Supplementary Table 1. Genetic variants identified in pancreatic cyst fluid.

Variant	Number (%)
KRAS	
p.G12D, c.35G>A	95 (15%)
p.G12V, c.35G>T	85 (14%)
p.G12R, c.34G>C	48 (8%)
p.G12I, c.34_35GG>AT	2 (1%)
p.G13D, c.38G>A	7 (1%)
p.Q61H, c.183A>C	16 (3%)
p.Q61H, c.183A>T	7 (1%)
p.Q61R, c.182A>G	9 (1%)
p.Q61K, c.181C>A	1 (1%)
p.Q61L, c.182_183AdelAAinsTC	1 (1%)
p.Q61L, c.182A>T	1 (1%)
GNAS	
p.R201H, c.602G>A	94 (15%)
p.R201C, c.601C>T	63 (10%)
p.R201S, c.601C>A	6 (1%)
p.Q227E, c.679C>G	3 (1%)
BRAF	
p.T599I, c.1796C>T	2 (1%)
p.V600E, c.1799T>A	1 (1%)
p.K601N, c.1803A>T	1 (1%)
p.Q612*, c.1834C>T	1 (1%)
CTNNB1	
p.S45F, c.134C>T	2 (1%)
p.S45Y, c.134C>A	1 (1%)
p.T41A, c.121A>G	1 (1%)
TP53	
p.R273H, c.818G>A	6 (1%)
p.R175H, c.524G>A	3 (1%)
p.R248W, c.742C>T	2 (1%)
p.R110L, c.329G>T	1 (1%)
p.R181C, c.541C>T	1 (1%)
p.R181P, c.542G>C	1 (1%)
p.G199L, c.595_596GG>TT	1 (1%)
p.Y234C, c.701A>G	1 (1%)
p.S241F, c.722C>T	1 (1%)
p.C242fs*5, c.722delC	1 (1%)
p.G245S, c.733G>A	1 (1%)
p.N247IS, c.740A>T	1 (1%)
p.D259Y, c.775G>T	1 (1%)
p.G266R, c.796G>C	1 (1%)
p.V274F, c.820G>T	1 (1%)
p.R280T, c.839G>C	1 (1%)
Homozygous deletion*	2 (1%)
PIK3CA	
p.H1047R, c.3140A>G	3 (1%)
p.E542K, c.1624G>A	3 (1%)
p.E545K, c.1633G>A	2 (1%)
p.Q546R, c.1637A>G	1 (1%)
p.Q546H, c.1638G>T	1 (1%)
p.Y1021C, c.3062A>G	1 (1%)
p.H1047Y, c.3139C>T	1 (1%)
PTEN	
T321fs*1	1 (1%)
Homozygous deletion*	1 (1%)
AKT1	
p.E17K, c.49G>A	1 (1%)

*Deletion is based on low sequencing coverage of amplicons for the gene of interest.