

Table S3. Metabolites impacted by CsrB overexpression.

Glycolysis Metabolite	Fold Change	Std. Dev.
Glyceraldehyde-3-phosphate	7.43	2.97
3Phosphoglycerate	4.65	0.70
Phosphoenolpyruvate	2.89	0.50
Pyruvate	4.37	1.08
Acetyl-CoA	7.62	0.67
G1P+G6P+F6P	3.32	0.61
TCA Metabolite	Fold Change	Std. Dev.
Oxaloacetate	6.36	1.93
Malate	11.22	3.59
Fumarate	5.27	3.91
Succinate	5.51	1.59
Oxoglutarate	0.80	0.10
cis-Aconitate	0.69	0.07
Citrate/Isocit	0.65	0.09
Glyoxylate	3.60	0.82
Amino Acid	Fold Change	Std. Dev.
Glycine	2.82	0.65
Alanine	7.89	0.94
Serine	3.18	0.95
Proline	6.15	3.11
Betaine	2.18	0.59
Valine	0.80	0.11
Threonine	28.30	5.83
Cysteine	0.48	0.05
Leucine	0.93	0.22
Isoleucine	0.70	0.14
Asparagine	44.42	19.29
Aspartate	8.41	2.52
Glutamine	15.25	9.15
Glutamate	13.58	8.13
Methionine	1.05	0.32
Phenylalanine*	2.51	0.95
Tyrosine	1.88	0.23
Tryptophan	4.87	2.88
Lysine	3.57	1.30
Histidine	3.80	2.25
Arginine	0.66	0.26

* An increase in phenylalanine (despite the complete deletion of pheA/L in BLR-DAJ) is attributed to accumulated prephenate which can be non-enzymatically converted to phenylpyruvate and transaminated to phenylalanine^a.

^a Olson, M. M., et al., 2007. Production of tyrosine from sucrose or glucose achieved by rapid genetic changes to phenylalanine-producing *Escherichia coli* strains. Applied microbiology and biotechnology. 74, 1031-40.