During the study period the patient underwent weekly chemotherapy treatments.

CTCs were identified using the AccuCyte-CyteFinder® system (RareCyte, Seattle, WA). Samples were collected over a period of 272 days following enrollment in the clinical trial. CTCs were isolated using the AccuCyte-CyteFinder® system from whole blood and ctDNA from plasma. We used next generation sequencing and computational biology tools to analyze genomic DNA from multiple CTCs, while blood cells (WBCs) and ctDNA from various time points. We observed somatic genomic aberrations in both CTCs and ctDNA that could be classified into three groups: a) static (variants that remain unchanged during the course of therapy), b) sample-specific (variants that are unique to each time point) and c) intermediate (variants that are short-lived but are present across multiple time points). Variants identified in the blood biopsy samples were compared with variants observed in primary breast tumor, metastatic bone marrow tumor and publically available pan-cancer datasets.

We then performed meta-analysis on somatic variants to identify changes in affected networks in response to therapy over time. Several key nodes were identified that could rationally have been targeted for therapy using compounds currently in clinical trials. We then compared and contrasted the perturbed networks obtained from the CTCs and ctDNA to better understand the etiology of TNBC.

These studies represent the first step of a synergistic partnership between the Clinical Site et al. (WGA). CTCs with available sequence data are indicated with arrows (n=6). Whole Genome Sequencing was also performed on cfDNA isolated from the plasma at each time point and c) an intermediate group that has variants that are unchanged during the course of therapy, b) a sample-specific group that is unique to each time point and c) an intermediate group that has variants that are short-lived but are present across multiple time points. Variants identified in the blood biopsy samples were compared with variants observed in primary breast tumor, metastatic bone marrow tumor and publically available pan-cancer datasets.

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