SUPPORTING INFORMATION

Two-Way Chemical Communication between Artificial and Natural Cells

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MATERIAL AND METHODS

Bacterial strains and media. Strains used in this study are listed in Table S4. *E. coli* and *P. aeruginosa* were grown in LB. *V. fischeri* was grown in LBS (10 g/L tryptone, 5 g/L yeast extract, 20 g/L NaCl, 50mM Tris-HCl, 0.3% glycerol) for experiments and either LBS or photobacterium broth (0.3 g/L NH_4Cl, 1 g/L $CaCO_3$, 5 g/L casein enzymatic hydrolysate, 0.01 g/L $FeCl_3$, 0.3 g/L $MgSO_4 \bullet 7H_2O$, 3 g/L KH_2PO_4, 30 g/L NaCl, 23.5 g/L sodium glycerophosphate, 2.5 g/L yeast extract) to make glycerol cell stocks. *V. harveyi* was grown in marine broth supplemented with 2% casamino acids when glycerol cell stocks were made or in Autoinducer Bioassay (AB) media (17.5 g/L NaCl, 12.3 g/L $MgSO_4 \bullet 7H_2O$, 2 g/L casamino acids, 10 mM potassium phosphate pH 7, 1 mM L-ariginine, 1% (v/v) glycerol) for the chemical communication experiments. When necessary, media were supplemented with antibiotic (100 µg/mL ampicillin, 50 µg/mL kanamycin, or 34 µg/mL chloramphenicol).

Genetic constructs. *lsrR, lsrK,* and the intergenic operon region of *lsr* were amplified from the genome of *E. coli* MG1655 by PCR. The gene coding for *Staphylococcus aureus* α-hemolysin (αHL) was synthesized by Genscript. T3 RNA polymerase (BBa_K346000), AiiA (BBa_C0160) and the following devices BBa_K575024, BBa_K575037, and BBa_T9002 were taken from the registry of standard biological parts. The gene encoding firefly luciferase was amplified from pBESTluc (Promega). Sequence information for the exploited constructs can be found in Table S5.

In vitro transcription-translation. The constructs encoding parts of the *E. coli* AI-2 quorum pathway were expressed with the PURE system (New England BioLabs). Each reaction contained

10 µL solution A, 7.5 µL solution B, 20 U RNase inhibitor, and 250 ng DNA, unless specifically stated otherwise. When needed, between 0 µM and 250 µM AI-2 or 0.5 mM of *S*-adenosyl-L-homocysteine (SAH) was added to the solution. The constructs designed to express parts of the quorum pathways of *P. aeruginosa* and *V. fischeri* used either a cell-free *E. coli* S30 extract for circular DNA (Promega) (20 µL premix, 15 µL S30 extract, 5 µL amino acids mix, 40 U of RNase inhibitor, and 2 µg of DNA) or the *E. coli* S30 T7 High Yield Protein Expression System (Promega) (20 µL S30 premix, 18 µL T7 S30 extract, 40 U of RNase inhibitor, and 1 µg of DNA). When needed, 10 µM of 3OC12 HSL, C8 HSL, 3OC6 HSL, or C4 HSL (Sigma Aldrich or Cayman Chemical) were added to induce expression, or 300 µM of acetyl coenzyme A and 0.5 mM of *S*-adenosyl-L-methionine (SAM) were added for the synthesis of *N*-Acyl homoserine lactones. Reactions were incubated at 37 °C for 4 h to 6 h. In vitro reactions assembled for the sensing of 3OC12 HSL were shaken (50 s orbital shaking, 1 mm orbital amplitude prior to fluorescence acquisition every min) in 384 microwell plates (781076 Greiner Bio One) during incubation in an Infinite m200 plate reader (Tecan). Negative controls were the same reactions in the absence of quorum molecules. Fluorescence was either measured with a Photon Technology International (PTI) QuantaMaster 40 UV−vis spectrofluorometer or a CFX96 Touch Real-Time PCR Detection System (Bio-Rad).

Enzymatic production of AI-2. AI-2 was enzymatically produced *in vitro* with 12 µM of the purified fusion protein HLPT[1] and 5 mM of *S*-adenosyl-L-homocysteine. Reactions were incubated overnight at 37 °C, 220 RPM. The protein was then removed by two chloroform extractions. The aqueous phase contained AI-2. Since the enzymatic reaction produces in a 1:1 ratio AI-2 and homocysteine, AI-2 was indirectly quantified using 5,5’-dithio-bis(2-nitrobenzoic acid) (DTNB).

The solution for quantification contained 10 µL of sample, 100 µL of Tris-HCl, pH 8, 50 µL of 2 mM DTNB, 50 µM sodium acetate, and 840 µL of water. After 5 min of incubation at room temperature, the absorbance at 412 nm was measured and the concentration of homocysteine was calculated by using the molar extinction coefficient (13,600 $M^{-1}cm^{-1}$) of the reaction product 5-thio-2-nitrobenzoic acid (TNB).

Vesicle stability. To test whether bacteria could break phospholipid vesicles, a dye leakage assay[2] was performed. Dehydrated aliquots of 1:2 POPC:cholesterol vesicles[11] were hydrated with 60 µL S30 *E. coli* extract for circular DNA template (Promega) supplemented with 4 µg of DNA (RL081A), 1 mM *S*-adenosyl methionine, 700 µM acetyl coenzyme A, and 80 mM calcein (Sigma). The vesicles were then extruded through a polycarbonate membrane with 1 µm pores (Whatman) with an Avanti mini-extruder and purified with a sepharose 4B (Sigma-Aldrich) column. Fluorescence was monitored with excitation and emission at 495 nm and 515 nm, respectively. Subsequently, 0.3% (v/v) Triton X-100 was added as a control to break the vesicles.

The effect of cholesterol on chemical communication. Dehydrated aliquots of POPC vesicles with either 0 mol%, 10 mol%, or 66 mol% cholesterol were hydrated with 50 µL S30 *E. coli* extract for circular DNA template (Promega) supplemented with 4 µg of DNA (NY013A), 1 mM *S*-adenosyl-L-methionine, and 700 µM acetyl coenzyme A. The experiments were run as described below in the cellular Turing test section.

Artificial cells that sense 3OC6 and C8 HSL. Aliquots of 1:2 POPC:cholesterol vesicles were formed as previously described[3]. 100 µL aliquots were rehydrated with 50 µL of S30 *E. coli* extract containing 20 µL S30 premix, 15 µL S30 extract, 5 µL amino acids mixture, 40 U of RNase inhibitor, and 4 µg of DNA (RL082A, RL093A or RL094A, see Table S5 for sequences). Vesicles were diluted 1:1 with LB supplemented with 0.7 mg/mL proteinase K, 0.07 mg/mL RNase A, and 170 U/mL RNase T1 (Thermo Fisher Scientific) to remove any residual activity in the extravesicular solution. Reactions were incubated at 30 °C for 4 h. For sensing of externally added 3OC6 HSL, 1 µM of synthetic 3OC6 HSL or C8 HSL (Cayman Chemical) was added to the artificial cells. For the sensing of *V. fischeri*, bacteria were first grown from 200 µL of a glycerol stock at 30 °C in LBS until OD^{600} ^{nm} = 1.8. The bacteria were then pelleted, and the supernatant filtered through a 0.2 µm membrane (Sartorious). The supernatant (100 µL) was then mixed with 50 µL of artificial cells. LBS was used as a negative control in place of the *V. fischeri* supernatant. Samples were incubated at 30 °C for 4 h, then the artificial cells were collected and loaded into 96 well plates. 0.3% (v/v) Triton X-100 was added to break the vesicles, and 150 µL of the luciferase assay reagent (Promega) was added to the samples. Luminescence was recorded immediately with a plate reader (Tecan).

Artificial sender cells. Dehydrated aliquots of 1:2 POPC:cholesterol vesicles [3,4] were hydrated with 50 µL of S30 T7 High-Yield Protein Expression System supplemented with 2 µg of DNA encoding the corresponding synthase behind a T7 promoter (constructs MC001A, MC002A, MC003A, NY018A, NY019A and JF005A, Table S5). For the production of acyl homoserine lactones, 1 mM *S*-adenosyl-L-methionine and 700 µM acetyl coenzyme A were added. The production of AI-2 required 1 mM *S*-adenosyl-L-homocysteine. For the experiment corresponding to Figure 2A, artificial cells were diluted 1:3 in buffer A (50 mM HEPES, 10 mM $MgCl_2$, 100 mM KCl, pH 7.6) plus 0.7 mg/mL proteinase K. Reactions were incubated at 37 °C for 6 h. In the meantime, the corresponding *E. coli* reporter strain was grown from one colony in LB supplemented with antibiotic until $OD^{600\ nm}$ = 0.5. Bacteria were pelleted, resuspended in fresh LB, and added to artificial cells to a final $OD^{600\ nm}$ = 0.1. Samples were incubated at 37 °C. Aliquots were removed every hour, diluted in PBS, and monitored by flow cytometry with a FACS canto A (BD biosciences). Positive controls contained 0.1 µM of the corresponding quorum molecule. LB was added in place of quorum molecules for the negative control. Parameters for each flow cytometry experiment were: Forward scatter (FSC) signal (Ex.: 488 nm, Type: Area, Voltage: 525); Side scatter (SSC) signal (Ex.: 488 nm, Em.: 488 +/- 10 nm, Type: Area, Width, Voltage: 403)’ Green channel (FITC) signal (Ex.: 488 nm, Em.: 530 +/- 30 nm, Type: Area, Voltage: 600); Threshold parameters (FCS: 200, SSC: 200, Threshold operator: And). For the experiment corresponding to Figure 2B, artificial sender cells were diluted 1:1 with *V. fischeri* MJ11 at OD^{600}=0.2-0.3 and 0.7 mg/mL Proteinase K, 0.07 mg/mL RNase A, and 170 U/mL RNase T1 (Thermo Fisher Scientific) were also added to avoid any residual activity of the S30 reactions outside the artificial cells. Samples were incubated at 30 °C in 96-well plates (Thermo Fischer Scientific, 216305) without shaking. Every hour luminescence was measured with an Infinite M200 plate reader (Tecan). After 3 h of incubation, 5 µL of each sample were serially diluted and 10 µL of the 10^{-5} fold dilution were plated on LBS agar following the “track dilution” method to enumerate the colony forming units (CFU) with one plating per sample per experiment. Pictures from luminescent bacteria colonies were captured in a dark room with an Olympus OM-D EM5 camera and a M-Zuiko ED

12-50 mm 1:3.5-6.3 EZ lens using an exposure of 40 s at F 5 and an ISO of 200. Negative control were liposomes encapsulating the S30 extract without DNA. For the experiment corresponding to Figure 2C, AI-2 was detected with *V. harveyi* BB170, a strain that can naturally sense AI-2 but has been engineered to not sense its own autoinducer *N*-(3-oxobutanoyl)homoserine lactone. The assay was performed as described by Vilchez et al[5]. Briefly, *V. harveyi* was grown overnight from a 200 µL glycerol stock in AB medium supplemented with 50 µg/mL kanamycin at 30 °C, 220 RPM. The day after, bacteria were diluted to $OD^{600\ nm}$ = 0.7 and grown for 1.5 h (to $OD^{600\ nm}$ = 1.1) in AB medium. The culture was then diluted 1:5000 and 90 µL were loaded into a white 96-well plate (Nunc). 10 µL of sample was added to each well. AB medium was used as a blank, and 100 µM of enzymatically produced AI-2 was used as a positive control. AI-2 activity was calculated by dividing the sample value by the blank. Plates were incubated at 30 °C and luminescence was monitored with Infinite M200 plate reader plate reader (Tecan) after 3 h.

Artificial cells that mediate communication with two different cell types. *E. coli* reporter strains were grown to $OD^{600\ nm}$ = 0.5 from one colony in LB supplemented with antibiotic. Bacteria were pelleted and resuspended in fresh LB. Dehydrated aliquots [3] of 1:2 POPC cholesterol vesicles were hydrated with 50 µL *E. coli* S30 extract for circular DNA supplemented with 4 µg of DNA encoding a 3OC6 HSL sensing device and the corresponding synthase (NY016A, RL079A, or RL080A, Table S5). 1 mM of *S*-adenosyl-L-methionine and 700 µM of acetyl coenzyme A were added for the synthesis of acyl homoserine lactones and 1 mM of SAH for the production of AI-2. When commercial 3OC6 HSL was used, 1 µM of 3OC6 HSL was added to 50 µL of artificial cells mixed with 50 µL of the corresponding *E. coli* reporter strain at a final $OD^{600\ nm}$ = 0.1. 0.7 mg/ mL of proteinase K were added, and the samples were incubated at 37 °C. Aliquots were collected after every hour, diluted in PBS, and monitored by flow cytometry. When the presence of *V. fischeri* 7744 was sensed, bacteria were grown at 28 °C in LBS supplemented with ampicillin until OD^{600} = 1.2. Cells were harvested and the supernatant mixed with 50 µL of artificial cells and 50 µL of the *E. coli* reporter strain. Samples were incubated at 37 °C. Aliquots were collected each hour, diluted in PBS, and monitored by flow cytometry. Positive controls contained 0.1 mM of 3OC12 HSL. Negative controls were in the absence of supplemental quorum molecules or *V. fischeri* supernatant. Unspecific fluorescence was determined by adding the supernatant of *V. fischeri* to the *E. coli* reporter strain. Samples collected at 6 h were analyzed with BD FACSDiva software. For AI-2 synthesis, samples were mixed with *V. harveyi* BB170, following the protocol described above for the *V. harveyi* bioluminescence assay.

Quorum quenching. Dehydrated aliquots of 1:2 POPC:cholesterol vesicles [3] were hydrated with 50 µL of S30 *E. coli* extract supplemented with 4 µg of DNA encoding AiiA behind a tet promoter or a 3OC6-C8 HSL responsive-AiiA production device. 1 U of DNaseI (Thermo Fisher Scientific), 0.07 mg/mL RNaseA, and 170 U/mL of RNase T1 (Thermo Fisher Scientific) were added to the extravesicular solution to remove any residual activity of the S30 *E. coli* extract outside of the artificial cells. When necessary, 1 µM of 3OC6 HSL and 1 µM of C8 HSL or an aliquot of a *V. fischeri* culture at $OD^{600\text{ nm}}$ = 0.2 were added to the outside of the vesicles. Reactions were incubated at 37 °C for 4 h. *P. aeruginosa* was grown from 200 µL of a glycerol stock in LB until $OD^{600\text{ nm}}$ = 0.3 and added to artificial cells in a 1:1 ratio. After 2 h of incubation at 37 °C at 220 RPM, cells were harvested and the supernatants mixed 1:20 with the 3OC12 HSL *E. coli* sensor strain. Samples were incubated at 37 °C. 2 µL were collected every hour, diluted 1:100 in PBS, and monitored by flow cytometry. Controls were performed by adding to the reporter strain a culture of *P. aeruginosa* grown in LB and with *V. fischeri* supernatant to monitor unspecific interaction. The positive control was the addition of 0.1 µM 3OC12 HSL to the *E. coli* reporter strain. Negative controls included samples without added quorum molecules. Samples were collected at 2 h and analyzed with BD FACSDiva software. The population distribution was analyzed and plotted with FlowJo software.

Cellular Turing test. Dehydrated aliquots of 1:2 POPC:cholesterol vesicles[3] were hydrated with 50 µL S30 *E. coli* extract for circular DNA template (Promega) supplemented with 4 µg of DNA, 1 mM *S*-adenosyl-L-methionine, and 700 µM acetyl coenzyme A. 200 µL glycerol stock of exponential phase *V. fischeri* MJ11 were grown in 5 mL of LBS (30 °C, 145 rpm) until $OD^{600\ nm}$ = 0.2-0.3. Cells were undiluted or mixed in a 1:1 ratio with either functional artificial cells encapsulating DNA plasmids (RL078A, NY009A, NY013A, or NY014A) coding for the different versions of *luxR* and the *luxI* or nonfunctional artificial cells containing DNA plasmid (RL081A) coding for *luxR* and T7 RNA polymerase. Extravesicle solutions contained 0.7 mg/mL Proteinase K, 0.07 mg/mL RNase A, and 170 U/mL RNase T1 (Thermo Fisher Scientific) to avoid any residual activity of the S30 *E. coli* extract outside of the artificial cells. Samples were incubated at 30 °C in 96-well plates (Thermo Fischer Scientific, 216305) without shaking. Every hour luminescence was measured with an Infinite M200 plate reader (Tecan). After 3 h of incubation, 5 µL of each sample were serially diluted and 10 µL of the 10^{-5} fold dilution were plated on LBS agar following the "track dilution" method to enumerate the colony forming units (CFU)[6] with one plating per sample per experiment. Pictures from luminescent bacteria colonies were captured in a dark room with an Olympus OM-D EM5 camera and a M-Zuiko ED 12-50 mm 1:3.5-6.3 EZ lens using an exposure of 40 s at F 5 and an ISO of 200. Noise reduction and an exposure setting of +1.0 EV were applied on the JPEG image files in Adobe Photoshop lightroom CC 2016 prior the cell counting. A crop of one of the resulting images is shown in (Figure S10). Single colonies were then counted manually. Subsequently, the rest of the samples were collected for RNA extraction. Total RNA was isolated with the GeneJET RNA Purification Kit (Thermo Fischer Scientific), and 500 ng of RNA was retro transcribed using the RevertAid Reverse Transcriptase kit (Thermo Fischer Scientific). 5 ng of cDNA was mixed with the iQ SYBR Green supermix (Bio-Rad) and supplemented with the appropriate primers. 10 µL reactions were loaded in 96-well plates (HSP9655 Bio-Rad), and the cDNA was quantified with a CFX96 Touch real-time PCR (Bio-Rad) with SYBR green detection. The real-time PCR run protocol was one initial cycle of denaturation at 95 °C for 3 min followed by 40 cycles of denaturation (95 °C, 10 s) and annealing + extension (60 °C, 30 s) followed by one melt curve cycle (55-95 °C with 0.5 °C, 40 s). The primers to quantify the gene expression of *luxA* and *luxB* were luxA FW: 5'-cagagtttggtcttacgggaaat-3' (150 nM), luxA REV: 5'-gggtgtgctgtcggaataac-3' (150 nM), luxB FW: 5'-attaccacccatcaccctgt-3' (250 nM), luxB REV: 5'-gtcactaaaaccaagaatgaagcg-3' (250 nM). Gene expression was normalized to the expression of the malate dehydrogenase (mdh) housekeeping gene that was amplified with the following primers mdh FW: 5'-cactctggtgttactatcttacctct-3' and mdh REV: 5'-acttctgttcccgcattttgg-3' (300 nM). Primers were designed with Primer3 software.

For RNA-seq analysis, total RNA was treated with DNase (RapidOut DNA Removal kit, Thermoscientific) prior to RNA quantification with a spectrofluorometric detection method using the Quantum-iT RiboGreen RNA assay kit (Life-Technologies). Library preparation and sequencing were performed at Edinburgh Genomics (Ashworth laboratories, University of Edinburgh). Briefly, libraries were prepared using the TruSeq stranded total RNA-seq kit (Illumina) and the depletion of ribosomal RNAs was accomplished with the RiboZero rRNA removal kit for Gram negative bacteria (Illumina). Libraries were then sequenced on one lane of an Illumina HiSeq2500 in high output mode with v4 chemistry to a length of 125 base paired end. The quality of the raw sequence data was assessed with FastQC1[7]. The average number of reads were 10,397,486, 11,006,173, and 11,077,471 for samples containing functional artificial cells, nonfunctional artificial cells, and no artificial cells, respectively. Reads in FASTQ format were mapped to the *V. fischeri* MJ11 genome reference sequence using bowtie [8]. Transcripts were assembled with cufflink and cuffmerge and the quantification of isoforms was with cuffdiff [9–11]. The sample size for the RNA-seq experiments was chosen based on the average number of reads per sample (10M), read length (200bp), preliminary results, and prior reports[12] showing an effect size of at least two for *lux* operon gene expression from activation by quorum sensing. Therefore, to ensure a statistical power of at least 0.8 at a significance level of 0.05 for a standard two-tailed t-test, the sample size was set to six. Differences in the mean between groups were assessed using an unpaired two-tailed standard t-test. Standard deviations are shown in the bar plots as a measure of variability. RNA-seq differentially expressed genes are determined by cufflinks/cuffdiff after *p* value adjustment for multiple comparisons using FDR (False Discovery Rate). The functional and clusterization analysis for the three sets of differently expressed coding sequences was with DAVID [13]. The Benjamini test threshold was set to 10^{-2}**.**

SUPPORTING FIGURES

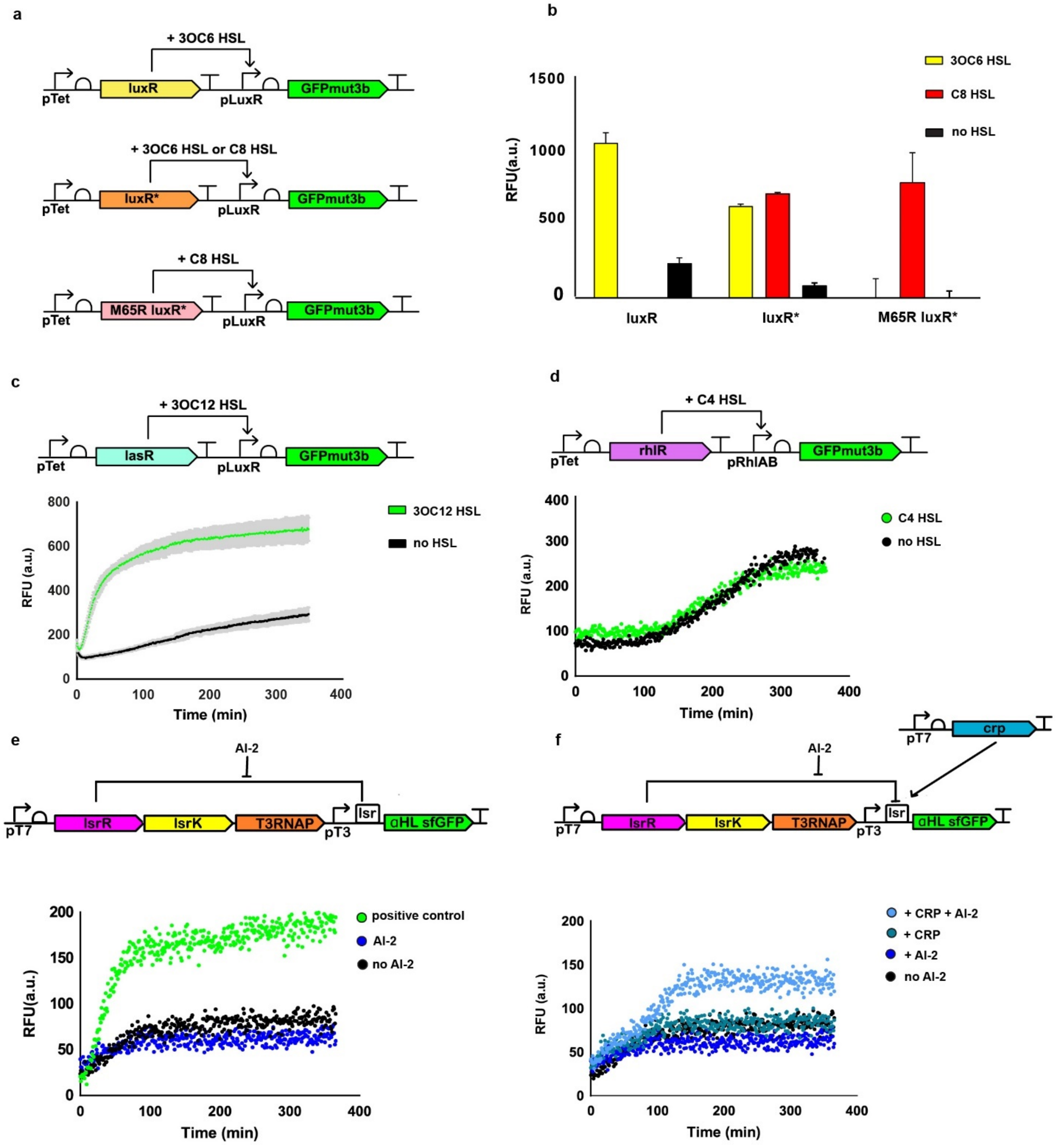

Figure S1. ***In vitro* sensing of quorum molecules.** (a) A schematic illustration of the genetic constructs for the sensing of 3OC6 HSL, 3OC6 HSL and C8 HSL, and C8 HSL is illustrated. (b) LuxR controlled *in vitro* expression of GFP was monitored by fluorescence spectroscopy for the genetic constructs shown in panel a (*n*=3 biological replicates, mean ± s.d.). (c) DNA encoding *lasR* for the sensing of 3OC12 HSL controlled the expression of GFP (*n*=3 biological replicates, mean ± s.d.). (d) The C4 HSL responsive, *rhlI* encoding construct was expressed *in vitro* (*n*=2 technical replicates). (e) The genetic circuit for sensing AI-2 was expressed with the PURE system (*n*=2 technical replicates). (f) CRP was added to the AI-2 sensing genetic circuit (*n*=2 technical replicates). RFU (Relative Fluorescence Units).

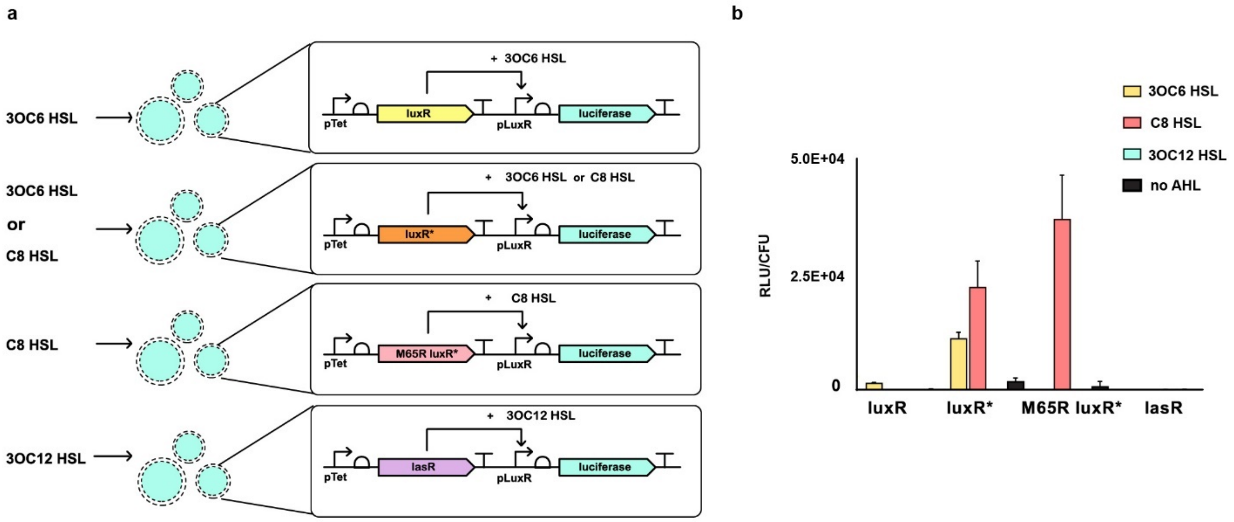

Figure S2. Artificial cells sense quorum molecules. Artificial cells carrying genetic constructs for the sensing of quorum molecules (a) were incubated with the corresponding HSL and monitored by luminescence (b) (*n*=3 technical replicates, mean ± s.d.). RLU/CFU (Relative luminescence Units/ Colony Forming Units per milliliter).

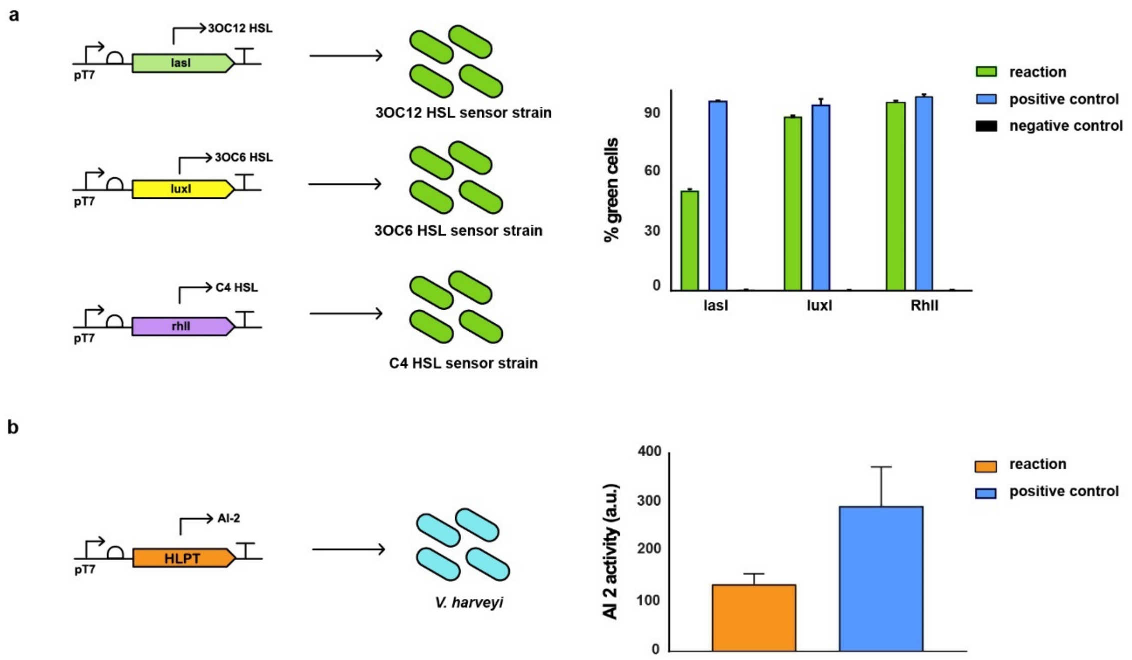

Figure S3. ***In vitro* production of quorum sensing molecules.** (a) Genetic constructs for the synthesis of 3OC12 HSL, 3OC6 HSL, and C4 HSL were expressed *in vitro*. After 6 h, samples were incubated with *E. coli* sensor strains and quantified by flow cytometry (*n*=3 technical replicates, mean ± s.d.). (b) Genetic constructs expressing the AI-2 synthesizing, HLPT fusion protein[1] were expressed *in vitro*. After 6 h, samples were incubated with *V. harveyi* BB170 and the luminescence (referred to as AI-2 activity) was measured. Samples were normalized against reactions without a DNA template (*n*=3 technical replicates, mean ± s.d.).

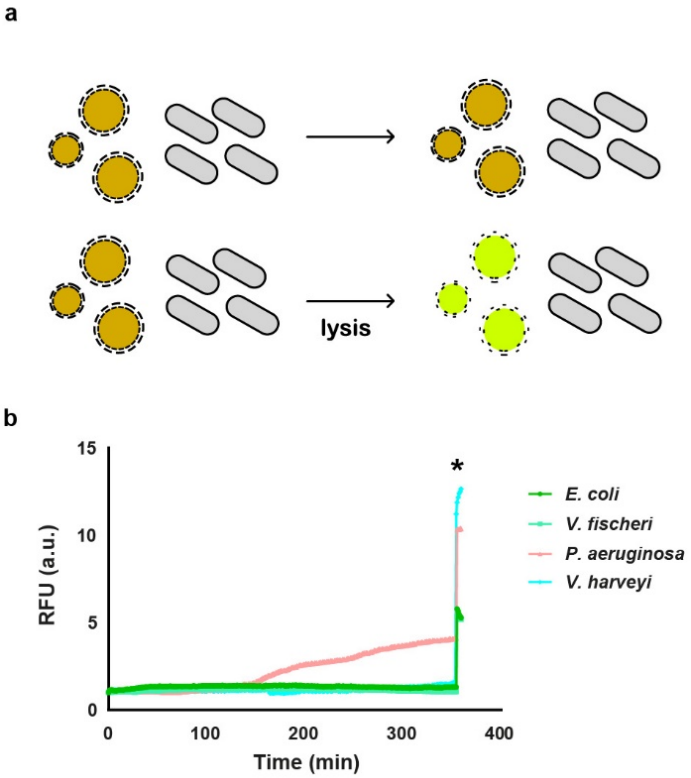

Figure S4. Artificial cell leakage assay. (a) Artificial cells supplemented with the self-quenching fluorophore calcein were incubated with different bacteria and monitored by fluorescence spectroscopy for 6 h. (b) *E. coli, V. fischeri, and V. harveyi* did not degrade the artificial cells under the same test conditions used for the chemical communication experiments, whereas the presence of *P. aeruginosa* compromised the integrity of the membrane. * indicates the addition of 0.3% (v/v) Triton X-100. RFU (Relative Fluorescence Units).

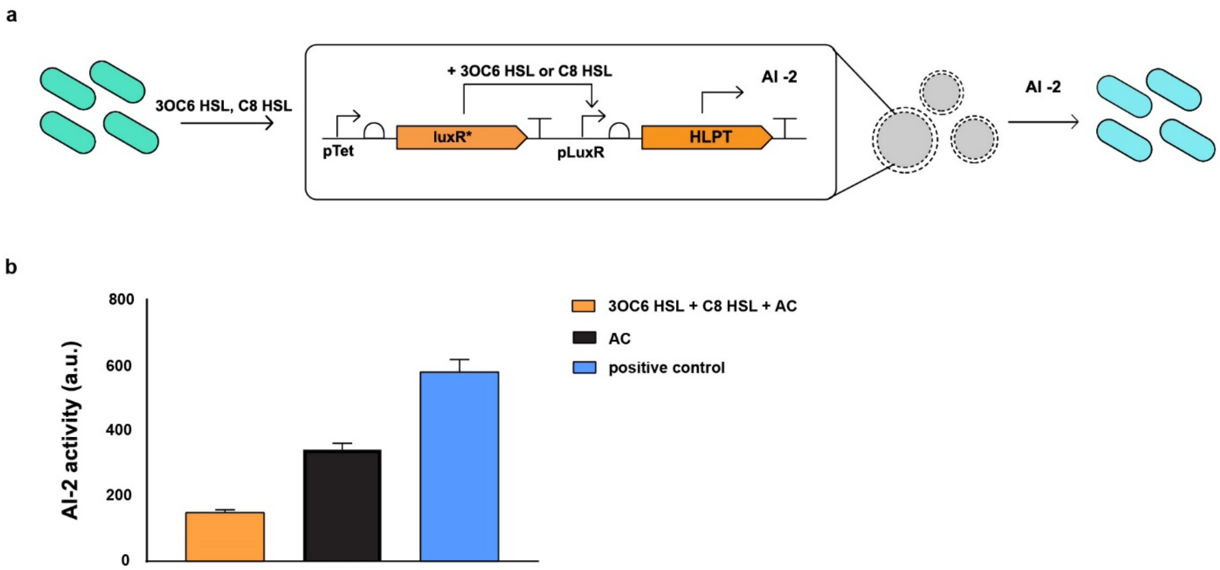

Figure S5. Artificial cells failed to produce AI-2 in response to quorum sensing molecules. (a) Artificial cells carrying a genetic construct to produce AI-2 in response to 3OC6 HSL and C8 HSL were incubated at 30 °C for 6 h. (b) Artificial cells were then mixed with *V. harveyi* BB170 and luminescence was monitored after 3 h (n=3 technical replicates, mean ± s.d.).

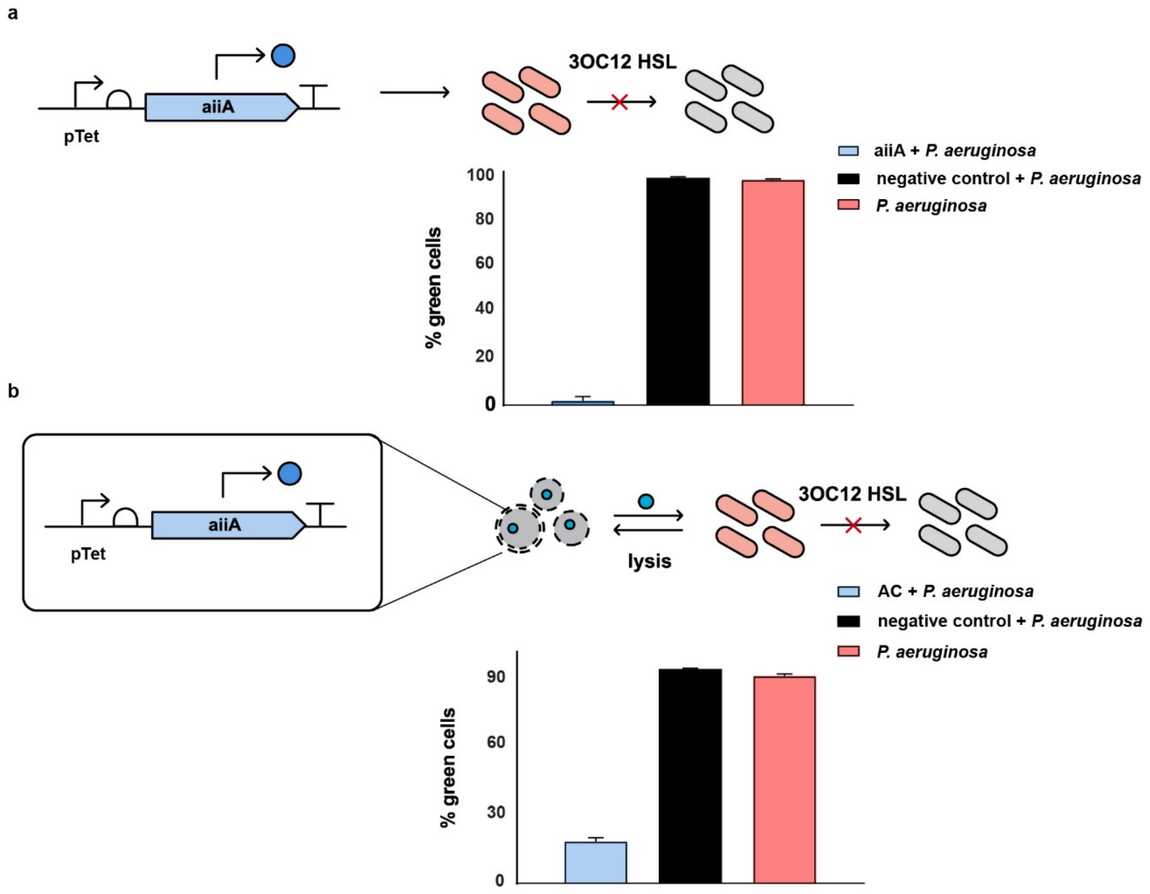

Figure S6. Artificial cells quench *P. aeruginosa* quorum sensing. (a) *In vitro* expressed AiiA was sufficient to degrade the 3OC12 HSL released by *P. aeruginosa.* 3OC12 HSL levels were assessed by flow cytometry of an *E. coli* reporter strain (*n*=3 technical replicates, mean ± s.d.). (b) Artificial cells carrying the same construct in panel a were capable of degrading *P. aeruginosa* secreted 3OC12 HSL (*n*=3 biological replicates, mean ± s.d.).

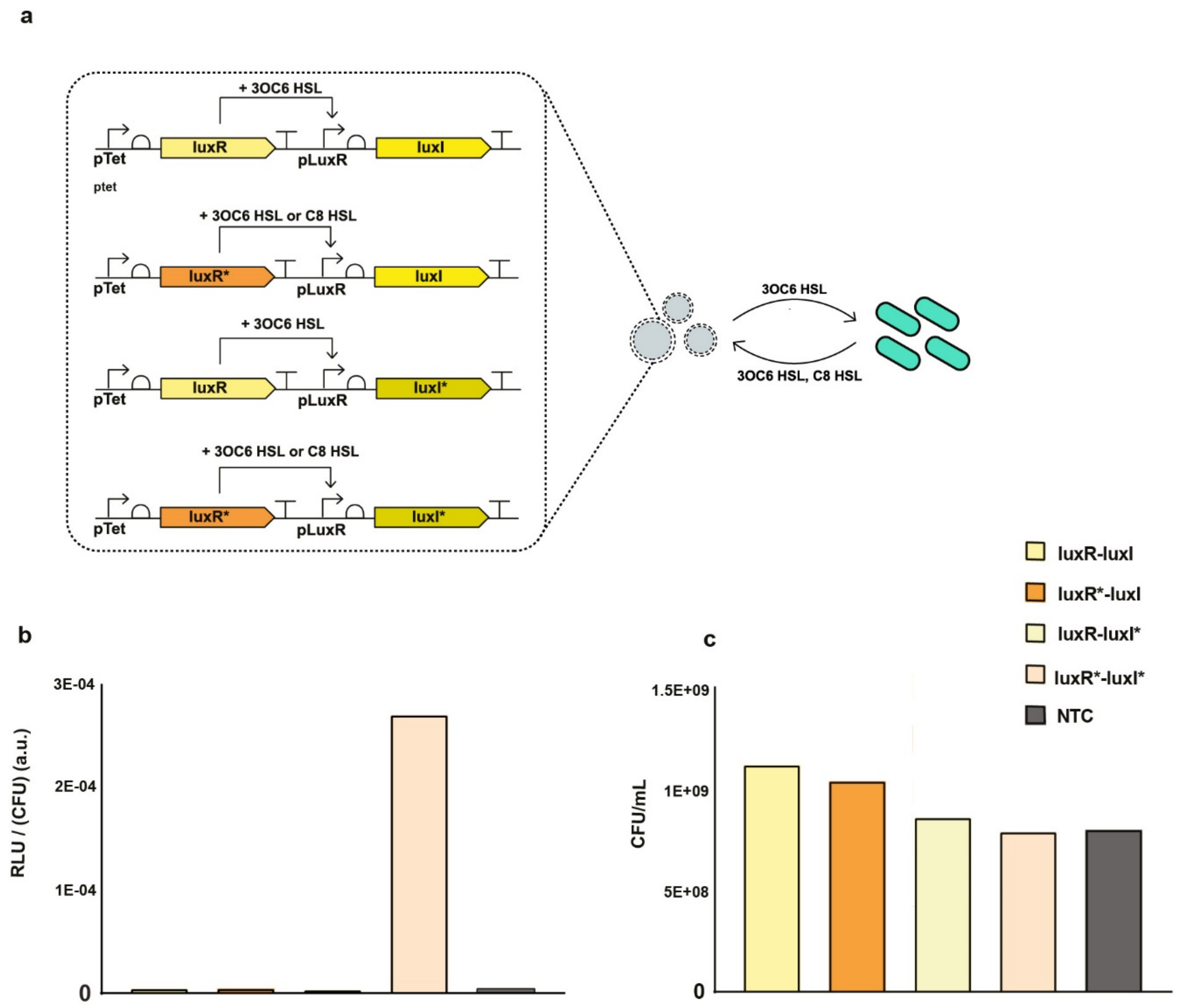

Figure S7. Screening of genetic constructs for the cellular Turing test. (a) A schematic illustration of the four genetic constructs tested for their ability to sense and produce 3OC6 HSL. (b) Luminescence data were acquired after 3 h of incubation of artificial cells with *V. fischeri* (*n*=1). (c) The number of viable cells per sample was determined by measuring the colony forming units (*n*=1). RLU/CFU (Relative Luminescence Units/Colony Forming Units per mililiter), CFU/mL (Colony Forming Units per mililiter).

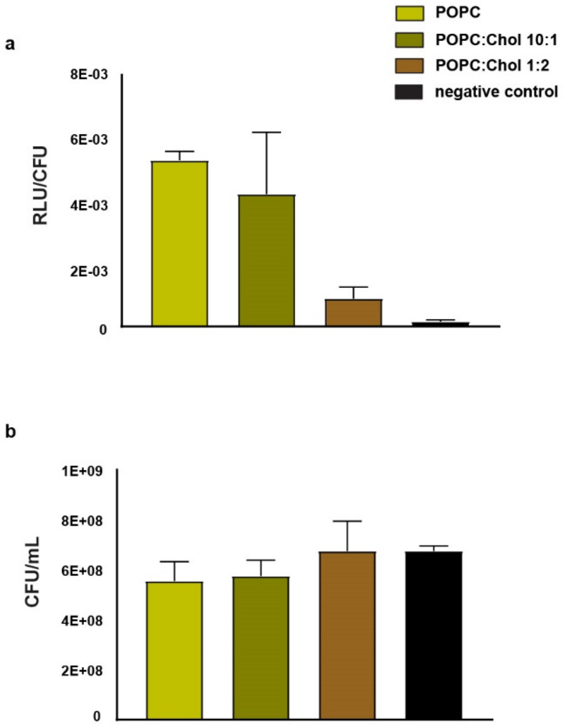

Figure S8. Influence of cholesterol on chemical communication. Artificial cells with different membrane compositions (POPC, 10:1 POPC:cholesterol, 1:2 POPC:cholesterol) containing DNA encoding LuxR* and LuxI* (NY013A) was incubated with *V. fischeri*. (a) The luminescent response per single cell of *V. fischeri* after 3 h showed a clear dependence on the concentration of cholesterol. (b) The number of viable *V. fischeri* cells per sample was determined by measuring the colony forming units. The negative control was an unencapsulated S30 reaction containing the same DNA and necessary components for transcription-translation. RLU/CFU (Relative Luminescence Units/Colony Forming Units per mililiter), CFU/mL (Colony Forming Units per mililiter).

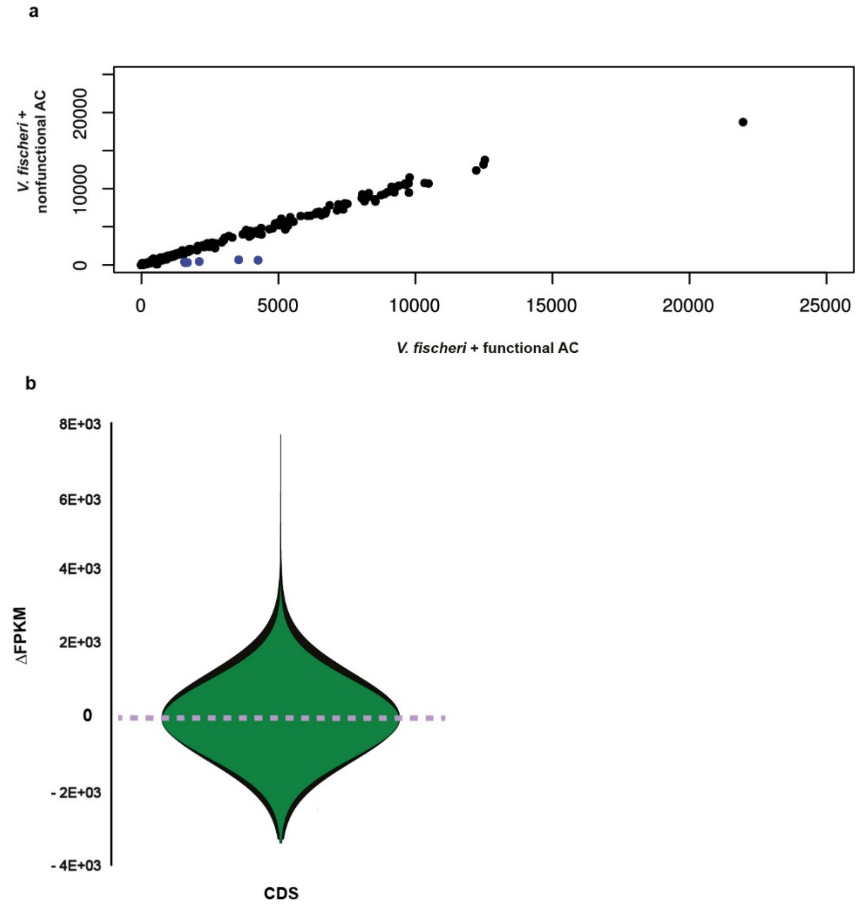

Figure S9. RNA sequencing data. (a) The correlation of *V. fischeri* gene expression in response to nonfunctional and functional artificial cells was highly correlated, r=0.99. Blue dots depict the genes falling off the correlation trend, including six out of the seven genes of the *lux* operon. (b) Distribution of the difference in FPKM per coding sequence between *V. fischeri*–*V. fischeri* with *V. fischeri*–functional artificial cells (green) and *V. fischeri*–*V. fischeri* with *V. fischeri*–nonfunctional artificial cells (black). FPKM (fragments per kilobase of transcript per million mapped reads), CDS (Coding DNA Sequences).

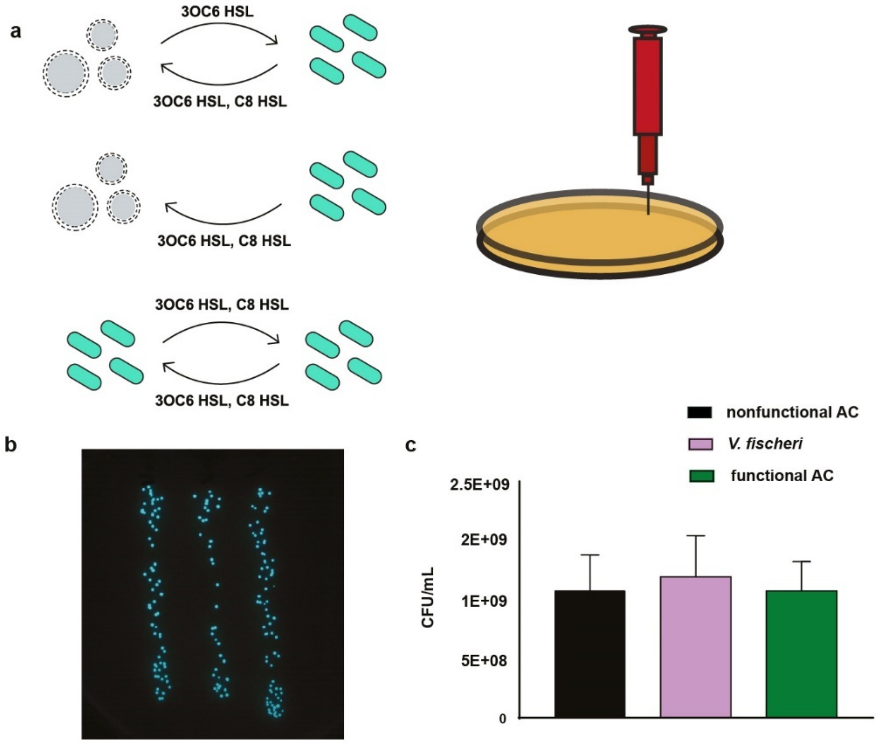

Figure S10. Determining the viable *V. fischeri* count for the cellular Turing test experiments. (a) A schematic illustration of the samples used for CFU enumeration. The number of cells was determined by track dilution with one plating per sample per experiment. (b) A representative picture of a plated sample of bacterial colonies used to calculate CFU. (c) No significant differences in number of viable cells were observed among the samples. (*n*=6 biological replicates, mean ± s.d.). CFU/mL (Colony Forming Units per milliliter).

SUPPORTING TABLES

Table S1. Enrichment analysis of the 81 differently expressed coding sequences that were commonly found for *V. fischeri* + functional artificial cells and *V. fischeri* + nonfunctional artificial cells with respect to *V. fischeri + V. fischeri*. Highlighted in grey are the significantly enriched ten gene sets with *FDR* $<10^{-2}$.

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006525~arginine metabolic process	8	10	3.3E-09	5096830, 5094984, 5098318, 5095180, 5093155, 5097146, 5095530, 5098218	46	17	2757	28.2	4.92E-07	4.92E-07	3.91E-06
GOTERM_BP_FAT	GO:0000103~sulfate assimilation	6	7.5	4.99E-08	5096365, 5094445, 5099740, 5100074, 5099138, 5096397	46	8	2757	44.95	7.48E-06	3.74E-06	5.96E-05
KEGG_PATHWAY	vfm00920:Sulfur metabolism	7	8.75	3.251E-07	5096365, 5094445, 5096432, 5099740, 5100074, 5099138, 5096397	40	14	1634	20.43	1.69E-05	1.69E-05	3.16E-04
SP_PIR_KEYWORDS	amino-acid biosynthesis	9	11.25	7.588E-07	5099805, 5096830, 5098318, 5097146, 5096432, 5095530, 5098218, 5099138, 5096397	80	68	7033	11.64	4.25E-05	4.25E-05	7.49E-04
KEGG_PATHWAY	vfi00330: Arginine and proline metabolism	9	11.25	9.292E-07	5096830, 5094984, 5098318, 5095180, 5093155, 5097146, 5095995, 5095530, 5098218	40	36	1634	10.21	4.83E-05	2.42E-05	9.03E-04
SP_PIR_KEYWORDS	arginine biosynthesis	5	6.25	1.781E-06	5096830, 5098318, 5097146, 5095530, 5098218	80	9	7033	48.84	9.97E-05	4.99E-05	1.76E-03
KEGG_PATHWAY	vfm00330:Arginine and proline metabolism	9	11.25	1.794E-06	5096830, 5094984, 5098318, 5095180, 5093155, 5097146, 5095995, 5095530, 5098218	40	39	1634	9.43	9.33E-05	3.11E-05	1.74E-03
GOTERM_BP_FAT	GO:0009064~glutamine family amino acid metabolic process	8	10	3.955E-06	5096830, 5094984, 5098318, 5095180, 5093155, 5097146, 5095530, 5098218	46	43	2757	11.15	5.93E-04	1.98E-04	4.72E-03
GOTERM_BP	GO:00065	5	6.25	4.139E-06	5096830,	46	8	2757	37.46	6.21E-04	1.55E-04	4.94E-03

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
_FAT	26~arginine biosynthetic process				5098318, 5097146, 5095530, 5098218							
GOTERM_BP_FAT	GO:0006790~sulfur metabolic process	8	10	2.73E-05	5099805, 5096365, 5094445, 5096432, 5099740, 5100074, 5099138, 5096397	46	57	2757	8.41	4.09E-03	8.20E-04	3.26E-02
GOTERM_BP_FAT	GO:0008652~cellular amino acid biosynthetic process	10	12.5	4.90E-05	5099805, 5096830, 5098318, 5094445, 5097146, 5096432, 5095530, 5098218, 5099138, 5096397	46	110	2757	5.45	7.33E-03	1.22E-03	5.85E-02
GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	10	12.5	6.08E-05	5099805, 5096830, 5098318, 5094445, 5097146, 5096432, 5095530, 5098218, 5099138, 5096397	46	113	2757	5.3	9.07E-03	1.30E-03	7.25E-02
SP_PIR_KEYWORDS	oxidoreductase	13	16.25	1.11E-04	5099805, 5094200, 5100277, 5095180, 5094467, 5099138, 5097770, 5096140, 5098116, 5094445, 5095530, 5096397, 5093448	80	299	7033	3.82	6.18E-03	2.07E-03	1.09E-01
KEGG_PATHWAY	vfm00020:Citrate cycle (TCA cycle)	6	7.5	1.17E-04	5094200, 5093157, 5100277, 5097920, 5096543, 5096140	40	22	1634	11.14	6.05E-03	1.52E-03	1.13E-01
GOTERM_BP_FAT	GO:0009084~glutamine family amino acid biosynthetic process	5	6.25	1.26E-04	5096830, 5098318, 5097146, 5095530, 5098218	46	17	2757	17.63	1.88E-02	2.37E-03	1.51E-01
GOTERM_BP_FAT	GO:0019344~cysteine biosynthetic process	4	5	2.15E-04	5094445, 5096432, 5099138, 5096397	46	8	2757	29.97	3.17E-02	3.58E-03	2.56E-01

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	vfi00920: Sulfur metabolism	5	6.25	2.34E-04	5094445, 5096432, 5099740, 5100074, 5096397	40	14	1634	14.59	1.21E-02	2.43E-03	2.27E-01
GOTERM_BP_FAT	GO:0000097~sulfur amino acid biosynthetic process	5	6.25	3.03E-04	5099805, 5094445, 5096432, 5099138, 5096397	46	21	2757	14.27	4.44E-02	4.53E-03	3.61E-01
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	10	12.5	3.58E-04	5099805, 5096830, 5098318, 5094445, 5097146, 5096432, 5095530, 5098218, 5099138, 5096397	46	142	2757	4.22	5.22E-02	4.87E-03	4.26E-01
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	10	12.5	3.77E-04	5099805, 5096830, 5098318, 5094445, 5097146, 5096432, 5095530, 5098218, 5099138, 5096397	46	143	2757	4.19	5.50E-02	4.70E-03	4.49E-01
GOTERM_BP_FAT	GO:0000096~sulfur amino acid metabolic process	5	6.25	4.38E-04	5099805, 5094445, 5096432, 5099138, 5096397	46	23	2757	13.03	6.35E-02	5.04E-03	5.21E-01
GOTERM_BP_FAT	GO:0006534~cysteine metabolic process	4	5	4.50E-04	5094445, 5096432, 5099138, 5096397	46	10	2757	23.97	6.53E-02	4.81E-03	5.36E-01
GOTERM_BP_FAT	GO:0009070~serine family amino acid biosynthetic process	4	5	8.07E-04	5094445, 5096432, 5099138, 5096397	46	12	2757	19.98	1.14E-01	8.04E-03	9.59E-01
KEGG_PATHWAY	vfm00650:Butanoate metabolism	5	6.25	8.31E-04	5099833, 5094200, 5100277, 5097920, 5096543	40	19	1634	10.75	4.23E-02	7.18E-03	8.05E-01
KEGG_PATHWAY	vfm00620:Pyruvate metabolism	6	7.5	1.31E-03	5099833, 5093157, 5100277, 5098542, 5093596, 5096140	40	36	1634	6.81	6.57E-02	9.66E-03	1.26E+00
SP_PIR_KEYWORDS	Cysteine biosynthesis	3	3.75	1.82E-03	5096432, 5099138, 5096397	80	6	7033	43.96	9.67E-02	2.51E-02	1.78E+00
GOTERM_BP	GO:00551	14	17.5	2.07E-03	5099805,	46	338	2757	2.48	2.67E-01	1.92E-02	2.45E+00

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
_FAT	14~oxidation reduction				5094200, 5100277, 5095180, 5094467, 5099138, 5097770, 5094788, 5098116, 5094445, 5094744, 5095530, 5096397, 5093448							
KEGG_PATHWAY	vfm00450:Selenoamino acid metabolism	4	5	2.38E-03	5096365, 5096432, 5099740, 5100074	40	12	1634	13.62	1.17E-01	1.54E-02	2.29E+00
GOTERM_BP_FAT	GO:0009069~serine family amino acid metabolic process	4	5	4.40E-03	5094445, 5096432, 5099138, 5096397	46	21	2757	11.42	4.84E-01	3.82E-02	5.13E+00
KEGG_PATHWAY	vfm00010:Glycolysis / Gluconeogenesis	5	6.25	4.86E-03	5093157, 5100277, 5098542, 5093596, 5096140	40	30	1634	6.81	2.24E-01	2.78E-02	4.62E+00
KEGG_PATHWAY	vfm00230:Purine metabolism	7	8.75	6.97E-03	5093686, 5096365, 5099740, 5098542, 5100074, 5095995, 5099174	40	74	1634	3.86	3.05E-01	3.57E-02	6.57E+00
GOTERM_BP_FAT	GO:0044272~sulfur compound biosynthetic process	5	6.25	7.14E-03	5099805, 5094445, 5096432, 5099138, 5096397	46	48	2757	6.24	6.59E-01	5.80E-02	8.20E+00
SP_PIR_KEYWORDS	heme	3	3.75	8.97E-03	5094788, 5096397, 5093448	80	13	7033	20.29	3.96E-01	9.60E-02	8.51E+00
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	11	13.75	9.37E-03	5093686, 5099805, 5096830, 5098318, 5094445, 5097146, 5096432, 5095530, 5098218, 5099138, 5096397	46	268	2757	2.46	7.56E-01	7.16E-02	1.06E+01
SMART	SM00116:CBS	3	3.75	1.03E-02	5099786, 5098938, 5096473	7	31	1123	15.53	6.04E-02	6.04E-02	4.85E+00
GOTERM_MF_FAT	GO:0048037~cofactor binding	9	11.25	1.55E-02	5094984, 5098116, 5094200,	48	224	3173	2.66	8.96E-01	8.96E-01	1.69E+01

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
					5093157, 5096432, 5095530, 5099138, 5096397, 5096140							
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	6	7.5	1.72E-02	5094788, 5094200, 5093157, 5099257, 5098542, 5099138	46	94	2757	3.83	9.26E-01	1.22E-01	1.87E+01
SP_PIR_KEYWORDS	Acyltransferase	5	6.25	1.96E-02	5096830, 5099833, 5093157, 5093155, 5097146	80	92	7033	4.78	6.69E-01	1.68E-01	1.77E+01
KEGG_PATHWAY	vfm00250:Alanine, aspartate and glutamate metabolism	4	5	2.24E-02	5096830, 5098318, 5099257, 5093650	40	26	1634	6.28	6.92E-01	1.01E-01	1.97E+01
KEGG_PATHWAY	vfm00190:Oxidative phosphorylation	4	5	2.48E-02	5094788, 5094200, 5097920, 5096543	40	27	1634	6.05	7.28E-01	1.03E-01	2.16E+01
KEGG_PATHWAY	vfm00632:Benzoate degradation via CoA ligation	3	3.75	2.67E-02	5094200, 5097920, 5096543	40	11	1634	11.14	7.55E-01	1.02E-01	2.31E+01
KEGG_PATHWAY	vfi00250:Alanine, aspartate and glutamate metabolism	4	5	2.73E-02	5096830, 5098318, 5099257, 5093650	40	28	1634	5.84	7.63E-01	9.76E-02	2.36E+01
GOTERM_MF_FAT	GO:0050662~coenzyme binding	7	8.75	2.89E-02	5098116, 5094200, 5093157, 5095530, 5099138, 5096397, 5096140	48	160	3173	2.89	9.86E-01	8.81E-01	2.94E+01
SP_PIR_KEYWORDS	nadp	3	3.75	2.93E-02	5095530, 5099138, 5096397	80	24	7033	10.99	8.11E-01	2.12E-01	2.55E+01
GOTERM_MF_FAT	GO:0016407~acetyltransferase activity	5	6.25	2.94E-02	5096114, 5096830, 5099833, 5093157, 5097146	48	80	3173	4.13	9.87E-01	7.64E-01	2.98E+01
GOTERM_MF_FAT	GO:0016667~oxidoreductase activity, acting on	4	5	3.13E-02	5094445, 5094467, 5099138, 5096397	48	47	3173	5.63	9.90E-01	6.85E-01	3.15E+01

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
	sulfur group of donors											
GOTERM_MF_FAT	GO:0009055~electron carrier activity	7	8.75	3.22E-02	5094788, 5094200, 5094467, 5094744, 5099138, 5096397, 5096140	48	164	3173	2.82	9.91E-01	6.12E-01	3.22E+01
SP_PIR_KEYWORDS	pyruvate	3	3.75	3.40E-02	5093157, 5100277, 5098542	80	26	7033	10.14	8.56E-01	2.15E-01	2.89E+01
GOTERM_MF_FAT	GO:0016209~antioxidant activity	3	3.75	3.44E-02	5094467, 5093448, 5097770	48	20	3173	9.92	9.94E-01	5.71E-01	3.40E+01
GOTERM_BP_FAT	GO:0009310~amine catabolic process	3	3.75	3.74E-02	5095180, 5093155, 5097935	46	19	2757	9.46	9.97E-01	2.38E-01	3.65E+01
GOTERM_BP_FAT	GO:0009063~cellular amino acid catabolic process	3	3.75	3.74E-02	5095180, 5093155, 5097935	46	19	2757	9.46	9.97E-01	2.38E-01	3.65E+01
INTERPRO	IPR002500:Phosphoadenosine phosphosulphate reductase	2	2.5	3.75E-02	5096365, 5094445	71	3	5525	51.88	9.99E-01	9.99E-01	3.76E+01
INTERPRO	IPR000362:Fumarate lyase	2	2.5	3.75E-02	5096830, 5099257	71	3	5525	51.88	9.99E-01	9.99E-01	3.76E+01
SP_PIR_KEYWORDS	transferase	15	18.75	4.32E-02	5096114, 5093157, 5093155, 5097146, 5096432, 5099740, 5097432, 5093686, 5096830, 5099833, 5094984, 5096365, 5098542, 5100074, 5098218	80	763	7033	1.73	9.16E-01	2.40E-01	3.53E+01
GOTERM_MF_FAT	GO:0004783~sulfite reductase (NADPH) activity	2	2.5	4.38E-02	5099138, 5096397	48	3	3173	44.07	9.98E-01	6.05E-01	4.12E+01
GOTERM_MF_FAT	GO:0004779~sulfate adenylyltransferase activity	2	2.5	4.38E-02	5096365, 5100074	48	3	3173	44.07	9.98E-01	6.05E-01	4.12E+01

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0004781~sulfate adenylyltransferase (ATP) activity	2	2.5	4.38E-02	5096365, 5100074	48	3	3173	44.07	9.98E-01	6.05E-01	4.12E+01
COG_ONTOLOGY	Amino acid transport and metabolism / Coenzyme metabolism	2	2.5	4.39E-02	5096365, 5094445	15	4	1257	41.9	3.61E-01	3.61E-01	2.36E+01
UP_SEQ_FEATURE	domain:N-acetyltransferase	2	2.5	4.39E-02	5096830, 5097146	16	2	676	42.25	8.26E-01	8.26E-01	3.35E+01
GOTERM_BP_FAT	GO:0019419~sulfate reduction	2	2.5	4.82E-02	5096365, 5094445	46	3	2757	39.96	9.99E-01	2.86E-01	4.46E+01
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	3	3.75	4.89E-02	5095180, 5093155, 5097935	46	22	2757	8.17	9.99E-01	2.79E-01	4.51E+01
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	3	3.75	4.89E-02	5095180, 5093155, 5097935	46	22	2757	8.17	9.99E-01	2.79E-01	4.51E+01
SP_PIR_KEYWORDS	arginine metabolism	2	2.5	5.49E-02	5095180, 5093155	80	5	7033	35.17	9.58E-01	2.71E-01	4.28E+01
INTERPRO	IPR000644:Cystathionine beta-synthase, core	3	3.75	5.81E-02	5099786, 5098938, 5096473	71	31	5525	7.53	1.00E+00	9.95E-01	5.22E+01
GOTERM_BP_FAT	GO:0009066~aspartate family amino acid metabolic process	3	3.75	7.07E-02	5099805, 5099257, 5093650	46	27	2757	6.66	1.00E+00	3.67E-01	5.83E+01
GOTERM_MF_FAT	GO:0016410~N-acyltransferase activity	4	5	7.55E-02	5096114, 5096830, 5093155, 5097146	48	67	3173	3.95	1.00E+00	7.59E-01	6.06E+01
KEGG_PATHWAY	vfi00450:Selenoamino acid metabolism	3	3.75	8.05E-02	5096432, 5099740, 5100074	40	20	1634	6.13	9.87E-01	2.52E-01	5.58E+01
GOTERM_BP_FAT	GO:0045333~cellular respiration	3	3.75	8.49E-02	5094788, 5094200, 5099257	46	30	2757	5.99	1.00E+00	4.13E-01	6.54E+01

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR000089:Biotin/lipoyl attachment	2	2.5	8.54E-02	5093157, 5095222	71	7	5525	22.23	1.00E+00	9.95E-01	6.67E+01
SMART	SM00421: HTH_LUXR	2	2.5	9.26E-02	5097659, 5097215	7	18	1123	17.83	4.42E-01	2.53E-01	3.72E+01
GOTERM_BP_FAT	GO:0006527~arginine catabolic process	2	2.5	9.41E-02	5095180, 5093155	46	6	2757	19.98	1.00E+00	4.35E-01	6.93E+01

Table S2. Enrichment analysis of the 94 differently expressed coding sequences for *V. fischeri* + nonfunctional artificial cells with respect to *V. fischeri* + *V. fischeri.*

GOTERM_BP_FAT	GO:0006189~'de novo' IMP biosynthetic process	4	4.26	8.40E-05	5097940, 5095472, 5093469, 5098195	47	6	2757	39.11	1.62E-02	1.62E-02	1.05E-01
GOTERM_BP_FAT	GO:0006188~IMP biosynthetic process	4	4.26	2.30E-04	5097940, 5095472, 5093469, 5098195	47	8	2757	29.33	4.36E-02	2.20E-02	2.86E-01
GOTERM_BP_FAT	GO:0046040~IMP metabolic process	4	4.26	2.30E-04	5097940, 5095472, 5093469, 5098195	47	8	2757	29.33	4.36E-02	2.20E-02	2.86E-01
GOTERM_BP_FAT	GO:0009168~purine ribonucleoside monophosphate biosynthetic process	4	4.26	6.53E-04	5097940, 5095472, 5093469, 5098195	47	11	2757	21.33	1.19E-01	4.14E-02	8.12E-01
GOTERM_BP_FAT	GO:0009126~purine nucleoside monophosphate metabolic process	4	4.26	6.53E-04	5097940, 5095472, 5093469, 5098195	47	11	2757	21.33	1.19E-01	4.14E-02	8.12E-01
GOTERM_BP_FAT	GO:0009127~purine nucleoside monophosphate biosynthetic process	4	4.26	6.53E-04	5097940, 5095472, 5093469, 5098195	47	11	2757	21.33	1.19E-01	4.14E-02	8.12E-01
GOTERM_BP_FAT	GO:0009167~purine ribonucleoside monophosphate metabolic process	4	4.26	6.53E-04	5097940, 5095472, 5093469, 5098195	47	11	2757	21.33	1.19E-01	4.14E-02	8.12E-01
GOTERM_BP_FAT	GO:0009161~ribonucleoside monophosphate metabolic process	4	4.26	1.39E-03	5097940, 5095472, 5093469, 5098195	47	14	2757	16.76	2.37E-01	6.53E-02	1.72E+00
GOTERM_BP_FAT	GO:0009156~ribonucleoside monophosphate biosynthetic process	4	4.26	1.39E-03	5097940, 5095472, 5093469, 5098195	47	14	2757	16.76	2.37E-01	6.53E-02	1.72E+00
GOTERM_BP_FAT	GO:0044271~nitrogen compound	12	12.77	3.59E-03	5097940, 5096595, 5099333,	47	268	2757	2.63	5.03E-01	1.30E-01	4.39E+00

	biosynthetic process				5099487, 5097435, 5097146, 5099025, 5095472, 5093469, 5100143, 5098195, 5096166							
KEGG_PATHWAY	vfm00230:Purine metabolism	7	7.45	4.01E-03	5097940, 5099350, 5094638, 5096722, 5095472, 5093469, 5098195	36	74	1634	4.29	2.01E-01	2.01E-01	3.89E+00
GOTERM_BP_FAT	GO:0009124~nucleoside monophosphate biosynthetic process	4	4.26	4.06E-03	5097940, 5095472, 5093469, 5098195	47	20	2757	11.73	5.46E-01	1.23E-01	4.95E+00
GOTERM_BP_FAT	GO:0009123~nucleoside monophosphate metabolic process	4	4.26	5.36E-03	5097940, 5095472, 5093469, 5098195	47	22	2757	10.67	6.48E-01	1.38E-01	6.49E+00
GOTERM_BP_FAT	GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process	6	6.38	7.48E-03	5097940, 5096595, 5095472, 5093469, 5100143, 5098195	47	75	2757	4.69	7.67E-01	1.66E-01	8.94E+00
GOTERM_BP_FAT	GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	6	6.38	7.48E-03	5097940, 5096595, 5095472, 5093469, 5100143, 5098195	47	75	2757	4.69	7.67E-01	1.66E-01	8.94E+00
GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	4	4.26	1.17E-02	5097940, 5095472, 5093469, 5098195	47	29	2757	8.09	8.99E-01	2.25E-01	1.37E+01
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	4	4.26	1.41E-02	5097940, 5095472, 5093469, 5098195	47	31	2757	7.57	9.36E-01	2.41E-01	1.62E+01
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	4	4.26	1.54E-02	5097940, 5095472, 5093469, 5098195	47	32	2757	7.33	9.51E-01	2.39E-01	1.76E+01
SP_PIR_KEYWORDS	cytoplasm	10	10.64	1.59E-02	5099350, 5094741, 5099487, 5093882, 5096673,	94	296	7033	2.53	6.24E-01	6.24E-01	1.49E+01

					5097146, 5094544, 5097559, 5100143, 5098195							
SP_PIR_KEYWORDS	purine biosynthesis	3	3.19	1.62E-02	5097940, 5095472, 5098195	94	15	7033	14.96	6.32E-01	3.93E-01	1.52E+01
GOTERM_BP_FAT	GO:0009259~ribonucleotide metabolic process	4	4.26	1.81E-02	5097940, 5095472, 5093469, 5098195	47	34	2757	6.9	9.71E-01	2.56E-01	2.04E+01
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	5	5.32	1.97E-02	5097940, 5096595, 5095472, 5093469, 5098195	47	63	2757	4.66	9.79E-01	2.57E-01	2.20E+01
KEGG_PATHWAY	vfi00230:Purine metabolism	6	6.38	2.66E-02	5097940, 5099350, 5094638, 5095472, 5093469, 5098195	36	81	1634	3.36	7.79E-01	5.30E-01	2.34E+01
GOTERM_BP_FAT	GO:0006399~tRNA metabolic process	5	5.32	2.92E-02	5093607, 5094741, 5097710, 5096673, 5100143	47	71	2757	4.13	9.97E-01	3.37E-01	3.09E+01
INTERPRO	IPR014729:Rossmann-like alpha/beta/alpha sandwich fold	4	4.26	3.03E-02	5093607, 5096827, 5098671, 5095818	83	46	5525	5.79	9.98E-01	9.98E-01	3.20E+01
GOTERM_BP_FAT	GO:0009264~deoxyribonucleotide catabolic process	2	2.13	3.31E-02	5099350, 5097559	47	2	2757	58.66	9.99E-01	3.53E-01	3.43E+01
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	4	4.26	3.57E-02	5097940, 5095472, 5093469, 5098195	47	44	2757	5.33	9.99E-01	3.57E-01	3.65E+01
GOTERM_MF_FAT	GO:0004638~phosphoribosylaminoimidazole carboxylase activity	2	2.13	4.93E-02	5097940, 5095472	54	3	3173	39.17	9.99E-01	9.99E-01	4.52E+01
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	4	4.26	4.94E-02	5097940, 5095472, 5093469, 5098195	47	50	2757	4.69	1.00E+00	4.39E-01	4.68E+01
SP_PIR_KEYWORDS	amino-acid biosynthesis	4	4.26	6.06E-02	5099333, 5099487, 5097146, 5096166	94	68	7033	4.4	9.78E-01	7.20E-01	4.67E+01
GOTERM_	GO:0034660	5	5.32	7.62E-02	5093607,	47	97	2757	3.02	1.00E+00	5.75E-01	6.28E+01

BP_FAT	~ncRNA metabolic process				5094741, 5097710, 5096673, 5100143							
GOTERM_BP_FAT	GO:0016042~lipid catabolic process	2	2.13	8.07E-02	5097258, 5093882	47	5	2757	23.46	1.00E+00	5.77E-01	6.50E+01
GOTERM_BP_FAT	GO:0009262~deoxyribonucleotide metabolic process	2	2.13	8.07E-02	5099350, 5097559	47	5	2757	23.46	1.00E+00	5.77E-01	6.50E+01
INTERPRO	IPR001150: Formate C-acetyltransferase glycine radical	2	2.13	9.94E-02	5098574, 5098553	83	7	5525	19.02	1.00E+00	1.00E+00	7.31E+01
INTERPRO	IPR003088: Cytochrome c, class I	2	2.13	9.94E-02	5099252, 5100068	83	7	5525	19.02	1.00E+00	1.00E+00	7.31E+01
INTERPRO	IPR019777: Formate C-acetyltransferase glycine radical, conserved site	2	2.13	9.94E-02	5098574, 5098553	83	7	5525	19.02	1.00E+00	1.00E+00	7.31E+01

Table S3. Enrichment analysis of the 26 differently expressed coding sequences for *V. fischeri* + functional artificial cells with respect to *V. fischeri* + *V. fischeri*. Highlighted in grey are the significantly enriched five gene sets with *FDR* <10^{-2}.

GOTERM_MF_FAT	GO:0016151~nickel ion binding	5	19.23	8.9E-08	5100389, 5097037, 5098484, 5100141, 5097212	17	10	3173	93.32	4.63E-06	4.63E-06	8.65E-05
SP_PIR_KEYWORDS	Chaperone	6	23.08	9.64E-08	5100389, 5099958, 5097037, 5098484, 5094048, 5100141	26	34	7033	47.74	3.28E-06	3.28E-06	8.48E-05
GOTERM_MF_FAT	GO:0043167~ion binding	12	46.15	1.142E-06	5098855, 5096094, 5100389, 5097037, 5098484, 5098990, 5095327, 5099644, 5099334, 5099244, 5100141, 5097212	17	459	3173	4.88	5.94E-05	2.97E-05	1.11E-03
GOTERM_MF_FAT	GO:0043169~cation binding	12	46.15	1.142E-06	5098855, 5096094, 5100389, 5097037, 5098484, 5098990, 5095327, 5099644, 5099334, 5099244, 5100141, 5097212	17	459	3173	4.88	5.94E-05	2.97E-05	1.11E-03
SP_PIR_KEYWORDS	cytoplasm	9	34.62	5.18E-06	5100389, 5099958, 5097037, 5098484, 5098990, 5099244, 5094048, 5100141, 5097212	26	296	7033	8.22	1.76E-04	8.80E-05	4.55E-03
GOTERM_MF_FAT	GO:0046872~metal ion binding	11	42.31	7.071E-06	5096094, 5100389, 5097037, 5098484, 5098990, 5095327, 5099644, 5099334, 5099244, 5100141, 5097212	17	430	3173	4.77	3.68E-04	1.23E-04	6.87E-03

GOTERM_MF_FAT	GO:0046914~transition metal ion binding	9	34.62	4.412E-05	5100389, 5097037, 5098484, 5098990, 5095327, 5099644, 5099334, 5100141, 5097212	17	306	3173	5.49	2.29E-03	5.73E-04	4.29E-02
SP_PIR_KEYWORDS	Nickel insertion	3	11.54	1.21E-04	5100389, 5097037, 5100141	26	5	7033	162.3	4.09E-03	1.37E-03	1.06E-01
SP_PIR_KEYWORDS	zinc	4	15.38	3.13E-03	5098990, 5095327, 5099644, 5099334	26	84	7033	12.88	1.01E-01	2.63E-02	2.72E+00
KEGG_PATHWAY	vfm00641:3-Chloroacrylic acid degradation	2	7.69	1.46E-02	5095327, 5099334	9	3	1634	121.04	2.66E-01	2.66E-01	1.08E+01
KEGG_PATHWAY	vfm00624:1- and 2-Methylnaphthalene degradation	2	7.69	1.46E-02	5095327, 5099334	9	3	1634	121.04	2.66E-01	2.66E-01	1.08E+01
GOTERM_BP_FAT	GO:0006457~protein folding	3	11.54	1.55E-02	5099958, 5098484, 5098672	13	45	2757	14.14	6.95E-01	6.95E-01	1.52E+01
GOTERM_BP_FAT	GO:0034308~monohydric alcohol metabolic process	2	7.69	1.73E-02	5095327, 5099334	13	4	2757	106.04	7.35E-01	4.85E-01	1.68E+01
GOTERM_BP_FAT	GO:0019627~urea metabolic process	2	7.69	1.73E-02	5098484, 5097212	13	4	2757	106.04	7.35E-01	4.85E-01	1.68E+01
GOTERM_BP_FAT	GO:0006069~ethanol oxidation	2	7.69	1.73E-02	5095327, 5099334	13	4	2757	106.04	7.35E-01	4.85E-01	1.68E+01
GOTERM_BP_FAT	GO:0006067~ethanol metabolic process	2	7.69	1.73E-02	5095327, 5099334	13	4	2757	106.04	7.35E-01	4.85E-01	1.68E+01
INTERPRO	IPR014183:Alcohol dehydrogenase class III/S-(hydroxymethyl)glutathione dehydrogenase	2	7.69	1.80E-02	5095327, 5099334	26	4	5525	106.25	7.19E-01	7.19E-01	1.71E+01
KEGG_PATHWAY	vfm00980:Metabolism of xenobiotic	2	7.69	1.95E-02	5095327, 5099334	9	4	1634	90.78	3.38E-01	1.86E-01	1.41E+01

	s by cytochrome P450											
GOTERM_MF_FAT	GO:0051903~S-(hydroxymethyl)glutathione dehydrogenase activity	2	7.69	2.00E-02	5095327, 5099334	17	4	3173	93.32	6.51E-01	1.90E-01	1.78E+01
GOTERM_MF_FAT	GO:0008270~zinc ion binding	4	15.38	2.54E-02	5098990, 5095327, 5099644, 5099334	17	130	3173	5.74	7.38E-01	2.00E-01	2.22E+01
GOTERM_MF_FAT	GO:0004022~alcohol dehydrogenase (NAD) activity	2	7.69	2.99E-02	5095327, 5099334	17	6	3173	62.22	7.94E-01	2.02E-01	2.55E+01
INTERPRO	IPR002328:Alcohol dehydrogenase, zinc-containing, conserved site	2	7.69	3.13E-02	5095327, 5099334	26	7	5525	60.71	8.92E-01	6.71E-01	2.80E+01
KEGG_PATHWAY	vfm00350:Tyrosine metabolism	2	7.69	3.38E-02	5095327, 5099334	9	7	1634	51.87	5.15E-01	2.14E-01	2.33E+01
SP_PIR_KEYWORDS	metal-binding	4	15.38	4.09E-02	5098990, 5095327, 5099644, 5099334	26	218	7033	4.96	7.58E-01	2.47E-01	3.07E+01
KEGG_PATHWAY	vfm00680:Methane metabolism	2	7.69	4.80E-02	5095327, 5099334	9	10	1634	36.31	6.44E-01	2.28E-01	3.16E+01
KEGG_PATHWAY	vfm00071:Fatty acid metabolism	2	7.69	5.27E-02	5095327, 5099334	9	11	1634	33.01	6.79E-01	2.03E-01	3.42E+01
INTERPRO	IPR013149:Alcohol dehydrogenase, zinc-binding	2	7.69	5.30E-02	5095327, 5099334	26	12	5525	35.42	9.78E-01	7.19E-01	4.31E+01
INTERPRO	IPR002085:Alcohol dehydrogenase superfamily, zinc-containing	2	7.69	5.30E-02	5095327, 5099334	26	12	5525	35.42	9.78E-01	7.19E-01	4.31E+01
INTERPRO	IPR013154:Alcohol dehydrogenase GroES-	2	7.69	5.30E-02	5095327, 5099334	26	12	5525	35.42	9.78E-01	7.19E-01	4.31E+01

	like											
GOTERM_MF_FAT	GO:0051082~unfolded protein binding	2	7.69	6.85E-02	5099958, 5098484	17	14	3173	26.66	9.75E-01	3.69E-01	4.98E+01
SP_PIR_KEYWORDS	nucleotide-binding	5	19.23	6.96E-02	5096094, 5099958, 5097037, 5099244, 5094048	26	445	7033	3.04	9.14E-01	3.36E-01	4.70E+01
GOTERM_BP_FAT	GO:0006547~histidine metabolic process	2	7.69	8.38E-02	5098990, 5094537	13	20	2757	21.21	9.99E-01	8.91E-01	6.02E+01
GOTERM_BP_FAT	GO:0009075~histidine family amino acid metabolic process	2	7.69	8.38E-02	5098990, 5094537	13	20	2757	21.21	9.99E-01	8.91E-01	6.02E+01

Table S4. Bacterial strains used in this study.

Strain	Plasmid	Use
3OC12 HSL *E. coli* TOP10 reporter	K575024	*E. coli* strain used to sense 3OC12 HSL
3OC12 HSL *E. coli* NEBexpress reporter	K575024	*E. coli* strain used to sense 3OC12 HSL
3OC6 HSL *E. coli* TOP10 reporter	T9002	*E. coli* strain used to sense 3OC6 HSL and leakage experiments
C4 HSL *E. coli* TOP10 reporter	K575037	*E. coli* strain used to sense C4SL
V. fischeri MJ11 (ATCC BAA-1741)		Strain used to perform the cellular Turing test, quorum quenching experiments, to sense 3OC6 HSL, and leakage experiments
V. fischeri 7744 (ATCC 7744)		Strain used to activate artificial cells able to produce 3OC12 HSL
V. harveyi BB170 (ATCC BAA-1117)		Strain used to sense AI-2 and leakage experiments
P. aeruginosa PT5 PAO1 wild-type[14]		Strain used for quorum quenching experiments and leakage experiments

Table S5. DNA sequences used in this study.

NAME	**NOTE**	**SEQUENCE***
JF005A	pT7-RBS-HLPT-T7 term	TAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAG*AAGGAG*ATATACATATG**ATG**CCGTTGTTAGATAGCTTCACAGTCGATCATACCCGGATGGAAGCGCCTGCAGTTCGGGTGGCGAAAACAATGAACACCCCGCATGGCGACGCAATCACCGTGTTCGATCTGCGCTTCTGCGTGCCGAACAAAGAAGTGATGCCAGAAAGAGGGATCCATACCCTGGAGCACCTGTTTGCTGGTTTTATGCGTAACCATCTTAACGGTAATGGTGTAGAGATTATCGATATCTCGCCAATGGGCTGCCGCACCGGTTTTTATATGAGTCTGATTGGTACGCCAGATGAGCAGCGTGTTGCTGATGCCTGGAAAGCGGCAATGGAAGACGTGCTGAAAGTGCAGGATCAGAATCAGATCCCGGAACTGAACGTCTACCAGTGTGGCACTTACCAGATGCACTCGTTGCAGGAAGCGCAGGATATTGCGCGTAGCATTCTGGAACGTGACGTACGCATCAACAGCAACGAAGAACTGGCACTGCCGAAAGAGAAGTTGCAGGAACTGCACATCggccgaaagatccgacctcgagat**ATG**AAAATCGGCATCATTGGTGCAATGGAAGAAGAAGTTACGCTGCTGCGTGACAAAATCGAAAACCGTCAAACTATCAGTCTCGGCGGTTGCGAAATCTATACCGGCCAACTGAATGGAACCGAGGTTGCGCTTCTGAAATCGGGCATCGGTAAAGTCGCTGCGGCGCTGGGTGCCACTTTGCTGTTGGAACACTGCAAGCCAGATGTGATTATTAACACCGGTTCTGCCGGTGGCCTGGCACCAACGTTGAAAGTGGGCGATATCGTTGTCTCGGACGAAGCACGTTATCACGACGCGGATGTCACGGCATTTGGTTATGAATACGGTCAGTTACCAGGCTGTCCGGCAGGCTTTAAAGCTGACGATAAACTGATCGCTGCCGCTGAGGCCTGCATTGCCGAACTGAATCTTAACGCTGTACGTGGCCTGATTGTTAGCGGCGACGCTTTCATCAACGGTTCTGTTGGTCTGGCGAAAATCCGCCACAACTTCCCACAGGCCATTGCTGTAGAGATGGAAGCGACGGCAATCGCCCATGTCTGCCACAATTTCAACGTCCCGTTTGTTGTCGTACGCGCCATCTCCGACGTGGCCGATCAACAGTCTCATCTTAGCTTCGATGAGTTCCTGGCTGTTGCCGCTAAACAGTCCAGCCTGATGGTTGAGTCACTGGTGCAGAAACTTGCACATGGC**TAA**GAATTCGAGCTCCGTCGACAAGCTTGCGGCCGCACTCGAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
K575024	pLasB-BBa_B0030-GFPmut3b-BBa_J2311-BBa_B0034-lasR	GCCCCTCGCTGAGCGCGTCCCGGAGCTGGGGGCAACCTAGCTGCCACCTGCTTTTCTGCTAGCTATTCCAGCGAAAACATACAGATTTCCGGCGAAATCAAGGCTACCTGCCAGTTCTGGCAGGTTTGGCCGCGGGTTCTTTTTGGTACACGAAAGCTACTAGAG*ATTAAAGAGGAGAAA*TACTAG**ATG**CGTAAAGGAGAAGAACTTTTCACTGGAGTTGTCCCAATTCTTGTTGAATTAGATGGTGATGTTAATGGGCACAAATTTTCTGTCAGTGGAGAGGGTGAAGGTGATGCAACATACGGAAAACTTACCCTTAAATTTATTTGCACTACTGGAAAACTACCTGTTCCATGGCCAACACTTGTCACTACTTTCGGTTATGGTGTTCAATGCTTTGCGAGATACCCAGATCATATGAAACAGCATGACTTTTTCAAGAGTGCCATGCCCGAAGGTTATGTACAGGAAAGAACTATATTTTTCAAAGATGACGGGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCGAGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACAACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAACAAAATACTCCAATTGGCGATGGCCCTGTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTGTAACAGCTGCTGGGATTACACATGGCATGGATGAACTATACAAA**TAA**TAATACTAGAGTTGACAGCTAGCTCAGTCCTAGGTATAATGCTAGCTACTAGAGATT*AAAGAGGAGAAA*TAC

		TAG**ATG**GCCTTGGTTGACGGTTTTCTTGAGCTGGAACGCTCAAGTGGAAAATTGGAGTGGAGCGCCATCCTCCAGAAGATGGCGAGCGACCTTGGATTCTCGAAGATCCTGTTCGGCCTGTTGCCTAAGGACAGCCAGGACTACGAGAACGCCTTCATCGTCGGCAACTACCCGGCCGCCTGGCGCGAGCATTACGACCGGGCTGGCTACGCGCGGGTCGACCCGACGGTCAGTCACTGTACCCAGAGCGTACTGCCGATTTTCTGGGAACCGTCCATCTACCAGACGCGAAAGCAGCACGAGTTCTTCGAGGAAGCCTCGGCCGCCGGCCTGGTGTATGGGCTGACCATGCCGCTGCATGGTGCTCGCGGCGAACTCGGCGCGCTGAGCCTCAGCGTGGAAGCGGAAAACCGGGCCGAGGCCAACCGTTTCATAGAGTCGGTCCTGCCGACCCTGTGGATGCTCAAGGACTACGCACTGCAAAGCGGTGCCGGACTGGCCTTCGAACATCCGGTCAGCAAACCGGTGGTTCTGACCAGCCGGGAGAAGGAAGTGTTGCAGTGGTGCGCCATCGGCAAGACCAGTTGGGAGATATCGGTTATCTGCAACTGCTCGGAAGCCAATGTGAACTTCCATATGGGAAATATTCGGCGGAAGTTCGGTGTGACCTCCCGCCGCGTAGCGGCCATTATGGCCGTTAATTTGGGTCTTATTACTCTC**TAA**TAA
K575037	BBa_J2311-BBa_B0034-rhlR-BBa_B0015-pRhlAB - BBa_B0034-GFPmut3b	TCCTGTGAAATCTGGCAGTTACCGTTAGCTTTCGAATTGGCTAAAAAGTGTTCTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**CGTAAAGGAGAAGAACTTTTCACTGGAGTTGTCCCAATTCTTGTTGAATTAGATGGTGATGTTAATGGGCACAAATTTTCTGTCAGTGGAGAGGGTGAAGGTGATGCAACATACGGAAAACTTACCCTTAAATTTATTTGCACTACTGGAAAACTACCTGTTCCATGGCCAACACTTGTCACTACTTTCGGTTATGGTGTTCAATGCTTTGCGAGATACCCAGATCATATGAAACAGCATGACTTTTTCAAGAGTGCCATGCCCGAAGGTTATGTACAGGAAAGAACTATATTTTTCAAAGATGACGGGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCGAGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACAACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAACAAAATACTCCAATTGGCGATGGCCCTGTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTGTAACAGCTGCTGGGATTACACATGGCATGGATGAACTATACAAA**TAA**TAATACTAGAGTTGACAGCTAGCTCAGTCCTAGGTATAATGCTAGCTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AGGAATGACGGAGGCTTTTTGCTGTGGTGGGACGGTTTGCGTAGCGAGATGCAGCCGATCCACGACAGCCAGGGCGTGTTCGCCGTCCTGGAAAAGGAAGTGCGGCGCCTGGGCTTCGATTACTACGCCTATGGCGTGCGCCACACGATTCCCTTCACCCGGCCGAAGACCGAGGTCCATGGCACCTATCCCAAGGCCTGGCTGGAGCGATACCAGATGCAGAACTACGGGGCCGTGGATCCGGCGATCCTCAACGGCCTGCGCTCCTCGGAAATGGTGGTCTGGAGCGACAGCCTGTTCGACCAGAGCCGGATGCTCTGGAACGAGGCTCGCGATTGGGGCCTCTGTGTCGGCGCGACCTTGCCGATCCGCGCGCCGAACAATTTGCTCAGCGTGCTTTCCGTGGCGCGCGACCAGCAGAACATCTCCAGCTTCGAGCGCGAGGAAATCCGCCTGCGGCTGCGTTGCATGATCGAGTTGCTGACCCAGAAGCTGACCGACCTGGAGCATCCGATGCTGATGTCCAACCCGGTCTGCCTGAGCCATCGCGAACGCGAGATCCTGCAATGGACCGCCGACGGCAAGAGTTCCGGGGAAATCGCCATCATCCTGAGCATCTCCGAGAGCACGGTGAACTTCCACCACAAGAACATCCAGAAGAAGTTCGACGCGCCGAACAAGACGCTGGCTGCCGCCTACGCCGCGGCGCTGGGTCTCATC**TAA**TAA
MC001A	pT7-RBS-lasI-T7 term	TAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAG*AAGGAG*ATATACAT**ATG**ATCGTTCAGATCGGTCGTCGTGAAGAGTTCGACAAAAAACTGCTGGGTGAAATGCACAAACTGCGTGCTCAGGTTTTCAAAGAACGTAAAGGTTGGGACGTTTCCGTTATCGACGAAATGGAAATCGACGGTTACGACGCTCTGTCCCCGTACTACATGCTGATCCAGGAAGACACCCCGGAAGCTCAGGTTTTCGGTTGCTGGCGTATCTTCGACACCACCGGTCCGTACATGCTGAAAAACACCTTCCCGGAACTGCTGCACGGTAAAGAAGCTCCGTGCTCCCCGCACATCTGGGAACTGTCCCGTTTCGCTATCAACTCCGGTCAGAAAGGTTCCCTGGGTTTCTCCGACTGCACCCTGGAAGCTATGCGTGCTCTGGCTCGTTACTCCTTGCAGAACGACATCCAGACCCTGGTTACCGTTACCACCGTTGGTGTTGAAAAAATGATGATCCGTGCTGGTCTGGACGTTTCCCGTTTCGGTCCGCACCTGAAAATCGGTATCGAACGTGCTGTTGCTCTGCGTATCGAACTGAACGCTAAAACCCAGATCGCTCTGTACGGTGGTGTTCTGGTTGAACAGCGTCTGGCTGTTTCC**TAA**GCGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGACTCGAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
MC002A	pT7-RBS-luxI-T7 term	TAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAG*AAGGAG*ATATACAT**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGAGTGGGACTTAGTTGTAGAAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGAAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAATTGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTAAAT**TAA**GCGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGACTCGAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
MC003A	pT7-RBS-rhlI-T7 term	TAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACAT**ATG**ATCGAACTGCTGTCCGAATCCCTGGAAGGTCTGTCCGCTGCTATGATCGCTGAACTGGGTCGTTACCGTCACCAGGTTTTCATCGAAAAACTGGGTTGGGACGTTGTTTCCACCTCCCGTGTTCGTGACCAGGAGTTCGACCAGTTCGACCACCCGCAGACCCGTTACATCGTTGCTATGTCCCGTCAGGGTATCTGCGGTTGCGCTCGTCTGCTGCCGACCACCGACGCTTACCTGCTGAAAGACGTTTTCGCTTACCTGTGCTCCGAAACCCCGCCGTCCGACCCGTCCGTTTGGGAACTGTCCCGTTACGCTGCTTCCGCTGCTGACGACCCGCAGCTGGCTATGAAAATCTTCTGGTCCTCCCTCCAGTGCGCTTGGTACCTGGGTGCTTCCTCCGTTGTTGCTGTTACCACCACCGCTATGGAACGTTACTTCGTTCGTAACGGTGTTATCCTCCAGCGTCTGGGTCCGCCGCAGAAAGTTAAAGGTGAAACCCTGGTTGCTATCTCCTTCCCGGCTTACCAGGAACGTGGTCTGGAAATGCTGCTGCGTTACCACCCGGAATGGCTCCAGGGTGTTCCGCTGTCCATGGCTGTT**TAA**GCGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGACTCGAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG

NY008A	pTet-BBa_B0034-lasR-BBa_B0015-pLuxR-BBa_B0032-GFPmut3b-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAGT**ATG**GCCTTGGTTGACGGTTTTCTTGAGCTGGAACGCTCAAGTGGAAAATTGGAGTGGAGCGCCATCCTCCAGAAGATGGCGAGCGACCTTGGATTCTCGAAGATCCTGTTCGGCCTGTTGCCTAAGGACAGCCAGGACTACGAGAACGCCTTCATCGTCGGCAACTACCCGGCCGCCTGGCGCGAGCATTACGACCGGGCTGGCTACGCGCGGGTCGACCCGACGGTCAGTCACTGTACCCAGAGCGTACTGCCGATTTTCTGGGAACCGTCCATCTACCAGACGCGAAAGCAGCACGAGTTCTTCGAGGAAGCCTCGGCCGCCGGCCTGGTGTATGGGCTGACCATGCCGCTGCATGGTGCTCGCGGCGAACTCGGCGCGCTGAGCCTCAGCGTGGAAGCGGAAAACCGGGCCGAGGCCAACCGTTTCATAGAGTCGGTCCTGCCGACCCTGTGGATGCTCAAGGACTACGCACTGCAAAGCGGTGCCGGACTGGCCTTCGAACATCCGGTCAGCAAACCGGTGGTTCTGACCAGCCGGGAGAAGGAAGTGTTGCAGTGGTGCGCCATCGGCAAGACCAGTTGGGAGATATCGGTTATCTGCAACTGCTCGGAAGCCAATGTGAACTTCCATATGGGAAATATTCGGCGGAAGTTCGGTGTGACCTCCCGCCGCGTAGCGGCCATTATGGCCGTTAATTTGGGTCTTATTACTCTC**TAA**CACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**CGTAAAGGAGAAGAACTTTTCACTGGAGTTGTCCCAATTCTTGTTGAATTAGATGGTGATGTTAATGGGCACAAATTTTCTGTCAGTGGAGAGGGTGAAGGTGATGCAACATACGGAAAACTTACCCTTAAATTTATTTGCACTACTGGAAAACTACCTGTTCCATGGCCAACACTTGTCACTACTTTCGGTTATGGTGTTCAATGCTTTGCGAGATACCCAGATCATATGAAACAGCATGACTTTTTCAAGAGTGCCATGCCCGAAGGTTATGTACAGGAAAGAACTATATTTTTCAAAGATGACGGGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCTTGTTAATAGAATCGAGTTAAAAGGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTGGAATACAACTATAACTCACACAATGTATACATCATGGCAGACAAACAAAAGAATGGAATCAAAGTTAACTTCAAAATTAGACACAACATTGAAGATGGAAGCGTTCAACTAGCAGACCATTATCAACAAAATACTCCAATTGGCGATGGCCCTGTCCTTTTACCAGACAACCATTACCTGTCCACACAATCTGCCCTTTCGAAAGATCCCAACGAAAAGAGAGACCACATGGTCCTTCTTGAGTTTGTAACAGCTGCTGGGATTACACATGGCATGGATGAACTATACAAA**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTT
NY009A	pTET-BBa_B0034-LUXR*-BBa_B0015-pluxR-BBa_B0032-luxI-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGGCGAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACAGCGGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATTCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGAGTGGGACTTAGTTGTAGAAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGAAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAATTGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTAAATTAA**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
NY013A	pTET-BBa_B0034-luxR*-BBa_B0015-pluxR-BBa_B0032-luxI*-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGGCGAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACAGCGGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATTCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGGGTGGGACTTAGTTGTTGGAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGGAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAAT

		TGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTAAAT**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
NY014A	pTET-BBa_B0034-luxR-BBa_B0015-pluxR-BBa_B0032-luxI*-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGACTAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACATCAGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATGCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAATTAA**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGGGTGGGACTTAGTTGTTGGAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGGAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAATTGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTAAAT**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
NY016A	pTET-BBa_B0034-luxR*-BBa_B0015-pluxR-BBa_B0032-HLPT-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGGCGAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACAGCGGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATTCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**CCGTTGTTAGATAGCTTCACAGTCGATCATACCCGGATGGAAGCGCCTGCAGTTCGGGTGGCGAAAACAATGAACACCCCGCATGGCGACGCAATCACCGTGTTCGATCTGCGCTTCTGCGTGCCGAACAAAGAAGTGATGCCAGAAAGAGGGATCCATACCCTGGAGCACCTGTTTGCTGGTTTTATGCGTAACCATCTTAACGGTAATGGTGTAGAGATTATCGATATCTCGCCAATGGGCTGCCGCACCGGTTTTTATATGAGTCTGATTGGTACGCCAGATGAGCAGCGTGTTGCTGATGCCTGGAAAGCGGCAATGGAAGACGTGCTGAAAGTGCAGGATCAGAATCAGATCCCGGAACTGAACGTCTACCAGTGTGGCACTTACCAGATGCACTCGTTGCAGGAAGCGCAGGATATTGCGCGTAGCATTCTGGAACGTGACGTACGCATCAACAGCAACGAAGAACTGGCACTGCCGAAAGAGAAGTTGCAGGAACTGCACATCggccgaaagatccgacctcgagatATGAAAATCGGCATCATTGGTGCAATGGAAGAAGAAGTTACGCTGCTGCGTGACAAAATCGAAAACCGTCAAACTATCAGTCTCGGCGGTTGCGAAATCTATACCGGCCAACTGAATGGAACCGAGGTTGCGCTTCTGAAATCGGGCATCGGTAAAGTCGCTGCGGCGCTGGGTGCCACTTTGCTGTTGGAACACTGCAAGCCAGATGTGATTATTAACACCGGTTCTGCCGGTGGCCTGGCACCAACGTTGAAAGTGGGCGATATCGTTGTCTCGGACGAAGCACGTTATCACGACGCGGATGTCACGGCATTTGGTTATGAATACGGTCAGTTACCAGGCTGTCCGGCAGGCTTTAAAGCTGACGATAAACTGATCGCTGCCGCTGAGGCCTGCATTGCCGAACTGAATCTTAACGCTGTACGTGGCCTGATTGTTAGCGGCGACGCTTTCATCAACGGTTCTGTTGGTCTGGCGAAAATCCGCCACAACTTCCCACAGGCCATTGCTGTAGAGATGGAAGCGACGGCAATCGCCCATGTCTGCCACAATTTCAACGTCCCGTTTGTTGTCGTACGCGCCATCTCCGACGTGGCCGATCAACAGTCTCATCTTAGCTTCGATGAGTTCCTGGCTGTTGCCGCTAAACAGTCCAGCCTGATGGTTGAGTCACTGGTGCAGAAACTTGCACATGGC**TAA**TACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
NY017A	pTET-BBa_B0034-luxR*-	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGGCGAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCT

	BBa_B0015-pluxR-BBa_B0032-aiiA-BBa_B0015	AATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACAGCGGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATTCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ACAGTAAAGAAGCTTTATTTCGTCCCAGCAGGTCGTTGTATGTTGGATCATTCGTCTGTTAATAGTACATTAACACCAGGAGAATTATTAGACTTACCGGTTTGGTGTTATCTTTTGGAGACTGAAGAAGGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAATAATGAAGGTCTTTTTAACGGTACATTTGTCGAAGGGCAGGTTTTACCGAAAATGACTGAAGAAGATAGAATCGTGAATATTTTAAAACGGGTTGGTTATGAGCCGGAAGACCTTCTTTATATTATTAGTTCTCACTTGCATTTTGATCATGCAGGAGGAAATGGCGCTTTTATAAATACACCAATCATTGTACAGCGTGCTGAATATGAGGCGGCGCAGCATAGCGAAGAATATTTGAAAGAATGTATATTGCCGAATTTAAACTACAAAATCATTGAAGGTGATTATGAAGTCGTACCAGGAGTTCAATTATTGCATACACCAGGCCATACTCCAGGGCATCAATCGCTATTAATTGAGACAGAAAAATCCGGTCCTGTATTATTAACGATTGATGCATCGTATACGAAAGAGAATTTTGAAAATGAAGTGCCATTTGCGGGATTTGATTCAGAATTAGCTTTATCTTCAATTAAACGTTTAAAAGAAGTGGTGATGAAAGAGAAGCCGATTGTTTTCTTTGGACATGATATAGAGCAGGAAAGGGGATGTAAAGTGTTCCCTGAATATATA**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
NY018A	pT7-RBS-luxI*-T7 term	TAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAG*AAGGAG*ATATACAT**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGGGTGGACTTAGTTGTTGGAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGGAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAATTGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTA**TAA**GCGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGACTCGAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
NY019A	pT7-RBS-E34G E63G luxI-T7 term	TAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAG*AAGGAG*ATATACAT**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGGGTGGACTTAGTTGTTGAAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGGAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAATTGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTA**TAA**GCGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGACTCGAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
RL054K	pT3-RBS-aHL-sfGFP	ATTAACCCTCACTAAAGGGAGAAATAATTTTGTTTAACTTTAAG*AAGGAG*AATAATCT**ATG**GATTCTGATATCAATATCAAAACCGGCACCACCGATATCGGCTCCAATACCACCGTTAAAACCGGTGATCTGGTGACCTATGATAAAGAAAACGGTATGCATAAAAAAGTGTTTTACTCGTTTATTGACGATAAAAACCATAACAAAAAACTGCTGGTCATCCGCACCAAAGGCACCATTGCGGGTCAATACCGTGTGTACTCCGAAGAAGGTGCGAACAAAAGCGGTCTGGCTTGGCCGTCTGCCTTTAAAGTGCAGCTGCAACTGCCGGATAATGAAGTGGCGCAGATTTCAGATTATTATCCGCGTAATAGCATCGATACCAAAGAATATATGAGTACCCTGACCTATGGTTTTAATGGCAATGTTACCGGTGATGATACGGGTAAAATTGGCGGTCTGATTGGCGCCAATGTGTCCATTGGTCATACGCTGAAATACGTGCAACCGGATTTCAAAACCATTCTGGAAAGTCCGACCGATAAAAAAGTGGGTTGGAAAGTTATCTTCAACAACATGGTGAATCAGAACTGGGGTCCGTACGATCGCGATTCCTGGAATCCGGTTTATGGCAATCAGCTGTTTATGAAAACCCGCAACGGTAGTATGAAAGCGGCGGATAATTTTCTGGACCCGAACAAAGCCTCAAGCCTGCTGTCCAGCGGTTTTAGCCCGGATTTTGCCACGGTTATTACCATGGATCGCAAAGCCAGCAAACAGCAGACCAACATTGATGTGATCTACGAACGTGTGCGTGATGATTATCAACTGCATTGGACCTCAACCAATTGGAAAGGCACCAATACCAAAGATAAATGGACGGATCGCAGTTCAGAACGCTACAAAATTGATTGGGAAAAAGAAGAAATGACCAACggatccggcagcggttct**ATG**CGTAAAGGCGAAGAGCTGTTCACTGGTGTCGTCCCTATTCTGGTGGAACTGGATGGTGATGTCAACGGTCATAAGTTTTCCGTGCGTGGCGAGGGTGAAGGTGACGCAACTAATGGTAAACTGACGCTGAAGTTCATCTGTACTACTGGTAAACTGCCGGTACCTTGGCCGACTCTGGTAACGACGCTGACTTATGGTGTTCAGTGCTTTGCTCGTTATCCGGACCATATGAAGCAGCATGACTTCTTCAAGTCCGCCATGCCGGAAGGCTATGTGCAGGAACGCACGATTTCCTTTAAGGATGACGGCACGTACAAAACGCGTGCGGAAGTGAAATTTGAAGGCGATACCCTGGTAAACCGCATTGAGCTGAAAGGCATTGACTTTAAAGAAGACGGCAATATCCTGGGCCATAAGCTGGAATACAATTTTAACAGCCACAATGTTTACATCACCGCCGATAAACAAAAAAATGGCATTAAAGCGAATTTTAAAATTCGCCACAACGTGGAGGATGGCAGCGTGCAGCTGGCTGATCACTACCAGCAAAACACTCCAATCGGTGATGGTCCTGTTCTGCTGCCAGACAATCACTATCTGAGCACGCAAAGCGTTCTGTCTAAAGATCCGAACGAGAAACGCGATCATATGGTTCTGCTGGAGTTCGTAACCGCAGCGGGCATCACGCATG

		GTATGGATGAACTGTACAAA**TAA**ACTAGTCTGCAGTCCGGCAAAAAAGGGCAAGGTGTCACCACCCTGCCCTTTTTCTTTAAAACCGAAAAGATTACTTCGCGT
RL059K	pT3-lsr intergenic region-aHL-sfGFP	ATTAACCCTCACTAAAGGGAGaAATTCATTCTTCACTTTGAACATATTTAAATCTTTAATGCAATTGTTCAGTTCTTGCTCATTTATATCTGTGATGGCAACCACAGTTTGACTCTACGAGCATGAACAAACGCAACCGTGAAAATCAAAATAGCATAAATTGTGATCTATTCGTCGGAAATATGTGCAATGTCCACCTAAGGTTATGAACAAATTAAAAGCAGAAATACATTTGTTCAAAACTCACCTGCAAAACTGAACGGGGGAAATACTAGA**ATG**GATTCTGATATCAATATCAAAACCGGCACCACCGATATCGGCTCCAATACCACCGTTAAAACCGGTGATCTGGTGACCTATGATAAAGAAAACGGTATGCATAAAAAAGTGTTTTACTCGTTTATTGACGATAAAAACCATAACAAAAAACTGCTGGTCATCCGCACCAAAGGCACCATTGCGGGTCAATACCGTGTGTACTCCGAAGAAGGTGCGAACAAAAGCGGTCTGGCTTGGCCGTCTGCCTTTAAAGTGCAGCTGCAACTGCCGGATAATGAAGTGGCGCAGATTTCAGATTATTATCCGCGTAATAGCATCGATACCAAAGAATATATGAGTACCCTGACCTATGGTTTTAATGGCAATGTTACCGGTGATGATACGGGTAAAATTGGCGGTCTGATTGGCGCCAATGTGTCCATTGGTCATACGCTGAAATACGTGCAACCGGATTTCAAAACCATTCTGGAAAGTCCGACCGATAAAAAAGTGGGTTGGAAAGTTATCTTCAACAACATGGTGAATCAGAACTGGGGTCCGTACGATCGCGATTCCTGGAATCCGGTTTATGGCAATCAGCTGTTTATGAAAACCCGCAACGGTAGTATGAAAGCGGCGGATAATTTTCTGGACCCGAACAAAGCCTCAAGCCTGCTGTCCAGCGGTTTTAGCCCGGATTTTGCCACGGTTATTACCATGGATCGCAAAGCCAGCAAACAGCAGACCAACATTGATGTGATCTACGAACGTGTGCGTGATGATTATCAACTGCATTGGACCTCAACCAATTGGAAAGGCACCAATACCAAAGATAAATGGACGGATCGCAGTTCAGAACGCTACAAAATTGATTGGGAAAAAGAAGAAATGACCAACggatccggcagcggttct**ATG**CGTAAAGGCGAAGAGCTGTTCACTGGTGTCGTCCCTATTCTGGTGGAACTGGATGGTGATGTCAACGGTCATAAGTTTTCCGTGCGTGGCGAGGGTGAAGGTGACGCAACTAATGGTAAACTGACGCTGAAGTTCATCTGTACTACTGGTAAACTGCCGGTACCTTGGCCGACTCTGGTAACGACGCTGACTTATGGTGTTCAGTGCTTTGCTCGTTATCCGGACCATATGAAGCAGCATGACTTCTTCAAGTCCGCCATGCCGGAAGGCTATGTGCAGGAACGCACGATTTCCTTTAAGGATGACGGCACGTACAAAACGCGTGCGGAAGTGAAATTTGAAGGCGATACCCTGGTAAACCGCATTGAGCTGAAAGGCATTGACTTTAAAGAAGACGGCAATATCCTGGGCCATAAGCTGGAATACAATTTTAACAGCCACAATGTTTACATCACCGCCGATAAACAAAAAAATGGCATTAAAGCGAATTTTAAAATTCGCCACAACGTGGAGGATGGCAGCGTGCAGCTGGCTGATCACTACCAGCAAAACACTCCAATCGGTGATGGTCCTGTTCTGCTGCCAGACAATCACTATCTGAGCACGCAAAGCGTTCTGTCTAAAGATCCGAACGAGAAACGCGATCATATGGTTCTGCTGGAGTTCGTAACCGCAGCGGGCATCACGCATGGTATGGATGAACTGTACAAA**TAA**ACTAGTCTGCAGTCCGGCAAAAAAGGGCAAGGTGTCACCACCCTGCCCTTTTTCTTTAAAACCGAAAAGATTACTTCGCGT
RL060K	pT7-RBS-lsrR-RBS-lsrK-RBS-T3 RNAP-T7 term	TAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAG*AAGGAG*ATATACC**ATG**GCAATCAACGATTCGGCAATTTCAGAACAGGGAATGTGTGAAGAAGAACAGGTCGCGCGGATCGCGTGGTTTTACTATCACGACGGGCTGACCCAGAGCGAGATCAGCGATCGTCTCGGCCTGACACGTTTGAAAGTGTCGCGATTGCTGGAGAAAGGGCATCAGTCCGGCATTATTCGCGTACAGATTAATTCTCGCTTTGAAGGCTGTCTGGAATATGAAACTCAATTACGTCGTCAGTTTTCGCTGCAACATGTCCGGGTGATCCCTGGGCTTGCGGATGCTGATGTCGGTGGGCGACTGGGGATAGGCGCGGCGCATATGTTGATGAGTTTACTTCAACCACAACAGATGCTGGCGATTGGTTTTGGCGAGGCAACCATGAATACGCTGCAACGCTTAAGTGGTTTTATTTCGTCACAGCAAATTCGCCTGGTCACGCTCTCCGGTGGCGTCGGTTCTTATATGACGGGAATCGGGCAGCTTAACGCGGCGTGCAGTGTGAATATTATTCCGGCTCCGTTGCGGGCATCCTCCGCTGACATTGCCCGTACGCTAAAAAATGAAAATTGCGTCAAAGATGTTCTGTTAGCCGCGCAAGCAGCGGATGTGGCGATTGTCGGCATTGGTGCTGTGAGTCAACAGGACGATGCGACAATCATTCGCTCCGGTTATATCAGCCAGGGCGAACAGTTAATGATTGGCCGAAAAGGGGCGGTTGGCGACATTTTAGGCTACTTTTTTGATGCAAAAGGTGACGTTGTCACGAATATCAAAATACATAACGAACTGATTGGCTTACCTTTAAGCGCGCTGAAGACCATACCCGTCCGGGTTGGCGTGGCAGGGGGAGAAAATAAAGCCGAAGCAATTGCCGCTGCAATGAAAGGCGGTTATATCAACGCACTGGTTACCGATCAGGACACAGCAGCGGCGATTTTACGTAGT**TAA**GCTAGCTGTTTAACTTTAAG*AAGGAG*ATATACC**ATG**GCTCGACTCTTTACCCTTTCAGAATCAAAGTACTACCTGATGGCGCTGGATGCAGGCACCGGAAGTATTCGGGCTGTGATATTCGACCTGGAAGGCAATCAAATAGCAGTGGGACAGGCGGAGTGGCGGCATCTGGCAGTACCGGACGTTCCTGGTTCTATGGAATTTGATCTCAACAAAAACTGGCAACTGGCGTGTGAGTGTATGCGCCAGGCGCTGCACAACGCCGGCATAGCCCCGGAGTATATCGCTGCCGTTTCGGCATGTTCGATGCGTGAAGGCATTGTTTTATATAATAATGAAGGAGCCCCGATCTGGGCCTGCGCCAATGTGGATGCCAGAGCGGCACGCGAAGTTAGCGAACTTAAAGAACTGCACAACAATACCTTTGAAAACGAAGTTTATCGCGCGACCGGACAAACACTGGCTTTAAGTGCCATCCCCAGATTACTTTGGCTGGCGCACCATCGTTCCGATATTTACCGTCAGGCATCAACCATCACCATGATCAGCGACTGGCTGGCCTATATGCTCAGCGGCGAACTGGCGGTGGATCCCTCTAACGCTGGCACCACGGGACTTCTTGATCTAACCACCCGTGACTGGAAACCTGCATTGCTGGATATGGCTGGCCTACGTGCCGATATTCTTTCTCCTGTCAAAGAAACCGGCACATTGCTGGGCGTGGTAAGTTCACAAGCGGCGGAACTCTGCGGTCTGAAGGCGGGCACTCCGGTGGTCGTTGGAGGAGGCGACGTGCAGCTTGGTTGCCTTGGGTTAGGCGTTGTGCGTCCGGCACAAACCGCGGTTCTTGGCGGCACATTCTGGCAGCAAGTTGTAAATTTAGCCGCGCCGGTGACAGACCCAGAAATGAACGTGCGCGTTAATCCTCATGTTATTCCTGGCATGGTACAAGCTGAATCTATAAGCTTTTTTACCGGACTCACCATGCGCTGGTTCCGCGATGCTTTCTGTGCCGAAGAAAAACTGATTGCCGAACGTTTAGGCATCGACACCTATACGCTGCTGGAAGAGATGGCCAGTCGGGTGCCGCCTGGGTCGTGGGGCGTAATGCCGATCTTCTCCGACAGAATGCGCTTTAAAACCTGGTATCACGCTGCGCCTTCCTTTATTAACTTGTCCATTGACCCGGATAAATGTAACAAAGCGACATTGTTCCGTGCGCTGGAAGAAAATGCGGCGATTGTATCAGCGTGTAACTTGCAGCAAATTGCTGATTTCTCGAATATTCATCCTTCATCGTTAGTCTTTGCAGGCGGAGGTTCAAAAGGGAAATTATGGAGTCAAATTCTCGCTGATGTCTCGGGATTACCCGTCAATATTCCGGTGGTCAAAGAAGCCACTGCATTAGGATGTGCCATTGCAGCTGGCGTCGGTGCCGGAATTTTTTCATCAATGGCAGAAACCGGAGAACGCCTGGTTCGCTGGGAACGGACGCACACACCAGACCCGGAAAAGCATGAACTTTATCAGGATTCACGCGATAAGTGGCAGGCAGTTTATCAGGATCAGCTGGGGCTGGTTGATCATGGACTGACGACGTCGTTATGGAAAGCGCCTGGGTTA**TAA**GAGCTCTTTAAACGAATTCGTT*AAGGAG*AATAATCT**ATG**AACATCATCGAAAACATCGAAAAGAATGACTTCTCAGAAATCGAACTGGCTGCTATCCCGTTCAACACACTGGCTGACCACTACGGAAGCGCCTTGGCTAAAGAGCAGTTGGCTTTAGAACATGAGTCTTATGAGCTAGGCGAGCGCCGCTTCCTCAAGATGCTTGAGCGTCAAGCGAAAGCTGGTGAGATTGCAGACAACGCAGCCGCTAAGCCGTTACTCGCTACGCTTCTCCCTAAGTTAACCACACGTATCGTCGAGTGGCTCGAAGAGTACGCATCGAAGAAAGGCCGCAAGCCTAGCGCATACGCACCGCTCCAGTTACTCAAGCCGGAGGCCTCCGCGTTTATCACCCTGAAAGTTATC

		CTTGCGTCACTAACCAGTACGAACATGACAACCATTCAGGCCGCTGCTGGTATGCTGGGGAAAGCCATTGAGGACGAGGCACGATTTGGGCGCATCCGTGACCTAGAAGCGAAGCACTTCAAGAAGCACGTTGAGGAACAGCTTAACAAGCGCCACGGGCAAGTCTACAAGAAAGCATTTATGCAGGTGGTCGAGGCCGATATGATTGGTCGAGGTCTGCTTGGTGGCGAGGCGTGGTCTAGCTGGGATAAAGAAACCACGATGCACGTAGGGATTCGCCTGATTGAAATGCTGATTGAATCCACGGGTCTGGTGGAATTACAGCGCCACAACGCAGGTAACGCAGGCTCTGACCATGAGGCACTGCAACTGGCCCAAGAGTACGTGGACGTATTAGCGAAGCGTGCAGGCGCTCTGGCGGGTATCTCTCCGATGTTCCAGCCGTGTGTCGTACCGCCGAAACCTTGGGTAGCAATCACAGGGGGCGGCTATTGGGCTAACGGTCGCAGACCTTTGGCACTCGTTCGCACTCACTCTAAGAAGGGCTTGATGCGCTACGAAGACGTTTACATGCCAGAAGTCTACAAGGCTGTGAACCTCGCGCAAAACACCGCATGGAAAATCAACAAGAAAGTTCTTGCTGTTGTCAATGAGATTGTTAACTGGAAGAATTGCCCGGTAGCAGACATTCCATCGCTGGAGCGCCAAGAGTTACCGCCTAAGCCTGACGACATTGACACCAACGAGGCAGCGCTCAAGGAGTGGAAGAAAGCCGCTGCTGGTATCTATCGCTTGGACAAGGCACGAGTGTCTCGCCGTATCAGCTTAGAGTTCATGCTGGAGCAGGCCAACAAGTTCGCAAGTAAGAAAGCAATCTGGTTCCCTTACAACATGGACTGGCGCGGTCGTGTGTACGCTGTGCCGATGTTCAACCCGCAAGGCAACGACATGACGAAAGGTCTGCTGACCCTTGCTAAAGGCAAGCCAATCGGTGAGGAAGGTTTCTACTGGCTGAAAATCCACGGTGCGAACTGTGCGGGTGTTGATAAGGTTCCATTCCCGGAGCGCATCGCGTTCATTGAGAAGCACGTAGACGACATTCTGGCTTGCGCTAAAGACCCAATCAATAACACTTGGTGGGCTGAGCAGGATTCACCGTTCTGTTTCCTCGCGTTTTGCTTCGAGTATGCAGGCGTTACGCACCACGGTCTGAGCTACAATTGCTCTCTGCCGCTGGCGTTCGACGGGTCTTGCTCTGGTATCCAGCACTTCTCCGCGATGCTCCGCGATGAGGTAGGCGGTCGTGCGGTTAACCTGCTGCCAAGCGAAACCGTGCAGGACATTTACGGCATCGTTGCACAGAAAGTAAACGAGATTCTCAAACAGGATGCAATCAACGGCACGCCTAACGAGATGATTACCGTGACCGACAAGGACACCGGGGAAATCTCAGAGAAGCTCAAACTTGGAACCTCAACGCTGGCGCAACAGTGGCTGGCATATGGTGTAACCCGTAGCGTAACTAAACGTTCGGTCATGACGCTGGCTTACGGTTCCAAGGAGTTCGGCTTTCGTCAACAGGTATTGGATGACACCATTCAGCCTGCAATTGACAGCGGTAAGGGCTTGATGTTCACCCAACCGAACCAAGCGGCTGGCTATATGGCTAAGCTGATTTGGGATGCGGTAAGCGTGACCGTAGTTGCAGCGGTTGAGGCGATGAACTGGCTCAAATCTGCCGCTAAGCTGCTGGCTGCTGAGGTCAAGGACAAGAAGACCAAGGAGATTCTGCGCCACCGTTGCGCGGTTCACTGGACTACGCCGGACGGCTTCCCGGTCTGGCAGGAATACCGCAAGCCACTCCAGAAGCGTCTCGATATGATTTTCTTAGGGCAATTCCGTCTGCAACCGACGATTAATACCCTCAAGGATTCAGGCATTGACGCACACAAGCAGGAGTCTGGCATCGCTCCTAACTTTGTTCACTCACAGGACGGTAGCCACCTCCGCATGACAGTCGTTTATGCTCACGAGAAGTATGGCATTGAGTCCTTTGCGCTCATCCATGACAGCTTTGGGACTATCCCGGCAGACGCTGGTAAGCTCTTTAAGGCTGTGCGTGAAACGATGGTTATCACCTATGAGAACAACGATGTGCTGGCAGACTTCTACTCTCAGTTTGCCGACCAGCTACACGAGACCCAACTGGACAAGATGCCTCCGCTTCCGAAGAAAGGAAACCTGAACCTGCAAGACATTCTCAAGTCTGACTTTGCCTTTGCA**TAA**CTCGAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
RL076A	pT7-RBS-CRP-T7 term	TAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAATTTTGTTTAACTTTAAG*AAGGAG*ATATACAT**ATG**GTGCTTGGCAAACCGCAAACAGACCCGACTCTCGAATGGTTCTTGTCTCATTGCCACATTCATAAGTACCCATCCAAGAGCACGCTTATTCACCAGGGTGAAAAAGCGGAAACGCTGTACTACATCGTTAAAGGCTCTGTGGCAGTGCTGATCAAAGACGAAGAGGGTAAAGAAATGATCCTCTCCTATCTGAATCAGGGTGATTTTATTGGCGAACTGGGCCTGTTTGAAGAGGGCCAGGAACGTAGCGCATGGGTACGTGCGAAAACCGCCTGTGAAGTGGCTGAAATTTCGTACAAAAAATTTCGCCAATTGATTCAGGTAAACCCGGACATTCTGATGCGTTTGTCTGCACAGATGGCGCGTCGTCTGCAAGTCACTTCAGAGAAAGTGGGCAACCTGGCGTTCCTCGACGTGACGGGCCGCATTGCACAGACTCTGCTGAATCTGGCAAAACAACCAGACGCTATGACTCACCCGGACGGTATGCAAATCAAAATTACCCGTCAGGAAATTGGTCAGATTGTCGGCTGTTCTCGTGAAACCGTGGGACGCATTCTGAAGATGCTGGAAGATCAGAACCTGATCTCCGCACACGGTAAAACCATCGTCGTTTACGGCACTCGT**TAA**GCGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGACTCGAGCACCACCACCACCACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
RL078A	pTET-BBa_B0034-luxR-BBa_B0015-pluxR-BBa_B0032-luxI-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGACTAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACATCAGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATGCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGAGTGGGACTTAGTTGTAGAAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGAAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAATTGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTAAAT**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCC

		TTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
RL079A	pTET-BBa_B0034-luxR-BBa_B0015-pluxR-BBa_B0032-lasI-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGACTAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACATCAGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATGCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ATCGTTCAGATCGGTCGTCGTGAAGAGTTCGACAAAAAACTGCTGGGTGAAATGCACAAACTGCGTGCTCAGGTTTTCAAAGAACGTAAAGGTTGGGACGTTTCCGTTATCGACGAAATGGAAATCGACGGTTACGACGCTCTGTCCCCGTACTACATGCTGATCCAGGAAGACACCCCGGAAGCTCAGGTTTTCGGTTGCTGGCGTATCTTCGACACCACCGGTCCGTACATGCTGAAAAACACCTTCCCGGAACTGCTGCACGGTAAAGAAGCTCCGTGCTCCCCGCACATCTGGGAACTGTCCCGTTTCGCTATCAACTCCGGTCAGAAAGGTTCCCTGGGTTTCTCCGACTGCACCCTGGAAGCTATGCGTGCTCTGGCTCGTTACTCCTTGCAGAACGACATCCAGACCCTGGTTACCGTTACCACCGTTGGTGTTGAAAAAATGATGATCCGTGCTGGTCTGGACGTTTCCCGTTTCGGTCCGCACCTGAAAATCGGTATCGAACGTGCTGTTGCTCTGCGTATCGAACTGAACGCTAAAACCCAGATCGCTCTGTACGGTGGTGTTCTGGTTGAACAGCGTCTGGCTGTTTCC**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
RL080A	pTet-BBa_B0034-luxR-BBa_B0015-pluxR-BBa_B0032-rhlI-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGACTAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACATCAGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATGCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ATCGAACTGCTGTCCGAATCCCTGGAAGGTCTGTCCGCTGCTATGATCGCTGAACTGGGTCGTTACCGTCACCAGGTTTTCATCGAAAAACTGGGTTGGGACGTTGTTTCCACCTCCCGTGTTCGTGACCAGGAGTTCGACCAGTTCGACCACCCGCAGACCCGTTACATCGTTGCTATGTCCCGTCAGGGTATCTGCGGTTGCGCTCGTCTGCTGCCGACCACCGACGCTTACCTGCTGAAAGACGTTTTCGCTTACCTGTGCTCCGAAACCCCGCCGTCCGACCCGTCCGTTTGGGAACTGTCCCGTTACGCTGCTTCCGCTGCTGACGACCCGCAGCTGGCTATGAAAATCTTCTGGTCCTCCCTCCAGTGCGCTTGGTACCTGGGTGCTTCCTCCGTTGTTGCTGTTACCACCACCGCTATGGAACGTTACTTCGTTCGTAACGGTGTTATCCTCCAGCGTCTGGGTCCGCCGCAGAAAGTTAAAGGTGAAACCCTGGTTGCTATCTCCTTCCCGGCTTACCAGGAACGTGGTCTGGAAATGCTGCTGCGTTACCACCCGGAATGGCTCCAGGGTGTTCCGCTGTCCATGGCTGTT**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
RL081A	pTET-BBa_B0034-luxR-BBa_B0015-pluxR-BBa_B0032-T7 RNAP-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGACTAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACATCAGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATGCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**AAACACGATTAACATCGCTAAGAACGACTTCTCTGACATCGAACTGGCTGCTATCCCGTTCAACACTCTGGCTGACCATTACGGTGAGCGTTTAGCTCGCGAACAGTTGGCCCTTGAGCATGAGTCTTACGAGATGGGTGAAGCACGCTTCCGCAAGATGTTTGAGCGTCAACTTAAAGCTGGTGAGGTTGCGGATAACGCTGCCGCCAAGCCTCTCATCACTACCCTACTCCCTAAGATGATTGCACGCATCAACGAC

		TGGTTTGAGGAAGTGAAAGCTAAGCGCGGCAAGCGCCCGACAGCCTTCCAGTTCCTGCAAGAAATCAAGCCGGAAGCCGTAGCGTACATCACCATTAAGACCACTCTGGCTTGCCTAACCAGTGCTGACAATACAACCGTTCAGGCTGTAGCAAGCGCAATCGGTCGGGCCATTGAGGACGAGGCTCGCTTCGGTCGTATCCGTGACCTTGAAGCTAAGCACTTCAAGAAAAACGTTGAGGAACAACTCAACAAGCGCGTAGGGCACGTCTACAAGAAAGCATTTATGCAAGTTGTCGAGGCTGACATGCTCTCTAAGGGTCTACTCGGTGGCGAGGCGTGGTCTTCGTGGCATAAGGAAGACTCTATTCATGTAGGAGTACGCTGCATCGAGATGCTCATTGAGTCAACCGGAATGGTTAGCTTACACCGCCAAAATGCTGGCGTAGTAGGTCAAGACTCTGAGACTATCGAACTCGCACCTGAATACGCTGAGGCTATCGCAACCCGTGCAGGTGCGCTGGCTGGCATCTCTCCGATGTTCCAACCTTGCGTAGTTCCTCCTAAGCCGTGGACTGGCATTACTGGTGGTGGCTATTGGGCTAACGGTCGTCGTCCTCTGGCGCTGGTGCGTACTCACAGTAAGAAAGCACTGATGCGCTACGAAGACGTTTACATGCCTGAGGTGTACAAAGCGATTAACATTGCGCAAAACACCGCATGGAAAATCAACAAGAAAGTCCTAGCGGTCGCCAACGTAATCACCAAGTGGAAGCATTGTCCGGTCGAGGACATCCCTGCGATTGAGCGTGAAGAACTCCCGATGAAACCGGAAGACATCGACATGAATCCTGAGGCTCTCACCGCGTGGAAACGTGCTGCCGCTGCTGTGTACCGCAAGGACAAGGCTCGCAAGTCTCGCCGTATCAGCCTTGAGTTCATGCTTGAGCAAGCCAATAAGTTTGCTAACCATAAGGCCATCTGGTTCCCTTACAACATGGACTGGCGCGGTCGTGTTTACGCTGTGTCAATGTTCAACCCGCAAGGTAACGATATGACCAAAGGACTGCTTACGCTGGCGAAAGGTAAACCAATCGGTAAGGAAGGTTACTACTGGCTGAAAATCCACGGTGCAAACTGTGCGGGTGTCGATAAGGTTCCGTTCCCTGAGCGCATCAAGTTCATTGAGGAAAACCACGAGAACATCATGGCTTGCGCTAAGTCTCCACTGGAGAACACTTGGTGGGCTGAGCAAGATTCTCCGTTCTGCTTCCTTGCGTTCTGCTTTGAGTACGCTGGGGTACAGCACCACGGCCTGAGCTATAACTGCTCCCTTCCGCTGGCGTTTGACGGGTCTTGCTCTGGCATCCAGCACTTCTCCGCGATGCTCCGAGATGAGGTAGGTGGTCGCGCGGTTAACTTGCTTCCTAGTGAAACCGTTCAGGACATCTACGGGATTGTTGCTAAGAAAGTCAACGAGATTCTACAAGCAGACGCAATCAATGGGACCGATAACGAAGTAGTTACCGTGACCGATGAGAACACTGGTGAAATCTCTGAGAAAGTCAAGCTGGGCACTAAGGCACTGGCTGGTCAATGGCTGGCTTACGGTGTTACTCGCAGTGTGACTAAGCGTTCAGTCATGACGCTGGCTTACGGGTCCAAAGAGTTCGGCTTCCGTCAACAAGTGCTGGAAGATACCATTCAGCCAGCTATTGATTCCGGCAAGGGTCTGATGTTCACTCAGCCGAATCAGGCTGCTGGATACATGGCTAAGCTGATTTGGGAATCTGTGAGCGTGACGGTGGTAGCTGCGGTTGAAGCAATGAACTGGCTTAAGTCTGCTGCTAAGCTGCTGGCTGCTGAGGTCAAAGATAAGAAGACTGGAGAGATTCTTCGCAAGCGTTGCGCTGTGCATTGGGTAACTCCTGATGGTTTCCCTGTGTGGCAGGAATACAAGAAGCCTATTCAGACGCGCTTGAACCTGATGTTCCTCGGTCAGTTCCGCTTACAGCCTACCATTAACACCAACAAAGATAGCGAGATTGATGCACACAAACAGGAGTCTGGTATCGCTCCTAACTTTGTACACAGCCAAGACGGTAGCCACCTTCGTAAGACTGTAGTGTGGGCACACGAGAAGTACGGAATCGAATCTTTTGCACTGATTCACGACTCCTTCGGTACCATTCCGGCTGACGCTGCGAACCTGTTCAAAGCAGTGCGCGAAACTATGGTTGACACATATGAGTCTTGTGATGTACTGGCTGATTTCTACGACCAGTTCGCTGACCAGTTGCACGAGTCTCAATTGGACAAAATGCCAGCACTTCCGGCTAAAGGTAACTTGAACCTCCGTGACATCTTAGAGTCGGACTTCGCGTTCGCG**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
RL086A	pTET-BBa_B0034-T33A S116A M135I luxR-BBa_B0015-pluxR-BBa_B0032-GFPmut3b-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGGCGAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACAGCGGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATTCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGAGTGGGACTTAGTTGTAGAAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGAAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAATTGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTAAAT**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
RL087A	pTET-BBa_B0034-T33A R65M S116A M135I luxR-BBa_B0015-pluxR-BBa_	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGGCGAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGATGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACAGCGGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATTCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTC

	B0032-GFPmut3b-BBa_B0015	GAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGAGTGGGACTTAGTTGTAGAAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGAAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAATTGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTAAAT**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
RL089C	pTET-BBa_B0034-aiiA-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**ACAGTAAAGAAGCTTTATTTCGTCCCAGCAGGTCGTTGTATGTTGGATCATTCGTCTGTTAATAGTACATTAACACCAGGAGAATTATTAGACTTACCGGTTTGGTGTTATCTTTTGGAGACTGAAGAAGGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAATAATGAAGGTCTTTTTAACGGTACATTTGTCGAAGGGCAGGTTTTACCGAAAATGACTGAAGAAGATAGAATCGTGAATATTTTAAAACGGGTTGGTTATGAGCCGGAAGACCTTCTTTATATTATTAGTTCTCACTTGCATTTTGATCATGCAGGAGGAAATGGCGCTTTTATAAATACACCAATCATTGTACAGCGTGCTGAATATGAGGCGGCGCAGCATAGCGAAGAATATTTGAAAGAATGTATATTGCCGAATTTAAACTACAAAATCATTGAAGGTGATTATGAAGTCGTACCAGGAGTTCAATTATTGCATACACCAGGCCATACTCCAGGGCATCAATCGCTATTAATTGAGACAGAAAAATCCGGTCCTGTATTATTAACGATTGATGCATCGTATACGAAAGAGAATTTTGAAAATGAAGTGCCATTTGCGGGATTTGATTCAGAATTAGCTTTATCTTCAATTAAACGTTTAAAAGAAGTGGTGATGAAAGAGAAGCCGATTGTTTTCTTTGGACATGATATAGAGCAGGAAAGGGGATGTAAAGTGTTCCCTGAATATATA**TAA**CGCTGATAGTGCTAGTGTAGATCGCTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
RL092A	pTET-BBa_B0034-lasR-BBa_B0015-pluxR-BBa_B0032-luciferase-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAGT**ATG**GCCTTGGTTGACGGTTTTCTTGAGCTGGAACGCTCAAGTGGAAAATTGGAGTGGAGCGCCATCCTCCAGAAGATGGCGAGCGACCTTGGATTCTCGAAGATCCTGTTCGGCCTGTTGCCTAAGGACAGCCAGGACTACGAGAACGCCTTCATCGTCGGCAACTACCCGGCCGCCTGGCGCGAGCATTACGACCGGGCTGGCTACGCGCGGGTCGACCCGACGGTCAGTCACTGTACCCAGAGCGTACTGCCGATTTTCTGGGAACCGTCCATCTACCAGACGCGAAAGCAGCACGAGTTCTTCGAGGAAGCCTCGGCCGCCGGCCTGGTGTATGGGCTGACCATGCCGCTGCATGGTGCTCGCGGCGAACTCGGCGCGCTGAGCCTCAGCGTGGAAGCGGAAAACCGGGCCGAGGCCAACCGTTTCATAGAGTCGGTCCTGCCGACCCTGTGGATGCTCAAGGACTACGCACTGCAAAGCGGTGCCGGACTGGCCTTCGAACATCCGGTCAGCAAACCGGTGGTTCTGACCAGCCGGGAGAAGGAAGTGTTGCAGTGGTGCGCCATCGGCAAGACCAGTTGGGAGATATCGGTTATCTGCAACTGCTCGGAAGCCAATGTGAACTTCCATATGGGAAATATTCGGCGGAAGTTCGGTGTGACCTCCCGCCGCGTAGCGGCCATTATGGCCGTTAATTTGGGTCTTATTACTCTC**TAA**CACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**GAAGACGCCAAAAACATAAAGAAAGGCCCGGCGCCATTCTATCCTCTAGAGGATGGAACCGCTGGAGAGCAACTGCATAAGGCTATGAAGAGATACGCCCTGGTTCCTGGAACAATTGCTTTTGTGAGTATTTCTGTCTGATTTCTTTCGAGTTAACGAAATGTTCTTATGTTTCTTTAGACAGATGCACATATCGAGGTGAACATCACGTACGCGGAATACTTCGAAATGTCCGTTCGGTTGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCACAGAATCGTCGTATGCAGTGAAAACTCTCTTCAATTCTTTATGCCGGTGTTGGGCGCGTTATTTATCGGAGTTGCAGTTGCGCCCGCGAACGACATTTATAATGAACGTAAGCACCCTCGCCATCAGACCAAAGGGAATGACGTATTTAATTTTTAAGGTGAATTGCTCAACAGTATGAACATTTCGCAGCCTACCGTAGTGTTTGTTTCCAAAAAGGGGTTGCAAAAAATTTTGAACGTGCAAAAAAAATTACCAATAATCCAGAAAATTATTATCATGGATTCTAAAACGGATTACCAGGGATTTCAGTCGATGTACACGTTCGTCACATCTCATCTACCTCCCGGTTTTAATGAATACGATTTTGTACCAGAGTCCTTTGATCGTGACAAAACAATTGCACTGATAATGAATTCCTCTGGATCTACTGGGTTACCTAAGGGTGTGGCCCTTCCGCATAGAACTGCCTGCGTCAGATTCTCGCATGCCAGGTATGTCGTATAACAAGAGATTAAGTAATGTTGCTACACACATTGTAGAGATCCTATTTTTGGCAATCAAATCATTCCGGATACTGCGATTTTAAGTGTTGTTCCATTCCATCACGGTTTTGGAATGTTTACTACACTCGGATATTTGATATGTGGATTTCGAGTCGTCTTAATGTATAGATTTGAAGAAGAGCTGTTTTTACGATCCCTTCAGGATTACAAAATTCAAAGTGCGTTGCTAGTACCAACCCTATTTTCATTCTTCGCCAAAAGCACTCTGATTGACAAATACGATTTATCTAATTTACACGAAATTGCTTCTGGGGGCGCACCTCTTTCGAAAGAAGTCGGGGAAGCGGTTGCAAAACGGTGAGTTAAGCGCATTGCTAGTATTTCAAGGCTCTAAAACGGCGCGTAGCTTCCATCTTCCAGGGATACGACAAGGATATGGGCTCACTGAGACTACATCAGCTATTCTGATTACACCCGAGGGGGATGATAAACCGGGCGCGGTCGGTAAAGTTGTTCCATTTTTTGAAGCGAAGGTTGTGGATCTGGATACCGGGAAAACGCTGGGCGTTAATCAGAGAGGCGAATTATGTGTCAGAGGACCTATGATTATGTCCGGTTATGTAAACAATCCGGAAGCGACCAACGCCTTGATTGACAAGGATGGATGGCTACATTCTGGAGACATAGCTTACTGGGACGAAGACGAACACTTCTTCATAGTTGACCGCTTGAAGTCTTTAATTAAATACAAAGGATATCAGGTAATGAAGATTTTTACATGCACACACGCTACAATACCTGTAGGTGGCCCCCGCTGAATTGGAATCGATATTGTTACAACACCCCAACATCTTCGACGCGGGCGTGGCAGGTCTTCCCGACGATGACGCCGGTGAACTTCCCGCCGCCGTTGTTGTTTTGGAGCACGGAAAGACGATGACGGAAAAAGAGATCGTGGATTACGTCGCCAGTAAATGAATTCGTTTTACGTTACTCGTACTACAATTCTTTTCATAGGTCAAGTAACAACCGCGAAAAAGTTGCGCGGAGGAGTTGTGTTTGTGGACGAAGTACCGAAAGGTCTTACCGGAAAACTCGACGCAAGAAAAATCAGAGAGATCCTCATAAAGGCCAAGAAGGGCGGAAAGTCCAAATTG**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTT

RL093A	pTET-BBa_B0034-T33A R65M S116A M135I-luxR-BBa_B0015-pluxR-BBa_B0032-luciferase-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGGCGAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGATGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACAGCGGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATTCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**GAAGACGCCAAAAACATAAAGAAAGGCCCGGCGCCATTCTATCCTCTAGAGGATGGAACCGCTGGAGAGCAACTGCATAAGGCTATGAAGAGATACGCCCTGGTTCCTGGAACAATTGCTTTTGTGAGTATTTCTGTCTGATTTCTTTCGAGTTAACGAAATGTTCTTATGTTTCTTTAGACAGATGCACATATCGAGGTGAACATCACGTACGCGGAATACTTCGAAATGTCCGTTCGGTTGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCACAGAATCGTCGTATGCAGTGAAAACTCTCTTCAATTCTTTATGCCGGTGTTGGGCGCGTTATTTATCGGAGTTGCAGTTGCGCCCGCGAACGACATTTATAATGAACGTAAGCACCCTCGCCATCAGACCAAAGGGAATGACGTATTTAATTTTTAAGGTGAATTGCTCAACAGTATGAACATTTCGCAGCCTACCGTAGTGTTTGTTTCCAAAAAGGGGTTGCAAAAAATTTTGAACGTGCAAAAAAAATTACCAATAATCCAGAAAATTATTATCATGGATTCTAAAACGGATTACCAGGGATTTCAGTCGATGTACACGTTCGTCACATCTCATCTACCTCCCGGTTTTAATGAATACGATTTTGTACCAGAGTCCTTTGATCGTGACAAAACAATTGCACTGATAATGAATTCCTCTGGATCTACTGGGTTACCTAAGGGTGTGGCCCTTCCGCATAGAACTGCCTGCGTCAGATTCTCGCATGCCAGGTATGTCGTATAACAAGAGATTAAGTAATGTTGCTACACACATTGTAGAGATCCTATTTTTGGCAATCAAATCATTCCGGATACTGCGATTTTAAGTGTTGTTCCATTCCATCACGGTTTTGGAATGTTTACTACACTCGGATATTTGATATGTGGATTTCGAGTCGTCTTAATGTATAGATTTGAAGAAGAGCTGTTTTTACGATCCCTTCAGGATTACAAAATTCAAAGTGCGTTGCTAGTACCAACCCTATTTTCATTCTTCGCCAAAAGCACTCTGATTGACAAATACGATTTATCTAATTTACACGAAATTGCTTCTGGGGGCGCACCTCTTTCGAAAGAAGTCGGGGAAGCGGTTGCAAAACGGTGAGTTAAGCGCATTGCTAGTATTTCAAGGCTCTAAAACGGCGCGTAGCTTCCATCTTCCAGGGATACGACAAGGATATGGGCTCACTGAGACTACATCAGCTATTCTGATTACACCCGAGGGGGATGATAAACCGGGCGCGGTCGGTAAAGTTGTTCCATTTTTTGAAGCGAAGGTTGTGGATCTGGATACCGGGAAAACGCTGGGCGTTAATCAGAGAGGCGAATTATGTGTCAGAGGACCTATGATTATGTCCGGTTATGTAAACAATCCGGAAGCGACCAACGCCTTGATTGACAAGGATGGATGGCTACATTCTGGAGACATAGCTTACTGGGACGAAGACGAACACTTCTTCATAGTTGACCGCTTGAAGTCTTTAATTAAATACAAAGGATATCAGGTAATGAAGATTTTTACATGCACACACGCTACAATACCTGTAGGTGGCCCCCGCTGAATTGGAATCGATATTGTTACAACACCCCAACATCTTCGACGCGGGCGTGGCAGGTCTTCCCGACGATGACGCCGGTGAACTTCCCGCCGCCGTTGTTGTTTTGGAGCACGGAAAGACGATGACGGAAAAAGAGATCGTGGATTACGTCGCCAGTAAATGAATTCGTTTTACGTTACTCGTACTACAATTCTTTTCATAGGTCAAGTAACAACCGCGAAAAAGTTGCGCGGAGGAGTTGTGTTTGTGGACGAAGTACCGAAAGGTCTTACCGGAAAACTCGACGCAAGAAAAATCAGAGAGATCCTCATAAAGGCCAAGAAGGGCGGAAAGTCCAAATTG**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
RL094A	pTET-BBa_B0034-T33A S116A M135I luxR-BBa_B0015-pluxR-BBa_B0032-luciferase-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGGCGAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACAGCGGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATTCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**GAAGACGCCAAAAACATAAAGAAAGGCCCGGCGCCATTCTATCCTCTAGAGGATGGAACCGCTGGAGAGCAACTGCATAAGGCTATGAAGAGATACGCCCTGGTTCCTGGAACAATTGCTTTTGTGAGTATTTCTGTCTGATTTCTTTCGAGTTAACGAAATGTTCTTATGTTTCTTTAGACAGATGCACATATCGAGGTGAACATCACGTACGCGGAATACTTCGAAATGTCCGTTCGGTTGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCACAGAATCGTCGTATGCAGTGAAAACTCTCTTCAATTCTTTATGCCGGTGTTGGGCGCGTTATTTATCGGAGTTGCAGTTGCGCCCGCGAACGACATTTATAATGAACGTAAGCACCCTCGCCATCAGACCAAAGGGAATGACGTATTTAATTTTTAAGGTGAATTGCTCAACAGTATGAACATTTCGCAGCCTACCGTAGTGTTTGTTTCCAAAAAGGGGTTGCAAAAAATTTTGAACGTGCAAAAAAAATTACCAATAATCCAGAAAATTATTATCATGGATTCTAAAACGGATTACCAGGGATTTCAGTCGATGTACACGTTCGTCACATCTCATCTACCTCCCGGTTTTAATGAATACGATTTTGTACCAGAGTCCTTTGATCGTGACAAAACAATTGCACTGATAATGAATTCCTCTGGATCTACTGGGTTACCTAAGGGTGTGGCCCTTCCGCATAGAACTGCCTGCGTCAGATTCTCGCATGCCAGGTATGTCGTATAACAAGAGATTAAGTAATGTTGCTACACACATTGTAGAGATCCTATTTTTGGCAATCAAATCATTCCGGATACTGCGATTTTAAGTGTTGTTCCATTCCATCACGGTTTTGGAATGTTTACTACACTCGGATATTTGATATGTGGATTTC

		GAGTCGTCTTAATGTATAGATTTGAAGAAGAGCTGTTTTTACGATCCCTTCAGGATTACAAAATTCAAAGTGCGTTGCTAGTACCAACCCTATTTTCATTCTTCGCCAAAAGCACTCTGATTGACAAATACGATTTATCTAATTTACACGAAATTGCTTCTGGGGGCGCACCTCTTTCGAAAGAAGTCGGGGAAGCGGTTGCAAAACGGTGAGTTAAGCGCATTGCTAGTATTTCAAGGCTCTAAAACGGCGCGTAGCTTCCATCTTCCAGGGATACGACAAGGATATGGGCTCACTGAGACTACATCAGCTATTCTGATTACACCCGAGGGGGATGATAAACCGGGCGCGGTCGGTAAAGTTGTTCCATTTTTTGAAGCGAAGGTTGTGGATCTGGATACCGGGAAAACGCTGGGCGTTAATCAGAGAGGCGAATTATGTGTCAGAGGACCTATGATTATGTCCGGTTATGTAAACAATCCGGAAGCGACCAACGCCTTGATTGACAAGGATGGATGGCTACATTCTGGAGACATAGCTTACTGGGACGAAGACGAACACTTCTTCATAGTTGACCGCTTGAAGTCTTTAATTAAATACAAAGGATATCAGGTAATGAAGATTTTTACATGCACACACGCTACAATACCTGTAGGTGGCCCCCGCTGAATTGGAATCGATATTGTTACAACACCCCAACATCTTCGACGCGGGCGTGGCAGGTCTTCCCGACGATGACGCCGGTGAACTTCCCGCCGCCGTTGTTGTTTTGGAGCACGGAAAGACGATGACGGAAAAAGAGATCGTGGATTACGTCGCCAGTAAATGAATTCGTTTTACGTTACTCGTACTACAATTCTTTTCATAGGTCAAGTAACAACCGCGAAAAAGTTGCGCGGAGGAGTTGTGTTTGTGGACGAAGTACCGAAAGGTCTTACCGGAAAACTCGACGCAAGAAAAATCAGAGAGATCCTCATAAAGGCCAAGAAGGGCGGAAAGTCCAAATTG**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA
T9002	pTET-BBa_B0034-luxR-BBa_B0015-pluxR-BBa_B0032-GFPmut3b-BBa_B0015	TCCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCACTACTAGAG*AAAGAGGAGAAA*TACTAG**ATG**AAAAACATAAATGCCGACGACACATACAGAATAATTAATAAAATTAAAGCTTGTAGAAGCAATAATGATATTAATCAATGCTTATCTGATATGACTAAAATGGTACATTGTGAATATTATTTACTCGCGATCATTTATCCTCATTCTATGGTTAAATCTGATATTTCAATCCTAGATAATTACCCTAAAAAATGGAGGCAATATTATGATGACGCTAATTTAATAAAATATGATCCTATAGTAGATTATTCTAACTCCAATCATTCACCAATTAATTGGAATATATTTGAAAACAATGCTGTAAATAAAAAATCTCCAAATGTAATTAAAGAAGCGAAAACATCAGGTCTTATCACTGGGTTTAGTTTCCCTATTCATACGGCTAACAATGGCTTCGGAATGCTTAGTTTTGCACATTCAGAAAAAGACAACTATATAGATAGTTTATTTTTACATGCGTGTATGAACATACCATTAATTGTTCCTTCTCTAGTTGATAATTATCGAAAAATAAATATAGCAAATAATAAATCAAACAACGATTTAACCAAAAGAGAAAAAGAATGTTTAGCGTGGGCATGCGAAGGAAAAAGCTCTTGGGATATTTCAAAAATATTAGGTTGCAGTGAGCGTACTGTCACTTTCCATTTAACCAATGCGCAAATGAAACTCAATACAACAAACCGCTGCCAAAGTATTTCTAAAGCAATTTTAACAGGAGCAATTGATTGCCCATACTTTAAAAAT**TAA**TAACACTGATAGTGCTAGTGTAGATCACTACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATATACTAGAGACCTGTAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTTATAGTCGAATAAATACTAGAG*TCACACAGGAAAG*TACTAG**ATG**ACTATAATGATAAAAAAATCGGATTTTTTGGCAATTCCATCGGAGGAGTATAAAGGTATTCTAAGTCTTCGTTATCAAGTGTTTAAGCAAAGACTTGAGTGGGACTTAGTTGTAGAAAATAACCTTGAATCAGATGAGTATGATAACTCAAATGCAGAATATATTTATGCTTGTGATGATACTGAAAATGTAAGTGGATGCTGGCGTTTATTACCTACAACAGGTGATTATATGCTGAAAAGTGTTTTTCCTGAATTGCTTGGTCAACAGAGTGCTCCCAAAGATCCTAATATAGTCGAATTAAGTCGTTTTGCTGTAGGTAAAAATAGCTCAAAGATAAATAACTCTGCTAGTGAAATTACAATGAAACTATTTGAAGCTATATATAAACACGCTGTTAGTCAAGGTATTACAGAATATGTAACAGTAACATCAACAGCAATAGAGCGATTTTTAAAGCGTATTAAAGTTCCTTGTCATCGTATTGGAGACAAAGAAATTCATGTATTAGGTGATACTAAATCGGTTGTATTGTCTATGCCTATTAATGAACAGTTTAAAAAAGCAGTCTTAAAT**TAA**TAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA

*Promoters are underlined, start and stop codons are in bold, the RBS is in italics, and linker sequences of encoded fusion proteins are in lowercase. The *lrs* intergenic region is in red.

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