Supplementary Information for
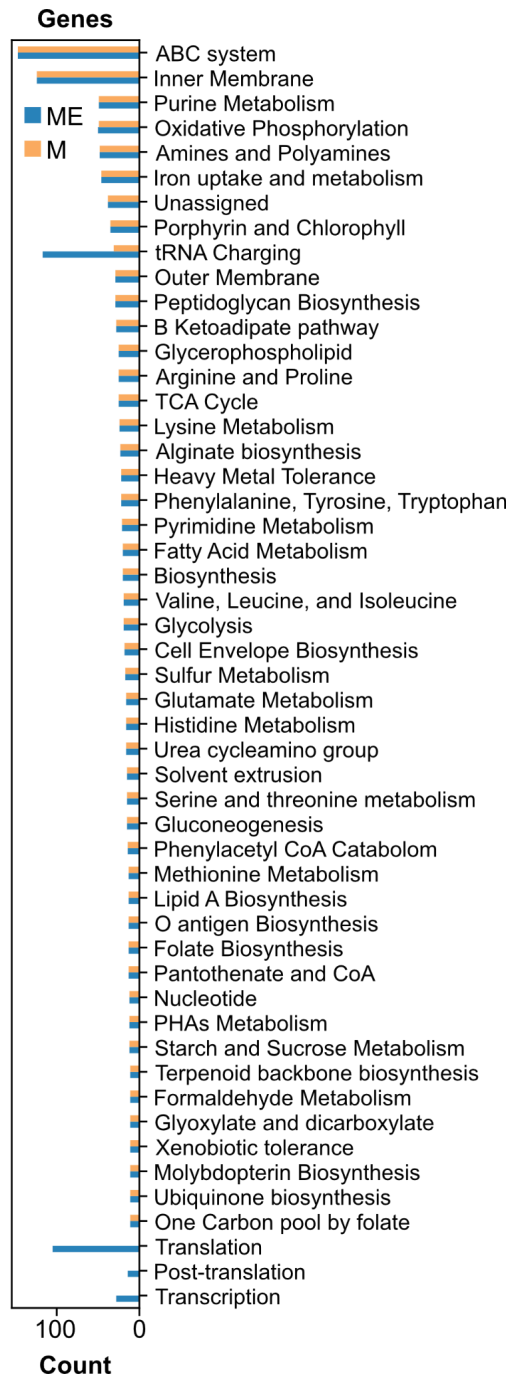
Model of metabolism and gene expression predicts proteome allocation in *Pseudomonas putida*

Juan D. Tibocha-Bonilla *et al.*
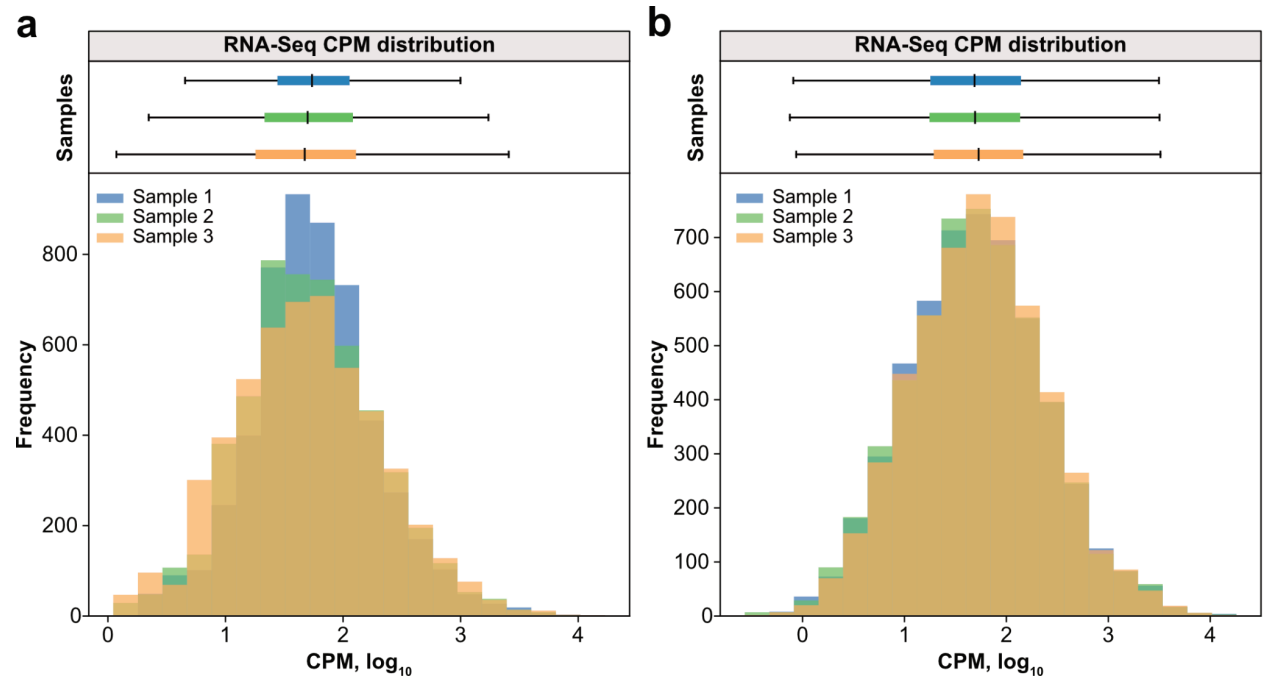
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This PDF file includes:

 Supplementary Figures 1 to 2

Genes

- ABC system
- Inner Membrane
- Purine Metabolism
- Oxidative Phosphorylation
- Amines and Polyamines
- Iron uptake and metabolism
- Unassigned
- Porphyrin and Chlorophyll
- tRNA Charging
- Outer Membrane
- Peptidoglycan Biosynthesis
- B Ketoadipate pathway
- Glycerophospholipid
- Arginine and Proline
- TCA Cycle
- Lysine Metabolism
- Alginate biosynthesis
- Heavy Metal Tolerance
- Phenylalanine, Tyrosine, Tryptophan
- Pyrimidine Metabolism
- Fatty Acid Metabolism
- Biosynthesis
- Valine, Leucine, and Isoleucine
- Glycolysis
- Cell Envelope Biosynthesis
- Sulfur Metabolism
- Glutamate Metabolism
- Histidine Metabolism
- Urea cycleamino group
- Solvent extrusion
- Serine and threonine metabolism
- Gluconeogenesis
- Phenylacetyl CoA Catabolom
- Methionine Metabolism
- Lipid A Biosynthesis
- O antigen Biosynthesis
- Folate Biosynthesis
- Pantothenate and CoA
- Nucleotide
- PHAs Metabolism
- Starch and Sucrose Metabolism
- Terpenoid backbone biosynthesis
- Formaldehyde Metabolism
- Glyoxylate and dicarboxylate
- Xenobiotic tolerance
- Molybdopterin Biosynthesis
- Ubiquinone biosynthesis
- One Carbon pool by folate
- Translation
- Post-translation
- Transcription

■ ME
■ M

100   0

Count

**Supplementary Figure 1. Breakdown of genes in their respective annotated pathways in
*i*Ppu1676-ME and the template M-model, *i*JN1462.**

Supplementary Figure 2. Multi-omic data (CPM) of *P. putida* KT2440 growth in glucose. a, Distribution of RNA-Seq raw read counts in the three biological replicate samples. **b,** Distribution of Ribo-Seq raw read counts in the three samples.