

Table S6. Validation of somatic mutations identified by targeted next generation sequencing.

Patient ID	Carcinoma							adj-IPMN							Relation status Discovery NGS	Relation status Validation NGS
	Gene	SNV position	Amino acid change	Mutation type	Consequence	Coverage	Variant allele frequency (%)	Gene	SNV position	Amino acid change	Mutation type	Consequence	Coverage	Variant allele frequency (%)		
<i>IPP05</i> <i>discovery</i> <i>NGS</i>	BRAF	Chr7:140481445 C>T	p.G455R	Substitution	Missense	505	9.1	RNF43	Chr17:56435615 G>A	p.L508fs	Substitution	Frameshift	366	13.6	Unrelated	Unrelated
	TP53	Chr17:7578449 C>T	p.A161T	Substitution	Missense	232	13.8									
	TP53	Chr17:7578521 G>C	p.L137V	Substitution	Missense	231	13.3									
	SMAD4	Chr18:48584754 C>T	p.P278S	Substitution	Missense	216	13.3									
<i>IPP05</i> <i>validation</i> <i>NGS</i>	TP53	Chr17:7578506 G>A	p.P142S	Substitution	Missense	248	30.5	RNF43	Chr17:56435615 G>A	p.L508fs	Substitution	Frameshift	236	5.5	Unrelated	Unrelated
	ARID1A	Chr1:27102176 C>T	p.I1701T	Substitution	Missense	373	7.8	GNAS	Chr20:57480529 C>G	p.A176G	Substitution	Missense	451	14.2		
	SMAD4	Chr18:48575209 C>T	p.R135X	Substitution	Nonsense	1269	7.3									
	RNF43	Chr17:56435126 C>T	p.D671N	Substitution	Missense	152	34.9									
<i>IPP09</i> <i>discovery</i> <i>NGS</i>	TP53	Chr17:7578388 C>T	p.R181H	Substitution	Missense	527	9.9	No mutations called					587	Unrelated	Unrelated	
	SMAD4	Chr18:48593477 C>T	p.Q410X	Substitution	Nonsense	923	5.6						843			
<i>IPP09</i> <i>validation</i> <i>NGS</i>	TP53	Chr17:7578388 C>T	p.R181H	Substitution	Missense	527	14.25	CDKN2A	Chr9:21971050 C>T	p.R103Q	Substitution	Missense	215	6.9	Unrelated	Unrelated
	SMAD4	Chr18:48593477 C>T	p.Q410X	Substitution	Nonsense	2732	7.6	RNF43	Chr17:56435644 C>G	p.C498S	Substitution	Missense	1012	11.6		
	ARID1A	Chr1:27101115 C>T	p.A1466V	Substitution	Missense	2760	8.65									
<i>IPP13</i> <i>discovery</i> <i>NGS</i>	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	1518	10.4	ARID1A	Chr1:27023438 G>A	p.A182T	Substitution	Missense	258	13	Unrelated	Unrelated
<i>IPP13</i> <i>validation</i>								RNF43	Chr17:56435227 C>A	p.S637I	Substitution	Missense	240	11.6		
<i>IPP15</i> <i>discovery</i> <i>NGS</i>	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	1518	10.4	RNF43	Chr17:56435227 C>A	p.S637I	Substitution	Missense	2824	9.5	Related	Related
	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	403	50.6	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	1629	41.2		
	GNAS	Chr20:57484421 G>A	p.R201H	Substitution	Missense	784	33	GNAS	Chr20:57484421 G>A	p.R201H	Substitution	Missense	1738	34.8		
	TP53	Chr17:7577570 C>T	p.M237I	Substitution	Missense	301	28.9	TP53	Chr17:7577570 C>T	p.M237I	Substitution	Missense	378	52.2		
	SMAD4	Chr18:48591919 G>A	p.R361H	Substitution	Missense	600	34	SMAD4	Chr18:48591919 G>A	p.R361H	Substitution	Missense	1314	13.85		
	GNAS	Chr20:57484610 C>T	p.R233C	Substitution	Missense	490	10.1									
<i>IPP15</i> <i>validation</i> <i>NGS</i>	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	2192	21.3	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	2060	32.3	Related	Related
	GNAS	Chr20:57484421 G>A	p.R201H	Substitution	Missense	990	29.8	GNAS	Chr20:57484421 G>A	p.R201H	Substitution	Missense	1761	29		
	TP53	Chr17:7577570 C>T	p.M237I	Substitution	Missense	870	7.4	TP53	Chr17:7577570 C>T	p.M237I	Substitution	Missense	1423	22.3		
	SMAD4	Chr18:48591919 G>A	p.R361H	Substitution	Missense	1927	22.9	SMAD4	Chr18:48591919 G>A	p.R361H	Substitution	Missense	2129	54.3		
	RNF43	Chr17:56437534 G>A	p.P310S	Substitution	Missense	348	23.6	RNF43	Chr17:56437534 G>A	p.P310S	Substitution	Missense	150	44.7		
	KRAS	Chr12:25398281 C>T	p.G13D	Substitution	Missense	2192	9.3	CDKN2A	Chr9:21971162 G>A	p.H66YH	Substitution	Missense	211	16.1		
	KRAS	Chr12:25398285 C>G	p.G12R	Substitution	Missense	2192	8.9									
<i>IPP19</i> <i>discovery</i> <i>NGS</i>	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	1310	36.9	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	1165	39	Related	Related
	TP53	Chr17:7578403 C>T	p.C176Y	Substitution	Missense	868	57.7	TP53	Chr17:7578403 C>T	p.C176Y	Substitution	Missense	561	92.3		
	RNF43	Chr17:56448280 C>T	p.A123T	Substitution	Missense	122	8.3	RNF43	Chr17:56437576 G>C	p.R296G	Substitution	Missense	182	9.7		
<i>IPP19</i> <i>validation</i> <i>NGS</i>	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	5573	39.7	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	3433	39.7	Related	Related
	TP53	Chr17:7578403 C>T	p.C176Y	Substitution	Missense	1901	70.1	TP53	Chr17:7578403 C>T	p.C176Y	Substitution	Missense	1539	70.1		
	CDKN2A	Chr9:21971150 G>A	p.P70S	Substitution	Missense	337	9.04									
<i>IPP22</i> <i>discovery</i> <i>NGS</i>	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	1153	18.8	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	315	33.1	Related	Related
	GNAS	Chr20:57484421 G>A	p.R201H	Substitution	Missense	1583	16.5	GNAS	Chr20:57484421 G>A	p.R201H	Substitution	Missense	1556	51.8		
	PIK3CA	Chr3:178952085 A>T	p.H1047L	Substitution	Missense	699	11.1	PIK3CA	Chr3:178952085 A>T	p.H1047L	Substitution	Missense	550	11.1		
	TP53	Chr17:7577124 C>A	p.V272L	Substitution	Missense	242	5.5	TP53	Chr17:7577124 C>A	p.V272L	Substitution	Missense	295	20.5		
<i>IPP22</i> <i>validation</i>	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	5044	13.9	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	4553	41.8	Related	Related
	GNAS	Chr20:57484421 G>A	p.R201H	Substitution	Missense	2372	14.4	GNAS	Chr20:57484421 G>A	p.R201H	Substitution	Missense	1587	40.6		

NGS	PIK3CA	Chr3:178952085 A>T	p.H1047L	Substitution	Missense	1373	19.9	PIK3CA	Chr3:178952085 A>T	p.H1047L	Substitution	Missense	1141	44.8		
	TP53	Chr17:7577124 C>A	p.V272L	Substitution	Missense	1308	5.4	TP53	Chr17:7577124 C>A	p.V272L	Substitution	Missense	3044	23.2		
	SMAD4	Chr18:48593443 G>A	p.W398X	Substitution	Nonsense	1100	21.1	SMAD4	Chr18:48593443 G>A	p.W398X	Substitution	Nonsense	757	77.1		
	RNF43	Chr17:56438293 delG	p.Q234fs	Deletion	Frameshift	195	14.4									
IPP31 discovery NGS	GNAS	Chr20:57484420 C>T	p.R201C	Substitution	Missense	108	59.2	GNAS	Chr20:57484420 C>T	p.R201C	Substitution	Missense	259	43		
	KRAS	Chr12:25398285 C>G	p.G12R	Substitution	Missense	444	24.1									
	TP53	Chr17:7572963 delT	p.K382fs	Deletion	Frameshift	217	10.7									
IPP31 validation NGS	KRAS	Chr12:25398285 C>G	p.G12R	Substitution	Missense	3235	31.6	KRAS	Chr12:25398285 C>G	p.G12R	Substitution	Missense	2919	11.4	Related	Related
	GNAS	Chr20:57484420 C>T	p.R201C	Substitution	Missense	1616	45	GNAS	Chr20:57484420 C>T	p.R201C	Substitution	Missense	991	12.9		
	TP53	Chr17:7572963 delT	p.K382fs	Deletion	Frameshift	3039	5.9									
	SMAD4	Chr18:48581219 G>A	p.E175K	Substitution	Missense	440	17.7									
IPP35 discovery NGS	KRAS	Chr12:25380277 G>T	p.Q61K	Substitution	Missense	1530	29.6	No mutations called						Unrelated	Unrelated	
	TP53	Chr17:7578406 C>T	p.R175H	Substitution	Missense	360	39									
	SMAD4	Chr18:48575677	p.L146X	Substitution	Nonsense	1422	40.3									
IPP35 validation NGS	KRAS	Chr12:25380277 G>T	p.Q61K	Substitution	Missense	16468	19.9	RNF43	Chr17:56435964 delG	p.R392fs	Deletion	Frameshift	689	13.8		
	TP53	Chr17:7578406 C>T	p.R175H	Substitution	Missense	3452	41.5	TGFBR2	Chr3:30713924 delG	p.G442fs	Deletion	Frameshift	2004	5.5		
	SMAD4	Chr18:48575677	p.L146X	Substitution	Nonsense	15024	34.4	PIK3CA	Chr3:178938877 G>A	p.E707K	Substitution	Missense	1313	27.3		
IPP36 discovery NGS	SMAD4	Chr18:48604769 C>T	p.R531W	Substitution	Missense	178	5.9	No mutations called						Unrelated	Unrelated	
	ARID1A	Chr1:27088766 C>T	p.S792F	Substitution	Missense	167	9									
IPP36 validation NGS	ARID1A	Chr1:27088766 C>T	p.S792F	Substitution	Missense	798	8.9	No mutations called								
IPP43 discovery NGS	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	329	11.9	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	1618	56.3	Unrelated	Unrelated
	GNAS	Chr20:57484420 C>T	p.R201C	Substitution	Missense	350	15.4	TP53	Chr17:7578263 G>A	p.R196X	Substitution	Missense	442	85.9		
	PIK3CA	Chr3:178951955 A>G	p.M1004V	Substitution	Missense	212	5.4	SMAD4	Chr18:48573625	p.K70fs	Deletion	Frameshift	117	7		
IPP43 validation NGS	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	6879	28.4	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	7125	57.3		
	CDKN2A	Chr9:21971111 G>A	p.H83Y	Substitution	Missense	1659	28.8	TP53	Chr17:7578263 G>A	p.R196X	Substitution	Missense	2016	87.4		
								SMAD4	Chr18:48573625	p.K70fs	Deletion	Frameshift	3352	5.4		
								RNF43	Chr17:56448297 T>C	p.R117H	Substitution	Missense	2168	62.8		
IPP44 discovery NGS	KRAS	Chr12:25380275 T>G	p.Q61H	Substitution	Missense	593	24.7	KRAS	Chr12:25380275 T>G	p.Q61H	Substitution	Missense	1650	37.8		
	RNF43	Chr17:56435571 C>T	p.M522I	Substitution	Missense	167	5.9									
	RNF43	Chr17:56435629 C>T	p.S503I	Substitution	Missense	167	5.6									
IPP44 validation NGS	KRAS	Chr12:25380275 T>G	p.Q61H	Substitution	Missense	12639	24.5	KRAS	Chr12:25380275 T>G	p.Q61H	Substitution	Missense	7238	35.6	Related	Related
IPP45 discovery NGS	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	841	26.4	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	604	21.1		
	SMAD4	Chr18:48575209 C>T	p.R135X	Substitution	Nonsense	1214	36.3	SMAD4	Chr18:48575209 C>T	p.R135X	Substitution	Nonsense	701	19.8		
IPP45 validation NGS	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	6270	24.6	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	10105	23.4	Related	Related
	SMAD4	Chr18:48575209 C>T	p.R135X	Substitution	Nonsense	2341	38.1	KRAS	Chr12:25380275 T>G	p.Q61QH	Substitution	Missense	3775	6		
	RNF43	Chr17:56438293 delG	p.Q234fs	Deletion	Frameshift	371	22.1	RNF43	Chr17:56438293 delG	p.Q234fs	Deletion	Frameshift	814	10.9		
	ARID1A	Chr1:27107101 delC	p.L2238fs	Deletion	Frameshift	294	7.2	ARID1A	Chr1:27107101 delC	p.L2238fs	Deletion	Frameshift	426	5.4		
								TP53	Chr17:7577124 C>A	p.V272L	Substitution	Missense	3563	25.3		

<i>IPP47</i> <i>discovery</i> <i>NGS</i>	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	2593	42.2	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	5188	45.8	Related	Related
	TGFBR2	Chr3:30732969 C>T	p.R553C	Substitution	Missense	288	64.6	TGFBR2	Chr3:30732969 C>T	p.R553C	Substitution	Missense	305	61		
	TP53	Chr17:7578484 delGAA	p.S149del	Deletion	In-Frame	633	54.3	TP53	Chr17:7578484	p.S149del	Deletion	In-Frame	1136	63.9		
<i>IPP47</i> <i>validation</i> <i>NGS</i>	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	1123	42.7	KRAS	Chr12:25398284 C>T	p.G12D	Substitution	Missense	13580	51	Related	Related
	TP53	Chr17:7578484 delGAA	p.S149del	Deletion	In-Frame	178	53.4	TP53	Chr17:7578484	p.S149del	Deletion	In-Frame	1628	64.6		
	TGFBR2	Chr3:30732969 C>T	p.R553C	Substitution	Missense	425	58.6									
<i>IPP50</i> <i>discovery</i> <i>NGS</i>	KRAS	Chr12:25398285 C>G	p.G12R	Substitution	Missense	683	5.5	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	5367	23.4	Related	Related
	KRAS	Chr12:25380282 G>A	p.A59V	Substitution	Missense	414	10.1	TP53	Chr17:7578263 A>G	p.R196X	Substitution	Nonsense	672	29.6		
	TP53	Chr17:7578263 A>G	p.R196X	Substitution	Nonsense	138	77									
	RNF43	Chr17:56440953 C>T	p.M128I	Substitution	Missense	301	7.8									
<i>IPP50</i> <i>validation</i> <i>NGS</i>	KRAS	Chr12:25398285 C>G	p.G12R	Substitution	Missense	24620	7.8	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	1469	23.4	Related	Related
	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	24620	5.2	TP53	Chr17:7578263 A>G	p.R196X	Substitution	Nonsense	625	29.6		
	TP53	Chr17:7578263 A>G	p.R196X	Substitution	Nonsense	138	90.7	PIK3CA	Chr3:178938796 G>C	p.V680L	Substitution	Nonsense	3494	40.7		
	PIK3CA	Chr3:178938796 G>C	p.V680L	Substitution	Nonsense	1129	43.4									
	CDKN2A	Chr9:21971093 C>T	p.G89S	Substitution	Missense	183	14.7									
<i>IPP54</i> <i>discovery</i> <i>NGS</i>	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	2932	9.9	KRAS	Chr12:25398284 C>G	p.G12A	Substitution	Missense	1102	9.9	Unrelated	Unrelated
	TP53	Chr17:7577124 C>A	p.V272L	Substitution	Missense	1336	9.5					528				
<i>IPP54</i> <i>validation</i> <i>NGS</i>	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	3221	6.2	KRAS	Chr12:25398284 C>G	p.G12A	Substitution	Missense	2786	9.5	Unrelated	Unrelated
	TP53	Chr17:7577124 C>A	p.V272L	Substitution	Missense	954	5.7									
<i>IPP56</i> <i>discovery</i> <i>NGS</i>	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	1833	5.6	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	1990	38.2	Related	Related
	TP53	Chr17:7578453 delGG	p.A159fs	Deletion	Frameshift	348	9	TP53	Chr17:7578453 delGG	p.A159fs	Deletion	Frameshift	378	65.4		
								GNAS	Chr20:57480495 G>A	p.E165K	Substitution	Missense	136	7.2		
								RNF43	Chr17:56435773 C>T	p.S455N	Substitution	Missense	230	6.3		
<i>IPP56</i> <i>validation</i> <i>NGS</i>	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	11208	10.9	KRAS	Chr12:25398284 C>A	p.G12V	Substitution	Missense	3376	61.8	Related	Related
	TP53	Chr17:7578453 delGG	p.A159Dfs	Deletion	Frameshift	885	10.1	TP53	Chr17:7578453 delGG	p.A159fs	Deletion	Frameshift	292	60.2		
	RNF43	Chr17:56435749 G>A	p.A463V	Substitution	Missense	364	27.8	RNF43	Chr17:56440764 G>A	p.Q152X	Substitution	Missense	2195	11.1		

adj-/dist-IPMN - adjacent/distant IPMN
 Bold indicates shared mutation to either of the other neoplasms
 SNV - Single nucleotide variation