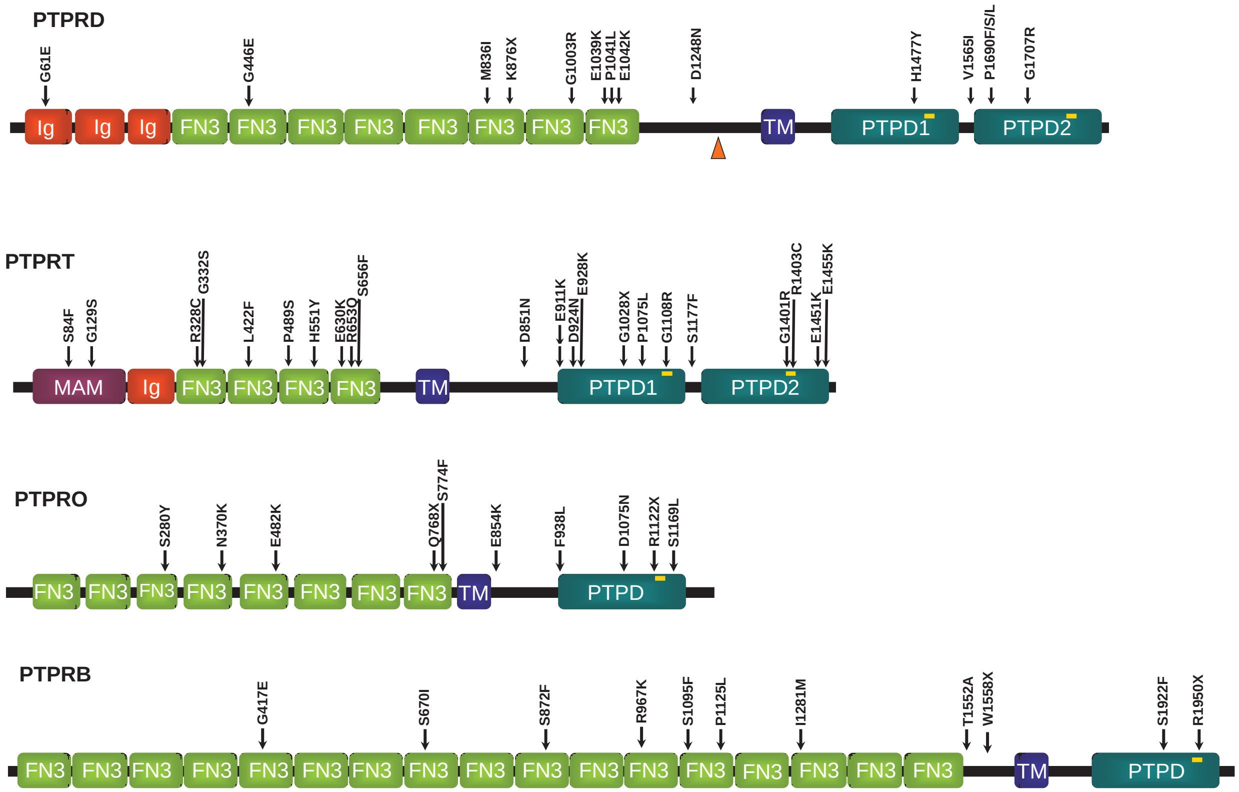
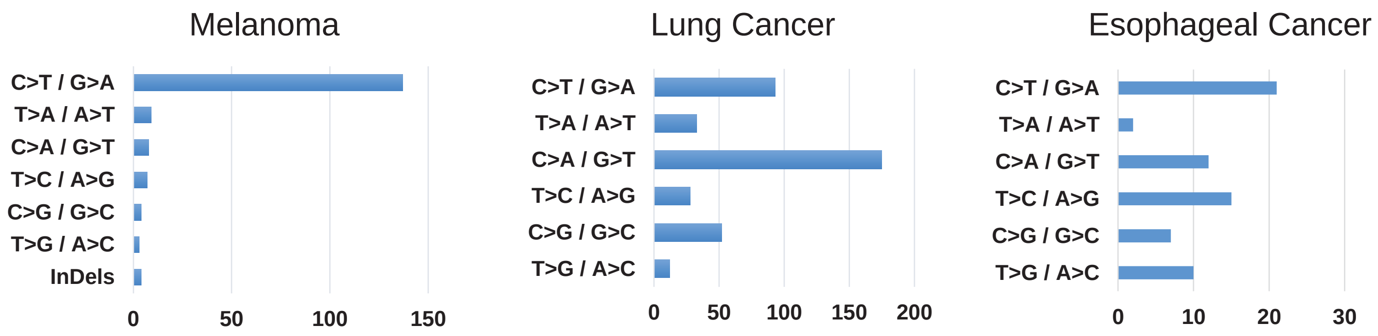
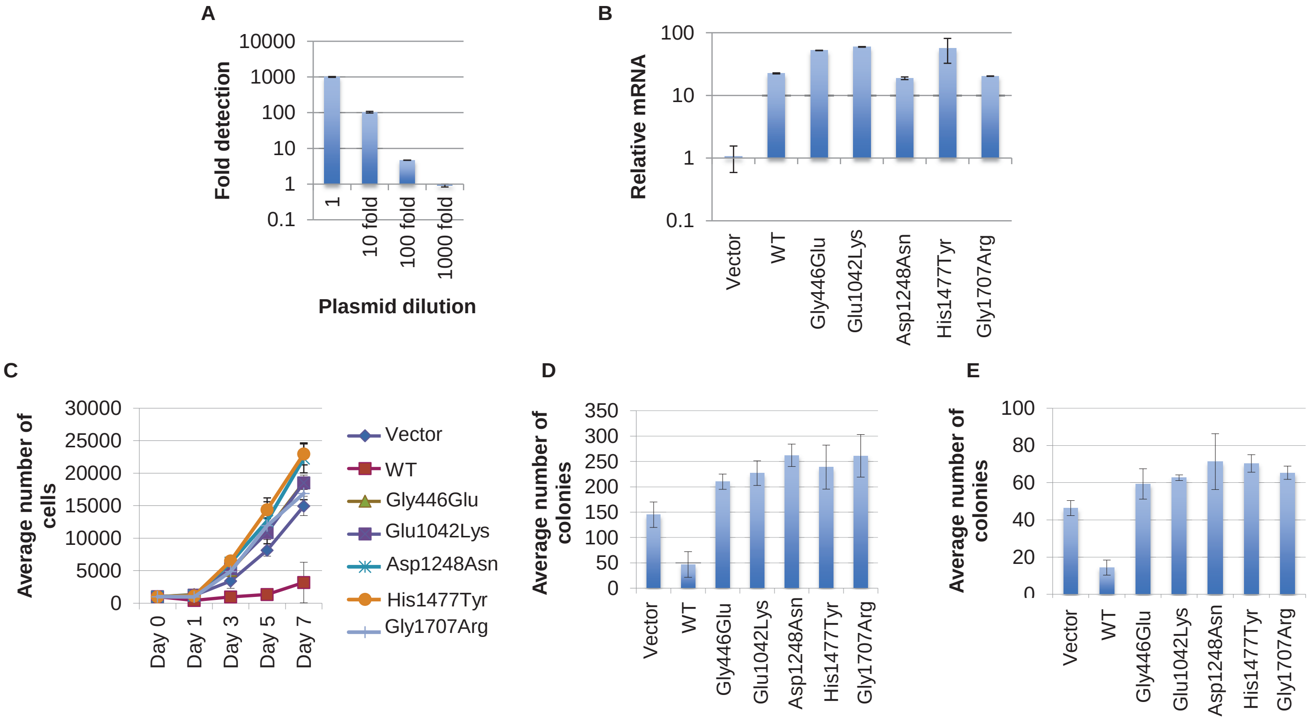


Supp. Figure S1. Schematics of mutations identified in *PTPRD*, *PTPRT*, *PTPRB* and *PTPRO*. Black arrow indicates location of somatic mutations. Boxes represent functional domains: MAM, meprin/A5/PTPμ protein-protein interaction domain; Ig, Ig-like C2-type domain; FN3, fibronectin type III domain; TM, transmembrane (single pass – type I) domain; PTPD1/2, catalytic phosphatase domain D1 (active site indicated in yellow) and D2 (active site indicated in yellow); PTPD, tyrosine-protein phosphatase domain; CS, cleavage site. Amino acid code are *: Stop, A: Ala, R: Arg, N: Asn, D: Asp, B: Asx, C: Cys, E: Glu, Q: Glu, Z: Glx, G: Gly, H: His, I: Ile, L: Leu, K: Lys, M: Met, F: Phe, P: Pro, S: Ser, T: Thr, W: Trp, Y: Tyr, and V: Val.



Supp. Figure S2. Spectra of single base pair substitutions mutation showed that C>T substitutions are frequent in the melanoma phosphatome. The number of mutation due to six classes of nucleotide substitutions causing nonsynonymous changes in the phosphatome screen is shown. The mutation type causing base pair substitution vs. number of incidence is represented by the histogram. Comparison with combined mutational spectrum of PTPRD, PTPRT, PTPRB, PTPRB and PTPRN2 in lung cancer and esophagus cancer is shown.



Supp. Figure S3. PTPRD mutants expressing Sk-Mel-2 have enhanced anchorage-dependent and -independent growth rate. (a) Validation of the *PTPRD* probe (Hs01551546_m1) using Taqman analysis on ABI 7500 instrument using *PTPRD* plasmid dilution. (b) Expression of WT PTPRD and mutants in Sk-Mel-2 pools as measured by Taqman probe. (c) Cellular proliferation of Sk-Mel-2 pooled clones transduced with an empty vector, WT PTPRD and indicated mutants was measured in the presence of 2% serum for 7 days. PTPRD mutant cells showed enhanced ability to grow compared with WT PTPRD expressing cells. (d) PTPRD mutants expressing Sk-Mel-2 have enhanced anchorage-independent growth rate. Anchorage-independent proliferation of Sk-Mel-28 cell clones expressing indicated constructs was analyzed by counting the number of colonies formed in soft agar. Graph indicates average number of colonies (+/-SD) formed after 14 days of growth by 2500 cells in 2% serum. (e) PTPRD mutants expressing Sk-Mel-2 have enhanced ability to form foci. Sk-Mel-2 pooled clones expressing the indicated empty vector (control), WT or mutant PTPRD constructs seeded at 1000 cells per T25 flask in 2% serum. The graph indicates average number of colonies (+/-SD) formed after 14 days of growth.

```
PTP1B/PTPN1 172            -LHFHYTTWPDFGVPESPASFLNFLFKVREFGSLSP
PTPRT human 1055  KKGYHEIRELRLFHFTSWPDHGVPCYATGLLGF---VRQVKFLNP
PTPRD human 1502  KNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAF---LRRVKTCNP
PTPRD dog   1502  KNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAF---LRRVKTCNP
PTPRD cow   1502  KNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAF---LRRVKTCNP
PTPRD mouse 1417  KNGSSEKREVRQFQFTAWPDHGVPEHPTPFLAF---LRRVKTCNP
                                  (D1521A)
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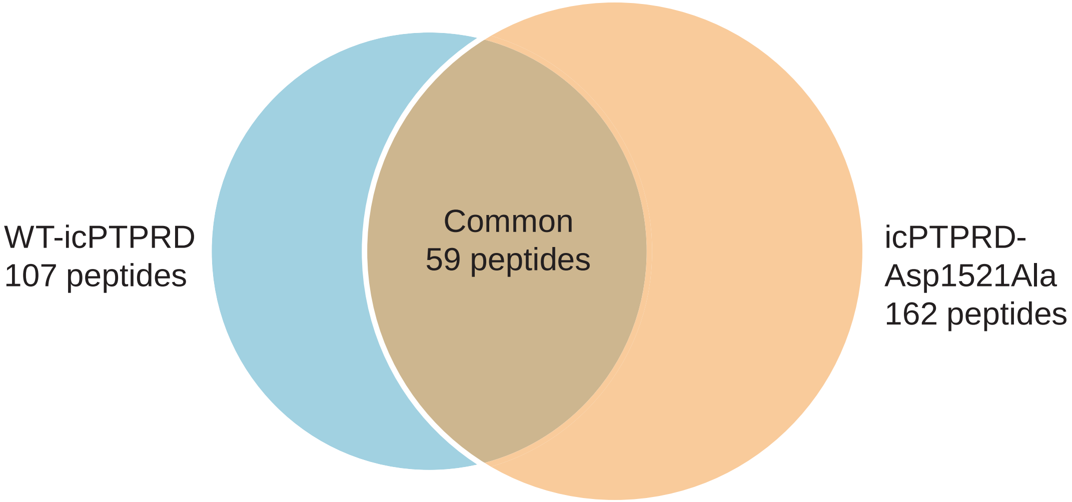
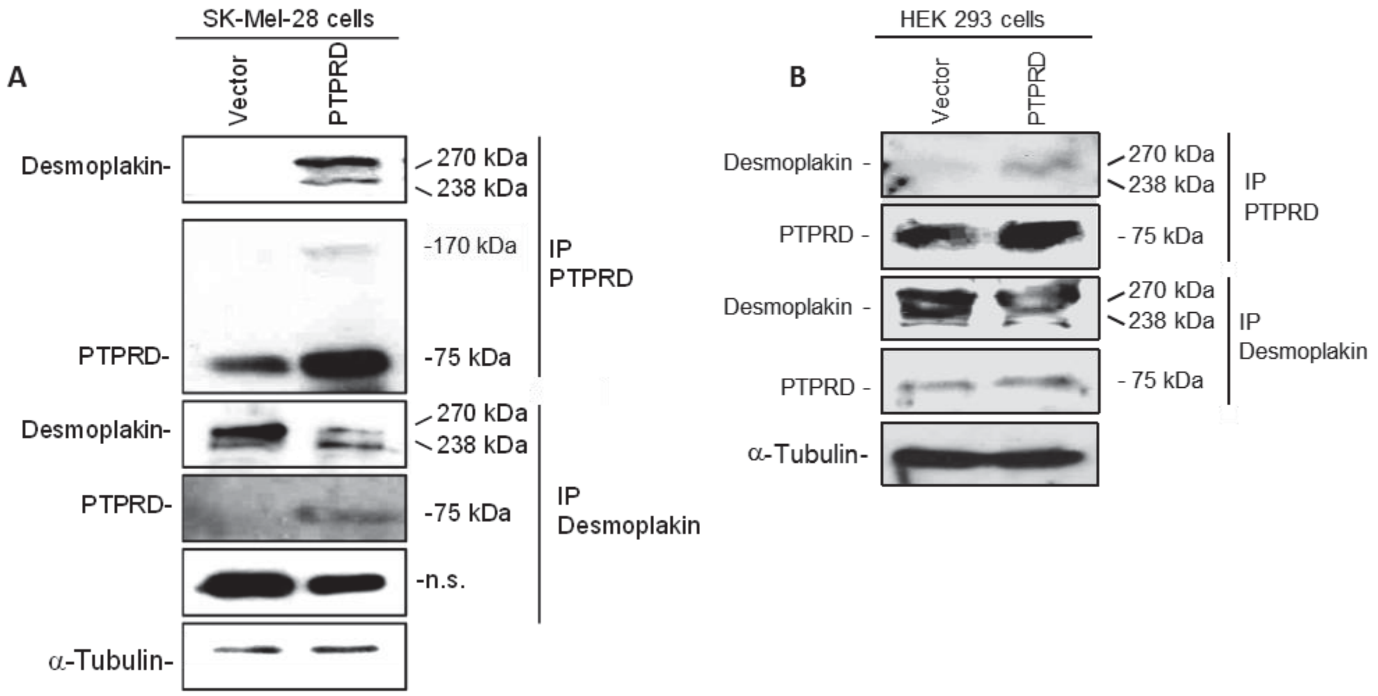
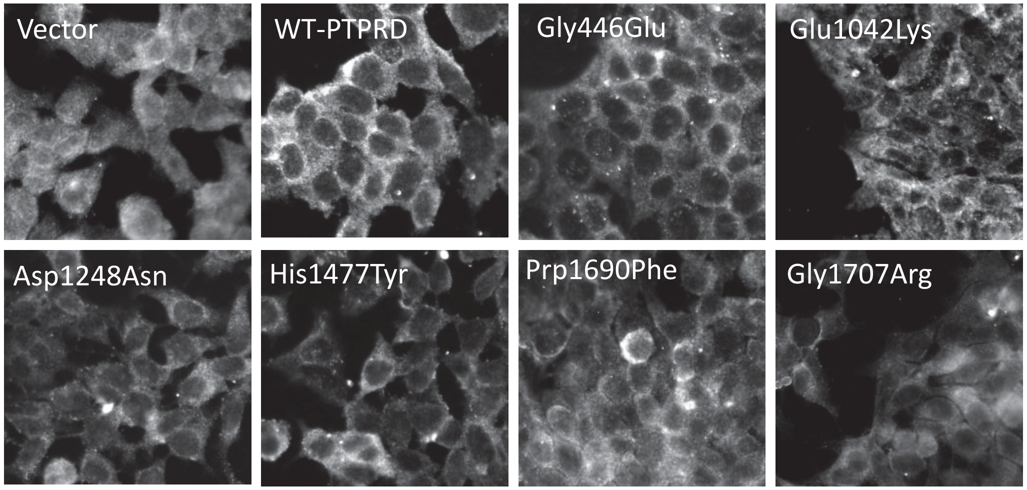
Supp. Figure S4. Sequence conservation of aspartic acid-1521 of human *PTPRD* and its orthologs with *PTP1B* and *PTPRT* for generation of a substrate-trapping mutant. Based on mechanistic studies of *PTP1B* and *PTPRT*, the residue highlighted in red was targeted to generate mutant PTPRD for use in substrate trapping immunoprecipitation. Asp1521Ala mutation in *PTPRD* is predicted to be similar to the Asp1071Ala mutation in *PTPRT* and Asp181Ala mutation in *PTP1B*, having higher substrate affinity and impaired phosphatase activity. Accession numbers are *PTPN1* (Homo sapien, NP_002818.1), *PTPRT* (Homo sapien, NP_008981.4), *PTPRD* (Homo sapien, NP_001035802.1), *PTPRD* (Canis lupus, NP_001035802.1), *PTPRD* (Bos taurus, XP_538659.2), *PTPRD* (Mus musculus, XP_002689639.2).



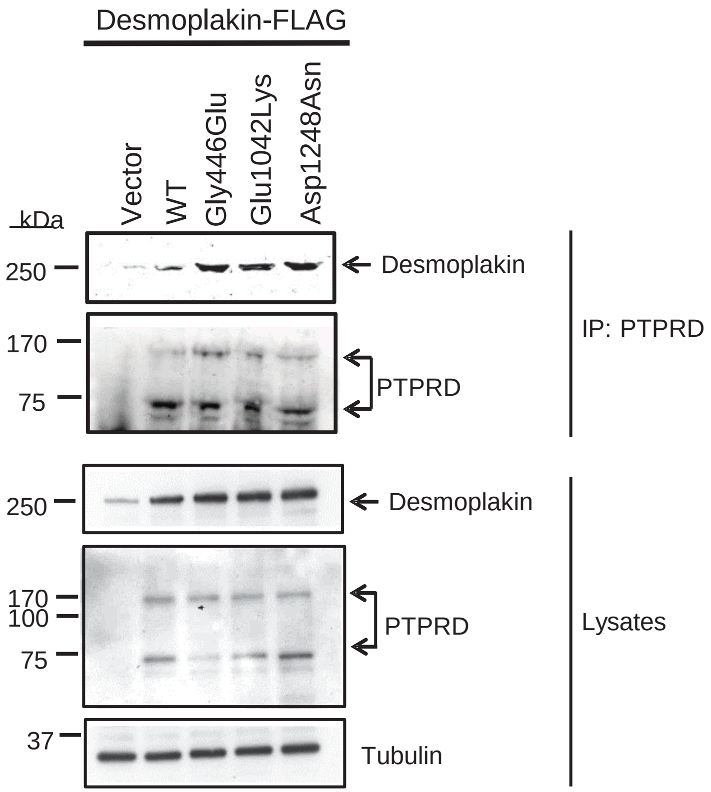
Supp. Figure S5. Venn-diagram showing common peptides pulled down by PTPRD. Blue color represents number of peptides in complex with WT icPTPRD, expressing both phosphatase domains of WT PTPRD. Orange color represents number of peptides in complex with icPTPRD-D1215A, expressing both phosphatase domains with Asp1521Ala substrate-trapping mutation in the first phosphatase domain. Merge area represents common peptides pulled down by both. Data normalized to control cell line is shown.



Supp. Figure S6. Desmoplakin interacts with overexpressed PTPRD in Sk-Mel-28 cells **(a)** and HEK 293 cells **(b)**. Immunoblots representing co-immunoprecipitation of desmoplakin and WT PTPRD by PTPRD and desmoplakin antibody. Lysates containing similar amount of total protein was determined by immunoblotting with anti α-tubulin.



Supp. Figure S7. Comparison of desmoplakin expression in WT PTPRD and mutant overexpressing Sk-Mel-28 pooled clones. Immuno-cytochemistry showing inverted images stained with desmoplakin Ab.



Supp. Figure S8. Desmoplakin interacts with WT and mutant PTPRD. PTPRD antibody was used to immunoprecipitate desmoplakin in HEK-293T cells expressing WT and mutant PTPRD. Western blot showing immunoprecipitated samples probed with FLAG antibody and PTPRD antibody. Expression of indicated proteins in whole cell lysates is also shown.

Supp. Table S1. Somatic mutations identified in PTPs

Gene	Other names	CCDS accession*	Ref Seq accession*	No. of mutations (% tumors affected) #	Tumor	Exon^	Nucleotide†	Amino Acid†	Functional domain‡	NRAS/BRAF mutation**
PTPRT	RPTPrho	42874.1	NM_133170.3	26 (22.5%)	12T	3, 18, 31	c.251C>T, c.2551G>A, c.4207C>T	p.Ser84Phe, p.Asp851Asn, p.Arg1403Cys	MAM,N/A,PTPD 2	NRAS
	KIAA0283				1T	3	c.385G>A	p.Gly129Ser	MAM	BRAF
					45T	7	c.994G>T	p.Gly332Cys (LOH)	FN3	BRAF
					52T	7,31	c.982C>T, c.4201G>A	p.Arg328Cys, p.Gly1401Arg	FN3,PTPD2	BRAF
					83T	8,32	c.1264C>T, c.4351G>A	p.Leu422Phe (LOH), p.Glu1451Lys	N/A,PTPD2	Both
					6T	9	c.1465C>T	p.Pro489Ser	N/A	BRAF
					68T	10,31	c.1651C>T, c.4194-14G>A	p.His551Tyr, p.nc	FN3,N/A	BRAF
					103T	12	c.1888G>A	p.Glu630Lys (LOH)	N/A	BRAF
					21T	12	c.1958G>A	p.Arg653Gln	N/A	BRAF
					5T	12	c.1967C>T	p.Ser656Phe	N/A	BRAF
					104T	18	c.2731G>A	p.Glu911Lys	N/A	None
					20T	18	c.2731G>A	p.Glu911Lys	N/A	BRAF
					39T	19,20,23,24	c.2782G>A, c.2904+9C>T, c.3082G>T, c.3224C>T	p.Glu928Lys, p.nc, p.Gly1028*, p.Pro1075Leu	N/A, PTPD1	None
					44T	19	c.2770G>A	p.Asp924Asn	N/A	NRAS
					80T	25	c.3322G>A	p.Gly1108Arg	PTPD1	BRAF
					41T	26	c.3530C>T	p.Ser1177Phe	N/A	BRAF
					74T	27	c.3771+11C>T	p.nc	N/A	NRAS
					30T	32	c.4363G>A	p.Glu1455Lys	PTPD2	BRAF
PTPRD	HPTP	43786.1	NM_002839.2	17 (18.5%)	34T	2	c.182G>A	p.Gly61Glu	Ig-I set	BRAF
	PTPD				13T	3,18	c.211-10C>T, c.3124G>A	p.nc, p.Glu1042Lys	N/A,N/A	None
	HPTPD				16T	10	c.1337G>A	p.Gly446Glu (LOH)	FN3	BRAF
	HPTP-delta				106T	18	c.3122C>T	p.Pro1041Leu	N/A	N/A
	R-PTP-delta				12T	18	c.3056-11C>T	p.nc (LOH)	N/A	NRAS
	MGC119750				48T	18	c.3115G>A	p.Glu1039Lys (LOH)	N/A	BRAF
	MGC119752				74T	17	c.2508G>A	p.Met836Ile (LOH)	FN3	NRAS
	MGC119753				32T	17	c.2626G>T	p.Lys876*	FN3	BRAF
	protein tyrosine phosphatase, receptor type, D				71T	17	c.3007G>A	p.G1003Arg	FN3	BRAF
	protein tyrosine phosphatase, receptor type,				21T	22	c.3742G>A	p.Asp1248Asn (LOH)	N/A	BRAF

Gene	Other names	CCDS accession*	Ref Seq accession*	No. of mutations (% tumors affected) #	Tumor	Exon^	Nucleotide†	Amino Acid†	Functional domain‡	NRAS/BRAF mutation**
	delta polypeptide									
	MGC119751				36T	31	c.5119G>A	p.G1707Arg	PTPD2	BRAF
	EC 3.1.3.48				52T	27	c.4429C>T	p.His1477Tyr (LOH)	PTPD1	BRAF
					86T	29	c.4693G>A	p.Val1565Ile (LOH)	PTPD1	BRAF
					6T	30	c.5068C>T, c.5069C>T	p.Pro1690Ser (tct), p.Pro1690Leu (ctt), p.Pro1690Phe (ttt)	PTPD2	NRAS
					83T	28	c.4661+6_446+7insACAGTTCAGGAATGGTAAGTT	p.nc	N/A	Both
PTPRB	PTPB	N/A	NM_001109754.1	19 (16.5%)	21T	5	c.1250G>A	p.G417Glu	N/A	BRAF
	HPTPB				6T	8	c.1781-5G>A	p.nc (LOH)	N/A	BRAF
	VEPTP				91T	8	c.2009G>A, c.2009T>A	p.Ser670Ile, p.Ser670Arg	FN3	BRAF
	HPTP-BETA				39T	11, 14, 27	c.2615C>T, c.3374C>T, c.5765C>T	p.Ser872Phe, p.Pro1125Leu, p.Ser1922Phe	FN3, N/A, N/A	None
	R-PTP-BETA				55T	12	c.2900G>A	p.Arg967Lys	FN3	None
	FLJ44133				7T	13	c.3284C>T	p.Ser1095Phe	FN3	NRAS
	MGC59935				58T	15, 18	c.3843A>G, c.4654A>G	p.Ile1281Met, p.Thr1552Ala	FN3, FN3	BRAF
	MGC142023				12T	17	c.4169-9T>A	p.nc	N/A	NRAS
	DKFZp686E2262				81T	17	c.4169-10T>C, c.4169-9T>A	p.nc, p.nc	N/A	BRAF
	DKFZp686H15164				88T	17	c.4169-10T>C, c.4169-9T>A	p.nc, p.nc	N/A	BRAF
					16T	18	c.4674G>A	p.Trp1558*	FN3	BRAF
					73T	19	c.4715-5C>T	p.nc	N/A	BRAF
					24T	28	c.5848C>T	p.Arg1950*	PTPc	NRAS
PTPRO	GLEPP1	8675.1	NM_030667.1	11 (12.7%)	95T	5	c.839C>A	**p.**Ser280Tyr	N/A	NRAS
	PTPU2				9T	6	c.1106-9T>A, c.1110C>G	p.nc, p.Asn370Lys	N/A	BRAF
	PTP-U2				85T	7	c.1444G>A	p.Glu482Lys	FN3	BRAF
	PTP-oc				21T	13	c.2302C>T	p.Gln768*	FN3	BRAF
					13T	14	c.2321C>T	p.Ser774Phe	FN3	None
					12T	16	c.2560G>A	p.Glu854Lys	N/A	NRAS
					24T	19	c.2814T>G	p.Phe938Leu	N/A	NRAS
					39T	23	c.3223G>A	p.Asp1075Asn	PTPc	None
					60T	24	c.3364C>T	p.Arg1122*	PTPc	NRAS
					45T	25	c.3506C>T	p.Ser1169Leu (LOH)	PTPc	BRAF
PTPRN2	IAR	5947.1	NM_002847.3	11 (12.7%)	13T	2	c.113-7C>T	p.nc	N/A	None
	ICAAR				32T	3, 14	c.202G>A, c.2149G>A	p.Asp68Asn, p.Glu717Lys	N/A	BRAF
	PTPRP				24T	5	c.536G>A	p.Arg179Lys	N/A	NRAS

Gene	Other names	CCDS accession*	Ref Seq accession*	No. of mutations (% tumors affected) #	Tumor	Exon^	Nucleotide†	Amino Acid†	Functional domain‡	NRAS/BRAF mutation**
	IA-2beta				36T	5	c.428G>A	p.Gly143Asp	N/A	BRAF
					96T	6	c.770C>T	p.Pro257Leu (LOH)	N/A	None
					35T	7	c.1063G>A	p.Ala355Thr	N/A	BRAF
					63T	9	c.1269G>A	p.Met423Ile (LOH)	N/A	NRAS
					34T	15	c.2345-7C>T	p.nc	N/A	BRAF
					44T	15	c.2276C>T	p.Pro759Leu	N/A	NRAS
					39T	16	c.2419-7C>T	p.nc	N/A	None
PTPRS	PTPSIGMA	12140.1	NM_002850.3	9 (10.1%)	31T	4	c.421C>T	p.Pro141Ser	Ig-I set	None
					37T	4	c.470C>T	p.Ala157Val	Ig-I set	BRAF
					49T	3,4	c.379+1G>T, c.543T>A	p.nc, p.Asn181Lys	Ig-I set	BRAF
					85T	9	c.860C>T	p.Pro287Leu	Ig-I set	BRAF
					24T	10	c.1532C>T	p.Pro511Leu	FN3	NRAS
					55T	26	c.4165G>A	p.Asp1389Asn	N/A	None
					95T	29	c.4531G>A	p.Glu1511Lys	PTPc	NRAS
					104T	34	c.5425C>T	p.Pro1809Ser	PTPc	None
PTPN13	PNP1	N/A	NM_080683.2	8 (8.9%)	103T	7	c.1196-6C>T	p.nc	N/A	BRAF
	FAP-1				29T	20	c.3224-7C>T	p.nc (LOH)	N/A	BRAF
	PTP1E				12T	21	c.3314-7T>G	p.nc	N/A	NRAS
	PTPL1				104T	28	c.4549C>T	p.Arg1517*	PDZ	None
	PTPLE				68T	28	c.4559A>G, c.4566A>G	p.Asn1520Ser, p.Ile1522Met (LOH)	PDZ	BRAF
	PTP-BL				39T	31	c.5246C>T	p.Ser1749Leu (LOH)	N/A	None
	PTP-BAS				17T	49	c.7385A>T	p.Gln2462Leu	PTPc	NRAS
	, DKFZp686J1497									
PTPRC	LCA	1397.1	NM_002838.4	7 (8.9%)	73T	13	c.1659+1G>A	p.nc	N/A	BRAF
	LY5				106T	14	c.1694G>T	p.Pro563Leu	FN3	N/A
	B220				69T	15	c.1721-9G>T	p.nc	N/A	BRAF
	CD45				45T	17	c.1972C>T	p.Gln656*	N/A	BRAF
	T200				68T	24	c.2689C>T	p.Gln895*	PTPD1	BRAF
	CD45R				23T	30	c.3406G>A	p.Glu1134Lys	PTPD2	BRAF
	GP180				64T	30	c.3458C>T	p.Ser1151Phe	PTPD2	BRAF
PTPRN	IA2	2440.1	NM_002846.2	8 (8.9%)	21T	3	c.193G>A	p.Gly65Arg	N/A	BRAF
	IA-2				52T	4	c.361C>T, c.365G>C	p.Pro121Ser, p.Arg122Pro	N/A	BRAF
	ICA512				4T	5	c.427C>T	p.Gln143*	N/A	BRAF
	R-PTP-N				8T	5	c.604G>A	p.Glu202Lys	N/A	BRAF

Gene	Other names	CCDS accession*	Ref Seq accession*	No. of mutations (% tumors affected) #	Tumor	Exon^	Nucleotide†	Amino Acid†	Functional domain‡	NRAS/BRAF mutation**
	FLJ16131				96T	6	c.785G>A	p.Gly262Glu	N/A	None
	IA-2/PTP				59T	9	c.1286C>T	p.Ser429Phe	N/A	BRAF
					50T	15	c.2192G>A	p.Gly731Glu (LOH)	N/A	BRAF
PTPRH	SAP1	33110.1	NM_002842.2	7 (7.6%)	55T	4,8	c.431G>A, c.1690-9C>T	p.Gly144Asp, p.nc	FN3,N/A	None
	FLJ39938				71T	4	c.458G>A	p.Gly153Glu	FN3	BRAF
	MGC133058				51T	6	c.1094C>T	p.Ser365Phe	FN3	BRAF
	MGC133059				39T	12	c.2384+11G>A	p.nc	N/A	None
					34T	18	c.2969C>T	p.Pro990Leu	PTPc	BRAF
					21T	20	c.3220C>T	p.Gln1074*	PTPc	BRAF
MTMR3	ZFYVE10	13871.1	NM_153050.2	5 (6.3%)	74T	10	c.835C>T	p.Arg279*	MTPc	NRAS
	FLJ32333				71T	11	c.881C>T	p.Ser294Phe	MTPc	BRAF
	KIAA0371				21T	14	c.1330C>T	p.Leu444Phe	N/A	BRAF
	FYVE-DSP1				72T	15	c.1548C>A	p.Phe516Leu	N/A	None
					39T	20	c.3455C>T	p.Pro1152Leu	FYVE-type	None
TNS1	TNS	2407.1	NM_022648.4	7 (6.3%)	32T	8, 21	c.666-7C>T, c.4523C>T	p.nc, p.Pro1508Leu	N/A,SH2	BRAF
	MXRA6				4T	15	c.1729C>T	p.Pro577Ser	N/A	BRAF
	MST091				50T	12	c.2362C>T	p.Pro788Ser (LOH)	N/A	BRAF
	MST122				18T	19	c.4330+9C>T	p.nc	N/A	None
	MST127,				58T	15, 21	c.2919-2921delG ,c.4498G>A	p.Pro921Valfs*12, p.Ala1500Thr (LOH)	N/A,SH2	BRAF
	MSTP091									
	MSTP122									
	MSTP127									
	MGC88584									
	DKFZp586K0617									
TNS4	CTEN	11368.1	NM_032865.5	8 (6.3%)	106T	1	c.206G>T	p.Ala69Val	N/A	N/A
	PP14434				39T	2	c.653C>T, c.683C>T	p.Ser218Leu, p.Ser228Phe	N/A	None
	FLJ14950				32T	3, 4	c.1055C>T, c.1289-10C>T	p.Pro352Leu, p.nc	N/A	BRAF
					55T	11	c.1940C>T	p.Thr647Ile	PTB	None
					21T	12,12	c.2141G>A, c.2140-2142delG	p.Arg714Lys (LOH), p.Glu713Cysfs*24	PTB	BRAF
PTPRE	PTPE	7657.1	NM_006504.4	4 (5.1%)	39T	9	c.11G>A	p.nc	N/A	None
	HPTPE				55T	1	c.32G>A	p.Gly11Asp	N/A	None
DKFZp313F1310	FLJ57799				13T	6	c.598G>A	p.Glu200Lys	PTPD1	None

Gene	Other names	CCDS accession*	Ref Seq accession*	No. of mutations (% tumors affected) #	Tumor	Exon^	Nucleotide†	Amino Acid†	Functional domain‡	NRAS/BRAF mutation**
R-PTP-EPSILON	FLJ58245				90T	15	c.1599+12C>T	p.nc	N/A	BRAF
PTPRJ	DEP1	7945.1	NM_002843.3	5 (5.1%)	32T	4	c.3874+3G>T	p.nc	N/A	BRAF
	SCC1				1T	7	c.1257-1275delGTCATCCCCGGACTCCG	p.Val420Leufs*14	FN3	BRAF
	CD148				74T	8	c.1561C>A, c.1562C>T	p.Pro521Thr/Pro521Leu or p.Pro521I	N/A	NRAS
R-PTP-ETA	HPTPeta				20T	11	c.2155C>T	p.Pro719Ser	N/A	BRAF
MTMR12	3-PAP	34138.1	NM_001040446.1	3 (3.8%)	83T	4	c.331G>T	p.Leu111Phe	N/A	Both
	PIP3AP				95T	7	c.583+9G>T	p.nc	N/A	NRAS
					20T	16	c.2038G>A	p.Glu680Lys (LOH)	N/A	BRAF
PTPN5	STEP	7845.1	NM_006906.1	3 (3.8%)	63T	2	c.13G>A	p.Gly5Arg	N/A	NRAS
	PTPSTEP				90T	6	c.508C>G	p.Pro170Ala (LOH)	N/A	BRAF
	FLJ14427				21T	7, 9	c.916G>A, c.1080+1G>A	p.Glu306Lys, p.nc	N/A	BRAF
PTPN12	PTPG1	5592.1	NM_002835.3	3 (3.8%)	7T	11	c.938G>G	p.Val313Gly	N/A	NRAS
	PTP-PEST				10T	13	c.1448G>T	p.Ser483Leu	N/A	BRAF
					2T	18	c.2314G>T	p.Pro772Ser	N/A	BRAF
PTPN21	PTPD1	9884.1	NM_007039.3	3 (3.8%)	21T	5	c.829G>A	p.Glu277Lys	FERM	BRAF
	PTPRL10				50T	13	c.1756G>C	p.Tyr586His	N/A	BRAF
					33T	13	c.2224G>A	p.Asp742Asn	N/A	BRAF
MTMR6	N/A	9313.1	NM_004685.3	2 (2.5%)	34T	10	c.1116G>C	p.Trp372Cys	N/A	BRAF
					13T	14	c.1808G>T	p.Ser603Phe	N/A	None
MTMR8	FLJ20126	14379.1	NM_017677.2	2 (2.5%)	17T	3	c.310G>A	p.Ala104Thr (LOH)	N/A	NRAS
					12T	14	c.2102G>T	p.Ser701Phe (LOH)	N/A	NRAS
PTPN23	HDPTP	2754.1	NM_015466.2	2 (2.5%)	12T	20	c.3773G>T	p.Pro1258Leu	PTPc	NRAS
	HD-PTP				13T	21	c.4015G>T	p.Arg1339*	PTPc	None
	KIAA1471									
	PTP-TD14									
	DKFZp564F0923									
PTP4A1	HH72	4965.1	NM_003463.3	1 (1.3%)	21T	2	c.25G>T	p.Pro9Ser	N/A	BRAF
	PRL1									
	PRL-1									

Gene	Other names	CCDS accession*	Ref Seq accession*	No. of mutations (% tumors affected) #	Tumor	Exon^	Nucleotide†	Amino Acid†	Functional domain‡	NRAS/BRAF mutation**
	PTPCAAX1 PTP(CAAX1) DKFZp779M0721									

*Accession numbers for mutated PTPs in Santa Cruz and GenBank. #Number of non-synonymous and splice site mutations observed and percent of tumors affected for each of the 23 genes in the panel of 79 melanoma cancers.

†Nucleotide and amino acid change resulting from mutation. When multiple mutations in the same gene in a tumor were observed, the mutations are separated by a comma. "*/X" refers to stop codon. "LOH" refers to cases wherein the wild-type allele was lost and only the mutant allele remained. "Splice site" refers to a case wherein the alteration affected 15 bases spanning the exon.

**Mutations previously observed in NRAS, BRAF. "None" refers no mutation observed. "Both" refers to both NRAS and BRAF mutation.

‡ Abbreviations for the functional domains: FERM: Four-point-one, Ezrin, Radixin, Moesin domain; FN3: Fibronectin Type III; FYVE-type: Fab1, YOTB, Vac1, EEA1-type zince finger domain; Ig: Immunoglobulin domain; IgCam: Immunoglobulin-containing cell adhesion molecules; Ig-like C2-type 1: immunoglobulin-like domain containing two cysteine residues; MAM:Meprin/A5-protein/PTPmu;

MTPc: myotubularin phosphatase domain; PDZ: PSD95, DlgA, zo-1 domain/glycine-leucine-glycine-phenylalanine domain; PTT: phosphatase tensin-type domain; PTPc: protein tyrosine phosphatase domain of PTPs containing single catalytic domains; PTPD1: protein tyrosine phosphatase domain 1 (of PTPs containing two catalytic domains); PTPD2: protein tyrosine phosphatase

domain 2 (of PTPs containing two catalytic domains); SH2: Src homology 2 domain; TM: transmembrane domain; PTB: Phosphotyrosine-binding domain

^Exon number were derived from Ensemble (http://uswest.ensembl.org/index.html)

‡Functional domains were derived from Pfam (http://pfam.sanger.ac.uk/)

p.nc : protein has not been analysed, an effect is expected but difficult to predict

c. : a coding DNA reference sequenced is used in this analysis.

All the variants have been submitted to the ClinVar database at http://www.ncbi.nlm.nih.gov/clinvar/. Accession numbers for ClinVar dataset are listed in Supp. Table S8.

Supp. Table S2. List of genes sequenced in PTP screen

Gene ID	CCDS	Accession	Gene Description
MTMR11	CCDS942.1	NM_181873	myotubularin related protein 11
PTPDC1	CCDS6708.1	NM_152422	protein tyrosine phosphatase domain containing 1
PTPRS	CCDS12139.1	NM_130853	protein tyrosine phosphatase, receptor type, S
PTPN13	n/a	NM_080683	protein tyrosine phosphatase, non-receptor type 13
PTPN6	CCDS41744.1	NM_080548	protein tyrosine phosphatase, non-receptor type 6
PTP4A2	CCDS348.1	NM_080391	protein tyrosine phosphatase type IVA, member 2
TNS4	CCDS11368.1	NM_032865	tensin 4
TNS1	CCDS2407.1	NM_022648	tensin 1
MTMR3	CCDS13870.1	NM_021090	myotubularin-related protein 3
MTMR8	CCDS14379.1	NM_017677	myotubularin related protein 8
MTMR2	CCDS8305.1	NM_016156	myotubularin-related protein 2
PTPN23	CCDS2754.1	NM_015466	protein tyrosine phosphatase, non-receptor type 23
MTMR9	CCDS5979.1	NM_015458	myotubularin-related protein 9
MTMR15	CCDS32186.1	NM_014967	myotubularin related protein 15
PTPN18	CCDS2161.1	NM_014369	protein tyrosine phosphatase, non-receptor type, 18
PTPLA	CCDS7121.1	NM_014241	protein tyrosine phosphatase-like, member A
PTPN22	CCDS864.1	NM_012411	protein tyrosine phosphatase, non-receptor type 22
PTP4A3	CCDS6382.1	NM_007079	protein tyrosine phosphatase type IVA, member 3
PTPRT	CCDS42874.1	NM_007050	protein tyrosine phosphatase, receptor type, T
PTPN21	CCDS9884.1	NM_007039	protein tyrosine phosphatase, non-receptor type 21
PTPRE	CCDS7657.1	NM_006504	protein tyrosine phosphatase, receptor type, E
PTPRU	CCDS334.1	NM_005704	protein tyrosine phosphatase, receptor type, U
PTPRCAP	CCDS8163.1	NM_005608	protein tyrosine phosphatase, receptor type, C-associated protein
PTPN14	CCDS1514.1	NM_005401	protein tyrosine phosphatase, non-receptor type 14
MTMR4	CCDS11608.1	NM_004687	myotubularin related protein 4
MTMR7	CCDS34851.1	NM_004686	myotubularin related protein 7
MTMR6	CCDS9313.1	NM_004685	myotubularin related protein 6
MTMR1	CCDS14695.1	NM_003828	myotubularin-related protein 1
PTP4A1	CCDS4965.1	NM_003463	protein tyrosine phosphatase type IVA, member 1
PTPRZ1	CCDS34740.1	NM_002851	protein tyrosine phosphatase, receptor-type, Z polypeptide 1
PTPRR	CCDS8998.1	NM_002849	protein tyrosine phosphatase, receptor type, R
PTPRO	CCDS8674.1	NM_002848	receptor-type protein tyrosine phosphatase O
PTPRN2	CCDS5947.1	NM_002847	protein tyrosine phosphatase, receptor type, N polypeptide 2
PTPRN	CCDS2440.1	NM_002846	protein tyrosine phosphatase, receptor type, N

Gene ID	CCDS	Accession	Gene Description
PTPRM	CCDS11840.1	NM_002845	protein tyrosine phosphatase, receptor type, M
PTPRK	CCDS5137.1	NM_002844	protein tyrosine phosphatase, receptor type, K
PTPRJ	CCDS7945.1	NM_002843	protein tyrosine phosphatase, receptor type, J
PTPRH	CCDS33110.1	NM_002842	protein tyrosine phosphatase, receptor type, H
PTPRG	CCDS2895.1	NM_002841	protein tyrosine phosphatase, receptor type, G
PTPRF	CCDS489.2	NM_002840	protein tyrosine phosphatase, receptor type, F
PTPRD	CCDS43786.1	NM_002839	protein tyrosine phosphatase, receptor type, D
PTPRC	CCDS1397.1	NM_002838	protein tyrosine phosphatase, receptor type, C
PTPRA	CCDS13038.1	NM_002836	protein tyrosine phosphatase, receptor type, A
PTPN12	CCDS5592.1	NM_002835	protein tyrosine phosphatase, non-receptor type 12
PTPN11	CCDS9163.1	NM_002834	protein tyrosine phosphatase, non-receptor type 11
PTPN9	CCDS10280.1	NM_002833	protein tyrosine phosphatase, non-receptor type 9
PTPN7	CCDS1423.1	NM_002832	protein tyrosine phosphatase, non-receptor type, 7
PTPN4	CCDS2129.1	NM_002830	protein tyrosine phosphatase, non-receptor type 4
PTPN3	CCDS6776.1	NM_002829	protein tyrosine phosphatase, non-receptor type 3
PTPN2	CCDS11865.1	NM_002828	protein tyrosine phosphatase, non-receptor type 2
PTPN1	CCDS13430.1	NM_002827	protein tyrosine phosphatase, non-receptor type 1
PTPRB	n/a	NM_001109754	protein tyrosine phosphatase, receptor type, B
PTPN20A	CCDS31191.1	NM_001042387	protein tyrosine phosphatase, non-receptor type 20A
PTPN20B	CCDS41514.1	NM_001042357	protein tyrosine phosphatase, non-receptor type 20B
MTMR12	CCDS34138.1	NM_001040446	myotubularin related protein 12
PTPN5	CCDS41626.1	NM_001039970	protein tyrosine phosphatase, non-receptor type 5
MTM1	CCDS14694.1	NM_000252	myotubularin 1

Supp. Table S3. List of PTP sequencing primers

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
1	79	MTMR12-1	MTMR12	1	CCDS34138.1	NM_001040446	M13-CAGCCGCTAGTGCTGGTG	GCAATCCCTTCTCGGCTC	GTAAAACGACGGCCAGT
2	79	MTMR12-2	MTMR12	2	CCDS34138.1	NM_001040446	M13-TTCTGAAAGCATGGCTTAATGTT	AAGCAGTGAGAACATTCCAGGT	GTAAAACGACGGCCAGT
3	79	MTMR12-3	MTMR12	3	CCDS34138.1	NM_001040446	M13-AAATAGGGCTGGAAAGCCTTTAG	CCCAAACTTCACCAAATGCAG	GTAAAACGACGGCCAGT
4	79	MTMR12-4	MTMR12	4	CCDS34138.1	NM_001040446	M13-AGGCAAGATGGTCTCGATCTC	CCAAGTTCAGGTCCAAACTCC	GTAAAACGACGGCCAGT
5	79	MTMR12-5	MTMR12	5	CCDS34138.1	NM_001040446	GCAGCACCTTTCCTCTCATTC	M13-CAACCTTCATGCAACGTAAGC	GTAAAACGACGGCCAGT
6	79	MTMR12-6	MTMR12	6	CCDS34138.1	NM_001040446	M13-AAGAACTTAGACACCTTGACTCTTGTC	AAATGAATCACTCAAGCAAGGG	GTAAAACGACGGCCAGT
7	79	MTMR12-7	MTMR12	7	CCDS34138.1	NM_001040446	M13-ATGGGCTTAGTGGAGGAAACC	GACAGCCAATGGGTATGGAG	GTAAAACGACGGCCAGT
8	79	MTMR12-8	MTMR12	8	CCDS34138.1	NM_001040446	M13-CTGAGCTGGTTCTGAACAGGG	AAGCCAAGGGCTTTCAGTAGG	GTAAAACGACGGCCAGT
9	79	MTMR12-9	MTMR12	9	CCDS34138.1	NM_001040446	M13-TTTAAATGCTAAGCTTATGTGTCCC	AAACGACGCAGGTGACACTC	GTAAAACGACGGCCAGT
10	79	MTMR12-10	MTMR12	10	CCDS34138.1	NM_001040446	M13-CATTTCCACACCCATTGACTG	AAAGGCACCAACTTTCACCTG	GTAAAACGACGGCCAGT
11	79	MTMR12-11	MTMR12	11	CCDS34138.1	NM_001040446	GGATTCTGCAGTTTGAGTCAGG	M13-TTGTAAGCAGGTGGCATGTTC	GTAAAACGACGGCCAGT
12	79	MTMR12-12	MTMR12	12	CCDS34138.1	NM_001040446	GGGCAGGAATATATCCCAGTATC	M13-GCAAAGGATTCCAAGGTTAGG	GTAAAACGACGGCCAGT
13	79	MTMR12-13	MTMR12	13	CCDS34138.1	NM_001040446	GTTATTGGCCCTTGCCTTTAG	M13-CTTTGCAAGCAGCAATCCTAC	GTAAAACGACGGCCAGT
14	79	MTMR12-14	MTMR12	14	CCDS34138.1	NM_001040446	M13-TCAGAAGTGCTTATTCCACAGC	AGTTTGCATGTCATCCTCTCG	GTAAAACGACGGCCAGT
15	79	MTMR12-15	MTMR12	15	CCDS34138.1	NM_001040446	M13-TGCCTGTGTCCAGAAGTATGTG	TCAACTCTGCAGACTGCTTCG	GTAAAACGACGGCCAGT
16	79	MTMR12-16a	MTMR12	16	CCDS34138.1	NM_001040446	GGCAACACTGATGTCTCTTGG	M13-GGAGCAGAGCGAAAGGAAAC	GTAAAACGACGGCCAGT
17	79	MTMR12-16b	MTMR12	16	CCDS34138.1	NM_001040446	AGCGCTACCTACGTTGGATTC	M13-GTAGCGTGACACAAATCCAGG	GTAAAACGACGGCCAGT
18	79	MTMR3-1	MTMR3	1	CCDS13870.1	NM_021090.3	M13-AAGGGAAAGAAGAGAGCCTTG	AAGAGACAACATCTAGCTCACAGG	GTAAAACGACGGCCAGT
19	79	MTMR3-2	MTMR3	2	CCDS13870.1	NM_021090.3	M13-GCCTGTTCACCTTGGTCTTTG	TCATCTTAAACAGTGGATTCTCAGG	GTAAAACGACGGCCAGT
20	79	MTMR3-3	MTMR3	3	CCDS13870.1	NM_021090.3	TACCATCCATTCAGCCAACTG	M13-TCTCCCAATTCTGTATGCCTC	GTAAAACGACGGCCAGT
21	79	MTMR3-4	MTMR3	4	CCDS13870.1	NM_021090.3	TTGATCCAGATAAGTTTGCAGTTC	M13-AAATATTTCAGGCACAAACTACTCAG	GTAAAACGACGGCCAGT
22	79	MTMR3-5	MTMR3	5	CCDS13870.1	NM_021090.3	M13-CACTACGAGTGGGCATTCTTG	AGGCCCAATAGATTGTGATGC	GTAAAACGACGGCCAGT
23	79	MTMR3-7	MTMR3	7	CCDS13870.1	NM_021090.3	GCCTTTAACTGGTTCTGTGGC	M13-CAGGTTAGCAGCAGCAGAGG	GTAAAACGACGGCCAGT
24	79	MTMR3-8	MTMR3	8	CCDS13870.1	NM_021090.3	AGGACTTGAAGCTGACCCAAC	M13-CCCATCAAGTGAAGCTCTGC	GTAAAACGACGGCCAGT
25	79	MTMR3-9	MTMR3	9	CCDS13870.1	NM_021090.3	TGCTTGTGGGTCTAATTCTGC	M13-TTGCCACTTATTTCAAATTGGG	GTAAAACGACGGCCAGT
26	79	MTMR3-10	MTMR3	10	CCDS13870.1	NM_021090.3	M13-TTAATCAGAAGCTGCAGTGGG	CATTTCAGACCCAGCAAGGAG	GTAAAACGACGGCCAGT
27	79	MTMR3-11	MTMR3	11	CCDS13870.1	NM_021090.3	GCCTCATCCTGAGACATGC	M13-TTTAACCGAATCACCACTCCC	GTAAAACGACGGCCAGT
28	79	MTMR3-12	MTMR3	12	CCDS13870.1	NM_021090.3	TTTCTGGGAGGCTGTTAGAGG	M13-GTTTCATGTGAGAACTGGCCC	GTAAAACGACGGCCAGT
29	79	MTMR3-13	MTMR3	13	CCDS13870.1	NM_021090.3	CCCGTCCTGACAGAGTAAATTG	M13-GGAACCAGTCCATCCAGAGAC	GTAAAACGACGGCCAGT
30	79	MTMR3-14	MTMR3	14	CCDS13870.1	NM_021090.3	M13-TGATCCTCATTTCCAGACATCC	CAACAGGGCCTAACTCACTCC	GTAAAACGACGGCCAGT
31	79	MTMR3-15a	MTMR3	15	CCDS13870.1	NM_021090.3	M13-CTCGCTCCAGAGATGCTACAG	CTCCACTCTCCTCTTTGGTGG	GTAAAACGACGGCCAGT
32	79	MTMR3-15b	MTMR3	15	CCDS13870.1	NM_021090.3	GTGACAACACAGTGCCTCTGG	M13-AGAACTGCTTCCTCCCTACCC	GTAAAACGACGGCCAGT
33	79	MTMR3-15c	MTMR3	15	CCDS13870.1	NM_021090.3	CATTGGACTTCACCAAGACCC	M13-TACATTCGGCTAAAGGCAAGG	GTAAAACGACGGCCAGT
34	79	MTMR3-15d	MTMR3	15	CCDS13870.1	NM_021090.3	AGGGTAGGGAGGAAGCAGTTC	M13-GTGGTGCAAGTTCCTTGAGTG	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
35	79	MTMR3-15e	MTMR3	15	CCDS13870.1	NM_021090.3	AGAGACAAGCCTGGTCGAGAG	M13-AGCCTACTCACCACCTCATCC	GTAAAACGACGGCCAGT
36	79	MTMR3-15f	MTMR3	15	CCDS13870.1	NM_021090.3	TAGCACCCTCCAGATGTACCC	M13-CCTGTACCAATCACCATGCAC	GTAAAACGACGGCCAGT
37	79	MTMR3-16	MTMR3	16	CCDS13870.1	NM_021090.3	M13-ACCTGTGTATCCCTCTCCCAG	GGTTCCCAGGAGCTAAGGTG	GTAAAACGACGGCCAGT
38	79	MTMR3-17a	MTMR3	17	CCDS13870.1	NM_021090.3	M13-TGGTCCTTGTGACTCTTGCTG	TGCAAACACCAATTTCAGAGG	GTAAAACGACGGCCAGT
39	79	MTMR3-17b	MTMR3	17	CCDS13870.1	NM_021090.3	M13-TCTGAATCATGCCATAGCTCAC	CCCAGGCTTCACCCTAGTAAG	GTAAAACGACGGCCAGT
40	79	MTMR3-18	MTMR3	18	CCDS13870.1	NM_021090.3	M13-GCTCCAGCACATGCAAATTAC	TGGTGCATCCCAAATCTGTC	GTAAAACGACGGCCAGT
41	79	MTMR6-1	MTMR6	1	CCDS9313.1	NM_004685	GGGAAGTGTTTCTAGGAGACGG	M13-CCAAGATGCTGAAAGTGGGAC	GTAAAACGACGGCCAGT
42	79	MTMR6-2	MTMR6	2	CCDS9313.1	NM_004685	CCTGTTTCTTGCTACCCTCAA	M13-GGCAGGAGTGATCTGGAGAC	GTAAAACGACGGCCAGT
43	79	MTMR6-3	MTMR6	3	CCDS9313.1	NM_004685	AACGTGAAGTTTGAGTGAGTATGTAAC	M13-TTTCTAATTACTTTCAGGCCAATATG	GTAAAACGACGGCCAGT
44	79	MTMR6-4	MTMR6	4	CCDS9313.1	NM_004685	M13-TCAAATGTATTCAGGTATTAGCCATC	CACAGACAACTTGCTACGCTG	GTAAAACGACGGCCAGT
45	79	MTMR6-5	MTMR6	5	CCDS9313.1	NM_004685	M13-TCAGCGTAGCAAGTTGTCTGTG	AACTGCTTGAACCGAGAGGTG	GTAAAACGACGGCCAGT
46	79	MTMR6-6	MTMR6	6	CCDS9313.1	NM_004685	TTTCTTCATCAAACTAGATAAGGAGGT	M13-AAGGATTGATTTCCTTAGTATCATTAGC	GTAAAACGACGGCCAGT
47	79	MTMR6-7	MTMR6	7	CCDS9313.1	NM_004685	M13-TTCCTTTAAACTGCCTCCTAGC	AATACATGCCTGATTTCTAAGAGTTG	GTAAAACGACGGCCAGT
48	79	MTMR6-8	MTMR6	8	CCDS9313.1	NM_004685	TTTGTAAGCACGGGAATAATAGAAA	M13-TTATCTGATGAATAGATACCAGCCC	GTAAAACGACGGCCAGT
49	79	MTMR6-9	MTMR6	9	CCDS9313.1	NM_004685	TCATTGCAGGCATAGCACTTC	M13-GATGCCAGTCTCATCATTTCC	GTAAAACGACGGCCAGT
50	79	MTMR6-10	MTMR6	10	CCDS9313.1	NM_004685	M13-AACGGAAATAATTTAAGTCACGAAAC	CACTCTTACCTCCCATCACGC	GTAAAACGACGGCCAGT
51	79	MTMR6-11	MTMR6	11	CCDS9313.1	NM_004685	TGCTAATGTAACAGTGCTTTAGGAA	M13-GAAGGGTACTCAGCTTTAGAAATACAA	GTAAAACGACGGCCAGT
52	79	MTMR6-12	MTMR6	12	CCDS9313.1	NM_004685	M13-TCTGAGACAAGGTTAGACTGTGAATAC	GCCTAGGATGCAGTGTTCG	GTAAAACGACGGCCAGT
53	79	MTMR6-13	MTMR6	13	CCDS9313.1	NM_004685	GTTCCGAATCTCACAGATTTACAG	M13-TCAATCAAAGTAGGGATGACCTG	GTAAAACGACGGCCAGT
54	79	MTMR6-14	MTMR6	14	CCDS9313.1	NM_004685	ACCATGTCATATGCATTAAATGTTTC	M13-TGGTTATGCTTACAGACCATCCTC	GTAAAACGACGGCCAGT
55	79	MTMR8-1	MTMR8	1	CCDS14379.1	NM_017677	M13-GACGAGAGTTTGAGCCAGGAC	AGAGGTGTTTGGTTGAAAGGG	GTAAAACGACGGCCAGT
56	79	MTMR8-2	MTMR8	2	CCDS14379.1	NM_017677	M13-TTATCTTGCTTTGAATGGCCC	TGATGACCAGAGCCAATAACTTG	GTAAAACGACGGCCAGT
57	79	MTMR8-3	MTMR8	3	CCDS14379.1	NM_017677	M13-GGTCATGCTGTTACCATTACGG	GCCCTGATCTTTCCATTATGC	GTAAAACGACGGCCAGT
58	79	MTMR8-4	MTMR8	4	CCDS14379.1	NM_017677	M13-GCCTTTATTTGCATTGTTTGATG	GAATGGCTGAATGTTGAATGG	GTAAAACGACGGCCAGT
59	79	MTMR8-5	MTMR8	5	CCDS14379.1	NM_017677	GCAGACAGGTAGAGGAGGAGG	M13-GCTACTAAGTGGCAGCATGAAAC	GTAAAACGACGGCCAGT
60	79	MTMR8-6	MTMR8	6	CCDS14379.1	NM_017677	CCTCTACTCATGGAACCTGGC	M13-TCACACTGAGGTGGGAAAGAC	GTAAAACGACGGCCAGT
61	79	MTMR8-7	MTMR8	7	CCDS14379.1	NM_017677	M13-GGTTCAGAATGAGGCATTGAG	GACTCTGCTCACCTGCTTGC	GTAAAACGACGGCCAGT
62	79	MTMR8-8	MTMR8	8	CCDS14379.1	NM_017677	M13-CATTTAACCTTTCTGCCTCAGC	CTTTCCACCATGGCACACTAC	GTAAAACGACGGCCAGT
63	79	MTMR8-9	MTMR8	9	CCDS14379.1	NM_017677	M13-TGCTTTAGGGACAGTATTTGGC	GACAGTCATCCATTAAGCTCTGC	GTAAAACGACGGCCAGT
64	79	MTMR8-10	MTMR8	10	CCDS14379.1	NM_017677	ATCTGAAATTTGAAGGCACCC	M13-TGCCATGTTCAACTTCCTCTTC	GTAAAACGACGGCCAGT
65	79	MTMR8-11	MTMR8	11	CCDS14379.1	NM_017677	CCTTGCCACTACCAACAGAGAC	M13-ATGCCAAATTCAGGGTGGTAG	GTAAAACGACGGCCAGT
66	79	MTMR8-12	MTMR8	12	CCDS14379.1	NM_017677	TGCTGCTTATCAGTTCAACAGG	M13-TACAGATGGTGGCAGCTATCC	GTAAAACGACGGCCAGT
67	79	MTMR8-13	MTMR8	13	CCDS14379.1	NM_017677	M13-CCCAATTATGAGCATGTCCAG	CAATTCAACTCCAAGCAGGC	GTAAAACGACGGCCAGT
68	79	MTMR8-14a	MTMR8	14	CCDS14379.1	NM_017677	M13-ATGAGGGAAAGATGTTGTGGG	AAGTTTCCAGAGATGCCAGTG	GTAAAACGACGGCCAGT
69	79	MTMR8-14b	MTMR8	14	CCDS14379.1	NM_017677	TGACCAATCCTCTTGGCTTT	M13-CATAGCCCTCTCTGGGACAA	GTAAAACGACGGCCAGT
70	79	MTMR8-15a	MTMR8	15	CCDS14379.1	NM_017677	CTGCAGCCCAAGCAGAGTAT	M13-GGCCCCACAGATTCCTAAGT	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
71	79	MTMR8-15b	MTMR8	15	CCDS14379.1	NM_017677	GAGAATGGCACCCTATCCAG	M13-GGCTTCACCCACTTAAACCA	GTAAAACGACGGCCAGT
72	79	PTP4A1-1	PTP4A1	1	CCDS4965.1	NM_003463	GATTGAAGAATTGCTGCTTCTTG	M13-TTCTGGGAACTGGAATTGTAGG	GTAAAACGACGGCCAGT
73	79	PTP4A1-2	PTP4A1	2	CCDS4965.1	NM_003463	TGATCTTCTGTTAACCAGCATACTT	M13-TTTCACAACTTCAAATCCTTGC	GTAAAACGACGGCCAGT
74	79	PTP4A1-3	PTP4A1	3	CCDS4965.1	NM_003463	M13-TCACATTTGGTAGACAACAGGG	TCAGAAGTATTATCTACCACCCTTCC	GTAAAACGACGGCCAGT
75	79	PTP4A1-4	PTP4A1	4	CCDS4965.1	NM_003463	M13-AGGGTGGTAGATAATACTTCTGAGTTG	AGAATGTAAGATCTTGATTTCCTGG	GTAAAACGACGGCCAGT
76	79	PTP4A1-5	PTP4A1	5	CCDS4965.1	NM_003463	CCACAAGAGAGGTGATGGTTG	M13-TCTGTCTAGCTTGAGGCCTGG	GTAAAACGACGGCCAGT
77	79	PTPN12-1	PTPN12	1	CCDS5592.1	NM_002835	GCTCCTGGAAGTTGTGGTGTC	M13-AGGTACACAAAGCACTGGCG	GTAAAACGACGGCCAGT
78	79	PTPN12-2	PTPN12	2	CCDS5592.1	NM_002835	AAATGAGTTGTGAGGAATTGGG	M13-CTACTTCCTTAACAGTGAAACTCAGG	GTAAAACGACGGCCAGT
79	79	PTPN12-3	PTPN12	3	CCDS5592.1	NM_002835	AATTACCCTGCTGGTACCTAGAGTC	M13-GCTGTTGGTATCATGTTTGAGC	GTAAAACGACGGCCAGT
80	79	PTPN12-4	PTPN12	4	CCDS5592.1	NM_002835	M13-GAAAGACACATTATTTGGAAATGG	GGACAAGATTTAAATTATTATCACACC	GTAAAACGACGGCCAGT
81	79	PTPN12-5	PTPN12	5	CCDS5592.1	NM_002835	M13-AGCCAATTATACTTCTCGGTGC	GTTTGAATTGCGCTATTGTGG	GTAAAACGACGGCCAGT
82	79	PTPN12-6	PTPN12	6	CCDS5592.1	NM_002835	CTCCATGCCTGCTAATGTGG	M13-TCCTTGGCGTCTATAAGCCTG	GTAAAACGACGGCCAGT
83	79	PTPN12-7	PTPN12	7	CCDS5592.1	NM_002835	GCATGTCTATCACTTCAAACATTTC	M13-GATTACAGGCATGAGCCACTG	GTAAAACGACGGCCAGT
84	79	PTPN12-8	PTPN12	8	CCDS5592.1	NM_002835	M13-GGCAGTTTAAATGAGCTGTGC	TACAAGGCCCTAGTCCCAAAC	GTAAAACGACGGCCAGT
85	79	PTPN12-9	PTPN12	9	CCDS5592.1	NM_002835	M13-CAGATGTTGCCATGAACACAC	CGGCCTTCACTACCTTTATTTC	GTAAAACGACGGCCAGT
86	79	PTPN12-10	PTPN12	10	CCDS5592.1	NM_002835	M13-GTGCCAAGCACAGTGTCTGAG	TGGGCAATAGCTCTATGAACAAG	GTAAAACGACGGCCAGT
87	79	PTPN12-11	PTPN12	11	CCDS5592.1	NM_002835	M13-AAACAAAGGTATAGTTGTTTGTTTCCC	AAATGTTAAGTGTCCTGGATATTCTTC	GTAAAACGACGGCCAGT
88	79	PTPN12-12	PTPN12	12	CCDS5592.1	NM_002835	TTGAAGTCTGGTCCTTCAGGC	M13-CAATTCATGGTAGTATCCACATTCTG	GTAAAACGACGGCCAGT
89	79	PTPN12-13a	PTPN12	13	CCDS5592.1	NM_002835	TTCGCAACCAGATTGTAATGG	M13-TGTTACACTGCAGTCCACACAAG	GTAAAACGACGGCCAGT
90	79	PTPN12-13b	PTPN12	13	CCDS5592.1	NM_002835	TGAGATTAAGAAGGTCCCTCTCC	M13-TTGCCTTCAGATAAATCAGGTATG	GTAAAACGACGGCCAGT
91	79	PTPN12-13c	PTPN12	13	CCDS5592.1	NM_002835	M13-AAATGTCGGTGATACTTCCCAG	AGCACCTGAATGTGTTGTTCC	GTAAAACGACGGCCAGT
92	79	PTPN12-14	PTPN12	14	CCDS5592.1	NM_002835	M13-AAACTGATCTAGATATTTGTGACAGGAA	CACCATGCCCAGCCTATAAT	GTAAAACGACGGCCAGT
93	79	PTPN12-15	PTPN12	15	CCDS5592.1	NM_002835	M13-TTCAGAAATATGCTTACCCAGAAA	TCTTAGTATAAGAAATGCCGATCAAA	GTAAAACGACGGCCAGT
94	79	PTPN12-16	PTPN12	16	CCDS5592.1	NM_002835	M13-CCCATAACAGACCCAGCTTTC	AAATCTCTTTCCCATTAGCCTGT	GTAAAACGACGGCCAGT
95	79	PTPN12-17	PTPN12	17	CCDS5592.1	NM_002835	TTCTGTGTGACCACAATAATACCTG	M13-TGACTAGTCCAAGCAACTTTGG	GTAAAACGACGGCCAGT
96	79	PTPN12-18	PTPN12	18	CCDS5592.1	NM_002835	M13-AATGAGAATGTCTGTGGACATGG	GTATAAGGCAGGTAGATGGTCCC	GTAAAACGACGGCCAGT
97	79	PTPN13-1	PTPN13	1	n/a	NM_080683.2	M13-TTTCCCTCCAATTCCTTTACC	TTCATACTCTGCCAAAGGCAC	GTAAAACGACGGCCAGT
98	79	PTPN13-2	PTPN13	2	n/a	NM_080683.2	M13-GCATTATCCATTGAAGTGATTGC	TTGAAACATGGTAGCCCATTG	GTAAAACGACGGCCAGT
99	79	PTPN13-3	PTPN13	3	n/a	NM_080683.2	M13-TATGCATAAAGGATGGGCTGG	CGTATAAACGTGTGGAAGAGCTATG	GTAAAACGACGGCCAGT
100	79	PTPN13-4	PTPN13	4	n/a	NM_080683.2	TGTGGTTCCTGTGATTCCTAGA	M13-TCAGCTCAAACATGCTATCATTC	GTAAAACGACGGCCAGT
101	79	PTPN13-5	PTPN13	5	n/a	NM_080683.2	TCTGAAATGAATTGGCCAGC	M13-TTACCAGATTTCAAAGCCAGG	GTAAAACGACGGCCAGT
102	79	PTPN13-6a	PTPN13	6	n/a	NM_080683.2	CATCACCATCCCATTTCACC	M13-TGAGGGCCAAAGATATCCAAG	GTAAAACGACGGCCAGT
103	79	PTPN13-6b	PTPN13	6	n/a	NM_080683.2	M13-AAGAAGATCTGGGCTTCATCC	TTCTACATTCATGGCTTCCCTC	GTAAAACGACGGCCAGT
104	79	PTPN13-6c	PTPN13	6	n/a	NM_080683.2	TTCATCCATGGACTTGCTTTG	M13-TGGAAGGGAGAACAGAAATTG	GTAAAACGACGGCCAGT
105	79	PTPN13-7	PTPN13	7	n/a	NM_080683.2	M13-AAACCCATTATTGGAACGCAT	CTACATCGTTATTTGAAGAAACTGCT	GTAAAACGACGGCCAGT
106	79	PTPN13-8	PTPN13	8	n/a	NM_080683.2	M13-GCAGTTTCTTCAAATAACGATGTAGTC	AAAGAATTGCGTGAACCTGG	GTAAAACGACGGCCAGT
107	79	PTPN13-9	PTPN13	9	n/a	NM_080683.2	AAATGAAATTTGCTTGATTAGCCTT	M13-CCAGTGGAAATGAATATGGGA	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
108	79	PTPN13-10	PTPN13	10	n/a	NM_080683.2	TCCATTTCTGTTATTGGTAAATTCC	M13-TCGGTTATCCTCATTCTTCCC	GTAAAACGACGGCCAGT
109	79	PTPN13-11	PTPN13	11	n/a	NM_080683.2	ATATCTTTGGATTTGCCACGG	M13-GAGGTCAGGCATGGTAACAAAC	GTAAAACGACGGCCAGT
110	79	PTPN13-12	PTPN13	12	n/a	NM_080683.2	GAGTGTCTCAGAGCTCCCTGC	M13-AAAGCAGACATTATCATTGATTGGA	GTAAAACGACGGCCAGT
111	79	PTPN13-13	PTPN13	13	n/a	NM_080683.2	CATGGAAATTAACCTTACATGCCT	M13-AGGAACCAAAGAAGCCTCAAA	GTAAAACGACGGCCAGT
112	79	PTPN13-14	PTPN13	14	n/a	NM_080683.2	CTTCATCTCTTAGCCAAAGCAAG	M13-GGGTTCAAATCATATCTGCCC	GTAAAACGACGGCCAGT
113	79	PTPN13-15	PTPN13	15	n/a	NM_080683.2	M13-CGGCCAAACCATATCATACAG	CACTGAATGGCAGAGTCTAAGG	GTAAAACGACGGCCAGT
114	79	PTPN13-16	PTPN13	16	n/a	NM_080683.2	M13-AAGTCAATATCCAGTGCCTAACAAG	CATGAAATTGAAATATTGGCTTCAC	GTAAAACGACGGCCAGT
115	79	PTPN13-17a	PTPN13	17	n/a	NM_080683.2	M13-GTGACTGAGCAATTAACACACTTTG	AGACCAGAAGTGAGCTGGCAC	GTAAAACGACGGCCAGT
116	79	PTPN13-17b	PTPN13	17	n/a	NM_080683.2	M13-ACCCTGATTGCCACACTTTG	TCACTCCTGCCAAAGATTCTG	GTAAAACGACGGCCAGT
117	79	PTPN13-17c	PTPN13	17	n/a	NM_080683.2	AATATGGGACGAGCAATCAGC	M13-CGCAACAGACTTTGAACTGAAG	GTAAAACGACGGCCAGT
118	79	PTPN13-18	PTPN13	18	n/a	NM_080683.2	M13-TGTGTTTCAGGCAGGCTAATC	CACAGATATCAAACGGTCTCCTG	GTAAAACGACGGCCAGT
119	79	PTPN13-18	PTPN13	18	n/a	NM_080683.2	CTGATGCAGAATCTTTGGCAG	M13-TGGCAATTAGGACATGGAACC	GTAAAACGACGGCCAGT
120	79	PTPN13-19a	PTPN13	19	n/a	NM_080683.2	M13-CTGGAGGACCAGCTGACTTG	AAGATGGAACACATTAAGTAATCACAG	GTAAAACGACGGCCAGT
121	79	PTPN13-19b	PTPN13	19	n/a	NM_080683.2	M13-AAATGCCCATTGGAGGATG	GGAACTCAAGACTCTTCATTGTTAGG	GTAAAACGACGGCCAGT
122	79	PTPN13-20a	PTPN13	20	n/a	NM_080683.2	GAGAAGCCTGGTTTGAAATGG	M13-TGAAAGTCTCTTTCTCGGTGG	GTAAAACGACGGCCAGT
123	79	PTPN13-20b	PTPN13	20	n/a	NM_080683.2	CATCTCGGAGAACTCCTTTGG	M13-GCAAGTTTGCAAAGTCATAGCC	GTAAAACGACGGCCAGT
124	79	PTPN13-21	PTPN13	21	n/a	NM_080683.2	AGCTTTGTCCTGGGCTAGGTT	M13-TGGAGGTATTTGATGTGTCCCT	GTAAAACGACGGCCAGT
125	79	PTPN13-22	PTPN13	22	n/a	NM_080683.2	CACTGCTTTGGCTAATGAATCC	M13-GGCATCAAAGAGTTTCTTAATGCTAC	GTAAAACGACGGCCAGT
126	79	PTPN13-23	PTPN13	23	n/a	NM_080683.2	M13-CAGAATTTGCCTGAGTCCCTC	CAGGCTTGGTTTCTTGATTAGC	GTAAAACGACGGCCAGT
127	79	PTPN13-24a	PTPN13	24	n/a	NM_080683.2	TCCACCTGGCCATTATCATAC	M13-GGGCATTAACTGTAATCCAACA	GTAAAACGACGGCCAGT
128	79	PTPN13-24b	PTPN13	24	n/a	NM_080683.2	AGCTTTGTCCTGGGCTAGGTT	M13-TGGAGGTATTTGATGTGTCCCT	GTAAAACGACGGCCAGT
129	79	PTPN13-25	PTPN13	25	n/a	NM_080683.2	ATACCATTGGAGTGCAGTAAGTACA	M13-CAGCATTATGAAACCATTCTGAAA	GTAAAACGACGGCCAGT
130	79	PTPN13-26	PTPN13	26	n/a	NM_080683.2	M13-TGAGATGGATTGGCCTTTCAG	AGTTGTCACATACAAGATAACATGCC	GTAAAACGACGGCCAGT
131	79	PTPN13-27a	PTPN13	27	n/a	NM_080683.2	CCCACTTCAGTCTCCAGCAC	M13-TCTGCCTAACCACTGTGAAGG	GTAAAACGACGGCCAGT
132	79	PTPN13-27b	PTPN13	27	n/a	NM_080683.2	tgttcctatgtaaacacagcatgtta	M13-catgatgaaaccaccacagc	GTAAAACGACGGCCAGT
133	79	PTPN13-28	PTPN13	28	n/a	NM_080683.2	M13-GAGACCGTGTCTCAACAACAAC	CCCTAAAGGGAAACTTTATGAACAC	GTAAAACGACGGCCAGT
134	79	PTPN13-29	PTPN13	29	n/a	NM_080683.2	GACAGACTTGACTTCTTCACTTGG	M13-TGGAAACAGAAAGCATAAACCG	GTAAAACGACGGCCAGT
135	79	PTPN13-30	PTPN13	30	n/a	NM_080683.2	CGTTGTGCCTATGATTTCCAT	M13-GGCTGTCATGACCTCCACATA	GTAAAACGACGGCCAGT
136	79	PTPN13-31	PTPN13	31	n/a	NM_080683.2	M13-ACGTGCAACAAAGAGGAGTTG	TCCTGCCAATTTAGTCTATGAATTAC	GTAAAACGACGGCCAGT
137	79	PTPN13-32	PTPN13	32	n/a	NM_080683.2	CTTGAGGCCAGGAGGATTG	M13-AAGTGAACAGCTGGCAGTGAA	GTAAAACGACGGCCAGT
138	79	PTPN13-33	PTPN13	33	n/a	NM_080683.2	M13-CAACATCCCAGAAATGTGAGTTT	ACGGTTACCTATGTGAGGCTCT	GTAAAACGACGGCCAGT
139	79	PTPN13-34	PTPN13	34	n/a	NM_080683.2	M13-GGAGAGAGACAATGTGCAGTCC	CAGAGACGAGAATGAATACTGGG	GTAAAACGACGGCCAGT
140	79	PTPN13-35	PTPN13	35	n/a	NM_080683.2	M13-TCTGTTTAACACCTTGTCCCTTTC	TGTTTGGACTAACCCTACTAGAAGTAAA	GTAAAACGACGGCCAGT
141	79	PTPN13-36	PTPN13	36	n/a	NM_080683.2	TCCAAATGTATCATTTATATCATGGC	M13-TCTCTGATTATTTCACCTTCTGGG	GTAAAACGACGGCCAGT
142	79	PTPN13-37	PTPN13	37	n/a	NM_080683.2	ACTGATGCCTCAGCCACTG	M13-CAGCCTCCCAAAGCACTG	GTAAAACGACGGCCAGT
143	79	PTPN13-38	PTPN13	38	n/a	NM_080683.2	M13-AAACGGGATCTGTCCAAGG	GGACTCCCAGCCTCTGTCTC	GTAAAACGACGGCCAGT
144	79	PTPN13-39	PTPN13	39	n/a	NM_080683.2	M13-TCCATCGTAGGCGACAGAAC	AAATTCTTCTAATCTTGGGCCAG	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
145	79	PTPN13-40	PTPN13	40	n/a	NM_080683.2	M13-CACTCAGAATCAGCCTTAATCAAC	TAATGATTTGGCATCACCGAC	GTAAAACGACGGCCAGT
146	79	PTPN13-41	PTPN13	41	n/a	NM_080683.2	M13-TCATGATCTTTGACTCATGCAA	GCAATCACGGAAAGAGTCCA	GTAAAACGACGGCCAGT
147	79	PTPN13-42	PTPN13	42	n/a	NM_080683.2	TGGACAACAGAACGAGACCC	M13-ATCCCAAGATCACAACACATTATC	GTAAAACGACGGCCAGT
148	79	PTPN13-43	PTPN13	43	n/a	NM_080683.2	M13-TTCCCAAGACTACCAGAAGGG	CCTCACTGCAGTAAATGTTTGG	GTAAAACGACGGCCAGT
149	79	PTPN13-44	PTPN13	44	n/a	NM_080683.2	AGCCTACACCCTGTTTCTTGC	M13-GCATGTTGTATGAACTTGCTGC	GTAAAACGACGGCCAGT
150	79	PTPN21-1	PTPN21	1	CCDS9884.1	NM_007039	M13-AGAGGATCGCTTTCTCCTGG	CTCCTGACCTTGTGATTCGC	GTAAAACGACGGCCAGT
151	79	PTPN21-2	PTPN21	2	CCDS9884.1	NM_007039	M13-GGTCAGGGATTAGTGCGACTG	TCCTTTGTGCCTAGTGAACCC	GTAAAACGACGGCCAGT
152	79	PTPN21-3	PTPN21	3	CCDS9884.1	NM_007039	M13-ACACACACAACCATGTGGGAT	TCATTGAGGTATTCCAAGTTCATTT	GTAAAACGACGGCCAGT
153	79	PTPN21-4	PTPN21	4	CCDS9884.1	NM_007039	M13-CCAAGCCAAGACTCATATCTGC	CAGGGAAAGCAGTCACACTTG	GTAAAACGACGGCCAGT
154	79	PTPN21-5	PTPN21	5	CCDS9884.1	NM_007039	M13-GTCAATGGCCATGATTCCTTC	GACTGGCTGCTTTCAACTTCC	GTAAAACGACGGCCAGT
155	79	PTPN21-6	PTPN21	6	CCDS9884.1	NM_007039	M13-CCCTCAGCATTCAGCACATAC	AACTTTGGTCACCAGGACCTC	GTAAAACGACGGCCAGT
156	79	PTPN21-7	PTPN21	7	CCDS9884.1	NM_007039	M13-AACCAGTCCAGGGAACTCTAGC	TTTGAAGAAAGCGGCTTATTG	GTAAAACGACGGCCAGT
157	79	PTPN21-8	PTPN21	8	CCDS9884.1	NM_007039	GACCTCGTGATCCACCCAC	M13-CTGCCTCCAAACACATACAGG	GTAAAACGACGGCCAGT
158	79	PTPN21-9	PTPN21	9	CCDS9884.1	NM_007039	TCTTTAGACAAACTCTGCATTAAACG	M13-TTTACCTTTCAAGAATTACAATGGTTC	GTAAAACGACGGCCAGT
159	79	PTPN21-10	PTPN21	10	CCDS9884.1	NM_007039	CCGACAGAGAACCTCCCTTCT	M13-AATATTAGGTTGGACCTATGGGAAA	GTAAAACGACGGCCAGT
160	79	PTPN21-11	PTPN21	11	CCDS9884.1	NM_007039	GTCATAGGGCTTGACATTGCC	M13-GCTTCATGATCTCCAAGCATTC	GTAAAACGACGGCCAGT
161	79	PTPN21-12a	PTPN21	12	CCDS9884.1	NM_007039	TAGATGAGGAAGCCGAAGCTC	M13-ATCTCGGGCTGGCTGTAGAC	GTAAAACGACGGCCAGT
162	79	PTPN21-12b	PTPN21	12	CCDS9884.1	NM_007039	M13-ATGTCGTCCAACCCTAGCATC	CTGTCCTCCTGGAACGTTTG	GTAAAACGACGGCCAGT
163	79	PTPN21-12c	PTPN21	12	CCDS9884.1	NM_007039	AACGTTCCAGGAGGACAGC	M13-TCCTCTTCTCCGCGTCTG	GTAAAACGACGGCCAGT
164	79	PTPN21-12d	PTPN21	12	CCDS9884.1	NM_007039	AGCCTGAGCTACAGCTTCCAC	M13-TGCTGTGGATTAGCATGGTG	GTAAAACGACGGCCAGT
165	79	PTPN21-12e	PTPN21	12	CCDS9884.1	NM_007039	M13-ACAAACGGAACAGCATCGAG	TTCCACGATGTTCTTCTTCCC	GTAAAACGACGGCCAGT
166	79	PTPN21-12f	PTPN21	12	CCDS9884.1	NM_007039	M13-TACGGCCATAAGAAGTCCCTG	GATGAGTGAAAGAAGCGCCAG	GTAAAACGACGGCCAGT
167	79	PTPN21-13	PTPN21	13	CCDS9884.1	NM_007039	TGTGTGTTCCTGGTCTTCAGTG	M13-ATCTCATGAAGGCATTTGCG	GTAAAACGACGGCCAGT
168	79	PTPN21-14	PTPN21	14	CCDS9884.1	NM_007039	M13-ACAGTGCTAGATTTGAAGCAGAAA	CCCAGCTTGCAGTACAGTTTG	GTAAAACGACGGCCAGT
169	79	PTPN21-15	PTPN21	15	CCDS9884.1	NM_007039	CAGCAAGGTTAAACAGGTTGC	M13-TTTCTCCACAGGTCAGGATTC	GTAAAACGACGGCCAGT
170	79	PTPN21-16	PTPN21	16	CCDS9884.1	NM_007039	M13-TCAGATGTGCCGTCTATGTGAG	TTCGGAAACATAAATGTTCCTCTC	GTAAAACGACGGCCAGT
171	79	PTPN21-17	PTPN21	17	CCDS9884.1	NM_007039	GCACCCAGTGCTCTTTATCTG	M13-ACAGTCCAAGGAAATGTGCG	GTAAAACGACGGCCAGT
172	79	PTPN21-18	PTPN21	18	CCDS9884.1	NM_007039	M13-GAGACTGTCCATCTCCCAACC	GTGGATCAAGTGTCAACGGG	GTAAAACGACGGCCAGT
173	79	PTPN23-1	PTPN23	1	CCDS2754.1	NM_015466	M13-CTCCCGTGACCAGTGACTTC	GGTTCAGATGAAGATGCAGGTG	GTAAAACGACGGCCAGT
174	79	PTPN23-2	PTPN23	2	CCDS2754.1	NM_015466	AATCCTGAGTCCTGGTTGGTG	M13-TCAAATGATCTGCCCACCTC	GTAAAACGACGGCCAGT
175	79	PTPN23-3	PTPN23	3	CCDS2754.1	NM_015466	TGGCATTTGTGAGTTAGCTGG	M13-CTATGCAGCAAGGAGAAGGG	GTAAAACGACGGCCAGT
176	79	PTPN23-4	PTPN23	4	CCDS2754.1	NM_015466	GCTTCATTACCTGCAGAGTCG	M13-GCCATCTGAAGAGCTGAAAGC	GTAAAACGACGGCCAGT
177	79	PTPN23-5	PTPN23	5	CCDS2754.1	NM_015466	M13-TCTGAGTTTCCCTGTTCCCTC	GTACAGGAGACCTTCATGCCC	GTAAAACGACGGCCAGT
178	79	PTPN23-6	PTPN23	6	CCDS2754.1	NM_015466	M13-GGAACATGTGGACATACCAGG	CCTGATTCAACAAAGCCAAGG	GTAAAACGACGGCCAGT
179	79	PTPN23-7	PTPN23	7	CCDS2754.1	NM_015466	M13-GGGAAGGATAAAGGGAAGGG	CAAGTTTCTTCCAGTCCTTCTGG	GTAAAACGACGGCCAGT
180	79	PTPN23-8	PTPN23	8	CCDS2754.1	NM_015466	M13-AGTGCACAGGTAGGGACGG	AAGAAGAAGAGACGCCACGAC	GTAAAACGACGGCCAGT
181	79	PTPN23-9	PTPN23	9	CCDS2754.1	NM_015466	M13-GATCTACTACTTCGCAGCCGTG	CACTTAAGACACCAGGCCTCC	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
182	79	PTPN23-10	PTPN23	10	CCDS2754.1	NM_015466	M13-TCATCTGATGGACAGGCAGG	CAGAGGGACAAGACCCTTCAC	GTAAAACGACGGCCAGT
183	79	PTPN23-11	PTPN23	11	CCDS2754.1	NM_015466	M13-CCTGAGGGTATAGGAGCAAGC	GAAGTCGTTGTCCTTCTTGGC	GTAAAACGACGGCCAGT
184	79	PTPN23-12	PTPN23	12	CCDS2754.1	NM_015466	M13-TGGCATCTACATGGGAAGTAGG	CTGTAACAGCTGGGTCTGTGG	GTAAAACGACGGCCAGT
185	79	PTPN23-13	PTPN23	13	CCDS2754.1	NM_015466	CCAGCATTGGACACTCTTCAG	M13-CTCACTGCAGAAGCGACAGAG	GTAAAACGACGGCCAGT
186	79	PTPN23-14	PTPN23	14	CCDS2754.1	NM_015466	M13-CTGACATCTTTGCCAAACTGG	TGGACATTTCATTCCTCTCCC	GTAAAACGACGGCCAGT
187	79	PTPN23-15	PTPN23	15	CCDS2754.1	NM_015466	M13-CAGATTGAGTGGTGAGGCTTG	TGATTCAGAGGAGTGGGTGTG	GTAAAACGACGGCCAGT
188	79	PTPN23-16	PTPN23	16	CCDS2754.1	NM_015466	CCTCACTTAAGCCCTGACCTG	M13-CCTTGTCCTCTGTGGGCAG	GTAAAACGACGGCCAGT
189	79	PTPN23-17	PTPN23	17	CCDS2754.1	NM_015466	M13-AATGGGCCAAGTACATGGAAG	GACACTCAGGGCCTCGACTC	GTAAAACGACGGCCAGT
190	79	PTPN23-18	PTPN23	18	CCDS2754.1	NM_015466	M13-CCACTCAGAGATGAAGGTGGG	CCAGATCTGCGTAGAAGTCCC	GTAAAACGACGGCCAGT
191	79	PTPN23-19	PTPN23	19	CCDS2754.1	NM_015466	M13-CCAGTCCTCTGCTCTTTCCC	TTCCACTGCCTCACTCTCCTC	GTAAAACGACGGCCAGT
192	79	PTPN23-20a	PTPN23	20	CCDS2754.1	NM_015466	M13-CAGGTTTGTGTGGCCCTG	GGCTGTATCAGCTGGGTGG	GTAAAACGACGGCCAGT
193	79	PTPN23-20b	PTPN23	20	CCDS2754.1	NM_015466	AGGAGAGTGAGGCAGTGGAAG	M13-AGGGTAGGTGTAAGGCGTGG	GTAAAACGACGGCCAGT
194	79	PTPN23-20c	PTPN23	20	CCDS2754.1	NM_015466	GTGGTGAGCAGTCCCTATGTG	M13-GGGTAGAGCTGGGTGTGTAGG	GTAAAACGACGGCCAGT
195	79	PTPN23-20d	PTPN23	20	CCDS2754.1	NM_015466	CAGCACCACTTCTCTTCTGGG	M13-CCCATGGGTCTGGTAGAAGG	GTAAAACGACGGCCAGT
196	79	PTPN23-20e	PTPN23	20	CCDS2754.1	NM_015466	M13-CACAAGCGTTTGGGCCTC	GTGAAGGCACCAGGTGGG	GTAAAACGACGGCCAGT
197	79	PTPN23-20f	PTPN23	20	CCDS2754.1	NM_015466	M13-CCTACACACCCAGCTCTACCC	GACAGTGTCCAGAGCTCCCAC	GTAAAACGACGGCCAGT
198	79	PTPN23-20g	PTPN23	20	CCDS2754.1	NM_015466	CTGCAGACCTGCTCTCCTCC	M13-GCAGCTGGCATTGATGTAGTC	GTAAAACGACGGCCAGT
199	79	PTPN23-20h	PTPN23	20	CCDS2754.1	NM_015466	GATGTGGGAGCTCTGGACAC	M13-TTGCTGAGGGACAGATAAGCC	GTAAAACGACGGCCAGT
200	79	PTPN23-20i	PTPN23	20	CCDS2754.1	NM_015466	M13-AGCCCCTGCCTACACACC	GGGACCTGGGTAGAGCTG	GTAAAACGACGGCCAGT
201	79	PTPN23-21	PTPN23	21	CCDS2754.1	NM_015466	M13-GAGGCTGAGATGGAGAAGGTG	CAGGAAGAGCCTATGAGCCAG	GTAAAACGACGGCCAGT
202	79	PTPN23-22	PTPN23	22	CCDS2754.1	NM_015466	M13-TAAGTGCTGTCCAGTCCTTGG	ATAGAGCAGTGCAAAGGCTCC	GTAAAACGACGGCCAGT
203	79	PTPN23-23	PTPN23	23	CCDS2754.1	NM_015466	ATTGTGCACTGCAGGTAGAGG	M13-TGCCTCATAGCAGAACCTGAG	GTAAAACGACGGCCAGT
204	79	PTPN23-24	PTPN23	24	CCDS2754.1	NM_015466	M13-GCAGGAGAAGGTGAGGATCTG	CCTGAGGAAGGTGGTTCTGAG	GTAAAACGACGGCCAGT
205	79	PTPN23-25a	PTPN23	25	CCDS2754.1	NM_015466	AAGCATCAGCCAGAAGGTGAG	M13-TCAGGTCTTGTTGAGTGTCCAG	GTAAAACGACGGCCAGT
206	79	PTPN23-25b	PTPN23	25	CCDS2754.1	NM_015466	ATTGCCAAGCTCAGCATTC	M13-GCCAAAGGCAGCAGAAATG	GTAAAACGACGGCCAGT
207	79	PTPN5-1	PTPN5	1	CCDS41626.1	NM_001039970	M13-ATGATCTGAAGCTGCCCTCTC	CCAAACCATAGCCAGGAAGAG	GTAAAACGACGGCCAGT
208	79	PTPN5-2	PTPN5	2	CCDS41626.1	NM_001039970	GAGGGAGCCTTCTTATCTTTGC	M13-AACGAAGAGCTATGGAGCAGC	GTAAAACGACGGCCAGT
209	79	PTPN5-3	PTPN5	3	CCDS41626.1	NM_001039970	M13-GCTTTGCTAATCGAGGGTGAC	CCTTATCCTCCTGCCTTCCAG	GTAAAACGACGGCCAGT
210	79	PTPN5-4	PTPN5	4	CCDS41626.1	NM_001039970	M13-GGACCTTAGAGGTTCAGGAGC	CAGGCAGAAGAACTTCAGGG	GTAAAACGACGGCCAGT
211	79	PTPN5-5	PTPN5	5	CCDS41626.1	NM_001039970	M13-CCACGGTAAGTAAGCTTTGGG	GATGGGAGCTGGTAGAAATCC	GTAAAACGACGGCCAGT
212	79	PTPN5-6	PTPN5	6	CCDS41626.1	NM_001039970	ATGGGCACTCCAGGAACAC	M13-CAGGAGTCAGAGTCAGGCATC	GTAAAACGACGGCCAGT
213	79	PTPN5-7	PTPN5	7	CCDS41626.1	NM_001039970	M13-GTTCCCAGCTGATCTCTCCC	ATGCTGAGTTCCAGGCACC	GTAAAACGACGGCCAGT
214	79	PTPN5-8	PTPN5	8	CCDS41626.1	NM_001039970	M13-ATGCGTCGTGAGCACTAACTC	CACCTCCTCCAGTCCTGTCAC	GTAAAACGACGGCCAGT
215	79	PTPN5-9	PTPN5	9	CCDS41626.1	NM_001039970	GCAGAAGAAGTGTGGGTATGC	M13-CCACACTCAGGCTCTTCACAG	GTAAAACGACGGCCAGT
216	79	PTPN5-10	PTPN5	10	CCDS41626.1	NM_001039970	M13-CTGTGAAGAGCCTGAGTGTGG	CTTACCGAGCCTCACATCTCC	GTAAAACGACGGCCAGT
217	79	PTPN5-11	PTPN5	11	CCDS41626.1	NM_001039970	CCTTGTGTATCTCTCCGCTGG	M13-TCCCAAGTCCATTCACCTCTC	GTAAAACGACGGCCAGT
218	79	PTPN5-12	PTPN5	12	CCDS41626.1	NM_001039970	M13-TCTCTATCTCTGGGCTGGTTTG	AGATGCTGGTGGCAATGAAG	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
219	79	PTPN5-13	PTPN5	13	CCDS41626.1	NM_001039970	GACAGAGTGGGACTGAGGAGC	M13-ATGCACATGTGGGTCTCTCC	GTAAAACGACGGCCAGT
220	79	PTPN5-14	PTPN5	14	CCDS41626.1	NM_001039970	M13-CTGGCAAGTGATTGCTACTCC	GAGGACAGAGGGAGCTGACTG	GTAAAACGACGGCCAGT
221	79	PTPRB-1	PTPRB	1	n/a	NM_001109754.1	GTCAGAATGGCAGCGTGG	M13-GAAAGTGGAGTGGGAATTTGG	GTAAAACGACGGCCAGT
222	79	PTPRB-2	PTPRB	2	n/a	NM_001109754.1	M13-AGAAAGTGTGGCTTGAGGAGC	TTTGTATCCCTGGAACTCAAATG	GTAAAACGACGGCCAGT
223	79	PTPRB-3	PTPRB	3	n/a	NM_001109754.1	AAAGTCTTCAAGCCATGTTCTTT	M13-TCCACTGTATCCCACAAGCTC	GTAAAACGACGGCCAGT
224	79	PTPRB-4	PTPRB	4	n/a	NM_001109754.1	GGAACACAAATGAATATGTGACTTCTA	M13-AAAGTGGATATGGGTCTTCTATACCTT	GTAAAACGACGGCCAGT
225	79	PTPRB-5	PTPRB	5	n/a	NM_001109754.1	CAAGGAATGTGGCTTGCAG	M13-GCTCCACTTCTCAGATTGGG	GTAAAACGACGGCCAGT
226	79	PTPRB-6	PTPRB	6	n/a	NM_001109754.1	M13-TGTCTCCTATCTACTGCTGCCC	CAGTTACGGCAGTTACCTGGG	GTAAAACGACGGCCAGT
227	79	PTPRB-7	PTPRB	7	n/a	NM_001109754.1	M13-AAATAAATGTTGAACTGAAACACGC	ATCCATAAAGCAATGCCCAG	GTAAAACGACGGCCAGT
228	79	PTPRB-8	PTPRB	8	n/a	NM_001109754.1	GAACTGAGAGTCTATAGCAACAACACA	M13-TTGTAAAGGCCAGGGATGAGT	GTAAAACGACGGCCAGT
229	79	PTPRB-9	PTPRB	9	n/a	NM_001109754.1	TGCTGACTGCAATAGACGACTC	M13-ATTGCTACAGCTCTGTGGTGC	GTAAAACGACGGCCAGT
230	79	PTPRB-10a	PTPRB	10	n/a	NM_001109754.1	M13-ATTGTCCCAGCTTGTCATCTG	GGCTTGGCTGAATGATGTTAG	GTAAAACGACGGCCAGT
231	79	PTPRB-10b	PTPRB	10	n/a	NM_001109754.1	M13-ttgtcccagcttgtcatctg	tcagattttgcaatcgttcc	GTAAAACGACGGCCAGT
232	79	PTPRB-11a	PTPRB	11	n/a	NM_001109754.1	M13-GTTGCCAGTTCCTTGAATGTG	TCGAAATACCTGAACTACCCG	GTAAAACGACGGCCAGT
233	79	PTPRB-11b	PTPRB	11	n/a	NM_001109754.1	M13-tgttgccagttccttgaatg	ccactgcatctattcaggttca	GTAAAACGACGGCCAGT
234	79	PTPRB-12a	PTPRB	12	n/a	NM_001109754.1	M13-GTTCTCTCAGTGGGTGCCAA	ATTTGTGAATAGCTGAGCCCG	GTAAAACGACGGCCAGT
235	79	PTPRB-12b	PTPRB	12	n/a	NM_001109754.1	M13-gtgccaaaacatcagaagca	caatctagcccttctccaggt	GTAAAACGACGGCCAGT
236	79	PTPRB-13a	PTPRB	13	n/a	NM_001109754.1	CAAATGCATCATCTTCTACCTGC	M13-TCTCCCAATGTTGCTTCATCC	GTAAAACGACGGCCAGT
237	79	PTPRB-13b	PTPRB	13	n/a	NM_001109754.1	M13-tgctccacttgtctctctgc	ctcaccctggggttcttaca	GTAAAACGACGGCCAGT
238	79	PTPRB-14a	PTPRB	14	n/a	NM_001109754.1	M13-TTCCCGTATCACTGAATCCAAC	GGAAACTAAGGACCAACCAAGG	GTAAAACGACGGCCAGT
239	79	PTPRB-14b	PTPRB	14	n/a	NM_001109754.1	M13-ctgctcccttctcctcactg	ccccacgattcattactgct	GTAAAACGACGGCCAGT
240	79	PTPRB-15	PTPRB	15	n/a	NM_001109754.1	M13-ATGTACGACTCACCCACATGC	ACAGTCCCTTCCCAAATTCAG	GTAAAACGACGGCCAGT
241	79	PTPRB-16a	PTPRB	16	n/a	NM_001109754.1	M13-TGATGTTGCTCAGCTATCTTATTTG	TCCAAGCCCTATTTGAGTAAGATG	GTAAAACGACGGCCAGT
242	79	PTPRB-16b	PTPRB	16	n/a	NM_001109754.1	M13-tggcatagctgtgattatgtga	tccatttgagaaataagagtagcaaa	GTAAAACGACGGCCAGT
243	79	PTPRB-17	PTPRB	17	n/a	NM_001109754.1	TCAGAGCTAGTTGGACCCAAAG	M13-TGGCAATCAGACAGGCTTATG	GTAAAACGACGGCCAGT
244	79	PTPRB-18	PTPRB	18	n/a	NM_001109754.1	M13-TCACACACACACAGTCTGATGC	AACAGGCTTTATTGCCCAAAG	GTAAAACGACGGCCAGT
245	79	PTPRB-19	PTPRB	19	n/a	NM_001109754.1	M13-TGGCCAGAGATAGTGGATGTG	AGCTCGCATGCATCAGTTG	GTAAAACGACGGCCAGT
246	79	PTPRB-20	PTPRB	20	n/a	NM_001109754.1	M13-CTACCCTGCTACCCACTGACC	CACCATCAGCCAATATCTCCC	GTAAAACGACGGCCAGT
247	79	PTPRB-21	PTPRB	21	n/a	NM_001109754.1	M13-AAGTAAATGCCTCATCGTGGG	AAGGGCTGAATTCATCAATGG	GTAAAACGACGGCCAGT
248	79	PTPRB-22	PTPRB	22	n/a	NM_001109754.1	M13-TTCCCTCCCTCAGAGATGTTG	TCCGGTTACTGTGAAGAGAAGC	GTAAAACGACGGCCAGT
249	79	PTPRB-23	PTPRB	23	n/a	NM_001109754.1	M13-AAGGGTAAGCACCACATTTGC	TTCTGCCTGAGTTGTACCTCG	GTAAAACGACGGCCAGT
250	79	PTPRB-24	PTPRB	24	n/a	NM_001109754.1	TGGCTTCTCTTCACAGTAACCG	M13-GCAGCCTCCTAACTTCTGAGC	GTAAAACGACGGCCAGT
251	79	PTPRB-25	PTPRB	25	n/a	NM_001109754.1	TCAGGGCTAATGCATGTTGAG	M13-GCATTCAGAGCTTGAGATTGTCC	GTAAAACGACGGCCAGT
252	79	PTPRB-26	PTPRB	26	n/a	NM_001109754.1	TTATCCTGCCTGAGCCTCATC	M13-GAGGAGTGGCATCTCCAGTG	GTAAAACGACGGCCAGT
253	79	PTPRB-27	PTPRB	27	n/a	NM_001109754.1	M13-AGACTTGGCAGAGACCTCCC	GGGTTTCACTTTGATGATGGG	GTAAAACGACGGCCAGT
254	79	PTPRB-28	PTPRB	28	n/a	NM_001109754.1	M13-ATTGCTTTAGCAGCTGATCCC	GCAACTCCTATGGGCTGAAAC	GTAAAACGACGGCCAGT
255	79	PTPRB-29	PTPRB	29	n/a	NM_001109754.1	TTCGCTGGTTCCTCTCTTGTAG	M13-GTTGGTCCAGACAAATCCTCC	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
256	79	PTPRB-30	PTPRB	30	n/a	NM_001109754.1	TCTCCCATAACTGGGAAGGG	M13-CCTTGTCAGATTAAGGTCCTGG	GTAAAACGACGGCCAGT
257	79	PTPRB-31	PTPRB	31	n/a	NM_001109754.1	CCAGAGACCATTAGTGAAGCG	M13-GGCTGGTTTCAAACTCTTAGGC	GTAAAACGACGGCCAGT
258	79	PTPRB-32	PTPRB	32	n/a	NM_001109754.1	M13-AGGCGATGGGCTAGAATCAC	CTCTGTAGGGCATGAAGCAAG	GTAAAACGACGGCCAGT
259	79	PTPRC-1	PTPRC	1	CCDS1397.1	NM_002838	M13-ATGCAGCTAGCAAGTGGTTTG	TGATGGTTTACAGCAGGCTTC	GTAAAACGACGGCCAGT
260	79	PTPRC-2	PTPRC	2	CCDS1397.1	NM_002838	M13-ATATTTGGGCTTTGTAAACATGG	TGTGATTTACTGTCAAGTTTGGG	GTAAAACGACGGCCAGT
261	79	PTPRC-3	PTPRC	3	CCDS1397.1	NM_002838	M13-GGGAGGAGCATACATTTAGGG	TTGGAGATCTTGCTTCCCTTC	GTAAAACGACGGCCAGT
262	79	PTPRC-4	PTPRC	4	CCDS1397.1	NM_002838	M13-TCGCAATTTGCTCCTTATAACC	TGGTTAGATTTCCTCACACCATTC	GTAAAACGACGGCCAGT
263	79	PTPRC-5	PTPRC	5	CCDS1397.1	NM_002838	TGTAGAATGCATGTGTCGTGG	M13-TTTGCATAATTTGGTGTTGATACG	GTAAAACGACGGCCAGT
264	79	PTPRC-6	PTPRC	6	CCDS1397.1	NM_002838	M13-CGAATGTCAAATCAAACGAGG	AAAGAAAGGAGCCCGAGGTAG	GTAAAACGACGGCCAGT
265	79	PTPRC-7	PTPRC	7	CCDS1397.1	NM_002838	CCGCCAATTAGATGCGTACC	M13-TAGTGGGTCCTGAAAGCTTGG	GTAAAACGACGGCCAGT
266	79	PTPRC-8	PTPRC	8	CCDS1397.1	NM_002838	TGAGGTCCTTGTTAGGGCAG	M13-CACCAGACTAGCTCCTGTGACC	GTAAAACGACGGCCAGT
267	79	PTPRC-9	PTPRC	9	CCDS1397.1	NM_002838	M13-CATGTTAGGAATGAATGAGGGC	AGAACAAGAGAGGCAGGGAGG	GTAAAACGACGGCCAGT
268	79	PTPRC-10	PTPRC	10	CCDS1397.1	NM_002838	M13-TGGTAATTTCCACAGATGTTTCA	TGGACTTTCATATACGACACCAAA	GTAAAACGACGGCCAGT
269	79	PTPRC-11	PTPRC	11	CCDS1397.1	NM_002838	M13-ACAGTGCCAATCTGGTGTGAC	AGCTTTGTGACTCACTGGCTC	GTAAAACGACGGCCAGT
270	79	PTPRC-12	PTPRC	12	CCDS1397.1	NM_002838	GAGTTCACTTGGAACAATGTGATG	M13-AAATGTGCCAGGTAAATGTGC	GTAAAACGACGGCCAGT
271	79	PTPRC-13	PTPRC	13	CCDS1397.1	NM_002838	M13-AAATGAGTGATTTATTCTTCAGGGTTT	TGTGAGCAGTGGTCTTAAAGTTATTT	GTAAAACGACGGCCAGT
272	79	PTPRC-14	PTPRC	14	CCDS1397.1	NM_002838	CCTTGAAGTTTAAAGCAAATCAGC	M13-TCCTCTTATGAATTCAACAAACCTT	GTAAAACGACGGCCAGT
273	79	PTPRC-15	PTPRC	15	CCDS1397.1	NM_002838	M13-TGGAGGTGATTATTCAACCAGTC	TGAAGTGGGCTGTATGCTGTC	GTAAAACGACGGCCAGT
274	79	PTPRC-16	PTPRC	16	CCDS1397.1	NM_002838	CTCTGCTCAAGGCTCTTCCTC	M13-GAGATTGCACCACCACACTTC	GTAAAACGACGGCCAGT
275	79	PTPRC-17	PTPRC	17	CCDS1397.1	NM_002838	M13-TGTGTACGAGGAGGAAAGAAGC	AAAGGCAAATGGCAATATAAATACAC	GTAAAACGACGGCCAGT
276	79	PTPRC-18	PTPRC	18	CCDS1397.1	NM_002838	GAGATTTGTTCTGAAAGTTGTCAATC	M13-CCCTGCATCTCCGTTTATCTC	GTAAAACGACGGCCAGT
277	79	PTPRC-19	PTPRC	19	CCDS1397.1	NM_002838	ATAAAGGAAGCTCGAAAGCCC	M13-CAGTGACATATGGGCTCACTTC	GTAAAACGACGGCCAGT
278	79	PTPRC-20	PTPRC	20	CCDS1397.1	NM_002838	M13-TGCCCAGAGAAATTCACAATC	TCTGTTCCCAAATCATCCTCC	GTAAAACGACGGCCAGT
279	79	PTPRC-21	PTPRC	21	CCDS1397.1	NM_002838	M13-ACCCAGGAAATACATTGCTGC	TCATCAGGCAGATACATGTGG	GTAAAACGACGGCCAGT
280	79	PTPRC-22	PTPRC	22	CCDS1397.1	NM_002838	TTCAGGACACATTAGTGGGAAATAG	M13-TGTTCTAACCACAGCTTTCATCC	GTAAAACGACGGCCAGT
281	79	PTPRC-23	PTPRC	23	CCDS1397.1	NM_002838	M13-TTTGTACTGGTACTCCCTTCCAC	TCTCTAACAGCCCTAGGCAGG	GTAAAACGACGGCCAGT
282	79	PTPRC-24	PTPRC	24	CCDS1397.1	NM_002838	AGAGACATCTTTCCCTTTGGC	M13-TGTGGTCATCTTTCTTCCACAG	GTAAAACGACGGCCAGT
283	79	PTPRC-25	PTPRC	25	CCDS1397.1	NM_002838	M13-TGCCATGAATTGTTCCAATATG	TCTGGTGAAGACTAAATGCAAGC	GTAAAACGACGGCCAGT
284	79	PTPRC-26	PTPRC	26	CCDS1397.1	NM_002838	TCTTTAGTGCATACTAGCCCTGTC	M13-TGACTGTGTGTCCCACATTAAAC	GTAAAACGACGGCCAGT
285	79	PTPRC-27	PTPRC	27	CCDS1397.1	NM_002838	TGTTGTTTGACATGGAATTATGTTC	M13-TCGCTTAATGAATGGCCC	GTAAAACGACGGCCAGT
286	79	PTPRC-28	PTPRC	28	CCDS1397.1	NM_002838	TGTTTCGCAAGATATGTTGTAATCTT	M13-GATGAAGCAAGCAATCCAAGAC	GTAAAACGACGGCCAGT
287	79	PTPRC-29	PTPRC	29	CCDS1397.1	NM_002838	M13-GCACAGACAGAGAAAGAAAGGG	TATATGATGGCCTTGCCTGC	GTAAAACGACGGCCAGT
288	79	PTPRC-30	PTPRC	30	CCDS1397.1	NM_002838	M13-AAATTACTCTATGCAGGCAAGGC	ACCAAGAGAGTGACCGACTCC	GTAAAACGACGGCCAGT
289	79	PTPRC-31	PTPRC	31	CCDS1397.1	NM_002838	TTTGGTTCTTGAAAGAGGTTGG	M13-AAGAACAAACGAGAGGAAAGGAG	GTAAAACGACGGCCAGT
290	79	PTPRC-32	PTPRC	32	CCDS1397.1	NM_002838	M13-TCATCCAATACTTCCACAAATAAATC	TTCTACAAATATTGGTTCGCTGC	GTAAAACGACGGCCAGT
291	79	PTPRD-1	PTPRD	1	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-AATTTCAGATCGGACAGACTCG	ATCTCTTTCAAAGGCTGGCTG	GTAAAACGACGGCCAGT
292	79	PTPRD-2	PTPRD	2	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	ATGTATGTCTTGATGGCGGTG	M13-AAGCAAGCAAGTAACGTAGAAACC	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
293	79	PTPRD-3	PTPRD	3	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-TCCACCACTGTATTGAGAGCTTTAG	AAGCACCATCACAATGCTAGTC	GTAAAACGACGGCCAGT
294	79	PTPRD-4	PTPRD	4	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-TGTTAGGTTCTCAACAAGCACTG	ACATCACAAACATGGACCACC	GTAAAACGACGGCCAGT
295	79	PTPRD-5	PTPRD	5	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	GTTGAGTGGACCTTCGCTTTG	M13-AATATAACAACACGGACCCTGC	GTAAAACGACGGCCAGT
296	79	PTPRD-6	PTPRD	6	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	TGTACGGTGCATGTCATGTGT	M13-GGATGGGCTTTCTAGAGGCAT	GTAAAACGACGGCCAGT
297	79	PTPRD-7a	PTPRD	7	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-AATGCGTGCAGGATCACTTAG	TTTGTGTTAGCACAGGTTCGC	GTAAAACGACGGCCAGT
298	79	PTPRD-7b	PTPRD	7	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	CATCACACTGACGTGGGACTC	M13-TCCTTCTCACCTCTTTGCACC	GTAAAACGACGGCCAGT
299	79	PTPRD-8	PTPRD	8	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-GCAGGTTACGCTAATGGAAGAAC	CAAAGCCTCCAAATAACCACTG	GTAAAACGACGGCCAGT
300	79	PTPRD-9	PTPRD	9	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-CTTCCCTTATTCCAGTTACCTTTG	GCAGGTTTGCTTATTGGTGAAG	GTAAAACGACGGCCAGT
301	79	PTPRD-10	PTPRD	10	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	TTGTCCTTATTGTTCGTTTATTTATTT	M13-TGAGCCTATTGAAAGACAGCA	GTAAAACGACGGCCAGT
302	79	PTPRD-11	PTPRD	11	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-TTTGAAAGAGAAACCTAAGTAAAGAAA	AAATAAGAGCAATTTCAGGATATGA	GTAAAACGACGGCCAGT
303	79	PTPRD-12	PTPRD	12	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	GTGGCAGCAAATCACACATTC	M13-TTTGTTAGTTCATGCATCCAAGC	GTAAAACGACGGCCAGT
304	79	PTPRD-13	PTPRD	13	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-ATTTGCAGAATGAAGGCAGAC	TGGACAAATTATGCACTTGGAC	GTAAAACGACGGCCAGT
305	79	PTPRD-14a	PTPRD	14	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-GAGTGGAACTCCCTCATTTGG	GCTGGAACAATAAGCTGCTCC	GTAAAACGACGGCCAGT
306	79	PTPRD-14b	PTPRD	14	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	TCTTATTCAGTGGCACCCTCC	M13-AAGGCCGTAAGCAGACAAATC	GTAAAACGACGGCCAGT
307	79	PTPRD-14c	PTPRD	14	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	AGAAGGCACCACTTCAACCTC	M13-AGCCAGACTTGCTTGACATTC	GTAAAACGACGGCCAGT
308	79	PTPRD-15	PTPRD	15	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	CTATGGTCCATGGTGGAAAGG	M13-CAAAGCACCAAACTGTCTCCC	GTAAAACGACGGCCAGT
309	79	PTPRD-16	PTPRD	16	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	AAAGCTAGTGCACATTGGTTTAGA	M13-TCTGAGCAGAAGAATCTTTCACTACAT	GTAAAACGACGGCCAGT
310	79	PTPRD-17	PTPRD	17	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-TTCAACCTCATTGGTCTGTGG	GCTAGGTATGGAGAAGCCAGC	GTAAAACGACGGCCAGT
311	79	PTPRD-18	PTPRD	18	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	CCAGTATCTTACCTCTACCTTAACAGG	M13-GATGGATATACCCACAAATCCC	GTAAAACGACGGCCAGT
312	79	PTPRD-19	PTPRD	19	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	TGCATCACACACTTATCATTAAATCC	M13-TCAACCACCTAAGGACAGCAG	GTAAAACGACGGCCAGT
313	79	PTPRD-20	PTPRD	20	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-GAGTGCAGGTGCAATTCTCTG	TTTGCTTGGGCAAGTCTCC	GTAAAACGACGGCCAGT
314	79	PTPRD-21	PTPRD	21	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-TATTTGCCTGCTTCCTCACCT	TTACTATATTGCTTGTGCAGACACTTT	GTAAAACGACGGCCAGT
315	79	PTPRD-22	PTPRD	22	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-CAGCTTCACAGTTAGGATCATCTTG	CCACCATGCACAGCCATC	GTAAAACGACGGCCAGT
316	79	PTPRD-23	PTPRD	23	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-CCATTAGGTCATGTCCCAGG	AGAAAGATAAGCCTTAGGGAAAGG	GTAAAACGACGGCCAGT
317	79	PTPRD-24	PTPRD	24	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-CCTTCAACAGCAACTCAAAGC	TGGAAGATCTATTTCATTCTTCACTG	GTAAAACGACGGCCAGT
318	79	PTPRD-25	PTPRD	25	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	CCAAAGGCTACAGGGTGGTAG	M13-TTAGCATAGGCCTCATTTGACC	GTAAAACGACGGCCAGT
319	79	PTPRD-26	PTPRD	26	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-TTTGAGTAGAAGTAATGGATGTAAGGTC	GGTTAAAGTAAAGCCACGACTCAA	GTAAAACGACGGCCAGT
320	79	PTPRD-27	PTPRD	27	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	GGGTACACTGCATTCAAACTGT	M13-CCAAGGGACTAAATGATGACCT	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
321	79	PTPRD-28	PTPRD	28	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-GGTTGATGTTTATGTATCCAGTGTG	GATGGTCCGGATTATGTCCAG	GTAAAACGACGGCCAGT
322	79	PTPRD-29	PTPRD	29	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-ATGAAGGGAGCTCATGGTTTC	GTCAAGTGGCAAGTGCTTCTC	GTAAAACGACGGCCAGT
323	79	PTPRD-30	PTPRD	30	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-TTCTTGTGGTCCGTATGCTTG	TGGTAATTTGGTTTGTCTAATAGGAAG	GTAAAACGACGGCCAGT
324	79	PTPRD-31	PTPRD	31	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	M13-GAAGTATGTCCACACCCAAGC	TGTTGAGAGAGTATGGAGTCCG	GTAAAACGACGGCCAGT
325	79	PTPRD-32	PTPRD	32	CCDS43786.1, CCDS6472.1	NM_002839, NM_130391	TTGGCAAAGTTAATCAACACCC	M13-TGCCCTGTATGGCTCAGAAG	GTAAAACGACGGCCAGT
326	79	PTPRE-1	PTPRE	1	CCDS7657.1	NM_006504	TCTCCTCATCATCACTGCCTG	M13-TTCAGCCACACCATTCTTCTC	GTAAAACGACGGCCAGT
327	79	PTPRE-2	PTPRE	2	CCDS7657.1	NM_006504	M13-AGGAAGAAGGGCTTATGGAGG	GGCACAGTGATACCCACCAG	GTAAAACGACGGCCAGT
328	79	PTPRE-3	PTPRE	3	CCDS7657.1	NM_006504	M13-ACCTGGTGGGTATCACTGTGC	CTCAAACGTCCATGTCACACC	GTAAAACGACGGCCAGT
329	79	PTPRE-4	PTPRE	4	CCDS7657.1	NM_006504	M13-TCAGCTTGGTTACTCAGTCGC	GCAAGGGTTCTGAGTCTTTGG	GTAAAACGACGGCCAGT
330	79	PTPRE-5	PTPRE	5	CCDS7657.1	NM_006504	M13-GGACAGCAGGTAGTTTGCTCC	GTCCTAGGTGCAAATGCTGAG	GTAAAACGACGGCCAGT
331	79	PTPRE-6	PTPRE	6	CCDS7657.1	NM_006504	GCTGAAATCCTACCCTTGTCG	M13-TGTGACAATTTACACTCCGGG	GTAAAACGACGGCCAGT
332	79	PTPRE-7	PTPRE	7	CCDS7657.1	NM_006504	GTGAGTCTGGGAAAGGTTTGG	M13-TAAGTCCTTGGTCTTGTTGGC	GTAAAACGACGGCCAGT
333	79	PTPRE-8	PTPRE	8	CCDS7657.1	NM_006504	M13-GCCTGAGAAGGGAGTGAACAG	TAAGCCACTGCATGTGTTTGG	GTAAAACGACGGCCAGT
334	79	PTPRE-9	PTPRE	9	CCDS7657.1	NM_006504	M13-GAGGCCTTCTGTAGTTGGGTG	GTCTGCCTATCACAGCCTGG	GTAAAACGACGGCCAGT
335	79	PTPRE-10	PTPRE	10	CCDS7657.1	NM_006504	M13-AGCAGCACATGTTCAGAGTCG	CATTGCCCATGAGGATGAG	GTAAAACGACGGCCAGT
336	79	PTPRE-11	PTPRE	11	CCDS7657.1	NM_006504	M13-AAAGTTGCATCCAGTGACCTG	AAAGATGAGGACGAGGGAGTC	GTAAAACGACGGCCAGT
337	79	PTPRE-12	PTPRE	12	CCDS7657.1	NM_006504	CTCTGACTCTTGCCTCACACC	M13-AATCATGGCTCAGGTATTGCC	GTAAAACGACGGCCAGT
338	79	PTPRE-13	PTPRE	13	CCDS7657.1	NM_006504	M13-GAGTGGTTTCCTTTGAGCAGG	ACAGCACACAGGAGCCCTTAG	GTAAAACGACGGCCAGT
339	79	PTPRE-14	PTPRE	14	CCDS7657.1	NM_006504	M13-TTTGCAAGCTTGTAGCAATGG	AGGTGTGAGCCATCGTGC	GTAAAACGACGGCCAGT
340	79	PTPRE-15	PTPRE	15	CCDS7657.1	NM_006504	M13-TCATTAGGCCTTAGGCTGTCC	GGGACATTTGTAATGAACGGG	GTAAAACGACGGCCAGT
341	79	PTPRE-16	PTPRE	16	CCDS7657.1	NM_006504	GGTCAACAAGCATTAACAGGC	M13-AGCCAATGGGACTAGGTGAAG	GTAAAACGACGGCCAGT
342	79	PTPRE-17	PTPRE	17	CCDS7657.1	NM_006504	M13-TAGGACAAGCAGGTTTCAGCC	CACAGCTGCGGGTACTGG	GTAAAACGACGGCCAGT
343	79	PTPRE-18	PTPRE	18	CCDS7657.1	NM_006504	M13-CTTCAGTGCTGATATGCAGGG	TTTACTGCGAAACATTGCAGC	GTAAAACGACGGCCAGT
344	79	PTPRE-19	PTPRE	19	CCDS7657.1	NM_006504	M13-GGAATTCTGCATGTGCCTAAA	CAACTGTATAGCAGGTGGCCTT	GTAAAACGACGGCCAGT
345	79	PTPRH-1	PTPRH	1	CCDS7657.1	NM_006504	M13-CTGGGTTCCACTTCCTCCTC	CTGAAGCCCTCTTCCTTCTCC	GTAAAACGACGGCCAGT
346	79	PTPRH-2	PTPRH	2	CCDS7657.1	NM_006504	M13-CTCCTCGACCCAGGAAAGAC	TCAGTACAATCCCTCCCAACC	GTAAAACGACGGCCAGT
347	79	PTPRH-3	PTPRH	3	CCDS7657.1	NM_006504	M13-TTTATGAGCGCCGTTGTTTC	TCCAACTAAAGAACCTGTCGC	GTAAAACGACGGCCAGT
348	79	PTPRH-4	PTPRH	4	CCDS7657.1	NM_006504	M13-GGTTAAGGAAGGGCTGGAAAG	GAAATCCGCTACGTTCTCCTG	GTAAAACGACGGCCAGT
349	79	PTPRH-5	PTPRH	5	CCDS7657.1	NM_006504	GCTGTGGTGAGCCGAGAT	M13-GTCAGCTCCCAACCACCC	GTAAAACGACGGCCAGT
350	79	PTPRH-6	PTPRH	6	CCDS7657.1	NM_006504	M13-CTGCTGGATGCAATGGTTAAG	CATCTCCTGAGCTGAGACTGC	GTAAAACGACGGCCAGT
351	79	PTPRH-7	PTPRH	7	CCDS7657.1	NM_006504	M13-AGCTAAGATGGTTGAGGGCAG	TACAGAGCCAGAGCCCAGAAG	GTAAAACGACGGCCAGT
352	79	PTPRH-8	PTPRH	8	CCDS7657.1	NM_006504	M13-AGGGCGTATCACTGTGTTCTG	AGCTCCCAAAGTCCTTTCATC	GTAAAACGACGGCCAGT
353	79	PTPRH-9	PTPRH	9	CCDS7657.1	NM_006504	M13-GGATATCTCAGCTTTGCTGTGG	TCATCTCTCAGCTCGCAAGG	GTAAAACGACGGCCAGT
354	79	PTPRH-10	PTPRH	10	CCDS7657.1	NM_006504	M13-AGGTAGTTTGGATTTGGCGAG	CCACTGATTTCCTCACAATGG	GTAAAACGACGGCCAGT
355	79	PTPRH-11	PTPRH	11	CCDS7657.1	NM_006504	M13-GTCAGCTGTCTTTGGACCAGG	TCCCTGAGTTCTGGTTTCTGC	GTAAAACGACGGCCAGT
356	79	PTPRH-12	PTPRH	12	CCDS7657.1	NM_006504	M13-TCCTCCTGTTTCTCATCCTCG	ATCCACCCTCTGACCTAGCTG	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
357	79	PTPRH-13	PTPRH	13	CCDS7657.1	NM_006504	M13-GGACTACAGGCGTGCAACAC	TTTGCTTAATCCCGAAAGCC	GTAAAACGACGGCCAGT
358	79	PTPRH-14	PTPRH	14	CCDS7657.1	NM_006504	M13-GGGTGCCATATAATCTCAGGG	AGGACTTGTTTCTCAAAGCGG	GTAAAACGACGGCCAGT
359	79	PTPRH-15	PTPRH	15	CCDS7657.1	NM_006504	TCCATGGGTCTTGGTCTTGTC	M13-CAGAGACCCTGGTTGAGGAAG	GTAAAACGACGGCCAGT
360	79	PTPRH-16a	PTPRH	16	CCDS7657.1	NM_006504	GCACGCCTGGAGAGATAAGAG	M13-TGGAGGAATCCGTAAGGTCTG	GTAAAACGACGGCCAGT
361	79	PTPRH-16b	PTPRH	16	CCDS7657.1	NM_006504	M13-GCACGCCTGGAGAGATAAGAG	TGGAGGAATCCGTAAGGTCTG	GTAAAACGACGGCCAGT
362	79	PTPRH-17	PTPRH	17	CCDS7657.1	NM_006504	M13-CATCTGCTGGTTCACATTTGG	GGAGGACCTGGCTTCTAGCAC	GTAAAACGACGGCCAGT
363	79	PTPRH-18	PTPRH	18	CCDS7657.1	NM_006504	M13-ACCTTCCACCCACTCCTCTG	CAGGGTCCCGTCTAACACAAC	GTAAAACGACGGCCAGT
364	79	PTPRH-19	PTPRH	19	CCDS7657.1	NM_006504	M13-ACACAGATCCCTCCAATCAGC	GGAATACGTACTGAGCCTGGG	GTAAAACGACGGCCAGT
365	79	PTPRH-20	PTPRH	20	CCDS7657.1	NM_006504	AGTCCCTCAGCAACACAGGAC	M13-CAGGAATCTGGGCTCAAGTG	GTAAAACGACGGCCAGT
366	79	PTPRJ-1	PTPRJ	1	CCDS7945.1	NM_002843	AGGAGGAGGCGAAGGAGAC	M13-GGGCAGGTGCAGTCAATG	GTAAAACGACGGCCAGT
367	79	PTPRJ-2	PTPRJ	2	CCDS7945.1	NM_002843	M13-GCTTAATGTGCTTCTTACCACCC	CTACAGAGCGAGGCTCCAAC	GTAAAACGACGGCCAGT
368	79	PTPRJ-3	PTPRJ	3	CCDS7945.1	NM_002843	M13-CCAAGTGTGCATTTCATTTCA	CAAGTGATCAATGGTTATCTCCAG	GTAAAACGACGGCCAGT
369	79	PTPRJ-4	PTPRJ	4	CCDS7945.1	NM_002843	TGGTGCAGGGAAGTCTAGGAG	M13-TTTCCAACAGGCAACTTGAAC	GTAAAACGACGGCCAGT
370	79	PTPRJ-5	PTPRJ	5	CCDS7945.1	NM_002843	GCTCCCAGCACTGAACCC	M13-CTCCATACACATGGAAGAGCAAT	GTAAAACGACGGCCAGT
371	79	PTPRJ-6	PTPRJ	6	CCDS7945.1	NM_002843	GGGAGCAGATATTGATGGAGC	M13-TCACTCAGAATCAGAATCACAGG	GTAAAACGACGGCCAGT
372	79	PTPRJ-7	PTPRJ	7	CCDS7945.1	NM_002843	M13-AGAGGAGGAAGGAACACTCCC	ACATCATGCATCCTGTGTCTG	GTAAAACGACGGCCAGT
373	79	PTPRJ-8	PTPRJ	8	CCDS7945.1	NM_002843	M13-GAGAGAGGGATCAGGTGTCCT	ATCTCTGCTTGATGGTTTCCA	GTAAAACGACGGCCAGT
374	79	PTPRJ-9	PTPRJ	9	CCDS7945.1	NM_002843	M13-CTCGACAGCACTTGGAGAGG	CTGGCCATCATTTAACCAGTG	GTAAAACGACGGCCAGT
375	79	PTPRJ-10	PTPRJ	10	CCDS7945.1	NM_002843	M13-ctgcaaggtcagcaccact	tcctggaattctacttaatctgtgc	GTAAAACGACGGCCAGT
376	79	PTPRJ-11	PTPRJ	11	CCDS7945.1	NM_002843	M13-CCCAGGATTCTGCTACTCCC	GTCCACACGTGCAGACCC	GTAAAACGACGGCCAGT
377	79	PTPRJ-12	PTPRJ	12	CCDS7945.1	NM_002843	M13-CTCTGCTCCTCACCAGTTTCC	TTACTCACATGCCTCAGTGGG	GTAAAACGACGGCCAGT
378	79	PTPRJ-13	PTPRJ	13	CCDS7945.1	NM_002843	CCCAACATCACCACCATGTAG	M13-GTCCCTGAGACGTGTCTGACC	GTAAAACGACGGCCAGT
379	79	PTPRJ-14	PTPRJ	14	CCDS7945.1	NM_002843	TTACAATGGGAAGCTGGAACC	M13-CACAGCTGGCCTTCTATGGAC	GTAAAACGACGGCCAGT
380	79	PTPRJ-15	PTPRJ	15	CCDS7945.1	NM_002843	TCTCTGGTGTTAGGGTCCCAG	M13-GCCAAATGCAGAACACTATGG	GTAAAACGACGGCCAGT
381	79	PTPRJ-16	PTPRJ	16	CCDS7945.1	NM_002843	M13-AATTAGCATTTGCAGCTTGGG	AAACTTCCAGATGGTCATGGTC	GTAAAACGACGGCCAGT
382	79	PTPRJ-17	PTPRJ	17	CCDS7945.1	NM_002843	M13-CCCTCTTGCCAAATTATACCC	CTCTGCGAACCCACAGTTG	GTAAAACGACGGCCAGT
383	79	PTPRJ-18	PTPRJ	18	CCDS7945.1	NM_002843	CCCTCTTGCCAAATTATACCC	M13-TTCTTTCAGCTACCTGCCACC	GTAAAACGACGGCCAGT
384	79	PTPRJ-19	PTPRJ	19	CCDS7945.1	NM_002843	M13-TCTATGGGACTGTTGGGCTG	AATGAATGGTTGTGGAAGTGG	GTAAAACGACGGCCAGT
385	79	PTPRJ-20	PTPRJ	20	CCDS7945.1	NM_002843	ATGTGACTTCTCTGTGCCACG	M13-GGGAAACAGCACATAGTCAACC	GTAAAACGACGGCCAGT
386	79	PTPRJ-21	PTPRJ	21	CCDS7945.1	NM_002843	M13-TTCGATGAAATCTTCAGTGTGC	CCAGCAGCAACGTAATAAACAG	GTAAAACGACGGCCAGT
387	79	PTPRJ-22	PTPRJ	22	CCDS7945.1	NM_002843	M13-TAGCCAGTCTCCCTTGTGAGG	TCCCAAGAAAGTAAATTTCCCAG	GTAAAACGACGGCCAGT
388	79	PTPRJ-23	PTPRJ	23	CCDS7945.1	NM_002843	M13-GCACTTTATCAGCTGCTGTGC	ACATTCCCTCTTAGGCTTTGC	GTAAAACGACGGCCAGT
389	79	PTPRJ-24	PTPRJ	24	CCDS7945.1	NM_002843	M13-TGTGACAGTGAAGGAAAGCAAG	ATTAGCTGGGCATGGTGTG	GTAAAACGACGGCCAGT
390	79	PTPRJ-25	PTPRJ	25	CCDS7945.1	NM_002843	GCTTGAACCGTTTGCTGTTG	M13-ATATGCAGCTTCATGCCCTC	GTAAAACGACGGCCAGT
391	79	PTPRN-1	PTPRN	1	CCDS2440.1	NM_002846	M13-ACGCAAATTAGCTTACGAGCC	TCATGACATTTCACCCTCACC	GTAAAACGACGGCCAGT
392	79	PTPRN-2	PTPRN	2	CCDS2440.1	NM_002846	M13-CAGGCCTGATTCCTACTCTCC	CCCAGTAGCCCTCTTCCTTTC	GTAAAACGACGGCCAGT
393	79	PTPRN-3	PTPRN	3	CCDS2440.1	NM_002846	M13-GAAGAAGGAAGACTTGCCTGG	CAAGATATGGGAAGGTGAGGC	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
394	79	PTPRN-4	PTPRN	4	CCDS2440.1	NM_002846	M13-TCACCCACTGAGTTTGTCCC	CCATTCCTGCACCTCTTTACC	GTAAAACGACGGCCAGT
395	79	PTPRN-5	PTPRN	5	CCDS2440.1	NM_002846	CCCGAATAGTTCTGCCTTGC	M13-CTGAGACCCTGGAGCCATC	GTAAAACGACGGCCAGT
396	79	PTPRN-6	PTPRN	6	CCDS2440.1	NM_002846	M13-CCTGTTCCACCAGGTAAGTCC	GCATAGATTGTCAGGGAAGGG	GTAAAACGACGGCCAGT
397	79	PTPRN-7	PTPRN	7	CCDS2440.1	NM_002846	M13-TCACTCACTCATCTGCATCCC	CCTGAAGCCTGACTCTTCCTC	GTAAAACGACGGCCAGT
398	79	PTPRN-8	PTPRN	8	CCDS2440.1	NM_002846	M13-CCAGGCTTAGGATGAGACCAG	ACCTTAGGCAATAACTTGCGG	GTAAAACGACGGCCAGT
399	79	PTPRN-9	PTPRN	9	CCDS2440.1	NM_002846	M13-GGTGTCCTCTCTGTACCCAGC	GGATTTCTGCCCTCTGCTTC	GTAAAACGACGGCCAGT
400	79	PTPRN-10a	PTPRN	10	CCDS2440.1	NM_002846	M13-AGAAGCAGAGGGCAGAAATCC	TTCAGTACAGCTGGGAGCATC	GTAAAACGACGGCCAGT
401	79	PTPRN-10b	PTPRN	10	CCDS2440.1	NM_002846	M13-GCCCAGCAGCAGAGGAAT	CAGGCGCTCCTTGTCTTG	GTAAAACGACGGCCAGT
402	79	PTPRN-11	PTPRN	11	CCDS2440.1	NM_002846	M13-CTTCCTTGCCTAAGATGCCC	GGTCTCCATCCTCTGTCTTGC	GTAAAACGACGGCCAGT
403	79	PTPRN-12a	PTPRN	12	CCDS2440.1	NM_002846	TATCTCTGCGACCTCAATCCC	M13-CCATCTGCTGGTGAGAAAGAG	GTAAAACGACGGCCAGT
404	79	PTPRN-12b	PTPRN	12	CCDS2440.1	NM_002846	M13-CCTGTCTTTGGCTGATGTGA	AACTGGGAGGACACACTGCT	GTAAAACGACGGCCAGT
405	79	PTPRN-13a	PTPRN	13	CCDS2440.1	NM_002846	M13-CTAATCTCCCAGCTTTGCCC	CCATTCAGTTCCGACCCTTAG	GTAAAACGACGGCCAGT
406	79	PTPRN-13b	PTPRN	13	CCDS2440.1	NM_002846	M13-CTCAGTGCTGCTCACTCTGG	GATGCCGGTTCTTTTTGATG	GTAAAACGACGGCCAGT
407	79	PTPRN-14	PTPRN	14	CCDS2440.1	NM_002846	M13-AGCCTAGGAGCCCAGAGTTG	GATCCTCCATGTATGCCTGTG	GTAAAACGACGGCCAGT
408	79	PTPRN-15a	PTPRN	15	CCDS2440.1	NM_002846	M13-GTGAAGGAATGGGATGGTGAG	GATGTAATCGCTCCGAGAAGG	GTAAAACGACGGCCAGT
409	79	PTPRN-15b	PTPRN	15	CCDS2440.1	NM_002846	M13-CAGTGTGTCCTCCCAGTTCA	CACACTGCTTGACACCATCC	GTAAAACGACGGCCAGT
410	79	PTPRN-16	PTPRN	16	CCDS2440.1	NM_002846	CTGACTTCCTGCCCTGTGAG	M13-CCTTGCTAGGATATCAGGCCC	GTAAAACGACGGCCAGT
411	79	PTPRN-17a	PTPRN	17	CCDS2440.1	NM_002846	M13-CTGACCCACTTGCTCTGACC	ATACGTGGTAGAGGGAGGCAC	GTAAAACGACGGCCAGT
412	79	PTPRN-17b	PTPRN	16	CCDS2440.1	NM_002846	M13-CCTACCAAGCAGAGCCAAAC	GGTCTGCACGTTCTTCAGGT	GTAAAACGACGGCCAGT
413	79	PTPRN-18	PTPRN	18	CCDS2440.1	NM_002846	M13-CAGGTGGGCTCTTAAAGGGAG	TGTATGAATCATGAGCAGGGC	GTAAAACGACGGCCAGT
414	79	PTPRN-19	PTPRN	19	CCDS2440.1	NM_002846	GTGGTTGGAGAGACCGAGAAG	M13-CCAGAAGTCAGAGGCCGAG	GTAAAACGACGGCCAGT
415	79	PTPRN-20	PTPRN	20	CCDS2440.1	NM_002846	M13-TCTCCAACCATCTTCCCTCTC	GTGCTGGATTTGGACTATGCC	GTAAAACGACGGCCAGT
416	79	PTPRN-21	PTPRN	21	CCDS2440.1	NM_002846	ATGAGCTTTCCTTCATCCTCG	M13-GACAACCTGCTCCTTCTGAGC	GTAAAACGACGGCCAGT
417	79	PTPRN-22a	PTPRN	22	CCDS2440.1	NM_002846	M13-CAAGGCTCTTTGCCTCCAG	GTAGGATGGTCATGGAGAGGG	GTAAAACGACGGCCAGT
418	79	PTPRN-22b	PTPRN	22	CCDS2440.1	NM_002846	GAAGGTGAACAAGTGCTACCG	M13-GGCTTTCCCTTCCTGACTCT	GTAAAACGACGGCCAGT
419	79	PTPRN-23	PTPRN	23	CCDS2440.1	NM_002846	ACCTTTCCCACCTGCTTCTG	M13-CTTCTGGCTTTCCCTTCCTG	GTAAAACGACGGCCAGT
420	79	PTPRN2-2	PTPRN2	2	CCDS5947.1	NM_002847	M13-TCTGGCTTCAGAATAATCGGC	TTCCATCCGCCTCCTCTC	GTAAAACGACGGCCAGT
421	79	PTPRN2-3	PTPRN2	3	CCDS5947.1	NM_002847	M13-CATTGCAAGGACGTGTGTGAC	GACGATCCCAGTAGGAAGCAC	GTAAAACGACGGCCAGT
422	79	PTPRN2-4	PTPRN2	4	CCDS5947.1	NM_002847	M13-TGAGAGGGAGGCTTACTTTGC	AGAAAGATGGTGGGTGCTTTG	GTAAAACGACGGCCAGT
423	79	PTPRN2-5	PTPRN2	5	CCDS5947.1	NM_002847	M13-CATGGTCATGGAGCAGCAAG	GACTAAGGAAACATGCCCAGG	GTAAAACGACGGCCAGT
424	79	PTPRN2-6	PTPRN2	6	CCDS5947.1	NM_002847	CGATGGAAATGTGACTCTTGC	M13-AAGAGCATGGTGCGTCTGTC	GTAAAACGACGGCCAGT
425	79	PTPRN2-7	PTPRN2	7	CCDS5947.1	NM_002847	ACAGGGTCAGGTGGATTTGAG	M13-CACTTGGTGAGCCAGCAGTC	GTAAAACGACGGCCAGT
426	79	PTPRN2-8	PTPRN2	8	CCDS5947.1	NM_002847	M13-CCTCACCTTTCGTATGGAGG	TCTTTGCATTTACCACGACTTTC	GTAAAACGACGGCCAGT
427	79	PTPRN2-9a	PTPRN2	9	CCDS5947.1	NM_002847	M13-ATAGACTGCACACACTTCGCC	CACACAGGAGCTTAGCCAGG	GTAAAACGACGGCCAGT
428	79	PTPRN2-9b	PTPRN2	9	CCDS5947.1	NM_002847	M13-GTCAGTCCATCGTCTGAGTGC	ATCAGGAGGAGCCACTGTCC	GTAAAACGACGGCCAGT
429	79	PTPRN2-10	PTPRN2	10	CCDS5947.1	NM_002847	TTGTTGCTGGAAACTCAGGTG	M13-GCTGCTGAAATCACCTTTCAC	GTAAAACGACGGCCAGT
430	79	PTPRN2-11	PTPRN2	11	CCDS5947.1	NM_002847	M13-AATGGAAACAAAGGTCATGGTG	GTGAGTCTCTCTCTGCCCTGG	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
431	79	PTPRN2-12	PTPRN2	12	CCDS5947.1	NM_002847	M13-TCCATTAAGGTAGGCGGGTC	ACCTTGGCTGAATTAACCTGC	GTAAAACGACGGCCAGT
432	79	PTPRN2-13	PTPRN2	13	CCDS5947.1	NM_002847	AGTTGCATTTGGAGACGTGTG	M13-GATACAGGAACAACTGCTGGG	GTAAAACGACGGCCAGT
433	79	PTPRN2-14	PTPRN2	14	CCDS5947.1	NM_002847	M13-GCCTGAACCTTGGATCTTAGC	CAGATGCTGGGTGTTGCAG	GTAAAACGACGGCCAGT
434	79	PTPRN2-15	PTPRN2	15	CCDS5947.1	NM_002847	M13-TTTCACTTAACGGTTGCATGG	CTGGTACACACAGGTCAGCAC	GTAAAACGACGGCCAGT
435	79	PTPRN2-16	PTPRN2	16	CCDS5947.1	NM_002847	CATTCAGAAGGGTGTGAGCAG	M13-AGAACCTTCCCACGTGATTTG	GTAAAACGACGGCCAGT
436	79	PTPRN2-18	PTPRN2	18	CCDS5947.1	NM_002847	M13-GTGCATTCAGAGATGCTCAGG	TAACGAATCCCATTCGGAGG	GTAAAACGACGGCCAGT
437	79	PTPRN2-19	PTPRN2	19	CCDS5947.1	NM_002847	M13-CTCAGTGCCTGAGGTTCGG	AAATCGCTCACGATTAACACG	GTAAAACGACGGCCAGT
438	79	PTPRN2-20	PTPRN2	20	CCDS5947.1	NM_002847	M13-TCAAACACACAGACCTTGCG	AACGCCCAATTGTATTTACCC	GTAAAACGACGGCCAGT
439	79	PTPRN2-21	PTPRN2	21	CCDS5947.1	NM_002847	M13-CATCCCACAAGCTACAAGCTG	CTGCAAACCACCTTCCTACG	GTAAAACGACGGCCAGT
440	79	PTPRN2-22	PTPRN2	22	CCDS5947.1	NM_002847	M13-TGGCTAGCAGGAGATTGACAG	TAGGACTTGAGATGTGGCTGC	GTAAAACGACGGCCAGT
441	79	PTPRN2-23	PTPRN2	23	CCDS5947.1	NM_002847	AATTTCTTTCTGCGAAATGGC	M13-TGACTACGGGAGAGCTAAGGG	GTAAAACGACGGCCAGT
442	79	PTPRO-1	PTPRO	1	CCDS8675.1	NM_030667	M13-CAGTTCGCCATTGTGAGCC	CCTCTCAAGACCACCAGGAAC	GTAAAACGACGGCCAGT
443	79	PTPRO-2	PTPRO	2	CCDS8675.1	NM_030667	M13-TTTAAGAAATAAGGCTTACCATAAACA	GTGGAGTCTGTCAATTCGAGC	GTAAAACGACGGCCAGT
444	79	PTPRO-3	PTPRO	3	CCDS8675.1	NM_030667	TGAGGAGTTTAGTGCCCACAG	M13-GAACCAGATGTTCTAGGCTTCC	GTAAAACGACGGCCAGT
445	79	PTPRO-4	PTPRO	4	CCDS8675.1	NM_030667	M13-GCCATAATTGTTTCAAACTTTCCA	GGGTAAGTCAGTTAATTATAACCTTTGG	GTAAAACGACGGCCAGT
446	79	PTPRO-5a	PTPRO	5	CCDS8675.1	NM_030667	M13-TTTCCGTTCGTATCGTAAACTTG	TCTGCTCTCAGTCTGCATTGG	GTAAAACGACGGCCAGT
447	79	PTPRO-5b	PTPRO	5	CCDS8675.1	NM_030667	TTTCCGTTCGTATCGTAAACTTG	M13-TCTGCTCTCAGTCTGCATTGG	GTAAAACGACGGCCAGT
448	79	PTPRO-5c	PTPRO	5	CCDS8675.1	NM_030667	tgcttgtgtacctgactcattaag	M13-AAAGCAGTGGGTGGTTTGG	GTAAAACGACGGCCAGT
449	79	PTPRO-6	PTPRO	6	CCDS8675.1	NM_030667	TTCATTAATCGACTTGTCTATACCCAG	M13-TCTGAGCATCATTAATCCCACC	GTAAAACGACGGCCAGT
450	79	PTPRO-7	PTPRO	7	CCDS8675.1	NM_030667	GACCTGAAGAGTTGCCAGTCC	M13-CTGGCTTCCTACAATTGCCTC	GTAAAACGACGGCCAGT
451	79	PTPRO-8	PTPRO	8	CCDS8675.1	NM_030667	M13-TTCTAGGTTCCCTTCAATGTTCAC	TGATAATGATTTGAGCTCGCAC	GTAAAACGACGGCCAGT
452	79	PTPRO-9	PTPRO	9	CCDS8675.1	NM_030667	M13-GAAGTTTGAGGCCATTGCTAA	TGTAAATTGCTCAGTCTTGGCT	GTAAAACGACGGCCAGT
453	79	PTPRO-10	PTPRO	10	CCDS8675.1	NM_030667	M13-AATAAGGACTGTTTCGCATGTGT	GGGTGAATGACTGGCACTTTC	GTAAAACGACGGCCAGT
454	79	PTPRO-11	PTPRO	11	CCDS8675.1	NM_030667	M13-GTTACCGGGACTATCGTGTGC	TGACGTGTCAATAAATGATTGCTTAG	GTAAAACGACGGCCAGT
455	79	PTPRO-12	PTPRO	12	CCDS8675.1	NM_030667	M13-AACAGAGAGGGAATGTGTCTGC	TGAATTGAGGAGCTCTTGCTG	GTAAAACGACGGCCAGT
456	79	PTPRO-13	PTPRO	13	CCDS8675.1	NM_030667	GCTCTTACCTACCTATATTTGAATTGG	M13-TGCTGTTAATTTCTATCAGTGAAACAC	GTAAAACGACGGCCAGT
457	79	PTPRO-14	PTPRO	14	CCDS8675.1	NM_030667	M13-AAGGGAATTGGTCAGATGGG	GAAGCTTGGGATTTCTTGGTG	GTAAAACGACGGCCAGT
458	79	PTPRO-15	PTPRO	15	CCDS8675.1	NM_030667	M13-ATCATCGTAAGCTCACTGCCC	TTTGTGTAAACAAGCAATCCTTTG	GTAAAACGACGGCCAGT
459	79	PTPRO-16a	PTPRO	16	CCDS8675.1	NM_030667	M13-TTTAATGCTGTGATGATAAGCTGG	CACCACTGTTTCAGTCCCTTG	GTAAAACGACGGCCAGT
460	79	PTPRO-16b	PTPRO	16	CCDS8675.1	NM_030667	TCTGCAGATGGCTAGGGAGT	M13-CTGCAGCAAAGTGTGGGATA	GTAAAACGACGGCCAGT
461	79	PTPRO-16c	PTPRO	16	CCDS8675.1	NM_030667	M13-ggttctgtttggttccctgt	cgctatacaacttaggtgtgcaa	GTAAAACGACGGCCAGT
462	79	PTPRO-17	PTPRO	17	CCDS8675.1	NM_030667	GCAAATGGGAAGTATAAAGTGCAG	M13-GACAAGCAATCTTTAATTGGAACG	GTAAAACGACGGCCAGT
463	79	PTPRO-18	PTPRO	18	CCDS8675.1	NM_030667	GAGATTTCTCCTATCAAGGAAGCTG	M13-ACATGACCGCAACACAAACC	GTAAAACGACGGCCAGT
464	79	PTPRO-19	PTPRO	19	CCDS8675.1	NM_030667	M13-GCAATGTCATATAGCAAAGGGC	AATCTCAGACGTGGCCTTGAG	GTAAAACGACGGCCAGT
465	79	PTPRO-20a	PTPRO	20	CCDS8675.1	NM_030667	TTTCAAGGACAGGAGAGCTGG	M13-TGTTTGACACATCCATATAGCCC	GTAAAACGACGGCCAGT
466	79	PTPRO-20b	PTPRO	20	CCDS8675.1	NM_030667	M13-CCGGTTCAACTGGATGACTT	TGGTCACATTTCACCCTCCT	GTAAAACGACGGCCAGT
467	79	PTPRO-21	PTPRO	21	CCDS8675.1	NM_030667	CATAGGTGTGTGATCCTTTGCC	M13-ACAGCAAGCATTTCATCAACG	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
468	79	PTPRO-22	PTPRO	22	CCDS8675.1	NM_030667	M13-TGTTTCATCTTCACCACGGTC	CGCTGGGTTAGGGTCTCC	GTAAAACGACGGCCAGT
469	79	PTPRO-23	PTPRO	23	CCDS8675.1	NM_030667	TAGCAGAGTCCTGGGTCATCC	M13-AAGGGCTTATGGAATGGTGAG	GTAAAACGACGGCCAGT
470	79	PTPRO-24	PTPRO	24	CCDS8675.1	NM_030667	ACTTGAAGCCGAGAGGCAG	M13-TTTGAAGCATATCATTGAATAATGG	GTAAAACGACGGCCAGT
471	79	PTPRO-25	PTPRO	25	CCDS8675.1	NM_030667	AAGCCATGATGTTCTAAGCTCTG	M13-TTTGTCCCATCCATCACATC	GTAAAACGACGGCCAGT
472	79	PTPRS-1a	PTPRS	1	CCDS12140.1	NM_002850	CTCCTCCATGAAGGTCTCCTG	M13-CACACACACAGCCATAAATGC	GTAAAACGACGGCCAGT
473	79	PTPRS-1b	PTPRS	1	CCDS12140.1	NM_002850	catcctggaatcggacagtg	M13-caggagtcacagcacagcac	GTAAAACGACGGCCAGT
474	79	PTPRS-2	PTPRS	2	CCDS12140.1	NM_002850	ATCCTTGCTTTCCTCCTCCTC	M13-AACGTGTCCACGAAGTCCAC	GTAAAACGACGGCCAGT
475	79	PTPRS-3a	PTPRS	3	CCDS12140.1	NM_002850	TAGCCCAGCCTAGACAGGAAC	M13-AACACAAAGCAGGAGGGTTTG	GTAAAACGACGGCCAGT
476	79	PTPRS-3b	PTPRS	3	CCDS12140.1	NM_002850	TCACAAACTTGCAGCCTGAG	M13-CACCGTGTATTTGACGATGG	GTAAAACGACGGCCAGT
477	79	PTPRS-4a	PTPRS	4	CCDS12140.1	NM_002850	ACTGGCTGTAAAGGATGGCAC	M13-CTGTCTGTCCTCCAGTAGTCCC	GTAAAACGACGGCCAGT
478	79	PTPRS-4b	PTPRS	4	CCDS12140.1	NM_002850	ACGTATGTGTTCCGGCTTG	M13-AGGTGCGTGATGAGCTTCTT	GTAAAACGACGGCCAGT
479	79	PTPRS-5	PTPRS	5	CCDS12140.1	NM_002850	GCCAAGCTAGGGCTTCCAG	M13-AACTAAGGCCCAGAGAGGGAC	GTAAAACGACGGCCAGT
480	79	PTPRS-6a	PTPRS	6	CCDS12140.1	NM_002850	M13-TCTCCTCCGCATCCTGTC	CCCACCTGTGCCTGAAGTC	GTAAAACGACGGCCAGT
481	79	PTPRS-6b	PTPRS	6	CCDS12140.1	NM_002850	M13-GCCCAAGAACTTCAAGGTGA	GATCCATGTCCTCTGGGCTA	GTAAAACGACGGCCAGT
482	79	PTPRS-7a	PTPRS	7	CCDS12140.1	NM_002850	CTGGGCCATAGTTTGTTACCC	M13-TCCGGTTCCATGGTGTAGTAG	GTAAAACGACGGCCAGT
483	79	PTPRS-7b	PTPRS	7	CCDS12140.1	NM_002850	M13-TAAATCCAAGAGCCAAGACGG	TTAAAGCACCGTGCATAACCC	GTAAAACGACGGCCAGT
484	79	PTPRS-8	PTPRS	8	CCDS12140.1	NM_002850	M13-AGGTGGACAGGTGACAATGG	GCAGCACACATAGGGACAAAG	GTAAAACGACGGCCAGT
485	79	PTPRS-9	PTPRS	9	CCDS12140.1	NM_002850	CCTCATCCCTCTCTGTCCC	M13-GAACAAAGCGGAGACAGGC	GTAAAACGACGGCCAGT
486	79	PTPRS-10	PTPRS	10	CCDS12140.1	NM_002850	AGGGACTTGGGACAGGACAG	M13-AAACTGAGCCTTAAGCCCTGC	GTAAAACGACGGCCAGT
487	79	PTPRS-11	PTPRS	11	CCDS12140.1	NM_002850	M13-GACTCATCCTGGAGCTGGG	GCATTGAATCTTGGATGACCC	GTAAAACGACGGCCAGT
488	79	PTPRS-12	PTPRS	12	CCDS12140.1	NM_002850	M13-GAGGCCTGAGTCAGCAACTG	GCCTCTGTAGCCGTGAGATG	GTAAAACGACGGCCAGT
489	79	PTPRS-13	PTPRS	13	CCDS12140.1	NM_002850	M13-GATCTGGAAGAGGTGAGGGC	AGCTGCCTGTGACTGACCAC	GTAAAACGACGGCCAGT
490	79	PTPRS-14	PTPRS	14	CCDS12140.1	NM_002850	CACCAGGGTCAAGGTTCTAGG	M13-TCTCTGAGACAACTCCTCCCTC	GTAAAACGACGGCCAGT
491	79	PTPRS-15	PTPRS	15	CCDS12140.1	NM_002850	TTCCAGAGGAGACCAAAGCTC	M13-CCATGGACCCGTATGACTAGG	GTAAAACGACGGCCAGT
492	79	PTPRS-16	PTPRS	16	CCDS12140.1	NM_002850	M13-GAAACCCTAGTCATACGGGTCC	TGGAGGTATTTGGGAATCCAG	GTAAAACGACGGCCAGT
493	79	PTPRS-17	PTPRS	17	CCDS12140.1	NM_002850	CCTTCTAACCACAGCTCACCC	M13-GCTTGTTCACTTCCAGGTTGG	GTAAAACGACGGCCAGT
494	79	PTPRS-18a	PTPRS	18	CCDS12140.1	NM_002850	M13-TCTCCCAGGAGTATGAGGTGAG	TATCTAAAGATGCCCAGTGGC	GTAAAACGACGGCCAGT
495	79	PTPRS-18b	PTPRS	18	CCDS12140.1	NM_002850	M13-CCAAATGCCTCCTGAACAAT	ACACCATACGCCAGAAGTCC	GTAAAACGACGGCCAGT
496	79	PTPRS-19	PTPRS	19	CCDS12140.1	NM_002850	TGAAGTACACGTCCCATGGTC	M13-GGCAAGAGAACAGGTGTCAGC	GTAAAACGACGGCCAGT
497	79	PTPRS-20	PTPRS	20	CCDS12140.1	NM_002850	M13-ACTTCTGGCGTATGGTGTGG	TAGTCAGCCTGGGTAGACACG	GTAAAACGACGGCCAGT
498	79	PTPRS-21	PTPRS	21	CCDS12140.1	NM_002850	M13-GGCCACTTGGGCATCTTC	ATGACGATAAAGCAGCCTGTG	GTAAAACGACGGCCAGT
499	79	PTPRS-22	PTPRS	22	CCDS12140.1	NM_002850	ACTGCAGGTACGTCCACCC	M13-CTGCCACCACCTTCTAGTCC	GTAAAACGACGGCCAGT
500	79	PTPRS-23	PTPRS	23	CCDS12140.1	NM_002850	M13-ACTAGAAGGTGGTGGCAGGG	CAGCTCTGTCTCCCACAAGAC	GTAAAACGACGGCCAGT
501	79	PTPRS-24	PTPRS	24	CCDS12140.1	NM_002850	M13-GTGTAGCTGTCACTGGCTTGG	AAGTACTGGTAGCGGGCAGAG	GTAAAACGACGGCCAGT
502	79	PTPRS-25	PTPRS	25	CCDS12140.1	NM_002850	M13-CATGCTGTGGGAGAACAATTC	TTGTATCCATCACCAACCAGG	GTAAAACGACGGCCAGT
503	79	PTPRS-26	PTPRS	26	CCDS12140.1	NM_002850	GGGTGAAGATAGGGAGGATGG	M13-CTGATCTGACCACCCGATTC	GTAAAACGACGGCCAGT
504	79	PTPRS-27	PTPRS	27	CCDS12140.1	NM_002850	M13-CCCATCTGGGCTGTTAGAGTC	AGGTGGCTGTACCCATCTCAC	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
505	79	PTPRS-28	PTPRS	28	CCDS12140.1	NM_002850	M13-GCCAAAGAGACCTTCTGCAAG	CTCGGAAATGGTGCAGAAAC	GTAAAACGACGGCCAGT
506	79	PTPRT-1a	PTPRT	1	CCDS42874.1	NM_007050	M13-AGCCTCCCGCCTCAGTTC	GAGCCCACACAACTTTCTCCTC	GTAAAACGACGGCCAGT
507	79	PTPRT-1b	PTPRT	1	CCDS42874.1	NM_007050	M13-gttaggactcgggggacac	gcccacacaactttctcctc	GTAAAACGACGGCCAGT
508	79	PTPRT-2	PTPRT	2	CCDS42874.1	NM_007050	M13-AGCCGACGAGACAGAGGTAAC	ATTCAGCCTTGGTTTGACCAC	GTAAAACGACGGCCAGT
509	79	PTPRT-3	PTPRT	3	CCDS42874.1	NM_007050	M13-CTTGATCTCTGGCCACTCCTC	GACCTAGCACCTGTAGGGAGAG	GTAAAACGACGGCCAGT
510	79	PTPRT-4	PTPRT	4	CCDS42874.1	NM_007050	CAGGGTAGCGTGCTGTCTTAAC	M13-GAAGGGATTGCAGGCTCTATG	GTAAAACGACGGCCAGT
511	79	PTPRT-5	PTPRT	5	CCDS42874.1	NM_007050	TCTTAAGTGCCAGTTCCACCC	M13-CTTGTGTTGCCATAGAGCTGC	GTAAAACGACGGCCAGT
512	79	PTPRT-6	PTPRT	6	CCDS42874.1	NM_007050	M13-ATATCCGTGTTGGGAGTCACC	ACCATAGTTTCTCCCGTTTGG	GTAAAACGACGGCCAGT
513	79	PTPRT-7	PTPRT	7	CCDS42874.1	NM_007050	M13-CCTTGTCGTCATGTGCTTGTAG	AGGCAAGAGGAAAGCCAGTC	GTAAAACGACGGCCAGT
514	79	PTPRT-8	PTPRT	8	CCDS42874.1	NM_007050	M13-TGTGTTCCCTGTTGTAGCAGAA	AAGCCTCATAACTGACTGCCAT	GTAAAACGACGGCCAGT
515	79	PTPRT-9	PTPRT	9	CCDS42874.1	NM_007050	GAGAACGTACAGCCCATCAGAC	M13-TGGGTATTCACCAATGTCAGG	GTAAAACGACGGCCAGT
516	79	PTPRT-10	PTPRT	10	CCDS42874.1	NM_007050	M13-CAGAATCTGCTGGCCAAGTTC	CTGGATCGTCCTAATTCCACC	GTAAAACGACGGCCAGT
517	79	PTPRT-11	PTPRT	11	CCDS42874.1	NM_007050	AGGCCTGGAAGGCTTCTTATC	M13-TCACATGATTCAACTGGAGGC	GTAAAACGACGGCCAGT
518	79	PTPRT-12	PTPRT	12	CCDS42874.1	NM_007050	M13-AGGAGAAGTTGGGTTGACACC	GCCCTGCTGACTTATCATTTG	GTAAAACGACGGCCAGT
519	79	PTPRT-13	PTPRT	13	CCDS42874.1	NM_007050	GGGAATGAGGTTTATGAGATGG	M13-TGTTGCCTAATCTTTCTCTGTGTG	GTAAAACGACGGCCAGT
520	79	PTPRT-14	PTPRT	14	CCDS42874.1	NM_007050	AAGTACCTGGCATGTCGTGG	M13-GGTGGAAAGACTGCTGATTCC	GTAAAACGACGGCCAGT
521	79	PTPRT-15	PTPRT	15	CCDS42874.1	NM_007050	M13-CCTCACAAGGAATTGGTCCTC	GAAGATCCCTGCTGGACAATG	GTAAAACGACGGCCAGT
522	79	PTPRT-16	PTPRT	16	CCDS42874.1	NM_007050	AACAGCCAACATGAAACATGG	M13-ACAGACACTTGGTTGGTGCAG	GTAAAACGACGGCCAGT
523	79	PTPRT-17	PTPRT	17	CCDS42874.1	NM_007050	M13-TAGAACACATGCATTGTCGGG	GCAAGCATCCATACCCTATGC	GTAAAACGACGGCCAGT
524	79	PTPRT-18	PTPRT	18	CCDS42874.1	NM_007050	M13-GTTGAGTCCCAAGTTGGTTCC	TGTAGCAAGGCTTTAGTGCCC	GTAAAACGACGGCCAGT
525	79	PTPRT-19	PTPRT	19	CCDS42874.1	NM_007050	M13-GGGTCTTACTTTGCCCTGTTG	CTAGGGATGGCAGTAAGGCTG	GTAAAACGACGGCCAGT
526	79	PTPRT-20	PTPRT	20	CCDS42874.1	NM_007050	AATGGGAGCAGTAACTGAGGG	M13-ATCAAGGAGGATCCAGACTGC	GTAAAACGACGGCCAGT
527	79	PTPRT-21	PTPRT	21	CCDS42874.1	NM_007050	M13-TTGCCACTTCTCTGGGAATAAC	GCTGGTGGAAACTCATTCCTC	GTAAAACGACGGCCAGT
528	79	PTPRT-22	PTPRT	22	CCDS42874.1	NM_007050	CACCAGTGTGGAGACTTGACC	M13-GAAGGGAAAGGACATTGCTTG	GTAAAACGACGGCCAGT
529	79	PTPRT-23	PTPRT	23	CCDS42874.1	NM_007050	TTGGGTTTATTTGGATGGGAC	M13-CTGGACGTAGAGCAGACCCTC	GTAAAACGACGGCCAGT
530	79	PTPRT-24	PTPRT	24	CCDS42874.1	NM_007050	M13-GCAGCAGCTATGGCTCCAC	GATGTATGCCACCATGACCAG	GTAAAACGACGGCCAGT
531	79	PTPRT-25	PTPRT	25	CCDS42874.1	NM_007050	GGGATAGGGCTGAATGCTAGG	M13-CTCTCACACCCAGGTCCTTTC	GTAAAACGACGGCCAGT
532	79	PTPRT-26	PTPRT	26	CCDS42874.1	NM_007050	AAATTTGGCCCTTTGGGTTAC	M13-TTACTGGAAGCTTGATGCTGG	GTAAAACGACGGCCAGT
533	79	PTPRT-27	PTPRT	27	CCDS42874.1	NM_007050	M13-TAGGCGAGTTAGGCTGAGTTG	AGAGCCCACCTTGTGTCTAGG	GTAAAACGACGGCCAGT
534	79	PTPRT-28	PTPRT	28	CCDS42874.1	NM_007050	M13-CTCAGTCCAGGCCTCATCATC	AATGGCTTGTCTGATGCTCG	GTAAAACGACGGCCAGT
535	79	PTPRT-29	PTPRT	29	CCDS42874.1	NM_007050	GTGCCAATGCACTCCAGG	M13-AGCACAACACAGACTCTTGGC	GTAAAACGACGGCCAGT
536	79	PTPRT-30	PTPRT	30	CCDS42874.1	NM_007050	CACCATGATGCTGCAGTCC	M13-TTGAGGGATGTTGAGTTGTGG	GTAAAACGACGGCCAGT
537	79	PTPRT-31	PTPRT	31	CCDS42874.1	NM_007050	AGGCTAAAGCCTTCACCATTG	M13-TTAGCAGCCAGGTGTTGAGTG	GTAAAACGACGGCCAGT
538	79	PTPRT-32	PTPRT	32	CCDS42874.1	NM_007050	GTAGAAGCAGGCATCAAGCAG	M13-CCCAGTTACTGCCATTCACAC	GTAAAACGACGGCCAGT
539	79	TNS1-1	TNS1	1	CCDS2407.1	NM_022648	GTCACACAGGGTGTGTATGGG	M13-TTGAAGACTCAGGCACGAGAG	GTAAAACGACGGCCAGT
540	79	TNS1-2a	TNS1	2	CCDS2407.1	NM_022648	CCATGGTTCTCTCTCTCCTCG	M13-GACCTGGGTGGAAAGTCACTG	GTAAAACGACGGCCAGT
541	79	TNS1-2b	TNS1	2	CCDS2407.1	NM_022648	M13-CCATGGTTCTCTCTCTCCTCG	GACCTGGGTGGAAAGTCACTG	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
542	79	TNS1-3	TNS1	3	CCDS2407.1	NM_022648	M13-ACAGTGAGTCAGTGCCAGGG	TCATCCAAGGACACATTCAGG	GTAAAACGACGGCCAGT
543	79	TNS1-4	TNS1	4	CCDS2407.1	NM_022648	M13-TTCTCCCTTAAATCCACACCC	GTCCTCATCGCTTCTCATTCC	GTAAAACGACGGCCAGT
544	79	TNS1-5	TNS1	5	CCDS2407.1	NM_022648	M13-TGTCTTCCCTCCAGGACAAAG	CTAGGCACAGCTATCCCATCC	GTAAAACGACGGCCAGT
545	79	TNS1-6	TNS1	6	CCDS2407.1	NM_022648	GGTCTAGGGCAATGTTCTTGG	M13-TCGGGCTGTCTGTTACTACCC	GTAAAACGACGGCCAGT
546	79	TNS1-7	TNS1	7	CCDS2407.1	NM_022648	M13-TCCCTTCACTGTCTCCTCTGC	CTAGTCTGGCTGTCTCCTGGG	GTAAAACGACGGCCAGT
547	79	TNS1-8	TNS1	8	CCDS2407.1	NM_022648	GGGCTGAAAGGACAGAGTCAG	M13-AGCCCAGGAGGAGTACCTGTC	GTAAAACGACGGCCAGT
548	79	TNS1-9	TNS1	9	CCDS2407.1	NM_022648	M13-GGTGTTGATGAGCTCTCCCTC	CCCACCATATCGTCTCAAACTG	GTAAAACGACGGCCAGT
549	79	TNS1-10	TNS1	10	CCDS2407.1	NM_022648	ACCTCAGGCAAGTAGGACAGG	M13-TGATCACTGTGGAACAGACCAG	GTAAAACGACGGCCAGT
550	79	TNS1-11	TNS1	11	CCDS2407.1	NM_022648	GTCCAGCTTAAGCCACTGGTC	M13-AGGCCAAGAGAAGCAAGGTC	GTAAAACGACGGCCAGT
551	79	TNS1-12a	TNS1	12	CCDS2407.1	NM_022648	M13-CTGGCAGAGTGGATGATACCC	TCATCGTCCAGGATGTCTGTC	GTAAAACGACGGCCAGT
552	79	TNS1-12b	TNS1	12	CCDS2407.1	NM_022648	M13-GGAACACACGCTTTCTGTGAG	CTCTGGTAGCCAGCTAAACCC	GTAAAACGACGGCCAGT
553	79	TNS1-12c	TNS1	12	CCDS2407.1	NM_022648	ACACTCTCTTCTCTGGACGGG	M13-ACTGTTCAATCTCCTGCTGGG	GTAAAACGACGGCCAGT
554	79	TNS1-12d	TNS1	12	CCDS2407.1	NM_022648	AGTGACCACCTCCCACTATGC	M13-GGAGGGACAGACTCCAGAGAG	GTAAAACGACGGCCAGT
555	79	TNS1-12e	TNS1	12	CCDS2407.1	NM_022648	ACACAAGTCCCAGAGTGTCCC	M13-ACCAGTGAAAGCAACATCTGC	GTAAAACGACGGCCAGT
556	79	TNS1-12f	TNS1	12	CCDS2407.1	NM_022648	CTACCCAGAGGCCCTGTCC	M13-GGGAACTCAGGGAGACTGG	GTAAAACGACGGCCAGT
557	79	TNS1-12g	TNS1	12	CCDS2407.1	NM_022648	M13-CCAGGTTCATGTCAATGGTG	GCCTGCTGGCTACAAGACTC	GTAAAACGACGGCCAGT
558	79	TNS1-13	TNS1	13	CCDS2407.1	NM_022648	M13-CCTCTGAGCTAGGAGGCACTG	TTGACCATCAGGTTTCTGGAG	GTAAAACGACGGCCAGT
559	79	TNS1-14	TNS1	14	CCDS2407.1	NM_022648	GGGCTGGTTAACTCACTGTCC	M13-ACAAGCAATGGAAGAGAAGGG	GTAAAACGACGGCCAGT
560	79	TNS1-15	TNS1	15	CCDS2407.1	NM_022648	M13-CTCACTAAGCGTGCCCTCAC	AAGGCTGCAAGGAAATCTGTC	GTAAAACGACGGCCAGT
561	79	TNS1-16	TNS1	16	CCDS2407.1	NM_022648	TGAACTCAGAAAGCTGCTCCC	M13-GCTCCGAGGCATAGTTGAGTC	GTAAAACGACGGCCAGT
562	79	TNS1-17	TNS1	17	CCDS2407.1	NM_022648	TCTGTGGACAGCGCAAATC	M13-CCTGAGTCCCAGTGAGGAAAG	GTAAAACGACGGCCAGT
563	79	TNS1-18	TNS1	18	CCDS2407.1	NM_022648	GGAGTCCAGGAAGCTGTGTTC	M13-ATAGGCAACAGATCCAGGAGG	GTAAAACGACGGCCAGT
564	79	TNS1-19	TNS1	19	CCDS2407.1	NM_022648	GCCTACTGCTTAACCTCCCTG	M13-TCATCTGGTGATGGCTCAAAC	GTAAAACGACGGCCAGT
565	79	TNS1-19a	TNS1	19	CCDS2407.1	NM_022648	M13-CGTCTGCCCAGAGAAACTACC	GAACCACAGATCCAGACCCTC	GTAAAACGACGGCCAGT
566	79	TNS1-19b	TNS1	19	CCDS2407.1	NM_022648	M13-GTCTACCAGGTTTCTGGCCTC	AGAGTGTGGGAGAAGGAGACG	GTAAAACGACGGCCAGT
567	79	TNS1-19c	TNS1	19	CCDS2407.1	NM_022648	CCTACTACCCTGGCCTGAGC	M13-CCAGAAGTCAGTGATTCACCC	GTAAAACGACGGCCAGT
568	79	TNS1-20	TNS1	20	CCDS2407.1	NM_022648	M13-GGGCCAGGACTTTGATGTATG	CCTACTGTCCAGCTTCAACCC	GTAAAACGACGGCCAGT
569	79	TNS1-21	TNS1	21	CCDS2407.1	NM_022648	AAAGAACGAAGGTCGGTAGGC	M13-TGATGGGAGTTAAGGTCCTGC	GTAAAACGACGGCCAGT
570	79	TNS1-22	TNS1	22	CCDS2407.1	NM_022648	GTCAGAGATTGGGAAAGCAGG	M13-GCCTGTCAGAAAGAACTTGGG	GTAAAACGACGGCCAGT
571	79	TNS1-23	TNS1	23	CCDS2407.1	NM_022648	M13-AGGGTAGAGGTGGAGGTTTCC	TCCTGAACAATCTGGCAAGTC	GTAAAACGACGGCCAGT
572	79	TNS1-24	TNS1	24	CCDS2407.1	NM_022648	M13-GTTGCAGAGCTCACCTTCAGC	CCAGATCCATTCTTCAGGGAG	GTAAAACGACGGCCAGT
573	79	TNS1-25	TNS1	25	CCDS2407.1	NM_022648	M13-CTCCCTGAAGAATGGATCTGG	AAATGTGTGGGTACACGGATG	GTAAAACGACGGCCAGT
574	79	TNS1-26	TNS1	26	CCDS2407.1	NM_022648	M13-AGTTGTGTGGACCTGCGATAG	TTACTCACACATGGGCAGACC	GTAAAACGACGGCCAGT
575	79	TNS1-27	TNS1	27	CCDS2407.1	NM_022648	GAATGCATCTGTGTGATCTTGG	M13-AGCCCTGGTTTCTAAATGTGC	GTAAAACGACGGCCAGT
576	79	TNS1-28	TNS1	28	CCDS2407.1	NM_022648	ACCTCTCTGAGTCCCTGATGC	M13-AGAGTGGTCAGGATTCATGGG	GTAAAACGACGGCCAGT
577	79	TNS4-1a	TNS4	1	CCDS11368.1	NM_032865	M13-GGAGCTCCTGGTTAGCAAGTG	a	GTAAAACGACGGCCAGT
578	79	TNS4-1b	TNS4	1	CCDS11368.1	NM_032865	M13-TAAACTGCAGAGGTCACCACC	TTGGTTAGGTTTGCACAGCAC	GTAAAACGACGGCCAGT

	# of Tumors sequenced	Primer	Gene	Exon	CCDS accession	Ref Seq accession	Forward Primer	Reverse Primer	Sequencing Primer
579	79	TNS4-2a	TNS4	2	CCDS11368.1	NM_032865	GATCTGAAGCCTGGGTCTGTC	M13-CTCCAGTCTTGGAGAAGCCAC	GTAAAACGACGGCCAGT
580	79	TNS4-2b	TNS4	2	CCDS11368.1	NM_032865	GAGACACGAAGCAGCAGTGAG	M13-AAATGCTTGAGGACAGCTTGAG	GTAAAACGACGGCCAGT
581	79	TNS4-3	TNS4	3	CCDS11368.1	NM_032865	GTTGCCCTAACACCCTGTCTG	M13-AATGTGTTGACTGGCTGTTGC	GTAAAACGACGGCCAGT
582	79	TNS4-4	TNS4	4	CCDS11368.1	NM_032865	M13-TGGTGGTTGAATGAAACCTTG	CTTCCCAGGACCCACTATTTG	GTAAAACGACGGCCAGT
583	79	TNS4-5	TNS4	5	CCDS11368.1	NM_032865	M13-CCGAGGAAGTAGGAACCACAG	GTCACCCTGAAAGCTAGTGCC	GTAAAACGACGGCCAGT
584	79	TNS4-6	TNS4	6	CCDS11368.1	NM_032865	ACTACAGGCATGTGAACCACG	M13-CCCTGCATGAGTAGAGCTTCC	GTAAAACGACGGCCAGT
585	79	TNS4-7	TNS4	7	CCDS11368.1	NM_032865	M13-AAGTCTCCGTTGTGAGCTGAG	CACAGCTAGGAGGTGGAGATG	GTAAAACGACGGCCAGT
586	79	TNS4-8	TNS4	8	CCDS11368.1	NM_032865	M13-GAGGTGGGAGATCTTCAAAGG	AAAGCTGAGATGGGAAACACG	GTAAAACGACGGCCAGT
587	79	TNS4-9	TNS4	9	CCDS11368.1	NM_032865	M13-CCACACACCCACTTTCTGTTG	CTGCAGCTGTCTCAGCTATCC	GTAAAACGACGGCCAGT
588	79	TNS4-10	TNS4	10	CCDS11368.1	NM_032865	GAGACTTCTTGGAGGACAGGG	M13-CCTACCCTCATTCTGTCACCC	GTAAAACGACGGCCAGT
589	79	TNS4-11	TNS4	11	CCDS11368.1	NM_032865	M13-CGGAAGTAAGTTCAAGGCTGG	GTCAGAATGGTGCCTCTTTCC	GTAAAACGACGGCCAGT
590	79	TNS4-12	TNS4	12	CCDS11368.1	NM_032865	M13-GAATGAGATGCAGGCTGAGG	TCTGTCAATATGGCCACAAGC	GTAAAACGACGGCCAGT

Supp. Table S4. Summary of number of base pairs sequenced

				Uncovered							
Gene Name	**# of Primers Used**	**# of Exons of the Gene**	**# of Covered Exons**	**# of Uncovered Exons**	**% of Coverage**	**# of NS mutations found**	**# of S mutations found**	**# of bps sequenced**	**# of bps sequenced in exon + splice sites**	**# of NS mutations per bp**	**# of S mutations per bp**
PTPRT	33	33	33	0	100.0	27	6	346,020	347,600	7.77E-05	1.73E-05
PTPRN2	22	25	23	2	92.0	11	0	240,555	242,135	4.54E-05	0.00E+00
TNS4	14	13	12	1	92.3	8	2	169,455	171,035	4.68E-05	1.17E-05
PTPRO	30	26	26	0	100.0	11	1	288,192	289,772	3.80E-05	3.45E-06
PTPRD	35	43	43	0	100.0	18	5	453,144	454,724	3.96E-05	1.10E-05
PTPRN	29	23	20	3	87.0	8	2	232,023	233,603	3.42E-05	8.56E-06
PTPRB	38	36	35	1	97.2	19	3	524,955	526,535	3.61E-05	5.70E-06
PTPN5	14	15	15	0	100.0	3	3	133,905	135,485	2.21E-05	2.21E-05
PTPRH	21	20	20	0	100.0	7	0	264,255	265,835	2.63E-05	0.00E+00
PTPRE	19	20	20	0	100.0	4	5	165,900	167,480	2.39E-05	2.99E-05
PTP4A1	5	5	5	0	100.0	1	0	41,001	42,581	2.35E-05	0.00E+00
PTPRC	32	34	33	1	97.1	7	0	309,048	310,628	2.25E-05	0.00E+00
PTPRS	34	40	37	3	92.5	9	2	461,676	463,256	1.94E-05	4.32E-06
MTMR3	23	18	17	1	94.4	5	1	283,926	285,506	1.75E-05	3.50E-06
MTMR12	17	16	16	0	100.0	3	0	177,039	178,619	1.68E-05	0.00E+00
PTPN12	20	18	18	0	100.0	3	0	184,860	186,440	1.61E-05	0.00E+00
TNS1	38	33	33	0	100.0	6	5	411,195	412,775	1.45E-05	1.21E-05
PTPN13	53	47	47	0	100.0	8	0	590,130	591,710	1.35E-05	0.00E+00
MTMR6	14	14	14	0	100.0	2	1	147,177	148,757	1.34E-05	6.72E-06
PTPRJ	25	26	25	1	96.2	5	0	316,869	318,449	1.57E-05	0.00E+00
MTMR8	17	14	14	0	100.0	2	1	166,848	168,428	1.19E-05	5.94E-06
PTPN21	23	18	18	0	100.0	3	0	278,238	279,818	1.07E-05	0.00E+00
PTPN23	34	25	23	2	92.0	2	1	387,732	389,312	5.14E-06	2.57E-06
Grand Total	**206**	**562**	**547**	**0**	**97.3**	**120**	**45**	**6,574,143**	**6,610,483**		

Supp. Table S5. Characteristics of melanoma patients with PTP mutations

Sample	Patient Age (years)	Patient Gender	Tumor Source	Matched normal source
1T	29	F	Lung	Blood
2T	30	M	Pectoral muscle	Blood
4T	34	F	Lung	Blood
5T	47	M	External iliac soft tissue	Blood
6T	42	M	Neck, soft tissue	Blood
7T	53	M	Stomach	Blood
8T	61	M	Inguinal soft tissue	Blood
9T	62	M	Back, subcutaneous	Blood
10T	55	M	Axillary soft tissue	Blood
12T	53	M	Upper arm, subcutaneous	Blood
13T	49	M	Chest wall, subcutaneous	Blood
16T	62	M	Lung	Blood
17T	33	M	Shoulder, subcutaneous	Blood
18T	55	M	Clavicle, soft tissue	Blood
20T	58	F	Axillary soft tissue	Blood
21T	59	M	Omentum	Blood
23T	44	M	Lung	Blood
24T	49	M	Axillary soft tissue	Blood
29T	51	M	Inguinal soft tissue	Blood
30T	53	F	Lung	Blood
31T	49	F	Thigh, subcutaneous	Blood
32T	58	M	Omentum	Blood
33T	33	M	Chest wall subcutaneous, & pleura	Blood
34T	31	M	Shoulder, subcutaneous	Blood
35T	23	F	Thigh, subcutaneous	Blood
36T	25	M	Thigh, subcutaneous	Blood
37T	38	F	Omentum	Blood
39T	56	M	Mesentery	Blood
41T	45	M	Neck, soft tissue	Blood
44T	56	M	Lung	Blood
45T	48	M	Mediastinum	Blood
48T	28	M	Back, soft tissue	Blood
49T	43	M	Thigh, subcutaneous	Blood
50T	49	F	Inguinal soft tissue	Blood

Sample	Patient Age (years)	Patient Gender	Tumor Source	Matched normal source
51T	50	F	Adnexa	Blood
52T	39	F	Lung	Blood
55T	60	M	Lung	Blood
58T	46	F	Hip, subcutaneous	Blood
59T	64	F	Abdomen, subcutaneous	Blood
60T	46	M	Flank, subcutaneous	Blood
63T	30	M	Jejunum	Blood
64T	32	F	Ovary	Blood
68T	49	M	Lung	Blood
69T	36	M	Axillary soft tissue	Blood
71T	67	M	Lung	Blood
72T	53	M	Liver	Blood
73T	45	F	Breast	Blood
74T	40	F	Lower extremity, subcutaneous	Blood
80T	36	F	Popliteal soft tissue	Blood
81T	60	F	Upper arm, subcutaneous	Blood
83T	33	F	Back, subcutaneous	Blood
85T	44	M	Chest wall, subcutaneous	Blood
86T	42	F	Liver	Blood
88T	37	F	Chest wall, subcutaneous	Blood
90T	19	M	Neck, soft tissue	Blood
91T	55	F	Subcostal soft tissue	Blood
95T	58	F	Inguinal soft tissue	Blood
96T	49	M	Inguinal soft tissue	Blood
103T	35	F	Axillary soft tissue	Blood
104T	56	M	Thigh, subcutaneous	Blood
106T	41	F	Lung	Blood

Supp. Table S6. Mass spectrometry data showing PTPRD interactome from icPTPRD-WT and icPTPRD-D1521A expressing Sk-Mel-28 cells induced by doxycycline for 24h

Protein peptides	Accession No.	icPTPRD-D1521A	icPTPRD-WT	Control
Receptor-type tyrosine-protein phosphatase delta OS=Homo sapiens GN=PTPRD PE=1 SV=2	P23468	307	202	
Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	O14744	137	104	89
Probable ATP-dependent RNA helicase DDX20 OS=Homo sapiens GN=DDX20 PE=1 SV=2	Q9UHI6	49	42	22
Component of gems 4 OS=Homo sapiens GN=GEMIN4 PE=1 SV=1	P57678	44	34	20
Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	Q8TEQ6	39	30	15
RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3	P98175	36	28	3
Influenza virus NS1A-binding protein OS=Homo sapiens GN=IVNS1ABP PE=1 SV=3	Q9Y6Y0	34	28	85
Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	Q71U36	32	34	31
Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	P21333	31	23	39
Spectrin alpha chain, brain OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	Q13813	31	14	127
Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	Q9BQA1	28	29	17
Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	Q13885	28	17	22
Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2	P23588	28	13	10
Spectrin beta chain, brain 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	Q01082	27	14	98
Methylosome subunit pICln OS=Homo sapiens GN=CLNS1A PE=1 SV=1	P54105	25	16	10
U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	O75643	20	13	
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	P11142	17	9	22

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Uncharacterized protein C9orf174 OS=Homo sapiens GN=C9orf174 PE=1 SV=2	Q9P1Z9	17	14	17
Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	O75533	16	9	
Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	P60891	16	9	25
Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	Q15393	16	17	
OTU domain-containing protein 4 OS=Homo sapiens GN=OTUD4 PE=1 SV=3	Q01804	16	10	4
Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2	P52732	15	16	
Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens GN=PRPSAP2 PE=1 SV=1	O60256	14	10	25
Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ACAP2 PE=1 SV=3	Q15057	13	13	36
Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1	Q9H4B7	12	6	8
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	P08670	12	7	17
RING finger protein 219 OS=Homo sapiens GN=RNF219 PE=1 SV=1	Q5W0B1	12	7	
Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1	Q15208	11	10	12
Survival of motor neuron protein-interacting protein 1 OS=Homo sapiens GN=SIP1 PE=1 SV=1	O14893	11	2	2
Serine/threonine-protein kinase RIO1 OS=Homo sapiens GN=RIOK1 PE=1 SV=2	Q9BRS2	11	7	
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	P19338	11	11	4
Terminal uridylyltransferase 4 OS=Homo sapiens GN=ZCCHC11 PE=1 SV=3	Q5TAX3	11	4	10
Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1	P62314	10	3	2
Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4	P31943	10	8	3
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	P15924	10	1	1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	Q9Y3F4	10	16	11
Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 PE=1 SV=2	Q14558	10	10	24
Mitogen-activated protein kinase kinase kinase 7 OS=Homo sapiens GN=MAP3K7 PE=1 SV=1	O43318	9	3	3
Spindlin-1 OS=Homo sapiens GN=SPIN1 PE=1 SV=3	Q9Y657	9	2	
Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1	P62316	9	5	3
IQ motif and SEC7 domain-containing protein 1 OS=Homo sapiens GN=IQSEC1 PE=1 SV=1	Q6DN90	9	9	2
Teneurin-3 OS=Homo sapiens GN=ODZ3 PE=2 SV=3	Q9P273	8	14	10
Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	P08107	8	5	3
Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	Q6P2Q9	8	4	
Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	Q00610	8	8	13
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	P07437	8	15	12
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	P62805	8		
U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2	Q8WWY3	7	7	2
Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1	P62318	7	1	1
Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens GN=SNRPB PE=1 SV=2	P14678	7	2	4
CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3	P27708	7	4	1
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	P23396	7	7	3
ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	Q08211	7	5	1
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	O43143	7	10	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3	P35573	7	3	4
Hypoxia-inducible gene 2 protein OS=Homo sapiens GN=HIG2 PE=1 SV=1	Q9Y5L2	7	5	6
Uncharacterized protein OS=Homo sapiens GN=LGR6	D6R9F0	7	4	10
116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1	Q15029	6	4	
Uncharacterized protein C11orf84 OS=Homo sapiens GN=C11orf84 PE=1 SV=3	Q9BUA3	6	4	
High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3	P09429	6	8	9
Calmodulin-regulated spectrin-associated protein 3 OS=Homo sapiens GN=KIAA1543 PE=1 SV=2	Q9P1Y5	6	4	
Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	P06748	6	2	1
E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=1 SV=1	P19474	6	1	22
U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1	O43290	6	1	
Transcription factor E2F7 OS=Homo sapiens GN=E2F7 PE=1 SV=3	Q96AV8	6	5	
Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2	P34931	6	5	5
C-Myc-binding protein OS=Homo sapiens GN=MYCBP PE=1 SV=3	Q99417	6	3	4
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	P07900	6	5	5
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	P62269	5		
40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	P62263	5		1
Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=1 SV=2	P35030	5	6	7
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2	P31040	5	4	5
Survival motor neuron protein OS=Homo sapiens GN=SMN1 PE=1 SV=1	Q16637	5	4	5

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	A5YKK6	5	3	
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	P14923	5	1	
Glycosyltransferase 25 family member 3 OS=Homo sapiens GN=CERCAM PE=2 SV=1	Q5T4B2	5	11	5
Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	P54652	5	3	7
Probable methylcytosine dioxygenase TET2 OS=Homo sapiens GN=TET2 PE=1 SV=3	Q6N021	5	1	1
Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2	P11908	5	4	24
60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	P05387	5	1	2
SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1	Q6P3W7	5	2	3
Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	P81605	5		2
Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	Q9Y2W1	5		
Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3	O94788	4	4	2
Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2	Q8N1F7	4	4	5
Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	P68363	4	3	4
Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1	Q58FF7	4	3	5
Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=5	P07814	4	1	2
Autophagy-related protein 2 homolog B OS=Homo sapiens GN=ATG2B PE=1 SV=5	Q96BY7	4	5	
Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	Q00839	4	4	
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	P22626	4		
Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	P68371	4	9	7

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	Q5D862	4		1
Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	Q13435	4	6	
Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	P55884	4		1
Bullous pemphigoid antigen 1 OS=Homo sapiens GN=DST PE=1 SV=4	Q03001	4	3	4
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3	O15294	4	2	
FAM30A protein OS=Homo sapiens GN=FAM30A	Q05DB7	4	2	3
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	Q86YZ3	4		
Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	P01614	4	2	2
40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	P62244	4	1	1
Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	Q13835	4	1	
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 OS=Homo sapiens GN=TAB1 PE=1 SV=1	Q15750	4	4	5
E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=2	Q9NS91	4	3	3
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	P13010	4	1	
Transcription elongation factor B polypeptide 1 OS=Homo sapiens GN=TCEB1 PE=1 SV=1	Q15369	4	4	2
EF-hand calcium-binding domain-containing protein 6 OS=Homo sapiens GN=EFCAB6 PE=1 SV=1	Q5THR3	4	1	3
Uncharacterized protein OS=Homo sapiens GN=DSTYK	C9J9G6	4	4	2
60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	P35268	4		2
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	P68104	4	1	2
E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2	P49792	4		7

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Ras-related protein Rab-19 OS=Homo sapiens GN=RAB19 PE=2 SV=2	A4D1S5	4	5	2
Caspase 3, apoptosis-related cysteine peptidase, isoform CRA_b OS=Homo sapiens GN=CASP3	A8MVM1	4	8	5
Gem-associated protein 6 OS=Homo sapiens GN=GEMIN6 PE=1 SV=1	Q8WXD5	4		1
Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1	P07477	4	3	1
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	P60709	4	3	4
Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF PE=1 SV=2	P10586	4	2	
Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1	Q13464	4		
Putative tyrosine-protein phosphatase TPTE OS=Homo sapiens GN=TPTE PE=2 SV=3	P56180	4	5	2
T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	P78371	4	2	6
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	P50990	4	1	4
Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	P20700	3	2	
Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	P23381	3		
Leucine-rich repeat-containing protein 42 OS=Homo sapiens GN=LRRC42 PE=1 SV=1	Q9Y546	3		
Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	P10599	3	2	2
E3 ubiquitin-protein ligase RNF180 OS=Homo sapiens GN=RNF180 PE=2 SV=2	Q86T96	3	7	
NACHT, LRR and PYD domains-containing protein 1 OS=Homo sapiens GN=NLRP1 PE=1 SV=1	Q9C000	3	3	1
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	P48643	3	1	4
Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	Q02413	3		
Protein phosphatase 1B OS=Homo sapiens GN=PPM1B PE=1 SV=1	O75688	3	2	4

Protein peptides	Accession No.	icPTPRD-D1521A	icPTPRD-WT	Control
Putative small nuclear ribonucleoprotein polypeptide E-like protein 1 OS=Homo sapiens GN=SNRPEL1 PE=5 SV=1	Q5VYJ4	3	1	
Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2	O75821	3		1
T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	Q99832	3	2	4
Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	Q13263	3	1	1
Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1	O00303	3		1
T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	P17987	3	4	4
cDNA FLJ43335 fis, clone NT2RI3006673, highly similar to Receptor-type tyrosine-protein phosphatase F (EC 3.1.3.48) OS=Homo sapiens	B3KWM1	3	1	
COL12A1 protein OS=Homo sapiens	Q86TG9	3	1	3
Cytospin-B OS=Homo sapiens GN=CYTSB PE=1 SV=1	Q5M775	3	6	3
40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	P60866	3		
Zinc finger protein 40 OS=Homo sapiens GN=HIVEP1 PE=1 SV=3	P15822	3		
Fibromodulin OS=Homo sapiens GN=FMOD PE=1 SV=2	Q06828	3	3	2
60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	P61353	3		1
60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	P39023	3		
DNA endonuclease RBBP8 OS=Homo sapiens GN=RBBP8 PE=1 SV=2	Q99708	3	3	5
Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=2	Q93008	3		
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	P62847	3	2	
Probable histone-lysine N-methyltransferase ASH1L OS=Homo sapiens GN=ASH1L PE=1 SV=2	Q9NR48	3	1	3
Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	Q15233	3	2	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	P11021	3	3	3
60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	P30050	3		1
40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	P39019	3	1	1
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	P25398	3		
DNA repair protein REV1 OS=Homo sapiens GN=REV1 PE=1 SV=1	Q9UBZ9	3		1
Zinc finger protein 202 OS=Homo sapiens GN=ZNF202 PE=1 SV=4	O95125	3		
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	P62277	3	1	
Zinc finger protein 510 OS=Homo sapiens GN=ZNF510 PE=2 SV=1	Q9Y2H8	3	6	3
60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	P62913	3	2	1
Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	Q9UMS4	3	3	
Phosphatidylinositol 4-kinase alpha OS=Homo sapiens GN=PI4KA PE=1 SV=3	P42356	3	1	1
60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	P18621	3		
Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2	Q99873	3		2
26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	P35998	3		1
PiggyBac transposable element-derived protein 2 OS=Homo sapiens GN=PGBD2 PE=2 SV=1	Q6P3X8	3	2	5
Putative uncharacterized protein DKFZp686G04235 OS=Homo sapiens GN=DKFZp686G04235	Q63HL4	3		
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	P62241	2	1	
Pulmonary surfactant-associated protein D OS=Homo sapiens GN=SFTPD PE=1 SV=2	P35247	2		
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	P05388	2	1	1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	P08238	2	2	2
POTE ankyrin domain family member B OS=Homo sapiens GN=POTEB PE=2 SV=1	Q6S5H4	2		
Solute carrier family 22 member 11 OS=Homo sapiens GN=SLC22A11 PE=1 SV=1	Q9NSA0	2	1	1
Cell division protein kinase 18 OS=Homo sapiens GN=CDK18 PE=1 SV=3	Q07002	2		
Sp110 nuclear body protein OS=Homo sapiens GN=SP110 PE=1 SV=5	Q9HB58	2	3	3
TGF-beta-activated kinase 1 and MAP3K7-binding protein 3 OS=Homo sapiens GN=TAB3 PE=1 SV=2	Q8N5C8	2	3	2
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	P62851	2		
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	P62266	2	1	
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	P62081	2	2	
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	P61247	2	1	
Putative uncharacterized protein OS=Homo sapiens	Q2NKY6	2	1	1
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	P12956	2	1	1
40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	P62857	2		1
TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 OS=Homo sapiens GN=TAB2 PE=1 SV=1	Q9NYJ8	2	3	
26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	O00487	2		
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	Q14204	2	3	16
Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	Q12905	2	3	
Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2	O15397	2	4	
Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	O00410	2		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Syntaxin-binding protein 3 OS=Homo sapiens GN=STXBP3 PE=1 SV=2	O00186	2	2	
Isoleucyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	P41252	2	3	1
Taste receptor type 2 member 42 OS=Homo sapiens GN=TAS2R42 PE=2 SV=1	Q7RTR8	2		1
Contactin-1 OS=Homo sapiens GN=CNTN1 PE=1 SV=1	Q12860	2		
Putative HIN1-like protein OS=Homo sapiens GN=HIN1L PE=5 SV=1	Q7RTX8	2	3	1
Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2	Q58FF8	2	2	4
26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	Q99460	2		3
PHD and RING finger domain-containing protein 1 OS=Homo sapiens GN=PHRF1 PE=1 SV=3	Q9P1Y6	2		
Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein OS=Homo sapiens GN=PREX2 PE=2 SV=1	Q70Z35	2		
Chromosome-associated kinesin KIF4A OS=Homo sapiens GN=KIF4A PE=1 SV=3	O95239	2		
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	P50991	2	3	4
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	Q13200	2		
26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	O43242	2		2
Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	P30086	2	2	2
Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 PE=1 SV=4	Q8NCM8	2		
Rotatin OS=Homo sapiens GN=RTTN PE=1 SV=3	Q86VV8	2	1	
Coiled-coil domain-containing protein 58 OS=Homo sapiens GN=CCDC58 PE=1 SV=1	Q4VC31	2	1	1
PHD finger protein 20 OS=Homo sapiens GN=PHF20 PE=1 SV=2	Q9BVI0	2		1
Protein tyrosine phosphatase, receptor type, F isoform 2 variant (Fragment) OS=Homo sapiens	Q59FI2	2		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1	Q12996	2		
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	P62249	2		2
Putative heat shock protein HSP 90-alpha A5 OS=Homo sapiens GN=HSP90AA5P PE=1 SV=1	Q58FG0	2	1	1
Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	P60228	2	2	
Vacuolar protein sorting-associated protein 8 homolog OS=Homo sapiens GN=VPS8 PE=1 SV=3	Q8N3P4	2		
Homeobox protein Hox-A5 OS=Homo sapiens GN=HOXA5 PE=1 SV=2	P20719	2	4	1
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	P60842	2		6
A disintegrin and metalloproteinase with thrombospondin motifs 15 OS=Homo sapiens GN=ADAMTS15 PE=2 SV=1	Q8TE58	2		
Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	P62736	2	5	5
Uncharacterized protein C19orf68 OS=Homo sapiens GN=C19orf68 PE=1 SV=2	Q86XI8	2	2	3
Histone-lysine N-methyltransferase SETD2 OS=Homo sapiens GN=SETD2 PE=1 SV=3	Q9BYW2	2		
Amiloride-sensitive cation channel 2, neuronal OS=Homo sapiens GN=ACCN2 PE=1 SV=3	P78348	2	1	
Neuropilin-1 OS=Homo sapiens GN=NRP1 PE=1 SV=3	O14786	2		
Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2	Q9P2R3	2	1	
Uncharacterized protein C10orf82 OS=Homo sapiens GN=C10orf82 PE=2 SV=2	Q8WW14	2	2	
Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	P22234	2	1	1
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Homo sapiens GN=UAP1L1 PE=2 SV=2	Q3KQV9	2		
Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	P84090	2	1	
Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	P14868	2		1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3	Q9Y2H1	2	3	4
DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	Q16531	2	1	
Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=2	Q9NZI8	2	2	1
Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	P33778	2	1	
Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2	P62987	2	2	1
Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1	Q9Y262	2	2	1
ATP-dependent RNA helicase DQX1 OS=Homo sapiens GN=DQX1 PE=2 SV=2	Q8TE96	2		
Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	Q13347	2		
U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=1 SV=3	P09012	2		
Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2	Q9NYF8	2		
Splicing factor 45 OS=Homo sapiens GN=RBM17 PE=1 SV=1	Q96I25	2		
Myosin light chain kinase, smooth muscle OS=Homo sapiens GN=MYLK PE=1 SV=4	Q15746	2	1	4
Gem-associated protein 7 OS=Homo sapiens GN=GEMIN7 PE=1 SV=1	Q9H840	2	1	1
Small nuclear ribonucleoprotein G-like protein OS=Homo sapiens PE=3 SV=2	A8MWD9	2	2	2
Small nuclear ribonucleoprotein F OS=Homo sapiens GN=SNRPF PE=1 SV=1	P62306	2		1
B-cell lymphoma/leukemia 11B OS=Homo sapiens GN=BCL11B PE=1 SV=1	Q9C0K0	2	1	1
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	P02545	2		
U2-associated protein SR140 OS=Homo sapiens GN=SR140 PE=1 SV=2	O15042	2	2	
Echinoderm microtubule-associated protein-like 6 OS=Homo sapiens GN=EML6 PE=2 SV=2	Q6ZMW3	2		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Pre-mRNA branch site protein p14 OS=Homo sapiens GN=SF3B14 PE=1 SV=1	Q9Y3B4	2	3	
MAP kinase-activated protein kinase 5 OS=Homo sapiens GN=MAPKAPK5 PE=1 SV=2	Q8IW41	2		
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	P62829	2	1	
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	P62750	2	1	1
Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1	O94906	2	2	
60S ribosomal protein L26-like 1 OS=Homo sapiens GN=RPL26L1 PE=1 SV=1	Q9UNX3	2		
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	P55072	2	1	
CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens GN=CD2BP2 PE=1 SV=1	O95400	2		
Protein KIAA1967 OS=Homo sapiens GN=KIAA1967 PE=1 SV=2	Q8N163	2		
6-pyruvoyl tetrahydrobiopterin synthase OS=Homo sapiens GN=PTS PE=1 SV=1	Q03393	2		
MORC family CW-type zinc finger protein 2 OS=Homo sapiens GN=MORC2 PE=1 SV=2	Q9Y6X9	2	6	
Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1	Q96DG6	2		3
Desmin OS=Homo sapiens GN=DES PE=1 SV=3	P17661	2		2
Spindlin-2A OS=Homo sapiens GN=SPIN2A PE=1 SV=3	Q99865	2		
60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	P32969	2		
60S acidic ribosomal protein P0-like OS=Homo sapiens GN=RPLP0P6 PE=5 SV=1	Q8NHW5	2	1	1
Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=2	O95819	2		
Uncharacterized protein OS=Homo sapiens GN=ASB18	C9JFL4	2		
Gem (Nuclear organelle) associated protein 4 OS=Homo sapiens GN=GEMIN4	Q8WUM5	2	4	3

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	O43175	2		5
60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	P18124	2	2	2
Inactive phospholipase C-like protein 2 OS=Homo sapiens GN=PLCL2 PE=1 SV=2	Q9UPR0	1		
Inactive Ufm1-specific protease 1 OS=Homo sapiens GN=UFSP1 PE=2 SV=2	Q6NVU6	1		
Inactive ubiquitin carboxyl-terminal hydrolase 50 OS=Homo sapiens GN=USP50 PE=2 SV=1	Q70EL3	1		1
Maltase-glucoamylase (Fragment) OS=Homo sapiens GN=MGAM	Q8TE24	1	1	
Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	P34932	1		1
Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	Q92598	1		
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	P04792	1		
Heat-stable enterotoxin receptor OS=Homo sapiens GN=GUCY2C PE=1 SV=2	P25092	1		
Hepatocyte growth factor receptor OS=Homo sapiens GN=MET PE=1 SV=4	P08581	1		
Hermansky-Pudlak syndrome 5 protein OS=Homo sapiens GN=HPS5 PE=1 SV=2	Q9UPZ3	1		
Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	Q14103	1	1	
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	P61978	1	2	1
Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2	P14866	1		1
High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8B OS=Homo sapiens GN=PDE8B PE=1 SV=2	O95263	1		
Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1	Q13547	1		
Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	P04908	1	3	
Histone-lysine N-methyltransferase MLL4 OS=Homo sapiens GN=WBP7 PE=1 SV=1	Q9UMN6	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3	Q16695	1		
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	Q14974	1		2
Histone-lysine N-methyltransferase MLL3 OS=Homo sapiens GN=MLL3 PE=1 SV=3	Q8NEZ4	1		
HIV Tat-specific factor 1 OS=Homo sapiens GN=HTATSF1 PE=1 SV=1	O43719	1		
Homeobox protein cut-like 1 OS=Homo sapiens GN=CUX1 PE=1 SV=3	P39880	1		
Homeobox protein Meis1 OS=Homo sapiens GN=MEIS1 PE=1 SV=1	O00470	1		
Homeodomain-interacting protein kinase 4 OS=Homo sapiens GN=HIPK4 PE=2 SV=1	Q8NE63	1		
Homer protein homolog 1 OS=Homo sapiens GN=HOMER1 PE=1 SV=2	Q86YM7	1		
Homer protein homolog 2 OS=Homo sapiens GN=HOMER2 PE=1 SV=1	Q9NSB8	1		
Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	Q16543	1	1	1
Huntingtin OS=Homo sapiens GN=HTT PE=1 SV=2	P42858	1		
Huntingtin-associated protein 1 OS=Homo sapiens GN=HAP1 PE=1 SV=3	P54257	1		
Hypermethylated in cancer 1 protein OS=Homo sapiens GN=HIC1 PE=1 SV=5	Q14526	1	1	
IL-18 receptor beta splice variant OS=Homo sapiens	Q2QDE5	1		3
Immunoglobulin superfamily member 2 OS=Homo sapiens GN=CD101 PE=1 SV=2	Q93033	1		
Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3	Q71UI9	1		
Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=1 SV=3	Q8WXH0	1	1	
Nuclear receptor co-repressor OS=Homo sapiens	Q7Z516	1	1	
Nuclear receptor coactivator 5 OS=Homo sapiens GN=NCOA5 PE=1 SV=2	Q9HCD5	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3	Q12769	1		
NTPase KAP family P-loop domain-containing protein 1 OS=Homo sapiens GN=NKPD1 PE=2 SV=1	Q17RQ9	1		
Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=1 SV=3	P05114	1		
Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2	Q6KC79	1		
NF-kappa-B inhibitor-like protein 1 OS=Homo sapiens GN=NFKBIL1 PE=1 SV=1	Q9UBC1	1		
Neuronal protein NP25 OS=Homo sapiens	Q7Z517	1		
Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1	Q9BYT8	1		
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	Q09666	1		1
Myosin-VIIb OS=Homo sapiens GN=MYO7B PE=2 SV=2	Q6PIF6	1		
Netrin receptor UNC5A OS=Homo sapiens GN=UNC5A PE=2 SV=3	Q6ZN44	1		
Nucleolar protein 3 (Apoptosis repressor with CARD domain), isoform CRA_a OS=Homo sapiens GN=NOL3	B4DFL0	1	1	
NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3 PE=1 SV=2	Q8TBC4	1		
Necdin OS=Homo sapiens GN=NDN PE=1 SV=1	Q99608	1		
Nebulin OS=Homo sapiens GN=NEB PE=1 SV=4	P20929	1	1	1
Nck-associated protein 5 OS=Homo sapiens GN=NCKAP5 PE=1 SV=2	O14513	1		
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=NDUFA10 PE=1 SV=1	O95299	1		
NACHT, LRR and PYD domains-containing protein 11 OS=Homo sapiens GN=NLRP11 PE=2 SV=2	P59045	1		
NACHT, LRR and PYD domains-containing protein 10 OS=Homo sapiens GN=NLRP10 PE=1 SV=1	Q86W26	1		
N-acetylglucosamine kinase OS=Homo sapiens GN=NAGK	B4DLZ5	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
0	Q76KP1	1		
Myotubularin-related protein 4 OS=Homo sapiens GN=MTMR4 PE=2 SV=2	Q9NYA4	1	1	
Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3	P11117	1		
Netrin receptor UNC5C OS=Homo sapiens GN=UNC5C PE=1 SV=2	O95185	1	1	5
Peptide chain release factor 1, mitochondrial OS=Homo sapiens GN=MTRF1 PE=1 SV=2	O75570	1		
Piwi-like protein 2 OS=Homo sapiens GN=PIWIL2 PE=2 SV=1	Q8TC59	1		
Phosphorylase b kinase gamma catalytic chain, skeletal muscle isoform OS=Homo sapiens GN=PHKG1 PE=2 SV=3	Q16816	1		
Phosphoinositol 3-phosphate-binding protein 3 (Fragment) OS=Homo sapiens GN=PLEKHA6	A5XEJ4	1		
Phosphatidylinositol transfer protein, beta (Fragment) OS=Homo sapiens GN=PITPNB	B3KYB7	1		
Phosphate-regulating neutral endopeptidase OS=Homo sapiens GN=PHEX PE=1 SV=1	P78562	1		
PHD finger protein 3 OS=Homo sapiens GN=PHF3 PE=1 SV=3	Q92576	1		
PHD finger protein 11 OS=Homo sapiens GN=PHF11 PE=1 SV=3	Q9UIL8	1		
Peripherin OS=Homo sapiens GN=PRPH PE=1 SV=2	P41219	1	1	4
Peripheral-type benzodiazepine receptor-associated protein 1 OS=Homo sapiens GN=BZRAP1 PE=1 SV=2	O95153	1	2	4
Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4	Q15154	1		
Peregrin OS=Homo sapiens GN=BRPF1 PE=1 SV=2	P55201	1		
Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	P67809	1		1
Peptidyl-prolyl cis-trans isomerase E OS=Homo sapiens GN=PPIE PE=1 SV=1	Q9UNP9	1		
Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3	Q9BZE4	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
PAX-9 protein (Fragment) OS=Homo sapiens GN=PAX-9	O95616	1	2	
Partner of Y14 and mago OS=Homo sapiens GN=WIBG PE=1 SV=1	Q9BRP8	1		
Paladin OS=Homo sapiens GN=PALD PE=1 SV=3	Q9ULE6	1		
Otolin-1 OS=Homo sapiens GN=OTOL1 PE=3 SV=1	A6NHN0	1		
Otoferlin OS=Homo sapiens GN=OTOF PE=1 SV=3	Q9HC10	1	3	
Orexin receptor type 1 OS=Homo sapiens GN=HCRTR1 PE=1 SV=2	O43613	1		
Olfactory receptor 8A1 OS=Homo sapiens GN=OR8A1 PE=2 SV=2	Q8NGG7	1		
Olfactory receptor 13C5 OS=Homo sapiens GN=OR13C5 PE=2 SV=1	Q8NGS8	1		
Numb-like protein OS=Homo sapiens GN=NUMBL PE=1 SV=1	Q9Y6R0	1		
Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3	Q12830	1		
Myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3	O43795	1		1
Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	Q02790	1		
Keratin-81-like protein OS=Homo sapiens PE=2 SV=3	A6NCN2	1		
Liprin-alpha-1 OS=Homo sapiens GN=PPFIA1 PE=1 SV=1	Q13136	1		
Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=4	P50851	1		
Leucine-rich repeat-containing protein LOC400891 OS=Homo sapiens PE=2 SV=2	Q6ZQY2	1		
Leucine-rich repeat-containing protein 15 OS=Homo sapiens GN=LRRC15 PE=1 SV=1	Q8TF66	1		
Leucine-rich repeat LGI family member 2 OS=Homo sapiens GN=LGI2 PE=1 SV=1	Q8N0V4	1		
Leucine-rich repeat and death domain-containing protein OS=Homo sapiens GN=LRDD PE=1 SV=2	Q9HB75	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Leptin receptor OS=Homo sapiens GN=LEPR PE=1 SV=2	P48357	1		
Left-right determination factor 1 OS=Homo sapiens GN=LEFTY1 PE=2 SV=1	O75610	1		
Laminin subunit gamma-2 OS=Homo sapiens GN=LAMC2 PE=1 SV=2	Q13753	1		
Kinesin-like protein KIFC2 OS=Homo sapiens GN=KIFC2 PE=1 SV=1	Q96AC6	1		
Myotilin OS=Homo sapiens GN=MYOT PE=1 SV=2	Q9UBF9	1		
Kinesin-like protein KIF15 OS=Homo sapiens GN=KIF15 PE=1 SV=1	Q9NS87	1		1
Low-density lipoprotein receptor-related protein 10 OS=Homo sapiens GN=LRP10 PE=1 SV=2	Q7Z4F1	1		1
Kelch-like protein 20 OS=Homo sapiens GN=KLHL20 PE=1 SV=4	Q9Y2M5	1		
Jouberin OS=Homo sapiens GN=AHI1 PE=1 SV=1	Q8N157	1		
Iporin OS=Homo sapiens GN=RUSC2 PE=1 SV=2	Q8N2Y8	1		
Interleukin-27 subunit alpha OS=Homo sapiens GN=IL27 PE=1 SV=2	Q8NEV9	1		
Interferon-induced protein with tetratricopeptide repeats 2 OS=Homo sapiens GN=IFIT2 PE=1 SV=1	P09913	1		
Interferon kappa OS=Homo sapiens GN=IFNK PE=1 SV=1	Q9P0W0	1		
Inter-alpha-trypsin inhibitor heavy chain H5 OS=Homo sapiens GN=ITIH5 PE=2 SV=2	Q86UX2	1		
Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	P17301	1	1	1
Insulin receptor substrate 4 OS=Homo sapiens GN=IRS4 PE=1 SV=1	O14654	1		
Inositol polyphosphate 1-phosphatase OS=Homo sapiens GN=INPP1 PE=1 SV=1	P49441	1	1	
Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens GN=ITPR2 PE=1 SV=2	Q14571	1		
Kinesin-like protein KIF3C OS=Homo sapiens GN=KIF3C PE=1 SV=3	O14782	1		1

Protein peptides	Accession No.	icPTPRD-D1521A	icPTPRD-WT	Control
Zymogen granule membrane protein 16 OS=Homo sapiens GN=ZG16 PE=1 SV=1	O60844	1		
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	P35579	1	1	2
Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2	P19105	1		
Myoneurin OS=Homo sapiens GN=MYNN PE=1 SV=1	Q9NPC7	1		
Myomegalin OS=Homo sapiens GN=PDE4DIP PE=1 SV=1	Q5VU43	1	1	
Myelin transcription factor 1-like protein OS=Homo sapiens GN=MYT1L PE=2 SV=2	Q9UL68	1		
Myelin gene regulatory factor OS=Homo sapiens GN=MRF PE=1 SV=3	Q9Y2G1	1		
Myelin expression factor 2 OS=Homo sapiens GN=MYEF2 PE=1 SV=3	Q9P2K5	1	1	
Multiple epidermal growth factor-like domains protein 8 OS=Homo sapiens GN=MEGF8 PE=1 SV=2	Q7Z7M0	1		1
Mucin-16 OS=Homo sapiens GN=MUC16 PE=1 SV=2	Q8WXI7	1	1	1
Mothers against decapentaplegic homolog 2 OS=Homo sapiens GN=SMAD2 PE=1 SV=1	Q15796	1		
Monocarboxylate transporter 8 OS=Homo sapiens GN=SLC16A2 PE=1 SV=2	P36021	1		
LON peptidase N-terminal domain and RING finger protein 3 OS=Homo sapiens GN=LONRF3 PE=1 SV=1	Q496Y0	1		3
Mitogen-activated protein kinase kinase kinase kinase 4 isoform OS=Homo sapiens GN=MAP4K4	Q5MD60	1		
Long-chain fatty acid transport protein 4 OS=Homo sapiens GN=SLC27A4 PE=1 SV=1	Q6P1M0	1		
Mitogen-activated protein kinase 6 OS=Homo sapiens GN=MAPK6 PE=1 SV=1	Q16659	1	1	
Microtubule-associated serine/threonine-protein kinase 2 OS=Homo sapiens GN=MAST2 PE=1 SV=2	Q6P0Q8	1		
Menin OS=Homo sapiens GN=MEN1 PE=1 SV=3	O00255	1		
MAP kinase-interacting serine/threonine-protein kinase 1 OS=Homo sapiens GN=MKNK1 PE=1 SV=1	Q9BUB5	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Mannose-P-dolichol utilization defect 1 protein OS=Homo sapiens GN=MPDU1 PE=1 SV=2	O75352	1		
E3 ubiquitin-protein ligase CHFR OS=Homo sapiens GN=CHFR PE=1 SV=2	Q96EP1	1		
Lysyl-tRNA synthetase OS=Homo sapiens GN=KARS PE=1 SV=3	Q15046	1		1
Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2	Q96N66	1		
Lysine-specific demethylase 6B OS=Homo sapiens GN=KDM6B PE=1 SV=4	O15054	1	1	
Low-density lipoprotein receptor-related protein 2 OS=Homo sapiens GN=LRP2 PE=1 SV=3	P98164	1		
Inosine-5'-monophosphate dehydrogenase 1 OS=Homo sapiens GN=IMPDH1 PE=1 SV=2	P20839	1		
Mitogen-activated protein kinase-binding protein 1 OS=Homo sapiens GN=MAPKBP1 PE=2 SV=4	O60336	1	3	1
ATR-interacting protein OS=Homo sapiens GN=ATRIP PE=1 SV=1	Q8WXE1	1		
Bromodomain containing protein 1 variant (Fragment) OS=Homo sapiens	Q59G93	1		
Bromodomain and WD repeat-containing protein 3 OS=Homo sapiens GN=BRWD3 PE=1 SV=2	Q6RI45	1		
Bridging integrator 3 OS=Homo sapiens GN=BIN3 PE=1 SV=1	Q9NQY0	1		
Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3	Q9Y6D5	1		1
Bone morphogenetic protein 1 OS=Homo sapiens GN=BMP1 PE=1 SV=2	P13497	1		
BolA-like protein 2 OS=Homo sapiens GN=BOLA2 PE=1 SV=1	Q9H3K6	1		
Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	Q13867	1		
Biogenesis of lysosome-related organelles complex 1 subunit 2 OS=Homo sapiens GN=BLOC1S2 PE=1 SV=1	Q6QNY1	1	2	1
Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4	Q13057	1		
Beclin 1-associated autophagy-related key regulator OS=Homo sapiens GN=ATG14 PE=1 SV=1	Q6ZNE5	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
BCL-6 corepressor OS=Homo sapiens GN=BCOR PE=1 SV=1	Q6W2J9	1		
E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2	O95714	1		
BAI1-associated protein 3 OS=Homo sapiens GN=BAIAP3 PE=1 SV=2	O94812	1		
C21orf2 protein OS=Homo sapiens GN=C21orf2	Q8N5X6	1		
ATP-dependent DNA helicase Q4 OS=Homo sapiens GN=RECQL4 PE=1 SV=1	O94761	1		
ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2	Q9UG63	1		
ATP-binding cassette sub-family C member 9 OS=Homo sapiens GN=ABCC9 PE=1 SV=2	O60706	1		
ATP-binding cassette sub-family A member 13 OS=Homo sapiens GN=ABCA13 PE=2 SV=2	Q86UQ4	1	4	3
ATP-binding cassette sub-family A member 12 OS=Homo sapiens GN=ABCA12 PE=1 SV=3	Q86UK0	1		
Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1	Q9UBB4	1	1	5
Armadillo repeat-containing protein 2 OS=Homo sapiens GN=ARMC2 PE=1 SV=4	Q8NEN0	1		
Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	P08758	1	1	
Ankyrin-3 OS=Homo sapiens GN=ANK3 PE=1 SV=3	Q12955	1	1	2
Angiopoietin-1 receptor OS=Homo sapiens GN=TEK PE=1 SV=2	Q02763	1		
Amyloid beta A4 precursor protein-binding family B member 3 OS=Homo sapiens GN=APBB3 PE=1 SV=2	O95704	1		
B-cell scaffold protein with ankyrin repeats OS=Homo sapiens GN=BANK1 PE=1 SV=3	Q8NDB2	1		1
Caspase recruitment domain-containing protein 14 OS=Homo sapiens GN=CARD14 PE=1 SV=2	Q9BXL6	1		
cDNA FLJ56880 OS=Homo sapiens	B7Z6C1	1		
cDNA FLJ56443, highly similar to Putative ATP-dependent RNA helicase DHX33 (EC 3.6.1.-) OS=Homo sapiens	B4DIS6	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
cDNA FLJ54153, weakly similar to Homo sapiens Mof4 family associated protein 1 (MRFAP1), mRNA OS=Homo sapiens	B4DTJ7	1		2
cDNA FLJ53883, highly similar to C-jun-amino-terminal kinase-interacting protein 1 OS=Homo sapiens	B7Z1L7	1		
cDNA FLJ53559 OS=Homo sapiens	B4DKG6	1		
cDNA FLJ53535 OS=Homo sapiens	B4DK98	1		
cDNA FLJ40285 fis, clone TESTI2027820 OS=Homo sapiens	Q8N7W1	1		
CDKN2A-interacting protein OS=Homo sapiens GN=CDKN2AIP PE=1 SV=2	Q9NXV6	1		
CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2	Q6YHK3	1		
C-C chemokine receptor type 5 OS=Homo sapiens GN=CCR5 PE=1 SV=1	P51681	1		
Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	P31944	1		
Bromodomain testis-specific protein OS=Homo sapiens GN=BRDT PE=1 SV=4	Q58F21	1		
Caspase recruitment domain-containing protein 6 OS=Homo sapiens GN=CARD6 PE=1 SV=2	Q9BX69	1		
C2 calcium-dependent domain-containing protein 4B OS=Homo sapiens GN=C2CD4B PE=2 SV=1	A6NLJ0	1		
Carnosine synthase 1 OS=Homo sapiens GN=CARNS1 PE=1 SV=3	A5YM72	1		
cAMP-specific 3',5'-cyclic phosphodiesterase 4D OS=Homo sapiens GN=PDE4D PE=1 SV=2	Q08499	1		
cAMP-specific 3',5'-cyclic phosphodiesterase 4A OS=Homo sapiens GN=PDE4A PE=1 SV=3	P27815	1	1	1
cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1 SV=1	P10644	1	1	3
cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB PE=1 SV=2	P22694	1		
cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2	P17612	1	1	1
Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	Q9NZT1	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=1 SV=3	Q8IWX8	1	1	
Cadherin-like protein 26 OS=Homo sapiens GN=CDH26 PE=2 SV=3	Q8IXH8	1		
Cadherin-24 OS=Homo sapiens GN=CDH24 PE=1 SV=1	Q86UP0	1	1	
Cadherin-11 OS=Homo sapiens GN=CDH11 PE=1 SV=2	P55287	1		
Alstrom syndrome protein 1 OS=Homo sapiens GN=ALMS1 PE=1 SV=3	Q8TCU4	1		3
Caspase-1 OS=Homo sapiens GN=CASP1 PE=1 SV=1	P29466	1	1	
28S ribosomal protein S33, mitochondrial OS=Homo sapiens GN=MRPS33 PE=1 SV=1	Q9Y291	1		
Amphoterin-induced protein 1 OS=Homo sapiens GN=AMIGO1 PE=1 SV=1	Q86WK6	1	1	
60S ribosomal protein L10-like OS=Homo sapiens GN=RPL10L PE=1 SV=3	Q96L21	1		
60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	P27635	1		1
60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	P05386	1	1	
5-hydroxytryptamine receptor 3A OS=Homo sapiens GN=HTR3A PE=1 SV=1	P46098	1		1
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4	P08865	1		
40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	P46781	1		
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	P62701	1	2	
40S ribosomal protein S27-like OS=Homo sapiens GN=RPS27L PE=1 SV=3	Q71UM5	1	1	
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	P15880	1	1	
40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	P08708	1	2	
60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	P50914	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	P46783	1	1	
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	Q07020	1	1	1
26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2	P48556	1		
26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	P51665	1		1
26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	Q15008	1	1	
26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens GN=PSMD10 PE=1 SV=1	O75832	1		
26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	P62195	1		
26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	P43686	1		1
26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	P17980	1		
26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	P62191	1		1
14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	P27348	1		1
14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	P61981	1		3
14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	Q04917	1		1
14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	P31946	1		3
40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	P62280	1		
7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1	Q7L2J0	1		
cDNA FLJ58538, highly similar to Homo sapiens leucine zipper transcription regulator 2 (LZTR2), mRNA OS=Homo sapiens	B4DK76	1		
Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	P61163	1	2	
Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1	O00116	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
A-kinase anchor protein 9 OS=Homo sapiens GN=AKAP9 PE=1 SV=3	Q99996	1		
A-kinase anchor protein 4 OS=Homo sapiens GN=AKAP4 PE=1 SV=1	Q5JQC9	1		
ADP-ribosylation factor GTPase-activating protein 3 OS=Homo sapiens GN=ARFGAP3 PE=1 SV=1	Q9NP61	1		2
Adenylyl cyclase-associated protein OS=Homo sapiens	B4DNA3	1		
Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5	Q01518	1	1	3
Adenylate cyclase type 4 OS=Homo sapiens GN=ADCY4 PE=1 SV=1	Q8NFM4	1	1	
ADAMTS-like protein 3 OS=Homo sapiens GN=ADAMTSL3 PE=2 SV=4	P82987	1		
Activating signal cointegrator 1 complex subunit 2 OS=Homo sapiens GN=ASCC2 PE=1 SV=3	Q9H1I8	1		4
60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	P26373	1		1
Abhydrolase domain-containing protein FAM108B1 OS=Homo sapiens GN=FAM108B1 PE=2 SV=1	Q5VST6	1	1	1
Amiloride-sensitive sodium channel subunit delta OS=Homo sapiens GN=SCNN1D PE=1 SV=2	P51172	1		
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 OS=Homo sapiens GN=PFKFB3 PE=1 SV=1	Q16875	1		
60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	P62917	1		
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	P62424	1		
60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	Q02878	1		
60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2	P61513	1	1	
60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	P18077	1		
60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	P42766	1		
60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	P49207	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	P46779	1		
60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	P61254	1		
60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	P83731	1		
60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	Q02543	1		
Actin-like protein 8 OS=Homo sapiens GN=ACTL8 PE=2 SV=1	Q9H568	1	1	
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	P13639	1		
DUX4 OS=Homo sapiens GN=DUX4	C3U395	1		
Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1	Q7L2H7	1	2	1
Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=1 SV=1	Q9UBQ5	1		1
Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1	O15372	1		
Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1	Q14152	1		
Eukaryotic translation initiation factor 2-alpha kinase 4 OS=Homo sapiens GN=EIF2AK4 PE=1 SV=3	Q9P2K8	1		
Eukaryotic translation initiation factor 2 subunit 3-like protein OS=Homo sapiens GN=EIF2S3L PE=1 SV=2	Q2VIR3	1	1	
Estrogen-related receptor gamma OS=Homo sapiens GN=ESRRG PE=1 SV=1	P62508	1		
Enhancer of filamentation 1 OS=Homo sapiens GN=NEDD9 PE=1 SV=1	Q14511	1		
Endoplasmic reticulum aminopeptidase 2 OS=Homo sapiens GN=ERAP2 PE=1 SV=2	Q6P179	1		
Embryonic polyadenylate-binding protein 2 OS=Homo sapiens GN=PABPN1L PE=2 SV=1	A6NDY0	1		
Eukaryotic translation initiation factor 4E transporter OS=Homo sapiens GN=EIF4ENIF1 PE=1 SV=2	Q9NRA8	1		2
Elongator complex protein 2 OS=Homo sapiens GN=ELP2 PE=1 SV=2	Q6IA86	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	P56537	1		
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	P24534	1	1	1
ELL-associated factor 2 OS=Homo sapiens GN=EAF2 PE=1 SV=1	Q96CJ1	1		
Ectonucleotide pyrophosphatase/phosphodiesterase family member 1 OS=Homo sapiens GN=ENPP1 PE=1 SV=2	P22413	1		
E3 UFM1-protein ligase 1 OS=Homo sapiens GN=KIAA0776 PE=1 SV=2	O94874	1		
E3 ubiquitin-protein ligase SMURF2 OS=Homo sapiens GN=SMURF2 PE=1 SV=1	Q9HAU4	1		
E3 ubiquitin-protein ligase PDZRN3 OS=Homo sapiens GN=PDZRN3 PE=1 SV=2	Q9UPQ7	1		1
E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	Q7Z6Z7	1		
E3 ubiquitin-protein ligase DZIP3 OS=Homo sapiens GN=DZIP3 PE=1 SV=2	Q86Y13	1		
E1A-binding protein p400 OS=Homo sapiens GN=EP400 PE=1 SV=3	Q96L91	1		1
Dynein heavy chain 7, axonemal OS=Homo sapiens GN=DNAH7 PE=1 SV=2	Q8WXX0	1	3	3
Dynein heavy chain 1, axonemal OS=Homo sapiens GN=DNAH1 PE=1 SV=3	Q9P2D7	1		
cDNA FLJ57338, moderately similar to Mus musculus UDP glucuronosyltransferase 2 family, polypeptide A2, mRNA OS=Homo sapiens	B4E2F4	1		
Elongator complex protein 3 OS=Homo sapiens GN=ELP3 PE=1 SV=2	Q9H9T3	1		1
Gamma-2-syntrophin OS=Homo sapiens GN=SNTG2 PE=1 SV=2	Q9NY99	1		
GUCA1B protein (Fragment) OS=Homo sapiens GN=GUCA1B	A4FUA1	1		
Guanine nucleotide-binding protein G(olf) subunit alpha OS=Homo sapiens GN=GNAL PE=1 SV=1	P38405	1		
Growth hormone-inducible transmembrane protein OS=Homo sapiens GN=GHITM PE=1 SV=2	Q9H3K2	1	1	
Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2	Q08378	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1	P49915	1		
Glycosyltransferase 54 domain-containing protein OS=Homo sapiens PE=2 SV=3	A6NG13	1	1	
Glycine N-acyltransferase OS=Homo sapiens GN=GLYAT PE=1 SV=3	Q6IB77	1	1	2
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	P04406	1		
Glutamyl aminopeptidase OS=Homo sapiens GN=ENPEP PE=1 SV=3	Q07075	1		1
Glutaminyl-tRNA synthetase OS=Homo sapiens GN=QARS PE=1 SV=1	P47897	1	1	
Glutamate dehydrogenase 2, mitochondrial OS=Homo sapiens GN=GLUD2 PE=1 SV=2	P49448	1		
Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4	Q04637	1		
Gem-associated protein 8 OS=Homo sapiens GN=GEMIN8 PE=1 SV=1	Q9NWZ8	1	2	
Dual specificity protein phosphatase 7 OS=Homo sapiens GN=DUSP7 PE=1 SV=3	Q16829	1		
FYVE, RhoGEF and PH domain-containing protein 4 OS=Homo sapiens GN=FGD4 PE=1 SV=2	Q96M96	1		
Frizzled-1 OS=Homo sapiens GN=FZD1 PE=1 SV=2	Q9UP38	1		
Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	O75369	1		
Ficolin-2 OS=Homo sapiens GN=FCN2 PE=1 SV=2	Q15485	1		
Fibrous sheath-interacting protein 2 OS=Homo sapiens GN=FSIP2 PE=1 SV=4	Q5CZC0	1		
F-box/WD repeat-containing protein 9 OS=Homo sapiens GN=FBXW9 PE=1 SV=2	Q5XUX1	1		
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	P49327	1	2	4
F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	P47756	1		1
Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	O43592	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	O14980	1	2	2
Exosome complex exonuclease RRP45 OS=Homo sapiens GN=EXOSC9 PE=1 SV=3	Q06265	1		
Exosome complex exonuclease RRP4 OS=Homo sapiens GN=EXOSC2 PE=1 SV=2	Q13868	1		
Girdin OS=Homo sapiens GN=CCDC88A PE=1 SV=2	Q3V6T2	1		7
Centrosomal protein of 152 kDa OS=Homo sapiens GN=CEP152 PE=1 SV=3	O94986	1		
Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4	Q13561	1		2
Coiled-coil domain-containing protein 18 OS=Homo sapiens GN=CCDC18 PE=1 SV=1	Q5T9S5	1		
Coiled-coil domain-containing protein 150 OS=Homo sapiens GN=CCDC150 PE=2 SV=2	Q8NCX0	1		
Codanin-1 OS=Homo sapiens GN=CDAN1 PE=1 SV=4	Q8IWY9	1	2	
Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2	P35606	1		3
Coagulation factor VIII OS=Homo sapiens GN=F8 PE=1 SV=1	P00451	1	1	1
Chromodomain-helicase-DNA-binding protein 8 OS=Homo sapiens GN=CHD8 PE=1 SV=4	Q9HCK8	1		
Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CHD6 PE=1 SV=4	Q8TD26	1		
Chromodomain-helicase-DNA-binding protein 2 OS=Homo sapiens GN=CHD2 PE=1 SV=2	O14647	1		
Chromobox protein homolog 6 OS=Homo sapiens GN=CBX6 PE=1 SV=1	O95503	1		
Charged multivesicular body protein 2b OS=Homo sapiens GN=CHMP2B PE=1 SV=1	Q9UQN3	1	1	
Collagen alpha-3(IV) chain OS=Homo sapiens GN=COL4A3 PE=1 SV=3	Q01955	1		
Centrosomal protein of 70 kDa OS=Homo sapiens GN=CEP70 PE=1 SV=2	Q8NHQ1	1		7
Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	P02748	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Centromere-associated protein E OS=Homo sapiens GN=CENPE PE=1 SV=2	Q02224	1		1
Centlein OS=Homo sapiens GN=CNTLN PE=2 SV=4	Q9NXG0	1		1
Cell division protein kinase 9 OS=Homo sapiens GN=CDK9 PE=1 SV=3	P50750	1		
Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2	Q99459	1	1	
Cell differentiation protein RCD1 homolog OS=Homo sapiens GN=RQCD1 PE=1 SV=1	Q92600	1		
Cell adhesion molecule-related/down-regulated by oncogenes OS=Homo sapiens GN=CDON PE=1 SV=2	Q4KMG0	1		
CEBPD protein OS=Homo sapiens GN=CEBPD	Q504X4	1		
cDNA FLJ77204 OS=Homo sapiens	A8K9T0	1		
cDNA FLJ60502, highly similar to homeodomain transcription factor 1 OS=Homo sapiens	B4DGS8	1		
cDNA FLJ60374 OS=Homo sapiens	B4DYY8	1	1	
cDNA FLJ58690, highly similar to Solute carrier family 2, facilitated glucosetransporter member 11 OS=Homo sapiens	B7Z6F0	1		
HAUS augmin-like complex subunit 7 OS=Homo sapiens GN=HAUS7 PE=1 SV=3	Q99871	1		
Centrosomal protein of 78 kDa OS=Homo sapiens GN=CEP78 PE=1 SV=1	Q5JTW2	1		
Cytotoxic and regulatory T-cell molecule OS=Homo sapiens GN=CRTAM PE=1 SV=2	O95727	1		
Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1	Q9UJU6	1		
DnaJ homolog subfamily C member 25 OS=Homo sapiens GN=DNAJC25 PE=2 SV=1	Q9H1X3	1		
DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	P31689	1		
DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens GN=POLR1C PE=1 SV=1	O15160	1		
DNA-directed RNA polymerase II subunit RPB7 OS=Homo sapiens GN=POLR2G PE=1 SV=1	P62487	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
DNA-binding protein SATB2 OS=Homo sapiens GN=SATB2 PE=1 SV=2	Q9UPW6	1		
DNA-binding protein A OS=Homo sapiens GN=CSDA PE=1 SV=4	P16989	1	1	1
DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5	P33991	1		
DNA polymerase epsilon catalytic subunit A OS=Homo sapiens GN=POLE PE=1 SV=5	Q07864	1		
Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1	Q9Y295	1		1
Desmoglein-4 OS=Homo sapiens GN=DSG4 PE=1 SV=1	Q86SJ6	1		
Collagen alpha-2(IV) chain OS=Homo sapiens GN=COL4A2 PE=1 SV=4	P08572	1		
Deoxyhypusine synthase OS=Homo sapiens GN=DHPS PE=1 SV=1	P49366	1		
cDNA FLJ58051, highly similar to Tetraspanin-7 OS=Homo sapiens	B4DDG0	1	1	
Cytosolic 5'-nucleotidase 3 OS=Homo sapiens GN=NT5C3 PE=1 SV=3	Q9H0P0	1	1	
Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	Q7L576	1		
Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	P22695	1	1	
Cyclin-dependent kinase 5 activator 1 OS=Homo sapiens GN=CDK5R1 PE=1 SV=1	Q15078	1		
CUGBP Elav-like family member 3 OS=Homo sapiens GN=CELF3 PE=1 SV=1	Q5SZQ8	1		
CST complex subunit STN1 OS=Homo sapiens GN=OBFC1 PE=1 SV=2	Q9H668	1		
Copper homeostasis protein cutC homolog OS=Homo sapiens GN=CUTC PE=1 SV=1	Q9NTM9	1		
Cooperator of PRMT5 OS=Homo sapiens GN=COPR5 PE=1 SV=3	Q9NQ92	1		
Contactin-6 OS=Homo sapiens GN=CNTN6 PE=1 SV=1	Q9UQ52	1		
Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3	Q96JB2	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Conserved oligomeric Golgi complex subunit 1 OS=Homo sapiens GN=COG1 PE=1 SV=1	Q8WTW3	1		
Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1	Q9BPX3	1		
Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2	Q14126	1		1
Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5	Q9UPN7	1		
Protocadherin gamma-A10 OS=Homo sapiens GN=PCDHGA10 PE=2 SV=1	Q9Y5H3	1		
Putative ATP-dependent RNA helicase DDX11-like protein 8 OS=Homo sapiens GN=DDX11L8 PE=1 SV=1	A8MPP1	1	2	1
Serine/threonine-protein kinase PDIK1L OS=Homo sapiens GN=PDIK1L PE=2 SV=1	Q8N165	1		
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	P30153	1		1
THAP domain-containing protein 9 OS=Homo sapiens GN=THAP9 PE=2 SV=2	Q9H5L6	1	4	2
Putative 60S ribosomal protein L13a-like MGC87657 OS=Homo sapiens PE=5 SV=1	Q6NVV1	1		1
Serine/threonine-protein kinase Nek3 OS=Homo sapiens GN=NEK3 PE=1 SV=2	P51956	1		
Pumilio domain-containing protein C14orf21 OS=Homo sapiens GN=C14orf21 PE=1 SV=1	Q86U38	1	6	2
Serine/threonine-protein kinase Nek11 OS=Homo sapiens GN=NEK11 PE=1 SV=2	Q8NG66	1		
Serpin B10 OS=Homo sapiens GN=SERPINB10 PE=1 SV=1	P48595	1		
Uncharacterized protein C10orf68 OS=Homo sapiens GN=C10orf68 PE=2 SV=1	Q9H943	1		
Proto-oncogene vav OS=Homo sapiens GN=VAV1 PE=1 SV=4	P15498	1		
Proto-oncogene serine/threonine-protein kinase mos OS=Homo sapiens GN=MOS PE=1 SV=1	P00540	1		
Protocadherin-17 OS=Homo sapiens GN=PCDH17 PE=2 SV=2	O14917	1	3	1
Putative uncharacterized protein (Fragment) OS=Homo sapiens	O95420	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Putative 40S ribosomal protein S10-like OS=Homo sapiens GN=RPS10P5 PE=5 SV=1	Q9NQ39	1	1	
Serine/threonine-protein kinase 16 OS=Homo sapiens GN=STK16 PE=1 SV=4	O75716	1		
Protein ITFG3 OS=Homo sapiens GN=ITFG3 PE=1 SV=1	Q9H0X4	1		2
U7 snRNA-associated Sm-like protein LSm11 OS=Homo sapiens GN=LSM11 PE=1 SV=2	P83369	1		
Titin OS=Homo sapiens GN=TTN PE=1 SV=2	Q8WZ42	1	1	2
Putative rhophilin-2-like protein OS=Homo sapiens PE=5 SV=2	A8MT19	1		
Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens GN=USP11 PE=1 SV=3	P51784	1		
Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1	Q16629	1		
Serine/threonine-protein kinase Nek4 OS=Homo sapiens GN=NEK4 PE=1 SV=2	P51957	1		
Thyroid receptor-interacting protein 11 OS=Homo sapiens GN=TRIP11 PE=1 SV=3	Q15643	1		
Tetratricopeptide repeat protein 34 OS=Homo sapiens GN=TTC34 PE=2 SV=2	A8MYJ7	1		2
Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens	B4DGT3	1		
Putative male-specific lethal-3 protein-like 2 OS=Homo sapiens GN=MSL3L2 PE=5 SV=1	P0C860	1		
Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	P26639	1		
Putative gonadotropin-releasing hormone II receptor OS=Homo sapiens GN=GNRHR2 PE=5 SV=3	Q96P88	1		1
UDP-N-acetylglucosamine transferase subunit ALG13 homolog OS=Homo sapiens GN=ALG13 PE=1 SV=2	Q9NP73	1	4	1
THO complex subunit 4 OS=Homo sapiens GN=THOC4 PE=1 SV=3	Q86V81	1		
Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1	O94804	1		
Protein naked cuticle homolog 2 OS=Homo sapiens GN=NKD2 PE=1 SV=1	Q969F2	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
TFIIH basal transcription factor complex helicase XPD subunit OS=Homo sapiens GN=ERCC2 PE=1 SV=1	P18074	1		
TEL2-interacting protein 1 homolog OS=Homo sapiens GN=TTI1 PE=1 SV=3	O43156	1	2	1
Protein phosphatase 1A OS=Homo sapiens GN=PPM1A PE=1 SV=1	P35813	1		2
Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2	Q99959	1		
Uncharacterized protein C20orf117 OS=Homo sapiens GN=C20orf117 PE=1 SV=2	O94964	1		
Mitogen-activated protein kinase 12 OS=Homo sapiens GN=MAPK12 PE=1 SV=3	P53778	1		
Single-chain Fv (Fragment) OS=Homo sapiens GN=scFv	Q65ZC8	1		
Uncharacterized protein C20orf152 OS=Homo sapiens GN=C20orf152 PE=2 SV=2	Q96M20	1		
Protein RMD5 homolog A OS=Homo sapiens GN=RMND5A PE=1 SV=1	Q9H871	1		
Uncharacterized protein C3orf20 OS=Homo sapiens GN=C3orf20 PE=1 SV=2	Q8ND61	1		
Protein LAS1 homolog OS=Homo sapiens GN=LAS1L PE=1 SV=2	Q9Y4W2	1		
Uncharacterized protein C3orf26 OS=Homo sapiens GN=C3orf26 PE=1 SV=2	Q9BQ75	1		
Uncharacterized protein C6orf150 OS=Homo sapiens GN=C6orf150 PE=1 SV=2	Q8N884	1		
Sodium channel protein type 10 subunit alpha OS=Homo sapiens GN=SCN10A PE=1 SV=2	Q9Y5Y9	1		
Tektin-4 OS=Homo sapiens GN=TEKT4 PE=2 SV=1	Q8WW24	1	1	
SLIT-ROBO Rho GTPase-activating protein 1 OS=Homo sapiens GN=SRGAP1 PE=1 SV=1	Q7Z6B7	1		
Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1	P13693	1		
Tetratricopeptide repeat protein 28 OS=Homo sapiens GN=TTC28 PE=1 SV=4	Q96AY4	1		2
Tetratricopeptide repeat protein 17 OS=Homo sapiens GN=TTC17 PE=1 SV=1	Q96AE7	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
SH3 domain-containing kinase-binding protein 1 OS=Homo sapiens GN=SH3KBP1 PE=1 SV=2	Q96B97	1		
Protein unc-79 homolog OS=Homo sapiens GN=KIAA1409 PE=2 SV=3	Q9P2D8	1		
Short stature homeobox protein 2 OS=Homo sapiens GN=SHOX2 PE=2 SV=4	O60902	1	1	
Uncharacterized protein C16orf73 OS=Homo sapiens GN=C16orf73 PE=2 SV=3	Q8N635	1	1	
Protein phosphatase 1D OS=Homo sapiens GN=PPM1D PE=1 SV=1	O15297	1		
Uncharacterized protein C17orf66 OS=Homo sapiens GN=C17orf66 PE=2 SV=2	A2RTY3	1		
U6 snRNA-associated Sm-like protein LSm4 OS=Homo sapiens GN=LSM4 PE=1 SV=1	Q9Y4Z0	1	1	
Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2	P37108	1		1
Ras and Rab interactor 3 OS=Homo sapiens GN=RIN3 PE=1 SV=4	Q8TB24	1		
Protein spire homolog 2 OS=Homo sapiens GN=SPIRE2 PE=1 SV=3	Q8WWL2	1		
Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2	Q8TF72	1	4	
Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	P06702	1		1
Protein rogdi homolog OS=Homo sapiens GN=ROGDI PE=2 SV=1	Q9GZN7	1		
Protein THEMIS OS=Homo sapiens GN=THEMIS PE=1 SV=3	Q8N1K5	1		1
Rho guanine nucleotide exchange factor 15 OS=Homo sapiens GN=ARHGEF15 PE=1 SV=4	O94989	1		
Rheumatoid factor RF-IP16 (Fragment) OS=Homo sapiens	A2J1P0	1		
Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=3	O95359	1		
Ribosomal protein S6 kinase delta-1 OS=Homo sapiens GN=RPS6KC1 PE=1 SV=2	Q96S38	1		
tRNA (adenine-N(1)-)-methyltransferase catalytic subunit TRMT61A OS=Homo sapiens GN=TRMT61A PE=1 SV=1	Q96FX7	1	1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
tRNA pseudouridine synthase A, mitochondrial OS=Homo sapiens GN=PUS1 PE=1 SV=3	Q9Y606	1		
Transcriptional adapter 2-beta OS=Homo sapiens GN=TADA2B PE=1 SV=2	Q86TJ2	1		
Ribosomal RNA-processing protein 7 homolog A OS=Homo sapiens GN=RRP7A PE=1 SV=2	Q9Y3A4	1		1
Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2	A6NHL2	1	1	1
Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1	Q14692	1		
Transcription termination factor, mitochondrial OS=Homo sapiens GN=MTERF PE=1 SV=1	Q99551	1	1	2
Rho GTPase-activating protein SYDE2 OS=Homo sapiens GN=SYDE2 PE=1 SV=1	Q5VT97	1		
Rho GTPase-activating protein 26 OS=Homo sapiens GN=ARHGAP26 PE=1 SV=1	Q9UNA1	1	1	
Rho GTPase-activating protein 19 OS=Homo sapiens GN=ARHGAP19 PE=1 SV=1	Q14CB8	1		
Transcription initiation factor IIE subunit beta OS=Homo sapiens GN=GTF2E2 PE=1 SV=1	P29084	1		
U7 snRNA-associated Sm-like protein LSm10 OS=Homo sapiens GN=LSM10 PE=1 SV=1	Q969L4	1		
Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2	Q00577	1		
S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2	Q00266	1		
RRP15-like protein OS=Homo sapiens GN=RRP15 PE=1 SV=2	Q9Y3B9	1		
rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2	P22087	1		
RUN domain-containing protein 3B OS=Homo sapiens GN=RUNDC3B PE=1 SV=1	Q96NL0	1		
RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	Q9Y265	1	1	1
Transmembrane and coiled-coil domain-containing protein 2 OS=Homo sapiens GN=TMCO2 PE=2 SV=1	Q7Z6W1	1		
RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	Q9Y230	1	1	4

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Tripartite motif-containing protein 49-like protein MGC161748 OS=Homo sapiens PE=2 SV=1	P0CI26	1		
Transmembrane protease serine 7 OS=Homo sapiens GN=TMPRSS7 PE=2 SV=2	Q7RTY8	1		
Retroviral-like aspartic protease 1 OS=Homo sapiens GN=ASPRV1 PE=1 SV=1	Q53RT3	1		
Transmembrane protein 14B OS=Homo sapiens GN=TMEM14B PE=2 SV=1	Q9NUH8	1		
Sal-like protein 3 OS=Homo sapiens GN=SALL3 PE=2 SV=2	Q9BXA9	1	1	
SCAN domain-containing protein 3 OS=Homo sapiens GN=SCAND3 PE=2 SV=1	Q6R2W3	1		
RING finger and SPRY domain-containing protein 1 OS=Homo sapiens GN=RSPRY1 PE=2 SV=1	Q96DX4	1		
RIMS-binding protein 3A OS=Homo sapiens GN=RIMBP3 PE=1 SV=3	Q9UFD9	1		
Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	Q8NDV7	1	1	
RNA binding motif protein, X-linked-like 1 (Fragment) OS=Homo sapiens GN=RBMXL1	Q5T9T9	1		
Putative uncharacterized protein ENSP00000383309 OS=Homo sapiens PE=5 SV=3	A8MUU9	1		1
Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3	P52565	1		
RalBP1-associated Eps domain-containing protein 1 OS=Homo sapiens GN=REPS1 PE=1 SV=3	Q96D71	1		
Rab9 effector protein with kelch motifs OS=Homo sapiens GN=RABEPK PE=1 SV=1	Q7Z6M1	1	2	
Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	P50395	1		
Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=2	Q53H96	1		
Tyrosine-protein phosphatase non-receptor type 21 OS=Homo sapiens GN=PTPN21 PE=1 SV=2	Q16825	1		
Serine hydroxymethyltransferase OS=Homo sapiens	B4DWA7	1		
TPR repeat-containing protein C10orf93 OS=Homo sapiens GN=C10orf93 PE=2 SV=2	Q5SR76	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Transcription factor BTF3 OS=Homo sapiens GN=BTF3 PE=1 SV=1	P20290	1		
U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2	P08621	1		
Putative uncharacterized protein DKFZp781D2453 OS=Homo sapiens GN=DKFZp781D2453	Q68DE7	1		
U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2	P09661	1	1	
Putative uncharacterized protein C13orf35 OS=Homo sapiens GN=C13orf35 PE=2 SV=1	Q6ZP68	1		
U2 small nuclear ribonucleoprotein B'' OS=Homo sapiens GN=SNRPB2 PE=1 SV=1	P08579	1		
Putative uncharacterized protein C12orf63 OS=Homo sapiens GN=C12orf63 PE=2 SV=2	Q6ZTY8	1		
Tyrosine-protein phosphatase non-receptor type 23 OS=Homo sapiens GN=PTPN23 PE=1 SV=1	Q9H3S7	1		
Ras-responsive element-binding protein 1 OS=Homo sapiens GN=RREB1 PE=1 SV=3	Q92766	1		
Retinol dehydrogenase 10 OS=Homo sapiens GN=RDH10 PE=1 SV=1	Q8IZV5	1		
Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1	Q9HB40	1		
Sentrin-specific protease 7 OS=Homo sapiens GN=SENP7 PE=1 SV=4	Q9BQF6	1		
Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=1 SV=1	Q14257	1	1	
RelA-associated inhibitor OS=Homo sapiens GN=PPP1R13L PE=1 SV=4	Q8WUF5	1		
Tubulin polyglutamylase TTLL6 OS=Homo sapiens GN=TTLL6 PE=2 SV=2	Q8N841	1		
Serine protease 55 OS=Homo sapiens GN=PRSS55 PE=2 SV=2	Q6UWB4	1		
RB1-inducible coiled-coil protein 1 OS=Homo sapiens GN=RB1CC1 PE=1 SV=3	Q8TDY2	1		
Signal recognition particle 68 kDa protein OS=Homo sapiens GN=SRP68 PE=1 SV=2	Q9UHB9	1		
Ras-related protein Rab-37 OS=Homo sapiens GN=RAB37 PE=1 SV=3	Q96AX2	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	P46940	1		6
Septin-12 OS=Homo sapiens GN=SEPT12 PE=1 SV=1	Q8IYM1	1		
Tumor protein 63 OS=Homo sapiens GN=TP63 PE=1 SV=1	Q9H3D4	1		
Transcription factor E2F1 OS=Homo sapiens GN=E2F1 PE=1 SV=1	Q01094	1	2	2
Type I inositol-3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4A PE=1 SV=1	Q96PE3	1		
Receptor-type tyrosine-protein phosphatase T OS=Homo sapiens GN=PTPRT PE=1 SV=5	O14522	1	1	
Zinc finger CCCH domain-containing protein 7B OS=Homo sapiens GN=ZC3H7B PE=1 SV=1	Q9UGR2	1		
Shugoshin-like 2 OS=Homo sapiens GN=SGOL2 PE=1 SV=2	Q562F6	1		
WD repeat-containing protein 87 OS=Homo sapiens GN=WDR87 PE=2 SV=3	Q6ZQQ6	1		
Xanthine dehydrogenase/oxidase OS=Homo sapiens GN=XDH PE=1 SV=4	P47989	1		
Spindlin-3 OS=Homo sapiens GN=SPIN3 PE=2 SV=1	Q5JUX0	1		
X-linked retinitis pigmentosa GTPase regulator OS=Homo sapiens GN=RPGR PE=1 SV=2	Q92834	1		
Zinc finger and BTB domain-containing protein 34 OS=Homo sapiens GN=ZBTB34 PE=2 SV=4	Q8NCN2	1		
Zinc finger protein 161 homolog OS=Homo sapiens GN=ZFP161 PE=2 SV=2	O43829	1		
Probable phospholipid-transporting ATPase IK OS=Homo sapiens GN=ATP8B3 PE=2 SV=4	O60423	1	1	1
Sperm-associated antigen 8 OS=Homo sapiens GN=SPAG8 PE=1 SV=2	Q99932	1		
Probable histone-lysine N-methyltransferase NSD2 OS=Homo sapiens GN=WHSC1 PE=1 SV=1	O96028	1		
Probable helicase with zinc finger domain OS=Homo sapiens GN=HELZ PE=1 SV=2	P42694	1		
Zinc finger FYVE domain-containing protein 1 OS=Homo sapiens GN=ZFYVE1 PE=1 SV=1	Q9HBF4	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Zinc finger FYVE domain-containing protein 9 OS=Homo sapiens GN=ZFYVE9 PE=1 SV=2	O95405	1		
Zinc finger matrin-type protein 2 OS=Homo sapiens GN=ZMAT2 PE=1 SV=1	Q96NC0	1		
UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	Q9Y224	1		
Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3	P35080	1		
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	P49748	1		
Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2	Q8IVF2	1		1
Protein AF1q OS=Homo sapiens GN=MLLT11 PE=2 SV=1	Q13015	1		
Uronyl 2-sulfotransferase OS=Homo sapiens GN=UST PE=2 SV=1	Q9Y2C2	1		
Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2	Q5VYK3	1		
Sorting nexin-20 OS=Homo sapiens GN=SNX20 PE=1 SV=1	Q7Z614	1		1
T-box transcription factor TBX5 OS=Homo sapiens GN=TBX5 PE=1 SV=2	Q99593	1		
TATA-binding protein-associated factor 172 OS=Homo sapiens GN=BTAF1 PE=1 SV=2	O14981	1		1
Spectrin beta chain, brain 3 OS=Homo sapiens GN=SPTBN4 PE=1 SV=2	Q9H254	1		1
Protein furry homolog-like OS=Homo sapiens GN=FRYL PE=1 SV=2	O94915	1		
Vesicular glutamate transporter 1 OS=Homo sapiens GN=SLC17A7 PE=2 SV=1	Q9P2U7	1		
Voltage-dependent L-type calcium channel subunit alpha-1C OS=Homo sapiens GN=CACNA1C PE=1 SV=4	Q13936	1		
TBC1 domain family member 8B OS=Homo sapiens GN=TBC1D8B PE=2 SV=2	Q0IIM8	1		
Spectrin beta chain, brain 4 OS=Homo sapiens GN=SPTBN5 PE=1 SV=1	Q9NRC6	1		
TBC1 domain family member 10B OS=Homo sapiens GN=TBC1D10B PE=1 SV=3	Q4KMP7	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
WAP, kazal, immunoglobulin, kunitz and NTR domain-containing protein 1 OS=Homo sapiens GN=WFIKKN1 PE=1 SV=1	Q96NZ8	1		
Splicing factor 3A subunit 2 OS=Homo sapiens GN=SF3A2 PE=1 SV=2	Q15428	1		
V_segment translation product (Fragment) OS=Homo sapiens GN=TCRBV18S1	A0A5B2	1		
Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	Q14247	1		
Zinc finger protein 536 OS=Homo sapiens GN=ZNF536 PE=1 SV=3	O15090	1		1
Splicing factor 3B subunit 5 OS=Homo sapiens GN=SF3B5 PE=1 SV=1	Q9BWJ5	1		
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	P11940	1	3	1
Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1	Q15366	1		2
Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	Q15365	1	1	4
Sushi domain-containing protein 2 OS=Homo sapiens GN=SUSD2 PE=1 SV=1	Q9UGT4	1		
Zinc finger protein 134 OS=Homo sapiens GN=ZNF134 PE=2 SV=2	P52741	1		
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	P23246	1		
Zinc finger protein 526 OS=Homo sapiens GN=ZNF526 PE=2 SV=2	Q8TF50	1		
Zinc finger protein 99 OS=Homo sapiens GN=ZNF99 PE=2 SV=2	A8MXY4	1		
StAR-related lipid transfer protein 9 OS=Homo sapiens GN=STARD9 PE=2 SV=2	Q9P2P6	1		
Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	O95347	1		
Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZZEF1 PE=1 SV=6	O43149	1		
Suppressor of cytokine signaling 7 OS=Homo sapiens GN=SOCS7 PE=1 SV=2	O14512	1		
SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3	Q9UH99	1		

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Zinc finger protein 648 OS=Homo sapiens GN=ZNF648 PE=1 SV=1	Q5T619	1		
Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=1 SV=1	Q9UHV9	1	1	
Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	Q15427	1	1	
Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial OS=Homo sapiens GN=DHTKD1 PE=2 SV=2	Q96HY7	1		1
PRO0195 OS=Homo sapiens	Q9UI79	1		
Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1	O75934	1		
Zinc finger protein 318 OS=Homo sapiens GN=ZNF318 PE=1 SV=2	Q5VUA4	1		
Zinc finger protein 35 OS=Homo sapiens GN=ZNF35 PE=2 SV=4	P13682	1		
Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1	Q8IXK0	1		
Prefoldin subunit 4 OS=Homo sapiens GN=PFDN4 PE=1 SV=1	Q9NQP4	1		
Zinc finger protein 528 OS=Homo sapiens GN=ZNF528 PE=2 SV=1	Q3MIS6	1		
Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2	O60925	1		
PRAME family member 20/21 OS=Homo sapiens GN=PRAMEF20 PE=2 SV=1	Q5VT98	1		
Potassium voltage-gated channel subfamily A member 2 OS=Homo sapiens GN=KCNA2 PE=1 SV=2	P16389	1		
Potassium channel subfamily K member 5 OS=Homo sapiens GN=KCNK5 PE=1 SV=1	O95279	1		
Synaptonemal complex protein 2-like OS=Homo sapiens GN=SYCP2L PE=1 SV=2	Q5T4T6	1		
Zinc finger protein 469 OS=Homo sapiens GN=ZNF469 PE=1 SV=3	Q96JG9	1		1
Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2	Q16186	1		1
Prefoldin subunit 5 OS=Homo sapiens GN=PFDN5 PE=1 SV=2	Q99471	1	1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Uncharacterized protein KIAA1109 OS=Homo sapiens GN=KIAA1109 PE=1 SV=1	Q2LD37	1	1	
Uncharacterized protein OS=Homo sapiens GN=RECQL4	C9JFV7	1		1
T-complex protein 10A homolog 2 OS=Homo sapiens GN=TCP10L PE=2 SV=1	Q8TDR4	1		
Protein CIP2A OS=Homo sapiens GN=KIAA1524 PE=1 SV=2	Q8TCG1	1		
T-complex protein 1 subunit zeta-2 OS=Homo sapiens GN=CCT6B PE=1 SV=4	Q92526	1		
Uncharacterized protein OS=Homo sapiens GN=PUM1	A6NDW8	1		
Protein FAM65B OS=Homo sapiens GN=FAM65B PE=1 SV=4	Q9Y4F9	1		
Protein FAM59A OS=Homo sapiens GN=FAM59A PE=1 SV=2	Q9H706	1		
Solute carrier family 22 member 13 OS=Homo sapiens GN=SLC22A13 PE=2 SV=2	Q9Y226	1		
Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3	Q99523	1		
Protein FAM73B OS=Homo sapiens GN=FAM73B PE=1 SV=1	Q7L4E1	1		
Uncharacterized protein OS=Homo sapiens GN=FBLN7	B8ZZC1	1		
Protein FAM5B OS=Homo sapiens GN=FAM5B PE=2 SV=2	Q9C0B6	1		
Protein Daple OS=Homo sapiens GN=CCDC88C PE=1 SV=3	Q9P219	1		
Uncharacterized protein OS=Homo sapiens GN=ARMC9	C9J535	1		
Protein FAM195B OS=Homo sapiens GN=FAM195B PE=1 SV=1	C9JLW8	1		
Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	Q99497	1		
Son of sevenless homolog 1 OS=Homo sapiens GN=SOS1 PE=1 SV=1	Q07889	1		
Protein FAM102A OS=Homo sapiens GN=FAM102A PE=2 SV=2	Q5T9C2	1	2	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Protein AKNAD1 OS=Homo sapiens GN=AKNAD1 PE=2 SV=2	Q5T1N1	1		
TAT protein OS=Homo sapiens	Q8WW92	1		
Uncharacterized protein OS=Homo sapiens	A8MY96	1		
Protein FAM172A OS=Homo sapiens GN=FAM172A PE=2 SV=1	Q8WUF8	1		
Solute carrier family 22 member 15 OS=Homo sapiens GN=SLC22A15 PE=2 SV=1	Q8IZD6	1	1	
Uncharacterized protein OS=Homo sapiens GN=SNTN	C9JRU3	1		1
Protein BAT2-like 2 OS=Homo sapiens GN=BAT2L2 PE=1 SV=2	Q9Y520	1		1
Uncharacterized protein OS=Homo sapiens GN=SUMO3	A8MU27	1		
Sodium/iodide cotransporter OS=Homo sapiens GN=SLC5A5 PE=1 SV=1	Q92911	1		
Uncharacterized protein C9orf84 OS=Homo sapiens GN=C9orf84 PE=2 SV=1	Q5VXU9	1		
Uncharacterized protein KIAA0141, mitochondrial OS=Homo sapiens GN=KIAA0141 PE=2 SV=3	Q14154	1		
Protein BAT2-like 1 OS=Homo sapiens GN=BAT2L1 PE=1 SV=2	Q5JSZ5	1		
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	P49368	1	1	5
T-complex protein 11-like protein 1 OS=Homo sapiens GN=TCP11L1 PE=1 SV=1	Q9NUJ3	1		
Sodium/hydrogen exchanger OS=Homo sapiens	B4DX51	1		
Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1	O43237			1
cDNA FLJ55789, highly similar to Rattus norvegicus basic leucine zipper and W2 domains 1 (Bzw1), mRNA OS=Homo sapiens	B4DLZ8			1
cDNA FLJ54712, highly similar to Tight junction protein ZO-2 OS=Homo sapiens	B7Z7T6			1
cDNA FLJ54162, moderately similar to CDP-diacylglycerol--inositol3-phosphatidyltransferase (EC 2.7.8.11) OS=Homo sapiens	B4DUV0		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	P02452		1	
Coatomer subunit zeta-1 OS=Homo sapiens GN=COPZ1 PE=1 SV=1	P61923			2
Coiled-coil domain-containing protein 33 OS=Homo sapiens GN=CCDC33 PE=1 SV=3	Q8N5R6		3	1
Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=3	P22105		1	
Cytochrome b5 reductase 4 OS=Homo sapiens GN=CYB5R4 PE=1 SV=1	Q7L1T6			1
Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens GN=EIF2B5 PE=1 SV=3	Q13144			1
cDNA FLJ57032, moderately similar to Tubulin-specific chaperone E OS=Homo sapiens	B7Z4X8		1	
Suppression of tumorigenicity 18 protein OS=Homo sapiens GN=ST18 PE=1 SV=1	O60284		1	
Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	P53618		1	2
Cylicin-1 OS=Homo sapiens GN=CYLC1 PE=1 SV=2	P35663		1	
Synaptonemal complex protein 3 OS=Homo sapiens GN=SYCP3 PE=2 SV=1	Q8IZU3		1	
Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	P53621			1
CCR4-NOT transcription complex subunit 10 OS=Homo sapiens GN=CNOT10 PE=1 SV=1	Q9H9A5		1	
Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	Q92616			1
cDNA FLJ46097 fis, clone TESTI2021112 OS=Homo sapiens	Q6ZRU3		1	
cDNA FLJ37345 fis, clone BRAMY2021142, highly similar to Homo sapiens transmembrane channel-like 7 (TMC7), mRNA OS=Homo sapiens	B3KSZ3			1
cDNA FLJ40178 fis, clone TESTI2017932 OS=Homo sapiens	Q8N7Z9			1
Transient receptor potential cation channel subfamily M member 8 OS=Homo sapiens GN=TRPM8 PE=2 SV=2	Q7Z2W7		1	
Coiled-coil domain-containing protein 147 OS=Homo sapiens GN=CCDC147 PE=2 SV=1	Q5T655		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
cDNA FLJ43252 fis, clone HEART2006909 OS=Homo sapiens	Q6ZUX1		1	
Coiled-coil domain-containing protein 36 OS=Homo sapiens GN=CCDC36 PE=1 SV=2	Q8IYA8			1
CDNA FLJ26488 fis, clone KDN05770, highly similar to Bumetanide-sensitive sodium-(potassium)-chloride cotransporter 2 OS=Homo sapiens	Q6ZP54		2	2
cDNA FLJ16186 fis, clone BRTHA2007060, moderately similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 OS=Homo sapiens	Q6ZNE1			1
Coiled-coil domain-containing protein 144A OS=Homo sapiens GN=CCDC144A PE=1 SV=1	A2RUR9			1
Transcription factor E2F2 OS=Homo sapiens GN=E2F2 PE=1 SV=1	Q14209		1	
Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3	Q9Y6G9			1
Collagen alpha-1(IV) chain OS=Homo sapiens GN=COL4A1 PE=1 SV=3	P02462			1
Coiled-coil domain-containing protein 14 OS=Homo sapiens GN=CCDC14 PE=2 SV=3	Q49A88			1
cDNA FLJ52272, highly similar to Rhabdoid tumor deletion region protein 1 OS=Homo sapiens	B7Z5X4			1
cDNA FLJ52882, highly similar to Pyruvate dehydrogenase (lipoamide) kinase isozyme 2 (EC 2.7.11.2) OS=Homo sapiens	B4DEF3		1	
Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3	Q13409			1
Transducin beta-like protein 3 OS=Homo sapiens GN=TBL3 PE=1 SV=2	Q12788			1
Transcriptional regulator ATRX OS=Homo sapiens GN=ATRX PE=1 SV=5	P46100			1
Coiled-coil domain-containing protein 125 OS=Homo sapiens GN=CCDC125 PE=2 SV=2	Q86Z20			1
cDNA FLJ53577, highly similar to pre-mRNA-splicing factor ATP-dependentRNA helicase DHX16 (EC 3.6.1.-) OS=Homo sapiens	B4DZ28		1	1
Cytochrome c oxidase subunit 6A1, mitochondrial OS=Homo sapiens GN=COX6A1 PE=1 SV=4	P12074		1	
cDNA FLJ32537 fis, clone SMINT2000400, highly similar to Homo sapiens FRG1 mRNA OS=Homo sapiens	Q96MD3			1
Coiled-coil domain-containing protein 110 OS=Homo sapiens GN=CCDC110 PE=2 SV=1	Q8TBZ0			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Translation initiation factor eIF-2B subunit beta OS=Homo sapiens GN=EIF2B2 PE=1 SV=3	P49770			1
Chloride channel protein ClC-Ka OS=Homo sapiens GN=CLCNKA PE=1 SV=1	P51800			1
Transcription factor EB OS=Homo sapiens GN=TFEB	B0QYS6		1	
TPH2 protein OS=Homo sapiens GN=TPH2	Q14CC5		1	
Chromosome 20 open reading frame 4 OS=Homo sapiens GN=C20orf4	A2A2Q9			1
Toll-like receptor 8 OS=Homo sapiens GN=TLR8 PE=1 SV=1	Q9NR97		1	
Conserved oligomeric Golgi complex subunit 2 OS=Homo sapiens GN=COG2 PE=1 SV=1	Q14746			1
Tetratricopeptide repeat protein 5 OS=Homo sapiens GN=TTC5 PE=1 SV=2	Q8N0Z6		1	1
Tissue factor pathway inhibitor 2 OS=Homo sapiens GN=TFPI2 PE=1 SV=1	P48307		1	
Tetratricopeptide repeat protein 7A OS=Homo sapiens GN=TTC7A PE=1 SV=3	Q9ULT0			1
Chromobox protein homolog 8 OS=Homo sapiens GN=CBX8 PE=1 SV=3	Q9HC52			1
Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2	Q8IX12		1	
Condensin-2 complex subunit H2 OS=Homo sapiens GN=NCAPH2 PE=1 SV=1	Q6IBW4		1	
Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	P12110			1
Taste receptor type 2 member 19 OS=Homo sapiens GN=TAS2R19 PE=1 SV=1	P59542		1	
Thrombospondin type-1 domain-containing protein 1 OS=Homo sapiens GN=THSD1 PE=1 SV=1	Q9NS62		1	1
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	Q9Y490			6
Cell growth-inhibiting protein 48c OS=Homo sapiens	B1H0U4			1
Threonyl-tRNA synthetase, mitochondrial OS=Homo sapiens GN=TARS2 PE=1 SV=1	Q9BW92		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Centriolin OS=Homo sapiens GN=CEP110 PE=1 SV=2	Q7Z7A1			1
Centromere protein C 1 OS=Homo sapiens GN=CENPC1 PE=1 SV=2	Q03188			1
T-box transcription factor TBX19 OS=Homo sapiens GN=TBX19 PE=1 SV=3	O60806			1
Complexin-2 OS=Homo sapiens GN=CPLX2 PE=1 SV=2	Q6PUV4			1
THAP domain-containing protein 5 OS=Homo sapiens GN=THAP5 PE=1 SV=2	Q7Z6K1		1	
Chaperone activity of bc1 complex-like, mitochondrial OS=Homo sapiens GN=CABC1 PE=1 SV=1	Q8NI60			1
Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3	P07358			1
Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3	O43396			1
Complement C1q tumor necrosis factor-related protein 5 OS=Homo sapiens GN=C1QTNF5 PE=1 SV=1	Q9BXJ0		1	1
Centrosome and spindle pole-associated protein 1 OS=Homo sapiens GN=CSPP1 PE=1 SV=4	Q1MSJ5		1	
Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	P10643			1
Cholecystokinin B receptor splice variant long isoform (Fragment) OS=Homo sapiens GN=CCKBR	A0SEH4			1
cDNA FLJ61364, highly similar to Gamma-glutamyltransferase 4 (EC 2.3.2.2) OS=Homo sapiens	B4DRZ0			1
Transcription factor SOX-12 OS=Homo sapiens GN=SOX12 PE=2 SV=2	O15370			2
Transcription factor jun-B OS=Homo sapiens GN=JUNB PE=1 SV=1	P17275		4	1
CWF19-like protein 2 OS=Homo sapiens GN=CWF19L2 PE=1 SV=4	Q2TBE0			1
cDNA FLJ58291, moderately similar to Neutral alpha-glucosidase C (EC 3.2.1.20) OS=Homo sapiens	B4DWC5			1
Testin OS=Homo sapiens GN=TES PE=1 SV=1	Q9UGI8		1	
CVWG5837 OS=Homo sapiens GN=UNQ5837	Q6UXY5			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
cDNA FLJ59202, moderately similar to Homo sapiens CGI-121 protein (CGI-121), mRNA OS=Homo sapiens	B4DHS0			1
cDNA FLJ59586, highly similar to Diacylglycerol kinase zeta (EC 2.7.1.107) OS=Homo sapiens	B7Z1L2			1
Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 SV=3	P20908		1	
Synaptophysin OS=Homo sapiens GN=SYP PE=1 SV=3	P08247		1	
Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	P12259		1	
cDNA FLJ60845, highly similar to Telomere-associated protein RIF1 OS=Homo sapiens	B4DS49		1	
CLASP2 protein OS=Homo sapiens GN=CLASP2	B2RTR1		1	
cDNA FLJ61332, highly similar to Rho-GTPase-activating protein 25 OS=Homo sapiens	B7Z5A5			1
Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	P00488			1
cDNA FLJ61688 OS=Homo sapiens	B4DK58			1
Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2	Q02388		1	1
Crumbs homolog 1 OS=Homo sapiens GN=CRB1 PE=1 SV=2	P82279			1
cDNA FLJ76742, highly similar to Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2, mRNA OS=Homo sapiens	A8K119			1
Testis-expressed sequence 15 protein OS=Homo sapiens GN=TEX15 PE=1 SV=2	Q9BXT5		1	
Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL17A1 PE=1 SV=3	Q9UMD9			1
Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1	O00560			2
Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909		1	
CLIP-associating protein 1 OS=Homo sapiens GN=CLASP1 PE=1 SV=1	Q7Z460			1
T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	P40227		2	5

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Tetratricopeptide repeat protein 25 OS=Homo sapiens GN=TTC25 PE=1 SV=2	Q96NG3			1
cDNA: FLJ22753 fis, clone KAIA0597 OS=Homo sapiens	Q9H5Z5		1	
Copine-5 OS=Homo sapiens GN=CPNE5 PE=1 SV=2	Q9HCH3			1
Synaptosomal-associated protein 29 OS=Homo sapiens GN=SNAP29 PE=1 SV=1	O95721			1
Uncharacterized protein KIAA0748 OS=Homo sapiens GN=KIAA0748 PE=1 SV=2	A2RU30		1	
Uncharacterized protein OS=Homo sapiens GN=SPIN2A	A6NMQ5		1	
Uncharacterized protein C9orf170 OS=Homo sapiens GN=C9orf170 PE=2 SV=1	A2RU37			1
Acyl-CoA dehydrogenase family member 11 OS=Homo sapiens GN=ACAD11 PE=1 SV=2	Q709F0			1
Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3	Q8N3C0			1
Uncharacterized protein C9orf172 OS=Homo sapiens GN=C9orf172 PE=3 SV=1	C9J069			1
Uncharacterized protein C9orf50 OS=Homo sapiens GN=C9orf50 PE=2 SV=1	Q5SZB4			1
Actin-binding protein IPP OS=Homo sapiens GN=IPP PE=2 SV=1	Q9Y573		2	
Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	P68133			1
Acetylcholine receptor subunit beta OS=Homo sapiens GN=CHRNB1 PE=1 SV=3	P11230			1
ADP-ribosylation factor-like protein 3 OS=Homo sapiens GN=ARL3 PE=1 SV=2	P36405		1	
A disintegrin and metalloproteinase with thrombospondin motifs 2 OS=Homo sapiens GN=ADAMTS2 PE=2 SV=2	O95450		1	1
Adseverin OS=Homo sapiens GN=SCIN PE=1 SV=4	Q9Y6U3			1
Uncharacterized protein KIAA1210 OS=Homo sapiens GN=KIAA1210 PE=2 SV=3	Q9ULL0			1
Uncharacterized protein KIAA1211 OS=Homo sapiens GN=KIAA1211 PE=1 SV=3	Q6ZU35		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	P17858		2	
Uncharacterized protein OS=Homo sapiens	C9JH24			1
Uncharacterized protein OS=Homo sapiens GN=INS	C9JNR5		1	
Uncharacterized protein OS=Homo sapiens GN=LIMS3	A6NEJ8			1
Uncharacterized protein OS=Homo sapiens GN=OR10J3	B5MD10			1
Uncharacterized protein OS=Homo sapiens GN=PLA2G4E	B7WPN2			1
Uncharacterized protein C13orf40 OS=Homo sapiens GN=C13orf40 PE=2 SV=2	Q8NDH2		1	
Uncharacterized protein KIAA0195 OS=Homo sapiens GN=KIAA0195 PE=1 SV=1	Q12767		1	
Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	P12814			1
Brefeldin A-inhibited guanine nucleotide-exchange protein 3 OS=Homo sapiens GN=ARFGEF3 PE=1 SV=3	Q5TH69			1
Aminoglycoside phosphotransferase domain-containing protein 1 OS=Homo sapiens GN=AGPHD1 PE=2 SV=2	A2RU49		1	
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	Q12904			1
Uncharacterized protein C14orf79 OS=Homo sapiens GN=C14orf79 PE=2 SV=2	Q96F83		1	
Alsin OS=Homo sapiens GN=ALS2 PE=1 SV=2	Q96Q42			1
Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3	P54920			1
Alpha-protein kinase 3 OS=Homo sapiens GN=ALPK3 PE=2 SV=2	Q96L96			1
Alpha-parvin OS=Homo sapiens GN=PARVA PE=1 SV=1	Q9NVD7			1
Alpha-methyl-acyl-CoA racemase OS=Homo sapiens	Q3KT79		1	
Adenylyl cyclase-associated protein 2 OS=Homo sapiens GN=CAP2 PE=1 SV=1	P40123			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2	P35611			1
Uncharacterized protein OS=Homo sapiens GN=UBE2D3	D6RGD0			1
Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT1 PE=2 SV=2	P26572			1
Alpha-(1,3)-fucosyltransferase OS=Homo sapiens GN=FUT4 PE=1 SV=3	P22083		1	
All-trans-retinol 13,14-reductase OS=Homo sapiens GN=RETSAT PE=2 SV=2	Q6NUM9			1
Uncharacterized protein C1orf103 OS=Homo sapiens GN=C1orf103 PE=1 SV=1	Q5T3J3			1
Alcohol dehydrogenase class 4 mu/sigma chain OS=Homo sapiens GN=ADH7 PE=1 SV=2	P40394		1	
Uncharacterized protein C1orf141 OS=Homo sapiens GN=C1orf141 PE=2 SV=1	Q5JVX7			1
A-kinase anchor protein 7 isoform gamma OS=Homo sapiens GN=AKAP7 PE=2 SV=1	Q9P0M2			1
A-kinase anchor protein 6 OS=Homo sapiens GN=AKAP6 PE=1 SV=3	Q13023			1
A-kinase anchor protein 11 OS=Homo sapiens GN=AKAP11 PE=1 SV=1	Q9UKA4			1
Uncharacterized protein C18orf25 OS=Homo sapiens GN=C18orf25 PE=1 SV=2	Q96B23		1	
Zinc finger protein 780B OS=Homo sapiens GN=ZNF780B PE=2 SV=1	Q9Y6R6		1	
60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	P62888		1	1
Zinc finger protein 185 OS=Homo sapiens GN=ZNF185 PE=1 SV=3	O15231		1	
Zinc finger protein 2 OS=Homo sapiens GN=ZNF2 PE=2 SV=3	Q9BSG1			1
Zinc finger protein 311 OS=Homo sapiens GN=ZNF311 PE=1 SV=2	Q5JNZ3			1
2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2	P12694		1	
Zinc finger protein 404 OS=Homo sapiens GN=ZNF404 PE=2 SV=1	Q494X3		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=1 SV=3	Q92552		1	
Zinc finger protein 451 OS=Homo sapiens GN=ZNF451 PE=2 SV=2	Q9Y4E5			1
Zinc finger protein 521 (Early hematopoietic zinc finger protein) (LYST-interacting protein LIP3). (Fragment) OS=Homo sapiens GN=ZNF521	Q8IYZ2			1
Zinc finger matrin-type protein 4 OS=Homo sapiens GN=ZMAT4 PE=2 SV=1	Q9H898		1	
Zinc finger protein 556 OS=Homo sapiens GN=ZNF556 PE=2 SV=1	Q9HAH1			1
Zinc finger CCHC-type and RNA-binding motif-containing protein 1 OS=Homo sapiens GN=ZCRB1 PE=1 SV=2	Q8TBF4			1
Zinc finger protein 92 homolog OS=Homo sapiens GN=ZFP92 PE=2 SV=3	A6NM28		1	
Zinc finger protein Rlf OS=Homo sapiens GN=RLF PE=1 SV=2	Q13129		1	
Zinc finger protein with KRAB and SCAN domains 5 OS=Homo sapiens GN=ZKSCAN5 PE=1 SV=1	Q9Y2L8		1	
26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	P62333			1
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	P63104			4
Zinc finger protein ZFPM2 OS=Homo sapiens GN=ZFPM2 PE=1 SV=3	Q8WW38		1	
Zinc-binding alcohol dehydrogenase domain-containing protein 2 OS=Homo sapiens GN=ZADH2 PE=1 SV=1	Q8N4Q0			1
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	P62258		1	4
Zona pellucida-binding protein 1 OS=Homo sapiens GN=ZPBP PE=2 SV=1	Q9BS86		1	
26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	O00232			2
WD repeat and FYVE domain-containing protein 3 OS=Homo sapiens GN=WDFY3 PE=1 SV=2	Q8IZQ1		1	1
UPF0027 protein C22orf28 OS=Homo sapiens GN=C22orf28 PE=1 SV=1	Q9Y3I0			1
UPF0585 protein C16orf13 OS=Homo sapiens GN=C16orf13 PE=1 SV=2	Q96S19			2

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
V(D)J recombination-activating protein 1 OS=Homo sapiens GN=RAG1 PE=1 SV=2	P15918			1
60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	P84098		1	
V4-6 protein (Fragment) OS=Homo sapiens GN=IGLV11-55	Q5NV87		1	
Vacuolar protein sorting-associated protein 11 homolog OS=Homo sapiens GN=VPS11 PE=1 SV=1	Q9H270			1
Vacuolar protein sorting-associated protein 53 homolog OS=Homo sapiens GN=VPS53 PE=1 SV=1	Q5VIR6		1	
Voltage-gated potassium channel subunit beta-1 OS=Homo sapiens GN=KCNAB1 PE=2 SV=1	Q14722		1	
von Willebrand factor A domain-containing protein 1 OS=Homo sapiens GN=VWA1 PE=2 SV=1	Q6PCB0			1
Zinc finger protein 167 OS=Homo sapiens GN=ZNF167 PE=2 SV=2	Q9P0L1			1
V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3	O75348			1
Amyloid beta A4 precursor protein-binding family A member 2 OS=Homo sapiens GN=APBA2 PE=1 SV=3	Q99767			1
WD repeat-containing protein 16 OS=Homo sapiens GN=WDR16 PE=1 SV=3	Q8N1V2		1	
5'-AMP-activated protein kinase subunit gamma-3 OS=Homo sapiens GN=PRKAG3 PE=2 SV=3	Q9UGI9			2
WD repeat-containing protein 70 OS=Homo sapiens GN=WDR70 PE=1 SV=1	Q9NW82		1	
WD repeat-containing protein C10orf79 OS=Homo sapiens GN=C10orf79 PE=2 SV=3	Q8NDM7			1
WD repeat-containing protein C2orf86 OS=Homo sapiens GN=C2orf86 PE=1 SV=2	O95876			1
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	P62753			1
Xin actin-binding repeat-containing protein 1 OS=Homo sapiens GN=XIRP1 PE=1 SV=1	Q702N8			1
Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens GN=ZC3H11A PE=1 SV=3	O75152		1	
Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3	Q7Z2W4		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
von Willebrand factor C and EGF domain-containing protein OS=Homo sapiens GN=VWCE PE=2 SV=2	Q96DN2			1
BTB/POZ domain-containing protein KCTD3 OS=Homo sapiens GN=KCTD3 PE=1 SV=2	Q9Y597		1	
Breakpoint cluster region protein OS=Homo sapiens GN=BCR PE=1 SV=2	P11274		1	1
Cadherin-4 OS=Homo sapiens GN=CDH4 PE=2 SV=2	P55283		1	
Cadherin-17 OS=Homo sapiens GN=CDH17 PE=1 SV=3	Q12864		1	
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	Q9BQE3			2
Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	Q13509		3	3
C5a anaphylatoxin chemotactic receptor OS=Homo sapiens GN=C5AR1 PE=1 SV=2	P21730			1
C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 OS=Homo sapiens GN=CPAMD8 PE=1 SV=2	Q8IZJ3			1
Tubulin beta-4 chain OS=Homo sapiens GN=TUBB4 PE=1 SV=2	P04350			2
C2 domain-containing protein 3 OS=Homo sapiens GN=C2CD3 PE=1 SV=4	Q4AC94		1	
Calbindin OS=Homo sapiens GN=CALB1 PE=1 SV=2	P05937		1	1
Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2	Q3ZCM7			1
Calcium-activated potassium channel subunit alpha-1 OS=Homo sapiens GN=KCNMA1 PE=1 SV=2	Q12791			1
BTB/POZ domain-containing protein KCTD18 OS=Homo sapiens GN=KCTD18 PE=2 SV=2	Q6PI47		1	
BTB/POZ domain-containing protein KCTD11 OS=Homo sapiens GN=KCTD11 PE=1 SV=1	Q693B1		1	
Tubulin polyglutamylase TTLL7 OS=Homo sapiens GN=TTLL7 PE=2 SV=2	Q6ZT98			1
Tubulin tyrosine ligase-like family, member 11 OS=Homo sapiens GN=TTLL11	B1AP70			1
Bromodomain containing 2 (Fragment) OS=Homo sapiens GN=BRD2	B0V072			2

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Bromodomain and WD repeat-containing protein 1 OS=Homo sapiens GN=BRWD1 PE=1 SV=4	Q9NSI6			1
Cytoplasmic tRNA 2-thiolation protein 1 OS=Homo sapiens GN=CTU1 PE=1 SV=1	Q7Z7A3			1
Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2	Q9UIG0			1
Ammonium transporter Rh type B OS=Homo sapiens GN=RHBG PE=1 SV=2	Q9H310			1
C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L PE=1 SV=3	O14523			1
CAP-Gly domain-containing linker protein 2 OS=Homo sapiens GN=CLIP2 PE=1 SV=1	Q9UDT6		1	
CB1 cannabinoid receptor-interacting protein 1 OS=Homo sapiens GN=CNRIP1 PE=1 SV=1	Q96F85			1
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	P07339			2
Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2	P21964			1
Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3 PE=1 SV=2	Q6ZXV5			1
Transmembrane channel-like 3 OS=Homo sapiens GN=TMC3	A2RTY2			1
Transmembrane protein 126A OS=Homo sapiens GN=TMEM126A PE=1 SV=1	Q9H061			1
Caskin-1 OS=Homo sapiens GN=CASKIN1 PE=1 SV=1	Q8WXD9			1
Carboxypeptidase D OS=Homo sapiens GN=CPD PE=1 SV=2	O75976		1	
Transmembrane protein 200A OS=Homo sapiens GN=TMEM200A PE=2 SV=1	Q86VY9		1	
Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2	P09493			1
CAP-Gly domain-containing linker protein 4 OS=Homo sapiens GN=CLIP4 PE=1 SV=1	Q8N3C7			1
BRCA1-A complex subunit MERIT40 OS=Homo sapiens GN=MERIT40 PE=1 SV=1	Q9NWV8		1	
Transmembrane protein C2orf18 OS=Homo sapiens GN=C2orf18 PE=1 SV=1	Q8N357			2

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
cAMP-specific 3',5'-cyclic phosphodiesterase 4B OS=Homo sapiens GN=PDE4B PE=1 SV=1	Q07343			2
Transmembrane protein ENSP00000382582 OS=Homo sapiens PE=4 SV=2	A8MUB7			1
Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	Q92973			1
Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4	Q99439			1
Calpain-7 OS=Homo sapiens GN=CAPN7 PE=1 SV=1	Q9Y6W3			1
Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4	P29144		1	
Calmodulin-regulated spectrin-associated protein 1 OS=Homo sapiens GN=CAMSAP1 PE=1 SV=2	Q5T5Y3			2
Calcium-transporting ATPase type 2C member 2 OS=Homo sapiens GN=ATP2C2 PE=1 SV=2	O75185		1	
Caprin-2 OS=Homo sapiens GN=CAPRIN2 PE=1 SV=1	Q6IMN6			1
Ankyrin repeat domain-containing protein 62 OS=Homo sapiens GN=ANKRD62 PE=2 SV=4	A6NC57		1	1
EF-hand calcium-binding domain-containing protein 1 OS=Homo sapiens GN=EFCAB1 PE=2 SV=1	Q9HAE3			1
Arginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	P54136		2	2
Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ARAP2 PE=1 SV=3	Q8WZ64			1
Uncharacterized protein C10orf46 OS=Homo sapiens GN=C10orf46 PE=2 SV=1	Q86Y37			1
Apoptosis regulator BAX OS=Homo sapiens GN=BAX PE=1 SV=1	Q07812			3
Apolipoprotein C-IV OS=Homo sapiens GN=APOC4 PE=1 SV=1	P55056			1
Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	P04114			1
AP-4 complex subunit epsilon-1 OS=Homo sapiens GN=AP4E1 PE=1 SV=2	Q9UPM8			1
Anti-folate binding protein (Fragment) OS=Homo sapiens GN=HuVH8B VH	A2NYQ9		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Unc-84 homolog B (C. elegans) OS=Homo sapiens GN=UNC84B	B0QY62			1
Uncharacterized protein C11orf47 OS=Homo sapiens GN=C11orf47 PE=2 SV=1	Q2NKK8			1
Armadillo repeat-containing protein 8 OS=Homo sapiens GN=ARMC8 PE=1 SV=2	Q8IUR7			1
Ankyrin repeat domain-containing protein 45 OS=Homo sapiens GN=ANKRD45 PE=2 SV=1	Q5TZF3		1	
Ankyrin repeat domain-containing protein 11 OS=Homo sapiens GN=ANKRD11 PE=1 SV=3	Q6UB99		1	
Ankyrin repeat and SAM domain-containing protein 1A OS=Homo sapiens GN=ANKS1A PE=1 SV=4	Q92625			1
Uncharacterized protein C11orf65 OS=Homo sapiens GN=C11orf65 PE=2 SV=1	Q8NCR3			1
Ankyrin repeat and fibronectin type-III domain-containing protein 1 OS=Homo sapiens GN=ANKFN1 PE=2 SV=2	Q8N957		1	
Angiotensin-converting enzyme 2 OS=Homo sapiens GN=ACE2 PE=1 SV=2	Q9BYF1		1	
Uncharacterized protein C12orf34 OS=Homo sapiens GN=C12orf34 PE=2 SV=1	Q5U5X8			1
AN1-type zinc finger and ubiquitin domain-containing protein 1 OS=Homo sapiens GN=ANUBL1 PE=2 SV=2	Q86XD8			1
Uncharacterized protein C12orf76 OS=Homo sapiens GN=C12orf76 PE=2 SV=1	Q8N812		1	
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	P07355			1
ATP-dependent RNA helicase DHX8 OS=Homo sapiens GN=DHX8 PE=1 SV=1	Q14562		1	
Brain protein 16-like OS=Homo sapiens GN=BRP16L PE=3 SV=1	P0CB43		1	
Tyrosine-protein kinase HCK OS=Homo sapiens GN=HCK PE=1 SV=5	P08631			1
Tyrosine-protein kinase JAK3 OS=Homo sapiens GN=JAK3 PE=1 SV=2	P52333			1
Tyrosine-protein phosphatase non-receptor type 9 OS=Homo sapiens GN=PTPN9 PE=1 SV=1	P43378			1
Bestrophin variant (Fragment) OS=Homo sapiens	Q59FK9		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
U5 small nuclear ribonucleoprotein 40 kDa protein OS=Homo sapiens GN=SNRNP40 PE=1 SV=1	Q96DI7		1	
Basic helix-loop-helix domain-containing protein KIAA2018 OS=Homo sapiens GN=KIAA2018 PE=1 SV=3	Q68DE3		1	
BAH and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=BAHCC1 PE=1 SV=3	Q9P281		1	
Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens GN=BIRC6 PE=1 SV=2	Q9NR09		2	1
Armadillo repeat protein deleted in velo-cardio-facial syndrome OS=Homo sapiens GN=ARVCF PE=1 SV=1	O00192			1
Ubiquitin carboxyl-terminal hydrolase 4 OS=Homo sapiens GN=USP4 PE=1 SV=3	Q13107		1	
Translin OS=Homo sapiens GN=TSN PE=1 SV=1	Q15631			1
ATP-dependent RNA helicase DDX39 OS=Homo sapiens GN=DDX39 PE=1 SV=2	O00148			1
Ubiquitin carboxyl-terminal hydrolase 8 OS=Homo sapiens GN=USP8 PE=1 SV=1	P40818			2
Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=1 SV=3	P61086			1
Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1	Q9NT62			1
Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A PE=1 SV=4	Q05086			1
UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	Q9NYU2			1
ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	P25705			1
UDP-glucuronosyltransferase 1A3 (Fragment) OS=Homo sapiens GN=UGT1A3	A9UKD1			1
Arylsulfatase G OS=Homo sapiens GN=ARSG PE=1 SV=1	Q96EG1			1
Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15 PE=1 SV=3	Q9Y4E8		2	1
LOC441239 protein OS=Homo sapiens GN=LOC441239	Q6P462			1
Leucine-rich repeat-containing protein 16A OS=Homo sapiens GN=LRRC16A PE=1 SV=1	Q5VZK9		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=1 SV=2	O60341		1	
Protein TANC2 OS=Homo sapiens GN=TANC2 PE=1 SV=3	Q9HCD6			1
Lysine-specific demethylase 3B OS=Homo sapiens GN=KDM3B PE=1 SV=2	Q7LBC6			1
Lymphotoxin-alpha OS=Homo sapiens GN=LTA PE=1 SV=2	P01374			1
Lymphocyte antigen 75 OS=Homo sapiens GN=LY75 PE=1 SV=2	O60449			1
Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2	P05455		1	
Protein tyrosine phosphatase type IVA 2 OS=Homo sapiens GN=PTP4A2 PE=1 SV=1	Q12974		1	
Low affinity immunoglobulin epsilon Fc receptor OS=Homo sapiens GN=FCER2 PE=1 SV=1	P06734			1
Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2	P40121			13
Protein Wnt-3a OS=Homo sapiens GN=WNT3A PE=1 SV=2	P56704			1
Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	Q14764			1
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	P00338		1	1
Protein Wnt-4 OS=Homo sapiens GN=WNT4 PE=1 SV=4	P56705			1
Protein-glutamine gamma-glutamyltransferase 4 OS=Homo sapiens GN=TGM4 PE=1 SV=2	P49221			1
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3	P11182			1
Leukocyte immunoglobulin-like receptor subfamily B member 4 OS=Homo sapiens GN=LILRB4 PE=1 SV=2	Q8NHJ6		1	
Leucyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2	Q9P2J5		1	1
Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=1	Q14517			1
Leucine-rich repeat-containing protein 7 OS=Homo sapiens GN=LRRC7 PE=1 SV=1	Q96NW7		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Leucine-rich repeat-containing protein 41 OS=Homo sapiens GN=LRRC41 PE=1 SV=3	Q15345		1	
Ran-binding protein 10 OS=Homo sapiens GN=RANBP10 PE=1 SV=1	Q6VN20			2
Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2	P36776			1
Protein pellino homolog 2 OS=Homo sapiens GN=PELI2 PE=1 SV=1	Q9HAT8			1
Protein fat-free homolog OS=Homo sapiens GN=FFR PE=1 SV=2	Q9UID3			1
MORN repeat-containing protein 4 OS=Homo sapiens GN=MORN4 PE=2 SV=1	Q8NDC4			1
MORC family CW-type zinc finger protein 4 OS=Homo sapiens GN=MORC4 PE=1 SV=2	Q8TE76		1	
Protein IWS1 homolog OS=Homo sapiens GN=IWS1 PE=1 SV=2	Q96ST2		1	
Protein kinase C eta type OS=Homo sapiens GN=PRKCH PE=1 SV=4	P24723		1	
Protein kinase C gamma type OS=Homo sapiens GN=PRKCG PE=1 SV=3	P05129		4	2
Protein kinase C-binding protein NELL2 OS=Homo sapiens GN=NELL2 PE=1 SV=1	Q99435		1	
Protein lunapark OS=Homo sapiens GN=LNP PE=1 SV=2	Q9C0E8		1	
Midline-1 OS=Homo sapiens GN=MID1 PE=1 SV=1	O15344		2	
Lysosomal-trafficking regulator OS=Homo sapiens GN=LYST PE=1 SV=3	Q99698		1	
Protein NOXP20 OS=Homo sapiens GN=FAM114A1 PE=1 SV=2	Q8IWE2			2
Protocadherin-23 OS=Homo sapiens GN=DCHS2 PE=2 SV=1	Q6V1P9			1
Methylcytosine dioxygenase TET1 OS=Homo sapiens GN=TET1 PE=1 SV=2	Q8NFU7			1
Methionyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	P56192		2	
Metalloproteinase 12-like protein OS=Homo sapiens	Q2VYF6			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Metal transporter CNNM4 OS=Homo sapiens GN=CNNM4 PE=1 SV=3	Q6P4Q7			1
Membrane-associated phosphatidylinositol transfer protein 3 OS=Homo sapiens GN=PITPNM3 PE=1 SV=2	Q9BZ71		1	
Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2	Q9UNF1			1
Melanoma ubiquitous mutated protein (Fragment) OS=Homo sapiens GN=MUM-1	Q13110		1	
Mastermind-like protein 2 OS=Homo sapiens GN=MAML2 PE=1 SV=2	Q8IZL2			2
Protein PROCA1 OS=Homo sapiens GN=PROCA1 PE=2 SV=2	Q8NCQ7		1	
Mannose 6-phosphate/insulin-like growth factor-II receptor (Fragment) OS=Homo sapiens	Q13661			1
Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1	P10620			1
Integral membrane protein 2A OS=Homo sapiens GN=ITM2A PE=1 SV=2	O43736		1	
Leucine-rich repeat-containing protein 39 OS=Homo sapiens GN=LRRC39 PE=2 SV=1	Q96DD0		1	
Intraflagellar transport protein 80 homolog OS=Homo sapiens GN=IFT80 PE=1 SV=3	Q9P2H3			1
Putative protein FAM90A2 OS=Homo sapiens GN=FAM90A2P PE=5 SV=2	Q658T7		1	1
Interleukin-22 receptor subunit alpha-1 OS=Homo sapiens GN=IL22RA1 PE=1 SV=1	Q8N6P7			1
Interleukin-1 receptor-associated kinase 4 OS=Homo sapiens GN=IRAK4 PE=1 SV=1	Q9NWZ3			1
Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	Q12906		2	
Interleukin 1 receptor accessory protein variant AcPb OS=Homo sapiens GN=IL1RAP	B1NLD0		1	
Interferon-induced, double-stranded RNA-activated protein kinase OS=Homo sapiens GN=EIF2AK2 PE=1 SV=2	P19525			1
Putative RNA exonuclease NEF-sp OS=Homo sapiens GN=44M2.3 PE=2 SV=1	Q96IC2		1	
IQ and AAA domain-containing protein 1 OS=Homo sapiens GN=IQCA1 PE=2 SV=1	Q86XH1			1

Protein peptides	Accession No.	icPTPRD-D1521A	icPTPRD-WT	Control
Putative uncharacterized protein BCR (Fragment) OS=Homo sapiens GN=BCR	Q12845			1
Putative myosin light chain kinase 3 OS=Homo sapiens GN=MYLK3 PE=2 SV=3	Q32MK0		1	
Putative uncharacterized protein C12orf77 OS=Homo sapiens GN=C12orf77 PE=2 SV=1	C9JDV5			1
Putative uncharacterized protein DKFZp686E2459 OS=Homo sapiens GN=DKFZp686E2459	Q7Z3D7		1	
Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2	P12268			1
Inner centromere protein OS=Homo sapiens GN=INCENP PE=1 SV=3	Q9NQS7			1
Putative uncharacterized protein FLJ36116 OS=Homo sapiens PE=2 SV=1	Q8N9X3			1
Putative zinc finger and BTB domain-containing protein 12-like protein OS=Homo sapiens PE=5 SV=4	A6NH08			1
Pyridoxal phosphate phosphatase PHOSPHO2 OS=Homo sapiens GN=PHOSPHO2 PE=1 SV=1	Q8TCD6			1
Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	O95373			3
Immunity-related GTPase family Q protein OS=Homo sapiens GN=IRGQ PE=1 SV=1	Q8WZA9			1
Slit homolog 3 protein OS=Homo sapiens GN=SLIT3 PE=2 SV=3	O75094		1	
Putative serpin A13 OS=Homo sapiens GN=SERPINA13 PE=5 SV=1	Q6UXR4			1
Keratin-associated protein 11-1 OS=Homo sapiens GN=KRTAP11-1 PE=1 SV=1	Q8IUC1			1
Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2	Q32MZ4			2
Leucine-rich repeat and calponin homology domain-containing protein 2 OS=Homo sapiens GN=LRCH2 PE=2 SV=2	Q5VUJ6		1	1
P-selectin OS=Homo sapiens GN=SELP PE=1 SV=3	P16109			1
Large proline-rich protein BAT2 OS=Homo sapiens GN=BAT2 PE=1 SV=3	P48634		1	
La-related protein 1B OS=Homo sapiens GN=LARP1B PE=1 SV=2	Q659C4		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	Q6PKG0		1	
PTB-containing, cubilin and LRP1-interacting protein OS=Homo sapiens GN=PID1 PE=1 SV=1	Q7Z2X4			1
Kinesin-like protein KIF23 OS=Homo sapiens GN=KIF23 PE=1 SV=3	Q02241			3
Kinesin-like protein KIF21B OS=Homo sapiens GN=KIF21B PE=1 SV=2	O75037			1
Putative protein FAM90A12 OS=Homo sapiens GN=FAM90A12 PE=3 SV=1	A8MX19			1
Putative ankyrin repeat domain-containing protein 30B-like OS=Homo sapiens GN=ANKRD30BL PE=2 SV=3	A7E2S9		1	
Multidrug resistance protein 1 OS=Homo sapiens	B5AK60			1
Putative ATP-dependent RNA helicase DHX57 OS=Homo sapiens GN=DHX57 PE=1 SV=2	Q6P158		1	
Kelch-like protein 8 OS=Homo sapiens GN=KLHL8 PE=2 SV=4	Q9P2G9			1
Kelch-like protein 31 OS=Homo sapiens GN=KLHL31 PE=2 SV=1	Q9H511		1	
Kelch-like protein 29 OS=Homo sapiens GN=KLHL29 PE=2 SV=2	Q96CT2		1	
Katanin p60 ATPase-containing subunit A-like 2 OS=Homo sapiens GN=KATNAL2 PE=2 SV=3	Q8IYT4			1
Putative heat shock protein HSP 90-alpha A2 OS=Homo sapiens GN=HSP90AA2 PE=1 SV=2	Q14568		1	1
Putative L-aspartate dehydrogenase OS=Homo sapiens GN=ASPDH PE=2 SV=2	A6ND91			1
IST1 homolog OS=Homo sapiens GN=KIAA0174 PE=1 SV=1	P53990			1
Isoleucyl-tRNA synthetase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2	Q9NSE4			1
Iroquois-class homeodomain protein IRX-6 OS=Homo sapiens GN=IRX6 PE=2 SV=3	P78412			1
Kinesin-like protein KIF16B OS=Homo sapiens GN=KIF16B PE=1 SV=2	Q96L93		1	
Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	Q99733			5

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
MST148 protein OS=Homo sapiens GN=MST148	Q7Z2R3			1
Oxygen-regulated protein 1 OS=Homo sapiens GN=RP1 PE=1 SV=1	P56715			1
PRO0899 OS=Homo sapiens	Q9P1L9			1
Probable ATP-dependent RNA helicase DDX28 OS=Homo sapiens GN=DDX28 PE=2 SV=2	Q9NUL7			1
Olfactory receptor 4N2 OS=Homo sapiens GN=OR4N2 PE=2 SV=1	Q8NGD1			1
Olfactory receptor 4C6 OS=Homo sapiens GN=OR4C6 PE=2 SV=1	Q8NH72			1
Olfactory receptor 1E1 OS=Homo sapiens GN=OR1E1 PE=2 SV=1	P30953			1
Probable ATP-dependent RNA helicase DDX4 OS=Homo sapiens GN=DDX4 PE=2 SV=2	Q9NQI0			1
Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2	P26196			1
PAB-dependent poly(A)-specific ribonuclease subunit 2 OS=Homo sapiens GN=PAN2 PE=1 SV=3	Q504Q3			1
Probable G-protein coupled receptor 156 OS=Homo sapiens GN=GPR156 PE=2 SV=2	Q8NFN8			1
Pregnancy-specific beta-1-glycoprotein 5 OS=Homo sapiens GN=PSG5 PE=2 SV=3	Q15238			1
Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	P55209		1	2
Probable N-acetyltransferase 8B OS=Homo sapiens GN=NAT8B PE=2 SV=1	Q9UHF3		1	
Nucleolar pre-ribosomal-associated protein 1 OS=Homo sapiens GN=URB1 PE=1 SV=4	O60287			1
Nuclear RNA export factor 2 OS=Homo sapiens GN=NXF2 PE=1 SV=1	Q9GZY0		2	
Nuclear receptor subfamily 1 group I member 2 OS=Homo sapiens GN=NR1I2 PE=1 SV=1	O75469		1	
Progesterone receptor OS=Homo sapiens GN=PGR PE=1 SV=4	P06401			1
Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	P35232		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	P12273		1	
Proline-rich protein 16 OS=Homo sapiens GN=PRR16 PE=2 SV=1	Q569H4			1
Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2	P49790		1	
Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=1 SV=1	Q9H173		1	
Poly [ADP-ribose] polymerase 14 OS=Homo sapiens GN=PARP14 PE=1 SV=2	Q460N5		1	
Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	P05155			1
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	Q8NC51		1	
PI-PLC X domain-containing protein 1 OS=Homo sapiens GN=PLCXD1 PE=2 SV=1	Q9NUJ7			1
Platelet-derived growth factor subunit B OS=Homo sapiens GN=PDGFB PE=1 SV=1	P01127			1
Pleckstrin homology domain-containing family A member 7 OS=Homo sapiens GN=PLEKHA7 PE=1 SV=2	Q6IQ23			1
Pleckstrin homology domain-containing family G member 5 OS=Homo sapiens GN=PLEKHG5 PE=2 SV=3	O94827			1
Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	Q15149			3
Phosphomannomutase 2 OS=Homo sapiens GN=PMM2 PE=1 SV=1	O15305			1
Poliovirus receptor-related protein 3 OS=Homo sapiens GN=PVRL3 PE=1 SV=1	Q9NQS3			1
P58 killer cell inhibitory receptor KIR-K7c (Fragment) OS=Homo sapiens	Q9UNB4		1	
Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1 OS=Homo sapiens GN=INPP5D PE=1 SV=2	Q92835		1	
N-terminal kinase-like protein OS=Homo sapiens GN=SCYL1 PE=1 SV=1	Q96KG9		1	
Poly(A) polymerase gamma OS=Homo sapiens GN=PAPOLG PE=1 SV=2	Q9BWT3			1
Phosphatidylinositol 3-kinase regulatory subunit alpha OS=Homo sapiens GN=PIK3R1 PE=1 SV=2	P27986			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1	Q13310		1	
Polycystin-1 OS=Homo sapiens GN=PKD1 PE=1 SV=3	P98161		2	4
Polypeptide N-acetylgalactosaminyltransferase 3 OS=Homo sapiens GN=GALNT3 PE=2 SV=2	Q14435			1
Peroxisome assembly protein 12 OS=Homo sapiens GN=PEX12 PE=1 SV=1	O00623		1	
Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	P26599			1
Potassium channel subfamily K member 2 OS=Homo sapiens GN=KCNK2 PE=2 SV=2	O95069		1	
Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=2	O60664			4
Paternally-expressed gene 3 protein OS=Homo sapiens GN=PEG3 PE=2 SV=1	Q9GZU2			1
Phosphatidylinositol-4-phosphate 5-kinase type-1 alpha OS=Homo sapiens GN=PIP5K1A PE=1 SV=1	Q99755			1
Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2	Q9Y623		1	
Protein BAT5 OS=Homo sapiens GN=BAT5 PE=1 SV=3	O95870		1	
Protein C20orf11 OS=Homo sapiens GN=C20orf11 PE=1 SV=1	Q9NWU2		1	
Protein CBFA2T3 OS=Homo sapiens GN=CBFA2T3 PE=1 SV=2	O75081			1
Myotubularin-related protein 7 OS=Homo sapiens GN=MTMR7 PE=1 SV=3	Q9Y216			2
Myotubularin-related protein 6 OS=Homo sapiens GN=MTMR6 PE=1 SV=2	Q9Y217			1
Protein cramped-like OS=Homo sapiens GN=CRAMP1L PE=1 SV=3	Q96RY5			1
Myotubularin-related protein 10 OS=Homo sapiens GN=MTMR10 PE=1 SV=3	Q9NXD2		1	
Protein CXorf40A OS=Homo sapiens GN=CXorf40A PE=1 SV=1	Q8TE69		1	
Myosin-XVI OS=Homo sapiens GN=MYO16 PE=1 SV=3	Q9Y6X6			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1	Q09161		1	
Myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2	O94832		1	1
NADPH oxidase 4 OS=Homo sapiens GN=NOX4 PE=1 SV=2	Q9NPH5		1	
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	P60660			1
Protein FAM179A OS=Homo sapiens GN=FAM179A PE=2 SV=2	Q6ZUX3		1	
Myosin light chain 6B OS=Homo sapiens GN=MYL6B PE=1 SV=1	P14649			1
Myomesin-2 OS=Homo sapiens GN=MYOM2 PE=2 SV=2	P54296		1	
Protein FAM55C OS=Homo sapiens GN=FAM55C PE=2 SV=1	Q969Y0			1
Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1	Q9NZM1			1
Multiple PDZ domain protein OS=Homo sapiens GN=MPDZ PE=1 SV=1	O75970		1	
Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1	Q9UNW1			1
Protein FAM69C OS=Homo sapiens GN=FAM69C PE=2 SV=3	Q0P6D2		1	
Ig heavy chain V-II region WAH OS=Homo sapiens PE=1 SV=1	P01824		1	
Myosin-VIIa OS=Homo sapiens GN=MYO7A PE=1 SV=1	Q13402		1	
Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	P60900			1
Protein FAM89A OS=Homo sapiens GN=FAM89A PE=2 SV=1	Q96GI7			1
Novel protein (KIAA0894) OS=Homo sapiens GN=RP11-476E15.3	Q5T925			1
Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	Q06323			1
Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	Q9UL46			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Nibrin OS=Homo sapiens GN=NBN PE=1 SV=1	O60934		1	
Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=2	Q96TA1			1
NHP2-like protein 1 OS=Homo sapiens GN=NHP2L1 PE=1 SV=3	P55769			1
Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1	P61289			1
NFAT5 protein OS=Homo sapiens GN=NFAT5	A2RRB4			1
Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2	Q92530			1
NACHT, LRR and PYD domains-containing protein 7 OS=Homo sapiens GN=NLRP7 PE=1 SV=1	Q8WX94			2
Neuron navigator 3 OS=Homo sapiens GN=NAV3 PE=1 SV=3	Q8IVL0		3	
N-acylsphingosine amidohydrolase (Acid ceramidase) 1, isoform CRA_c OS=Homo sapiens GN=ASAH1	D3DSQ1			1
Proteasome subunit alpha type-7-like OS=Homo sapiens GN=PSMA8 PE=1 SV=3	Q8TAA3			1
Neurobeachin-like protein 1 OS=Homo sapiens GN=NBEAL1 PE=2 SV=3	Q6ZS30		1	
Neurabin-2 OS=Homo sapiens GN=PPP1R9B PE=1 SV=2	Q96SB3		1	
Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	P49720			1
Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4	P28070			1
Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=1 SV=3	Q8NF91			1
Negative elongation factor A OS=Homo sapiens GN=WHSC2 PE=1 SV=3	Q9H3P2			1
Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2	Q86VF7		1	
Protein ALO17 OS=Homo sapiens GN=KIAA1618 PE=1 SV=2	Q9HCF4		2	
ProSAP-interacting protein 1 OS=Homo sapiens GN=PROSAPIP1 PE=2 SV=1	O60299		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	P28066			1
Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2	P42224			4
E3 ubiquitin-protein ligase ZNRF2 OS=Homo sapiens GN=ZNRF2 PE=1 SV=1	Q8NHG8		1	
Seven transmembrane helix receptor OS=Homo sapiens	Q8NHC2			1
SH3 and multiple ankyrin repeat domains protein 1 OS=Homo sapiens GN=SHANK1 PE=1 SV=2	Q9Y566		1	
ESF1 homolog OS=Homo sapiens GN=ESF1 PE=1 SV=1	Q9H501			1
E-selectin OS=Homo sapiens GN=SELE PE=1 SV=1	P16581		1	
Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	P58107		1	
Ephexin-1 OS=Homo sapiens GN=NGEF PE=2 SV=2	Q8N5V2		1	3
Eosinophil lysophospholipase OS=Homo sapiens GN=CLC PE=1 SV=2	Q05315		1	
SH3 domain-binding protein 1 OS=Homo sapiens GN=SH3BP1 PE=1 SV=3	Q9Y3L3		1	
Seven transmembrane helix receptor OS=Homo sapiens	Q8NHB3		1	
EMILIN-2 OS=Homo sapiens GN=EMILIN2 PE=1 SV=3	Q9BXX0		1	
SETMAR protein (Fragment) OS=Homo sapiens GN=SETMAR	Q96H41			1
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	P26641			1
Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	P29692			2
Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2	P40763		1	
Similar to dual specificity phosphatase 9 (Fragment) OS=Homo sapiens	Q8N4A4		1	
EH domain-binding protein 1-like protein 1 OS=Homo sapiens GN=EHBP1L1 PE=1 SV=2	Q8N3D4		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Egl nine homolog 1 OS=Homo sapiens GN=EGLN1 PE=1 SV=1	Q9GZT9			1
EGF-like domain-containing protein C3orf50 OS=Homo sapiens GN=C3orf50 PE=2 SV=1	Q0D2K5			1
Single-stranded DNA-binding protein 3 OS=Homo sapiens GN=SSBP3 PE=1 SV=1	Q9BWW4			1
EF-hand calcium-binding domain-containing protein 5 OS=Homo sapiens GN=EFCAB5 PE=1 SV=2	A4FU69			1
Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1	P46060			1
Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	P14625		3	1
Exocyst complex component 5 OS=Homo sapiens GN=EXOC5 PE=1 SV=1	O00471		1	
Serine protease HTRA2, mitochondrial OS=Homo sapiens GN=HTRA2 PE=1 SV=2	O43464			1
Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3	Q96AE4		1	1
Fanconi-associated nuclease 1 OS=Homo sapiens GN=FAN1 PE=1 SV=4	Q9Y2M0			1
Fanconi anemia group A protein OS=Homo sapiens GN=FANCA PE=1 SV=2	O15360		1	
Serine/arginine repetitive matrix protein 5 OS=Homo sapiens GN=SRRM5 PE=2 SV=3	B3KS81		1	
F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	P52907			1
Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	P55060			6
Exostosin-like 1 OS=Homo sapiens GN=EXTL1 PE=1 SV=2	Q92935		1	1
Serine/threonine-protein kinase MRCK beta OS=Homo sapiens GN=CDC42BPB PE=1 SV=2	Q9Y5S2			1
Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	P05198		1	1
Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens GN=EXD2 PE=1 SV=1	Q9NVH0		2	1
E3 ubiquitin-protein ligase synoviolin OS=Homo sapiens GN=SYVN1 PE=1 SV=2	Q86TM6			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=1 SV=2	O60645		1	
Excitatory amino acid transporter 1 OS=Homo sapiens GN=SLC1A3 PE=1 SV=1	P43003		1	
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens GN=PPP2R5D PE=1 SV=1	Q14738			1
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1	P67775			1
Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit beta OS=Homo sapiens GN=PPP2R3B PE=1 SV=2	Q9Y5P8			1
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	P62136			1
Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	P29508		4	
Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1	Q99613		2	
Serpin B4 OS=Homo sapiens GN=SERPINB4 PE=1 SV=2	P48594		1	
SET domain-containing protein 5 OS=Homo sapiens GN=SETD5 PE=1 SV=2	Q9C0A6		1	
Serine/threonine-protein kinase Nek1 OS=Homo sapiens GN=NEK1 PE=1 SV=2	Q96PY6		1	
Disintegrin and metalloproteinase domain-containing protein 2 OS=Homo sapiens GN=ADAM2 PE=1 SV=2	Q99965		1	
SLAIN motif-containing protein 2 OS=Homo sapiens GN=SLAIN2 PE=1 SV=2	Q9P270		1	
DNA2-like helicase OS=Homo sapiens GN=DNA2 PE=1 SV=3	P51530		1	
DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	P11388			1
Spermine oxidase OS=Homo sapiens GN=SMOX PE=1 SV=1	Q9NWM0		1	
DNA repair protein complementing XP-C cells OS=Homo sapiens GN=XPC PE=1 SV=4	Q01831			1
DNA polymerase theta OS=Homo sapiens GN=POLQ PE=1 SV=1	O75417		1	
Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	Q15459		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
DNA ligase 1 OS=Homo sapiens GN=LIG1 PE=1 SV=1	P18858		1	
DNA dC->dU-editing enzyme APOBEC-3F OS=Homo sapiens GN=APOBEC3F PE=1 SV=3	Q8IUX4		1	
Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3	Q8NB90		1	
Disks large-associated protein 1 OS=Homo sapiens GN=DLGAP1 PE=1 SV=1	O14490			1
Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1	Q96SI9			2
Disheveled-associated activator of morphogenesis 2 OS=Homo sapiens GN=DAAM2 PE=2 SV=3	Q86T65			2
Dipeptidyl peptidase 4 OS=Homo sapiens GN=DPP4 PE=1 SV=2	P27487			1
Dipeptidyl aminopeptidase-like protein 6 OS=Homo sapiens GN=DPP6 PE=1 SV=2	P42658			1
DET1 homolog OS=Homo sapiens GN=DET1 PE=1 SV=2	Q7L5Y6			1
Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	P16949		1	
Sterol regulatory element-binding protein 2 OS=Homo sapiens GN=SREBF2 PE=1 SV=2	Q12772			1
Structural maintenance of chromosomes protein 1B OS=Homo sapiens GN=SMC1B PE=1 SV=2	Q8NDV3		1	
Structure-specific endonuclease subunit SLX4 OS=Homo sapiens GN=SLX4 PE=1 SV=3	Q8IY92			1
Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	Q9Y6N5			1
Cytosolic purine 5'-nucleotidase OS=Homo sapiens GN=NT5C2 PE=1 SV=1	P49902			1
DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2	P26358		1	
Dynein heavy chain 17, axonemal OS=Homo sapiens GN=DNAH17 PE=2 SV=2	Q9UFH2		1	
E3 ubiquitin-protein ligase RNF149 OS=Homo sapiens GN=RNF149 PE=2 SV=2	Q8NC42			1
Sodium/potassium/calcium exchanger 2 OS=Homo sapiens GN=SLC24A2 PE=2 SV=1	Q9UI40		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Solute carrier family 12 (Potassium/chloride transporters), member 4, isoform CRA_e OS=Homo sapiens GN=SLC12A4	B3KUS0			1
E3 ubiquitin-protein ligase MARCH11 OS=Homo sapiens GN=MARCH11 PE=2 SV=3	A6NNE9			1
Solute carrier family 2, facilitated glucose transporter member 9 OS=Homo sapiens GN=SLC2A9 PE=1 SV=2	Q9NRM0		1	
Solute carrier family 22 member 3 OS=Homo sapiens GN=SLC22A3 PE=1 SV=1	O75751			1
E2F3 protein OS=Homo sapiens GN=E2F3	Q499G5			1
Sorbin and SH3 domain-containing protein 1 OS=Homo sapiens GN=SORBS1 PE=1 SV=2	Q9BX66		1	
Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1	P63167			1
Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens GN=SPATA5L1 PE=1 SV=2	Q9BVQ7			1
Dynein heavy chain 2, axonemal OS=Homo sapiens GN=DNAH2 PE=1 SV=3	Q9P225			2
FERM domain-containing protein 4A OS=Homo sapiens GN=FRMD4A PE=1 SV=3	Q9P2Q2			1
Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3	Q13596			1
Dynamin-1 OS=Homo sapiens GN=DNM1 PE=1 SV=2	Q05193		1	
Sorting nexin-16 OS=Homo sapiens GN=SNX16 PE=1 SV=2	P57768			1
Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3	Q14203		1	1
Sorting nexin-29 OS=Homo sapiens GN=SNX29 PE=1 SV=2	Q8TEQ0			1
Dual oxidase 1 OS=Homo sapiens GN=DUOX1 PE=1 SV=1	Q9NRD9			1
DPY30 domain-containing protein 1 OS=Homo sapiens GN=DYDC1 PE=1 SV=1	Q8WWB3		1	
Double-stranded RNA-specific editase 1 OS=Homo sapiens GN=ADARB1 PE=1 SV=1	P78563			1
Docking protein 3 OS=Homo sapiens GN=DOK3 PE=1 SV=2	Q7L591		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Sperm acrosome membrane-associated protein 3 OS=Homo sapiens GN=SPACA3 PE=1 SV=1	Q8IXA5		1	
Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3	Q8TE73		1	3
HEAT repeat-containing protein 5A OS=Homo sapiens GN=HEATR5A PE=1 SV=2	Q86XA9			1
F-box only protein 10 OS=Homo sapiens GN=FBXO10 PE=2 SV=3	Q9UK96		1	
Hephaestin-like protein 1 OS=Homo sapiens GN=HEPHL1 PE=2 SV=2	Q6MZM0			1
Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2	Q99575		1	
Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2	P69891		1	
Helicase-like transcription factor OS=Homo sapiens GN=HLTF PE=1 SV=2	Q14527		1	
Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1	Q8IY67		1	
Ribose-phosphate pyrophosphokinase 3 OS=Homo sapiens GN=PRPS1L1 PE=1 SV=2	P21108			1
Ribosomal protein S6 kinase alpha-6 OS=Homo sapiens GN=RPS6KA6 PE=1 SV=1	Q9UK32			1
Heat shock protein beta-2 OS=Homo sapiens GN=HSPB2 PE=1 SV=2	Q16082			1
HES5 protein OS=Homo sapiens GN=HES5	Q5M8T3			1
RILP-like protein 1 OS=Homo sapiens GN=RILPL1 PE=1 SV=1	Q5EBL4			1
Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1	Q13151		1	
HCG2011465 (Fragment) OS=Homo sapiens GN=hCG_2011465	Q8WW44			1
HCG1990398 OS=Homo sapiens GN=hCG_1990398	Q9BZU2		1	
RING finger protein 146 OS=Homo sapiens GN=RNF146 PE=1 SV=1	Q9NTX7		1	
Harmonin OS=Homo sapiens GN=USH1C PE=1 SV=3	Q9Y6N9		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
H(+)/Cl(-) exchange transporter 5 OS=Homo sapiens GN=CLCN5 PE=1 SV=1	P51795		1	
RING finger protein 150 OS=Homo sapiens GN=RNF150 PE=2 SV=2	Q9ULK6			1
Guanylate cyclase soluble subunit alpha-3 OS=Homo sapiens GN=GUCY1A3 PE=1 SV=2	Q02108		1	
Guanine nucleotide-binding protein-like 1 OS=Homo sapiens GN=GNL1 PE=1 SV=2	P36915			1
RNA 3'-terminal phosphate cyclase-like protein OS=Homo sapiens GN=RCL1 PE=1 SV=3	Q9Y2P8		1	
Guanine nucleotide exchange factor DBS OS=Homo sapiens GN=MCF2L PE=1 SV=2	O15068		1	
Ribosomal protein S6 modification-like protein B OS=Homo sapiens GN=RIMKLB PE=2 SV=2	Q9ULI2		1	
Receptor-type tyrosine-protein phosphatase zeta OS=Homo sapiens GN=PTPRZ1 PE=1 SV=4	P23471		1	1
Ran-binding protein 9 OS=Homo sapiens GN=RANBP9 PE=1 SV=1	Q96S59		1	1
Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1	P54868		1	
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3	Q16836		1	
Hydrocephalus-inducing protein homolog OS=Homo sapiens GN=HYDIN PE=1 SV=2	Q4G0P3			1
Hyaluronan mediated motility receptor OS=Homo sapiens GN=HMMR PE=1 SV=2	O75330			1
Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	Q13283			1
Ras-associating and dilute domain-containing protein OS=Homo sapiens GN=RADIL PE=1 SV=4	Q96JH8			1
Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3	P62491			3
Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	P51149			1
Rho guanine nucleotide exchange factor 16 OS=Homo sapiens GN=ARHGEF16 PE=1 SV=1	Q5VV41		1	
Receptor-type tyrosine-protein phosphatase S OS=Homo sapiens GN=PTPRS PE=1 SV=2	Q13332			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
GTPase IMAP family member 6 OS=Homo sapiens GN=GIMAP6 PE=2 SV=1	Q6P9H5			1
Regulator of G-protein signaling 9 OS=Homo sapiens GN=RGS9 PE=1 SV=1	O75916			1
REST corepressor 3 OS=Homo sapiens GN=RCOR3 PE=1 SV=2	Q9P2K3			1
Reticulon-4-interacting protein 1, mitochondrial OS=Homo sapiens GN=RTN4IP1 PE=1 SV=2	Q8WWV3		1	
Highly divergent homeobox OS=Homo sapiens GN=HDX PE=1 SV=1	Q7Z353		1	
Rho GTPase-activating protein 11B OS=Homo sapiens GN=ARHGAP11B PE=1 SV=1	Q3KRB8		1	
Rho guanine nucleotide exchange factor 1 OS=Homo sapiens GN=ARHGEF1 PE=1 SV=2	Q92888		1	
Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1	P55795		1	
Rho guanine nucleotide exchange factor 10-like protein OS=Homo sapiens GN=ARHGEF10L PE=1 SV=2	Q9HCE6			1
Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	P52597		1	
Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2	Q32P51		1	
Homeobox protein Nkx-2.3 OS=Homo sapiens GN=NKX2-3 PE=1 SV=2	Q8TAU0			1
Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=3	Q14192			1
GDP-fucose protein O-fucosyltransferase 2 OS=Homo sapiens GN=POFUT2 PE=2 SV=3	Q9Y2G5			1
Gasdermin-B OS=Homo sapiens GN=GSDMB PE=1 SV=2	Q8TAX9			1
GAS2-like protein 3 OS=Homo sapiens GN=GAS2L3 PE=1 SV=1	Q86XJ1		1	
Gamma-tubulin complex component 2 OS=Homo sapiens GN=TUBGCP2 PE=1 SV=2	Q9BSJ2			1
Gamma-aminobutyric acid receptor subunit epsilon OS=Homo sapiens GN=GABRE PE=2 SV=2	P78334			2
Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1	Q02383		2	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	P47929		1	
Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	P17931			3
Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	P09382			2
GTP-binding protein Rhes OS=Homo sapiens GN=RASD2 PE=1 SV=1	Q96D21			1
Four-jointed box protein 1 OS=Homo sapiens GN=FJX1 PE=2 SV=1	Q86VR8			1
Semaphorin-6D OS=Homo sapiens GN=SEMA6D PE=1 SV=1	Q8NFY4		1	
Forkhead box protein F2 OS=Homo sapiens GN=FOXF2 PE=1 SV=2	Q12947		1	
FKSG42 OS=Homo sapiens GN=FKSG42	Q9BZ74		1	
Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1	P35270			1
Seprase OS=Homo sapiens GN=FAP PE=1 SV=5	Q12884			1
Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2	Q9UHD8			1
Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1	Q13501			2
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	P02751		4	
FERM, RhoGEF and pleckstrin domain-containing protein 2 OS=Homo sapiens GN=FARP2 PE=1 SV=3	O94887			1
FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (Chondrocyte-derived) (Fragment) OS=Homo sapiens GN=FARP1	Q5JV91			1
Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3	P42285		1	
Separin OS=Homo sapiens GN=ESPL1 PE=1 SV=3	Q14674			2
Glutamine-rich protein 2 OS=Homo sapiens GN=QRICH2 PE=1 SV=1	Q9H0J4		1	
F-box/LRR-repeat protein 18 OS=Homo sapiens GN=FBXL18 PE=2 SV=2	Q96ME1			1

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Graves disease carrier protein OS=Homo sapiens GN=SLC25A16 PE=2 SV=3	P16260			1
GRAM domain-containing protein 1B OS=Homo sapiens GN=GRAMD1B PE=1 SV=1	Q3KR37			1
GPI ethanolamine phosphate transferase 2 OS=Homo sapiens GN=PIGG PE=1 SV=1	Q5H8A4			1
GON-4-like protein OS=Homo sapiens GN=GON4L PE=1 SV=1	Q3T8J9			1
RNA polymerase II transcription factor SIII subunit A3-like-1 OS=Homo sapiens GN=TCEB3CL PE=2 SV=1	Q3SY89			1
RUN and FYVE domain-containing protein 4 OS=Homo sapiens GN=RUFY4 PE=2 SV=2	Q6ZNE9			1
Glycosyltransferase 1 domain-containing protein 1 OS=Homo sapiens GN=GLT1D1 PE=2 SV=2	Q96MS3		1	
Glycogenin-1 OS=Homo sapiens GN=GYG1 PE=1 SV=4	P46976		2	
Glycerophosphodiester phosphodiesterase domain-containing protein 1 OS=Homo sapiens GN=GDPD1 PE=1 SV=2	Q8N9F7			1
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	P06396			1
Ryanodine receptor 2 OS=Homo sapiens GN=RYR2 PE=1 SV=3	Q92736		1	
Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2	P04279		8	
Glutamate receptor, ionotropic kainate 1 OS=Homo sapiens GN=GRIK1 PE=1 SV=1	P39086		1	1
Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	P14136			1
GH3 domain-containing protein OS=Homo sapiens GN=GHDC PE=1 SV=2	Q8N2G8		1	
General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2	O60763			2
General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	P78347			1
General transcription factor 3C polypeptide 2 OS=Homo sapiens GN=GTF3C2 PE=1 SV=2	Q8WUA4			1
Secreted frizzled-related protein 1 OS=Homo sapiens GN=SFRP1 PE=1 SV=1	Q8N474		1	

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	**Control**
Secretory phospholipase A2 receptor OS=Homo sapiens GN=PLA2R1 PE=1 SV=2	Q13018		1	1
Semaphorin-6C OS=Homo sapiens GN=SEMA6C PE=2 SV=4	Q9H3T2			1
GTP-binding protein 5 OS=Homo sapiens GN=GTPBP5 PE=2 SV=1	Q9H4K7		1	
Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	O76003			1

icPTPRD-D1521A: intracellular PTPRD having two phosphatase domains and bearing D1521A mutation;

icPTPRD-WT: intracellular PTPRD having two phosphatase domains; Control: Vector alone

Supp. Table S7. Mass spectrometry data showing minimum of two peptides from PTPRD interactome obtained from icPTPRD-WT and icPTPRD-D1521A expressing Sk-Mel-28 cells induced by doxycycline for 24h

Protein peptides	Accession No.	icPTPRD-D1521A	icPTPRD-WT	
RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3	P98175	33	25	Common
Probable ATP-dependent RNA helicase DDX20 OS=Homo sapiens GN=DDX20 PE=1 SV=2	Q9UHI6	27	20	Common
Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	Q15393	16	17	Common
Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2	P52732	15	16	Common
Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	O14744	48	15	Common
Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	Q8TEQ6	24	15	Common
Component of gems 4 OS=Homo sapiens GN=GEMIN4 PE=1 SV=1	P57678	24	14	Common
U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	O75643	20	13	Common
Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	Q9BQA1	11	12	Common
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	O43143	7	10	Common
Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	O75533	16	9	Common
RING finger protein 219 OS=Homo sapiens GN=RNF219 PE=1 SV=1	Q5W0B1	12	7	Common
Serine/threonine-protein kinase RIO1 OS=Homo sapiens GN=RIOK1 PE=1 SV=2	Q9BRS2	11	7	Common
IQ motif and SEC7 domain-containing protein 1 OS=Homo sapiens GN=IQSEC1 PE=1 SV=1	Q6DN90	7	7	Common
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	P19338	7	7	Common
E3 ubiquitin-protein ligase RNF180 OS=Homo sapiens GN=RNF180 PE=2 SV=2	Q86T96	3	7	Common
Methylosome subunit pICln OS=Homo sapiens GN=CLNS1A PE=1 SV=1	P54105	15	6	Common

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	
OTU domain-containing protein 4 OS=Homo sapiens GN=OTUD4 PE=1 SV=3	Q01804	12	6	Common
Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	Q13435	4	6	Common
MORC family CW-type zinc finger protein 2 OS=Homo sapiens GN=MORC2 PE=1 SV=2	Q9Y6X9	2	6	Common
Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4	P31943	7	5	Common
Transcription factor E2F7 OS=Homo sapiens GN=E2F7 PE=1 SV=3	Q96AV8	6	5	Common
U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2	Q8WWY3	5	5	Common
Autophagy-related protein 2 homolog B OS=Homo sapiens GN=ATG2B PE=1 SV=5	Q96BY7	4	5	Common
Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	Q6P2Q9	8	4	Common
116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1	Q15029	6	4	Common
Uncharacterized protein C11orf84 OS=Homo sapiens GN=C11orf84 PE=1 SV=3	Q9BUA3	6	4	Common
Calmodulin-regulated spectrin-associated protein 3 OS=Homo sapiens GN=KIAA1543 PE=1 SV=2	Q9P1Y5	6	4	Common
ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	Q08211	6	4	Common
Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	Q00839	4	4	Common
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	P23396	4	4	Common
Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2	O15397	2	4	Common
Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2	P23588	18	3	Common
CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3	P27708	6	3	Common
CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	A5YKK6	5	3	Common
Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	Q9UMS4	3	3	Common

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	
TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 OS=Homo sapiens GN=TAB2 PE=1 SV=1	Q9NYJ8	2	3	Common
Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	Q12905	2	3	Common
Pre-mRNA branch site protein p14 OS=Homo sapiens GN=SF3B14 PE=1 SV=1	Q9Y3B4	2	3	Common
Ras-related protein Rab-19 OS=Homo sapiens GN=RAB19 PE=2 SV=2	A4D1S5	2	3	Common
Putative tyrosine-protein phosphatase TPTE OS=Homo sapiens GN=TPTE PE=2 SV=3	P56180	2	3	Common
Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1	P62316	6	2	Common
Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	P08107	5	2	Common
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3	O15294	4	2	Common
Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF PE=1 SV=2	P10586	4	2	Common
Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	P20700	3	2	Common
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	P62847	3	2	Common
Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	Q15233	3	2	Common
Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1	P07477	3	2	Common
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	P62081	2	2	Common
Syntaxin-binding protein 3 OS=Homo sapiens GN=STXBP3 PE=1 SV=2	O00186	2	2	Common
Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	P60228	2	2	Common
Uncharacterized protein C10orf82 OS=Homo sapiens GN=C10orf82 PE=2 SV=2	Q8WW14	2	2	Common
U2-associated protein SR140 OS=Homo sapiens GN=SR140 PE=1 SV=2	O15042	2	2	Common
Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1	O94906	2	2	Common

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	
NACHT, LRR and PYD domains-containing protein 1 OS=Homo sapiens GN=NLRP1 PE=1 SV=1	Q9C000	2	2	Common
Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3	O94788	2	2	Common
Transcription elongation factor B polypeptide 1 OS=Homo sapiens GN=TCEB1 PE=1 SV=1	Q15369	2	2	Common
Uncharacterized protein OS=Homo sapiens GN=DSTYK	C9J9G6	2	2	Common
Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2	P04279	0	8	Not Common
Glycosyltransferase 25 family member 3 OS=Homo sapiens GN=CERCAM PE=2 SV=1	Q5T4B2	0	6	Not Common
Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	Q9Y3F4	0	5	Not Common
Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2	Q8TF72	1	4	Not Common
Teneurin-3 OS=Homo sapiens GN=ODZ3 PE=2 SV=3	Q9P273	0	4	Not Common
Pumilio domain-containing protein C14orf21 OS=Homo sapiens GN=C14orf21 PE=1 SV=1	Q86U38	0	4	Not Common
Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	P29508	0	4	Not Common
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	P02751	0	4	Not Common
Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	P04908	1	3	Not Common
Otoferlin OS=Homo sapiens GN=OTOF PE=1 SV=3	Q9HC10	1	3	Not Common
Homeobox protein Hox-A5 OS=Homo sapiens GN=HOXA5 PE=1 SV=2	P20719	1	3	Not Common
Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	Q71U36	1	3	Not Common
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	P07437	0	3	Not Common
Transcription factor jun-B OS=Homo sapiens GN=JUNB PE=1 SV=1	P17275	0	3	Not Common
Caspase 3, apoptosis-related cysteine peptidase, isoform CRA_b OS=Homo sapiens GN=CASP3	A8MVM1	0	3	Not Common

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	
Neuron navigator 3 OS=Homo sapiens GN=NAV3 PE=1 SV=3	Q8IVL0	0	3	Not Common
UDP-N-acetylglucosamine transferase subunit ALG13 homolog OS=Homo sapiens GN=ALG13 PE=1 SV=2	Q9NP73	0	3	Not Common
Cytospin-B OS=Homo sapiens GN=CYTSB PE=1 SV=1	Q5M775	0	3	Not Common
Zinc finger protein 510 OS=Homo sapiens GN=ZNF510 PE=2 SV=1	Q9Y2H8	0	3	Not Common
Spindlin-1 OS=Homo sapiens GN=SPIN1 PE=1 SV=3	Q9Y657	9	2	Not Common
PAX-9 protein (Fragment) OS=Homo sapiens GN=PAX-9	O95616	1	2	Not Common
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	P62701	1	2	Not Common
40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	P08708	1	2	Not Common
Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	P61163	1	2	Not Common
Gem-associated protein 8 OS=Homo sapiens GN=GEMIN8 PE=1 SV=1	Q9NWZ8	1	2	Not Common
Codanin-1 OS=Homo sapiens GN=CDAN1 PE=1 SV=4	Q8IWY9	1	2	Not Common
Rab9 effector protein with kelch motifs OS=Homo sapiens GN=RABEPK PE=1 SV=1	Q7Z6M1	1	2	Not Common
Protein FAM102A OS=Homo sapiens GN=FAM102A PE=2 SV=2	Q5T9C2	1	2	Not Common
Isoleucyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	P41252	1	2	Not Common
Putative HIN1-like protein OS=Homo sapiens GN=HIN1L PE=5 SV=1	Q7RTX8	1	2	Not Common
Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	P68371	0	2	Not Common
Protein kinase C gamma type OS=Homo sapiens GN=PRKCG PE=1 SV=3	P05129	0	2	Not Common
Coiled-coil domain-containing protein 33 OS=Homo sapiens GN=CCDC33 PE=1 SV=3	Q8N5R6	0	2	Not Common
Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	P14625	0	2	Not Common

Protein peptides	Accession No.	icPTPRD-D1521A	icPTPRD-WT	
THAP domain-containing protein 9 OS=Homo sapiens GN=THAP9 PE=2 SV=2	Q9H5L6	0	2	Not Common
Actin-binding protein IPP OS=Homo sapiens GN=IPP PE=2 SV=1	Q9Y573	0	2	Not Common
6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	P17858	0	2	Not Common
Midline-1 OS=Homo sapiens GN=MID1 PE=1 SV=1	O15344	0	2	Not Common
Methionyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	P56192	0	2	Not Common
Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	Q12906	0	2	Not Common
Nuclear RNA export factor 2 OS=Homo sapiens GN=NXF2 PE=1 SV=1	Q9GZY0	0	2	Not Common
Protein ALO17 OS=Homo sapiens GN=KIAA1618 PE=1 SV=2	Q9HCF4	0	2	Not Common
Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1	Q99613	0	2	Not Common
Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1	Q02383	0	2	Not Common
Glycogenin-1 OS=Homo sapiens GN=GYG1 PE=1 SV=4	P46976	0	2	Not Common
Mitogen-activated protein kinase-binding protein 1 OS=Homo sapiens GN=MAPKBP1 PE=2 SV=4	O60336	0	2	Not Common
Protocadherin-17 OS=Homo sapiens GN=PCDH17 PE=2 SV=2	O14917	0	2	Not Common
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	P11940	0	2	Not Common
Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1	P62314	8	1	Not Common
U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1	O43290	6	1	Not Common
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	P14923	5	1	Not Common
Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	P06748	5	1	Not Common
Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	Q13835	4	1	Not Common

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	P13010	4	1	Not Common
Putative small nuclear ribonucleoprotein polypeptide E-like protein 1 OS=Homo sapiens GN=SNRPEL1 PE=5 SV=1	Q5VYJ4	3	1	Not Common
cDNA FLJ43335 fis, clone NT2RI3006673, highly similar to Receptor-type tyrosine-protein phosphatase F (EC 3.1.3.48) OS=Homo sapiens	B3KWM1	3	1	Not Common
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	P62277	3	1	Not Common
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	P62241	2	1	Not Common
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	P62266	2	1	Not Common
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	P61247	2	1	Not Common
Rotatin OS=Homo sapiens GN=RTTN PE=1 SV=3	Q86VV8	2	1	Not Common
Amiloride-sensitive cation channel 2, neuronal OS=Homo sapiens GN=ACCN2 PE=1 SV=3	P78348	2	1	Not Common
Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2	Q9P2R3	2	1	Not Common
Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	P84090	2	1	Not Common
DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	Q16531	2	1	Not Common
Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	P33778	2	1	Not Common
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	P62829	2	1	Not Common
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	P55072	2	1	Not Common
60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	P62913	2	1	Not Common
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	P15924	9	0	Not Common
Survival of motor neuron protein-interacting protein 1 OS=Homo sapiens GN=SIP1 PE=1 SV=1	O14893	9	0	Not Common
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	P62805	8	0	Not Common

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	
Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	Q13885	6	0	Not Common
Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1	P62318	6	0	Not Common
Mitogen-activated protein kinase kinase kinase 7 OS=Homo sapiens GN=MAP3K7 PE=1 SV=1	O43318	6	0	Not Common
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	P62269	5	0	Not Common
Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	Q9Y2W1	5	0	Not Common
Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1	Q9H4B7	4	0	Not Common
40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	P62263	4	0	Not Common
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	P22626	4	0	Not Common
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	Q86YZ3	4	0	Not Common
Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1	Q13464	4	0	Not Common
Probable methylcytosine dioxygenase TET2 OS=Homo sapiens GN=TET2 PE=1 SV=3	Q6N021	4	0	Not Common
Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	P81605	3	0	Not Common
Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens GN=SNRPB PE=1 SV=2	P14678	3	0	Not Common
Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	Q5D862	3	0	Not Common
Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	P55884	3	0	Not Common
Gem-associated protein 6 OS=Homo sapiens GN=GEMIN6 PE=1 SV=1	Q8WXD5	3	0	Not Common
60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	P05387	3	0	Not Common
Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3	P35573	3	0	Not Common
Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	P23381	3	0	Not Common

Protein peptides	Accession No.	icPTPRD-D1521A	icPTPRD-WT	
Leucine-rich repeat-containing protein 42 OS=Homo sapiens GN=LRRC42 PE=1 SV=1	Q9Y546	3	0	Not Common
Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	Q02413	3	0	Not Common
40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	P60866	3	0	Not Common
Zinc finger protein 40 OS=Homo sapiens GN=HIVEP1 PE=1 SV=3	P15822	3	0	Not Common
60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	P39023	3	0	Not Common
Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=2	Q93008	3	0	Not Common
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	P25398	3	0	Not Common
Zinc finger protein 202 OS=Homo sapiens GN=ZNF202 PE=1 SV=4	O95125	3	0	Not Common
60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	P18621	3	0	Not Common
Putative uncharacterized protein DKFZp686G04235 OS=Homo sapiens GN=DKFZp686G04235	Q63HL4	3	0	Not Common
40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	P62244	3	0	Not Common
60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	P35268	2	0	Not Common
Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2	O75821	2	0	Not Common
Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1	O00303	2	0	Not Common
60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	P61353	2	0	Not Common
60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	P30050	2	0	Not Common
DNA repair protein REV1 OS=Homo sapiens GN=REV1 PE=1 SV=1	Q9UBZ9	2	0	Not Common
26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	P35998	2	0	Not Common
Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=5	P07814	2	0	Not Common

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	P68104	2	0	Not Common
SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1	Q6P3W7	2	0	Not Common
C-Myc-binding protein OS=Homo sapiens GN=MYCBP PE=1 SV=3	Q99417	2	0	Not Common
Pulmonary surfactant-associated protein D OS=Homo sapiens GN=SFTPD PE=1 SV=2	P35247	2	0	Not Common
POTE ankyrin domain family member B OS=Homo sapiens GN=POTEB PE=2 SV=1	Q6S5H4	2	0	Not Common
Cell division protein kinase 18 OS=Homo sapiens GN=CDK18 PE=1 SV=3	Q07002	2	0	Not Common
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	P62851	2	0	Not Common
26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	O00487	2	0	Not Common
Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	O00410	2	0	Not Common
Contactin-1 OS=Homo sapiens GN=CNTN1 PE=1 SV=1	Q12860	2	0	Not Common
PHD and RING finger domain-containing protein 1 OS=Homo sapiens GN=PHRF1 PE=1 SV=3	Q9P1Y6	2	0	Not Common
Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein OS=Homo sapiens GN=PREX2 PE=2 SV=1	Q70Z35	2	0	Not Common
Chromosome-associated kinesin KIF4A OS=Homo sapiens GN=KIF4A PE=1 SV=3	O95239	2	0	Not Common
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	Q13200	2	0	Not Common
Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 PE=1 SV=4	Q8NCM8	2	0	Not Common
Protein tyrosine phosphatase, receptor type, F isoform 2 variant (Fragment) OS=Homo sapiens	Q59FI2	2	0	Not Common
Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1	Q12996	2	0	Not Common
Vacuolar protein sorting-associated protein 8 homolog OS=Homo sapiens GN=VPS8 PE=1 SV=3	Q8N3P4	2	0	Not Common
A disintegrin and metalloproteinase with thrombospondin motifs 15 OS=Homo sapiens GN=ADAMTS15 PE=2 SV=1	Q8TE58	2	0	Not Common

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	
Histone-lysine N-methyltransferase SETD2 OS=Homo sapiens GN=SETD2 PE=1 SV=3	Q9BYW2	2	0	Not Common
Neuropilin-1 OS=Homo sapiens GN=NRP1 PE=1 SV=3	O14786	2	0	Not Common
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Homo sapiens GN=UAP1L1 PE=2 SV=2	Q3KQV9	2	0	Not Common
ATP-dependent RNA helicase DQX1 OS=Homo sapiens GN=DQX1 PE=2 SV=2	Q8TE96	2	0	Not Common
Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	Q13347	2	0	Not Common
U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=1 SV=3	P09012	2	0	Not Common
Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2	Q9NYF8	2	0	Not Common
Splicing factor 45 OS=Homo sapiens GN=RBM17 PE=1 SV=1	Q96I25	2	0	Not Common
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	P02545	2	0	Not Common
Echinoderm microtubule-associated protein-like 6 OS=Homo sapiens GN=EML6 PE=2 SV=2	Q6ZMW3	2	0	Not Common
MAP kinase-activated protein kinase 5 OS=Homo sapiens GN=MAPKAPK5 PE=1 SV=2	Q8IW41	2	0	Not Common
60S ribosomal protein L26-like 1 OS=Homo sapiens GN=RPL26L1 PE=1 SV=1	Q9UNX3	2	0	Not Common
CD2 antigen cytoplasmic tail-binding protein 2 OS=Homo sapiens GN=CD2BP2 PE=1 SV=1	O95400	2	0	Not Common
Protein KIAA1967 OS=Homo sapiens GN=KIAA1967 PE=1 SV=2	Q8N163	2	0	Not Common
6-pyruvoyl tetrahydrobiopterin synthase OS=Homo sapiens GN=PTS PE=1 SV=1	Q03393	2	0	Not Common
Spindlin-2A OS=Homo sapiens GN=SPIN2A PE=1 SV=3	Q99865	2	0	Not Common
60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	P32969	2	0	Not Common
Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=2	O95819	2	0	Not Common
Uncharacterized protein OS=Homo sapiens GN=ASB18	C9JFL4	2	0	Not Common

Protein peptides	**Accession No.**	**icPTPRD-D1521A**	**icPTPRD-WT**	
Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	Q13263	2	0	Not Common
40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	P39019	2	0	Not Common
Phosphatidylinositol 4-kinase alpha OS=Homo sapiens GN=PI4KA PE=1 SV=3	P42356	2	0	Not Common
Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	P01614	2	0	Not Common
Receptor-type tyrosine-protein phosphatase delta OS=Homo sapiens GN=PTPRD PE=1 SV=2	P23468			
icPTPRD-D1521A: intracellular PTPRD having two phosphatase domains and bearing D1521A mutation; icPTPRD-WT: intracellular PTPRD having two phosphatase domains; Control: Vector alone				

Supp. Table S8. List of ClinVar accession numbers for the PTP variants. Variants can be accessed at http://www.ncbi.nlm.nih.gov/clinvar/

HGVS name	Phenotype descriptions	Date last evaluated	Gene symbol	ClinVarAccession
NM_133170.3:c.251C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154775
NM_133170.3:c.2551G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154776
NM_133170.3:c.4207C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154777
NM_133170.3:c.385G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154778
NM_133170.3:c.994G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154779
NM_133170.3:c.982C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154780
NM_133170.3:c.4201G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154781
NM_133170.3:c.1264C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154782
NM_133170.3:c.4351G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154783
NM_133170.3:c.1465C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154784
NM_133170.3:c.1651C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154785
NM_133170.3:c.4194-14G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154786
NM_133170.3:c.1888G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154787
NM_133170.3:c.1958G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154788
NM_133170.3:c.1967C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154789
NM_133170.3:c.2731G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154790

HGVS name	Phenotype descriptions	Date last evaluated	Gene symbol	ClinVarAccession
NM_133170.3:c.2782G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154791
NM_133170.3:c.2904+9C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154792
NM_133170.3:c.3082G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154793
NM_133170.3:c.3224C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154794
NM_133170.3:c.2770G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154795
NM_133170.3:c.3322G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154796
NM_133170.3:c.3530C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154797
NM_133170.3:c.3771+11C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154798
NM_133170.3:c.4363G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRT	SCV000154799
NM_002839.2:c.182G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154800
NM_002839.2:c.211-10C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154801
NM_002839.2:c.3124G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154802
NM_002839.2:c.1337G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154803
NM_002839.2:c.3122C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154804
NM_002839.2:c.3056-11C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154805
NM_002839.2:c.3115G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154806
NM_002839.2:c.2508G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154807
NM_002839.2:c.2626G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154808

HGVS name	Phenotype descriptions	Date last evaluated	Gene symbol	ClinVarAccession
NM_002839.2:c.3007G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154809
NM_002839.2:c.3742G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154810
NM_002839.2:c.5119G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154811
NM_002839.2:c.4429C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154812
NM_002839.2:c.4693G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154813
NM_002839.2:c.5068C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154814
NM_002839.2:c.5069C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154815
NM_002839.2:c.4661+6_446+7insACAGTTCAGGAATGGTAAGTT	Cutaneous Malignant Melanoma	2014-06-02	PTPRD	SCV000154816
NM_001109754.1:c.1250G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154817
NM_001109754.1:c.1781-5G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154818
NM_001109754.1:c.2009G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154819
NM_001109754.1:c.2009T>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154820
NM_001109754.1:c.2615C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154821
NM_001109754.1: c.3374C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154822
NM_001109754.1:c.5765C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154823
NM_001109754.1:c.2900G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154824
NM_001109754.1:c.3284C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154825
NM_001109754.1:c.3843A>G	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154826

HGVS name	**Phenotype descriptions**	**Date last evaluated**	**Gene symbol**	**ClinVarAccession**
NM_001109754.1:c.4654A>G	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154827
NM_001109754.1:c.4169-9T>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154828
NM_001109754.1:c.4169-10T>C	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154829
NM_001109754.1:c.4674G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154830
NM_001109754.1:c.4715-5C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154831
NM_001109754.1:c.5848C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRB	SCV000154832
NM_030667.1:c.839C>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154833
NM_030667.1:c.1106-9T>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154834
NM_030667.1:c.1110C>G	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154835
NM_030667.1:c.1444G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154836
NM_030667.1:c.2302C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154837
NM_030667.1:c.2321C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154838
NM_030667.1:c.2560G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154839
NM_030667.1:c.2814T>G	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154840
NM_030667.1:c.3223G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154841
NM_030667.1:c.3364C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154842
NM_030667.1:c.3506C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRO	SCV000154843
NM_002847.3:c.113-7C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154844

HGVS name	**Phenotype descriptions**	**Date last evaluated**	**Gene symbol**	**ClinVarAccession**
NM_002847.3:c.202G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154845
NM_002847.3:c.2149G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154846
NM_002847.3:c.536G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154847
NM_002847.3:c.428G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154848
NM_002847.3:c.770C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154849
NM_002847.3:c.1063G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154850
NM_002847.3:c.1269G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154851
NM_002847.3:c.2345-7C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154852
NM_002847.3:c.2276C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154853
NM_002847.3:c.2419-7C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRN2	SCV000154854
NM_002850.3:c.421C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRS	SCV000154855
NM_002850.3:c.470C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRS	SCV000154856
NM_002850.3:c.379+1G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRS	SCV000154857
NM_002850.3:c.543T>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRS	SCV000154858
NM_002850.3:c.860C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRS	SCV000154859
NM_002850.3:c.1532C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRS	SCV000154860
NM_002850.3:c.4165G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRS	SCV000154861
NM_002850.3:c.4531G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRS	SCV000154862

HGVS name	**Phenotype descriptions**	**Date last evaluated**	**Gene symbol**	**ClinVarAccession**
NM_002850.3:c.5425C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRS	SCV000154863
NM_080683.2:c.1196-6C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPN13	SCV000154864
NM_080683.2:c.3224-7C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPN13	SCV000154865
NM_080683.2:c.3314-7T>G	Cutaneous Malignant Melanoma	2014-06-02	PTPN13	SCV000154866
NM_080683.2:c.4549C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPN13	SCV000154867
NM_080683.2: c.4559A>G	Cutaneous Malignant Melanoma	2014-06-02	PTPN13	SCV000154868
NM_080683.2: c.4566A>G	Cutaneous Malignant Melanoma	2014-06-02	PTPN13	SCV000154869
NM_080683.2:c.5246C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPN13	SCV000154870
NM_080683.2:c.7385A>T	Cutaneous Malignant Melanoma	2014-06-02	PTPN13	SCV000154871
NM_002838.4:c.1659+1G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRC	SCV000154872
NM_002838.4:c.1694G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRC	SCV000154873
NM_002838.4:c.1721-9G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRC	SCV000154874
NM_002838.4:c.1972C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRC	SCV000154875
NM_002838.4:c.2689C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRC	SCV000154876
NM_002838.4:c.3406G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRC	SCV000154877
NM_002838.4:c.3458C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRC	SCV000154878
NM_002846.2:c.193G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN	SCV000154879
NM_002846.2:c.361C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRN	SCV000154880

HGVS name	Phenotype descriptions	Date last evaluated	Gene symbol	ClinVarAccession
NM_002846.2:c.365G>C	Cutaneous Malignant Melanoma	2014-06-02	PTPRN	SCV000154881
NM_002846.2:c.427C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRN	SCV000154882
NM_002846.2:c.604G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN	SCV000154883
NM_002846.2:c.785G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN	SCV000154884
NM_002846.2:c.1286C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRN	SCV000154885
NM_002846.2:c.2192G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRN	SCV000154886
NM_002842.2:c.431G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRH	SCV000154887
NM_002842.2:c.1690-9C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRH	SCV000154888
NM_002842.2:c.458G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRH	SCV000154889
NM_002842.2:c.1094C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRH	SCV000154890
NM_002842.2:c.2384+11G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRH	SCV000154891
NM_002842.2:c.2969C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRH	SCV000154892
NM_002842.2:c.3220C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRH	SCV000154893
NM_153050.2:c.835C>T	Cutaneous Malignant Melanoma	2014-06-02	MTMR3	SCV000154894
NM_153050.2:c.881C>T	Cutaneous Malignant Melanoma	2014-06-02	MTMR4	SCV000154895
NM_153050.2:c.1330C>T	Cutaneous Malignant Melanoma	2014-06-02	MTMR5	SCV000154896
NM_153050.2:c.1548C>A	Cutaneous Malignant Melanoma	2014-06-02	MTMR6	SCV000154897
NM_153050.2:c.3455C>T	Cutaneous Malignant Melanoma	2014-06-02	MTMR7	SCV000154898

HGVS name	**Phenotype descriptions**	**Date last evaluated**	**Gene symbol**	**ClinVarAccession**
NM_022648.4:c.666-7C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154899
NM_022648.4:c.4523C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154900
NM_022648.4:c.1729C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154901
NM_022648.4:c.2362C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154902
NM_022648.4:c.4330+9C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154903
NM_022648.4:c.2919-2921delG	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154904
NM_022648.4:c.4498G>A	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154905
NM_032865.5:c.206G>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154906
NM_032865.5:c.653C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154907
NM_032865.5:c.683C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154908
NM_032865.5:c.1055C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154909
NM_032865.5:c.1289-10C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154910
NM_032865.5:c.1940C>T	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154911
NM_032865.5:c.2141G>A	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154912
NM_032865.5:c.2140-2142delG	Cutaneous Malignant Melanoma	2014-06-02	TNS1	SCV000154913
NM_006504.4:c.11G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRE	SCV000154914
NM_006504.4:c.32G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRE	SCV000154915
NM_006504.4:c.598G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRE	SCV000154916

HGVS name	Phenotype descriptions	Date last evaluated	Gene symbol	ClinVarAccession
NM_006504.4:c.1599+12C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRE	SCV000154917
NM_002843.3:c.3874+3G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRJ	SCV000154918
NM_002843.3:c.1257-1275delGTCATCCCCGGACTCCG	Cutaneous Malignant Melanoma	2014-06-02	PTPRJ	SCV000154919
NM_002843.3:c.1561C>A	Cutaneous Malignant Melanoma	2014-06-02	PTPRJ	SCV000154920
NM_002843.3:c.1562C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRJ	SCV000154921
NM_002843.3:c.2155C>T	Cutaneous Malignant Melanoma	2014-06-02	PTPRJ	SCV000154922
NM_001040446.1:c.331G>T	Cutaneous Malignant Melanoma	2014-06-02	MTMR12	SCV000154923
NM_001040446.1:c.583+9G>T	Cutaneous Malignant Melanoma	2014-06-02	MTMR12	SCV000154924
NM_001040446.1:c.2038G>A	Cutaneous Malignant Melanoma	2014-06-02	MTMR12	SCV000154925
NM_006906.1:c.13G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPN5	SCV000154926
NM_006906.1:c.508C>G	Cutaneous Malignant Melanoma	2014-06-02	PTPN5	SCV000154927
NM_006906.1:c.916G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPN5	SCV000154928
NM_006906.1:c.1080+1G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPN5	SCV000154929
NM_002835.3:c.938G>G	Cutaneous Malignant Melanoma	2014-06-02	PTPN12	SCV000154930
NM_002835.3:c.1448G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPN12	SCV000154931
NM_002835.3:c.2314G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPN12	SCV000154932
NM_007039.3:c.829G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPN21	SCV000154933
NM_007039.3:c.1756G>C	Cutaneous Malignant Melanoma	2014-06-02	PTPN21	SCV000154934

HGVS name	**Phenotype descriptions**	**Date last evaluated**	**Gene symbol**	**ClinVarAccession**
NM_007039.3:c.2224G>A	Cutaneous Malignant Melanoma	2014-06-02	PTPN21	SCV000154935
NM_004685.3:c.1116G>C	Cutaneous Malignant Melanoma	2014-06-02	MTMR6	SCV000154936
NM_004685.3:c.1808G>T	Cutaneous Malignant Melanoma	2014-06-02	MTMR6	SCV000154937
NM_017677.2:c.310G>A	Cutaneous Malignant Melanoma	2014-06-02	MTMR8	SCV000154938
NM_017677.2:c.2102G>T	Cutaneous Malignant Melanoma	2014-06-02	MTMR8	SCV000154939
NM_015466.2:c.3773G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPN23	SCV000154940
NM_015466.2:c.4015G>T	Cutaneous Malignant Melanoma	2014-06-02	PTPN23	SCV000154941
NM_003463.3:c.25G>T	Cutaneous Malignant Melanoma	2014-06-02	PTP4A1	SCV000154942