GENE EXPRESSION DATA AND FTIR SPECTRA PROVIDE A SIMILAR PHENOTYPIC DESCRIPTION OF BREAST CANCER CELL LINES IN 2D AND 3D CULTURES

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SUPPLEMENTARY MATERIALS

Negative	Positive
210772 at	219216 at
41553 at	212721 [_] at
216154 at	$217725 \ x$ at
207870 ⁻ at	213225 at
210636 at	209379 s at
215701 at	202314 at
207696 at	203543 s at
214920 at	205089 at
216702 x at	212248 at
216611 s at	201963 at
216500 at	217936 at
215987 at	217930_dt 209430_at
207496 at	209450_at
207490_{at}	204200_dt 21/31/_s_at
210441_dt 211333_s_at	$21+51+5_{at}$
211355_ <u>s_</u> at	202959_at 216713_at
215297_{at}	210/15_at 212170_at
$210070_{s_{at}}$	212179_{at}
$2141/1_5_at$	209032_{at}
200390_x_at	201407_5_at
213019_5_at	202900_S_at
214032_x_at	222119_8_at
200340_a	208802_at 218064_a_at
200305_at	218004_5_at
207150_at	212470_at
202648_at	215936_s_at
213494_s_at	200686_s_at
213999_at	204516_at
221546_at	21250/_at
213903_s_at	206095_s_at
211446_at	214683_s_at
21/53/_x_at	218289_s_at
206948_at	20212/_at
221141_x_at	218043_s_at
210279_at	201448_at
220799_at	202861_at
213//4_s_at	201737_s_at
216351_x_at	208924_at
207679_at	2086/1_at
215811_at	212615_at
210322_x_at	212616_at
222259_s_at	220553_s_at
215151_at	218989_x_at
34210_at	218422_s_at
206035_at	212454_x_at
222287_at	201084_s_at
217482_at	203552_at
203161_s_at	200914_x_at
207294_at	212177_at
216834_at	212176_at
213907_at	209571_at

Table S1. List of Affymetrix probe set identifiers representing genes which are differentially expressed in 2D or 3D culture conditions. The left (right) column reports the 50 probe sets with the most downregulated (upregulated) expression levels in a 3D culture if compared to a 2D culture.

	HCC1500	HCC1569	ZR751	BT549	Hs578T	MDAMB231	MDAMB361	MCF7	SKBR3	T47D	MCF12A	MDAMB468	MDAMB436
HCC1500	1.00E+00												
HCC1569	5.60E-14	1.00E+00											
ZR751	0.00E+00	0.00E+00	1.00E+00										
BT549	0.00E+00	4.44E-16	0.00E+00	1.00E+00									
Hs578T	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.00E+00								
MDAMB231	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.00E+00							
MDAMB361	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.00E+00						
MCF7	0.00E+00	1.00E+00											
SKBR3	0.00E+00	1.00E+00											
T47D	0.00E+00	8.52E-07	0.00E+00	1.00E+00									
MCF12A	0.00E+00	1.00E+00											
MDAMB468	0.00E+00	1.00E+00											
MDAMB436	0.00E+00	5.83E-14	0.00E+00	1.00E+00									

2D cultures

3D cultures

11001500	1.000												
HCC1500	1.00E+00												
HCC1569	3.89E-13	1.00E+00											
ZR751	0.00E+00	0.00E+00	1.00E+00										
BT549	0.00E+00	0.00E+00	0.00E+00	1.00E+00									
Hs578T	0.00E+00	0.00E+00	2.22E-16	0.00E+00	1.00E+00								
MDAMB231	0.00E+00	0.00E+00	1.11E-16	0.00E+00	8.89E-07	1.00E+00							
MDAMB361	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.00E+00						
MCF7	0.00E+00	1.00E+00											
SKBR3	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.65E-04	0.00E+00	1.00E+00				
T47D	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.27E-07	0.00E+00	1.09E-08	1.00E+00			
MCF12A	0.00E+00	0.00E+00	4.98E-07	0.00E+00	1.00E+00								
MDAMB468	7.10E-08	1.45E-09	4.41E-07	0.00E+00	7.78E-12	1.00E+00							
MDAMB436	1.11E-16	4.44E-16	7.33E-15	0.00E+00	8.87E-09	1.00E+00							

Table S2. Comparison of the FTIR spectra of 13 breast cancer cell lines using multivariate analysis of variance (MANOVA). P-values are reported in the table. For each cell line, 50 spectra were randomly extracted from our spectral library. The MANOVA was calculated from the scores of the spectra projected on the first 6 PCs obtained by PCA applied in the 1800-1000 cm⁻¹ region on 650 spectra used to characterize the cell lines either in 2D or 3D culture conditions. Values smaller than 10^{-16} appear as 0. Off-diagonal p-values larger than 10^{-16} are shaded.



Figure S1. A. Loadings plot for the first 2 PCs obtained by applying PCA on the mean spectra of each cell line grown in 2D and 3D culture conditions. **B.** Score plot representing the projection of the spectra on PC1 and PC2. The numbering and color code of the spectra in the score plot correspond to those reported in Table 1. **C.** Score plot representing the projection of the spectra on PC1 and PC2. The numbering of the spectra in the score plot correspond to those reported in Table 1. **C.** Score plot corresponds to the numbering reported in Table 1. Colors have been modified to group cell lines according to their molecular subtype: basal A (red), basal B (green) and luminal (blue). The variance explained by each PC appears on the axes. PCA has been computed after mean centering in the 1800-1480 cm⁻¹ spectral range.



Figure S2. Discriminant vector obtained by linear combination of the first 6 PCs to achieve the best discrimination between 2D and 3D cell cultures based on the FTIR spectral signatures. Wavenumber values are assigned to the main maxima and minima of the vector.