

1 Nishikawa and Duncan, SUPPLEMENTAL TABLE S1.

2
3 **TABLE S1. Relative quantification analysis of *fimSR* and *fimA*-related genes expression in strains**
4 **33277 and W83 by $\Delta\Delta C_T$ method.**

5	6	7	8	9	10	11	12
Strain	gene	Avg C_T^a	Avg ΔC_T^b	ΔC_T SD ^c	$\Delta\Delta C_T^d$	RQ ^e	
8	33277	<i>fimA</i>	16.230375	11.657747	0.04586264	0.0	1.0
9	33277	<i>fimS</i>	22.32254	17.749912	0.022366915	0.0	1.0
10	33277	<i>fimR</i>	19.506887	14.934259	0.04442617	0.0	1.0
11	33277	<i>fimX</i>	14.920545	10.347916	0.023265244	0.0	1.0
12	33277	<i>pgmA</i>	15.927211	11.354582	0.028491484	0.0	1.0
13	33277	<i>glk</i>	18.928392	14.355764	0.010255761	0.0	1.0
14	33277	16SrRNA	4.5726285	-	-	-	-
15	W83	<i>fimA</i>	24.91251	19.980543	0.015474653	8.322796	0.0031231209
16	W83	<i>fimS</i>	23.901964	18.969997	0.02164793	1.2200851	0.4292574
17	W83	<i>fimR</i>	20.96205	16.030083	0.018008143	1.0958233	0.46786904
18	W83	<i>fimX</i>	22.938131	18.006165	0.01901394	7.658249	0.0049503664
19	W83	<i>pgmA</i>	23.331947	18.39998	0.011158608	7.0453987	0.007570484
20	W83	<i>glk</i>	18.695807	13.76384	0.0141396765	-0.59192467	1.5072562
21	W83	16SrRNA	4.9319673	-	-	-	-

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23 a. Average threshold cycle (C_T) of three independent reactions. Each reaction contains an equal amount
24 of cDNA templates from three biological replicates.

25 b. (Avg C_T of each gene) – (Avg C_T of 16SrRNA)

26 c. Standard deviation of ΔC_T

27 d. Avg ΔC_T – (33277 Avg ΔC_T)

28 e. $2^{-\Delta\Delta C_T}$

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