

Supplementary Analysis and Statistical Methods

Analysis of Quebec and Georgia Microarray Data

Illumina DASL transcript intensities were interpreted in GenomeStudio, and data were quantile normalized and scaled per processing batch. Average, rank invariant, and cubic spline normalization methods were considered, but yielded lower Pearson R^2 coefficients between RNA replicates and ruled out on this basis. Multiple RNA replicates were mean combined to assess transcript expression per patient/tumor and data were further analyzed on this basis.

Differential Analysis

Differentially regulated probes were computed using permutation testing in the R package “samr” (1) where 500 permutations determined a false discovery rate (FDR) less than 1% in conjunction with a minimum fold-change of 1.5-fold difference in expression.

Hierarchical Clustering

Hierarchically clustered heatmaps were generated in R/Bioconductor (2) using the “heatmap.2” function of the “gplots” package with a Euclidean distance dissimilarity metric and an average linkage clustering algorithm. Heatmaps used probe-level data which were normalized (Z-score) for visualization purposes.

KEGG Pathways

KEGG signal transduction pathways were obtained from the KEGG database (<http://www.genome.jp/kegg/>) (3) and mapped via Entrez gene ID. Overrepresented KEGG pathways were assessed by Fisher’s exact test. Two by two tables were built using the number of transcripts upregulated in the TN subtype and in a given pathway compared to non-upregulated transcripts and non-pathway transcripts (see example below). Fisher’s exact test was calculated using the R/Bioconductor (2) “fisher.test” function of the “stats” package. P-values were corrected for multiple hypothesis testing using Bonferroni’s correction for KEGG signal transduction pathways. Pathway expressions were calculated as the mean of the normalized (Z-score) gene components for each KEGG pathway, where each cohort analyzed with separate normalization for each cohort analyzed. Differentially expressed pathways between breast cancer subtypes were calculated using permutation testing in the R/Bioconductor package “samr” (1) with a FDR less than 1%, in conjunction with a t-statistic determined p-value corrected for multiple hypothesis test using Bonferroni’s correction.

QC-BCP	Wnt	Non-Wnt	Total
Upregulated in TN	8	93	101
Not upregulated in TN	34	1401	1435
Total	42	1494	1536

P = 0.00481

HMEC Oncogenic Pathways

Data for adenoviral transfected Human Mammary Epithelial Cells (HMECs) published by Bild *et al.* (4) were downloaded from GEO (series GSE3158). Probes, uniquely and differentially regulated, in an oncogenic HMEC model were calculated between the given pathway and all other samples: both green fluorescent protein (GFP) control and transfected oncogenic HMEC samples. Methods to determine differential expression were consistent with those applied to our data, i.e. permutation testing (500 permutations), a minimum fold-change of 1.5, and a FDR less than 1%. Experimental pathway regulation was calculated using similar methods as those applied to estimate canonical pathway expression, except pathway induced genes increased the pathway metric and inhibited genes decreased the metric. Specifically, probe-level data were first normalized (Z-score), pathway induced probes were summed, pathway inhibited probes were subtracted, and the total was divided by the number of pathway probes available on the given platform. Data across platforms were mapped by Entrez gene identifiers. Differential pathway regulation was assessed by permutation testing (permutations = 500, FDR < 1%) and a p-value with Bonferroni's correction applied.

LWS Data

The LWS-81 gene signature determined by treating PC9 and H2030 lung cancer cells with Wnt3A and published by Nguyen *et al.* (5) was matched across platforms by Entrez gene identifier. Probes with increased expression after treatment with Wnt3A were deemed Wnt+, and those with negative expression were denoted Wnt-. Pathway metrics were built using the same method applied to the Bild *et al.* oncogenic pathways: this includes normalization, summing Wnt+ probes, subtracting Wnt- probes and dividing by the total number of probes. Differential analysis was conducted using consistent methods. Significance was determined by p-value with Bonferroni's correction applied in combination with permutation testing.

Wnt/ β -catenin Classifier

The Wnt classifier was built using a closest shrunken centroid approach implemented in R/Bioconductor (2) using the package "pamr" (6). To aptly characterize Wnt/ β -catenin signaling we trained a classifier to identify β -catenin signaling as compared to both normal (GFP) and other oncogenic signaling (E2F3, Myc, Ras, and Src) using the adenoviral vector transformed HMEC data published by Bild *et al.* (4). Feature selection was based on a threshold yielding a FDR of 1% or less determined using the function "pamr.fdr" and 500 permutations. In cross validation the model was 100% sensitive, identifying all β -catenin transfected cells, and 97.83% specific, identifying all but one other sample correctly.

Cross Validation of Wnt Classifier

		Classifier	
		β -catenin	Other
Actual	β -catenin	9	0
	Other	1	45

This classifier was applied to the meta-analysis of 11 studies covering 1,878 primary tumor expression profiles (7-15). Application of the classifier to Affymetrix, Agilent, and Illumina data sets, followed the recommendations of pamr software (6). Specifically, data was consistently normalized within Affymetrix, Agilent, and Illumina platforms. In cross platform comparisons probes were mean averaged to gene level, samples were normalized, feature selection was limited those available on the given platform. The classifier retained the same cross-validation sensitivity and specificity regardless of platform. Multiple experiments within platforms were batch adjusted using the “pamr.batchadjust” R function of the “pamr” package.

Meta-analysis Data Sets

Data for breast cancer meta-analyses (7-16) were downloaded from Gene Expression Omnibus (GEO; <http://www.ncbi.nlm.nih.gov/geo/>) (17). CEL files for Affymetrix HG-U133A chips (GEO platform: GPL96) were loaded into Expression Console and MAS 5.0 normalized with a target intensity of 600 and exported in a linear format. Agilent data was downloaded using the normalized series matrix files for the UNC custom array (GEO platform: GPL1390) and duplicate samples between the UNNCH studies were removed. Additionally, samples with a degraded RNA profile, as identified by the authors since publication (<https://genome.unc.edu/>), were also removed. Clinical data for the UNCCCH studies were ascertained from the GEO deposits. Metastasis data for the EMC-286, EMC-192, and MSKCC-99 data sets are those published by Bos *et al.* (8).

Meta-Analysis Data Sets															
Data Set	GEO	PMID	Size	Platform	Clinical & Outcome Data										
					Intrinsic Subtype	ER	PR	HER2	Grade	Node	Chemo Treatment	Hormone Treatment	Relapse	Mets	OS
EMC-192	GSE12276	19421193	192	Affy	N	N	N	N	N	N	Y	Y	N	Y	N
EMC-286	GSE2034	15721472	286	Affy	N	Y	N	N	N	Y	Y	Y	N	Y	N
Georgia	GSE18539		143	Illm	N	Y	Y	Y	N	N	N	N	N	N	Y
GGI-327	GSE6532	17401012	327	Affy	N	Y	Y	N	Y	Y	Y	Y	Y	Y	N
MSKCC-99	GSE2603	16049480	99	Affy	N	Y	Y	Y	Y	Y	N	N	N	Y	N
Quebec	GSE17650		97	Illm	N	Y	Y	Y	N	N	N	N	N	N	N
STH-159	GSE1456	16280042	159	Affy	Y	N	N	N	Y	N	Y	N	Y	N	Y
UNCCCH-186	GSE10886	19204204	186	Agil	Y	N	N	N	Y	Y	N	PA	Y	N	Y
UNCCCH-67	GSE6128	17663798	67	Agil	Y	Y	N	N	Y	Y	N	PA	Y	N	Y
UNCCCH-73	GSE3165	19291283	73	Agil	Y	Y	N	N	Y	Y	N	PA	Y	N	Y
Uppsala-249	GSE4922	17079448	249	Affy	N	Y	N	N	Y	Y	N	Y	Y	N	N

PA: partial data

Analysis of Classifier Data

Patients classified as Wnt+ and Wnt- were analyzed for overrepresentation in pathological determined subtypes, intrinsic subtypes, histological grade, and lymph node status using Fisher's exact test implemented in R/bioconductor (2) using the function "fisher.test" of the stats package. A representative example of a two by two table is provided below.

TN Subtype / Classifier	Wnt+	Wnt-	Total
TN	52	103	155
non-TN	4	151	155
Total	56	254	310

P = 6.3x10⁻¹⁴

Kaplan-Meier analyses were created in R/Bioconductor (2) using the "survfit" function of the "survival" package. Significant differences in survival were calculated using a log-rank test p-value implemented in R/Bioconductor using the "survdif" function of the "survival" package.

Reference List

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