**Supplemental Table Legends**

**Table S1. List of hubs and raw data for network analysis**

Metabolites in common between Met-Met and Met-Gene networks and genes in common between Met-Gene and Gene-Gene networks.

**Table S2. Prognostic Value of Metabolite and Gene Hubs on Patient Survival**

**(A) Prognostic Value of Metabolite Hubs on Patient Survival**

P values were calculated by fitting Cox proportional hazard model using survival times as output and the indicated metabolites as input. P values that are <0.05 are bolded. \*, #, $ indicate the metabolite not included in the 9 (\*), 8 (#), or 7 ($) metabolite signature, respectively.

**(B) Prognostic Value of Gene Hubs on Patient Survival**

Prognostic survival determined using PROGgeneV2 in the indicated studies with the indicated impact of high or low gene expression on survival.

**Table S3. Genes highly correlated with AQP7 gene expression in human breast cancer patient tumor tissue**

Pearson’s and Spearman’s correlation coefficients of 0.7-0.96 identify genes from cBioportal, TCGA, and METABRIC that correlate with Aquaporin expression.

**Table S4. Raw data and heatmaps for metabolomics of cell lines and tumors**