

Cohorts for Figure 1

<p>Transcriptomic data – Primary breast cancers <i>Guy's</i> <i>SCAN-B</i> <i>METABRIC</i> <i>TCGA breast cancer</i> <i>ICGC</i> References [26-30]</p>	<p>Samples: Total primary breast cancer samples, $n = 6173$: Guy's: primary TNBC, $n = 131$; HER2+, $n = 32$; ER+, $n = 14$; SCAN-B: primary TNBC, $n = 165$; HER2+, $n = 420$; ER+, $n = 2425$; METABRIC: primary TNBC, $n = 101$; HER2+, $n = 117$; ER+, $n = 347$; TCGA: primary TNBC, $n = 112$; HER2+, $n = 158$; ER+, $n = 426$; ICGC: primary TNBC, $n = 73$; HER2+, $n = 4$; ER+, $n = 182$</p> <p style="text-align: right;">(Figure 1A, 1B; Supplementary Figure 1)</p>
<p>Transcriptomic data – Post-neoadjuvant chemotherapy-resistant residual TNBCs <i>Matched baseline-residual TNBC cohort</i> References [31]</p>	<p>Samples: Total matched primary and residual TNBC samples, $n = 27$ of which: King's College London: ($n = 8$); Royal Marsden Hospital ($n = 9$); The Netherlands Cancer Institute ($n = 10$).</p> <p style="text-align: right;">(Figure 1C)</p>

Cohorts for Figure 2

<p>Single-cell RNA sequencing data: <i>scRNA-seq cohort</i> References [32]</p>	<p>Samples: Total samples, $n = 27$ primary samples, 150290 cells, of which: TNBC ($n = 8$ samples, 54819 cells); HER2+ ($n = 6$ samples, 31917 cells); ER+ ($n = 13$ samples, 63554 cells).</p> <p style="text-align: right;">(Figure 2A, 2B, 2C; Supplementary Figure 2A, 2B, 3A, 3B)</p>
<p>Spatial transcriptomic data: <i>Spatial transcriptomic cohort</i> References [33]</p>	<p>Samples: TNBC samples, $n = 22$ patients, with 43 tumor sections of which: Primary (pre-treatment), $n = 13$ patients with 26 tumor sections; Residual (post-NAC), $n = 9$ patients with 17 tumor sections.</p> <p style="text-align: right;">(Figure 2D)</p>

Cohort for Figure 3

<p>Transcriptomic data - cell line: <i>Cancer Cell Line Encyclopedia (CCLE)</i> (https://portals.broadinstitute.org/ccle)</p>	<p>Samples: CCLE database was used to characterize mRNA expression of EGFR, cyclin A, cyclin E and CDK2 in human cell lines.</p> <p style="text-align: right;">(Figure 3B)</p>
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Supplementary Table 1. Summary of transcriptomic datasets from different patient cohorts.