Supplemental information to: **The CreC regulator of *Escherichia coli*, a new target for metabolic manipulations**

Manuel S. Godoy, Pablo I. Nikel, José G. Cabrera Gomez, and M. Julia Pettinari

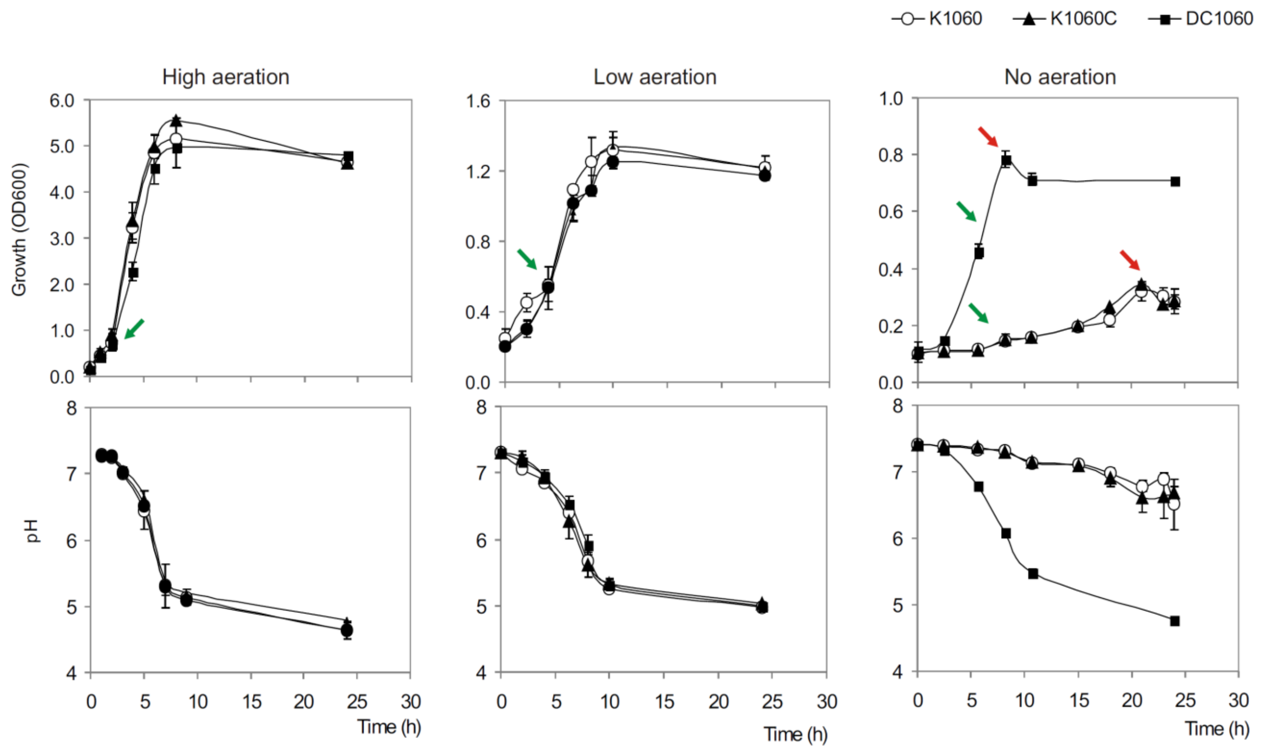

FIG S1: Growth and pH curves of cultures (M9 minimal medium containing 30 g liter^{-1} glucose) grown in the three different aeration conditions studied in this work (high aeration, low aeration, and no aeration). The arrows indicate the sampling times corresponding to exponential phase (green arrows) or early stationary phase (red arrows) used to measure the specific AckA and LdhA activities.

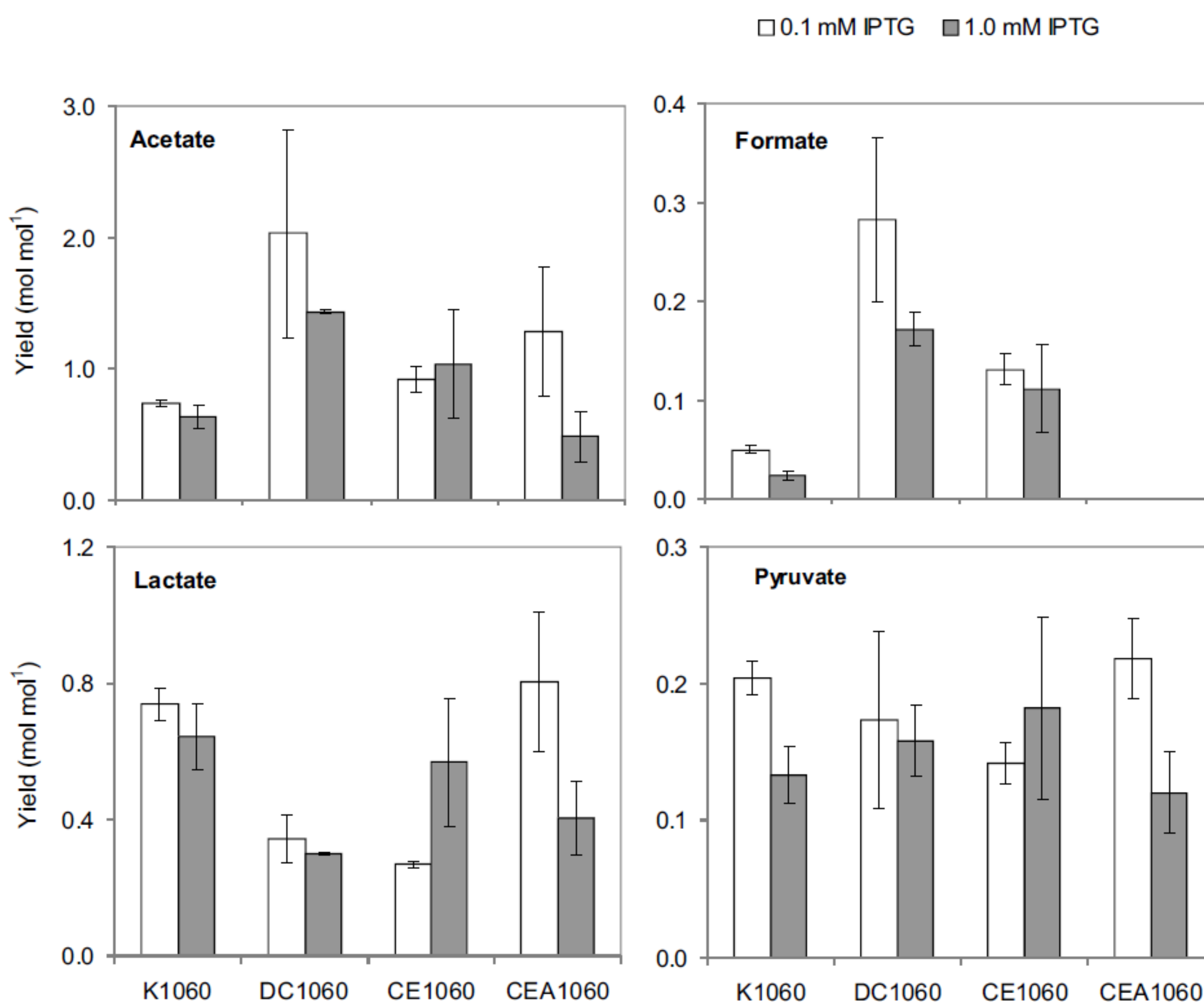

FIG S2: Profile of organic acids formation in the *E. coli* strains under study. Cells were grown in M9 minimal medium containing 30 g liter^{-1} glucose and 100 mM $NaHCO_3$ under low aeration for 48 h. The *E. coli* strains tested were K1060 (wild-type strain), DC1060 (Δ*creC*), CE1060 (Δ*creC* Δ*adhE*), and CEA1060 (Δ*creC* Δ*adhE* Δ*ackA*). All bacteria were transformed with plasmids pSBF2 (carrying *FDH1*^{Cb}, a NADH-forming formate dehydrogenase from *Candida boidinii*) and pEcPpc (carrying *ppc*^{Ec}, the endogenous phosphoenolpyruvate carboxylase from *E. coli*). The expression of the genes in these plasmids was induced by addition of isopropyl-β-D-1-thiogalactopyranoside (IPTG) at two concentrations (0.1 mM and 1.0 mM). Metabolites were assayed in culture supernatants and the results are reported as yield of the corresponding acids on glucose (mol mol^{-1}). Results represent the average ± standard deviation from duplicated measurements from at least two independent cultures.