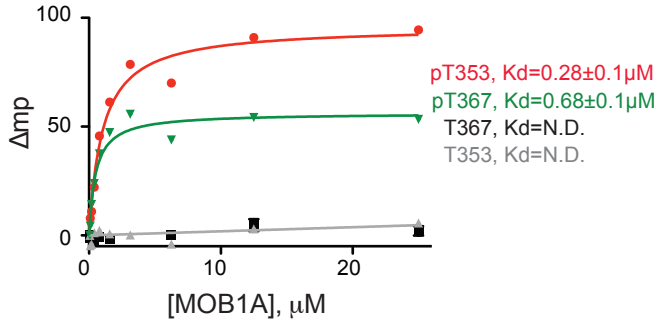
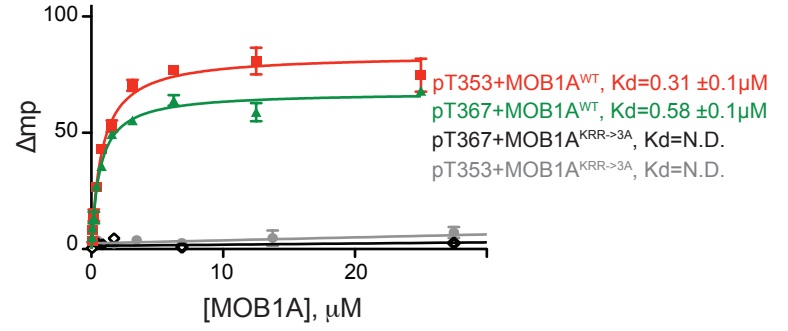


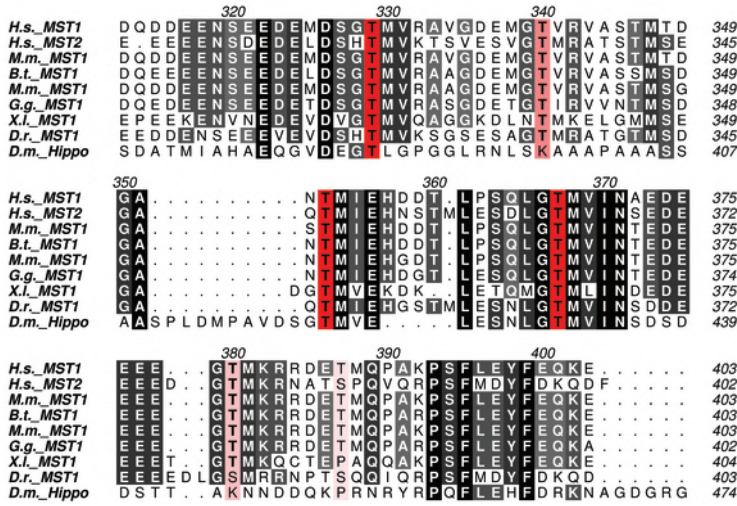
A



B

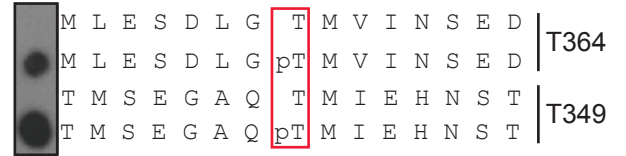


C

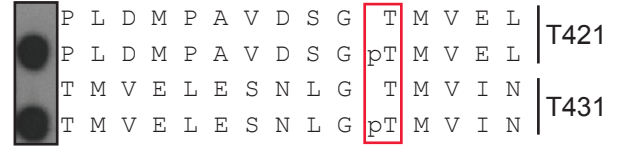


D

Human MST2

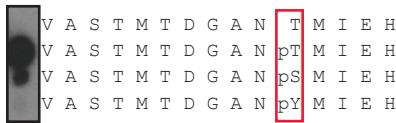


Drosophila Hippo



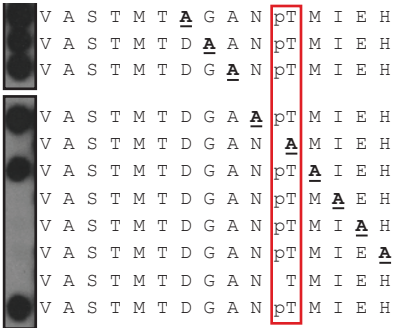
A

T353 peptide

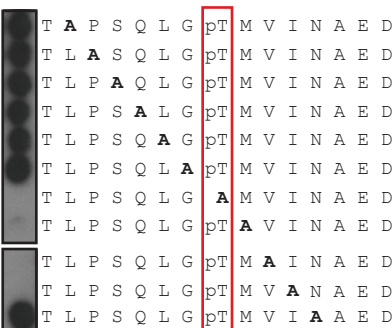


B

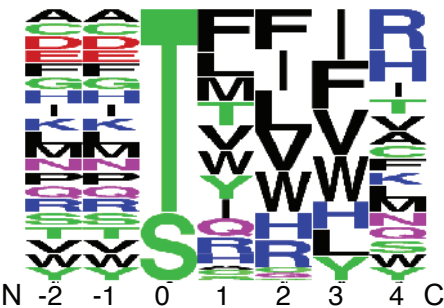
T353 peptide



T367 peptide



C

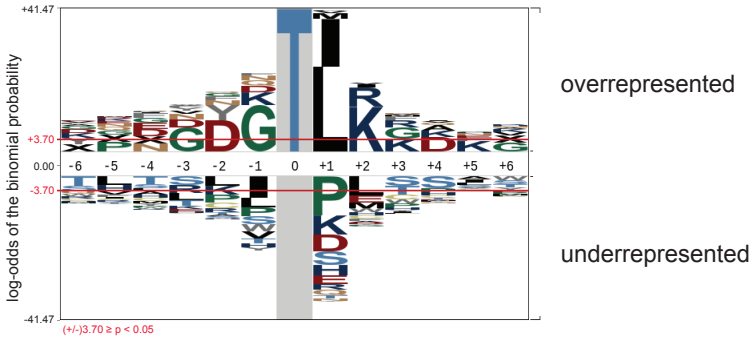


D

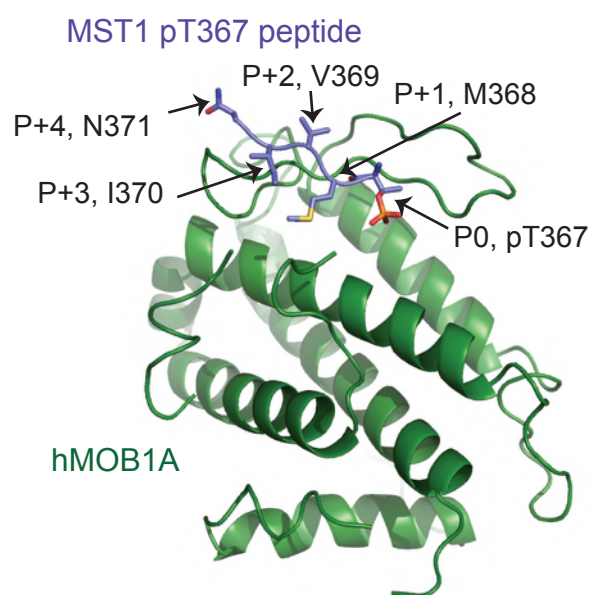
T329	S	G	pT	M	V	R	A
T340	M	G	pT	V	R	V	A
T353	A	N	pT	M	I	E	H
T367	L	G	pT	M	V	I	N
T380	E	G	pT	M	K	R	R
T387	A	E	pT	M	Q	P	A

Kd = 46.5μm
Kd = 66.1μm
Kd = 0.28μm
Kd = 0.68μm
Kd = 185μm
Kd N.D.

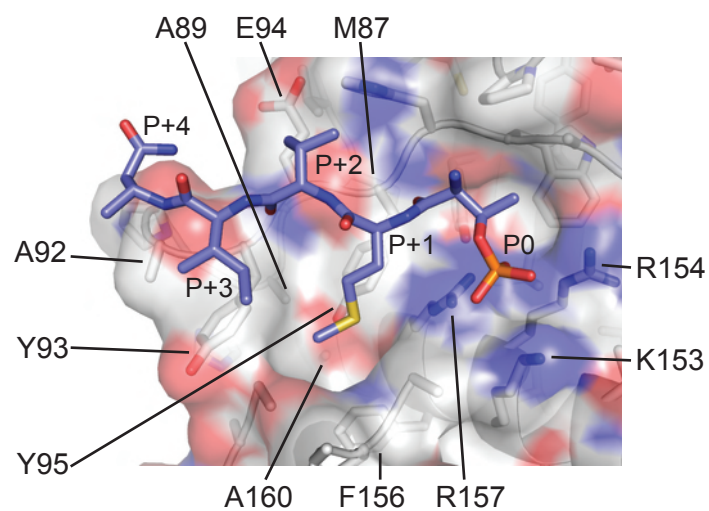
E



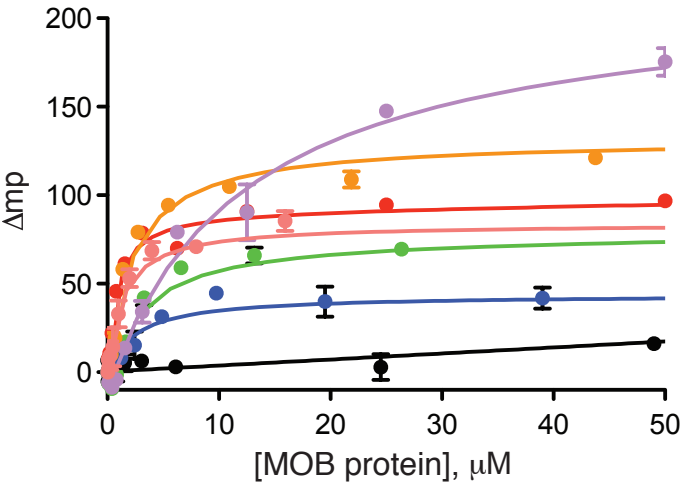
A



B

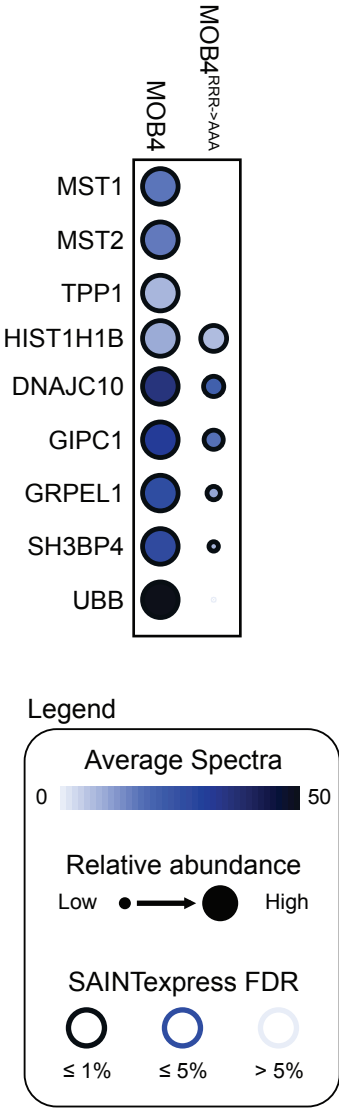


A

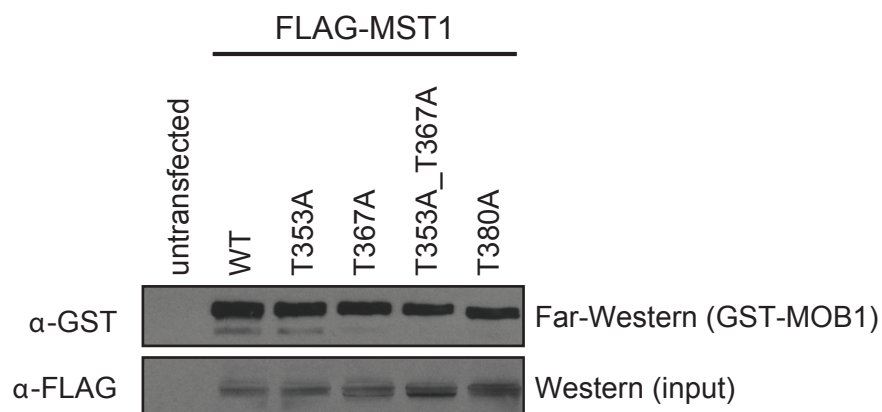


MOB Protein	Overall identity to HsMOB1A, %	Projected phospho-binding residues	Kd, μM (to MST1 pT367 peptide)
MOB1A	100	KRR	0.67 \pm 0.09
MOB1B	96	KRR	0.78 \pm 0.09
MOB2	37	RHH	N. D.
MOB3A	50	SRR	2.9 \pm 0.8
MOB3B	50	CRR	2.6 \pm 0.9
MOB3C	49	TRR	2.3 \pm 0.3
MOB4	21	RRR	12.2 \pm 2.1
ScMob1	48	RRR	29.3 \pm 3.7

B



A



B

