



S5 Fig. The ROC performance against known HCV entry factors of the *in silico* predictions and Li et al.'s siRNA experiment. As described in the main text, using a cutoff of at least 70% sequence conservation to find SLiMs (Fig 1A), we identified 15 of the 19 known HCV entry factors before complex analysis and 9 after, and Li et al. (Li et al. (2014) *PLoS Pathog*, 10(5), e1004163) identified 8 (see Table 1). In all, the *in silico* method identified 899 (231 after complex analysis), and Li et al.'s experiment 45, hepatocyte surface proteins as potential HCV entry factors. In this figure, the cutoff of HCV E1/E2 sequence conservation was varied from 0% to 100%, at which the same procedure as described in Fig 1 was carried out, and sensitivity and specificity for the resulting predictions were calculated to generate the ROC curves, on which the performance obtained at 70% sequence conservation cutoff is indicated. AUC: Area Under Curve.