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Genome-Wide Hypomethylation and Cancer Risk—Letter
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Genome-Wide Hypomethylation and Cancer Risk—Response
Kevin Brennan and James M. Flanagan

INFOGRAPHIC: Chronic social isolation is linked to increased mammary tumor growth in rodent models of breast cancer. In the SV40-T antigen mouse model of “triple-negative” breast cancer, the heightened stress response elicited by social isolation has been associated with increased expression of metabolic genes in the mammary gland before invasive tumors develop (i.e., during the carcinoma in situ stage). To further understand the mechanisms underlying how accelerated mammary tumor growth is associated with social isolation, mammary gland adipose tissue was separated from adjacent ductal epithelial cells and individual cell types were analyzed for changes in metabolic gene expression. The cover micrograph depicts representative nonadipocytes (epithelial/stromal cells) and mammary adipocytes (not shown) following collagenase treatment/centrifugation. Increased metabolic gene expression specific to the mammary adipocytes of socially isolated mice coincided with increased adipocyte glucose metabolism, lipid synthesis, and leptin secretion. Results from this study suggest that exposure to a chronic stressor (social isolation) results in specific metabolic reprogramming in mammary gland adipocytes that, in turn, contributes to increased proliferation of adjacent preinvasive malignant epithelial cells. Metabolites and/or tumor growth-promoting proteins secreted from adipose tissue could identify biomarkers and/or targets for breast cancer prevention. See article by Volden and colleagues (beginning on page 634) for more information.