

**Site Specific Genomic Alterations in a Well-Differentiated Pancreatic Neuroendocrine Tumor  
With High-Grade Progression**

<b>SUPPLEMENTARY TABLE 1. Copy Number Gains as Assigned by the Ion Reporter CNV Calling Algorithm</b>				
<b>ISCN Names</b>	<b>Size, kb</b>	<b>Likely Ploidy</b>	<b>CNV Confidence</b>	<b>Genes in CNV region</b>
<b>PanNET high grade tumor area</b>				
7q21.2	1004	×3	42.10	AKAP9; CDK6; SAMD9
4q22.1-q24	18104	×3	25.34	AFF1; NFKB1; TET2
19q13.2	11	×3	25.33	CIC
3p22.1	14	×3	21.66	CTNNB1
17q25.3	8	×3	21.06	RNF213; LOC100294362
8p11.21	1	×3	17.80	KAT6A
5q22.2	9	×3	17.68	APC
9p24.1-p22.3	7134	×3	17.43	PTPRD; PSIP1
9q33.1-q34.12	13263	×3	16.66	TLR4; ABL1
5q35.2-q35.3	149	×3	16.13	FGFR4; NSD1
13q33.1	1	×7	14.33	ERCC5
14q32.31	4	×3	13.24	HSP90AA1
8q22.3	32	×3	13.10	UBR5
<b>PanNET low grade tumor area</b>				
14q32.13-q32.33	9702	×3	242.30	DICER1; TCL1A; BCL11B; HSP90AA1; AKT1
8p11.23p11.21	4479	×3	60.40	GPR124; FGFR1; KAT6A; IKBKB
17p13.1-p11.2	9552	×3	55.75	TP53; PER1; MIR6883; AURKB; FLCN
7q31.33-q36.1	25691	×3	55.66	GRM8; SMO; TRIM24; BRAF; EPHB6; EZH2; KMT2C
9p21.3-p13.3	13109	×3	55.46	CDKN2A; CDKN2B-AS1; CDKN2B; TAF1L; FANCG
18q11.2-q21.1	25160	×3	47.87	ZNF521; CDH2; SMAD2; MBD1
12q12-q13.12	3140	×3	38.46	ARID2; KMT2D
4q13.1-q22.1	25215	×3	38.08	LPHN3; AFF1
3q27.3-q29	8161	×3	32.67	LOC100131635; BCL6; LPP; TNK2
4q12	449	×3	29.80	PDGFRA; KIT
12q13.12-q13.2	7044	×3	29.24	KMT2D; ATF1; SMUG1; ERBB3
3p11.1-q22.2	45467	×3	28.07	EPHA3; GATA2; EPHB1
8q24.3	6	×3	27.46	RECQL4
3p22.2-p22.1	4187	×3	25.49	MLH1; ITGA9; ITGA9-AS1; MYD88; CTNNB1