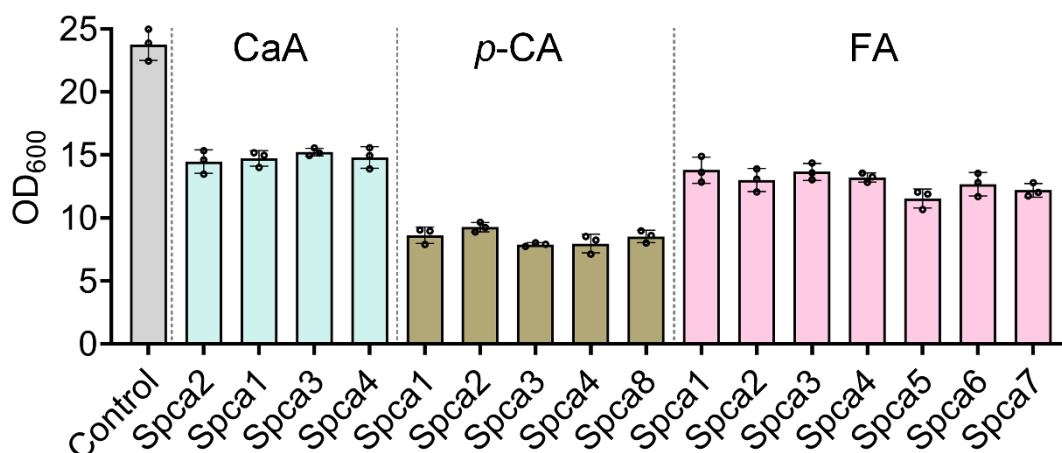
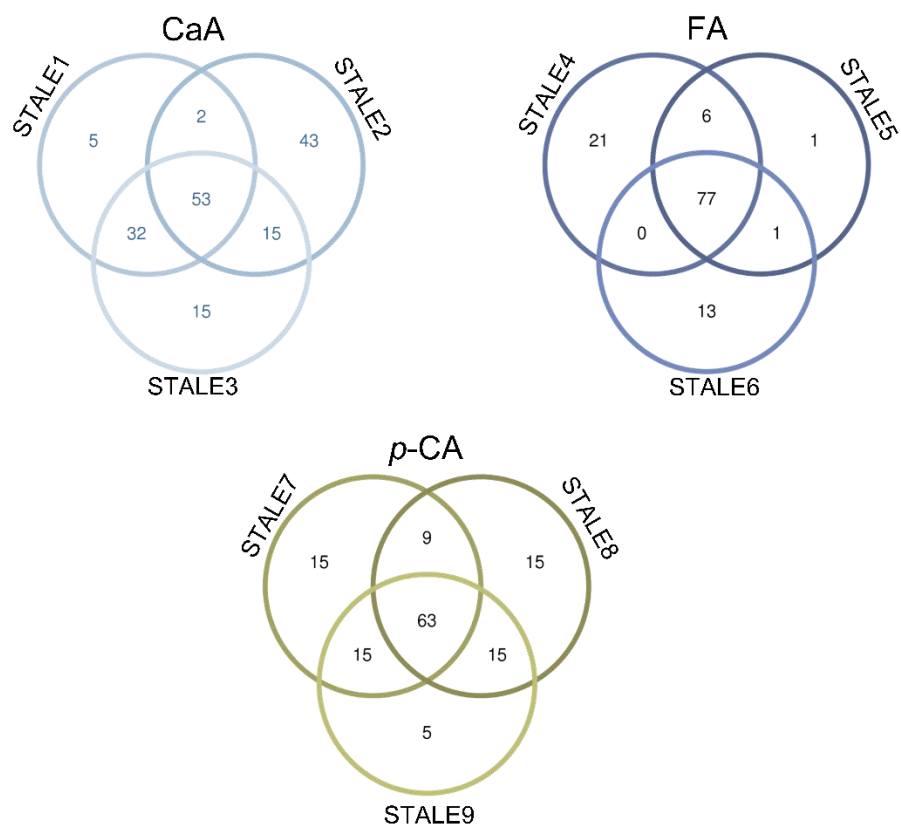


**Engineering a robust and autonomous biological funneling for efficient
valorization of lignin-related aromatics**

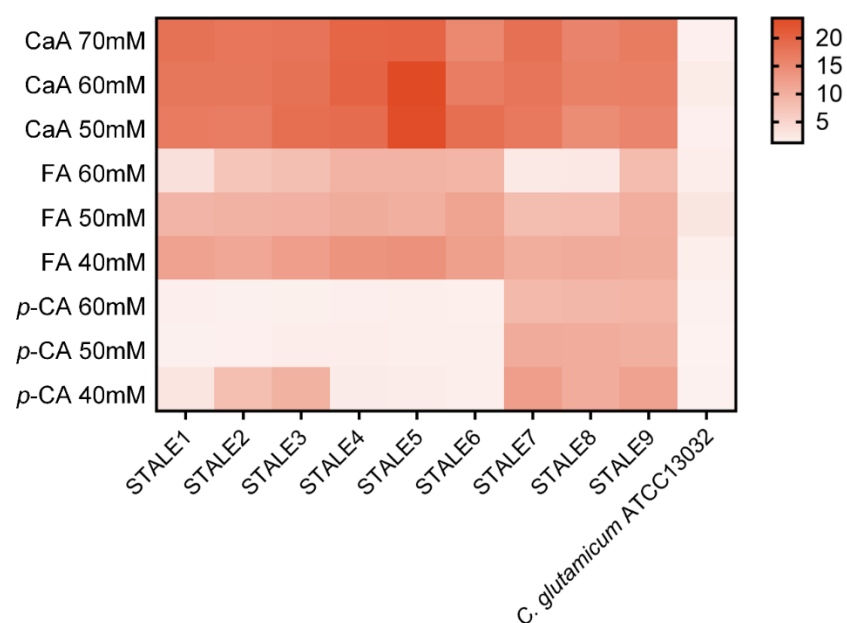
Xu et al.



Supplementary Figure 1. Final OD₆₀₀ values for wild type *C. glutamicum* in defined CGXII media with Spca1-Spca8 cultured in in defined CGXII media supplied with CaA, *p*-CA, and FA, respectively. Total substrate inputs supplied in five sequential pulses over 56 h for respective strains: CaA was supplied in strains Spca1–Spca4, with total inputs of 45.45, 46.35, 47.68 and 47.22 mM, respectively. (light green bars). Total *p*-CA inputs were 48.65, 48.22, 48.00, 47.98 and 48.27 mM for strains Spca1–Spca4 and Spca8, respectively (dark brown bars). Total FA inputs were 43.48, 43.20, 43.35, 43.72, 43.30, 43.72 and 42.82 mM for strains Spca1–Spca7, respectively, (pink bars). Abbreviations: FA, ferulic acid; *p*-CA, *p*-coumaric acid; CaA, caffeic acid. Values are presented as mean $\pm$ s.d. (n = 3 independent biological replicates). Source data are provided as a Source Data file.

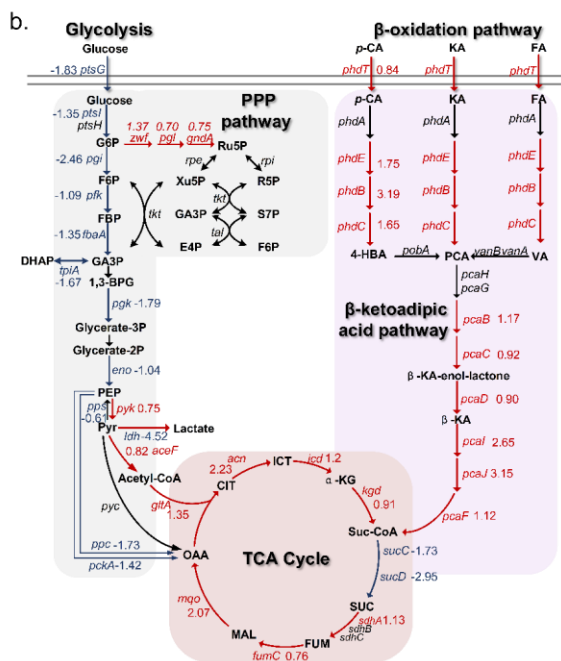


Supplementary Figure 2. Mutation profiles following ALE of CaA, FA, and *p*-CA. Venn diagrams of mutation sites (SNVs and InDels) in STALE1-STALE3, STALE4-STALE6, and STALE7-STALE9 strains. Abbreviations: FA, ferulic acid; *p*-CA, *p*-coumaric acid; CaA, caffeic acid.



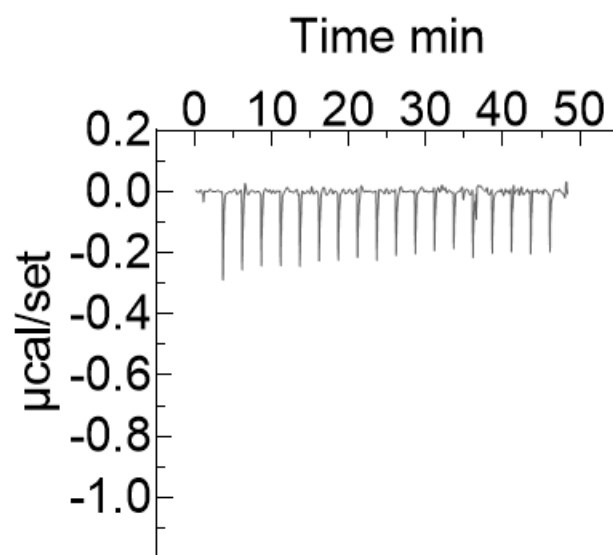
Supplementary Figure 3. Cross-tolerance to all three substrates in STALE1-STALE9.

Abbreviations: FA, ferulic acid; *p*-CA, *p*-coumaric acid; CaA, caffeic acid. Values are presented as mean $\pm$ s.d. (n = 3 independent biological replicates). Source data are provided as a Source Data file.

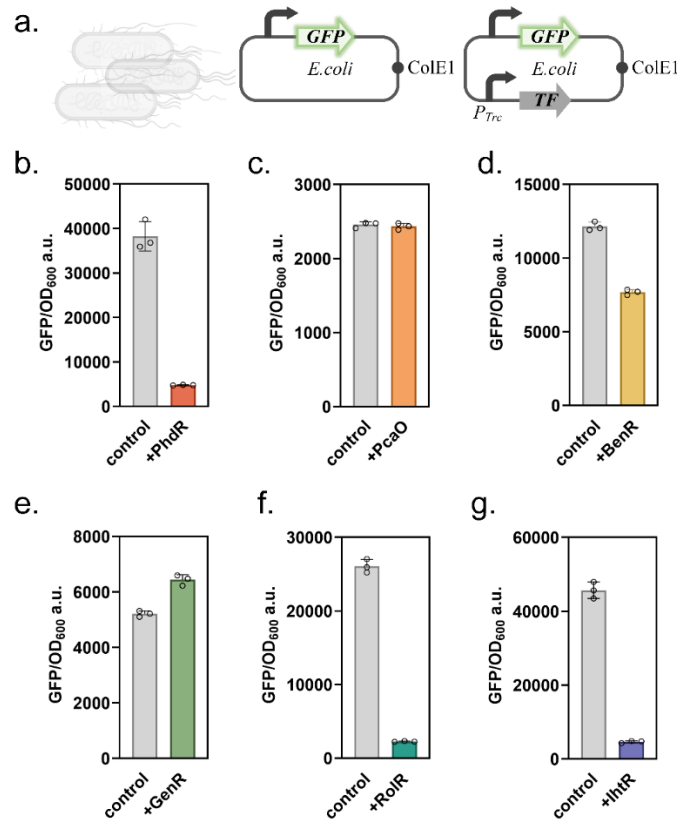


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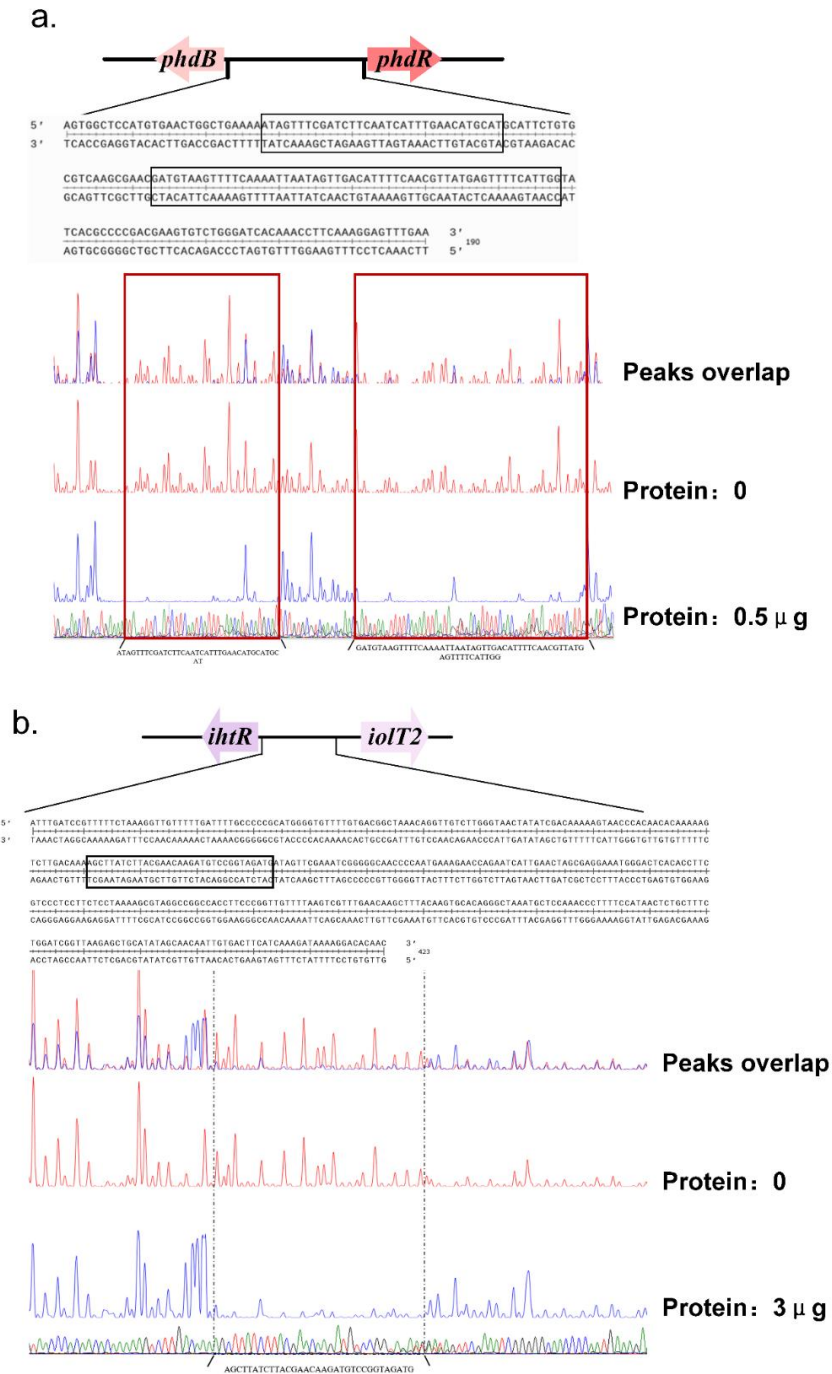
encodes phosphoenolpyruvate carboxykinase; *acn* encodes aconitate hydratase; *icd* encodes NADP-dependent isocitrate dehydrogenase; *kgd* encodes α -ketoglutarate dehydrogenase; *sucC* encodes succinate-CoA ligase subunit beta; *sucD* encodes succinate-CoA ligase subunit alpha; *fumC* encodes class II fumarate hydratase; *mgo* encodes malate dehydrogenase; *phdT* encodes MHS family transporter; *phdA* encodes acyl-CoA ligase; *phdE* encodes enoyl-CoA hydratase; *phdB* encodes 3-hydroxyacyl-CoA dehydrogenase; *phdC* encodes 3-oxoacyl-CoA ketohydrolase; *pobA* encodes 4-hydroxybenzoate-3-hydroxylase; *vanAB* encodes vanillate O-demethylase; *pcaHG* encodes protocatechuate-3,4-dioxygenase; *pcaB* encodes β -carboxy-*cis,cis*-muconate lactonizing enzyme; *pcaC* encodes γ -carboxymuconolactone decarboxylase; *pcaD* encodes β -keto adipate enol-lactone hydrolase; *pcaIJ* encodes β -keto adipate succinyl-CoA transferase; *pcaF* encodes β -keto adipyl-CoA thiolase.



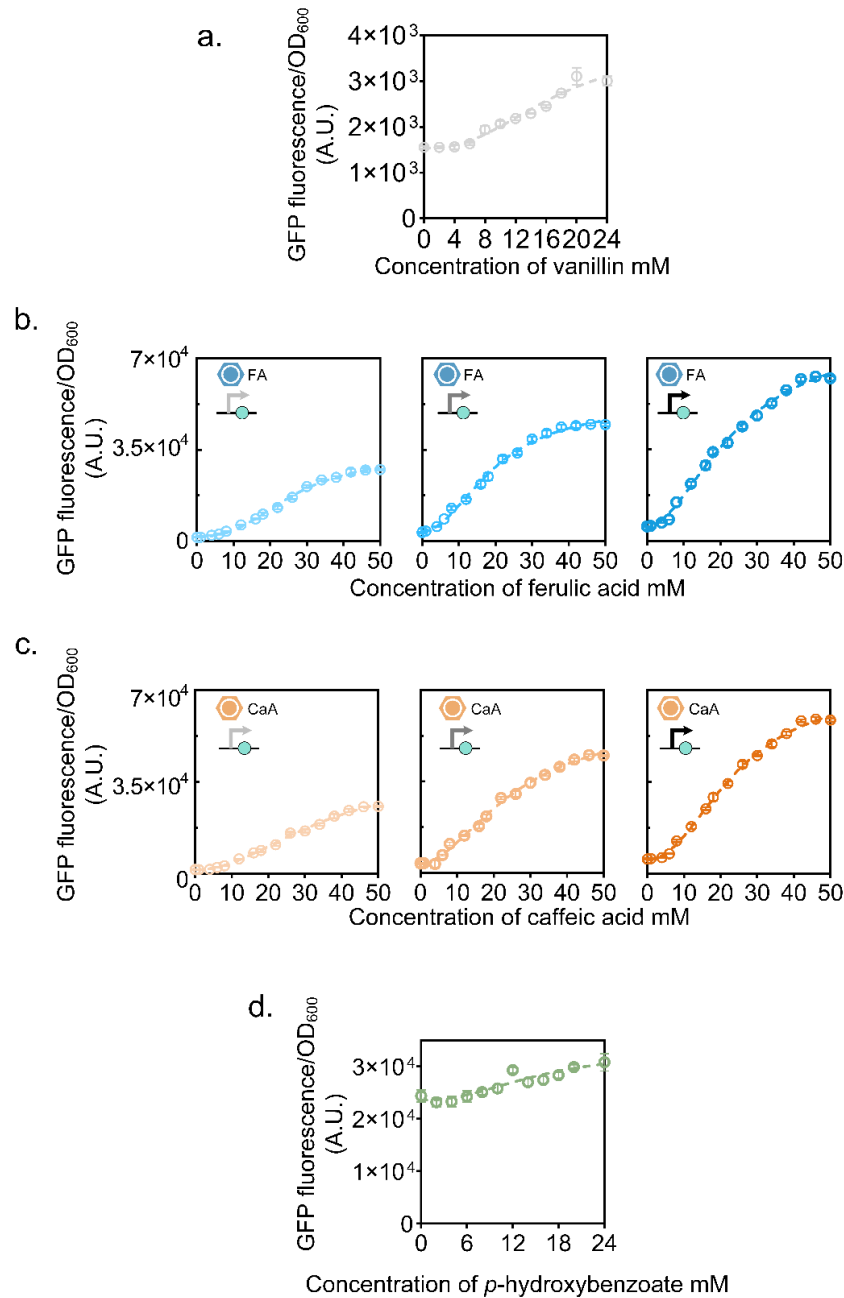
Supplementary Figure 5. Control experiment of isothermal titration calorimetry of PhdR with ligands, in which protein desalting buffer was titrated with PhdR. Source data are provided as a Source Data file.



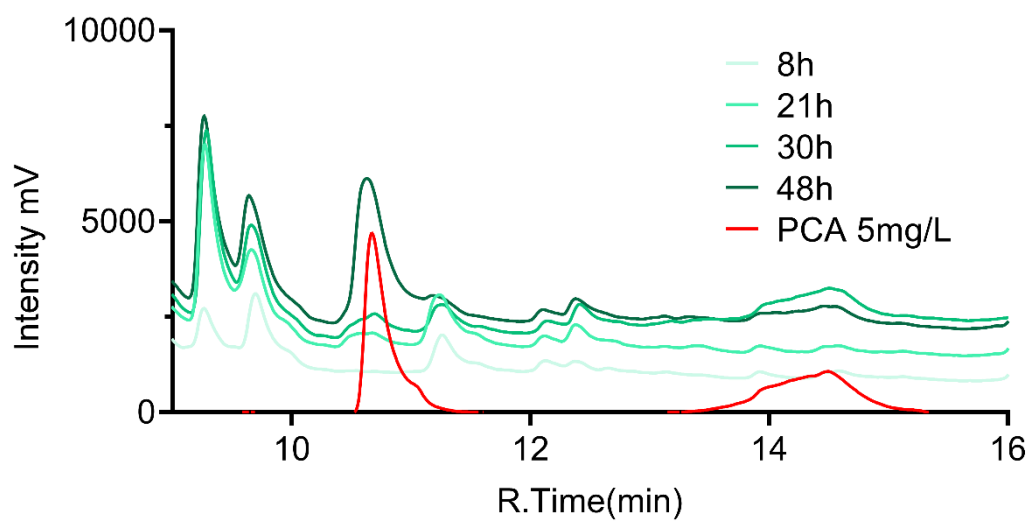
Supplementary Figure 6. Functional validation of aTFs. **a.** Schematic representation of plasmids with and without aTF expression in *E. coli*. Comparison of fluorescence intensity with and without phdR (**b**), PcaO (**c**), BenR (**d**), GenR (**e**), RolR (**f**), and IhtR (**g**) expression in *E. coli*. Values are presented as mean $\pm$ s.d. ($n = 3$ independent biological replicates). Source data are provided as a Source Data file.



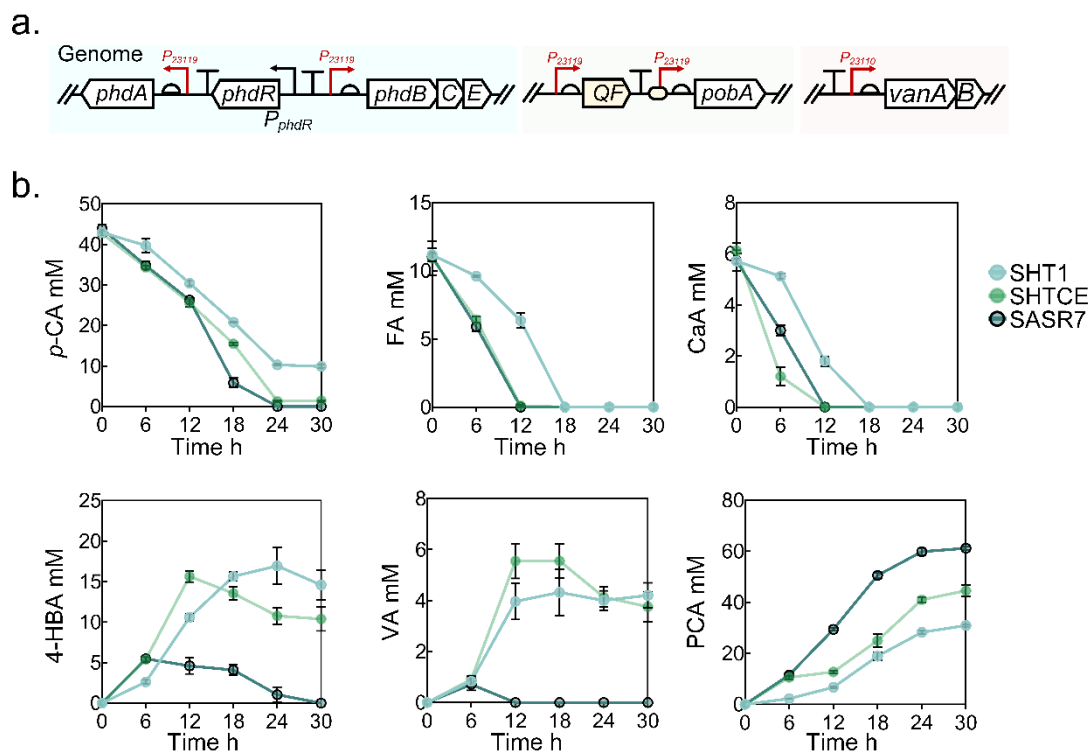
Supplementary Figure 7. Identification of PhdR and IhtR binding sites on promoters.
 DNase I footprinting of PhdR (a), and IhtR (b).



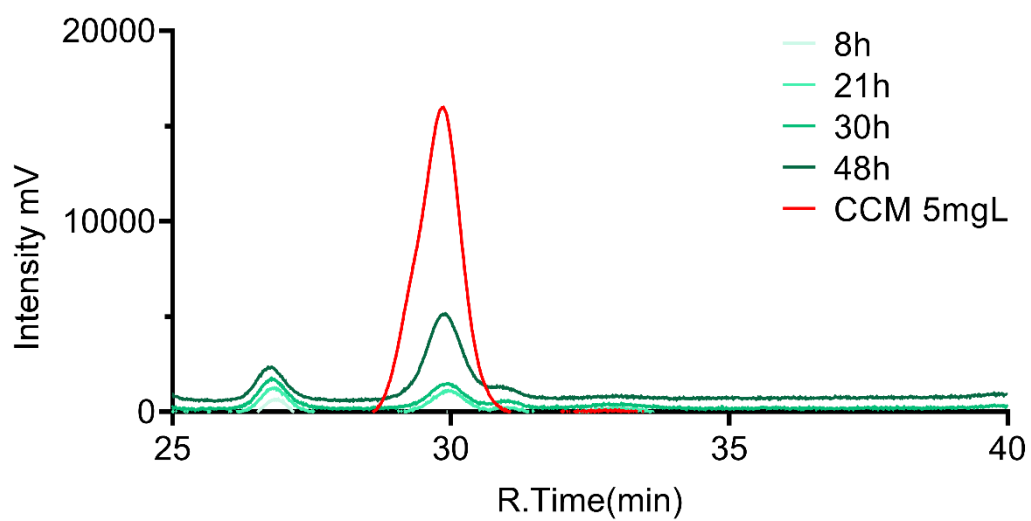
Supplementary Figure 8. Dose-response profiles of native biosensors and the optimized hybrid promoters. **a.** Initial dose-response curve of the VanR-VA- P_{vanA} . Dose-response curves of the optimal three *phd* hybrid promoters ($P_{Bba-23110-O2}$, $P_{Bba-23106-O2}$, $P_{Bba-23119-O2}$) supplemented with FA (**b**) and CaA (**c**). **d.** Dose-response Curve of engineered hybrid promoters of PcaO-4-HBA- P_{pobA} . Abbreviations: FA, ferulic acid; CaA, caffeic acid. Values are presented as mean $\pm$ s.d. ($n = 3$ independent biological replicates). Source data are provided as a Source Data file.



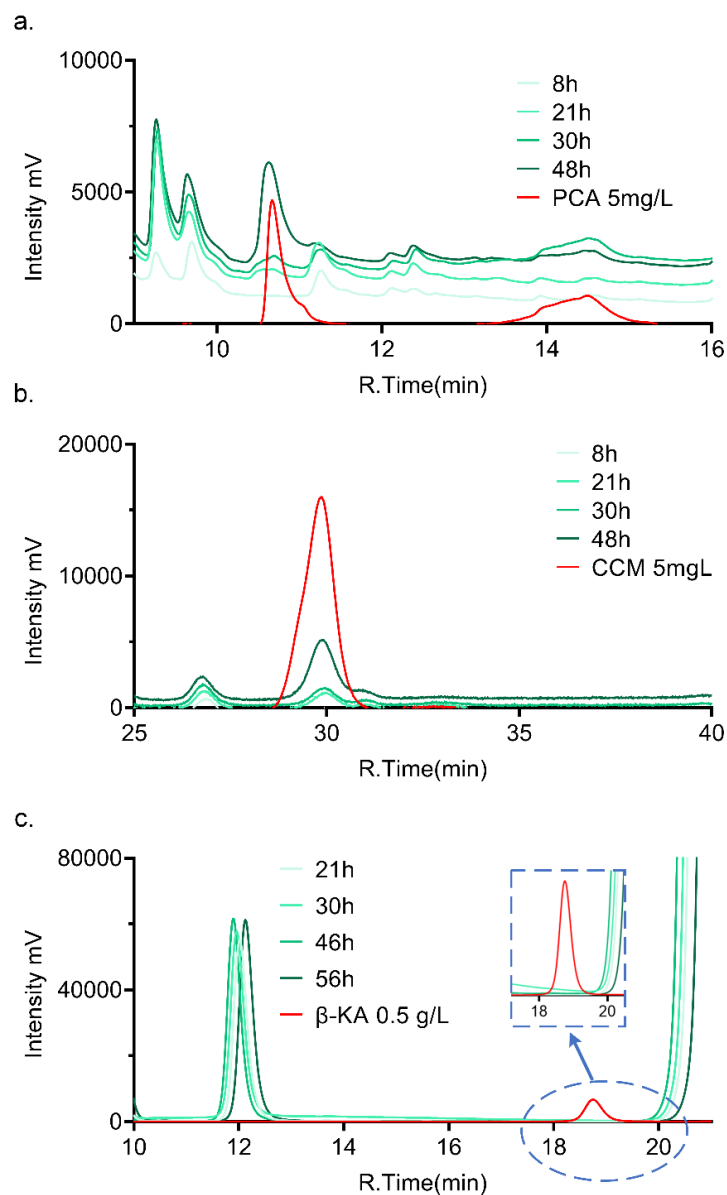
Supplementary Fig. 9. HPLC analysis of protocatechuic acid (PCA) produced by strain SASR7 grown on 10 g/L glucose as the sole carbon source. The red line represents the 5 mg/L PCA standard, with a retention time of approximately 10.6 min. Source data are provided as a Source Data file.



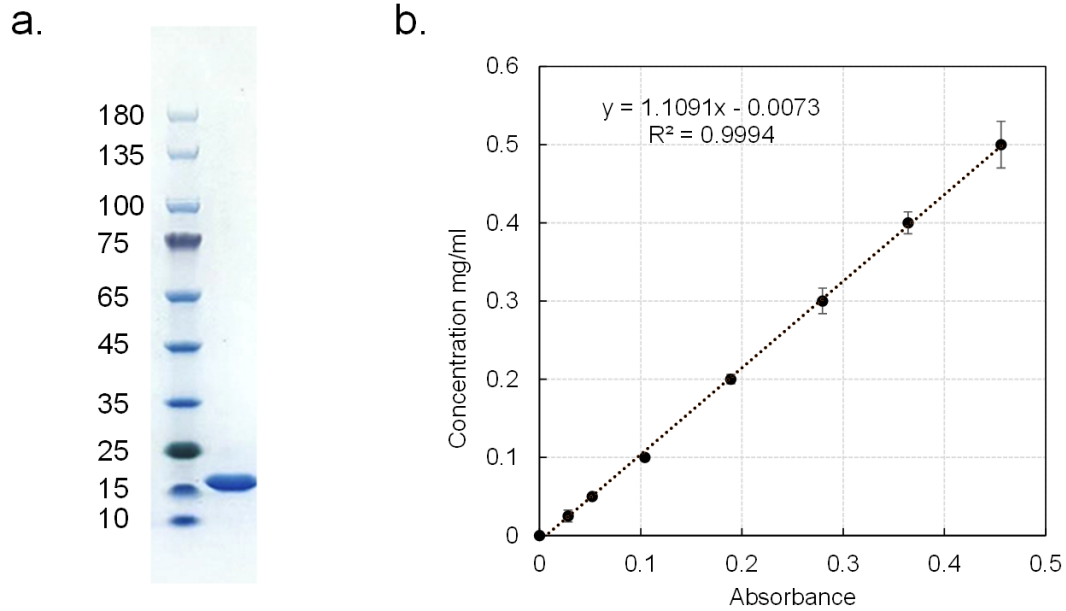
Supplementary Fig. 10. Construction of SHTCE and comparative fermentation performance with SHT1 and SASR7. a. Schematic illustration of the genome integration strategy for SHTCE. Native promoters of the target gene clusters were replaced with constitutive promoters of defined strengths to enable constitutive expression of all biological funneling genes (*phdAEBC*, *vanAB*, and *pobA*). The specific promoters used are indicated in red in the schematic. Regulatory elements, gene organization, and integration loci are shown as depicted. **b.** Time-course fermentation profiles of strains SHT1, SHTCE, and SASR7 cultivated with a mixed phenylpropanoid substrate containing of *p*-CA, FA, and CaA at a molar ratio of 4:1:0.5. Residual substrate concentrations (*p*-CA, FA, and CaA), intermediate metabolites 4-HBA and VA, and the final product PCA are shown over time. Abbreviations: FA, ferulic acid; *p*-CA, *p*-coumaric acid; CaA, caffeic acid; PCA, protocatechuic acid; 4-HBA, *p*-hydroxybenzoate; VA, vanillic acid. Values are presented as mean $\pm$ s.d. ($n = 3$ independent biological replicates). Source data are provided as a Source Data file.



Supplementary Fig. 11. HPLC analysis of *cis,cis*-muconic acid (CCM) produced by strain SASR7-C1 grown on 10 g/L glucose as the sole carbon source. The red line represents the 5 mg/L CCM standard, with a retention time of approximately 30 min. Source data are provided as a Source Data file.



Supplementary Fig. 12. HPLC analysis of β -Ketoadipic acid (β -KA) produced by strain SASR7-K19 grown on 10 g/L glucose as the sole carbon source. β -KA was derivatized to levulinic acid according to previously reported methods (see Methods). The red line represents the 5 mg/L levulinic acid standard, with a retention time of approximately 18.6 min.



Supplementary Fig. 13. Verification and quantification of PhdR protein purification. **a.** SDS-PAGE analysis of PhdR after multi-step purification; **b.** Standard curve of the BCA protein quantification kit, with the absorbance at 562 nm on the x-axis and the protein concentration on the y-axis. Values are presented as mean $\pm$ s.d. ($n = 3$ independent biological replicates).

Supplementary Table 1. Sequences of heterologous enzyme.

Gene	Suorce	Amino acid sequence
<i>praI^{Paj}</i>	<i>Paenibacillus sp. JJ-1b</i>	MRTQVGIAGAGPAGLLSHLLYLQGIIESIIENRTREEIEGTIRAGVLEQGTVDLMNQMGVGARMMKEGHFHEGFELRFNGRGRHINVELTGGKYVTVYAQHEVIKDLVAARLQTGGQIH FNVGDVSLHDVDTSSPKIRFRPNKDGELEIECDFIAGCDGFRGSPRAIPQSVRKEYQKVYPFSWLGLVEAPPSAHELIYANHERGFALVSTRSPQIQRLYLQVDAQDHIDNWSDDRI WSELHARLETRDGFKLLEGPFIQKQIVSMRSFVCDPMQHGRFLAGDAAHIVPPTGAKGLNLAADVQVLARGLEAYKAGKMEILNRCTEICLRRIWKAERFSWFMTTMLHRDQGHPT FERGIQLAELDYVTSSRAASTSLAENYIGLPMEF*
<i>pobA^{Ppu}</i>	<i>Pseudomonas putida KT2440</i>	MKTQVAIIAGAPSGLLGQLLHKAGIDNIIVERQTAEYVLGRIRAGVLEQGTVDLLREAGVAERMDREGLVHEGVELLVGRRQRDLKALTGGKTVMVYGGTEVTRDLMQAREASGAPII YSAANVQPHLEKGEKPYLTFEKDGRVQRIDCDYIAGCDGFHGISRQSIPEGVLKQYERVYPFGWLGLSDTPPVNHELIIYAHHERGFALCSQRSQTRSRYLQVPLQDRVEEWSDERF WDELKARLPAEVAADLVTPALEKSIAPLRSLVVEPMQYGHFLVGDAAHIVPPTGAKGLNLAASDVNYLYRILVKVYHEGRVDLLAQYSPLALRRVWKGERFSWFMTQLLHDFGSHKD AWDQKMQEADREYFLTSPAGLVNIAENYVGLPFEEVA*
<i>vanAB^{Ppu}</i>	<i>Pseudomonas putida KT2440</i>	<i>vanA</i> : MYPKNTWYVACTPDEIATKPLGRQICGEKIVFYRARENQVAAVEDFCPHRGAPLSLGYVEDGNLVCYHGLVMGCDGKTVSMPGQVRVGFPCNKTFAAVERYGFIWWWPGDQAQAD PALIPHLEWAVSDEWAYGGGLFHIGCDYRLMIDNMDLTHETVYHASSIGQKEIDEAPPVTTVTGDEVVTARHMENIMAPPFWRMALRGNLADDVPVDRWQICRFTPPSHVLIEVGVA HAGKGGYHAEAQHKASSIVDFITPESDTSIWYFWGMARNFAAHDQTLTDNIREGQGKIFSEDLERQQQNLLAHPERNLLKLNIDAGGVQSRKVLRIIAQERAPQPQLIATSANPA* <i>vanB</i> : MIDAVVVSNDQAGGICSELAADGSLLPASAGAHIDVHLDPGLVRQYSLCNHPEERHRYLIGVLNDPASRGGSRLHEQVQAGARLRISAPRNLFLAEGAQRSLFFAGGIGITPILC MAEQLSDSGQAFELHYCARSSERAFFVERIRSAPFADRLFVHFDEQPETALDIAQVLGNPQDDVHLVYVCGPGGFMQHVLDASGLGWQEANLHREYFAAAPVDASNDGSFAVQVGST GQVFEVPADRTVVQVLEENGIEIAMSCEQGICGTCLTRVLQGTDPDHRDLFTEEEQALNDQFTPCCSRSKTPLLVDI*
<i>vanAB^{Acb}</i>	<i>Acinetobacter sp ADP1</i>	<i>vanA</i> : MDVIIHKIHLTPSIRAFELISANGSDLPADFAGSHIDVHLKNGLTRQYSLNCCSEQHRYVIGVLHDENSRGGSRCIHQDYREGDHLNIGTPRNLFEIHSKTQKAVLFAGGIGITPILSMAY RLKHQQIPFELHYFVRSHEMIAFYGNLTEHFPEQIHFIHQNSQETQCEMSKVLVEEAPDRHLYVCGPAGFMQFVMDSAQQAGWSDEQLHQEHFVAPQIDQSQNEAFTIEVLGSDRKIEV SAHQATATQALLEHGFDPVPSCEQGICGTCTIRVVSCTPDHRDVFMTDEEHALNDQFTPCCSRAKSKILVIDLA* <i>vanB</i> : MFIKNAWYVACRPEEIQDKPLGRTICGEKIVFYRGKENKVAAVEDFCPHRGAPLSLGYVEDGHLVCGYHGLVMGCEGKTIAMPAQRVGGFPCNKAYAVVEKYGFIWWWPGEKSLANE DLPTLEWADHPESYGGGLFHIQCDYRLMIDNMDLTHETVYHSSSIGQKEIDEALPVTKVDGDHVVTERYMENIAPPFWQMALRGHNLADDVPVDRWQRCHFFAPSNVHIEVGVAH AGHGGYNAPKDKKVASVVDFITPETETSHWYFWGMARNFQPENQQLTDQIREGQGKIFTEDLEMLEQQQQNLRNPQRQLMLNIDAGGVQSRKIIDRLAKENSPSPQDTQRKFPNI RVI*
<i>vanAB^{Cef}</i>	<i>Corynebacterium efficiens</i>	<i>vanA</i> : MCGGDTRKFYPLFYCRSAHAGLNCDSQHQLSMSLSDSSLDSSHSSRLTFPQKAEAPMTTTSASSTASSTTTAKILPHPLNAWYVAAWDHEVTSKGIISRTIANKPLALYRTQDGRAVALAD ACWHRLAPLSKGKLTGRDGIQCPYHGLVYNSAGRCMSMPAQETLNPSSAAVASFPVVEQYRYIWWWLGDPTLADPTTVPDMHQMTHPEWTGDGKTIAACNYQLVDNLMDLTHEEFV HSSSIGQDELSEADFVETHTEDSVTVSRWMDRIDPPPFWQKNMNDKFPGYEGKVDWRWQIIHYYPSTICIDVGAKAGTGAPEGDRSQGVNGYVMNTITPETDRSSHYFWSFQRNYRL DSQLITTQLRDGVHGVFGEDEEMLTAAQAEIDANPDYEFYNLNDAGGMWVRRILEKALEAENRLHIPTTSAPVRKES* <i>vanB</i> : MGSPHPGKPGGGGEPPAHPHIRTGQEGVLMGTGSATNLLWQNAEVIATTEIADRIRRLRPEHPHKVVRPGEHLKVVDINGQQTERSYSIVDADPEGAEVSLTVFHTPNRGGSTFM HSLVPGQRITVTGPQQDFPLRIGAPRYVLVAGGIGITAIRGMAGLLRRLGADYTIHYAARSPEAMAYREELIAEHGDRHLHYLDSSESVTLIDIPALIDTIDSGTELYMCGPIRLMDAIRRAWRE RELDPTNLRFEFTFGNSGWFLPESFRVTIPRLGVSTEISENESILEALEKIGVEMMSDCRRGECGLCQVKVLDREGQIDHRDVFFSDRQKASEKLCAVSRVASTSAAPVPGNSLTELITP DNDSTAPGGRNIHLTIDVP*
<i>aroY</i>	<i>Enterobacter cloacae</i> ATCC 13047	MQNPINDLRSAIALLQRHPGHYIETDHPVDPNAELAGVYRHIGAGGTVKRPTRTGPAMMFNSVKGYPGSRILVGMHASRERAALLLGCVPKSLAQHVQAVKNPVPVVPVSPASQAPCQ EQVYFADDPDFDLRKLPAPTNTPIDAGPFFCLGLVLASDPEDTSLTDVTIHLRCVQERDELSMFLAAGRHIIEVFRKKAEEAGKPLPVTINMGLDPAIYIGACFEAPTPFGYNELGVAGAL RQQPVVLVQGVAVKEKAIARAEIIIEGELLPGVRVREDQHTNTGHAMPEFFPGYCGEANPSLPVIKVAVTMRNHAILQTLVGPGEHTTLAGLPTASIRNAVEEAIPGFLQNVYAHTAGG GKFLGILQVKKRQPSDEGRQGQAALIALATYSELKNILVDEVDIFDSDDLWAMTTRMQGDVSITTLPGIRGHQLDPSQSPDYSTSIRGNISCKTIFDCTVPWALKARFERAPFMEVD TPWAPELFSDDK*
<i>ecdB</i>		MRLIVGMTGATGAPLGVALLQALRDMPEVETHLVMSKWAKTTIELETPYTAQDVAALADVHSPADQAATISSGSFRTDGMIVIPCSMKTLGIRAGYAEGLVGRAADVVLKEGRKLVLV PRETPLSTIHLENMLALSRMGVAMVPPMPAYYNHPQTADDITQIHVTRVLDDQFGLHEHKKARRWNLQAQAHFSQENNDGI*
<i>ecdD</i>		MICPRCADEQIEVMATSPVKGIWTVYQCCHCLYTWRDTEPLRRTSREHYPEAFRMTQKDIDEAPQVPTIPPLL*

Supplementary Table 2. Sequences of key mutations used to validate the tolerance mechanisms after ALE in this study.

Gene name	Sequence
wzz*	ATGGAATTAAGGGAATACGCGACAATCCTGATGAAGAATTGGGTGTTGATCGTTATCGCATCCATTCTTGAATTGCAGCGGGCGCTGGTTTTCCCTTCTAGCTACACCGGAGTATC AGTCACGTAAGTGTATGTATCGGTGCGGTGCGGGGGCTGGGACAACCTCTGACATGGTTCAAGGTGCTAACTTTTCGCGTCAGATTGTGAATAGTTATGTTGATGTCATTAAGAC GGGTGTTGTTCTAGAGCCGGTTGTTGATGAGCTTGGTCTGGAGTTGACGGCTAACCAAGTTGAGTTCTCATATCAGTGCAGCTTCTCCTGCTGATACTGCGTTGATCAACATCACTGCT TCTAGTCCCTTCTCCTCAGCAGCGCGCTGAGATCGCCAATGCAGTGGGGGAGAGTTTCAAGAATGTGATTAGACTGAATTGGAACCAAGACTCCGGCGATGGCATGAGCCCGATTAA CCTGACTACTACTCAGGTGGCTCTGGAACCATCTTCTCCGGTCAGTCTAATGTGATGATGAATATCCTCCTCGGCCACTTGTAGGTCTTGCAATAGGTGTTGGTATTGCAGTGCTT CGCGCGGCTTTGGATACTCGTATTCCTTGCAGGATATTGAAGAGGTTACTGATAAGCCACTTTTGGGCGGAATCATTGCGGATTCTGAAGTTGAGAAGCACCCGTTGATCATT AGCACAAGCCGCATAGTCTATTGCGGAGTCTTTCTGCGGTTACGTAACCTGCAGTTCCTAACGTCGCGCGCTCATCTTCAGTATTTGTTATCTCCTCTGCTAATCCTGGTGA GGGTAAAGTCAACCACTTCTGTAAACCTAGCTTTGGCGCTTGCAGAGGCCGGCTCCCGTGTAGCGCTGATCGAAGCTGATCTTCGCTTGCCACGAGTGAGCAAGTACCTCGGAGTTG AGGGCAACGCAGGTCTGACTGACATTCTCATTGGCAAGGCCGAGGTTAATGATGTGTTGCAGCGTTGGGGTAGGACTCAGTTGTAATCTCCCGGCAGGGCGCATTCGCCGAAC CCGAGTGAGTTGCTTGGTTGAGCTGAGATGGACAAGGTCATTGCGGAGCTTGAGGAAAGCTTTGATTATGTGATCATCGATGCCCCCTCCGGCGTTGGCGGTTACCGATGCTGCAGT TATTGGTCATGGCAAGGCTGGCATCCTGATTGCGGTCTCCGCAGGTTCTACAAAGAAGCCTGAGTTGGAAGCTACGCTGTCCACGCTTGAGAAATGCGGATGCCAATGTTGTTGGCG TTGTCGCTACGATGCTCCCGCTAAGTCTGTGGCTGGTTATGGCTACGGAAATTACGGCTACGGCGACACCTCCAAATCAATGCCCTAAGCCCGACAACACCGAAGTAAACACCA CCGATGCTTCCAAGGCCAACAATGAGCAATAG
CGL_RS1820*	ATGTCAAATATTTTTATGAAGGGATCCTGCAGAATCTAATTCAAGATGGGTGGGATGTGCACCTTGTTCAAATCCAGGCCAGTTGGGAAGAAATTAAGTAAAGCTCATAC TATCGAGATGTCTAGAGAGATTTCAATAGGTACCGATGTTAAATCATTATTTAATTGGGTGCTATTGCTTAGGAAAATTCGTCGAAGAGTGCTGATAGTTGGAATCCGAAAGCTTCAT TGCTGGGAGTCGTGGCAGCACGAATTGCTCGAGTGCCACATGGGCTGCGCTCTGAACTGTTTTAGGCTTAAAAAGAAGATTCTAGTGTTTTTGAAT ATTTGACCCAGTTGTTTGCACATCAAACTTTGGCTGTAAGTCAATCTCTGAAGAAAGCAATTGAAGATGCGCACCTCGTTTTAAAGGAAGAGTGCAAGCTTAGGTTATGGCAGTATG AATGGAGTTGAGCTTGATCGCTTTAGAGTCCATCCCTGAAGAGAAATTATCTGCTCGTAATGCTTTAAACCTGCCTAGTAAATCTGTCATTGTTGGTTTTGTCGGCAGAATAAATAA GATAAGGGAGGAGATCTTCTCGCTGCTCTTACAAAACATGAGGCTTTTACCCGATTGCGACTGCATCTCTTAATTATTGGTGAATTGGAAGACGATGACTTGCGAGAAGCATTCTTA AATTAGTTAATGAAGGGCAGGTTACGATTACAGGATGGATTGATTTCCCTGAAGAACCATTAGCTGCAGTTGATGTTTTGCTTCACCCAACTCAGCGAGAAGGTTAGGTATGCTTTG CTGGAAGCTCAGGCTATGGGAGTGCTGTATTGACGAATGCTGTGACTGGAACAGTTGATGCAGTAACAAGTGGAGAAGGTGGCTTTTTTGCCGATGACGATTCTGTTGAGTCTGG GTTTCTAAGATTGATTATTAGTTTCCGATCCTAAGTTAAGAGACCGGATGGGACGTGCTGGTCGCCAGTTGTGTGAGCTCGTTTCAATCGTGATGATGTCGCAGCTCGTTTCAGTC ATTTCTGTGGAACAATTCAAAAAATAG
lexA* (upstream)	TTCAAACTCCCGCCTCAATTGTTTGGCCACATCTTAACCTTTAGCCACGACACGTTGGAACACCAATACCGTTACATGTTGACTAAGTTTCTATGTTGATTATAGCACCCCGTTT GAACGTTGTCTAGAGAAGATTTAAAAATCTCGAACACTCGTACCATTTCCGCAGGAAAACCTGTATGGTTGGAAACTAGAAATACTGACAGAGGTTGGAATAGCTCAGCATTGAGCTT CAGAAGTTCACACTGGATGAACCTCATCAAGAGTGAACATGGAAGCGAACAGAGTTTTAGTGCTTTAACGGGCAACAATGAGAGGAAGGGAACGGAAG
atsR*-1 (upstream 1)	AGCATAGAACTAAACAGTATGCTTGTCTGCTAAATGTGAATTTTAAAGAGATTATCCACACAATTACGAAAAAACAGATTGCCACAAATTAGTCTTCGAACCTTTAATCAACACC ACACCCAAAGCTAAACTTGCCTGCTGTTGTGTAAATTTGCATTGAGGCTGAAAAATTCCTAAAGGGACTCCGTCCGAATAATTGGAAGGCCAGAGAAGACAGTCAACTCCTAGAGTAA GGATAATC
atsR*-2 (upstream 2)	AGCATAGAACTAAACAGTATGCTTGTCTGCTAAATGTGAATTTTAAAGAGATTATCCACACAATTACGAAAAAACAGATTGCCACAAATTAGTCTTCGAACCTTTAATCAACACC ACACCCAAAGCTAAACTTGCCTGCTGTTGTGTAAATTTGCATTGAGGCTGAAAAATTCCTAAAGGGACTCCGTCCGAATAATTGGAAGGCCAGAGAAGACAGTCAACTCCTAGAGTAA GGATAATC
atsR*-3	GTGTGCGGGCTTAGAGAAACAAAAAGGCTGCTACGCGGACAGCATTGTACGCTGCTGCTGCGGAGATCGCCTTGATGGAAGGCCCTGAGGCGTTACGGTTGCGGCCATTGCAG CTGCAGCCGGGTCTCCCCAGGACTTTTCACTAATCTTCCCTTCTCGGGAAGACGCATTGGTGCAATTTGTGGTCAATTCGCGTTACAGGAACCTACGGATCAGCTATACGAGTTTC CTACAAGCGTGCCCCACGAGATGCCATTGAACAATTTGGTGATAAACCAATTGCGGGATGGCGATGACGCTATGGATTCTTTCAGCGCAATGTTTCGAATCGGTGAGATCCTTGAA ATCTTGACCCCATCAAGTGTGTTATCGATAAGGAGCGACTCATTGCTCCGTTGCTTGAGTTGATGTTGAAAGCTGACAAAGACCTTGACAAGTTGATGCGGCAACTCTGATCCATTT GCATGCAGCGCAATTGCAACCTCGCTGCATACGTTTTACCAAGCTTCCGAGCCCCGGACATAGAAGATGGAGTCGATTGATCCGTGCGGCATGCGCCTGGATTAAGAAATAA

Supplementary Table 3. Operators of biosensors constructed and characterized in this study.

Allosteric transcription factor	Operator sequences	Reference
PhdR	ATAGTTTCGATCTTCAATCATTTGAACATGCATGCAT	This study
	GATGTAAGTTTTCAAAATTAATAGTTGACATTTCAACGTTATGAG	
IhtR	AGCTTATCTTACGAACAAGATGTCCGGTAGATG	This study
PcaO	GTTCGCAAGGCGAAC	1
	AACCCCTGACCTTCGGGGTT	
BenR	GTCACACACCGCTT	2
	CCTAGGAATCCCCTAAT	
	TTTAGGGCTATCCCTAGT	
GenR	ATTCCGCTATGTGGAATCTAAGTATTCGCCCTCAGGAAACGGGGG	3
	ATAATCACTCTTTCCAGATAGCGGAATCCCTT	
	ATCACACGCACCAGAATCGGGAGG	
RolR	AAAATCTGAACCCTTGTTCAATTATGAAT	4
VanR	AACTAACTAAGAGTTTAGGTATTTGGTT	5

Supplementary references

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