



Correction to: The Emerging Roles of Steroid Hormone Receptors in Ductal Carcinoma in Situ (DCIS) of the Breast

Hugo Villanueva¹ · Sandra L. Grimm¹ · Sagar Dhamne² · Kimal Rajapakshe¹ · Adriana P. Visbal¹ · Christel M. Davis³ · Erik A. Ehli³ · Sean M. Hartig¹ · Cristian Coarfa¹ · Dean P. Edwards^{1,2}

Published online: 21 November 2018

© Springer Science+Business Media, LLC, part of Springer Nature 2018

Correction to: Journal of Mammary Gland Biology and Neoplasia (2018) 23:237–248
<https://doi.org/10.1007/s10911-018-9416-0>

The original version of this article unfortunately contained mistakes.

1) Middle initials for “Sandra Grimm” and “Adriana Visbal” were missing. Kindly see above author group for their complete names.

2) In Fig. 3, two figures embedded into one. Below is the correct Fig. 3.

The online version of the original article can be found at <https://doi.org/10.1007/s10911-018-9416-0>

✉ Dean P. Edwards
deane@bcm.edu

¹ Department of Molecular and Cellular Biology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

² Department of Pathology and Immunology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

³ Avera Institute for Human Genetics, 3720 W 69th St, Sioux Falls, SD 57108, USA

Fig. 3 Global gene expression analysis in engineered DCIS.COM cells. a Summary of gene expression changes found by microarray analysis of the DCIS.COM cell lines after a 24-h hormone treatment. The Illumina HumanHT-12 v4.0 Gene Expression Beadchip Assay was used. Genes were selected based on the criteria of a fold-change greater than 1.25 with a *p* value of less than 0.05. The patterned areas indicate commonly regulated genes, with the solid color showing genes uniquely expressed in that cell line. **b** Dendrogram integrating our gene expression profiling of ER+/PR+ DCIS.COM cells with a public specimen cohort of patient DCIS and tumor samples (normal-like, basal, HER2-enriched, and luminal subtypes)

