

Description of Additional Supplementary Files:

Supplementary Data 1: CRISPRi-seq data comprising sample metadata, raw and normalized sgRNA counts, and differential sgRNA enrichment results within and between growth conditions. Differential enrichment was tested using the R package DESeq2, fitting a negative binomial Generalized Linear Model and testing for significance with a two-tailed Wald test against an absolute log₂ fold change threshold of 1. P-values were adjusted for multiple comparisons using the procedure of Benjamini and Hochberg.

Supplementary Data 2: RNA-seq data for wild-type and Δspv_0647 mutant strains, comprising raw and normalized read counts, and differential expression results as tested by R package DESeq2, fitting a negative binomial Generalized Linear Model and testing for significance with a two-tailed Wald test against an absolute log₂ fold change threshold of 1. P-values were adjusted for multiple comparisons using the procedure of Benjamini and Hochberg.

Supplementary Data 3: FoldSeek results generated through the online submission portal (<https://search.foldseek.com>) for UniProt accession number A0A0H2ZQ31 (SPV_0647), listing matches to the PDB100 data base.

Supplementary Data 4: GC-FAME results listing relative fatty acid levels per sample.

Supplementary Data 5: Proteo-transcriptomic data comprising raw and normalized quantifications for detected transcripts and proteins, and differential expression results. For transcripts, these were determined using the R package DESeq2, fitting a negative binomial Generalized Linear Model and testing for significance with a two-tailed Wald test against an absolute log₂ fold change threshold of 1. For proteins, they were generated using R package DEP with label-free quantifications (LFQ values) as input, fitting a linear model and moderating t-statistic estimates by an empirical Bayes approach through the R package limma. P-values were adjusted for multiple comparisons by controlling the false discovery rate.