

**Table S1.** Summary of [<sup>3</sup>H]-L-glutamine and [<sup>3</sup>H]-L-leucine uptake IC<sub>50</sub> values for breast cancer cells treated with varying concentrations of BenSer.

Cell line	<sup>3</sup> H]-L-glutamine IC <sub>50</sub>				<sup>3</sup> H]-L-leucine IC <sub>50</sub>			
	MCF-7	HCC1806	MDA-231	MCF10a	MCF-7	HCC1806	MDA-231	MCF10a
IC <sub>50</sub>	37.85	17.19	15.37	3.901	3.789	2.87	3.001	17.63
Span (%)	= 100	= 91.81	= 80.01	= 65.15	= 93.74	= 97.71	= 98.58	= 100

**Supplementary Table 2.** Summary of Kruskal-Wallis tests with Dunn’s multiple comparisons correction on inter-subtype comparisons of gene expression (mRNA log<sub>2</sub> values) of putative BenSer targets *SLC7A5*, *SLC3A2*, *SLC7A8*, *SLC1A5*, *SLC1A4*, *SLC38A1*, and *SLC38A2* in the METABRIC dataset (n=2509). Data were grouped into the “PAM50 + Claudin-low” subtypes based on clinical attribute data retrieved from [www.cbioportal.org/](http://www.cbioportal.org/). \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, \*\*\*\*p < 0.0001, ns=not significant.

Subtype comparison pairs	Gene								
	<i>SLC7A5</i>	<i>SLC3A2</i>	<i>SLC7A8</i>	<i>SLC43A1</i>	<i>SLC43A2</i>	<i>SLC1A4</i>	<i>SLC1A5</i>	<i>SLC38A1</i>	<i>SLC38A2</i>
Basal vs. HER2	****	ns	****	ns	**	****	**	****	****
Basal vs. Luminal A	****	***	****	****	****	****	****	****	ns
Basal vs. Luminal B	****	ns	****	*	****	****	ns	****	**
Basal vs. Normal	****	ns	****	**	***	****	****	****	*
Claudin-low vs. HER2	***	ns	****	ns	****	****	****	****	*
Claudin-low vs. Luminal A	****	***	****	****	****	****	ns	****	ns
Claudin-low vs. Luminal B	**	ns	****	ns	****	****	****	****	ns
Claudin-low vs. Normal	***	ns	****	*	****	****	ns	****	ns
HER2 vs. Luminal A	****	ns	****	**	ns	ns	****	ns	****
HER2 vs. Luminal B	****	**	****	ns	****	ns	****	ns	****
HER2 vs. Normal	****	ns	ns	ns	ns	ns	****	ns	*
Luminal A vs. Luminal B	****	****	***	ns	ns	ns	****	ns	ns
Luminal A vs. Normal	***	ns	***	ns	ns	ns	ns	ns	ns
Luminal B vs. Normal	ns	ns	ns	ns	*	ns	****	ns	ns