# Ancestry as a potential modifier of gene expression in breast tumors from Colombian women

**Silvia J. Serrano-Gómez[1,2], María Carolina Sanabria-Salas[1], Jone Garay[3], Melody C. Baddoo[4], Gustavo Hernández-Suarez[1], Juan Carlos Mejía[5], Oscar García[6], Lucio Miele[7], Laura Fejerman[8☯, Jovanny Zabaleta[3,9☯]***

**1** Grupo de investigación en Biología del Cáncer, Instituto Nacional de Cancerología, Bogotá D. C, Colombia, **2** Programa de doctorado en Ciencias Biológicas, Pontificia Universidad Javeriana, Bogotá D. C, Colombia, **3** Stanley S. Scott Cancer Center, LSUHSC, New Orleans, LA, United States of America, **4** Tulane University School of Medicine, New Orleans, LA, United States of America, **5** Grupo de Patología, Instituto Nacional de Cancerología, Bogotá D. C, Colombia, **6** Grupo de Seno y Tejidos blandos, Instituto Nacional de Cancerología, Bogotá D. C, Colombia, **7** Department of Genetics, LSUHSC, New Orleans, LA, United States of America, **8** Department of Medicine, Institute of Human Genetics, University of California San Francisco, San Francisco, CA, United States of America, **9** Department of Pediatrics, LSUHSC, New Orleans, United States of America

☯ These authors contributed equally to this work.

* jzabal@lsuhsc.edu

## Abstract

### Background

Hispanic/Latino populations are a genetically admixed and heterogeneous group, with variable fractions of European, Indigenous American and African ancestries. The molecular profile of breast cancer has been widely described in non-Hispanic Whites but equivalent knowledge is lacking in Hispanic/Latinas. We have previously reported that the most prevalent breast cancer intrinsic subtype in Colombian women was Luminal B as defined by St. Gallen 2013 criteria. In this study we explored ancestry-associated differences in molecular profiles of Luminal B tumors among these highly admixed women.

### Methods

We performed whole-transcriptome RNA-seq analysis in 42 Luminal tumors (21 Luminal A and 21 Luminal B) from Colombian women. Genetic ancestry was estimated from a panel of 80 ancestry-informative markers (AIM). We categorized patients according to Luminal subtype and to the proportion of European and Indigenous American ancestry and performed differential expression analysis comparing Luminal B against Luminal A tumors according to the assigned ancestry groups.

### Results

We found 5 genes potentially modulated by genetic ancestry: *ERBB2* (log2FC = 2.367, padj<0.01), *GRB7* (log2FC = 2.327, padj<0.01), *GSDMB* (log2FC = 1.723, padj<0.01, *MIEN1* (log2FC = 2.195, padj<0.01 and *ONECUT2* (log2FC = 2.204, padj<0.01). In the