

Supplemental Materials:

Proteogenomic Analysis of *Burkholderia* Species Strains 25 and 46 Isolated from Uraniferous Soils Reveals Multiple Mechanisms to Cope with Uranium Stress

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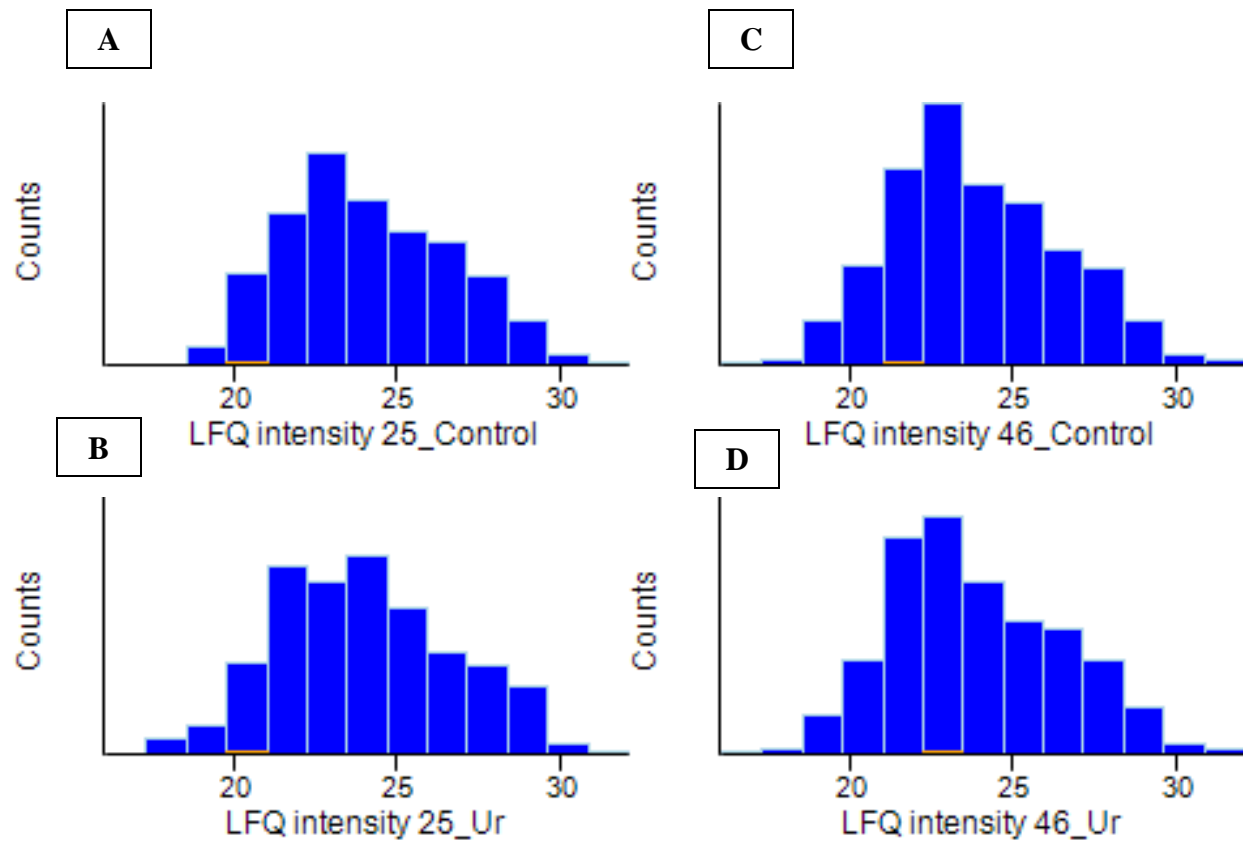
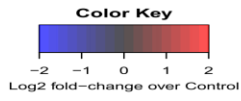


Figure S1. Shown are the label free quantification (LFQ) proteomics data analysed using Perseus software for A and B, strain 25 in the presence and absence of uranium and; C, D, strain 46 in the presence and absence of uranium, respectively. Data were $\log_2(x)$ transformed and histograms were plotted.

A



B

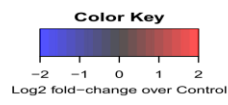


Figure S2. Heat maps from SRS-25 (left) and SRS-46 (right) show the of relative abundance of all the identified proteins between control and uranium amended microcosms. The proteins were sorted on the basis of their fold change value as compared to their control. Gradient of fold change is shown by color code where blue represents the lower most fold change value and red represents the highest fold change value.

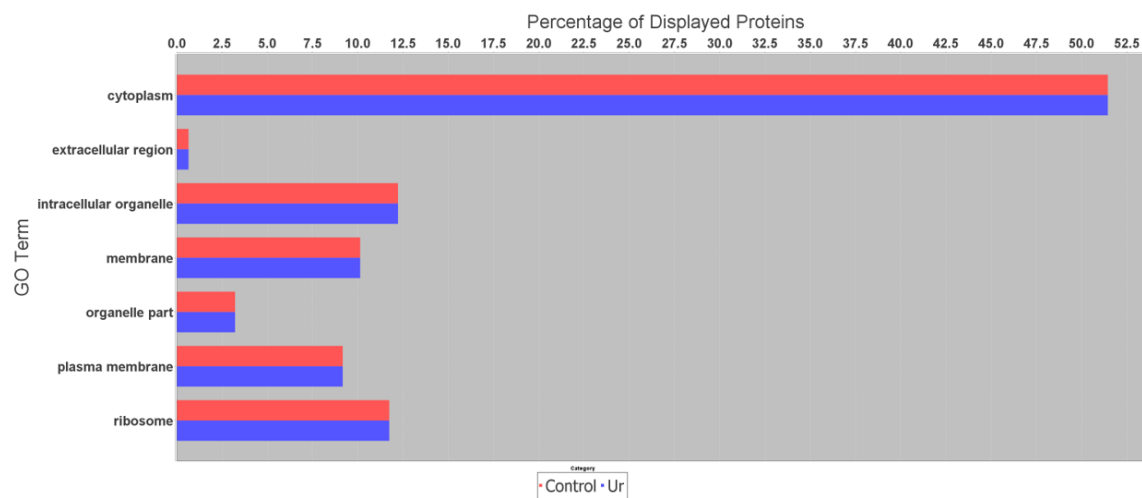
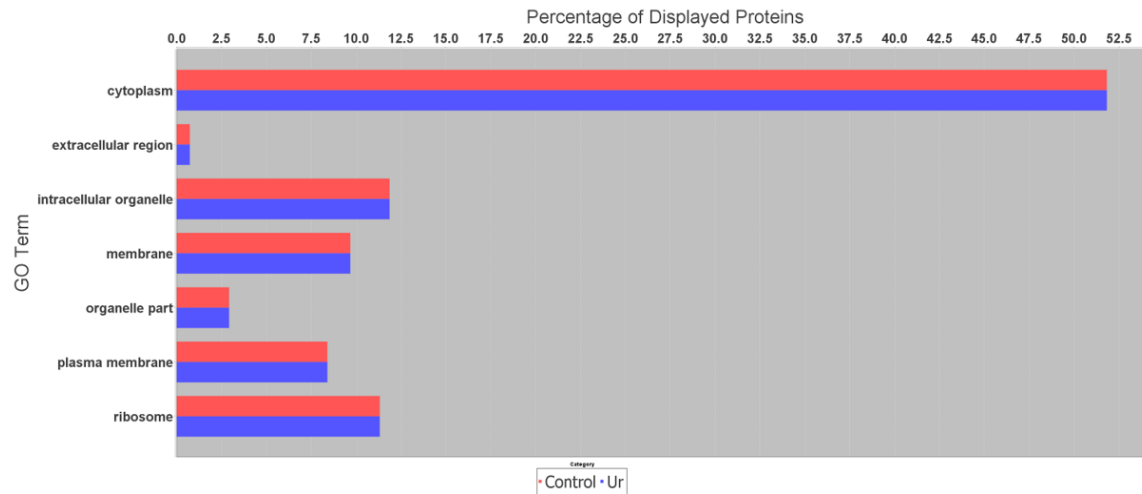


Figure S3. Plotted are proteins obtained from strains SRS-25 (top) and SRS-46 (bottom) with or without uranium exposure, analyzed by Scaffold software using gene ontology (GO) analysis tool.