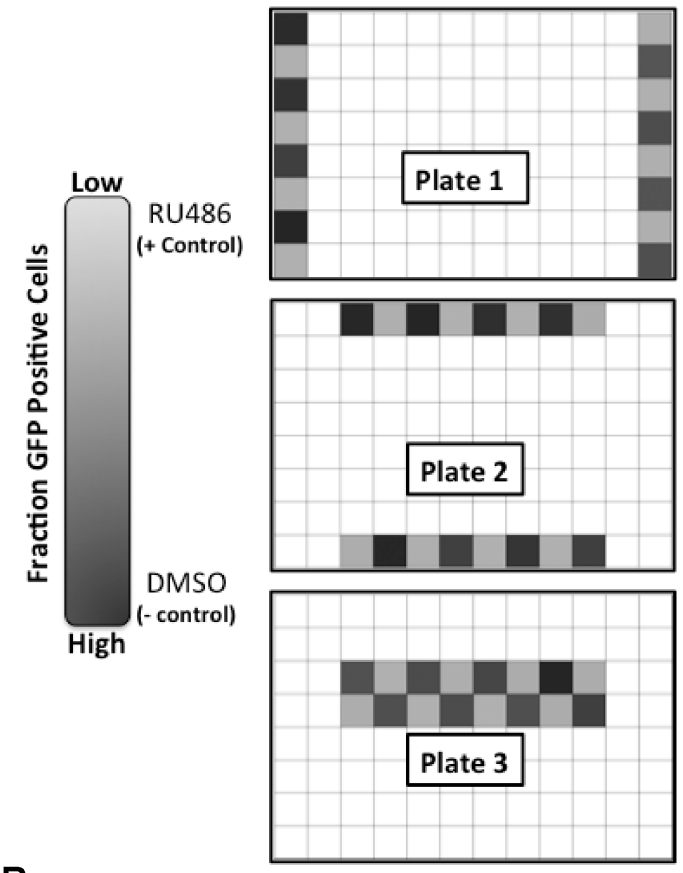
A high content assay to identify small molecule modulators of a cancer stem cell population in luminal breast cancer

Supplementary Material

Byong Hoon Yoo,[1] Sunshine Daddario Axlund,[2] Peter Kabos,[4] Brian G. Reid,[1] Jerome Schaack,[3] Carol A. Sartorius,[2] and Daniel V. LaBarbera[1]

[1]Department of Pharmaceutical Sciences, The Skaggs School of Pharmacy and Pharmaceutical Sciences; Departments of [2]Pathology, [3]Microbiology, and [4]Medical Oncology School of Medicine; The University of Colorado Denver Anschutz Medial Center, Aurora, CO, USA.

A



B

	Z' factor	S/N	S/B	%CV
Plate 1	0.49	148	20	16
Plate 2	0.71	58	16	7
Plate 3	0.55	53	14	12

Supplementary Figure S1.

High-content assay validation.

(**A**) Maps of 3 different 96-well plates for assay validation, including: 8 positive (1 μM RU486) and 8 negative (0.5% DMSO) controls per plate. All control wells were treated with 100 nM progesterone. Plate maps were generated using the Operetta® imager and Harmony® software, and the scale bar next to the maps depicts the quantitative GFP intensity per well.

(**B**) Statistical parameters of assay validation including: signal to noise (S/N), signal to background (S/B), and % coefficient of variation (%CV).