

友泽仁信  
Youze renxin  
友泽仁信

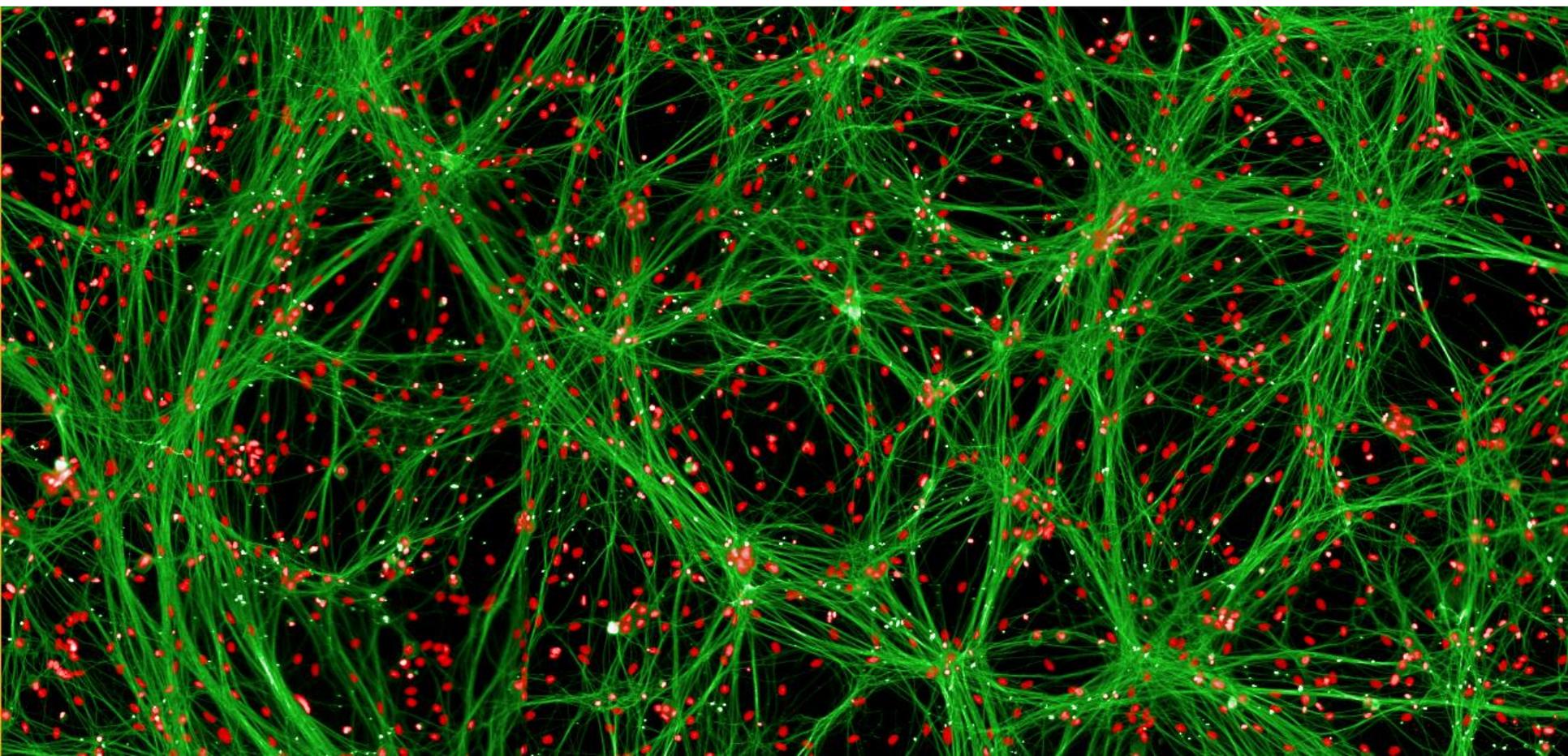
# 高内涵细胞影像信息技术

——由图像采集迈向数据挖掘



技术支持 于雪梅

济南友泽仁信贸易有限公司

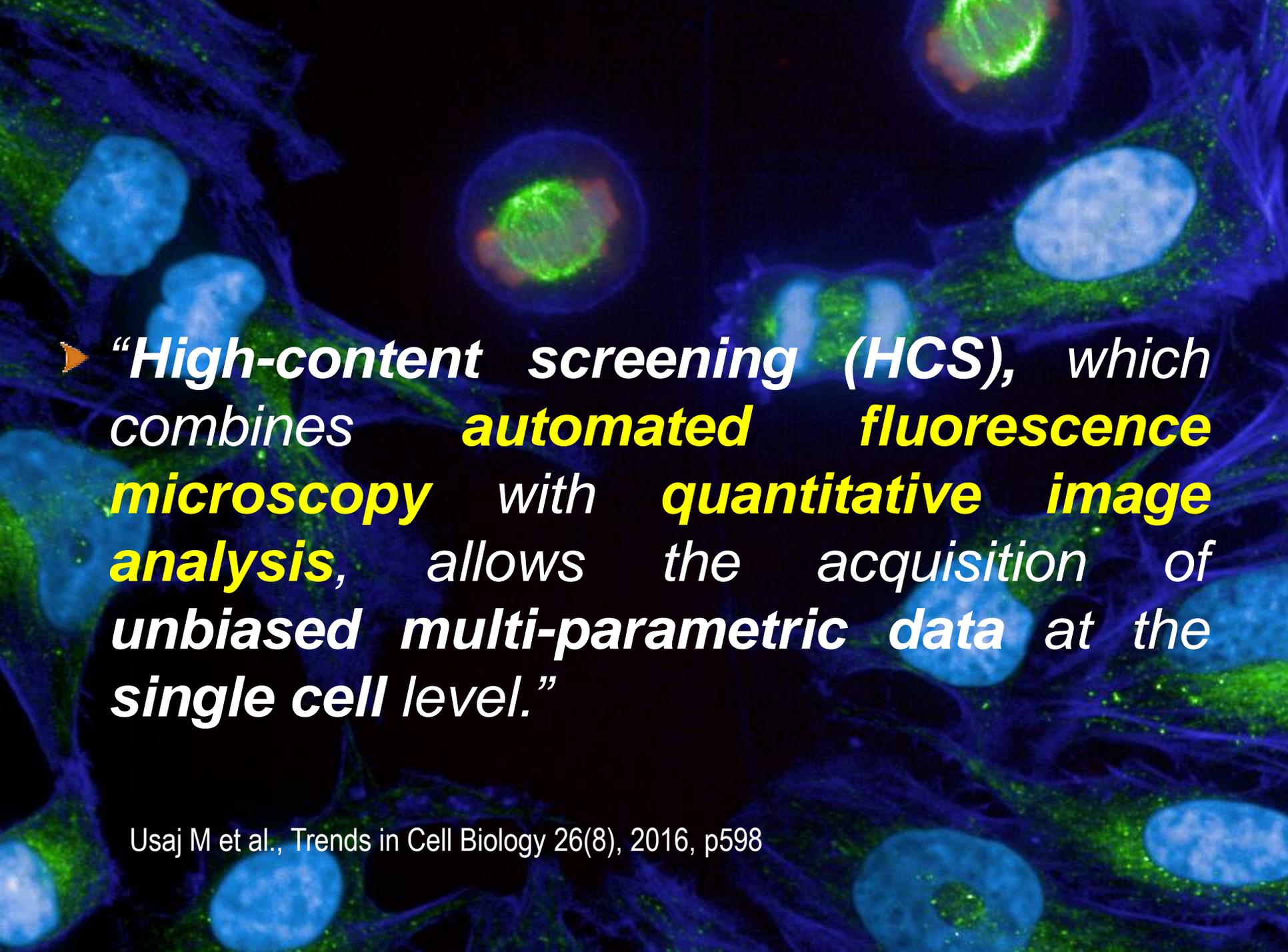


# PerkinElmer覆盖分子、细胞、动植、组织一系列产品

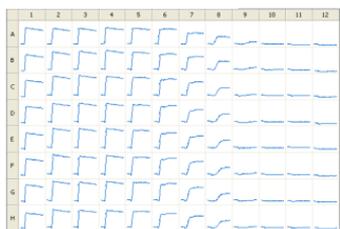
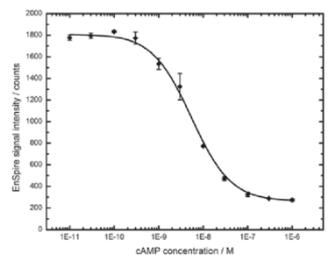


责任心  
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- 
- “**High-content screening (HCS)**, which combines **automated fluorescence microscopy** with **quantitative image analysis**, allows the acquisition of **unbiased multi-parametric data** at the **single cell level.**”

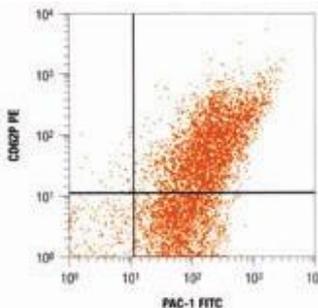
# 什么是高内涵？



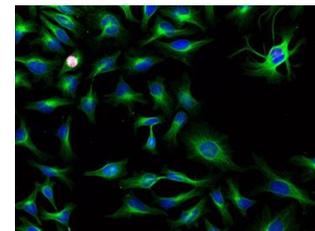
酶标仪

高通量  
成像

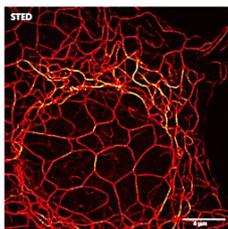
流式  
细胞仪



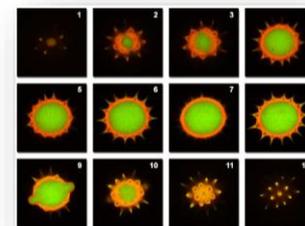
荧光  
显微镜



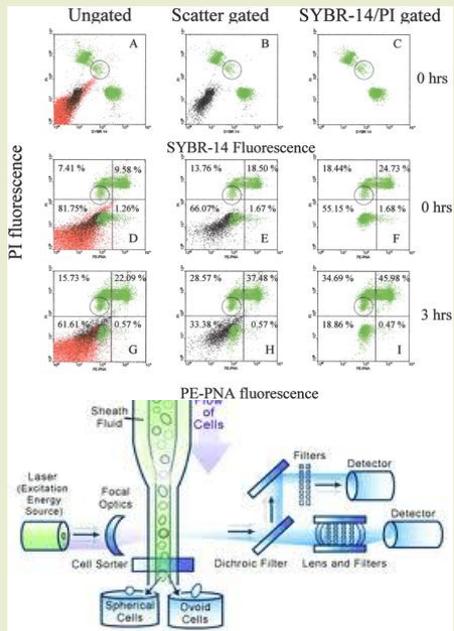
超高  
分辨



共聚焦



# 共聚焦技术vs. 流式细胞技术vs. 高内涵技术



## 激光共聚焦（玻片）

- 样本准备量大、试剂消耗量大
- 清晰的亚细胞结构图像
- 成像耗时长、效率低
- 简单细胞定量

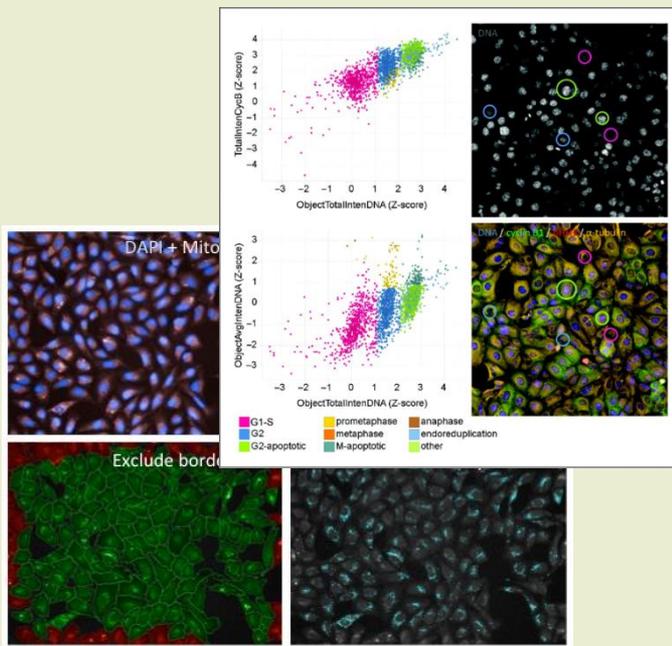
无客观批量的定量结果



## 流式细胞技术（消化细胞）

- 血液或其他液体
- 消化后的组织样品
- 样品消耗量大
- 精确的细胞水平定量结果

无亚细胞结构信息



## 高内涵技术（孔板）

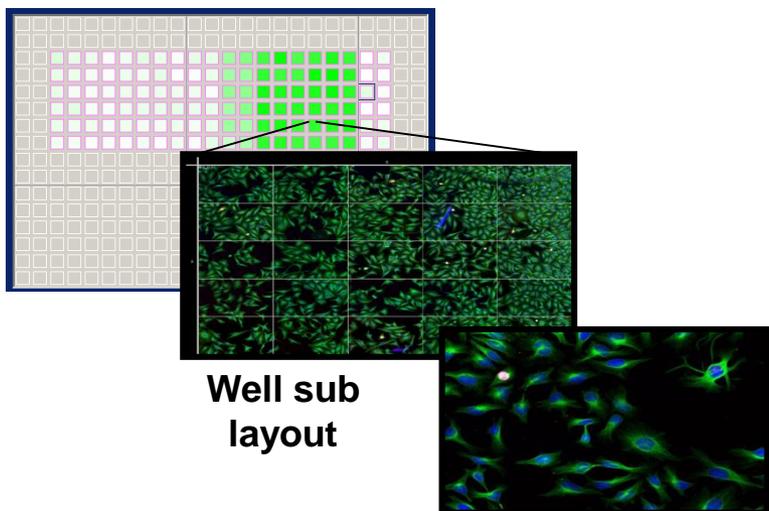
- 成像实验设计体系完整
- 清晰的亚细胞结构图像
- 精细单细胞、细胞器水平分析
- 丰富的细胞器水平软件自动算法
- 客观高效的批量数据统计结果

基于亚细胞结构的  
客观批量单细胞定量

# 高内涵的工作流程:



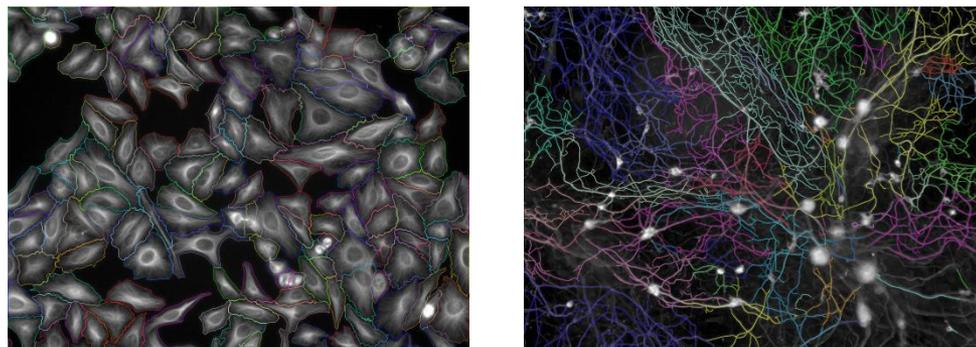
## 1. 自动扫描



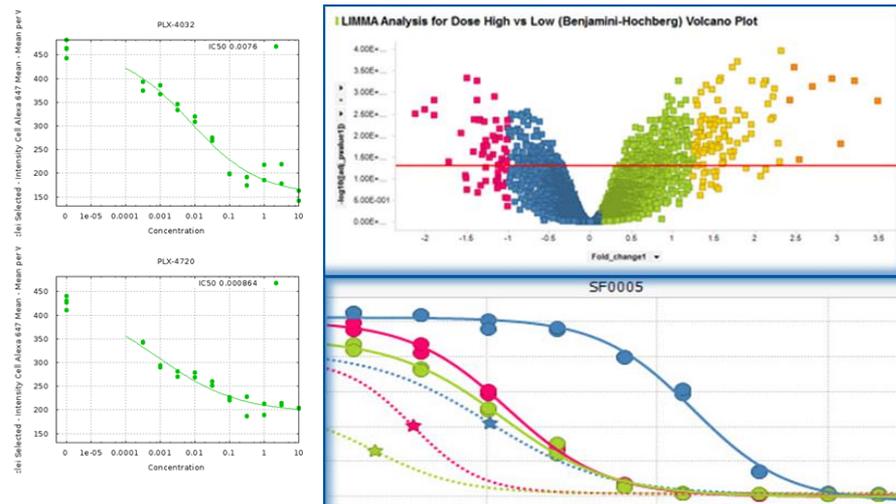
Well sub layout

Multi color image field

## 2. 图像分析



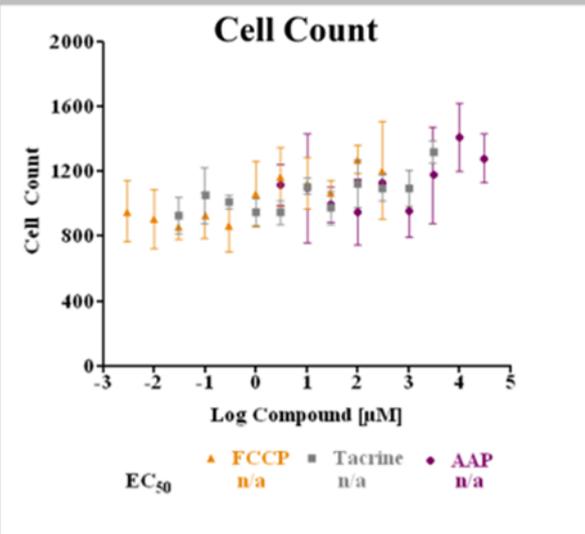
## 3. 数据可视化及数据挖掘



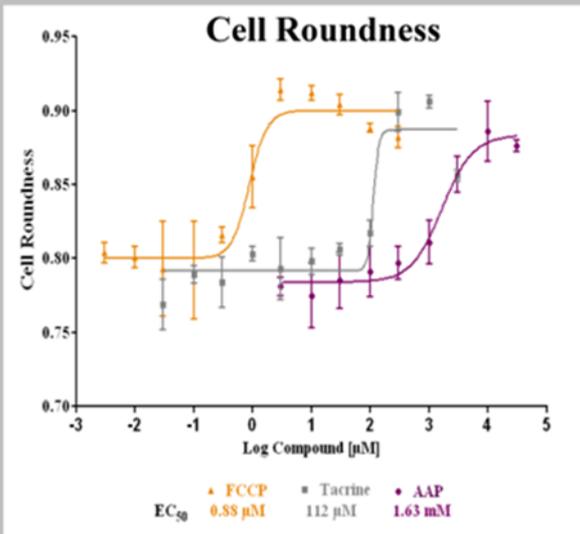
# 单细胞形态获取 + 流畅自动使用过程



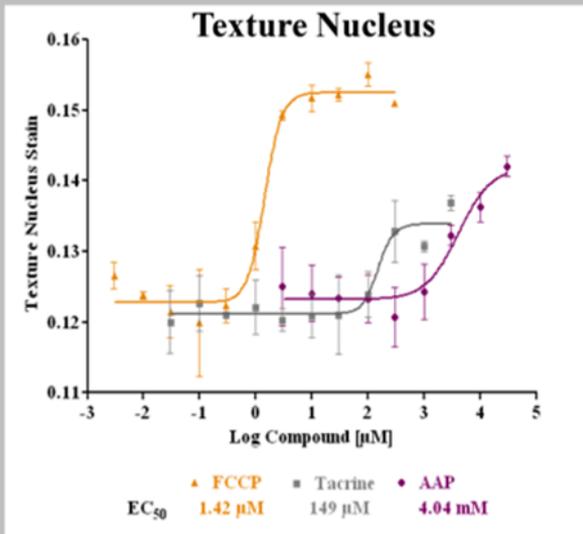
A



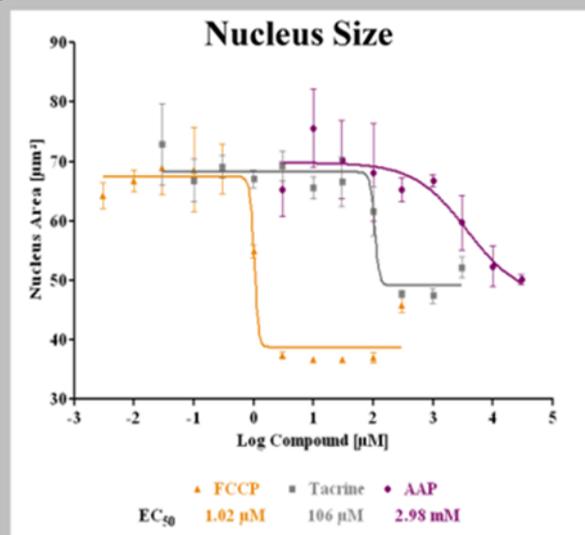
B



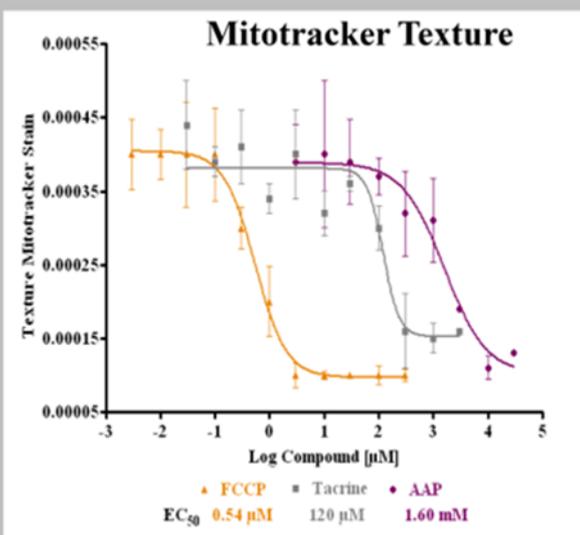
C



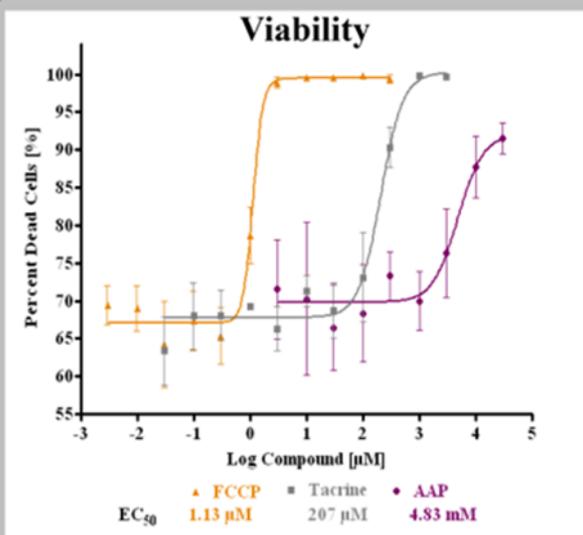
D



E



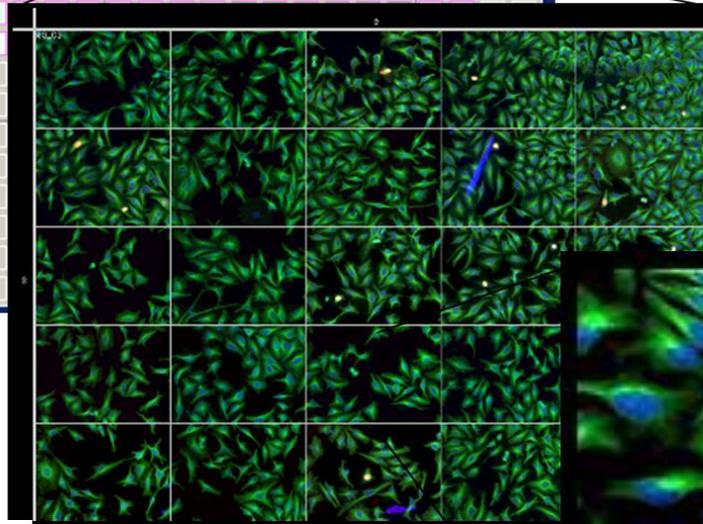
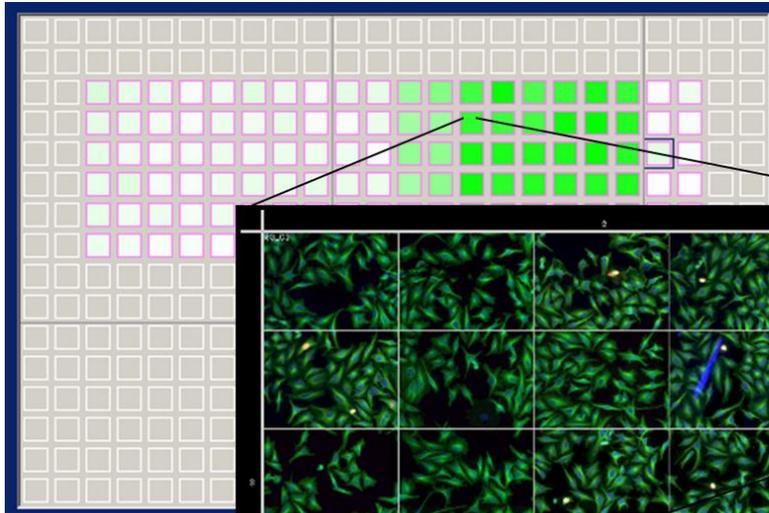
F



# 高内涵提供平行采样，提供更准确的细胞信息

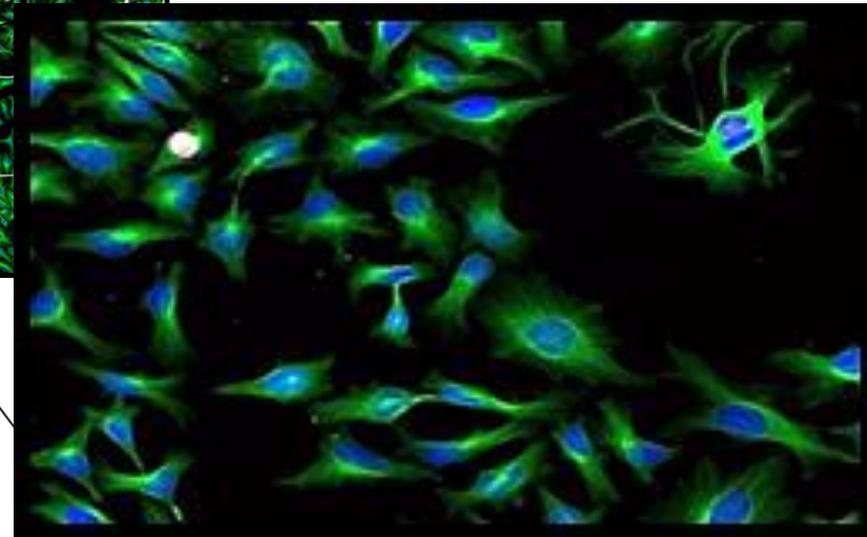
- ▶ High Content Screening is single cells based and Multi-parameter outputs

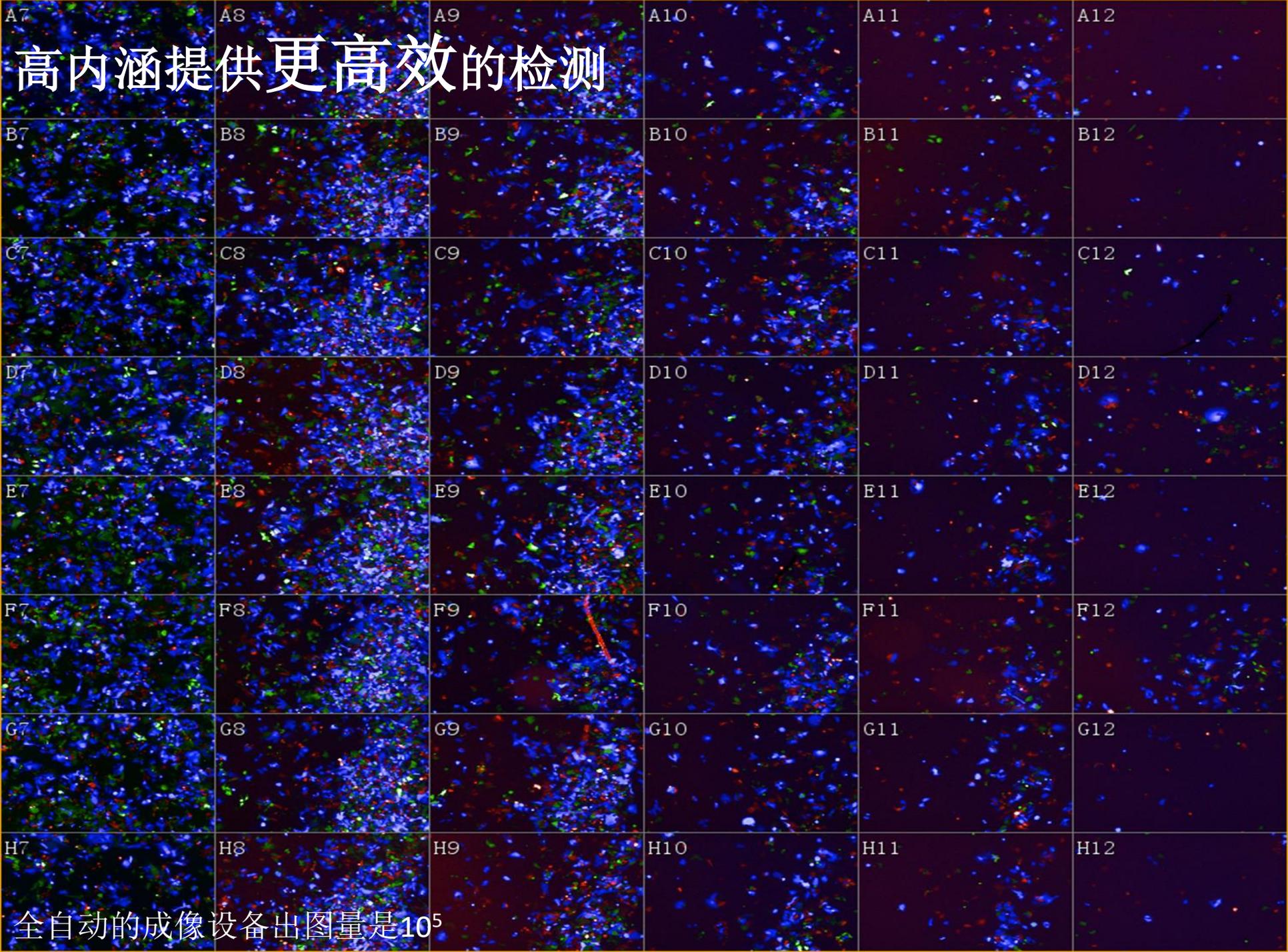
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友泽仁信



Vell sub layout

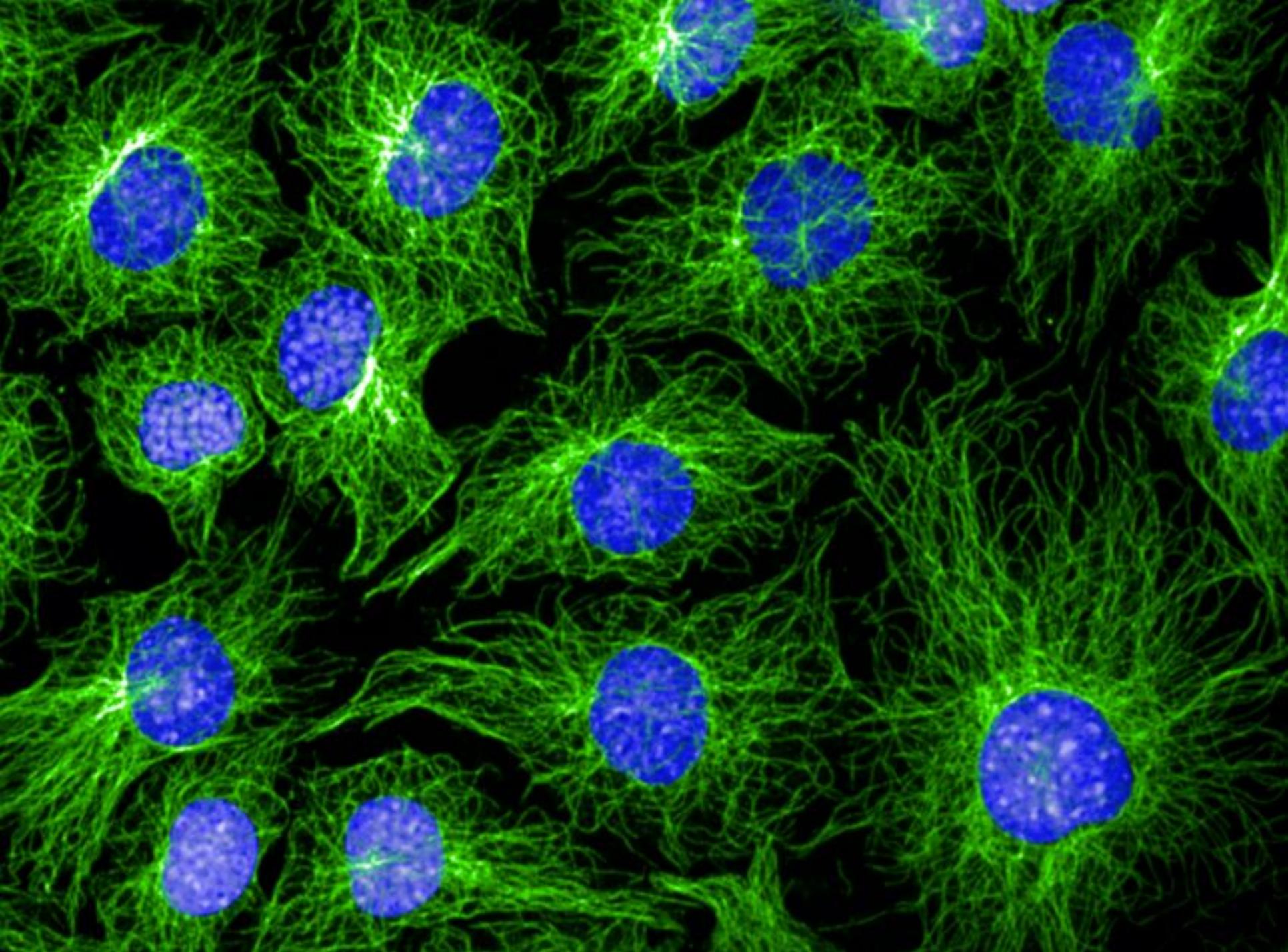
Multi color image field



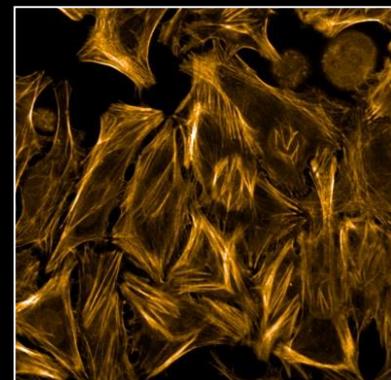
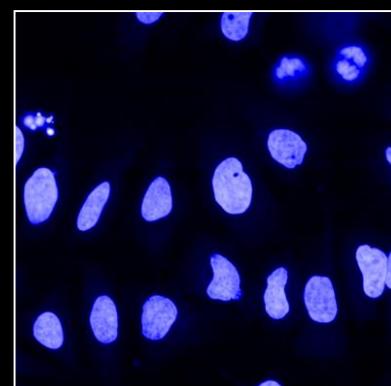
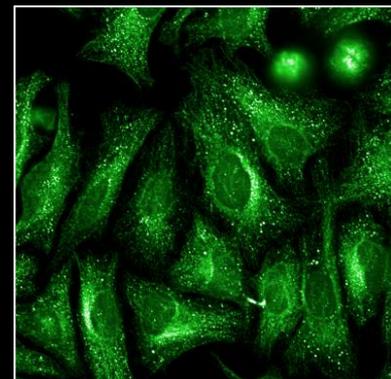
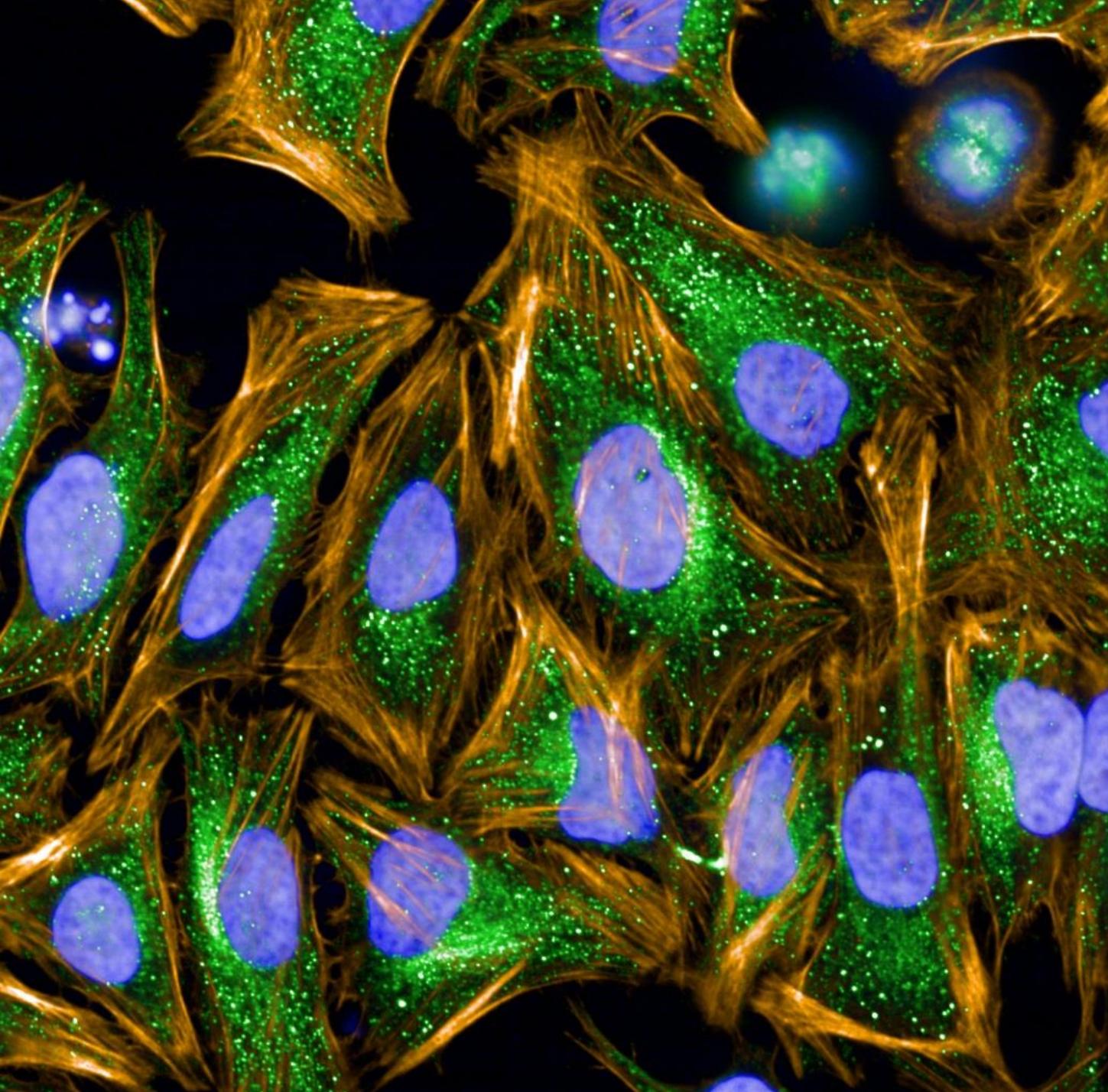


高内涵提供更高效率的检测

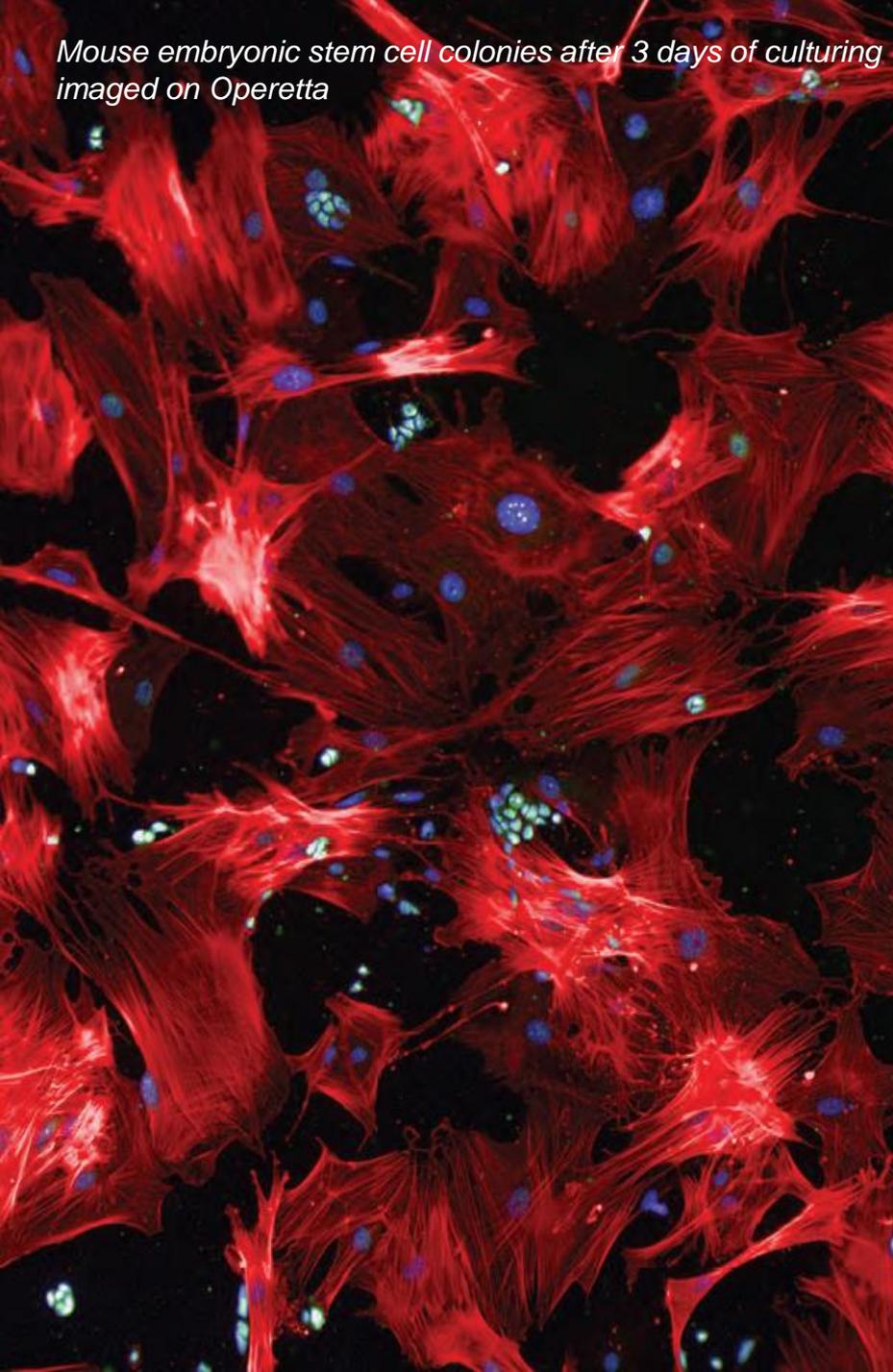
全自动的成像设备出图量是 $10^5$



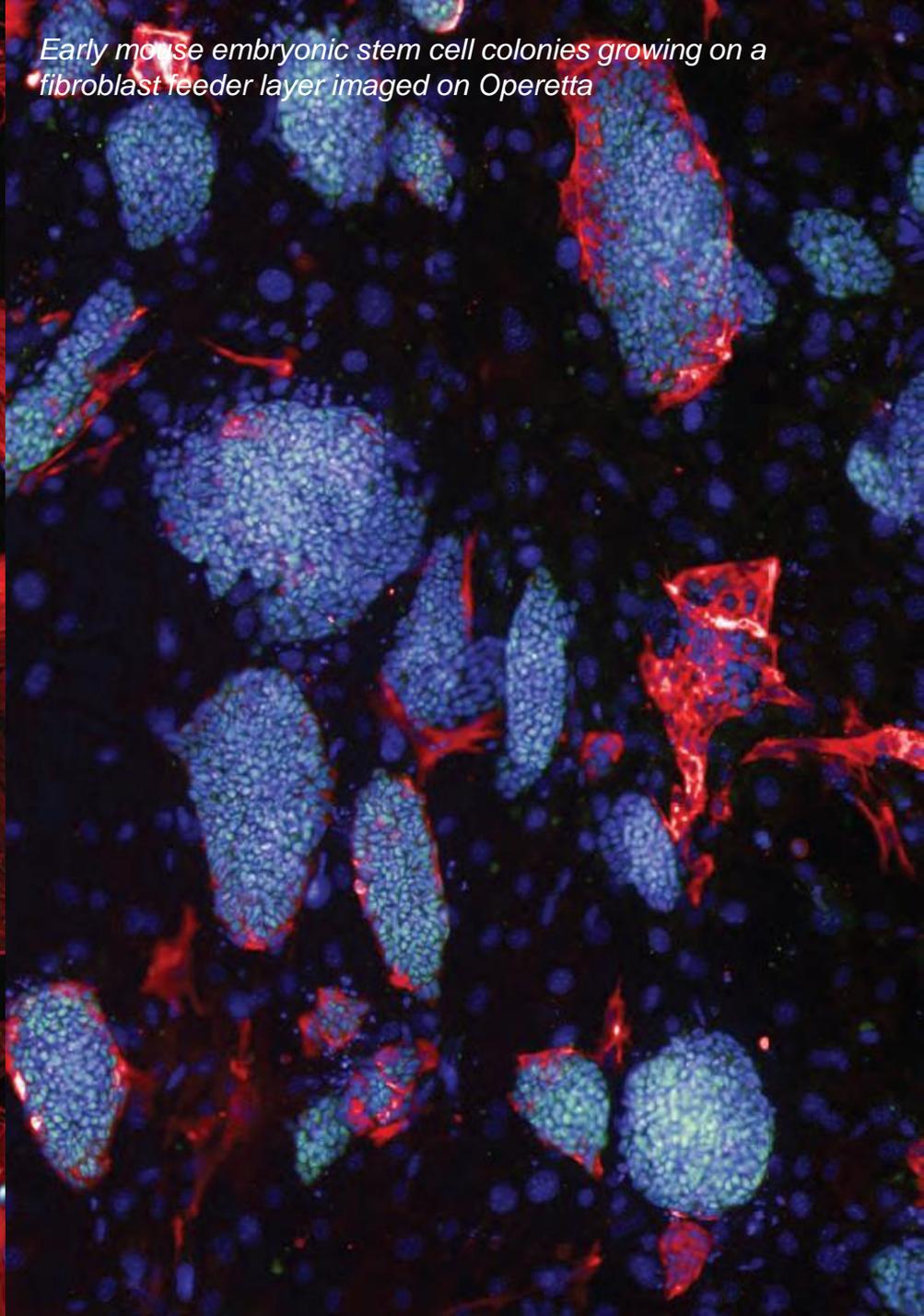
63x Water (NA 1.15)  
Confocal

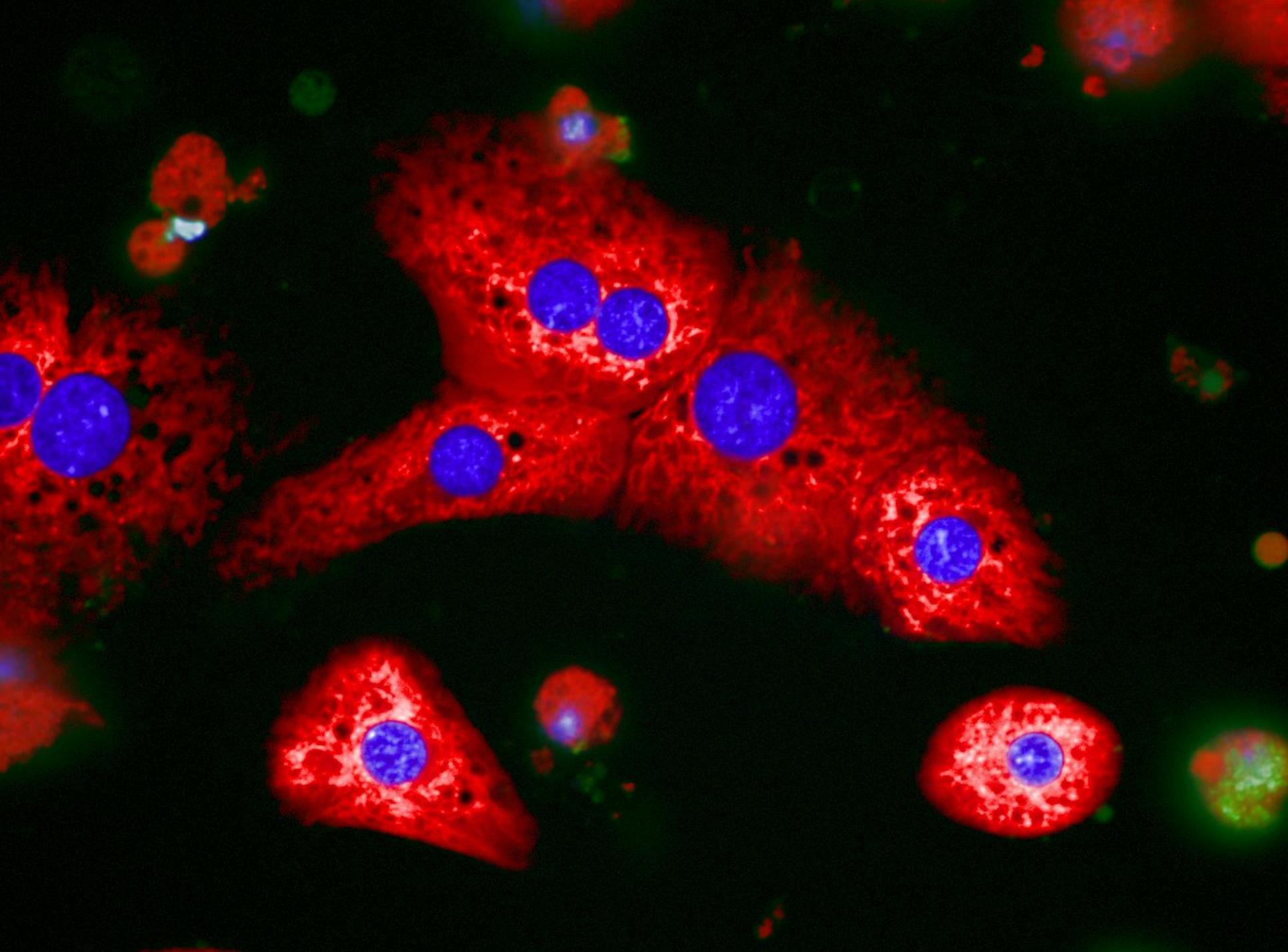


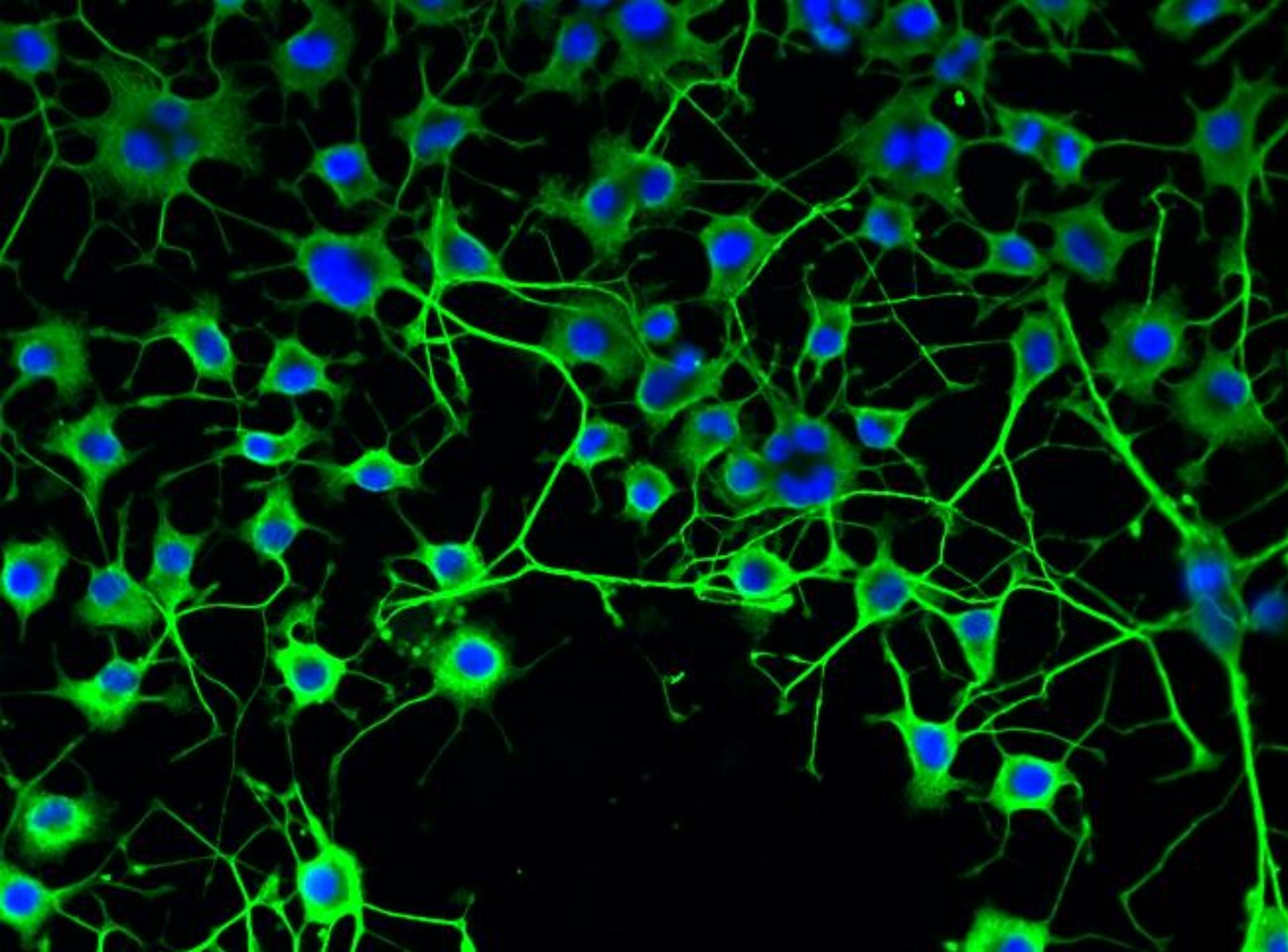
*Mouse embryonic stem cell colonies after 3 days of culturing imaged on Operetta*



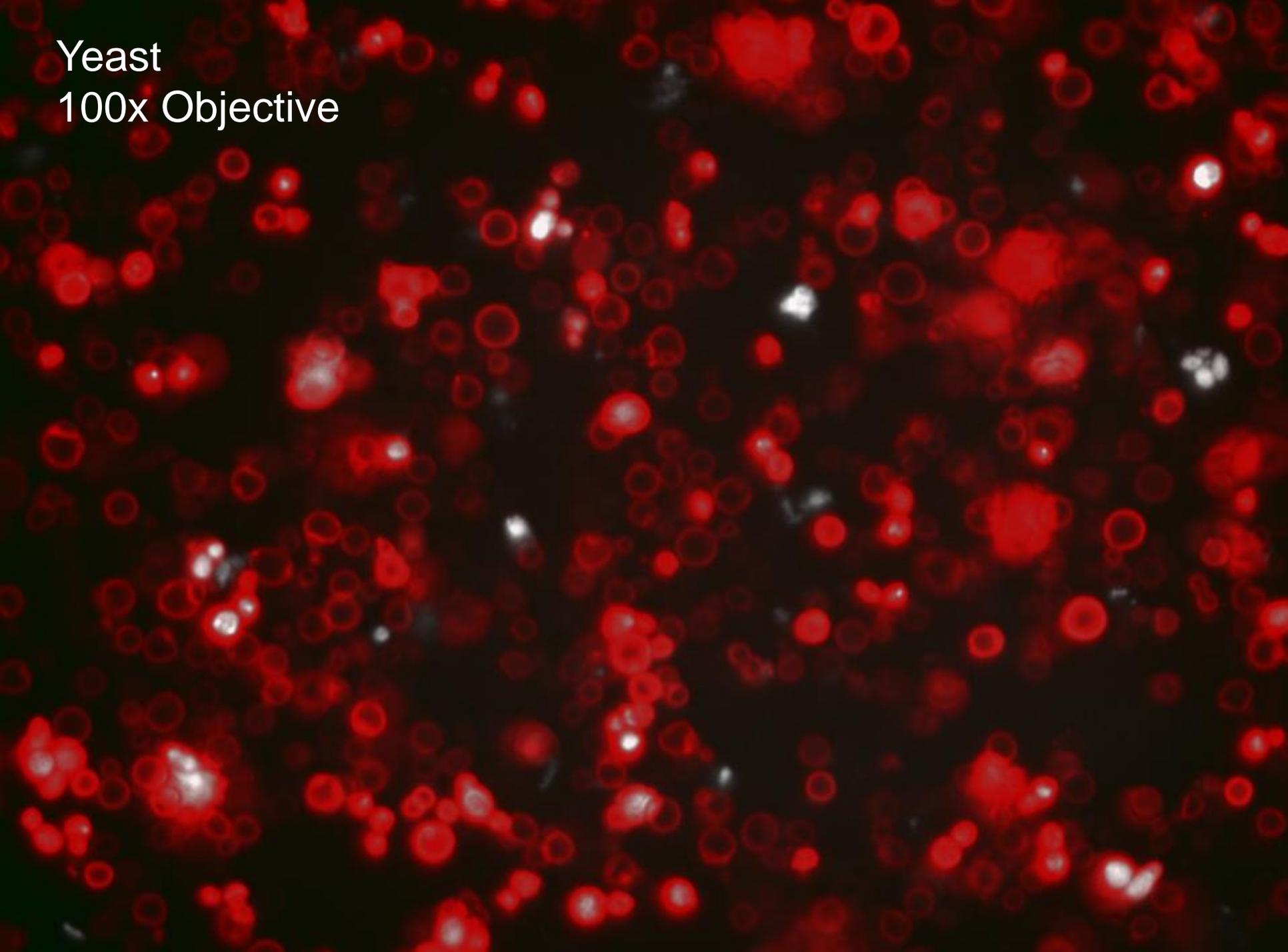
*Early mouse embryonic stem cell colonies growing on a fibroblast feeder layer imaged on Operetta*







Yeast  
100x Objective

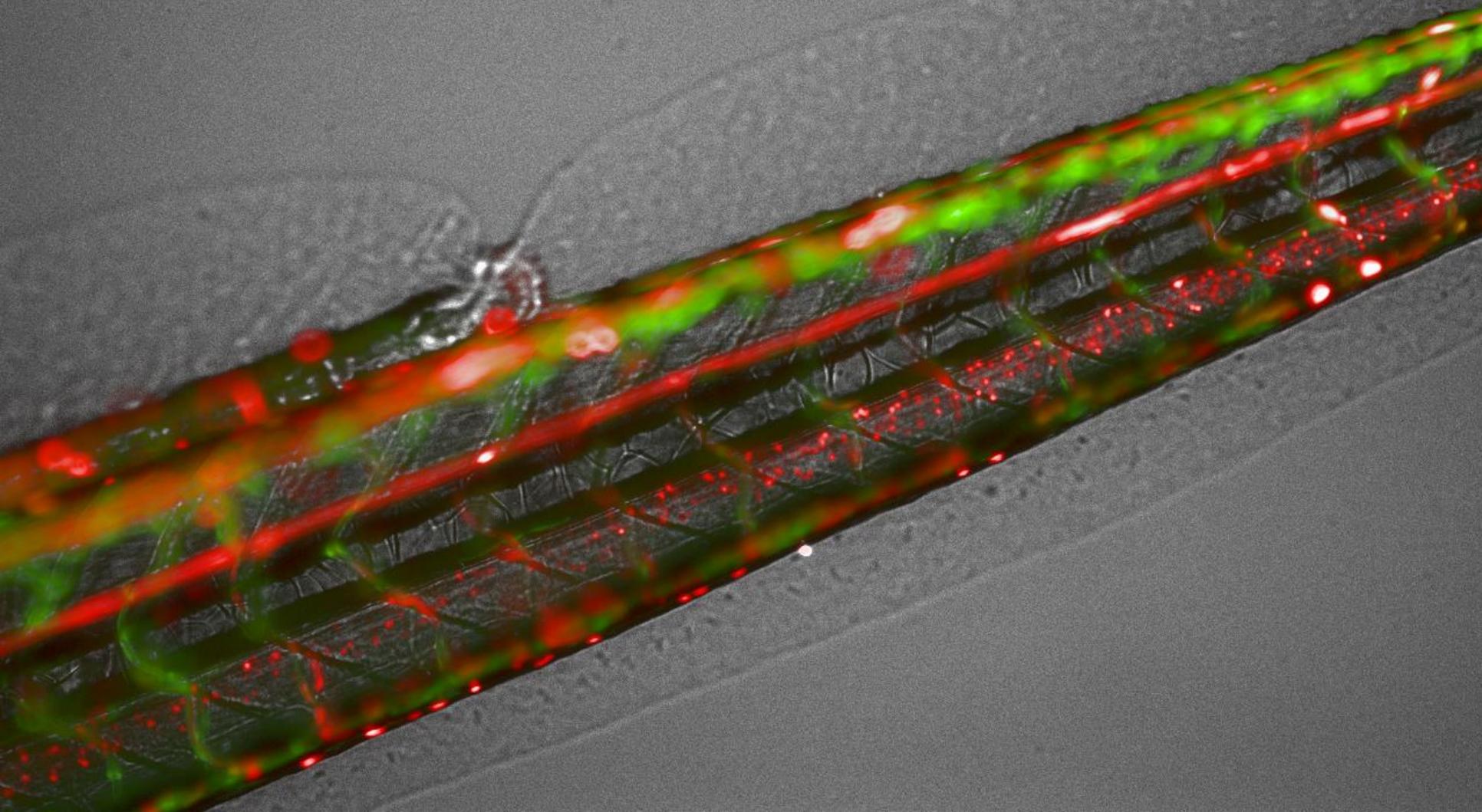


# Zebrafish

Brightfield

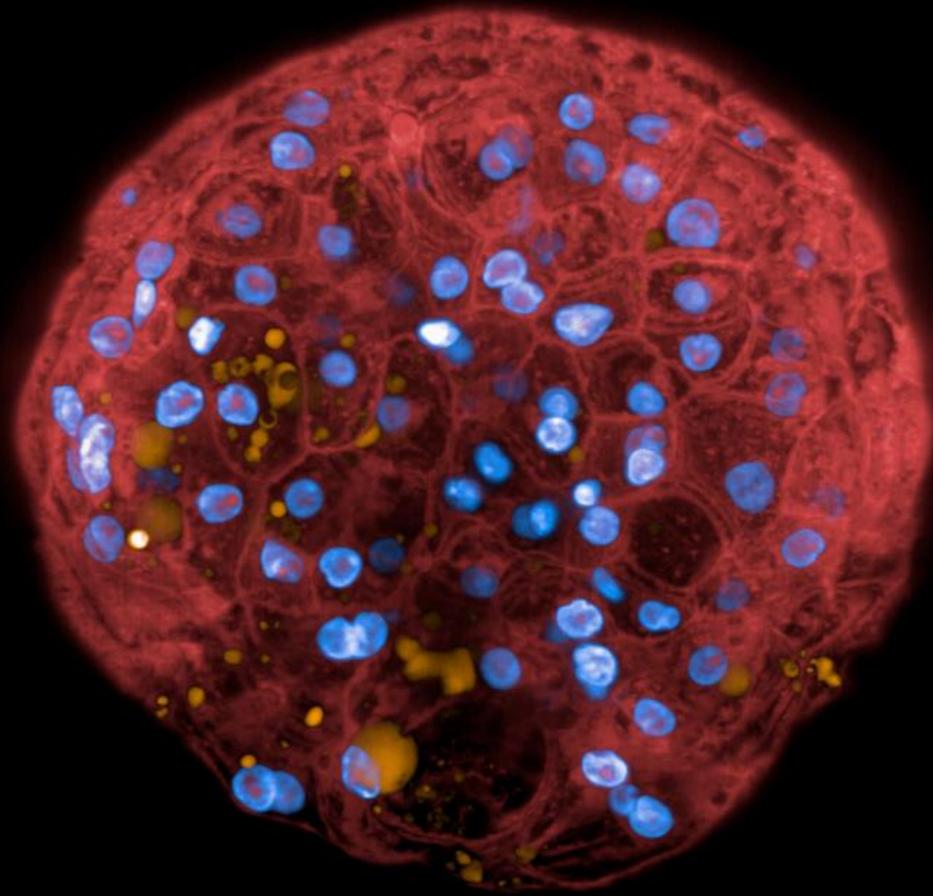
GFP – Vascular Structure

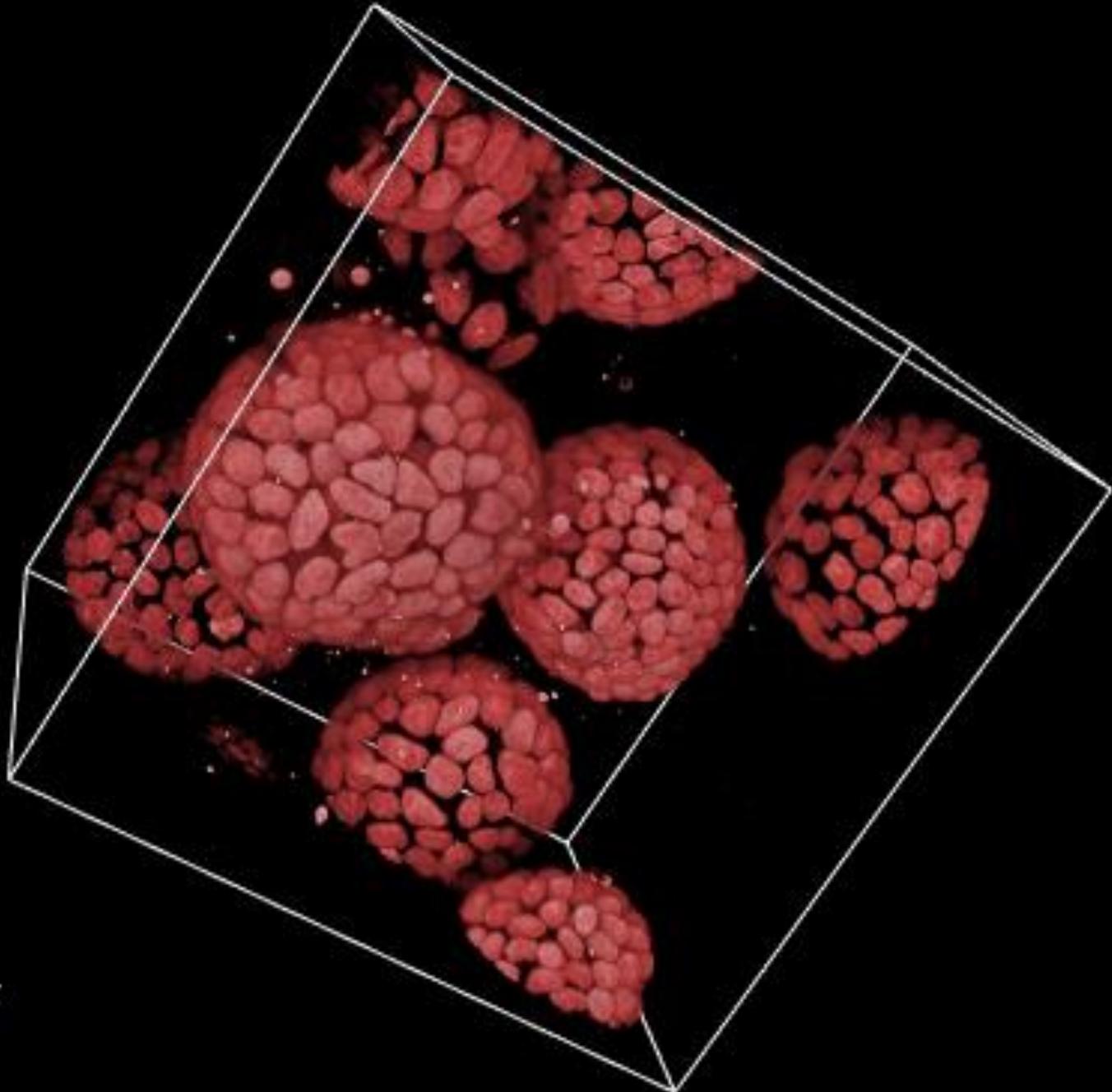
dsRED – Red Blood Cells



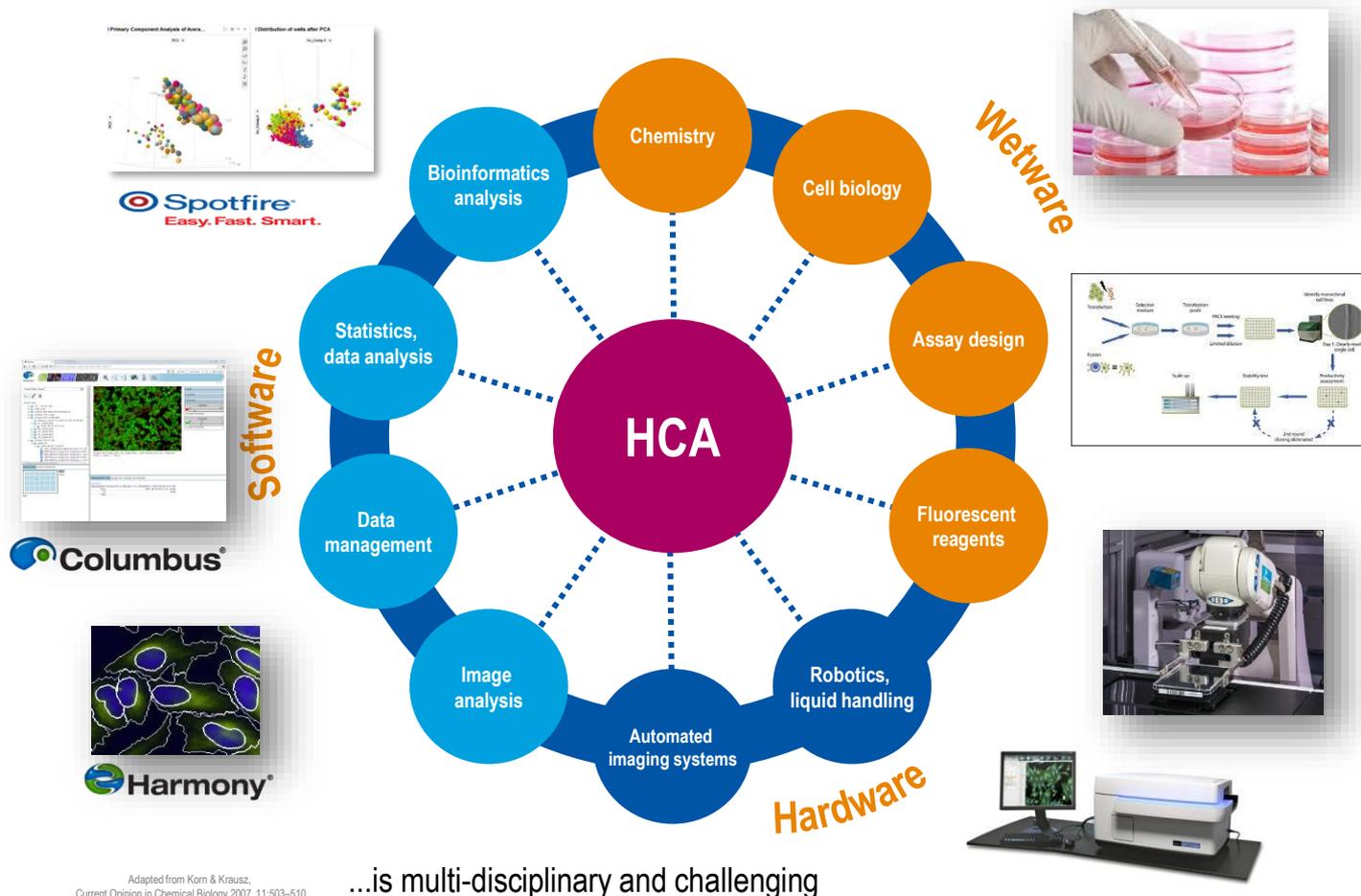
*c. elegans* brightfield





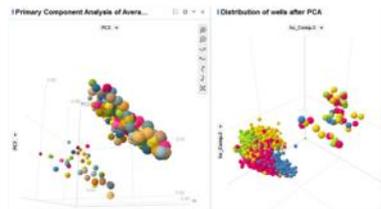


# PerkinElmer提供HCS整体技术方案！从实验设计、硬件、到软件数据分析

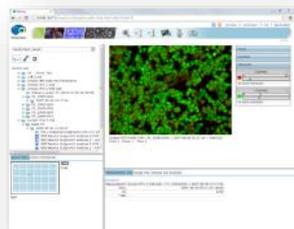


Adapted from Korn & Krausz,  
Current Opinion in Chemical Biology 2007, 11:503-510

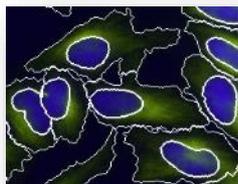
...is multi-disciplinary and challenging



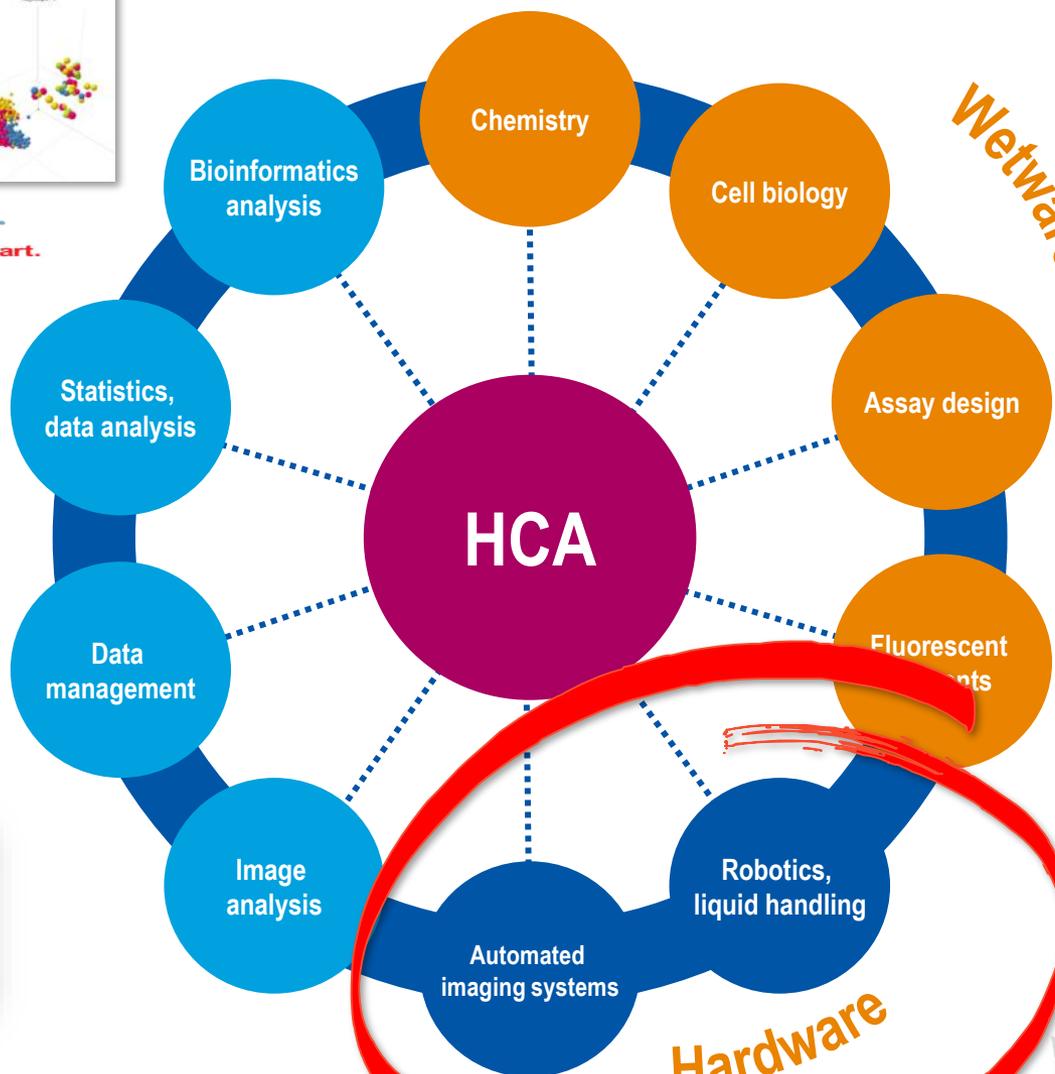
Spotfire  
Easy. Fast. Smart.



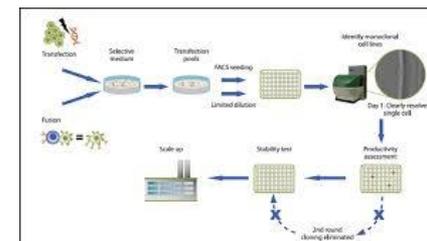
Columbus



Harmony



Wetware

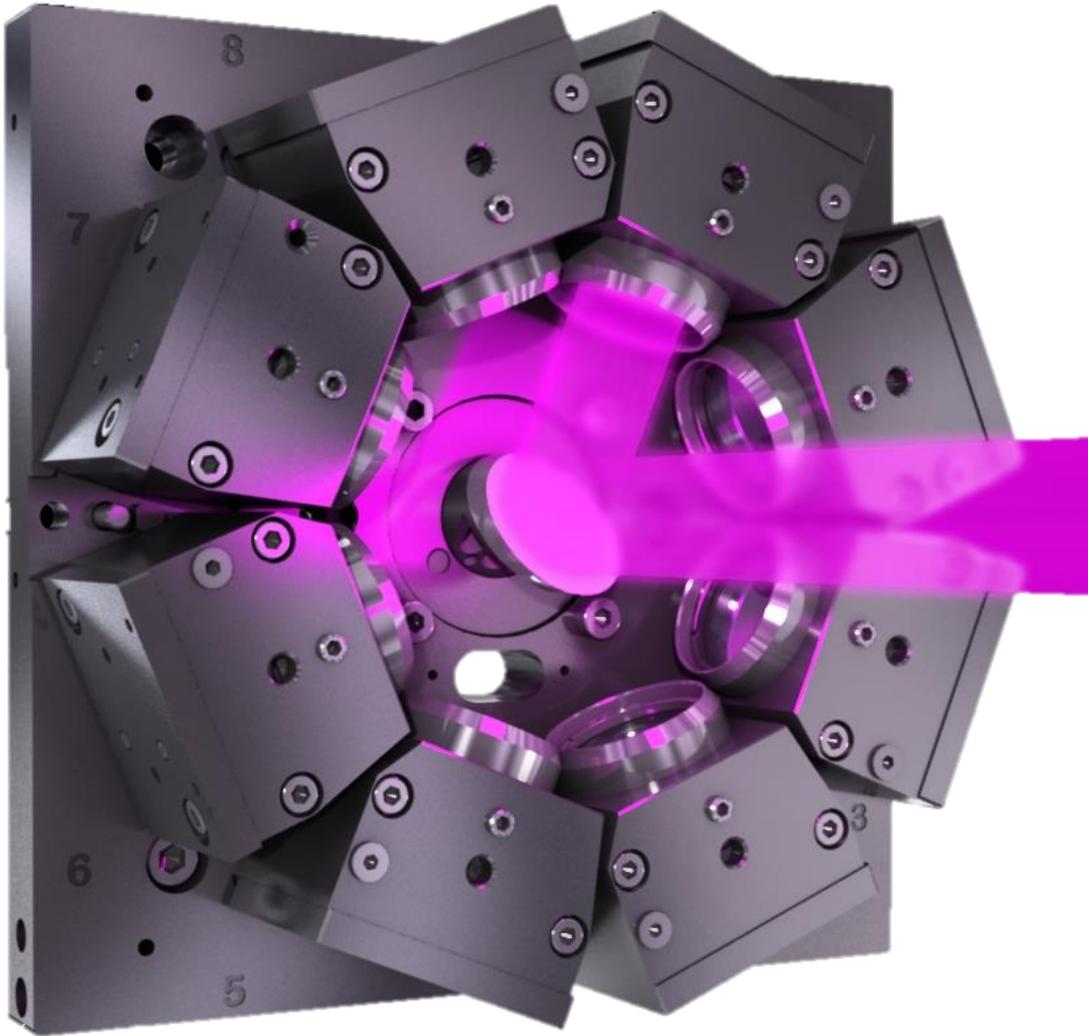


# 专业高内涵设计，避免外接部件



无需专业光路维护，无外漏光纤，无需暗室

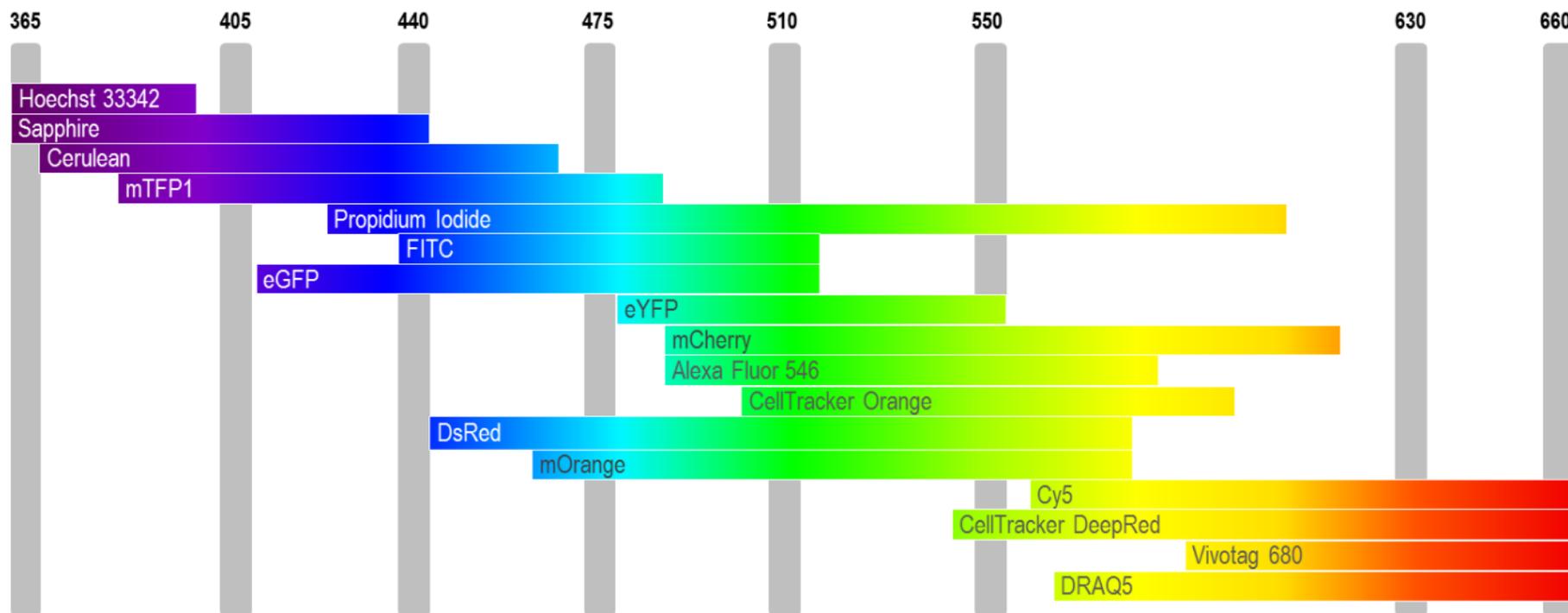
**Operetta CLS**



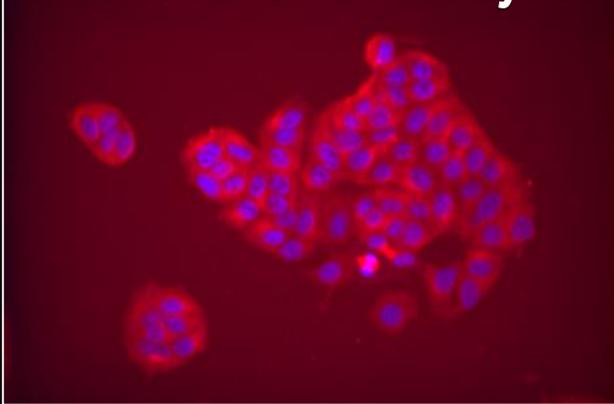
- 共聚焦专用高功率LED
- 免光纤设计，提高激发光能量

# 系统如何兼容更多染料

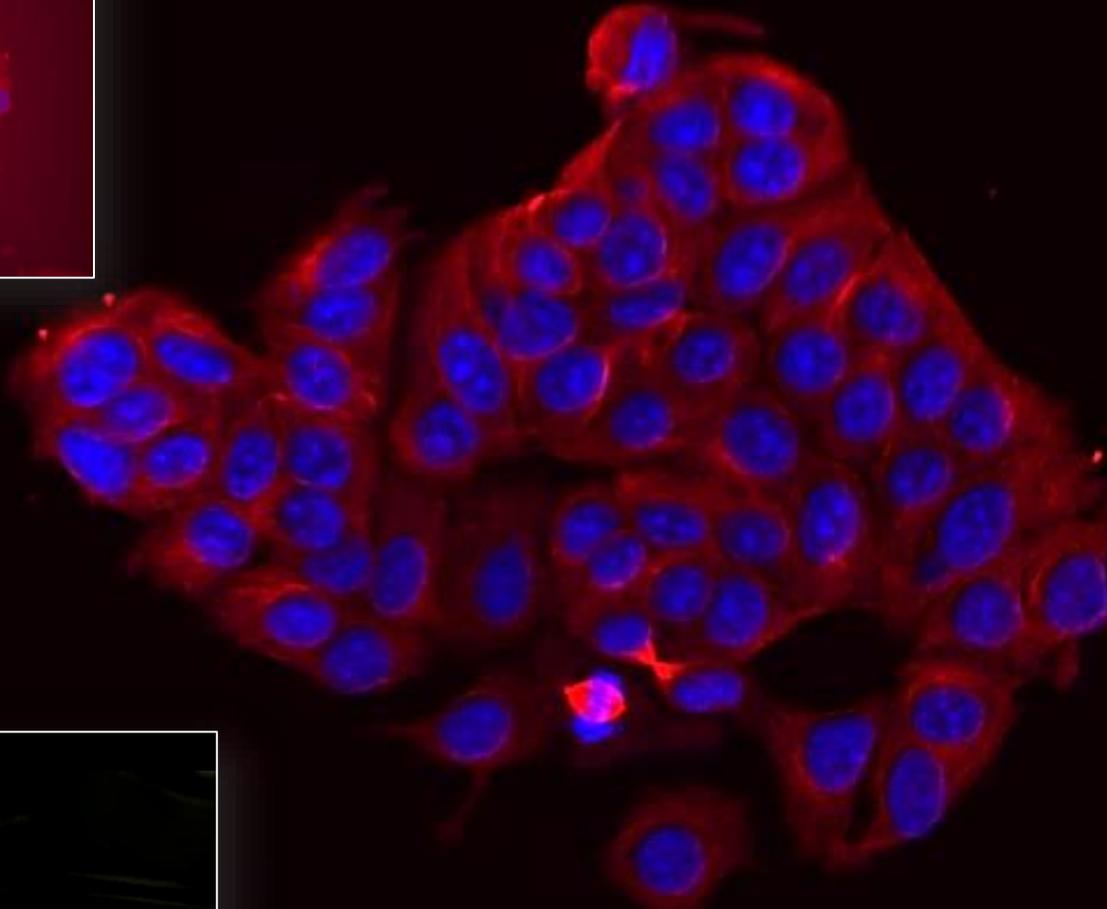
涵盖从UV 到NIR 广泛的激发谱线，适合多种应用需求



**20x 0.4 N.A. Air Objective**

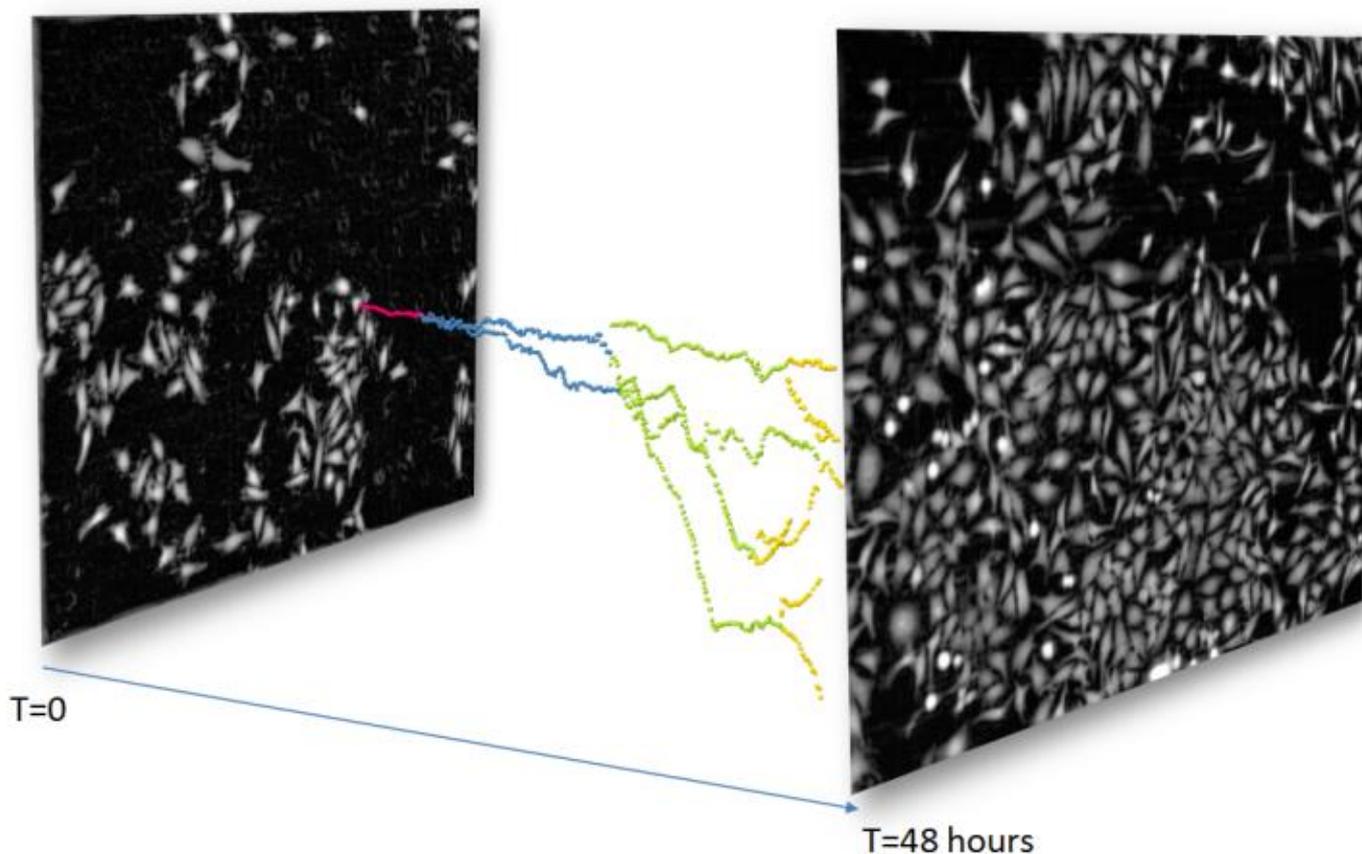


**20x 0.7 N.A. Water Objective**



- 中高端市场唯一配备水镜的高内涵系统
- 透光量是普通空气镜的3~4倍

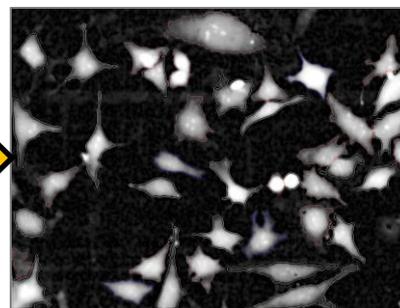
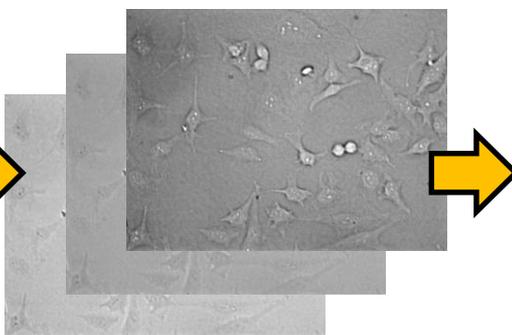
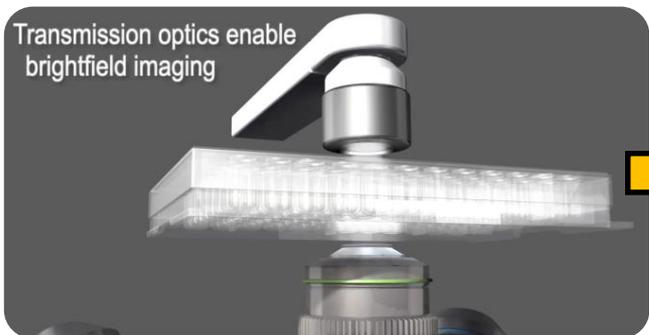
硬件优势：近红外单色LED，荧光级别高信噪比的非标记成像，实施无标记细胞检测



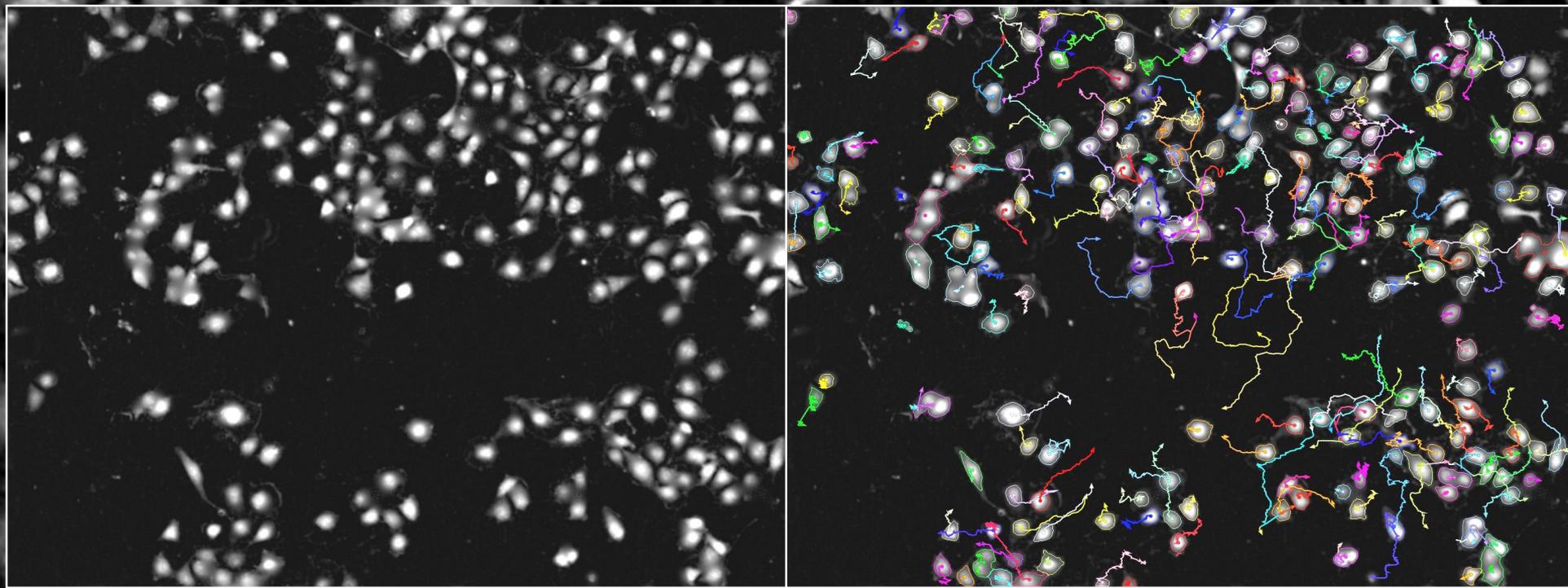
单色光源

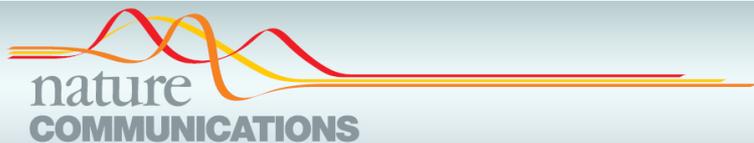
焦距包围成像

数字转换



# 南京大学：DPC模式下的细胞分裂和运动轨迹追踪





## ARTICLE

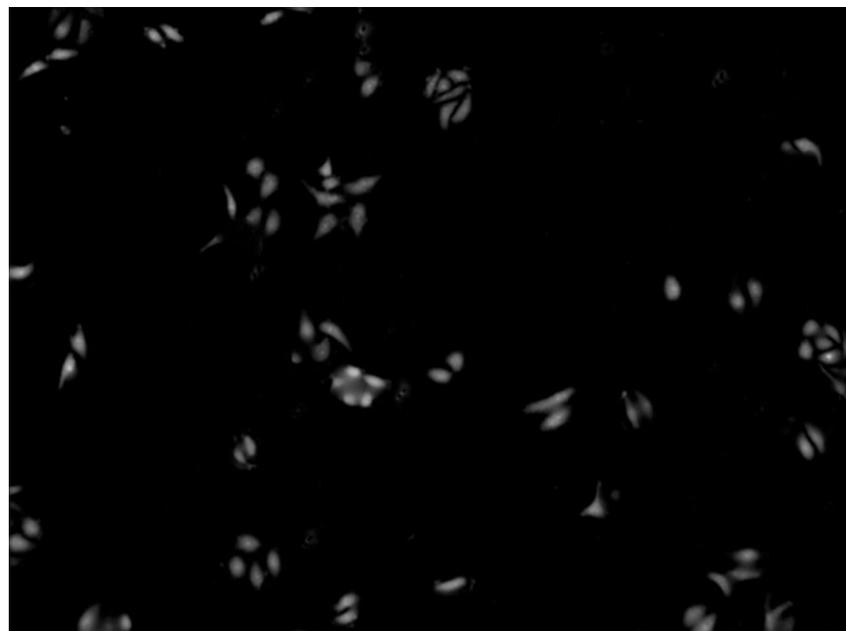
Received 13 Jul 2013 | Accepted 2 Jan 2014 | Published 27 Jan 2014

DOI: 10.1038/ncomms4195

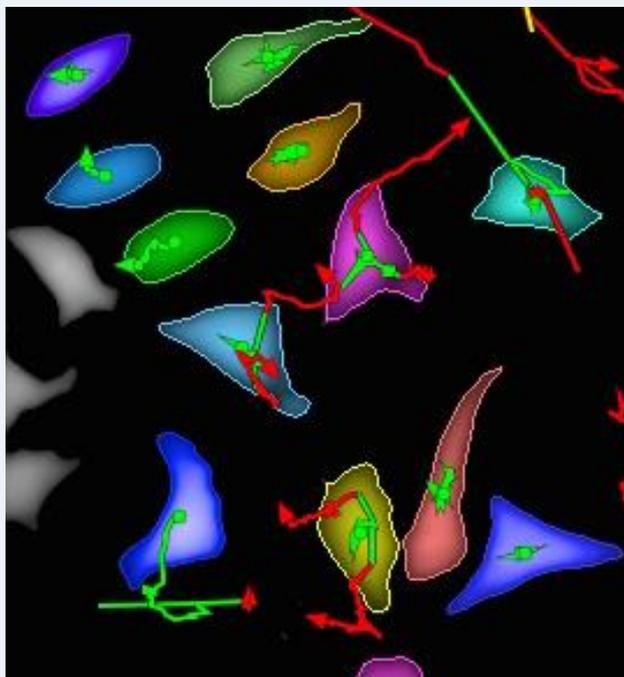
OPEN

# Clonal culturing of human embryonic stem cells on laminin-521/E-cadherin matrix in defined and xeno-free environment

a cell incubator. After that, the plates were transferred into a high throughput imaging system (**Operetta** PerkinElmer) equipped with an environmental control unit (37 °C, 5% CO<sub>2</sub>). For [Supplementary Movies 1 and 2](#), the brightfield images were taken once in 15 min during 24 h after plating using Harmony software (PerkinElmer), exported and analysed using ImageJ software (NIH, the United States). For [Supplementary Movie 3](#), the images were taken **once in 30 min for 5 days**. For migration



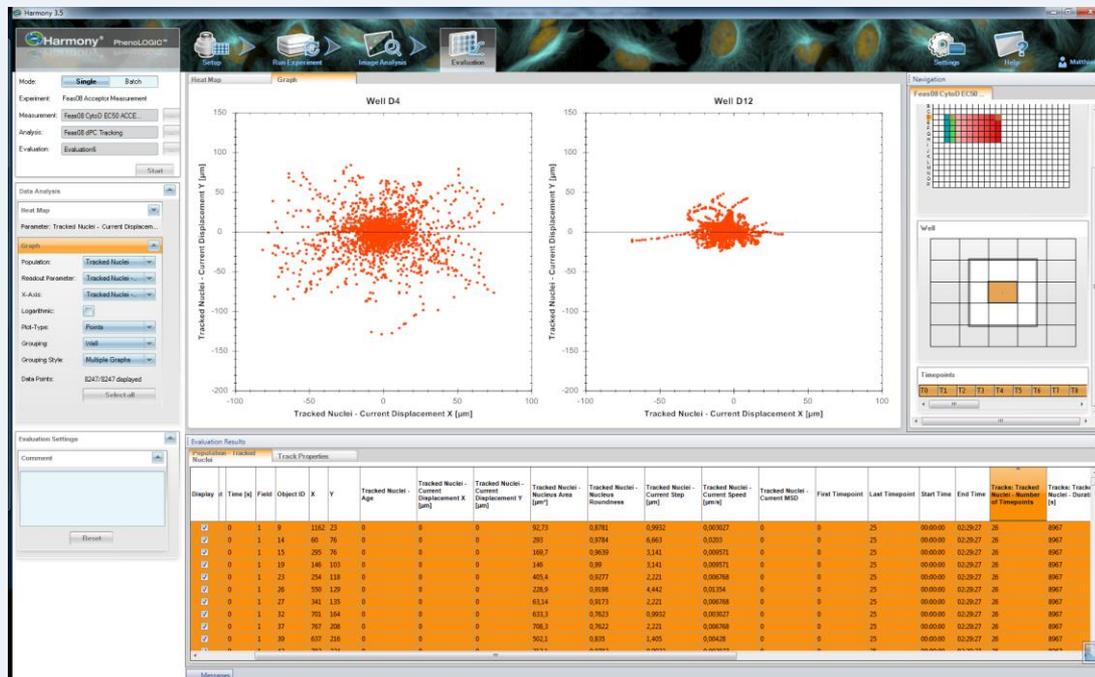
# 无标记迁移、代次分析



Tracking of dividing cells on a digital phase contrast image

Green: Track of first generation

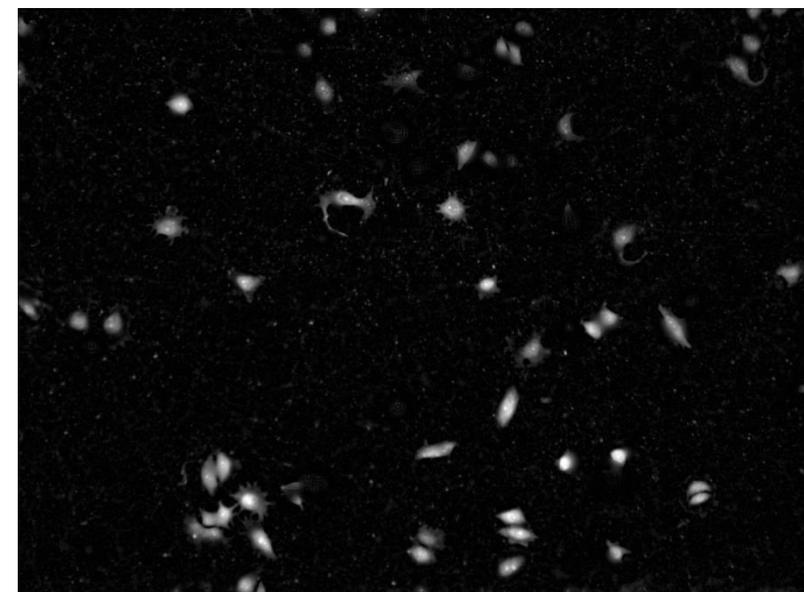
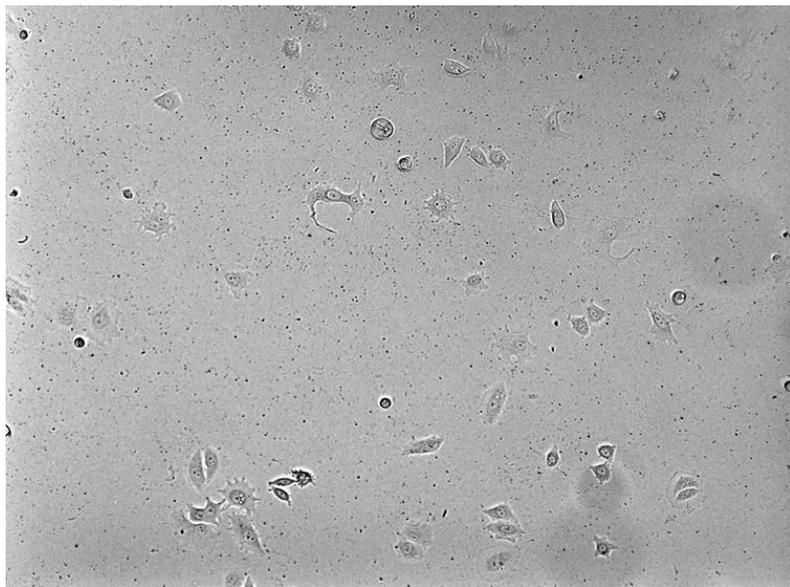
Red: Second generation



untreated

treated

Longitudinal cell studies to quantify dynamic behavior



细胞计数

细胞形态分析

细胞迁移能力分析

细胞世代分析

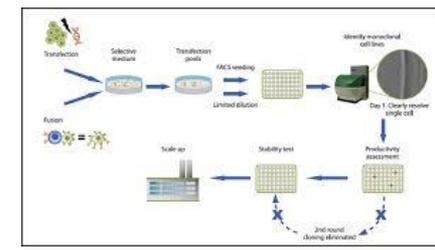
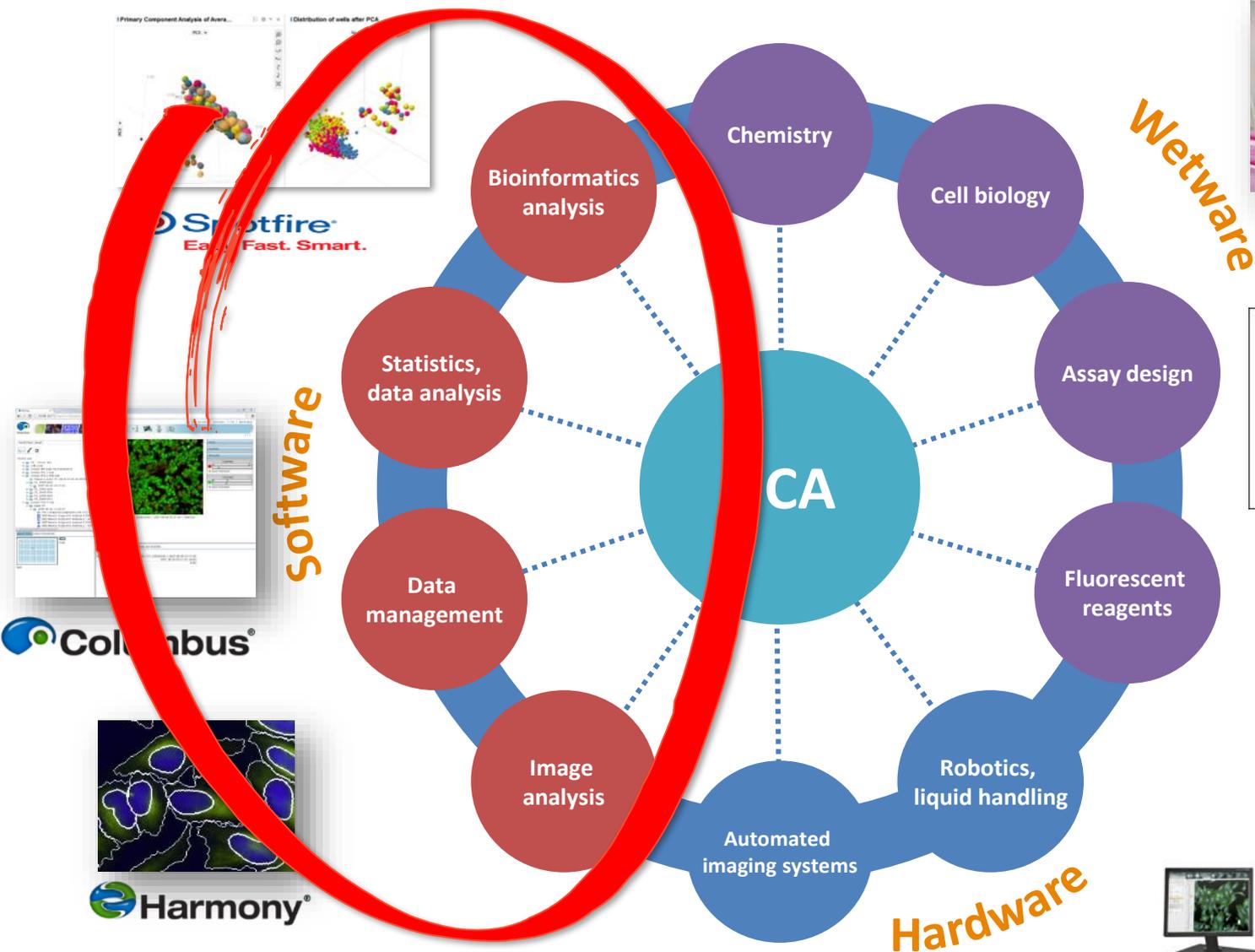
神经细胞分析

克隆形成

微组织形态学分析

细胞浆/膜蛋白表达分析

# 高内涵分析平台建设



...is multi-disciplinary and challengin

# 软件优势：简介的界面和流程设计，让使用越来越简单

## Global Control

## Navigation Bar

The screenshot displays the Harmony 3.1 software interface. At the top, there is a navigation bar with icons for Setup, Run Experiment, Image Analysis, and Evaluate. Below this is a central image analysis window showing a multi-color fluorescence image of cell colonies. To the left is a settings pane with various analysis options. To the right is an image control panel with channels and overlays. Below the image is a results table.

Object No	Colony Area [µm²]	Colony Roundness	Oct-4 Intensity Mean	Oct-4 Intensity Sum	Cytokeratin Intensity
23	25959.5	0.825158	1705.93	4.49085E+07	840.48
24	6780.18	0.721567	2038.73	1.399843E+07	3099.3
25	15795.8	0.789085	3.03767E+07	913.78	
26	33091	0.587872	7.180663E+07	1155.5	
27	35560.2	0.645448	7.654893E+07	1039.6	

Image Control

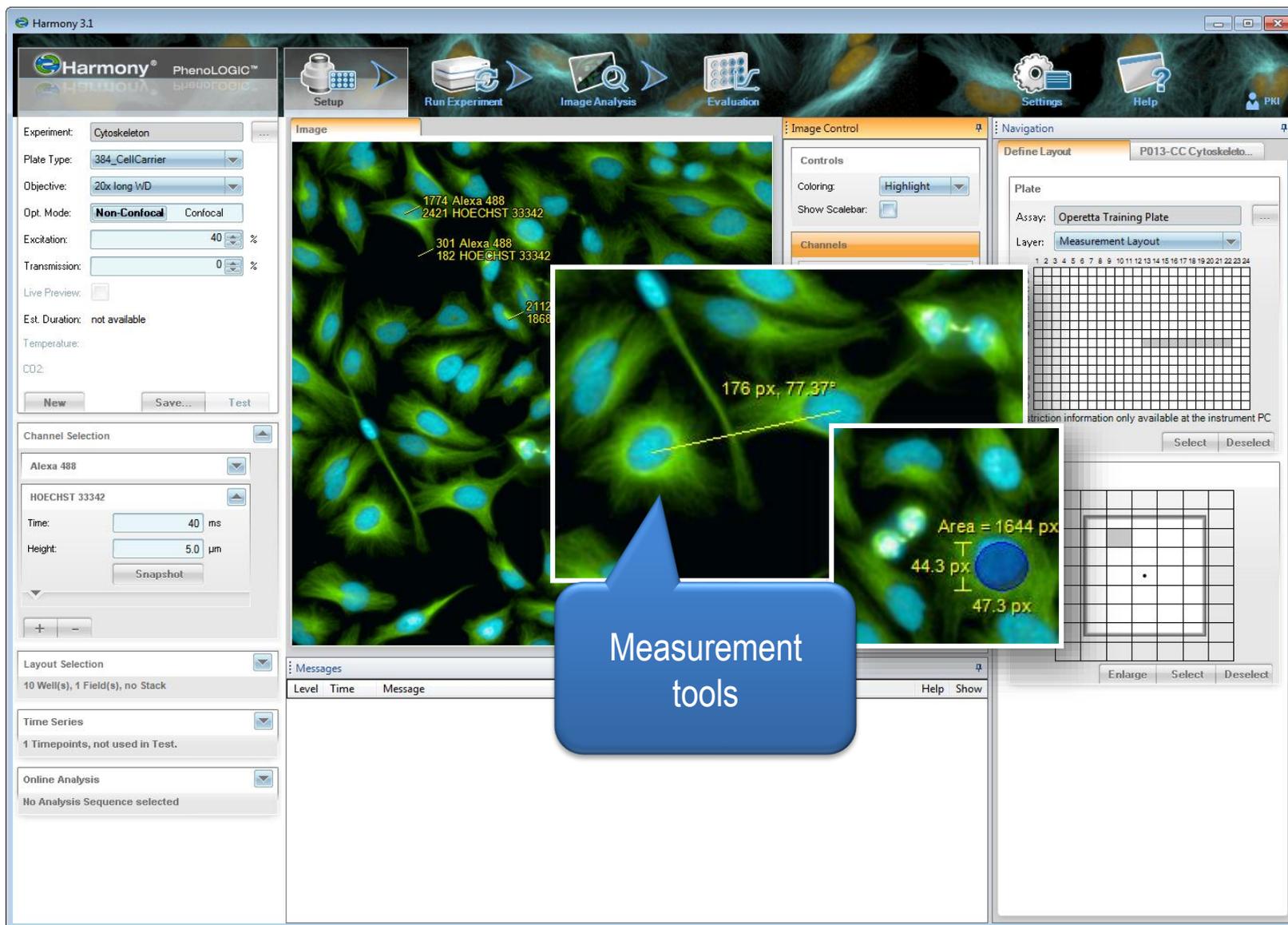
Plate Navigation



Settings Pane

Results

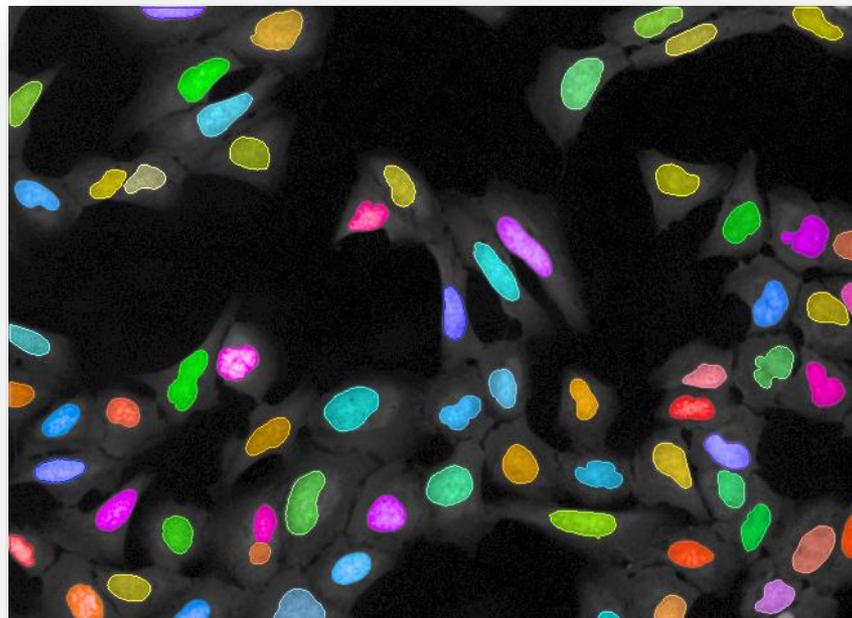
# 软件优势: Image View Tools 图像查看功能



Show intensities, measure

# 图像分析的分析模块 building blocks

- Find Nuclei 
- Find Cells 
- Find Cytoplasm 
- Find Spots 
- Find Micronuclei 
- Find Texture Regions 
- Find Image Regions 
- Find Neurites 



- Calc. Intensity 
- Calc. Morphology 
- Calc. Texture 
- Calc. Properties  $a^2+b$
- Select Cell Region 
- Select Region 
- Select Population 



Tracking object

# 一键化操作的细胞检测——15步 VS 1步

传统软件选择细胞核，必须先填写最大细胞核，最小细胞核直径尺寸，测量背景数值，测量细胞数值，细胞减去背景。。。



4 Move the cursor to the opposite edge of the object and note the Length value.

2 Select the Arrow tool as shown in the following figure.



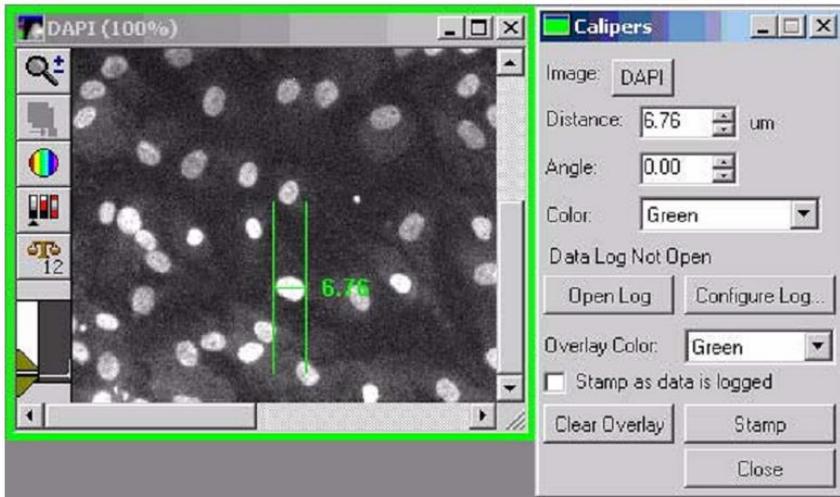
3 Move the arrow cursor over the dimmest part of the dimmest object in the image. As you move the cursor, the XY coordinates and the gray-level value of the pixel under the cursor are indicated at the bottom of the MetaPress Software desktop. The XY coordinates are in parentheses and the gray-level value is to the right of the arrow. For example:

(101, 80) -> 366

4 Note the gray-level value of the object.

5 Move the cursor just outside the object to the background of the image and note the gray-level value of the background.

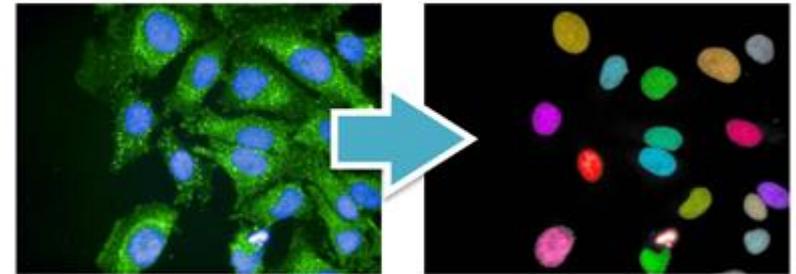
In the following example, the value is 10 pixels (or 12.87 μm). This number represents the cell width in pixels. If the image is calibrated, then the length is in pixels and calibrated units.



## PE Harmony

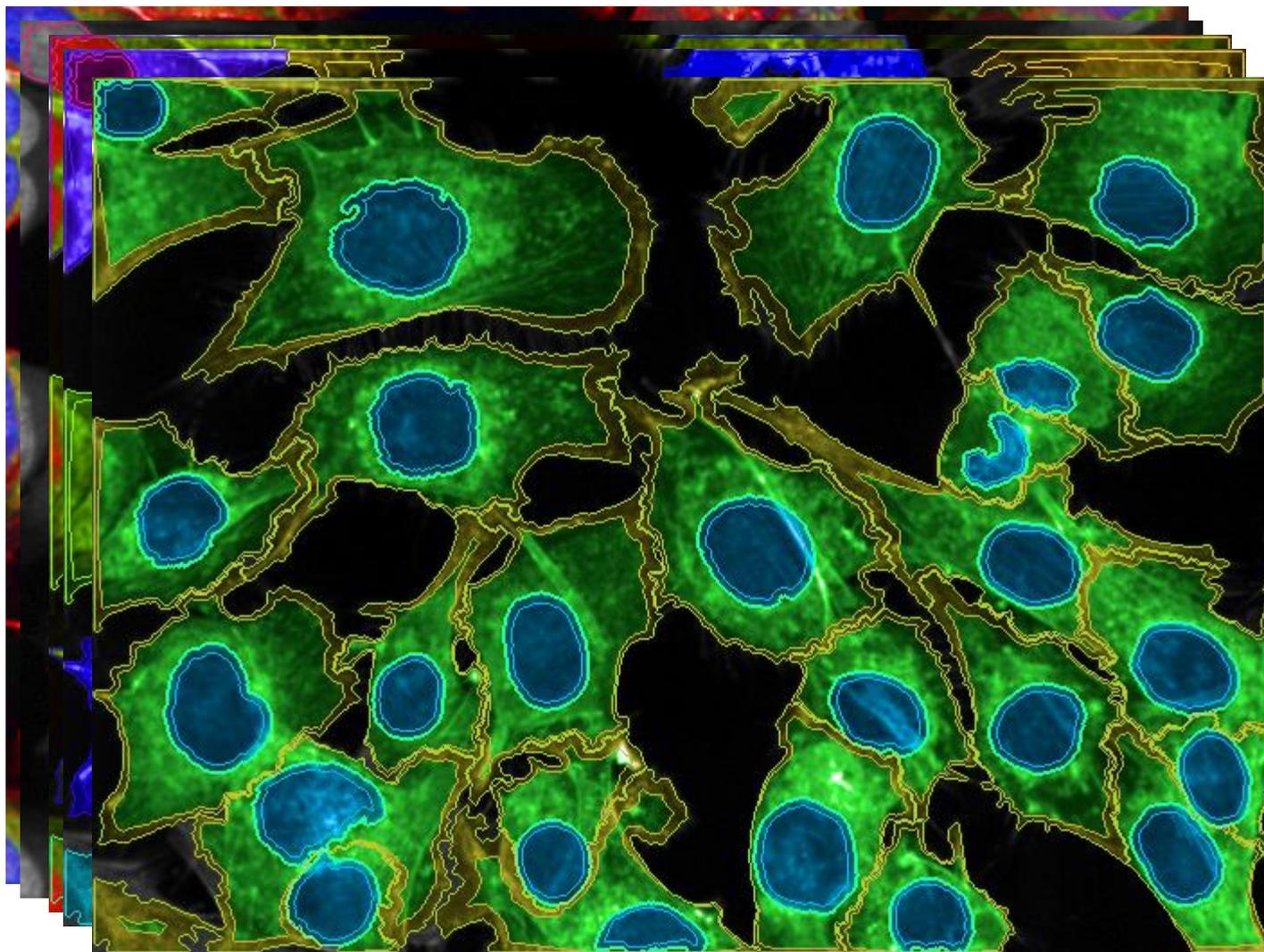
Step 1. Find Nuclei is good enough for getting the numbers.

①



Summary		Properties Nuclei					
Property	Mean	CV %	StdDev	Median	Max	Min	Sum
Area [μm²]	266.571	34.539	92.071	249.36	440.55	86.4	4531.71
Area [px²]	9728.12	34.5385	3359.94	9100	16077	3153	165378
Intensity DRAQ5	1739.34	19.949	346.98	1650.77	2977.42	1395.94	29568.7
Contrast DRAQ5	0.426285	14.5611	0.0620718	0.415831	0.649076	0.354963	7.24685

# 怎么完成细胞的高内涵分析?



Image



Find nuclei



Find cytoplasm



Segmentation



Content analysis



Quantity

Calculate Morphology Properties

Population: Nuclei  
Region: Cytoplasm

Method: STAR

Channel: Alexa 488

Symmetry   
Threshold Compactness   
Axial   
Radial   
Profile

Profile Inner Region: Nucleus  
Profile Width: 4 px

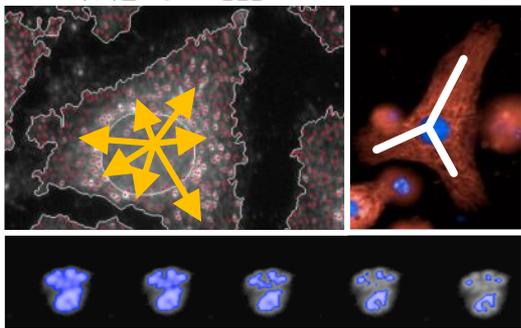
Sliding Parabola

Sliding Parabola   
Curvature: 10  
Use for Center

## Profile

„At inside of plasma membrane“  
„Center of cytoplasm“  
„Outside of nuclear membrane“  
„Inside of nuclear membrane“  
„In the center of the nucleus“

Weighed intensity...



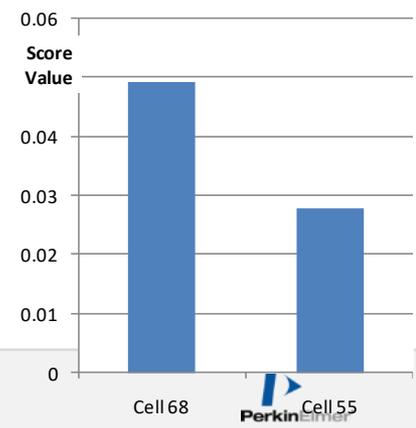
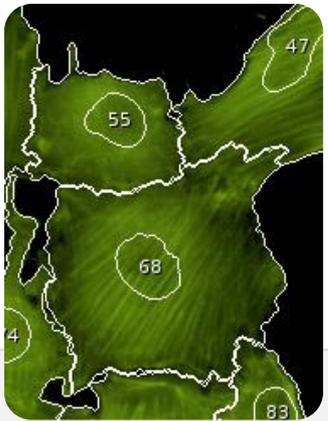
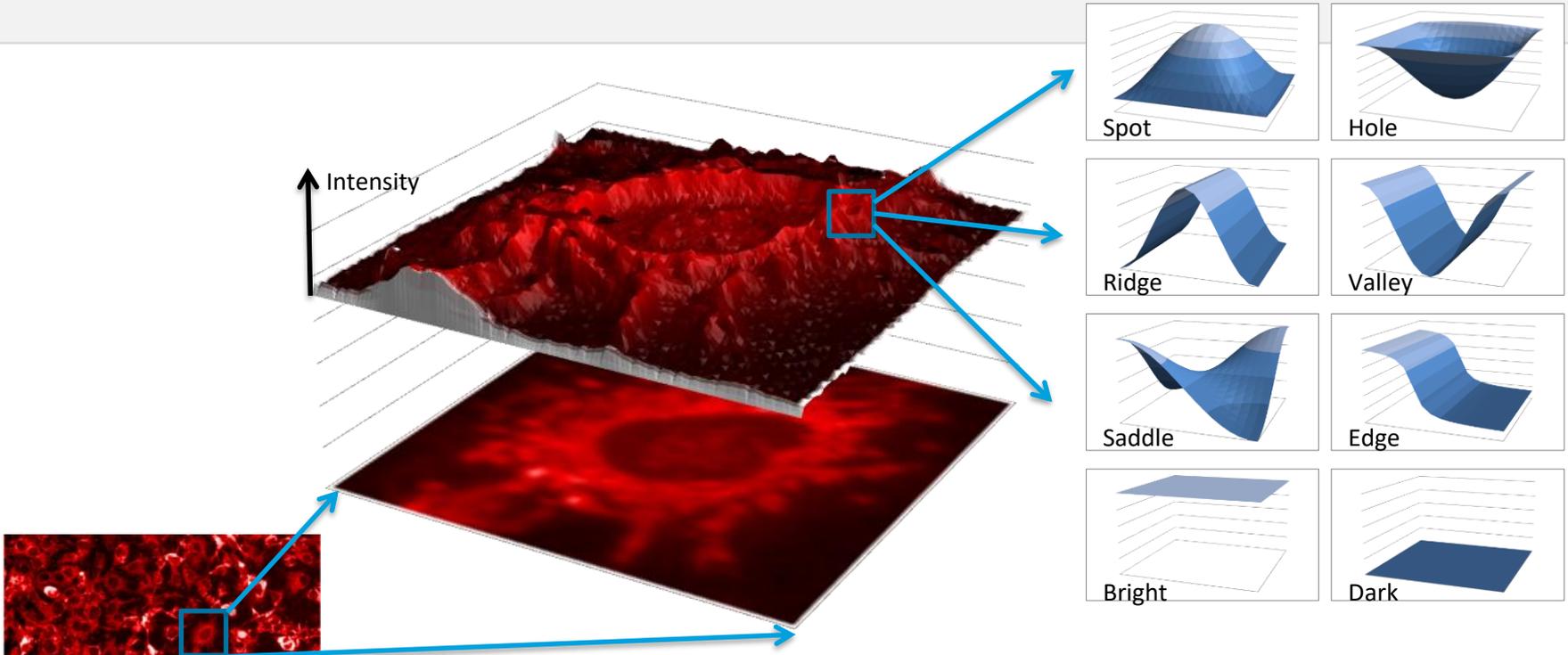
Profile 1/5 image.

STAR = Symmetry (对称性), Threshold Compactness (信号密度),  
Axial (轴向), Radial (放射性)

Profile: 亚细胞分区

识别越来越精准!

# 纹理分析——量化“看上去不一样”的细胞



对比越来越显著！

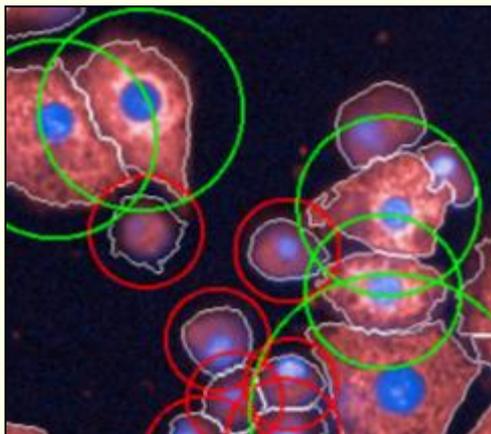
# 软件优势：软件自学习，轻松分组样品，不仅仅是细胞分类

The screenshot displays the Harmony 4.0 software interface. The top navigation bar includes buttons for Setup, Run Experiment, Image Analysis, Evaluation, Settings, Help, Operetta, Operetta (Simulation), and Hartwig. The main workspace is divided into several panels:

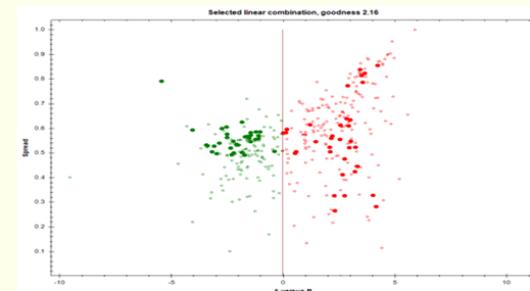
- Left Panel:** A grid of image thumbnails showing cell phenotypes under different Demecolcine concentrations: Phenotype A (0 μM), Phenotypes A and B (0.03 μM), and Phenotype B (1.6 μM). Below this are larger images showing cell segmentation and classification results.
- Center Panel:** A large microscopy image of a cell culture well. A red circle highlights a specific cell, labeled with the number '3'.
- Right Panel:** A 'Navigation' window showing a 96-well plate layout (8 rows x 12 columns) for 'Oris MDA-MB-231 - M...'. A 'Well' view below shows a zoomed-in grid with a highlighted well.
- Bottom Right Panel:** A scatter plot titled 'Selected linear combination, goodness 3.66'. The y-axis is labeled 'Signal' and the x-axis is 'A versus B'. The plot shows two distinct clusters of data points, one green and one red, separated by a vertical line.

# 细胞纹理自学习——转化观察经验为软件语言

## Train on dead cells



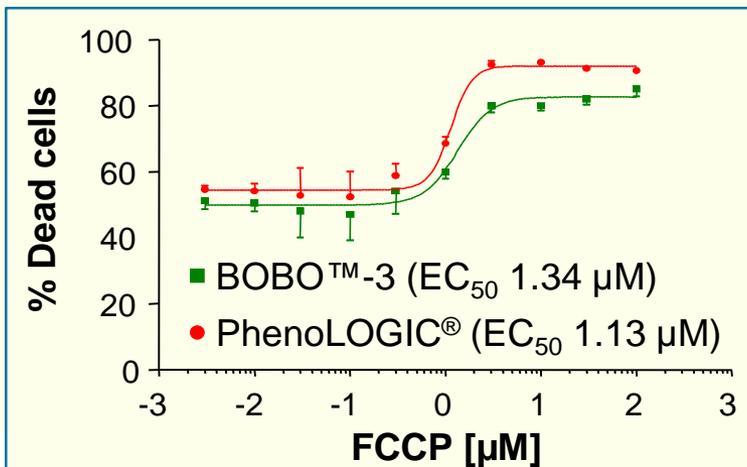
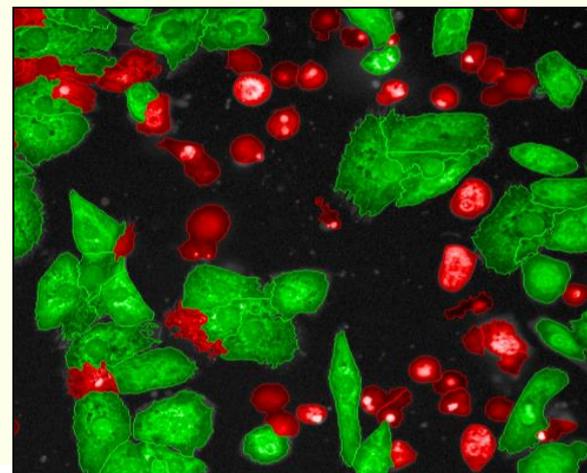
## PhenoLOGIC



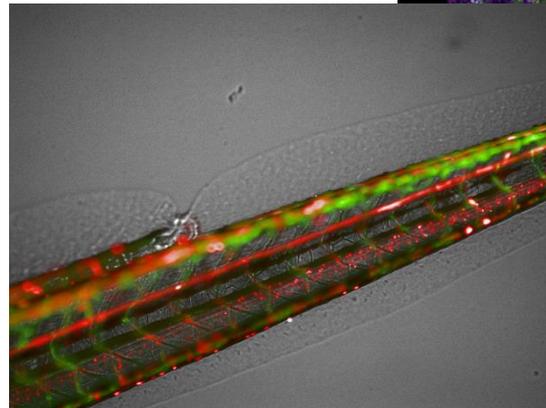
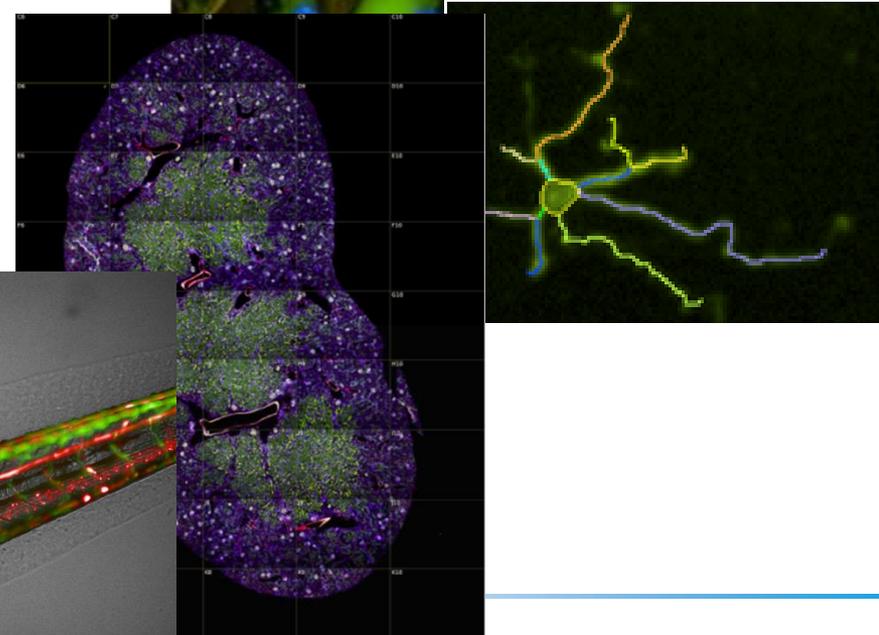
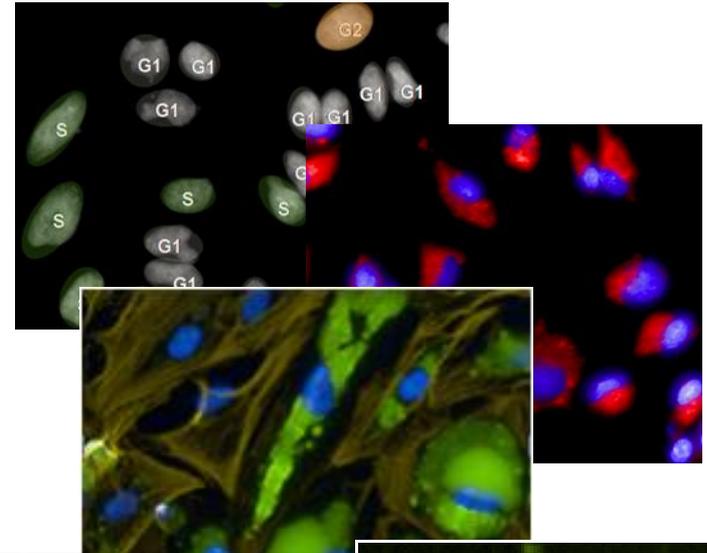
4 out of 29 properties used to calculate a classifier



## Classification result



- ▶ 肿瘤研究 (细胞周期、细胞增殖与凋亡、细胞迁移等分析)
- ▶ 炎症研究 (GPCR、信号通路研究)
- ▶ 心血管疾病研究 (动脉硬化分析)
- ▶ 中枢神经及疼痛研究 (神经元分析)
- ▶ 靶点验证 (RNA干扰分析)
- ▶ 病毒研究 (病毒滴度测定, 抗病毒药物筛选等)
- ▶ 干细胞及分化研究
- ▶ 药物筛选



# 39种预制分析方案

- 蛋白表达量分析
- 细胞形态学分析
- 核质转位
- 细胞凋亡
- 细胞周期分析
- 细胞毒性分析
- 细胞迁移
- 细胞自噬
- 干细胞克隆分析
- 无标记代次分析
- 神经细胞神经元检测
- 3D MicroTissue

## Chapter 4 – Ready-Made Solutions

**Image Analysis Sequence: Quantification of Marker in Cytoplasm**

**Input Image**  
Channel 1:  
Combined nuclear and  
cytoplasmic stain image

Channel 2:  
Signal image

Untreated  
control:  
Nuclei cytosol

Labeled  
caspase-3  
antibody

Treated cells



**Image Segmentation**

**Find Nuclei**  
Finds nuclear outlines using  
the nuclear stain image

**Find Cytoplasm**  
Finds cytoplasmic outlines  
around each of the previously  
detected nuclei

Nuclear region  
overlaid on the  
nuclear stain image (untreated  
cells)

Detected  
cytoplasmic  
outlines

Results of  
detection on  
treated cells

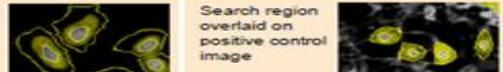


**Define Region of Interest**

**Select Cell Region**  
Select the region to search for  
the marker in the cytoplasm.  
The region is based on the  
detected nuclei and cytoplasm  
outlines.

Search region  
overlaid on the  
signal stain image (control)

Search region  
overlaid on  
positive control  
image



**Quantify Properties in Regions and Calculate Ratios of Properties**

**Calculate Intensity Properties**  
Mean signal intensity in the  
selected region

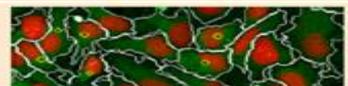
Object No	Intensity ROI Mean
1	313.703
2	352.387
3	318.887
4	336.194
5	255.301

Object No	Intensity ROI Mean
1	2686.62
2	2533.06
3	5270.26
4	348.249
5	3180.67

**Identify Subpopulations**

**Select Population**  
Identify cells with a high  
marker intensity ("Marker  
positive" or "POS")

Cells with a marker  
intensity > 1000 units  
are marked with yellow dots



**Readout Values**

<b>Total Number of Cells</b>	For information and quality control
<b>Mean Marker Intensity</b>	Marker intensity within the cell population
<b>Fraction of positive cells</b>	Fraction of cells showing the marker, e.g. "responders" to a treatment
<b>Mean marker intensity in POS cells</b>	Mean marker intensity of the "responders"

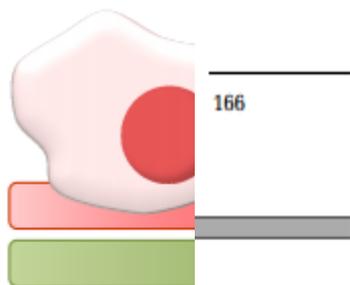
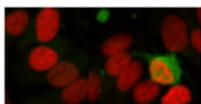


Figure 5-1: Schematic representation of cell fragmentation and caspase-3 activation.

### 5.1.1 Introduction

There are two main pathways of apoptosis: the extrinsic pathway, which is mediated by death receptors, and the intrinsic pathway, which is mediated by mitochondrial cytochrome c. Both pathways eventually lead to the activation of caspases, which are the executioners of apoptosis. In this analysis, we focus on the intrinsic pathway, which is mediated by mitochondrial cytochrome c and caspase-3.

We describe a high-content screening assay to identify compounds that induce apoptosis in cells. The assay is based on the detection of nuclear fragmentation and caspase-3 activation. The assay is performed in a 96-well plate using a ready-made analysis pipeline.

### 5.1.2 Materials

CellCarrier 384-well (Corning # 676090); HeLa cells (ATCC #72400) + 10% FBS (Sigma #H15-002); Hoechst33342 (Sigma #9023); Caspase-3 antibody, Alexa Fluor 488 conjugate (Molecular Probes #A10242).

6E3 or			
	1	2	3
A			
B			
C			
D			
E			
F			
G			
H			
I			
J			
K			
L			
M			
N			
O			
P			

Figure 5-2: Plate layout.

### Image Acquisition

- ▶ Use the 2-camera system to acquire the images.
- ▶ Open the Ready-Made Analysis Pipeline.
- ▶ Load the image sequence (e.g., from a folder).
- ▶ Load the sequence as described in the software.
- ▶ Adapt the parameters for the acquisition of the samples (e.g., exposure time).
- ▶ Switch to the Ready-Made Analysis Pipeline.
- ▶ Optional: Run the analysis on a subset of the samples.
- ▶ **Run** the analysis.

Dye	Ex./1 Max.
DRAQ5™ (nucleus/cytoplasm, specific stain for nucleic acids)	647 /
Cleaved-caspase-3 antibody (Alexa Fluor® 488 conjugate)	494 /

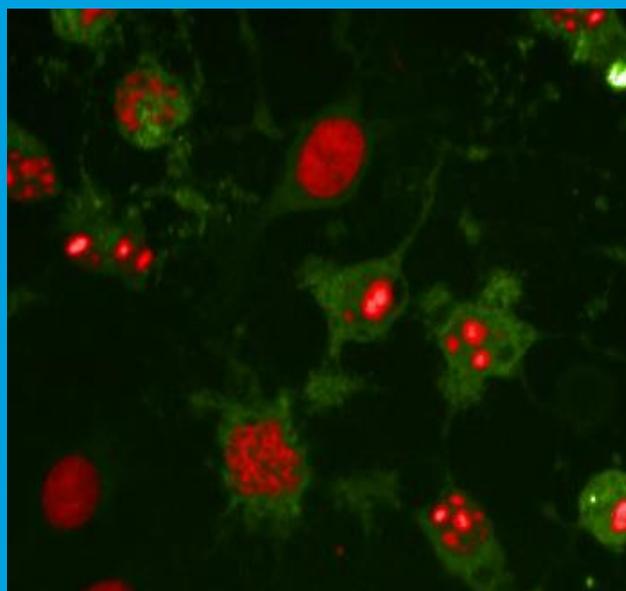
Table 5-1: Fluorescence channels.

### Image Analysis

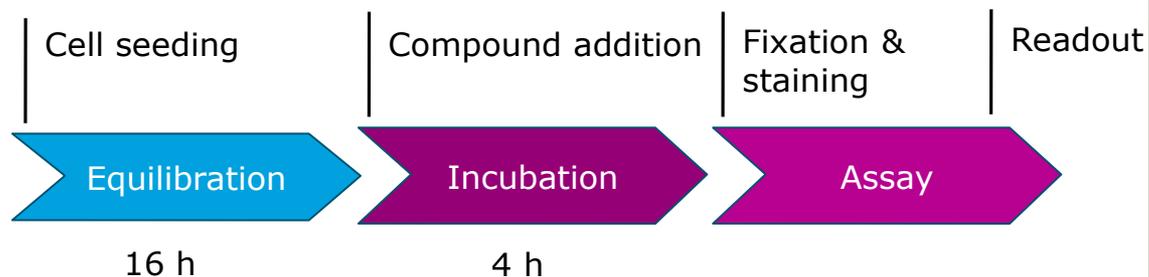
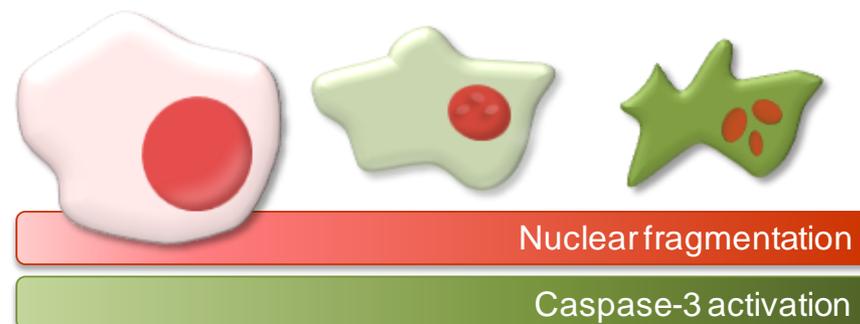
- ▶ Load the analysis pipeline.
- ▶ Select the **Find Nuclei** detection method. The general description and special hints or fragments are described in the software.
- ▶ Adjust the threshold for the **Population building** method. The "Population building" method is described in the software (4.6) for the "Population building" method.

The ready-made analysis pipeline is built using the following building blocks:

Image Analysis: RMA Apoptosis 1		
Input Images	DRAQ5™ nuclear stain channel	Alexa 488 Caspase-3 channel
Image Segmentation		
Find Nuclei	Detects Nuclei in the DRAQ5 channel	
Definitions of Regions of Interest		
Select Cell Region	Define an enlarged region of interest (ROI) in the DRAQ5 channel by setting the outer border of the nuclear region to - 80 % and the inner border to 100 % (see section 4.11.3). With this region ( <b>MarkerROI</b> ) we will later quantify the intensity of the Alexa 488 detection channel.	
Select Region	Define a shrunken selection of the nuclei ( <b>NucFragROI</b> ) by scaling down the outer border about 2 pixels (px)	
Quantifying Properties in Regions		
Calculate Intensity Properties	Use the <b>MarkerROI</b> to quantify properties of the marker channel (caspase-3):	
	<ul style="list-style-type: none"> <li>- Mean Intensity of the marker</li> <li>- Standard Deviation of the marker</li> <li>- Median Intensity of the marker</li> </ul>	
Calculate Intensity Properties (2)	Quantify the properties of the nucleus, using <b>NucFragROI</b> as a region in the nuclear channel:	
	<ul style="list-style-type: none"> <li>- Coefficient of Variance (CV) Intensity</li> <li>- Sum Intensity</li> </ul>	
Calculate Morphology Properties	Quantify the properties of the nucleus, using the standard Nuclear region:	
	<ul style="list-style-type: none"> <li>- Area of a nucleus</li> </ul>	
Select Subpopulation		
Select Population	Apply a threshold to find a population which has a high mean marker intensity (to be adjusted). This population is defined as apoptotic cells.	
Calculate Readout Values		
Define Results	Select and calculate values to report back as the results for each well	



## 细胞凋亡研究



# 凋亡检测 – 成像

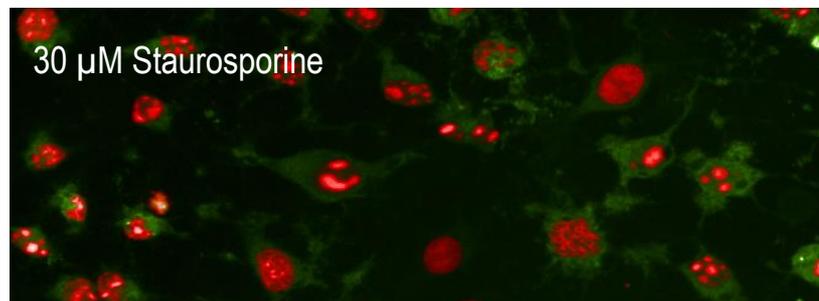
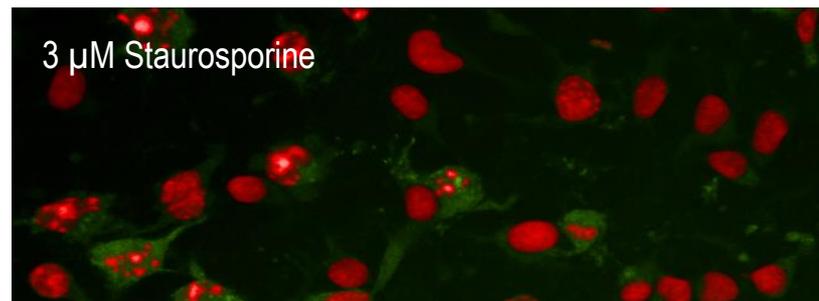
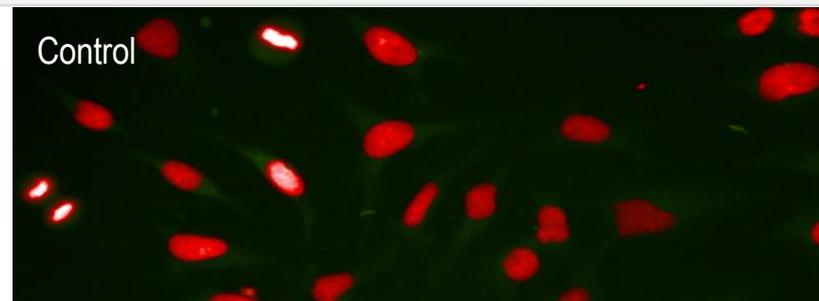
Caspase 3 活化      Alexa Fluor® 488  
   labeled anti caspase-3 antibody

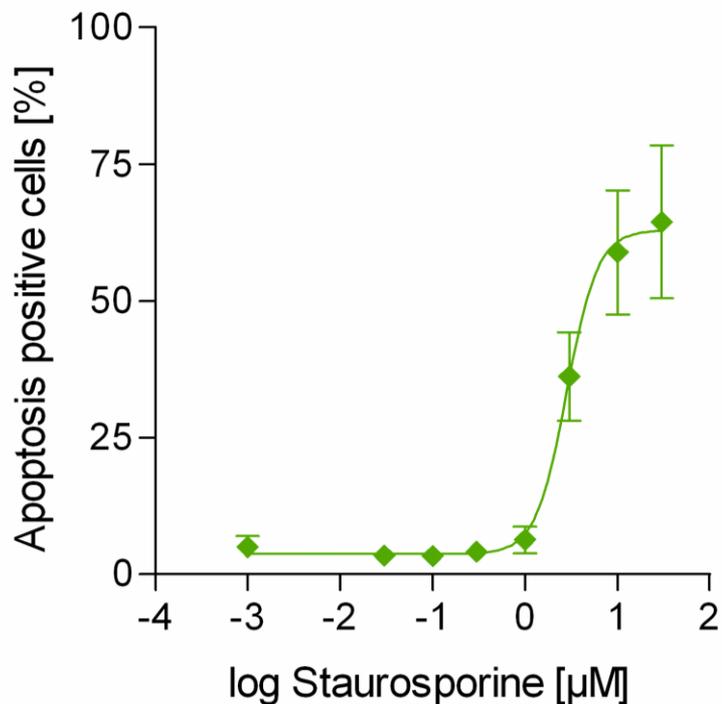
细胞计数              DRAQ5™

细胞核大小            DRAQ5™

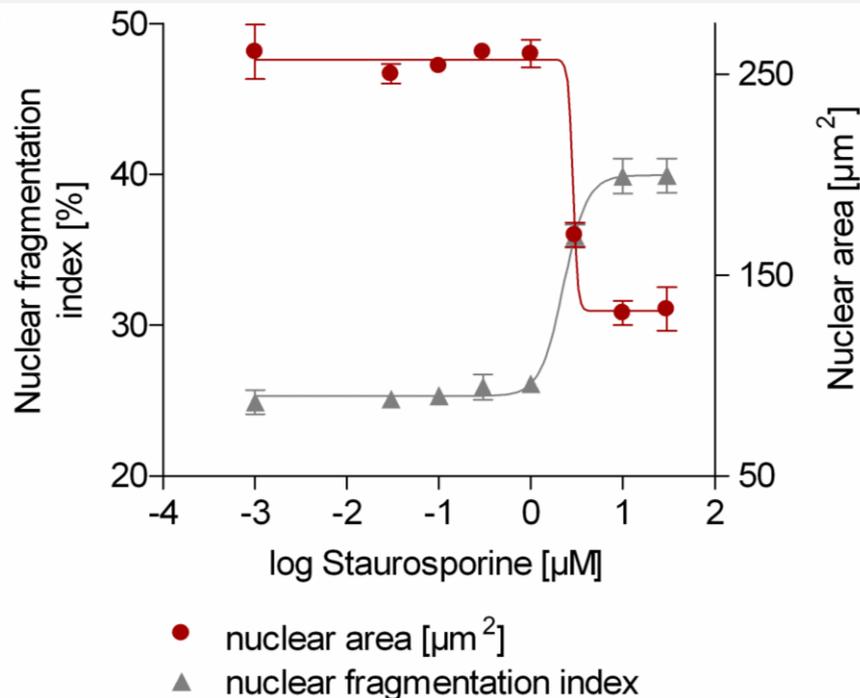
细胞核碎片化         DRAQ5™

- 20x long WD 物镜成像
- 增加十字胞碱浓度导致caspase-3增加
- 药物处理后的细胞核表现出典型的凋亡现象，核皱缩，面积变小，亮度增加；在凋亡晚期细胞核碎片化

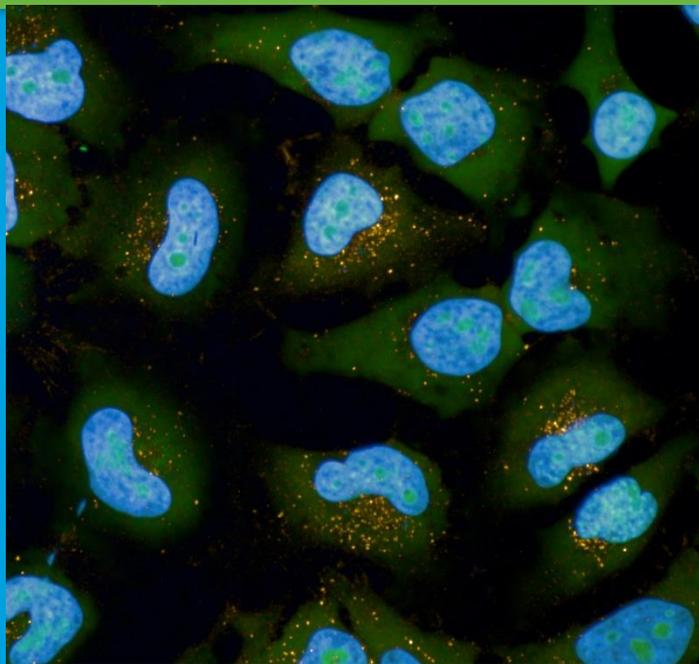




EC<sub>50</sub> 2.824



- Caspase-3 based readout (left) and nuclear morphology based readout (right) show **similar EC<sub>50</sub> values** for staurosporine.
  - a. 样本制备简单，检测通量高。不需要消化细胞的过程，可以批量对96或者384个样本进行处理制备，批量对样本进行数据读取。
  - b. 单次实验获得的实验结果内容丰富，不仅有凋亡标志蛋白的定量检测，还可以同时分析细胞核的形态学变化。



## 细胞自噬研究

Data generated in the PerkinElmer  
Application Lab, Hamburg

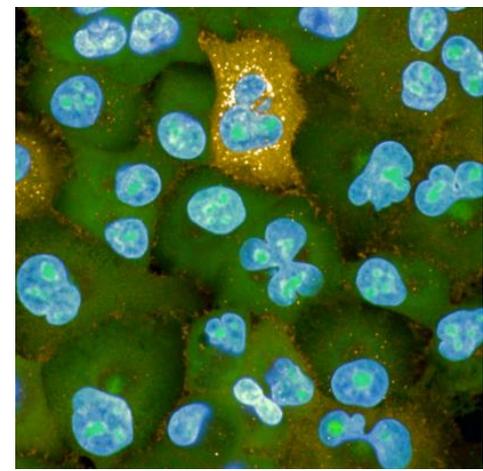
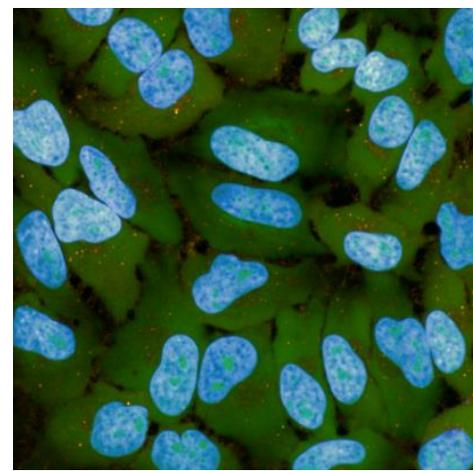
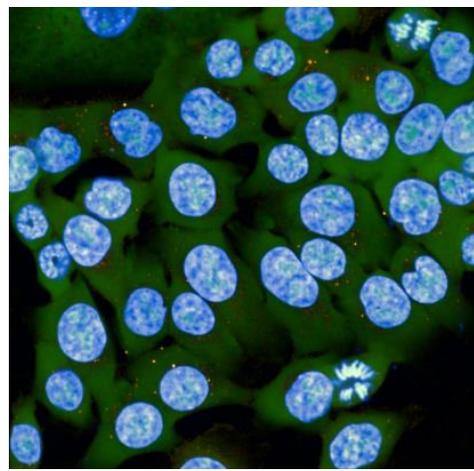
# Autophagy in three cell lines

HCT 116

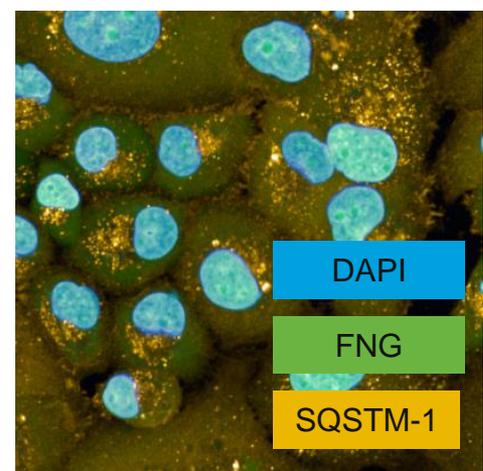
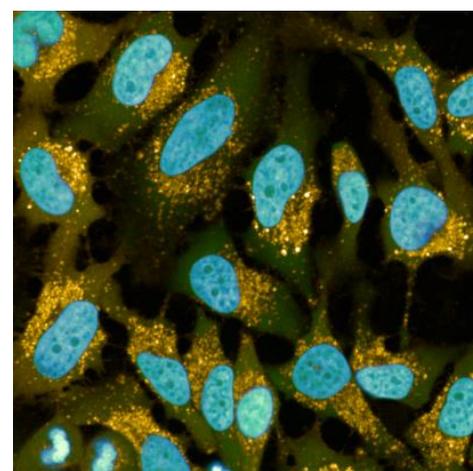
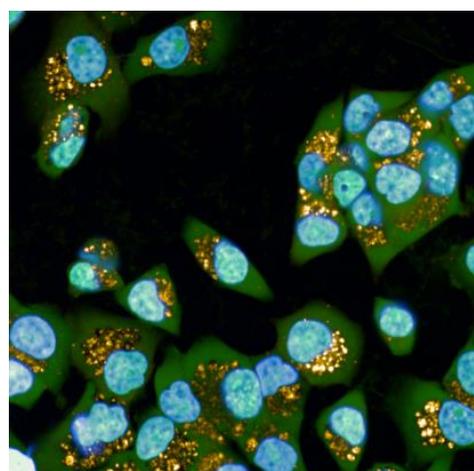
HeLa

PANC-1

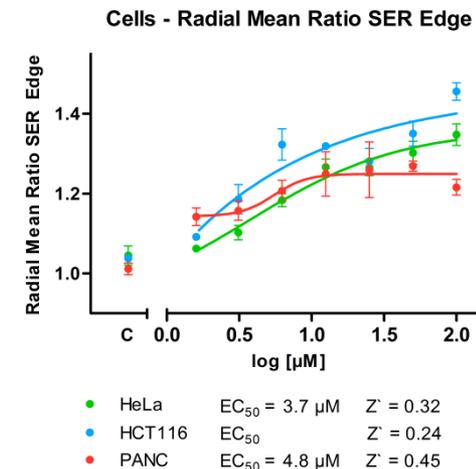
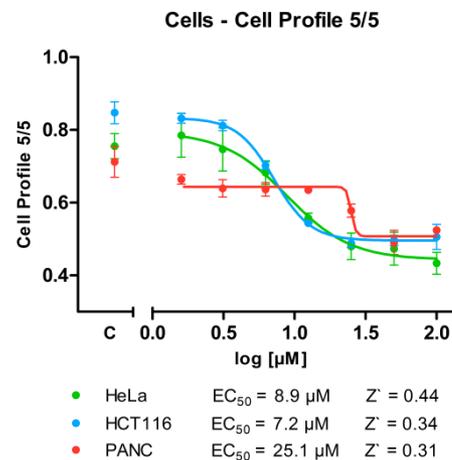
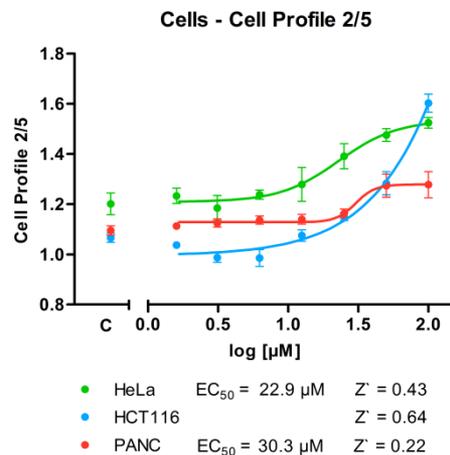
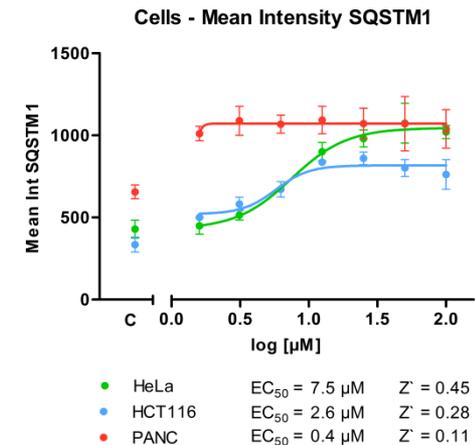
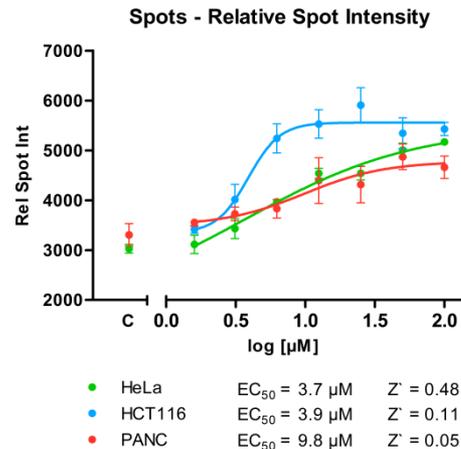
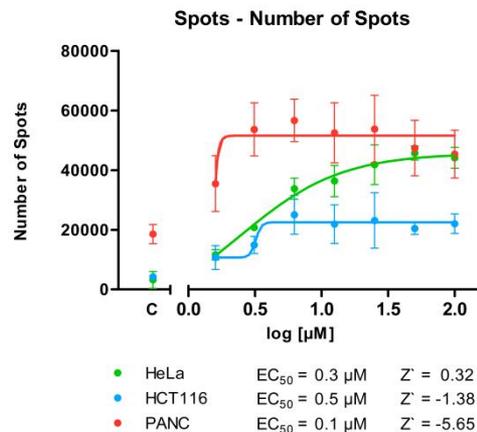
Controls

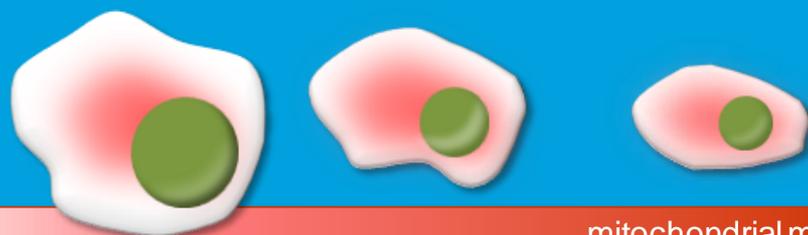
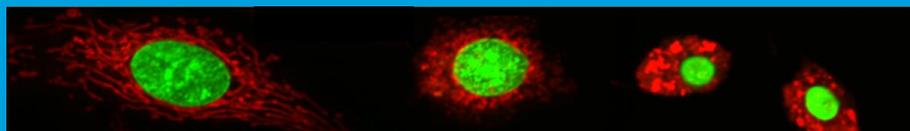


Chloroquine  
50μM



# Examples of individual properties





mitochondrial mass

nuclear area

## 细胞毒性研究

Data generated in the PerkinElmer  
Application Lab

Cell seeding

Equilibration

24 h

Compound  
addition

Incubation

24 h

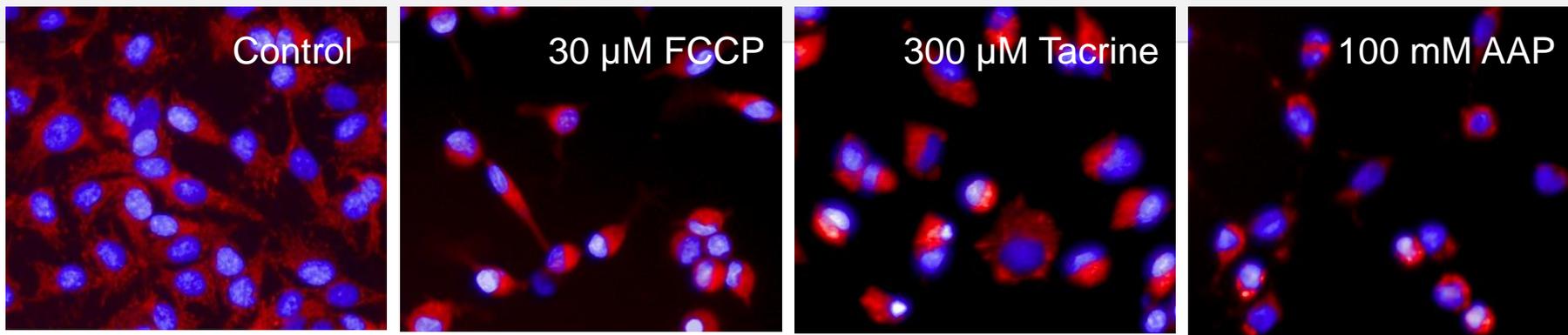
Live cell  
staining

Labeling

40 min

Readout

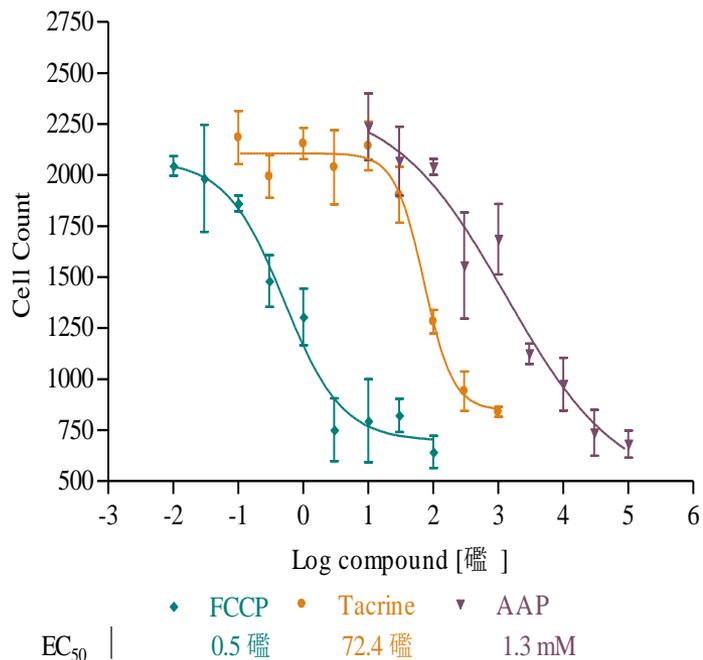
Imaging



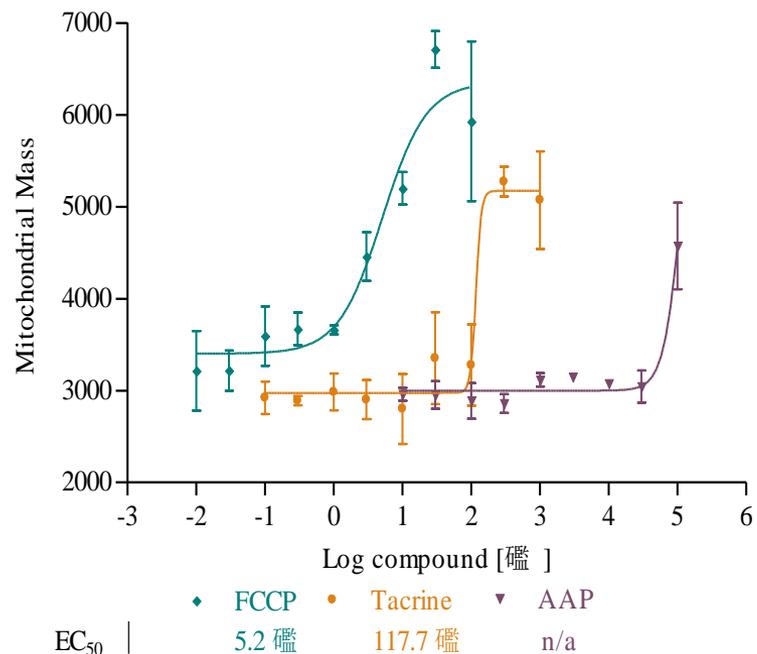
细胞计数  
线粒体数量  
细胞核增大/皱缩

Hoechst 33342  
MitoTracker® Deep Red  
Hoechst 33342

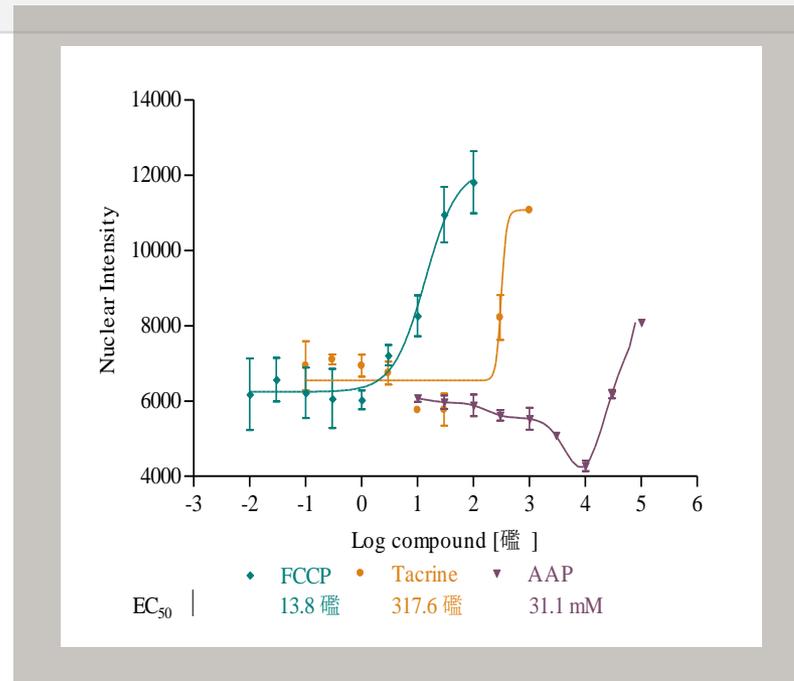
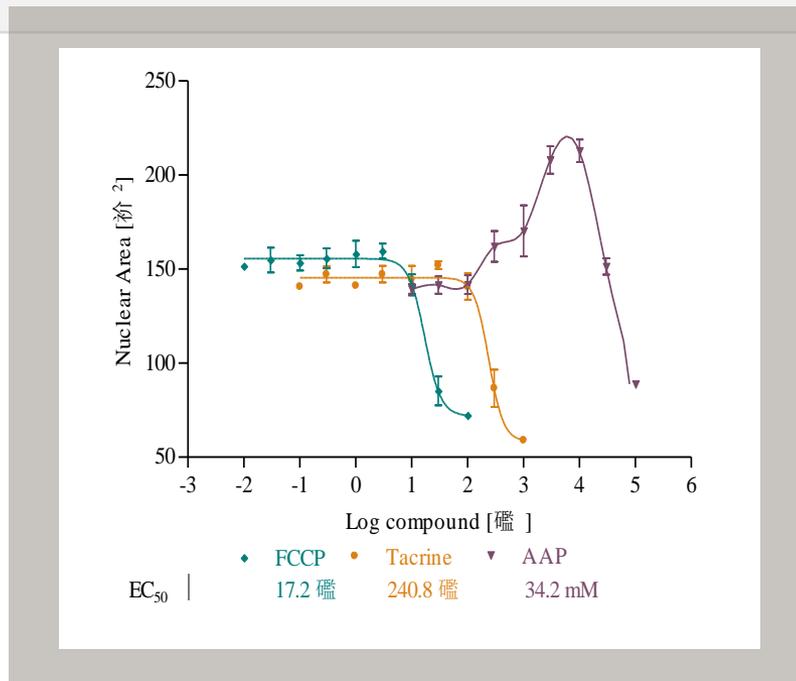
- ▶ 20x long WD 物镜成像
- ▶ 对HepG2细胞进行3种化合物处理 (Carbonyl Cyanide P-(Trifluoromethoxy) Phenylhydrazone , Tacrine and Acetaminophen) , 观察到细胞毒性
- ▶ 处理后细胞数量减少, 线粒体数量增多, 细胞核变小



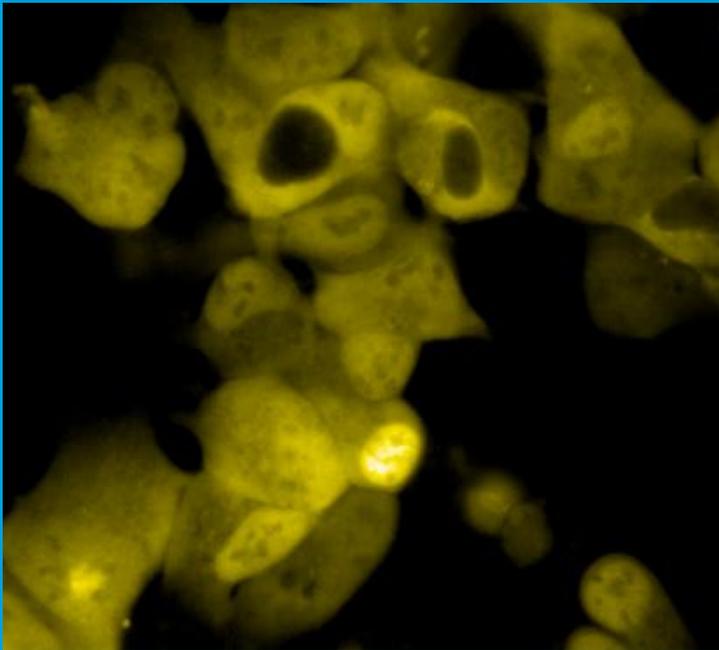
细胞数目变化与化合物浓度的关系，随药物浓度增加，细胞数目逐渐减少



线粒体密度的曲线：  
线粒体在细胞毒作用早期就受到影响，这里线粒体功能紊乱主要表现为线粒体呼吸作用增强



- 细胞损伤后通常会造造成细胞核皱缩
- FCCP 和 Tacrine 导致细胞核皱缩，同时细胞核荧光强增大
- AAP 最初导致细胞核增大，很可能是因为诱导细胞坏死，然后细胞核皱缩
- 高内涵支持我们做多个浓度梯度，支持我们同时做多个维度的表型分析，有助于我们发现这些隐藏的但实际上很重要的表型，有助于对化合物作用机制进行分类。

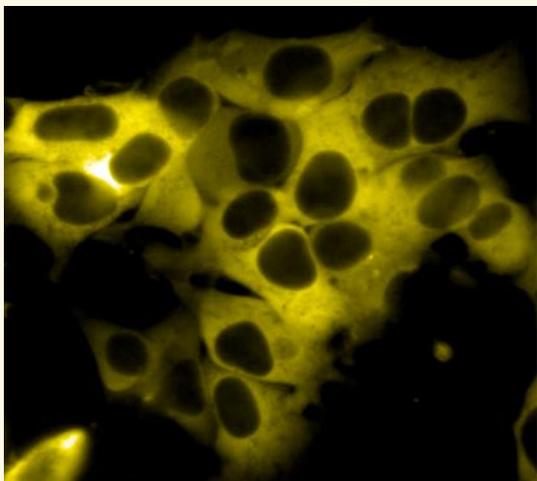


## 蛋白转位研究

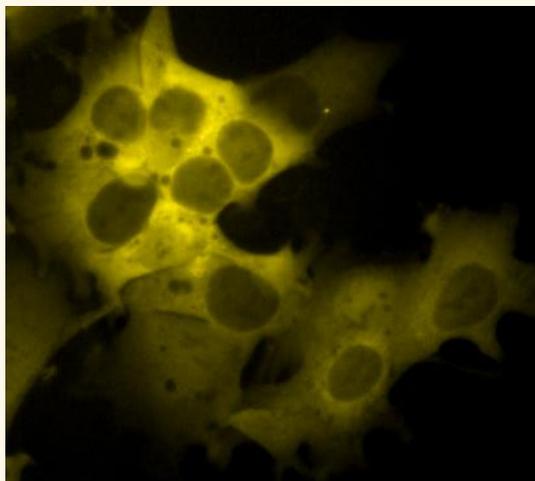
Data generated in the PerkinElmer  
Application Lab

## HaloTag<sup>®</sup> TMR ligand染活细胞

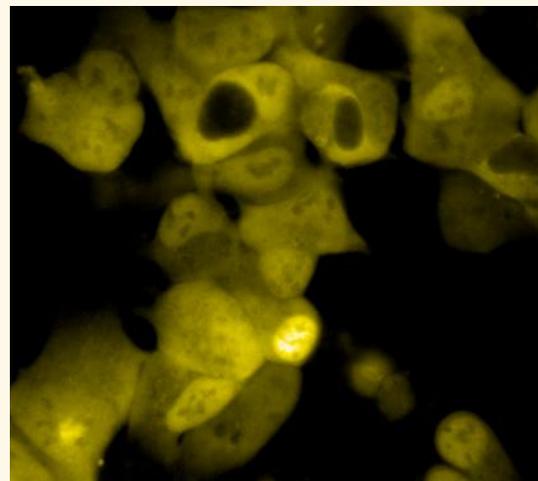
HaloTag<sup>®</sup> TMR ligand (fused to p65 subunit of NF- $\kappa$ B); 30 min post-TNF $\alpha$  addition



0 ng/ml TNF $\alpha$



0.5 ng/ml TNF $\alpha$

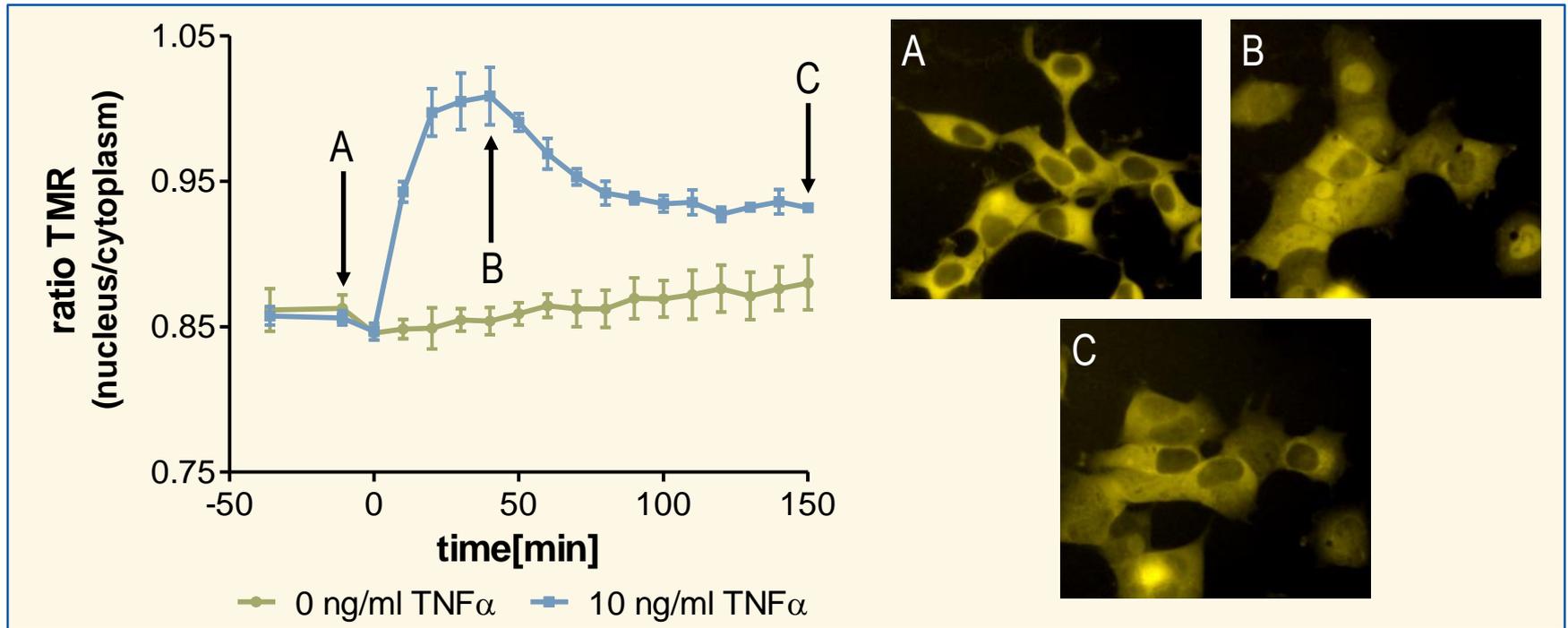


50 ng/ml TNF $\alpha$

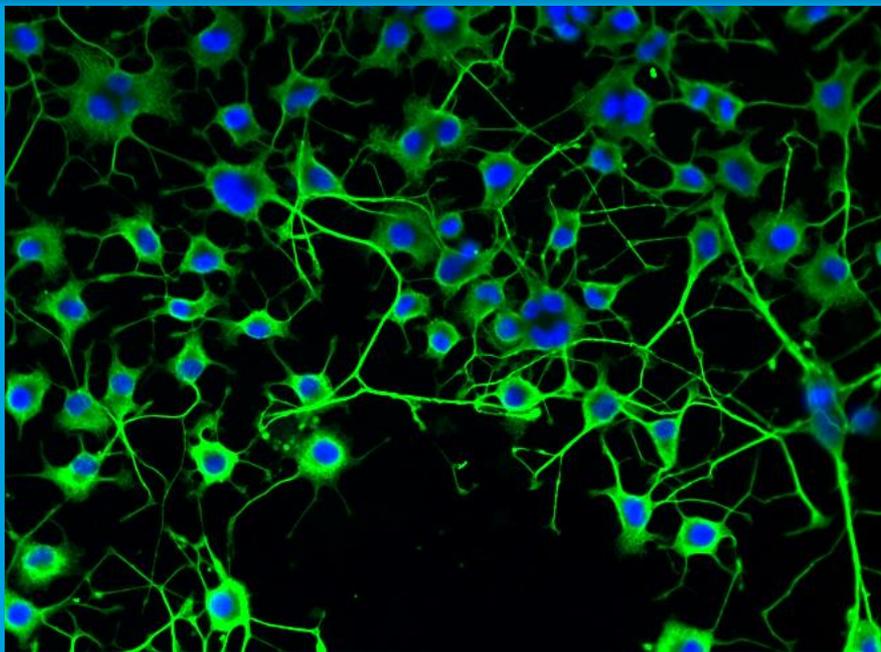
- HEK293细胞稳定表达NF- $\kappa$ B家族带 HaloTag<sup>®</sup> 融合标签的p65 (p65-HT)，通过HaloTag<sup>®</sup> TMR 配体透过细胞膜染活细胞
- 用不同浓度TNF $\alpha$  刺激NF- $\kappa$ B 信号
- 用Operetta<sup>®</sup> 高内涵系统成像，40x LWD 物镜荧光宽场

# NF- $\kappa$ B转位具有时间效应

- ▶ 通过Harmony<sup>®</sup> 高内涵成像和分析软件计算
- ▶ 计算NF- $\kappa$ B荧光 信号的核质比



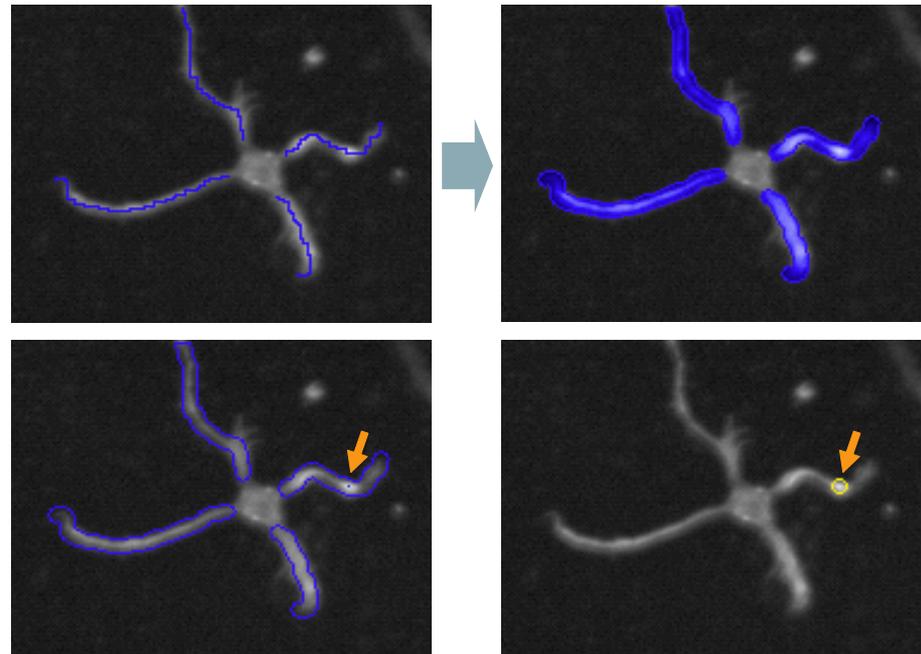
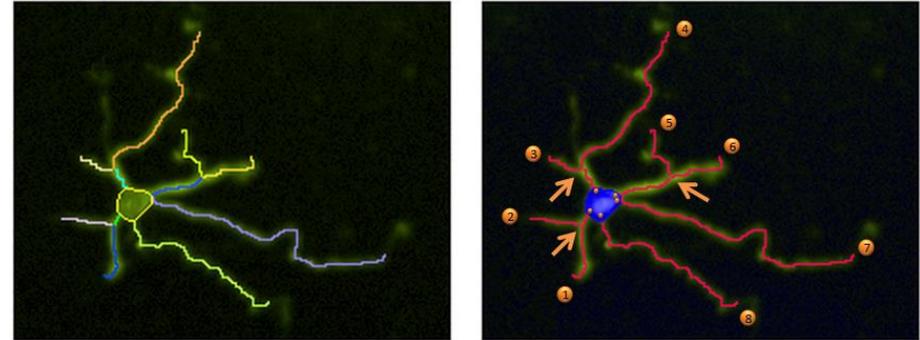
- 刺激30min后，核内p65-HT百分比 达到最高值
- 与固定终点分析相反，向实验中添加时间维度，允许鉴定抑制NF- $\kappa$ B易位的化合物以及影响细胞核中NF- $\kappa$ B分子驻留时间的化合物



## 神经细胞研究

Data generated in the PerkinElmer  
Application Lab

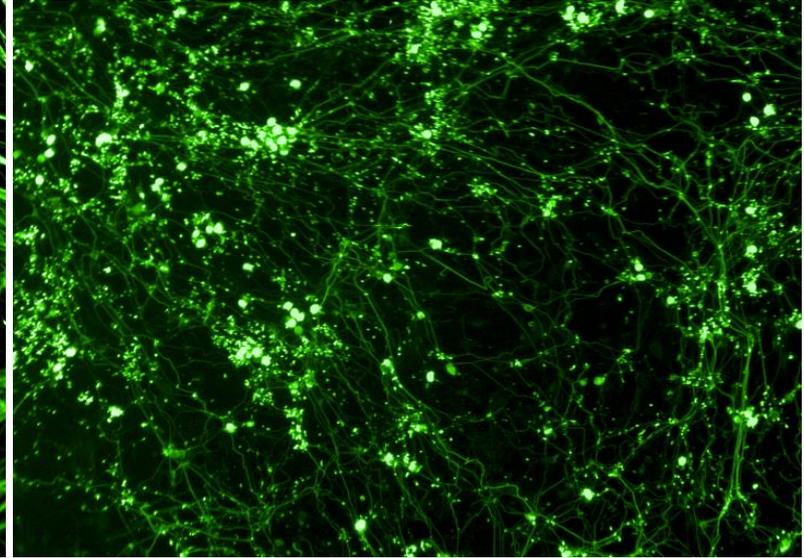
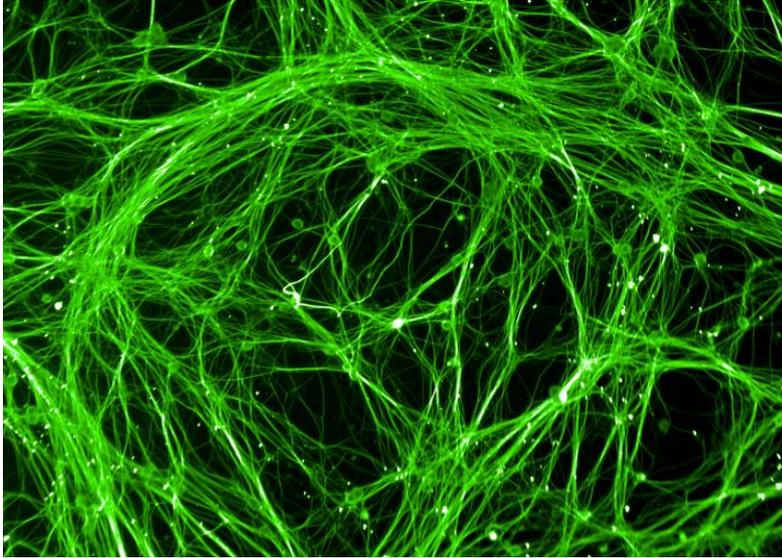
- Powerful neurite analysis
  - Left: individual segments (different colors)
  - Right: Roots (circles), nodes (arrows), and ends (numbers)
- Unique colocalization analysis
  - Neurites can be used as search mask for signals colocalized on neurites ⇒ essential for axon analysis
  - Middle: mask created from neurites
  - Lower: Spot identification on neurite (arrow)



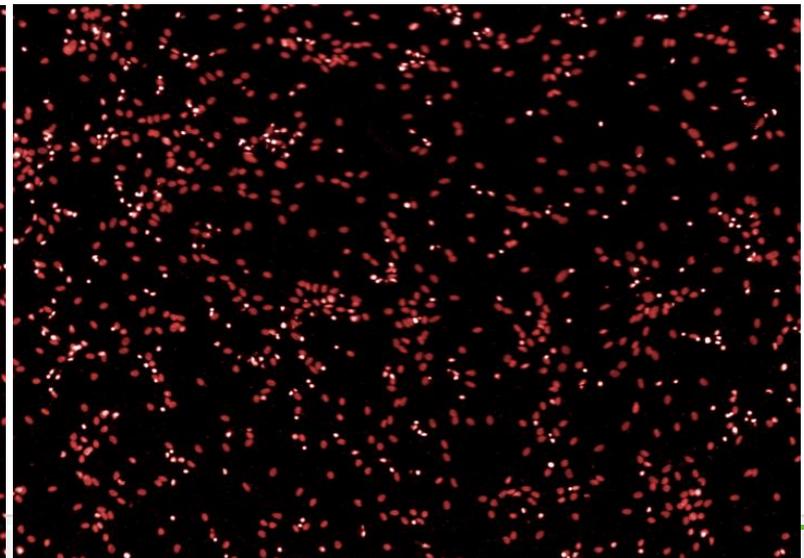
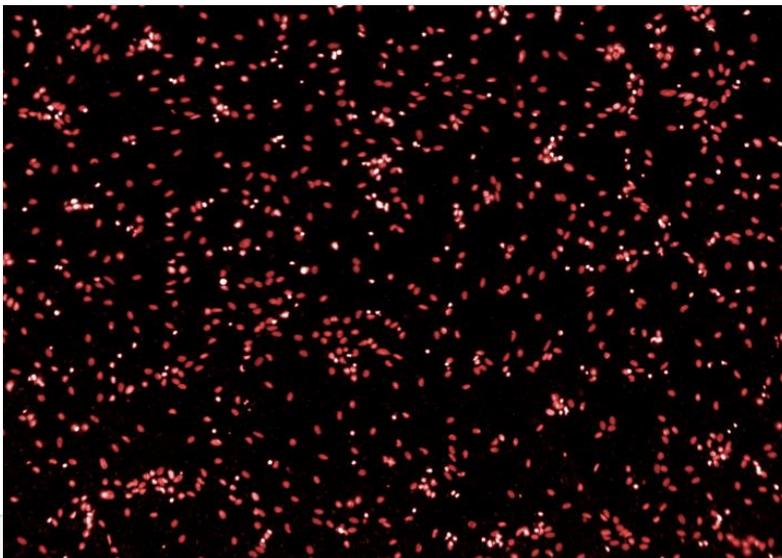
NGF treated

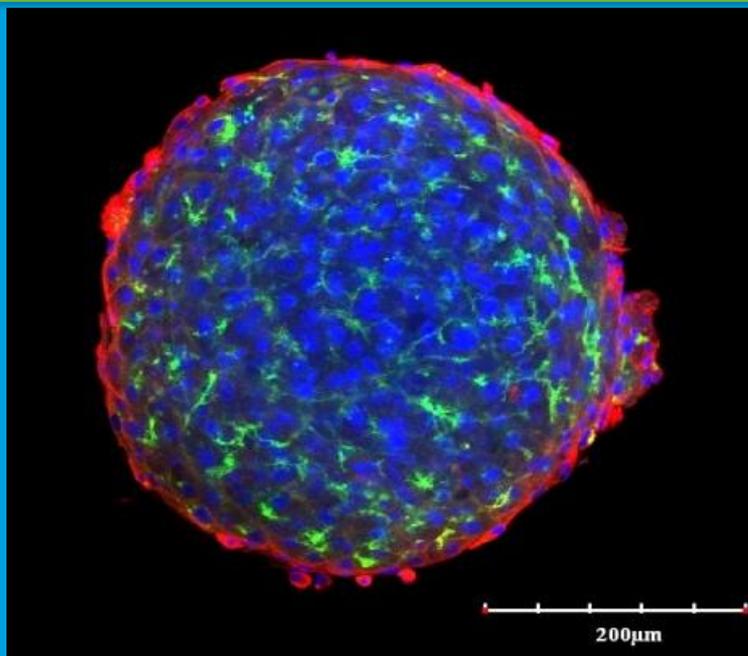
infected

Tuj1-A488  
Axons



Draq5  
Nuclei





## 3D微组织研究

Data generated in the PerkinElmer  
Application Lab

*Immunofluorescence image of hepatocytes  
co-cultured with non parenchymal cells (NPC).*

*Green: DPP-IV (bile canalicular marker),*

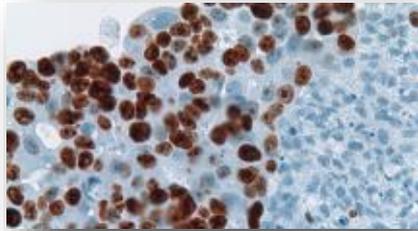
*Blue: DAPI,*

*Red: ICAM-1 (endothelial marker)*

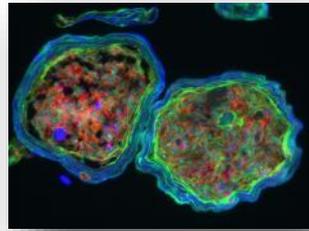
© 2014 PerkinElmer

# What are Microtissues (MTs) or Spheroids?

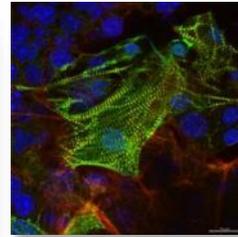
- ▶ 自组装的细胞群
- ▶ 体外三维细胞模型：最接近体内的模型 《Nature medicine》
- ▶ 细胞产生内源性细胞外基质（ECM）
- ▶ 细胞 - 细胞和细胞 - ECM相互作用
- ▶ 不同的细胞可以长成MT ...



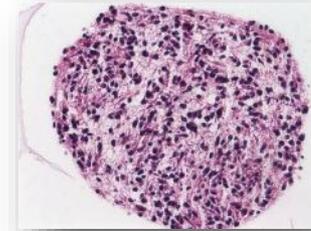
**Tumor MTs**



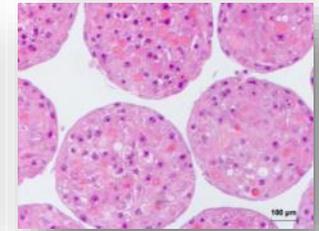
**Skin MTs**



**Embryoid  
Bodies**



**Neuro MTs**



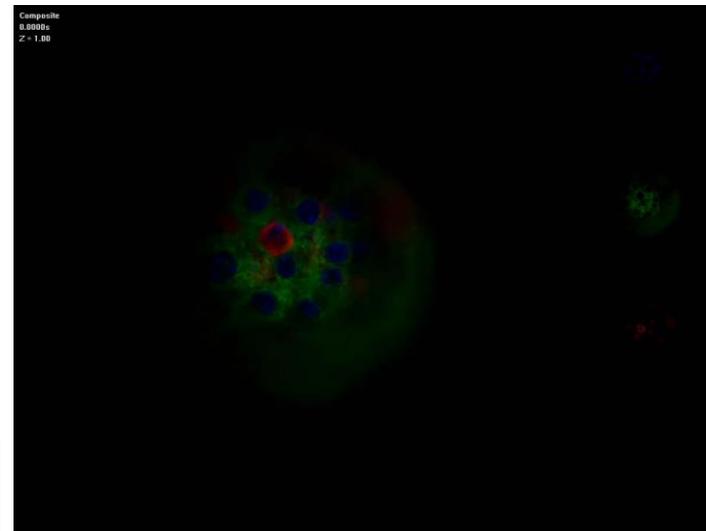
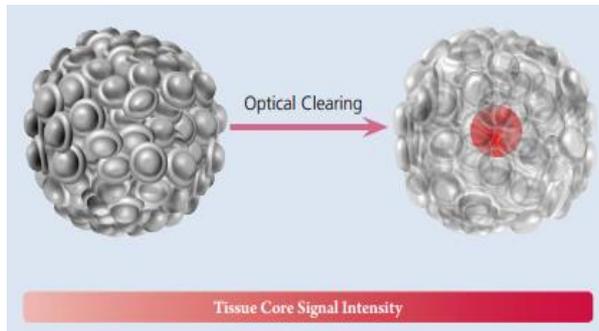
**Liver MTs**

Physiologically relevant 3D cell model

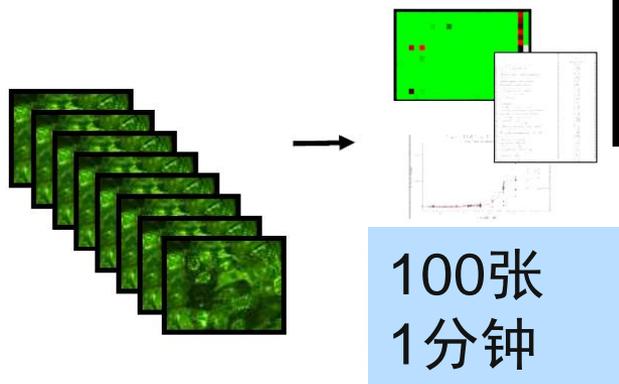
Data courtesy of InSpher<sup>in</sup>sphero

# HCS benefit

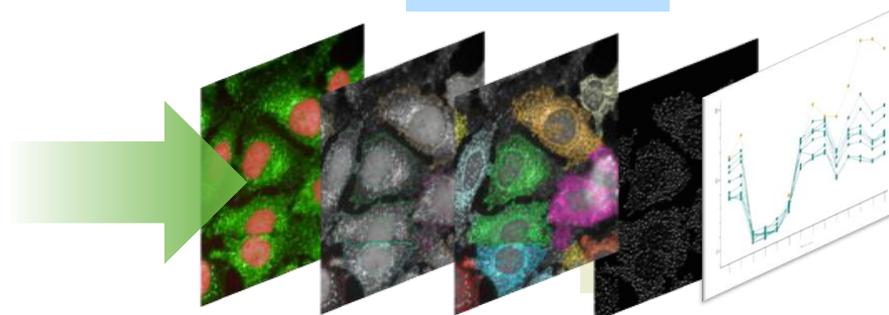
水镜—  
Z轴更深扫描深度



更快的扫描速度



全面的分析功能



# 特色模块 Intelligent Acquisition – PreciScan

## PreciScan

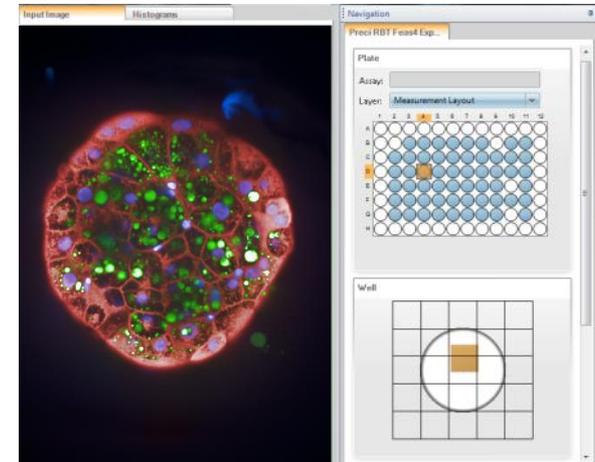
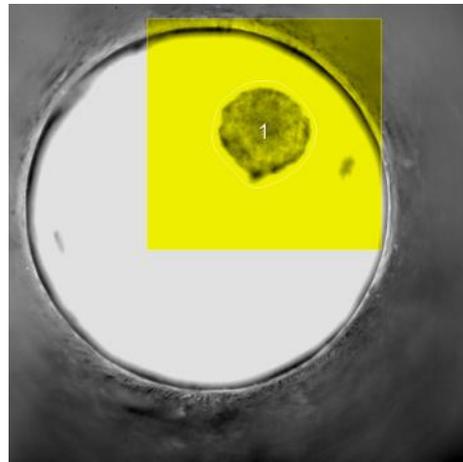
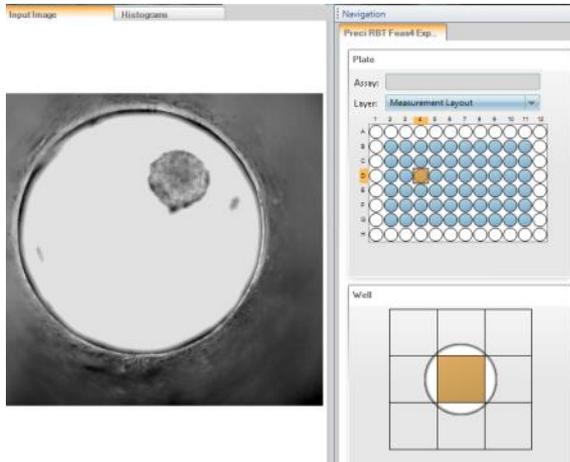
PreScan – Meas (10x)



„Find Microtissue“ Analysis

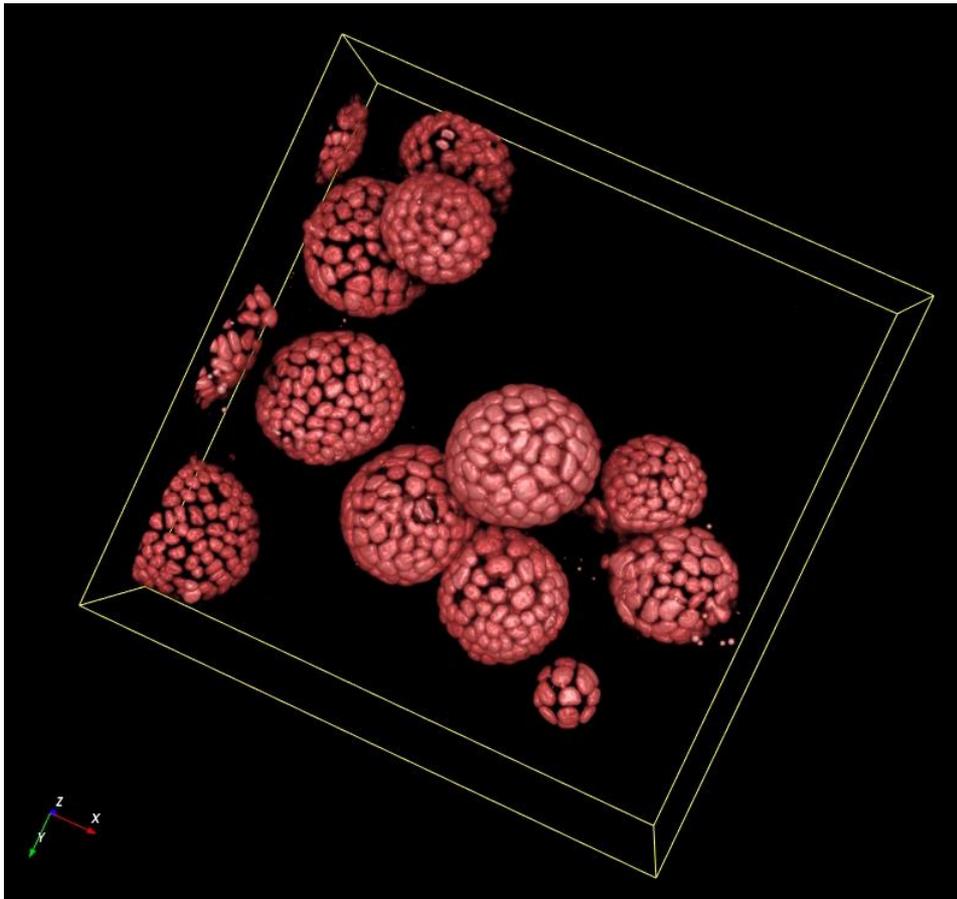


ReScan – Meas (40x)



Identify x/y positions of tissues for ReScan measurement

ReScan only wells that contain tissues



# 肾微组织体积等参数计算

Harmony 4.8

Harmony PhenoLOGIC™

Analysis: \*RMS 3D Analysis - Cysts  
Measurement: RMS\_3DCysts\_Drao5\_63x...

Analysis Sequence

Input Image  
Using: 3D Analysis, FFC None

Find Image Region

Output Population: Cysts

Calculate Position Properties

Output Properties: Cyst

Calculate Morphology Properties

Population: Cysts  
Region: Cyst  
Method: Standard

Volume:   $\mu\text{m}^3$   
Surface Area:   
Number of Fragments:   
Equivalent Ellipsoid Axes:   
Object Box Size:   
Sphericity:   
Inner Sphere Radius:   
Object Height:   
Maximum Thickness:   
Footprint Area:   
Maximum Crosssection Area:   
Maximum Inner Disk Radius:

Property Prefic: Cyst

Select Population  
Output Population: Cysts Selected

Find Nuclei  
Output Population: Nuclei

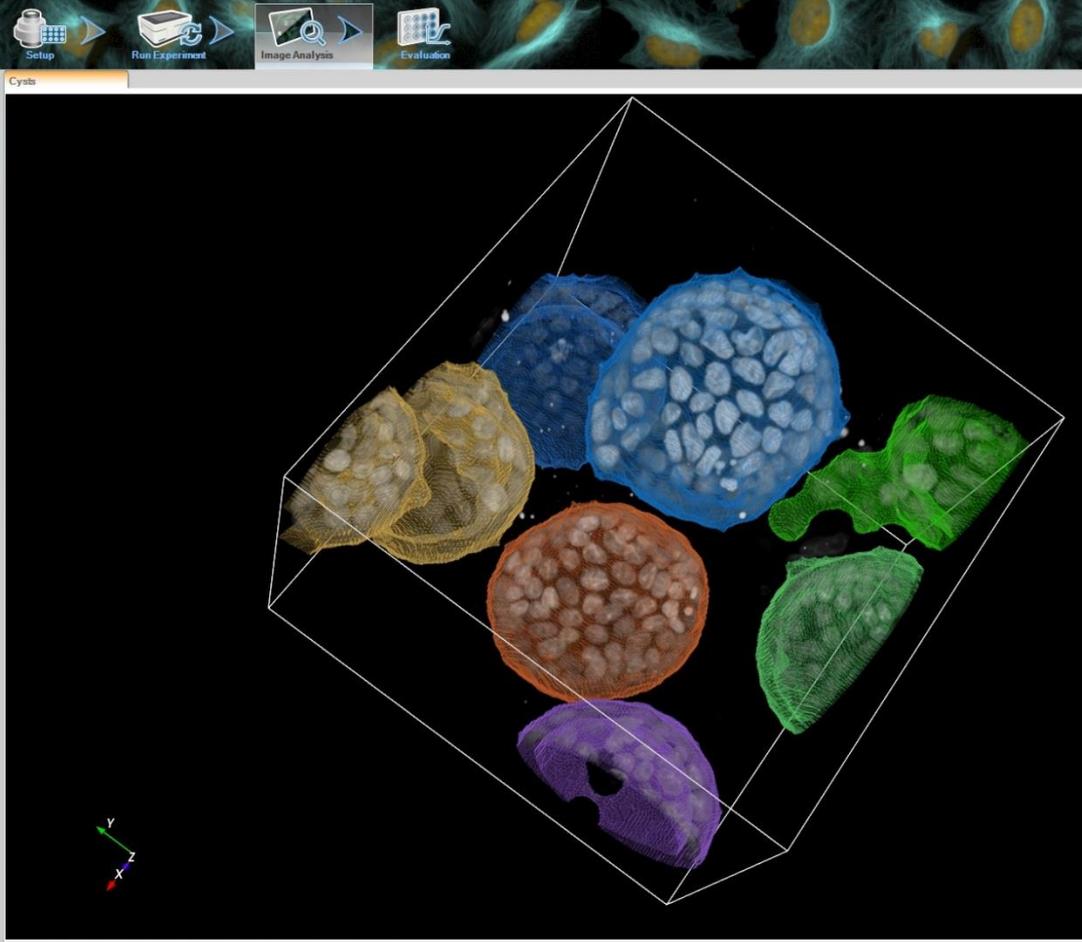
Find Cytoplasm  
Output Regions: Cell and Cytoplasm

Select Region  
Region Prefic: Raw Lumen  
Select Region (2)  
Output Region: Raw Lumen Resized  
Select Region (3)  
Output Region: Lumen

Calculate Morphology Properties (2)  
Output Properties: Standard

Calculate Morphology Properties (3)  
Output Properties: Standard

Calculate Properties



	微球1	微球2
体积	449087	258566
表面积	36259	24461
球圆度	0.77	0.80
长轴	105.1	85.96
短轴	88.4	73.7
内径	41.1	34.7
投影	7643.5	5219.8

Image Analysis Results

Object No	Cyst Centroid X in Image [ $\mu\text{m}$ ]	Cyst Centroid Y in Image [ $\mu\text{m}$ ]	Cyst Centroid Z in Image [ $\mu\text{m}$ ]	Cyst Contact Area with Image Sides [%]	Cyst Contact Area with Bottom [%]	Cyst Contact Area with Top [%]	Cyst Volume [ $\mu\text{m}^3$ ]	Cyst Surface Area [ $\mu\text{m}^2$ ]	Cyst Sphericity	Cyst Number of Fragments	Cyst Ellipsoid Longest Axis Length [ $\mu\text{m}$ ]	Cyst Ellipsoid Medium Axis Length [ $\mu\text{m}$ ]	Cyst Ellipsoid Shortest Axis Length [ $\mu\text{m}$ ]	Cyst Ellipsoid Short/Long Axis Ratio	Cyst Ellipsoid Tilt (deg)	Cyst Ellipsoid Orientation (deg)	Cyst Object Box Longest Length [ $\mu\text{m}$ ]	Cyst Object Box Medium Length [ $\mu\text{m}$ ]	Cyst Object Box Shortest Length [ $\mu\text{m}$ ]
1	-50.8352	6.79678	56.9846	2.31501	0	0	449087	36359	0.779997	1	105.084	93.7514	88.4141	0.841366	74.9312	-0.347706	109.583	98.8764	94.1476
5	35.4407	-4.33401	89.0785	0	0	0	258566	24461.6	0.80238	1	85.9672	78.507	73.6845	0.857124	80.8639	-43.8056	86.3738	84.055	76.0123
7	-63.1599	66.0492	118.454	6.93935	0	2.34437	144736	24203.3	0.550799	1	96.8139	82.7053	48.5246	0.501215	81.8305	11.0933	91.2772	81.9984	59.533
2	42.2782	77.1401	67.5663	6.53201	0	0	132560	35006.5	0.35915	1	161.764	80.9295	54.3955	0.336265	50.7634	-18.2954	139.299	81.7541	68.4734
4	83.708	-54.0512	77.1691	6.12084	0	0	64904.7	21253.5	0.367484	1	95.4258	91.6117	46.8646	0.491111	88.79	89.7666	82.3207	83.5362	43.8407
6	-11.3401	-80.7919	86.2702	4.04908	0	0	51335.1	17568.9	0.380202	1	102.74	70.4804	42.923	0.417785	51.3871	-1.81618	89.354	72.7561	54.2648
3	-73.7304	-74.4944	51.5813	5.34112	0	0	49052.1	15803.4	0.410051	1	82.4312	58.7788	56.9753	0.691186	53.4664	-34.569	105.662	63.0243	61.6709

# 腔内体积

Harmony 4.8

Harmony<sup>®</sup> PhenoLOGIC™

Analysis: \*RMS 3D Analysis - Cysts  
Measurement: RMS\_3DCysts\_Drag5\_63x...

New Save... Test

Analysis Sequence

Input Image

Using: 3D Analysis, FFC None

Find Image Region

Output Population: Cysts

Calculate Position Properties

Output Properties: Cyst

Calculate Morphology Properties

Output Properties: Standard

Select Population

Output Population: Cysts Selected

Find Nuclei

Output Population: Nuclei

Find Cytoplasm

Output Regions: Cell and Cytoplasm

Select Region

Region Prefix: Raw Lumen

Select Region (2)

Output Region: Raw Lumen Resized

Select Region (3)

Population: Cysts Selected

Region:

Method: ResizeRegion (µm)...

Direction: XYZ

Fixed Aspect Ratio: 1

Outer Border XY: -5 µm

Outer Border Z: -5 µm

Output Region: Lumen

Calculate Morphology Properties (2)

Output Properties: Standard

Calculate Morphology Properties (3)

Output Properties: Standard

Calculate Properties

Output Properties: By Related Population

Define Results

Output: 13 Well Results, 12 Object Results

体积: 198838um<sup>3</sup>  
115632um<sup>3</sup>  
距离: 2.33um  
表面积: 18804um<sup>2</sup>  
13351um<sup>2</sup>

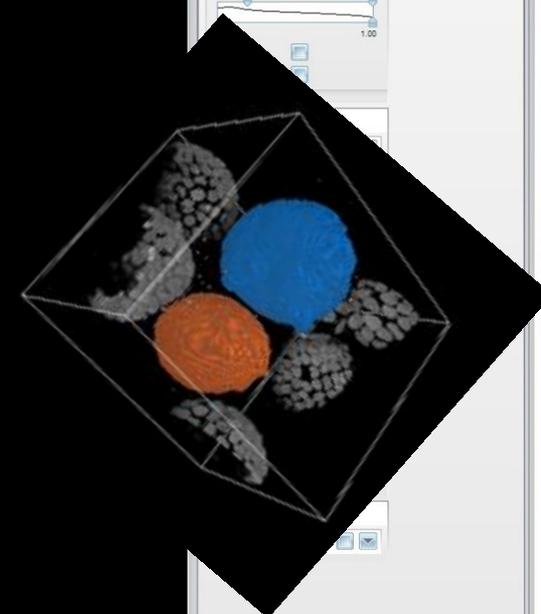
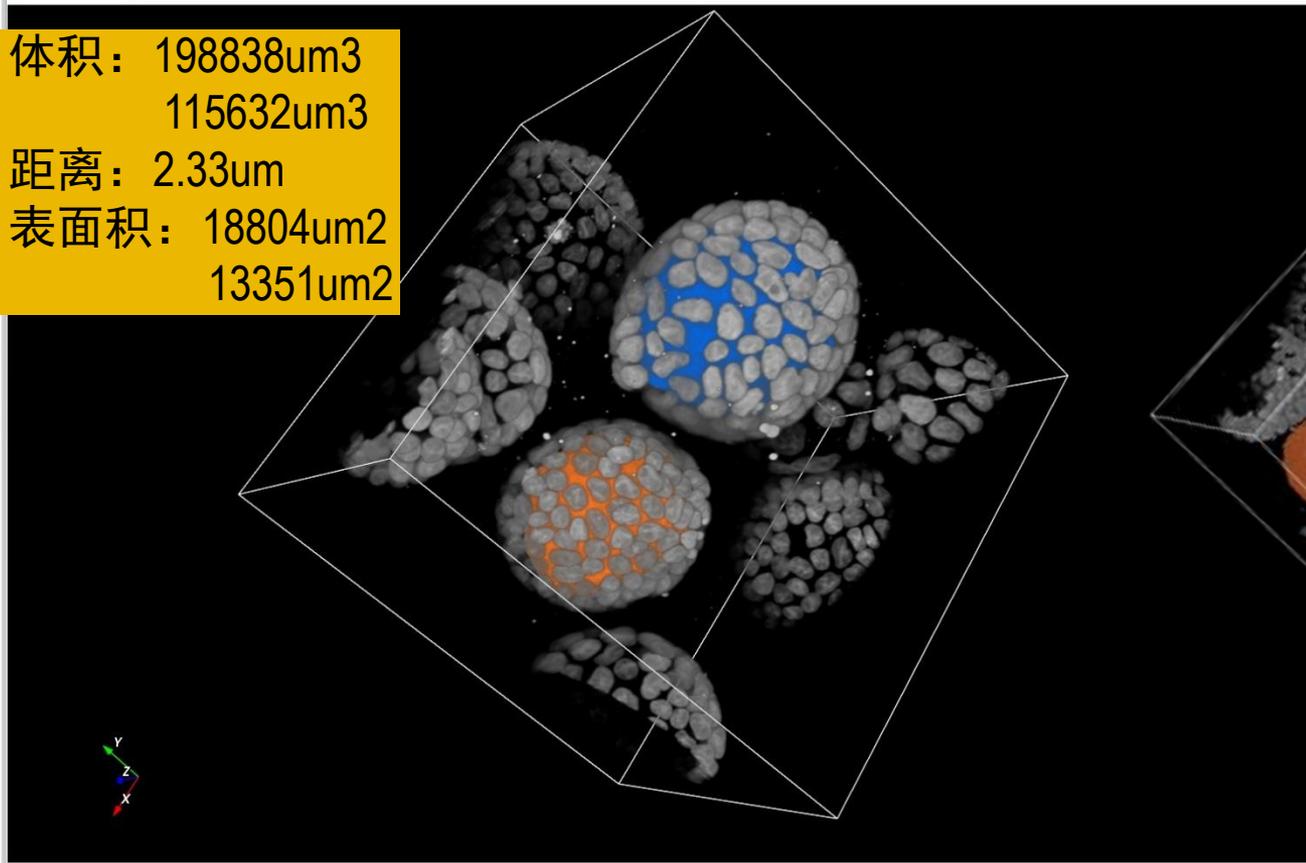


Image Control

Controls

Representation: XYZ 3D

Coloring: Highlight

Show Scale: 20 100 1.00

Left Mouse Button: 3D Rotate, with CTRL: 2D Rotate, with Shift: 2D Shift Mousewheel Zoom Size: 360x360x300, 148 MB

Image Analysis Results

Summary Properties Cysts Selec...

Population: Cysts Selected	Value						
Number of Objects	2						
Property	Mean	CV %	StdDev	Median	Max	Min	Sum
Cyst Centroid X in Image [µm]	-7.69722	-792.576	61.0063	-7.69722	35.4407	-50.8352	-15.3944
Cyst Centroid Y in Image [µm]	1.23139	639.17	7.87065	1.23139	6.79678	-4.33421	2.46277
Cyst Centroid Z in Image [µm]	73.0316	31.074	22.6939	73.0316	89.0785	56.9848	146.063
Cyst Contact Area with Image Sides [%]	1.1575	141.421	1.63696	1.1575	2.31501	0	2.31501
Cyst Contact Area with Bottom [%]	0	NaN	0	0	0	0	0
Cyst Contact Area with Top [%]	0	NaN	0	0	0	0	0
Cyst Volume [µm <sup>3</sup> ]	353826	38.0748	134719	353826	449087	258566	707653
Cyst Surface Area [µm <sup>2</sup> ]	30410.3	27.664	8412.71	30410.3	36359	24461.6	60820.6
Cyst Sphericity	0.791188	2.00044	0.0158273	0.791188	0.80238	0.779997	1.58238

# 微球内细胞计数

Harmony 4.8

Harmony® PhenoLOGIC™

Setup Run Experiment Image Analysis Evaluation

Analysis: RMS 3D Analysis - Cysts  
Measurement: RMS\_3DCysts\_Draq5\_63k...

Analysis Sequence

Input Image

Using: 3D Analysis, FFC None

Find Image Region

Output Population: Cysts

Calculate Position Properties

Output Properties: Cyst

Calculate Morphology Properties

Output Properties: Standard

Select Population

Output Population: Cysts Selected

Find Nuclei

Channel: DRAQ5

ROI: Cysts Selected

Cyst

Method: A

Common Threshold: 0.29

Volume: > 120  $\mu\text{m}^3$

Output Population: Nuclei

Find Cytoplasm

Output Regions: Cell and Cytoplasm

Select Region

Region Prefix: Raw Lumen

Select Region (2)

Output Region: Raw Lumen Resized

Select Region (3)

Output Region: Lumen

Calculate Morphology Properties (2)

Output Properties: Standard

Calculate Morphology Properties (3)

Output Properties: Standard

Calculate Properties

Output Properties: By Related Population

Define Results

Output: 13 Well Results, 12 Object Results

微球1: 细胞计数: 153  
细胞体积: 1327 $\mu\text{m}^3$   
微球2: 细胞计数: 144  
细胞体积: 813 $\mu\text{m}^3$

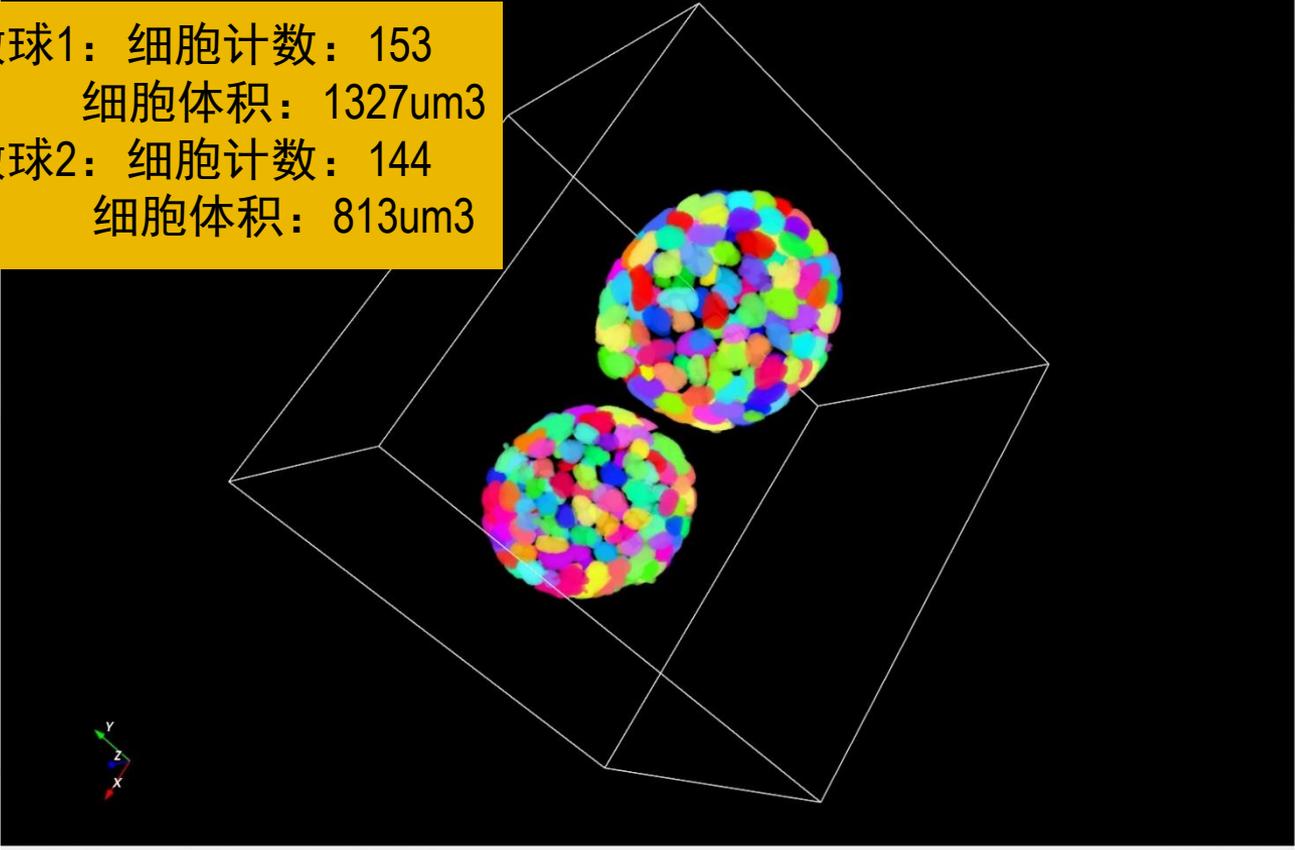


Image Control

Controls

Representation: MY2 3D

Coloring: Highlight

Show Scale: 20 53 1.00

Shade: [ ]

Clip Box: [ ]

Channels

DRAQ5 [ ]

Regions

Nucleus [ ]

Color: Rainbow

Style: Solid

Overlays

ROI [ ]

Highlighted Objects [ ]

Left Mouse Button: 3D Rotate, with CTRL; 2D Rotate, with Shift; 2D Shift  
Mousewheel: Zoom  
Size: 360x360x300, 148 MB

Image Analysis Results

Summary Properties Nuclei

Population: Nuclei	Value						
Number of Objects	297						
Property	Mean	CV %	StdDev	Median	Max	Min	Sum
Nucleus Volume [ $\mu\text{m}^3$ ]	599.367	73.0703	437.959	520.97	4523.17	128.364	178012
Nucleus Volume [px $^3$ ]	33803.6	73.0703	24773.4	29469	255856	7261	1.00684E+07

Harmony Phenologic™

Analysis: \*3D distance to untouched cell  
 Measurement: G1 - Measurement 1b

Load PreScan

New Save... Test

Analysis Sequence

Input Image

Using: 3D Analysis, FFC None

Find Image Region

Output Population: Image Region

Select Region

Output Region: Image Region Resized

Find Image Region (2)

Output Population: Image Region (2)

Calculate Morphology Properties

Output Properties: Standard

Calculate Position Properties

Output Properties: Image Region

Select Population

Output Population: Image Region (2) Selected

Select Population (2)

Output Population: Image Region (2) Selected S...

Select Population (3)

Output Population: cell selected

Calculate Position Properties (2)

Population: cell selected

Region: Image Region

Method: Gross Population

Population B: Image Region

Region B: Image Region

ROI Border Distance:

Nearest Object Distance:

Overlap:

Property Prefix: Image Region

Define Results

	Mean	CV%	Sum
离区域距离 [um]	3.63	61.81	10.89
重叠程度[%]	0	NA	0

	离区域距离 [um]
Cell 1	1.79
Cell 2	6.13
Cell 3	2.98

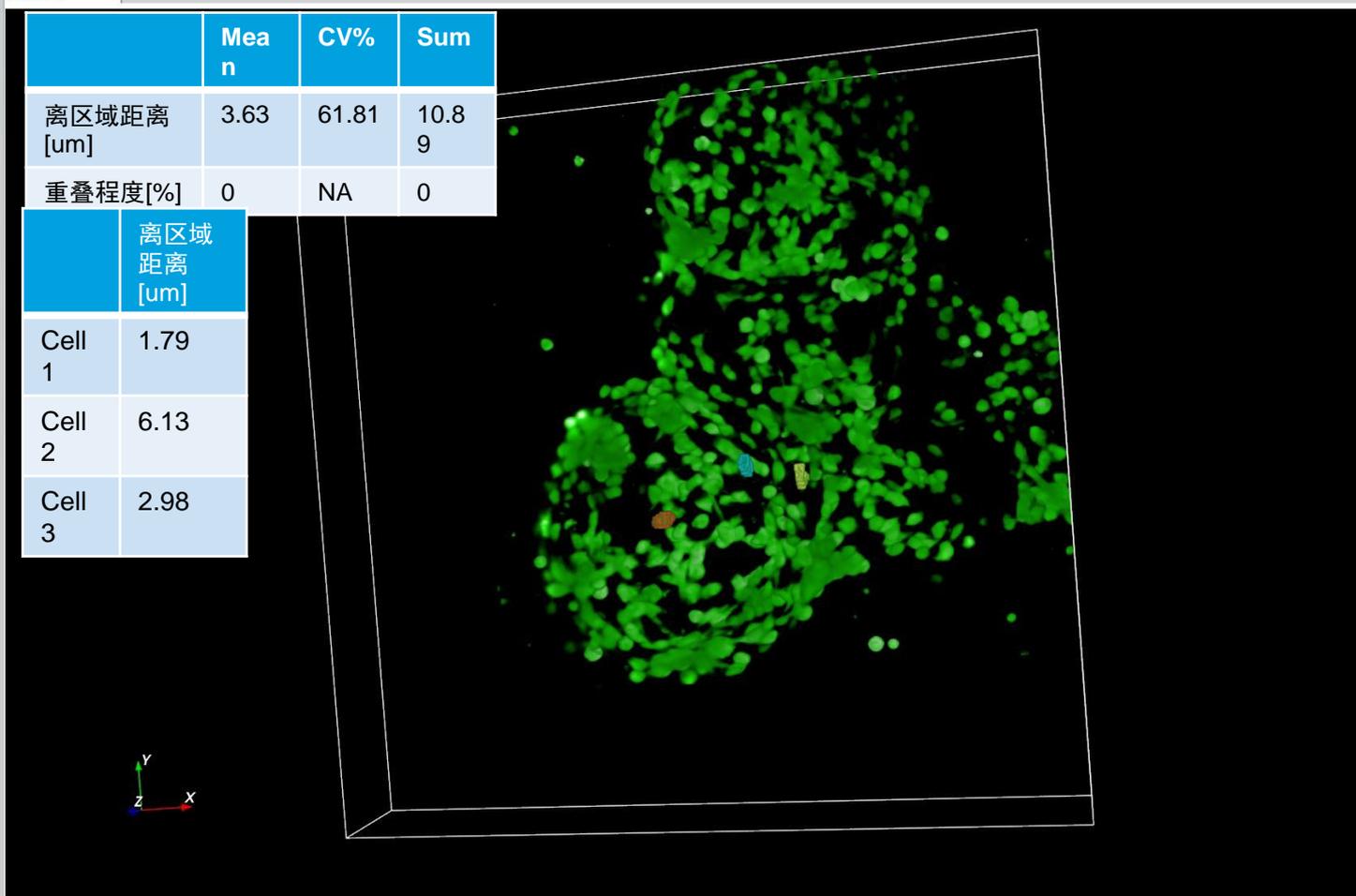


Image Control

Controls

Representation: XYZ 3D

Coloring: Highlight

Show Scale: 27 80 0.61

Shade: 0.61

Clip Box:

Channels

Alexa 488

Color: #1ff906

217 8728

Auto Contrast: 1.01

EthD-1

Color: #20f807

149 1241

Auto Contrast: 0.83

Regions

Image Region

Color: Rainbow

Style: Border

Overlays

Region B

Highlighted Objects

Left Mouse Button: 3D Rotate, with CTRL: 2D Rotate, with Shift: 2D Shift

Mousewheel: Zoom

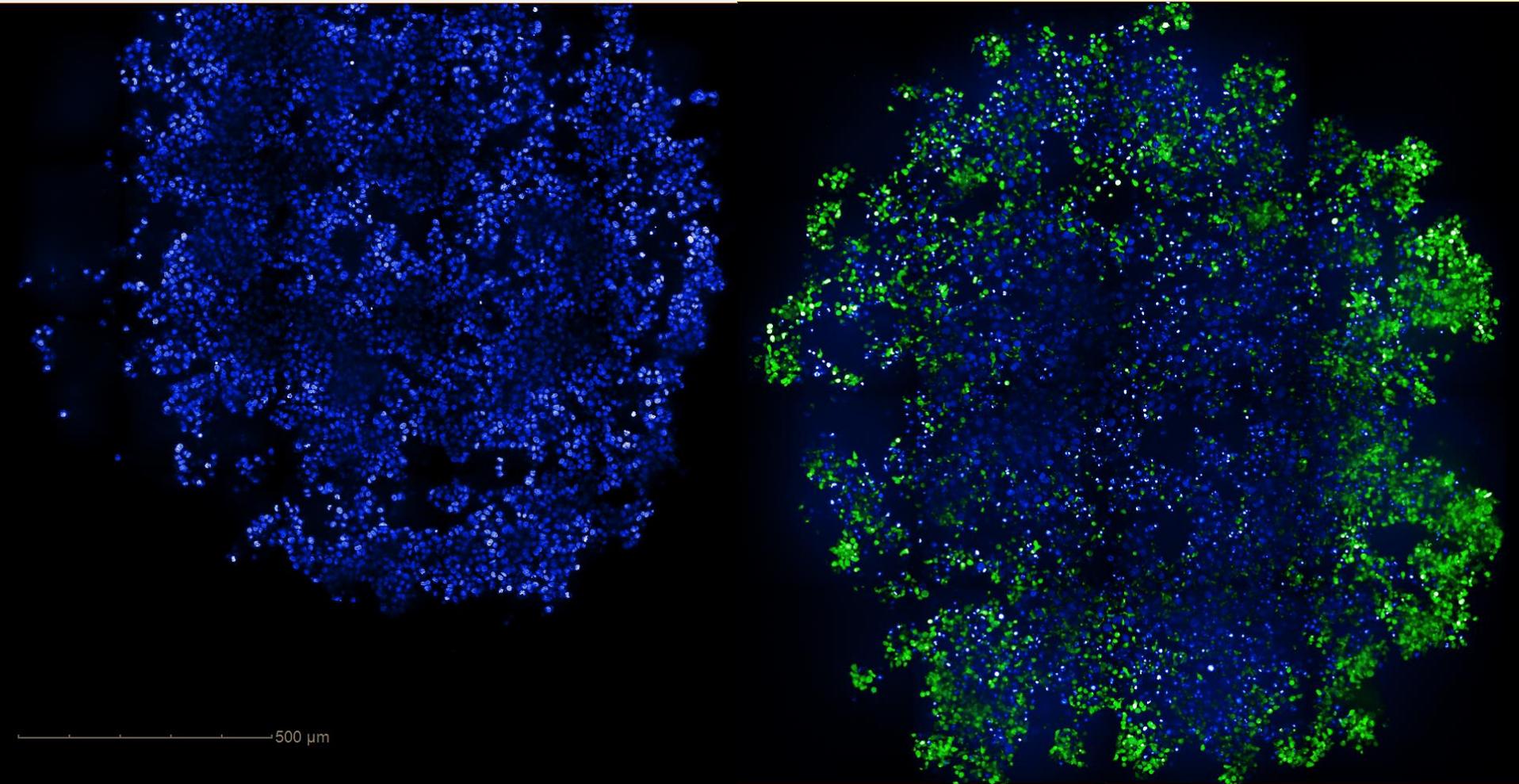
Size: 360x360x35, 17 MB

Image Analysis Results

Summary	Properties cell selected
---------	--------------------------

Population: cell selected	Value
Number of Objects	3
Property	Mean CV % StdDev Median Max Min Sum
Image Region Volume [um³]	2143.4 40.9582 877.898 1764.9 3147.06 1518.24 6430.21
Image Region Surface Area [um²]	1073.02 23.8439 255.649 947.451 1387.39 904.213 3216.06
Image Region Centroid X in Well [um]	-2091.77 -3.15185 65.9298 -2081.97 -2031.29 -2182.05 -6275.32
Image Region Centroid Y in Well [um]	-384.594 -6.01409 23.1298 -376.559 -366.553 -410.67 -1153.78
Image Region Centroid Z in Well [um]	52.6945 42.5511 22.4221 50.9814 75.9328 31.1852 158.083
Image Region Centroid X in Image [um]	43.4212 151.837 65.5296 53.2211 103.802 -26.8598 130.264

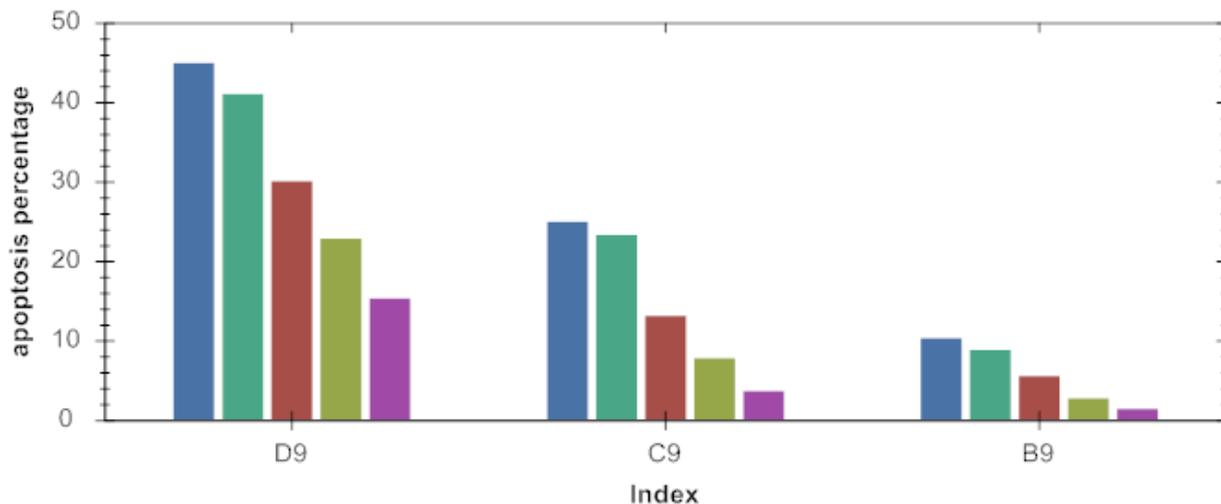
# 3D微组织CAR-T杀伤实验



凋亡细胞检测 分层计算Car-T细胞浸润

# 分析结果

## 肿瘤凋亡细胞百分比

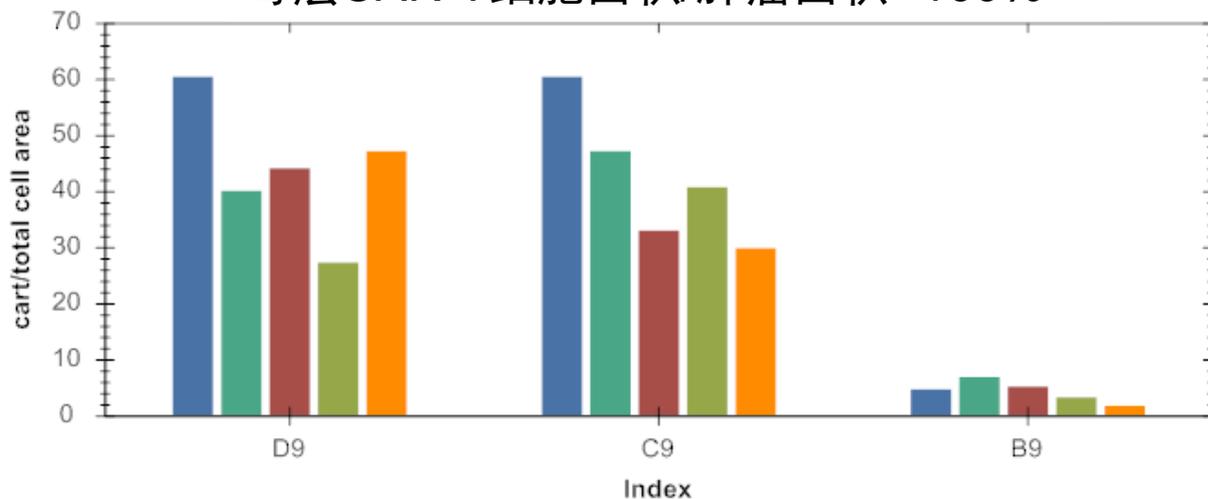


B9: 癌细胞

C9: 癌细胞+CAR-T a

D9: 癌细胞+CAR-T b

## 每层CAR-T细胞面积/肿瘤面积\* 100%



结论:

CAR-T a和b组会导致肿瘤凋亡

CAR-T 细胞浸润肿瘤与肿瘤凋亡有高度相关性

# Our Customer Base

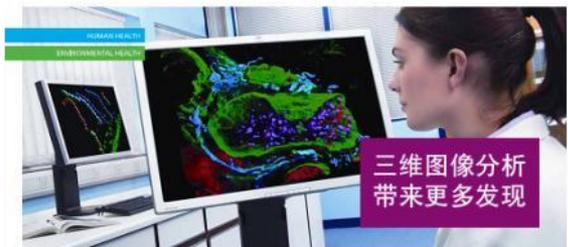


# 国内高内涵系统代表用户

中国科学院上海药物所	3台	蒋华良所长	瑞金医院	陈赛娟院士
东方肝胆医院		王红阳院士	罗氏中国研发中心	
重庆第三军医大学		万瑛	复旦大学 医学院	闻玉梅院士
中国中医科学院			中南大学湘雅医院	3台
中国科学院上海生化细胞所	2台		首都医科大学	
厦门大学 分子疫苗学和分子诊断学国家重点实验室、药学院	2台		南京高新生物医药公共服务平台有限公司	2台
北京大学 医学部、肿瘤医学 童坦君院士 尚永丰院士	4台		北京生命科学研究所 邵峰院士	王晓东院士、
南京中医药大学			军事医学科学院	2台
南京大学		华子春院长	中科院动物所	2台 周琪院士
天津中医药大学		张伯礼院士	中科院病毒所	



# 专业的高内涵技术交流活动。



Velocity三维细胞图像分析软件培训会——北京/上海



User Meetings

## 专业的应用支持团队



庞圣如



郭晓



高晓勇



马文瑞



白宗良



石晓月  
活体专家



王瑜  
高内涵专家



赖萌  
细胞影像专家



刘治东  
药筛专家



钱帮国  
病理专家



李想  
影像专家



黄幸  
活体专家



孙兵  
影像专家



张勇  
活体专家



刘欣毅  
酶标专家



刘文苑  
影像专家



周洪波  
活体专家



赵茵  
药筛专家



谢轶谦  
药筛专家



于雪梅

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