Supplementary Materials for

Proteomic Analysis of Integrin-Associated Complexes Identifies RCC2 as a Dual Regulator of Rac1 and Arf6

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Supplementary Material

Methods
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Methods

Western blotting

Following SDS-PAGE, resolved proteins were transferred to nitrocellulose membrane (Whatman, Maidstone, UK). Membranes were blocked with casein blocking buffer (Sigma-Aldrich, Poole, UK) and probed with primary antibodies diluted in blocking buffer containing 0.05% (v/v) Tween 20. Membranes were washed with Tris-buffered saline (10 mM Tris-HCl, pH 7.4, 150 mM NaCl) containing 0.05% (v/v) Tween 20 and incubated with species-specific fluorescent dye–conjugated secondary antibodies diluted in blocking buffer containing 0.05% (v/v) Tween 20. Membranes were washed in the dark, then scanned using the Odyssey infrared (IR) imaging system (LI-COR Biosciences, Cambridge, UK) to visualize bound antibodies. For quantification of relative band densities, the Odyssey software (version 1.1; LI-COR Biosciences) was used to calculate net pixel volume (the background-corrected sum of the pixel intensity values multiplied by the area of the feature).

Coomassie staining

Following SDS-PAGE, total protein was visualized by incubating gels in Coomassie staining solution [0.025% (w/v) Coomassie Brilliant Blue R-250, 10% (v/v) acetic acid, 25% (v/v) propanol] for 1 hour at room temperature. Gels were then destained in 10% (v/v) acetic acid, washed with distilled H_2O, and scanned using the Odyssey IR imaging system.

In-gel proteolytic digestion

In-gel digestion with trypsin was carried out as described by Shevchenko et al. (*1*) and adapted to enable high-throughput processing in 96-well plates. Following Coomassie staining, gels were washed with distilled H_2O, and lanes were sliced into 30 slices and chopped into ~1-mm^3 pieces. Gel pieces from each slice were transferred to separate wells of a perforated V-bottomed 96-well plate (Proxeon, Odense, Denmark) and shrunk by dehydration in acetonitrile

(ACN) for 5 min. ACN was removed by centrifugation (289 × *g*, 1 min), and gel pieces were dried in a vacuum centrifuge and then rehydrated in reduction buffer (10 mM dithiothreitol, 25 mM NH_4HCO_3) for 1 hour at 56°C. Supernatant was removed by centrifugation, and gel pieces were incubated with alkylation buffer (55 mM iodoacetamide, 25 mM NH_4HCO_3) for 45 min at room temperature in the dark. Gel pieces were washed with 25 mM NH_4HCO_3 for 10 min. Gel pieces were then shrunk in ACN (5 min), washed with 25 mM NH_4HCO_3 (5 min), and shrunk again in ACN (5 min). Gel pieces were dried in a vacuum centrifuge before rehydration with digestion buffer (25 mM NH_4HCO_3) containing 12.5 ng/µl sequencing-grade modified trypsin (Promega, Southampton, UK) for 45 min at 4°C. Samples were then incubated for 16 hours at 37°C.

Peptides were collected from the digestion buffer by centrifugation into a V-bottomed 96-well storage plate (Thermo Fisher Scientific, Waltham, MA, USA). Remaining peptides were extracted from the gel matrix with 20 mM NH_4HCO_3 (20 min) and collected by centrifugation. Peptide extraction was repeated a further two times with 5% (v/v) formic acid in 50% (v/v) ACN. Pooled extracts were concentrated to 20 µl and ACN was removed by vacuum centrifugation. Samples were stored at −20°C until analysis by liquid chromatography–tandem mass spectrometry (LC-MS/MS).

LC-MS/MS analysis

LC-MS/MS analysis was performed using a nanoACQUITY UltraPerformance LC system (Waters, Elstree, UK) coupled online to a 4000 Q TRAP triple-quadrupole linear ion trap analyzer (Applied Biosystems, Framingham, MA, USA). Samples (5 µl) were concentrated and desalted on a Symmetry C_{18} preparative column (20 mm length, 180 µm inner diameter, 5 µm particle size, 100 Å pore size; Waters). Peptides were separated on an ACQUITY UltraPerformance LC bridged ethyl hybrid C_{18} analytical column (100 mm length, 75 µm inner diameter, 1.7 µm particle size, 130 Å pore size; Waters) using a 40-min linear gradient from 1% to 30% (v/v) ACN in 0.1% (v/v) formic acid at a flow rate of 300 nl/min at 50°C.

The mass spectrometer was instructed to acquire enhanced-resolution and product ion scans for peptides with ion counts greater than 250,000 counts per second, with a precursor ion mass-to-charge ratio (*m*/*z*) selection window of *m*/*z* 400–1600. Information-dependent acquisition (Analyst, version 1.4.1; Applied Biosystems) was used to acquire tandem mass spectra over the range *m*/*z* 140–1400 for the two most intense peaks, which were excluded for 12 seconds after two occurrences. Spectra were extracted, charge-state deconvoluted, and deisotoped using the Mascot Search script (mascot.dll, version 1.6b9; Matrix Science, London, UK) as a plug-in for Analyst.

Peak list files were searched against a modified version of the IPI Human database (version 3.34, release date 2nd October 2007, containing 67,756 sequences) containing ten additional contaminant and reagent sequences of non-human origin. Searches were submitted to an in-house Mascot server (version 2.2.03; Matrix Science) (*2*). Carbamidomethylation of cysteine was set as a fixed modification and oxidation of methionine was allowed as a variable modification. Only tryptic peptides were considered, with up to one missed cleavage permitted. Monoisotopic precursor mass values were used, and only doubly and triply charged precursor ions were considered. Mass tolerances for precursor and fragment ions were 1.5 D and 0.5 D, respectively.

To validate the proteomic datasets generated by MS, multiple database search engines and rigorous statistical algorithms at both the peptide and protein level were employed (*3*, *4*). To achieve this, data validation was performed using Scaffold (version Scaffold_2_00_05; Proteome Software, Portland, OR, USA), which models the score distributions of the entire dataset of spectra. Database search files generated by Mascot were imported into Scaffold and further analyzed using the search engine X! Tandem (version 2007.01.01.1) (*5*) implemented from within Scaffold. X! Tandem searches were conducted against the same protein sequence database and using the same search parameters as the associated Mascot search, except that X! Tandem allowed *S*-carbamoyl-methylcysteine cyclization (pyro-carbamidomethylation of cysteine) at N-termini as a variable modification by default.

Peptide identifications were accepted if they could be established with at least 90% probability as determined by the PeptideProphet algorithm (*3*). PeptideProphet uses curve fitting to model all peptide matches in a dataset as a two-component mixture of distributions representing correct and incorrect identifications and applies Bayesian statistics to compute the probability that a peptide match is correct. Protein identifications were accepted if they were assigned at least two unique, validated peptides and could be established with at least 99% probability as determined by the ProteinProphet algorithm (*4*).

Data deposition

Mass spectrometric data were converted using PRIDE Converter (version 2.0.1) (*6*) and deposited in the PRIDE database (http://www.ebi.ac.uk/pride) (*7*) under accession numbers 9985–9992.

Quantification using spectral counting

Label-free quantification of relative protein abundance was performed using spectral counting (*8–12*). Relative protein abundance was calculated on the basis of the unweighted spectral count assigned to each identified protein by Scaffold. The unweighted spectral count includes spectra matched to peptides shared between multiple proteins if there is independent evidence that these proteins are present. To normalize the data, spectral counts were expressed as a percentage of the total number of spectra observed in the entire sample. Mean normalized spectral counts were calculated using data from three independent FN and VCAM-1 affinity isolations and two independent VCAM-1(D40A) control isolations.

Hierarchical clustering analysis

Agglomerative hierarchical clustering was performed using Cluster 3.0 (C Clustering Library, version 1.37) (*13*). Quantitative data (mean normalized spectral counts) were used for hierarchical clustering. Protein hits were hierarchically clustered on the basis of uncentered Pearson correlation, and

distances between hits were computed using a complete-linkage matrix. Clustering results were visualized using Java TreeView (version 1.1.1) (*14*) and MultiExperiment Viewer (version 4.1.01) (*15*).

Interaction network analysis

The open-source platform Cytoscape (version 2.6.0) (*16*) was used to visualize protein–protein interaction networks. Proteins specifically enriched in FN and VCAM-1 affinity purifications (enriched at least two-fold over the control on the basis of mean normalized spectral count) were mapped onto a human interactome constructed from a union of human protein interaction datasets, which combines literature-curated interactions reported in the IntAct, DIP, BIND, and HPRD databases, two published interactomes (*17*, *18*), and a further integrated dataset (*19*) (release date 15th May 2007; available at http://cytoscape.org/cgi-bin/moin.cgi/Data_Sets/; provided by A. G. Garrow, Unilever, Sharnbrook, UK), and a literature-curated interactome of integrin adhesion complexes (*20*). It was possible to map 386 of the 406 proteins specifically enriched to FN and 181 of the 185 proteins specifically enriched to VCAM-1 onto this interactome. Paxillin, which was not identified by MS analysis, but which was specifically enriched in FN and VCAM-1 affinity purifications over control as determined by Western blotting, was imputed to the mapped datasets. Removal of paxillin from our interactome models did not affect overall network architecture. Mean normalized spectral counts of proteins specifically enriched in FN and VCAM-1 affinity purifications were further normalized to the mean normalized spectral count of β_1 integrin in each dataset. These β_1 integrin–normalized data were used to calculate the ratio of enrichment to FN-induced complexes over VCAM-1–induced complexes for each protein. The $\log_2$-transformed enrichment data were mapped as an attribute onto each protein (node) of our networks and represented visually by node color. Model layouts were constructed using the attribute circle layout implemented in Cytoscape.

The overall human interactome network, $G = (N, E)$, consists of a set of nodes N ($|N| = 10{,}204$) and a set of known interactions (edges) E ($|E| = 58{,}723$),

excluding self-interactions. The subnetwork induced by a set of proteins, $N' \subset N$, is defined as $G' = (N', E')$, where E' is the set of all edges in E that join two nodes in N'. The clustering coefficient $c(n)$ of each node n was calculated according to the definition of Watts and Strogatz (*21*), and the overall clustering coefficient for each network was defined as the mean of $c(n)$ over all nodes having degree $k(n) \geq 2$. For each set of experimentally identified proteins N', 10,000 random samples N'_{rand} of size $|N'|$ nodes were taken from N, chosen such that the distribution of degrees within the full network G was the same for each N'_{rand} as that for N'. For each random sample, the induced subnetwork G'_{rand} was examined and its number of edges and clustering coefficient calculated. P values for these properties were calculated as the proportions of random samples having values greater than or equal to the experimentally determined protein sets.

Interaction network analysis revealed that proteins recruited to both $\alpha_5\beta_1$–FN and $\alpha_4\beta_1$–VCAM-1 complexes were linked into expansive networks through multiple connectors, which were distinctly non-random, with significantly higher numbers of interactions and clustering coefficients than those observed for control simulations (table S3).

GTPase activity assays

Nine-centimeter tissue culture–treated plastic dishes (Corning BV Life Sciences, Haarlemmermeer, The Netherlands) were coated with 10 μg/ml bovine FN (Sigma-Aldrich) in phosphate-buffered saline (PBS) containing 1 mM calcium and 0.5 mM magnesium (Lonza Bioscience, Wokingham, UK) for 2 hours at room temperature and blocked with 10 mg/ml filtered, heat-denatured bovine serum albumin (BSA) for 30 min at room temperature. Cells were detached with 0.5 mg/ml trypsin and maintained in suspension in DMEM for 30 min before plating (1×10^6 cells per dish) or harvesting from suspension by centrifugation. Active Rac1 was affinity purified from lysates prepared in buffer A [20 mM HEPES, pH 7.4, 10% (v/v) glycerol, 140 mM NaCl, 1% (v/v) NP-40, 0.5% (w/v) sodium deoxycholate, 4 mM EGTA, 4 mM EDTA, 50 μg/ml leupeptin, 50 μg/ml

aprotinin, 1 mM AEBSF] using 300 µg GST-PAK CRIB domain immobilized on agarose beads. Beads were incubated with the lysates for 1 hour and then washed 3 times with buffer A. Active Arf6 was affinity purified from lysates prepared in buffer B [50 mM Tris, pH 7.5, 10% (v/v) glycerol, 100 mM NaCl, 2 mM $MgCl_2$, 50 µg/ml leupeptin, 50 µg/ml aprotinin, 1 mM AEBSF] supplemented with 1% (v/v) Triton X-100, 0.5% (w/v) sodium deoxycholate, and 0.1% (w/v) SDS using 300 µg GST-GGA3 (VHS-GAT domain) immobilized on agarose beads. Beads were incubated with the lysates for 1 hour and then washed 3 times with buffer B supplemented with 1% (v/v) NP-40. Active GTPase was eluted in reducing sample buffer, resolved by SDS-PAGE, and analyzed by Western blotting. For all experiments, equivalent loading between time points was confirmed by blotting the crude lysate for mitochondrial Hsp70 and Rac1 or Arf6. The significance of changes in abundance was established using a paired Student's *t*-test of normally distributed small samples (n = 4–8).

Adhesion formation assay

Glass coverslips (13-mm diameter) were coated with 10 µg/ml bovine FN in PBS containing 1 mM calcium and 0.5 mM magnesium overnight at 4°C and blocked with 10 mg/ml filtered, heat-denatured BSA for 30 min at room temperature. MEF cells transfected with control siRNA or siRNA directed against RCC2 were detached with 0.5 mg/ml trypsin and maintained in suspension in DMEM for 20 min before plating (1.25×10^4 cells per coverslip). Cells were allowed to spread at 37°C in a humidified 8% (v/v) CO_2 atmosphere. Cells were fixed at appropriate time points with 4% (w/v) paraformaldehyde, permeabilized with 0.5% (w/v) Triton X-100 in PBS, and blocked with 3% (w/v) BSA in PBS. Fixed cells were stained for vinculin with hVIN-1 monoclonal IgG and a Cy2-conjugated secondary IgG (Stratech Scientific, Newmarket, UK). Coverslips were mounted in ProLong antifade reagent (Invitrogen, Paisley, UK) and photographed on a Deltavision RT microscope (Applied Precision, Issaquah, WA, USA) using a 60×/NA 1.42 Plan Apo objective and CH350 camera (Photometrics, Tucson, AZ, USA). Images were compiled and analyzed using ImageJ (version 1.410;

National Institutes of Health, Bethesda, MD, USA). The total area of adhesion complexes per cell was calculated by automatically recording the area of fluorescence intensity above an empirically determined threshold after rolling-ball background subtraction. The same threshold was used for all conditions within a single experiment. For each time point, adhesion area was compared between control and knockdown cells using a Student's *t*-test.

Cell spreading assay

Ninety-six–well plates (Corning BV Life Sciences) were coated with protein ligands diluted in PBS for 60–90 min at room temperature and blocked with 10 mg/ml filtered, heat-denatured BSA for 30–60 min at room temperature. Cells were detached with 0.5 mg/ml trypsin and resuspended to 1×10^5 cells/ml in DMEM containing 25 mM HEPES, 4.5 mg/ml glucose, and L-glutamine. Plates were incubated at 37°C in a humidified 5% (v/v) CO_2 atmosphere for various times, ranging from 10 min to 90 min, as indicated. Cells were fixed with 5% (w/v) glutaraldehyde for 30 min, and wells were washed with PBS. The degree of cell spreading was assessed as a percentage of the total number of cells counted, using phase-contrast microscopy. At least 100 cells in four to six randomly chosen high-powered fields were counted per treatment point. Data were plotted using SigmaPlot (version 8.0; Systat Software, London, UK) using the sigmoidal non-linear regression algorithm to calculate estimates of half-maximal spreading.

Generation of cell-derived matrix

Twenty-four–well plates (Corning BV Life Sciences) were seeded with telomerase-immortalized human fibroblasts at 5×10^4 cells/ml and cultured for 11 days, changing the growth medium every other day for fresh medium supplemented with 50 µg/ml ascorbic acid to stabilize matrix fibrils. Mature matrix was denuded of fibroblasts by lysis with 20 mM NH_4OH and 0.5% (v/v) Triton X-100 in PBS, followed by digestion with 10 µg/ml DNase I (Roche

Diagnostics, Burgess Hill, UK) in PBS containing 1 mM calcium and 0.5 mM magnesium.

Cell migration assays

MEF cells were seeded at 8×10^3 cells/ml and allowed to spread for 3 hours on cell-derived matrix in 24-well plates at 37°C in a humidified 5% (v/v) CO_2 atmosphere. Cells were also seeded on FN-coated wells to measure random migration. To monitor cell movements, images were acquired on an AS MDW live cell imaging system (Leica Microsystems GmbH, Wetzlar, Germany) using a 5×/NA 0.15 Plan Fluotar objective and a Coolsnap HQ camera (Photometrics) at 10-min intervals for 12 hours. Cells were maintained at 37°C in a humidified 5% (v/v) CO_2 atmosphere, and point visiting was used to allow multiple positions to be imaged within the same time course. Images were converted to stacks using ImageJ, and migration paths of non-dividing, non-clustered cells were manually tracked and analyzed using MTrackJ (version 1.3.0; E. Meijering, Erasmus MC – University Medical Center Rotterdam, Rotterdam, The Netherlands) and Chemotaxis and Migration Tool (version 1.01; G. Trapp, ibidi GmbH, Martinsried, Germany) plug-ins to ImageJ. Directionality (persistence) was determined by dividing the linear displacement (Euclidean distance) of a cell after 12 hours by the total distance moved (accumulated distance). Migration paths of 10 cells in three randomly chosen fields were tracked in triplicate wells for each cell type (n = 90). The significance of changes in accumulated distance and persistence was determined using a Z-test to account for large sample size.

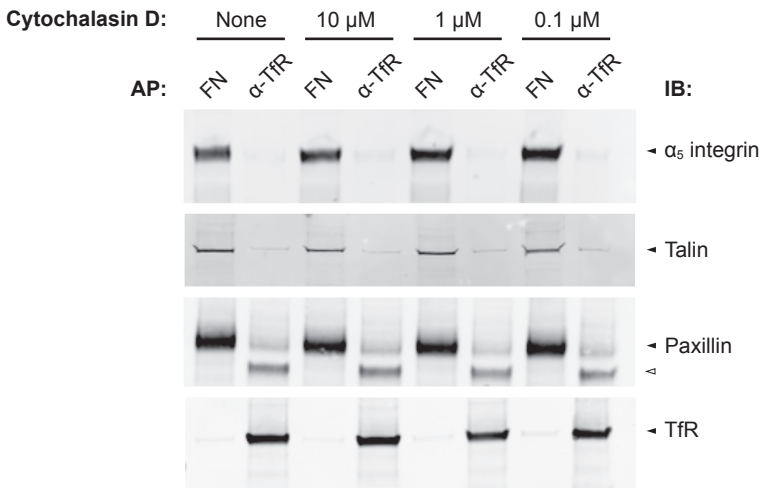

Fig. S1. Disruption of the actin cytoskeleton does not affect recruitment of talin and paxillin to isolated $\alpha_5\beta_1$–FN complexes. $\alpha_5\beta_1$–FN complexes were affinity isolated in the presence of the cell membrane–permeable crosslinker DTBP and a range of concentrations of the actin-disrupting agent cytochalasin D, as indicated. Samples were analysed by Western blotting. Bead-coated proteins used for each affinity purification (AP) and proteins probed for by immunoblotting (IB) are indicated. Mouse IgG fragments are indicated by a white arrowhead.

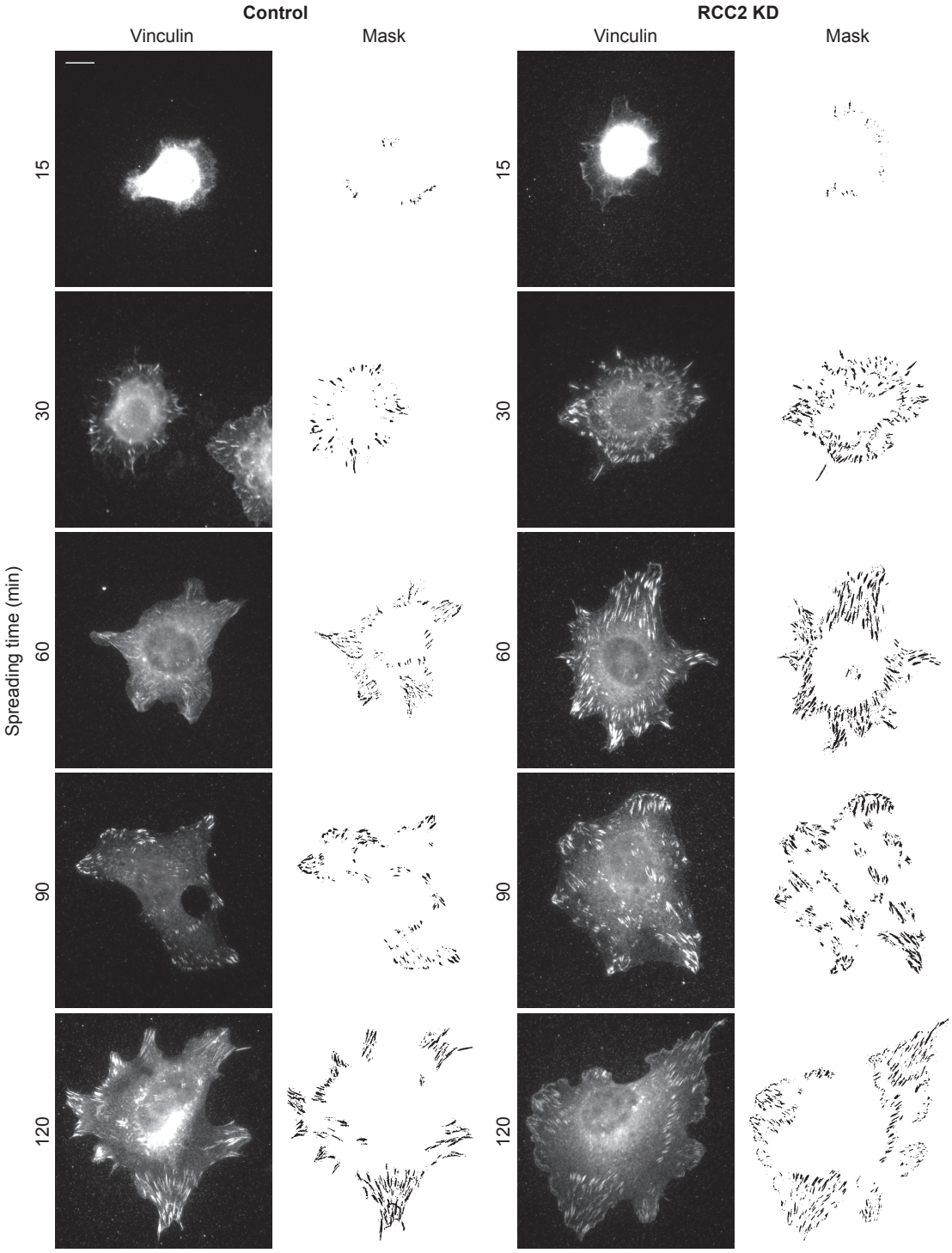

Fig. S2. Knockdown of RCC2 accelerates adhesion formation. MEF cells transfected with control or RCC2 antisense oligonucleotides were plated onto FN and allowed to spread for 15–120 min, as indicated, before fixing and staining for vinculin. Masks were generated by thresholding the pixel intensity of background-subtracted images and used to measure adhesion area. Masks are representative of two separate experiments (n = 45). 60-min spreading images are reproduced in Fig. 5B. Bar = 10 μm.

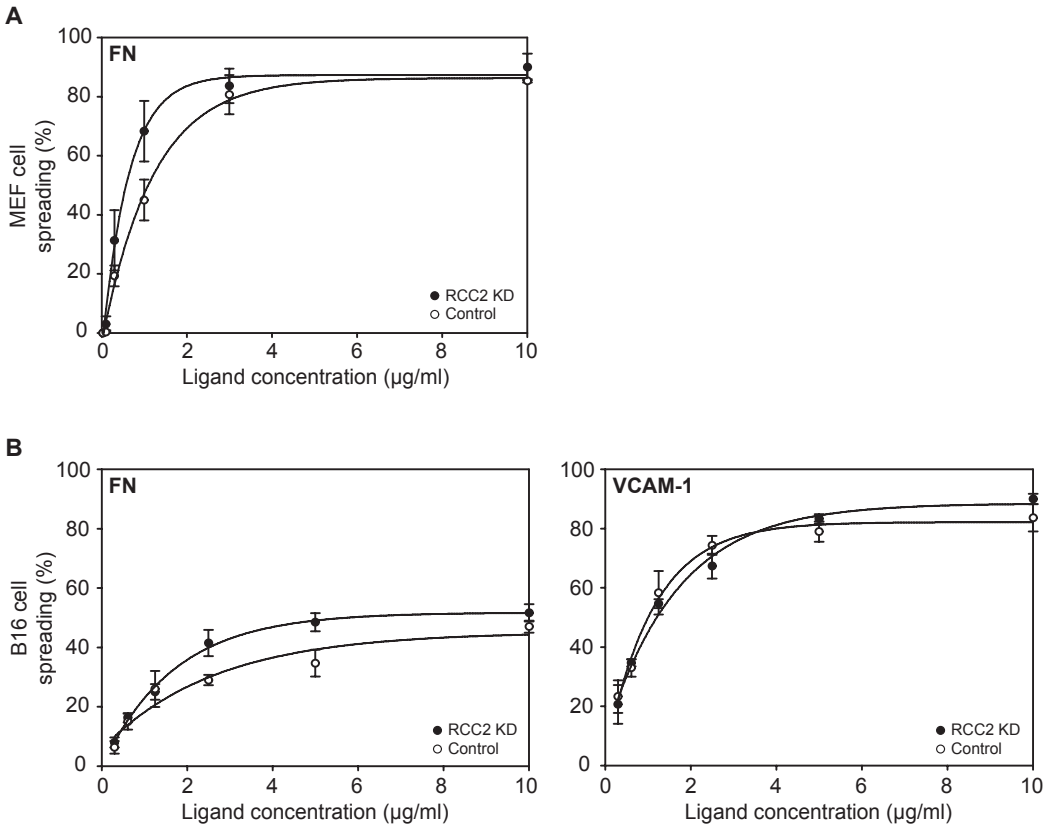

Fig. S3. Knockdown of RCC2 augments FN-mediated cell spreading. (**A** and **B**) The percentage of MEF cells on FN (A) or B16-F10 cells on FN or VCAM-1 (B) counted as spread was plotted as a function of ligand concentration. MEF cells were allowed to spread for 60 min; B16-F10 cells were allowed to spread for 90 min.

Table S1. Hierarchical clustering analysis of proteins identified in FN, VCAM-1, and VCAM-1(D40A) affinity purifications (full datasets).

Hierarchical clustering	Selected cluster (Fig. 2)	Gene symbol	Protein name	Mean normalized spectral count (% of total spectra) x10^{3}			Specific enrichment?*	
				FN	VCAM-1	VCAM-1(D40A)	FN	VCAM-1
	B	SEC31A	Isoform 1 of Protein transport protein Sec31A	0	1.41	0	–	Yes
	B	SNAP29	Synaptosomal-associated protein 29	0	1.41	0	–	Yes
	B	TRAPPC3	Uncharacterized protein TRAPPC3	0	1.41	0	–	Yes
	B	PSME3	Isoform 1 of Proteasome activator complex subunit 3	0	1.41	0	–	Yes
	B	LYPLA2	Acyl-protein thioesterase 2	0	1.41	0	–	Yes
	B	MSI2	Isoform 1 of RNA-binding protein Musashi homolog 2	0	1.41	0	–	Yes
	B	SSRP1	FACT complex subunit SSRP1	0	1.24	0	–	Yes
	B	ASNS	Asparagine synthetase	0	1.24	0	–	Yes
	B	EIF6	Eukaryotic translation initiation factor 6	0	2.19	0	–	Yes
	B	MCM4	DNA replication licensing factor MCM4	0	1.24	0	–	Yes
	B	BYSL	Bystin	0	2.19	0	–	Yes
	B	SLC2A1	Solute carrier family 2, facilitated glucose transporter member 1	0	1.24	0	–	Yes
	B	EMD	Emerin	0	2.19	0	–	Yes
	B	RPL38	60S ribosomal protein L38	0	1.24	0	–	Yes
	B	SEPT11	Septin-11	0	2.19	0	–	Yes
	B	CSNK1A1	Casein kinase I isoform alpha (Casein kinase 1, a1)	0	1.24	0	–	Yes
	B	FKBP4	FK506-binding protein 4	0	2.19	0	–	Yes
	B	PYCR2	Pyrroline-5-carboxylate reductase 2	0	1.24	0	–	Yes
	B	TALDO1	Transaldolase	0	2.19	0	–	Yes
	B	TYMS	Thymidylate synthase	0	1.24	0	–	Yes
	B	VDAC1	Voltage-dependent anion-selective channel protein 1	0	2.19	0	–	Yes
	B	ACAT1	Acetyl-CoA acetyltransferase, mitochondrial precursor	0	1.24	0	–	Yes
	B	CENTD2	Isoform 3 of Centaurin-delta 2	0	2.19	0	–	Yes
	B	CNBP	Zinc finger protein 9	0	1.24	0	–	Yes
	B	PTPN11	Isoform 1 of Tyrosine-protein phosphatase non-receptor type 11 (SHP2)	0	2.19	0	–	Yes
	B	TOP1	DNA topoisomerase 1	0	1.24	0	–	Yes
	B	STAT5B	Signal transducer and activator of transcription 5B	0	2.19	0	–	Yes
	B	ACO2	Aconitase 2, mitochondrial	0	1.24	0	–	Yes
	B	UBR4	Isoform 1 of Zinc finger UBR1-type protein 1	0	2.65	0	–	Yes
	B	BOLA2;BOLA2B	BolA-like protein 2	0	1.41	0	–	Yes
	B	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	0	1.41	0	–	Yes
	B	PAFAH1B3	Platelet-activating factor acetylhydrolase IB subunit gamma	0	1.41	0	–	Yes
	B	MRPL43	Mitochondrial ribosomal protein L43	0	1.41	0	–	Yes
	B	SNRPA1	U2 small nuclear ribonucleoprotein A'	0	1.87	0	–	Yes
	B	PSMB6	Proteasome subunit beta type-6 precursor	0	1.87	0	–	Yes
	B	CHD4	Isoform 1 of Chromodomain-helicase-DNA-binding protein 4	0	1.87	0	–	Yes
	B	AP2S1	Isoform 1 of AP-2 complex subunit sigma-1	0	2.11	0	–	Yes
	B	HRB	Isoform 1 of Nucleoporin-like protein RIP	0	3.59	0	–	Yes
	B	NUP188	Isoform 1 of Nucleoporin NUP188 homolog	0	5.15	0	–	Yes
	B	ARF1	ADP-ribosylation factor 1 (Arf1)	0	4.59	0	–	Yes
	B	ATP5O	ATP synthase subunit O, mitochondrial precursor	0	4.84	0	–	Yes
	B	IMMT	Isoform 1 of Mitochondrial inner membrane protein	0	4.84	0	–	Yes
	B	STRAP	Serine-threonine kinase receptor-associated protein	0	3.28	0	–	Yes
	B	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor	0	3.28	0	–	Yes
	B	THOC2	THO complex 2 isoform 1	0	3.11	0	–	Yes
	B	HBG1;HBE1	Hemoglobin subunit gamma-1	0	8.08	0	–	Yes
	B	PSMD3	26S proteasome non-ATPase regulatory subunit 3	0	4.53	0	–	Yes
	B	ITGA4	Integrin alpha-4 precursor (α$_4$ integrin)	0.99	18.27	0	Yes	Yes
	B	UBE2N	Ubiquitin-conjugating enzyme E2 N	0.87	2.11	0	Yes	Yes
	B	EPN1	Isoform 1 of Epsin-1	0.87	2.11	0	Yes	Yes
	B	ATP5C1	Isoform Liver of ATP synthase gamma chain, mitochondrial precursor	0.87	2.19	0	Yes	Yes
	B	PRMT5	Protein arginine N-methyltransferase 5	0.87	2.19	0	Yes	Yes
	B	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor	0.87	2.19	0	Yes	Yes
	B	STIP1	Stress-induced-phosphoprotein 1	0.87	1.87	0	Yes	Yes
	B	RCC1	Regulator of chromosome condensation 1 isoform a	2.65	5.54	0	Yes	Yes
	B	RPL13A	60S ribosomal protein L13a	2.30	4.68	0	Yes	Yes
	B	MRPS23	Mitochondrial ribosomal protein S23	0.99	3.27	0	Yes	Yes
	B	ILF3	Isoform 1 of Interleukin enhancer-binding factor 3	1.31	4.53	0	Yes	Yes
	B	PSMA6	Proteasome subunit alpha type-6	0.99	3.11	0	Yes	Yes
	B	NUP205	Nuclear pore complex protein Nup205	0.99	3.11	0	Yes	Yes
	B	RAC1	Isoform A of Ras-related C3 botulinum toxin substrate 1 precursor (Rac1)	2.85	9.05	0	Yes	Yes
	B	NARG1	Isoform 1 of NMDA receptor-regulated protein 1	0.87	1.24	0	Yes	Yes
	B	SNRP70	Isoform 1 of U1 small nuclear ribonucleoprotein 70 kDa	0.87	1.24	0	Yes	Yes
	B	NHP2L1	NHP2-like protein 1	1.74	2.49	0	Yes	Yes
	B	RAB5C	Ras-related protein Rab-5C (Rab5C)	2.18	3.27	0	Yes	Yes
	B	LGALS1	Galectin-1	0.87	1.41	0	Yes	Yes
	B	PSMB2	Proteasome subunit beta type-2	1.31	2.11	0	Yes	Yes
	B	MCM6	DNA replication licensing factor MCM6	1.49	2.49	0	Yes	Yes
	B	RPL36	60S ribosomal protein L36	3.17	5.30	0	Yes	Yes
	B	DIMT1L	Probable dimethyladenosine transferase	3.52	6.39	0	Yes	Yes
		VTA1	Vacuolar protein sorting-associated protein VTA1 homolog	0	4.38	2.82	–	–
		SYK	Isoform Short of Tyrosine-protein kinase SYK	0	4.53	2.82	–	–
		PSMD2	26S proteasome non-ATPase regulatory subunit 2	0	4.05	2.82	–	–
		ATXN2L	Isoform 1 of Ataxin-2-like protein	0	6.16	4.58	–	–
		PSMA3	Isoform 1 of Proteasome subunit alpha type-3	0	5.93	2.82	–	Yes
		HIP1R	Huntingtin-interacting protein 1-related protein	1.77	6.94	6.26	–	–
		VDAC2	Voltage-dependent anion-selective channel protein 2	0.87	4.05	2.82	–	–
		STMN1	Stathmin	0.99	3.59	2.29	–	–
		PPIL1	Peptidyl-prolyl cis-trans isomerase-like 1	1.98	6.16	4.58	–	–
		UPF1	Isoform 1 of Regulator of nonsense transcripts 1	4.38	10.21	7.67	–	–
		LYPLA1	Isoform 1 of Acyl-protein thioesterase 1	2.30	5.46	4.58	–	–
		PLEC1	Plectin 1 isoform 1	7.88	18.66	15.33	–	–
		DRG1	Developmentally-regulated GTP-binding protein 1	1.86	3.59	2.82	–	–
		BAT1	Isoform 2 of Spliceosome RNA helicase BAT1	6.91	12.71	9.86	–	–
		MIF	Macrophage migration inhibitory factor	2.61	5.14	3.44	–	–
		RPL22	60S ribosomal protein L22	4.16	8.28	5.73	–	–
		HIST1H4F;HIST2H4B;	Histone H4	26.18	47.69	33.93	–	–
		FBL	rRNA 2'-O-methyltransferase fibrillarin	4.63	7.58	5.64	–	–
		DDX21	Isoform 1 of Nucleolar RNA helicase 2	15.85	26.59	19.56	–	–
		CAD	CAD protein	6.50	13.27	7.93	–	–
		KRT9	Keratin, type I cytoskeletal 9	10.05	22.33	13.04	–	–
		RPS18	40S ribosomal protein S18	9.30	21.83	11.46	–	–
		PPIH	Peptidyl-prolyl cis-trans isomerase H	2.18	7.49	3.44	–	Yes
		TRIM28	Isoform 1 of Transcription intermediary factor 1-beta	3.51	8.26	2.82	–	Yes
		PDCD6	Programmed cell death protein 6	4.28	11.39	3.44	–	Yes
		SRM	Spermidine synthase	3.63	6.39	2.82	–	Yes
		RPS19	40S ribosomal protein S19	5.58	10.62	4.58	–	Yes
		HSPE1	10 kDa heat shock protein, mitochondrial	4.79	9.27	4.58	–	Yes
		RPL17	60S ribosomal protein L17	3.72	7.26	2.29	–	Yes
		RPS8	40S ribosomal protein S8	9.66	16.84	6.26	–	Yes
	C	ZW10	Centromere/kinetochore protein zw10 homolog	0.87	0	0	Yes	–
	C	NDUFA9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial precursor	0.87	0	0	Yes	–
	C	NOLA2	H/ACA ribonucleoprotein complex subunit 2	0.87	0	0	Yes	–
	C	PELP1	Isoform 1 of Proline-, glutamic acid- and leucine-rich protein 1	0.87	0	0	Yes	–
	C	ERLIN2	Isoform 1 of Erlin-2 precursor	0.87	0	0	Yes	–
	C	POLR2C	DNA-directed RNA polymerase II subunit RPB3	0.87	0	0	Yes	–
	C	LRBA	Lipopolysaccharide-responsive and beige-like anchor protein	0.87	0	0	Yes	–
	C	LOC442497;SLC3A2	Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform a (CD98hc)	0.87	0	0	Yes	–
	C	RPA2	Isoform 1 of Replication protein A 32 kDa subunit	0.87	0	0	Yes	–
	C	DSCR2	Isoform 1 of Down syndrome critical region protein 2	0.87	0	0	Yes	–
	C	TKT	Transketolase	0.87	0	0	Yes	–
	C	TNFSF5IP1	Tumor necrosis factor superfamily, member 5-induced protein 1	0.87	0	0	Yes	–
	C	FLOT2	Flotillin 2	0.87	0	0	Yes	–
	C	GLUD1	Glutamate dehydrogenase 1, mitochondrial precursor	0.87	0	0	Yes	–
	C	PSMC6	26S protease regulatory subunit S10B	0.87	0	0	Yes	–
	C	MRPS34	Mitochondrial 28S ribosomal protein S34	0.87	0	0	Yes	–
	C	FDFT1	Squalene synthetase	0.87	0	0	Yes	–
	C	RNH1	Ribonuclease inhibitor	0.87	0	0	Yes	–
	C	C1QBP	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor	2.61	0	0	Yes	–
	C	PSMD13	HSPC027	0.87	0	0	Yes	–
	C	DDX18	ATP-dependent RNA helicase DDX18	1.31	0	0	Yes	–
	C	ARF6	ADP-ribosylation factor 6 (Arf6)	0.87	0	0	Yes	–
	C	RSU1	Ras suppressor protein 1 (Rsu-1)	1.31	0	0	Yes	–
	C	SAR1A	GTP-binding protein SAR1a	0.87	0	0	Yes	–
	C	ILK	Integrin-linked protein kinase (ILK)	1.31	0	0	Yes	–
	C	HMGA1	Isoform HMG-I of High mobility group protein HMG-I/HMG-Y	0.87	0	0	Yes	–
	C	COPG	Coatomer subunit gamma	1.31	0	0	Yes	–
	C	PFKL	Isoform 1 of 6-phosphofructokinase, liver type	0.87	0	0	Yes	–
	C	SEPT9	Isoform 1 of Septin-9	1.31	0	0	Yes	–
	C	NUP210	Isoform 1 of Nuclear pore membrane glycoprotein 210 precursor	0.87	0	0	Yes	–
	C	CPNE1	Copine-1	1.31	0	0	Yes	–
	C	BAG2	BAG family molecular chaperone regulator 2	0.87	0	0	Yes	–
	C	CLIC2	Chloride intracellular channel protein 2	1.31	0	0	Yes	–
	C	PSMA2	Proteasome subunit alpha type-2	0.87	0	0	Yes	–
	C	COMT	Isoform Membrane-bound of Catechol O-methyltransferase	1.31	0	0	Yes	–
	C	EIF3K	Eukaryotic translation initiation factor 3 subunit 12	0.87	0	0	Yes	–
	C	SEC61B	Protein transport protein Sec61 subunit beta	1.31	0	0	Yes	–
	C	TTC9C	Tetratricopeptide repeat protein 9C	0.87	0	0	Yes	–
	C	SPTBN1	Isoform Short of Spectrin beta chain, brain 1	1.31	0	0	Yes	–
	C	EIF4H;LOC653994	Isoform Short of Eukaryotic translation initiation factor 4H	0.87	0	0	Yes	–

Table S1, continued.

Hierarchical clustering	Selected cluster (Fig. 2)	Gene symbol	Protein name	Mean normalized spectral count (% of total spectra) x10^3			Specific enrichment?*	
				FN	VCAM-1	VCAM-1(D40A)	FN	VCAM-1
	C	NDUFV2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial precursor	1.31	0	0	Yes	–
	C	KARS	Lysyl-tRNA synthetase	0.87	0	0	Yes	–
	C	RBBP4	Histone-binding protein RBBP4	1.31	0	0	Yes	–
	C	PRPF19	Pre-mRNA-processing factor 19	0.87	0	0	Yes	–
	C	NDUFA2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	1.31	0	0	Yes	–
	C	TPR	Nucleoprotein TPR	0.87	0	0	Yes	–
	C	QARS	Glutaminyl-tRNA synthetase	1.31	0	0	Yes	–
	C	G6PD	Isoform Short of Glucose-6-phosphate 1-dehydrogenase	0.87	0	0	Yes	–
	C	UBE2L3	Ubiquitin-conjugating enzyme E2 L3	1.31	0	0	Yes	–
	C	ACACA	Isoform 1 of Acetyl-CoA carboxylase 1	0.87	0	0	Yes	–
	C	RAE1	mRNA export factor	1.31	0	0	Yes	–
	C	IPO4	Isoform 1 of Importin-4	8.34	0	0	Yes	–
	C	PAICS	Multifunctional protein ADE2	6.93	0	0	Yes	–
	C	–	Similar to fibronectin 1 isoform 4 preproprotein isoform 10	335.50	0	0	Yes	–
	C	RPL6	60S ribosomal protein L6	13.39	0	0	Yes	–
	C	NARS	Asparaginyl-tRNA synthetase, cytoplasmic	0.87	0	0	Yes	–
	C	VPS28	Vacuolar protein sorting-associated protein 28 homolog	1.86	0	0	Yes	–
	C	RPLP2	60S acidic ribosomal protein P2	2.18	0	0	Yes	–
	C	MDN1	Midasin	0.87	0	0	Yes	–
	C	GSTK1	Glutathione S-transferase kappa 1	1.86	0	0	Yes	–
	C	RPL15	60S ribosomal protein L15	2.18	0	0	Yes	–
	C	EMG1	Probable ribosome biogenesis protein NEP1	0.87	0	0	Yes	–
	C	CLIC5	Isoform 1 of Chloride intracellular channel protein 5	1.86	0	0	Yes	–
	C	PTGES3	Prostaglandin E synthase 3	2.18	0	0	Yes	–
	C	NAT10	N-acetyltransferase 10	0.87	0	0	Yes	–
	C	STX4	Syntaxin-4	1.86	0	0	Yes	–
	C	PPID	40 kDa peptidyl-prolyl cis-trans isomerase	2.18	0	0	Yes	–
	C	PAFAH1B2	Platelet-activating factor acetylhydrolase IB subunit beta	0.87	0	0	Yes	–
	C	LASP1	Isoform 1 of LIM and SH3 domain protein 1 (LASP1)	1.86	0	0	Yes	–
	C	PDCD5	Programmed cell death protein 5	2.18	0	0	Yes	–
	C	NDUFA5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	0.87	0	0	Yes	–
	C	TGM2	Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	24.48	0	0	Yes	–
	C	PRKCB1	Isoform Beta-I of Protein kinase C beta type (PKCb)	0.87	0	0	Yes	–
	C	SNRPE	Small nuclear ribonucleoprotein E	2.18	0	0	Yes	–
	C	CAP1	Adenylyl cyclase-associated protein 1	3.17	0	0	Yes	–
	C	U2AF1	Splicing factor U2AF 35 kDa subunit	0.87	0	0	Yes	–
	C	SNRPB	Isoform SM-B' of Small nuclear ribonucleoprotein-associated proteins B and B'	2.18	0	0	Yes	–
	C	VPS35	Vacuolar protein sorting-associated protein 35	3.72	0	0	Yes	–
	C	DLD	Dihydrolipoyl dehydrogenase, mitochondrial precursor	0.87	0	0	Yes	–
	C	KRT31	Keratin, type I cuticular Ha1	3.72	0	0	Yes	–
	C	NECAP2	Isoform 1 of Adaptin ear-binding coat-associated protein 2	5.82	0	0	Yes	–
	C	PSMD5	Uncharacterized protein PSMD5	0.87	0	0	Yes	–
	C	CUGBP2	CUG triplet repeat, RNA binding protein 2 isoform 2	6.93	0	0	Yes	–
	C	RPA1	Replication protein A 70 kDa DNA-binding subunit	0.87	0	0	Yes	–
	C	HMGB1	High mobility group protein B1	7.86	0	0	Yes	–
	C	MRPS6;SLC5A3	Mitochondrial 28S ribosomal protein S6	0.87	0	0	Yes	–
	C	SUB1	Activated RNA polymerase II transcriptional coactivator p15	12.47	0	0	Yes	–
	C	RPL29	60S ribosomal protein L29	6.29	0	0	Yes	–
	C	FLOT1	Flotillin-1	6.27	0	0	Yes	–
	C	DNAJB1	DnaJ homolog subfamily B member 1	1.77	0	0	Yes	–
	C	AP2A2	AP-2 complex subunit alpha-2	30.22	0	0	Yes	–
	C	SRP14	Signal recognition particle 14 kDa protein	1.74	0	0	Yes	–
	C	AHNAK	AHNAK nucleoprotein isoform 1	1.74	0	0	Yes	–
	C	STXBP3	Syntaxin-binding protein 3	1.74	0	0	Yes	–
	C	IDI1	Isopentenyl-diphosphate delta isomerase	1.74	0	0	Yes	–
	C	PRPS2	Isoform 1 of Ribose-phosphate pyrophosphokinase 2	1.74	0	0	Yes	–
	C	RAB7A	Ras-related protein Rab-7a (Rab7A)	1.74	0	0	Yes	–
	C	PRPF4	Isoform 1 of U4/U6 small nuclear ribonucleoprotein Prp4	1.74	0	0	Yes	–
	C	HADHA	Trifunctional enzyme subunit alpha, mitochondrial precursor	1.74	0	0	Yes	–
	C	LCP1	Plastin-2	1.74	0	0	Yes	–
	C	ITGAV	Isoform 1 of Integrin alpha-V precursor (α_v integrin)	1.74	0	0	Yes	–
	C	C22orf28	UPF0027 protein C22orf28	1.77	0	0	Yes	–
	C	RPL31	60S ribosomal protein L31	2.30	0	0	Yes	–
	C	PGAM5	Isoform 1 of Phosphoglycerate mutase family member 5 precursor	1.77	0	0	Yes	–
	C	JTV1	Multisynthetase complex auxiliary component p38	2.30	0	0	Yes	–
	C	DHX30	Isoform 1 of Putative ATP-dependent RNA helicase DHX30	1.77	0	0	Yes	–
	C	SLC25A1	Tricarboxylate transport protein, mitochondrial precursor	2.30	0	0	Yes	–
	C	POLR1C	Isoform 1 of DNA-directed RNA polymerases I and III subunit RPAC1	1.77	0	0	Yes	–
	C	DAB2	Isoform 1 of Disabled homolog 2 (Disabled-2)	2.30	0	0	Yes	–
	C	CPSF6	Isoform 1 of Cleavage and polyadenylation specificity factor subunit 6	5.44	0	0	Yes	–
	C	NOP5/NOP58	Nucleolar protein 5	1.77	0	0	Yes	–
	C	KIDINS220	KIDINS220 protein	14.82	0	0	Yes	–
	C	MRPL13	39S ribosomal protein L13, mitochondrial	1.77	0	0	Yes	–
	C	PDLIM5	PDZ and LIM domain protein 5	1.77	0	0	Yes	–
	C	COPE	Epsilon subunit of coatomer protein complex isoform c	1.77	0	0	Yes	–
	C	ACLY	ATP-citrate synthase	3.29	0	0	Yes	–
	C	KRT5	Keratin, type II cytoskeletal 5	3.46	0	0	Yes	–
	C	FAU	40S ribosomal protein S30	3.48	0	0	Yes	–
	C	IGF2BP3	Isoform 1 of Insulin-like growth factor 2 mRNA-binding protein 3	3.48	0	0	Yes	–
	C	EIF2S3	Eukaryotic translation initiation factor 2 subunit 3	3.63	0	0	Yes	–
	C	THEM2	Thioesterase superfamily member 2	0.99	0	0	Yes	–
	C	ST13	Hsc70-interacting protein	0.99	0	0	Yes	–
	C	CLTB	Isoform Non-brain of Clathrin light chain B	0.99	0	0	Yes	–
	C	SUPT5H	Isoform 1 of Transcription elongation factor SPT5	0.99	0	0	Yes	–
	C	CKAP5	Cytoskeleton-associated protein 5	0.99	0	0	Yes	–
	C	ARHGEF1	ARHGEF1 protein (p115RhoGEF)	0.99	0	0	Yes	–
	C	BAT3	Isoform 1 of Large proline-rich protein BAT3	0.99	0	0	Yes	–
	C	APOBEC3C;APOBEC3	Probable DNA dC->dU-editing enzyme APOBEC-3C	0.99	0	0	Yes	–
	C	CLNS1A	Methylosome subunit pICln	0.99	0	0	Yes	–
	C	LSM12	Isoform 1 of Protein LSM12 homolog	0.99	0	0	Yes	–
	C	CNN2	Calponin-2	0.99	0	0	Yes	–
	C	TK1	Thymidine kinase 1, soluble	0.99	0	0	Yes	–
	C	NAPG	Gamma-soluble NSF attachment protein	0.99	0	0	Yes	–
	C	APOLD1;DDX47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 2	0.99	0	0	Yes	–
	C	ABCF1	Isoform 1 of ATP-binding cassette sub-family F member 1	0.99	0	0	Yes	–
	C	GDI2	Rab GDP dissociation inhibitor beta	0.99	0	0	Yes	–
	C	VPS26A	Vacuolar protein sorting-associated protein 26A	0.99	0	0	Yes	–
	C	C1orf58	BRO1 domain-containing protein BROX	0.99	0	0	Yes	–
	C	GSTO1	Glutathione transferase omega-1	0.99	0	0	Yes	–
	C	PGK1	Phosphoglycerate kinase 1	0.99	0	0	Yes	–
	C	PDAP1	28 kDa heat- and acid-stable phosphoprotein	0.99	0	0	Yes	–
	C	PSMB5	Proteasome beta 5 subunit	0.99	0	0	Yes	–
	C	RPL28	60S ribosomal protein L28	0.99	0	0	Yes	–
	C	RBM12;CPNE1	RNA-binding protein 12	0.99	0	0	Yes	–
	C	SNAP23	Isoform SNAP-23a of Synaptosomal-associated protein 23	0.99	0	0	Yes	–
	C	RPS15	40S ribosomal protein S15	0.99	0	0	Yes	–
	C	FEN1	Flap endonuclease 1	0.99	0	0	Yes	–
	C	GNAI3	Guanine nucleotide-binding protein G	0.99	0	0	Yes	–
	C	MT-CO2	Cytochrome c oxidase subunit 2	0.99	0	0	Yes	–
	C	PRMT1	HMT1 hnRNP methyltransferase-like 2 isoform 1	0.99	0	0	Yes	–
	C	HSPG2	Basement membrane-specific heparan sulfate proteoglycan core protein precursor	1.49	0	0	Yes	–
	C	EIF3F	Eukaryotic translation initiation factor 3 subunit 5	0.99	0	0	Yes	–
	C	ALDH1B1	Aldehyde dehydrogenase X, mitochondrial precursor	1.49	0	0	Yes	–
	C	SNRPA	U1 small nuclear ribonucleoprotein A	0.99	0	0	Yes	–
	C	ANKRD25	Isoform 1 of Ankyrin repeat domain-containing protein 25	1.49	0	0	Yes	–
	C	CNOT1	CCR4-NOT transcription complex, subunit 1 isoform a	0.99	0	0	Yes	–
	C	NCBP1	Nuclear cap-binding protein subunit 1	1.49	0	0	Yes	–
	C	PFKP	6-phosphofructokinase type C	0.99	0	0	Yes	–
	C	ARL2;SNX15	ADP-ribosylation factor-like protein 2 (Arf-like protein 2)	1.49	0	0	Yes	–
	C	NOLA1	Isoform 1 of H/ACA ribonucleoprotein complex subunit 1	0.99	0	0	Yes	–
	C	USP15	Isoform 1 of Ubiquitin carboxyl-terminal hydrolase 15	1.49	0	0	Yes	–
	C	RPS23	40S ribosomal protein S23	0.99	0	0	Yes	–
	C	SEC22B	Vesicle-trafficking protein SEC22b	1.49	0	0	Yes	–
	C	OLA1	Isoform 1 of Obg-like ATPase 1	0.99	0	0	Yes	–
	C	SEC23B	Protein transport protein Sec23B	1.49	0	0	Yes	–
	C	SFRS1	Isoform ASF-1 of Splicing factor, arginine/serine-rich 1	0.87	0	0	Yes	–
	C	SF3B1	Splicing factor 3B subunit 1	1.31	0	0	Yes	–
	C	SET	Isoform 1 of Protein SET	2.48	0	0	Yes	–
	C	SMCHD1	Structural maintenance of chromosomes flexible hinge domain containing 1	0.87	0	0	Yes	–
	C	TTLL12	Tubulin–tyrosine ligase-like protein 12	1.31	0	0	Yes	–
	C	BZW2	Basic leucine zipper and W2 domain-containing protein 2	2.48	0	0	Yes	–
	C	GALE	UDP-glucose 4-epimerase	0.87	0	0	Yes	–
	C	NUP155	Isoform 1 of Nuclear pore complex protein Nup155	1.31	0	0	Yes	–
	C	HNRPDL	Isoform 1 of Heterogeneous nuclear ribonucleoprotein D-like	4.95	0	0	Yes	–
	C	ARPC4	Actin-related protein 2/3 complex subunit 4 (Arp2/3, subunit 4)	0.87	0	0	Yes	–
	C	TFAM	Transcription factor A, mitochondrial precursor	1.31	0	0	Yes	–
	C	DKFZp686D0972	Hypothetical protein LOC345651	4.95	0	0	Yes	–
	C	HMGB2	High mobility group protein B2	9.33	0	0	Yes	–
	C	SSBP1	Single-stranded DNA-binding protein, mitochondrial precursor	8.94	0	0	Yes	–
	C	COPB1	Coatomer subunit beta	0.99	0	0	Yes	–
	C	NACA	Nascent polypeptide-associated complex subunit alpha	5.98	0	0	Yes	–
	C	ATP6V1B2	Vacuolar ATP synthase subunit B, brain isoform	1.77	0	0	Yes	–
	C	PHGDH	Phosphoglycerate dehydrogenase	2.65	0	0	Yes	–

Table S1, continued.

Hierarchical clustering	Selected cluster (Fig. 2)	Gene symbol	Protein name	Mean normalized spectral count (% of total spectra) x10^3 FN	VCAM-1	VCAM-1(D40A)	Specific enrichment?[a] FN	VCAM-1
	C	MAP4	Isoform 1 of Microtubule-associated protein 4	1.77	0	0	Yes	–
	C	PUF60	Isoform 1 of Poly	2.65	0	0	Yes	–
	C	AKR1C1	Aldo-keto reductase family 1 member C1	1.77	0	0	Yes	–
	C	YES1	Proto-oncogene tyrosine-protein kinase Yes	2.65	0	0	Yes	–
	C	EPB41	Isoform 1 of Protein 4.1	1.77	0	0	Yes	–
	C	DBN1	Isoform 1 of Drebrin	2.65	0	0	Yes	–
	C	FAM62B	Isoform 2 of Protein FAM62B	1.77	0	0	Yes	–
	C	PDHB	Isoform 1 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor	7.81	0	0	Yes	–
	C	RPS26;LOC728937;LC	40S ribosomal protein S26	1.98	0	0	Yes	–
	C	SEC24C	Protein transport protein Sec24C	1.98	0	0	Yes	–
	C	YWHAG	14-3-3 protein gamma	1.98	0	0	Yes	–
	C	RCC2	Protein RCC2	11.14	0	0	Yes	–
	C	CBX3;LOC653972	Chromobox protein homolog 3	7.78	0	0	Yes	–
	C	TUBB6	TUBB6 protein	19.30	0	0	Yes	–
	C	RAB11A	Ras-related protein Rab-11A (Rab11A)	2.73	0	0	Yes	–
	C	EIF5B	Eukaryotic translation initiation factor 5B	3.23	0	0	Yes	–
	C	RAB35	Ras-related protein Rab-35 (Rab35)	4.28	0	0	Yes	–
	C	SSB	Lupus La protein	3.23	0	0	Yes	–
	C	HNRPH2	Heterogeneous nuclear ribonucleoprotein H'	7.44	0	0	Yes	–
	C	VIL2	Villin 2 (Ezrin)	11.82	0	0	Yes	–
	C	USP39	U4/U6.U5 tri-snRNP-associated protein 2	2.64	0	0	Yes	–
	C	SIPA1	Signal-induced proliferation-associated protein 1	1.77	0	0	Yes	–
	C	KIAA0368	KIAA0368 protein	2.36	0	0	Yes	–
	C	MRPS28	Mitochondrial 28S ribosomal protein S28	1.77	0	0	Yes	–
	C	PCNA	Proliferating cell nuclear antigen	2.36	0	0	Yes	–
	C	SF3A3	Splicing factor 3A subunit 3	1.77	0	0	Yes	–
	C	SNRPD3	Small nuclear ribonucleoprotein Sm D3	2.36	0	0	Yes	–
	C	SEPT2	Septin-2	6.37	0	0	Yes	–
	C	HIST1H2AA	Histone H2A type 1-A	10.88	0	0	Yes	–
	C	PKM2	Isoform M2 of Pyruvate kinase isozymes M1/M2	5.03	0	0	Yes	–
	C	YWHAH	14-3-3 protein eta	3.92	0	0	Yes	–
	C	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	4.14	0	0	Yes	–
	C	KRT81	Keratin, hair, basic, 1	2.85	0	0	Yes	–
	C	CAND1	Isoform 1 of Cullin-associated NEDD8-dissociated protein 1	4.10	0	0	Yes	–
	C	C14orf166	Protein C14orf166	3.05	0	0	Yes	–
	C	CSNK2A1	Casein kinase II subunit alpha (Casein kinase 2, a1)	2.64	0	0	Yes	–
	C	MPP1	55 kDa erythrocyte membrane protein	5.13	0	0	Yes	–
	C	H2AFV	Histone H2AV	7.92	0	0	Yes	–
	C	ACTR3	Actin-related protein 3 (Arp3)	10.11	0	0	Yes	–
	C	ITGA5	Integrin alpha-5 precursor (α$_5$ integrin)	38.98	0	0	Yes	–
	C	LRRC59	Leucine-rich repeat-containing protein 59	4.06	0	0	Yes	–
	C	CORO1B;PTPRCAP	Coronin-1B	2.79	0	0	Yes	–
	C	PSMB3	Proteasome subunit beta type-3	2.79	0	0	Yes	–
	C	EIF5	Eukaryotic translation initiation factor 5	2.79	0	0	Yes	–
	C	IGF2R	Cation-independent mannose-6-phosphate receptor precursor	2.79	0	0	Yes	–
	C	SFRS3	Splicing factor, arginine/serine-rich 3	7.82	0	0	Yes	–
	C	HDAC1	Histone deacetylase 1	2.76	0	0	Yes	–
	C	YWHAQ	14-3-3 protein theta	3.92	0	0	Yes	–
	C	BMP2K	Isoform 1 of BMP-2-inducible protein kinase	6.25	0	0	Yes	–
	C	TRAP1	Heat shock protein 75 kDa, mitochondrial precursor	25.72	0	0	Yes	–
	C	RAB10	Ras-related protein Rab-10 (Rab10)	3.46	0	0	Yes	–
	C	QKI	Isoform 1 of Protein quaking	9.16	0	0	Yes	–
	C	PDIA6	Isoform 1 of Protein disulfide-isomerase A6 precursor	3.07	0	0	Yes	–
	C	TPM3	Tropomyosin 3 isoform 4	3.51	0	0	Yes	–
	C	MRTO4	mRNA turnover protein 4 homolog	4.22	0	0	Yes	–
	D	PPP2CA	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	3.35	1.24	0	Yes	Yes
	D	MCM2	DNA replication licensing factor MCM2	3.53	1.24	0	Yes	Yes
	D	RAP1B	Ras-related protein Rap-1b precursor (Rap1b)	7.82	2.81	0	Yes	Yes
	D	AARS	Alanyl-tRNA synthetase, cytoplasmic	4.12	1.41	0	Yes	Yes
	D	ALDOA	Fructose-bisphosphate aldolase A	6.24	2.11	0	Yes	Yes
	D	HIST1H2BJ	Histone H2B type 1-J	14.85	4.97	0	Yes	Yes
	D	RPL8	60S ribosomal protein L8	5.02	1.41	0	Yes	Yes
	D	ENO1	Isoform alpha-enolase of Alpha-enolase	15.99	4.53	0	Yes	Yes
	D	KPNA2	Importin subunit alpha-2	8.07	2.19	0	Yes	Yes
	D	MRLC2	Myosin regulatory light chain	4.10	1.24	0	Yes	Yes
	D	STON2	Isoform 1 of Stonin-2	12.59	4.05	0	Yes	Yes
	D	KRT18	Keratin, type I cytoskeletal 18	14.31	4.53	0	Yes	Yes
	D	IQGAP1	Ras GTPase-activating-like protein IQGAP1	29.09	8.73	2.82	Yes	Yes
	D	MACF1	Isoform 1 of Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (ACF7)	6.02	1.24	0	Yes	Yes
	D	RANBP5	RAN binding protein 5	6.82	1.41	0	Yes	Yes
	D	FLNB	Isoform 1 of Filamin-B	20.16	4.21	0	Yes	Yes
	D	VASP	Vasodilator-stimulated phosphoprotein (VASP)	6.61	1.41	0	Yes	Yes
	D	HNRPF	Heterogeneous nuclear ribonucleoprotein F	16.54	3.51	0	Yes	Yes
	D	TARS	Threonyl-tRNA synthetase, cytoplasmic	9.56	1.87	0	Yes	Yes
	D	VCL	Isoform 1 of Vinculin	13.91	2.81	0	Yes	Yes
	D	ANP32B	Isoform 1 of Acidic leucine-rich nuclear phosphoprotein 32 family member B	7.88	1.41	0	Yes	Yes
	D	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	14.00	2.49	0	Yes	Yes
	D	MYH9	Myosin-9 (Myosin IIA)	16.81	3.11	0	Yes	Yes
	D	FARSB	Phenylalanyl-tRNA synthetase beta chain	7.58	1.87	0	Yes	Yes
	D	XPO1	Exportin-1	11.56	2.65	0	Yes	Yes
	D	ATP5A1	ATP synthase subunit alpha, mitochondrial precursor	14.90	3.28	0	Yes	Yes
		ATP5B	ATP synthase subunit beta, mitochondrial precursor	23.60	3.43	2.82	Yes	–
		FAM62A	Isoform 1 of Protein FAM62A	23.42	5.39	3.44	Yes	–
		NCL	Isoform 1 of Nucleolin	39.57	9.51	9.07	Yes	–
		KIAA1967	Uncharacterized protein KIAA1967	4.16	0	2.29	–	–
		YBX1	Nuclease sensitive element-binding protein 1	4.56	0	2.29	Yes	–
		HSD17B10	Isoform 1 of 3-hydroxyacyl-CoA dehydrogenase type-2	3.66	0	2.29	–	–
		PPA1	Inorganic pyrophosphatase	4.59	0	2.82	–	–
		MATR3	Matrin-3	13.17	0	8.45	–	–
		RPL23A;hCG_16001	60S ribosomal protein L23a	6.45	0	2.82	Yes	–
		PA2G4	Proliferation-associated protein 2G4	6.54	0	2.82	Yes	–
		HSPA5	HSPA5 protein	7.90	0	2.82	Yes	–
		GART	Isoform Long of Trifunctional purine biosynthetic protein adenosine-3	8.59	0	2.29	Yes	–
		UBE2M	NEDD8-conjugating enzyme Ubc12	6.43	1.41	2.29	Yes	–
		GSTP1	Glutathione S-transferase P	7.94	1.24	3.44	Yes	–
		RPL7	60S ribosomal protein L7	11.14	1.41	2.82	Yes	–
		EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component	14.99	2.65	4.23	Yes	–
		SF1	Isoform 1 of Splicing factor 1	15.74	2.19	4.58	Yes	–
		LDHA	Isoform 1 of L-lactate dehydrogenase A chain	6.30	2.81	2.29	Yes	–
		KRT2	Keratin, type II cytoskeletal 2 epidermal	17.16	7.66	5.73	Yes	–
		DIAPH1	Diaphanous 1	8.13	4.38	2.29	Yes	–
		ANXA1	Annexin A1	28.84	16.14	8.55	Yes	–
		SYNCRIP	Isoform 1 of Heterogeneous nuclear ribonucleoprotein Q	11.87	6.70	4.58	Yes	–
		SFRS9	Splicing factor, arginine/serine-rich 9	9.64	5.38	3.44	Yes	–
		EEF2	Elongation factor 2	50.62	28.41	16.74	Yes	–
		PPP1CA	Protein phosphatase 1, catalytic subunit, alpha isoform 3	8.87	4.67	4.23	Yes	–
		YWHAE	14-3-3 protein epsilon	8.25	3.97	3.44	Yes	–
		XRCC5	ATP-dependent DNA helicase 2 subunit 2	19.36	9.20	8.45	Yes	–
		SND1	Staphylococcal nuclease domain-containing protein 1	14.52	6.55	7.04	Yes	–
		HNRPK	Heterogeneous nuclear ribonucleoprotein K	37.46	18.17	19.03	Yes	–
		DDX1	ATP-dependent RNA helicase DDX1	8.05	2.81	2.29	Yes	–
		CCT2	T-complex protein 1 subunit beta	26.55	9.98	7.93	Yes	–
		PRDX6	Peroxiredoxin-6	11.42	3.35	3.44	Yes	–
		YWHAZ	14-3-3 protein zeta/delta	16.59	5.30	4.58	Yes	–
		TOMM34	Mitochondrial import receptor subunit TOM34	6.01	1.41	3.44	–	–
		RANBP1	Ran-specific GTPase-activating protein	7.78	2.19	4.23	–	–
		FUS	Isoform Short of RNA-binding protein FUS	5.28	1.87	2.29	Yes	–
		CCT4	T-complex protein 1 subunit delta	18.23	6.39	7.67	Yes	–
		XRCC6	ATP-dependent DNA helicase 2 subunit 1	14.52	5.15	6.52	Yes	–
		SMAP1L	Isoform 1 of Stromal membrane-associated protein 1-like	4.84	1.41	2.29	Yes	–
		TUBB2C	Tubulin beta-2C chain	135.65	33.72	60.58	Yes	–
		ACP1	Isoform 1 of Low molecular weight phosphotyrosine protein phosphatase	3.23	2.11	2.29	–	–
		RPS13	40S ribosomal protein S13	5.15	3.27	3.44	–	–
		RPSA	40S ribosomal protein SA	18.22	11.16	11.89	–	–
		TAGLN2	Transgelin-2	21.53	12.94	14.54	–	–
		HNRPA3	Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	18.86	11.63	11.27	–	–
		TCP1	T-complex protein 1 subunit alpha	17.24	10.44	10.75	–	–
		CCT8	T-complex protein 1 subunit theta	24.48	14.67	14.97	–	–
		EIF3E	Eukaryotic translation initiation factor 3 subunit 6	5.82	3.43	4.23	–	–
		VIM	Vimentin	57.31	34.11	42.12	–	–
		GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	15.53	8.66	10.31	–	–
		HNRPH1	Heterogeneous nuclear ribonucleoprotein H	35.48	19.20	23.88	–	–
		RPS9	40S ribosomal protein S9	14.19	7.80	8.55	–	–
		TARDBP	TDP43	16.76	8.66	10.22	–	–
		HNRNPU	Heterogeneous nuclear ribonucleoprotein U isoform a	38.80	20.12	20.96	–	–
		CLIC1;DDAH2	Chloride intracellular channel protein 1	36.00	19.66	20.18	–	–
		TUBA1B	Tubulin alpha-1B chain	79.81	43.68	46.25	–	–
		KRT8	Keratin, type II cytoskeletal 8	35.57	17.16	20.08	–	–
		HSPD1	60 kDa heat shock protein, mitochondrial precursor	54.43	26.05	33.31	–	–

Table S1, continued.

Hierarchical clustering	Selected cluster (Fig. 2)	Gene symbol	Protein name	Mean normalized spectral count (% of total spectra) x10^3 FN	VCAM-1	VCAM-1(D40A)	Specific enrichment?* FN	VCAM-1
		PI4KA	Isoform 1 of Phosphatidylinositol 4-kinase alpha	0.99	1.24	0	Yes	Yes
		SCRIB	Isoform 1 of Protein LAP4	0.99	1.24	0	Yes	Yes
		PSMB1	Proteasome subunit beta type-1 precursor	2.30	2.81	0	Yes	Yes
		RUVBL2	RuvB-like 2	2.65	3.28	0	Yes	Yes
		PSMD11	Proteasome 26S non-ATPase subunit 11 variant (Fragment)	1.98	2.19	0	Yes	Yes
		EPS15	Epidermal growth factor receptor substrate 15	5.21	6.08	0	Yes	Yes
		RPL27A	60S ribosomal protein L27a	7.90	9.20	0	Yes	Yes
		PSMA5	Proteasome subunit alpha type-5	2.18	2.19	0	Yes	Yes
		TIA1	TIA1 protein	3.96	3.97	0	Yes	Yes
		ARPC3	Actin-related protein 2/3 complex subunit 3	1.31	1.41	0	Yes	Yes
		EIF3B	Isoform 1 of Eukaryotic translation initiation factor 3 subunit 9	5.02	5.39	0	Yes	Yes
		MLLT4	Isoform 4 of Afadin	4.63	5.00	0	Yes	Yes
		CORO1C	Coronin-1C	5.29	5.62	0	Yes	Yes
		RPS25	40S ribosomal protein S25	5.09	5.30	0	Yes	Yes
		NDUFS3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor	1.31	1.24	0	Yes	Yes
		RALY	Isoform 1 of RNA-binding protein Raly	2.36	2.19	0	Yes	Yes
		MYH10	Isoform 1 of Myosin-10	15.19	14.27	0	Yes	Yes
		RAP2B	Ras-related protein Rap-2b precursor	2.48	2.11	0	Yes	Yes
		DHX15	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	7.26	6.24	0	Yes	Yes
		PRDX3	Peroxiredoxin 3 isoform b	3.72	3.27	0	Yes	Yes
		YWHAB	Isoform Long of 14-3-3 protein beta/alpha	6.53	5.77	0	Yes	Yes
		RPL35	60S ribosomal protein L35	2.61	2.11	0	Yes	Yes
		MYL4	Myosin light polypeptide 4	10.24	8.04	0	Yes	Yes
		KRT10	Keratin, type I cytoskeletal 10	14.81	11.54	0	Yes	Yes
		GTPBP4	Nucleolar GTP-binding protein 1	1.77	1.24	0	Yes	Yes
		GMPS	GMP synthase	3.07	2.19	0	Yes	Yes
		LY6G5B;CSNK2B	Casein kinase II subunit beta	2.18	1.41	0	Yes	Yes
		GLRX3	Glutaredoxin-3	1.86	1.24	0	Yes	Yes
		PDCD10	Programmed cell death protein 10	2.73	1.87	0	Yes	Yes
		CAPZA1	F-actin-capping protein subunit alpha-1	6.82	4.67	0	Yes	Yes
		DDX6	Probable ATP-dependent RNA helicase DDX6	3.64	2.19	0	Yes	Yes
		RPL21;LOC729402;LO	60S ribosomal protein L21	2.18	1.24	0	Yes	Yes
		LDHB	L-lactate dehydrogenase B chain	2.18	1.24	0	Yes	Yes
		MYL6	Isoform Non-muscle of Myosin light polypeptide 6	6.83	3.97	0	Yes	Yes
		MSN	Moesin	34.18	19.83	0	Yes	Yes
		RPS24	Isoform 1 of 40S ribosomal protein S24	6.95	3.89	0	Yes	Yes
	E	CACYBP	Isoform 1 of Calcyclin-binding protein	2.65	1.24	0	Yes	Yes
	E	FLJ12529	Isoform 1 of Cleavage and polyadenylation specificity factor subunit 7	5.41	2.49	0	Yes	Yes
	E	EEF1B2	Elongation factor 1-beta	4.56	2.19	0	Yes	Yes
	E	NAPA	Alpha-soluble NSF attachment protein	2.85	1.41	0	Yes	Yes
	E	RPL10A	60S ribosomal protein L10a	11.93	5.92	0	Yes	Yes
	E	SF3B14	Pre-mRNA branch site protein p14	2.79	1.41	0	Yes	Yes
	E	YTHDF2	Isoform 1 of YTH domain family protein 2	2.79	1.41	0	Yes	Yes
	E	THOC4	THO complex subunit 4	5.28	2.65	0	Yes	Yes
	E	SRI	Sorcin	4.16	2.11	0	Yes	Yes
	E	RPS7	40S ribosomal protein S7	7.64	3.89	0	Yes	Yes
	E	ANXA2	Annexin A2 isoform 1	16.19	8.35	0	Yes	Yes
	E	MAPRE1	Microtubule-associated protein RP/EB family member 1 (EB1)	2.65	1.41	0	Yes	Yes
	E	RPS17	40S ribosomal protein S17	3.48	1.87	0	Yes	Yes
	E	ITGB1	Integrin beta 1 isoform 1A precursor (β$_1$ integrin)	48.92	26.14	0	Yes	Yes
	E	FSCN1	Fascin	3.29	1.41	0	Yes	Yes
	E	HIST1H1B	Histone H1.5	4.41	1.87	0	Yes	Yes
	E	MDH2	Malate dehydrogenase, mitochondrial precursor	7.88	3.51	0	Yes	Yes
	E	MCM3	DNA replication licensing factor MCM3	3.23	1.24	0	Yes	Yes
	E	ZYX	Zyxin	5.50	2.19	0	Yes	Yes
	E	TLN1	Talin-1	565.91	228.54	28.82	Yes	Yes
	E	AP2M1	AP-2 complex subunit mu-1	16.54	8.58	2.82	Yes	Yes
	E	NPM1	Isoform 1 of Nucleophosmin	24.00	12.40	4.23	Yes	Yes
	E	URP2	Isoform 2 of Unc-112-related protein 2 (Kindlin-3)	40.72	22.62	4.58	Yes	Yes
	E	AP2B1	Isoform 1 of AP-2 complex subunit beta-1	72.83	35.44	5.73	Yes	Yes
		CAPZB	Isoform 1 of F-actin-capping protein subunit beta	5.50	8.89	2.82	Yes	Yes
		RPL18	60S ribosomal protein L18	6.26	9.43	3.44	–	Yes
		RPL14	60S ribosomal protein L14	5.90	7.88	2.29	Yes	Yes
		RPL5	60S ribosomal protein L5	11.10	14.27	4.23	Yes	Yes
		DYNC1H1	Dynein heavy chain, cytosolic	6.45	7.16	3.44	–	Yes
		RPS2	40S ribosomal protein S2	9.54	10.46	5.11	–	Yes
		RPS16	40S ribosomal protein S16	5.52	5.84	2.29	Yes	Yes
		HSPA1B;HSPA1A	Heat shock 70 kDa protein 1	25.81	26.06	11.89	Yes	Yes
		ILF2	Interleukin enhancer-binding factor 2	9.55	11.86	5.11	–	Yes
		RPL24	60S ribosomal protein L24	13.26	15.37	5.64	Yes	Yes
		PSMA7	Isoform 1 of Proteasome subunit alpha type-7	2.73	3.27	2.29	–	–
		RPS3A	40S ribosomal protein S3a	14.42	17.33	12.25	–	–
		GCN1L1	GCN1-like protein 1	8.55	10.30	6.88	–	–
		PFN1	Profilin-1	6.65	7.40	4.58	–	–
		RPL23	60S ribosomal protein L23	7.70	8.74	5.73	–	–
		RPLP0	60S acidic ribosomal protein P0	16.03	16.63	11.37	–	–
		TUFM	Tu translation elongation factor, mitochondrial	2.36	3.59	2.29	–	–
		RPS11	40S ribosomal protein S11	9.44	13.35	9.07	–	–
		CCT3	T-complex protein 1 subunit gamma	13.99	20.83	14.09	–	–
		PRDX1	Peroxiredoxin-1	25.90	35.18	17.19	–	Yes
		VAPA	Vesicle-associated membrane protein-associated protein A	6.43	5.62	2.29	Yes	Yes
		RPL4	60S ribosomal protein L4	11.81	10.46	4.23	Yes	Yes
		EIF4A1	Eukaryotic initiation factor 4A-I	14.11	13.58	4.23	Yes	Yes
		TFRC	Transferrin receptor protein 1	6.20	4.84	2.29	Yes	Yes
		CCT5	T-complex protein 1 subunit epsilon	16.97	12.01	5.11	Yes	Yes
		ACTN4	Alpha-actinin-4	68.92	51.33	22.90	Yes	Yes
		PICALM	Isoform 1 of Phosphatidylinositol-binding clathrin assembly protein	32.56	22.24	11.46	Yes	–
		KPNB1	Importin subunit beta-1	15.76	11.70	4.23	Yes	Yes
		KRT1	Keratin, type II cytoskeletal 1	52.78	38.30	13.75	Yes	Yes
		CFL1	Cofilin-1	6.89	4.30	3.44	Yes	–
		XPO5	Isoform 1 of Exportin-5	8.23	5.92	5.11	–	–
		CCT6A	T-complex protein 1 subunit zeta	18.75	13.51	11.63	–	–
		EEF1D	Elongation factor 1-delta	14.13	10.77	7.67	–	–
		TOP2A	Isoform 2 of DNA topoisomerase 2-alpha	6.95	5.60	4.58	–	–
		RBMX	Heterogeneous nuclear ribonucleoprotein G	9.02	7.26	5.64	–	–
		CCT7	T-complex protein 1 subunit eta	19.83	16.69	11.89	–	–
		HSP90AA1	Isoform 1 of Heat shock protein HSP 90-alpha	74.58	61.84	53.03	–	–
		RPS10	40S ribosomal protein S10	7.82	5.39	3.44	Yes	–
		CLTC	Isoform 1 of Clathrin heavy chain 1	351.53	249.39	154.46	Yes	–
		ELAVL1	ELAV-like protein 1	16.79	12.56	7.93	Yes	–
		RPL12	60S ribosomal protein L12	17.96	13.19	7.93	Yes	–
		HIST1H2BK	Histone H2B type 1-K	60.44	45.65	25.74	Yes	–
		PHB	Prohibitin	14.07	13.04	6.52	Yes	Yes
		STOM	Erythrocyte band 7 integral membrane protein	13.79	12.27	6.52	Yes	–
		AP2A1	Adaptor-related protein complex 2, alpha 1 subunit isoform 2	78.30	69.68	37.18	Yes	–
		FLNC	Gamma filamin variant	32.93	29.95	18.15	–	–
		FLNA	Filamin-A	125.79	105.69	60.79	Yes	–
		MEMO1	Protein MEMO1	0	0	2.29	–	–
		SFRS6	Isoform SRP55-1 of Splicing factor, arginine/serine-rich 6	0	0	2.82	–	–
		LSM3	U6 snRNA-associated Sm-like protein LSm3	0	0	2.29	–	–
		SF3B3	Isoform 1 of Splicing factor 3B subunit 3	0	0	2.82	–	–
		DNAJC7	DnaJ homolog subfamily C member 7	0	0	2.29	–	–
		PSMA1	Isoform Short of Proteasome subunit alpha type-1	0	0	2.82	–	–
		SDHB	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor	0	0	2.29	–	–
		TNPO1	Transportin-1	0	0	2.82	–	–
		NUP214	Nuclear pore complex protein Nup214	0	0	9.96	–	–
		FTL	Ferritin-like protein	0	0	2.29	–	–
		EBNA1BP2	Probable rRNA-processing protein EBP2	0	0	2.82	–	–
		ANKRD17	Ankyrin repeat domain protein 17 isoform a	0	0	2.29	–	–
		ADAMTSL4	Isoform 1 of ADAMTS-like protein 4 precursor	0	0	2.82	–	–
		CHMP2B	Charged multivesicular body protein 2b	0	0	2.29	–	–
		PUM1	Pumilio homolog 1	0	0	3.44	–	–
		ETF1	Eukaryotic peptide chain release factor subunit 1	0	0	4.23	–	–
		PTPN23	Tyrosine-protein phosphatase non-receptor type 23	0	0	4.58	–	–
		CHCHD3	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3	0	0	5.64	–	–
		KRT6A	Keratin, type II cytoskeletal 6A	0	0	8.02	–	–
		CHMP2A	Charged multivesicular body protein 2a	0	0	5.11	–	–
		BAT2D1	HBxAg transactivated protein 2	0	0	7.93	–	–
		FCGR2A	Low affinity immunoglobulin gamma Fc region receptor II-a precursor	0	0	7.93	–	–
		EIF3I	Eukaryotic translation initiation factor 3 subunit 2	0	1.41	7.04	–	–
		NSUN2	tRNA	0	4.05	21.32	–	–
		INPPL1	Isoform 1 of Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2	0	2.19	15.95	–	–
		AKR7A2	Aflatoxin B1 aldehyde reductase member 2	1.49	0	5.73	–	–
		KRT16	Keratin, type I cytoskeletal 16	2.48	0	11.46	–	–
		IGF2BP2	Insulin-like growth factor 2 mRNA-binding protein 2	3.05	0	9.17	–	–
		MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic	0	1.24	4.58	–	–
		RARS	Isoform Complexed of Arginyl-tRNA synthetase, cytoplasmic	0	2.19	7.04	–	–
		NUP93	Nuclear pore complex protein Nup93	0	1.87	4.23	–	–
		PIK3R2	Phosphatidylinositol 3-kinase regulatory subunit beta	0	4.05	9.34	–	–
		CD2AP	CD2-associated protein	0	3.43	9.34	–	–
		PCMT1	Isoform 1 of Protein-L-isoaspartate(D-aspartate) O-methyltransferase	1.86	4.67	9.17	–	–
		KIAA0174	Isoform 1 of Uncharacterized protein KIAA0174	1.98	3.59	6.26	–	–
		RPS21	40S ribosomal protein S21	3.05	5.39	10.22	–	–
		EIF4G1	Eukaryotic translation initiation factor 4 gamma, 1 isoform 2	6.42	11.39	20.80	–	–

Table S1, continued.

Hierarchical clustering	Selected cluster (Fig. 2)	Gene symbol	Protein name	Mean normalized spectral count (% of total spectra) x10^3			Specific enrichment?[a]	
				FN	VCAM-1	VCAM-1(D40A)	FN	VCAM-1
		CAPN1	Calpain-1 catalytic subunit	2.73	2.65	6.88	–	–
		KHSRP	KH-type splicing regulatory protein	21.20	18.81	50.57	–	–
		CDC2	Putative uncharacterized protein DKFZp686L20222	9.01	11.31	26.43	–	–
		VARS	Valyl-tRNA synthetase	11.35	13.50	28.46	–	–
		ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	0	2.11	2.29	–	–
		RAC2	Ras-related C3 botulinum toxin substrate 2 precursor	0	4.92	5.73	–	–
		IGHG1	IGHG1 protein	0	98.80	119.55	–	–
		VCAM1	Isoform 1 of Vascular cell adhesion protein 1 precursor	0	126.51	159.38	–	–
		SDCBP	Syntenin-1	0	8.90	8.02	–	–
		HBZ	Hemoglobin subunit zeta	0.87	4.59	5.73	–	–
		HBA2;HBA1	Hemoglobin subunit alpha	6.95	21.45	27.94	–	–
		EIF3EIP	Eukaryotic translation initiation factor 3 subunit 6 interacting protein	0.99	2.49	2.82	–	–
		ASCC3L1	Isoform 1 of U5 small nuclear ribonucleoprotein 200 kDa helicase	7.17	16.67	20.61	–	–
		HEATR1	HEAT repeat-containing protein 1	0	1.24	2.29	–	–
		COPA	Coatomer protein complex, subunit alpha isoform 1	0	1.24	2.29	–	–
		SNX3	Isoform 1 of Sorting nexin-3	0	1.41	2.29	–	–
		HBE1	Hemoglobin subunit epsilon	1.74	18.63	26.53	–	–
		CHMP4B	Charged multivesicular body protein 4b	1.49	6.88	11.63	–	–
		HBG2;HBG1;HBE1	Hemoglobin subunit gamma-2	6.83	23.07	36.48	–	–
		PDCD6IP	PDCD6IP protein	8.85	36.69	54.97	–	–
		DDOST	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase precursor	1.31	0	2.82	–	–
		NQO1	NAD	2.30	0	5.73	–	–
		RSL1D1	Ribosomal L1 domain-containing protein 1	1.31	0	2.29	–	–
		RBM3	Putative RNA-binding protein 3	1.31	0	2.29	–	–
		RFC4	Replication factor C subunit 4	1.49	0	2.82	–	–
		CIRBP	Cold-inducible RNA-binding protein	1.77	0	2.82	–	–
		SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor	1.49	0	2.29	–	–
		EIF4G2	Eukaryotic translation initiation factor 4 gamma 2	6.48	0	9.69	–	–
		DECR1	2,4-dienoyl-CoA reductase, mitochondrial precursor	2.64	1.41	5.11	–	–
		MBNL1	Isoform EXP42 of Muscleblind-like protein 1	4.83	1.41	9.96	–	–
		DNM2	Isoform 1 of Dynamin-2	5.09	1.41	9.96	–	–
		UBAP2L	Isoform 1 of Ubiquitin-associated protein 2-like	13.24	3.51	23.35	–	–
		RPS20	40S ribosomal protein S20	3.72	1.41	5.11	–	–
		MARS	Methionyl-tRNA synthetase, cytoplasmic	5.38	1.87	7.93	–	–
		CSE1L	Isoform 1 of Exportin-2	5.43	1.87	6.52	–	–
		RBM14;TMEM137	Isoform 1 of RNA-binding protein 14	10.07	4.53	12.77	–	–
		SNRPF	Small nuclear ribonucleoprotein F	1.74	0	2.29	–	–
		SLC25A5	ADP/ATP translocase 2	1.86	0	2.29	–	–
		ESD	S-formylglutathione hydrolase	2.36	0	2.29	–	–
		KIF2C	Kinesin family member 2C	2.65	0	2.82	–	–
		PABPC4	Isoform 1 of Polyadenylate-binding protein 4	6.59	0	6.88	–	–
		IGF2BP1	Insulin-like growth factor 2 mRNA-binding protein 1	12.10	1.41	13.13	–	–
		CIP29	Nuclear protein Hcc-1	3.25	0	2.82	–	–
		H2AFY	H2A histone family, member Y isoform 2	3.07	0	2.82	–	–
		TCERG1	Isoform 1 of Transcription elongation regulator 1	7.64	0	6.88	–	–
		HNRPAB	Isoform 2 of Heterogeneous nuclear ribonucleoprotein A/B	6.02	0	4.58	–	–
		RAVER1	RAVER1	15.72	3.28	13.92	–	–
		CLTA	Isoform Non-brain of Clathrin light chain A	3.35	5.00	8.02	–	–
		RPS27	40S ribosomal protein S27	2.61	3.97	5.73	–	–
		PHB2	Prohibitin-2	5.52	8.50	11.37	–	–
		PABPC1	Isoform 1 of Polyadenylate-binding protein 1	14.00	21.93	28.89	–	–
		GRB2	Isoform 1 of Growth factor receptor-bound protein 2	6.81	12.86	16.48	–	–
		LMNB1	Lamin-B1	1.77	1.87	2.82	–	–
		FUBP3	Isoform 1 of Far upstream element-binding protein 3	8.11	9.05	13.40	–	–
		EWSR1	CDNA FLJ32119 fis, clone PEBLM1000034, highly similar to RNA-BINDING PROTEIN EWS	1.74	2.11	3.44	–	–
		HSPB1	Heat shock protein beta-1	13.21	14.51	25.02	–	–
		MCM5	DNA replication licensing factor MCM5	5.05	7.01	9.07	–	–
		BUB3	Mitotic checkpoint protein BUB3	12.32	15.21	20.53	–	–
		MCM7	Isoform 1 of DNA replication licensing factor MCM7	6.93	8.43	10.48	–	–
		GNB2L1	Lung cancer oncogene 7	19.05	21.86	28.63	–	–
		HNRPM	Isoform 1 of Heterogeneous nuclear ribonucleoprotein M	75.71	87.77	118.74	–	–
		RPS15A	40S ribosomal protein S15a	2.61	5.84	5.73	–	–
		PRPF8	Pre-mRNA-processing-splicing factor 8	4.10	8.88	8.55	–	–
		RPL9	60S ribosomal protein L9	2.73	4.53	5.11	–	–
		RPS4X	40S ribosomal protein S4, X isoform	8.57	14.35	16.21	–	–
		–	Serum albumin precursor	288.73	462.51	491.37	–	–
		IARS	Isoleucyl-tRNA synthetase, cytoplasmic	6.25	10.92	10.75	–	–
		HIST1H1D	Histone H1.3	16.42	29.17	26.43	–	–
		PRKDC	Isoform 1 of DNA-dependent protein kinase catalytic subunit	43.44	72.50	68.19	–	–
		RPL26	60S ribosomal protein L26	5.23	4.53	5.11	–	–
		TIAL1	TIA-1 related protein isoform 2	5.26	4.59	5.11	–	–
		RPS12	Ribosomal protein S12	5.96	5.38	5.73	–	–
		HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0	6.87	6.09	6.52	–	–
		RPL10	60S ribosomal protein L10	4.65	3.73	4.23	–	–
		EEF1A1	Elongation factor 1-alpha 1	74.23	58.84	69.08	–	–
		C1orf57	Probable UPF0334 kinase-like protein C1orf57	6.95	5.70	6.88	–	–
		NUDT21	Cleavage and polyadenylation specificity factor subunit 5	12.56	10.46	12.51	–	–
		ACTB	Actin, cytoplasmic 1	136.56	111.28	131.01	–	–
		RPL7A	60S ribosomal protein L7a	15.70	12.65	12.51	–	–
		RPS3	40S ribosomal protein S3	27.71	23.70	23.35	–	–
		HSP90AB1	Heat shock protein HSP 90-beta	105.38	95.86	91.26	–	–
		ACTR2	Actin-related protein 2	2.76	2.19	2.82	–	–
		PRDX2	Peroxiredoxin-2	10.11	7.94	10.31	–	–
		FUBP1	Isoform 1 of Far upstream element-binding protein 1	13.57	10.61	14.18	–	–
		–	Trypsin - Sus scrofa (Pig).	103.22	82.19	108.19	–	–
		EIF4A3	Eukaryotic initiation factor 4A-III	4.14	3.11	4.23	–	–
		HNRPH3	Isoform 1 of Heterogeneous nuclear ribonucleoprotein H3	35.47	27.01	37.01	–	–
		HNRNPA2B1	Isoform B1 of Heterogeneous nuclear ribonucleoproteins A2/B1	61.20	46.97	64.76	–	–
		APRT	Adenine phosphoribosyltransferase	5.03	4.84	5.73	–	–
		FASN	Fatty acid synthase	58.53	54.92	67.14	–	–
		PARP1	Poly [ADP-ribose] polymerase 1	21.27	18.96	23.78	–	–
		ATAD3A	ATPase family, AAA domain containing 3A	6.15	8.74	8.45	–	–
		EPRS	Glutamyl-prolyl tRNA synthetase	11.98	18.64	18.41	–	–
		RPL30	60S ribosomal protein L30	6.63	8.73	9.96	–	–
		RPS14	40S ribosomal protein S14	9.61	12.94	14.80	–	–
		LMNA	Isoform A of Lamin-A/C	13.79	17.63	20.08	–	–
		RAN	GTP-binding nuclear protein Ran	8.35	9.67	11.10	–	–
		RPL11	Isoform 1 of 60S ribosomal protein L11	8.57	10.13	10.48	–	–
		YARS	Tyrosyl-tRNA synthetase, cytoplasmic	4.38	5.47	4.23	–	–
		KRT19	Keratin, type I cytoskeletal 19	12.79	14.75	13.04	–	–
		SFPQ	Isoform Long of Splicing factor, proline- and glutamine-rich	14.23	13.89	13.04	–	–
		HNRNPC	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	25.61	24.81	24.93	–	–
		HIST1H2AD	Histone H2A type 1-D	53.31	53.20	51.98	–	–
		HSPA8	Isoform 1 of Heat shock cognate 71 kDa protein	49.48	53.53	55.23	–	–
		RPS27A;UBB;UBC	Ubiquitin and ribosomal protein S27a precursor	69.62	68.36	74.97	–	–
		CAPNS1	Calpain small subunit 1	3.66	1.41	3.44	–	–
		SNRPD1	Small nuclear ribonucleoprotein Sm D1	3.05	1.24	2.29	–	–
		DARS	Aspartyl-tRNA synthetase, cytoplasmic	5.29	1.87	4.23	–	–
		NONO	Non-POU domain-containing octamer-binding protein	7.58	2.49	5.64	–	–
		VAMP8	Vesicle-associated membrane protein 8	2.18	1.41	2.29	–	–
		TUBB	Tubulin beta chain	158.67	99.70	158.95	–	–
		RPL3	60S ribosomal protein L3	4.14	2.19	4.23	–	–
		RPS5	40S ribosomal protein S5	11.38	6.09	11.63	–	–
		EIF3D	Eukaryotic translation initiation factor 3 subunit 7	3.64	2.19	4.23	–	–
		DHX9	146 kDa protein	41.88	24.97	45.63	–	–
		DAZAP1	Isoform 1 of DAZ-associated protein 1	12.27	6.63	10.22	–	–
		VCP	Transitional endoplasmic reticulum ATPase	12.22	6.40	9.07	–	–
		LARS	Leucyl-tRNA synthetase, cytoplasmic	13.06	7.01	10.22	–	–
		PTBP1	Isoform 1 of Polypyrimidine tract-binding protein 1	25.61	12.87	19.65	–	–
		EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	8.27	5.15	6.52	–	–
		RPL13	60S ribosomal protein L13	10.93	6.72	9.07	–	–
		DDX3X	ATP-dependent RNA helicase DDX3X	28.25	19.74	22.73	–	–
		RPS6	40S ribosomal protein S6	11.36	7.81	10.22	–	–
		LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial precursor	16.96	12.00	15.59	–	–
		HNRNPA1	Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	36.32	22.94	32.59	–	–
		LOC646195;RPS28;LC	40S ribosomal protein S28	2.18	1.41	3.44	–	–
		DDX17	DEAD box polypeptide 17 isoform 1	22.22	12.48	32.43	–	–
		RBM4	Isoform 1 of RNA-binding protein 4	7.81	6.55	16.74	–	–
		HIST2H3A;HIST2H3C	Histone H3.2	7.88	7.08	15.59	–	–
		SNRPD2	Small nuclear ribonucleoprotein Sm D2	7.32	6.08	12.51	–	–
		PCBP2	Poly(rC)-binding protein 2	10.55	8.59	17.88	–	–
		DDX5	Probable ATP-dependent RNA helicase DDX5	37.71	29.74	62.30	–	–
		G3BP1	Ras GTPase-activating protein-binding protein 1	6.15	4.53	7.93	–	–
		HNRNPR	Heterogeneous nuclear ribonucleoprotein R	12.97	9.67	17.26	–	–
		PCBP1	Poly(rC)-binding protein 1	14.56	9.69	16.48	–	–
		HSPA9	Stress-70 protein, mitochondrial precursor	16.81	12.56	20.18	–	–
		EIF3A	Eukaryotic translation initiation factor 3 subunit 10	5.92	5.62	8.45	–	–
		HNRPD	Isoform 1 of Heterogeneous nuclear ribonucleoprotein D0	12.25	11.39	18.15	–	–
		EEF1G	Elongation factor 1-gamma	12.84	11.47	19.29	–	–
		HNRNPL	Heterogeneous nuclear ribonucleoprotein L isoform a	16.10	13.97	24.67	–	–
		PPIA;LOC654188;PPIA	Peptidyl-prolyl cis-trans isomerase A	18.06	15.13	25.64	–	–

[a]Proteins enriched by at least 2.0-fold over the VCAM-1(D40A) control sample (see table S2) were regarded as specific. Proteins not enriched in a specific adhesion complex are indicated by a dash (–).

Table S2. Specifically enriched proteins identified in FN and VCAM-1 affinity purifications.

			Fold enrichment over VCAM-1(D40A)[b]		Specific enrichment?[c]		Hops from β, integrin[d]	
Gene symbol	Protein name	Accession number(s)[a]	FN	VCAM-1	FN	VCAM-1	FN	VCAM-1
AARS	Alanyl-tRNA synthetase, cytoplasmic	IPI00027442,IPI00784131	ND	ND	Yes	Yes	4	7
ACTN4	Alpha-actinin-4	IPI00013808	3.01	2.24	Yes	Yes	1	1
ALDOA	Fructose-bisphosphate aldolase A	IPI00465439	ND	ND	Yes	Yes	2	NC
ANP32B	Isoform 1 of Acidic leucine-rich nuclear phosphoprotein 32 family member B	IPI00007423,IPI00759824	ND	ND	Yes	Yes	4	NC
ANXA2	Annexin A2 isoform 1	IPI00418169,IPI00455315	ND	ND	Yes	Yes	3	5
AP2B1	Isoform 1 of AP-2 complex subunit beta-1	IPI00220991,IPI00333383,IPI00784156,	12.71	6.18	Yes	Yes	5	NC
AP2M1	AP-2 complex subunit mu-1	IPI00022256,IPI00619900	5.87	3.04	Yes	Yes	5	NC
ARPC3	Actin-related protein 2/3 complex subunit 3 (Arp2/3, subunit 4)	IPI00005162	ND	ND	Yes	Yes	3	NC
ATP5A1	ATP synthase subunit alpha, mitochondrial precursor	IPI00440493	ND	ND	Yes	Yes	2	2
ATP5C1	Isoform Liver of ATP synthase gamma chain, mitochondrial precursor	IPI00478410	ND	ND	Yes	Yes	3	3
CACYBP	Isoform 1 of Calcyclin-binding protein	IPI00395627,IPI00552308	ND	ND	Yes	Yes	3	5
CAPZA1	F-actin-capping protein subunit alpha-1	IPI00005969	ND	ND	Yes	Yes	NC	NC
CAPZB	Isoform 1 of F-actin-capping protein subunit beta	IPI00026185,IPI00218782,IPI00642256	1.95	3.16	Yes	Yes	NC	NC
CCT5	T-complex protein 1 subunit epsilon	IPI00010720	3.32	2.35	Yes	Yes	NC	NC
CORO1C	Coronin-1C	IPI00008453,IPI00867509,IPI00867575	ND	ND	Yes	Yes	NC	NC
DDX6	Probable ATP-dependent RNA helicase DDX6	IPI00030320	ND	ND	Yes	Yes	4	NC
DHX15	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	IPI00396435	ND	ND	Yes	Yes	2	2
DIMT1L	Probable dimethyladenosine transferase	IPI00004459	ND	ND	Yes	Yes	NC	NC
EEF1B2	Elongation factor 1-beta	IPI00178440,IPI00414723	ND	ND	Yes	Yes	3	6
EIF3B	Isoform 1 of Eukaryotic translation initiation factor 3 subunit 9	IPI00396370,IPI00719752,IPI00747447	ND	ND	Yes	Yes	4	6
EIF4A1	Eukaryotic initiation factor 4A-I	IPI00025491	3.34	3.21	Yes	Yes	4	6
ENO1	Isoform alpha-enolase of Alpha-enolase	IPI00465248	ND	ND	Yes	Yes	4	NC
EPN1	Isoform 1 of Epsin-1	IPI00002495,IPI00027082,IPI00397365,	ND	ND	Yes	Yes	3	7
EPS15	Epidermal growth factor receptor substrate 15	IPI00292134,IPI00385325	ND	ND	Yes	Yes	4	6
FARSB	Phenylalanyl-tRNA synthetase beta chain	IPI00300074	ND	ND	Yes	Yes	×	×
FLJ12529	Isoform 1 of Cleavage and polyadenylation specificity factor subunit 7	IPI00550821,IPI00719106	ND	ND	Yes	Yes	NC	NC
FLNB	Isoform 1 of Filamin-B	IPI00289334,IPI00382696,IPI00477536,	ND	ND	Yes	Yes	1	1
FSCN1	Fascin	IPI00163187,IPI00747810	ND	ND	Yes	Yes	NC	5
GLRX3	Glutaredoxin-3	IPI00008552	ND	ND	Yes	Yes	NC	NC
GMPS	GMP synthase	IPI00029079	ND	ND	Yes	Yes	4	NC
GTPBP4	Nucleolar GTP-binding protein 1	IPI00385042,IPI00736402	ND	ND	Yes	Yes	3	5
HIST1H1B	Histone H1.5	IPI00217468	ND	ND	Yes	Yes	NC	NC
HIST1H2BJ	Histone H2B type 1-J	IPI00515061	ND	ND	Yes	Yes	NC	NC
HNRPF	Heterogeneous nuclear ribonucleoprotein F	IPI00003881	ND	ND	Yes	Yes	3	8
HSPA1B;HSPA1A	Heat shock 70 kDa protein 1	IPI00304925,IPI00845339,IPI00847536	2.17	2.19	Yes	Yes	2	2
ILF3	Isoform 1 of Interleukin enhancer-binding factor 3	IPI00219330,IPI00298788,IPI00298789,	ND	ND	Yes	Yes	4	NC
IQGAP1	Ras GTPase-activating-like protein IQGAP1	IPI00009342	10.32	3.10	Yes	Yes	3	NC
ITGA4	Integrin alpha-4 precursor (α_4 integrin)	IPI00009803	ND	ND	Yes	Yes	1	1
ITGB1	integrin beta 1 isoform 1A precursor (β_1 integrin)	IPI00645194	ND	ND	Yes	Yes	0	0
KPNA2	Importin subunit alpha-2	IPI00002214	ND	ND	Yes	Yes	4	7
KPNB1	Importin subunit beta-1	IPI00001639	3.73	2.77	Yes	Yes	4	7
KRT1	Keratin, type II cytoskeletal 1	IPI00220327	3.84	2.79	Yes	Yes	4	NC
KRT10	Keratin, type I cytoskeletal 10	IPI00009865	ND	ND	Yes	Yes	NC	NC
KRT18	Keratin, type I cytoskeletal 18	IPI00554788,IPI00784347	ND	ND	Yes	Yes	2	2
LDHB	L-lactate dehydrogenase B chain	IPI00219217	ND	ND	Yes	Yes	6	NC
LGALS1	Galectin-1	IPI00219219	ND	ND	Yes	Yes	1	1
LYG5B;CSNK2B	Casein kinase II subunit beta	IPI00010865,IPI00640088	ND	ND	Yes	Yes	3	7
MACF1	Isoform 1 of Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (ACF7)	IPI00256861,IPI00513991,IPI00550385,	ND	ND	Yes	Yes	NC	NC
MAPRE1	Microtubule-associated protein RP/EB family member 1 (EB1)	IPI00017596	ND	ND	Yes	Yes	4	NC
MCM2	DNA replication licensing factor MCM2	IPI00184330	ND	ND	Yes	Yes	4	NC
MCM3	DNA replication licensing factor MCM3	IPI00013214	ND	ND	Yes	Yes	3	NC
MCM6	DNA replication licensing factor MCM6	IPI00031517	ND	ND	Yes	Yes	4	NC
MDH2	Malate dehydrogenase, mitochondrial precursor	IPI00291006	ND	ND	Yes	Yes	NC	NC
MLLT4	Isoform 4 of Afadin	IPI00023461,IPI00759546	ND	ND	Yes	Yes	2	2
MRLC2	Myosin regulatory light chain	IPI00033494,IPI00220573,IPI00604523	ND	ND	Yes	Yes	NC	NC
MRPS23	Mitochondrial ribosomal protein S23	IPI00032881	ND	ND	Yes	Yes	NC	NC
MSN	Moesin	IPI00219365	ND	ND	Yes	Yes	6	NC
MYH10	Isoform 1 of Myosin-10 (Myosin IIB)	IPI00397526,IPI00479307,IPI00790503	ND	ND	Yes	Yes	4	NC
MYH9	Myosin-9 (Myosin IIA)	IPI00019502	ND	ND	Yes	Yes	4	NC
MYL4	Myosin light polypeptide 4	IPI00384992,IPI00798256	ND	ND	Yes	Yes	4	NC
MYL6	Isoform Non-muscle of Myosin light polypeptide 6	IPI00335168,IPI00744444,IPI00789605,	ND	ND	Yes	Yes	NC	5
NAPA	Alpha-soluble NSF attachment protein	IPI00009253	ND	ND	Yes	Yes	5	NC
NARG1	Isoform 1 of NMDA receptor-regulated protein 1	IPI00032158,IPI00386189	ND	ND	Yes	Yes	4	NC
NDUFS3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor	IPI00025796	ND	ND	Yes	Yes	×	×
NHP2L1	NHP2-like protein 1	IPI00026167	ND	ND	Yes	Yes	3	8
NPM1	Isoform 1 of Nucleophosmin	IPI00220740,IPI00549248	5.68	2.93	Yes	Yes	4	3
NUP205	Nuclear pore complex protein Nup205	IPI00472675,IPI00783781	ND	ND	Yes	Yes	2	NC
PDCD10	Programmed cell death protein 10	IPI00298558	ND	ND	Yes	Yes	NC	NC
PHB	Prohibitin	IPI00017334,IPI00791634	2.16	2.00	Yes	Yes	4	5
PI4KA	Isoform 1 of Phosphatidylinositol 4-kinase alpha	IPI00070943	ND	ND	Yes	Yes	NC	NC
PPP2CA	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	IPI00008380	ND	ND	Yes	Yes	1	1
PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	IPI00554737	ND	ND	Yes	Yes	NC	5
PRDX3	Peroxiredoxin 3 isoform b	IPI00024919,IPI00374151	ND	ND	Yes	Yes	NC	NC
PRMT5	Protein arginine N-methyltransferase 5	IPI00441473	ND	ND	Yes	Yes	3	NC
PSMA5	Proteasome subunit alpha type-5	IPI00291922	ND	ND	Yes	Yes	3	6
PSMA6	Proteasome subunit alpha type-6	IPI00029623	ND	ND	Yes	Yes	3	6
PSMB1	Proteasome subunit beta type-1 precursor	IPI00025019	ND	ND	Yes	Yes	2	5
PSMB2	Proteasome subunit beta type-2	IPI00028006	ND	ND	Yes	Yes	3	6
PSMD11	Proteasome 26S non-ATPase subunit 11 variant (Fragment)	IPI00105598	ND	ND	Yes	Yes	3	6
RAB5C	Ras-related protein Rab-5C	IPI00016339	ND	ND	Yes	Yes	4	NC
RAC1	Isoform A of Ras-related C3 botulinum toxin substrate 1 precursor (Rac1)	IPI00010271,IPI00219675	ND	ND	Yes	Yes	2	NC
RALY	Isoform 1 of RNA-binding protein Raly	IPI00011268,IPI00216044,IPI00642213,	ND	ND	Yes	Yes	NC	NC
RANBP5	RAN binding protein 5	IPI00329010,IPI00793443	ND	ND	Yes	Yes	4	7
RAP1B	Ras-related protein Rap-1b precursor (Rap1b)	IPI00015148	ND	ND	Yes	Yes	NC	NC
RAP2B	Ras-related protein Rap-2b precursor (Rap2b)	IPI00018364	ND	ND	Yes	Yes	NC	NC
RCC1	Regulator of chromosome condensation 1 isoform a	IPI00001661,IPI00747309,IPI00787306	ND	ND	Yes	Yes	5	5
RPL10A	60S ribosomal protein L10a	IPI00412579,IPI00827508	ND	ND	Yes	Yes	3	6
RPL13A	60S ribosomal protein L13a	IPI00304612,IPI00398964	ND	ND	Yes	Yes	3	6
RPL14	60S ribosomal protein L14	IPI00002821,IPI00069693,IPI00555744,	2.57	3.44	Yes	Yes	3	6
RPL21;LOC729402;L	60S ribosomal protein L21	IPI00247583	ND	ND	Yes	Yes	3	6
RPL24	60S ribosomal protein L24	IPI00306332	2.35	2.73	Yes	Yes	3	6
RPL27A	60S ribosomal protein L27a	IPI00398135,IPI00456758,IPI00827619	ND	ND	Yes	Yes	3	6
RPL35	60S ribosomal protein L35	IPI00412607	ND	ND	Yes	Yes	3	6
RPL36	60S ribosomal protein L36	IPI00216237	ND	ND	Yes	Yes	3	6
RPL4	60S ribosomal protein L4	IPI00003918	2.79	2.47	Yes	Yes	3	6
RPL5	60S ribosomal protein L5	IPI00000494	2.63	3.38	Yes	Yes	3	6
RPL8	60S ribosomal protein L8	IPI00012772,IPI00797230	ND	ND	Yes	Yes	3	6
RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor	IPI00025874	ND	ND	Yes	Yes	3	NC
RPS16	40S ribosomal protein S16	IPI00227492	2.41	2.55	Yes	Yes	3	5
RPS17	40S ribosomal protein S17	IPI00221093	ND	ND	Yes	Yes	3	6
RPS24	Isoform 1 of 40S ribosomal protein S24	IPI00029750,IPI00219486,IPI00847986	ND	ND	Yes	Yes	3	6
RPS25	40S ribosomal protein S25	IPI00012750,IPI00401105,IPI00478694	ND	ND	Yes	Yes	3	6
RPS7	40S ribosomal protein S7	IPI00013415	ND	ND	Yes	Yes	3	6
RUVBL2	RuvB-like 2	IPI00029104	ND	ND	Yes	Yes	4	NC
SCRIB	Isoform 1 of Protein LAP4	IPI00410666,IPI00425560,IPI00425562,	ND	ND	Yes	Yes	NC	NC
SF3B14	Pre-mRNA branch site protein p14	IPI00032827	ND	ND	Yes	Yes	3	9
SNRP70	Isoform 1 of U1 small nuclear ribonucleoprotein 70 kDa	IPI00219483,IPI00290204	ND	ND	Yes	Yes	3	8
SRI	Sorcin	IPI00027175,IPI00414264	ND	ND	Yes	Yes	NC	NC
STIP1	Stress-induced-phosphoprotein 1	IPI00013896	ND	ND	Yes	Yes	3	3
STON2	Isoform 1 of Stonin-2	IPI00103521,IPI00337705	ND	ND	Yes	Yes	5	7
TARS	Threonyl-tRNA synthetase, cytoplasmic	IPI00329633	ND	ND	Yes	Yes	3	NC
TFRC	Transferrin receptor protein 1	IPI00022462	2.70	2.11	Yes	Yes	NC	NC
THOC4	THO complex subunit 4	IPI00328840	ND	ND	Yes	Yes	3	7
TIA1	TIA1 protein	IPI00743479	ND	ND	Yes	Yes	NC	NC
TLN1	Talin-1	IPI00784273	19.64	7.93	Yes	Yes	1	1
UBE2N	Ubiquitin-conjugating enzyme E2 N	IPI00003949,IPI00376844	ND	ND	Yes	Yes	NC	NC
URP2	Isoform 2 of Unc-112-related protein 2 (Kindlin-3)	IPI00216699,IPI00397834	8.88	4.93	Yes	Yes	1	1
VAPA	Vesicle-associated membrane protein-associated protein A	IPI00170692,IPI00374657	2.81	2.45	Yes	Yes	NC	NC
VASP	Vasodilator-stimulated phosphoprotein (VASP)	IPI00301058	ND	ND	Yes	Yes	2	2
VCL	Isoform 1 of Vinculin	IPI00291175,IPI00307162	ND	ND	Yes	Yes	2	2
XPO1	Exportin-1	IPI00298961,IPI00784388	ND	ND	Yes	Yes	4	4
YTHDF2	Isoform 1 of YTH domain family protein 2	IPI00306043	ND	ND	Yes	Yes	×	×
YWHAB	Isoform Long of 14-3-3 protein beta/alpha	IPI00216318,IPI00759832	ND	ND	Yes	Yes	1	1
ZYX	Zyxin	IPI00020513	ND	ND	Yes	Yes	2	2

Table S2, continued.

			Fold enrichment over VCAM-1(D40A)[b]		Specific enrichment?[c]		Hops from β, integrin[d]	
Gene symbol	Protein name	Accession number(s)[a]	FN	VCAM-1	FN	VCAM-1	FN	VCAM-1
ABCF1	Isoform 1 of ATP-binding cassette sub-family F member 1	IPI00013495,IPI00792186	ND	0	Yes	−	NC	−
ACACA	Isoform 1 of Acetyl-CoA carboxylase 1	IPI00011569,IPI00396015,IPI00396018,	ND	0	Yes	−	2	−
ACLY	ATP-citrate synthase	IPI00021290,IPI00394838	ND	0	Yes	−	3	−
ACTR3	Actin-related protein 3 (Arp3)	IPI00028091	ND	0	Yes	−	4	−
AHNAK	AHNAK nucleoprotein isoform 1	IPI00021812	ND	0	Yes	−	NC	−
AKR1C1	Aldo-keto reductase family 1 member C1	IPI00029733	ND	0	Yes	−	NC	−
ALDH1B1	Aldehyde dehydrogenase X, mitochondrial precursor	IPI00103467	ND	0	Yes	−	×	−
ANKRD25	Isoform 1 of Ankyrin repeat domain-containing protein 25	IPI00470559,IPI00760928,IPI00760962	ND	0	Yes	−	×	−
ANXA1	Annexin A1	IPI00218918	3.37	1.89	Yes	−	2	−
AP2A1	Adaptor-related protein complex 2, alpha 1 subunit isoform 2	IPI00793223	2.11	1.87	Yes	−	4	−
AP2A2	AP-2 complex subunit alpha-2	IPI00016621	ND	0	Yes	−	4	−
APOBEC3C;APOBEC	Probable DNA dC->dU-editing enzyme APOBEC-3C	IPI00555878	ND	0	Yes	−	NC	−
APOLD1;DDX47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 2	IPI00023972,IPI00397372	ND	0	Yes	−	×	−
ARF6	ADP-ribosylation factor 6 (Arf6)	IPI00215920	ND	0	Yes	−	2	−
ARHGEF1	ARHGEF1 protein (p115RhoGEF)	IPI00339379,IPI00395605,IPI00433169,	ND	0	Yes	−	3	−
ARL2;SNX15	ADP-ribosylation factor-like protein 2 (Arf-like protein 2)	IPI00003326	ND	0	Yes	−	NC	−
ARPC4	Actin-related protein 2/3 complex subunit 4 (Arp2/3, subunit 4)	IPI00554811,IPI00744414	ND	0	Yes	−	4	−
ATP5B	ATP synthase subunit beta, mitochondrial precursor	IPI00303476	8.38	1.22	Yes	−	3	−
ATP6V1B2	Vacuolar ATP synthase subunit B, brain isoform	IPI00007812,IPI00848320	ND	0	Yes	−	×	−
BAG2	BAG family molecular chaperone regulator 2	IPI00000643	ND	0	Yes	−	3	−
BAT3	Isoform 1 of Large proline-rich protein BAT3	IPI00465123,IPI00513728,IPI00640922,	ND	0	Yes	−	4	−
BMP2K	Isoform 1 of BMP-2-inducible protein kinase	IPI00337426	ND	0	Yes	−	NC	−
BZW2	Basic leucine zipper and W2 domain-containing protein 2	IPI00022305	ND	0	Yes	−	NC	−
C14orf166	Protein C14orf166	IPI00006980,IPI00792100	ND	0	Yes	−	NC	−
C1orf58	BRO1 domain-containing protein BROX	IPI00065500	ND	0	Yes	−	×	−
C1QBP	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor	IPI00014230	ND	0	Yes	−	2	−
C22orf28	UPF0027 protein C22orf28	IPI00550689	ND	0	Yes	−	NC	−
CAND1	Isoform 1 of Cullin-associated NEDD8-dissociated protein 1	IPI00100160,IPI00746694	ND	0	Yes	−	NC	−
CAP1	Adenylyl cyclase-associated protein 1	IPI00008274	ND	0	Yes	−	NC	−
CBX3;LOC653972	Chromobox protein homolog 3	IPI00297579	ND	0	Yes	−	NC	−
CCT2	T-complex protein 1 subunit beta	IPI00297779	3.35	1.26	Yes	−	3	−
CCT4	T-complex protein 1 subunit delta	IPI00302927	2.38	0.83	Yes	−	NC	−
CFL1	Cofilin-1	IPI00012011	2.00	1.25	Yes	−	2	−
CKAP5	Cytoskeleton-associated protein 5	IPI00028275,IPI00472887	ND	0	Yes	−	NC	−
CLIC2	Chloride intracellular channel protein 2	IPI00221328,IPI00514835	ND	0	Yes	−	NC	−
CLIC5	Isoform 1 of Chloride intracellular channel protein 5	IPI00027193,IPI00165936,IPI00294443,	ND	0	Yes	−	4	−
CLNS1A	Methylosome subunit pICln	IPI00004795	ND	0	Yes	−	4	−
CLTB	Isoform Non-brain of Clathrin light chain B	IPI00014589,IPI00216472	ND	0	Yes	−	3	−
CLTC	Isoform 1 of Clathrin heavy chain 1	IPI00024067,IPI00455383	2.28	1.61	Yes	−	2	−
CNN2	Calponin-2	IPI00015262	ND	0	Yes	−	NC	−
CNOT1	CCR4-NOT transcription complex, subunit 1 isoform a	IPI00186010	ND	0	Yes	−	NC	−
COMT	Isoform Membrane-bound of Catechol O-methyltransferase	IPI00011284,IPI00375513	ND	0	Yes	−	NC	−
COPB1	Coatomer subunit beta	IPI00295851	ND	0	Yes	−	3	−
COPE	Epsilon subunit of coatomer protein complex isoform c	IPI00399319,IPI00465132	ND	0	Yes	−	3	−
COPG	Coatomer subunit gamma	IPI00001890,IPI00783982	ND	0	Yes	−	2	−
CORO1B;PTPRCAP	Coronin-1B	IPI00007058	ND	0	Yes	−	NC	−
CPNE1	Copine-1	IPI00018452,IPI00852917	ND	0	Yes	−	4	−
CPSF6	Isoform 1 of Cleavage and polyadenylation specificity factor subunit 6	IPI00012998,IPI00030654,IPI00647126	ND	0	Yes	−	NC	−
CSNK2A1	Casein kinase II subunit alpha	IPI00016613,IPI00741317,IPI00744507,	ND	0	Yes	−	2	−
CUGBP2	CUG triplet repeat, RNA binding protein 2 isoform 2	IPI00410277,IPI00607544,IPI00845479,	ND	0	Yes	−	NC	−
DAB2	Isoform 1 of Disabled homolog 2 (Disabled-2)	IPI00179438,IPI00783245	ND	0	Yes	−	4	−
DBN1	Isoform 1 of Drebrin	IPI00003406,IPI00295624,IPI00794221	ND	0	Yes	−	5	−
DDX1	ATP-dependent RNA helicase DDX1	IPI00293655	3.51	1.23	Yes	−	4	−
DDX18	ATP-dependent RNA helicase DDX18	IPI00301323	ND	0	Yes	−	NC	−
DHX30	Isoform 1 of Putative ATP-dependent RNA helicase DHX30	IPI00411733,IPI00477295	ND	0	Yes	−	NC	−
DIAPH1	Diaphanous 1	IPI00030876,IPI00783474	3.54	1.91	Yes	−	3	−
DKFZp686D0972	Hypothetical protein LOC345651	IPI00003269	ND	0	Yes	−	×	−
DLD	Dihydrolipoyl dehydrogenase, mitochondrial precursor	IPI00015911	ND	0	Yes	−	6	−
DNAJB1	DnaJ homolog subfamily B member 1	IPI00015947	ND	0	Yes	−	3	−
DSCR2	Isoform 1 of Down syndrome critical region protein 2	IPI00030770,IPI00401072	ND	0	Yes	−	×	−
EEF2	Elongation factor 2	IPI00186290	3.02	1.70	Yes	−	2	−
EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component	IPI00003519	3.55	0.63	Yes	−	2	−
EIF2S3	Eukaryotic translation initiation factor 2 subunit 3	IPI00297982	ND	0	Yes	−	4	−
EIF3F	Eukaryotic translation initiation factor 3 subunit 5	IPI00654777	ND	0	Yes	−	4	−
EIF3K	Eukaryotic translation initiation factor 3 subunit 12	IPI00033143	ND	0	Yes	−	4	−
EIF4H;LOC653994	Isoform Short of Eukaryotic translation initiation factor 4H	IPI00014263,IPI00220894	ND	0	Yes	−	4	−
EIF5	Eukaryotic translation initiation factor 5	IPI00022648	ND	0	Yes	−	4	−
EIF5B	Eukaryotic translation initiation factor 5B	IPI00299254	ND	0	Yes	−	4	−
ELAVL1	ELAV-like protein 1	IPI00301936	2.12	1.58	Yes	−	3	−
EMG1	Probable ribosome biogenesis protein NEP1	IPI00025347	ND	0	Yes	−	NC	−
EPB41	Isoform 1 of Protein 4.1	IPI00003921,IPI00218697,IPI00218698,	ND	0	Yes	−	3	−
ERLIN2	Isoform 1 of Erlin-2 precursor	IPI00026942	ND	0	Yes	−	×	−
FAM62A	Isoform 1 of Protein FAM62A	IPI00022133,IPI00746655	6.81	1.57	Yes	−	NC	−
FAM62B	Isoform 2 of Protein FAM62B	IPI00409635	ND	0	Yes	−	×	−
FAU	40S ribosomal protein S30	IPI00019770,IPI00397098	ND	0	Yes	−	3	−
FDFT1	Squalene synthetase	IPI00020944	ND	0	Yes	−	5	−
FEN1	Flap endonuclease 1	IPI00026215	ND	0	Yes	−	5	−
FLNA	Filamin-A	IPI00302592,IPI00333541	2.07	1.74	Yes	−	1	−
FLOT1	Flotillin-1	IPI00027438	ND	0	Yes	−	NC	−
FLOT2	Flotillin 2	IPI00789008,IPI00795979	ND	0	Yes	−	NC	−
FUS	Isoform Short of RNA-binding protein FUS	IPI00221354,IPI00260715,IPI00428056,	2.30	0.81	Yes	−	3	−
G6PD	Isoform Short of Glucose-6-phosphate 1-dehydrogenase	IPI00216008,IPI00289800	ND	0	Yes	−	NC	−
GALE	UDP-glucose 4-epimerase	IPI00553131	ND	0	Yes	−	NC	−
GART	Isoform Long of Trifunctional purine biosynthetic protein adenosine-3	IPI00025273	3.75	0	Yes	−	3	−
GDI2	Rab GDP dissociation inhibitor beta	IPI00031461	ND	0	Yes	−	3	−
GLUD1	Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801,IPI00027146	ND	0	Yes	−	NC	−
GNAI3	Guanine nucleotide-binding protein G	IPI00220578	ND	0	Yes	−	NC	−
GSTK1	Glutathione S-transferase kappa 1	IPI00219673	ND	0	Yes	−	2	−
GSTO1	Glutathione transferase omega-1	IPI00019755,IPI00642936	ND	0	Yes	−	NC	−
GSTP1	Glutathione S-transferase P	IPI00219757	2.31	0.36	Yes	−	2	−
H2AFV	Histone H2AV	IPI00018278,IPI00218448,IPI00249267,	ND	0	Yes	−	×	−
HADHA	Trifunctional enzyme subunit alpha, mitochondrial precursor	IPI00031522	ND	0	Yes	−	4	−
HDAC1	Histone deacetylase 1	IPI00013774	ND	0	Yes	−	3	−
HIST1H2AA	Histone H2A type 1-A	IPI00045109,IPI00219037	ND	0	Yes	−	×	−
HIST1H2BK	Histone H2B type 1-K	IPI00419833,IPI00477495,IPI00816252	2.35	1.77	Yes	−	×	−
HMGA1	Isoform HMG-I of High mobility group protein HMG-I/HMG-Y	IPI00179700	ND	0	Yes	−	3	−
HMGB1	High mobility group protein B1	IPI00419258	ND	0	Yes	−	4	−
HMGB2	High mobility group protein B2	IPI00219097	ND	0	Yes	−	3	−
HNRPDL	Isoform 1 of Heterogeneous nuclear ribonucleoprotein D-like	IPI00011274,IPI00045498,IPI00845282	ND	0	Yes	−	NC	−
HNRPH2	Heterogeneous nuclear ribonucleoprotein H'	IPI00026230	ND	0	Yes	−	3	−
HNRPK	Heterogeneous nuclear ribonucleoprotein K	IPI00216049,IPI00216746,IPI00514561,	1.97	0.95	Yes	−	3	−
HSPA5	HSPA5 protein	IPI00003362	2.80	0	Yes	−	2	−
HSPG2	Basement membrane-specific heparan sulfate proteoglycan core protein precursor (Perlecan)	IPI00024284	ND	0	Yes	−	NC	−
IDI1	Isopentenyl-diphosphate delta isomerase	IPI00220124	ND	0	Yes	−	×	−
IGF2BP3	Isoform 1 of Insulin-like growth factor 2 mRNA-binding protein 3	IPI00658000,IPI00746216	ND	0	Yes	−	NC	−
IGF2R	Cation-independent mannose-6-phosphate receptor precursor	IPI00289819	ND	0	Yes	−	NC	−
ILK	Integrin-linked protein kinase (ILK)	IPI00013219	ND	0	Yes	−	1	−
IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	IPI00291510	ND	0	Yes	−	3	−
IPO4	Isoform 1 of Importin-4	IPI00156374,IPI00398009	ND	0	Yes	−	3	−
ITGA5	Integrin alpha-5 precursor (α_5 integrin)	IPI00306604	ND	0	Yes	−	1	−
ITGAV	Isoform 1 of Integrin alpha-V precursor (α_V integrin)	IPI00027505,IPI00555991	ND	0	Yes	−	1	−
JTV1	Multisynthetase complex auxiliary component p38	IPI00011916	ND	0	Yes	−	NC	−
KARS	Lysyl-tRNA synthetase	IPI00014238,IPI00307092	ND	0	Yes	−	NC	−
KIAA0368	KIAA0368 protein	IPI00157790	ND	0	Yes	−	NC	−
KIDINS220	KIDINS220 protein	IPI00384909	ND	0	Yes	−	NC	−
KRT2	Keratin, type II cytoskeletal 2 epidermal	IPI00021304	2.99	1.34	Yes	−	NC	−
KRT31	Keratin, type I cuticular Ha1	IPI00032513,IPI00796364	ND	0	Yes	−	3	−
KRT5	Keratin, type II cytoskeletal 5	IPI00009867	ND	0	Yes	−	3	−
KRT81	Keratin, hair, basic, 1	IPI00182655,IPI00182655,IPI00760863	ND	0	Yes	−	NC	−
LASP1	Isoform 1 of LIM and SH3 domain protein 1 (LASP1)	IPI00000861	ND	0	Yes	−	3	−
LCP1	Plastin-2	IPI00010471	ND	0	Yes	−	NC	−
LDHA	Isoform 1 of L-lactate dehydrogenase A chain	IPI00217966	2.75	1.23	Yes	−	6	−
LOC442497;SLC3A2	Solute carrier family 3 (activators of dibasic and neutral a.a. transport), member 2 isoform a (CD98hc)	IPI00027493,IPI00554481,IPI00554611,	ND	0	Yes	−	1	−
LRBA	Lipopolysaccharide-responsive and beige-like anchor protein	IPI00022555,IPI00477088	ND	0	Yes	−	NC	−
LRRC59	Leucine-rich repeat-containing protein 59	IPI00396321	ND	0	Yes	−	4	−
LSM12	Isoform 1 of Protein LSM12 homolog	IPI00410324,IPI00867714	ND	0	Yes	−	NC	−
MAP4	Isoform 1 of Microtubule-associated protein 4	IPI00220113,IPI00333281,IPI00396171,	ND	0	Yes	−	NC	−
MDN1	Midasin	IPI00167941	ND	0	Yes	−	NC	−
MPP1	55 kDa erythrocyte membrane protein	IPI00215610	ND	0	Yes	−	4	−
MRPL13	39S ribosomal protein L13, mitochondrial	IPI00022403	ND	0	Yes	−	NC	−
MRPS28	Mitochondrial 28S ribosomal protein S28	IPI00022276,IPI00791486,IPI00795922	ND	0	Yes	−	×	−
MRPS34	Mitochondrial 28S ribosomal protein S34	IPI00169413,IPI00658155,IPI00845406	ND	0	Yes	−	NC	−
MRPS6;SLC5A3	Mitochondrial 28S ribosomal protein S6	IPI00305668	ND	0	Yes	−	NC	−
MRTO4	mRNA turnover protein 4 homolog	IPI00106491	ND	0	Yes	−	NC	−
MT-CO2	Cytochrome c oxidase subunit 2	IPI00017510	ND	0	Yes	−	NC	−
NACA	Nascent polypeptide-associated complex subunit alpha	IPI00023748,IPI00797126	ND	0	Yes	−	NC	−
NAPG	Gamma-soluble NSF attachment protein	IPI00293817	ND	0	Yes	−	NC	−
NARS	Asparaginyl-tRNA synthetase, cytoplasmic	IPI00306960,IPI00646656	ND	0	Yes	−	NC	−

Table S2, continued.

			Fold enrichment over VCAM-1(D40A)[b]		Specific enrichment?[c]		Hops from β, integrin[d]	
Gene symbol	Protein name	Accession number(s)[a]	FN	VCAM-1	FN	VCAM-1	FN	VCAM-1
NAT10	N-acetyltransferase 10	IPI00300127	ND	0	Yes	−	NC	−
NCBP1	Nuclear cap-binding protein subunit 1	IPI00019380	ND	0	Yes	−	3	−
NCL	Isoform 1 of Nucleolin	IPI00604620,IPI00827674	4.36	1.05	Yes	−	3	−
NDUFA2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	IPI00219381	ND	0	Yes	−	×	−
NDUFA5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	IPI00412545,IPI00554681	ND	0	Yes	−	NC	−
NDUFA9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial precursor	IPI00003968	ND	0	Yes	−	NC	−
NDUFV2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial precursor	IPI00291328,IPI00412122,IPI00646556	ND	0	Yes	−	NC	−
NECAP2	Isoform 1 of Adaptin ear-binding coat-associated protein 2	IPI00018188,IPI00073436	ND	0	Yes	−	6	−
NOLA1	Isoform 1 of H/ACA ribonucleoprotein complex subunit 1	IPI00302176,IPI00607820	ND	0	Yes	−	NC	−
NOLA2	H/ACA ribonucleoprotein complex subunit 2	IPI00041325	ND	0	Yes	−	NC	−
NOP5/NOP58	Nucleolar protein 5	IPI00006379	ND	0	Yes	−	×	−
NUP155	Isoform 1 of Nuclear pore complex protein Nup155	IPI00026625,IPI00376609	ND	0	Yes	−	3	−
NUP210	Isoform 1 of Nuclear pore membrane glycoprotein 210 precursor	IPI00291755,IPI00783433	ND	0	Yes	−	NC	−
OLA1	Isoform 1 of Obg-like ATPase 1	IPI00290416	ND	0	Yes	−	3	−
PA2G4	Proliferation-associated protein 2G4	IPI00299000,IPI00794875,IPI00807557	2.32	0	Yes	−	4	−
PAFAH1B2	Platelet-activating factor acetylhydrolase IB subunit beta	IPI00026546	ND	0	Yes	−	4	−
PAICS	Multifunctional protein ADE2	IPI00217223	ND	0	Yes	−	4	−
PCNA	Proliferating cell nuclear antigen	IPI00021700	ND	0	Yes	−	4	−
PDAP1	28 kDa heat- and acid-stable phosphoprotein	IPI00013297	ND	0	Yes	−	NC	−
PDCD5	Programmed cell death protein 5	IPI00023640	ND	0	Yes	−	NC	−
PDHB	Isoform 1 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor	IPI00003925,IPI00549885,IPI00798351	ND	0	Yes	−	6	−
PDIA6	Isoform 1 of Protein disulfide-isomerase A6 precursor	IPI00299571,IPI00644989	ND	0	Yes	−	NC	−
PDLIM5	PDZ and LIM domain protein 5	IPI00007935	ND	0	Yes	−	4	−
PELP1	Isoform 1 of Proline-, glutamic acid- and leucine-rich protein 1	IPI00006702,IPI00178047,IPI00787089	ND	0	Yes	−	5	−
PFKL	Isoform 1 of 6-phosphofructokinase, liver type	IPI00332371,IPI00784216	ND	0	Yes	−	3	−
PFKP	6-phosphofructokinase type C	IPI00009790,IPI00643196	ND	0	Yes	−	3	−
PGAM5	Isoform 1 of Phosphoglycerate mutase family member 5 precursor	IPI00788907	ND	0	Yes	−	3	−
PGK1	Phosphoglycerate kinase 1	IPI00169383	ND	0	Yes	−	NC	−
PHGDH	Phosphoglycerate dehydrogenase	IPI00011200,IPI00642548	ND	0	Yes	−	NC	−
PICALM	Isoform 1 of Phosphatidylinositol-binding clathrin assembly protein	IPI00216184,IPI00290738,IPI00400849	2.84	1.94	Yes	−	3	−
PKM2	Isoform M2 of Pyruvate kinase isozymes M1/M2	IPI00479186,IPI00784179	ND	0	Yes	−	5	−
POLR1C	Isoform 1 of DNA-directed RNA polymerases I and III subunit RPAC1	IPI00005179,IPI00217386	ND	0	Yes	−	3	−
POLR2C	DNA-directed RNA polymerase II subunit RPB3	IPI00018288	ND	0	Yes	−	3	−
PPID	40 kDa peptidyl-prolyl cis-trans isomerase	IPI00003927	ND	0	Yes	−	NC	−
PPP1CA	Protein phosphatase 1, catalytic subunit, alpha isoform 3	IPI00027423,IPI00550451	2.10	1.11	Yes	−	2	−
PRDX6	Peroxiredoxin-6	IPI00220301	3.32	0.97	Yes	−	NC	−
PRKCB1	Isoform Beta-I of Protein kinase C beta type (PKCb)	IPI00010466,IPI00219628	ND	0	Yes	−	3	−
PRMT1	HMT1 hnRNP methyltransferase-like 2 isoform 1	IPI00018522,IPI00215734,IPI00382516	ND	0	Yes	−	3	−
PRPF19	Pre-mRNA-processing factor 19	IPI00004968	ND	0	Yes	−	3	−
PRPF4	Isoform 1 of U4/U6 small nuclear ribonucleoprotein Prp4	IPI00150269,IPI00218435	ND	0	Yes	−	3	−
PRPS2	Isoform 1 of Ribose-phosphate pyrophosphokinase 2	IPI00219617,IPI00718888	ND	0	Yes	−	NC	−
PSMA2	Proteasome subunit alpha type-2	IPI00219622	ND	0	Yes	−	3	−
PSMB3	Proteasome subunit beta type-3	IPI00028004	ND	0	Yes	−	3	−
PSMB5	Proteasome beta 5 subunit	IPI00375704,IPI00479306	ND	0	Yes	−	3	−
PSMC6	26S protease regulatory subunit S10B	IPI00021926	ND	0	Yes	−	3	−
PSMD13	HSPC027	IPI00549672	ND	0	Yes	−	3	−
PSMD5	Uncharacterized protein PSMD5	IPI00477981	ND	0	Yes	−	3	−
PTGES3	Prostaglandin E synthase 3	IPI00015029,IPI00789101,IPI00789698	ND	0	Yes	−	3	−
PUF60	Isoform 1 of Poly (FUSE-binding protein−interacting repressor)	IPI00069750,IPI00100716,IPI00788826,	ND	0	Yes	−	2	−
QARS	Glutaminyl-tRNA synthetase	IPI00026665	ND	0	Yes	−	NC	−
QKI	Isoform 1 of Protein quaking	IPI00385562,IPI00410032,IPI00410118,	ND	0	Yes	−	4	−
RAB10	Ras-related protein Rab-10	IPI00016513	ND	0	Yes	−	4	−
RAB11A	Ras-related protein Rab-11A	IPI00020436,IPI00429190,IPI00795676	ND	0	Yes	−	4	−
RAB35	Ras-related protein Rab-35	IPI00300096	ND	0	Yes	−	NC	−
RAB7A	Ras-related protein Rab-7a	IPI00016342	ND	0	Yes	−	NC	−
RAE1	mRNA export factor	IPI00019733	ND	0	Yes	−	3	−
RBBP4	Histone-binding protein RBBP4	IPI00328319,IPI00645329	ND	0	Yes	−	4	−
RBM12;CPNE1	RNA-binding protein 12	IPI00550308	ND	0	Yes	−	NC	−
RCC2	Protein RCC2	IPI00465044	ND	0	Yes	−	3	−
RNH1	Ribonuclease inhibitor	IPI00550069	ND	0	Yes	−	3	−
RPA1	Replication protein A 70 kDa DNA-binding subunit	IPI00020127	ND	0	Yes	−	4	−
RPA2	Isoform 1 of Replication protein A 32 kDa subunit	IPI00013939,IPI00646500,IPI00646957,	ND	0	Yes	−	4	−
RPL12	60S ribosomal protein L12	IPI00024933	2.27	1.66	Yes	−	3	−
RPL15	60S ribosomal protein L15	IPI00470528,IPI00550032	ND	0	Yes	−	3	−
RPL23A;hCG_16001	60S ribosomal protein L23a	IPI00021266,IPI00789159,IPI00793523,	2.29	0	Yes	−	3	−
RPL28	60S ribosomal protein L28	IPI00182533,IPI00816097	ND	0	Yes	−	3	−
RPL29	60S ribosomal protein L29	IPI00419919,IPI00796934	ND	0	Yes	−	3	−
RPL31	60S ribosomal protein L31	IPI00026302	ND	0	Yes	−	3	−
RPL6	60S ribosomal protein L6	IPI00329389,IPI00790342,IPI00867533	ND	0	Yes	−	3	−
RPL7	60S ribosomal protein L7	IPI00030179,IPI00472171	3.95	0.50	Yes	−	3	−
RPLP2	60S acidic ribosomal protein P2	IPI00008529	ND	0	Yes	−	3	−
RPS10	40S ribosomal protein S10	IPI00008438	2.27	1.57	Yes	−	3	−
RPS15	40S ribosomal protein S15	IPI00216153	ND	0	Yes	−	3	−
RPS23	40S ribosomal protein S23	IPI00218606,IPI00739952	ND	0	Yes	−	3	−
RPS26;LOC728937;L	40S ribosomal protein S26	IPI00186712,IPI00655650	ND	0	Yes	−	3	−
RSU1	Ras suppressor protein 1 (Rsu-1)	IPI00017256,IPI00377066,IPI00643346	ND	0	Yes	−	2	−
SAR1A	GTP-binding protein SAR1a	IPI00015954	ND	0	Yes	−	4	−
SEC22B	Vesicle-trafficking protein SEC22b	IPI00006865	ND	0	Yes	−	NC	−
SEC23B	Protein transport protein Sec23B	IPI00017376	ND	0	Yes	−	NC	−
SEC24C	Protein transport protein Sec24C	IPI00024661,IPI00647787	ND	0	Yes	−	NC	−
SEC61B	Protein transport protein Sec61 subunit beta	IPI00220835	ND	0	Yes	−	NC	−
SEPT2	Septin-2	IPI00014177	ND	0	Yes	−	3	−
SEPT9	Isoform 1 of Septin-9	IPI00455033,IPI00784614,IPI00784808,	ND	0	Yes	−	4	−
SET	Isoform 1 of Protein SET	IPI00072377,IPI00301311,IPI00646059,	ND	0	Yes	−	2	−
SF1	Isoform 1 of Splicing factor 1	IPI00294627,IPI00386114,IPI00386117,	3.43	0.48	Yes	−	4	−
SF3A3	Splicing factor 3A subunit 3	IPI00029764	ND	0	Yes	−	3	−
SF3B1	Splicing factor 3B subunit 1	IPI00026089	ND	0	Yes	−	3	−
SFRS1	Isoform ASF-1 of Splicing factor, arginine/serine-rich 1	IPI00215884,IPI00218591,IPI00218592	ND	0	Yes	−	3	−
SFRS3	Splicing factor, arginine/serine-rich 3	IPI00010204,IPI00843996	ND	0	Yes	−	2	−
SFRS9	Splicing factor, arginine/serine-rich 9	IPI00012340	2.80	1.56	Yes	−	3	−
SIPA1	Signal-induced proliferation-associated protein 1	IPI00305305	ND	0	Yes	−	NC	−
SLC25A1	Tricarboxylate transport protein, mitochondrial precursor	IPI00294159	ND	0	Yes	−	NC	−
SMAP1L	Isoform 1 of Stromal membrane-associated protein 1-like	IPI00102856,IPI00645261,IPI00645838	2.11	0.61	Yes	−	×	−
SMCHD1	Structural maintenance of chromosomes flexible hinge domain containing 1	IPI00847644	ND	0	Yes	−	×	−
SNAP23	Isoform SNAP-23a of Synaptosomal-associated protein 23	IPI00010438	ND	0	Yes	−	5	−
SND1	Staphylococcal nuclease domain-containing protein 1	IPI00140420	2.06	0.93	Yes	−	NC	−
SNRPA	U1 small nuclear ribonucleoprotein A	IPI00012382	ND	0	Yes	−	3	−
SNRPB	Isoform SM-B' of Small nuclear ribonucleoprotein-associated proteins B and B'	IPI00027285,IPI00329512,IPI00395674,	ND	0	Yes	−	3	−
SNRPD3	Small nuclear ribonucleoprotein Sm D3	IPI00017964	ND	0	Yes	−	3	−
SNRPE	Small nuclear ribonucleoprotein E	IPI00029266,IPI00068430	ND	0	Yes	−	3	−
SPTBN1	Isoform Short of Spectrin beta chain, brain 1	IPI00005614,IPI00328230,IPI00333015,	ND	0	Yes	−	3	−
SRP14	Signal recognition particle 14 kDa protein	IPI00293434	ND	0	Yes	−	3	−
SSB	Lupus La protein	IPI00009032	ND	0	Yes	−	3	−
SSBP1	Single-stranded DNA-binding protein, mitochondrial precursor	IPI00029744	ND	0	Yes	−	NC	−
ST13	Hsc70-interacting protein	IPI00032826,IPI00218038	ND	0	Yes	−	3	−
STOM	Erythrocyte band 7 integral membrane protein	IPI00219682	2.12	1.88	Yes	−	NC	−
STX4	Syntaxin-4	IPI00029730,IPI00644806,IPI00797749	ND	0	Yes	−	4	−
STXBP3	Syntaxin-binding protein 3	IPI00297626	ND	0	Yes	−	4	−
SUB1	Activated RNA polymerase II transcriptional coactivator p15	IPI00221222	ND	0	Yes	−	3	−
SUPT5H	Isoform 1 of Transcription elongation factor SPT5	IPI00298058,IPI00479229,IPI00655641,	ND	0	Yes	−	4	−
SYNCRIP	Isoform 1 of Heterogeneous nuclear ribonucleoprotein Q	IPI00018140,IPI00402182,IPI00402183,	2.59	1.46	Yes	−	3	−
TFAM	Transcription factor A, mitochondrial precursor	IPI00020928	ND	0	Yes	−	NC	−
TGM2	Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	IPI00294578	ND	0	Yes	−	1	−
THEM2	Thioesterase superfamily member 2	IPI00020530	ND	0	Yes	−	NC	−
TK1	Thymidine kinase 1, soluble	IPI00299214,IPI00791117	ND	0	Yes	−	NC	−
TKT	Transketolase	IPI00643920,IPI00788802,IPI00792641	ND	0	Yes	−	NC	−
TNFSF5IP1	Tumor necrosis factor superfamily, member 5-induced protein 1	IPI00644482	ND	0	Yes	−	NC	−
TPM3	Tropomyosin 3 isoform 4	IPI00178083,IPI00218319,IPI00479185	ND	0	Yes	−	NC	−
TPR	Nucleoprotein TPR	IPI00022970,IPI00742682	ND	0	Yes	−	3	−
TRAP1	Heat shock protein 75 kDa, mitochondrial precursor	IPI00030275	ND	0	Yes	−	NC	−
TTC9C	Tetratricopeptide repeat protein 9C	IPI00175096	ND	0	Yes	−	×	−
TTLL12	Tubulin--tyrosine ligase-like protein 12	IPI00029048	ND	0	Yes	−	NC	−
TUBB2C	Tubulin beta-2C chain	IPI00007752	2.24	0.56	Yes	−	NC	−
TUBB6	TUBB6 protein	IPI00646779	ND	0	Yes	−	NC	−
U2AF1	Splicing factor U2AF 35 kDa subunit	IPI00005613	ND	0	Yes	−	3	−
UBE2L3	Ubiquitin-conjugating enzyme E2 L3	IPI00021347	ND	0	Yes	−	4	−
UBE2M	NEDD8-conjugating enzyme Ubc12	IPI00022597	2.81	0.61	Yes	−	5	−
USP15	Isoform 1 of Ubiquitin carboxyl-terminal hydrolase 15	IPI00000728,IPI00219504,IPI00219505	ND	0	Yes	−	NC	−
USP39	U4/U6.U5 tri-snRNP-associated protein 2	IPI00419844	ND	0	Yes	−	NC	−
VIL2	Villin 2 (Ezrin)	IPI00746388	ND	0	Yes	−	5	−
VPS26A	Vacuolar protein sorting-associated protein 26A	IPI00411426	ND	0	Yes	−	2	−
VPS28	Vacuolar protein sorting-associated protein 28 homolog	IPI00007155	ND	0	Yes	−	NC	−
VPS35	Vacuolar protein sorting-associated protein 35	IPI00018931	ND	0	Yes	−	NC	−
XRCC5	ATP-dependent DNA helicase 2 subunit 2	IPI00220834	2.29	1.09	Yes	−	4	−
XRCC6	ATP-dependent DNA helicase 2 subunit 1	IPI00465430,IPI00644712	2.23	0.79	Yes	−	3	−
YBX1	Nuclease sensitive element-binding protein 1	IPI00031812	1.99	0	Yes	−	3	−
YES1	Proto-oncogene tyrosine-protein kinase Yes	IPI00013981,IPI00477734	ND	0	Yes	−	NC	−
YWHAE	14-3-3 protein epsilon	IPI00000816	2.40	1.16	Yes	−	2	−
YWHAG	14-3-3 protein gamma	IPI00220642	ND	0	Yes	−	2	−
YWHAH	14-3-3 protein eta	IPI00216319	ND	0	Yes	−	3	−
YWHAQ	14-3-3 protein theta	IPI00018146	ND	0	Yes	−	3	−
YWHAZ	14-3-3 protein zeta/delta	IPI00021263	3.62	1.16	Yes	−	3	−
ZW10	Centromere/kinetochore protein zw10 homolog	IPI00011631	ND	0	Yes	−	3	−
−	Similar to Fibronectin 1 isoform 4 preproprotein isoform 10	IPI00714673	ND	0	Yes	−	1	−

Table S2, continued.

			Fold enrichment over VCAM-1(D40A)[b]		Specific enrichment?[c]		Hops from β, integrin[d]	
Gene symbol	**Protein name**	**Accession number(s)[a]**	**FN**	**VCAM-1**	**FN**	**VCAM-1**	**FN**	**VCAM-1**
ACAT1	Acetyl-CoA acetyltransferase, mitochondrial precursor	IPI00030363,IPI00440499	0	ND	−	Yes	−	NC
ACO2	Aconitase 2, mitochondrial	IPI00017855,IPI00790739	0	ND	−	Yes	−	NC
AP2S1	Isoform 1 of AP-2 complex subunit sigma-1	IPI00219840	0	ND	−	Yes	−	NC
ARF1	ADP-ribosylation factor 1 (Arf1)	IPI00215914,IPI00215917	0	ND	−	Yes	−	2
ASNS	Asparagine synthetase	IPI00554777	0	ND	−	Yes	−	NC
ATP5O	ATP synthase subunit O, mitochondrial precursor	IPI00007611	0	ND	−	Yes	−	3
BOLA2;BOLA2B	BolA-like protein 2	IPI00301434	0	ND	−	Yes	−	×
BYSL	Bystin	IPI00328987	0	ND	−	Yes	−	NC
CENTD2	Isoform 3 of Centaurin-delta 2	IPI00639996,IPI00828080	0	ND	−	Yes	−	NC
CHD4	Isoform 1 of Chromodomain-helicase-DNA-binding protein 4	IPI00000846,IPI00455210	0	ND	−	Yes	−	NC
CNBP	Zinc finger protein 9	IPI00430812,IPI00430813	0	ND	−	Yes	−	6
CSNK1A1	Casein kinase I isoform alpha	IPI00167096,IPI00183400,IPI00790374	0	ND	−	Yes	−	6
DYNC1H1	Dynein heavy chain, cytosolic	IPI00456969,IPI00477531	1.88	2.08	−	Yes	−	NC
EIF6	Eukaryotic translation initiation factor 6	IPI00010105	0	ND	−	Yes	−	4
EMD	Emerin	IPI00032003	0	ND	−	Yes	−	NC
FKBP4	FK506-binding protein 4	IPI00219005	0	ND	−	Yes	−	NC
GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	IPI00026268	0	ND	−	Yes	−	NC
HBG1;HBE1	Hemoglobin subunit gamma-1	IPI00220706	0	ND	−	Yes	−	NC
HRB	Isoform 1 of Nucleoporin-like protein RIP	IPI00304693,IPI00607616,IPI00736669	0	ND	−	Yes	−	5
HSPE1	10 kDa heat shock protein, mitochondrial	IPI00220362	1.04	2.02	−	Yes	−	NC
ILF2	Interleukin enhancer-binding factor 2	IPI00005198	1.87	2.32	−	Yes	−	NC
IMMT	Isoform 1 of Mitochondrial inner membrane protein	IPI00009960,IPI00470829,IPI00554469	0	ND	−	Yes	−	NC
LYPLA2	Acyl-protein thioesterase 2	IPI00027032,IPI00027618,IPI00513881,	0	ND	−	Yes	−	NC
MCM4	DNA replication licensing factor MCM4	IPI00018349	0	ND	−	Yes	−	NC
MRPL43	Mitochondrial ribosomal protein L43	IPI00334579,IPI00428285,IPI00428286,	0	ND	−	Yes	−	NC
MSI2	Isoform 1 of RNA-binding protein Musashi homolog 2	IPI00073713,IPI00167806,IPI00792475	0	ND	−	Yes	−	×
NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor	IPI00604664	0	ND	−	Yes	−	NC
NUP188	Isoform 1 of Nucleoporin NUP188 homolog	IPI00385001,IPI00477040	0	ND	−	Yes	−	NC
PAFAH1B3	Platelet-activating factor acetylhydrolase IB subunit gamma	IPI00014808	0	ND	−	Yes	−	NC
PDCD6	Programmed cell death protein 6	IPI00025277	1.24	3.31	−	Yes	−	NC
PPIH	Peptidyl-prolyl cis-trans isomerase H	IPI00007346	0.63	2.18	−	Yes	−	NC
PRDX1	Peroxiredoxin-1	IPI00000874	1.51	2.05	−	Yes	−	NC
PSMA3	Isoform 1 of Proteasome subunit alpha type-3	IPI00171199,IPI00419249	0	2.10	−	Yes	−	6
PSMB6	Proteasome subunit beta type-6 precursor	IPI00000811,IPI00789119	0	ND	−	Yes	−	6
PSMD3	26S proteasome non-ATPase regulatory subunit 3	IPI00011603	0	ND	−	Yes	−	6
PSME3	Isoform 1 of Proteasome activator complex subunit 3	IPI00030243,IPI00219445	0	ND	−	Yes	−	6
PTPN11	Isoform 1 of Tyrosine-protein phosphatase non-receptor type 11 (SHP2)	IPI00658023	0	ND	−	Yes	−	2
PYCR2	Pyrroline-5-carboxylate reductase 2	IPI00470610	0	ND	−	Yes	−	NC
RPL17	60S ribosomal protein L17	IPI00413324	1.62	3.17	−	Yes	−	6
RPL18	60S ribosomal protein L18	IPI00215719	1.82	2.74	−	Yes	−	6
RPL38	60S ribosomal protein L38	IPI00215790	0	ND	−	Yes	−	6
RPS19	40S ribosomal protein S19	IPI00215780	1.22	2.32	−	Yes	−	6
RPS2	40S ribosomal protein S2	IPI00013485,IPI00479366	1.87	2.05	−	Yes	−	6
RPS8	40S ribosomal protein S8	IPI00216587	1.54	2.69	−	Yes	−	6
SEC31A	Isoform 1 of Protein transport protein Sec31A	IPI00305152,IPI00515103,IPI00746182,	0	ND	−	Yes	−	NC
SEPT11	Septin-11	IPI00019376	0	ND	−	Yes	−	NC
SLC2A1	Solute carrier family 2, facilitated glucose transporter member 1	IPI00220194	0	ND	−	Yes	−	NC
SNAP29	Synaptosomal-associated protein 29	IPI00032831	0	ND	−	Yes	−	NC
SNRPA1	U2 small nuclear ribonucleoprotein A'	IPI00297477	0	ND	−	Yes	−	8
SRM	Spermidine synthase	IPI00292020	1.29	2.27	−	Yes	−	NC
SSRP1	FACT complex subunit SSRP1	IPI00005154	0	ND	−	Yes	−	NC
STAT5B	Signal transducer and activator of transcription 5B (Stat5B)	IPI00103415	0	ND	−	Yes	−	2
STRAP	Serine-threonine kinase receptor-associated protein	IPI00294536,IPI00796172	0	ND	−	Yes	−	NC
TALDO1	Transaldolase	IPI00550488,IPI00744692	0	ND	−	Yes	−	5
THOC2	THO complex 2 isoform 1	IPI00158615	0	ND	−	Yes	−	×
TOP1	DNA topoisomerase 1	IPI00413611	0	ND	−	Yes	−	9
TRAPPC3	Uncharacterized protein TRAPPC3	IPI00647089	0	ND	−	Yes	−	NC
TRIM28	Isoform 1 of Transcription intermediary factor 1-beta	IPI00438229	1.25	2.93	−	Yes	−	NC
TYMS	Thymidylate synthase	IPI00103732,IPI00221108	0	ND	−	Yes	−	NC
UBR4	Isoform 1 of Zinc finger UBR1-type protein 1	IPI00640981,IPI00646605,IPI00746934,	0	ND	−	Yes	−	NC
VDAC1	Voltage-dependent anion-selective channel protein 1	IPI00216308	0	ND	−	Yes	−	5

[a]Human International Protein Index (IPI) database identifier(s).

[b]Fold enrichments of proteins identified in FN or VCAM-1 affinity isolations versus the VCAM-1(D40A) control isolation were calculated from mean normalized spectral counts (table S1). Fold enrichments of proteins detected in FN or VCAM-1 affinity isolations but not in the VCAM-1(D40A) control isolation could not be determined (ND). Fold enrichments of proteins not identified in either FN or VCAM-1 affinity isolations are indicated by zero (0).

[c]Proteins enriched by at least 2.0-fold over the VCAM-1(D40A) control sample were regarded as specific. Proteins not enriched in a specific adhesion complex are indicated by a dash (−).

[d]Number of direct protein–protein interactions between selected protein and β_1 integrin based on analysis of the $\alpha_4\beta_1$–FN and $\alpha_4\beta_1$–VCAM-1 interaction networks. Proteins that did not link to the major interconnected interaction networks derived from $\alpha_4\beta_1$–FN and $\alpha_4\beta_1$–VCAM-1 adhesion complexes were deemed not connected (NC). Proteins not present in the human interactome, and, therefore, that could not be mapped onto the interactome, are indicated by a cross (×). Proteins not enriched in a specific adhesion complex are indicated by a dash (−).

Table S3. Protein–protein interaction network statistics.

	Full network[a]	FN-induced network[a,b]	VCAM-1–induced network[a,b]
Nodes	10204	386	181
Edges	58723	2814 (P = 0.0011)	864 ($P < 1 \times 10^{-4}$)
Clustering coefficient	0.178	0.541 (P = 0.0006)	0.671 (P = 0.0025)

[a]The properties of the overall protein–protein interaction network and the subnetwork models generated for $\alpha_5\beta_1$–FN and $\alpha_4\beta_1$–VCAM-1 affinity isolations are shown.
[b]*P*-values indicate significantly greater numbers of edges and clustering coefficients in the induced subnetworks when compared to networks induced by degree-matched random samples of the same size.

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