Birth of a Photosynthetic Chassis: A MoClo Toolkit Enabling Synthetic Biology in the Microalga Chlamydomonas reinhardtii

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Abstract

Microalgae are regarded as promising organisms to develop innovative concepts based on their photosynthetic capacity that offers more sustainable production than heterotrophic hosts. However, to realize their potential as green cell factories, a major challenge is to make microalgae easier to engineer. A promising approach for rapid and predictable genetic manipulation is to use standardized synthetic biology tools and workflows. To this end we have developed a Modular Cloning toolkit for the green microalga *Chlamydomonas reinhardtii*. It is based on Golden Gate cloning with standard syntax, and comprises 119 openly distributed genetic parts, most of which have been functionally validated in several strains. It contains promoters, UTRs, terminators, tags, reporters, antibiotic resistance genes, and introns cloned in various positions to allow maximum modularity. The toolkit enables rapid building of engineered cells for both fundamental research and algal biotechnology. This work will make *Chlamydomonas* the next chassis for sustainable synthetic biology.

Keywords: Algal biotechnology, *Chlamydomonas reinhardtii*, modular cloning, synthetic biology.

There is an urgent need to decarbonize the world economy due to depletion of fossil fuel reserves coupled with accumulation of greenhouse gases produced by their combustion. One alternative to the use of fossil fuels is to use photosynthetic microorganisms, such as microalgae, as green cell factories to produce fuels and chemicals from atmospheric CO_2 in a sustainable process driven by sunlight[1, 2]. The fixed carbon can be redirected towards compounds that can be used in the fuel, food, cosmetic and pharmaceutical industries, such as proteins, alcohols, alkanes, lipids, sugars, pigments or terpenes[3-5]. By contrast with land plant-based photoproduction, microalgae do not compete with agriculture and can be grown at high yields even at large scale[4, 6], including on waste streams, thus minimizing inputs[3]. The green microalga *Chlamydomonas reinhardtii* (referred to hereafter as "Chlamydomonas") has been extensively engineered for basic research and industrial biotechnology[4, 6-8]. Its nuclear and organellar genomes are sequenced and annotated, molecular biology techniques and culture conditions are highly developed, and its physiology and metabolism are well understood[9-13]. Moreover, the metabolic plasticity and cellular compartments of Chlamydomonas offer great potential for advanced metabolic engineering strategies[14, 15]. Chlamydomonas has already been engineered for production of the biodiesel precursor bisabolene[8], the terpene patchoulol[7], and recombinant proteins as well as enzymes such as an HIV antigen[16] and xylanase[17]. Despite these proofs of concept however, engineering of Chlamydomonas is still slow due to a lack of standardized resources and tools[11]. Development of the field of algal synthetic biology offers the means to enable design and construction of microalgal cells with defined and predictable properties[18]. Besides biotechnological applications, the transition from empirical to synthetic approaches also provides the opportunity to answer fundamental biological questions using new concepts and approaches based on understanding by construction rather than deconstruction.

Synthetic biology approaches, predicated on the Design-Build-Test-Learn cycle[19], make organisms easier to engineer through the use of standardized parts and their assembly to simplify the building of designed DNA molecules[19]. Among available standards[20], the Golden Gate Modular Cloning (MoClo) technology, based on Type IIS restriction enzymes, offers extensive standardization and allows the assembly of complex multigenic DNA from basic gene parts (*e.g.* promoters, CDS, terminators) in just two steps[21, 22]. The method accelerates and multiplies the possibilities to permute multiple genetic elements, and makes facile the building of multigene constructs for full metabolic pathways[23]. MoClo is efficient and versatile, but relies on intensive upfront generation of a standardized library of basic building blocks, the gene parts, that have been domesticated to remove Type IIS sites, and codon optimized for the host as appropriate. MoClo toolkits have already been developed for a few model organisms[24-29] although not yet for microalgae.

Here, we report the generation of a MoClo toolkit composed of more than 100 gene parts codon-optimized for the Chlamydomonas nuclear genome. These genetic parts were designed to provide maximum modularity to end-users, and to facilitate the development of engineered strains for fundamental and green biotechnological applications, through iterative design and testing. We provide functional validation and characterization of many gene parts in several Chlamydomonas strains. This kit is available to the community, to allow Chlamydomonas to become the next chassis for sustainable synthetic biology approaches.

RESULTS

Standard and content of the Chlamydomonas MoClo kit

Standardization is the key to efficient building. The Chlamydomonas MoClo kit adopts the syntax proposed by the plant synthetic biology community including the OpenPlant

Consortium[30] (Fig. 1). This syntax is defined for level 0 plasmids containing standard gene parts (promoters, coding sequences, untranslated regions, etc.) and assigns strict fusion sites for 10 cloning positions. In a single step, standardized parts can be assembled into modules (Transcriptional Unit, TU, level 1) and modules into devices (multigenic construct, level M or 2) according to the original MoClo syntax[22] (Supplementary Fig. 1). Our Chlamydomonas MoClo toolkit is composed of a set of 119 parts representing 67 unique genetic elements available at different positions within the standard, thereby providing maximum modularity to designers (Fig. 1, Fig. 2). The kit recapitulates most of the standard genetic elements previously developed for Chlamydomonas which we "domesticated" by removing *Bpi*I and *Bsa*I restriction sites (the two enzymes used by the MoClo strategy[22], Supplemental Figure 1) from their sequences by DNA synthesis or PCR-based mutagenesis. The available gene parts encompass 7 promoters coupled or not to their original 5'UTR, the corresponding 5'UTR and the *CrTHI4* riboswitch, 8 immunological or purification tags in positions leading to N- or C-terminal translational fusions, 9 signal and targeting peptides, 12 reporters, 5 antibiotic resistance genes, the foot and mouth virus (FMDV) 2A peptide which allows expression of two or more proteins from a single transcriptional unit[17, 31, 32], 2 micro RNA (miRNA) backbones and associated controls, and six 3'UTR-terminators (Fig. 1b, Fig. 2 and Supplementary Table 1). All sequences and plasmids are available through the public Addgene repository (http://www.addgene.org/).

Constitutive promoters and reporter genes

Five antibiotic resistance genes are used as selectable markers for Chlamydomonas but also can function as reporter genes[33, 34]. We assembled three modules that allow control of the expression of the *aadA* gene, conferring spectinomycin resistance, by three constitutive

promoters: P_{PSAD} and $P_{\beta TUB2}$ with or without the first intron of β*TUB2* (pCM1-1 to 3, Supplementary Table 3). The transformation efficiency of the three modules in UVM4[35] cells was estimated by counting spectinomycin resistant colonies and showed resistance frequencies within the same range (Fig. 3a). The presence of the first β*TUB2* intron significantly increased the transformation efficiency as previously observed with the presence of *RBCS2* introns in the *ble* marker[33, 36, 37]. Alternative reporters are bioluminescent proteins, which allow more sensitive and quantitative analysis of gene expression. The kit contains *Gaussia princeps* luciferase, the brightest luciferase established in Chlamydomonas[38], as well as the redesigned Nanoluciferase (NanoLuc) which provides a stable and strong luminescence signal[39]. Chlamydomonas NanoLuc was specifically developed for our MoClo kit through recoding to match the codon bias of Chlamydomonas, and cloned at 6 different positions within the standard. This new part was first tested with the most widely used promoter/terminator combination (P_{AR} promoter / T_{RBCS2} terminator) for strong constitutive expression in Chlamydomonas. The corresponding module (pCM1-04) was assembled with another module conferring paromomycin resistance (Supplementary Fig. 2) into a device (pCMM-1) that was introduced into the genome of the D66 strain (CC-4425, Fig. 3b). Among paromomycin resistant colonies, 34.8% ± 8.3 (N=48, mean ± SEM) were luminescent. The signal was variable between clones due to genomic position effects[40, 41] but was linear from 50 to 5 x 10^5 cells (Fig. 3b and Supplementary Fig. 2). By contrast, non-expressing transformants (resistant to paromomycin only) or the D66 recipient strain displayed only a faint signal, 3 orders of magnitude lower, and saturating swiftly (Fig. 3b, inset). The modularity of the MoClo strategy allows rapid assessment of combinations of multiple parts. For example, we assembled 4 modules where NanoLuc expression is controlled by all possible combinations of the two most common constitutive promoters (P_{AR} and P_{PSAD}) and terminators (T_{RBCS2} and

T_{PSAD}) (Fig. 3b, pCM1-4 to 7, Supplementary Table 3). Each module was assembled with the paromomycin resistance module (pCMM-1 to 4, Supplementary Table 4) and introduced into the Chlamydomonas genome. Bioluminescence levels were averaged over hundreds of transformants to account for the genome position effect[40, 41]. The strengths of the two promoters were found to be comparable, whilst T_{PSAD} appeared to confer robust expression from both promoters, 10-fold higher than T_{RBCS2} (Fig. 3c). In a distinct context (strain, reporter sequence, culture conditions, etc.), the same genetic element may perform differently[31, 35]. Such context sensitivity can be overcome by taking advantage of the modularity of the Chlamydomonas MoClo kit, which allows for the rapid characterization of all possible parts combinations. These results also confirmed the performance of the Chlamydomonas NanoLuc reporter and its employability for detailed understanding and characterization of genetic circuits especially if coupled with automated cell-sorting microfluidic devices[42].

Control of gene expression

To build genetic circuits, the fine-tuning of gene expression is a prerequisite. Multiple parts enabling controlled gene expression have therefore been implemented. The activity of the P_{NIT1} promoter can be controlled by switching the nitrogen source since it is strongly repressed by ammonium and highly induced on nitrate[34, 43, 44]. A module where P_{NIT1} controls expression of the *ble-GFP* gene (pCM1-8) conferred strong zeocin resistance in the CC-1690 strain but only when ammonium was replaced by nitrate as nitrogen source. By contrast, the P_{PSAD} promoter (pCM1-9) conferred strong antibiotic resistance on both nitrogen sources (Fig. 4a and Supplementary Fig. 3a-c). The vitamin B_{12}-repressible promoter P_{METE}[45] allowed conditional functional complementation of the photosynthetic mutant *nac2-26* (CC-4421), which lacks photosystem II due to the absence of the TPR-like protein NAC2 required for

stability of the *psbD* mRNA encoding the D2 reaction center protein[46]. *nac2-26* mutant cells engineered with a module harboring the *NAC2* coding sequence under the control of the P_{METE} promoter (pCM1-10) could grow photoautotrophically in the absence of vitamin B_{12}, but growth was compromised by increasing its concentration by amounts as low as 5 ng/L (Fig. 4b).

Regulation of gene expression can also be controlled by vitamin B_1 (thiamine) at the level of the transcript through riboswitches[47, 48]. Binding of thiamine pyrophosphate to the *THI4* riboswitch (RS) results in alternative splicing and retention of an 81 bp upstream open reading frame, ultimately interfering with translation[47, 48]. The RS also responds when cells are grown in the presence of the thiamine biosynthetic intermediate 4-methyl-5-(2-hydroxyethyl) thiazole (HET), but not with 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP)[47]. A module combining P_{AR} and *THI4 (RS)* to drive expression of the *ble-GFP* gene (pCM1-11) conferred conditional zeocin sensitivity in the UVM4 strain[35]. Resistance was compromised by thiamine or HET but not HMP (Fig. 4c and Supplementary Fig. 3d), thereby demonstrating the efficient repression of the transgene through the *THI4* riboswitch.

Finally, to allow targeted repression of gene expression, a microRNA precursor sequence derived from the pre-miR1157 and used for the generation of artificial miRNAs (amiRNA)[49] was re-designed for compatibility with the Golden Gate cloning method. To demonstrate its effectiveness in driving gene repression, a specific amiRNA sequence directed against the *MAA7* gene, whose repression provides resistance to 5'-fluoroindole (5'-FI)[50], was inserted into the microRNA precursor. A control random sequence ("scrambled") amiRNA was inserted into the same backbone. These parts were placed under the control of P_{PSAD} and T_{PSAD} (pCM1-12 and 13) and assembled with a paromomycin resistance module (pCM1-27). The same amiRNA sequences were introduced into the previously established pChlamiRNA3 vector[49] as

controls. After transformation of the CC-1690 strain, 36% of paromomycin-resistant cells displayed resistance to 5'-FI with the device targeting *MAA7* (pCMM-5) but not with the scrambled amiRNA (pCMM-6) (Fig. 4d and Supplementary Fig. 3f). A modified 5' rapid amplification of cDNA ends (5'-RACE) assay revealed that the *MAA7* transcript was most frequently cleaved at a site corresponding to positions 10 and 11 of the amiRNA, as expected for a specific action of the miRNA (Fig. 4d). The properties of controllable parts can also be combined as shown for P_{NIT1} control of amiRNA-dependent gene repression[34]. An amiRNA strategy recently proved useful for concerted metabolic engineering of a biodiesel precursor in Chlamydomonas[8]. The versatility of the MoClo kit opens new possibilities for sophisticated metabolic engineering strategies, *e.g.* the specific downregulation of up to six target genes with one level M assembly.

Multiple fusion tags for detection and purification of gene products.

Protein fusion tags are indispensable tools used to improve protein expression yields, enable protein purification, and accelerate the characterization of protein structure and function[51]. Our MoClo kit includes multiple epitope and affinity tags known to be functional in Chlamydomonas. The modularity of the MoClo assembly allows rapid assessment of the best tagging strategy through a rapid design/build/test/learn cycle. We took advantage of the well characterized *rap2* mutant (Δ*FKBP12*), which is insensitive to rapamycin[52], to test the functionality of five tags (Fig. 5a,b). We designed and built 5 devices allowing strong constitutive expression of N- or C-terminal tagged FKBP12 coupled to a paromomycin module (pCMM-7 to 11, Fig. 5c-h and Supplementary Table 4). The engineered strains were selected on paromomycin and the functionality of the fusion protein was tested by assessing sensitivity to rapamycin. Protein extracts were probed by immunoblotting using FKBP12-specific and tag-

specific antibodies (Fig. 5d-h). All tags allowed detection (Fig. 5d-h) or purification (Fig. 5i) of FKBP12 even though some were not functional for restoring rapamycin sensitivity. The test revealed that pCMM-9 outperforms other devices since it provides a WT-like phenotype and expression level coupled to a strong and specific Myc signal with no significant processing of the protein. These results demonstrate the importance of the modularity provided by the Chlamydomonas MoClo toolkit for designing optimal fusion proteins.

Visualization and targeting of proteins in living cells

Fluorescent protein tags allow the temporal and spatial monitoring of dynamic expression patterns at cellular and subcellular scales[53]. Natural and synthetic metabolic pathways can be optimized through spatial organization since cell compartments offer many advantages, such as isolation of metabolic reactions and generation of concentration gradients[14]. In a eukaryotic chassis like Chlamydomonas, organelles such as microbodies, mitochondria and chloroplasts can be engineered to implement or improve metabolic pathways[15]. The Chlamydomonas MoClo kit includes 11 targeting and signal peptides that allow the targeting of fusion proteins to mitochondria, chloroplast, nucleus, secretory pathway, ER and peroxisome-like microbodies. The functionality of the targeting and signal peptides and of the five fluorescent proteins (mVenus - yellow, mCherry - red, mRuby2 - red, Clover - green, mCerrulean3 - cyan) included in the toolkit was tested. Eight modules (pCM1-19 to 26, Supplementary Table 3) combining diverse fluorescent proteins and targeting sequences were assembled into devices with an antibiotic resistance module (pCMM-12 to 19). All devices were found to behave as expected and provided the expected fluorescent signal in the targeted compartment (Fig. 6). The fluorescent and targeting parts of the Chlamydomonas MoClo toolkit, most of which have been validated here, enable engineering in the third dimension[14] *i.e.* isolation and

organization in multiple cellular compartments, and offer new tools for biological design/build/test cycles.

Discussion

The Chlamydomonas MoClo toolkit presented here provides more than 100 domesticated gene parts to allow advanced synthetic biology in microalgae. Numerous parts of multiple types have been characterized and validated in different genetic backgrounds[10] and culture conditions, and can be readily used for biological design without further development. With the efficiency and modularity of the MoClo strategy, molecular cloning is no longer a limiting step for engineering Chlamydomonas cells. Indeed, from design to building, a complex device of up to six different genes/modules can be obtained within a week using the standardized parts provided in our kit. The modularity will also enable combinatorial assembly by shuffling part libraries[54] and determine *a posteriori* which combination is the most relevant. The development of gene-editing technologies in Chlamydomonas, including Zinc-finger nucleases[55, 56] and several CRISPR-Cas9 approaches[55, 57-59], together with the development of high-throughput microfluidics[42] are beginning to gather pace. Coupling these resources to our standardized MoClo toolkit will facilitate the use of Chlamydomonas as the photosynthetic chassis for innovative synthetic biology approaches aimed at fundamental and biotechnological applications. We expect that the creativity of designers, released from the time constraints associated with classical cloning strategies, will allow rapid expansion of the standard gene parts, modules and devices through open distribution, notably using the Addgene repository. We invite the community to openly share their parts through Addgene and/or our consortium (contact M. Schroda). The development of the Chlamydomonas MoClo toolkit constitutes a complete step-change in the fields of microalgal biology and

biotechnology. The parts developed for the MoClo toolkit may also be employed in other microalgal species since the orthogonality of several Chlamydomonas transcriptional units has been demonstrated in multiple hosts, including the industrially relevant species *Chlorella ellipsoidea*, *Nannochloropsis sp.* and *Dunaliella salina*[60]. Synthetic approaches will allow engineering of microalgae in a predictable and efficient manner and thereby offer great potential to couple environmental protection, energy transition and bioeconomic growth[4].

Methods

All chemicals were obtained from Sigma-Aldrich, unless otherwise specified.

Escherichia coli and *Chlamydomonas reinhardtii* strains, transformation and growth conditions.

Bacterial growth was performed at 37°C in LB broth supplemented with agar (20% m/V), spectinomycin (50 µg/mL), ampicillin or carbenicillin (50 or 100 µg/mL, respectively) and X-gal (40 µg/mL) when required. Chemically competent *E. coli* DH10β (New England Biolabs) were used for transformation (by heat shock following the manufacturer's instructions) and maintenance of plasmids. All plasmids of the kit were maintained and amplified in TOP10 *E. coli* strain prior to submission to Addgene.

C. reinhardtii strains[35, 46, 52, 61, 62], culture and transformation conditions are recapitulated in Supplementary Table 5. They were grown in Tris-Acetate-Phosphate (TAP) medium[63] supplemented with agar (1.6 % m/V), spectinomycin (100 µg/mL), paromomycin (15 µg/mL), zeocin (ThermoFisher Scientific, 10 to 15 µg/mL), 5-fluoroindole (20 µM) or rapamycin (LC Laboratories, 1 µM) when required. For *NIT1* promoter characterization (Figure 4a), a modified TAP medium lacking nitrogen source (TAP-N) was used instead, and was

supplemented with 4 mM KNO_3 (nitrate) or 7.5 mM NH_4Cl (ammonium). For NAC2 autotrophy test (Figure 4b), cells were grown in minimal media (HSM) for selection of complemented strains. The responsiveness to B12 was assessed on plate and then in liquid. Cells were grown for 15 days in HSM until 1-5 x10^7 cells/mL concentration prior to inoculation in a 96-well plate at a concentration of 10^5 cells/mL in 200 µL of HSM. For response assays (Figure 4c) thiamine (Melford Laboratories Ltd.), 4-methyl-5-(2-hydroxyethyl) thiazole (HET) and 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP, Fluorochem UK) were added to TAP media at a final concentration of 10 µM.

For transformation by electroporation (see Supplementary Table 5), a TAP culture of 1-5 x 10^6 cells/mL was concentrated 100 times in TAP complemented with 60 mM sucrose or the MAX Efficiency Transformation reagent for Algae (ThermoFisher scientific) and 25-250 µL were incubated with 80-300 ng of DNA for 10-30 min on ice in a 0.4 cm gapped cuvette (BioRad) prior to electroporation (BioRad Gene Pulser Xcell). The cells were then left to recover in TAP complemented with 40-60 mM sucrose for 16 h under appropriate light and shaking conditions (typically 50 µmol photon m^{-2} s^{-1} at 100 rpm) prior to plating on TAP-agar plates with adapted antibiotics. Transformation by glass-beads method followed previously published protocols[7, 64]. Briefly, after growth in TAP until 5 x 10^6 cells/mL, cells were concentrated 30 times and 5 x 10^7 cells were mixed with DNA using glass beads. After 2-fold dilution with TAP, 2.5 x 10^7 cells were spread onto TAP agar plates containing 100 µg ml^{-1} spectinomycin. Plates were incubated for 16 h in the dark prior to light exposition (30 µmol photon.m^{-2}.s^{-1}). When colony counting was performed (Figure 3a), it was 8 days after the beginning of light. In both cases, the transformation protocol leads to insertion of a linear DNA in a random location within the nuclear genome.

Design. All *in silico* sequence designs and analysis were performed with Serial Cloner, Benchling, SnapGene, ApE or Genome Compiler. For exogenous parts, reverse translation was performed with Serial Cloner using *C. reinhardtii* nuclear genome codon frequency (http://www.kazusa.or.jp/codon/cgi-bin/showcodon.cgi?species=3055).

amiRNAs can be generated using DNA parts pCM0-068 and pCM0-069. Both are derived from the endogenous pre-miR1157[65], but differ in the way in which the amiRNA specific sequence is introduced. pCM0-069/pCMM-20 is analogous to pChlamyRNA3[65], and a dsDNA fragment containing the amiRNA/loop/amiRNA* sequence is introduced into a *Spe*I site inside the miRNA precursor sequence. pCM0-068 presents two divergently oriented *Bpi*I sites, allowing the cloning of the dsDNA fragment by Golden Gate. In this last case, the dsDNA fragment is formed by the annealing of two oligos with the following sequence: 1) sense oligo (5' AGTA-(MIRNA*SEQ)-TCTCGCTGATCGGCACCATGGGGGTGGTGGTGATCAGCGCTA-(MIRNA SEQ)-T 3'), 2) anti-sense oligo (5'CAGT-A-(rev com MIRNA SEQ)-TAGCGCTGATCACCACCACCCCCATGGTGCCGATCAGCGAGA-(rev com MIRNA*SEQ) 3'). There are online tools that help with the design of the amiRNA sequence (http://wmd3.weigelworld.org/cgi-bin/webapp.cgi).

Parts repository. All sequences listed in Supplementary Table 2 were deposited in Addgene. Physical distribution of the DNA is performed through Addgene. We invite the community to share their future parts through Addgene and/or with our consortium (contact M. Schroda) which will make them available to the community.

Parts cloning. All PCR reactions were performed using the Phusion DNA polymerase, KOD Xtreme Hot Start DNA polymerase (Merck) or Q5 DNA polymerase purchased from New

England Biolabs (NEB) following the manufacturer's instructions adapted to GC-rich DNA, typically duration of hybridization and polymerization was doubled and/or GC enhancer solution was used. Molecular biology kits were purchased from Macherey-Nagel, peqLab, NEB or QIAgen (gel extraction and miniprep kits). Primers were produced by Eurofins Genomics or Sigma-Aldrich while synthesized parts were obtained from Genecust, DC Biosciences, IDTDNA or Sigma-Aldrich.

MoClo Assembly Conditions. All Restriction/ligation reactions were performed using *BbsI* or *BbsI*-HF (*BpiI* is an isoschizomer) or *BsaI*-HF (NEB or ThermoFisher) together with T4 ligase (NEB) in a medium containing the NEB CutSmart buffer and 1 mM ATP (with stock of 10 mM solubilized in 0.1 M Tris-HCl, pH 7.9). Typical ratio between destination plasmid (100 fmol) and entry plasmid/parts was 1:2. To facilitate handling of the kit for end-users, we provide detailed protocols and reaction mix calculators for each type of assembly: level 0 for parts (Supplementary Table 6), level 1 for modules (Supplementary Table 7) and level M for devices (Supplementary Table 8).

Quality Control of generated DNAs. All plasmids were controlled by differential restriction. In addition, all level 0 plasmids were sequenced with specific primers. Sequencing was performed by Eurofins Genomics, Source BioSciences UK, Seqlab, Macrogen, Microsynth, GATC Biotech or Core Facility (CeBiTec, Bielefeld University).

NanoLuc activity determination. Reagents were purchased from Promega (ref. N1110) and activity was determined as previously described[39]. For screening, *C. reinhardtii* colonies were transferred into a 96-well plate containing 100 µL of TAP in each well. After gentle

resuspension, 50 µL was transferred into a solid white 96-well plate to which 50 µL of Nano-Glo substrate diluted in the provided buffer (2% V/V) was added and gently mixed by pipetting. Luminescence was measured at 460 nm with a CLARIOstar plate reader (BMG Labtech). For promoter/terminator combination assessment experiment (Figure 3c), all *C. reinhardtii* colonies from a transformation event were pooled and resuspended in TE buffer (50 mM Tris-HCl pH 7.9, 1 mM EDTA) complemented with anti-protease (1 tablet per 50 mL, Sigma-Aldrich: S8830). The cells were lysed by vortexing 10 seconds twice in the presence of glass beads (about 1:5 ratio beads/cells V/V) prior to two centrifugations (20000 g for 10 min at 4°C) to clarify the supernatant. The protein concentration was then determined using Bradford reagent with a Bovine Serum Albumin standard curve and the concentration was standardized to 0.5 g/L. The activity was determined in a 96-well plate in a final volume of 50 µL (1:1 with nano-Glo resuspended in provided lysis buffer) per well. NanoLuc activity was determined on 6 different increasing protein quantities (0.1 to 2.5 µg) for each assay, allowing to assess linearity of the signal.

Absorbance measurement of cultures growing in microtiter plates

Growth in microtiter plates was determined by measuring the optical density of each well at 730 nm. Microtiter plates containing 180-200 µL culture were incubated under constant light (125 µmol photon.m^{-2}.s^{-1}) at 25°C and 40 rpm orbital shaking. For density determination, cultures were resuspended by pipetting and 100 µL of cell suspension was transferred to a new microtiter plate containing 50 µL TAP 0.03% Tween-20. Optical density of each well was determined at 730 nm in a CLARIOstar plate reader (BMG Labtech). Plates were shaken for 6-10 sec at 600 rpm before measurement.

RNA extraction and miRNA-mediated cleavage mapping

RNA isolation was carried out as previously described[49] (a detailed protocol can be found at http://www.plantsci.cam.ac.uk/research/davidbaulcombe/methods/downloads/smallrna.pdf/view), with the following modifications: Cells were centrifuged and resuspended in 0.25 mL of water and mixed with 0.25 mL Lysis buffer (50 mM Tris-HCl pH 8.0, 200 mM NaCl, 50 mM EDTA, 2% SDS, 1 mg/mL proteinase K). Lysis buffer was incubated at 50°C for 5 min prior mixing with cells. Cell suspension was then incubated at 25°C for 20 min. Finally, 2 mL of PureZol (Biorad) was added and samples were snap-frozen. RNA quality was assessed in gel and quantified in Nanodrop (ThermoFisher scientific).

miRNA cleavage site determination was performed as previously described[66]. Briefly, 10 µg of total RNA was ligated with an RNA oligo (5' CGACUGGAGCACGAGGACACUGACAUGGAC UGAAGGAGUAGAAA 3') using T4 RNA ligase for 1 h at 37°C. RNA was extracted with phenol:chloform and precipitated with ethanol and sodium acetate. The precipitated RNA was retrotranscribed into cDNA by SuperScript IV reverse transcriptase (ThermoFisher scientific), using random hexamers and following manufacturer's recommendations. Two µL of the cDNA was used as template of a PCR using primers FJN456 (5'- CGACTGGAGCACGAGGACACTGA) and FJN495 (5'- TGGGGTAGGGGTGGGGGCCAG). Two µL of this PCR was used as template of a second PCR with primers FJN457 (5'- GGACACTGACATGGACTGAAGGAGTA) and FJN496 (5'- TGACCCAGTCGCGGATGGCCT). PCR was resolved in a 2% agarose gel and the specific band was isolated from the gel and cloned into pGEM-T easy (Promega) for sequencing.

Immuno-blotting. Chlamydomonas cells expressing FKB12 fusion proteins from liquid cultures were collected by centrifugation 4000 g for 5 min at room temperature (RT), washed in 50 mM Tris-HCl pH 7.5, and resuspended in a minimal volume of the same solution. Cells were lysed

399 by two cycles of slow freezing to -80°C followed by thawing at RT. The soluble cell extract was
400 separated from the insoluble fraction by centrifugation (15000 g for 20 min at 4°C). Total
401 protein extracts (15 µg) were then subjected to 15% SDS-PAGE.
402 mCherry-expressing cells were harvested at 3500 rpm for 2 min (4 °C) and resuspended in
403 60 µL of DTT-carbonate buffer (0.1 M DTT, 0.1 M Na_2CO_3). After freezing at -20 °C and thawing,
404 55 µL of SDS-Sucrose buffer were added (5 % SDS, 30 % sucrose). Samples were then boiled
405 for 45 s at 95 °C, followed by 2 min incubation on ice and 13000 g centrifugation for 2 min at
406 RT. Protein extracts corresponding to 2 µg of Chlorophyll were then separated using 12% SDS-
407 PAGE.
408 For immunoblot analyses, proteins were then transferred to nitrocellulose membranes (Bio-
409 Rad, 162-0115 or Amersham Protran). After blocking with 3 to 5% low-fat Milk in PBS for 1 h
410 at RT, membranes were incubated with primary antibody in 5% low-fat Milk in PBS for 16 h at
411 4°C. After 4 washes in PBS - 0.1% tween-20 (TPBS), the membranes were incubated with
412 secondary antibody in 5% low-fat Milk in PBS for 1 h at RT, and subsequently washed 4 time
413 in TPBS prior to chemi-luminescence revelation using ECL. Primary antibodies used were anti-
414 FKBP12 [52] (1/5000 dilution; secondary was anti-rabbit 1/10000), anti-FLAG (Sigma-Aldrich
415 F1804, 1/5000 dilution; secondary was anti-mouse 1/5000), anti-STREP (IBA, Catalog N. 2-
416 1509-001, 1/5000 dilution; conjugated to HRP), anti-cMYC (Sigma-Aldrich M4439, 1/2500
417 dilution; secondary was anti-mouse 1/5000), anti-HA (Sigma-Aldrich H9658, 1/5000 dilution;
418 secondary was anti-mouse 1/2500) and anti-PRPL1[67]. For mCherry serum, rabbits were
419 immunized against purified full-length mCherry protein containing an N-terminal His_6-tag.
420
421 **Microscopy.** For mCherry experiments (Figure 6b-e), images were taken at 100x magnification
422 with a BX53F microscope (Olympus). Fluorescence images for the detection of mCherry were

taken using a TRITC filter. For other fluorescent proteins (Figure 6f-h), microscopy was performed as previously described [7, 68].

Accession numbers. All parts accession numbers and the corresponding references are listed in Supplementary Table 2.

ASSOCIATED CONTENT

Supporting Information.

Supplementary Figure 1 - MoClo assembly workflow reflecting the abstraction hierarchy

Supplementary Figure 2 - Variability of Nanoluc expression in pCMM-1 transformants.

Supplementary Figure 3 - Control of gene expression, complementary data.

Supplementary Table 1 - list of all unique parts of the Chlamy MoClo kit

Supplementary Table 2 - list of all parts of the Chlamy MoClo kit: level 0 plasmids

Supplementary Table 3 - list of all modules used for the Chlamy MoClo kit validation: level 1 plasmids

Supplementary Table 4 - list of all modules used for the Chlamy MoClo kit validation: level M plasmids

Supplementary Table 5 - list of Chlamydomonas reinhardtii strains and associated transformations

Supplementary Table 6 - level 0 ligation file: protocol and reaction mix calculator to clone parts.

Supplementary Table 7 - level 1 ligation file: protocol and reaction mix calculator to assemble modules.

Supplementary Table 8 - level M ligation file: protocol and reaction mix calculator to assemble devices.

Abbreviation.

MoClo: Modular Cloning, TU: Transcriptional Unit, RBCS2: Ribulose Bisphosphate Carboxylase oxygenase Small subunit 2,HSP70: Heat Shock Protein 70, AR: HSP70A/RBCS2,

TUB2: Tubulin 2, PSAD: Photosystem I reaction center subunit II, HET: 4-methyl-5-(2-hydroxyethyl) thiazole, HMP: 4-amino-5-hydroxymethyl-2-methylpyrimidine, amiRNA: artificial micro RNA, TAP: Tris Acetate Phosphate

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Author Contribution.

SDL, AGS, MS, PEJ, OK, JLC and GP created the consortium that led this study.

PC, FJN, FW, PM, DCB, GP, JLC, OK, PEJ, MS, AGS and SDL designed the study and wrote the manuscript.

PC, FJN, FW, PM, KB, KJL, MEPP, PA, AGR, SSG, JN, BS, JT, RT, LW, KV, TB, KS, MC, FdC, AD, MdM, JH, WH, CHM designed parts, modules and devices, performed the experiments, and/or analyzed data.

Competing Financial Interests statement.

The authors declare no competing financial interest.

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696 **Graphical Abstract**

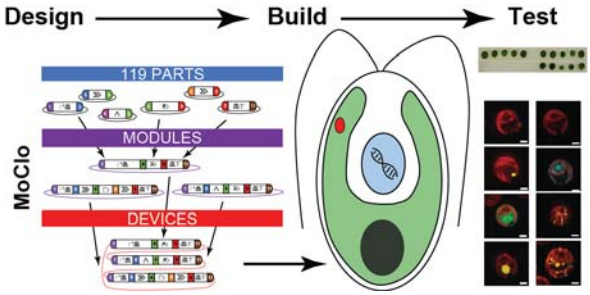
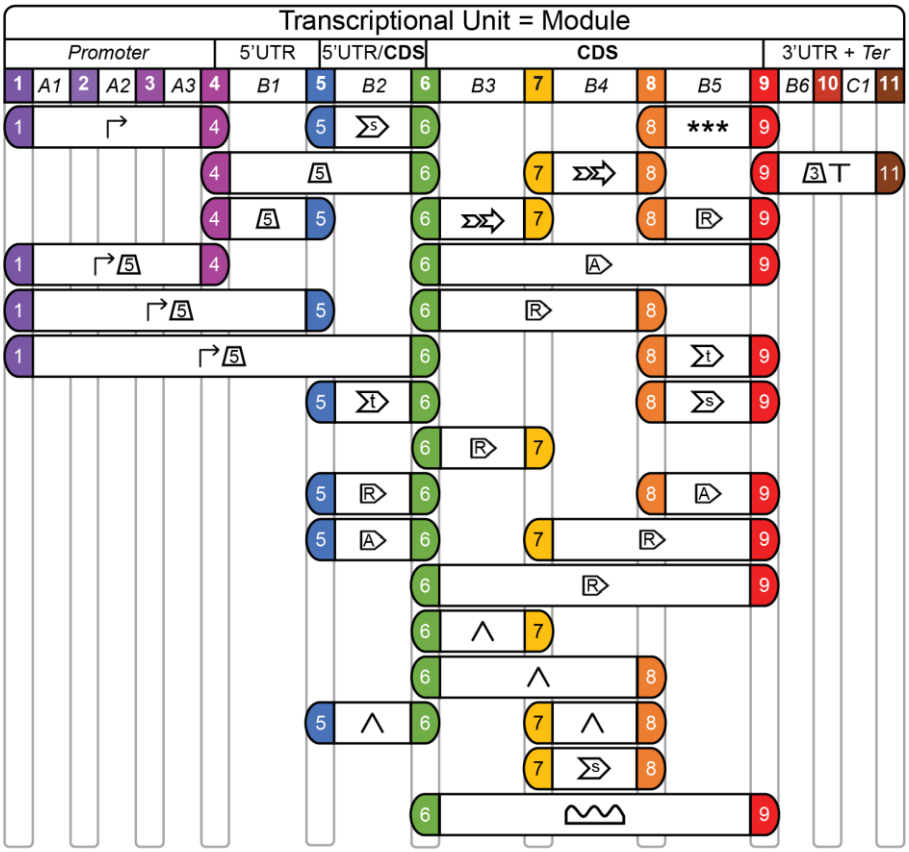
697 

Figure 1.

a.



b.

Types of part (*non transcribed*; **translated**)	SBOL	Parts	Unique parts
Promoters		7	7
Promoters + 5'UTR		15	7
5'UTR		12	6
Introns		4	1
Signal and Targeting peptides		11	9
Immuno and purification tags		15	8
Reporter genes		34	12
Antibiotic Resistance genes		8	5
3'UTR / *Terminators*		6	6
2A peptide		2	1
amiR		4	4
Multi-Stop	***	1	1
Total		119	67

Figure 1. Overview of the Chlamydomonas MoClo toolkit.

(**a**) Type and position of parts used following the Plant MoClo Syntax[30]. Symbols correspond to the SBOL2.0 visual[69] representation described in **b**. Each of the 11 fusion sites defining a part position is represented with a color and a number. Positions presented are representative of the whole set of each part type. Parts in italicized letters are non-transcribed, parts in regular letters are transcribed and parts in bold letters are transcribed and translated.

(**b**) Table summarizing unique and total gene parts available. The SBOL2.0 symbols are indicated for each type. When the SBOL2.0 standard was not existing for a part type, the symbol proposed before[28] was used, or defined here.

Figure 2

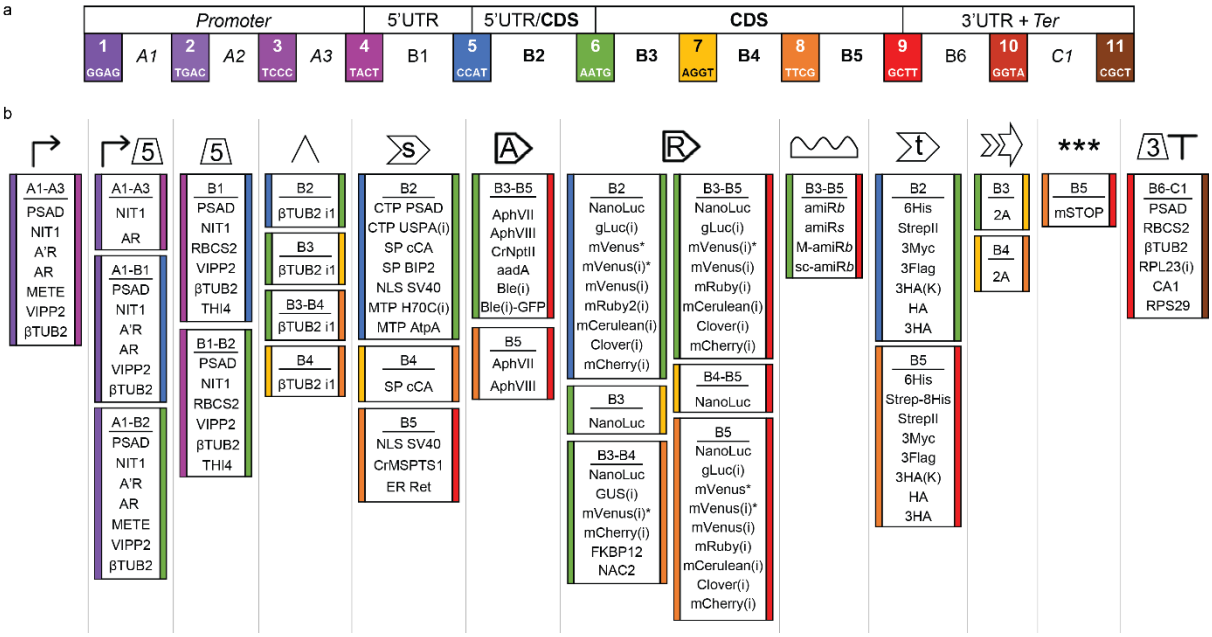


Figure 2. List of parts in function of their type and assembly position.

(a) Plant MoClo syntax[30] indicating the color code for fusion sites used in this figure.

(b) All parts in the Chlamydomonas MoClo kit are classified primarily by their function, indicated by SBOL2.0 visual code[69] as in Fig. 1 (from left to right: promoters, promoter+5'UTR, 5'UTR, introns, antibiotic resistance genes, reporter genes, artificial microRNA, immunological and purification tags, 2A peptide, and 3'UTR+terminators). Colored stripes on the left and right sides of each box represent the fusion sites in 5' and 3' of the position, respectively, and follow the color code on top. AR and A'R stand for HSP70A/RBCS2 and HSP70A467/RBCS2, respectively[36]. A star (*) indicates that the part contains extra restriction sites as in pOpt vectors[68] while the same part unmarked does not. An (i) indicates the presence of an intron within the part (*cf.* Supplementary Table 2). For amiRNA (amiR) backbones, *b* and *s* mean that *Bpi*I and *Spe*I site are within the backbone for amiR cloning, respectively, while M and sc mean that the target amiR sequence for *MAA7* and the control scrambled sequence were introduced into the miR1157 backbone, respectively (cf. Fig. 4). mSTOP stands for multi-STOP.

Figure 3.

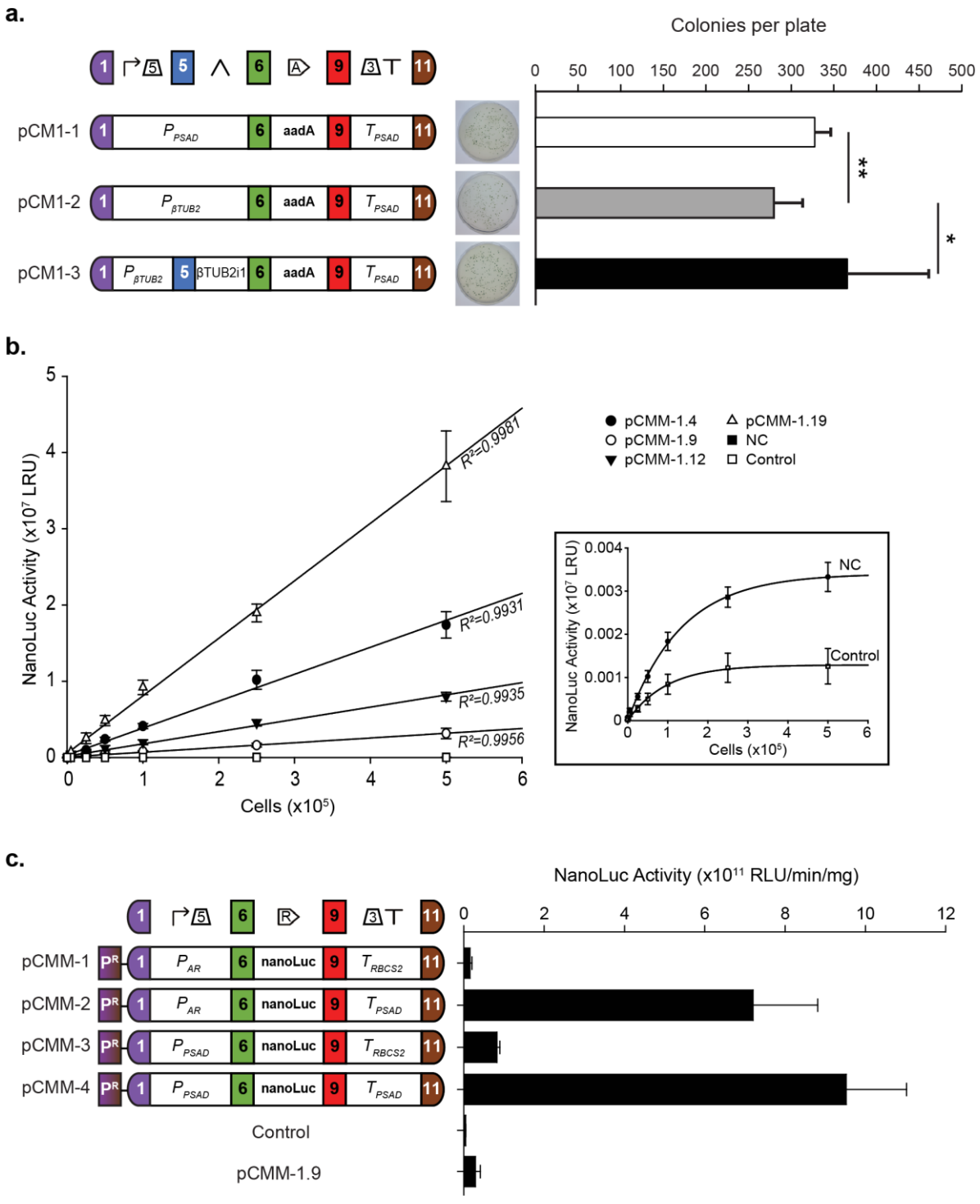


Figure 3. Constitutive promoters and reporter genes.
(**a**) Average number of spectinomycin resistant colonies after transformation of UVM4 cells (mean ± SD, N=11) for the three modules (pCM1-3, where pCM stands for plasmid Chlamydomonas Moclo). Representative transformation plates are shown.
(**b**) Linearity of NanoLuc activity as a function of cell number. NanoLuc activity for 4 independent clones transformed with the pCMM-1 device (pCMM-1.X), one non-expressing clone (NC) and the recipient strain (CC-4425 noted as control) are presented (N=3, mean ± SEM). Linear regression and correlation coefficient (R^2) are shown. The NC and control are shown in the inset on a different scale.

(**c**) Average NanoLuc activity of D66 (CC-4425) cells transformed with 4 devices (pCMM-1 to 4) harboring promoter/terminator combinations to drive NanoLuc expression coupled to a paromomycin resistance module (represented as P^R, left, Supplementary Fig. 2). Luminescence levels are represented as mean ± SEM (average of a total of more than 400 clones from 3 biological replicates). The negative and positive controls are the recipient strain and the pCMM-1.9 strain (shown in **b**), respectively.
a,c *p<0.05; **p< 0.01 assessed by Student's t-test, SBOL2.0[69] visual of module designs are shown above the devices.

Figure 4.

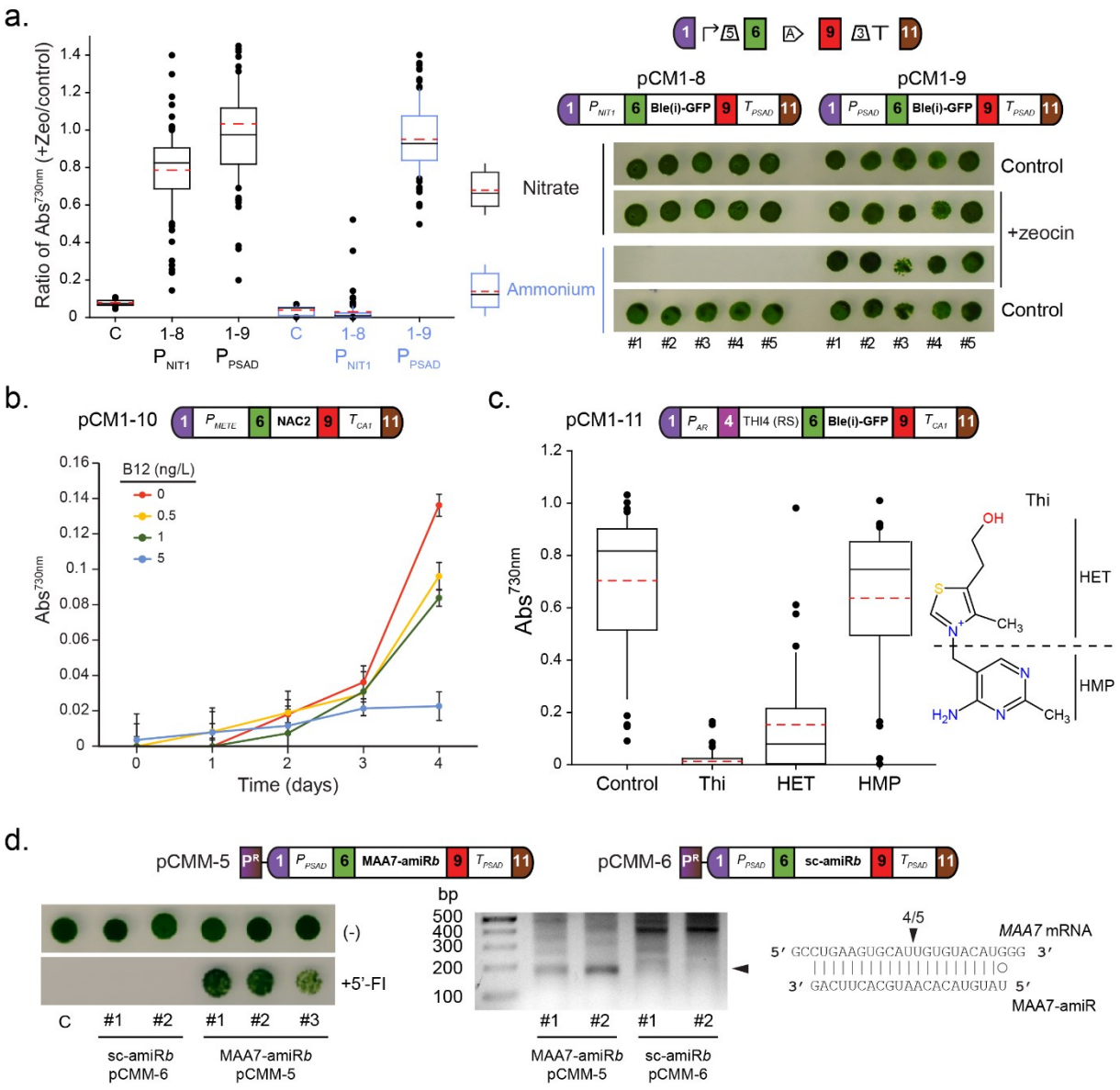


Figure 4. Control of gene expression.

(**a**) Control of gene expression by the nitrogen source. Zeocin resistant colonies (conferred by *Ble(i)-GFP*) selected after transformation of CC-1690 cells with each of the two represented modules ("1-8" for pCM1-8 and "1-9" for pCM1-9) were grown in TAP-nitrogen ± zeocin (15 µg/mL) supplemented with either 7.5 mM $(NH_4)Cl$ (ammonium, blue) or 4 mM KNO_3 (nitrate, black) and their growth was followed (Absorbance at 730 nm). The plot shows the ratio between the growth in the presence and absence of zeocin (C is the non-transformed CC-1690 strain). The right panel shows cells grown in similar conditions but on solid media. Results presented (N=16 for control CC-1690 and N=86 for each other conditions) correspond to one out of three independent transformations (for the other two, see Supplementary Fig. 3).

(**b**) Control of gene expression by vitamin B_{12}. Conditional complementation of *nac2-26* cells with the pCM1-10 module expressing NAC2 under P_{METE} control. Complemented strains were selected for photoautotrophic growth on solid minimal medium and the cells were grown in liquid minimal medium supplemented with the indicated amount of vitamin B_{12}. Data are mean ± SD (N=3).

(**c**) Control of gene expression by vitamin B_1. Average growth (absorbance at 730 nm after 7 days of growth, N=40) of UVM4 cells transformed with the pCM1-11 module designed to express constitutively *Ble(i)-GFP* transcripts containing the *THI4* riboswitch in the 5'UTR. After culture in TAP, the cells were transferred to TAP+zeocin (10 µg/mL) supplemented with 10 µM thiamine (Thi), 10 µM 4-methyl-5-(2-hydroxyethyl) thiazole

(HET) or 10 µM 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP) or not (control). The chemical structure of Thi is represented on the right and the HET and HMP moieties are indicated (See also Supplementary Fig. 3). (**d**) Targeted gene knockdown with artificial miRNA. Paromomycin resistant cells selected after transformation of CC-1690 cells by each of the two represented devices (pCMM-5 and pCMM-6), carrying an amiRNA cloned with *Bpi*I and directed against *MAA7* (MAA7-amiR*b*) or a random sequence ('scrambled': sc-amiR*b*), were grown in the absence (denoted (-)) or presence of 5'-fluoroindole (+5'-FI) (left panel). C indicates non-transformed cells. Clones resistant to 5'FI were analyzed by a modified 5'-RACE assay. A specific 173 bp PCR band (black arrowhead) was amplified only from the 5'-FI resistant transformants and not from ones expressing the amiRNA with scrambled sequence (middle panel and Supplementary Fig. 3). Sequencing revealed that the most frequent cleavage occurred at positions opposed to positions 10 and 11 of the amiRNA (right panel, black arrowhead). P^R represents the paromomycin resistance module (pCM1-27, Supplementary Fig. 2a).
a, c The box and whisker plots show the 10^{th} (lower whisker), 25^{th} (base of box), 75^{th} (top of box) and 90^{th} (top whisker) percentiles. The line within the box is the median, the dashed red line is the mean. Outliers are plotted as individual data points.

Figure 5.

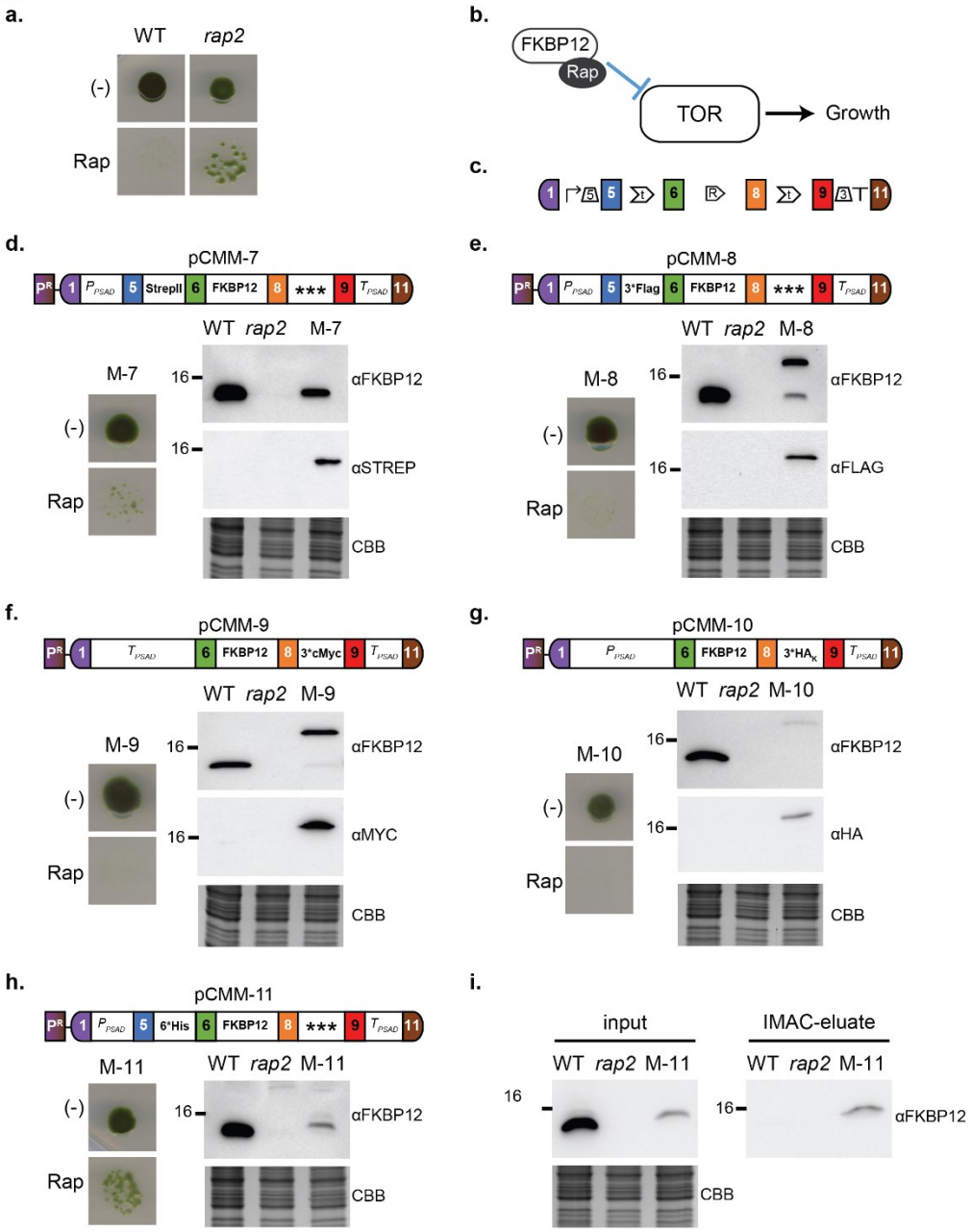


Figure 5. Design, build and test of five fusion tags

(**a**) Phenotype of recipient (WT) and Δ*FKBP12* (*rap2*) strains in the presence (Rap) or absence (-) of 1 µM rapamycin.

(**b**) Molecular mechanism underlying the *rap2* phenotype. Target Of Rapamycin (TOR) is inhibited by rapamycin only in the presence of FKBP12 (mutated in *rap2*). Upon formation of the tripartite TOR/FKBP12/rapamycin complex, TOR is inhibited and growth is arrested[52].

(**c**) SBOL2.0 visual[69] of module designs for functional complementation of *rap2*.

(**d-h**) Phenotype in the presence (Rap) or absence (-) of 1 µM rapamycin and detection of tagged proteins in soluble extracts by immunoblotting with antibodies against either FKBP12 (αFKBP12) or the appropriate tag (indicated within each panel). Each device is indicated in the upper part of the panel. CBB: Coomassie Brilliant Blue staining of a duplicate gel loaded with the same samples and shown as loading control.

(**i**) Purification through ion-metal affinity chromatography (IMAC) of 6His-FKBP12 expressed from the same device as in **h**.

P^R represents the paromomycin resistance module (pCM1-27, Supplementary Fig. 2a). *rap2* cells transformed with pCMM-X are indicated as M-X in each panel. Data are representative of 3 biological replicates.

Figure 6.

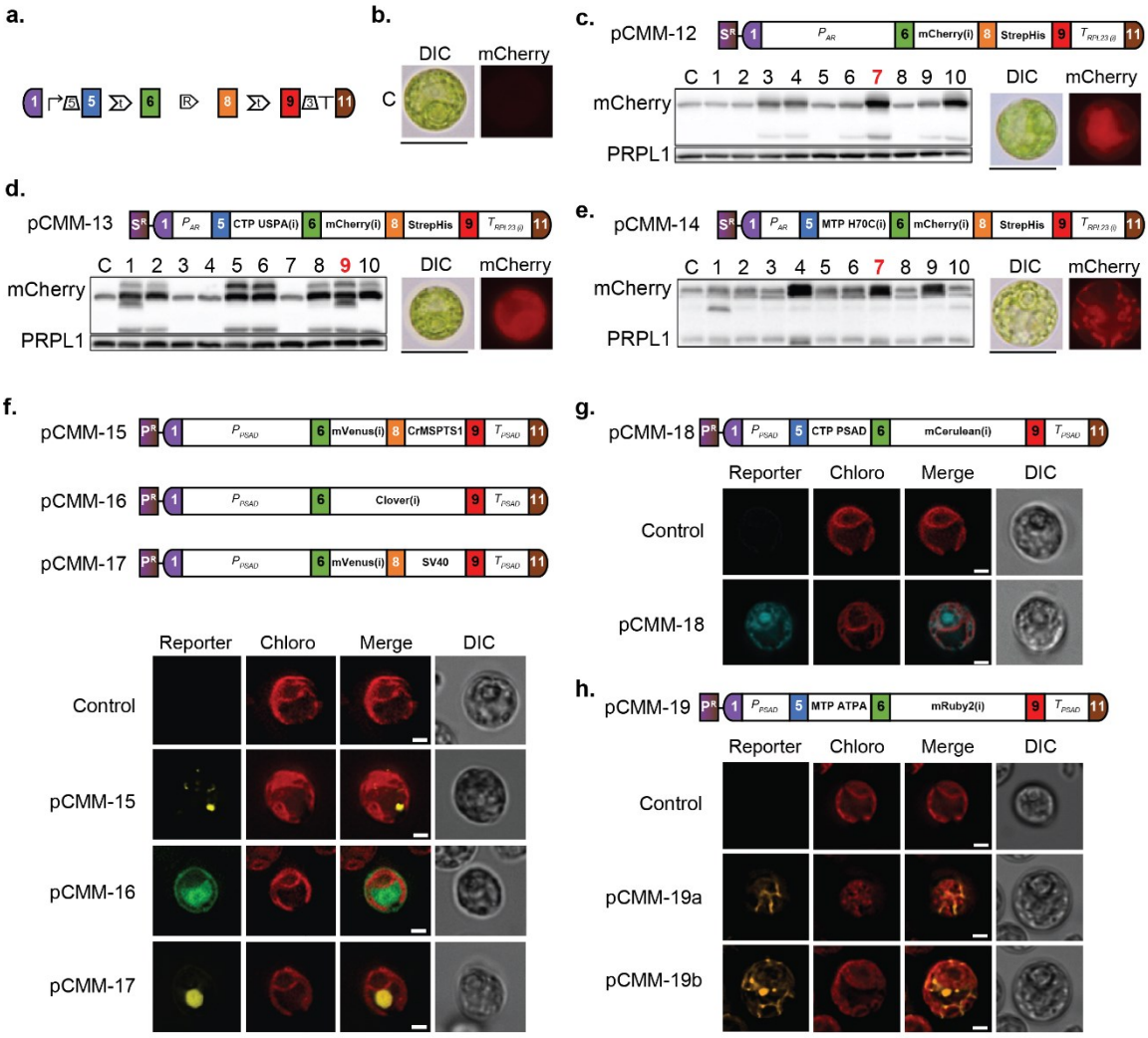
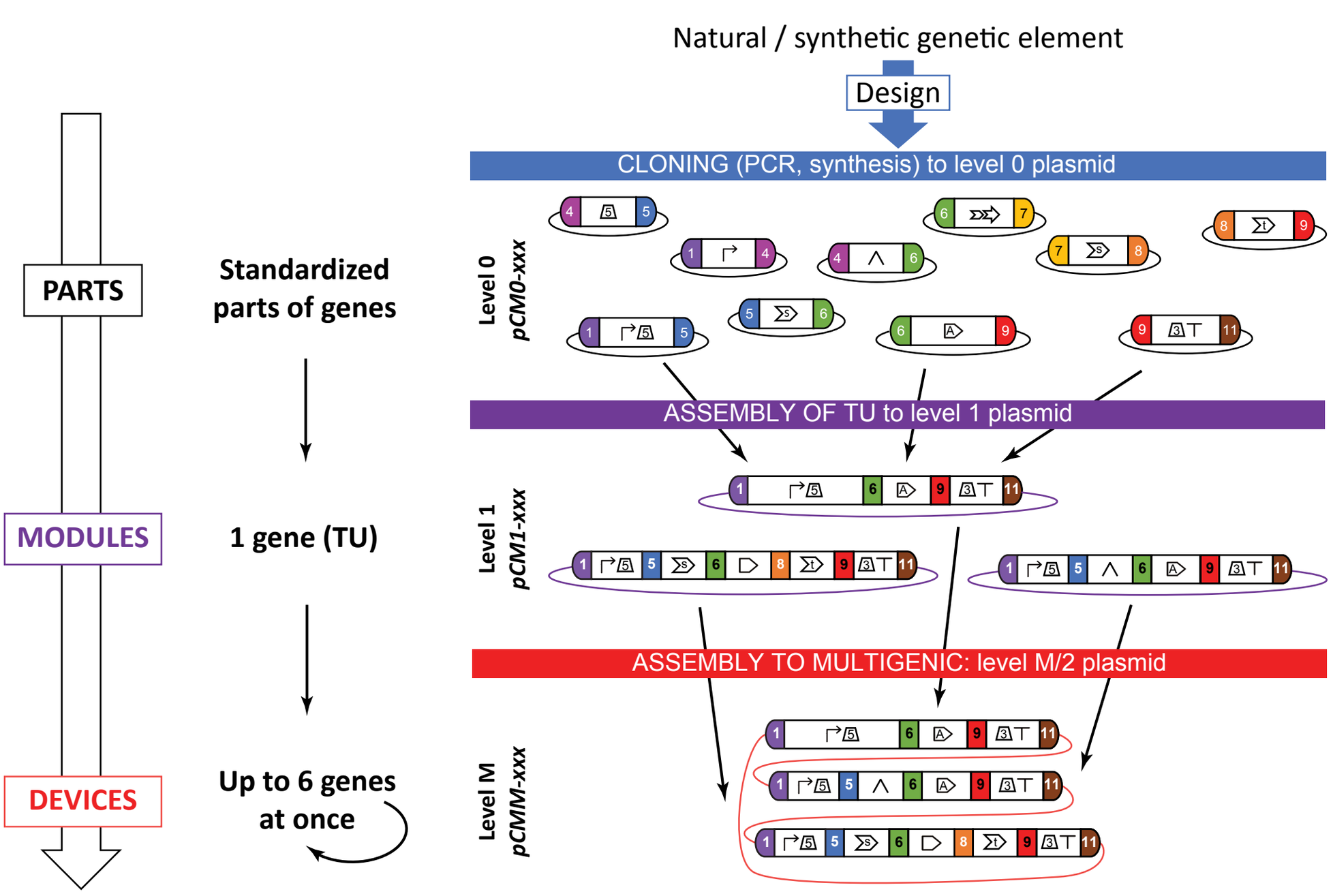
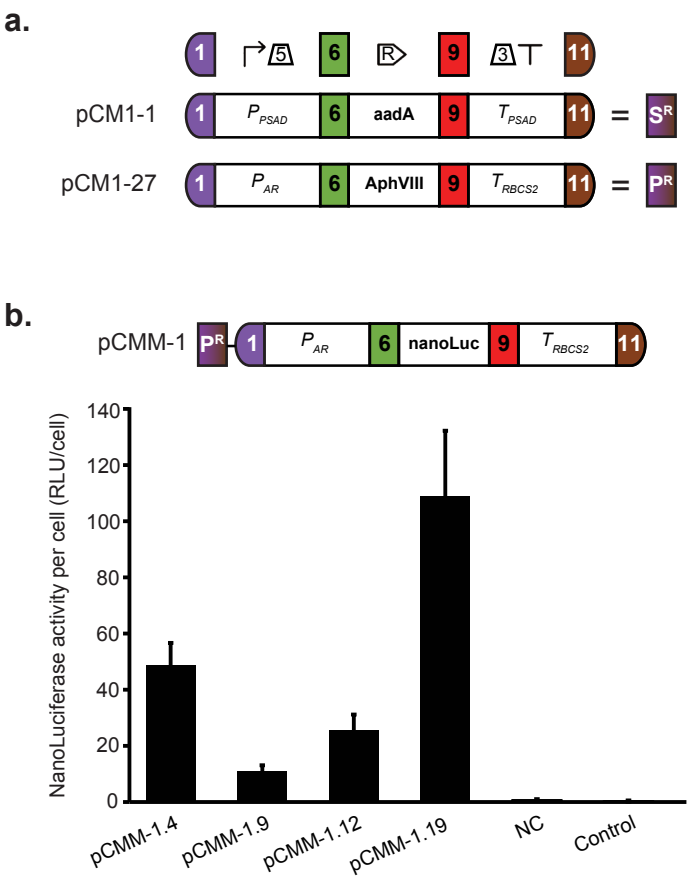


Figure 6. Targeting reporter genes to different subcellular compartments.

(**a**) SBOL2.0[69] visual syntax for modules used.
(**b**) Visible light ("DIC") and fluorescence signal ("mCherry") of the UVM4 recipient strain used as control ("C") for panels **c**-**e**.
(**c-e**) mCherry targeting to the (**c**) cytosol with no transit peptide, (**d**) chloroplast with CTP USPA (Chloroplast Transit Peptide of Universal Stress Protein A) or (**e**) mitochondria with MTP H70C (Mitochondrial Transit Peptide of HSP70C) in UVM4 cells transformed with the indicated devices (pCMM-12 to 14). In each panel, an anti-mCherry immunoblot analysis of transformants is shown. Note that the anti-mCherry antibody cross-reacts with a protein of similar size present in control cells (C). An anti-PRPL1 immunoblot is shown as loading control. The transformant strain number indicated in red corresponds to the images (bars are 10 µm) presented on the right.
(**f-h**) Fluorescent marking of (**f**) microbodies with mVenus-CrMSPTS1 (Malate Synthase PTS1-like sequence), cytosol with Clover or the nucleus with mVenus-SV40 (Simian Virus 40 nuclear localization signal), (**g**) the chloroplast with CTP PSAD-mCerulean (Chloroplast Transit Peptide of PSAD), (**h**) mitochondria with MTP ATPA-mRuby2 (Mitochondrial Transit Peptide of ATPA) after transformation of UVM4 cells with the indicated devices (pCMM-15 to 19). Images of representative transformants are grouped with the corresponding control image (recipient strain) according to the filter used. pCMM-19a and pCMM-19b show two images taken on different z-axis on the same cell. "Chloro" refers to chlorophyll autofluorescence. The Scale bars represent 2 µm.
S^R and P^R represent respectively modules conferring resistance to spectinomycin (S^R=pCM1-1, Fig. 3a and Supplementary Fig. 2a) and paromomycin (P^R=pCM1-27, Supplementary Fig. 2a).



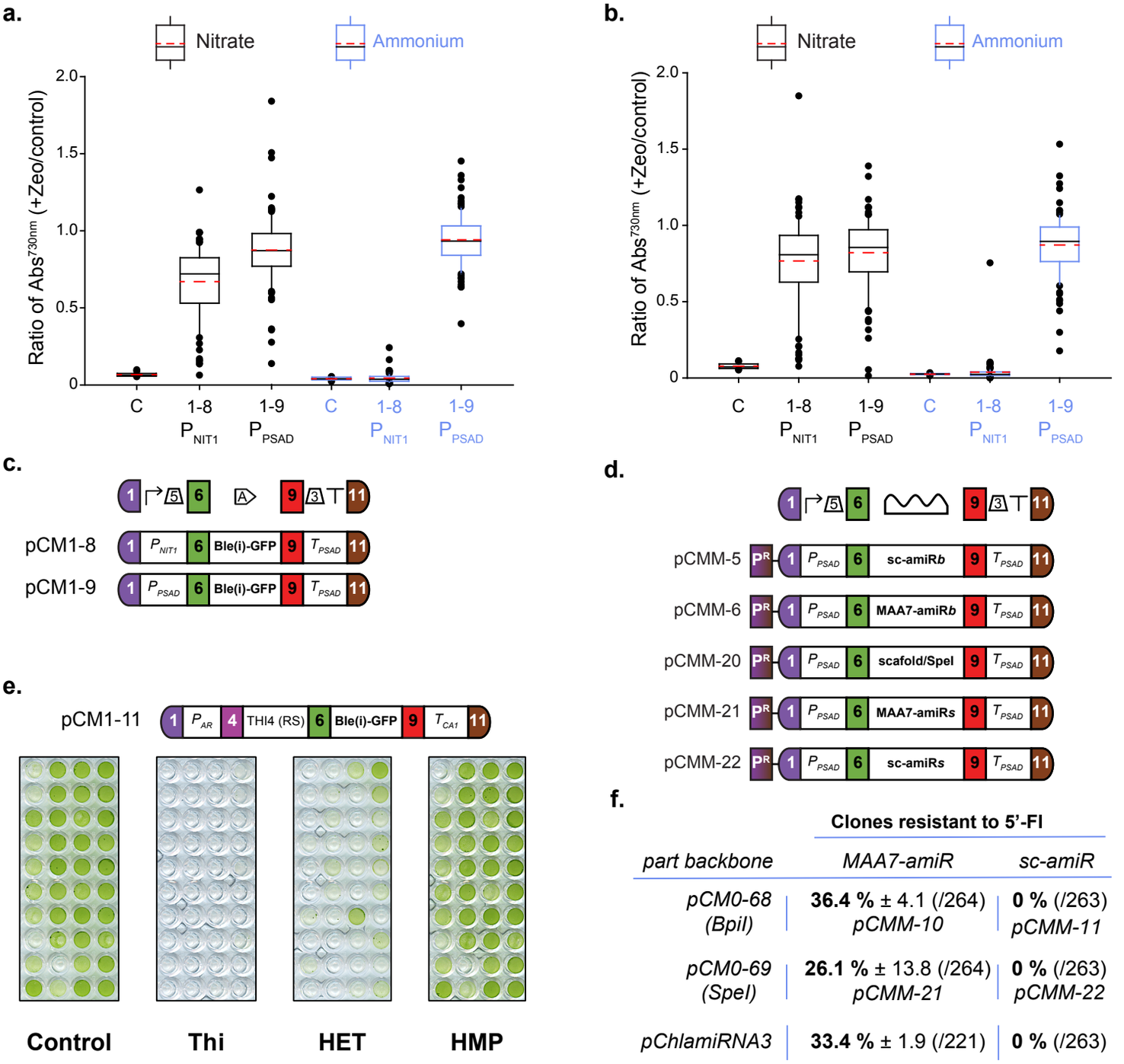
Supplementary Figure 1. MoClo assembly workflow reflecting the abstraction hierarchy.
We followed the original MoClo syntax[22] updated[30]. After design of a gene part controlled in silico for full compatibility until level M assembly, the part is cloned with *BpiI* (equivalent to *BbsI*) into the appropriate level 0 plasmid (Spectinomycin bacterial resistance). After quality control (QC) by restriction and sequencing, the resulting clone is registered in the part database as a pCM0-xxx (where pCM stands for plasmid Chlamydomonas Moclo). To generate the desired Transcriptional Unit (TU), the compatible parts are assembled with *BsaI* into the appropriate level 1 plasmid (Ampicillin bacterial resistance). After QC by restriction, the clone is registered as pCM1-xxx in the module database. Finally, to assemble a device, up to 6 modules at a time are assembled with the corresponding end-linker[22] by *BpiI* into a level M or 2 plasmid (Spectinomycin or kanamycin bacterial resistance, respectively). After QC by restriction, the clone is registered as pCMM-xxx in the device database. New assembly from this device can be performed to assemble more modules to the device[22]. Parts are represented in SBOL2.0 visual code[69] (see also Fig. 1).



Supplementary Figure 2. Variability of Nanoluc expression in pCMM-1 transformants.

a. Schemes of the spectinomycin (SR) and paromomycin (PR) resistance modules.

b. NanoLuc activity averaged (N=3, mean ± SEM) per line and expressed as RLU (Relative Luminescence Unit) per cell (same data as in Fig. 3b) of four independent NanoLuc-expressing transformants, one non-expressing clone (noted NC) and the recipient strain (CC-4425, noted control).



f.

part backbone	Clones resistant to 5'-FI: *MAA7-amiR*	Clones resistant to 5'-FI: *sc-amiR*
pCM0-68 (BpiI)	**36.4 %** ± 4.1 (/264) *pCMM-10*	**0 %** (/263) *pCMM-11*
pCM0-69 (SpeI)	**26.1 %** ± 13.8 (/264) *pCMM-21*	**0 %** (/263) *pCMM-22*
pChlamiRNA3	**33.4 %** ± 1.9 (/221)	**0 %** (/263)

Supplementary Figure 3. Control of gene expression, complementary data.
(a-b) Results from the two additional transformation assays performed independently from that presented in Fig. 4a. Control of gene expression by the nitrogen source. Zeocin resistant colonies (*Ble*) selected after transformation of CC-1690 cells by each of the two represented modules ("1-8" stands for pCM1-8 and "1-9" for pCM1-9,) were grown in TAP-nitrogen ± zeocin supplemented with either 7.5 mM $(NH_4)Cl$ (ammonium, blue) or 4 mM KNO_3 (nitrate, black) and their growth was followed (absorbance at 730 nm). The plot shows the ratio between growth in the presence and absence of zeocin (C is non-transformed CC-1690). Results presented (N =16 for CC-1690 "C" and N=86 for all others) correspond to two out of three independent transformations (the other is shown in Fig. 4a). The box and whisker plots show the 10th (lower whisker), 25th (base of box), 75th (top of box) and 90th (top whisker) percentiles. The line within the box is the median, the dashed red line is the mean. Outliers are plotted as individual data points.
(**c**) Modules used to generate data presented in figure 4a and in **a** and **b**.
(**d**) Modules used to generate results presented in figure 4d and in **f**.
(**e**) Module used to generate results presented in Figure 4c (top) and image of the cultures used to generate these data. Cultures in TAP+zeocin supplemented or not (control) with 10 µM of thiamine (Thi), 10 µM of 4-methyl-5-(2-hydroxyethyl) thiazole (HET), or 10 µM of 4-amino-5-hydroxymethyl-2-methylpyrimidine (HMP).
(**f**) Percentage of transformants resistant (± SD) to the metabolic drug 5-fluoroindole (5'-FI, used at 20 µM). The CC-1690 strain was transformed with devices (indicated under each result, design in d) containing the amiRNA sequence targeting the *MAA7* gene or a scrambled sequence as a negative control, cloned into the amiRNA backbone with *BpiI* or *SpeI*, corresponding to parts pCM0-79 and pCM0-80, respectively. The pChlamiRNA3 construct containing the same miRNA backbone was used as a positive control. Average of three independent transformations, the total number of transformants screened for 5'-FI resistance in each experiment is indicated in parenthesis.