

Supplemental figure legends

Figure S1. Mass spectrometry of tryptic peptides of YFP fusion proteins recovered from upper and lower bands of HES-1 expressed the HuEV-A vector. Coverage maps were prepared using Byonic software. Shown is the sequence of HES1 tag and N terminus. Amino acids denoted in green are peptides identified in this analysis. Each green line under a peptide denotes the number of times the peptide has been identified in this analysis (spectral counts). A red line below a peptide indicates that the corresponding amino acid carries a modification (in vivo or in vitro). For instance, cysteines are reduced and alkylated with iodoacetamide prior to analysis and are therefore all underlined in red. The red arrow indicates the beginning of the protein and end of the tag.

Figure S2. Mass spectrometry of tryptic peptides of YFP fusion proteins recovered from upper and lower bands of URI as in figure S1. Shown in a) is the sequence of the URI tag as in S1. URI protein spectral counts downstream of the tag are shown in b).

Figure S3. Standard curve of YFP amounts versus fluorescence reading (excitation 475nm, emission 527nm). The R^2 and equation of the best-fit trend-line for the experimental points is also reported.

Figure S4. a) HeLa cells were plated and transfected with Fugene-HD (Promega) in different size wells according with the parameters reported in the table. b) After lysis of the cells in each of the wells, the YFP fluorescence of 10 ml of solution used for IP was

measured. The range of variability between two separate FLIP measurements (var.) is reported.

Figure S5. Tet-ON HeLa cells were transfected with the HuEV-A construct encoding the target protein with an N-terminal FLAG, YFP (Venus) and V5 tag under a tet-inducible promoter. These cells were stimulated with 0, 50 or 1000 ng/ml doxycycline. Immunoprecipitation (IP) was carried out using 5 µg of either IgG, tested CDI mAb, or 5 µg of FLAG-M2 (Sigma). Immunoblotting was performed using rabbit Anti-FLAG (1:1000 dilution, Cell Signaling #2368). The arrow indicates the predicted molecular weight of the target protein.

HES1_TOP_Band

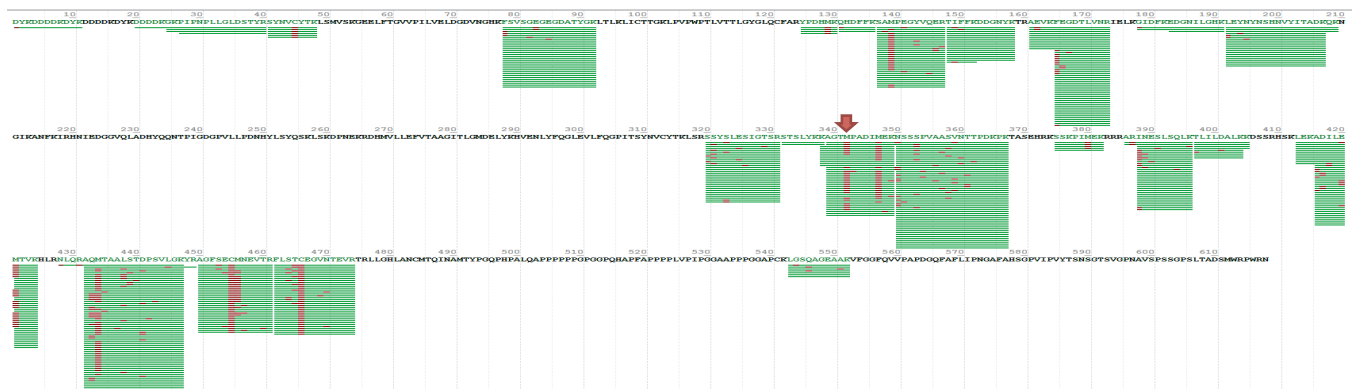
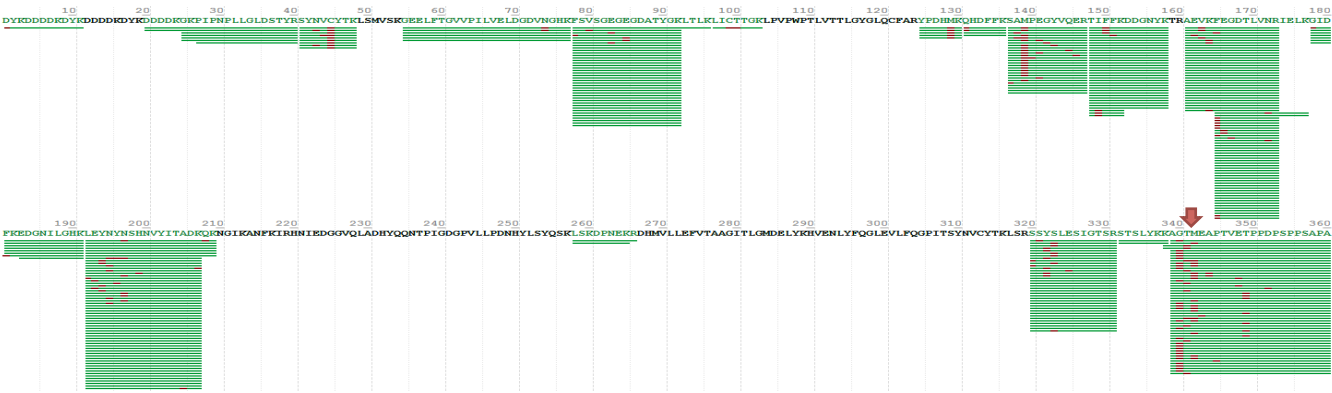


Figure S2 a)

URI _ TOP _ Band_Tag_sequence_Portion



URI _ BOTTOM _ Band_Tag_sequence_Portion

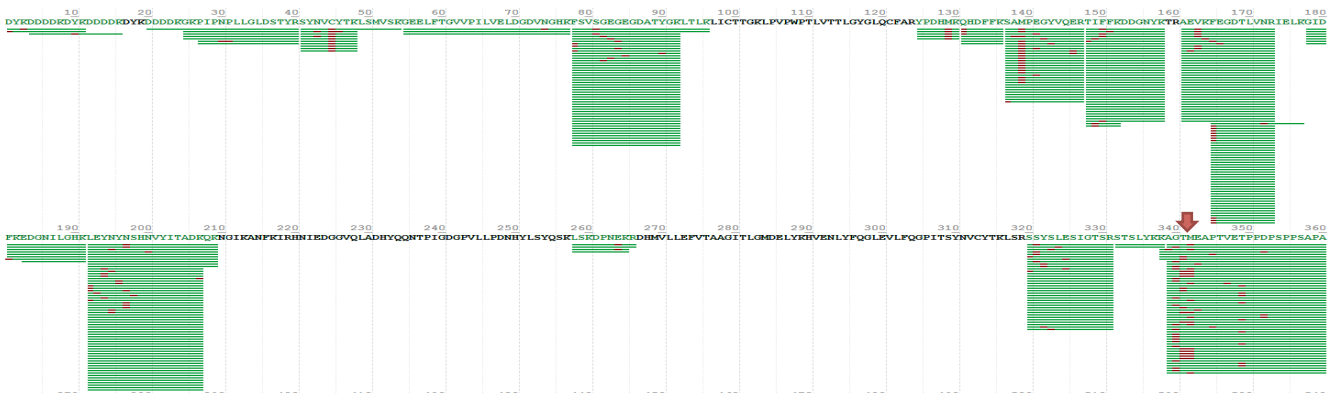
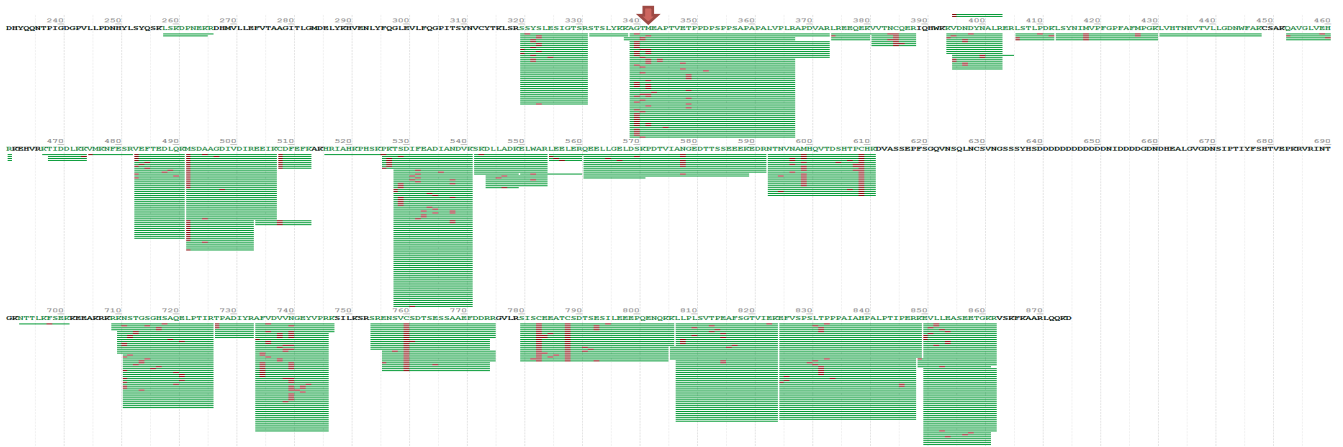


Figure S2 b)

URI_Top_Band_Protein_sequence_Portion



URI _ Bottom _ Band _ Protein _ sequence _ Portion

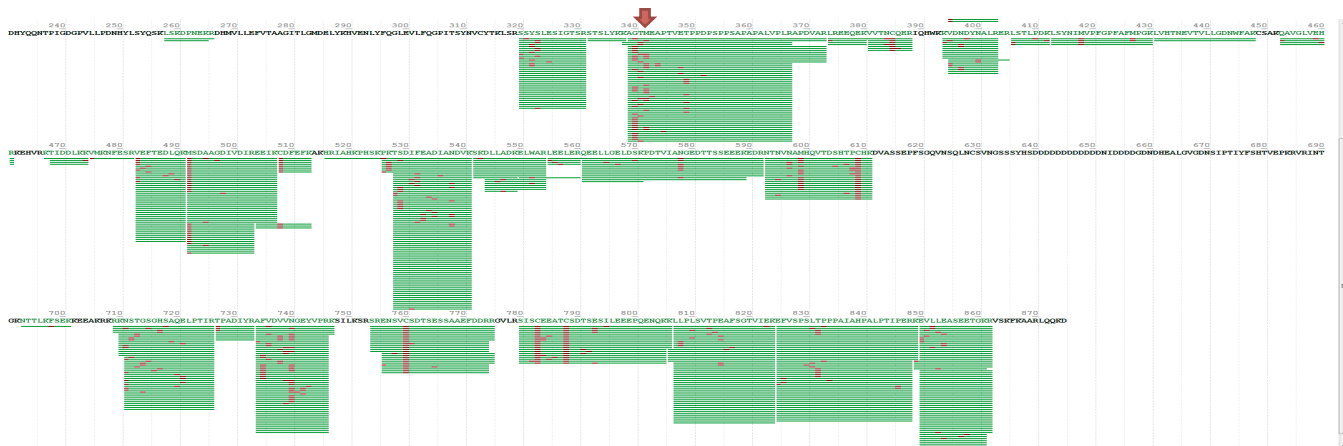


Figure S3

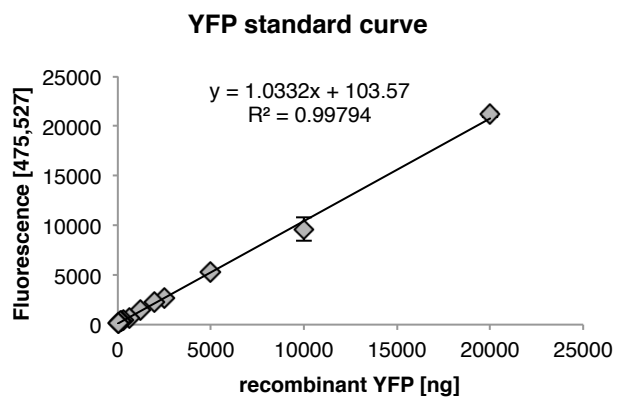


Figure S4

A

	cells/well [X10 ⁶]	media [ul]	DNA [ug]	OPTIMEM [uL]	Fugene-HD
96 well/plate	0.02	100	0.075	10	0.225
48 well/plate	0.03	200	0.1	10	0.4
24 well/plate	0.06	400	0.2	25	0.8
12 well/plate	0.12	800	0.4	25	1.5
6 well/plate	0.3	2000	0.75	50	3
6cm plates	0.6	2500	1.5	100	6

B

SAMPLES USED FOR IP	YFP fluorescence	var.
94 wells	22.5	8.9
48 wells	51.5	17.4
24 wells	52	5.4
12 wells	282	30.8
6 wells	819.5	18.8
6cm plate	1434.5	76.8

Figure S5-1

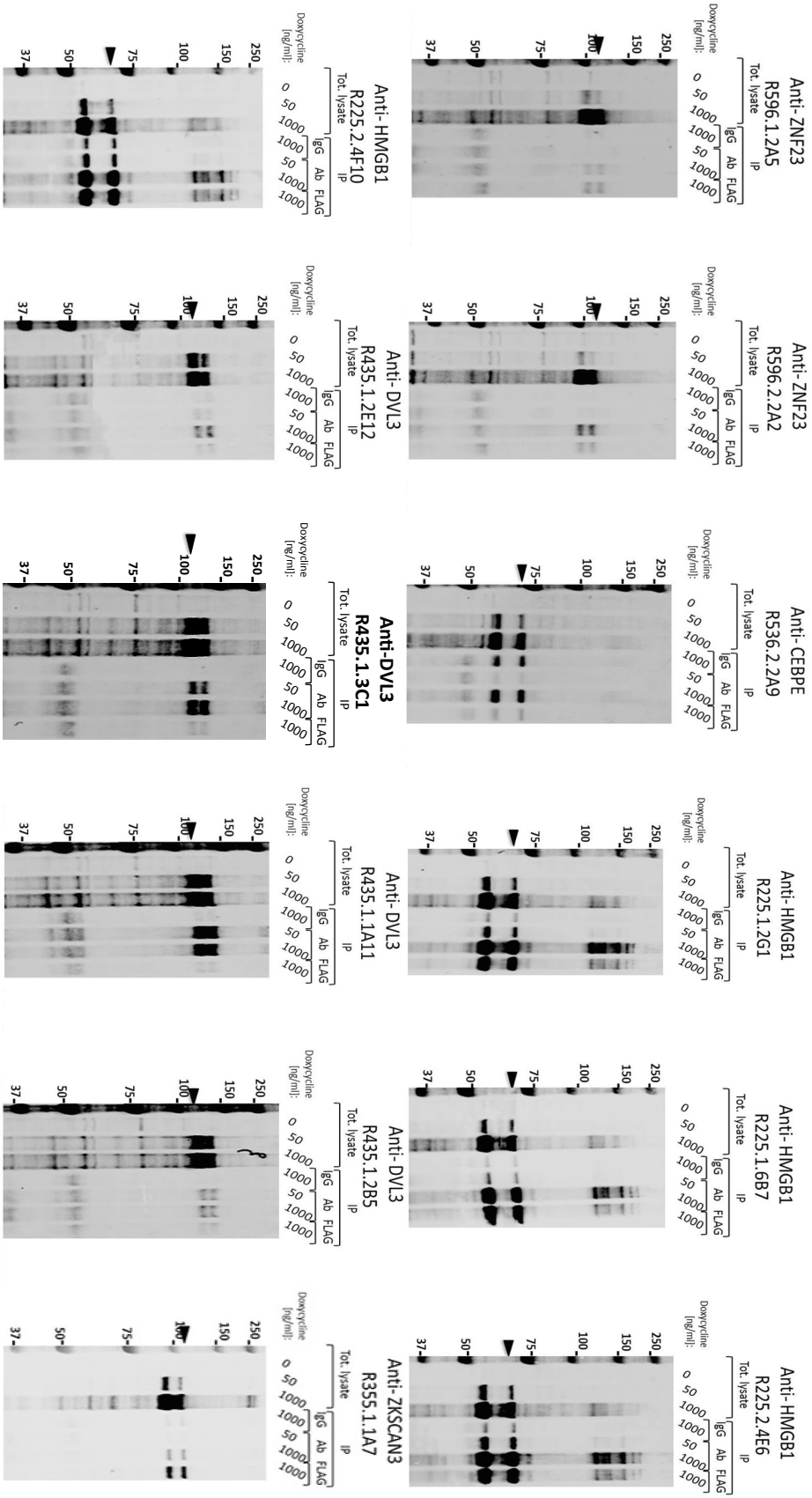


Figure S5-2

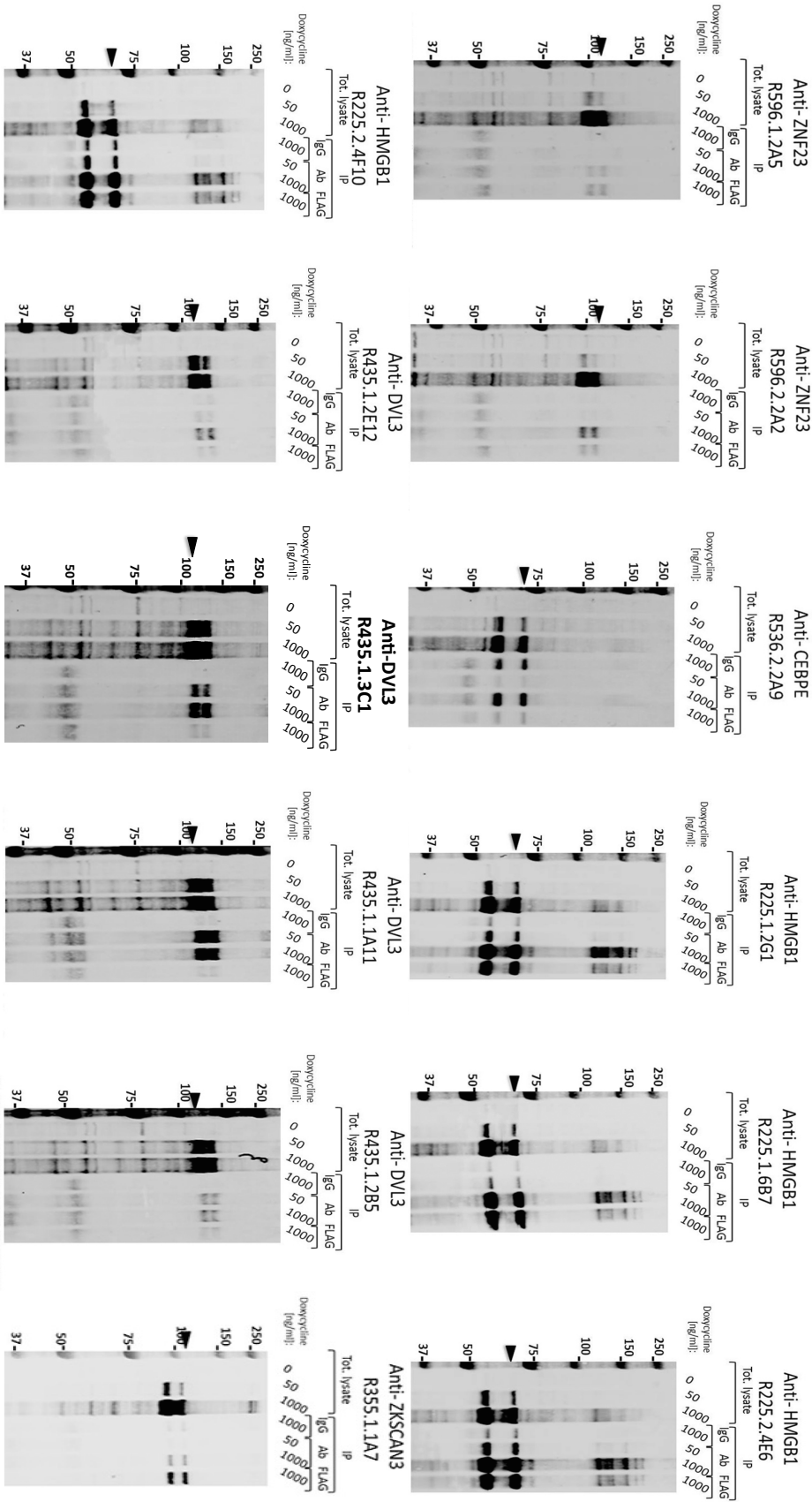


Figure S5-3

