

Electronic Supplementary Material

African Swine Fever Virus Protein E199L Promotes Cell Autophagy through the Interaction of PYCR2

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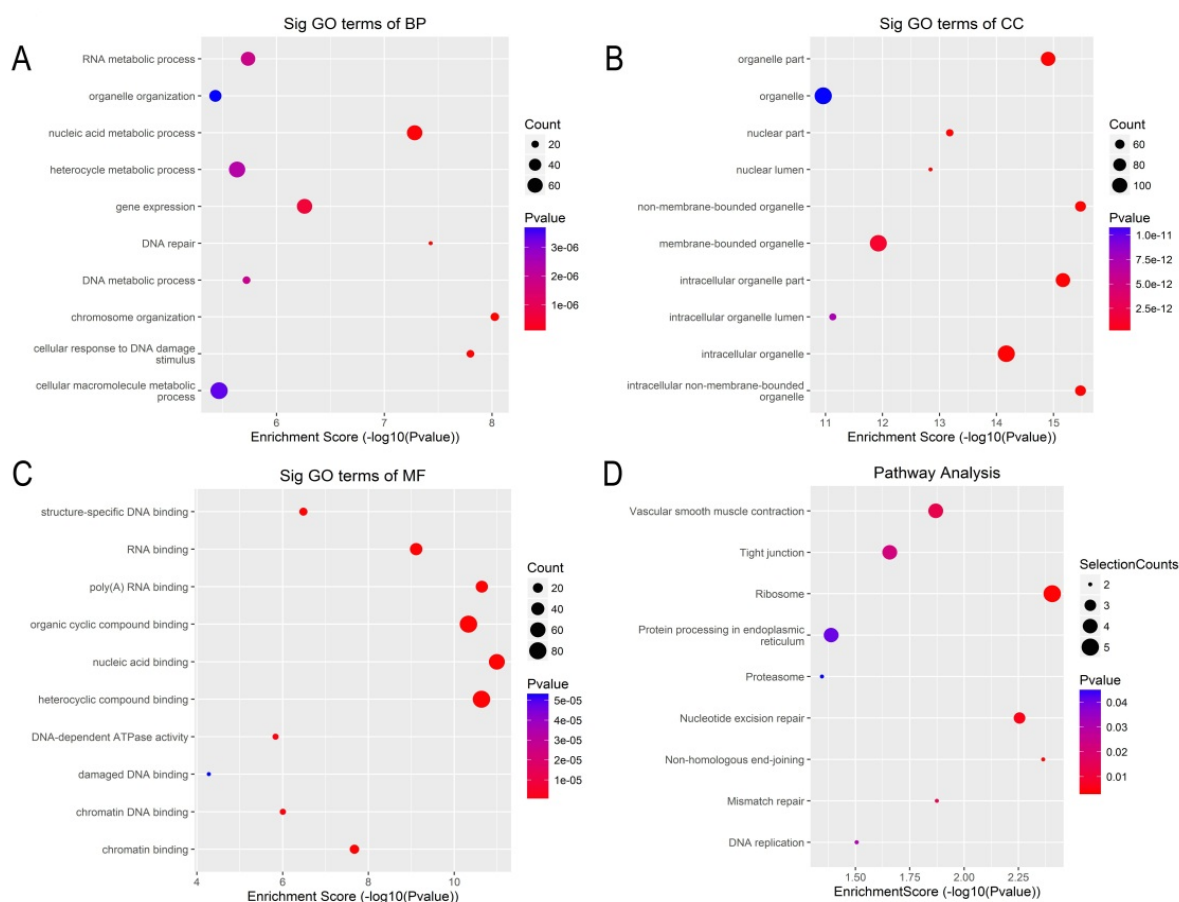


Fig. S1 Gene ontology (GO) and KEGG pathway analysis of E199L-interacting proteins. **A, B, C** The ontology covers three domains: Biological Process, Cellular Component and Molecular Function. Fisher's exact test is used to find if there is more overlap between the gene list and the GO annotation list. The P -value denotes the significance of GO terms enrichment in the genes. The lower the P -value, the more significant the GO term (P -value ≤ 0.05 is recommended). The dot plot shows the enrichment score values of the top ten most significant enrichment terms. **D** Pathway analysis is a functional analysis mapping gene to KEGG pathways. The Fisher P -value denotes the significance of the pathway correlated to the conditions. The smaller, the more significant (The recommend P -value cut-off is 0.05.) The dot plot shows the top ten Enrichment score ($-\log_{10}(P\text{-value})$) value of the significant enrichment pathway.

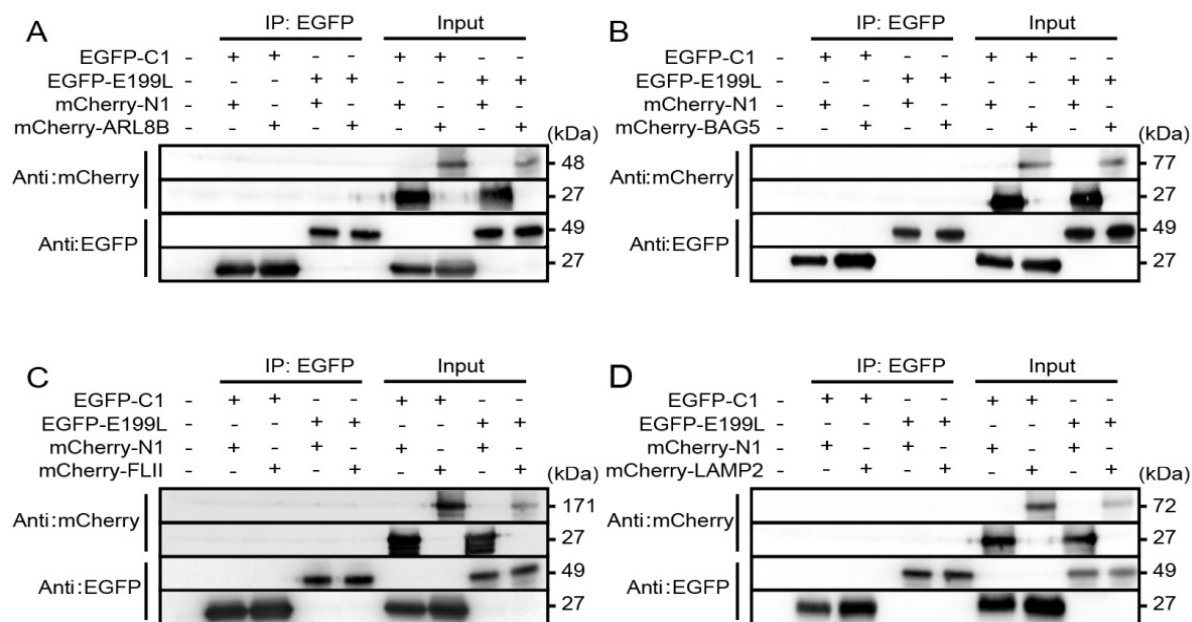


Fig. S2 ASFV E199L protein cannot interact with 4 host proteins. Vero cells were co-transfected with EGFP-C1, EGFP-E199L, mCherry-N1 and (A) mCherry-ARL8B/ (B) mCherry-BAG5/ (C) mCherry-FLII/ (D) mCherry-LAMP2 plasmid in pairs and immunoprecipitation was performed with anti-EGFP antibody. Immunoblotting analysis was performed with anti-EGFP antibody and anti-mCherry antibody. Blots are representative of the 3 independent experiments.