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4 **Supporting Information for**
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6 Release factor inhibiting antimicrobial peptides improve non-
7 standard amino acid incorporation in wild-type bacterial cells.
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13
14 The data that support the findings of this study are available from the
15 corresponding author.
16

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33 **SI Methods**

34 **Reagents**

35 Antibiotics and nsAAs were purchased from Sigma, except for **AbK**, which was purchased
36 from TOCRIS. Apidaecin 1b was purchased from AnaSpec. Api137 was purchased from NovoPro
37 Biosciences Inc. N-3-oxo-octanoyl-L-Homoserine lactone (NHL) was purchased from Cayman
38 Chemical and stock solutions with it were made in ethyl acetate (acidified with 0.01% acetic acid)
39 to 1 mg mL⁻¹. nsAA stock solutions were prepared in water with minimal base or acid, e.g. 0.3 M
40 KOH to prepare 0.2 M **Bpa** stock solution, except for **Cou** stock, which was prepared in DMSO
41 at concentrations of 100–200 mM. Aqueous apidaecin (to 5–20 mg mL⁻¹) stocks and nsAA stock
42 solutions were filter-sterilized and stored at -20 °C before use. DNA oligonucleotides and gBlocks
43 were synthesized by IDT.

44 **In Vitro Protein Translation Assay.**

45 The recombinant MjBpaRS was prepared as previously described¹. *tRNA_{CUA}^{Tyr}* was prepared
46 by *in vitro* transcription and purified as previously described². PURExpress® and PURExpress®
47 and Δ RF123 Kit were purchased from NEB and the cell-free translation experiments were set-up
48 following the manufacturer's instructions supplemented with 20 ng μL⁻¹ linearized DNA templates
49 (T7-(UAG)₀-sfGFP, T7-(UAG)₁-sfGFP, or T7-(UAG)₂-sfGFP, see also below), MjBpaRS (to 10
50 μM final) and *tRNA_{CUA}^{Tyr}* (to 5 μM final) in 5 μL reactions per condition. 4 μL of these reaction
51 mixtures were transferred to a Corning® 384 Well flat bottom, low flange, white polystyrene assay
52 and relative fluorescence units for sfGFP was measured at excitation/emission wavelengths of 485
53 nm/528 nm using a Biotek spectrophotometric plate reader at 37 °C over 8 hours. The signal values
54 were normalized to peak fluorescence magnitude within an experiment and the graph was plotted
55 indicating the standard deviation between repeats in shade. Graphs were plotted and analyzed in
56 Prism 8.2.1 for Windows, GraphPad Software, www.graphpad.com.

57

58 **Growth Media and Growth Conditions.**

59 Unless otherwise noted, cultures were grown in 2xYT medium (16 g L⁻¹ bacto tryptone, 10
60 g L⁻¹ bacto yeast extract, 5 g L⁻¹ sodium chloride) supplemented with antibiotics to retain the
61 plasmids. nsAA incorporation experiments with autoinduction (e.g. **SI Figure 6**) were done in
62 GMML minimal media [1× M9 (Sigma-Aldrich M-6030) /1 mM MgSO₄/0.1 mM CaCl₂/8.5 mM
63 NaCl /5 μM Fe₂SO₄ /1% v/v glycerol /0.3 mM leucine] supplemented with 10% 2xYT, 0.05%
64 glucose and 0.05% arabinose. Typically, *Agrobacterium tumefaciens* C58 cells were grown in LB
65 at 30 °C, C321 strains were grown at 34 °C, and the rest of the *E. coli* strains at 37 °C. To check
66 the sensitivity of a given species to the apidaecins, overnight cultures were adjusted to OD₆₀₀ ~0.5

67 and serially diluted (2×10^{-1} dilutions). 2 μL of each dilution was spotted on solid media (e.g. LB)
68 containing Api137 of different concentrations up to 750 $\mu\text{g mL}^{-1}$.

69 **Growth Curves.**

70 Overnight cultures (grown in 2xYT) were diluted to $\text{OD}_{600} = 0.05$ into media with different
71 concentrations of apidaecins; either 2xYT (for experiments in **SI Figure 2 and 9b**) or into GMML
72 supplemented with appropriate antibiotics 10% 2xYT (final), 0.05% glucose and 0.05% arabinose
73 (for experiments in **SI Figure 8b, 8d, 10g**) in a Corning® 96 Well clear flat bottom plate. OD_{600}
74 was recorded every minute using a Biotek spectrophotometric plate reader set to 30 °C with
75 continuous shaking over at least 18 hours. At least three technical and two biological repeats were
76 plotted (indicating the standard deviation between repeats in shade). Exceptions were the high
77 apidaecins concentrations where the availability of the peptide was limiting, e.g. 1280 $\mu\text{g mL}^{-1}$
78 Api1b. The growth curves were analyzed in Prism 8.2.1 for Windows, GraphPad Software,
79 www.graphpad.com. The growth parameters were predicted by fitting the growth data to logistic
80 growth models and the two-tail P values were determined by t-test.

81 **Lambda Phage lysis assay**

82 In order to induce the C321 λ cI857 lysogens, freezer stocks of the cells were streaked on
83 LB agar plates and incubated overnight at 30 °C. Several colonies were screened for temperature
84 sensitivity at 42 °C. Parallel liquid cultures were set up in LB supplemented with 5mM MgSO₄ at
85 30 °C. Overnight cultures from the temperature sensitive isolates were diluted 1:100 in the same
86 medium containing Api137 at indicated concentrations. Once the cells reached $\text{OD}_{600} \sim 0.1$ (grown
87 at 30 °C with good aeration) the temperature was shifted to 42 °C for 15 min. The cells were then
88 diluted to $\text{OD}_{600} \sim 0.05$ in a Corning® 96 Well clear flat bottom plate. OD_{600} was recorded every
89 minute using a Biotek spectrophotometric plate reader set to 37 ° with continuous shaking.

90

91 **Cloning and strain engineering**

92 For routine PCR and Gibson assembly procedures Q5® High-Fidelity 2X Master Mix and
93 Gibson Assembly® Master Mix from NEB were used and primers were designed following the
94 manufacturer's instructions. (T7-(UAG)₂-sfGFP DNA template was generated by linearizing and
95 amplifying the pBAD-Ub-UAG-sfGFP_151UAG plasmid with primers Pri1 and Pri2 (**SI Tables**
96 **1–2**). The template was cleaned up and concentrated by phenol-chloroform extraction and ethanol
97 precipitation before use in cell-free translation experiments. Routinely, new plasmids were
98 constructed using parts from existing plasmids, e.g. p006-GFP-pBAD (Addgene Plasmid
99 #108315) as the plasmid backbone for the new pBAD-PopZ plasmids (**SI Table 2**), or gBlocks
100 (IDT) via Gibson assembly and cloning into NEB® 5-alpha Competent *E. coli*.

101 Of note, a shortened backbone from pDULE-ABK (Addgene Plasmid #49086, with total
102 vector size of 7590) was used to construct the new pDule plasmids, e.g. pDule-MbAbKRS-
103 2xtRNA with total vector size of 4577 bp. The pDule-MbAbKRS-2xtRNA plasmid series contains
104 two copies of *tRNACUA^{Pvu}I* genes under proK and lpp promoters.

105 Simple site-directed mutagenesis of reporter plasmids, e.g. PopZ-(UAG)₂-sfGFP to PopZ-
106 (UAG)₆-sfGFP, were performed using Q5® Site-Directed Mutagenesis Kit from NEB® following
107 the manufacturer's instructions.

108 Strains that are used in the nsAA incorporation experiments were generated by
109 transforming electrocomponent cells, BL21 (E. cloni EXPRESS BL21(DE3), Lucigen), DH10B
110 (E. cloni 10G, Lucigen) or other strains including *E. coli* Nissle 1917 and *A. tumefaciens* that are
111 made electrocompetent and handled as described^{3,4}. Cultures from at least 3 separate colonies were
112 frozen and used for the nsAA incorporation assays as biological replicates. Routinely, new

113 sequences were verified via Sanger sequencing by Genewiz and NGS-based complete plasmid
114 sequencing by MGH DNA Core (**SI Table 2**).

115

116 **nsAA Incorporation Assays.**

117 nsAA incorporation was quantified using at least 3 biological and technical replicates as
118 described previously⁵ with the following modifications: in general, strains harboring indicated
119 reporter and aaRS/tRNA plasmids were inoculated from frozen stocks in biological triplicates
120 and grown to confluence overnight in 96-well deep well plates. Experimental cultures were
121 inoculated at 1:10 dilutions of the overnight in 96-well deep well plates containing 100 µL of
122 either 2xYT, GMML, or LB (for *A. tumefaciens*) media supplemented with antibiotics, inducers
123 and nsAAs (or no nsAA). Cells were incubated shaking at their optimal temperatures. In
124 experiments with apidaecins, the peptide (or water control) was added at around OD₆₀₀ of 0.5–
125 0.8, typically after 2–4 h of growth, as adding the peptide earlier was either toxic or did not result
126 in an improvement in nsAA incorporation. The cells were then further incubated until the
127 cultures reached confluence (16–24 h). Cells were then centrifuged (5,000 g for 3 min), the
128 supernatant was removed by decanting the plates and the pellets were washed with 1 mL PBS at
129 least once (three times for experiments with **Cou**) and resuspended in 1 mL PBS. 100 µL of the
130 cell suspensions were transferred to a Corning® 96 Well clear flat bottom, black polystyrene
131 plates and absorbance at 600 nm (i.e. OD₆₀₀) and relative fluorescence units (RFU, with
132 excitation/emission wavelengths of 485 nm/528 nm for sfGFP and 390 nm/450 nm for **Cou**)
133 were measured using a Biotek spectrophotometric plate reader. The read data were blanked and
134 further processed as reported in figures, e.g. the reporter fluorescence was normalized by the
135 OD₆₀₀ reading to obtain RFU/OD₆₀₀. Typically, these individual intensity values were further

136 normalized to the highest average signal within an experiment and the data were plotted and
137 analyzed in Prism 8.2.1 for Windows.

138 Specifically, in experiments leading to **Figures 2c** and **SI Figures 4c–d 5a, 6a** we used
139 cells harboring the reporter plasmid pZE21/Ub-UAG-sfGFP_151UAG (ColE1 origin, KanR,
140 under Tet induction) and pEVOL aaRS/tRNA_{CUA} plasmids (p15A origin, CmR, tRNA genes
141 constitutively expressed, aaRS genes under arabinose induction) as previously described⁵. In
142 these experiments, arabinose (to final 0.2%) was present throughout, including the initial
143 inoculation of the frozen stocks, because the constitutive expression of the aaRS genes did not
144 affect the growth. After the cells were diluted into 2xYT supplemented with arabinose,
145 kanamycin (to final 25 µg mL⁻¹), chloramphenicol (to final 12.5 µg mL⁻¹), and nsAAs, at around
146 OD₆₀₀ of 0.5–0.8, typically after 2–4 h of growth, sfGFP expression was induced by the addition
147 of anhydrotetracycline (100 ng mL⁻¹ final) together with the addition of the apidaecin peptides.
148

149 For experiments with *A. tumefaciens*, overnight cultures of *A. tumefaciens* cells harboring
150 the plasmids pTD114_sfGFP-1ATG (pBBR1 origin, GmR, under NHL induction) and
151 pYW15c_MjBpaRS (pSa origin, AmpR, MjBpaRS and *tRNA*_{CUA}^{Tyr} genes constitutively expressed
152 under PN25 and proK promoters, respectively) were diluted 1:10 in LB supplemented with
153 gentamycin (to final 125 µg mL⁻¹), carbenicillin (to final 125 µg mL⁻¹) and **Bpa** (or no nsAA). At
154 around OD₆₀₀ of 0.5–0.8 (after 3–4 h of growth at 30 °C), sfGFP expression was induced by the
155 addition of NHL (1 µg mL⁻¹ final) together with the addition of the apidaecin peptide.
156

157 For experiments leading to **Figures 2d, 3, 4** and **SI Figures 6b–g, 7, 8a, 8c, 9c, 10c and**
158 **10d** the new auto-inducible reporter system was used. In these experiments *E. coli* cells harbored

159 two plasmids: an auto-inducible reporter plasmid (ColE1 origin, KanR, under arabinose
160 induction), and a pDule aaRS/tRNA_{CUA} plasmid (p15A origin, TcR, aaRS and tRNA genes
161 constitutively expressed, under GlnS and proK promoters, respectively). In any strain the
162 reporter plasmid was either of the pBAD-Ub-UAG-sfGFP_151UAG, pBAD-PopZ-(UAG)₀-
163 sfGFP, pBAD-PopZ-(UAG)₂-sfGFP, pBAD-PopZ-(UAG)₆-sfGFP or pBAD-PopZ-(UAG)₈-
164 sfGFP. The aaRS/tRNA_{CUA} plasmid was either of the pDule-MjBpaRS, pDule-MjCouRS, pDule-
165 Sc5OHWRS, pDule-MbAbKRS-2xtRNA, pDule-MbAbKRS-2xtRNA-RBS1-api1b, pDule-
166 MbAbKRS-2xtRNA-RBS2-api1b, pDule-MbAbKRS-2xtRNA-RBS1-apiB5, pDule-MbAbKRS-
167 2xtRNA-RBS1-apiB8, and pDule-MbAbKRS-2xtRNA-RBS1-apiC3) (**SI Table 2**). In these
168 experiments, overnight cultures were grown in 2xYT supplemented with 25 µg mL⁻¹ kanamycin
169 and 5 µg mL⁻¹ tetracycline. The cells were then directly diluted 1:10 in GMML supplemented
170 with kanamycin (to final 12.5 µg mL⁻¹), tetracycline (to final 2.5 µg mL⁻¹), glucose (to final
171 0.05%), arabinose (to final 0.05%), and nsAAs (or no nsAA). In conditions involving
172 exogenously added peptides, at around OD₆₀₀ of 0.5–0.8 (after 3–4 h of growth at 37 °C)
173 apidaecin peptides were added. Otherwise, the cells were incubated until the cultures reached
174 confluence (16–24 h) and they were as detailed above.

175

176 Protein Sequence Analysis by LC-MS/MS

177 Excised gel bands were cut into approximately 1 mm³ pieces. Gel pieces were then
178 subjected to a modified in-gel trypsin digestion procedure ⁶. Gel pieces were washed and
179 dehydrated with acetonitrile for 10 min. followed by removal of acetonitrile. Pieces were then
180 completely dried in a speed-vac. Rehydration of the gel pieces was with 50 mM ammonium
181 bicarbonate solution containing 12.5 ng/µl modified sequencing-grade trypsin (Promega,

182 Madison, WI) at 4°C. After 45 min., the excess trypsin solution was removed and replaced with
183 50 mM ammonium bicarbonate solution to just cover the gel pieces. Samples were then placed
184 in a 37°C room overnight. Peptides were later extracted by removing the ammonium bicarbonate
185 solution, followed by one wash with a solution containing 50% acetonitrile and 1% formic acid.
186 The extracts were then dried in a speed-vac (~1 hr). The samples were then stored at 4°C until
187 analysis.

188 On the day of analysis, the samples were reconstituted in 5 - 10 µl of HPLC solvent A
189 (2.5% acetonitrile, 0.1% formic acid). A nano-scale reverse-phase HPLC capillary column was
190 created by packing 2.6 µm C18 spherical silica beads into a fused silica capillary (100 µm inner
191 diameter x ~30 cm length) with a flame-drawn tip⁷. After equilibrating the column each sample
192 was loaded via a Famos auto sampler (LC Packings, San Francisco CA) onto the column. A
193 gradient was formed, and peptides were eluted with increasing concentrations of solvent B
194 (97.5% acetonitrile, 0.1% formic acid). As peptides eluted, they were subjected to electrospray
195 ionization and then entered into an LTQ Orbitrap Velos Pro ion-trap mass spectrometer (Thermo
196 Fisher Scientific, Waltham, MA). Peptides were detected, isolated, and fragmented to produce a
197 tandem mass spectrum of specific fragment ions for each peptide. Peptide sequences (and hence
198 protein identity) were determined by matching protein databases with the acquired fragmentation
199 pattern by the software program, Sequest (Thermo Fisher Scientific, Waltham, MA)⁸. All
200 databases include a reversed version of all the sequences and the data was filtered to between a
201 one and two percent peptide false discovery rate.

202

203 **Image acquisition and quantification.**

204 For imaging, bacterial cells were resuspended in minimal volume of 1 x PBS. 1 μ L of this
205 cell suspension was spotted to the coverslips (typically, 24X50 mm coverslips; #1.5) and an 8x8-
206 mm wide, 2-mm thick PBS-agarose pad (SeaKem LE Agarose) was laid on top of the cells. Phase
207 and fluorescence images were acquired using a Nikon Ti2 Eclipse inverted microscope equipped
208 with a Plan Apo Lambda DM 60X (1.4 NA, Ph3) oil objective and Andor Zyla sCMOS camera.
209 NIS-Element AR software was used for image acquisition. For quantitative comparisons, the
210 samples were imaged in the same session with the same image conditions across. Image processing
211 was performed in FIJI. Images were scaled, cropped and rotated without interpolation. Linear
212 adjustment was performed to optimize contrast and brightness of the images. Figure construction
213 was performed in Adobe Illustrator. The relative fluorescence units of **Cou** and sfGFP signal
214 intensities were quantified using a FIJI plugin, MicrobeJ⁹, where cells were identified in the phase
215 contrast channel with width limit from 0.3 to 2 μ m and length above 1 μ m. Fluorescence intensities
216 at the cell poles and the rest of the cell body then quantified and averaged within individual cells
217 ($N > 100$) using the ‘polarity’ mode in MicrobeJ. Violin plots (**Figure 3e** and **SI Figure 7c**) were
218 plotted and analyzed in Prism 8.2.1 for Windows,

219

220 **Partial recoding by multiplex automated genome engineering (MAGE)**

221 Previously designed MAGE oligos were ordered from IDT with standard desalting and 2
222 phosphorothioate bonds at each terminus (**SI Table 1**).¹⁰ A master stock solution with a mixture
223 of these 13 oligos to reach final concentrations of 30 μ M for each oligo. As a negative control,
224 MAGE-Neg control was prepared to 400 μ M. pORTMAGE protocol was performed as
225 previously described¹¹. Briefly, an overnight culture of cells harboring pORTMAGE-3 plasmid

226 (Addgene Plasmid # 72678) was diluted 100-fold into 20–30 mL 2xYT + kanamycin (to final 25
227 µg mL⁻¹), and grown at 30 °C with aeration until mid-log growth was achieved (OD600 ~0.55–
228 0.65). Lambda Red was induced in a shaking water bath (42 °C, 300 rpm, 15 minutes), then
229 induced culture tubes were cooled rapidly on ice for at least 5 minutes. Electrocompetent cells
230 were prepared at 4 °C by pelleting 10 mL of culture (centrifuge at 16,000 g at 5 min) and
231 washing the cell pellet twice with 1 mL ice cold deionized water (dH₂O) and eventually
232 resuspending cells in 250 µL cold dH₂O. 55 µL of the cells were mixed with 5 µL of the oligo
233 mixture. Cells were transferred to 0.1 cm cuvettes, electroporated (BioRad GenePulser™, 1800
234 V, 200 Ω, 25 µF), and then immediately resuspended in 0.5 mL SOC medium. The cells were
235 allowed to recover 1 h at 30 °C at 250rpm. To select for Api 137 resistant colonies, 100 µL of
236 these cells were plated on LB + Api 137 (750 µg mL⁻¹). For continued MAGE cycling 4.5 mL
237 2xYT + kanamycin (to final 25 µg mL⁻¹) were added and cultures were recovered to mid-log
238 phase before being induced for the next cycle. Colonies on LB + Api 137 plates appeared after as
239 little as 2 MAGE cycles with the mixture of the 13 oligos, but not with the negative control. The
240 resistant isolates were tested for their ability to incorporate nsAAs after the pORTMAGE
241 plasmid was cured. The presence of codon replacements were confirmed using allele-specific
242 colony PCR using primer sets specific for 13 genes and following the MASC-PCR protocol as
243 described¹⁰.

244

245 **Library Generation Flow Cytometry and Cell Sorting.**

246 Apidaecin peptide library was constructed using pDule-MbAbKRS-2xtRNA-RBS1-api1b
247 as the template. First, the plasmid backbone was linearized using primers Pri3 and Pri4. The library
248 insert sequence, Ultra1, was acquired as one 200 bp PAGE purified Ultramer (IDT). Ultra1 (to

final 1 μ M) was further amplified by Pri5 and Pri6. The insert (~125 ng) is assembled into the backbone (~400 ng) in a 150 μ L Gibson assembly reaction (NEB 50 °C, 1h). The product was then cleaned and concentrated by ethanol precipitation and the entire product was electro-transformed into *E. cloni* 10G SUPREME (Lucigen) cells that already harbored the pBAD-Ub-UAG-sfGFP_151UAG plasmid. After cells were recovered in SOC for 1 h, overnight cultures were set up by adding 4 mL 2xYT supplemented with kanamycin (to final 25 μ g mL⁻¹) and tetracycline (to final 5 μ g mL⁻¹) at 37 °C with aeration. In parallel, dilutions were plated to estimate the library size. 50 colonies were randomly selected and sequenced (Genewiz) in order to estimate library diversity and quality.

The library was directly diluted 1:10 in GMML supplemented with kanamycin (to final 12.5 μ g mL⁻¹), tetracycline (to final 2.5 μ g mL⁻¹), glucose (to final 0.05%), arabinose (to final 0.05%), and **BocK** (to 2 mM). After the cells were incubated overnight at 37 °C, they were washed twice with 1 mL 1 x PBS and diluted for fluorescence activated sorting in a Sony MA900 Cell Sorter. Cells displaying the top ~0.0005% and ~0.02% of fluorescence activation (~2,000 cells) were collected into 2xYT. After 30 min recovery, dilutions of the recovery were plated on LB + tetracycline (to final 10 μ g mL⁻¹). The next day, 30 colonies from each sort were sequenced. Library variants of interest were grown overnight, miniprepped, and retransformed into *E. cloni* 10G cells for further analysis in nsAA incorporation assays.

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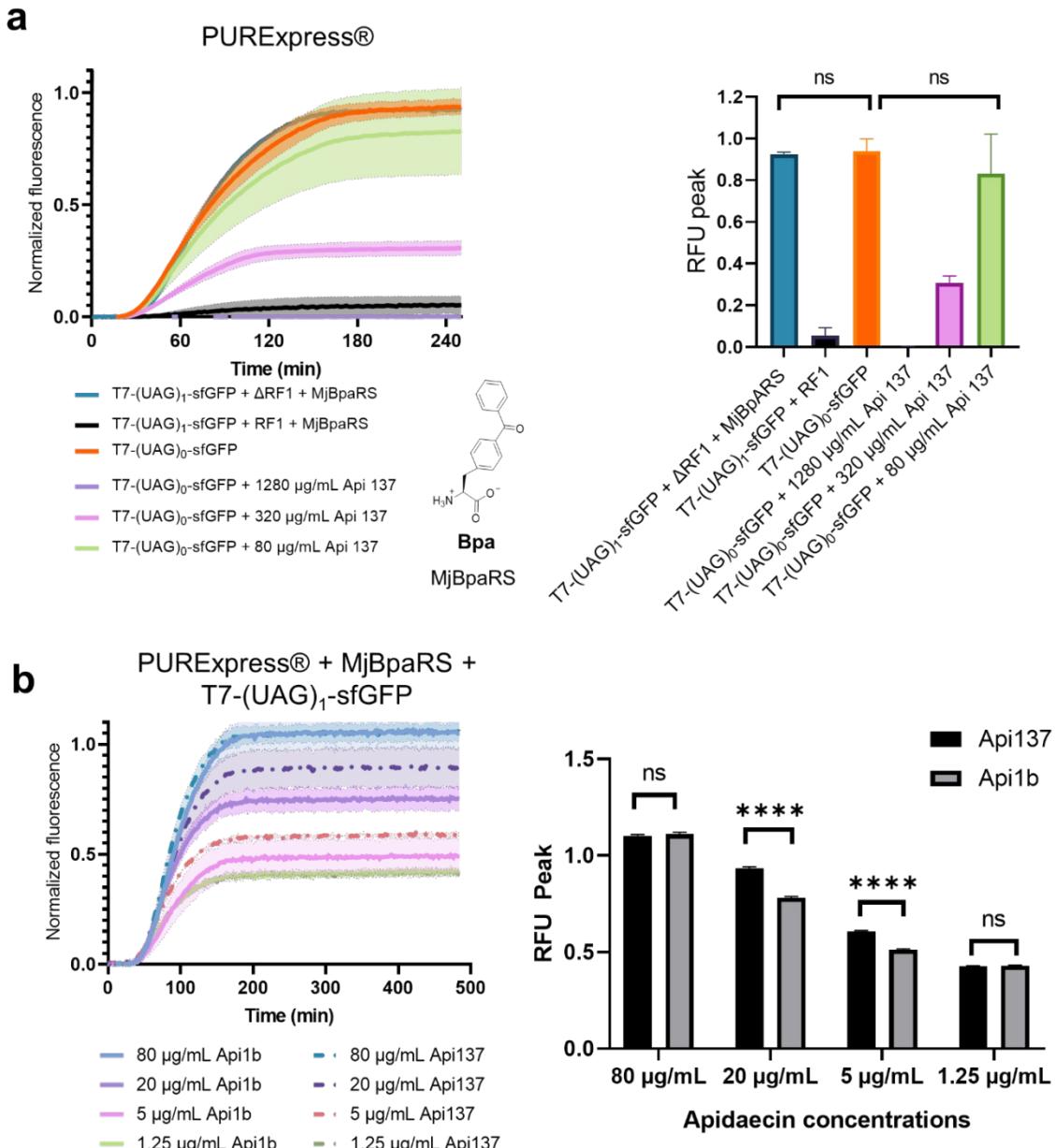
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271 **SI References**

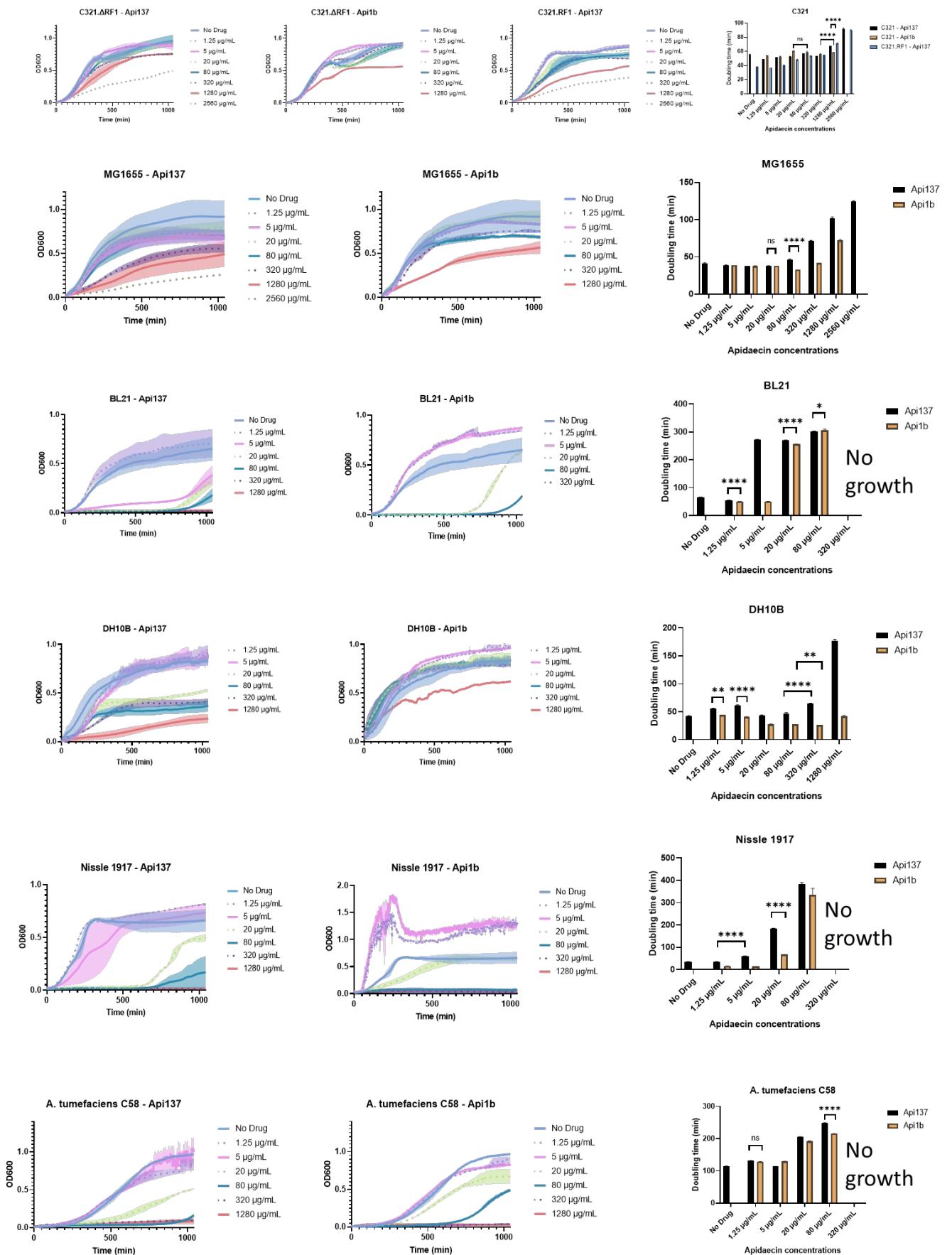
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309

310 **SI Figure 1.** Apidaecins improved nsAA incorporation in a cell-free translation system. a) In the
 311 cell-free protein translation system PURE, addition of purified MjBpaRS/*tRNA^{UUA}_{CUA}* pair and their
 312 cognate nsAA, **Bpa**, expressed an in-frame amber containing sfGFP construct (T7-(UAG)₁-
 313 sfGFP) comparably to a construct without ambers (T7-(UAG)₀-sfGFP). Api137 inhibited cell-
 314 free translation at concentrations higher than 80 µg mL⁻¹. b) At the same concentrations, Api137,
 315 a synthetic apidaecin analog, promoted nsAA-dependent increase of T7-(UAG)₁-sfGFP signal
 316 significantly better than the naturally occurring Api1b. Maximum relative fluorescence units
 317 (RFU) for each condition are shown on right panels. ****, P < 0.0001



319 **SI Figure 2.** Apidaecins are toxic to different Gram-negative bacteria where RF1 function is
320 essential. In a dose-manner, apidaecins inhibited growth of different Gram-negative bacteria in
321 liquid media. This inhibition typically manifested itself as a reduction in final cell mass or as a
322 prolonged doubling time (right panels). In general, Api137 was a more potent inhibitor than
323 Api1b, and RF1+ strains (including C321.RF1) was more sensitive than C321. Δ RF1. Among *E.*
324 *coli* strains tested, Nissle 1937 was the strain that was the most sensitive to apidaecins followed
325 by BL21, DH10B, MG1655, C321.RF1 and C321. Δ RF1. ****, $P < 0.0001$; **, $P \leq 0.007$; *, $P =$
326 0.0116

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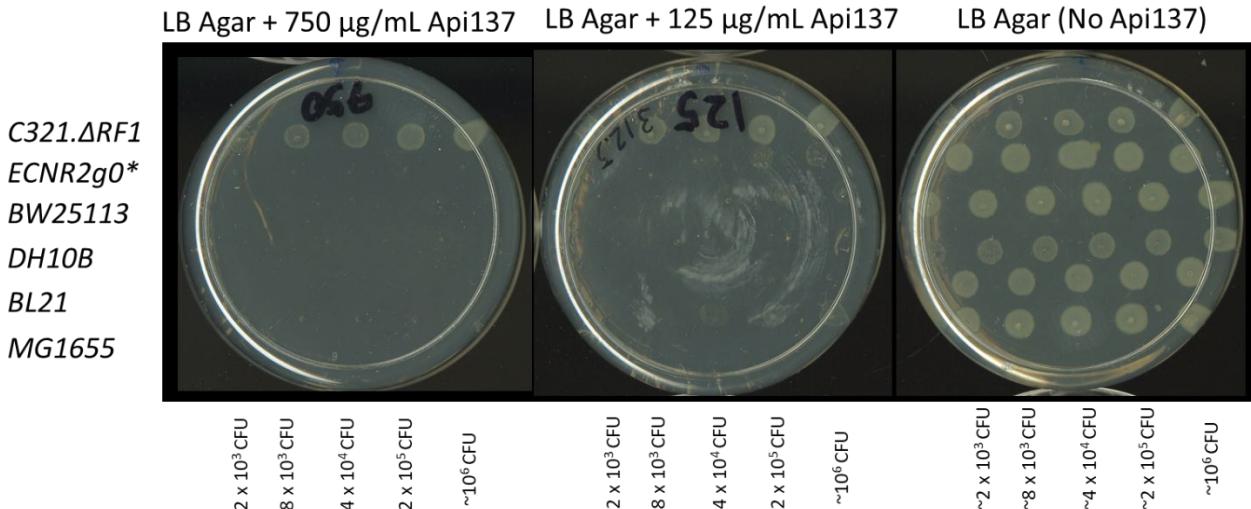
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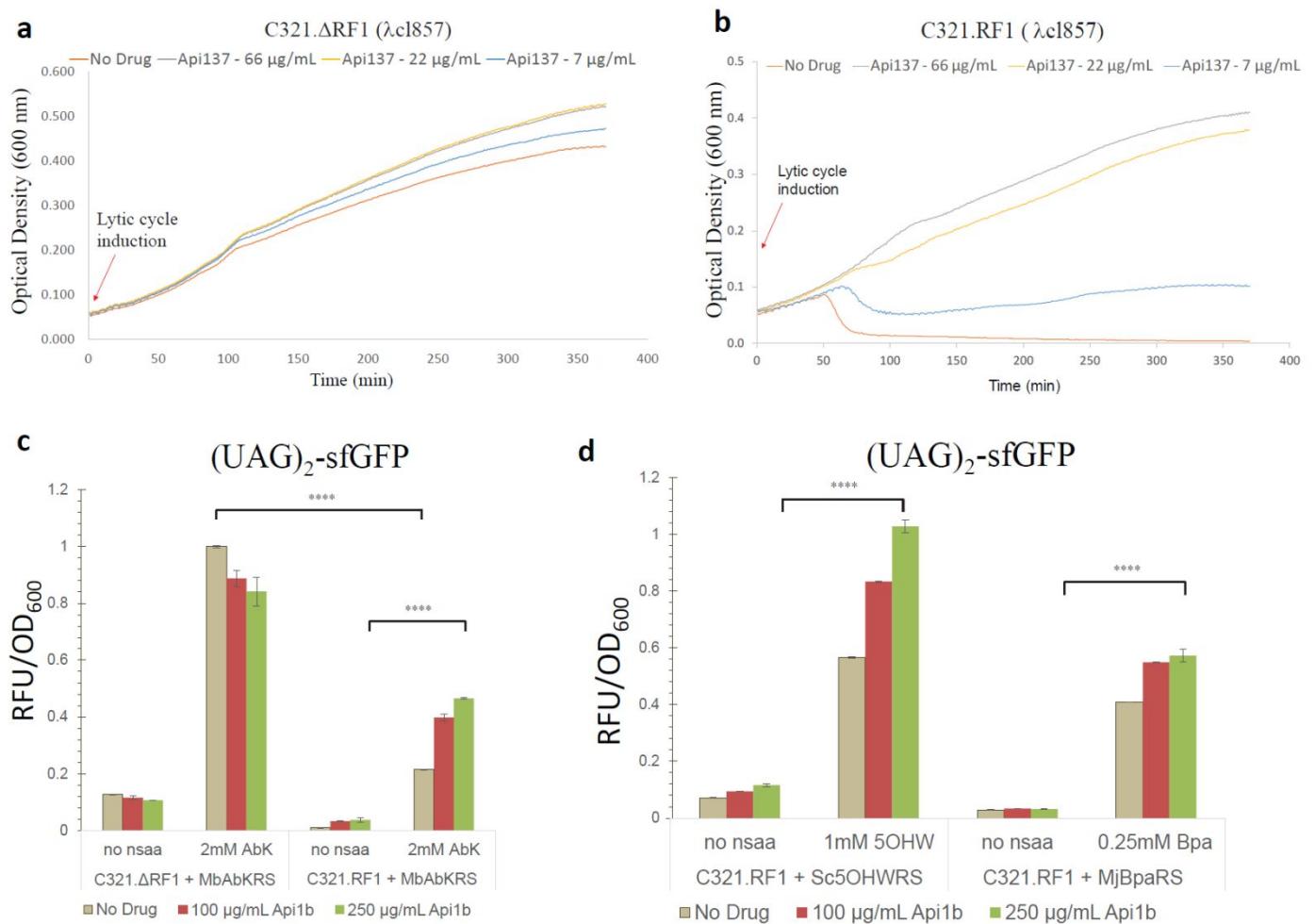
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336 **SI Figure 3.** Apidaecins inhibit colony formation of different *E. coli* strains where RF1 function
337 is essential. In LB solid media, Api137 (down to 125 µg mL⁻¹) was toxic to cells from different
338 *E. coli* strains, except the recoded MG1655 lacking native UAGs and RF1 (C321.DRF1).
339 ECNR2gO* is the MG1655 non-recoded and RF1+ parental strain of C321.
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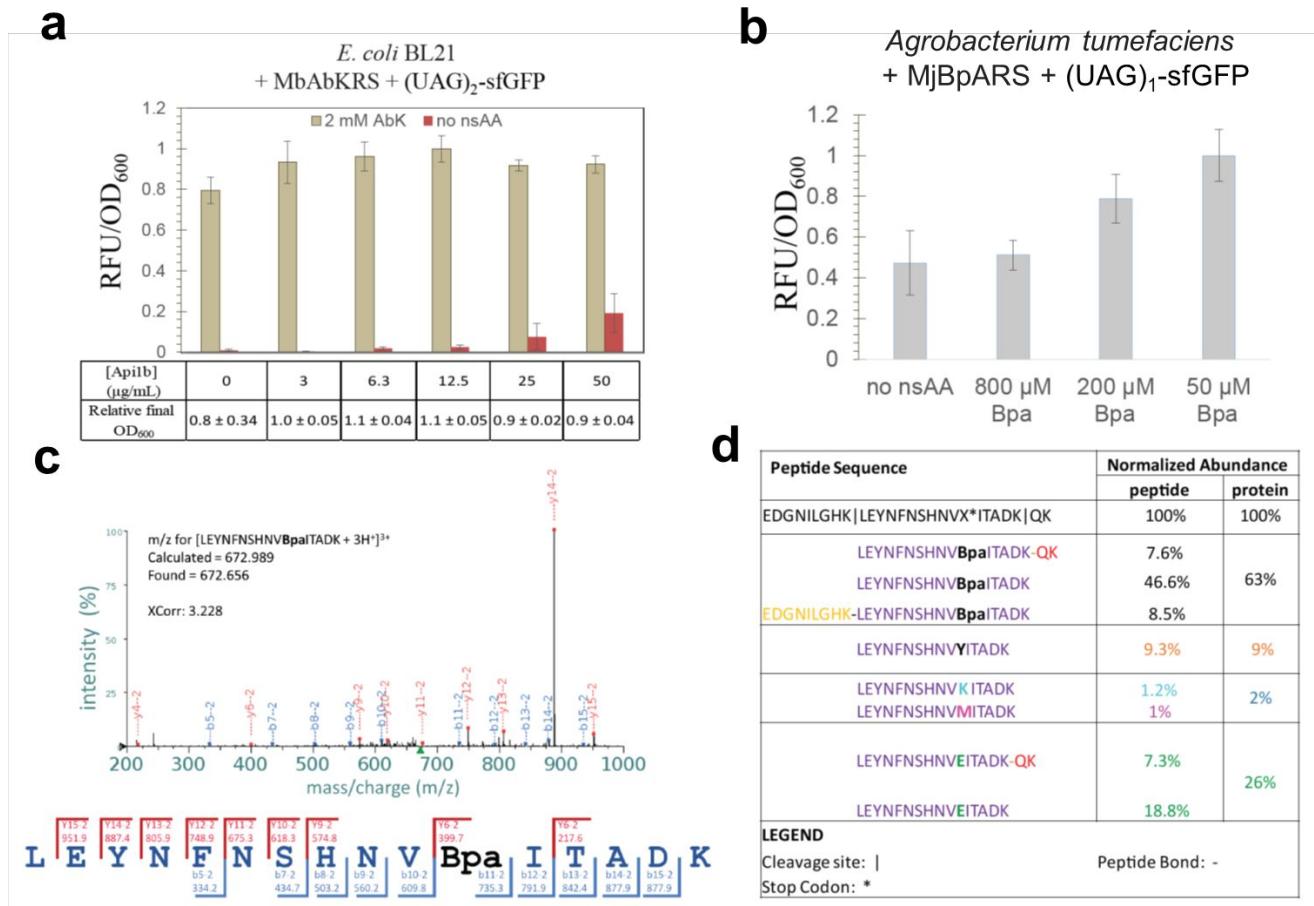
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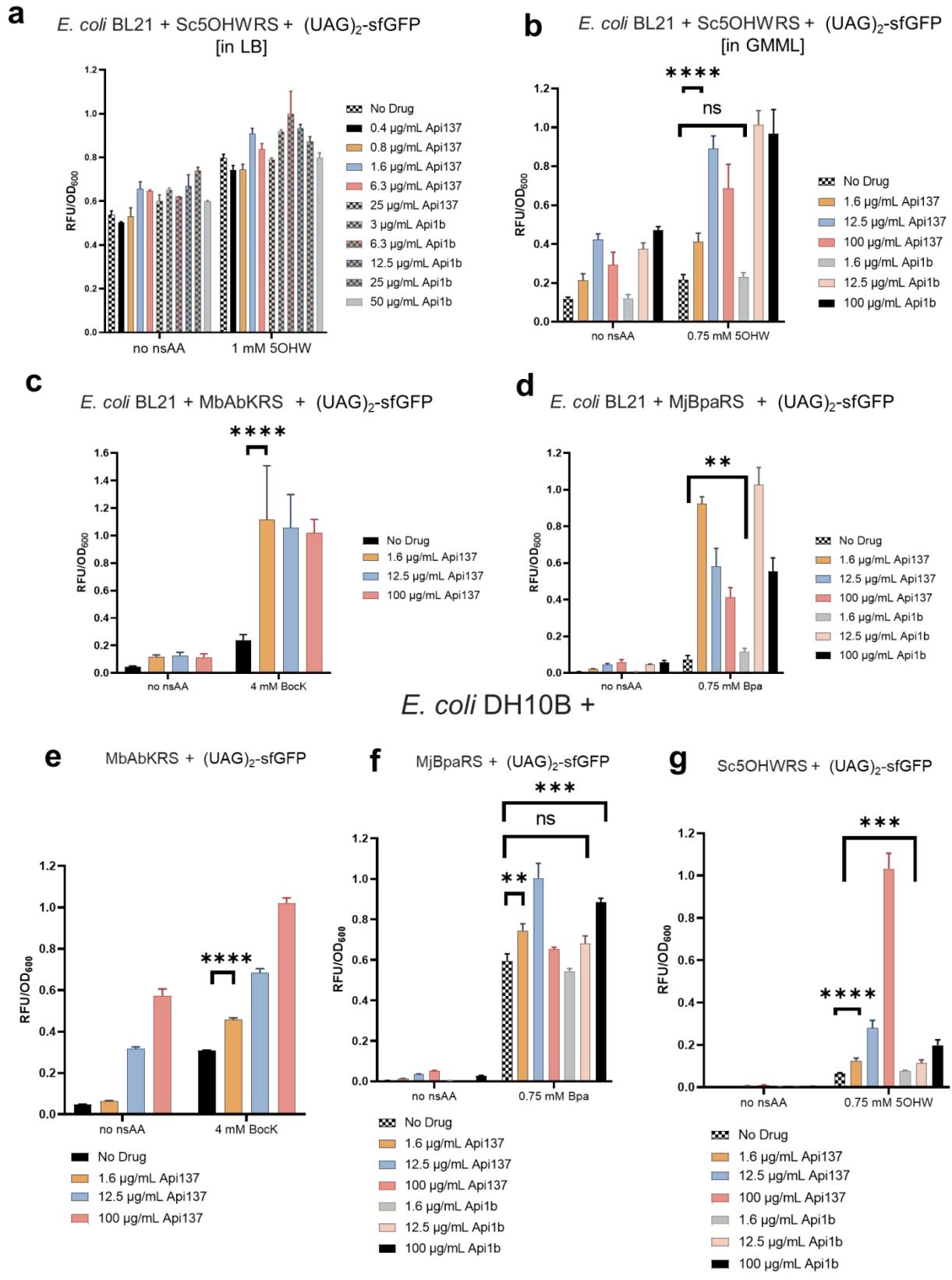
344 **SI Figure 4.** Apidaecins confer conditional phage resistance and improve nsAA incorporation in
345 *E. coli* cells with redundant RF1 functionality. a) In liquid media, C321. Δ RF1 is resistant to λ
346 phage-induced lysis and to Api137. b) In a dose dependent manner, Api137 rescued lysis of
347 C321.RF1 (λ cl857) cells upon λ phage lytic cycle induction. c) Api1b stimulated **AbK**-
348 dependent sfGFP signal increase in C321.RF1, but not in C321. Δ RF1 cells expressing
349 MbAbKRS /*tRNA_{CUA}^{D₁₃₁}* system. d) Api1b improved **5OH**- and **Bpa**-dependent sfGFP signal
350 increase in C321.RF1 expressing Sc5OHWRS/*tRNA_{CUA}^{T_{yr}}* and MjBpaRS/*tRNA_{CUA}^{T_{yr}}* systems. ****,
351 $P < 0.0001$

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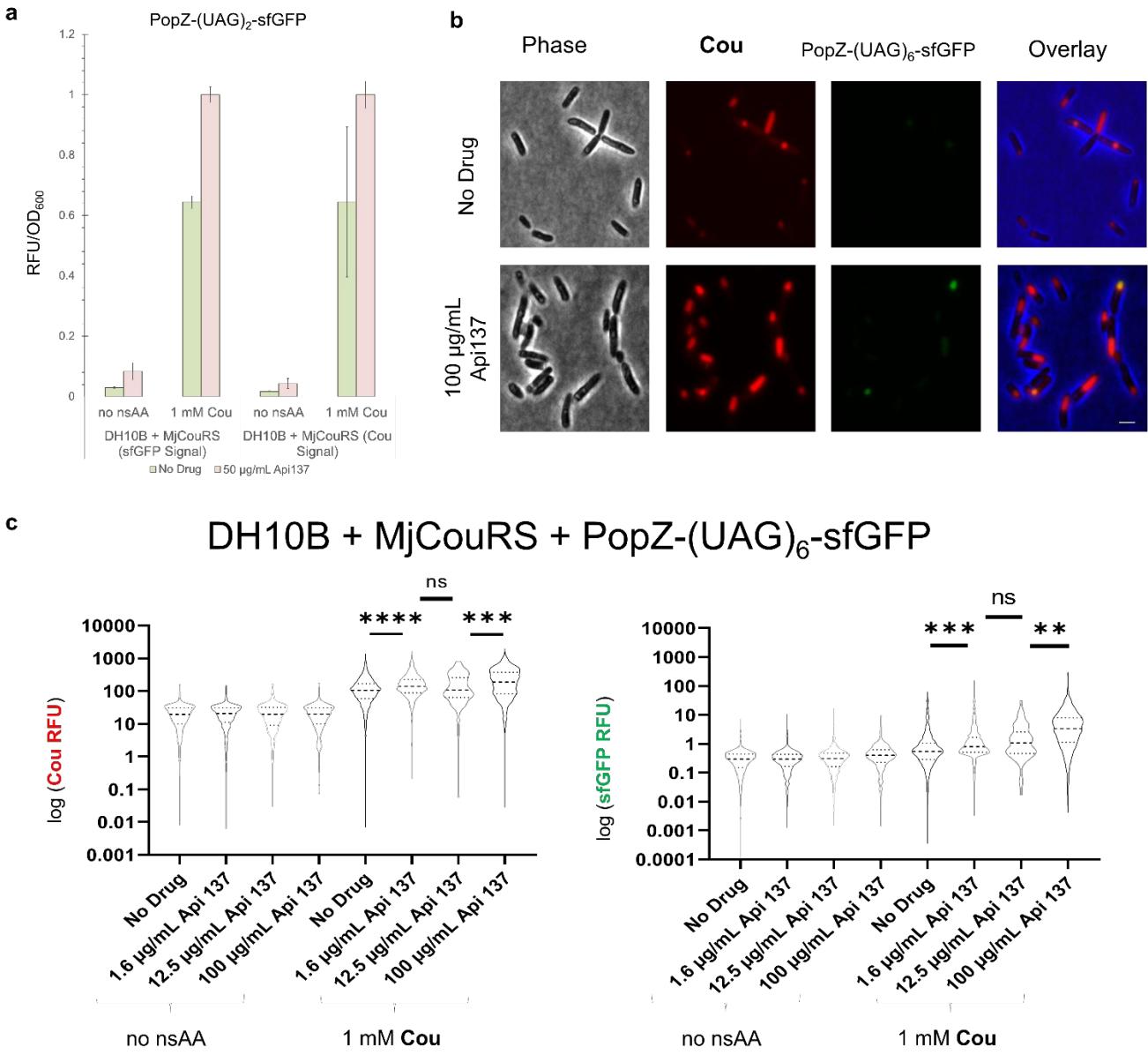


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354 **SI Figure 5.** Exogenously added apidaecins improve nsAA-dependent sfGFP signal increase in
 355 different bacteria. a) in a dose-dependent manner and with minimal effect in final cell density
 356 (manifested by the drop of the relative final OD₆₀₀ compared to no drug controls), Api1b
 357 improved AbK-dependent sfGFP signal increase in *E. coli* BL21 cells, b) *A. tumefaciens*
 358 (constitutively expressing MjBpARS/*tRNA*_{CUA}^{Tyr}) expressed (UAG)₁-sfGFP optimally at 50 μM
 359 **Bpa**. c-d) Tandem mass spectrometry (MS/MS) fragmentation analysis of the trypsin digested
 360 (UAG)₁-sfGFP construct from *A. tumefaciens* (grown in LB) confirmed **Bpa** incorporation at the
 361 expected amber position. c) A MS-MS spectra for a representative **Bpa**-containing peptide. d)
 362 Relative abundances are based on ion count of detected relevant peptides with **Bpa** and the other
 363 natural amino acids.

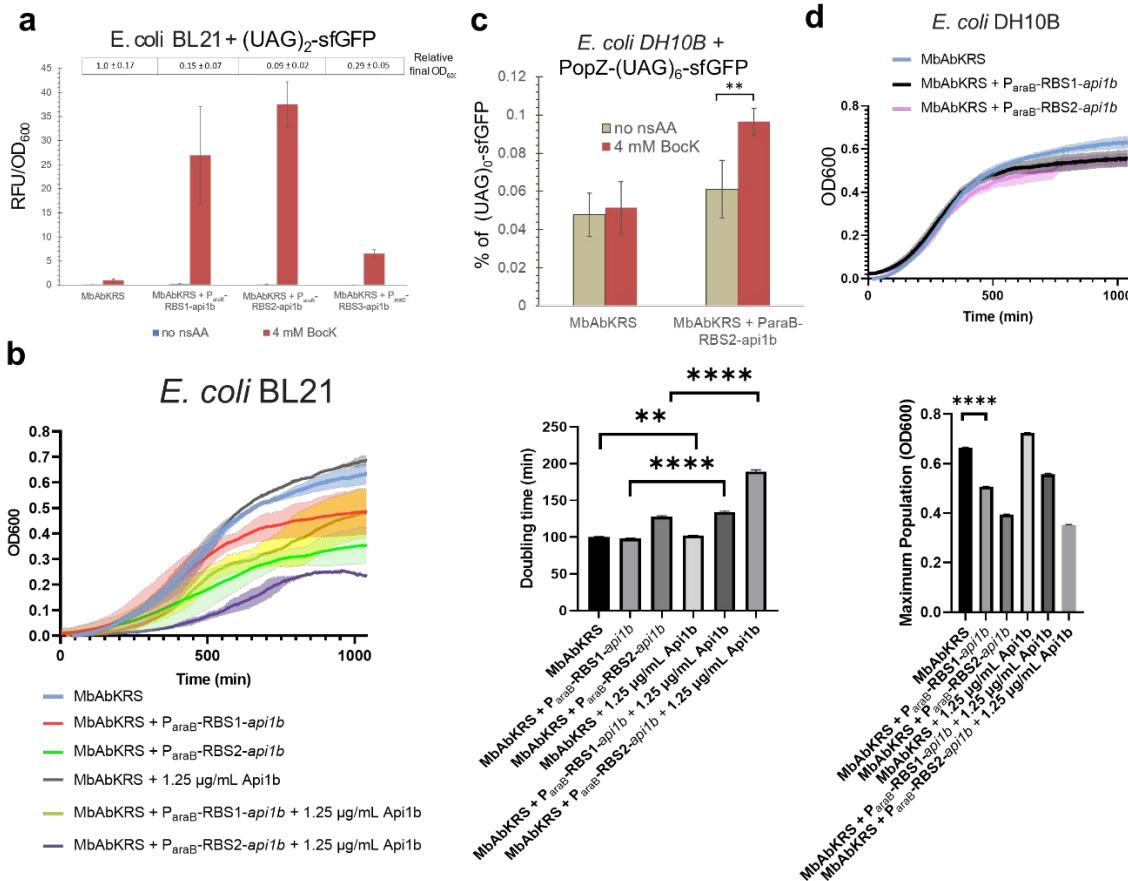


365 **SI Figure 6.** a) The Sc5OHWRs/*tRNA*_{CUA}^{T_{rrn}} in LB results in high back-ground (no nsAA) signal
366 occluding the effects of apidaecins. b) The new autoinducable reporter system in GMML
367 minimal media results in strong signal (+ nsAA) over back-ground (no nsAA). In a dose
368 dependent manner, apidaecins improve nsAA-dependent sfGFP expression in both BL21 (a-d)
369 and DH10B (e-f) expressing PopZ-(UAG)₂-sfGFP reporter and Sc5OHWRs/*tRNA*_{CUA}^{T_{rrn}} (a,b,g),
370 or MbAbKRS /*tRNA*_{CUA}^{P_{vrl}}(c,e), or MjBpaRS/*tRNA*_{CUA}^{T_{vr}} (d,f) systems. b) In BL21 cells expressing
371 the Sc5OHWRs/*tRNA*_{CUA}^{T_{rrn}} and PopZ-(UAG)₂-sfGFP, Api137, or Api1b improved sfGFP signal
372 up to ~4, or ~5 fold. c) In BL21 cells expressing the MbAbKRS /*tRNA*_{CUA}^{P_{vrl}} and PopZ-(UAG)₂-
373 sfGFP, Api137 improved OD₆₀₀ normalized sfGFP signal up to ~10 fold. d) In BL21 cells
374 expressing the MjBpARS/*tRNA*_{CUA}^{T_{vr}} and PopZ-(UAG)₂-sfGFP, Api137, or Api1b improved
375 sfGFP signal up to ~13, or ~14 fold. e) In DH10B expressing the MbAbKRS /*tRNA*_{CUA}^{P_{vrl}} and
376 PopZ-(UAG)₂-sfGFP, Api137 improved sfGFP signal up to ~3 fold. f) In DH10B expressing the
377 MjBpARS/*tRNA*_{CUA}^{T_{vr}} and PopZ-(UAG)₂-sfGFP, Api137 improved sfGFP signal up to ~2 fold. g)
378 In DH10B expressing the Sc5OHWRs/*tRNA*_{CUA}^{T_{rrn}} and PopZ-(UAG)₂-sfGFP, Api137, or Api1b
379 improved sfGFP signal up to ~16, or ~3 fold. ****, P < 0.0001; ***, P ≤ 0.005; **, P ≤ 0.0076.
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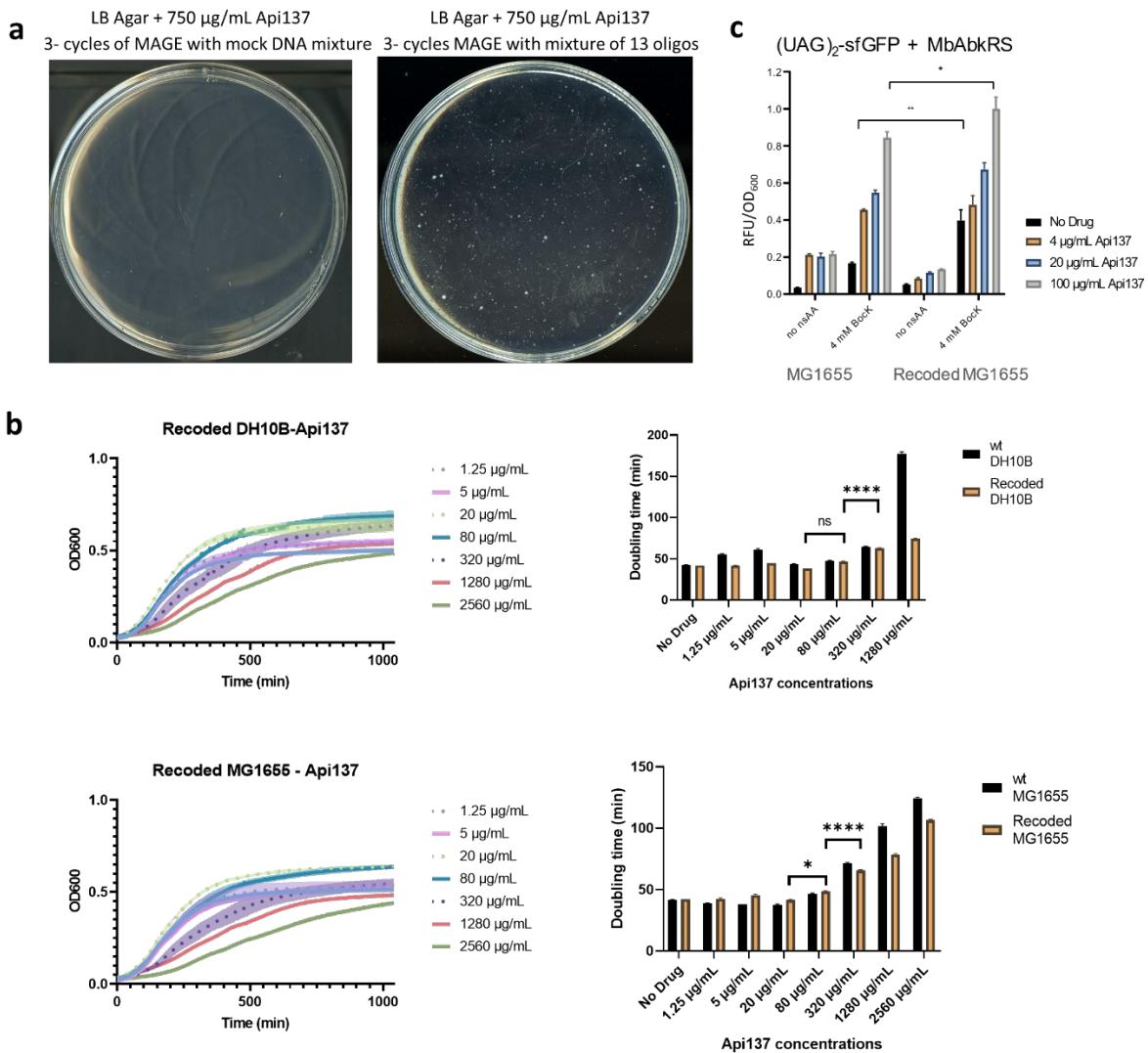
383 **SI Figure 7.** Apidaecins improve specific, multi-site incorporation of **Cou**. a) Bulk
 384 measurements of DH10B expressing MjCouRS/*tRNA^{Tyr}_{CUA}* and PopZ-(UAG)₂-sfGFP show that
 385 Api137 treatment increases spectrally distinct sfGFP and Cou signals to the comparable extend.
 386 b) Micrographs showing subcellular signals from **Cou** (false colored in red) and PopZ-(UAG)₆-
 387 sfGFP fusion (false colored in green) colocalized at the poles of the DH10B *E. coli* cells imaged
 388 in phase, DAPI, and EGFP channels and overlayed on phase (false colored in blue) c) Violin
 389 plots of single cell quantification by light microscopy showed that Api137 improved both Cou
 390 and sfGFP signals comparably. An exception was DH10B cells expressing PopZ-(UAG)₆-sfGFP
 391 treated with highest concentration of Api137 tested (100 µg mL⁻¹). Under these conditions, the
 392 **Cou** signal improvement was ~2 fold, but the sfGFP signal improvement was ~5 fold. The scale
 393 bars are 2 µm. ****, P <0.0001; ***, P ≤ 0.004; **, P = 0.0035.



395
396 **SI Figure 8.** a) Three ribosome binding sequences of different strengths (RBS2>RBS1>RBS3)
397 were designed using the RBS calculator tool (<https://salislab.net/software/>)¹². Arabinose operated
398 autoinduction of *api1b* improved **BocK** incorporation up to ~37 fold while showing significant
399 toxicity depending on the gene's RBS-strength. b) Growth curves (left), generation times
400 (middle) and final OD (right) of BL21 cells auto-inducibly expressing MbAbKRS and P_{araB}-
401 RBS1-*api1b* or P_{araB}-RBS2-*api1b*. Exogenously added Api1b further sensitized *api1b* expressing
402 cells but did not affect the growth of MbAbKRS control cells. 1.25 µg mL⁻¹ Api1b reduced the
403 growth rate of MbAbKRS control cells only 2% but it reduced the growth rate of *api1b*
404 expressing cells ~30%. Growth of these *api1b* expressing cells were completely inhibited in the
405 presence of higher Api1b concentrations tested (>10 µg mL⁻¹). c) In-cell autoinduction of *api1b*
406 genes had a dramatically less effect on nsAA incorporation in DH10B compared to BL21. d)
407 P_{araB}-RBS1-*api1b* or P_{araB}-RBS2-*api1b* expression did not inhibit the growth of DH10B. The
408 RBS sequences are RBS1: GGAGGTAAAAAA, RBS2:GGAGTTAAGGAGGTAAAAAA, and
409 RBS3: GGAGGTAAAAAAATGCCGTAAAGGAGGTAAAAAA. ****, P < 0.0001; **, P ≤
410 0.007.

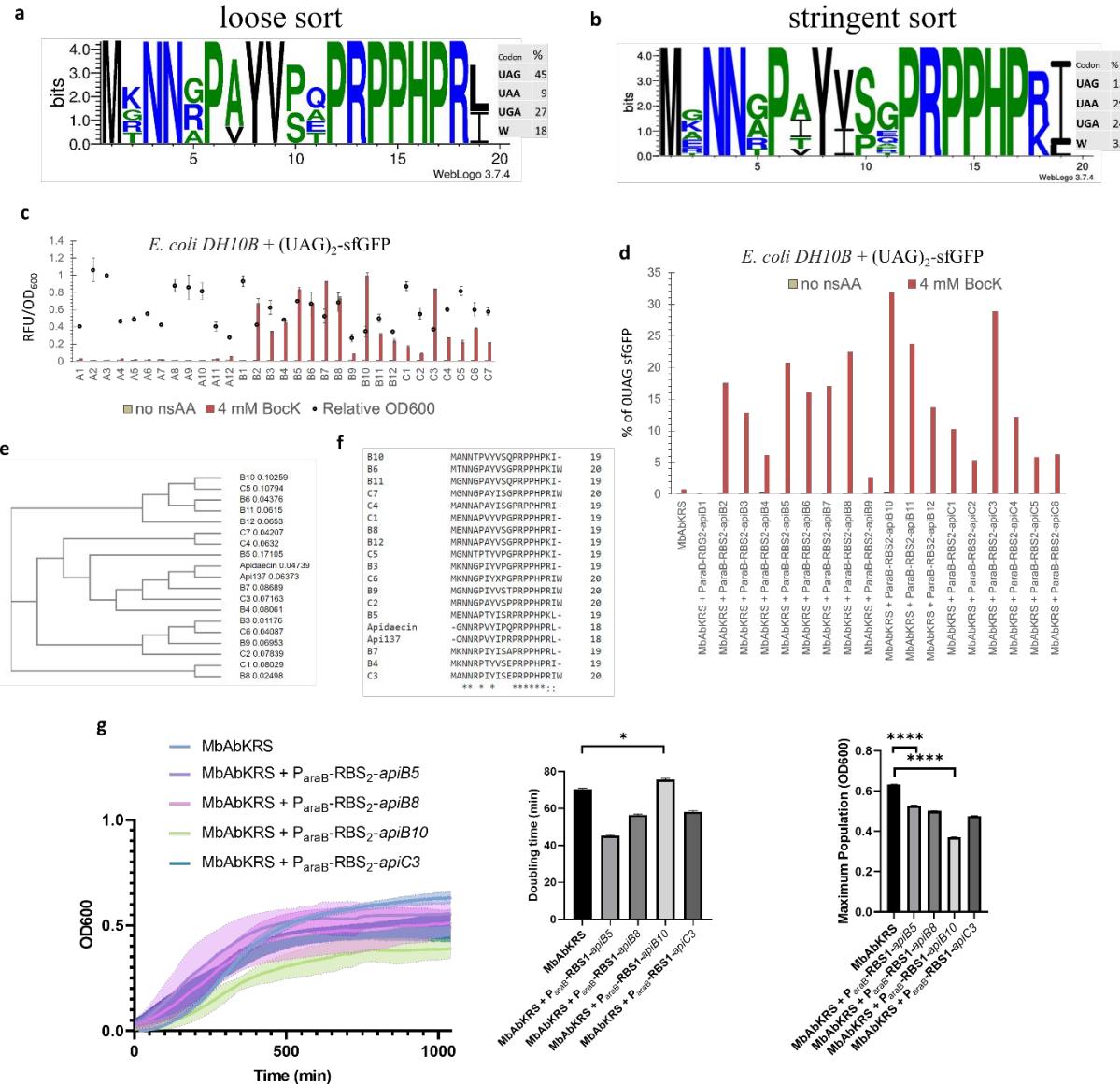
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414 **SI Figure 9.** RF1 inhibition by apideacins can facilitate recoding efforts toward improved nsAA
 415 incorporation. a) Cells recoded by a mixture of oligos specifically targeting essential genes
 416 formed colonies on Api137 containing selective plates. Same experimental set-up with a random
 417 oligo did not result into spontaneously resistant mutants. b) Growth curves (left) and generation
 418 times (right) of ‘partially recoded’ DH10B and MG1655 in the presence of different [Api137]
 419 show that partially recoded strains are more apidaecin-resistant than the wild-type parents (right,
 420 from **SI Figure 2**). c) Partially recoded MG1655 cells incorporated **BocK** more efficiently than
 421 the wild-type even in the absence of Api137. ****, $P < 0.0001$; **, $P \leq 0.0082$; *, $P \leq 0.0366$.



422

423 **SI Figure 10.** In-cell autoinduction allows evolution of new apidaecin-like peptides that show
424 improved nsAA incorporation and decreased cell toxicity. a–b) Enriched apiaecin-like peptide
425 variants from the loose (a) or stringent (b) sorts do not converge to common sequences. c–d) In-
426 cell autoinduction of variants from the stringent sort improved BocK incorporation but also
427 affected the cell growth to different extends in DH10B cells. e–f) a Neighbor-joining
428 phylogenetic tree without distance corrections (e), and multiple sequence alignment of relevant
429 apidaecin variants (f) generated using Clustal Omega Multiple Sequence Alignment tool¹³. g)
430 Growth curves (left), generation times (middle) and final OD (right) of DH10B cells auto-
431 inducibly expressing MbAbKRS and *apiB5*, *apiB8*, *apiB10*, or *apiC3*. ***, P < 0.0001; *, P =
432 0.0113.
433

Pri1	GTAATACGACTCACTATAAGGGTTAACTTTAAGAAGGAGATATACAT ATGCAGATTTGTG
Pri2	TTAGTGGTGGTGGTGGTGGT
Ultra1	GGTGGATAAAAATCTCTGCTTGAGGCCAATGCTTNSCCGACTCTG DNSAACTATVNSCGAAAACTCGATAGGATTACCAGGCCAATAA AAATTTCAAGTCGGACCTGTTACCGGAAAGAGTCTGACGGCAA AGAGCACCTGGAAGAATTACTATGGTGRVCTTCDSCCAGDBSGGT TCGGGATGTACTCGGG
Pri3	CGGAAGATCTGTTTGAAGTTC
Pri4	AAAATCTGAAGCTCTCATCAAAG
Pri5	GATACTGAACCTTCAAAACAGATCTCCGGGTGGATAAAAATCTCT GCTTG
Pri6	CCAGAAACTCTTGATGAGAGCTTCAAGATTCCCAGTACATCC CG
MAGE-Neg control	T*C*ATGTTGCTTCATGTGATCTGGATAGCGGGAAAAACATTGTACA TACAGAGTAGTTACGAGAGTTGGCCATGGTACTGGGAGCTGCA
MAGE_murF_TAA	g*t*taaagccggaataatattgaccaaatgtcggccagccaaTtaacatgtcccattctcctgtaaagcgc gtactaccttcca*t*g
MAGE_pgpA_TAA	g*t*cgtaggattaaataagagttccaggcctgatgagacgtgacaagcgtcacatcaggcatcggtgcacaat tacgacagaataccca*g*c
MAGE_sucB_TAA	g*a*taatgccttacgtcactacgtcaggtaaaactattacacgtccagcagcagacgcgtcgat cttcagcaacttt*t*g
MAGE_lolA_TAA	a*a*agtattatccaaaaatcgagcgacagattgctactcaggtgccttactacgttgatcatctaccgtgac gccttgcggcggg*g*t
MAGE_lpxK_TAA	a*g*cgacattcatgactccatcaatcgaaacgcgtccgcggcgtaaattgtccagaagccagaaggtagt tgcgtaaagcagttcg*c*t
MAGE_fabH_TAA	c*c*aggaaacacaaatgcgtcatgtttaatccttatcttagaaacgaaccagcgcggagccccag gtgaatccaccccaa*a*g
MAGE_hemA_TAA	c*a*taggcgtaaatgcacccgtaaaaaaaaagaaaatgtactgttactccagccgaggctgcgcaga atattcaggcgttcgt*t*a
MAGE_fliN_TAA	g*a*tatcattactccgtcgagcgaatgcgcgcctgagccgttaatgtatgtatgcataaccacgtactgtcaatct tccgcgcgggttc*t*g
MAGE_hda_TAA	a*g*ttcggataaggcgttcgcgcgcatccgacaataaacaccttattacaacttcagaattttcacaaacg aatgttcgttt*a*c
MAGE_mreC_TAA	a*g*caacagcgtaatgaggaaagagagccagattaccagcgtccctggctacgtatgcgtccattattgc cctccggcgcacgcgc*a*g
MAGE_coaD_TAA	a*t*caggcgtatgcaccatttcgtccggagaatgtccatcaggcgtatggcgaagttagcgttaacgttt atgcggatggatg*t*c
MAGE_atpE_TAA	t*a*ggttaacgttctgatattgtctttaaataaaagcaacgcgttattacgcgcacagcgaacatcacgtacagaccc agacctaagcgcg*a*t*c
MAGE_yaff_TAA	t*t*taggttgggtgagtgggggttgttaaggacggggagagtcgggtattattacgaaagccgcgtcc cgcaaggactgacgc*c*a

437 **SI Table 2.** Sequences of new constructs. Promoter sequences – blue highlight; RBS sequences –
438 purple highlight; relevant ORFs – red; stop codons underlined; terminator sequences – green
439 highlight. In-frame amber stop codons are highlighted in black

Name	Sequence
T7- (UAG) ₂ - sfGFP	GTAATACGACTCACTATAAGGGTTAACTTTAAGAAGGGAGATATACATATGCAGATTGGTGAAGACCTTACAGGTAAAGACGATT ACCCGGAGGTGGAGTCCTCGGACACCACATCGATAATGTAATCAAAATCCAAGATAAGGAAGGAATCCCTCAGACCGAGCAA CGTCTGATTTCGCAGGTAAACAACCTGGAGGATGGTCGACGCCCTTCGGACTACAACATCCAGAAAGAATCACCTTCATTGG TTCTCGCTCTCGTGGAGGAATAGTTGTTGTGCAGGAGCTTGATCCAAGGGCGAGGGAGCTTTACTGGCGTAGTACCAATTCT CGTAGAGCTCGATGGCGATGTAATGCCATAAGTTTCCGTACGCCAGGGCGAGGGCGATGCAACTAACGGCAAGCTCAC TCTCAAGTTATTTGACTACTGGCAAGCTCCCAGTACCATGCCAATCTCGTAACTACTCTGACCTATGCCGACAAATGTTTT CCCCGTATCCAGATCACATGAAGCAACATGATTTTTAAGTCCGCAATGCCAGAGGGCTATGACAAAGGCCACTATTAGCT TAAGGATGATGCCACCTATAAGACTCGCGCAGAGGTTAAAGTTGAGGGCATACTCTGTAATTCGATTGAGCTCAAGGGATT GATTGTAAGGAGGATGGCAATATTCTCGGCCATAAGTGGAGTATAATTCCATAATGTAATAGATTACCGCAGATAAGC AAAAGAATGGCATTAAGGCAATTAAAGATTGCGATAATGTTAGGAGGATGGCTCCGACACTCGCAGATCATTATCAACAAA ATACTCAATTGGCGATGCCCACTACTCTCCAGATAATCATTATCTCCACTCAATCGTGTCTCCAAAGATCCAATGAG AAGCGGATCACATGGTACTCCTGGAGTTGTAACTGCAGCAGGCTTACTCATGGCATGGTGAAGCTCTATAAGCTGAGCACC ACCAACCACCACTAA
pTD114_sf GFP- 1ATG	GTAAAACGACGGCCAGTGAGCGCGCTAATACGACTCACTATAAGGGCGAATTGGAGCTACGTGCAGATCTGCACATAGGCCACA CCCTGAATGAGATGTTCTCCGTACGTTCTGGCTAGCCCGAAAGAGGAGAAATTAACTATGGCATCAAGGGCGAGGA GCTCTTACTCGCTAGTACCAATTCTCGTAGAGCTCGATGGCGATGTAATGCCATAAGTTTCCGTACGCCAGGGCGAG GGCGATGCAACTAACCGCAAGCTCACCTCAAGTTATTTGTAACTACTGGCAAGCTCCAGTACCATGGGCAACTCTGTAACTA CTCTGACCTATGGCGTACATGTTCCCGTATCCAGATCACATGAAGCAACATGATTTTTAAGTCCGCAATGCCAGAGGGC TATGTACAAGAGCGCACTATTAGCTTAAGGATGATGGCACCTATAAGACTCGCGCAGAGGTTAAAGTTGAGGGCATACTCTG TAAATCGCATTGAGCTCAAGGGATTGATTTAAGGAGGATGGCAATATTCTCGGCCATAAGCTGGAGTATAATTCAATTCCA TAATGTAATAGATTACCGCAGATAAGCAAAAGAATGGCATTAAGGCAATTAAAGATTGCGCATAATGTTAGGAGGATGGCTCCGT ACAACTCGCACTATTCAACAAATACTCCAATTGGCGATGGCCAGTACTCTCCAGATAATCATTATCTCCACTCAAT CCGTGCTCCAAAGATCCAATGAGAAGCGCGATCACATGGTACTCTGGAGTTGTAACTGCAGCAGGCACTACTATGGCAT GGATGAGCTATAAGCTCGAGCACCAACCAACCACTAAAGTCTAGAGGATGCCCTTGGCCACCTCACTAAAAGCTGGTGA ACTGCTCAGGGCGCATCCGACTCTGTTAGAAGTAGTGTGCAACTCCGTCATCCCGTACCGTGGCGTACAGTAAAGTGGAGG CGTCAAATGACTGTACAACGTGTTAGGGCAATCGCAATTGACACTAGCAGACCTCCCGATCGAGTTCGAAACTTGAACTCTG ACTCTCAGATGAGTTCCCGGATGGCGAGCGCGTAAGATGGGCTTGTGCGGACGTCGAAGCGCTTATGGCTTCCGTAG CTTGACCGGGACGCTGTTGACTTGACCCCTTCGACGTCGGCGATCTCCTCATCGTCTGCCAGCGCAATCCATCTCAGATAGG TGGCCTCCTCGGATCGAGCCATCGCGCATCTCCCGGTTAGGGTGGTGAAGGAATGAGATGCGGGCATGGATCTGCCGAT GGTGCAGCGCTGCGACTGCATCGATCTCCGATCGAGATCGTACCCGTTGTCGATGCCATCGTAACATCGACATAAAG CCGTTGGCGTCTGATGGTATTGTGATGCCAGCGGATGCCGAATCGGATGCGTGGTCATAAGAAGGCACGCTGCTCTCG ACAGCGTCGGCGCTGTCGCCGACCCGACCAGGTGAAGATGTGCTTCCGGACCTCCGGCGTTGACGCCGATCGAGCGCTTC GAACCTCTGTCGAAGTAGGGTATTGCGCATGTCGCGCAGCCGGTCTCAGGATGCACTCATGCCCTGATCGCGCAAGAT CAGTCAGTTGTCAGCCAGTGTGCACTCCATACCTCTATCGGTTGTCAGTAGCCTTCTGCTAGTCTCTGCAAGGAATTG ATATCAAGCTTATCGATACCGTCACCTCGAGGGGGGGCCCGTACCCAGCTTTGTCCTTACTGAGGGTTAATTGCGCCT GGCGTAATCATGGTCAAGCTGTTCTGTTGAAATTGTTATCCGTCACAATTCCACACAAACATACGAGCCGAAGCATAAAG TGTAAGGCTGGGTGCTTAATGAGTGAAGCTAACATTATGCGTTGCGTCACTGCCGCTTCCAGTCGGGAAACCTGT CGTCCAGCTGCTTAATGAGTGAACGGCAACCGCGGGAGAGGGCGTTGCGTATTGGCGCATGCAATAAAACACTGTTGAAATT ATTAAGCATTCTGCCGACATGGAAAGCCATCACAAACGGCATGTAACCTGAACTCGCAGGGCATCAGGACACTTGTGCTT GTATAATATTGCCCCATGGAGCGCACCCGTGGAAACGGATGAAGGCACGAAACCCAGTTGACATAAGCTGTTGCGTAA GTAATGCAAGTAGCGTATGCGCTACCGCAACTGGTCAAGGACCGGAGCGGGTGGTAACGGCGCAGTGGCGTT CATGGCTTGTATGACTGTTTTGTAAGTCTATGCCCGGGCATCCAAGCAGCAAGCGCGTTACGCCGTGGTGCATGTTG TGTATGGAGCAGCAACGATGTTACGAGCAGCAACGATGTTACGAGCAGGGCGATGCCCTAAACAAAGTTAGGTGGCTCA AGTATGGCAGTACCGTCACATGAGGCTCGGCCCTGACCAAGTCACCATGCGGCTGCTTGTGATCTTCGGTGTGAGTT CGGAGACGTAGCCACCTACTCCACATCGCCGACTCGGATTACCTCGGGACTTGTGCTCGTAGTAAGACATTGATCGCGCTT GCTGCCCTCGGACCAAGAAGCGGGTTGCGCTCGCGCTACGTTCTGCCAAGTTGAGCAGCCGCTAGTGAAGATCTA TCTATGATCTCGCAGTCTCCGGAGAGCACCGGAGGCGAGGGCATGGCCACCCGCTACATCTCTCAAGCTGAGGCCAACGC GCTTGGCTTATGTCATCGTCAAGCAGATTACGGTACGATCCCGCAGTGGCTCTATACAAAGTGGCATACGGGAA GAAGTGTGCACTTGTATGACCCAAAGTACCGCCACCTAACAACTGTTCAAGGCCAGTCGGGCTTGTGAGTGGCGTGG TCGGTAAATTGTCACAACCCGCAAGTGGCACTTTGGGGAAATGTGCGGCCGCTTCTGCTGGCGCTGGCGCTGTTCTG GCGCTGGACTTCCGCTTCCGTCAGCAGCTTCTGCCACGCCCTGATGATGCCGGCGCTTGGCTGATGCCCTTCTGCGCAT ACGGCCCCAGGGCGTCCAGAACGGGCTCAGGCCTCCGAAGGTCTGGGCCGCTTGGCTGATGCCCTTCTGCGCAT CTCACGCGCTCTCGCGGCCCTGAGGGCAGGCTICATACCCCTGCCAACCGCTTGTGAGTGGCGCTGGCCACGGCTCCGGC GTCTCAACGCGCTTGTGAGATTCCCGACTTCTGCCAATCCCTCGCGTACAGGCCGCTGACGCCGCTGGCTGACGCCGCTT GACCGTGGCCACTGGTGGCGCTCCAGGGCTCGTAGAACGCGCTGAGTGGCGCTGACGCCGCTGGCTGATGCCCGT TGCAGCCCTAGATGCCACAGCGGCCAACAGCTGGTGTGCGGGCTCATCGCCTGTTGCGCTGGCGATGACGCCG ACAGCCTGCCGCTCGCGTACGCCAACAGCGGGTACATGTCGGGCTGGTTCGTCACGGTGGATGCTGCGCTACGAT GCGATCCGCCCCGACTTGTGCCAGCCACTITGTCGCTTCTCGAAGAACGCCGCTGCTGTTGCGCTGGCGACTTCCACC

	ATTCGGGCTGGCGTCATGACGTACTGACCGCAACACAGCGCTTGC CGCCGCTTCTGGCAGCAACTCGCGCAGTCGG CATCGCTTCATCGGTGCTGCTGGCGCCAGTGCCTCTCTGGCGCTCGTGGCGTCAAGCGTTGGCGCTCGCGCTCGCG AGGC GTGCTTGAGACTGGCCACGTTGCCATTTCGCCAGCTTGCATGATCGCTATGCCCATGCCCTGCC CCCTTTGGTGTCCAACCGGCTCGACGGGGCAGCGCAAGGCCTGCCTCCGGCGGGCCACTCAATGCTGAGTAACTCACTAG ACTTTGCTCGCAAAGTCGTGACCGCTACGGCGCTCGGGCCCTACGGCTCTCCGGCTCGCTCGCCCTCGCGCTCG CGCTCCCTGCCAGCCGTGGATATGTGGACGATGCCCGAGCGGCCACCGCTGGCTCGCTCGCCCTCGGCC TGCTGGACAAGCTGATGGACAGGCTGCCAGCAGCTGACCACAGGGATTGCCACCGCTACCCAGCCTCGACCACA TACCCACCGGCTCCAAC TGCGGCCCTGGGCCCTGCCCATCAATT TTAATT TCTGGGAAAGCCTCCGGCTCGGC CTGCGCGCTCGCCGGTTGAGACCCAAGTGGAAAGGCGGTCAAGGCTCGCGCAGCACCGCAGCGCTGGCCTTGAC GCCCTGGAACGCCAACGCCATGCGAGTGGGGCACTGAAGGGCAAGGCCCGCTGCCGCCCCGAGCCTCACGCC GAGTGGGGGGGTTCAAGGGGGAGCCGCGCACCTGGCAAGGCCAGGGCGACTGCCAAGAGCTCATTGCCGACCCCCCGCAATAG AGGGCGAAATGCGAAAGACTTAAAATCAACA ACTTAAAAGGGGGTACGCAACAGCTCATTGCCGACCCCCCGCAATAG CTCATTGCGTAGGTTAAAGAAAATCTGTAATTGACTGCCACTTACGCAACGCATAATTGTTGCGCCTGCCAAAAGTTGCA GCTGATTGCGATGGTGGCGCAACCGTGGCACCCTACCGCATGGAGATAAGCATGGCACCGCAGTCAGAGAAAATCGGCAT TCAAGCAAGAACAAAGCCGTCACTGGGTGCAAACCGAACGCAAGCGCATGAGGCCTGGCGGGCTTATGAGGAAAC CCACGGCGCAATGCTGCACTCACCTCGTGGCGCAGATGGGCCACCAAGACCCACGCCGCAATGCTGCGCATCACCTCGTGG CGCAGATGGGCCACCAAGACCCGCTGGTGTGCGCAGCCAGAACACTTCAAGCTCATGCCAGCTTGTGGCGACGGTCAATA CGCAGTCAAGGACTGGTGGCGAGCGCTGGATCTCCGCTGAAGCTCAACGGCCCGGCCACCGTGTGGCCTACGTGGTCAAT GACCGCGTGGCGGGCCAGCCCGCAGGAGCAGTGGCCTGTGGTGTAGTGGCGCCTGGTGTGATCACCGACGACAG ACGAATCGCTGGGGCATGGCACCTGGCAGCCGATCCGGCATGGAAACCAGACCTGCCAGCCTGACCGAACCGAGGAATGG AGGAGCCGCCAGCCAGCCGGCATTCCGGCATGGAAACCAGACCTGCCAGCCTGACCGAACCGAGGAATGGAACGGCG GGGCAGCAGCCTGCCATGCCGATGCCGATGGCGTGGCGTGGTCTGGACGATGGCGAGCCGTTGGAGGCCACCGGTCACGCTG CCGCGCCGGTAGCACTGGGTGCGCAGCAACCCGTAAAGTGCCTGTCAGTCCAGACTATGCCGTAGGCCCTGGTGTGATCAC CTTGTGCGCTCCCGCGTGGCTGCGGTCATGGAGCCGGCACCTGACCTGAATGGAAGCGGGCACCTCGTAAACGG ATTCAACCGCTGGGTTATCAGGCTCTGGAGGAGAAGATGATCATCTGCAATTACCTCCACGGGGAGGCGCTGAC TGGCCTCAGGCATTGAGAACACGGTCAACTGCTCCGGTAGTCATAAACCGGTAACACGCAATAGACATAAGCGGCT ATTAAACGACCCCTGCCCTGAACCGACGACGGGTCGAATTGCTTGAATTCTGCATTATCCGCTATTATCACTATT GCGTAGCAACCAGCGTTAAAGGGACCAATACTGCCATTAAAAAAATTACGCCCGCCCTGCCACTCATCGCAGTCAGGCC TGGTTAAAATGAGCTGATTTAACAAAATTAAACGCAATTAAACAAAATTAAACGCTTACAATTCCATTGCCATTCA GCTGCGCAACTGTTGGAGGGCGATCGGTGCGGGCTTCGCTATTACGCCAGCTGGCAGGAGGGATGTGCTGCAAGGC ATTAAGTGGTAACGCCAGGGTTTCCAGTCACGACGTT
pYW15c MjBpaRS	CATGGCTCGAGAAA TCAAAAAAAATTATTGCTTGTGAGCGGATAACAAATTATAATA GATTCAATTGAGCGGATAACAAATT TCACACAGAATTCA AAAGAGGAGAAA TTAACT ATGGATGAATTGAGATGATCAAGCTAATACATCTGAAATCATCAGTGA AGAGGAATTACGTGAGGTGTTGAAAAAAGATGAGGAAGATCCGCTGGCATGGATTGAGCCTCCGGTAAGATT CATCTGGCAC TATCTCAGGATAAAAAGATGATCGACTTACAAATGCCGGGTTGCGACATCATCATCTGTTGGCGACTTACATGCTATTAAA TCAGAAGGGAGAACCTGACGAAATTGCAAGATTGGGATTACAACAAGAAGGTATTGAGGCGATGGGACTGAAGCGAAGTA TCTTATGGCTCACCTTTCAGTTGATAAGGACTACACTTAAATGTATATGCCATTAAAGACTACCCCTGAAGCGTGGC GCCGCTCGATGGAGCTTACGCCGTGAGGACGAAAACCCAAAAGTAGCGAAGTGTATCTAACATGCAAGTGAATACCT CACATTATCTGGTGTGACGTCGCCGTGGCGGAATGGAGCAGCGTAAACCCACATGTTAGCTGAGTTACTCCAAAAAA GGTGGCTGTATCCACAATCTCTTCAAGGGCTGGACGGTAAGGCAAATAGGTTATCCAAAGGCAACTTATCGCAGTG GATGATGCTGAGAGATTGCCGCAAGGATTAAAAGGCCATTGTCCCAGGGAGTTGCGAGGGAAATCCTTATGGAAA TCGCAAAACTCTCTGGAATATCTTTAACCATAAAAGCTCCAGAGAACAGTTGGAGGAGACCTGACGGTAAATTCTGAC GCTTGAATCCCTGTTAAAGAACAAAGAACCTGACCCGATGGACTTGAAAAACCCGTTAGCCGAAGAGCTTATCAA AAATTAGCTGAGGCTTAA AA CTGCGAGTTCAACCGCTAAATTGCTGAGAATT CA AAAAAGCCGACCC CTGACAG CGGGCTT TTTTTCGACCTTAACATGAGAGGATTGACGGCTAACTAAGCCGCTGCTGACTTCTCGCCGATCAAAGGATTTGCTAT TAAGGGATTGACGAGGGCGTATCTGCGCAGTAAGATGCGCCCGATT CCGGCGGTAGTT CAGCAGGGCAGACGGCAGCT AAATCCGATGGCAGGGGTTCAAAATCCCTCCGCCGACCA AATTGAAAAGCTGCTCAACGAGCAGGTTTTGCA CATGCGAGCTGGTACCCCGGTCGACCTGCAAGCAAGCTTAAATTAGCTGACCATGGTGCAGCAATTCTGAAAGACCAAAGGGCT CGTGATACGCCATTATTGTTATTAGGTTAATGTCATGATAAAATGGTTCTTAGACGCTCAGGTGGCAGCTTCTGGGAAATGTCGCG GAACCCCTATTGTTATTCTAAATACATGTCAGGCTCATGAGACAATAACCCCTGATAAAATGCTTCAATAAT TGAAAAGGAAGAGTATGAGTATTCAACATTCCGTCGCCCTTATTCCCTTTGCGGCATTGCTCTGTTGCTCAC CCAGAACGCTGGTAAAGTAAAAGATGCTGAAGATCAGTGGGTACGAGTGGACTTAAAGTTCTGCTATGTCGCGGGTATTATCCG TGTTGACGCCGGCAAGAGCAACTCGGTGCCGATACACTATTCTCAGAATGACTTGGTTGAGTACTCAGTCAGAAAAG CATTTACGGATGCCATGACAGTAAGAGAATTGCACTGCTGCCATAACCATGAGTGTAAACACTGCGGCCAACTTACTCTGA CAACGATGCCAGGGACCAAGGAGCTAACCGCTTTGCAACACATGGGGATCATGTAACCTGCTGTCGTTGGGAAACCGG AGCTGAATGAAGCCATACCAACAGCGAGCGTGCAGCACCCAGCTGGCAGCAATGCGCAACACGGTGGCAGGAAACTTAAACTG GCGAACTACTACTAGCTCCGGCAACAAATTAAATAGACTGGATGGAGGCCGATAAAGTTGCGAGGACCAACTCTCGCCTCG CCTTCCGGCTGGTTATTGCTGATAAAATCTGGAGCCGGTGGAGCGTGGCTCGCGGTATATTGCGACTGCGACTGGGGCAGAT GGTAAGCCCTCCCGTATCGTAGTTACACGACGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATGCTGAGATA GGTGCCTCACTGATTAAGCATGGTAACTGTCAGACCAAGTTACTCATATAACTTTAGATTGATTAAAACCTCATTTAATT AAAAGGATCTAGGTAAGATCCTTTGATAATCTCATGACCAAATCCCTAACGCTGAGTTTCTGCTTCACTGAGCGTCAGACCC CGTAGAAAAGATCAAAGGATCTTCTGAGATCCTTCTGGAGACCTAACCTGAAAGGTAACTGGCTTCAGCAGAGCGCAG GCCGGTGGTTTTGCCAGACAGAGGCCAGCTGGAGCGAAGGCCACTACCGAAGCTGAGATAACCTACAGCGTGGCTGAG TCCCTCTAGTGTAGCCGTTAGTACGGGCCACTCTGAAAGGTAACGACTTCTGCTGAGTACCTGCTGCTGCTGCTG GTGGCTGCTGCCAGTGGCAGTAAGTCGTGCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCG GAACGGGGGGTTCCGTGACACAGCCAGCTGGAGCGAAGGCCACTACCGAAGCTGAGATAACCTACAGCGTGGCTGAG GCGCCACGCTCCCGAAGGGAGAAAGGCCAGAGTATCCGGAAGCGCAGGGTGGAAACAGGAGAGCGCAGGAGGGAGCTT CCAGGGGAAACGCCGGTATCTTATAGTCCTGCGGGTTGCCACCTCTGACTTGAAGGCGTCAAGGCTGAGCTGATTT GTGATGCTCGTCAAG

	TGGCGAACGCAAGCCAAGCCGAGAAGAAAAGCGCACCGGGCCGCGACGCCACCAGAGAAATGAGGAACACCAGATGTCGTTTCAG AAGACGGCTGCACTGAACGTAGAACGCCACTGCACTATAGCAGCGGAGGGITGGATCCATCAGGCACAGCAGGGCTGCTGCC GGCCATCAGCGGACGCAGGGAGACTTCCGCAACCGGCCGTTCGATGCGGACCGATGGCCTTCGCGCAGGGGTAGTGAATCC GCCAGGATTGACTTGCCTGCCCTACCTCTCACTAGTGAGGGCGCAGCGCATCAAGCGGTAGCGCACTCCGCCACCGCAA CTTCACTGCACATCGTGTAAATCATCGTGTAGAGACCGTGGGAATGGCCGAGCGAGATCTGACCGGTTCAATGCGTGTGTTCTACCGCACGTTG GCGGAGCAAGGCCGTCGCAACGAGTGGCGAGGGTGTGGTGTGGCGGGTTCTGATGCCCTGTTCTACCGCACGTTG AAGGCAGCTGAAAGGTCTGGTCATACATGTATGGCGACGCACCGACACCGCTCCGTGGATCGGTCAATGCGTGTGCTGCC AAAACCCAGAACACCAGGCCAGGAATGCCCGCGCAGGATACTTCCGCTCAAGGGCGTGGGAAGCGCAACGCCGCTGCC TCGGCCTGGTCTTCAGCCACCATGCCCGTGCACGCACAAAGCTCATCGCGTGTGAAGCGATTCACAGATGTCGCTG TTCATCCGCGTCCAGCTGTTGAGTTCTCCAGAAGCGTTAATGTCGTTCTGATAAAGCGGGCATGTTAAGGGCGTT CCTGTTGGTCACTGTGCTCCGTGAAAGGGGATTCTGTCATGGGGTAATGATACCGATGAAACAGAGAGAGGATGCTCAC GATACTGGTTACTGTGATGAAACATGCCCGTTACTGGAACGTTGAGGGTAAACAACCTGGCGGTATGGATGCGCGGGACCA GAGAAAAATCACTCAGGGTCAATGCCAGCGCTTCGTTAATACAGATGAGGTGTTCCACAGGGTAGCCAGCAGCATCCTGCC GCAGATCCGAAACATAATGGTCAGGGCCTGACTCCCGTTCCAGACTTACGAAACACCGAAACCGAAGACCATTGTT GTTGCTCAGGTCGAGACGTTGAGCAGCAGTCGCTTCAGGTCGCTCGCGTATCGGTGATTCTGTAACCAGTAAGG ACCCCAGCCTAGCCGGTCTCAACGACAGGAGCAGCATGCGCACCGTGGCCAGGACCAACGCTGCCAGATGCG CCCGTGCCTGCTGGAGATGGCGACGCAGTGATGGATATGTCGCAAGGGTTGGTTCGCGATTACAGTCTCGCCAGCGCAGGC AGTCAGTGCAGGAGAAGCGGAAGGCGAGAGTAGGGAACTGCCAGCTTAAAGCTGCGGCTCCCTGGCGTTCTGATAACGAGTAA TCGTTAATCCGAAATAACGTTAAACCGGTTCCGGGGTTTTTATGGGGGAGTTAGGGAAAGGACATTGCTGAGAATAT TTAAGGGCGCTGTCACTTGCCTGATATGAGAATTATTAACCTTATAATGAGAATTTAGGAAAGGACACTTAAATAAGATA CGTTGCTTTTCGATTGATGAAACACCTATAATTAACACTATTCTATTATTTATGATTTGTTATATAACATATTCTAGTTGTT AAAGAGAATTAAGAAAATAATCTGAAAATAATAAAGGAAATCAGTTATGACAACCTGACGGCTACATCATTCACTTCT TCACAACCGGACCGAACTCGCTCGGCTGGCCCGGTGCAATTAAATACCGCGAGAAATAGAGTTGATCGTCAAAACCAA CATTGCGACCGACGGTGGCGATAGGCATCCGGTGGTCTCAAAGCAGCTTCGCTGGCTGATACTGGTCTCGCGCCAGCT TAAGACGCTAATCCCTACTGCTGGCGAAAAGATGTCAGACAGCGCAGGGCACAAGCAAACATGCTGCGACGCTGGCGAT ATCAAATTGCTGCTGCGAGTGCAGTACTGACTGACAGCTCCGCTGATACCGATTATCCATCGTGGATGGAGCAGACTCG TTAATCGCTTCCATGCGCCGAGTAAACATTGCTCAAGCAGATTATCGCCAGCAGCTCCGAAATGCCCTTCCCCCTGCGC GTTAATGATTGCCCCAACAGGCTGCTAAATGCGCTGGTCTCATCGCCAGGAAAGAACCCCGTATTGCAAAATATTGAC GGCCAGTTAGCCATTGCCCCAGTGGCGCGAGAAAGTAAACCCACTGGTGTACCCATTGCGAGCCTCCGATTTTACCC CCGTAGTGTGATGAAACTCTCTCTGGCGGGAAACAGCAAATATCACCCGCTGGCAAACAAATCTCGTCCCTGATTTTACCC CCTGACCGGAATGGTGGAGATTGAGAATATAACCTTCACTCCAGCGGTGCGTCAAAAAAAATCGAGATAACCGTTGGCCTC AATCGGCGTTAAACCGCCACCGAGTGGCATTAAACGAGTATCCGGCAGCAGGGGATCATTGCGCTCAGCCATACTTTC ATACTCCGCCATTAGAGAAAGAACCAATTGCTCATTCGATCAGCATGCCGCTACTGCTGCTTACTGGCTCTCTCGCT AACCAAACCGTAACCCGCTTAAATAAAAGCATTCTGTAACAAACAGGGACCAAAGCCATGACAAAACCGCTAACAAAGGT CTATAATCACGGCAAAAGTCCACATTGCTGATGACTGACTGACAGCTCCGCTACACTTGTCTATGCCATGACATTAAATCCATAAGATTAG CGGATCCTACCTGACGCTTATCGCAACTCTCTACTGTTCTCCATACCGGTTTAAGGGAGTAAAAAAATGCAAGGTT AGACTTTAACAGGTAAAGCAGTACCTGGAGGTGGAGTCCCGACACCATCGATAATGAAAATCAAAATCAAGATAAGG AAGGAATCCCTCCAGACCAGCAACGCTGATTTCGCAGGTAACAAACTGGAGGTGGTGCACGCTTCCGACTACAACATCCA GAAAGAATCTACCCCTCATTTGGTCTGCGCTGCGTGGAGGA[TAG]TTGTTGTCAGGAGCTGCTGATCCAAGGGCGAGGAGCTC TTTACTGGCGTAGTACCAATTCTGCTAGAGCTCGATGGCAGTGTAAATGCCATAAGTTCCGACGCCACTCTCGTAACACTCTG ATGCAACTAACGGCAAGCTCACTCTCAAGTTTATTGACTACTGCAAGCTCCAGTACCGGCCACTCTCGTAACACTCTG ACCTATGGCGTACAATGTTTCCCGTATCCAGATCATGAGAACCAATGTTTAAAGTCCGCAATGCCAGAGGGGATATG ACAAGAGCGCACTATTGCTTAAAGGATGATGGCACCTATAAGACTCGCGAGGGTAAAGTTGAGGGCAGACTCTCGTAAT CGCATTGAGCTCAAGGGCATTGATTAAAGGAGGATGGCAATAATTCTGCCATAAGCTGGAGTATAATTCAATTCCATAATG TA[TAG]ATTACCGCAGATAAGCAAAGAATGGCATTAAAGGCGAATTAAAGTCCGCAATGTCGAGGATGGCTCCGTAACAC TCGCAGATCATTATAACAAAATCTCAATTGGCGATGGCCAGACTCTCCAGATAATCATTATCTCCACTCAATCCGTG CTCTCCAAAGATCCAAATGAGAAGCGCGATCACATGGTACTCTGGAGTTGTAACTGCAAGCAGGCCATTACTCATGGCATGGATG AGCTCTATAAGCTCGAGCACCACCAACCACTAACCCAAAGGGCGACACCCCTAATTAGCCCGCGA[AAGGCCAGTC TTTCGACTGAGCCCTTCGTTTATGATGCCAGITCCCTACTCTCGCATGGGAGTCCCAACACTACCATCGCGCTACGG CGTTTACCTCTGAGTTCCGGCATGGGTCAGGTGGGACCCAGCGCTACTGCCGAGGCA[AAACAAGGGGTTGTTAGGCCATAT TCAGGTATAATGGGCTCGCATAATGTCAGAATTGTTGAGGTTAAACACTGACCCCTATTGTTTATTTCTAAATACA TTCAAAATGTTATCCGCTCATGAGACAATAACCCCTGATAAAATGCTTCAATAATATTGAAAAGGAAAGAATATGAGGCCATATTCAA CGGGAAACGTCGAGGCCGCGATTAAATTCCAACATGGATGCTGTTATATGGGTATAAATGGGCTCCGATAATGTCGGGCAAT CAGGTGGCAGAACATCTATCGCTTGTATGGGAAGGCCGATGCGCCAGAGTTGTTCTGAAACATGGCAAGGTTAGCCTGCGCAATGA TGTTCAGAGATGGTCAGACTAAACTGGCTGACGGAATTATGCCACTTCGACCATCAAGCATTATCCGTACTCCGT
pBAD-Ub- UAG- sfGFP_151 UAG	GGGGTTCTGTCACACAGCCAGCTGGAGCGAACGACCTACACCGAACCTGAGATACCTACAGCGTGTAGCTATGAGAAAGGCC ACGCTTCCCGAAGGGAGAAAGCGGACAGGTATCCGTAAGCGGAGGGTCCGAAACAGGAGAGCGCACAGGAGGGAGCTCCAGG GGGAAACGCTGGTATCTTATAGCTCTGCGGGTTGCGCACCTCTGACTTGAAGCGTGTGATTTTGTGATGTCGTCGTCAGGGGG GGAGCTATGGAAAAACGCCAGCAACGCCGCTTTTACGGTTCTGCCCTTTGCTGCCCTTTGCTCACATGTTCTTCTGCC TTATCCCTGATTCTGTTGATAACCGTATTACGCCCTTGTAGTGAGCTGAGCTGATACCGCTGCCAGCCGAACGACCGAGCGCAGCG AGTCAGTGCAGGAGAAGCGGAAGGCGAGAGTAGGGAACTGCCAGCTTAAAGCTGCGGCCCCCTGGCGGTTCTGATAACGAGTAA TCGTTAATCCGAAATAACGTTAAACCGGTTCCGGGGTTTTTATGGGGGAGTTAGGGAAAGGACATTGCTGAGAATAT TTAAGGGCGCTGTCACTTGCCTGATATGAGAATTATTAACCTTATAATGAGAATTTAGGAAAGGACACTTAAATAAGATA CGTTGCTTTTCGATTGATGAAACACCTATAATTAACACTATTCTATTATTTATGATTTGTTATATAACATATTCTAGTTGTT AAAGAGAATTAAGAAAATAATCTGAAAATAATAAAGGAAATCAGTTATGACAACCTGACGGCTACATCATTCACTTCT TCACAACCGGACCGAACTCGCTCGGCTGGCCCGGTGCAATTAAATACCGCGAGAAATAGAGTTGATCGTCAAAACCAA CATTGCGACCGACGGTGGCGATAGGCATCCGGTGGTCTCAAAGCAGCTTCGCTGGCTGATACTGGTCTCTCGCCAGCT TAAGACGCTAATCCCTACTGCTGGCGAAAAGATGTCAGACAGCGCAGGGCACAAGCAAACATGCTGCGACGCTGGCGAT ATCAAATTGCTGCTGCGAGTGCAGTACTGACTGACTGACAGCTCCGCTGATACCGATTATCCATCGTGGATGGAGCAGACTCG TTAATCGCTTCCATGCGCCGAGTAAACATTGCTCAAGCAGATTATCGCCAGCAGCTCCGAAATGCCCTTCCCCCTGCGC GTTAATGATTGCCCCAACAGGCTGCTAAATGCGCTGGTCTCATCGCCAGGAAAGAACCCCGTATTGCAAAATATTGAC GGCCAGTTAGCCATTGCCCCAGTGGCGCGAGAAAGTAAACCCACTGGTGTACCCATTGCGAGCCTCCGATTTTACCC CCGTAGTGTGATGAAACTCTCTCTGGCGGGAAACAGCAAATATCACCCGCTGGCAAACAAATCTCGTCCCTGATTTTACCC CCTGACCGGAATGGTGGAGATTGAGAATATAACCTTCACTCCAGCGGTGCGTCAAAAAAAATCGAGATAACCGTTGGCCTC AATCGGCGTTAAACCGCCACCGAGTGGCATTAAACGAGTATCCGGCAGCAGGGGATCATTGCGCTCAGCCATACTTTC ATACTCCGCCATTAGAGAAAGAACCAATTGCTCATTCGATCAGCATGCCGCTACTGCTGCTTACTGGCTCTCTCGCT AACCAAACCGTAACCCGCTTAAATAAAAGCATTCTGTAACAAACAGGGACCAAAGCCATGACAAAACCGCTAACAAAGGT CTATAATCACGGCAAAAGTCCACATTGCTGATGACTGACTGACAGCTCCGCTACACTTGTCTATGCCATGACATTAAATCCATAAGATTAG CGGATCCTACCTGACGCTTATCGCAACTCTCTACTGTTCTCCATACCGGTTTAAGGGAGTAAAAAAATGCAAGGTT AGACTTTAACAGGTAAAGCAGTACCTGGAGGTGGAGTCCCGACACCATCGATAATGAAAATCAAAATCAAGATAAGG AAGGAATCCCTCCAGACCAGCAACGCTGATTTCGCAGGTAACAAACTGGAGGTGGTGCACGCTTCCGACTACAACATCCA GAAAGAATCTACCCCTCATTTGGTCTGCGCTGCGTGGAGGA[TAG]TTGTTGTCAGGAGCTGCTGATCCAAGGGCGAGGAGCTC TTTACTGGCGTAGTACCAATTCTGCTAGAGCTCGATGGCAGTGTAAATGCCATAAGTTCCGACGCCACTCTCGTAACACTCTG ATGCAACTAACGGCAAGCTCACTCTCAAGTTTATTGACTACTGCAAGCTCCAGTACCGGCCACTCTCGTAACACTCTG ACCTATGGCGTACAATGTTTCCCGTATCCAGATCATGAGAACCAATGTTTAAAGTCCGCAATGCCAGAGGGGATATG ACAAGAGCGCACTATTGCTTAAAGGATGATGGCACCTATAAGACTCGCGAGGGTAAAGTTGAGGGCAGACTCTCGTAAT CGCATTGAGCTCAAGGGCATTGATTAAAGGAGGATGGCAATAATTCTGCCATAAGCTGGAGTATAATTCAATTCCATAATG TA[TAG]ATTACCGCAGATAAGCAAAGAATGGCATTAAAGGCGAATTAAAGTCCGCAATGTCGAGGATGGCTCCGTAACAC TCGCAGATCATTATAACAAAATCTCAATTGGCGATGGCCAGACTCTCCAGATAATCATTATCTCCACTCAATCCGTG CTCTCCAAAGATCCAAATGAGAAGCGCGATCACATGGTACTCTGGAGTTGTAACTGCAAGCAGGCCATTACTCATGGCATGGATG AGCTCTATAAGCTCGAGCACCACCAACCACTAACCCAAAGGGCGACACCCCTAATTAGCCCGCGA[AAGGCCAGTC TTTCGACTGAGCCCTTCGTTTATGATGCCAGITCCCTACTCTCGCATGGGAGTCCCAACACTACCATCGCGCTACGG CGTTTACCTCTGAGTTCCGGCATGGGTCAGGTGGGACCCAGCGCTACTGCCGAGGCA[AAACAAGGGGTTGTTAGGCCATAT TCAGGTATAATGGGCTCGCATAATGTCAGAATTGTTGAGGTTAAACACTGACCCCTATTGTTTATTTCTAAATACA TTCAAAATGTTATCCGCTCATGAGACAATAACCCCTGATAAAATGCTTCAATAATATTGAAAAGGAAAGAATATGAGGCCATATTCAA CGGGAAACGTCGAGGCCGCGATTAAATTCCAACATGGATGCTGTTATATGGGTATAAATGGGCTCCGATAATGTCGGGCAAT CAGGTGGCAGAACATCTATCGCTTGTATGGGAAGGCCGATGCGCCAGAGTTGTTCTGAAACATGGCAAGGTTAGCCTGCGCAATGA TGTTCAGAGATGGTCAGACTAAACTGGCTGACGGAATTATGCCACTTCGACCATCAAGCATTATCCGTACTCCGT

	ATGCATGGTTACTACCACCGATCCCCGAAAAAACAGCGTTCAGGTATTAGAAGAAATATCTGATTCAAGGTGAAAATATTGT TGATGCCTGGCAGTGTCTCGCCGGTGTGCACTCGATTCTGTGTTGATCGAGTGATTTGATGACGAGCGTAATGGCTGGCCTGTTGAACAAGTC CAGGGCAATCAGAATGAATAACGGTTGGTGTGATCGAGTGATTTGATGACGAGCGTAATGGCTGGCCTGTTGAACAAGTC TGGAAAGAAATGCAAAACTTTGCCATTCTCACCGGATTCACTCGTCACTCATGGTATTCTCACTTGATAACCTTATTGCA CGAGGGAAATTAATAGGTTGATTGATGTTGGACGAGTCGAACGACCGATAACAGGATCTGCCATCTGAACTGCGTCTCGGAGTTCTCGGAGTTCTCCATTACAGAAACGGCTTTCAAAAATATGGTATTGATAATCTGATATGAATAATTGCAATTICA TTTGATGCTGATGAGTTCTAAGCGGCGCCATCGAATGGCGCAAACCGTTCAGGTTACGTTACGATGTCGAGAGTATGCCGTTCTCTTACAGACGTTCC CGCGTGTGAACCAAGGCCACGTTCTCGGAAACCGCGGAAAAGTGGAAAGCGGCGATGCCGAGCTGAATTACATTCCC AACCGCGTGGCACAACAACTGGGGCAACAGTCGTTCTGCTGTTGCCACCTCCAGTCTGCCAGTCTGCCAGCAGCGCGTGC AAATTGTCGGCCGATTAAATCTCGCCGCAACTGGTGCAGCGTGTGTTGCTGATGTTGCACTTAACTATCGCTGATGACGAGGCCAT TGCTGTGAAAGCTGCTGCACTATGTTCCGGTTATTCTGATGTCGACCGAGACACCCATCAACAGTATTATTCTCCC ATGAGGACGGTACCGCACTGGCGTGGAGCATCTGGTCGATTGGTCACCGCAAATCCGCTGTTAGCGGGCCATTAAAGTTC TGTCTCGGCGCTCTCGTCTGGCTGGCATAAAATATCTCACTCGCAATCAAATTCAAGCGATAGCGGTGCTGGCTGCCAGC AC TGGAGTGCATGTCGGTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCACTCGATGCTGGTCCAACGATC AGATGGCGTGGCGCAATGCGGCCATTACCGAGTCGGGCTGCGCGTTGGTGCAGATACTCGGTAGTGGGATACGACGATA CCGAAGATAGCTCATGTTATATCCGCCGTTAACCCACATCAAACAGGATTTCGCGTCTGCCAGTCTACTGGTAAAAGAAAACACCCCTGGGCC CAATACGAAACCGCCTCTCCCGCGCTTGGCGATTCAATATGCGACAGGTTCCGACTGAAAGCAGGTTCCGACTGAGCGTCAAAAGCAGCTT CGCCTGGCTGATACTGGTCTCGCGCCAGCTAACAGCCTAACCTTAACTGCTGGCGAAAAGATGTGACAGACGCGACGGC GACAAGCAAACATGCTGTGCACGCTGGCGATATCAAATTGCTGCTGCCAGGTGATCGTGTACTGACAAGCCTCGCGTA CCCGATTATCCATCGTGGATGGAGCGACTCGTTAACGCTCCATGCGCCGCACTAACATTGCTCAAGCAGATTATCGCCAG CAGCTCGAATAGGCCCTTCCCTGCCCCCGCTTAATGATGCCCCAACACGGTCGCTGAAATTGCGCTGGTGCCTCATCC GGGCGAAAAGAACCCCGTATTGCAAATATTGACGGCCAGTTAACGGCATTATGCCAGTAGGCGCGCGACGAAAGTAACCCAC TGGTGTGACCATTCGCGAGCTCCGGATGACGACCGTGTGATGTAATCTCTGGCGGGAAACAGCAAATACCCGGTGGCGG AAACAAATTCTCGTCCCTGATTTCACCAACCCCGTACCGCGAACGGTGGAGATTGAGAATATAACCTTCACTCCAGCGGTGG TCGATAAAAAAAATCGAGATAACCGTGGCTAACGGCGCTAACGGCGAACAGTGGCATTAAACAGGATATCCGGCAGC AGGGGATCATTGCGCTCAGCCATACTTCTACACTCCGCCATTAGAGAAGAAGAACCAATTGCTCATATTGATCAGACATTG CCGTCACTGCGTCTTACTGGCTTCTCGCTAACAAACCGTAACCCCGCTTATTAAGAACGATTCTGACGCTTITATCGCAACTCTACTGTTCTCATACCCGTT TTAAGGAGTAAAATGTCGATCAGTCAAGAACCTACAATGGAGAAATCTCGCTCATTGACGATCATCTCGGAG GATGACGGCCGGCGAGCTGGCGCGGAAGCGCGCCCCCGCCCGGAAACCGAACCTGCAACGGTGTGCTGCGAC GAGGTTCTGGAATTGACGGATCCGATCGCGCCCGAGCCCGAGCTGCCGCTGGAGACTGTCGGCGACATGACCGTCTATTGCG CGCCGGAACCTGAGTCGGAACCCGCTAACAGCCGCCGCCGGCGCTCCGGTGTGATCGCGACGAAGTCGCCAGCAGCTGG TCGCGTCTCGGCCGCTTCGGCCGCCGGCGAGCGCCTCGCAGCTGAGCTGCCCTGCTGATGCCAAGGACGGTCGGACGCT GGAAGACGTCGACGCGAGCTGCTGCGCCCGTCTCAAGGAGTGGCTGGACAGAACCTGCCGCGCATCGTCAAGGAGT GGAGGAGAAGTGCAGCGTATCTCGGAGCCGGGGTGTGTTCTGGTACCGCATCAGCGAGGAGGAGCTTACT GCGTAGTACCAATTCTCGTACAGGCTGATGGGATGAAATGGCCAATAGTTCTCGTACGCGCGAGGGCGAGGGCGATGCA ACTAACGGCAAGCTCACTCTCAAGTTATTGTACTACTGGCAAGCTCCAGTACCATGGCCAATCTCGTAACTACTCTGACCTA TGGCGTCAATGTTCTCCGCTATCCAGATCACATGAAGCAACATGATTCTTAACTGCGCAAGAGGCTATGTAACAG AGCGCACTATTAGCTTAAAGGATGATGGCACCTATAAGACTCGCCAGAGGTAAGGTTGAGGGCGATACTCTGTAATCGCAT TGAGCTAAGGGCATTGATTAAAGGAGGATGGCAATATTCTCGCCATAAGCTGGAGTATAATTCAATTCCATAATGTATAC ATTACCGCAGATAAGCAAAGAATGGCATTAAGGCGAATTAAAGGCGATGCTCCAGTACTCTCCAGATAATGTTCTGACGCA GATCATTATCAACAAATCTCAATTGGCGATGGCCAGTACTCTCCAGATAATGTTCTCCACTCAATCCGTCGCTCTC CAAAGATCCAATGAGAAGCGCGACATGGTACTCTGGAGTTGTAACTCGAGCAGGCAATTACTCATGGCATGGTGAAGCTC TATAAGCTCGAGCACCAACACCAACTAACCCCAAGGGGACACCCCTAATTAGCCGGCGAAGGGCCAGTCTTCGACT GAGCCTTCTGTTATTGATGCTGGCAGTCCCTACTCTCGTACGGGAGTCCCACACTACCATGGCGTACCGCGTACGGCTGTTCA AAATGGGCTCGCGATAATGTCAGAATTGTTAATTGTTGTAACACTGACCCCTATTGTTATTCTAAATACATTCAAATA TGTATCCGCTCATGAGACAATAACCTGATAAAATGCTCAATAATATTGAAAAGAAGAATATGAGCCATATTCAACGGGAA CGTCAAGGGCCGAGTAAATTCAACATGGATGCTGATTATGGTATAATGGGCTCGCGATAATGTCGGGCAATCAGGTG
pBAD- PopZ- (UAG) ₀ - sfGFP	GATACCTACAGCGTGAAGCTGATGAGAAAGCGCCACGCTTCCGAAGGGAGAAAGGGCGAACAGGTATCCGTAAGCGGCAGGGTC GGAACAGGAGAGCGCACGGAGGGAGCTTCAGGGGGGAGGACCGCTTCCAGGGGGGAGGACCGCATGGGATAACCGTATTACGCCCTTGTGAGCTGATAC CGCTGCCGAGCCAAACGACCGAGCGCAGCGAGTCAGTGAAGCGAGGAAGCGGAAGGGAGAGTAGGAAACTGCCAGCTTAAGCT AACTAAGCAGAAGGCCCTGACGGATGGCCTTTTGCCTTACAAACTCTTCTGTTGAAAACGACGCCAGTCTTAAGCT CGGGCCCTTGTGCTCACATGTTCTTCTCGCTTATCCCTGATTCTGTTGATAACCGTATTACGCCCTTGTGAGCTGATAC AACTAAGCAGAAGGCCCTGACGGATGGCCTTTTGCCTTACAAACTCTTCTGTTGAAAACGACGCCAGTCTTAAGCT CGGGCCCTTGTGCTCACATGTTCTTCTCGCTTATCCCTGATTCTGTTGATAACCGTAAAACGACGCCAGTCTCGGGGTTTTATGGGG GGAGTTAGGGAAAGAGCATTGCTGAGATTTAAGGGCCCTGTCACTTGTGTTGATGAGATATGAGAATTATTAAACCTTATAAAT GAGAAAAGAACGCACTTAAAGATACGTTGCTTCTGATGTAACACCTATAATTAAACTATTCTCATTTATTAT GATTTTTGATATACATATTCTAGTTGTTAAAGAGAATTAAAGAAAATAATTCTGAAACACCTATAATTAAACTATTCTCATTTATTAT GACAACCTGACGGCTACATCATCTACCTTCTACAACCCGACCGAACTCGCTCGGGCTGGCCCGGTGATTTTAAATAC CCGCGAGAAATAGAGTGTGCTAACACATTGCGACCGACGGTGGCGATAGGCATCCGGGTGGTGTCTCAAAGCAGCTT CGCCTGGCTGATACTGGTCTCGCGCCAGCTAACAGCCTAACCTTAACTGCTGGCGAAAAGATGTGACAGACGCGACGGC GACAAGCAAACATGCTGTGCACGCTGGCGATATCAAATTGCTGCTGCCAGGTGATCGTGTACTGACAAGCCTCGCGTA CCCGATTATCCATCGTGGATGGAGCGACTCGTTAACGCTCCATGCGCCGCACTAACATTGCTCAAGCAGATTATCGCCAG CAGCTCGAATAGGCCCTTCCCTGCCCCCGCTTAATGATGCCCCAACACGGTCGCTGAAATTGCGCTGGTGCCTCATCC GGGCGAAAAGAACCCCGTATTGCAAATATTGACGGCCAGTTAACGGCATTATGCCAGTAGGCGCGCGACGAAAGTAACCCAC TGGTGTGACCATTCGCGAGCTCCGGATGACGACCGTGTGATGTAATCTCTGGCGGGAAACAGCAAATACCCGGTGGCGG AAACAAATTCTCGTCCCTGATTTCACCAACCCCGTACCGCGAACGGTGGAGATTGAGAATATAACCTTCACTCCAGCGGTGG TCGATAAAAAAAATCGAGATAACCGTGGCTAACGGCGCTAACGGCGAACAGTGGCATTAAACAGGATATCCGGCAGC AGGGGATCATTGCGCTCAGCCATACTTCTACACTCCGCCATTAGAGAAGAAGAACCAATTGCTCATATTGATCAGACATTG CCGTCACTGCGTCTTACTGGCTTCTCGCTAACAAACCGTAACCCCGCTTATTAAGAACGATTCTGACGCTTITATCGCAACTCTACTGTTCTCATACCCGTT TTAAGGAGTAAAATGTCGATCAGTCAAGAACCTACAATGGAGAAATCTCGCTCATTGACGATCATCTCGGAG GATGACGGCCGGCGAGCTGGCGCGGAAGCGCGCCCCCGCCGGAAACCGAACCTGCAACGGTGTGCTGCGAC GAGGTTCTGGAATTGACGGATCCGATCGCGCCCGAGCCCGAGCTGCCGCTGGAGACTGTCGGCGACATGACCGTCTATTGCG CGCCGGAACCTGAGTCGGAACCCGCTAACAGCCGCCGCCGGCGCTCCGGTGTGATCGCGACGAAGTCGCCAGCAGCTGG TCGCGTCTCGGCCGCTTCGGCCGCCGGCGAGCGCCTCGCAGCTGAGCTGCCCTGCTGATGCCAAGGACGGTCGGACGCT GGAAGACGTCGACGCGAGCTGCTGCGCCCGTCTCAAGGAGTGGCTGGTGTGTTCTGGTACCGCATCAGCGAGGAGCAGCTTACT GCGTAGTACCAATTCTCGTACAGGCTGATGGGATGAAATGGCCAATAGTTCTCGTACGCGCGAGGGCGAGGGCGATGCA ACTAACGGCAAGCTCACTCTCAAGTTATTGTACTACTGGCAAGCTCCAGTACCATGGCCAATCTCGTAACTACTCTGACCTA TGGCGTCAATGTTCTCCGCTATCCAGATCACATGAAGCAACATGATTCTTAACTGCGCAAGAGGCTATGTAACAG AGCGCACTATTAGCTTAAAGGATGATGGCACCTATAAGACTCGCCAGAGGTAAGGTTGAGGGCGATACTCTGTAATCGCAT TGAGCTAAGGGCATTGATTAAAGGAGGATGGCAATATTCTCGCCATAAGCTGGAGTATAATTCAATTCCATAATGTATAC ATTACCGCAGATAAGCAAAGAATGGCATTAAGGCGAATTAAAGGCGATGCTCCAGTACTCTCCAGATAATGTTCTGACGCA GATCATTATCAACAAATCTCAATTGGCGATGGCCAGTACTCTCCAGATAATGTTCTCCACTCAATCCGTCGCTCTC CAAAGATCCAATGAGAAGCGCGACATGGTACTCTGGAGTTGTAACTCGAGCAGGCAATTACTCATGGCATGGTGAAGCTC TATAAGCTCGAGCACCAACACCAACTAACCCCAAGGGGACACCCCTAATTAGCCGGCGAAGGGCGAAGGGCCAGTCTTCGACT GAGCCTTCTGTTATTGATGCTGGCAGTCCCTACTCTCGTACGGGAGTCCCACACTACCATGGCGTACCGCGTACGGCTGTTCA AAATGGGCTCGCGATAATGTCAGAATTGTTAATTGTTGTAACACTGACCCCTATTGTTATTCTAAATACATTCAAATA TGTATCCGCTCATGAGACAATAACCTGATAAAATGCTCAATAATATTGAAAAGAAGAATATGAGCCATATTCAACGGGAA CGTCAAGGGCCGAGTAAATTCAACATGGATGCTGATTATGGTATAATGGGCTCGCGATAATGTCGGGCAATCAGGTG

	GACAATCTATCGCTTGTATGGGAAGCCGATGCGCCAGAGTTGTTCTGAAACATGGCAAAGGTAGCGTGTCCAATGATGTTACA GATGAGATGGTCAGACTAAACTGGCTGACGGAATTATGCCACTTCCGACCATCAAGCATTITATCCGACTCCTGATGATGCAT GGTTACTCACCCTGCGATCCCCGGAAAAAACAGCGTCCAGGTATTAGAAGAATATCCTGATTTCAGGTGAAAATATTGTTGATG GCTGGCAGTGTTCCTGCGCCGGTTGACTCGATTCCCTGTTGATAATTGCTTAAACAGCGATCGGTATTTCGCTCGCTCAGGG GCAATCACGAATGAATAACGGTTGGTTGATGCGAGTGATTGATGACGAGCGTAATGGCTGGCCTGTTGAAACAAGTCTGGAAA GAAATGCATAAACTTTGCCATTCTCACCGGATTCACTCGTCACTCATGGTATTCTCACTTGATAACCTTATTGACGAGGG GAAATTAATAGGTGATTGATGTTGGACGAGTCGGAATCGCAGACCGATACCGATCTGCCATCCTATGGAACGCGCTCGG GAGTTTCTCCTTCACTACAGAAACGGCTTTCAAAATATGGTATTGATAATCCTGATATGAATAAAATTGCAATTTCATTGAT GCTCGATGAGTTTCTAAGCGGCCATCGAATGGCGAAAACCTTCGCGGTATGGCATGATAGCGCCGGAAAGAGAGTC ATTCAAGGTGGTGAATGAAACCGTAACGTTATACGATGTCGAGAGTATGCCGTGCTCTTATCAGACCCTTCCCCTG GTGAAACCAAGGGCAGGCCACGTTCTGCGAAAACCGGGAAAAGTGAACGGCGATGCCGGAGCTGAAATTCACTCCAAACGG GTGGCACAACAACTCGCGGCAAACAGTCGTTGATGGCGTCCACCTCAGTCTGGCTGACCGCGCTGCAACATTG TCGCGCGATTAAATCTCGCGCCATCAACTGGGTGCAAGCGTCAGTGGGCTGATCATTAACTATCGCTGGATGACCAGGATGCC AAGCGCGGTGCAACTATCTCGCGCAACCGCTGAGTCAACTATCGCTGGGCTTATTCTGATGTCGCTGACCAG GGAAGCTGCTGCACTATGTTCCGGCTTATTCTGATGTCGCTGACCAGACCCATCAACAGTATTATTTCTCCATGAGG ACGGTACCGCACTGGCGTGGAGCATCTGGTCGATTGGTCACCGCAAATCGCGCTGTTAGCGGGCCATTAAAGTTCTG GGCGCTCTGCGTCTGGCTGGCATAAAATCTCACTCGCAATCAAATTCAAGCTGGCAGCTGGCTGGAGACGCTG GGCGCTGCTGGCTGGCATAAAATCTCACTCGCAATCAAATTCAAGCTGGCAGCTGGCTGGAGACGCTG TGCCATGTCGGGTTTCAACAAACCTGCAATGCTGATGAGGGCATCTGGCTGCGGATATCGGTAGTGGGATACGACG GCGCTGGCGCAATCGCGCCATTACCGAGTCCGGCTGCGTGGGATATCGGTAGTGGGATACGACG GATACTGCTATGTTATACCGCGTTAACCCACATCAAACAGGATTTCGCGTGTGGGCAAACCGCGTGGACCGCTG AACTCTCAGGGCAGCGGTGAAAGGGCAATCAGCTGTTGCACTGGTAAAGAAAACCCCTGGCGCCAA CGAAACCGCCTCTCCCAGCGCTGGCGATTCAATTGCAAGCTGGCAGACAGGTTCCGACTGAAAGCGGGAGTGA CATGACAAAATCCCTAACGTGAGTTACCGCGCCTGTTCCACTGAGCGTCAAGACCCCGTAGAAAAGATCAAAGG GATCTTCTGCGCTAACGAGTCTGCTGTTGCAAACAAAAAACCGCGTACCGAGCGTGGGTTGCTGCCAGTGG GCTACCAACTTTCCGAAGGTAACGGCTCAGCAGAGCGCAGATAACAAACTGTTCTCTAGTGTAGCCGTAGTTAG ACCACTCAAGAACACTGTTAGCACCGCTACATACCTCGCTGTCAATTCTGTTACAGTGGCTGCTGCCAGTGG TGTCTTACGGGTTGACTCAAGACGATAGTACCGGATAAGGCGCAGCGGTGGCTGAACGGGGGTTCTG AGCTTGGAGCGAACGACCTACACCGAAC PopZ- (UAG) ₂ - sfGFP ORF (rest is same as pBAD- PopZ- (UAG) ₀ - sfGFP)
PopZ- (UAG) ₆ - sfGFP ORF (rest is same as pBAD- PopZ- (UAG) ₀ - sfGFP)	ATGTCCGATCAGTCTCAAGAACCTACAATGGAGGAATCCTCGCCCTCATTGACGATCATCTCGAGGGATGACCGCGCCGG AGCCTGCGGCCAGCGGCCCGCCGCCGAAACCGAACCTGAACCGGTGTCGTCGACGACGAGGGTTCTGGAATTGA CGGATCCGATCGCGCCCGAGCCGAGCTGCCCGCTGGAGACTGTCGGCAGACATCGACGCTATTGCGCCGGAACCTGAGTC GGAACCGGCTACACGCCGCCGGCGCTCCGCTGTTGATCGCAGAAGTCGCCAGCAGCTGTCGGCGTTTGGCCGCT TCGGCCGCGCGAGCGCCCTCGCAGCCTGAGCTGCTGCTGATGCCAAGGACGGTGGACGCTGGAGACGCTG GAGCTGCTGCCGGCTGCTAACGGAGTGGTGGACGAAACCTGCCGATCGTGGAGACGACAGGTTGAGGAAGAGTC CGTATCTCGGGGACCGGGTACGGTGGGTTCTGGTACCTAGCATCAAGGTTCTGGAGGAGCTTACTG ATTCTCGTAGAGCTGATGGCGATGTAATGGCCATAAGCTGGAGTATAATTCAATTCCATAATGATA CTGACACTACGGTACAGTGGCTGCTGGAGGTTGTAACGAGCAGGATTACTCATGGCATGGATGAGCT GACTATTACCGCATTAAGGCAATTAAAGGAGGATGGCTCCCGATAATGTTGAGGAGTGGCTCCG CATTGATTAAAGGAGGATGGCAATTCTCGGCCATAAGCTGGAGTATAATTCAATTACATTACCGCAGATA AGCAAAGAATGGCATTAAGGCAATTAAAGGAGGATGGCTCCGATAATGTTGAGGAGTGGCTCCG ACAAGAGCGCACTATTAGCTTAAGGATGATGGCACCTATAAGACTCGCGCAGAGGTAAGGTTGAGGGCG CGCATTGAGCTCAAGGGATTGTTAAAGGAGGATGCAATTCTCGGCCATAAGCTGGAGTATAATTCA AAACTCCAATTGGCGATGGCCAGTACTCTCCAGATAATGTTGAGGAGTGGCTCCG TA[TAGATTACCGCATTAAGGAAAGAATGGCATTAAGGCAATTAAAGGAGGATGGCTCCG TCGAGCATTTACCAAAACTCCAATTGGCGATGGCCAGTACTCTCCAGATAATCATTATCTCCACTCAATCCGTG CTCTCCAAAGTCCAATGAGAAGCGCGATCACATGGTACTCTGGAGGTTGTAACGAGCAGGATTACTCATGG AGCTCTAAGCTCGAGCACCACCAACCAACTAA
PopZ- (UAG) ₈ - sfGFP ORF (rest is same as pBAD- PopZ-	ATGTCCGATCAGTCTCAAGAACCTACAATGGAGGAATCCTCGCCCTCATTGACGATCATCTCGAGGGATGACCGCGCCGG AGCCTGCGGCCAGCGGCCCGCCGCCGAAACCGAACCTGAACCGGTGTCGTCGACGACGAGGGTTCTGGAATTGA CGGATCCGATCGCGCCCGAGCCGAGCTGCCCGCTGGAGACTGTCGGCAGACATCGACGCTATTGCGCCGGAACCTGAGTC GGAACCGGCTACACGCCGCCGGCGCTCCGCTGTTGATCGCAGAAGTCGCCAGCAGCTGTCGGCGTTTGGCCGCT TCGGCCGCGCGAGCGCCCTCGCAGCCTGAGCTGCTGCTGATGCCAAGGACGGTGGACGCTGGAGACGCTG GAGCTGCTGCCGGCTGCTAACGGAGTGGTGGACGAAACCTGCCGATCGTGGAGACGACAGGTTGAGGAAGAGTC CGTATCTCGGGGACCGGGTACGGTGGGTTCTGGTACCTAGCATCAAGGTTCTGGAGGAGCTTACTG GGCAGGAGCTTTACTGGCGTAGACCAATTCTCGTAGAGCTCGATGGCGATGTAATGGCCATAAGGTTCTCG AGGAGCTTACTGAGCTCGATGGCGATGTAATGGGATAAGCTTACTGAGCTGGCAAGCTCCAGTACCATGG CGTAACACTCTGACCTATGGCGTACAATGTTTCCGCTATCCAGATCACATGAAGCAACATGATT TTAAGTCCGCAATG

(UAG) ₀ -sfGFP)	CAGAGGGCTATGTACAAGAGCGCACTATTAGCTTAAGGATGATGGCACCTATAAGACTCGCGAGAGGTAAAGTTGAGGGCG ATACTCTCGTAAATCGCATTGAGCTCAAGGGCATTGATTTAAGGAGGATGCCAATATTCTGGCCATAAGCTGGAGTATAATT CAATTCCCATATGTA TAG ATTACCGAGATAAGCAAAGAACATGGCATTAAAGGCAATTAAAGATTCCGCTCATAATGTGGAGGA TGGCTCGTACAACCTCGCAGATCATTATCAACAAAATACTCCAATTGGCGATGGCCAGTACTCCTCCAGATAATCATTATCT CCACTCAATCCGTGCTCTCAAAGATCCAATGAGAAGCGCGATCACATGGTACTCCTGGAGTTGTAACTGCAGCAGGCATTAC TCATGGCATGGATGAGCTCTATAAGCTCGAGCACCACCAACCAACTAA
pDule-MjBpaRS (includes a copy of <i>tRNA^{Tyr}_{CUA}</i> gene)	GCGCCGTTAAGGCTAAACTGAAAGACAAGTTGGTACTCGCCTCCAAAGCCAGTTACCTCGGTTCAAAGAGTTGGTAGC TCAGAGAACCTTCGAAAAACGCCCTGCAAGCGGTTTTTCGTTTCAAGAGCAAGAGATTACGCGCAGACCAAAACGATCTCAA GAAGATCATCTTATTAATCAGATAAAATATTCTAGATTTCAGTGAATTATCTCTCAAATGTAGCACCTGAGTCAGCCCCAT ACGATATAAGTGTAAATCTCATGTTGACAGCTTATCATCGATAAGCTTAAATGCGGTAGTTTACAGTAAATGCTAACCG AGTCAAGGAGCTTGGTACGGTCAACCGTACTAGGGCTGTTCTAACTGAGGAGTCAGTCACTATGCGGTACCTTGCGTAT TTATGCGGTAGTTGGTACGGTCAACCGTACTAGGGCTGTTCTAACTGAGGAGTCAGTCACTATGCGGTACCTTGCGTAT GCGTTGATGCAATTCTATGCGCACCCGTTCTGGAGACTGTGGACCGCTTGGCCGCCAGTCTGCTCGTACTCGTACT TGGAGCCACTATCGACTACGCCATGGGACACACCCGCTGTGGATCTCTACGCCGGACGCGATCGTGGCCGATCACC GGGCCACAGGTGCGGTTGCTGGCCTATATGCCGACATACCGATGGGAAGATCGGGCTGCCACTTCGGGCTCATGAGC GCTTGTTCGGCGTGGGTATGGTGCAGGCCCGTGGCGGGGACTGTGGCGCCATCTCTTGATGACCGTACCCCTGCG CGGCGGTGCTCAACGGCTCAACCTACTACTGGGCTGTTCTAACTGAGGAGTCAGCATAAGGAGAGCGTCAACCGT GAGAGCCTTCAACCCAGTCAAGGCTCTCCGGTGGCGGGGACTGACTATCTGCGGTACCTATGCGGTACCTTGCGTAT AACTCGTAGGACAGGTGCGGAGCGCTCTGGTCAATTGCGGTACCTTGCGTACGGTCCGCCACAAACGTTGGCGAGAAGCAGGCC GCTTGGGTATTGGAATCTGCAACCGCTCTGCTCAAGCCTTCTGACTGGTCCGCCACAAACGTTGGCGAGAAGCAGGCC ATTATGCCGGCATGGCGGCCACGCACTGGGCTACGTTCTGCTGGCGTACGCCATGCTGTCAGGCTGATTTATGCCCTGGCGAGC TCAAGGATCGCTCGGGCTTACCGCTAACTTCGATATTGACGGGCTGATCGTACGGGATTTATGCCCTGGCGAGC ACATGGAACGGGTTGGCATGGATTGTAGGGCGGCCCTATACCTTGTCTGCTCCCGCGTTGCGTGCAGGAGCCGG CCACCTCGACCTGAATGGAAGGCCGGCACCTCGTAACGGATTCACCAAGAATTGGAGCCAATCAATTCTGCGGAGA ACTGTGAATGCGCAACCAAACCTTGGCAGAACATATCCATCGCTCCG TATAAGATCATCGGTTATACTGTTACGTT GAGGAATCCCATTGAGCAATTGAAATGATAAAGAGAAACACATCTGAAATTATCAGCGAGGAGTAAAGAGAGGTTTA AAAAAGATGAAAATCTGCTGGTATAGGTTGAACCAAGTGGTAAATACATTAGGGATTATCTCAAATAAAAAGATG ATTGATTACAAAATGCTGGATTGATATAATTATTTGCTGATTACACGCTTAACTAAACCGAGAAGGAGTTGGATGA GATTAGAAAATAGGAGATTATAACAAAAAGTTTGAGCAATTGGGTTAAAGGCAAAATATCTTATGGAAGTCCTTCCAG CTTGATAAGGATTATACACTGAATGTCTATAGATTGGTTAAAAGTACCTTAAAAGAGCAAGAAGGAGTATGAACTTATAG CAAGAGGGATGAAAATCCAAGGTTGCTGAAGTTATCTCAAATAATGCAAGGTTAACAGACTTATCTGGCGTTGATGT TGCAAGTTGGGGATGGAGCAGAGAAAATACACATGTTAGCAAGGGAGCTTACCAAAAAGGTTGTTGATTCACAACCC TGTTCTAACGGGTTGGAGAAGGAAGGAAAGTAGGTTCTCAAAAGGGAAATTATAGCTGTTGACTCTCCAGAAGGATT AGGGCTAACGAAAGAACACTGCCCAGCTGGAGTTGAGGAAATCCAATAATGGAGATAGCTAACATTCTCCTGAA TATCCTAACACAAAAAGGCCAGAAAATTTGGTGGAGATTGACGTTAACAGTATGAGGAGTTAGGAGAGTTTATTA ATAAGGAATTGCACTAACGGATTAAAATGCTGTAGCTGAAGAACTTAAAGATTGAGCCAATTAGAAAGAGATTAT ATAAGTCGACCATCATCATCATCCACCTGGCGACCTGCACCGTACCTGAACCAAGAAAGGTGAACGGACAAATCCGT AAAATCGGTGACTACAACAAAAAGTTGCAAGCGATGGGCTGAAAGCGAAATACGTTACGGTTCTGAATGGATGCTGGAC AAAGACTACACCTGAAACGTTACCGTCTGGCGTAAAACCACCCCTGAAACCGTGCCTGTTCTATGAACTGATCGCGCGT AAGACGAAAACCGAAAAGTGTGGAGTTATCTACCCGATCATGCGAGGTTAACGGTATCCACTAACAAAGGTTGACCTGGT TGGTGGTATGGAACAGCGTAAATCCACATGCTGGCGTGAACTGCTGCCAAAAAAAGGTTGATCCACACCCGGTTCTG ACCGGCTGGACGGTGAAGGTAATTGCTCTCTAACAGGTAACCTCATCGGGTTGACCGACTCTGGGAAAGAACCTCGT GAAAATCAAAAAGCGTACTGCCCGGGTTGTTGAGGTAACCCGATCATGGAACCGTAAACTCTTACGAAGAAGTGAATCTGTT TGACCATCAAAGGCTGGAAAAATTGGTGGTGAACCTGACCGTTAACCTGAAAGGAGTACGACGAAATCTGTTCAAAAACAAAGA ACTGCACCCGATGGACCTGAAAAACCGGGTTGCGGAAGAACGACTGATCAAACATCTGGAACCGATCCGTAACGCTGTAACTGCA GTTTCAAACGCTAACATTGCTGATCGCTACGCTTATAGGCTACATGATCTCTGCAATATATTGAGTTGCGTGTGTTGTAGG CCGGATAAGGCGTACGCCGATCCGGCAAGAACAGCAACATCCAAACGCCGCGTTACGCCGCGTTTTCTGCTTTCT TCGCGAATTAACTCGCTTCGCAACATGTCAGGACCCGTTATTGACTACCGGAAGCAGTGTGACCGCTGCTCTCAAATGCC AGGCCAGGTTGCTCAGGCTCTCGGGTGGAGGTAATAATTGACGATATGACTCGTACGTCACGGCTAACGCGCTGACTT CTCGCCGATCAAAGCATTGAAAGTGCAGGAAGAACGACTAACAGGGAGTGAAGAGGGCCGCGAACAGCGTTTCCATAGGCTCC GCCCCCTGACAAGCATCACGAAATCTGACGCTAACATGAGTGGCGAACCCGACAGGACTATAAGATAACCAAGGCGTT CCCCCTGGCGCTCCCTCGTGCCTCTCTGTTCCCTGCCCTGGTTACCGGTGTCATCCGCTGTTATGCCCGTGTGCTCATT CCACGCTGACACTCAGTCCGGTAGGCAGTTCGCTCAAGCTGACTGATGACGAAACCCCCCGTTGCTCAGTCCGACCGCTGC CCTTATCCGTAACTATCGTCTGAGTCCAACCGGAAAGACATGCAAAGCACCACGGCAGCAACTGGTAATTGATTAG AGGAGTTAGCTTGAAGTCA
pDule-MjCouRS (includes a copy of	GCGCCGTTAAGGCTAAACTGAAAGACAAGTTGGTACTCGCCTCCAAAGCCAGTTACCTCGGTTCAAAGAGTTGGTAGC TCAGAGAACCTTCGAAAAACGCCCTGCAAGCGGTTTTTCGTTTCAAGAGCAAGAGATTACGCGCAGACCAAAACGATCTCAA GAAGATCATCTTATTAATCAGATAAAATATTCTAGATTTCAGTGAATTATCTCTCAAATGTAGCACCTGAAAGTCAGCCCCAT ACGATATAAGTGTAAATCTCATGTTGACAGCTTATCATCGATAAGCTTAAATGCGGTAGTTTACAGTAAATGCTAACCG AGTCAGGCACCGTGTATGAAATCTAACATGCGCTACGTCATCCTCGGCCACCGTACCCCTGGATGCTGTAGGCATAGGCTTGG

	<p>AGCAGTGTGACCGTGTGCTCTCAAATGCCCTGAGGCCAGTTGCTCAGGCTCTCCCGTGAGGAATAATTGACGATATGATCA</p> <p>GTGCACGGCTAACTAAGCGGCCCTGCTGACTTCTGCCGATCAAAGGCATTGGCTATTAAAGGGATTGACGAGGCCGATCTGC</p> <p>GCAGTAAGATGCGCCCCGCATTGAAGCGGGTGGCTCAAGGGTAGAGCTGGCGCTCTAAAGCGCCTGGTTGCAAGGTCAAGTC</p> <p>GTCCGCTTCACCAATTCGAAAAGCCTGCTAACGAGCAGGCTTTTGATGCAGTCAGGAGCTCAGGCTCAAGTCTGCAATT</p> <p>ATTTCTGCCATTATCGCTTCAAACGCTAAATTGCTGATGCGCTACGCTTATCAGGCTACATGATCTGCAATATATTGAGT</p> <p>TGCGTGTCTTGTAGGCCGATAAGGCCTACGCCGATCCGGAAAGAAACAGCAAACAAATCCAAAAGGCCAGGAACCCTGAGCGTT</p> <p>GTTTTCTGCTTCTCGCAATTAACTCGCTTCGACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCCTGAGCGTT</p> <p>TTATCTGTTGTGCTGAGTACGCTCTCGTAGTGTAGGACAAATCCGCCGGAGCTGCTCTCTGTTGCTACTGACGGGTGG</p> <p>TGCGTAACGCCAAAGCACCGCCGACATCAGCGCTAGCGGAGTGTATACTGCTTACTATGTTGCACTGATGAGGGTGTAGT</p> <p>GAAGTGTCTCATGGCAGGAGAAAAAGCTGACCCTGGCTAGCAGAATATGTAACAGGATATATCCGCTTCCTCGCT</p> <p>CACTGACTCGTACCGCTCGTCTCGACTGCCAGGGAAATGGCTACGCCGACCCCTGCGCTTGTGGATCTACGCCGGACGCTCGT</p> <p>ACAGGTGCGGTTGCTGGCCTATACCGCAGATGGGAAGATCGGGCTCGGCACTTCGGCTCATGAGCGCTT</p> <p>TCGGCGTGGGATGGTGGCAGGCCCCGTCGGGGGACTGTTGGCGCCATCTCTGCAATGCCATTCTGGCGCGT</p> <p>GCTCAACGCCCTCAACCTACTATGGGCTGCTTCAATGCGAGGAGTCGATAAGGGAGAGCGTGCACCGATGCCCTGAGAGGC</p> <p>TTCAACCCAGTCAGCTCTCCGGTGGCGCGGGCATGACTATGCGCCACTTATGACTGCTCTTATCATGCAACTCGT</p> <p>AGGACAGGTGCCGGCAGCGCTGGGTATTTCGGGAGGGACCGCTTCGCTGGAGCGCAGCATGATGCCCTGCGTT</p> <p>GTATTCCGAATCTTGACGCCCTCGCTAACGCTTCGACTGGTCCGCCACAAACGTTGGCAGAGCAGGCCATTATCG</p> <p>CCGCATGGCGCCGACGCACTGGCTACGCTT</p>
pDule-MbAbKRS-2xtRNA (includes two copies of <i>tRNA^{PvuI}_{CUA}</i> gene)	<p>TAACTATATGCGAAACCTCGATAGGATTACCAAGGCCAATAAAAAATTTCGAAGTCGGACCTGTTACCGGAAAGAGTCGAC</p> <p>GGCAAAGAGCACCTGGAAAGAAATTACTATGGTGAECTCGCTCAGATGGGTCGGGATGACTCGGGAAAATCTGAGGCTCTCA</p> <p>TCAAAGAGTTCTGGACTATCTGAAATCTGACTCTGAAATCTGAGGAGATCTCTGATGGTCTTGGGGATACTCTGATATAATG</p> <p>CACGGGGACCTGGAGCTTCTCGGCACTGCTGGCCAGTTCTCTGATAGAGAATGGGGATTGACAACAAACATGGATAGGT</p> <p>CAGGTTTGGTCTGAACGCTTCTCAAGGTTATGCACTGCGCTTAAACATTAAAGGGCATCAAGGTCGAATCTACTATAA</p> <p>TGGGATTTCACCAATCTAATGCACTGAGTTCAAACGCTAAATTGCCGATGCCGCTACGCTTATCAGGCC</p> <p>TACATGATCTGCAAATCCGCTTATGCGCTTACCGGATAGGCTACGCCGATCCGGCAAGAAACAGCAAACAAATCCAAAACGCC</p> <p>GTTCAGCGCGTTTCTGCTTCTCGCAATTAACTCGCTTCTCGCACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACC</p> <p>GCTCGAGCGTTTATCTGTTGCTGCTGAGCTACGCTCTCTGAGTAGGACAAATCCGCCGGAGCTGCTCTCTGCTCAGCTAC</p> <p>TGACGGGGTGGTGCCTACCGGAAACAGCACCGCCGACATCAGCGCTAGCGCAGTGTAGTATACTGGCTTACTATGTTGGACTGAT</p> <p>GAGGGTGTAGTGAAGTGTCTCATGTCAGGAGAAAAAAGGCTGCGCAGGAGAAATGGCTACGCCGCTAGCAGAATATGTAACAGGATATT</p> <p>CCGCTTCTCGCTCACTGACTCGTACGCTCTCGTCTCGACTGCCGAGCGGGAAATGGCTACGACGGGGGGAGATTCTCTGAGGAGATCTCTG</p> <p>GGAAGATGCCAGGAAGATACTAACAGGGAAAGTGAAGGGCCGCGCAAAGCGTTTCTCATAGGCTCCGCCCTGGCGCTCCC</p> <p>CATCAGAAATCTGACGCTAAATCAGTGGTGGCGAAACCCGACAGGACTATAAAGATAACCCGCTTCCCTGGCGCTTCTCATCCACGCC</p> <p>TCGTGCGCTCTCCTGTTCCGCTTACCGGTTACCGGTTACCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGG</p> <p>AGTCCGGTAGGAGCTTCTGCTTACGCTGACTGTATGACGAACCCCCCTGCTAGTCCGACCGCTGCCCTTACCGGTAAC</p> <p>ATCGTCTGAGTCCACCCGAAAGACATGCAAAGCACCCTGCTGAGCTGGTAATTGATTAGAGGAGTTAGTCTGTA</p> <p>AGTCATGCGCCGTTAAGCTAAACTGAAAGGACAAGTTGGTACTGCGCTCTCCAAGCCAGTTACCTCGGTTCAAAAGAGIT</p> <p>GGTAGCTCAGAGAAACCTCTGAAAAACGCCCTGCAAGGCCGTTTCTGTTTCTGAGAGCAAGGATACGCCAGCAGACCAAACAG</p> <p>ATCTCAAGAGATCTTATTAACTAGATAAAATATTCTAGATTTCAGTCAATTATCTCTCAATAGTACGACCTGAAGTC</p> <p>GCCCCATACGATATAAGTGTAACTCTCATGTCAGCTTACATCGATAAGCTTAAATGCGTAGTTTACAGTTAAATTG</p> <p>CTAACCGAGTCAGGCCACCGTGTATGAAATCTAACATGCGCTACGCTCATCCGACCCGTCACCCGATGCTGAGGCTA</p> <p>GGCTTGGTTATGCCGGTACTGCCGGCTTCTGCGGGATATGTCGCTTCCGACAGCATGCCAGTCAGTCACTATGCCGCTGCTAGC</p> <p>GCTATATGCGTTATGCAATTCTATGCGCACCCGTTCTGGAGCAGCAGTCCGACCGCTTGGCCGCCAGCTCTGCTCGCTT</p> <p>CGCTACTTGGAGCCACTATCGACTACGCCATGGCGACCCGCTCTGGAGCTGCCGACGCTCGTGGCCCTGCGCTTACCGGCGACGCTCGTGGCC</p> <p>CATCACCGGCCACAGGTGCCGGTGTGGCCATATGCCGACATCAGGAGTGGGAAGATGCCGCTGCCACCTCGGGCT</p> <p>ATGAGCGCTTGGTGGCGGGTGTGGAGCTGGCAGGCCCCGGTGGCCGGGGGACTGTTGGCCGCCATCTCTGCAATGCCATT</p> <p>TTGCGCGGCCGCTCAACGCCACTACTGGGCTGCTCTCTAATGCAAGGAGTCGCTGCAATAGGGAGAGCGCTGACCGAT</p> <p>GCCCTTGAGAGCCTCAACCCAGTCAGCTCTCCGGTGGCGCGGGCATGACTATGCGCCGACTTATGACTGCTTCTCTT</p> <p>TCATGCAACTCGTAGGACAGGTGCCGGACGCCGCTCTGGGTATTTCGGGAGGGACCGCTTCGCTGGAGCGCAGCATGATCGG</p> <p>CCTGTCGCTTGCCTTACCGGAAATCTGCAAGCCCTCGCTCAAGCTTCTGACTGGTCCGCCACCAAACGTTCCGGAGAGC</p> <p>AGGCCATTATGCCGGCATGGCGGCCAGCAGCTGGGCTACGCTTCTGCTGGCGCTGCAAGGCCAGGCTGAGTGGCTTCC</p> <p>TATGATTCTCTGCTTCCGGCGCTTACCGCTAACCTGCTACGCTTCTGCTGGAGCTGCTGAGGCTGAGTACGACCATCAGGGA</p> <p>CAGCTTCAAGGATCTGCTGCCGCTTACCGCTAACCTGCTACGCTTCTGCTGGAGCTGCTGAGGCTGAGTGGCTTCC</p> <p>GAGCACATGGAACGGGTTGGCATGGGATGGGAGTGGGAGCTGGCGCCCTATACCTTGCTGCTCCCGCGTGGCTGCGCTGCGATGGAGC</p> <p>CGGGCCACCTGCAACCTGAATGGAAGGCCGGCACCTCGCTAACCGGATTCAACCAACTCCATCGCGTCCGCCATCTCAGCAGGCCACGCCGCGCATCTCG</p> <p>GGCTCTTGCACTGCAACCATCTCTGCCGGCGGTGCTCAACGCCCTCAACCTACTACTGGGCTGCTTCTTAATGCAAGGAGTCG</p> <p>ATAAGGGAGAGCGTCTGGCAGAAGGGGGATGTCGCAAGGCAATTAGGGTAACGCCAGGGTTCCAGTCAGCACGACGTT</p>

	<p>GTAAAACGACGCCAGTCCAAGCTTAAAAAAATCCTTAGCTTCGCTAAGGATCTCGAGTGGCGGAAACCCCCGGGAACTCAA CCCGGCTGAACGGATTAGAGTCATTCGATCTACATGATCAGGTTCCGAATTCAGCGTACAAGTATAACACAAGTTTTAT GTTGAGAATATTTTTGATGGGAGGCATTTCGCTATTAAAGGGATTGACGAGGGCGTATCTGCGCAGTAAGATGCGCCCCCGCATI GGAAACCTGATCATGTAGATCGAATGGACTCTAAATCCGTCAGCCGGGTTAGATTCCCGGGTTCCGCCAATTGCAAAAGCC TGCTCAACGAGCAGGTTTIGCAIGGCCCTCGGGTTGTCAGCCCTGCTCCGCTTATAAGATCATACAGCCGTTACGTTGTTAC GCTTGAGGAATCCCATAATGGATAAAAACCATTAGATGTTAATATCTGCACCGGGCTCTGGATGTCAGGACTGGCACGCT CCACAAAATCAAGCACCATGAGGTCTCAAGAAGTAAAATATACATTGAAATGGCGTGTGGAGACCATTTGTTGTAATAATTCC AGGAGTGTAGAACAGCCAGAGCATTCAAGACATCATAAGTACAGAAAAACCTGCAAACGATGTAGGGTTCTGGACGAGGATATC AATAATTTCACAAGATCAACCGAAAGCAAAACAGTGTGAAAGTTAGGGTAGTTCTGCTCAAAGGTCAAAGGCTATGACCT CCGAAATCAGTTCAAGGGCTCGAAGCCCTCTGGAAAATTCTGTTCTGCAAAGGCAACACATCAGATCTGACCT CGCTGCAAATCAACTCAAATTCGCTGTCCCGCATCGGCTCTGCTCTCACTTACAAGAACGCCAGCTGATAGGGTTGAG GCTCTCTTAAGTCCAGAGGATAAAATTCTCAAATATGGCAAAGCTTCAAGGAACTTGACCTGTAATTGACAAGAAGAA AAAACGATTTCAGCGCTCTACCAATGATAGAGAAGACTACCTCGTAAACTCGAACGTGATATTACGAAATTTCGAGA CCGGGTTCTGGAGATAAAGTCTCTATCCTTATCCGGCGAATCGTGGAGAGAATGGTATTAAATAATGATACTGAACTT TCAAAACAGATCTCCGGTGGATAAAATCTGTTGAGGCCAATGCTGCCCCGACTCTGTA </p>
pDule-MbAbKRS-2xtRNA-RBS1-api1b (includes two copies of tRNA ^{Pv1} _{CUA} gene)	<p>TAACTATATGCAAAACTCGATAGGATTACCAGGCCAATAAAAATTCGAAGTCGGACCTTGTACCGGAAAGAGTCTGAC GGCAAAGAGCACCTGGAAGAATTACTATGGTAACCTCGCTCAGATGGGTCGGGATGACTCGGGAAAATCTGAAAGCTCTCA TCAAAGAGTTCTGGAACATCTGGAATTCGACTCTCGAAATCTGAGGAGATTCTCTGCTATGGCTTCTGGGGATACTCTGATATAATG CACGGGGACCTGGAGCTTCTCGCAGTCGTCGGCCAGTTCTCTGATAGAGAATGGGGTATTGACAAACATGGATAGGTG CAGGTTTGGTCTGGAACCTGCTCAAGGTTATGACGCGCTTAAACATTAAAGGGCATCAAGGTCGAATCTACTATAA TGGGATTCAACCAATCTAAACTGCAGTTCAAACGCTAAATTGCGTATGCGCTACGCTTATCAGGCTACATGATCTGCAA TATATTGAGTTGCGTCTTGTAGGCCGATAAGGCGTTCACGCCGATCCGGCAAGAAACAGCAAAACAATCCAAAACGCCG GTTCAGGGCGTTTCTGCTTCTCGAATTAAATTCCGGAGAAGAAACCAATTGTCATATTGCATACGACATGCGTC ACTGCGCTTTACTGGCTCTCTCGTAACCAAACCGTAACCCCGCTTAAAGCATTGTAACAAAGCGGGACCAAGG CATGACAAAACCGCTAACAAAGTGTCTAATACCGCAGAAAGTCCACATTGATTTGACCGCGCTCACACTTGTCTAT GCCATAGCATTTCATCCATAAGGATTAGGCCATCTGACGCTTACCTGACGCTTATTCGCAACTCTACTGTTCTCATACCCGTTTTA AGGAGGTAAAAGGTTAATATCGCCCGTATACATTCCTCAGCACCCACGCCGACCCCTTAGTTCCGACATGTGA GCAAAGAGCCAGCAAAGGCCAGGAACCGCTCGAGCGTTTATCTGTTGTTGCGTGAACGCTCTCTGAGTAGGACAATTC GCCGGGAGCTGCTCCCTCTGTCAGCTACTGACGGGGTGGTGCTAACGGCAAAGCACCCTGGGACATCAGCGTAGCGGAGT GTATACTGGCTTACTATGTTGCACTGATGAGGGTGTCACTGAGGTGTTCTGACTGCTTATGTCAGGAGAAAAAGGCTGCA CCGGTCAAGCAGGAGATTCTCTGAGATGCCAGGAAGATGCGAGGAAAGTACTTAACAGGGAAGTGTAGAGAGGGCCGCGAACAGCG TGGCTTACAGGCTCCGCCCCCTGACAAGCATCAGGAAATCTGACGCTCAACATTAGTGGTGGCGAACCCGCAAGGACTATAAG TTTCCATAGGCTCCGCCCCCTGACAAGCATCAGGAAATCTGACGCTCAACATTAGTGGTGGCGAACCCGCAAGGACTATAAG ATACAGGCGTTCCGCCCCCTGGCGCTCCCTGTCGCTCTGCTCTGCTTCTGCTTACCGGTTGTCATTCCGCTTATGCCC GCGTTTGTCTCATCCACCGCTGACACTCAGTCCGGTAGGCGTCAAGCTGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG TCCGACCGCTGCGCTTATCCGTAACTATCGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG GTAATTGATTAGAGGAGTTAGTCTGTAAGTCACTGCGCCGTTAAGGCTAAACTGAAAGGACAAGTTGGTACTGCGCTCTC CAAGCCAGTACCTCGGTTAACAGAGTTGGTAGCTAGCAGAGAACCTCGAAAAACCGCCCTGCAAGGCCGTTTCTGTTTCA GCAAGAGATTACCGCAGACCAAAACGATCTCAAGAAGATCATCTTATTAGATAAAATATTCTAGATTTCAGTGAATT ATCTCTCAAATGTAGCACCTGAAAGTCAGCCCATACGGATATAAGGTTGAAATTCTCATGTTGACGCTTACATCGATAAGCTT AATGCGTAGTTATCAGGTTAAATTGCTAACCGCAGTCAGGACCCGTGTATGAAATCTAACATGCGCTCATCGTCATCTCGG CACCGTCACCCCTGGATGCTGAGGCTAGGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG ATCGCCAGTCACTATGGCTGCTGCTGCTATGCGTATGCGTTGATGCAATTCTCATGCGCACCGCTTCTCGGAGACTGTCGACCC CTTGGCCGCCGCCCCAGTCTGCTGCTTCTGCTACTTGGAGGCCACTACGACTACCGCAGTCATGGCACCACACCGCTCTGTGGA TCCTCTACGCCGAGCAGTCGTTGCGCCATCACCGGCCACAGGTGCGGTTGCTGGCCCTATATGCCGACATCACCAGATGG GGAAGATCGGGCTGCCACTTCGGGCTCATGAGCGTITGTTCGGGTGGGTATGGTGGCAGGCCCGTGGCCGGGGACTGTTG GGGCCATCTCTTGCACTGCCACATTCTGCGGCCGCGTCTCAACGGCTAACCTACTACTGGCTGCTTCTTAATGCAAGGA GTCGCATAAGGGAGAGCGTCGACCGATGCCCTGAGAGGCCCTAACCCAGTCAGCTCTCCGGTGGGCCGGCATGACTATC GTCGCCGCTATTGACTGTCTTATCATGCACTGAGGCCAGGGTGGCTGGGCTGGCGCAGCGCTCTGGGTATGGCGCAGGACCG CTTTCGCTGGAGCGCGAGCATGCCCTGCTGCTTGGTATTGGAATCTGCAACGCCCTGCTCAAGCTTCTGCTACTGGTC CCGCCACAAACGTTCTGGAGAAGCAGGCCATTATGCCGCGATGGCGGCCAGCAGCTGGCTACGCTTCTGCTGGCTTCCG GACCGCAGGCTGGATGGCTTCCCCATTATGATTCTCTGCTTCCGGCGCATGGGATGCCGCTTGTGAGGCCATGCTGTCCA GGCAGGTAGATGACGACCATCAGGACAGCTTCAGGATCGCTCGGGCTTCTACAGCTTAACCTGATCATGGACCGCTGAT CGTCACGGCGATTATGCCCTCGCGAGCACATGGAACGGGTTGGCATGGATTGTTAGGGCCGCCCTATACCTTGTCTGCTC CCCAGCTTGTGCGTCCGGTGCATGGAGCCGGCACCTCGACCTGAATGGAAGCCGGCCACCTCGCTAACGGATTACCAACTCC AAGAATTGGAGCCAATCAATTCTGCGGAGAATGTAATGCGCAAACCAACCTTGGCAGAACATCATCCATCGCGTCCGCCATC TCCAGCAGCCGACGCCGCGCATCTCGGCCCTCTGCACTGCCACCTGACGACCATTCCTGGCGGCCGCTGCTCAAGGCCCTCAACCTACTAC TGGGCTGCTCTTAATGCAAGGAGTCGCTAACAGGGAGAGCGCTGGCGAAGGGGGATGTCGCTGCAAGGCCGATTAAAGGGTAA CGCCAGGGTTTCCAGTCACGGCGTGTAAACGACGCCAGTGCCTAACGCTTAAAGGAAATCTTCTGCTAACGGATCTG CAGTGGCGGAAACCCCCGGGAATCTAACCCGCTGAAACGGATTAGTCCATTGATCATGATCAGGTTCCGAATTGAGCG TTACAAGTATTACACAAAGTTTTATGTTGAGAATTTTTGATGGGAGGCATTGCTTAAAGGGATTGACGAGGGCGTAT CTGCGCAGTAAGATGCGCCCCGCATTGGAAACCTGATCATGAGATGCAATGACTCTAAATCCGTTAGCCGGGTTAGATTCCC GGGGTTCCGCCAATTGCAAAAGCCGCTCAACGAGCAGGCTTGGCCATCCCTCGGGTTGTCAGCCTGCTCCCGCTTATAAAG ATCATACGCCGTTAACCGTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG TCTGGATGTCAGGACTGGCACGCTCCACAAAATCAAGCAGCACCATGAGGTCTCAAGAAGTAAAATACATTGAAATGGCGTGTG GAGACCATCTTGTGAATAATTCCAGGAGTTGAGAACAGCCAGAGCATTGACGACATCAACTGAGAACAGTGTGAAAGTTAGGGTAGTT GATGTAGGGTTCTGGACGAGGATATCAATAATTCTCACAGTTCAAGGGCTCCGAAGCCCTCTGGAAAATTCTGTTCTGCAAGAGCATCA ACGAACACATCCAGATCTGTAACCTCGCCTGAAAATCAACTCCAAATTGCTGTTCCGCTCGCTCCCTACTAC AAGAAGCCAGCTGAGGGTTGAGGCCAGAGGATAAAATTCTCTAAATATGGCAAAGCCCTTCAGGGAACTT </p>

	GAGCCTGAACTTGTGACAAGAAGAAAAAACGATTTCAGCGGCTCTATAACCAATGATAGAGAAGACTACCTCGTAAACTCGAA CGTGATATTACGAAATTTCGTAGACCGGGGTTTCTGGAGATAAAGTCTCTATCCCTATTCCGGCGAATACGTGGAGAGAAT GGGTATTAATAATGATACTGAACCTTCAAAACAGATCTCCGGGTTGATAAAAATCTCTGCTTGAGGCCAATGCTTGGCCCCGACT CTGTA
pDule-MbAbKRS-2xtRNA-RBS2-api1b (rest is same as pDule-MbAbKRS-2xtRNA-RBS1-api1b)	GAGAAGAAACCAATTGTCCATATTGCATCAGACATTGCCGTACTCGTCTTTACTGGCTCTCTCGCTAACCAAACCGTAACC CCGCTTATTAAAAGCATCTGTAAACAAAGCGGGACCAAGCCATGACAAAAACCGCTAACAAAAGTGTCTATAATCACGGCAGA AAAGTCCACATTGATTATTIGCACGGCGTACACTTTGCTATGCCATAGCATTTCATCCATAAGATTAGCGGATCTACCTGACG CTTTTATCGCAACTCTACTGTTTCTCATACCCGTTTTAAGGAGGTAaaaaATGGGTAATAATCGCCCGTATA CATTCCTCAGCCACGCCGCCACCCACGCCCTTAGTCGACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGCTCGAGCGTTTA GCGTTTATCTGTTGCTCGGTGAACGCTCTCTGAGTAGGACAAATCCGCCGGAGCTGCCCTCTGTTCACTGACGGGTTGACGG GGTGGTGCCTAACGGAAAAGCACGCCGGACATCAGCGTAGCGGAGTGTATACTGGTTACTATGTTGGCACTGA
pDule-MbAbKRS-2xtRNA-RBS1-apiB5 (rest is same as pDule-MbAbKRS-2xtRNA-RBS1-api1b)	GAGAAGAAACCAATTGTCCATATTGCATCAGACATTGCCGTACTCGTCTTTACTGGCTCTCTCGCTAACCAAACCGTAACC CCGCTTATTAAAAGCATCTGTAAACAAAGCGGGACCAAGCCATGACAAAAACCGCTAACAAAAGTGTCTATAATCACGGCAGA AAAGTCCACATTGATTATTIGCACGGCGTACACTTTGCTATGCCATAGCATTTCATCCATAAGATTAGCGGATCTACCTGACG CTTTTATCGCAACTCTACTGTTTCTCATACCCGTTTTAAGGAGGTAaaaaATGAAAATAATGCACCCATATACGTACAC AACCACGCCGCCACCCAAAATATAATTTCGACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGCTCGAGCGTTTA TCTGTTGTTGCTCGGTGAACGCTCTCTGAGTAGGACAAATCCGCCGGAGCTGCCCTCTGTTCACTGACTGACGGGTTGTTG GTAACGGCAAAGCACGCCGGACATCAGCGTAGCGGAGTGTATACTGGTTACTATGTTGGCACTGA
pDule-MbAbKRS-2xtRNA-RBS1-apiB8 (rest is same as pDule-MbAbKRS-2xtRNA-RBS1-api1b)	GAGAAGAAACCAATTGTCCATATTGCATCAGACATTGCCGTACTCGTCTTTACTGGCTCTCTCGCTAACCAAACCGTAACC CCGCTTATTAAAAGCATCTGTAAACAAAGCGGGACCAAGCCATGACAAAAACCGCTAACAAAAGTGTCTATAATCACGGCAGA AAAGTCCACATTGATTATTIGCACGGCGTACACTTTGCTATGCCATAGCATTTCATCCATAAGATTAGCGGATCTACCTGACG CTTTTATCGCAACTCTACTGTTTCTCATACCCGTTTTAAGGAGGTAaaaaATGAAAATAATGCACCCATATACGTATCAC GACCACGCCGCCACCCAAAATATAATTGATTCGACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGCTCGAGCGTTTA TCTGTTGTTGCTCGGTGAACGCTCTCTGAGTAGGACAAATCCGCCGGAGCTGCCCTCTGTTCACTGACTGACGGGTTGTTG GTAACGGCAAAGCACGCCGGACATCAGCGTAGCGGAGTGTATACTGGTTACTATGTTGGCACTGA
pDule-MbAbKRS-2xtRNA-RBS1-apiB10 (rest is same as pDule-MbAbKRS-2xtRNA-RBS1-api1b)	GAGAAGAAACCAATTGTCCATATTGCATCAGACATTGCCGTACTCGTCTTTACTGGCTCTCTCGCTAACCAAACCGTAACC CCGCTTATTAAAAGCATCTGTAAACAAAGCGGGACCAAGCCATGACAAAAACCGCTAACAAAAGTGTCTATAATCACGGCAGA AAAGTCCACATTGATTATTIGCACGGCGTACACTTTGCTATGCCATAGCATTTCATCCATAAGATTAGCGGATCTACCTGACG CTTTTATCGCAACTCTACTGTTTCTCATACCCGTTTTAAGGAGGTAaaaaATGGCAATAATACACCGTATACGTATCAC AACCACGCCGCCACCCAAAATATAATTTCGACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGCTCGAGCGTTTA TCTGTTGTTGCTCGGTGAACGCTCTCTGAGTAGGACAAATCCGCCGGAGCTGCCCTCTGTTCACTGACTGACGGGTTGTTG GTAACGGCAAAGCACGCCGGACATCAGCGTAGCGGAGTGTATACTGGTTACTATGTTGGCACTGA
pDule-MbAbKRS-2xtRNA-RBS1-apiC3 (rest is same as pDule-MbAbKRS-2xtRNA-RBS1-api1b)	GAGAAGAAACCAATTGTCCATATTGCATCAGACATTGCCGTACTCGTCTTTACTGGCTCTCTCGCTAACCAAACCGTAACC CCGCTTATTAAAAGCATCTGTAAACAAAGCGGGACCAAGCCATGACAAAAACCGCTAACAAAAGTGTCTATAATCACGGCAGA AAAGTCCACATTGATTATTIGCACGGCGTACACTTTGCTATGCCATAGCATTTCATCCATAAGATTAGCGGATCTACCTGACG CTTTTATCGCAACTCTACTGTTTCTCATACCCGTTTTAAGGAGGTAaaaaATGGCAATAATGCACCCGTATACGTACCAA AACCACGCCGCCACCCAAAATATAATTGGTCGACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGCTCGAGCGTTTA TCTGTTGTTGCTCGGTGAACGCTCTCTGAGTAGGACAAATCCGCCGGAGCTGCCCTCTGTTCACTGACTGACGGGTTGTTG GTAACGGCAAAGCACGCCGGACATCAGCGTAGCGGAGTGTATACTGGTTACTATGTTGGCACTGA