

Table 3S. Comparison of *arcA* microarray expression data between *H. influenzae* and *E. coli*

<i>H. influenzae</i>		RAA6V/ RdV		<i>E. coli</i> homolog	Salmon <i>et al.</i> <i>arcA</i> -/ <i>arcA</i> +		Liu and De Wulf <i>arcA</i> -/ <i>arcA</i> +	
Gene ID	Function	Fold change	P value		Fold change	P value	Fold change	P value
HI0007	Formate dehydrogenase, beta subunit (<i>fdxH</i>)	7.8	1.12E-09	<i>fdnH</i>	-1.62	3.26E-02		
				<i>fdoH</i>	2.32	5.08E-02		
HI0008	Formate dehydrogenase, gamma subunit (<i>fdxI</i>)	9.7	5.42E-09	<i>fdnI</i>	-2.18	5.89E-03		
HI0009	FdhE protein (<i>fdhE</i>)	9.7	8.39E-10	<i>fdhE</i>	1.92	1.65E-02		
HI0018	Uracil DNA glycosylase (<i>ung</i>)	2.5	1.01E-05	<i>ung</i>				
HI0026	Lipoate biosynthesis protein A (<i>lipA</i>)	2.6	4.08E-07	<i>lipA</i>	1.82	1.47E-01		
HI0174	Conserved hypothetical protein	2.3	1.75E-05	<i>ycfB</i>	-1.36	9.44E-02		
HI0608	Conserved hypothetical protein	5.5	3.65E-10	<i>yfbS</i>	-1.91	4.08E-03		
HI0747	NADH dehydrogenase (<i>ndh</i>)	10.7	4.06E-11	<i>ndh</i>	3.93	6.47E-03	-3.5	2.64E-02
HI0889	Serine hydroxymethyltransferase (serine methylase) (<i>glyA</i>)	2.4	4.11E-06	<i>glyA</i>	1.04	8.47E-01		
HI0890	Dephospho-CoA kinase	2.5	4.83E-05	<i>coaE</i> (<i>yacE</i>)				
HI1218	L-lactate permease (<i>lldP</i>)	44.0	1.20E-08	<i>lctP</i> (<i>lldP</i>)			11.4	2.0E-04
HI1444	5,10 methylenetetrahydrofolate reductase (<i>metF</i>)	5.6	4.91E-06	<i>metF</i>				
HI1661	2-oxoglutarate dehydrogenase E2 component (<i>sucB</i>)	2.8	5.33E-07	<i>sucB</i>	15.50	1.14E-03		
HI1662	2-oxoglutarate dehydrogenase E1 component (<i>sucA</i>)	2.6	6.71E-07	<i>sucA</i>	11.14	1.85E-03		
HI1727	Argininosuccinate synthetase (<i>argG</i>)	4.8	5.02E-07	<i>argG</i>	-1.82	5.94E-03		
HI1728	Conserved hypothetical protein	3.5	1.54E-06	<i>yfeP</i>	-1.78	4.54E-03		
HI1730	Conserved hypothetical protein	3.0	1.48E-06	<i>ybgK</i>				
HI1731	Conserved hypothetical protein	5.9	2.52E-09	<i>ybgJ</i>				
HI1739.1	L-lactate dehydrogenase (<i>lldD</i>)	3.2	1.79E-10	<i>lctD</i> (<i>lldD</i>)			11.4	2.0E-04
HI0590	Putrescine-ornithine antiporter (<i>potE</i>)	-2.5	3.06E-08	<i>potE</i>	-1.50	1.87E-02		
HI0591	Ornithine decarboxylase (<i>speF</i>)	-4.0	2.54E-08	<i>speF</i>				
HI0592	Conserved hypothetical protein	-4.4	4.62E-08	no homolog				
HI0884	Aerobic respiration control protein ArcA (<i>arcA</i>)	-654.8	2.72E-12	<i>arcA</i>	-2.09	2.37E-03		
HI1349	Conserved hypothetical protein, similar to dps protein family	-3.4	1.43E-07	<i>dps</i>				

Similarities and differences across species in putative ArcA regulons. *H. influenzae arcA* microarray expression data (from Tables 1 and 2, columns RAA6V/ RdV) was compared to *E. coli arcA* microarray expression data of Salmon *et al.* (Salmon, K.A., *et al.* 2005. *J. Biol. Chem.* 280: 15084-15096) and Liu and De Wulf (Liu, X. and P. De Wulf. 2004. *J. Biol. Chem.* 279:12588-12597).

Putative *E. coli* homologs in bold have expression data from either microarray sets of Salmon *et al.* or Liu and De Wulf that show agreement with the *H. influenzae* array data in anaerobic expression ratios in the $\Delta arcA$ mutant, RAA6V vs. the parent strain, RdV. Fold change values represent an increase (positive) or decrease (negative) in gene expression in the $\Delta arcA$ mutant vs. parent strain, RdV. *E. coli* homologs with blank entries are genes whose expression levels did not meet the authors' criteria for minimum signal detection on the array.