Supplemental Table S2. The Top 20 Genomic Alterations in N0 and N1b PTMCs

Hugo symbol	Case ID (No.)		Chromosome	Start position	End position	cDNA change	Protein change	Variant classification	VAF	Allelic depth	
	N0	N1b								Reference	Variant
DPP6	2		7	153750096	153750096	c.191G>A	p.G64D	Missense	0.09	64	6
		21	7	153750140	153750140	c.235G>A	p.E79K	Missense	0.06	79	5
		23	7	153750096	153750096	c.191G>A	p.G64D	Missense	0.09	73	7
		27	7	153750140	153750140	c.235G>A	p.E79K	Missense	0.06	79	5
PGS1		18	17	76394393	76394393	c.472A>C	p.K158Q	Missense	0.22	25	7
		19	17	76394393	76394393	c.472A>C	p.K158Q	Missense	0.18	32	7
		25	17	76394393	76394393	c.472A>C	p.K158Q	Missense	0.15	29	5
		27	17	76394393	76394393	c.472A>C	p.K158Q	Missense	0.15	41	7
BRAF	2		7	140453136	140453136	c.1799T>A	p.V600E	Missense	0.2	16	4
	14		7	140453136	140453136	c.1799T>A	p.V600E	Missense	0.18	14	3
		20	7	140453136	140453136	c.1799T>A	p.V600E	Missense	0.33	10	5
DDX11	2		12	31237922	31237922	c.500G>C	p.R167T	Missense	0.1	26	3
			12	31237978	31237978	c.556C>T	p.R186W	Missense	0.1	27	3
		21	12	31254785	31254785	c.2071A>G	p.I691V	Missense	0.09	41	4
		25	12	31237978	31237978	c.556C>T	p.R186W	Missense	0.14	24	4
GBA	2		1	155208310	155208310	c.586A>C	p.K196Q	Missense	0.44	10	8
		15	1	155208310	155208310	c.586A>C	p.K196Q	Missense	0.22	21	6
		22	1	155208310	155208310	c.586A>C	p.K196Q	Missense	0.24	18	6
RHPN2	8		19	33517507	33517507	c.217G>A	p.V73M	Missense	0.09	32	3
	14		19	33517507	33517507	c.217G>A	p.V73M	Missense	0.07	53	4
		22	19	33493842	33493842	c.825G>T	p.M275I	Missense	0.08	36	3
SLC4A8		17	12	51853889	51853889	c.1010C>A	p.T337K	Missense	0.1	38	4
		18	12	51882642	51882642	c.2446A>C	p.K816Q	Missense	0.24	16	5
		19	12	51882642	51882642	c.2446A>C	p.K816Q	Missense	0.26	23	8
ADAMTS9	1		3	64601832	64601832	c.2828G>T	p.S943I	Missense	0.1	38	4
		20	3	64582510	64582510	c.4175G>T	p.G1392V	Missense	0.07	57	4
AP3S1	7		5	115249078	115249078	c.473C>T	p.P158L	Missense	0.08	48	4
	10		5	115249078	115249078	c.473C>T	p.P158L	Missense	0.08	36	3
ARHGAP5	2		14	32561340	32561340	c.1465G>A	p.E489K	Missense	0.11	39	5
	8		14	32561340	32561340	c.1465G>A	p.E489K	Missense	0.06	47	3
ATP10B	7		5	160029664	160029664	c.3283A>C	p.K1095Q	Missense	0.14	86	14
	8		5	160029664	160029664	c.3283A>C	p.K1095Q	Missense	0.19	66	15
CYP4F2	14		19	15989696	15989696	c.1448C>G	p.A483G	Missense	0.09	41	4
		17	19	15989696	15989696	c.1448C>G	p.A483G	Missense	0.16	21	4
			19	15989730	15989730	c.1414A>G	p.T472A	Missense	0.19	17	4
DAAM2		19	6	39851764	39851764	c.1872T>G	p.N624K	Missense	0.13	26	4
		22	6	39835584	39835584	c.727T>A	p.Y243N	Missense	0.14	30	5
DNHD1	10		11	6588461	6588461	c.11722C>A	p.L3908M	Missense	0.06	60	4
		16	11	6559947	6559947	c.3232C>T	p.R1078C	Missense	0.07	69	5

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Supplemental Table S2. Continued

Hugo symbol	Case ID (No.)		Chromosome	Start position	End position	cDNA change	Protein change	Variant classification	VAF	Allelic depth	
	N0	N1b								Reference	Variant
FCGBP	2		19	40392347	40392347	c.8157G>C	p.Q2719H	Missense	0.13	21	3
		27	19	40389741	40389741	c.8441T>C	p.V2814A	Missense	0.09	51	5
FNDC3B	7		3	172052852	172052852	c.1760A>C	p.H587P	Missense	0.20	80	20
	8		3	172052852	172052852	c.1760A>C	p.H587P	Missense	0.16	70	14
HCAR3	14		12	123200527	123200527	c.758A>G	p.H253R	Missense	0.12	23	3
		26	12	123200527	123200527	c.758A>G	p.H253R	Missense	0.14	19	3
HELZ		16	17	65191567	65191567	c.449T>C	p.L150P	Missense	0.07	54	4
		25	17	65144769	65144769	c.2537A>G	p.D846G	Missense	0.06	67	4
HLA-DRB5	8		6	32497931	32497931	c.71C>T	p.S24F	Missense	0.1	75	8
		26	6	32497918	32497918	c.84G>C	p.L28F	Missense	0.11	69	9
			6	32497928	32497928	c.74C>G	p.P25R	Missense	0.11	66	8
MUC16	5		19	9085096	9085096	c.6719C>A	p.P2240H	Missense	0.1	46	5
		21	19	9008290	9008290	c.39262A>G	p.N13088D	Missense	0.19	22	5
			19	9008292	9008292	c.39260T>C	p.L13087P	Missense	0.19	22	5

PTMC, papillary thyroid microcarcinoma; VAF, variants allele frequency.