

# JCB Data Viewer

Bringing New Dimensions  
to Published Image Data

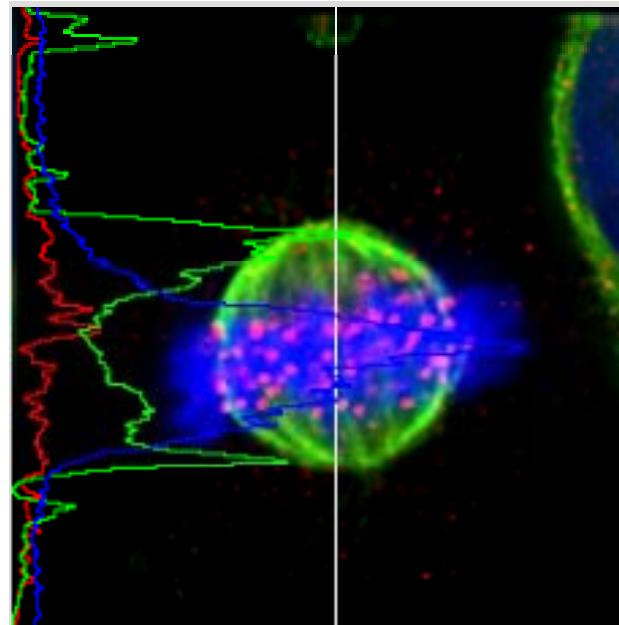
Liz Williams, PhD  
Executive Editor, *The Journal of Cell Biology*  
[lwilliams@rockefeller.edu](mailto:lwilliams@rockefeller.edu)

THE ROCKEFELLER  
UNIVERSITY  
PRESS  
QUALITY AND INTEGRITY

# Why would a publisher be interested in OME/OMERO?

## Our goals as a publisher:

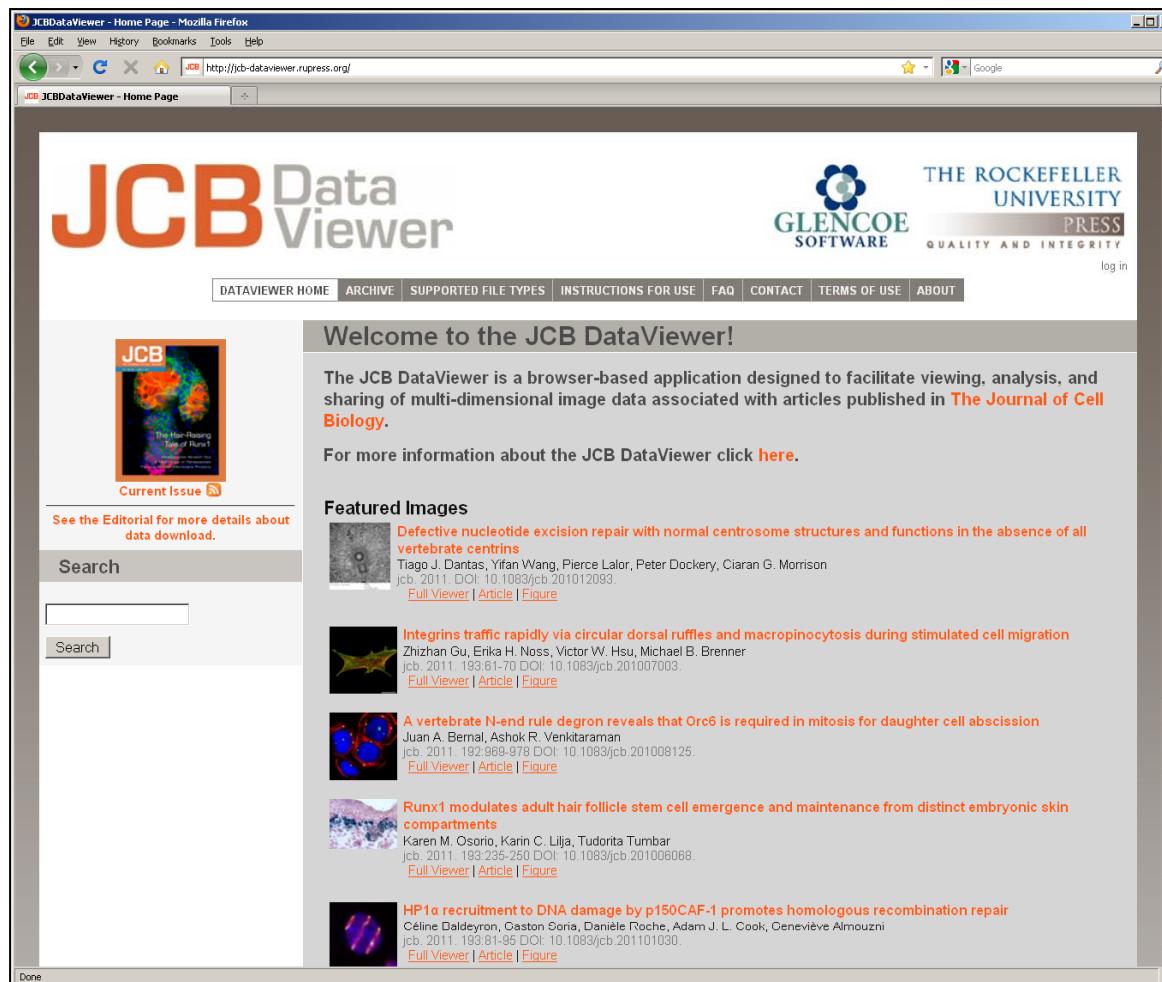
- To ensure that our authors have an effective medium for publishing their image data.
- To ensure that our readers have an effective medium for accessing and assessing published image data.
- To ensure the integrity of the scientific record.



- An OMERO-based, browser-based application for viewing, sharing, and archiving original, unprocessed image data associated with *JCB* papers.
- Enables presentation and sharing of image data acquired using a wide variety of light microscope and gel documentation systems.
- Allows users (editors, reviewers, readers) to perform simple analyses of the data within the application and to download the data in the open OME-TIFF format for more in-depth analysis with their software of choice.
- Enables multidimensional publishing – far beyond what is possible with standard PDFs and html.

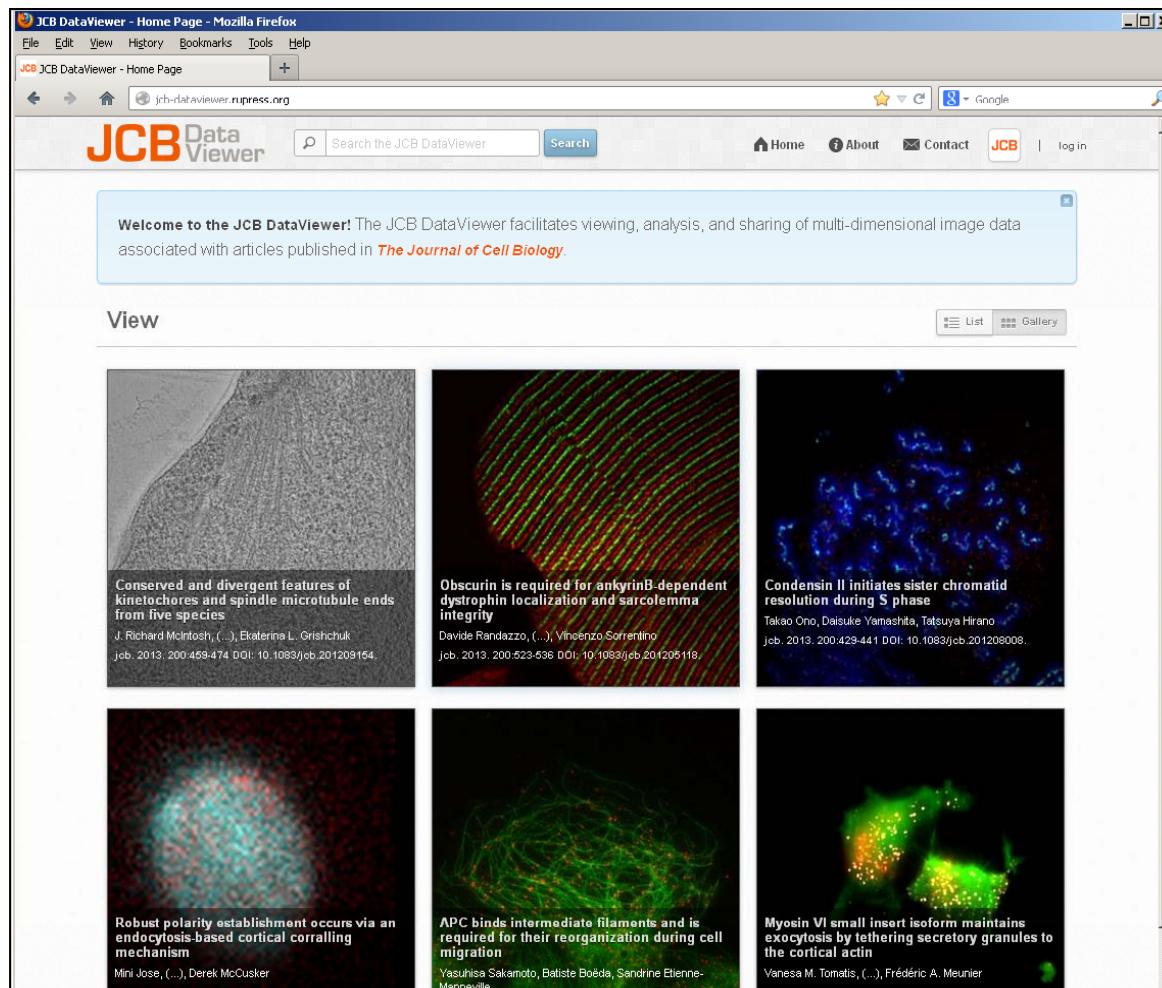


circa 2012



<http://jcb-dataviewer.rupress.org>

circa 2013



<http://jcb-dataviewer.rupress.org>

# The JCB DataViewer: Supported File Types

A screenshot of a Mozilla Firefox browser window displaying the 'About the JCB DataViewer application | Supported File Types - Mozilla Firefox' page. The URL in the address bar is [jcb-dataviewer.rupress.org/jcb/page/imageformats/](http://jcb-dataviewer.rupress.org/jcb/page/imageformats/). The page title is 'JCB DataViewer'. On the left, there is a sidebar with links: 'About', 'Instructions for Use', 'Supported File Types' (which is the active tab), 'FAQ', and 'Terms of Use'. The main content area is titled 'Supported File Types' and contains a table with three columns: 'Format', 'Extensions', and 'Comments'. The table lists numerous file formats, many of which have specific comments describing their characteristics or requirements.

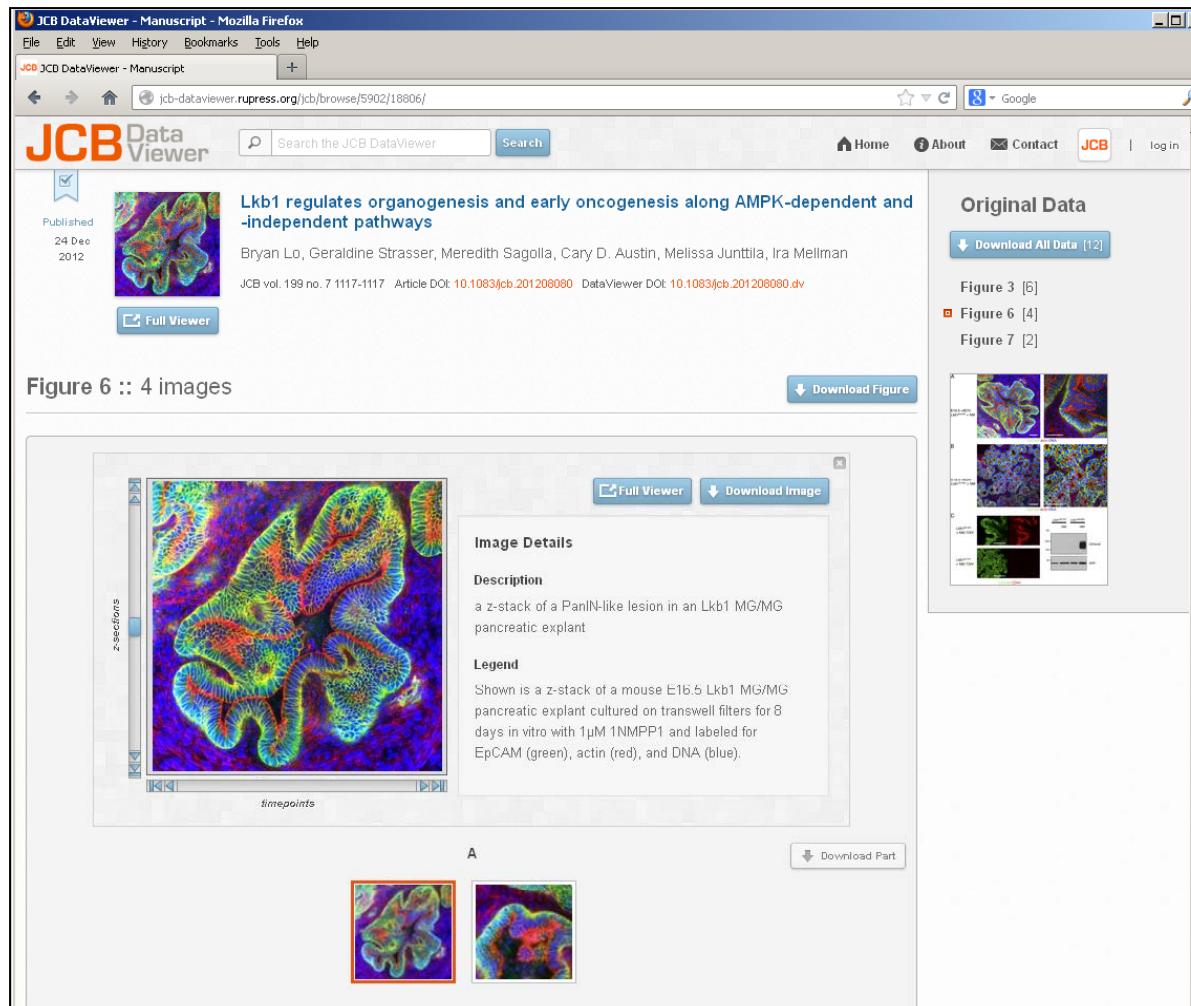
Format	Extensions	Comments
Adobe Photoshop PSD	.psd	
Alicona 3D	.a3d	
Amersham Biosciences GEL	.gel	
Amira Mesh	.am, .amiramesh, .grey, .hx, .labels	
Analyze 7.5	.img, .hdr	
Animated PNG	.png	
Aperio SVS TIFF	.svs	
ARF	.arf	
AVI (Audio Video Interleave)	.avi	Uncompressed (raw) or compressed with select lossless compression codecs (e.g., Apple ProRes (rpza))
Bio-Rad PIC	.pic, .xml, .raw	Excluding multi-plane "stitched" files and annotated ROI images
Bitplane Imaris	.ims	
Bitplane Imaris 3 (TIFF)	.ims	
Bitplane Imaris 5.5 (HDF)	.ims	
Cellomics	.c01	
CompuX Simple-PCI	.cxd	
DeltaVision	.dv, .v3d, .v3d_d3d, .dvlog	
DICOM	.dicom, .dcm, .jp2, .j2k, .j2kr, .raw	Uncompressed only
EPS (Encapsulated PostScript)	.eps, .epsi, .ps	
EvoTec/PerkinElmer Opera Flex	.flex	
FEI	.img	
FITS (Flexible Image Transport System)	.fits	
Gatan Digital Micrograph	.dm3	

Using Bioformats,  
more than 75 PFFs  
are supported.

## 1. single image analysis

# JCB Data Viewer

## The Mini Viewer



<http://jcb-dataviewer.rupress.org>

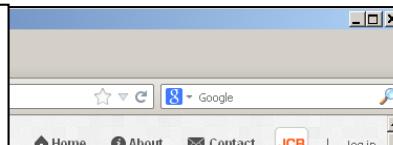
Lo et al (2012)

# JCB Data Viewer

## The Mini Viewer



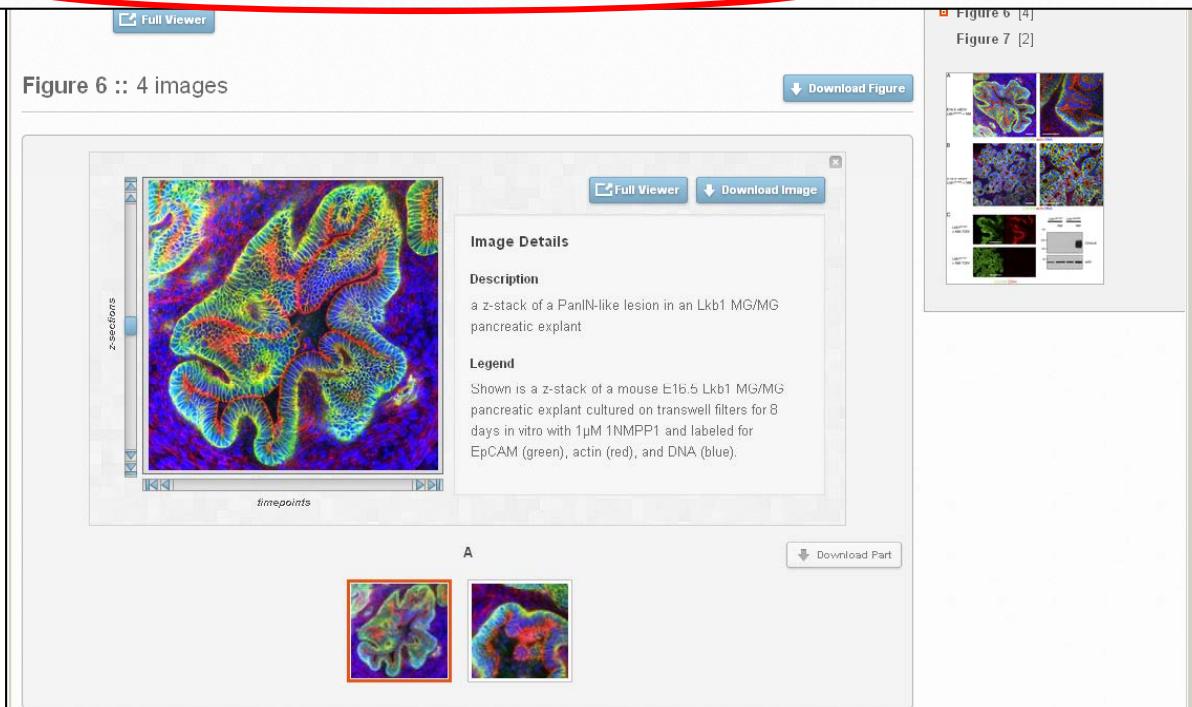
### Attribution & Maneuverability



#### Lkb1 regulates organogenesis and early oncogenesis along AMPK-dependent and -independent pathways

Bryan Lo, Geraldine Strasser, Meredith Sagolla, Cary D. Austin, Melissa Junntila, Ira Mellman

JCB vol. 199 no. 7 1117-1118 Article DOI: [10.1083/jcb.201208080](https://doi.org/10.1083/jcb.201208080) DataViewer DOI: [10.1083/jcb.201208080.dv](https://doi.org/10.1083/jcb.201208080.dv)



<http://jcb-dataviewer.rupress.org>

Lo et al (2012)

# JCB Data Viewer

## The Mini Viewer

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**Annotation**

**Image Details**

**Description**  
a z-stack of a PanIN-like lesion in an Lkb1 MG/MG pancreatic explant

**Legend**  
Shown is a z-stack of a mouse E16.5 Lkb1 MG/MG pancreatic explant cultured on transwell filters for 8 days in vitro with 1 $\mu$ M 1NMPP1 and labeled for EpCAM (green), actin (red), and DNA (blue).

**Figure 6 :: 4 images**

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**Figure 6 [4]**  
**Figure 7 [2]**

A

[Download Part](#)

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Lo et al (2012)

# JCB Data Viewer

## The Mini Viewer

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**Sharing & Re-analysis**

**Download Image**

**Download Figure**

**Download All Data [957]**

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# JCB Data Viewer

## The Mini Viewer

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**Sharing & Re-analysis**

**Download Image**

**Download Figure**

**Download All Data [957]**

**Mining**

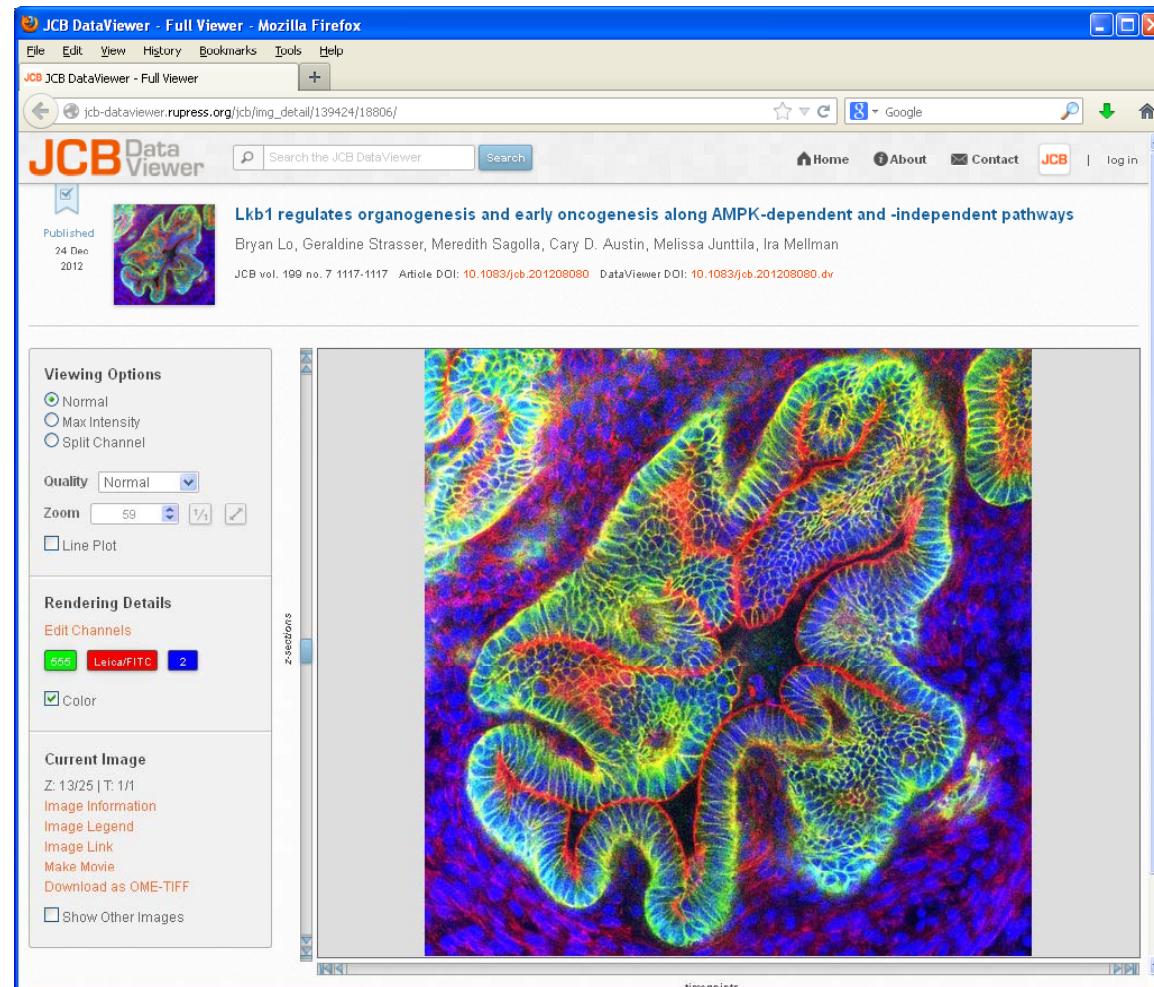
**Search the JCB DataViewer**

**Search**

<http://jcb-dataviewer.rupress.org>

# JCB Data Viewer

## The Full Viewer



<http://jcb-dataviewer.rupress.org>

Lo et al (2012)

# JCB Data Viewer

## The Full Viewer

Annotation

ver - Mozilla Firefox

Image Information

Basic Information

**Image name:** a z-stack of a PanIN-like lesion in an Lkb1 MG/MG pancreatic explant

**Author:** Bryan Lo, Geraldine Strasser, Meredith Sagolla, Cary D. Austin, Melissa Juntila, Ira Mellman

**Publication:** Lkb1 regulates organogenesis and early oncogenesis along AMPK-dependent and -independent pathways

**Publication ID:** jcb. 2012. 199:1117-1130 DOI: 10.1083/jcb.201208080.

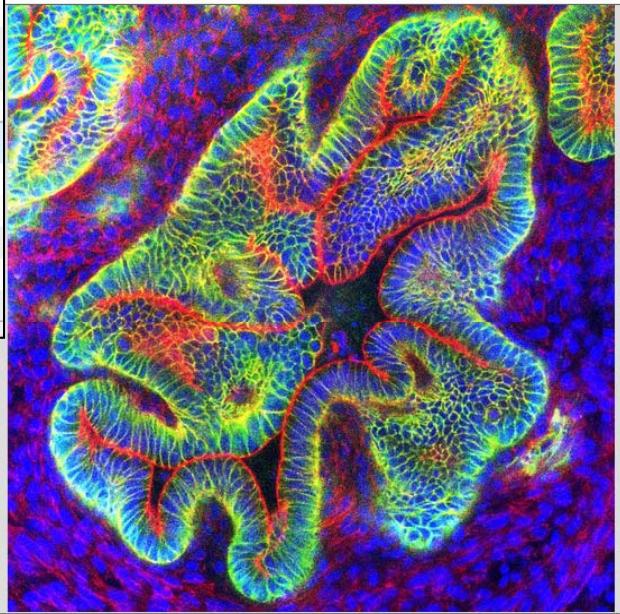
**Created on:** Sun Apr 22 2012

Dimensions

Image Size	Pixel Size
X: 1024px	X: 0.3784µm
Y: 1024px	Y: 0.3784µm
Z: 25	Z: 1.0071µm
T: 1	

Color

Current Image  
Z: 13/25 | T: 1/1  
[Image Information](#)  
[Image Legend](#)  
[Image Link](#)  
[Make Movie](#)  
[Download as OME-TIFF](#)  
 Show Other Images



<http://jcb-dataviewer.rupress.org>

Lo et al (2012)

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ver - Mozilla Firefox

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Y: 1024px	Y: 0.3784 $\mu$ m
Z: 25	Z: 1.0071 $\mu$ m
T: 1	

Color

**Attribution & Maneuverability**

**Link to This Page**

[http://jcb-dataviewer.rupress.org/jcb/img\\_detail/M39424/18806/?c=1|0:255\\$00F](http://jcb-dataviewer.rupress.org/jcb/img_detail/M39424/18806/?c=1|0:255$00F)

<http://jcb-dataviewer.rupress.org>

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T: 1	

Color

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**Link to This Page**

[http://jcb-dataviewer.rupress.org/jcb/img\\_detail/M39424/18806/?c=1|0:255\\$00F](http://jcb-dataviewer.rupress.org/jcb/img_detail/M39424/18806/?c=1|0:255$00F)

**Data Presentation**

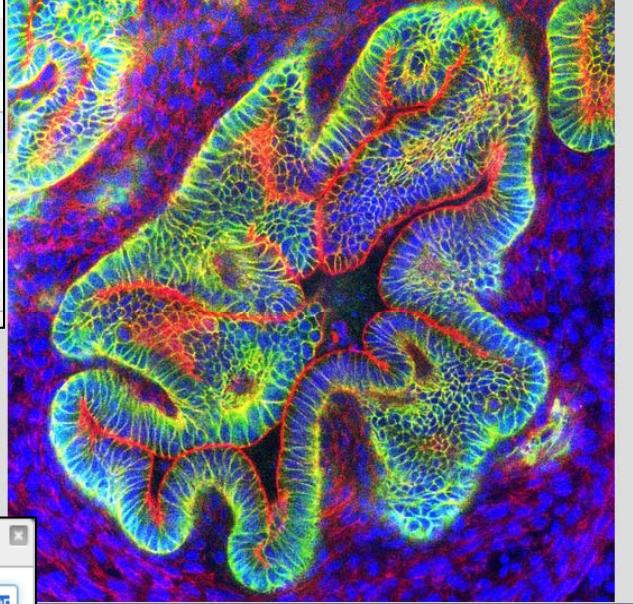
**Make Movie**

**Axis:** Z

**Format:** Quicktime .mov (Mac)

**Frames per second:** 3

**Make Movie**



timepoints

<http://jcb-dataviewer.rupress.org>

Lo et al (2012)

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## The Full Viewer

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**Image Information**

**Basic Information**

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T: 1	

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Link to This Page

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timepoints

Data Presentation

**Make Movie**

**Axis:** Z

**Format:** Quicktime .mov (Mac)

**Frames per second:** 3

**Make Movie**

Data Analysis

Viewing Options

- Normal
- Max Intensity
- Split Channel

Quality Normal

Zoom 59

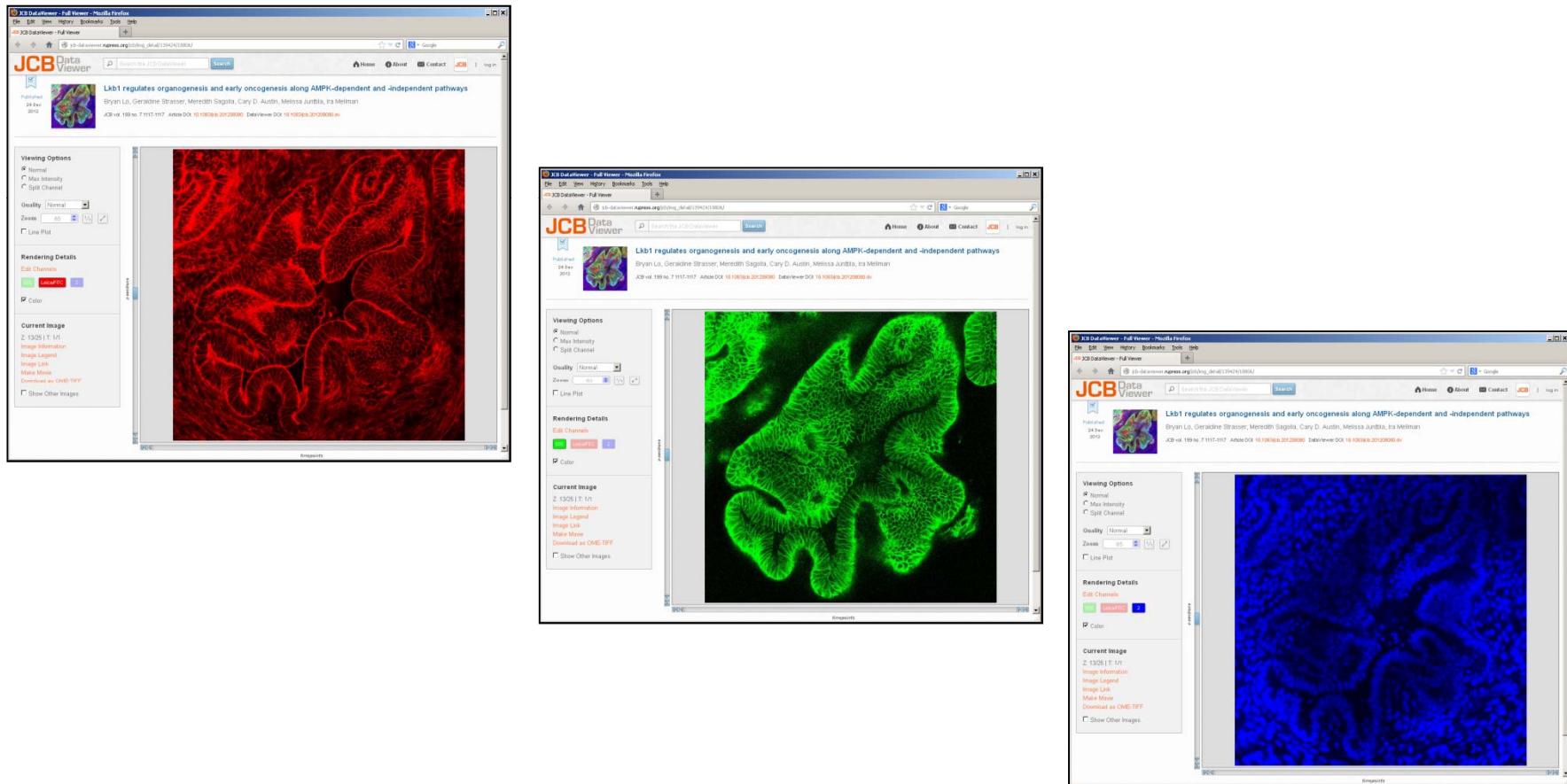
Line Plot

Axis: Horizontal

Y = 983

# JCB Data Viewer

## Split-Channel View

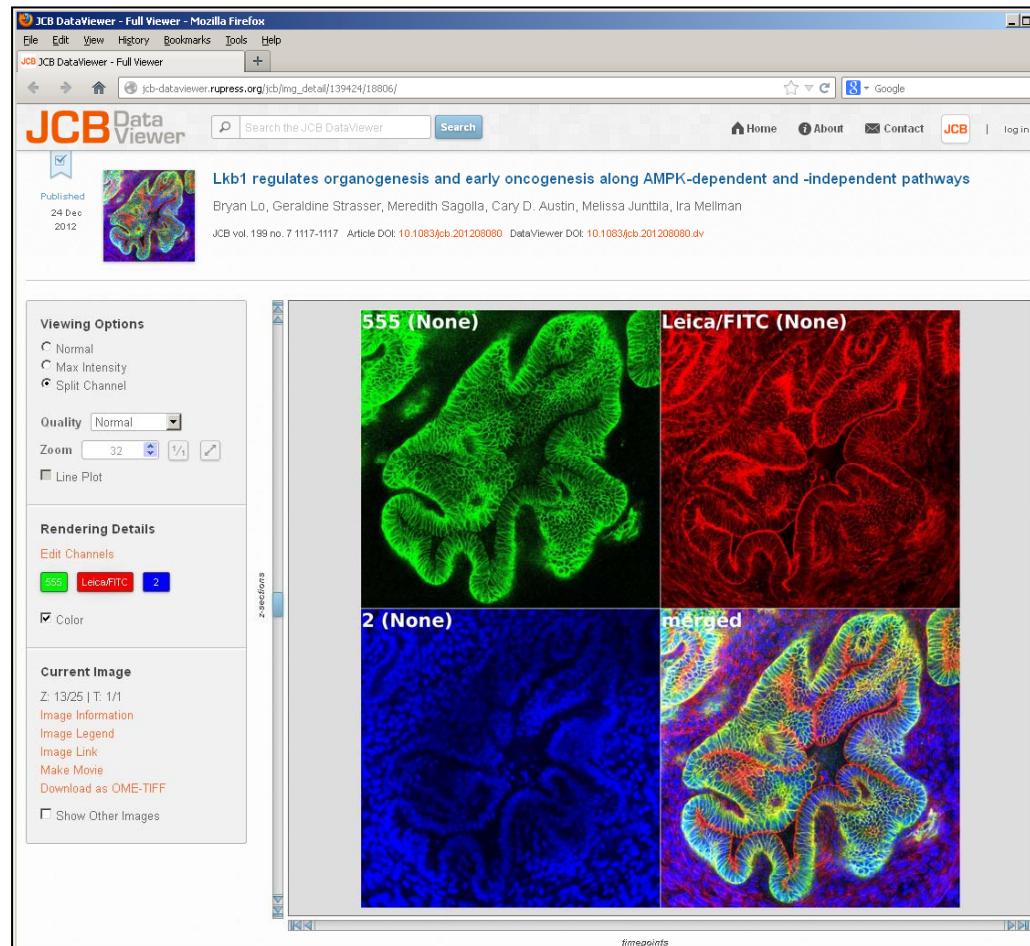


<http://jcb-dataviewer.rupress.org>

Lo et al (2012)

# JCB Data Viewer

## Split-Channel View



<http://jcb-dataviewer.rupress.org>

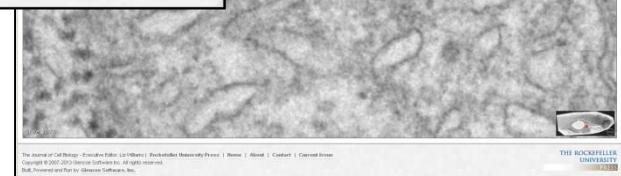
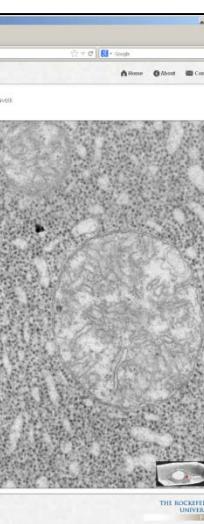
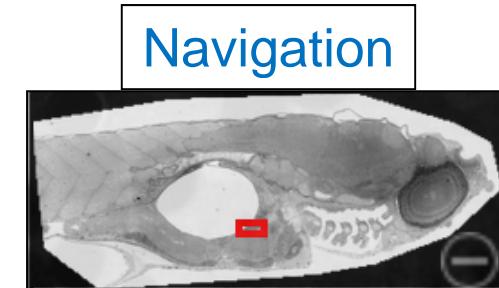
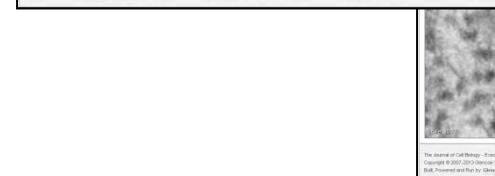
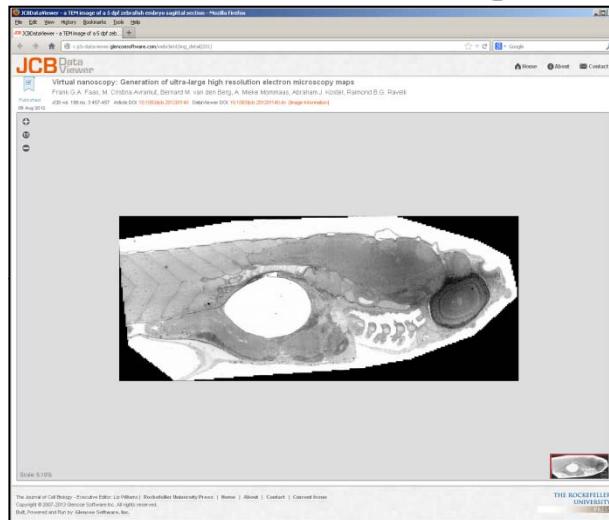
Lo et al (2012)

## 2. ultra-large, tiled image hosting

## What do we mean by an “ultra-large” image?

- 26000 tiled EMs
- 921600 pixels x 380928 pixels
- 281 gigapixels
- 1.6 nm resolution (16 million dpi)

## Ultra-large, high-resolution, tiled images

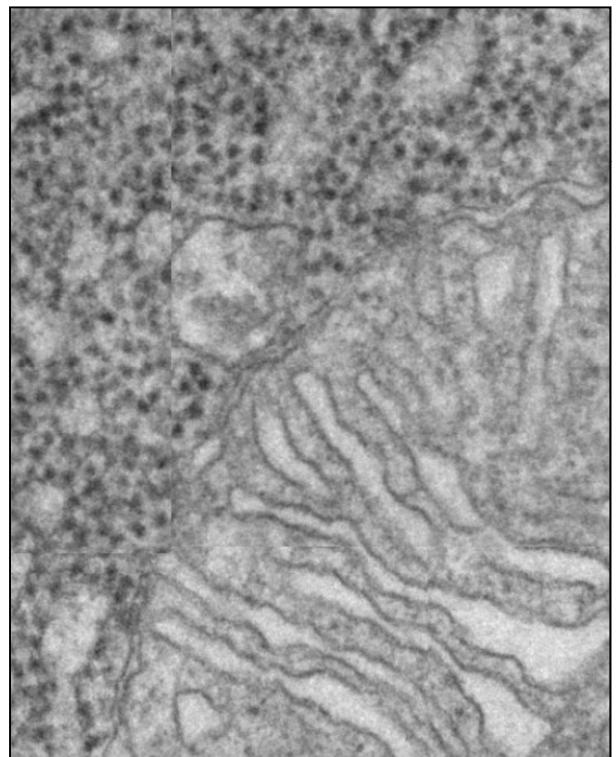
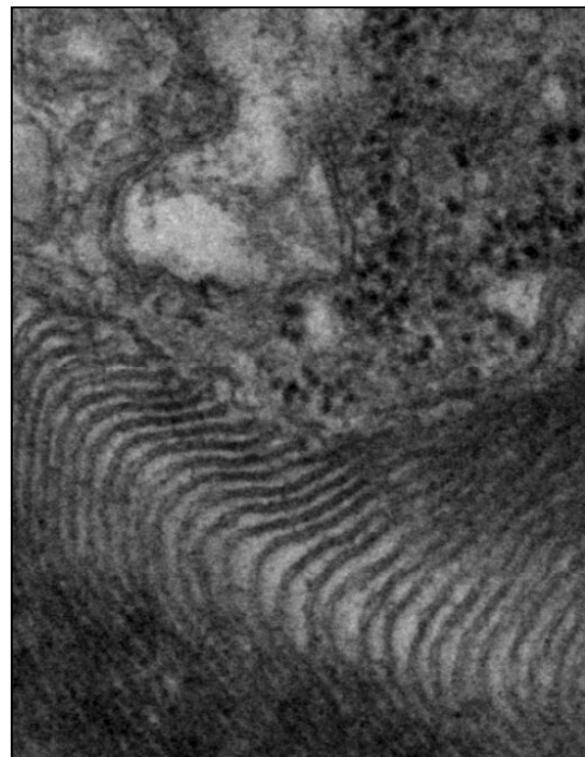
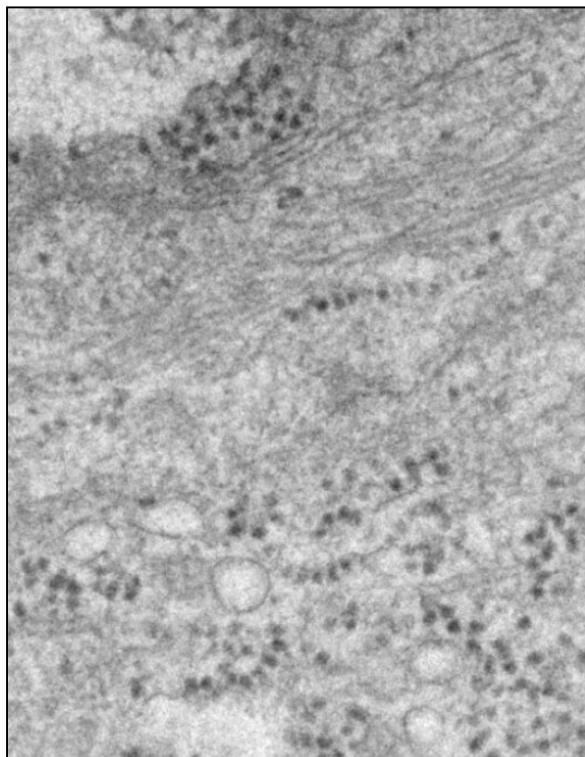


Navigation

<http://jcb-dataviewer.rupress.org>

Faas et al (2012)

## Ultra-large, high-resolution, tiled images



<http://jcb-dataviewer.rupress.org>

Faas et al (2012)

### 3. high-content screen analysis

## Six high-content screens hosted to date:

from “small”:

Srikumar et al (2013)

- 12 384-well plates (only 25% full)
- 3 fields per well
- 2 channels per field
- 2 quantitative datapoints per gene scored as a ‘hit’ (290 total)

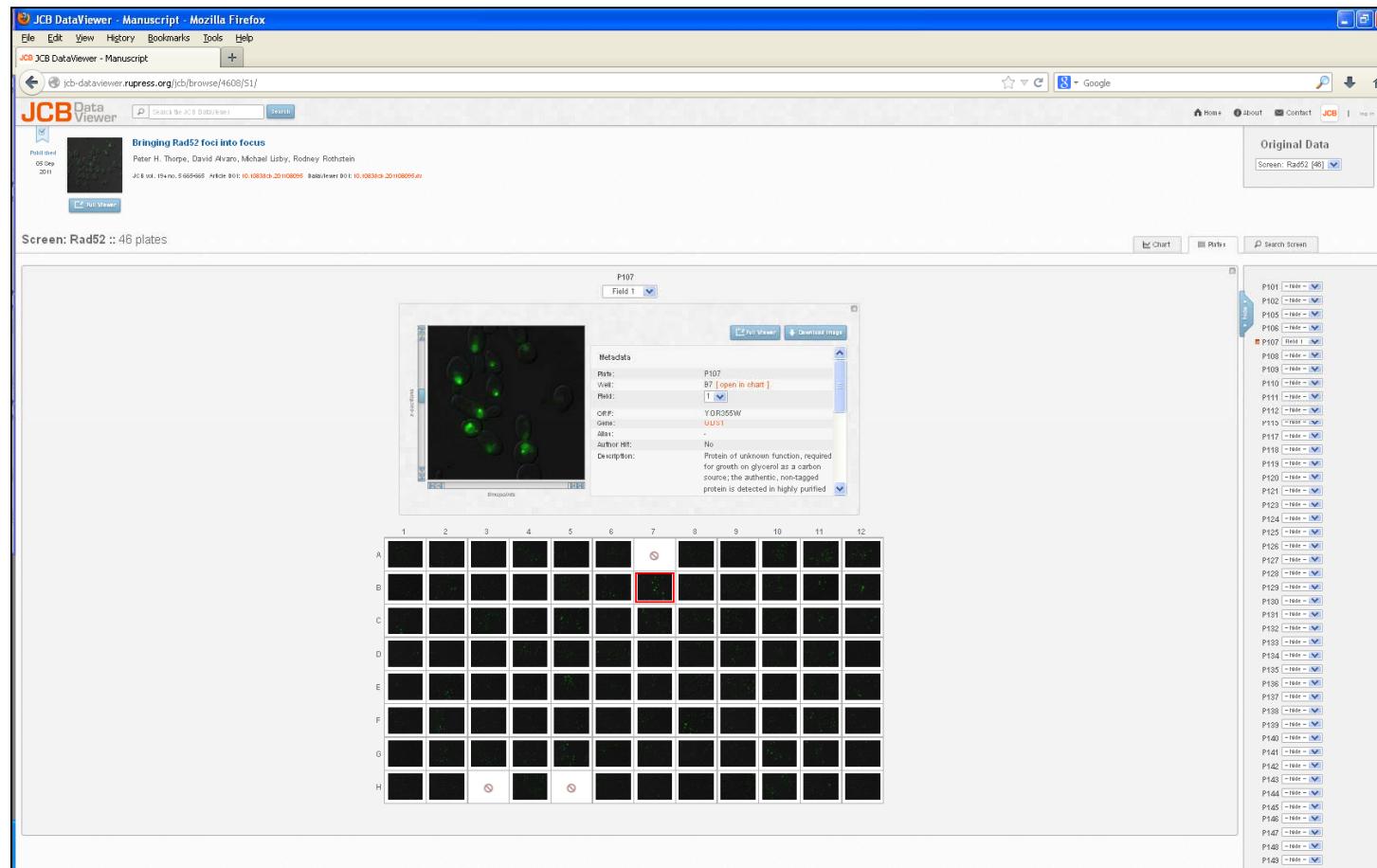
to “large and complicated”:

Breker et al (2013)

- 85 384-well plates
- 3 fields per well
- 3 channels per field (brightfield and 2 fluorescence channels)
- 97920 total images
- 1 qualitative & 1 quantitative datapoint per strain per treatment (26650 total)
- cross-plate datasets (2 untreated and 3 treated datasets per strain)

# JCB Data Viewer

## HCS Data – Plate View

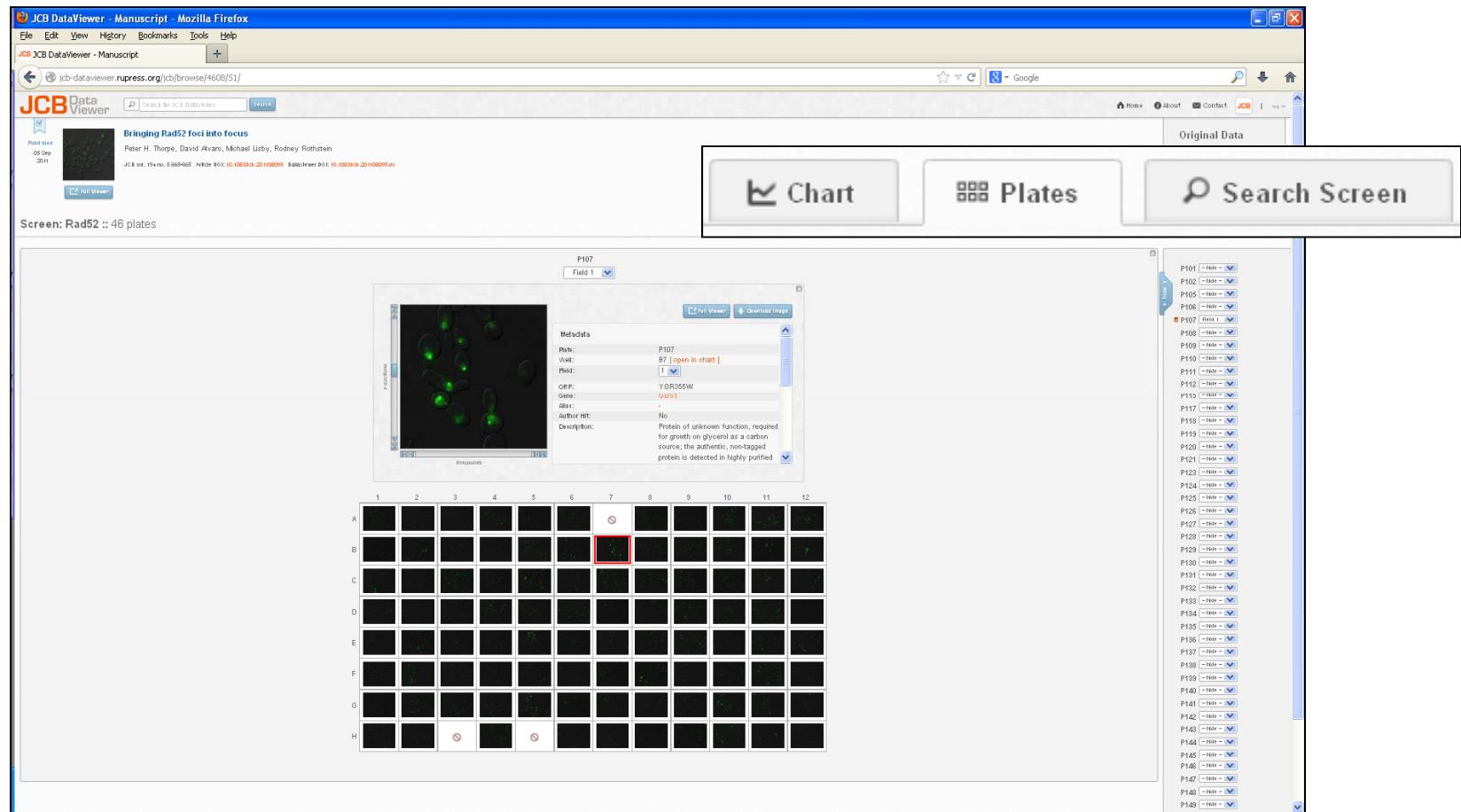


<http://jcb-dataviewer.rupress.org>

Thorpe et al (2011)

# JCB Data Viewer

## HCS Data – Plate View



<http://jcb-dataviewer.rupress.org>

Thorpe et al (2011)

# JCB Data Viewer

## HCS Data – Plate View

Full Dataset Archiving & Sharing

Bringing Rad52 foci into focus  
Peter H. Thorpe, David Alvaro, Michael Lisby, Rodney Rothstein  
JCB 181, 194-205; Article first published online October 5, 2011; DOI: 10.1083/jcb.20100295; eLife article DOI: 10.1083/jcb.20100295.e

Screen: Rad52 :: 46 plates

P107  
Field 1

Metadata

Plate: P107  
Well: B7 [open in chart]  
Field: 1  
Cell Type: YDR355W  
Gene: UUS1  
Alias:  
Author Hit: No  
Description: Protein of unknown function, required for growth on glycerol as a carbon source; the authentic, non-tagged protein is detected in highly purified

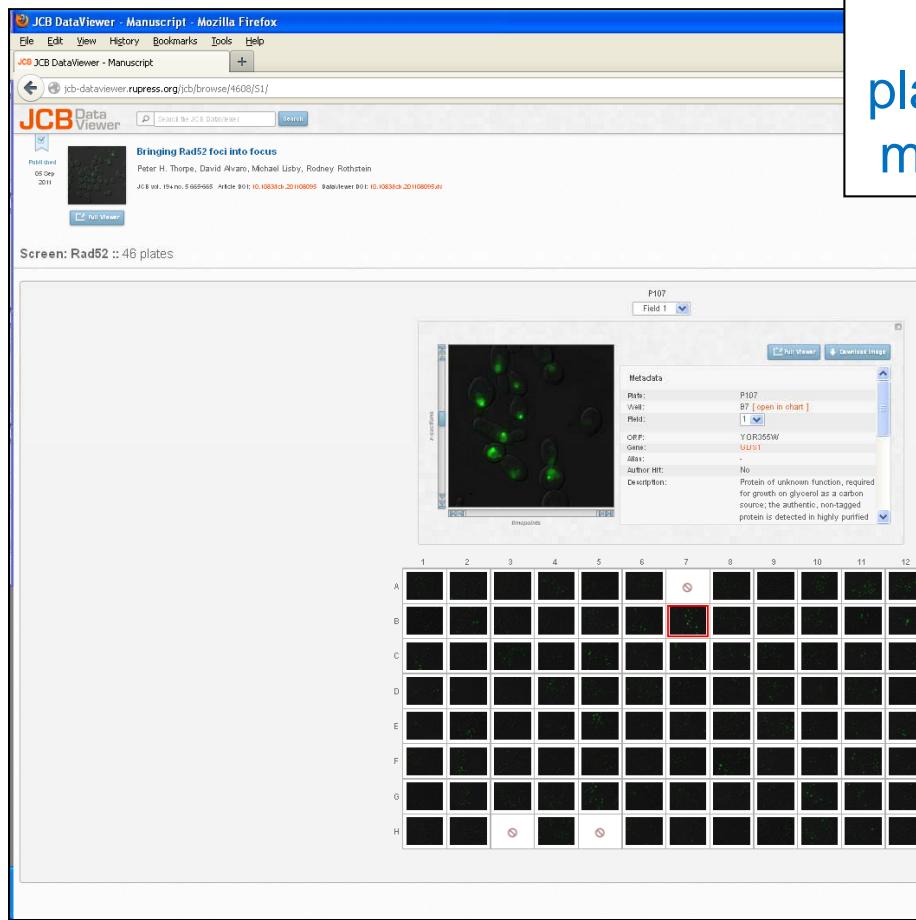
	1	2	3	4	5	6	7	8	9	10	11	12
A												
B												
C												
D												
E												
F												
G												
H												

<http://jcb-dataviewer.rupress.org>

Thorpe et al (2011)

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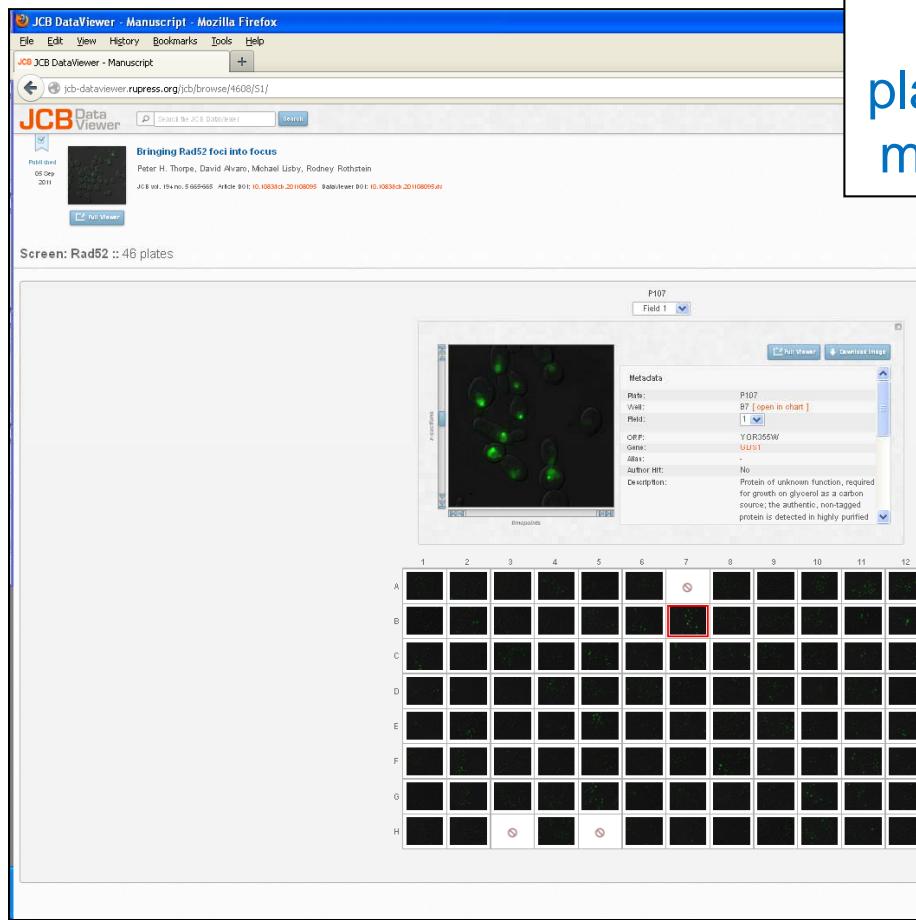


Maneuverability between plate arrays, single image data, metadata, and phenotypic data

Metadata	
Plate:	P107
Well:	B7 [ open in chart ]
Field:	1
ORF:	YOR355W
Gene:	GDS1
Alias:	-
Author Hit:	No
Description:	Protein of unknown function, required for growth on glycerol as a carbon source; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
GO Biological Process:	generation of precursor metabolites and energy, cellular respiration
GO Molecular Function:	not available
GO Cellular Component:	nucleus, mitochondrion, cytoplasm
GO Term:	cellular respiration, cytoplasm, generation of precursor metabolites and energy, mitochondrion, nucleus
Record no.:	
Strain:	
Batch:	
Cells:	198
Foci:	24
% of Foci:	12

# JCB Data Viewer

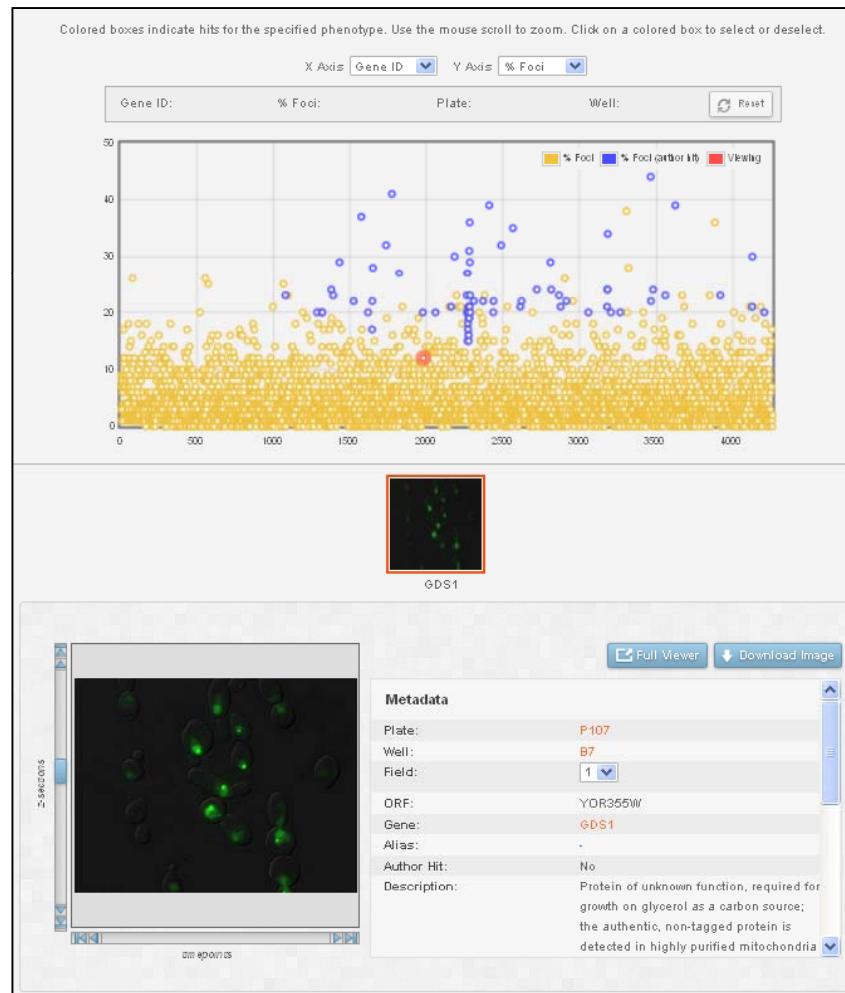
## HCS Data – Plate View



Maneuverability between plate arrays, single image data, metadata, and phenotypic data

Metadata	
Plate:	[ open in chart ]
Well:	
Field:	
ORF:	YOR355W
Gene:	GDS1
Alias:	-
Author Hit:	No
Description:	Protein of unknown function, required for growth on glycerol as a carbon source; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
GO Biological Process:	generation of precursor metabolites and energy, cellular respiration
GO Molecular Function:	not available
GO Cellular Component:	nucleus, mitochondrion, cytoplasm
GO Term:	cellular respiration, cytoplasm, generation of precursor metabolites and energy, mitochondrion, nucleus
Record no.:	
Strain:	
Batch:	
Cells:	198
Foci:	24
% of Foci:	12

## HCS Data – Chart View (quantitative)

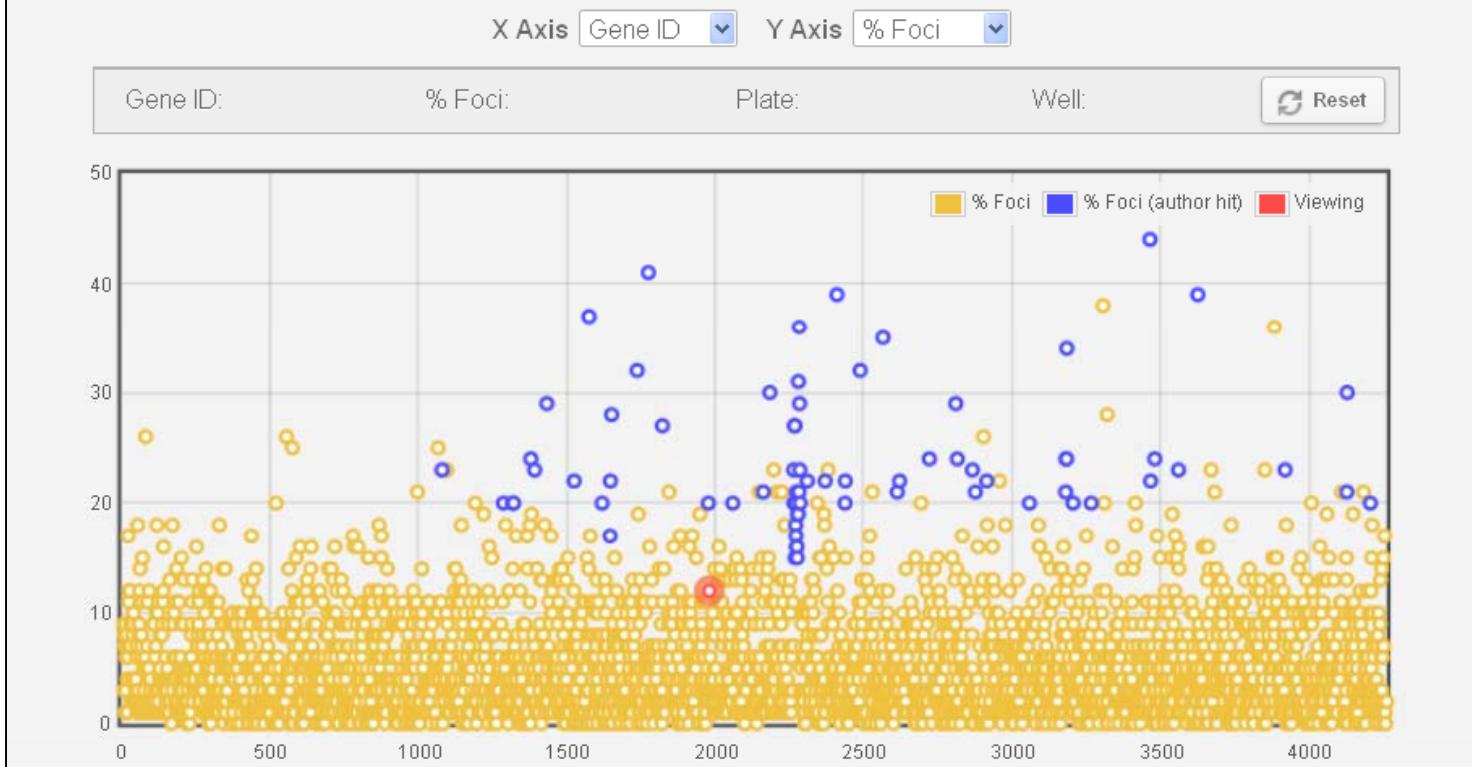


<http://jcb-dataviewer.rupress.org>

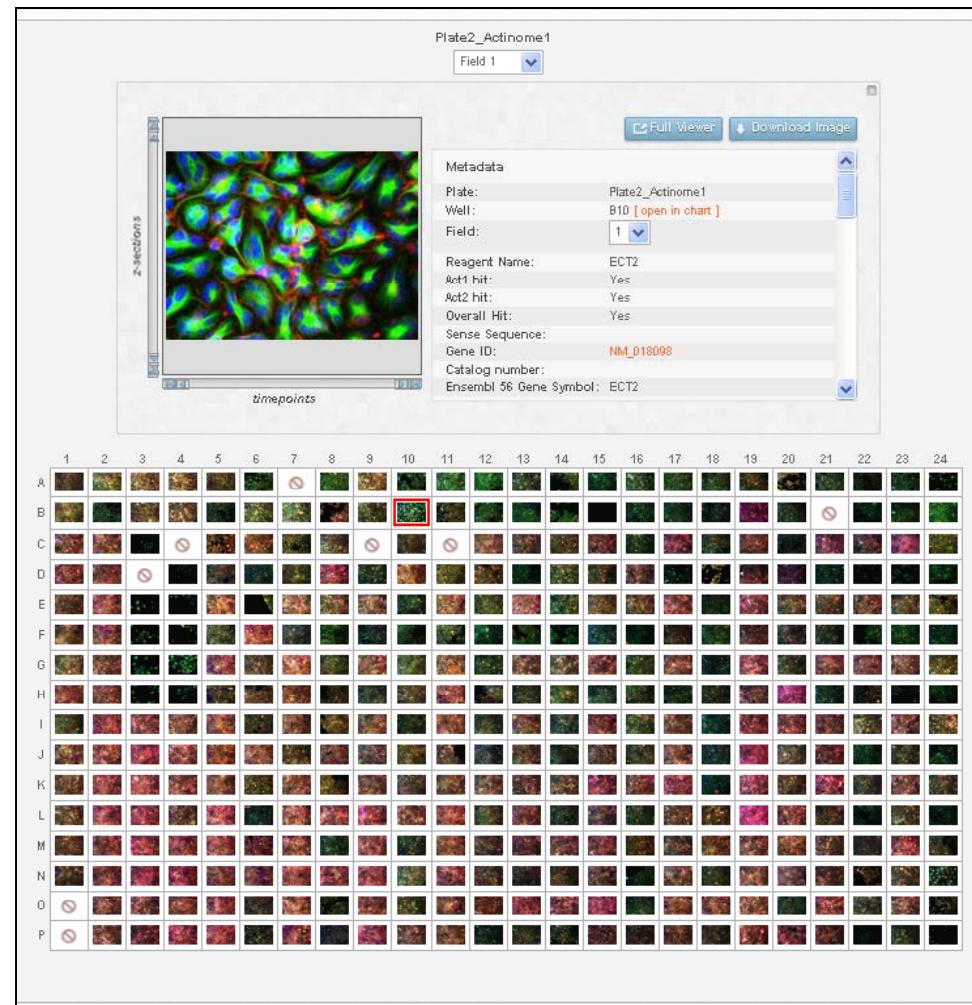
Thorpe et al (2011)

# HCS Data – Chart View (quantitative)

Colored boxes indicate hits for the specified phenotype. Use the mouse scroll to zoom. Click on a colored box to select or deselect.



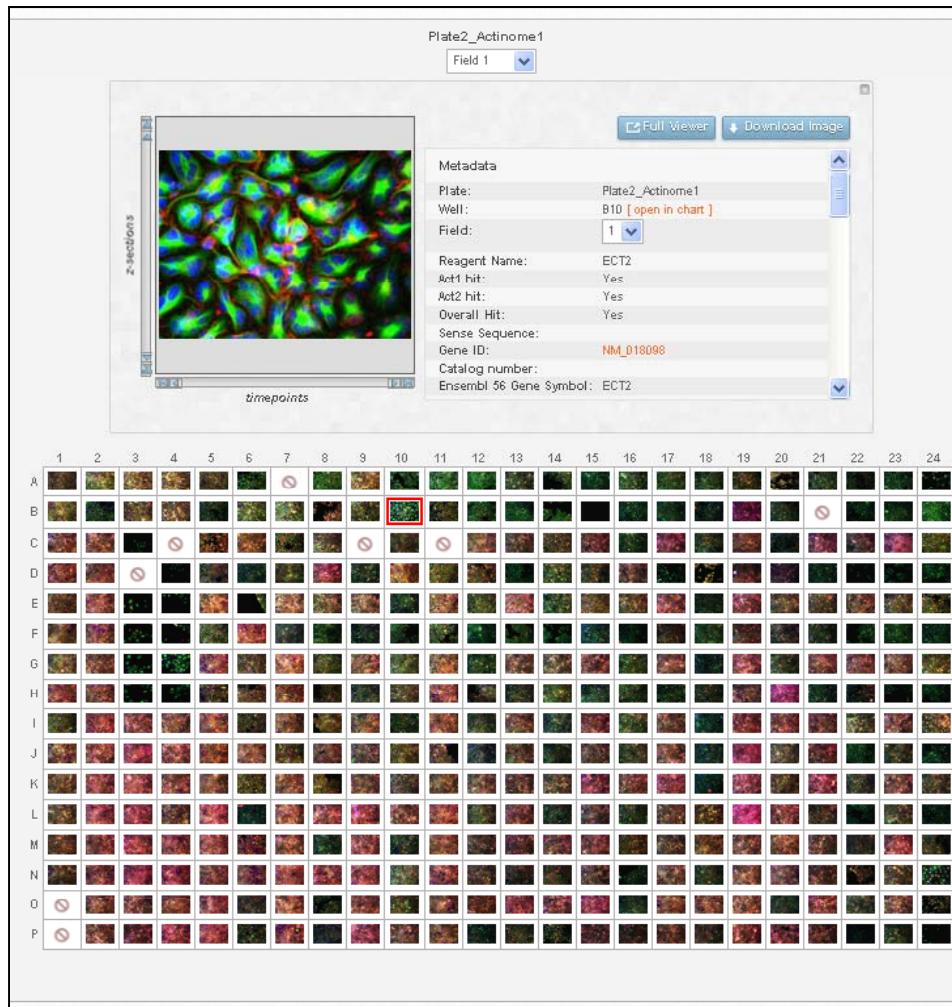
## HCS Data – Plate View



<http://jcb-dataviewer.rupress.org>

Rohn et al (2011)

## HCS Data – Plate View



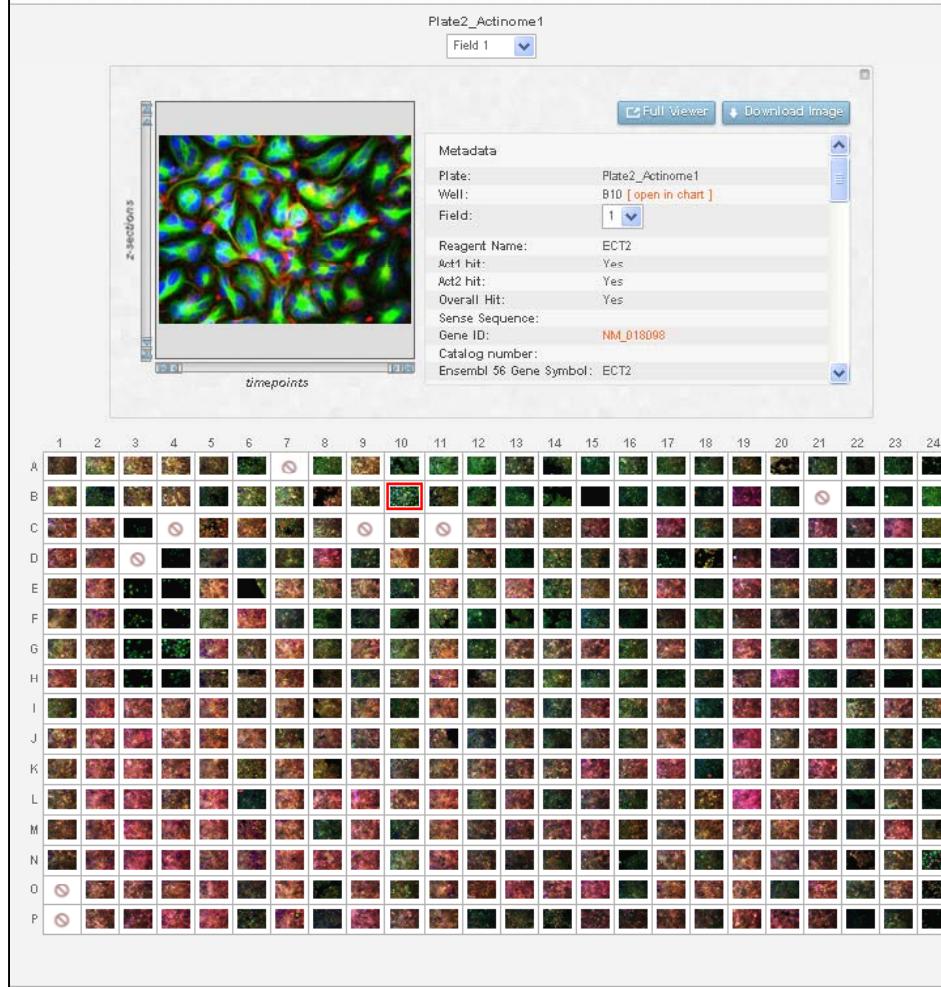
Metadata	
Plate:	Plate2_Actinome1
Well:	B10 [open in chart]
Field:	2
Reagent Name:	ECT2
Act1 hit:	Yes
Act2 hit:	Yes
Overall Hit:	Yes
Sense Sequence:	
Gene ID:	NM_018098
Catalog number:	
Ensembl 56 Gene Symbol:	ECT2
More actin:	No
More peripheral actin:	No
More cytoplasmic actin:	Yes
More actin over nucleus:	Yes
More filopodia:	No
Increased width of lamellae:	Yes
Less actin:	No
Fewer filopodia:	No
Decreased width of lamellae:	No
Nuclear actin ring:	No
More actin puncta:	Yes
More actin stress fibers:	No
More transverse actin stress fibers:	No
More cortical actin stress fibers:	No
More zigzag actin stress fibers:	Yes
Disorganized peripheral actin:	Yes
Increased cell size:	Yes
Decreased cell size:	No
Variable cell size:	No
Cell shape round:	No
Cell shape spiky:	No
Cell shape bipolar or elongated:	No
Cell shape geometric:	No
Cell shape variable:	No
Decreased cell number:	Yes
Increased cell number:	No
More multinucleate cells:	Yes
Increased DNA area:	Yes
Decreased DNA area:	No
Missshapen DNA:	Yes
Apoptotic DNA:	No
Increased mitotic index:	No
Microtubules disorganized:	Yes
Microtubule processes:	No
Microtubule clumps:	No
Microtubule nuclear ring:	No
Microtubule nuclear bracket:	No
More microtubules:	No
Loss of cell monolayer:	Yes
Motile lamellae:	No

<http://jcb-dataviewer.rupress.org>

Rohn et al (2011)

## HCS Data – Plate View

[ open in chart ]

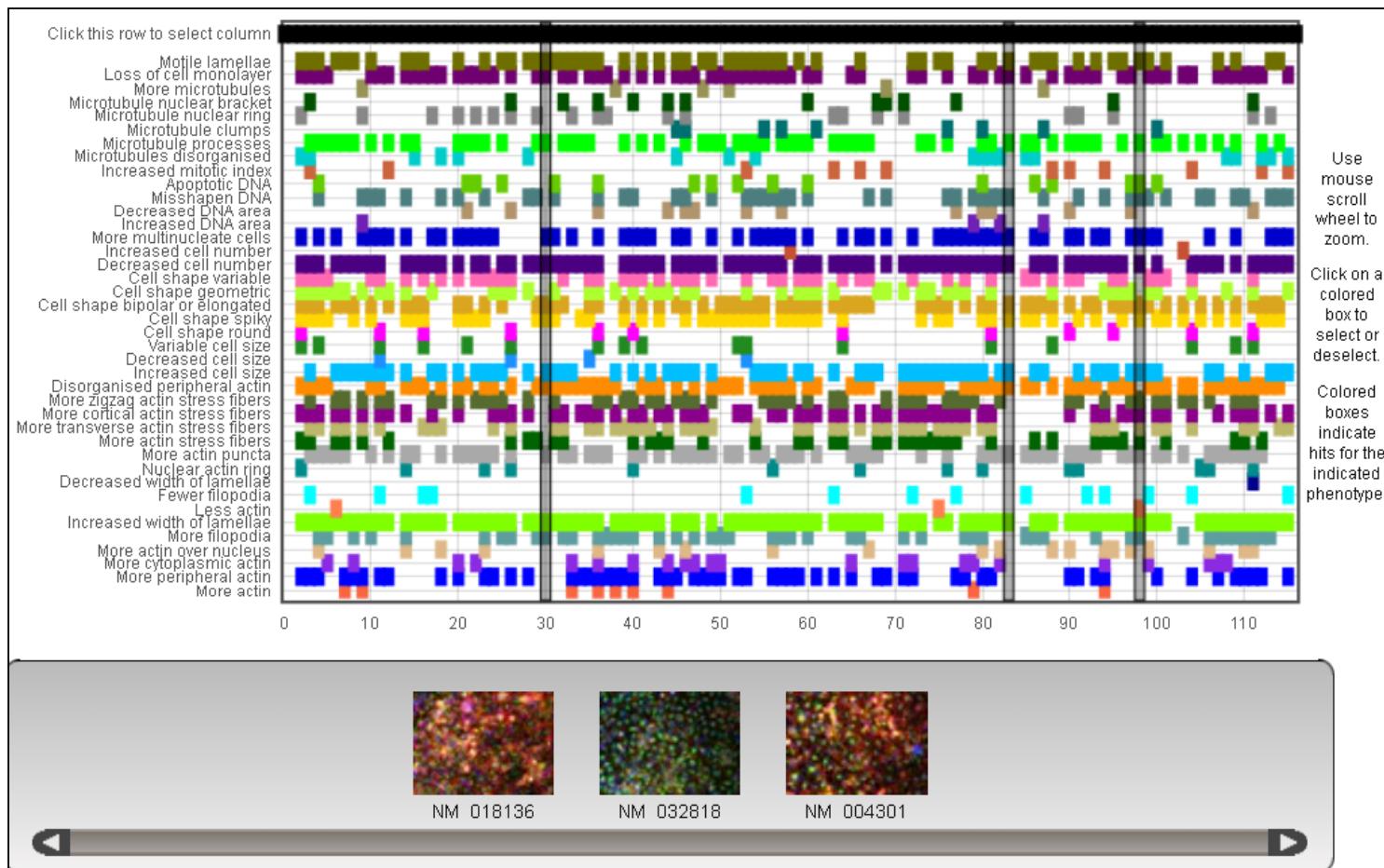


Reagent Name:	ECT2
Act1 hit:	Yes
Act2 hit:	Yes
Overall Hit:	Yes
Sense Sequence:	
Gene ID:	NM_018098
Catalog number:	
Ensembl 56 Gene Symbol:	ECT2
More actin:	No
More peripheral actin:	No
More cytoplasmic actin:	Yes
More actin over nucleus:	Yes
More filopodia:	No
Increased width of lamellae:	Yes
Less actin:	No
Fewer filopodia:	No
Decreased width of lamellae:	No
Nuclear actin ring:	No
More actin puncta:	Yes
More actin stress fibers:	No
More transverse actin stress fibers:	No
More cortical actin stress fibers:	No
More zigzag actin stress fibers:	Yes
Disorganized peripheral actin:	Yes
Increased cell size:	Yes
Decreased cell size:	No
Variable cell size:	No
Cell shape round:	No
Cell shape spiky:	No
Cell shape bipolar or elongated:	No
Cell shape geometric:	No
Cell shape variable:	No
Decreased cell number:	Yes
Increased cell number:	No
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Microtubules disorganized:	Yes
Microtubule processes:	No
Microtubule clumps:	No
Microtubule nuclear ring:	No
Microtubule nuclear bracket:	No
More microtubules:	No
Loss of cell monolayer:	Yes
Motile lamellae:	No

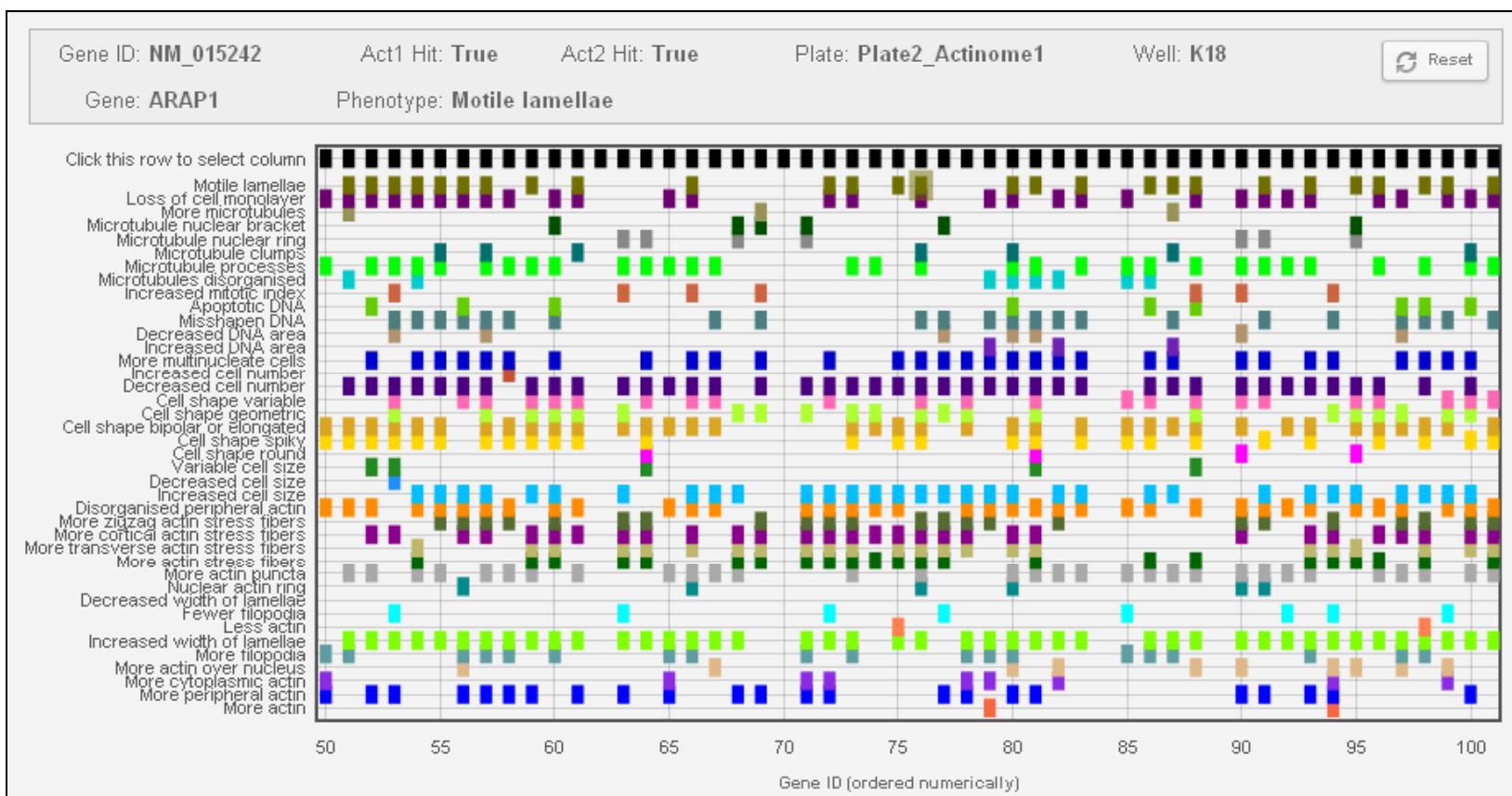
<http://jcb-dataviewer.rupress.org>

Rohn et al (2011)

## HCS Data – Chart View (qualitative)

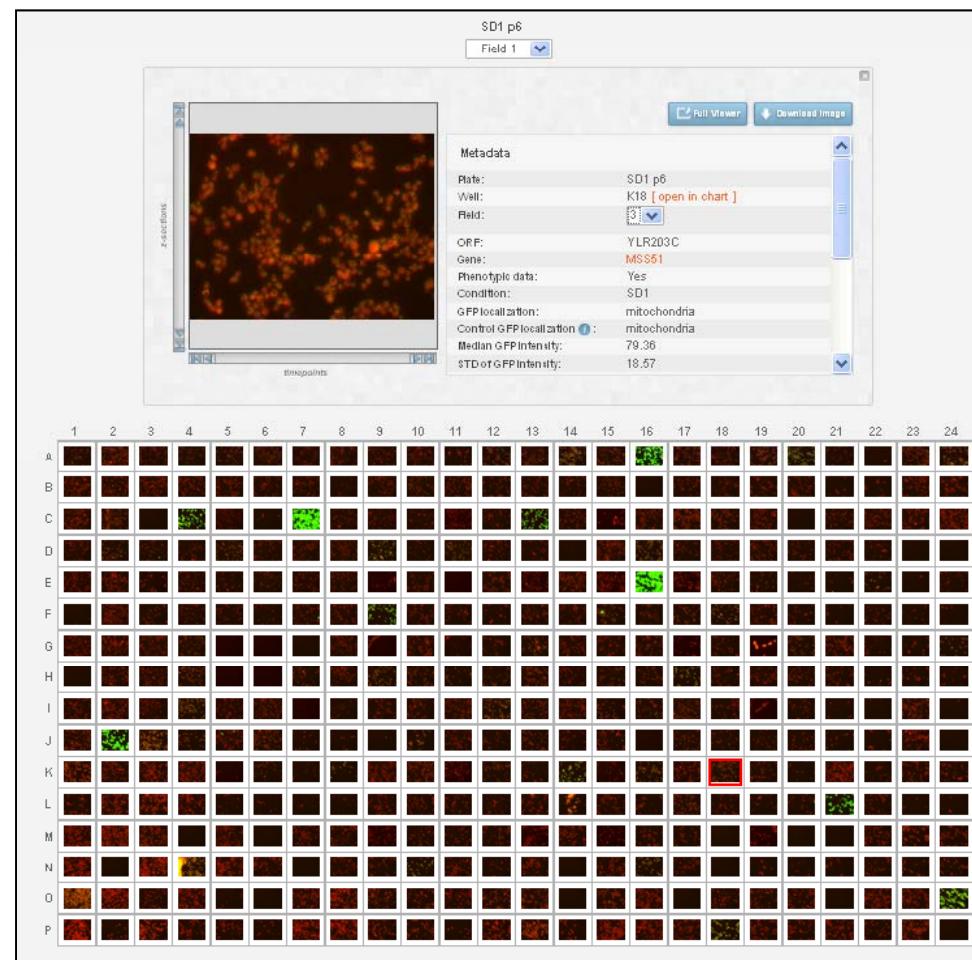


# HCS Data – Chart View (qualitative)



# JCB Data Viewer

## HCS Data – Plate View

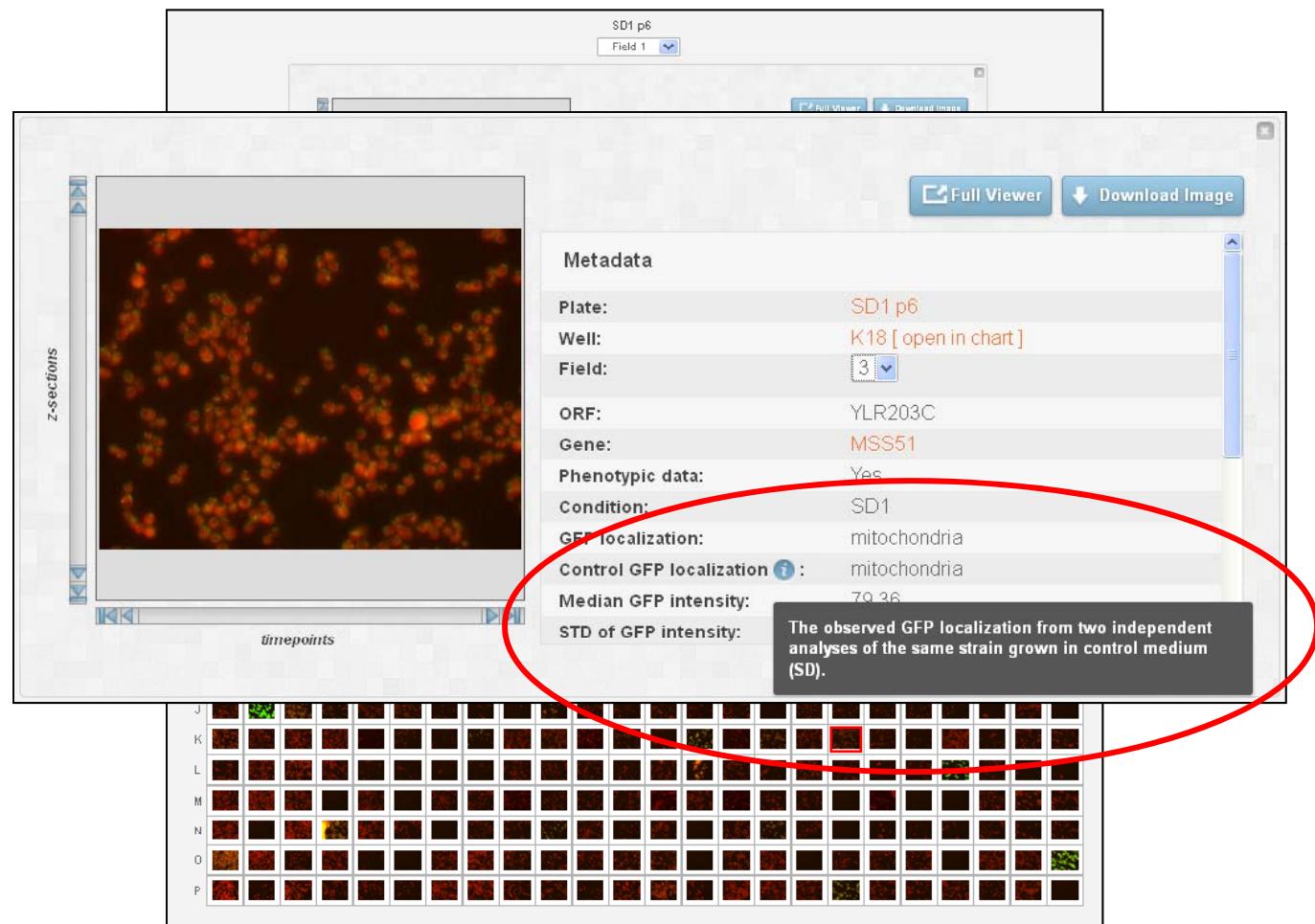


<http://jcb-dataviewer.rupress.org>

Breker et al (2013)

# JCB Data Viewer

## HCS Data – Plate View

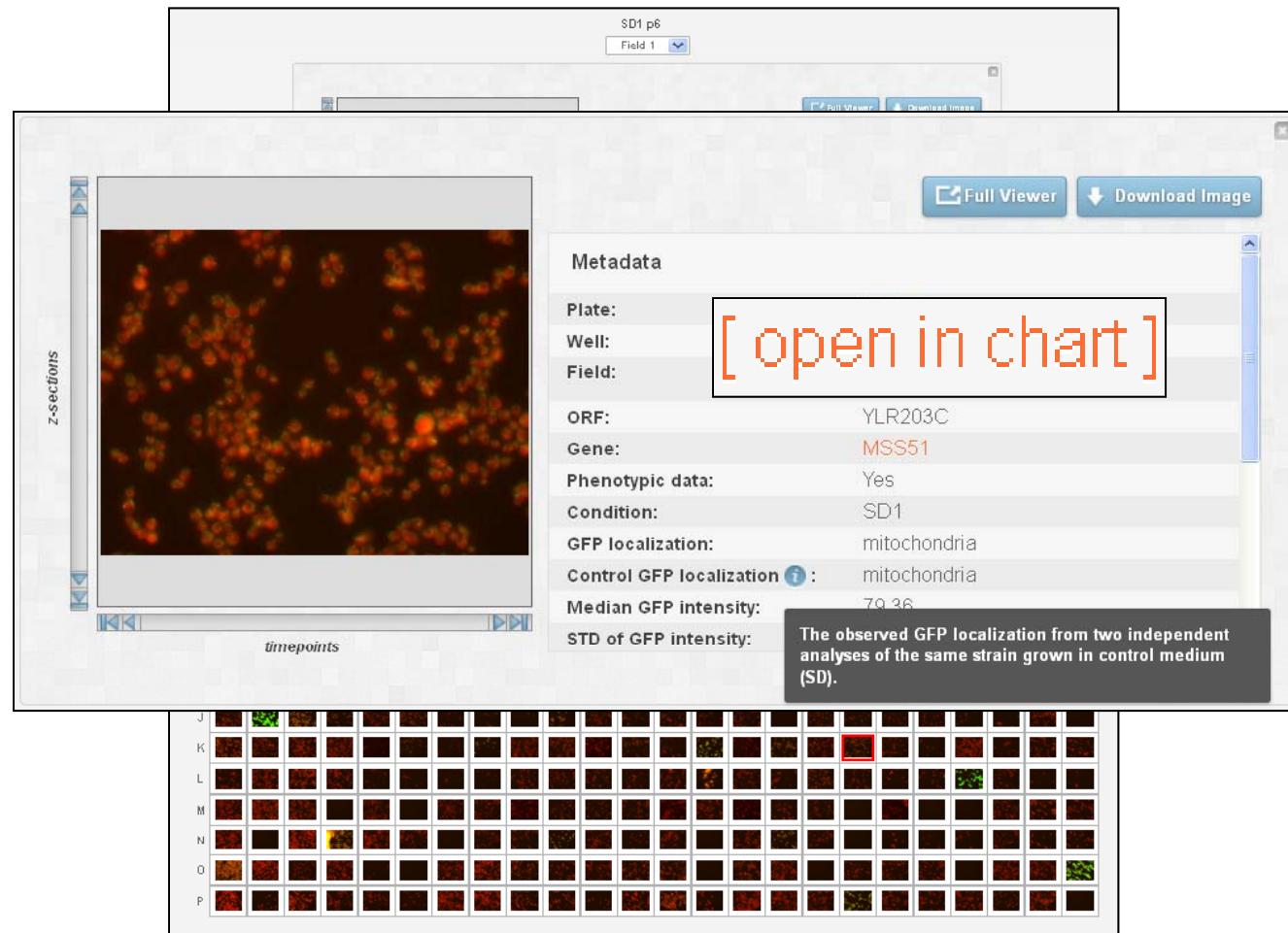


<http://jcb-dataviewer.rupress.org>

Breker et al (2013)

# JCB Data Viewer

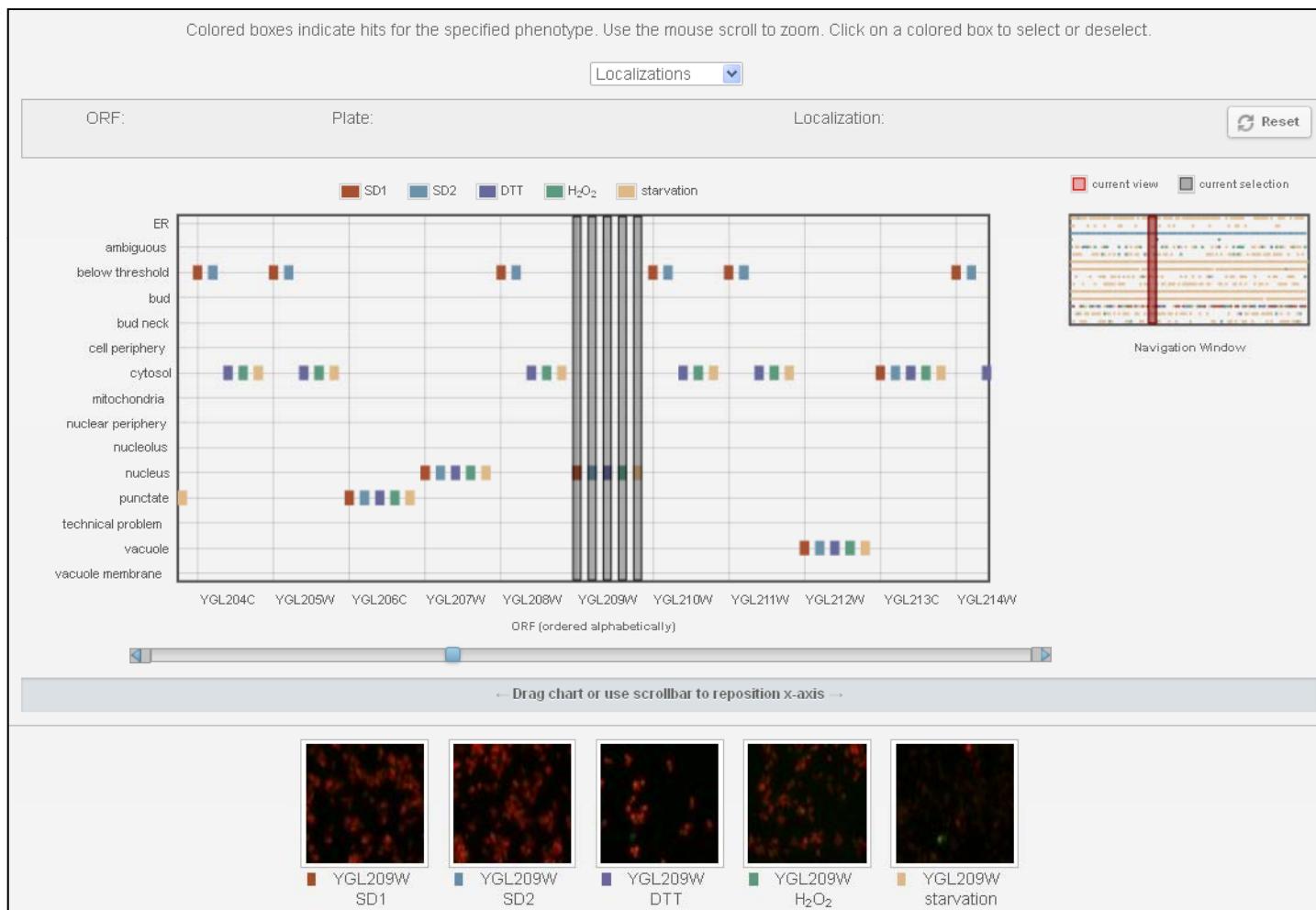
## HCS Data – Plate View



<http://jcb-dataviewer.rupress.org>

Breker et al (2013)

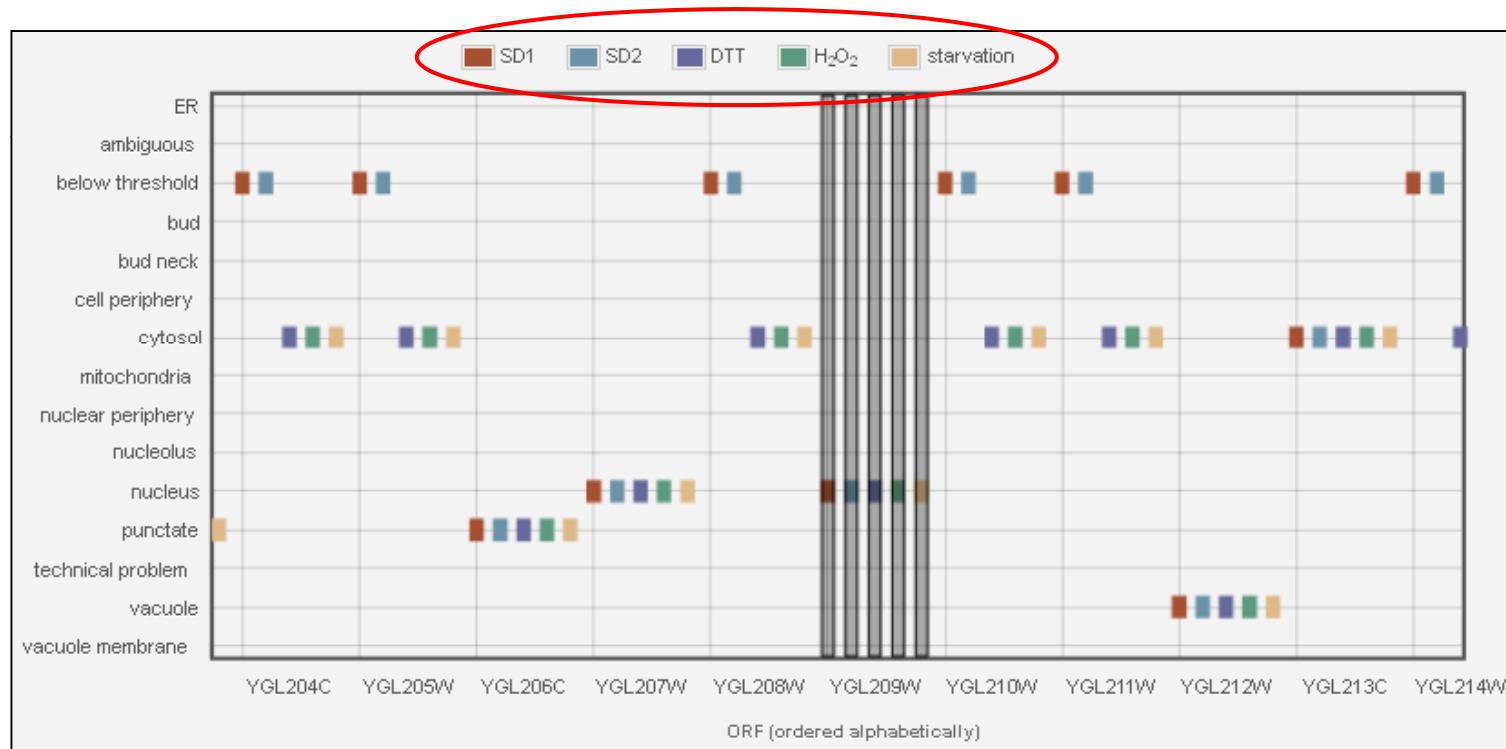
# HCS Data – Chart View (qualitative)



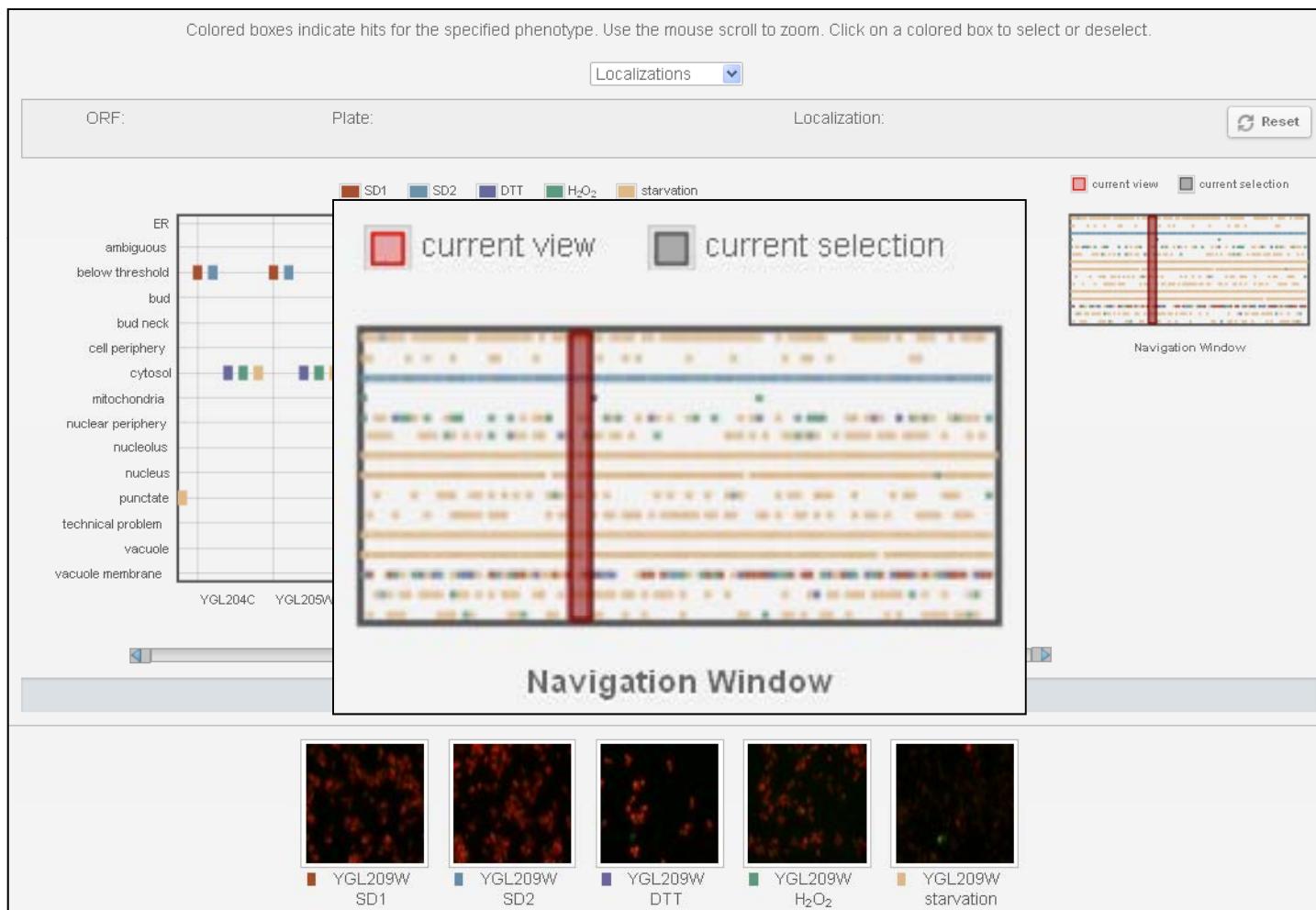
<http://jcb-dataviewer.rupress.org>

Breker et al (2013)

## HCS Data – Chart View (qualitative)



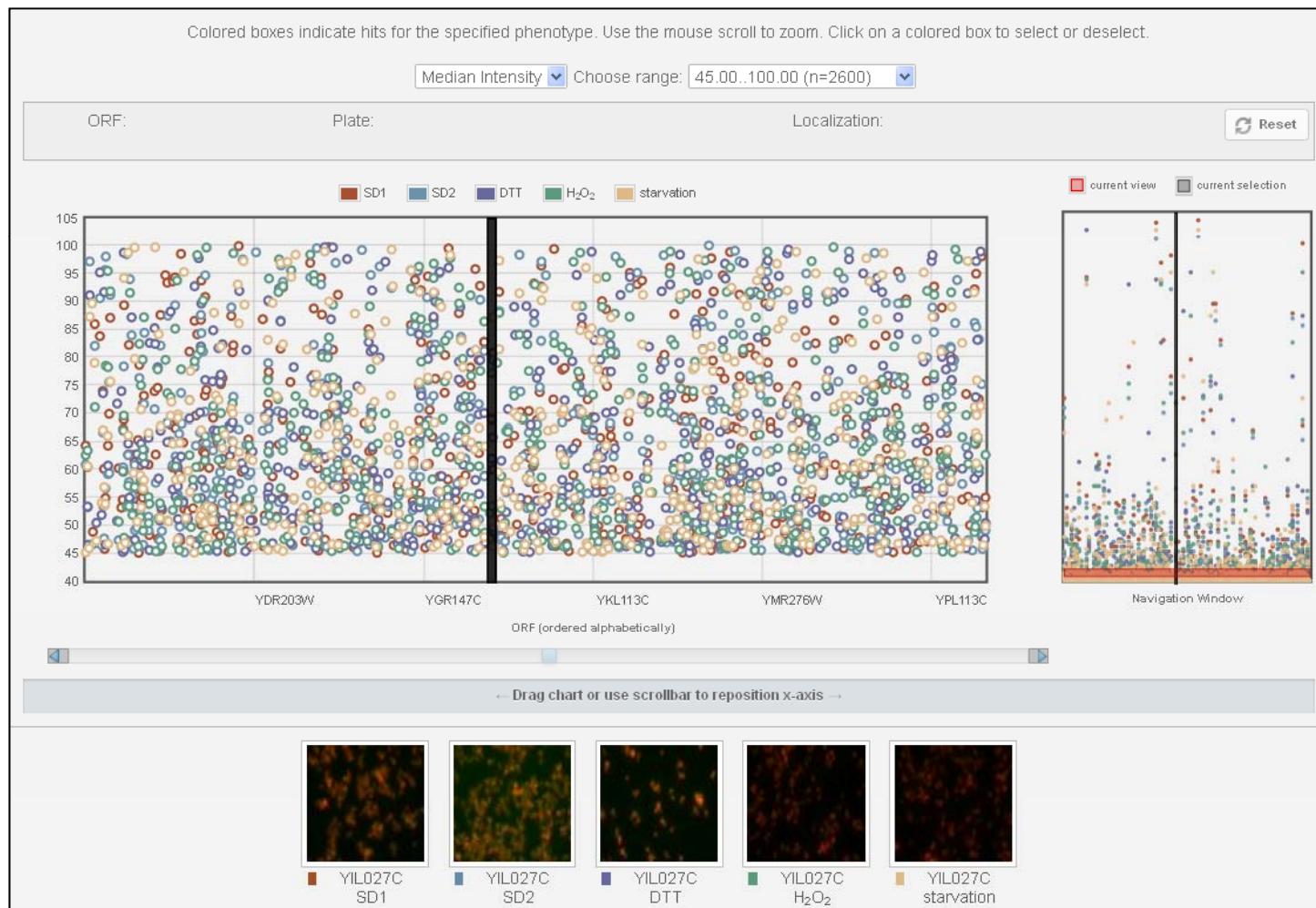
## HCS Data – Chart View (qualitative)



<http://jcb-dataviewer.rupress.org>

Breker et al (2013)

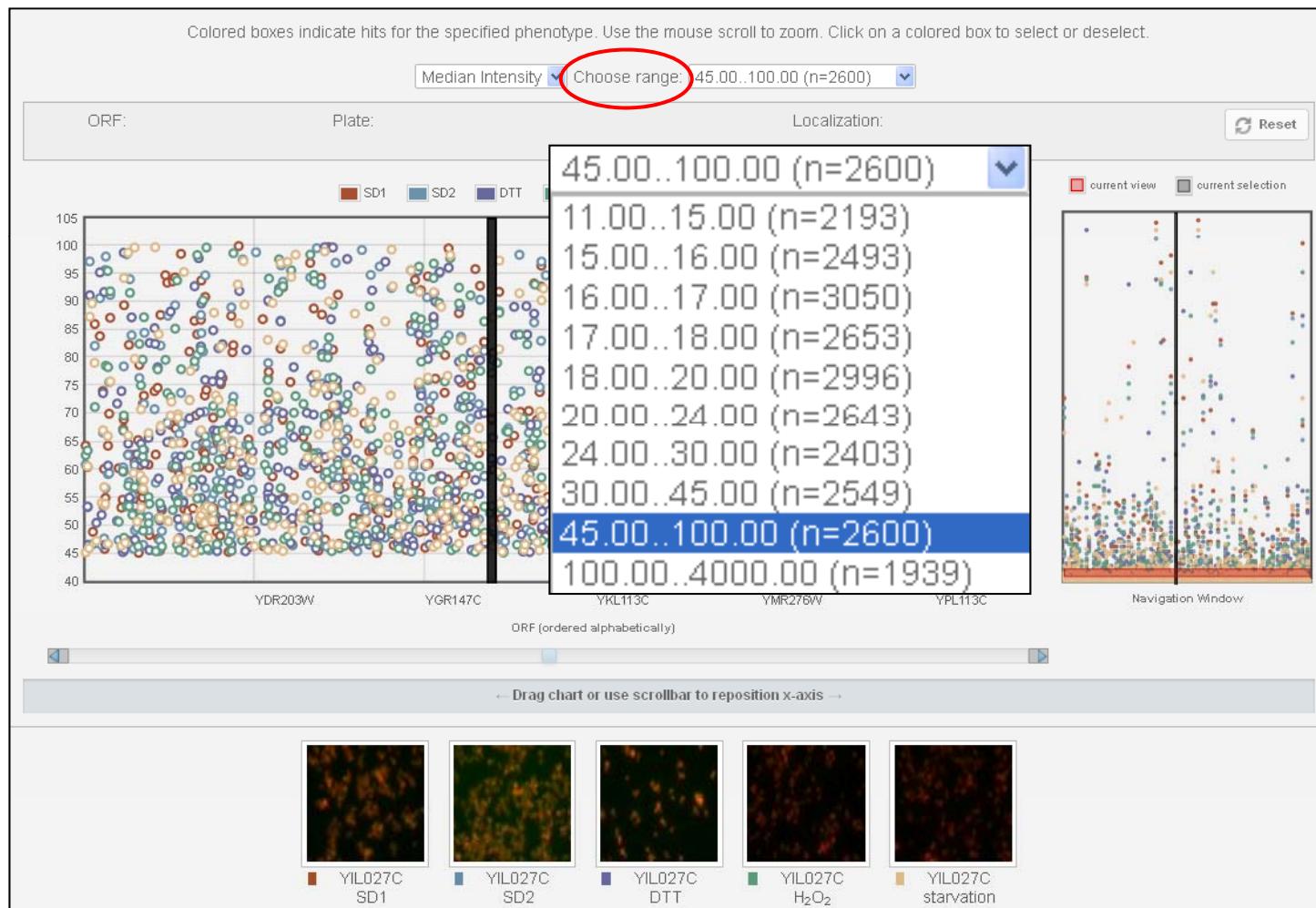
# HCS Data – Chart View (quantitative)



<http://jcb-dataviewer.rupress.org>

Breker et al (2013)

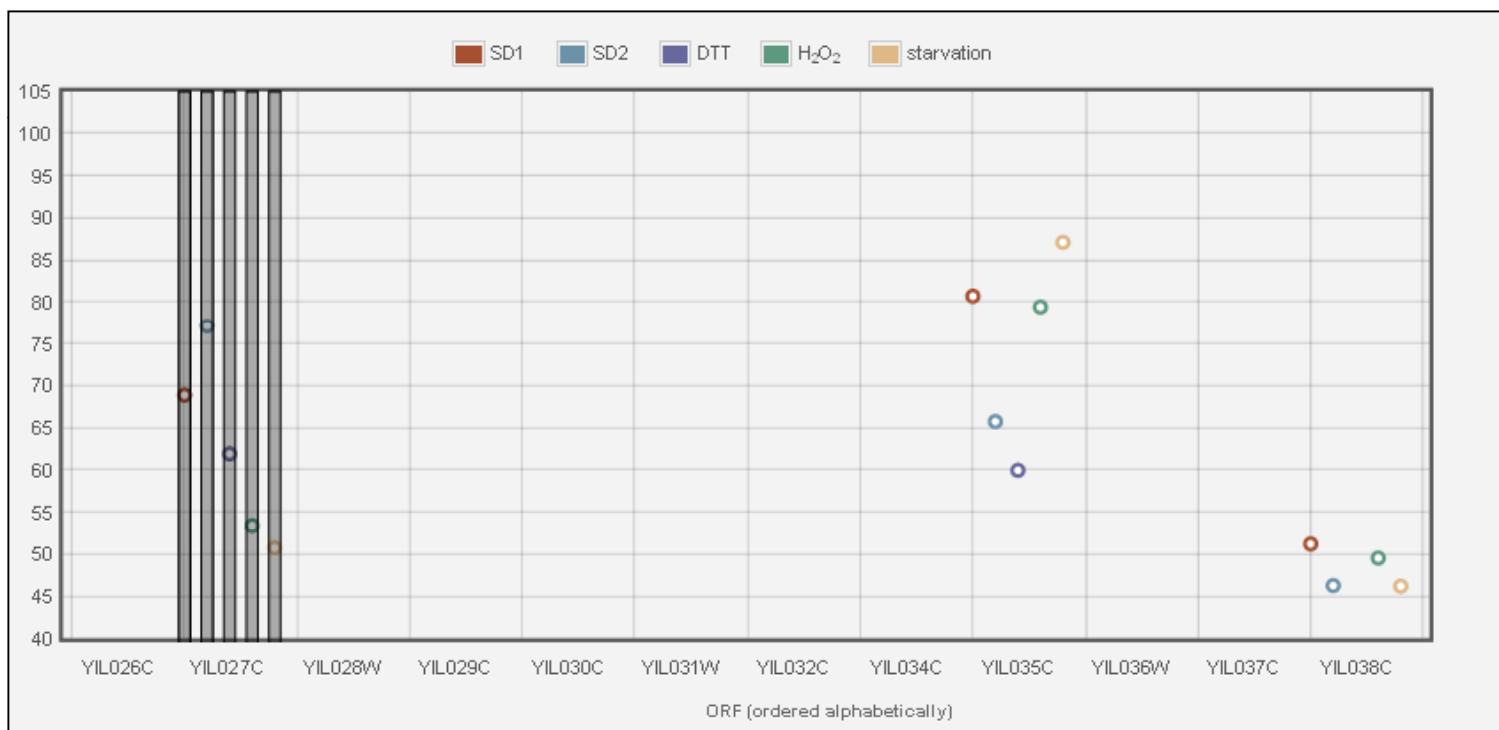
## HCS Data – Chart View (quantitative)



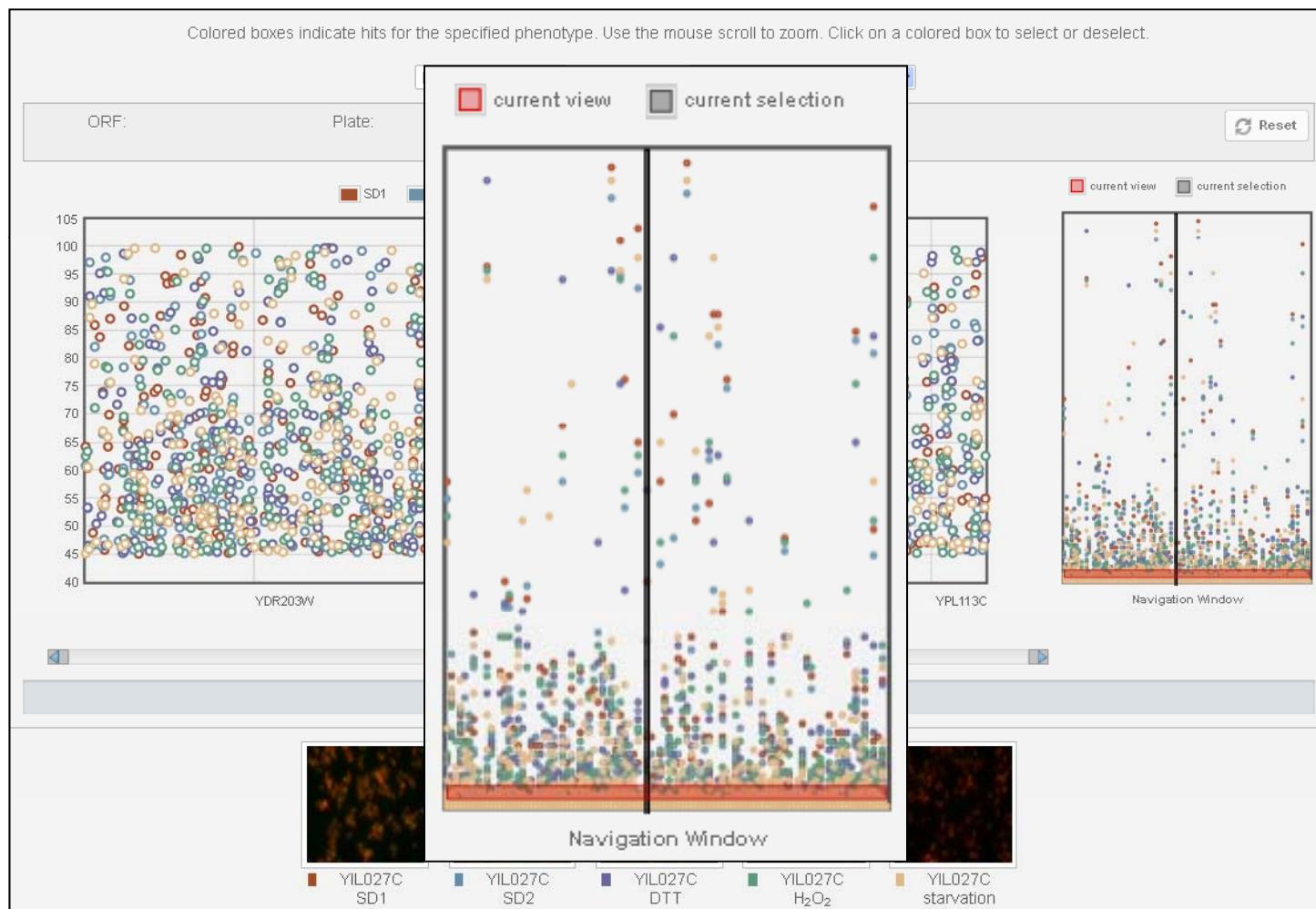
<http://jcb-dataviewer.rupress.org>

Breker et al (2013)

## HCS Data – Chart View (quantitative)



## HCS Data – Chart View (quantitative)



- Browser-based viewing of original, raw image files in >75 PFFs (from single images to massively tiled images to plate-arrayed HCS datasets)
- Image data-metadata linking
- Tools for single image analysis
- Tools for complex HCS dataset visualization and analysis
- Tools to enhance image data-published data maneuverability (e.g., direct image links, citation information and links, data DOIs)
- Raw image downloading in OME-TIFF format
- Database-wide search functionality.

# Multidimensional Publishing

difference in the amount of Aurora B in unaligned and apparently aligned chromosomes ([Fig. 5 A](#)). We detected no change in chromosome staining with anti-phosphohistone H3 ([Fig. 5 A](#)) or anti-phospho-CENP-A (not depicted) after Bod1 depletion. Because both are markers of Aurora B activity ([Zeitlin et al., 2001](#)), these results suggest that Aurora B kinase activity was not dramatically impaired by the loss of Bod1. To further assay the function of Aurora B, we determined the localization of MCAK, which localizes to the inner centromere in its phosphorylated form but concentrates at kinetochores in its dephosphorylated state ([Andrews et al., 2004](#)). At unaligned sister kinetochores or in kinetochore pairs not yet fully under tension, MCAK is predominantly located at the inner centromere ([Fig. 5 B; Andrews et al., 2004](#)). In Bod1<sup>sirNA</sup> cells, we observed that although total MCAK present at unaligned centromeres was similar to control cells ([Fig. 5 C](#)), its precise localization was abnormal, forming multiple foci stretching out to one or both sister kinetochores.

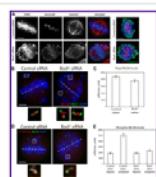


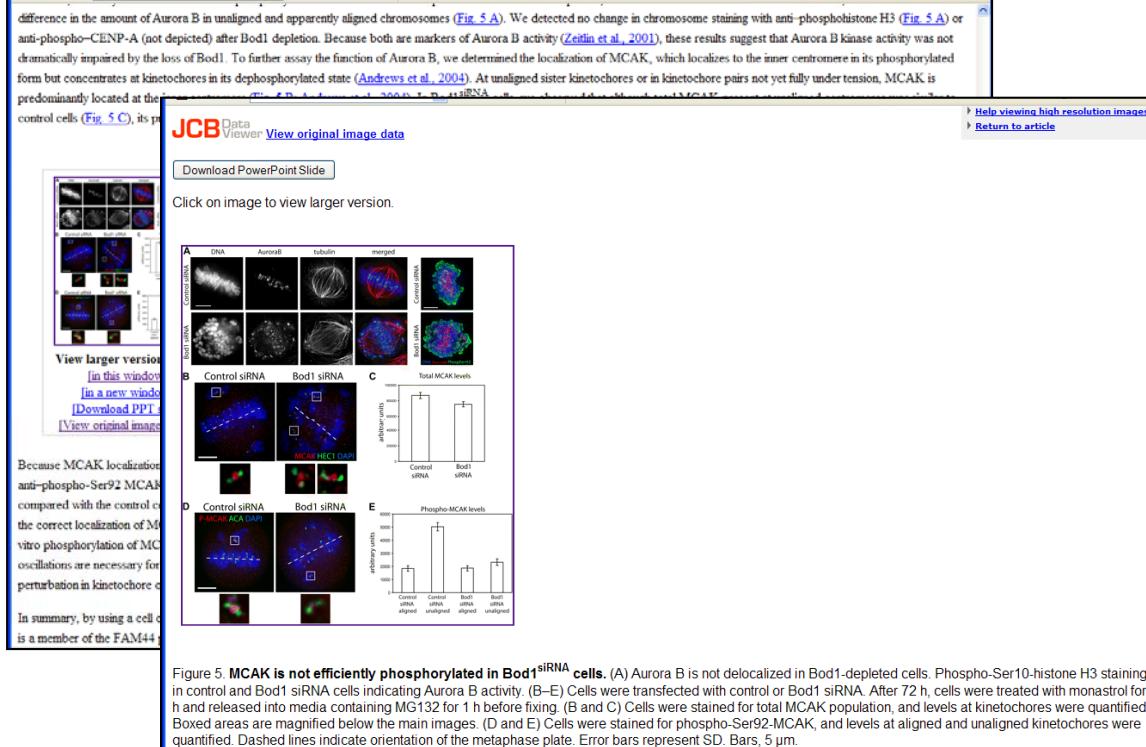
Figure 5. MCAK is not efficiently phosphorylated in Bod1<sup>sirNA</sup> cells. (A) Aurora B is not delocalized in Bod1-depleted cells. Phospho-Ser10-histone H3 staining in control and Bod1 siRNA cells indicating Aurora B activity. (B–E) Cells were transfected with control or Bod1 siRNA. After 72 h, cells were treated with monastrol for 3 h and released into media containing MG132 for 1 h before fixing. (B and C) Cells were stained for total MCAK population, and levels at kinetochores were quantified. Boxed areas are magnified below the main images. (D and E) Cells were stained for phospho-Ser92-MCAK, and levels at aligned and unaligned kinetochores were quantified. Dashed lines indicate orientation of the metaphase plate. Error bars represent SD. Bars, 5 μm.

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Because MCAK localization to centromeres and kinetochores depends on the state of MCAK phosphorylation, we examined the levels of phosphorylated MCAK using an anti-phospho-Ser92 MCAK antibody ([Andrews et al., 2004](#)). Phosphorylation of MCAK was substantially reduced at the inner centromere of unaligned chromosomes in Bod1<sup>sirNA</sup> cells compared with the control cells ([Fig. 5, D and E](#)). These results suggest that Bod1 depletion impairs the formation of bioriented attachments across sister kinetochores, possibly by impairing the correct localization of MCAK at centromeres and, thereby, preventing its phosphorylation and timely correction of syntelic attachments. We have not detected any effect of Bod1 on the *in vitro* phosphorylation of MCAK by Aurora B (unpublished data), so Bod1 may modulate MCAK phosphorylation by interacting with other proteins. Aurora B activity and kinetochore oscillations are necessary for syntelic correction ([Lampson et al., 2004](#)), and our data further suggest that syntelic correction may require MCAK phosphorylation. Whether there is any subtle perturbation in kinetochore oscillations in Bod1-depleted cells is not yet known and will require much higher resolution live cell imaging.

In summary, by using a cell cycle-dependent analysis of the *Xenopus* chromatin proteome, we have identified a novel protein required for proper chromosome biorientation called Bod1. Bod1 is a member of the FAM44 protein family and is highly conserved throughout metazoans. Depletion of Bod1 in human cells causes severe biorientation defects, although kinetochores appear to

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difference in the amount of Aurora B in unaligned and apparently aligned chromosomes (**Fig. 5 A**). We detected no change in chromosome staining with anti-phosphohistone H3 (**Fig. 5 A**) or anti-phospho-CENP-A (not depicted) after Bod1 depletion. Because both are markers of Aurora B activity (Zeitlin et al., 2001), these results suggest that Aurora B kinase activity was not dramatically impaired by the loss of Bod1. To further assay the function of Aurora B, we determined the localization of MCAK, which localizes to the inner centromere in its phosphorylated form but concentrates at kinetochores in its dephosphorylated state (Andrews et al., 2004). At unaligned sister kinetochores or in kinetochore pairs not yet fully under tension, MCAK is predominantly located at the control cells (**Fig. 5 C**), its p

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**Bod1, a Novel Kinetochore Protein Required for Chromosome Biorientation**

IM Porter, S E McClelland, G A Khoudjani, C J Hunter, J S Andersen, A D McIntosh, J J Blow, J R Swedlow

Published: 22 Oct 2007

JCB vol. no. - Article DOI: [10.1083/jcb.200704098](https://doi.org/10.1083/jcb.200704098) DataViewer DOI: [10.1083/jcb.200704098.dv](https://doi.org/10.1083/jcb.200704098.dv)

**Original Data**

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**Figure 4** [5] [View](#)

**Figure 5** [8] [View](#)

**Figure 5 :: 8 images**

A

B

C

D

Because MCAK localization anti-phospho-Ser92 MCAK compared with the control cells the correct localization of MCAK in vitro phosphorylation of MCAK oscillations are necessary for perturbation in kinetochore oscillations.

In summary, by using a cell cycle inhibitor, we show that MCAK is a member of the FAM44 family.

Figure 5. MCAK is not effluxed from the nucleus in control and Bod1 siRNA cells. Cells were arrested in metaphase and released into media containing cycloheximide for 1 h and then fixed. Boxed areas are magnified and shown below. Dashed lines indicate the position of the centromeres. Scale bars, 10  $\mu$ m. Quantification of the data is shown in Fig. 5B. Dashed lines indicate the position of the centromeres. Scale bars, 10  $\mu$ m. Quantification of the data is shown in Fig. 5B.

# Multidimensional Publishing

difference in the amount of Aurora B in unaligned and apparently aligned chromosomes (**Fig. 5 A**). We detected no change in chromosome staining with anti-phosphohistone H3 (**Fig. 5 A**) or anti-phospho-CENP-A (not depicted) after Bod1 depletion. Because both are markers of Aurora B activity (Zeitlin et al., 2001), these results suggest that Aurora B kinase activity was not dramatically impaired by the loss of Bod1. To further assay the function of Aurora B, we determined the localization of MCAK, which localizes to the inner centromere in its phosphorylated form but concentrates at kinetochores in its dephosphorylated state (Andrews et al., 2004). At unaligned sister kinetochores or in kinetochore pairs not yet fully under tension, MCAK is predominantly located at the control cells (**Fig. 5 C**), its position in the Bod1 siRNA cells is indistinguishable from the control cells.

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**A** DNA AuroraB tubulin

**B** Control siRNA Bod1 siRNA

**C** Control siRNA Bod1 siRNA

**D** Control siRNA Bod1 siRNA

**E** Control siRNA Bod1 siRNA

**F** MCAK ACA DAPI

**Figure 5 :: 8 images**

Because MCAK localization anti-phospho-Ser92 MCAK compared with the control cells shows the correct localization of MCAK. In vitro phosphorylation of MCAK oscillations are necessary for perturbation in kinetochore orientation. In summary, by using a cell cycle marker, we show that MCAK is a member of the FAM44 family.

**Figure 5. MCAK is not efficiently phosphorylated in control and Bod1 siRNA cells. Cells were transfected with control or Bod1 siRNA for 3 h and released into media containing mitotic conditions for 2 h. Cells were fixed and stained for phospho-Ser92 MCAK and total MCAK. Boxed areas are magnified and shown below. Dashed lines indicate quantification. Dashed lines indicate quantification.**

**Bod1, a Novel Kinetochore Protein Required for Chromosome Biorientation**  
IM. Porter, S.E. McClelland, G.A. Khoudjani, C.J. Hunter, J.S. Andersen, A.D. McAnish, J.J. Blow, J.R. Swedlow  
JCB vol. no. - Article DOI: 10.1089/jcb.200704098 DataViewer DOI: 10.1089/jcb.200704098

Original Data

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[Figure 4 \[5\]](#)

[Figure 5 \[6\]](#)

**Figure 5 :: 8 images**

**Image Details**

Description: Control siRNA Aurora B

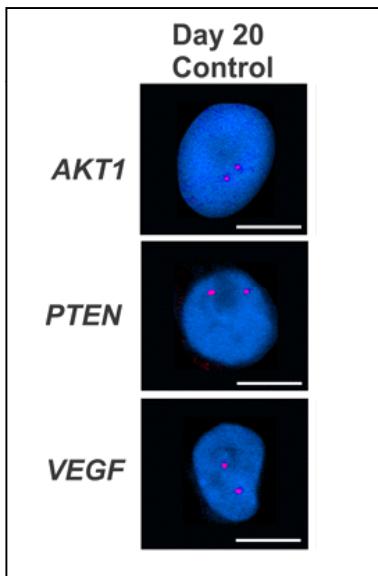
Legend:

Figure 5. MCAK is not efficiently phosphorylated in Bod1 siRNA cells. (A) Aurora B is not delocalized in Bod1-depleted cells. Phospho-Ser10-histone H3 staining in control and Bod1 siRNA cells indicating Aurora B activity. (B-E) Cells were transfected with control or Bod1 siRNA. After 72 h, cells were transfected with mitomycin C for 3 h, fixed, and stained for phospho-Ser92 MCAK and total MCAK. Boxed areas are magnified and shown below. Dashed lines indicate quantification. Dashed lines indicate quantification.

**A**

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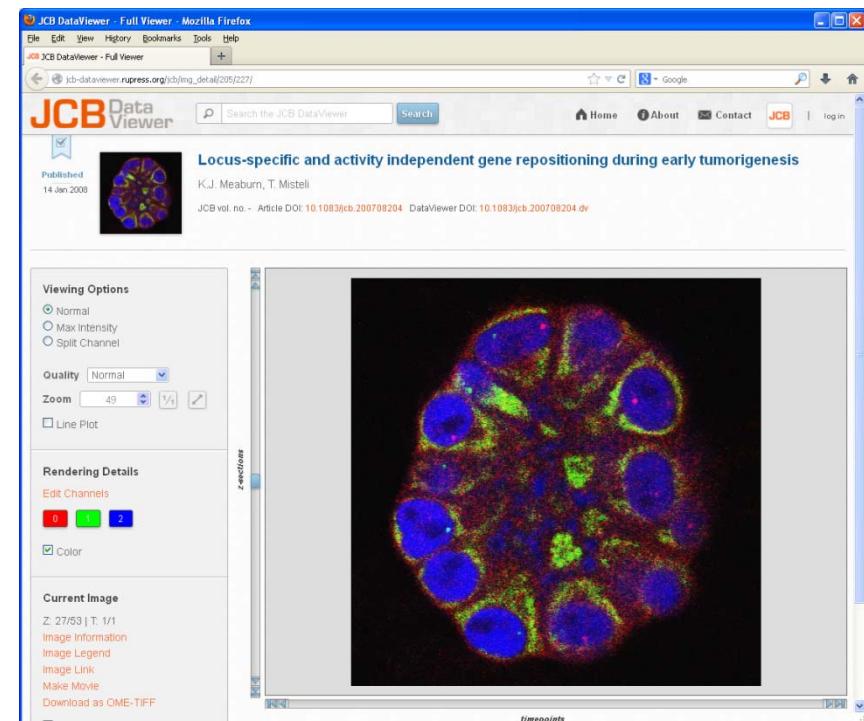
# Data Access and Validation



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**Voluntary participation rate (as of June 10, 2013):**

2.03 TB of image data (published and unpublished)

→ 313 published manuscripts

→ 1164 published figures

→ 204,935 published images

→ 1,309,621 individual image frames

## Where do we go from here?

- Continue to expand the range of data we can host and the tools available to analyze and access those data.
- Continue to promote a new standard for sharing and archiving of published image data.
- *...an international repository for all published image data?*



# JCB Data Viewer

<http://jcb-dataviewer.rupress.org>

*with special thanks to Emma Hill, Mike Rossner, and:*

