

Figure S1. CSCs are enriched in sphere culture population. A, Representative images of tumors formed in the *in vivo* limiting dilution assay (1 × 10³, 10⁴ and 10⁵ cells/site). Scale bar = 10 mm. **B**, Expression levels of Sox2 in MCF7 and PDC #1 cells were compared between cells cultured under adherent and sphere conditions. Actin was used for loading control. **C**, (Left) Immunofluorescence images of Nanog staining in PDC #1 cells cultured under adherent and sphere conditions are shown. Nuclei were counterstained with DAPI. Arrows indicate cells with strong Nanog staining. Scale bar = 50 µm. (Right) The intensities of Nanog staining were quantified by using ImageJ software. One hundred cells in each slide were counted (mean ±SD, n = 3; ***p < 0.001). **D**, (Left) Immunofluorescence images of Myc staining in PDC #1 cells cultured under adherent and sphere conditions are shown. Nuclei were quantified by using ImageJ software. One hundred cells in each slide were counted (mean ±SD, n = 3; ***p < 0.001). **D**, (Left) Immunofluorescence images of Myc staining were quantified by using ImageJ software. One hundred cells with DAPI. Arrows indicate cells with strong Myc staining. Scale bar = 50 µm. (Right) The intensities of software. One hundred cells in each slide were quantified by using ImageJ software. One hundred cells in each slide were quantified by using Myc staining. Scale bar = 50 µm. (Right) The intensities of Myc staining were quantified by using ImageJ software. One hundred cells in each slide were quantified by using ImageJ software. One hundred cells in each slide were quantified by using ImageJ software. One hundred cells in each slide were quantified by using ImageJ software. One hundred cells in each slide were quantified by using ImageJ software. One hundred cells in each slide were quantified by using ImageJ software. One hundred cells in each slide were counted (mean ±SD, n = 3; ***p < 0.001).

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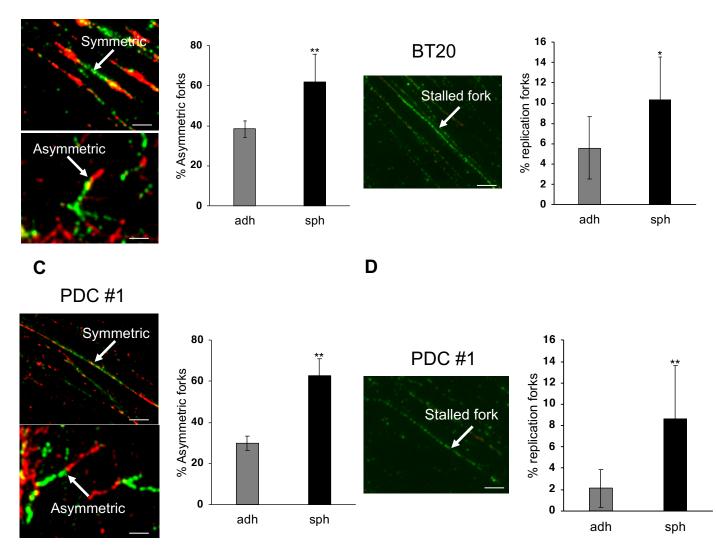


Figure S2. DNA replication stress is upregulated in CSC-enriched spheroid cells. A,C, Proportion of asymmetric forks, representative of replication stress. Thirty bidirectional forks in each slide were counted. Three slides for each population were prepared (mean \pm SEM, n = 3; **p < 0.01). Scale bar = 10 µm. B, D, Proportion of stalled forks, labeled only with green was calculated. Two hundred labeled forks in each slide were counted. Three slides for each population were prepared (mean \pm SEM, n = 3; **p < 0.01). Scale bar = 5 µm.

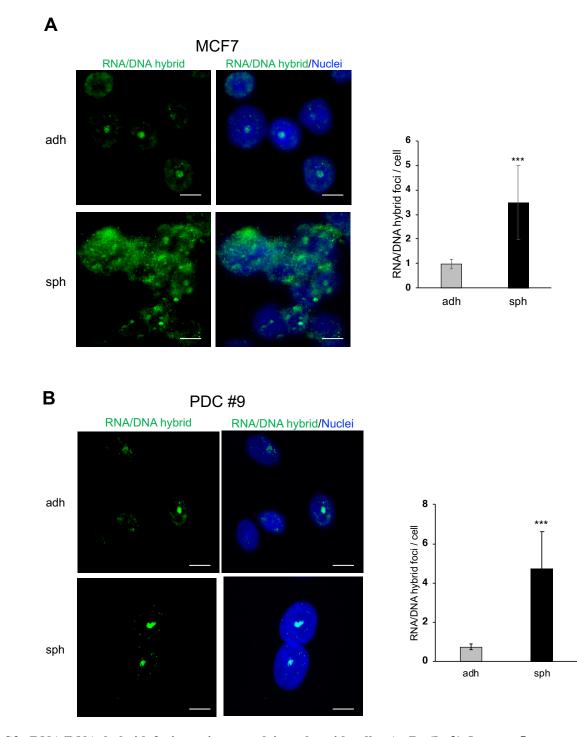


Figure S3. RNA/DNA hybrid foci are increased in spheroid cells. A, B, (Left) Immunofluorescence images of RNA/DNA hybrid staining in cells cultured in the adherent and sphere conditions are shown. (Right) Number of RNA/DNA hybrid foci in each cell was counted and compared between the two conditions. Hundred cells in each slide were counted. Three slides for each population were prepared (mean \pm SEM, n = 3; ***p < 0.001). Scale bar = 10 µm.

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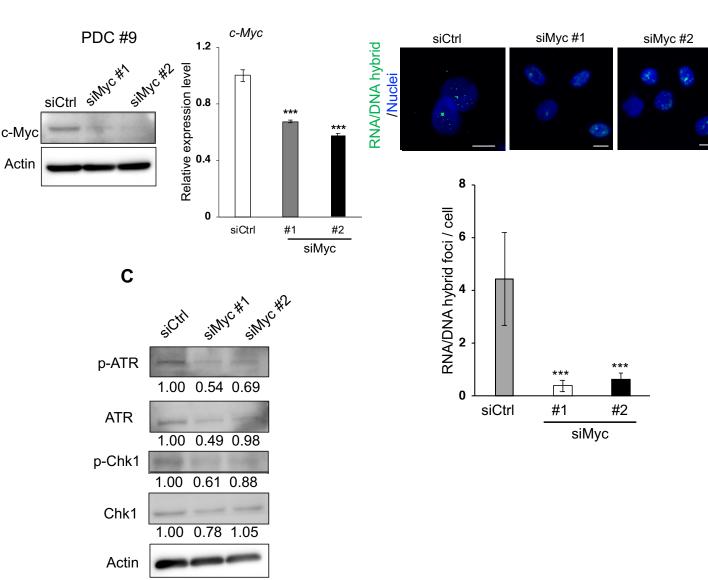


Figure S4. c-Myc expression contributes to replication stress. A, Knockdown efficiencies of siRNAs targeting *c*-*Myc* (siMyc #1 and #2) or control siRNA (siCtrl) in PDC#9 was compared by immunoblotting (left) and qPCR (right) (mean \pm SEM, n = 3; ***p < 0.001). B, Number of RNA/DNA hybrid foci in each cell was counted and compared among spheroid cells treated with siCtrl, *siMyc* #1, and *siMyc* #2. Scale bar = 10 µm. Hundred cells in each slide were counted. Three slides for each population were prepared (mean \pm SEM, n = 3; ***p < 0.001). C, Expression levels of ATR, p-ATR, Chk1 and p-Chk1 as determined by immunoblotting, were compared among cells treated with siCtrl, *siMyc* #1, and *siMyc* #2. Expression was quantified by ImageJ and normalized to Actin.

В

PANTHER Overrepresentation Test

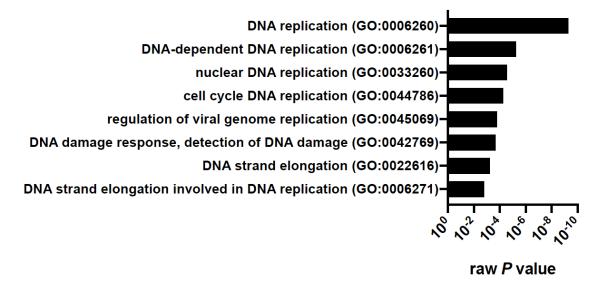


Figure S5. Gene Ontology (GO) enrichment analysis (<u>http://pantherdb.org/about.jsp</u>). Genes of which expression levels are >1.5 fold in spheroid cells than in adherent cells were analyzed.

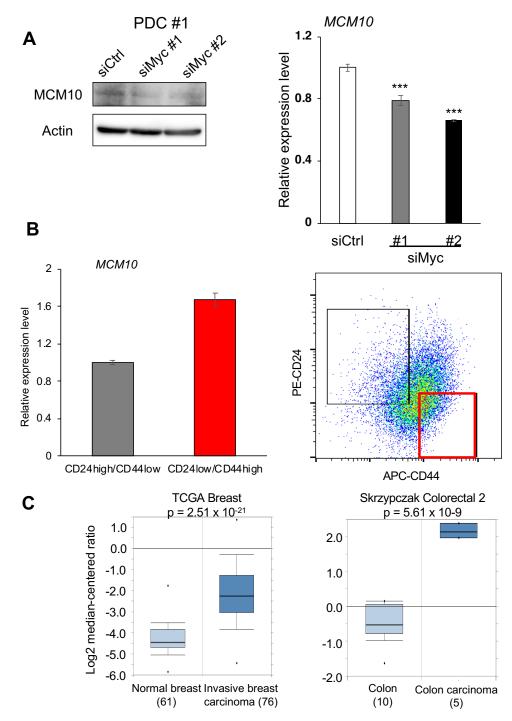


Figure S6. MCM10 expression is associated with c-Myc expression and upregulated in cancer stem-like cells and in cancer tissues. A, Expression level of MCM10 in PDC#1 in sphere conditions treated with siCtrl, *siMyc* #1 and *siMyc* #2 was compared by immunoblotting (left) and qPCR (right) (mean \pm SEM, n = 3; ***p < 0.001). Actin was used for loading control. **B**, Expression level of *MCM10* was compared by qPCR between the CD24^{-/low}/CD44^{high} CSC-enriched population and the CD24^{high}/CD44^{low} control population. The PDC #6 cells were analyzed. (mean \pm SEM, n = 3; *p < 0.05). **C**, *MCM10* expression was compared between non-malignant cells and cancer cells in breast and colon using the Oncomine cancer gene expression database (Left; TCGA Breast, Right; Skrzypczak Colorectal 2). P-values were calculated by Student's t-test.

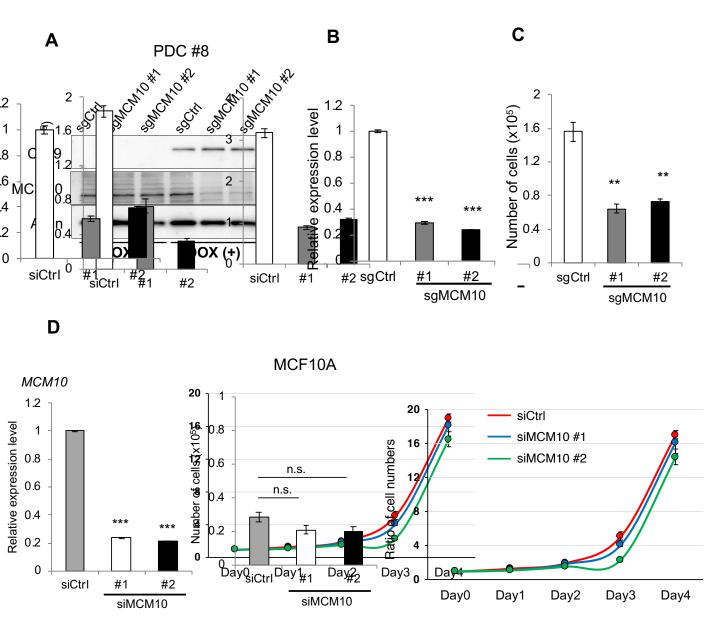
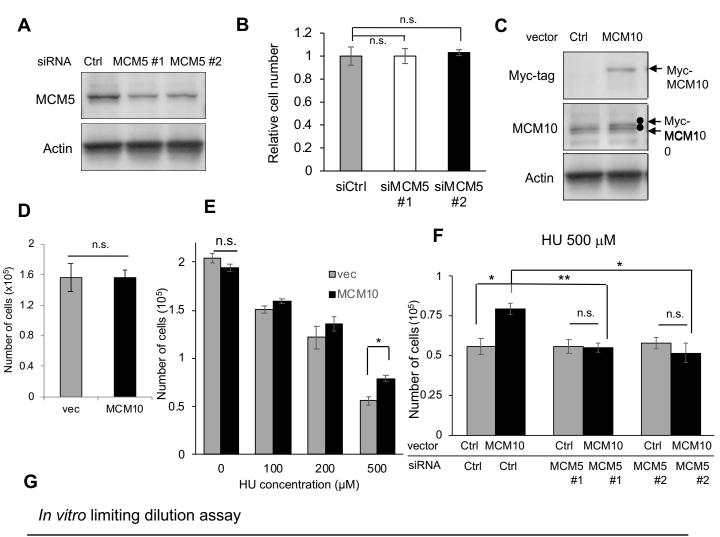


Figure S7. MCM10 plays important roles for proliferation of cancer cells. A, B, DOX-inducible knockout in PDC #8 (sgMCM10) and control cells (shCtrl) were compared by immunoblotting (A) and qPCR (B) (mean \pm SEM, n = 3; ***p < 0.001). C, Cells were seeded in 12-well plates (10,000 cells/well) and cultured. Then they were harvested and counted after 4 days (mean \pm SEM, n = 3; **p < 0.01). D, MCF10A treated with siCtrl or *siMCM10*. Knockdown efficiencies of siRNAs (left) and cell proliferation (middle and right) were compared.



		- CSC	Probability						
	63	125	250	500	1000	2000	frequency	(vs shCtrl)	
shCtrl	0/8	1/8	5/8	7/8	8/8	8/8	1/319	-	
shMCM10 #1	0/8	0/8	1/8	4/8	8/8	8/8	1/652	0.0456	
shMCM10 #2	0/8	0/8	1/8	3/8	8/8	8/8	1/716	0.0241	

Figure S8. MCM5 is involved in the functions of MCM10 and MCM10 plays important roles for sphere formation in vitro. A, B, Expression levels of MCM5 were compared in MCF7 cells treated with siCtrl or *siMCM5* (A). Number of cells were counted after 4 days (mean \pm SEM, n = 3) (B). C,D, Expression levels of endogenous MCM10 and Myc-tagged MCM10, as determined by immunoblotting, were compared among cells transfected with the indicated expression vectors (C). Number of cells were counted after 4 days (mean \pm SEM, n = 3)(D). E,F, MCF7 cells were transfected with the Myc-tagged MCM10 or empty vector (E). MCF7 cells were transfected with the Myc-tagged MCM10 or empty vector with indicated siRNAs (F). Cells were seeded in a 12-well plate (10,000 cells/well). Forty-eight hours later, they were treated with indicated concentrations of HU for an additional 48 h. Cells were harvested and counted (mean \pm SEM, n = 3; **p < 0.01, *p < 0.05). G, In vitro limiting dilution assay for MCM10-depleted cells in patient-derived breast cancer cells: 2,000, 1,000, 500, 250, 125, or 63 cells were seeding. CSC frequency and p-values were determined using the ELDA software.

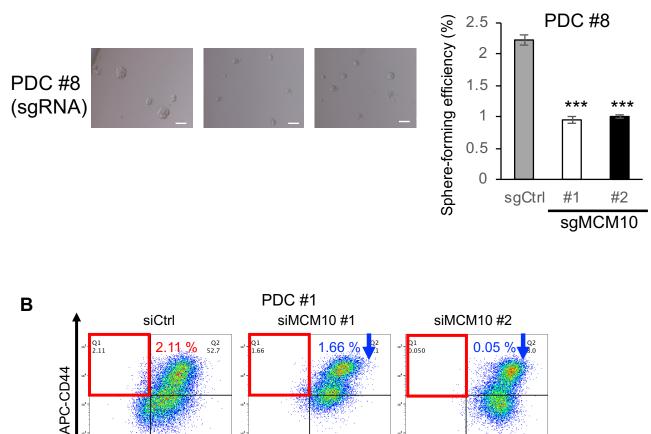


Figure S9. MCM10 plays important roles for CSC properties. A (Left) Representative images of tumor spheres. DOX-inducible *MCM10* knockout PDC #8 cells were cultured under sphere conditions. Scale bar = 100 μ m. (Right) Quantification of tumor sphere formation efficiency. Spheres were formed for 6 days (mean ± SEM, n = 4; ***p < 0.001). **B**, PDC#1 treated with siCtrl, *siMCM10* #1 or *siMCM10* #2 were stained with CD44 and CD24 antibodies, and then subjected to flow cytometry analysis.

PE-CD24

Q3 23.4 Q4 0.23

101

Q3 41.8

Q4 1.77

Q3 34.9

Q4 10.3

Table S1. Characteristics of clinical breast tumors used in this stud	ły
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PDC (#)	ER	PgR	HER2	Molecular subtypes			
1	-	-	0	Triple negative			
2	3+	3+	2+ (FISH+)	Luminal HER2			
3	3+	-	3+	Luminal HER2			
4	-	-	2+ (FISH+)	HER2			
5	-	-	2+ (FISH-)	Luminal like			
6	+	+	2+ (FISH-)	Luminal like			
7	-	+	-	Luminal like			
8	-	-	-	Ovarian cancer			
9	+	+	-	Luminal like			

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Rank	Gene symbol	· · · ·	ļ		Gene symbol	i			Gene symbol			Gene symbol	
1	GMNN	37.044			CENPL	3.325			NSL1	1.746		PSMA4	1.128
2	SPC25	28.289			ORC1	3.265			PSMC3	1.743		PSMB3	1.114
3	RPS27A	27.516			RFC2	3.244			PSMA3	1.739	1	CDKN1B	1.108
4	PSME1	21.896			PPP2R5B	3.204			PMF1	1.733		PPP2R5C	1.108
5	MCM10	15.916			CDC20	3.180	ļ		RPA2	1.720	155		1.105
6	CDT1	15.123			MCM4	3.153			PSMA5	1.707	156		1.103
7	PSMC2	13.974			RANBP2	3.138			PSMD11	1.700		CDK2	1.094
8	CENPI	13.831			MCM6	3.083			RPA1	1.698	158		1.020
9	AURKB	12.728		59	CENPN	3.048	ļ		CENPT	1.646	159		0.989
10	CDC6	12.029			PPP2R5A	2.991			PSMB7	1.645	160		0.896
11	BIRC5	9.943			INCENP	2.967			PSMD12	1.644		PSMD3	0.885
12	GINS2	9.823		62	MCM7	2.926			PSMD1	1.634	162	PSMB4	0.880
13	SKA1	9.493		63	POLD3	2.837		113	PSMA2	1.616	163	MAPRE1	0.868
14	NDC80	9.282		64	CASC5	2.796		114	PAFAH1B1	1.608	164	PSMB10	0.844
15	CENPM	8.938		65	PSMA1	2.785		115	PSMD6	1.595	165	KIF2A	0.822
16	ERCC6L	8.639		66	KIF20A	2.776		116	POLD2	1.564	166	KNTC1	0.814
17	PSMD9	8.307		67	RAD21	2.735		117	PSMA7	1.533	167	E2F3	0.773
18	NUF2	7.717		68	DNA2	2.724		118	RFC4	1.528	168		0.768
19	CDC45	7.440		69	LIG1	2.710		119	POLA2	1.519	169	STAG2	0.766
20	KIF2C	7.041		70	CENPP	2.706		120	CLIP1	1.509	170	POLD4	0.695
21	NUDC	7.037		71	SKA2	2.696		121	PSME2	1.509	171	SEH1L	0.626
22	PRIM1	6.714		72	SPC24	2.657		122	POLE2	1.489	172	PSMB2	0.624
23	ZWINT	6.504		73	PPP2CB	2.635		123	PSMB1	1.467	173	PSMC6	0.610
24	CDCA8	6.473		74	MAD2L1	2.634		124	UBA52	1.466	174	RFC5	0.548
25	CENPK	6.246		75	FBXO5	2.612		125	CCNA2	1.461	175	PSME4	0.533
26	MLF1IP	5.954		76	CDKN1A	2.611		126	PSMB5	1.451	176	RCC2	0.502
27	ZWILCH	5.924		77	RPA3	2.554		127	ORC4	1.405	177	CKAP5	0.496
28	KIF18A	5.346		78	CCNA1	2.552		128	PSMD14	1.402	178	NDEL1	0.472
29	GINS1	5.281		79	CENPO	2.513		129	PSMD8	1.377	179	CLASP1	0.438
30	FEN1	5.251		80	DSN1	2.460			ORC3	1.366	180	RANGAP1	0.436
31	E2F1	4.845		81	MCM3	2.456		131	PSMB8	1.352		CENPC1	0.417
32	GORASP1	4.819		82	NUP85	2.418		132	PSMD13	1.344	182	B9D2	0.320
33	CENPA	4.714		83	PSMF1	2.379		133	PSMD2	1.336		PSMC1	0.121
34	PLK1	4.472		84	DBF4	2.332		134	MIS12	1.320	184	RPS27	0.020
35	SGOL2	4.429		85	MCM8	2.249		135	XPO1	1.316			
36	BUB1	4.375		86	POLE	2.223		136	PSMD4	1.282			
37	E2F2	4.169		87	PSMC4	2.145		137	GINS4	1.275			
	ITGB3BP	4.135		88	SEC13	2.123		138	NUP107	1.271			
39	TAOK1	3.893		89	MCM2	2.109		139	CENPH	1.269			
40	PCNA	3.872		90	STAG1	1.914		140	PSMA6	1.253			
41	ORC6	3.823		91	PSMA8	1.895			ORC5	1.211			
42	SMC3	3.778		92	PPP2R1A	1.836		142	ZW10	1.187			
43	MCM5	3.717		93	NUP133	1.833		143	PRIM2	1.182			
44	CENPQ	3.709		94	SMC1A	1.804		144	PSMB9	1.167			
45	SGOL1	3.628		95	PSMC5	1.799		145	PSMB6	1.157			
46	RFC3	3.606		96	PPP2R5E	1.790		146	NUP43	1.156			
47	CDC7	3.542		97	ORC2	1.776		147	POLA1	1.147			
48	KIF23	3.485		98	PSMD10	1.773		148	PSMD7	1.138			
49	APITD1	3.353		99	NUP37	1.771			RB1	1.131			
50	BUB1B	3.351		100	BUB3	1.767		150	AHCTF1	1.129			

Table S2. Genes included in Reactome_DNA_Replication gene set and the ratios of expression levels of each gene, sphere cells (SPH) / adherent cells (ADH)