**SUPPLEMENTARY MATERIAL**

**Tracking response to neoadjuvant systemic therapy through cfDNA profiling in early breast cancer**

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**Supplementary Figure S1: Cell-free DNA (cfDNA) concentration at baseline.** Box plots showing the association between cfDNA concentration at baseline with clinical and pathological variables. In all panels, the boxes show the median and interquartile range. The whiskers extend to the full range of the data points. In all panels, the *p*-values were calculated using the Wilcoxon rank sum test. All tests were two-sided.

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**Supplementary Figure S2: Cell-free DNA (cfDNA) concentration on-treatment.** Box plots showing the association between cfDNA concentration on-treatment with clinical and pathologic variables. In all panels, the boxes show the median and interquartile range. The whiskers extend to the full range of the data points. In all panels, the *p*-values were calculated using the Wilcoxon rank sum test. All tests were two-sided.

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**Supplementary Figure S3: Cell-free DNA (cfDNA) concentration post-treatment.** Box plots showing the association between cfDNA concentration post-treatment with clinical and pathologic variables. In all panels, the boxes show the median and interquartile range. The whiskers extend to the full range of the data points. In all panels, the *p*-values were calculated using the Wilcoxon rank sum test. All tests were two-sided.

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**Supplementary Figure S4: ctDNA fraction at baseline.** Box plots showing the association between ctDNA fraction, defined as the number of variants detected in cfDNA as a fraction of the aggregate set of variants detected in the given patient, at baseline with clinical and pathologic variables. In all panels, the boxes show the median and interquartile range. The whiskers extend to the full range of the data points. In all panels, the *p*-values were calculated using the Wilcoxon rank sum test. All tests were two-sided.

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**Supplementary Figure S5: ctDNA fraction at baseline.** Box plots showing the association between ctDNA fraction, defined as the maximum allele fraction (AF) of any detected variant, at baseline with clinical and pathologic variables. In all panels, the boxes show the median and interquartile range. The whiskers extend to the full range of the data points. In all panels, the *p*-values were calculated using the Wilcoxon rank sum test. All tests were two-sided.

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**Supplementary Figure S6: ctDNA fraction at baseline.** Box plots showing the association between ctDNA fraction, defined as the mean allele fraction (AF) of all detected variants, at baseline with clinical and pathologic variables. In all panels, the boxes show the median and interquartile range. The whiskers extend to the full range of the data points. In all panels, the *p*-values were calculated using the Wilcoxon rank sum test. All tests were two-sided.