SCIENTIFIC ABSTRACT
Epithelial mesenchymal transition (EMT) in tumor tissue has been implicated as a potential biomarker for chemotherapy and immunotherapy resistance. However, it is unknown whether an EMT gene signature of circulating tumor cells (CTC) can also predict chemotherapy or immunotherapy response. This pilot study aims to serially profile CTC by RNA-seq and correlate the expressions of genes with treatment response in patients with metastatic breast cancer. Data collected will set the stage for a larger study testing a prediction model based on CTC molecular signature for treatment stratification in patients with advanced cancers.