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EasyCloneYALI: CRISPR/Cas9-Based Synthetic Toolbox for Engineering of the Yeast Yarrowia lipolytica

Carina Holkenbrink, Marie I. Dam, Kanchana R. Kildegaard, Johannes Beder, Jonathan Dahlin, David Doménech Belda, and Irina Borodina*

The oleaginous yeast Yarrowia lipolytica is an emerging host for production of fatty acid-derived chemicals. To enable rapid iterative metabolic engineering of this yeast, there is a need for well-characterized genetic parts and convenient and reliable methods for their incorporation into yeast. Here, the EasyCloneYALI genetic toolbox, which allows streamlined strain construction with high genome editing efficiencies in Y. lipolytica via the CRISPR/Cas9 technology is presented. The toolbox allows marker-free integration of gene expression vectors into characterized genome sites as well as marker-free deletion of genes with the help of CRISPR/Cas9. Genome editing efficiencies above 80% were achieved with transformation protocols using non-replicating DNA repair fragments (such as DNA oligos). Furthermore, the toolbox includes a set of integrative gene expression vectors with prototrophic markers conferring resistance to hygromycin and nourseothricin.

1. Introduction

The oleaginous yeast Yarrowia lipolytica is an attractive host for industrial production of fatty-acid derived chemicals, organic acids, and enzymes.[1–3] Y. lipolytica is commercially used for production of omega-3 eicosapentaenoic acid,[4] and a number of other processes are emerging, such as production of lipids from unsterile feedstocks[5] and bioremediation of oil-contaminated environments.[6]

Development of a strain into an efficient industrial cell factory requires multiple rounds of metabolic engineering. The engineering efforts so far have been hampered by limited genome targeting efficiencies in Y. lipolytica and by the requirement for selection markers, which need to be recycled. The low genome targeting efficiencies are due to a high rate of non-homologous end joining (NHEJ) for repair of DNA double-strand (ds) breaks in contrast to Saccharomyces cerevisiae, where the homologous recombination (HR) mechanism is the dominating repair pathway.[7,8]

To overcome the above-mentioned limitations of marker-based genome editing, the CRISPR/Cas9 system has been successfully implemented in several yeast species.[9] The most widely applied CRISPR/Cas9 system for genome editing combines three parts: 1) a sgRNA,[10] composed of a site-specific crRNA fused to a tracrRNA, which binds Cas9 endonuclease; 2) the Cas9 endonuclease, capable of creating dsDNA breaks; and 3) a dsDNA repair template, which is used by the HR pathway to repair the dsDNA break. Three previous studies have successfully applied the CRISPR/Cas9 technology in Y. lipolytica for single knockouts of genes and insertion of expression constructs, reaching 90–100% correct genome edit efficiencies after 2–4 days recovery phase after transformation.[11–13] Due to the long recovery, during which the cells divide through multiple generations, it is imperative to use replicating repair templates, e.g., with the repair elements cloned into episomal vectors. We have developed a CRISPR/Cas9 method, which achieves high genome editing efficiency using non-replicating DNA repair templates. For gene deletions/mutations, we use synthetic double-stranded oligos as repair templates, while for gene insertions, we use linearized non-replicating vectors.

The genome engineering toolbox EasyCloneYALI, presented in this study, comprises a set of integrative expression vectors which allow expression of one or two genes per vector and integration into highly expressed intergenic genome sites. Five vectors can be integrated with the help of the CRISPR/Cas9 technology, reaching efficiencies above 80%. Eleven vectors can be integrated with the help of dominant selection markers, with 30–100% efficiency. Further, we provide vectors and protocols for knockout of up to two genes simultaneously using the
CRISPR/Cas9 system. Using 90 bp double-stranded oligos as DNA repair templates, we obtained efficiencies of 90% for individual knockouts and 66–68% for double knockouts. To ease and accelerate plasmid construction, all plasmids in this toolbox are standardized and allow recycling of biobricks. The vectors are assembled by USER cloning. The vectors can be obtained via AddGene. We provide detailed protocols in the Supporting Information.

2. Experimental Section

A detailed step-by-step protocol for the EasyCloneYALI toolbox is provided as supplementary material. All the vectors can be obtained individually or as a set from AddGene.

2.1. Strains and Media

Yarrowia lipolytica GB20[14] was a kind gift of Volker Zickermann. The genotype of the GB20 is mus51Δ(=ku70), nmg1-Htg2, ndh2i, lys11°, leu2°, ura3°, MatB. All the strains in this study were derived from Y. lipolytica GB20, which are listed in Supporting Information Table S1. Y. lipolytica strains were grown at 30°C and 250 rpm in standard yeast peptone dextrose (YPD, Sigma–Aldrich), synthetic complete (SC, Sigma–Aldrich) or mineral medium.[15] For growth on solid media, YPD and SC medium were supplemented with 20 g L−1 agar. When necessary for selection, the YPD medium was supplemented with 250 mg L−1 nourseothricin or 50–100 mg L−1 hygromycin B. To screen for successful thi6 knockout strains, the cells were spotted on mineral medium agar without addition of thiamine. Escherichia coli strain DH5α was used for cloning and plasmid propagation. E. coli was grown in Lysogeny Broth (LB) supplemented with 100 mg L−1 ampicillin and when needed with 15 g L−1 agar.

2.2. Design of crRNAs and Assembly of gRNA Vectors

Optimal target-specific crRNA sequences (20 bp) were identified with the help of the online tool “CHOPCHOP” (http://chopchop.cbu.uib.no/).[16] To predict suitable crRNAs, the genomic target region/gene was entered, and the Y. lipolytica CL1B122 genome sequence and standard settings were chosen. One high-ranking crRNA sequence was chosen for plasmid construction. The crRNA-encoding DNA was ordered as two complementary primers encoding overhangs for plasmid construction. The crRNA-encoding DNA was transformed into the parent strain using a lithium chloride method.[17] The vectors were then gel purified. To construct plasmids pCfB4132 and pCfB4589, biobricks BB1243 and BB1388, respectively, were circularized by self-ligation with T4 ligase.

2.3. Plasmid Construction

All biobricks used in this study are listed in Supporting Information Table S3. Biobricks were amplified by PCR with Phusion U (Thermo Fisher Scientific) under the following conditions: 98°C for 5 min, 30 cycles of 98°C for 10 s, 52°C for 10 s, 72°C for 30 s, 11 kb−1, 72°C for 10 min, and gel purified. The templates and primers used for PCR amplification of each biobrick are listed in Supporting Information Table S3. All vectors were assembled by USER cloning according to Supporting Information Table S2. A typical USER reaction was composed of 0.5 μL CutSmart buffer (NEB), 0.5 μL USER enzyme and 0.8 to 1 μL of each biobrick/linearized parent vector/oligonucleotide (10 μmol). If necessary, water was added to adjust the volume to a total of 5 μL. The reaction was incubated at 37°C for 25 min and 25°C for 10 min followed by transformation into E.coli. Correct assembly was verified by DNA sequencing. The parent vectors for USER reaction were prepared by digestion with restriction endonuclease FastDigest AssI (Life Technologies) and sticky ends obtained by nicking with Nb.BsmI (New England Biolabs). The vectors were then gel purified.

To construct plasmids pCfB4132 and pCfB4589, biobricks BB1243 and BB1388, respectively, were circularized by self-ligation with T4 ligase.

2.4. Strain Construction

DNA was transformed into the parent strain using a lithium-acetate-based protocol.[17] In detail, the parent strain was incubated for 24 hr at 30°C on solid medium prior to transformation. Integration plasmids were linearized with the endonuclease NcoI (Thermo Fisher Scientific) and gel purified. 5 × 10⁷ cells of the parent strain were resuspended in 1 mL sterile water in a 1.5-mL Eppendorf tube. The cells were collected by centrifugation at 3000 × g for 5 min and the water decanted. This washing step was repeated once more. DNA was added to the cell pellet, and mixed by carefully flicking the tube. Then 100 μL transformation mix was added to the tube and mixed by flicking the tube. For integrating vectors with selection marker cassettes, 500 ng DNA was used per transformation. For CRISPR/Cas9 mediated transformations, 500–1000 ng of gRNA plasmid and either 2 nmole of 90 bp double stranded oligonucleotide (if multiple 2 nmole of each) or 500 ng of linearized
promoters were grown overnight in 5 mL SC medium in a microplate reader (Biotek). Biomass was measured as absorbance at 600 nm, and emission at 528 nm. Strains were tested for the cytometry data sets were analyzed and interpreted by FlowJo.

2.8. Determination of Growth Rates
A pre-culture of each *Y. lipolytica* strain was grown in 5 mL SC medium in 13-mL tubes overnight at 30 °C and 250 rpm. The growth rates were determined in 96-well microtiter well plates (Greiner Bio-One). Each well was filled with 150 μL mineral medium and inoculated with 2.5 μL pre-culture. The plates were sealed with Breathe-Easy sealing membrane (Z380059; Sigma–Aldrich) to allow online optical density measurements. The plate was cultivated in a microtiter plate reader (ELx808, BioTek) at 30 °C for 42 hr with agitation. The optical density was measured at 600 nm every 30 min.

3. Results and Discussion

3.1. Construction of the Vectors for the EasyCloneYALI Toolbox

The EasyCloneYALI toolbox enables three key genome-editing operations (Figure 1). 1) The integration of one or two gene expression cassettes into a defined genomic locus using auxotrophic/resistance markers for selection (Figure 1A); 2) The marker-free integration of one or two gene expression cassettes using the CRISPR/Cas9 technology (Figure 1B); and 3) The marker-free knockout/mutation of genes using the CRISPR/Cas9 technology (Figure 1C). To facilitate the integration of gene expression cassettes, we chose to construct integrative expression vectors that target specific intergenic sites. Initially, we choose 11 target regions according to the following criteria. The regions of ca. 5000 bp should be unique, not containing ORFs or other non-coding RNA elements, and the adjacent five ORFs must have high expression levels in both exponential growth phase and under nitrogen limitation. The exact genome location of the integration sites are listed in Supporting Information Table S5. The integration sites were named after their chromosome location, e.g., IntA_1. We constructed 11 integration vectors containing an EasyClone cloning site for standardized cloning.[15] We flanked by the pex20 and lip2 terminator sequences (Figure 2A). The two terminator sequences are in turn each flanked by a 500 bp region homologous to the selected integration site, named up- and downstream region. The set of vectors described in Figure 1A additionally contain a selection marker cassette downstream of the Cas9 cleavage site or of the ORF, and was ordered from Integrated DNA Technologies. The 90mers were designed either to introduce a stop codon and a frame-shift mutation (replacing the PAM motif (NGG)) or for a complete removal of the ORF.

2.5. Design of Double-Stranded 90mer Repair Template for Gene Knockouts via CRISPR/Cas9
To obtain gene knockouts via the CRISPR/Cas9 technology, cells were transformed with a 90 bp double-stranded DNA repair template. The repair template encoded 45 bp up- and 45 bp downstream of the Cas9 cleavage site or of the ORF, and was ordered from Integrated DNA Technologies. The 90mers were designed either to introduce a stop codon and a frame-shift mutation (replacing the PAM motif (NGG)) or for a complete removal of the ORF.

2.6. Phenotyping of Δgfp, Δhph, and Δthi6
Strains were tested for the Δgfp phenotype by resuspending cells in Milli-Q water and measuring biomass and fluorescence in a microplate reader (Biotek). Biomass was measured as absorbance at 600 nm, and fluorescence with excitation at 485 nm and emission at 528 nm. Strains were tested for the Δhph and Δthi6 phenotypes by resuspending cells in Milli-Q water and plating on solid YPD medium with hygromycin and on mineral medium without thiamine, respectively (Supporting Information Figure S4).

2.7. Fluorescence Measurements with FACS
*Y. lipolytica* strains expressing humanized recombinant green fluorescent protein (*hrgfp*) under the control of different promoters were grown overnight in 5 mL SC medium in 13-mL tubes at 30 °C and 250 rpm agitation. An adequate volume was then used to inoculate 500 μL of mineral medium in a 96-deep-well microtiter plate with air-penetrable lid (EnzyScreen) to an initial OD600 of 0.1. Cells were grown at 30 °C and 300 rpm at 5 cm orbit cast for 24–72 hr. For FACS analysis, 30 μL culture was added to 150 μL phosphate buffered saline (PBS) buffer. Cells were then analyzed by flow cytometry using a BD Biosciences Fortessa flow 867 cytometer (Becton Dickinson) with a blue laser (488 nm). For each strain, 10,000 single-cell events were recorded. Flow cytometry data sets were analyzed and interpreted by FlowJo software (Tree Star, Inc.). Outliers were removed from the forward-scattered light (FSC) and side-scattered light (SSC) data sets plot, with the rule for outliers set at 90% quantile region. Cells were analyzed for their mean values. A two-tailed T-tests (p-value <0.05) prove significant difference in fluorescence between Int_B and the remaining 11 integration sites.
by NotI recognition sites allowing excision for yeast transformation. The genome editing via the CRISPR/Cas9 technology required DNA repair templates, either in form of marker-free integration vectors or double-stranded oligonucleotides, respectively (Figure 1B and C). The design of the marker-free integration vectors is similar to the integration vectors with markers but devoid of selection markers (Figure 2A). Further, both applications require the expression of a gRNA from an episomal vector (Supporting Information Figure S1). The episomal vector pCfB3405 was inspired by the P-POT1 plasmid.[20] The vector is composed of the Pot1 promoter fused to the CEN1 sequence for replication in Y. lipolytica,[21] adjacent to the EasyClone cloning site.[15] Further, the plasmid contains a nat resistance marker for selection on the antibiotic nourseothricin, as well as an ampicillin resistance cassette and puC ori for propagation in E.coli. Next, the gRNA expression cassette was cloned into the linearized vector pCfB3405. The gRNA expression cassette is composed of four elements: the tRNA-Gly (YALI0A04565r), functioning as RNA III polymerase promoter (encoded by BB1635), the crRNA sequence (target specific 20 bp), followed by the tracrRNA sequence fused to the RPR1 terminator sequence (encoded by BB1636) (Supporting

<table>
<thead>
<tr>
<th>Int. sites</th>
<th>PrExp1-Ura3</th>
<th>PrExp1-Hph</th>
<th>PrTetron-Nat</th>
</tr>
</thead>
<tbody>
<tr>
<td>IntB</td>
<td>pCfB4586</td>
<td>pCfB4132</td>
<td>pCfB4848</td>
</tr>
<tr>
<td>IntA,1</td>
<td>pCfB5935</td>
<td>pCfB4780</td>
<td></td>
</tr>
<tr>
<td>IntC,1</td>
<td>pCfB6577</td>
<td>pCfB4781</td>
<td></td>
</tr>
<tr>
<td>IntC,2</td>
<td>pCfB6578</td>
<td>pCfB4782</td>
<td></td>
</tr>
<tr>
<td>IntC,3</td>
<td></td>
<td>pCfB4786</td>
<td></td>
</tr>
<tr>
<td>IntD,1</td>
<td>pCfB4796</td>
<td>pCfB4780</td>
<td></td>
</tr>
<tr>
<td>IntE,1</td>
<td>pCfB4778</td>
<td>pCfB6574</td>
<td>pCfB4666</td>
</tr>
<tr>
<td>IntE,2</td>
<td>pCfB6575</td>
<td>pCfB4779</td>
<td></td>
</tr>
<tr>
<td>IntE,3</td>
<td>pCfB6576</td>
<td>pCfB4783</td>
<td></td>
</tr>
<tr>
<td>IntE,4</td>
<td>pCfB5219</td>
<td>pCfB4787</td>
<td></td>
</tr>
<tr>
<td>IntF,1</td>
<td>pCfB5791</td>
<td>pCfB5690</td>
<td>pCfB4784</td>
</tr>
<tr>
<td>IntF,2</td>
<td>pCfB5681</td>
<td>pCfB4785</td>
<td></td>
</tr>
</tbody>
</table>

Figure 1. EasyCloneYALI toolbox applications. A) The EasyCloneYALI toolbox contains a set of 27 standarized vectors for integration of gene expression cassettes into defined genome loci (named Int(chromosome)_#). B) A marker-free integration of gene expression cassettes into defined genomic loci is mediated by CRISPR/Cas9. C) Marker-free gene deletions with CRISPR/Cas9. A Cas9-expressing strain is transformed with a target-specific gRNA vector and a DNA repair template. The DNA repair template can be designed to introduce point mutations (frame-shift, premature stop-codon, amino acid changes) or to delete the entire ORF.
marker cassette, allowing growth on D-serine.[24] This plasmid has been used for genome engineering of Y. lipolytica strains resistant to hygromycin (unpublished data). We integrated the Cas9 gene as we were unable to maintain to episomal plasmids in one cell. A detailed description of the molecular cloning workflow can be found in the supplementary handbook.

3.2. Evaluation of Genome Integration Sites

To validate how the integration of a gene expression cassette into the genome integration sites affects gene expression levels and cell growth, hrgfp was cloned into each of the 11 integration vectors under the control of the GPD promoter and transformed into Y. lipolytica ST3683. GFP fluorescence was used to evaluate hrgfp expression levels (Figure 2B). All 11 strains (ST5143-ST5149, ST5235-5238) displayed higher fluorescence levels, with 44–139% increase, compared to the control strain (ST4296) which express hrgfp from a previously described integration site IntB.[23] The majority replicate clones differed not more than 11% in emitted fluorescence from each other, which indicates that no multiple integrations have occurred. Only two out of 28 clones showed a 30% and 50% increase in fluorescence compared to their respective replicate clones. The growth rate of the strains was not affected by the integration of the gene expression cassette (Supporting Information Table S6).

3.3. Compatibility of Y. lipolytica Promoters with the Standarized EasyCloneYALI System

To ease the usage of the EasyCloneYALI toolbox and to decrease the lab workload, promoter and gene biobricks contain standardized overhangs. Twelve frequently used Y. lipolytica promoters were adapted to the EasyClone system and cloned to control hrgfp expression. The vectors were integrated into the Y. lipolytica genome and GFP fluorescence was used to evaluate hrgfp expression levels (Figure 2C). We detected promoter activities for the fba1, icl1, yat1, ilv5, tef1, exp, gpd, and tef1in promoters. The DNA sequences of the promoters can be found in supplementary data. No fluorescence could be detected for the strains expressing hrgfp from the gpat, dga1, ggm1, or fba1in promoters. The tefin promoter (tef promoter combined with its intron) has previously shown to provide a 17-fold increase in expression compared to the tef promoter alone.[25] However, when we introduced the EasyClone linker between the tef promoter’s intron and hrgfp, fluorescence level was similar to the TEF promoter without intron. To test whether the EasyClone linker influenced the promoter activity, we fused hrgfp directly to the tefin promoter, omitting the start codon of hrgfp as described previously.[25] This strain showed fluorescence levels 7.4-fold higher than the strain expressing hrgfp from the EasyClone-adapted tefin promoter. To test whether the linker also influenced promoter strength of a non-intronic promoter, we constructed a strain expressing hrgfp from the gpd promoter without EasyClone linker. In this case the EasyClone-adapted gpd promoter led to 24% higher fluorescence levels than the GPD promoter without the EasyClone linker. As
standardization of biobricks facilitates the workflows, we decided to proceed with the positively evaluated EasyClone-standardized promoters.

3.4. Selection Marker-Mediated Integration of Gene Expression Cassettes

The Y. lipolytica strains used in this study lack Ku70p, which is involved in DNA double-strand repair by non-homologous end-joining (NHEJ).\[^7,8\] Deletion of ku70 gene in Y. lipolytica has been shown to increase the rate of DNA double-strand breaks repaired by homologous recombination.\[^7,8\] The strain is slightly higher sensitive to UV light.\[^7\] We constructed a set of integration vectors harboring auxothrophic or antibiotic selection markers (Figure 1A). Then we determined the integration efficiencies of the vectors containing a nourseothricin selection marker targeting different integration sites (Figure 3A). The vectors integrated with more than 50% efficiency, with exception of vector targeting site IntE1, for which the efficiency was ca. 30%.

3.5. Validation of Genome Editing via CRISPR/Cas9 Technology

Vectors constructed for marker-free integration into the genome were evaluated by transforming the linearized integration vectors together with their corresponding gRNA vector into strain ST5010 (Δku70 hrgfp hph Cas9) (Figure 1B and Supporting Information Table S7). Strain ST5010 grows at a maximum specific growth rate of 0.21 ± 0.04 hr\(^{-1}\) similar to its parent strain (0.19 ± 0.06 hr\(^{-1}\)) and did not seem to be affected by constitutive Cas9 expression. Also, the Cas9 expression vector pCfB4906 integrated with an efficiency of 67% similar to the empty IntB integration vector. For marker free integration, we tested two gRNA vectors for each integration site. Three days post transformation, colonies were screened for correct integration of the EasyCloneYALI vectors by colony PCR. The integration efficiencies, with exception of vector targeting site IntE1, for which the efficiency was ca. 30%, ranged from 0% to 95% (Supporting Information Table S7). For five out of the 11 sites, IntC_2, IntC_3, IntD_1, IntE_1 and IntE_3, integration efficiencies of above 80% could be obtained, and 30% for IntE_4 (Figure 3B). For the remaining sites, only 0–12% of the colonies had the vector correctly integrated. Interestingly, the two gRNA sequences tested for integration site IntE_3 lead to 95% and 12% efficiency, respectively, although they target the same genomic region overlapping in 15 out of 20 nucleotides (Supporting Information Figure S3). We are currently investigating this difference in more detail. The simultaneous integration of two integration vectors was not successful.

We evaluated the EasyCloneYALI toolbox for knockout of genes, by targeting hrgfp, hph, and thi6 allowing an easy phenotypic screening. Knockout of hrgfp leads to loss of fluorescence, knockout of hph loss of resistance to hygromycin, and without thi6 the cells are unable to grow without thiamine supplementation in the medium. The repair templates were designed to introduce a premature stop-codon and a frame-shift into hrgfp and hph, and to delete the whole ORF of thi6 (Figure 1C). We validated the toolbox for single, double, and triple knockout of genes (Figure 3C). For all three single genes knockouts, efficiencies of around 90% could be achieved, while the knockout-efficiencies for two genes simultaneously varied depending on the gene combination — between 6% and 66% (Figure 3C). The knockout of three genes simultaneously was not successful. To confirm that the dsDNA break generated by CRISPR/Cas9 was repaired via the HR pathway, colony PCR was performed on all confirmed Δthi6 colonies of a transformation targeting gfp and thi6 simultaneously. 100% of the 14 Δthi6 colonies that had repaired the dsDNA break by using the supplied double-stranded oligonucleotide.
Following the EasCloneYALI toolbox manual, a new strain can be obtained within 6 days, comparable to the protocol described by Ref. [13]. The transformation is performed on Day 1 (4 hr required), followed by 2–3 days incubation on selective plates. On Day 3 the colonies are genotyped by colony PCR and correct clones are inoculated in non-selective media for gRNA vector removal overnight. A diluted suspension of the overnight culture is ready for a new round of transformation on Day 6. Optionally the strain can be tested for sensitivity towards nourseothricin to confirm gRNA vector loss.

4. Discussion

We demonstrated that the EasyCloneYALI toolbox can be used for reliable and fast strain engineering of *Y. lipolytica*. We identified 11 intergenic sites with high gene expression levels and validated that integration of gene expression cassettes into these sites did not affect the growth. For marker-mediated integration of the expression vectors, we determined integration efficiencies of 33% to 100%. Similar efficiencies of 56% and 85% have been previously reported for Δku70 strains[7,8] or 73% for *ku70*-repressed strains[26] The CRISPR/Cas9-mediated integration of gene expression constructs into sites IntC_2, IntC_3, IntD_1, IntE_1, and IntE_3 occurred with efficiencies above 80%. A previous study reported efficiencies of 47% to 69%.[13] For single genome edits, efficiencies above 80% could be achieved, compared to 58% and 100% knockout efficiency reported for a Δku70 strain by Gao et al.[11] and Schwartz et al.[12] in 2016 (Figure 3). When deleting different combinations two genes variable efficiencies of 5.9% to 66% were obtained while a triple knockout was not successful (Figure 3C). Gao et al.[11] achieved efficiencies of 36% and 19% for a double and triple gene knockout, respectively, using a plasmid-based CRISPR/Cas9 system in a *ku70* strain and 4 days of recovery time.[13] Comparisons of these knockout efficiencies should be taken with caution as the studies target different genes and experimental protocols. In the EasyCloneYALI protocols, linear DNA fragments, as commercial double-stranded oligonucleotides or PCR products, can be used as repair templates instead of episomal vectors, and time-consuming cloning of plasmids can be avoided. Additionally, the toolbox allows the knockout of two genes or integration of two gene expression cassettes simultaneously (Figures 2 and 3). The EasyCloneYALI integration vectors have been used for multiple rounds of genome engineering and no loss of already integrated cassettes could be detected[27] By standardizing molecular cloning, promoter and gene biobricks as well as linearized parent plasmids can be reused and easily exchanged between lab members.

**Abbreviations**

Cas9, CRISPR-associated nuclease; CRISPR, Clustered Regularly Interspaced Short Palindromic Repeats; HR, homologous recombination; NHEJ, non-homologous end joining.

**Supporting Information**

Supporting Information is available from the Wiley Online Library or from the author.

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**Conflict of Interest**

The authors declare no financial or commercial conflict of interest.

**Keywords**

CRISPR/Cas9, integrative vectors, metabolic engineering, *Yarrowia lipolytica*, yeast

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