

**Table S2.**

<b>Tumor subtype</b> (No. patient)	<b>Cohort</b> (N=817)	<b>Her2</b> (N=120)	<b>Basal</b> (N=107)	<b>Luminal A</b> (N=201)	<b>Luminal B</b> (N=122)
<b>No. of tumors with amplification (%)</b> (FAK vs c-Myc)	129 (15.79) vs 173 (21.2)	27 (22.5) vs 38 (31.7)	32 (29.9) vs 51 (47.7)	21 (10.5) vs 26 (12.94)	33 (27.1) vs 39 (32.0)
<b>Spearman correlation</b>	0.73**	0.58*	0.68*	0.79**	0.77**
<i>p</i> value	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
<b>No. of tumors with mRNA upregulation (%)</b> (FAK vs c-Myc)	306 (37.5) vs. 53 (6.5)	49 (40.8) vs. 5 (4.2)	62 (57.9) vs. 24 (22.4)	62 (30.9) vs. 1 (0.5)	70 (57.4) vs. 4 (3.3)
<b>Spearman correlation</b>	0.073	-0.0035	0.14	0.11	0.065
<i>p</i> value	0.036	0.974	0.15	0.13	0.47

\*\* : A strong correlation.

\* : Intermediate correlation.