EUROPEAN JOURNAL OF CANCER XXX (2008) 326–328

available at www.sciencedirect.com

ScienceDirect

journal homepage: www.ejconline.com

Erratum

Erratum to ‘When should I start using a new biomarker: Focus on Expression arrays’ [EJC Supplement, 5 (2007) 97–104]

*C. Desmedt, C. Sotiriou**

Institut Jules Bordet, Functional Genomics and Translational Research Unit, Fonds National de la Recherche Scientifique (F.N.R.S), Université Libre de Bruxelles (U.L.B.), Brussels, Belgium

The Publisher regrets the following errors which appeared in the above mentioned article.

Page 98, 2nd column, lines 17 and 18, the text ‘Current limitations for transferring gene expression signatures from bench to bedside’ is a main heading.

Page 98, 2nd column, line 32, ‘Technology-related considerations’ is a subheading.

Page 99, 2nd column, line 14, Table 1 should be cited at the end of this line and is also missing from the article. The Table is shown below.

Page 101, 2nd column, line 19, ‘Clinical validation’ is a subheading.

Page 102, 1st column, line 4, Fig. 1 is cited but is missing from the article. The figure is shown below.

DOI of original article: 10.1016/S1359-6349(07)70029-0

* Corresponding author. Tel.: +32 2 5413428; fax: +32 2 5380858.
E-mail address: christos.sotiriou@bordet.be (C. Sotiriou).

doi:10.1016/j.ejca.2007.11.012

Table 1 – Main gene expression profiling studies with prognostic implications in breast cancer

Type of Study	Signature	Type of Microarray Platform	Samples (Characteristics)	Main Findings	Reference
'Fishing-expedition' approach	70-gene prognostic signature	Long-oligonucleotides (Agilent Hu25K-24,479 oligonucleotides)	78 (all <55 years old, LN– and untreated)	Prediction of clinical outcome, defined as presence of distant metastases at the 5-year mark	[2]
			295 (including 61 from previous study/ both treated and untreated/ 151 LN– and 144 LN+)	Validation of [2]	[3]
		Long-oligonucleotides (Custom-designed 'Mammaprint®')	307 (T1-T2 tumours from pts < 61 yrs old, LN–, and untreated)	Independent validation of [2] and [3]	[50]
	76-gene prognostic signature (60 genes for ER+ and 16 genes for ER- tumours)	Short-oligonucleotides (Affymetrix U133A-22,283 probe-sets)	286 (untreated LN– pts/ training set:115 and validation set: 171)	Prediction of clinical outcome, defined as presence of distant metastases at the 5-year mark	[4]
		Short-oligonucleotides (Custom-made Affymetrix VDX2-297 genes)	180 (untreated LN–)	Validation of [4]	[5]
		Short-oligonucleotides (Affymetrix U133A-22,283 probe-sets)	198 (T1-T2 tumours from pts < 61 years old, LN–, and untreated from ref .14)	Independent validation of [4] and [5]	[51]
'Hypothesis-driven' approach	Fibroblast Core	cDNA (43,000 features)	Fibroblasts from ten anatomic sites	Identification of similarities between tumours and wounds	[6]
	Serum Response list (512 genes)	Long-oligonucleotides (Agilent Hu25K-24,479 oligonuicleotides)	295 (from ref. 11)	Robustness, scalability and integration of this signature to predict survival	[7]
	Gene Expression Grade Index (97 genes)	Short-oligonucleotides (Affymetrix U133A-22,283 probe-sets)	189 (training set: 64 ER+ pts and validation set: 125 untreated pts)+ 3 publicly available datasets (from refs 2,4,11)	Identification of Genomic Grade associated with histological grade able to classify histological grade 2 pts into high and low risks of recurrence	[10]
		Short-oligonucleotides (Affymetrix U133A-22,283 probe-sets)	335 (ER+ both untreated and Tam-treated/ 86 from ref 25) + 4 publicly available datasets (from refs 2,4,11,12)	Definition of distinct subtypes of ER+ tumours with the Genomic Grade	[16]
	Death-from-cancer signature (11 genes)	Short-oligonucleotides (Affymetrix U95Av2-12,625 probe-sets)	Mouse/human comparative approach for the identification of the signature and validation on 1153 cancer patients from which 97 were breast cancer patients	Identification of an 11-gene stem-cell resembling signature	[8]
	Invasiveness Gene Signature (186 genes)	Short-oligonucleotides Short-oligonucleotides (Affymetrix U133A and B-~45,000 probe-sets)	Comparison of six CD44+/ CD24-or low cells isolated from breast cancers with normal epithelial cells from three mammoplasties+ Validation on ref. X and Y	Identification of a tumourigenic breast cancer signature	[9]

CT: chemotherapy; LN: lymph node status; pts: patients; IFN: interferon; ER: oestrogen-receptor.

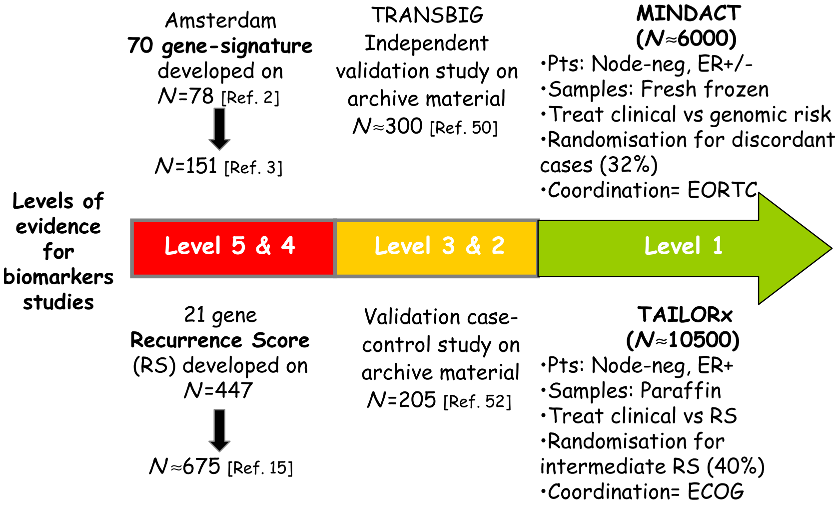

Fig. 1 – Schematic illustration of the validation strategy of the 70-gene signature [2,3,50] and of the Recurrence Score [15].