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Overexpression of the BCL11A Transcription Factor in Basal-like Versus Luminal Breast Cancer Cells

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Overexpression of the BCL11A Transcription Factor in Basal-like Versus Luminal Breast Cancer Cells

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Abstract: Gene expression profiling identifies discrete subtypes of breast cancers such as luminal, basal-like, and HER2+. Luminal breast cancers respond well to anti-hormonal therapies, and express estrogen (ER) and/or progesterone (PR) receptors. ER, PR, and HER2 are absent in basal-like or triple negative breast cancers, rendering them less responsive to anti-hormonal therapies. Forty percent of luminal breast tumors contain 'luminobasal' cells that express the marker cytokeratin 5 (CK5) commonly used to identify basal-like breast cancers. Here we ask- what are these luminobasal cells in luminal tumors? Our models include a pure luminal cell line (E-3) and a pure luminobasal cell line (EWD-8) derived from a parental luminal breast cancer cell line grown in mice. Guided by large microarray datasets comparing women's primary luminal and basal-like breast cancers, we chose to examine the expression profile of BCL11A between our E-3 and EWD-8 breast cancer cell lines. BCL11A is a transcription factor whose function within breast cancer cells is not fully known; however, microarray profiling indicates that the EWD-8 luminobasal cells express significantly higher levels of BCL11A mRNA relative to luminal cells. Our data confirms this overexpression of BCL11A in the EWD-8 cells, and is associated with the differential expression of accepted luminal and basal-like markers. Future studies will focus on knocking out a specific exon from the BCL11A gene using the Crispr/Cas9 system and assessing the effects in luminobasal cells.