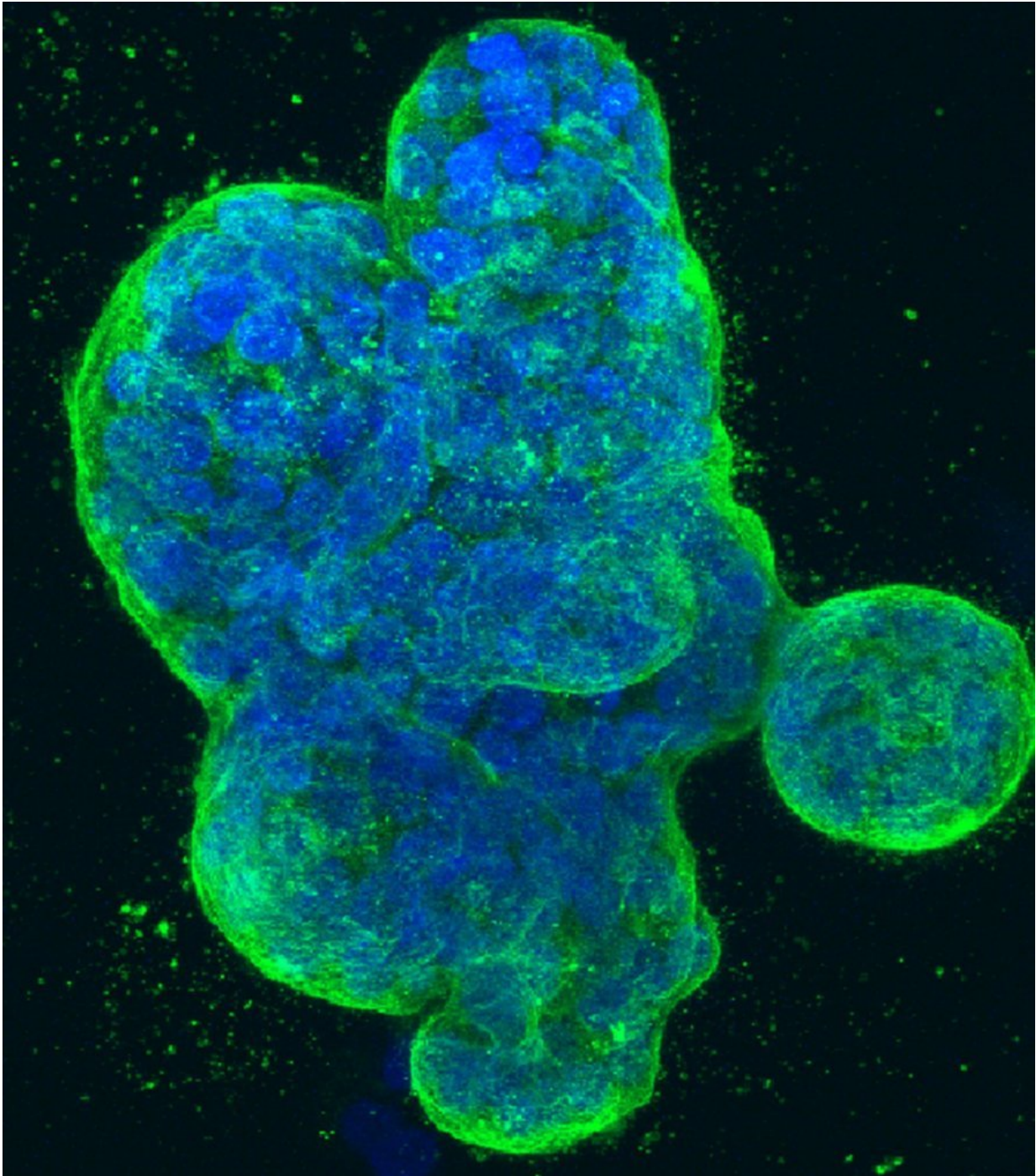


New breast cancer targets

May 4 2018



Three-dimensional culture of human breast cancer cells, with DNA stained blue and a protein in the cell surface membrane stained green. Image created in 2014 by Tom Misteli, Ph.D., and Karen Meaburn, Ph.D. at the NIH IRP.

Genome-wide association studies (GWAS) have identified more than 150 genetic variations associated with increased risk for breast cancer. Most of these variants are not located in protein-coding gene regions but are assumed to regulate the expression of certain genes.

One way to figure out what these variants are doing is to conduct a cis-eQTL analysis. That's a way of detecting changes in the expression of genes presumably regulated by a nearby variant.

Using four large-scale data sets from normal and cancerous breast tissue samples, Xingyi Guo, Ph.D., and colleagues identified 101 candidate [breast cancer](#) susceptibility genes with variant-associated gene expression changes. In [breast cancer cells](#) grown in culture, the researchers also demonstrated how three genes promoted tumor growth by disrupting normal cell behavior.

Their findings, published May 3 in the *American Journal of Human Genetics*, reveal potential target genes associated with an increased risk of breast cancer and provide additional insights into the underlying genetic and biological mechanisms that drive this common cancer.

More information: Xingyi Guo et al. A Comprehensive cis -eQTL Analysis Revealed Target Genes in Breast Cancer Susceptibility Loci Identified in Genome-wide Association Studies, *The American Journal of Human Genetics* (2018). [DOI: 10.1016/j.ajhg.2018.03.016](https://doi.org/10.1016/j.ajhg.2018.03.016)

Provided by Vanderbilt University

Citation: New breast cancer targets (2018, May 4) retrieved 25 April 2024 from <https://medicalxpress.com/news/2018-05-breast-cancer.html>

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