

SUPPLEMENTARY MATERIALS

SCLEROSING EPITHELIOID MESENCHYMAL NEOPLASM

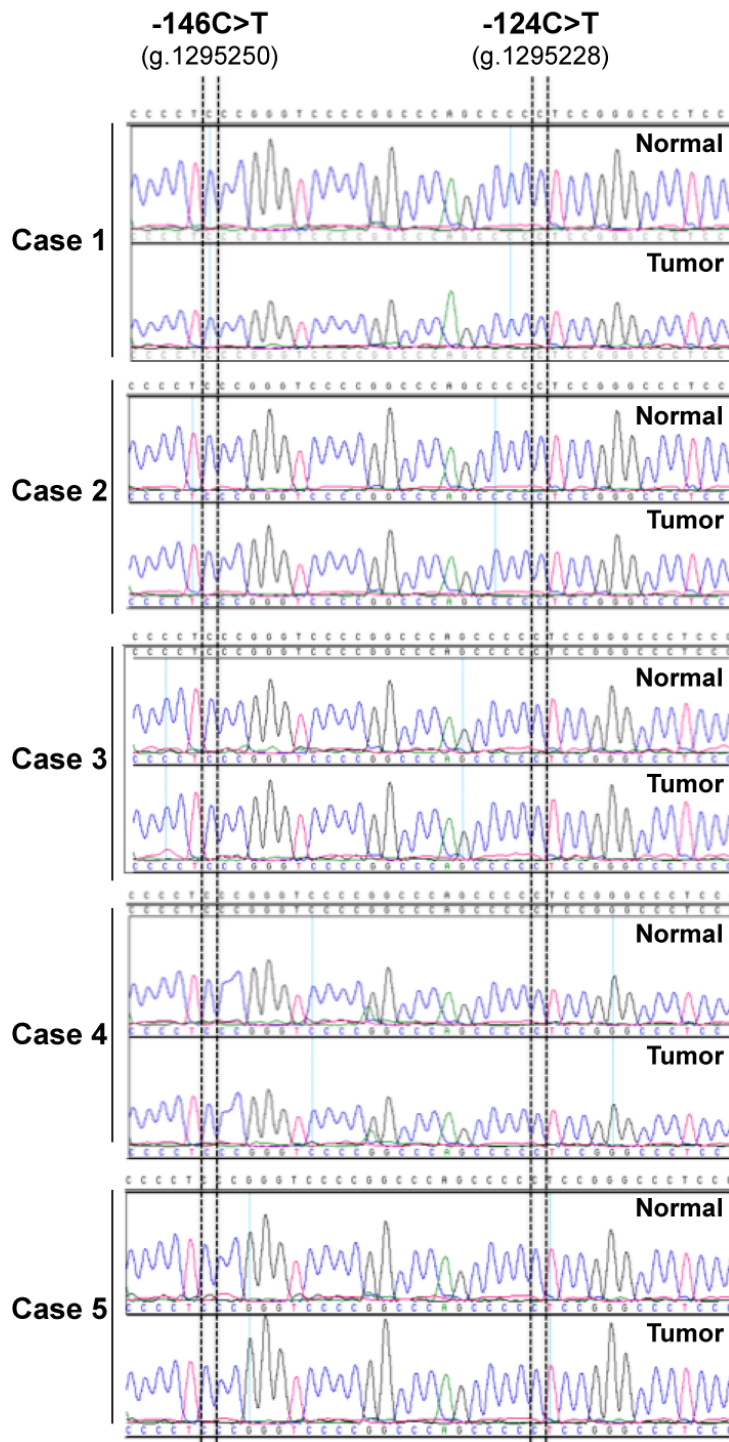
A PROPOSED NEW ENTITY

Basturk et al.

Supplementary Figure 1

Supplementary Tables 1-5

Supplementary Figure 1



Supplementary Figure 1: *TERT* promoter mutation assessment using Sanger sequencing. Representative Sanger sequence electropherograms of the *TERT* promoter region encompassing the -124C>T and -146C>T hotspot sites in both tumor and matched normal samples.

Supplementary Table 1. List of Antibody Sources

Antibody	Source	Dilution	Pretreatment
AE1:AE3	BioGenex	1:2K	CC1 (Ventana)
CK18	Dako	1:1K	CC1 (Ventana)
CD99	Biolegend	1:400	CC1(Ventana)
Vimentin	Dako	1:1K	CC1(Ventana)
Chromogranin	Dako	1:2K	CC1 (Ventana)
Synaptophysin	Dako	1:800	CC1 (Ventana)
PR	Ventana	1:2	CC1 (Ventana)
CD10	Ventana	1:2	CC1 (Ventana)
β -catenin	B.D. Transduction	1:500	CC1 (Ventana)
Trypsin	BioDesign	1:3K	Protease 1 (Ventana)
Chymotrypsin	BioDesign	1:3K	Protease I (Ventana)
TTF1	Dako	1:100	CC1Ventana
HepPar-1	Dako	1:2K	CC1 (Ventana)
MUC4	Santa Cruz	1:2K	ER2 (BOND RX)
Desmin	Dako	1:1K	CC1 (Ventana)
Myogenin	Ventana	Prediluted	CC1 (Ventana)
INI1 (BAF-47)	BD Transduction	1 :500	ER2 (BOND RX)
CD117	Dako	1:2K	CC1 (Ventana)
DOG1	Ventana	Predilute	CC1 (Ventana)
S100	Dako	1:2K	CC1 (Ventana)
HMB45	Dako	1:100	CC1 (Ventana)
Melan-A	Dako	1:100	ER2 (BOND RX)
CD31	Dako	1:700	CC1 (Ventana)
ERG	AbCam	1:150	CC1 (Ventana)
CD21	Dako	1:250	Protease 1 (Ventana)
CD35	Dako	1:100	Protease 1 (Ventana)
CD45	Dako	1:1500	ER2 (BOND RX)
BCL2	Dako	1:200	ER2 (BOND RX)
ALK	Ventana	Prediluted	CC1 (Ventana)
CD34	Dako	1:1K	ER2 (BOND RX)
STAT6	Cell Marque	1:250	ER2 (BOND RX)

Supplementary Table 2. Summary of the Cases Analyzed

Case	Age	Sex	Size (cm)	Site	Type of Surgery	Outcome (months)	Whole Exome Sequencing	RNA-Sequencing	Archer FusionPlex	Methylation Profiling	TERT Promoter Mutation Analysis
1	30	F	1.8	Head	Whipple	NED (80)	Yes	Yes	Yes	Yes	Yes
2	26	F	1.5	Body	Distal pancreatectomy	NED (53)	Yes	Yes	Yes	Yes	Yes
3	46	F	1.3	Neck	Excision	NED (80)	Failed sequencing	No	Failed sequencing	No	Yes
4	57	F	N/A	Neck	Excision	NED (49)	Yes	Yes	Yes	Yes	Yes
5	51	F	1.6	Tail	Distal pancreatectomy	NED (94)	Yes	Yes	Yes	Yes	Yes
6	75	M	5.0	Head	Whipple	NED (24)	No	Yes	Yes	Yes	No
7	28	M	2.5	Tail	Distal pancreatectomy	NED (19)	No	Yes	No	Yes	No
8	29	F	5.8	Head	Whipple	NED (8)	No	No	No	No	No

NED: No evidence of disease, M: Male, F: Female

Supplementary Table 3: Whole Exome Sequencing Statistics

Sample ID	Target Territory	Total Reads	Mean Target Coverage (X)	Percent Target Bases 2X	Percent Target Bases 20X	Percent Target Bases 50X	Percent Target Bases 100X
Case 1 Tumor	51189318	159363872	188,7	0,997319	0,98791	0,955375	0,827839
Case 1 Normal	51189318	126707046	169,1	0,997683	0,985519	0,937057	0,774402
Case 2 Tumor	51189318	165483550	179,9	0,997606	0,984639	0,934641	0,776301
Case 2 Normal	51189318	117884140	99,9	0,996391	0,946146	0,795804	0,452161
Case 4 Tumor	51189318	160857195	210,6	0,997744	0,987486	0,951548	0,842403
Case 4 Normal	51189318	124572297	168,6	0,997673	0,972803	0,907256	0,735289
Case 5 Tumor	51189318	160778048	215,7	0,997976	0,989503	0,957902	0,854018
Case 5 Normal	51189318	160966246	195,4	0,997863	0,988541	0,954148	0,832857

Supplementary Table 4. MSKCC-Solid Fusion Panel

Target name	NCBI_reference sequence	Target_exons	Direction	Assay_type
ALK	NM_004304	19,20,21,22	5'	fusion
ALK	NM_004304	C1156Y, G1202R, D1203N, S1206Y, F1174L, L1196M, G1269A	N/A	mutation
BCOR	NM_001123385	7,8	5'	fusion
BCOR	NM_001123385	7,14,15	3'	fusion
BRAF	NM_004333	7, 8, 9, 10, 11, 12	5'	fusion
BRAF	NM_004333	7, 8	3'	fusion
BRAF	NM_004333	15		V600E
BRAF	NM_004333	16	5'	splice variant
BRAF	NM_004333	1,2,3,13	3'	splice variant
CAMTA1	NM_015215	8,9,10	5'	fusion
CCNB3	NM_033031	2,3,4,5,6	5'	fusion
CIC	NM_015125	19,20	3'	fusion
COL6A3	NM_004369.2	8,9,10,11	3'	fusion
DNAJB1	NM_006145	1,2	3'	fusion
EGFR	NM_005228	1	3'	(2-7 exon skipping event)
EGFR	NM_005228	24, 25	3'	fusion
EGFR	NM_005228	7,8,9,16,20	5'	fusion
EPC1	NM_025209	9,10,11	3'	fusion
ERBB2	NM_004448	23, 24, 25, 26	3'	fusion
ERBB2	NM_004448	4,5	5'	fusion
ERG	NM_004449	2, 3, 4, 5, 6, 7, 8, 9, 10, 11	5'	fusion
ETV6	NM_001987	1,2,3,4,5,6	3'	fusion
ETV6	NM_001987	2,3,5,6,7	5'	fusion
EWSR1	NM_005243	4,5,6,7,8,9,10,11,12,13	3'	fusion
FGFR1	NM_015850	2,8,9,10	5'	fusion
FGFR1	NM_015850	17	3'	fusion
FGFR2	NM_000141.4	16, 17	3'	fusion
FGFR2	NM_000141.4	2,8,9,10	5'	fusion
FGFR3	NM_000142	8, 9, 10	5'	fusion
FGFR3	NM_000142	16, 17, intron 18	3'	fusion
FOSB	NM_006732.2	1,2	5'	fusion
FOXO1	NM_002015	1,2,3	5'	fusion
FOXO1	NM_002015	1,2,3	3'	fusion
FUS	NM_004960	4,5,6,7,8,9,10,11,14	3'	fusion
GLI1	NM_005269	4,5,6,7	5'	fusion
GLI1	NM_005269	4,5,6,7	3'	fusion
GRB7	NM_005310	10, 11, 12	5'	fusion
HMGA2	NM_003483	1,2,3,4,5	3'	fusion

Target name	NCBI_reference sequence	Target_exons	Direction	Assay_type
JAK3	NM_000215	10,11,12,17,18,19	5'	fusion
JAZF1	NM_175061	2,3,4	3'	fusion
KIT	NM_000222.2	1	3'	fusion
MAML2	NM_032427	2,3	5'	fusion
MAML2	NM_032427	2	3'	fusion
MEAF6	NM_001270875	4,5	3'	fusion
MET	NM_000245	13	3'	fusion
MET	NM_000245	2, 13, 14, 15, 16	5'	fusion
MGEA5	NM_012215	12,13	5'	fusion
MKL2	NM_014048	11,12,13	5'	fusion
MYB	NM_001130173	7, 8, 9, 11, 12, 13, 14, 15, 16	3'	fusion
NCOA1	NM_147223	12,13,14,15	5'	fusion
NCOA2	NM_006540	11,12,13,14	5'	fusion
NOTCH1	NM_017617.3	26, 27, 28, 29	5'	fusion
NOTCH1	NM_017617.3	2, 4, 29, 30, 31	3'	fusion
NOTCH2	NM_024408	26, 27, 28	5'	fusion
NOTCH2	NM_024408	5, 6, 7	3'	fusion
NR4A3	NM_173200	3,4	5'	fusion
NRG1	NM_004495	1, 2, 3, 6	5'	fusion
NTRK1	NM_002529	8, 10, 11, 12, 13,	5'	fusion
NTRK2	NM_006180	11,12,13,14,15,16,17	5'	fusion
NTRK3	NM_002530	13,14,15,16	5'	fusion
NTRK3	NM_002530	13,14,15	3'	fusion
NTRK3	NM_001007156	15	5'	fusion
PDGFB	NM_002608	2,3	5'	fusion
PDGFRA	NM_006206.4	10, 11,12,13,14	5'	fusion
PDGFRA	NM_006206.4	7	3'	(exons 8,9 deletion)
PHF1	NM_024165	1,2	5'	fusion
PIK3CA	NM_006218	2	5'	fusion
PLAG1	NM_002655	1,2,3,4	5'	fusion
PPARG	NM_015869	1,2,3	5'	fusion
PRKACA	NM_002730	2	5'	fusion
RET	NM_020975	8,9,10,11,12,13	5'	fusion
RET	NM_020975	V804M/L	N/A	mutation
ROS1	NM_002944	31,32,33,34,35,36,37	5'	fusion
RSPO2	NM_178565	1,2	5'	fusion
RSPO3	NM_032784	2	5'	fusion
SS18	NM_001007559	10,11	5'	fusion
SS18	NM_001007559	4,5,6,8,9,10	3'	fusion
STAT6	NM_001178078	1,2,3,4,5,6,7,16,17,18,19	5'	fusion

Target_name	NCBI_reference_sequence	Target_exons	Direction	Assay_type
TAF15	NM_139215	6,7	5'	fusion
TAF15	NM_139215	5,6,7	3'	fusion
TCF12	NM_207036	4,5,6	3'	fusion
TFE3	NM_006521	3,4,5,6	5'	fusion
TFEB	NM_007162	1,2,3,4	5'	fusion
TFG	NM_006070	4,5,6,7	3'	fusion
TFG	NM_006070	6	5'	fusion
TMPRSS2	NM_005656	1,2,3,4,5,6	3'	fusion
TMPRSS2	NM_001135099	1	3'	fusion
USP6	NM_004505	1,2,3	5'	fusion
YWHAE	NM_006761	5	3'	fusion

Supplementary Table 5: Non-synonymous somatic mutations identified in sclerosing epithelioid mesenchymal neoplasm of the pancreas using whole-exome sequencing

Case ID	Chromosome	Position	Ref Allele	Alt Allele	Gene Symbol	AA Change	Variant Class	Tumor MAF	Normal MAF	Tumor Depth	Normal Depth	LOH	Hotspot	Cancer Cell Fraction	Clonality	Pathogenicity	Mutation Taster	Provean	FATHMM	CHASM	Cancer gene (Census, Kandath, Lawrence)
Case 1	5	149216399	ACAG	A	PPARGC1B	p.S799del	In_Frame_Del	0,1	0	60	75	No	No	0,34	Subclonal	Passenger	D
Case 1	1	109839676	G	A	MYBPHL	p.S189F	Missense_Mutation	0,057553957	0	139	140	No	No	0,2	Subclonal	Passenger	D	D	T	Passenger	.
Case 1	1	220921886	A	G	MARCH2	p.S5G	Missense_Mutation	0,303030303	0	33	21	No	No	1	Clonal	Passenger	N	N	T	Passenger	.
Case 1	19	45719334	A	G	EXOC3L2	p.I313T	Missense_Mutation	0,27027027	0	37	47	No	No	0,92	Clonal	Passenger	D	D	T	Passenger	.
Case 1	20	2945612	C	G	PTPRA	p.S60C	Missense_Mutation	0,316326531	0	98	87	No	No	1	Clonal	Passenger	D	N	T	Passenger	.
Case 1	4	88535868	A	G	DSPP	p.N685S	Missense_Mutation	0,05	0,006060606	180	165	No	No	0,17	Subclonal	Passenger	N	N	D	Passenger	.
Case 1	5	79550736	C	G	MSH3	p.P64A	Missense_Mutation	0,208791209	0,040816327	91	98	No	No	0,71	Subclonal	Passenger	N	N	D	Passenger	.
Case 1	8	143396416	C	T	TSNARE1	p.R341Q	Missense_Mutation	0,316831683	0	101	109	No	No	1	Clonal	Passenger	N	D	T	Passenger	.
Case 2	1	169080619	C	G	ATP1B1	p.L37V	Missense_Mutation	0,39516129	0	124	27	No	No	1	Clonal	Passenger	D	N	T	Passenger	.
Case 2	11	67250716	A	T	AIP	p.Q29H	Missense_Mutation	0,253623188	0	138	66	No	No	1	Clonal	Likely pathogenic	D	N	D	Passenger	.
Case 2	13	113174211	G	A	TUBGCP3	p.R624W	Missense_Mutation	0,2	0	15	13	No	No	0,84	Clonal	Passenger	D	D	T	Passenger	.
Case 2	19	39961096	G	A	SUPT5H	p.G537D	Missense_Mutation	0,195121951	0	123	98	No	No	0,82	Clonal	Likely pathogenic	D	D	.	Driver	.
Case 2	2	207632160	C	A	FASTKD2	p.T248N	Missense_Mutation	0,263157895	0	114	56	No	No	1	Clonal	Passenger	D	D	T	Passenger	.
Case 2	2	31572613	C	T	XDH	p.E970K	Missense_Mutation	0,087591241	0	137	63	No	No	0,37	Subclonal	Passenger	D	N	T	Passenger	.
Case 2	6	83823058	C	T	DOPEY1	p.T233I	Missense_Mutation	0,238095238	0,026315789	84	38	No	No	1	Clonal	Passenger	D	N	T	Passenger	.
Case 2	7	139285169	G	A	HIPK2	p.S810F	Missense_Mutation	0,32	0	25	13	No	No	1	Clonal	Passenger	D	N	T	Passenger	.
Case 4	19	17303578	GCAAGCCC	G	MYO9B	p.Q946Cfs*32	Frame_Shift_Del	0,171428571	0	35	36	No	No	1	Clonal	Passenger
Case 4	3	158523190	G	GA	MFS1	p.A135Dfs*32	Frame_Shift_Ins	0,303797468	0	79	46	No	No	1	Clonal	Passenger
Case 4	13	103268760	AAAAATC	A	TPP2	p.K136_L137del	In_Frame_Del	0,08	0	100	90	No	No	0,83	Clonal	Passenger
Case 4	1	10397468	T	G	KIF1B	p.M1054R	Missense_Mutation	0,080188679	0	212	149	No	No	0,83	Clonal	Passenger	D	N	T	Passenger	.
Case 4	1	152552214	T	C	LCE3D	p.R67G	Missense_Mutation	0,298507463	0	134	176	No	No	1	Clonal	Passenger	N	N	T	Passenger	.
Case 4	1	210273703	A	G	SYT14	p.K399R	Missense_Mutation	0,043478261	0	92	39	No	No	0,45	Subclonal	Passenger	D	N	T	Passenger	.
Case 4	1	235872551	G	C	LYST	p.P3328R	Missense_Mutation	0,285714286	0	259	168	No	No	1	Clonal	Passenger	D	D	T	Passenger	.
Case 4	1	9322316	C	A	H6PD	p.S315Y	Missense_Mutation	0,244094488	0	127	111	No	No	1	Clonal	Passenger	N	D	D	Passenger	.
Case 4	11	118629499	T	C	DDX6	p.N326S	Missense_Mutation	0,104477612	0	67	38	No	No	1	Clonal	Passenger	D	D	T	Passenger	TRUE (Census)
Case 4	11	124620727	C	T	VSIG2	p.A104T	Missense_Mutation	0,056451613	0	124	79	No	No	0,58	Subclonal	Passenger	D	D	T	Passenger	.
Case 4	11	6479504	C	A	TRIM3	p.A52S	Missense_Mutation	0,05511811	0	127	103	No	No	0,57	Subclonal	Likely pathogenic	D	N	D	Passenger	.
Case 4	12	42631435	T	C	YAF2	p.M40V	Missense_Mutation	0,040462428	0	173	170	No	No	0,42	Subclonal	Passenger	D	N	T	Passenger	.
Case 4	14	47120429	A	G	RPL10L	p.W171R	Missense_Mutation	0,278074866	0	187	184	No	No	1	Clonal	Passenger	D	D	T	Passenger	.
Case 4	15	48807632	A	T	FBN1	p.C474S	Missense_Mutation	0,069651741	0,00621118	201	161	No	No	0,72	Subclonal	Likely pathogenic	D	D	D	Driver	.
Case 4	17	79857882	G	A	ANAPC11	p.R166H	Missense_Mutation	0,253333933	0	150	136	No	No	1	Clonal	Passenger	D	N	.	Passenger	.
Case 4	17	916353	T	C	ABR	p.M615V	Missense_Mutation	0,089108911	0,011363636	101	88	No	No	0,92	Clonal	Passenger	D	N	T	Passenger	.
Case 4	18	12264319	T	A	CIDEA	p.L66H	Missense_Mutation	0,059233449	0	287	251	No	No	0,61	Subclonal	Passenger	D	D	T	Passenger	.
Case 4	18	8796237	A	T	SOGA2	p.E673V	Missense_Mutation	0,074074074	0	135	114	No	No	0,76	Clonal	Passenger	D	D	T	Passenger	.
Case 4	2	162175353	G	A	PSMD14	p.R6K	Missense_Mutation	0,323353293	0	167	116	No	No	1	Clonal	Passenger	D	N	.	Passenger	.
Case 4	20	56078582	T	C	CTCF	p.T584A	Missense_Mutation	0,038461538	0	312	251	No	No	0,4	Subclonal	Passenger	N	N	T	Passenger	.
Case 4	23	117880972	G	T	IL13RA1	p.C95F	Missense_Mutation	0,245033113	0,008196721	151	122	No	No	1	Clonal	Likely pathogenic	D	D	D	Passenger	.
Case 4	4	89649797	C	T	FAM13A	p.E987K	Missense_Mutation	0,301587302	0	189	142	No	No	1	Clonal	Passenger	D	D	T	Passenger	.
Case 4	5	140755031	G	A	PCDHGA6	p.V461I	Missense_Mutation	0,254847645	0	361	344	No	No	1	Clonal	Passenger	N	N	T	Passenger	.
Case 4	7	1538115	G	C	INTS1	p.A453G	Missense_Mutation	0,053571429	0	112	136	No	No	0,55	Subclonal	Passenger	D	D	T	Passenger	.
Case 4	8	105001556	G	A	RIMS2	p.R984Q	Missense_Mutation	0,080536913	0	149	116	No	No	0,83	Clonal	Passenger	D	D	T	Passenger	.
Case 4	3	114069908	G	C	ZBTB20	p.Y339*	Nonsense_Mutation	0,071856287	0	334	317	No	No	0,74	Subclonal	Passenger	A
Case 5	6	1390977	TCAC	T	FOXF2	p.H272del	In_Frame_Del	0,142857143	0	49	46	No	No	1	Clonal	Passenger	D
Case 5	1	40363301	C	T	MYCL	p.V310M	Missense_Mutation	0,063636364	0,004405286	220	227	No	No	0,7	Subclonal	Passenger	D	N	T	Passenger	.
Case 5	11	55607204	T	C	OR5D16	p.I326T	Missense_Mutation	0,1	0	120	158	No	No	1	Clonal	Passenger	N	N	T	Passenger	.
Case 5	14	47613364	G	A	MDGA2	p.R237W	Missense_Mutation	0,111111111	0	117	90	No	No	1	Clonal	Passenger	D	.	T	Passenger	.
Case 5	16	28507445	G	C	APOBR	p.E361D	Missense_Mutation	0,113207547	0	53	54	No	No	1	Clonal	Passenger	N	N	T	Passenger	.
Case 5	19	13041497	G	A	FARSA	p.R72W	Missense_Mutation	0,06	0,004273504	250	234	No	No	0,66	Subclonal	Passenger	D	D	T	Passenger	.
Case 5	19	8400664	G	A	KANK3	p.P16L	Missense_Mutation	0,166666667	0	18	20	No	No	1	Clonal	Passenger	D	N	T	Passenger	.
Case 5	23	103268162	G	T	H2BFWT	p.A24D	Missense_Mutation	0,039130435	0,004366812	230	229	No	No	0,43	Subclonal	Passenger	N	N	T	Passenger	.
Case 5	3	186256514	C	G	CRYGS	p.V170L	Missense_Mutation	0,032921811	0	243	204	No	No	0,36	Subclonal	Passenger	N	N	T	Passenger	.
Case 5	3	25835620	C	A	OXSM	p.P339T	Missense_Mutation	0,098591549	0	142	130	No	No	1	Clonal	Passenger	N	D	.	Passenger	.
Case 5	6	46216564	G	C	RCAN2	p.R99G	Missense_Mutation	0,073529412	0	136	122	No	No	0,81	Clonal	Likely pathogenic	D	D	.	Driver	.

Supplementary Table 6. Fusion candidate genes and/or readthroughs identified by RNA-sequencing analysis of sclerosing epithelioid mesenchymal neoplasm of the pancreas.

Case ID	Fusion Caller	5' Gene	3' Gene	5' Mapping	3' Mapping	Fusion Type	Crossing Reads	Encompassing Reads	In Frame	Driver Probability (Oncofuse)	5' Cancer Gene	3' Cancer Gene
Case 1	STAR-Integrate	TMF1	EOGT	3:69072356-	3:69061905-	Read_Through	3	2	No	0.115484304	No	No
Case 1	Bowtie-Integrate, BWA-Integrate	D28390	TUBA1A	12:49658967-	12:49580616-	Intra_Chromosomal	16	14	Yes	0.000759567	No	No
Case 1	Bowtie-Integrate, BWA-Integrate	D28390	TUBA1B	12:49658967-	12:49523505-	Intra_Chromosomal	17	9	Yes	0.00000785	No	No
Case 2	STAR-Integrate, Bowtie-Integrate, BWA-Integrate, Bowtie-Fusioncatcher	ANXA2	NOP10	15:60674541-	15:34634309-	Intra_Chromosomal	10	8	No	0.005854542	No	No
Case 4	STAR-Integrate, BWA-Integrate	GRM5	NCL	11:88345998-	2:232320629-	Intra_Chromosomal	10	2	No	0.44815709	No	No
Case 4	STAR-Integrate	FAM188A	ITGA8	10:15839218-	10:15699585-	Read_Through	6	17	Yes	0.299599166	No	No
Case 4	MAPSplice	TMEM222	SNORA20,TCP1	1:27651816+	6:160201405-	Intra_Chromosomal	3	10	Yes	0.208586963	No	No
Case 4	Bowtie-Integrate, BWA-Integrate	FBXO25	FAM157A	8:385707+	3:197907626+	Inter_Chromosomal	2	2	No	0.07415937	No	No
Case 4	Bowtie-Integrate, BWA-Integrate	GATSL2	GTF2I	7:74867229-	7:74143124+	Intra_Chromosomal	17	9	No	0.004563057	No	No
Case 4	STAR-Fusion	CLPS	CPA1	6:35764982-	7:130027665+	Intra_Chromosomal	2	1	No	0.000532411	No	No
Case 5	STAR-Fusion	RN7SL4P	RN7SL166P	3:15780256+	13:20311178-	Intra_Chromosomal	3	1	No	0.948277221	No	No
Case 5	STAR-Integrate	AMY2B	PNLIP	1:104116558+	10:118318664+	Inter_Chromosomal	3	6	No	0.125810357	No	No
Case 5	STAR-Integrate	GRM5	NCL	11:88345998-	2:232320629-	Inter_Chromosomal	4	3	No	0.011146112	No	No
Case 5	STAR-Integrate, BWA-Integrate	CPA1	CELA3B	7:130022050-	1:22315755+	Inter_Chromosomal	2	6	No	0.004802719	No	No
Case 5	STAR-Integrate	CLPS	AMY2A	6:35764978-	1:104163177+	Inter_Chromosomal	7	2	Yes	0.004125734	No	No
Case 5	Bowtie-Integrate, BWA-Integrate	LOC100288142	NBPF1	1:145316684-	1:16892954-	Intra_Chromosomal	110	468	No	0.000674527	No	Yes
Case 6	STAR-Integrate, Bowtie-Integrate, BWA-Integrate, Bowtie-Fusioncatcher, MAPSplice, STAR-Fusion	KAT6B	DNAH7	10:76603236+	2:196651895-	Inter_Chromosomal	4	17	Yes	0.985546392	Yes	No
Case 6	STAR-Integrate, Bowtie-Integrate, BWA-Integrate, Bowtie-Fusioncatcher	UCK2	ZMIZ1	1:165865567+	10:80878672+	Inter_Chromosomal	5	17	No	0.591263951	No	No
Case 6	STAR-Integrate, Bowtie-Integrate, BWA-Integrate	NFATC2	NUTM2A	20:50051725-	10:88992360+	Inter_Chromosomal	5	8	Yes	0.204184399	Yes	Yes
Case 6	STAR-Integrate, Bowtie-Integrate, BWA-Integrate, Bowtie-Fusioncatcher	FAM210B	PGAP1	20:54934247+	2:197767466-	Inter_Chromosomal	5	7	No	0.158507156	No	No
Case 6	STAR-Integrate, Bowtie-Integrate, BWA-Integrate, Bowtie-Fusioncatcher	CAMK2G	SNCG	10:75632748-	10:88719390+	Intra_Chromosomal	10	9	No	0.027357488	No	No
Case 6	MAPSplice, STAR-Fusion, STAR-Integrate	CAMK2G	SNCG	10:75632747-	10:88719390+	Intra_Chromosomal	7	10	Yes	0.027357488	No	No
Case 6	Bowtie-Integrate, BWA-Integrate	MNAT1	SLC38A6	14:61346653-	14:61449226+	Read_Through	2	2	No	0.000108277	No	No
Case 7	STAR-Integrate, Bowtie-Integrate, BWA-Integrate, STAR-Fusion	PANX1	HEPHL1	11:93886796+	11:93815584+	Intra_Chromosomal	18	25	No	0.013503835	No	No
Case 7	Bowtie-Integrate, BWA-Integrate	DTX2	UPK3B	7:76133760+	7:76140972+	Read_Through	2	4	Yes	0.006634333	No	No