TABLE S1 – Strains, plasmids, and primers used in this study.

Strains

Strain	Genotype or relevant characteristics
WN150	"wild-type" *Salmonella enterica* serovar Typhimurium strain 14028s [2]
WN1405	Δ*efp* mutation (deletion of base-pairs 145-424) in WN150 [2]
BW25113	"wild-type" E. coli, parental strain used for the Keio collection [1]
MW1014	Δ*efp* of Keio collection with kanamycin cassette removed using FLP recombinase [2]

Plasmids

Plasmid	Description	Reference
pXG10sf-LacZ	**pXG10sf plasmid for generating translational fusions to super-folder GFP.**	4
pXG10sf-AtpD	**pXG10sf with AtpD ORF and 74bp upstream inserted between NsiI and NheI sites**	2
pXG10sf-AtpD P214L	pXG10sf-AtpD with the PPG motif mutated to PLG	2
pXG10sf-AtpD - AtpA 12aa	pXG10sf-AtpD with the 12 codons immediately upstream of the PPG motif replaced by those of AtpA	2
pXG10sf-AtpD - AtpA 180-PPG	pXG10sf-AtpD with codons 129-212 replaced with codons 180-279 of AtpA.	this work
pXG10sf-AtpD - AtpA 120-PPG	pXG10sf-AtpD with codons 86-212 replaced with codons 120-279 of AtpA.	this work
pXG10sf-AtpD - AtpA 60-PPG	pXG10sf-AtpD with codons 43-212 replaced with codons 60-279 of AtpA.	this work
pXG10sf-AtpD - AtpA ATG-PPG	pXG10sf-AtpD with codons 1-212 replaced with codons 1-279 of AtpA.	this work
pXG10sf-AtpD - AtpA UTR-PPG	pXG10sf-AtpD with 5' UTR and codons 1-212 replaced with 5' UTR and codons 1-279 of AtpA.	this work
pXG10sf-AtpD - AtpA UTR	pXG10sf-AtpD with the 5' UTR replaced by that of AtpA	this work
pXG10sf-AtpD - AtpA UTR-60 & 12aa	pXG10sf-AtpD with 5' UTR and codons 1-43 replaced with 5' UTR and codons 1-60 of AtpA, and with the 12 codons immediately upstream of the PPG motif replaced by those of AtpA	this work
pXG10sf-AtpD - AtpA UTR-120 & 12aa	pXG10sf-AtpD with 5' UTR and codons 1-86 replaced with 5' UTR and codons 1-120 of AtpA, and with the 12 codons immediately upstream of the PPG motif replaced by those of AtpA	this work

pXG10sf-AtpD - AtpA UTR-180 & 12aa	pXG10sf-AtpD with 5' UTR and codons 1-129 replaced with 5' UTR and codons 1-180 of AtpA, and with the 12 codons immediately upstream of the PPG motif replaced by those of AtpA	this work
pXG10sf-AtpD - AGAGG::AGAG**C**	pXG10sf-AtpD with point mutation altering the SD sequence to AGAG**C**	this work
pXG10sf-AtpD - AGAGG::AGA**C**G	pXG10sf-AtpD with point mutation altering the SD sequence to AGA**C**G	this work
pXG10sf-AtpD - AtpA UTR from -75-61	pXG10sf-AtpD with 5' UTR bases -74-61 replaced by bases -75-61 of AtpA	this work
pXG10sf-AtpD - AtpA UTR from -60-46	pXG10sf-AtpD with 5' UTR bases -60-46 replaced by those of AtpA	this work
pXG10sf-AtpD - AtpA UTR from -45-31	pXG10sf-AtpD with 5' UTR bases -45-31 replaced by those of AtpA	this work
pXG10sf-AtpD - AtpA UTR from -30-16	pXG10sf-AtpD with 5' UTR bases -30-16 replaced by those of AtpA	this work
pXG10sf-AtpD - AtpA UTR from -15-1	pXG10sf-AtpD with 5' UTR bases -15-1 replaced by those of AtpA	this work
pXG10sf-AtpD - AGAGG::AG**G**AGG	pXG10sf-AtpD with G insertion to mutate the SD sequence to AG**G**AGG	this work
pXG10sf-AtpD - AUG::**G**UG	pXG10sf-AtpD with point mutation altering the start codon to **G**UG	this work
pXG10sf-AtpD - AUG::**U**UG	pXG10sf-AtpD with point mutation altering the start codon to **U**UG	this work
pXG10sf-AtpD - AtpA UTR from -45-31 & AGAGG::AG**G**AGG	pXG10sf-AtpD with 5' UTR bases -45-31 replaced by those of AtpA **and** with G insertion to mutate the SD sequence to AG**G**AGG	this work
pXG10sf-AtpD - AtpA UTR & P214L	pXG10sf-AtpD with the 5' UTR replaced by that of AtpA and with the PPG motif mutated to PLG	this work
pXG10sf-AtpD - AtpA UTR from -45-31 & P214L	pXG10sf-AtpD with 5' UTR bases -45-31 replaced by those of AtpA **and** with the PPG motif mutated to PLG	this work
pXG10sf-AtpD - AtpA UTR & 12aa	pXG10sf-AtpD with the 5' UTR replaced by that of AtpA **and** with the 12 codons immediately upstream of the PPG motif replaced by those of AtpA	this work
pXG10sf-AtpD - AtpA 12aa & AGAGG::AG**G**AGG	pXG10sf-AtpD with the 12 codons immediately upstream of the PPG motif replaced by those of AtpA **and** with G insertion to mutate the SD sequence to AG**G**AGG	this work
pXG10sf-AtpD - AtpA UTR from -45-31 & 12aa	pXG10sf-AtpD with 5' UTR bases -45-31 replaced by those of AtpA **and** with the 12 codons immediately upstream of the PPG motif replaced by those of AtpA	this work

pXG10sf-AtpA	**pXG10sf [1] with AtpA ORF and 75bp upstream inserted between NsiI and NheI sites**	2
pXG10sf-AtpA R279P	pXG10sf-AtpA with the RPPG motif mutated to PPPG	2
pXG10sf-AtpA P281L	pXG10sf-AtpA with the PPG motif mutated to PLG	2
pXG10sf-AtpA - AtpD 12aa	pXG10sf-AtpA with the 12 codons immediately upstream of the PPG motif replaced by those of AtpD	2
pXG10sf-AtpA - AtpD 129-PPG	pXG10sf-AtpA with codons 180-279 replaced with codons 129-212 of AtpD.	this work
pXG10sf-AtpA - AtpD 86-PPG	pXG10sf-AtpA with codons 120-279 replaced with codons 86-212 of AtpD.	this work
pXG10sf-AtpA - AtpD 43-PPG	pXG10sf-AtpA with codons 60-279 replaced with codons 43-212 of AtpD.	this work
pXG10sf-AtpA - AtpD ATG-PPG	pXG10sf-AtpA with codons 1-279 replaced with codons 1-212 of AtpD.	this work
pXG10sf-AtpA - AtpD UTR-PPG	pXG10sf-AtpA with 5' UTR and codons 1-279 replaced with 5' UTR and codons 1-212 of AtpD.	this work
pXG10sf-AtpA - AtpD UTR	pXG10sf-AtpA with the 5' UTR replaced by that of AtpD	this work
pXG10sf-AtpA - AtpD UTR-43 & 12aa	pXG10sf-AtpA with 5' UTR and codons 1-60 replaced with 5' UTR and codons 1-43 of AtpD, and with the 12 codons immediately upstream of the PPG motif replaced by those of AtpD	this work
pXG10sf-AtpA - AtpD UTR-86 & 12aa	pXG10sf-AtpA with 5' UTR and codons 1-120 replaced with 5' UTR and codons 1-86 of AtpD, and with the 12 codons immediately upstream of the PPG motif replaced by those of AtpD	this work
pXG10sf-AtpA - AtpD UTR-129 & 12aa	pXG10sf-AtpA with 5' UTR and codons 1-180 replaced with 5' UTR and codons 1-129 of AtpD, and with the 12 codons immediately upstream of the PPG motif replaced by those of AtpD	this work
pXG10sf-AtpA - AGGGGA::AGG**A**GG	pXG10sf-AtpA with A base moved two positions upstream to alter the SD sequence to AGG**A**GG	this work
pXG10sf-AtpA - AtpD UTR from -74-61	pXG10sf-AtpA with 5' UTR bases -75-61 replaced by bases -74-61 of AtpD	this work
pXG10sf-AtpA - AtpD UTR from -60-46	pXG10sf-AtpA with 5' UTR bases -60-46 replaced by those of AtpD	this work
pXG10sf-AtpA - AtpD UTR from -45-31	pXG10sf-AtpA with 5' UTR bases -45-31 replaced by those of AtpD	this work
pXG10sf-AtpA - AtpD UTR from -30-16	pXG10sf-AtpA with 5' UTR bases -30-16 replaced by those of AtpD	this work

pXG10sf-AtpA - AtpD UTR from -15-1	pXG10sf-AtpA with 5' UTR bases -15-1 replaced by those of AtpD	this work
pXG10sf-AtpA - AtpD UTR & AGAGG::AG**G**AGG	pXG10sf-AtpA with the 5' UTR replaced by that of AtpD and with G insertion to mutate the SD sequence to AG**G**AGG	this work
pXG10sf-AtpA - AtpD UTR from -30-1	pXG10sf-AtpA with 5' UTR bases -30-1 replaced by those of AtpD	this work
pXG10sf-AtpA - AtpD UTR from -30-1 & AGAGG::AG**G**AGG	pXG10sf-AtpA with 5' UTR bases -30-1 replaced by those of AtpD **and** with G insertion to mutate the SD sequence to AG**G**AGG	this work
pXG10sf-AtpA -AtpD UTR & P281L	pXG10sf-AtpA with the 5' UTR replaced by that of AtpD **and** with the PPG motif mutated to PLG	this work
pXG10sf-AtpA - AtpD 12aa & AGGGGA::AGG**A**GG	pXG10sf-AtpA with the 12 codons immediately upstream of the PPG motif replaced by those of AtpD **and** with A base moved two positions upstream to alter the SD sequence to AGG**A**GG	this work
pBAD30XS	**pBAD30mw700 [2] with an xhoI & an speI cloning site at forth codon position of gfp**	3
pBAD30XSG	pBAD30XS with start codon changed from AUG to GUG	this work
pBAD30XST	pBAD30XS with start codon changed from AUG to UUG	this work
pBAD30XSA	pBAD30XS with start codon changed from AUG to AUC	this work
pBAD30XSC	pBAD30XS with start codon changed from AUG to CUG	this work
pBAD30XS2	**pBAD30XS with PPPPPP inserted between the xhoI and speI sites**	3
pBAD30XS2G	pBAD30XS2 with start codon changed from AUG to GUG	this work
pBAD30XS2T	pBAD30XS2 with start codon changed from AUG to UUG	this work
pBAD30XS2A	pBAD30XS2 with start codon changed from AUG to AUC	this work
pBAD30XS2C	pBAD30XS2 with start codon changed from AUG to CUG	this work
pBAD30XS63	**pBAD30XS with LPPP (yeiG) inserted between the xhoI and speI sites**	3
pBAD30XS63G	pBAD30XS63 with start codon changed from AUG to GUG	this work
pBAD30XS63T	pBAD30XS63 with start codon changed from AUG to UUG	this work
pBAD30XS63A	pBAD30XS63 with start codon changed from AUG to AUC	this work
pBAD30XS63C	pBAD30XS63 with start codon changed from AUG to CUG	this work
pBAD30XS71	**pBAD30XS with MGLDPGLRTG inserted between the xhoI and speI sites**	this work

pBAD30XS71G	pBAD30XS71 with start codon changed from AUG to GUG	this work
pBAD30XS71T	pBAD30XS71 with start codon changed from AUG to UUG	this work
pBAD30XS71A	pBAD30XS71 with start codon changed from AUG to AUC	this work
pBAD30XS71C	pBAD30XS71 with start codon changed from AUG to CUG	this work
pBAD30XS75	**pBAD30XS with PPPP inserted between the xhoI and speI sites**	this work
pBAD30XS75G	pBAD30XS75 with start codon changed from AUG to GUG	this work
pBAD30XS75T	pBAD30XS75 with start codon changed from AUG to UUG	this work
pBAD30XS75A	pBAD30XS75 with start codon changed from AUG to AUC	this work
pBAD30XS75C	pBAD30XS75 with start codon changed from AUG to CUG	this work

Primers

Purpose	Cloning details	Primer Name	Primer Sequence (5' to 3')
pXG10sf-AtpD - AtpA #-PPG	Inserts using pXG10sf-AtpA as template [3]. Inserted by Gibson cloning [5]	atpA PPG R	ATGCAACGCGCAGACGGTTTCCCGGCGGACGACGGAGCAGCAGGGAGATCTGAC
		atpA 180 F	GTCAAACTCTCAGGAACTGCTGGAAACCGACGCCATCATCAACCAGCGCGACTCC
		atpA 120 F	AGTCCCGGTAGGTAAAGCTACGCTGGGTGTTGATAATGACGGCTTCTCTGCCGTTGAAGC
		atpA 60 F	TGGTAATGAGAAGCTGGTGCTGGAAGTTGCTATCGCACTGAACCTGGAGCGCGAC
		atpA ATG F	AACCAGGTTATTTCGTAGAGGATTTAAGATGCAACTGAATTCCACCGAAATCAGCGAACT
		UTR F	CGCCCGGTAGTGATCTTATTTCATTATGGTG
	Around the world (ATW) plasmid fragments using pXG10sf-AtpD as template [3]	atpD PPG F	CCGCCGGGAAACCGTCTGCG
		atpD 129 R	GGTTTCCAGCAGTTCCTGAGAGTTTGAC
		atpD 86 R	ACCCAGCGTAGCTTTACCTACCG
		atpD 43 R	AACTTCCAGCACCAGCTTCTCATTACC
		atpD ATG R	CTTAAATCCTCTACGAAATAACCTGGTTAAACCGC

		UTR R	GAGACGTTGATTGGCACGTAAGAGGTTCCAAC
pXG10sf-AtpA - AtpD #-PPG	Inserts using pXG10sf-AtpD as template [3]. Inserted by Gibson cloning [5]	atpD PPG R	CGCCCGGGAATGCTTCACGTCCTGGCGGCTCGTTCATCTGGCCATACACCAGGG
		atpD 129 F	AGACCGGTAAAACCGCGCTGGCTATCGGTATCAAAGTTATCGACCTGATGTGTCCGTTCG
		atpD 86 F	GGGTGCGCCAATTGACGGTAAAGGTCCGCGTATCATGAACGTCCTGGGCGAACCGG
		atpD 43 F	AATGATCTCCCTGCCGGGTAACCGTTACCAGCAGCAGCTTGGCGGCGGTATTGTG
		atpD ATG F	CGTCTTGCAGTCTTAAGGGGACTGGAGCATGGCTACTGGAAAGATTGTCCAGGTAATCGG
		UTR F	as above
	ATW plasmid fragments using pXG10sf-AtpA as template [3]	atpA PPG F	CCGCCAGGACGTGAAGCATTCCC
		atpA 180 R	GATAGCCAGCGCGGTTTTACCGG
		atpA 120 R	CGGACCTTTACCGTCAATTGGCGC
		atpA 60 R	GTAACGGTTACCCGGCAGGGAGATC
		atpA ATG R	GCTCCAGTCCCCTTAAGACTGCAAGAC
		UTR R	as above
pXG10sf-AtpD - AtpA UTR-# & 12aa	Inserts using pXG10sf-AtpA as template [3]. Inserted by Gibson cloning [5]	UTR F	as above
		atpA ATG R	as above
		atpA 60 R	as above
		atpA 120 R	as above
		atpA 180 R	as above
	ATW plasmid fragments using pXG10sf-AtpD - AtpA 12aa as template [3]	UTR R	as above
		atpD ATG F	as above
		atpD 43 F	as above
		atpD 86 F	as above
		atpD 129 F	as above
pXG10sf-AtpA - AtpD UTR-# & 12aa	Inserts using pXG10sf-AtpD as template [3]. Inserted by Gibson	UTR F	as above
		atpD ATG R	as above
		atpD 43 R	as above

	cloning [5]	atpD 86 R	as above
		atpD 129 R	as above
	ATW plasmid fragments using pXG10sf-AtpA - AtpD 12aa as template [3]	UTR R	as above
		atpA ATG F	as above
		atpA 60 F	as above
		atpA 120 F	as above
		atpA 180 F	as above
pXG10sf-AtpD - AtpA UTR from -75-61	ATW PCR followed by Gibson cloning [5]	atpD-A -75-61 F	CACATGCATATGGTCATTGATGGCCACCGAGATCGTCTCG GGGGCCGC
		atpD-A -75-61 R	GCCATCAATGACCATATGCATGTGCTCAGTATCTCTATCAC TGATAGGGATGTCAATCTC
pXG10sf-AtpD - AtpA UTR from -60-46	ATW PCR and Gibson cloning [5]	atpD-A -60-46 F	GAGTATTACTCAGGAACTAGCGTACGCGGCCGTGGGGGCC GCCGCGGTTTAAC
		atpD-A -60-46 R	TACGCTAGTTCCTGAGTAATACTCAGTATCTCTATCACTGA TAGGGATGTC
pXG10sf-AtpD - AtpA UTR from -45-31	ATW PCR and Gibson cloning [5]	atpD-A -45-31 F	CTTGAGCGCCTTGCATTAACCAGGTTATTTCGTAGAGGATT TAAGATGGC
		atpD-A -45-31 R	TGGTTAATGCAAGGCGCTCAAGGAGACGATCTCGGTGAGT TCCTGAG
pXG10sf-AtpD - AtpA UTR from -30-16	ATW PCR and Gibson cloning [5]	atpD-A -30-16 F	TGACGTCTTGCAGTCTCGTAGAGGATTTAAGATGGCTACT GGAAAGATTGTCCAGG
		atpD-A -30-16 R	CCTCTACGAGACTGCAAGACGTCACCGCGGCGGCCCCCGA GACGATC
pXG10sf-AtpD - AtpA UTR from -15-1	ATW PCR and Gibson cloning [5]	atpD-A -15-1 F	TTATTTTAAGGGGACTGGAGCATGGCTACTGGAAAGATTG TCCAGG
		atpD-A -15-1 R	CATGCTCCAGTCCCCTTAAAATAACCTGGTTAAACCGCGG CG
pXG10sf-AtpA - AtpD UTR from -74-61	ATW PCR and Gibson cloning [5]	atpA-D -75-61 F	ATACTGAGTATTACTCAGGAACTAGCGTACGCGGCCGTCT TGAG
		atpA-D -75-61 R	TAGTTCCTGAGTAATACTCAGTATCTCTATCACTGATAGGG ATGTCAATC
pXG10sf-AtpA - AtpD UTR from -60-46	ATW PCR and Gibson cloning [5]	atpA-D -60-46 F	ATGGCCACCGAGATCGTCTCCTTGAGCGCCTTGCAGACGT CTTGC
		atpA-D -60-46 R	AAGGAGACGATCTCGGTGGCCATCAATGACCATATGCATG TGCTCAGTATCTC

pXG10sf-AtpA - AtpD UTR from -45-31	ATW PCR and Gibson cloning [5]	atpA-D -45-31 F	TGGGGGCCGCCGCGGTGACGTCTTGCAGTCTTAAGGGGAC TGGAGCATGC
		atpA-D -45-31 R	TCACCGCGGCGGCCCCCACGGCCGCGTACGCTGCCATCAA TGACC
pXG10sf-AtpA - AtpD UTR from -30-16	ATW PCR and Gibson cloning [5]	atpA-D -30-16 F	TGCATTAACCAGGTTATTTTAAGGGGACTGGAGCATGCAA CTG
		atpA-D -30-16 R	CCTTAAAATAACCTGGTTAATGCAAGGCGCTCAAGACGGC C
pXG10sf-AtpA - AtpD UTR from -15-1	ATW PCR and Gibson cloning [5]	atpA-D -15-1 F	TCTCGTAGAGGATTTAAGATGCAACTGAATTCCACCGAAA TCAGCG
		atpA-D -15-1 R	TTGCATCTTAAATCCTCTACGAGACTGCAAGACGTCTGCA AGGC
pXG10sf-AtpD - AGAGG::AGAG**C**	ATW PCR and Gibson cloning [5]	atpD GAGC SD F	TTATTTCGTAGAGCATTTAAGATGGCTACTGGAAAGATTG TCCAGG
		atpD GAGC SD R	CATCTTAAATGCTCTACGAAATAACCTGGTTAAACCGCGG C
pXG10sf-AtpD - AGAGG::AGA**C**G	ATW PCR and Gibson cloning [5]	atpD GACG SD F	TTATTTCGTAGACGATTTAAGATGGCTACTGGAAAGATTG TCCAGG
		atpD GACG SD R	CATCTTAAATCGTCTACGAAATAACCTGGTTAAACCGCGG C
pXG10sf-AtpD - AGAGG::AG**G**AGG	ATW PCR and Gibson cloning [5]	atpD start mut F	TGGCTACTGGAAAGATTGTCCAGGTAATCGGCGCCGTGGT CG
		atpD AGGAGG SD R	TGGACAATCTTTCCAGTAGCCATCTTAAATCCTCCTACGAA ATAACCTGGTTAAACCGC
pXG10sf-AtpA - AGGGGA::AGG**A**G G	ATW PCR and Gibson cloning [5]	atpA AGGAGG SD F	AGTCTTAAGGAGGCTGGAGCATGCAACTGAATTCCACCG
		atpA AGGAGG SD R	ATGCTCCAGCCTCCTTAAGACTGCAAGACGTCTGCAAGGC G
pXG10sf-AtpD - AUG::**G**UG	ATW PCR and Gibson cloning [5]	atpD start mut F	as above
		atpD GTG start R	TGGACAATCTTTCCAGTAGCCACCTTAAATCCTCTACGAA ATAACCTGGTTAAACCGC
pXG10sf-AtpD - AUG::**U**UG	ATW PCR and Gibson cloning [5]	atpD start mut F	as above
		atpD TTG start R	TGGACAATCTTTCCAGTAGCCAACTTAAATCCTCTACGAA ATAACCTGGTTAAACCGC
pXG10sf-AtpD -	ATW PCR and Gibson	atpD start mut F	as above

AtpA UTR from -45-31 & AGAGG::AG**G**AGG	cloning [5] using pXG10sf-AtpD - AtpA UTR from -45-31 as template	atpD-A UTR 30-44 AGGAGG SD R	TGGACAATCTTTCCAGTAGCCATCTTAAATCCTCCTACGAA ATAACCTGGTTAATGCAAG
pXG10sf-AtpD - AtpA UTR & P214L	ATW PCR and Gibson cloning [5] using pXG10sf-AtpD - AtpA UTR as template	atpD P214L SDM F [3]	TGGCCAGATGAACGAGCCGCTGGGAAACCGTCTGCGCGTT G
		atpD P214L SDM R [3]	CAACGCGCAGACGGTTTCCCAGCGGCTCGTTCATCTGGCC A
pXG10sf-AtpD - AtpA UTR from -45-31 & P214L	ATW PCR and Gibson cloning [5] using pXG10sf-AtpD P214L as template	atpD-A -45-31 F	as above
		atpD-A -45-31 R	as above
pXG10sf-AtpD - AtpA UTR from -45-31 & 12aa	ATW PCR and Gibson cloning [5] using pXG10sf-AtpD 12aa as template	atpD-A -45-31 F	as above
		atpD-A -45-31 R	as above
pXG10sf-AtpD - AtpA 12aa & AGAGG::AG**G**AGG	ATW PCR and Gibson cloning [5] using pXG10sf-AtpD - AtpA 12aa as template	atpD start mut F	as above
		atpD AGGAGG SD R	as above
pXG10sf-AtpA - AtpD UTR & AGAGG::AG**G**AGG	ATW PCR and Gibson cloning [5] using pXG10sf-AtpA - AtpD UTR as template	atpD start mut F	as above
		atpA-D UTR AGGAGG SD R	TTCGGTGGAATTCAGTTGCATCTTAAATCCTCCTACGAAAT AACCTGGTTAAACCGCGGC
pXG10sf-AtpA - AtpD UTR from -30-1	ATW PCR and Gibson cloning [5] using pXG10sf-AtpA - AtpD UTR -15-1 as template	atpA ATG F	as above
		atpA-D UTR 30-1 R	CTACGAAATAACCTGGTTAATGCAAGGCGCTCAAGACGGC CGCG
pXG10sf-AtpA - AtpD UTR from -30-1 & AGAGG::AG**G**AGG	ATW PCR and Gibson cloning [5] using pXG10sf-AtpA - AtpD UTR -15-1 as template	atpA-D UTR 30-1 AGGAGG F	AACCAGGTTATTTCGTAGGAGGATTTAAGATGCAACTGAA TTCCACCGAAATCAGCGAAC
		atpA-D UTR 30-1 R	as above
pXG10sf-AtpA - AtpD UTR & P281L	ATW PCR and Gibson cloning [5] using	atpA P281L SDM F [3]	CCTGCTGCTCCGTCGTCCGCTGGGACGTGAAGCATTCCCG GGCGACGTATTCTACCTCC

	pXG10sf-AtpA - AtpD UTR as template	atpA P281L SDM R [3]	CCCGGGAATGCTTCACGTCCCAGCGGACGACGGAGCAGC AGGGAGATCTGACGGTAAGC
pXG10sf-AtpA - AtpD 12aa & AGGGGA::AGG**A**GG	ATW PCR and Gibson cloning [5] using pXG10sf-AtpA - AtpD 12aa as template	atpA AGGAGG SD F	as above
		atpA AGGAGG SD R	as above
Replace AUG with GUG in pBADXS	Site directed mutagenesis (SDM)	1FS	AATTCAGGAGGAATTTACCGTGAGTAAAC
		1RS	TCGAGTTTACTCACGGTAAATTCCTCCTG
Replace AUG with UUG in pBADXS	SDM	2FS	AATTCAGGAGGAATTTACCTTGAGTAAAC
		2RS	TCGAGTTTACTCAAGGTAAATTCCTCCTG
Replace AUG with CUG in pBADXS	SDM	3FS	AATTCAGGAGGAATTTACCCTGAGTAAAC
		3RS	TCGAGTTTACTCAGGGTAAATTCCTCCTG
Replace AUG with AUC in pBADXS	SDM	4FS	AATTCAGGAGGAATTTACCATCAGTAAAC
		4RS	TCGAGTTTACTGATGGTAAATTCCTCCTG

Table S1 References

1. Baba T, Ara T, Hasegawa M, Takai Y, Okumura Y, Baba M, Datsenko KA, Tomita M, Wanner B, Mori H (2006) Construction of Escherichia coli K-12 in-frame, single-gene knockout mutants: the Keio collection. *Mol Syst Biol* 2: 2006 0008.

2. Hersch SJ, Wang M, Zou SB, Moon KM, Foster LJ, Ibba M, Navarre WW (2013) Divergent protein motifs direct elongation factor P-mediated translational regulation in Salmonella enterica and Escherichia coli. *MBio* 4: e00180-00113.

3. Elgamal S, Katz A, Hersch SJ, Newsom D, White P, Navarre WW, Ibba M (2014 *in review*) EF-P dependent pauses integrate proximal and distal signals during translation. *In review at the time of submission*

4. Corcoran CP, Podkaminski D, Papenfort K, Urban JH, Hinton JC, Vogel J (2012) Superfolder GFP reporters validate diverse new mRNA targets of the classic porin regulator, MicF RNA. *Mol Microbiol* 84: 428-445.

5. Gibson DG, Young L, Chuang RY, Venter JC, Hutchison CA, Smith HO (2009) Enzymatic assembly of DNA molecules up to several hundred kilobases. *Nat Meth* 5: 343-345