IPP17											
Carcinoma						IPMN					
Gene Symbol	Transcript Accession	Nucleotide change	Amino Acid	Consequence	Allele Frequency	Gene Symbol	Transcript Accession	Nucleotide change	Amino Acid	Consequence	Allele Frequency
ACAP2	**CCDS33924.1**	**chr3: 195063234 C>T**	**C165Y**	**Missense**	**19**	**ADCY8**	**CCDS33924.1**	**chr8: 131964235 C>T**	**V374M**	**Missense**	**29**
ADAMTS1	CCDS33524.1	chr21: 28212054 T>G	E627A	Missense	11	**ASH1L**	**CCDS6363.1**	**chr1: 155307924 T>C**	**N2920S**	**Missense**	**16**
ADCY8	**CCDS6363.1**	**chr8: 131964235 C>T**	**V374M**	**Missense**	**36**	**CLNK**	**CCDS1113.2**	**chr4: 10542196 G>T**	**P175H**	**Missense**	**14**
AR	CCDS14387.1	chrX: 66765158 T>A	L57Q	Missense	15	CLU	CCDS47024.1	chr1: 155307924 T>C	R127H	Missense	23
ARL11	CCDS9419.1	chr13: 50204931 delCTT	F117del	In-frame deletion	10	**CPN1**	**CCDS47832.1**	**chr10: 101816891 T>A**	**Y297F**	**In-frame deletion**	**13**
ASH1L	**CCDS1113.2**	**chr1: 155307924 T>C**	**N2920S**	**Missense**	**16**	**CSRNP2**	**CCDS7486.1**	**chr12: 51458139 delTCT**	**E340del**	**In-frame deletion**	**13**
C7orf26	CCDS5353.1	chr7: 6647641 C>T	A400V	Missense	13	**CTNNB1**	**CCDS8807.1**	**chr3: 41266136 T>C**	**S45P**	**Missense**	**11**
CLNK	**CCDS47024.1**	**chr4: 10542196 G>T**	**P175H**	**Missense**	**14**	**ERF**	**CCDS2694.1**	**chr19: 42752892 G>A**	**R458C**	**Missense**	**15**
COMT	CCDS13770.1	chr22: 19951169 G>A	V124M	Missense	11	FBP2	CCDS12600.1	chr9: 97325736 C>A	S238I	Missense	13
CORIN	CCDS3477.1	chr4: 47645243 G>C	A663G	Missense	14	**HOXB3**	**CCDS6711.1**	**chr17: 46629769 C>T**	**G23D**	**Missense**	**13**
CPN1	**CCDS8807.1**	**chr10: 101816891 T>A**	**Y297F**	**In-frame deletion**	**9**	**KRTAP13**	**CCDS11528.1**	**chr21: 31797951 T>C**	**T94A**	**Missense**	**14**
CSRNP2	**CCDS2694.1**	**chr12: 51458139 delTCT**	**E340del**	**In-frame deletion**	**17**	**MAGEB4**	**CCDS13591.1**	**chrX: 30260590 C>T**	**T113M**	**Missense**	**14**
CTNNB1	**CCDS47443.1**	**chr3: 41266136 T>C**	**S45P**	**Missense**	**11**	**MEGF8**	**CCDS14221.1**	**chr19: 42857116 insC**	**D1065Gfs**	**Frameshift**	**13**
DST	CCDS12600.1	chr6: 56362247 C>T	R4095H	Missense	10	**MTF1**	**CCDS12604.2**	**chr1: 38323197 T>A**	**D45V**	**Missense**	**15**
ERF	**CCDS5465.1**	**chr19: 42752892 G>A**	**R458C**	**Missense**	**20**	MYT1L	CCDS30676.1	chr2: 1893222 C>T	G769R	Missense	12
GLI3	CCDS3796.1	chr7: 42006048 G>A	R875C	Missense	18	**NTRK3**	**CCDS46222.1**	**chr15: 88476298 G>T**	**P612T**	**Missense**	**13**
GLRB	CCDS6719.1	chr4: 158058014 C>G	R196G	Missense	12	**OR5R1**	**CCDS10340.1**	**chr11: 56185228 C>T**	**V161I**	**Missense**	**18**
HABP4	CCDS34393.1	chr9: 99227746 C>T	R214*	Nonsense	11	**OR6N1**	**CCDS31530.1**	**chr1: 158736147 G>A**	**A109V**	**Missense**	**14**
HLA-C	CCDS11528.1	chr6: 31239837 C>T	M4I	Missense	13	**PBX4**	**CCDS30905.1**	**chr19: 19681407 C>G**	**E143D**	**Missense**	**15**
HOXB3	**CCDS55217.1**	**chr17: 46629769 C>T**	**G23D**	**Missense**	**20**	SLC12A1	CCDS12406.1	chr15: 48559885 G>A	R761Q	Missense	17
KIF13B	CCDS45002.1	chr8_28991628 G>T	P905T	Missense	12	**SYT3**	**CCDS10129.2**	**chr19: 51135864 G>A**	**A118V**	**Missense**	**18**
KNTC1	CCDS13591.1	chr12: 123047234 C>T	P531L	Missense	24	**THOC7**	**CCDS12798.1**	**chr3: 63823666 C>T**	**R113Q**	**Missense**	**13**
KRAS	**CCDS3927.1**	**Chr12: 25398284 C>A**	**G12V**	**Missense**	**3**	**ACAP2**	**CCDS2900.1**	**chr3: 195063234 C>T**	**C165Y**	**Missense**	**13**
KRTAP13-3	**CCDS14221.1**	**chr21: 31797951 T>C**	**T94A**	**Missense**	**17**	**ZNF157**	**CCDS14278.1**	**chrX: 47272856 C>T**	**R462***	**Nonsense**	**15**
LIFR	CCDS12604.2	chr5: 38493788 C>A	C662F	Missense	18						
MAGEB4	**CCDS30676.1**	**chrX: 30260590 C>T**	**T113M**	**Missense**	**21**						
MEGF8	**CCDS10340.1**	**chr19: 42857116 insC**	**D1065Gfs***	**Frameshift**	**14**						
MTF1	**CCDS44981.1**	**chr1: 38323197 T>A**	**D45V**	**Missense**	**24**						
NTRK3	**CCDS32941.1**	**chr15: 88476298 G>T**	**P612T**	**Missense**	**19**						
OAS3	CCDS31530.1	chr12: 113400644 T>C	V674A	Missense	13						
OR10H4	CCDS30905.1	chr19: 16060236 G>A	R140H	Missense	12						
OR5R1	**CCDS35100.1**	**chr11: 56185228 C>T**	**V161I**	**Missense**	**19**						
OR6N1	**CCDS12406.1**	**chr1: 158736147 G>A**	**A109V**	**Missense**	**13**						
PALM2-AKAP2	CCDS6943.1	chr9: 112899162 G>T	M446I	Missense	13						
PBX4	**CCDS55701.1**	**chr19: 19681407 C>G**	**E143D**	**Missense**	**19**						
POMT1	CCDS11425.1	chr9: 134382860 C>G	S129C	Missense	14						
PRKCQ	CCDS14661.1	chr10: 6539181 C>T	N/A	Splice site	12						
PTRF	CCDS2749.2	chr17: 40574907 A>G	L70P	Missense	11						
SETD2	CCDS47643.1	chr3: 47087996 insT	Q2360Rfs*	Frameshift	10						
SGCE	NM_020979	chr7: 94259126 G>A	S46F	Missense	12						
SH2B2	CCDS5307.1	chr7: 101944178 C>T	S158L	Missense	22						
SMOC2	CCDS12798.1	chr6: 168999654 C>T	T276M	Missense	13						
SYT3	**CCDS2900.1**	**chr19: 51135864 G>A**	**A118V**	**Missense**	**22**						
THOC7	**CCDS189.1**	**chr3: 63823666 C>T**	**R113Q**	**Missense**	**20**						
UBR4	CCDS14278.1	chr1: 19470491 C>T	R2721Q	Missense	10						
ZNF157	**CCDS33924.1**	**chrX: 47272856 C>T**	**R462***	**Nonsense**	**14**						

Bold indicates shared mutation to either of the other neoplasms
WES - Whole exome sequencing

IPP39											
Carcinoma						IPMN					
Gene Symbol	Transcript Accession	Nucleotide change	Amino Acid	Consequence	Allele Frequency	Gene Symbol	Transcript Accession	Nucleotide change	Amino Acid	Consequence	Allele Frequency
AARD	CCDS34935.1	chr8: 117950666 C>T	R62W	Missense	23	AKAP6	CCDS9644.1	chr14: 33292742 G>A	G1908E	Missense	19
ADRA1D	CCDS13079.1	chr20: 4228962 C>G	A215P	Missense	20	CYP11A1	CCDS32291.1	chr15: 74635350 C>T	V320I	Missense	11
ARHGAP25	CCDS33214.2	chr2: 69015032 C>T	A137V	Missense	22	EBF3	CCDS31314.1	chr10: 131665431 C>A	G329V	Missense	15
BCL11B	CCDS9950.1	chr14: 99642296 G>A	R293C	Missense	20	EPHA5	CCDS3513.1	chr4: 66361174 G>A	S333L	Missense	15
BMPR1B	CCDS58919.1	chr4: 96036909 A>G	H137R	Missense	20	FNIP1	CCDS34227.1	chr5: 131013522 C>A	A465S	Missense	16
C3orf56	NM_001007534	chr3: 126916036 G>A	V170I	Missense	29	GNAS	CCDS13472.1	chr20: 57484421 G>A	R201H	Missense	13
C5	CCDS6826.1	chr9: 123751851 T>C	K1050R	Missense	17	**KRAS**	**NM_033360**	**chr12: 25398284 C>T**	**G12D**	**Missense**	**9**
FAM111B	CCDS7972.1	chr11: 58877117 G>T	E7*	Nonsense	25	KRAS	CCDS33469.1	chr12: 25398284 C>A	G12V	Missense	17
FAN1	CCDS32186.1	chr15: 31221509 G>A	R899Q	Missense	25	LPIN3	CCDS42773.1	chr20: 39984570 G>A	A567T	Missense	12
GPR126	CCDS47489.1	chr6: 142711444 C>A	H424Q	Missense	24	MYO3B	CCDS44529.1	chr2: 171248925 G>A	D571N	Missense	13
HMHA1	CCDS58637.1	chr19: 1085931 C>G	L1129V	Missense	23	OR52L1	CCDS47045.1	chr11: 6007674 C>T	G163R	Missense	18
INSR	CCDS12176.1	chr19: 7174603 G>A	R372*	Nonsense	19	PDS5A	CCDS45120.1	chr4: 39874641 T>C	N801D	Missense	20
KLHL8	CCDS3617.1	chr4: 88084735 G>A	S600F	Missense	20	PPM1A	CCDS54909.1	chr14: 60749941 C>T	R247*	Nonsense	11
KLK13	CCDS12822.1	chr19: 51563757 G>A	R58W	Missense	28	PROB1	CCDS2788.1	chr5: 138730650 G>T	P41T	Missense	11
KRAS	**CCDS7270.1**	**chr12: 25398284 C>T**	**G12D**	**Missense**	**5**	QARS	CCDS2809.1	chr3: 49136670 G>A	A544V	Missense	23
LRRTM3	CCDS44196.1	chr10: 68687143 C>T	R157W	Missense	23	RBM6	CCDS11607.1	chr3: 50005076 T>C	F73S	Missense	20
MAGI3	CCDS31690.1	chr1: 114092184 C>A	Q122K	Missense	28	RNF43	CCDS11934.1	chr17: 56440659 C>A	E187*	Nonsense	19
MCAM	CCDS9408.1	chr11: 119185669 G>A	L92F	Missense	21	SMAD2	CCDS41423.1	chr18: 45372160 G>A	R337C	Missense	17
MED4	CCDS9600.1	chr13: 48660533 delG	A83Dfs*	Deletion	23	SPTA1	NM_032102	chr1: 158606537 C>T	R1735Q	Missense	11
MYH6	CCDS13241.1	chr14: 23869994 T>C	N445S	Missense	21	SRSF8	CCDS9095.1	chr11: 94800748 A>G	S120G	Missense	10
NCOA6	CCDS4039.1	chr20: 33330375 G>A	P1229S	Missense	19	TDG	CCDS6280.1	chr12: 104373729 insA	I98Nfs*6	Frameshift	12
OTP	CCDS44404.1	chr5: 76932981 G>A	P38S	Missense	25	VPS13B	CCDS11043.1	chr8: 100829840 T>C	Y2749H	Missense	22
PCDH15	CCDS7853.1	chr10: 55581796 G>T	A1899D	Missense	20	ZZEF1	CCDS9644.1	chr17: 3945788 insAC	F2081Cfs*	Frameshift	11
PRMT3	CCDS1296.2	chr11: 20414471 T>C	I109T	Missense	28						
PRRC2C	CCDS1698.1	chr1: 1715535911 T>C	Y2557H	Missense	28						
PUM2	CCDS46221.1	chr2: 20458002 A>T	N/A	Splice site	24						
PXDN	CCDS33312.1	chr2: 1668825 G>A	T438M	Missense	19						
SCN3A	CCDS44233.1	chr2: 165997469 G>A	R571C	Missense	24						
SHC1	CCDS4282.1	chr1: 154938685 C>A	G402V	Missense	19						
TCERG1	CCDS47253.2	chr5: 145886595 G>A	R912H	Missense	23						
TP53	CCDS11118.1	chr17: 7579389 G>A	Q100*	Nonsense	26						
TPO	CCDS1643.1	chr2: 1488501 G>A	R491H	Missense	21						
ZBED4	CCDS33677.1	chr22: 50277325 G>C	L5F	Missense	29						
ZFYVE9	CCDS563.1	chr1: 52740239 C>T	S910F	Missense	24						

Bold indicates shared mutation to either of the other neoplasms
WES - Whole exome sequencing

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Carcinoma

Gene Symbol	Transcript Accession	Nucleotide change	Amino Acid	Consequence	Allele Frequency
ANKRD66	CCDS59024.1	chr6: 46726491 G>A	A197T	Missense	25
AXIN2	CCDS11662.1	chr1763545677 G>A	A306V	Missense	25
BRINP3	CCDS1373.1	chr1: 190067855 G>A	R532W	Missense	24
C11orf87	CCDS31672.1	chr11: 109294783 G>A	A142T	Missense	24
CCDC138	CCDS2080.1	chr2: 109411098 C>T	A166V	Missense	27
COL11A1	CCDS778.1	chr1: 103400084 C>T	G1174E	Missense	26
CSMD2	CCDS380.1	chr1: 34190221 G>A	A887V	Missense	21
CUL2	CCDS55709.1	chr10: 35349820 T>C	Y119C	Missense	24
DNAH11	NM_001277115	chr7: 21813561 G>A	E3094K	Missense	21
DPH1	CCDS42228.1	chr17: 1936810 C>T	R30W	Missense	31
DYNC2H1	CCDS44717.1	chr11: 103074424 T>G	L2744V	Missense	28
EFCAB6	CCDS14049.1	chr22: 44067871 G>A	T541M	Missense	21
GLTSCR1	CCDS46134.1	chr19: 48182734 A>T	I103F	Missense	44
GPR83	CCDS8297.1	chr11: 94113733 C>T	R285H	Missense	23
FAT3	NM_001008781	chr11: 92600283 C>T	T4012M	Missense	10
HMG20B	CCDS45919.1	chr19: 3574502 C>T	T90M	Missense	27
KCNN3	CCDS30880.1	chr1: 154680646 C>T	A668T	Missense	23
LCP1	CCDS9403.1	chr13: 46730707 T>A	N/A	Splice site	24
MAML1	CCDS34315.1	chr5: 179193055 C>A	F348L	Missense	23
KRAS	**NM_033360**	**chr12: 25398284 C>A**	**G12V**	**Missense**	**17**
NCAM1	NM_001242607	chr11: 113105856 G>A	A625T	Missense	19
NKTR	CCDS2702.1	chr3: 42681221 G>A	R1342K	Missense	12
NRAP	CCDS7579.1	chr10: 115389371 C>G	K672N	Missense	12
PARD3B	CCDS42806.1	chr2: 206166406 G>T	G809C	Missense	20
PAX1	CCDS13146.2	chr20: 21689325 T>A	I349N	Missense	27
RAB5C	CCDS58551.1	chr17: 40280713 T>C	Y124C	Missense	24
RNF43	CCDS11607.1	chr17: 56448297 C>G	R117P	Missense	15
SCN1A	CCDS54413.1	chr2: 166868765 G>A	R1245*	Nonsense	23
SLC25A2	CCDS4258.1	chr5: 140682964 C>T	V157M	Missense	20
TAS2R7	CCDS8631.1	chr12: 10954530 G>A	R214*	Nonsense	26
THSD7B	NM_001080427	chr2: 138414717 C>T	A1425V	Missense	11
TLN2	CCDS32261.1	chr15: 63053928 G>A	A1563T	Missense	23
ZFP92	CCDS59177.1	chrX: 152686571 C>T	R246C	Missense	22
ZNF853	CCDS59048.1	chr7: 6662459 C>T	R613C	Missense	33

IPMN

Gene Symbol	Transcript Accession	Nucleotide change	Amino Acid	Consequence	Allele Frequency
ASXL3	CCDS45847.1	chr18: 31325865 C>A	P2018Q	Missense	20
CCDC138	CCDS2080.1	chr2: 109403362 delCC	P29Rfs*	Frameshift	14
COL4A5	CCDS35366.1	chrX: 107683415 G>A	W20*	Nonsense	19
COL4A5	CCDS35366.1	chrX: 107863584 G>A	G869R	Missense	10
CPSF2	CCDS9902.1	chr14: 92597401 G>A	V25I	Missense	17
CRTAP	CCDS2657.1	chr3: 33155736 G>A	S56N	Missense	31
DDX46	CCDS34240.1	chr5: 134143463 insC	I661Hfs*	Frameshift	16
ERCC4	CCDS32390.1	chr16: 14014057 T>G	M12R	Missense	19
FBXW5	CCDS7014.1	chr9: 139837046 C>T	G210R	Missense	21
FER1L6	CCDS43767.1	chr8: 125082711 T>C	Y1280H	Missense	14
GABPA	CCDS13575.1	chr21: 27136946 A>C	E328D	Missense	32
GAS2L2	CCDS11298.1	chr17: 34072898 C>T	A540T	Missense	11
GJA9	CCDS432.1	chr1: 39340513 G>A	R420W	Missense	12
GJB6	CCDS9291.1	chr13: 20797606 G>A	T5M	Missense	26
GNAS	CCDS13472.1	chr20: 5748442 C>T	R201C	Missense	36
IER5	CCDS1343.1	chr1: 181058784 C>T	P249L	Missense	22
KIAA1468	CCDS11979.2	chr18: 59931372 A>G	N834S	Missense	27
KRAS	**NM_033360**	**chr12: 25398284 C>A**	**G12V**	**Missense**	**17**
KRAS	NM_033360	chr12: 25398285 C>A	G12C	Missense	40
LYRM1	CCDS10593.1	chr16: 20931526 A>T	Y81F	Missense	11
MXRA5	CCDS14124.1	chrX: 3239279 G>C	P1483A	Missense	14
NCKAP1L	CCDS31813.1	chr12: 54911345 delTC	F375Y	Deletion	28
NHSL2	NM_001013627	chrX: 71358833 A>C	S479R	Missense	15
NUP205	CCDS34759.1	chr7: 135282758 G>A	E693K	Missense	29
OR4P4	CCDS31504.1	chr11: 55406626 G>T	E265*	Nonsense	45
OR5B12	CCDS31551.1	chr11: 58207143 G>T	T161N	Missense	19
PGBD1	CCDS4648.1	chr6: 28269445 A>G	N605S	Missense	21
PINK1	CCDS211.1	chr1: 20977000 A>C	N521T	Missense	11
PIP4K2B	CCDS11329.1	chr17: 36927497 T>C	Y279C	Missense	17
PNLIP	CCDS7594.1	chr10: 118306809 delAAG	E18del	In-frame deletion	14
PSME4	CCDS33197.2	chr2: 54197866 G>A	P19L	Missense	15
RP1L1	CCDS43708.1	chr8: 10467124 G>C	P1495R	Missense	10
RTN3	CCDS58141.1	chr11: 63486681 A>C	D236A	Missense	29
SEC14L6	CCDS54518.1	chr22: 30934816 T>C	Q43R	Missense	14
THBS4	CCDS4049.1	chr5: 79378293 C>A	R917S	Missense	19
TIAM1	CCDS13609.1	chr21: 3263915 C>A	G45W	Missense	24
TMCO4	CCDS198.1	chr1: 20020994 C>T	R478H	Missense	13
TNXB	NM_019105	chr6: 32064098 C>T	R511H	Missense	10
TPCN1	CCDS44985.1	chr12: 113711468 A>T	N385Y	Missense	11
TTLL11	CCDS48012.1	chr9: 124855090 T>G	K203T	Missense	26
UTP11L	CCDS429.1	chr1: 38489286 C>G	R250G	Missense	29
ZC3H12D	NM_207360	chr6: 149795534 G>T	A49D	Missense	15
ZNF865	CCDS58681.1	chr19: 56125418 C>T	P145L	Missense	30

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