

TABLE S2 Genes differentially regulated in *arcA* mutant strain versus WT strain, grown in duck serum

Gene/locus name	Function or description of product	Fold change in expression	p-value	q-value
<i>grxA</i>	glutaredoxin 1	-16.3	4.60E-06	0.004279
<i>flgB</i>	cell-proximal portion of basal-body rod FlgB	-14.6	0.001120	0.056753
<i>FlgD</i>	flagellar hook formation protein FlgD	-10.0	0.001539	0.064927
<i>FlgE</i>	flagellar biosynthesis, hook protein FlgE	-7.0	0.001448	0.063975
<i>motA</i>	flagellar motor protein MotA	-6.4	1.40E-05	0.007796
<i>ydgR</i>	putative tripeptide transporter permease	-6.4	0.001257	0.058511
<i>FeoB</i>	ferrous iron transport protein B	-6.0	2.07E-05	0.009627
<i>fliM</i>	Flagellar motor switch protein	-5.2	0.002583	0.077688
<i>fhuC</i>	iron-hydroxamate transporter subunit	-5.1	0.003364	0.087784
<i>fliD</i>	flagellar capping protein	-4.7	0.000139	0.025915
<i>amtB</i>	putative ammonium transporter	-4.6	0.001037	0.054607
<i>fliH</i>	flagellar assembly protein	-4.6	0.000892	0.050819
<i>FlgK</i>	flagellar hook-associated protein	-4.5	6.26E-05	0.017471
<i>fliK</i>	flagellar hook-length control protein	-4.4	0.003865	0.094289
<i>fliA</i>	flagellar biosynthesis sigma factor FliA	-4.2	0.001138	0.056753
<i>glnQ</i>	glutamine ABC transporter ATP-binding component	-4.2	0.002283	0.074080
<i>motB</i>	flagellar motor protein	-4.1	0.000682	0.045341
<i>fliC</i>	flagellin	-4.0	0.000221	0.030852
<i>yjdE</i>	putative amino acid/amine transport protein, cryptic	-4.0	0.003041	0.084496
<i>glnP</i>	glutamine transport protein GlnP	-3.9	0.001508	0.064759
<i>CheA</i>	chemotaxis protein CheA	-3.9	5.80E-05	0.017471
<i>cheW</i>	positive regulator of CheA protein activity	-3.7	0.000211	0.030852
<i>flgH</i>	flagellar basal body L-ring protein precursor	-3.5	0.003964	0.094430
<i>cheY</i>	chemotaxis protein CheY	-3.5	0.001637	0.065296
<i>adiY</i>	putative regulatory protein AdiY	-3.3	0.003795	0.093765
<i>cheR</i>	chemotaxis regulator, protein-glutamate methyltransferase	-3.3	0.000890	0.050819
<i>ahpC</i>	alkyl hydroperoxide reductase, C22 subunit	-3.3	0.001125	0.056753
<i>tar</i>	methyl-accepting chemotaxis protein II	-3.3	0.003669	0.092843
<i>oppD</i>	oligopeptide transport ATP-binding protein OppD	-3.2	0.000808	0.050819
<i>fliG</i>	flagellar motor switch protein G	-3.2	0.001927	0.069285
<i>oppB</i>	oligopeptide transport permease protein	-3.2	0.000180	0.030852
<i>citE</i>	citrate lyase beta chain	-3.2	0.000557	0.041502

<i>APECO1_4385</i>	fructose-specific PTS system IIA component	-3.1	0.002645	0.078566
<i>citF</i>	citrate lyase alpha chain	-3.1	0.002195	0.072548
<i>flgI</i>	flagella basal body P-ring-like protein FlgI	-3.0	0.003323	0.087538
<i>cydA</i>	cytochrome d terminal oxidase, subunit I	-3.0	0.002588	0.077688
<i>gst</i>	glutathione S-transferase	-2.9	0.002125	0.072548
<i>cheZ</i>	chemotaxis regulator, protein phosphatase for CheY	-2.9	0.001194	0.057478
<i>oppC</i>	oligopeptide transporter subunit	-2.8	0.000986	0.054607
<i>ybjM</i>	conserved hypothetical protein YbjM	-2.7	0.004209	0.094788
<i>fdhF</i>	formate dehydrogenase-H, selenopolypeptide subunit	-2.7	0.002684	0.078873
<i>flgL</i>	flagellar hook-associated protein FlgL	-2.6	0.001671	0.065513
<i>thrB</i>	homoserine kinase	-2.6	0.003279	0.087538
<i>APECO1_3052</i>	conserved hypothetical protein	-2.5	0.001309	0.059587
<i>frdB</i>	iron-sulfur protein subunit of fumarate reductase	-2.1	0.004294	0.094788
<i>tsr</i>	methyl-accepting chemotaxis protein I, serine sensor receptor	-2.1	0.002751	0.079994
<i>zntA</i>	lead, cadmium, zinc and mercury transporting ATPase	-2.1	0.002335	0.074080
<i>livM</i>	leucine/isoleucine/valine transporter subunit LivM	-2.0	0.003461	0.089486
<i>yihF</i>	conserved hypothetical protein	2.2	0.003691	0.092843
<i>fliR</i>	flagellar biosynthetic protein FliR	2.3	0.002534	0.077688
<i>znuA</i>	adhesin-like protein	2.4	0.001253	0.058511
<i>APECO1_1702</i>	conserved hypothetical protein	2.4	0.001794	0.066992
<i>APECO1_1174</i>	hypothetical protein	2.4	0.002164	0.072548
<i>ybiL</i>	putative tonB-dependent receptor YbiL precursor	2.4	0.002961	0.084496
<i>gudD</i>	glucarate dehydratase	2.6	0.004337	0.094788
<i>fimH</i>	type 1 fimbrial adhesin FimH	2.8	0.004051	0.094788
<i>iclR</i>	aceBAK operon repressor	2.9	0.000880	0.050819
<i>phoE</i>	outer membrane pore protein E precursor	2.9	0.004260	0.094788
<i>cirA</i>	ferric iron-catecholate outer membrane transporter	2.9	0.003913	0.094289
<i>NmpC</i>	outer membrane porin protein	2.9	0.001987	0.070225
<i>yggR</i>	conserved hypothetical protein	3.0	0.001027	0.054607
<i>APECO1_1700</i>	putative NADH-dependent flavin oxidoreductase	3.0	0.003050	0.084496
<i>APECO1_4448</i>	putative fructose-bisphosphate aldolase	3.1	0.003255	0.087538
<i>APECO1_4058</i>	hypothetical protein	3.2	0.003917	0.094289
<i>crl</i>	crl transcriptional regulator	3.2	0.001734	0.066338
<i>APECO1_3393</i>	conserved hypothetical protein	3.4	0.000482	0.041502
<i>yaaX</i>	conserved hypothetical protein	3.4	0.000566	0.041502

<i>bglH</i>	carbohydrate-specific outer membrane porin, cryptic	3.5	0.003319	0.087538
<i>APECO1_2187</i>	putative hexuronate transporter , D-galactonate transporter	3.7	0.000339	0.037864
<i>APECO1_1629</i>	conserved hypothetical protein	3.7	0.003674	0.092843
<i>yjcG</i>	putative symporter YjcG	3.7	0.003991	0.094430
<i>yhjE</i>	putative metabolite transport protein YhjE	3.7	0.001032	0.054607
<i>ybcS2</i>	bacteriophage lambda lysozyme-like protein	3.8	0.001466	0.063975
<i>ycgF</i>	conserved hypothetical protein	3.8	0.000264	0.03353
<i>yjiJ</i>	putative permease	4.0	0.000580	0.041502
<i>cycA</i>	transport of D-alanine, D-serine, and glycine	4.1	0.00459	0.098662
<i>APECO1_2625</i>	putative 2-keto-3-deoxygalactokinase	4.1	0.004346	0.094788
<i>ydcJ</i>	conserved hypothetical protein	4.2	0.004384	0.094875
<i>yjiK</i>	SdiA-regulated	4.2	0.000508	0.041502
<i>YlaC</i>	conserved hypothetical protein	4.2	7.19E-05	0.018243
<i>malK</i>	maltose/maltodextrin transport ATP-binding protein MalK	4.3	0.001323	0.059587
<i>mgo</i>	malate:quinone oxidoreductase	4.3	0.000448	0.041502
<i>APECO1_2112</i>	FimF protein precursor	4.3	0.001580	0.064927
<i>glcB</i>	malate synthase G	4.4	0.001803	0.066992
<i>yjaE</i>	Regulator of sigma D	4.4	0.001588	0.064927
<i>metF</i>	5,10-methylenetetrahydrofolate reductase	4.6	0.002494	0.077688
<i>IclR</i>	Bacterial transcriptional regulator,	4.7	0.000204	0.030852
<i>metA</i>	homoserine O-succinyltransferase MetA	4.9	0.004344	0.094788
<i>yigI</i>	conserved hypothetical protein	5.0	0.000308	0.037352
<i>FimA</i>	P pilus assembly protein, pilin FimA	5.0	0.001166	0.057068
<i>APECO1_2442</i>	conserved hypothetical protein	5.1	0.000765	0.049697
<i>glcC</i>	conserved hypothetical protein	5.4	0.002041	0.071217
<i>fimA</i>	type 1 fimbriae major subunit FimA	5.6	0.002990	0.084496
<i>CreD</i>	colicin E2 resistance	6.0	0.000189	0.030852
<i>fimD</i>	outer membrane usher protein FimD precursor	6.1	0.000360	0.038607
<i>APECO1_4163</i>	putative oxalyl-CoA decarboxylase	6.2	0.001936	0.069285
<i>yfdV</i>	putative transporter protein	6.7	0.002330	0.074080
<i>ydcI</i>	putative transcriptional regulator YdcI	7.2	0.003092	0.084627
<i>fimI</i>	FimI fimbrial protein	7.5	0.000443	0.041502
<i>APECO1_279</i>	conserved hypothetical protein	7.6	0.001824	0.066992
<i>envR</i>	putative acrEF/envCD operon repressor	7.6	0.000623	0.042437
<i>PapD</i>	type I fimbrial chaperone	8.2	3.06E-05	0.012203
<i>ybgO</i>	conserved hypothetical protein	8.7	0.000558	0.041502
<i>yjcH</i>	conserved hypothetical protein	9.2	0.002209	0.072548
<i>YfdX</i>	conserved hypothetical protein	9.4	0.000244	0.032421
<i>APECO1_282</i>	conserved hypothetical protein	9.7	0.000328	0.037864

<i>putP</i>	proline:sodium symporter	10.3	0.001604	0.064927
<i>kgtP</i>	alpha-ketoglutarate permease	10.5	8.06E-05	0.018753
<i>yneI</i>	aldehyde-dehydrogenase like protein YneI	10.9	2.17E-06	0.003032
<i>ybiW</i>	putative formate acetyltransferase 3	11.3	0.004220	0.094788
<i>fruA</i>	PTS system, fructose-like-2 IIC component	11.5	0.004233	0.094788
<i>yfdW</i>	formyl-coenzyme A transferase	11.5	0.000491	0.041502
<i>APECO1_1268</i>	transaldolase-like protein	11.7	0.002201	0.072548
<i>nanA</i>	N-acetylneuraminic lyase	11.8	0.000452	0.041502
<i>malG</i>	maltose transport system permease protein MalG	12.9	0.000412	0.041502
<i>malE</i>	Maltose-binding periplasmic proteins	13.0	0.000613	0.042437
<i>ptsA</i>	phosphoenolpyruvate-protein phosphotransferase PtsA	14.4	0.003783	0.093765
<i>putA</i>	delta-1-pyrroline-5-carboxylate dehydrogenase	15.7	0.004241	0.094788
<i>glcD</i>	glycolate oxidase subunit D	17.5	4.03E-05	0.014079
<i>ybiY</i>	putative pyruvate formate lyase activating enzyme	20.3	0.001689	0.065513
<i>lldD</i>	L-lactate dehydrogenase, FMN-linked	24.6	0.000112	0.022287
<i>malF</i>	maltose transport system permease protein MalF	25.2	0.000554	0.041502
<i>lldR</i>	DNA-binding transcriptional repressor	31.9	0.000111	0.022287
<i>lamB</i>	maltoporin precursor	32.4	0.000532	0.041502
<i>malM</i>	maltose operon periplasmic protein precursor MalM	32.6	0.000850	0.050819
<i>acs</i>	acetyl-CoA synthetase	33.1	0.003057	0.084496
<i>yjhT</i>	conserved hypothetical protein , N- acetylneuraminic acid mutarotase; Provisional	33.9	0.002518	0.077688
<i>lldP</i>	L-lactate permease	36.6	0.000840	0.050819
<i>glcF</i>	glycolate oxidase iron-sulfur subunit	42.5	7.25E-06	0.005058