	65.2*
5	b	$\alpha$ -proteobacteria	$\alpha$ -proteobacterium	C1-4	--
6	b	$\gamma$ -proteobacteria	<i>P. stutzeri</i>	C5-1	63.0*
7	b	$\gamma$ -proteobacteria	<i>Marinobacter</i> sp.	C10-5	55.7
8	b	$\gamma$ -proteobacteria	<i>Marinobacter</i> sp.	D3-15	55.7
9	b	Gram positive	<i>Staphylococcus</i> <i>saprophyticus</i>	D3-16	37*
10	b	$\gamma$ -proteobacteria	<i>Marinobacter</i> sp.	D5-10	55.7

11	b	$\gamma$ -proteobacteria	<i>P. stutzeri</i>	D7-6	63.0*
12	b	$\gamma$ -proteobacteria	<i>P. stutzeri</i>	D8-12	63.0*
13	b	$\gamma$ -proteobacteria	<i>Marinobacter sp.</i>	E1-7	55.7
14	b	$\gamma$ -proteobacteria	<i>P. stutzeri</i>	E4-2	63.0*
15	b	Gram positive bacteria	<i>Bacillus methanolicus</i>	F6-2	43*
1	c	Gram positive bacteria	<i>B. methanolicus</i>	F7-3	43*
2	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i>	F9-1	63.0*
3	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i>	F9-2	63.0*
4	c	$\gamma$ -proteobacteria	<i>Marinobacter sp.</i>	2-25	55.7
5	c	$\alpha$ -proteobacteria	<i>Pseudomonas sp.</i>	G-179	63.0*
6	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i> 17592	ATCC 17592	60.9
7	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i> DSM 50238	DSM 50238	64.9
8	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i> 17594	ATCC 17594	63.8
9	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i> 17595	ATCC 17595	61.5
10	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i> 17587	ATCC 17587	62.3
11	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i> CCUG 11256	CCUG 11256	65.0
12	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i> 17591	ATCC 17591	61.4
13	c	$\gamma$ -proteobacteria	<i>P. stutzeri</i> DNSP21	DNSP21	63.4
14	c	$\gamma$ -proteobacteria	<i>P. balearica</i> DSM 6083	DSM 6083	64.4
15	c	$\gamma$ -proteobacteria	<i>Escherichia coli</i>	S17-1/ $\lambda_{pir}$	55.1*
1	d	Yeast	<i>Saccharomyces cerevisiae</i>	Yeast Genomic	

				DNA	
2	d	Yeast	<i>S. cerevisiae</i>	Yeast- <i>mfa1</i>	
3	d	Yeast	<i>S. cerevisiae</i>	Yeast- <i>mfa2</i>	
4	d	Yeast	<i>S. cerevisiae</i>	Yeast- <i>ras1</i>	
5	d	Yeast	<i>S. cerevisiae</i>	Yeast- <i>act1</i>	
6	d	Yeast	<i>S. cerevisiae</i>	Yeast- <i>ste3</i>	
7	d	$\gamma$ -proteobacteria	<i>Shewanella sp.</i>	7-1	49*
8	d	$\gamma$ -proteobacteria	<i>Shewanella sp.</i>	7-2	49*
9	d	$\gamma$ -proteobacteria	<i>Shewanella gelidimarina</i>	11-1	48
10	d	$\gamma$ -proteobacteria	<i>Shewanella sp.</i>	11-2	49*
11	d	$\gamma$ -proteobacteria	<i>Shewanella sp.</i>	14-2	49*
12	d	$\gamma$ -proteobacteria	<i>Shewanella sp.</i>	PS-2 (SQ26)	49*
13	d	$\gamma$ -proteobacteria	<i>Shewanella sp.</i>	PS-3 (SQ26)	49*
14	d	$\gamma$ -proteobacteria	<i>S. woodyi</i>	PV-3	39
15	d	--	--	--	--
1	e	$\gamma$ -proteobacteria	<i>Pseudomonas fluorescens</i>	ATCC 17397	60.54
2	e	$\gamma$ -proteobacteria	<i>Pseudomonas putida</i>	ATCC 12633	63.0*
3	e	$\gamma$ -proteobacteria	<i>P. putida</i>	DSM4476	63.0*
4	e	$\gamma$ -proteobacteria	<i>Pseudomonas chlororaphis</i>	ATCC 17811	63.0*
5	e	$\gamma$ -proteobacteria	<i>P. fluorescens</i>	ATCC 17467	60.54
6	e	$\gamma$ -proteobacteria	<i>P. fluorescens</i>	ATCC 13525	60.54
7	e	$\gamma$ -proteobacteria	<i>Pseudomonas aureofaciens</i>	ATCC 13985	63.0*

8	e	$\gamma$ -proteobacteria	<i>P. fluorescens</i>	ATCC 17400	60.54
9	e	$\gamma$ -proteobacteria	<i>Pseudomonas aeruginosa</i>	ATCC 27583	66.1
10	e	$\gamma$ -proteobacteria	<i>P. aeruginosa</i>	ATCC 15692	63.0*
11	e	$\gamma$ -proteobacteria	<i>P. stutzeri</i> KC	KC	63.0*
12	e	$\gamma$ -proteobacteria	<i>P. stutzeri</i>	Tm300	63.0*
13	e	$\gamma$ -proteobacteria	<i>Pseudomonas mendocina</i>	ATCC 25411	63.0*
14	e	--	--	--	--
15	e	--	--	--	--

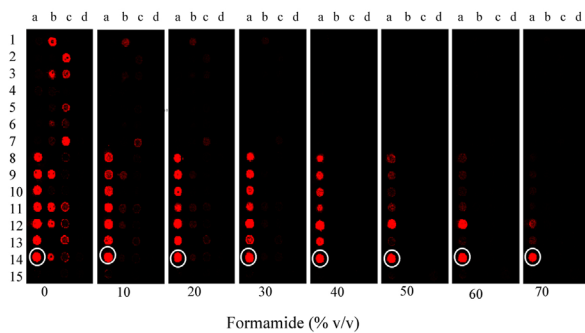
<sup>+</sup>The species presented in the fifth column (e) were added for experiments evaluating species relationships.

\*Genus average.

<sup>#</sup>For phylogenetic relationships between most of the strains, please refer to the references 15, 26, 28, 30, 43, and 46.

## Supporting Figures

SI\_Figure 1.



SI\_Figure 2.

