

RESEARCH ARTICLE

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

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## 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* ( $\log_2FC = 2.367$ ,  $\text{padj} < 0.01$ ), *GRB7* ( $\log_2FC = 2.327$ ,  $\text{padj} < 0.01$ ), *GSDMB* ( $\log_2FC = 1.723$ ,  $\text{padj} < 0.01$ ), *MIEN1* ( $\log_2FC = 2.195$ ,  $\text{padj} < 0.01$ ) and *ONECUT2* ( $\log_2FC = 2.204$ ,  $\text{padj} < 0.01$ ). In the