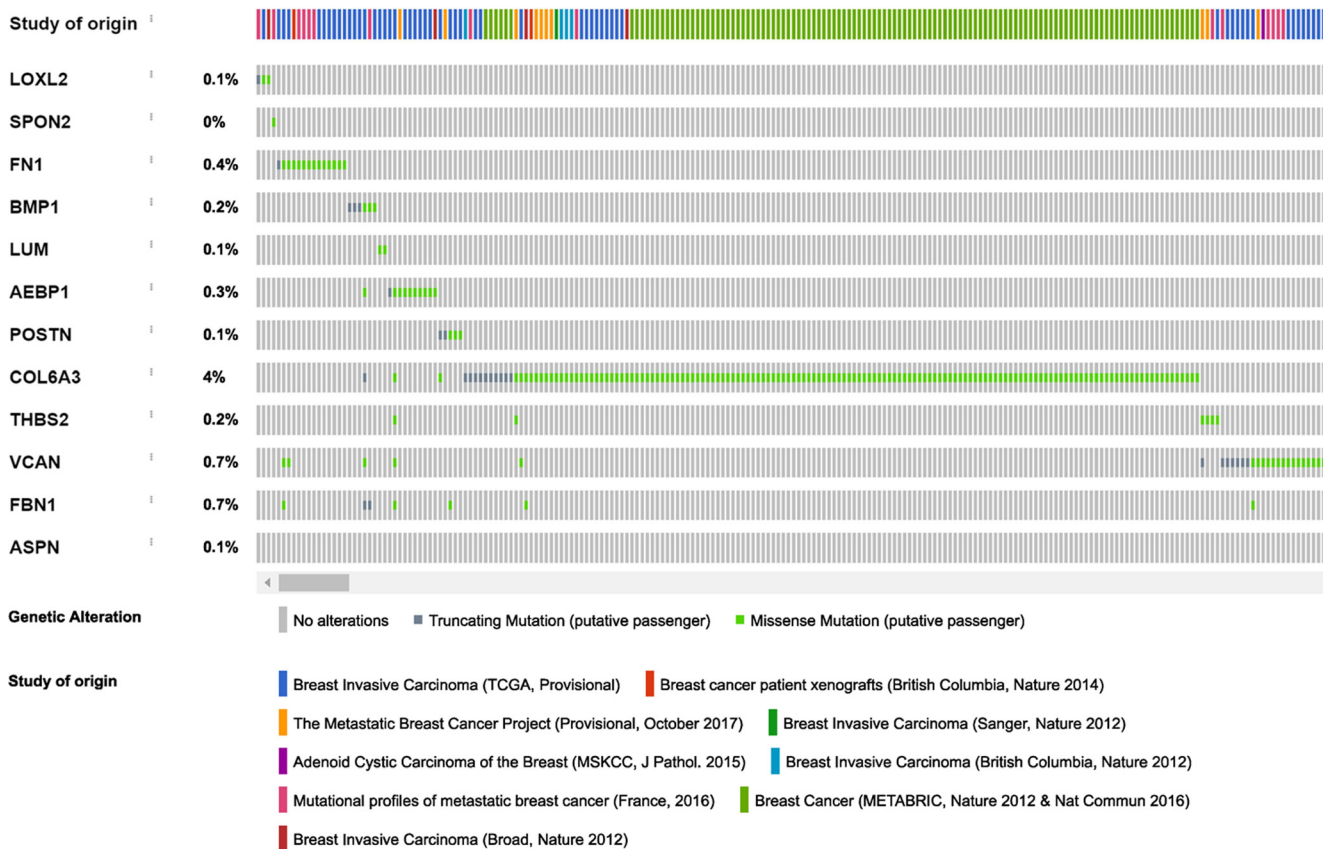


Single-cell RNA sequencing reveals gene expression signatures of breast cancer-associated endothelial cells

SUPPLEMENTARY MATERIALS



Supplementary Figure 1: *In silico* analysis of breast cancer databases. TCGA analysis for ECM-related gene expression via the cBioPortal database.