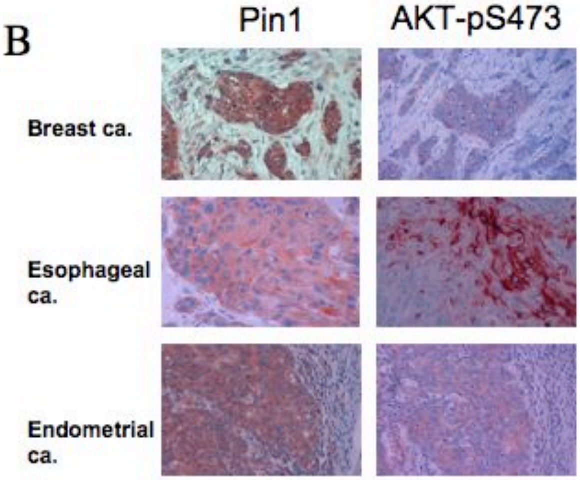
Supplementary Figure S1

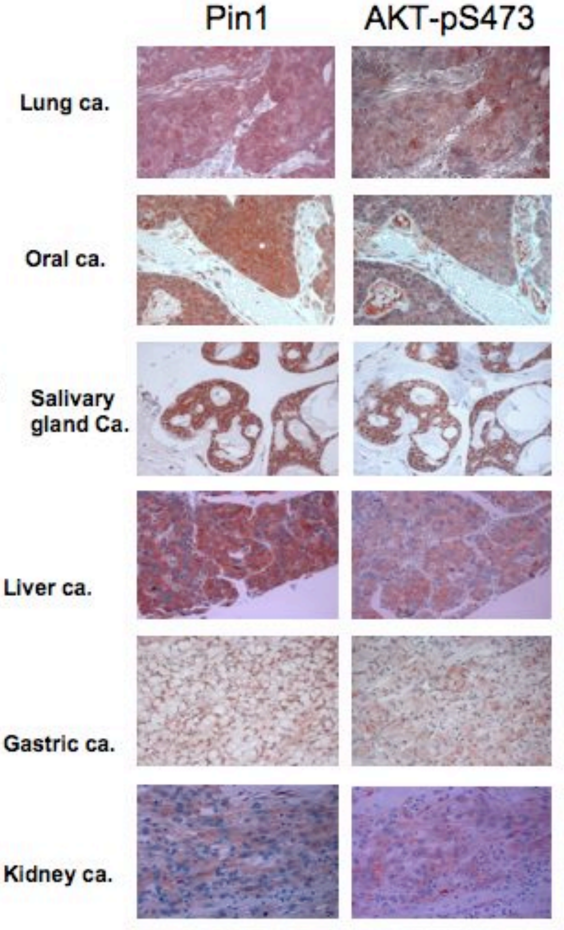
A

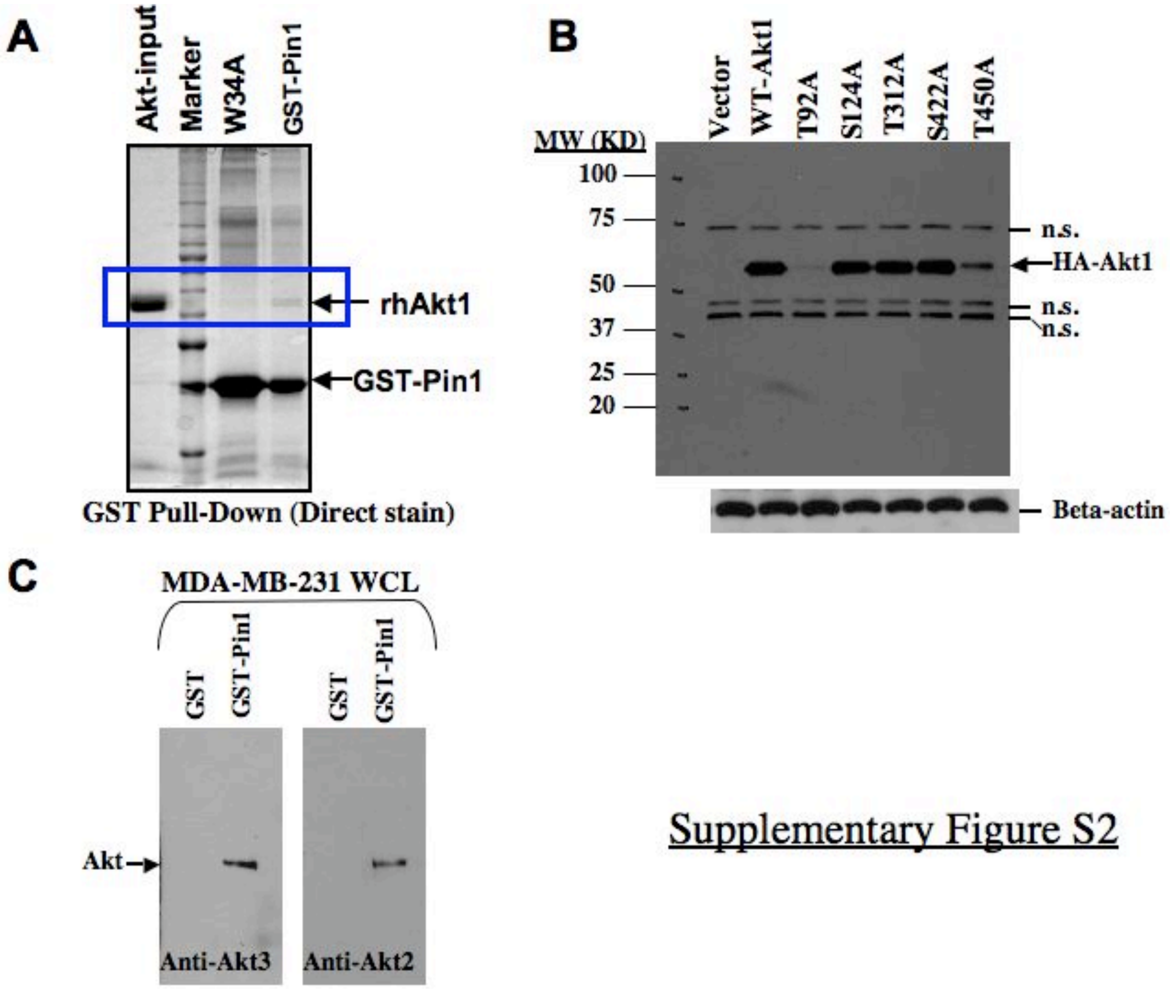
		Pin1 staining		
		Low (L)	High (H)	Total
*Cyclin D1	L	48 (41.7%)	33 (28. 7%)	81 (70.4%)
	H	13 (11.3%)	21 (18.3%)	34 (29.6%)
Total		61 (53.0%)	54 (47.0%)	115(100%)

* $r=0.192$, $p< 0.05$

B

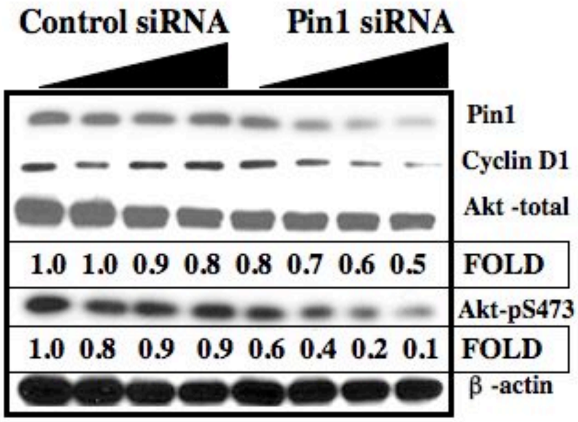






Supplementary Figure S2

Supplementary Figure S3



Supplementary Table 1. Ser/Thr-Pro sites on human Akt1 protein

Ligand	Position							
	-3	-2	-1	0		+1	+2	+3
Pin1 PPIase substrate		A	A	pS/T	P	F	NH	Np
Pin1 concensus binding sites	W	F	Y	pS/T	P	R	L	X
	Y	I	R			F	I	
	F		F			W		
MPM2 concensus binding sites	Y	W	F	pS/T	P	L	X	X
	F	F	L			I		
S/T P sites on Akt1								
T92 P	H	V	E	pT	P	E	E	R
S124 P	R	S	G	pS	P	S	D	N
T312 P	F	C	G	pT	P	E	Y	W
S422 P	K	K	L	pS	P	P	F	K
T450 P	I	T	I	pT	P	P	D	Q

Supplementary Table 2

T92 and T450-Pro (Akt1) motifs are conserved evolutionarily

	T92-Pro	**T450-Pro**
sp|P31749| KRAC_HUMAN	HVE-**T**-**P**EEREE	QMITI-**T**-**P**PDQ
tr|Q9BWB6| Akt1-Mouse	HVE-**T**-**P**EEREE	QMITI-**T**-**P**PDQ
sp|P47196| KRAC_RAT	HVE-**T**-**P**EEREE	QMITI-**T**-**P**PDQ
tr|O57513| Akt1-Gallus	HVE-**T**-**P**EEREE	QMITI-**T**-**P**PDQ
tr|Q98TY9| Akt1-Xenopus	HVD-**S**-**P**EEREE	QMITI-**T**-**P**PDQ
sp|Q60823|AKT2_MOUSE	HVD-**S**-**P**DEREE	QSITI-**T**-**P**PDR
sp|P31751| AKT2_HUMAN	HVD-**S**-**P**DEREE	QSITI-**T**-**P**PDR
tr|Q7ZX15| Akt2-Xenopus	HVD-**T**-**P**EEREE	QSITL-**T**-**P**PDR
sp|P47197| AKT2_RAT	HVD-**S**-**P**DEREE	QSITI-**T**-**P**PDR
sp|Q9Y243| AKT3_HUMAN	HVD-**T**-**P**EEREE	QTITI-**T**-**P**PEK
sp|Q9WUA6| AKT3_MOUSE	HVD-**T**-**P**EEREE	QTITI-**T**-**P**PEK
tr|Q8UUX0| Akt2-Zebrafish	HVD-**S**-**N**SEREE	QTITV-**T**-**P**PDQ
sp|Q63484|AKT3_RAT	HVD-**T**-**P**EEREE	QTITI-**T**-**P**PEK
tr|Q24293| AKT1-DROSOPHIA	AVE-**S**-**E**LERHE	ESVEL-**T**-**P**PDP
tr|Q17942| AKT1-C. elegans	YAE-**S**-**A**EVRQR	QPVQL-**T**-**P**PSR