Supplementary Materials

ROR1 Potentiates FGFR Signaling in Basal-Like Breast Cancer

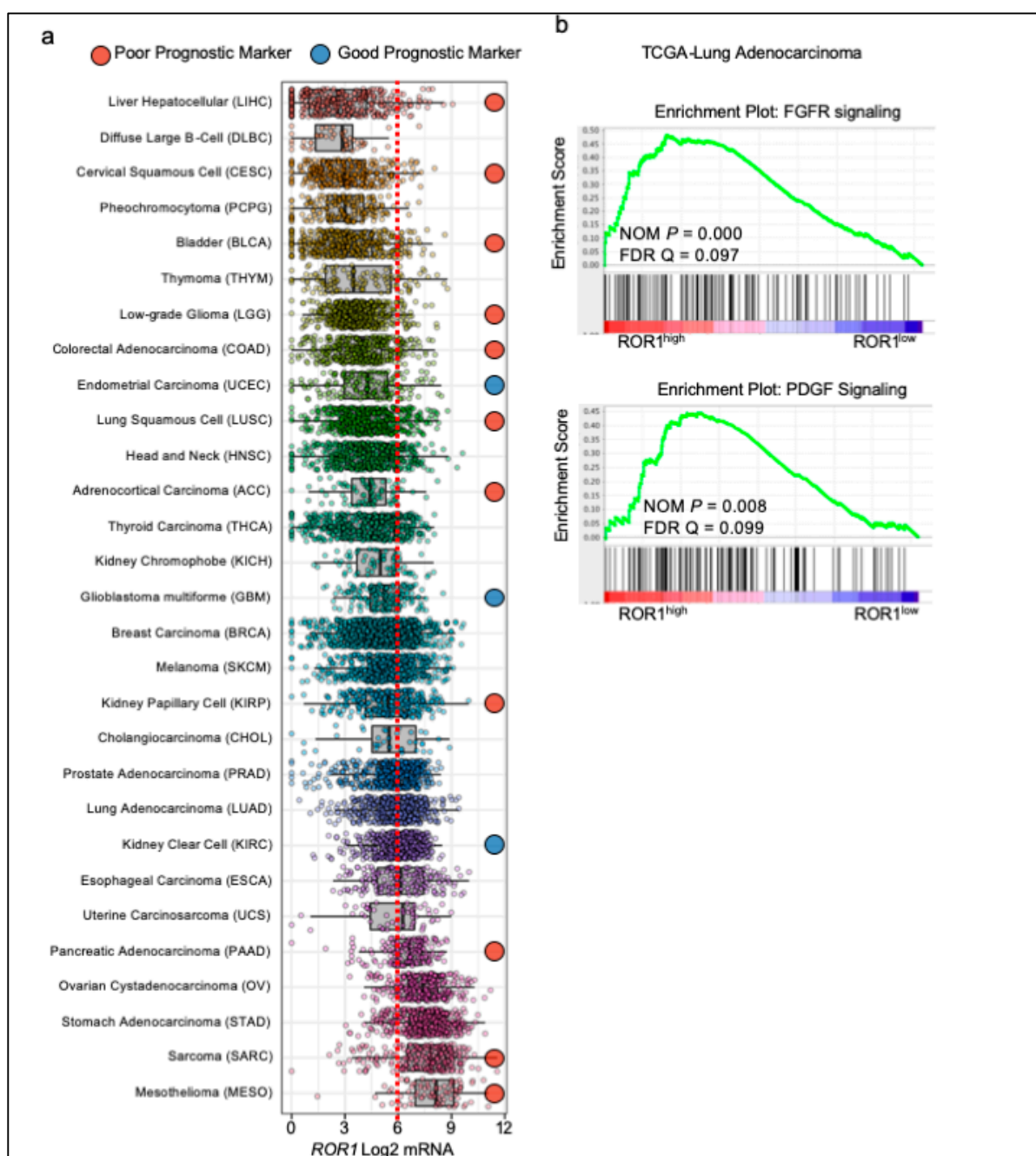**Gaurav Pandey, Nicholas Borcherding, Ryan Kolb, Paige Kluz, Wei Li, Sonia Sugg, Jun Zhang, Dazhi A. Lai and Weizhou Zhang**

Figure S1. Supplementary Figures to Figures 1 and 4. (**a**) ROR1 expression summary in different cancer types across TCGA Pan Can cohort. Brown: labeled points indicate ROR1 expression is a poor prognosis marker. Blue dots indicate ROR1 expression predicts good survival. (**b**) Enrichment plot for FGFR and PDGFR genesets showing enrichment in ROR1-high expressing group in the TCGA lung adenocarcinoma (LUAC) dataset.
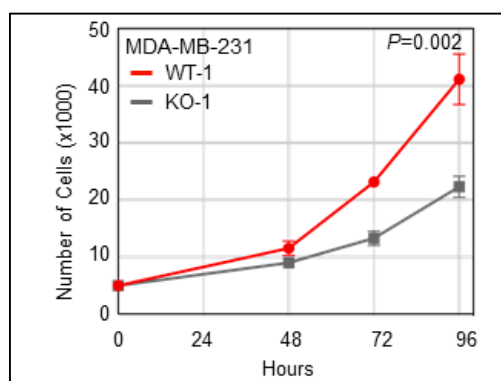
Figure S2. ROR1 promotes cell growth in MDA-MB-231 cells. Cells in Figure 2d were used for cell growth assay. Briefly, 5000 WT or KO cells were seeded and total cell numbers were counted at 48, 72 and 96 h later (n = 3).
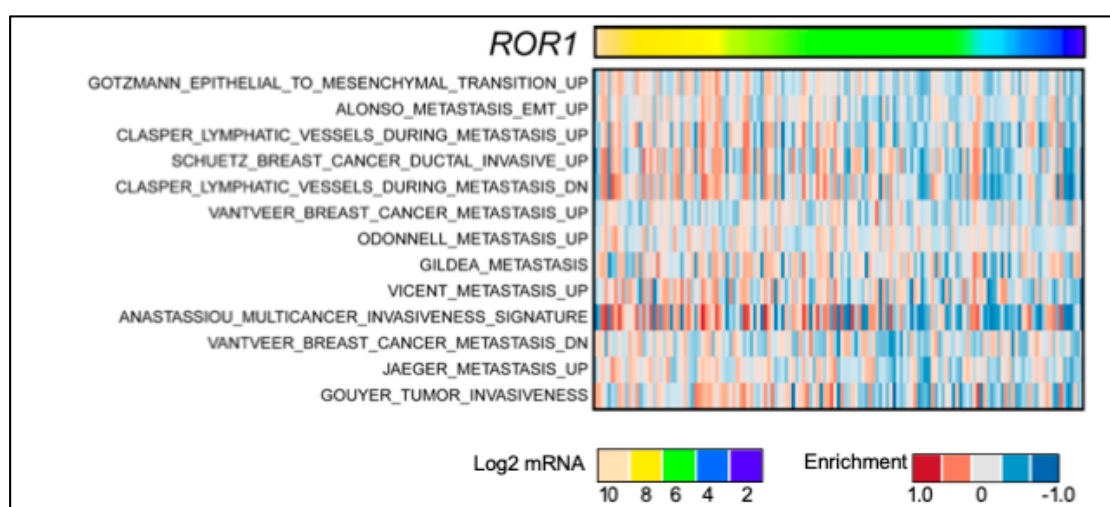

Figure S3. ROR1 expression is correlated with metastasis and EMT genesets in BLBC. Ingenuity Pathway Analysis (IPA) for upstream regulators comparing the $ROR1^{high}$ versus $ROR1^{low}$ tertiles in the BLBC samples in the TCGA. Enriched in ROR1-high specimens are those pathways involved in metastasis and EMT.