All Three Endogenous Quinone Species of *Escherichia coli* Are Involved in Controlling the Activity of the Aerobic/Anaerobic Response Regulator ArcA

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DOI
10.3389/fmicb.2016.01339

Publication date
2016

Document Version
Other version

Published in
Frontiers in Microbiology

Citation for published version (APA):
Supplementary Figure 1. **Plasmid maps of new constructs used in this study.** Plasmids were based on pDOC-K (Lee et al., 2009). A: pDOC-S-ubiCA. The *ubiCA* sites are flanked by I-SceI restriction sites, sizes are approximations. B: pDOC-K-yoeG-ParaMenH. The *yoeG* sites are flanked by I-SceI restriction sites, sizes are approximations.
Supplementary Figure 2A-D. **Quinone pool redox state of *E. coli* MG1655.** Redox state (open figures) and concentration (closed figures) of all quinones in *E. coli* MG1655. A: All quinones together; B: UQ; C: DMK; D: MK. The bar above indicates N2 (gray) or air (white) sparging. Data based on the average of three biologically independent replicates. Error bars indicate standard deviation.
Supplementary Figure 2E-G. Quinone pool redox state of *E. coli* UQ- (i.e. AV34), DMK- and MK-only mutant strains. Redox state (open figures) and concentration (closed figures) of all quinones in *E. coli* MG1655. E: AV34 (UQ-only); F: DMK-only; G: MK-only. The bar above indicates N2 (gray) or air (white) sparging. Data based on the average of three biologically independent replicates. Error bars indicate standard deviation.
Supplementary Figure 3: Exo-metabolite analysis of various E. coli strains. A: Metabolites of E. coli MG1655; B: E. coli AV34; C: E. coli DMK-only; D: E. coli MK-only. The bar above each panel indicates sparging with N₂ (gray) or air (white). Data represent the average of three biologically independent replicates, error bars indicate the standard deviation.