

1 **Supplemental Data: The intra viral protein interaction network of hepatitis C**
2 **virus.**

3 Nicole Hagen^{2,*}, Karen Bayer^{1,*}, Kathrin Rösch², Michael Schindler^{1,2,3,#}

4 ¹Institute of Virology, Helmholtz Zentrum Munich, German Research Center for
5 Environmental Health, Munich, Germany

6 ²Heinrich Pette Institute, Leibniz Institute for Experimental Virology, Hamburg,
7 Germany

8 ³Institute of Medical Virology and Epidemiology of Viral Diseases, University Clinic
9 Tübingen, Tübingen, Germany

10

11 *These authors contributed equally

12 #Corresponding author:

13 Michael Schindler

14 michael.schindler@helmholtz-muenchen.de

15 Fon +49-(0)89-3187-4609

16

17

18

19

20

21

22

1 **Supplemental Figure S1: Quantitative and statistical analyses of FRET signals**
2 **in 293T and Huh7.5 cells.**

3 Number of independent experiments (n), mean value % FRET+ cells (MF), and
4 standard deviations (SD) are indicated. Analyses were performed for both
5 combinations (YFP-protein A + CFP-protein B & CFP-protein A + YFP-protein B). For
6 calculation of statistical significance, mean FRET signals of n experiments were
7 compared to the negative control FRET signal (CFP-fusion with YFP-only) with the
8 two-tailed unpaired Student's t test (Graph Pad Prism 5.0). Significance levels are
9 indicated as follows: p<0.05 (*), p<0.01 (**) and p<0.001 (***)
10 Grey boxes depict
11 mean FRET values \geq 10 % (numbers in red). This threshold was arbitrarily introduced
12 as additional stringency criterion to define robust FRET of cotransfected fusion
13 proteins. Some mean FRET values below 10 % also reached statistical significance.
14 These values are shown in green. Primary data for transfection of 293T cells are
15 accessible within the supplemental data set (see below).

16

17

18

19

20

21

22

A																					
B		Core		E1		E2		p7		NS2		NS3		NS4A		NS4B		NS5A		NS5B	
		293T	Huh7.5	293T	Huh7.5	293T	Huh7.5	293T	Huh7.5	293T	Huh7.5	293T	Huh7.5	293T	Huh7.5	293T	Huh7.5	293T	Huh7.5		
Core	C-A + Y-B	n	9	8																	
	MF	67.93	44.89																		
	SD	14.88	25.25																		
		***	***																		
E1	C-A + Y-B	n	9	7	9	not tested															
	MF	3.91	2.87	1.88																	
	SD	3.33	3.53	2.35																	
		ns	*	*																	
E2	Y-A + C-B	n	12	1																	
	MF	1.84	0.90																		
	SD	2.84	.																		
		ns																			
p7	C-A + Y-B	n	9	3	11	not tested	18	13													
	MF	0.9	0.00	0.44		62.29	47.12														
	SD	1.91	0.00	0.45		28.53	34.40														
		ns	ns	ns		***	***														
NS2	Y-A + C-B	n	23	6	17	7															
	MF	21.11	3.00	74.76	42.21																
	SD	17.46	3.71	17.68	10.45																
		***	*	***	***																
NS3	C-A + Y-B	n	9	3	10	2	17	13	23	11											
	MF	6.43	0.00	0.18	0.35	18.36	34.92	29.30	6.69												
	SD	11.16	0.00	0.23	0.50	20.68	31.22	18.37	4.66												
		ns	ns	ns		***	**	***	***												
NS4A	Y-A + C-B	n	15	5	16	14	19	17	24	6	38	8									
	MF	27.78	0.62	16.41	7.69	6.88	4.67	8.03	6.64	24.46	19.70										
	SD	32.91	1.28	17.37	10.61	32.95	21.98	26.82	8.93	24.46	19.70										
		**	ns	***	*	***	*	**	ns	***	***										
NS4B	C-A + Y-B	n	10	3	11	not tested	40.11	16.60	40.73	6.18	60.31	56.30									
	MF	0.09	0.00	0.34		32.95	21.98	26.82	8.93	24.46	19.70										
	SD	0.19	0.00	0.35		32.95	21.98	26.82	8.93	24.46	19.70										
		ns	ns	ns		***	*	***	ns	***	***										
NS5A	Y-A + C-B	n	35	3	34	9	39	2	32	6											
	MF	15.54	1.03	17.78	4.22	8.81	0.30	22.54	14.05												
	SD	21.20	1.79	14.09	8.47	18.43	0.42	24.18	11.29												
		**	ns	***	ns	ns	ns	**	**												
NS5B	C-A + Y-B	n	9	1	11	3	14	2	14	4	23	7	28	13							
	MF	0.28	0.00	1.88	0.00	2.18	7.05	8.00	0.40	2.90	4.84	9.64	12.72	9.95	24.16						
	SD	0.35	.	4.57	0.00	2.13	5.87	9.87	0.45	10.5	11.65	ns	ns	ns	ns	***	***				
		ns	ns	**	**	**	***	**	ns	ns	ns										
NS4A	Y-A + C-B	n	8	not tested	10	not tested	14	2	10	not tested	22	not tested	20	8	10	not tested					
	MF	0.20	not tested	0.07	not tested	5.49	0.35	0.16	not tested	0.71	not tested	2.99	11.44	4.31	18.44	**	ns				
	SD	0.49	ns	0.09	ns	17.50	0.50	0.21	ns	1.34	ns	4.31	18.44	2.65	ns	ns	ns	ns	ns		
		ns	ns	ns	ns	ns	.	ns	ns	ns											
NS4B	Y-A + C-B	n	9	not tested	4.79	not tested	10	not tested	10	not tested	9	not tested	20	14							
	MF	0.54	not tested	9.36	not tested	0.60	not tested	0.60	not tested	2.00	not tested	27.97	2.46	23.88	2.65						
	SD	0.48	ns	ns	ns	1.05	ns	ns	ns	3.38	ns	***	*	ns	ns						
		**	ns	**	**	**	ns	*	ns	ns	ns										
NS5A	Y-A + C-B	n	8	not tested	1.08	not tested	10	not tested	11	not tested	9	not tested	8	not tested							
	MF	0.64	not tested	0.14	not tested	0.09	not tested	0.62	not tested	0.36	not tested	0.23	not tested	0.93	not tested						
	SD	1.27	ns	ns	ns	0.18	ns	1.40	ns	0.56	ns	0.28	ns	2.10	ns	ns	ns	ns	ns		
		ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns			
NS5B	C-A + Y-B	n	11	not tested	1.00	not tested	1.88	ns	1.80	not tested	0.14	not tested	10	not tested	9	not tested					
	MF	0.30	not tested	1.00	not tested	1.00	ns	1.80	not tested	0.17	not tested	0.15	not tested	1.07	not tested						
	SD	0.61	ns	*	ns	ns	ns	ns	ns												
		ns	.	ns	ns	ns															
NS5B	Y-A + C-B	n	20	6	20	4	18	6	14	not tested	13	not tested	12	not tested	20	9					
	MF	13.11	3.90	23.62	20.55	12.97	18.42	4.07	not tested	1.34	not tested	0.91	not tested	1.10	not tested	7.06					
	SD	10.43	6.82	21.94	5.03	15.34	15.36	7.74	ns	1.40	not tested	0.19	not tested	1.62	not tested	9.50	**				
		***	ns	***	***	***	**	ns	ns	ns											

p < 0.05 *
 p < 0.01 **
 p < 0.001 ***

n number of experiments
 MF mean value % FRET+ cells
 SD standard deviation

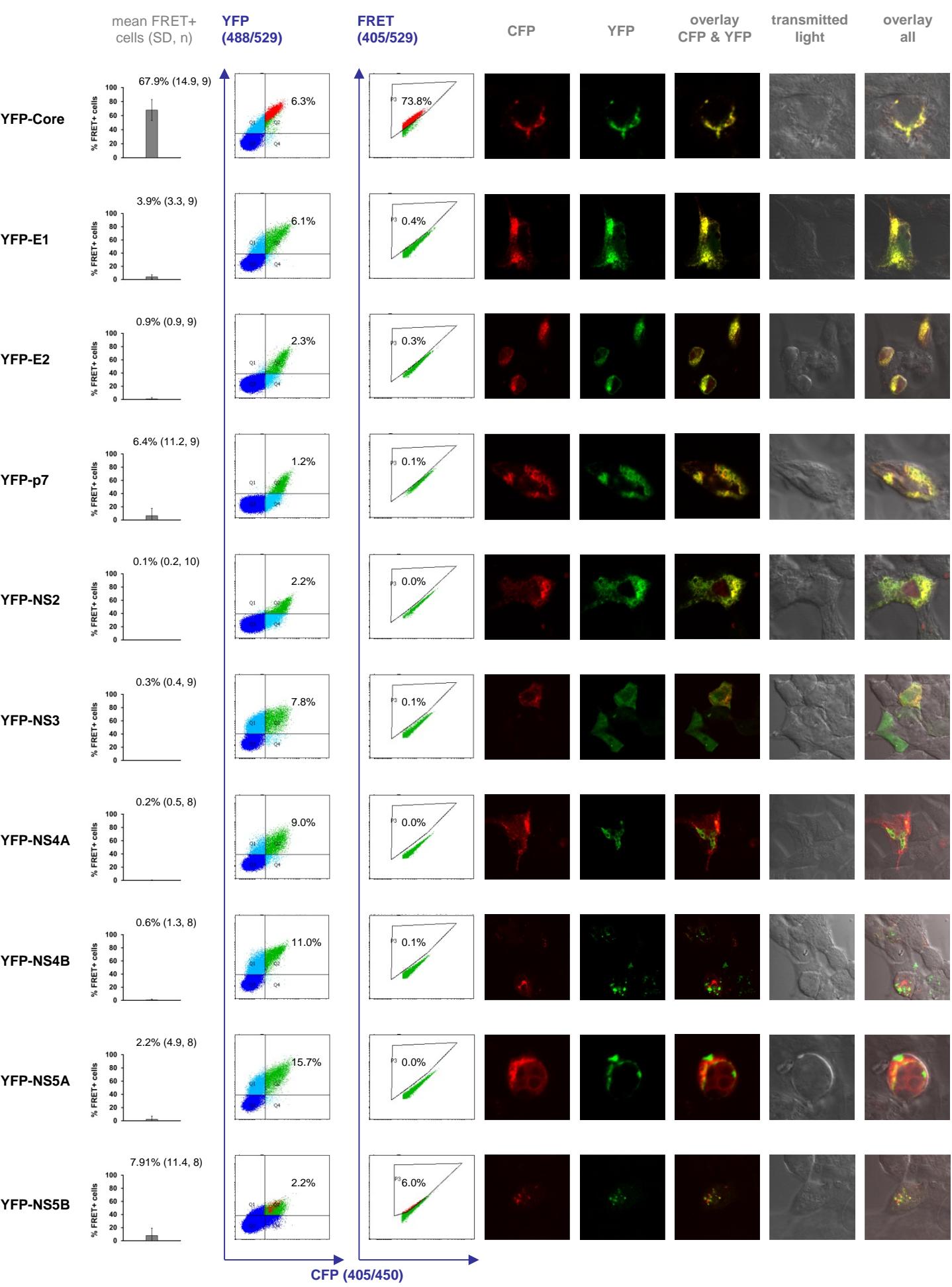
mean above 10 % threshold
 mean below 10 % threshold
 not significant

1 **Supplemental Dataset: FRET results of HCV CFP and YFP fusion proteins**
2 **transfected in 293T cells.**

3 The percentage of FRET+ cells (mean) from the indicated number of experiments (n)
4 as well as standard deviation (SD) is presented in every graph (left panel). We
5 furthermore show a representative example of the cotransfection efficiency (%
6 cotransfected cells) and the percentage of FRET+ cells according to the gating
7 strategy previously established (Banning et al., 2010 PLoS ONE 5(2): e9344).
8 Furthermore, the subcellular localization of the respective fusion proteins was
9 analysed by confocal microscopy (right panel; CFP is false colored in red and YFP in
10 green).

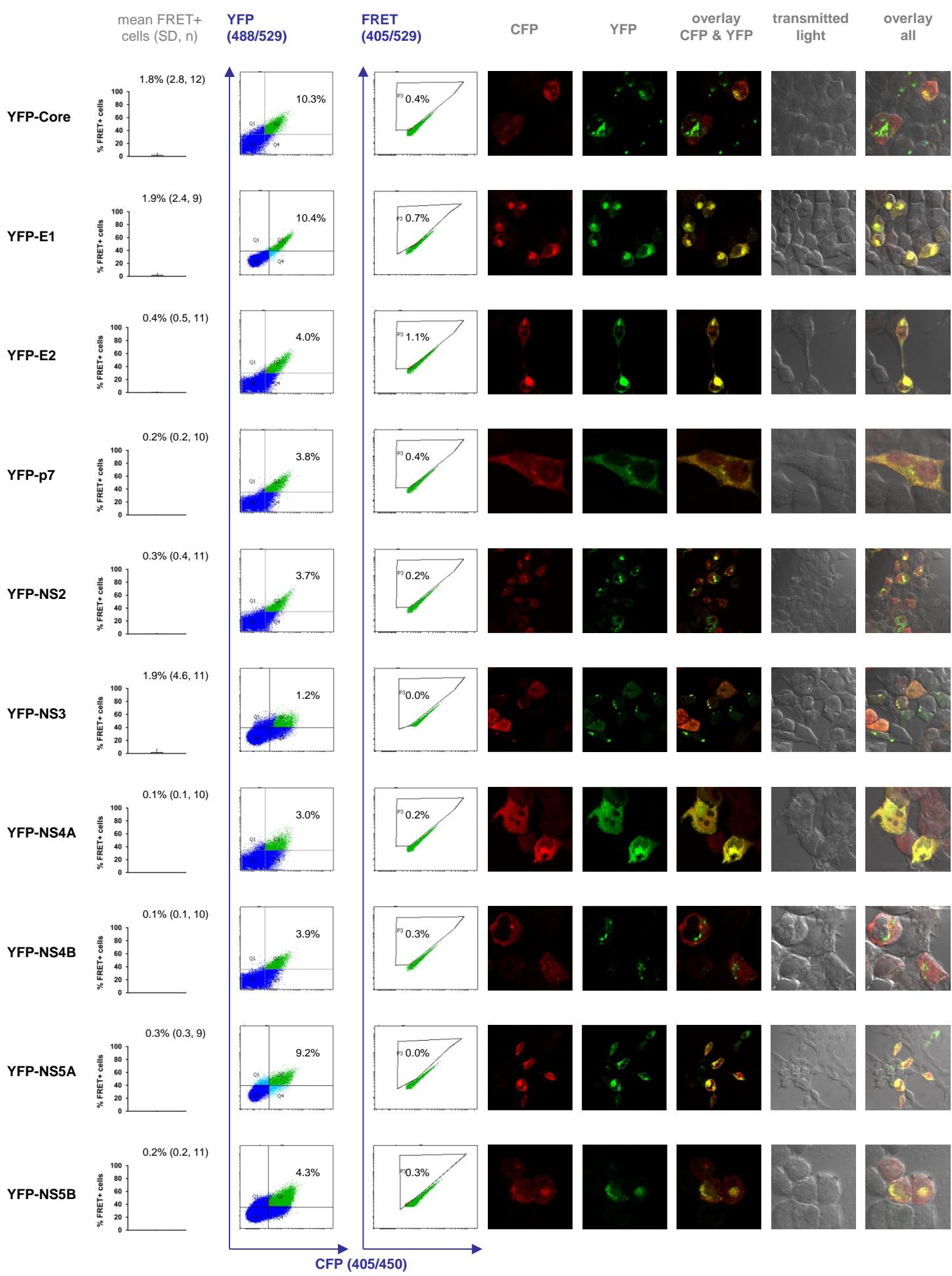
CFP-Core
tested with:

Interaction via FACS-FRET



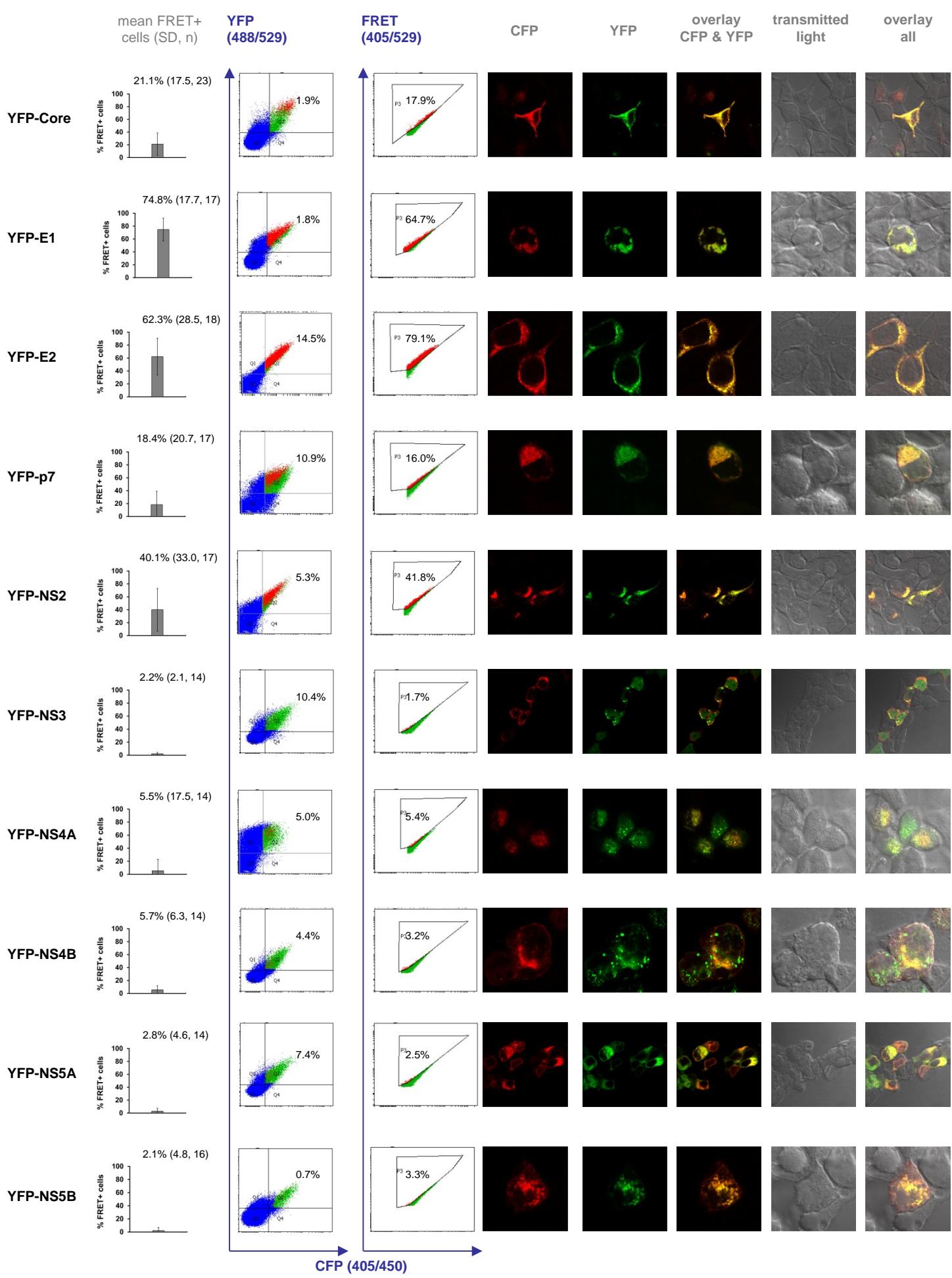
CFP-E1

tested with:

Interaction via FACS-FRET**Colocalization via CLSM**

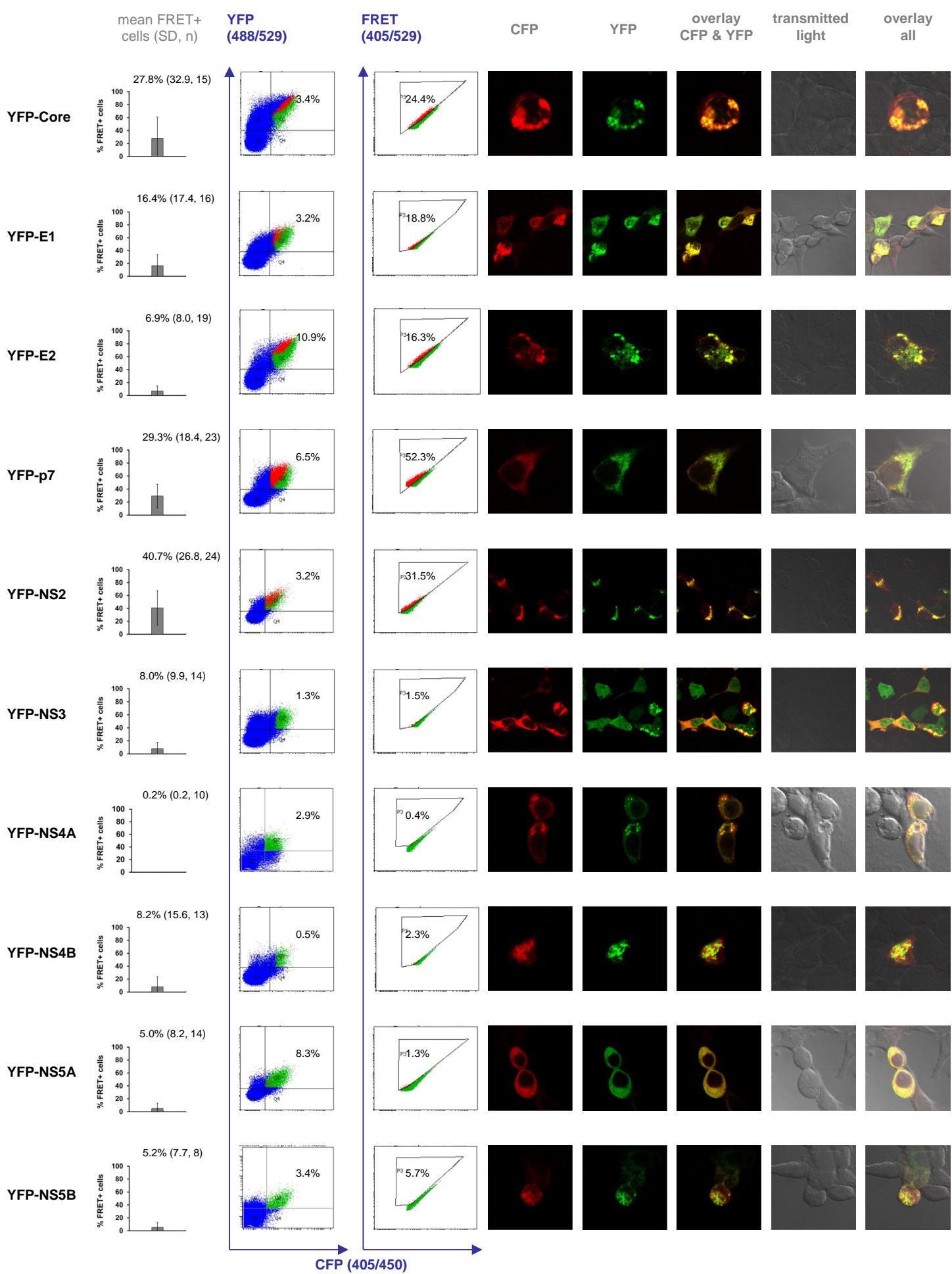
CFP-E2

tested with:

Interaction via FACS-FRET**Colocalization via CLSM**

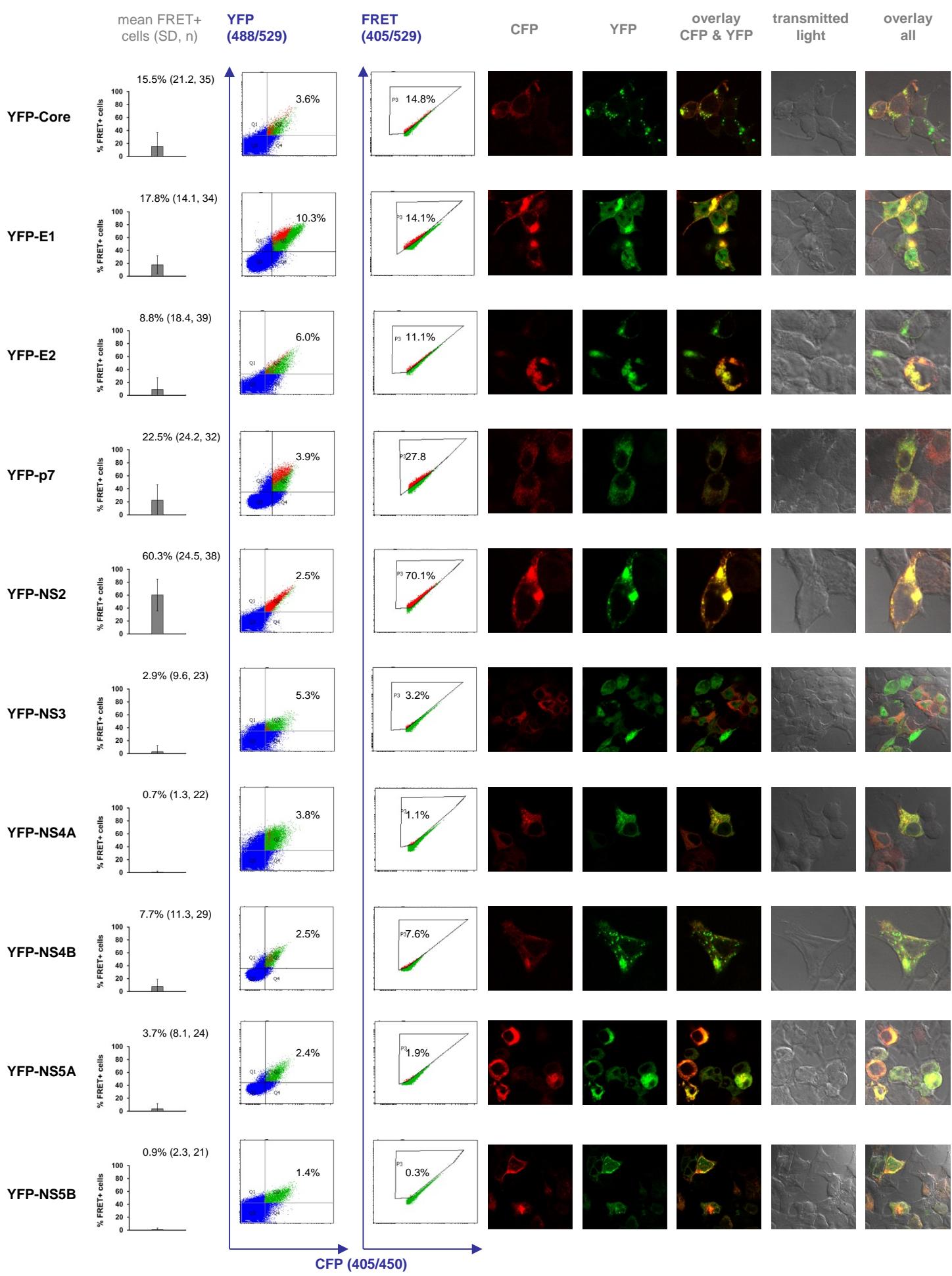
CFP-p7

tested with:

Interaction via FACS-FRET**Colocalization via CLSM**

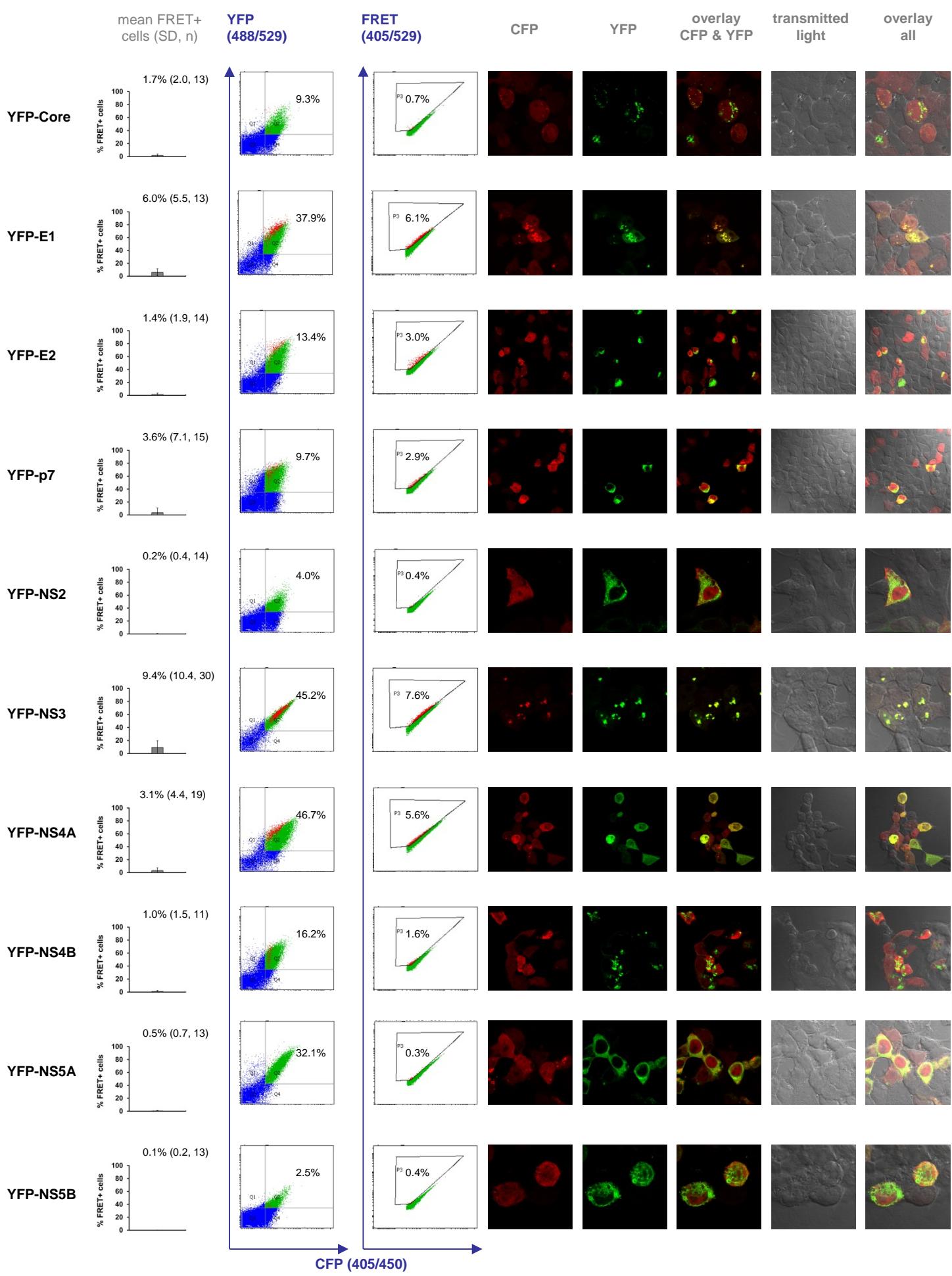
CFP-NS2

tested with:

Interaction via FACS-FRET**Colocalization via CLSM**

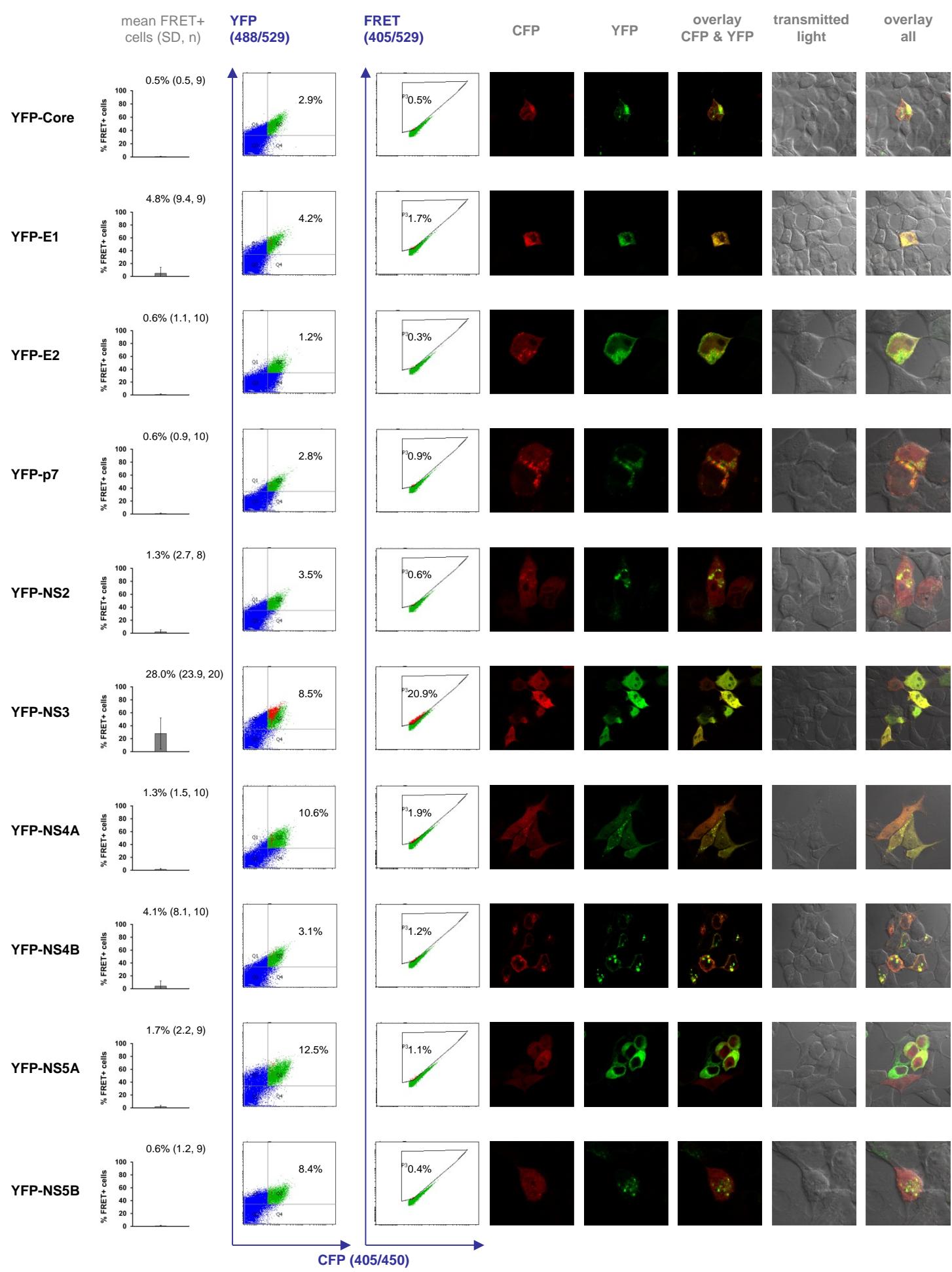
CFP-NS3

tested with:

Interaction via FACS-FRET**Colocalization via CLSM**

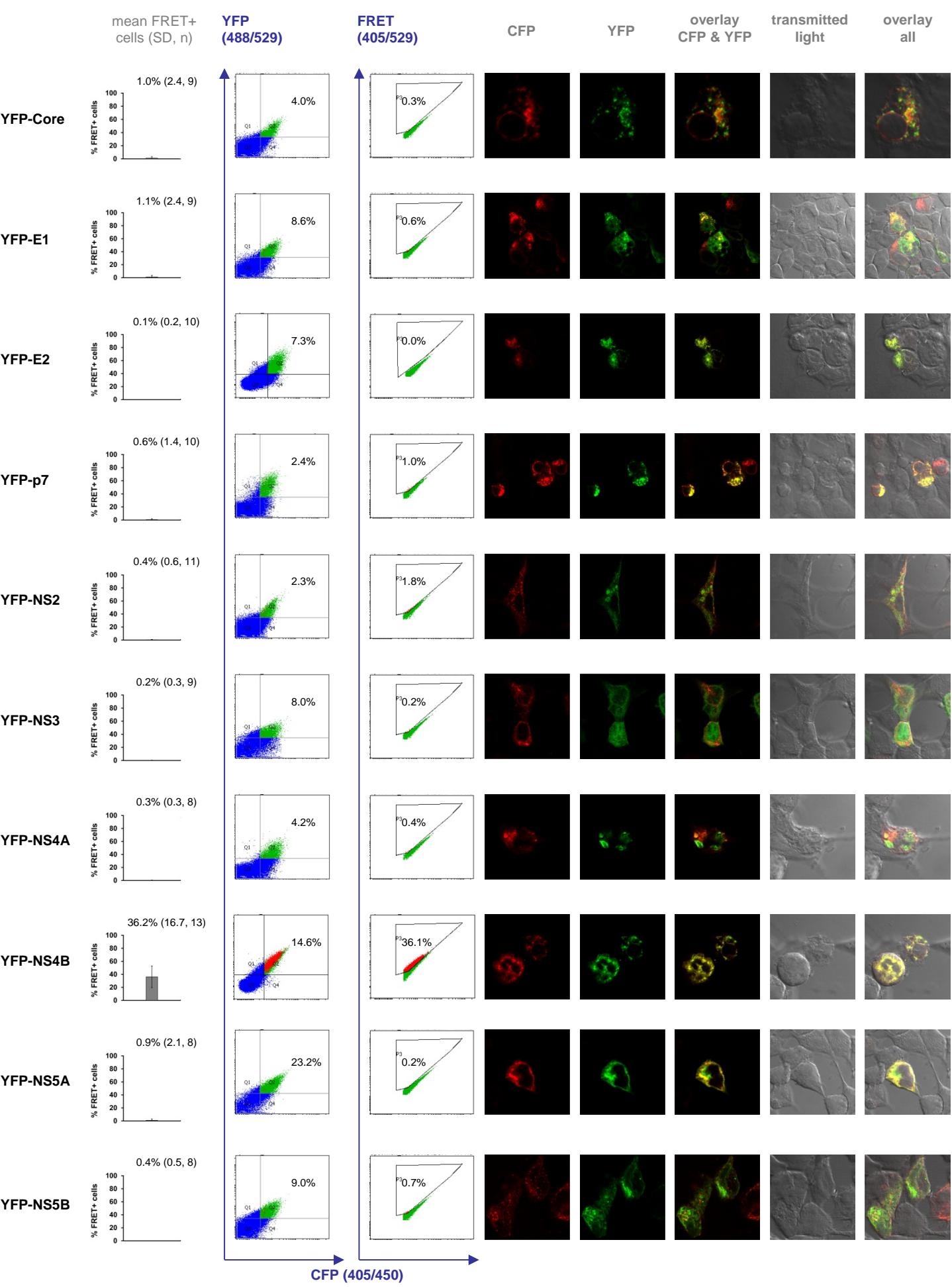
CFP-NS4A
tested with:

Interaction via FACS-FRET



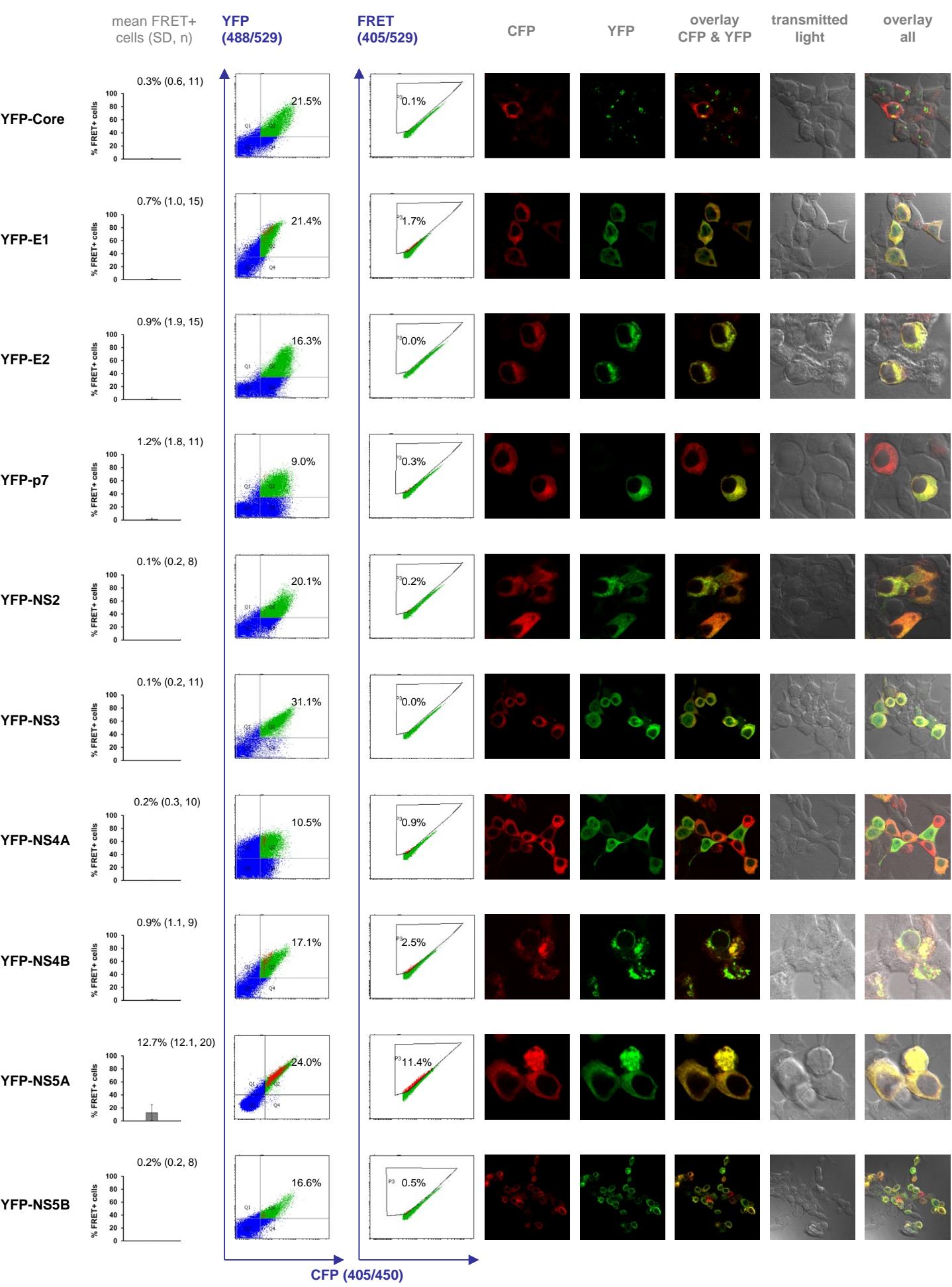
CFP-NS4B
tested with:

Interaction via FACS-FRET



CFP-NS5A
tested with:

Interaction via FACS-FRET



CFP-NS5B
tested with:

Interaction via FACS-FRET

