Supporting Information

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SI Materials and Methods

Cultured Cell Lines. The cultured plastic-adherent melanoma lines 1363-mel, 2048-mel, 1558-mel, 1102-mel, 397-mel, and 1087-mel were initiated from enzymatic digests of metastatic lesions. The EBV-B cell lines 1363-EBV, 2048-EBV, 1558-EBV, 1102-EBV, and 1087-EBV were generated from PBMCs according to standard methods and were maintained as suspension cultures. The MCF7 breast cancer cell line and LoVo, a colon cancer cell line, were obtained from the American Type Culture Collection. The 293 HEK cells expressing HLA-DRβ1*0101 were generated as described previously (1). All cell lines were maintained at 37 °C, 5% CO_2 in medium consisting of RPMI 1640 plus 10% heat-inactivated FCS, 2 mM L-glutamine, 10 mM Hepes buffer, and antibiotics. Cultures were certified to be free of *Mycoplasma* contamination by PCR.

Isolation of HLA-DR-Associated Peptides. Cells (total number, 0.3×10^9 to 1.2×10^9 per cell line) were lysed in a solution of 20 mM Tris·HCl, pH 8.0; 150 mM NaCl with 1% CHAPS; 1 mM PMSF; 5 μg/mL aprotinin; 10 μg/mL leupeptin; 10 μg/mL pepstatin A; and 1:100 dilutions of phosphatase inhibitor cocktails I and II (Sigma–Aldrich), to prevent potential dephosphorylation of peptides during extraction. The lysate was centrifugated and then run over an Econocolumn (Bio-Rad) containing the pan-HLA-DR-specific mAb L243 bound to recombinant protein A fastflow Sepharose beads (Amersham Pharmacia Biotech). After overnight incubation at 4 °C, peptides were eluted from HLA-DR molecules with 10% acetic acid (HOAc) and separated by using a 10-kDa cutoff ULTRAFREE-MC filter (Millipore). Extracts were stored at −80 °C.

Phosphopeptide Enrichment. Samples were taken to dryness, reconstituted in 20–30 μL of 1:1:1 acetonitrile to methanol to aqueous acetic acid (0.01%), loaded at 1 μL/min onto an activated Fe^{3+}-immobilized metal-affinity chromatography column (360-μm o.d. and 150-μm i.d.; Polymicro Technologies) packed with 7–8 cm of POROS 20 MC packing material (PerSeptive Biosystems) and eluted with 12 μL of 50 mM ascorbic acid in 0.1% HOAc (Sigma–Aldrich) onto a microcapillary precolumn (360-μm o.d. and 75-μm i.d.) containing 5 cm of C18 irregular reverse-phase packing material (5- to 20-μm particles; YMC).

Peptides. Peptides used in this study were synthesized with Fmoc chemistry, isolated by HPLC to >90% purity, and validated with mass spectrometry (Global Peptides and Pi Proteomics). Peptides included: B-$Raf_{586-614}$ V600E, (B-Raf mut; EDLTVKIGDFGLATEKSRWSGSHQFEQLS); B-Raf mut pT599 (pB-Raf mut; EDLTVKIGDFGLA[pT]EKSRWSGSHQFEQLS); wild-type B-$Raf_{586-614}$ (B-Raf wt; EDLTVKIGDFGLATVKSRWSGSHQFEQLS); B-Raf wt pT599 (pB-Raf wt; EDLTVKIGDFGLA[pT]VKSRWSGSHQFEQLS); MART-$_{100-111}$ pS108 (pMART-1; Table 1); tensin-$3_{1433-1445}$ pS1441 (pTensin-3; Table 1); influenza $HA_{307-319}$ (PKYVKQNTLKLAT); and mutant triosephosphate isomerase (TPI_{26-38} T28I or TPImut; IGILNAAKVPADT).

1. Wang RF, Wang X, Atwood AC, Topalian SL, Rosenberg SA (1999) Cloning genes encoding MHC class II-restricted antigens: Mutated CDC27 as a tumor antigen. *Science* 284:1351–1354.

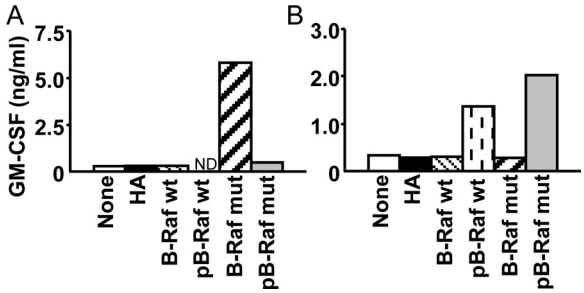


Fig. S1. CD4$^+$ T cells discriminate the presence of a phosphate moiety on candidate B-Raf peptides. B-Raf mut-specific CD4$^+$ T cell cultures were generated from the PBMCs of melanoma patients whose tumors harbored B-Raf mut. T cells raised against candidate B-Raf mut (*A*) or B-Raf mut^{pT599} (pB-Raf mut; *B*) peptides were assessed for reactivity after an overnight coculture with peptide-pulsed APCs. GM-CSF secretion from T cells was measured by ELISA. ND, not done.

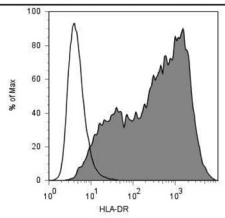
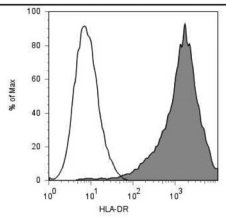
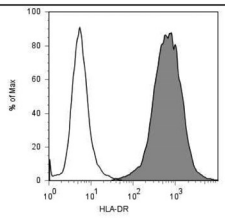
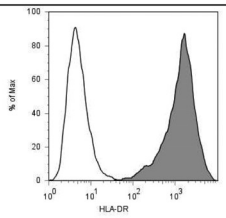
Patient No.	HLA-DR genotype	Mel	EBV
1363	β1*0101		
2048	β1*0101, 0404 β4*0103		

Fig. S2. HLA-DR expression on melanoma and EBV-B cells used for phosphopeptide isolation. Cells were analyzed by flow cytometry for expression of HLA-DR (mAb L243, isotype IgG2a). HLA-DR expression is shown in solid gray, and isotype controls appear in open field.

Table S1. Characteristics of HLA-DR-associated phosphopeptides selectively expressed by EBV-transformed B cells

Source protein	Location*	Phosphopeptide†	1363-EBV	2048-EBV	Known phosphosite (score)‡
1363-EBV and 2048-EBV					
B lymphocyte antigen CD20	PM	$_{25}$SGPKPLFRRMpSSLVGPTQ$_{42}$	−	+§	N (0.945)
		$_{26}$GPKPLFRRMpSS$_{36}$	−	+§	
		$_{26}$GPKPLFRRMpSSL$_{37}$	−	+§	
		$_{26}$GPKPLFRRMpSSLV$_{38}$	−	+§	
		$_{26}$GPKPLFRRMpSSLVG$_{39}$	++	++§	
		$_{26}$GPKPLFRRMpSSLVGP$_{40}$	++	+++§	
		$_{26}$GPKPLFRRMpSSLVGPT$_{41}$	++	+++§	
		$_{26}$GPKPLFRRMpSSLVGPTQ$_{42}$	++	+++§	
		$_{26}$GPKPLFRRMpSSLVGPTQS$_{43}$	−	+§	
Lymphoid-restricted membrane protein	ERM	$_{130}$ApSPTIEAQGTSPAHDN$_{145}$	−	++	N (0.991)
		$_{130}$ApSPTIEAQGTSPAHDNI$_{146}$	−	+	
		$_{130}$ApSPTIEAQGTSPAHDNIA$_{147}$	−	++	
		$_{402}$SSpSWRILGSKQSEHRP$_{417}$	+	−	N (0.994)
1363-EBValone					
ADAM 8	PM	$_{758}$pSPPFPVPVYTRQAPKQVIK$_{776}$	+	−	N (0.677)
B lymphocyte antigen CD19	PM	$_{328}$DPTRRFFKVpTPPPGSGPQ$_{345}$	+	−	N (0.238)
Germinal center B cell-expressed transcript 2 protein	C	$_{142/76}$RpSPEDEYELLMPHRISSH$_{159/93}$	+	−	N (0.998)
		$_{143/77}$pSPEDEYELLMPHRISSH$_{159/93}$	+	−	
		$_{143/77}$SPEDEYELLMPHRIpSSH$_{159/93}$	+	−	N (0.737)
		$_{149/83}$ELLMPHRIpSSHF$_{160/94}$	+	−	
		$_{149/83}$ELLMPHRIpSSHFL$_{161/95}$	+	−	
Interleukin-2 receptor subunit-β	PM	$_{282}$TPDPSKFFSQLpSSEHGGDV$_{300}$	+	−	N (0.905)
		$_{282}$pTPDPSKFFSQLSSEHGGDVQ$_{301}$	+	−	N (0.772)
Optineurin	C/G	$_{473}$pSDFHAERAAREK$_{484}$	+	−	N (0.073)
Phosphoglycerate kinase 1	C	$_{203}$pSPERPFLAILGGAKVADK$_{220}$	+	−	Y (0.997)
		$_{203}$pSPERPFLAILGGAKVADKIQ$_{222}$	+	−	
Solute carrier family 12, member 6, isoform a	PM	$_{1050}$TKDKYMASRGQKAKpSMEG$_{1067}$	+	−	N (0.993)
TNFAIP3-interacting protein 1	C/N	$_{559}$VPHHGFEDWpSQIR$_{571}$	+	−	N (0.483)
Tumor necrosis factor receptor superfamily member 8	PM	$_{513/50}$KIEKIpYIMKADTVIVG$_{528/65}$	++	−	N (0.771)
		$_{514/51}$IEKIpYIMKADTVIVG$_{528/65}$	+	−	
UPF0501 protein KIAA1430	UK	$_{136}$EESpSDDGKKY$_{145}$	+	−	Y (0.458)
Xenotropic and polytropic retrovirus receptor 1	PM	$_{657}$KNRpSWKYN$_{664}$	+	−	N (0.995)
		$_{657}$KNRpSWKYNQ$_{665}$	+	−	
		$_{657}$KNRpSWKYNQSISLR$_{670}$	+	−	
		$_{657}$KNRpSWKYNQSISLRRP$_{672}$	++	−	
		$_{658}$NRpSWKYNQSISLR$_{670}$	+	−	
		$_{658}$NRpSWKYNQSISLRRP$_{672}$	+	−	
		$_{659}$RpSWKYNQSISLRRP$_{672}$	++	−	
2048-EBV alone					
BCL2-associated transcription factor 1	N	$_{653}$RRIDIpSPSTLR$_{663}$	−	+	N (0.970)
		$_{653}$RRIDIpSPSTLRK$_{664}$	−	+	
Caspase recruitment domain-containing protein 11	C	$_{509}$RAKpSPISLK$_{517}$	−	+	N (0.996)
Chromatin-modifying protein 1a	C/E/N	$_{49/177}$ESpSVRSQEDQLSR$_{61/189}$	−	+	Y (0.986)
		$_{49/177}$ESpSVRSQEDQLSRR$_{62/190}$	−	++	
Interleukin-10 receptor-β chain	PM	$_{293}$DKLpSVIAEDSESGKQ$_{307}$	−	+	N (0.498)
		$_{293}$DKLpSVIAEDSESGKQN$_{308}$	−	+	
		$_{293}$DKLpSVIAEDSESGKQNP$_{309}$	−	+	
		$_{293}$DKLpSVIAEDSESGKQNPG$_{310}$	−	++	
		$_{293}$DKLpSVIAEDSESGKQNPGDS$_{312}$	−	+	
		$_{294}$KLpSVIAEDSESGKQN$_{308}$	−	+	
		$_{294}$KLpSVIAEDSESGKQNP$_{309}$	−	++	
		$_{294}$KLpSVIAEDSESGKQNPG$_{310}$	−	+	
NADH-ubiquinone oxidoreductase flavoprotein 3	MTM	$_{88}$NLELSKFRMPQPSSGREpSPRH$_{108}$	−	+§	N (0.997)
		$_{91}$LSKFRMPQPSSGREpSPRH$_{108}$	−	+§	
Protein FAM40A	N	$_{318}$PPLPEDSIKVIRNMRAApSPPA$_{338}$	−	++§	Y (0.981)
Ras association domain-containing protein 6	C	$_{184/152/140}$RTMpSEAALVRK$_{194/162/150}$	−	++	N (0.614)
SH2 domain containing 3C isoform 1	C¶/M¶	$_{80}$MPRPpSIKKAQNSQAARQ$_{96}$	−	+§	N (0.997)
Tax1-binding protein 1, isoform 1 or 2	C	$_{106}$THKGEIRGASTPFQFRA*pSpS*P$_{125}$	−	+	N (0.955/0.996)
		$_{107}$HKGEIRGASTPFQFRA*pSpS*P$_{125}$	−	++	
UPF0492 protein C20orf94	UK	$_{391}$STIQNpSPTKK$_{400}$	−	+	N (0.953)

−, not detected; +, <6 copies per cell; ++, 6–50 copies per cell; +++, 51–140 copies per cell.

*In the localization column: C, cytoplasm; E, endosome; ER, endoplasmic reticulum; ERM, endoplasmic reticulum membrane; G, Golgi; GM, Golgi membrane; M, membrane; MTM, mitochondrial membrane; N, nucleus; PM, plasma membrane; and UK, unknown.

†pS, pT, and pY correspond to serine, threonine, or tyrosine-associated phosphorylated residues, respectively. Italics indicate the exact site of phosphorylation could not be determined.

‡Phosphosites searched in the Phospho-ELM database [Diella F, Gould CM, Chica C, Via A, Gibson TJ (2008) *Nucleic Acids Res* 36:D240–D244]. Values in parentheses show the score from the NetPhos 2.0 Server [Viner NJ, Nelson CA, Deck B, Unanue ER (1996) *J Immunol* 156:2365–2368] indicating the probability for the site to be phosphorylated, scale 0–1.0. Higher scores indicate greater confidence in the prediction, with the designated binding threshold at 0.500. In cases of undefined phosphorylation sites (italicized), both scores are given.

§Peptides containing Met^{ox}.

¶Hypothetical localization.

Table S2. Characteristics of HLA-DR-associated phosphopeptides commonly expressed by melanoma and EBV-B cells

Source protein	Location*	Phosphopeptide†	1363-mel	1363-EBV	2048-mel	2048-EBV	Known phosphosite (score)‡
Elongin A	N§	$_{122}$RSYpSPDHRQK$_{131}$	−	−	++	nm	Y (0.974)
Ferritin heavy chain	C	$_{171}$FDKHTLGDpSDNES$_{183}$	++	−	++	nm	Y (0.603)
Frizzled-6	PM	$_{617}$EPA*pS*PAA*pS*ISRLSGEQVDGKG$_{637}$	−	−	−	+	N (0.240/0.951)
		$_{620}$SPAASISRLpSGEQVDGKG$_{637}$	+	−	−	−	N (0.996)
		$_{623}$ASISRLpSGEQVDGKG$_{637}$	++	−	−	−	
		$_{623}$ApSISRLpSGEQVDGKG$_{637}$	++	−	−	−	N (0.951 and 0.996)
		$_{623}$ApSISRLSGEQVDGKG$_{637}$	++	−	+	−	N (0.951)
		$_{623}$A*pS*I*pS*RLSGEQVDGKGQ$_{638}$	−	−	+	−	N (0.951/0.141)
Insulin like growth factor 2 receptor	LM	$_{2392}$TTKpSVKALSSLHG$_{2404}$	−	−	+	−	N (0.673)
		$_{2392}$TTKpSVKALSSLHGDD$_{2406}$	−	−	++	−	
		$_{2392}$TTKpSVKALSSLHGDDQ$_{2407}$	−	−	++	−	
		$_{2392}$TTKpSVKALSSLHGDDQD$_{2408}$	−	−	++	nm	
		$_{2392}$TTKpSVKALSSLHGDDQDS$_{2409}$	−	−	+	++	
		$_{2393}$TKpSVKALSSLHGDD$_{2406}$	−	−	+	−	
		$_{2393}$TKpSVKALSSLHGDDQ$_{2407}$	−	−	+	nm	
		$_{2393}$TKpSVKALSSLHGDDQD$_{2408}$	−	−	+	nm	
		$_{2394}$KpSVKALSSLHGDDQ$_{2407}$	−	−	+	−	
		$_{2394}$KpSVKALSSLHGDDQD$_{2408}$	−	−	+	nm	
		$_{2392}$TTKSVKALSSLHGDDQDpSED$_{2411}$	−	−	−	+++	Y (0.977)
		$_{2392}$TTKSVKALSSLHGDDQDpSEDE$_{2412}$	−	−	−	nm	
		$_{2394}$KSVKALSSLHGDDQDpSEDE$_{2412}$	−	−	−	nm	
		$_{2476}$KLVSFHDDpSDEDL$_{2488}$	−	−	−	nm	N (0.996)
Lipolysis-stimulated lipoprotein receptor	PM	$_{324/287/305}$APSTYAHLpSPAK$_{335/398/316}$	+	−	−	−	N (0.958)
		$_{324/287/305}$APSTYAHLpSPAKTPPPP$_{340/303/321}$	+	++	−	−	
Plakophilin-4	PM	$_{206}$NRAMRRVpSSVPSR$_{218}$	−	−	+	−	N (0.996)
		$_{206}$NRAMRRVpSSVPSRAQ$_{220}$	−	−	+	−	
		$_{278}$RPA*pS*P*pT*AIRRIGSVTSRQT$_{296}$	−	−	−	+	Y (0.997)/ N (0.043)
Sequestosome-1	N/C/E	$_{332}$pSGGDDDWTHLSSKEVDPST$_{350}$	−	+	−	−	Y (0.991)
		$_{332}$pSGGDDDWTHLSSKEVDPSTG$_{351}$	−	++	−	−	
		$_{332}$pSGGDDDWTHLSSKEVDPSTGE$_{352}$	−	+	−	−	
		$_{332}$pSGGDDDWTHLSSKEVDPSTGEL$_{353}$	−	+	−	−	
		$_{332}$pSGGDDDWTHLSSKEVDPSTGELQ$_{354}$	−	+	−	−	
		$_{333}$GGDDDWTHLpSSKEVDPS$_{349}$	++	−	+	−	N (0.954)
		$_{333}$GGDDDWTHLpSSKEVDPSTG$_{351}$	−	−	+	−	
		$_{334}$GDDDWTHLpSSKEVD$_{347}$	−	−	+	−	
		$_{334}$GDDDWTHLpSSKEVDP$_{348}$	−	−	++	−	
		$_{334}$GDDDWTHLpSSKEVDPS$_{349}$	+++	−	++	−	
		$_{334}$GDDDWTHLpSSKEVDPST$_{350}$	−	−	+	−	
		$_{334}$GDDDWTHLpSSKEVDPSTG$_{351}$	+++	+	+	−	
		$_{335}$DDDWTHLpSSKEVDPS$_{349}$	++	+	−	−	
		$_{335}$DDDWTHLpSSKEVDPSTG$_{351}$	−	+	−	−	
		$_{336}$DDWTHLpSSKEVDPS$_{349}$	++	−	−	−	
		$_{337}$DWTHLpSSKEVDPS$_{349}$	++	−	−	−	
		$_{337}$DWTHLpSSKEVDPSTG$_{351}$	++	−	−	−	
		$_{338}$WTHLpSSKEVDPS$_{349}$	+++	−	−	−	
		$_{338}$WTHLpSSKEVDPSTG$_{351}$	++	nm	−	−	
Sorting nexin-17	C/E	$_{402}$GpTLRRSDSQQAVK$_{414}$	−	−	+	+	N (0.899)
		$_{402}$GpTLRRSDSQQAVKS$_{415}$	−	−	+	−	
		$_{402}$GpTLRRSDSQQAVKSPP$_{417}$	−	−	+	−	
UPF0555 protein KIAA0776	UK	$_{783}$VLKSRK*pS*p*S*VTEE$_{794}$	−	−	+	++	N (0.990)/Y (0.997)

−, not detected; +, <6 copies per cell; ++, 6–50 copies per cell; +++, 51–140 copies per cell; and nm, not measured.

*In the localization column: C, cytoplasm; E, endosome; LM, lysosome membrane; N, nucleus; NM, nuclear membrane; PM, plasma membrane; and UK, unknown.

†pS, pT, and pY correspond to serine, threonine, or tyrosine-associated phosphorylated residues, respectively. Italics indicate the exact site of phosphorylation could not be determined.

‡Phosphosites searched in the Phospho-ELM database [Diella F, Gould CM, Chica C, Via A, Gibson TJ (2008) *Nucleic Acids Res* 36:D240–D244]. Values in parentheses show the score from the NetPhos 2.0 Server [Viner NJ, Nelson CA, Deck B, Unanue ER (1996) *J Immunol* 156:2365–2368] indicating the probability for the site to be phosphorylated, scale 0–1.0. Higher scores indicate greater confidence in the prediction, with the designated binding threshold at 0.500. In cases of undefined phosphorylation sites (italicized), both scores are given.

§Hypothetical localization.

Table S3. Characteristics of source proteins generating HLA-DR-restricted phosphopeptides

Source protein	Accession number	Known phosphoprotein?	Function	Other names
ADAM 8	P78325	N	Cellular trafficking	A disintegrin and metalloproteinase domain 8, Cell surface antigen MS2, CD156a
Amino-terminal enhancer of split	Q08117	N	Transcriptional regulation	GRG protein, Protein ESP1, Gp130-associated protein GAM
Ankyrin repeat domain-containing protein 54	Q6NXT1	Y	Unknown	NA
Anoctamin-8	Q9HCE9	N	Ion transport	Transmembrane protein 16H
AP-3 complex subunit-Δ-1	O14617	Y	Trafficking	Adapter-related protein complex 3 subunit-Δ-1, AP-3 complex subunit-Δ, Δ-adaptin
BCL2-associated transcription factor 1	A2RU75	N	Transcription factor	NA
B lymphocyte antigen CD19	P15391	Y	Receptor/signal transduction	Differentiation antigen CD19, B lymphocyte surface antigen B4, Leu-12
B lymphocyte antigen CD20	P11836	Y	Receptor/signal transduction	Membrane-spanning 4-domains subfamily A member 1, B lymphocyte surface antigen B1, Leu-16, Bp35
Casein kinase II subunit-β	P67870	Y	Signal transduction	Phosvitin, G5a
Caspase recruitment domain-containing protein 11	Q9BXL7	N	Signal transduction	CARD-containing MAGUK protein 3, Carma 1
Chromatin-modifying protein 1a	Q9HD42	N	Cell cycle/protein trafficking	Chromatin-modifying protein 1a, Vacuolar protein sorting-associated protein 46-1
Claudin-11	O75508	N	Cell adhesion	Oligodendrocyte-specific protein
Elongin A	Q14241	Y	Transcriptional regulation	Transcription elongation factor B polypeptide 3, RNA polymerase II transcription factor SIII subunit A1, SIII p110, Elongin 110-kDa subunit
Emerin	P50402	Y	Protein binding	NA
Ferritin heavy chain	P02794	Y	Ion storage	Cell proliferation-inducing gene 15 protein
FLJ20689	Q9H3M3	N	Unknown	NA
Frizzled-6	O60353	Y	Receptor/Signal transduction	NA
Germinal center B-cell-expressed transcript 2 protein	Q8N6F7	Y	Signal transduction*	Germinal center-associated lymphoma protein
Insulin-like growth factor 2 receptor	P11717	Y	Metabolism	Cation-independent mannose-6-phosphate receptor, M6P/IGF2 receptor, 300 kDa mannose 6-phosphate receptor, CD222
Insulin receptor substrate 2	Q9Y4H2	Y	Receptor/signal transduction	NA
Interleukin 1 receptor accessory protein	Q9NPH3	N	Receptor/signal transduction	NA
Interleukin-2 receptor subunit-β	P14784	Y	Receptor/signal transduction	High-affinity IL-2 receptor subunit-β, P70-75, CD122
Interleukin-10 receptor-β chain	Q08334	N	Receptor/signal transduction	IL-10R2, Cytokine receptor family 2 member 4, CDw210b
Lipolysis-stimulated lipoprotein receptor	Q86X29	Y	Receptor/metabolism	NA
LUC7-like isoform b	Q53G47	Y	Unknown	NA
Lymphoid-restricted membrane protein	Q12912	N	Metabolism	Protein Jaw1
Matrix-remodeling-associated protein 7	P84157	N	Unknown	Transmembrane anchor protein 1
Melanoma antigen recognized by T cells 1	Q16655	N	Unknown	MART-1, Melan-A, Antigen SK29-AA, Antigen LB39-AA

Source protein	Accession number	Known phosphoprotein?	Function	Other names
Membrane-associated progesterone receptor component 1	O00264	Y	Receptor	NA
NADH-ubiquinone oxidoreductase flavoprotein 3	P56181	N	Metabolism	NADH-ubiquinone oxidoreductase 9-kDa subunit, Complex I-9kD, Renal carcinoma antigen NY-REN-4
NF-κB inhibitor-interacting Ras-like protein 2	Q9NYR9	N	Signal regulation	IκB-interacting Ras-like protein 2
Optineurin	Q96CV9	Y	Signal transduction/protein trafficking	Optic neuropathy-inducing protein, E3-14.7K-interacting protein, FIP-2, Huntingtin-interacting protein L, Huntingtin yeast partner L, NEMO-related protein, Transcription factor IIIA-interacting protein
Phosphoglycerate kinase 1	P00558	Y	Metabolism	Primer recognition protein 2, Cell migration-inducing gene 10 protein
Plakophilin-4	Q99569	Y	Cell adhesion	p0071
Probable fibrosin-1 long-transcript protein isoform 2	Q9HAH7	Y	Unknown	NA
Protein FAM40A	Q5VSL9	Y	Unknown	NA
Ras association domain-containing protein 6	Q6ZTQ3	N	Signal transduction	NA
Sequestosome-1	Q13501	Y	Signal transduction	Phosphotyrosine-independent ligand for the Lck SH2 domain of 62 kDa, Ubiquitin-binding protein p62, EBI3-associated protein of 60 kDa
SH2 domain containing 3C isoform 1	Q8N5H7	Y	Signal transduction	Novel SH2-containing protein 3
Small acidic protein	O00193	Y	Unknown	NA
Solute carrier family 12, member 6, isoform a	Q9UHW9	Y	Ion transport	Electroneutral potassium chloride cotransporter 3, K-Cl cotransporter 3
Sorting nexin-17	Q15036	Y	Trafficking*	NA
Synaptojanin-170	O43426	Y	Metabolism	Synaptic inositol-1,4,5-trisphosphate 5-phosphatase 1
Tax1-binding protein 1, isoform 1 or 2	Q86VP1	N	Signal transduction	TRAF6-binding protein
Tensin-3	Q68CZ2	Y	Cellular structure	Tumor endothelial marker 6, Tensin-like SH2 domain-containing protein 1
Tetraspanin-10	Q9H1Z9	N	Unknown	Oculospanin
TNFAIP3 interacting protein 1	Q15025	Y	Signal regulation	Nef-associated factor 1, HIV-1 Nef-interacting protein, Virion-associated nuclear shuttling protein, Nip40-1
Transmembrane protein 184C	Q9NVA4	N	Unknown	Transmembrane protein 34
Tumor necrosis factor receptor superfamily member 8	P28908	N	Receptor/signal transduction	CD30L receptor, Lymphocyte activation antigen CD30, KI-1 antigen, CD30
UPF0492 protein C20orf94	Q5VYV7	N	Unknown	NA
UPF0501 protein KIAA1430	Q9P2B7	Y	Unknown	NA
UPF0555 protein KIAA0776	O94874	Y	Unknown	NA
Xenotropic and polytropic retrovirus receptor 1	Q9UBH6	Y	Receptor/signal transduction	Protein SYG1 homolog, Xenotropic and polytropic murine leukemia virus receptor X3

NA, not applicable.
*Hypothetical function.