Supporting Tables

Table S1. Transposon insertion mutants with altered P_{pilY1}-*lacZ* reporter activity.

Gene[a]	Number of insertions	Miller unit (liquid)[b]	Miller unit (surface)[b]	Function/pathway
WT	N/A	72±2	147±9	
fimS	1	19±1	75±13	Putative histidine kinase; Alginate biosynthesis
algR	1	17±2	17±5	Response regulatory protein; Alginate biosynthesis,
vfr	5	36±6	38±5	Cyclic AMP receptor protein, transcriptional regulator
pilJ	2	42±1	50±6	Putative methyl-accepting chemotaxis protein
pilK	2	40±2	40±4	Putative methyltransferase
chpA	1	39±7	50±1	Putative chemotaxis protein, histidine kinase
fimV	2	33±3	44±7	Putative aspartate-semialdehyde dehydrogenase;TFP biosynthesis;
pilC	3	26±3	33±6	Inner membrane platform protein; TFP biosynthesis;
fimU	2	17±3	16±0	Minor pilin of TFP
pilY1	2	973±51	5726±126	TFP twitching activity; swarming

				activity
truB	4	38±18	52±14	tRNA pseudouridine 55 synthase
rnpA	1	24±5	41±1	Ribonuclease P protein component
rrmJ	1	29±4	70±1	Cell division protein
sucD	1	41±1	72±7	Succinyl-CoA synthetase alpha chain
thrH	1	44±10	95±15	Homoserine kinase
rbfA	1	50±21	N/A	Ribosome-binding factor A
gshA	1	38±2	61±2	Glutamate--cysteine ligase
miaA	1	20±2	18±1	Delta 2-isopentenylpyrophosphate transferase
nuoN	1	32±2	69±3	Putative methyltransferase, NADH dehydrogenase I chain N
pepA	1	34±0	55±1	Leucine aminopeptidase
Intergenic *PA14_28510-28520*	1	34±2	44±1	Intergenic region of 28520 and 28510. Both are hypothetic proteins
PA14_01510	1	55±5	N/A	Putative plasmid stabilization system protein
PA14_05210	1	25±2	25±3	Putative membrane protein
PA14_11970	1	39±2	47±1	Methylpurine-DNA glycosylase family protein
PA14_13900	1	39±1	50±2	Hypothetical protein
PA14_15290	1	31±2	49±2	Putative regulatory protein

PA14_39440	1	29±1	43±5	Hypothetical protein
PA14_41150	1	18±5	12±2	Putative permease of ABC transporter
PA14_46510	1	36±3	46±3	Hypothetical protein
PA14_59180	1	39±6	N/A	Topoisomerase I - like protein
PA14_60060	1	45±10	N/A	Hypothetical protein
PA14_72220	1	33±3	N/A	Conserved hypothetical protein

[a] Sites of transposon insertion are located within the coding sequences of the indicated genes. In bold indicate genes investigated in this study.

[b] Cells were grown in either M8 liquid broth to log phase ($OD_{600} = 0.5$), or on M8 swarming agar (0.5% agar) surface overnight. The Miller units (mean ±SD) from at least three biological replicates were shown.