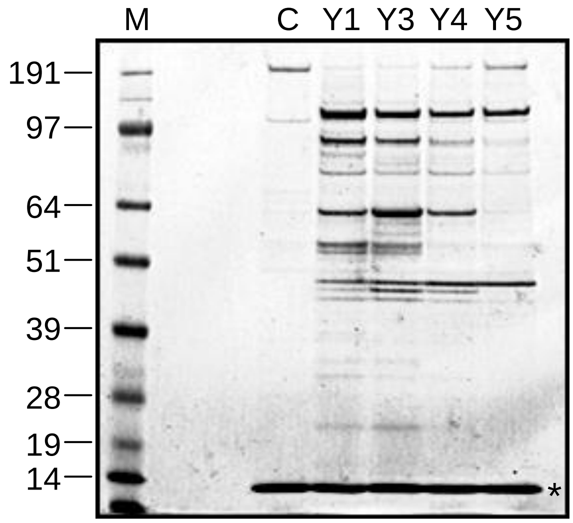
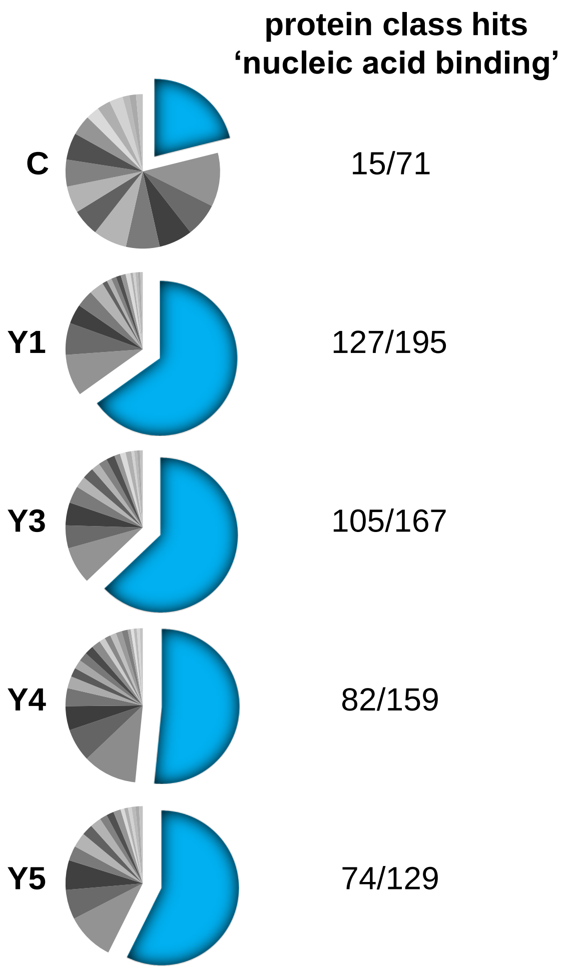
Köhn_Figure S1

A



B



C

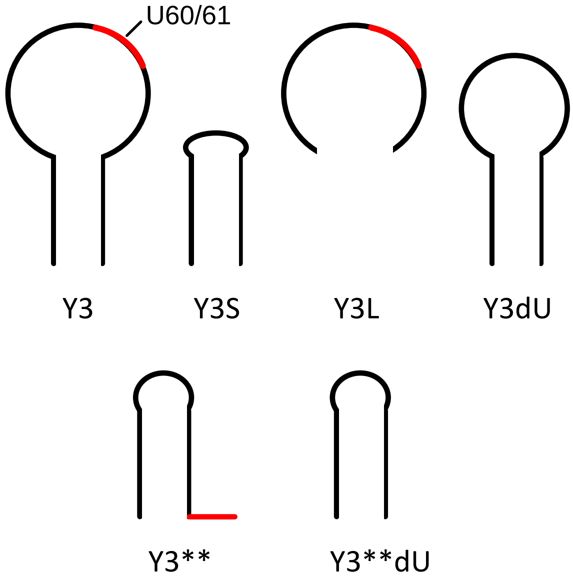
	Protein (Gene Symbol)	C	Y1	Y3	Y4	Y5
	Ro60 (TROVE2)		46,8 39	52,2 52	53,0 64	50,7 63
	La (SSB)	6,1 7	76,2 175	77,2 171	77,2 211	78,2 222
	HNRNPK		53,8 76	17,7 5	5,0 1	7,8 3
	MATR3	3,8 2	56,6 129	60,6 161		
	IGF2BP1	10,1 10	61,2 102	61,2 182	60,3 163	48,4 49
	ELAVL1		3,4 1	50,6 40	3,4 1	3,4 1
	YBX1		60,8 51	63,9 83	65,1 68	60,8 35
	PUF60	5,6 1	34,9 23	14,3 9	17,0 7	60,3 68
	RPL13		6,2 1	10,0 2		
3'-end processing factors	CPSF160 (CPSF1)		4,3 6	11,4 16		
	CPSF100 (CPSF2)		1,7 1	16,1 10		
	CPSF73 (CPSF3)			5,3 3		
	CPSF30 (CPSF4)			14,1 3		
	hFIP1 (FIP1L1)		2,9 1	14,8 7		
	WDR33			11,0 13		
	Symplekin (SYMPK)		2,2 2	4,1 4		

XX: Peptide coverage (PC) in %

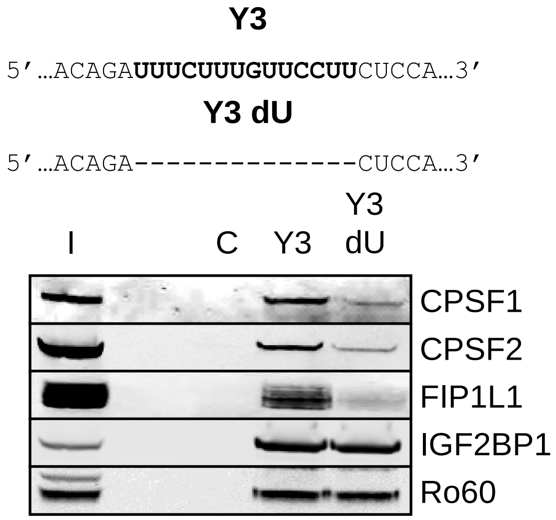
XX: Peptide spectral matches (PSMs)

Köhn_Figure S1

D



E



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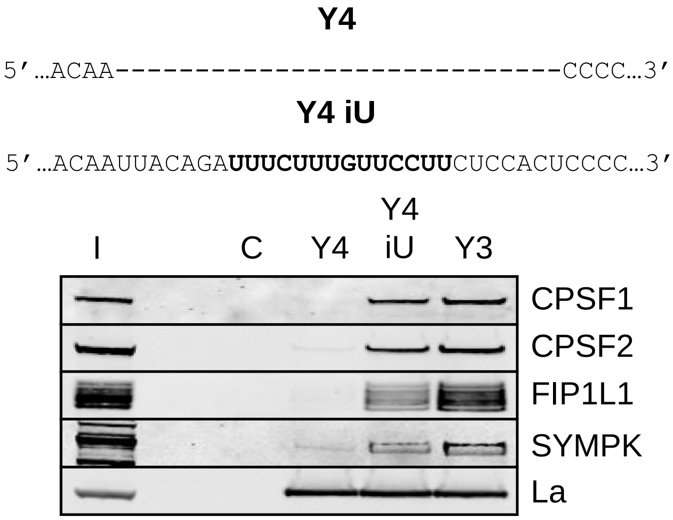
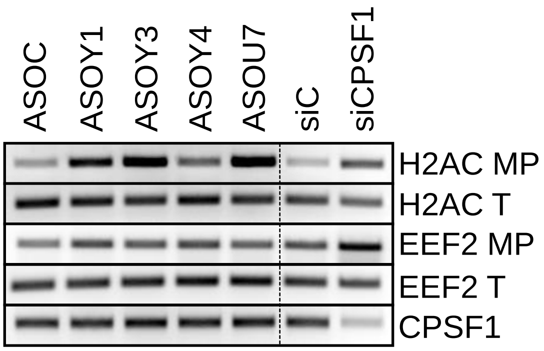
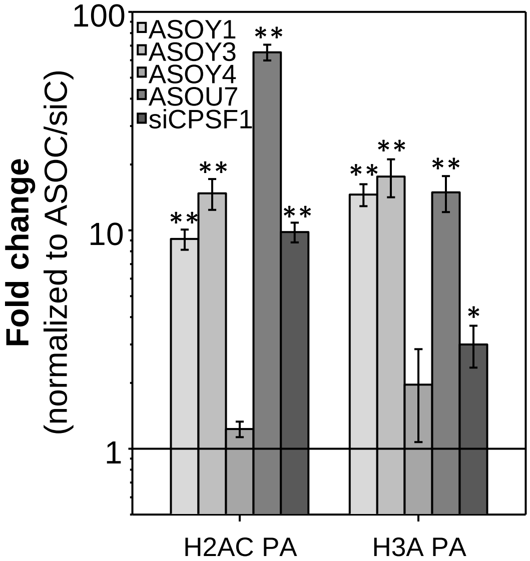


G



H



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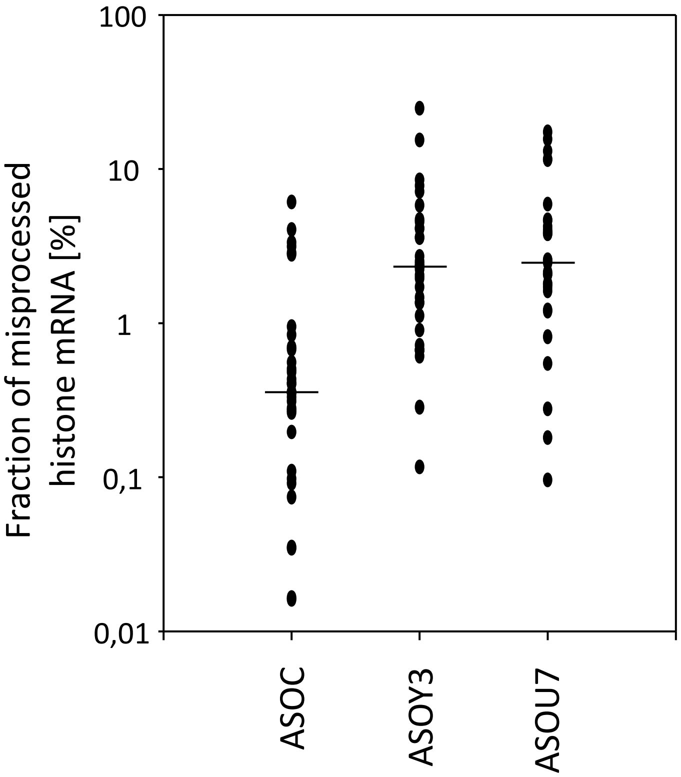
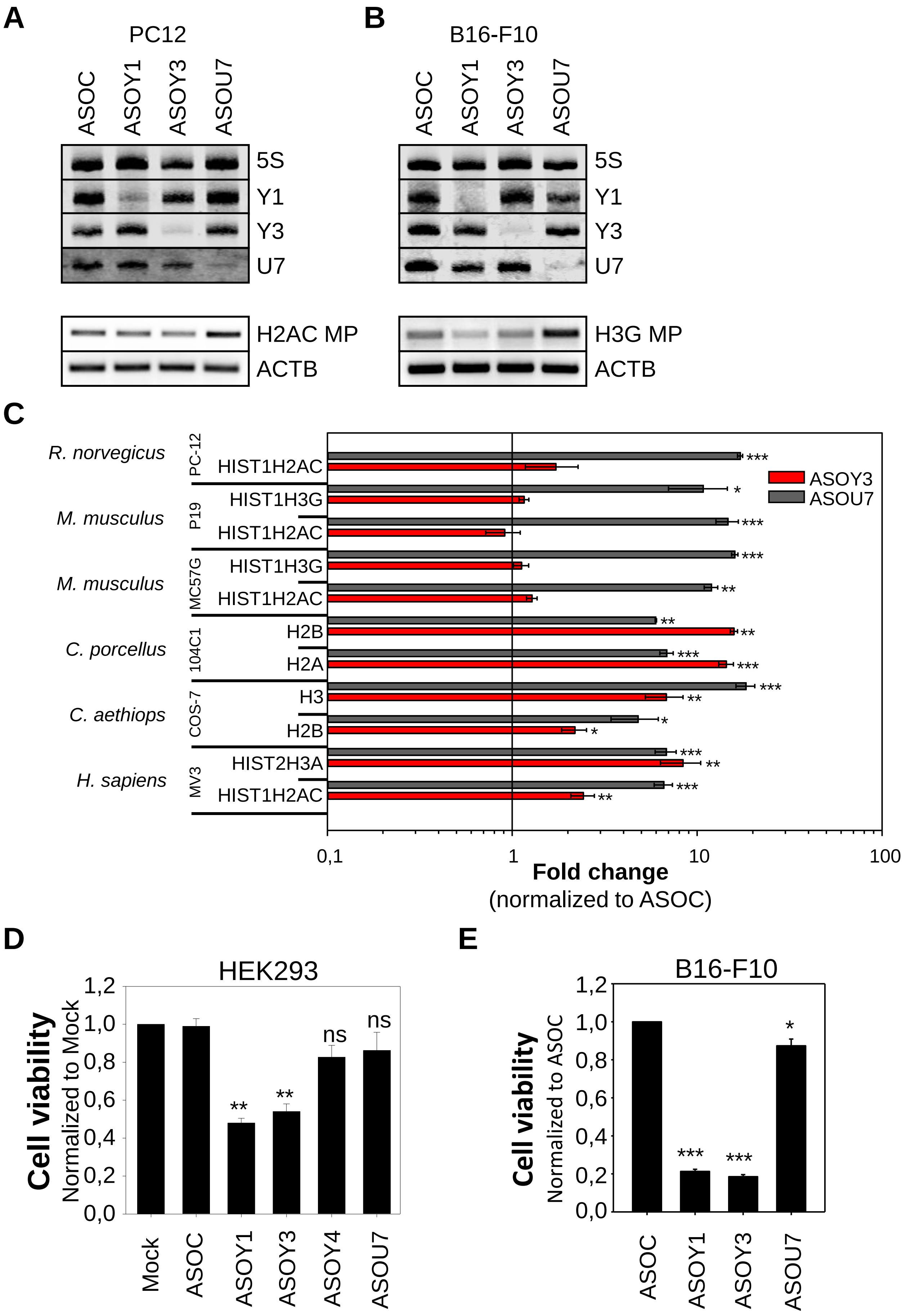

100
10
1
0,1
0,01
Fraction of misprocessed histone mRNA [%]
ASOC
ASOY3
ASOU7

Köhn_Figure S3



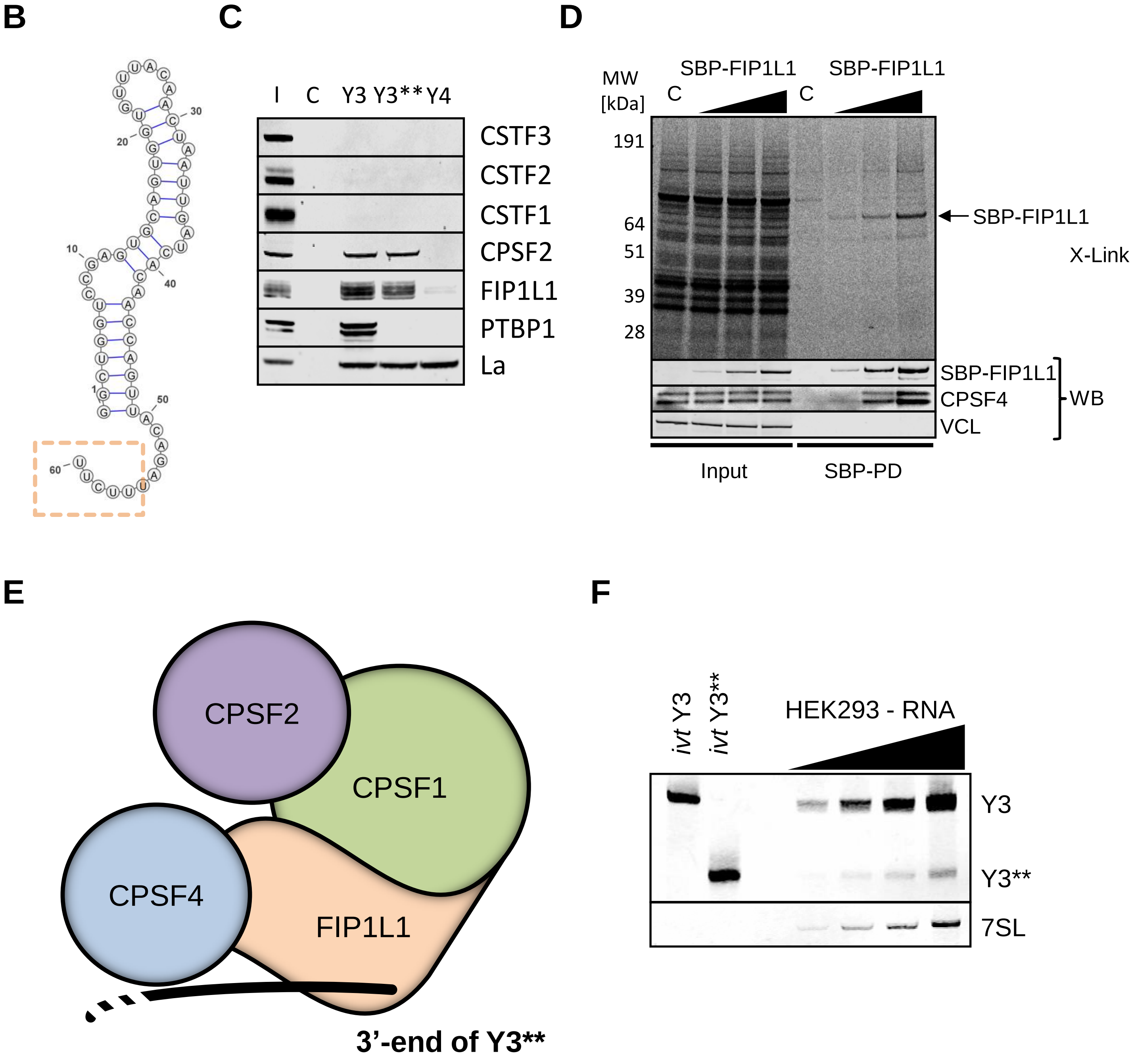
Köhn_Figure S4

A

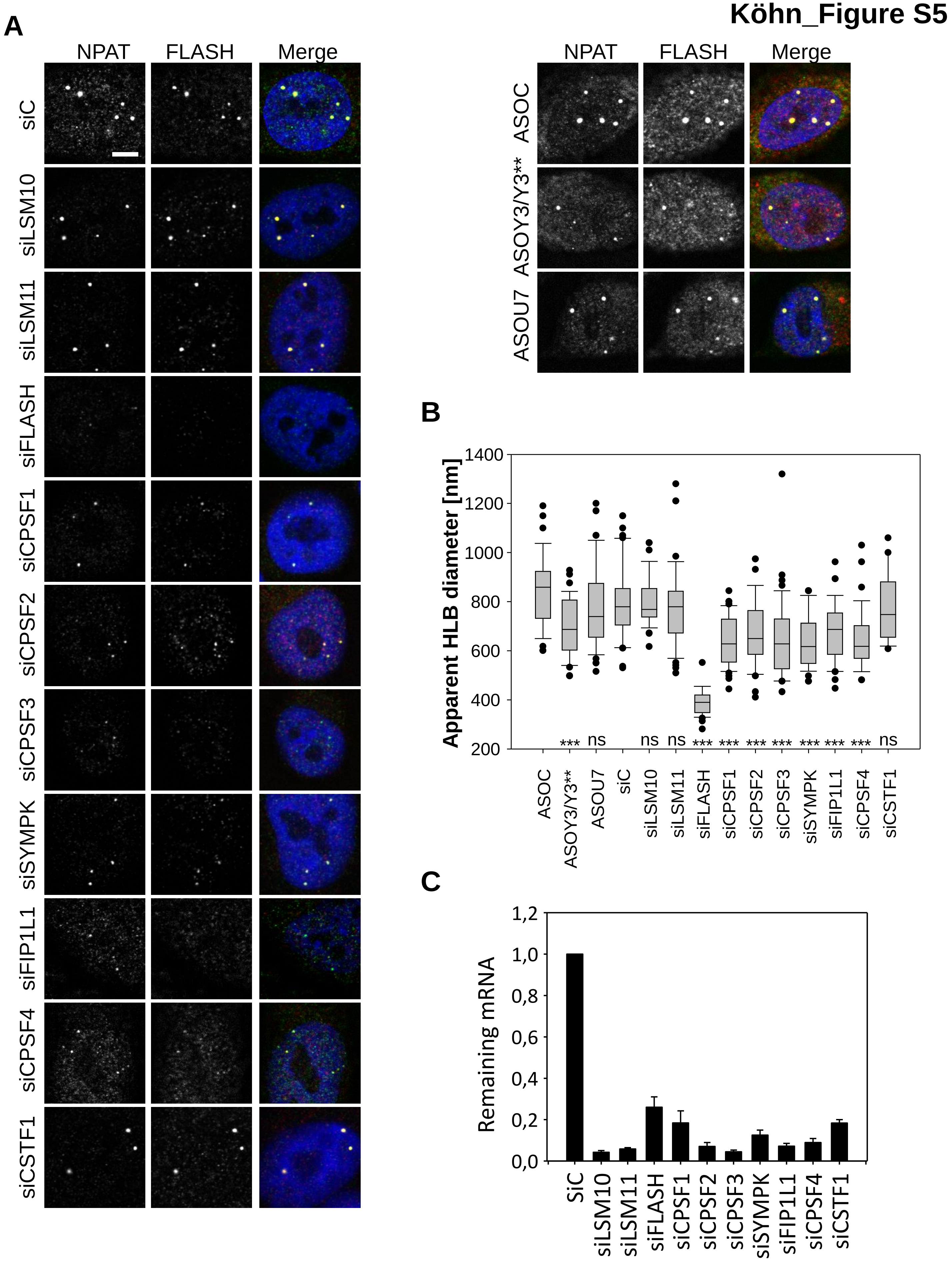
ASO/siRNA site

```
Y3 FL   GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTTTGTTCCTTCTCCACTCCCACTGCTTCACTTGACTAGCCTTTT
#1      GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTTTGTT
#2      GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTTT
#3      GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTTT
#4      GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTTT
#5      GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTT
#6      GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTT
#7      GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTT
#8      GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTT
#9      GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTT
#10     GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTACAGATTTCTA
```

T = T60   T = T61

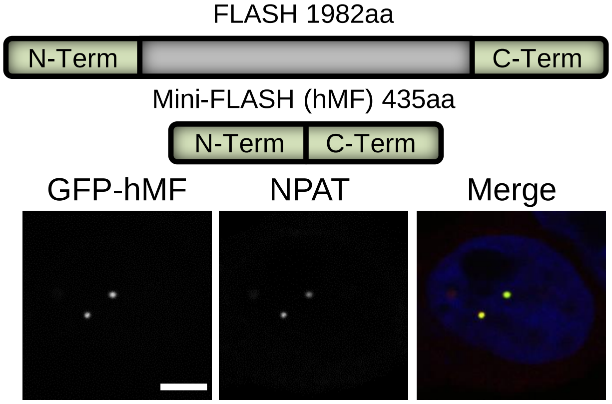


Köhn_Figure S5



Köhn_Figure S5

D



E