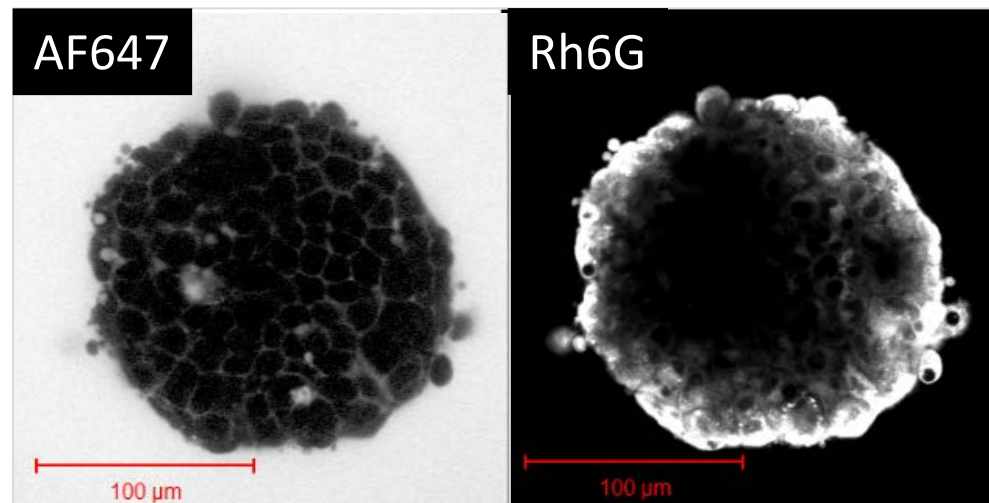
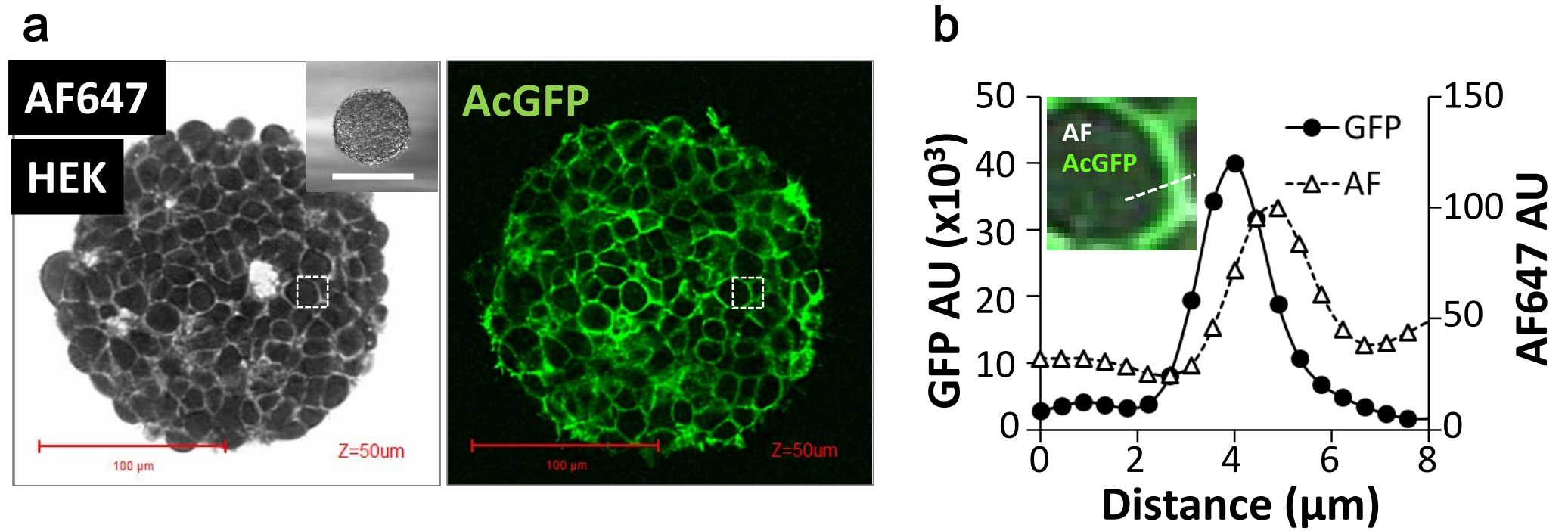


Extended Data Figure 1



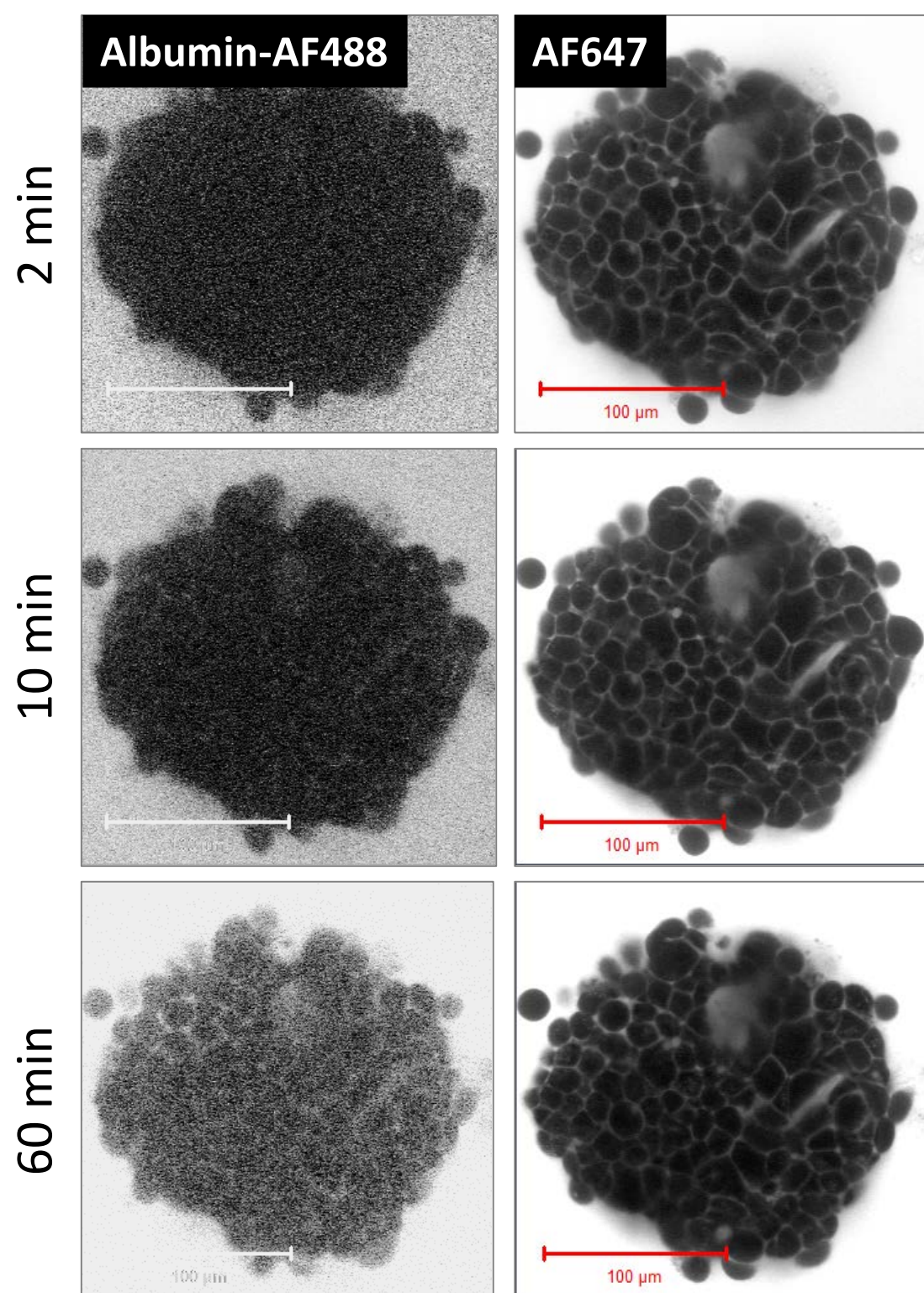
Extended Data Figure 1. The hydrophobicity of the fluorescent dye affects the inflow diffusion rate of the dye into the target spheroid. Dual-color confocal microscopy was performed for HepG2 spheroid NCI using the hydrophilic fluorescent dye AF647 (left) and the hydrophilic fluorescent dye Rhodamine 6G (Rh6G, right). One hour after the addition of the two dyes, compared to AF647, Rh6G fluorescence was observed with marked accumulation only in peripheral cells but little in the core region. Bar; 100 μm. The images were prepared by ZEN software (Zeiss, Jena, Germany).

Extended Data Figure 2



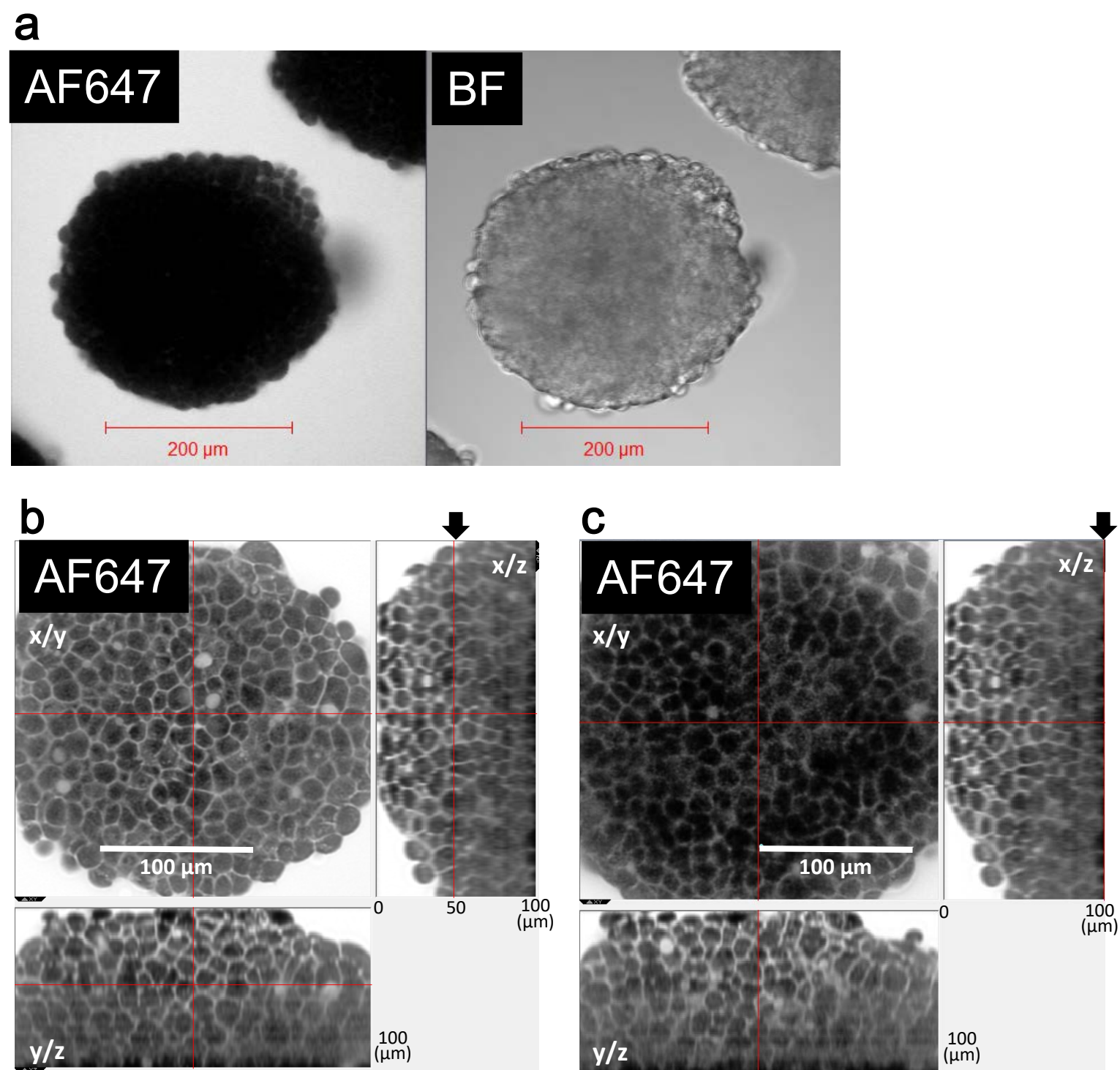
Extended Data Figure 2. NCI accurately visualizes the intercellular space of the spheroid. (a) A dual-color confocal image of a representative HEK293T (HEK) spheroid with transient expression of plasma membrane-targeting AcGFP in the cytosol. NCI with AF647 (left) and AcGFP images (right). Bar: 100 μm . Dashed rectangle: enlarged area in the inset (b). Inset: bright field. Bar: 200 μm . (b) Merged histograms of AcGFP (solid circles) and AF647 (blank triangles) fluorescence intensity along the dashed line in the inset. Inset: Merged image of the indicated dashed square in each image in (a). Square size: 16 \times 16 μm . The AcGFP signal (green: intracellular side of the plasma membrane) was located beneath the AF647 signal (white: intercellular). The images were prepared by ZEN software.

Extended Data Figure 3



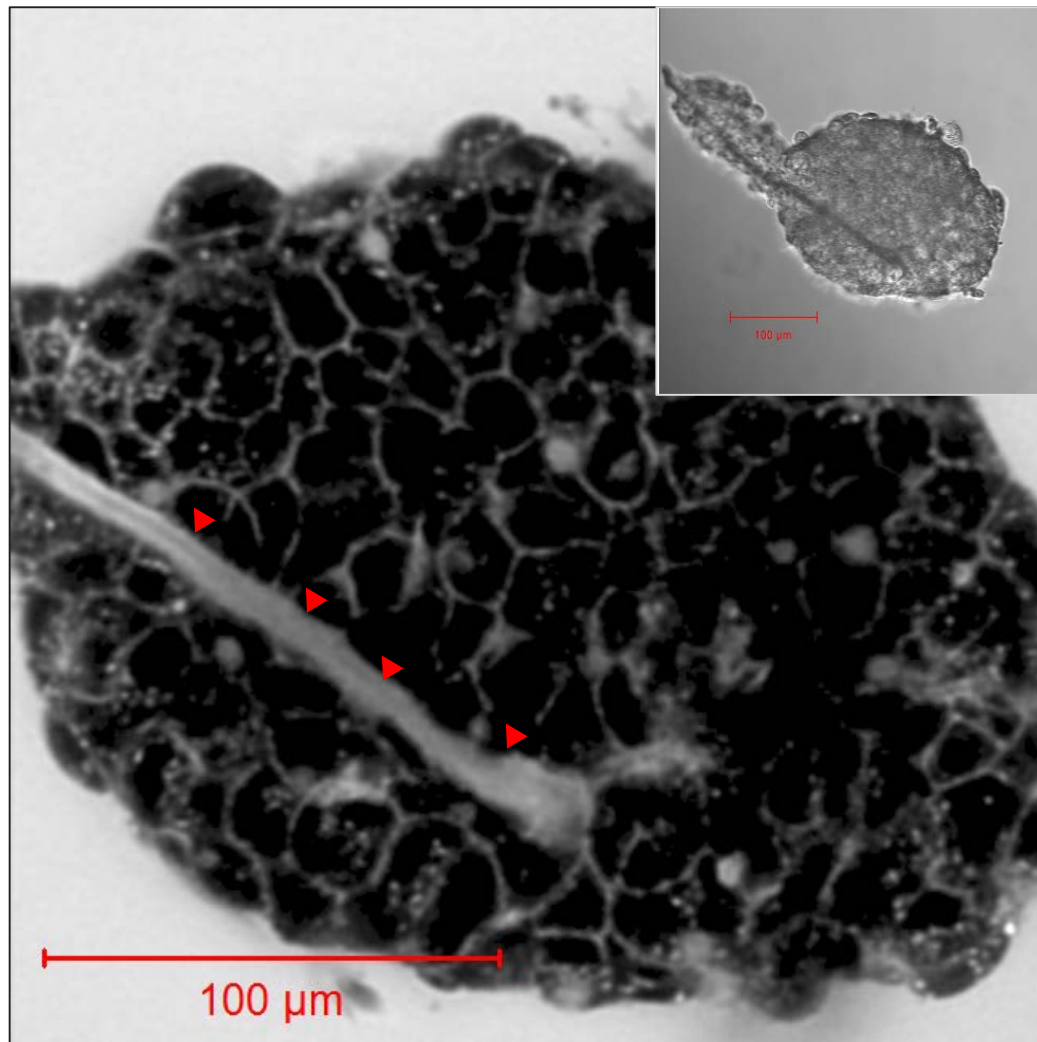
Extended Data Figure 3. The molecular weight of the dye can affect the inflow diffusion rate into the core region of the target spheroids. AF488-conjugated albumin was added to the medium of HepG2 spheroids together with AF647. Dual-color confocal imaging was performed at the same z position of the spheroid over a time course of 2, 10, and 60 min after the addition of dye. Higher molecular weight of dye yielded slower diffusion rates. Bar: 100 μm. The images were prepared by ZEN software.

Extended Data Figure 4



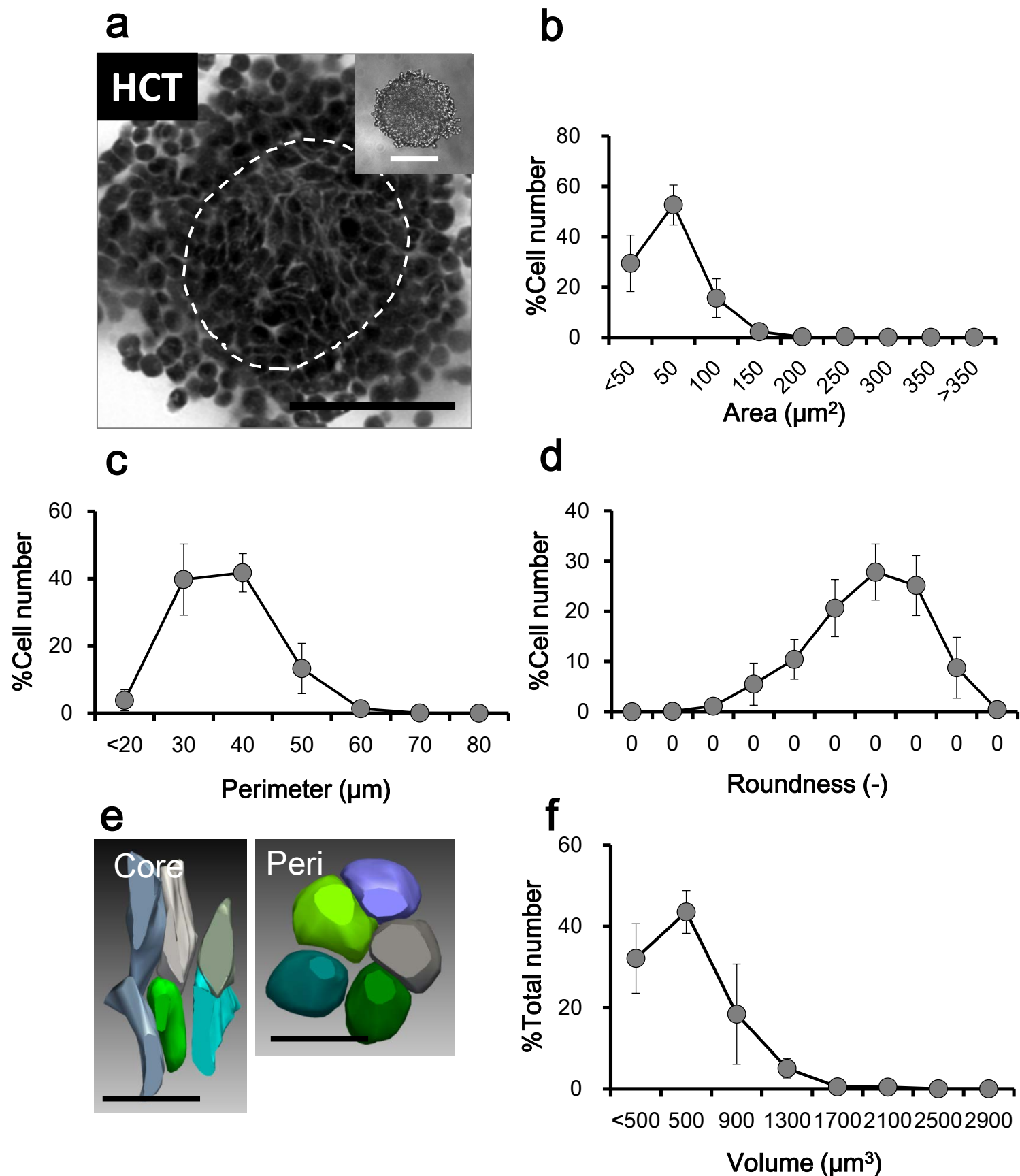
Extended Data Figure 4. NCI visualizes the cells in the deep core region of HepG2 spheroids. (a) Low-magnification image of the HepG2 spheroid acquired by NCI (left: AF647) and bright field (right: BF). (b, c) Confocal images of the same spheroid in (a) at (b) 50 μm and (c) 100 μm distance from the adhesion plane with the orthogonal images. Bar: 100 μm. Arrow: z position of the x/y plane. Individual cells can be identified by the separation of fluorescent signals in the intercellular space. The images were prepared by ZEN software.

Extended Data Figure 5



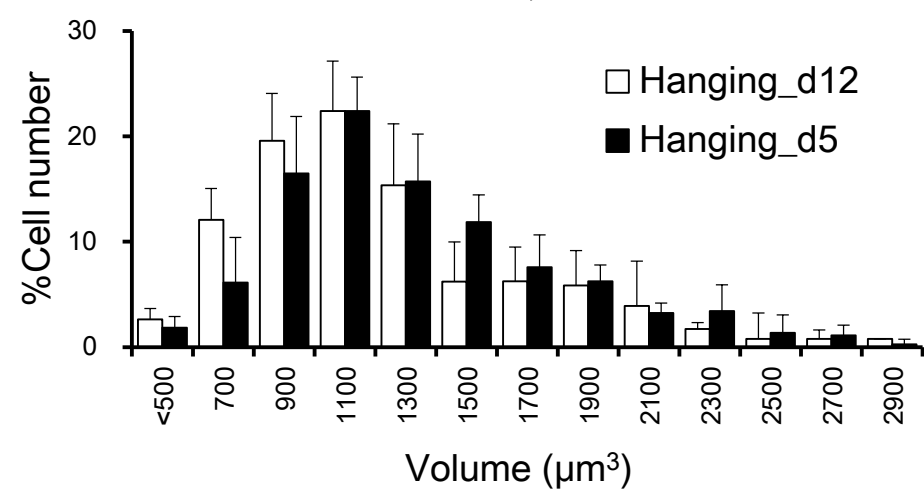
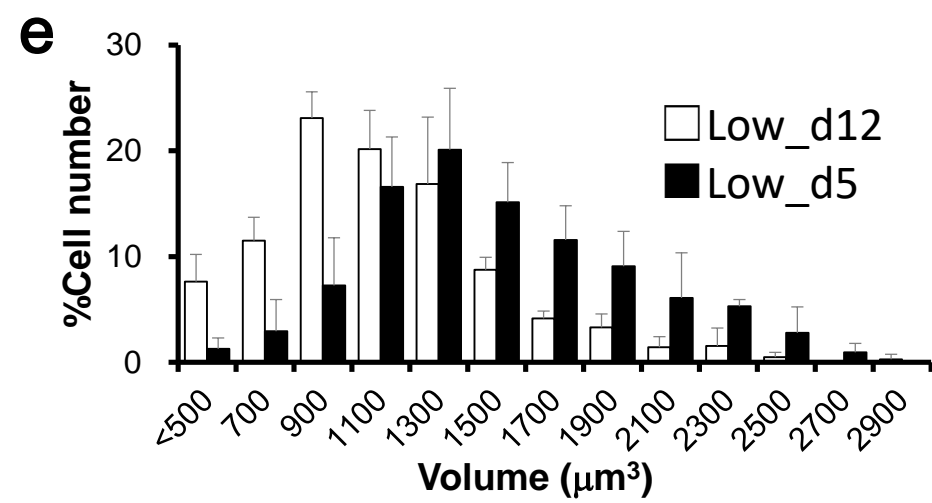
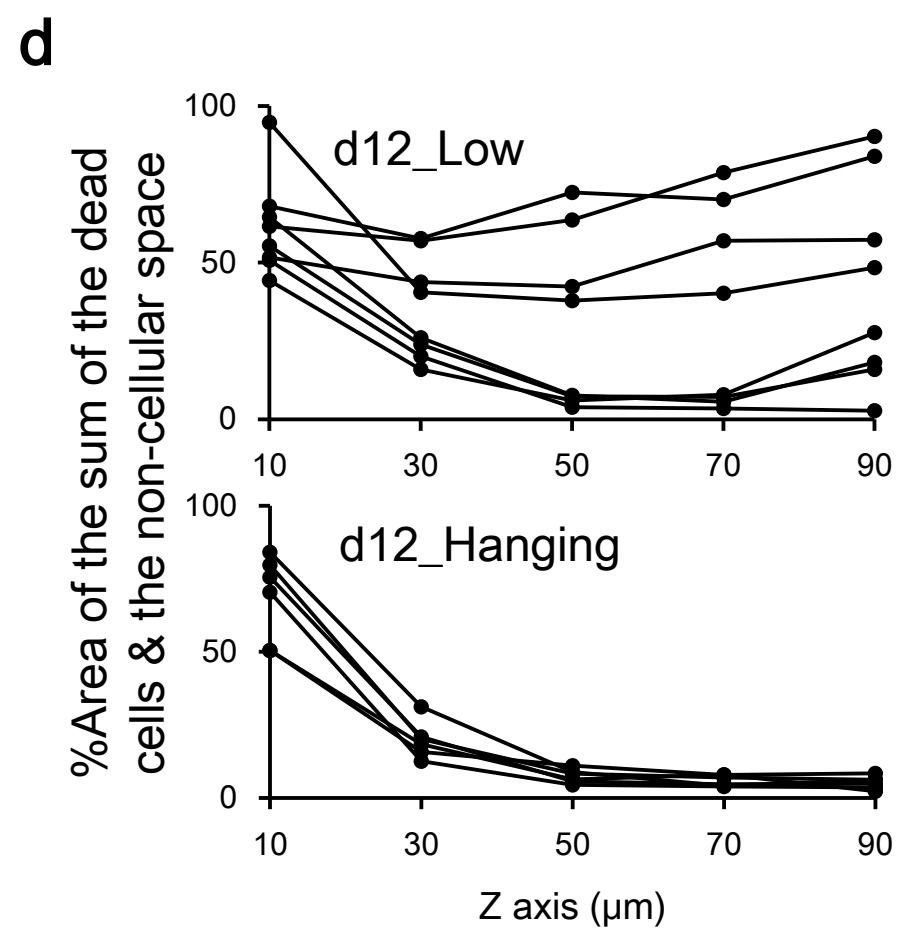
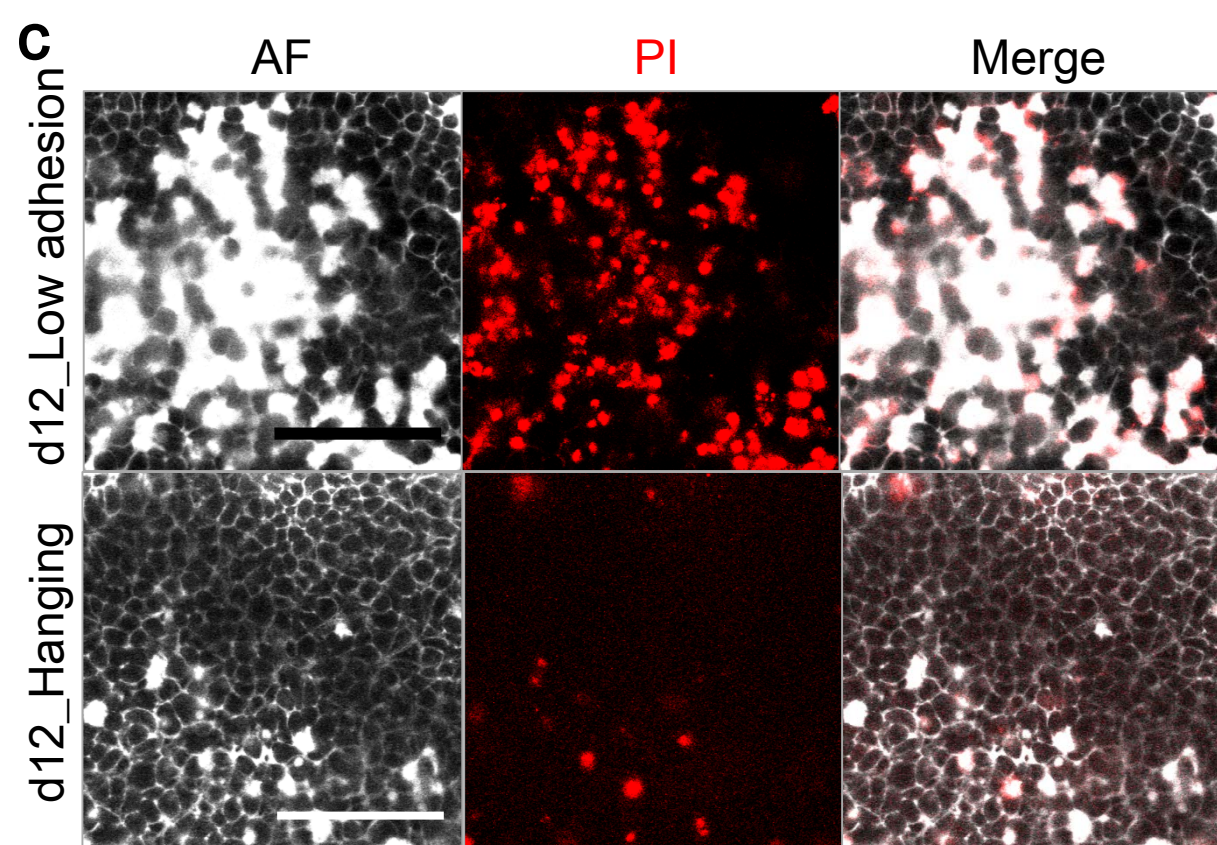
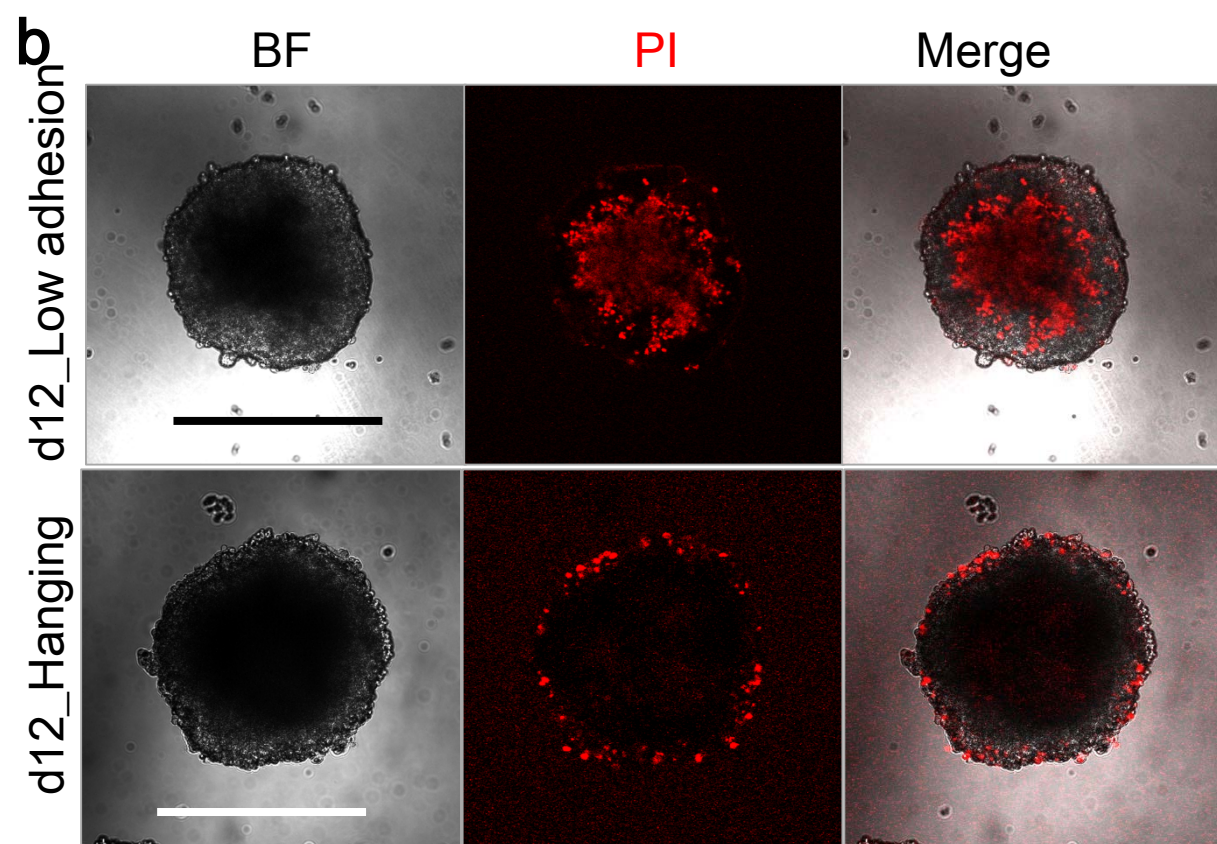
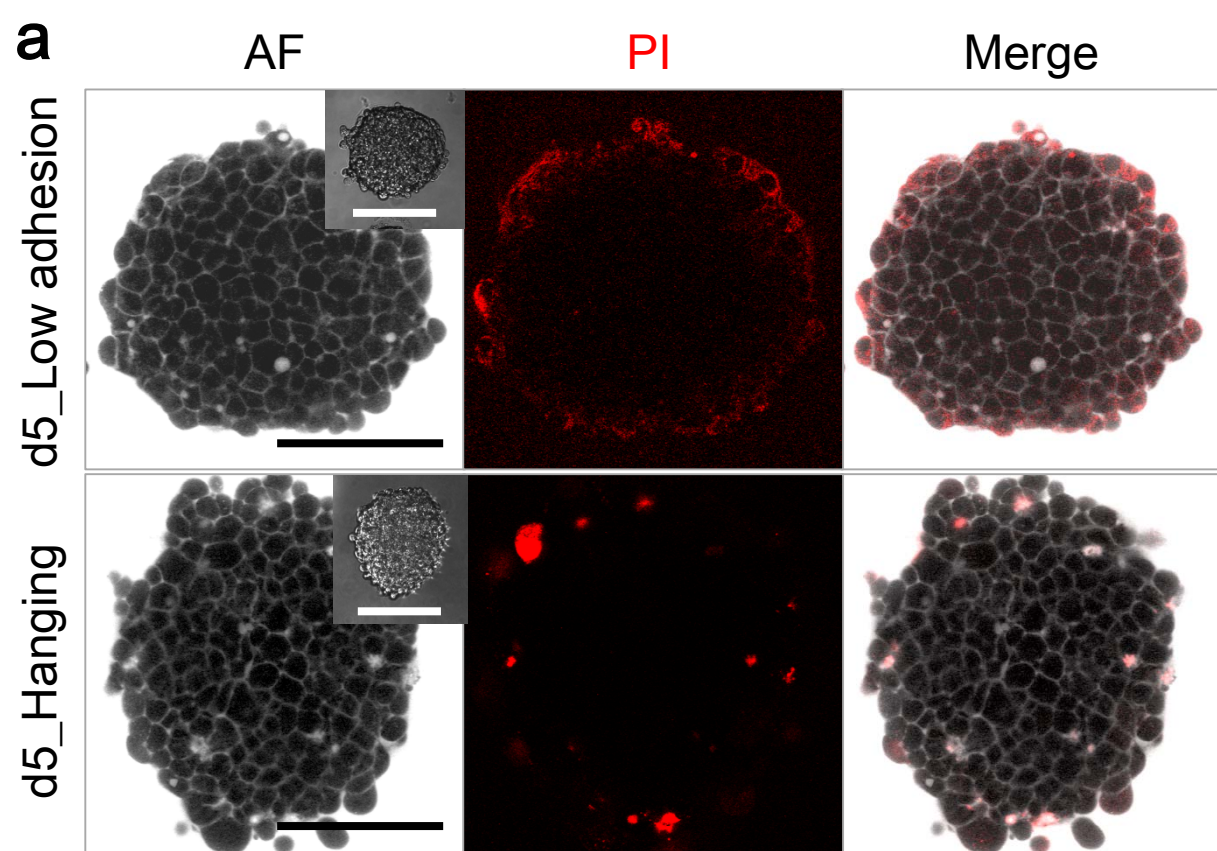
Extended Data Figure 5. NCI can visualize non-cellular insoluble components in spheroids. Representative NCI image of day 5 HepG2 spheroid that embeds insoluble filament component penetrating the dye (arrowhead), which might have originated from debris in the medium. Scale bar: 100 μm . Inset: Low-magnitude image of the spheroid in the bright field. Bar: 100 μm . The images were prepared by ZEN software.

Extended Data Figure 6



Extended Data Figure 6. NCI of a colon cancer-delivered cell line, HCT-116 (HCT). (a) Representative NCI image of HCT spheroids on day 5 of culture. The dashed line indicates the boundary between the inner tight and outer rough-cell-packaging areas. Bar: 100 μm . Inset: Bright fields. Bar: 200 μm . (b-d) Histograms of the individual cellular contours in the spheroid confocal images analyzed by the (b) area, (c) perimeter, and (d) roundness. N = 4. (e) Representative images of the reconstructed 3D structures of individual core cells in HCT spheroids. Each cell is indicated by a different color. Core: core cells; Peri: peripheral cells in (a). (f) Volumetric histogram of the spheroid core cells measured in the same way as in Figure 1i. N = 3. The images of (a) were prepared by ZEN software, and the structural parameters (b-d), 3D reconstruction of (e) and individual cell volumes of (f) were calculated by NeuroLucida (MBF Bioscience, Williston, VT, US).

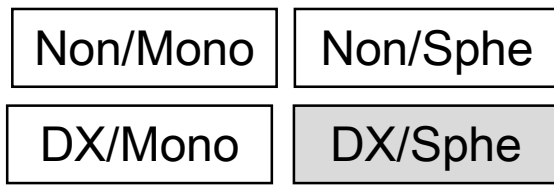
Extended Data Figure 7



Extended Data Figure 7. NCI shows the difference in structural characteristics and viability of two spheroids cultured under different conditions. (a) HepG2 spheroids cultured for 5 days in a low-adhesion culture plate (upper) and by hanging drop method (lower) visualized by NCI (left column), propidium iodide (PI, middle), and merged (right). Bar: 100 μm . A slight difference was observed between the two spheroids. (b) HepG2 spheroids cultured under the same conditions as in (a) for 12 days. Bright field image (left), confocal image with PI (middle), and merged (right). Scale bar: 500 μm . Clear PI accumulation, which may indicate cell death, was observed in the spheroid core region, which was cultured using a low-adhesion culture plate. (c) Confocal image of the core region of spheroids (b) 100 μm above the adhesion plane. NCI (left column), PI (middle), and merged (right). Scale bar: 100 μm . (d) The content of the area of the sum of dead cells and non-cellular space against the entire scanned area aligned along the z-axis from the adhesion plane to 90 μm . Upper: low-adhesion plate. N = 8. Lower: hanging drop method. N = 6. Each line indicates individual spheroid data. (e) Volumetric histograms of individual core cells of HepG2 spheroids cultured in the low-adhesion culture plate (upper panel) and by hanging drop method (lower panel). The five-day culture data are shown in the solid column, and 12 day culture data are shown in the blank column. The low-adhesion culture plate showed a peak shift in the cell volume histogram. The images of (a-c) were prepared by ZEN software, and calculation of the fluorescence intensity in (d) were by Fiji software (<https://imagej.net/Fiji>). The volume of the individual cells of (e) were calculated by Neurolucida.

Extended Data Figure 8

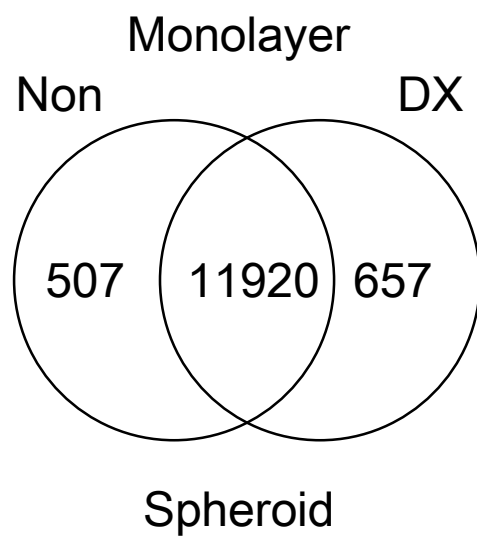
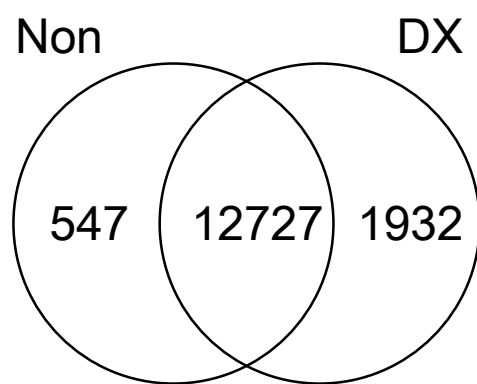
a



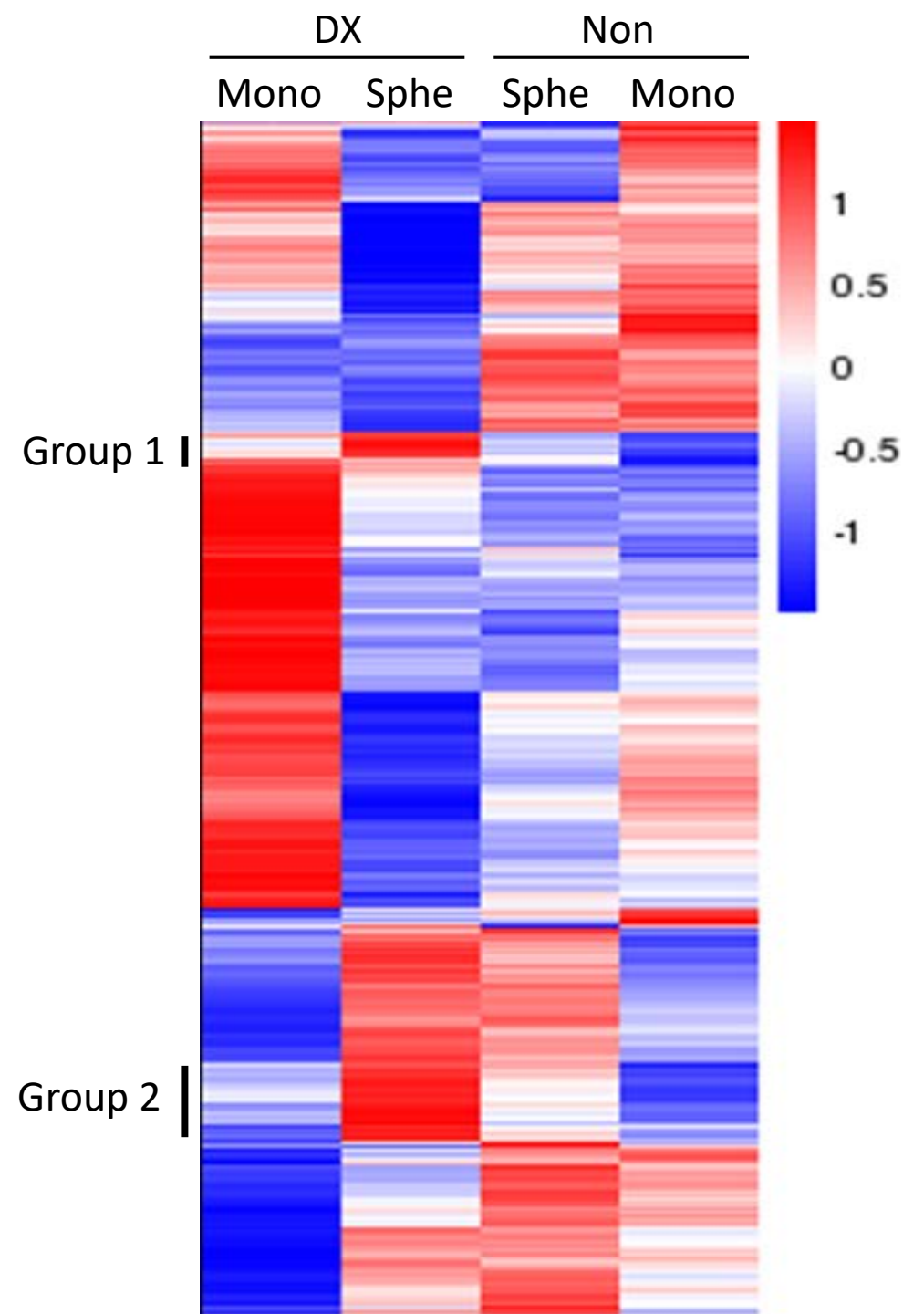
mRNA

- > Library (adaptor ligation)
- > PCR
- > QC
- > Seq (illumina HiSeq6000)
- > Mapping (Human genome: TopHat2)
- > Exp. Quantification (HTSeq)
- > Dif. Exp. Anal. (DESeq)
- > Norm. (DESeq)
- > FDR est. (BH)
- > GO Enrichment

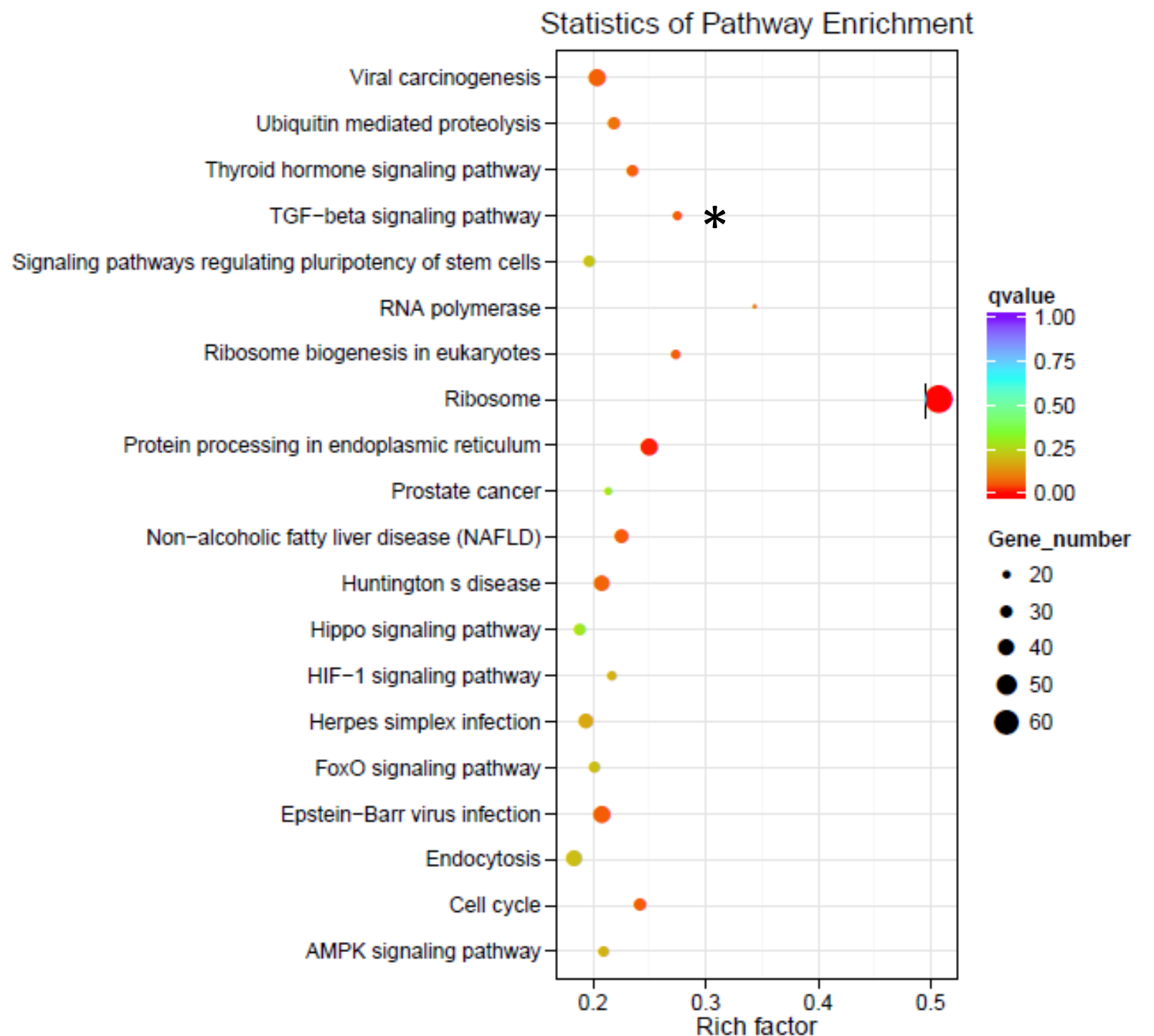
b



c



d



Extended Data Figure 8. Transcriptomic analysis of HepG2 cells under various culture conditions. (a) Schema of transcriptomic analysis. The four conditions in HepG2 cells cultured with monolayer (Mono) or spheroid (Sphe) with/without DX were compared. QC, quality control; FDR, false discovery rate; BH, Benjamini –Hochberg. (b) Venn diagrams representing the number of unique and common genes between the two RNA-seq samples. (c) FPKM cluster analysis (heat map) using the $\log_{10}(\text{FPKM}+1)$ value. The color range from red to blue represents the $\log_{10}(\text{FPKM}+1)$ value from large to small. Overall, 3,795 of 12,427 genes analyzed were found to be differentially expressed after multiple testing corrections (FDR estimation BH, <0.05). The upregulated gene clusters in DX-treated spheroids were named Group 1 (84 genes) and Group 2 (126 genes), and the list is shown in Extended Data Figure 9 (Group 1) and 10 (Group 2). (d) KEGG enrichment scatter plot of DX enhancement in spheroids. Dot size represents the number of different genes, and color indicates the q-value. Asterisk: TGF- β signaling pathway.

Extended Data Figure 9

Gene ID	Gene Name
ENSG00000137509	prolylcarboxypeptidase(PRCP)
ENSG00000089063	transmembrane protein 230(TM230)
ENSG00000156467	ubiquinol-cytochrome c reductase binding protein(UQCRB)
ENSG00000105438	KDEL endoplasmic reticulum protein retention receptor 1(KDEL1)
ENSG00000127184	microRNA 3607(MIR3607)
ENSG00000179222	MAGE family member D1(MAGED1)
ENSG00000099624	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit(ATP5D)
ENSG00000177600	ribosomal protein lateral stalk subunit P2(RPLP2)
ENSG00000065978	Y-box binding protein 1(YBX1)
ENSG00000139644	transmembrane BAX inhibitor motif containing 6(TMBIM6)
ENSG00000111275	aldehyde dehydrogenase 2 family (mitochondrial)(ALDH2)
ENSG00000166794	peptidylprolyl isomerase B(PPIB)
ENSG00000142541	ribosomal protein L13a(RPL13A)
ENSG00000167004	protein disulfide isomerase family A member 3(PDIA3)
ENSG00000170889	ribosomal protein S9(RPS9)
ENSG00000101439	cystatin C(CST3)
ENSG00000163041	H3 histone family member 3A(H3F3A)
ENSG00000169100	solute carrier family 25 member 6(SLC25A6)
ENSG00000105193	ribosomal protein S16(RPS16)
ENSG00000160014	calmodulin 3(CALM3)
ENSG00000109472	carboxypeptidase E(CPE)
ENSG00000130707	argininosuccinate synthase 1(ASS1)
ENSG00000167526	ribosomal protein L13(RPL13)
ENSG00000143870	protein disulfide isomerase family A member 6(PDIA6)
ENSG00000166710	beta-2-microglobulin(B2M)
ENSG00000160213	cystatin B(CSTB)
ENSG00000155368	diazepam binding inhibitor, acyl-CoA binding protein(DBI)
ENSG00000161944	asialoglycoprotein receptor 2(ASGR2)
ENSG00000138207	retinol binding protein 4(RBP4)
ENSG00000197249	serpin family A member 1(SERPINA1)
ENSG00000198931	adenine phosphoribosyltransferase(APRT)
ENSG00000170540	ADP ribosylation factor like GTPase 6 interacting protein 1(ARL6IP1)
ENSG00000115268	ribosomal protein S15(RPS15)
ENSG00000110492	midkine (neurite growth-promoting factor 2)(MDK)
ENSG00000136942	ribosomal protein L35(RPL35)
ENSG00000132386	serpin family F member 1(SERPINF1)
ENSG00000173457	protein phosphatase 1 regulatory inhibitor subunit 14B(PPP1R14B)
ENSG00000233927	ribosomal protein S28(RPS28)
ENSG00000120885	microRNA 6843(MIR6843)
ENSG00000221983	ubiquitin A-52 residue ribosomal protein fusion product 1(UBA52)
ENSG00000162244	ribosomal protein L29(RPL29)
ENSG00000142534	ribosomal protein S11(RPS11)
ENSG00000109861	cathepsin C(CTSC)
ENSG00000149273	ribosomal protein S3(RPS3)
ENSG00000153574	ribose 5-phosphate isomerase A(RPIA)
ENSG00000065154	ornithine aminotransferase(OAT)
ENSG00000112306	ribosomal protein S12(RPS12)
ENSG00000136156	integral membrane protein 2B(IT2B)
ENSG00000135744	angiotensinogen(AGT)
ENSG00000158104	4-hydroxyphenylpyruvate dioxygenase(HPD)
ENSG00000131143	cytochrome c oxidase subunit 41(COX41)
ENSG00000117632	microRNA 3917(MIR3917)
ENSG00000135940	cytochrome c oxidase subunit 5B(COX5B)
ENSG00000118137	apolipoprotein A1(APOA1)
ENSG00000116221	mitochondrial ribosomal protein L37(MRPL37)
ENSG00000125827	thioredoxin related transmembrane protein 4(TM4)
ENSG00000159199	ATP synthase, H+ transporting, mitochondrial Fo complex subunit C1 (subunit 9)(ATP5G1)
ENSG00000186468	ribosomal protein S23(RPS23)
ENSG00000063177	ribosomal protein L18(RPL18)
ENSG00000140988	ribosomal protein S2(RPS2)
ENSG00000147257	glypican 3(GPC3)
ENSG00000129824	ribosomal protein S4, Y-linked 1(RPS4Y1)
ENSG00000147255	immunoglobulin superfamily member 1(IGSF1)
ENSG00000105372	ribosomal protein S19(RPS19)
ENSG00000124299	peptidase D(PEPD)
ENSG00000161203	adaptor related protein complex 2 mu 1 subunit(AP2M1)
ENSG00000093010	microRNA 4761(MIR4761)
ENSG00000137818	ribosomal protein lateral stalk subunit P1(RPLP1)
ENSG00000178445	glycine decarboxylase(GLDC)
ENSG00000163902	ribophorin I(RPN1)
ENSG00000155660	protein disulfide isomerase family A member 4(PDIA4)
ENSG00000083845	ribosomal protein S5(RPS5)
ENSG00000169174	proprotein convertase subtilisin/kexin type 9(PCSK9)
ENSG00000243147	mitochondrial ribosomal protein L33(MRPL33)
ENSG00000244038	dolichyl-diphosphooligosaccharide--protein glycosyltransferase non-catalytic subunit(DDOST)
ENSG00000177556	antioxidant 1 copper chaperone(ATOX1)
ENSG00000175899	alpha-2-macroglobulin(A2M)
ENSG00000167996	ferritin heavy chain 1(FTH1)
ENSG00000206503	major histocompatibility complex, class I, A(HLA-A)
ENSG00000125995	reactive oxygen species modulator 1(ROMO1)
ENSG00000101444	adenosylhomocysteinase(AHCY)
ENSG00000123131	peroxiredoxin 4(PRX4)
ENSG00000149547	EI24, autophagy associated transmembrane protein(EI24)
ENSG00000105640	ribosomal protein L18a(RPL18A)

Extended Data Figure 9. The contents of Group 1 of the heat map shown in Extended Data Fig. 8b.

Extended Data Figure 11

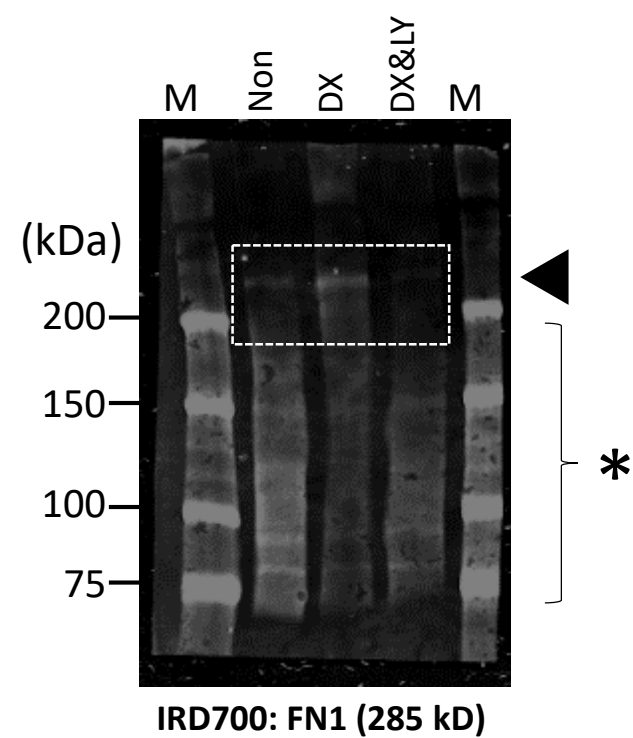
	Gene	FPKM			
		Non_Sphe	Dx_Sphe	Non_Mono	Dx_Mono
Integrin	ITGA1	13	16	19	19
	ITGA2	10	4	22	10
	ITGA2B	0	1	0	13
	ITGA3	1	1	3	6
	ITGA4	0	0	0	0
	ITGA5	0	0	0	1
	ITGA6	33	27	26	24
	ITGA7	2	1	3	9
	ITGA8	0	0	0	0
	ITGA9	0	0	0	1
	ITGA10	0	0	2	2
	ITGA11	0	0	0	0
	ITGAD	0	0	0	0
	ITGAE	22	28	20	18
	ITGAL	7	5	10	7
	ITGAM	0	0	0	6
	ITGAV	47	50	85	55
	ITGAX	0	0	0	0
	ITGB1	328	481	389	378
	ITGB1BP1	80	85	53	52
	ITGB1BP2	0	0	1	0
	ITGB1P1	0	0	0	1
	ITGB2	6	12	20	20
	ITGB3	0	0	0	0
	ITGB3	0	0	0	0
	ITGB3BP	24	24	18	8
	ITGB4	2	2	4	13
	ITGB5	69	82	142	130
ITGB6	0	0	0	0	
ITGB7	1	0	1	3	
ITGB8	0	0	0	0	
ITGBL1	0	0	0	0	

	Gene	FPKM			
		Non_Sphe	Dx_Sphe	Non_Mono	Dx_Mono
Proteoglycan	CSPG4P4Y	0	0	0	0
	CSPG4	0	0	0	1
	CSPG4P1Y	0	0	0	0
	CSPG4P2Y	0	0	0	0
	CSPG4P3Y	0	0	0	0
	CSPG4P5	0	0	0	0
	CSPG5	0	1	0	5
	HAPLN1	0	0	0	0
	HAPLN2	0	0	0	3
	HAPLN3	0	0	0	0
	HAPLN4	0	0	0	0
	HSPG2	30	54	148	320
	IMPG1	0	0	0	0
	IMPG2	0	0	0	0
	IMPG2	0	0	0	0
	LEPRE1	61	96	120	178
	PRG2	0	0	0	0
	PRG3	0	0	0	0
	PRG4	0	0	0	0
	SPOCK1	0	0	0	0
	SPOCK2	34	55	192	311
	SPOCK3	0	0	0	0
	TSKU	42	5	44	50

	Gene	FPKM			
		Non_Sphe	Dx_Sphe	Non_Mono	Dx_Mono
Collagen	COL1A1	0	0	1	3
	COL1A2	0	0	0	1
	COL2A1	171	312	157	288
	COL4A1	0	0	0	0
	COL4A2	1	0	1	1
	COL4A3	0	0	0	0
	COL4A4	0	0	0	0
	COL4A5	1	1	0	1
	COL4A6	0	0	0	0
	COL5A1	0	1	1	1
	COL5A2	1	1	1	2
	COL5A3	0	0	0	0
	COL6A1	3	5	5	23
	COL6A2	0	0	0	2
	COL6A5	0	0	0	0
	COL6A6	0	0	0	0
	COL7A1	15	21	73	97
	COL8A1	0	0	0	0
	COL8A2	0	0	0	1
	COL9A1	0	0	0	1
	COL9A3	84	141	293	437
	COL9A2	12	16	45	76
	COL10A1	0	0	0	0
	COL11A1	0	0	0	0
	COL11A2	0	0	1	3
	COL12A1	0	0	0	0
	COL13A1	0	0	0	0
	COL14A1	0	0	0	1
	COL15A1	0	0	0	0
	COL16A1	7	8	7	11
	COL17A1	0	0	0	1
	COL18A1	55	100	175	200
	COL19A1	0	0	0	0
	COL20A1	0	0	0	3
	COL21A1	78	116	97	68
	COL22A1	0	0	0	0
	COL23A1	0	0	0	0
	COL24A1	0	0	0	0
	COL25A1	0	0	0	0
	COL27A1	55	57	144	248
COL28A1	0	0	0	1	

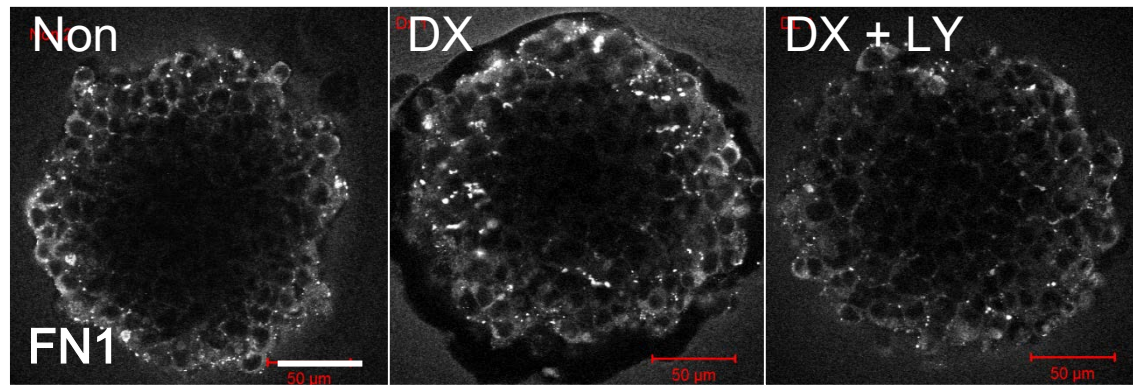
Extended Data Figure 11. Systematic comparison of the transcription mass (FPKM) of the ECM-related gene series expressed in HepG2 cells under several culture conditions. All data were obtained from RNA-seq results.

Extended Data Figure 12



Extended Data Figure 12. The whole image of immunoblotting analysis of fibronectin expression shown in Fig. 4g. Arrowhead: non-disassembled FN (285 kDa). Asterisk: a putative disassembled FN. Dashed rectangle: area shown in Fig. 4g. The image was prepared by Odyssey system (LI-COR, Lincoln, NB, USA).

Extended Data Figure 13



Extended Data Figure 13. Immunofluorescence of fibronectin in HepG2 spheroids after drug treatment. Day 5 HepG2 spheroids of non-treated or treated with DX or with DX and the TGFR inhibitor (LY) were embedded in the Smear Gell, fixed, permeabilized with detergent, and immunostained with rat anti-FN1 antibody and fluorescence-conjugated secondary antibody. Images were acquired using the confocal microscopy. Scale bar: 50 μm . The images were prepared by ZEN software (Zeiss, Jena, Germany),