

Case No.	Antigen	Parental tissue	TG1	TG2 – TG6	TG8
UXE-001	AE1/AE3	+	+	+	+
	ER	+	+/- or ++	-	-
	TP53	WT	WT	WT	WT
	PTEN	-	-	-	-
	ARID1A	-	-	-	-
	PAX8	+	+	+	+
	PAX2	+focal	- or +focal	-	-
	PMS2	+	NA	NA	NA
	MSH6	+	+	+	+
UXE-004	AE1/AE3	+	+	+	+/-
	ER	++	+/- or ++	++	++
	TP53	WT	WT	WT	WT
	PTEN	-	-	-	-
	ARID1A	-	-	-	-
	PAX8	+/-	+/-	+	+
	PAX2	-	-	-	-
	PMS2	-partly	- or +/-	NA	NA
	MSH6	+	+	+	+
UXE-005	AE1/AE3	+	+/-	+	+
	ER	++	+/-	++	++
	TP53	+partly	WT	WT	WT
	PTEN	-	-	+	+
	ARID1A	+	+	+	+
	PAX8	+/-	-	+	+
	PAX2	-	-	-	-
	PMS2	+	+	+	+
	MSH6	+	+	+	+
UXE-008	AE1/AE3	+/-	- or +/-	-	+/-
	ER	+/-	- or +	-	-
	TP53	WT	WT	WT	WT
	PTEN	-	-	-	-
	ARID1A	-	-	-	-
	PAX8	+	- or +	-	-
	PAX2	+focal	- or +focal	-	-
	PMS2	+	+	+	+
	MSH6	+	+	+	+
UEX-009	AE1/AE3	+/-	+/-	+/-	+/-
	ER	-	-	-	-
	TP53	WT	WT	WT	WT
	PTEN	+focal	+	+	+
	ARID1A	-	-	-	-
	PAX8	+/-	-	+/-	+/-
	PAX2	-	-	-	-
	PMS2	+	+	+	+
	MSH6	+	+	+	+
UXE-010	AE1/AE3	+	+	+	+
	ER	+	+/++	++	++
	TP53	WT	WT	WT	WT
	PTEN	-	-	-	-
	ARID1A	-	-	-	-
	PAX8	+	+	+	+
	PAX2	+focal	+focal	- or +focal	- or +focal
	PMS2	+	+	+	+
	MSH6	-	-	-	-

Supplementary Table S1 Summary of immunohistochemistry for parental tissues and PDXs

AE1/AE3, PAX8: +, positive; +/-, including negative cell groups; -, almost all negative cells

ER: ++, >50%; +, 10-50%; +/-, 1-10%; -, 0-1% positive cells

TP53: WT, scattered positive cells; +, mutant patterns with almost all positive cells

ARID1A, MSH6: +, retained; -, lost

PAX2, PTEN: +, focal, including negative cell groups; -, almost all negative cells

PMS2: +, retained; +/-, including negative cell groups; -, lost; NA, poor staining

Case No.	Gene Name	Variant Function	AA change	Variant rate (%)	
				Parental tissue	PDX-TG8
001	<i>MTOR</i>	nonsynonymous SNV	G305C	4.3	
			K1815T		10.4
	<i>ARID1A</i>	frameshift deletion	S634fs*12	9.5	40.8
		frameshift insertion	Y1027*	14.7	47.7
		nonsynonymous SNV	R1833C		22.4
	<i>JAK1</i>	nonsynonymous SNV	R542C	4.4	
	<i>NFE2L2</i>	nonsynonymous SNV	E82D	4.2	
	<i>IL7R</i>	nonsynonymous SNV	N65S		27.6
	<i>PIK3R1</i>	nonframeshift deletion	I405del	7.5	39.6
		splicing	—		39.7
	<i>MET</i>	nonsynonymous SNV	M1229V	3.4	
	<i>NOTCH1</i>	nonsynonymous SNV	E681D	3.6	
	<i>ATM</i>	nonsynonymous SNV	R2832H	8.8	50.8
		nonframeshift deletion	F627fs*22		26.7
	<i>SETBP1</i>	nonsynonymous SNV	R1456C		38.1
	<i>KEAP1</i>	nonsynonymous SNV	R354W	1.7	
	<i>CHEK2</i>	nonsynonymous SNV	R474H	4.0	
			R145Q	12.2	51.9
	<i>EP300</i>	stopgain SNV	R202*	3.9	

Case No.	Gene Name	Variant Function	AA change	Variant rate (%)	
				Parental tissue	PDX-TG8
004	<i>MTOR</i>	nonsynonymous SNV	A2532V	41.5	
		stopgain SNV	G845*	2.9	50.1
	<i>ARID1A</i>	stopgain SNV	R1989*	89.9	99.9
	<i>JAK1</i>	nonsynonymous SNV	R873H	2.6	47.7
			R93H		50.1
	<i>NOTCH2</i>	stopgain SNV	G929*	42.2	
		nonsynonymous SNV	C547R	45.6	49.5
	<i>TPM3</i>	nonsynonymous SNV	A203V	33.8	
	<i>NTRK1</i>	nonsynonymous SNV	E413K	49.2	49.9
	<i>MDM4</i>	nonsynonymous SNV	A472T	2.4	48.4
	<i>AKT3</i>	nonsynonymous SNV	P69Q	33.3	
		stopgain SNV	Y312*		48.2
	<i>MYCN</i>	nonsynonymous SNV	P44L	55.7	61.8
	<i>ALK</i>	nonsynonymous SNV	S1561L	42.0	44.8
			P1551S	2.5	57.0
	<i>MSH2</i>	nonsynonymous SNV	G204E		47.0
	<i>BCL2L11</i>	nonsynonymous SNV	G156R	43.0	
	<i>NFE2L2</i>	nonsynonymous SNV	F70C	44.2	50.1
			V591G		48.6
	<i>ERBB4</i>	nonsynonymous SNV	E1121D	43.6	49.6
			T731M		49.5

004	<i>BRAD1</i>	stopgain SNV	R641*	1.8	
	<i>RAF1</i>	nonsynonymous SNV	K439E	41.6	
	<i>CTNNB1</i>	nonsynonymous SNV	R225H	43.3	
			A522T	2.7	48.1
			M735L	46.6	49.9
			K133N		49.8
	<i>SETD2</i>	nonsynonymous SNV	P2379L	44.8	50.7
			D790Y	3.0	48.7
		frameshift insertion	R1407fs*8		37.0
	<i>BAP1</i>	nonsynonymous SNV	S341N		46.5
	<i>PBRM1</i>	frameshift deletion	F1018fs*15	36.4	
		nonsynonymous SNV	D901G	45.5	48.9
	<i>PIK3CA</i>	nonsynonymous SNV	E81K	51.4	55.6
	<i>FGFR3</i>	nonsynonymous SNV	G493S	40.5	
	<i>PDGFRA</i>	nonsynonymous SNV	G898D	2.0	48.7
	<i>KIT</i>	nonsynonymous SNV	D419N	44.2	49.1
	<i>MAP3K1</i>	nonsynonymous SNV	S1299R	47.6	50.4
	<i>PIK3R1</i>	stopgain SNV	R386*	46.3	51.7
		nonsynonymous SNV	D560G	44.5	49.3
	<i>APC</i>	nonsynonymous SNV	A501D	1.8	48.7
			P1665H		47.6
	<i>FGFR4</i>	nonsynonymous SNV	C271Y	1.4	44.1
	<i>ROS1</i>	nonsynonymous SNV	R2210I	46.4	47.3
		frameshift deletion	N1767fs*22	36.5	
	<i>MAP3K4</i>	nonsynonymous SNV	V562A	40.9	
			G857E		47.4
	<i>FGFR</i>	nonsynonymous SNV	R671C	35.4	
	<i>MET</i>	nonsynonymous SNV	S752Y	47.3	48.8
			V1362I	42.0	
			P210T		49.0
	<i>SMO</i>	nonsynonymous SNV	T336A	49.7	60.4
	<i>NRG1</i>	nonsynonymous SNV	A531A	41.8	
			R220H		50.1
	<i>FGFR1</i>	nonsynonymous SNV	R250W	1.8	46.7
	<i>JAK2</i>	frameshift deletion	K302fs*8	35.8	
		nonsynonymous SNV	V392M	2.6	50.6
		stopgain SNV	E1006*	42.1	
	<i>CDKN2A</i>	nonsynonymous SNV	G67D		36.1
	<i>PTCH1</i>	nonsynonymous SNV	S1359R	33.5	
			L254S		47.8
	<i>TSC1</i>	nonsynonymous SNV	V219A	36.6	
	<i>KIF5B</i>	nonsynonymous SNV	Y649H	42.0	
	<i>RET</i>	nonsynonymous SNV	F195L	2.5	49.0
	<i>PTEN</i>	nonsynonymous SNV	R130Q	46.2	47.9
		frameshift insertion	N323fs*2	41.3	
	<i>NT5C2</i>	nonsynonymous SNV	R367Q	44.7	52.6
	<i>FGFR2</i>	nonsynonymous SNV	A53V		43.1

004	<i>IGF2</i>	nonsynonymous SNV	G49S	80.8	99.7
	<i>ATM</i>	stopgain SNV	R1730*	47.1	48.6
		nonsynonymous SNV	S978Y		51.5
	<i>KRAS</i>	nonsynonymous SNV	G12A	42.9	65.1
	<i>ARID2</i>	stopgain SNV	Q965*	2.0	48.4
	<i>CDK4</i>	nonsynonymous SNV	K106N	41.9	
	<i>POLE</i>	nonsynonymous SNV	S1931F	2.6	47.1
			V411L	34.5	39.7
	<i>FLT3</i>	nonsynonymous SNV	Y597C	3.0	49.4
			F316V	2.5	47.2
	<i>BRCA2</i>	stopgain SNV	E790*	45.3	48.6
		nonsynonymous SNV	I1065S	46.6	51.2
	<i>RB1</i>	nonsynonymous SNV	R857C	42.8	
	<i>NTRK3</i>	nonsynonymous SNV	R536K		49.9
	<i>IGF1R</i>	nonsynonymous SNV	V732M		46.0
	<i>CREBBP</i>	nonsynonymous SNV	R1786C	2.0	44.9
			R624C	2.0	48.7
	<i>TP53</i>	stopgain SNV	R196*	45.2	47.6
	<i>NF1</i>	nonsynonymous SNV	V212F	2.2	49.7
	<i>ERBB2</i>	nonsynonymous SNV	R968I		49.0
	<i>KEAP1</i>	nonsynonymous SNV	D165N	43.2	
	<i>SMARCA4</i>	nonsynonymous SNV	E861K	45.4	49.9
	<i>NOTCH3</i>	nonsynonymous SNV	V905M	2.0	47.7
			A564T	38.0	41.4
	<i>JAK3</i>	nonsynonymous SNV	E1019D	33.1	
	<i>PIK3R2</i>	nonsynonymous SNV	A190V	62.2	
	<i>AKT2</i>	nonsynonymous SNV	Q472R	45.2	
	<i>ACTN4</i>	nonsynonymous SNV	R95W		44.8
	<i>AXL</i>	nonsynonymous SNV	A848V		46.5
	<i>POLD1</i>	nonsynonymous SNV	A308V	2.2	53.1
			T747A	3.3	52.7
	<i>EP300</i>	nonsynonymous SNV	P428S	44.1	49.5
		stopgain SNV	R1312*	2.4	43.2
	<i>ARAF</i>	frameshift deletion	R255fs*37		40.5

Case No.	Gene Name	Variant Function	AA change	Variant rate (%)	
				Parental tissue	PDX-TG8
005	<i>ARID1A</i>	stopgain SNV	Y1027*		48.4
	<i>PIK3CA</i>	nonsynonymous SNV	C378Y	61.5	67.0
		nonframeshift deletion	E453del	53.0	58.6
	<i>TP53</i>	nonsynonymous SNV	G245S	40.9	
		splicing	—	43.4	99.9
	<i>BRCA1</i>	nonsynonymous SNV	P1136S		46.0
	<i>SETBP1</i>	nonsynonymous SNV	S1492R	45.9	47.8
	<i>ACTN4</i>	nonsynonymous SNV	R695L	43.7	

Case No.	Gene Name	Variant Function	AA change	Variant rate (%)	
				Parental tissue	PDX-TG8
008	<i>ARID1A</i>	frameshift deletion	D1850fs*33	81.4	90.3
	<i>NRAS</i>	nonsynonymous SNV	Q61L	47.9	49.1
			G12D	46.3	49.8
	<i>IDH1</i>	nonsynonymous SNV	R132H	62.8	64.3
	<i>CTNNB1</i>	nonsynonymous SNV	Y333F	49.4	50.3
	<i>PIK3CA</i>	nonsynonymous SNV	R88Q	57.0	58.0
			E726K	46.3	48.6
	<i>PTEN</i>	stopgain SNV	R130*	31.2	29.0
		splicing	—	63.7	65.0
	<i>NOTCH3</i>	nonsynonymous SNV	N1597K	51.5	49.7

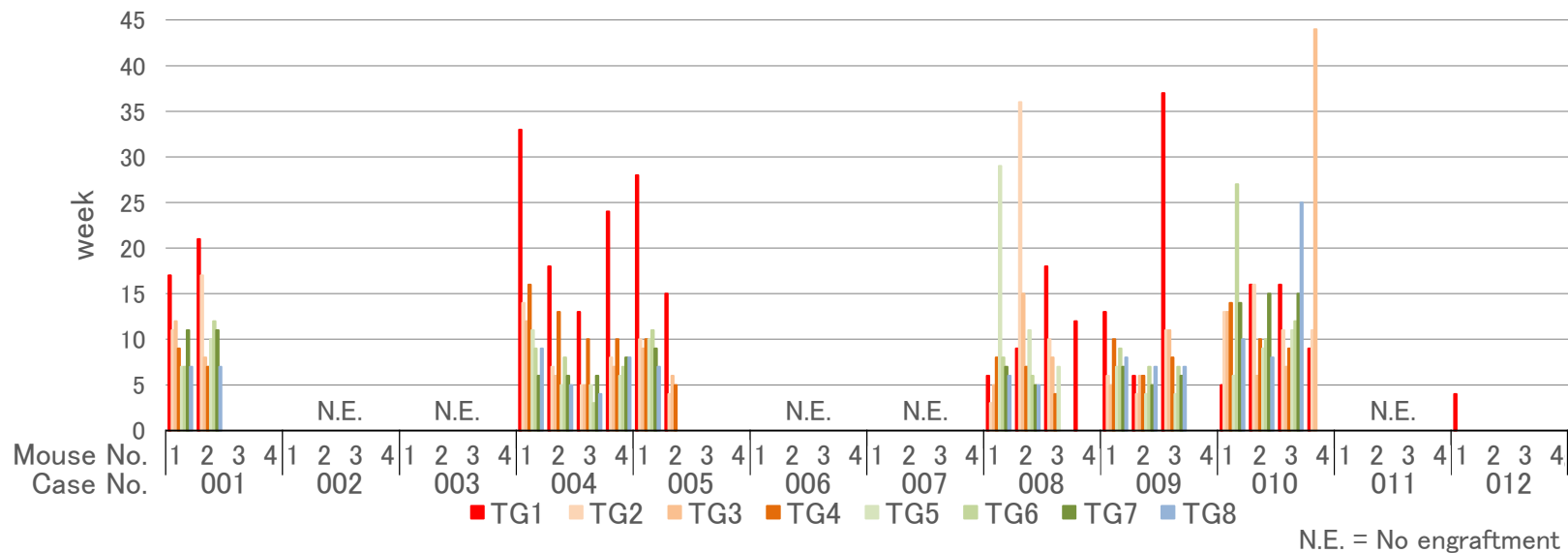
Case No.	Gene Name	Variant Function	AA change	Variant rate (%)	
				Parental tissue	PDX-TG8
009	<i>ARID1A</i>	frameshift insertion	H203fs*197	41.2	43.1
		nonframeshift deletion	P21delP		31.8
	<i>PIK3R1</i>	nonframeshift insertion	N453_T454insN	25.5	32.0
	<i>KRAS</i>	nonsynonymous SNV	G12V	34.5	47.4

Case No.	Gene Name	Variant Function	AA change	Variant rate (%)	
				Parental tissue	PDX-TG8
010	<i>MTOR</i>	stopgain SNV	R2018*	35.8	50.2
		nonsynonymous SNV	R2060W		16.1
	<i>ARID1A</i>	frameshift deletion	D1850fs*33	31.9	38.8
		frameshift insertion	D1850fs*4	40.8	58.0
	<i>FBXW7</i>	nonsynonymous SNV	R689W	35.4	49.2
	<i>IL7R</i>	frameshift deletion	R267fs*28		43.4
	<i>ROS1</i>	nonsynonymous SNV	G1915R	37.5	51.9
	<i>MYC</i>	nonsynonymous SNV	A59V		44.0
	<i>PTEN</i>	stopgain SNV	R233*	38.6	48.2
	<i>HRAS</i>	nonsynonymous SNV	A59T		46.5
	<i>ATM</i>	nonsynonymous SNV	R1973I		47.7
	<i>FLT3</i>	nonsynonymous SNV	T432M	49.4	49.9
	<i>BRCA2</i>	frameshift deletion	S1650fs*20	34.6	45.7
	<i>NF1</i>	frameshift deletion	Y628fs*3	14.9	
		frameshift insertion	I679fs*21	22.9	
	<i>BRCA1</i>	frameshift deletion	K654fs*47	35.5	42.7
	<i>KDM6A</i>	stopgain SNV	R393*		44.1

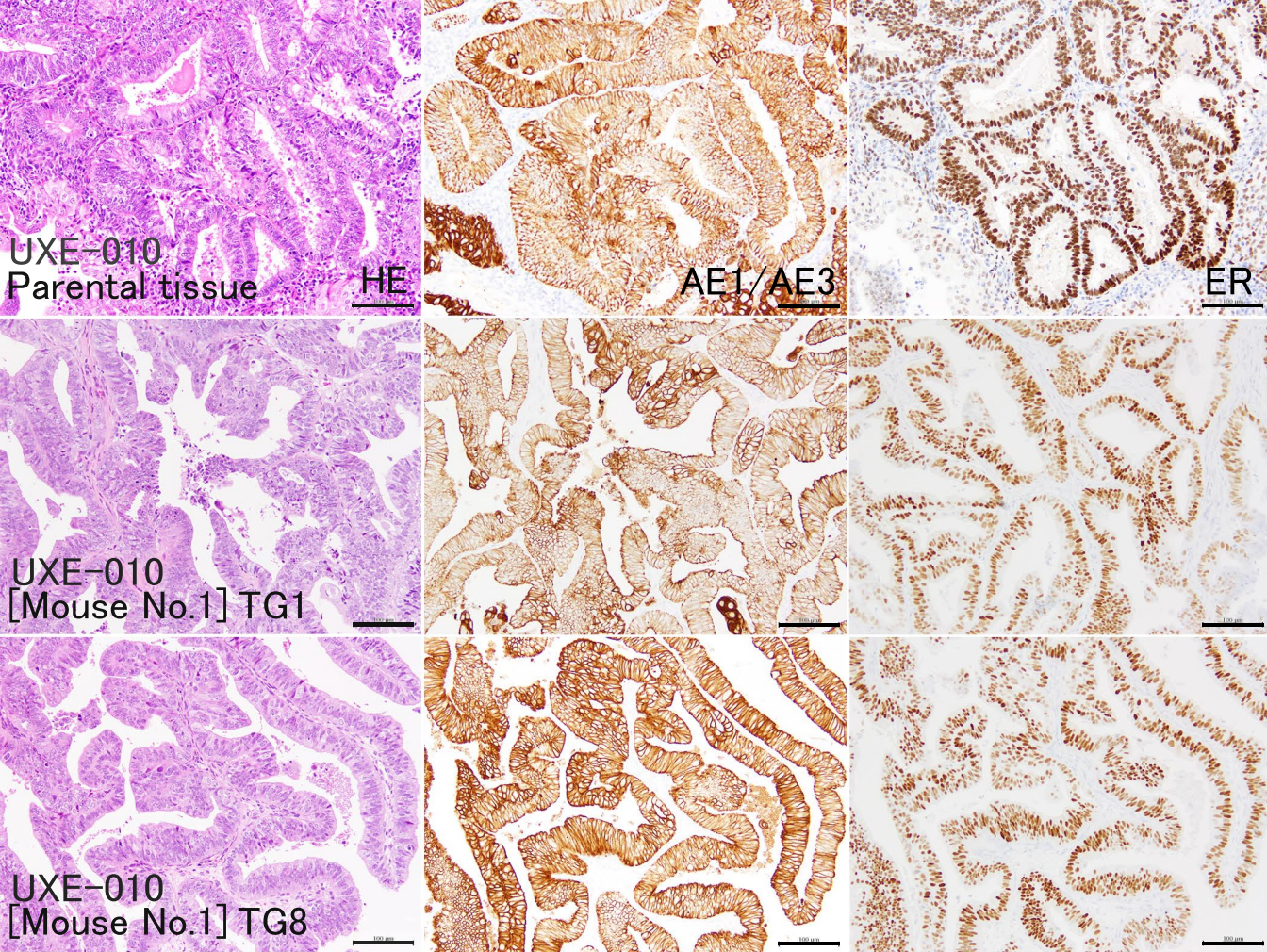
Supplementary Table S2 Variant rates of cancer-associated genes between original tumor tissues and TG8-PDXs.

Gene	NCBI RefSeq	Forward primer	Reverse primer
<i>MYC</i>	NM_002467	CCCTCAACGTTAGCTTCACC	AGCAGCTCGAATTTCTTCCA
<i>IL7R</i>	NM_002185	TGCATGGCTACTGAATGCTC	GCCTTAATCCCCTTTGTGGT

Supplementary Table S3 **Primer sequences (5' → 3') for Sanger sequencing**

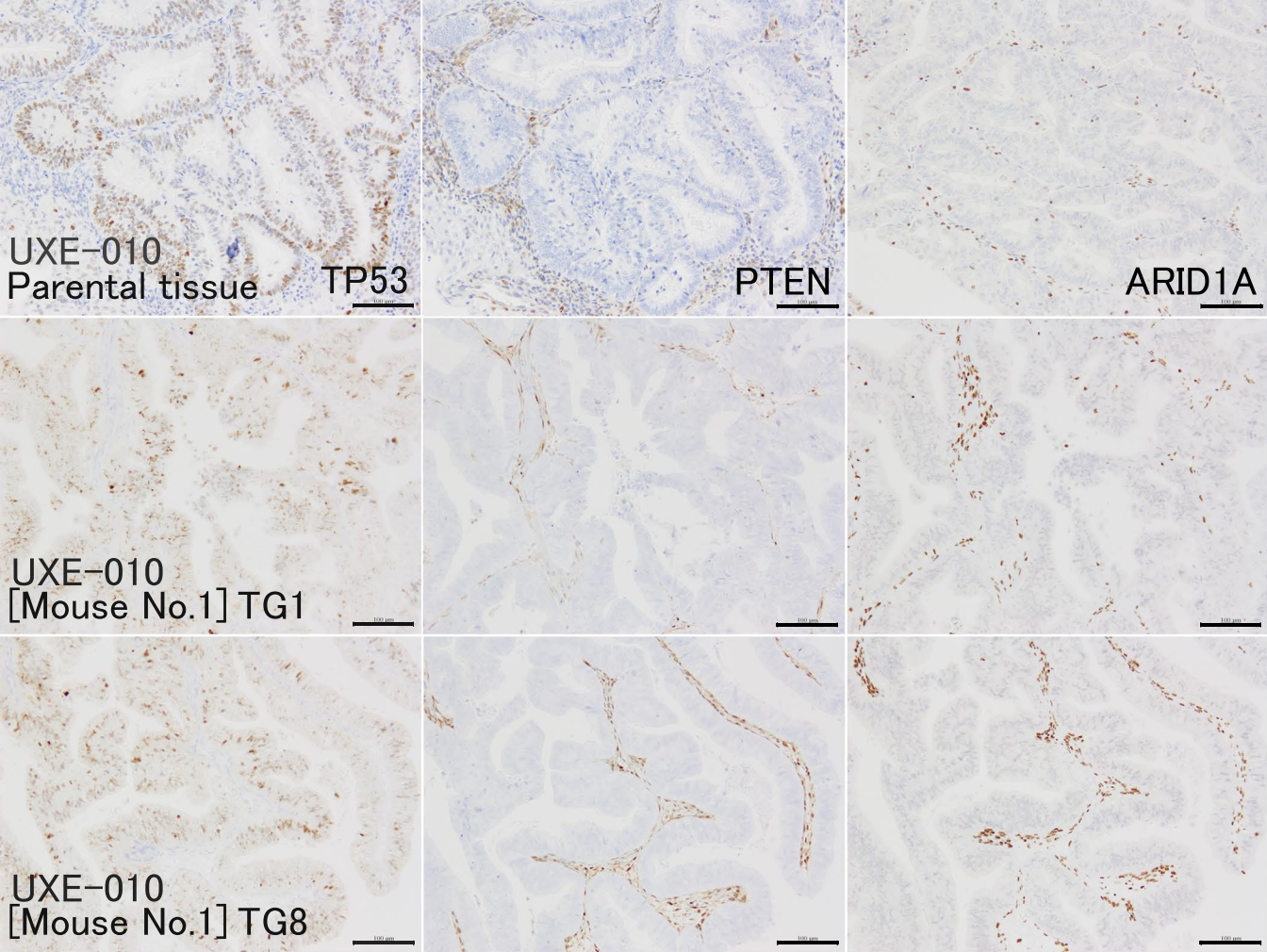


Supplementary Figure S1 Duration from implantation to passaging to the next generation, which could represent the growth of PDXs) in each mouse



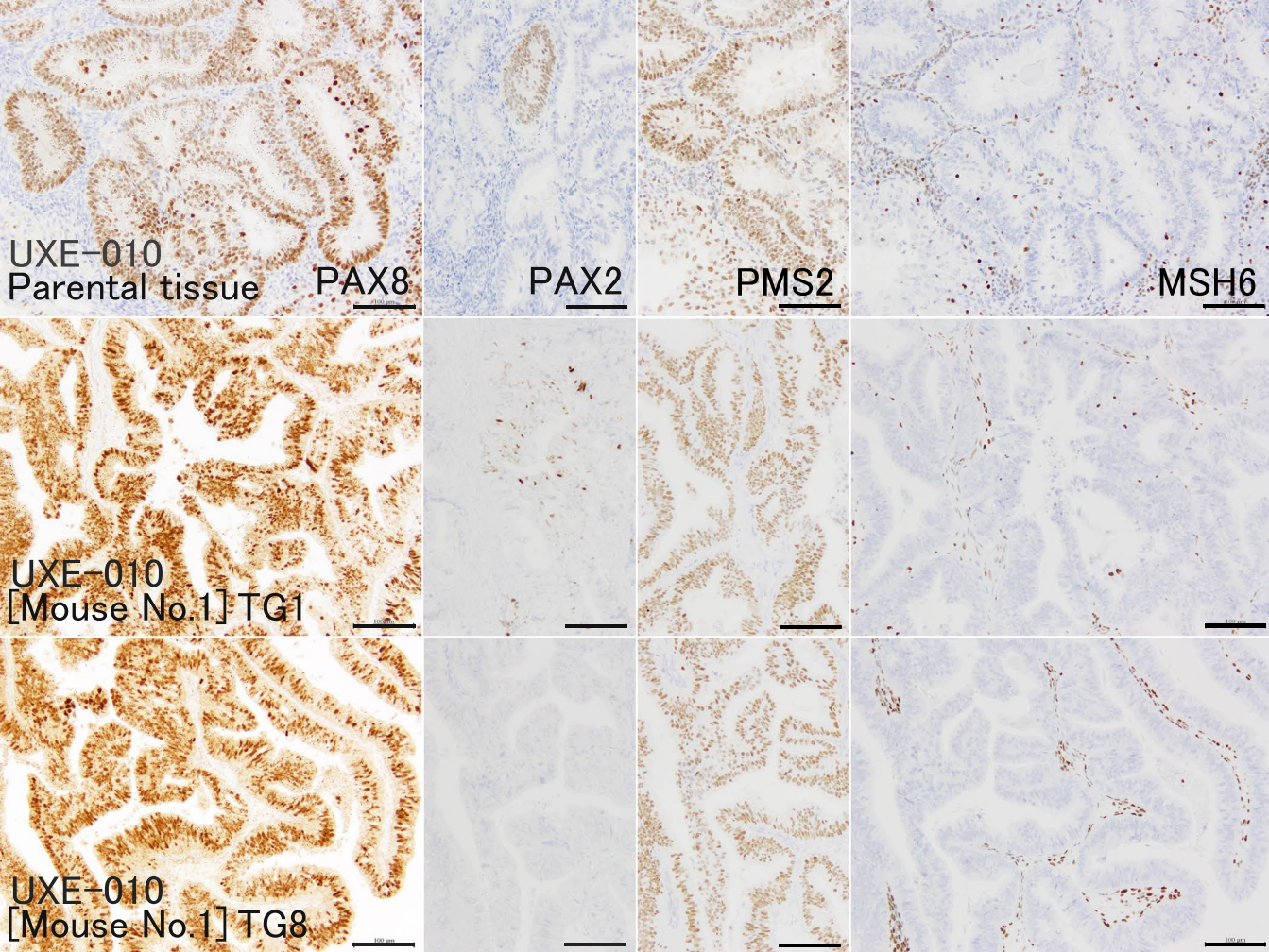
Supplementary Figure S2A

Histological and immunohistochemical photographs of a parental tissue and PDXs. Left panels, HE staining. Middle and right panels present immunohistochemical staining, using a serial section of the each left HE stained setcion.



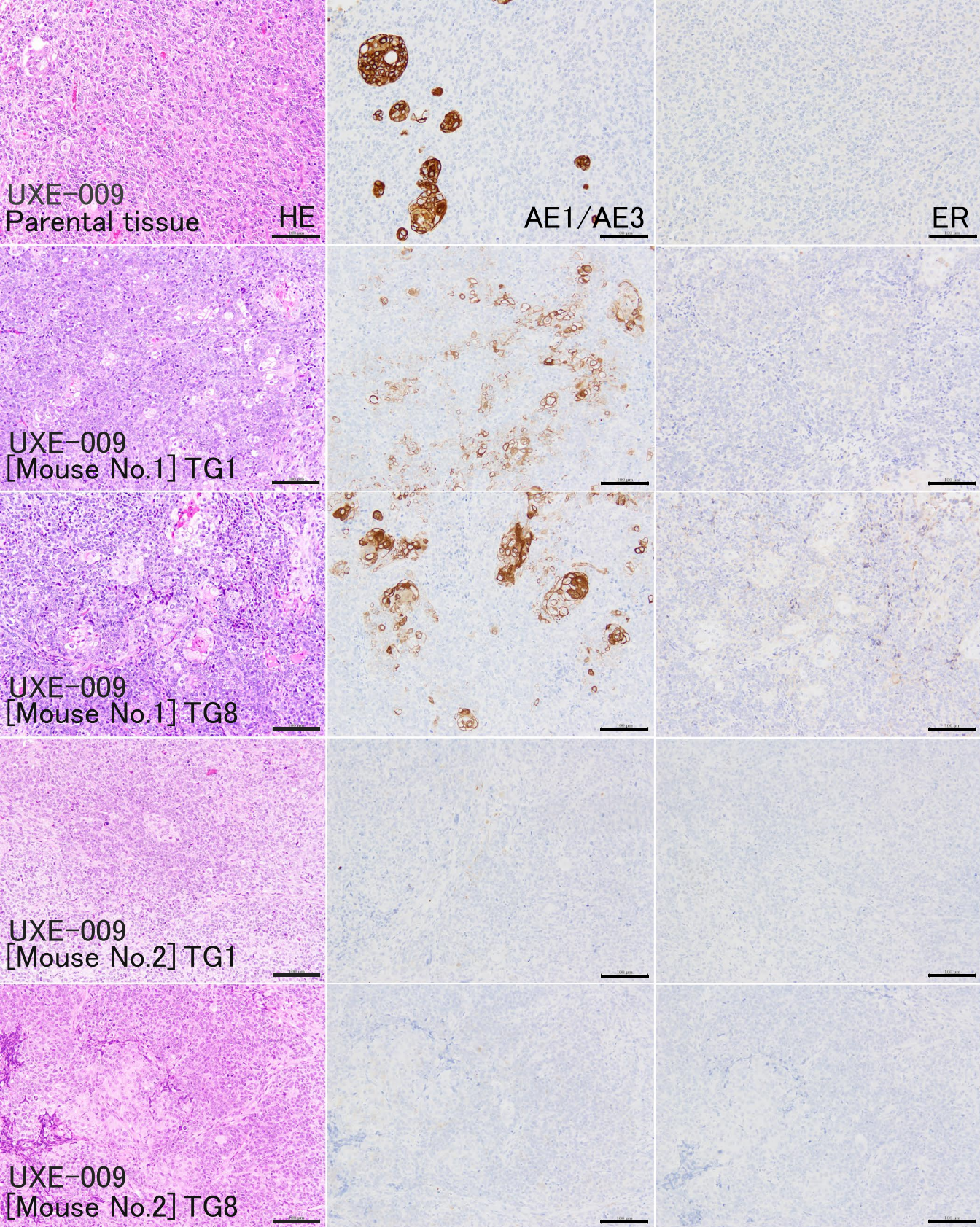
Supplementary Figure S2B

Immunohistochemical photographs of a parental tissue and PDXs, using a serial section of the each HE stained setcion.



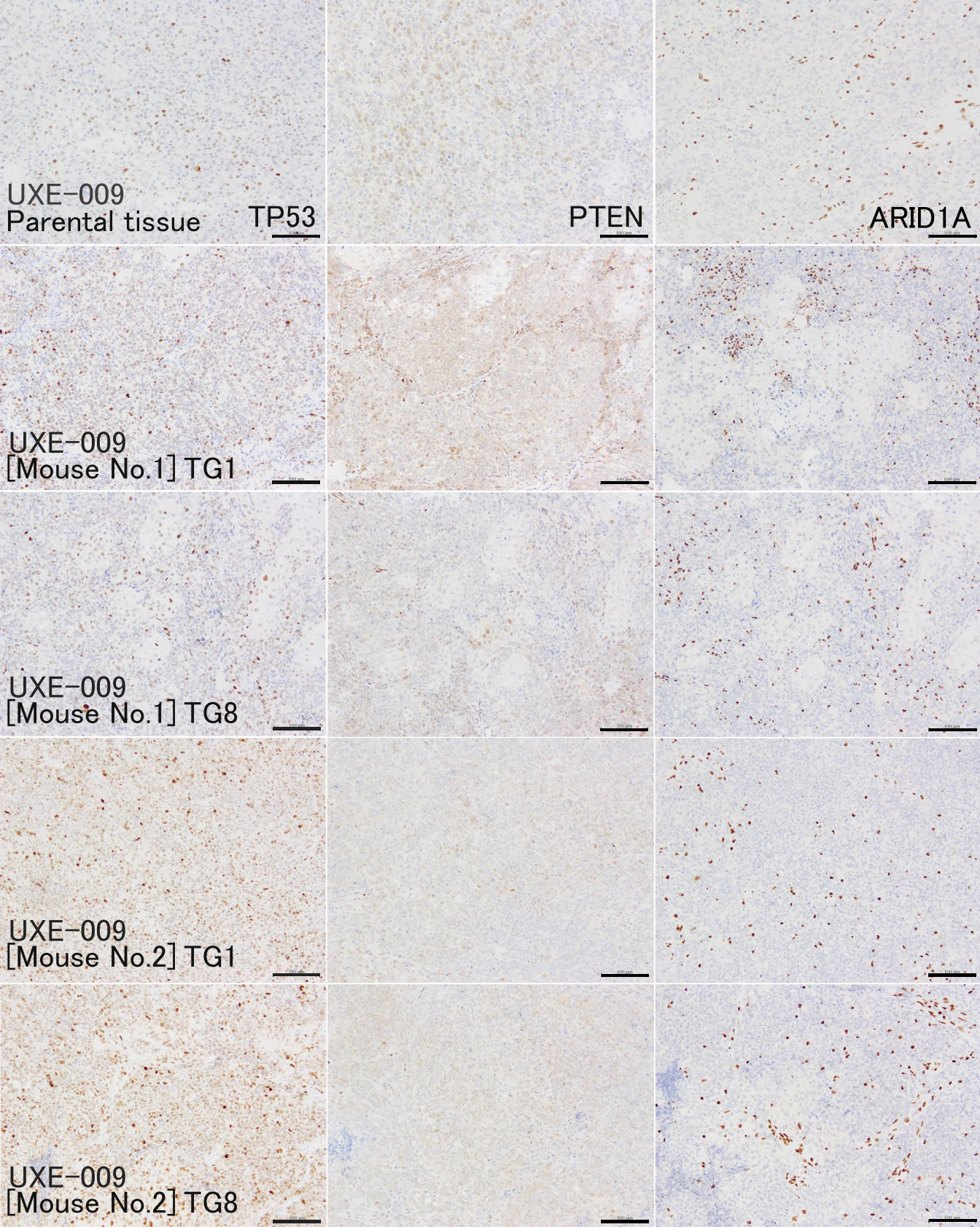
Supplementary Figure S2C

Immunohistochemical photographs of a parental tissue and PDXs, using a serial section of the each HE stained setction.



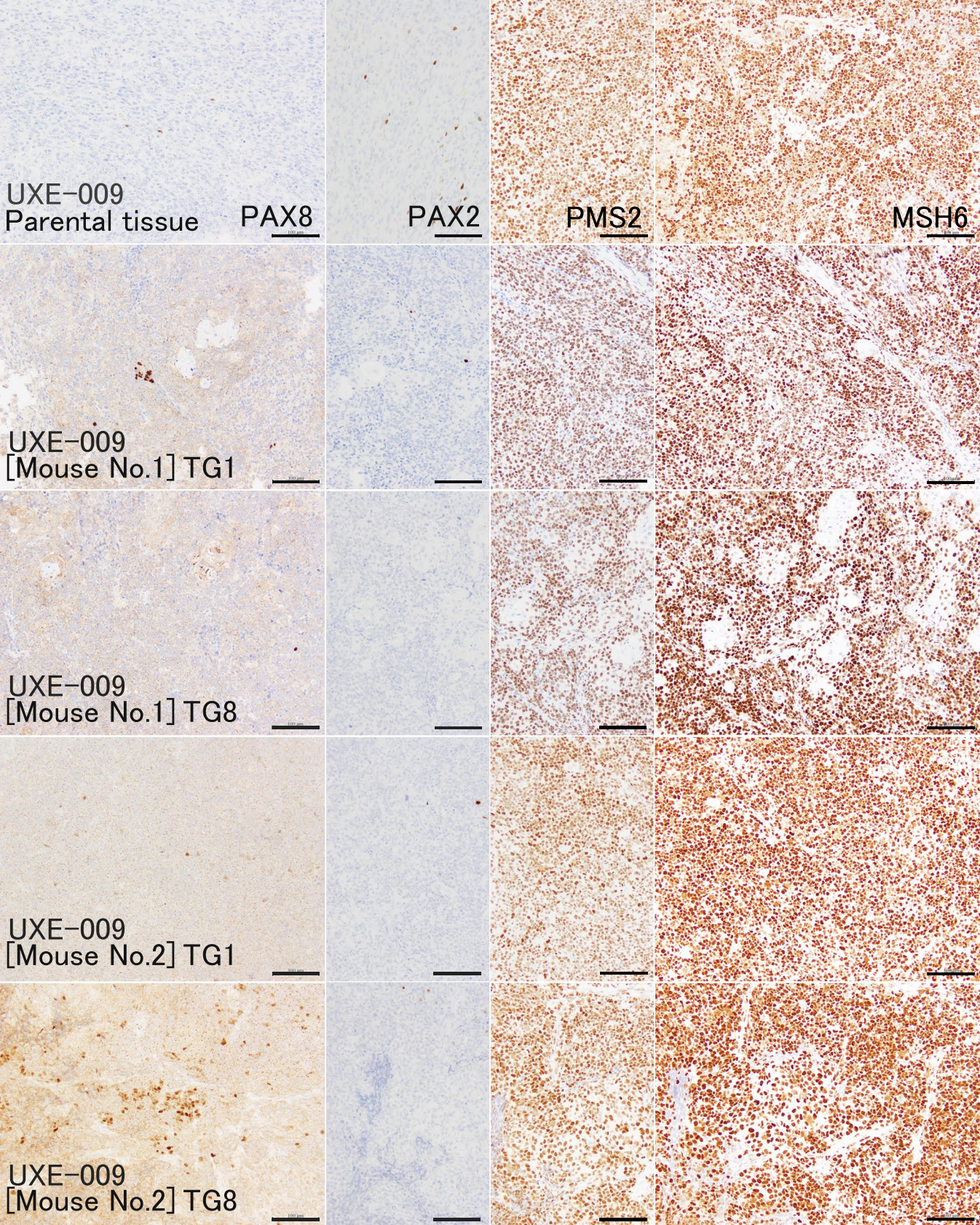
Supplementary Figure S3A

Histological and immunohistochemical photographs of a parental tissue and PDXs. Left panels, HE staining. Middle and right panels present immunohistochemical staining, using a serial section of the each left HE stained setcion.

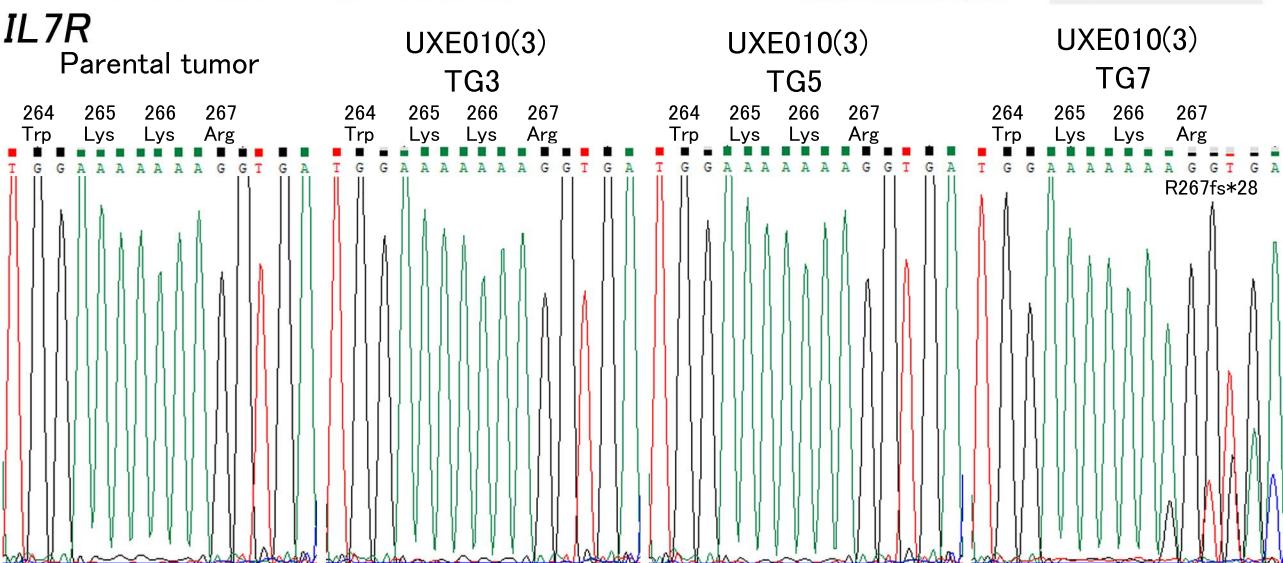
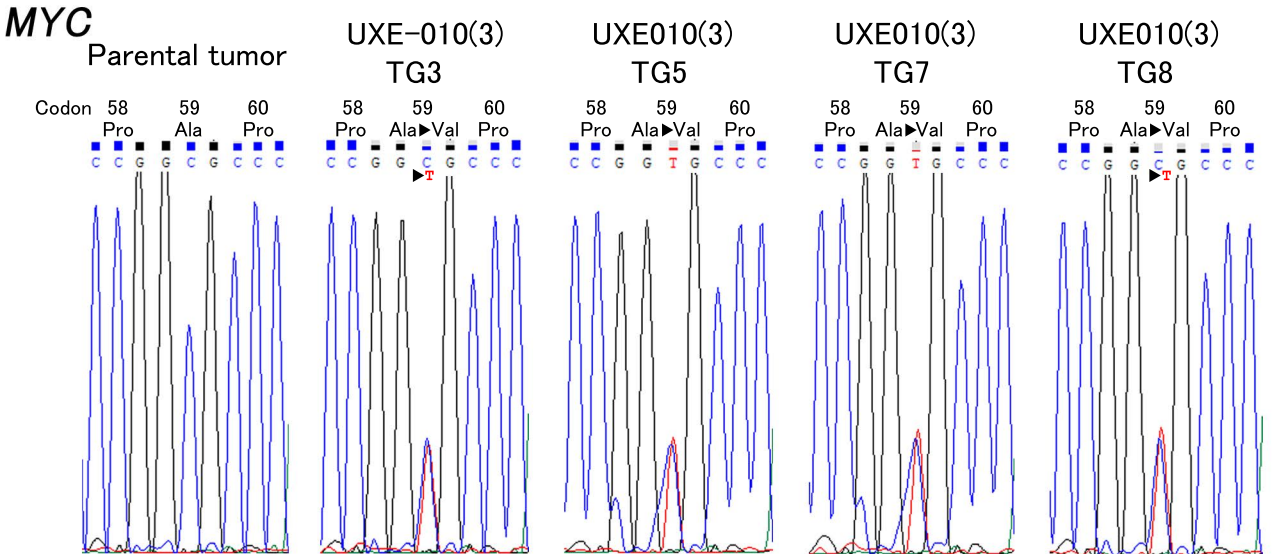


Supplementary Figure S3B

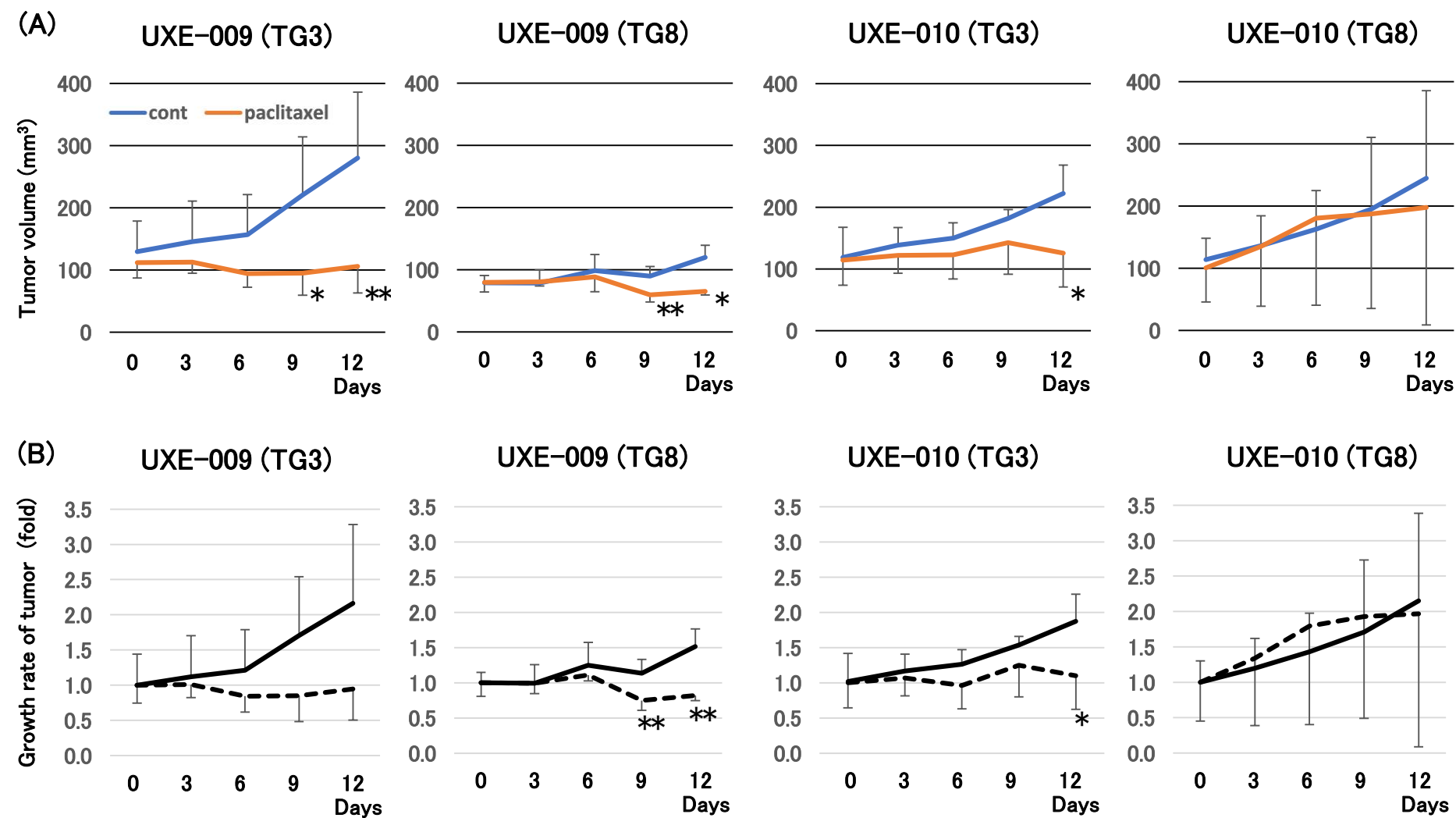
Immunohistochemical photographs of a parent tissue and PDXs, using a serial section of the each HE stained setcion.



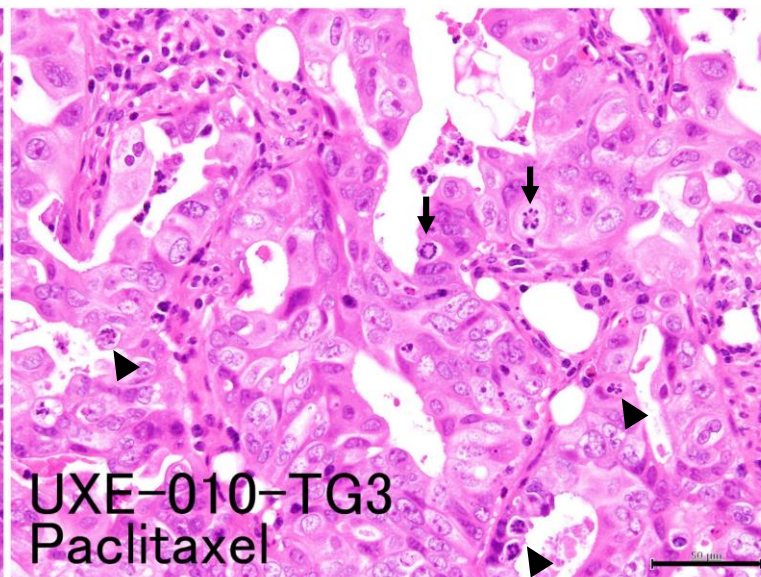
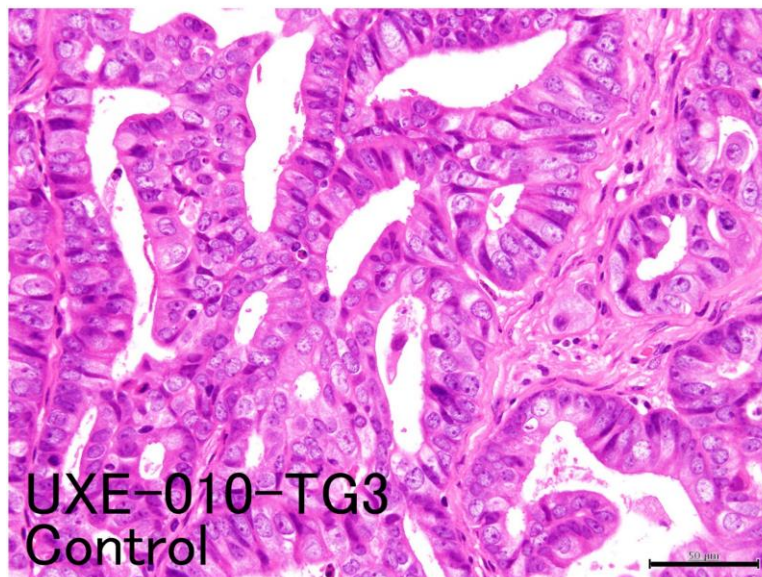
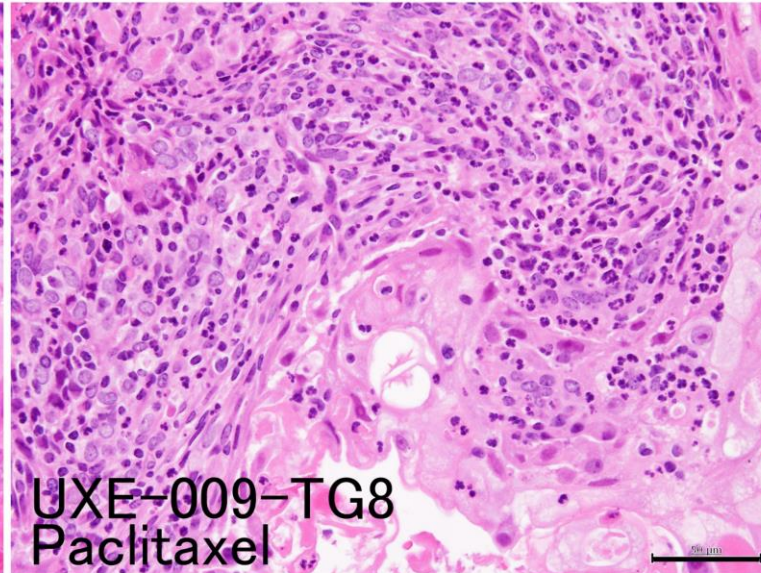
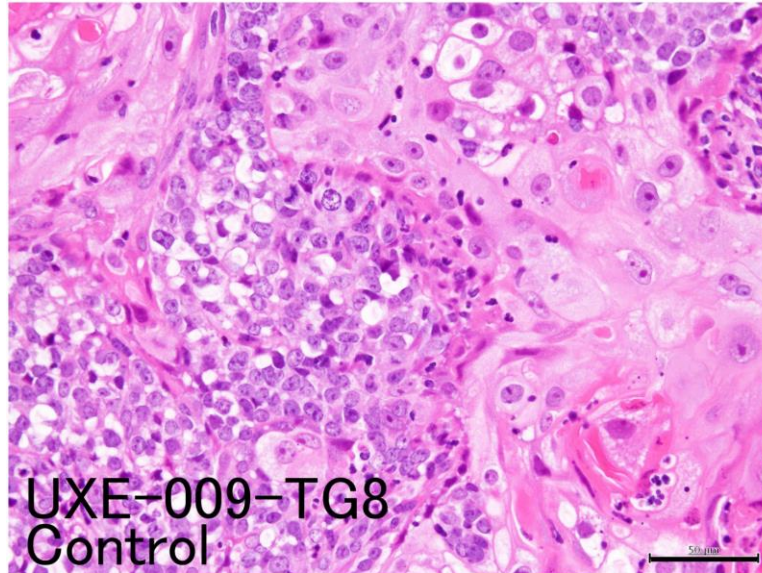
Supplementary Figure S3C
 Immunohistochemical photographs of a parental tissue and PDXs, using a serial section of the each HE stained setcion.



Supplementary Figure S4 Changes in variants of principal cancer-associated genes between original tumors and UXE-010-PDXs



Supplementary Figure S5. Growth curves of PDXs of the control and paclitaxel (20 mg/kg bodyweight, intraperitoneally, once three days up to 5 times)-treated mice. TG3 and 8, Trans Generation 1 and 8. (A) Tumor volumes. (B) Growth rate of tumors (vs. volume on Day 0). *, ** $P < 0.05$, 0.01 vs. control. Bar=S.D.



Supplementary Figure S6

Upper panels; apoptotic tumor cells are obvious in a paclitaxel-treated UXE-009-PDX.
Lower panels; tumor cell with apoptotic (arrowheads) and mitotic arrest (arrows) findings are scattered in a paclitaxel-treated UXE-010-PDX. Bar=50 μ m.