Supplementary table 5. Mutation calling of whole exome sequencing data from primary duct cell lines at later passages (P25).

PD47_CT	Chr	Consequence	VAF	Cancer related gene (Cosmic)	PD47_CTS	Chr	Consequence	VAF	Cancer related gene (Cosmic)	PD51_CT	Chr	Consequence	VAF	Cancer related gene (Cosmic)	PD51_CTS	Chr	Consequence	VAF	Cancer related gene (Cosmic)	PD62_CT	Chr	Consequence	VAF	Cancer related gene (Cosmic)
CDKN2B	9	p.L80fs	90%	yes	**TP53**	17	p.N115fs	93%	yes	**TP53**	17	p.R116del	100%	yes	**TP53**	17	p.R116del	90%	yes	**CDKN2A**	9	p.L78fs	100%	yes
CDKN2A	9	p.L78fs	71%	yes	**CDKN2A**	9	p.L78fs	73%	yes	**CDKN2A**	9	p.L78fs	85%	yes	**CDKN2A**	9	p.L78fs	82%	yes	**TP53**	17	p.N115fs	92%	yes
TGFBR1	9	p.17_20del	50%	yes	ENTHD1	22	p.G290W	64%	no	DOK7	4	p.A187fs	80%	no	PCYOX1	2	p.P331T	76%	no	SH3GL3	15	p.L17F	83%	no
TP53	17	p.R116fs	37%	yes	PLEK	2	p.Q343X	58%	no	POGK	1	p.G459V	76%	no	TMEM182	2	p.I169M	75%	no	NID1*	1	p.N1099fs	81%	no
ALYREF	17	p.P2A	31%	no	**SMAD4**	18	p.R97fs	56%	yes	NADSYN1	11	p.Q348X	75%	no	REPIN1	7	p.L2M	75%	no	FBXO22	15	p.C117Y	81%	no
OPHN1	X	p.M499I	30%	no	CNNM1	10	p.K396N	54%	no	AOC1	7	p.S633L	72%	no	PCYOX1	2	p.S376L	74%	no	MMP8	11	p.R292H	67%	no
CDKL3	5	p.Y115F	29%	no	FSIP2	2	p.D5692Y	54%	no	CNTNAP2	7	p.C569S	69%	yes	ARHGEF15	17	p.S505L	73%	no	MTNR1B	11	p.T50I	59%	no
ERBB2	17	p.P1100S	28%	yes	LRIG2	1	p.S303C	51%	no	ADAM19	5	p.G303D	67%	no	NADSYN1	11	p.Q348X	73%	no	ZNF804B	7	p.H274Q	58%	no
NID1*	1	p.R1100G	26%	no	OPHN1	X	p.M499I	48%	no	TMEM182	2	p.I169M	67%	no	AOC1	7	p.S633L	73%	no	EPB41L5	2	p.D458N	55%	no
NRDE2	14	p.E773fs	23%	no	OR6Q1	11	p.C145X	47%	no	REPIN1	7	p.L2M	65%	no	PCYOX1	2	p.S409F	70%	no	SARM1	17	p.P664L	52%	no
IGSF9	1	p.V487M	21%	no	ALYREF	17	p.P2A	43%	no	PCYOX1	2	p.P331T	64%	no	TTC39B	9	p.E391Q	68%	no	RBM10	X	p.N222K	52%	yes
PLEK	2	p.Q343X	21%	no	MAGEE2	X	p.N425K	39%	no	KIAA1551	12	p.E615K	63%	no	PEG3	19	p.S997C	68%	no	ATP5C1	10	p.L174V	50%	no
CACNA1E	1	p.Q1870K	19%	no	TGFBR1	9	p.17_20del	37%	yes	PLEKHN1	1	p.E403X	57%	no	EXOC7	17	p.S323C	66%	no	SPRR2G	1	p.P15H	48%	no
ABCA4	1	p.R124H	16%	no	CACNA1C	12	p.T538M	37%	no	CUL5	11	p.E762Q	57%	no	POGK	1	p.G459V	65%	no	C17orf53	17	p.G148D	48%	no
SPTLC3	20	p.T347P	15%	no	CDKL3	5	p.Y115F	35%	no	RHOJ	14	p.A190T	53%	no	CUL5	11	p.E762Q	63%	no	KIAA2018	3	p.S1435G	46%	no
XDH	2	p.E734D	14%	no	CHD7	8	p.P2665L	29%	no	C12orf49	12	p.Q74E	53%	no	CNTNAP2	7	p.C569S	62%	yes	TREML2	6	p.Q151L	41%	no
FOXE1	9	p.169_169de	13%	no	TMEM132C	12	p.G411R	27%	no	EXOC7	17	p.S323C	52%	no	ADAM19	5	p.G303D	46%	no	LAMA2	6	p.S659L	41%	no
KSR1	17	p.T136P	11%	no	NCOR2	12	p.N678T	17%	no	CLSTN3	12	p.T951fs	33%	no	TAL1	1	p.R38X	46%	yes	ZNF124	1	p.R194C	35%	no
NTHL1	16	p.R263C	10.9%	no	NOXO1	16	p.L352R	15%	no	BCAR1	16	p.Q302H	46%	no	C12orf49	12	p.Q74E	44%	no	CSF1R	5	p.H437Y	25%	yes
					DLGAP3	1	p.T763P	13%	no	NETO1	18	p.W134X	40%	no	KIAA1551	12	p.E615K	44%	no	AIM1L	1	p.531_548del	22%	no
					DRD4	11	p.S308P	12%	no	NPFFR2	4	p.Y140C	38%	no	RHOJ	14	p.A190T	43%	no	ANKLE1	19	p.C640F	18%	no
					RBMX	X	p.T77fs	10%	no	ERICH3	1	p.A652P	37%	no	TMC8	17	p.R11fs	43%	no	SHANK1	19	p.Q1184P	15%	no
					MUC16	19	p.S13888N	10%	yes	ZNF398	7	p.E117G	34%	no	NPFFR2	4	p.Y140C	42%	no	PRG4	1	p.T657P	14%	no
										PREX1	20	p.A1344E	33%	no	DOK7	4	p.A187fs	42%	no	EHBP1L1	11	p.K1219Q	13%	no
										FGR	1	p.G192D	31%	no	PLEKHN1	1	p.L80fs	40%	no	KRT18	12	p.M58fs	13%	no
										IFT122	3	p.V272I	29%	no	BMP3	4	p.Q338H	39%	no	C1RL	12	p.G250D	12%	no
										HIST1H1B	6	p.A119V	29%	no	FGR	1	p.G192D	39%	no	MUC16	19	p.S12510F	11%	yes
										POPDC2	3	p.S185C	27%	no	ERICH3	1	p.A652P	37%	no	SEC16B	1	p.Q96K	10%	no
										MAN1A2	1	p.S393F	26%	no	ZNF398	7	p.E117G	37%	no					
										EPHA10	1	p.Q45E	26%	no	NETO1	18	p.W134X	36%	no					
										FBN1	15	p.C1905X	24%	no	OTOP2	17	p.C443X	35%	no					
										JADE2	5	p.M61V	24%	no	EPHA10	1	p.Q45E;	34%	no					
										TAL1	1	p.R38X	24%	yes	CACNG8	19	p.R275C	34%	no					
										PFKM	12	p.E733X	23%	no	PREX1	20	p.A1344E	34%	no					
										MTF1	1	p.A737S	22%	no	AMPD3	11	p.E519Q	33%	no					
										SF3A1	22	p.Q242X	21%	no	SLC8A3	14	p.F480L	33%	no					
										OTOP2	17	p.C443X	15%	no	CLSTN3	12	p.T951fs	31%	no					
															RPL9	4	p.N15fs	29%	no					
															JADE2	5	p.M61V	28%	no					
															PFKM	12	p.E733X	24%	no					
															FBN1	15	p.C1905X	23%	no					
															MTF1	1	p.A737S	23%	no					
															TBKBP1	17	p.A484D	22%	no					
															POPDC2	3	p.S185C	21%	no					
															BCAR1	16	p.Q302H;	21%	no					
															POLG	15	p.52_53del	21%	yes					
															SMAD4	18	p.R97fs	18%	yes					
															TCHH	1	p.R68C	16%	no					
															SF3A1	22	p.Q242X	16%	no					
															PABPC1	8	p.E156fs	12%	yes					
															TTLL11	9	p.79_80del	11%	no					
															MUC17	7	p.T2916S	10%	no					

Chr: Chromosome
VAF: Variant allele frequency
Consequence: Amino acid change
* off-target effect
Grey highlight: SNV detected in earlier passage (P10)