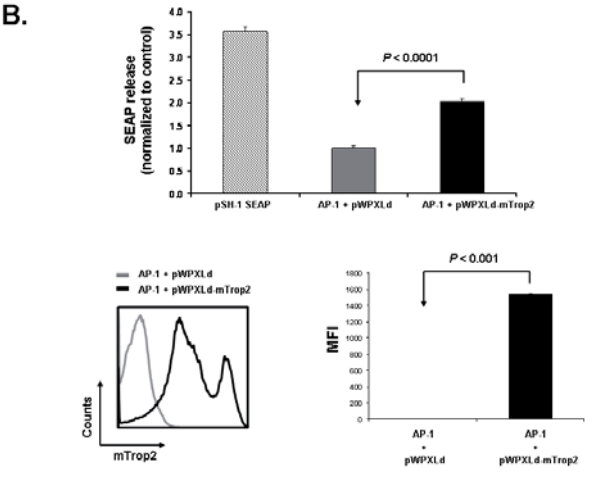
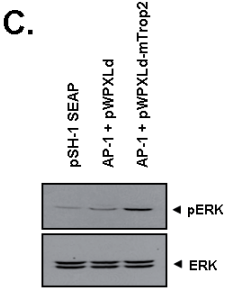
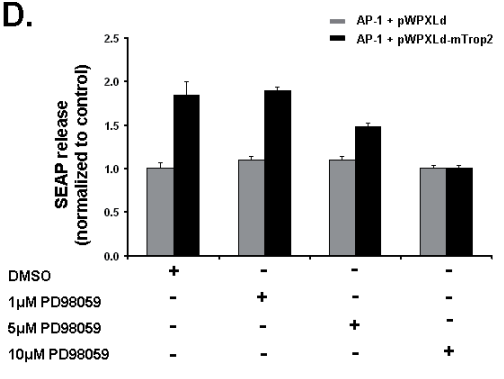
A.
Cytoplasmic Tail
PIP2-binding motif
hTrop-2 298-323 TNRRKSGKYKKVEI KELGELRKEPSL
mTrop-2 292-317 TKRRKSGKYKKVEL KELGEMRSEPSL
303
Species
Cytoplasmic Tail
Sequence Identity
PIP2-binding motif
Trop-2 (Homo sapiens) TNRRKSGKYKKVEI KELGE LR KEPSL
Trop-2 (Mus musculus) TKRRKSGKYKKVELKELGEMRSEPS L 84%
Trop-2 (Bos taurus) TNRRKSGKYKKVEI KELGE I RQKPSL 80%
Trop-2 (Monodelphis domestica) RKSGK YEKVEI KEMGEM 82%
Trop-2 (Xenopus laevis) RRKRGKYQKAEMKELNEMQQEAS 65%


B.
SEAP release (normalized to control)
P < 0.0001
pSH-1 SEAP
AP-1 + pWPXLd
AP-1 + pWPXLd-mTrop2
AP-1 + pWPXLd
AP-1 + pWPXLd-mTrop2
Counts
mTrop2
P < 0.001
MFI
AP-1 + pWPXLd
AP-1 + pWPXLd-mTrop2


C.
pSH-1 SEAP
AP-1 + pWPXLd
AP-1 + pWPXLd-mTrop2
pERK
ERK


D.
AP-1 + pWPXLd
AP-1 + pWPXLd-mTrop2
SEAP release (normalized to control)
DMSO
1μM PD98059
5μM PD98059
10μM PD98059