

Table I. Matching our list of genes with published gene signatures related with breast cancer metastasis

Publication	Array Platform	Samples description	Gene signatures	Matching
Van't Veer et al. Gene expression profiling predicts clinical outcome of breast cancer. Nature, 2002.	Agilent 24479 60-mer oligos	97 samples from LN- patients	231 prognosis reporters (risk of distant metastasis)	0 (bone, brain, liver and lung)
			430 Brca1 reporters	0 (bone, brain, and lung) HMGCS2 (liver)
			2460 ER- reporters	AIF1, FLI1, LCP2, PTPRC (bone) 0 (brain,liver) DSC2, UGT8 (lung)
Ramaswamy et al. A molecular signature of metastasis in primary solid tumors. Nat Genet, 2003.	Rosetta inkjet (24479 genes; breast adenocarcinoma) oligonucleotide microarrays.	279 primary tumors of diverse types (lung, breast, prostate)	128 genes separating metastasis from primary tumors able to distinguish patients with good versus poor prognosis	0 (bone, brain, liver and lung)
Nevins et al. Towards integrated clinico-genomic models for personalized medicine: combining gene expression signatures and clinical factors in breast cancer outcomes prediction. Human mol. genetics, 2003.	Multiple gene expression signatures “metagenes”	86 LN+ breast cancer patients	143 predictors of lymph node metastasis	PTPRC (bone) SQLE (brain) 0 (liver and lung)
			165 predictors of breast cancer recurrence	CSF1 (bone) LIG1 (brain) 0 (liver) PIGR (lung)
Wang et al. Gene expression profiles to predict distant metastasis of lymph-node negative primary breast cancer. The lancet, 2005.	Affymetrix U133A 25-mer oligos	LN- and LN+ patients with invasive breast cancer	76-gene signature to distinguish LN- primary breast cancer to develop distant metastasis within 5 years	0 (bone, brain, liver and lung)
Naderi et al. A gene-expression signature to predict survival in breast cancer across independent data sets. Oncogene, 2006.	Agilent 22575 60-mer oligos	135 tumor samples (no criteria for selection)	70-gen prognostic signature (risk of metastasis)	0 (bone, brain, liver and lung)
Nuyten et al. Predicting a local recurrence after breast-conserving therapy by gene expression profiling. Breast Cancer Res, 2006.	Agilent 24479 60-mer oligos	161 patients in stage I and II breast cancer with age < 53 years	70-gene predictor of local recurrence	0 (bone, brain, liver and lung)
Feng et al. Differentially expressed genes between primary cancer and paired lymph node metastases predict clinical outcome of node-positive breast cancer patients. Breast Cancer Res Treat, 2006	Operon 70-mer two-color 21239 probes	35 patients: primary tumor and lymph node metastasis paired samples	79 differentially expressed genes between primary samples and metastasis samples	PTPRC (bone) LUM (brain) 0 (liver) PIGR (lung)
Minn et al. Genes that mediate breast cancer metastasis to lung. Nature, 2005	Affymetrix U133A	82 breast cancer patients (Primary tumors)	95 genes predictors of lung metastasis	CSF1 (bone) 0 (brain, liver, lung)

Klein et al. Identification of brain- and bone-specific breast cancer metastasis genes. Cancer Letters, 2008	Affymetrix U133A	8 bone metastases, 18 brain metastases and 3 primary tumours	51 brain metastasis specific genes (vs. bone metastasis)	0 (bone, brain, liver UGT8 (lung)
Bos et al. Genes that mediate breast cancer metastasis to the brain. Nature, 2009	Affymetrix U133A	CN34-BrM2 and MDA231-BrM2 brain metastatic cell lines. 368 breast cancer primary tumors	17 genes whose expression was correlated with brain relapse	0 (bone, brain, liver, lung)
			26 genes whose expression was increased in brain metastatic cell lines but not in bone or lung metastatic cell lines	0 (bone, brain, liver, lung)