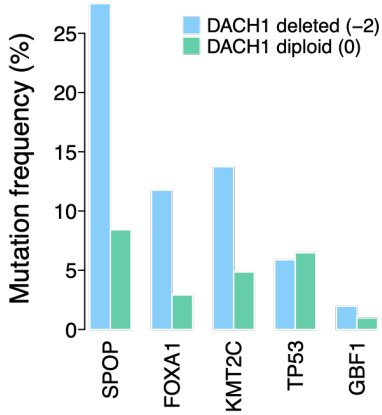


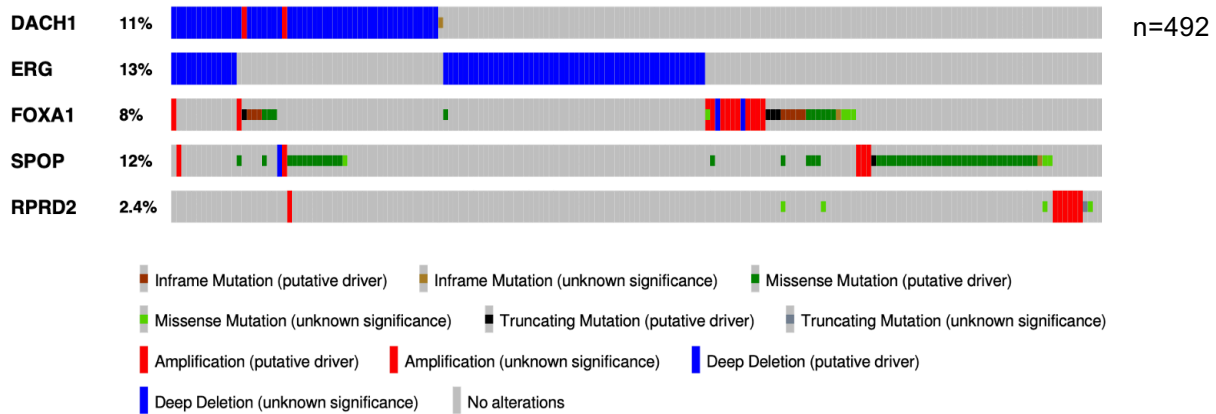
**A**



DACH1 SCNA	-2	-1	0	1	2	Sum
Samples	51	126	309	4	2	492
	Del		Dip			

	DACH1 Del (n=51)	DACH1 diploid (n=309)	p val Fisher test	p.adj (Bonf)
SPOP	14	26	0.0023	0.012
FOXA1	6	9	0.0158	0.079
KMT2C	7	15	0.0583	0.29
TP53	3	20	1.0	1.0
GBF1	1	3	0.4617	1.0

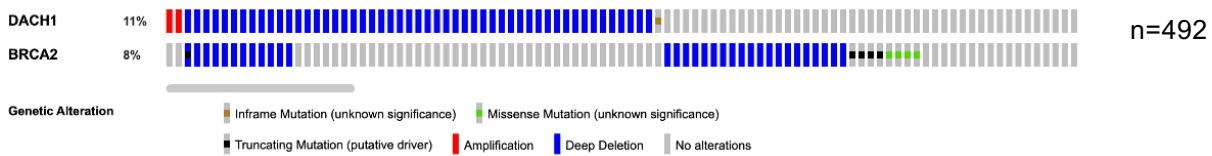
**B**



**C**

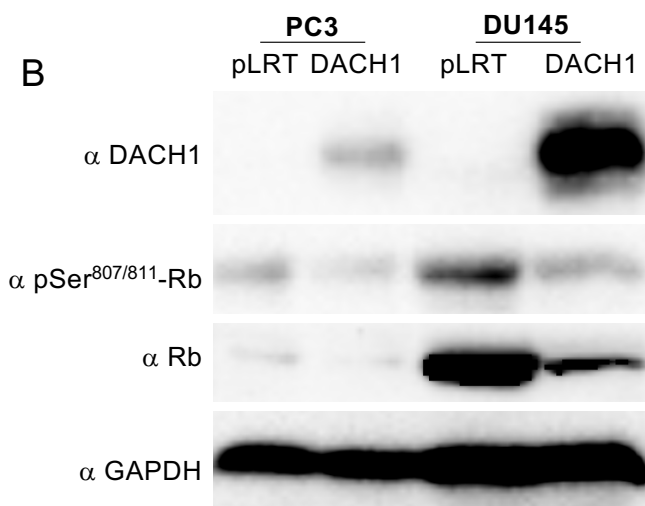
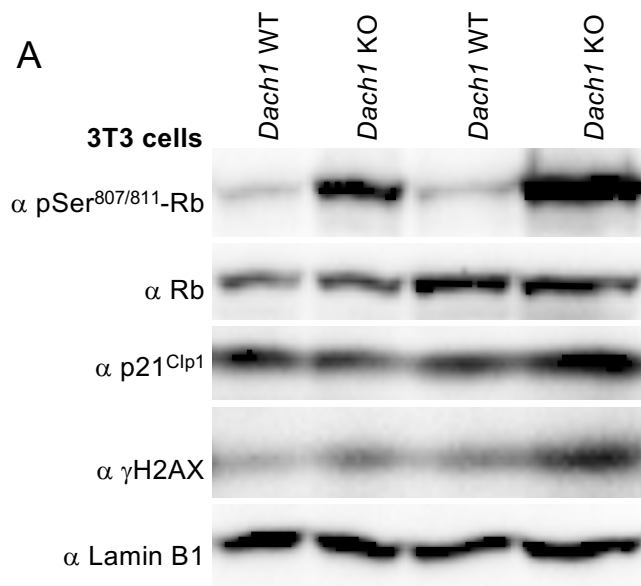
A	B	Neither	A Not B	B Not A	Both	Log2 Odds Ratio	p-Value	q-Value	Tendency
DACH1	ERG	386	41	52	13	1.235	0.015	0.051	Co-occurrence
	FOXA1	407	45	31	9	1.393	0.022	0.054	Co-occurrence
	SPOP	394	37	44	17	2.041	<0.001	<0.001	Co-occurrence
	RPRD2	427	53	11	1	-0.449	0.613	0.613	Mutual exclusivity
ERG	FOXA1	389	63	38	2	-1.622	0.078	0.156	Mutual exclusivity
	SPOP	367	64	60	1	<-3	0.001	0.006	Mutual exclusivity
FOXA1	RPRD2	415	65	12	0	<-3	0.179	0.256	Mutual exclusivity
	SPOP	398	33	54	7	0.645	0.214	0.267	Co-occurrence
SPOP	RPRD2	442	38	10	2	1.218	0.254	0.282	Co-occurrence
RPRD2	SPOP	422	58	9	3	1.278	0.177	0.256	Co-occurrence

**D**

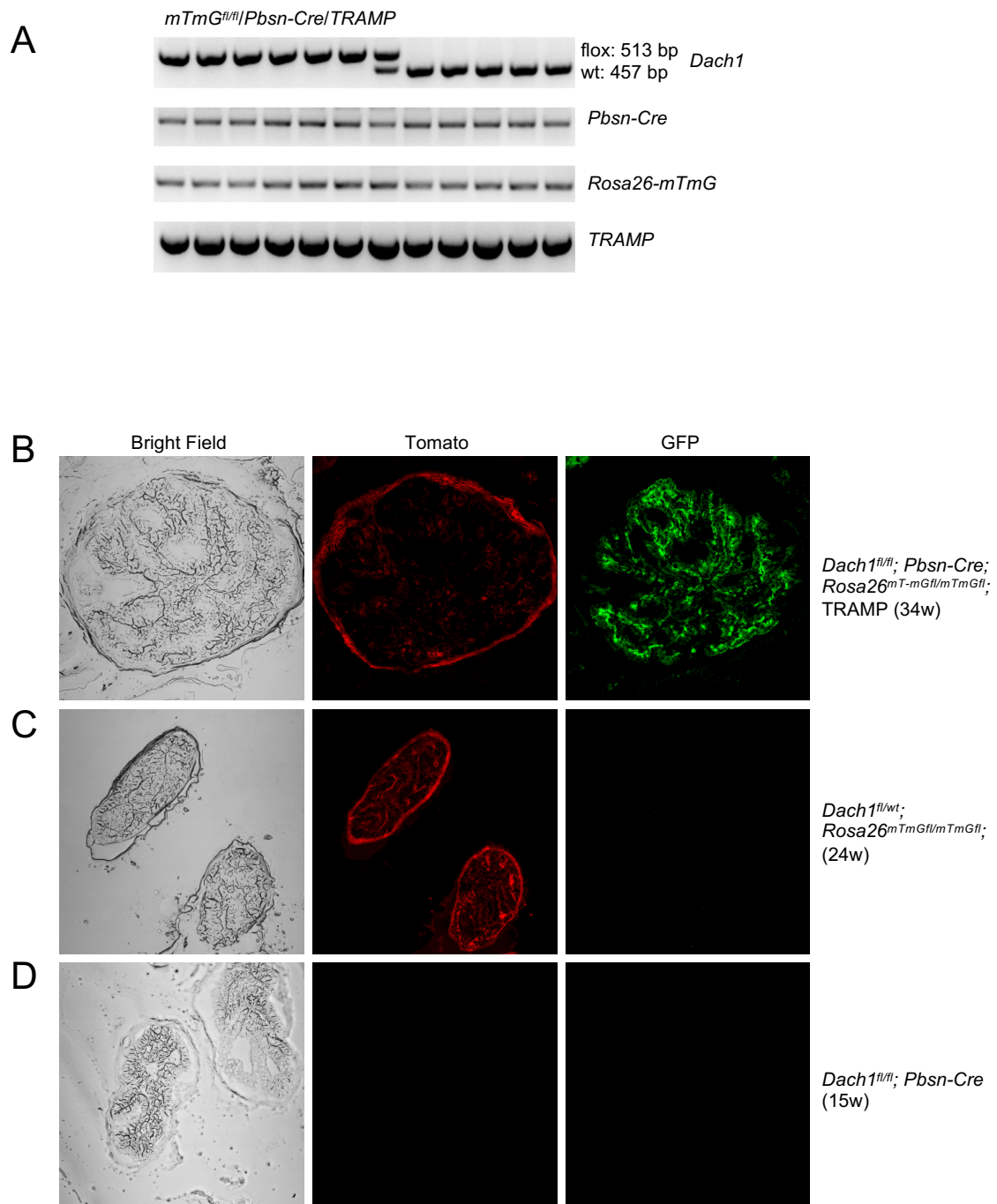


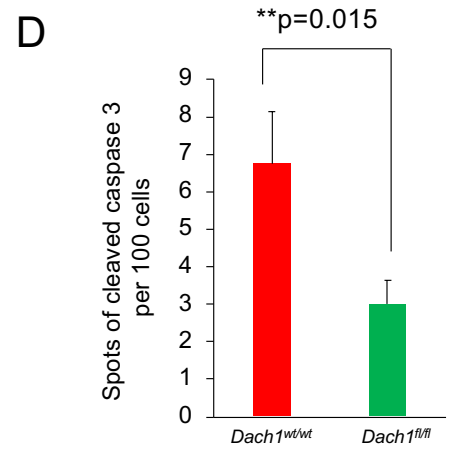
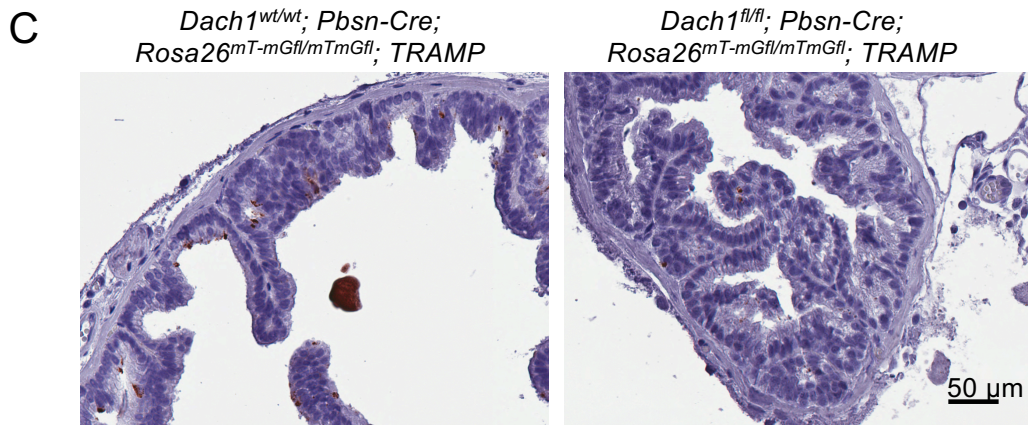
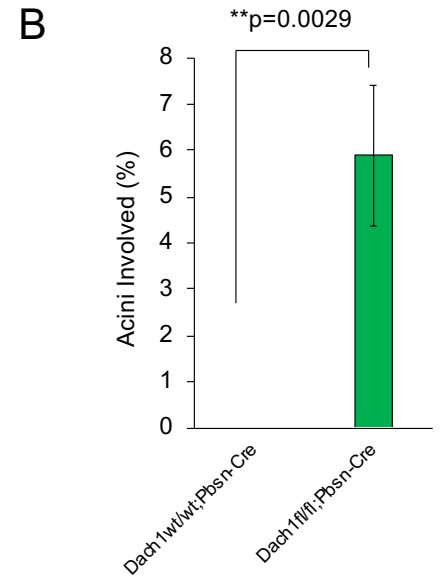
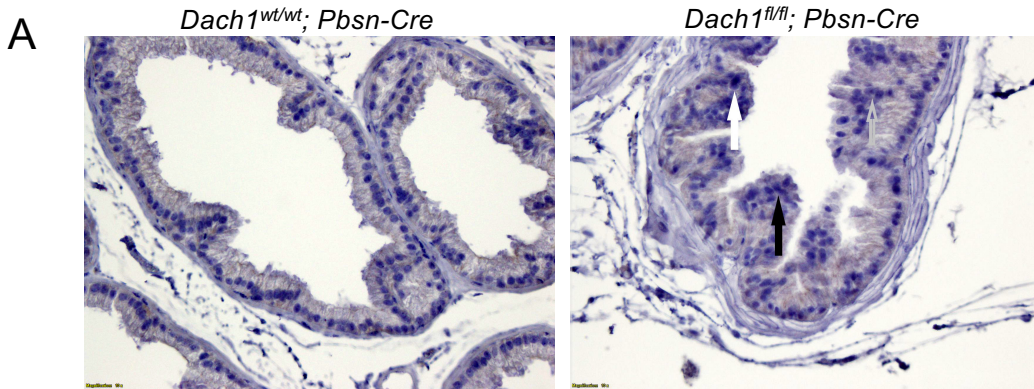
A	B	Neither	A Not B	B Not A	Both	Log2 Odds Ratio	p-Value	q-Value	Tendency
DACH1	BRCA2	410	42	28	12	2.065	<0.001	0.007	Co-occurrence

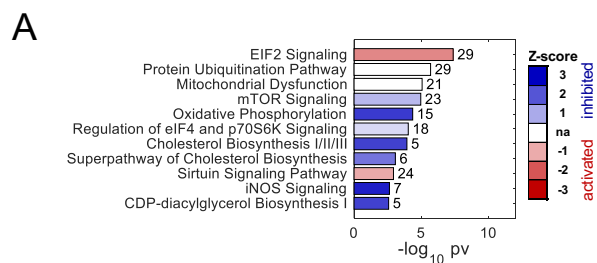






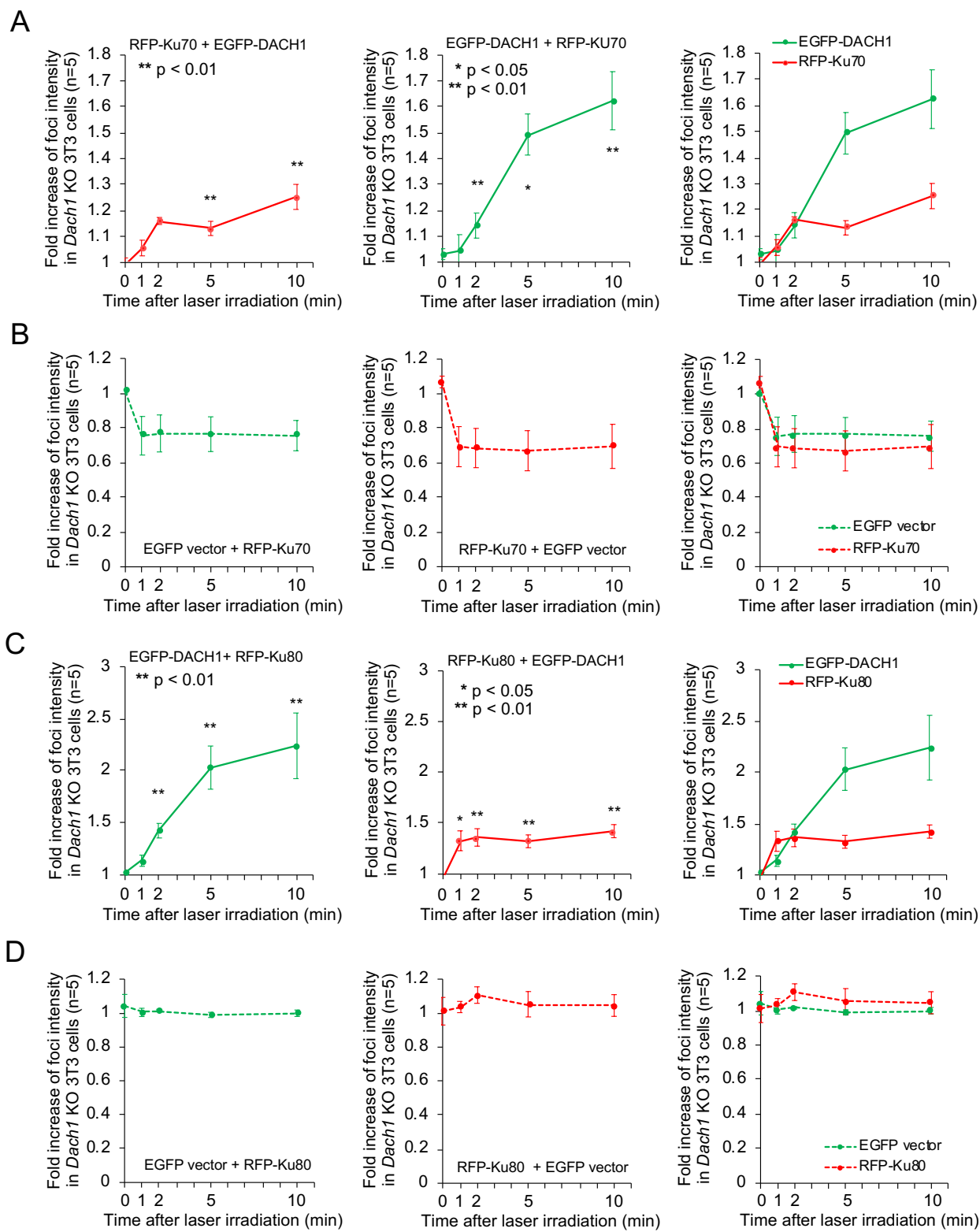


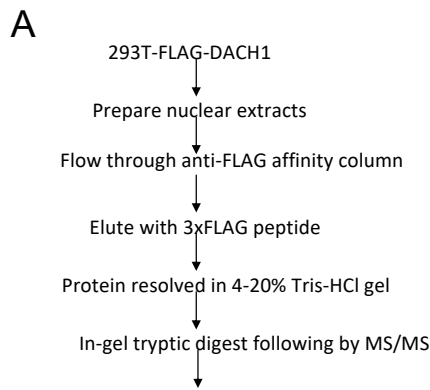




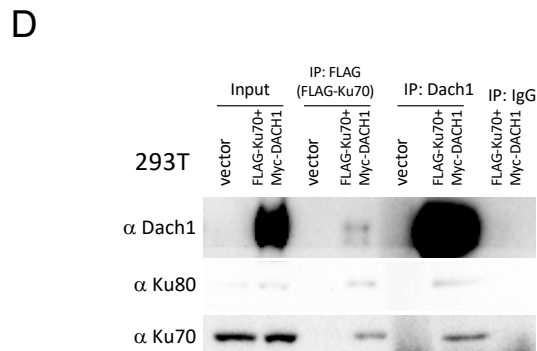
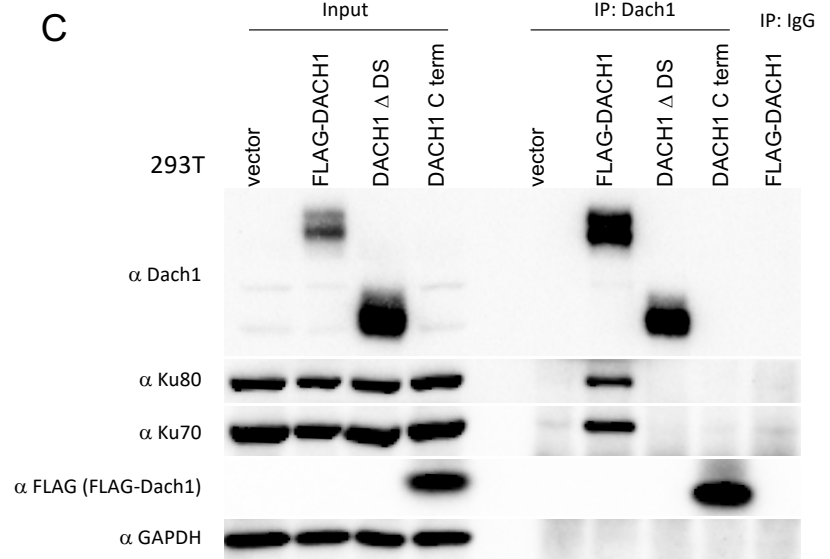
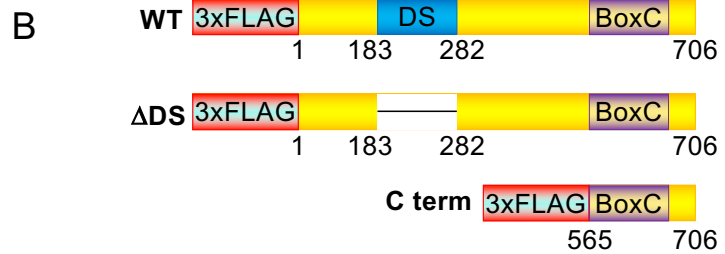
**B**

Canonical Pathway	<i>p</i>	WT/KO Z	N
EIF2 Signaling	4.27E-08	1.41	29
Protein Ubiquitination Pathway	2.04E-06	NaN	29
Mitochondrial Dysfunction	8.71E-06	NaN	21
mTOR Signaling	1.1E-05	-0.83	23
Oxidative Phosphorylation	4.37E-05	-2.32	15
Regulation of eIF4 and p70S6K Signaling	9.33E-05	-0.45	18
Cholesterol Biosynthesis I	0.000117	-2.24	5
Cholesterol Biosynthesis II (via 24,25-dihydrocholesterol)	0.000117	-2.24	5
Cholesterol Biosynthesis III (via Desmosterol)	0.000117	-2.24	5
Superpathway of Cholesterol Biosynthesis	0.000851	-1.63	6
Sirtuin Signaling Pathway	0.001175	1	24
iNOS Signaling	0.002344	-2.65	7
CDP-diacylglycerol Biosynthesis I	0.002692	-2.24	5





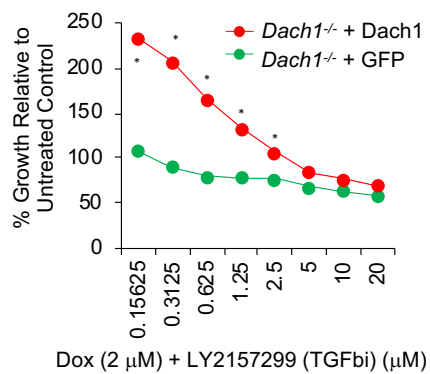
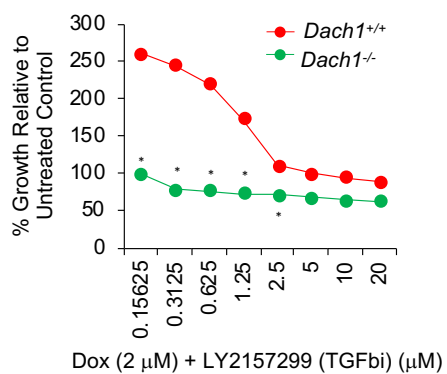
11	C2	ATP-dependent DNA helicase 2 subunit 2 (EC 3.6.1.-) (ATP-dependent DNA helicase II 80 kDa subunit)
15	G2	ATP-dependent DNA helicase 2 subunit 1 (ATP-dependent DNA helicase II 70 kDa subunit) (Lupus Ku aut)



**E**

Kinase Predictor V2 Score	Human Kinase Short Name	Human UniProt. ID	Kinase Predictor V2 Score - Proximity
639	ERK1	P27361	1440
629	ERK2 (MAPK1)	P28482	1439
596	JNK1 (MAPK8)	P45983	1367
596	JNK3 (MAPK10)	P53779	1367
594	ERK5 (MAPK7)	Q13164	1347
590	p38g MAPK (MAPK1)	P53778	1337
580	CDK2	P24941	1327
578	p38a MAPK (MAPK1)	Q16539	1326
578	CDK1 (CDC2)	P06493	1319
575	JNK2 (MAPK9)	P45984	1316
575	p38d MAPK (MAPK1)	Q15264	1313
561	CDKL5 (STK9)	Q76039	1299
557	CDK3	Q00526	1284
552	p38b MAPK (MAPK1)	Q15759	1278

A



B

