

LNCaP	ND-BA	ND	ND-BQ
SNAI1	--	--	--
VIM	--	--	--
Ki67	--	--	--
p16	--	--	--
CDH1	--	--	--
MDA MB 231	ND-BA	ND	ND-BQ
SNAI1	--	--	--
VIM	0.683 *	0.607 **	--
Ki67	--	--	--
no p16 expression			
no CDH1 expression			
MCF-7	ND-BA	ND	ND-BQ
CDH1	--	--	--
SNAI1	--	--	--
Ki67	--	--	--
no p16 expression			
VIM - Ct values above optimal range			

Table S1: qPCR analysis of genes implicated in EMT, proliferation and apoptosis. *P(H1)= 0.008

**P(H1)= 0.004 -- No significant change. Statistical analysis was performed using Relative Expression Software Tool (REST) ¹. Number of randomizations: 2000

1. M. W. Pfaffl, G. W. Horgan and L. Dempfle, *Nucleic Acids Res*, 2002, **30**, e36.