Supplemental Materials

Molecular Biology of the Cell

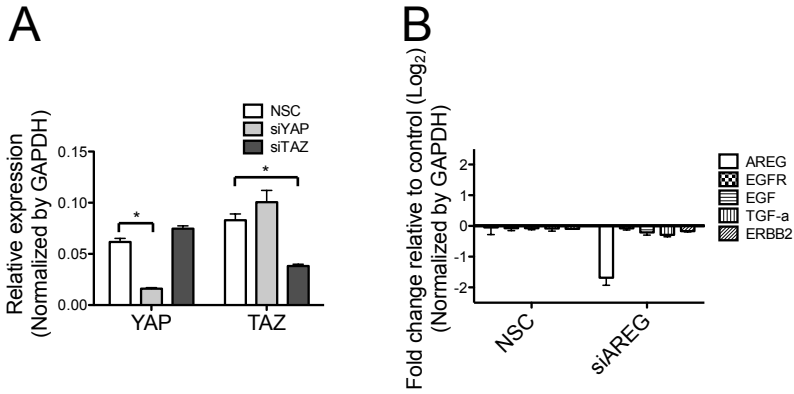
Lin et al.

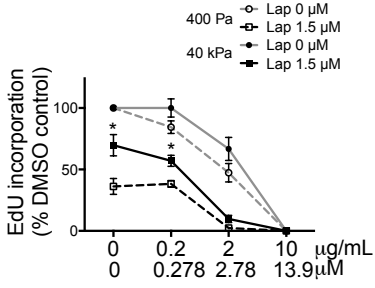
Additional file 1: Figure S1. Knockdown efficiency in siRNA experiments.(A) Expression levels of YAP and TAZ measured by qRT-PCR in HCC1569 with NSC siRNA, YAP or TAZ knockdown by siRNA for 72 h. (B) Fold change of expression levels of various receptors and ligands of the HER family were measured by qRT-PCR in HCC1569 with NSC siRNA or AREG knockdown by siRNA after 72 h.

Additional file 2: Figure S2. Verteporfin has a synergistic effect with lapatinib. Line graphs show the relative incorporation of EdU, expressed as a percentage of DMSO-treated cells in HCC1569 cultured on 400 Pa or 40 kPa PA gels for 48 h, and then treated with lapatinib (1.5 μM) together with verteporfin (0, 0.2, 2, 10 μg/mL), or DMSO for 48 h. (n = 3, 500 cells/condition/experiment, * $p < 0.05$).

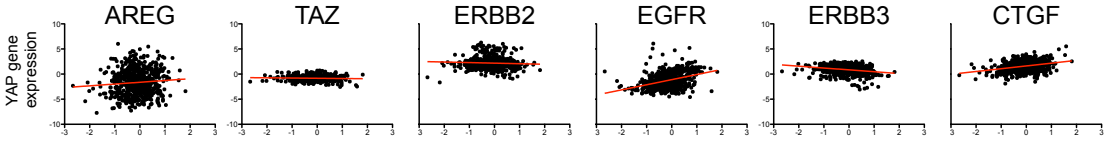
Additional file 3: Figure S3. Correlation between YAP gene expression with expression of a number of Hippo and HER-related genes in the TCGA dataset. Summary table shows correlation between *YAP* and *ERBB2* gene expression with the other indicated genes. Pearson's r statistic is shown. Below, regression plots show examples of the fit for all tumor types.

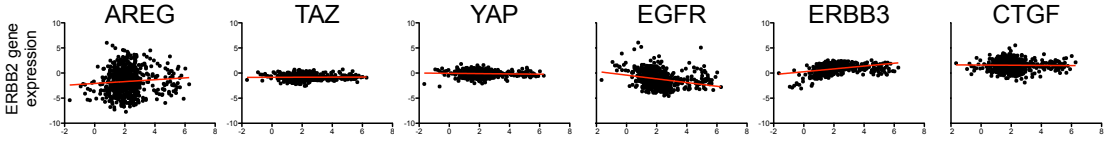
Additional file 4: Figure S4. Responses to changes in microenvironmental stiffness for 49 different receptor tyrosine kinases (RTK). (A) Images of RTK array membranes that were probed with extracts from HCC1569 cells. HCC1569 were grown for 48 h on 400 Pa or 40 kPa PA gel for 48 h, treated with lapatinib (1.5 μM) or DMSO, and then harvested at 1 h or 48 h after lapatinib treatment. (B) Bar graphs showing quantification of intensity of phosphorylation on EGFR, HER2, HER3, VEGFR1, and RYK RTKs. (C) A complete table of the RTKs represented on the blot.#


A
Relative expression
(Normalized by GAPDH)
0.15
0.10
0.05
0.00
NSC
siYAP
siTAZ
*
*
YAP
TAZ
B
Fold change relative to control (Log2)
(Normalized by GAPDH)
2
1
0
-1
-2
AREG
EGFR
EGF
TGF-a
ERBB2
NSC
siAREG

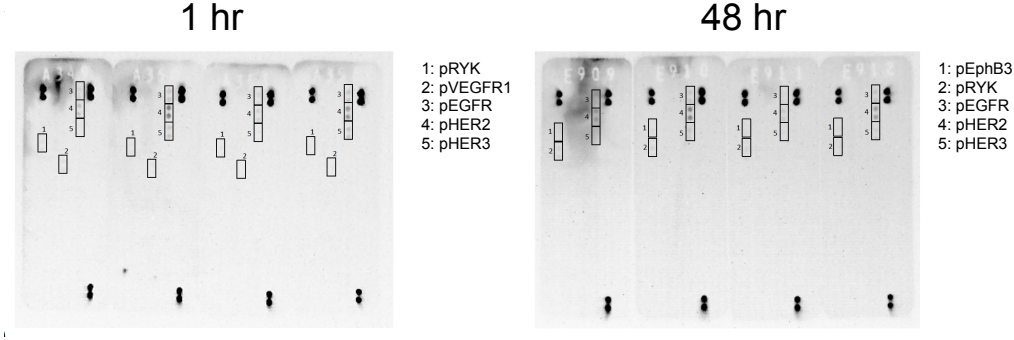

400 Pa
Lap 0 µM
Lap 1.5 µM
40 kPa
Lap 0 µM
Lap 1.5 µM
EdU incorporation
(% DMSO control)
100
50
0
*
*
0
0
0.2
0.278
2
2.78
10
13.9
µg/mL
µM

		AREG	TAZ	ERBB2	EGFR	ERBB3	CTGF
YAP	Pearson r	0.0825	-0.05424	-0.05704	0.3713	-0.2447	0.3115
	P value	0.0452	0.1883	0.1664	< 0.0001	< 0.0001	< 0.0001
	Significant	*	ns	ns	***	***	***
		AREG	**TAZ**	**YAP**	**EGFR**	**ERBB3**	**CTGF**
ERBB2	Pearson r	0.08503	0.01709	-0.05704	-0.2654	0.3689	-0.02014
	P value	0.039	0.6787	0.1664	< 0.0001	< 0.0001	0.6253
	Significant	*	ns	ns	***	***	ns

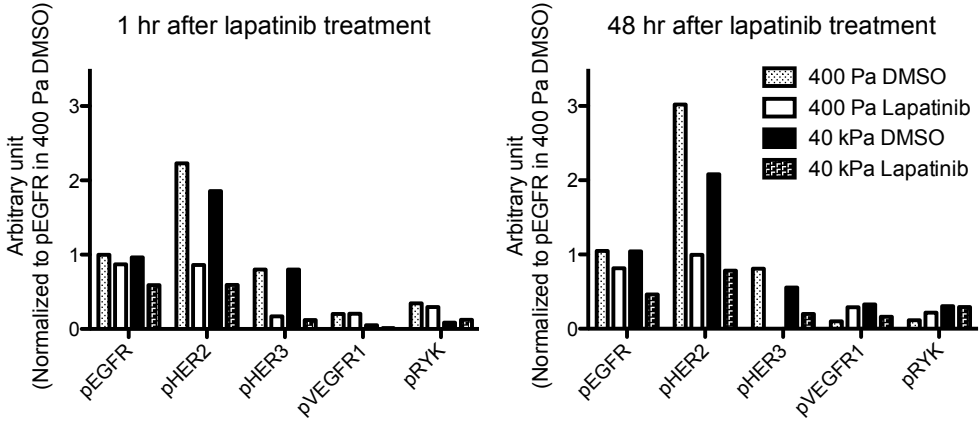




A

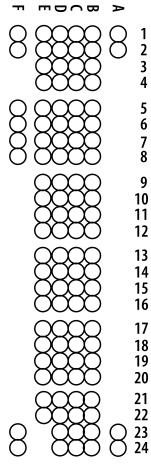


B



C

Human Phospho-RTK Array Coordinates



Refer to the table below for the Human Phospho-RTK Array coordinates.

Coordinate	Receptor Family	RTK/Control	Coodinate	Receptor Family	RTK/Control
A1, A2	Reference Spots	——	D1, D2	Tie	Tie-2
A23, A24	Reference Spots	——	D3, D4	NGF R	TrkA
B1, B2	EGF R	EGF R	D5, D6	NGF R	TrkB
B3, B4	EGF R	ErbB2	D7, D8	NGF R	TrkC
B5, B6	EGF R	ErbB3	D9, D10	VEGF R	VEGF R1
B7, B8	EGF R	ErbB4	D11, D12	VEGF R	VEGF R2
B9, B10	FGF R	FGF R1	D13, D14	VEGF R	VEGF R3
B11, B12	FGF R	FGF R2α	D15, D16	MuSK	MuSK
B13, B14	FGF R	FGF R3	D17, D18	Eph R	EphA1
B15, B16	FGF R	FGF R4	D19, D20	Eph R	EphA2
B17, B18	Insulin R	Insulin R	D21, D22	Eph R	EphA3
B19, B20	Insulin R	IGF-I R	D23, D24	Eph R	EphA4
B21, B22	Axl	Axl	E1, E2	Eph R	EphA6
B23, B24	Axl	Dtk	E3, E4	Eph R	EphA7
C1, C2	Axl	Mer	E5, E6	Eph R	EphB1
C3, C4	HGF R	HGF R	E7, E8	Eph R	EphB2
C5, C6	HGF R	MSP R	E9, E10	Eph R	EphB4
C7, C8	PDGF R	PDGF Rα	E11, E12	Eph R	EphB6
C9, C10	PDGF R	PDGF Rβ	E13, E14	Insulin R	ALK
C11, C12	PDGF R	SCF R	E15, E16	——	DDR1
C13, C14	PDGF R	Flt-3	E17, E18	——	DDR2
C15, C16	PDGF R	M-CSF R	E19, E20	Eph R	EphA5
C17, C18	RET	c-Ret	E21, E22	Eph R	EphA10
C19, C20	ROR	ROR1	F1, F2	Reference Spots	——
C21, C22	ROR	ROR2	F5, F6	Eph R	EphB3
C23, C24	Tie	Tie-1	F7, F8	——	RYK
			F23, F24	Control (-)	PBS