

Supplementary Figures

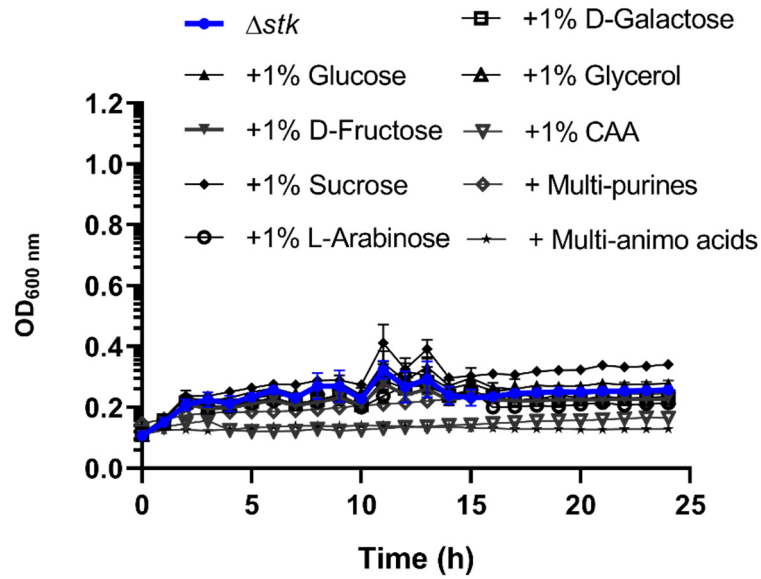


Figure S1. Growth analysis of Δstk strains. (A) The growth of Δstk strain in CDM or CDM supplemented with each indicated nutrient. Growth was monitored with an automatic plate reader with shaking at 37°C. Data are presented as means \pm SD of triplicate.

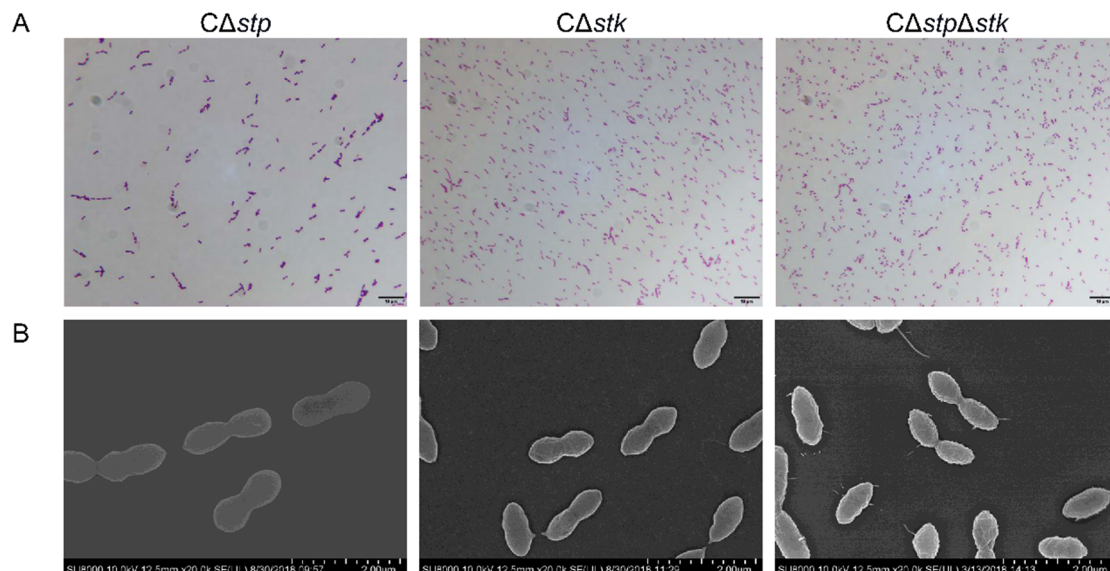


Figure S2. Morphological analysis of $C\Delta stp$, $C\Delta stk$, and $C\Delta stp\Delta stk$ strains. Gram staining (A) and scanning electron microscopy (SEM) (B) analysis of $C\Delta stp$, $C\Delta stk$, and $C\Delta stp\Delta stk$ strains.

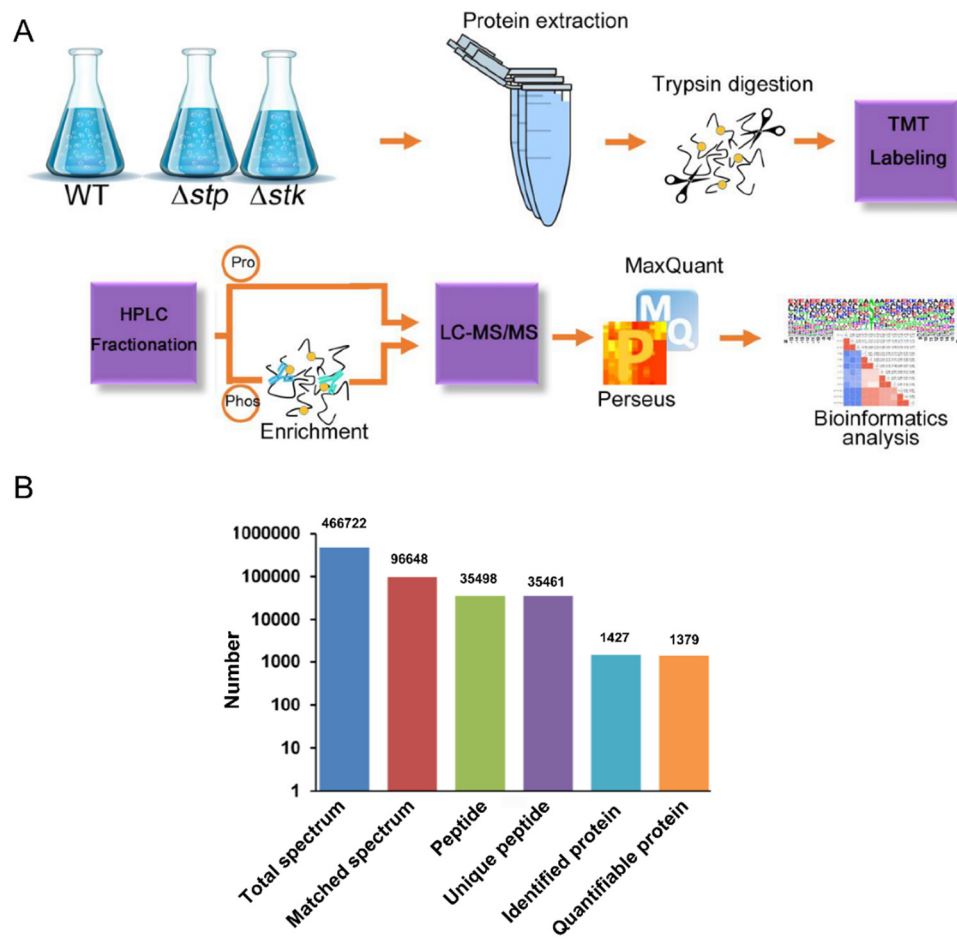


Figure S3. Comparative proteomic analysis between the WT and Δstp or Δstk strains. (A) The systematic workflow of the quantitative profiling of the global mass spectrum. (B) The basic statistics of mass spectrum data.

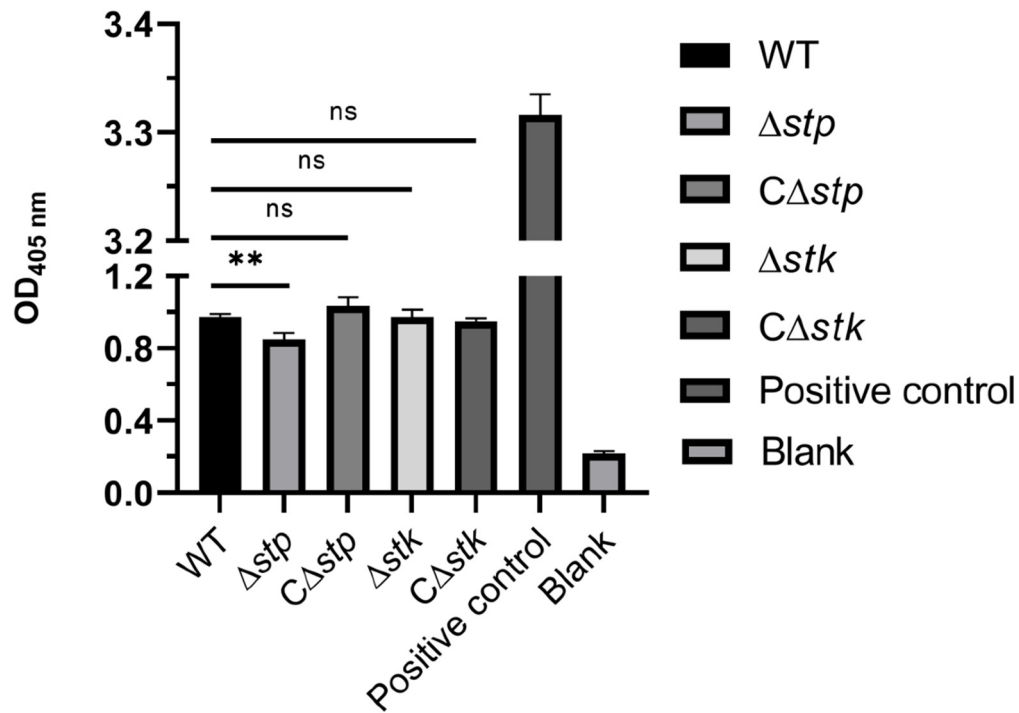


Figure S4. Phosphatase activity assay. Cells at the mid-log phase of each indicated strain were collected, washed three times with buffer1 [20 mM Tris-HCl (pH 8.0) and 200 mM NaCl₂], resuspended in lyse buffer [50 mM Tris-HCl (pH 8.0), 150 mM NaCl₂, 100 U/mL mutanolysin (Sigma), and 1 mM PMSF], and lysed by sonication. The amount of total protein loaded was normalized using a Micro BCA protein assay kit (Cwbiotech, China). Samples were mixed with buffer2 [50 mM Tris-HCl (pH 8.0), 2 mM MnCl₂, and 20 mM p-nitrophenyl phosphate (p-NPP)], and incubated at 37°C for 10 min. The absorbance at 405 nm was then measured. Purified recombinant STP protein was used as the positive control, the reaction buffer2 used as the blank. Data are presented as means \pm SD of triplicate. Statistical significance was determined by two-tailed, unpaired Student's *t*-tests (ns, *p* value > 0.05; *, *p* value < 0.05).