

AI Cell Health Analysis - Precision in Segmentation of Diverse Glial Cell Morphologies

Gillian Lovell

Sartorius UK Ltd, Royston, Hertfordshire, UK

Correspondence

Email: askascientist@sartorius.com

Abstract

Live cell imaging assays can yield valuable insight into biological models and have been used extensively for screening drug candidates. The images acquired can not only provide data on compound cytotoxicity but additional information on the non-toxic effects which compounds may have on cells. This is particularly useful when using valuable or easily perturbed samples such as glial cells.

Accurate cell segmentation is the first and most critical stage of turning images into quantitative and reproducible data. Incucyte® AI Cell Health Analysis uses a neural network (AI model) for segmentation, which was trained using manually annotated images of a wide range of adherent and non-adherent cell types. As a result the AI model adapts well to changes in morphology and a single algorithm can be used to robustly segment all

of the observed cell morphologies, resulting in comparable data across the biological models. Segmentation of cells such as low contrast primary astrocytes is exceptionally challenging due to their unclear boundaries and lack of cytoplasmic features, and since these cells are expensive, difficult to extract and highly sensitive, the ability to perform label-free analysis is particularly valuable.

Application Highlight

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Glial cells can have a multitude of morphologies depending on their origin, function, and activation state and adapting to these various shapes is challenging. The image panel in Figure 1 highlights the diversity of these types of cells with the segmentation mask displayed as a yellow outline around the cell boundary. Glioblastoma line A172 are rapidly growing adherent, high-contrast cells with extended protrusions. Microglia cell line BV2 grow in a semi-adherent manner and are therefore more rounded, high-contrast, and tend to grow in clusters. Primary astrocytes from the cortical region of rat brain are flat, low-contrast cells with minimal texture.

T98G are another human glioblastoma cell line which exhibit a different healthy morphology to A172. The image displays this cell line in the presence of chemotherapeutic Taxol (paclitaxel) which is used to induce cell death.

The segmentation of Taxol-treated T98G also demonstrates how well the AI Cell Health Analysis adapts to heterogeneous morphologies within a single image. This can also be observed during compound treatment (Figure 2A) as cells drastically change appearance during the transition between a live, healthy morphology to apoptotic.

Glioblastoma cells were treated with high and low concentrations of a panel of chemotherapeutic compounds. Doxorubicin (DOX) – a DNA intercalator – appeared to have differential impact on cells at low versus high concentrations. The images show that the low concentration of doxorubicin caused a small amount of cell death, while remaining live cells became enlarged and flattened compared to the healthy phenotype; the high concentration induced apoptosis in almost all the cells.

AI Cell Health Analysis accurately segmented the live, dead, and morphologically altered cells while the second neural network classified cells as live (green colored outline) or dead (red colored outline). The use of AI Cell Health for quantification ensured that data could be directly compared across different cell types and compound treatment groups, providing valuable insight into compound effects (Figure 2B).

Figure 1: AI Cell Health Analysis Accurately Segments Glial Cells with Diverse Morphologies

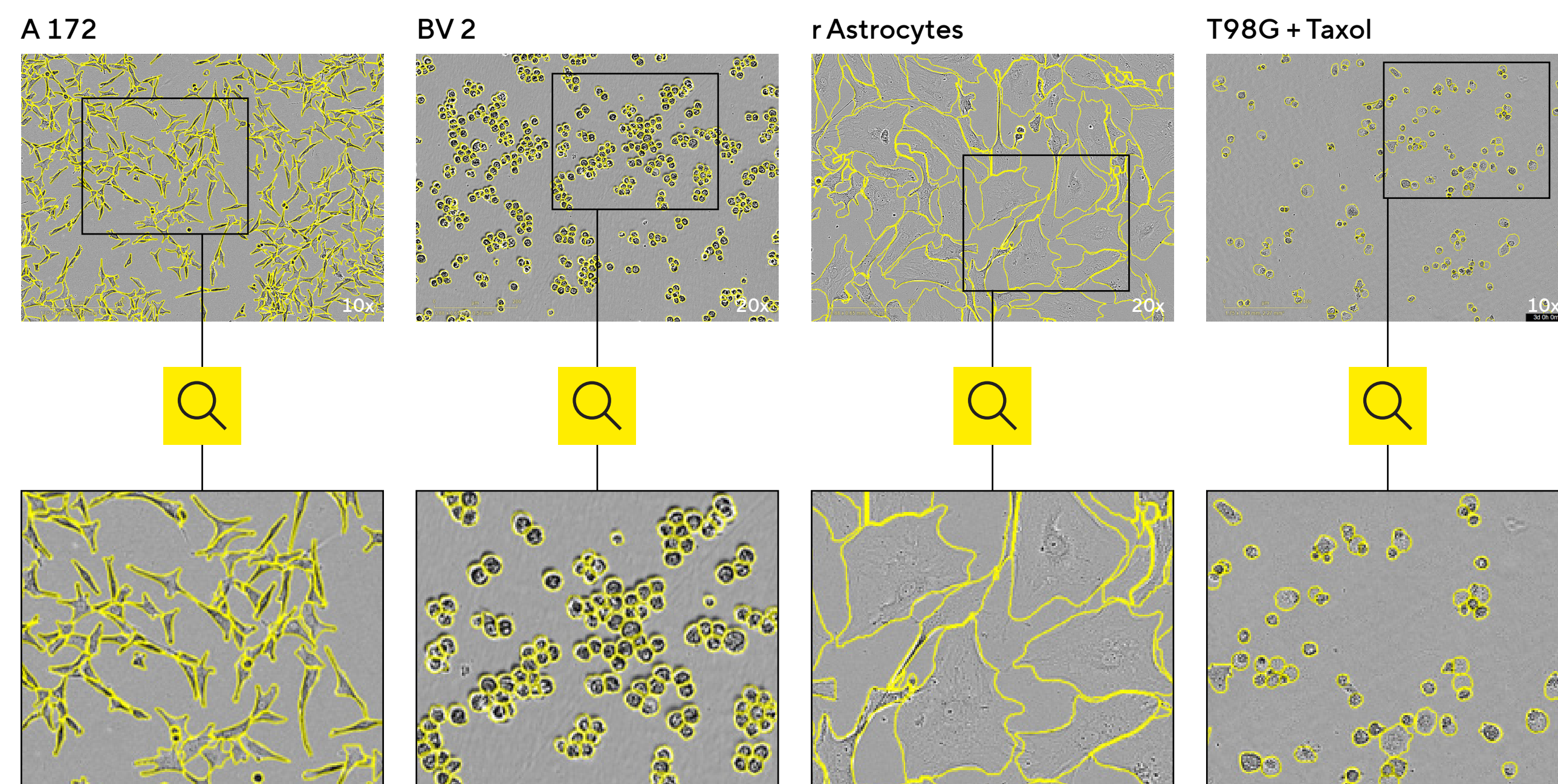
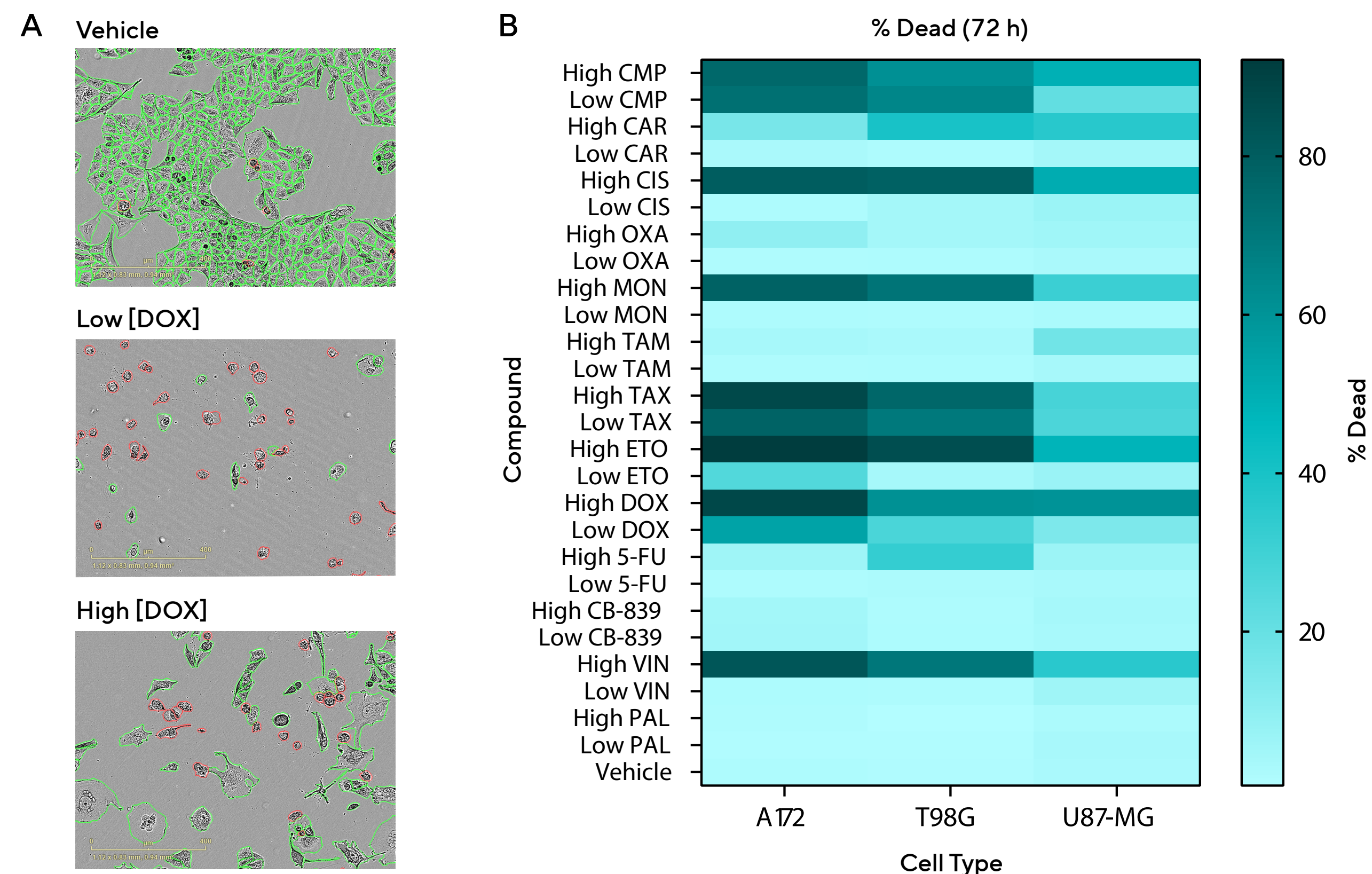


Figure 2: Label-Free Screening of Glioblastoma Responses to Chemotherapeutic Compounds



North America

Sartorius Corporation
565 Johnson Avenue
Bohemia, NY 11716
USA
Phone +1 734 769 1600
Email: orders.US07@sartorius.com

Europe

Sartorius UK Ltd
Longmead Business Centre
Blenheim Road
Epsom
Surrey, KT19 9QQ
United Kingdom
Phone +44 1763 227400
Email: euordersUK03@sartorius.com

Asia Pacific

Sartorius Japan K.K.
4th Floor, Daiwa Shinagawa North Bldg.
1-8-11, Kita-Shinagawa 1-chome
Shingawa-Ku
Tokyo 140-0001
Japan
Phone +813 6478 5202
Email: euordersUS07@sartorius.com

 **Find out more** www.sartorius.com/incucyte

 **For questions, email:** AskAScientist@sartorius.com