SUPPORTING INFORMATION

A multiscale study of the role of dynamin in the regulation of glucose uptake

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The materials presented in this file of Supporting Information complement the experimental methods reported in the main manuscript. Additionally, some experimental results are also presented:

- effect of cell numbers on the magnitude of glucose uptake;
- effect of insulin concentration on the magnitude of glucose uptake;
- details of the Student t-test performed on the dataset shown in in Figure 4D and E.
- indications of the reversibility of dynasore *in vivo.*

S1. Experimental Methods

S1.1 Fabrication of the electrochemical chips

The chips were initially designed in Clewin 4 and fabricated from PDMS using standard soft lithographic techniques.[1] Briefly, to make the master of the microfluidic system, a 100 µm thick SU-8 photoresist layer was spin-coated on a clean Si wafer, and patterned through a Cr mask. After developing and silane functionalization of the SU-8 master, a 10:1 poly(dimethylsiloxane) (PDMS) mixture was poured on the SU-8 structure and polymerized in an oven at 100 °C for 1 h. Also, a ~200 µm thick PDMS membrane was made by pouring the required quantity of uncured PDMS in a petri dish. To close the channels, the resulting patterned PDMS layer was bound to another PDMS surface or to a piece of clean microscope slide after surface-activation with air plasma (12 W for 70 s).

The sample chamber, where the cell-on-paper sample was inserted during the experiment, was made of two identical pieces as described in Figure 2A, which were themselves made of four layers. In the first iteration of the chip, five layers were required,[2] but the design was here simplified, largely because a thin membrane for gas exchange is not needed for the short experiments described here.

First, a thick (~4 mm) piece of PDMS (layer 1 in Figure S1A) was used to provide mechanical strength to the system. A fluidic connection was established by punching a Ø 1.5 mm porthole across layer 1. A second layer, featuring a 100 µm deep channel made of a 6 mm disk connected to a 100 µm wide microchannel (Figure S1B) was prepared. The 6 mm disk was then cut out with a 6 mm biopsy punch, thus opening a large hole through the layer, connected to the 100 µm channel. The approximate overall thickness of this layer was ~300 µm. Layer 2 was then bonded to layer 1, with the channels facing down, to close the channels. Layer 3 was a piece of porous polycarbonate membrane (3 µm pores, 11.3% overall porosity, Millipore, USA) closing the 6 mm hole pierced across layer 2. Uncured PDMS was carefully painted over the surface of layer 2 to allow for the bonding of the polycarbonate membrane. Finally, layer 4, which is a ~200 µm thick layer of PDMS with a 6 mm hole opened with a biopsy punch, was glued using PDMS over layers 2 and 3 to complete the device. During the fabrication, great care was given to the alignment of the 6 mm holes to form a smooth sample chamber.

The detection chamber (see Figure 2A) was simply made by bonding a ~4 mm thick piece of PDMS featuring the microfluidic system shown in Figure S1C to a piece of glass microscope slide. Before that, Ø 1.5 mm portholes were punched at each extremity of the chip, for the inlet and outlet, and a Ø 0.75 mm hole was punched in the center of the 1 mm square present at the center of the microfluidic design, to allow for the insertion of the sensor. Fluid connections were completed by inserting tubings into the port holes. The fluid flows were actuated from a computer-controlled Nemesys system (Cetoni GmbH, Germany) featuring two low-pressure pump modules.

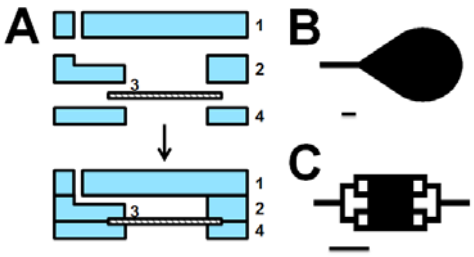


Figure S1: Chip design, A) Fabrication of one half of the sample chamber. Layers 1, 2 and 4 are made of PDMS. Layer 3 is a piece of porous polycarbonate membrane. Layer 2 features a microfluidic channel, described in B) (bar shows 1 mm), and the area corresponding to the disk in this panel is opened with a biopsy puncher. C) Layout of the detection chamber (bar shows 1 mm), the sensor is positioned at the center of the 1 mm square which has been previously opened with a Ø 0.75 mm punch.

S1.2 Electrode fabrication

The sensor was prepared by threading a Ø 51 µm Pt wire, Teflon coated, and a Ø 75 µm Ag wire, Teflon coated (both from Science Products GmbH, Germany) in the lumen of a 20 G blunt syringe needle (H. Sigrist & Partner AG, Switzerland).[3–5] The extremities of the wires were stripped of the Teflon with a flame and attached to connection wires using conductive silver paste. A third connection wire is also attached with silver paste to the metal of the needle. The lumen of the needle is filled with fluid epoxy (EPO-TEK 302-3M, Epoxy Technologies Inc., USA), to

secure the wires in place, and the system is let to set overnight. The general layout of the sensor is recapitulated on Figure 2B. The connections are then secured in place using heat-shrink tubing, and the tip of the needle is gently polished, finishing with 0.05 µm alumina slurry, to expose the three electrodes: the Pt working electrode (WE), the Ag|AgCl pseudo reference electrode (RE), and the stainless steel of the needle used as a counter electrode (CE).

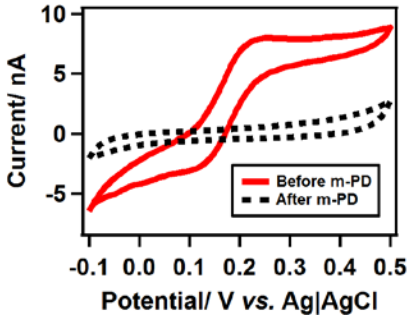


Figure S2: Typical voltammograms (*SR*= 100 mV s^{-1}) performed at the clean Pt surface in 1 mM FcMeOH in PBS before and after deposition of the poly-(m-phenylenediamine) (m-PD) film.

S1.3 Electrode functionalization

All the electrochemical tests were performed using an Iviumstat potentiostat (Ivium Technologies, Netherlands). All the potentials mentioned in this work are reported vs the Ag|AgCl pseudo reference. Before each set of experiments, the sensor was carefully polished with fine sandpaper and alumina slurry (0.05 µm particles). The sensor was then sonicated for 5 minutes in isopropyl alcohol and rinsed in water. A layer of chloride was deposited on the Ag electrode by immersing the sensor in 3 M KCl. Several current steps (-20 µA for 1 s followed by 20 µA for 9 s) were applied for 1 min.

The sensor was modified using a variation from a method presented by others.[6–8] The WE was cleaned electrochemically in 0.1 M H_2SO_4 by running 10 cyclic voltammogram (CV) cycles from -0.3 V to 1.0 V (scan rate *SR*= 500 mV s^{-1}). The quality of the electrode response is tested by running a CV in 1 mM ferrocenemethanol (FcMeOH) in phosphate buffered saline (PBS; pH= 7.4). Then, a layer of poly-(m-phenylenediamine) (m-PD) was electropolymerized on the WE. This part works as an exclusion membrane, thus improving the selectivity of the sensor. This was performed by placing the sensor in a solution of 100 mM m-PD in PBS, and applying the following potentials: 20 s at 0.0 V, 5 mins at 0.7 V and 5 mins at 0.0 V. The sensor is rinsed with water and the quality of the membrane is tested by running another CV in 1 mM FcMeOH. As shown in Figure S2, the anodic signal originating from the probe is abolished, thus showing the integrity of the m-PD membrane. In the second step, the sensor is modified with glucose oxidase (GOx) by dipping it in the following solution: 60 mg ml^{-1} GOx, 30 mg ml^{-1} bovine serum albumin, 60 mg ml^{-1} poly(ethylene glycol) diglycidyl ether and 2% v/v glycerol in PBS. This layer is then hardened by placing the sensor at ~50 ˚C for 2 hours.

The sensor was finally rinsed and inserted into the detection chamber, as shown in Figure 2A, so that the electrodes are in the lumen of the channels. Solutions of glucose in HEPES buffer were then used, at a flow rate *Q* of 1 µl s^{-1}, to test the detection device, as described below.

S1.4 Cell culture

C2C12 cells were maintained in high glucose DMEM media supplemented with 10 % fetal bovine serum, 2 mM L-glutamine, non-essential amino acids, 20 mM HEPES and 1 % penicillin streptomycin solution in a 5 % CO_2 humid atmosphere at 37 °C. The cells were grown in cell culture flasks and were sub-cultured every 2-3 days to avoid high cell density which may trigger differentiation.

S1.5 Fluorescence imaging of the cell-seeded paper patches

The paper patches containing cells were rinsed in PBS and fixed for 10 mins in 3.7 % formaldehyde in PBS at room temperature. The patches were rinsed in PBS and then permeabilized in 0.5 % Triton X-100 in PBS for 5 mins at room temperature. The patches were rinsed twice in PBS and then exposed to a 50 µl drop of 100 nM fluorescently labeled phalloidin (Phalloidin-Atto 514, Sigma-Aldrich) in PBS for 30 min at room temperature, in the dark. The patches were then rinsed thrice in PBS and mounted with a Fluoroshield mounting medium containing 4',6-diamidino-2-phenylindole (DAPI). The samples were imaged with an epifluorescence Image 2M microscope (Carl Zeiss). The software ImageJ was used to improve the quality of the image. When the processing was simply used to facilitate the topological analysis of the images (such as in Figure 2E and F), only the brightness and contrast were modified on each image individually.

S1.6 Imaging and quantification of GLUT4 translocation

To image the translocation of GLUT4, C2C12 were seeded on poly(L-lysine) coated microscope coverslips and incubated overnight in 2 ml of media. The next morning, the cells were serum starved for ~4 hours in 2 ml of serum-free media. At the end of the starvation period, and if required by the experimental conditions, 1 µM dynasore was added to the media and the coverslips were incubated for 10 minutes. Insulin (1 µg ml^{-1}) was then added to the media and the coverslip was incubated for another 10 minutes. Before that, a 5:1 mixture of primary anti-GLUT4 N-20 antibody produced in goat (200 µg ml^{-1}, Santa Cruz Biotechnology Inc., Texas, USA) and secondary anti-goat antibody labeled with CF™ 488A (2 mg ml^{-1}, produced in chicken) was prepared and incubated for 10 minutes at room temperature in the dark. The anti-GLUT4 N-20 targets an extracellular epitope of the GLUT4 and is therefore suitable for the analysis of the surface expression of the transporter.[9] A 20 µl drop of the antibody mixture was then added to the 2 ml of media in which the coverslips are incubated, for each experimental condition. The coverslips are then left at 4 ˚C for 1 hour to allow for epitope labeling while still inhibiting endocytosis of the antibodies. After this step, the coverslips are rinsed with PBS twice, fixed, permeabilized and mounted as described above.

The samples were imaged with an epifluorescence Image 2M microscope (Carl Zeiss). For the GLUT4 translocation analysis, the imaging was carried out on the same day for the two experimental conditions, and the same microscope setting were used to allow for comparison. The image processing was performed on the two images, corresponding to the two experimental conditions, simultaneously. Here, the contrast and brightness were modified, and the background was removed using the ImageJ specific function.

For the fluorometric measurements, the cells were grown to ~90% confluency in a 24-well plate, in 0.5 ml of medium. The samples were labeled for GLUT4 (5 µl of the 5:1 antibody mixture added to each well), fixed and rinsed as described above, but not permeabilized, and the plates were analyzed with a Victor 3.0 multilabel counter (Perkin-Elmer, MA, USA) using the fluorescein configuration (excitation filter 485 nm, emission filter 535 nm, bottom counting, 0.1 s measurement time). To account for the background, several wells were kept antibody-free, all the other preparation steps remaining unchanged. The average signal from these wells was subtracted to the signal obtained from the wells which were labeled with antibodies, for

each technical repeat. The final fluorescence value associated to each well was the median of 2-3 repeated measurements performed at different sites of the wells. This was to ensure that the incomplete cell coverage does not alter the validity of the data. Finally, each well signal was normalized to the average signal obtained for control. The results from three plates were pooled to obtain the data presented in the text.

S1.7 Worm maintenance and preparation

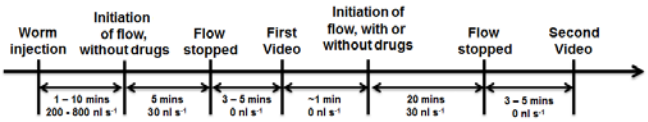
C. elegans were cultured at 20 °C, in Ø 90 mm Petri dishes, on nematode growth media (NGM) seeded with *Escherichia coli* strain OP50 bacteria. The strain used in this study was the wild-type N2 strain, as obtained from the Caenorhabditis Genetics Center (University of Minnesota). In all the experiments, YA worms were harvested from the plates and suspended in solution prior to each introduction in the microfluidic system by rinsing the plates with fresh S-medium.

For the RNAi studies, RNAi clones *dyn-1* (C02C6.1) were purchased from GeneService and sequence verified. Bacteria were grown in Luria Broth (LB) with 100 µg/mL ampicillin and 12.5 µg/mL tetracycline overnight in a thermal shaker at 37 ^{o}C. The following day, 50 µL of the confluent bacterial cultures were used to inoculate freshly prepared LB medium containing only ampicillin (100 µg/mL). The new cultures were grown until reaching an optical density between 0.6-0.8. Plates were induced overnight at room temperature with 2 mM isopropyl β-D-1-thiogalactopyranoside (IPTG) and seeded with 90 µL of the culture of HT115 bacteria expressing the RNAi clones for the *dyn-1* gene or the empty vector. L4 worms were transferred on the RNAi plates and removed after 24 h of treatment. YA worms were then collected for introduction in the microfluidics system.

S1.8 Worm mobility assay

The chip design is shown in Figure S3A.[10] The main feature of the chip is a 2 x 2 mm^2 microfluidic chamber, dedicated to adult nematode maintenance and treatment, connected to three inlets – In1, In2 and In3 – dedicated respectively to worms loading, S medium refreshing and treatment injection, and two outlets – Out1 and Out2 – fitted respectively with 60 µm and 30 µm filters. These filters allow for size selection of the nematodes, so that only adult worms are retained in the chamber. Microchannels are 40 µm high, while the height of the chamber is 130 µm. The microfluidic chips were prepared by standard soft lithography using a 2-layer SU-8 master. Briefly, the master was fabricated by depositing a 40 µm-thick SU-8 pattern on a Si 4-inch wafer, followed by a second 90 µm-thick SU-8 layer on top of the first, which corresponds to the worm chamber. These two SU-8 layers are shown in Figure S3A as layer 1 and layer 2, respectively. Then, this master was used as a mold for PDMS casting. A liquid PDMS mixture (10:1 base to curing agent weight ratio) was degassed, poured onto the mold and cured at 100 °C for 1 h. Finally, after de-molding, each PDMS chip was diced, the inlets and outlets were punched into the PDMS and each chip was bonded to a 26 mm x 76 mm glass slide, using air-plasma surface activation. Hereafter tubings were plugged in the PDMS holes. The microfluidic chip was integrated onto an inverted microscope (Axio Observer, Zeiss) equipped with a precisExcite High-Power LED Illumination system (Visitron, Puchheim, Germany) for bright field imaging. A 5x/0.12 A-Plan Zeiss objective was used. Videos were recorded with a Pixelink B681 CMOS Camera. The microfluidic operations were controlled using Nemesys syringe pumps (Cetoni, Korbussen, Germany).

For the worm mobility assay, a mixed population of worms was suspended in 200 µl of S medium and aspirated into a tubing connected to the device. With a *Q* ranging from 200 to 800 nl s^{-1}, the unsynchronized worms were injected in the microfluidic chamber from inlet In1 (Figure S3B). Worm synchronization was automatically performed hydrodynamically through Out1. This outlet filter was tailored with 60 µm wide and 800 µm long channels, in such a way that only adult worms were retained in the chamber, while younger worms were washed away by the flow. The number of worms retained in the chamber (median 10 worms, 1st- 3rd quartiles 7- 12 worms, 30 measurements) was controlled by adjusting the volume of the injected solution, from 5 µl up to 20 µl. After worm synchronization, Out1 was closed and Out2 opened (Figure S3C). The worms were then exposed to a constant *Q* of 30 nl s^{-1} of S medium, without any drug or glucose, from In2 for 5 min, to remove the residues of OP50 bacteria and any metabolic waste from the chamber, and also to expose the worms to a basal level of hydrodynamic conditions. The tailored filters cast on the Out2 side, *i.e.* 30 µm wide channels, prevented the adult worms from escaping. At that point, the flow was stopped, and the first video was recorded (5 sec, 20 fps). After the first recording, the second solution (S medium without/ with 200 mM glucose and without/ with the appropriate concentration of dynasore) was injected for 20 min, at *Q*= 30 nl s^{-1}, from In3 (Figure S3D). Finally, the second video was recorded. In order to avoid any effect of the flow on worm motility, the flow was stopped for 3-5 min before starting both recordings (Figure S3E). The time sequence of the worm mobility assay is shown in Scheme S1.



Scheme S1: Time sequence of the worm mobility assay.

Each video was converted to grayscale and processed using a custom routine written in IgorPro (WaveMetrics, USA) to extract a mobility score. The data processing routine is summarized in Figure S4. First, the area of interest, corresponding to the central chamber, was selected and extracted from each frame. Each of these reduced frames was then converted to a binary image using a user-defined threshold. This threshold was adjusted so that the shape of the worms appears clearly, but most the other features, such as debris or the edges of the PDMS channels, are cancelled. The same threshold was used for each frame of the video. The number of white pixels, corresponding to a '1' value, were counted for each frame and averaged over the duration of the video, thus providing a measure of the fraction of the image that is occupied by the worms. In a second step, the binary video was differentiated using the forward difference method. The number of non-null pixels, indicative of worm motion, was counted for each frame, and these values were averaged over the whole video. This value, describing the rate of change of the frames and therefore the worm activity, was normalized to the average worm area computed above, thus providing the mobility score for this video. The values of interest, reported in Figure 4, are actually the variation of this mobility score, before and after the treatments, defined as the ratio of the score after the treatment to the score before the treatment. To prevent from overloading the memory of the computer, the algorithm was typically run over 3 s of the video. The rest of the file was used to ensure the behavior of the worm was consistent over the duration of the video. To guarantee the relevance of the computed mobility

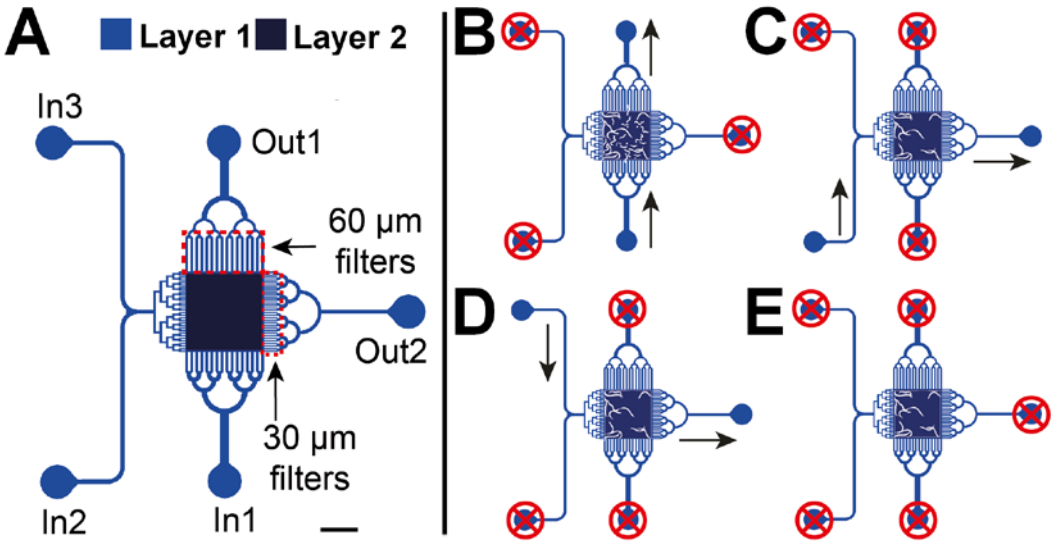


Figure S3: Design and operations of the microfluidic device. A- Schematic of the microfluidic device, comprising the 130 µm thick culture chamber, the 3 inlets (In1, In2 and In3), and the 2 outlets (Out1 and Out2), which are 40 µm thick. Out1 and Out2 are fitted with filters, respectively 60 µm and 30 µm wide, tailored to retain the adult worms in the chamber (scale bar= 1 mm). B- A mixed population of worms is injected from In1 into the culture chambers, where adults are retained, while younger worms are filtered out through Out1. C- Fresh S medium is injected from In2 in order to remove debris and provide clean medium to the worms. D- The treatment is given to the worms through In3. E- For 3-5 min before the recordings, no flow is provided to the worm chamber.

value, it was important to ensure that the worms were not overlaid or crowded, which would have impaired the computation of the worm area, for instance. This was facilitated by injecting only a few worms in the chamber. Also, by stopping the flow, it allowed the worms to swim freely and therefore to spread evenly in the chamber. Finally, the videos were captured at a point where the worms were found to be isolated from each other. The time sequence of the worm mobility assay is shown in Scheme S1.

S1.9 Total glucose measurement in worms

An unsynchronized culture of N2 *C. elegans* was harvested from its culture plate and suspended in S medium. The population was centrifugated at 5000 RPM for 3 minutes and rinsed in water twice, and then resuspended in S medium and incubated for 2 hours to allow for the purge of the intestinal tract. The worm suspension was then split between 9 individual wells of a 24-well plate (230 µl of solution per well, corresponding to ~2,700 worms per well). Microscopic observation confirmed that comparable worm populations were introduced in each well. Each well was supplemented with 230 µl of S medium, without or with glucose or dynasore, so that 3 wells contain 200 mM glucose, 3 wells contain 200 mM glucose and 10 µM dynasore and the last three wells are controls and only contain S medium. The plate is then incubated for one hour. The content of each well was then harvested and placed in an individual Eppendorf tube, so that each condition was described by 3 samples. Each sample was washed 3 times with DI water, as described above, and the worm population was resuspended in 100 µl 2 mM HCl and heated to 95°C for one hour. This process was used to lyse the worms and hydrolyze the glycogen to obtain the total glucose content. At the end of the heating, no worm could be observed in the solution. The acid was then neutralized with 2 mM NaOH (pH~ 7) and the lysates where kept at -20 ˚C.
To measure the glucose content, the lysates were diluted 10x in PBS. An electrochemical glucose sensor, prepared as described above was used to quantify the glucose levels by placing it directly in the vial containing the diluted sample, *i.e.* not using the microfluidic system.

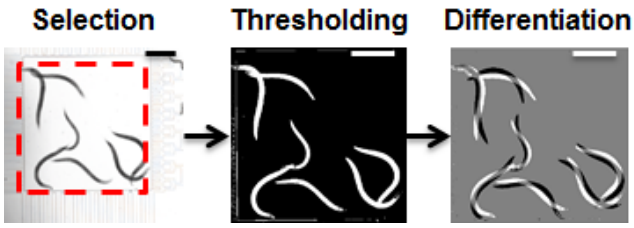


Figure S4: Data processing routine for the worm mobility assay. Selection- Each frame is extracted from a video, and the area of interest is selected. The surrounding area is cropped from the frame to reduce file size. Thresholding- each frame is converted to a binary image with a user-adjusted threshold, so that the area corresponding to the worms is isolated. Differentiation- the time differential between successive binary frames is computed. On each panel, the scale bars show 0.5 mm.

S1.10 Data processing

As detailed elsewhere,[2] the dead-volume time T_{DV}, *i.e.* the delay between the injection of a plug of analyte and the time when it is detected by the potentiostat, is subtracted from the time axis, so that 0 s corresponds to the time when the stimulating buffer enters the detection chamber. In our setup, T_{DV} was typically in the 60 s to 100 s range.
The traces were filtered with a binomial filter, over 11 points. The baseline is fitted with a decaying exponential and subtracted from the signal and converted to concentration using the calibration data. The section of the recorded data normally corresponding to the presence of insulin buffer in the chamber is not taken into account in the background fitting. The main parameter extracted from these data is the decrease in glucose concentration at t= 250 s, $\Delta[glucose]_{250s}$, which corresponds to the amount of glucose absorbed by the cells from the 5 mM buffer. Where applicable, the data are reported as average ± standard deviation (SD), and the number of individual measurements is described using the notation *n*. Comparisons between two different datasets were performed with a two-tailed Student's t-test, or with a 1-way ANOVA in the case of more

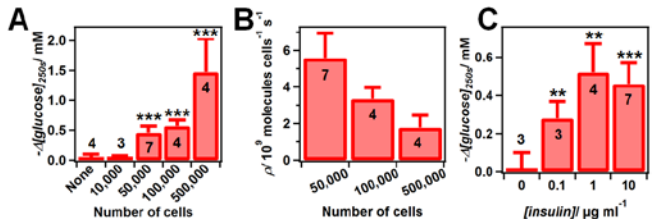


Figure S5: Optimization of the glucose uptake assay. A- Effect of increasing number of cells on the paper patch on $\Delta[glucose]_{250s}$ (10 µg ml^{-1} insulin, Q= 1 µl s^{-1}). B- The uptake rate per cell ρ was computed from the data shown in A-. C- Effect of insulin concentration on glucose uptake (50,000 cells, Q= 1 µl s^{-1}). The number of experiments n is shown in each bar. **: p<0.01; ***: p<0.001 in comparison to control (i.e. no cells or no insulin)

than 2 datasets, followed by post hoc two-tailed Student's t-tests.

S2. Effect of cell number on glucose uptake

As shown in Figure S5A, the number of C2C12 seeded on the paper patch was modified. As expected, the magnitude of glucose uptake increased with the number of cells (p= 1.5 10^{-8}, one-way ANOVA). Additionally, no clear signal could be recorded for 10,000 cells, but the glucose decay was easily quantifiable for 50,000 cells (p= 9.2 10^{-5} for a two-tailed Student's t-test). As a consequence, 50,000 cells were seeded on the paper patches in the following tests. In a previous report focusing at dopamine exocytosis from neuron-like PC12 cells,[2] we have found that the response of the cells-on-paper system scaled well with the number of cells seeded on the paper patch. In contrast, as shown in Figure S5B, ρ, the number of glucose molecules captured per cell per second at t= 250 s was dependent on the number of cells introduced into the system. More specifically, the activity of each cell decreases as more cells are seeded. A possible explanation for this is that the high cell density case depletes strongly the glucose in the buffer, thus preventing further uptake. In any case, this observation shows that some negative interactions or feedback loops can occur when a system is built from individual cells, and that careful characterization can be needed when a bottom-up approach is considered for biological samples.

S3. Effect of insulin concentration

The response of the system to different insulin concentrations was also tested (Figure S5C) for 50,000 cells. Increasing concentrations were found to increase the magnitude of glucose uptake (p= 1.6 10^{-4}, one-way ANOVA). An insulin concentration of 1 µg ml^{-1} was found sufficient to induce a maximal response. This level of insulin was therefore chosen for the following experiments. The concentration needed to induce half of the maximal concentration was ~0.1 µg ml^{-1}, which corresponds to ~15 nM. This value is in good agreement with the one reported using a scintillation assay.[11]

S4. Worm mobility assay

Tables S1 and S2 show the p-values obtained for the post-hoc Student's t tests run on the datasets shown in Figures 4D and E. Furthermore, the reversibility of dynasore was investigated. To this purpose, a mobility assay (n= 1 chip, 11 worms) was carried out with 0 mM glucose and 1 µM dynasore. After the 20 min of exposure to the drug, the mobility ratio was measured as 0.65. At this point, S medium only was injected once again in the chip to remove dynasore, in the same conditions. Another video was taken after 20 min of dynasore recovery, and the mobility ratio, in comparison to the video recorded before the exposure to dynasore, was 0.81. A recovery in mobility of 24% was therefore achieved upon dynasore washing, hence indicating that the effect of the drug can be reversed. The recovery though was not complete, possibly because of worm starvation on-chip or stress.

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Table S1: Summary of the *p*-values obtained for the post-hoc Student's t test performed on the worm mobility assay (Figure 4D). The bottom row lists the number *n* of chip used for each condition.

		0 mM glucose						200 mM glucose					
	[dynasore]	0 nM	1 nM	10 nM	100 nM	1 µM	10 µM	0 nM	1 nM	10 nM	100 nM	1 µM	10 µM
0 mM glucose	0 nM		0.6007	0.2333	0.3531	0.2575	0.0282	**0.0000**	**0.0080**	**0.0025**	**0.0001**	**0.0017**	0.0120
	1 nM			0.1710	0.2402	0.1672	0.0279	**0.0000**	0.0114	**0.0038**	**0.0002**	**0.0034**	0.0111
	10 nM				0.4598	0.9756	0.1316	**0.0009**	0.0618	0.0125	**0.0006**	0.0129	0.0688
	100 nM					0.5029	0.0390	**0.0000**	**0.0079**	**0.0023**	**0.0001**	**0.0011**	0.0183
	1 µM						0.1275	**0.0015**	0.0725	0.0110	**0.0004**	0.0145	0.0629
	10 µM							0.3261	0.8876	0.1404	**0.0087**	0.2200	0.8185
200 mM glucose	0 nM								0.3103	0.0279	**0.0001**	0.0997	0.5449
	1 nM									0.0900	**0.0050**	0.1343	0.9069
	10 nM										0.0921	0.4871	0.1500
	100 nM											0.0265	**0.0061**
	1 µM												0.2737
	10 µM												
n		3	3	3	3	4	3	7	3	3	5	3	4

Table S2: Summary of the p-values obtained for the post-hoc Student's t test performed on the worm mobility assay (Figure 4E). The bottom row lists the number *n* of chip used for each condition.

		0 mM glucose			200 mM glucose			200 mM L-glucose		
	[dynasore]	0 mM	100 nM	10 µM	0 mM	100 nM	10 µM	0 mM	100 nM	10 µM
0 mM glucose	0 mM		0.2333	0.0282	**0.0000**	**0.0001**	0.0120	0.0693	**0.0071**	0.0167
	100 nM			0.1316	**0.0009**	**0.0006**	0.0688	0.4785	0.0706	0.1477
	10 µM				0.3261	**0.0087**	0.8185	0.2187	0.9274	0.6163
200 mM glucose	0 mM					**0.0001**	0.5449	**0.0043**	0.1114	0.0289
	100 nM						**0.0061**	**0.0002**	**0.0029**	**0.0020**
	10 µM							0.1141	0.7083	0.4290
200 mM L-glucose	0 mM								0.8518	0.9372
	100 nM									0.5325
	10 µM									
n		3	3	3	7	5	4	5	3	3