

Table W1. Proteins Analyzed and Antibodies Used in This Study.

	Antibody	Distributor	Dilution	
	p ^{S118} ERα	No. 2511	Cell Signaling, Danvers, MA	1:2000
	FAK	No. 3285	Cell Signaling, Danvers, MA	1:2000
	GSK3-β	No. 9315	Cell Signaling, Danvers, MA	1:1000
	p ^{S9} GSK3-β	No. 9336	Cell Signaling, Danvers, MA	1:1000
	HSP27	No. 2402	Cell Signaling, Danvers, MA	1:1000
	ILK	No. 3856	Cell Signaling, Danvers, MA	1:2000
	MET	No. 3127	Cell Signaling, Danvers, MA	1:1000
	PAI-1	AHP1100	Serotec, Oxford, United Kingdom	1:5000
	PI3K	No. 4292	Cell Signaling, Danvers, MA	1:1000
	p38	No. 9212	Cell Signaling, Danvers, MA	1:1000
	p ^{T180/Y182} p38	No. 4631	Cell Signaling, Danvers, MA	1:1000
	ROCK	No. 4035	Cell Signaling, Danvers, MA	1:1000
	p ^{S727} STAT3	No. 9136	Cell Signaling, Danvers, MA	1:1000
	uPA	Ab19893	Abcam, Cambridge, United Kingdom	1:500

Table W2. Patient and Disease Characteristics Related to the Collective of 52 Node-Positive Patients Analyzed to Study Protein Expression Correlations between Primary Tumor and Lymph Node Metastases.

Factor	Patient Collective (n = 52)	
	No. Patients	%
Age		
<50	6	11.5
≥50	46	88.5
Tumor state		
T1	11	21.2
T2	31	59.6
T3	7	13.5
T4	3	5.8
Nodal status		
N1	22	42.3
N2	16	30.8
N3	14	26.9
Subtype		
Ductal	38	73.1
Lobular	10	19.2
Ductal-lobular	2	3.8
Other	2	3.8
Distant metastasis		
Positive	0	0.0
Negative	50	96.2
Unknown	2	3.8
Grading		
1	1	1.9
2	24	46.1
3	27	51.9
Hormone receptor status		
Positive	41	78.9
Negative	10	19.2
Unknown	1	1.9

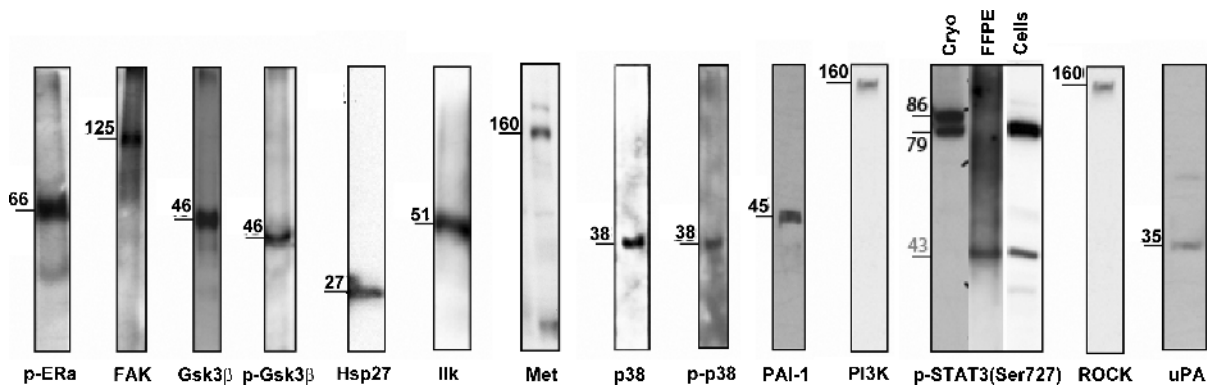


Figure W1. Validation of antibody specificity by Western blot analysis. All antibodies were validated using breast cancer FFPE tissue samples unless stated otherwise.

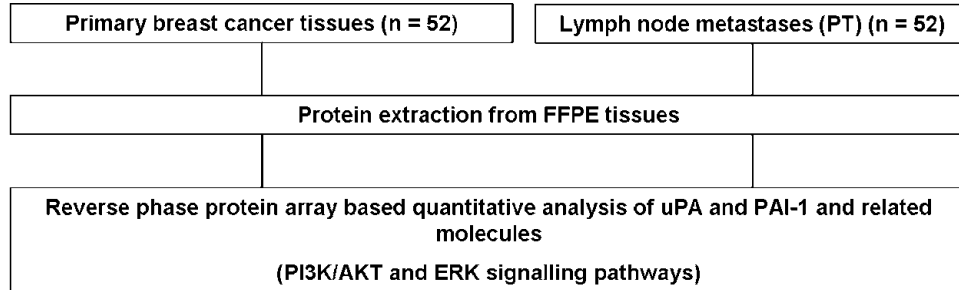


Figure W2. Strategy for the analysis of the collective used in this study.

Table W3. Correlation of the Expression of the 14 Analyzed Signaling Molecules between Primary Tumors and Lymph Node Metastases.

	r_s	P (two-sided)
FAK	0.597	.000
GSK3- β	0.270	>.999
pGSK3- β	0.646	.000
ILK	0.697	.000
MET	0.603	.001
PI3K	0.655	.000
ROCK	0.571	.000
pp38	0.576	.000
p38	0.651	.000
PAI-1	0.173	>.999
uPA	0.566	.008
pSTAT3	0.453	.000
pER	0.446	.000

The Spearman correlation coefficient r_s and P values are shown. All P values are adjusted for multiple testing as described in the Materials and Methods section. Statistically significant correlations are in bold face emphases.

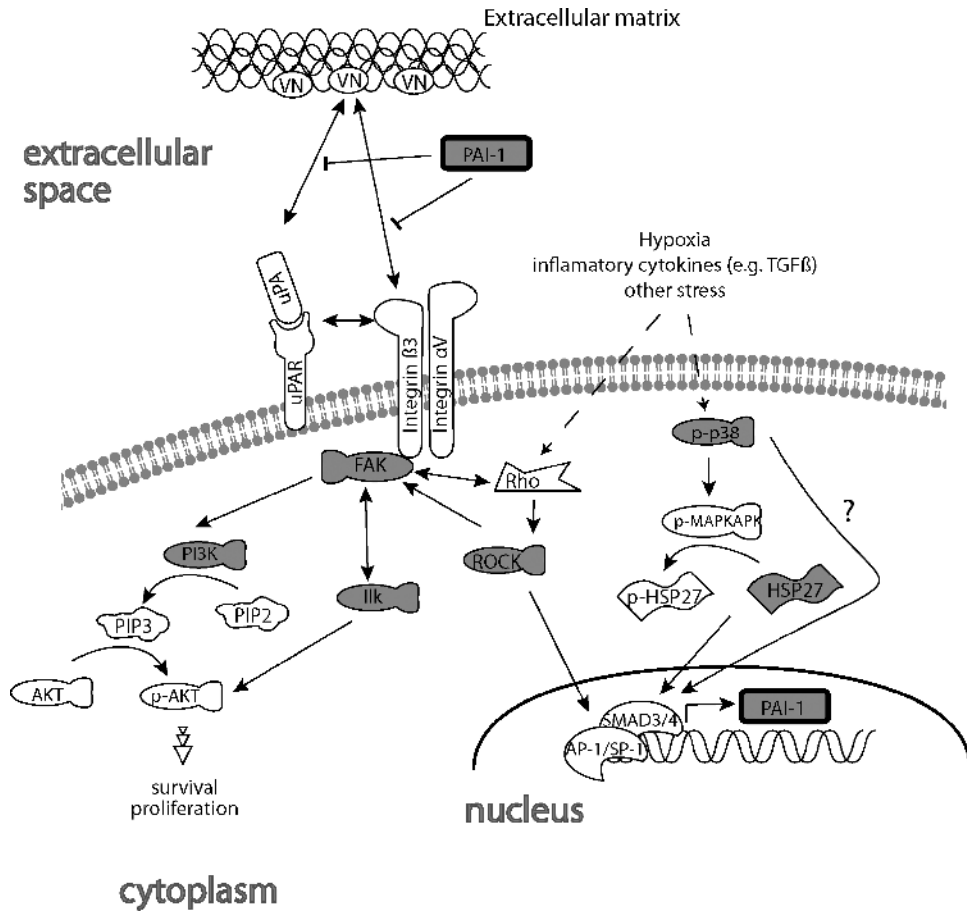


Figure W3. Overview of pathways correlating with high PAI-1 expression (gray). PAI-1 expression was found to be correlated with several proteins involved in AKT signaling (FAK, ILK, ROCK, and PI3K), supporting the assumption that PAI-1 is involved in the activation of AKT through integrin $\alpha_V\beta_3$ -induced PI3K activation. Furthermore, PAI-1 correlates with HSP27 and pp38, which are known to increase PAI-1 expression through transcription factor activation.