Supporting Information

Bioconversion of xylose to ethylene glycol and glycolate in engineered *Corynebacterium glutamicum*

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Table S1. Oligonucleotides used for gene cloning in this study.

Name	Relevant characteristics (5' → 3')	Source
crRNA-*iolR*-*SpeI*-fwd	TATactagtAGGTCTTCGAAGAGTTCGGCTGGCATCTACAACAGTAGAAATTC	This study
crRNA-*ald*-*SpeI*-fwd	TATactagtTGCGGTGCCACGTGCGACCTCACAATCTACAACAGTAGAAATTC	This study
crRNA-*SpeI*-rev	TATactagtATTTAAATAAAACGAAAGGC	This study

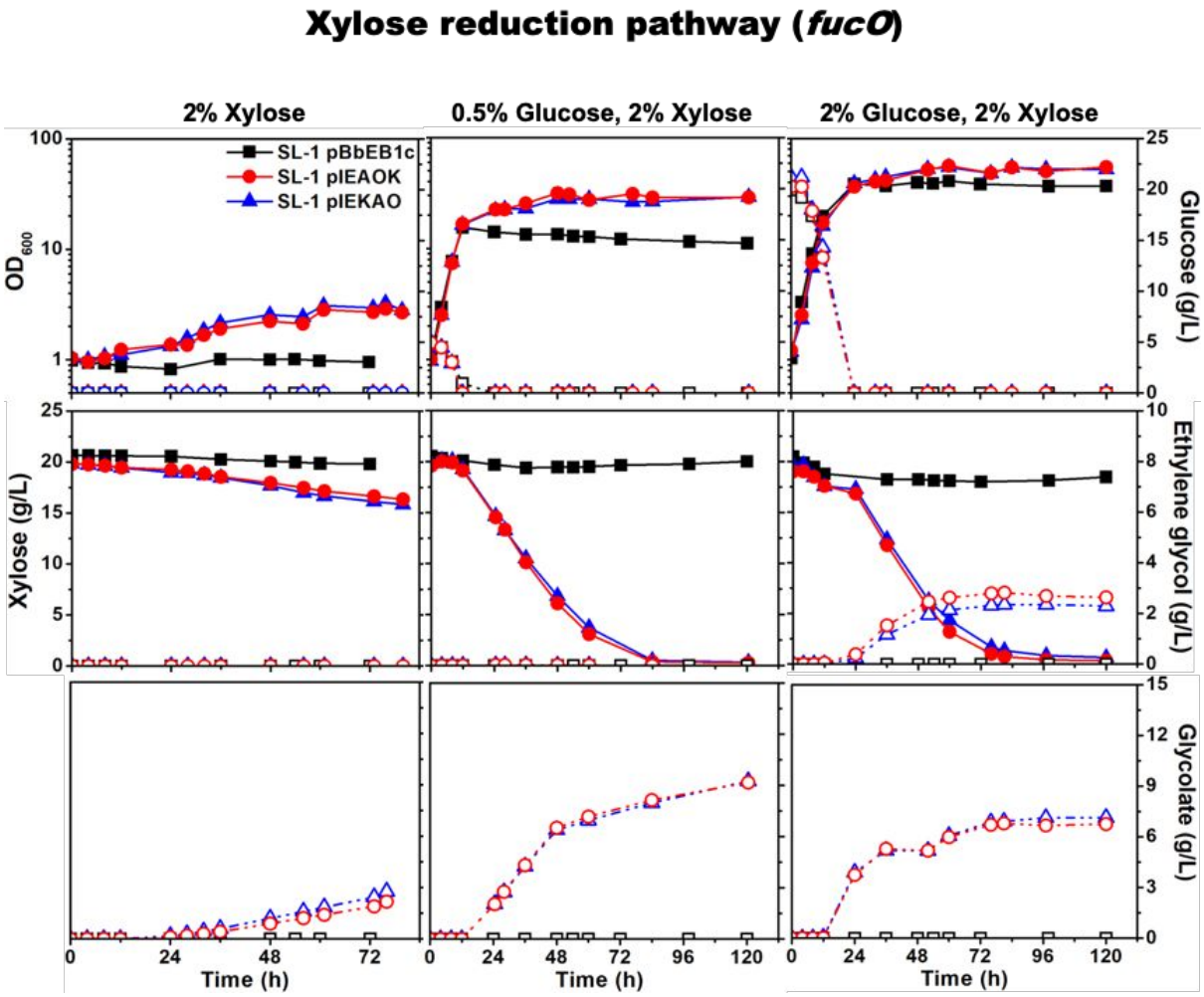
Note: The restriction enzyme sites were shown as lower cases. Target specific-protospacer regions of the sgRNAs were underlined.

Table S2. Single strand oligonucleotides used for the CoryneCR12-STOP

Name	Relevant characteristics (5' → 3')	Source
ssODN_*iolR*	GCGGTCGAGGTCTTCGAAGAGTTCGGC**Tta**CCAAATGGGAGCTTCGGTGGT CATGATGT	This study
ssODN_*ald*	ACGTCCGCTGCGGTGCCACGTGCGACCT**atC**AGAAAACTTCACCAGTGACA GGTGAAAT	This study

Note: Edited bases were shown as lower cases and stop codon sites were shown in bold.

Figure S1. Time course of growth, xylose consumption and ethylene glycol production in engineered *C. glutamicum* with the *fucO* gene expression



Growth and carbon source consumption in recombinant *C. glutamicum* for production of ethylene glycol. Optical densities at 600 nm (OD_{600}; solid symbol; solid line) and glucose (open symbol; dashed line) concentrations [upper row], xylose (solid symbol; solid line) and ethylene glycol (open symbol; dashed line) concentrations [middle row], and glycolate (open symbol; dashed line) concentrations [lower row] in the medium were measured for *C. glutamicum* SL-1 pBbEB1c (black square in A & B), SL-1 pIEAOK (red circle in A) or SL-1 pIEKAO (blue triangle in A). Either xylose (2% wt/vol) as the sole carbon source [left panel], a mixture of xylose (2% wt/vol) and glucose (0.5% wt/vol) [middle panel], or a mixture of xylose (2% wt/vol) and glucose (2% wt/vol) [right panel] in CgXII medium were used. Data represents mean values of triplicate cultivations, and error bars represent standard deviations. See the details in Table 1 for the strain used.

Figure S2. Sequence chromatograms of editing sites at the *iolR* and *ald* gene of *C. glutamicum*.