

**Fig. S1**

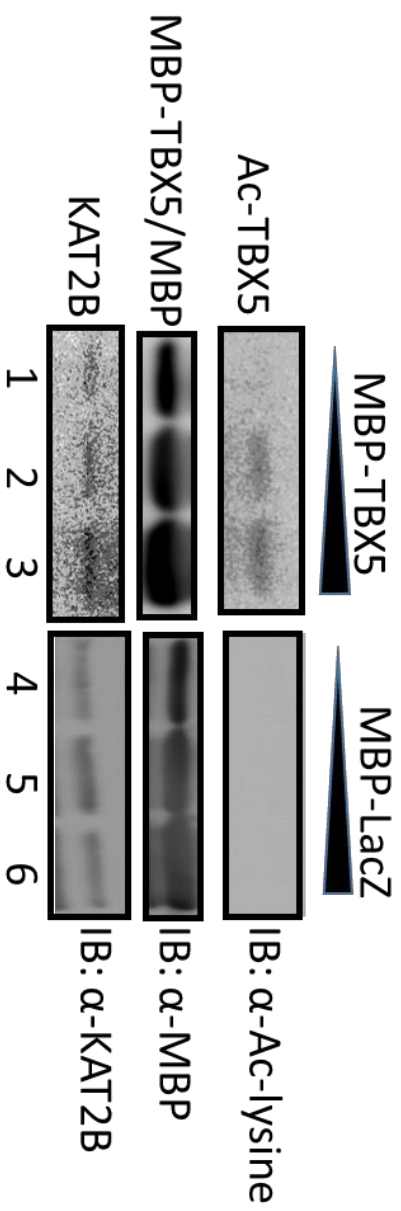


Fig. S2

A Prediction of acetylation residues by PredMod

Position	Confidence	Site
126	14	KWSYTGKAEFAMP
20	14	PLEPDAKDLPDCDS
234	12	ENNPFAKGFRRGSD
325	7	QIYHCTKRKKEEC
88	6	RMFPSPYKVKVTGL
221	5	TSYQNHKITQLKI

B

The online Acetylation predictor PHOSIDA  
<http://www.phosida.com>

Protein  
 TBX5

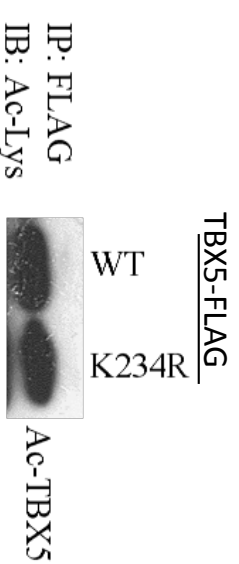
Predicted sites  
 K78 (91%), K157 (90%),  
 K234 (100%)

C

Prediction of acetylation sites by PALL (Prediction of acetylation on Internal Lysine)

Peptide	Position	Score	Threshold
PLEPDAKDLPDCDS	20	0.48	0.2
DLPCDSKPEASALG	27	0.98	0.2
ALGAPSKSPSSPQ	37	1.29	0.2
FPSYKVKVTGLNP	90	0.76	0.2
VSFQKLKLTNNHL	159	0.46	0.2
NNFGSKNTAFCT	197	0.51	0.2
ENNPFAKGFRRGSD	234	1.60	0.2
RSTVRQKVASNHS	266	0.89	0.2
TDHPYKPYMETS	340	0.61	0.2

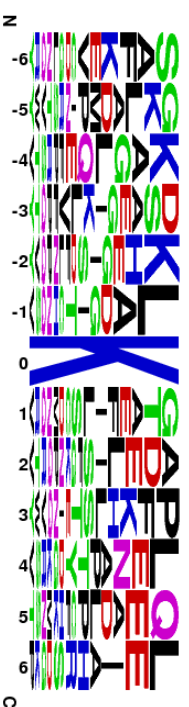
D



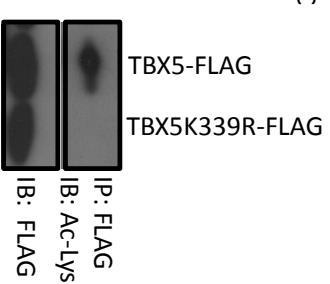
**A** KAT2B/2A Acetylation motif

P53 (NP\_000537) : 314-SSPQPKKKPLDGG-326  
 c/EBPβ (NP\_034013) : 95- YGAKPSKKPADYG-107  
 FOXO1 (NP\_062713) : 239-EGGKSGKSPRRRA-251  
 F111 (NP\_002008) : 374-TESSMYKYPSDIS-386  
 BUB1B (NP\_001202) : 244-RVGGALKAPSQNR-256  
 GAGA (NP\_001034015) : 319-PRAKRAKHPPGTE-231  
 MEF2C (NP\_002388) : 233-NKNNQAKSPPMN-245  
 Cyclin A (NP\_001228) : 89- PWRKANSKQPAFTI-101  
 Cyclin A (NP\_001228) : 106-AEKFAQKPAESQ-118  
 E2F1 (NP\_005216) : 114-HPGKGVKSPGERS-126  
 CTTA (NP\_000237) : 138-VGQKSQKRPFEE-150  
 MYOD (NP\_002469) : 96- WACKACKRKTTNA-108  
 KUT70 (NP\_001460) : 536-PEGKVTKRKHDFE-548  
 ERRalpha (NP\_004442) : 156-GRRGKYKRRPEVD-168  
 ERRalpha (NP\_004442) : 132-QACRFTKCLRVM-144  
 P65 (NP\_068810) : 308-TEKSIKTKKSPFS-320  
 Rb (NP\_000312) : 867-NPPKPLKLRFDI-879  
 CDK2 (NP\_001789) : 27-GEVVALKIRLDT-39  
 TALL1 (NP\_003180) : 215-PTHPPDKLISKNE-227  
 PTEN (NP\_000305) : 122-IHCKAGKGRGVM-134  
 IRF-2 (NP\_002190) : 72- PDPKTKANFRCA-84  
 EVI1 (NP\_001192123) : 558-TRRKDEKPLTPVP-570  
 PKM2 (NP\_002645) : 299-IEIPAEKVFLAQK-311  
 P38 (NP\_001306) : 146-IIHRDLKPSNLAV-158  
 P38 (NP\_001306) : 47- GLRVAVKKLSRPF-159

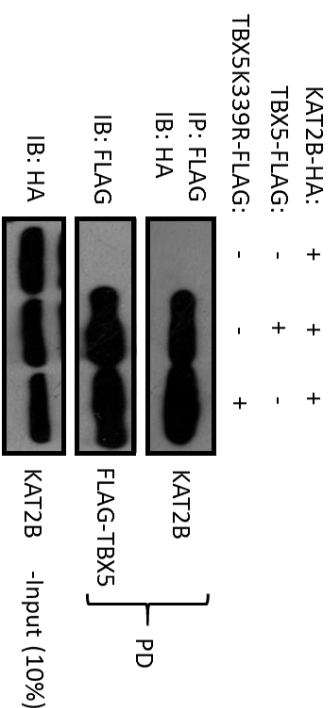
**B** Non-acetylated proteins



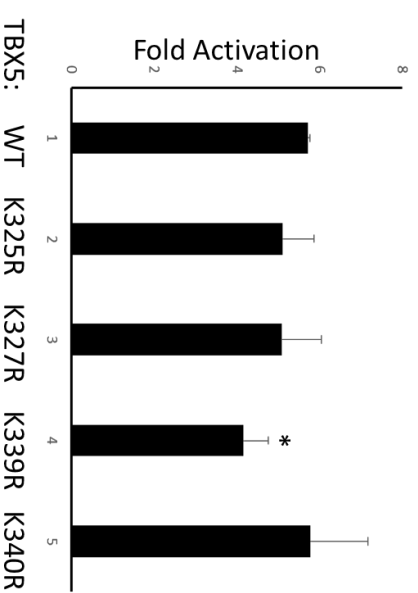
**C**



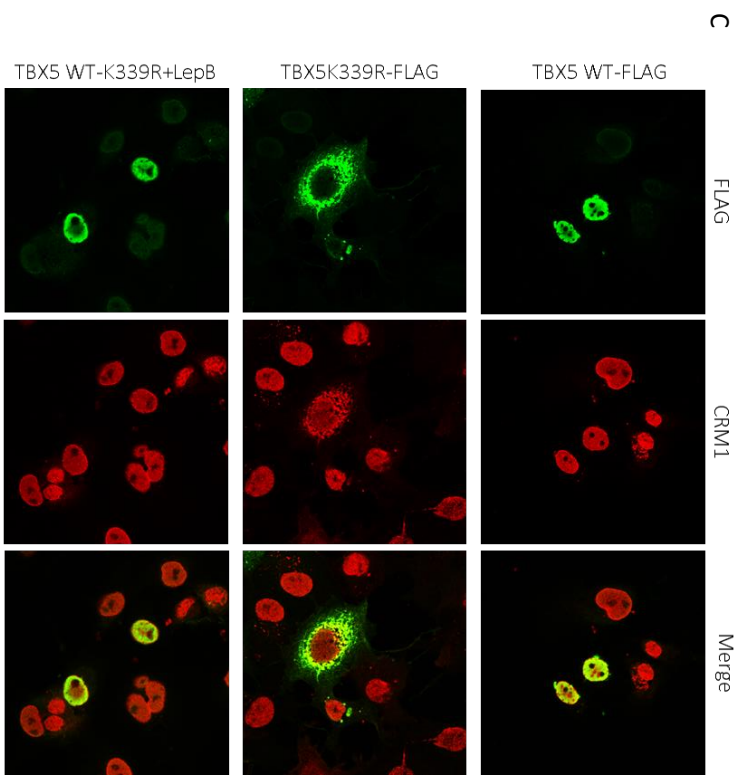
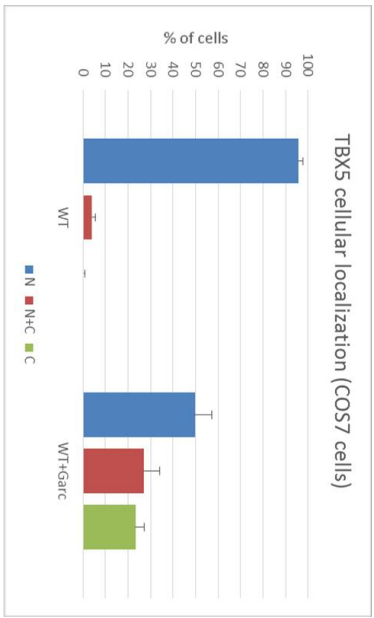
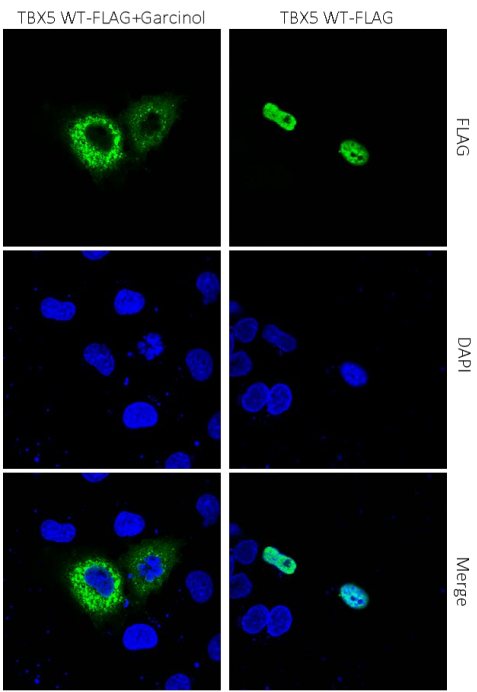
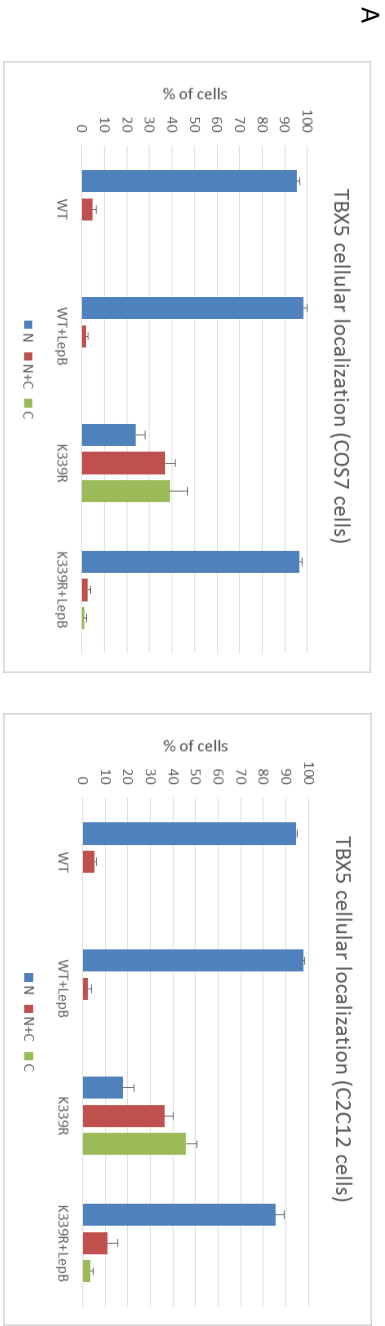
**D**



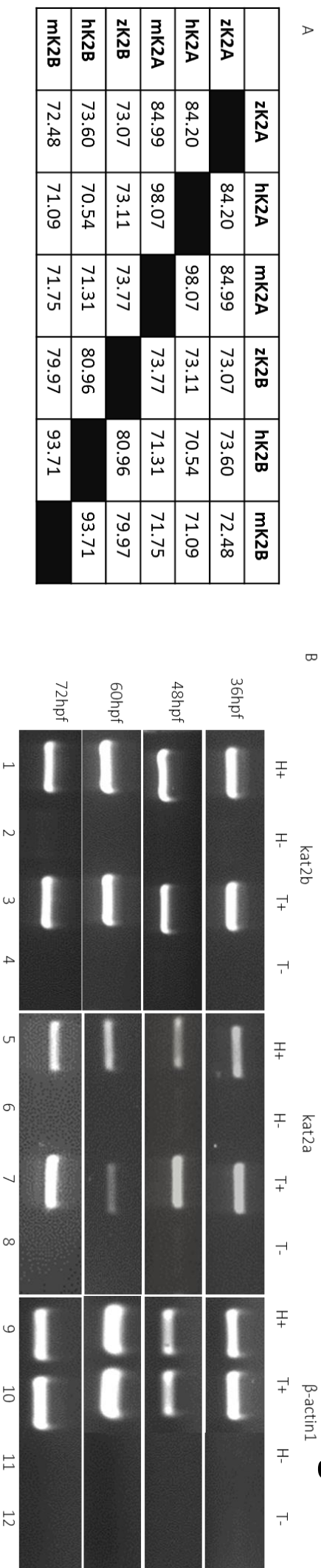
**E**

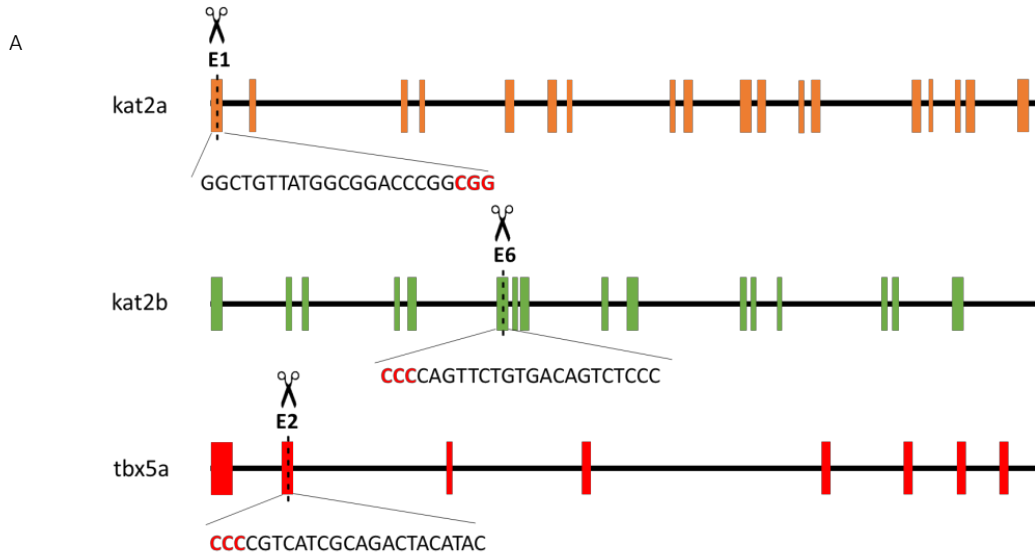


**Fig. S4**

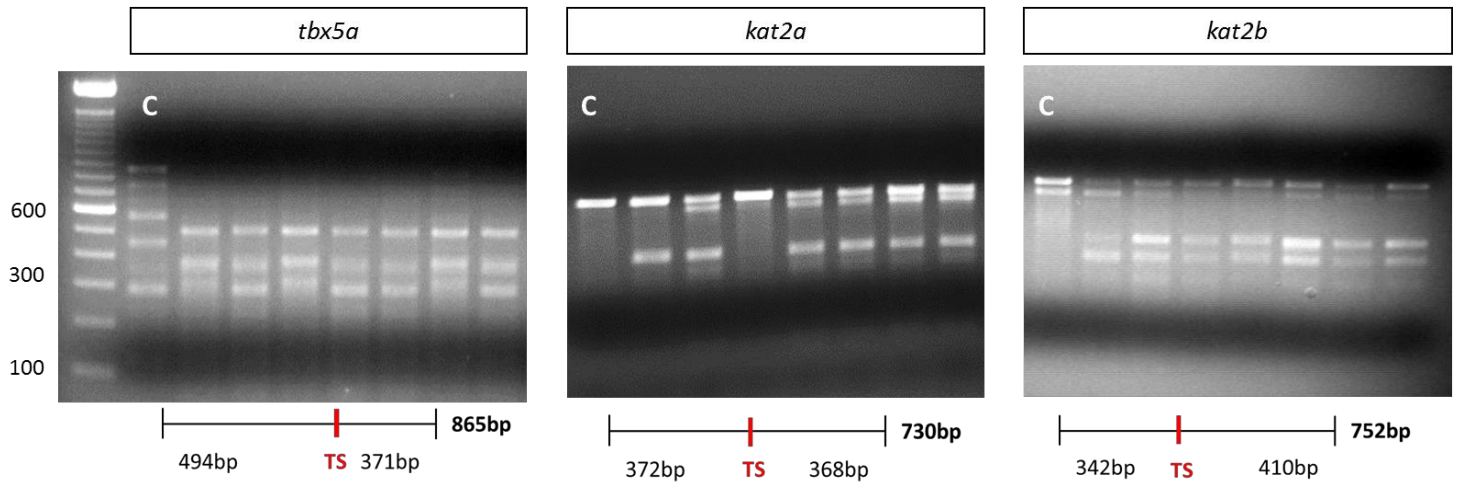


**Fig. S5**





B



C

	<i>kat2a</i> mild/severe	<i>kat2a</i> control	<i>kat2b</i> mild/severe	<i>kat2b</i> control	<i>tbx5a</i> mild/severe	<i>tbx5a</i> control
Embryos analyzed	40	20	40	20	40	20
Embryos harbouring mutations	38 (95%)	1 (5%)	39 (98%)	2 (10%)	40 (100%)	1 (5%)
Rate of mutagenesis	88%	25%	79%	30%	82%	20%