# Additional files

Additional file 1: **Fig. S1** Identification of different protein intermediates by LC-MSMS mass spectrometry. Proteins were broken into peptides with trypsin, and then the peptides were broken into fragment ions by a tandem mass spectrometer. More than 30% of the peptides matching with the target protein were considered to be correct. Figures show the alignment results of VP2 and N48K mutant proteins separated via Native PAGE. (**a**–**e**) Protein intermediates were extracted from VP2 protein. (**f**–**j**) Protein intermediates were extracted from N48K mutant protein.