

Table S3. Cells lacking bS21-2 have significant changes in transcript abundance. RNA-Seq was used to compare genome-wide transcript abundance from wild-type cells with an empty vector (LVS pF), cells lacking bS21-2 and containing an empty vector (LVS Δ rpsU2 pF), and bS21-2 mutant cells with bS21-2-V ectopically expressed (LVS Δ rpsU2 pF-rpsU2-V). Transcripts with significant differences in cells lacking bS21-2 compared to wild-type (>2 -fold change, adjusted p-value <0.05) are highlighted in yellow (columns E, G, I). All changes were complemented by ectopic expression of bS21-2-V (column G). Base mean (column D) reflects a measure of transcript abundance across all strains. NA = not available, generally due to low read abundance.