

Supplementary materials for

A pathway independent multi-modular ordered control system based on thermosensors and CRISPRi improves bioproduction in *Bacillus subtilis*

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Table. S1 Primers used in this study

Primer	Sequence
futc-F1	AGAGGCGATTATGTTGGCATTG
futc-R1	CGGATAGCCCAGATCCAGATT
manB-F1	TGGCGGCATTGAAGTTACC
manB-R1	TCATCAACGGGAGGGAAGTC
ndk-F1	TCAGAGCCGTGGATGATGTT
ndk-R1	ACCTGTATTCGCAATGGTGTG
gmk-F1	CCAAGAGAGGGCGAAGTGA
gmk-R1	AAGCGTCTGTTCAACATAATCG
zwf-F1	AGCACACGCACAGCCAAT
zwf-R1	CTCCAAGAAAGGGCAACTTCAT
pfkA-F1	GGTCAGCAGCACTCGGAGAA
pfkA-R1	GCGGCAAGAAGCACAGTATT
lytC-F1	GACTTCTTTCTCAAGGAGTCC
lytC-R1	GAAACACTCCTGCCGTAAG
FL-hbs-F	CGTTCACGCACCTCGAAGTTACC
FL-hbs-R	CGGTTGCAGAAGCAAGCGAATTG
ameye-D-F	CGGAAGAAACATTTGGCTAATTCCCCATTGAGGGCAAG
ameye-D-R	TGTGAAGGAACTGTTCTTTTTCTTT
ameye-F	CTGGATTTTTATTGCTGTTTCATT
ameye-R	AGTTCAGCTCAGTGATACCTG
ameye-S-F	GATAGCTTCTCGTTCAGGCGAGCGGATAACAATTTACACAG
ameye-S-R	TCTTTTTTGTTGACATGTGTACATTTACCTCCTTTG
ameye-U-F	GCAAAACGATTCAAAACCTCT
ameye-U-R	GTGAAATTGTTATCCGCTCGCCTGAACGAGAAGCTATC
CI857-F	CAAAGGAGGTGAAATGTACACATGTCAACAAAAAAGAAACCGC
CI857-R	CCCTCAATGGGGAATTAGCCAAATGTTTCTTCCGG
Pveg-NF1	AACACCTTATTAACGTTGATATNAACACCGTGCGTGTTNACATACCTCT GGCGGTGATAA
Pveg-NF2	AACACCTTATTAACGTTGATATTNNNNNCGTGCCNNNNNGACATACCTCT GGCGGTGATAA
Pveg-NF3	AACACCTTATTAACGTTGATATTAACACNNNNNGTGTTGACATACCTCT GGCGGTGATAA
Pveg-NR	AATATCAACGTTAATAAGGTGTTAGATATTTAT

H-Pveg5-F	CATGGATGAACTGTACAAATAACTGCAGGTCGACGTCC
H-Pveg5-R	CGCACGGTGTTAATATCAACGTTAATAATAGAGCGCAACGCAATTAATG
Pveg5-F	CATTAATTGCGTTGCGCTCTATTATTAACGTTGATATTAACACCGTGCG
Pveg5-R	GTCGACCTGCAGTTATTTGTACAGTTCATCCATGCCA
npre-F	CTTGCGGCAGCCATCTTCAC
npre-R	GCCATCGTCACCCACTTA
ganA-F	GTGATGTCAAAGCTTGAAAAACG
ganA-R	TTTTCCAAAGCAATAACGCTGGA
bpr-F	TTAGGCGCATTAAACAGTCGGC
bpr-R	GGATGAATAATCGCGTCAAAC
epr-F	TTGTGCAGACTCTGAAAAGGT
epr-R	ACTGAAGCCGACTAAAATCGGC
apre-F	AACATCAGGATGCTGACAAATAAAA
apre-R	AGAGGGTAAAGAGTGAGAAGC
ldh-R	TTGAAGGCAGGAAGGCT
ldh-F	GCAACAAAATTGCCTGATGG

Table. S2 Plasmids used in this study

Plasmid	Characteristics	Ref.
pHTa0	ColE1 Amp ^r , Cm ^r , <i>E. coli</i> - <i>B. subtilis</i> shuttle vector, $\Delta P_{grac}::$ <i>egfp</i>	Lab stock
pHTa1	pHTa0 derivate, P _R - <i>egfp</i>	This work
pHTa1-2	pHTa0 derivate, P _{veg} - <i>egfp</i>	This work
pHTa2	pHTa0 derivate, P _{veg1} - <i>egfp</i>	This work
pHTa3	pHTa0 derivate, P _{veg2} - <i>egfp</i>	This work
pHTa4	pHTa0 derivate, P _{veg3} - <i>egfp</i>	This work
pHTa5	pHTa0 derivate, P _{veg4} - <i>egfp</i>	This work
pHTa6	pHTa0 derivate, P _{veg5} - <i>egfp</i>	This work
pP43-mCherry	ColE1 Amp ^r , RepB Km ^r , <i>E. coli</i> - <i>B. subtilis</i> shuttle vector, mCherry expressed from P ₄₃	This work
pLCT-dCpf1	pMB1 Spec ^r , Cm ^r P _{veg5} -dCpf1 integrant expression at <i>nprE</i> locus of <i>B. subtilis</i>	This work
pLCT2-dCpf1	pMB1 Spec ^r , Cm ^r P _{veg} -dCpf1 integrant expression at <i>ganA</i> locus of <i>B. subtilis</i>	This work

Table S3. Sequences of genetic parts used in this study

Name	Sequence
<i>P_{veg}</i>	TTATTAACGTTGATATAATTTAAATTTTATTTGACAAAAATGGGCTCGTGTT GTACAATAAATGT
<i>P_{veg1}</i>	TTATTAACGTTGATATAATTTAAATTTTATTTGACATAACACCGTGCGTGTT GTACAATAAATGT
<i>P_{veg2}</i>	TTATTAACGTTGATATTAACACCGTGCGTGTTGACAAAAATGGGCTCGTGT TGTACAATAAATGT
<i>P_{veg3}</i>	TTATTAACGTTGATATAATTTAAATTTTATTTGACAAAAATGGGCTCGTGTT GTACAATAAATGTAGTAACACCGTGCGTGTTG
<i>P_{veg4}</i>	TTATTAACGTTGATATTAACACCGTGCGTGTTGACAAAAATGGGCTCGTGT TGTACAATAAATGTAGTACCTCTGGCGGTGATAA
<i>P_{veg5}</i>	TTATTAACGTTGATATTAACACCGTGCGTGTTGACATACCTCTGGCGGTGA TAATACAATAAATGT
<i>P_{veg32}</i>	TTATTAACGTTGATATTTATTGCGTGCATGTTGACATACCTCTGGCGGTGA TAATACAATAAATGT
<i>P_{veg34}</i>	TTATTAACGTTGATATTAACACGGGTAGTGTTGACATACCTCTGGCGGTGA TAATACAATAAATGT
<i>P_{veg37}</i>	TTATTAACGTTGATATTGGCGGCGTGCTCGTTGACATACCTCTGGCGGTG ATAATACAATAAATGT
<i>zwf</i> - crRNA1	GCAAAACGAAAATTGTATCCGTC
<i>zwf</i> - crRNA2	TGCGCGGACAATATCATGCTGGT
<i>zwf</i> - crRNA3	GTGAAAGACGGCTTACACTGGTG
<i>pfkA</i> - crRNA1	CAACGGATACGCGGGATTGATCA
<i>pfkA</i> - crRNA2	CATGTGTAGGTGTACCGGTACA
<i>pfkA</i> - crRNA3	AAGAAGAAACAAATCTTGAAACT
<i>lytC</i> - crRNA1	GCCGATAACTCAGTGAAAAGAGT
<i>lytC</i> -	AACGGCTTCTTATATGCAGACGC

crRNA2

lytC-

TCAGTATACATGCAAATGCTAAT

crRNA3

ATGTCAACAAAAAAGAAACCGCTGACACAAGAACAACCTGGAAGATGCAAG
AAGACTGAAAGCAATTTATGAAAAAAGAAAAATGAACTGGGCCTGTCACA
AGAATCAGTTGCAGATAAAATGGGCATGGGCCAAAGCGGCGTTGGCGCA
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TTTTCTGCAACCGCTGAATCCGCAATATCCGATGATTCCGTGCAATGAAT
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TTTGGCTAA

CJ⁸⁵⁷

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TCAAACACGGCGCGGATATGGGCATTGCCTTTGATGGCGATTTTGACCGC
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GGCCTGCTGGCAGAAGCATTCTCGAAAAAATCCCGGCGCGAAGATCA

manB

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futC

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GCCAGTCGATTATGTTGAACAGACGCTTCAAGATGGAAGAACGCTTTTTT

gmk

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 TCGTGACACGAGGAACAGAAACAGACGCTCTGATTGAAAATCGAATGAAA
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 AGGTTGAATAA

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 AGATTTTAGCGACGGATATTGATGAAAAAGCATTGGAAAAAGCGAAAAAA
 GGCGTTTATCAGGAGCGGTCTTTACA

Table S4 Hill-equation fitting parameters of gene expression fine-tuning

Promoter	y_{min}	y_{max}	K	n	R^2
P_{veg5}	19.97805 ± 14.5704	2378.71118 ± 29.95501	38.21927 ± 0.04872	62.02255 ± 2.92182	0.99959

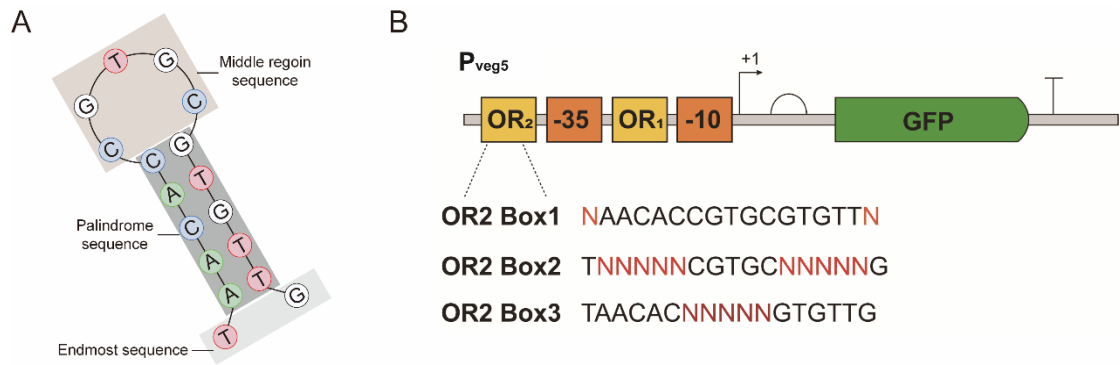


Figure S1 (A) Modular OR₂ sequence, including endmost sequence module (T and G), palindrome sequence module (AACAC and GTGTT) and middle region sequence module (CGTGC). (B) Three type of promoter mutation libraries at the OR₂ region.

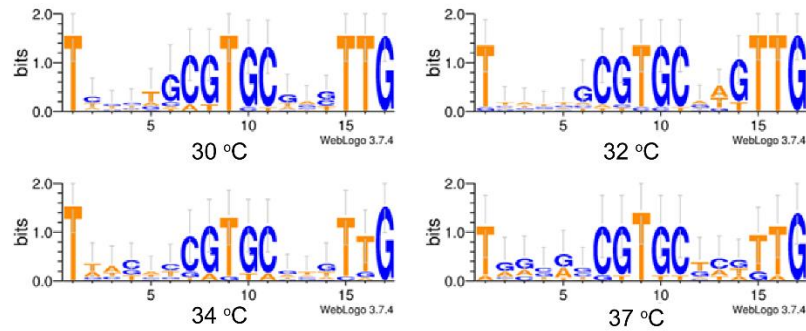


Figure S2 Sequence features at OR₂ region of promoter variants with different transition points (30, 32, 34 and 37 °C).

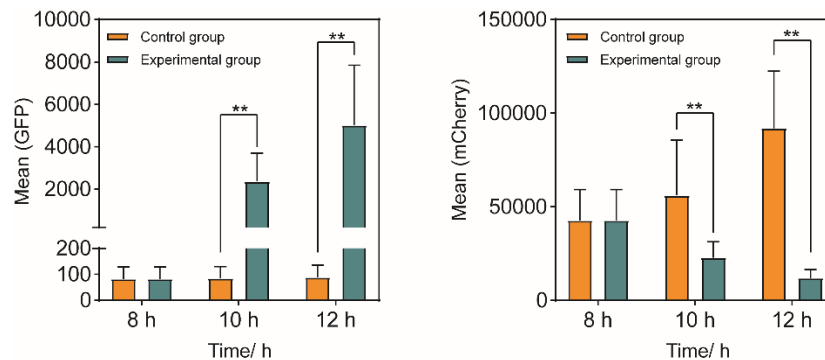


Figure S3 The switching effects of bifunctional temperature-responsive genetic circuits. The control group was cultured under constant temperature fermentation at 32 °C for 12 h and the experimental group was cultured by using single-switch control (0-8 h at 32 °C and 8-12 h at 39 °C).

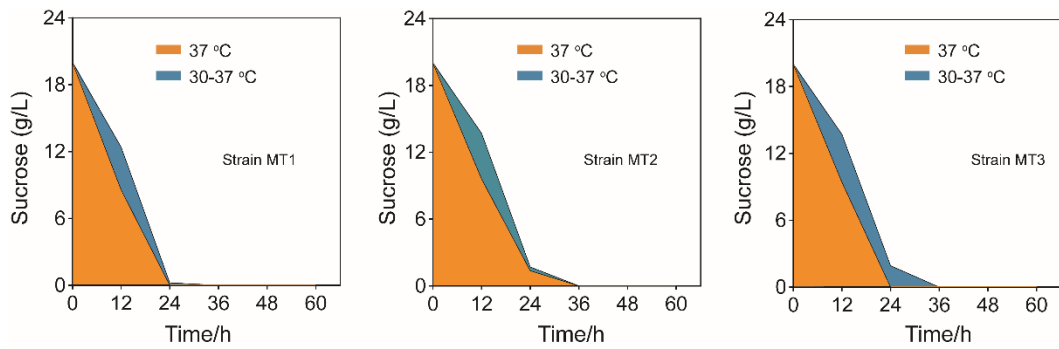


Figure S4 The sucrose concentration of strain MT1, MT2 and MT3 under different bioprocesses, including constant temperature fermentation at 37 °C for 60 h and single-switch control (0-12 h at 30 °C and 12-60 h at 37 °C).

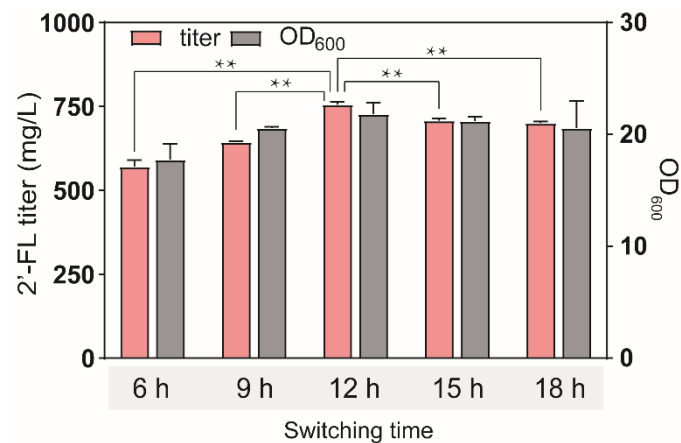


Figure S5 The cell growth and 2'-FL titer of strain MT3 (*manB* and *futC* were driven by P_{veg34}) under single-switch control from 30 to 37 °C with different switching times (6, 9, 12, 15 and 18 h). The statistical analysis is based on Student's *t*-test. All data were the average of three independent studies with standard deviations. ** $P < 0.01$.

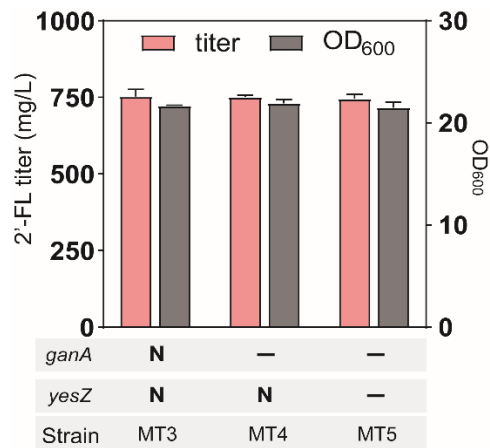


Figure S6 OD₆₀₀ and 2'-FL titer of strain MT3, MT4 and MT5 with single-switch control (0-12 h at 30 °C and 12-60 h at 37 °C). The strain MT4 was obtained by knocking out gene *ganA* of strain MT3, and MT5 was obtained by knocking out *yesZ* of strain MT4. 'N' means no knockout and '-' means knockout. All data were the average of three independent studies with standard deviations.

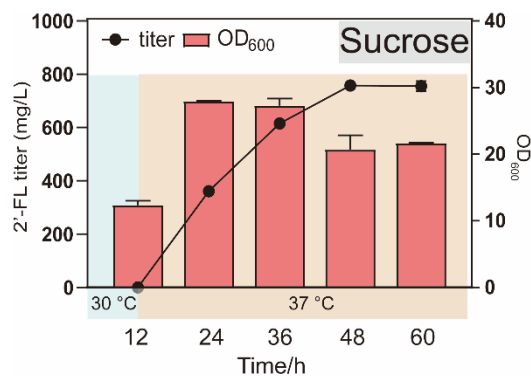


Figure S7 The fermentation process of strain MT3. Trends of OD₆₀₀ and 2'-FL titer in shake flask with single-switch control. Data are presented as mean ± s.d. of three replicates.

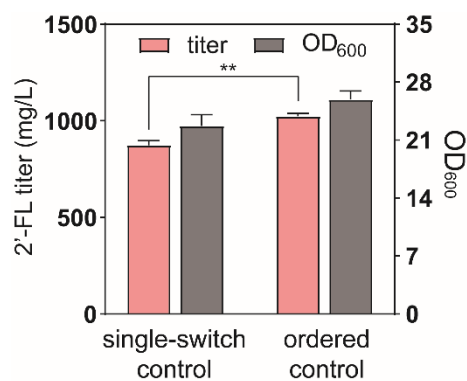


Figure S8 OD₆₀₀ and 2'-FL titer of strain MT14 under different control strategies, including

single-switch control and ordered control (0-12 h at 30 °C ,12-18 h at 34 °C and 12-60 h at 37 °C). The statistical analysis is based on Student's *t*-test. All data were the average of three independent studies with standard deviations. ***P* < 0.01.

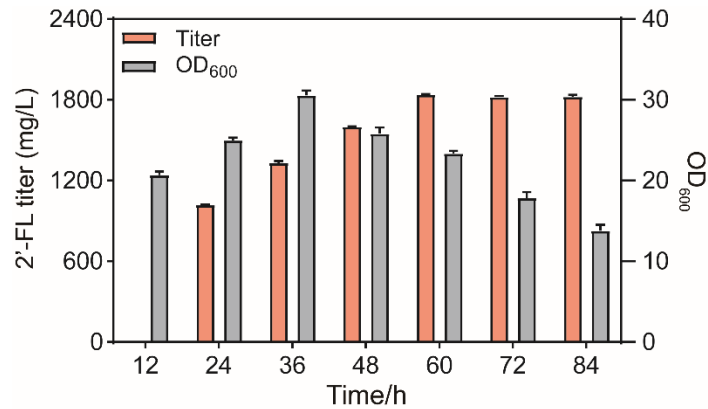


Figure S9 The OD₆₀₀ and 2'-FL titer of strain MT17 for 84 h. All data were the average of three independent studies with standard deviations.

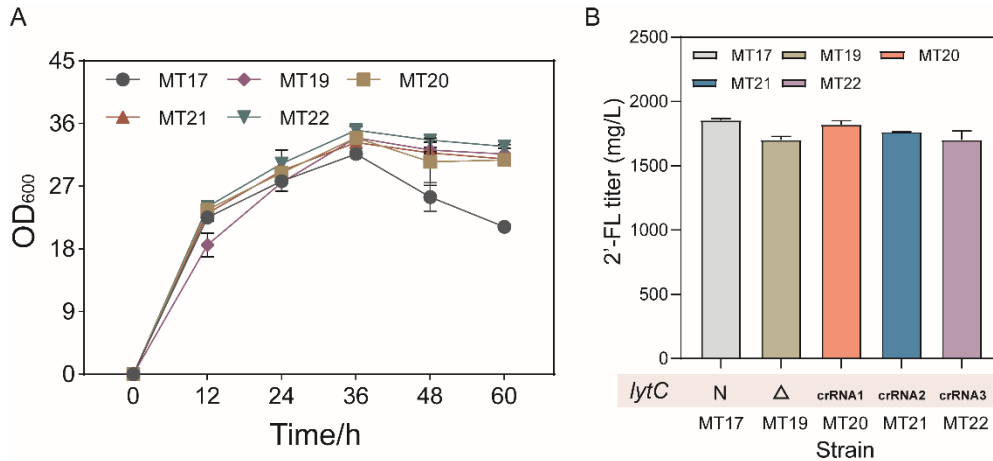


Figure S10 (A) The OD₆₀₀ of recombinant strains with knocking out or knocking down *lytC* in shake flask. (B) The 2'-FL production of recombinant strains in shake flask. "N" means the native gene *lytC* was not engineered. "Δ" means the gene *lytC* was knocked out. The strain MT19 was obtained by knocking out *lytC* directly from the control strain MT17. Three crRNAs that targeted to different positions on *lytC*, driven by the promoter *P_{veg5}*, were integrated into the genome of MT17, resulting in the strains MT20 (crRNA1), MT21 (crRNA2) and MT22 (crRNA3), respectively. All data were the average of three independent studies with standard

deviations.

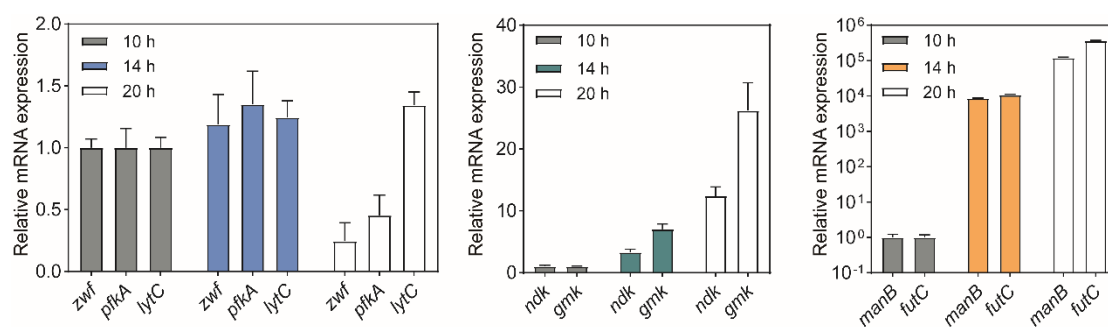


Figure S11 Relative normalized expression of genes *manB*, *futC*, *ndk*, *gmK*, *lytC*, *zwf* and *pfkA* in strain MT17 by using multi-modular ordered control (0-12 h at 30 °C, 12-18 h at 34 °C and 18-80 h at 37 °C). Data are presented as mean \pm s.d. of three replicates.

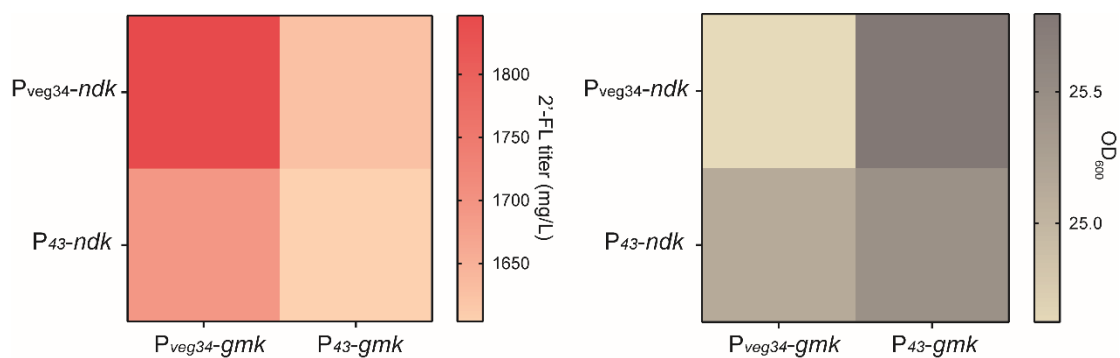


Figure S12 The cell growth and 2'-FL titer of GTP recycling-modified strains, including MT17, and the recombinant strains with constitutive overexpression of GTP supply by promoter *P₄₃*. The statistical analysis is based on Student's *t*-test. All data were the average of three independent studies with standard deviations.