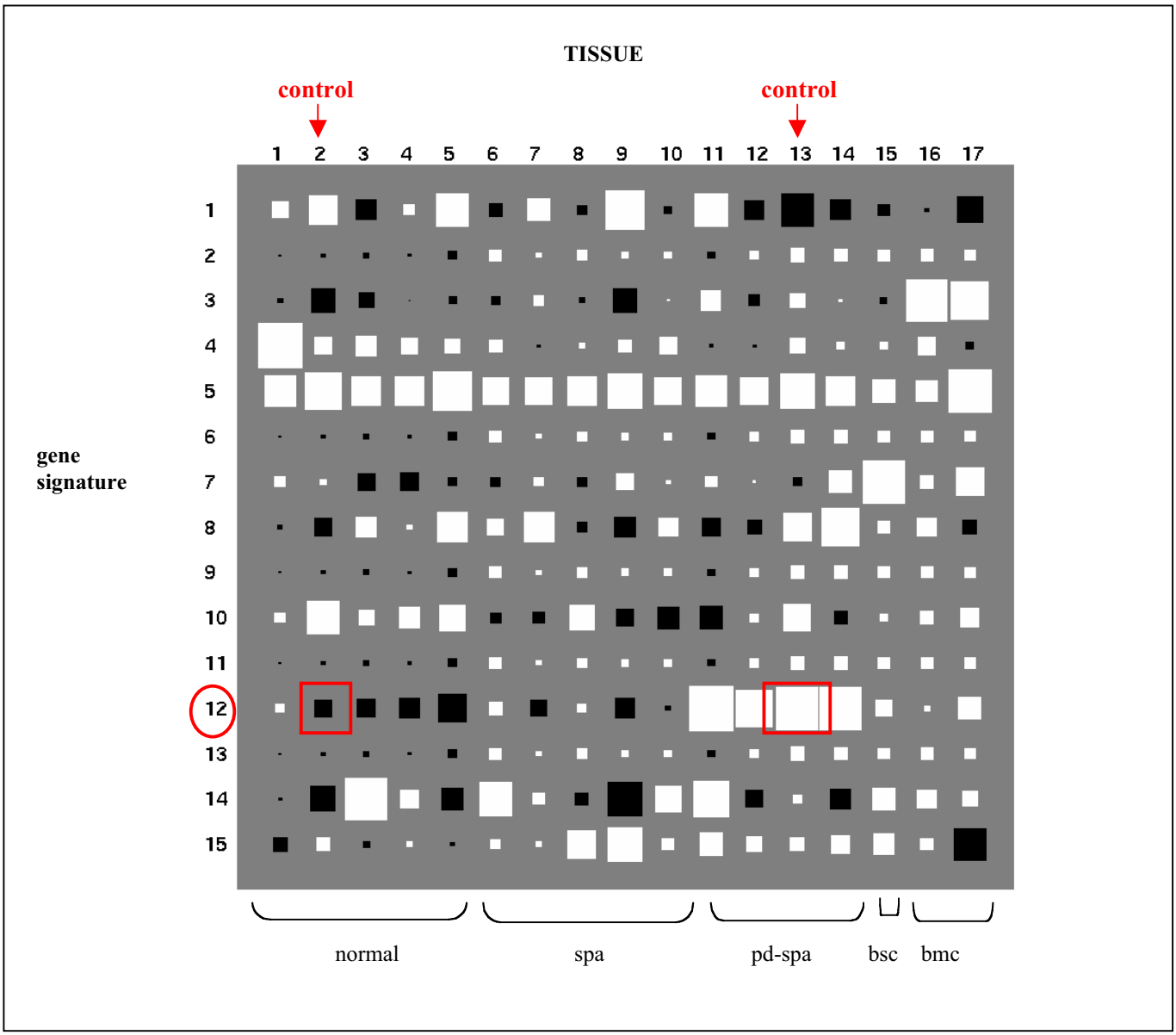
A decomposition model to track gene expression signatures: preview on observer-independent classification of ovarian cancer
Martoglio, Miskin, Smith, and MacKay (2002) Bioinformatics

Gene signatures revealed by independent component analysis (ICA) of ovarian cDNA array data. Assessment of ICA results: fixing the matrix and testing with new sample data.
Hidden gene expression profiles (gene signatures) unveiled in the initial independent component analysis (ICA) run on 15 ovarian tailored cDNA array data were fixed and quantified in two independent tissues not previously tested (tissues 2 (normal), and 13 (pd-spa)). Tissue 13 showed a prominent amount of gene signature 12, similar to other pd-spa samples (tissues 11,12, and 14), while tissue 2 displayed an amount similar to other normal tissues (especially tissues 3, 4, and 5). Both of these observations were in accordance with the respective histopathological classification of the control tissue samples, confirming the definition of tissue-specific gene signatures. Intra-tissue type differences could then be assessed based on a number of further defined gene signatures.