

**Table S2.** Cells lacking bS21-2 exhibit genome-wide changes in protein abundance. Data-independent acquisition (DIA) mass spectrometry analysis of cellular lysates was used to quantify genome-wide protein abundance in wild-type cells (WT), cells lacking bS21-1 (delt\_rpsU1), cells lacking bS21-2 (delt\_rpsU2), and cells lacking bS21-3 (delt\_rpsU3). Each deletion strain was compared to wild-type, but significant changes (>1.5-fold change, adjusted p-value <0.05, excluding bS21) were only observed in the cells lacking bS21-2. Cells are highlighted if the fold-change (columns R, U, and X) is greater than 1.5 (log2FC>0.58 or <-0.58). Green indicates less abundant in deletion strains compared to wild-type, and red indicates more abundant. Adjusted p-values are highlighted red if <0.05 (columns T, W, and Z).