When cancer spreads to a secondary tissue, or metastasizes, is when the hope for a cure becomes the hope for a treatment. Breast cancer is puzzling because it has a specific propensity to spread to the bone, brain, liver, and lung tissues, but not to the skin, heart, uterus, or spleen, and relapse often occurs ten or twenty years after initial remission. Although this pattern of spread was observed more than a century ago, the only explanations still remain hypotheses. The current prevailing explanation is the initial, 120-year old seed and soil hypothesis, which states that metastasis depends upon a unique relationship between metastatic cells (the seeds) and hospitable microenvironments (the soils).

To this end, we have created a biomaterial-based phenotyping platform to observe how metastatic breast cancer cells differentiate between diverse secondary sites. Collectively, we identified unique phenotypes of cells that spread specifically to the bone, brain, and lung, establishing a connection between \textit{in vitro} phenotype and \textit{in vivo} fate. In sum, we have used phenotyping to understand the non-random nature of metastatic spread in breast cancer, toward creating a predictive diagnostic tool and informing safe and efficacious drug design for tissue-specific metastasis.

\textbf{Figure 1.} \textbf{A.} Breast cancer spread is not random, and is hypothesized to be mediated by “seed and soil” interactions. \textbf{B.} Schematic of phenotypic screen performed on metastatic breast cancer cells across three different microenvironments. Cells metastasizing to the same site are phenotypically similar.