Supplemental Table S3. Pathogenicity of Mutation Based on Clinvar or CADD Score Specific to the N0 PTMCs

Case ID	Hugo symbol	Chromosome	Start position	End position	cDNA change	Protein change	Variant classification	Variants allele frequency	Allelic depth		Clinvar	CADD score
									Reference	Variant		
Case 1	MACF1	1	39913536	39913536	c.19631G>A	p.R6544Q	Missense	0.35	47	25		35
	RFX3	9	3263077	3263077	c.1463C>A	p.A488D	Missense	0.08	37	3		34
	CPT1A	11	68527117	68527117	c.2155G>T	p.G719C	Missense	0.07	43	3		33
	VWF	12	6219688	6219688	c.384G>T	p.K128N	Missense	0.07	41	3		33
	FAM19A3	1	113269253	113269253	c.393C>A	p.V131V	Silent	0.13	26	4		38
	RSPH3	6	159403614	159403614	c.599T>C	p.L200P	Missense	0.08	45	4		31
	FCHSD2	11	72549871	72549871	c.1780G>T	p.E594*	Nonsense	0.16	21	4		46
Case 2	AGMAT	1	15906635	15906635	c.478G>T	p.G160*	Nonsense	0.06	46	3		40
	GBA	1	155208310	155208310	c.586A>C	p.K196Q	Missense	0.44	10	8	Pathogenic	24
	BRAF	7	140453136	140453136	c.1799T>A	p.V600E	Missense	0.2	16	4	Pathogenic	32
	DNAJC27	2	25190101	25190101	c.149G>T	p.G50V	Missense	0.25	12	4		32
	AASS	7	121738875	121738875	c.1452G>T	p.L484F	Missense	0.06	115	8		31
	NDRG3	20	35315980	35315980	c.235G>T	p.D79Y	Missense	0.14	24	4		34
Case 3	C17orf66	17	34191774	34191774	c.441G>A	p.W147*	Nonsense	0.12	23	3		36
	ABHD10	3	111700766	111700766	c.278C>A	p.A93E	Missense	0.06	83	5		34
	ABCB4	7	87083867	87083867	c.328G>T	p.E110*	Nonsense	0.13	28	4		39
Case 4	PLCB2	15	40582975	40582975	c.3100G>T	p.E1034*	Nonsense	0.08	46	4		43
Case 5	SERAC1	6	158541607	158541607	c.1016G>T	p.G339V	Splice site	0.11	31	4		32
	SACS	13	23939347	23939347	c.415G>A	p.G139R	Missense	0.08	47	4		34
Case 6	ATP8B4	15	50189710	50189710	c.2476G>T	p.A826S	Missense	0.06	60	4		31
	MRGBP	20	61429987	61429987	c.319C>A	p.L107I	Missense	0.06	63	4		33
Case 7	CLK3	15	74914836	74914836	c.468T>G	p.Y156*	Splice site	0.13	94	14		36
	EFNB3	17	7612804	7612804	c.933T>G	p.Y311*	Nonsense	0.25	68	23		36
Case 8	ATP10D	4	47538939	47538939	c.1380C>A	p.Y460*	Nonsense	0.05	75	4		35
	DPP9	19	4690922	4690922	c.1564G>T	p.E522*	Nonsense	0.14	18	3		38
	KCNJ14	19	48967933	48967933	c.1210G>T	p.E404*	Nonsense	0.07	76	6		42
	PIGO	9	35089182	35089182	c.3177C>A	p.S1059R	Missense	0.06	60	4		31
	RBL2	16	53515605	53515605	c.3107C>A	p.P1036H	Missense	0.08	45	4		34
Case 9	UTRN	6	144844251	144844251	c.5833C>T	p.Q1945*	Nonsense	0.14	71	12		44
	TATDN3	1	212977951	212977951	c.382C>A	p.R128S	Missense	0.06	72	5		34
	HNRNPUL2	11	62483338	62483338	c.2053G>T	p.G685W	Missense	0.11	32	4		31
Case 10	ALDH1L1	3	125869347	125869347	c.916G>T	p.D306Y	Missense	0.1	38	4		32
	UHRF2	9	6493905	6493905	c.1577C>A	p.A526D	Missense	0.12	30	4		32
	ZZEF1	17	3916896	3916896	c.8426T>A	p.L2809*	Nonsense	0.07	62	5		57
	SSH2	17	27959250	27959250	c.2881G>T	p.E961*	Nonsense	0.09	42	4		35
	PIK3C3	18	39542573	39542573	c.377C>A	p.T126K	Missense	0.06	45	3		34
	PPP1R12C	19	55603038	55603038	c.2242G>T	p.E748*	Nonsense	0.1	46	5		39
	NPAS2	2	101541636	101541636	c.61C>A	p.R21S	Missense	0.11	34	4		34
	MCF2L2	3	183013223	183013223	c.1540G>T	p.E514*	Nonsense	0.11	47	6		37
	PDE3A	12	20792832	20792832	c.2192C>A	p.P731Q	Missense	0.21	15	4		32
	FNDC3A	13	49772296	49772296	c.2669C>A	p.S890*	Nonsense	0.05	118	6		41
	ZDHHC8	22	20127115	20127115	c.341C>A	p.P114Q	Missense	0.05	95	5		33

(*Continued to the next page*)

Supplemental Table S3. Continued

Case ID	Hugo symbol	Chromosome	Start position	End position	cDNA change	Protein change	Variant classification	Variants allele frequency	Allelic depth		Clinvar	CADD score
									Reference	Variant		
Case 11	FUCA1	1	24192087	24192087	c.418G>T	p.E140*	Nonsense	0.14	23	4		40
	IREB2	15	78775682	78775682	c.1319C>A	p.S440*	Nonsense	0.1	38	4		40
	SLC6A2	16	55732392	55732392	c.1401C>A	p.Y467*	Nonsense	0.05	89	5		32
Case 12	USH2A	1	216052393	216052393	c.8271T>G	p.Y2757*	Nonsense	0.06	149	9	Pathogenic	39
	COPG1	3	128993762	128993762	c.2338G>T	p.G780W	Missense	0.08	45	4		34
	NMUR2	5	151775094	151775094	c.863G>T	p.R288L	Missense	0.06	58	4		35
	PKD2L1	10	102056920	102056920	c.1002G>A	p.W334*	Nonsense	0.08	45	4		39
	ST6GAL-NAC1	17	74623557	74623557	c.940G>T	p.E314*	Nonsense	0.11	34	4		36
Case 13	MPL	1	43814638	43814638	c.1433C>A	p.S478*	Nonsense	0.07	39	3		38
	MCF2L2	3	183056646	183056646	c.428G>A	p.R143K	Missense	0.09	40	4		31
	ENPP2	8	120629477	120629477	c.584G>A	p.C195Y	Missense	0.09	39	4		31
	OR2AG2	11	6789604	6789604	c.585T>G	p.Y195*	Nonsense	0.09	43	4		34
	DHX34	19	47865762	47865762	c.1405C>T	p.Q469*	Nonsense	0.16	38	7		40
	LANCL2	7	55468998	55468998	c.810C>A	p.Y270*	Nonsense	0.13	27	4		42
	FAM117A	17	47810016	47810016	c.263G>T	p.R88L	Missense	0.07	71	5		34
Case 14	BRAF	7	140453136	140453136	c.1799T>A	p.V600E	Missense	0.18	14	3	Pathogenic	32
	CAMKK2	12	121690480	121690480	c.1145G>T	p.C382F	Missense	0.11	32	4		34

CADD, Combined Annotation-Dependent Depletion; PTMC, papillary thyroid microcarcinoma.