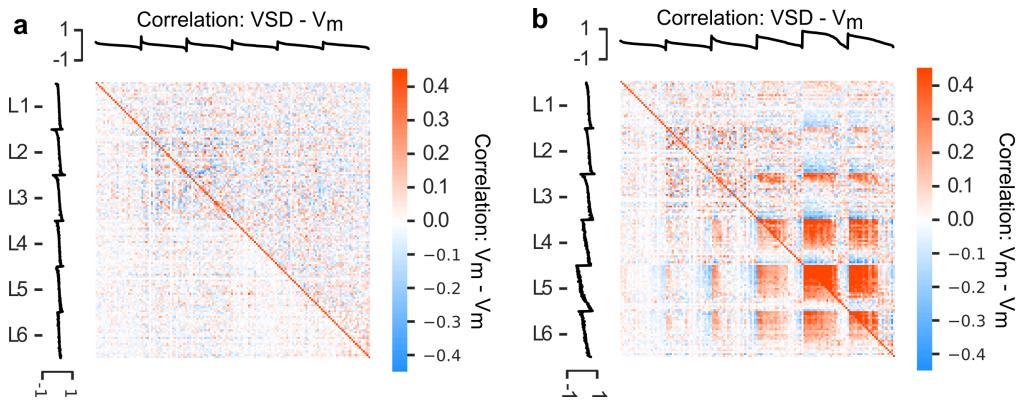


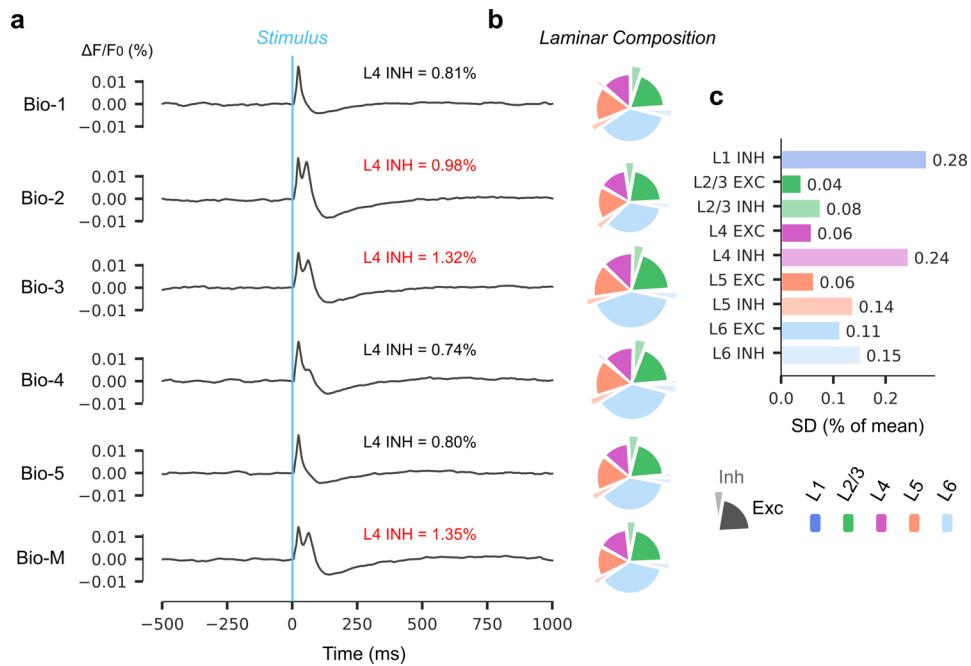
Supplementary information

Fig. 1: Pairwise V_m correlations



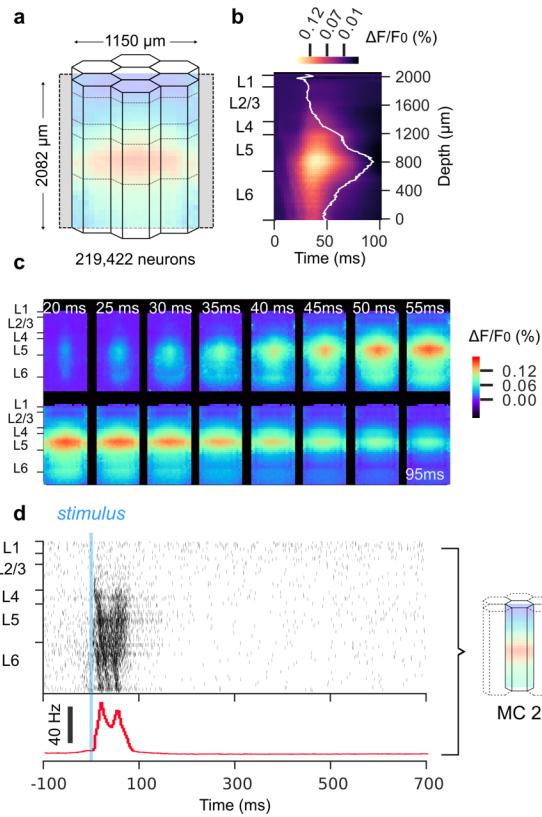
a, Pairwise membrane potential correlations between neurons (300 per layer) for spontaneous network activity. Upper triangle: correlations computed using thresholded traces (-55 mV). Lower triangle: correlations computed on raw traces including spikes. Top and left margins: V_m -VSD correlations for each cell, sorted by strength within each layer (filtered and unfiltered, respectively). **b**, Same as in **a**, but for evoked activity (single stimulus, 60 contiguous TC fibers at NMC center).

Fig. 2: Individual NMC responses



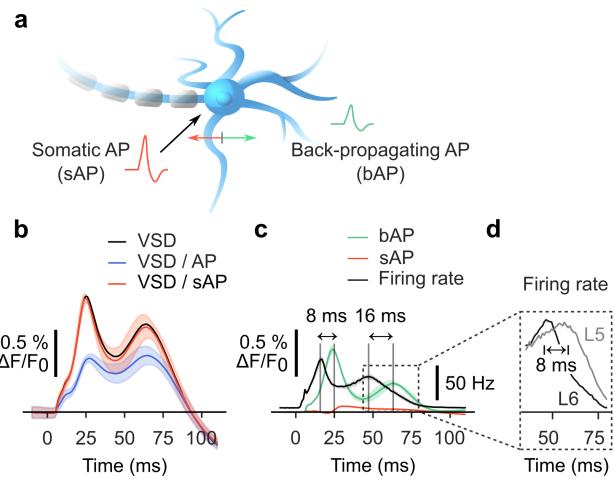
a, Spatially averaged VSD data for Bio-1-5 and Bio-M, $[Ca^{2+}]_o = 1.25$ mM. Vertical blue line indicates stimulus. Text indicates percent deviation from mean in L4 inhibitory populations (black: subcritical response; red: supercritical response). **b**, Number of cells by layer (color) and cell type (standard or exploded pie slices) for each individual microcircuit. Radius of each pie plot is proportional to the total number of neurons. **c**, Standard deviations (percent deviation from mean) for numbers of neurons by layer and cell type.

Fig. 3: Sagittal view VSDI dynamics



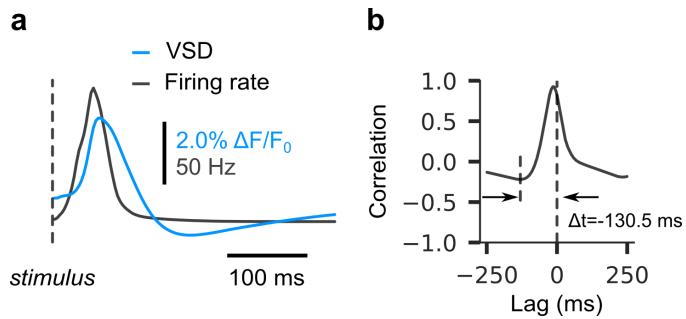
a, Mosaic configuration of NMC model (7 concentric columns), with sagittal imaging plane (indicated in gray) bisecting the volume along the y-axis (depth). **b**, Linescan of cross-sectional VSD activity: matrix of time series data for a vertical line through the center of the imaging plane. White line overlay is sum of each matrix row (i.e. the integral over time for each depth). **c**, VSDI data for a sagittal slice through the mosaic in 5 ms intervals (20–95 ms post-stimulus). **d**, Top: raster plot of 2000 randomly sampled cells in the central column (MC 2). Bottom: same data as above, but in time histogram format.

Fig. 4: Forward- and backward-propagating action potentials



a, Schematic illustrating forward- and backward-propagating APs. Red: APs occurring at the soma/axon initial segment (sAP). Green: back-propagating APs occurring in dendritic arbors (bAP). **b**, Time domain comparison of filtered VSD signals. Black: full signal, no filtration. Blue: VSD signal computed with thresholded V_m (-55 mV), all spikes excluded. Red: VSD signal computed with thresholded V_m (-55 mV), only spikes in somatic compartments excluded. **c**, Comparison of VSD signal contributions by bAP (green) and sAP (red), with firing rate overlay (black). **d**, L6 and L5 mean firing rates during time window in dashed box in **c**.

Fig. 5: Anticorrelation lag time between VSDI and population firing rate for evoked responses



a, VSDI activity (blue line) and population firing rate (black line) in a 350 ms poststimulus time window (averaged over n=10 trials). Dashed horizontal line indicates stimulus onset. **b**, Cross-correlogram of traces in **a** (VSD vs. firing rate) for lags spanning the interval [-250 ms, 250 ms]. Time lag associated with anticorrelation peak (-130.5 ms) framed by horizontal arrows.

Table 1 Wavefront Propagation Velocities

Publication	Min. speed	Max. speed	Wavefront quantification	Experiment protocol	Anesthesia	Brain region	Animal
Petersen et al., 2003a	33 µm/ms (barrel arc)	60 µm/ms (barrel row)	Gaussian fit (cross-sectional)	whisker deflection (in vivo)	urethane or halothane	barrel cortex	rat P21-P28
Fehérvári et al., 2015	47+/-12 µm/ms	66+/-15 µm/ms	amplitude threshold (50% peak)	50 µA current injection (in vivo)	urethane	visual cortex (V1)	mouse P56-P140
Ferezou et al., 2006	27+/-7 µm/ms (urethane)	30+/-7 µm/ms (awake)	amplitude threshold (50% peak)	spontaneous (in vivo)	urethane or isoflurane or none	barrel cortex	mouse
Lippert et al., 2007	200+/-100 µm/ms	200+/-100 µm/ms	--	whisker deflection (in vivo)	isoflurane	barrel cortex	rat
Petersen et al., 2003b	<10 µm/ms	>100 µm/ms	amplitude threshold (50% peak)	spontaneous (in vivo)	urethane or ketamine/xylazine or halothane	barrel cortex	rat/mouse P21-P35
Contreras and Llinas, 2001	181+/-44 µm/ms (L2/3)	217+/-53 µm/ms (L5/6)	--	white matter stimulation 1-5V, 100µs (in vitro)	sodium pentobarbital	visual and somatosensory cortex	guinea pig
Chavane et al., 2011	90 µm/ms	90 µm/ms	2D Gaussian fit	sinusoidal luminance gratings (in vivo)	althesin (3 mg/kg/h) and pancuronium bromide (0.2 mg/kg/h)	visual cortex	cat
Civillico and Contreras, 2005	30 µm/ms (single whisker)	196 µm/ms (multiple whiskers)	amplitude threshold (2x SD of baseline per pixel)	whisker deflection (in vivo)	ketamine-xylazine (100 mg/kg i.p., 20 mg/kg i.p. respectively)	barrel cortex	mouse
NMC	~10 µm/ms	~20 µm/ms	2D Gaussian fit	whisker deflection (in silico)	--	somato-sensory cortex	rat

Algorithm 1: 2D Gaussian surface fit

```

input :A surface arr of size  $n \times m$ 
output:A 2D Gaussian fit

/* compute 2D surface
Function 2DGauss( $h, x, y, \sigma_x, \sigma_y$ ):
  return  $h \cdot \exp -\frac{1}{2} \left[ \left( \frac{x}{\sigma_x} \right)^2 + \left( \frac{y}{\sigma_y} \right)^2 \right]$ 

/* compute first-order moments of arr
Function Moments(arr):
  total  $\leftarrow$  sum of entries in arr
   $x_0 \leftarrow \frac{1}{\text{total}} \sum (\{\text{row of arr}\} \times \{\text{row index}\})$  // 1st moment in x
   $y_0 \leftarrow \frac{1}{\text{total}} \sum (\{\text{col of arr}\} \times \{\text{col index}\})$  // 1st moment in y
  r  $\leftarrow$  row of arr at index int(x)
  c  $\leftarrow$  column of arr at index int(y)
   $\sigma_x \leftarrow \sqrt{\sum |(r - \text{index of } r) \times r|^2 / \sum r}$ 
   $\sigma_y \leftarrow \sqrt{\sum |(c - \text{index of } c) \times c|^2 / \sum c}$ 
  h  $\leftarrow$  max of arr
  return  $x_0, y_0, h, \sigma_x, \sigma_y$ 

/* compute 2D surface
Function Fitgauss(arr):
   $x_0, y_0, h, \sigma_x, \sigma_y \leftarrow$  Moments(arr)
  x  $\leftarrow$   $n \times m$  matrix of row indices
  y  $\leftarrow$   $n \times m$  matrix of column indices
  def err_fn ( $x, y, \text{arr}$ ):
    return 2DGauss( $x - x_0, y - y_0, h, \sigma_x, \sigma_y$ ) - arr
  return LeastSq(err_fn, x, y, arr) // least-squares fit using
    scipy.optimize

/* main routine
Function Main(arr):
  params = Fitgauss(arr)

```