

Supplementary Information

A Nanobiosensor for Dynamic Single Cell Analysis during Microvascular Self-Organization

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Fig. S1

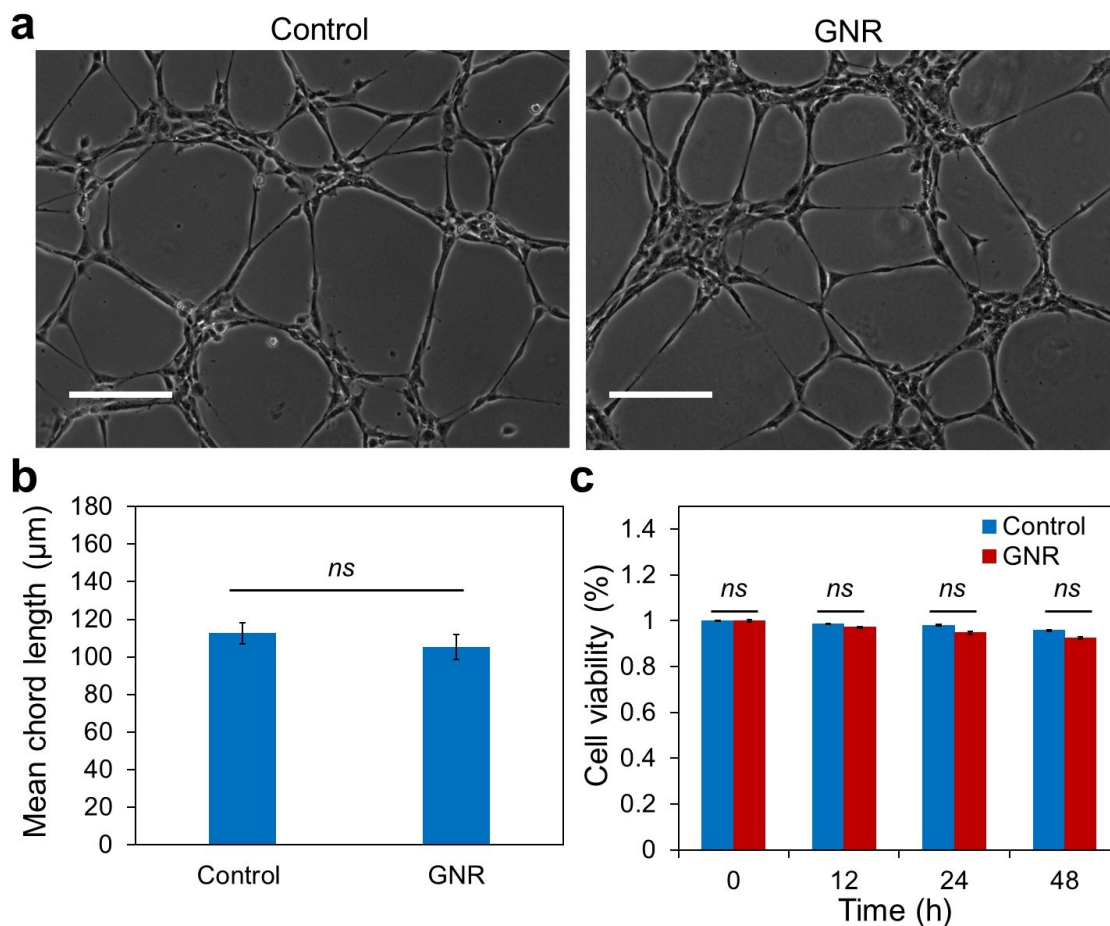


Fig. S1. The GNR-LNA nanobiosensor for investigating microvascular self-organization. (a) Microvascular networks with and without GNRs. Scale bars, 200 μm . Images are representative of three independent experiments. (b) The mean chord lengths of microvascular networks with and without GNR. (c) The viability of HUVECs with and without GNRs. Data represent over 100 cells in each group and are expressed as mean \pm s.e.m. ($n=5$, ns, not significant; unpaired Student's t -test).

Fig. S2

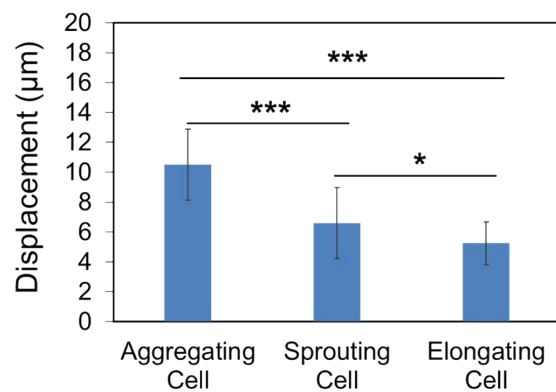


Fig. S2. The maximum displacement of cell subpopulations. Data represent over 100 cells in each group and are expressed as mean \pm s.e.m. ($n=3$, $*P<0.05$, $**P<0.01$, $***P<0.001$; unpaired Student's t -test).

Fig. S3

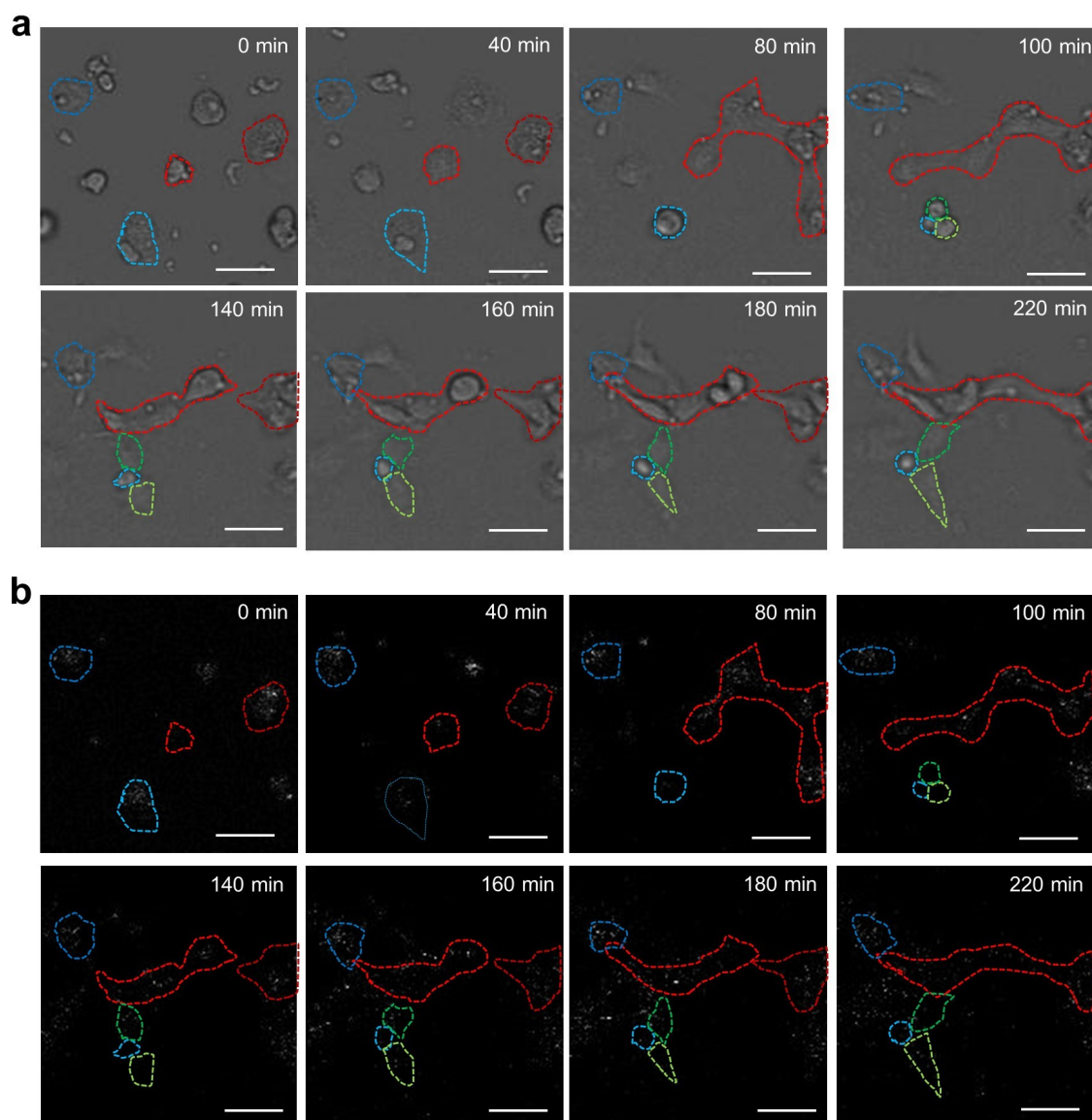


Fig. S3. Dynamic single cell analysis. (a) Bright-field images of endothelial cells during microvascular self-organization. (b) Fluorescence images of endothelial cells during microvascular self-organization. The cells were treated with random probes. Dotted lines indicate the cell morphology. Scale bars, 50 μm. Images are representative from three independent experiments.

Fig. S4

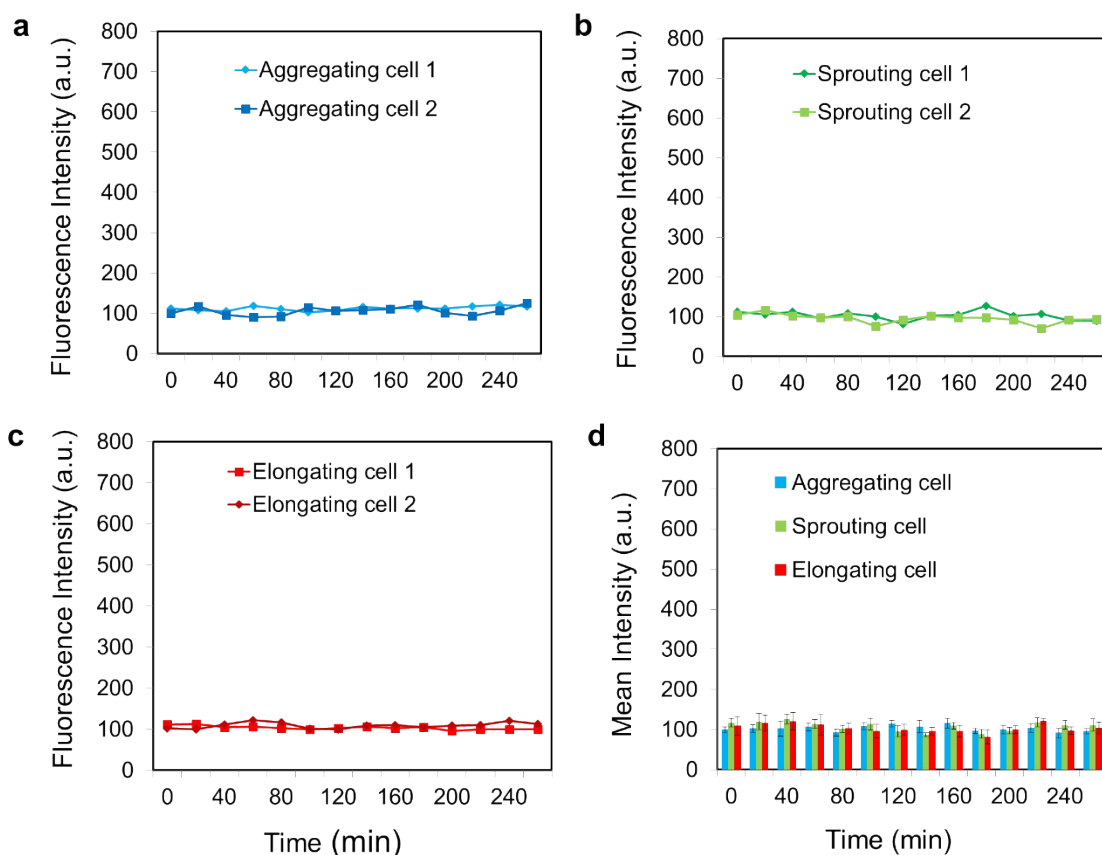


Fig. S4. The intensity of random probe during microvascular self-organization. (a-c) Tracking of fluorescence intensity of the random probe in representative (a) aggregating cells, (b) sprouting cells and (c) elongating cells. (d) Comparison of the average fluorescence intensities in cell subpopulations. Data represent over 100 cells in each group and expressed as mean \pm s.e.m. (n=3).

Fig. S5

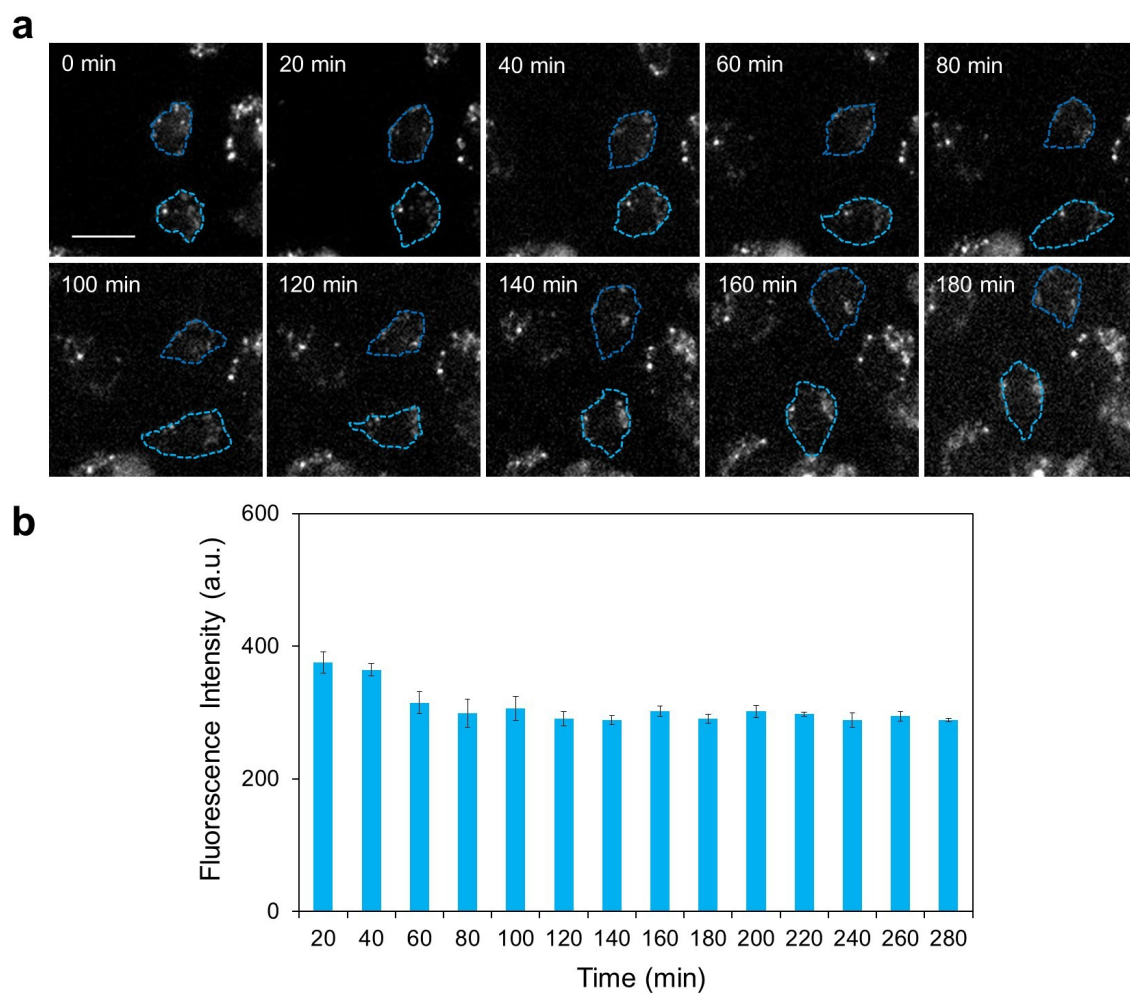


Fig. S5. Dynamic tracking of aggregating cells. (a) DII4 mRNA tracking of aggregating cells during microvascular structure formation. (b) Average intensity of DII4 mRNA expression of aggregating cells. Data represent over 100 cells and expressed as mean \pm s.e.m. (n=3).

Fig. S6

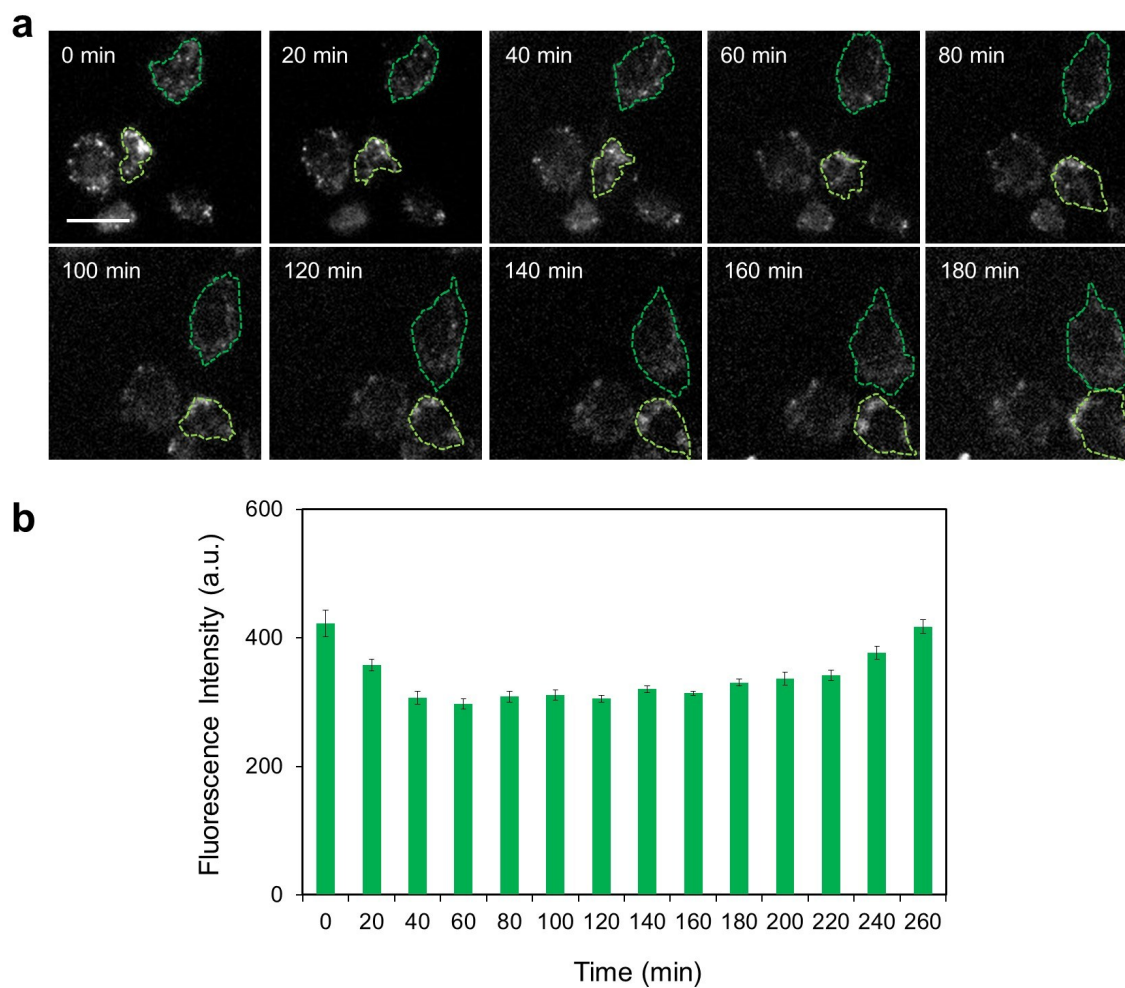


Fig. S6. (a) DII4 mRNA tracking of sprouting cells during microvascular structure formation. (b) Average intensity of DII4 mRNA expression of aggregating cells. Data represent over 100 cells and expressed as mean \pm s.e.m. (n=3).

Fig. S7

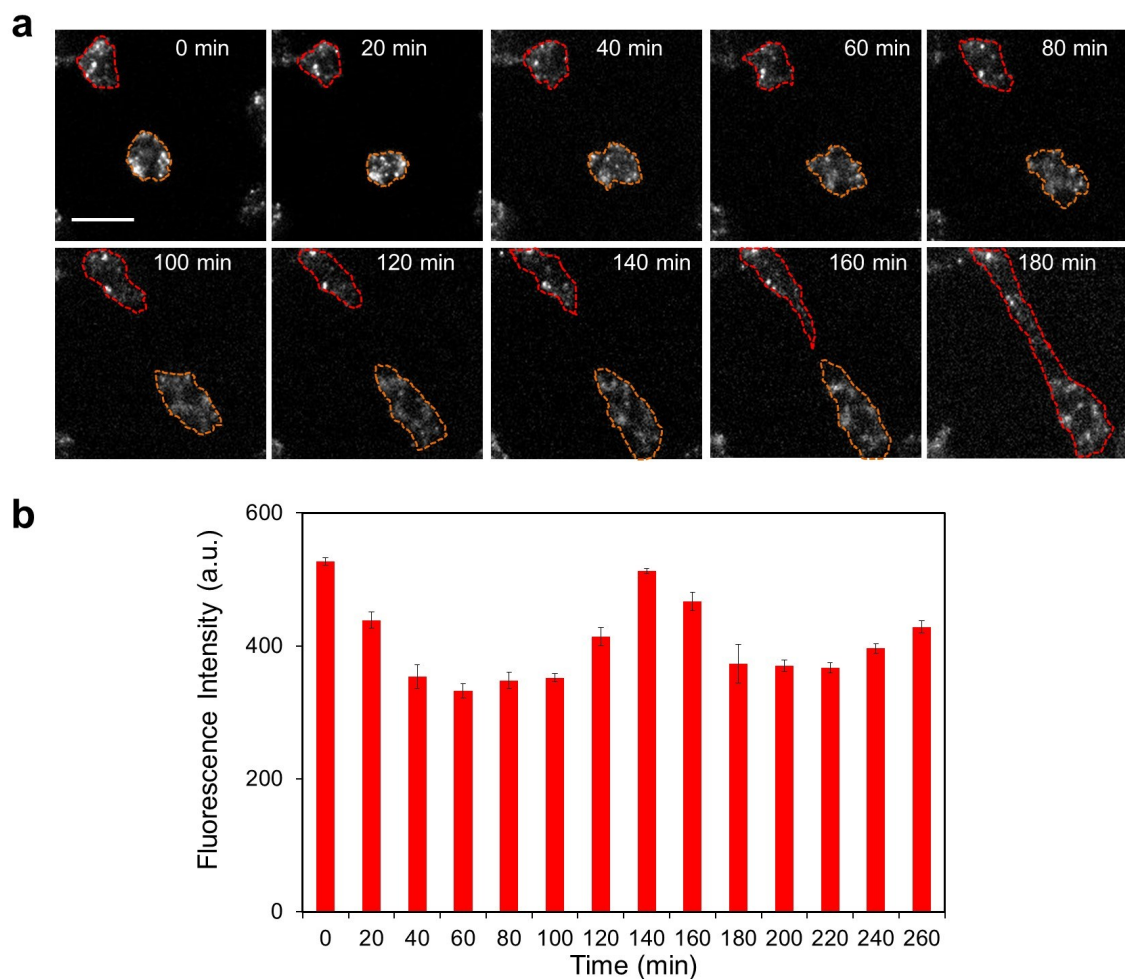


Fig. S7. (a) DII4 mRNA tracking of aggregating cells during microvascular structure formation. (b) Average intensity of DII4 mRNA expression of elongating cells. Images are representative of three independent experiments. Data represent over 100 cells and expressed as mean \pm s.e.m. (n=3).

Fig. S8

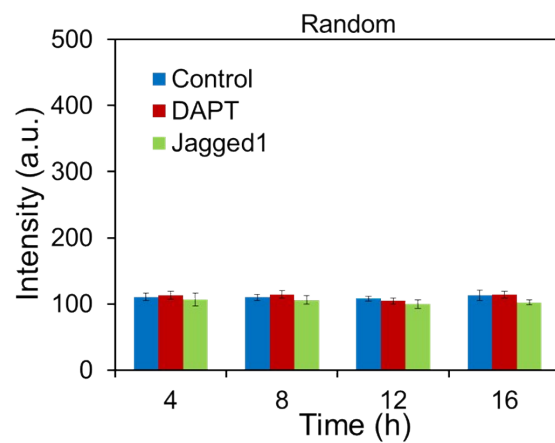


Fig. S8. Mean fluorescent intensity comparison of random probe in microvascular networks. Data represent over 100 cells in each group and are expressed as mean \pm s.e.m. (n=5).

Fig. S9

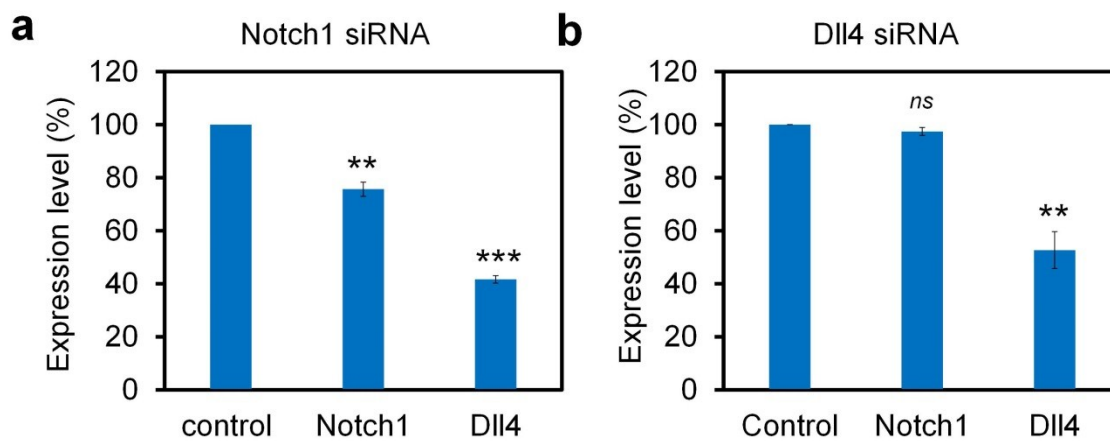


Fig. S9. Quantification of western blot results of Notch1 and DII4 expression in HUVEC networks with (a) DII4 siRNA and (b) Notch1 siRNA. Data are representative from three independent experiments. (n=3, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$; unpaired Student's t -test).

Tab. S1

Tab. S1. LNA probes and synthetic DNA target sequences

Name		Sequence (5'-3')	Fluorophore
DII4	Probe	+AA+GG+GC+AG +TT+GG+AG+AG+GG+TT	/56-FAM
	Target	AACCCTCTCCA ACTGCCCTT	
Random	Probe	+AC+GC+GA+CA+AG+CG+CA+CC+GA+TA	/56-FAM
	Target	TATCGGTGCGCTTGTCGCGT	

* + represents LNA monomer

Tab. S2

Tab. S2. Kolmogorov–Smirnov two sample test results

Treatment	DII4 mRNA		Random	
	DAPT	Jag1	DAPT	Jag1
h	1	1	0	0
p-value	1.57E-22	4.41E-15	0.556	0.2606
statistic (<i>D</i>)	0.7	0.57	0.11	0.14