

Supplementary Table 3: List of accession numbers of RNA seq data used for calculating RPKM

GSE63858	Ribosome profiling of <i>E. coli</i> K-12 MG1655 MOPS rich media with 0.2% glucose
GSE72899	Clarifying the translational pausing landscape in bacteria by ribosome profiling (1)
GSE72899	COLOMBOS v2.0: an ever expanding collection of bacterial expression compendia (2)
E-MTAB-2802	Comprehensive Mapping of the <i>Escherichia coli</i> Flagellar Regulatory Network (3)
GSE54901	Deciphering Fur transcriptional regulatory network highlights its complex role (4)
GSE66482	Decoding genome-wide GadEWX-transcriptional regulatory networks reveals multifaceted cellular responses to acid stress in <i>Escherichia coli</i> (5)
GSE46740	Genome-scale reconstruction of the sigma factor network in <i>Escherichia coli</i> : topology and functional states (6)
E-MTAB-2903	Identification of bacterial sRNA regulatory targets using ribosome profiling (7)
GSE55199	Global Transcriptional Start Site Mapping Using Differential RNA Sequencing Reveals Novel Antisense RNAs in <i>Escherichia coli</i> (8)
GSE41940	Rho and NusG suppress pervasive antisense transcription in <i>Escherichia coli</i> (9)
E-MTAB-4240	SuhB Associates with Nus Factors To Facilitate 30S Ribosome Biogenesis in

	<i>Escherichia coli</i> (10)
GSE69856	The ribonuclease polynucleotide phosphorylase can interact with small regulatory RNAs in both protective and degradative modes (11)
GSE82343	Modulation of global transcriptional regulatory networks as a strategy for increasing kanamycin resistance of EF-G mutants
GSE40313	Genomic analysis reveals epistatic silencing of "expensive" genes in <i>Escherichia coli</i> K-12 (12)
GSE104504	Transcriptome data for wild type , Δfis , Δcya mutants in Early Exponential, Mid Exponential growth phase generated in-house (unpublished)

BIBLIOGRAPHY

1. **Mohammad F, Woolstenhulme CJ, Green R, Buskirk AR.** 2016. *Cell Rep* **14**:686–694.
2. **Meysman P, Sonogo P, Bianco L, Fu Q, Ledezma-Tejeida D, Gama-Castro S, Liebens V, Michiels J, Laukens K, Marchal K, Collado-Vides J, Engelen K.** 2014. *Nucleic Acids Res* **42**:D649–D653.
3. **Fitzgerald DM, Bonocora RP, Wade JT.** 2014. *PLoS Genet* **10**:e1004649.
4. **Seo SW, Kim D, Latif H, O'Brien EJ, Szubin R, Palsson BO.** 2014. *Nat Commun* **5**:4910.
5. **Seo SW, Kim D, O'Brien EJ, Szubin R, Palsson BO.** 2015. *Nat Commun* **6**:7970.
6. **Cho B-K, Kim D, Knight EM, Zengler K, Palsson BO.** 2014. *BMC Biol* **12**:4.
7. **Wang J, Rennie W, Liu C, Carmack CS, Prévost K, Caron M-P, Massé E, Ding Y, Wade JT.** 2015. *Nucleic Acids Res* gkv1158.
8. **Thomason MK, Bischler T, Eisenbart SK, Förstner KU, Zhang A, Herbig A, Nieselt K, Sharma CM, Storz G.** 2015. *J Bacteriol* **197**:18–28.
9. **Peters JM, Mooney RA, Grass JA, Jessen ED, Tran F, Landick R.** 2012. *Genes Dev* **26**:2621–2633.
10. **Singh N, Bubunenko M, Smith C, Abbott DM, Stringer AM, Shi R, Court DL, Wade JT.** 2016. *mBio* **7**:e00114-16.
11. **Bandyra KJ, Sinha D, Syrjanen J, Luisi BF, De Lay NR.** 2016. *RNA* **22**:360–372.
12. **Srinivasan R, Chandraprakash D, Krishnamurthi R, Singh P, Scolari VF,**

Krishna S, Seshasayee ASN. 2013. Mol Biosyst **9**:2021.