# Multiplexed immunofluorescence reveals protein expression alterations in breast cancer

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Breast cancers are highly variable and the specific characteristics of a tumor determine treatment response and patient outcome. Genetic sequencing has improved our understanding of the genetic changes that underlie cancer phenotypes; however, less is known about differences in protein expression among breast cancers.

A new study in *JCI Insight* reports the use of a multiplexed immunostaining platform to examine the protein expression within breast tumors. Research teams led by Ingo Mellinghoff and Steven Larsen of Memorial Sloan Kettering Cancer Center, and Fiona Ginty of GE Global Research evaluated expression of 27 proteins in single cells within paraffin-fixed sections from patients with untreated stage II/III breast cancer.

The researchers identified 8 clusters of proteins that were co-expressed within cancer cells. A third of the breast tumors expressed only one of the 8 clusters, while the remaining tumors contained multiple protein co-expression clusters that occurred in discrete and interspersed patterns.

These results indicate that multiplexed immunofluorescence is a useful technique to interrogate cell populations and signaling networks within a tumor to enhance our understanding of tumor biology.

  **More information:** Anup Sood et al, Multiplexed

immunofluorescence delineates proteomic cancer cell states associated with metabolism, *JCI Insight* (2016). DOI: 10.1172/jci.insight.87030

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