

TABLE S2 Summary of genes down-regulated in CF74ΔT6SS

gene_id	gene	product	direction	log2 (fold_change)	p_value
CFCDC_1858	<i>fadE</i>	acyl-CoA dehydrogenase	-	4.7248	0.0004
CFCDC_0190	<i>dctA</i>	C4-dicarboxylate transporter DctA	+	4.1448	0.0005
CFCDC_0561	<i>tdcD</i>	propionate/acetate kinase	+	4.3434	0.0005
CFCDC_4286	<i>fadB</i>	multifunctional fatty acid oxidation complex subunit alpha	+	4.3653	0.0005
CFCDC_4142	<i>eutE</i>	ethanolamine utilization protein EutE	-	5.1795	0.0007
CFCDC_4137	<i>eutB</i>	ethanolamine ammonia-lyase heavy chain	-	3.3633	0.0019
CFCDC_0566	<i>yhaN</i>	hypothetical protein	+	3.2808	0.0021
CFCDC_0857	<i>fucl</i>	L-fucoseisomerase	-	3.2808	0.0022
CFCDC_3969	<i>glpT</i>	sn-glycerol-3-phosphate transporter	-	4.2163	0.0024
CFCDC_3968	<i>glpQ</i>	glycerophosphodiesterphosphodiesterase	-	3.9251	0.0023
CFCDC_0730	<i>nupG</i>	nucleoside permease	-	3.1852	0.0028
CFCDC_3221	<i>ydcI</i>	LysR family transcriptional regulator	+	3.1349	0.0032
CFCDC_3925	<i>yejG</i>	hypothetical protein	-	3.1227	0.0033
CFCDC_1759	<i>glpF</i>	glycerol uptake facilitator protein	-	3.3001	0.0038
CFCDC_4365	<i>rbsC</i>	ribose ABC transporter permease protein	-	3.0266	0.0044
CFCDC_3886	<i>mglC</i>	galactoside ABC transporter permease	-	2.9828	0.0049
CFCDC_1758	<i>glpK</i>	glycerol kinase	-	4.2824	0.0059
CFCDC_4145	<i>eutD</i>	phosphotransacetylase	-	4.6111	0.0064
CFCDC_4146	<i>eutT</i>	putative cobalaminadenosyltransferase in ethanolamine utilization	-	4.9507	0.0066
CFCDC_0555	<i>garL</i>	2-dehydro-3-deoxyglucarate aldolase	+	2.9971	0.0066
CFCDC_2679	<i>flgK</i>	flagellar hook-associated protein FlgK	+	2.7308	0.0081
CFCDC_2777	<i>ycgG</i>	cyclic diguanylatephosphodiesterase (EAL) domain protein	+	2.8694	0.0081
CFCDC_1404	<i>ykgE</i>	putative dehydrogenase subunit	+	2.8490	0.0086
CFCDC_0133	<i>aldB</i>	aldehyde dehydrogenase B	+	2.6538	0.0091
CFCDC_0972	<i>srlE</i>	PTS system glucitol/sorbitol-specific transporter subunit IIBC	-	3.2798	0.0101
CFCDC_0970	<i>srlD</i>	sorbitol-6-phosphate dehydrogenase	-	2.5405	0.0101
CFCDC_2314	<i>sdhB</i>	succinate dehydrogenase iron-sulfur subunit	+	2.6016	0.0103
CFCDC_2434	<i>bssR</i>	biofilm formation regulatory protein BssR	+	3.1236	0.0109
CFCDC_0553	<i>garD</i>	D-galactaratedehydratase	-	2.4598	0.0109
CFCDC_4287	<i>fadA</i>	3-ketoacyl-CoA thiolase (fatty oxidation complex beta subunit)	+	2.5207	0.0112
CFCDC_3603	<i>fliD</i>	flagellar capping protein	+	2.4715	0.0121
CFCDC_3888	<i>mglB</i>	galactose-binding transport protein	-	2.4402	0.0134
CFCDC_0764	<i>ygfH</i>	putative coenzyme A transferase	-	2.8255	0.0134
CFCDC_3230	<i>cybB</i>	cytochrome b561	-	2.4055	0.0145
CFCDC_4126	<i>ucpA</i>	short chain dehydrogenase	-	2.6212	0.0150
CFCDC_4138	<i>eutA</i>	reactivating factor for ethanolamine ammonia lyase	-	3.2983	0.0156
CFCDC_0580	<i>uxaC</i>	uronateisomerase	+	2.4525	0.0169
CFCDC_3274	<i>pspE</i>	thiosulfate: cyanidesulfurtransferase	-	2.3057	0.0172
CFCDC_1720	<i>fdoG</i>	formate dehydrogenase-O, major subunit	-	2.8665	0.0173
CFCDC_2712	<i>fecA</i>	ferric citrate outer membrane transporter	-	2.2564	0.0193

CFCDC_0556	<i>garR</i>	Rossmann-fold NAD(P)(+)-binding proteins	+	2.2884	0.0198
CFCDC_2228	<i>citX</i>	2'-(5"-triphosphoribosyl)-3'-dephospho-CoA:apo-citrate lyase	-	3.2284	0.0199
CFCDC_3887	<i>mglA</i>	galactose/methyl galactoside transporter ATP-binding protein	-	2.2698	0.0209
CFCDC_3435	<i>yeaW</i>	putative 2Fe-2S cluster-containing dioxygenase subunit	+	2.3347	0.0210
CFCDC_3522	<i>cheR</i>	chemotaxismethyltransferaseCheR	-	3.3468	0.0217
CFCDC_1057	<i>rbsA</i>	ribose transport system ATP-binding protein	+	2.9488	0.0265
CFCDC_1937	<i>prpD</i>	2-methylcitrate dehydratase	+	2.2329	0.0270
CFCDC_1952	<i>mhpR</i>	DNA-binding transcriptional activator MhpR	-	2.6395	0.0273
CFCDC_3279	<i>pspA</i>	phage shock protein A	-	2.1112	0.0279
CFCDC_3036	<i>fumA</i>	fumaratehydratase class I, aerobic	+	2.4143	0.0281
CFCDC_2658	<i>bssS</i>	biofilm formation regulatory protein BssS	-	2.5172	0.0287
CFCDC_3602	<i>fliC</i>	bacterial flagellin C-terminal helical region	-	2.9404	0.0291
CFCDC_0531	<i>mtr</i>	tryptophan permease	+	2.0987	0.0295
CFCDC_1422	<i>yjiO</i>	multidrug efflux system protein	-	2.0906	0.0230
CFCDC_3689	<i>yeel</i>	hypothetical protein	+	2.1230	0.0308
CFCDC_3438	<i>fadD</i>	long-chain-fatty-acid--CoA ligase	-	2.0986	0.0311
CFCDC_1060	<i>iolC</i>	5-dehydro-2-deoxygluconokinase	+	2.3009	0.0339
CFCDC_1757	<i>glpX</i>	fructose 1,6-bisphosphatase II	-	1.9895	0.0374
CFCDC_1053	<i>iolA</i>	methylmalonate-semialdehyde dehydrogenase	+	2.0254	0.0377
CFCDC_3605	<i>fliT</i>	flagellar biosynthesis protein FliT	+	2.8783	0.0386
CFCDC_0378	<i>bfd</i>	bacterioferritin-associated ferredoxin	+	3.0138	0.0388
CFCDC_1962	<i>fbpC</i>	ferric transporter ATP-binding subunit	-	1.9560	0.0429
CFCDC_2680	<i>flgL</i>	flagellar hook-associated protein FlgL	+	1.9116	0.0436
CFCDC_0188	<i>ldrD</i>	toxic polypeptide, small	+	3.3786	0.0434
CFCDC_2668	<i>flgM</i>	anti-sigma28 factor FlgM	-	2.1278	0.0464
CFCDC_3529	<i>motA</i>	flagellar motor protein MotA	-	2.7427	0.0466
CFCDC_0291	<i>glpD</i>	glycerol-3-phosphate dehydrogenase	-	2.3828	0.0495
CFCDC_1513	<i>caiF</i>	DNA-binding transcriptional activator CaiF	+	1.9368	0.0496
CFCDC_2221	<i>ybdQ</i>	hypothetical protein	-	2.3263	0.0450

