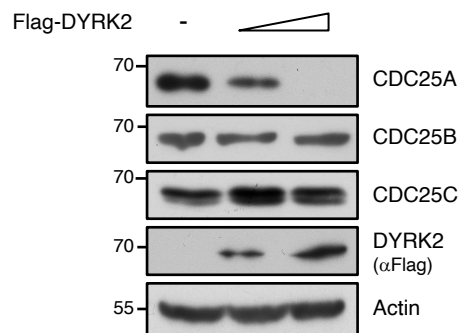
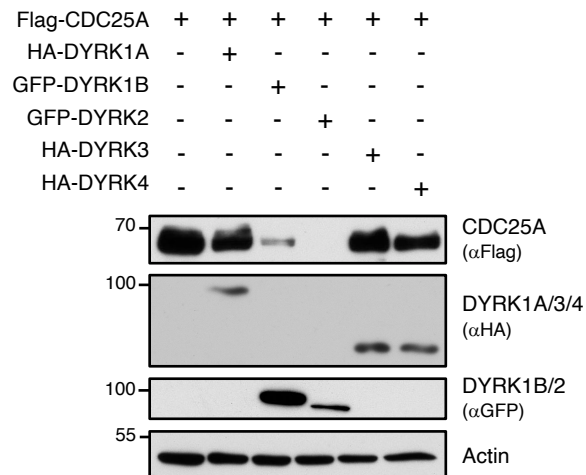
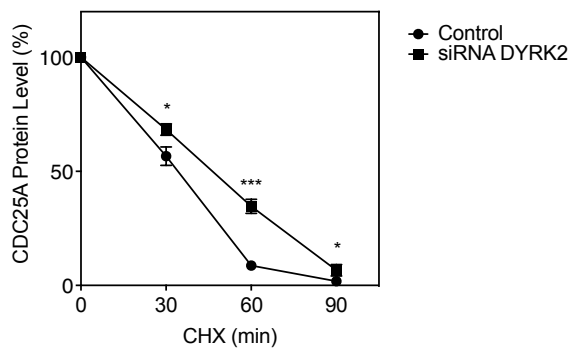
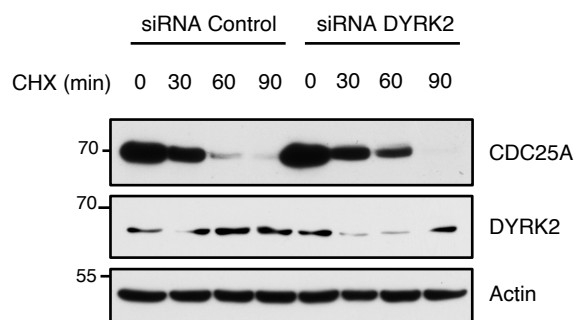
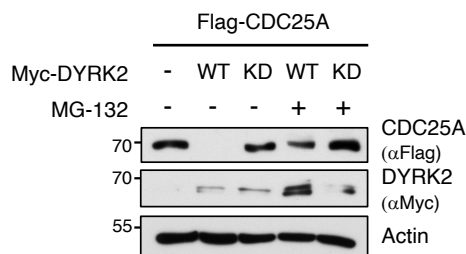
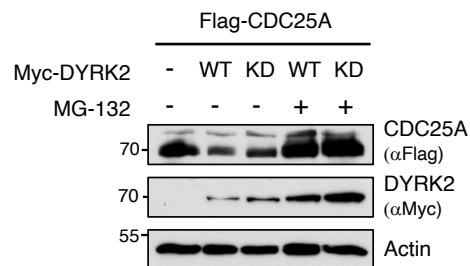
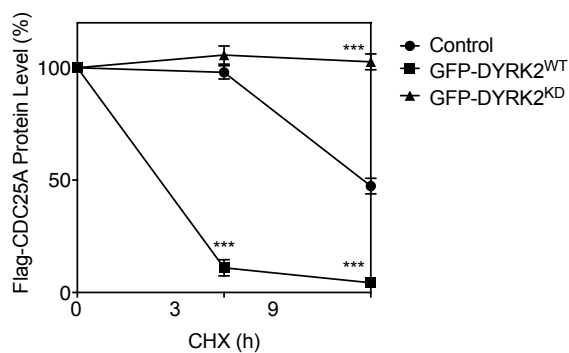
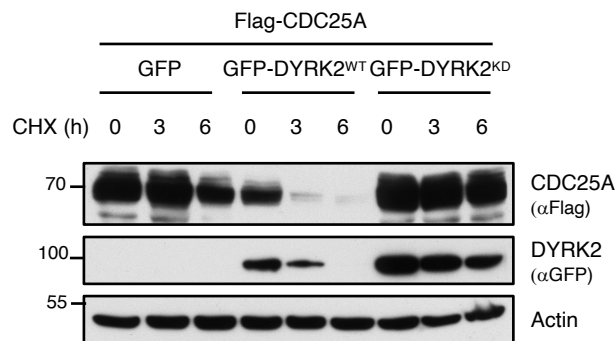
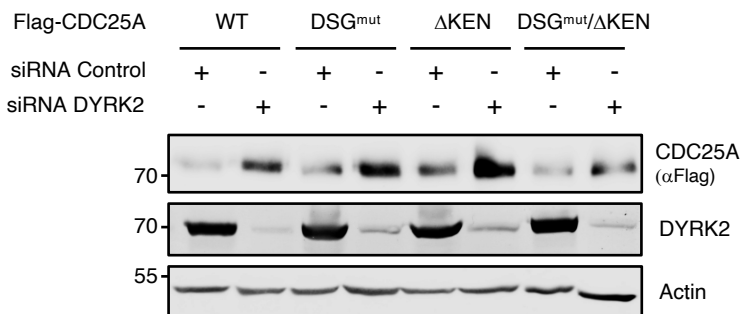


A**B****C**

A**B****C****D**

A

CDC25A

4 GPEPPHRRLLF
 PPHRRLLFACS
 RRRLLFACSPPP
 LLFACSPPPASQ
 ACSPPPASQPVV 27

337 LIGDFSKGYLFH
 DFSKGYLFHTVA
 KGYLEFHTVAGKH
 LFHTVAGKHQDL 357

373 FANLIKEFVIID
 LIKEFVIIDCRY
 EFVIIDCRYPYE
 IIDCRYPYEYEG
 CRYPYEYEGGHI 396

421 DGKRVIVVFHCE
 RVIVVFHCEFSS
 VVFHCEFSSEGR
 FSSERGPRMCRY
 ERGPRMCRYVRE
 PRMCRYVRERDR
 CRYVRERDR LGN 453

DYRK2

4 HLHVGSHAHGQI
 VGS SHAHQIQVQ
 HAHGQIQVQQLF
 GQIQVQQLFEDN
 QVQQLFEDNSNK
 QLFEDNSNKRTV 30

29 RTVLTTQPNGLT
 LTTQPNGLTTVG
 QPNGLTTVGKTG
 GLTTVGKTGLPV 48

81 TPEQAMKQYMOK
 QAMKQYMQKLT
 KQYMQKLTAFEH
 MQKLTAFEHHEI
 LTAFEHHEIFSY 105

112 GLNAKKRQGMTG
 AKKRQMTGGPN
 RQMTGGPNNGG
 MTGGPNNGGYDD
 GPNNGGYDDQGG
 NGGYDDDDQGSYV
 YDDDDQGSYVQVP
 DQGSYVQVPHDH
 SYVQVPHDHVAY
 QVPHDHVAYRYE 150

286 QGRSGIKVIDFG
 SGIKVIDFGSSC
 KVIDFGSSCYEH
 DFGSSCYEHQRV 306

328 MPIDMWSLGCIL
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 SLGCILAEILLT
 CILAEILLTGYPL 348

B

GFP-DYRK2

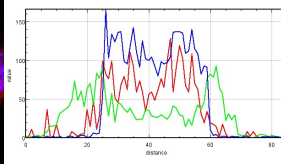
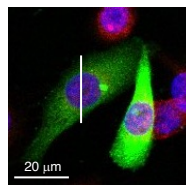
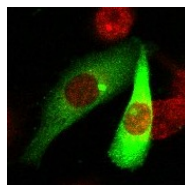
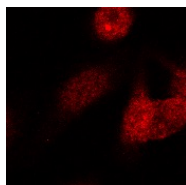
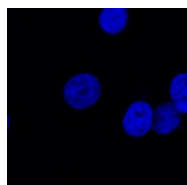
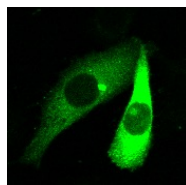
DAPI

CDC25A

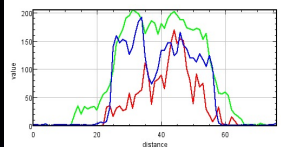
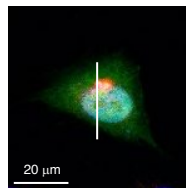
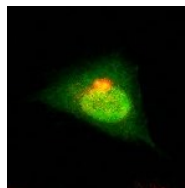
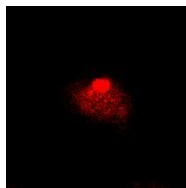
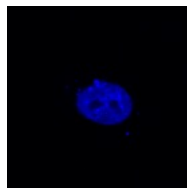
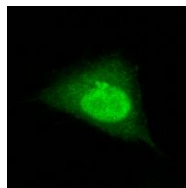
MERGE

RGB Profile

CONTROL



ETP



C

GFP-DYRK2

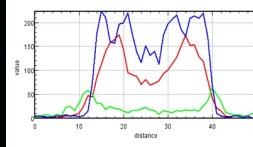
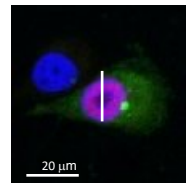
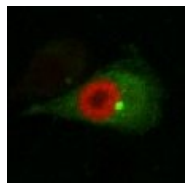
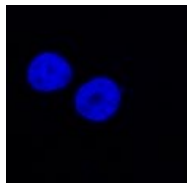
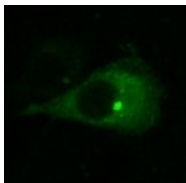
DAPI

FLAG-CDC25A

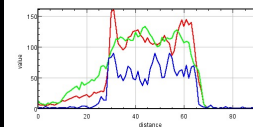
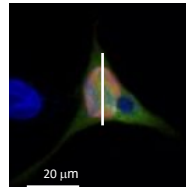
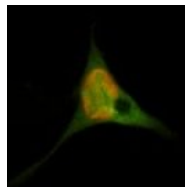
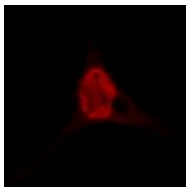
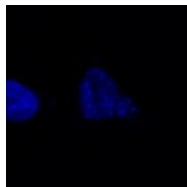
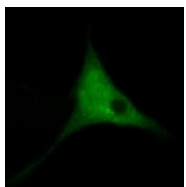
MERGE

RGB Profile

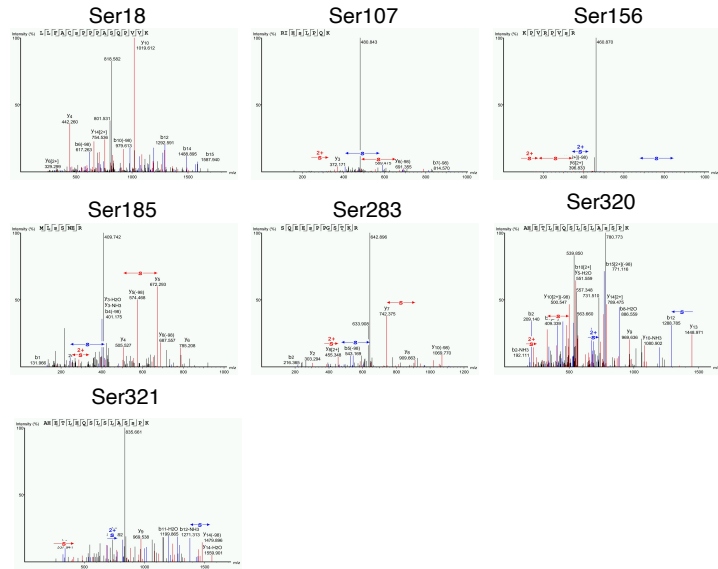
CONTROL

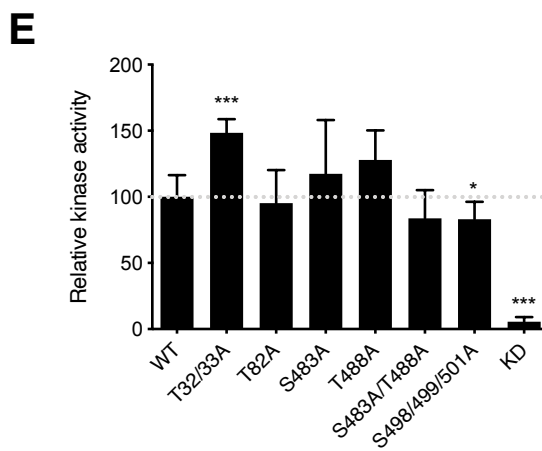
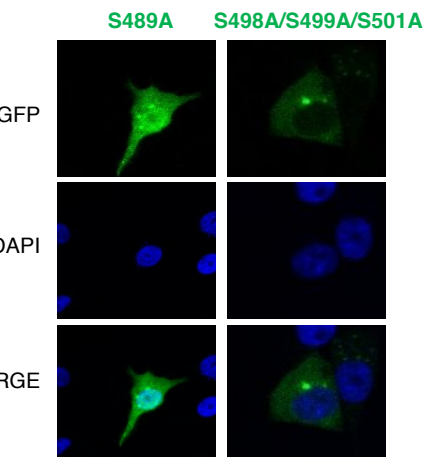
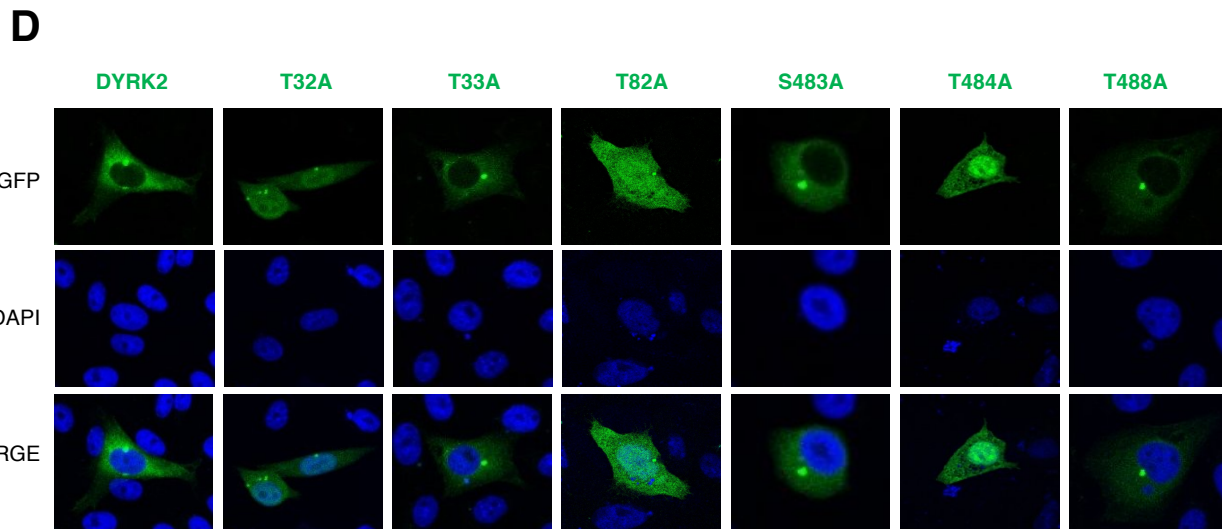
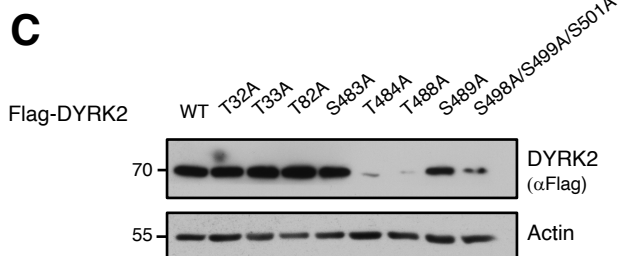
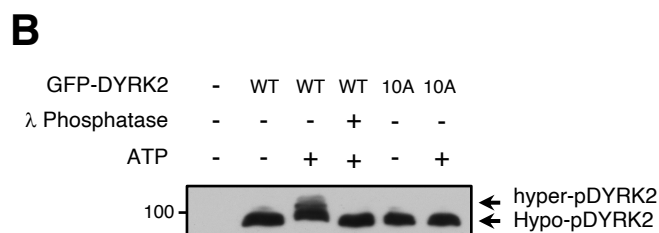
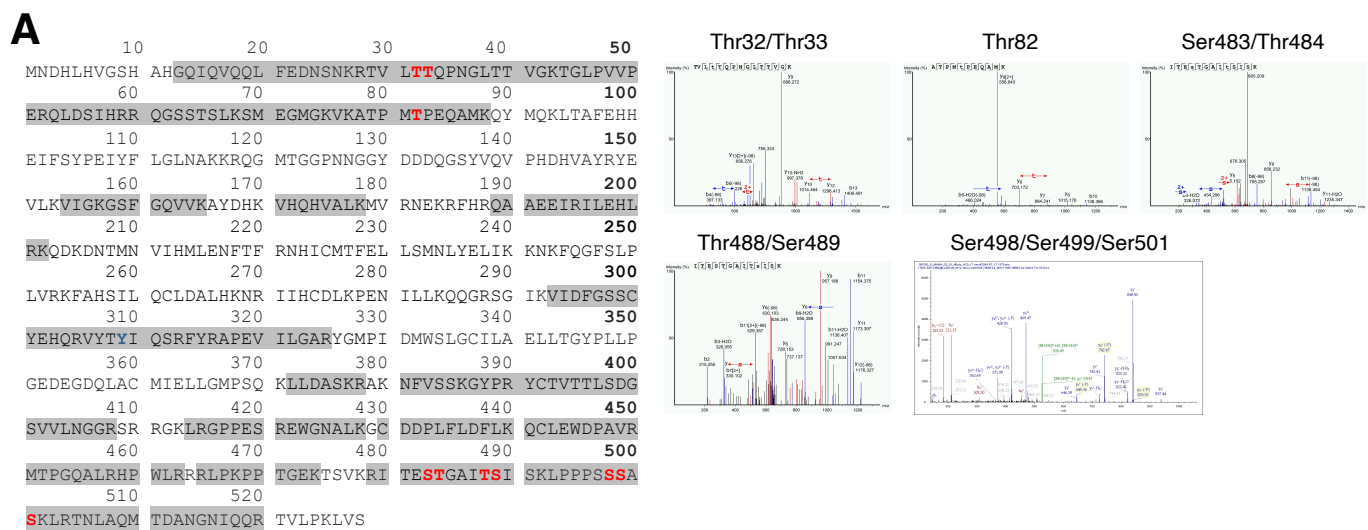


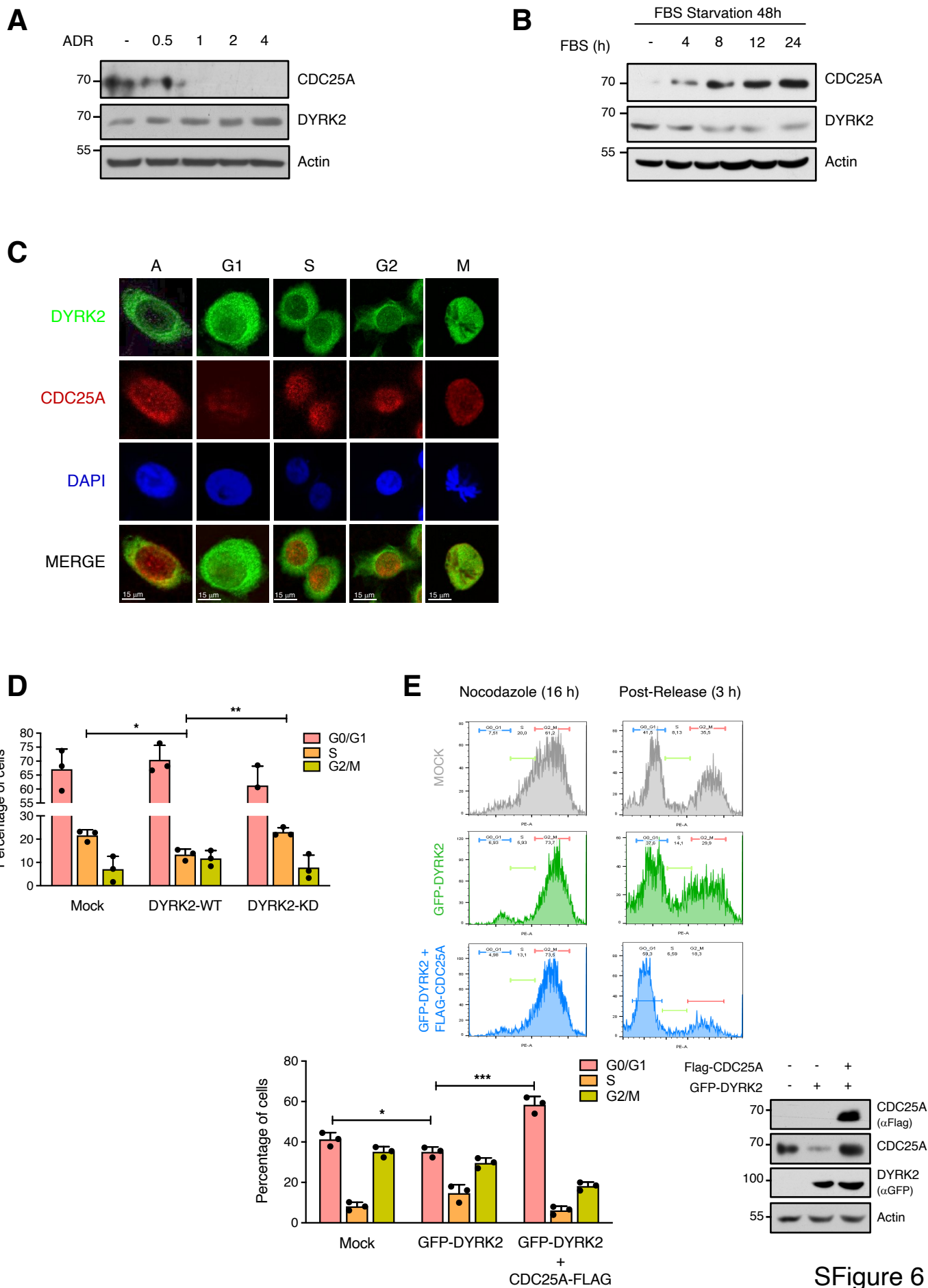
ETP



10	20	30	40	50
MELGPEPPHR	RRLLFAC	SPP	PASQPVVKAL	FGASAAGLS PVTNLIVTMD
60	70	80	90	100
QLQGLGSDYE	QPLEVKNSN	LQRMGSSEST	DSGFC	LDSPG PLDSKENLEN
110	120	130	140	150
PMRRIHSLPQ	KLLGCSPALK	RSHSDSLDHD	IFQLIDPDEN	KENEAFFFK
160	170	180	190	200
PVRPVSRGCL	HSHGLQEGKD	LFTQRONSAP	ARML	SSNERD SSEPGNFIFL
210	220	230	240	250
FTPQSPVTAT	LSDEDDGFVD	LLDGENLKNE	EETPSCMASL	WTAPLVMRTT
260	270	280	290	300
NLDNRCKLFD	SPSLCSSSTR	SVLKRPERSQ	EE	SPPGSTKR RKSMGASPK
310	320	330	340	350
ESTNPEKAHE	TLHQSLSLAS	SPKGTIENIL	DNDPRDLIGD	FSKGYLFHTV
360	370	380	390	400
AGKHQDLKYI	SPEIMASVLN	GKFANLIKEF	VIIDCRYPYE	YEGGHIKGA
410	420	430	440	450
NLMHEEEVED	FLKKPIVPT	DGKR	VIVVFH	CEFSSERGPR MCRYVRERDR
460	470	480	490	500
LGNEYPKLHY	PELYVLKGGY	KEFFMK	CQSY	CEPPSYRPMH HEDFKEDLKK
510	520			
FRTKSRTWAG	EKSKREMYSR	LKKL		

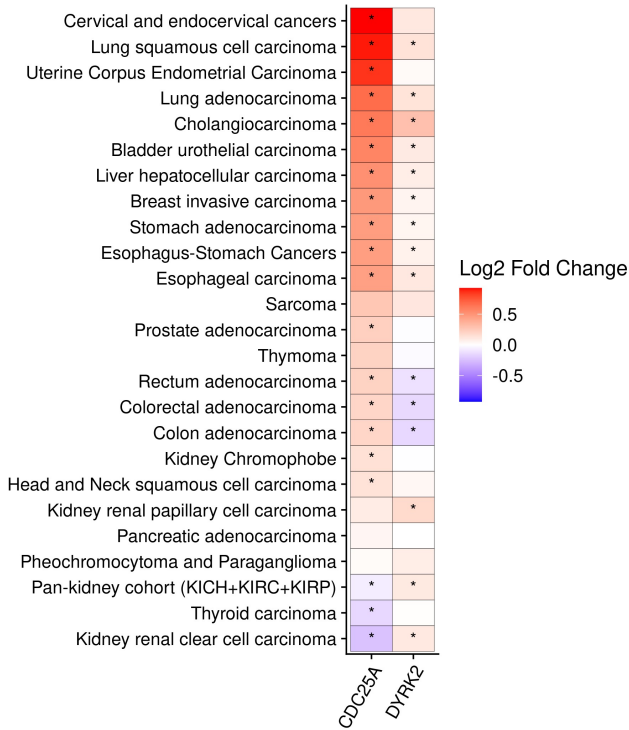






SFigure 6

A



B

