



**Supplementary Figure S2.** Targeted transcript analysis of Neddylaton and SUMOylation pathway genes in response to AAV2 infection. Approximately  $8 \times 10^4$  HeLa cells were infected with scAAV2-EGFP vectors at an MOI of  $5 \times 10^3$  vgs/cell. At various time points, total RNA from each of the treated condition in HeLa cells was isolated and transcript levels of Neddylaton target genes (**a, i-iv**) and SUMOylation target genes (**b, i-iv**) were measured by qPCR. Beta-actin was used as an endogenous control for the normalization of data. Each time point had its own mock-treated control cells, and their transcript level is denoted by *dotted line*. Data presented are representative set from two independent biological replicates. Paired *t*-test was performed to determine the statistical significance. Data are expressed as mean  $\pm$  SD,  $n=3$ ,  $*p \leq 0.05$ . qPCR, quantitative polymerase chain reaction.