

A modular high-throughput approach for advancing synthetic biology in the chloroplast of *Chlamydomonas*

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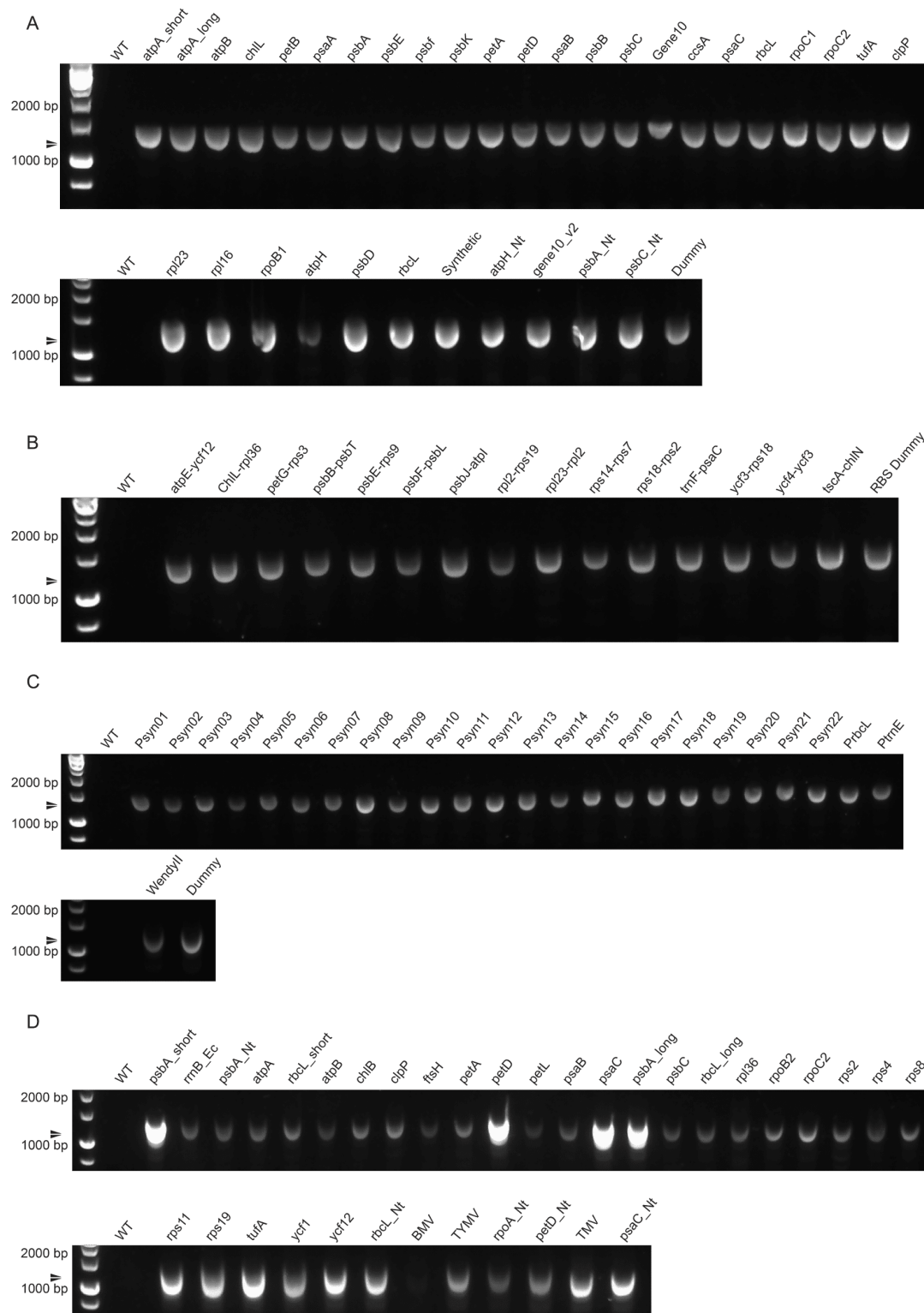
Supplementary table 4: Mass Spectrometry parameters for energy metabolites

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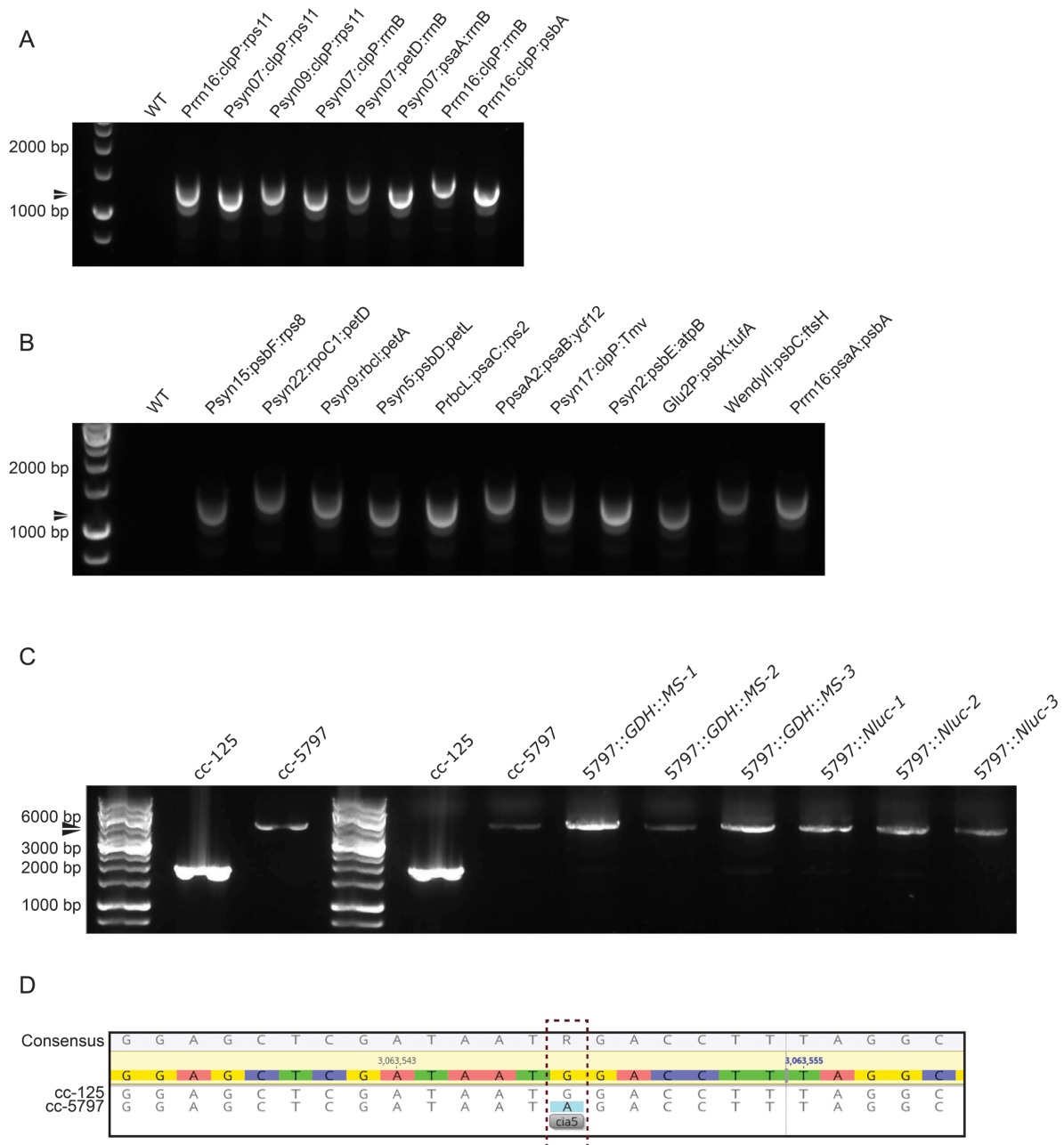
Supplementary table 6: Primers used in this study

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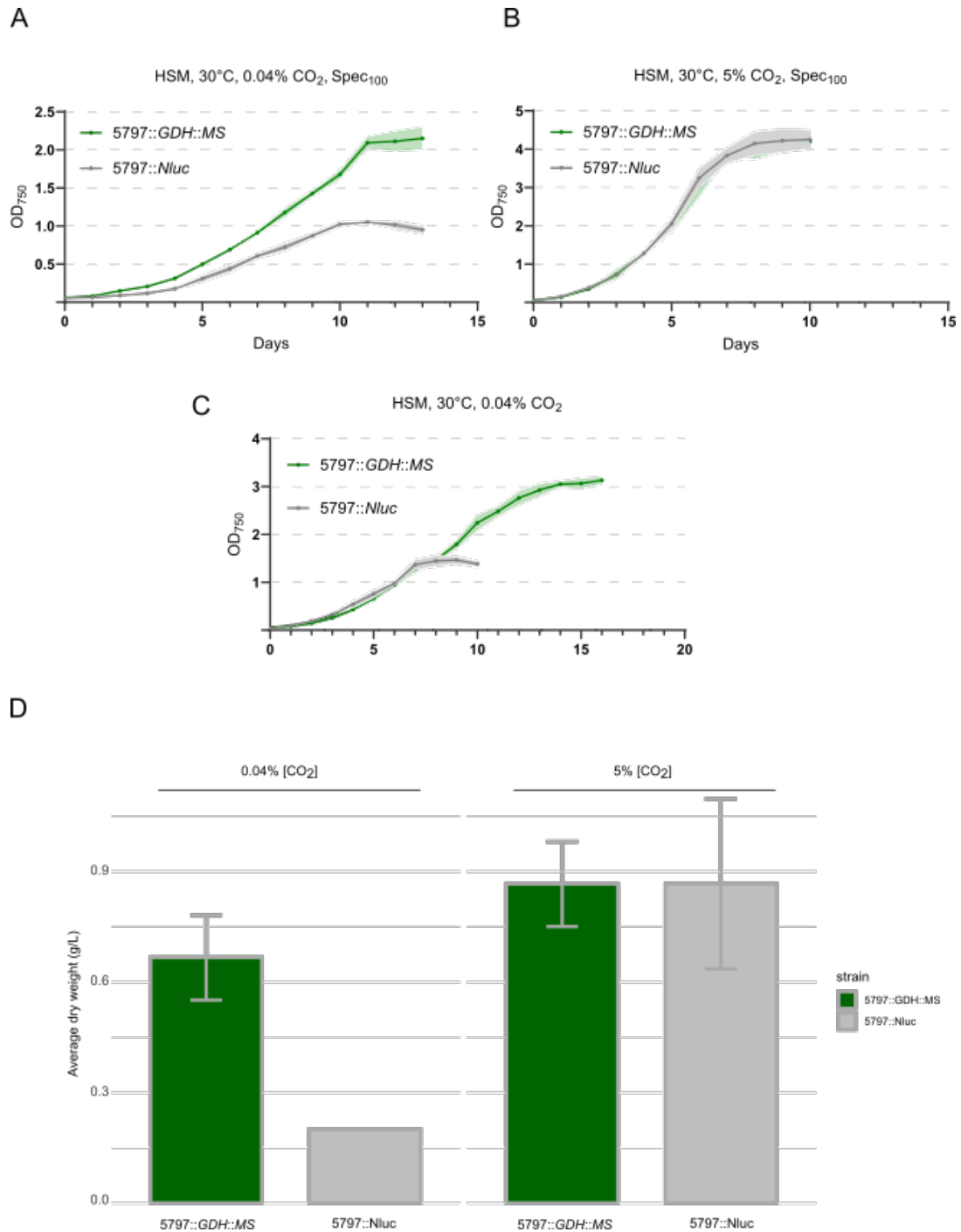
Supplementary Figures



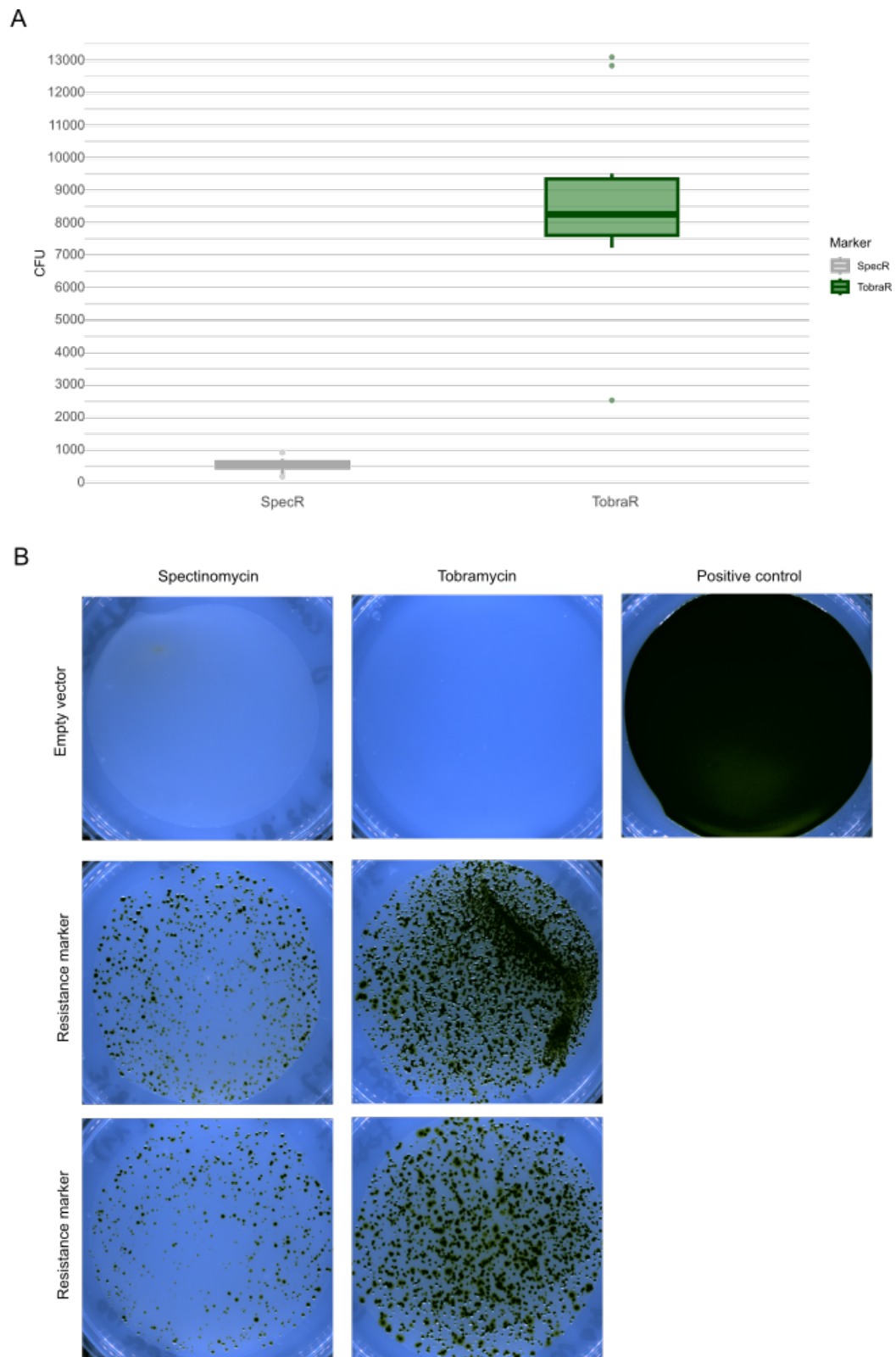
Supplementary figure 1: Gel analysis of cPCR amplification for the NanoLuc reporter gene in transplastomic strains, characterized in Figures 3–4, featuring one representative colony for each construct. A distinct band, approximately 1100–1300 bp in size, is observed in the genetically modified strains, absent in the WT. **a–d**, cPCR for NanoLuc in strains containing various 5'UTRs, IEEs, Promoters, and 3'UTRs respectively.



Supplementary figure 2: cPCR and sequencing for strain genomic characterization. **a-b**, Gel analysis of cPCR amplification for the NanoLuc reporter gene in transplastomic strains, characterized in Figures 5, featuring one representative colony for each construct. A distinct band, approximately 1100-1300 bp in size, is observed in the genetically modified strains, absent in the WT. **c** cPCR analysis of the glycolate dehydrogenase gene in cc-125 WT, cc-5797 mutant, and all engineered strains depicted in Figure 6. The transition from a 2000 bp band in cc-125 to a 6000 bp band in cc-5797, attributable to an insertion cassette. This band shift is consistently present in all engineered cc-5797 strains, verifying the insertion cassette's presence across these variants. **d**, Sequencing analysis reveals a point mutation at the *cia5* locus in the nuclear genome of the cc-5797 mutant, absent in the cc-125 WT. A dark red dotted-lined box highlights this mutation, confirming the previously reported genotype.

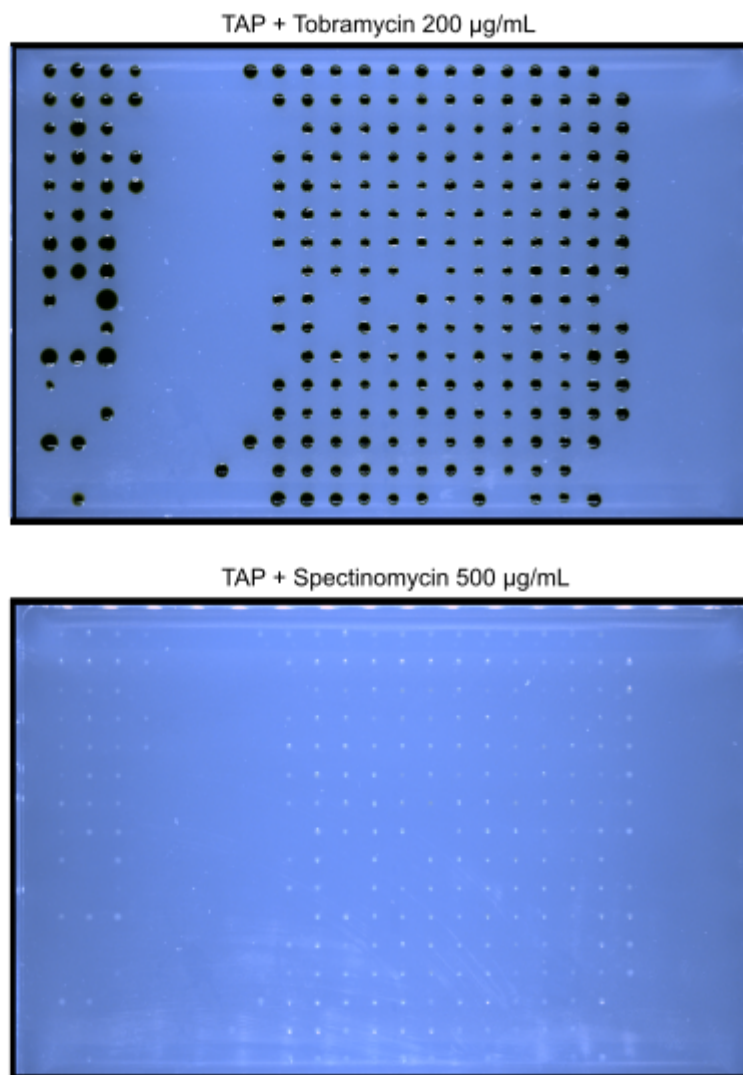


Supplementary figure 3: Growth and biomass production analyses of transplastomic strains containing the synthetic photorespiration bypass. **a-c**, Growth curve of engineered strains and control at ambient CO₂ (**a**) and 5% CO₂ (**b**) both with selection pressure (Spectinomycin 100 µg/mL) and ambient CO₂ without selection pressure (**c**), all shown as OD₇₅₀ over time (days). Engineered strains (5797::GDH::MS, in green) reach a two-fold final OD over the control strains (5797::Nluc, in grey) in ambient CO₂ but behave similarly in 5% CO₂. The same phenotype is observed when removing the selection pressure in **c**. $n_{\text{biological}}=3$ for each curve. **d**, Mean and standard deviations of measured dry weight of the south engineered strains after 13 days of growth for $n_{\text{biological}}=3$. The average dry weight is comparable for both control strains (5797::Nluc, in grey) and engineered strains (5797::GDH::MS, in green) in high CO₂ concentration (5%), while a three-fold increase can be observed in the engineered strains in ambient CO₂ concentrations (0.04%).

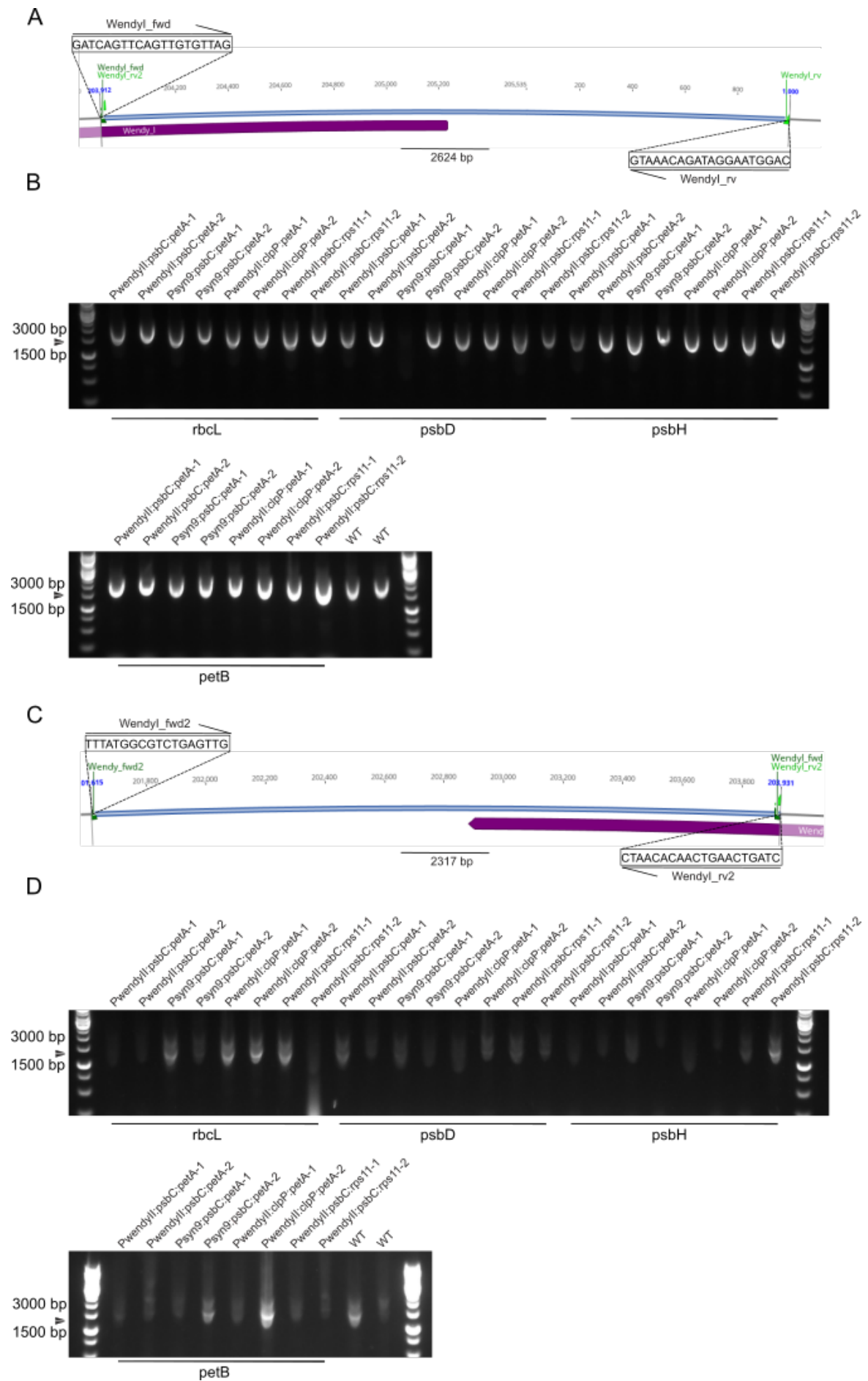


Supplementary figure 4: Comparison of the selection efficiency for the Spectinomycin and Tobramycin antibiotic resistance markers. **a**, Mean and standard deviations of Colony Forming Unit (CFU) count per plate after transformation of both markers in the WT strain, n=11. The Tobramycin marker leads to an order of magnitude increase in the number of colonies obtained after transformation. Box plot shows median as solid line, the box with lower and upper quartile, and the whiskers representing the data points that fall within 1.5 times the interquartile range (IQR) from the lower and upper quartiles. Any data point outside this range is considered as outlier. **b**, Example of a transformation plate for the selection markers. Two different selection marker systems are shown with two replicates and one negative controls for each one, as well as a positive control showing cell viability. Successful selection after chloroplast transformation can be observed,

notably with a high efficiency for tobramycin-based selection (100 µg/mL) over Spectinomycin-based selection (100 µg/mL).

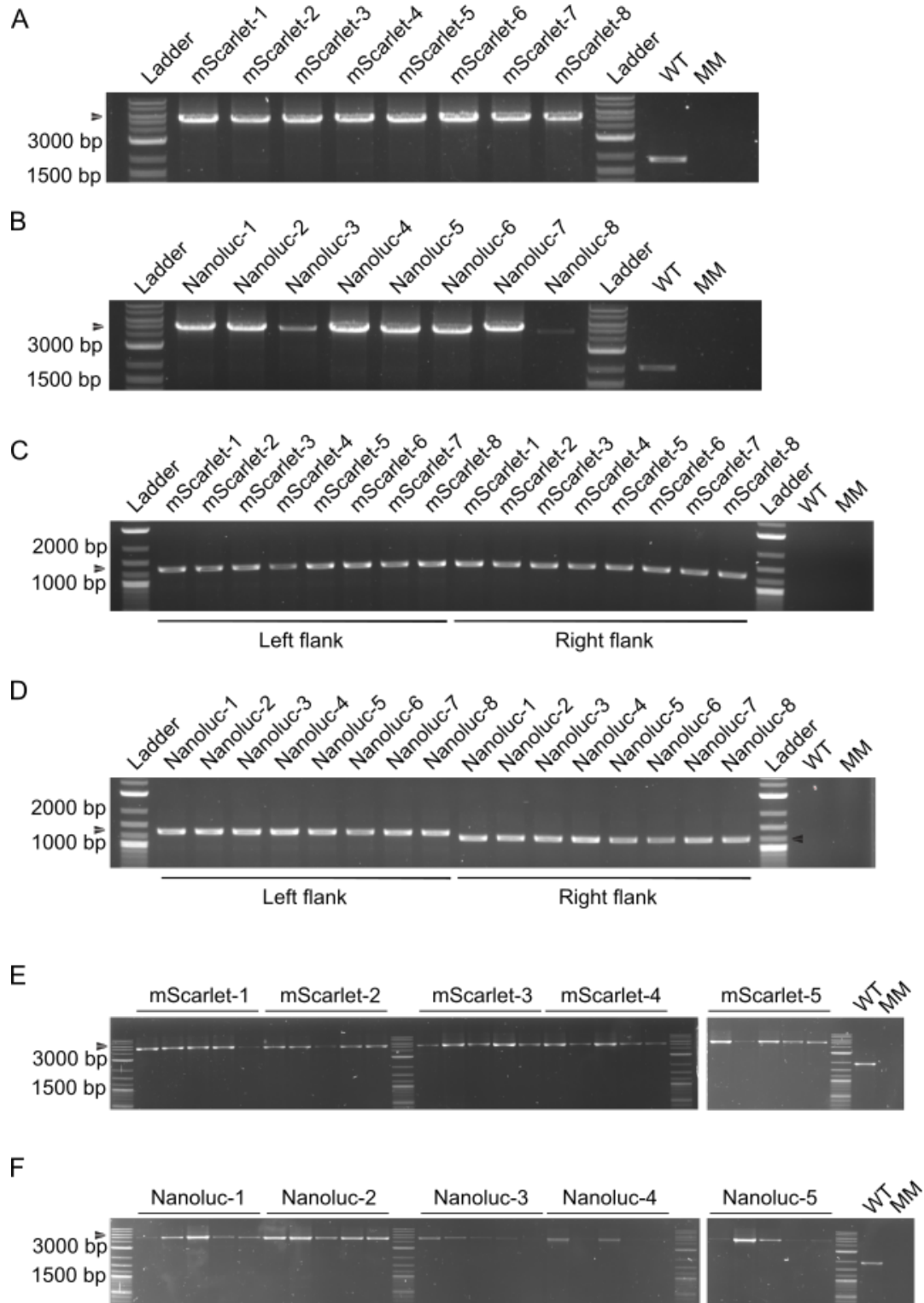


Supplementary figure 5: Cross-resistance assessment between Tobramycin and Spectinomycin markers. a, Tobramycin resistant transformants restreaked on two different media: TAP supplemented with Tobramycin (200 µg/mL, top plate) and TAP supplemented with Spectinomycin (500 µg/mL, bottom plate). Concentrations of antibiotic were chosen according to standard concentrations used for restreaks after confirmed integration and homoplasmy.



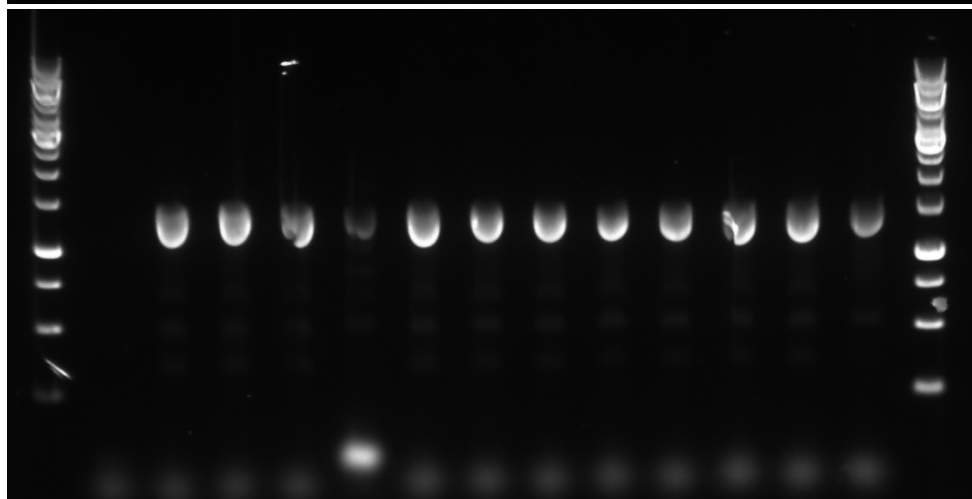
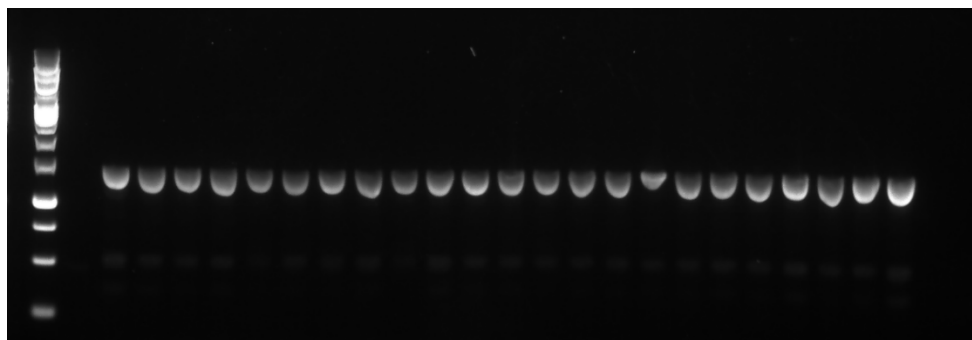
Supplementary figure 6: Gel analysis of cPCR amplification of the Wendyl locus, in transplastomic strains characterized in Figure 5c, featuring two representative colonies for each construct, including four constructs per integration sites. Schematics for the first and second PCRs are shown in panels **a** and **c** respectively. **b and d**, PCR 1 and 2, respectively covering the right and left border of the Wendyl gene. A distinct band, approximately 2100-2300 bp and 2500-2600 bp in size (for **b** and **d** respectively), is observed in all strains, including the WT, indicating that no recombination event took place for that locus. GeneRuler 1kb Plus (Thermo Fischer Scientific) was used as ladder for these gels.

Supplementary figure 7: Gel analysis of cPCR amplification of the WendyII locus, in transplastomic strains characterized in Figure 5c, featuring two representative colonies for each construct, including four constructs per integration sites. Schematics for the first and second PCRs are shown in panels **a** and **c** respectively. **b** and **d**, PCR 1 and 2, respectively covering the right and left border of the WendyII gene. A distinct band, approximately 700-800 bp and 2500-2700 bp in size (for **b** and **d** respectively), is observed in all strains, including the WT, indicating that no recombination event took place for that locus. GeneRuler 1kb Plus (Thermo Fischer Scientific) was used as ladder for these gels.

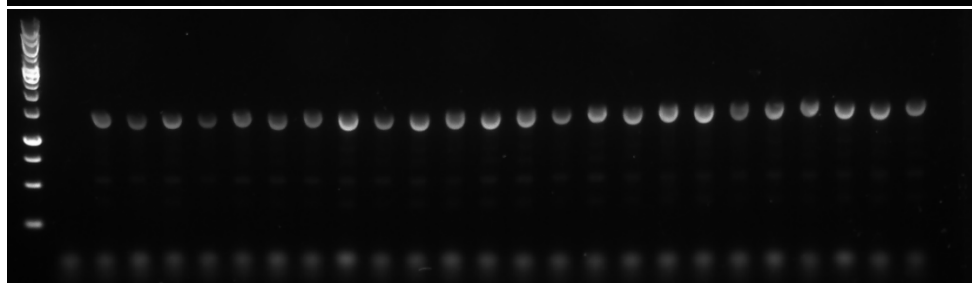
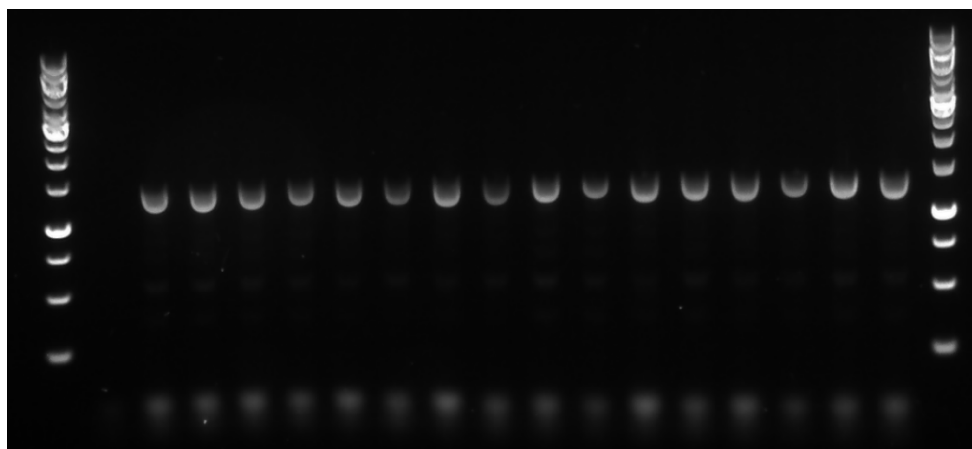


Supplementary figure 8: Gel analysis of Homoplasmy cPCR amplification of mScarlet-I and Nanoluc transplastomic strains. mScarlet strains analyzed in Figure 2d-e and Nanoluc strains analyzed in Figures 2c and 3a-c were selected for confirming homoplasmy in colonies selected through the high-throughput pipeline. Panels **a-d** feature 8 clones per construct. The 1kb plus NEB ladder was used for these gels. **a-b**, cPCR covering the entire integrated fragment, homologies included, using the HomPCR_Confirm_01/ 02. Expected bands of 5400 bp can be observed for mScarlet strains in **a**, and of 5217 bp for Nanoluc strains in **b**. A smaller band around 1980 bp is observed for WT, characteristic of the amplification of the WT locus. No bands appear in the MasterMix control (MM). **c-d**, cPCR confirming left and right flank integration of the cassette, binding in each homology and reporter gene, using the HomPCR_Confirm_03/04 for the left flank, and HomPCR_Confirm_05/06 and 07/08 for the right flank of mScarlet-I and Nanoluc respectively. Expected bands of 1360 and 1318 bp are present in mScarlet strains left and right flanks in **a**. Similarly, expected bands of 1360 and 1192 bp are present in Nanoluc strains in **b**. **e-f**, After restreaking of colonies 1 to 5 for both mScarlet (mScarlet-1 to mScarlet-5) and Nanoluc (Nanoluc-1 to Nanoluc-5) transplastomic strains, 5 individual colonies were picked (each individual lane) and subjected to the homology cPCR shown in **a-b**. Each individual colonies for both mScarlet and Nanoluc clones displays the expected bands of 5400 and 5217 bp respectively, supporting homoplasmy for the population. The characteristic WT band of 1980 bp was observed, while no band appeared for the MM control.

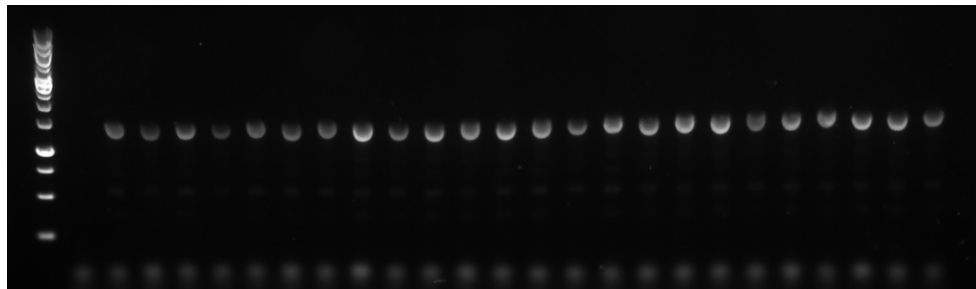
A



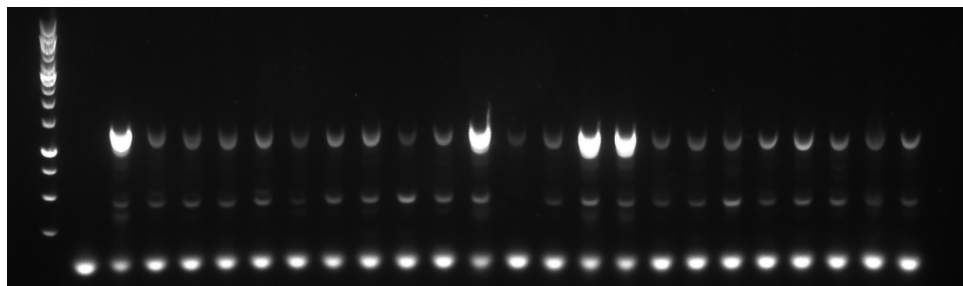
B



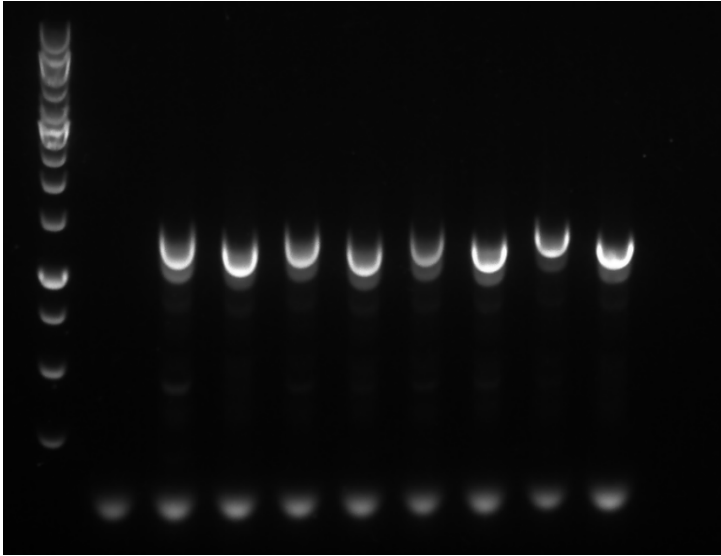
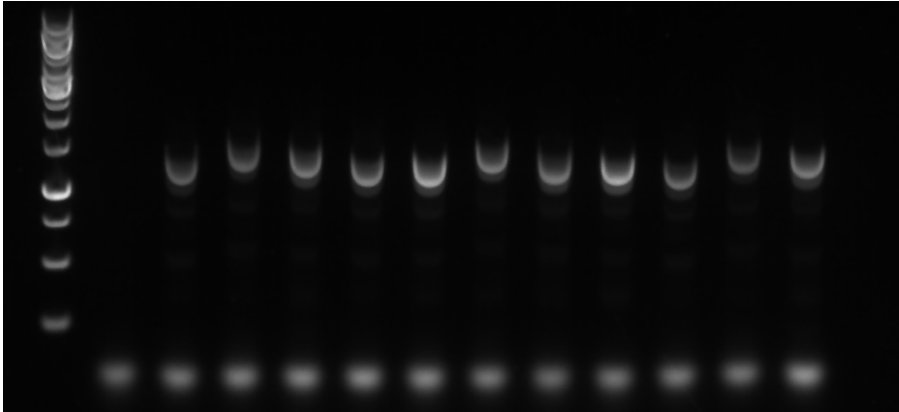
C



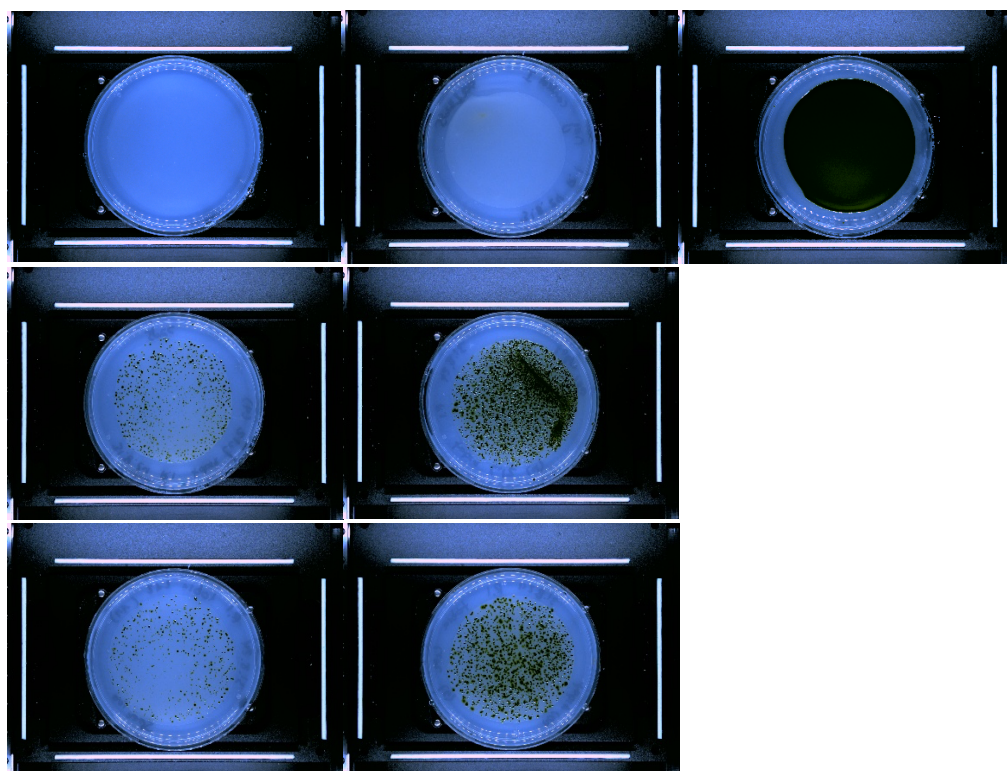
D



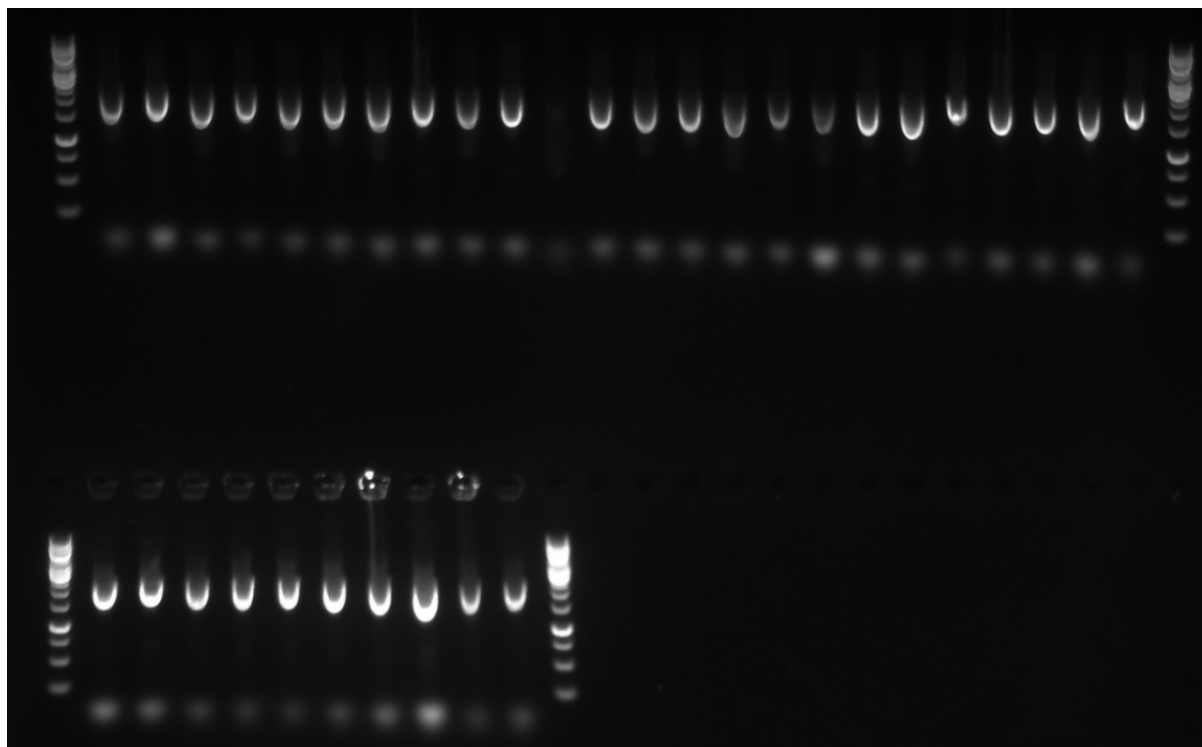
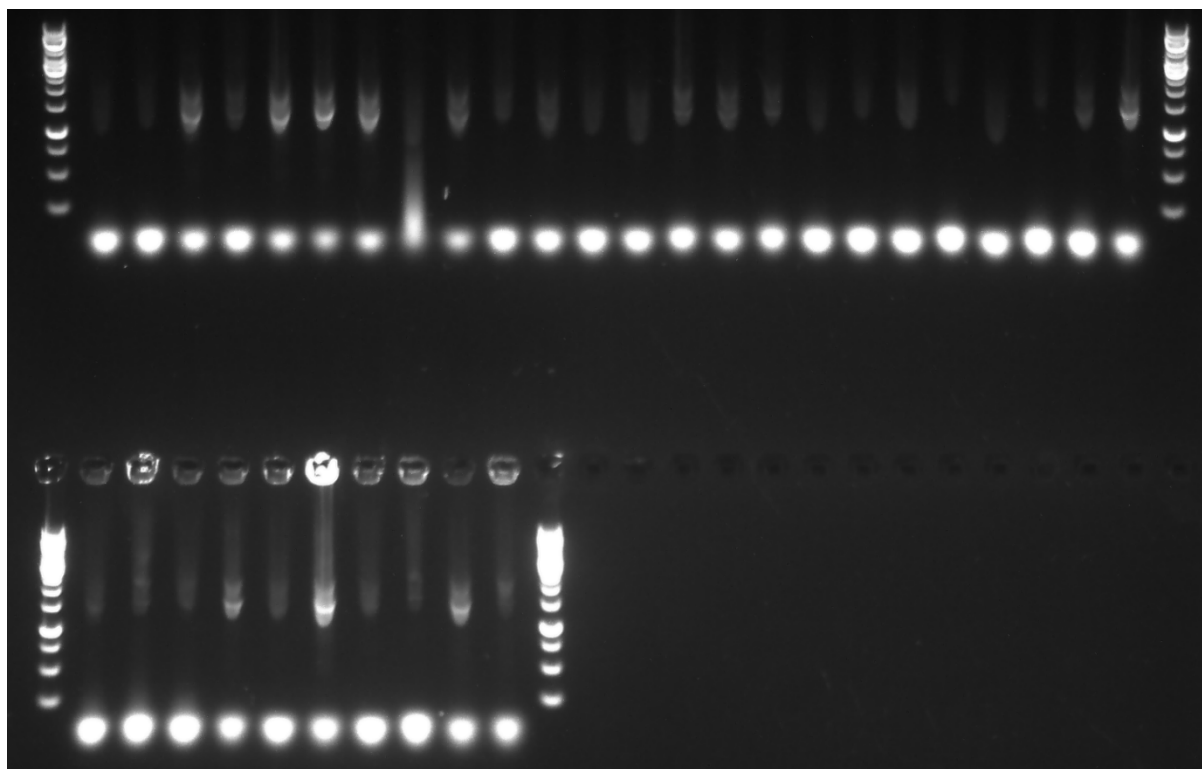
Supplementary figure 9: Unprocessed gels of Supplementary figure 1 depicted cPCR confirming Nanoluc integration in transplastomic strains.

A**B****C**

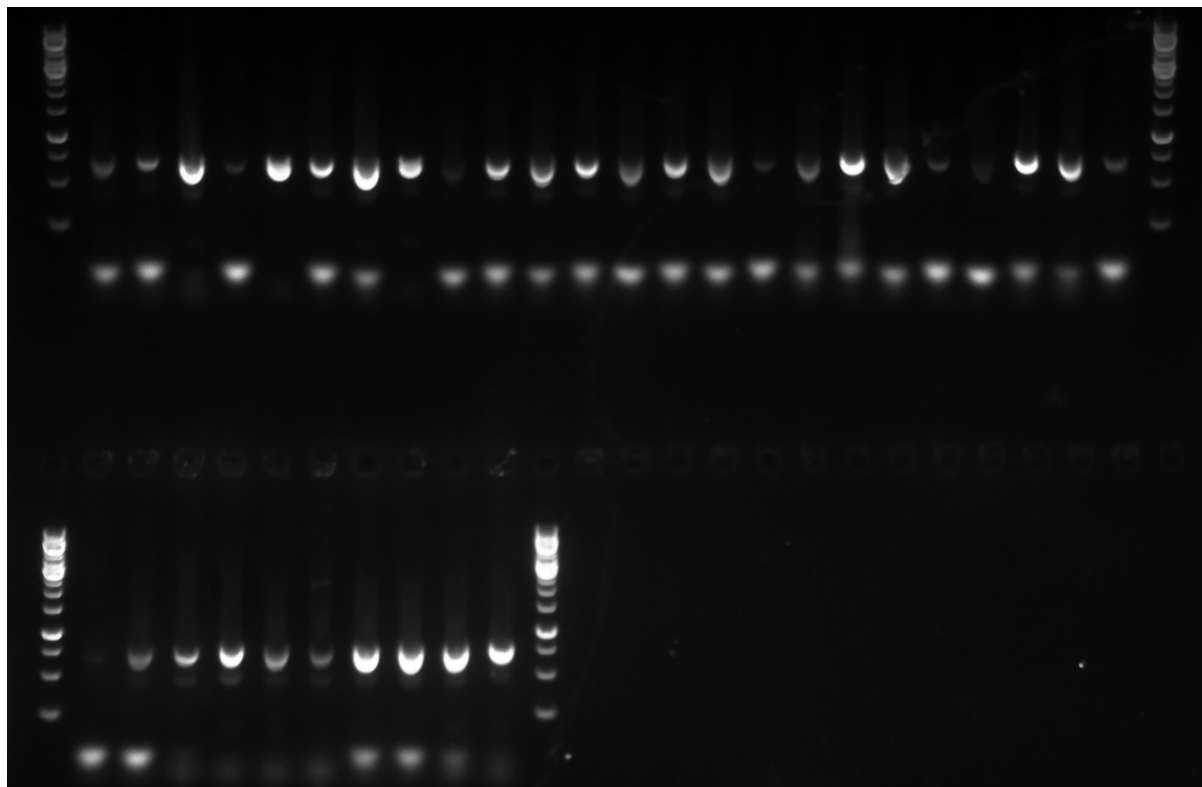
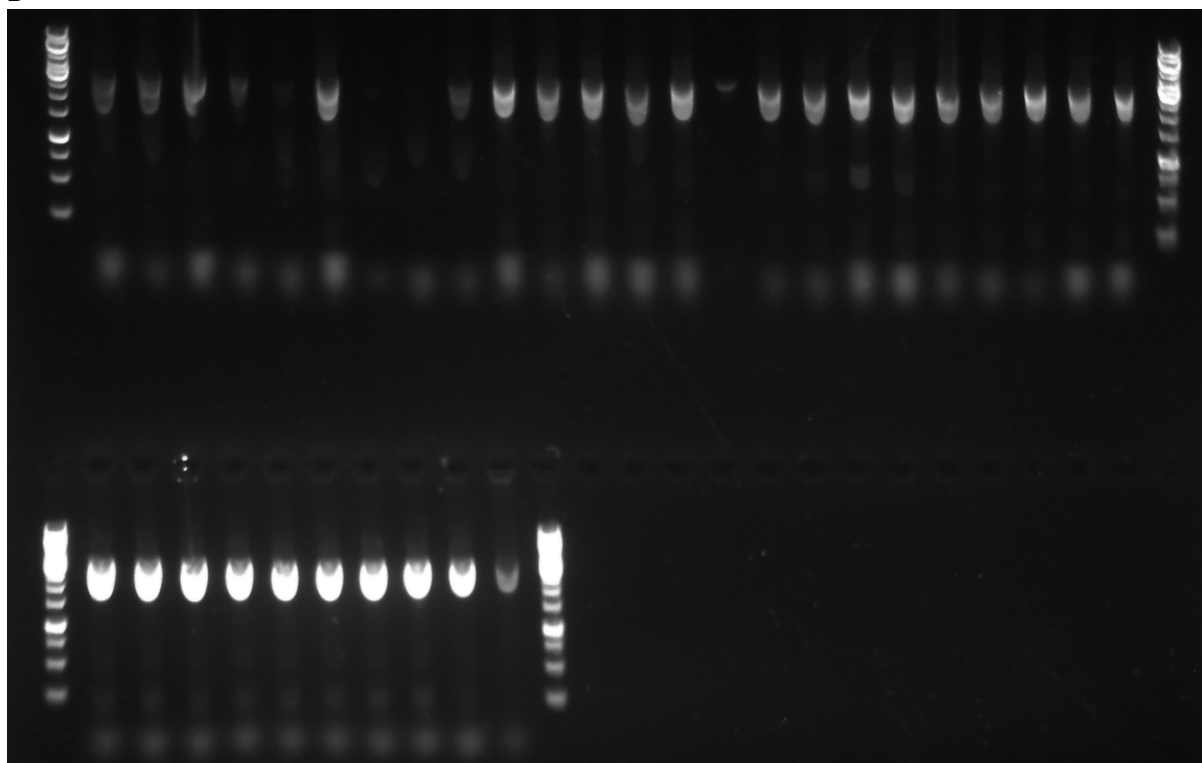
Supplementary figure 10: Unprocessed gels of Supplementary figure 2 depicted cPCR confirming Nanoluc integration in transplastomic strains, alongside cPCR confirming that the mutant strain cc-5797 contains a cassette in the Glycolate Dehydrogenase locus.



Supplementary figure 11: Unprocessed plate pictures of Tobramycin chloroplast transformation showed in Supplementary figure 4 panel B.

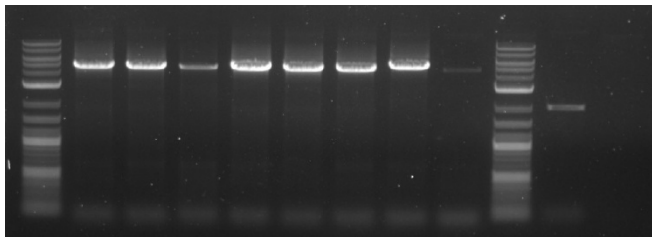
A**B**

Supplementary figure 12: Unprocessed gels of Supplementary figure 6, panels b and d, depicted cPCR confirming Nanoluc integration in transplastomic strains, in Wendyl locus right and left borders, to identify any homologous recombination event.

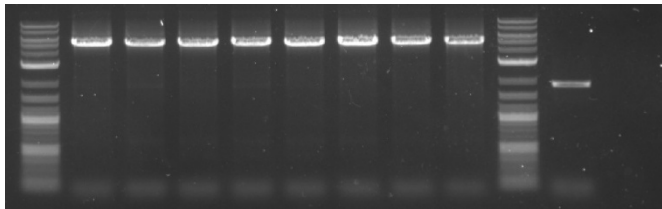
A**B**

Supplementary figure 13: Unprocessed gels of Supplementary figure 7, panels b and d, depicted cPCR confirming Nanoluc integration in transplastomic strains, in WendyII locus right and left borders, to identify any homologous recombination event.

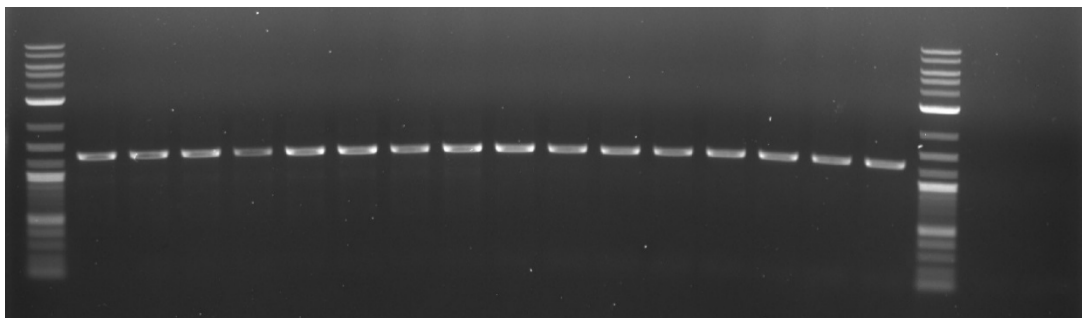
A



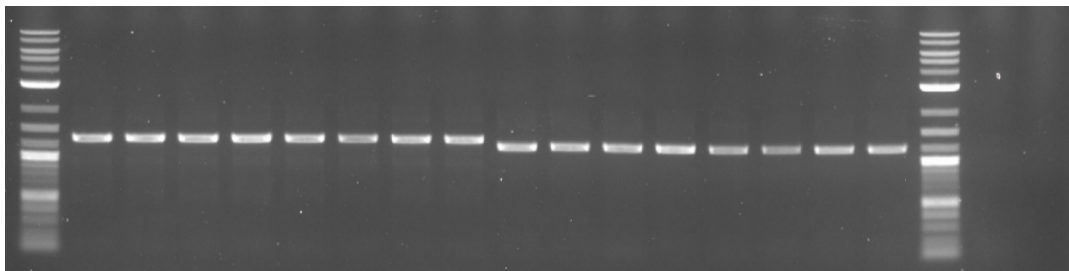
B



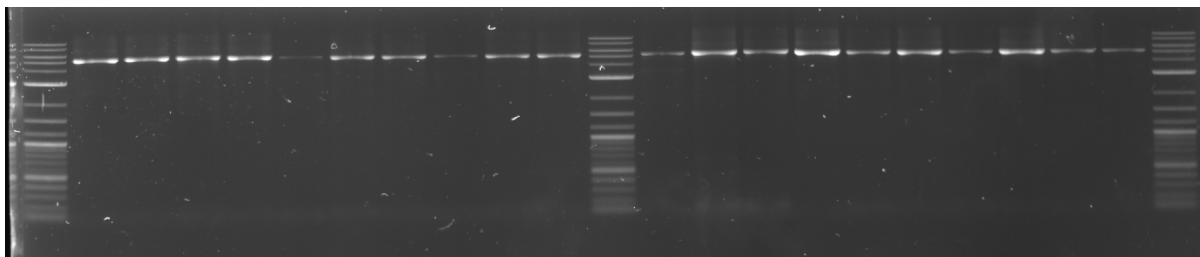
C



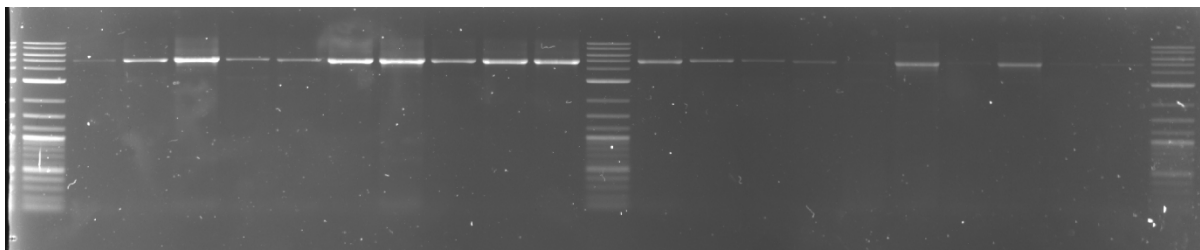
D

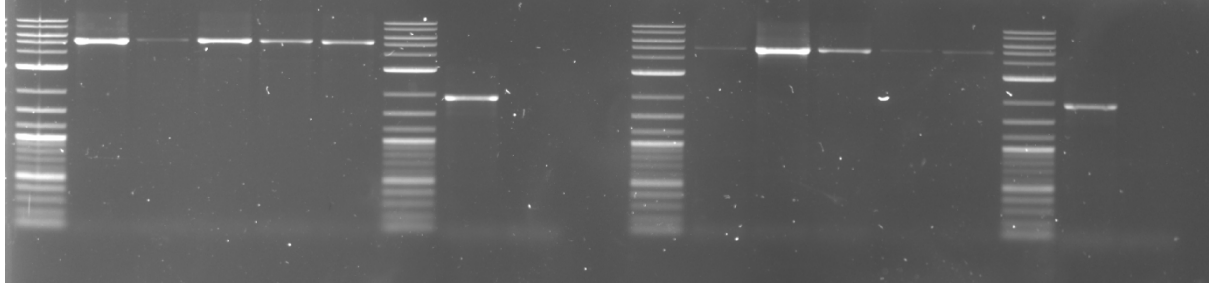


E



F



G

Supplementary figure 14: Unprocessed gels of Supplementary figure 8. a-b cPCR to assess homoplasmy in transplastomic strains, for Nanoluc and mScarlet constructs respectively. c-d, cPCR confirming left and right flank integration of the constructs in the chosen locus, for nanoluc and mScarlet constructs respectively. e-g, cPCR to assess homoplasmy in transplastomic strains after two rounds of restreaking to isolate single clones, for mScarlet and Nanoluc respectively constructs respectively.

Supplementary Text

Supplementary text 1: Fluorescence microscopy settings for each fluorophore, chlorophyll and brightfield.

mCherry

Excitation laser:	561 nm
Laser power:	2.5%
Pinhole:	103
Imaging mode:	SUPERRES
Master gain:	750
Digital gain:	1.5
Main beam splitter (MBS):	488/561/633
Second beam splitter (SBS):	LP 570
Emission dual filters:	BP 420-480 + BP 495-620

mScarlet-I

Excitation laser:	561 nm
Laser power:	2.5%
Pinhole:	109
Imaging mode:	SUPERRES
Master gain:	750
Digital gain:	1.5
Main beam splitter (MBS):	488/561/633
Second beam splitter (SBS):	LP 570
Emission dual filters:	BP 420-480 + BP 495-620

mVenus

Excitation laser:	514 nm
Laser power:	5%
Pinhole:	103
Imaging mode:	SUPERRES

Master gain:	775
Digital gain:	1.0
Main beam splitter (MBS):	458/514
Second beam splitter (SBS):	LP 525
Emission dual filters:	BP 420-480 + BP 495-550

mCerulean

Excitation laser:	458 nm
Laser power:	5%
Pinhole:	103
Imaging mode:	SUPERRES
Master gain:	775
Digital gain:	1.0
Main beam splitter (MBS):	458/561
Second beam splitter (SBS):	SP 615
Emission dual filters:	BP 465-505 + LP 525

Chlorophyll

Excitation laser:	633 nm
Laser power:	1%
Pinhole:	103
Imaging mode:	SUPERRES
Master gain:	720
Digital gain:	1.0
Main beam splitter (MBS):	488/561/633
Second beam splitter (SBS):	BP 570-625
Emission dual filters:	BP 570-620 + LP 645

Brightfield

Excitation laser:	561 nm
Laser power:	2%
Pinhole:	76.4
Imaging mode:	T-PMT
Master gain:	150

Digital gain: 1.0

Supplementary text 2: PIXL colony detection parameters. Imaging settings and algorithm selection.

Mode:	White
Gain:	39.4%
Gamma:	39.4%
Exposure:	10ms
Saturation:	34.4
White Balance - Red:	34.4%
White Balance - Green:	25%
White Balance - Blue:	74.3
Focus:	Auto
Lighting power:	70%
Algorithm:	Colony Separation
Organism:	<i>S. cerevisiae</i> (dark colonies)
Blueness Filter:	0 - 1
Circularity Filter:	0 - 1
Greenness Filter:	0 - 1
Intensity Filter:	0 - 1
Proximity Filter:	0 - 100
Radius Filter:	0.25 – 2.5
Redness Filter:	0 - 1

Supplementary text 3: FACS analysis settings.

Laser (mScarlet-I):	561 nm
Filter (mScarlet-I):	570-630 nm
Filter Gain (mScarlet-I):	40%
Laser (Chlorophyll):	638 nm
Filter (Chlorophyll):	690-750 nm
Filter Gain (Chlorophyll):	40%

Supplemental text 4: criteria for selecting integration sites

We evaluated four distinct chloroplast integration sites in this study. We began with the well-established *psbH* locus, widely used in *C. reinhardtii* chloroplast engineering¹.

To expand upon previously reported sites, we designed three additional loci (*psbD*, *rbcL*, and *petB*) using similar criteria:

1. We placed each insertion near a photosynthetic gene to allow for photosynthetic selection in knockout strains, similar like what has been reported for the *psbH* integration site.
2. We aimed to minimize interference with neighboring genes by reviewing RNA-seq data to avoid genome regions of high or antisense transcription^{2,3}.
3. We searched for a specific orientation of neighboring genes. For instance, at the *rbcL* and *psbD* loci, flanking genes are oriented away from the insertion site (divergent orientation), thereby reducing the likelihood of antisense transcription. In the case of *petB*, the gene faces the integrated cassette, but low transcriptional activity at that locus, based on RNA-seq evidence, made it a worthwhile comparison for evaluating different genomic contexts.
4. We ensured compatibility with our modular cloning system by removing internal restriction sites without disrupting adjacent genes.

These criteria would also allow for integration at next to the *psbF* site in the chloroplast genome of *C. reinhardtii*, which we have not explored yet. Additionally, future work could compare our sites to integration in the inverted repeats, which have been demonstrated to increase the gene expression strength due to the higher gene dosage.

Supplemental text 5: Design and in-depth analysis of synthetic chloroplast promoters

To develop a minimal chloroplast promoter scaffold in *C. reinhardtii*, we began with the commonly used *rrn16* promoter, which is 217 base pairs (bp) in length. By annotating the -35 and -10 sequence motifs, located near the midpoint of this 217 bp region, we hypothesized that the promoter could be shortened without significantly reducing its activity. Through iterative truncations, we arrived at a minimal scaffold of only 46 bp.

Building on this minimal promoter, we designed 22 synthetic variants to achieve a range of expression strengths and to explore fundamental design principles. The variants can be broadly grouped as follows:

Ten variants preserving the original -35 and -10 boxes and randomizing the other base pairs

Maintained -35 box (TTGACA) and -10 box (TAAATT), while randomizing all other positions.

Twelve variants with targeted changes relative to the *rrn16* promoter

Psyn11: Modified only upstream (5') of the -10 box. Decrease in expression.

Psyn12: Modified only downstream (3') of the -35 box. Relatively high expression.

Psyn13: Modified all bp between the -35 and -10 motifs. Low expression.

Psyn14: Modified the region immediately downstream of the -10 box. Data currently unavailable.

Psyn15: Modified only upstream (5') of the -35 box. Very high expression.

Psyn16: Incorporated scattered base-pair changes across the entire scaffold.

Psyn17: Replaced 17 bp between the -35 and -10 boxes with sequence from the *psaA* promoter. Very high expression.

Psyn18: Replaced 23 bp between the -35 and -10 boxes with *psaA* sequence. Low expression.

Psyn19: Added the RUA-box 5' of the -35 box (derived from the tobacco *rrn16* promoter). High expression, but not exceeding other strong promoters.

Psyn20: Substituted the native -10 box (TAAATT) with the canonical bacterial consensus (TATAAT). One of the highest expression levels observed.

Psyn21: Changed every base outside the -35 and -10 motifs to its complementary nucleotide (A→T, T→A, G→C, C→G). Very low expression.

Psyn22: Modified every base 5' of the -35 box and 3' of the -10 box. Very high expression.

For benchmarking, we also included two endogenous reference promoters (*Pwendy II* and *PtrnE*). Both share the same -35 box, the same distance between the -35 and -10 motifs, and an even more bacterial-like -10 box, leading to robust expression in *C. reinhardtii*.

These experiments revealed several important trends:

Proximal region to the -10 box: Positions immediately upstream (5') of the -10 motif play a key role in maintaining high expression. In particular, a conserved G two nucleotides 5' of the -10 box was shared by many strong promoters.

Sequence upstream of -35 and downstream of -10: Modifications in these regions did not generally affect expression (e.g., the region 5' of the -35 box, which is crucial in tobacco, appeared nonessential in *C. reinhardtii*).

Spacing between -35 and -10 motifs: Psyn17 and Psyn18 showed that changing this distance strongly impacts expression.

Substituting the native -10 motif: Replacing TAAATT with the bacterial consensus TATAAT (Psyn20) yielded especially high expression.

Collectively, these findings highlight the utility of synthetic promoter libraries in uncovering critical regulatory elements and informing more advanced synthetic biology efforts in chloroplast engineering.

Supplemental text 6: Manual for the Chloroplast Modular Cloning System

Type IIs restriction enzymes

Unlike conventional Type II restriction enzymes, which cleave DNA within their recognition sequences, Type IIS restriction enzymes cut outside their recognition sequences at defined distances (Figure 1). This property allows for the flexible design of overhangs, enabling a single enzyme to generate up to 256 distinct 4-base pair overhangs. This capability has led to the development of the Golden Gate cloning technique, now one of the most widely used cloning methods. Commonly used Type IIS enzymes include BsaI, BsmBI, BpiI (BbsI), PaeI (AarI), and SapI.

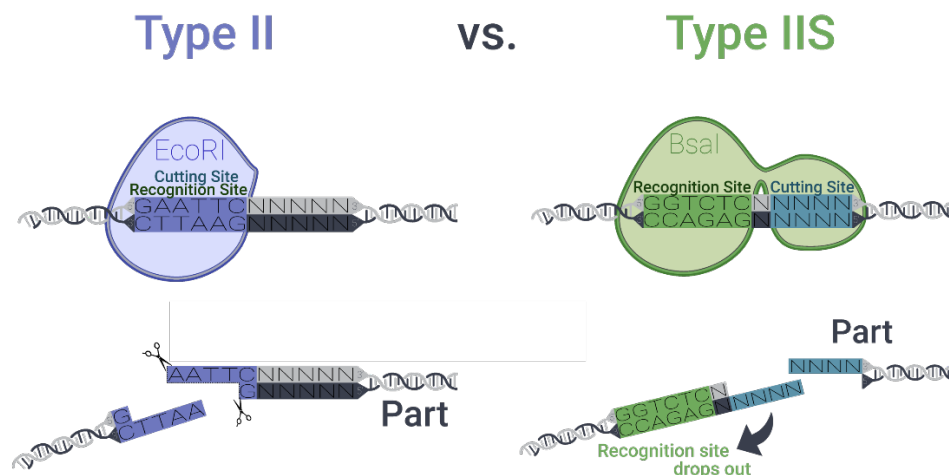


Figure 1 General principle of Type IIs restriction enzymes

While Type II restriction enzymes cleave DNA within their recognition sequence, Type IIS restriction enzymes cut DNA adjacent to their recognition sites, allowing the 4-base pair cut site to be freely chosen.

Golden Gate cloning allows these enzymes to be combined in a single "one-pot" reaction with T4 ligase, eliminating the need for separate restriction and ligation steps. Because the recognition sites for Type IIS enzymes are cleaved off during digestion and are not included in the final assembly (Figure 1), correctly assembled constructs are not cleaved further. This feature enables the cycling of restriction enzyme digestion and ligation steps, which increases the efficiency of obtaining correctly assembled constructs.

General introduction

Following the initial development of Golden Gate cloning and the subsequent creation of the widely adopted Modular Cloning (MoClo) standard syntax, which employs standardized overhangs generated by Type IIS restriction enzymes such as BsaI, BpiI, and BsmBI, a consensus has emerged within the plant synthetic biology community. The widely adopted Phytobrick standard in the plant synthetic biology community has been successfully adapted for a range of photosynthetic organisms, including cyanobacteria, plants, mosses, plant chloroplasts, and even for nuclear engineering in *Chlamydomonas reinhardtii*, standardizing and characterizing genetic parts is essential. Although different cloning systems employ varying strategies for assembling multigene constructs, most are

compatible with the assembly of single transcription units from standardized parts. Our system, utilizes a hierarchical assembly approach, similar to the common Plant MoClo and the Chlamydomonas MoClo system, rather than the iterative cloning scheme used in the GoldenBraid/Loop assembly standard.

The following sections provide a detailed explanation of our cloning system.

The general Modular cloning scheme

In our hierarchical cloning scheme, individual Level 0 parts are first cloned into a universal acceptor vector. A Level 0 part represents the DNA sequence of a fundamental genetic element—such as a promoter, 5'UTR, coding sequence, or 3'UTR—flanked by a standardized 4-bp overhang and BsaI recognition sites.

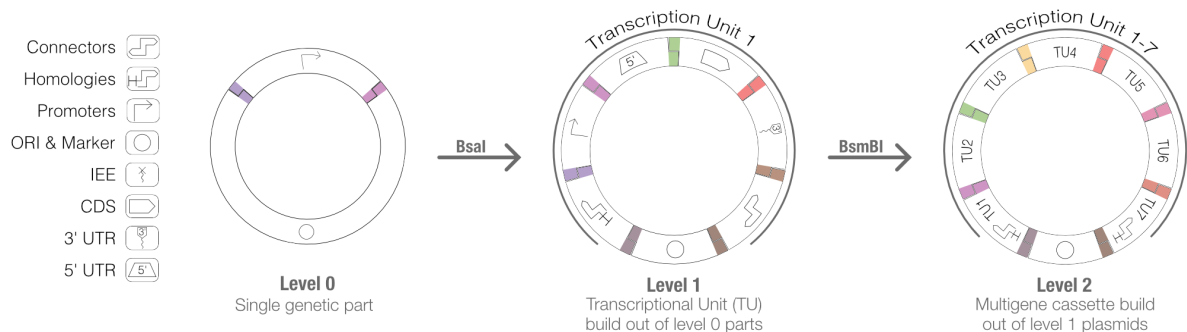


Figure 2 The hierarchical modular cloning scheme

New parts are first domesticated and assembled into a universal acceptor vector (Level 0). These parts can then be combined in a one-pot reaction to create Level 1 plasmid containing a single transcriptional unit. Optionally, these single transcriptional units can be further assembled into a multigene cassette. (Level 2).

These parts are then assembled into a single transcriptional unit using a one-pot Golden Gate reaction with BsaI, combining 5–9 Level 0 parts into a Level 1 assembly.

Next, 2–7 transcriptional units are integrated into a Level 2 multigene cassette via another one-pot Golden Gate reaction using BsmBI. In our system, the arrangement and order of transcription units are defined by the chosen connectors (detailed explanation below), rather than by the acceptor vectors used in the Level 1 assembly.

To enable selection of successfully assembled plasmids, different antibiotic markers are used at each assembly stage. In our system, Level 0 employs chloramphenicol, Level 1 uses carbenicillin (or ampicillin), and Level 2 utilizes kanamycin selection.

Domesticating new Level 0 parts

New Level 0 parts are generated using PCR products or synthesized DNA. These linear sequences are then assembled into a single standardized universal acceptor vector. In contrast to other methods that require multiple acceptor vectors, only one is needed because standardized overhangs are incorporated into the PCR primers or synthesized sequence. The specific overhangs are detailed in Table 1.

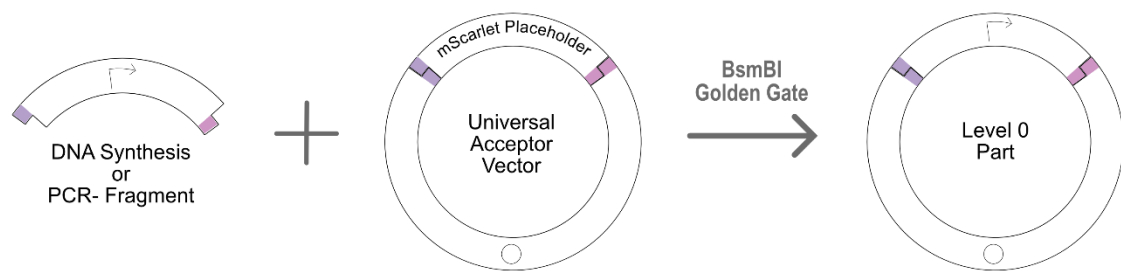


Figure 3 Domesticating new Level 0 Parts

PCR or DNA synthesis fragments that include standardized overhangs and BsmBI recognition sites are assembled into the Universal Acceptor vector. This vector features an mScarlet placeholder, enabling pink/white colony screening.

The unique overhangs assign the position within the Level 1 assembly for the subsequent cloning steps. For some overhangs, additional nucleotides are appended. For example, overhangs in the 3'UTR position (**GCTTAA**, **GGTAA**) incorporate stop codons, while those at the tag positions (**CCATG**, **GGAATG**, **GCTTTA**) include extra bases to ensure that fusion tags remain in frame.

For the domestication of new coding sequences, the original start and stop codons are removed. The start codon is reintroduced as part of the Golden Gate overhang for the CDS, which prevents double start codons, while the stop codon is incorporated into the 3'UTR/terminator sequence. This design allows for the modular addition of C-terminal tags. For most Level 0 assemblies, the BsmBI enzyme is used. However, for new Connector/Integration site homology parts, the enzyme PaqCI is required along with the alternative Universal acceptor vector. This is because these parts contain BsmBI recognition sites, which are necessary for the subsequent assembly of multi-gene constructs.

Table 1 Overhangs for creating new Level 0 parts via DNA synthesis/PCR

Level 1 overhangs are indicated in blue. BsmBI sites (**CGTCTC/GAGACG**) are indicated. For connector overhangs PaqCI sites are used.

Position	Sequence
1_5'Connector_fwd	AAC CACCTG CATATCTCG AACACGTCTC GNNNN
1_5'Connector_rv	GGAGT GAGATAT GCAGGT TT
2_Promoter_fwd	AAC CGTCTC GCTCG GGAG
2_Promoter_rv	TACTT GAGG GAGACG AA
3_5'UTR_fwd	AAC CGTCTC GCTCG TACT
3_5'UTR_rv	AATGT GAGG GAGACG AA
3a_5'UTR_fwd	AAC CGTCTC GCTCG TACT
3a_5'UTR_rv	CCATT GAGG GAGACG AA
3b_n-tag_fwd	AAC CGTCTC GCTCG CCATG
3b_n-tag_rv	GGAATG TGAGG GAGACG AA
4_CDS_fwd	AAC CGTCTC GCTCG AATG
4_CDS_rv	GCTTT GAGG GAGACG AA
5_3'UTR+Terminator_fwd	AAC CGTCTC GCTCG GCTTAA
5_3'UTR+Terminator_rv	CGCTT GAGG GAGACG AA
5a_c-tag_fwd	AAC CGTCTC GCTCG GCTTTA

5a_c-tag_rv	GGTATGAGG GAGAC GAA
5b_3'UTR+Terminator_fwd	AAC CGTCTC GCTCG GGTAA
5b_3'UTR+Terminator_rv	CGCT TGAGG GAGAC GAA
6_3'Connector_fwd	AAC CACCTGC ATATCTCG CGCT
6_3'Connector_rv	NNNNG GAGACGAGACT GAGATAT GCAAGTGTT
7-8_E.coli_ORI+Resistance_fwd	AAC CGTCTC GCTCG GAGAC
7-8_E.coli_ORI+Resistance_rv	AACAT GAGG GAGAC GAA

Our version of the universally acceptor vector, allows for pink/white selection after cloning and transformation, due to the mScarlet placeholder cassette in the vector. Except of this mScarlet placeholder cassette this vector is sequence identical to the commonly used (in the plant synthetic biology community) Universal acceptor vector (Addgene #68161). Another aspect, which needs to be considered when creating new Level 0 Part is that internal enzyme recognition sites for at least BsaI and BsmBI have to be removed within the part sequence to not interfere with the subsequent cloning process.

Assembly of Level 1 Transcription Units

To construct a single transcriptional unit (Level 1), 5–9 Level 0 parts are assembled in a one-pot reaction using BsaI. The overhangs on these parts adhere to the widely adopted Phytobrick standard, which is also employed in the modular cloning system for nuclear engineering in *Chlamydomonas*, including the A1–C1 overhangs (Figure 4).

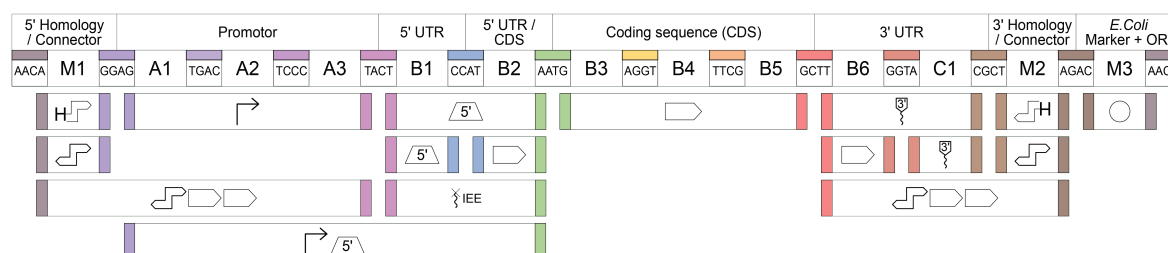


Figure 4 Part types and positioning of the chloroplast modular cloning system

The modular design of the system provides high flexibility by offering 5'UTRs, promoters, IEEs, and tags as separate, independently selectable parts. The chloroplast modular cloning systems adheres to the widely adopted Phytobrick standard, including the A1–C1 overhangs. These overhangs are complemented by two additional overhangs for the connectors/homology parts, as well as the *E. coli* marker and origin.

Compared to the modular cloning system for nuclear engineering in *Chlamydomonas*, our system brings several new features, such as the additional connector/homology parts, the possibility of building polycistronic transcription units via IEEs and a few more.

Our system differs from the traditional modular cloning architecture by not using the conventional Level 1 and Level 2 acceptor vectors to dictate the placement of the transcription units in subsequent assembly steps. Instead, this function is performed by connector parts that contain BsmBI sites and specific overhangs to define the arrangement of multigene constructs. The following sections provide a detailed explanation of these homology parts/connectors and other new features.

New in our Chloroplast Modular cloning System:

Chloroplast genome homology parts and connectors

To adapt the Modular Cloning (MoClo) approach for chloroplast engineering, the standard MoClo positions have been extended with additional Connector/Homology positions. These

extensions enable site-directed integration into the plastome and support multigene assembly. Four specific regions of the chloroplast genome are available as homology sites for precise, site-specific integration. For multigene assemblies, the 5' homology region is incorporated into the first transcription unit and the 3' homology region into the last transcription unit. Alternatively, these homology parts can be used within a single transcription unit to integrate a single gene of interest.

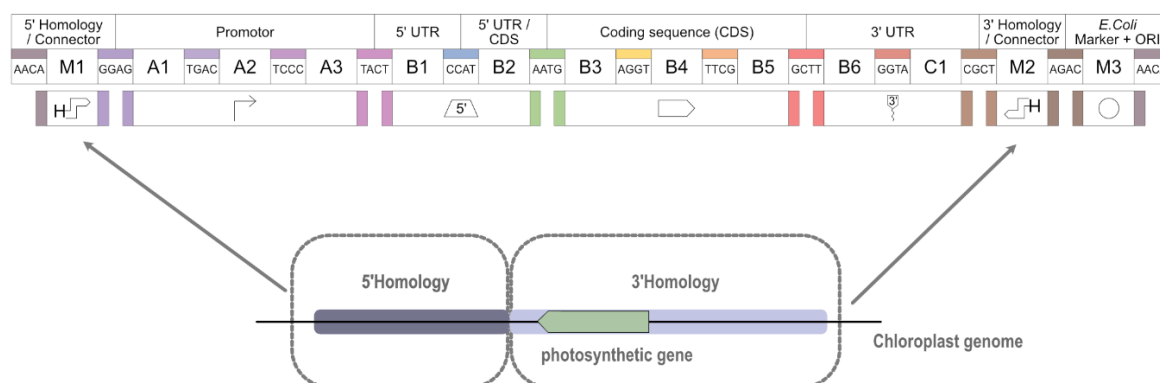


Figure 5 Homology parts of the chloroplast genome of *Chlamydomonas reinhardtii*

Chloroplast regions for four distinct integration sites are provided as homology parts within the extended Modular Cloning framework, supplementing the standard Phytobrick part positions. Notably, one homology part also includes a photosynthetic gene, which can be leveraged for photosynthetic selection strategies.

The same modular cloning position as the homology parts (M1 and M2) are also used for the connector parts. These connector parts are used within a Level 1 assembly to define the order of transcription units within a multigene Level 2 assembly. These parts include BsmBI sites and the different overhangs for the respective position of the transcription unit.

Our system features several types of connector parts—including short, long, and reverse connectors (detailed below). Each type comprises seven distinct connectors corresponding to the seven positions in a Level 2 multigene assembly.

One advantage of connector-based assembly is its increased flexibility: no end linkers are required, and new functions can be easily incorporated into the connector parts. The 5' and 3' connectors are selected independently to construct a Level 1 plasmid, allowing one to seven Level 1 plasmids to be combined into a Level 2 plasmid without needing the end linkers that other modular cloning systems require (Figure 6).

To design and assemble multigene constructs, the rule for selecting connectors is as follows: 5'Con(N) connects to 3'Con(N-1). For example, the 5' connector of the second transcription unit (5'Connector_2) must connect to the 3' connector of the first transcription unit (3'Connector_1). Additionally, the total number of transcription units in the final assembly must be considered, since the last unit must end with 3'Homology for the integration in the chloroplast genome and to properly connect to the Level 2 backbone.

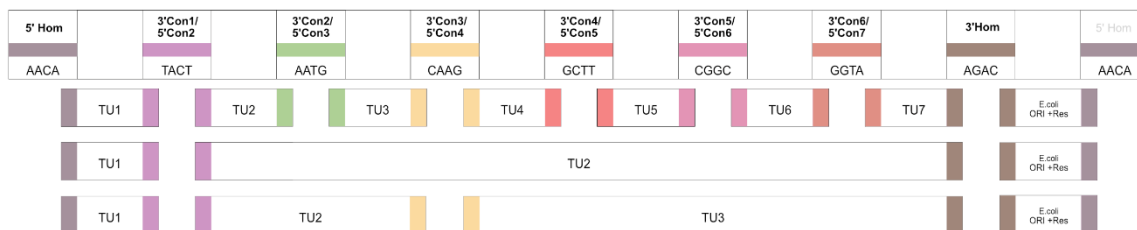


Figure 6 Connector parts define the position of transcription units (TU) within a multigene assembly. The position of the Level 1 transcription units within a multigene Level 2 assembly is dictated by the 4bp BsmBI overhangs with the connector parts. Our cloning systems allows assembly for up to 7 TU's but the number of TU's can be chosen highly flexibly, by the selection of the specific connector parts in the Level 1 assembly. The first TU always includes the 5'Homology and the last TU always includes the 3'homology for the integration into the chloroplast genome

Example for the assembly of a Level 2 Multi-gene constructs

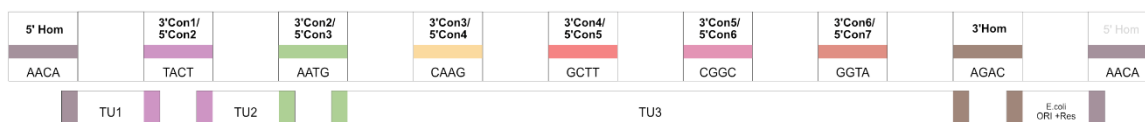


Figure 7 Example of a multigene assembly with three transcription units. The first transcription unit (TU1) uses a 5' homology part (selected from one of four chloroplast integration sites) combined with 3' Connector-1. The second transcription unit (TU2) is built with 5' Connector-2 and 3' Connector-2. The third transcription unit (TU3) incorporates 5' Connector-3 paired with the corresponding 3' homology part matching the chosen 5' homology site.

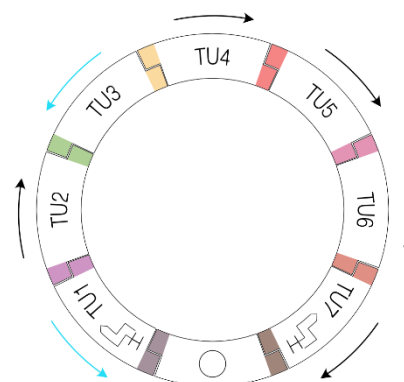
An example of assembling a Level 2 multigene construct is as follows:

- **First Transcription Unit:**
 - Use a 5' Homology part for the connector position (selectable from four chloroplast integration sites).
 - Use 3' Connector-1.
- **Second Transcription Unit:**
 - Use 5' Connector-2.
 - Use 3' Connector-2.
- **Third Transcription Unit:**
 - Use 5' Connector-3.
 - Use the corresponding 3' Homology part that matches the chosen 5' Homology site.

These three Level 1 plasmids are subsequently combined with a Level 2 acceptor vector in a BsmBI Golden Gate reaction. The connectors selected during the Level 1 assembly determine the final order of transcription units in the multigene construct (Figure 7).

Additional features: Reversing of Transcription units

Our modular cloning system also includes a set of reverse connectors that allow the orientation of transcription units to be switched (Figure 8). This is particularly important because natural 3'UTRs often lack strong termination signals, leading to read-through transcription. Such read-through can produce antisense RNA that interferes with the expression of neighbouring genes. By inverting the direction of transcription units, this issue can be circumvented. Additionally, homology parts for plastome integration have been designed with an inversion option for all available integration sites as well.



Level 2

Figure 8 Reverse connectors allow switching of the transcription unit directionality. In this example TU1 and TU3 are in the reverse orientation

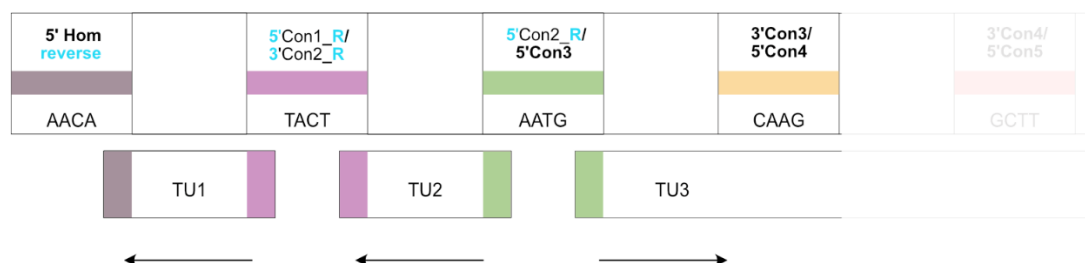


Figure 9 Example of reverse connector usage

For assembling reverse transcription units, reverse connectors and reverse homologies are employed. In the first transcription unit, a 5' homology part is paired with a reversed 5'Connector-1 (serving as the 3' connector). The second transcription unit uses a reversed 5'Connector-2 along with a reversed 3'Connector. The third transcription unit, oriented in the forward direction, is constructed using the standard 5'Connector-3 and 3'Connector-3. These three Level 1 transcription units are subsequently combined in a Level 2 assembly.

For reverse transcription unit assembly, the same naming scheme and rules apply, with each connector number corresponding to its position in the multigene assembly (Figure 9). The only difference is that the inverted versions of the 5' and 3' connectors must be used. This approach allows the orientation of up to seven transcription units to be independently selected.

Additional features: Building polycistronic operons via Intercistronic expression elements (IEEs) and operon connectors.

One feature that has not traditionally been incorporated into the Modular Cloning approach is the construction of polycistronic operon structures. Standard Modular Cloning assemblies rely on separate transcription units composed of promoters, 5'UTRs, coding sequences, and 3'UTRs/terminators. To integrate polycistronic design into this framework, a method was needed to “skip” the promoter and terminator positions. This was achieved by extending the connector position to bypass these regions. In this work, 14 novel operon connectors were designed and constructed, enabling the assembly of operons with up to seven genes expressed from a single polycistronic mRNA. These new operon connector parts can be adapted for any Modular Cloning toolkit designed for bacterial chassis, thereby facilitating polycistronic expression.

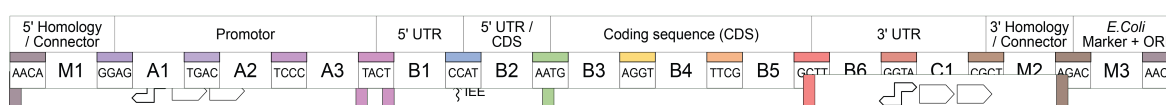


Figure 10 Operon connectors & IEE parts enable the construction of polycistronic multigene assemblies

Operon parts are included in our modular cloning system to “skip” promoter and 3'UTR/Terminator positions. When combined with intercistronic expression elements (IEEs), these parts enable the assembly of polycistronic multigene constructs.

Although polycistronic expression is native to chloroplasts due to their bacterial origin, primary polycistronic transcripts often require post-transcriptional processing into monocistronic fragments. To implement polycistronic gene expression for chloroplast engineering, the necessary intercistronic expression elements (IEEs) were integrated into our system in place of the 5'UTR. Combined with the operon connectors described above, this design allows for the construction of modular polycistronic constructs for chloroplast expression.

For example, a polycistronic construct can be built by designing the first transcription unit to include a promoter and a 3' operon connector, while the second transcription unit contains a 5' operon connector, one of 11 distinct IEE parts, and a 3'UTR. This configuration allows two genes of interest to be expressed from a single polycistronic transcript.

Additional features: Placeholder parts

To facilitate the characterization of entire libraries of a specific part type, it would be ideal to pre-build Level 2 assemblies with a placeholder that can later be exchanged with library elements. However, exchangeable parts have not been implemented within the Modular Cloning framework. Therefore we have designed and constructed placeholder parts that can be removed after the assembly process. In standard Golden Gate cloning, the recognition sites are eliminated in the final construct; therefore, these placeholders must be designed to retain BsaI recognition sites after assembly. This was achieved by incorporating the reverse BsaI recognition sequence.

To simplify the identification of correct assemblies, a GFP cassette—expressed in *E. coli*—was selected as the placeholder. These placeholder parts have been designed and constructed for most positions defined by the standardized Phytobrick and MoClo syntax, making them universally replaceable in all MoClo toolkits that adhere to this standard.

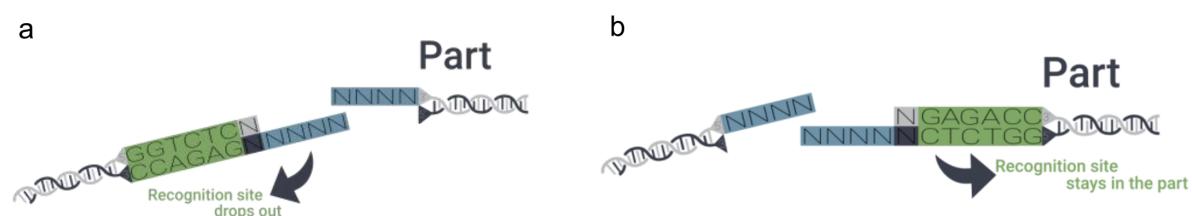


Figure 11 Design and function of modular placeholder parts

BsaI is a Type IIS restriction enzyme that cuts outside of its recognition sequence. In the standard Golden Gate cloning approach (a), the recognition site is removed during assembly. By contrast, using the reverse BsaI recognition sequence (b) allows the site to remain in the final construct. This retained recognition site enables the design of placeholder parts that can be removed in subsequent cloning rounds.

The placeholder parts are treated as regular parts during the Golden Gate assembly, with only a minor protocol adjustment required: the final step in the thermocycler should be a 16°C ligation step. Without this step, the placeholder would be excised from the assembled plasmid. Once assembled, colonies can be identified by green fluorescence due to the GFP cassette. The resulting Level 2 plasmid can then be used for the insertion of part libraries at the placeholder position.

Supplementary Tables

Supplementary Table 1: Mass Spectrometry parameters for CoAs.

Name	Precursor Ion	Product Ion	Collision energy [V]	Fragmentor Voltage [V]	Cell Accelerator Voltage [V]	Dwell time [msec]	Polarity
CoA	768.12	428	35	380	5	220	Positive
		261.1	35	380	5	220	Positive
ACoA	810.1	428	31	380	5	220	Positive
		302.2	31	380	5	220	Positive

Supplementary Table 2: Mass Spectrometry parameters for organic acids.

Name	Precursor Ion	Product Ion	Collision energy [V]	Fragmentor Voltage [V]	Cell Accelerator Voltage [V]	Dwell time [msec]	Polarity
Citrate	191	111.1	11	380	5	20	Negative
		85.1	14	380	5	20	
Alphaketoglutarate	145.1	101.1	5	380	5	20	Negative
		57.2	8	380	5	20	
Malate	133.1	115.1	8	380	5	20	Negative
		71.2	14	380	5	20	
Succinate	117.2	73.2	9	380	5	20	Negative
		55.1	15	380	5	20	
Fumarate	115.1	71.2	4	380	5	20	Negative
		27.3	9	380	5	20	
Lactate	89.2	89.2	0	380	5	20	Negative
		71.3	10	380	5	20	
Pyruvate	87.1	87.1	0	380	5	20	Negative
		43.1	4	380	5	20	
Glycolate	75.2	75.2	0	380	5	20	Negative
		47.2	6	380	5	20	
Glyoxylate	73.2	73.2	0	380	5	20	Negative
		45.2	7	380	5	20	

Supplementary Table 3: Mass Spectrometry parameters for amino acids.

Compound	Precursor	Product	Dwell time [msec]	Fragmenter Voltage [V]	Collision Energy [V]	Cell Accelerator Voltage [V]	Polarity
Tryptophane	205.1	188	20	380	7	5	Positive
		145.9	20	380	17	5	Positive
Tyrosine	182.1	165	20	380	6	5	Positive
		136.1	20	380	12	5	Positive
Arginie	174.9	116	20	380	12	5	Positive
		70.2	20	380	29	5	Positive
Phenylalanine	166.1	120.2	20	380	13	5	Positive
		103.1	20	380	32	5	Positive
Histidine	156.1	110.1	20	380	16	5	Positive
		83	20	380	30	5	Positive
Methionine	150.1	133	20	380	7	5	Positive
		104	20	380	7	5	Positive
Glutamate	148.1	84.1	20	380	17	5	Positive
		56.1	20	380	34	5	Positive
Glutamine	147.2	130.1	20	380	8	5	Positive
		84.2	20	380	17	5	Positive
Lysine	147.1	130.1	20	380	8	5	Positive
		84.1	20	380	19	5	Positive
Aspertate	134.1	88	20	380	9	5	Positive
		74	20	380	14	5	Positive
Asparagine	133.	87.1	20	380	17	5	Positive
		74.2	20	380	16	5	Positive
Isoleucine	132.1	86.1	20	380	8	5	Positive
		69.1	20	380	18	5	Positive
Leucine	132.1	86.1	20	380	8	5	Positive
		30.3	20	380	18	5	Positive
Threonine	120.2	74.1	20	380	8	5	Positive
		55.9	20	380	18	5	Positive
Valine	118.1	72	20	380	9	5	Positive
		55.1	20	380	23	5	Positive
Proline	116	70	20	380	15	5	Positive
		43.3	20	380	35	5	Positive
Serine	106.1	60.2	20	380	12	5	Positive
		42.2	20	380	11	5	Positive
Alanine	90	44.1	20	380	12	5	Positive
Glycine	76.1	30.3	20	380	32	5	Positive
		28.3	20	380	32	5	Positive

Supplementary Table 4: Mass Spectrometry parameters for energy metabolites.

Name	Precursor Ion	Product Ion	Collision energy [V]	Fragmentor Voltage [V]	Cell Accelerator Voltage [V]	Dwell time [msec]	Polarity
NAD	664.1	524	18	380	5	50	Positive
		428	26	380	5	50	Positive
NADH	666.1	649	17	380	5	50	Positive
		514	23	380	5	50	Positive
NADP	744.1	604	20	380	5	50	Positive
		508	32	380	5	50	Positive
NADPH	746.1	729	17	380	5	50	Positive
		135.8	40	380	5	50	Positive
AMP	346	96	24	380	5	50	Negative
		78.9	30	380	5	50	Negative
ADP	425.9	327.8	17	380	5	50	Negative
		133.9	22	380	5	50	Negative
ATP	505.9	407.9	21	380	5	50	Negative
		158.8	28	380	5	50	Negative

Supplementary Table 5: Sequences of all the parts of interest.

MoClo part	Part type	Sequence
pME_Cp_0_1_001_psbH_5'Homology_Cr	5' Homology	GAATTGTCAATTTTAAATGTACACTTAGTTGAAAGTGCC CCTGTCCCCTTGGCCATATTTAACAGAAGTTATTTATAA CGCAGCTGTTTTTGGAGTCTATAAATTTATAACATCAG TACTATGGATTTCCTTTAGTTTTATGGCCTAGGACGT CCCCTCCCCTTCGATGCTGGAGGCATCCTTTTACGGGA CAATAAAATAAATTTGTTGCCTCGCTATCGGCTAACAA GTTCTTCGGAGTATATAAATATAGGATGTTAATACTG CTATAAACTTTAGTTGCCCAATATTTATATTAGGACGCC AGTGGCAGTGGTACCGCCACTGCCTGCTTCGCAGTATA TAAATATAGGCAGTTGGCAGGCAACTGCCACTGACGTC CTATTTTAATACTCCCAAGTTTACTTGCCTAGGCAGTTG GCAGGCAACAAATTTATTTATTGTCCACTAAAATTTATT TGCCCGAAGGGGACGTCCACTAAAATTTATTTACCCGA AGGGGACGTCCTAATATAAATATGGGGATGTCAATGCT CCGTTAGGAAGTAACTAACGTTTTTCAAATAAATTTTAT CCCGGAGGGAAGTAGGCAGTAGCCCGCCACTGTCATC CTTTAAGTGGATCTCTGTCAGGCAATTTGCTTACACCT TTAAATTAATAAATTTAAATTTAAAGAAAAGTGAGCTATT AACGCGTTTATCTTAACG

CCTCTGTTGGAGCTTCTCCCTTCCCTTACGGGACATC
CCCTTCCCTTACGGGATATTTATATACTCCGAAGGACG
TCCCTTCGGGCAAATAAATTTTAGTGGCAGTTGCAAA
GTATTAATATCGTATATAAATATCCTGCCAACTGCCTAG
GCAAGTAAACTTAGGGATTTAATGCTCCGTTAGGACG
TCCCTTCCCTTCGGGACGTCCCTTACGGGAATATA
ATATTAGTGACGTCCCTTCGGGCAAATGAATTTAG
TGGCAGTTGCCTGCCAACTGCCGATTTATATACTGC
GATAAACTTTAGTTGCCGAAGGGGTTTACATACAATT
TATTTATTGTACCACTGCCACTAATTTTATATTCCGTA
AGGGGACGTCCTCCTTCCCTTCGGGCAAGTAACTTA
GGAGTATGTAAACCTGCTAGCGCAGCAAATAAATTTTA
TTCTAAGTTTACTTGCCCGAAGGGGAAGGAGGAAGCA
GGCAGTTGCCTCCTTCCCTTCCCTTCGGGACGTCCCC
TTCGGGATTTTAAATGCTCCGTTAGGAGGCAAATAAATT
TAGTGGCAGTTGCCTGCCAACTGCCTCCTTCGGAGTA
TTAAATAGGACGTCCCTTACGGGAATATAAATATTA
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AAATAGGATGTAACTACTGCGGAGCAGGCAGTGCGG
TACCACTGCCACTGGCGTCCTCCTTCGGAGTATGTAAA
CATTCTATATTTATATACTGCGATAAACTTTAGTTGCC
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GCCACTAAAATTTATTTACCCGAAGGGGACGTCCTTCC
CCTTCCCTTCGGGACGTCACTGGCAGTTGCCTGCCAA
CTGCCTAATATAAATATTGGGCAAGTAACTTAGGAGT
ATATAAATATAGGATTTTAATACTCCGAAGGAGGCAGT
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AAACGGTGGTTATTCCAGGCCAACTTATGAAATGCAA
GTACCATCAGATATTGCTAGCATGGATACG

pME_Cp_0_1_005_rbcl_5'Homology_Cr	5' Homology	GTAAAAACACATAACTCCACGTAAGCGCATTTTCTTACA ATCAAAGAATGCCAATTGTTCTTTGCTTGTTGTAAGA AAAAGTAGGCTTTTTCTTTGAAAACATTTTCAGCATATTC AACAACTTTTATAGATTGGTTTAGCGGATGATGGGACT CGAACCCACAACCTCGAAGTTGGAAGGATCGCACTCTA CCGATTGAGTTACATCCGCTTTAGTATGTTACTATTTCT TTTATTATAACTTATAAAATATAATACATAAAGATAAAT TCTATAATAAAAAGCTAAGATTTTATTTTCTGGCAGAT CGTAATTTATAAAGACAGGCAAATTTAAACAAAAGATA ACTTTAGAACTTAATTTTAAAAATGTAAATGATGTTTA GGTATTTAACCTAAACACCATAAAAAATAAACGATGT TTATGCTATTCACATAAACATCATGAAAAATAAAATTA AAGTTTGTCAATAGTATCAAATTCGAATTTAATTTCTTT CCAACTTCACATGCAGCAGCAAGTTCTGGTGACCATT TACAAGCTGAACGAATTACGTCGCCACCTTCACGAGCA AGGTCACGACCTTCGTTACGAGCTTGAGTACAAGCTTC AAGAGCTACACGGTTAGCTGCAGCACCTGGAGCGTTA CCCCAAGGGTGACCTAGAGTACCACCACCGAACTGAA GACATGCGTCATCACCGAAGATTTCACTAAAGCTGGC ATGTGCCATACGTGAATACCACCTGAAGCAACTGGCAT AACACCTGGCATTGAACACCACTTTGAGTGAAGTAAA TACCACGGCTACGGTCTTTTTCAACGTAGTCATCACGCA TTAAGTCTACGAAACCTAGAGTAACCTCACGTTACCTT CTAGTTTACCTACAACAGTACCAGAGTGAAGGTGGTCA CCACCAGACATACGAAGAGCTTTAGCAAGAACACGGA AGTGAATACCGTGGTTACGTTGACGGTCAATAACCGCG TGCATAGCACGGTGGATGTGTAGAAGAAGACCGTTGT CACGACAGTAGATAGCTAATGAAGTGTTAGCTGTGAA ACCACCTGTTAAGTAGTCGTGCATAATAAGGTACAC CTAATTTCTTTAGCACATACTGCAGTTTCATCATTTCTTC ACAAGTACCAGCAGTAGCGTTTAAAGTAGTGACCTTTAA CTTCACCTGTTTCTGCTTGAGCTTTGTAAATAGCTTCAG CAACGAAAAGGAAACGGTCACGCCAACGCATGAATGG TTGTGAGTTTACGTTTTCGTCGCTTTAGTAAAGTCAAG ACCACCACGTAAACATTCATAAACTGCACGACCGTAGT TTTTAGCTGAAAGACCTAATTTAGGTTTGATTGTACAAC CTAAAAGACCACGACCATATTTGTTTAATTTGTCACGTT CTACCTGAATACCGTGTGGAGGACCTACGAATGTTTTA ACGTAAGCAGGTGGAATACGAAGGTCTTCAAGACGTA GAGCACGTAAAGCTTTGAAACCGAATACGTTACCTACA ATAGAAGTGAACATGTTAGTTACTGAACCTTCTTCGAA TAAGTCGATTGGGTAAGCTACGTAAGCAATGTATTGGT TGTCTTCACCGGAACTGGTTCGATATCGTAACAACGA CCTTTGTAACGGTCAAGACTTGTTAAACCGTCAGTCCAT ACTGTAGTCCATGTACCTGTTGAAGATTCAGCAGCTAC AGCAGCACCATTCCTTCAGGTGGAACACCTGGTTGTG GAGTCATACGGAATGCAGCTAAAATATCAGTATCTCTT ACTACGTAATCAGGTGTGTAGTATGTTAAACGGTAGTC TTTTACACCGGCTTTGAATCCAGCACCTGCTTTAGTTTC TGTTTGTGGAACCATTTATATAAATAAATGTAACCTCTT TTGACGATCCTAAAATAATCTGTCCGGAAATATAATTTA AAAATTGTTGAAAAATTTTAAATACATTTAAATATATTA TATATTTAGAAAATAAAAAATAATGTAACTAGCAAATT TATGTAATTGTCTTATCAGTCGAGCATAGAAAGGCCT TTAGGTATATGTCGGTCGTCTTACGCAGTTTACTTAC
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pME_Cp_0_1_007_petB_5'Homology_Cr

5' Homology

GATTGACGTTTTGCACTAGCGCCGCCAGATAAAATTTTCT
TTTTTTACTGTATCTTTTCCTTTTGTTTTGCGGTGCCAC
TTTTAAATAATCCACTTTTTCCATTTCTTTTTTCCAAC
TCTTTAGAACGATCTTCCATATGGATATTAATTAATAAA
CCACAAATTTGGTTACATAATTCATCATCTAAATATTGC
ATTAATAATACCATACGACGACGGAAAAATAAGTTATA
AATATCAGTCCACTGTGCAGGTAATCTTCACCCCAACA
ATAAATAATACGAGGTAATCCAATCGGCATAAATTACT
TTGTTAATAAAATGTTGTGTTTTATTAATACTAGTCTAA
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CTACGTTAACTTAAATGCCTTCGGCCGGATTGAAC
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CTAAATGTGTTAAATGCATACACAATTTTTGTGTTAGAC
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pME_Cp_0_1_010_psbD_5'Homology_Cr

5' Homology

GGTTTGGAAATAATAAAATCGAAAAAAGAATTCACTC
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pME_Cp_0_2_001_16s_Prom_Cr	Promoter	CAGGCAACAAATTTATTTATTGTCCCGTAAGGGGAAGG GGAAAAACAATTATTATTTACTGCGGAGCAGCTTGTTA TTAGAAATTTTTATTAAAAAAAATAAAAAATTTGACAA AAAAAATAAAAAAGTTAAATTA AAAACACTGGGAAT GTTCTAACAATCATAAAAAAATCAAAGGGTTTAAAT CCCGACAAAATTTAACTTTAAAGAGT
pME_Cp_0_2_003_psaA2_Prom_Cr	Promoter	TTTAAAATAAGTAAAAATAATTTGTAAACCAATAAAAA ATATATTTATGGTATAATATAAC
pME_Cp_0_2_025_psbA_Prom_Nt	Promoter	GATCTACATACACCTTGGTTGACACGAGTATATAAGTC ATGTTTACTGTTG
pME_Cp_0_2_035_rrn16_short_Prom_Nt	Promoter	ATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAG GGGGCAGGGATGGCTATATTTCTGGGA
pME_Cp_0_2_036_rrn16_long_Prom_Nt	Promoter	GCTCCCCGCCGTCGTTCAATGAGAATGGATAAGAGGC TCGTGGGATTGACGTGAGGGGGCAGGGATGGCTATAT TTCTGGGAGCGAACTCCGGGCGAATACGAAGCGCTTG GATACAGTTGTAGGGAGGGATTT
pME_Cp_0_2_057_Synthetic_promoter_01	Promoter	CGAAATATAATTTGACATAAAAACTATATAATTTTAAAT TAAATAC

pME_Cp_0_2_058_Synthetic_promoter_02	Promoter	AATAATTTGATTTGACAAAAATAAGTTACAAGTTAAAT TAAATC
pME_Cp_0_2_059_Synthetic_promoter_03	Promoter	TATATTGAATTTTGACATAAATAAGTTATAACAATAAAT TAATAAC
pME_Cp_0_2_060_Synthetic_promoter_04	Promoter	ATGATTACTATTTGACATTTATAAATTTATATTTAAAT AGAAAC
pME_Cp_0_2_061_Synthetic_promoter_05	Promoter	ATAAACATATTTTGACATAAATAATATAATATCTAAAT TACTAAT
pME_Cp_0_2_062_Synthetic_promoter_06	Promoter	CAAGCAATCAATTGACATTATAAATTATATAAATTAAT TAAAAAC
pME_Cp_0_2_063_Synthetic_promoter_07	Promoter	CAGATAATAATTTGACAATTTAAAAAATATATATAAAT TCTAATC
pME_Cp_0_2_064_Synthetic_promoter_08	Promoter	TCATAAAAGTTTGGACAAAATTGTATTATAAATTTAAAT TAATTAG
pME_Cp_0_2_065_Synthetic_promoter_09	Promoter	ATAATATATATTTGACATACATTTATTTTTAAGCTAAAT AACATT
pME_Cp_0_2_066_Synthetic_promoter_10	Promoter	AATTAATAAATTTGACATTATATTTTACATCTATTAAAT CAGTAC
pME_Cp_0_2_067_Synthetic_promoter_11	Promoter	AAAAATAAAATTTGACAAAAAATAATTTTACATAAA TTAAAAAC
pME_Cp_0_2_068_Synthetic_promoter_12	Promoter	AAAAATAAAATTTGACATTATTATTTTAAAAAGTTAAAT TAAAAAC
pME_Cp_0_2_069_Synthetic_promoter_13	Promoter	AAAAATAAAATTTGACAATTTATTAATTTACTTAAAT TAAAAAC
pME_Cp_0_2_070_Synthetic_promoter_14	Promoter	AAAAATAAAATTTGACAAAAAATAAAAAAGTTAAAT TTTTCAAT
pME_Cp_0_2_071_Synthetic_promoter_15	Promoter	TATTATTGACAAAAAATAAAAAAGTTAAATTTAAAT AC
pME_Cp_0_2_072_Synthetic_promoter_16	Promoter	AATGGCAATTTGACAACAAGCAAGTAAAGGGTTAAAT AAGAAC
pME_Cp_0_2_073_Synthetic_promoter_17	Promoter	AAAAATAAAATTTGACAAAAAATAATTTATGGTAAAT TTAAAAAC
pME_Cp_0_2_074_Synthetic_promoter_18	Promoter	AAAAATAAAATTTGACAACCAATAAAAAATATATTTAT GGTAAATTTAAAAAC
pME_Cp_0_2_075_Synthetic_promoter_19	Promoter	AAAATGTGGGATTGACAAAAAATAAAAAAGTTAAAT TTAAAAAC
pME_Cp_0_2_076_Synthetic_promoter_20	Promoter	AAAAATAAAATTTGACAAAAAATAAAAAAGTTATAAT ATAAAAAAC
pME_Cp_0_2_077_Synthetic_promoter_21	Promoter	ATTTTTATTGACATTTTTTTTATTTTTCATAAATTTTTT G
pME_Cp_0_2_078_Synthetic_promoter_22	Promoter	TTCAGGTTTTATTGACAAAAAATAAAAAAGTTAAAT TTATTCTC
pME_Cp_0_2_079_rbcL_promoter_Cr	Promoter	ACAAGTACATAAATTTGCTAGTTTACATTATTTTTATT CTAAATATATAATATATT
pME_Cp_0_2_080_tRNA_Glu2_promoter_Cr	Promoter	CAACTAAGTGACATTAAAAATTGACAATTCAATTTTT TTAATTATAATATATAT
pME_Cp_0_2_081_Wendyll_promoter_Cr	Promoter	AATATATTTATTTGACATAAATATATTTATGTGATATAA TATATT
pME_Cp_0_2_082_pDummy_Cr	Promoter	CCCCTGGCGCCCTT

pME_Cp_0_2_083_Promoter_Placeholder_Cr	Promoter	GAAAGTGAAACGTGATTTTCATGCGTCATTTTGAACATT TTGTAAATCTTATTTAATAATGTGTGCGGCAATTCACAT TTAATTTATGAATGTTTTCTTAACATCGCGGCAACTCAA GAAACGGCAGGTTTCGGATCTTAGCTACTAGAGAAAGA GGAGAAATACTAGATGCGTAAAGGCGAAGAGCTGTTT ACTGGTGTGTCCTTATTTCTGGTGGAAGCTGGATGGTGA TGTCACCGGTCATAAGTTTTCCGTGCGTGCGGAGGGTG AAGGTGACGCACTAATGGTAACTGACGCTGAAGTT CATCTGTACTACTGGTAACTGCCGTTCTTGGCCGA CTCTGGTAACGACGCTGACTTATGGTGTTTCACTGCTTT GCTCGTTATCCGGACCATATGAAGCAGCATGACTTCTT CAAGTCCGCCATGCCGGAAGGCTATGTGCAGGAACGC ACGATTTCTTTAAGGATGACGGCACGTACAAAACGCG TGCGGAAGTGAAATTTGAAGGCGATACCCTGGTAAAC CGCATTGAGCTGAAAGGCATTGACTTTAAAGAGGACG GCAATATCCTGGGCCATAAGCTGGAATACAATTTTAAC AGCCACAATGTTTACATCACCGCCGATAAACAAAAA TGGCATTAAAGCGAATTTTAAATTCGCCACAACGTGG AGGATGGCAGCGTGCAGCTGGCTGATCACTACCAGCA AAACACTCCAATCGGTGATGGTCTGTTCTGCTGCCAG ACAATCACTATCTGAGCACGCAAAGCGTTCTGTCTAAA GATCCGAACGAGAAACGCGATCATATGGTTCTGCTGG AGTTCGTAACCGCAGCGGGCATCACGCATGGTATGGA TGAAGTGTACAAATGACCAGGCATCAAATAAACGAAA GGCTCAGTCGAAAGACTGGGCCTTCGTTTTATCTGTT GTTTGTGGTGAACGCTCTCTACTAGAGTCACACTGGC TCACCTTCGGGTGGGCCTTTCTGCGTTTATA
pME_Cp_0_3_001_atpA_5'UTR_Cr	5'UTR	TTTACCTTTTTTTAATTTGCATGATTTTAATGCTTATGC TATCTTTTTTATTTAGTCCATAAAACCTTTAAAGGACCTT TTCTTATGGGATATTTATTTTCTAACAAAGCAATCG GCGTCATAAACTTTAGTTGCTTACGACGCCTGTGGACG TCCCCCCTTCCCCTTACGGGCAAGTAACTTAGGGATT TTAATGCAATAAAATAAATTTGTCCTCTTCGGGCAAATGA ATTTTAGTATTTAAATATGACAAGGGTGAACCATTACTT TTGTTAACAAGTGATCTTACCACTCACTATTTTTGTTGA ATTTTAACTTATTTAAATTTCTCGAGAAAGATTTTAA AATAAACTTTTTAATCTTTATTTATTTTTCTTTTTT
pME_Cp_0_3_002_atpA_5'UTR_Cr	5'UTR	ACTATATAAATACATTTACCTTTTTATAAATACATTTACC TTTTTTTTAATTTGCATGATTTTAATGCTTATGCTATCTT TTTTATTTAGTCCATAAAACCTTTAAAGGACCTTTTCTTA TGGGATATTTATTTTCTAACAAAGCAATCGGCGTCA TAACTTTAGTTGCTTACGACGCCTGTGGACGTCCCCC CTTCCCCTTACGGGCAAGTAACTTAGGGATTTTAATG CAATAAATAAATTTGTCCTCTTCGGGCAAATGAATTTTA GTATTTAAATATGACAAGGGTGAACCATTACTTTTGTTA ACAAGTGATCTTACCACTCACTATTTTTGTTGAATTTTA AACTTATTTAAATTTCTCGAGAAAGATTTTAAAAATAAA CTTTTTAATCTTTATTTATTTTTCTTTTTT
pME_Cp_0_3_003_atpB_5'UTR_Cr	5'UTR	ATATATATAGTTAAATGAAAAAATAAAAAATAAGCGT TAGTGAATAATACTTTTTATATATAAATTTCTACTATATGT TTGAGCTTCCTTTTATATAAATTTTAAATTTATAACAAGT TACACTCTCAGTTAAAGGTGCCTTTTGAAAGTAAAGC CACAATGTTTACATACTAGGCAGTGGCGATACCACTGC CACTGGCGTCCTCCTTCGGAGTATGTAACATGCTAAG TTTACTTGCCCGAAGGGGAAGGAGGAGGTTCTTATTTT AAATTACCTAAGATAAAGTTTCCTTCGGGGTTTATACGT AAGAATTTAAGTAAAAATAAGTTAAAAATATGA

pME_Cp_0_3_004_chlL_5'UTR_Cr	5'UTR	ATATATAAAATAAAAAAACGTTAGTAATTCAAAAGTT TTAATATTATACAATTGAACTATTATGTATTAATATAA GAATGTCACCTCTTACCATAATTTCTATACTCCAAAGTAA CTTTTACATAAAATGTCCCCTCTGGGGCTGCCTCCTTCC CCTTCCCCTTCGGGTATATAAATATAGGGCAAGTAAAC TTAGCATAAACTTTAGTTGCCGAAGGGGTTTACATAC TCCGAAGGAGGACAAAATTTATTTATTGTGGTACAATAA ATAAATTGTATGTAAACCCCTTTCGGGTAAGTAAAGTTT ATCACGGCAATAAGTTTCTGCTTACGCAGTATTATATCT GACGCAGTATTATATAAGAAGTTGGCAGGATAAAAAAT GTGTAAGTATGGCAATCTTTTAAATAGTGTTCAATTCA TTTAAGGCAGATAAAAAAGAAAAAGTCCACAGGATTTA ATTTTGAATAGTTCTCTATCAAAAAAGGTTGCCGAAC A
pME_Cp_0_3_005_petB_5'UTR_Cr	5'UTR	ATAACTTTAATTTAACTTTAAATAATTAAGCTACACAT TTTTTTAGTCTTAAGAAAGCCTAATGGTCATGTCACAAT CTTATAAAAAATTTAT
pME_Cp_0_3_006_psaA_5'UTR_Cr	5'UTR	ATATGATGTAAAAAACTATTTGTCTAATTTAATAACC ATGCATTTTTTATGAACACATAATAATTAAGCGTTGC TAATGGTGTAATAATGTATTTATTAATTAATAATTG TTATTATAAGGAGAAATCC
pME_Cp_0_3_007_psbA_5'UTR_Cr	5'UTR	ACCATGCTTTTAATAGAAGCTTGAATTTATAAAATAAAA TATTTTACAATATTTTACGGAGAAATTAACCTTTAA AAAAATTAACAT
pME_Cp_0_3_008_psbE_5'UTR_Cr	5'UTR	ATAATACATTGATTATAAAGCAGACAAATTGTTGAAAA AGCTAAGTAAGCACACTTAGGAGGTATTTTTT
pME_Cp_0_3_009_psbF_5'UTR_Cr	5'UTR	ATTATATTTATTTTAACTAATATTTACATAAATTTTAA CGAGTTAGCTTAATACAAAAGGTAAATTACCCTATTT ATTTTTATTAATT
pME_Cp_0_3_010_psbK_5'UTR_Cr	5'UTR	TTTGATTTTAGAAAGAAAAACGAGCTTTAAGGTGAGC TTATTTTGTTCGTGTAAATTTTTAAATCTAAGGTGTA TAGACAAAAATCTACATTTTCATATGCTAAAAACATACT CTTTACGGGTACGCGAATGTTAGGTAAATTTTACAAC TAACTCTATGGTTGTGGGAAGAAAACCAATACATAGA GATATTTTAAAAAGATATCTCTCACTTTAATAGATTTT ATTATAAATACTATCAACAATTTCTTAACTTTTTAATGA AGGATATTT
pME_Cp_0_3_011_petA_5'UTR_Cr	5'UTR	GAGAAGAAAAAAATAAAATTTAAATAGTAATTATGAA TGTAATTACTTATGCTTACTTTTTAGCTAGATAAAAC TTGTTGAGGCTGCTTAGTTGCACCTTCTCGTACCCGTA TGGGTAGGGGTTTATCCACGAAAAATTTCTATTTTAA ATAGGAGTCCAGTTGAAAAGCACTGGAATCCCCTTAT AGATAAATTAATATCTATTTTAAATTTGAATAGTTTTTA TTCTAGTTTCGTTTTAAGATTAATAAAATT
pME_Cp_0_3_012_petD_5'UTR_Cr	5'UTR	AAAAATTTTATAGCATGTAAACATTAGAAATACAGCATA ATTGGAGTAAAAGAAAAATTTAAACTTTTACATTGAA AAGTTTATGGCGTTTTGGCTTTATAAAATAAAAACTTT TCGGAACGGCTAAACCATATTTATTATCATTAAAAATTTA TTTGCCCGAAGGGGACGTATCCGAAATAGAACAAATG CCAAAATCTACTAAATTAGATTAAAAATAGTTTTAAAAAT GGATAGATTTAAATAAAAAACAGAAGTAAATGTAATT CTGTCCCTTTTACAGGGTGGTATCTCTAAAAACCAGG GCTTGCCCAATCAACAATTTAAAGCTTATTTAGTTTTAT TGAAAATTAACGGATAAATAAAT

pME_Cp_0_3_013_psaB_5'UTR_Cr	5'UTR	CAATGTTACTCGTGGATGGCTTTGGTATTTAGGCGTA GCATGCAGTAAATATATGGCCAATGGCTCCTCTTTAG CAAGTTCTCAACTTAAATGCAATCTCTAACGAGAATC TAAAGCTCAGAAATATATTTGAATTTAAATTTCCACAG GATTATGGCGTAGTCATAATCAACTAAAAATCTTTT TAAATTTTAAATTTACTTTTTACGCTTTTGTATGCAAA GTTTGCTTGCACCTGAATAGTTTTATTAATTTTATTT AATGGTAGTTTAAAGTAGTAATTTACTTCAATTAACA AAAAAATCCTAATTGTTTATCCCTTTAAAGAGCGCTT AAAGTTTTTTTACTTAGTGAAGTAAAAATACCGCTCCCT TCTGGTATTTTTCTTTGATTTAACAATTAGCATTTTAA CCTTTACTTTTCTCTCAGTGTTATACTGCTTAAAGTTT TTAGGTCATTAGATAATTTAATAATATTACATATAGG GAGTAAGACAATTTT
pME_Cp_0_3_014_psbB_5'UTR_Cr	5'UTR	AATTTAATTTAAATCTTAAAAATTTTTTTTAAACATAGT TAATTAATTTTTTAAAGATTTTAAATTAATGTAGAAATT AATTTCTTTTATTTTATAACCTTGTAATAATTAAGTAA AAAAATCAGTAAAAATTTTTT
pME_Cp_0_3_015_psbC_5'UTR_Cr	5'UTR	TATTTAAGTGTTACAAAGAAATTGAATTTAATCTCAAA ATACATTTTTGAAATTTTTTATATTATTTTAGTATCT AAAAAAAAGCATTTGCTATTAGTAGGACAGTTGTCATG TTAATGGAGCTTACTTTACCTTAGTATATAAGGTAATTT AAATATAAAAAGATTTAAATTTATGTTTTAATTAACAA TTAAAAACGATTAAGTTGTTTAAATCACTTTATTTAA TAAATATGATCTAAATTATTTTAAATTTACTTTCCAAT GCAATTTTAGCACAAATAAATTAGATCATATTTAAAT ACAAGTTATAAAATTTCTATTCTTAAAAACAACATTATTT TACTCTGTGTTTTAAAAATGTTGGAGATAAGCTTTTGT CCTTAATTTCTTTGGATTAATATGGTACAAGAGGATTTT TGTTGTTAAAGGTTTACCATATTTATTTATATGGG TGGACGTTAAAAATTTAAATTTTATTTAAGCAAACT TTATAGAAATCAAATAATTTGTACGGAGGTAATGCAA A
pME_Cp_0_3_016_gene10_5'UTR_T7	5'UTR	AGACCACAACGGTTTCCCTCTAGAAATAATTTGTTTAA CTTTAAGAAGGAGATATACAT
pME_Cp_0_3_017_ccsA_5'UTR_Cr	5'UTR	TTAAGAATTGGTAGTTTTTGAACATAACAGTGACATAA AACTGGTAAAAGACATCCCTGTAAGAGAAATGCATAT GGTGAATTACACAATAAATTTTAAAAATAAAGCTCTGA CAAGCCTCTCCCTTTGCGATATACATGCTCTGTTAGG ATATAATTCTGCCTAAGTTCCTAACAAAGGGTTTACTTT TTCTCGGGGAATGGTTTGTACTTTGTTTTAAATCTTTT TCAAAGAATGTCAATCTCCTATAAAGGGAGGAACATTA CTCATGG
pME_Cp_0_3_018_psaC_5'UTR_Cr	5'UTR	TGGACAAAAGCAGTCATTCAAATATAGGTATGAGGA GAGAAATATATGCGCCGCAAGGCGCACTGCCACTGCTT AATATAAATACCTTGTTTAAAGTCGATTCTCAATCTTCTT TTTGATATGGAGATGACATATTTAGCACACGCAAAAA TATAGCATCTTTAAAAATTAACTTAAATTTAAAT
pME_Cp_0_3_019_rbcL_5'UTR_Cr	5'UTR	AAATGTATTTAAATTTTTCAACAATTTTAAATTATATT TCCGGACAGATTATTTTAGGATCGTCAAAGAAGTTAC ATTTATTTATATAA
pME_Cp_0_3_020_rpoC1_5'UTR_Cr	5'UTR	ATAGTGATGTAATTGCGGATGTATAAATTTCACTAAAA TGTTATATCAACCTTAAAGGGCCCCGAAATGGTTCATT ATACCCGAAGCGAATTGTAGTTACTACCTGCTACCTCT TCAGGTATATGTACCAACTGGCGTCCCTTACAGGTAC ACAGTAAGTAATAAGTTACTACTTCTCGAGACAGAAC CAATGTCCCCCTTCGGGCTGGCACGGCCATGTTATTTAT ATATCCAAATGAGGTAGCCTTGTTAGCTATACATAAAA TATGGTTTTTCTGGTTAAAAATCTTAAGCTTAATAAA GCTTTATATGTTAGTTCGACTTTGTAGCCCCGCAGTCGT

		TTATGTGTGAGATCTAATGCTTTATCGGGATTAGTTTCA AAGGACTTTACCCACATAGAAGTACCATATAAAATTGC ATTTTATTAACATTAAGCTACAAGAAAATCCTTTTAAT ATTTATT
pME_Cp_0_3_021_rpoC2_5'UTR_Cr	5'UTR	TTAAAATTATATAAAAAGCTAGTTATCCTGCTACCTCTA CCTTACCGACTCCTAACAGAATATAAATATACTCCGACG ACGTTTAGTATTATACTTAGAGGCAGTTGAAATCTAGTT CCTCCGGGAGTGCTTGGAACCAATTTCAATCAAATTA ACCAAGATAAATATAAAAAATGATTTTAAACGTTTGA CTTTAATCTTCCATTCGTTAT
pME_Cp_0_3_023_tufA_5'UTR_Cr	5'UTR	AACAGAAGTACTGTAGTTTTTTAAATTATACCTAAACCT GAAAAATTGGATTATATAGCAATAACACTATTAAGAAC TATATATTAATAATGTCAATACTATCCCGTAGGGACTATG AACTAAACACCTATCCGAATGTTAATGCTTAGTGAG CAAAGTATGCAGTATTTATCTACAAAAAGGAGAAACT CTTACCTCTGGTTAGAGGTTTCTTTTAAATGTTTGAAG CATTAACAATCTAATTCAAAAGAAGTGACTAAATAAT AATTTATTAATAACACAT
pME_Cp_0_3_024_clpP_5'UTR_Cr	5'UTR	TTTAAGTTTAACGTAGAGCCAATATTTGTTTGAATTTAT CTATTTTTTAAACCATTTTGGTTTAAATTTTATTTGCT TCAAAGGAGCTGTAAACGGTACTTTAATTTTACAGT AGCACTCGCAGAGCTTATTTACGTGCAAATAAAGCTC TATCTACTAGGATATTAGACTAGTATTAATAAAACACA ACATTTTATTAACAAAGTAATTT
pME_Cp_0_3_025_rpl23_5'UTR_Cr	5'UTR	AGTTCCTTTTATTTTAAATAGAAAAAACTTATTA CGTCTTTTGGAGGATTACACATACTGTAAAAACGCCAA TTGTAGTCAAAATCTAGATTCTGGTTAGGCAATAGAGG ATATTTTCTTTCCCTGTGGAATCTATAACTATAGCTGCT ATACAGACCCGAAAGAAAGCAATATATACTGGTCAGG AACTAACTTCTCTGTTCTAAGAAGTTTACATACCACA AAAAACAACGGTATTACTTGGTTTAAAGTTGATTTTAA AATAAATGTTTGGTTGATATATAAAAAAAATTTCACTT TTCTT
pME_Cp_0_3_026_rpl16_5'UTR_Cr	5'UTR	GATTAACTAATTTTACCATAAGTATTCTGTTTTAATAA ATTTATGCCCATGAACGCTGCCAAAGGAGGCAGTGGCT CGCCACTGCCCCCTTACGGGTACATAAATGTCCTAACTT GATATTTATTTACCTGTAAGGGTTAGCCTATAGGCGAG GTAAATAAATTTAAGTCAGCCATAGCTATTCTAGAGTA TAACGTGTACGTATCCTTACGGGTACGTACACGTTATA CTCAGTTAGCAGGGACTTGTTAGCCTATAAGCGAGATA AGTACACTTGGCCAACGGTTTATATTAATATACTCCAGC AGAAGAACAATTAAGTAAATCTAAAAATATCTATCT TTTTGCTGAAGAATTGCGGAAAAATCGATAGTATTGTT CATTGTATAAAGTGTACGTACCCGTTAAGGGTACGTAC ACTTTAATGCAAGATAAACAAAAATCAATACATATTACT AGTTACTAGTATAAAGTACAATTGATTTCTGTGATTTG TAGCTTTTAAATTAATTTTAAATTAAGTGTACATAAA AATTTAAATTAATAAAAAAC

pME_Cp_0_3_027_rpoB1_5'UTR_Cr	5'UTR	TTTCACGCACAAGGTGGAAATTGATTGATTAGCTTTAA AATTCAAATTAATAAATGGCATAATGGAGAAAATACC TTTCTTTAAACTAACCTAACAAATTAGGTAATTGAACCA GGGTAAGCTTTTTTAGCTAAATCCCTTCAGAAGCTAAC ATGCTAACTTTCCATAAAATTACATAACTTTTTGCTGAT GGTTTGAGCTAATAGGGCCGTATTCAAGTATAATATTA TATTGCCATCGGCTTTTGGGTATAAAATATTACCTTATG CTACCATCCAGCCTTAAAGGGAAGTGATTTAGCTGCT TTATAGTATATAAATTTAAGTTAACTTACAAGTGAGTTA ACATAAGGCCAGTTGTTTAGCAAACTGCCTCCTTCGG AGTATTAATAAGGCAGTGGCAATACCACTGCCACTGG CGTCCTAAGTATATAAATATTAAGTGGCGTGCATGTGT CTTAGTTTCAAGAGTTTACATCCTCTTAAGTTTACTTG CCCGAAGGGGAAGAATGCAGGGTTAGACAAAGAAAC ATGACTCACTGTCTAT
pME_Cp_0_3_030_atpH_5'UTR_Cr	5'UTR	CAACCAAAGAATATAATATTCTTTGGTTGTTATCGATTT TATTGATTCATTTAGGAGGAAATA
pME_Cp_0_3_031_psbD_5'UTR_Cr	5'UTR	AATACACAATGATTAAAATTAATAATAATAAAATTTAAC GTAACGATGAGTTGTTTTTTATTTTGGAGATACACGCA
pME_Cp_0_3_032_rbcL_5'UTR_Nt	5'UTR	ATGTATTTGGCAAATCAAATACCATGGTCTAATAATCA AACATTCTGATTAGTTGATAATATTAGTATTAGTTGGAA ATTTTGTGAAAGATTCTGTGAAAAGTTTCATTAACACG GAATTCGTGTGCGAGTAGACCTTGTTGTTGTGAGAATTC TTAATTCATGAGTTGTAGGGAGGGATT
pME_Cp_0_3_033_Synthetic_5'UTR_Sy	5'UTR	AAATTCGATAGAGATGAAATTGGAGCTCTAGAGAATTC AGTTGTAGGGAGGGATCC
pME_Cp_0_3_039_atpH_5'UTR_Nt	5'UTR	GATATTGACTAGTGCTAGTTATATATGAAATGAACTAA AGATATATTTTACTACTCTAGGGGATTCTAATAGACTAG AAGTCCTTCCGGCCCTTGACTGTGAATTGAATGAA TAAACGGATGAAATCAAGAAATAATTCAACTAACAGTT CGAACCAAGAAATGGAAGAACGAAAGTCGTATGGGT CACAAAGACTCTGTGGCTAAAAAGTAAAAAGATATAT CGAAGTAGTTCTGATGATTCAATAATCTTATTACTTCAA TCCGAAGTTCTTAGTTACTTCGACTGGATGAGTCCTAGC GAGGGAATAATTAAGTCATAACTCATTGGTTGATTGTA TCATTAACCATTTCTTTTTTTGGTACGAGGAACTTATC
pME_Cp_0_3_061_gene103longer_5'UTR_T7	5'UTR	GGCAGACCACAACGGTTTCCCACTAGAAATAATTTTGT TTAACTTTAAGAAGGAGATATACAT
pME_Cp_0_3_064_psbA_5'UTR_Nt	5'UTR	AATAAAAAGCCTTCCATTTTCTATTTTGATTGTAGAAA ACTAGTGTGCTTGGGAGTCCCTGATGATTAAATAAACC AAGATTTTACC
pME_Cp_0_3_065_psbC_5'UTR_Nt	5'UTR	GTTATTTGTACCAGTAACCGGTTTATGGATGAGTGCTC TTGGAGTAGTCGGTCTAGCCCTGAACCTACGTGCCTAT GACTTCGTTTCTCAGGAAATTCGCGCAGCGGAAGATCC TGAATTTGAGACTTTCTACACCAAAAATATTCTCTTAA CGAAGGTATTCGCGCTTGGATGGCGGCTCAAGATCAG CCTCATGAAAACCTTATATCCCTGAGGAGGTTCTACCA C
pME_Cp_0_3_091_Synthetic_5'UTR_1	5'UTR	GTTATTATAAGGAGAAATCC
pME_Cp_0_3_091_Synthetic_5'UTR_2	5'UTR	ATATGATGTAGATTCATTTAGGAGGAAATA
pME_Cp_0_3_091_Synthetic_5'UTR_3	5'UTR	ATATGATGTAATCAAATAAAACGAAAGGCTCAGTCGAA AGACTGGGCCTTTCGTTTTATGATTCATTTAGGAGGAA ATA
pME_Cp_0_3_091_Synthetic_5'UTR_4	5'UTR	ATATGATGTAATCAAATAAAACGAAAGGCTCAGTCGAA AGACTGGGCCTTTCGTTTTATGTTATTATAAGGAGAAA TCC

pME_Cp_0_03_092_RBS_dummy	5'UTR	TGTCAGGATACCCGA
pME_Cp_0_3_093_RBS_Placeholder	5'UTR	GAAAGTGAAACGTGATTTTCATGCGTCATTTTGAACATT TTGTAAATCTTATTTAATAATGTGTGCGGCAATTCACAT TTAATTTATGAATGTTTTCTTAACATCGCGGCAACTCAA GAAACGGCAGGTTTCGGATCTTAGCTACTAGAGAAAGA GGAGAAATACTAGATGCGTAAAGGCGAAGAGCTGTTC ACTGGTGTGTCCTTATTCTGGTGGAAGTGGATGGTGA TGTCACGGTCATAAGTTTTCCGTGCGTGGCGAGGGTG AAGGTGACGCAACTAATGGTAAACTGACGCTGAAGTT CATCTGTAATACTGGTAAACTGCCGGTTCCTTGCCGA CTCTGGTAACGACGCTGACTTATGGTGTTCAAGTCTTT GCTCGTTATCCGGACCATATGAAGCAGCATGACTTCTT CAAGTCCGCCATGCCGGAAGGCTATGTGCAGGAACGC ACGATTTCTTTAAGGATGACGGCACGTACAAAACGCG TGCGGAAGTGAAATTTGAAGGCGATACCCTGGTAAAC CGCATTGAGCTGAAAGGCATTGACTTTAAAGAGGACG GCAATATCCTGGGCCATAAGCTGGAATACAATTTTAAC AGCCACAATGTTTACATCACCGCCGATAAACAAAAA TGGCATTAAAGCGAATTTTAAATTCGCCACAACGTGG AGGATGGCAGCGTGCAGCTGGCTGATCACTACCAGCA AAACACTCCAATCGGTGATGGTCTGTCTGCTGCCAG ACAATCACTATCTGAGCACGCAAAGCGTCTGTCTAA GATCCGAACGAGAAACGCGATCATATGGTCTGCTGG AGTTCGTAACCGCAGCGGGCATCACGCATGGTATGGA TGAAGTGTACAAATGACCAGGCATCAATAAACAGAAA GGCTCAGTCGAAAGACTGGGCCTTCGTTTTATCTGTT GTTTGTGCGTGAACGCTCTCTACTAGAGTCACACTGGC TCACCTTCGGGTGGGCCTTCTGCGTTTATA
pME_Cp_0_3IEE_001_atpE-ycf12_IEE_Cr	IEE	TTTCACTTATCAACAAATCCCTAATAAGAAAGTAGTAT ATGTTCTATTAGAGGGTTTGTAAAATTATCTAGAGCTA TTCAAGTCTGATAGAGTTGAACAGTATACTCTTTGGGT AAATACATAGATCTAACATTATTTAAAGTTTATGTTCTT GTTACTTTTTGATTTTGTATATAAAAAAATTTTTTCAT
pME_Cp_0_3IEE_003_chlL-rpl36_IEE_Cr	IEE	TAAGAATAAAGCAGCTTTAAATACTTTCCTGTTTATAAT TTAGGAAATTAATGGATATTTGTTGAAACTAATCCCC AGTTGGATACCCATTGGTAGTTAATTGCCACTGCCTGCT TCACCTTACAAAATGTATGGACACAAAACGGCTAATAA ATACAGACTCCCGGTGGCATTGTTGGCTGCTTCGCC TGAAAGGAGAAAGTGATTTCTTCTTATTAGCTAATCT ATTCTTTTCTGTTTGGTAAATAATAGCGTCTCATAT CCATATCTATAACAAAAAGTTAAATGTTTAAATTTTAA AGTCTTTTTTACATTAATAAACACTTTTAATTGATGGGA CATCTTTAGTTTTTAAATAAATAAAGATGCACCCTCAA ACTGTCAGTTCATTAACCCAAATTATTTAATTTGGATGC ATATAAGCGAATTGACTTCAAACTAATAAAATTTTT
pME_Cp_0_3IEE_004_petG-rps3_IEE_Cr	IEE	TATTTATAAACTAACTACCTCCAATGAAAGAGGTAGT TTATAACCCAATCAAAATGTTTTACCTTTTCTTCTCTAT GGACGGAATACAAATAACAATTGCATTGTTACTCTCGA CTGGTTTCTAGCTTTACTGTCAGGTGTTTATATTATGCT ACTGTACCTTTTCCCAAGCAAGAATATACTTAAGGTATA GAAATATAAACAAGCATCCCGAAGAAAAAAGGGGTTA TTTTCTATGTTTATTACATAAAGACATTTGATTGTTT AATCTATATAATTGAAAATAGCTTTATTTCTTTATTAAC GTATGGGAACCTTTTACTGTTTAGTTTGTGTTTGCCTATT TGTAAGGTCTATTTAAATATATCCTTTTGTGTTTGCCTG CAACTAAAAAGTTTACTTAGATACTTCGTAGCTCCATT TACTTGCCGGGGATTGTTAGCTCTTTTCAAAGAAATG ATTTTTCACGTTGGAAAAATCAACTTTGTATTTAGTACT CTACTAACAAATACTATTTAATTCCTAGTAATGGAGTAG TATTGGATGGTTAATTTCTATTTTAAACAGAGTAAGCAT TACTTACTTGAATTTTAAATTATAATTAATTTATTTATA

AACAGGTTCTAAAGAAGCTATAACACACATTGTATTTT
 ATTTTTTTTAACGTTGTACAAATGTTTAGAATAAAAAATA
 CGTGTTTTGCACCTTGAAATGGCTCCAGTTTTCTAAACT
 AATGTTTTCAAAGGAGATGTGTTCAACATCAATTAGCTT
 ACTTTAATTTTCAATTTAAAAAATTTGT

pME_Cp_0_3IEE_005_psaC-petL_IEE_Cr	IEE	TTTTTAAATTCACCTTGGCGTTTAAAAAACCTTTAAAAAA GGGAGTATCTTGGTGAGATCCTCCATAAATTTTAAATT AGGTAGCCTCTTCTTTGGGTACATTTATTAATATAAAT GTGCCCAAAGTTCTTAACAAGAAAATATAAATCCCAT AAACTTTTGGCTTATTTAATTGGAACGTTTACTTTTAAA AACTATATAAAAAATTAACAACCTTACAAAGTTGGTTTA AAGTATCTATTTAATGTTTTTCAATCATTTTAATAAATA ATGACATGCACAAGAACCTTATTAGTTTTAAATCGCAT GTTAGCTTTAAAAGCTAATTTGTTTGCACTCTGTGAA ATCTTATTTGAATGTGTCAGGGGTAAACAAGACTCTTCC AGCCAAAGGCAGTGCCGGGTGTAACAAACGGCTTTATTC TATCCCATTTAGGATGCCAATGACAGTTAGAAAGCCTT GATATTCTTAAAGCAGTCAAGCATCACTATTAAATTGTT CACAGTCCGCATATTTTATTTGATCTTTTGAGAAGATA AAAATTACCTTCCGCTTTTGCAAAAAATTTAGCCGAAGA GTTTGATTTAACTAATTCAGTTAAAAATGATTTTTGAT TTTAATTATATCCATATTTTT
pME_Cp_0_3IEE_007_psbB-psbT_IEE_Cr	IEE	GTTTTCTTTTCTGGCAGTTGGCAGAGAATGTGTTTGTC TCCTTACCGAGTATAAAACCACTCTGCAAGTACAACCTG CCACTGTGGTCGCCTTACGTGGTTTAGTTACACGTAAG GCGACGTCCTTTAGGTATTTAAAAGTTTTACTTACAGAA CTTATTTATACATGGAGGGCTCCACAGCAGCAAAGTTG TATAAGTTTAAAAAAGCACTCTCTTTTGGGACTGCTTA GCAAATTACCTAATTTTACTTTTAAACCTTTAACACTTT ACTATGATTCTTTTATAGCCATACACTTGAAATTCCTCA AGTATTTTAAAACATTTTAAAAATGTTTAGTGCAATG TTCATTTTAAGGTAATTTCAATAGATACTTTTGCTTTGTA GCTAAAGTATGCATTTATAATTAACCTAATTCAAAAAA ATCAAAATACATTTTACTTTTT
pME_Cp_0_3IEE_008_psbE-rps9_IEE_Cr	IEE	TTAATCTAAAAACTTTTTTACTTAGAAAAATTTTTCTAA GTAAAAAAAGTACCTTTTCAAACCATCTATATAATCTT GGCAAAGGCATTTAATTTGGGTCTACCACACATAATGA TTAAAAAAAACGTAAATCCTAAAGAAAAAGTCCATTGA TGTCAGTTAGCATAACTCACGTACAAGAAATAATAATA TGATAGTAATATAAGATATATATAGGAGTTTCATAAA GATAAAGAAAGCTTTTATAGTATTTTAAAAAATATTG TTCATAAATAAACATGAGCAACTGGCACTAGTCTAGAT GACTAATAGGGTAAAAGATTAGTTCTAATCATTGTGCT TTTAGCGCACTTTCTAGACTTTGTGATATGGTAGGTTTT ACAATGAATATCGTCCATTTTCTCTTAACAGAATCATA AATCTCAACAGGAACTAAATCCCTTGTTGTTATTTGC AAAATATTTTTTATAGTTTATTTTGATTGCTTGAGTTT AATTTCAATTTAAATGGTAACATTTATATTTTGAAAGA CGATTTTGTATAATTTAACGCATGTGCGAATTAATAATT TGTGACAAGCATTTTCCGATATGTACAATACATTTGAA ACTCTATTAAAAATTTATTGGCCGAAATCAGTCATATAA CCTAAAAAATAGGTTACTTACCAGAAGGAGAGCATAAA

		AAATTTTATATGGGAAGTGTAAATATGGCTTTAGCAAAA GATGAAAAAATCTCTCATTGTTTTTCAGTTGCTTTTAG GTATTATGTTGTATTTTAAAGGGGTGTCGGATGTCCTT TAAAAAATATAGAAATAAGCAAATTAATAATTTATTTT TGT
pME_Cp_0_3IEE_009_psbF-psbL_IEE_Cr	IEE	GTATTCGTCCCTAAAAGAACGTTAGTACGCTGTAGCGA AATCCTTTCTGGATATTTGTATATCCAAAGGGCGGCTG TGGCTGTAGATATTTACATACTCCATGCTTGCCTAGAT ATTTATATTAGGATTTTAATACTCCCATGCTTTGCATAG ATATTTATATTCCCGTAAGGGGATGCCGGAGGCATTGA AGGAGGCAGTTGGCAGGATATTTATATACTCCGAAGG GACTTCTTAGCCGATAGGCGAGGCAACTGCCTCCTTCG GAGTATATAAATATCCACTGGCATCCCGTAAGGGGATG CCGAAGGCAGGCTATATTAATATCAACTGACGTCCTAA TTTATGGACTTTTTTAGAACTGCCTGCAGCTTTTGGGCA AGAAAATTGATTACAATAGCCTAACCTTTGAGTCCATCC ACAGTAAGGATAGCTTAAATCCCTAAAGGGATCGTTA TTTTACCTAGAACACACTCAAAAGGAAAAGGATATTAT GACTTTAATAAATAACCAAAACGTTATTTTATAGTTAT AGACATTAGTTAATGAGTAAATAATTTATAGGCTATC TTTTTAATGTAAACTCATTAAATAAGTTAGACCG
pME_Cp_0_3IEE_010_psbJ-atpI_IEE_Cr	IEE	TCAAAATTAAATTTTTTGTTTAGGCAGTTGGCTATGCCT CAACTCACTTACGGGATTTACATACTCCGTAaaaaaaga TGTTAGTGGCAAGTTACTGCCTATTCGAAAAAATTTGA AGCCCTTATCAAGCTTCCACATAGCGTTTTAGATGGTTT GTTTTCCAACAATCCATCTTTTTATATTTGTTATGAAA ATAGCAGTTTATTTAGACTTTTGCATCAATCCATAGGAT TGTATATACCAGATTTTAAACAAATATGTTTTACAATTT TTTCTTGTAACATAACCTTACTTACGTGTCCTCCTTAGG GCTAACAAATAACAAAGCATACCTAATACGGTTAAAG CTTGGCAAACGTGAGGGCTGTAAACAGCATAAGTTAT CCAAAAAAGAGACACTCAAATATGGAGTTCCTAATACT GCTAAAGCTAGAATTGTTCTTGCTTGCAAATATACATCA TTTTTGGAATGCTATAATCTTACCACCTTTTTAAAGGA CTCACCTGTTTAATACTGTAATCGCTTTTAGGTAGAGAA CTATCTTTGTATTCACCATATTCTTCTGTCACATGCACAG CAATATAATACGTAAGTACAATTGTTAAAAAATAGA TAATAACTGGTCATTATTTATAGTGGTTATTATTAATA TATTAATATCTTTCAATAATTGGTAAGAATTTTATTAC ATTTT

pME_Cp_0_3IEE_013_rpl2-rps19_IEE_Cr	IEE	CTAATTAAAGATAGGTCAATTTAAACAAGTGGCCTCTT TTGGCTATTTATTTACCCCTTCCCCTTACGGGACAATA AATAAATTTGTTGGCAGGCAACTGCCTCCTCCCCTTCG GGCAAGTAAACTTAGAATAAAATTTATTTGCTGCGCTA GCAGGTTTACATACTCCTAAGTTTACTTGCCCGAAGGG GAAGGAGGACGTCCCCTTACGGGAATATAAATATTAGT GGCAGTGGTACAATAAATAAATAGTATATAAATATCGG CAGTTGGCAGGCAACTGCCACTGACGTCCACTAAAATT TATTCTTTCTCGGGGACAATAAATAAATTTGCTCCTGTAA AGGGACGTAAAATAGCAGTAAGCATAAGTATGGCCAC TTGCTTAAATTTTACAATATTAATAAATTTCTAGAAATA ATAAAGTTTTGGTTGATAAATTTTAACTGTTAATTGTTT GTTTAACTTTATAGATATCGGGACTTAGTAAGTCTAA AGTCGCTAAAAACAACCAAGTTTCAGATAAACATTTGTTT CAACTGATTGGTTGTTTTGTTTATCCTTAGAGTTTATA TATCTTAACTCTATATTGGGTAAACCACTATAATGGTCA TATGTTGGAAAAATCCAATAAATTTCAATTTAATGTGG AATTTAAAAAGCTCATATGTACTTAAATAGACAATTGT TAAACATGAATAGAAAATATTACCTACTTTATTTTTAT AAATACAGCTTTAGCCATTATTATAAATTCAAAAGTCA TTTTAAAAAATCAA
pME_Cp_0_3IEE_015_rpl23-rpl2_IEE_Cr	IEE	TGGCTGATTTAAAAATAGGCAGTGGCGGTACCACTGCCA CTGGCGTCTCTCAAGAACAAAGATATTTTTAA CTCTAAGTTTATTTGCCAAAGAGGCAGAGAAACATTG TACCAGAAATGACAGCTTTTGTAGTTTAGGGATATACA TAGCCAAAGCTCTAGGATCTATCCAAAAATCACTGTCA TGCCGCCCCTCAAGGGGAATCAGTAGACTTTACAGTGT ATCCCTTTACCGGTATAGTAATCTTTTGCTTATTTTAGAA GCAAGTATCATATAAATAAATTTGTAAATAAAAAATAT ACTTAATTTTTTAATAAAAAAGGGTTATTTTCTAATAAT AAATCTAGCTATTAAGTGGTAACCTATCTATCGGCTAA ACCCTTTAATATGCAAAGGCCCGTTTAAGGTGCCAATG CGTAGTTGAAAAACACCTTTCCCTTTTCCCTGCGGGAC GCCAGTAGATAAAATATCGGCAGTTGGCAGGCAACTGC CACTGACGTCCCGTAAGGGGAAAGGGACGTCTGCCA ACTGCTGAGGCAAATGAATTTTAGTGGAATGTTACCG CCACTGGCGTCCCGTAAGGGGAAAGGGAGGAGCTCGA ACGAGGTTGTTAGTGGTCCACTTTTAATTGTTTGACTC CTCATGAGAGCTGAAAGACAGGCTGTAAATTTTATTAG TACCTAATCTATAAATAGTAAACAACCTAAAAACATAA TT
pME_Cp_0_3IEE_018_rps14-rps7_IEE_Cr	IEE	TTTCGTTTTGATATCGTAACTTAGTTATATGCATATCTA TTAAGTAGCGATTTTCAAAGAGGCAGTTGGCAGGACG TCCCCTTACGGGAATATAAATATTAGTGGCAGTGGTAC CGCCACTGCCTATATTTATATACTCCGAAGGAACCTGTT AGCCGATAGGCGAGGCAACAAATTTATTTATTGTATAT AAATATCCAATAAAATTTATTTGCCCGAAGGGGACGTC CTATTAACCATCACATAACTAAAATTGCTTATTTGGTA TGAAAGTTTGCATCTATTTAACCATTTAGTAAAAATAA TGATGCTTTTTTAAATAAAA

pME_Cp_0_3IEE_019_rps18-rps2_IEE_Cr	IEE	CAAATCCAGTGTTATAAAAACTTGCTAAGTACTTAAAT CTCAGCGAAAAGCTAGATATCGATTTTCTACTAGTATTG TCTTAATAGAAAAAGTTATTAATAGAAAAGAAAAATA TAAAAATCAATAGTGGATTTTGAATAGAAATTGAATGC CTTACAACTTTTCTGCTTCAGACACATAATAAGTTAGA GATAACCCCTTTATGGCATAAAATGTCTTTGTTATGTGG CAGCCCCGAAAGGGAAGTCTACTAACTCGTTAAAGGCT GCGCTCCAGATTAATATTCTGCGAAGGATATCGCCTG ATAGGTAAATAAATTTTAACTGGCATCCCTTTACGGGA TAACATTTATTGGCTGCCTCGCTATCGGCTAACCACTT CGGGCAAGTCAACTTAGAATAACATTTATTTACTGCGC TAGCAGGTTTACATACTAGGCAGTGGTGGTACCACTGC CACTGGCGTCCTCCTCGGAGTATGTAAACATTCAATAT TTATATTAGGACGTCCCCTTCGGGTAAATAAATTTTAGT GGCAGTTGGCAAGATATTTATATACAATATTAATACTTC GCAACTGCCACTGACGTCCTTCCCCTTCGGGCAAGTAA ACTTAGAATAAAATTTATTTGCTGCGTTAGCAGGTTTAC ATACTCCTAAGTTTACTTGCCTCCTTCGGAGTATATAAA TATCCCGAAGGGGAAGGAGGACGTCCCCTTACGGGAA TATAAATATTAGTGGCAGTGGTACAATAAATAAATAGT ATATAAATATCCCGTAAGGGGAAGGGGACAAATTTATT TATTGTCCTAGGTACATAAATGTTTAAGCAGTTTAAAG GCCTGACGGGCTCAATTTCT
pME_Cp_0_3IEE_020_trnF-psaC_IEE_Cr	IEE	GCCGGGATAGCTCAGTTGGTAGAGCAAAGCATTGAAA ATGCTTGGGTACCGGTTCAAGTCCGGTTCCTGGCAAT TCCCTAATGGACCAAAAGCAGTCATTCAAATATAGGTA TGAGGAGAGAAAATATATGCGCCGCAAGGCGCACTGCC ACTGCTTAATATAAATACCTTGTTTAAAGTCGATTCTCA ATCTTCTTTTGATATGGAGATGACATTTTAGCACAAC GCAAAAATATAGCATCTTTAAAAATTAACCTAAAATTTA AAT
pME_Cp_0_3IEE_021_ycf3-rps18_IEE_Cr	IEE	AAAAGATGTTGACCCTTTTGACTTGAAGTTGCCAGATT GATTTTTACTCTTCTCTAAGCCATATTTAATACTTTGTA AGGAAAATATAAATACCTATTGATATAAATAAAAACAA ATTGCAGCCCTCAGTGGCAATTTATTTACCTAGGCCG CCAGCGGCAGTGGTACCACCACTGCCGCTGGTGTTCTT AAGAAGAAAAGGTTTAGATATTTTCTTTGGGGCTGTA CAACAGCAAGATTAATATGCTTTATGGAGAAGCTGTAT TCTCAATGGTCTAAGCTGCTTCAAATTTTATAAAAACT ACTTTAGTTACTAAGTAGTATTTTCGCAATTTATATTTAA ATTTTTATTTATTT
pME_Cp_0_3IEE_022_ycf4-ycf3_IEE_Cr	IEE	AATACTGATTTTAAAAATTTTATAGAGATTAAATAAAAA CAAAACGTCTAAACAGATGTTATTAAGCTGCACCTTTG GCGCAGCTTAAAAGGCACGTTGCCTAATATTACTACAG TACAAAAATGTAATTGTTATAGTTATAAGTACTTAGTTT CAATAAATCGCTGATTTTATTTTAA
pME_Cp_0_3IEE_023_IEE5_v2	IEE	GACTTGTA AAAAATATGACGCTCTTTTCTTTGGTTTATA GTATTTGGAAAAGCAAAATGTTTAGACATCTGGTTTAA AGACAGTATACTACTTGATTGCACCTTTGGCCGTATAGT AGATCATAGGTTAAAAGGCTATTTGTACATAAGTAGAC TTTTACATTTTAATTTTTTTGTAAGTTTGAATACATTTAG TTAATTAAGTTTATAGATTTTAAATTA AAAAGCTCCCTT GTATGAGGAAGTAGGTTGTCCACAGGGATTGCTTAA AATCTAACAAAAATACATTTCCGTTAAATTAAGATGGG TGTAGCATCTCGCTGCTATACTTCACCAAAAGATCTTAC TTCCACATACCCTGTTTGTGACCAAGTAAGTGTTTACTT TTAGATTTAACGTGTTTATAACATTTAAGTAATTAT

pME_Cp_0_3IEE_023_tscA-chlN_IEE_Cr	IEE	GACTTGTA AAAATATGACGCTCTTTTCTTTGGTTTATA GTATTGGAAAAAGCAAAATGTTTAGACATCTGGTTTAA AGACAGTATACTACTTGATTGCACCTTTGGCCGTATAGT AGATCATAGGTTAAAAGGCTATTTGTACATAAGTAGAC TTTTACATTTTAATTTTTTTGTAAGTTTGAATACATTTAG TTAATTAAGTTTGTAGTTTTTAAATTA AAAAGCTCCCTT GTATGAGGAAGTAGGTTGTCCACAGGGATTGCTTAA AATCTAACAAAAATACATTTCCGTTAAATTAAGATGGG TG TAGCATCTCGCTGCTATACTTCACCAAAAGATCTTAC TTCCACATACCCTGTTTGTGACCAAGTAAGTGTTTACTT TTAGATTTAACGTGTTTATAACATTTAAGTAATTAT
pME_Cp_0_3b_003_strep-tag	N-terminal Tag	ATGTGGAGCCACCCGAGTTCGAGAAGGGAATG
pME_Cp_0_3b_024_His-Tag	N-terminal Tag	CACCATCACCACCATCAT
pME_Cp_0_3b_025_Hibit-tag	N-terminal Tag	CCATGGTTTCTGGTTGGCGTTTATTTAAGAAAATTTCTG GAATG
pME_Cp_0_3b_026_flag-tag	N-terminal Tag	GATTATAAAGATGACGATGACAAAGGTGACTATAAGG ATGATGATGATAAAGGTGACTACAAAGACGACGATGA TAAA
pME_Cp_0_3b_027_HA-tag	N-terminal Tag	TATCCATATGATGTACCAGATTACGCAAAATACCCATAC GATGTTCTGATTATGCTGGTTATCCTTATGATGTTCCA GATTATGCT
pME_Cp_0_3b_028_myc-tag	N-terminal Tag	GAACAAAACTTATTTTCAGAGGAAGATTTAAACGGTGA GCAAAAATTAATTTCTGAGGAAGACTTAAATGGTGAAC AAAACTGATTTTCGGAGGAAGATCT
pME_Cp_0_4_001_Nanoluc	CDS	GTTTTCACTTTAGAAGACTTCGTAGGTGACTGGCGTCA AACAGCAGGTTATAATTTAGACCAAGTTTTAGAACAAG GTGGTGATCAAGTTTATTCCAAAATTTAGGTGTTTCTG TTACTCCAATTCAACGTATCGTATTAAGTGGTGA AAAAT GGTCTTAAAAATTGACATCCATGTTATTATTCCTTATGAA GGTCTTTCAGGTGACCAATGGGTCAAATTGAAAAAAT TTTTAAAGTAGTTATCCTGTAGATGACCATCACTTTAA AGTAATTTTACACTATGGTACTTTAGTAATTGATGGCGT TACACCTAATATGATTGACTACTTTGGTCGTCCTTATGA AGGTATTGCTGTTTTGATGGTAAAAAATCACAGTTA CAGGTACATTATGGAATGGTAATAAAATTATTGACGAA CGTTTAATCAATCCTGATGGTTCATTATTATCCGTGTT ACAATTAATGGTGTTACAGGTTGGCGTCTTTGTGAACG TATCCTTGCT
pME_Cp_0_4_005_aadA_with_stop_codon	CDS	GCAATGCGTACTCCAGAAGAACTTAGTAATCTTATTAA AGATTTAATTGAACAATACACTCCAGAAGTGAAAAATGT CCATGGCTCGTGAAGCGGTTATCGCCGAAGTATCGACT CAACTATCAGAGGTAGTTGGCGTCATCGAGCGCCATCT CGAACCGACGTTGCTGGCCGTACATTTGTACGGCTCCG CAGTGGATGGCGGCCTGAAGCCACACAGTGATATTGA TTTGCTGGTTACGGTGACCGTAAGGCTTGATGAAACAA CGCGGCGAGCTTTGATCAACGACCTTTTGAAACTTCG GCTTCCCCTGGAGAGAGCGAGATTCTCCGCGCTGTAGA AGTCACCATTGTTGTGCACGACGACATCATTCCGTGGC GTTATCCAGCTAAGCGCGAACTGCAATTTGGAGAATGG CAGCGCAATGACATTCTTGACGGTATCTTCGAGCCAGC CACGATCGACATTGATCTGGCTATCTTGCTGACAAAAG CAAGAGAACATAGCGTTGCCTTGGTAGGTCCAGCGGC GGAGGAACTCTTTGATCCGGTTCCTGAACAGGATCTAT TTGAGGCGCTAAATGAAACCTTAACGCTATGGAACCTCG CCGCCGACTGGGCTGGCGATGAGCGAAATGTAGTGC TTACGTTGTCCCGCATTTGGTACAGCGCAGTAACCGGC AAAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAA TGGAGCGCCTGCCGGCCAGTATCAGCCCGTCATACTT GAAGCTAGGCAGGCTTATCTTGGACAAGAAGATCGCTT

GGCCTCGCGCGCAGATCAGTTGGAAGAATTTGTTCACT
 ACGTGAAAGGCGAGATCACTAAGGTAGTTGGCAAATA
 A

pME_Cp_0_4_007_mScarlet-I	CDS	GTTTCAAAAGGTGAAGCAGTAATTAAGAATTTATGCG TTTCAAAGTTCATATGGAAGGTTCTATGAATGGTCACG AATTTGAAATTGAAGGTGAAGGTGAAGGTCGTCCATAT GAAGGTACACAACTGCTAAATTAAGAATAACAAAAG GTGGTCCATTACCTTTTAGTTGGGATATTTATCTCCAC AATTTATGTATGGTTCACGTGCATTTATTAACACCCAG CAGACATTCCAGATTACTATAACAATCATTCCCAGAA GGTTTCAAATGGGAACGTGTTATGAACTTGAAGATGG TGGTGCAGTTACTGTAACACAAGATACATCATTAGAAG ATGGTACTTTAATTTATAAAGTTAAATTACGTGGTACAA ATTTTCCACCTGATGGTCCTGTAATGCAAAAAAACA ATGGGTTGGGAAGCTTCAACTGAACGTTTATATCCTGA AGATGGTGTATTAAGAAGGTGATTAATAATGGCATTAC GTTTAAAGATGGTGGTCGTTATTTAGCTGACTTTAAA ACAACTTATAAAGCAAAAAACCTGTTCAAATGCCTGG TGCTTAAACGTTGATCGTAAATTAGACATTACTTCACA CAATGAAGATTATACAGTAGTTGAACAATATGAACGTA GTGAAGGTCGTCATTCTACAGGTGGTATGGATGAATTA TATAAA
pME_Cp_0_4_008_tdTomato	CDS	GTTTCAAAAGGTGAAGAAGTAATTAAGAATTCATGCG TTTTAAAGTACGTATGGAAGGTTCTATGAATGGTCATG AATTTGAAATTGAAGGTGAAGGTGAAGGTCGTCCATAT GAAGGTACACAAACAGCAAAATTAAGAATTACTAAAG GTGGTCCATTACCATTGCTTGGGATATTTAAGTCCAC AATTTATGTACGGTTCAAAAGCTTATGTAACATCCA GCAGACATTCCAGATTATAAAAAATTAAGTTTTCCAGA AGGTTTTAAATGGGAACGTGTAATGAATTCGAAGATG GTGGTTTAGTTACAGTTACTCAAGACTCAAGTTTACAA GATGGTACATTAATTTATAAAGTTAAATGCGTGGTAC TAATTTTCCACCTGATGGTCCAGTTATGCAAAAAA CTATGGGTTGGGAAGCAAGTACAGAACGTTTATATCCA CGTGATGGTGTTTTAAAGGTGAAATTCACCAAGCATT AAAATTAAGAAGATGGTGGTCACTATTTAGTTGAATTTA AAACAATTTATATGGCAAAAAACCTGTACAATTACCT GGTATTACTATGTTGATACTAAATTAGACATTACTTCT CACAATGAAGATTACACTATTGTAGAACAATATGAACG TAGTGAAGGTCGTACCATTTATTTTAGGTCACGGTAC TGGTTCTACAGGTTCAAGTTCATCTGGTACTGCTTCAA GTGAAGATAATAACATGGCAGTAATTAAGAATTTATG CGTTTTAAAGTACGTATGGAAGGTTCTATGAATGGTCA TGAATTCGAAATTGAAGGTGAAGGTGAAGGTCGTCCA TATGAAGGTACTCAAACTGCAAAATTAAGAATACTAA AGGTGGTCCATTACCTTTCGCATGGGATATTTATCACC ACAATTCATGTATGGTTCTAAAGCTTATGTTAAACATCC AGCTGATATTCCTGATTATAAAAAATTAAGTTTTCCAGA AGGTTTCAAATGGGAACGTGTAATGAATTTGAAGATG GTGGTTTAGTTACAGTAACCTCAAGATTCATCTTACAAG

ATGGTACTTTAATTTATAAAGTTAAAATGCGTGGTACA
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 TCAGAAGGTCGTACCATTTATTCTTATATGGTATGGAC
 GAATTATACAAA

pME_Cp_0_4_009_mVenus	CDS	GTTTCAAAAGGTGAAGAATTATTCACAGGTGTTGTACC AATTTTAGTTGAATTAGATGGTGATGTTAATGGTCACA AATTCTCAGTATCTGGTGAAGGTGAAGGTGATGCAACA TACGGTAAATTAACTTTAAATTAATTTGTACTACAGGT AAATTACCAGTTCCTTGGCCAACATTAGTTACTACATTA GGTACGGTTTACAATGTTTTGCACGTTACCCAGACCAT ATGAAACAACATGACTTTTTCAAAGTGCTATGCCAGA AGGTTATGTACAAGAACGTACTATTTTTTCAAAGACG ATGGTAATTATAAACACGTGCAGAAGTAAATTCGAA GGTGATACATTAGTTAATCGTATTGAATTAAGGTAT TGATTTTAAAGAAGATGGTAATTTTAGGTCACAAAT TAGAATATAATTACAACCTACATAATGTTTATATTACAG CAGATAAACAAAAAACGGTATTAAAGCTAATTTTAAA ATTCGTCACAATATTGAAGATGGTGGTGTTCATTAGC AGATCATTATCAACAAATACTCCAATTGGTGATGGTC CTGTATTATTACCTGATAACCATTACTTATCATACAAA GTAAATTATCAAAAGACCCTAATGAAAAACGTGATCAT ATGGTATTATTAGAATTTGTTACAGCAGCTGGTATTACA TTAGGTATGGATGAATTATATAAA
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pME_Cp_0_4_010_mCerulean3	CDS	ATGGTAAGTAAAGGTGAAGAATTATTTACTGGTGTAGT TCCAATTTTAGTTGAATTAGACGGTGACGTTAATGGTC ATAAATTTCTGTTTCAGGTGAAGGTGAAGGTGATGCT ACTTACGGTAAATTAACTTTAAATTTATTTGTACAAC GGTAATTAACAGTACCTTGGCCTACATTAGTAACCTAC ATTAACATGGGGTGTCAATGTTTTGCACGTTATCCAG ATCACATGAAACAACATGATTTCTTTAAATCAGCTATGC CAGAAGGTTATGTACAAGAAGTACAATTTCTTTAAA GATGACGGTAACTATAAACACGTGCAGAAGTTAAAT TGAAGGTGATACATTAGTTAATCGTATTGAATTAAGG GTATTGATTTCAAAGAAGATGGTAATTTTAGGTCAT AAATTAGAATACAATGCTATTAGTGATAATGTTTATATT ACTGCTGATAAACAAAAAACGGTATTAAAGCTAACT CAAAAATTCGTCACAATATTGAAGATGGTTCAGTTCAATT AGCTGATCATTATCAACAAAAACACCAATTGGTGATG GTCCAGTTTTATTACCTGATAATCACTACTTAAGTACAC AATCTAAATTATCTAAAGACCCAAATGAAAAACGTGAC
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CACATGGTTTTATTAGAATTTGTTACAGCAGCAGGTATT
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pME_Cp_0_4_022_aac6-aph2-Tobramycin-
marker CDS

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CAACTTCTTAAACACTAACTTAGAAACAAACGTTAAAAAT
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pME_Cp_0_4_023_ptxD-marker

CDS

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GCCAGATCGTGTTGATGCTGATTTCTTACAAGCTTGTC
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GCTGAATTAGCTATTGGTTTAGCTGTAGGTTTAGGTCG
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pME_Cp_0_4_026_Arg9-marker

CDS

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TAGTTGATGCAGCTCGTGATATGGGTGTTATGGCAATT
ACTGCAGGTAAAGGTGATGTTATCGTTTAGTTCACCT

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pME_Cp_0_4_033_Firefly-luciferase_v2.0

CDS

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 AAAAAAGGTGGTAAAATTGCTGTT

pME_Cp_0_4_035_aphA6-Kanamycin- marker	CDS	ATGACCATGGAATTACCAAATATTATTCAACAATTTATC GGAAACAGCGTTTTAGAGCCAAATAAAATTGGTCAGTC GCCATCGGATGTTTATTCTTTAATCGAAATAATGAAAC TTTTTTCTTAAGCGATCTAGCACTTTATATACAGAGAC AACATACAGTGTCTCTCGTGAAGCGAAAAATGTTGAGTT GGCTCTCTGAGAAATTAAAGGTGCCTGAACTCATCATG ACTTTTCAGGATGAGCAGTTTGAATTCATGATCACTAA AGCGATCAATGCAAAACCAATTCAGCGCTTTTTTTAAC AGACCAAGAATTGCTTGCTATCTATAAGGAGGCACTCA ATCTGTTAAATTCAATTGCTATTATTGATTGTCCATTAT TTCAAACATTGATCATCGGTTAAAAGAGTCAAAATTTT TATTGATAACCAACTCCTTGACGATATAGATCAAGATG ATTTTGACACTGAATTATGGGGTGACCATAAACTTAC CTAAGTCTATGGAATGAGTTAACCGAGACTCGTGTGGA AGAAAGATTGGTTTTTCTCATGGCGATATCACGGATA GTAATATTTTTATAGATAAATTCAATGAAATTTATTTTT AGATCTTGGTCGTGCTGGGTTAGCAGATGAATTTGTAG ATATATCCTTTGTTGAACGTTGCCTAAGAGAGGATGCA TCGGAGGAACTGCGAAAAATTTTTAAAGCATTTAA AAATGATAGACCTGACAAAAGGAATTATTTTTTAAAC TTGATGAATTGAAT
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pME_Cp_0_4_059__malate_synthase_Cm CDS

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pME_Cp_0_5_001_psbA_3'UTR_Cr

3'UTR

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pME_Cp_0_5_005_rrnB_3'UTR_Ec	3'UTR	GTAGAAACGCAAAAAGGCCATCCGTCAGGATGGCCTT CTGCTTAATTTGATGCCTGGCAGTTTATGGCGGGCGTC CTGCCCCGCCACCCTCCGGGCCGTTGCTTCGCAACGTTT AAATCCGCTCCCGGCGGATTTGTCTACTCAGGAGAGC GTTACCCGACAAACAACAGATAAAACGAAAGGCCAG TCTTCGACTGAGCCTTTCGTTTTATTGATG
pME_Cp_0_5_006_psbA_3'UTR_Nt	3'UTR	TCCTGGCCTAGTCTATAGGAGGTTTTGAAAAGAAAGGA GCAATAATCATTTTCTTGTCTATCAAGAGGGTGCTATT GCTCCTTCTTTTTT
pME_Cp_0_5_007_atpA_3'UTR_Cr	3'UTR	TTTTAATTAAGTAGGAACCTCGGTATATGCTCTTTGGG GTCTTATTAGCTAGTATTAGTTAACTAACAAAAGATCAA TATTTTAGTTTGTTTTATATATTTTATTACTTAAGTAGTA AGGATTTGCATTTAGCAATCTTAAACTTAAGTAATAA TCTATAAATAAAATATATTTTCGCTTTAAACTTATAAA AATTATTTGCTCGTTATAAGCCTAAAAAACGTAGGAT CTCTACGAGATATTACATTGTTTTTTCTTTAATTGGCTT TAATATTACTTTGTATATATAAACCAAAGTACTTGTTAA TAGTTATTAAATTATATTAACATACAGTACAAAGAAAT TTTTTGCTAAAAAAGTATGTTAACATTAATAATTTTG TTTATACAG
pME_Cp_0_5_009_rbcL_3'UTR+rbcL-CDS_Cr	3'UTR	GTAACAAGCTCGTAACGAAGGTCGTGACCTTGCTCGT GAAGGTGGCGACGTAATTCGTTTCAGCTTGTAATGATC TCCAGAACTTGCTGCTGCATGTGAAGTTTGAAAGAAA TTAAATTCGAATTTGATACTATTGACAACTTTAATTTTT ATTTTTCATGATGTTTATGTGAATAGCATAAACATCGTT TTTATTTTTATGGTGTTAGGTTAAATACCTAAACATCA TTTTACATTTTTAAAAATTAAGTTCTAAAGTTATCTTTGT TTAAATTTGCCTGTCTTTATAAATTACGATGTGCCAGAA AAATAAAATCTTAGCTTTTATTATAGAATTTATCTTTAT GTATTATATTTATAAGTTATAATAAAAGAAATAGTAAC ATACTAAAGCGGATGTA
pME_Cp_0_5_010_atpB_3'UTR_Cr	3'UTR	TTTAATTTTTTATGTGTAATTAATAAATATTTGGACA CCATTAAAGTTGTTTTCTTCTTAAAGAGCCAATTTATTTTA ATTACAC
pME_Cp_0_5_011_chlB_3'UTR_Cr	3'UTR	AAATAATCTAAATTTTCAGGATGAAATACTGCGCTAGC GGGCAGTCACAACTACTATCTTCGAACGCAG
pME_Cp_0_5_012_clpP_3'UTR_Cr	3'UTR	TAATATGGAATTCATCTTTTAGTTGTGTAGCTTGCTATAA GATATTACTCTAACTGGTCTATAGCTTGACCGCAGGTTA CATATATATTCGTTTTTATATTAAGGGATATCACTACAA G
pME_Cp_0_5_013_ftsH_3'UTR_Cr	3'UTR	TAATATTTAAACAGTATTAATAAAACATACGGCAGCTTC TAACTGCACCATGTGAATACTATTTCTTGTGCTAGTTAC TCTCACTCCGCTTCGTTATTGTGTAGCCCTGTAAGGAAC GTCCAACCTAACCATATCTATATCCCTAATAAATTATCTTC CCCGAGAAAAGAGTAAATTAGGGTCTGTAGATATAAG GGCTGCACGATAGCGTAAACAACACCAATAAAAGTAA GCCATTTTCATGGTTATACTGCTCATGGACAAAAAATT GAATAACTTGCAAATTATAATGACGAGGGTTAAGCAAT GGTACACTCATGGTGGCAAGTTCGATAAACTTTAGTTA CCC

pME_Cp_0_5_015_petA_3'UTR_Cr	3'UTR	TATTTAATTTTTGTAGGGCTGCTGTGCAGCTCCTACAA ATTTTAGTATGTTATTTTTAAAGTTTGATATACTGAAAA CAAAGTTCTACTTGAACGATATTTAGCTTTAATGCTAT AATATAGCGGACTAAGCCGTTGGCAATTTAGCTGCCAA TTAATTTTATTCGAAGGATGTAAACCTGCTAACGATATT TATATATAAGCATTTTAATACTCCGAGGGAGGCCTCTA ACCTTTAGCAAGTAAGTAACTTCCCCTTCGGGGCAGC AAGGCAGCAGATTTAAATTCTCCAAAGGAGGCAGTTG ATATCAGTAAACCCCTTCGATGACTCTGGCATTGATGC AAAGCATGGGGAACTAAAGTTCCTCCACTGCCTCCTT CCCCTTCCCTTCGGGACGTCCCCTTCCCCTACGGGCA AGTAACTTAGGGATTTAATGCAATAAATAAATTTGT CCCCTACGGGACGTCAGTGGCAGTTGCGAAGTATTAA TATTGTATATAAATATAGAATGTTTACATACTCCGAAGG AGGACGTCAGTGGCAGTGGTACCGCACTGCCTATTTT AATACTCCGAAGGAGGCAGTGGTGGTCCCCTGCCACT AAAATTTATTTGC
pME_Cp_0_5_017_petD_3'UTR_Cr	3'UTR	TCTAAAATTTTAAATTTCCCTCTAGGGTTGCAATACGAT TTGCAACCCTGAAGGGGGAAAACTGAGTTCTGTCATTT TTTTAAGAACTCCATCAATAAATTGTGTCTTAGCAGATA ATGCGGGTAAATAACACCCTTGTTATCCTACAAAATA GGAGATTCCATTTAATTTAAACCAAAACAATAACTTAGT TACAAC
pME_Cp_0_5_018_petL_3'UTR_Cr	3'UTR	TTTATTAATGAGTAAAACACGCTAATGGGTTTTTACTA CTACATTTTTTATATATAATTGTAAGAGCACAGCAACGT GCTCTTACATTTTCCGTTATTTAAGTACCTAACTAAAT CAAATAAATGCGTTAAGTTTGAGACTGCAAAGCTGCCA
pME_Cp_0_5_019_psaB_3'UTR_Cr	3'UTR	TGTAATGTACTTTATTTACTACCTCATCAGATCAGCATA TACGTGCGACCCGATGTGGTACTTTTAAATCGGTTAGA CATTTAGT
pME_Cp_0_5_020_psaC_3'UTR_Cr	3'UTR	TTTTTTAATTCACCTGGCGTTTAAAAACCTTTAAAAAA GGGAGTATCTTGGTGAGATCCTCCATAAATTTTAAATT AGGTAGCCTCTTCTTTGGGTACATTTATTAATATAAAT GTGCCCAAAGTTCTTAACAAGAAAATATAAATCCCAT AAACTTTTGGCTTATTTAATTGGAAC
pME_Cp_0_5_021_psaA_3'UTR_Cr	3'UTR	TTTTTTTTTAACTAAAATAAATCTGGTTAACCATACCT GGTTTATTTTAGTTTATACACACTTTTCATATATATATAC TTAATAGCTACCATAGGCAGTTGGCAG
pME_Cp_0_5_022_psaC_3'UTR_Cr	3'UTR	TTTTTATTATTATTAATTTGGGTTGTTACCATGTAACA ACCAATTTTACAACATCAGATTTGTTATTTACTAACA AACCATTGAAATCGCTCATCTGACACGGAATGCCAA TCTTTTAATAACTTTATAGCATTTTCTA
pME_Cp_0_5_026_rbcL_3'UTR_Cr	3'UTR	TTTTTATTTTCATGATGTTTATGTGAATAGCATAAACAT CGTTTTTATTTTATGGTGTTTAGGTT
pME_Cp_0_5_028_rpl36_3'UTR_Cr	3'UTR	AAATCTACTTTAGGAAGCCCTTTCCCCTCCCCTTCGG GACGTCCCCTTCGGGCAAATAAATTTTAGTGGACGTCA GTGGCAGTTGCCTGCCAACTGCCGATTTTATATACTA GGCAGTGGCGGTACCACTGCCACTGACGTCCTAAGTTT ACTTGCCCAATTTTATATTAGGCAGTTGGCAGGCAAC TGCCACTGACGTCCGAAGGGGAAGGGGAAGGAGGC AGTTGCCTGCCAACTGCCTCCTTACGGAGTATTAAT AGGCAGTGGCGGTACCACTGCCACTGACGTCCTAATAT AAATATTAGGGCGTCCCGTAAGAGGACGTCATAGGCA AGTAGACTTAAGGAAGCCAGTTGATATTTATTTACGCC AAAAGGAGGTAAGTAACCTATGTTTCGCTATTTCTGTCT AAATGCGCT

pME_Cp_0_5_030_rpoB2_3'UTR_Cr	3'UTR	TTCTATGCATAAATGAAATTATTTTATTATTTTTTAATC ACTTTATGAATCTGGTTCTTTTCATTTTTTAGAATCTTGTT AGCAAATTTCTCTACCAGAATGGGATGGCATTGGCAGT TGGAAAACCCGGTACAAGTCAATACATTCTTTAGTTTTT TGCATATTCGAAAGGACGTCCCCTTACGGGACGTCCCT TTTGGGACGCCAGTGGACGTCACTGGCAGTGGTACCG CCACTGCCTCCTTCCCCTTCCCCTTCGGGACGTCCCCT ACGGGAATATAAATATTAGTGGCAGTTGCCTCCTTCCC TTTCCCCTTCGGGACGTCCCCTTACGGGAATATAAATAT TAGTGGCAGTTGCCTCCTTCCCCTTCCCCTTCGGGACGT CCCCTTACGGGAATATAAATATTAGTGGCAGTTGCCTC CTTCCCCTTCCCCTTCGGGACGTCCCCTTACGGGAATAT AAATATTAGTGGCAGTTGCCTCCTTCCCCTTCGGGCAA GTAAACTTAGGAGTATATAAATATAGGATGTTAATACT GCGGAGCAGGCAGTGGCGGTACCACTGCCACTAAAAT TTATTTGCCCGAAGGGGACGTCTGCCAACTGCCTAGG CAGCCAATAAAATTTATCGCAGTATATGTATATGCTTCC CCTTCTGGGATAGAAGTAAACATCTCCGAAGGCACGTT CTTACGGTCTATATATTCTTGCACTGGCTTGCAGTGC TACTAATGTAATGTTCCCAAGGGGTTAATCCCATTGA AG
pME_Cp_0_5_031_rpoC2_3'UTR_Cr	3'UTR	AATTCTTTCTTTTTGTTAAAAGATTCTAAAAGTAAAGT ATTAACCTT
pME_Cp_0_5_032_rps2_3'UTR_Cr	3'UTR	ATACTAACCATATGGTTTAGTTTTTTTTTAGTTGTCATTC TAGGACGTCCCCTTACGGGAATATAAATATTAGTGGCA GTGGTACCGCCACTGCCTGCTCCGCAGTATTAAACATCCT ATTTTAATACTCCGAAGGAGGCAGTTGGTTCAGCCTCT GCCATTCAAGTAGATATACCAACGAGGATATTCTTTT AATATCCTCGTTGGGTATATCTACTTTTTGATTAGTATTT ATATACTTAATATGCAAATATTCC
pME_Cp_0_5_034_rps4_3'UTR_Cr	3'UTR	TTTAATCGGTAAAAATCCCAGGTAGTTGCACCTTTCCT TCAGGACGTCCCCTTCCCCTTCGGGACAATAAATAAAT TGTTGCCTGCCAACAAATTTATTTATTGTATTAATAAG AATAAAATTTATTTGCTGCGGTAGCAGGTTTACATACA ATTTATTTATTGTACCACTGCCACTGGCGTCCTCCTCG GAGTATGTAAACATGCTAAGTTTACTTGCCCAATATTTA TATTAGGCAGTTGGCAGGCACTGCCACTAAAATTTAT TTACCCGAAGGGGACGTCCCGAAGGGGAAGGGGAAG GAGGACGTCCCCTTACGGGAATATAAATATTAGTGGAC GTCAGTGGCGGTACCACTGCCACTGGCGTCCTATATTT ATATACTCCTAAGTTTACTTGCCCAATATTTATATACCC GAAGGGGAAGGGGAAGCATATAAATATACTTCGGAGT ATATAAATATAGGATGTTAATACTGCGGAGCAGGCAGT TGGCAGGACGTCCCCTTCGGGATTTAATGCTCCGTTA GGAGGCAAATAAATTTTAGTGGCAGTGGTACCGCCACT GCCTGCTTCCTCCTTCGGAGTATGTAAACCCCTTCGGGC AACTAAAGTTTATCGCAGTATATAAATATAGGCAGTTG GCAGGCAACTGCCACTGACGTCTATATTTATATACTCC GAAGGAACCTTGTTAGCCGATAGGCGAGGCAACTGCCA CTAAAATTTATTTGCCCGAAGGGGACGTCCACTAATAT TTATATTCCCCTAAGGGGACAAATTTATTTATTGCATTA AAATCCCTAAGTTTACTTGCTCCTTCGGAGTATATAAA TATCCCGTAAGGGGAAGGGGACGTCTAGTATATAAA TATCGGCAGTTGGCAGGCAACAAATTTATTTATTGTCCC GTAAGGGTTTGCAAGAATACTGTAAGGGGATGTCTTTT TAAATTCATTCAAAAAAATCAAAATAAAACTATTATAA TTTTGACCAATTACCAATAAATTACCAGATTAAATGT ATTTTATTTTCCAAATTATACCAG

pME_Cp_0_5_035_rps8_3'UTR_Cr	3'UTR	CAATTGGTAACTTTAGAAAAATTAGAAATAAATCCTAT GCTGCAAAATATTCTTTTGAGTCGCCTTCCAATTAATA AATTATTTAAACACGTTTTGTAAATCGGTAGGCTAGC AGTTGTTGTTCCCAATCTCTATTTACTATAAGTAAATTT CAAAATAAATTAATGTAATACCCTCTCCCAAGTGGTA CTATACTAACTAAATTGACATACTGCTAAATTAATTTA AGTAATATTTACAAGGTCAACTTCTGTCAATAATTAGAT TTTAAATAAGTGTTTTTGGGAGGAAAGGTAAATACAT TTCTGGTACCTCTGGTGATGCCATATTAATATTTTAC AGAGGTAGCCAGTTTTAAATTTATAAAAAA
pME_Cp_0_5_036_rps11_3'UTR_Cr	3'UTR	TTTTTAAAAAATTAAAGATATACCAATTTATTTTTGTAT ACAAGTTTTATAGTGCAATATTTTTATAAAATATTTCTT GATTATGCTTGAGTTTTAGTATTTTACCATGCTCATGTC AACCATAAACTTGTATACAAAACATTAACAATTTTTTAT TTATTGAAATTGAAATTTATTTCTATTTAAAAATGCAG
pME_Cp_0_5_038_rps19_3'UTR_Cr	3'UTR	TTTTTGTATTTTACTGCTATTTGGTACACCTTAGTTTC TAACTAATTTCTATAAACTACTATTCTTGCAGTTAACC GGAATATAAACATCGACTTTGGGAAACCAAGTTGGTAA GAACTTGTTGTCTTGCAGCTCTTTCGCGCTGCCAGAC GGCAAGTTCTTTCCCTTCGGAAGGCAGCTAATTATGTT TATAGTCTATTTGCAATGCCACTCTGAGTAAATAAATTT CCCCTTGTGATATTAATATGAGCTGCCACTACCATCCT CTTAGAAGTATATAAATATGCACTGGCATCCTAGAGAA ATTAATTACTTTTATAGCTATAGAATGCTTGTTAAGGGA TTTACTACTATAAAATTAATGTGCTCCTTGGGGTAAATA CACTTAATAAATCCCTTAGGTATTTAAATAGCCTATTT GGGTAAAGGCTTTTTAAATATGTAATAAATTATATATAT TAGTTTTATGTGGTTTTTATATCTATGGGAACCTTACTT TTTTTACTGTAAATTCCTAGTTAAGAGTAATAAGAGC C
pME_Cp_0_5_039_tufA_3'UTR_Cr	3'UTR	TTTCACATTTAAATTCATAACGAGCCCTTAACGGACGT CCCCTTTGGGATGCCAAGGCTCTGTTAGGATATAATAC TGCGTAAGCAGGAATTTGCTATTTATTTACCCGAAAAG GTTTCGACCATAGGTGAGGACAAATTTATTTATTGTGGT ACCGCCACTGCCTCCTTCGGAGTATTAATAATCCTATATT TATATTCTCTGAAAAAAGTTCCCTTCGGG
pME_Cp_0_5_040_ycf1_3'UTR_Cr	3'UTR	AAATATGCCATATTTTTACTAATTTTATATCCAAGACAT TGTATGCTTATAAATAAAGAAGATGCTTTCATCTCTAA AGATGAG
pME_Cp_0_5_041_ycf12_3'UTR_Cr	3'UTR	TTTAAATAGCATAGCAATTGCTAGCCTTATAAAATGTA TGTACCTGAAAGTGACGTTTAGACTTTTCGGGTACATAC ATACTTCTTAATAACAAAGAAAAATTTGTTACAAACA CACATTAACACTTATAAATAGCTTACTTTAATCTGCATA GCAGCTTCTTGAACGTATTTATTATGTATTCTGAAGTTTA TATCTTTATGGTCATATAAAGGCTGTTTGTGACAATCTT TAAAGTTAATGACTAAGAAACAATATTGGAGATCAAC
pME_Cp_0_5_042_rbcL_3'UTR_Nt	3'UTR	AAACAGTAGACATTAGCAGATAAATTAGCAGGAAATA AAGAAGGATAAGGAGAAAGAACTCAAGTAATTATCCT TCGTTCTCTTAATTGAATTGCAATTAAACTCGGCCCAAT CTTTTACTAAAAGGATTGAGCCGAATA
pME_Cp_0_5_043_BMV_3'UTR_Bv	3'UTR	GGTGCCCTTTGAGAGTCTACTTTTGCTCTCTTCGGAAGA ACCTTAGGGGTTTCGTGCATGGGCTTGCATAGCAAGTC TAGATGCGGGTACCGTACAGTGTTGAAAAACACTGTAA ATCTCTAAAAGAAACCA
pME_Cp_0_5_044_TYMV_3'UTR_Tv	3'UTR	GTTCTCGATCTTTAAATCGTTAGCTCGCCAGTTAGCGA GGTCTGTCCCAACACGACAGATAATCGGGTGCAACTCC CGCCCTTTTCCGAGGGTCATCGGAACC

pME_Cp_0_5_045_rpoA_3'UTR_Nt	3'UTR	ATCTATTGGACTTACTTAGTGAAAAATAGATTGAACTCT TTAGCACAATTAATATATTAATATATCATATATTTCAAAA TAAATTCAGAATTAATGAATAGATGTATCTAGGGAG AATTCGCTTTGAAGAACTATTCCCTAGATACACATGTC GTGTTATTTACAATTGAATCAATTTAAAAAT
pME_Cp_0_5_046_petD_3'UTR_Nt	3'UTR	ATTTTTAAATTGATTCAATTGTGAAATAACACGACATGT GTATCTAGGGAATAGTTTCTTCAAAGCGAATTCTCCCTA GATACATCTATTCAATTTAATTCTGAATTTATTTGAATA TATGATATATTAATATATTAATTGTGCTAAAGAGTTTCA ATCTATTTTCACTAAGTAAGTCCAATAGAT
pME_Cp_0_5_047_TMV_3'UTR_Tv	3'UTR	ATAAATAACGGATTGTGTCCGTAATCACACGTGGTGCG TACGATAACGCATAGTGTTTTCCCTCCACTTAAATCGA AGGGTTGTGCTTGGATCGCGCGGGTCAAATGTATATG GTTTCATATACATCCGCAGGCACGTAATAAAGCGAGGG GTTTCAATCCCCCGTTACCCCGGTAGGGGCCCA
pME_Cp_0_5_048_psaC_3'UTR_Nt	3'UTR	TACGTTTCGAGAAAACCTCTACTTGAATCCATTTAATTTTT TTTACCGACAAACCTGTGCTCGAAAATCACAATATTTTG AGCACGGGTTTTTATG
pME_Cp_0_5_049_TDumy	3'UTR	ACTCAGTTGTAGTAACGAGCGGATAGATTCCCAGACCC ACCTTCACGGGCGGTAGCAGGACCTCAATAATAGGATT TTCG
pME_Cp_0_05_050_Terminator_Placeholder	3'UTR	GAAAGTGAAACGTGATTTTCATGCGTCATTTTGAACATT TTGTAAATCTTATTTAATAATGTGTGCGGCAATTCACAT TTAATTTATGAATGTTTTCTTAACATCGCGGCAACTCAA GAAACGGCAGGTTCCGATCTTAGCTACTAGAGAAAGA GGAGAAATACTAGATGCGTAAAGGCGAAGAGCTGTTT ACTGGTGTGTCCTTATTCTGGTGGAAGTGGATGGTGA TGTC AACGGTCATAAGTTTTCCGTGCGTGCGAGGGTG AAGGTGACGCAACTAATGGTAACTGACGCTGAAGTT CATCTGTACTACTGGTAACTGCCGTTCTTGGCCGA CTCTGGTAACGACGCTGACTTATGGTGTTCAGTGCTTT GCTCGTTATCCGGACCATATGAAGCAGCATGACTTCTT CAAGTCCGCCATGCCGGAAGGCTATGTGCAGGAACGC ACGATTTCTTTAAGGATGACGGCACGTACAAAACGCG TGCGGAAGTGAAATTTGAAGGCGATACCCTGGTAAAC CGCATTGAGCTGAAAGGCATTGACTTTAAAGAGGACG GCAATATCTGGGCCATAAGCTGGAATACAATTTTAAC AGCCACAATGTTTACATCACCGCCGATAAACAAAAAAA TGGCATTAAAGCGAATTTTAAATTCGCCACAACGTGG AGGATGGCAGCGTGCAGCTGGCTGATCACTACCAGCA AAACACTCCAATCGGTGATGGTCTGTTCTGCTGCCAG ACAATCACTATCTGAGCACGCAAAGCGTTCTGTCTAAA GATCCGAACGAGAAACGCGATCATATGGTTCTGCTGG AGTTTCGTAACCGCAGCGGCATCACGCATGGTATGGA TGAAGTGTACAAATGACCAGGCATCAAATAAACGAAA GGCTCAGTCGAAAGACTGGGCCTTCGTTTTATCTGTT GTTTGTGCGGTGAACGCTCTCTACTAGAGTCACACTGGC TCACCTTCGGGTGGGCCTTCTGCGTTTATA
pME_Cp_0_5a_001_Strep-tag	C-terminal Tag	GCTTTATGGAGCCACCCGAGTTCGAGAAGGGGTA
pME_Cp_0_5a_002_His-tag	C-terminal Tag	GCTTTACACCATCACCACCATCATGGGTA
pME_Cp_0_5a_003_Hibit-tag	C-terminal Tag	GCTTTAGTTTCTGGTTGGCGTTTATTTAAGAAAATTTCT GGGTA
pME_Cp_0_5a_004_flag-tag	C-terminal Tag	GATTATAAAGATGACGATGACAAAGGTGACTATAAGG ATGATGATGATAAAGGTGACTACAAAGACGACGATGA TAAA

pME_Cp_0_5a_005_HA-tag	C-terminal Tag	TATCCATATGATGTACCAGATTACGCAAAATACCCATAC GATGTTCTGATTATGCTGGTTATCCTTATGATGTTCCA GATTATGCT
pME_Cp_0_5a_006_myc-tag	C-terminal Tag	GAACAAAACTTATTTTCAGAGGAAGATTAAACGGTGA GCAAAAATTAATTTCTGAGGAAGACTTAAATGGTGAAC AAAACTGATTTTCGGAGGAAGATCT
pME_Cp_0_6_005_psbH_3'Hom_v2_Cr	3'Homology	TGCCACTGCCGAATATAAATATGGTTGAGTTGCTTAGT TTACCTTAGCGAAAAGAAGACTTAGCAGCTAGCCTTAA CAAACAGTTTTATATTTTATGTTTGTAAATAAAATT AAGAACTTTAGCTAAAGTTTCCCACTCATAGAAACG TCATCTAAAATTAAGAAGTGTGTAATTTCTAAAATG ATTAATAAGAATGCTGCAATAAAAGGATAAATACAGC CATTAAACAGTTGTACCCAGCCTGGTAATACTTTACC TGCTTCTGAGTTAAGTGGACGTAATAAAGTACCTAATG GTGTAACATAAACAGGTTCTTGGAAGTCTGAATTTACTT TTGATGGTTTAGCTTTAGAAGTTCCTGTTGCCATAATTG ATTAATGAATTAAGCGTTATTAGCGCTATTTTATTAC TTTCTGTAAAAAATAAGGAAAATATCTTCAGTGCATTCT CCTCTCAGGATTATAAATACTCTGAGGATAACGTTCTCT CGTCAAGGGGTTGCTTCTGTGAGTATAGAAACCTACT AGCACAAGAAATAAATTGCATAAAAATGTATTTACCTA GGACCGCAGTAGGCAGTCCCTTTTCCCTTCAGAACTG CCTGCTTTAAAAGAATGAAAAAAGTGCCTGTCTGGTA AGTAAAAGTCTTTAATTACTCACTAAAGACGATCTAGA AGTTCTTTGTTCATTTTTATTTAATATAATTTGTTAT ATAAAAATTAATAATTTTTAATTAATGTTAACTTTGT AAGGACAGTTTCAAAGTGACATGAATGGCTACTGCAA AAACGAAGTAAGTTATTCTTCTCAGGGCAAAATTTTG AGTAGATTAATTTTGTTAAAAATGTGGGACACAGTCG TCAAGTCTTTGAACTATCTAAGAGATATGTTGAAAAG AGAATAATTTTATTATTAATGAGCTATGGAAAGTCCA GCTTTTTTCTTACCTTTTTTATGGTTTCTTCTGTTAAG TGTAAGTGGCTATTCAGTTTATGTTAGTTTGGTCCACC TTCAAAAAAATTACGTGATCCTTTGAAGAACACGAAG ATTAACAAGTTAAAAAGTACTATTTTACAAGTGACTT CGGTGCCTC
pME_Cp_0_6_006_psbH_5'Hom-reversed_v2_Cr	5'Homology Reversed	CGTTAAGATAAACGCGTTAATAGCTCACTTTTCTTTAAA TTTAATTTTTAATTTAAAGGTGAAGCAAATTGCCTGAC GAGAGATCCACTTAAAGGATGACAGTGGCGGGCTACT GCCTACTTCCCTCCGGGATAAAATTTATTTGAAAAACGT TAGTTACTTCTAACGGAGCATTGACATCCCATATTTA TATTAGGACGTCCCCTTCGGGTAAATAAATTTTAGTGG ACGTCCCCTTCGGGCAATAAATTTTAGTGGACAATAA ATAAATTTGTTGCTGCCAAGTGCCTAGGCAAGTAAAC TTGGGAGTATTAATAAGGACGTGAGTGGCAGTTGCCT GCCAAGTGCCTATATTTATATACTGCGAAGCAGGCAGT GGCGGTACCACTGCCACTGGCGTCTAATATAAATATT GGGCAACTAAAGTTTATAGCAGTATTAACATCCTATATT TATATACTCCGAAGGAAGTGTAGCCGATAGGCGAGG CAACAAATTTATTTATTGTCCCGTAAAGGATGCCTCCA GCATCGAAGGGGAAGGGGACGTCTAGGCCATAAAAC TAAAGGGAAATCCATAGTAAGTATGTTATAAATTTAT AGACTCCAAAAAACAGCTGCGTTATAAATAACTTCTGT TAAATATGGCCAAGGGGACAGGGGCACTTTCAACTAA GTGTACATTAAAAATTGACAATTC

pME_Cp_0_6_007_psbA_3'Hom_Cr	3'Homology	AAAGTATTTGTCGTCTACGATATGTAAATCTGTCGTCTA CGATATGTAAATTTGAGCTCTTATGGCCTCTACATCGAG GTTTATTATCTTACCGAAGGTAAATGCCTTCGTGGATCT TATGGGACGTGATGTGGTCTTCCTGGTTGTTCTATATGT GAATCTGTCGTTTACAATATGTAAATTTGAGCTCTTATG AGCTCTACATCGAGGTTTATTATCTTACCGAAGGTAAT GCCTTCGTGGATCTTATGGGACGTGATGCGGTCTTCCT GGTTGTTCTATATGTGAATCTGTCGTTTACAATATGTAA ATTTGAGCTCTTATGAGCTCTACATCGAGGTTTATTATC TTACCGAAGGTAAATGCCTTCGTGGATTTTTTGGGACG TGCTGTGGTCTTCCTAGTTGTTCTATAATCACTTCGTGA CAGCCTGTTGGCTTACATTTATTTTATACGCTGTTATA TTTATACGCTGTTAGACAAGTTTAAATACATAAATTTTT ATTAGTCTATCGACCGTTAATTGCTTAACTTACCGAAGG TTAATCGCTTTACTTACCGAAGGTTAATCGCTTTACTTA CCGAAGGTTAATTGCTTAACTTACTGAAGGTTAATCGC TTTACTTACCGAAGGTTAATTGCTTAACTTACTGAAGGT TAATCGCTTTACTTACCGAAGGTTAATCCAATTTTTTTT CGCCATATGTAGACGTTTAAATTGCTACAACGTTATTAGC CTTTCGTCGCTATCAAATCGGTTCAAGATATATACACTT TATTCACTTTCGTTTATATTATGGCTGGATTAGGTCTTTT AGTTAATTAAAATTTACATATTTAATGCTATTTATTATTA TTGCAATTGCATTAAATATTTTTTAAAAAAATTAATC TTCAGCTATATTAGTAAATAACCCATAAATAGTTTCAAT TGGAATAATTGGAATTGGATATGGACTAGTTTTATTTTC TTCTAATAACTTTAATATCGCTGGA
pME_Cp_0_6_009_rbcl_3'Hom_Cr	3'Homology	CAACGAACACGGCTACCTTCAGTAATTTTTAAACCATCA CCTAATAATACCGCACCTACGTTGTTTGCTTCTAAGTTA AGTGCAATACCTAAAGTACCATCTTCAATTCAGTAA TTCACCTGACATTGCTTTTTCTAAACCATAAATACGAGC AATACCGTCACCTACTTGGAAAACGATACCGAAATCTA CCATTTTCACTTCTGGAGTGTATTGTTCAATTAATCTTT AATAAGATTACTAAGTTCTTCTGGAGTACGCATTGCCAT AAAAAGAAAAATAAATAAAAGATTAAAAAGTTTAT TTTTAAATCTTCTCGAGAATTTTAAATAAGTTTAAAA TTCAACAAAAATAGTGAGTGGTAAGATCACTTGTTAAC AAAAGTAATGGTTCACCTTGTCTATTTAAATACTAAA ATTCATTTGCCGAAGAGGACAAATTTATTTATTGCATT AAAATCCCTAAGTTTACTTGCCGTAAGGGGAAGGGG GGGACGTCCACAGGCGTCGTAAGCAACTAAAGTTTAT GACGCCGATTGCTTTGTTAGGAAAATATAAATATCCCA TAAGAAAAGGTCCTTTAAAGGTTTTATGGACTAAATAA AAAAGATAGCATAAGCATTAAATCATGCAAAATTAATA AAAAGGTAAATGTATTTATAAAAAGGTAAATGTATTTA TATAGTATTTATATTATAGCATAATAATAAATATATTTA TAAATTGATTGTTCTTAGAGCTAAAAGAGAAGAACAAT GGGTTTATAGGTATTTGAGATCCAGTTATAAAAATGA CTTTTGACGTTTATGGTATATAAACAACGCTCTAATAA AGTCTACTATATTGGAGAGGAGTGAACAGTGGCCTCG CTTATCCCCTGACAGGAATATACATG

pME_Cp_0_6_013_petB_3'Hom_Cr	3'Homology	CTTGTGCAAATAAATAGCACACTCTTGCATATCTATATT TTAAGATGTCAGCTTTTGTATTGATTGAGTTGTATATTT TATTTACTTTACTAGGGTGTTTATATATTCCTTTTGGG GTTGCCAGATAGTTATATAACCAATCACAACAACAGT AAAAATTGAAGTTTATTTACCCAAAGGGGTGTATCCCC TTTGGGTAAATAAACTTCAATGGCCAAGTGCCTTGGA ACTTACGTAGCAGCCTAAAAAAGCTAGTCTTATATCC GAAGCAAGTAAAAGAAATGGATATTAATATTATAGA GGACCTGAAATACCTTGTTTACGAATCATTAGAAGTG CATTAAACATGAAAACAGCTGTTAAAAGTGGTAATACGA AAGTGTGTAACTGTAGAAACGTGTTAAAGTTGCTTGA CCAACACCAACACCACCACGTAATAACTCAACAATGAA ACCACCAACACCTGGGATTGCATCAGGAACACCTGTTA CAATTTTAACCGCCAGTAACCAACTTGGTCCCATGGTA ATGAATAACCTGTTACACCAAAAGAACTGTACATACA GCCATGATTACACCTGTAACCCATGTTAATTCACGTGG ACGTTTGAAACCACCTGTTAAATATACACGGAAACGT GTAAACCATCATAAGAACCATCATACTAGCTGACCAA CGGTGAATTGAACGAATTAACCAACCAAGTTAACATC AGTCATAATGTATTGTACTGATGCGAAAGCTTCTGCTA CTGTTGGACGGTAGTAGAAAGTCATAGCAAAACCACT AGCTACTTGACAAGGAAACATGTAAGTAATACCAC CAATACAGTAGAAAATATTTACGTGTGGTGAACATAT TTACTTGTAATATCATCAGCAATTGCTTGAATTTCTAAA CGTTCTTCAAACCAATCGTATACTTTACTCATATAAAAT TTTTATAAGATTGTGACATGACCATTAGGCTTTCTTAAG ACTAAAAAATGTGTAGCTTAATTATTTAAAGTTTAAAT TAAAGTTATAATATATATTATATATAAAATAAAAAAAC GTTAGTAATTCAAAAGTTTAAATATTATACAATTGAACT ATTATGTATTAATATAAGAATGTCACCTCTTACCATAT TTCTACTCCAAAGTAACTTTTACATAAATGTCCCTC TGGGGCTGCCTCCTTCCCCTTCCCCTTCGGGTATATAAA TATAGGGCAAGTAACTTAGCATAACTTTAGTTGCC GAAGGGGTTTACATACTCCGAAGGAGGACAAATTTATT TATTGTGGTACAATAAATAAATTGTATGTAAACCCCTTT CGGGTAACTAAAGTTTATCACGGCAATAAGTTTCTGCT TACGCAGTATTATATCTGACGCAGTATTATATAAGAAG TTGGCAGGATAAAAAATGTGTAAGTATGGCAATCTTTTA AAATAGTGTTCAATTCAATTAAGGCAGATAAAAAAGAAA AAAGTCCACAGGATTTAATTTGAATAGTTCTCTATCAA AAAAAGGTTTGCCGAACAATGTTTTATTCTGGAGTTT GATTTTATGAAATTAGCTGTTTACGGAAGGTGGTAT TGAAAAATCAACGACAAGTTGTAATATTTGATTGCTTT AGCAAAACGTGGTAAAAAAGTGTTACAAATTGGTTGT GATCCTAAACATGATAGTACTTTTACATTGACAGGGTTT TTAATTCCAACCATTTATTGATACATTAAGTTCTAAAGAT TATCATTATGAAGATATTGGCC
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		AGGGGACGTCCCGAAGGGGAAGGGGACGTCCTAACG GAGCATTAATAATCCCTAAGTTTACTTGCCTAGGCAGTT GGCAGGATATTTATATACGATATTAATACTTTGCAACTG CCACTAAATTTATTTGCCCGAAGGGGACGTCCTTCGG AGTATATAAATATCCCGTAAGGGGAAGGGGATGTCCC GTAAGGGGAAGGGGAGAAGCTCCAACAGAGG
pME_Cp_0_6_021_petB_5'Hom- reversed_Cr	5'Homology Reversed	GCGGTTTCTGCCAGATCCCCGTTGGCCATTGATAAG GGGTAGCTATAAATTAACCATAGTTATATTCTGGTTAA AGGATCGGAACTAACCCCAAGTCTCTAGTCTAAACAAA AAATTGTGTATGCATTTAACACATTTAGTGTTTTAACT AGACAAAAAAATTAAGTATGATATTATAAAAGTAATA TTTTTTAGCCTTCGTGATGGAAGTGGTAGACATCCTGGT TTTAGGAACCAAGTGCTGAAAGGCGTGCCGGTTCAAATC CGCCCGAAGGCATTTTAAGTTTAACGTAGAGCCAATAT TTGTTTGAATTTATCTATTTTTTAAACCATTTTGGTTTAA AATTTTTATTTGCTTCAAAGGAGCCTGTAAACGGTACTT TAATTTTTACAGTAGCACTCGCAGAGCTTATTTACGTGC AAATAAAAGCTCTATCTACTAGGATATTAGACTAGTATT AATAAAACACAACATTTTATTAACAAAGTAATTTATGCC GATTGGAGTACCTCGTATTATTTATTGTTGGGGTGAAG AATTACCTGCACAGTGGACTGATATTATAACTTTATTT TCCGTCGTCGTATGGTATTTTAAATGCAATATTAGATG ATGAATTATGTAACCAAATTTGTGGTTTATTAATTAATA TCCATATGGAAGATCGTTCTAAAGAGTTGGAAAAAAA GAAATGGAAAAAAGTGGATTATTTAAAAGTGGCACCCG CAAAAACAAAAGGAAAAGATACAGTAAAAAAGAAAA TTTATCTGGCGGCGCTAGTGCAAAACGTCAATC

pME_Cp_0_6_022_rbcl_5'Hom-reversed_Cr	5'Homology Reversed	GTAAGTAACTGCGTAAGACGACCGACATATACCTAAA GGCCCTTTCTATGCTCGACTGATAAGACAAGTACATAA ATTTGCTAGTTTACATTATTTTTATTTCTAAATATATAA TATATTTAAATGTATTTAAAAATTTTCAACAATTTTTAAA TTATATTTCCGGACAGATTATTTAGGATCGTCAAAAGA AGTTACATTTATTTATATAAATGGTTCACAAACAGAAA CTAAAGCAGGTGCTGGATTCAAAGCCGGTGTAAGA CTACCGTTTAACTACTACACACCTGATTACGTAGTAAG AGATACTGATATTTAGCTGCATTCCGTATGACTCCACA ACCAGGTGTTCCACCTGAAGAATGTGGTGCTGCTGTAAG CTGCTGAATCTTCAACAGGTACATGGACTACAGTATGG ACTGACGGTTTAAACAAGTCTTGACCGTTACAAAGGTCG TTGTTACGATATCGAACCAGTTCGGGGTGAAGACAACC AATACATTGCTTACGTAGCTTACCAATCGACTTATTCTG AAGAAGGTTTCACTAATAACATGTTCACTTCTATTGTA GGTAACGTATTCGGTTTCAAAGCTTTACGTGCTCTACGT CTTGAAGACCTTCGTATTCACCTGCTTACGTTAAAAACA TTCGTAGGTCCTCCACACGGTATTCAGGTAGAACGTGA CAAAATTAACAAATATGGTCGTGGTCTTTTAGGTTGTA CAATCAAACTAAATTAGGTCTTTCAGCTAAAACTAC GGTCGTGCAGTTTATGAATGTTTACGTGGTGGTCTTGA CTTTACTAAAGACGACGAAAAACGTAACTCACAACCAT TCATGCGTTGGCGTGACCGTTTCTTTTCGTTGCTGAAG CTATTTACAAAGCTCAAGCAGAAACAGGTGAAGTTAAA GGTCACTACTTAAACGCTACTGCTGGTACTTGTGAAGA AATGATGAAACGTGCAGTATGTGCTAAAGAATTAGGT GTACCTATTATTATGCACGACTACTTAACAGGTGGTTTC ACAGCTAACACTTCATTAGCTATCTACTGTCGTGACAAC GGTCTTCTTCTACACATCCACCGTGCTATGCACGCGGTT ATTGACCGTCAACGTAACCACGGTATTCACCTCCGTGTT CTTGCTAAAGCTCTTCGTATGTCTGGTGGTGACCACCTT CACTCTGGTACTGTTGTAGGTAACTAGAAGGTGAACG TGAAAGTTACTCTAGGTTTTCGTAGACTTAATGCGTGATG ACTACGTTGAAAAAGACCGTAGCCGTGGTATTTACTTC ACTCAAGACTGGTGTTCATGCCAGGTGTTATGCCAGT TGCTTCAGGTGGTATTCACGTATGGCACATGCCAGCTT TAGTTGAAATCTTCGGTGATGACGCATGTCTTCAGTTC GGTGGTGGTACTCTAGGTCACCCTTGGGGTAACGCTCC AGGTGCTGCAGCTAACCGGTAGCTCTTGAAGCTTGTA CTCAAGCTCGTAACGAAGGTGCTGACCTTGCTCGTGAA GGTGGCGACGTAATTCGTTACGCTTGTAATGGTCACC AGAACTTGCTGCTGCATGTGAAGTTTGGAAGAAATTA AATTCGAATTTGATACTATTGACAACTTTAATTTTTATT TTTCATGATGTTTATGTGAATAGCATAAACATCGTTTTT ATTTTTATGGTGTTAGGTTAAATACCTAAACATCATTT TACATTTTTAAATTAAGTTCTAAAGTTATCTTTGTTTA AATTTGCCTGTCTTTATAAATTACGATGTGCCAGAAAAA TAAATCTTAGCTTTTATTATAGAATTTATCTTTATGTA TTATATTTTATAAGTTATAATAAAAGAAATAGTAACATA CTAAAGCGGATGTAACCTCAATCGGTAGAGTGCGATCCT TCCAAGTTGAGGTTGTGGGTTGAGTCCCATCATCCG CTAAACCAATCTATAAAAGTTGTTGAATATGCTGAAAT GTTTTCAAAGAAAAAGCCTAGTTTTCTTTTACAACAAG CAAAGAACAATTGGCATTCTTTGATTGTAAGAAAATGC GCTTACGTGGAGTTATGTGTTTTTAC
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pME_Cp_0_6_023_psbD_5'Hom-
reversed_Cr

5'Homology
Reversed

CACAAAGCAGTTCTAGTCCCATATATATAACTATATATA
ACCCGTTTAAAGATTTATTTAAAAATATGTGTGAAAAA
ATGCTTATTTTTAATTTATTTTATATAAGTTATAATATT
AAATACACAATGATTAAAAATTAAATAATAATAAATTTAA
CGTAACGATGAGTTGTTTTTATTTTGGAGATACACGC
AATGACAATTGCGATCGGTACATATCAAGAGAAACGC
ACATGGTTCGATGACGCTGATGACTGGCTTCGTCAGA
CCGTTTCGTATTCGTAGGTTGGTCAGGTTTATTACTATT
CCCTTGTGCTTACTTTGCATTAGGTGGTTGGTTAACTGG
TACTACTTTCGTTACTTCATGGTATACGCATGGTTTAGC
TACTTCTTACTTAGAAGGTTGTAACCTCTTAACAGCAGC
TGTTTCTACACCTGCTAACAGTATGGCTCACTCTCTTCT
ATTTGTTGGGGTCCAGAAGCTCAAGGTGATTTCACTC
GTTGGTGTCAACTTGGTGGTTTATGGGCATTGTTGCT
TTACACGGTGCAATTTGGTTTAAATTGGTTTCATGCTTCGT
CAGTTTGAAATTGCTCGTTCAAGTAACTTACGTCCATAC
AACGCAATTGCTTCTCAGCACCAATTGCTGTATTGCTT
TCAGTATTCCTAATTTACCCATTAGGTCAATCAGGTTGG
TTCTTTGCACCTAGTTTCGGTGTAGCTGCTATCTTCCGT
TTCATTTTATTCTTCCAAGGTTTCCCAACTGGACACTTA
ACCCATTCCACATGATGGGTGTTGCTGGTGTTTAGGT
GCTGCTTTATTATGTGCTATTCACGGTGCTACTGTTGAA
AACACATTATTGGAAGACGGTGACGGTGCTAACACATT
CCGTGCATTCAACCCTACACAGGCTGAAGAAACATACT
CTATGGTACTGCTAACCGTTTCTGGTCACAAATCTTCG
GTGTTGCTTTCTTAACAAACGTTGGCTTCACTTCTTCA
TGTTATTAGTTCCAGTAACTGGTCTTTGGATGAGTGCTA
TTGGTGTTGTAGGTTTAGCTCTAACTTACGTGCTTACG
ACTTCGTATCACAAGAGATTCTGTGCTGCTGAAGACCCT
GAATTCGAAACATTCTACACTAAAAACATTCTTCTTAAC
GAAGGTATTCGTGCTTGGATGGCTGCTCAAGACCAACC
ACACGAACGTTTAGTATTCCCTGAAGAAGTATTACCAC
GTGGTAACGCTCTATAATATATTTTATATAAATTACCA
ATACTAATTAGTATTGGTAATTTATATTACTTTATTATTT
AAAAGAAAATGCCCTTTGGGGCTAAAAATCACATGA
GTGCTTGAGCCGTATGCGAAAAAATCGCATGTACGGT
TCTTTAGGAGGATTTAAAAATATAAAAAATAAAAAAAC
AAATCCTACCTGACTAAACCAGGACATTTTTCACGTA
CTGTCAAAGGTCCAAACACAACAACCTTGGATTGGAA
CCTTCACGCAGATGCTCATGACTTTGACAGTCATACAA
GTGATCTAGAAGAAATTTCTAGAAAAGTATTCAGTGCA
CACTTTGGTCAATTAGGTATCATTTTCATTTGGTTAAGT
GGGTGCGACACGAAGACGTATATATTTTATAGTTTAA
AAAGATACTTTTACACTGTAGTTGAAAAGTAAAGCAC
TTTTAAAAATCAAAGCAGTATAAGGCAATTATTTGCATT
TTGCTTTAGTTCTTTTATTTTTTCAGAAAAACTTACTTT
TTAGTTTCAATTATGTCTAAAAAGACAGAAGTGGTTTAT
CATATAAAAAGATTTTACAATCCACTTTTAAAAATC
TTTTGGTTTTTTATTTAAATCTATACTCTTAATACAAATG
GCAGATCCTAAATCCTGTAAAGACATCCCCTTAAGGGA
CGGTTTTATCAAGTTCCATAGCCTAACAGAGGTAAATC
CATTTTAATAACCACAAAGCGTTTATCGTTAAAAATAAA
TACTAATATATGTAACGTGTAAAAATAATTTTTAATAT
TATTAAGGATACTCAAAAAAATACATTAACAAGTCTA
ATAGAACACAAAATGTATTAATCAGCTAGGTCTGAAA
AAACTTTAATTTATTTTAAGGACATCTCGCTCTTTGG
GTATAGCAATTCAATTGATTTGCTCTATATTTATATCCCT
AAACTAGATAAACTTTGTAGAACTATAAATTTTATGCA
GTTTATCCGAAATTAAGTCAAACGTTTTTTCTTTGAG
TGAATCTTTTTTTTCGATTTTATTATTCCAAACC

Supplementary Table 6: List of primers used in this study.

Primer	Target	Sequence	Purpose
oRI0025	MoClo backbone	CGGTTCTGCTGGCCTTTTGC	Sequencing Lvl1 fw
oRI0026	MoClo backbone	GATAGGTGCCTCACTGATTAAG	Sequencing Lvl1 rv
oRI0027	MoClo backbone	CTATAAAAATAGGCGTATCACGA GGC	Sequencing Entry vector fwd
oRI0028	MoClo backbone	CGAGTCAGTGAGCGAGGAAGC	Sequencing Entry vector rv
oRI0202	MoClo backbone	GTGAGCTATTAACGCGTTTATCT TAAC	Sequencing Lvl2 fw
oRI0203	MoClo backbone	GTAAACTAAGCAACTCAACCATA TTTATATTC	Sequencing Lvl2 rv
oRI0343	Nanoluciferase	CCAACCTGTAACACCATTAAATTG	cPCR to confirm integration of Nanoluc rv
oRI0642	psbH locus	CTCTAGACGATGGGGGC	cPCR to confirm integration in psbH locus fw
oRI0643	psbN locus	GTTTATATGCTCGACAAAATGAC TTTC	cPCR to confirm integration in psbN locus rv
oRI0733	Glycolate dehydrogenase	GGTCTCGTTGCGGGACGTCCTG CCAAC	cPCR to confirm Glycolate dehydrogenase integration fw
oRI0734	Glycolate dehydrogenase	GGTCTCGCGCTGCAGGCAACAA ATTTATTTATTGTC	cPCR to confirm Glycolate dehydrogenase integration rv
oRI0738	Malate synthase	GGTCTCGAGCGGGGTAACATAA GTTTATC	cPCR to confirm Malate synthase integration fw
oRI0739	Malate synthase	GGTCTCGCATTCGCTAATGGGA GAATATATTTATTTGAC	cPCR to confirm Malate synthase integration rv
oRI0736	Kanamycin	GGTCTCGGTTGATGCGAGTGAT TTTGATG	cPCR to confirm Kanamycin integration fw
oRI0737	Kanamycin	GGTCTCGCAACCAAACCGTTAT TCATTCCG	cPCR to confirm Kanamycin integration rv
oRI0745	Tobramycin	CATTAAAGGGAAGTCATCGTC	cPCR to confirm Tobramycin integration fw
oRI0746	Tobramycin	CATTGAAAACGGTCGTAAAG	cPCR to confirm Tobramycin integration rv
aadA_rv_57_54	Spectinomycin	CAGATCAGTTGGAAGAATTTG	cPCR to confirm Spectinomycin integration rv
aadA_rv_63_60	Spectinomycin	CATACTGAAGCTAGGCAGGC	cPCR to confirm Spectinomycin integration rv
Nanoluc_fwd_61_59	Nanoluciferase	CCTGATGGTTCATTATTATTCCG TG	cPCR to confirm integration of Nanoluc fw
Nanoluc_fwd_58_55	Nanoluciferase	CAATTAATGGTGTTACAGGTTG	cPCR to confirm integration of Nanoluc fw
Nanoluc_fwd_62_59	Nanoluciferase	GTTACAGGTTGGCGTCTTTG	cPCR to confirm integration of Nanoluc fw
petB_fwd_59_56	petB locus	ACAGGTGATTTTCTTCAATACC	cPCR to confirm integration in petB locus for Homoplasmy fw
petB_fwd_63_60	petB locus	GTTCCAGTTTAACCATTCGTTG	cPCR to confirm integration in petB locus for Homoplasmy fw
petB_rv_57_55	petB locus	ACCTCCGTAAATAACATCTTC	cPCR to confirm integration in petB locus for Homoplasmy rv
petB_rv_60_57	petB locus	CAATCTACACCCCATAACC	cPCR to confirm integration in petB locus for Homoplasmy rv
petB_rv_63_60	petB locus	CACAATCTACACCCCATAACC	cPCR to confirm integration in petB locus for Homoplasmy rv
psbD_fwd_59_56	psbD locus	AGGCGATTTGTTTCACTTAAG	cPCR to confirm integration in psbD locus for Homoplasmy fw
psbD_fwd_62_59	psbD locus	CCGTGATACATCTTCGAAAGTAA G	cPCR to confirm integration in psbD locus for Homoplasmy fw
psbD_rv_57_54	psbD locus	CTTGTTTTTCGGGTATTGAG	cPCR to confirm integration in psbD locus for Homoplasmy rv
psbD_rv_63_60	psbD locus	TTCCCGATACTTTGTCTGCTTG	cPCR to confirm integration in psbD locus for Homoplasmy rv

psbH_cPCR_hom_fwd_2	psbH locus	CTTTAAGTGGATCTCTCGTC	cPCR to confirm integration in psbH locus for Homoplasmy fw
psbH_cPCR_Hom_fwd_3	psbH locus	AAGTGGATCTCTCGTCAG	cPCR to confirm integration in psbH locus for Homoplasmy fw
psbH_cPCR_homology_fwd	psbH locus	GAAAAGTGAGCTATTAACGC	cPCR to confirm integration in psbH locus for Homoplasmy fw
psbH_fwd_60_57	psbH locus	CATTGCGAAAATACTGGTGC	cPCR to confirm integration in psbH locus for Homoplasmy fw
psbH_fwd_60_57_2	psbH locus	GCTAGTCATTGCGAAAATACTG	cPCR to confirm integration in psbH locus for Homoplasmy fw
psbH_rv_58_56	psbH locus	GTTTATATGCTCGACAAAATGAC	cPCR to confirm integration in psbH locus for Homoplasmy rv
psbH_rv_59_57	psbH locus	ATGCTCGACAAAATGACTTTC	cPCR to confirm integration in psbH locus for Homoplasmy rv
rbcl_fwd_57_55	rbcl locus	GTCTAACCGATTTTATAATGCG	cPCR to confirm integration in rbcl locus for Homoplasmy fw
rbcl_fwd_59_57	rbcl locus	GTTAACAAGTTATTCCCACTGTG	cPCR to confirm integration in rbcl locus for Homoplasmy fw
rbcl_rv_57_55	rbcl locus	GTCAACTACACGACCTAAG	cPCR to confirm integration in rbcl locus for Homoplasmy rv
rbcl_rv_60_57	rbcl locus	CAGGAATTTTCAGCGATTTTACC	cPCR to confirm integration in rbcl locus for Homoplasmy rv
tobra_rv_56_58	Tobramycin	GGTGACTCAGGTATTATTGATG	cPCR to confirm integration of Tobramycin rv
tobra_rv_57_55	Tobramycin	TTGGTGACTCAGGTATTATTG	cPCR to confirm integration of Tobramycin rv
tobra_rv_58_56_2	Tobramycin	CAAGAATTCATTGAAAACGGTC	cPCR to confirm integration of Tobramycin rv
tobra_tmv_rv_59_56	Tobramycin	CGCTTAAATAAATAACGGATTGTG	cPCR to confirm integration of Tobramycin rv
petB_fwd_5'Hom	petB locus	GTTAGTTCCGATCCTTTAACC	cPCR to confirm integration in petB locus for Homoplasmy fw
psbD_fwd_5'Hom	psbD locus	GTCATTGCGTGTATCTCC	cPCR to confirm integration in psbD locus for Homoplasmy fw
psbH_rv_58_56	psbH locus	GTTTATATGCTCGACAAAATGAC	cPCR to confirm integration in psbH locus for Homoplasmy fw
rbcl_fwd_5'Hom	rbcl locus	CTTTAGGTATATGTCGGTCG	cPCR to confirm integration in rbcl locus for Homoplasmy fw
Wendyl_fwd	Wendyl locus	GATCAGTTCAGTTGTGTTAG	cPCR to confirm the lack of integration in the Wendyl locus fw
Wendyl_fwd2	Wendyl locus	TTTATGGCGTCTGAGTTG	cPCR to confirm the lack of integration in the Wendyl locus fw
Wendyl_rv	Wendyl locus	GTAAACAGATAGGAATGGAC	cPCR to confirm the lack of integration in the Wendyl locus rv
Wendyl_rv2	Wendyl locus	CTAACACAACCTGAAGTATG	cPCR to confirm the lack of integration in the Wendyl locus rv
Wendyll_fwd	Wendyll locus	CAAATGCGTTAAGACTTCC	cPCR to confirm the lack of integration in the Wendyll locus fw
Wendyll_fwd_2	Wendyll locus	CCTTAAAGGGTGAATGTATATAC	cPCR to confirm the lack of integration in the Wendyll locus fw
Wendyll_rv	Wendyll locus	CCAGTATTTTCGCAATGAC	cPCR to confirm the lack of integration in the Wendyll locus rv
Wendyll_rv_2	Wendyll locus	GGAAGTCTTAACGCATTTG	cPCR to confirm the lack of integration in the Wendyll locus rv
HomPCR_Confirm_01	psbH locus fwd	GAATTCGAATCCGCGTTTTC	cPCR to assess the homoplasmic state of engineered strains in psbH locus
HomPCR_Confirm_02	psbH locus rv	TAAGTAGGGTTCTCAGAGGC	cPCR to assess the homoplasmic state of engineered strains in psbH locus
HomPCR_Confirm_03	psbH locus left flank fwd	GAATTCGAATCCGCGTTTTC	cPCR to confirm integration of the left flank of genetic constructs in psbH locus
HomPCR_Confirm_04	psbH locus left flank rv	GGCTTATCTTGGACAAGAAGAA G	cPCR to confirm integration of the left flank of genetic constructs in psbH locus
HomPCR_Confirm	psbH locus	GTAGTGAAGGTCGTCATTCTAC	cPCR to confirm integration of the

irm_05	right flank mScarlet-I fw		right flank of the mScarlet-I construct in psbH locus
HomPCR_Conf irm_06	psbH locus right flank mScarlet-I rv	TAAGTAGGGTTCTCAGAGGC	cPCR to confirm integration of the right flank of the mScarlet-I construct in psbH locus
HomPCR_Conf irm_07	psbH locus right flank Nanoluc fw	CATATATATATACTTAATAGCTA CCATAGGC	cPCR to confirm integration of the right flank of the Nanoluc construct in psbH locus
HomPCR_Conf irm_08	psbH locus right flank Nanoluc rv	TAAGTAGGGTTCTCAGAGGC	cPCR to confirm integration of the right flank of the Nanoluc construct in psbH locus

Supplementary Table 7: List of Genbank Accession code per construct.

Plasmid Name	Genbank Accession code
pME_Cp_UAV_sfGFP	PX069915
pME_G_E_004_UAV_mScarlet-I	PX069916
pME_G_E_007_UAV_sfGFP_PaqCI	PX069914
pME_Cp_0_1_001_psbH_5'Hom_Cr	PX069917
pME_Cp_0_1_004_psbA_5'Hom_Cr	PX069918
pME_Cp_0_1_005_rbcl_5'Hom_Cr	PX069919
pME_Cp_0_1_007_petB_5'Hom_Cr	PX069920
pME_Cp_0_1_010_psbD_5'Hom_Cr	PX069921
pME_G_0_1_003_5C1RLF	PX069922
pME_G_0_1_005_5C1RSF	PX069923
pME_G_0_1_006_5C1SR	PX069924
pME_G_0_1_007_5C2LF	PX069925
pME_G_0_1_008_5C2SF	PX069926
pME_G_0_1_009_5C2SR	PX069927
pME_G_0_1_010_5C3LF	PX069928
pME_G_0_1_011_5C3SF	PX069929
pME_G_0_1_012_5C3SR	PX069930
pME_G_0_1_013_5C5LF	PX069931
pME_G_0_1_014_5C5SF	PX069932
pME_G_0_1_015_5C5SR	PX069933
pME_G_0_1_016_5C7LF	PX069934
pME_G_0_1_017_5C7SF	PX069935
pME_G_0_1_019_5C7OSR	PX069936
pME_G_0_1_022_5C4SF	PX069937
pME_G_0_1_023_5C6SF	PX069938
pME_G_0_1-2_001_OC5'1	PX171811
pME_G_0_1-2_002_OC5'2	PX171812
pME_G_0_1-2_003_OC5'3	PX171813
pME_G_0_1-2_004_OC5'4	PX171814
pME_G_0_1-2_005_OC5'5	PX171815

pME_G_0_1-2_006_OC5'6	PX171816
pME_G_0_1-2_007_OC5'7	PX171817
pME_B_0_2_020_Pdummy	PX171457
pME_Cp_0_2_001_rrn16_prom_Cr	PX171467
pME_Cp_0_2_003_psaA2_prom_Cr	PX171468
pME_Cp_0_2_004_rrn16_prom_short_Cr	PX171469
pME_Cp_0_2_057_Synthetic_promoter_01	PX171470
pME_Cp_0_2_058_Synthetic_promoter_02	PX171471
pME_Cp_0_2_059_Synthetic_promoter_03	PX171472
pME_Cp_0_2_060_Synthetic_promoter_04	PX171473
pME_Cp_0_2_061_Synthetic_promoter_05	PX171474
pME_Cp_0_2_062_Synthetic_promoter_06	PX171475
pME_Cp_0_2_063_Synthetic_promoter_07	PX171476
pME_Cp_0_2_064_Synthetic_promoter_08	PX171477
pME_Cp_0_2_065_Synthetic_promoter_09	PX171478
pME_Cp_0_2_066_Synthetic_promoter_10	PX171479
pME_Cp_0_2_067_Synthetic_promoter_11	PX171480
pME_Cp_0_2_068_Synthetic_promoter_12	PX171481
pME_Cp_0_2_069_Synthetic_promoter_13	PX171482
pME_Cp_0_2_070_Synthetic_promoter_14	PX171483
pME_Cp_0_2_071_Synthetic_promoter_15	PX171484
pME_Cp_0_2_072_Synthetic_promoter_16	PX171485
pME_Cp_0_2_073_Synthetic_promoter_17	PX171486
pME_Cp_0_2_074_Synthetic_promoter_18	PX171487
pME_Cp_0_2_075_Synthetic_promoter_19	PX171488
pME_Cp_0_2_076_Synthetic_promoter_20	PX171489
pME_Cp_0_2_077_Synthetic_promoter_21	PX171490
pME_Cp_0_2_078_Synthetic_promoter_22	PX171491
pME_Cp_0_2_079_rbcL_promoter_Cr	PX171492
pME_Cp_0_2_080_tRNA_Glu2_promoter_Cr	PX171493
pME_Cp_0_2_081_Wendyll_promoter_Cr	PX171494
pME_G_0_2_001_Promoter_placeholder	PX171819
pME_Cp_0_2-3_001_psbD_Prom_5UTR_Cr	PX171460
pME_Cp_0_2-3_002_rbcL_Prom_5UTR_Cr	PX171461
pME_Cp_0_2-3_003_atpA_Prom_5UTR_Cr	PX171462
pME_Cp_0_2-3_004_psbA_Prom_5UTR_Cr	PX171463
pME_G_0_2-3_005_Placeholder	PX171818
pME_Cp_0_2-3a_002_psbD_Prom_5'UTR_Cr	PX171464
pME_Cp_0_2-3a_003_rbcL_Prom_5'UTR_Cr	PX171465
pME_Cp_0_2-3a_004_atpA_Prom_5UTR_Cr	PX171466
pME_B_0_3_009_5'UTR_dummy	PX171458
pME_Cp_0_3_001_atpA_5'UTR_Cr	PX171495
pME_Cp_0_3_002_atpA_5'UTR_Cr	PX171496
pME_Cp_0_3_003_atpB_5'UTR_Cr	PX171497

pME_Cp_0_3_004_chlL_5'UTR_Cr	PX171498
pME_Cp_0_3_005_petB_5'UTR_Cr	PX171499
pME_Cp_0_3_006_psaA_5'UTR_Cr	PX171500
pME_Cp_0_3_007_psbA_5'UTR_Cr	PX171501
pME_Cp_0_3_008_psbE_5'UTR_Cr	PX171502
pME_Cp_0_3_009_psbF_5'UTR_Cr	PX171503
pME_Cp_0_3_010_psbK_5'UTR_Cr	PX171504
pME_Cp_0_3_011_petA_5'UTR_Cr	PX171505
pME_Cp_0_3_012_petD_5'UTR_Cr	PX171506
pME_Cp_0_3_013_psaB_5'UTR_Cr	PX171507
pME_Cp_0_3_014_psbB_5'UTR_Cr	PX171508
pME_Cp_0_3_015_psbC_5'UTR_Cr	PX171509
pME_Cp_0_3_016_gene10_5'UTR_T7	PX171510
pME_Cp_0_3_017_ccsA_5'UTR_Cr	PX171511
pME_Cp_0_3_018_psaC_5'UTR_Cr	PX171512
pME_Cp_0_3_019_rbcL_5'UTR_Cr	PX171513
pME_Cp_0_3_020_rpoC1_5'UTR_Cr	PX171514
pME_Cp_0_3_021_rpoC2_5'UTR_Cr	PX171515
pME_Cp_0_3_023_tufA_5'UTR_Cr	PX171516
pME_Cp_0_3_024_clpP_5'UTR_Cr	PX171517
pME_Cp_0_3_025_rpl23_5'UTR_Cr	PX171518
pME_Cp_0_3_026_rpl16_5'UTR_Cr	PX171519
pME_Cp_0_3_027_rpoB1_5'UTR_Cr	PX171520
pME_Cp_0_3_030_atpH_5'UTR_Cr	PX171521
pME_Cp_0_3_031_psbD_5'UTR_Cr	PX171522
pME_Cp_0_3_032_rbcL_5'UTR-full_Nt	PX171523
pME_Cp_0_3_033_Synthetic_5'UTR_1_Sy	PX171524
pME_Cp_0_3_039_atpH_5'UTR_Nt	PX171525
pME_Cp_0_3_061_gene10v2_5'UTR_T7	PX171526
pME_Cp_0_3_064_psbA_5'UTR_Nt	PX171527
pME_Cp_0_3_065_psbC_5'UTR_Nt	PX171528
pME_Cp_0_3_091_Synthetic_5'UTR_2_Sy	PX171529
pME_Cp_0_3_092_Synthetic_5'UTR_3_Sy	PX171530
pME_Cp_0_3_093_Synthetic_5'UTR_4_Sy	PX171531
pME_Cp_0_3_094_Synthetic_5'UTR_5_Sy	PX171532
pME_G_0_3_001_5'UTR_Placeholder	PX171820
pME_Cp_0_3a_001_gene10_5'UTR_T7	PX171533
pME_Cp_0_3a_002_petA_5'UTR_Cr	PX171534
pME_Cp_0_3a_003_psaA_5'UTR_Cr	PX171535
pME_Cp_0_3a_004_psbE_5'UTR_Cr	PX171536
pME_Cp_0_3a_005_rbcL_5'UTR_Cr	PX171537
pME_Cp_0_3a_006_atpE-ycf12_IEE_Cr	PX171538
pME_Cp_0_3a_007_rps14-rps7_IEE_Cr	PX171539
pME_Cp_0_3a_008_psbE-rps9_IEE_Cr	PX171540

pME_Cp_0_3a_009_ycf4-ycf3_IEE_Cr	PX171541
pME_Cp_0_3a_010_tscA-chlN_IEE_Cr	PX171542
pME_Cp_0_3a_011_psbC_5'UTR_Cr	PX171543
pME_G_0_3a_001_Placeholder	PX171821
pME_Cp_0_3b_024_His-Tag	PX171544
pME_Cp_0_3b_025_Hibit-tag	PX171545
pME_Cp_0_3b_026_Flag-tag	PX171546
pME_Cp_0_3b_027_HA-tag	PX171547
pME_Cp_0_3b_028_myc-tag	PX171548
pME_Cp_0_3b_029_mScarlet-I	PX171549
pME_Cp_0_3b_030_mCerulean	PX171550
pME_Cp_0_3b_031_mVenus	PX171551
pME_G_0_3b_0002_Placeholder	PX171822
pME_Cp_0_3IEE_001_atpE-ycf12_IEE_Cr	PX171552
pME_Cp_0_3IEE_003_chlL-rpl36_IEE_Cr	PX171553
pME_Cp_0_3IEE_004_petG-rps3_IEE_Cr	PX171554
pME_Cp_0_3IEE_005_psaC-petL_IEE_Cr	PX171555
pME_Cp_0_3IEE_007_psbB-psbT_IEE_Cr	PX171556
pME_Cp_0_3IEE_008_psbE-rps9_IEE_Cr	PX171557
pME_Cp_0_3IEE_009_psbF-psbL_IEE_Cr	PX171558
pME_Cp_0_3IEE_010_psbJ-atpI_IEE_Cr	PX171559
pME_Cp_0_3IEE_013_rpl2-rps19_IEE_Cr	PX171560
pME_Cp_0_3IEE_015_rpl23-rpl2_IEE_Cr	PX171561
pME_Cp_0_3IEE_018_rps14-rps7_IEE_Cr	PX171562
pME_Cp_0_3IEE_019_rps18-rps2_IEE_Cr	PX171563
pME_Cp_0_3IEE_020_trnF-psaC_IEE_Cr	PX171564
pME_Cp_0_3IEE_021_ycf3-rps18_IEE_Cr	PX171565
pME_Cp_0_3IEE_022_ycf4-ycf3_IEE_Cr	PX171566
pME_Cp_0_3IEE_023_tscA-chlN_IEE5_Cr	PX171567
pME_Cp_0_4_001_Nanoluc	PX171568
pME_Cp_0_4_005_aadA	PX171569
pME_Cp_0_4_006_mScarlet	PX171570
pME_Cp_0_4_007_mScarlet-I	PX171571
pME_Cp_0_4_008_tdTomato	PX171572
pME_Cp_0_4_009_mVenus	PX171573
pME_Cp_0_4_010_mCerulean3	PX171574
pME_Cp_0_4_011_iLov	PX171575
pME_Cp_0_4_012_FlucS284T	PX171576
pME_Cp_0_4_022_aac6-aph2-marker	PX171577
pME_Cp_0_4_023_ptxD-marker	PX171578
pME_Cp_0_4_024_CrCD-negative-marker	PX171579
pME_Cp_0_4_026_Arg9-marker	PX171580
pME_Cp_0_4_033_Firefly-luciferase_v2	PX171581
pME_Cp_0_4_034_aadA	PX171582

pME_Cp_0_4_035_aphA6	PX171583
pME_G_0_4_001_CDS_Placeholder	PX171823
pME_B_0_5_012_3'UTR_dummy	PX171459
pME_Cp_0_5_001_psbA_3'UTR_Cr	PX171584
pME_Cp_0_5_005_rrnB_3'UTR_Ec	PX171585
pME_Cp_0_5_006_psbA_3'UTR_Nt	PX171586
pME_Cp_0_5_007_atpA_3'UTR_Cr	PX171587
pME_Cp_0_5_009_rbcl_3'UTR_rbcl-CDS_Cr	PX171588
pME_Cp_0_5_010_atpB_3'UTR_Cr	PX171589
pME_Cp_0_5_011_chlB_3'UTR_Cr	PX171590
pME_Cp_0_5_012_clpP_3'UTR_Cr	PX171591
pME_Cp_0_5_013_ftsH_3'UTR_Cr	PX171592
pME_Cp_0_5_015_petA_3'UTR_Cr	PX171593
pME_Cp_0_5_017_petD_3'UTR_Cr	PX171594
pME_Cp_0_5_018_petL_3'UTR_Cr	PX171595
pME_Cp_0_5_019_psaB_3'UTR_Cr	PX171596
pME_Cp_0_5_020_psaC_3'UTR_Cr	PX171597
pME_Cp_0_5_021_psbA_3'UTR_Cr	PX171598
pME_Cp_0_5_022_psbC_3'UTR_Cr	PX171599
pME_Cp_0_5_026_rbcl_3'UTR_Cr	PX171600
pME_Cp_0_5_028_rpl36_3'UTR_Cr	PX171601
pME_Cp_0_5_030_rpoB2_3'UTR_Cr	PX171602
pME_Cp_0_5_031_rpoC2_3'UTR_Cr	PX171603
pME_Cp_0_5_032_rps2_3'UTR_Cr	PX171604
pME_Cp_0_5_034_rps4_3'UTR_Cr	PX171605
pME_Cp_0_5_035_rps8_3'UTR_Cr	PX171606
pME_Cp_0_5_036_rps11_3'UTR_Cr	PX171607
pME_Cp_0_5_038_rps19_3'UTR_Cr	PX171608
pME_Cp_0_5_039_tufA_3'UTR_Cr	PX171609
pME_Cp_0_5_040_ycf1_3'UTR_Cr	PX171610
pME_Cp_0_5_041_ycf12_3'UTR_Cr	PX171611
pME_Cp_0_5_042_rbcl_3'UTR_Nt	PX171612
pME_Cp_0_5_043_BMV_3'UTR_Bv	PX171613
pME_Cp_0_5_044_TYMV_3'UTR_Tv	PX171614
pME_Cp_0_5_045_rpoA_3'UTR_Nt	PX171615
pME_Cp_0_5_046_petD_3'UTR_Nt	PX171616
pME_Cp_0_5_047_TMV_3'UTR_Tv	PX171617
pME_Cp_0_5_048_psaC_3'UTR_Nt	PX171618
pME_G_0_5_001_3'UTR_Placeholder	PX171831
pME_G_0_5-6_006_OC3'1	PX171824
pME_G_0_5-6_007_OC3'2	PX171825
pME_G_0_5-6_008_OC3'3	PX171826
pME_G_0_5-6_009_OC3'4	PX171827
pME_G_0_5-6_010_OC3'5	PX171828

pME_G_0_5-6_011_OC3'6	PX171829
pME_G_0_5-6_012_OC3'7	PX171830
pME_Cp_0_5a_002_His-tag	PX171619
pME_Cp_0_5a_003_Hibit-tag	PX171620
pME_Cp_0_5a_004_Flag-tag	PX171621
pME_Cp_0_5a_005_HA-tag	PX171622
pME_Cp_0_5a_006_myc-tag	PX171623
pME_Cp_0_5a_007_mScarlet-I	PX171624
pME_Cp_0_5b_001_psbA_3'UTR_Cr	PX171625
pME_Cp_0_5b_002_atpB_3'UTR_Cr	PX171626
pME_Cp_0_5b_003_petL_3'UTR_Cr	PX171627
pME_Cp_0_5b_004_psbA_3'UTR_Nt	PX171628
pME_Cp_0_5b_005_TMV_3'UTR_Tv	PX171629
pME_Cp_0_5b_006_ftsH_3'UTR_Cr	PX171630
pME_Cp_0_6_005_psbH_3'Hom_Cr	PX171631
pME_Cp_0_6_006_psbH_5'Hom_rev_Cr	PX171632
pME_Cp_0_6_007_psbA_3'Hom_Cr	PX171633
pME_Cp_0_6_009_rbcL_3'Hom_Cr	PX171634
pME_Cp_0_6_013_petB_3'Hom_Cr	PX171635
pME_Cp_0_6_019_psbD_3'Hom_Cr	PX171636
pME_Cp_0_6_020_psbA_5'Hom_rev_Cr	PX171637
pME_Cp_0_6_021_petB_5'Hom_rev_Cr	PX171638
pME_Cp_0_6_022_rbcL_5'Hom_rev_Cr	PX171639
pME_Cp_0_6_023_psbD_5'Hom_rev_Cr	PX171640
pME_G_0_6_004_3C1LR	PX171832
pME_G_0_6_006_3C1SR	PX171833
pME_G_0_6_008_3C2LR	PX171834
pME_G_0_6_009_3C2SR	PX171835
pME_G_0_6_011_3C3LR	PX171836
pME_G_0_6_012_3C3SR	PX171837
pME_G_0_6_014_3C5LR	PX171838
pME_G_0_6_015_3C5SR	PX171839
pME_G_0_6_018_3C7LR	PX171840
pME_G_0_6_019_3C7SR	PX171841
pME_G_0_6_021_3C1SF	PX171842
pME_G_0_6_022_3C2SF	PX171843
pME_G_0_6_023_3C3SF	PX171844
pME_G_0_6_024_3C4SF	PX171845
pME_G_0_6_025_3C5SF	PX171846
pME_G_0_6_026_3C6SF	PX171847
pME_G_0_6_027_3C7SF	PX171848
pME_Cp_0_7-8_003_Amp_ColE1_mScarlet	PX171641
pME_Cp_0_7-8_004_Amp_ColE1_sfGFP	PX171642
pME_Cp_0_7-8_005_Kan_ColE1_mScarlet	PX171643

pME_Cp_0_7-8_006_Kan_CoIE1_sfGFP	PX171644
pME_Cp_2_001_Promoter_PH_Meas_construct	PX171645
pME_Cp_2_002_5'UTR_PH_Meas_construct	PX171646
pME_Cp_2_003_3'UTR_PH_Meas_construct	PX171647
pME_Cp_2_005_atpA_5'UTR_Cr_Meas_construct	PX171648
pME_Cp_2_006_atpB_5'UTR_Cr_Meas_construct	PX171649
pME_Cp_2_007_chlL_5'UTR_Cr_Meas_construct	PX171650
pME_Cp_2_008_petB_5'UTR_Cr_Meas_construct	PX171651
pME_Cp_2_009_psaA_5'UTR_Cr_Meas_construct	PX171652
pME_Cp_2_010_psbA_5'UTR_Cr_Meas_construct	PX171653
pME_Cp_2_011_psbE_5'UTR_Cr_Meas_construct	PX171654
pME_Cp_2_012_psbF_5'UTR_Cr_Meas_construct	PX171655
pME_Cp_2_013_psbK_5'UTR_Cr_Meas_construct	PX171656
pME_Cp_2_014_petA_5'UTR_Meas_construct	PX171657
pME_Cp_2_015_petD_5'UTR_Meas_construct	PX171658
pME_Cp_2_016_psaB_5'UTR_Cr_Meas_construct	PX171659
pME_Cp_2_017_psbB_5'UTR_Cr_Meas_construct	PX171660
pME_Cp_2_018_psbC_5'UTR_Cr_Meas_construct	PX171661
pME_Cp_2_019_gene10_5'UTR_T7_Meas_construct	PX171662
pME_Cp_2_020_ccsA_5'UTR_Cr_Meas_construct	PX171663
pME_Cp_2_021_psaC_5'UTR_Cr_Meas_construct	PX171664
pME_Cp_2_022_rbcL_5'UTR_Cr_Meas_construct	PX171665
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pME_Cp_2_029_rpoB1_5'UTR_Cr_Meas_construct	PX171672
pME_Cp_2_030_atpH_5'UTR_Cr_Meas_construct	PX171673
pME_Cp_2_031_psbD_5'UTR_Cr_Meas_construct	PX171674
pME_Cp_2_032_rbcL_5'UTR_Nt_Meas_construct	PX171675
pME_Cp_2_033_Synthetic_5'UTR_Meas_construct	PX171676
pME_Cp_2_034_atpH_5'UTR_Nt_Meas_construct	PX171677
pME_Cp_2_035_gene10_5'UTR_v2_T7_Meas_construct	PX171678
pME_Cp_2_036_psbA_5'UTR_Nt_Measurment_construct	PX171679
pME_Cp_2_037_psbC_5'UTR_Nt_Meas_construct	PX171680
pME_Cp_2_038_5'UTR_Dummy_Meas_construct	PX171681
pME_Cp_2_039_psbA_3'UTR_Cr_Meas_construct	PX171682
pME_Cp_2_040_rrnB_3'UTR_Ec_Meas_construct	PX171683
pME_Cp_2_041_psbA_3'UTR_Nt_Meas_construct	PX171684
pME_Cp_2_042_atpA_3'UTR_Cr_Meas_construct	PX171685
pME_Cp_2_043_rbcL_3'UTR_CDS_Cr_Meas_construct	PX171686
pME_Cp_2_044_atpB_3'UTR_Cr_Meas_construct	PX171687

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pME_Cp_2_047_ftsH_3'UTR_Cr_Meas_construct	PX171690
pME_Cp_2_048_petA_3'UTR_Cr_Meas_construct	PX171691
pME_Cp_2_049_petD_3'UTR_Cr_Meas_construct	PX171692
pME_Cp_2_050_petL_3'UTR_Cr_Meas_construct	PX171693
pME_Cp_2_051_psaB_3'UTR_Cr_Meas_construct	PX171694
pME_Cp_2_052_psaC_3'UTR_Cr_Meas_construct	PX171695
pME_Cp_2_053_psbA_3'UTR_Cr_Meas_construct	PX171696
pME_Cp_2_054_psbC_3'UTR_Cr_Meas_construct	PX171697
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pME_Cp_2_060_rps2_3'UTR_Cr_Meas_construct	PX171703
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pME_Cp_2_063_rps19_3'UTR_Cr_Meas_construct	PX171706
pME_Cp_2_064_tufA_3'UTR_Cr_Meas_construct	PX171707
pME_Cp_2_065_ycf1_3'UTR_Cr_Meas_construct	PX171708
pME_Cp_2_066_ycf12_3'UTR_Cr_Meas_construct	PX171709
pME_Cp_2_067_rbcL_3'UTR_Nt_Meas_construct	PX171710
pME_Cp_2_068_BMV_3'UTR_Meas_construct	PX171711
pME_Cp_2_069_TYMV_3'UTR_Meas_construct	PX171712
pME_Cp_2_070_rpoA_3'UTR_Nt_Meas_construct	PX171713
pME_Cp_2_071_petD_3'UTR_Cr_Meas_construct	PX171714
pME_Cp_2_072_TMV_3'UTR_Meas_construct	PX171715
pME_Cp_2_073_psaC_3'UTR_Nt_Meas_construct	PX171716
pME_Cp_2_074_3'UTR_Dummy_Meas_construct	PX171717
pME_Cp_2_097_mScarlet-I_Meas_construct	PX171718
pME_Cp_2_098_CDS_PH_Meas_construct	PX171719
pME_Cp_2_100_tdTomato_Meas_construct	PX171720
pME_Cp_2_101_mVenus_Meas_construct	PX171721
pME_Cp_2_120_Fluc_Meas_construct	PX171722
pME_Cp_2_121_Syn_Prom_01_Meas_construct	PX171723
pME_Cp_2_122_Syn_Prom_02_Meas_construct	PX171724
pME_Cp_2_123_Syn_Prom_03_Meas_construct	PX171725
pME_Cp_2_124_Syn_Prom_04_Meas_construct	PX171726
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pME_Cp_2_129_Syn_Prom_09_Meas_construct	PX171731

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pME_Cp_2_132_Syn_Prom_12_Meas_construct	PX171734
pME_Cp_2_133_Syn_Prom_13_Meas_construct	PX171735
pME_Cp_2_134_Syn_Prom_14_Meas_construct	PX171736
pME_Cp_2_135_Syn_Prom_15_Meas_construct	PX171737
pME_Cp_2_136_Syn_Prom_16_Meas_construct	PX171738
pME_Cp_2_137_Syn_Prom_17_Meas_construct	PX171739
pME_Cp_2_138_Syn_Prom_18_Meas_construct	PX171740
pME_Cp_2_139_Syn_Prom_19_Meas_construct	PX171741
pME_Cp_2_140_Syn_Prom_20_Meas_construct	PX171742
pME_Cp_2_141_Syn_Prom_21_Meas_construct	PX171743
pME_Cp_2_142_Syn_Prom_22_Meas_construct	PX171744
pME_Cp_2_143_rbcL_Prom_Cr_Meas_construct	PX171745
pME_Cp_2_144_trnA_Glu2_Prom_Cr_Meas_construct	PX171746
pME_Cp_2_145_Wendyll_Prom_Cr_Meas_construct	PX171747
pME_Cp_2_146_IEE_Meas_construct	PX171748
pME_Cp_2_148_Prom_Dummy_Meas_construct	PX171749
pME_Cp_2_151_5'UTR_Dummy_IEE_Meas_construct	PX171750
pME_Cp_2_152_atpE-ycf12_IEE_Cr_IEE_Meas_construct	PX171751
pME_Cp_2_153_chlL-rpl36_IEE_Cr_IEE_Meas_construct	PX171752
pME_Cp_2_154_petG-rps3_IEE_Cr_IEE_Meas_construct	PX171753
pME_Cp_2_155_psbB-psbT_IEE_Cr_IEE_Meas_construct	PX171754
pME_Cp_2_156_psbE-rps9_IEE_Cr_IEE_Meas_construct	PX171755
pME_Cp_2_157_psbF-psbL_IEE_Cr_IEE_Meas_construct	PX171756
pME_Cp_2_158_psbJ-atpI_IEE_Cr_IEE_Meas_construct	PX171757
pME_Cp_2_159_rpl2-rps19_IEE_Cr_IEE_Meas_construct	PX171758
pME_Cp_2_160_rpl23-rpl2_IEE_Cr_IEE_Meas_construct	PX171759
pME_Cp_2_161_rps14-rps7_IEE_Cr_IEE_Meas_construct	PX171760
pME_Cp_2_162_rps18-rps2_IEE_Cr_IEE_Meas_construct	PX171761
pME_Cp_2_163_trnF-psaC_IEE_Cr_IEE_Meas_construct	PX171762
pME_Cp_2_164_ycf3-rps18_IEE_Cr_IEE_Meas_construct	PX171763
pME_Cp_2_165_ycf4-ycf3_IEE_Cr_IEE_Meas_construct	PX171764
pME_Cp_2_166_tscA-chlN_IEE5_Cr_IEE_Meas_construct	PX171765
pME_Cp_2_185_mScarlet-I_His-tag	PX171766
pME_Cp_2_186_mScarlet-I_Hibit-tag	PX171767
pME_Cp_2_187_mScarlet-I_Flag-tag	PX171768
pME_Cp_2_188_mScarlet-I_HA-tag	PX171769
pME_Cp_2_189_mScarlet-I_c-Myc-tag	PX171770
pME_Cp_2_295_Tobra_test_construct	PX171771
pME_Cp_2_296_Arg_test_construct	PX171772
pME_Cp_2_297_PtxD_test_construct	PX171773
pME_Cp_2_298_mCerulean_Meas_construct	PX171774
pME_Cp_2_299_Psyn15_5'psbF_3'rps8_psbH_locus	PX171775

pME_Cp_2_300_Psyn22_5'rpoC1_3'petD_psbH_locus	PX171776
pME_Cp_2_301_Psyn9_5'rbcl_3'petA_psbH_locus	PX171777
pME_Cp_2_302_Psyn5_5'psbD_3'petL_psbH_locus	PX171778
pME_Cp_2_303_PrbcL_5'psaC_3'rps2_psbH_locus	PX171779
pME_Cp_2_304_PpsaA2_5'psaB_3'ycf12_psbH_locus	PX171780
pME_Cp_2_305_Psyn17_5'clpP_3'TMV_psbH_locus	PX171781
pME_Cp_2_306_Psyn2_5'psbE_3'atpB_psbH_locus	PX171782
pME_Cp_2_307_PGlu2_5'psbK_3'tufA_psbH_locus	PX171783
pME_Cp_2_308_PWendyll_5'psbC_3'ftsH_psbH_locus	PX171784
pME_Cp_2_309_Prrn16_5'psaA_3'psbA_psbH_locus	PX171785
pME_Cp_2_310_Psyn7_5'clpP_3'rps11_psbH_locus	PX171786
pME_Cp_2_311_Psyn9_5'clpP_3'rps11_psbH_locus	PX171787
pME_Cp_2_312_Prrn16_5'clpP_3'rps11_psbH_locus	PX171788
pME_Cp_2_312_Psyn7_5'clpP_3'rrnB_psbH_locus	PX171789
pME_Cp_2_313_Psyn7_5'petD_3'rrnB_psbH_locus	PX171790
pME_Cp_2_314_Psyn7_5'psaA_3'rrnB_psbH_locus	PX171791
pME_Cp_2_315_Prrn16_5'clpP_3'rrnB_psbH_locus	PX171792
pME_Cp_2_316_Prrn16_5'clpP_3'psbA_psbH_locus	PX171793
pME_Cp_2_317_PWendyll_5'clpP_3'petA_psbH_locus	PX171794
pME_Cp_2_318_Psyn9_5'psbC_3'petA_psbH_locus	PX171795
pME_Cp_2_319_PWendyll_5'psbC_3'rps11_psbH_locus	PX171796
pME_Cp_2_320_PWendyll_5'psbC_3'petA_psbH_locus	PX171797
pME_Cp_2_321_PWendyll_5'clpP_3'petA_rbcL_locus	PX171798
pME_Cp_2_322_Psyn9_5'psbC_3'petA_rbcL_locus	PX171799
pME_Cp_2_323_PWendyll_5'psbC_3'rps11_rbcL_locus	PX171800
pME_Cp_2_324_PWendyll_5'psbC_3'petA_rbcL_locus	PX171801
pME_Cp_2_325_PWendyll_5'clpP_3'petA_psbD_locus	PX171802
pME_Cp_2_326_Psyn9_5'psbC_3'petA_psbD_locus	PX171803
pME_Cp_2_327_PWendyll_5'psbC_3'rps11_psbD_locus	PX171804
pME_Cp_2_328_PWendyll_5'psbC_3'petA_psbD_locus	PX171805
pME_Cp_2_329_PWendyll_5'clpP_3'petA_petB_locus	PX171806
pME_Cp_2_330_Psyn9_5'psbC_3'petA_petB_locus	PX171807
pME_Cp_2_332_PWendyll_5'psbC_3'petA_petB_locus	PX171808
pME_Cp_2_333_PWendyll_5'psbC_3'rps11_petB_locus	PX171809
pME_Cp_2_334_South_Pathway	PX171810

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