CYTELY

Cytely documentation.

Accelerate discovery. A guide to uploading images, building workflows, and exploring your data in Cytely.

CYTELY DOCUMENTATION

Contents

Cytely Documentation

Cytely is a cloud-native platform for data-driven microscopy. It treats microscopy images like flow cytometry data, linking quantitative metrics (scatter plots, gates) directly to visual evidence, so you can explore whole populations without losing single-cell context.

Start here

If you're new, follow the Quickstart to go from a fresh account to your first analyzed dataset, or read Key concepts for the ideas behind the platform.

Core areas

The Get started tour walks through the three tabs you'll spend all your time in:

- **Images** - uploading files, organizing groups, and reviewing per-field detections.
- **Workflow builder** - the node-based pipeline: let Cytely build it for you or build it yourself, and inspect each step's live preview.
- **Data explorer** - plots, gates, cropped images, the overview map, and how to export or share your results.

Quickstart

Create your account, upload images, and explore your first analysis in Cytely Essentials.

This guide walks through getting from a fresh Cytely account to your first analyzed dataset in the Data explorer.

Create your account

Go to the Cytely web client at app.cytely.io and choose **Need an account?**. Enter your email and a password, then follow the confirmation link sent to your inbox. You can also sign up with a Google account.

Upload images

Once signed in, drag and drop image files onto the dashboard or click **Upload** and browse to your data. Cytely supports most common microscopy file formats, including open formats like `TIFF` and `OME-TIFF` and vendor-specific formats like `.nd2` and `.czi`.

Track progress in the upload panel at the bottom of the page. When the files finish uploading, click **Configure dataset**, then **Start analysis** in the lower right corner.

Image analysis

Next, create the workflow that will analyze your images. Choose **Build workflow for me** and share your instructions, or click **Build yourself** to build one from

scratch. See the full guide in Workflow builder.

Cytely then runs the analysis in the background. Runtime depends on dataset size and complexity. You'll receive an email as soon as the results are ready.

Explore your results

Follow the link in the completion email. Cytely first asks you to confirm whether the analysis looks acceptable - zoom in, scroll through, then accept or reject with feedback. From there you land in the Data explorer, where you can build scatter plots, draw gates, and inspect cropped objects against the overview map.

Key concepts

The ideas behind Cytely - a cloud-native platform that treats microscopy data like flow cytometry so you can explore populations without losing single-cell context.

Data–driven microscopy

Traditional microscopy analysis is a linear, manual bottleneck - acquiring data, shuffling files across hard drives, and running fragile scripts or manual counts. Cytely replaces that with a unified cloud environment that links **quantitative metrics** (scatter plots, gates) directly to **visual evidence** (cell images), so you can explore whole populations while still inspecting single cells instantly.

Acquisition & ingestion

Every experiment starts by ingesting images into Cytely's secure cloud. You can drag and drop existing files from the dashboard - see the Quickstart for the full upload flow - or stream data directly from a microscope with Cytely Bridge. Either way, Cytely preserves acquisition metadata and creates a single lab context - a digital twin of the experiment ready for analysis.

Cytely Bridge

Cytely Bridge is middleware that connects your microscope's software to the Cytely Cloud. As the microscope scans, images stream to the cloud with standardised parameters and full metadata. During analysis you can also click **Trigger acquisition** to instruct the microscope to re-image objects of interest at higher resolution.

Bridge currently supports **Nikon NIS-Elements** via the JOBS module, with **Zeiss** support in alpha.

Workflow Builder

The Workflow Builder is a visual, no-code environment for defining how Cytely identifies cells and objects. Instead of a black-box analysis, you build a transparent, reproducible pipeline by connecting nodes - for example a Gaussian filter to reduce noise, a background segmentation, a watershed to separate touching cells, a size filter to drop debris, and finally an object measurement node that extracts area, circularity, and intensity for every detected object. Running the workflow processes the whole dataset in parallel in the cloud.

Ready–to–go assays & Replicate

Cytely ships a library of pre-validated **assays** (for example a standard phagocytosis assay or a HeLa transfection efficiency workflow). You can also **Replicate** any existing workflow, tweak parameters for your sample, and save the result as a new custom assay - turning analyses into reusable, shareable building blocks.

Data Explorer

The Data Explorer is where Cytely's cytometric approach shows up. Scatter plots sit at the top, a gallery of cropped cell images sits bottom-left, and the full overview map sits bottom-right. Draw a gate on a plot and the gallery and map instantly filter to just the cells inside it, so an outlier on a graph is one click away from the actual cell in the sample.

Plots are not created automatically. You add each scatter plot, histogram, bar chart, or table yourself in the Data Explorer and choose the measurements it uses.

Sharing & replicating

A Cytely share link opens a full interactive Data Explorer for collaborators - they can inspect your gates and click through plots. Changes a recipient makes to the shared view are not saved back to your dataset, and the link does not give access to other experiments in your account. Because the analysis workflow travels with the dataset, a reviewer can also re-run your exact pipeline, or Replicate it against their own data, making reproducibility the default rather than an afterthought.

An account can also hold a **team** with more than one user. Team members can open each other's datasets, adjust each other's workflows, and add or remove plots and gates in the Data Explorer.

Experiments & the workspace

Every dataset in Cytely lives in an experiment. Here's how experiments are organized, what the tabs inside one do, and which controls are always within reach.

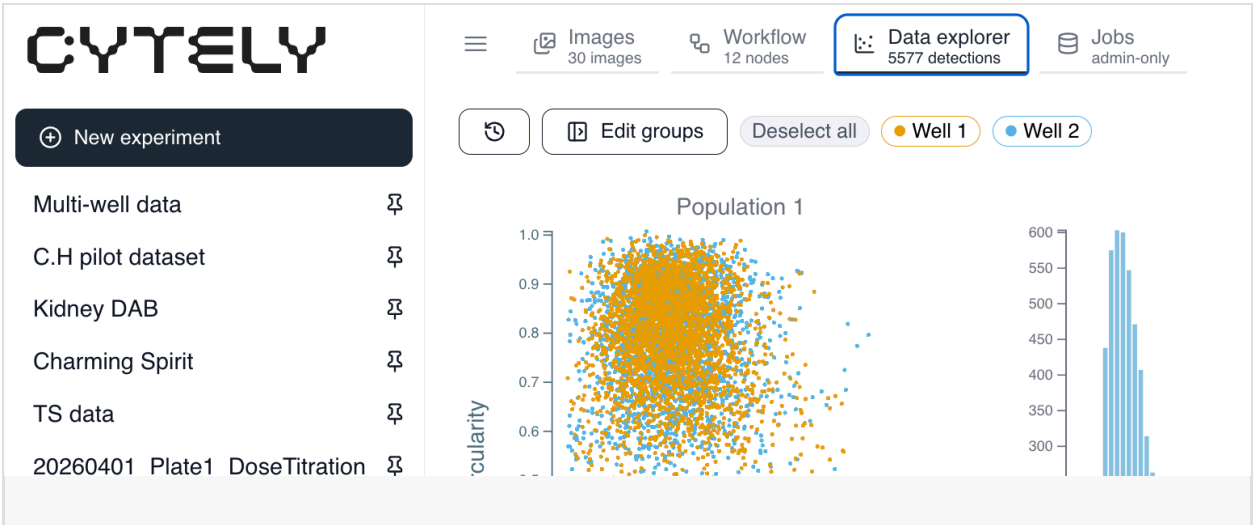
The dataset list

The left sidebar lists every dataset you have access to. A dataset bundles a set of images, the workflow that analyzes them, and the Data explorer layout built on the results - so a whole study stays in one place.

The **...** menu on each entry lets you **pin** a dataset to the top of the list, rename it, or delete it. Pinning is the simplest way to keep the handful of studies you are actively working on above older archives.

Adding a new dataset

Click **+ New experiment** at the top of the sidebar to create another dataset. This is available at any time, including when you already have datasets open.



The New experiment button at the top of the dataset sidebar creates a new dataset.

Tabs inside a dataset

- **Images** - upload, organize, and review the raw fields. See Uploading & reviewing.
- **Workflow** - the node-based analysis pipeline. See Workflow builder. This tab is not available to every account - see Who can build workflows.
- **Data explorer** - plots, gates, and per-object inspection of the results. See Data explorer.

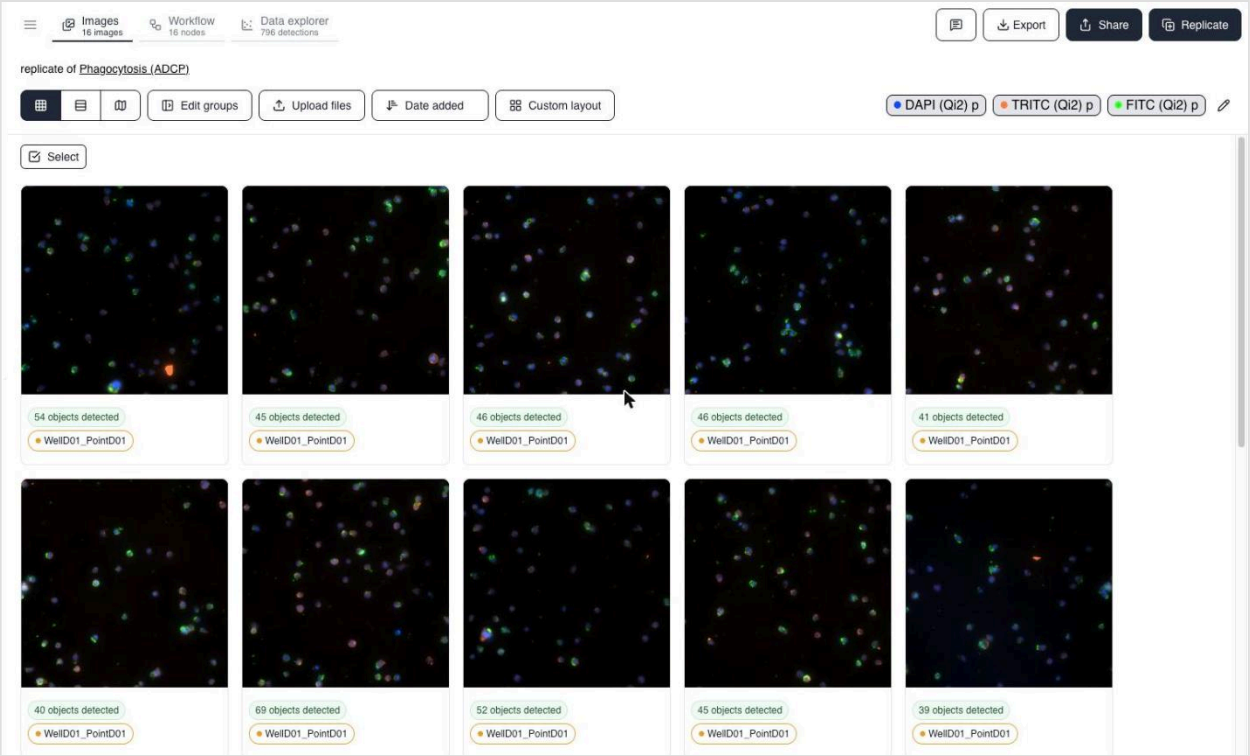
Global controls

The controls in the top-right corner are available from most tabs, so you rarely have to navigate away from what you are doing.

- **Microscope control** - lists the microscopes connected to your account, each with an online or offline indicator, for live acquisition through Cytely Bridge.
- **Export** - downloads the per-object measurement table as CSV. See Exporting & sharing.
- **Share** - generates a read-only public link and copies it to your clipboard immediately. There is no confirmation dialog, so treat one click as publishing the view.
- **Replicate** - creates a new replicate of the experiment, either by uploading fresh data or by including existing data, so a proven setup can be rerun on the next batch.

Uploading & reviewing images

The Images tab is where every dataset starts. Drop your files in, organize them, and inspect what Cytely detected.



The Images tab in Gallery view - thumbnails, detection counts, and group tags.

Uploading files

Drag and drop files anywhere on the Images tab, or click **Upload files** to browse. Cytely supports raw microscopy formats with intact metadata - `.nd2`, `.czi`, and `TIFF`.

For live acquisition, connect your microscope with Cytely Bridge to stream fields straight into the workspace.

Uploads run in the background - track them in the progress panel at the bottom of the page. Cytely creates a new dataset as soon as the first file lands and begins

reading channel and metadata information.

Gallery, table, and map views

Switch between **Gallery**, **Table**, and **Map** layouts from the toolbar. Reorder with **Date added** (or by name, group, or detection count). Each card shows the file name, its group tag, and - once analyzed - how many objects were detected in that field.

- **Gallery** - thumbnail grid. **Custom layout** changes the arrangement, from 1×16 through 6×3, so you can trade thumbnail size for how much of the dataset fits on screen.
- **Table** - one row per file with the filename, acquisition timestamp, and per-row download and delete actions.
- **Map** - a zoomable plot of stage positions, showing where each field sits on the slide or plate.

Select turns on checkboxes for bulk actions: download, move to another experiment, or delete every checked image at once.

In **Map** view, **Select** also enables spatial selection: hold `Shift` and drag with the left mouse button to rubber-band select every field inside the box. Hold `Cmd` (`Ctrl` on Windows) and drag to add another box to the existing selection, or hold `Cmd` and click individual fields to add them one at a time.

Channels

The colored channel pills above the grid toggle each fluorescence channel on or off in the thumbnails (for example DAPI, TRITC, FITC). Use the pencil icon to rename channels or change the pseudo-color each channel is assigned in the composite thumbnails.

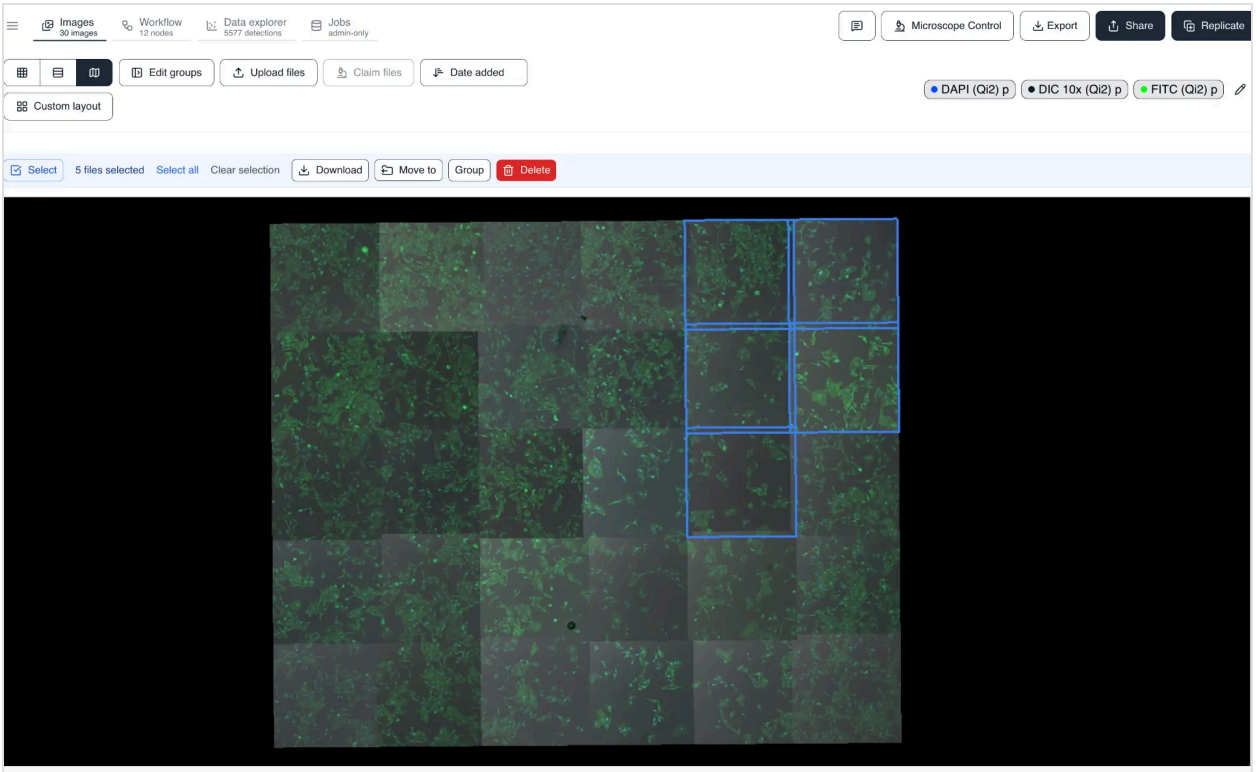
Grouping images

Click **Edit groups** to organize files into named replicates or conditions (e.g. `WellD01_PointD01`). Groups follow your data through analysis and appear as coloring in the Data explorer.

Add groups by hand with **Add group**, or let **Auto group** infer them from filenames and acquisition metadata (typically one group per well). Data explorer widgets and statistics are computed per group. Groups can be created or changed after the analysis has run - the Data explorer updates to reflect them.

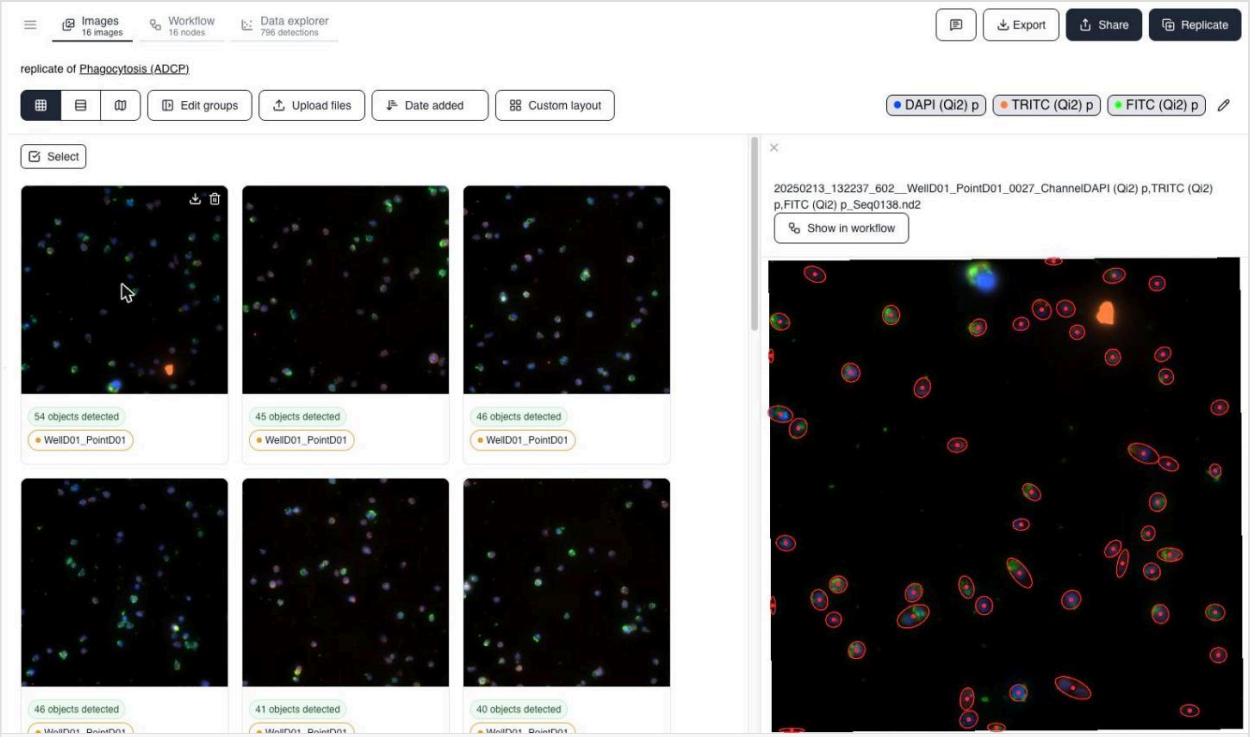
Groups can also be created spatially in **Map** view: open the map, click **Select**, select the images you want, then click **Group** and give the group a name.

In the grouping view, a file can be moved into another existing group by dragging it onto that group.



Map view with Select active: selected fields are outlined in blue and Group creates a named group from them.

Inspecting a single image



Clicking a thumbnail opens the full field with the detection overlay and a Show in workflow link.

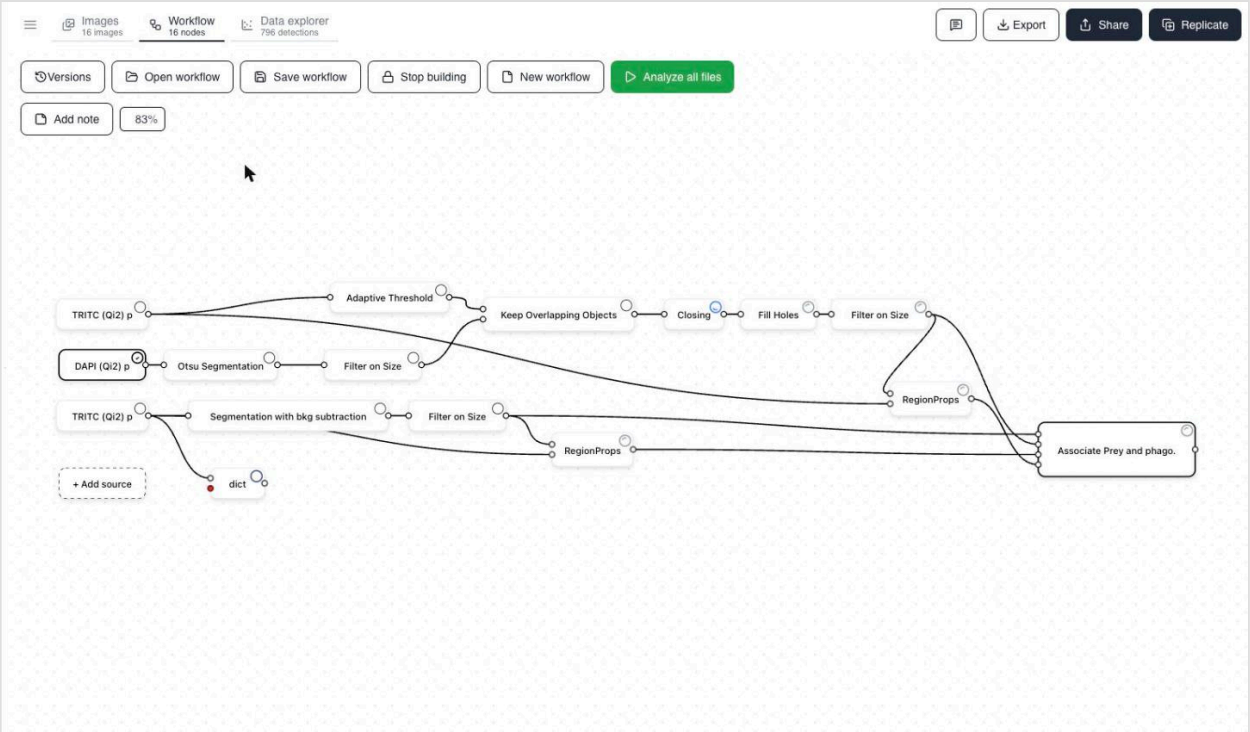
Click any thumbnail to open a side panel with the full-resolution image, an outline overlay marking every detected object, and a **Show in workflow** link that jumps straight to the Workflow tab with that file preloaded as the node preview source - useful for auditing or debugging a specific field of view.

Starting an analysis

Once at least one image is uploaded, click **Configure dataset** and then **Start analysis** in the lower right. Cytely summarizes the dataset and asks how you want to proceed - see Workflow builder for the two paths available.

Workflow builder

A visual, node-based pipeline that turns raw channels into per-object measurements.



A typical workflow: source channels on the left, aggregation sink on the right.

The Workflow tab shows your analysis as a graph. Source channels on the left feed into a chain of processing and measurement steps (nodes), which converge on a final aggregation (*sink*) node on the right. Every node produces data that downstream nodes can consume.

Building a workflow

Press **Start analysis** and assemble the pipeline in the visual builder, or start from a saved template. See Build a workflow using workflow builder.

Who can build workflows

Direct access to the Workflow tab is not enabled for every account. It is switched on for you in advance if your team is set up to build pipelines - most new accounts start without it.

If it is not enabled, then whenever you upload data to a new dataset and press **Start analysis**, Cytely asks how you want the workflow made:

- **Build the workflow for me** - the Cytely team builds and runs the pipeline for you. Once you choose this, the workflow is no longer editable by you for that dataset.
- **I want to build a workflow myself** - the Workflow tab opens and you assemble the pipeline in the visual builder.

The choice is made per dataset at the point you start the analysis, so pick "I want to build a workflow myself" if you expect to tune the pipeline yourself later.

Typical pipeline shape

Most workflows follow the same rough pattern:

1. **Segmentation** turns raw channel intensities into object masks. Channels are often segmented separately (e.g. Otsu for nuclei, Adaptive Threshold for a marker), then combined.
2. **Morphological clean-up** - closing gaps, filling holes, and keeping overlapping objects - tidies up the masks.
3. **Filter on size** removes noise and oversized artifacts, leaving only well-formed objects.
4. **Measurement** nodes (like Morphology) quantify each object.
5. **Aggregation** at the sink node links related objects - for example, associating "prey" with their parent phagocytes and rolling measurements up per cell.

Toolbar

- **Versions** - browse and roll back workflow history.
- **Open / Save / New workflow** - reuse pipelines across datasets.
- **Stop building** - lock editing on a finished workflow.
- **Analyze all files** - (re)run the pipeline across the full dataset. Cytely processes in the background and emails you when results are ready.
- **Add note** - annotate the canvas with context for collaborators.

The canvas can extend beyond the visible area in either direction and does not auto-fit: drag empty canvas space to pan, and use the zoom-percent control to fit more of the pipeline on screen.

Workflows are not guaranteed to persist between sessions, so use **Save workflow** once a pipeline works and **Open workflow** to bring it back.

Build a workflow using workflow builder

For full control, assemble the pipeline yourself in the visual builder and tune each node against its live preview.

Pick a source image

Open the Workflow tab and choose a representative image as the preview source. Every node's live preview renders against that image, so it should reflect the kind of data you're analyzing.

Add source channels

Add a source node per channel you want to analyze (for example DAPI for nuclei, TRITC for a marker). The colored channel pills on each source node control which acquisition channel it emits into the pipeline.

Add analysis steps

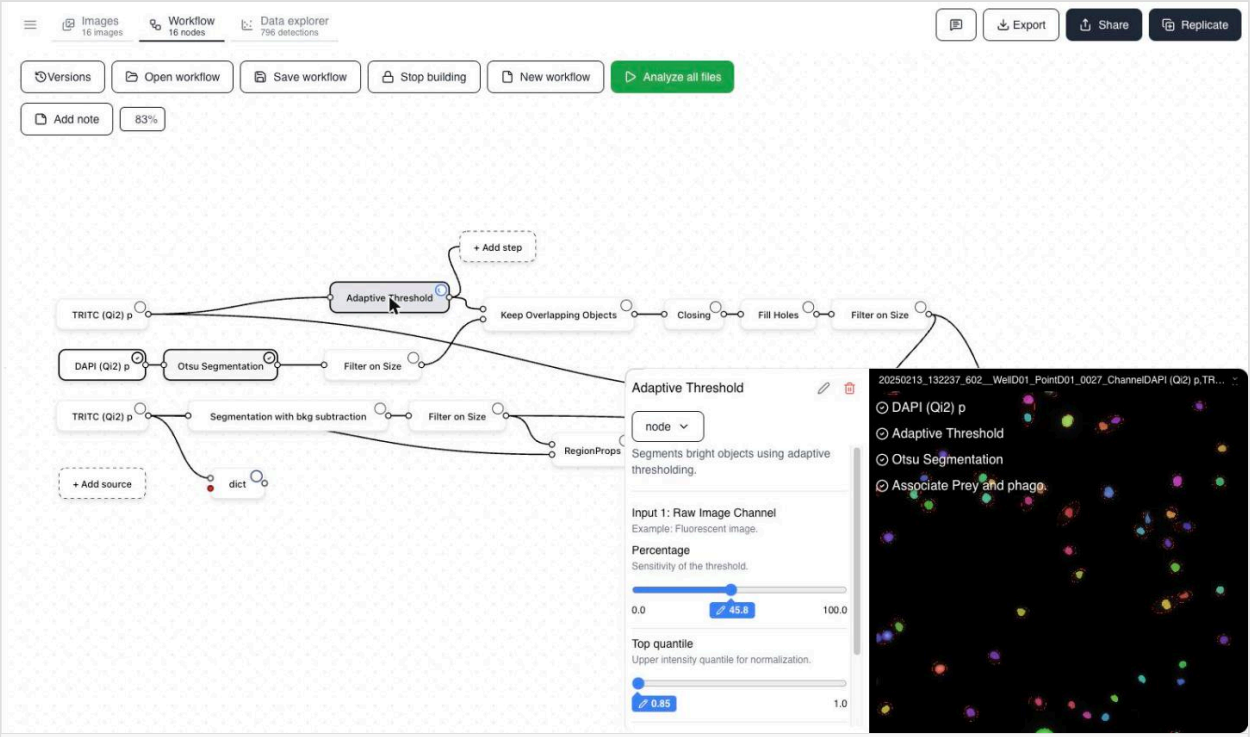
Click **+ Add step** on any node's output to append the next step. Cytely offers a searchable library of algorithms grouped by category - segmentation, filtering, morphology, measurement, and aggregation.

A typical branch looks like: *Source channel → Segmentation → Clean-up (Closing, Fill Holes) → Filter on Size → Morphology*. Branches for different channels usually converge on a final aggregation node that links them together (for example *Associate Prey and phagocyte*).

Node detail panel

Clicking any node opens a detail panel with a plain-language description of what the step does, its expected inputs (with examples of the kinds of upstream nodes it accepts), and any tunable parameters - usually a mix of sliders and numeric fields.

The preview panel



A node's detail panel with tunable parameters and the live preview updating on the source image.

The preview on the right renders the node's output overlaid on the chosen source image. Above the image is a **breadcrumb** of every upstream step currently included in the preview, so you can see exactly which chain of operations produced the visible result. Adjust a parameter and the preview updates as soon as the pipeline re-runs.

Layers

The preview is built from **layers**: every node that is currently selected adds one.

How each kind of output is drawn:

- **Source channels** show the image they contain (nuclei stain, membrane stain, and so on) as an intensity image.
- **A single intensity image** - a source channel or a processed intensity image on its own - is displayed in grayscale.
- **More than one intensity image** at the same time is displayed in the color assigned to each source channel, so the layers can be told apart.
- **Binary and labeled images** are drawn in random colors. For labeled images each label gets its own color.
- **Output nodes** draw oval shapes where objects were detected. These ovals are not the actual segmentation mask - they are a marker showing where objects were found.

Preview–visibility toggle

Every node has a small circle in its top-right corner. This is a **preview toggle**, not a pipeline switch. Unchecking it removes that step from the breadcrumb and drops its layer from the preview - but the node itself and all its connections remain active in the pipeline. It only changes what you're currently inspecting, not what the workflow computes.

Switching preview channels

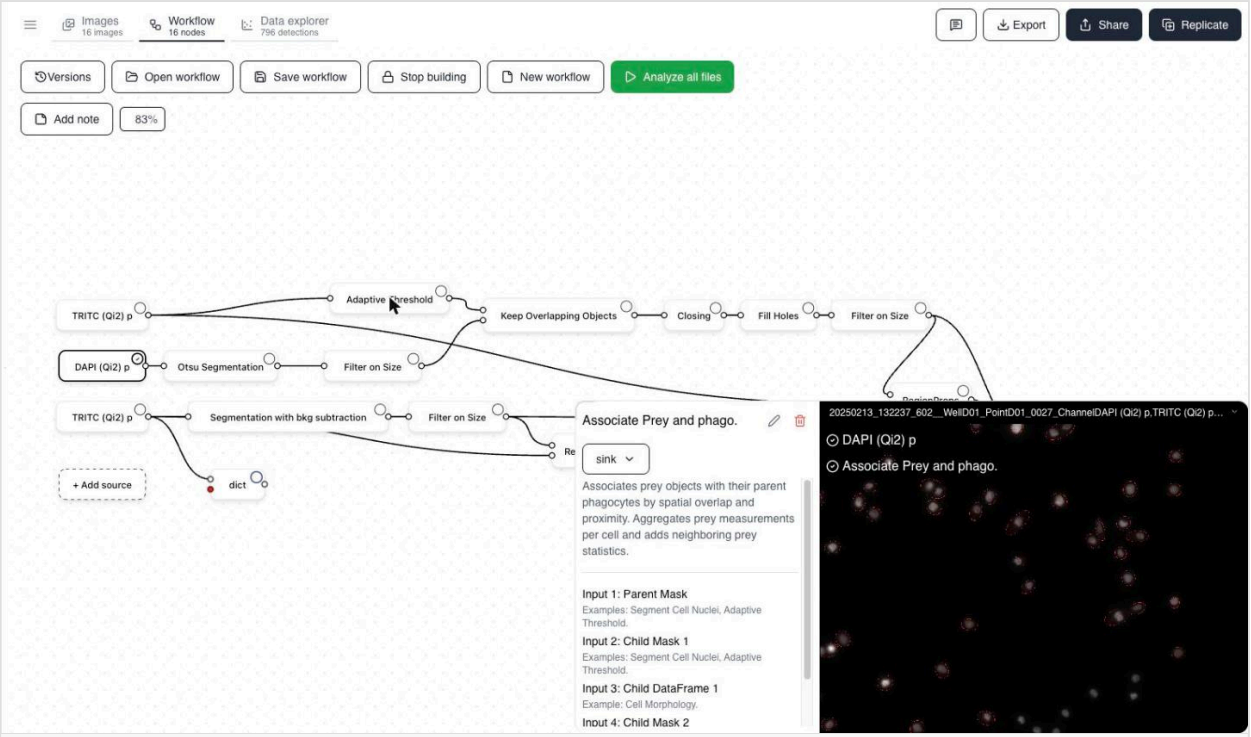
The preview panel exposes channel pills matching your source image, so you can flip between channels to sanity-check overlays against different underlying data.

The bin icon in the preview panel deletes the node you are currently inspecting.

Canvas shortcuts

- **Select multiple nodes** - hold `Shift` and drag on the canvas to rubber-band select every node inside the box.
- **Delete a selection** - press `Backspace` to remove the selected node, or all currently selected nodes at once.
- **Delete a single node** - open the node and click the bin icon in the preview window.

Run the workflow

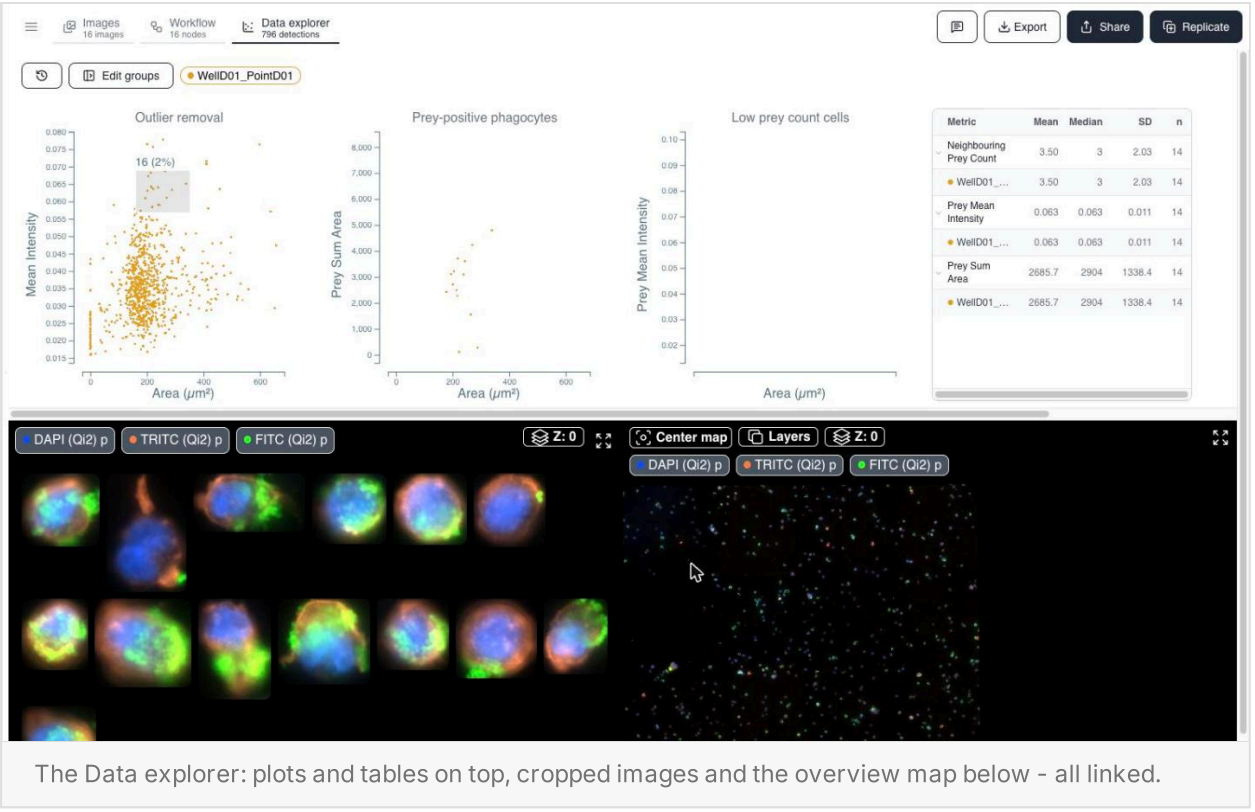


Separate channel branches typically converge on an aggregation node - here, Associate Prey and phagocyte.

When you're happy, click **Analyze all files** to run the pipeline across the whole dataset. Save the workflow with **Save workflow** so you can reapply it to future datasets, and use **Versions** to review or roll back changes.

Data explorer

Interactively explore every detected object across plots, tables, cropped images, and the overview map.



The Data explorer: plots and tables on top, cropped images and the overview map below - all linked.

The Data explorer opens once your analysis is complete. It's the interactive workspace where cytometry-style gating meets microscopy: every plot, table, and image tile is linked to the same underlying detections, so a selection anywhere updates everywhere.

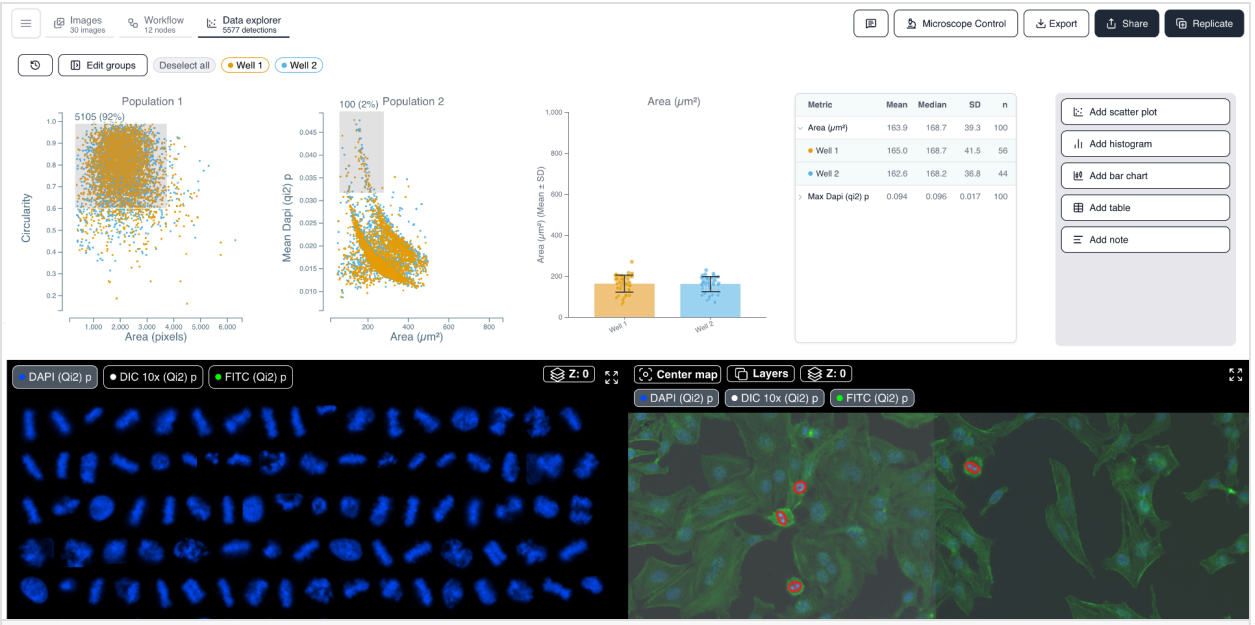
Reviewing the analysis first

Before you land in the Data explorer, Cytely asks you to confirm that the analysis is acceptable. Zoom, scroll through your dataset, and either accept with the green

button or reject with the red button and a short description of what you expected instead.

The four linked panels

The workspace is split into two rows, shown below with scatter plots, a bar chart, and a statistics table on top, and cropped object images alongside the overview map on the bottom.



A populated Data explorer: gated scatter plots and stats on top, cropped nuclei and the outlined overview map on the bottom.

- **Upper panel - plots and tables.** Scatter plots, histograms, statistics tables, and free-form notes you build up to explore your populations. See Plots & gating.
- **Lower-left panel - cropped images.** A gallery of object thumbnails for the current gated population, so you can visually verify what a selection contains.
- **Lower-right panel - overview map.** The full uploaded fields with detected objects outlined, showing spatial context.

All four are cross-filtered - see Cross-filtering & inspection for how they interact.

Widgets

The upper panel is a customisable board. Add a **scatter plot**, **histogram**, **bar chart**, **table**, **note**, or a **preset** layout, and break any of them down by group. **Edit columns** controls which measurements a widget uses - Area, Centroid X/Y, Circularity, Major axis length, Max and Mean intensity, and other measurements.

If the workflow changes and a widget points at a column that no longer exists, the widget shows a warning card instead of a plot. Use **Edit columns** on that card to repoint it at current measurements or clear the stale ones.

Sample view and map view

Toggle between **Sample view**, which works at the object level, and **Map view**, a 96-well plate heatmap. Pick the metric that colors the wells (for example total detections) and read the scale from the legend - a fast way to spot edge effects or a failed well before digging into single objects.

Single–cell montage

The montage panel shows a crop per detected cell, with channel toggles so you can check a marker on its own, and a Z-slice indicator for stacks.

Groups

The tag chips at the top of the workspace (for example `WellD01_PointD01`) reflect the groups you set up in the Images tab. Use **Edit groups** to adjust them; the statistics table and plots recolor to match.

Ready to export or share?

See Exporting & sharing for how to download CSVs, save layouts, and share interactive links with collaborators.

Plots & gating

The building blocks of an analysis in the Data explorer: plots, gates, tables, and notes.

Scatter plots

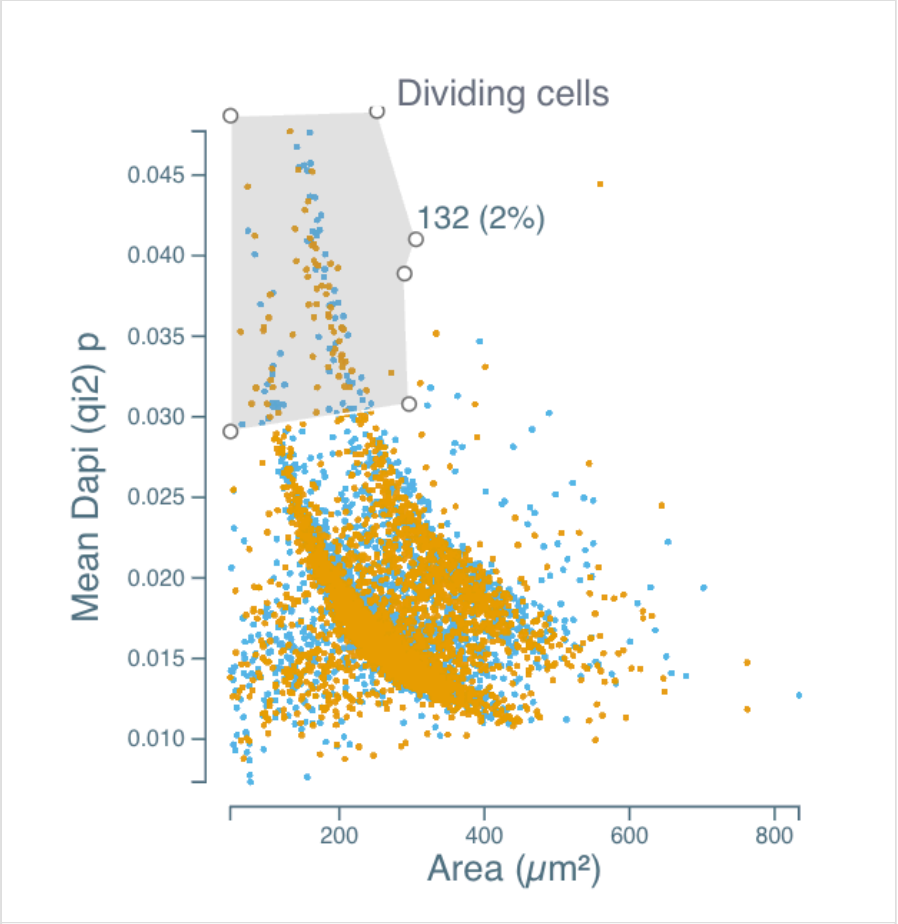
Click **Add scatter plot** and pick an X and Y parameter - area, intensity, circularity, or any measured feature. Add as many plots as you need; each one is a lens on the same underlying detections.

Each point is one detected object, colored by group. In the example below, mean DAPI intensity is plotted against object area, and the two wells are overlaid in orange and blue.

Gates

Drag with the left mouse button on a scatter plot to draw a **gate** - a rectangle or polygon selection that defines a subpopulation. Move a gate by dragging its interior; resize it by dragging its edges.

A gate is named and reports how many objects it contains, both as an absolute count and as a share of the parent population - here `132 (2%)` small, bright nuclei labelled "Dividing cells".



A scatter plot with a polygon gate. The gate label shows its name and the number and percentage of objects it captures.

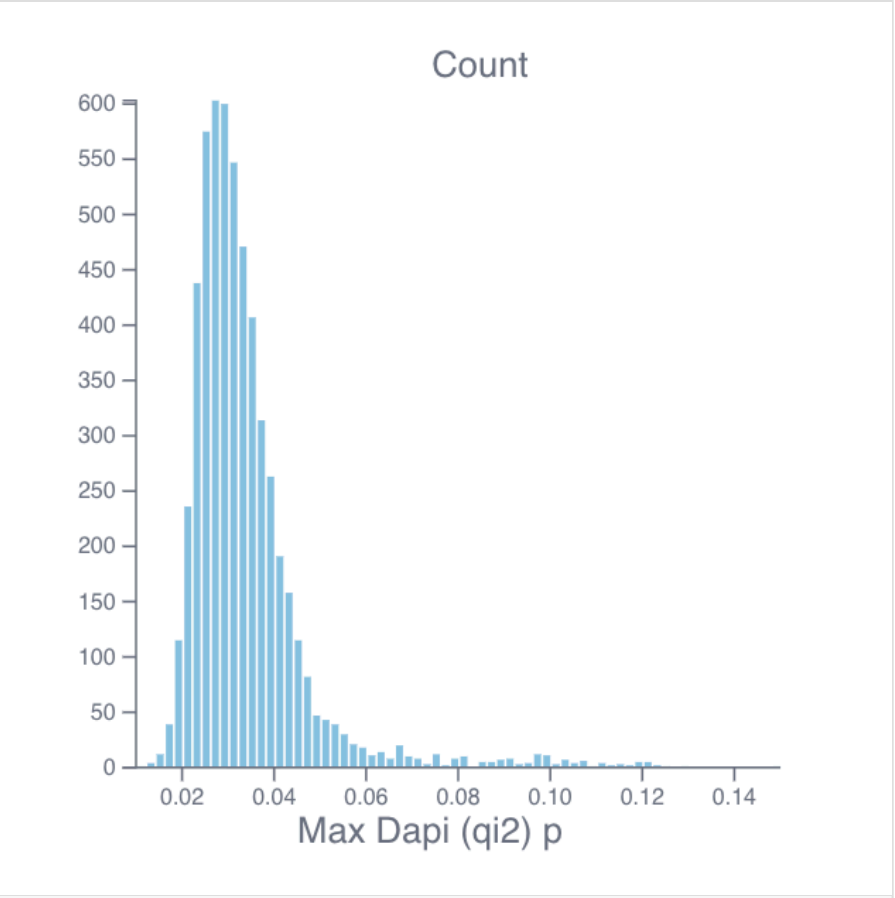
Plots downstream of a gate update to show only the objects it contains, so **chaining gates** lets you narrow to very specific populations step by step - for example, "all phagocytes → prey-positive phagocytes → high-intensity prey".

Plot shortcuts

- **Zoom** - hold `Space` and scroll (or use a two-finger gesture on a touchpad) over a scatter plot to zoom in and out.
- **Change an axis range** - drag directly on the axis you want to rescale.
- **Log scale** - right-click an axis to switch it to a logarithmic scale.

Histograms

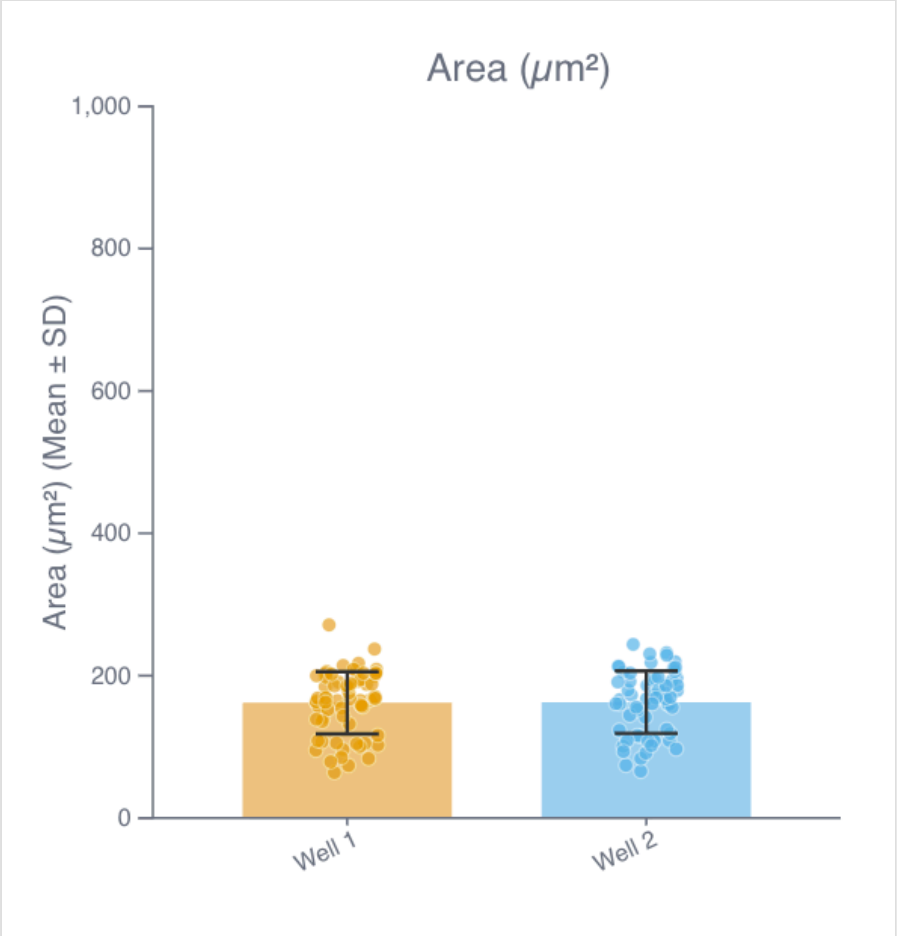
Click **Add histogram** and pick a parameter to see its distribution - useful for comparing intensities between subpopulations or across groups.



A histogram of max DAPI intensity. The y-axis is object count per bin, making skew and outlier tails easy to spot.

Bar charts

Click **Add bar chart** and pick a parameter to compare it across groups. Each bar is the group mean with error bars showing the standard deviation, and the individual objects are overlaid as jittered points so you can see the spread behind the summary.



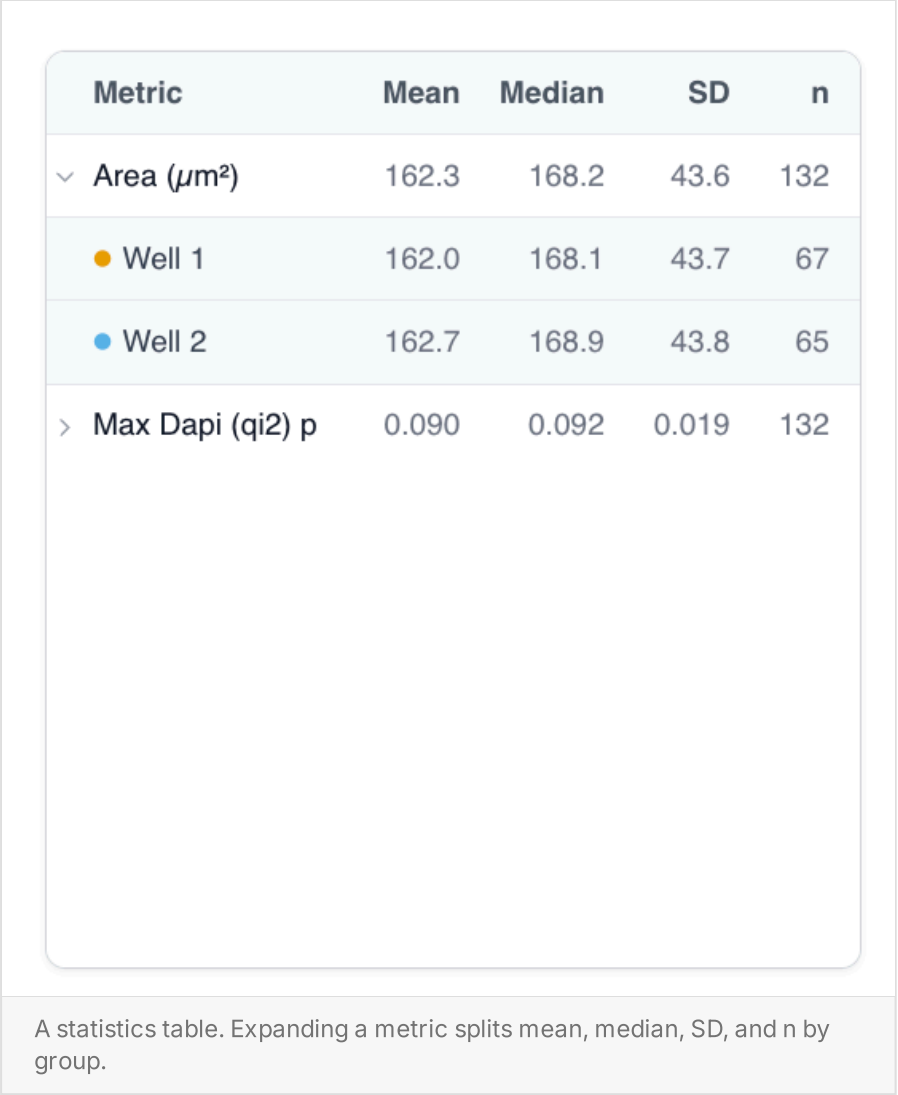
A bar chart comparing mean area between two wells. Error bars show standard deviation; each dot is a single object.

Bar charts respect the active gates, so gating first and then adding a bar chart compares only the population you selected.

Statistics tables

Click **Add table** and choose the parameters you want to summarize. Cytely reports **mean**, **median**, **standard deviation**, and **object count** (`n`) for the currently gated population, split by group.

Each metric is a row you can expand to break the numbers down per group, with the group colors matching the plots.



Metric	Mean	Median	SD	n
Area (μm²)	162.3	168.2	43.6	132
Well 1	162.0	168.1	43.7	67
Well 2	162.7	168.9	43.8	65
Max Dapi (qi2) p	0.090	0.092	0.019	132

A statistics table. Expanding a metric splits mean, median, SD, and n by group.

Notes

Because Cytely datasets can be shared, it's worth annotating them. Add a free-form note with **Add note** to capture context, conditions, and interpretation next to the data.

Phagocytosis assay table

If your dataset contains phagocytosis data, click **Add phagocytosis assay** to add a table of assay-level metrics like iMOP and phagocytosis score.

Cross–filtering & inspection

A selection anywhere in the Data explorer updates everywhere. Here's how the four panels stay in sync.

Everything is linked

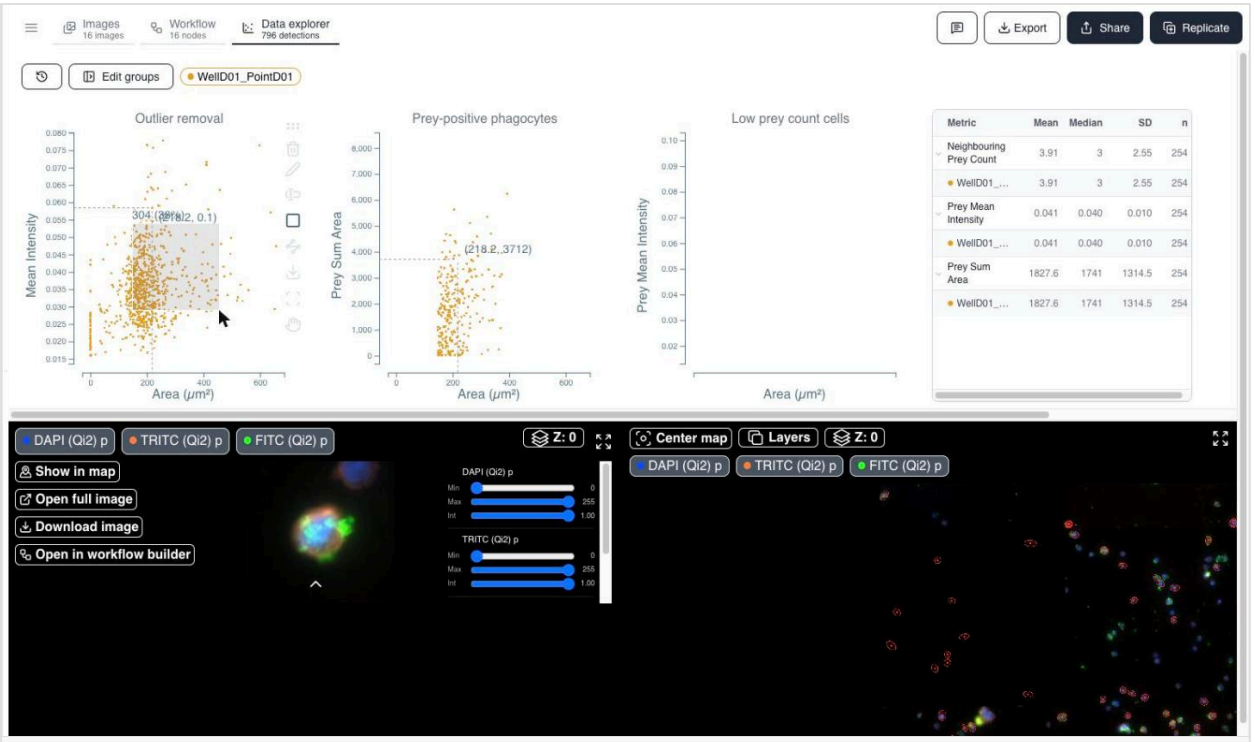


Figure 1. Drawing a gate on a scatter plot instantly filters the cropped images, the map, and every other plot.

Scatter plots, histograms, statistics tables, cropped images, and the overview map are all backed by the same per-object dataset. Draw a gate on any plot and every other panel instantly filters to match - the table recalculates, the gallery shows only matching objects, and the map highlights their positions (Figure 1).

Cropped images

The lower-left panel shows a thumbnail per object in the current gated population, so you can visually confirm what a selection actually contains (Figure 1, lower left).

Overview map

The lower-right panel shows the full uploaded fields with detected objects outlined in purple (Figure 1, lower right). **Center map** recenters on the currently selected object.

Inspecting a single object

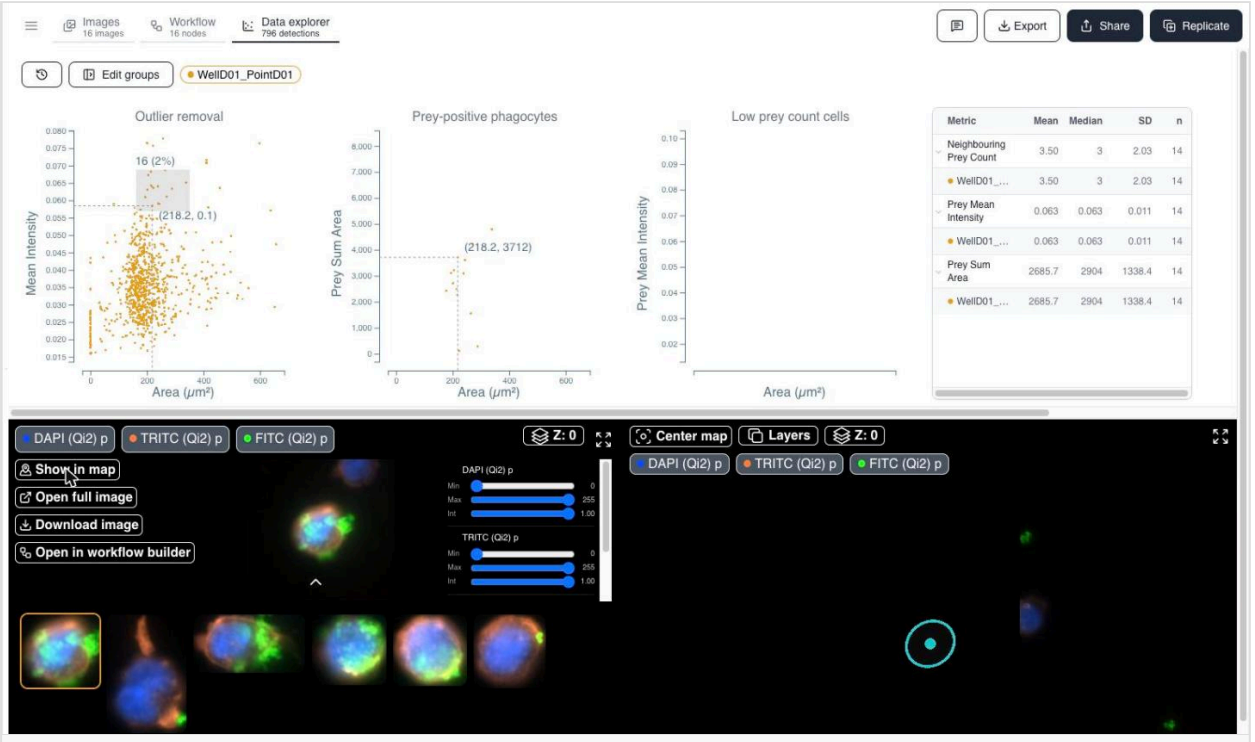


Figure 2. Show in map centers the overview on the selected object, marked with a cyan circle.

Click any thumbnail in the cropped images panel to open it. Cytely exposes (Figure 2):

- **Per-channel intensity sliders** - Min, Max, and Int for each channel, so you can adjust brightness/contrast for that single view.
- **Show in map** - centers the overview map on that object, marked with a cyan circle.
- **Open full image** - opens the parent field of view at full resolution.
- **Download image** - saves the cropped image locally.
- **Open in workflow builder** - jumps to the Workflow tab with that object's parent image as the preview source, so you can inspect exactly which pipeline steps produced it.

Exporting & sharing

Take your results out of Cytely - as CSV, as a reusable layout, or as an interactive link.

Export CSV

Use **Export → Export CSV** at the top-right of the plots panel. When the download progress bar completes, click the download icon to save the file. The CSV contains every parameter for every detected object; if you've applied gates, the last gate that contained each row appears in the `Gate presence` column.

Export plots and gates

Use **Export → Export Plots and gates** to download your current Data-explorer layout as a file.

Save and re–apply plots and gates

The plot toolbar has two star icons. The **star with a plus** saves the current plots and gates, and the **star** re-applies a saved set to the current dataset.

Share a link

Click **Share** at the top-right of the plots panel to copy a link to your clipboard. Anyone with the link - Cytely account or not - can open the same plots and gates and interact with them. Changes a recipient makes to the shared view are not

saved back to your dataset, and the link does not give access to other experiments in your account.