

Appendix for

Yuan et al., "Chk1 and 14-3-3 proteins inhibit atypical E2Fs
to prevent a permanent cell cycle arrest"

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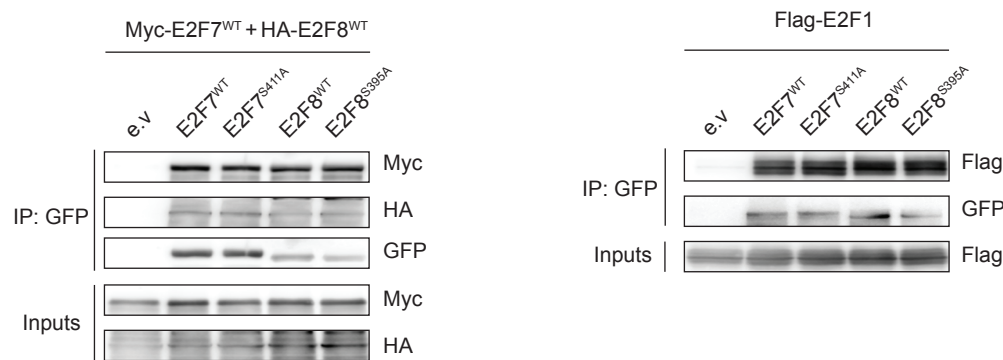
Appendix Figure S1

Legend:

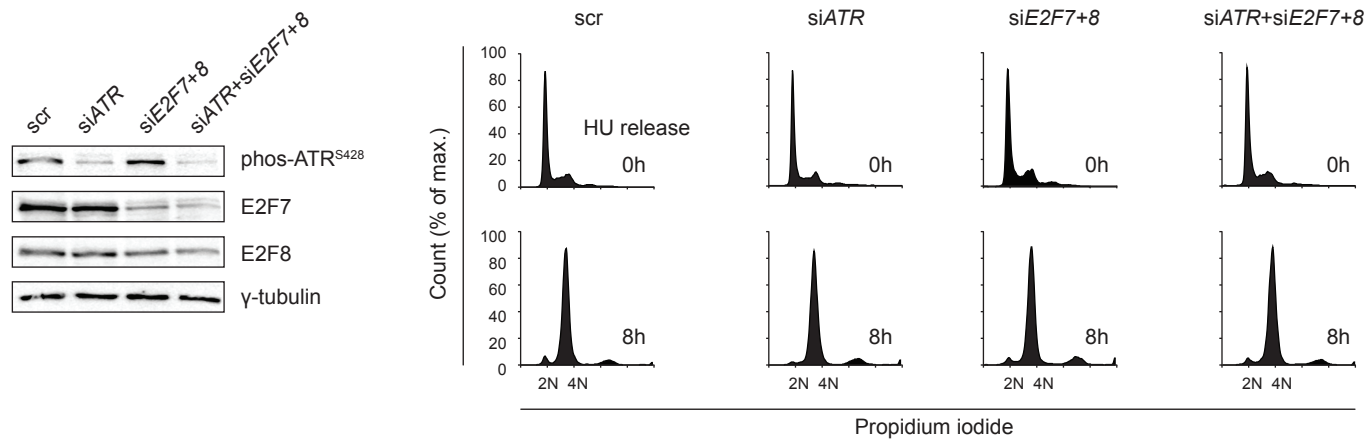
A The co-immunoprecipitation experiments revealed that homo- and hetero dimerization between the atypical E2Fs and their binding to E2F1 was not affected by Chk1/14-3-3.

B The function of ATR in regulation of E2F7/8 using siRNA against *ATR* under HU arrest/release conditions. Knockdown efficiency of *ATR* and *E2F7*, *E2F8* was confirmed by immunoblotting (left). Then cells were harvested at indicated timepoints and subjected to flow cytometry for cell cycle profile analysis (right).

A



B



Appendix Table S1. Enriched interaction partners between wildtype and alanine mutant E2F7

Legend: This table lists the binding partners that bind differently to wildtype and alanine mutant version of E2F7, based on the additional SILAC experiment.

More binding to alanine mutant
Less binding to alanine mutant

Gene Symbol	Protein Name	logwtHsaL	logwtLsaH
ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	-2,30	1,32
AKR1C3	Aldo-keto reductase family 1 member C3	-1,79	0,68
ANXA1	Annexin A1;Annexin	-1,49	0,61
ATP5H	ATP synthase subunit d, mitochondrial	-1,38	0,90
ATP5O	ATP synthase subunit O, mitochondrial	-1,73	0,54
AURKA	Aurora kinase A	-2,28	0,56
HSPA1A	Heat shock 70 kDa protein 1A/1B	-1,64	0,54
KIAA0101	PCNA-associated factor	-1,17	0,98
NAMPT;NAMPTL	Nicotinamide phosphoribosyltransferase	-1,51	0,87
SERPINB1	Leukocyte elastase inhibitor	-1,80	0,68
SERPINB5	Serpin B5	-2,07	1,27
SERPINB8	Serpin B8	-1,74	0,66
ACTG1	Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed	0,56	-2,16
AHNAK	Neuroblast differentiation-associated protein AHNAK	0,80	-2,20
ALPP	Alkaline phosphatase, placental type	0,86	-3,03
CALD1	Caldesmon	1,02	-2,47
CNN2	Calponin-2	1,23	-2,13
CTPS1	CTP synthase 1	0,86	-1,88
DNAJA2	DnaJ homolog subfamily A member 2	0,52	-2,01
FHL2	Four and a half LIM domains protein 2	0,94	-1,99
IL18	Interleukin-18	1,17	-2,55
KRT17	Keratin, type I cytoskeletal 17	0,73	-3,64
LIMA1;TRMT1	LIM domain and actin-binding protein 1	0,86	-4,08
MAP2K3	Dual specificity mitogen-activated protein kinase kinase 3	0,83	-1,70
MAP4	Microtubule-associated protein;Microtubule-associated protein 4	0,62	-2,02
MPRIP	Myosin phosphatase Rho-interacting protein	0,58	-2,97
MT1X	Metallothionein-1X	0,85	-1,52
MT2A;MT1G	Metallothionein-2;Metallothionein-1G	0,87	-1,50
MYH9	Myosin-9	1,02	-4,70
MYL6;PDE6H	Myosin light polypeptide 6	0,85	-4,09
PALLD	Palladin	0,75	-2,04
PBDC1	Protein PBDC1	0,87	-1,81
PDLIM7	PDZ and LIM domain protein 7	0,88	-2,26
PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	0,57	-2,45
RAI14	Ankyrin	0,79	-2,46
RTCA	RNA 3-terminal phosphate cyclase	0,73	-2,13
STAT3	Signal transducer and activator of transcription 3;Signal transducer and activator of transcription	0,87	-1,58
TPM1	Tropomyosin alpha-1 chain	1,93	-2,90
TPM4	Tropomyosin alpha-4 chain	0,83	-2,21
TUBA1B	Tubulin alpha-1B chain	0,51	-1,97
TUBA4A	Tubulin alpha-4A chain	1,01	-2,58
TUBB	Tubulin beta chain	0,61	-2,02
TUBB2A	Tubulin beta-2A chain	0,52	-2,29
TUBB3	Tubulin beta-3 chain	0,99	-2,27
TUBB6	Tubulin beta-6 chain	1,05	-3,01
TUBB8	Tubulin beta-8 chain	0,56	-1,84
UPP1	Uridine phosphorylase 1	0,98	-1,98
YWHAB	14-3-3 protein beta/alpha;14-3-3 protein beta/alpha, N-terminally processed	1,01	-3,08
YWHAE	14-3-3 protein epsilon	0,80	-3,26
YWHAG	14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed	0,81	-2,76
YWHAQ	14-3-3 protein theta	0,60	-1,82
YWHAZ	14-3-3 protein zeta/delta	0,73	-2,50