Table S1. Genes of *E. coli* encoding metabolic-related functions regulated by the ArcBA and CreBC two-component systems. Data were compiled from Lynch and Lin [1] and Salmon et al. [2], and the specific references cited below.

ArcBA system			
Gene(s)	**Function(s)**	**Regulation**	**Ref.**
aceBA	Isocitrate lyase (AceA); catalyzes the cleavage of isocitrate or the condensation of glyoxylate and succinate. Malate synthase A (AceB); converts acetyl-CoA and glyoxylate into malate and CoA	–	[3]
acnA, *acnB*	Aconitase; catalyzes the reversible isomerization of citrate and iso-citrate *via cis*-aconitate in the TCA cycle	–	[4]
cydAB	Cytochrome *d* oxidase; catalyzes the oxidation of ubiquinol-8 during oxic respiration as O_2 becomes limiting	+	[5,6]
cyoABCDE	Cytochrome *o* oxidase; catalyzes the oxidation of ubiquinol-8 during oxic respiration under O_2-rich growth conditions	–	[5]
fumAC	Fumarase; interconverts fumarate and L-malate in the TCA cycle, and participates in the reductive pathway from oxaloacetate to succinate during anoxic growth	+	[7]
glcDEF	Glycolate oxidase; converts glycolate into glyoxylate in the glyoxylate shunt	–	[6]
gltA	Citrate synthase; catalyzes the condensation of acetyl-CoA and oxaloacetate to form citrate	–	[8]
icd	Isocitrate dehydrogenase; catalyzes the conversion of isocitrate to α-ketoglutarate, thereby forming NADH and CO_2	–	[6]
lldPRD	L-Lactate permease, regulator, and dehydrogenase, which interconvert pyruvate and L-lactate	–	[6]
lpdA	Lipoamide dehydrogenase; a component of the pyruvate dehydro-genase complex, α-ketoglutarate dehydrogenase, and the glycine-cleavage multi-enzyme systems	–	[9]
mdh	Malate dehydrogenase; catalyzes the reversible oxidation of malate to oxaloacetate, thereby forming NADH	–	[6]
ndh	Respiratory NADH dehydrogenase II; a membrane-bound (but non-H^+–translocating) monomeric flavoprotein	+	[6,10]
pflB	Pyruvate-formate lyase; catabolizes pyruvate under anoxic conditions	+	[11,12]
ptsG	D-Glucose–specific permease of the sugar phosphotransferase system	–	[13]
sdhCDAB	Succinate dehydrogenase; oxidizes succinate to fumarate and transfers electrons to ubiquinone in the oxic respiratory chain	–	[6]
sucABCD	Succinyl-CoA synthase; catalyzes the interconversion of succinyl-CoA and succinate by means of GTP hydrolysis, both in the TCA cycle and the reductive branch	–	[14]
CreBC system			
Gene	**Function(s)**	**Regulation**	**Ref.**
pta-ackA	Phosphate acetyltransferase (Pta) catalyzes the conversion of acetyl-CoA into acetyl-*P*, whereas acetate kinase (AckA) converts acetyl-*P* into acetate, thereby forming ATP	+	[15]
talA	Transaldolase A; converts D-glyceraldehyde-3-*P* and D-sedoheptulose-7-*P* into D-fructose-6-*P* and D-erythrose-4-*P* in the non-oxidative branch of the PP pathway	+	[15]

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