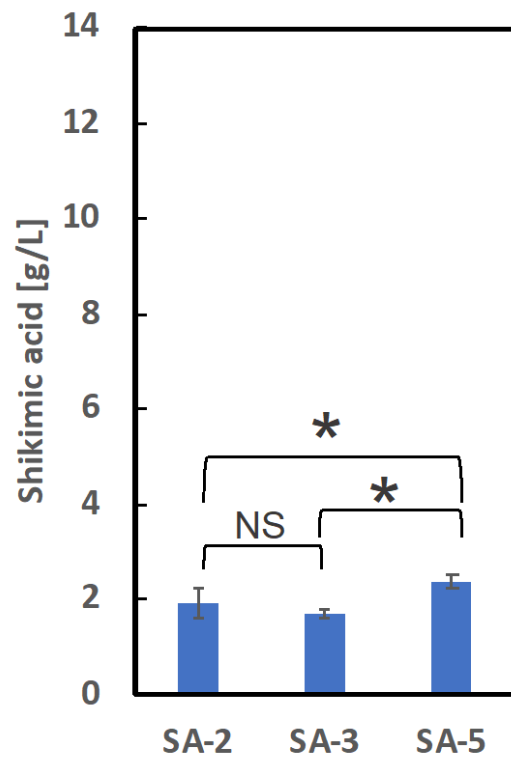


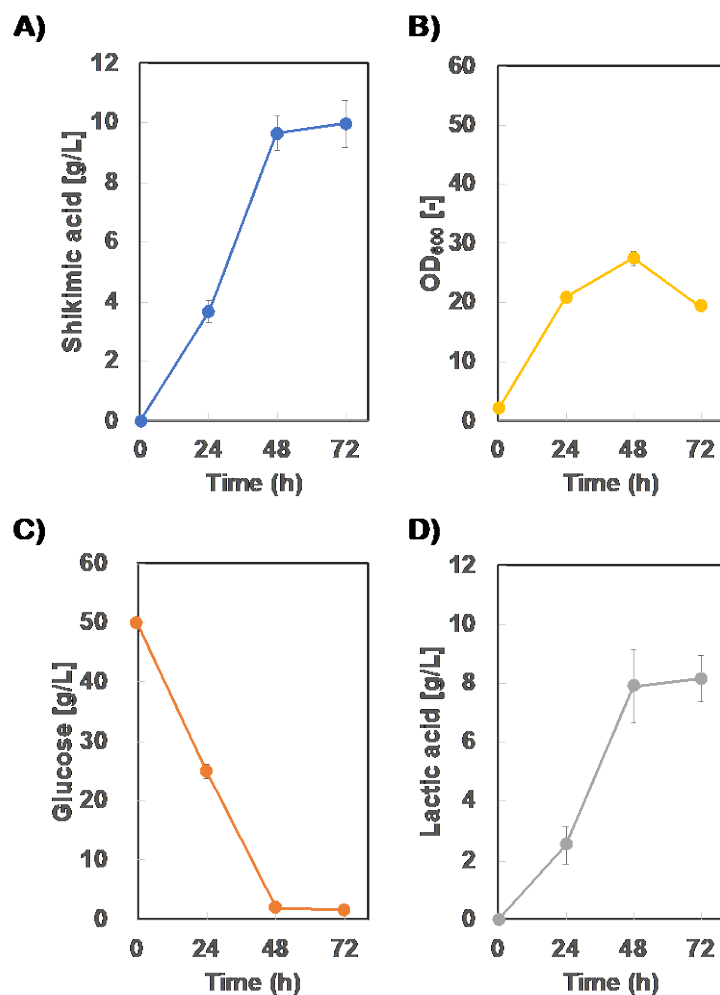
Supplementary Material

1 Supplementary Data

1.1 Supplementary Figure



Supplementary Figure 1. Culture profiles of strain SA-2, SA-3 and SA-5. The data are presented as the average of three independent experiments, and error bars indicate the standard deviation. P values were computed using the two-tailed Student's t-test (*, $P < 0.05$).



Supplementary Figure 2. Culture profiles of strain SA-8. (A) Shikimic acid production, (B) cell growth, (C) glucose consumption, (D) lactic acid accumulation. The data are presented as the average of three independent experiments, and error bars indicate the standard deviation.

2 Supplementary table

2.1 Supplementary Table S1 Oligonucleotide primers used in this study.

Oligonucleotide primers	Sequence
Δ aroK_up_fw	5'- CATGATTACGAATTCTTCGATGGACTACAG -3'
Δ aroK_up_rv	5'- GGTTTAATTAATCGCCTCTAAACCTTC -3'
Δ aroK_down_fw	5'- GAAGGTTTAGAGGCGATTAATTAAACC -3'
Δ aroK_down_rv	5'- AGTGCCAAGCTTTGGCTGATTGCC -3'
Δ qsuD_up_fw	5'- CATGATTACGAATTCTGGCGGTGGCTGAA -3'
Δ qsuD_up_rv	5'- CGAGGTTTTACTGACTCCTACTTTTTGAGATTTG -3'
Δ qsuD_down_fw	5'- CAAATCTCAAAAAGTAGGAGTCAGTAAAACCTCG -3'

Δ qsuD_down_rv 5'- GACTCTAGAGGATCCCATCACTTGCTCCCT -3'

Δ qsuB_up_fw 5'- ACATGATTACGAATTCCAGTGTTTCATCATGGGTGCCATTG -3'

Δ qsuB_up_rv 5'- CACGATGCAACTGCTCTTTGGTTTTACTGAGCCGCGAGTTG -3'

Δ qsuB_down_fw 5'- CGGCTCAGTAAAACCAAAGAGCAGTTGCATCGTGCAGCAG -3'

Δ qsuB_down_rv 5'- CGACTCTAGAGGATCCCAATGAAATCAACACCCTCAGGTTCCG -3'

Δ nagD_up_fw 5'- ACATGATTACGAATTCGTCCGAGTCCACGATGGTGTGG -3'

Δ nagD_up_rv 5'- GCTGCTCATCTGGTACGTGCACCATTGTCCCTGTTTTGGGC -3'

Δ nagD_down_fw 5'- CAGGGACAATGGTGCACGTACCAGATGAGCAGCAGTTCAC -3'

Δ nagD_down_rv 5'- CGACTCTAGAGGATCCGTGAACTGCTGCTCATCTGGTACGTG -3'

gnd_S361F_up_fw 5'- CTATGACATGATTACGAATTCGTCCATCGCTGCCAA -3'

gnd_S361F_up_rv 5'- GGGTCGACGTCCCAGTTGTTCTCGTCAAAGCCAGCCTTGATCTCGTC -3'

gnd_S361F_down_fw 5'- GCTTTGACGAGAACAACACTGGGACGTGACCCTCGCGACCTCGCTAC -3'

gnd_S361F_down_rv 5'- CGACTCTAGAGGATCCCCGGGTAAAGCTTCAACCT -3'

aroK_up_fw 5'- CATGATTACGAATTCGTAATTTCCATTGGT -3'

aroK_up_rv 5'- CCAGATAGAGAATTCCTCTAAACCTTCGA -3'

aroK_down_fw 5'- TCTGTTGTTCTCGACCGATTAATTAAACCG -3'

aroK_down_rv 5'- AGACTCTAGAGGATCCGATCAGTTTCGTAA-3'

P_aroG_T_fw 5'- TCGAAGGTTTAGAGGGAATTCTCTATCTGG -3'

P_aroG_T_rv 5'- CGGTTTAATTAATCGGTCGAGAACAACAGA -3'

Δcg2392_up_fw 5'- ACATGATTACGAATTCCTTGAGCACTCGGCGCAAGACGATAG -3'

Δ cg2392_up_rv 5'- GGGATATCAACTGTCCAACCTCATTAGCAATTAGTCCTTCACAG CGTCGAAAACG -3'

Δ cg2392_down_fw 5'- CGCTGTGAAGGACTAATTGCTAATGAGTTGGACAGTTGATATCCCTAAAGAAGTTCTCCC -
3'

Δ cg2392_down_rv 5'- CGACTCTAGAGGATCCCTCGCTGAGACGGTAAAGATCAGCGGTG -3'

pta_up_fw 5'- ACATGATTACGAATTCAATGTGGAGTATGTGAGCGGGGGTTC -3'

pta_up_rv 5'- GCTGCTGGCGGCCGCCAGCCTGAACCTTCTCATTGATGACACTTCAG -3'

pta_down_fw 5'- GGTTTCAGGCTGGCGGCCGCCAGCAGCATTACCGCTGAACAAGAGCC -3'

pta_down_rv 5'- CGACTCTAGAGGATCCGTTGGGTTTCGGGTTAACAGCACAGTC -3'

ldh_up_fw 5'- ACATGATTACGAATTCCCGATAAAGCCAGCGCCCATATTT -3'

ldh_up_rv 5'- GATTTCATAATCTTGACGCGGCCGCTTTCGATCCCCTTCCTGATTTCCC -3'

ldh_down_fw 5'- GATCGAAAGCGGCCGCGTCAAGATTATGAAATCCATCGTCGGCGATG -3'

ldh_down_rv 5'- CGACTCTAGAGGATCCGCGATGTCTTCCTCACCGTATTCACCGTG -3'

aroK-H36_fw 5'- GAATTCTCTATCTGGTGCCCTAAACGGGGG -3'

aroK-term_re 5'- GTCGAGAACAACAGATAAAAACGAAAGGCC -3'

pta-H36_fw 5'- AAGGTTTCAGGCTGGCGGCCGCCATTCAGGCTGCGCAACTGTTG -3'

pta-term_re 5'- ATGCTGCTGGCGGCCGCTGTTATGTGCCTGGCTCCTAATCAAAGCTG -3'

ldh-H36_fw 5'- AGTGGGATCGAAAGCGGCCGCCATTCAGGCTGCGCAACTGTTG -3'

ldh-term_re 5'- AATCTTGACGCGGCCGCTGTTATGTGCCTGGCTCCTAATCAAAGCTG -3'

aroG_fw 5'- GAGTAGCATGGGATCCATGAGTTGGACAGTTGATATCCCTAAAGAAGTTCTCCCTG -3'

aroG_rv 5'- ACAGCCAAGCCTCGAGTTAGTTACGCAGCATTTCTGCAACGAGGAAAGC -3'

aroB_fw 5'- GAGTAGCATGGGATCCATGAGCGCAGTGCAGATTTTCAACACCGTC -3'

aroB_rv 5'- ACAGCCAAGCCTCGAGTTAGTGGCTGATTGCCTCATAAGCACTCTGTAAATCTTG -3'

qsuC_fw 5'- TAGGAGTAGCATGGGATCCATGCCTGGAAAAATT -3'

qsuC_rv 5'- CAAAACAGCCAAGCCTCGAGCTACTTTTTGAGATT -3'

aroE1_fw 5'- GAGTAGCATGGGATCCATGGTCAACTACGTCGACAGGGAAACAACCCTG -3'

aroE1_rv 5'- ACAGCCAAGCCTCGAGTTACTTGGAGAACTCCTCCGCAGCAATGATCTG -3'

aroE3_fw 5'- GAGTAGCATGGGATCCATGGGTTCTCACATCACTCACCGGGC -3'

aroE3_rv 5'- ACAGCCAAGCCTCGAGTTAGTGTTCTTCTGAGATGCCTAAAGACTCTTCCAAAGCCTC -3'

tkt-tal_fw 5'- GAGTAGCATGGGATCCATGACCACCTTGACGCTGTCACCTG -3'

tkt-tal_rv 5'- ACAGCCAAGCCTCGAGCTACTTCAGGCGAGCTTCCATGGACTCAAG-3'

pck_fw 5'- GAGTAGCATGGGATCCATGACTACTGCTGCAATCAGGGGCCTTC-3'

pck_rv 5'- ACAGCCAAGCCTCGAGTTAAGCGTGAGCTGCTGAAATGCGG-3'

RT-aroG_fw 5'- TTGCATACGCTGACAAGCTC -3'

RT-aroG_rv 5'- TGCCTCAACAGCCTGGATAA -3'

RT-aroB_fw 5'- CTGCGCCTTTACGAAACTGA -3'

RT-aroB_rv 5'- TGGGAGCCTTCGACTTCTTT -3'

RT-ldh_fw 5'- GCATACGCATACGCACTGAT -3'

RT-ldh_rv 5'- CATGACGTTGCCTTCGAGTT -3'

RT-cg3177_fw 5'- GCATACGCATACGCACTGAT -3'

RT-cg3177_rv 5'- CATGACGTTGCCTTCGAGTT -3'
