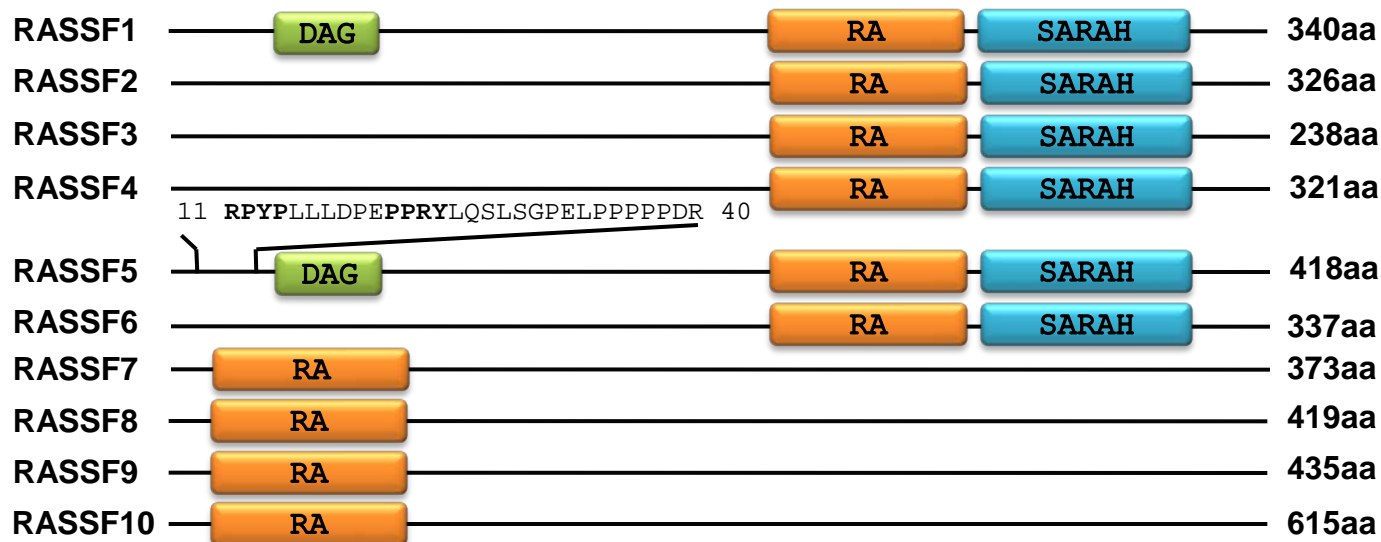


Supplementary Figure 1

A



B

Sequence alignment of RASSF5 DAG domain across three samples (F5A, F5B, F5C). The alignment shows conserved residues and a gap in F5C.

```

F5A MAMASPAIGQRRPYPLLLDPEPPRYLQSLSGPELPPPPDRSSRLCVPAPLSTAPGAREGRSARRAARGNLEPPPRASRPARPLRPGLQQLRRRPGAPRPRDVR SIFEQPDPRVPAERG 120
F5B MAMASPAIGQRRPYPLLLDPEPPRYLQSLSGPELPPPPDRSSRLCVPAPLSTAPGAREGRSARRAARGNLEPPPRASRPARPLRPGLQQLRRRPGAPRPRDVR SIFEQPDPRVPAERG 120
F5C -----MTVDSSMS----- 8

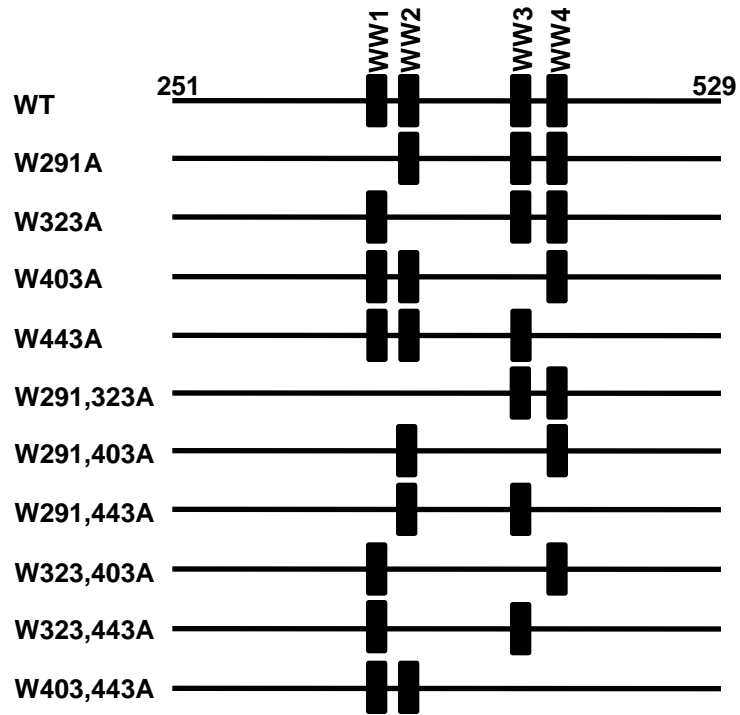
F5A EGHCF AELVLPGGPGWCDL CGREVL RQALR CTNCKFTCHPECRSLIQLD CSQQEGLSRDRPSP ESTLTVTF S QNVCKPVEETQR PPTLQEIKQKIDSYNTREKNCLGMKLS EDGTYTGFI 240
F5B EGHCF AELVLPGGPGWCDL CGREVL RQALR CTNCKFTCHPECRSLIQLD CSQQEGLSRDRPSP ESTLTVTF S QNVCKPVEETQR PPTLQEIKQKIDSYNTREKNCLGMKLS EDGTYTGFI 240
F5C -----SGYCSLD--EELED CFFTAKTTFFRNAQSK-----HLSKNVCKPVEETQR PPTLQEIKQKIDSYNTREKNCLGMKLS EDGTYTGFI 87

F5A KVHLKLR RPVTVPAGIR PQSIYDAI KEVNLAATTDKRTS FYLPLDAIKQLHISSTTTVSEVIQGLLKKFMVVDNPQKFALFKRIHKDGVLFQKLSIADRPLYLRLLAGPDTEVLSFVLK 360
F5B KVHLKLR RPVTVPAGIR PQSIYDAI KEVNLAATTDKRTS FYLPLDAIKQLHISSTTTVSEVIQGLLKKFMVVDNPQKFALFKRIHKDGVGCLLHP----- 336
F5C KVHLKLR RPVTVPAGIR PQSIYDAI KEVNLAATTDKRTS FYLPLDAIKQLHISSTTTVSEVIQGLLKKFMVVDNPQKFALFKRIHKDGVLFQKLSIADRPLYLRLLAGPDTEVLSFVLK 207

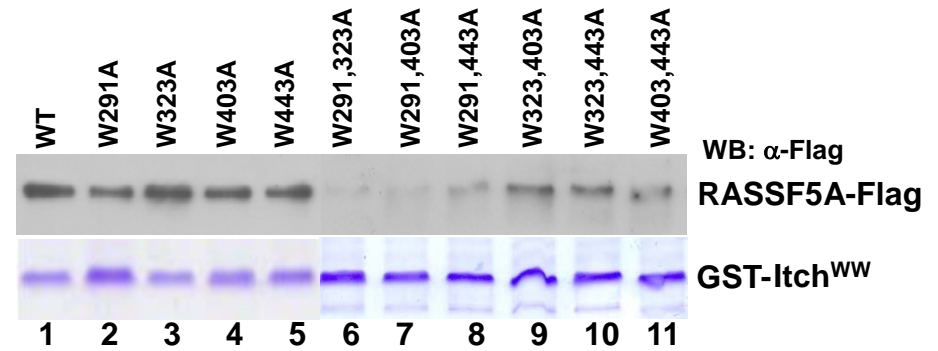
F5A ENETGEVEWDAFSIPELQNFLTILEKEEQDKIQVQKKYDKFRQKLEEALRESQ GKPG 418
F5B ----- 418
F5C ENETGEVEWDAFSIPELQNFLTILEKEEQDKIQVQKKYDKFRQKLEEALRESQ GKPG 265
  
```

Supplementary Figure 2

A

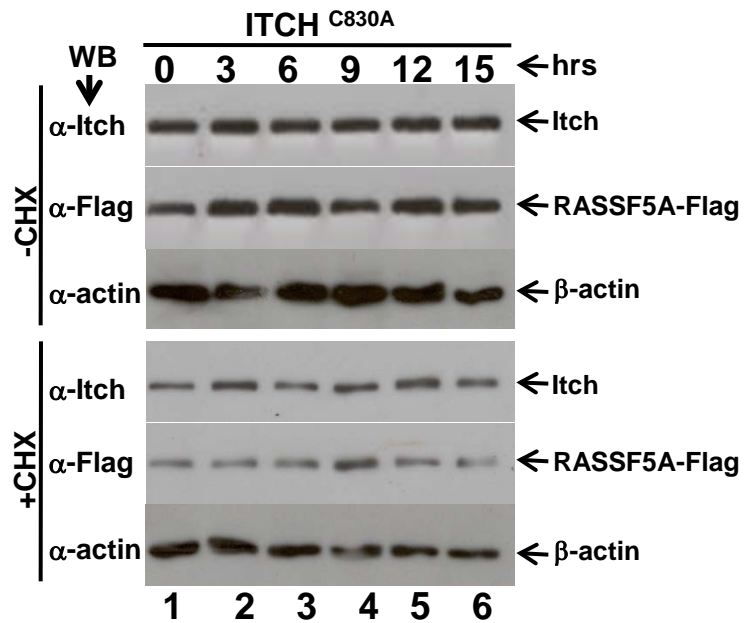


B

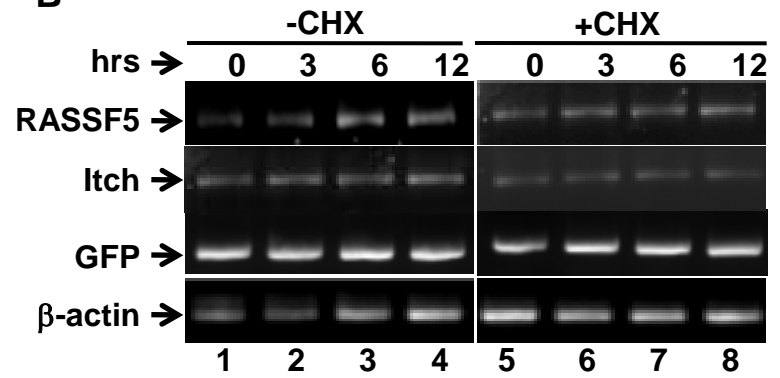


Supplementary Figure 3

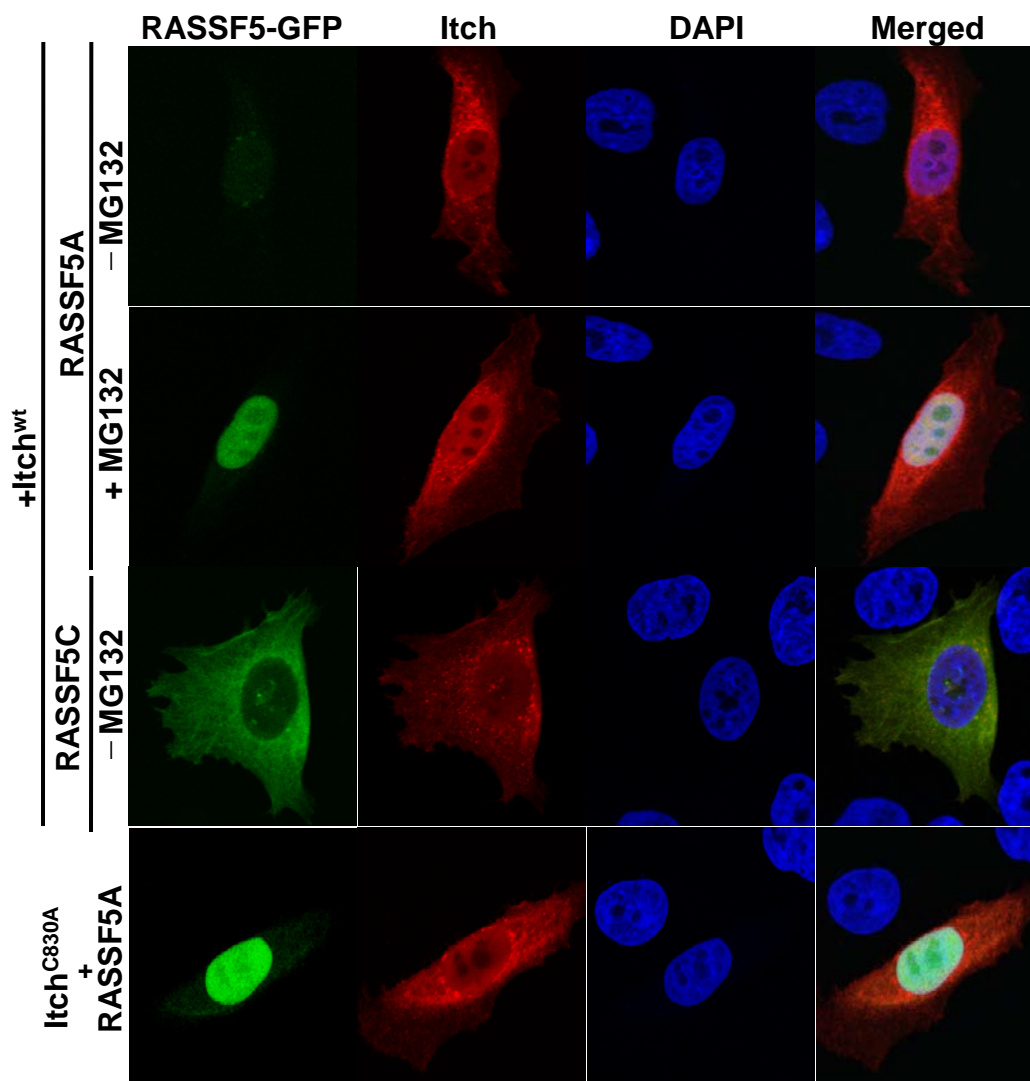
A



B



Supplementary Figure 4

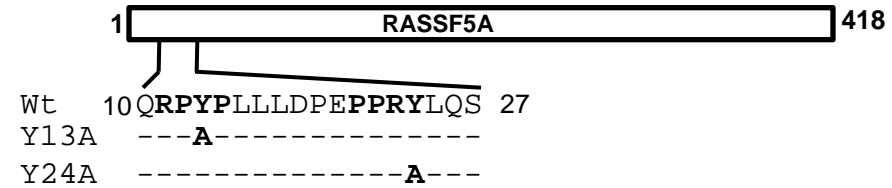


Supplementary Figure 5

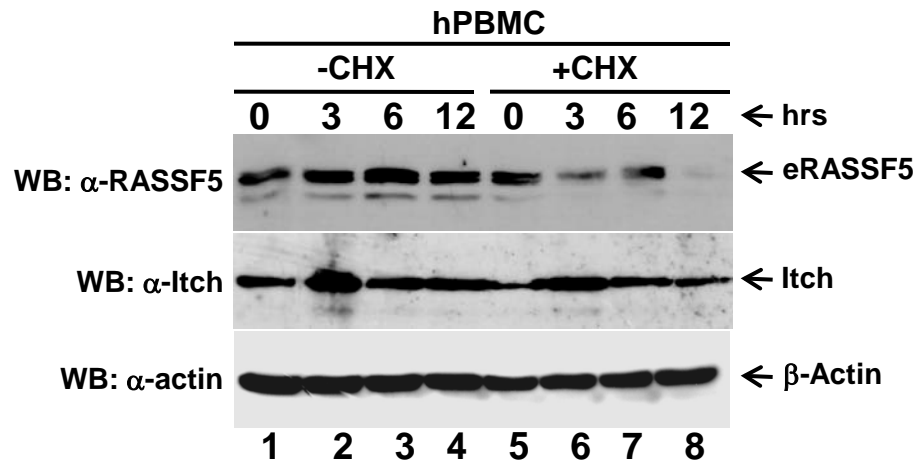
A

			↓ ↓ ↓		
p73	: 419	QLLQRPSHLQ	PPSY	GPVLSPMNKV	442
c-Jun	: 157	GGFSASLHSE	PPVY	ANLSNFNPGA	180
LATS-1	: 363	VPAGTVNRQF	PPPY	PLTAANGQSP	386
	: 549	VAEAPNYQGF	PPPY	PKHLLHQNPS	569
P63	: 530	SMPSTSHCTF	PPPY	PTDCSIVSFL	553
SMAD1	: 214	SPFQMPADTF	PPAY	LPPEDPMTQD	237
EBBR4	:1022	YLVPQAFNIE	PPIY	TSRARIDSNR	1045
	:1043	SNRSEIGHSE	PPAY	TPMSGNQFVY	1066
	:1288	FSLKPGTVLE	PPPY	RHRNTVV	1308
RUNX1	: 345	GSATRYHTYL	PPPY	PGSSQAQGGP	368
WBP2	: 187	DGAMGYVQPF	PPPY	PGPMEPPVSG	210
	: 239	NVYMPTSQPE	PPPY	YPPEDKKT	260
RASSF5	: 11	RPYPLLLDPE	PPRY	LQSLSGPELP	34

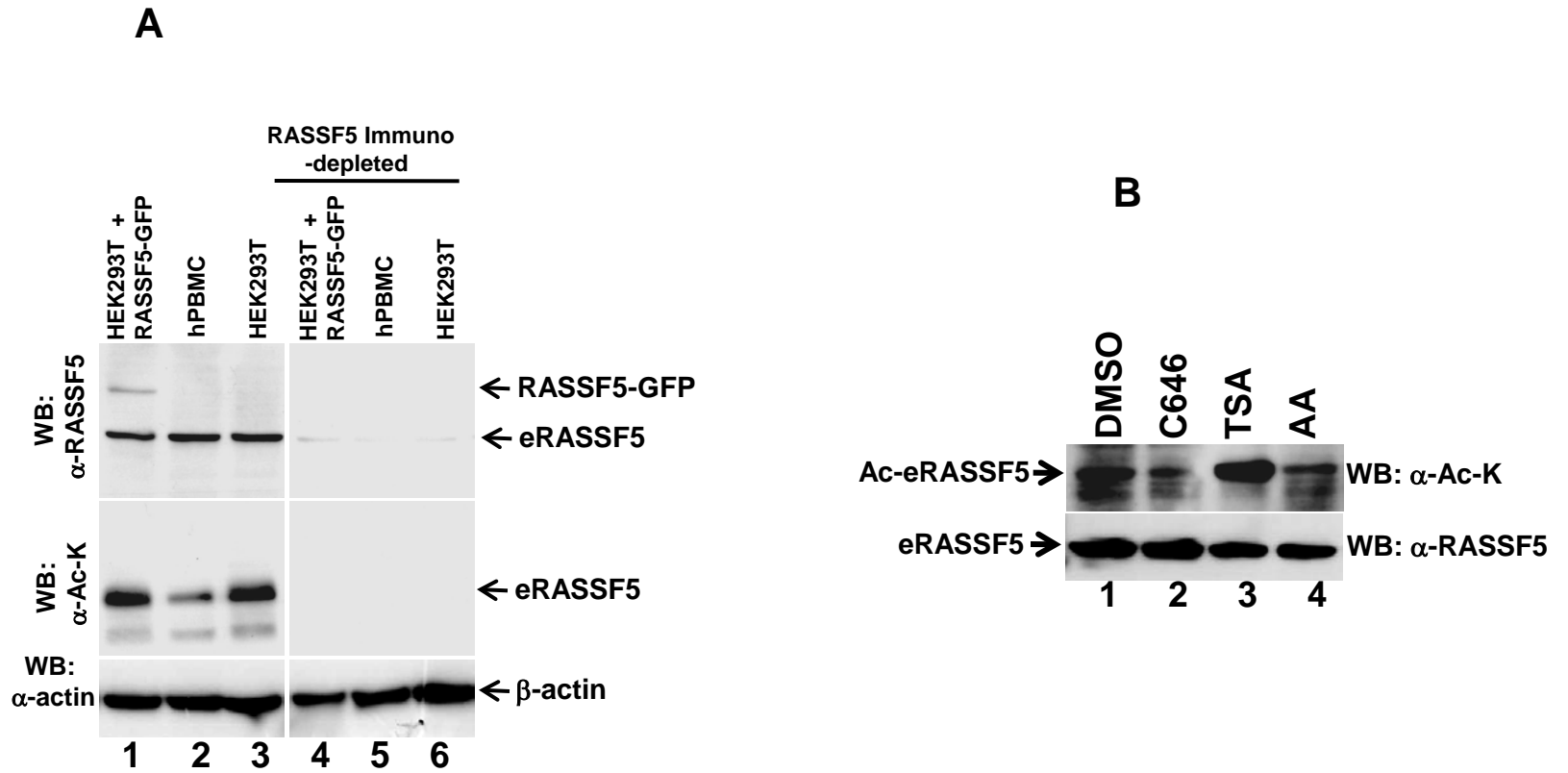
B



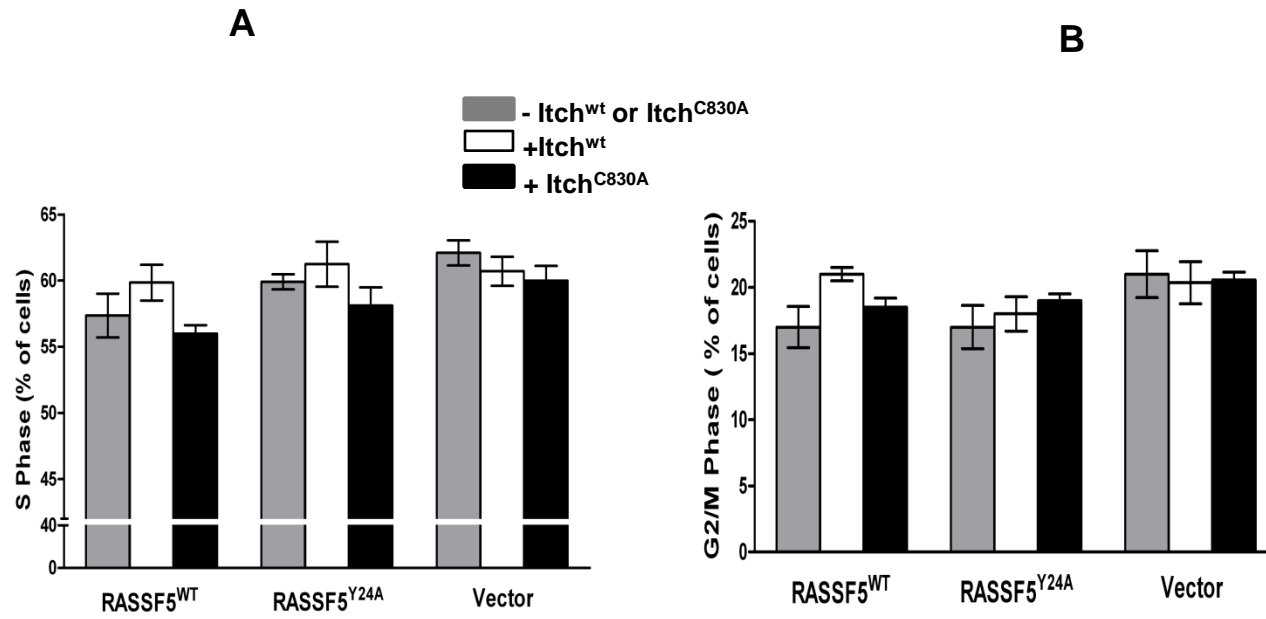
Supplementary Figure 6



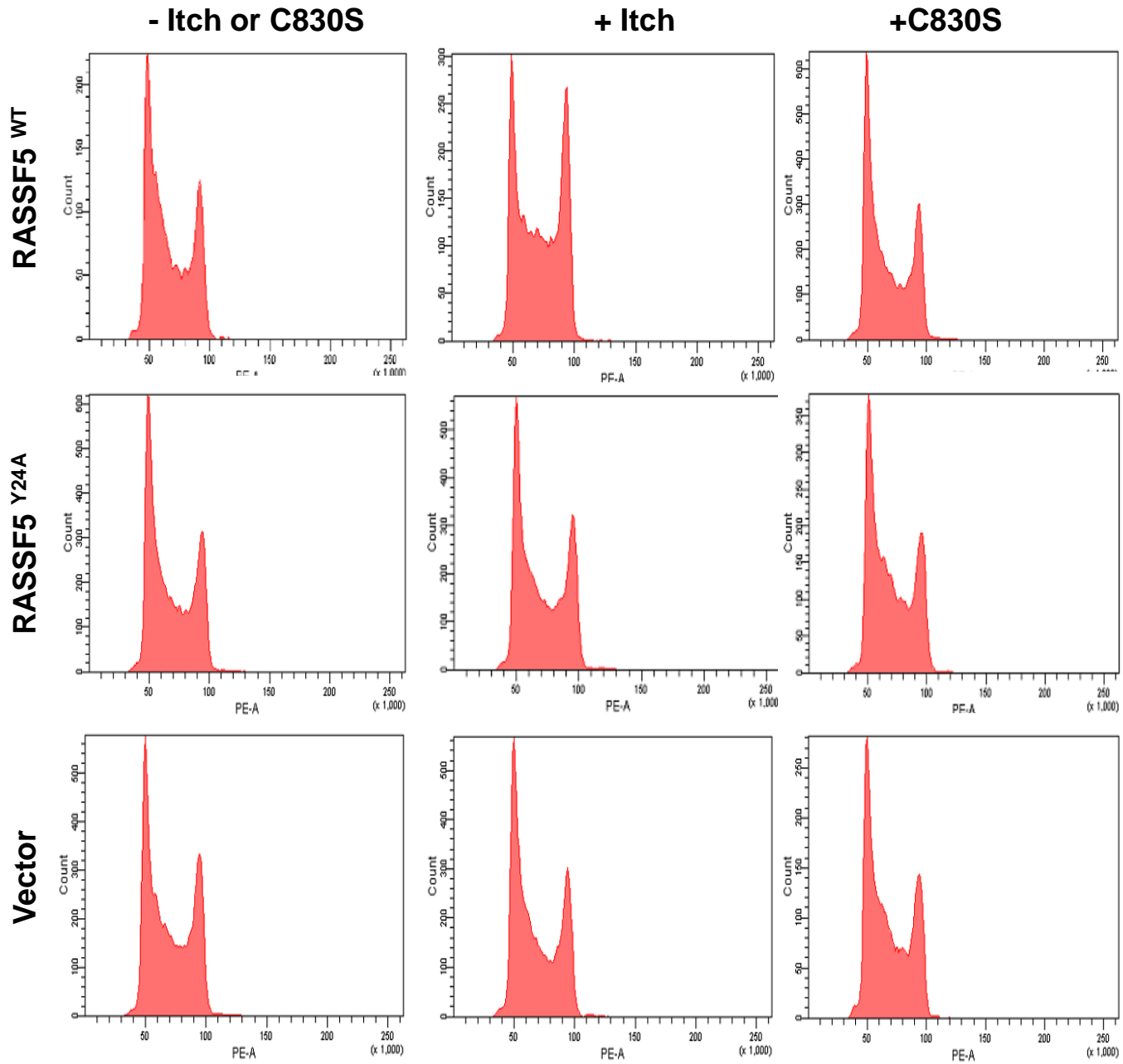
Supplementary Figure 7



Supplementary Figure 8

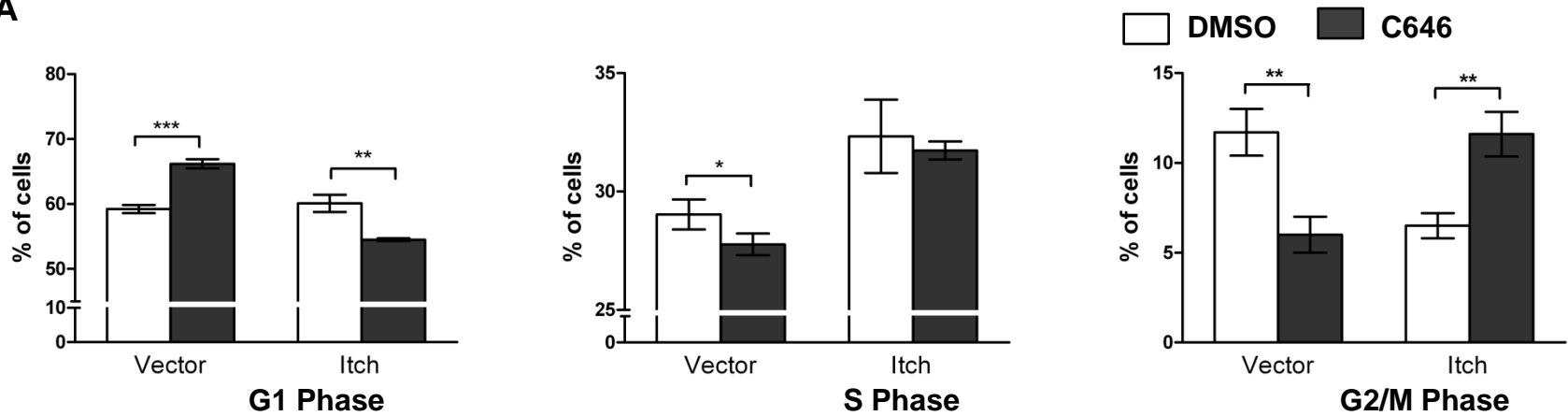


Supplementary Figure 8C



Supplementary Figure 9

A



B

