

**Table S3 Comparison of the crc-regulated genes and predicated crc-binding genes**

PA#	Gene	Fold change	SD	Protein
PA0117		<b>2.1</b>	<b>0.8</b>	probable short chain dehydrogenase
PA0129	gabP	<b>1.7</b>	<b>0.1</b>	gamma-aminobutyrate permease
PA0133		<b>2.3</b>	<b>1.4</b>	probable transcriptional regulator
PA0430	metF	<b>1.8</b>	<b>0.4</b>	5,10-methylenetetrahydrofolate reductase
PA0585		<b>-1.7</b>	<b>1.0</b>	hypothetical protein
PA0782	putA	<b>-1.5</b>	<b>0.1</b>	proline dehydrogenase PutA
PA0783	putP	<b>1.7</b>	<b>0.1</b>	sodium/proline symporter PutP
PA0831	oruR	<b>1.6</b>	<b>0.0</b>	transcriptional regulator OruR
PA0872	phhA	<b>-2.3</b>	<b>0.6</b>	phenylalanine-4-hydroxylase
PA1617		<b>2.0</b>	<b>0.8</b>	probable AMP-binding enzyme
PA1991		<b>1.6</b>	<b>0.2</b>	probable iron-containing alcohol dehydrogenase
PA2081	kynB	<b>1.5</b>	<b>0.6</b>	kynurenine formamidase, KynB
PA2332		<b>1.5</b>	<b>0.2</b>	probable transcriptional regulator
PA2338		<b>7.5</b>	<b>0.7</b>	probable binding protein component of ABC maltose/mannitol transporter
PA2482		<b>-2.9</b>	<b>0.7</b>	probable cytochrome c
PA2760		<b>3.9</b>	<b>2.0</b>	probable outer membrane protein precursor
PA2776		<b>1.6</b>	<b>0.0</b>	conserved hypothetical protein
PA2886	atuA	<b>2.1</b>	<b>0.7</b>	expressed protein with apparent function in citronellol catabolism
PA2890	atuE	<b>1.8</b>	<b>0.0</b>	putative isohexenylglutaconyl-CoA hydratase
PA3027		<b>2.0</b>	<b>0.2</b>	probable transcriptional regulator
PA3038		<b>1.7</b>	<b>0.5</b>	probable porin
PA3161	himD	<b>2.0</b>	<b>0.1</b>	integration host factor beta subunit
PA3183	zwf	<b>2.2</b>	<b>0.2</b>	glucose-6-phosphate 1-dehydrogenase
PA3190		<b>1.6</b>	<b>0.5</b>	probable binding protein component of ABC sugar transporter
PA3215		<b>2.1</b>	<b>0.4</b>	probable transcriptional regulator
PA3283		<b>-6.4</b>	<b>4.3</b>	conserved hypothetical protein
PA3300	fadD2	<b>2.5</b>	<b>1.2</b>	long-chain-fatty-acid--CoA ligase
PA3482	metG	<b>1.7</b>	<b>0.5</b>	methionyl-tRNA synthetase
PA3537	argF	<b>2.6</b>	<b>0.3</b>	ornithine carbamoyltransferase, anabolic
PA3959		<b>1.6</b>	<b>0.7</b>	hypothetical protein
PA4070		<b>1.7</b>	<b>0.6</b>	probable transcriptional regulator
PA4090		<b>-2.8</b>	<b>0.5</b>	hypothetical protein
PA4094		<b>2.1</b>	<b>0.6</b>	probable transcriptional regulator
PA4247	rplR	<b>1.5</b>	<b>0.2</b>	50S ribosomal protein L18
PA4471		<b>-20.8</b>	<b>20.5</b>	hypothetical protein
PA4570		<b>-7.1</b>	<b>5.7</b>	hypothetical protein
PA4571		<b>3.2</b>	<b>1.9</b>	probable cytochrome c
PA4733	acsB	<b>1.6</b>	<b>0.2</b>	acetyl-coenzyme A synthetase
PA4770	lldP	<b>-1.7</b>	<b>0.8</b>	L-lactate permease
PA4937	rnr	<b>-1.5</b>	<b>0.2</b>	exoribonuclease RNase R
PA4983		<b>1.8</b>	<b>0.9</b>	probable two-component response regulator
PA4985		<b>1.5</b>	<b>0.3</b>	hypothetical protein
PA5056	phaC1	<b>1.6</b>	<b>0.4</b>	poly(3-hydroxyalkanoic acid) synthase 1
PA5060	phaF	<b>-1.5</b>	<b>0.2</b>	polyhydroxyalkanoate synthesis protein PhaF
PA5075		<b>2.0</b>	<b>0.5</b>	probable permease of ABC transporter
PA5112	estA	<b>1.7</b>	<b>0.6</b>	esterase EstA
PA5152		<b>4.2</b>	<b>1.0</b>	probable ATP-binding component of ABC transporter
PA5167		<b>5.3</b>	<b>1.5</b>	probable c4-dicarboxylate-binding protein

PA5168		<b>9.7</b>	<b>4.5</b>	probable dicarboxylate transporter
PA5220		<b>1.5</b>	<b>0.5</b>	hypothetical protein
PA5235	glpT	<b>1.9</b>	<b>0.4</b>	glycerol-3-phosphate transporter
PA5285		<b>1.5</b>	<b>0.1</b>	hypothetical protein
PA5301		<b>2.4</b>	<b>0.8</b>	probable transcriptional regulator
PA5324		<b>3.8</b>	<b>1.4</b>	probable transcriptional regulator
PA5348		<b>5.4</b>	<b>0.9</b>	probable DNA-binding protein
PA5442		<b>3.0</b>	<b>1.4</b>	conserved hypothetical protein