Supporting Information Carbon Source Utilization

To reveal a more representative metabolic profile for *E. coli* IrrE-expressing strains BioLog assays were performed on *E. coli* IrrE-expressing strains and compared with similar analyses of *E. coli* control strain. The major differences between the strains are briefly described below.

We noted that the 44 substrates utilized by the control strain could be divided further into two broad categories. 41substrates were stromgly utilized (>100U). The remaining 3 substrates were weakly utilized (50 to 100U) by control strain. For the 44 utilized substrates, the IrrE-expressing *E. coli* strain had no significant effect on utilization of theβ-methyl-D-glucoside, acetic acid, α-hydroxybutyric acid, N-acetyl-D-glucosamine, L-arabinose, D-galactose, D-melibiose, D-psicose, D-trehalose, D-gluconic acid, D-glucuronic acid, α-ketoglutaric acid, inosine, uridine, thymidine and D-glucose-6-phosphate. The genetic basis accounting for significant differences between the strains are described. Included as substrates in GN2 MicroPlates are 19 amino acids, amino acid analogs and dipeptides. The IrrE-expressing strain and the control cell was negative (<50U) for utilization of D-alanine, L-glutamic acid, L-histidine, L-leucine, L-ornithine, L-phenylalanine, L-proline; the amino acid analogs L-alaninamide, hydroxy-L-proline; and the dipeptides glycyl-L-glutamic acid, L-pyroglutamic acid (data not shown). The utilization of the amino acids L-alanine, L-asparagine, L-aspartic acid, D-serine, L-serine, L-threonine; and the dipeptides L-alanyl-glycine, glycyl-L-aspartic acid were serverely decreased in the IrrE-expressing strain.

Supplementary Information Table S5. Comparison of the *E. coli* control strain and transformant strain expressing IrrE metabolism by BIOLOG GN2 plate

BioLog compound [a]	Control strain [b]	IrrE-expressing strain [b]	Fold change [c]
α-D-Lactose	176	10	-17.6
Pyruvic Acid Methyl Ester	193	15	-12.9
L-Rhamnose	230	25	-9.1
L-Serine	364	43	-8.5
D-Galactonic Acid Lactone	195	24	-8.1
Glycyl-L-Aspartic Acid	174	26	-6.7
D-Serine	195	34	-5.7
L-Threonine	156	28	-5.6
Bromosuccinic Acid	107	21	-5.1
L-Alanyl-Glycine	83	17	-4.9
Succinic Acid Mono-Methyl Ester	90	22	-4.1
D,L-Lactic Acid	147	37	-4
L-Alanine	130	33	-3.9
L-Aspartic Acid	160	45	-3.6
L-Asparagine	221	63	-3.5
D,L-α-Glycerol Phosphate	172	52	-3.2
Dextrin	173	76	-2.3
Succinic Acid	126	56	-2.3
Maltose	362	167	-2.2
L-Fucose	260	152	-1.7
Glycerol	192	113	-1.7
D-Galacturonic Acid	259	176	-1.5
D-Fructose	**227**	**302**	1.3

α -D-Glucose-1-Phosphate	**220**	**326**	1.5
D-Mannose	**232**	**410**	1.8
α -D-Glucose	**167**	**327**	2
Glucuronamide	**115**	**243**	2.1
D-Mannitol	**208**	**456**	2.2
D-Sorbitol	**16**	**97**	6.1

[a] Chemical compounds or growth/metabolic substrates tested in the BIOLOG GN2 plate, where there was a significant difference between the *E. coli* control strain and the IrrE-expressing strain.
[b] The average signal for each BIOLOG GN2 well was calculated as the mean of the signal from *E. coli* control strain or the IrrE-expressing strain in three independent PM array experiments. Wells where there was no much difference are not shown
[c] Statistically significant changes in arbitrary units are given as ratio of sample versus control (fold-change).