

<b>Characteristic</b>		<b>Number</b>	<b>percent</b>
<b>Age group</b>	<i>≤ 50 years</i>	78	31.5%
	<i>&gt;50 years</i>	170	68.5%
<b>Tumor size</b>	<i>≤2cm</i>	126	50.8%
	<i>&gt;2cm</i>	122	49.2%
<b>Axillary LN metastasis</b>	<i>No</i>	136	54.8%
	<i>Yes</i>	112	45.2%
<b>SBR grade</b>	<i>I</i>	48	19.4%
	<i>II</i>	116	46.8%
	<i>III</i>	84	33.9%
<b>ER status</b>	<i>Negative</i>	36	14.6%
	<i>Positive</i>	210	85.4%
	<i>Missing</i>	2	
<b>PR status</b>	<i>Negative</i>	60	24.5%
	<i>Positive</i>	185	75.5%
	<i>Missing</i>	3	
<b>Her2 status</b>	<i>Negative</i>	217	90%
	<i>Positive</i>	24	10%
	<i>Missing</i>	7	
<b>Adjuvant Hormonal treatment</b>	<i>No</i>	56	22.6%
	<i>Yes</i>	192	77.4%
<b>Adjuvant (or neoadj) chemotherapy</b>	<i>No</i>	108	43.5%
	<i>Yes</i>	140	56.5%
<b>TIF1<math>\gamma</math></b>	<i>Low</i>	143	64.1%
	<i>High</i>	80	35.9%
	<i>Missing</i>	25	
<b>TGF<math>\beta</math>1</b>	<i>Low</i>	142	69.6%
	<i>High</i>	62	30.4%
	<i>Missing</i>	44	
<b>Nuclear SMAD4</b>	<i>Low</i>	125	72.3%
	<i>High</i>	48	27.7%
	<i>Missing</i>	75	
<b>Cytoplasmic SMAD4</b>	<i>Low</i>	82	47.4%
	<i>High</i>	91	52.6%
	<i>Missing</i>	75	

*Table S1: Clinicopathological characteristics and biomarker expression in the tested patients' population (248 patients)*

Marker		TIF1 $\gamma$ low		TIF1 $\gamma$ high		P value*	TGF $\beta$ 1 low		TGF $\beta$ 1 high		P value*
		No.	(%)	No.	(%)		No.	(%)	No.	(%)	
<b>Nuclear SMAD 4</b>	Low	66	(71.7%)	46	(73%)	P=0.86	85	(75.2%)	27	(67.5%)	P=0.34
	High	26	(28.3%)	17	(27%)		28	(24.8%)	13	(32.5%)	
<b>Cytopl. SMAD4</b>	Low	40	(43.5%)	31	(49.2%)	P=0.48	50	(44.2%)	19	(47.5%)	P=0.7
	High	52	(56.5%)	32	(50.8%)		63	(55.8%)	21	(52.5%)	
<b>SMAD loss</b>	Yes	33	(35.9%)	27	(42.9%)	P=0.38	45	(39.8%)	15	(37.5%)	P=0.8
	No	59	(64.1%)	36	(57.1%)		68	(60.2%)	25	(62.5%)	
<b>TGF<math>\beta</math>1</b>	Low	81	(70.4%)	47	(68.1%)	P=0.74					
	high	34	(29.6%)	22	(31.9%)						

*Table S2: Absence of correlations between expression of TGF $\beta$ 1, TIF1 $\gamma$ , cytoplasmic and nuclear SMAD4.*

*\*Correlations tested by Pearson's Chi square test*

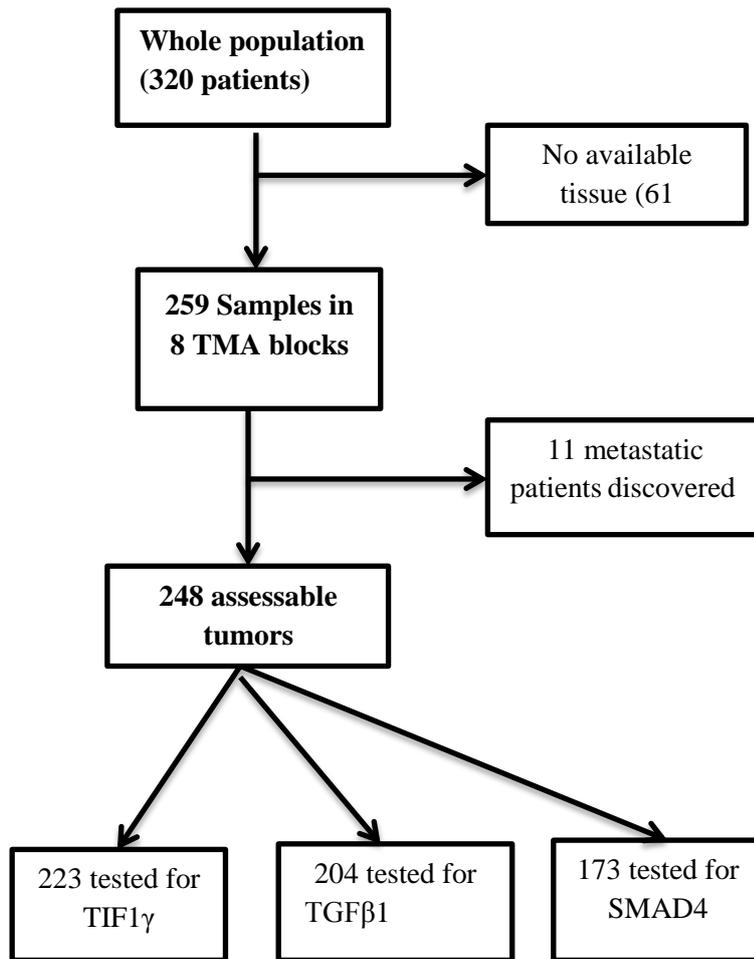


Figure S1: A flowchart of the whole population and subsets tested for different biomarkers