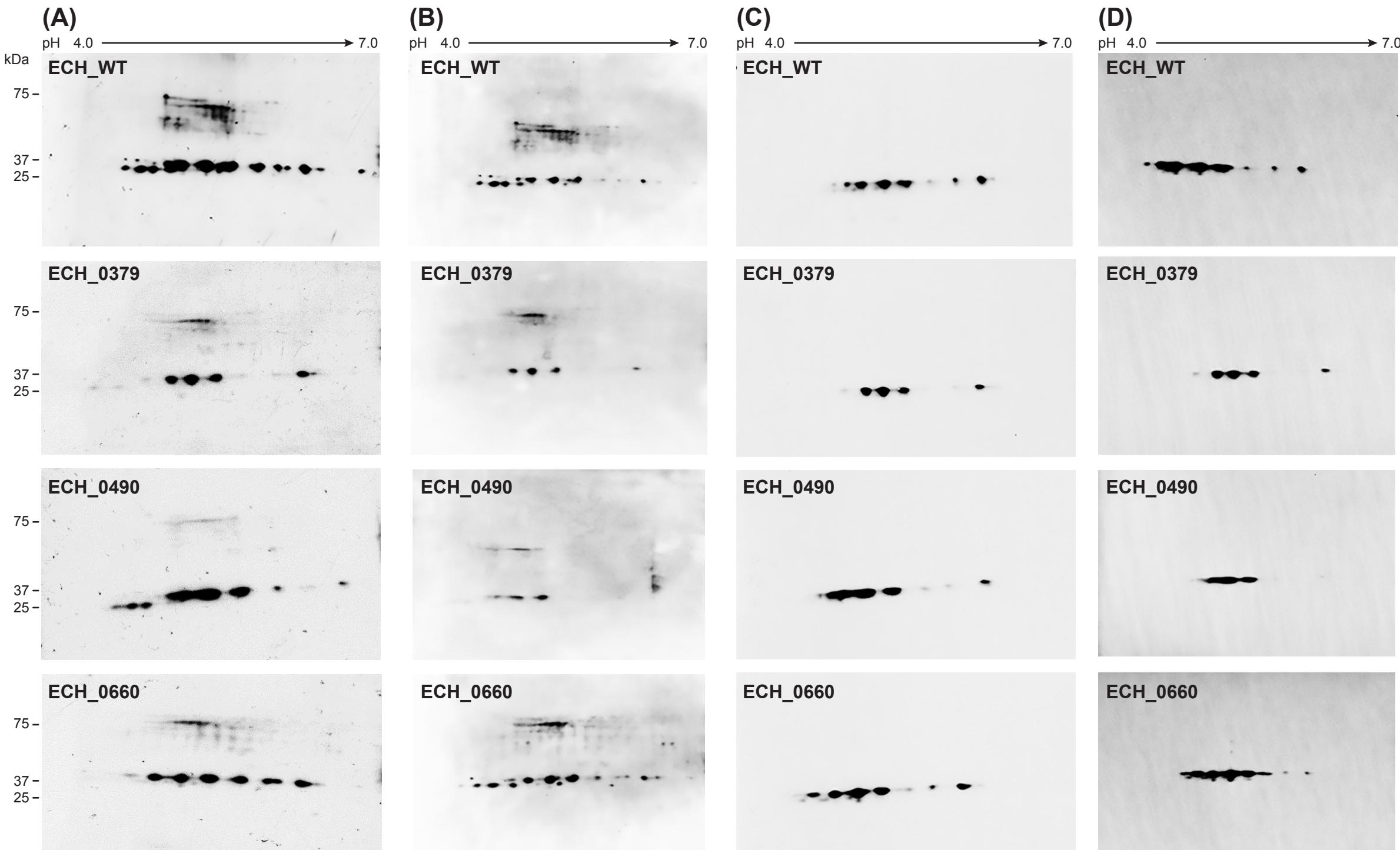
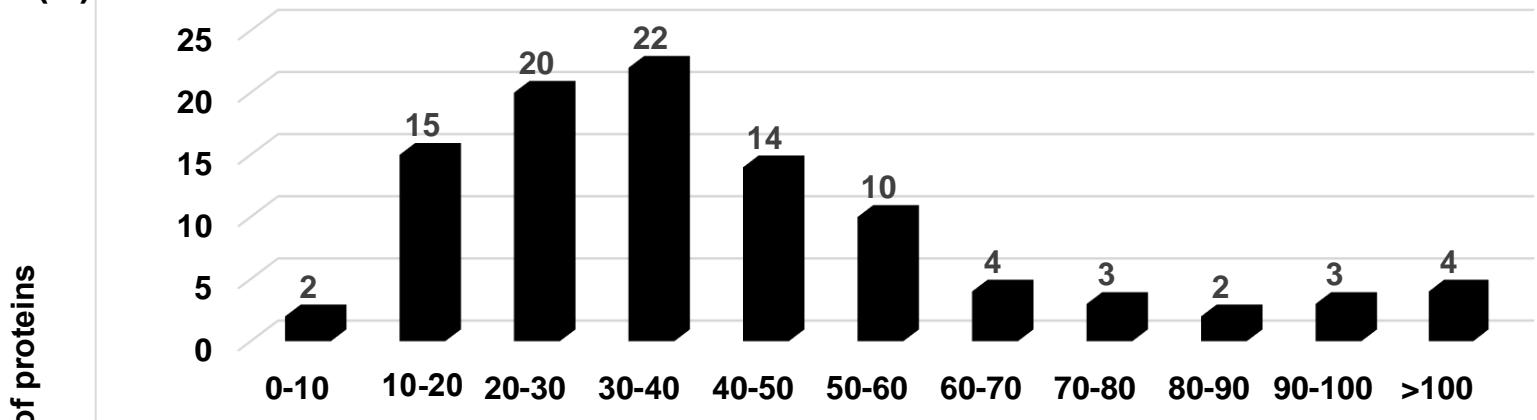


**Supplementary Figure 1.** Workflow of sample preparation, LC-MS/MS analysis and proteins quantitation of *E. chaffeensis* wildtype and mutants organisms.



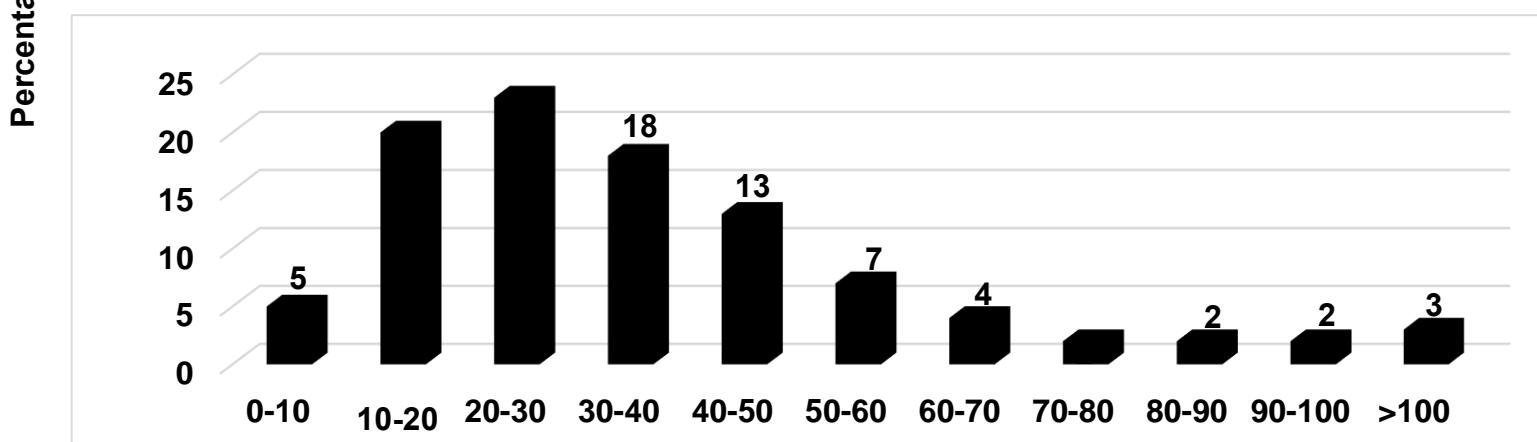
**Supplementary Figure 2.** Replicates of *E. chaffeensis* wildtype and mutants' proteomes immunolabelled with polyclonal sera (Panels A and B) and with p28 MAb (Panels C and D).

(A)



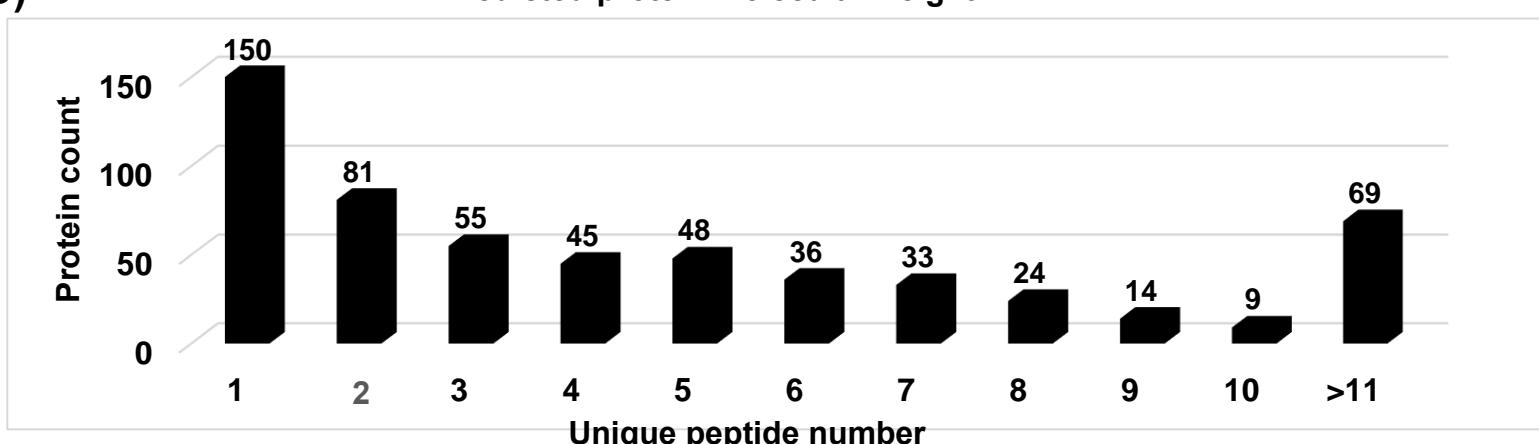
(B)

Observed experimental protein molecular weight

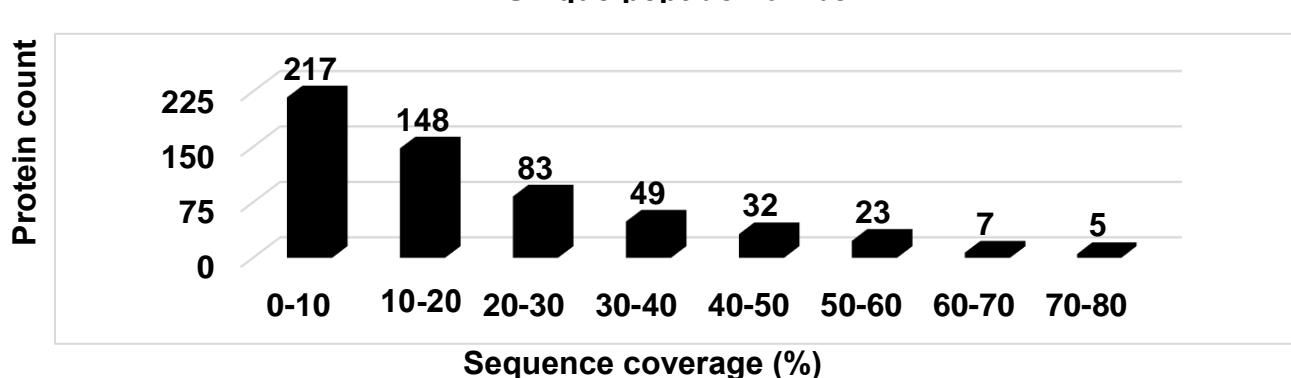


(C)

Predicted protein molecular weight



(D)



**Supplementary Figure 3.** Distribution of experimental (A) and predicted proteins molecular weights (B) obtained from proteomics data and genome sequence (NC\_007799.1). Unique peptides of the detected proteins (C), and protein sequence coverage (D). The number of proteins in each of the categories is presented above each bar.