Supporting Information

Methods

1. Focused ultrasound system and acoustic characterization

The FUS system that was designed and built in house is composed of an air-backed spherically curved transducer (frequency: 1.025 MHz; diameter/radius of curvature: 4/3 cm) that is attached to a water filled 3D printed cone with an exit window made of thin Mylar membrane (**Fig. 1A**). The system is mounted on a 3D positioning system and target localization in X-Y directions (left/right, superior/inferior) is performed with needle guidance (**Fig. 1A**).

The FUS transducer spatial profile was modeled using the Field II program (**Fig. S1**). The experimental spatial characterization of the FUS was performed with a 0.2 mm hydrophone (ONDA, HNC-0200, Sunnyvale, CA, USA) that was attached to a motor-driven 3D scanning system (Velmex, 3 axis UniSlide System MSU2004, Bloomfield, NY, USA). We also measured the efficiency of the transducer, by comparing the electrical power input to the FUS, which was measured with an RF power meter (Agilent, E4419B RF Power Meter, Santa Clara, CA 95051USA) to the acoustic power output, which was determined with the radiation force balance method using a digital balance (Mettler-Toledo, Dual Range XS205, Columbus, OH, USA). The FUS transducer was 56% efficient.

Ultrasound gel and plastic cranial windows ensured good acoustic coupling with the targeted region (< 5% inertial losses). The -6dB transverse and axial focal region of the FUS system is 2 mm and 9 mm respectively.

2. Experimental protocol.

All animal procedures were performed according to the guidelines of the Public Health Policy on the Humane Care of Laboratory Animals and approved by the Institutional Animal Care and Use Committee of Massachusetts General Hospital. Human *HER2*-amplified and estrogen dependent BT474 breast cancer cells that were genetically modified to express green fluorescent protein were stereotactically implanted in the brain of mice with cranial windows, as previously described (1, 2). After cell implantation, tumor growth was monitored using Gluc measurements, as described before (3). When tumors reached a size of \sim 20-40 mm³, we performed BTB disruption using FUS exposures (10 msec bursts, every 1 sec for 2 min) and concurrent i.v. administration of

Fig. S1. Comparison of model predications with experimental profiles of the focused ultrasound system.

microbubbles (20 µl/kg, Definity, Lantheus Medical Imaging) **(Fig. 1B)**. A 480 kPa peak negative pressure (based on absolute characterization of the FUS system was used throughout the present study. To cover the entire tumor and its periphery we performed four non-overlapping sonications (X-Y directions).

Shortly after sonication, the pharmacokinetics and intratumoral uptake and clearance of the autofluorescent chemotherapeutic agent doxorubicin was measured for 20 minutes using intravital multiphoton microscopy (4). Briefly, the animals were anesthetized and their heads were immobilized on a motorized x-y stage (H101A ProScan II, Prior Scientic) and the tumor margin was localized by intravital multiphoton microscopy. One area of interest was defined for sequential imaging of doxorubicin uptake, based on local vessel architecture and presence of tumor cells. Prior to injection of doxorubicin, one z-stack image was acquired at intervals of 1.38µm, spanning a depth of 100-200 µm. One plane in the vicinity of 50% depth of the z-stack image was chosen and used for subsequent X-Y serial imaging. Three to four sequential images were acquired at 20 sec intervals before intravenous injection of 150µl doxorubicin at a concentration of 7 mg/ml over 30 sec (7.5 mg/kg). Following administration of doxorubicin, continuous sequential image acquisition at 20 sec intervals was continued for a total of 40-50 X-Y images. 8 animals were used in total (#4 FUS-treated and #4 non-FUS treated). For consistency in the notation of the experiments/modeling, Cv is the doxorubicin intensity/concentration in the vessel, Ce is the doxorubicin intensity/concentration in the extracellular/interstitial space, and Ci is the doxorubicin intensity/concentration that has been internalized in the cells.

In separate experiments the antibody-drug conjugate ado-trastuzumab emtansine (T-DM1) (5 mg/kg) was administered i.v. immediately after the sonications. The animals were sacrificed at 4 hours or at 5 days post treatment and the intratumoral distribution of T-DM1 in the brain tumors was determined through tissue staining for human IgG and quantification of fluorescence, as previously described (1).

3. Image analysis.

To analyze the data from the intravital imaging, small image motion artifacts were corrected using the image registration function "imregtform" Matlab

(Matlab2016b, Mathworks, Natick, MA) that had as input the local vessel architecture. After registration the vessels were segmented using semiautomatic thresholding of the doxorubicin images, which used as vessel marker, and the doxorubicin kinetics were determined in a 20 x 20 pixel region of interest (ROI) in the vessel and interstitial space (**Fig. 2A**). The drug penetration measurement of doxorubicin was performed by determining the drug profile perpendicular to the vessel using maximum intensity projection across the series of images. The doxorubicin intracellular kinetics were determined on segmented cells. Cell segmentation was performed using the "roipoly" function of Matlab from the thresholded images.

Brains were collected and fixed at the specified time points post-T-DM1 injection (4 hours and 5 days), then embedded in OCT and frozen. Tissues were sectioned (10 µM) and immunostained for CD31 (Millipore, MAB1398Z, mouse mAb, 1:200) and human IgG (Invitrogen, Cat# A-21091, 1:100) as previously described(1). Stained and mounted tissues were imaged on a fluorescent slide scanner (TissueFAXS, Ragon Institute of MGH, MIT, and Harvard) using a 20 x objective (pixel:micron ratio = 0.5). Penetration distance of T-DM1 from vessels was characterized as previously described (1). Area fraction of T-DM1 was quantified using ImageJ software.

4. Single cell doxorubicin kinetics analysis

Magnified images of doxorubicin uptake by endothelial cells (EC) in a brain tumor after FUS-BBB/BTB disruption is shown in **Fig. S2.**

5. Overview of mathematical models for drug transport.

Our mathematical modeling framework simulates the convective and diffusive transport of anticancer agents through the blood stream and across the endothelium into the interstitial space of a tumor along with their uptake by tumor cells. To quantify different tumor micro-environmental drug transport parameters (e.g. BTB diffusion coefficient, vessel wall effective porosity, etc.), we use a simplified tumor cord geometry and experiment-specific parameter-fitting procedures based on the experimentally determined interstitial drug PK of the two different therapeutic agents. The choice of a tumor cord geometry allows us to keep the multidimensional fitting procedures computationally tractable. Then, to study the influence of the spatial structural heterogeneity

Doxorubicin / cancer cells (GFP)

Fig. S2. Doxorubicin uptake by endothelial cells (EC) in a brain tumor after FUS-BBB/BTB disruption. A) Representative sequential images from intravital multiphoton microscopy of doxorubicin in the breast cancer BM model after FUS-BTB disruption. Red: doxorubicin autofluorescence; green: GFP-positive BT474-Gluc cancer cells. B) Magnified image to demonstrate uptake by three segmented endothelial cells. C) Segmented endothelial cells and vessel wall. Color scale shows significant doxorubicin retention by the endothelial cells.

(e.g. vascularity) of the brain tumor microenvironment on the interstitial drug transport after FUS-BTB disruption, we reformulated our model using a vascular network geometry and the previously fitted model parameters.

For the tumor cord geometry model, the computational domain include luminal, vascular wall and interstitial subdomains (**Fig. 4B**). A formal description of the model along with a detailed discussion of the initial and boundary conditions

6. 2D tumor cord model for doxorubicin and T-DM1 interstitial pharmacokinetics

In this section, we describe the details of the Physiologically Based Pharmacokinetic (PBPK) model using 2D tumor cord model. The main processes to be described are the diffusive and convective transport of the agents through the blood stream and across the endothelium into the interstitial space along with their uptake by tumor cells. **Table S2** provides a list of notations used in this work. The computational domain, which is based on the two-dimensional planar model, includes luminal, vascular wall and interstitial subdomains (**Fig. S3**). The luminal domain, with one inlet and one outlet, has a diameter of 30μm, and the vessel wall thickness is 5μm (6). The whole domain is discretized using triangular elements with an average mesh edge length of 3um that is considered are provided below (**SI methods, Section 6**). The geometry of vascular network model is generated based on a previously validated percolation method to mimic the tumorlike vascular structure (**Fig.5A**) (5). A formal description of the model along with a detailed discussion of the initial and boundary conditions considered are provided below (**SI methods, Section 7**).

refined around the vascular wall (mesh edge length 1μm along the vascular wall).

For the flow problem, we assume blood and interstitial fluid to be homogeneous, Newtonian, and incompressible fluids with constant viscosity, μ. Inside the vessel, flow is modeled with the Stokes equation. The flow through vascular wall and interstitial space, which is modeled as isotropic porous medium (with porosity $ε_v$ and $ε_i$ respectively), is described by the Brinkman equation (with a characteristic hydraulic conductivity K). This approach was selected as it provides more flexibility in defining the boundary conditions, as compared to Darcy's law (7). Boundary conditions are as follow: constant velocity, V_{rbc}, at the inlet, a reference pressure at the luminal outlet of 5 mmHg, no-slip velocity at the solid interfaces of the vascular wall subdomain, and a pressure of 1 mmHg at the interstitial outlets,

Fig. S3. Mathematical model for doxorubicin and T-DM1 interstitial pharmacokinetics. A) A summary of governing equations and boundary conditions used in the specific subdomain in the mathematical model. B) Schematic illustration of the processes included in the model. C) Mathematical model formulation for cell kinetics of doxorubicin and T-DM1. D) A notation table with transport parameters.

where V_{rbc} is a model parameter (Table S3). Continuity of the pressure and velocity fields is enforced across the subdomain boundaries. V_{rbc} was experimentally measured via particle velocimetry of fluorescently labeled red blood cells (8).

For the anticancer agent transport problem, we define the extracellular concentration of any agent as a continuous scalar field, Ce, relative to a peak concentration in the bloodstream inside the vessel. The agent undergoes convection (based on the previously described flow problem), diffusion, and cellular uptake in the interstitial space. This process is modeled as a convection-diffusion problem in the luminal and vascular wall subdomains with diffusion coefficients D_b and D_v , and a reaction-convection-diffusion problem in the interstitial subdomain with diffusion coefficient Di and an agent-specific reaction term. Boundary concentrations profiles at the luminal inlet, which are experimentally measured drug concentration profiles for doxorubicin (**Fig. 2B**) and constant for T-DM1, and outflow (Neumann boundary conditions) at the rest of boundaries of the computational domain.

The model accounts for the doxorubicin and T-DM1 cellular uptake in the vascular wall and interstitium (reaction term in the reactionconvection-diffusion) as follows. For doxorubicin, cellular uptake in the vascular wall and interstitial space is assumed to undergo reversible cellular uptake (9) and a non-reversible intracellular drug binding to the cell nucleus (extension to the classical model to account for the binding of doxorubicin to DNA), which define two scalar fields for the intracellular concentration, C_i , and bound concentration, Cb, respectively (**Fig. S3**). The reversible drug uptake is modeled based on

Michaelis-Menten kinetics for a given maximum binding rate, porosity, and Michaelis-Menten kinetics constant (9, 10). The agent binds to the nucleus at a constant rate. The T-DM1 kinetics account for agent binding/unbinding to cancer cells/matrix and non-reversible internalization into cancer cells in the interstitial space only given constant binding, unbinding, and internalization rates and tissue porosity (6, 10, 11), which define two additional scalar fields for the bound and internalized concentrations, C_b and C_i , internalized concentrations, C_b and respectively. A summary of the model governing equations, along with the specific subdomains they are applied to, and the imposed boundary conditions are provided in **Fig. S3**.

The parameters of the mathematical model were fitted to the experimental data using a numerical optimization procedure based on an agent-specific objective function and initial values for the model parameters taken from the literature, see **Table S3** and **S4** for doxorubicin and T-DM1, respectively. For doxorubicin, we defined the objective function as the L2-norm of the difference between the experimentally measured pharmacokinetics at a given experiment-specific distance from the vessel wall and the output of the model at the same distance. The experimentally measured doxorubicin pharmacokinetics and equivalent mathematical model output are shown in **Fig. 4B**. Due to the unavailability of experimentally measured T-DM1 pharmacokinetic measurements, we devised a procedure to recover T-DM1 pharmacokinetics in the interstitium based on the experimentally determined T-DM1 penetration data.

We assumed that T-DM1 fluorescence is detectable for relative concentrations above 0.05. This gives us a bound concentration value for any given penetration distance. We then assumed that the concentration goes from 0 to 0.05 over a period of 4 hours and that the dynamics are governed by the analytic solution of a one-dimensional advection-diffusion problem where the TDM1 concentration is given for a distance *x* from the vessel and time *t*:

$$
C_b(x,t) = \frac{C_0}{2} \operatorname{erfc}\left(\frac{x - ut}{\sqrt{4D_x t}}\right), \qquad \textbf{[S1]}
$$

where $C_0=0.05$, u is the interstitial flow velocity obtained from the matching doxorubicin model (non-FUS vs FUS), $D_x=4 \times 10^{-2}$ μ m²/s is a reference diffusion value, and *erfc* is the complementary error

function. The T-DM1 profiles based on equation [1] for control (no-FUS) and FUS treated along a schematic of the experimental methodology described above are shown in **Fig. 4B**.

This model fit procedure was performed for each set of experimental data available, *i.e.* four repetitions of each experiment class (doxorubicin in non-FUS, doxorubicin after FUS, T-DM1 in non-FUS, T-DM1 after FUS). Statistics in **Table 1, Table 2,** and **Fig. 4** are computed over these repetitions.

The model considers that BTB disruption occurs immediately after the ultrasound exposure (sonication) and remains open for 4 hours after the sonications (12–17). Molecular weight dependent closing of the barrier was not included in 2D tumor cord modeled, as it is expected to have a marginal impact on doxorubicin due to its fast clearance (10 min), whereas in T-DM1 the interstitial drug distribution was measured at 4 hours, hence effective values were used. Systemic agent clearance from the blood plasma and antibody degradation in the tumor tissue were ignored in the current model.

7. Vasculature network model for doxorubicin and T-DM1 interstitial pharmacokinetics

To study the impact of tumor heterogeneity in interstitial transport, we expanded the 2D tumor cord model to a two-dimensional vascular network based model. The vascular network with one inlet and five outlets is generated using the previously validated percolation method for the generation of synthetic tumor-like vascular networks (18), shown in **Fig. 5A**. The computational domain consists of two subdomains, vasculature (average diameter 15 µm) and interstitial space. The whole domain is discretized using triangular elements with an average mesh edge length of 3μm. The mesh is refined around the vascular wall (average mesh edge length 0.8μm along the vascular wall). Inside the vessel, blood flow is modeled following the approach employed in the 2D tumor cord model. Transvascular fluid transport is modeled using Starling's law and assuming no osmotic pressure difference (6). The rate of transvascular fluid flow is defined as:

$$
J_f = L_p (P_v - P_i), \qquad [\textbf{S2}]
$$

where $L_p = \frac{\varepsilon_v r_0^2}{8 \mu d}$ is the hydraulic conductivity of the vessel wall, P_y and P_i are vascular and interstitial pressure respectively, ε_v is the void fraction at vessel wall, r_0 is the pore radius and d is the vessel wall thickness. The flow inside interstitial space is modeled with Darcy's Law. For boundary conditions, we define a constant pressure of 25 mmHg at the inlet and 5 mmHg at the luminal outlet, and zero pressure at the interstitial outlets (19).

The anticancer agent transport in the luminal subdomain is modeled as a convection-diffusion problem, and a reaction-convection-diffusion problem in the interstitial subdomain, as described for the 2D tumor cord model. For transvascular anticancer agent transport, we first calculate the Péclet number across the vessel wall

$$
P_e = \frac{L_p (P_v - P_i)(1 - \sigma_f)}{P}, \qquad \textbf{[S3]}
$$

where σ_f is the reflection coefficient and P is the vascular diffusive permeability,

$$
\sigma_f = 1 - W, P = \frac{H D_v}{d}, \quad \textbf{[S4]}
$$

and H and W are the diffusive and convective hindrance factors that depend on the relative size of the particles to the pores (20).

$$
H = \varphi (1 - 2.1044\alpha + 2.089\alpha^3 - 0.948\alpha^5),
$$

\n
$$
[\mathbf{S5}]
$$

\n
$$
W = \varphi (2 - \varphi) \left(1 - \frac{2}{3} \alpha^2 - 0.163\alpha^3 \right),
$$
 [S6]

where α is the particle size to pore size ratio and $\omega = (1 - \alpha)^2$.

The rate of drug transvascular transport I_s across the vessel wall is modeled using Starling's approximation (6, 20). When the Péclet number is less than or equal to 1, the Kedem-Katchalsky equation is used

$$
J_s = J_f \left(1 - \sigma_f\right) \frac{\Delta C}{\ln(C_v/C_e)} + \Delta C, \quad \text{[S7]}
$$

where ΔC is the anticancer agent concentration difference across the vessel wall. When the Péclet number is greater than 1, the Patlak equation is used

$$
J_s = J_f \left(1 - \sigma_f\right) \frac{C_v e^{Pe} - C_e}{e^{Pe} - 1}, \quad \textbf{[S8]}
$$

For boundary condition, we use agent-specific concentrations profiles at the luminal inlet as described before, outflow (Neumann boundary condition) at the luminal outlet and the concentration at the rest of the boundary is set to be zero.

Fig. S4. Pressure distribution and transvascular pressure difference with varies pore sizes. A) Qualitative demonstration of pressure field and transvascular pressure difference for doxorubicin with pore diameter of 10m and 400nm. Quantification of transvascular pressure difference as a function of vessel wall pore diameter for the percolation model B) Doxorubicin C) T-DM1. Quantification of drug transvascular flux as a function of vessel wall pore diameter D) Doxorubicin E) T-DM1

In addition, in the case that FUS is applied, to model the blood brain barrier closure, we incorporate an exponential decay for porosity ε _v for both agents and vessel wall diffusive coefficient D_v for doxorubicin to baseline value

$$
\varepsilon_v = C_{\varepsilon_v} e^{-Rt} + B_{\varepsilon_v}, \qquad \textbf{[S9]}D_v = C_{D_v} e^{-Rt} + B_{D_v}, \qquad \textbf{[S10]}
$$

where R is the constant that describes the rate of exponential decay, which is extracted from the decay of measured MRI contrast agent transfer coefficient reported by Park, et al (21). B_{ε_n,D_n} are the baseline value that we fitted with the control experiments using the 2D tumor cord model. C_{ε_n,D_n} are the values that we fitted using the FUS experiments.

To study influence of vascular pore size on transvascular transport, we performed simulations using vascular network based model with an average of previously fitted transport parameters (**Table 1 and 2**). The transvascular drug transport is defined as transvascular mass flux normalized by the average transvascular concentration difference and it is calculated at a certain region of interest in the vascular network (19) (**Fig. 5B**). **Fig. S4. A** indicates an elevated interstitial fluid pressure after FUS-BBB/BTB disruption and a transvascular pressure difference drop as pore diameter increases for doxorubicin. **Fig. S4. B-E** shows the transvascular pressure difference and drug transvascular flux for the two different agents as a function of pore diameter. Both pressure difference across the vessel wall and drug transvascular flux are higher after FUS-BBB/BTB disruption as compared to control group (non-FUS). Then we conducted sensitivity analysis to study the relative importance of the different transport parameters and intracellular drug kinetics using different administration protocols with the experiment-specific and drug-specific (fitted) model parameters (**Fig. 5C, Table 1 and 2**). Other parameters used in the vascular network model is shown in **Table S5**.

Fig. S5. A) Simulated doxorubicin administration using the Weibull probably distribution function. B) Intracellular drug kinetics for bolus vs infusion administration

Fig. S6. A**)** T-DM1 intracellular drug kinetics for different at low (left) and high (right) perfusion regions in the percolation model. B) T-DM1 intracellular drug kinetics 10 fold higher dose.

8. Modeling doxorubicin administration protocol

The bolus administration experimental data were fitted using the analytical form of the Weibull probably distribution function (PDF)

$$
f(x) = \frac{kC}{\lambda} \left(\frac{x}{\lambda}\right)^{k-1} e^{-\left(\frac{x}{\lambda}\right)^k}, \quad [S11]
$$

Varying the different parameters, C, λ, and k, allowed us to control independently the shape and the scale of the vascular drug concentration profile, while warranting a constant dose (area under the curve) as we move from bolus to infusion. Good fitting with the experimental values was obtain for C=2.72, λ=2, and k=1.4. By varying λ different drug administration protocols can be attained (**Fig. S5A**). These curves were then used as input to the numerical simulations (time-dependent drug concentration profiles at the luminal inlet). **Fig. S5B** shows the intercellular doxorubicin concentration as a function of time for the different administration protocols based on Weibull PDF.

9. Model parameter fit.

The parameters of the mathematical model were fitted using a numerical optimization procedure based on initial reference values taken from the literature (**Table S3 and S4**) and an agent-specific objective function. Sixteen models were fitted comprising four repetitions of each class of experiment: non-FUS vs FUS and doxorubicin vs T-DM1. For doxorubicin, we took advantage of experimentally determined doxorubicin kinetics measured 20 µm from the vessel wall to define the objective function as the difference between this measurement and the output of the model at the same point. To quantify the rate of cellular transmembrane transport from the single cell kinetic measurements of more than one cell type (**Fig. 6**), we redefined the objective function to each cell type in turn and fitted for changes in the rate of cellular transmembrane transport by assuming homogeneous well-mixed cell populations (22). The ratio of the endothelial cell populations was set to be 75% of the total vasculature cell population (23). For T-DM1, we reused the agent-independent model parameters $ε_v$ and $ε_i$ (fitted values from doxorubicin model), and fit the rest. Due to the unavailability of experimentally measured T-DM1 pharmacokinetic measurements, we devised the procedure described above (**SI methods, Section 6**) to recover T-DM1 pharmacokinetics in the

interstitium based on the experimentally determined T-DM1 penetration data.

10. Sensitivity analysis

For both agents, we performed sensitivity analyses for the 16 fitted models (4 per case) in order to compare the sensitivity of each model to changes in each of their parameters as well as differences before and after FUS treatment using vasculature network model. Mathematically, we numerically approximate the derivative of the intracellular agent concentration C_i with respect to any parameter P_i , *i.e.* $\frac{\partial C_i}{\partial P_i}$. To be able to compare the sensitivities to different parameters and also across different experiment classes we employed the following normalized measure of sensitivity $S =$ σ_i $max(C_i)$ σc_i $\frac{\partial C_l}{\partial P_l}$, where σ_l is the standard deviation of P_i across the four repetitions of each experiment class and $max(C_i)$ is the peak intracellular concentration measured. S should be interpreted as the relative change in C_i for a given change of P_i that is equally likely for all i.

11. Numerical implementation

The simulations were performed using the commercial package COMSOL (version 5.2a, Burlington, MA, USA), which uses the finite element method to solve the partial differential equations in the model numerically. The computational domain for the 2D tumor cord model and the percolation model was discretized with an average element size of 3μm, and with the grid being refined near the vessel walls in order to be able to capture a larger gradient. For optimization, we employed the Nelder-Mead method with a maximum number of iterations of 1000. For doxorubicin, duration of the simulation was dictated by its clearance that according to the multiphoton microscopy measurements was approximately 12 mins. For T-DM1, duration of the simulation was dictated by time point of immunostaining (4 hours).

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Table S1. Summary of studies reporting the impact of FUS-BBB/BTB disruption on the delivery of anticancer agents in murine in brain

tumor models. Data form the first clinical trial have also been included. Note that the delivery of some nanoparticle formulations reported in the literature was magnetically or acoustically actuated.

^a All models are orthotropic; **^b** Magnetic actuation of the drug into the tumor interstitial space after FUS-BBB/BTB disruption; **^c** The drug might have been propelled into the tumor by the microbubble collapse after the application of FUS. Review Criteria: Information for the data in Table I was compiled by searching the PubMed and Web of Science databases for articles published before March 1st 2018, including early-release publications. Search terms included "focused ultrasound brain tumor", "ultrasound blood tumor barrier disruption", "ultrasound blood tumor barrier disruption", "focused ultrasound blood brain barrier glioma", and "focused ultrasound blood tumor barrier glioma". Full articles were checked for additional material when appropriate, and articles that cite key publications were checked.

Table S2. Notations

Table S3. Doxorubicin model parameters

Table S4. T-DM1 model parameters.

Table S5. Vascular network model parameters.

