

Table S2: Breast Cancer Data pathway analysis results of genes. Ingenuity Pathway Analysis Canonical Pathways from Genes involved in Gene-Metabolite Pairs of the Tumor Correlated Cluster and Tumor Anti-Correlated Cluster. P-values are all calculated from right-tailed Fisher's Exact Test.

Tumor Correlated Cluster			Tumor Anti-Correlated Cluster		
<i>Name</i>	<i>p-value</i>	<i>Overlap</i>	<i>Name</i>	<i>p-value</i>	<i>Overlap</i>
Oxidative Phosphorylation	2.00E-15	16.5% (18/109)	Hepatic Fibrosis/Hepatic Stellate Cell Activation	1.21E-06	8.7% (16/183)
Mitochondrial Dysfunction	4.98E-14	11.7% (20/171)	FAK Signaling	3.56E-05	10.1% (10/99)
Protein Ubiquitination Pathway	5.50E-04	4.2% (11/265)	Actin Cytoskeleton Signaling	7.28E-05	6.6% (15/227)
GDP-mannose Biosynthesis	2.27E-03	33.3% (2/6)	Signaling by Rho Family GTPases	1.94E-04	6.0% (15/248)
Pyridoxal 5'-phosphate Salvage Pathway	9.01E-03	6.2% (4/65)	Circadian Rhythm Signaling	5.18E-04	15.2% (5/33)