

Supporting Information

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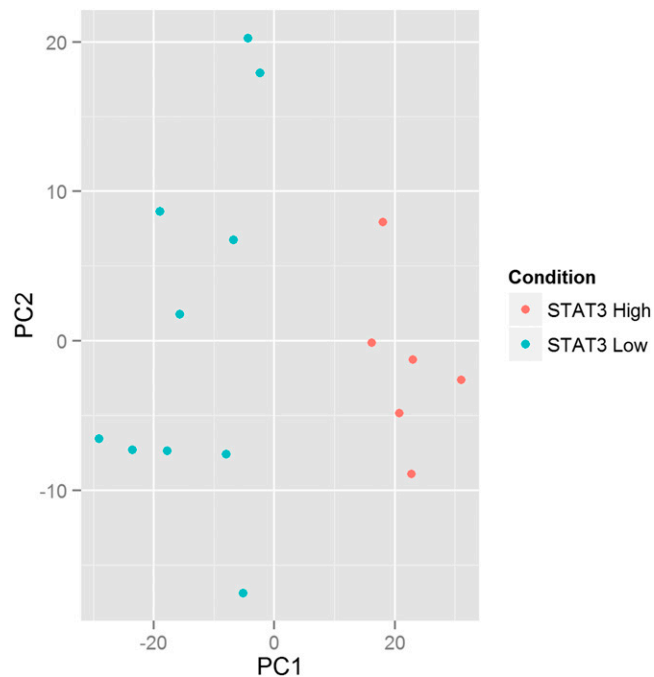


Fig. S1. Principal components analysis of differentially expressed genes detected in basal-like breast cancer. Genes differentially expressed when comparing STAT3 high (red) with STAT3 low (blue) patients were analyzed via principal components analysis to determine the overall difference in groups when comparing principal variance characteristics. Each patient is graphed along the component of highest variance on the x axis and the second highest variance on the y axis. Despite the smaller sample size of the basal-like group, the 438 differentially expressed genes clearly divide patients into separate sections of the graph as determined by the first principal component (PC).

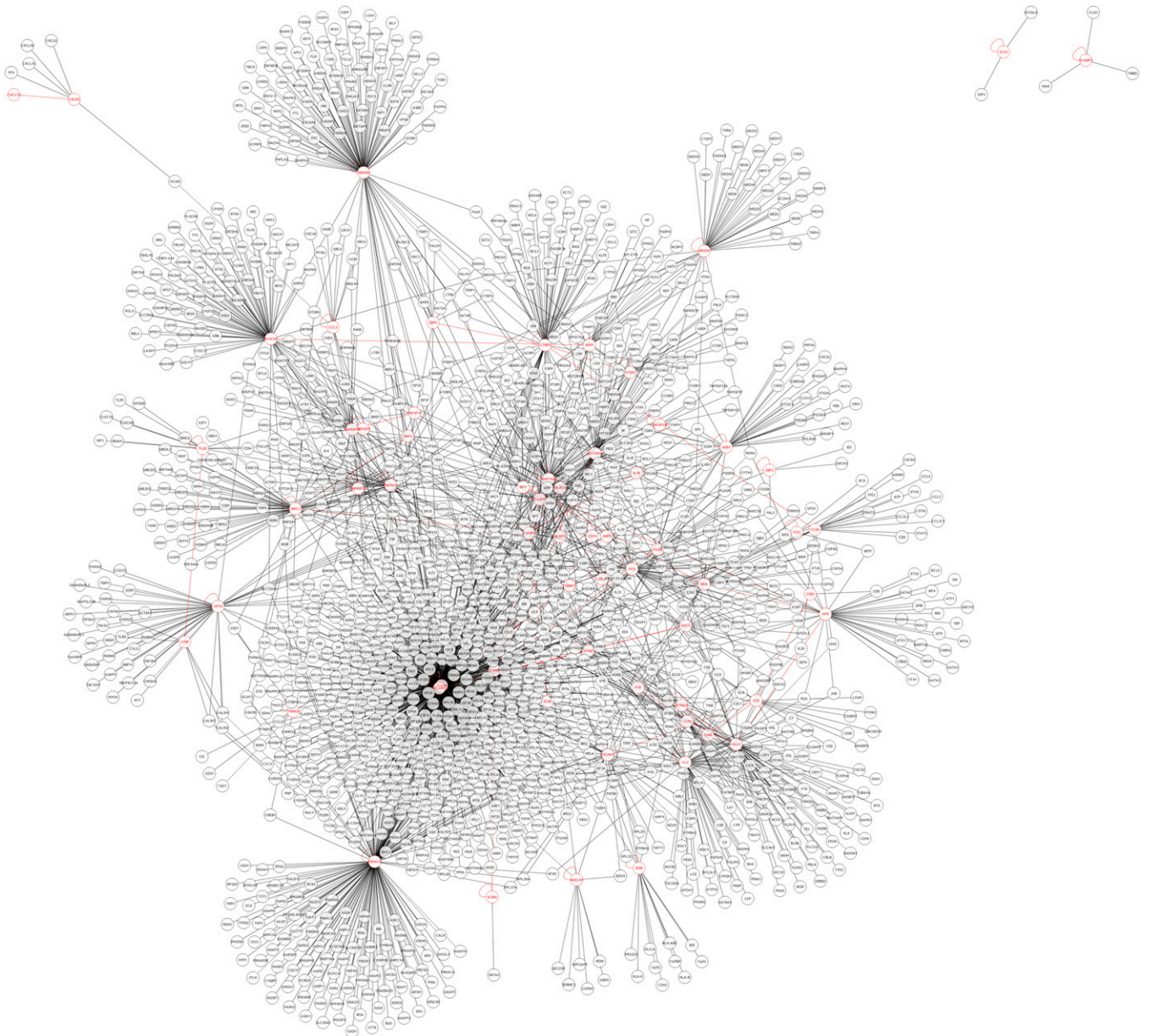


Fig. S2. Predicted protein interaction network for differentially expressed genes. Differentially expressed genes were analyzed for potential interactions via g:GOST in g:Profiler. Black lines indicate connections between genes not detected in the analysis, whereas red lines indicate known interactions between differentially expressed genes.

Table S2. Differentially regulated microRNAs by breast cancer subtype with FDR-adjusted *P* value <0.1

microRNA	Log ₂ fold change	Cancer association	Ref.
Luminal A			
hsa-mir-128-2	0.88	Mammary cell transformation	(1)
hsa-mir-128-1	0.74	p70S6K1 degradation	(2)
hsa-mir-483	-1.23	Overexpressed in epithelial malignancies	(3)
hsa-mir-224	-1.4	Associated with colorectal cancer proliferation	(4)
hsa-mir-1180	0.89	No direct evidence	
hsa-mir-145	-0.88	Inhibition of lung cancer	(5)
hsa-mir-107	0.47	Cell-cycle arrest in lung cancer	(6)
hsa-mir-214	-0.73	PTEN degradation in ovarian cancer	(7)
hsa-mir-299	-0.85	Degrades osteopontin in breast cancer	(8)
hsa-mir-423	0.5	Promotes proliferation in hepatocellular carcinoma	(9)
Luminal B			
hsa-mir-326	2.393873	MDR1 regulation in breast cancer	(10)
hsa-mir-3677	1.899579	No direct evidence	
hsa-mir-92a-2	0.979293	Hepatocellular carcinoma development	(11)
hsa-mir-215	1.677733	Positive regulator of p53	(12)
hsa-mir-760	1.946421	Plasma-level potential colorectal cancer biomarker	(13)
Basal-like			
hsa-mir-375	-3.05893	Associated with cervical cancer carcinogenesis	(14)
hsa-mir-183	-1.9353	Alteration of cellular migration in breast cancer	(15)
hsa-mir-3161	2.798385	No direct evidence	
hsa-mir-142	1.98575	Negative regulator of proliferation in pancreatic cancer	(16)
hsa-mir-196a-2	-2.17022	Polymorphism associated with cancer susceptibility	(17)
hsa-mir-3690	-1.48909	No direct evidence	
hsa-mir-150	1.398504	Promotes malignant behavior in breast cancer cells	(18)
hsa-mir-20b	-2.02197	Affects VEGF expression	(19)
hsa-mir-182	1.758854	Potential breast cancer biomarker	(20)
hsa-mir-342	1.98575	Associated with HER2 expression	(21)
hsa-mir-222	1.398886	Important for epithelial-mesenchymal transition in breast cancer	(22)
hsa-mir-3614	1.758854	No direct evidence	
hsa-mir-363	-1.75518	Regulation of metastasis and tumorigenesis	(23)

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Dataset S1. Patient reverse-phase protein array data expressed as a z score for all patients analyzed for each cancer subtype

[Dataset S1](#)

Dataset S2. List of differentially expressed genes used in this study

[Dataset S2](#)