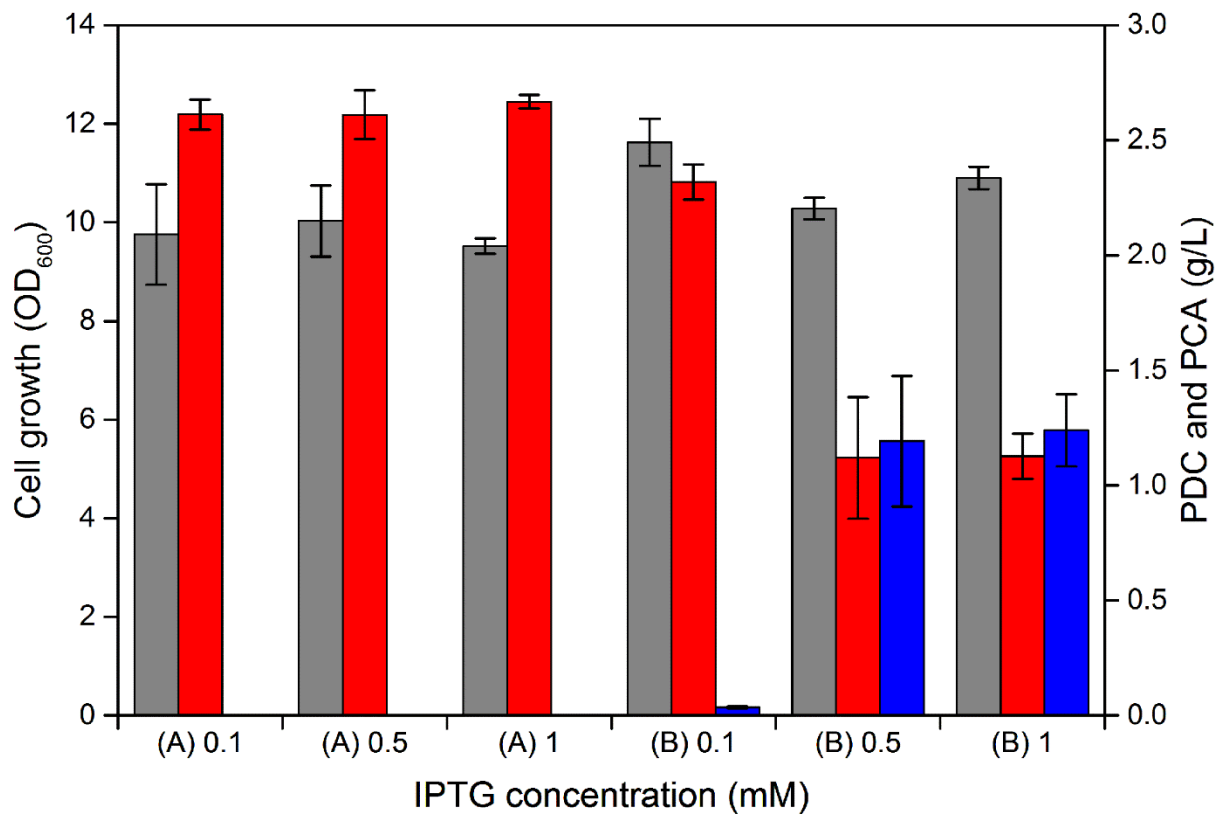
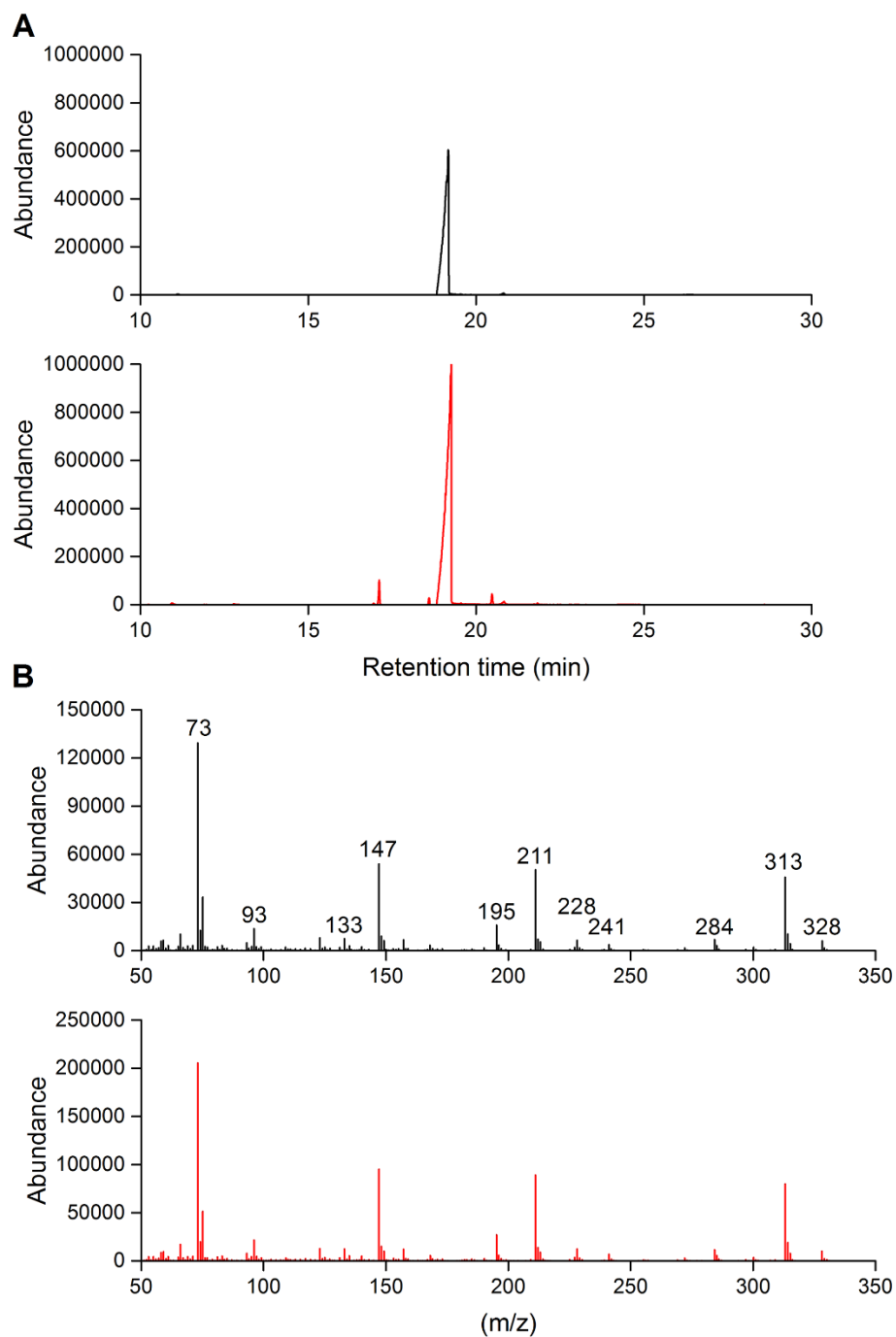


Supporting Information



Supplementary Figure S1. PCA-feeding experiments against different PmdABC recombinants under various IPTG induction levels. Cells of *E. coli* W3110 harboring pTacABC (A) and of *E. coli* BL21(DE3) harboring pETABC (B) were induced at 4 h when OD₆₀₀ was ca. 0.6, and PCA was fed at 12 h at a final concentration of 2.5 g/L. Samples were withdrawn 24 h after feeding PCA. Numbers in x-axis imply IPTG concentration in mM. Symbols are: gray box, cell growth (OD₆₀₀); red box, PDC concentration (g/L); blue box, residual PCA concentration (g/L).



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12 **Supplementary Figure S2.** Identification of PDC production by GC-MS. (A) Gas

13 chromatogram of the trimethylsilylated (TMS) derivative of authentic PDC compound (upper

14 black) and of PDC produced in flask culture (lower red). (B) Mass spectrum of the TMS

15 derivative of authentic PDC compound (upper black) and of PDC produced in flask culture
16 (lower red).

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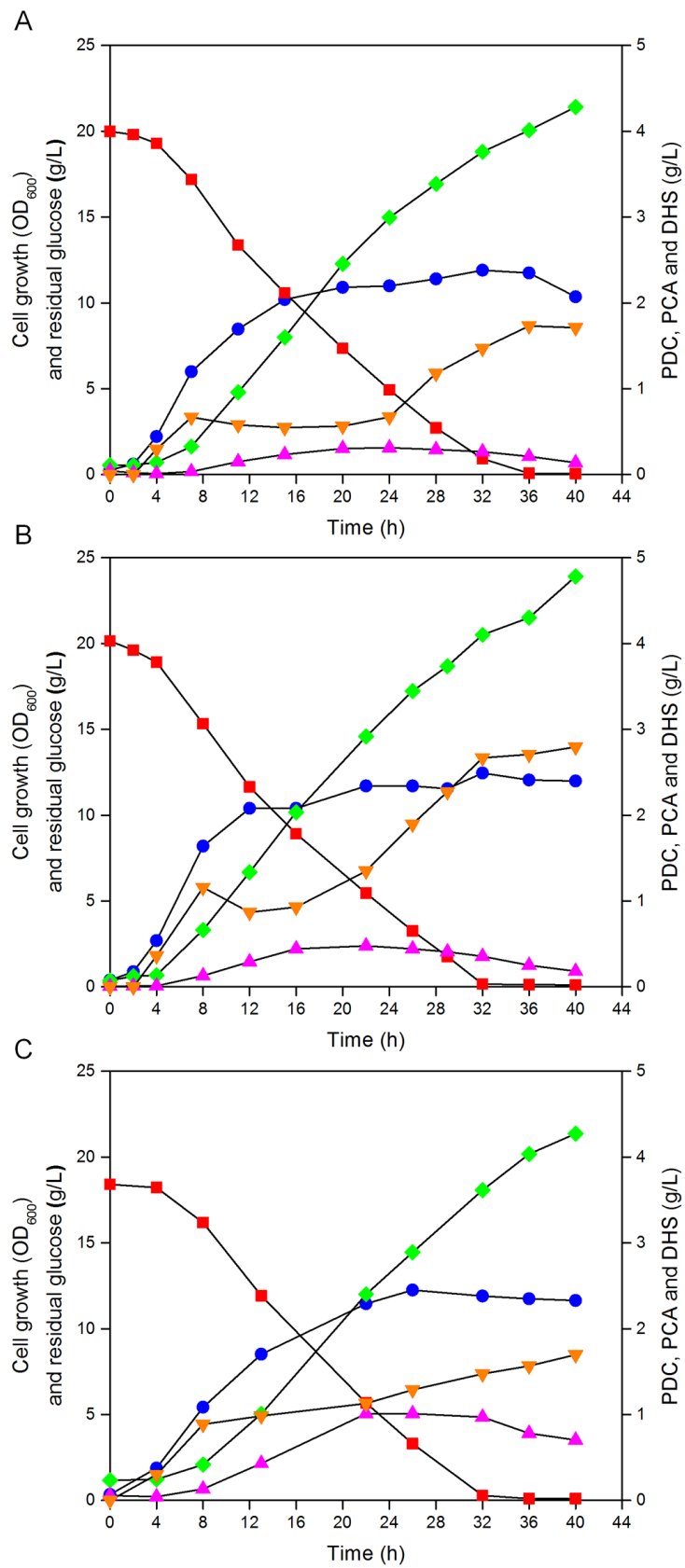
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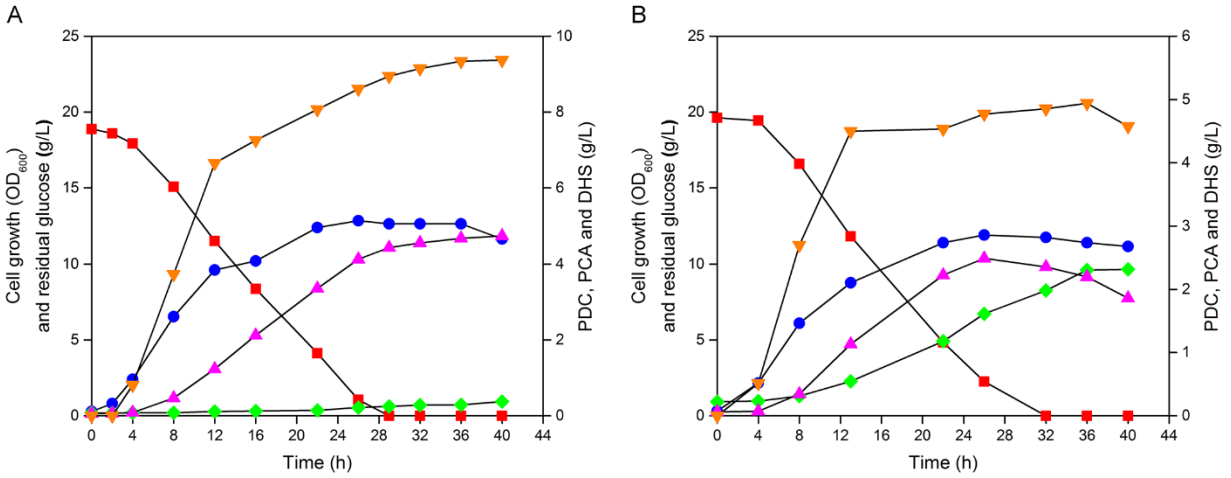
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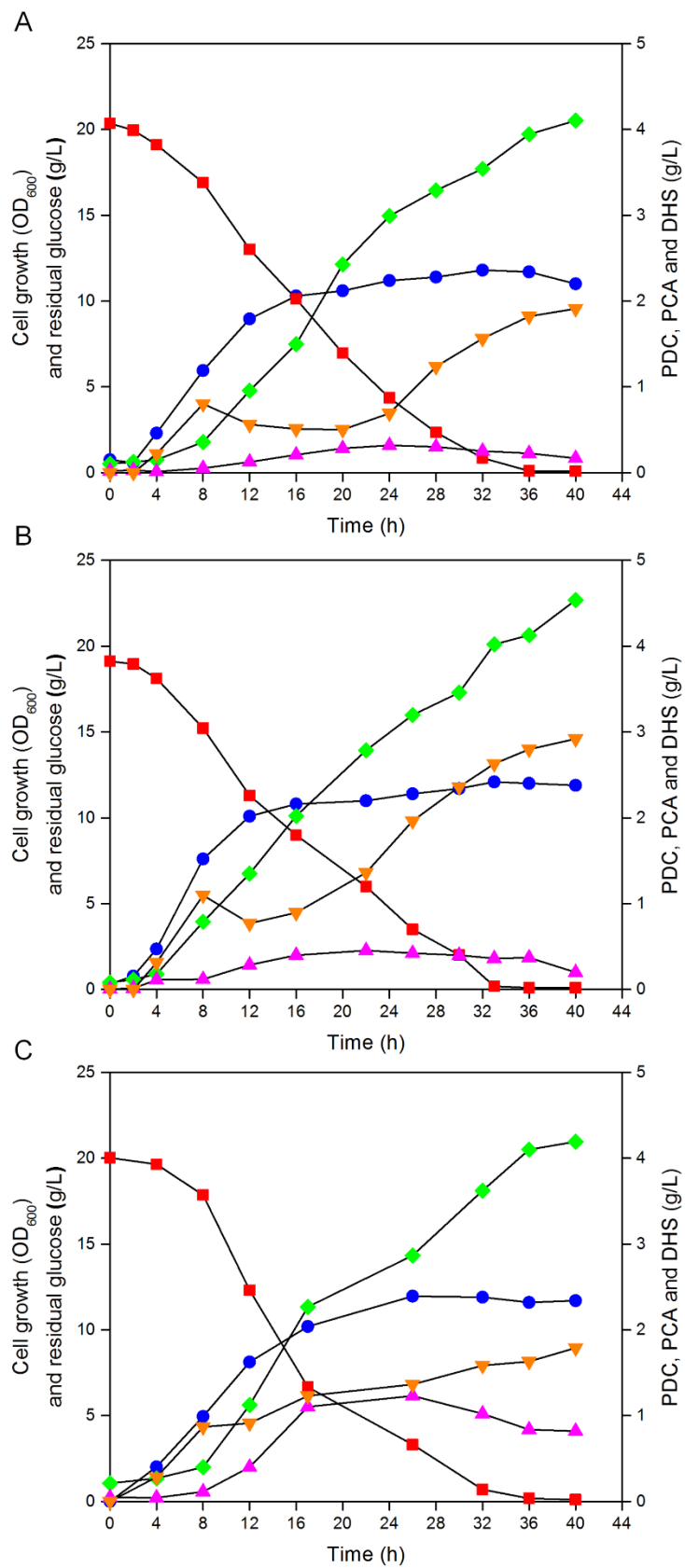
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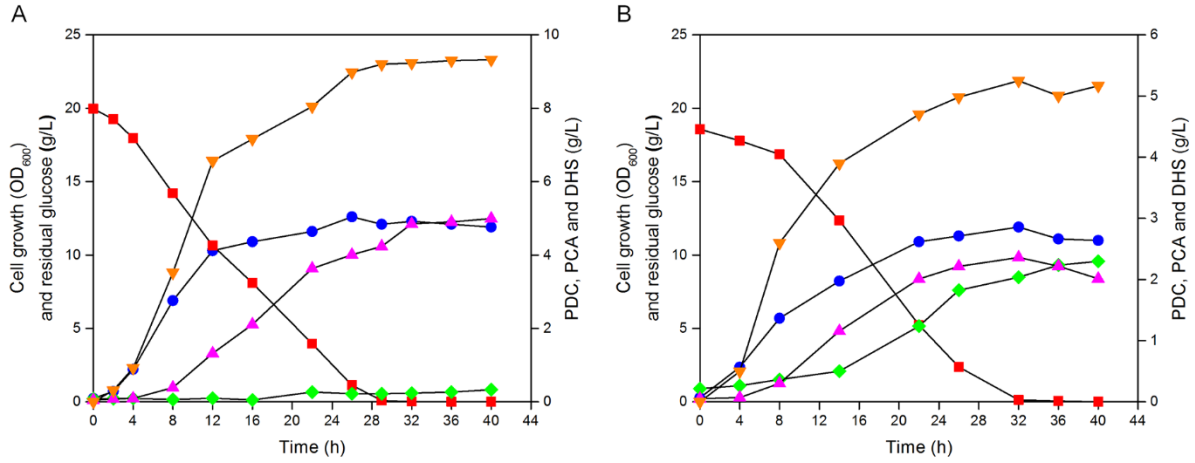
Supplementary Figure S3. Batch fermentation profiles of the engineered strain GYT1 harboring pTacFABC and pBBR1G^{fbr}-EcA under dissolved oxygen (DO) levels of 25% (A), 40% (B) and 80% (C) of air saturation. Symbols are: blue circle, cell growth (OD₆₀₀); red square, residual glucose concentration (g/L); green diamond, PDC concentration (g/L); magenta triangle, PCA concentration (g/L); orange inverted triangle, DHS concentration (g/L).



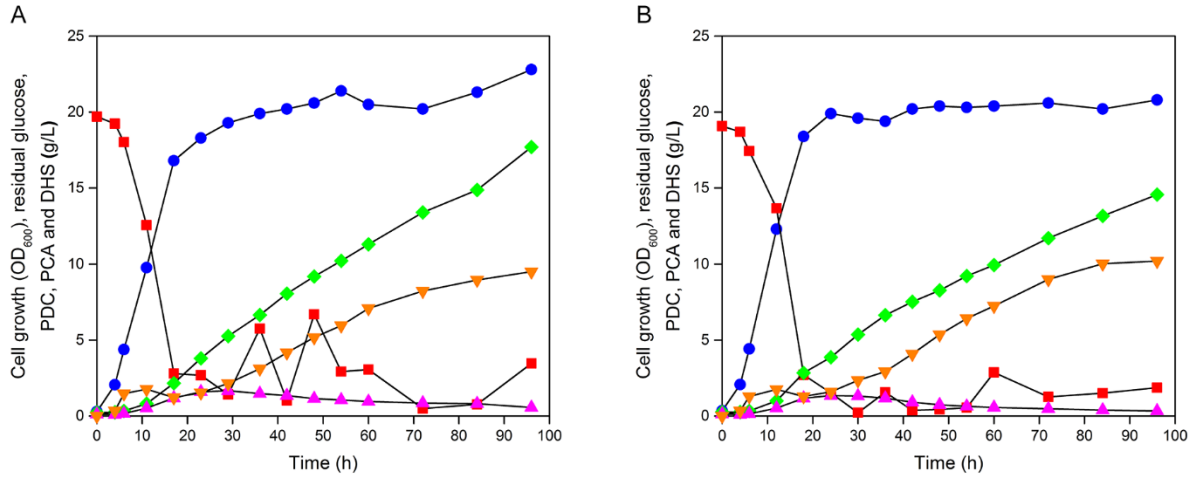
Supplementary Figure S4. Batch fermentation profiles of the engineered strain GYT7 harboring pTacFABC and pBBR1G^{fbr}-EcA (A), and GYT6 harboring pTacFABC and pBBR1G^{fbr}-EcA (B). Symbols are: blue circle, cell growth (OD₆₀₀); red square, residual glucose concentration (g/L); green diamond, PDC concentration (g/L); magenta triangle, PCA concentration (g/L); orange inverted triangle, DHS concentration (g/L).



Supplementary Figure S5. Batch fermentation profiles of the engineered strain GYT1 harboring pTacFABC and pBBR1G^{fbr}-EcA under dissolved oxygen (DO) levels of 25% (A), 40% (B) and 80% (C) of air saturation in one additional replicate. Symbols are: blue circle, cell growth (OD₆₀₀); red square, residual glucose concentration (g/L); green diamond, PDC concentration (g/L); magenta triangle, PCA concentration (g/L); orange inverted triangle, DHS concentration (g/L).



Supplementary Figure S6. Batch fermentation profiles of the engineered strain GYT7 harboring pTacFABC and pBBR1G^{fbr}-EcA (A), and GYT6 harboring pTacFABC and pBBR1G^{fbr}-EcA (B) in one additional replicate. Symbols are: blue circle, cell growth (OD₆₀₀); red square, residual glucose concentration (g/L); green diamond, PDC concentration (g/L); magenta triangle, PCA concentration (g/L); orange inverted triangle, DHS concentration (g/L).



Supplementary Figure S7. Fed-batch fermentation profiles of GYT1 harboring pTacFABC and pBBR1G^{fbr}-EcA in two additional independent replicates. Symbols are: blue circle, cell growth (OD₆₀₀); red square, residual glucose concentration (g/L); green diamond, PDC concentration (g/L); magenta triangle, PCA concentration (g/L); orange inverted triangle, DHS concentration (g/L).

92 **Supplementary Table S1.** DHS Dehydratases of Various Microbial Origins

Name	Size (aa)	Organism	Identity (%)	Accession No.
AroZ	617	<i>Klebsiella pneumonia</i>	100	ABR77558
AsbF	280	<i>Bacillus thuringiensis</i>	6.0	ARP57354
QuiC	486	<i>Acinetobacter sp.</i> ADP1	11.5	CAG68556
QsuB	618	<i>Corynebacterium glutamicum</i>	39.4	BAB97815
Qa-4	359	<i>Neurospora crassa</i>	11.6	EAA30378
QutC	348	<i>Aspergillus nidulans</i>	11.7	AAC71790

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113 **Supplementary Table S2.** DNA Sequence of *E. coli*-codon Optimized *asbF* Gene

Name	Codon optimized sequence
<i>asbF</i>	atgaaatatagcctgtgcaccattagcttccgccaccaactgattagctttaccgacatcgtgcaattcgcgtatgagaa cggcttcgaggggtatcgaactgtggggcaccacgcgcagaacctgtatatgcaagagcgtgaaaccaccgagcg tgaactgaactttctgaaggacaaaaacctggagatcacatgattagcgactacctggatatcagcctgagcgcg atttcgaaaagaccattgagaaaagcgaacagctggttgtgctggcgaactggtcaacaccaaaaaatccgtacc tttgcgggtcagaagggcagcaaagacttttagcgagcaagagcgtaggagtattgtgaaacgtatccgtaagatttg cgatgtgttcgcgcaacacaacatgtacgttctgctggaaacccacccgaacacctgaccgacacctgccgagc accattgaactgctggaggaagttaaccacccgaacctgaagatcaacctggactttctgcacatttgggaaagcgg gcgaacccgatcgatagcttccaccgtctgaaaccgtggaccctgcactaccactttaagaacattagcagcgcgga ttatctgcacgtgttcgagccgaacaacgtttatgcggcggcggttagccgtattggtatggtgccgctgttcgaagg cattgttaactatgacgagatcattcaggaagtgcgtggtaccgacctgttcgcgagcctggagtggtttggccacaa cagcaaagaatcctgaaagaagaatgaagggtgctgattaaccgcaaactggaagttgtgaccagctaa

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Supplementary Table S3. SHK Importers from Different Microbial Sources

Name	Size (aa)	Organism	Identity (%)	Accession No.
EcShiA	438	<i>Escherichia coli</i>	100	APC52228
KpShiA	440	<i>Klebsiella pneumonia</i>	35.2	ARM22236
RoShiA	462	<i>Rhodococcus opacus</i> PD630	33.4	AHK28521
AsShiA	445	<i>Acinetobacter sp.</i> ADP1	65.3	CAG67191

154 **Supplementary Table S4.** Oligonucleotides Used in This Study

Primer name	Sequence (5'-3')
pET(pmdABC)-f	CGGTTTTTCCAAAGCCATATATGTATATCTCCTTC
pET(pmdABC)-r	AGCAGCTGAGCGCGGATTGATGAGATCCGGCTGCTAACAA
pmdABC(pET)-f	TTGTTAGCAGCCGGATCTCATCAATCCGCGCTCAGCTGCT
pmdABC(pET)-r	GAAGGAGATATACATATATGGCTTTGGAAAAACCG
pmdABC(pTac)-f	TAACAATTTACACAGGAAAAATGGCTTTGGAAAAACCGTA
pmdABC(pTac)-r	GGTACCGAGCTCGAATTCTGTCAATCCGCGCTCAGCTGCT
pTac(pmdABC)-f	AGCAGCTGAGCGCGGATTGACAGAATTCGAGCTCGGTACC
pTac(pmdABC)-r	TACGGTTTTTCCAAAGCCATTTTCCTGTGTGAAATTGTTATCCG
asbF-f	AGACAGGAATTCATGAAATATTCGCTATGTACC
asbF-r	AGACAGCTGCAGTTACGAAGTTACTACTTC
asbF ^{opt} -f	AGACAGGAATTCATGAAATATAGCCTGTGCAC
asbF ^{opt} -r	AGACAGCTGCAGTTAGCTGGTCACAACCTTC
aroZ(pTrc)-f	TCACACAGGAAACAGACCATATGCTGCGCTCTATCGCCAC
aroZ(pTrc)-r	GGGTACCGAGCTCGAATTCCCTAACAATACTGCATCGCCG
pTrc(aroZ)-f	CGGCGATGCAGTATTGTTAGGGAATTCGAGCTCGGTACCC
pTrc(aroZ)-r	GTGGCGATAGAGCGCAGCATATGGTCTGTTTCCTGTGTGA
qsuB-f	AGACAGGAGCTCATGCGTACATCCATTGCCACTG
qsuB-r	AGACAGTCTAGACTAGTTTGGGATTCCCCGCTC
trc-asbF-f	CCAACATAGTAAGCCAGTATACACTCCGTTGACAATTAATCATCC
trc-asbF-r	GGACTGTTGGGCGCCATCTCCTTGAAGAGTTTGTAGAAACG
aroG ^{fbr} (pBBR1)-f	TTCACACAGGAAACAGCTATGAATTATCAGAACGACG
aroG ^{fbr} (pBBR1)-r	AGCTTATCGATACCGTCGACTTACCCGCGACGCGCTTTTA
pBBR1(aroG ^{fbr})-f	TAAAAGCGCGTCGCGGGTAAGTCGACGGTATCGATAAGCT
pBBR1(aroG ^{fbr})-r	CGTCGTTCTGATAATTCATAGCTGTTTCCTGTGTGAA
RBS-tktA-f	CTTGATATCGAATTCCTGCAGCCCCGGGACAGGAAACAGACCAT ATGTCCTCAC
RBS-tktA-r	ACCGCGGTGGCGGCCGCTCTAGAACTAGTGTTACAGCAGTTCTT TTGC
RBS-EcA-f	AGACAGAAGCTTACAGGAAACAGCTATGGACTCCACGCTCATC
RBS-KpA-f	AGACAGAAGCTTACAGGAAACAGCTATGAGCAATCCACAAGAC AACAC
RBS-KpA-r	AGACAGACTAGTTCAGGCGCTTTCCGCCCCGGGAG
RBS-RoA-f	AGACAGAAGCTTACAGGAAACAGCTATGAGCGTCGAGGAAACA GCG
RBS-RoA-r	AGACAGGGATCCTCATGCGGGGACCCCGTCCTTC
RBS-AsA-f	AGACAGAAGCTTACAGGAAACAGCTATGGCTTCAAATTTATCAT C
RBS-AsA-r	AGACAGGGATCCTTATTTGCCTGTAACATAACCAG
aroE-KO-f	AATCCGCGATGCCCTGACGGGTGAACTGTTTCGACAGGGGTAA CATAATGTAGGTGACACTATAGAACGCG
aroE-KO-r	TCACGCGGACAATTCCTCCTGCAATTGCTTTATAACTGGTTCTAC GTCAGTAGTGGATCTGATGGGTACC

aroE-KOEX-f	GCGGCGTTCCCGGTTGTGCCTGGTGAAACGGGGGGGCGTTTAA ATCCTTCAGAAATCCGCGATGCCCTGA
aroE-KOEX-r	TTTTTTATTCTCGTCCCACTCTTCCCTGTCCGGAAACTGGATGGC CTGATTCACGCGGACAATTCCTCCT
pykF-KO-r	GAAAGCAAGTTTCTCCCATCCTTCTCAACTTAAAGACTAAGACT GTCATGTAGGTGACACTATAGAACGCG
pykF-KO-r	GATATACAAATTAATTACAAAAGCAATATTACAGGACGTGAAC AGATGCTAGTGGATCTGATGGGTACC
pykF-KOEX-f	AGGCACCACCACTTTCGTAATACCGGATTTCGCTTTCGGGCAGTG CGCCAGAAAGCAAGTTTCTCCCATC
pykF-KOEX-r	ATTGCTTCTGGTTATCGATTAAATAAAAAAGCGCCCATCAGGG CGCTTCGATATACAAATTAATTCACA
pykA-KO-r	TTATTTTCATTTCGGATTTCATGTTCAAGCAACACCTGGTTGTTTCA GTCAACGGAGTATTACATTAGGTGACACTATAGAACGCG
pykA-KO-r	GTTGAACATCATTGAACGTAGGCCGGATGTGGCGTTTTTCGCC GCATCCGGCAACGTACTAGTGGATCTGATGGGTACC
pykA-KOEX-f	CCTAATCTTATACGACATCCGAATGAGATTAAATTTATCGCCATCGC GGCGTTATTTTCATTTCGGATTTC
pykA-KOEX-r	GGCCTTCGCCTGATGATAAGTTCAAGTTTGCTTCAGAATATTCGA AATCTGTTGAACTATCATTGAAC
Ptrc(ppsA)-f	GCATTTTCATTTTTATGGTTTCGTTTATACCGATGGTTTATGTGGAA ATTGCGCGTCATACACATACGATT
Ptrc(ppsA)-r	ATGCCGAGTTGGTTATACCAAAGCACCAGCGGTGACGAGCCATT GTTGGACATGGTCTGTTTCCTGTGTG
Ptrc(ppsA)-EX-f	TTATGTCTGGTTTATAAAATGAACCTTCAATTTTATTTTTTATGAA AACAGCATTTCATTTTTATGGT
Ptrc(ppsA)-EX-r	TCATTTACCCAGGGAGGCATTTTTGCCCCCAACCCTGTCTACAT CATTCATGCCGAGTTGGTTATACC
Ptrc(shiA)-f	ATCTTCCATCGAATTTTTTCATGTTGCCGCTAATCAGCCATAAAAT CATTTTCGCGTCATACACATACGATT
Ptrc(shiA)-r	CTTAACGAAAGCGTCCCTTCATCGGGACGAGTGGAGATGAGCG TGGAGTCCATGGTCTGTTTCCTGTGTG
Ptrc(shiA)-EX-f	GTGGGTCTCTGCTTAATCCTTAAACAACACCAGCAACTCCTGC GCTTTCATCTTCCATCGAATTTTTTC
Ptrc(shiA)-EX-r	AGTCGACGACGGCACCAGCGAAGCTGCCTAACGCAGCTCGTCG GGCGCGACTTAACGAAAGCGTCCCTTC
Ptrc(sthA)-f	TCCAATAAAACGTCAGGGCAAAAGTAAGAAACAGACAAAGCA AAGGCCGCCGCGTCATACACATACGATT
Ptrc(sthA)-r	CCGCCGGGGCCGGAACCTATTACTATGGCATCGTAATCGTAGGA ATGTGGCATGGTCTGTTTCCTGTGTG
Ptrc(sthA)-EX-f	TACGTACAGCGGAAACCTGCCGCTTAAACGGAGAGTATCGTCGA TAAAAATCCAATAAAACGTCAGGG
Ptrc(sthA)-EX-r	TAAC TGCGACGCGCGCACCTTGCTTAACCAGGCCATTGCAGCG CCTTCGCCGCCGGGGCCGGAACCTATTAC CCCATTGCAGCGCCTTCGCCGCCGGGGCCGGAACCTATTACTAT

P _{trc} (sthA ^m)-r	GGCATCATAGTCATAGGAATGTGGCATGGTCTGTTTCCTGTGTG CATTTTGATAACGCTCGATAACTGCGACGCGCGCACCTTGCTTA
P _{trc} (sthA ^m)-EX-r	ACCAGGCCCATTCAGCGCCTTCG

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