## **A fluoride-responsive genetic circuit enables** *in vivo* **biofluorination in engineered**  *Pseudomonas putida*

Calero *et al.*

### **Supplementary Table 1. Bacterial strains and plasmids used in this study.**



<sup>a</sup> *FRS*, fluoride-responsive riboswitch; *Antibiotic markers*: Amp, ampicillin; Gm, gentamicin; Km, kanamycin; Nal, nalidixic acid; and Str, streptomycin.



# **Supplementary Table 2. Oligonucleotides used in this study.**

#### **Supplementary Table 3. Transitions and optimized parameters for fluorometabolites detection by mass spectrometry.**<sup>a</sup>



<sup>a</sup> 5′-FDA, 5′-fluoro-5′-deoxyadenosine; 5′-FDRP, 5′-fluoro-5′-deoxy-D-ribose 1-phosphate; DP, declustering potential; EP, entrance potential; CE, collision energy; CXP, collision exit potential; RT, retention time.



**Supplementary Table 4. NMR characterization of chemically-synthesized 5′-fluoro-5′-deoxyadenosine.** a

<sup>a</sup> Int., integrals; Mult., multiplicities; s, singlet; d, doublet; t, triplet; m, multiplet.

<sup>b</sup> This assignment is unambiguous and could also be for  $N_1$ . Assignments of the NH<sub>2</sub> group are not possible due to exchange of the labile protons.

Note: Both 1D as well as 2D homo- and hetero-nuclear spectra were used to assign all the resonances. The <sup>1</sup>H and <sup>19</sup>F chemical shifts were obtained from 1D-NMR spectra, whereas the <sup>13</sup>C and <sup>15</sup>N chemical shifts were obtained from 2D-edited heteronuclear single quantum correlation (HSQC)-, heteronuclear multiple bond correlation (HMBC)- and heteronuclear 2 bond correlation (H2BC)-spectra. The presence of 19F in the molecule enables the extraction of both one and two bond *J* coupling constants between <sup>19</sup>F and <sup>13</sup>C (<sup>1</sup>J<sub>FC5</sub><sup> $\cdot$ </sup> and 2*J*FC4′) from the HSQC spectrum as well as two and three bond *J* coupling constants between 19F and 1H (2J<sub>FH5'</sub> and 3J<sub>FH4'</sub>) from the 1D-NMR spectra.



**Supplementary Fig. 1. Structural organization of** *FluoroBricks***. (A)** The standard design followed to test different parts of the biofluorination pathway includes a defined set of synthetic biology parts; i.e. promoters, ribosome binding sites (RBS), coding sequences, His tags and transcriptional terminators. All coding sequences used in this work were codon-optimized to ensure proper expression and translation in *P*. *putida*. Individual transcriptional units (*FluoroBrick*) are easily composable into more complex designs by one-step *USER* cloning or restriction/ligation according to the rules of the Standard European Vector Architecture<sup>3,8</sup>. (B) Nomenclature used for the plasmids containing FluoroBricks. Plasmids are named with the initials *FB* followed by a code of numbers and letters, standing out for the promoter and coding sequence used. An *H* superscript indicates the presence of a  $6\times$  histidine tag in the sequence.



**Supplementary Fig. 2. Chemical synthesis of 5′-fluoro-5′-deoxyadenosine.** The starting point was 2′,3′ isopropylidene-6-chloropurine riboside [6-Chloro-9-(2,3-O-isopropylidene-β-D-ribofuranosyl)-9H-purine] (1), which was converted to the primary fluoride (**2**) by treatment with tosyl fluoride (TsF) and tetrabutylammonium fluoride (TBAF) in tetrahydrofuran (THF). Next, (**2**) was aminated to 2′,3′ isopropylidenated-5′-fluoro-5′-deoxy-adenosine (**3**) with NH<sup>3</sup> in *tert*-butanol (*t*-BuOH). The last step, carried at room temperature (rt), was the deprotection of (**3**) with 90% (v/v) formic acid to yield 5′-fluoro-5′ deoxyadenosine. This protocol is based on the synthesis proposed by Ashton & Scammells<sup>9</sup>.



**Supplementary Fig. 3. NMR characterization of chemically-synthesized 5′-fluoro-5′-deoxyadenosine. (A)** 1D 1H-NMR spectrum of 5′-fluoro-5′-deoxyadenosine (5'-FDA). **(B)** Overview 19F-NMR spectrum. The large hums are background signals originating from the probe. **(C)** Zoom-in of the decoupled 19F-NMR spectrum. **(D)** Zoom-in of the coupled 19F-NMR spectrum.



**Supplementary Fig. 4. Measurement of fluorometabolites by LC-MS/MS. (A)** Chromatograms of cell-free extracts of *P*. *putida* KT2440 bearing plasmid pFB·1F1 (or an empty plasmid, used as a negative control), compared to the chromatogram obtained for a chemically-synthesized 5′-fluoro-5′-deoxyadenosine (5′-FDA) standard. The characteristic retention time for 5′-FDA (in min) is shown above the peak corresponding to the fluorometabolite. **(B)** Chromatograms of cell-free extracts of *P*. *putida* KT2440 bearing plasmid pFB·1F1PH1 (or plasmid pFB·1F1, used as a negative control), compared to the chromatogram obtained for an enzymatically-synthesized 5′-fluoro-5′-deoxy-D-ribose 1-phosphate (5′-FDRP) standard. The characteristic retention time for 5′-FDRP (in min) is shown above the peak corresponding to the fluorometabolite. Souce data are provided as a Source Data file.



**Supplementary Fig. 5.** *In vivo* **biosynthesis of 5′-fluoro-5′-deoxyadenosine in a** *crcB* **mutant of** *P***. putida.** (A) Growth curves of *P. putida* KT2440∆*crcB*::FRS-T7RNAP containing the plasmid modules with the fluorinase of *S. xinghaiensis* (pFB·1F2, blue circles) compared to the growth of *P. putida* KT2440 $\triangle$ crcB::FRS-T7RNAP with an empty plasmid (gray circles). Addition of NaF at 5 mM to the cultures is indicated with a vertical black arrow (F– ). Error bars correspond to standard deviations of three different biological replicates. **(B)** Intracellular concentration of 5′-FDA in the cells after 24 and 48 h of induction of the fluoride-dependent riboswitch with 5 mM NaF. CDW, cell dry weight. Data are presented as mean values and error bars correspond to standard deviations of three different biological replicates. Source data are provided as a Source Data file.



**Supplementary Fig. 6.** *In vitro* **biosynthesis of 5′-fluoro-5′-deoxyadenosine and 5′-fluoro-5′-deoxy-Dribose 1-phosphate. (A)** Structure of plasmid constructs carrying the genes encoding fluorinases and phosphorylases from *Streptomyces* sp. MA37 (*flA1* and *flB1*) and *S*. *xinghaiensis* (*SxflA* and *SxflB*) under transcriptional regulation of the XylS/*Pm* expression system. FlB1 was tagged in the *N*-terminal domain using a 6× histidine tag (NHis); T0 and T1 indicate synthetic transcriptional terminators. **(B)** *In vitro* biosynthesis of 5′-fluoro-5′-deoxyadenosine (5′-FDA) and 5′-fluoro-5′-deoxy-D-ribose 1-phosphate (5′- FDRP) using cell-free extracts of *P*. *putida* KT2440 with selected fluorinases and phosphorylases in the configurations described in **(A)**. Data are presented as mean values and error bars correspond to the standard deviations of three different biological replicates. Source data underlying Supplementary Figure 6b are provided as a Source Data file.



**Supplementary Fig. 7. Quantification of alive and dead** *P***.** *putida* **cells under biofluorination conditions.** Cultures of *P. putida* KT2440::FRS-T7RNAP bearing plasmid pFB·1F2 (encoding a fluorinase from *S*. *xinghaensis*) or plasmid pFB·1F2PH1 (encoding fluorinase and phosphorylase from *S*. *xinghaensis* and *Streptomyces* sp. MA37, respectively), were added or not with 15 mM NaF (indicated as +F and –F, respectively). Cells harvested from these cultures were treated with propidium iodide, and the fraction of dead cells was determined measuring fluorescence at an excitation/emission wavelength of 544/612 nm (blue bars). Growth was determined by measuring OD<sup>600</sup> (grey bars), and the *specific death* was determined by normalizing the fluorescence reading corresponding to dead cells to the OD<sub>600</sub> (orange bars). A culture of the same strain bearing an empty plasmid, added (+F) or not (–F) with NaF, was used as a control. Further controls included cultures supplemented with 15 mM NaCl (+Cl) or heated at 95°C for 5 min as indicated in the figure. Representative results from three different biological replicates are shown, and dots indicate individual measurements. Source data are provided as a Source Data file.

### **Supplementary References**

- 1. Meselson, M. & Yuan, R. DNA restriction enzyme from *E*. *coli*. *Nature* **217**, 1110-1114 (1968).
- 2. Bagdasarian, M. *et al.* Specific purpose plasmid cloning vectors. II. Broad host range, high copy number, RSF1010-derived vectors, and a host-vector system for gene cloning in *Pseudomonas*. *Gene* **16**, 237-247 (1981).
- 3. Silva-Rocha, R. *et al.* The Standard European Vector Architecture (SEVA): a coherent platform for the analysis and deployment of complex prokaryotic phenotypes. *Nucleic Acids Res.* **41**, D666-D675 (2013).
- 4. Choi, K.H. *et al.* A Tn*7*-based broad-range bacterial cloning and expression system. *Nat. Methods* **2**, 443- 448 (2005).
- 5. Calero, P., Jensen, S.I. & Nielsen, A.T. Broad-host-range *ProUSER* vectors enable fast characterization of inducible promoters and optimization of *p*-coumaric acid production in *Pseudomonas putida* KT2440. *ACS Synth. Biol.* **5**, 741-753 (2016).
- 6. Volke, D.C., Turlin, J., Mol, V. & Nikel, P.I. Physical decoupling of XylS/*Pm* regulatory elements and conditional proteolysis enable precise control of gene expression in *Pseudomonas putida*. *Microb. Biotechnol.* **13**, 222-232 (2020).
- 7. Aparicio, T., de Lorenzo, V. & Martínez-García, E. CRISPR/Cas9-based counterselection boosts recombineering efficiency in *Pseudomonas putida*. *Biotechnol. J.* **13**, e1700161 (2018).
- 8. Sánchez-Pascuala, A., de Lorenzo, V. & Nikel, P.I. Refactoring the Embden-Meyerhof-Parnas pathway as a whole of portable *GlucoBricks* for implantation of glycolytic modules in Gram-negative bacteria. *ACS Synth. Biol.* **6**, 793-805 (2017).
- 9. Ashton, T.D. & Scammells, P.J. An improved synthesis of 5′-fluoro-5′-deoxyadenosines. *Bioorg. Med. Chem. Lett.* **15**, 3361-3363 (2005).