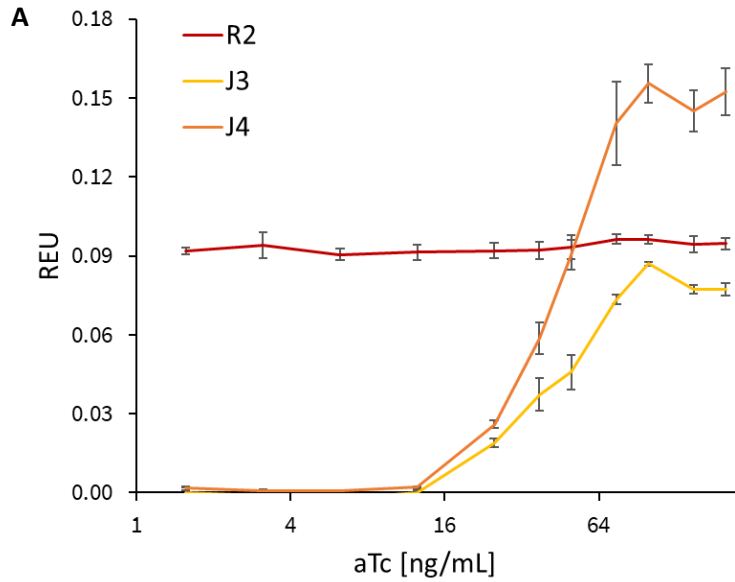


regulated by numerous mechanisms including but not limited to PII (*glnB*) and PZ (*glnZ*), which are key regulatory proteins responsive to the intracellular nitrogen status (1-4). Amongst others, by interacting with the histidine kinase/phosphatase activity of NtrB (*glnL*), PII and PZ affect the phosphorylation state and activity of NtrC (*glnG*), a central transcriptional regulator of numerous genes, including *glnA* encoding GS and *nifA* encoding the nitrogen fixation global transcriptional regulator that affects transcription of the nitrogenase complex NifHDK and many of its accessory *nif* genes(5, 6). Furthermore, PII and PZ form a complex with AmtB (ammonia membrane diffusion transporter) and DraG to affect nitrogenase ribosylation and ammonia sensing and possibly transport (7-10). DraG (nitrogenase ADP-ribosylhydrolase) opposes the activity of DraT (nitrogenase ADP-ribosyltransferase), which deactivates NifHDK by ribosylation. Furthermore, the activities of PII and PZ are in part controlled by their post-translational uridylylation state, which is in turn controlled by the bidirectional UT/UR (uridylyltransferring/uridylylremoving, *glnD*) based on intracellular nitrogen, carbon, and energy status (11). Usually PII and PZ are uridylylated under nitrogen starvation. The directionality and activity of ATase are also thought to be directly modulated by small molecules such as glutamine and alpha-ketoglutarate (α KG) that bind the regulatory region separating the adenylyltransferring and adenylylremoving domains (2, 3). NifL functions as an anti-activator to NifA in some species, such as *A. vinelandii*, and is itself under complex regulation not shown here(12). Other abbreviations: GDH (glutamate dehydrogenase, *gdhA*, *gdhB*), GOGAT (glutamine 2-oxoglutarate amidotransferase (glutamate synthase), *gltBD*).

Figure S2: Testing genetic circuits in *A. brasilense* through red fluorescent protein (RFP) readout.



B

$$REU_X = \frac{\left[\frac{FI}{OD_{600}} \right]_X - \left[\frac{FI}{OD_{600}} \right]_{EV}}{\left[\frac{FI}{OD_{600}} \right]_{R1} - \left[\frac{FI}{OD_{600}} \right]_{EV}}$$

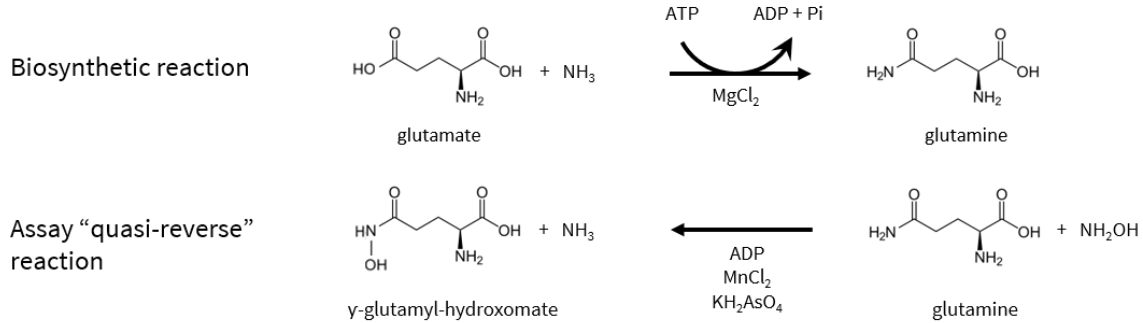
[A] Genetic circuits were tested on pTS7 with circuit gene of interest (GOI) = RFP [see Fig S21 for diagrams and part sequences]. Cells were inoculated and induced with anhydrotetracycline (aTc) at OD_{600} 0.5 in 200 μ L volumes in a 96-well plate at 300 rpm and 30°C. OD_{600} and fluorescence (575/15 excitation and 615/16 emission) were determined 48 h later and relative expression units (REUs) were calculated as shown in

[B]. In the absence of standard genetic tools in *A. brasilense*, the R1 circuit on pTS7 with GOI = RFP was

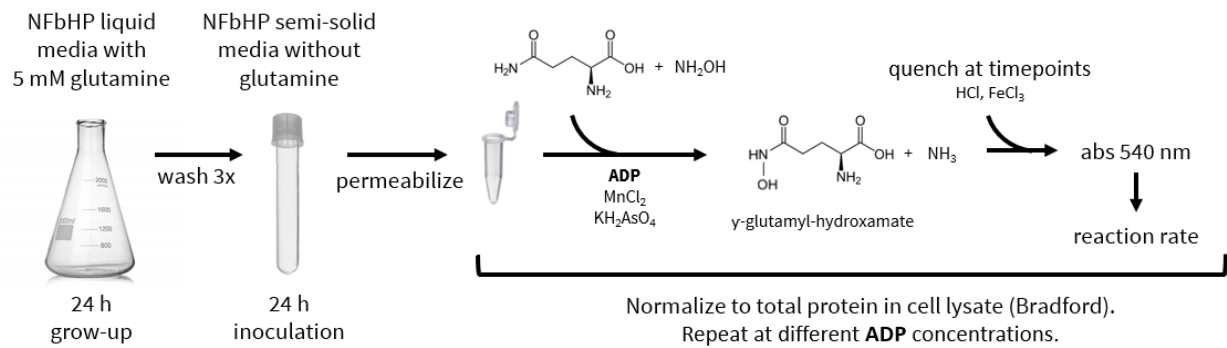
defined as the standard. FI denotes fluorescence intensity, EV denotes empty vector control, X denotes the circuit to be characterized. Error bars are standard deviations of n=4 biological replicates. See [Fig S21] for genetic circuit diagrams and part sequences.

Figure S3: Glutamine synthetase (GS) activity measurements.

A



B

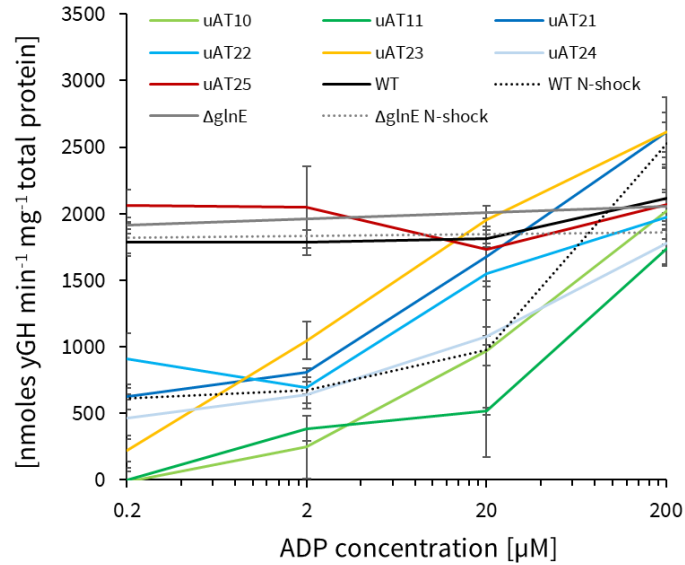


C

$$GS \text{ adenylation state} \approx \frac{\text{total activity} - \text{unadenylylated activity}}{\text{total activity}} \cdot 12 \approx \frac{\left[\frac{dyGH}{dt}\right]_{200\mu\text{M ADP}} - \left[\frac{dyGH}{dt}\right]_{0.2\mu\text{M ADP}}}{\left[\frac{dyGH}{dt}\right]_{200\mu\text{M ADP}}} \cdot 12$$

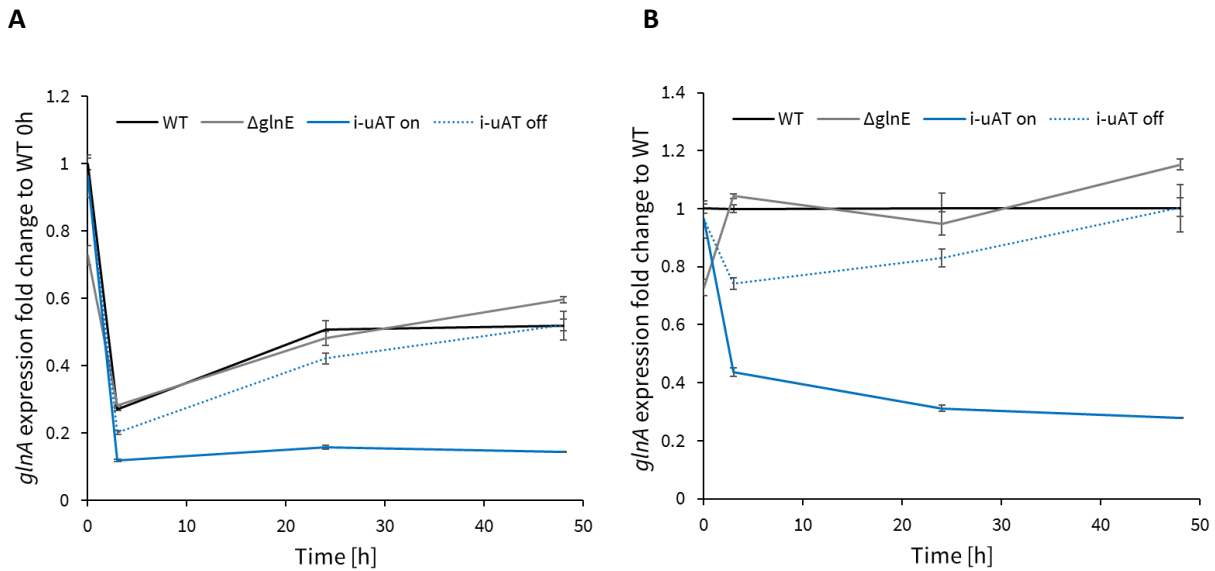
[A] Biosynthetic GS activity and quasi-reverse reaction of the γ -glutamyl hydroxamate assay. **[B]** Schematic of γ -glutamyl hydroxamate (γ GH) assay to determine glutamine synthetase activity of permeabilized whole cells. **[C]** Conversion of glutamine synthetase activities determined by the γ -glutamyl hydroxamate assay to adenylation state.

Figure S4: Average glutamine synthetase (GS) activity measured by γ -glutamyl hydroxamate (yGH) production at multiple ADP concentrations.



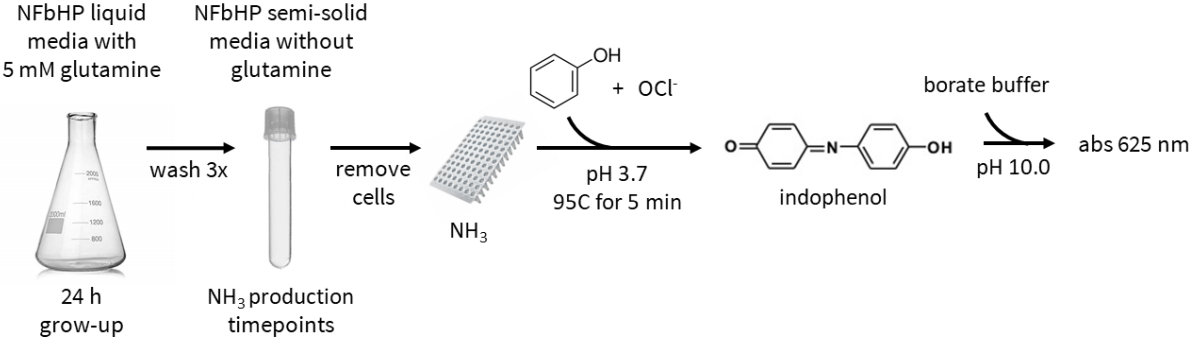
Constitutively unidirectional adenylyltransferases (uAT) expressing *A. brasilense* $\Delta glnE$ strains [circuit R2 from pTS7, see Fig S21] were inoculated at OD₆₀₀ of 0.1 in semisolid NFbHP media and cells were processed as in [Fig S3B]. Rates were taken between 5 and 10 min timepoints and are normalized to total protein content determined by the Bradford assay. Wild-type (WT) and $\Delta glnE$ controls are not expressing uATs. Error bars are standard deviations of n=4 technical replicates. The N-shock controls show GS native adenylylation behavior after a 30 mM ammonium chloride shock 30 minutes prior to cell permeabilization.

Figure S5: Effect of uAT expression on *glnA* transcription under nitrogen fixing conditions.



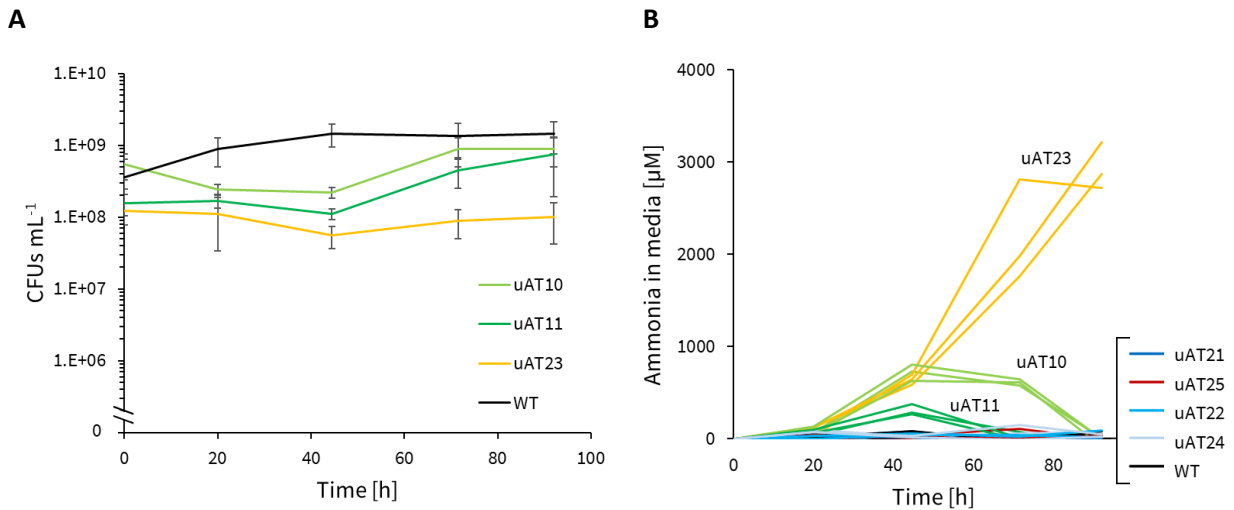
Reverse transcription quantitative polymerase chain reaction (RT-qPCR) analysis of *glnA* transcription levels in *A. brasilense* wild-type (WT), Δ *glnE*, and Δ *glnE* expressing plasmid uAT10 from the inducible circuit J3 [Fig S21] in the on and off states. To establish nitrogen fixing conditions, cells were inoculated in semisolid NFbHP media at OD₆₀₀ 0.1 and the on-state cultures induced with 200 ng/mL anhydrotetracycline at 0 h; biological replicate tubes were setup such that one tube would be harvested and extracted for RNA at each timepoint. Error bars show technical triplicates by RT-qPCR. Fold changes in **[A]** are relative to WT at 0 h (immediately after grow-up in NFbHP with 5 mM glutamine), and relative to WT at each timepoint in **[B]**. Fold changes were computed using the Pfaffl method, incorporating primer efficiencies and *glyA* as a previously reported housekeeping control gene(13, 14).

Figure S6: Ammonia measurements.



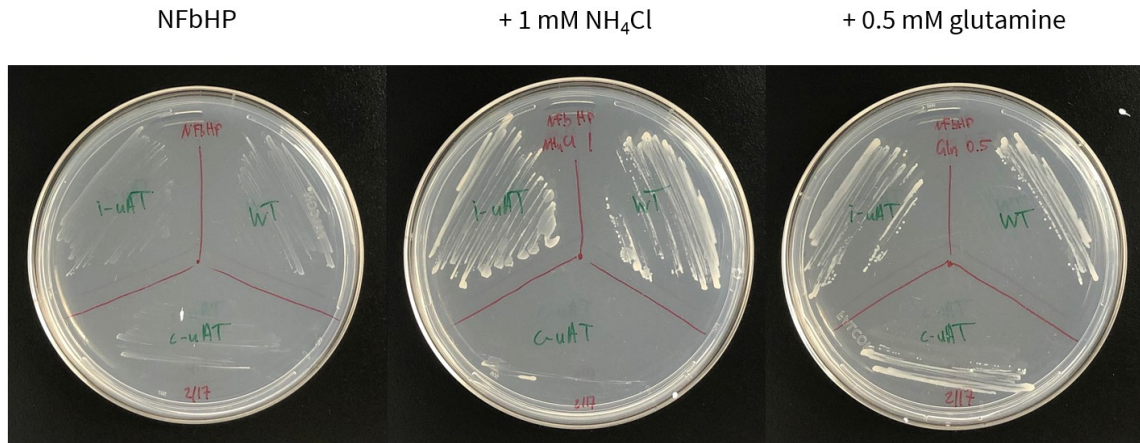
Schematic of indophenol assay to determine ammonia concentration in media.

Figure S7: Colony forming units (CFUs) of constitutive unidirectional adenylyltransferase (uAT) expressing *A. brasilense* Δ *glnE* strains.



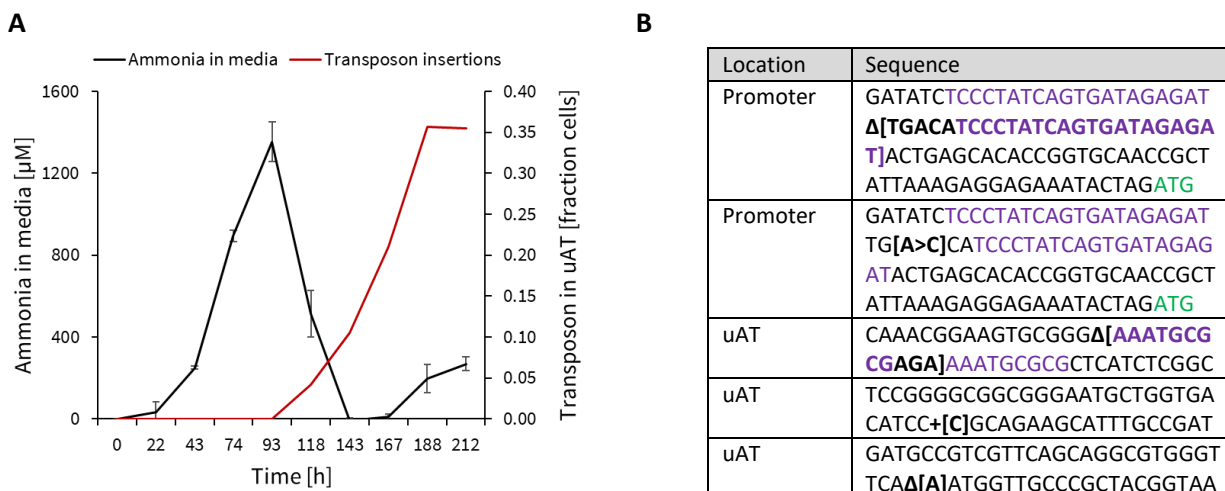
Strains were inoculated at OD₆₀₀ of 0.1 in semisolid NFbHP media [circuit R2 from pTS7, see Fig S21]. **[A]** CFUs were counted from plating culture dilutions on LB agar plates. Error bars are standard deviations of biological triplicates. Ammonia in media is shown in Fig 2C and reproduced here in **[B]** for convenience to show the growth trade-off during ammonia production.

Figure S8: Role of supplemental glutamine on colony formation of uAT expressing strains grown on solid media.



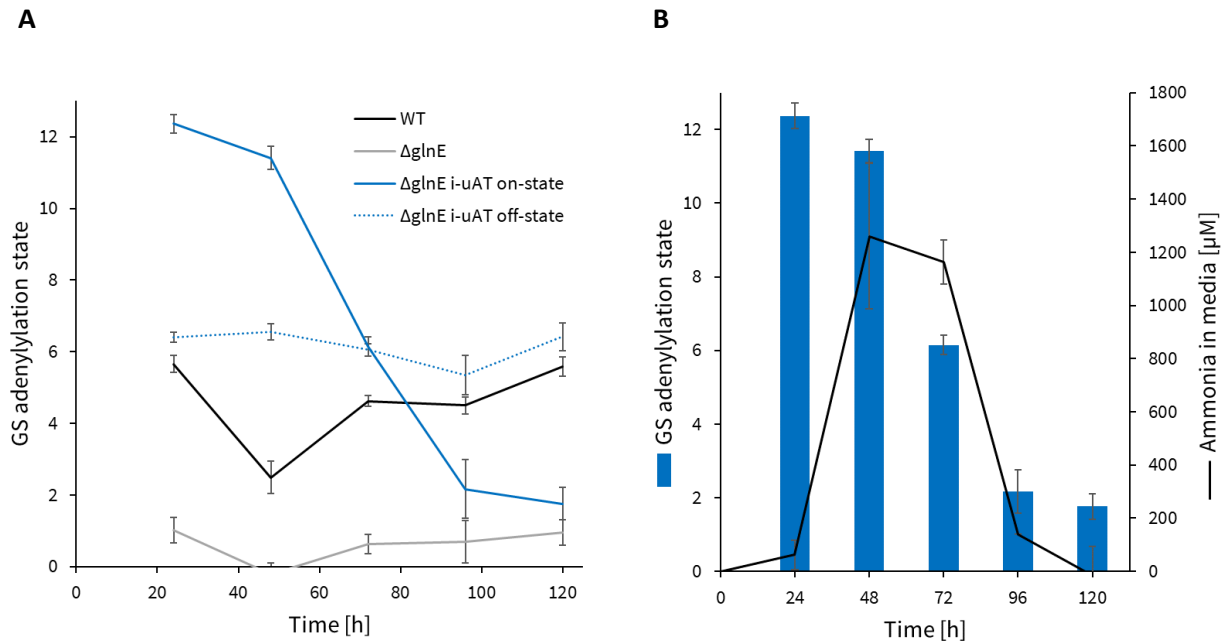
A. brasilense wild-type (WT), $\Delta glnE$ constitutive uAT (c-uAT), and $\Delta glnE$ inducible uAT (i-uAT) expressing strains were plated on NFbHP media with either no added nitrogen source, 1 mM NH₄Cl or 0.5 mM glutamine. The glutamine concentration used was half that of NH₄Cl to keep the concentration of total nitrogen the same. uAT strains are stable chromosome integrations of c-uAT and i-uAT circuits [Fig S21] to allow for antibiotic free plating and growth comparison alongside WT. Plates were imaged after 2 days at 30°C.

Figure S9: Strain stability of ammonia production.



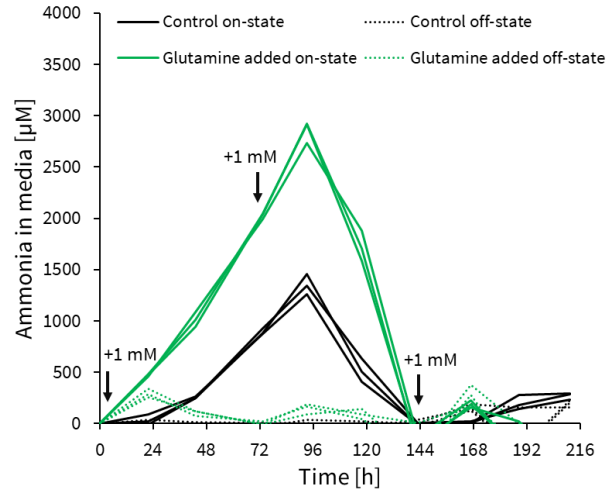
[A] Average time course data of ammonia in the media of *A. brasilense* $\Delta glnE$ with inducible on-state (200 ng mL⁻¹ anhydrotetracycline) expression of uAT10 on circuit J3 from pTS7 [see Fig S21 for genetic circuit diagram and parts] inoculated and induced in semisolid NFbHP media at OD₆₀₀ of 0.1. Ammonia concentrations were determined by the indophenol assay; error bars are standard deviations of biological triplicates [see Fig S4 for assay]. Transposon insertions were quantified by plating cultures at timepoints, PCR amplifying the uAT cassette of individual colonies, and evaluating amplicon length on a DNA agarose gel. 8 colonies were screened per biological replicate culture per timepoint, their transposon insertions summed, and converted to a fraction estimating the total number of cells containing transposons in the uAT cassette at each time point. **[B]** Examples of other, non-transposon mutations found by sequencing; mutational sites have been bolded, repeats colored in purple, and start codons colored in green.

Figure S10: Glutamine synthetase adenylylation changes as ammonia is depleted over time.



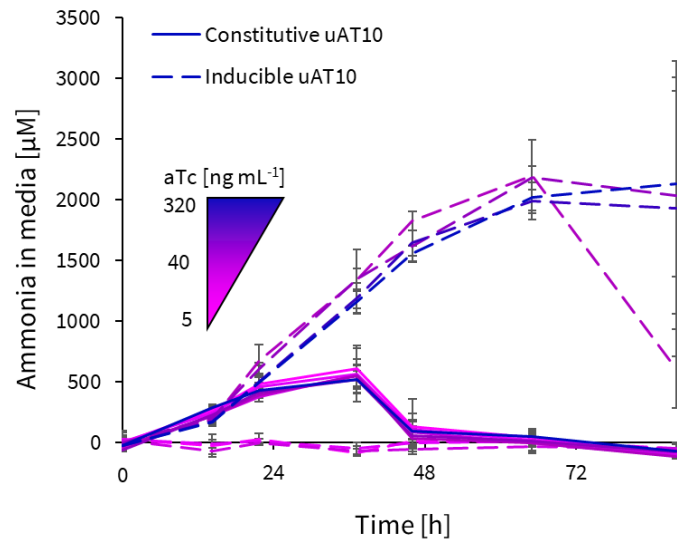
[A] Glutamine synthetase (GS) adenylylation state time-courses under nitrogen fixing conditions for *A. brasilense* wild-type (WT), *glnE* knockout ($\Delta glnE$), and inducible uAT (i-uAT) expression in the $\Delta glnE$ strain either on-state or off-state. **[B]** Ammonia production time course in the i-uAT on-state cultures overlaid onto GS adenylylation. Cells were inoculated in semisolid NFbHP media at OD_{600} 0.1 and the on-state cultures induced with 200 ng/mL anhydrotetracycline at 0 h. The i-uAT in this experiment is pT57 plasmid expressed uAT10 on circuit J3 [Fig S21]. Ammonia was quantified by the indophenol procedure [Fig S5] and GS adenylylation state by the γ -glutamyl hydroxamate assay [Fig S3]. All error-bars are standard deviations of technical triplicates.

Figure S11: Effect of the addition of exogenous glutamine on ammonia production.



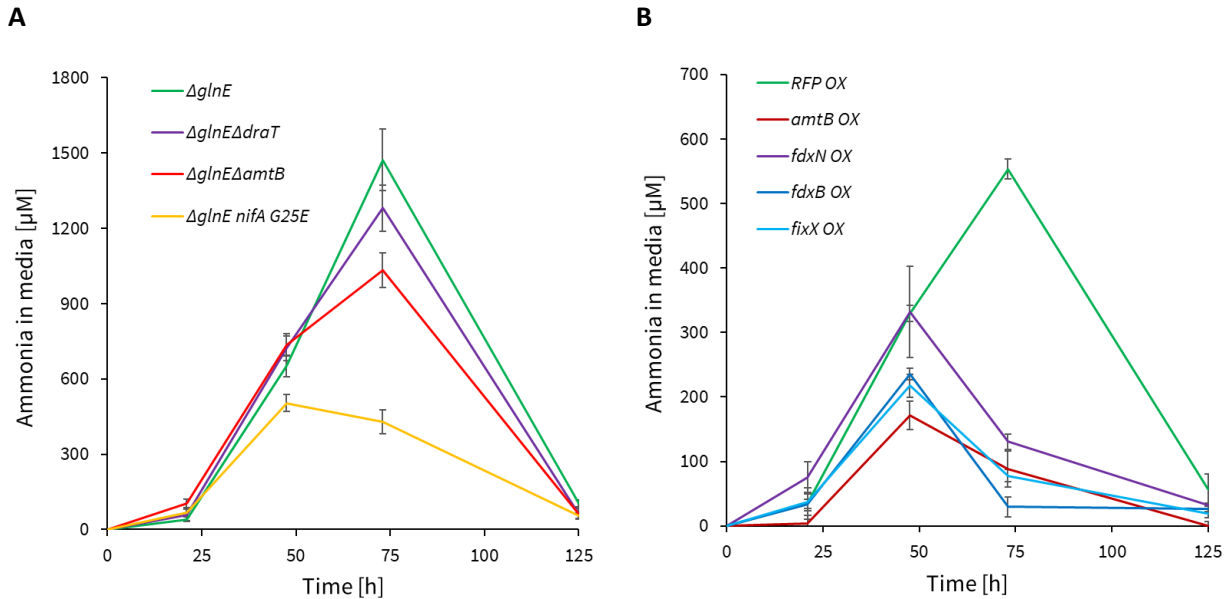
Ammonia production time-courses under nitrogen fixing conditions for *A. brasilense* $\Delta glnE$ expressing plasmid uAT10 from the inducible circuit J3 [Fig S21] with exogenous glutamine added to the media at indicated timepoints. Cells were inoculated in semisolid NFbHP media at OD_{600} 0.1 and the on-state cultures induced with 200 ng/mL anhydrotetracycline at 0 h. Ammonia was quantified by the indophenol procedure [Fig S6].

Figure S12: Ammonia production controlled inducibly.



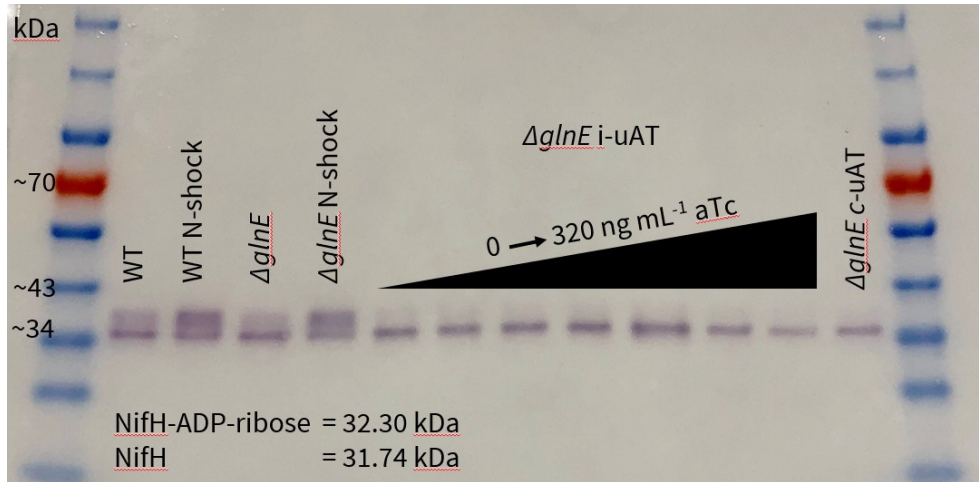
Average time course data of ammonia in the media of *A. brasilense* $\Delta glnE$ with constitutive (circuit R2) and inducible (circuit J3) expression of uAT10 from pTS7 [see Fig S21 for genetic circuit diagrams and parts] inoculated and induced in semisolid NFbHP media at OD_{600} of 0.1 at different anhydrotetracycline (aTc) inducer concentrations. Ammonia concentrations were determined by the indophenol assay; error bars are standard deviations of biological triplicates [see Fig S4 for assay].

Figure S13: Optimizing ammonia production through metabolic engineering.



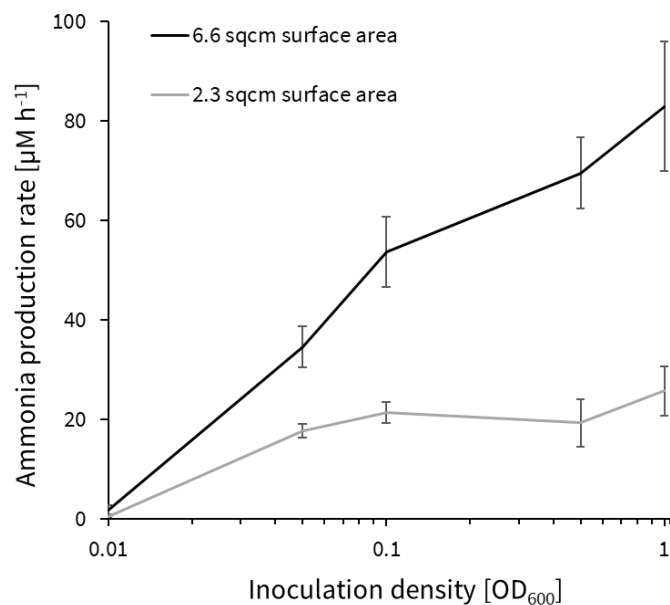
[A] For the knockout lines, native copies of *draT* and *amtB* were independently deleted in the *A. brasilense* $\Delta glnE$ strain to generate double knockouts and the N-terminal region of *nifA* was mutated at G25E by double homologous recombination (15). In these strains, uAT10 was inducibly expressed on the J3 circuit from the pTS7 plasmid. Cells were inoculated in NFbHP at OD₆₀₀ of 0.1 and induced to on-state with 200 ng mL⁻¹ anhydrotetracycline. **[B]** For the overexpression (OX) lines, red fluorescent protein (RFP), *amtB*, *fdxN*, *fdxB*, and *fixX* were expressed as GOI2 on the OX3 circuit, with uAT10 being the first GOI [see Fig S21 for genetic circuit diagrams and parts]. Strains were assayed in the same way as in panel **[A]**. All ammonia concentrations were determined by the indophenol assay; error bars are standard deviations of biological triplicates [see Fig S4 for assay].

Figure S14: Effect of uAT expression on nitrogenase post-translational regulation.



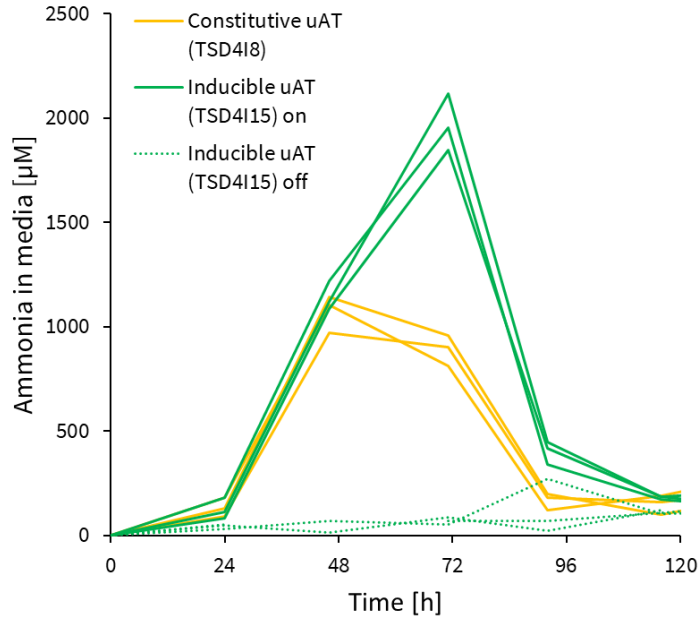
Nitrogenase activity is post-translationally deactivated by ADP-ribosylation through DraT and reactivated by hydrolysis of this post-translational modification through DraG [Fig S1]. Activation states of nitrogenase are shown above by Western blotting of nitrogenase subunit NifH in *A. brasilense* wild-type (WT), $\Delta glnE$, and $\Delta glnE$ stably expressing either constitutive uAT10 (c-uAT) or inducible uAT10 (i-uAT) across different anhydrotetracycline (aTc) inducer concentrations as indicated [Fig S21]. For this, cells were inoculated in semisolid NFbHP media at OD₆₀₀ 0.1 and induced as indicated at 0 h; cells were harvested at 24 h. Nitrogen shocks (N-shocks) denote addition of 20 mM NH₄Cl for 30 minutes prior to cell harvesting.

Figure S15: Gas diffusion limits ammonia production in semisolid media.



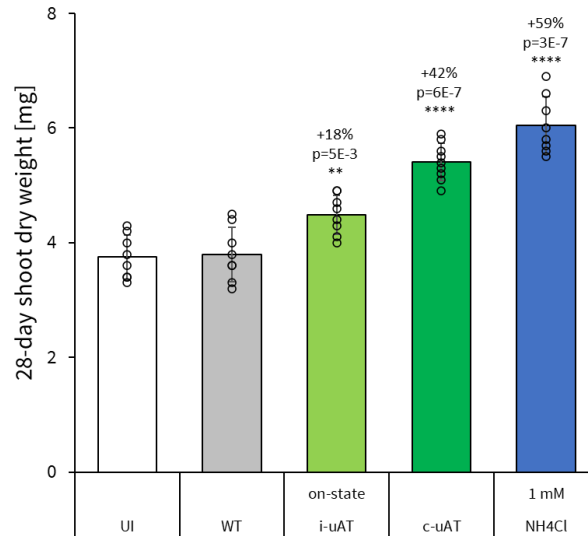
A. brasilense ΔglnE transformed with pTS7 carrying inducible circuit J3 with GOI = uAT10 was inoculated and induced to on-state (200 ng mL^{-1} anhydrotetracycline) at various ODs in 5 mL volumes in both 15 mL falcon tubes (surface area = 2.3 cm^2) and 50 mL falcon tubes (surface area = 6.6 cm^2). Average ammonia production rates were determined by the indophenol method between 24 and 48 h timepoints. Error bars are standard deviations of biological triplicates.

Figure S16: Chromosomally integrated uAT ammonia production.



Time course data of ammonia in the media of *A. brasilense* ΔglnE stable lines for constitutive (TSD418) and inducible (TSD4115) uAT10 unidirectional adenylyltransferases expression [see Fig S21 for genetic circuit diagrams, parts, and notes]. Strains were inoculated in semisolid NFbHP media at OD_{600} of 0.1 and on-state samples were induced with 200 ng mL^{-1} anhydrotetracycline. Ammonia concentrations were determined by the indophenol assay [see Fig S4 for assay].

Figure S17: Effect of uAT expressing *A. brasilense* $\Delta glnE$ strains on shoot dry weight of *S. viridis* in the absence of added sugar in the media.



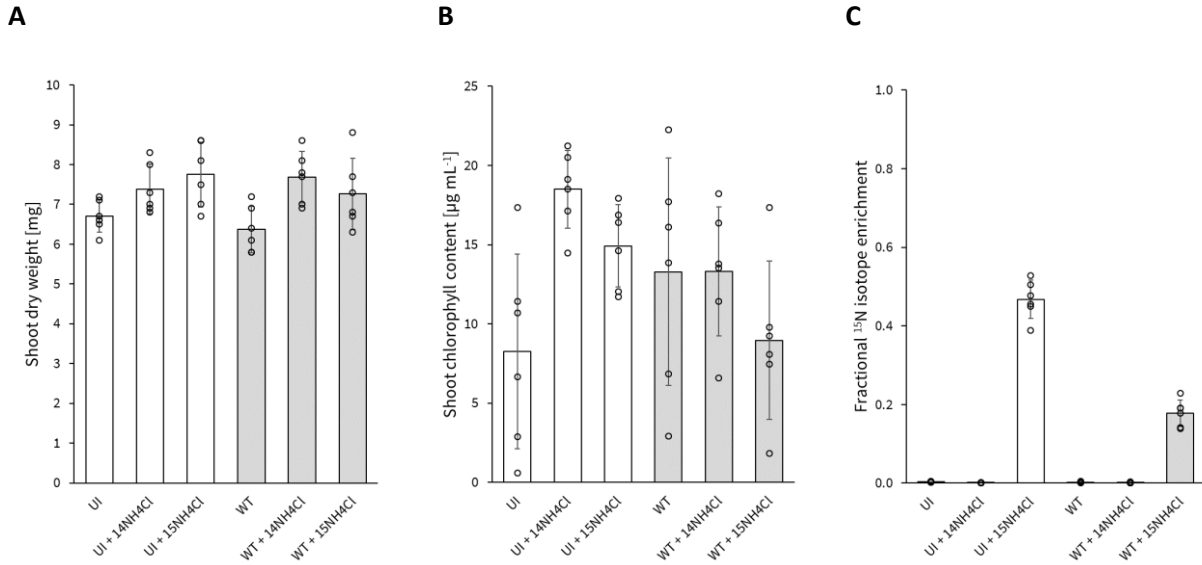
A. brasilense wild-type (WT) and $\Delta glnE$ strains with chromosomally integrated constitutive and inducible uAT10 circuits [Figs S16 and S21] were introduced at OD₆₀₀ 0.1 to 14 day old *S. viridis* plants growing gnotobiotically in modified 1/5 strength NFbHP with sodium lactate dropped out. At the time of inoculation, the i-uAT replicates were induced with 200 ng mL⁻¹ anhydrotetracycline. After an additional 14 days, shoot dry weights were collected. Percent growth promotion values are indicated above each bar and stars indicate p-values of statistical significance compared to WT using a two-sided homoscedastic t-test. All error bars are standard deviations of n=8-9 biological replicates.

Figure S18: Calculation of fractional enrichment of ¹⁵N isotopes in pheophytin.

$$\begin{aligned}
 & \text{fractional } ^{15}\text{N enrichment} \\
 = & \frac{\langle \frac{m}{z} \rangle_X - \langle \frac{m}{z} \rangle_{STD}}{(\text{number of N atoms in molecule}) \cdot (15\text{N neutron mass}) \cdot (\text{maximal enrichment above nat. abundance})} \approx \frac{\langle \frac{m}{z} \rangle_X - \langle \frac{m}{z} \rangle_{STD}}{4 \cdot 0.997 \cdot 0.996} \\
 & \text{where } \langle m/z \rangle = \sum_{\text{isotopes}} (\text{isotope mass} \cdot \text{relative abundance})
 \end{aligned}$$

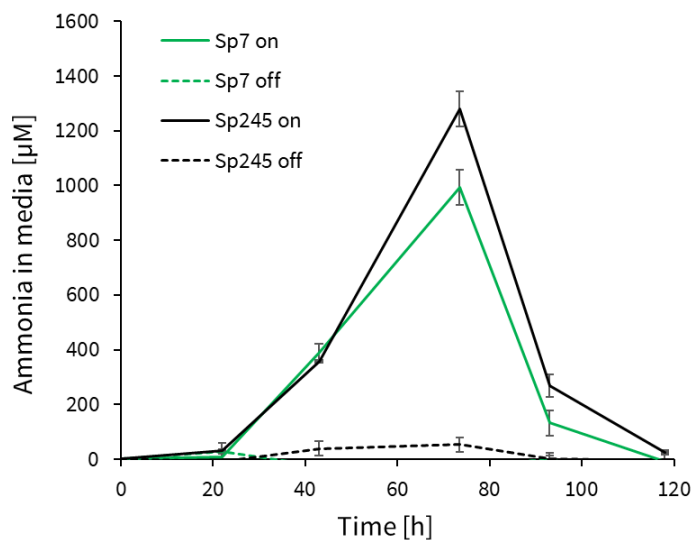
X denotes sample, STD denotes an authentic chlorophyll standard processed to pheophytin and assayed identically to samples of interest, and relative abundances have been normalized to 1. Calculation assumes natural abundance to be 0.4%.

Figure S19: Fertilized controls of *S. viridis* ¹⁵N isotope integration either uninoculated (UI) or wild-type (WT) *A. brasilense* inoculated.



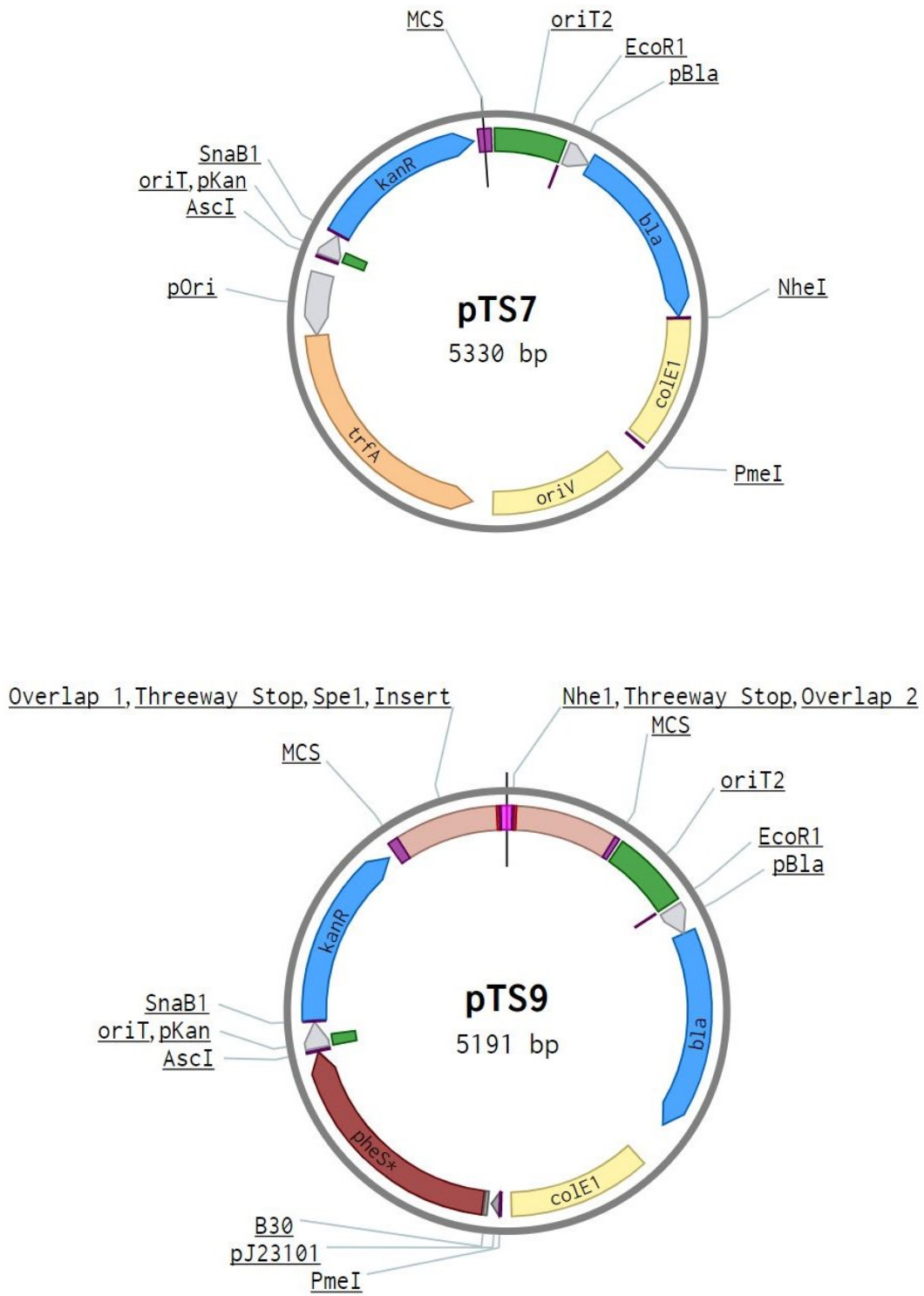
Ammonium chloride fertilizer was introduced at 1 mM and microbes were introduced at OD₆₀₀ 0.1 to 14 day old *S. viridis* plants growing gnotobiotically in modified 1/5 strength NFbHP at room atmosphere. At 14 days post inoculation, shoot dry weight **[A]** and total chlorophyll content **[B]** were collected. Chlorophyll was converted to pheophytin for isotopic analysis **[C]** to determine fractional enrichment of the ¹⁵N isotope [see S12 for calculation]. All error bars are standard deviations of n=6 biological replicates.

Figure S20: Broad applicability of unidirectional adenylyltransferase (uAT) inducible ammonia production.



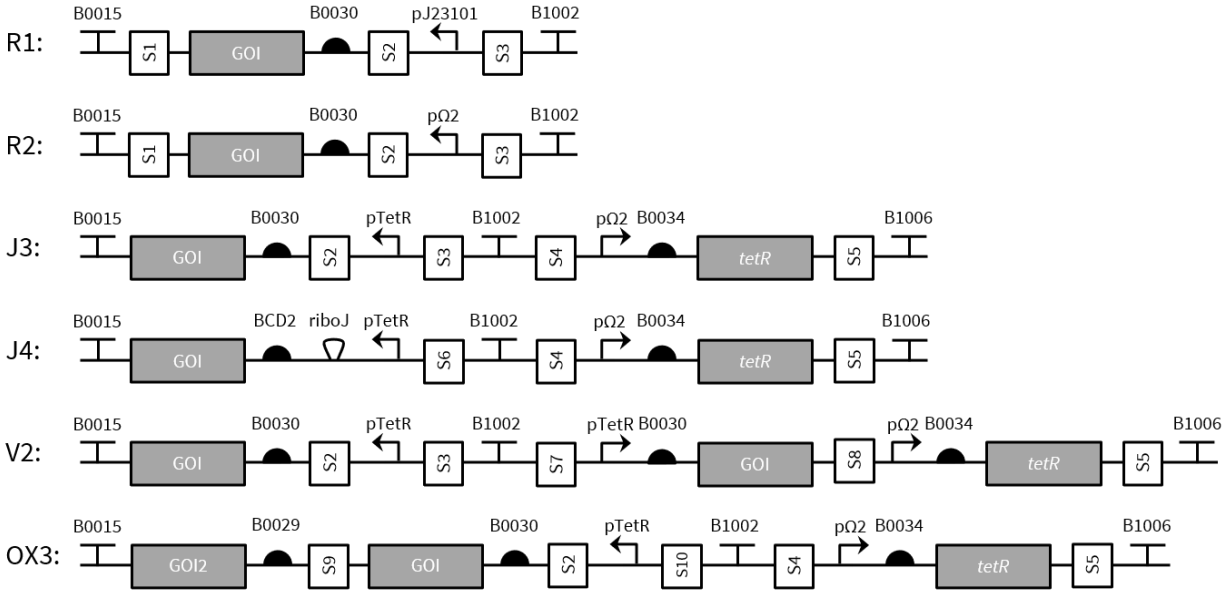
The native *glnE* of *A. brasilense* Sp7 was disrupted and the J3 inducible circuit with uAT10 was inserted in a single step. This engineering was accomplished by single homologous recombination with a pTS7 plasmid that carried 1000 bp of *glnE* homology instead of *oriV* and *trfA*. The Sp245 control is the *A. brasilense* Sp245 Δ *glnE* strain carrying the J3 inducible circuit with uAT10 on a plasmid. Strains were inoculated in semisolid NFbHP media at an OD_{600} of 0.1 and on-state samples were induced with 200 ng mL^{-1} anhydrotetracycline. Error bars are standard deviations of biological triplicates. [See Fig S21 for genetic circuits and parts].

Figure S21A: Plasmids designed for *A. brasilense* used in this work.



The *oriV* broad host range origin for replication and kanamycin resistance were used for positive selection on our replicative plasmids (pTS7), while our integrative plasmids carried a negative selection marker and 0.5-1.0 kb homologous genomic regions instead of *oriV* for chromosome editing (pTS9). We find *pheS** to be highly effective as a negative selection maker in *A. brasilense*, compared to other standard markers such as *sacB* (16). Overlaps 1 and 2 of pTS9 are 500-1000 bp of chromosome upstream and downstream of loci of interest; insert is the sequence to add or replace between homologous regions. Genetic circuit inserted into either plasmid are shown in [Fig S21B] and part sequences are shown in [Fig S21C]. Sequences of these plasmids have been deposited at GenBank with accession numbers MW835297 for pTS7 and MW835298 for pTS9.

Figure S21B: Genetic circuit diagrams.



Abbreviations are as follows, genes of interest (GOI): red fluorescent protein (RFP) for circuit testing or unidirectional adenylyltransferase (uAT) for ammonia production. Circuits R1 and R2 are for constitutive expression, J3 and J4 are for inducible expression. RFP data of these circuits is shown in [Figs S2A-B]. Circuit V2 contains a second copy of GOI for increased evolutionary stability (recommended to be codon refactored) [Fig 3C], while circuit OX3 contains polycistronic GOI2 for overexpression of an additional gene of interest, such as *amtB*, *fdxB*, *fdxN*, or *fixX* [Fig S13B]. All part sequences are shown and annotated in [Fig S21C]. Sequences of these circuits have been deposited at GenBank with accession numbers MW835306-MW835311 in the order they are shown above; GOI place holders for these submissions are as follows: GOI=RFP for circuits R1 and R2; GOI=uAT10 for circuits J3, J4, V2, and OX3; GOI2=RFP for circuit OX3.

Figure S21C: Sequences of genetic parts used in plasmids [Fig S21A] and circuits [Fig S21B]. All part sequences below are shown in their forward direction as depicted in [Fig S21B]; promoter, ribosome binding site (RBS), terminator, and spacer directions correspond to the genes they are flanking. Note: RBSs are separated 6 bp from gene start codons - those spacers are not shown. Parts named BBa are from the BioBrick Registry of Standard Biology Parts; other part sources are either described if common, or referenced if specific. GenBank accession numbers are shown for deposited sequences (all uATs).

Name	Notes	Sequence
<i>colE1</i>	Origin of replication from pUC19	TTGAGATCCTTTTTTCTGCGCTAATCTGCTGCTTGCACAAACAAAAACCACCGTACCAGCGGTGGTTTG TTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGTAACTGGCTTCAGCAGAGCGCAGATACCAAATA CTGTTCTTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCCTACATACCTCGCTC TGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAAGTCGTGCTTACCGGTTGGACTCAAGACGA TAGTTACCGGATAAGGCGCAGCGGTGGGGTGAACGGGGGGTTCTGTGCACACAGCCAGCTTGGAGCGA ACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGA AAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGG GAAACGCCTGGTATCTTATAGTCTGTGCGGGTTCCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCT CGTCAGGGGGCGGAGCCTATGAAAA
<i>oriV</i>	Origin of replication from pEAQ-HT (17)	CCGGGAGGGTTTCGAGAAGGGGGGACCCCCCTTCGGCGTGCAGCGTCCAGCGCACAGGGCGCAGCCC TGTTAAAAACAAGGTTTATAAATATTGGTTTAAAAAGCAGGTTAAAAGACAGGTTAGCGGTGGCCGAAAA ACGGGCGGAAACCTTGCAAATGCTGGATTTTCTGCTGTGGACAGCCCTCAAATGTCAATAGGTGCGC CCCTCATCTGTGCACTCTGCCCTCAAGTGTCAAGGATCGCGCCCTCATCTGTGAGTGTGCGCCCT CAAGTGTCAATACCGCAGGGCACTTATCCCGAGGCTTGTCCACATCATCTGTGGGAAACTCGCGTAAATC AGGCGTTTTGCGCGATTTGCGAGGGTGGCCAGCTCCACGTGCGCGCGCGAAATCGAGCCTGCCCTCATCT GTCAACGCCGCGGGGTGAGTCGGCCCTCAAGTGTCAACGTCCGCCCTCATCTGTGAGTGGGGCCA AGTTTTCCGCGAGGTATCCACAACGCCGGCGCGGTGTCTCGCACAGGCTTCGACGCGCTTTCGCG CGCGTTGCGAGGGCCATAGACGGCCGACGCCAGCGGCGAGGGCAACCAGCCCG
<i>trfA</i>	Required for <i>oriV</i> , also from pEAQ-HT (17)	ATGAATCGGACGTTTGACCGGAAGGCATACAGGCAAGAACTGATCGACGCGGGTTTTCCGCCGAGGAT GCCGAAACCATCGAAGCCGACCGTCATGCGTGCGCCCGCGAAACCTTCCAGTCCGTGCGCTCGATGG TCCAGCAAGCTACGGCCAAGATCGAGCGCGACAGCGTGCAACTGGCTCCCCCTGCCCTGCCCGCCATC GGCCCGGTGGAGCGTTACGTGCTCTCGAACAGGAGGCGGCAAGTTTGGCGAAGTCGATGACCATCGA CACGCGAGGAACTATGACGACCAAGAAGCGAAAAACCGCCGCGAGGACCTGGCAAAACAGGTACGCG AGGCCAAGCAGGCCGCTTGTGAAACACACGAAGCAGCAGATCAAGGAAATGCAGCTTTCCTTGTTCGA TATTGCGCCGTGGCCGGACACGATGCGAGCGATGCCAAACGACACGCGCCGCTCTGCCCTGTTCAACCAG CGCAACAAGAAATCCCGCGCAGGGCGTGCAAAAAAGGTCATTTTTCCACGTCAACAAGGACGTGAAG ATCACCTACACCGCGTCGAGCTGCGGGCCGACGATGACGAACTGGTGTGGCAGCAGGTGTTGGAGTAC GCGAAGCGCACCCCTATCGGCGAGCCGATCACCTTCAGTTCACGAGCTTTCAGGACCTGGGCTGGT CGATCAATGGCCGTTATTACGAAGGCCGAGGAATGCTGTCGCGCTACAGGCGACGGCGATGGGCT TCAGTCCGACCGCTTGGGCACCTGGAATCGGTGTCGCTGCTGCACCGCTTCCGCGTCTGGACCGTGG CAAGAAACGTCCTGTTGCCAGGTCCTGATCGACGAGGAAATCGTCGTGCTGTTTGTGGCGACACTAC ACGAAATTCATATGGGAGAAGTACCGCAAGCTGTGCGCGACGGCCGACGGATGTTGACTATTTTCAGCT CGCACCGGAGCGTACCCGCTCAAGCTGAAACCTTCCGCCTCATGTGCGGATCGGATTCCACCCCGCT GAAGAAAGTGGCGCAGCAGGTGCGCGAAGCCTGCGAAGATTGCGAGGCGAGCGGCTGGTGGAAACAG CCTGGGTCAATGATGACCTGGTGCATTGCAACGCTAG
<i>oriT</i>	Origin of transfer (also functions as a promoter and is part of pKan) from pBBR1	GGTCACGACTTTGCGAAGCAAAGTCTAGTGAGTATACTCAAGCATTGAGTGG

<i>oriT2</i>	Origin of transfer from pVO155 (18)	GATAGGTGGGCTGCCCTTCTGGTTGGCTTGGTTTCATCAGCCATCCGCTTGCCCTCATCTGTTACGCCGGC GGTAGCCGGCCAGCCTCGCAGAGCAGGATTCCCGTTGAGCACCGCCAGGTGCGAATAAGGGACAGTGAA GAAGGAACACCCGCTCGCGGGTGGCCCTACTTCACCTATCCTGCCCGGCTGACGCCGTTGGATACACCAA GGAAAGTCTACACGAACCCCTTGGCAAACCTGTATATCGTGCGAAAAAGGATGGATATACCGAAAAAA TCGCTATAATGACCCGAAGCAGGGTTATGACGCCGAAAAACG
<i>bla</i>	Ampicillin resistance from pUC19	ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTGCGGCATTTGCTTCTCTGTTTTGCTCACCC AGAAACGCTGGTAAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGA TCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCGAAGAACGTTTTCAATGATGAGCACTTTTAAAG TTCTGCTATGTGGCGCGTATTATCCGTATTGACGCCGGGCAAGAGCAACTCGGTGCGCCGATACACTAT TCTCAGAATGACTTGGTTGAGTACTCACCAGTACAGAAAAAGCATCTTACGGATGGCATGACAGTAAGAG AATTATGCAGTGTGCCATAACCATGAGTGATAAACAAGTGGCCAACTACTTCTGACAACGATCGGAGG ACCGAAGGAGCTAACCGCTTTTTGCAACAATGGGGGATCATGTAACCTGCCTTGATCGTTGGGAACCG GAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGC GCAAACTATTAAGTGGCAACTACTTACTAGCTTCCCGGCAACAATTAAGACTGGATGGAGGGGAT AAAGTTGCAGGACCACTTCTGCGCTGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGG TGAGCTGGGTCTCGCGGTATCATTGACGACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCT ACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCTCACTGA TTAAGCATTGGTAA
<i>kanR</i>	Kanamycin resistance from pBBR1	ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACT GGGCACAACAGACAATCGGCTGCTGTGATGCCCGCTGTTCCGGCTGTGACGCGAGGGGCGCCCGTTCT TTTTGTCAAGACGACCTGTCGGTCCCTGAATGAAGTCAAGGACGAGGAGCGCGGCTATCGTGGCTG GCCACGACGGCGTTCCTTGCAGCTGTGCTCGAGCTTGTCACTGAAGCGGGAAGGGACTGGCTGCTAT TGGCGAAGTGGCGGGCAGGATCTCTGTCTCATCTCACCTTGTCTCTGCCGAGAAAGTATCCATCATGGCT GATGCAATGCGCGGCTGCATACGCTTGTATCCGGCTACCTGCCATTGACACCACGAAACATTCGCA TCGAGCGAGCAGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGG GGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGCGCGCATCCCGACGCGGAGGATCTCGTCTGTA CCCATGGCGATGCCTGCTTCCGAATATCATGGTGAAAATGGCCGTTTTCTGGATTATCGACTGTGGC CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCG GCGAATGGGTGACCGCTTCTCGTGTTCACGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTAT CGCCTTCTGACGAGTCTTCTGA
<i>pheS*</i>	<i>E. coli pheS</i> mutated at T254A and A307G(16)	ATGCTGGACGCCCTGAAAGACGAAGTCTGAGCCAAGTGAACCGCGCCGGTATCTGGCGGCTCTAGAG GAAGTGC CGGTGACCGCTCTCGGCAAGAAAGGTAGGATCACCGGCTCATGAAAGAGCTTGGGGGCTTG TCGCCGATGAACCGCGAAGCTGGGCAACAGCTGAACGCCCTGAAGGATGAAATCGCCGCGCGGATC GACGGGCGAAGGCCGACCTGGCCCGCCCATCTCGAGGCGCGTTCAGGCGGAGCGCATTGATGTA ACCCTCCCGGTGCGACCGGAGACCGAAGGGCGCATCCATCCTATCTCACAACCATAGACGAAATGGTCC CCATCTTCCGCTGAAATGGGCTTTCCGTGGCAGAAGGCCCGATGTGGAAGACGATTTTCATAATTTACC GCCCTTAACCTTCCACCCGGCCACCCCGCAGGGACATGCATGACACCTTCTATCTGCCCGACGAGGTGA CAAGAAAATGCTGCTCAGGACGCACACCTCCCGGTGCAGGTCGCGACGATGCTCAACAAGAAGCCCCG ATCCGCATCATTGCTCCCGTCTGACGTATCGTTACAGTATGATATGACCCACACCCCGATGTTCCATCAA ATCGAGGATTGGTGTAGACGAAGCAACCCATATGGCCATCTGAAGGGATGCTGATCGAATTTTGTG GCGCGTCTTCGATGTCGACGATTTGCCGTTGCGTTTCCGTCTAGCTTCTTCCCTTTCGCTGAACCCCTCAG CGAAGTTGACATCGGTTGCAGCAGGAAGGGCGGTAAGTCAAGCTGGGCAACTACGGAGACTGGCTCGA AATCTGGGCTGCGGTATGGTGCATCCCAATGTCTGGAAGCTGCGGTATCGACTCCACCAAGTACCGA GGCTTCGGCTTCGGATGGGAATCGAGCGGTGGCCATGCTGAAGTACGGGATCCCTGACCTGCGCACCT TCTCGAAGCTGACCTCCGGTGGTTGAAACATTATTA
pKan	Native <i>kanR</i> promoter from pBBR1	GGTCACGACTTTGCGAAGCAAAGTCTAGTGAGTATACTCAAGCATTGAGTGGCCCGCCGGAGGCACCGCC TTGCGCTGCCCGCTCGAGCCGGTTGGACACCAAAAGGGAGGG
pBla	Native <i>bla</i> promoter from pUC19	TTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTTTTTTCTAAATACATTCAAATATGATCCGCTCAT GAGACAATAACCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGT
pOri	Native <i>trfA</i> promoter from pEAQ-HT (17)	TGTGGCGCAACGATGCCGGCGACAAGCAGGAGCGCACCGACTTCTCCGCATCAAGTGTITTTGGCTCTCA GGCCGAGGCCACGGCAAGTATTTGGCAAGGGTTCGCTGGTATTCTGTCAGGGCAAGATTGCGAATAAC CAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACCGACTTATTGCGGATAAGGTGGATTATCTGGA CACCAAGGCACCGGGGTCAAATCAGGAATAAGGGCACATTGCCCGCGGTGAGTCGGGGCAATCCC GCAAGGAGGGTGA
pJ23101	BBa_J23101	TTTACAGCTAGCTCAGTCTAGGTATTATGCTAGC
pTetR	BBa_R0040	TCCTATCAGTGATAGAGATTGACATCCCTATCAGTGATAGAGATACTGAGCAC
pΩ2	Composite promoter (this work)	GAACCGGAATTGCCAGCTGGGGCGTCCAAACACAATGCCTTGGCCAGTAGACATAAGCCTTCTCGGTC TGTAGGCTGTAATGACAGTGAAGCAACCCGTTGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCGG AAGAGAGTCAATTCAGGGTGAAGTACTACTCATTAGGCACCCAGGCTTACACTTTATGCTTCCGGCT CGTATGTTGTGGAAATTGTG

riboJ	Previously reported for reliable gene expression (19)	AGCTGTACCCGGATGTGCTTCCGGTCTGATGAGTCCGTGAGGACGAAACAGCCTCTACAAATAATTTGT TAA
B0029	BBa_B0029	TTCACACAGGAAACC
B0030	BBa_B0030	ATTAAAGAGGAGAAA
B0034	BBa_B0034	AAAGAGGAGAAA
BCD2	Previously reported for reliable gene expression (20)	GGGCCCAAGTTCACTTAAAAAGGAGATCAACAATGAAAGCAATTTTCGACTGAAACATGTTAACCATGCT AAGGAGGTTTTCTA
B1002	BBa_B1002	CGCAAAAACCCCGCTTCGGCGGGGTTTTTCGC
B1006	BBa_B1006	AAAAAAAACCCCGCCCTGACAGGGCGGGTTTTTTTT
B0015	BBa_B0015	CCAGGCATCAAATAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTGTCCGGT AACGCTCTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCGCGTTTATA
Threeway stop	Stop codons frameshifted to stop every ORF (this work)	TAGCTAACTGA
S1	Spacer (this work)	TCGAAGTACTAGTTAGATGATAGGAT
S2	Spacer (this work)	ACCGGTGCAACCGCT
S3	Spacer (this work)	CGCAGGAGCTAGGCAGCGCTCCACGATATC
S4	Spacer (this work)	GCGACCTGCGTCGCCTAGAGCGAG
S5	Spacer (this work)	TAGTAGGCTAGAAACCTAGATGATGATTT
S6	Spacer (this work)	CGCAGGAGCTAGGCAGCGCTCCACGATATCTTTTCAGCAGGACGCACTGACC
S7	Spacer (this work)	GCGACCTGGGTCTATGTTGGGTTTGACATC
S8	Spacer (this work)	CACGTGGCGTCGCCTAGAGCGAG
S9	Spacer (this work)	CAATTGACATGAGTTACTGGCCCTGATTTCTCCGCTTCTAATACCGACA
S10	Spacer (this work)	CGCAGGAGCTAGGCAGCGCTCCACGATATCTCCCTATCAGTGATAGAGATTGACA
<i>uAT10</i>	<i>E. coli glnE</i> 423-946, similar to AT-C 425-946 (2)	ATGGCACATATGACCAATGTGCGCCGGGTGTTAATGAATTGATTGGCGACGATGAAAGTGAAACTCAGG AAGAGTCGCTGTCGGAACAGTGGCGTGAGCTGTGGCAGGATGCGTTGCAGGAAGATGACACTACGCCAG TGCTGGCGCATCTTAGCGAGGATGATCGAAACAGGTGCTAACGCTGATTGCCGATTTCCGCAAAGAGCT GGATAAGCGCACCATCGGGCCGCGAGGACGTCAGGTGCTCGACCATCTGATGCCGATCTGCTAAGTGAT GTCTGTGCGCGTGAAGACGCTGCCGTTACGCTGTCGCGCATTACCGCCTTGCTGGTGGGGATTGTTACCC GCACCACTATTTAGAATTGCTCAGTGAATTCCTCCGCGGCGCTTAAACATTTGATTTCTCTGTGTGCCGCT CGCCGATGATTGCCAGCCAGCTGGCGGTTATCCATTATTGCTGGATGAATTGCTCGATCCAAACACCCCTT TACCAGCCGACGGCGACCGATGCCTACCGGATGAGTTGCGCCAGTATTTGCTGCGCGTGCCGGAAGATG

	Accession: MW835299	ACGAAGAGCAACAGCTTGAGGCGCTGCGTCAGTTCAAACAGGCGCAGCTGTTACGCATCGCCGACGCG ATATCGCCGGTACGCTACCGGTGATGAAAGTGAGCGATCACTAACCTGGCTGGCGGAAGCCATGATAGA TGCCGTCGTTACGACAGGCGTGGGTTCAAATGGTTCGCCGCTACGGTAAGCCGAATCACTGAACGAACGC GAAGGGCGTGGTTTTGCGGTGGTACGGCAAGCTGGGCGGCTGGGAGTTAGGCTACAGTTCGGAT CTTGACCTTATCTTCTCCATGATTGCCAATGGATGCGATGACTGACGCGTGAAGCGGAAATCGACGGGC GGCAGTTTTATCTGCGTCTGGCGAACGCATTATGCATCTGTTACGACGCTACCTCTCCGGCATTITGT ATGAAGTGGATGCTGACTGCGTCCGTCGGGGCGCGGGAATGCTGGTACATCCGCAGAAAGCATTG CCGATTATCAGAAAACGAGGCGCTGGACGTGGGAACATCAGGCGCTGGTGCCTGCGCGTGTAGTGTACG GCGATCCGACGCTCACCAGCCTTTGACGCGTGCCTGCGAGATTATGACGCTGCCGCTGAAGGTAA AACTCTGCAACGGAAGTGCGGGAAATGCGCGAGAAAATGCGCGCTCATCTCGGCAATAAACATCGCGA TCGCTTTGATATCAAAGCTGATGAAGGGGAATTACCGATATCGAATTTATTACCAATATCTGGTGTTC GCTACGCTCATGAAAACCGAAGTTAACGCGCTGGTACAGCAACGTCGCTATTCTGAACTACTGGCGCA AAACGACATTATGGAAGAGCAGGAAGCGATGGCGCTGACCGGTGTTACACTACGCTTCGCGATGAACTT CATCATCTGGCATTACAGGAATTGCCGGCCATGTGTCGGAGGATTGCTTACCAGCAGAGCGTGAAGTGG TGGGGCAAGCTGGCAGAAAGTGGTGGGAAGAATGA
<i>uAT11</i>	<i>E. coli glnE</i> , 609-946 (3) Accession: MW835300	ATGGACGAAGAGCAACAGCTTGAGGCGTGCCTGAGTTCAAACAGGCGCAGCTGTTACGCATCGCCGCA GCGGATATCGCCGGTACGCTACCGGTGATGAAAGTGAGCGATCACTAACCTGGCTGGCGGAAGCCATG ATAGATGCCGTCGTTACGACGGCGTGGGTTCAAATGGTTCGCCGCTACGGTAAGCCGAATCACTGAACG AACCGGAAGGGCGTGGTTTTGCGGTGGTACGGCAAGCTGGGCGGCTGGGAGTTAGGCTACAGTT CCGATCTTGACCTTATCTTCTCCATGATTGCCAATGGATGCGATGACTGACGCTGAGCGGGAATCGAC GGGCGCAGTTTTATCTGCTGCTGGCGCAACGCTATTATGCATCTGTTACGACGCTGATCTCCGGCAG TTTTGATGAAGTGGATGCTGACTGCGTCCGTCGGGGCGCGGGAATGCTGGTACATCCGAGAAAGC ATTTGCCGATTATCAGAAAACGAGGCTGGACGTGGGAACATCAGGCGCTGGTGCCTGCGCGTGTAGT GTACGGCGATCCGACGCTCACCAGCCTTTGACGCGTGCCTGCGAGATTATGACGCTGCCGCGTGAA GGTAAAACCTGCAACGGAAGTGCGGGAAATGCGCGAGAAAATGCGCGCTCATCTCGGCAATAAACAT CGCGATCGCTTATGATATCAAAGCTGATGAAGGGGAATTACCGATATCGAATTTATTACCAATATCTGGT GTTGCGCTACGCTCATGAAAACCGAAGTTAACGCGCTGGTACAGCAACGTCGCTATTCTGAACTACTG GCGAAAACGACATTATGGAAGAGCAGGAAGCGATGGCGCTGACCGGTGTTACACTACGCTTCGCGAT GAACCTCATCATCTGGCATTACAGGAATTGCCGGCCATGTGTCGGAGGATTGCTTACCAGCAGAGCGTG AACTGGTGCGGGCAAGCTGGCAGAAAGTGGCTGGTGGGAAGAATGA
<i>uAT21</i>	<i>A. brasilense glnE 449-1003</i> homologous to <i>uAT10</i> (this work) Accession: MW835301	ATGCTCGCCGGTGGAGACCGCTACGCCGAGCTGTTGAGGAGGCGCCGCTGCTGTCGGCCCCGGC AACCTCGTCTTACCAGGACCGACGACACCCCGCACGGTGAAGACGCTGGCCGCGATGGGCTACCGC GACCCAGCCGGGTCATCGCCGTGGTCTCCACCTGGCACCGCGGGCGCTACCGTCCACCCGCTCGGGCC GCGCGGGGAGCTGCTGACCGAGCTGGTCCGGCCATGCTAACGAGCTGGCGAAGACCCCGCCCCGG ACGACGCGCTGGTTAAGTTCGACAGCTTCTGAGCGGCTTCCGGCGGGGCTGGGGCTGTTCTCGCTGT CATCGCAACCCCTGGCTGCTCGCCGTGCTGCGGAGATCATGGGCACGGCGCGCAGCTGGCCGAGAC GTTGTCGCGCAACCCGCTGCTGCTGACCGCGTGTGTCGCCGACTTCTTCGACCCGCTGCCGACCGCG CGGGGCTGACCCGGAGTACCAGCCTTCATCGCCGGGCGCACAACTTCGAGGATGTGCTGACCTGTC GCGCGCTGGACCAACGACGAGCCTTCCGCGCCGGGCGCACATCTGCGCGCATCACCGACGGCGA CCGCTCGCGCCCTTCTCGCGATCTGCGCGAGCTGGTGGTGGCGGAGCTGGCCGCCGCGTGGAGGA GGAGTTCGCCGCCGCCACGGCCGATCCCGCGCGCCTGGTGGTGGTGGCGATGGGCAAGCTAGG CAGCCGCGAGCTCACCATCACTCCGACATCGACCTGATCGTGGTCTACGAGTGGCCGCGGACCCCGC CAGTCGGACGGAGCCGAGCCGCTGCCCCCAACGAGTATTACATCAAGCTGACGACGCTGACCAACG CCATCACCGCCCGATGGCCGACGGCGGCTGTACGAGGTGGACATGCGGCTGCGCCGCTGGGCAACG CCGGTCCGCTCGCCACCGCTGGACGCTTACCAGCTATCAGGCAAGGATGCTGGACGTGGGAGCA CATGGCCCTGACCCGCGCCGCTCATCGGCAAGTATCCGGCGCGGCGATCCGGCGCTGGGTGATAAG GTCGAGTGGCGATCCGCGGTGTGCTGACCGCCCGCGCACCCGGCAAGGTGCTGCGGGACGTCGCC GACATGCGCCGCCATCGACAAGGAGTTCGACACCAACCCGTTGGAACGTCGCAATACGCGCCGCTG GGCCTGATCGACATCGAGTTCAGGCCCCAGTATCTCCAGCTCCGTCACGGCCACGCGATCCGGACATCT GTCATCGCCACGACCGCGCCCTGCTCAACGCCGCTGCGGGCGGGCTGCTGGCGCGGAGGTGGCGGA GGAGCTGGTGGCGACGCTGAAGCTGTGGCGGGGGTGCAGGGCTTCTGCGCTGACCAACGACGGCGT GCTCGATCCGCGGAGGTTTTGCCCCACCTGCGGGAGGGCTCTGCGCGCCGCTTCCCGACGAGGAG CCGGCGGTTGACTTCGCCGCGCTCGACAGAGAATCCGGGACATCGCCGCCGCGCCACCGCAATTCG TGCGCTGGTGCAGGAGCCGCGCTCAAGGCTGCTCCCCAGAGACCAACGAAGAAGCCAACTCCCAT GA
<i>uAT22</i>	<i>A. brasilense glnE 481-1003</i> (this work) Accession: MW835302	ATGCCCGCACGGTGAAGACGCTGCGCGCATGGGCTACCGCACCCAGCCGGGTCATCGCCGTGGTC TCCACCTGGCACCGCGGGCGCTACCGTCCACCCGCTCGGGCCGCGCGGGAGCTGCTGACCGAGCTG GTGCCGCCATGCTGAACGAGCTGGCAAGACCCCGCCCGACGACGCTGGTTAAGTTCGACAGC TTCTGGAGCGGCTTCCGCGGGGCTGGGCTGTTCTCGCTGTTATCGCAACCCGCTGCTCGCCCT GGTCGCGGAGATCATGGGCACGGCGCGAGCTGGCCGAGACGTTGTCGCGCAACCCGCTGCTGCTCGA CGCCGTGCTGTCGCCGACTTCTCGACCGCTGCCGACGCGGGGGCTGACCGCGAGTACCAGCGC TTATCGCCGGGGCGCAACTTCGAGGATGTGCTGACCTGTGCGGGCGTGGACCAACGACGACGCT TCCGCGCGGGGGCGACATCTGCGCGCATACCGACGCGGACCGCTGCGGCCCTTCTCGCCGATCT GGCCGACGTGGTGGTGGCGAGCTGGCCGCCGCTGGAGGAGGATTCGCCCGCCGCGCCGCGCAT CCCCGCGGGCGCTGGTGGTGGTGGCGATGGGCAAGCTAGGCGAGCCGCGAGCTCACCATCACTCCGA CATCGACCTGATCGTGGTCTACGAGGTGCCCGGGCACCCGACGCTGGACGGAGCAAGCCGCTGGC

		<p>CCCCAACGAGTATTACATCAAGCTGACGCAGCGCCTGACCAACGCCATCACCGCCCCGATGGCCGACGGG CGGCTGTACGAGGTGACATGCGGCTGCGCCGTCGGGCAACGCCGGTCCGCTCGCCACCCGCGTGGAC GCCTTCACCGCCTATCAGGCCAAGGATGCCTGGACGTGGGAGCACATGGCCCTGACCCGCGCCCGGTCA TCGGCAGTGATTCCGGCGGCGGATCCGGCGTGGTATAAGGTCGAGTCGGCGATCCCGCGTGTGC TGACCGGCCCGCGACCCGGCAAGGTGCTGCGGGACGTGCGCCGACATGCGCCGCGGCATCGCAAGG AGTTCCGACACCAACCCGTGGAACGTCAAATACGCCCGGGCGGCTGATCGACATCGAGTTCACGGC CCAGTATCTCCAGTCCGTACGGCCACGCGCATCCGACATCCTGTCCATCGCCACAGCCGCGCCCTGC TCAACGCCGCTGCGGCCGGGTGCTGGCGCCGGAGGTGGCGGAGGAGCTGGTGGCGACGCTGAAGCTG TGGCGCGGGTGACGGGCTTCTGCGCCTGACCACCGACGGCGTCTCGATCCGCGGACAGTTTCGCCCA CCCTGCGGGAGGGCTCTGCGCGCCGCTTCCGGACGAGGAGCCGGCGTTGACTTCGCCGCGCTCGA CAGCAGAATCCGGGACATCGCCGCCGCGCCACCGCCATTTCTGGCGTGGTGGAGGAGCCGGCGTCA AGGCTGCCTCCCCAGAGACCAACGAAGAAGCCAACTCCCATGA</p>
uAT23	<p><i>A. brasilense</i> <i>glnE</i> 506-1003 (this work)</p> <p>Accession: MW835303</p>	<p>ATGCACC CGGGCGCTACCCTCCACCCGCTCGGGCCGCGCGGGAGCTGCTGACCAGCTGGTGCCG GCCATGCTGAACGAGCTGGCGAAGACCCCGCCCGGACGACGCGCTGGTTAAGTTCGACAGCTTCTGG AGCGGCTTCCGGCGGGGTGCGGCTGTTCTCGCTGTTATCGCCAACCCCTGGCTGCTGCCCTGGTCGC GGAGATCATGGGCACGGCGCCGACGTGGCCGAGACGTTGTCCGCAACCCCTGCTGCTCGACGCCGT GCTGTCGCCGACTTCTCGACCCGCTGCCCGACGCGGGGCTGACGCCGAGTACCAGCGTTCATC GCCGGGGCGACAACCTCGAGGATGTGCTGACCCTGTGCGCGCGCTGACCAACGACCCAGCGCTTCCGC GCCGGGGCGACATCTGCGCGCATACCCGACGGCGACCCTGCGGCCCTTCTCGCCGATCTGGCCG ACGTGGTGGTCCGGAGCTGGCCGCCGCTGGAGGAGGAGTTCGCCGCCCGCACGGCCGATCCCCG GCGCGCCTGGGTGCTGGCGATGGGCAAGCTAGCGACGCCGCGAGCTACCTCGACATCG ACCTGATCGTGGTCTACGAGGTGCCGCGGGCACCCGCCAGTCGGACGGAGCAAGCCGCTGGCCCCA ACGAGTATTACATCAAGCTGACGCAGCGCTGACCAACGCCATCACCGCCCGATGGCCGATGGCGGCT GTACGAGGTGGACATGCGGCTGCGCCGTCGGGCAACGCCGTCGCTCGCCACCGCGCTGGACGCTTC ACCGCTATCAGGCCAAGGATGCTGGACGTGGGAGCACATGGCCCTGACCCGCGCCCGCTCATCGGCA GTATTCCGGCGGGCGGATCCGGCGTGGGTATAAGGTCGAGTCGGCGATCCCGGCTGTGCTGACCCG GCCCGCGCACCCGGCAAGGTGCTGCGGGACGTCGCCGACATGCGCCGCGCATCGACAAGGAGTTCG GCACCACAACCCGTGGAACGTCAAATACGCCCGGGCGGCTGATCGACATCGAGTTCAGGCCCCAGTA TCTCAGCTCCGTACGGCCACGCGCATCCGGACATCCTGTCCATCGCCACAGCCGCGCCCTGCTCAACG CCGCTGCGGCCGGGTGCTGGCGCCGAGGTGGCGGAGGAGTGGTGGCGACGCTGAAGCTGTGGCGG CGGGTGCAGGGTCTTCTGCGCTGACCCACCGACGGCGTCTCGATCCGCGGAGTTTCGCCACCCCTGC GGGAGGGCTTCTGCGCGCCGCTTCCGGACGAGGAGCCGGCGTTGACTTCGCCGCGCTCGACAGCA GAATCCGGGACATCGCCGCCGCGCCACCGCCATTTCTGGCGTGGTGGAGGAGCCGGCGTCAAGGCT GCCTCCCCAGAGACCAACGAAGAAGCCAACTCCCATGA</p>
uAT24	<p><i>A. brasilense</i> <i>glnE</i> 529-1003 (this work)</p> <p>Accession: MW835304</p>	<p>ATGCTGAACGAGCTGGCGAAGACCCCGCCCGGACGACGCGCTGGTTAAGTTCGACAGCTTCTGGAGC GGCTTCCGGCGGGGTGCGGCTGTTCTCGTGTTCATCGCCAACCCCTGGCTGCTGCCCTGGTCCGGA GATCATGGGCACGGCGCCGACGTGGCCGAGAGCTTTGTCCGCAACCCCTGCTGCTCGACCGCTGTG TCGCCGACTTCTTCGACCCGCTGCCGACGCGGGGCTGACGCCGGATACCAGCGTTCATCGCCG GGGCGACAACCTCGAGGATGTGCTGACCCTGTGCGGCGCTGGACCAACGACCCAGCGTTCGCGCCG GGGCGACATCTGCGCGCATACCCGACGGCGACCCTGCGGCCCTTCTCGCCGATCTGGCCGACGT GGTGGTCCGGAGCTGGCCGCCGCTGGAGGAGGAGTTCGCCGCCCGCACGGCCGATCCCCGGCGG CGCTGGTGGTGGTGGCGATGGGCAAGCTAGGCAGCCGGCAGCTACCATCACTCCGACATCGACCT GATCGTGGTCTACGAGGTGCCGCCGGCACCCGCCAGTCGGACGGAGCCAAAGCCGCTGGCCCCAACGA GTATTACATCAAGCTGACGCAGCGCTGACCAACGCCATCACCGCCCGATGGCCGACGGCGGCTGTAC GAGTGGACATGCGGCTGCGCCGTCGGGCAACGCCGTCGCTCGCCACCGCGTGGACGCTTCACC GCATCAGGCCAAGGATGCTGGACGTGGGAGCACATGGCCCTGACCCGCGCCCGCTCATCGGACGT GATCCGGCGGGCGGATCCGGCGTGGGTATAAGGTCGAGTCGGCGATCCCGGCTGTGCTGACCGGC CCGCGCACCCGGCAAGGTGCTGCGGGACGTCGCCGACATGCGCCGCCGATCGACAAGGAGTTCGCG ACCACAACCCGTGGAACGTCAAATACGCCCGGGCGGCTGATCGACATCGAGTTCAGGCCCCAGTATC TCCAGTCCGTACGGCCACGCGCATCCGGACATCCTGTCCATCGCCACAGCCGCGCCCTGCTCAACGCC GCTGCGGCCGGCTGCTGGCGCCGGAGGTGGCGGAGGAGTGGTGGCGACGCTGAAGCTGTGGCGGCG GGTGCAGGGTCTTCTGCGCCTGACCACCGACGGCGTCTCGATCCGCGGACAGTTTCGCCACCCCTGCGG GAGGGCTTCTGCGCGCCGCTTCCGGACGAGGAGCCGGCGTTGACTTCGCCGCGCTCGACAGCAGA ATCCGGGACATCGCCGCCGCGCCACCGCCATTTCTGGCGTGGTGGAGGAGCCGGCGTCAAGGCTGC CTCCCCAGAGACCAACGAAGAAGCCAACTCCCATGA</p>
uAT25	<p><i>A. brasilense</i> <i>glnE</i> 625-1003 homologous to uAT11 (this work)</p> <p>Accession: MW835305</p>	<p>ATGAACCTCGAGGATGTGCTGACCCTGTCGCGGCGCTGGACCAACGACCCAGCGCTTCCGCGCCGGGGCGC ACATCTGCGCGCATACCCGACGGCGACCCTGCGGCCCTTCTCGCCGATCGGCCGACGTGGTGGT GCCGGAGCTGGCCGCCGCTGGAGGAGGAGTTCGCCGCCGCCACGGCCGATCCCGCGCGGCGCTG GGTGGTGGTGGCGATGGGCAAGCTAGGCAGCCGGCAGCTACCATCACTCCGACATCGACTCATCGT GGTCTACGAGGTGCCCGGGCACCCGCCAGTCGGACGGAGCAAGCCGCTGGCCCCAACGAGTATTA CATCAAGTGACGCAGCGCTGACCAACGCCATCACCGCCCGATGGCCGACGGCGGCTGTACGAGGT GGACATGCGGCTGCGCCGTCGGGCAACGCCGTCGCTCGCCACCGCGTGGACGCTTCACCGCCTAT CAGGCCAAGGATGCTGGACGTGGGAGCACATGGCCCTGACCCGCGCCCGCTCATCGGACGATGATTC GGCGCGGCGGATCCGGCGTGGGTATAAGGTCGAGTCGGCGATCCGCGGATCGGCGTGTGCTGACCGCGC GACCCGGCAAGGTGCTGCGGGACGTCGCCGACATGCGCCGCCGATCGACAAGGAGTTCGGCACCCACC AACCCGTGGAACGTCAAATACGCCCGGGCGGCTGATCGACATCGAGTTCAGGCCCCAGTATCTCCAGC</p>

		TCCGTCACGGCCACGCGCATCCGGACATCCTGTCCATCGCCACCAGCCGCGCCTGCTCAACGCCGCTGCG GCCGGGCTGCTGGCGCCGAGGTGGCGGAGGAGCTGGTGCGACGCTGAAGCTGTGGCGCCGGGTGCA GGGCTTCTGCGCCTGACCACCAGCGGCTGCTCGATCCGCGGAGGTTTCCGCCACCCTGCGGGAGGGG CTCTCGCGCCGCTTCCCGGACGAGGAGCGGGGTTGACTTCGCCGCGCTCGACAGCAGAAATCCGGG ACATCGCGCCCGCCACCGCCATTTCTGGCGCTGGTCGAGGAGCCGCGCTCAAGGCTGCCTCCCC AGAGACCAACGAAGAAGCCAACTCCCATGA
<i>RFP</i>	BBa_E1010	ATGGCCAGCAGCGAAGACGTTATCAAAGAGTTCATGCGCTTTAAGGTCGGGATGGAAGGCAGCGTAAAC GGTCATGAATTCGAGATCGAAGGAGAAGGTGAAGGGCGTCCCTATGAGGGCAGCAGACGGCTAAGCTC AAAGTGACGAAGGGTGGACCTCTGCCGTTTGTGGGACATCCTGTGCGCCAGTTTCAAGTATGGCAGCA AGGCGTATGTGAAGCATCCGGCCGACATCCCTGATTATCTGAAACTCAGTTTCCCGGAAGGTTTCAAGTGG GAACGAGTGATGAACTTCGAGGACGGCGGCGTGTACGCGTACACAGGACAGTAGCTTGCAGGACGGC GAATTCATTTAAGGTCAACTTCGAGGGACCAACTTCCGTCAGATGGCCGGTGTATGCAGAAAAAGA CTATGGGTTGGGAGGCAAGCACCAGCGTATGTATCCGGAGGATGGAGCCCTTAAGGGTGAGATCAAGA TGCGGTTGAAGCTGAAGGATGGGGGCCATTACGATGCGGAGGTTAAACCACCTATATGGCGAAAAAC CAGTCCAGCTCCCGGGCGGTATAAGACGGATATTAAGCTGGACATCACCAGTCATAACGAAGACTACAC CATCGTCGAGCAATACGAGCGCGCAAGGGCGGCAATTCACGGGTGCCTGA
<i>tetR</i>	BBa_R0040 with LVA tag removed and codon refactored for <i>A. brasilense</i> codon usage	ATGTCGCCCTGGACAAGAGTAAGGTCATTAATTCGCTTGAATGCTGAACGAAGTCGGCATCGAGG GTTTGACCACCCGGAAGCTGGCTCAGAAGCTGGGTGTCGAACAGCCGACGTTGACTGGCATGTGAAGA ACAAGAGGGCGTTGCTCGATGCGCTCGCCATCGAAATGCTCGATCGCCACCATACGCATTTCTGTCTCT GAGGGTGAATCGTGGCAAGACTTCTGCGGAACAATGCCAAATCTTCCGCTGCGCTCTTGTGCCACCG TGATGGCGCAAGGTGCATCTGGGACCCCTCCGACGGAAGCAAGTATGAGACACTAGAGAACCACT CGCGTTTCTGCAACAGGGTTTTAGCCTGGAACGCCCTGTATGCGTTGTGCGCGGTGGGACATTTCA CTCTCGGCTGCGTCTTGGAGGACAGGAGCATCAGGTGGCGAAGGAAGAGCGTAAACCCCAACGACCG ATTCTATGCCCGGCTGCTGCGGACGGCATCGAACTTTTCGACCACCAAGGAGCTGAACCGGCGTCTCT GTTGCGTTTGGAACTCATTATTTGCGGTTTGGAGAAACAGCTTAAGTGCGAATCCGGATCATGA
<i>amtB</i>	From the <i>A. brasilense</i> genome	ATGAGCCGCTCTTACCCTCGCCGCGGACGATGGCGGCGATTCTGGGCTTGGCCGGTCTGCCTGCCG CCGCCCTCGCCAGGAAGCGGCCCGCCGCGGCGGACGCCACCCTGAGCAGCGGCGACACGGCTTGGGA TGCTGGTCCGACGGCGCTGGTTCTGTTATGACCATCCCGGGTCTGGCCCTGTTCTACGGCGGATGGTC CGCAAGATGAACGTGCTGTGCGTGTGATGACAGAGCTTCGCGATCTGCTGCTGCTGATGACATCCTGTGG TCTTCGCGGTTACAGCATCGCCTTACCAGGACCCCGTATTTCCGCGACCTTTCGAAGTTATGCTG GCCGGCATACCAAGGACAGCCTGACGGGCGTATTCCGGAGACGATCTTGTGCTTCCAGATGACCTT CGCCATCATACGCGGCCCTGATACCGGCGCCTTCGCCGACCGCATGAAGTTCTCCTCGATGCTGTCT TCACGGGCTGTGGTGTGATGCTACGCGCCGATCACCCTGGGTCTGGGGTCCGGGCGGCTATCT GGCGGGTACGGCGTGTGATTACCGGCGGACCGTGGTGCATCAACGCGGGCTGGCCGGTCT CGTCGCCCATCGTGTGGGCAAGCGCAAGGGCTACCCGAACGAGAATTCGCCCGCACAACTGGTG CTCAGCCTGATCGGCGCCTCGATGCTGTGGGTGGGCTGTTGCGCTTCAACGCGGGTCCGCGGTGGCCG CCGACGGCGGTGGGCGATGGCCATGCTGGTACGCAGATCGCCGCCGCCACCGCCGATGTCTGGCT GCTGGTGCAGTGGGCCACCAAGGGCAAGCCCTCGTCTCGGCATCATCTCCGGCGCATCGCCGGTCTG GTCGCCATACCCCGCCCTCGGGTTCGTGCGTCCGACCGGCGCCTGGTATCGGTCTGGCCGCGGCG TGATCTGCTACTGGGCGCCACCGCCTGAAGCGCGCCCTCGGCTATGACACTGCTGGAGCGCTTCGG CGTGACGGCGTGGGCGCATCGTGGCGCCATCCTGACCGGCTTTCGCCAGGAAGCCATCGGCGG TACCGCGGCGCCTGGAAGGCAACGTGGCCAGATCTGGACGAGGTCTACGGCATCCTGGCCACCATC GCCTACTCGCGGTCGGCTCCTCATCATCTGAAGGTATCGACGTGGTGTGGGCGCTTGTGTGACGA GGACGTCGAGCGGACGGCCTGGACCTCGCCCTGCACGGCGAGACCATCCACTAA
<i>fdxB</i>	From the <i>A. brasilense</i> genome	ATGGCTGAGTTCGTGACCGGACACCCGCGGCGGCCCTGGACGCCAAATTCGTGAAAGCATC GACCAGAAGATGTGCATCGGCTGCGGCCGCTGCTTCAAGGTCTGCGGCGCGACGTGCTGGAGCTGATC GGCATACCGAGGACGGGACATCGTCGACGCTTCGACGACGAGGCCGAGAAGAAGGTGATGAGCGTC AAGAACGCGGCAATTCATCGGCTGCGAAAGCTGCGGCAAGGTCTGTTCCAAGAAGTGCATCACCCACT TGCCCCAGCGGCGCTGA
<i>fdxN</i>	From the <i>A. brasilense</i> genome	ATGGCTTACAAGATCAAGGCTTCCGACTGCACCGCCTGCGGCGCCTGCGAGGCCGAGTGGCCGAACAACG CCATCAGCTTCAAGAAAGGCGCCTACGCCATCAACGCGGACCTGTGACCGAGTGAAGGGCCAGTTCTC CAGCCCGCAATGCGCTCGGTCTGCCGGCCGACTGCTGCGTCCCGGCTGA
<i>fixX</i>	From the <i>A. brasilense</i> genome	ATGAGCATCGTGGTCAAGATCGAAGAGAAGTGTACCAGAACCCTACATCGTGGACGAGAGCCGGCCG CACATCCAGATCCGCAACGACGCGGTCTGCAAGTCTCGAGTCCCAGGCTGACCCGCTGCTGCCCCG CGGCTGCTACAGCAAGAAGGACGAGACCGGCGAGCGTGTGACGCTGGCCACCGACGGCTGCTGGAATGCGGCA CCTGCCGCGTGTGCTGCCAGGACAAGGAAAATATTCAGTGGGACTACCCACGGGGCGGCTACGGCATCA GTTATAAGTTTGGTTGA

Figure S21D: Sequence of chromosome modifications reported in this work. Lowercase letters are 100 bp flanking genomic regions, and uppercase letters are inserted sequences. All sequences have been deposited at GenBank and accession numbers are shown.

Name	Notes	Sequence
TSD4	<i>glnE</i> deletion Accession: MW835312	tcggtgtcccggcagcggtgccgctgtgtcacagttgaccggaccctcgaccgccacctctctgctcagttcttgtcagggatagc cgaccTAGCTAACTGAACCATCATGTCTCTCCATAATGCACCTCCAGAATTATGAGTAGGTAGgccaagcca acaacgccagcgaagccaacacgcgccccgatcgaggtcgccacccggccccgacttcacatgccacggatggcggcggaagc gt
TSI8 and TSD4I8	Constitutive uAT insertion: R2 circuit where GOI = <i>uAT10</i> , without spacers and B1002, and with B0034 replacing B0030 [Fig S21B] Accession: MW835313	aacgccccggcctgtggcggtgcagagcagctggcgccgaatcggtgatggccccggtgagcgatcaggtgcacctgtggaagac ctgatgacccggtgcgcaccgcgccgacatggcagctggcgaggtgcagcgcgaagaacgagctgacccaacctgatT AGCTAACTGAACTAGTGAACCGAATTCAGCTGGGGCGTCCAAACACAATGCCTTGCCCAAGTAGAC ATAAGCCTTCTCGGTCTGTAGGCTGTAATGCAGGTAGCGAACCCGTTGGTGAAACACCTTCGCGGTATG GCATGATAGCGCCCGGAAGAGATCAATTAGGTTAGCTCAGTACTAGGACCCACCGAGCTTTAC ACTTTATGCTTCCGGCTCGTATGTTGTGGAAATTGTGTCTAGAGAAAGAGGAACTCCAGATGGCAC ATATGACCAATGTGCGCCGGGTGTTAATGAATTGATTGGCGACGATGAAAGTAACTCAGGAAGAGTCTG GCTGTCGGAACAGTGCGTGAAGTGTGGCAGGATGCGTTGCAGGAAGATGACTACGCCAGTGTCTGGC GCATCTTAGCAGGATGATCGCAACAGGTGTAACGCTGATTGCCGATTCCGCAAAGAGTGGATAAG CGCACCATCGGGCCGCGAGGACGTGAGGTGCTCGACCATCTGATGCCGCATCTGCTAAGTATGCTGTTG CGCGTGAAGACGCTGCCGTTACGCTGTCGCGCATTACCGCTTGCTGGTGGGGATTGTTACCCCGACCAAC TATTTAGAATTGCTCAGTGAATCCCCGCGGCCTAAACATTTGATTTCTGTGTGCCGCTCGCCGATG ATTGCCAGCAGTGCGCGTTATCCATTATTGCTGGATGAATGCTCGATCCAAACACCCCTTACCAGCC GACGGCGACCGATGCCTACCGCATGAGTTCGCGCAGATTTGCTGCGCGTGGCCGAAGATGACGAAGA GCAACAGCTTGAAGCGCTGCGTCAGTTCAAACAGGCGCAGCTGTTACGCATCGCCGAGCGGATATCGCC GGTACGCTACCGGTGATGAAAGTGAAGCATCACTTAACCTGGCTGGCCGAAGCCATGATAGATGCCCC GTTACGAGGCGTGGTTCAAATGTTGCCCCGCTACGGTAAGCCGAATCACTGAAACGAACCGGAAGGG CGTGGTTTTGCGTGGTTCGCTACGGCAAGCTGGGCGGCTGGGAGTTAGGCTACAGTTCGATCTTGACC TTATCTCTCCATGATTGCCCAATGGATGCGATGACTGACGGTGAAGGGAAATCGACGGCGGCGAGTT TTATCTGCTTGGCGCAACGCATTATGCATCTGTTCAGTACGGCTACCTCTTCGGCATTGTTGTATGAAGT GGATGCTCGACTGCTCCGTCGGGGCGCGGAAATGCTGGTACATCGCAGAAGCAATTTGCGGATTAT CAGAAAAACGAGGCGCTGACGCTGGGAACATCAGGCGCTGGTGGCTGGCGTGTAGTGTACGGCGATCCG CAGCTCACCGCAGCTTTGACGCAAGTGGTGGCGAGATTATGACGCTGCCGCGTGAAGGTAACACTCTGC AAACGGAAGTGCGGAAATGCAGAGAAATGCGCGCTCATCTCGCAATAAATCACTCGCATCGCTTTG ATATCAAAGCTGATGAAGGGGGAATTACCGATATCGAATTTATTACCCAATATCTGGTGTTCGCTACGCT CATGAAAAACGAAGTAAACGCGTGGTCAAGCAACGCTGCGTATTCTGGACTACTGGCGAAAACGACA TTATGGAAGAGCAGGAAGCGTGGCGCTACCCGTGCTTACACTACGCTTCGCGATGAAGTTTATCATCT GGCATTACAGGAATTCGGGGCCATGTGTCGGAGGATTGCTTACCGCAGAGCGTGAAGTGGTGGCGGC AAGCTGGCAGAAAGTGGTGGTGGGAAACCCGGGCATCACCATCACCATCACTGAACCGGTCCAGGCATC AAATAAACGAAAGGCTCAGTCGAAAGACTGGGCTTTTCTGTTTTATCTGTTGTTGTTCGGTGAACGCTCTC TACTAGAGTCACTGGCTCACCTCGGGTGGGCTTTCTGCGTTTATAGATAGCGATATGATAATGTATT GGCTAGCTGAGTAGGTAGgacctgaacccagggtggagcgccagctcgcccgccggagacggggcggtgctggcggc cctgatgacatctggcgaacatcgccaacgcccagggaagcgtcggggacaaggccaacccccgacacctggaggatgggagg aggccccggcgctgcaacggcggga
TSI15 and TSD4I15	Inducible uAT insertion: J3 circuit where GOI = <i>uAT10</i> [Fig S21B] Accession: MW835314	aacgccccggcctgtggcggtgcagagcagctggcgccgaatcggtgatggccccggtgagcgatcaggtgcacctgtggaagac ctgatgacccggtgcgcaccgcgccgacatggcagctggcgaggtgcagcgcgaagaacgagctgacccaacctgatT AGCTAACTGAACTAGTCAATACATTATCATATCGTATCTATAAACGCAGAAAGGCCACCCGAAGGTGAG CCAGTGTGACTCTAGTAGAGAGCGTTCCACCAGACAACAACAGATAAAAAAGGACAAAGCCAGTCTTTTCGACT GAGCCTTTCTGTTTTATTGATGCCTGGACCGTTCAGTGTGGTGTGATGGTCGCCGGTTCTTCCACCA GCCACTTCTGCAGCTTCCCGCACCAGTTCAGCTCTGCGGTGAAGCAATCTCCGACACATGGCCCGGC AATTCCTGTAATGCCAGATGATGAAGTTATCGCGAAGCGTGTGTAAGCACGGGTCAGCGCCATCGCTT CCTGCTCTCCATAATGTCGTTTTGCGCCAGTAGTTCAGAATAACGACGTTGTCTGACCAGCGGTTA CTCGTTTTTCATGAGCGTAGCGCAACACAGATATTGGTAATAAATCGATACCGTAAATTCCTTTTATC CAGCTTTGATATCAAAGCATCGCGATGTTTATTGCCGAGATGAGCGCGCATTCTCGCGCATTCCCGC ACTTCCGTTTCAGAGTTTTACCTTACGCGCAGCGTCATAATCTCGCGACGACTGCGTCAAAGTGGCG GGTGGAGCTGGGATCGCCGTACTACAGCGCACGCCAGCGCTGATGTTCCACGCTCCAGGCCTCG TTTTCTGATAATCGGCAAATGCTTCTGCGGATGTCACCAGCATTCCCGCCGCCCGGACGGACGCAGTCG AGCATCCACTTCATACAAAATGCCGAAGAGGTACGCGTACTGAACAGATGATAATGCGTTGCCGACAG

		<p>CGCAGATAAAACTGCCGCCGTCGATTTCCCGCTCACCGTCAGTCATCGCATCCATTGGGCAATCATGGAG GAAGATAAGGTCAAGATCGGAACTGTAGCCTAACTCCCAGCCGCCAGCTTGCCGTAGCCGACCACCGCA AAACCACGCCCTTCGCGTTTCAGGTGATTGGGCTTACCGTAGCGGGCAACCATTTGAACCACGCCTG CTGAACGACGGCATCTATCATGGCTTCCGCCAGCCAGGTTAAGTGATCGCTCACTTTATCACCGGTAGCG TACCGGCGATATCCGCTGCGGCGATGCGTAAACAGCTGCGCCTGTTTGAACCTGACGACGCGCCTCAAGCTG TTGCTCTTCGTCATCTTCCGGCACGCGCAGCAAATACTGGCGCAACTCATCGCGGTAGGCATCGGTCGCCG TCGGCTGGTAAAGGGTGTGGATCGAGCAATTCATCCAGCAATAATGGATAACGCGCCAGCTGGCTGGC AATCATCGGCGACGCGGCACACAGAGAAATCAAATGTTTAAAGCGCCGCGGGGAATTCATGAGCAATTC AAATAGGTGGTGGGTAACAATCCCCACCAGCAAGGCGGTAATGCGCGACAGCGTAACGGCAGCGTCT TCACGCGCACAGACATCACTTAGCAGATGCGGCATCAGATGGTCGAGCACTGACGTCCTCGCGGCCGA TGGTGGCTTATCCAGCTCTTTCGGGAAATCGGCAATCAGCGTTAGCACCTGTTTGCATCATCTCGCTA AGATGCGCCAGCACTGGCGTAGTGTCTTCTGCAACGCATCCTGCCACAGCTCACGCCACTGTTCCGA CAGCGACTTCTCTGAGTTTCACTTTCATCGTCGCAATCAATTCATTAACACCCGGCGCACATTGGTCAT ATGTGCCATAGTATTTCTCTCTTAAATAGCGGTTGCACCGGTGTGCTCAGTATCTTATCACTGATAGG GATGTCAATCTTATCACTGATAGGGAGATATCGTGGAGCGCTGCCTAGCTCCTGCGGCGAAAAACCCC GCCGAAGCGGGTTTTTTGCGGCGACCTGCGTCGCTAGAGCGAGGAACCGGAATTGCCAGCTGGGGCG TCCAAACACAAATGCCTTGCCCGTAGACATAAGCCTTCTCGGTCTGTAGGCTGTAATGCAGGTAGCGA ACCCGTTGGTGCAAAACCTTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGAGTT AGCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGTCTA GAGAAAGAGGAGAACTCGAGATGTCCCGCTGGACAAGAGTAAGGTCATTAATTCGCTTGGAAATTGC TGAACGAAGTCGGCATCGAGGGTTTTGACCACCCGGAAGCTGGCTCAGAAGCTGGGTGTCGAACAGCCGA CGTTGTACTGGCATGTGAAGAACAAGAGGGCGTTGCTCGATGCGCTCGCCATCGAAATGCTCGATCGCCA CCATACGATTTCTGTCTTTGAGGGTGAATCGTGCAAGACTTCTGCGGAACAATGCCAAATCTTTCC GCTGCGCTCTTTGTCACCGTGATGGCGCAAGGTGCATCTGGGCACCCGTCGACGGAAGAGCA TGAGACTAGAGAACCAGCTCGGTTTTCTGCCAACAGGGTTTTAGCCTGGAAAACGCCCTGTATGCGT TGTGCGCGGTGGGACATTTCACTCTCGGCTGCGTCTTGGAGGACCAAGGAGCATCAGGTGCGGAAGGAAG AGCGTGAAACCCCAACGACCGATTCTATGCCGCCGCTGCTGCGGCAGGCGATCGAACTTTTCGACCACCA AGGAGCTGAACCGGCTTCTGTTGCGTTTTGGAACCTATTATTTGCGGTTTGGAGAAAACAGCTTAAAGTGC GAATCCGGATCATGATAATAGTAGGCTAGAAACCTAGATGATGATTTAAAAAAAACCCCGCCCTGAC AGGGCGGGTTTTTTTTGTGCGTGATACGACAGATGGTTTGGCTAGCTGAGTAGGTA</p> <p><i>Ggaccctgaacccca ggtggagcgcagctgcccgcgcccggagacgggaggctggtcggccgctgatgcatctggcgaacgcatccgcaacccgagg aagcgctgcccgaaggccaccacccccgcacctggaggagtgggaggaggccccgggctcgaacccgga</i></p>
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