



**Fig. S5. *In vitro* inhibition effect of benidipine hydrochloride on different strains of SFTSV. (a)** Phylogenetic analysis of SFTSV strains based on S segment (1727 bp).

Neighbor-joining tree was conducted using Kimura 2-parameter model by means of Molecular Evolutionary Genetics Analysis software, version 5.0. Bootstrap analysis of 1,000 replicates was applied to assess the reliability of the reconstructed phylogenies. Scale bars indicate estimated evolutionary distance. The bold indicates the strains used in this study. **(b-g)** Vero cells were treated with benidipine hydrochloride or vehicle (DMSO), and infected with SFTSV strain WCH, HNXy2017-50, or HNXy2017-66 (MOI = 1). At 36 hours post infection (p.i.), the intracellular and supernatant viral RNA was measured with quantitative RT-PCR. Effects of benidipine hydrochloride on intracellular and supernatant vRNA of SFTSV WCH **(b and c)**, SFTSV HNXy2017-50 **(d and e)** and SFTSV HNXy2017-66 **(f and g)** were indicated. Comparison of mean values between drug treated group and vehicle group was performed by student's *t* test. \*  $P < 0.05$ ; \*\*  $P < 0.01$ ; \*\*\*  $P < 0.001$ .  $R^2$  was estimated by nonlinear regression model (curve fit).