Utilization of Bioinformatics and Immunocytochemistry to Examine Gap Junction Expression in Breast Cancers Cells

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Breast cancer is known for its diverse clinical classifications and expressing different levels of membrane proteins such as ion channels and gap junctions. This diversity allows more variations in cell polarization, which can lead to enhanced directional ion fluxes in certain breast cancer subtypes. We utilized the interactive web portal UALCAN to evaluate the gene expression data of gap junctions, ion exchange channels and cytoskeletal proteins in breast cancer tissues. Our data showed several gene targets (e.g., GJA1(Cx43),GJB2(Cx26) increased expression during tumor development compared to normal breast tissue. Immunocytochemistry protocols were developed to examine the spatial expression of GJB2(Cx26) in MCF10A (normal breast cells) and MCF7 (weakly metastatic) breast cancer cell lines under static conditions. Primary antibodies to GJB2(Cx26) were visualized using fluorescein conjugated anti-mouse IgG (H+L) secondary antibodies. Our data suggests that the use of genomic and proteomic expression data is an effective approach for identifying differential expression differences in normal and malignant tissues.

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