

Supplementary Figures S1 and S2

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Subpopulation-proteomics reveal growth rate, but not cell cycling, as a major impact on protein composition in *Pseudomonas putida* KT2440

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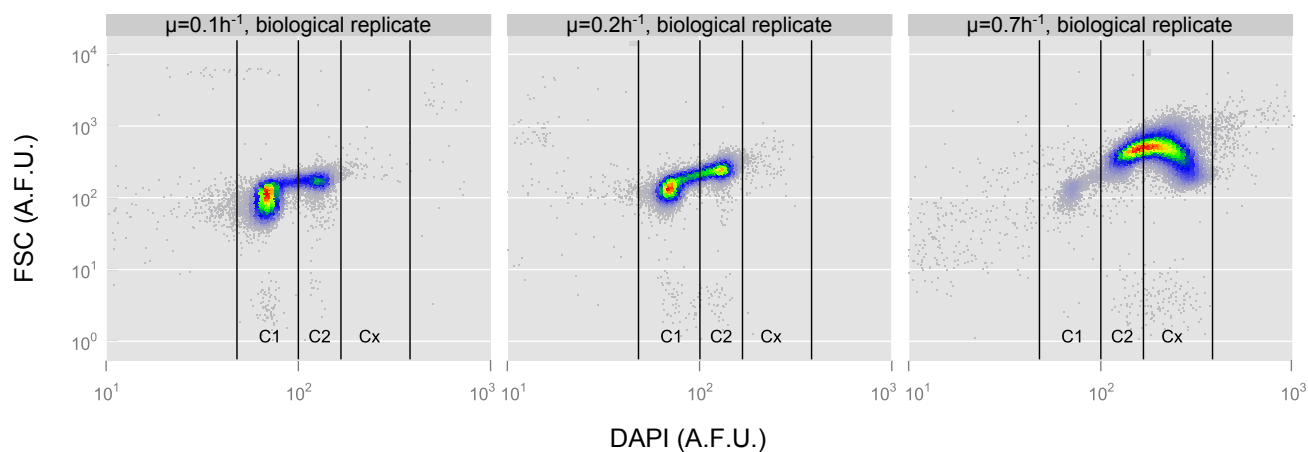
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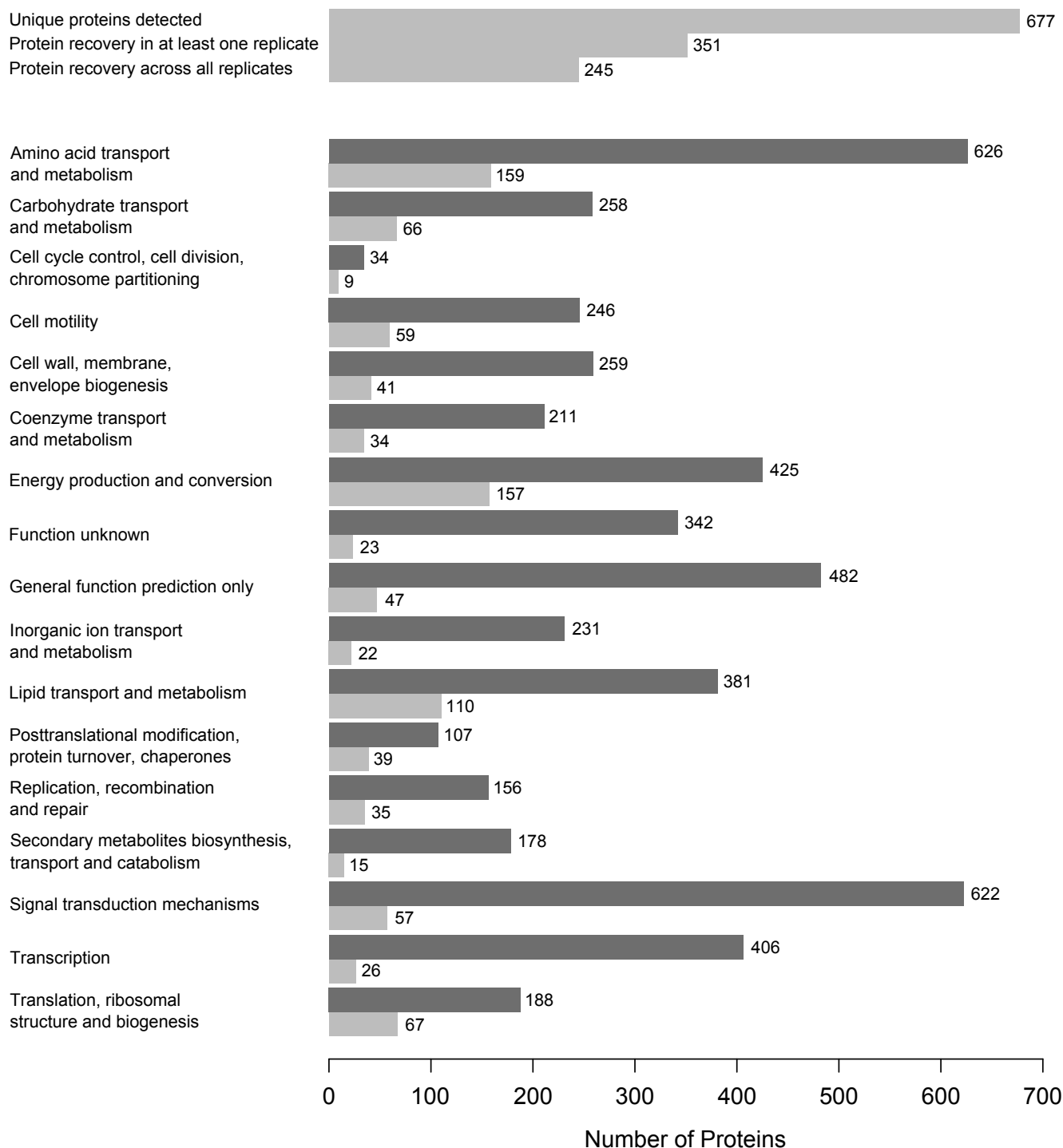
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Supplementary Fig. S1 Replicate dataset of dot plots of DNA content (DAPI, in arbitrary fluorescence units (A.F.U.)) versus forward scatter (FSC, in A.F.U.) at different growth rates 0.1 h^{-1} , 0.2 h^{-1} and 0.7 h^{-1} . Cells of *P. putida* KT2440 grown at steady state conditions in chemostats were stained with DAPI and analyzed by flow cytometry. The DNA content and the forward scatter increased with increasing growth rate. The indicated gates (C1, C2, Cx) were used for sorting 5×10^6 cells per subpopulation for further mass spectrometric analysis.



Supplementary Fig. S2 Overview of the total protein detection and protein annotation. Overall, 677 unique proteins were identified, 351 proteins were detected in at least one replicate of all subpopulations and 245 proteins were found across all replicates. Functional annotation was carried out using the COG database (Tatusov et al. 1997). 707 different functions of 647 unique proteins could be annotated into 17 categories. The total number of proteins of *Pseudomonas putida* KT2440 annotated in one specific category (dark grey bars) is compared to the number of proteins recovered in this study (light grey bars).