

# Endogenous enzymes enable the reductive glycine pathway in yeast across a broad range of formate concentrations

## Supplementary Table S1

Level 0 constructs used in this study

Level 0 Plasmid Name	Promoter	Gene	Terminator	Selection Marker	Level 0 backbone
<i>pCLJ3</i>	<i>PYK1</i>	<i>GCV1</i>	<i>PYK1</i>	<i>URA3</i>	<i>pLOA_0-1</i>
<i>pCLJ6</i>	<i>TEF1</i>	<i>GCV2</i>	<i>TEF1</i>	<i>URA3</i>	<i>pLOA_1-2</i>
<i>pCLJ9</i>	<i>TEF2</i>	<i>GCV3</i>	<i>TEF2</i>	<i>URA3</i>	<i>pLOA_2-3</i>
<i>pCLJ12</i>	<i>RPL3</i>	<i>MIS1</i>	<i>RPL3</i>	<i>URA3</i>	<i>pLOA_3-4</i>
<i>pCLJ15</i>	<i>RPL3</i>	<i>MIS1</i>	<i>RPL3</i>	<i>URA3</i>	<i>pLOA_3-R</i>
<i>pCLJ18</i>	<i>CWP2</i>	<i>LPD1</i>	<i>CWP2</i>	<i>URA3</i>	<i>pLOA_4-R</i>

## Supplementary Table S2

Primers used in this study

Oligo Name	Sequence
CL_00003	ATGCTATAATCAAAAAAATTGTGTTTAAGAGATTC
CL_00004	TTTACTGCTTGTAGTAATGTGTGGGCAC
CL_00011	GGACACTGTATCTGCTACGCTGTTTATAATGCTAGTATTTTGGAGATTAATCTCAGTACA
CL_00012	GAATCTCTAAACACAATTTTTTTGATTATAGACATTGTGATGATGTTTTATTTGTTTTGATTGGTGTCT
CL_00013	GTGCCACACATTACTACAAGCAGTAAAAAGAATCATGATTGAATGAAGATATT
CL_00014	GCAGCGTTTATTGTGCGAATCTCACTTTAGCATTATGTACCCATGTATAACCTTCC
CL_00017	ATGCTTAGGACAAGAGTACTGC
CL_00018	TCATTCAGTTTCGTTGCAATTC
CL_00025	GATTCGCACAATAAACGCTGCTTCTGTTATAGCTTCAAAATGTTTCTACTCCTTTTT
CL_00026	GGAGAGCAGTCACTCTTGTCCCTAAGCATTGTAATTAACCTTAGATTAGATTGCTATGCT
CL_00027	GAAGAAATTGCGAACGAACTGAATGAGGAGATTGATAAGACTTTTCTAGTTGCA
CL_00028	GTCCCTTTATTGAGAGTTTCACAGAATCTAAGATAGCGCCGATCAAAGTATTT
CL_00031	ATGTTACGCACTACTAGACTATGGACCACCCG
CL_00032	TCAGTCATCATGAACCAAGTGTCTTTTCG
CL_00039	GTGAACTCTCAATAAAGGGACTTCGTCGGGGCCGTATACTTACATATAGTAGATG
CL_00040	CGGGTGGTCCATAGTCTAGTAGTGCCTAACATGTTTAGTTAATTATAGTTGCTTGACCGTATATTC
CL_00041	CGAAAAGACACTGGTTCATGATGACTGAGAGTAATAATTATTGCTTCCATATAATAT
CL_00042	GCAACTACTTTTCTATTCACTGGGAAGGAGGGGTAGCGACGGATTAAT
CL_00045	ATGTTGTCGAGACTATCTTTATTGAGTAACTCG
CL_00046	AAAATAGACCTTCAATTTACCGTCGTCG

CL_00054	CGAGTACTCAATAAAGATAGTCTCGACAACATGATTGATTGTTGTAGTAACTGTGTTGTTTC
CL_00055	CGACGACGGTGAAATTGAAGGTCTATTTTAAGAAGTTTTGTTAGAAAATAAATCA
CL_00056	GGGCAGGTATCCGAACTGAACTTATTAGCAATATAATGGACGGGT
CL_00059	AAAAAATGATGAATTGAATTGAAAAGCTAGCAATATAATGGACGGGT
CL_00062	AATGTTAAGAATCAGATCACTCCTAAATAATAAGCG
CL_00063	TCAACAATGAATAGCTTTATCATAGGCAGCC
CL_00070	AGTTTCGGATACCTGCCCAATAGAGTCTAATAGACAAGGTGCTATGAGTGAA
CL_00071	CGCTTATTATTTAGGAGTGATCTGATTCTTAACATTTTTTTTTCTTGTTAGTGTGTAGCGAA
CL_00072	GGCTGCCTATGATAAAGCTATTCATTGTTGAGAAATCTCTGATTTTTTATAATATCTATATGGCT
CL_00073	AATAAAAAAAAAAATGATGAATTGAATTGAAAAGCTAAAAAAGATCCCACCGTAGCACACC
CL_000151	ACTCTATTGGGCAGGTATCCGAACTGAACTTATTAGGGGTAGCGACGGATTAATGGCATA
CL_000153	AAATCAAAAAAAAAAGAATAAAAAAAAAAATGATGAATTGAATTGAAAAGCTAGGGGTAGCGACGGATTAATGGCATA
CL_000154	GAAACACATTAATCCCAACAACAAGTATGCCATTAATCCGTCGCTACCCCTAGCTTTTCAATTCAATTCATCATT
CL_000155	GCACACAAGTTTGTGCTTTTCGTGCATGATATTAATAGCTTGGCAGCAACAGGACTAGGATGAGTAGCAGCA