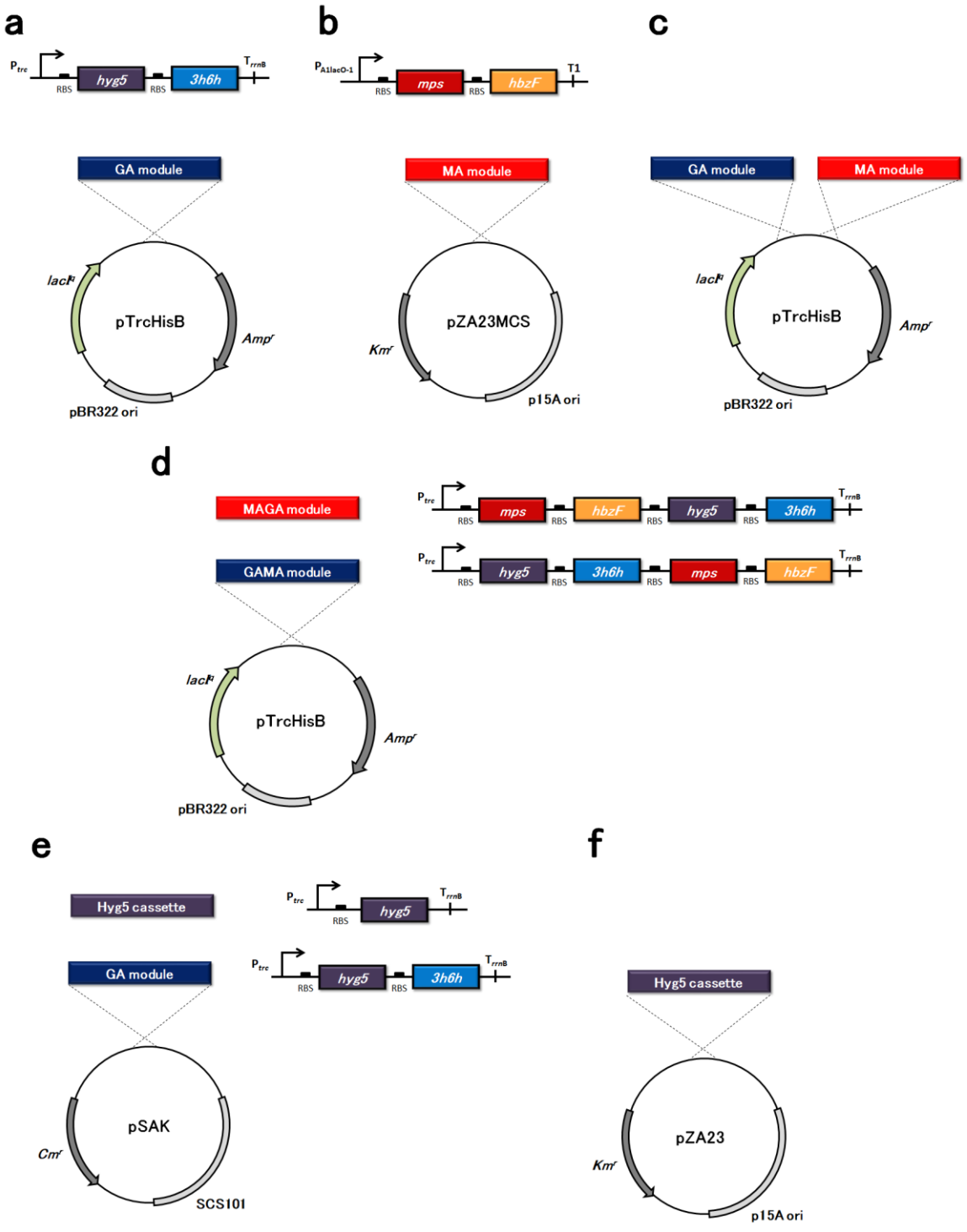
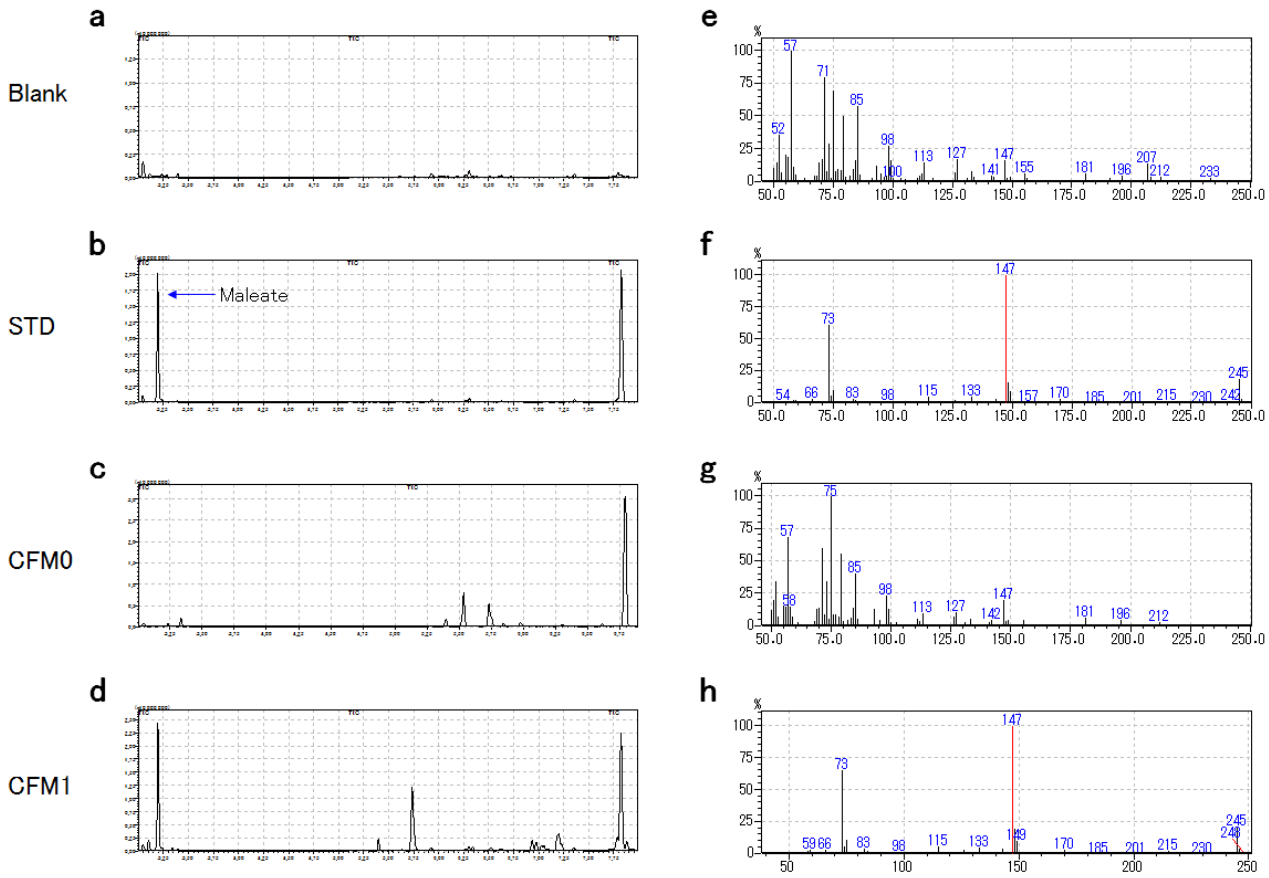
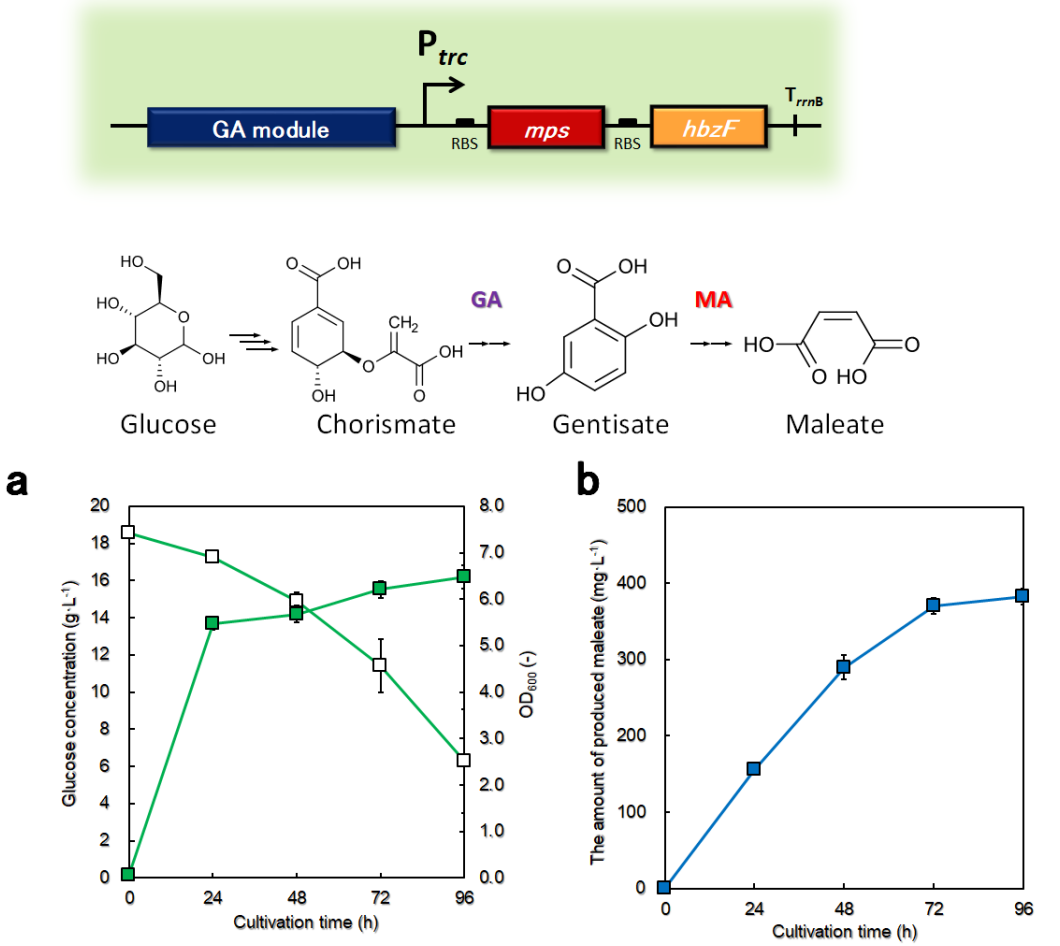

a
b
c
GA module
MA module
GA module
MA module
pTrcHisB
pZA23MCS
pTrcHisB
pBR322 ori
p15A ori
pBR322 ori
d
MAGA module
GAMA module
pTrcHisB
pBR322 ori
e
Hyg5 cassette
GA module
pSAK
SCS101
f
Hyg5 cassette
pZA23
p15A ori

**Supplementary Figure 1 | Maps of the plasmids constructed in this study.** (**a**) pTrcHisB carrying the GA module (pTcgl3026, pT3hb6h, and pTxlnD). (**b**) pZA23MCS carrying the MA module (pZA23psal, pZA23ppu1, pZA23palc, pZA23rsp, and pZA23ppu2). (**c**) pTrcHisB carrying the GA and MA modules (pT2c101-104 and pT2c201-204). (**d**) pTrcHisB carrying the MAGA or GAMA module (pT2t01 or pT2t02). (**e**) pSAK carrying the Hyg5 cassette or GA module (pS09 or pS10). (**f**) pZA23MCS carrying the Hyg5 cassette (pA09).

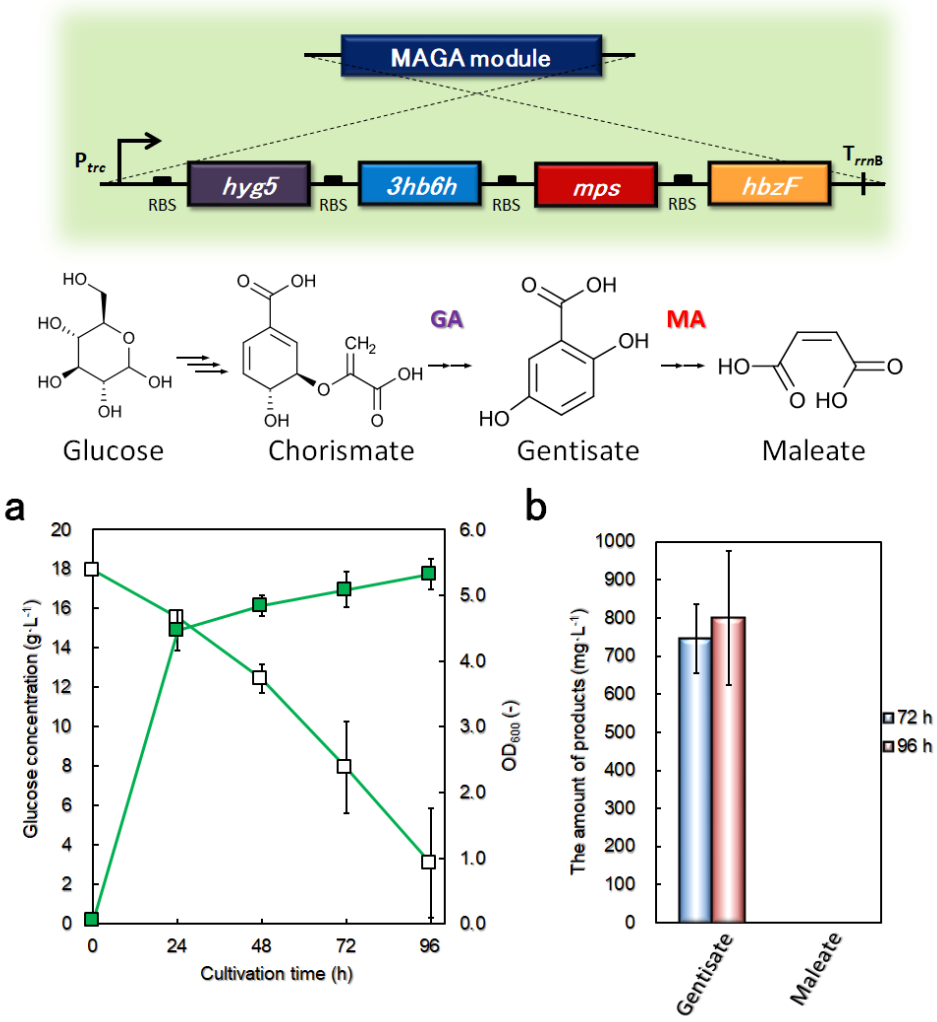



**Supplementary Figure 2 | Confirmation of maleate production by gas chromatography–mass spectrometry analysis.** (**a–d**) GC–MS chromatograms of maleate production. (**e–h**) MS spectra at 3.2 min in the GC–MS analysis. Each pair of **a** and **e**, **b** and **f**, **c** and **g**, and **d** and **h** presents the results for a blank, standard sample, CFM0, and CFM1, respectively.



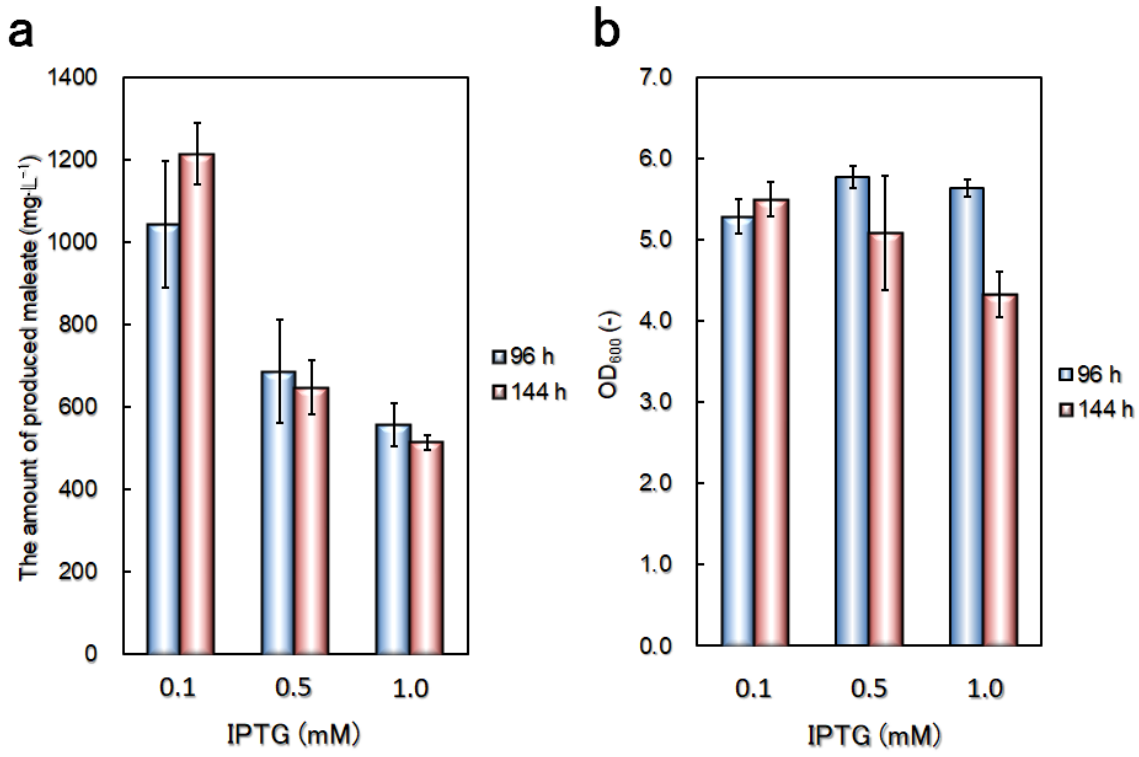

**Supplementary Figure 3 | Culture profile of CFM9 during maleate production.**

Time courses of (**a**) the glucose concentration (open symbols) and $OD_{600}$ (filled symbols), and (**b**) the amount of produced maleate. Data are presented as the mean ± standard deviation of three independent experiments ($n$ = 3).

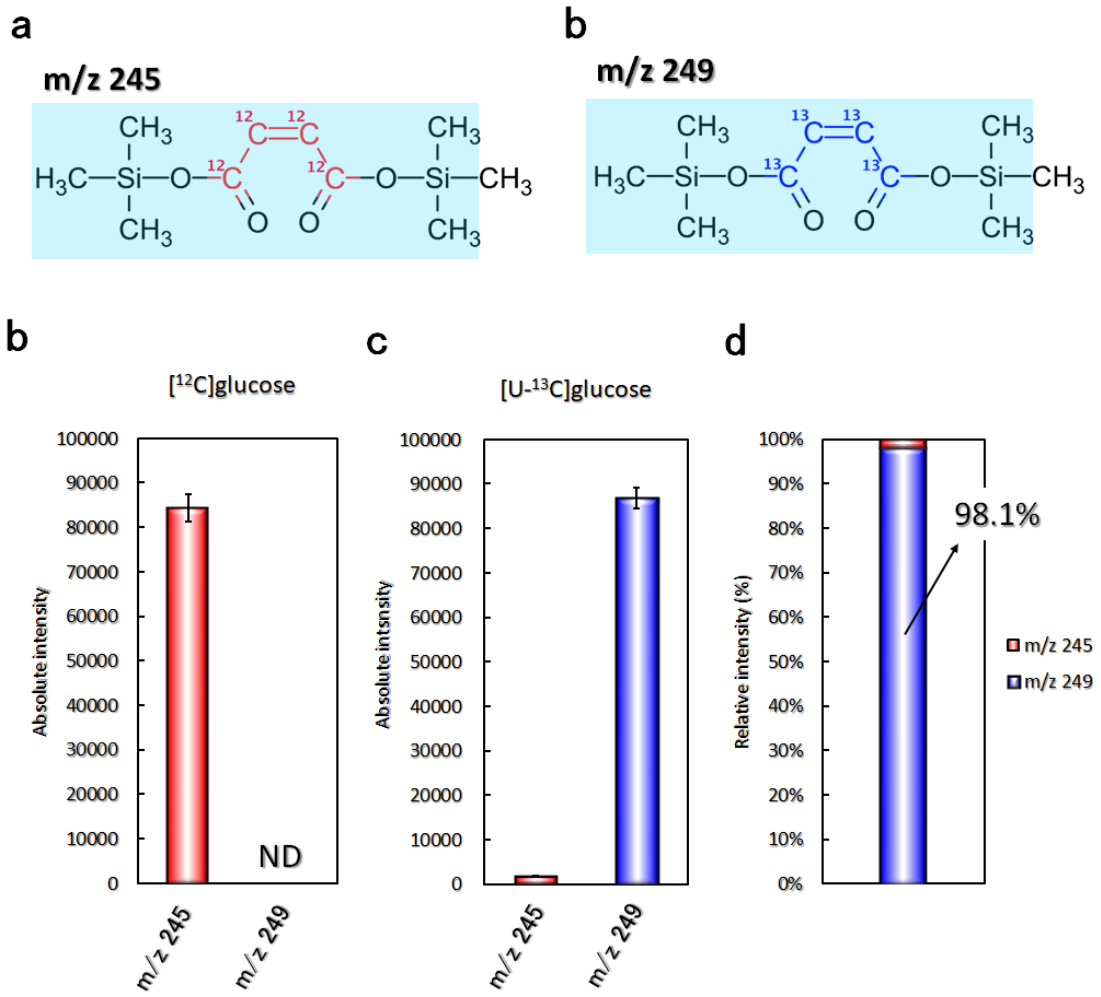



**Supplementary Figure 4 | Culture profile of CFMt2 during maleate production.**

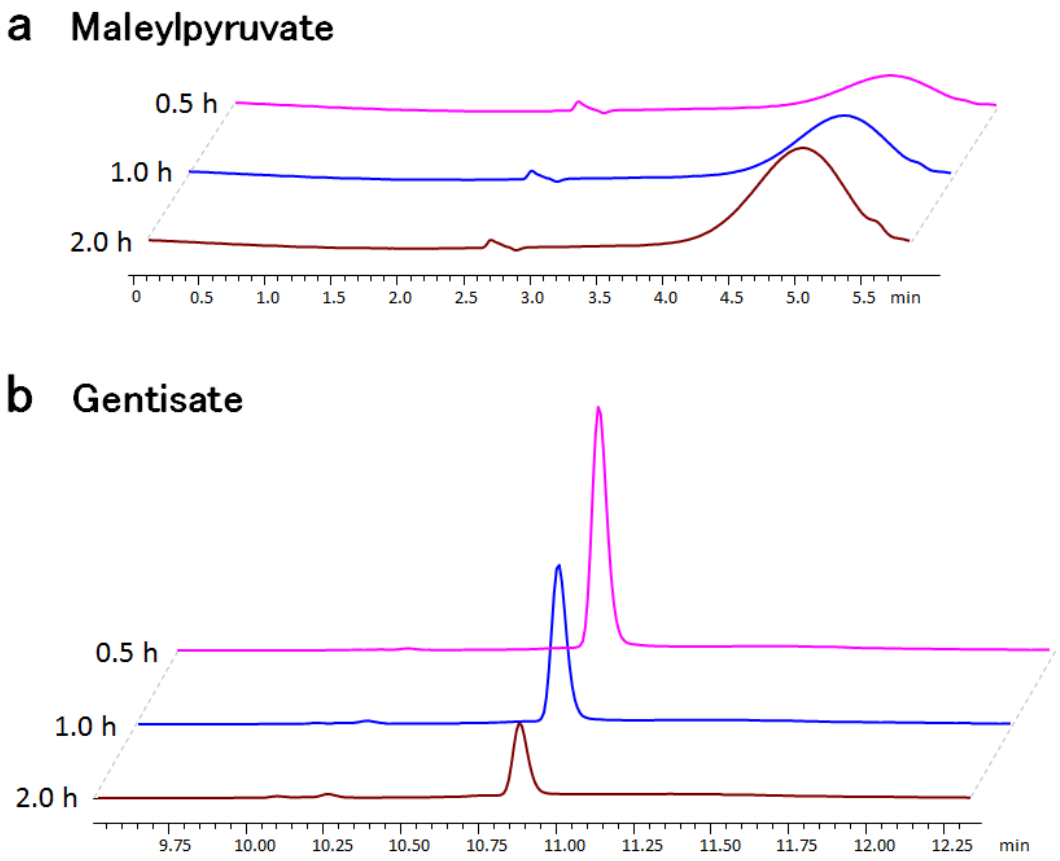
Time courses of (**a**) the glucose concentration (open symbols) and $OD_{600}$ (filled symbols), and (**b**) the amounts of produced maleate and gentisate. Data are presented as the mean ± standard deviation of three independent experiments ($n$ = 3).




**Supplementary Figure 5 | Effects of the concentration of β-D-1-thiogalactopyranoside (IPTG).** (**a**) Amounts of maleate produced by CFMt1 after 96 and 144 h of cultivation. (**b**) $OD_{600}$ values of CFMt1 after 96 and 144 h of cultivation. Data are presented as the mean ± standard deviation of three independent experiments ($n$ = 3).




**Supplementary Figure 6 | Labeling pattern of maleate produced by CMtS101 cultured using [$^{12}$C]glucose or [U-$^{13}$C]glucose as the carbon source.** (**a**) Structure of maleate–bis(trimethylsilyl) ester derivative and m/z of the demethylated product. (**b**) Absolute intensity of m/z = 245 and 249 in the case of using [$^{12}$C]glucose. (**c**) Absolute and (**d**) relative intensity of m/z = 245 and 249 in the case of using [U-$^{13}$C]glucose. Data are presented as the mean ± standard deviation of three independent experiments (*n* = 3).




**Supplementary Figure 7 | Time-course high-performance liquid chromatography chromatograms** of (**a**) maleylpyruvate formation and (**b**) gentisate consumption in enzymatic conversion of gentisate to maleylpyruvate.

**Supplementary Table 1. Summary of the amounts of consumed glucose and yields of produced gentisate in cultures of CFG1-3.** Data are presented as the mean ± standard deviation of three independent experiments ($n$ = 3).

| | **Strains** | | |
|---|---|---|---|
| | **CFG1** | **CFG2** | **CFG3** |
| Consumed glucose ($g \cdot L^{-1}$) | 5.7 ± 0.8 | 5.9 ± 0.5 | 17.9 ± 0.6 |
| Gentisate yield ($mol \cdot mol^{-1}$) | 0.165 ± 0.022 | 0.130 ± 0.002 | 0.022 ± 0.007 |

**Supplementary Table 2. Summary of the amounts of consumed glucose and yields of produced maleate in eight transformants.** Data are presented as the mean ± standard deviation of three independent experiments ($n$ = 3).

| | Strains | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | CFM1 | CFM2 | CFM3 | CFM4 | CFM5 | CFM6 | CFM7 | CFM8 |
| Consumed glucose ($g \cdot L^{-1}$) | 3.4 ± 0.1 | 4.8 ± 1.3 | 7.8 ± 0.6 | 6.0 ± 0.1 | 2.8 ± 0.1 | 1.2 ± 0.2 | 0.9 ± 0.2 | 1.1 ± 0.1 |
| Maleate yield ($mol \cdot mol^{-1}$) | 0.189 ± 0.018 | 0.477 ± 0.0093 | 0.0868 ± 0.0085 | 0.0842 ± 0.0086 | 0.117 ± 0.010 | 0.0896 ± 0.0401 | 0.0749 ± 0.0014 | 0.0528 ± 0.0023 |

**Supplementary Table 3. Amounts of produced organic acids.** Data are presented as the mean ± standard deviation of three independent experiments ($n$ = 3).

| Strains | Time (h) | Produced by-products (mg·L$^{-1}$) | | | | |
|---|---|---|---|---|---|---|
| | | Acetate | Pyruvate | Lactate | Formate | Malate |
| CFM00 | 24 | 2,890 ± 310 | 21 ± 21 | ND | ND | 31 ± 4 |
| | 48 | 4,750 ± 330 | 76 ± 15 | 36 ± 3 | ND | 19 ± 6 |
| | 72 | 5,370 ± 89 | 157 ± 4 | 126 ± 10 | ND | ND |
| CFM01 | 24 | ND | ND | ND | ND | ND |
| | 48 | ND | ND | ND | ND | ND |
| | 72 | ND | ND | ND | ND | ND |
| CFM1 | 72 | ND | ND | ND | 14 ± 3 | ND |
| | 94 | 17 ± 30 | ND | ND | 17 ± 5 | ND |
| | 144 | 540 ± 440 | ND | ND | 20 ± 5 | ND |
| CFMt1 | 72 | ND | ND | ND | 5 ± 5 | ND |
| | 94 | 40 ± 35 | ND | ND | 11 ± 3 | ND |
| | 144 | 640 ± 400 | ND | ND | 18 ± 6 | ND |
| CFMtS09 | 24 | ND | ND | ND | ND | ND |
| | 48 | ND | ND | ND | ND | ND |
| | 72 | 82 ± 4 | ND | ND | ND | ND |
| CFMtS10 | 24 | ND | ND | ND | ND | ND |
| | 48 | 16 ± 27 | ND | ND | ND | ND |
| | 72 | 74 ± 11 | ND | ND | ND | ND |
| CFMtS091 | 24 | ND | ND | ND | ND | ND |
| | 48 | ND | ND | ND | ND | ND |
| | 72 | ND | ND | ND | ND | ND |
| CFMtS101 | 24 | ND | ND | ND | ND | ND |

| | | | | | |
|---|---|---|---|---|---|
| 48 | ND | ND | ND | ND | ND |
| 72 | ND | ND | ND | ND | ND |

ND, not detected.

**Supplementary Table 4. Strains, plasmids, and transformants used in this study**

| Strains or plasmids | Genotype | Source or reference |
|---|---|---|
| Strains | | |
| NovaBlue | *endA1 hsdR17*(rK12$^-$mK12$^+$) *supE44 thi-I gyrA96 relA1 lac* recA1/F' [*proAB*$^+$ *lacI*$^q$ ZΔ*M15*::Tn*10*(Tet$^r$)]; used for gene cloning | Novagen |
| BL21 (DE3) pLysS | F$^-$ *ompT hsdS*($r_B^- m_B^-$) *gal dcm* λ(DE3) pLysS (Cam$^r$) (λ(DE3): *lac*I, *lac*UV5-T7 gene 1,*ind*1,*sam7*,*nin5* ); used for protein expression | TaKaRa Bio |
| ATCC 31882 | L-Phenylalanine-overproducing strain | American Type Culture Collection |
| CFT3 | ATCC31882 *ptsHI*::$P_{A1lacO-1}$-*Glk-GalP*Δ*pykF*Δ*pykA* | [1] |
| CFT5 | ATCC31882 *ptsHI*::$P_{A1lacO-1}$-*Glk-GalP*Δ*pykF*Δ*pykA*Δ*phe*Δ*tyrA* | [1] |
| CFG0 | CFT5 harboring pTrcHisB | This study |
| CFG1 | CFT5 harboring pTcgl3026 | This study |
| CFG2 | CFT5 harboring pT3hb6h | This study |
| CFG3 | CFT5 harboring pTxlnD | This study |
| CFMP0 | CFT5 harboring pZA23MCS | This study |
| CFMP1 | CFT5 harboring pZA23psal | This study |
| CFMP2 | CFT5 harboring pZA23ppu1 | This study |
| CFMP3 | CFT5 harboring pZA23palc | This study |
| CFMP4 | CFT5 harboring pZA23rsp | This study |
| CFMP5 | CFT5 harboring pZA23ppu2 | This study |
| CFM1 | CFT5 harboring pT2c101 | This study |
| CFM2 | CFT5 harboring pT2c102 | This study |
| CFM3 | CFT5 harboring pT2c103 | This study |
| CFM4 | CFT5 harboring pT2c104 | This study |

| | | |
|---|---|---|
| CFM5 | CFT5 harboring pT2c201 | This study |
| CFM6 | CFT5 harboring pT2c202 | This study |
| CFM7 | CFT5 harboring pT2c203 | This study |
| CFM8 | CFT5 harboring pT2c204 | This study |
| CFM9 | CFT5 harboring pT2c301 | This study |
| CFMt1 | CFT5 harboring pT2t01 | This study |
| CFMt2 | CFT5 harboring pT2t02 | This study |
| CMtS00 | CFMt1 harboring pSAK | This study |
| CMtS01 | CFMt1 harboring pS01 | This study |
| CMtS02 | CFMt1 harboring pS02 | This study |
| CMtS03 | CFMt1 harboring pS03 | This study |
| CMtS04 | CFMt1 harboring pS04 | This study |
| CMtS05 | CFMt1 harboring pS05 | This study |
| CMtS06 | CFMt1 harboring pS06 | This study |
| CMtS07 | CFMt1 harboring pS07 | This study |
| CMtS08 | CFMt1 harboring pS08 | This study |
| CMtS09 | CFMt1 harboring pS09 | This study |
| CMtS10 | CFMt1 harboring pS10 | This study |
| CMtS091 | CMtS09 harboring pA09 | This study |
| CMtS101 | CMtS10 harboring pA09 | This study |
| BL21MP | BL21 (DE3) pLysS harboring pETM1 | This study |
| | | |
| Plasmids | | |
| pTrcHis B | $P_{trc}$, pBR322 ori, $Amp^r$ | Life Technologies |
| pZA23MCS | $P_{AlacO1}$, p15A ori, $Km^r$ | Expressys |
| pZA33luc | $P_{AlacO1}$, luciferase gene, p15A ori, $Cm^r$ | Expressys |

| | | |
|---|---|---|
| pZS4Int-laci | *lacI*$^{q}$, SC101 ori, Spec$^{r}$ | Expressys |
| pSAK | $P_{AlacO1}$, SC101 ori, Cm$^{r}$ | This study |
| pET-22b(+) | $P_{T7}$, pBR322 ori, Amp$^{r}$ | Novagen |
| pTcgl3026 | pTrcHis B containing *hyg5* from *Streptomyces hygroscopicus* ATCC 29253 and *cgl3026* from *Corynebacterium glutamicum* | This study |
| pT3hb6h | pTrcHis B containing *hyg5* and *3hb6h* from *Rhodococcus jostii* RHA1 | This study |
| pTxlnD | pTrcHis B containing *hyg5* and *xlnD* from *Pseudomonas alcaligenes* NCIMB 9867 | This study |
| pZA23hbzF | pZA23MCS containing *hbzF* from *P. alcaligenes* NCIMB 9867 | This study |
| pZA23psal | pZA23MCS containing *mps0* from *Pseudaminobacter salicylatoxidans* and *hbzF* | This study |
| pZA23ppu1 | pZA23MCS containing *sgp1* from *Pseudomonas putida* and *hbzF* | This study |
| pZA23palc | pZA23MCS containing *mps1* from *P. alcaligenes* NCIMB 9867 and *hbzF* | This study |
| pZA23rsp | pZA23MCS containing *mps2* from *Rhodococcus* sp. strain NCIMB 12038 and *hbzF* | This study |
| pZA23ppu2 | pZA23MCS containing *mps3* from *P. putida* and *hbzF* | This study |
| pT2c101 | pT3hb6h containing *mps2* with $P_{AlacO1}$ promoter | This study |
| pT2c102 | pT3hb6h containing *mps3* with $P_{AlacO1}$ promoter | This study |
| pT2c103 | pT3hb6h containing *mps1* with $P_{AlacO1}$ promoter | This study |
| pT2c104 | pT3hb6h containing *sgp1* with $P_{AlacO1}$ promoter | This study |
| pT2c201 | pTcgl3026 containing *mps2* with $P_{AlacO1}$ promoter | This study |
| pT2c202 | pTcgl3026 containing *mps3* with $P_{AlacO1}$ promoter | This study |
| pT2c203 | pTcgl3026 containing *mps1* with $P_{AlacO1}$ promoter | This study |
| pT2c204 | pTcgl3026 containing *sgp1* with $P_{AlacO1}$ promoter | This study |

| | | |
|---|---|---|
| pTmpsR | pTrcHis B containing *mps2* and *hbzF* | This study |
| pT2c301 | pT3hb6h containing *mps2* and *hbzF* with $P_{trc}$ promoter | This study |
| pZAt01 | pZA23MCS containing *mps2*, *hbzF*, *hyg5*, and *3hb6h* in tandem | This study |
| pT2t01 | pTrcHis B containing *mps2*, *hbzF*, *hyg5*, and *3hb6h* in tandem | This study |
| pT2t02 | pTrcHis B containing *hyg5*, *3hb6h*, *mps2*, and *hbzF* in tandem | This study |
| pS01 | pSAK containing $aroF^{fbr}$ with $P_{AlacO1}$ promoter | This study |
| pS02 | pSAK containing $aroG^{fbr}$ with $P_{AlacO1}$ promoter | This study |
| pS03 | pSAK containing *tktA* with $P_{AlacO1}$ promoter | This study |
| pS04 | pSAK containing *ppc* with $P_{AlacO1}$ promoter | This study |
| pS05 | pSAK containing *maeB* with $P_{AlacO1}$ promoter | This study |
| pS06 | pSAK containing *ppsA* with $P_{AlacO1}$ promoter | This study |
| pS07 | pSAK containing *glk* with $P_{AlacO1}$ promoter | This study |
| pS08 | pSAK containing *galP* with $P_{AlacO1}$ promoter | This study |
| pS09 | pSAK containing *hyg5* with $P_{trc}$ promoter | This study |
| pS10 | pSAK containing *hyg5* and *3hb6h* in tandem under $P_{trc}$ promoter | This study |
| pA09 | pZA23MCS containing *hyg5* with $P_{trc}$ promoter | This study |
| pETM1 | pET-22b(+) containing *mps2* | This study |

Abbreviations: Amp, ampicillin; Km, kanamycin; Cm, chloramphenicol; Spec, spectinomycin.

**Supplementary Table 5. Oligonucleotide primers used in this study**

| Oligonucleotide primers | Sequence |
|---|---|
| 3hb6h_f | 5′-ATCTGCAGCTGGTACTTAAAGAGGTATATAATGAGCAATCTGCAGGATGC-3′ |
| 3hb6h_r | 5′-ATTCCCATATGGTACTTAGCTTGCACGATCGCTGC-3′ |
| xlnD_f | 5′-ATCTGCAGCTGGTACTTAAAGAGGTATATAATGCACAACAACATTCTGAT-3′ |
| xlnD_r | 5′-ATTCCCATATGGTACTTATTTGTATTTCTCGACGG-3′ |
| plac_to_ptrc_f | 5′-CTCCTGAGTAGGACACGAGGCCCTTTCGTCTTCAC-3′ |
| plac_to_ptrc_r | 5′-CGCTCCCGGCGGATTTCTAGGGCGGCGGATTTGTC-3′ |
| inv_ptrc_840_f | 5′-AATCCGCCGGGAGCGGATTTGAACG-3′ |
| inv_ptrc_840_r | 5′-TGTCCTACTCAGGAGAGCGTTCACC-3′ |
| mpr_hbz_ptrc_f | 5′-TATCGAATTCCTGCACGACCGGAATTATCGATTAA-3′ |
| mpr_hbz_ptrc_r | 5′-ATCCCCCGGGCTGCAATCTGTATCAGGCTGAAAAT-3′ |
| inv_ptrc_f | 5′-TATCGAATTCCTGCACGACCGGAATTATCGATTAA-3′ |
| inv_ptrc_r | 5′-ATCCCCCGGGCTGCAATCTGTATCAGGCTGAAAAT-3′ |
| ptrc_to_ptrc_840_f | 5′-CTCCTGAGTAGGACATGTTGACAATTAATCATCCG-3′ |
| ptrc_to_ptrc_840_r | 5′-CGCTCCCGGCGGATTAAGGCCCAGTCTTTCGACTG-3′ |
| ptrc_rbs_pz_psti_f | 5′-TATCGAATTCCTGCACGACCGGAATTATCGATTAA-3′ |
| ptrc_rbs_pz_psti_r | 5′-ATCCCCCGGGCTGCAATCTGTATCAGGCTGAAAAT-3′ |
| inv_pZ_ptsi_f | 5′-TGCAGCCCGGGGGATCCCAT-3′ |
| inv_pZ_ptsi_r | 5′-TGCAGGAATTCGATATCTTA-3′ |
| mpr_to_ptrc_f | 5′-CATCATCATCATGGTATGACCGCAACCGAACCGCA-3′ |
| 3hb6h_to_ptrc_r | 5′-TCTCGAGCTCGGATCTTAGCTTGCACGATCGCTGC-3′ |
| mpr_hbz_to_pt_hind_f | 5′-CATATGGGAATTCGAGCGGATAACAATTTCACACA-3′ |
| mpr_hbz_to_pt_hind_r | 5′-CCGCCAAAACAGCCAACGCGTACCATGGGATCCCC-3′ |
| cmr_f | 5′-GAGCTCGATATCAAATTACG-3′ |

| | |
|---|---|
| cmr_r | 5′-GTGAAGACGAAAGGGCCTCG-3′ |
| sc101_f | 5′-CCTAGGGTACGGGTTTTGCT-3′ |
| sc101_r | 5′-TTTGATATCGAGCTCCGCTTGGACTCCTGTTGATA-3′ |
| palac_f | 5′-CCCTTTCGTCTTCACAAATTTATCAAAAAGAGTGT-3′ |
| palac_r | 5′-AACCCGTACCCTAGGGTCTAGGGCGGCGGATTTGT-3′ |
| arof_f | 5′-AGAGGAGAAAGGTACATGAATTATCAGAACGACGA-3′ |
| arof_r | 5′-GGGGGGGCCCGGTACTTACCCGCGACGCGCTTTTA-3′ |
| arog_f | 5′-AGAGGAGAAAGGTACATGCAAAAAGACGCGCTGAA-3′ |
| arog_r | 5′-GGGGGGGCCCGGTACTTAAGCCACGCGAGCCGTCA-3′ |
| tkta_f | 5′-AGAGGAGAAAGGTACATGTCCTCACGTAAAGAGCT-3′ |
| tkta_r | 5′-GGGGGGGCCCGGTACTTACAGCAGTTCTTTTGCTT-3′ |
| ppc_f | 5′-AGAGGAGAAAGGTACATGAACGAACAATATTCCGC-3′ |
| ppc_r | 5′-GGGGGGGCCCGGTACTTAGCCGGTATTACGCATAC-3′ |
| maeb_f | 5′-AGAGGAGAAAGGTACATGGATGACCAGTTAAAACA-3′ |
| maeb_r | 5′-GGGGGGGCCCGGTACTTACAGCGGTTGGGTTTGCG-3′ |
| ppsa_f | 5′-AGAGGAGAAAGGTACATGTCCAACAATGGCTCGTC -3′ |
| ppsa_r | 5′-GGGGGGGCCCGGTACTTATTTCTTCAGTTCAGCCA-3′ |
| glk_f | 5′-AGAGGAGAAAGGTACATGACAAAGTATGCATTAGT-3′ |
| glk_r | 5′-GGGGGGGCCCGGTACTTACAGAATGTGACCTAAGG-3′ |
| galp_f | 5′-AGAGGAGAAAGGTACATGCCTGACGCTAAAAAACA-3′ |
| galp_r | 5′-GGGGGGGCCCGGTACTTAATCGTGAGCGCCTATTT-3′ |
| ptrc_psak_r | 5′-AGTCCAAGCGGAGCTTGTTGACAATTAATCATCCG-3′ |
| ptrc_psak_f | 5′-ATTTGATATCGAGCTAAGGCCCAGTCTTTCGACTG-3′ |
| ptrc_pza23_f | 5′-TATCATGACATTAACTGTTGACAATTAATCATCCG-3′ |
| ptrc_pza23_r | 5′-AGTCAGTGAGCGAGGAAGGCCCAGTCTTTCGACTG-3′ |
| inv_pza23_f | 5′-CCTCGCTCACTGACTCGCTA-3′ |

| | |
|---|---|
| inv_pza23_r | 5′-GTTAATGTCATGATAATAAT-3′ |
| mps2_pet22_f | 5'-AGAAGGAGATATACAATGACCGCAACCGAACCGCA-3' |
| mps2_pet22_r | 5'-CTCGAGTGCGGCCGCTGCACCTTCGCTAATATAGG-3' |

**Supplementary Table 6. Summary of proteins for maleate production.**

| Name | Species | NCBI accession | EC number |
|---|---|---|---|
| Hyg5 | *Streptomyces hygroscopicus* | O30478.1 | 4.1.3.45 |
| Cgl3026 | *Corynebacterium glutamicum* ATCC 13032 | Q8NLB6.1 | 1.14.13.24 |
| 3HB6H | *Rhodococcus jostii* RHA1 | 5HYM_A | 1.14.13.24 |
| XlnD | *Pseudomonas alcaligenes* NCIMB 9867 | AAG39455.1 | 1.14.13.24 |
| Mps0 | *Pseudaminobacter salicylatoxidans* | AAQ91293 | 1.13.11.4 |
| Sgp1 | *Pseudomonas putida* | ACO92375.1 | 1.13.11.4 |
| Mps1 | *Pseudomonas alcaligenes* NCIMB 9867 | AF173167_1 | 1.13.11.4 |
| Mps2 | *Rhodococcus* sp. strain NCIMB 12038 | ADT78164.1 | 1.13.11.4 |
| Mps3 | *Pseudomonas putida* | WP_047604952.1 | 1.13.11.4 |
| HbzF | *Pseudomonas alcaligenes* NCIMB 9867 | ABD64512.1 | 3.7.1.23 |

## Supplementary Note 1

**Sequence of *3hb6b*:**

ATGAGCAATCTGCAGGATGCCCGTATTATCATTGCCGGTGGTGGTATTGGTGG

TGCAGCAAATGCACTGGCACTGGCCCAGAAAGGTGCAAATGTTACCCTGTTT

GAACGTGCAAGCGAATTTGGTGAAGTTGGTGCAGGTCTGCAGGTTGGTCCG

CATGGTGCACGTATTCTGGATAGCTGGGGTGTTCTGGATGATGTTCTGAGCCG

TGCATTTCTGCCGAAAAATATCGTTTTTCGTGATGCCATTACCGCAGAAGTTC

TGACCAAAATTGATCTGGGTAGCGAATTTCGTGGTCGTTATGGTGGTCCGTAT

TTTGTTACCCATCGTAGCGATCTGCATGCAACCCTGGTTGATGCAGCACGTGC

AGCCGGTGCAGAACTGCATACCGGTGTTACCGTTACCGATGTTATTACCGAAG

GTGATAAAGCAATTGTGAGCACCGATGATGGTCGTACCCATGAAGCAGATATT

GCACTGGGTATGGATGGTCTGAAAAGCCGTCTGCGTGAAAAAATCAGCGGTG

ATGAACCGGTTAGCAGCGGTTATGCAGCATATCGTGGCACCACCCCGTATCGT

GATGTTGAACTGGATGAAGATATTGAAGATGTGGTGGGTTATATTGGTCCGCG

TTGTCATTTTATTCAGTATCCGCTGCGTGGTGGTGAAATGCTGAATCAGGTTG

CAGTTTTTGAAAGTCCGGGATTCAAAAACGGCATTGAAAATTGGGGTGGTCC

GGAAGAACTGGAACAGGCATATGCACATTGCCATGAAAATGTTCGTCGCGGT

ATTGATTATCTGTGGAAAGATCGTTGGTGGCCGATGTATGATCGTGAACCGAT

TGAAAACTGGGTTGATGGTCGCATGATTCTGCTGGGTGATGCCGCACATCCG

CCTCTGCAGTATCTGGCAAGCGGTGCAGTTATGGCAATCGAAGATGCAAAAT

GTCTGGCAGATTATGCAGCCGAAGATTTTAGCACCGGTGGTAATAGCGCATGG

CCTCAGATTCTGAAAGAAGTTAATACCGAACGCGCACCGCGTTGTAATCGTAT

TCTGACCACCGGTCGTATGTGGGGTGAACTGTGGCATCTGGATGGCACCGCA

CGTATTGCACGTAATGAACTGTTTCGTACCCGTGATACCAGCAGCTATAAATA

CACCGATTGGCTGTGGGGTTATAGCAGCGATCGTGCAAGCTAA

**Sequence of *xlnD*:**

ATGCACAACAACATTCTGATTGCCGGTGCAGGTATTGGTGGTCTGAGCGCAG

CACTGGGTCTGGCACGTAAAGGTATGCGTAGCATTGTTCTGGAAAAAGCACC

GGAACTGGGTGAAATTGGTGCCGGTATTCAGCTGGCACCGAATGCATATCAT

GCACTGGATGCCCTGGGTATTGGCGAAGTTGCACGTCAGACCGGTGTTCATG

TTGATAAACTGCTGTGGATGGATGGTATGACCGATAAAGAAATTGCAAGCGTT

CCGCTGGCAAATCGTTTTCGTGAATTTTTTGGTAATCCGTATGCCGTTATTCAC

CGTGCAGATTTTCATGGTCTGCTGGTTGAAGCATGTCATAAAACCGGTCTGGT

GGAAGTTCGTACCAATGCCGAAGTTGTTGATTATGAAAACTTTCCGGATCGTG

TTGAAGCCATTCTGCATGATGGTAGCTGTATTAATGGTGCAGTTCTGGTTGGT

GCAGATGGTCTGTGGTCAAATGTTCGTCAGAAAGTTATTGGTGATGGTGATCC

GCGTGTTAGCGGTCATACAACCTATCGTAGCGTTATTCCGGCAGAAGATATGC

CGGAAGAACTGCGTTGGAATATGAGCACCGCATGGGCAGGCGAAGGTTGTC

ATATGGTTCATTATCCGCTGAAAGGTGGCAAAGTTTTTAATCTGGTTCTGACC

AGCAATAGCGGTGCAAGCGAACCGGAAGCCGGTGTTCCGGTTACCACCGAT

GAAGTTTTTGAAAAATTCAAAACCATGAAACGTCGTCCGACCAGCCTGATTC

ATAAAGGTAATAATTGGAAACGTTGGGTGCTGTGCGATCGTGATCCGCTGCCG

AATTGGGTTGATGGTCGTGTTACCCTGCTGGGTGATGCAGCACATCCGATGAT

GCAGTATATGGCACAGGGTGCAAGCATGGCAATTGAAGATGCAGTTTGTCTG

GCATTTGAACTGGGTCGTGAAATGGATCCGGTTAGCGCACTGAAAAAATACA

ATCGTGCACGTTTTGCACGTACCGCACGTGTTCAGACCTATAGCCGTTATGCA

AGCGATTTTATCTATCATGCAAAAGGTGGTGCAGCAGCAATGCGTAATGAACT
GATGGGTGGCATGACCCCGACCGATTTTTTCCAGTGGATTAATTGGCTGTATG
GCAAAGAAACCGTCGAGAAATACAAATAA

**Sequence of *cgl3026*:**

ATCTGCAGCTGGTACTTAAAGAGGTATATAATGAGCCTGCCGCATAGTGATGA
ACTGCGTGGTCAGAAAATTATCATTAGCGGTGGTGGTATTGGTGGTGCAGCC
GGTGCACTGGCACTGGCCCTGCGTGGTGCCGATGTTACCCTGTATGAACGTG
CAGCAGAATTTAAAGAAGTTGGCGCAGGTCTGCAGATTGGTCCGCATGGTTG
GCGTATGCTGGAAAGCTGGGGTCTGCTGGATCAGATTGTTGTTGCAGGTTATC
TGCCGGAAGATATGCAGTTTCGTGATGCAGTTAATCGTGAAACCATTCTGACC
ATGCGTTTTGATGAAGAATTTCAGCAGCATTATGGTGGTCGTTATCTGGTTATT
CATCGTAGCGATCTGCTGAATATCCTGGTTACCAATGCCGAAGCAGCGGGTGC
AAAACTGCACAATGGTGTTCTGGTTACCGATAGCCGTACCGTTGATGGTGGCA
TTGAAGTTGATATTGAAAGCAGCATCAATAAAGGCGAGGATAACAAAACCCT
GCTGGTTGATGCATTTCTGGCATTTGATGGTATTCATAGCGTGATGCGTAAAA
AACTGGTGGATGATGCACCGGTTGCAAGCAGCTATGTTGCATATCGTGGCAC
CAGCAAACTGGCCGAAGATGCAGAAATGAAAGATCTGAAAAGCGTGATTGG
TTATATTGGACCGCATGTGCATTTTATTCAGTATCCGCTGCGTGGCGGTGAACT
GCTGAATCAGGTTGCAGTTTTTGAAAGCCAGCGCTATCTGGATGGTCGTACC
GCAGGCGATATTCCGGAAGATTGGGGTAATCCGGAAGAACTGGATCGTGCAT
ATAATCATTGTGATCCGTTTATTCAGGATCGTCTGGATACCCTGTGGCGTAATA
ATTGGTGGCAGATGAGCGATCGTGAACCGCTGGAAAATTGGCGTATTGGTCG
CATGCTGCTGCTGGGAGATGCAGCACATGCACCGCTGCAGTATCTGGCAAGC

GGTGCAGTTATGGCAATGGAAGATGCGGAAGCAGTTGCACTGTTTGCAGCAG

ATGCAGCCCGTGCAGGTAATCTGGATTGGGAAGAAGTTCTGGCAGAAGTTGA

AGCAGAACGTCGTCCGCGTTGTAGCCGTATTCAGACCGTTGGTCGTTTTTGG

GGTGAACTGTGGCATGTTGAAGGCACCGCACGTCTGATTCGTAATGAAGTTT

TTCGTCAGGCAGATCGTAATGGCTGGTTTATCTATGCCGATTGGCTGTGGGGT

TATGATGCAAGCAAACGTGCACATATTGCAAATCCGGAACTGGGTGAAATGC

CGCAGGCACTGAAAGAATGGCGTTATGCACTGCTGGAACAGAAATAAGTAC

CATATGGGAAT

**Sequence of *hbzF*:**

GTCGACGGTATCGATTTCATTAAAGAGGAGAAAGGTATGAAAATCTGCCGCT

TTAATGAAAATCGTCTGGGTGTTGTTGATGGTGATGAAGTTCTGGATGTTACC

GAAGCACTGAGCGTTCTGCCGAGCTATGAATATCCGCTGCCTGGTTATGATCC

GCTGATTAAACATCTGGATGCACTGCTGGCACGTATTGAAACCCTGATTAAAG

ATGCACCGCGTATTCTGCTGGCAGATGTTCGTCTGCTGAGTCCGGTTGCAAAT

CCGGGTAAAATCATTGCAGCACCGATTAACTATACCCGTCATCTGCAAGAAGT

GCTGGCCGATAGCGCAATTAACAATGGTGTTGCAAGCTTTACCCAGCATATCA

AAAAAAGCGGTCTGTTTCTGAAAGCAAATAGCAGCCTGGCTGGTGCCGGTG

AAGGTGTTGCACTGAGCCATCAGGATCGTCGTAATGATCATGAAGTTGAACT

GGCCATTGTGATTGGTAAAACCGCACGTAATGTTCCGCGTGAAAAAAGCCTG

GAATATGTTGCAGGTTATTGCATTGGTATTGATATGACCGTTCGTGGTCCGGAA

GAACGTAGCTTTCGTAAAAGTCCGGATAGCTATACCATTCTGGGTCCGTGGCT

GGTTACCCGTGATGAAATTGATAGTCCGGGTGAACTGCAGATGAGCCTGAAA

GTTAATGGTGAAGTTCGTCAGAATGCAAATACCAGCGATCTGATTCTGGGTGT

GGAAGAACTGGTTGAATTTGCAAGCAGCTTTTATACCCTGCATCCGGGTGAT

GTGATTATTAGCGGTACACCGGAAGGTGTGGGTCCGGTTAATCCTGGTGATGC

CATGCTGGCGGAAATTGAACGTATTGGCACCATGACCATTGCAATTCGTAGCG

TTGACTACAAGGATGACGATGACAAGTAAGATATCGAATTCCTG

**Sequence of *mps0*:**

ATTAAAGAGGAGAAAGGTACCATGCAGAACGAAAAACTGGATCATGAAAGC

GTTACCCAGGCAATGCAGCCGAAAGATACACCGGAACTGCGTGCACTGTATA

AAAGCTTTGAAGAAGAAAGCATTATTCCGCTGTGGACACAGCTGGGTGATCT

GATGCCGATTCATCCGAAAAGCAAAGCAGTTCCGCATGTTTGGAAATGGTCA

ACCCTGCTGCGTCTGGCACGTAAAAGCGGTGAACTGGTTCCGGTTGGTCGTG

GTGGTGAACGTCGTGCACTGGGTCTGGCAAATCCGGGTCTGGGTGGTAATGC

ATATATTAGCCCGACCATGTGGGCAGGTATTCAGTATCTGGGTCCGCGTGAAA

CCGCACCGGAACATCGTCATAGCCAGAATGCATTTCGTTTTGTTGTTGAAGGT

GAAGGTGTTTGGACCGTTGTTAATGGTGATCCGGTTCGTATGAGCCGTGGTGA

TCTGCTGCTGACACCGGGTTGGTGTTTTCATGGTCATCATAATGATACCGATC

AGCCGATGGCATGGATTGATGGTCTGGATATTCCGTTTAGCCAGCAGATGGAT

GTTGGCTTTTTTGAATTTGGTAGCGATCGTGTTACCGATTATGCAACCCCGAAT

TTTAGCCGTGGCGAACGTCTGTGGTGTCATCCTGGTCTGCGTCCGCTGAGCG

GTCTGCAGAATACCGTTGCAAGCCCGATTGGTGCATATCGTTGGGAATTTACC

GATCGTGCCCTGACCGAACAGCTGCTGCTGGAAGATGAAGGTCAGCCTGCA

ACCGTTGCACCGGGTCATGCAGCAATTCGTTATGTTAATCCGACCACAGGTG

GTGATGTTATGCCGACCCTGCGTTGTGAATTTCATCGTCTGCGTGCAGGCACC

GAAACCGCAACCCGTAATGAAGTTGGTAGCACCGTTTTTCAGGTTTTTGAAG

GTGCCGGTGCAGTTGTTATGAATGGTGAAACCACCAAACTGGAAAAAGGCG
ATATGTTTGTTGTTCCGAGCTGGGTTCCGTGGTCACTGCAGGCAGAAACCCA
GTTTGACCTGTTTCGTTTTAGTGATGCTCCGATTATGGAAGCACTGAGCTTTAT
GCGTACCAAAATTGAAGGCCAGAAACATCATCATCATCATCATTAAGGGCCCC
CCCTCGAG

**Sequence of *sgp1*:**

ATTAAAGAGGAGAAAGGTACCATGAATACCGCACCGAATACCCAGAGCACCA
GCGCACGTGCAGCATATTATCGTCGTATTGATGCATTTGCACTGACACCGCTG
TGGGAAAGCCTGCATGCACTGGTTCCGAAAACCCCGACCACCGCAATTGAA
CCGGCACTGTGGCGTTATGCAGAAGTTCGTCCGCTGCTGGCAGAAAGCGGTG
AACTGATTAGCGCAATGGAAGCAGAACGTCGTGTTCTGATTCTGGAAAATCC
GGCACTGCGTGGTCAGAGCGCAATTACCCAGAGTCTGTATGCAGGTCTGCAG
CTGATTCTGCCTGGTGAAGTTGCACCGGCACATCGTCATAGCCAGAGCGCAC
TGCGTCTGGTTCTGGAAGGTGAAACCGCATTTACCGCAGTTGATGGTGAACG
TATTCCGATGACACCGGGTGATTTTATCATTACTCCGGCACATACCTGGCATGA
TCACGGTAATACCGGTAATGATGCAGTTGTTTGGCTGGATGGTCTGGATATTC
CGCTGGTTCGTTTTTTTGAAGCAGGTTTTGCAGAAAAAGCCGAAGAAAGCG
TTCAGCGTGTTAGCCGTGCAGAAGGTGATAGCCTGGCACGTTATGGTAGCAA
TCTGGTTCCGCTGGATAGCCGTCGTGATGCAGCACAGCCGAGCCGTCTGTGT
CATTATCCGTATAAACATACCCGTGCAGCACTGGCAGATCTGGCACGTGGTGA
TGCAGATCCGCATTATGGTCATGCACTGCGTTTTAACAATCCGGAAACCGGTC
ATAGCCCGATGCCGACCATTGGCACCTTTATTCAGCTGCTGCCTGCCGGTTTT
GAAACCCGTACCCGTCGTAGCACCGATAGCACCATTGTTTGTTGTCTGGAAG

GCGGTGGCACCGCACAGGTTGGTGAACGCACCTTTCAGTTTGCACAGAATGA

TATTTTTGTGATCCCGAGCTGGTCAGCCCTGCGTCTGCAGGCAGGTCCGGAA

ACAGTTCTGTTTAGCTATAGCGATCGTCCGGTTCAGCAGGCACTGGGTCTGTG

GAAAGAAGAACGTATTCATCATCATCATCATCATTAAGGGCCCCCCCTCGAG

**Sequence of *mps1*:**

ATTAAAGAGGAGAAAGGTACCATGAGCTTTACCGAAAAACCGGCAGTTACC

AAAGAACGCAAAGAGTTTTATAGCAAACTGGAAAGCCATGATCTGGCACCG

CTGTGGGAAGTTCTGAATGAAGTTGTTACCACCAAACCGAAAAGCAATTGTG

CACCGCATCTGTGGGAATTTGAAGTTGCAAAAGAATTTCTGATGGAAGCAGG

CACCCTGATTACCGCAAAAGAAGCAGAACGTCGCGTACTGATTCTGGAAAAT

CCGGGTCTGAAAGGTCTGAGCCGTATTACCACCAGTCTGTATGCAGGTCTGC

AGCTGATTCTGCCTGGTGAAGTGGCACCGACCCATCGTCATAGCCAGAGCGC

ACTGCGTTTTGTTGTTGATGGTGGTGGCGCATGTACCAGCGTGGATGGTGAA

CGTACCACCATGCAGGTTGGTGATTTTGTTATTACCCCTCCGTGGGCATGGCA

TGATCACGTTAATGATAGCGATAAACCGATGATTTGGATGGATGGTCTGGATC

TGCCGATGGTTACCCTGTTTGATACCAGCTTTGCCGAAGGTTATGGTGAAGAT

ATTCAAGAAATTACCCGTCCGAATGGTGATAGCCTGGCACGTTATGGTGCAAA

TATGCTGCCGGTTGATTTTAAACAGAAAGGCCTGAGCAGCCCGATTTTTAACT

ATCCGTATGAACGTAGCCGTGAAGCACTGGAAGCAATGAAAAAAGCAAATG

AATGGGATCCGTGTCATGGTCTGAAAATGCAGTATATTAACCCGCTGGATGGT

ATGGCAGCAATGCCGACCATTAGCAGCTTTATTCAGCTGCTGCCGAAAGAATT

CCGTACCCAGACCTATCGTAGCACCGATGCAACCGTTTTTAGCGTTATTGAAG

GTCAGGGTAAAACCCGCATTGGTGATAAAGTGTTTTTCTGGAAAGCGAAAGA

TACCTTTGTTGTTCCGAGTTGGTATCCGGTTGAACATGAAGCAAGCAGTGATG
CAGTTCTGTTTAGCTATAGCGATCGTGTTGCACAGCAGAAACTGGGTTTTTGG
CGTGAAAGCCGTAATCATCATCATCATCATCATTAAGGGCCCCCCCTCGAG

**Sequence of *mps2*:**

ATTAAAGAGGAGAAAGGTACCATGACCGCAACCGAACCGCATGTTGATGATG
ATCCGGCACTGAAACAGCTGTATACCGATTTTGAAGCAGAACATCTGAATCC
GCTGTGGACACAGCTGGGTGATCTGATGCCGATGACCCCGACCAGCCGTGCA
GTTCCGTTTGTTTGGAAATGGTCAACCCTGTATCCGCTGGCACAGCGTGCCG
GTGATCTGGTTCCGGTTGGTCGTGGTGGTGAACGTCGTGCAATTGCCCTGGC
AAATCCGGGTCTGGGTGGTGTTCCGTATGTTACCCCGACCCTGTGGGCAGCA
ATTCAGTATCTGGGTCCGAAAGAAGTTGCACCGGAACATCGTCATGCACAGA
ATGCATTTCGTTTTGTTGTTGAAGGTGAAGGTGTTTGGACCGTTGTTAATGGT
GATCCGGTTGCAATGCGTCGTGGTGATTTTCTGCTGACACCGGGTTGGCATTT
TCATGGTCATCATAATGAAACCGATCAGCCGATGGCATGGATTGATGGTCTGG
ATATCCCGTTTGTTCATTATACCGATACCGGCTTTTTTGAATTTGGCAGCGAAA
ATGTTACCGATGATAGCACACCGGATGTTAGCCGTAGCGAACGTCTGTGGGC
ACATCCTGGTCTGCGTCCGCTGGTTGGCCTGGATGCAAAAACCAGCAGCCCG
ATTGCAGCATATCGTTGGGAACACACCGATGCAGCACTGCGTGAACAGCTGG
CACTGGAAGATGAAGGTTATGCAGCAACCACCGAACCGGGTCATGCAGCAG
TTCGTTATACCAATCCGACCACAGGTGGTGATGTTATGCCGACCATTCGTGCA
GAATTTCATCGTCTGCGTGCGGGTGCACATACCCGTCCGCGTCGTGATGTTGG
TAGCACCGTTTATCAGGTTTTTGAAGGTAGCGGTCGTTTTGTGCTGGGTGGTC
AGACCCGTACCGTGGGTAAAGGTGATATGATTGTTGTTCCGAGCTGGACCGA

ATGGTCAATTGAAGCCGATACCGAATTTGACCTGTTTGCATTTAGTGATGCAC
CGATTGTTGAACGTCTGCATTTTCACCGTACCTATATTAGCGAAGGTGCACAT
CATCATCATCATCATTAAGGGCCCCCCCTCGAG

**Sequence of *mps3*:**

ATTAAAGAGGAGAAAGGTACCATGAACAACAACGATAATATTGGCACCGCAC
GTGCAGATTTTTATCAGCGTATTGATAGCCAGGCACTGTTTCCGCTGTGGGAA
CAGCTGCATAATCTGGTTCCGCCTCAGCCGACCACCACCTGTGTTCCGGCAC
TGTGGCGTTTTAGCGAAGTTCGTCCGTATCTGATGGAAGCAGGTCAGCTGATT
AGTGCCGAAGAAGCAGTTCGTCGCGTTCTGGTTCTGGAAAATCCGGGTATTC
GTGGTCAGGCAAGCATTACCCCGAGCCTGTATGCAGGTCTGCAGCTGATTCT
GCCTGGTGAAATTGCACCGAGCCATCGTCATAGCCAGAGCGCACTGCGTTTT
GTTGTTGAAGGTAAAGGTGCATATACCGCAGTTGATGGTGAACGTACCACCA
TGCATCCGGGTGATTTCATTATTACCCCGTCATGGACCTGGCATGATCACGGTA
ATCCGAGCGAAACCGAAGGTGGTGAACCGGTTATTTGGCTGGATGGTCTGGA
TATTCCGACCGTTCGTTTTTATGGTGCAGGTTTTGCAGAAAATTATCCGCAGG
CAGTTCAGCCGGTTTCACGTCCGGATGGTAATAGCCTGGCACGTTATGGTGCG
AATATGCTGCCGCTGCGTCATGAAGTTCAGGGTGCAACCAGCCCGATTTTTAG
CTATCCGTATGCACGTACCCGTGAAGCACTGGCAACCCTGGAACAGCAGGGT
GAAGTTGATGCATGGGATGGTGTTAAACTGCGTTATGTTAATCCGGCAACCGG
TGGTTGGGCAATGCCGACCATTGGTACATGCATGCAGCTGCTGCCTCGTGGTT
TTGCGGGTAAAACCGCACGTTGTACCGATGCAACCGTTTATAGCGTTGTGGA
AGGTCGTGGTCGTGCAATTATTGGTGGTCAGACCTTTCATTTTGAACCGAAA
GATACCTTTGTTGTTCCGAGCTGGGTGACCCTGAGTCTGCAGGCAGATGATG

CATGTGTTCTGTTTAGCTATAGCGATCGTCCGGTTCAAGAAGCCCTGGGTCTG
CTGCGTGAAGCCCGTGAACATCATCATCATCATCATTAAGGGCCCCCCCTCGA
G

**Sequence of *aroF*$^{fbr}$:**

GGATCCATTAAAGAGGAGAAAGGTACCATGCAAAAAGACGCGCTGAATAAC
GTACATATTACCGACGAACAGGTTTTAATGACTCCGGAACAACTGAAGGCCG
CTTTTCCATTGAGCCTGCAACAAGAAGCCCAGATTGCTGACTCGCGTAAAAG
CATTTCAGATATTATCGCCGGGCGCGATCCTCGTCTGCTGGTAGTATGTGGTCC
TTGTTCCATTCATGATCCGGAAACTGCTCTGGAATATGCTCGTCGATTTAAAG
CCCTTGCCGCAGAGGTCAGCGATAGCCTCTATCTGGTAATGCGCGTCTATTTT
GAAAAACCCCGTACCACTGTCGGCTGGAAAGGGTTAATTAACGATCCCCATA
TGGATGGCTCTTTTGATGTAGAAGCCGGGCTGCAGATCGCGCGTAAATTGCT
GCTTGAGCTGGTGAATATGGGACTGCCACTGGCGACGGAAGCGTTAGATctgA
ATAGCCCGCAATACCTGGGCGATCTGTTTAGCTGGTCAGCAATTGGTGCTCGT
ACAACGGAATCGCAAACTCACCGTGAAATGGCCTCCGGGCTTTCCATGCCGG
TTGGTTTTAAAAACGGCACCGACGGCAGTCTGGCAACAGCAATTAACGCTAT
GCGCGCCGCCGCCCAGCCGCACCGTTTTGTTGGCATTAACCAGGCAGGGCAG
GTTGCGTTGCTACAAACTCAGGGGAATCCGGACGGCCATGTGATCCTGCGCG
GTGGTAAAGCGCCGAACTATAGCCCTGCGGATGTTGCGCAATGTGAAAAAGA
GATGGAACAGGCGGGACTGCGCCCGTCTCTGATGGTAGATTGCAGCCACGGT
AATTCCAATAAAGATTATCGCCGTCAGCCTGCGGTGGCAGAATCCGTGGTTGC
TCAAATCAAAGATGGCAATCGCTCAATTATTGGTCTGATGATCGAAAGTAATA
TCCACGAGGGCAATCAGTCTTCCGAGCAACCGCGCAGTGAAATGAAATACG

GTGTATCCGTAACCGATGCCTGCATTAGCTGGGAAATGACCGATGCCTTGCTG
CGTGAAATTCATCAGGATCTGAACGGGCAGCTGACGGCTCGCGTGGCTTAAT
CTAGAGGCATCAAATAAAACAAGCTT

**Sequence of *aroG*$^{fbr}$:**

GGATCCATTAAAGAGGAGAAAGGTACCATGAATTATCAGAACGACGATTTAC
GCATCAAAGAAATCAAAGAGTTACTTCCTCCTGTCGCATTGCTGGAAAAATT
CCCCGCTACTGAAAATGCCGCGAATACGGTTGCCCATGCCCGAAAAGCGATC
CATAAGATCCTGAAAGGTAATGATGATCGCCTGTTGGTTGTGATTGGCCCATG
CTCAATTCATGATCCTGTCGCGGCAAAAGAGTATGCCACTCGCTTGCTGGCGC
TGCGTGAAGAGCTGAAAGATGAGCTGGAAATCGTAATGCGCGTCTATTTTGA
AAAGCCGCGTACCACGGTGGGCTGGAAAGGGCTGATTAACGATCCGCATATG
GATAATAGCTTCCAGATCAACGACGGTCTGCGTATAGCCCGTAAATTGCTGCT
TGATATTAACGACAGCGGTCTGCCAGCGGCAGGTGAGTTTCTCaacATGATCA
CCCCACAATATCTCGCTGACCTGATGAGCTGGGGCGCAATTGGCGCACGTAC
CACCGAATCGCAGGTGCACCGCGAACTGGCATCAGGGCTTTCTTGTCCGGTC
GGCTTCAAAAATGGCACCGACGGTACGATTAAAGTGGCTATCGATGCCATTAA
TGCCGCCGGTGCGCCGCACTGCTTCCTGTCCGTAACGAAATGGGGGCATTCG
GCGATTGTGAATACCAGCGGTAACGGCGATTGCCATATCATTCTGCGCGGCGG
TAAAGAGCCTAACTACAGCGCGAAGCACGTTGCTGAAGTGAAAGAAGGGCT
GAACAAAGCAGGCCTGCCAGCACAGGTGATGATCGATTTCAGCCATGCTAAC
TCGTCCAAACAATTCAAAAAGCAGATGGATGTTTGTGCTGACGTTTGCCAGC
AGATTGCCGGTGGCGAAAAGGCCATTATTGGCGTGATGGTGGAAAGCCATCT
GGTGGAAGGCAATCAGAGCCTCGAGAGCGGGGAGCCGCTGGCCTACGGTAA

GAGCATCACCGATGCCTGCATCGGCTGGGAAGATACCGATGCTCTGTTACGTC

AACTGGCGAATGCAGTAAAAGCGCGTCGCGGGTAATCTAGAGGCATCAAATA

AAACAAGCTT

Underline: Initiation and termination codons

*The codons encoding amino acid changes with respect to the original sequence are indicated as small letters.

**Supplementary references**

1. Noda, S., Shirai, T., Oyama, S. & Kondo, A. Metabolic design of a platform *Escherichia coli* strain producing various chorismate derivatives. *Metab. Eng.* **33**, 119–129 (2016).