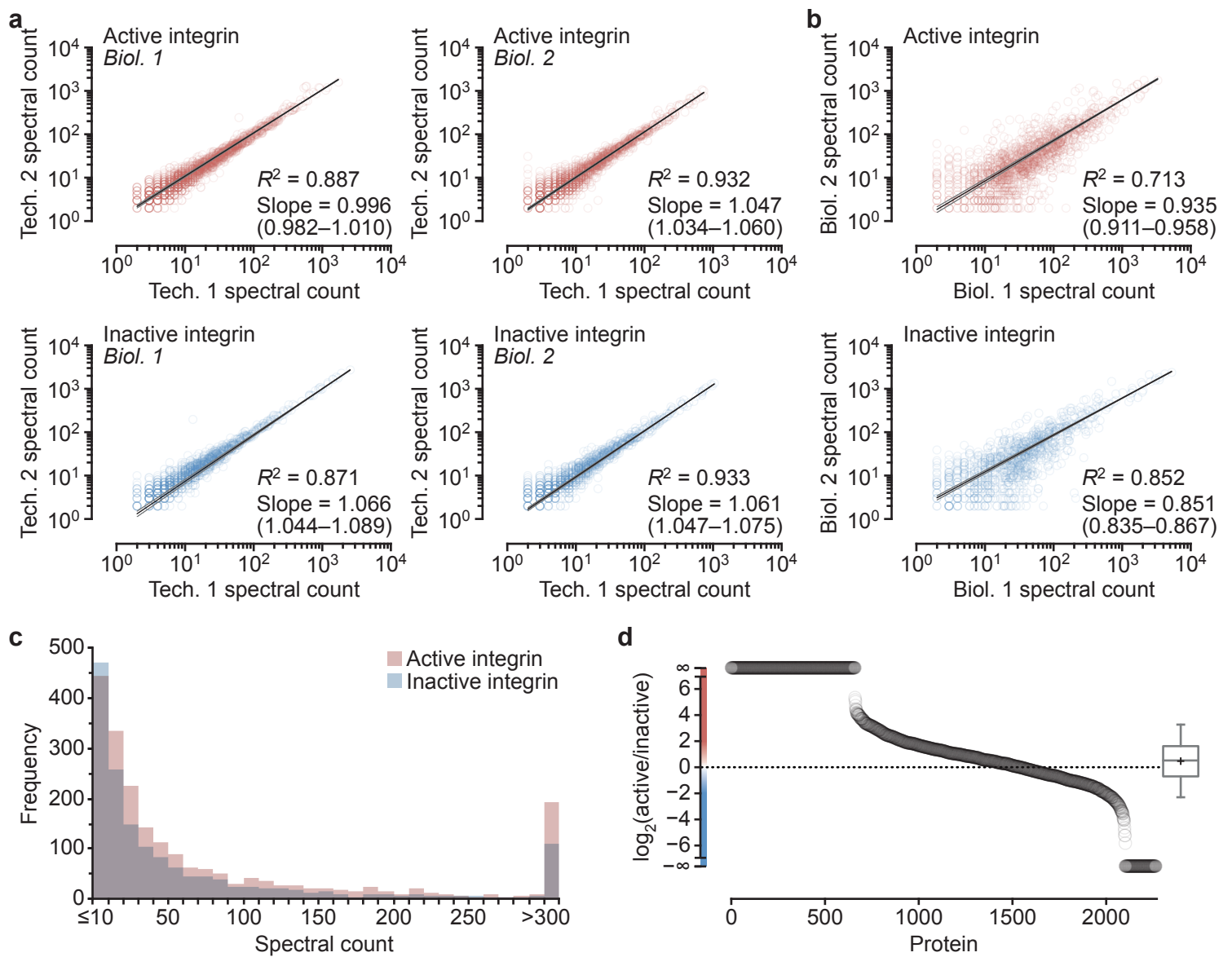
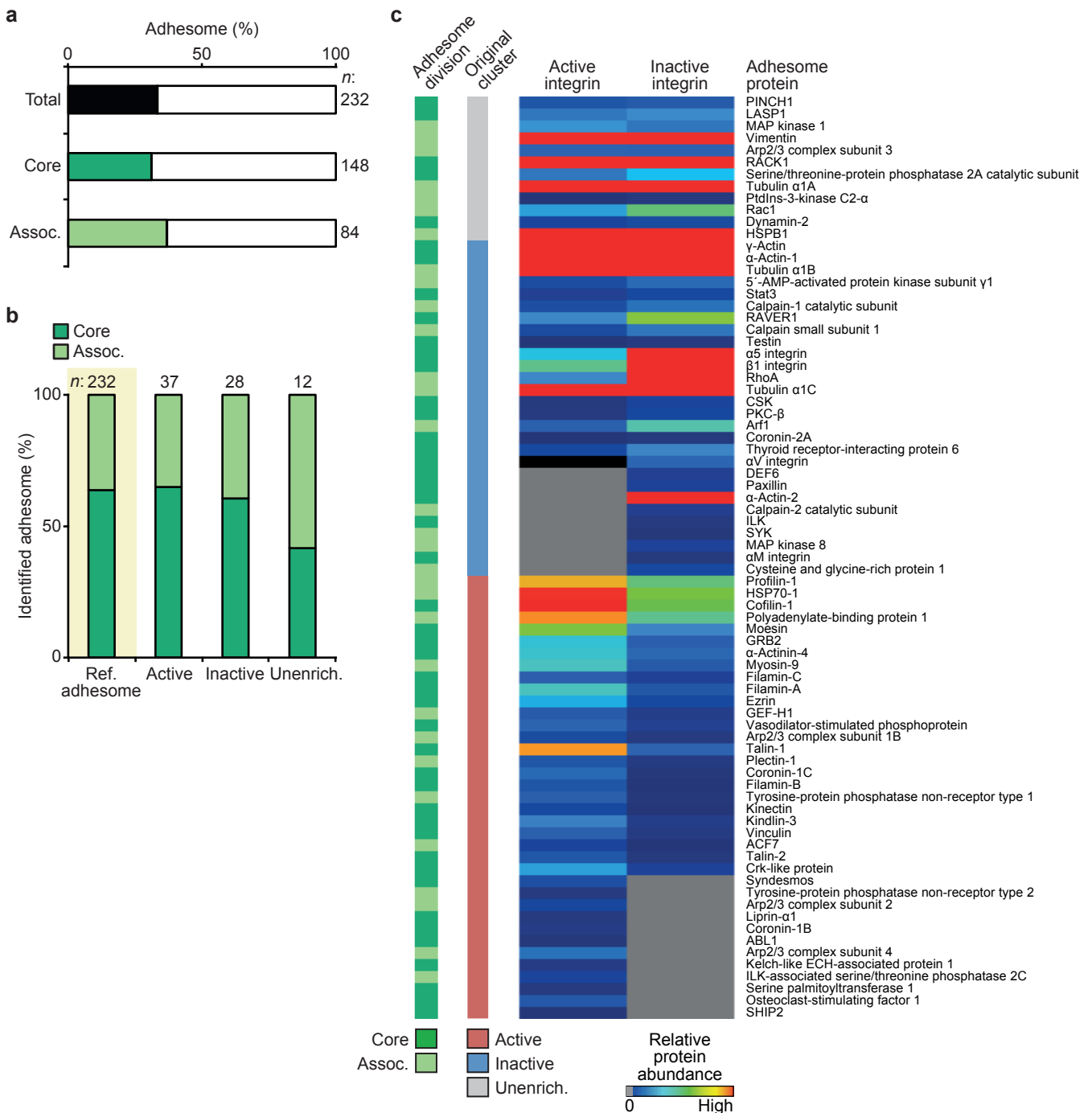


Supplementary Figure 1 | Morphology of cells spread on activity-specific anti-integrin mAbs.

(a,b) HFFs were spread on FN or stimulatory or inhibitory anti- $\beta 1$ integrin mAbs for 1 h. Cell areas (a) and perimeters (b) were measured using ImageJ. Box-and-whisker plots shows the median (line), mean (plus sign), 25th and 75th percentiles (box) and 5th and 95th percentiles (whiskers) ($n = 31$, 31 and 33 cells for FN, stimulatory and inhibitory, respectively). Comparisons between the three independent groups were determined by Kruskal–Wallis test with Dunn’s multiple comparisons test.

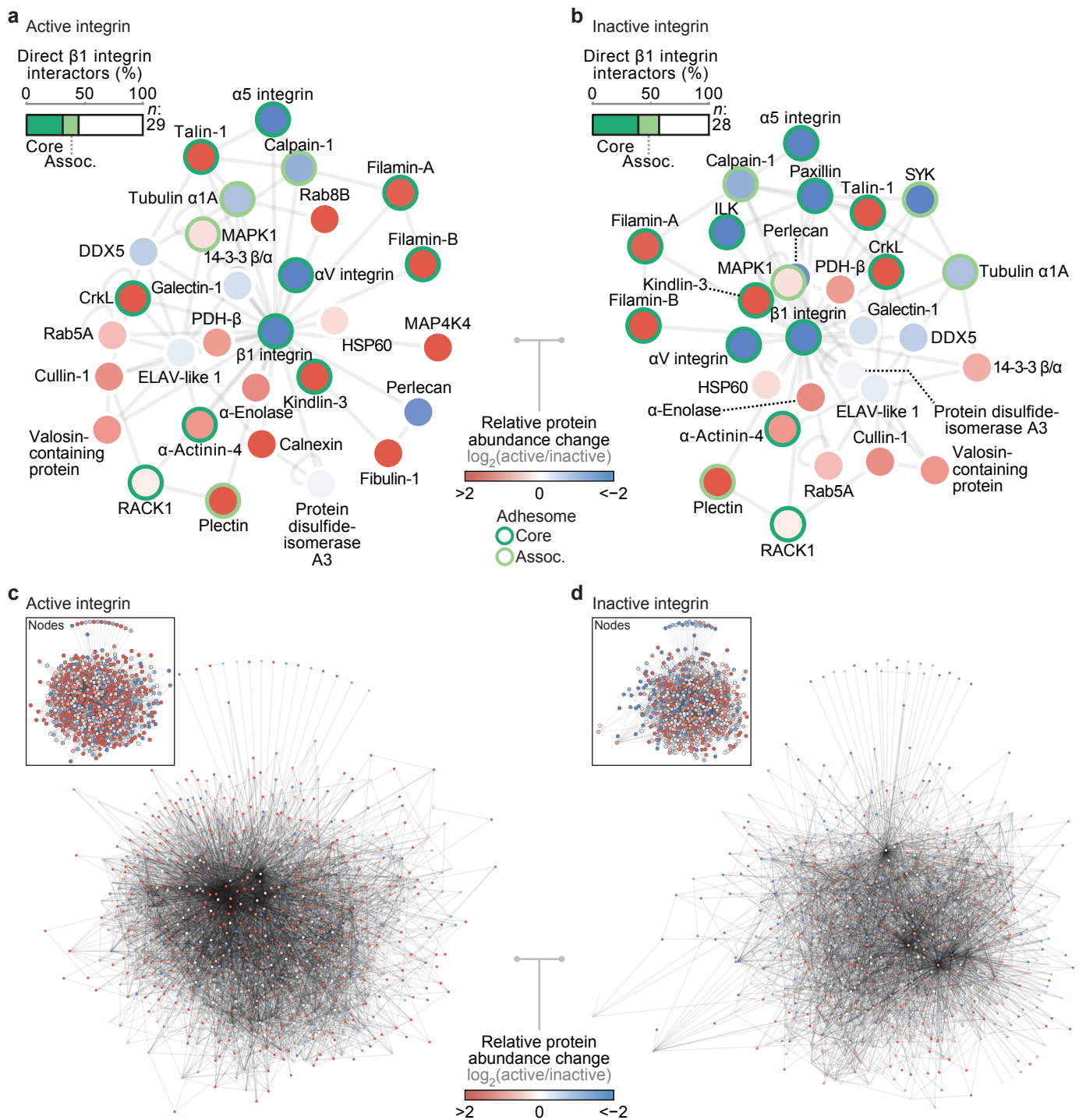


Supplementary Figure 2 | Quantification and reproducibility of MS data. (a,b) Spectral counts of proteins identified in active (red circles) and inactive (blue circles) integrin complexes were compared between technical replicate (a) and biological replicate (b) analyses. Proteins detected in both compared samples are displayed. Log–log lines (black lines) and associated 95% confidence bands (thin grey lines) were calculated by nonlinear regression analysis (least squares fit). Goodness of fit (R^2) and slope best fit values (95% confidence interval in parentheses) are displayed. Hougaard's measure of skewness was < 0.10 (almost linear) for all slope best fits. (c) Frequency distribution of spectral counts of proteins identified in active (red) and inactive (blue) integrin data sets. Bins, 10 spectral counts. (d) Abundance ratios of proteins identified in active relative to inactive integrin complexes were determined from normalised spectral counts and \log_2 transformed. Colour bar indicates higher relative abundance in the active (red) or inactive (blue) integrin data sets. Non-infinite abundance ratios were normally distributed (non-Gaussian distribution $P > 0.05$; D'Agostino & Pearson omnibus normality test), with median abundance ratio 0.52 (0.40–0.60, 95% confidence interval). Box-and-whisker plot shows the median (line), mean (plus sign), 25th and 75th percentiles (box) and 5th and 95th percentiles (whiskers).



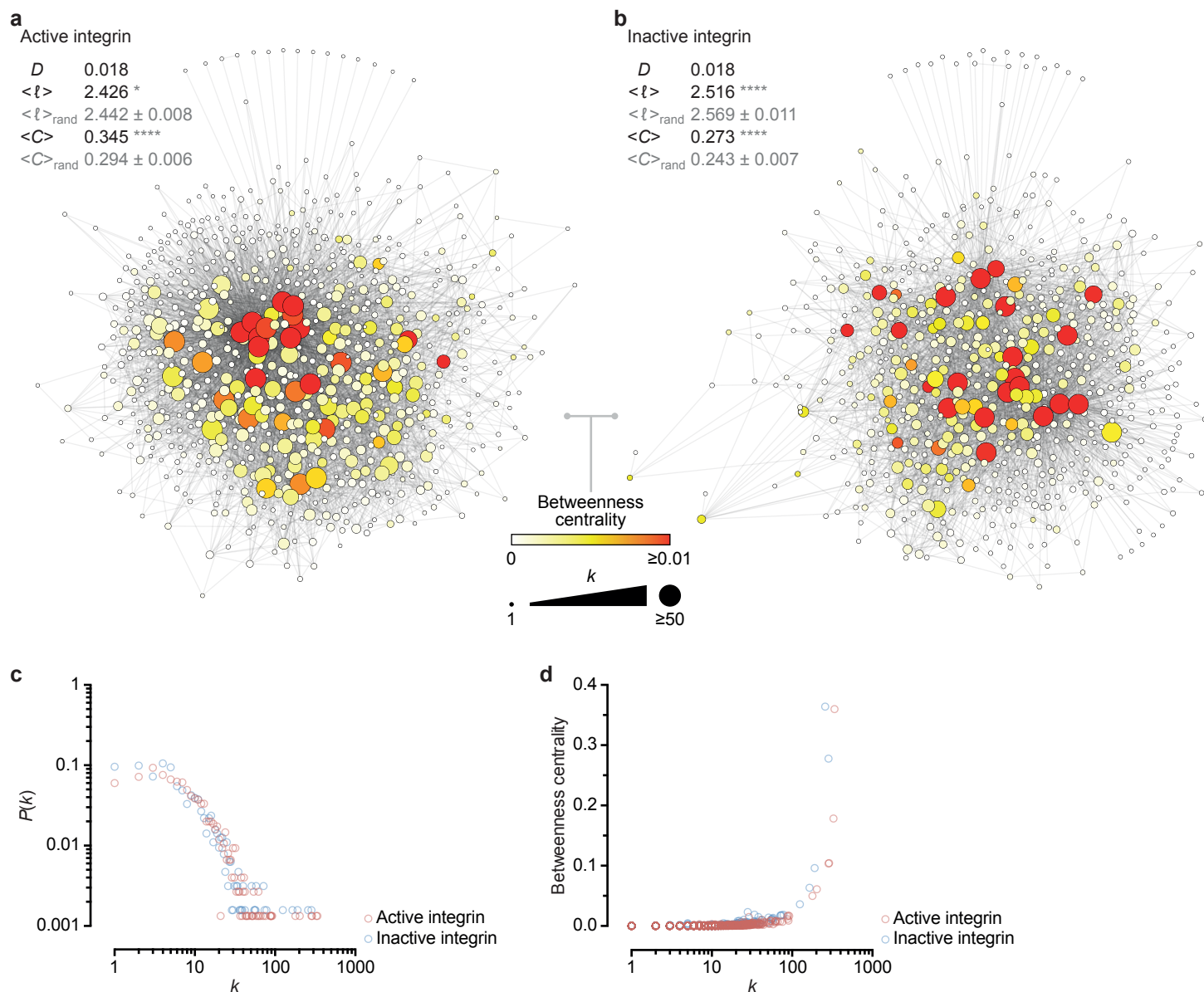
Supplementary Figure 3 | Adhesome components identified in activation state-dependent integrin complexes.

(a) Proportions of the literature-curated adhesome¹ identified by MS. Of the total reported adhesome ($n = 232$ proteins), 77 proteins (33%) were identified by MS. Adhesome divisions of reported intrinsic (core) components (46 proteins; 31%) and transiently or peripherally associated components (31 proteins; 37%) were represented to a similar extent in the MS data. (b) Proportions of identified adhesome proteins reported as core or associated adhesome components. Of the identified adhesome proteins enriched in active integrin complexes ($n = 37$ proteins), 24 proteins (65%) were core adhesome components; of those enriched in inactive integrin complexes ($n = 28$ proteins), a similar proportion (17 proteins; 61%) were core adhesome components. These proportions are similar to the 64% of the total adhesome reported as core components (yellow box, reference adhesome). In contrast, identified adhesome proteins with similar abundance in both data sets (unenriched) were fewer ($n = 12$ proteins) and had a smaller proportion of core adhesome components (5 proteins; 42%). This may reflect a relatively transient or peripherally associated set of proteins recruited to integrin complexes in an activation state-independent manner. (c) Heat map shows relative protein abundance (normalised spectral count) for identified adhesome components (grey, not detected). Clusters of differentially enriched proteins are indicated, and protein order is preserved from the original hierarchical clustering analysis (see Fig. 1d and Supplementary Table 1 for full, hierarchically clustered MS data). Heat bar (left) indicates the distribution of core and associated adhesome components.

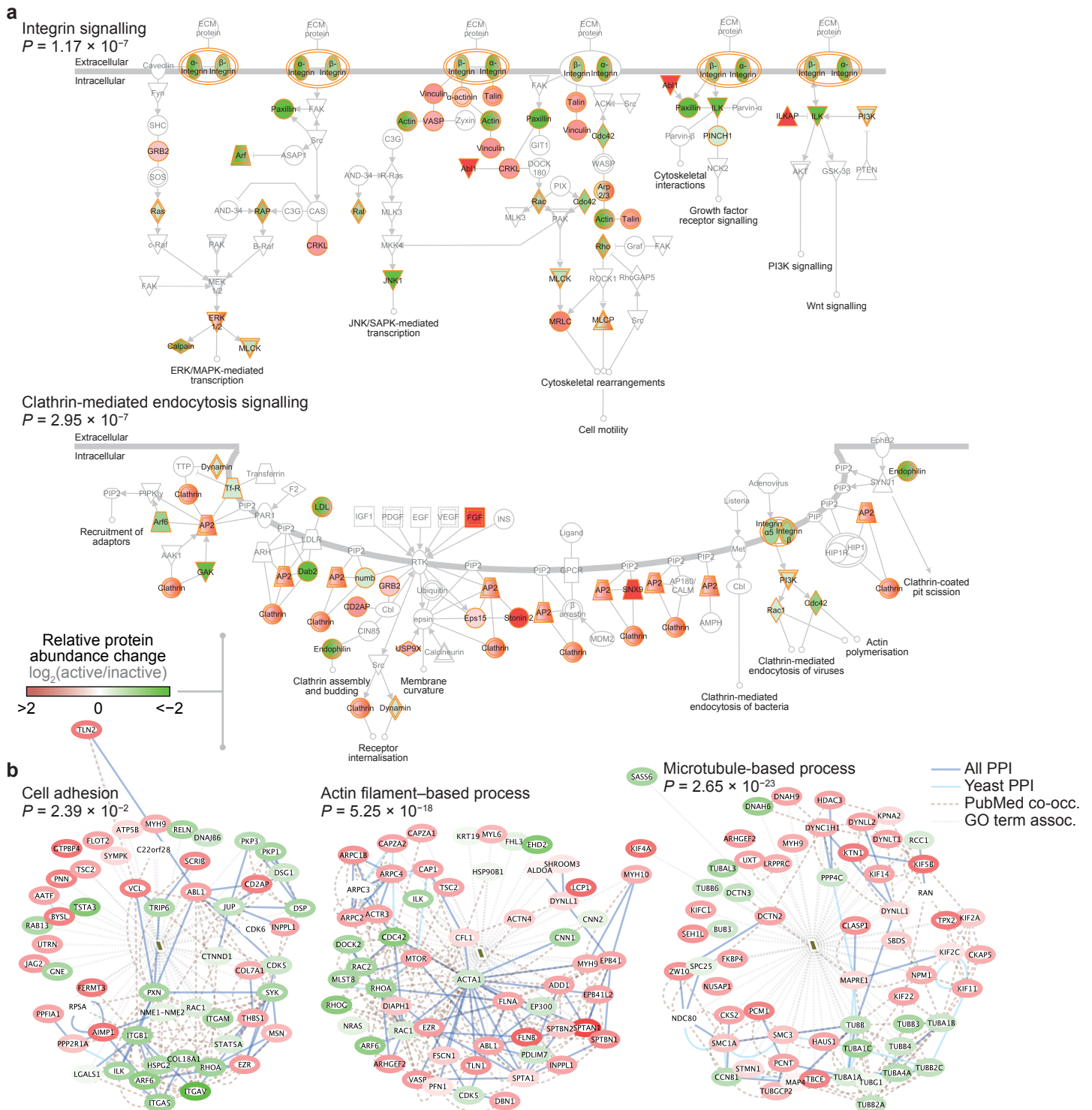


Supplementary Figure 4 | Interaction network analysis of activation state-dependent integrin complexes.

(a–d) Quantitative MS data for all proteins identified in the integrin data sets were mapped onto a merged, multi-source interactome database to generate active and inactive integrin interactomes (see methods for details). Of the identified proteins reported to interact directly with $\beta 1$ integrin (the one-hop interactions networks) ($n = 29$ and 28 for active and inactive integrin, respectively), 13 proteins (45%) in the active integrin network (a) and 16 proteins (57%) in the inactive integrin network (b) were reported adhesome components. Of these adhesome components, 69% were intrinsic (core) adhesome components in the active (9 proteins) and inactive (11 proteins) integrin networks. Analysis of the $\beta 1$ integrin two-hop interaction networks (proteins reported to interact directly with $\beta 1$ integrin or with $\beta 1$ integrin-binding partners) identified 751 proteins in the active integrin network (c, inset) and 636 proteins in the inactive integrin network (d, inset), which represents 9% and 7% of the total reported $\beta 1$ integrin two-hop interactome, respectively. These networks were highly interconnected, with 5152 and 3556 protein interactions in the active (c) and inactive (d) integrin networks, respectively. Nodes (circles) represent proteins identified by MS and are coloured according to protein enrichment in active (red) or inactive (blue) integrin complexes (\log_2 transformed). Edges (grey lines) represent reported protein-protein interactions. Networks were clustered using the yFiles Organic algorithm implemented in Cytoscape.

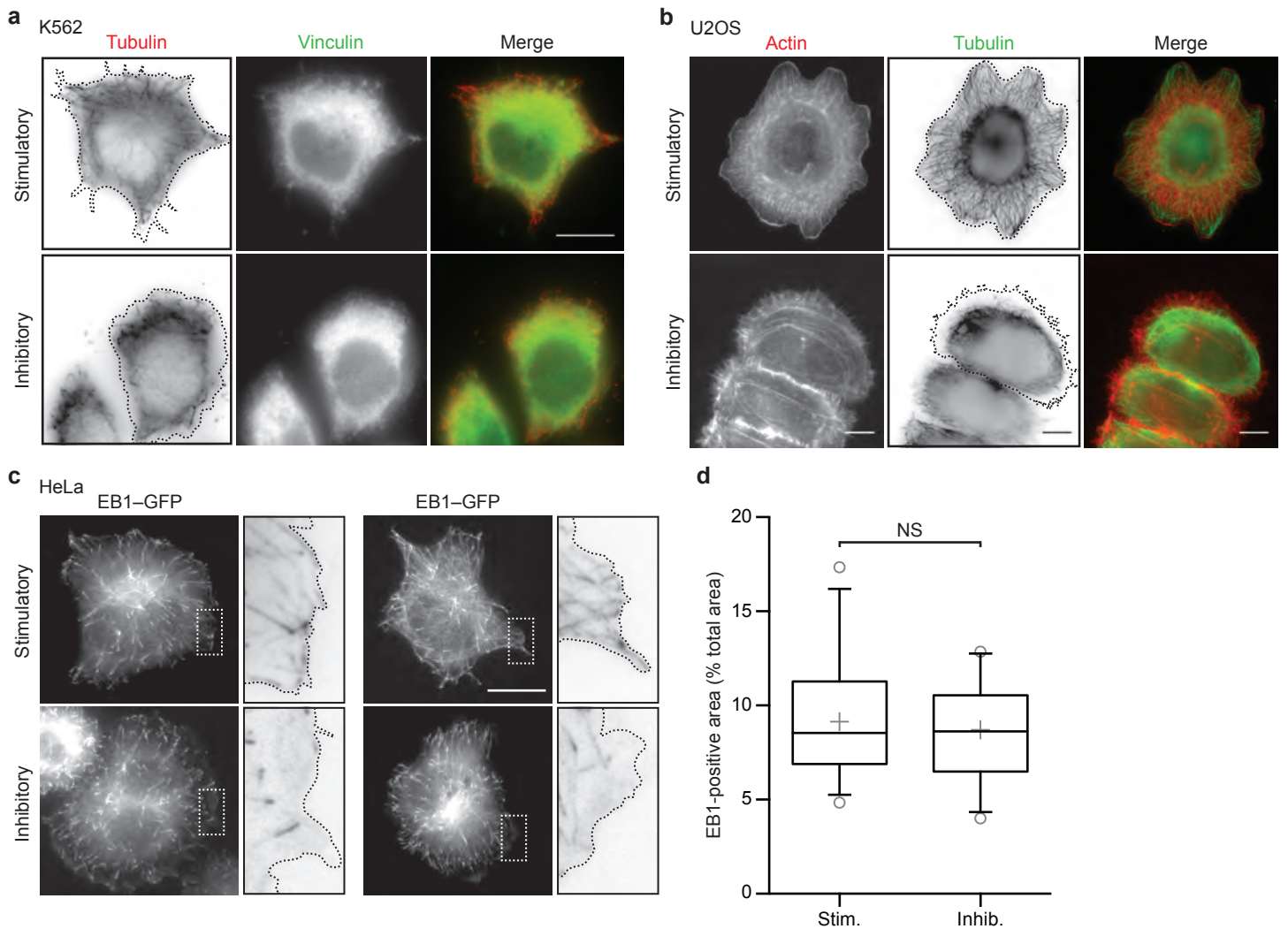


Supplementary Figure 5 | Topological analysis of integrin adhesion complex networks. (a,b) $\beta 1$ integrin two-hop interaction networks constructed from the active (a) and inactive (b) integrin data sets were clustered using the yFiles Organic algorithm implemented in Cytoscape. Self-interactions were removed and topological parameters were computed using NetworkAnalyzer: D , network density; $\langle \ell \rangle$, average shortest path length; $\langle C \rangle$, average clustering coefficient. Shortest path length represents the ability of two nodes (proteins; circles) in a network to interact via the smallest number of edges (protein-protein interactions; grey lines). For both integrin networks, this value was smaller than those expected by random network simulations ($\langle \ell \rangle_{\text{rand}}$, grey font), indicating highly interconnected (navigable) networks. Nodes are sized according to degree (number of interactions; k) and coloured according to betweenness centrality. Betweenness centrality represents the potential of a node to be part of the shortest path length between different pairs of nodes in the network and is a measure of the load on or the flow of network traffic through the node. High betweenness centrality equates to a network bottleneck (high-traffic node). The clustering coefficient represents the capacity for groups of nodes to interact. A high clustering coefficient equates to highly interconnected clusters in the network. Clustering coefficients of both networks were larger than those of random simulations ($\langle C \rangle_{\text{rand}}$, grey font), indicating that the proteins identified by MS have a tendency to form groups within the networks, in line with the proposed modular nature of the adhesome^{2,3}. Random networks were generated from 10^5 degree-preserving edge shuffles of each network. Results are mean \pm s.d. ($n = 10^4$ rounds of randomisation). * $P < 0.05$, **** $P < 0.0001$; two-tailed one-sample Z test. (c,d) Plots show the relationship between degree and the degree distribution, $P(k)$ (c), or betweenness centrality (d) for the active and inactive integrin networks. Highly connected proteins correlated with increased betweenness centrality, suggesting that hubs may influence the adhesion networks through both direct and indirect interactions.



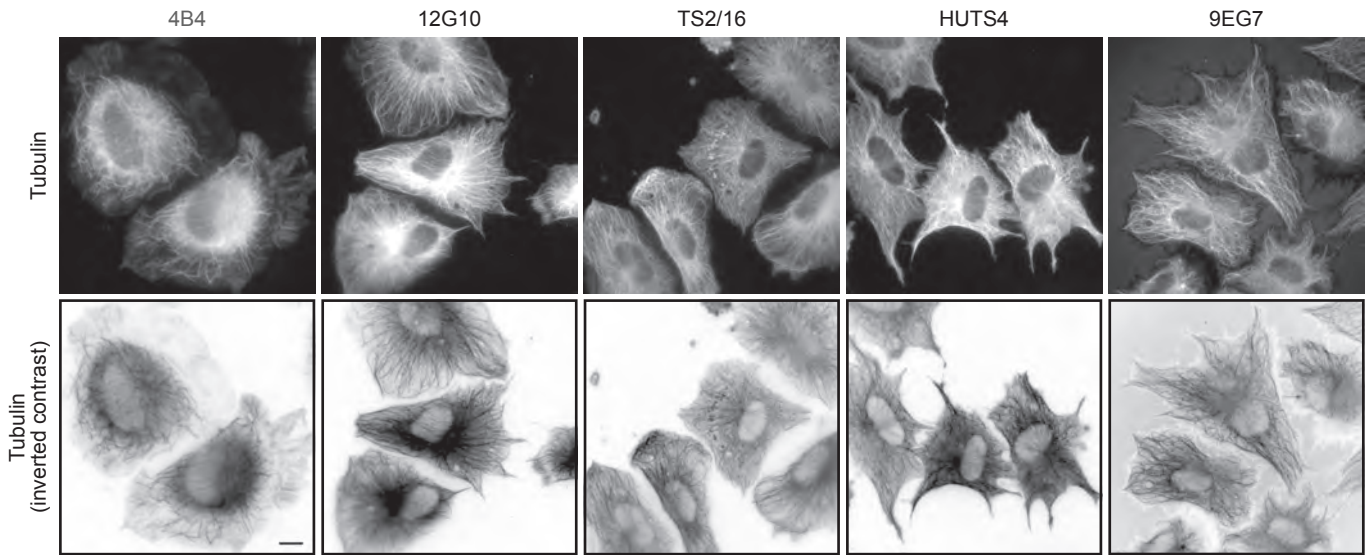
Supplementary Figure 6 | Pathway and functional interaction network analyses of activation state-dependent integrin complexes.

(a) Overrepresented canonical pathways that contain a number of adhesome proteins were selected ($P < 0.0001$; Fisher's exact test). Coloured nodes (shapes) represent proteins identified by MS and are coloured according to protein enrichment in active (red) or inactive (green) integrin complexes (\log_2 transformed). Nodes with multiple colours comprise quantitative contributions from multiple identified subunits or members of a complex or group. Grey nodes represent pathway members not identified in the integrin data sets. Edges (grey lines) represent direct functional interactions (no arrowhead, binding only; pointed arrowhead, acts on, including binding; blunt arrowhead, inhibits, including binding; blunt arrowhead with pointed arrowhead, inhibits and acts on, including binding; circular arrowhead, leads to). (b) Functional interaction networks for overrepresented adhesion and cytoskeleton Gene Ontology terms were selected ($P < 0.05$; Fisher's exact test). Nodes (ovals) represent proteins identified by MS, and node borders are coloured according to protein enrichment in active (red) or inactive (green) integrin complexes (\log_2 transformed). Edges (lines) represent reported protein-protein interactions (blue solid lines), literature co-occurrence (brown dashed lines) or Gene Ontology term association (grey dotted lines). A number of the adhesion-related enzymes in the integrin signalling pathway (a) and the cell adhesion and actin filament networks (b) (e.g. RhoA, Rac1, Cdc42 and Arf6) were enriched in inactive integrin complexes. Furthermore, excluding tubulin, most (41 proteins; 80%) of the proteins in the overrepresented microtubule-based process network (b) were enriched in active integrin complexes.



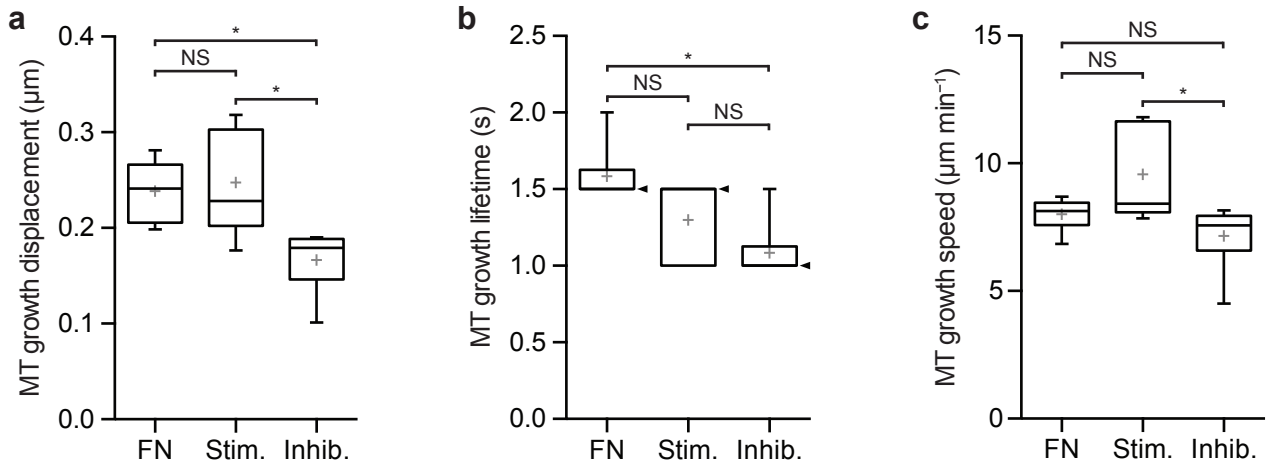
Supplementary Figure 7 | Microtubule growth in cells spread on stimulatory and inhibitory anti- β 1 integrin mAbs.

(a) K562 cells were stained for α -tubulin (red) and vinculin (green). (b) U2OS cells were stained for actin (red) and α -tubulin (green). (c) HeLa cells expressing EB1-GFP were imaged to visualise microtubule plus ends. Two representative images are shown. Inverted contrast images correspond to areas highlighted in white dotted boxes; black dotted lines indicate cell periphery. Scale bars, 10 μ m. (d) HFF cells were stained for EB1. Regions away from the cell periphery with areas of at least 40 μ m² were selected at random, and the amount of EB1-positive signal was determined as a percentage of the total measured area. Box-and-whisker plot shows the median (line), mean (plus sign), 25th and 75th percentiles (box) and 5th and 95th percentiles (whiskers) ($n = 26$ and 29 cell areas for stimulatory and inhibitory, respectively). Comparison between the two independent groups was determined by two-tailed Mann-Whitney test.



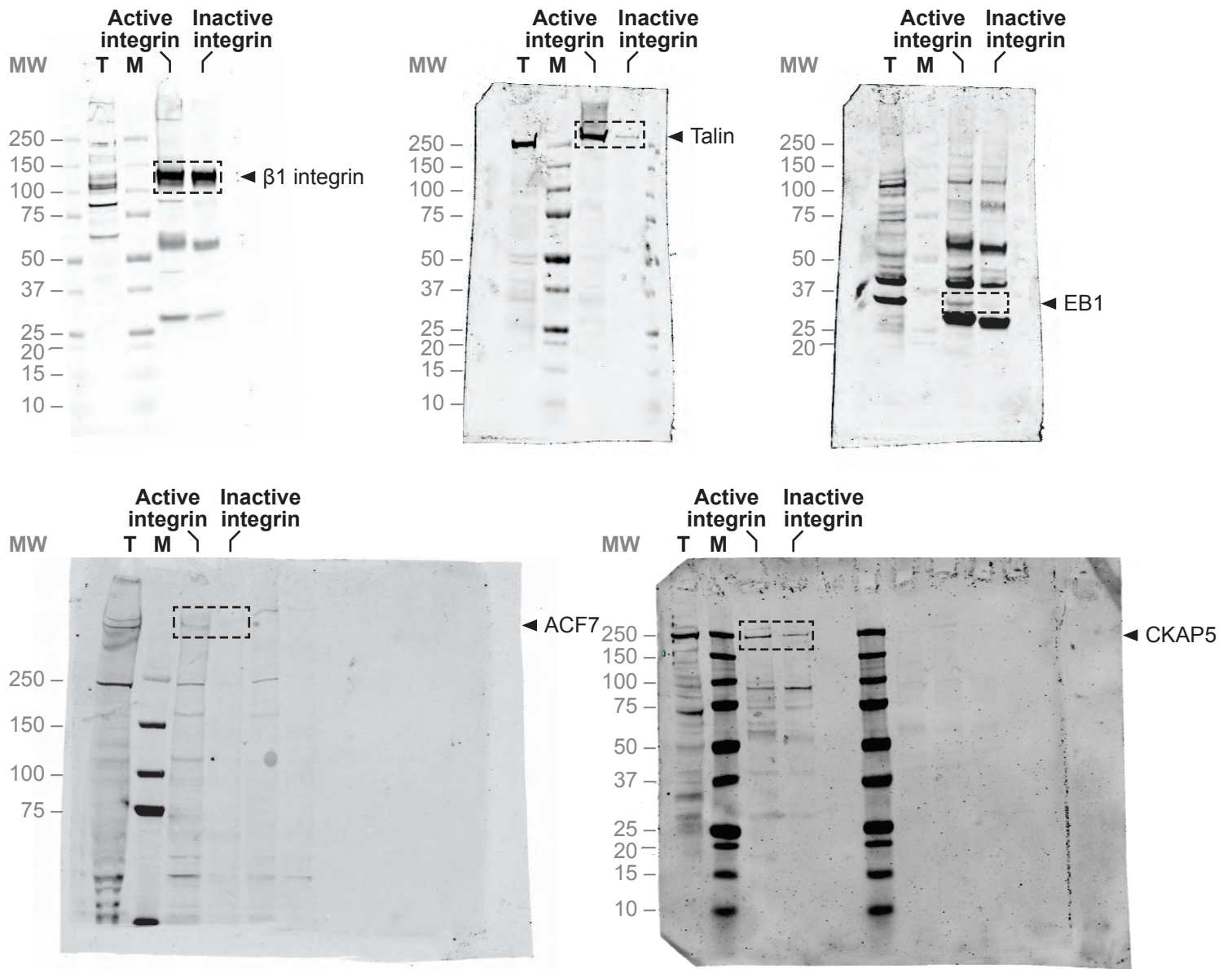
Supplementary Figure 8 | Microtubule growth in cells spread on additional stimulatory anti- β 1 integrin mAbs.

HFF cells were spread on the inhibitory and stimulatory mAbs used throughout this study (4B4 and 12G10, respectively) in addition to other stimulatory anti- β 1 integrin mAbs (TS2/16, HUTS4 and 9EG7). Cells were stained for α -tubulin and imaged to visualise microtubule growth to the cell periphery. Inverted contrast images are also shown. Scale bar, 10 μ m.



Supplementary Figure 9 | Microtubule growth dynamics in cells spread on activity-specific anti-integrin mAbs.

(a–c) HeLa cells expressing EB3–GFP were spread on FN, stimulatory and inhibitory mAbs and imaged by live TIRF microscopy. Microtubule plus-end dynamics were tracked and analysed using plusTipTracker⁴ (see Supplementary Movies 3–5). Median values for displacement (a), lifetime (b) and speed (c) of +TIP comet track growth were determined for each cell from at least 700 tracks per cell. Box-and-whisker plots show the median (line), mean (plus sign), 25th and 75th percentiles (box) and 5th and 95th percentiles (whiskers) ($n = 6, 5$ and 6 cells for FN, stimulatory and inhibitory, respectively). Arrowheads indicate obscured median lines. * $P < 0.05$; Kruskal–Wallis test with Dunn’s multiple comparisons test.



Supplementary Figure 10 | Original blots. Dashed boxes indicate cropped regions shown in Figure 4a. Arrowheads indicate expected band position for each protein probed. MW, molecular weight (kDa), grey font; T, total cell lysate; M, molecular weight marker.

Supplementary Table 1 | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	API Accession	UniProtKB Accession	Gene name	Protein name	Relative abundance (mean normalized spectral count) x10 ³			Fold enrichment (active/inactive)		Specific enrichment (active/inactive)		Cluster ¹	Adhesome ²	Hierarchical clustering
					MW (kDa)	Active integrin	Inactive integrin	Active integrin	Inactive integrin	Active integrin	Inactive integrin			
252	PI00129318	P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	36	2.036	2.266	0.90	False	False	Unenriched	-	-	
406	PI00115380	Q01611	NCP1	Nuclear cap binding protein subunit 1	92	0.321	0.280	0.90	False	False	Unenriched	-	-	
62	PI00121743	P02008	HBZ	Hemoglobin subunit zeta	16	14.302	15.861	0.90	False	False	Unenriched	-	-	
237	PI00121493	P06866	RPL20	40S ribosomal protein S20	13	5.655	6.277	0.90	False	False	Unenriched	-	-	
1325	PI00107485	N01644	NUP43	Isomorph 1 of Nup93 homologous phosphoprotein phosphohydrolase 2	20	0.324	0.359	0.90	False	False	Unenriched	-	-	
246	PI00131517	Q14566	MCM6	DNA replication licensing factor MCM6	93	0.835	0.910	0.92	False	False	Unenriched	-	-	
434	PI00108865	P06780	CANX2B	Caspein kinase II subunit beta	25	1.783	1.952	0.91	False	False	Unenriched	-	-	
611	PI00120252	P30101	PDK4	Protein disulfide-isomerase 4b	52	0.023	0.022	0.91	False	False	Unenriched	-	-	
640	PI00373877	Q58K21	ZNF326	Isomorph 1 of Zinc finger protein 326	66	0.390	0.427	0.91	False	False	Unenriched	-	-	
39	PI00121565	P09551	HNRNP1A	Isomorph A1-B of Heterogeneous nuclear ribonucleoprotein A1	39	7.671	8.432	0.91	False	False	Unenriched	-	-	
1369	PI00100324	Q13617	TRAPPC3	Trafficking protein particle complex subunit 3	20	0.414	0.456	0.92	False	False	Unenriched	-	-	
1220	PI00107339	Q98944	GNB1L	Isomorph 1 of Guanine nucleotide-binding protein beta-like protein 1	36	0.252	0.278	0.91	False	False	Unenriched	-	-	
90	PI00376798	P62913	RPL11	Isomorph 1 of 60S ribosomal protein L11	20	9.149	9.906	0.92	False	False	Unenriched	-	-	
201	PI00100843	P40182	XRN2	40S ribosomal protein S5	109	0.204	0.217	0.94	False	False	Unenriched	-	-	
1302	PI00117509	Q8IUR0	TRAPPC5	Trafficking protein particle complex subunit 5	21	0.408	0.441	0.93	False	False	Unenriched	-	-	
68	PI00121570	P39019	RPL59	40S ribosomal protein S19	16	13.384	14.196	0.94	False	False	Unenriched	-	-	
568	PI00100151	Q8I906	XRN2	Isomorph 1 of 5' to 3' exonuclease XRN2	109	0.204	0.217	0.94	False	False	Unenriched	-	-	
885	PI00132650	Q8NH45	NUP35	Nucleoporin NUP35	35	0.584	0.624	0.94	False	False	Unenriched	-	-	
1208	PI00101688	Q9Y488	TELO2	Telomere length regulation protein TEL2 homolog	92	0.067	0.072	0.93	False	False	Unenriched	-	-	
171	PI00101830	P33992	MCM5	DNA replication licensing factor MCM5	82	1.344	1.329	1.01	False	False	Unenriched	-	-	
49	PI00105448	P05787	KRT8	Keratin, type II cytoskeletal 8	54	6.229	6.216	1.00	False	False	Unenriched	-	-	
1031	PI001002895	P63272	SPT4	Transcription elongation factor SPT4	13	0.836	0.834	1.00	False	False	Unenriched	-	-	
843	PI00105596	P48070	KTM6	Proteasome subunit beta type 6	209	0.708	0.704	1.01	False	False	Unenriched	-	-	
157	PI001064304	P62826	RAN	GTP-binding nuclear protein Ran	24	5.233	5.082	1.03	False	False	Unenriched	-	-	
310	PI001027252	Q59623	PHB2	Prohibitin 2	33	2.064	2.017	1.02	False	False	Unenriched	-	-	
785	PI001003588	Q14254	ETS1E1	Eukaryotic translation elongation factor 1 epsilon-1	200	0.827	0.881	1.02	False	False	Unenriched	-	-	
1289	PI00171665	Q8NF94	NUP37	Nucleoporin Nup37	37	0.195	0.190	1.03	False	False	Unenriched	-	-	
1451	PI00120142	Q8WV12	NUPC202	Nucleic acid-containing protein 2	18	2.244	0.238	1.03	False	False	Unenriched	-	-	
118	PI00116565	P42937	PNA	Peptidyl prolyl co-trans isomerase A	85	8.868	9.275	0.96	False	False	Unenriched	-	-	
261	PI00129355	Q92499	DDX1	ATP-dependent RNA helicase DDX1	82	0.976	1.020	0.96	False	False	Unenriched	-	-	
256	PI00121044	Q8JUM9	RALY	Isomorph 1 of RNA-binding protein Raly	30	2.600	2.709	0.96	False	False	Unenriched	-	-	
1076	PI00110241	Q8I906	UBR5	Ubiquitin-like protein 5	16	1.979	1.750	0.96	False	False	Unenriched	-	-	
377	PI00120706	P69891	HGB1	Hemoglobin subunit gamma-1	16	20.032	20.879	0.96	False	False	Unenriched	-	-	
1104	PI001025717	Q17541	MTX2	Mexitin-2	30	0.331	0.345	0.96	False	False	Unenriched	-	-	
1224	PI00121128	Q15247	CIL2F	Chloride intracellular channel protein 2	20	0.365	0.384	0.96	False	False	Unenriched	-	-	
645	PI001000811	F28072	PSMB6	Proteasome subunit beta type-6	25	1.141	1.177	0.97	False	False	Unenriched	-	-	
461	PI001029744	Q04837	SGBP1	Single-stranded DNA-binding protein, mitochondrial	17	2.499	2.598	0.96	False	False	Unenriched	-	-	
663	PI00101854	Q14847	CABP8	Calcium-inducible RNA-binding protein	19	1.217	1.217	0.96	False	False	Unenriched	-	-	
966	PI001003217	Q99436	PSMB7	Proteasome subunit beta type-7	30	0.322	0.334	0.96	False	False	Unenriched	-	-	
482	PI001003482	Q16698	DCR1	2,4-dienoyl-CoA reductase, mitochondrial	36	1.214	1.226	0.99	False	False	Unenriched	-	-	
372	PI001005513	Q10181	UBR2	Splicing factor UBR2 55 kDa subunit	29	2.025	2.049	0.99	False	False	Unenriched	-	-	
628	PI001295485	Q95757	HSP9AL	Heat shock 70 kDa protein 9L	94	0.070	0.071	0.99	False	False	Unenriched	-	-	
147	PI001016010	Q13365	PCBP1	Poly(C)-binding protein 1	37	4.024	4.028	1.00	False	False	Unenriched	-	-	
680	PI001021719	Q14254	HAT1E1	Human acetyltransferase type B catalytic subunit	100	0.527	0.528	1.00	False	False	Unenriched	-	-	
463	PI001011274	Q14979	HNRPLD	Isomorph 1 of Heterogeneous nuclear ribonucleoprotein D-like	46	2.010	2.018	1.00	False	False	Unenriched	-	-	
687	PI001202219	P35606	COPB2	Coatomer subunit beta 2	102	0.225	0.226	1.00	False	False	Unenriched	-	-	
248	PI001206369	Q80213	NSUN2	RNA (cytosolic 5'-methyltransferase NSUN2	85	0.866	0.879	0.99	False	False	Unenriched	-	-	
259	PI001017303	P43246	MST2	DNA mismatch repair protein Msh2	105	0.676	0.687	0.99	False	False	Unenriched	-	-	
515	PI001219757	P09211	GSTP1	Glutathione S-transferase P	23	1.700	1.731	0.98	False	False	Unenriched	-	-	
408	PI001011200	Q43175	PHGDH	D-3-phosphoglycerate dehydrogenase	57	1.048	1.088	0.98	False	False	Unenriched	-	-	
100	PI001292145	P48668	KRT6A	Keratin, type II cytoskeletal 6A	30	3.469	3.704	0.98	False	False	Unenriched	-	-	
1834	PI001015011	Q8NKH8	FBX12	Isomorph 1 of F-box/LRR-repeat protein 12	37	0.058	0.060	0.97	False	False	Unenriched	-	-	
1924	PI001095952	Q8I906	PHF3	Peptidyl prolyl co-trans isomerase	33	0.065	0.067	0.97	False	False	Unenriched	-	-	
52	PI001011296	P62260	RPL20	40S ribosomal protein S20	18	13.833	15.218	0.95	False	False	Unenriched	-	-	
172	PI001054788	P05783	KRT18	Keratin, type I cytoskeletal 18	48	3.139	3.703	0.85	False	False	Unenriched	-	-	
255	PI001037385	Q75400	PPP4R4A	Isomorph 1 of Pre-mRNA-processing factor 40 homolog A	109	0.473	0.558	0.85	False	False	Unenriched	-	-	
911	PI001078612	P48021	LMNB1	Nuclear lamina protein LMNB1	38	0.178	0.178	0.85	False	False	Unenriched	-	-	
901	PI001095498	Q8JUC8	CDK11A	PITSLRE serine/threonine protein kinaseCDK11	90	0.140	0.166	0.84	False	False	Unenriched	-	-	
134	PI001013936	Q15717	ELAVL1	ELAV-like protein 1	39	3.563	4.235	0.84	False	False	Unenriched	-	-	
328	PI001055363	Q17802	TAGLN2	Transgelin-2	22	1.566	1.584	0.84	False	False	Unenriched	-	-	
1060	PI001038625	Q80723	HNRN	Hornrin	282	0.040	0.047	0.85	False	False	Unenriched	-	-	
449	PI001217966	P00338	LDHA	Isomorph 1 of L-lactate dehydrogenase A chain	37	1.140	1.127	0.87	False	False	Unenriched	-	-	
10	PI001220138	Q10181	SIRT	Isomorph 2 of Sirtuin 6 nuclear effector molecule homolog	102	0.442	0.510	0.87	False	False	Unenriched	-	-	
772	PI001000861	Q14847	LASP1	Isomorph 1 of LIM and SH3 domain protein 1	30	0.486	0.790	0.87	False	False	Unenriched	-	-	
288	PI001008240	P56192	MARS	Methionyl-tRNA synthetase, cytoplasmic	101	0.692	0.805	0.86	False	False	Unenriched	-	-	
543	PI001001346	Q14847	MARS	Peptidyl prolyl co-trans isomerase H	19	1.933	1.933	0.86	False	False	Unenriched	-	-	
1533	PI001061989	Q96919	CDC45	Sorcin	28	1.129	0.149	0.87	False	False	Unenriched	-	-	
241	PI001055689	Q9Y380	C22orf28	UPF027 protein C22orf28	55	1.275	1.444	0.88	False	False	Unenriched	-	-	
10	PI001002156	Q10181	STUB1	Isomorph 1 of STUB1 homologous and U-box containing protein 1	18	0.402	0.558	0.88	False	False	Unenriched	-	-	
251	PI001012066	Q15366	PCBP2	poly(C)-binding protein 2 isomorph b	38	4.271	4.802	0.89	False	False	Unenriched	-	-	
100	PI001008438	P46783	RPL10	40S ribosomal protein S10	19	7.035	7.944	0.89	False	False	Unenriched	-	-	
159	PI001021719	Q14254	RPL20	40S ribosomal protein S14	18	7.624	8.605	0.89	False	False	Unenriched	-	-	
1379	PI001045436	P04040	CAT	Catalase	60	0.126	0.142	0.89	False	False	Unenriched	-	-	
753	PI001074421	Q60773	EIF4E2	Eukaryotic translation initiation factor 4E type 2	28	0.741	0.838	0.88	False	False	Unenriched	-	-	
773	PI001003863	P47472	ACAT1	Acetyl-CoA acetyltransferase, mitochondrial	10	0.489	0.553	0.88	False	False	Unenriched	-	-	
1512	PI001045438	P44773	TPP1	Putative uncharacterized protein TPP1	20	0.088	0.087	0.88	False	False	Unenriched	-	-	
1287	PI001328815	Q8I906	USP48	USP48 protein	121	0.057	0.064	0.89	False	False	Unenriched	-	-	
85	PI001798360	P62979	SANP1	SANP1 protein	18	9.747	11.992	0.83	False	False	Unenriched	-	-	
717	PI001010777	Q17313	HDAC9	Protein HDAC9 homolog 2	34	0.642	0.769	0.83	False	False	Unenriched	-	-	
657	PI001015217	P07195	LDHB	L-lactate dehydrogenase B chain	37	0.979	1.179	0.83	False	False	Unenriched	-	-	
458	PI001017412	P35250	RFC2	Isomorph 1 of Replication factor C subunit 2	39	0.907	1.094	0.83	False	False	Unenriched	-	-	
1127	PI00121128	P62616	CIL1E	ADP-ribosylation factor-like protein 1	20	0.342	0.413	0.83	False	False	Unenriched	-	-	
320	PI001013774	Q13547	HDAC1	Histone deacetylase 1	55	0.936	1.144	0.82	False	False	Unenriched	-	-	
864	PI001010324	Q8M040	LSM12	Isomorph 1 of Protein LSM12 homolog	22	0.861	1.047	0.82	False	False	Unenriched	-	-	
1435	PI001000949	Q10250	PCAF	Proteasome inhibitor PIS1 subunit	50	0.134	0.165	0.81	False	False	Unenriched	-	-	
1480	PI001293350	Q95958	TM2XN	Transmembrane-associated protein X	33	0.144	0.177	0.81	False	False	Unenriched	-	-	
1382	PI001291559	Q9Y782	RN202	E3 ubiquitin-protein ligase BR1A	114	0.047	0.058	0.81	False	False	Unenriched	-	-	
1799	PI001004416	Q14847	CANX2A	Charged multivesicular-body protein 2a	25	0.088	0.102	0.82	False	False	Unenriched	-	-	
669	PI001032406	Q06884	DNAI2A	DnaI homolog subfamily A member 2	46	0.424	0.528	0.80	False	False	Unenriched	-	-	
649	PI001029733	Q04828	AKR1C1	Aldo-keto reductase family 1 member C1	37	0.596	0.743	0.80	False	False	Unenriched	-	-	
1457	PI001021230	P14625	HSP90A	Endoplasmic reticulum chaperone HSP90A	82	0.226	0.280	0.80	False	False	Unenriched	-	-	
1126	PI00101380	P41223	MTOR	Protein BUD31 homolog	17	0.555	0.695	0.80	False	False	Unenriched	-	-	
1300	PI001291646	Q15741	MTHFD1L	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	106	0.056	0.070	0.80	False	False	Unenriched	-	-	
313	PI001012535	P31688	RNAP2	DnaI homolog subfamily A member 1	15									

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	API Accession	UniProtKB Accession	Gene name	Protein name	Protein MW (kDa)	Relative abundance (mean normalized spectral counts) × 10 ³		Fold enrichment (active/inactive)		Specific enrichment [†]		Adhesome [‡]	Hierarchical clustering
						Active integrin	Inactive integrin	Active integrin [†]	Inactive integrin [†]	Active integrin [†]	Inactive integrin [†]		
826	IP00430812	P62333	CNBP	Isomorph 1 of Cellular nuclear acid-binding protein	19	1.121	1.078	1.04	False	False	Unenriched	-	
428	IP00021926	P62333	PSM6C	26S protease regulatory subunit S10B	44	1.054	1.012	1.04	False	False	Unenriched	-	
177	IP00021926	P62333	PSM6C	26S protease regulatory subunit S10B	44	1.054	1.012	1.04	False	False	Unenriched	-	
641	IP00007019	Q9Y3C6	PRLL	Prolyl 4-hydroxylase	68	1.040	1.014	1.04	False	False	Unenriched	-	
1656	IP00128658	Q8R9H5	WDR74	Isomorph 1 of Set1/Asf2 histone methyltransferase complex subunit ASF2	69	0.942	0.940	1.05	False	False	Unenriched	-	
43	IP00418471	P08670	VIM	Vimentin	54	5.789	5.413	1.07	False	False	Unenriched	YES	
1466	IP00001134	Q9YS80	RBM7	RNA-binding protein 7	31	0.221	0.206	1.07	False	False	Unenriched	-	
186	IP00020023	Q02543	RPL8A	60S ribosomal protein L8a	21	4.742	4.415	1.07	False	False	Unenriched	-	
2002	IP00155601	Q9H069	MACROD1	MACRO domain-containing protein 1	36	0.098	0.091	1.08	False	False	Unenriched	-	
1017	IP00016339	P51148	RAB5C	Ras-related protein Rab-5C	23	0.654	0.607	1.08	False	False	Unenriched	-	
658	IP00172580	Q72324	NUP54	Nucleoporin 54kDa variant (Fragment)	56	0.496	0.462	1.07	False	False	Unenriched	-	
1415	IP00017767	Q9Y735	MGST2	Microsomal glutathione S-transferase 2	17	0.496	0.465	1.07	False	False	Unenriched	-	
784	IP00063729	Q96011	THOC3	THO complex subunit 3	42	0.411	0.387	1.06	False	False	Unenriched	-	
1125	IP00005162	O15145	ARPC3	Actin-related protein 2/3 complex subunit 74	21	0.504	0.477	1.06	False	False	Unenriched	YES*	
1316	IP00021906	Q8W0X3	RPS19B1	Active regulator of SMT1	15	0.643	0.608	1.06	False	False	Unenriched	-	
157	IP00411058	P08965	RPS4	33 kDa protein	33	8.620	7.824	1.10	False	False	Unenriched	-	
425	IP00017334	P35232	PIH1	Prohibitin	30	1.745	1.589	1.10	False	False	Unenriched	-	
848	IP00029048	Q13576	IQGA2	Isomorph 1 of Ras GTPase-activating-like protein IQGA2	181	0.054	0.049	1.10	False	False	Unenriched	-	
471	IP00029535	P52789	PSMA4	Proteasome subunit alpha type-4	29	1.527	1.384	1.10	False	False	Unenriched	-	
1305	IP00011736	Q15437	SEC28B	Protein transport protein Sec28B	86	0.093	0.084	1.11	False	False	Unenriched	-	
1720	IP00005791	O14777	NDC80	Kinetochore protein NDC80 homolog	74	0.050	0.045	1.11	False	False	Unenriched	-	
314	IP00028270	Q71000	HSP90AA1	Isomorph 1 of Heat shock protein HSP 90-alpha	98	4.937	4.433	1.11	False	False	Unenriched	-	
1507	IP00024088	Q96828	POB1	Isomorph 1 of Polyglutamine-binding protein 1	38	0.193	0.173	1.11	False	False	Unenriched	-	
624	IP00029186	Q14604	USP10	Ubiquitin carboxyl-terminal hydrolase 10	88	0.350	0.321	1.09	False	False	Unenriched	-	
1089	IP00021742	P09105	HBO1	Isomorph 1 of HBO1 protein	16	0.891	0.816	1.09	False	False	Unenriched	-	
1010	IP00000764	P01962	DCAF2	DDK1- and CLK4-associated factor 2	60	0.332	0.306	1.08	False	False	Unenriched	-	
1763	IP00067959			36 kDa protein	36	0.050	0.046	1.09	False	False	Unenriched	-	
133	IP00419373	P51991	HNRNP3A3	Isomorph 1 of Heterogeneous nuclear ribonucleoprotein A3	40	3.932	3.377	1.16	False	False	Unenriched	-	
1121	IP00030781	P23284	STX2	Isomorph alpha of Signal transducer and activator of transcription 1 alpha/beta	83	0.096	0.083	1.16	False	False	Unenriched	-	
1273	IP00029566	P34932	HSPA4	Heat shock 70 kDa protein	94	0.118	0.101	1.17	False	False	Unenriched	-	
177	IP00074604	Q721M5	RPS27L	40S ribosomal protein S27-like	9	15.863	13.558	1.17	False	False	Unenriched	-	
1582	IP00053925	Q03117	AIP	Anti-hydrocortisone receptor interacting protein	38	0.068	0.061	1.17	False	False	Unenriched	-	
541	IP00031514	P40937	RPCS	Replication factor C subunit 5	38	0.942	0.837	1.13	False	False	Unenriched	-	
728	IP00021961	P24666	ACPI	Isomorph 1 of Low molecular weight phosphotyrosine protein phosphatase	18	1.440	1.278	1.13	False	False	Unenriched	-	
36	IP00048226	P02246	GNX1L	Guanine nucleotide-binding protein subunit beta-2-like 1	35	10.477	9.276	1.13	False	False	Unenriched	YES	
1056	IP00037570	Q53682	SEC13	Protein SEC13 homolog	36	0.398	0.351	1.13	False	False	Unenriched	-	
1226	IP00016752	Q52120	FAM88B	Protein FAM88B	37	0.344	0.304	1.13	False	False	Unenriched	-	
388	IP00046204	Q12324	PNB2	Peptidyl prolyl 4-trans isomerase B	24	2.347	2.047	1.15	False	False	Unenriched	-	
650	IP00015833	Q9N663	CHCHD3	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	26	1.135	0.999	1.14	False	False	Unenriched	-	
1087	IP00005537	P52815	MRLP12	Mitochondrial dicarboxylate carrier	48	0.251	0.220	1.14	False	False	Unenriched	-	
589	IP00028985	Q96842	THOC5	THO complex subunit 5	38	0.858	0.743	1.15	False	False	Unenriched	-	
1624	IP00018235	Q9UBV8	PEF1	Peftin	30	0.170	0.147	1.16	False	False	Unenriched	-	
149	IP00079560	Q04637	EIF4G1	EIF4G protein	172	0.687	0.595	1.15	False	False	Unenriched	-	
1585	IP00009501	P61970	NUP72	Nuclear transport factor 2	14	0.216	0.188	1.15	False	False	Unenriched	-	
1674	IP00155562	Q9R9V8	RNF126	Isomorph 2 of RING finger protein 126	34	0.178	0.154	1.16	False	False	Unenriched	-	
30	IP00021741	P02100	HBE1	Hemoglobin subunit epsilon	16	21.577	20.239	1.07	False	False	Unenriched	-	
242	IP00016832	P52786	PSMA1	Isomorph 3 of Proteasome subunit alpha type-1	30	2.429	3.400	0.71	False	False	Unenriched	-	
422	IP00015695	Q04049	WRB2	WD repeat-containing protein 82	86	1.047	0.961	0.72	False	False	Unenriched	-	
1021	IP00078309	P41250	GARS	Glycyl-tRNA synthetase	83	0.139	0.193	0.72	False	False	Unenriched	-	
273	IP00011213	Q13151	HNRNPAD	Heterogeneous nuclear ribonucleoprotein AD	31	2.590	3.582	0.72	False	False	Unenriched	-	
980	IP00010218	Q9H081	ACPC2	Kinetochore protein ACPC2	28	0.948	0.948	0.72	False	False	Unenriched	-	
1146	IP00019755	P78417	GSTO1	Glutathione S-transferase omega-1	28	0.342	0.475	0.72	False	False	Unenriched	-	
543	IP00021298	Q13630	CPFS	Isomorph 1 of Cleavage and polyadenylation specificity factor subunit 6	59	0.569	0.814	0.70	False	False	Unenriched	-	
583	IP00040590	P22952	RPL23A	Nucleolar phosphoprotein 23	33	0.098	0.100	0.98	False	False	Unenriched	-	
637	IP00000549	P61564	WRB5	WD repeat-containing protein 5	37	0.568	0.811	0.70	False	False	Unenriched	-	
1569	IP00020915	P30044	PBXD5	Isomorph 1 of Peroxisome biogenesis factor 5, mitochondrial	22	0.252	0.358	0.70	False	False	Unenriched	-	
711	IP00010201	P48552	PSMD8	Proteasome 26S non-ATPase subunit 8	40	0.543	0.807	0.68	False	False	Unenriched	-	
925	IP00030435	Q9R9W8	NFSPNAP1	Protein Nfspan1 homolog 1	33	0.262	0.368	0.71	False	False	Unenriched	-	
849	IP00041399	Q13643	FNH3	Four and a half LIM domains protein 3	31	0.474	0.667	0.71	False	False	Unenriched	-	
1080	IP00021918	Q92817	DDX39A	ATP-dependent RNA helicase DDX39A	54	0.264	0.387	0.68	False	False	Unenriched	-	
87	IP00037639	Q72794	KIF77	Keratin 77	62	2.614	3.876	0.67	False	False	Unenriched	-	
1049	IP00013949	Q43765	SGTA	Small glutamine-rich tetrapeptide repeat-containing protein alpha	34	0.324	0.480	0.68	False	False	Unenriched	-	
1049	IP00054451	P02246	GNX1L	Guanine nucleotide-binding protein subunit beta-2-like 1	35	1.256	1.568	0.67	False	False	Unenriched	-	
1048	IP00010717	Q03426	MVK	Mevalonate kinase	42	0.168	0.250	0.67	False	False	Unenriched	-	
699	IP00029200	P19623	SRM	Spermidine synthase	34	0.646	0.952	0.68	False	False	Unenriched	-	
903	IP00020249	NUP92	NUP92	Nuclear pore large G1-methylated nucleoporin	86	0.193	0.267	0.68	False	False	Unenriched	-	
156	IP00088541	Q92841	DDX17	Isomorph 4 of Probable ATP-dependent RNA helicase DDX17	80	3.354	4.927	0.68	False	False	Unenriched	-	
893	IP00006408	Q9Y314	NSOP	Nitric oxide synthase interacting protein	33	0.410	0.602	0.68	False	False	Unenriched	-	
643	IP00024689	P62333	PSM6B	Isomorph 2 of Proteasome subunit alpha type-6	38	0.602	0.848	0.68	False	False	Unenriched	-	
906	IP00030469	P52594	ADGF1	Isomorph 2 of Arf-GAP domain and FG repeats-containing protein 1	54	0.237	0.348	0.68	False	False	Unenriched	YES	
1805	IP00021638	P21796	VDAC1	Voltage-dependent anion-selective channel protein 1	31	0.098	0.143	0.69	False	False	Unenriched	-	
50	IP00054676	P69892	HBE2	Hemoglobin subunit gamma-2	16	21.329	20.825	0.69	False	False	Unenriched	-	
279	IP00024068	Q9WUM4	POC5GIP	Programmed cell death interacting protein 5	67	0.627	0.903	0.69	False	False	Unenriched	-	
622	IP00059292	Q56472	MAGOH8	Protein magi nashi homolog	17	1.343	1.950	0.69	False	False	Unenriched	-	
1058	IP00013810	Q43709	WBSK22	Isomorph 1 of Uncharacterized methyltransferase WBSK22	32	0.225	0.328	0.69	False	False	Unenriched	-	
1499	IP00025584	Q04049	WRB2	WD repeat-containing protein 82	130	0.049	0.040	0.70	False	False	Unenriched	-	
2076	IP00078313	Q9H2C5	METTL11	Methyltransferase-like protein 14	52	0.035	0.050	0.70	False	False	Unenriched	-	
220	IP00012340	Q13242	SFRS9	Splicing factor, arginine/serine-rich 9	26	3.110	3.977	0.78	False	False	Unenriched	-	
16	IP00039678	P20261	HNRNP2B1	Isomorph B1 of Heterogeneous nuclear ribonucleoproteins A2/B1	37	13.927	17.446	0.79	False	False	Unenriched	-	
947	IP00020806	P49721	PSM82	Proteasome subunit beta type-2	23	1.666	2.114	0.79	False	False	Unenriched	-	
407	IP00019321	P15927	RPA2	Isomorph 1 of Replication protein A 32 kDa subunit	29	0.509	0.642	0.79	False	False	Unenriched	-	
127	IP00013420	Q92825	FAR5A	Phenylalanyl-tRNA synthetase alpha chain	58	0.186	0.240	0.77	False	False	Unenriched	-	
1438	IP00018497	Q32C08	TIMM50	Isomorph 2 of Mitochondrial import inner membrane translocase subunit TIM50	50	0.120	0.155	0.77	False	False	Unenriched	-	
752	IP00011770	Q00483	NDFU44	NAH domain containing [ubiquitin] 1 alpha subcomplex subunit 4	9	2.184	2.817	0.78	False	False	Unenriched	-	
1007	IP00021167	Q75507	TRAF3	Isomorph 1 of Interferon-inducible double-stranded RNA-dependent protein kinase activator A	43	0.443	0.443	0.77	False	False	Unenriched	-	
721	IP00030512	Q94979	SEC13A	Isomorph 1 of Protein transport protein SEC13A	122	0.138	0.180	0.77	False	False	Unenriched	-	
727	IP00029581	P23258	TUBG1	Tubulin gamma 1 chain	51	0.340	0.443	0.77	False	False	Unenriched	-	
157	IP00020881	P52597	HNRNP28	Heterogeneous nuclear ribonucleoprotein F	46	3.983	5.186	0.77	False	False	Unenriched	-	
1588	IP00029486	Q99556	DUSP9	Dual specificity protein phosphatase 9	42	0.096	0.125	0.77	False	False	Unenriched	-	
1574	IP00018029	Q9U088	BAAP2	Isomorph 5 of Bran-specific angiogenesis inhibitor 1-associated protein 2	57	0.071	0.092	0.77	False	False	Unenriched	-	
1811	IP00029558	Q02243	TRAF3B	NADH dehydrogenase [ubiquinone] 1 subunit C2	154	0.180	0.234	0.77	False	False	Unenriched	-	
379	IP00047145	P08727	KRT19	Keratin, type I cytoskeletal 19	44	4.441	5.868	0.76	False	False	Unenriched	-	
711	IP00007682	P38806	ATF7V1A	V-type protein ATPase catalytic subunit C	68	0.289	0.382	0.76	False	False	Unenriched	-	
61	IP00017954	P35599	TRAF3	Isomorph 1 of Polyubiquitin tract-binding protein 3	76	3.458	4.855	0.76	False	False	Unenriched	-	
1547	IP00070581	Q9R0W9	FANCD2	Isomorph 1 of Fancconi anemia group D2 protein	166	0.028	0.037	0.76	False	False	Unenriched	-	
792	IP00021826	P62140	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	37	1.734	2.275	0.76	False	False	Unenriched	-	
1564	IP00000606	Q02243	TRAF3	Isomorph 1 of Polyubiquitin tract-binding protein 3	76	3.458	4.855	0.76	False	False	Unenriched		

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	IPI Accession	UniProtKB Accession	Gene name	Protein name	Relative abundance (mean normalized spectral counts) × 10 ³			Fold enrichment (active/inactive)		Specific enrichment [†]		Cluster [‡]	Adhesome [§]	Hierarchical clustering
					MW (kDa)	Active integrin	Inactive integrin	Active integrin [†]	Inactive integrin [†]	Active integrin [†]	Inactive integrin [†]			
682	IP00027996	P57757	CORO7	Isomorf 1 of Coronin 7	101	0.185	0.261	0.51	False	False	Unenriched	–	–	
1874	IP00021739	G01740	GCYF1	PEK2 amino acid-rich with GY domain-containing protein 1	115	0.018	0.024	0.15	False	False	Unenriched	–	–	
359	IP00031570	Q98507	C1orf57	Nucleoside-triphosphatase C1orf57	201	2.157	4.230	0.51	False	False	Unenriched	–	–	
419	IP00015947	P25685	DNAH1B	DnaJ homology subfamily B member 1	38	0.942	1.849	0.51	False	False	Unenriched	–	–	
1750	IP00054711	P14923	JUP	junction plakoglobin	60	0.086	0.168	0.51	False	False	Unenriched	–	–	
802	IP00179026	Q9JUC4	MCT51	Isomorf 1 of Malinact 1 cell-amplified sequence 1	21	0.559	1.100	0.51	False	False	Unenriched	–	–	
1801	IP00012833	P60510	PP94C	Serine/threonine-protein phosphatase 4 catalytic subunit	35	0.072	0.142	0.51	False	False	Unenriched	–	–	
208	IP00020783	Q9JUC4	STAT5A	Signal transducer and activator of transcription 5A	91	1.239	0.60	0.60	False	False	Unenriched	–	–	
479	IP00001738	Q99567	NUP88	Nuclear pore complex protein Nup88	84	0.403	0.667	0.60	False	False	Unenriched	–	–	
301	IP00045631	Q60341	KDM1	Isomorf 1 of Lysine-specific histone demethylase 1	99	0.558	0.918	0.61	False	False	Unenriched	–	–	
254	IP00079306	P28071	PSR85	Proteasome subunit beta type-5	28	2.410	3.976	0.61	False	False	Unenriched	–	–	
1020	IP00024795	Q8NF91	SYNE1	Isomorf 4 of Nesprin-1	1005	0.002	0.003	0.67	False	False	Unenriched	–	–	
1024	IP00007935	Q9H6C4	PDLIM5	PDZ and LIM domain protein 5	64	0.116	0.190	0.61	False	False	Unenriched	–	–	
364	IP00015651	P19754	RCC1	5-adenosylmethionine synthetase isomorf type-2	44	0.394	0.662	0.60	False	False	Unenriched	–	–	
705	IP00007155	Q9JUK1	VPS28	Vacuolar protein sorting-associated protein 28 homolog	25	0.662	1.108	0.60	False	False	Unenriched	–	–	
143	IP00083708	Q9Y523	PRKAC	Isomorf 2 of Protein kinase C- δ -like 2	317	0.336	0.560	0.60	False	False	Unenriched	–	–	
1405	IP00081573	Q11428	TGDF1	Isomorf 4 of Treacle protein	156	0.003	0.009	0.60	False	False	Unenriched	–	–	
18	IP00017617	P17844	DDX5	Probable ATP-dependent RNA helicase DDX5	69	5.706	9.123	0.63	False	False	Unenriched	–	–	
633	IP00080449	Q9JUN5	FP1L1	Isomorf 3 of Tre-1-like 3	58	0.420	0.675	0.62	False	False	Unenriched	–	–	
32	IP00017963	P08779	KRT16	Keratin, type I cytoskeletal 16	53	6.723	10.935	0.61	False	False	Unenriched	–	–	
188	IP00030725	P02538	KRT6A	Keratin, type II cytoskeletal 6A	60	4.422	7.197	0.61	False	False	Unenriched	–	–	
975	IP00128505	Q8RWR3	GTSE1	Gamete-specific factor 1	19	0.602	0.982	0.61	False	False	Unenriched	–	–	
718	IP00011257	Q84917	ACR3	Isomorf 1 of Cell division cycle and apoptosis regulator protein 1	133	0.084	0.136	0.62	False	False	Unenriched	–	–	
1303	IP00033030	P16186	ADRM1	Proteasomal ubiquitin receptor ADRM1	42	0.156	0.253	0.62	False	False	Unenriched	–	–	
375	IP00041007	Q7Z2W4	ZC3HAV1	Isomorf 1 of Zinc finger CCHC-type antiviral protein 1	101	0.404	0.652	0.62	False	False	Unenriched	–	–	
1109	IP00010369	Q9C623	WRHG1	WD repeat-containing protein 61	302	0.391	0.62	0.62	False	False	Unenriched	–	–	
442	IP00021742	Q8W222	HCG_204502	ANHD1-EP48P3 protein	277	0.347	0.551	0.63	False	False	Unenriched	–	–	
734	IP000165361	Q8H8T7	DGJUN1D5	DCN1-like protein 5	28	0.576	0.914	0.63	False	False	Unenriched	–	–	
874	IP00007321	Q75620	LPLA1	Acyl-protein thioesterase 1	49	0.586	0.929	0.63	False	False	Unenriched	–	–	
716	IP00007611	P48047	ATPSO	ATP-synthase subunit O, mitochondrial	23	0.833	1.312	0.63	False	False	Unenriched	–	–	
181	IP00079518	P33991	MCM4	DNA replication licensing factor, MCM4	93	0.851	1.335	0.64	False	False	Unenriched	–	–	
1513	IP00001605	Q9JUK4	NTR1	NTF-2-related export protein 1	60	0.315	0.484	0.64	False	False	Unenriched	–	–	
165	IP00007188	P05141	SLC25A5	ADP/ATP translocase 2	33	2.981	4.610	0.65	False	False	Unenriched	–	–	
1225	IP000165171	Q9Q6F8	DGCR14	Protein DGCR14	53	0.128	0.198	0.65	False	False	Unenriched	–	–	
178	IP00021638	Q97972	PCALD1	Isomorf 2 of Phosphatidylinositol-binding clathrin assembly protein	62	1.414	2.201	0.65	False	False	Unenriched	–	–	
1586	IP00025585	Q9JUF8	CGBP1	CGG triplet repeat-binding protein 1	19	0.155	0.242	0.64	False	False	Unenriched	–	–	
714	IP00014550	Q8N188	DNM2	dynamine 2 isomorf 2	98	0.164	0.256	0.64	False	False	Unenriched	–	YES	
1183	IP00007811	P13864	CDK6	Cyclin dependent protein kinase 4	64	1.008	1.574	0.64	False	False	Unenriched	–	–	
104	IP00000873	P26640	VARS	Valyl-tRNA synthetase	140	0.982	1.473	0.67	False	False	Unenriched	–	–	
915	IP00009253	P54920	NAPA	Alpha-synuclein NTF attachment protein	33	0.456	0.682	0.67	False	False	Unenriched	–	–	
41	IP00025512	Q9J979	HSP90A	Heat shock protein beta-1	23	10.911	16.447	0.65	False	False	Unenriched	–	YES	
531	IP00082189	P22061	PCMT1	Isomorf 2 of Protein-L-isospartate(D-aspartate) O-methyltransferase	30	1.073	1.617	0.66	False	False	Unenriched	–	–	
1375	IP00039813	Q6ZK17	LNH2B8	Isomorf 1 of Protein lin-28 homolog B	27	0.149	0.225	0.66	False	False	Unenriched	–	–	
958	IP00002373	Q9JUK3	NDR1	RNA-binding protein NDR1	66	0.250	0.377	0.66	False	False	Unenriched	–	–	
790	IP00010302	Q99419	CNN3	Calponin-3	34	0.515	0.778	0.66	False	False	Unenriched	–	–	
345	IP00002460	P20073	ANXA7	Isomorf 1 of Annexin A7	53	1.031	1.573	0.66	False	False	Unenriched	–	–	
1353	IP00030309	P54254	POLR2H	DNA-directed RNA polymerases I, II, and III subunit RPABC3	17	0.322	0.492	0.65	False	False	Unenriched	–	–	
311	IP00019516	Q9JUK4	RPLP0	Ribosome-associated phospholipase 1	49	0.586	0.929	0.65	False	False	Unenriched	–	–	
1351	IP00081600	Q14475	HBE1	Epiplon-globin (Fragment)	4	13.072	19.914	0.66	False	False	Unenriched	–	–	
1277	IP00018249	Q60726	CTNND1	Isomorf 1A8 of Catenin-1 delta-1	107	0.035	0.053	0.66	False	False	Unenriched	–	–	
1427	IP00011297	Q95573	ACSL3	Long-chain-fatty-acyl-CoA ligase 3	64	0.084	0.136	0.66	False	False	Unenriched	–	–	
1921	IP00080795	Q8RWF8	UPF040 protein	UPF040 protein	9	0.366	0.510	0.66	False	False	Unenriched	–	–	
798	IP00029130	Q14677	CLINT1	Clathrin interactor 1	70	0.258	0.396	0.65	False	False	Unenriched	–	–	
1227	IP00020895	P49757	NLME1	Isomorf 1 of Protein numb homolog	65	0.128	0.198	0.65	False	False	Unenriched	–	–	
1161	IP00005040	P11310	ACADM	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	47	0.216	0.331	0.65	False	False	Unenriched	–	–	
1940	IP00055639	Q9H615	SMG1	411 kDa protein	411	0.006	0.009	0.67	False	False	Unenriched	–	–	
1421	IP00002160	P09397	HNRK1	Isomorf 1 of Porphobilinogen deaminase	39	0.111	0.170	0.65	False	False	Unenriched	–	–	
1503	IP00001960	Q9Y696	CLIC4	Chloride intracellular channel family 4	29	0.161	0.248	0.65	False	False	Unenriched	–	–	
1906	IP00034803	Q6G6V3	C2orf79	Uncharacterized protein C2orf79	16	0.113	0.173	0.65	False	False	Unenriched	–	–	
1632	IP00045211	Q9H6A6	WRHG2	WD repeat-containing protein 62	85	0.390	0.62	0.65	False	False	Unenriched	–	–	
1637	IP00000005	P01111	NRAS	GTPase NRAS	21	0.189	0.289	0.65	False	False	Unenriched	–	–	
1	IP00021440	P63261	ACTG1	Actin, cytoplasmic 1	42	49.453	107.033	0.46	False	False	Inactive	YES	–	
112	IP00013559	P55227	KRT9	Keratin, type I cytoskeletal 9	62	8.198	12.711	0.64	False	False	Inactive	–	–	
358	IP00029078	P19013	KRT4	keratin 4	64	0.599	1.305	0.46	False	False	Inactive	–	–	
521	IP00023530	Q00335	CKD5	Cell division protein kinase 5	33	1.353	2.957	0.46	False	False	Inactive	–	–	
41	IP00014688	Q14368	BUB3	Isomorf 1 of Mitotic checkpoint protein BUB3	37	4.063	6.950	0.45	False	False	Inactive	–	–	
196	IP00021428	P68133	ACTA1	Actin, alpha skeletal muscle	42	32.231	70.888	0.45	False	False	Inactive	YES*	–	
73	IP00014856	Q14157	UBAP2L	Isomorf 1 of Ubiquitin-associated protein 2-like	115	1.319	2.895	0.46	False	False	Inactive	–	–	
66	IP00025512	Q9J979	HSP90A	Heat shock protein beta-1	23	10.911	16.447	0.46	False	False	Inactive	–	–	
933	IP00021749	Q92540	SMG7	Isomorf 1 of Protein SMG7	127	0.091	0.200	0.46	False	False	Inactive	–	–	
299	IP00029048	Q14166	TLIL2	Tubulin-tyrosine ligase-like protein 2	74	0.516	1.139	0.45	False	False	Inactive	–	–	
13	IP00021204	P55998	KRT2	Keratin, type I cytoskeletal 2 epidermal	66	9.840	22.999	0.45	False	False	Inactive	–	–	
221	IP00018693	Q97411	ANR1	Adrenic phospholipid transferase	66	0.946	1.236	0.45	False	False	Inactive	–	–	
674	IP00041706	Q9JUF5	TUBB6	46 kDa protein	46	12.385	27.688	0.45	False	False	Inactive	–	–	
235	IP00021298	P04350	TUBB4	Tubulin beta-4 chain	50	21.541	48.079	0.45	False	False	Inactive	–	–	
1217	IP00021692	Q9N856	MRN1	Isomorf 1 of Mre114-like protein 1	45	6.220	11.395	0.45	False	False	Inactive	–	–	
1115	IP00002922	Q98207	TBL1X1	F-box-like/WD repeat-containing protein TBL1X1	56	0.132	0.284	0.45	False	False	Inactive	–	–	
1448	IP00009480	Q96627	CDP58	CDP58 signalosome subunit protein	23	0.172	0.383	0.45	False	False	Inactive	–	–	
723	IP00086469	Q9JUF5	TUBB6	Tubulin beta-6 chain	47	12.272	27.810	0.44	False	False	Inactive	–	–	
862	IP00027485	P06730	EF4E	Eukaryotic translation initiation factor 4E	25	0.432	0.977	0.44	False	False	Inactive	–	–	
3	IP00038236	P52272	HNRPMP	Isomorf 2 of Heterogeneous nuclear ribonucleoprotein M	74	17.816	37.612	0.47	False	False	Inactive	–	–	
15	IP00029645	P63010	EF3A1	Elongation factor 3-alpha 1	50	18.176	38.404	0.47	False	False	Inactive	–	–	
409	IP00010118	Q96P08	QKI	Isomorf 4 of Protein quaking	40	0.940	1.987	0.47	False	False	Inactive	–	–	
319	IP00037397	P52948	NUP98	Isomorf 5 of Nuclear pore complex protein Nup88-Nup96	196	0.229	0.482	0.48	False	False	Inactive	–	–	
7	IP00079277	Q98863	TUBA1B	Tubulin alpha-1B chain	47	17.980	37.664	0.47	False	False	Inactive	–	YES	
1444	IP00047860	Q51619	UBAP2	Ubiquitin-associated protein 2 (UBAP2), transcript variant 1	73	0.235	0.494	0.48	False	False	Inactive	–	–	
992	IP00047307	P54619	PRKAG1	5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1, SUBUNIT 1	39	0.264	0.557	0.47	False	False	Inactive	–	YES	
1418	IP00010122	Q9JUK3	NDR1	Isomorf 1 of Nucleoside diphosphate	66	0.200	0.370	0.47	False	False	Inactive	–	–	
1129	IP00037541	Q96464	FUBP1	Isomorf 1 of Far upstream element-binding protein 1	68	0.777	1.631	0.48	False	False	Inactive	–	–	
1228	IP00016513	P63026	RAB10	Ras-related protein Rab-10	23	0.870	1.825	0.48	False	False	Inactive	–	–	
734	IP00020581	Q95811	ENHS1	Ewing sarcoma breakpoint region 1 isomorf 1	124	0.509	0.928	0.48	False	False	Inactive	–	–	
1086	IP00005948	Q9H620	MR1	Isomorf 1 of Methylthioesterase-1-phosphate isomerase	39	0.185	0.397	0.47	False	False	Inactive	–	–	
130	IP00037261	Q6824	FUBP3	Isomorf 1 of Far upstream element-binding protein 3	62									

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	IP1 Accession	UniProtKB Accession	Gene name	Protein name	Relative abundance (mean normalized spectral count) x10 ³		Fold enrichment (active/inactive)		Specific enrichment [†]		Adhesome [‡]	Hierarchical clustering
					Protein MW (kDa)	Active integrin	Inactive integrin	Active integrin	Inactive integrin	Cluster [§]		
847	IP00033130	Q9JBU0	SAE1	SUMO-activating enzyme subunit 1	38	0.262	0.683	0.38	False	False	Inactive	
1493	IP00375622	Q78920	CTF84	1 of 2 Cytosolic polyubiquitin element-binding protein 4	30	0.044	0.115	0.38	False	False	Inactive	
155	IP00165230	DZAF1	DZAF1	Isomorph of DAZ-associated protein 1	41	1.783	4.813	0.37	False	False	Inactive	
22	IP00013877	P31942	HNRNP33	Isomorph of Heterogeneous nuclear ribonucleoprotein H3	37	7.551	20.190	0.37	False	False	Inactive	
1112	IP00025084	P09522	CTPK1	Catalin small subunit 1	67	0.255	0.118	0.37	False	False	Inactive	YES*
29	IP00026592	Q9Y446	PKP3	Plakophilin-3	87	0.465	1.249	0.37	False	False	Inactive	
1059	IP00078934	P14923	JUP	Junction plakoglobin	63	0.752	2.015	0.37	False	True	Inactive	
510	IP0029242	P17812	CTPS	CTP synthase 1	69	0.325	0.885	0.37	False	False	Inactive	
72	IP00025815	Q13148	TARDP	TDPA3	45	2.792	7.591	0.37	False	False	Inactive	
949	IP00328938	Q9BWD0	RNF138	Isomorph of E3 ubiquitin-protein ligase RNF138	28	0.357	0.972	0.37	False	False	Inactive	
145	IP00564481	Q9N056	MIRN1	Putative uncharacterized protein MIRN1	36	1.986	5.400	0.37	False	False	Inactive	
1008	IP00022597	P61081	UBE2M	NEDD8-conjugating enzyme Ubc2	21	0.384	1.051	0.37	False	False	Inactive	
1911	IP00024097	Q9JUG8	TES	Isomorph of 1 of Testin	48	0.021	0.058	0.36	False	False	Inactive	YES
217	IP00021700	P48634	BAT2	Isomorph of 1 of Large proline-rich protein BAT2	229	0.223	0.516	0.36	False	False	Inactive	
719	IP00016008	P11413	GPDP	Isomorph Long of Glucosa-6-phosphate 1-dehydrogenase	64	0.169	0.466	0.36	False	False	Inactive	
1721	IP00022079	Q9Y609	NCOA3	Isomorph of 2 of Nuclear coactivator coactivator 3	154	0.007	0.019	0.37	False	False	Inactive	
1627	IP00024530	P36404	ARL2	ADP-ribosylation factor-like protein 2	51	0.120	0.330	0.36	False	False	Inactive	
366	IP00004273	P49756	RBM25	Isomorph of 1 of RNA-binding protein 25	100	0.279	0.781	0.36	False	False	Inactive	
195	IP00554777	P08243	ASNS	Asparagine synthetase [glutamine-hydrolyzing]	64	0.901	2.515	0.36	False	False	Inactive	
1003	IP00309578	Q43488	ARX7A2	Altaxon B1 aldolase reductase member 2	40	0.241	0.673	0.36	False	False	Inactive	
852	IP00024530	Q89Y56	HLEF2	Isomorph of 1 of HEAT repeat-containing protein 2	49	0.104	0.291	0.36	False	False	Inactive	
1557	IP00304932	Q43159	R8R8	Ribosomal RNA-processing protein 8	51	0.042	0.119	0.35	False	False	Inactive	
382	IP00078906	P38838	LAP3	Isomorph of 2 of Cytosol aminopeptidase	53	0.399	1.081	0.21	False	False	Inactive	
576	IP00021175	Q90626	Sectm	Sectm	22	0.609	2.828	0.22	False	False	Inactive	
700	IP00003923	P11772	UMPS	Isomorph of 1 of Uridine 5'-monophosphate synthase	55	1.074	0.816	0.21	False	False	Inactive	
44	IP00036064	Q86848	ITGAS	Integrin alpha 5	112	1.082	5.174	0.21	False	True	Inactive	YES
1153	IP00124805	Q94788	ALDH1A2	Isomorph of 1 of Retinal dehydrogenase 2	52	0.066	0.117	0.21	False	False	Inactive	
570	IP00041280	Q86K55	CARM1	Isomorph of 1 of Histone-arginine methyltransferase CARM1	63	0.194	0.973	0.20	False	False	Inactive	
1113	IP00018627	Q6GZ21	NAT13	Isomorph of 1 of N-acetyltransferase 13	19	0.231	1.154	0.20	False	False	Inactive	
1570	IP00078407	Q86947	DISS2	Isomorph of 1 of RNA-dihydroxyisopentyl synthase 3-like	72	0.040	0.098	0.20	False	False	Inactive	
38	IP00021756	P05556	ITGB1	Isomorph Beta-1 of Integrin beta 1	88	1.549	7.572	0.20	False	False	Inactive	YES
1716	IP00068145	Q8P956	C7orf27	Isomorph of 1 of HEAT repeat-containing protein C7orf27	88	0.008	0.040	0.20	False	False	Inactive	
1153	IP00028791	P18732	CAQ1	Probable cytosolic iron-sulfur protein assembly protein CAQ1	88	0.223	0.233	0.20	False	False	Inactive	
1549	IP00002324	Q9N219	MAT2B	Isomorph of 1 of Methionine adenosyltransferase 2 subunit beta	38	0.047	0.233	0.20	False	False	Inactive	
967	IP00022822	P39060	COL1A1	Isomorph of 2 of Collagen alpha-1(XVII) chain	154	0.035	0.173	0.20	False	False	Inactive	
2961	IP00012460	P19024	LGTN	Isomorph of 1 of Lignin	65	0.016	0.076	0.20	False	False	Inactive	
326	IP00000897	P42694	HEL2	HEL2 protein	219	0.100	0.532	0.19	False	True	Inactive	
555	IP00021593	Q14687	GSE1	Isomorph of 1 of Genetic suppressor element 1	136	0.086	0.455	0.19	False	False	Inactive	
1215	IP00013999	P15976	GATL3	Isomorph of 1 of Tyrosyl transferase factor	43	0.083	0.443	0.19	False	False	Inactive	
1352	IP00010080	Q95747	OXSR1	Serine/threonine-protein kinase OXSR1	58	0.043	0.238	0.18	False	False	Inactive	
1760	IP00030096	Q15286	RAB35	Ras-related protein Rab-35	23	0.219	1.201	0.18	False	False	Inactive	
740	IP00022103	Q18621	DNCE2	Segment polarity protein-disc-large homolog DNL-2	79	0.028	0.454	0.18	False	False	Inactive	
1542	IP00084996	Q9C066	DNAH6	Isomorph of 1 of Dyx19c1 heavy chain 6, axonemal	476	0.002	0.011	0.18	False	False	Inactive	
415	IP000641384	Q15027	SEC16A	SEC16 homolog A	252	0.077	0.304	0.25	False	False	Inactive	
547	IP00028935	P18466	KDM3B	Isomorph of 1 of Lysine-specific demethylase 3B	150	0.040	0.243	0.25	False	False	Inactive	
648	IP00048871	Q9Y530	UHRF10	Uncharacterized protein Gorf130	17	0.899	3.616	0.25	False	False	Inactive	
56	IP00005780	Q15294	OGT	Isomorph of 3 of UDP-N-acetylglucosamine-6-phosphate N-acetylglucosaminyltransferase 110 kDa subunit	117	0.100	0.382	0.26	False	False	Inactive	
697	IP00013933	P15924	DSP	Isomorph DPH of Desmoplamin	332	0.027	0.105	0.26	False	False	Inactive	
1507	IP00033568	Q9H747	PTGE2	Prostaglandin G/H synthase 2	42	0.069	0.263	0.26	False	False	Inactive	
1532	IP00024802	Q14981	BTAF1	TATA-binding protein-associated factor 172	207	0.010	0.037	0.27	False	False	Inactive	
817	IP00049389	Q86V86	METTL11A	Protein of unknown function DUF358, methyltransferase-like family protein	25	0.314	1.211	0.26	False	False	Inactive	
484	IP00024033	Q9H254	PTK23	Tyrosine-protein phosphatase non-receptor-type 23	165	0.018	0.031	0.26	False	False	Inactive	
1047	IP00020944	P37268	F0F17	Squalene synthetase	48	0.122	0.474	0.26	False	False	Inactive	
1360	IP00008771	Q10314	HHEX	Hematopoietically-expressed homeobox protein HHEX	30	0.084	0.328	0.26	False	False	Inactive	
1590	IP00010706	Q9H456	RIIAP2	Interferon alpha response factor 2	15	0.284	1.016	0.26	False	False	Inactive	
305	IP00022977	P12277	CKB	Creatine kinase B	43	0.605	2.756	0.22	False	False	Inactive	
245	IP00095406	Q9NT26	RBM12	Putative uncharacterized protein DKF2667H197 (Fragment)	100	0.293	1.327	0.22	False	False	Inactive	
604	IP00036218	Q8P947	SGR2	SCR-like protein 2	102	0.462	1.622	0.22	False	False	Inactive	
1390	IP000878754	Q86U11	PRPF39	Isomorph of 1 of Pre-mRNA-processing factor 39	78	0.009	0.042	0.21	False	False	Inactive	
466	IP000478231	P61586	RHOA	Transforming protein RhoA	22	0.779	3.392	0.23	False	False	Inactive	
766	IP00022184	Q18732	CAQ1	Isomorph of 3 of Pumilio homolog 2	88	0.221	0.962	0.23	False	False	Inactive	
884	IP00021843	Q9R063	TUBA1C	Tubulin alpha-1C chain	50	7.557	32.785	0.23	False	True	Inactive	YES*
672	IP000395347	Q171C2	LARP4	Isomorph of 1 of La-related protein 4	81	0.149	0.659	0.23	False	False	Inactive	
878	IP00020454	P12707	DCX	Developmental protein DCX	33	0.283	1.060	0.23	False	False	Inactive	
511	IP00016669	Q15382	RHEB	GTP-binding protein Rheb	20	0.677	2.968	0.23	False	False	Inactive	
1928	IP00024281	Q14893	SFP1	Isomorph of 1 of Survival of motor neuron protein-interacting protein 1	32	0.031	0.138	0.22	False	False	Inactive	
941	IP00023505	Q15639	MKP13	Isomorph of 1 of Mitogen-activated protein kinase phosphatase 13	49	0.408	1.493	0.23	False	False	Inactive	
1120	IP00002857	Q15639	MKP14	Isomorph CSBP2 of Mitogen-activated protein kinase 14	41	0.105	0.472	0.22	False	False	Inactive	
1180	IP000789069	Q9NVU2	ARL8B	ADP-ribosylation factor-like protein 8B	21	0.192	0.812	0.24	False	False	Inactive	
3751	IP00023846	Q86V95	FAM83A	Isomorph of 1 of Protein FAM83A	47	0.023	0.103	0.24	False	False	Inactive	
1327	IP00029035	Q96444	TP53RK	TP53-regulating kinase	28	0.116	0.492	0.24	False	False	Inactive	
1774	IP00027838	Q98024	RBM4B	RNA-binding protein 4B	40	0.529	2.244	0.24	False	False	Inactive	
1664	IP00012122	P41240	CEK	Tyrosine-protein kinase CEK	51	0.040	0.162	0.25	False	False	Inactive	YES
2080	IP00013929	Q15923	TCF3	Isomorph E12 of Transcription factor E2-alpha	68	0.015	0.061	0.25	False	False	Inactive	
435	IP00015046	Q9N604	RBM22	Isomorph of 1 of Pre-mRNA-splicing factor RBM22	47	0.502	1.492	0.34	False	False	Inactive	
842	IP00017596	Q86N64	TTCC	Tetratricopeptide repeat protein 5C	20	0.385	1.143	0.34	False	False	Inactive	
212	IP00033371	P17801	PTL	Isomorph of 1 of 6-phosphotransferase, beta type	42	0.834	3.484	0.34	False	False	Inactive	
914	IP000745793	P14635	CNB1	G2/mitotic-specific cyclin B1	48	0.152	0.450	0.34	False	False	Inactive	
1838	IP00021917	P11908	PHF2	Isomorph of 1 of Ribose-phosphate pyrophosphokinase 2	35	0.329	0.979	0.34	False	False	Inactive	
833	IP00011706	Q10767	ESD	S-fructose-bisphosphate hydrolase	34	0.235	0.701	0.34	False	False	Inactive	
775	IP00007750	P68366	TUBA4A	Tubulin alpha-4A chain	50	7.680	32.899	0.34	False	False	Inactive	
1752	IP00010296	Q8RY85	SMAP1	Isomorph of 1 of Stromal membrane-associated protein 1	50	0.071	0.210	0.34	False	False	Inactive	
1128	IP00016812	Q15639	RAP1A	Isomorph of 1 of Ras-related protein RAS1	34	0.204	0.746	0.34	False	False	Inactive	
561	IP00019345	P62834	SAL1	Ras-related protein Rap-1A	21	0.923	2.683	0.34	False	False	Inactive	
1872	IP00087071	Q10224	SLIT1A3	Isomorph of 1 of Slitrotonin receptor 3	34	0.085	0.244	0.35	False	False	Inactive	
148	IP00024971	Q14748	TEBTD1	Isomorph of 1 of Transcription elongation regulator 1	43	0.165	0.498	0.31	False	False	Inactive	
729	IP00030607	Q9H029	RBM38	Isomorph of 1 of RNA-binding protein 38	25	0.443	1.424	0.31	False	False	Inactive	
49	IP00030357	Q60374	DHFR	Dihydrofolate reductase	21	0.857	2.789	0.31	False	False	Inactive	
1159	IP00021628	Q10771	PKCE	Isomorph Beta-1 of Protein kinase C beta type	72	0.189</						

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	IPI Accession	UniProtKB Accession	Gene name	Protein name	Relative abundance (mean normalised spectral count) × 10 ³			Fold enrichment (active/inactive)		Specific enrichment		Cluster*	Adhesome*	Hierarchical clustering
					MW (kDa)	Active integrin	Inactive integrin	Active integrin	Inactive integrin	Active integrin	Inactive integrin			
1661	IP00027547	P61605	DCD	Dermicidin	11	0.092	1.074	0.09	False	True	Inactive	-	-	
1309	IP00021434	R08134	RHOC	Rho-related GTP-binding protein RhoC	22	0.229	0.291	0.09	False	True	Inactive	-	-	
1541	IP00038480	Q86U90	YRC	Yrc domain-containing protein, mitochondrial	29	0.025	0.286	0.09	False	True	Inactive	-	-	
1055	IP00184821	Q13057	COASY	Isomorph of bifunctional coenzyme A synthase	62	0.052	0.419	0.12	False	True	Inactive	-	-	
807	IP00037645	Q82642	YRN2	Isomorph of Y ₂ exoribonuclease 1	153	0.029	0.233	0.12	False	True	Inactive	-	-	
1729	IP00023556	Q9N977	SU12	Isomorph of RNA polymerase II subunit domain phosphatase SU12	23	0.047	0.384	0.12	False	True	Inactive	-	-	
940	IP00041356	Q9R937	VSPA4	Vacuolar protein sorting-associated protein 4A	49	0.053	0.444	0.12	False	True	Inactive	-	-	
712	IP00013561	Q13620	TSG1	GDP-L-fucose synthase	36	0.140	1.212	0.12	False	True	Inactive	-	-	
1515	IP00018783	Q98Y32	ITPA	Inosine triphosphatase	21	0.072	0.618	0.12	False	True	Inactive	-	-	
1955	IP00291928	P61106	RAB14	Ras-related protein Rab-14	24	0.105	0.921	0.11	False	True	Inactive	-	-	
1546	IP00020980	Q92ND4	EH2	EH domain-containing protein 2	61	0.012	0.109	0.11	False	True	Inactive	-	-	
690	IP00023647	ADAV11	UBA6	Isomorph of Ubiquitin-like modifier-activating enzyme 6	118	0.018	0.356	0.05	False	True	Inactive	-	-	
709	IP00301204	Q9NB87	RDH13	Retinol dehydrogenase 13	36	0.082	1.254	0.07	False	True	Inactive	-	-	
1154	IP00011539	P12882	HCK9B	Hemectox protein-like 9B	28	0.051	0.768	0.07	False	True	Inactive	-	-	
1085	IP00029737	Q60488	ACSL4	Isomorph of Long-chain-fatty-acyl-CoA ligase 4	79	0.019	0.317	0.06	False	True	Inactive	-	-	
1395	IP00010782	Q96046	GMPPA	Isomorph of 1 of Manose-1-phosphate guanylyltransferase alpha	46	0.022	0.358	0.06	False	True	Inactive	-	-	
1845	IP00405659	Q9R909	UBQLA2	Ubiquitin-2	66	0.016	0.259	0.06	False	True	Inactive	-	-	
630	IP00374068	Q6UJ74	ADAMTSL4	Isomorph of 1 of ADAMTS-like protein 4	117	0.017	0.428	0.04	False	True	Inactive	-	-	
871	IP00178375	Q43314	PPSPK2	Isomorph of 2 of Inositol hexakisphosphate and diphosphoinositil-pentakisphosphate kinase 2	138	0.007	0.216	0.03	False	True	Inactive	-	-	
591	IP00027505	P67796	ITGAV	Isomorph of 1 of integrin alpha-V	116	0.009	0.522	0.02	False	True	Inactive	YES	-	
877	IP00012728	P53121	ACSL1	Isomorph of 1 of Long-chain-fatty-acyl-CoA ligase 1	78	0.013	0.483	0.03	False	True	Inactive	-	-	
888	IP00472996	Q8ND24	RNF214	RING finger protein 214	78	0.013	0.482	0.03	False	True	Inactive	-	-	
1546	IP00028876	P55212	CASP6	Isomorph of Alpha of Caspase-6	38	0	0.233	ND	Inactive	False	True	Inactive	-	
1729	IP00179713	Q9R902	IGFBP2	Isomorph of 1 of Insulin-like growth factor 2 mRNA-binding protein 2	65	0.293	ND	Inactive	False	True	Inactive	-	-	
1359	IP00181702	Q95104	SFRS15	Isomorph of 1 of Splicing factor, arginine/serine-rich 15	126	0	0.105	ND	Inactive	False	True	Inactive	-	-
1608	IP00011726	Q02442	KTDC1	Isomorph of 1 of RNA 3'-terminal phosphatase cyclase	39	0	0.291	ND	Inactive	False	True	Inactive	-	-
1274	IP00006050	Q9P4C2	FAM151A	Isomorph of 1 of Protein FAM151A	100	0	0.152	ND	Inactive	False	True	Inactive	-	-
1536	IP00147874	Q9N945	NANS	Sialic acid synthase	40	0	0.309	ND	Inactive	False	True	Inactive	-	-
1930	IP00291800	Q9N9A8	EIF4ENF1	Isomorph of 1 of Eukaryotic translation initiation factor 4E transporter	108	0	0.030	ND	Inactive	False	True	Inactive	-	-
1974	IP00328798	Q9N9A8	RCL6	Isomorph of 1 of B-cell lymphoma 9-like protein	157	0	0.037	ND	Inactive	False	True	Inactive	-	-
1982	IP00004924	Q9H4E7	DFE6	Differentially expressed protein in FDCP 6 homolog	74	0	0.112	ND	Inactive	False	True	Inactive	YES	-
2166	IP00294618	Q92733	PRCC	Proline-rich protein PRCC	52	0	0.064	ND	Inactive	False	True	Inactive	-	-
1599	IP00744702	Q9N9E5	FAM125A	Isomorph of 1 of Multivesicular body subunit 12A	29	0	0.430	ND	Inactive	False	True	Inactive	-	-
1977	IP00031411	Q14517	FAT1	507 kDa protein	507	0	0.009	ND	Inactive	False	True	Inactive	-	-
1963	IP00013466	Q43681	ASNA1	ATPase ASNA1	39	0	0.142	ND	Inactive	False	True	Inactive	-	-
1873	IP00214562	P76509	RLN1	Retinoin factor 1	385	0	0.015	ND	Inactive	False	True	Inactive	-	-
2071	IP000002487	P42898	MTHFR	Methyltetrahydrofolate reductase	75	0	0.096	ND	Inactive	False	True	Inactive	-	-
1368	IP00031301	P41273	TM5SF9	Tumor necrosis factor ligand superfamily member 9	27	0	0.675	ND	Inactive	False	True	Inactive	-	-
1603	IP00159222	Q9N9A0	TCF20	Isomorph of 1 of Transcription factor 20	212	0	0.045	ND	Inactive	False	True	Inactive	-	-
1814	IP00007182	Q9BVC4	MLST8	Isomorph of 3 of Target of rapamycin complex subunit LST8	24	0	0.115	ND	Inactive	False	True	Inactive	-	-
2032	IP00091508	Q9R9B6	METTL1	34 kDa protein	34	0	0.211	ND	Inactive	False	True	Inactive	-	-
2062	IP00020239	Q12843	METTL9	Isomorph of 1 of Methyltransferase-like protein 9	37	0	0.217	ND	Inactive	False	True	Inactive	-	-
533	IP00087440	P43487	RANBP1	Putative uncharacterized protein RANBP1	19	0	0.380	ND	Inactive	False	True	Inactive	-	-
1206	IP00021328	Q6N9X0	IRGC	Interferon-inducible GTPase 5	50	0	0.053	ND	Inactive	False	True	Inactive	-	-
1467	IP00001735	Q9R9L8	NCKO2	Isomorph of 1 of Nuclear receptor corepressor 2	276	0	0.025	ND	Inactive	False	True	Inactive	-	-
1530	IP00055071	Q9R9W2	PLN41	Plen-41	211	0	0.045	ND	Inactive	False	True	Inactive	-	-
939	IP00026288	P62873	GMB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	27	0	0.071	ND	Inactive	False	True	Inactive	-	-
258	IP00382804	Q14222	EEF1A1	EEF1A1 protein (Fragment)	24	0	4.266	ND	Inactive	False	True	Inactive	-	-
2257	IP00002149	Q9R9L8	SAR1B	GTP-binding protein SAR1B	22	0	0.377	ND	Inactive	False	True	Inactive	-	-
1168	IP00413730	Q9N919	ACSS2	Acetyl-coenzyme A synthetase, cytoplasmic	79	0	0.280	ND	Inactive	False	True	Inactive	-	-
493	IP00128330	Q9R9V1	PPSPK1	Isomorph of 5 of Inositol hexakisphosphate and diphosphoinositil-pentakisphosphate kinase 1	133	0	0.084	ND	Inactive	False	True	Inactive	-	-
1645	IP00021317	Q14657	Torsin1	Torsin-1	38	0	0.073	ND	Inactive	False	True	Inactive	-	-
1692	IP00215191	P84085	ARIS	ADP-ribosylation factor 1	37	0	0.552	ND	Inactive	False	True	Inactive	-	-
770	IP00390130	Q9R9U5	TUBB6	Tubulin beta-2C chain	45	0	60.600	ND	Inactive	False	True	Inactive	-	-
2258	IP00016711	Q9N9K2	TUBA1C	Isomorph of 1 of Tubulin alpha chain class 3	50	0	0.502	ND	Inactive	False	True	Inactive	-	-
2205	IP00011488	Q13043	STR4	Isomorph of 1 of Serine/threonine-protein kinase 4	46	0	0.069	ND	Inactive	False	True	Inactive	-	-
1230	IP00215918	P18085	ARF4	ADP-ribosylation factor 4	21	0	2.065	ND	Inactive	False	True	Inactive	-	-
2215	IP00306439	Q9R9V7	C18orf55	TIM21-like protein, mitochondrial	28	0	0.118	ND	Inactive	False	True	Inactive	-	-
2256	IP00024502	Q9N9R5	UBQLN4	Ubiquitin-4	64	0	0.086	ND	Inactive	False	True	Inactive	-	-
2182	IP00043808	Q9NZ20	DTL	Isomorph of 1 of Denticles-like protein homolog	79	0	0.056	ND	Inactive	False	True	Inactive	-	-
1768	IP00013111	Q13617	CUL2	Cullin-2	90	0	0.098	ND	Inactive	False	True	Inactive	-	-
2211	IP00004567	Q9N9M4	PRMT7	Isomorph of 1 of Protein arginine N-methyltransferase 7	78	0	0.042	ND	Inactive	False	True	Inactive	-	-
2249	IP00393994	Q20A6	MOB2	Isomorph of 1 of Mps one binder kinase activator-like 2	27	0	0.082	ND	Inactive	False	True	Inactive	-	-
1054	IP00031420	Q9R9V1	UGN9	UDP-glucose 5-epimerase	55	0	0.251	ND	Inactive	False	True	Inactive	-	-
2117	IP00292827	Q9P289	MST4	Serine/threonine-protein kinase MST4	47	0	0.047	ND	Inactive	False	True	Inactive	-	-
1726	IP00182938	Q43865	ANCLY1	Isomorph of 1 of Putative adenylosuccinyltransferase 1	59	0	0.103	ND	Inactive	False	True	Inactive	-	-
1951	IP00023522	Q9N9A6	SH3GLB2	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	79	0	0.098	ND	Inactive	False	True	Inactive	-	-
1926	IP00024540	Q9N9A6	SH3GLB2	Isomorph of 1 of Endophilin-82	44	0	0.085	ND	Inactive	False	True	Inactive	-	-
1647	IP00008475	Q01581	HMGCS1	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	57	0	0.194	ND	Inactive	False	True	Inactive	-	-
1728	IP00017509	Q13422	PNP1	Isomorph of 1 of Phosphoprotein 1	83	0	0.060	ND	Inactive	False	True	Inactive	-	-
1404	IP00065149	Q9SC06	IRAK1	Interleukin-1 receptor-associated kinase 1 isoform 3	57	0	0.284	ND	Inactive	False	True	Inactive	-	-
2185	IP00021907	P28161	GM22	Glutathione S-transferase Mu 2	26	0	0.085	ND	Inactive	False	True	Inactive	-	-
1879	IP00295741	P07858	CTSB	Cathepsin B	36	0	0.167	ND	Inactive	False	True	Inactive	-	-
2045	IP00001640	Q9R9L5	GAMT1	N10-adenine-specific DNA methyltransferase 1	50	0	0.168	ND	Inactive	False	True	Inactive	-	-
2046	IP00001640	Q9R9L5	GAMT1	N10-adenine-specific DNA methyltransferase 1	53	0	0.168	ND	Inactive	False	True	Inactive	-	-
1678	IP00047727	Q9N9V4	KIF78	Isomorph of 1 of Keratin, type II cytoskeletal 78	27	0	0.587	ND	Inactive	False	True	Inactive	-	-
1980	IP00157965	Q9R9V1	NEB	NEB domain protein 1 (Negative regulator of ubiquitin-like proteins 1) (Renal carcinoma antigen NYN-RE18); Isoform 2	22	0	0.107	ND	Inactive	False	True	Inactive	-	-
1651	IP00220630	P49023	PN2	Isomorph of Alpha of Paxillin	61	0	0.136	ND	Inactive	False	True	Inactive	-	-
957	IP00013232	Q13422	IKZF1	Isomorph of IK3 of DNA-binding protein Ikaros	68	0	0.067	ND	Inactive	False	True	Inactive	-	-
1789	IP00054527	P02726	ACTA2	ACTA2 protein (Fragment)	37	0	27.448	ND	Inactive	False	True	Inactive	YES*	-
1806	IP00046951	Q9R9W2	HMG20B	Isomorph of 1 of SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin subfamily E member 1-related	36	0	0.082	ND	Inactive	False	True	Inactive	-	-
1828	IP00017993	P35326	SRP2A	Small proline-rich protein 2A	8	0	0.902	ND	Inactive	False	True	Inactive	-	-
1835	IP00300096	Q15235	CRPT	Nucleotide nucleoside-related phosphatase (carboxylating)	50	0	0.206	ND	Inactive	False	True	Inactive	-	-
2255	IP00166394	Q9N9V6	ARMCD10	Isomorph of 1 of Armadillo repeat-containing protein 10	38	0	0.085	ND	Inactive	False	True	Inactive	-	-
2261	IP00031545	Q14571	ITPR2	Isomorph of 1 of Aradillo repeat-containing protein type 2	308	0	0.011	ND	Inactive	False	True	Inactive	-	-
2265	IP00045112	P12035	KRT5	Keratin 5	64	0	0.760	ND	Inactive	False	True	Inactive	-	-
2004	IP00074931	Q9R9Y8	GORASP2	Golgi reassembly-stacking protein 2	49	0	0.056	ND	Inactive	False	True	Inactive	-	-
1294	IP00088911	Q13620	TSG1	Actin alpha 1 skeletal muscle protein	51	0	0.051	ND	Inactive	False	True	Inactive	-	-
2212	IP00039845	Q9N9E7	PANK4	Pantothenate kinase 4	86	0	0.051	ND	Inactive	False	True	Inactive	-	-
1770	IP00007401	Q15397	IPO8	Importin-8	120	0	0.087	ND	Inactive	False	True	Inactive	-	-
1821	IP00078409	Q9R9P3	HAT1P2	Isomorph of 1 of Orotidyltransferase HAT1P2	27	0	0.225	ND	Inactive	False	True	Inactive	-	-
1864	IP00030751	Q15014	ZNF69	Zinc finger protein 609	115	0	0.054	ND	Inactive	False	True	Inactive	-	-
1156	IP00041900	Q27270	KIAA0907	Isomorph of 1 of UPP460 protein KIAA0907	65	0	0.195	ND	Inactive	False	True	Inactive	-	-
2110	IP00024928	Q92608	DOCK2	Isomorph of 1 of Dedicator of cytokinesis protein 2	212	0	0.013	ND	Inactive	False	True	Inactive	-	-
2159	IP00049488	Q9R9V5	PPP1R15	Isomorph of 1 of Fork-associated inhibitor	89	0	0.044	ND	Inactive	False				

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	API Accession	UniProtKB Accession	Gene name	Protein name	Protein MW (kDa)	Relative abundance (mean normalized spectral counts) × 10 ³		Fold enrichment (active/inactive) (integrin ⁺)		Specific enrichment [†]		Adhesome [‡]	Hierarchical clustering
						Active integrin	Inactive integrin	Active integrin	Inactive integrin	Active integrin	Inactive integrin		
2195	PI00007304	Q95376	AHRH2	Protein araline-2 homolog	58	0	0.076	ND (inactive)	False	True	Inactive	-	
1897	PI00152200	Q57653	PRH1	Integrin α 2 PHD finger protein 19	23	0	0.228	ND (inactive)	False	True	Inactive	-	
1997	PI00093183	Q98927	DGCR6L	DGCR6 protein	25	0	0.233	ND (inactive)	False	True	Inactive	-	
1999	PI00024664	P45974	UBPS	Ubiquitin Long Ubiquitin carboxyl-terminal hydrolase 5	96	0	0.029	ND (inactive)	False	False	Inactive	-	
2020	PI00115683	Q13569	TUBB3	Tubulin beta 3 chain	50	0	1.003	ND (inactive)	False	False	Inactive	-	
1198	PI00739464			Actin, gamma 1	17	0	0.325	ND (inactive)	False	False	Inactive	-	
2152	PI00067799	Q8BTU1	BHDH2	Isomorphin α 3 hydroxybutyrate dehydrogenase type 2	27	0	0.143	ND (inactive)	False	True	Inactive	-	
1962	PI00001676	Q17430	NROCK4	Isomorphin α 2 Nuclear protein localization protein 4 homolog	69	0	0.054	ND (inactive)	False	True	Inactive	-	
1803	PI00021264	PS1911	CNN1	Calponin-1	33	0	0.269	ND (inactive)	False	True	Inactive	-	
1913	PI00783502	Q53E70	CRT2	CRIB-regulated transcription coactivator 2	72	0	0.090	ND (inactive)	False	True	Inactive	-	
2158	PI00165454	Q26910	SRN1	Sulfiredoxin-1	14	0	0.193	ND (inactive)	False	False	Inactive	-	
1432	PI00294739	Q9Y2E3	SAMHD1	Isomorphin α 1 of SAM domain and HD domain-containing protein 1	73	0	0.233	ND (inactive)	False	True	Inactive	-	
1953	PI00062882	Q12743	CTU1	Cytoplasmic tRNA 2-thiolation protein 1	36	0	0.073	ND (inactive)	False	False	Inactive	-	
2019	PI00055062	Q56127	DHRH1	Dehydrogenase/reductase SDR family member 1	34	0	0.129	ND (inactive)	False	True	Inactive	-	
2149	PI00058949	O14976	GAK	Cyclin-G-associated kinase	143	0	0.015	ND (inactive)	False	False	Inactive	-	
1756	PI00152089	Q8T803	CkxR38	Isomorphin α 1 of Uncharacterized protein CkxR38	37	0	0.149	ND (inactive)	False	True	Inactive	-	
2111	PI00025340	Q56500	P5MP	Pyridoxal-phosphate phosphatase	0	32	0.128	ND (inactive)	False	False	Inactive	-	
1942	PI00442073	P21251	CSRP1	Cysteine and glycine-rich protein 1	21	0	0.219	ND (inactive)	False	True	Inactive	YES	
2096	PI00296370	Q9JUC8	LCMT1	Putative uncharacterized protein LCMT1	39	0	0.142	ND (inactive)	False	True	Inactive	-	
2138	PI00306871	Q52680	KATZA	Isomorphin α 1 of Histone acetyltransferase KATZA	94	0	0.029	ND (inactive)	False	False	Inactive	-	
152	PI00302925	P09990	CTB	59 kDa protein	59	2.687	1.971	1.44	False	False	Active	-	
841	PI00031521	P40938	RFC3	Replication factor C subunit 3	41	0.416	0.290	1.43	False	False	Active	-	
194	PI00177963	P62336	SNRPD2	Small nuclear ribonucleoprotein Sm D2	14	8.673	6.011	1.44	False	False	Active	-	
812	PI00460208	P05174	DNAH1	Triosephosphate isomerase 1 isomorphin 2	24	3.766	2.537	1.44	False	False	Active	-	
523	PI00328319	Q90208	RBBP4	Histone-binding protein RBBP4	48	0.938	0.650	1.44	False	False	Active	-	
410	PI00470891	Q75334	CSDE1	Isomorphin α 1 of Gold shock domain-containing protein E1	89	0.636	0.441	1.44	False	False	Active	-	
647	PI00241175	Q14818	PSMA7	Isomorphin α 1 of Proteasome subunit alpha type-7	198	1.222	0.848	1.44	False	False	Active	-	
238	PI00384456	PS7201	MSH6	Isomorphin α 1 of GTP- γ -DNA mismatch repair protein Msh6	153	0.546	0.376	1.45	False	False	Active	-	
253	PI00292566	P17987	TCF1	T-complex protein 1 subunit alpha	60	1.634	1.124	1.45	False	False	Active	-	
274	PI00212623	YWH4Z2	YWH4Z2	14-3-3 protein zeta/delta	28	3.096	2.135	1.45	False	False	Active	-	
340	PI00303020	P26156	DDX6	Probable ATP-dependent RNA helicase DDX6	54	1.249	0.857	1.46	False	False	Active	-	
593	PI00216691	Q70737	PRF1	Prorhin-1	15	2.400	1.646	1.46	False	False	Active	YES	
283	PI00376005	Q97990	EIF5A	Isomorphin α 2 Eukaryotic translation initiation factor 5A-1	20	3.755	2.575	1.46	False	False	Active	-	
671	PI00555878	Q9NRW3	APORC3C1	Probable DNA dCpG-dT-editing enzyme APORC3-C	23	1.180	0.809	1.46	False	False	Active	-	
1191	PI00292695	Q12824	SMARCB1	Isomorphin α 1 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	44	0.252	0.173	1.46	False	False	Active	-	
1025	PI00214249	Q99614	PCP2	Isomorphin α 1 of mental retardation syndrome-related protein 1	70	0.124	0.084	1.48	False	False	Active	-	
82	PI00140420	Q7K274	SNF1	Staphylococcal nuclease domain-containing protein 1	102	2.070	1.464	1.41	False	False	Active	-	
526	PI00293919	P62195	PSMCS5	26S protease regulatory subunit 8	46	0.886	0.627	1.41	False	False	Active	-	
254	PI00292425	Q99760	RFC2	Isomorphin α 1 of Kinesin-like motor protein RFC2	85	0.943	0.665	1.42	False	False	Active	-	
796	PI00290416	Q9N7K5	OLA1	Isomorphin α 1 of Obj-like ATPase 1	45	0.534	0.377	1.42	False	False	Active	-	
166	PI00031415	P62081	RPS7	40S ribosomal protein S7	22	4.907	3.436	1.43	False	False	Active	-	
374	PI00268020	Q9N072	CNOT1	Isomorphin α 1 of CCR-NOT transcription complex subunit 1	199	0.289	0.209	1.43	False	False	Active	-	
744	PI00302619	Q10570	CFP1	Cleavage and polyadenylation specificity factor subunit 1	161	0.147	0.103	1.43	False	False	Active	-	
1053	PI00294178	P30154	PPP2R1B	Isomorphin α 1 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	66	0.323	0.226	1.43	False	False	Active	-	
832	PI00131998	P17980	PSM6	26S protease regulatory subunit 6a	49	0.470	0.328	1.43	False	False	Active	-	
623	PI00005511	Q7R7V0	PHF5A	PHD finger-like domain-containing protein 5A	12	2.748	1.928	1.43	False	False	Active	-	
1236	PI00031681	P24941	CDK2	Cell division protein kinase 2	34	1.063	0.747	1.42	True	False	Active	-	
64	PI00191058	Q5T6W2	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	49	5.216	3.748	1.39	False	False	Active	-	
588	PI00795769			52 kDa protein	52	0.622	0.450	1.40	False	False	Active	-	
620	PI00080552	O76003	GLRX3	Glutaredoxin-3	37	0.588	0.420	1.40	False	False	Active	-	
1607	PI00224605	Q14578	CTT	Isomorphin α 1 of Citron rho-interacting kinase	231	0.013	0.010	1.30	False	False	Active	-	
160	PI00218907	P05583	HMG2	High mobility group protein 2	24	3.985	2.800	1.40	False	False	Active	-	
332	PI00052273	P22102	GART	Isomorphin α 1 of Trifunctional purine biosynthetic protein adenosine-3	108	0.579	0.386	1.50	False	False	Active	-	
1074	PI00119316	Q13155	AMP2	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	35	0.356	0.238	1.50	False	False	Active	-	
17	PI00179130	P02979	UBA1	ubiquitin and ribosomal protein S27a precursor	18	1.714	1.247	1.40	False	False	Active	-	
319	PI00788907	Q9G651	PGAM5	Isomorphin α 1 of Serine/threonine-protein phosphatase PGAM5, mitochondrial	32	1.886	1.283	1.47	False	False	Active	-	
670	PI00220835	P60468	SGS3	Protein transport protein SecY1 subunit beta	10	3.449	2.345	1.47	False	False	Active	-	
974	PI00745613	Q9N903	EXOSC4	Exosome complex exonuclease RRP41	28	0.465	0.315	1.47	False	False	Active	-	
89	PI00219156	P62888	RPL30	60S ribosomal protein L30	13	16.921	11.420	1.48	False	False	Active	-	
610	PI00291093	P19388	POLR2E	DNA-directed RNA polymerases I, II, and III subunit RPAPC1	25	1.558	1.051	1.48	False	False	Active	-	
717	PI00152881	Q99760	SHROD2	RNAP family member 3 protein 2	117	0.200	0.139	1.48	False	False	Active	-	
331	PI00302850	P62314	SNRPD1	S1.828 nuclear ribonucleoprotein Sm D1	13	5.828	3.923	1.49	False	False	Active	-	
517	PI00282840	Q86911	THOC4	THO complex 4	28	1.716	1.156	1.48	False	False	Active	-	
264	PI00184200	Q99760	MCMD2	DNA replication licensing factor MCM2	70	0.852	0.574	1.48	False	False	Active	-	
1252	PI00220637	P49591	SARS	Seryl-tRNA synthetase, cytoplasmic	59	0.190	0.128	1.48	False	False	Active	-	
2016	PI00384339	P08107	HSPAL1	Heat shock 70 kDa protein 1	70	2.894	1.958	1.48	False	False	Active	YES	
1358	PI00254590	Q99760	RAB32A2	Isomorphin α 1 of Rab GTPase-activating protein non-catalytic subunit 3	150	0.047	0.033	1.43	False	False	Active	-	
673	PI00070818	Q9JUK6	CFP5	Cleavage and polyadenylation specificity factor subunit 5	77	0.344	0.231	1.49	False	False	Active	-	
818	PI00292975	Q9P246	RBM27	RNA-binding protein 27	119	0.189	0.127	1.49	False	False	Active	-	
1059	PI00289610	Q92768	HMG2L	Isomorphin α 2 of Histone deacetylase 2	69	0.407	0.279	1.46	False	False	Active	-	
25	PI00083857	Q9N039	HNRNPJ	Isomorphin α 1 of Heterogeneous nuclear ribonucleoprotein U	91	5.059	3.346	1.51	False	False	Active	-	
287	PI00018465	Q99832	CC7	T-complex protein 1 subunit eta	59	1.519	1.005	1.51	False	False	Active	-	
536	PI00292623	P60900	PSM6B	Proteasome subunit alpha type-6	27	1.520	1.004	1.51	False	False	Active	-	
1040	PI00166983	Q99760	PKA1	Phosphotransferase kinase 1	45	0.310	0.205	1.51	False	False	Active	-	
185	PI00029731	P18077	RPL35A	60S ribosomal protein L35a	13	6.697	4.413	1.52	False	False	Active	-	
45	PI00202781	P49327	FA3N	Fatty acid synthase	273	1.271	0.836	1.52	False	False	Active	-	
115	PI00225491	P08442	EIF4L1	Eukaryotic initiation factor 4A-1	46	3.021	2.056	1.52	False	False	Active	-	
2264	PI00087157	P78362	SRPK2	Putative uncharacterized protein SRPK2 (Fragment)	82	0.304	0.200	1.52	False	False	Active	-	
54	PI00101740	P23246	SFPO	Isomorphin α 1 of Splicing factor, proline- and glutamine-rich	76	3.604	2.353	1.53	False	False	Active	-	
1634	PI00115100	Q9N053	MTFCD2	Cytosolic oxidase subunit 2	28	0.151	0.100	1.54	False	False	Active	-	
285	PI00182757	Q9N163	KIAA1967	Isomorphin α 1 of Protein KIAA1967	103	0.847	0.624	1.36	False	False	Active	-	
300	PI00293434	P37108	SRP14	Signal recognition particle 14 kDa protein	15	4.954	3.638	1.36	False	False	Active	-	
243	PI00112932	Q9N012	SNRPB	U1 small nuclear ribonucleoprotein A	71	2.498	1.498	1.37	False	False	Active	-	
62	PI00221091	P62244	RPS15A	40S ribosomal protein S15a	15	15.069	11.019	1.37	False	False	Active	-	
723	PI00299214	P04183	TKL1	Thymidine kinase, cytosolic	25	1.014	0.742	1.37	False	False	Active	-	
389	PI00220442	P05180	YWHAG	14-3-3 protein gamma 1	36	3.438	2.511	1.37	False	False	Active	-	
48	PI00051159	Q92616	GCN11	Translational activator GCN1	293	1.090	0.795	1.37	False	False	Active	-	
1394	PI00554681	Q16718	NDR4F5	NAH domain thymosin [β -tubulin] 1 alpha subcomplex subunit 5	13	0.659	0.481	1.37	False	False	Active	-	
151	PI00090328	P18912	EIF4A3	Eukaryotic initiation factor 4A-III	47	2.827	1.960	1.37	False	False	Active	-	
433	PI00294159	PS3007	SLC25A1	Tricarballoylate transport protein, mitochondrial	34	1.472	1.073	1.37	False	False	Active	-	
2037	PI00384265	Q9N282	FAM120A	Isomorphin α 1 of Constitutive coactivator of PP1A-gamma-like protein 1	125	0.014	0.011	1.27	False	False	Active	-	
Q26838	PI00002874	Q99760	PCNA2	Proliferating cell nuclear antigen 2	22	5.899	4.130	1.43	False	False	Active	-	
609	PI00396371	P27816	MAP4	Isomorphin α 1 of Microtubule-associated protein 4	121	1.213	0.854	1.38	False	False	Active	-	
791	PI00746351	Q9Y211	DS3	Isomorphin α 1 of Exosome complex exonuclease RRP44	109	0.207	0.151	1.37	False	False	Active	-	
370	PI00258000	Q90249	IGFBP3	Isomorphin α 1 of Insulin-like growth factor 3, IGF-binding protein 3	62	0.943	0.683	1.38	False	False	Active	-	
930	PI00294955	Q9Y420	LSM4	U5 snRNP-associated Sm-like protein LSM4	15	0.859	0.622	1.38	False	False	Active	-	
1469	PI00087174	Q9Y417	MVCBP	C-Myc-binding protein	12	0.756	0.547	1.38	False	False	Active	-	
552	PI00543520	Q92940	TKT	Transferrin receptor	60	0.489	0.359	1.33	False	False	Active	-	

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	IPI Accession	UniProtKB Accession	Gene name	Protein name	Protein MW (kDa)	Relative abundance (mean normalized spectral count) × 10 ³		Fold enrichment (active/inactive)		Specific enrichment [†]		Cluster [‡]	Adhesome [§]	Hierarchical clustering
						Active integrin	Inactive integrin	Active integrin	Inactive integrin	Active integrin	Inactive integrin			
240	IP00219155	P61353	RPL27	60S ribosomal protein L27	16	5.261	2.899	1.81	False	False	Active			
1202	IP00179597	P10249	STAM1	150 kDa Spectrin alpha chain, erythrocyte	17	0.517	0.284	1.82	False	False	Active			
1659	IP00071444	Q8UNK3	RML26L1	60S ribosomal protein L26-like 1	17	1.653	0.910	1.82	False	False	Active			
65	IP00418880	P61247	RPL3A	40S ribosomal protein S3a	30	8.250	4.500	1.83	False	False	Active			
493	IP00301923	Q90760	CK2S1	Isomorph of Cell division protein kinase 9	45	1.010	0.551	1.83	False	False	Active			
590	IP00203344	Q92797	SYMPK	Isomorph 1 of Sympkin	141	0.242	0.132	1.83	False	False	Active			
385	IP00305068	Q94906	PRPF6	Pre-mRNA processing factor 6	107	0.539	0.294	1.83	False	False	Active			
1090	IP00215541	Q12913	PCSD2	Isomorph 3 of PC1 domain-containing protein 2	42	0.363	0.198	1.83	False	False	Active			
390	IP00018278	Q71109	H2AFV	Histone H2A.V	14	34.940	19.125	1.83	False	False	Active			
666	IP00292059	P49790	NUP133	Nuclear pore complex protein Nup133	154	0.182	0.100	1.82	False	False	Active			
1292	IP00222074	P62549	SPTA1	Isomorph 1 of Spectrin alpha chain, erythrocyte	280	0.036	0.020	1.80	False	False	Active			
2131	IP00292134	P42566	EP515	Isomorph 1 of Epidermal growth factor receptor substrate 15	99	0.020	0.011	1.82	False	False	Active			
280	IP00016339	Q14974	KPNB1	Importin subunit beta-1	97	0.952	0.542	1.76	False	False	Active			
801	IP00301923	Q12913	TRSP1	Heat shock protein 75 kDa, mitochondrial	80	1.293	0.738	1.75	False	False	Active			
53	IP00216592	P07910	HNRNPCC	Isomorph C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	32	9.569	5.411	1.77	False	False	Active			
472	IP00171159	P25788	PSMA3	Isomorph 2 of Proteasome subunit alpha type-3	28	1.731	0.983	1.76	False	False	Active			
745	IP00383046	Q95056	CMBL2	Carboxymethylchitinase homolog 2	28	0.818	0.464	1.76	False	False	Active			
1384	IP00001146	P62312	SLM6	U6 snRNP-associated S-like protein Lsm6	9	1.287	0.729	1.77	False	False	Active			
545	IP00555747	Q13310	PABPC4	Isomorph 2 of Poly(ADP-ribose) binding protein 4	70	1.817	1.048	1.73	False	False	Active			
1228	IP00316179	Q98075	C1orf26	Uncharacterized protein C1orf26	32	0.520	0.295	1.73	False	False	Active			
116	IP00545723	P17635	RPL10	60S ribosomal protein L10	29	6.006	3.474	1.73	False	False	Active			
1842	IP00215911	P27695	AMEX1	DNA-(apurinic or apyrimidinic site) lyase	36	1.126	0.073	1.73	False	False	Active			
1084	IP00507746	Q92066	NLDC	Nuclear migration protein nucleic	38	0.362	0.207	1.75	False	False	Active			
1810	IP00010029	Q15205	PHF21	Phosphoethanolamine 2	28	0.103	0.059	1.75	False	False	Active			
20	IP00186290	P13639	IEF2	Elongation factor 2	95	1.664	0.955	1.75	False	False	Active			
243	IP00644127	P41252	EAR5	Isomorph 1 of RNA polymerase, cytoplasmic	145	0.725	0.289	2.51	False	False	Active			
333	IP00216230	P42166	TARPO	Lamina-associated polypeptide 2, isoform alpha	99	0.458	0.187	2.50	False	False	Active			
323	IP00202822	P51532	SMARCA4	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin 4 isoform D	188	0.391	0.155	2.52	False	False	Active			
579	IP00505882	P32322	PKRC1	Pyruvate-5-carboxylase reductase	36	1.172	0.466	2.52	False	False	Active			
746	IP00303962	P91024	HSP95A	HSP95 protein class A	82	0.773	0.307	2.52	False	False	Active			
338	IP00465044	Q92958	PRKCC2	Protein RCK2	56	1.283	0.516	2.49	False	False	Active			
486	IP00297982	P41091	EIF252	Eukaryotic translation initiation factor 2 subunit 3	55	1.073	0.430	2.50	False	False	Active			
1083	IP0029624	P43021	NCAPD2	Condensin complex subunit 1	22	0.147	0.052	2.47	False	False	Active			
146	IP00413324	P18621	RPL17	60S ribosomal protein L17	21	7.266	2.965	2.45	False	False	Active			
191	IP00003377	Q13629	SFRS7	Isomorph 1 of Splicing factor, arginine/serine-rich 7	27	5.887	2.400	2.45	False	False	Active			
606	IP00251485	P08610	DIAPH1	Isomorph 1 of Protein diaphanous homolog 1	49	3.255	1.409	2.45	False	False	Active			
654	IP00296068	Q99460	PSMD1	Isomorph 1 of 26S proteasome non-ATPase regulatory subunit 1	106	0.309	0.125	2.47	False	False	Active			
11	IP00081836	Q96045	HCT112AG	Histone H2A type 1-H	14	68.037	27.630	2.46	False	False	Active			
295	IP00310720	P48543	CTCS	T11 complex protein 3 subunit epsilon	11	1.558	0.633	2.46	False	False	Active			
629	IP00202520	P34897	SHMT2	Serine hydroxymethyltransferase, mitochondrial	56	0.722	0.293	2.46	False	False	Active			
779	IP00206670	Q15370	TEC2B	Translation elongation factor B polypeptide 2	13	1.562	0.632	2.47	False	False	Active			
1568	IP00236588	Q28214	RPM252	RNA-binding protein with multiple splicing 1	22	0.147	0.060	2.45	False	False	Active			
187	IP00331691	P32969	RPL9	60S ribosomal protein L9	22	6.127	2.378	2.58	False	False	Active			
260	IP00216237	Q9Y3U8	RPL36	60S ribosomal protein L36	12	8.467	3.287	2.58	False	False	Active			
1362	IP00206297	Q96097	ASHPPTP	L-aminoadipate-semialdehyde dehydrogenase (phosphoantithiopyridine) transferase	36	0.282	0.109	2.59	False	False	Active			
202	IP00291939	P24683	SMC1A	Structural maintenance of chromosomes protein 1A	143	0.803	0.313	2.57	False	False	Active			
524	IP00021187	Q9Y265	RUVBL1	Isomorph 1 of RuvB-like 1	50	0.989	0.385	2.57	False	False	Active			
206	IP00290770	P49368	CTC3	Eukaryotic transcription TCP1, subunit 3 isoform B	60	1.760	0.686	2.57	False	False	Active			
757	IP00007074	P49457	YARS	Tyrosyl-RNA synthetase, cytoplasmic	62	0.183	0.071	2.62	False	False	Active			
1018	IP00222533	P47813	EIF1AX	Eukaryotic translation initiation factor 1A, X-chromosomal	16	0.797	0.311	2.56	False	False	Active			
735	IP00567050	Q15372	EIF3H	Eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa, isoform CRA_b	42	0.669	0.261	2.56	False	False	Active			
1896	IP00166293	Q9N257	HIST1H2B	Histone H2B type 2-B	14	21.808	8.531	2.56	False	False	Active			
599	IP00459672	Q9UNM6	HSPC027	HSPC027	43	0.988	0.389	2.54	False	False	Active			
575	IP00545737	P30153	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform 1	65	0.668	0.264	2.53	False	False	Active			
586	IP00785611	Q96097	RPL29	9 kDa protein	9	8.796	3.427	2.56	False	False	Active			
715	IP00419919	P47914	RPL29	60S ribosomal protein L29	18	1.348	0.530	2.54	False	False	Active			
1371	IP00404127	Q9N922	ASF1B	Histone chaperone ASF1B	22	0.128	0.050	2.56	False	False	Active			
42	IP00450498	Q96874	PA2G4	Poly (ADP-ribose) polymerase 1	113	3.333	1.370	2.43	False	False	Active			
417	IP00219994	P55060	CSE1L	Isomorph 3 of Exprin-2	108	0.871	0.359	2.43	False	False	Active			
353	IP00465248	Q67373	ENO1	Isomorph alpha-enolase of Alpha-enolase	47	1.613	0.667	2.42	False	False	Active			
710	IP00213723	Q13526	PNR1	Peptidyl-prolyl-4-trans isomerase NIMA-interacting 1	12	0.741	0.292	2.53	False	False	Active			
489	IP00207208	R30876	POLR2B	DNA-directed RNA polymerase II subunit RPB2	134	0.354	0.146	2.42	False	False	Active			
824	IP00200042	P43886	PSMC4	Isomorph 1 of 26S proteasome regulatory subunit 4B	47	0.526	0.217	2.42	False	False	Active			
6	IP00296337	P78527	PRKDC	Isomorph 1 of Protein tyrosine kinase catalytic subunit	459	3.255	1.355	2.41	False	False	Active			
584	IP00006980	Q9Y224	C14orf166	UPF0568 protein C14orf166	28	1.302	0.540	2.41	False	False	Active			
324	IP00219430	Q9J0E7	SMC3	Structural maintenance of chromosomes protein 3	142	0.543	0.226	2.40	False	False	Active			
585	IP00297572	Q28214	AGR	Intron binding protein aquarius	102	0.213	0.089	2.39	False	False	Active			
1662	IP00306290	Q43592	XPOT	Exportin-T	110	0.036	0.015	2.40	False	False	Active			
135	IP00217975	P20700	LMNB1	Lamin B1	66	2.788	1.186	2.35	False	False	Active			
46	IP00215953	Q28214	DDX21	Isomorph 1 of Nuclear RNA helicase 2	87	4.355	1.849	2.36	False	False	Active			
881	IP00815770	Q64993	SMK3	Isomorph 1 of Sorting nexin 3	19	1.020	0.433	2.36	False	False	Active			
67	IP00299573	P62424	RPL7A	60S ribosomal protein L7a	30	8.757	3.694	2.37	False	False	Active			
129	IP00299900	Q9J080	PA2G4	Protein tyrosine kinase catalytic subunit 2G4	44	4.443	1.878	2.37	False	False	Active			
1172	IP00013100	Q13616	CUL1	Protein associated with Cullin 1	90	0.116	0.049	2.37	False	False	Active			
949	IP00215610	Q00013	SFBP2	55 kDa erythrocyte membrane protein	52	0.428	0.185	2.31	False	False	Active			
793	IP00212845	Q15020	SPTBN2	Isomorph 1 of Spectrin beta chain, brain 2	271	0.023	0.010	2.30	False	False	Active			
1221	IP00294979	P49690	RAN	Ran GTPase-activating protein 1	64	0.241	0.050	2.35	False	False	Active			
106	IP00247583	P46778	RPL21	60S ribosomal protein L21	19	7.413	3.235	2.29	False	False	Active			
959	IP00202567	Q98779	SRAPB2	U2 small nuclear ribonucleoprotein B'	25	1.535	0.670	2.29	False	False	Active			
607	IP00202127	Q17694	PNR1	Peptidyl-prolyl-4-trans isomerase NIMA-interacting 1	68	0.414	0.181	2.31	False	False	Active			
1392	IP00219839	Q63683	HMC2	Isomorph 2 of Hypermethylated in cancer 2 protein	64	0.178	0.077	2.31	False	False	Active			
396	IP00315119	P43658	DMNT1	Isomorph 1 of DNA (cytosine-5)-methyltransferase 1	190	0.290	0.127	2.28	False	False	Active			
1429	IP00181636	Q98801	HIST1H2A	Isomorph 2 of Integrator complex subunit 1	118	0.084	0.028	2.29	False	False	Active			
1605	IP00294402	Q9J080	OCRL3	Isomorph 1 of Origin recognition complex subunit 3	82	0.062	0.027	2.30	False	False	Active			
163	IP00297211	Q60204	SMARCA5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	122	1.185	0.421	2.81	False	False	Active			
763	IP00014042	Q95133	IMPOT2	Importin-										

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	API Accession	UniProtKB Accession	Gene name	Protein name	Relative abundance (mean normalized spectral counts) × 10 ³			Fold enrichment (active/inactive)		Specific enrichment [†]		Adhesome [‡]	Hierarchical clustering
					MW (kDa)	Active integrin	Inactive integrin	Active integrin	Inactive integrin	Active integrin	Inactive integrin		
371	IP0009560	Q13691	INMT	Isomerase 1 of Mitochondrial inner membrane protein	84	0.774	0.386	2.01	False	False	Active		
55	IP0021700	P62701	RPS4	60S ribosomal protein S4, X isoform	30	9.643	4.785	2.02	False	False	Active		
9	IP0030313	Q93709	HIST1H2BH	Histone H2B type 1-H	14	77.372	38.470	2.01	False	False	Active		
455	IP0016387	Q14658	FSCN1	Fascin	55	0.914	0.454	2.01	False	False	Active		
1565	IP0002704	P49642	PRM1	DNA primase small subunit	50	0.079	0.039	2.03	False	False	Active		
94	IP0017297	P43243	MATR3	Matrin-3	95	2.016	0.979	2.06	False	False	Active		
556	IP00047330	Q9Y3A5	SBD5	Ribosome maturation protein SBD5	29	1.463	0.712	2.05	False	False	Active		
677	IP00031522	P49293	HADNA	Trifunctional enzyme subunit alpha, mitochondrial	26	0.415	0.205	2.06	False	False	Active		
501	IP00170692	Q9P0L0	VAPA	Isomerase 1 of Vesicle-associated membrane protein-associated protein A	28	1.780	0.862	2.06	False	False	Active		
1430	IP00003824	Q13356	PNL2	Isomerase 1 of Peptidyl prolyl cis-trans isomerase-like 2	59	0.116	0.056	2.07	False	False	Active		
185	IP0021772	P29537	RPL5	60S ribosomal protein L5	28	4.513	2.263	2.05	False	False	Active		
655	IP00220528	P62306	SNRPF	Small nuclear ribonucleoprotein F	10	4.132	2.017	2.05	False	False	Active		
619	IP00019912	P51659	HSD17B4	Peroxisomal multifunctional enzyme type 2	80	0.482	0.236	2.04	False	False	Active		
1171	IP00205821	P49912	LEB3	Isomerase 1 of Alpha-1,6-glucosylase 3	113	0.084	0.042	2.05	False	False	Active		
303	IP00021700	P12004	PCNA	Proliferating cell nuclear antigen	29	2.652	1.274	2.08	False	False	Active		
179	IP00013917	P25398	RPS12	40S ribosomal protein S12	15	9.778	4.702	2.08	True	False	Active		
618	IP00022809	P62273	RPS29	40S ribosomal protein S29	7	5.071	2.438	2.08	False	False	Active		
132	IP00046161	Q13838	BAT1	Isomerase 1 of Spliceosome RNA helicase BAT1	49	3.088	1.480	2.09	False	False	Active		
1009	IP00006052	Q9UHV9	PFND2	Prefoldin subunit 2	17	1.237	0.593	2.09	False	False	Active		
1046	IP00024245	P45880	VDAC2	Isomerase 2 of Voltage-dependent anion-selective channel protein 2	30	0.497	0.238	2.09	False	False	Active		
990	IP00038424	Q12650	GART	GARS-GART-GART (Fragment)	18	1.145	0.552	2.07	False	False	Active		
1134	IP00163084	Q9HC27	XAB2	Pre-mRNA-splicing factor XFP1	100	1.335	0.665	2.08	False	False	Active		
1084	IP00007163	Q10J45	LSM7	U6 snRNA-associated Sm-like protein LSM7	12	1.020	0.492	2.07	False	False	Active		
227	IP00013088	Q43707	ACTN4	Alpha-actinin-4	105	1.376	0.639	2.18	False	False	Active	YES	
213	IP00012345	Q13247	SFRS6	Isomerase 1 of Splicing factor, arginine/serine-rich 6	40	2.658	1.217	2.18	False	False	Active		
474	IP00016413	P68400	CSM2A1	CSM2A1	46	1.124	0.515	2.18	False	False	Active		
373	IP00379044	Q9N127	NUP93	Nuclear pore complex protein Nup93	95	0.328	0.151	2.17	False	False	Active		
1192	IP00022879	Q9Y3D8	AK6	Adenylyl kinase isoenzyme 6	20	0.623	0.287	2.17	False	False	Active		
1073	IP00012369	Q13257	MAD2L1	Mitotic spindle assembly checkpoint protein MAD2A	24	0.537	0.247	2.17	False	False	Active		
162	IP00021270	P32643	RPL26	60S ribosomal protein L26	18	7.171	3.254	2.20	False	False	Active		
226	IP00022774	P55072	VCP	Transitional endoplasmic reticulum ATPase	89	1.301	0.591	2.20	False	False	Active		
1240	IP00413995	Q80879	UGL2G2	Golgii autophagy, golgin subfamily A, 2	113	0.086	0.039	2.21	False	False	Active		
1456	IP00013598	Q9BVC5	Actn5	Actinin-5	26	0.252	0.114	2.21	False	False	Active		
1747	IP00215381	Q43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	11	0.939	0.420	2.20	False	False	Active			
1495	IP00023287	Q9Y3B4	SFB14	Pre-mRNA branch site protein p14	15	2.761	1.243	2.22	False	False	Active		
230	IP00029779	P73781	CTC2	T-complex protein 1 subunit beta	52	0.299	0.048	2.21	False	False	Active		
1240	IP00011528	Q95048	CSF1	Cleavage stimulation factor subunit 1	48	0.182	0.082	2.22	False	False	Active		
495	IP00064777	Q00303	EIF3F	HC1784554, isoform CRA_a	39	1.405	0.631	2.23	False	False	Active		
355	IP00007163	Q10J45	HSP90	Stress 70 protein, mitochondrial	78	1.577	0.713	2.23	False	False	Active		
1773	IP00023287	Q9Y3D3	MRPS16	28S ribosomal protein S16, mitochondrial	15	0.293	0.131	2.24	False	False	Active		
1032	IP00029728	P18074	ERCC2	TFII basal transcription factor complex helicase subunit	87	0.128	0.057	2.25	False	False	Active		
275	IP00078781	Q9N259	NUP205	Nuclear pore complex protein Nup205	103	0.389	0.188	2.12	False	False	Active		
886	IP00337307	Q8Z629	TMT2A	Isomerase 1 of rRNA (uracil-5)-methyltransferase homolog A (Fragment)	69	0.280	0.132	2.12	False	False	Active		
797	IP00073602	Q58K66	EXOC56	Exosome complex exocyst MTR3	28	1.016	0.479	2.12	False	False	Active		
938	IP00228206	Q75121	ZC3H11A	Zinc finger CCH domain-containing protein 11A	85	0.105	0.050	2.10	False	False	Active		
976	IP00010030	Q10460	YTHDC2	Probable ATP-dependent RNA helicase YTHDC2	160	0.083	0.039	2.13	False	False	Active		
896	IP00008922	Q11629	IFTM2	Interferon-induced transmembrane protein 2	15	1.646	0.783	2.10	False	False	Active		
572	IP00064271	P52692	EF1D	Isomerase 2 of Elongation factor 1 delta	17	0.716	0.339	2.11	False	False	Active		
571	IP00010305	Q95637	EIF5	Eukaryotic translation initiation factor 5	27	1.667	0.781	2.11	False	False	Active		
1521	IP00022334	Q04181	ORIT1	Ornithine aminotransferase, mitochondrial	49	0.113	0.054	2.09	False	False	Active		
1254	IP00039262	P11177	PDB9	Isomerase 1 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	39	0.321	0.152	2.11	False	False	Active		
1694	IP00013088	Q43707	ACTN4	Isomerase 1 of Actinin-like protein N2A	78	0.482	0.223	2.13	False	False	Active		
334	IP00415258	H09429	HMG81	High mobility group protein B1	25	4.580	2.144	2.14	False	False	Active		
1922	IP00292071	Q95985	TOP3B	Isomerase 1 of DNA topoisomerase 3-beta-1	97	0.029	0.014	2.07	False	False	Active		
729	IP00031443	Q94905	YPC1	Eukaryotic translation initiation factor 3 subunit K	25	1.136	0.526	2.16	False	False	Active		
1130	IP00005179	Q15160	ROP13C	Isomerase 1 of GNA-DIRECTED RNA polymerases I and III subunit RPA1C	39	0.329	0.152	2.16	False	False	Active		
1474	IP00024742	Q14949	UCDCK9	Cytochrome b-c1 complex subunit 8	10	0.705	0.328	2.15	False	False	Active		
103	IP00045248	Q97474	NRX1	Isomerase 1 of Nucleophosmin 1	33	0.810	0.375	2.15	False	False	Active		
103	IP000783271	P42704	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	158	1.547	0.494	3.13	True	False	Active		
83	IP00021088	P46781	RPS9	40S ribosomal protein S9	23	9.659	3.080	3.14	True	False	Active		
307	IP00011569	Q13085	ACACA	Isomerase 1 of Acetyl-CoA carboxylase 1	26	1.014	0.463	2.11	False	False	Active		
1341	IP00009659	Q9N0G5	RPRD1B	Regulation of nuclear pre-mRNA domain-containing protein 1B	37	0.387	0.124	3.12	True	False	Active		
1534	IP00017669	Q96963	SMARCC1	Isomerase 1 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	47	0.175	0.056	3.13	False	False	Active		
184	IP00045969	Q10294	MYL1	Cytoskeletal myosin I heavy chain 1	53	2.096	0.948	2.21	False	False	Active		
786	IP00038492	P12829	MYL4	Myosin light chain 4	22	1.329	0.429	3.10	True	False	Active		
977	IP00022793	P55084	HADHB	Trifunctional enzyme subunit beta, mitochondrial	51	0.460	0.148	3.11	True	False	Active		
265	IP00021266	P62750	RPL23A	60S ribosomal protein L23	18	6.577	3.127	3.13	False	False	Active		
707	IP00030078	Q15269	PWP2	Periodic tryptophan protein 2 homolog	102	0.294	0.096	3.06	False	False	Active		
403	IP00006932	Q9Y3B3	LUCLT2	RNA-binding protein Luc2-like 2	54	1.008	0.347	3.08	True	False	Active		
1694	IP00013088	Q43707	ACTN4	Cytochrome c oxidase subunit 6B1	103	0.403	0.133	3.03	False	False	Active		
40	IP00018793	P11388	TOP2A	Isomerase 3 of DNA topoisomerase 2-alpha	179	2.188	0.688	3.18	False	False	Active		
102	IP00019502	P35579	MTH9	Isomerase 1 of Myosin-9	227	1.251	0.393	3.18	True	False	Active	YES	
64	IP00046203	P49338	NCL	Nucleolin	77	7.219	2.275	3.17	False	False	Active		
662	IP00015790	Q5YVX3	ECM39	KAM488B protein	224	0.137	0.043	3.19	False	False	Active		
729	IP00029345	Q5UJ90	RIF1	Isomerase 1 of Telomerase-associated protein RIF1	174	0.093	0.029	3.21	False	False	Active		
304	IP00039598	P62910	RPL32	60S ribosomal protein L32	28	5.496	1.712	3.21	True	False	Active		
392	IP00021229	Q03041	H0189	Vglin	141	0.476	0.148	3.22	False	False	Active		
836	IP00024284	Q92973	TNPO1	Isomerase 1 of Transporin-1	102	0.270	0.084	3.21	False	False	Active		
1372	IP00039736	Q89177	ZC3H14	Isomerase 1 of Zinc finger CCH domain-containing protein 14	83	0.076	0.024	3.17	False	False	Active		
600	IP00013536	Q92955	DMG1	Downstreamless-regulated GTP-binding protein 1	41	1.070	0.346	3.08	False	False	Active		
1263	IP00079373	Q8N590	DOC8	Isomerase 1 of Dedicator of cytokinesis protein 8	239	0.041	0.012	3.42	False	False	Active		
813	IP00013536	Q96753	TFM3	Isomerase 2 of Tropomyosin alpha-3 chain	29	0.824	0.254	3.24	False	False	Active		
932	IP00032633	Q14628	TAF5	Thousand RNA synthetase, cytoplasmic	105	0.095	0.026	3.25	False	False	Active		
598	IP00025418	Q02388	COL7A1	Isomerase 1 of Collagen alpha-1(VII) chain	295	0.029	0.009	3.22	False	False	Active		
1599	IP00034379	Q9N383	MRP43	Mitochondrial ribosomal protein L34 (MRP43), transcript variant 4	29	0.295	0.091	3.24	False	False	Active		
55	IP00024067	Q9N043	CLTC	Isomerase 1 of Clathrin heavy chain 1	103	0.011	0.003	3.01	False	False	Active		
169	IP00009342	P46640	IQGAP1	Ras GTPase-activating-like protein IQGAP1	189	0.800	0.265	3.02	False	False	Active		
362	IP00041733	Q12123	DNK90	Isomerase 1 of Putative ATP-dependent RNA helicase DNK90	134	0.585	0.194	3.02	False	False	Active		
182	IP00079566	P57371	RPL24	19 kDa ribosomal protein	19	8.188	2.748	3.00	False	False	Active		
290	IP00029861	Q14980											

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	API Accession	UniProtKB Accession	Gene name	Protein name	Relative abundance (mean normalized spectral count) × 10 ³		Fold enrichment (active/inactive)		Specific enrichment [†]		Cluster [‡]	Adhesome [§]	Hierarchical clustering
					Protein MW (kDa)	Relative abundance (mean normalized spectral count) × 10 ³	Fold enrichment (active/inactive)	Active	Inactive	Active			
1136	PI0001297	Q13442	PODPI	28 kDa heat- and acid-stable phosphoprotein	21	0.686	0.188	3.65	False	False	Active	-	-
621	PI0002177	Q17340	PI3K	Programmed cell death protein 6	22	1.899	0.158	9.67	True	False	Active	-	-
867	PI0017843	P40603	RCOL	ATP-dependent DNA helicase Q1	73	0.248	0.068	3.65	False	False	Active	-	-
173	PI0030017	Q9H040	NAT10	N-acetyltransferase 10	116	1.321	0.362	3.65	False	False	Active	-	-
1060	PI0000964	Q9R068	UBQL	ubiquitin-specific protease 9, N-linked isoform 4	290	0.042	0.011	3.82	True	False	Active	-	-
1103	PI0003160	Q95602	POB1A	DNA-directed RNA polymerase I subunit RPA1	195	0.062	0.017	3.65	False	False	Active	-	-
1189	PI0030630	Q9H559	PDHA1	Mitochondrial PDHA1	46	0.399	0.109	3.66	False	False	Active	-	-
1255	PI0002083	Q96622	GPT1	G1 to S phase transition 1 isoform 2	65	0.058	0.016	2.63	False	False	Active	-	-
78	PI0005001	P39023	RPL3	60S ribosomal protein L3	46	5.318	1.393	3.82	True	False	Active	-	-
199	PI0002429	Q9H583	HEAT1	HEAT repeat-containing protein 1	242	0.529	0.138	3.83	False	False	Active	-	-
1175	PI0002103	P15104	HDRX	Histone H2A	15	19.260	5.033	3.83	False	False	Active	-	-
1420	PI0002513	P24539	ATP5F1	ATP synthase subunit b, mitochondrial	29	0.261	0.068	3.84	False	False	Active	-	-
317	PI0040022	Q14690	PCDD11	Protein RPP5 homolog	209	0.374	0.099	3.78	False	False	Active	-	-
475	PI0002125	P29748	FEN1	Flap endonuclease 1	43	1.273	0.336	3.79	False	False	Active	-	-
577	PI0000971	Q93252	LMNB2	Lamin-B2	70	0.860	0.227	3.79	True	False	Active	-	-
720	PI0003240	Q9Y933	LSM2	U6 snRNA-associated 5m-like protein LSM2	11	2.939	0.776	3.79	True	False	Active	-	-
1537	PI0003856	P36033	ATP9A1E1	V-type proton ATPase subunit E 1	26	0.285	0.076	3.75	False	False	Active	-	-
1589	PI0000594	Q9U466	DDX20	Probable ATP-dependent RNA helicase DDX20	92	0.081	0.021	3.86	False	False	Active	-	-
93	PI0074268	P12270	GTR	Nucleoprotein TR	267	0.920	0.228	4.04	True	False	Active	-	-
1045	PI0001826	Q9Y050	TOP2	Aspartate aminotransferase, mitochondrial	47	0.505	0.126	4.01	False	False	Active	-	-
75	PI0000136	Q14980	NLMA1	Isoform 3 of Nuclear mitotic apparatus protein 1	237	1.088	0.274	3.97	True	False	Active	-	-
312	PI0000578	Q01130	SFRS2	Splicing factor, arginine/serine-rich 2	25	2.915	0.735	3.97	True	False	Active	-	-
935	PI0009707	Q17513	KIAA0664	Protein KIAA0664	147	1.154	0.293	3.95	False	False	Active	-	-
685	PI0000071	Q17845	SRF12	Isoform 3 of Splicing factor, arginine/serine-rich 13A	22	1.303	0.328	3.97	True	False	Active	-	-
1544	PI0001385	P31949	S100A11	Protein S100-A11	12	0.648	0.164	3.95	False	False	Active	-	-
686	PI00024919	P30448	PHOX3	Thioredoxin-dependent peroxide reductase, mitochondrial	28	1.216	0.305	3.99	True	False	Active	-	-
911	PI00029276	P41224	MBF	Macrophage migration inhibitory factor	12	1.062	0.262	3.99	False	False	Active	-	-
702	PI00029200	Q8WVY3	PPP31	Isoform 1 of U4/U5 snRNP ribonucleoprotein Prp31	55	0.602	0.155	3.88	True	False	Active	-	-
450	PI0000882	P54886	ALDH18A1	Isoform Long of Delta 1-pyridoxal-5-carboxylate synthetase	87	0.796	0.204	3.90	True	False	Active	-	-
1595	PI0015911	Q14580	DIMC9	Isoform 4 of Death-inducing cell factor 9	12	1.078	0.271	3.95	False	False	Active	-	-
1116	PI00078096	Q7L106	BZW1	Isoform 1 of Basic leucine zipper and W2 domain-containing protein 1	48	0.480	0.123	3.90	True	False	Active	-	-
281	PI00029750	P62847	RPS24	Isoform 1 of 40S ribosomal protein S24	15	7.308	1.669	4.38	True	False	Active	-	-
158	PI0002089	Q79531	SFRS1	Splicing factor 38 subunit 1	147	1.037	0.273	3.85	True	False	Active	-	-
439	PI0000675	Q9R028	DDX23	Eukaryotic ATP-dependent RNA helicase DDX23	96	0.636	0.146	4.36	True	False	Active	-	-
123	PI0002012	Q14152	EF3A	Evolutionary transition initiation factor 3 subunit A	167	1.181	0.277	4.26	True	False	Active	-	-
497	PI0002027	Q15467	SMC2	Isoform 1 of Structural maintenance of chromosomes protein 2	136	0.205	0.051	4.29	True	False	Active	-	-
97	PI00087827	P18124	RPL7	Putative uncharacterized protein RPL7 (Fragment)	32	7.436	1.739	4.28	True	False	Active	-	-
994	PI0017642	Q96624	AURKB	Serine/threonine-protein kinase 12	39	0.458	0.107	4.28	False	False	Active	-	-
316	PI0011559	Q29713	SMC1A	Isoform 1 of Structural maintenance of chromosomes protein 4	112	0.497	0.115	4.32	True	False	Active	-	-
398	PI00043975	P151311	ERK	Erin	69	0.946	0.219	4.32	True	False	Active	-	-
512	PI00072160	Q92974	ARHGFB2	Rho/Rac guanine nucleotide exchange factor 2	121	0.408	0.094	4.34	True	False	Active	YES	-
519	PI00021285	P14678	SNRPB	Isoform SM-B' of Small nuclear ribonucleoprotein-associated proteins B and B'	25	1.850	0.430	4.30	True	False	Active	-	-
1148	PI00021743	Q17478	DXH29	ATP-dependent RNA helicase DXH29	155	0.073	0.017	4.29	True	False	Active	-	-
1025	PI00031058	P50552	VASP	Vasodilator-stimulated phosphoprotein	40	0.495	0.115	4.30	True	False	Active	YES	-
400	PI00041157	Q10567	NOP56	Nucleolar protein 56	96	1.016	0.242	4.20	False	False	Active	-	-
748	PI0010447	Q87A02	SMARCC2	Isoform 1 of SWI/SNF complex subunit SMARCC2	133	0.331	0.079	4.19	True	False	Active	-	-
764	PI00030990	Q9Y932	C1orf77	Isoform 1 of Uncharacterized protein C1orf77	26	0.983	0.232	4.24	True	False	Active	-	-
454	PI00022062	P61004	HSP51	10 kDa heat shock protein, mitochondrial	11	6.303	1.523	4.14	True	False	Active	-	-
534	PI00021290	P14396	ATP13B2	ATP-binding cassette, type B, member 2	134	0.378	0.091	4.20	True	False	Active	-	-
1440	PI0047748	Q6P062	CTR9	RNA polymerase-associated protein CTR9 homolog	134	0.034	0.008	4.25	False	False	Active	-	-
1684	PI00029719	Q94832	MYO1D	Myosin-Id	116	0.047	0.011	4.27	False	False	Active	-	-
1061	PI0017035	Q8N164	SMAD2	Leucine-rich repeat-containing protein 47	63	0.068	0.016	4.12	False	False	Active	-	-
1222	PI00032831	Q95721	SMAP29	Synaptosomal-associated protein 29	29	3.992	0.995	4.13	False	False	Active	-	-
1173	PI00031158	Q9N8V8	CMAS	Isoform 1 of N-acetylneuraminyl cytidyltransferase	48	0.302	0.073	4.14	False	False	Active	-	-
35	PI0000928	Q9PQ29	PPP2R1B	Macrophage-organizing signaling factor 8	28	1.642	0.396	4.09	True	False	Active	-	-
846	PI00032849	Q9Y9C1	NOP16	Nucleolar protein 16	21	1.070	0.219	4.89	True	False	Active	-	-
597	PI00009922	Q62673	SURP	SRA stem-loop-interacting RNA-binding protein, mitochondrial	12	3.486	0.711	4.90	True	False	Active	-	-
436	PI0015605	Q14588	BMX9	Isoform 1 of RNA-binding protein 9	59	0.122	0.028	4.26	True	False	Active	-	-
1182	PI000219673	Q9Y203	GSTK3	Glutathione S-transferase kappa 3	25	0.645	0.131	4.92	True	False	Active	-	-
741	PI00013927	P51665	PSMD7	26S proteasome non-ATPase regulatory subunit 7	37	0.907	0.184	4.93	True	False	Active	-	-
981	PI0002028	Q9U709	TRAF3	Probable ATP-dependent RNA helicase DDX41	70	0.427	0.088	4.68	True	False	Active	-	-
769	PI00054742	Q9R225	APIS	Isoform 2 of Apoptosis inhibitor 5	57	0.499	0.104	4.80	True	False	Active	-	-
837	PI00021728	P20042	EF252	Eukaryotic translation initiation factor 2 subunit 2	38	0.669	0.138	4.85	True	False	Active	-	-
512	PI0005687	Q15460	HNRNPUL2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	85	0.085	0.020	4.73	False	False	Active	-	-
804	PI000304187	Q9NWL13	RMN28	RNA-binding protein 28	86	0.260	0.055	4.73	False	False	Active	-	-
708	PI00019844	Q33629	USP39	U4/U5 snRNP-associated protein 2	65	0.517	0.110	4.70	True	False	Active	-	-
1129	PI00021256	Q14589	RPS19	19S ribosomal protein S19	32	0.360	0.076	4.61	True	False	Active	-	-
348	PI000412607	P42766	RPL35	60S ribosomal protein L35	15	5.266	1.177	4.47	True	False	Active	-	-
502	PI00011603	Q43242	PSMD3	26S proteasome non-ATPase regulatory subunit 3	61	0.956	0.212	4.51	True	False	Active	-	-
955	PI0007422	P16180	RPL32	40S ribosomal protein S24	8	2.852	0.656	4.30	True	False	Active	-	-
1210	PI00009407	P61803	DAK1	Dolichyl-diphosphoglycosyltransferase protein glycosyltransferase subunit DA01	12	1.482	0.328	4.52	True	False	Active	-	-
1307	PI00187011	Q9J478	ZC3H4	Zinc finger CCH domain-containing protein 4	140	0.089	0.020	4.45	True	False	Active	-	-
960	PI00021417	Q42890	SART1	U4/U5 snRNP-associated protein 1	90	0.258	0.056	4.61	True	False	Active	-	-
435	PI00012143	Q43395	HNRNPR	Isoform 1 of Heterogeneous nuclear ribonucleoprotein R	64	2.387	0.537	4.43	True	False	Active	-	-
883	PI000748303	Q96K61	ZFR	Putative uncharacterized protein ZFR	115	0.203	0.044	4.61	True	False	Active	-	-
1778	PI00101587	Q9NWL18	MERT140	Isoform 1 of BRCA1-A complex subunit MERT140	37	1.138	0.230	4.60	False	False	Active	-	-
876	PI00070943	P43396	PLA2	Isoform 1 of Phospholipidase A2 kinase alpha	231	0.094	0.020	4.70	True	False	Active	-	-
1335	PI00012970	Q00743	PP6C	Isoform 1 of Serine/threonine phosphatase 6 catalytic subunit	35	1.144	0.232	4.50	True	False	Active	-	-
1439	PI00043517	Q15347	HMG83	21 kDa protein	21	0.429	0.094	4.56	True	False	Active	-	-
1262	PI00169413	Q42930	MSPS24	28S ribosomal protein S24, mitochondrial	62	0.178	0.036	4.55	True	False	Active	-	-
543	PI00033979	Q92888	ARHGFE1	Isoform 2 of Rho guanine nucleotide exchange factor 1	99	0.105	0.020	5.25	False	False	Active	-	-
424	PI00046294	Q9Y459	CDCL5	Cell division cycle 5-like protein	92	0.528	0.099	5.33	True	False	Active	-	-
235	PI00026684	Q57820	MRPS41	Isoform 8 of MRPS complex subunit alpha-1	109	0.188	0.036	5.31	True	False	Active	-	-
924	PI00013830	Q13573	SNW1	SNW domain-containing protein 1	61	0.286	0.054	5.30	True	False	Active	-	-
1638	PI00039629	Q17460	CLASP1	Isoform 1 of CLIP-associated protein 1	169	0.041	0.008	5.13	True	False	Active	-	-
549	PI00041169	Q17551	ANXA2	Isoform 2 of Anexasin A2	40	1.231	0.255	4.82	True	False	Active	-	-
1373	PI00005160	Q15143	APPC18	Actin-related protein 2/3 complex subunit 18	41	0.256	0.048	5.33	True	False	Active	YES*	-
302	PI00041361	P11387	TOP2	DNA topoisomerase 1	91	0.920	0.175	5.26	True	False	Active	-	-
1281	PI000791573	Q15101	SUGT1	Isoform 2 of Suppressor of G2 allele of SKP1 homolog	62	0.278	0.052	5.35	True	False	Active	-	-
888	PI00074471	Q8T5C8	PNP1T	Polynucleotide nucleoside transferase 1, mitochondrial	86	0.239	0.046	5.20	True	False	Active	-	-
931	PI00051403	Q48444	ANCN1	Coatomer subunit delta	57	0.361	0.069	5.23	False	False	Active	-	-
1126	PI00083547	Q15113	H	RED protein	66	0.208	0.040	5.17	False	False	Active	-	-
1174	PI00025086	Q20674	COX5A	Cytochrome c oxidase subunit 5A, mitochondrial	17	1.419	0.270	5.26	True	False	Active	-	-
29	PI00028994	Q9Y490	TAL1	Tal1	270	2.487	0.487	5.11	True	False	Active	YES	-
545	PI00029464	Q15535	DNB1	DNA damage-binding protein 1	127	0.331	0.064	5.17	True	False	Active	-	-
829	PI000291200	Q8WUM0	NUP133	Nuclear pore complex protein NUP133	129	0.206							

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	UPI Accession	UniProtKB Accession	Gene name	Protein name	Relative abundance (mean normalized spectral count) × 10 ³		Fold enrichment (active/inactive)		Specific enrichment [†]		Adhesome [‡]	Hierarchical clustering
					Protein MW (kDa)	Inactive integrin	Active integrin	Active integrin	Inactive integrin	Cluster [§]		
1223	PI000202425	Q6P616	RPRD1A	isoform 1 of Regulation of nuclear pre-mRNA domain-containing protein 1A	86	0.340	0.031	10.97	True	False	Active	
1295	PI000000719	Q13420	EPF2B	isoform 1 of Translation initiation factor eIF-2B subunit delta	58	0.261	0.023	11.25	True	False	Active	
1297	PI000006298	Q13427	PF1G	isoform 1 of Peptidyl-prolyl cis-trans isomerase G	39	0.015	0.017	0.87	True	False	Active	
509	PI00021394	Q6Q832	DKC1	H/ACA ribonucleoprotein complex subunit 4	58	0.923	0.096	9.61	True	False	Active	
595	PI00015290	Q9H465	NCLG	isoform 1 of Nuclear pore complex NCLG	128	0.314	0.023	6.12	True	False	Active	
978	PI000302281	Q9N9Y3	DDX56	Probable ATP-dependent RNA helicase DDX56	62	3.307	0.032	9.59	True	False	Active	
986	PI000240812	Q9NT15	PDS5B	16S kDa protein	165	0.078	0.008	9.75	True	False	Active	
247	PI000200970	Q91609	SUPT15H	FACT complex subunit SPT15	120	0.026	0.001	10.26	True	False	Active	
573	PI00069817	Q9UG60	BA21B	isoform 1 of Tyrosine-protein kinase BA21B	171	0.248	0.024	10.33	True	False	Active	
1135	PI000102079	P23588	EF4B	Eukaryotic translation initiation factor 4B	69	0.193	0.019	10.16	True	False	Active	
856	PI000296229	Q9H922	BIRC1	Ribosome-protein factor 1 homolog	36	0.156	0.055	10.11	True	False	Active	
1036	PI000152929	P62310	LSM3	U6 snRNA-associated Sm-like protein LSM3	12	1.662	0.164	10.13	True	False	Active	
525	PI000385042	Q9B274	GTPBP4	Nucleolar GTP-binding protein 1	74	0.711	0.071	10.01	True	False	Active	
1015	PI000214351	P35958	PSMC2	26S proteasome regulatory subunit 7	49	0.453	0.045	10.07	True	False	Active	
1336	PI000182180	Q9NAM0	OTUD6B	OTU domain containing 6B	37	0.300	0.030	10.00	True	False	Active	
1378	PI00012837	P33176	KIF5B	Kinesin 1 heavy chain	110	0.120	0.012	10.00	True	False	Active	
68	PI00021652	P45973	CKB5	Chromatin domain homolog 5	22	1.748	0.165	10.59	True	False	Active	
788	PI00016697	P16157	ANKK1	isoform 1 of Ankyrin-1	206	0.143	0.013	11.00	True	False	Active	
996	PI00006252	Q12904	AIMP1	Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	34	0.623	0.058	10.74	True	False	Active	
601	PI00074595	Q98848	EBNA1BP2	Probable RNA-processing protein EBP2	35	1.171	0.113	10.36	True	False	Active	
1052	PI00003527	Q96019	AT16A	isoform 1 of Actin-like protein 6A	49	0.437	0.042	10.40	True	False	Active	
1066	PI00000733	Q9Y511	UTP18	U3 small nuclear RNA-associated protein 18 homolog	64	0.267	0.026	10.27	True	False	Active	
1258	PI00064570	Q9H923	SRB2	18 kDa protein	18	0.964	0.092	10.48	True	False	Active	
1329	PI000113122	Q16543	CCDC37	Hsp90 co-chaperone Cdc37	40	0.314	0.030	10.47	True	False	Active	
329	PI00016801	Q90367	GLUD1	Glutamate dehydrogenase 1, mitochondrial	61	1.675	0.181	9.25	True	False	Active	
1185	PI000158020	Q90801	SFRS14	isoform 1 of Putative splicing factor, arginine/serine-rich 14	120	0.101	0.011	9.18	True	False	Active	
96	PI000044213	P46013	MIR67	isoform Long of Argonaute 1-7	39	0.025	0.008	9.19	True	False	Active	
695	PI000328753	Q86J92	KTNI	isoform 1 of Kinectin	156	0.214	0.023	9.30	True	False	Active	YES
944	PI000300131	P42127	TMPO	isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma	51	1.545	0.167	9.25	True	False	Active	
5401	PI00020702	Q92013	NDP1	isoform 1 of Isocitrate dehydrogenase (NAD) subunit alpha, mitochondrial	49	1.302	0.153	9.15	True	False	Active	
1005	PI000797126	Q13765	NACA	nascent polypeptide-associated complex alpha subunit isoform A	95	0.258	0.028	9.21	True	False	Active	
553	PI00005648	Q14151	SARF2	Scarfoid attachment factor 2	107	0.434	0.046	9.43	True	False	Active	
1012	PI00064328	Q14742	PRMT5	protein arginine methyltransferase 5 isoform b	60	0.590	0.066	9.12	True	False	Active	
1013	PI00064328	Q14744	PRMT5	protein arginine methyltransferase 5 isoform b	71	0.261	0.028	9.32	True	False	Active	
1037	PI000218993	Q92598	HSPH1	isoform Beta of Heat shock protein 105 kDa	92	0.113	0.012	9.42	True	False	Active	
1519	PI000112010	P91923	DNAH3	28S ribosomal protein S28, mitochondrial	46	0.968	0.209	9.24	True	False	Active	
679	PI000033768	Q00541	PE51	isoform 1 of Pescadillo homolog	68	0.525	0.058	9.05	True	False	Active	
940	PI00032553	Q9BY28	WOR18	WD repeat-containing protein 18	47	0.507	0.056	9.05	True	False	Active	
1063	PI000334190	Q9U012	STOM2	Stomatolysin protein 2	39	0.609	0.057	9.05	True	False	Active	
984	PI000102752	Q96137	RBM15	isoform 1 of Putative RNA-binding protein 15	107	0.168	0.018	9.33	True	False	Active	
868	PI000550766	Q96773	RBP1	Ribosomal RNA processing protein 1 homolog A	53	0.504	0.056	9.00	True	False	Active	
1082	PI000374481	Q12796	CEHW	isoform 3 of Centromere protein 1	65	0.590	0.056	9.04	True	False	Active	
758	PI000000643	Q95816	BAG2	BAG family molecular chaperone regulator 2	24	1.269	0.151	8.40	True	False	Active	
1001	PI000430472	Q9N300	ASC3	Activating signal co-receptor 1 complex subunit 3	251	0.066	0.008	8.25	True	False	Active	
144	PI000072280	Q12880	TOP2B	isoform Beta-2 of DNA topoisomerase 2-beta	183	0.866	0.116	8.33	True	False	Active	
587	PI000166969	Q86U07	FERM3T	isoform 2 of Fermin family homolog 3	85	0.790	0.088	8.30	True	False	Active	YES
1344	PI00030911	Q9BVA0	VAMP8	Vesicle-associated membrane protein 8	11	1.492	0.179	8.34	True	False	Active	
1051	PI000106495	Q98943	NCAPG	Condensin complex subunit 3	114	0.161	0.019	8.47	True	False	Active	
1402	PI000021716	Q92691	MFRP2	28S ribosomal protein S28, mitochondrial	49	0.958	0.118	8.22	True	False	Active	
858	PI000071715	Q9Y221	NIP7	isoform 1 of 60S ribosome subunit biogenesis protein NIP7 homolog	20	1.124	0.131	8.58	True	False	Active	
897	PI000469490	Q4D011	RPL7L1	60S ribosomal protein L7-like 1	29	0.777	0.091	8.54	True	False	Active	
966	PI000168388	Q9H464	PRMT5	isoform 1 of Signal recognition particle 68 kDa protein	64	0.077	0.004	8.88	True	False	Active	
993	PI00015282	P78395	PRAME	Melanoma antigen preferentially expressed in tumours	58	0.294	0.034	8.65	True	False	Active	
1183	PI000050638	P14441	UBL4A	Ubiquitin-like protein 4A	18	0.800	0.092	8.70	True	False	Active	
1017	PI000334499	Q9U011	NUP2	isoform 1 of Nuclear autoantigenic sperm protein	86	0.203	0.021	8.70	True	False	Active	
1265	PI00008477	Q9ULW0	TPX2	Targeting protein for Xkp2	86	0.133	0.015	8.87	True	False	Active	
457	PI000376317	Q9P219	EDC4	isoform 1 of Enhancer of mRNA decapping protein 4	152	0.366	0.052	7.04	True	False	Active	
560	PI000212223	Q22341	PAK2	Multifunctional protein PAK2	50	0.388	0.076	7.07	True	False	Active	
527	PI00016910	Q9V613	EF3C	Eukaryotic translation initiation factor 3 subunit C	105	0.555	0.081	6.85	True	False	Active	
393	PI00008529	P05387	RPLP2	60S acidic ribosomal protein P2	12	6.710	0.996	6.74	True	False	Active	
540	PI00022079	Q9H923	GMP7	GMP anchorage [glutamine-hydroxylysyl]	72	0.670	0.076	8.76	True	False	Active	
224	PI000304612	P40429	RPL13A	60S ribosomal protein L13a	24	4.072	0.553	7.36	True	False	Active	
574	PI000291175	P18206	VCL	isoform 1 of Vinculin	117	0.456	0.062	7.35	True	False	Active	YES
1000	PI000179001	Q92061	HMG1A	isoform HMG1 of High mobility group protein HMG-1/HMGY-1	42	1.698	0.288	6.88	True	False	Active	
1214	PI00006865	Q75396	SEC22B	Vesicle-trafficking protein SEC22B	25	0.657	0.088	7.47	True	False	Active	
1286	PI000203078	Q91750	C1orf68	Skin-specific protein 32	26	0.562	0.076	7.39	True	False	Active	
311	PI000321156	Q9H923	ATP2B1	isoform 1 of ATP2B complex subunit beta	65	0.955	0.113	7.23	True	False	Active	
456	PI000301323	Q9N9V1	DX18	ATP-dependent RNA helicase DDX18	75	0.782	0.108	7.24	True	False	Active	
632	PI000294891	P46087	NOP2	Putative uncharacterized protein NOP2	94	0.473	0.065	7.28	True	False	Active	
736	PI000287515	Q86U04	MTDH	Protein LINC	68	0.584	0.067	8.21	True	False	Active	
1140	PI000789041	Q9H307	PNN	isoform 1 of Pinn	82	0.146	0.020	7.30	True	False	Active	
1441	PI000412771	Q9Y566	CD2AP	CD2-associated protein	71	0.134	0.018	7.44	True	False	Active	
1118	PI000702094	Q9B9Y5	AHCY1	transcription factor 415	253	0.031	0.004	7.75	True	False	Active	
1069	PI000184002	Q15813	TUBE1	Tubulin-specific chaperone E	59	0.923	0.044	7.34	True	False	Active	
1238	PI000295889	Q9J132	SMP19	Signal recognition particle 19 kDa protein	16	0.900	0.123	7.32	True	False	Active	
298	PI000256861	Q9J9P3	MACF1	isoform 2 of Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	620	0.139	0.020	7.95	True	False	Active	YES
508	PI000071422	Q92691	ANP2	isoform 1 of Actin- nucleator-rich nuclear phosphoprotein 2 family member B	29	1.465	0.186	7.98	True	False	Active	
754	PI000129113	Q9Y221	USP4	Ubiquitin carboxyl-terminal hydrolase 14	56	0.562	0.070	8.03	True	False	Active	
897	PI000006213	Q15154	PCM1	isoform 1 of Pericentriolar material 1 protein	228	0.131	0.016	8.19	True	False	Active	
1312	PI000793443	Q90440	IPSC	isoform 1 of Importin 5	124	0.125	0.016	7.81	True	False	Active	
477	PI000064379	Q9Y243	NOP58	Nucleolar protein 58	60	1.109	0.138	8.04	True	False	Active	
503	PI000328887	Q13895	BYSL	Bystin	50	1.224	0.151	8.11	True	False	Active	
2260	PI000312499	Q9Y401	TIAP2	Tiap2	272	0.134	0.014	8.15	True	False	Active	YES*
1000	PI000213000	Q14232	EIF2B1	Translation initiation factor eIF-2B subunit alpha	34	0.591	0.077	7.68	True	False	Active	
1403	PI000132356	P33240	CFP2	isoform 1 of Cleavage stimulation factor subunit 2	61	0.163	0.022	7.41	True	False	Active	
749	PI000044559	Q9H923	DMT1L	Probable dimethylthioesterase transferase	65	0.313	0.031	7.71	True	False	Active	
1278	PI00021248	P53350	PLK1	Serine/threonine-protein kinase PLK1	68	0.149	0.019	7.84	True	False	Active	
1364	PI000411614	Q79717	WH0L1	WD repeat and HMG-box DNA-binding protein 1	126	0.069	0.009	7.67	True	False	Active	
1576	PI000207717	Q16729	GEM1A	Component of gems	120	0.17						

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	IPI Accession	UniProtKB Accession	Gene name	Protein name	Protein MW (kDa)	Relative abundance (mean normalized spectral count) × 10 ³		Fold enrichment (active/inactive)		Specific enrichment (active/inactive)		Cluster*	Adhesome*	Hierarchical clustering
						Active integrin	Inactive integrin	Active integrin	Inactive integrin	Active integrin	Inactive integrin			
1617	IP00200685	P50613	CDK7	Cell division protein kinase 7	39	0.129	0	NO (active)	True	False	Active	-		
2193	IP00161477	Q8V973	ELP3	Isomorph 1 of Elocator complex protein 3	62	0.129	62	NO (active)	True	False	Active	-		
1490	IP00032881	Q9Y309	MRRP23	28S ribosomal protein S23, mitochondrial	22	0.570	0	NO (active)	True	False	Active	-		
1231	IP00002134	Q146401	PSMD5	26S proteasome non-ATPase regulatory subunit 5	56	0.234	0	NO (active)	True	False	Active	-		
1643	IP0003870	Q8V977	CAT5A4	Cancer/testis antigen family 45 member A45A6	21	0.384	0	NO (active)	True	False	Active	-		
1157	IP0002880	Q14146	URB2	Unlikely ribosome biogenesis protein 2 homolog	171	0.095	0	NO (active)	True	False	Active	-		
1356	IP00062336	Q86P16	RPRD1A	Isomorph 2 of Regulator of nuclear pre-mRNA domain-containing protein 1A	33	0.371	0	NO (active)	True	False	Active	-		
1579	IP00015962	Q10814	Cat6p4	Cat6p4	21	0.345	0	NO (active)	True	False	Active	-		
1215	IP00007004	Q9Y389	RBP15	RRP15-like protein	31	0.397	0	NO (active)	True	False	Active	-		
1123	IP00470883	Q6MZP3	STAG2	stromal antigen 2 isomorph	146	0.111	0	NO (active)	True	False	Active	-		
2151	IP00295400	P28081	WRNS	Isomorph 1 of Tyrosylphosphoryl-ATPase synthase, cytoplasmic	53	0.057	0	NO (active)	False	False	Active	-		
1665	IP00025264	Q86874	CYCL1	Cytochrome c1, heme protein, mitochondrial	35	0.144	0	NO (active)	True	False	Active	-		
2188	IP00067943	Q86876	TSEN4A	RNA splicing endonuclease 3A homolog	27	0.080	0	NO (active)	False	False	Active	-		
2154	IP00794240	Q8V915	MRRP39	Putative uncharacterized protein MRRP39	38	0.074	0	NO (active)	False	False	Active	-		
1581	IP00012149	Q00566	MPHCPH10	US small nuclear ribonucleoprotein protein MPP10	79	0.096	0	NO (active)	True	False	Active	-		
1925	IP00299977	Q9N9X4	PHF11	14 kDa phosphohistone phosphatase	14	0.334	0	NO (active)	True	False	Active	-		
1760	IP00062437	Q86F42	DHML2	Dynein light chain 2, cytoplasmic	100	3.593	0	NO (active)	True	False	Active	-		
2041	IP00103087	R9WJ05	EMN6G	Gen-associated protein 6	19	0.114	0	NO (active)	True	False	Active	-		
1860	IP0006442	Q13842	COL1	Collin	63	0.114	0	NO (active)	True	False	Active	-		
1484	IP00107745	Q52242	LUC7L3	Isomorph 1 of Luc7-like protein 3	51	0.198	0	NO (active)	True	False	Active	-		
1555	IP00002564	P18987	TYCC1	DNA repair protein TYCC1 protein	67	0.072	0	NO (active)	True	False	Active	-		
1996	IP00055086	Q9NMV9	Cl2orf111	Cell cycle regulator Mat88Bb homolog	80	0.037	0	NO (active)	False	False	Active	-		
1247	IP00465128	P48379	BAT3	Isomorph 1 of Large proline-rich protein BAT3	119	0.114	0	NO (active)	True	False	Active	-		
1386	IP00454540	Q9N971	PAL1P1	21-activated protein kinase-interacting protein 1	44	0.172	0	NO (active)	True	False	Active	-		
956	IP00290460	Q75821	EF3G	Eukaryotic translation initiation factor 3 subunit G	36	0.574	0	NO (active)	True	False	Active	-		
1178	IP00239815	Q86966	CHR12A	Isomorph 1 of Chrin	77	0.145	0	NO (active)	True	False	Active	-		
1285	IP00395568	Q8V900	PHF6	Isomorph 1 of PHF finger protein 6	42	0.214	0	NO (active)	True	False	Active	-		
1681	IP00164949	Q8V907	THL1	Isomorph NLF-C Negative elongation factor C/D	66	0.087	0	NO (active)	True	False	Active	-		
905	IP00393747	Q15061	WR43	WD repeat-containing protein 43	75	0.283	0	NO (active)	True	False	Active	-		
1218	IP00174673	Q86812	FN1	Fibronectin type 1 isomorph 4 prepropeptide isomorph 10	253	0.037	0	NO (active)	True	False	Active	-		
2148	IP00478834	Q9N9W6	ARGU1	Isomorph 1 of Arginine and glutamate-rich protein 1	33	0.087	0	NO (active)	True	False	Active	-		
1787	IP00305383	Q12695	UOCCR2	Cytochrome b-c1 complex subunit 2, mitochondrial	48	0.136	0	NO (active)	True	False	Active	-		
1862	IP00216682	Q17065	STOM	Erythrocyte band 7 integral membrane protein	122	0.189	0	NO (active)	True	False	Active	-		
1876	IP00293867	P30046	DDT	D-dopamine decarboxylase	13	0.244	0	NO (active)	True	False	Active	-		
1781	IP00006211	Q92502	VAPB	Isomorph 1 of Vesicle-associated membrane protein-associated protein B/C	27	0.429	0	NO (active)	True	False	Active	-		
1642	IP00216597	Q8V919	CTSL5	Cancer/testis antigen family 45 member A5	20	0.507	0	NO (active)	True	False	Active	-		
2169	IP0018895	PE2487	RPLR2G	DNA-directed RNA polymerase II subunit RPB2	19	0.076	0	NO (active)	False	False	Active	-		
2196	IP00106928	Q86A45	PTPN2	Protein tyrosine phosphatase, non-receptor type 2	41	0.053	0	NO (active)	False	False	Active	-	YES	
1640	IP00471764	Q8V904	TRAF3	Isomorph alpha 3 subunit	116	0.097	0	NO (active)	False	False	Active	-		
2000	IP00089902	Q02218	OGDH	2-oxoglutarate dehydrogenase, mitochondrial	116	0.030	0	NO (active)	False	False	Active	-		
1245	IP00004795	P54105	CLN15A	Methylsulfonium subunit p1Cin	26	0.612	0	NO (active)	True	False	Active	-		
1248	IP00000702	Q8V900	PHF6	Protein, glutamic acid-, leucine-rich protein 1 (PCLP1)	42	0.123	0	NO (active)	True	False	Active	-		
1666	IP00032649	A3N883	SBN01	Isomorph 1 of Protein strawberry notch homolog 1	154	0.016	0	NO (active)	False	False	Active	-		
963	IP00179680	Q14617	AP3D1	Isomorph 1 of AP-3 complex subunit delta-1	137	0.149	0	NO (active)	True	False	Active	-		
1286	IP00041537	Q8V908	FIBP3	Peptidyl-prolyl-cis-trans isomerase FIBP3	28	0.507	0	NO (active)	True	False	Active	-		
2078	IP00470743	Q8V904	TRAF3	Isomorph 1 of AT-rich interactive domain-containing protein 2	197	0.013	0	NO (active)	True	False	Active	-		
1633	IP00873809	Q9Y3X1	SNX9	Sorting nexin-9	46	0.146	0	NO (active)	True	False	Active	-		
830	IP00102069	Q12407	EF3M	Eukaryotic translation initiation factor 3 subunit M	43	0.738	0	NO (active)	True	False	Active	-		
1099	IP00454664	Q9N911	TEC10	Tec10-expressed sequence 10 protein	121	0.010	0	NO (active)	True	False	Active	-		
887	IP00454369	Q15070	DST	dystonin isomorph 2	650	0.004	0	NO (active)	False	False	Active	-		
2227	IP00001364	Q9Y386	GCFC1	Isomorph 1 of GC-rich sequence DNA-binding factor homolog	105	0.021	0	NO (active)	False	False	Active	-		
2028	IP00295236	Q15002	POLR2B	Polymorph protein SUI2	83	0.043	0	NO (active)	True	False	Active	-		
1820	IP00008247	Q8V904	ANAPCS	Isomorph 1 of Anaphase-promoting complex subunit 5	85	0.064	0	NO (active)	True	False	Active	-		
1840	IP00065109	P12532	CKMT1A	Isomorph 1 of Creatine kinase U-type, mitochondrial	47	0.204	0	NO (active)	True	False	Active	-		
1740	IP00170766	Q8V904	RBM17	Splicing factor 45	43	0.136	0	NO (active)	True	False	Active	-		
1545	IP00040353	P52657	GT72A2	Transcription initiation factor IIA subunit 2	12	0.540	0	NO (active)	True	False	Active	-		
1299	IP00790299	Q9N9W9	SLTM	68 kDa protein	68	0.117	0	NO (active)	True	False	Active	-		
2209	IP00061037	Q8V902	CHC101	Coiled-coil neck-coiled-coil helix domain-containing protein 1	16	0.194	0	NO (active)	False	False	Active	-		
2222	IP00063903	Q8V905	USMG65	Up-regulated during skeletal muscle growth protein 5	6	0.336	0	NO (active)	False	False	Active	-		
1836	IP00216412	Q8V973	QSOX1	Isomorph 2 of Coiled-coil domain-containing protein QSOX1	83	0.022	0	NO (active)	False	False	Active	-		
1790	IP00022125	Q8V900	ANP	Actin-dependent neuroprotection homeobox protein	124	0.053	0	NO (active)	True	False	Active	-		
1475	IP00011857	Q13112	CHAF1B	Chromatin assembly factor 1 subunit B	61	0.169	0	NO (active)	True	False	Active	-		
2122	IP00020984	P17824	CANX	Calnexin	27	0.056	0	NO (active)	True	False	Active	-		
1523	IP00025796	Q15043	NOL5B	NOL5B dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	50	0.346	0	NO (active)	True	False	Active	-		
2040	IP00435554	A43665	RG310	Isomorph 3 of Regulator of G-protein signaling 10	21	0.069	0	NO (active)	False	False	Active	-		
1091	IP00003886	Q8V972	GNL3	Isomorph 2 of Guanine nucleotide-binding protein-like 3	61	0.324	0	NO (active)	True	False	Active	-		
1195	IP00221114	Q8V904	TRIM33	Isomorph 1 of E3 ubiquitin-protein ligase TRIM33	63	0.101	0	NO (active)	True	False	Active	-		
1422	IP00018500	Q9P856	ARID3A	AT-rich interactive domain-containing protein 3A	63	0.198	0	NO (active)	True	False	Active	-		
1033	IP00026320	Q95071	UBR5	E3 ubiquitin-protein ligase UBR5	309	0.042	0	NO (active)	True	False	Active	-		
1132	IP00145590	Q8V904	MIR59P	MIR59A domain-interacting nuclear phosphoprotein	34	0.075	0	NO (active)	True	False	Active	-		
1234	IP00149473	P20290	BT3	Isomorph 2 of Transcription factor BT3	18	0.736	0	NO (active)	True	False	Active	-		
1363	IP00069070	Q9Y399	MRRP2	Mitochondrial 28S ribosomal protein S2	36	0.320	0	NO (active)	True	False	Active	-		
936	IP00015660	Q8V986	VOK1	Serine/threonine-protein kinase VOK1	45	0.475	0	NO (active)	True	False	Active	-		
991	IP00300659	Q8V919	PAR1B	Parafibromin	61	0.387	0	NO (active)	True	False	Active	-		
1885	IP00177437	Q8V920	CRNK1	Isomorph 1 of Crooked-neck-like protein 1	100	0.022	0	NO (active)	False	False	Active	-		
1825	IP00327791	Q95707	PD94	Ribonuclease P protein subunit p29	25	0.245	0	NO (active)	True	False	Active	-		
815	IP00784561	Q17425	SLTFH	Isomorph 1 of Transcription elongation factor SP76	199	0.119	0	NO (active)	True	False	Active	-		
872	IP00156374	Q8V920	IPO4	Isomorph 1 of Importin-4	119	0.238	0	NO (active)	True	False	Active	-		
1068	IP00028005	P57740	NUP107	Nuclear pore complex protein Nup107	106	0.187	0	NO (active)	True	False	Active	-		
1146	IP00331428	Q8V900	MAL2	Protein MAL2 homolog	93	0.482	0	NO (active)	True	False	Active	-		
1878	IP00434390	Q8V924	ASCC1	Activating signal co-receptor 1 complex subunit 1 (ASCC1)	44	0.139	0	NO (active)	True	False	Active	-		
1857	IP00218493	P04992	HRP11	Hydroxaphane-guanine phosphoribosyltransferase	25	0.173	0	NO (active)	True	False	Active	-		
1271	IP00426911	Q8V905	ET1	Eukaryotic peptide chain release factor subunit 3	49	0.075	0	NO (active)	True	False	Active	-		
2239	IP00300060	Q9N982	WDR70	WD repeat-containing protein 70	73	0.020	0	NO (active)	False	False	Active	-		
2247	IP00003310	P12435	RPL11	RPL11 protein	14	0.103	0	NO (active)	False	False	Active	-		
1987	IP00000000	Q8V922	UTP3	Something about silencing protein 10	55	0.065	0	NO (active)	True	False	Active	-		
1488	IP00306708	Q8V905	PK8	T-lymphocyte-activated killer cell-originated protein kinase	37	0.212	0	NO (active)	True	False	Active	-		
2197	IP00419626	Q12777	MRLP55	Isomorph 1 of 35S ribosomal protein L55, mitochondrial	19	0.163	0	NO (active)	True	False	Active	-		
2228	IP00011384	Q8V949	ENH1	Enrichment-containing protein 1	61	0.033	0	NO (active)	True	False	Active	-		
1903	IP00009598	Q92905	CPMS2	SWP395-associated complex subunit 5	38	0.186	0	NO (active)	True	False	Active	-		
1233	IP00242273	Q92925	SOMNO2	SOM/SNF-related matrix-associated actin-dependent regulator of chromatin 2 isomorph 2	57	0.241	0	NO (active)	True	False	Active	-		
1165	IP00201434	Q8V916	TRAF3	Isomorph beta-like protein 2	121	0.796	0	NO (active)	True	False	Active	-		
2210	IP00217143	Q8V948	SDHA	SDHA protein	57	0.053	0	NO (active)	False	False	Active	-		
1639	IP00027448	Q17964	ATP5L	ATP synthase subunit g, mitochondrial	11	0.890	0	NO (active)	True	False	Active	-		
1666	IP00002938	Q8V943	AR17	Activator of basal transcription 17	63	0.222	0	NO (active)	True	False	Active	-		
1580	IP00156032	Q13601	KRR1	KRR1 small subunit processome component homolog	44	0.139	0	NO (active)	True	False	Active	-		
1838	IP00015351	Q86294	C1orf128	Isomorph 1 of UPR0424 protein C1orf128	24	0.225	0	NO (active)	True	False	Active	-		
1389	IP00024423	Q9Y394	DDX3L	Probable ATP-dependent RNA helicase DDX3	46	0.075	0	NO (active)	True	False	Active	-		
1431	IP00493194	Q95983	MDB3	Isomorph 1 of Methyl-CpG-binding domain protein 3	33	0.284	0	NO (active)	True	False	Active	-		
1383	IP00303105	P63												

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	PII Accession	UniProtKB Accession	Gene name	Protein name	Relative abundance (mean normalized spectral count) × 10 ³			Fold enrichment (active/inactive)		Specific enrichment		Adhesome*	Hierarchical clustering
					MW (kDa)	Active integrin	Inactive integrin	Active integrin	Inactive integrin	Cluster†			
2203	PI0002203	Q9P287	BCIP	Isomorphous of BRCA2 and CDKN1A-interacting protein	36	0.080	0	NO (active)	True	False	Active	-	
2213	PI0003699	SAP98BP	Isomorphous of SAP98-binding protein	32	0.101	32	NO (active)	True	False	Active	-		
1668	PI0002533	Q6R81	CIAPIN1	Isomorphous of Anomorphin	32	2.200	0	NO (active)	True	False	Active	-	
1776	PI0000826	Q67514	HERC2	Probable E3 ubiquitin-protein ligase HERC2	527	0.007	0	NO (active)	False	False	Active	-	
2125	PI0003027	Q6V64	CORF1	Uncharacterized protein (Corf1)	24	0.025	0	NO (active)	False	False	Active	-	
2157	PI0015465	Q8TC07	TBC1D15	TBC1 domain family, member 15 isoform 1	82	0.040	0	NO (active)	False	False	Active	-	
1520	PI0012736	Q75347	TBCA	Tubulin-specific chaperone A	13	0.903	0	NO (active)	True	False	Active	-	
1658	PI0012773	Q61161	MTA1	Isomorphous of Metastasis-associated protein MTA1	81	0.084	0	NO (active)	True	False	Active	-	
1387	PI0003890	Q9ULH0	KIDIN220	Isomorphous of 2 of Kinase D-interacting substrate of 220 kDa	186	0.076	0	NO (active)	True	False	Active	-	
1433	PI0009290	Q9NVA2	SEPT11	Isomorphous of Septin-11	49	0.259	0	NO (active)	True	False	Active	-	
425	PI0012654	Q14939	NDC2	Isomorphous of Nucleolar and coiled-body phosphoprotein 1	75	0.913	0	NO (active)	True	False	Active	-	
934	PI0001040	Q9HWJ5	SF3B5	Splicing factor 3B subunit 5	10	2.685	0	NO (active)	True	False	Active	-	
1098	PI0002884	Q2NL82	TSR1	Pre-mRNA processing protein TSR1 homolog	92	0.221	0	NO (active)	True	False	Active	-	
1832	PI0000701	Q21450	HSS1L	Isomorphous of 1 of HSS1-like proteins	75	0.054	0	NO (active)	True	False	Active	-	
627	PI0001570	P35544	FALU	Ubiquitin-like protein falu and ribosomal protein S30 precursor	14	2.201	0	NO (active)	True	False	Active	-	
861	PI0002397	Q9H054	DDX47	Probable ATP-dependent RNA helicase DDX47	51	0.626	0	NO (active)	True	False	Active	-	
2215	PI0002943	Q65646	GABRA9	GA-binding protein alpha chain	55	0.035	0	NO (active)	False	False	Active	-	
1478	PI0012740	Q8IWA0	WOR5	WD repeat-containing protein 75	65	0.080	0	NO (active)	True	False	Active	-	
1270	PI0000708	Q55478	NSA2	Ribosome biogenesis protein NSA2 homolog	30	0.439	0	NO (active)	True	False	Active	-	
902	PI0003022	Q6G207	WOR12	Ribosome biogenesis protein WOR12	48	0.524	0	NO (active)	True	False	Active	-	
2063	PI0001028	Q55519	SSE11	Splicing factor arginine-serine-rich 11	32	0.111	0	NO (active)	True	False	Active	-	
1937	PI0002086	Q9N015	MRLP15	39S ribosomal protein L15, mitochondrial	33	0.153	0	NO (active)	True	False	Active	-	
1816	PI0014410	Q9NRW05	MRLP22	Isomorphous of 39S ribosomal protein L22, mitochondrial	24	0.237	0	NO (active)	True	False	Active	-	
1796	PI0001091	Q61007	DRG2	Putative uncharacterized protein DRG2	556	0.003	0	NO (active)	False	False	Active	-	
1792	PI0007914	P55039	DRG2	Putative uncharacterized protein DRG2	38	0.066	0	NO (active)	False	False	Active	-	
1328	PI0006400	Q6XG10	YALEF3	Isomorphous of 1 of Yef N-terminal domain-containing protein 3	33	0.076	0	NO (active)	False	False	Active	-	
918	PI0016822	Q9N805	GLT2D1	Procollagen galactosyltransferase 1	72	0.346	0	NO (active)	True	False	Active	-	
2048	PI0002109	Q9C005	DY30	Protein dy30 homolog	11	0.164	0	NO (active)	False	False	Active	-	
2111	PI0001836	Q9NVA2	NPE1	Nucleophosmin homolog 1	53	0.068	0	NO (active)	True	False	Active	-	
1809	PI0002954	Q15058	KIF4	Kinesin-like protein KIF4	69	0.189	0	NO (active)	True	False	Active	-	
1896	PI0004832	Q92759	DRG2	Putative uncharacterized protein DRG2	38	0.066	0	NO (active)	False	False	Active	-	
1941	PI0001839	Q92759	DRG2	Putative uncharacterized protein DRG2	38	0.066	0	NO (active)	False	False	Active	-	
1712	PI0016496	Q11318	PIRHA	General transcription factor III subunit 4	52	0.090	0	NO (active)	True	False	Active	YES	
2189	PI0001420	Q07021	C1QB	Complement component 1 Q subcomponent-binding protein, mitochondrial	31	0.065	0	NO (active)	False	False	Active	-	
2107	PI0003467	Q9H392	WHS2	Wolf-Hirschhorn syndrome candidate 2-binding protein	59	0.043	0	NO (active)	True	False	Active	-	
1725	PI0002921	Q25457	TOPBP1	DNA topoisomerase 2-binding protein 1	136	0.029	0	NO (active)	True	False	Active	-	
1983	PI0007808	Q14254	FLOT2	FLOT2	47	0.086	0	NO (active)	True	False	Active	-	
1567	PI0006493	Q9691	EP400	Isomorphous of E1A-binding protein p400	340	0.017	0	NO (active)	True	False	Active	-	
1613	PI0000769	Q14807	KIF23	Kinesin-like protein KIF23	73	0.092	0	NO (active)	True	False	Active	-	
1561	PI0002176	Q8Y181	FTS3	Putative RNA methyltransferase 3	97	0.071	0	NO (active)	True	False	Active	-	
1891	PI0009749	Q6M67	WFS12	Zinc finger protein 512	65	0.039	0	NO (active)	True	False	Active	-	
1044	PI0007946	Q23044	STIP3	STIP3 protein	68	0.286	0	NO (active)	True	False	Active	-	
904	PI0003813	Q9H8H0	NOL11	Nucleolar protein 11	81	0.275	0	NO (active)	True	False	Active	-	
2382	PI00064171	Q14151	WRN	Putative uncharacterized protein RPL179P	21	1.272	0	NO (active)	False	False	Active	-	
1824	PI0002107	Q14809	WRN	Werner syndrome ATP-dependent helicase	163	0.033	163	NO (active)	True	False	Active	-	
1839	PI0007415	Q8H2U1	DKH36	Isomorphous of Probable ATP-dependent RNA helicase DKH36	115	0.034	0	NO (active)	True	False	Active	-	
1794	PI0006153	Q6E613	MRLP35	39S ribosomal protein L35, mitochondrial	12	0.462	0	NO (active)	True	False	Active	-	
937	PI0002028	Q9N919	UTP6	U3 small nucleolar RNA-associated protein 6 homolog	70	0.258	0	NO (active)	True	False	Active	-	
2217	PI0003541	Q9N497	TIMELSS	Isomorphous of Protein timeless homolog	139	0.010	0	NO (active)	False	False	Active	-	
2143	PI0002030	Q9N913	ACT103	Acyl-coenzyme A thioesterase 13	15	2.020	0	NO (active)	False	False	Active	-	
2075	PI0003880	Q13766	RPN2	ribophosin II isoform 2 precursor	68	0.062	0	NO (active)	False	False	Active	-	
1862	PI0004014	Q13616	DCM4	50 kDa protein	50	0.199	0	NO (active)	True	False	Active	-	
1766	PI0003293	Q8Y183	SRM1	Serine/arginine repetitive matrix protein 1	104	0.058	0	NO (active)	True	False	Active	-	
1649	PI0003617	P42696	RBM34	Isomorphous of RNA-binding protein 34	49	0.146	0	NO (active)	True	False	Active	-	
1207	PI0003021	Q11171	EPH4	Isomorphous of Protein tyrosine kinase 4	92	0.171	0	NO (active)	True	False	Active	-	
2208	PI0001906	P35613	BSG	Isomorphous of 2 of Basigin	29	0.122	0	NO (active)	False	False	Active	-	
1954	PI0008400	Q94874	KIAA0776	Isomorphous of E3 UFM1-protein ligase 1	90	0.047	0	NO (active)	True	False	Active	-	
1569	PI0004290	Q48600	DEF	Digitonin-sugar expansion factor homolog	83	0.099	0	NO (active)	True	False	Active	-	
1365	PI0002128	P04080	CSTB	Cystatin B	11	1.237	0	NO (active)	True	False	Active	-	
1481	PI0006474	Q9Y5Y2	NUP87	Cytosolic Fe-S cluster assembly factor NUP87	29	0.112	0	NO (active)	True	False	Active	-	
1713	PI0007681	Q8Y811	KIF18B	Kinesin family member 18B	93	0.027	0	NO (active)	True	False	Active	-	
1604	PI0001316	P82650	MRLP22	28S ribosomal protein S22, mitochondrial	41	0.221	0	NO (active)	True	False	Active	-	
1641	PI0001104	P61024	CX518	Cyclin-dependent kinase regulatory subunit 1	10	0.576	0	NO (active)	True	False	Active	-	
1679	PI0002179	Q8U052	EN2C	Isomorphous of E1A/Rb/MS2-interacting/CAF2 family member 1	28	0.055	0	NO (active)	True	False	Active	-	
1243	PI0002102	Q8N8F6	AVL9	Isomorphous of 2 of Late secretory pathway protein AVL9 homolog	65	0.031	0	NO (active)	False	False	Active	-	
742	PI00009471	Q9JUN4	WDR3	WD repeat-containing protein 3	106	0.231	0	NO (active)	True	False	Active	-	
2251	PI0001178	Q14807	RBM21	RNA-binding motif protein 2, like 1	36	0.018	0	NO (active)	True	False	Active	-	
696	PI0001188	Q9Y379	NOCL2	Nucleolar complex protein 2 homolog	85	0.337	0	NO (active)	True	False	Active	-	
2343	PI0002913	Q67566	HGFC4	Hepatocyte growth factor activator	71	0.036	0	NO (active)	True	False	Active	-	
2097	PI0002699	Q97996	THBS3	Thrombospondin 3	117	0.029	0	NO (active)	True	False	Active	-	
1846	PI0000660	Q95831	AFM1	Isomorphous of Apoptosis-inducing factor 1, mitochondrial	67	0.060	0	NO (active)	True	False	Active	-	
1855	PI0002903	Q05005	KPN3	Isomorphous of Nucleolar protein alpha 3	58	0.099	0	NO (active)	True	False	Active	-	
869	PI0006627	Q6G617	CCDC124	Coiled-coil domain-containing protein 124	26	0.778	26	NO (active)	True	False	Active	-	
2240	PI0001073	Q9N161	COMM	COMM domain-containing protein 3	22	0.115	0	NO (active)	True	False	Active	-	
1719	PI0007400	Q9N805	GNS3	Isomorphous of DNA replication complex GINS protein PSF3	25	0.115	0	NO (active)	True	False	Active	-	
2124	PI0006552	Q9JW11	CND17	CCR4-NOT transcription complex subunit 7	33	0.199	0	NO (active)	True	False	Active	-	
1848	PI0002546	P64802	PAH4182	Platelet-activating factor acetylhydrolase B subunit beta	30	0.219	0	NO (active)	True	False	Active	-	
1887	PI00038531	Q9JUN4	ZMYND8	Isomorphous of 2 of Protein kinase C-binding protein 1	67	0.070	0	NO (active)	True	False	Active	-	
1910	PI00010748	Q9JUN4	HSP70	Hsp70-binding protein 1	44	0.116	0	NO (active)	True	False	Active	-	
1291	PI0003070	Q13616	DCM4	Isomorphous of 50 kDa protein	50	0.197	0	NO (active)	True	False	Active	-	
2202	PI00018139	Q9N500	SFRS2P	Isomorphous of SFRS2-interacting protein	129	0.011	0	NO (active)	False	False	Active	-	
1775	PI0002931	PPR310	PPR310	Serine/threonine-protein phosphatase 1 regulatory subunit 10	99	0.033	0	NO (active)	True	False	Active	-	
1350	PI0004421	Q15291	CFP1	Isomorphous of 1 of Cytosolic F-actin-binding interacting protein 1	145	0.039	0	NO (active)	True	False	Active	-	
2086	PI00031489	P06132	UROD	Uroporphyrinogen decarboxylase	41	0.111	0	NO (active)	True	False	Active	-	
1788	PI00074787	P42695	NACPO3	Uncoupling-2 complex subunit D3	169	0.021	0	NO (active)	True	False	Active	-	
1390	PI00052708	Q8T800	UTP5D	U3 small nucleolar RNA-associated protein 15 homolog	55	0.025	0	NO (active)	True	False	Active	-	
2342	PI00027241	Q60827	URB1	Nucleolar pre-ribosomal-associated protein 1	254	0.087	0	NO (active)	True	False	Active	-	
911	PI00002646	Q8UB89	UXT	Protein UXT	18	0.140	0	NO (active)	True	False	Active	-	
771	PI00051073	Q60213	DKH16	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DKH16	119	0.205	0	NO (active)	True	False	Active	-	
840	PI00013891	Q13595	TRA2A	Isomorphous of Long of Transformer-2 protein homolog alpha	33	0.958	0	NO (active)	True	False	Active	-	
2141	PI00079749	Q12846	STX4	Syntaxin 4 (Placental), isoform CRA_c	34	0.133	0	NO (active)	True	False	Active	-	
1462	PI0001177	Q14809	SEPT2	Isomorphous of 1 of Septin-2	42	0.260	0	NO (active)	True	False	Active	-	
1867	PI00003194	Q16637	SMN1	Isomorphous of SMN of Survival motor neuron protein	32	0.079	0	NO (active)	True	False	Active	-	
1818	PI0002929	Q14258	TRIM25	E3 ubiquitin ligase TRIM25	71	0.086	0	NO (active)	True	False	Active	-	
1853	PI0001901	Q15611	AD21	Isomorphous of 1 of Alpha-2-macroglobin	81	0.073	0	NO (active)	True	False	Active	-	
1859	PI00008274	Q01518	CAP1	Isomorphous of Adenylyl cyclase-associated protein 1	52	0.155	0	NO (active)	True	False	Active	-	
1449	PI00045429	P62987	UBA52	Ubiquitin and ribosome protein L40 precursor	15	18.649	0	NO (active)	True	False	Active	-	
844	PI00029098	Q9N919	SMR8	Signal recognition particle receptor subunit beta	32	0.072	0	NO (active)	True	False	Active	-	
2154	PI00016230	Q9E21	MRLP37	39S ribosomal protein L37, mitochondrial	48	0.042	0	NO (active)	True	False	Active	-	
1979	PI00034159	P61421	ATP6V0D1	V-type protein ATPase subunit d 1	40	0.189	0	NO (active)	True	False	Active	-	
1784	PI00024408	Q12830	BTF1	Isomorphous of 2 of Nucleosome-remodeling factor subunit BTF1	325	0.038	0	NO (active)	False	False	Active	-	
1793	PI00029331	Q9N912	POP1	Ribonuclease P/MRP protein subunit POP1	119	0.047	0	NO (active)	True	False	Active	-	
1764	PI00033984	Q8TC12	RDH11	Isomorphous of 1 of Retinol dehydrogenase 11	35	0.173	0	NO (active)	True	False	Active	-	
1895	PI00031461	Q9J395	GDJ2	Rap GTP dissociation inhibitor beta	51	0.138	0	NO (active)	True	False	Active	-	
1713	PI00025												

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	IPi Accession	UniProtKB Accession	Gene name	Protein name	Protein MW (kDa)	Relative abundance (mean normalized spectral count) × 10 ³			Fold enrichment (active/inactive)		Cluster*	Adhesome*	Hierarchical clustering
						Active	Inactive	Integrin [†]	Active	Inactive			
1162	IP00032957	P63279	UBE2I	SUMO-conjugating enzyme UBE2I	18	0.632	0	NO (active)	True	False	Active	-	
1517	IP00305492	Q43396	TYRKL	Threonine-like protein 5	32	0.212	0	NO (active)	True	False	Active	-	
1935	IP00854619	Q9NS58	SAMSN1	Putative uncharacterized protein SAMSN1	50	0.108	0	NO (active)	False	False	Active	-	
1767	IP00840414	Q17280	Cblor114	Uncharacterized protein Cblor114	42	0.137	0	NO (active)	True	False	Active	-	
1779	IP0014832	Q9H822	ITRM6	Islet 1 of Tropicamide motif-containing protein 56	81	0.018	0	NO (active)	False	False	Active	-	
1829	IP00040155	Q49426	GLV1	Islet 1 of Putative oxidoreductase GLV1	61	0.083	0	NO (active)	True	False	Active	-	
2066	IP00101659	Q96P11	NSUN5	Islet 2 of Putative methyltransferase NSUN5	50	0.058	0	NO (active)	False	False	Active	-	
2105	IP00212116	P48912	TSN4	Islet 1 of Elongation factor 1c, mitochondrial	25	0.095	0	NO (active)	True	False	Active	-	
2215	IP00384122	Q80T77	DLST	Dihydrolyipolysine-residue succinyl-proteinase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	40	0.063	0	NO (active)	False	False	Active	-	
2244	IP00303106	Q98773	PSMG3	Proteasome assembly chaperone 3	13	0.194	0	NO (active)	True	False	Active	-	
1959	IP00143566	NDUFA6	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6	18	0.230	0	NO (active)	True	False	Active	-	
1984	IP00220317	P09884	POLA1	DNA polymerase alpha catalytic subunit	166	0.015	0	NO (active)	True	False	Active	-	
1288	IP00027898	Q9NS22	C21orf70	Islet 1 of Uncharacterized protein C21orf70	25	0.432	0	NO (active)	True	False	Active	-	
997	IP0015838	Q9N938	LYAR	Cell growth-regulating nuclear protein	40	0.326	0	NO (active)	True	False	Active	-	
1004	IP00202860	P55209	NAP111	Nucleosome assembly protein 1-like 1	45	0.360	0	NO (active)	True	False	Active	-	
2175	IP00007812	P21281	ATP6V1B2	V-type proton ATPase subunit B, brain isoform	57	0.044	0	NO (active)	False	False	Active	-	
965	IP00399996	Q70703	RGM7TD1	Mitochondrial ribonuclease P protein 4	47	0.423	0	NO (active)	True	False	Active	-	
1217	IP00185146	Q96P70	IMPOT9	Importin 9	116	0.099	0	NO (active)	True	False	Active	-	
1761	IP00060606	Q98Y98	MRSM26	28S ribosomal protein S26, mitochondrial	24	0.282	0	NO (active)	True	False	Active	-	
1880	IP00111118	P31350	RRM2	ribonucleotide reductase M2 polypeptide isoform 1	51	0.057	0	NO (active)	True	False	Active	-	
970	IP00250708	Q96607	DDX27	Probable ATP-dependent RNA helicase DDX27	20	0.238	0	NO (active)	True	False	Active	-	
2212	IP00431082	Q96C22	HAUS1	Islet 1 of HAUS augmin-like complex subunit 1	32	0.085	0	NO (active)	False	False	Active	-	
1971	IP00217104	Q9M6G7	NLN2L2	Melanoma-associated antigen G1	34	0.085	0	NO (active)	True	False	Active	-	
1615	IP00000726	Q9H441	NMNAT1	Nicotinamide mononucleotide adenylyltransferase 1	52	0.257	0	NO (active)	True	False	Active	-	
2281	IP00219538	P06746	POLB	DNA polymerase beta	38	0.076	0	NO (active)	True	False	Active	-	
2120	IP0024567	Q9N2M5	GLTSCR2	Glioma tumor suppressor candidate region 2 protein	54	0.027	0	NO (active)	False	False	Active	-	
1933	IP00160421	Q9H945	MRLP3	39S ribosomal protein L38, mitochondrial	47	0.244	0	NO (active)	True	False	Active	-	
1423	IP00005705	P36873	PPP1CC	Islet 1 of Serine/threonine-protein phosphatase PP1 gamma catalytic subunit	37	0.458	0	NO (active)	False	False	Active	-	
1414	IP00413100	Q98UJ1	PLD8E1	Islet 1 of Flecitin homology-like domain family B member 1	151	0.097	0	NO (active)	True	False	Active	-	
2200	IP00101962	Q9P055	COX2C137	Colic acid oxidase	20	0.104	0	NO (active)	False	False	Active	-	
1656	IP00005740	Q43402	COX4NB	Neighbor of COX4	24	0.234	0	NO (active)	True	False	Active	-	
1669	IP00306400	Q98W19	KPC1	Kinesin-like protein KPC1	74	0.073	0	NO (active)	True	False	Active	-	
1946	IP0042862	Q98W45	PRLA	Peglyl-prolyl-cis-trans isomerase like 4	32	0.076	0	NO (active)	True	False	Active	-	
1972	IP00329594	Q9P031	CCDC59	Thyroid transcription factor 1-associated protein 26	29	0.112	0	NO (active)	True	False	Active	-	
1879	IP00329692	P30419	NMT1	Islet 1 of Glycylpeptide N-tetradecanoyltransferase 1	57	0.102	0	NO (active)	True	False	Active	-	
1990	IP00304803	Q9H919	GAPR3	GAP repeat sequence	37	0.054	0	NO (active)	False	False	Active	-	
2043	IP00945795	P43307	SSR1	Putative uncharacterized protein SSR1	30	0.185	0	NO (active)	False	False	Active	-	
1122	IP00219871	Q95777	LSM8	U6 snRNA-associated 5m-like protein LSM8	10	1.447	0	NO (active)	True	False	Active	-	
1761	IP00008437	Q9H919	PLD8E1	Probable ribosome biogenesis protein PLD8E1	20	0.220	0	NO (active)	True	False	Active	-	
1029	IP0015196	P78346	RP30	Ribonuclease P protein subunit p30	29	0.522	0	NO (active)	True	False	Active	-	
1349	IP00303099	Q93H42	CDCAF	Borealin	31	0.555	0	NO (active)	True	False	Active	-	
1945	IP00164422	Q9H919	ZCNCB	Islet 2 of Zinc finger CCHC domain-containing protein 8	51	0.071	0	NO (active)	True	False	Active	-	
973	IP00791325	Q15387	KIAA0020	Pumilio domain-containing protein KIAA0020	17	0.215	0	NO (active)	True	False	Active	-	
2120	IP00087759	Q14686	MLL2	564 kDa protein	564	0.003	0	NO (active)	False	False	Active	-	
1869	IP00007828	Q17031	CLKP	ATP-dependent Ctp proteinase ATP-binding subunit ctp-like, mitochondrial	60	0.059	0	NO (active)	True	False	Active	-	
1616	IP00294575	P30360	COX7	Cytochrome c oxidase subunit 7, mitochondrial	92	0.043	0	NO (active)	True	False	Active	-	
2206	IP00290514	Q9N988	INT59	Integrator complex subunit 9	74	0.019	0	NO (active)	False	False	Active	-	
2214	IP00328257	Q10607	APB1	Islet 1 of AP-1 complex subunit beta-1	105	0.456	0	NO (active)	True	False	Active	-	
1708	IP0045449	Q9W065	RAO2B8	UV excision repair protein RAO2B homolog B	42	0.111	0	NO (active)	True	False	Active	-	
1786	IP0020091	P61158	ACTR3	Actin-related protein 3	47	0.139	0	NO (active)	True	False	Active	-	
1526	IP00221226	Q15213	WR46	WD repeat-containing protein 46	68	0.053	0	NO (active)	True	False	Active	-	
1949	IP00012462	Q9H441	EF2A	Eukaryotic translation initiation factor 2A	60	0.053	0	NO (active)	True	False	Active	-	
2177	IP00010653	Q9G282	REK4	Islet 1 of RNA exonuclease 4	47	0.054	0	NO (active)	True	False	Active	-	
1737	IP00000296	Q98W19	C3orf10	Islet 1 of Probable protein BRCK1	9	0.392	0	NO (active)	True	False	Active	-	
1945	IP00008248	Q9H919	ANAPC1	Anaphase-promoting complex subunit 7, isoform A	67	0.194	0	NO (active)	True	False	Active	-	
1944	IP00106502	Q14145	KEAP1	Kelch-like ECH-associated protein 1	70	0.072	0	NO (active)	True	False	Active	YES	
1994	IP00219005	Q02790	F8BP4	Peglyl-prolyl-cis-trans isomerase F8BP4	52	0.039	0	NO (active)	False	False	Active	-	
1527	IP0021438	Q19527	FLT3	Fms-like tyrosine kinase 3	47	0.168	0	NO (active)	True	False	Active	-	
1976	IP0010845	Q00217	NDUFS8	NADH dehydrogenase (ubiquinone) iron-sulfur protein 8, mitochondrial	24	0.168	0	NO (active)	True	False	Active	-	
1471	IP00553153	Q9HJ22	ATP1F1	Putative uncharacterized protein DKF26564G0422	12	0.756	0	NO (active)	True	False	Active	-	
1741	IP00021255	Q9H811	LRB4	Islet 1 of Uppolysaccharidase-responsive and hege-like anchor protein	50	0.073	0	NO (active)	True	False	Active	-	
1446	IP00023591	Q00577	PURA	Transcriptional activator protein Pur-alpha	35	0.253	0	NO (active)	True	False	Active	-	
1738	IP00024043	Q98Y01	MRLP13	39S ribosomal protein L13, mitochondrial	21	0.312	0	NO (active)	True	False	Active	-	
1573	IP00032255	Q05058	PD03	Procollagen lyase-2, oxoglutarate 5-dioxygenase 3	37	0.073	0	NO (active)	True	False	Active	-	
1652	IP00032799	Q9H919	Q9H919	37 kDa protein	37	0.185	0	NO (active)	True	False	Active	-	
1736	IP00328170	Q13724	MOGS	Mannosyl-oligosaccharide glucosidase	92	0.035	0	NO (active)	True	False	Active	-	
1282	IP00166865	Q9H811	CS2D	CGSD (iron sulfur domain-containing) protein 2	60	0.178	0	NO (active)	True	False	Active	-	
1789	IP00029159	P49559	MRE11A	DOUBLE-STRAND BREAK REPAIR PROTEIN MRE11A	81	0.286	0	NO (active)	True	False	Active	-	
2231	IP00010244	Q92912	MRSF11	Islet 1 of 28S ribosomal protein S11, mitochondrial	21	0.168	0	NO (active)	False	False	Active	-	
2167	IP00221479	Q9H919	HEICL	Putative uncharacterized protein HEICL	33	0.005	0	NO (active)	True	False	Active	-	
1900	IP00168165	Q75122	CLASP2	CLASP2 protein	166	0.038	0	NO (active)	True	False	Active	-	
1902	IP00005657	Q15212	PF06	Prefoldin subunit 6	15	0.120	0	NO (active)	False	False	Active	-	
1347	IP00025640	Q14737	PCDO5	Programmed cell death protein 5	14	1.162	0	NO (active)	True	False	Active	-	
2183	IP00063827	Q9H441	ABHD4B	Islet 1 of ABHD4B domain-containing protein 14B	20	0.098	0	NO (active)	True	False	Active	-	
2228	IP00032911	P62380	TBR1	TATA box-binding protein-like protein 1	21	0.120	0	NO (active)	True	False	Active	-	
1828	IP00306719	Q98W59	CHD1	chromatin remodeler CHD1	51	0.064	0	NO (active)	True	False	Active	-	
3870	IP00191364	P63305	SKP1	Islet 1 of E3-ubiquitin-protein ligase SKP1	21	0.099	0	NO (active)	True	False	Active	-	
2107	IP00141816	Q15603	MRLP2	39S ribosomal protein L2, mitochondrial	33	0.100	0	NO (active)	True	False	Active	-	
2050	IP00291238	P15804	NDUPE2	NADH dehydrogenase (ubiquinone) flavoprotein 2, mitochondrial	27	0.080	0	NO (active)	False	False	Active	-	
2181	IP00306446	Q17028	ZNF4	Zinc finger protein 24	42	0.034	0	NO (active)	True	False	Active	-	
1199	IP00294211	Q26220	HKX38	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	141	0.061	0	NO (active)	True	False	Active	-	
1141	IP00087498	Q56409	ESCO2	N-acyltransferase ESCO2	68	0.042	0	NO (active)	False	False	Active	-	
1601	IP00141451	P39237	SERPINE6	Serpin B6	68	0.192	0	NO (active)	False	False	Active	-	
1737	IP00783302	Q96V77	PTCD3	Islet 1 of Pentatricopeptide repeat-containing protein 3, mitochondrial	79	0.071	0	NO (active)	True	False	Active	-	
1903	IP00795263	Q98G46	DNAAK19	Putative uncharacterized protein DNAAK19	10	0.216	0	NO (active)	False	False	Active	-	
1918	IP00021578	Q9NS28	KPNAB	Importin subunit alpha-4	50	0.056	0	NO (active)	True	False	Active	-	
1942	IP00018463	Q9Y307	TM6M2	Mitochondrial import inner membrane translocator Tim16	14	0.360	0	NO (active)	True	False	Active	-	
1957	IP00104177	Q17283	PING1	Islet 1 of Pogo transposable element with ZNF domain	155	0.033	0	NO (active)	True	False	Active	-	
1655	IP00186474	Q9H919	FAM127A	Protein FAM127A	13	0.255	0	NO (active)	True	False	Active	-	
1809	IP00298828	P02749	AP0H	Beta-2-glycoprotein 1	38	0.093	0	NO (active)	False	False	Active	-	
2000	IP00496705	Q9V829	MORC3	MORC Family CW-type zinc finger 3	107	0.020	0	NO (active)	False	False	Active	-	
2127	IP00212921	Q56134	ATP5J2	Putative uncharacterized protein ATP5J2	11	0.121	0	NO (active)	True	False	Active	-	
1177	IP00007729	Q9UMY1	NOL7	Islet 1 of Nuclear pore protein 7	29	0.472	0	NO (active)	True	False	Active	-	
2165	IP00505095	Q9NWS0	PHI1	PHI1 domain-containing protein 1	32	0.063	0	NO (active)	True	False	Active	-	
1143	IP00000948	Q9Y493	TBL2	Transducin beta-like protein 2	10	0.386	0	NO (active)	True	False	Active	-	
2162	IP0002182	P47755	CAPZ2	F-actin-capping protein subunit alpha-2	33	0.229	0	NO (active)	True	False	Active	-	
1110	IP00470596	Q14966	ZNF638	Islet 1 of Zinc finger protein 638	221	0.053	0	NO (active)	True	False	Active	-	
1536	IP00212526	Q9BXT5	RBM12B	Putative uncharacterized protein RBM12B	103	0.103	0	NO (active)	True	False	Active	-	
2163	IP00987649	Q9H919	Q9H919	113 kDa protein	113	0.013	0	NO (active)	True	False	Active	-	
1892	IP00018240	Q9N4U7	SDAD1	Islet 1 of Protein SDAD1 homolog	80	0.068	0	NO (active)	True	False	Active	-	
1147	IP00089860	Q14676	MDC1	Islet 1 of Mediator of DNA damage checkpoint protein 1	196	0.046	0	NO (active)	True	False	Active	-	
2168	IP00212119	Q17517	TIP1	Islet 1 of Tight junction protein ZO-1	71	0.061	0	NO (active)	True	False	Active	-	
2090	IP00062599	Q96645	SMARCD1	71 kDa protein	71	0.061	0	NO (active)	True	False	Active	-	

Supplementary Table 1 (cont.) | Hierarchical clustering analysis of proteins identified in active or inactive integrin adhesion complexes.

#	IPI Accession	UniProtKB Accession	Gene name	Protein name	Protein MW (kDa)	Relative abundance (mean normalized spectral count) $\times 10^3$		Fold enrichment (active/inactive)		Specific enrichment ¹		Cluster ²	Adhesome ³	Hierarchical clustering
						Active integrin	Inactive integrin	Integrin ⁴	Integrin ⁵	Active integrin	Inactive integrin			
1646	IP0029135	Q14759	LBR	Lamin-B receptor	71	0.057	0	ND (active)	True	False	Active	-	-	
2021	IP0004488	Q16864	ATP9F1F	V-type proton ATPase subunit F	13	0.139	0	ND (active)	False	False	Active	-	-	
1597	IP0002613	P49247	RPIA	Ribose-5-phosphate isomerase	33	0.282	0	ND (active)	True	False	Active	-	-	
1311	IP0022009	Q85168	NDUFB4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	15	0.413	0	ND (active)	True	False	Active	-	-	
2054	IP0018024	Q9N966	HMG20A	Isoform 1 of High-mobility group protein 20A	40	0.052	0	ND (active)	False	False	Active	-	-	
2030	IP0000617	Q15355	PPM1G	Protein phosphatase 1G	59	0.073	0	ND (active)	True	False	Active	-	-	
1648	IP0000715	Q60216	RAD21	Double-strand break repair protein rad21 homolog	72	0.100	0	ND (active)	True	False	Active	-	-	
1995	IP0001023	Q13065	FHL1	Protein flightless-1 homolog	145	0.029	0	ND (active)	True	False	Active	-	-	
1958	IP00171248	O75530	EED	Isoform 3 of Polycomb protein EED	46	0.063	0	ND (active)	True	False	Active	-	-	
1988	IP00220961	P05937	CALB1	Calbindin	30	0.180	0	ND (active)	True	False	Active	-	-	
2082	IP00451731	Q55182	NDUFA7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	13	0.310	0	ND (active)	True	False	Active	-	-	
2174	IP00003406	Q16643	DBN1	Isoform 1 of Drebirin	71	0.028	0	ND (active)	False	False	Active	-	-	
2055	IP00456048	Q80483	COMM2D	COMM domain-containing protein	23	0.125	0	ND (active)	True	False	Active	-	-	
2098	IP00416057	Q53148	RNMT	Isoform 2 of RNA methylase N ⁷ methyltransferase	58	0.050	0	ND (active)	False	False	Active	-	-	
2116	IP00461676	Q2V666	PMF1	HCG1999356, isoform CRA_c	20	0.090	0	ND (active)	False	False	Active	-	-	
1620	IP00799472	Q9N257	INCENP	Isoform 2 of inner centromere protein	105	0.051	0	ND (active)	True	False	Active	-	-	
2112	IP00221742	Q8UP22	PLC	phosphoinositide 3-kinase	22	0.160	0	ND (active)	True	False	Active	-	-	
1594	IP00004859	P54132	BLM	Bloom syndrome protein	159	0.029	0	ND (active)	True	False	Active	-	-	
1939	IP00208122	O75475	PSP1	Isoform 1 of PCA and SFRS1-interacting protein	60	0.042	0	ND (active)	False	False	Active	-	-	
1986	IP00216034	Q9NNU2	C20orf11	Protein C20orf11	27	0.187	0	ND (active)	True	False	Active	-	-	
2036	IP00100791	Q13889	GTF2I3	General transcription factor III subunit 3	38	0.051	0	ND (active)	False	False	Active	-	-	
2067	IP00305442	Q9BSL1	UBACL1	Ubiquitin-associated domain-containing protein	45	0.080	0	ND (active)	True	False	Active	-	-	
2173	IP00169000	P62675	MPP5C	Isoform 1 of 28S ribosomal protein S5, mitochondrial	48	0.073	0	ND (active)	False	False	Active	-	-	
2154	IP00396058	Q80402	NCAPG2	Isoform 2 of Condensin-2 complex subunit C2	132	0.022	0	ND (active)	True	False	Active	-	-	
1881	IP00154528	Q96888	SMC6	Isoform 1 of Structural maintenance of chromosomes protein 6	126	0.026	0	ND (active)	True	False	Active	-	-	
2050	IP00026519	P30405	PFH	Pepdyl-prolyl co-trans isomerase f, mitochondrial	22	0.160	0	ND (active)	False	False	Active	-	-	
1550	IP00031168	Q60256	PP5A-P2	Phosphoribosyl pyrophosphate synthase-associated protein 2	145	0.209	0	ND (active)	True	False	Active	-	-	
1366	IP00305289	P52732	KIF11	Kinesin-like protein KIF11	119	0.087	0	ND (active)	True	False	Active	-	-	
1529	IP00202606	Q75683	SURF6	Surfact locus protein 6	41	0.167	0	ND (active)	True	False	Active	-	-	
1602	IP00747053	Q59427	ERCC1	Testis basal transcription factor complex helicase XPR3 subunit	41	0.253	0	ND (active)	True	False	Active	-	-	
1273	IP00218466	P61619	SEC61A1	Protein transport protein SecE1 subunit alpha isoform 1	53	0.156	0	ND (active)	True	False	Active	-	-	
1409	IP00414836	Q92882	OSTP1	Osteonectin-stimulating factor 1	24	0.360	0	ND (active)	True	False	Active	YES	-	
2012	IP00128900	Q55111	PCF2S	Isoform 1 of Polycomb group RING finger protein 5	50	0.106	0	ND (active)	True	False	Active	-	-	
1863	IP00303383	Q12972	PPP1R8	Isoform Alpha of Nuclear inhibitor of protein phosphatase 1	38	0.106	0	ND (active)	True	False	Active	-	-	
2085	IP00302238	Q9NY61	AATF	Protein AATF	63	0.051	0	ND (active)	True	False	Active	-	-	
2142	IP00014622	Q99259	CNPE1	Capsin-1	45	0.037	0	ND (active)	False	False	Active	-	-	
1407	IP00005822	Q9UJX2	CDC23	Isoform 1 of Cell division cycle protein 23 homolog	69	0.142	0	ND (active)	True	False	Active	-	-	
2106	IP00025285	O75348	ATP9F1G1	V-type proton ATPase subunit G 1	14	0.314	0	ND (active)	True	False	Active	-	-	
1462	IP00224594	Q80161	SNAP23	Isoform Alpha-Delta of 26S proteasome non-ATPase regulatory subunit 4	42	0.253	0	ND (active)	True	False	Active	-	-	
2139	IP00183603	Q9NRP0	OSTC	Oligosaccharyltransferase complex subunit OSTC	17	0.119	0	ND (active)	False	False	Active	-	-	
1849	IP00874020	Q9H0M5	PCBD2	Pterin-4-alpha-carbonylamine dehydratase 2	14	0.453	0	ND (active)	True	False	Active	-	-	
1619	IP00244020	Q15311	CNPE3	Capsin-3	60	0.121	0	ND (active)	False	False	Active	-	-	
1932	IP00016932	Q15357	INPPL1	Isoform 1 of Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2	139	0.022	0	ND (active)	False	False	Active	YES	-	
2146	IP00329528	Q9Y486	VRBP	Isoform 1 of Protein VRBP	169	0.017	0	ND (active)	True	False	Active	-	-	
2015	IP00101428	Q80161	SNAP23	Isoform SNAP-23a of Synaptosomal-associated protein 23	42	0.141	0	ND (active)	True	False	Active	-	-	
1970	IP00007142	Q75817	PDP2	Ribonuclease P protein subunit p20	16	0.203	0	ND (active)	True	False	Active	-	-	
2094	IP00220202	Q15007	WTAP	Isoform 1 of Pre-mRNA-splicing regulator WTAP	44	0.074	0	ND (active)	True	False	Active	-	-	
1504	IP00202496	Q75607	NPM3	Nucleoplasm-3	19	0.133	0	ND (active)	False	False	Active	-	-	
1847	IP00171291	Q9N942	MPP1L7	39S ribosomal protein L17, mitochondrial	47	0.227	0	ND (active)	True	False	Active	-	-	
1447	IP00550638	Q9G2L1	POLR1E	Isoform 2 of DNA-directed RNA polymerase I subunit RPA49	47	0.138	0	ND (active)	True	False	Active	-	-	
1424	IP00121593	Q9I496	CLTA	Isoform Non-bran of Clathrin light chain A	24	0.534	0	ND (active)	True	False	Active	-	-	
1311	IP00033025	Q15181	SPY1	S1 Hsp protein	51	0.279	0	ND (active)	True	False	Active	-	-	
1479	IP00292168	Q9Y234	ASF1A	Histone chaperone ASF1A	23	0.094	0	ND (active)	False	False	Active	-	-	
1949	IP00293396	Q43747	APFG1	adaptor-related protein complex 1, gamma 1 subunit isoform A	92	0.060	0	ND (active)	True	False	Active	-	-	
1313	IP00170296	Q90773	SIRPB	Paired amphipathic helix protein Sirpb	145	0.081	0	ND (active)	True	False	Active	-	-	
1670	IP00373538	P35251	RFC1	Isoform 1 of Replication factor C subunit 1	128	0.034	0	ND (active)	True	False	Active	-	-	
1516	IP00299635	Q9N909	BIRC5	baculoviral IAP repeat-containing 5	530	0.010	0	ND (active)	True	False	Active	-	-	
2145	IP00293126	Q99426	TBCB	Tubulin-binding cofactor B	22	0.053	0	ND (active)	False	False	Active	-	-	
2052	IP00304409	Q9Y2V2	CARHSP1	Calcium-regulated heat stable protein 1	16	0.113	0	ND (active)	False	False	Active	-	-	
1812	IP00004497	P11274	BCKR	Isoform 1 of Breakpoint cluster region protein	143	0.022	0	ND (active)	True	False	Active	-	-	
1621	IP00126440	Q13888	GTF2H2	General transcription factor IIH subunit 2	44	0.180	0	ND (active)	True	False	Active	-	-	
2007	IP00217557	Q8XK66	NRM	Isoform 1 of Nurin	29	0.147	0	ND (active)	True	False	Active	-	-	
2065	IP00019495	Q63172	DYNLT1	Dynein light chain Tctex-type 1	12	0.210	0	ND (active)	False	False	Active	-	-	
2119	IP00205721	Q9N962	COPS1	COP9 signalosome complex subunit 3	45	0.030	0	ND (active)	False	False	Active	-	-	
1505	IP00000162	Q8NEJ9	NGDN	Isoform 1 of Neurogranin	36	0.282	0	ND (active)	True	False	Active	-	-	
1535	IP00032206	P50479	PDLIM4	Isoform 1 of PDZ and LIM domain protein 4	35	0.177	0	ND (active)	True	False	Active	-	-	
1763	IP00178651	Q9N942	RNMT1	Isoform 1 of RNA methylase N ⁷ , N ² -dimethylguanosine tRNA methyltransferase	69	0.107	0	ND (active)	True	False	Active	-	-	
1412	IP00440222	Q6LA44	MSH6	Sperm protein	37	0.080	0	ND (active)	True	False	Active	-	-	
2023	IP00026113	P78316	NOP14	Isoform 1 of Nuclear protein 14	98	0.026	0	ND (active)	False	False	Active	-	-	
1434	IP00107113	Q17544	UTP45A	Isoform 1 of U3 small nuclear RNA-associated protein 14 homolog A	96	0.098	0	ND (active)	False	False	Active	-	-	
2128	IP00024551	Q9NPA0	C15orf24	UPF0480 protein C15orf24	26	0.055	0	ND (active)	False	False	Active	-	-	
1807	IP00297593	Q70021	USP34	Isoform 1 of Ubiquitin carboxyl-terminal hydrolase 34	404	0.009	0	ND (active)	True	False	Active	-	-	
1964	IP00027139	Q9N941	CLIC5	Isoform 2 of Chloride intracellular channel protein 5	47	0.098	0	ND (active)	True	False	Active	-	-	
2108	IP00003636	Q94884	ATXN10	Ataxin-10	53	0.038	0	ND (active)	True	False	Active	-	-	
2133	IP00099433	Q8WY85	MYST4	Isoform 1 of Histone acetyltransferase MYST4	231	0.008	0	ND (active)	False	False	Active	-	-	
2013	IP00202094	P78560	CRADD	Death domain-containing protein CRADD	23	0.094	0	ND (active)	False	False	Active	-	-	
2059	IP00303346	Q9I498	MPP1L7	Isoform 2 of Mortality factor 4-like protein 1	37	0.095	0	ND (active)	True	False	Active	-	-	
1628	IP000910781	Q67644	GPI	Ribose-6-phosphate isomerase	64	0.106	0	ND (active)	True	False	Active	-	-	
2058	IP00294908	Q14728	PP2R5D	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	69	0.037	0	ND (active)	True	False	Active	-	-	
1569	IP00100815	Q8WTT2	NDCB	Nuclear complex protein 3 homolog	93	0.077	0	ND (active)	True	False	Active	-	-	
1477	IP00032459	Q9Y272	AP3M1	AP-3 complex subunit mu-1	47	0.166	0	ND (active)	True	False	Active	-	-	
2092	IP00031479	Q14554	POU5F1	Protein disulfide-isomerase A5	60	0.042	0	ND (active)	True	False	Active	-	-	
1690	IP00110898	Q13144	EIF2B5	Translation initiation factor eIF-2B subunit epsilon	80	0.052	0	ND (active)	True	False	Active	-	-	
2093	IP00102997	Q86555	WRNIP1	Isoform 2 of ATPase WRNIP1	69	0.052	0	ND (active)	True	False	Active	-	-	
2025	IP002946134	Q9P038	FGF2	Isoform 1 of Heparin-binding growth factor 2	31	0.046	0	ND (active)	False	False	Active	-	-	
2060	IP00188113	P63201	COPS2	Isoform 2 of COP9 signalosome complex subunit 2	52	0.038	0	ND (active)	False	False	Active	-	-	
2132	IP00185859	Q98812	MRLP45	39S ribosomal protein L45, mitochondrial	35	0.132	0	ND (active)	True	False	Active	-	-	
198	IP000911039	P08107	HSPAL1A	Heat shock 70 kDa protein 1A, mitochondrial	64	1.716	0	ND (active)	True	False	Active	-	-	
2077	IP00141290	Q9P118	MRLP14	39S ribosomal protein L14, mitochondrial	16	0.261	0	ND (active)	True	False	Active	-	-	
1850	IP00007024	Q9Y300	FAM96B	Protein FAM96B	18	0.160	0	ND (active)	False	False	Active	-	-	
2070	IP00304885	Q03188	CENPC1	Centromere protein C 1	107	0.024	0	ND (active)	True	False	Active	-	-	
1484	IP002059762	Q9VW22	LYPLAL1	Isoform 1 of Lipophospholipase-like protein 1	26	0.224	0	ND (active)	True	False	Active	-	-	
1844	IP00142044	Q8YB88	SUPV3L1	ATP-dependent RNA helicase SUPV3L1, mitochondrial	88	0.070	0	ND (active)	True	False	Active	-	-	
1522	IP00100160	Q86P96	CAND1	Isoform 1 of Cullin-associated NEDD8-dissociated protein 1	136	0.067	0	ND (active)	True	False	Active	-	-	
1460	IP00101572	P62309	SNRPG	Small nuclear ribonucleoprotein G	8	0.441	0	ND (active)	False	False	Active	-	-	
1950	IP00292221	Q9HY92	RFP1	Ribosome production factor 1	40	0.108	0	ND (active)	True	False	Active	-	-	
2033	IP00023409	Q9B277	UPF3B	Isoform 1 of Regulator of nonsense transcripts 3B	58	0.075	0	ND (active)	True	False	Active	-	-	
2065	IP00101524	Q8UB89	TFP1L1	Isoform 1 of Tufelin-interacting protein-11	97	0.015	0	ND (active)	False	False	Active	-	-	
2039	IP00293476													

Supplementary Table 2 (cont.) | Functional enrichment analysis of proteins differentially enriched in integrin adhesion complexes.

Cluster ¹	Term ^{2,3}	Proteins ⁴	Count (proteins per term)	Fold enrichment	Corrected P value
Inactive	GTP binding	EEF1A1, RAB8A, GNAI3, TUBB2A, RAB1A, CDC42, RAC2, GNB1, RAB35, ARF4, RHEB, RAB13, RAB27A	13	8.66	9.76E-06
Inactive	P-loop	ARL2, RAB8A, GNAI3, DTYMK, ARF5, ARF5, RAB1A, CDC42, ARF1, RAC2, RAB35, ARF4, RHEB, RAB13, NSF, RAB27A	16	6.16	1.77E-05
Inactive	Kinase	COASY, PFKFB4, GNE, PKRAG1, FN3, DTYMK, DCK, PIP5K2, PIP5K1, TTN, PMVK, MST4, CMPK1, CBX, IK, PAPS1, CSK, SYK, DVL3, IRAK1, PFKL, PFKF, PFKM, OXSR1, STK4, CDK5, GAK, PRKX, TP53RK, PANK4, PMPK, RPS6KA3, RPS6KA1, MAPK14, PRK2, RMPK, MAPK9, PRK2	38	2.46	3.10E-04
Inactive	Multifunctional enzyme	MTFHD1, PMPK, COASY, UMP5, PFKFB4, ATIC, GNE, TSTA3, PAPS1, RINGT, FDF1	11	7.01	1.24E-03
Inactive	Protein transport	NUP98, TSG1D1, VPS37B, ARF6, ARF5, RAB1A, FAMIL25A, SEC16A, SNF8, RAB23, VPS4A, RAB11A, SAR1B, SAR1A, NSF, EIFENF1, RAB8A, IPO8, C18ORF55, NUP1, ARF1, RAB35, ARF4, TOMM20, RAB14, RAB13, RAB10, XPO1, VPS25	29	2.67	1.87E-03
Inactive	Prenylated cysteine	CDK4, RAB8A, FRK2, RAB35, RAB13, RAB1A, RAB27A	7	13.58	3.25E-03
Inactive	Ligase	ADCS, CPTS, RCTD1, AAR5, UBA6, SAEL1, AANS, ACS2, RN214, CNOT4, MKRN2, UBE2N, MTFHD1, UHRF1, ACS1, UBA1, UBA2, UBE2N, RN213, ACS4, AAC5	21	3.07	7.05E-03
Inactive	Phosphotransferase	PKFB4, PFKL, DTYMK, PFKF, DCK, PFKM, CDK5, PRKCB, RPS6KA3, RPS6KA1, MAPK14, MKL2, MAPK8, CSK, SYK	16	3.55	1.79E-02
Inactive	Palmpolantar keratoderma	KRT9, JUP, KRT6B, DSG1, KRT14, DSP	6	14.09	1.80E-02
Inactive	Monomer	RPS6KA3, CBR1, RPS6KA1, PKM2, ARF4, FOXR, RHEB	7	10.08	2.02E-02
Inactive	Magnesium	ADCS, TTN, MSTA, ITGAM, FDF1, ACS4, RHOD, SAR1B, ACS4, NSF, IRAK1, PFKL, PFKF, PDKP, PFKM, OXSR1, STK4, LAR3, RPS6KA3, ITFA, RPS6KA1, PKM2, RHEB, PRP2, SRXN1	25	2.52	2.31E-02
Inactive	mRNA processing	RBM12, RBM4, SFI, PRPF39, CASC3, RINGT, HNRNPA3, RBM4B, HNRNPH3, SRB2, TARDBP, KHSRP, CFSF7, QKI, RBM38, SIFI, RBM14, RBM25, SSU72	18	3.09	3.02E-02
Inactive	Heterodimer	CAPN1, S100A8, TUBB2A, ITGAS, ITGAV, TUBA4A, CAPN2, TGB1, TUBA1B, ITGAM, CAPN1	11	4.77	3.11E-02
Unenriched	Acetylation	KRCX5, LDH8, LDHA, POLM5, WDR82, BTK, NONO, RBM8A, RPLP0, UZAF1, RPL11, RPL12, EIF2B3, RAN, PTBP1, JUP, MAPK1, SPAG9, NME2, KRT19, RPS18, PPI1CA, RPS19, RPS18, RPS16, RPS17, RFC2, RPS11, MCT51, NEK7, ALDOA, HSD17B10, FPL11, CHCHD3, DUSP12, TAGLN2, ACP1, ACAT1, HNRNPA3, C10RF57, IDH2, RPS20, PRPF40A, HNRNPA3, RPSA, SRP54, LGALS1, PHB, GARS, DDX1, EPRS, HBA1, DDX5, RPS5, HNRNPA1, HNRNPA2B1, VDAC1, WDR61, LASP1, NIPSNAP1, NUF12, GNB2L1, RAB5C, TSNAX, TCOF1, C22ORF28, DGC14, YBK1, LSM14A, ACTR2, CDPB2, RHP18, GNAS, ATP5O, RBM42, SLC25A5, UFL1L, PFK3C2A, CCTA, DECF1, CLIC1, HNR9B1, GNB2, ROCI1, CLIC4, EEF1G, FARSA, THOC3, POLR2B, LINC5, NCB1, LINC11, NUPR2, POLR2A, NUP214, DDX19A, PCMT1, MARS, MAT2A, CNAO2B, MAGCD01, SGT4, EEF1E1, PSMC10, PHGDH, YWHAQ, HSPA4L, USP48, DNM2, MMS19, RALY, NCBP1, ZC3H4V1, IQGAP2, MTFHD1, CBRF, AIP, PPP4C, DARS, HNRNPA2B1, CORO7, PPP1CB, PSMA2, ADRM1, PSMA1, PSMA4, HSPB1, EDF1, PDCD6IP, RNM20, XRN2, RPS1, CHMP2A, CNBP, SRM, KARS, TTC4, SPZC5, PSMB6, PSMB1, ARPC3, DDX3X, ZNF326, HNRNPF, PSMB2, DNAA1, HNRNPO, EFB1, HIST2H3A, WDOR, SAPI8, SMG1, AK2, CSDR3F3, PSMD6, PPIH, HDAC1, PPIA, POLD1, E1FH, SEC13, HSPD1, DNAA1B, HNRNPH1, EFB2, HSP90A1, METAP1, PRDX5, PRDX2, CAD, BUD31, RPS1, ACTR1A, MAGOHB, HSPD92, HNR9B1, HSP90A1, HSCAM, SMOX1, GIBB1, NUPR2, CDK4, MCM3, CDK4, MCM6, SARNP, EFAF4, EFAF2, UCHL5, HMB1, HBG2, UBE2Z, GSTP1, SEC23B, KRT6C, VPS29, KRT6A, VIM, HAT1, VARS, ANKX7, RPA2, RPA2, KRT8, NUDT21, HSPA4, CNI2, UCK2, YES1, GADPH, NSUN2, GTF3C4, GICF3, PSTRIP2, NSD2, ATXN2, HSP90B1, KRT77, PHB2, ANXA11, LSM12, HNB1, RNF40	260	1.80	8.50E-31
Unenriched	Phosphoprotein	KRCX5, LDH8, LDHA, HNR8, SEC13A, POLM5, STATA3, KRPR, WDR82, BTK, NONO, WDR74, DDX17, RBM8A, RPLP0, SFRS9, UZAF1, PQB91, RPL11, RPL12, NUP35, CDC45, CCAR1, RAN, RCOF1, PTBP1, AIP, MAPK1, SPAG9, KRT19, NME2, PPI1CA, RPS18, KRT17, RPS17, RPS14, CNBP, RPS10, POLD1, MCT51, NEK7, FUS, GUC1, ALDOA, FPL11, CHCHD3, F1G2, IGF2BP1, RCL1, TAGLN2, ACP1, HNRNPA3, RAC1, RPS20, PRPF40A, HNRNPA3, RPSA, PHB, LGALS1, DDX1, GARS, EPRS, NDC80, HBA1, DDX5, HNRNPA1, RPS5, HNRNPA2, VDAC1, SYNE1, RPL18A, NUP62, LASP1, GNB2L1, TCOF1, TSNAX, POA6, C22ORF28, DGC14, YBK1, LSM14A, ANKRD17, CORP2, RRP18, USP10, CTBP1, NDUFB10, UFD01, SLC25A5, PIK3C2A, CTF6, APOC1, CLIC1, GTF2B, HNRPO, GNB2, FANCD2, CDK11A, EEF1G, FARSA, SRCAP, RBM33, NOB1, NUPR2, RPL22, POLR2A, SIRT, NUP214, PRR21A, TRIP11, ACTL3, EFB1, HSPB1, CMIP, RPS10, MVK, FELO, PDCD6IP, MCT51, NEK7, ACTB2, CNBP, MAGEA1, IGF2BP1, RCL1, ACP1, LINC28B, DNAA2, MMS19, RALY, NCBP1, ZC3H4V1, RBM3, E1FH, GARS, MAT2A, CSNK2B, ELAV1, STAT1, SGT4, TRIM21, CAPRN1, NRAS, CENB2, TRFC, RPL23, PHGDH, YWHAQ, HSPA4L, USP48, TRMT112, PDCD6IP, RNM20, DCUN1D5, XRN2, CPM2A, AFG1, LINC28B, KARS, TSC4, PSMA4, PSMB7, DDX3X, ARPC3, PSMB1, ZNF326, HNRNPF, NUBM, PRKRA, HNRNPO, DNAA1, E1FH, DNAA2, HIST2H3A, CSTF3, WDOR, SMOX1, GIBB1, PSMC6, NOSIP, HDAC1, PPIA, POLD1, E1FH, SEC13, HSPD1, HNRNPH1, HSP90A1, METAP1, CAD, RPS1, PRMT1, PCBP1, PCBP2, MAGOHB, CAT, TUBA1A, CLINT1, IMPDH2, PSM59, KHDH81, HSP90A1, SSBP1, NUP98, HMB1, G3BP1, CDK6, MCM3, CDK4, MCM6, SARNP, EFAF1, ATROV1A, EFAF2, CFSF4, CFSF4, HBG2, CFSF2, GTF1, KRT6C, KRT6A, VIM, HAT1, CTNND1, COMT, VARS, STUB1, RNF126, TYMS, RPA2, PSMB3, KRT5, KRT6, NUDT21, KRT1, LARS, HSPA4, CNI2, UCK2, YES1, GADPH, NSUN2, GTF3C4, GICF3, PSTRIP2, NSD2, ATXN2, HSP90B1, KRT77, PHB2, ANXA11, LSM12, HNB1, RNF40	66	6.14	8.54E-30
Unenriched	RNA-binding	RALY, EFB2C, ZC3H4V1, RBM3, TIMM50, RBM7, YBK1, RPS3, NONO, ANKRD17, DDX17, RBM8A, RPLP0, PCBP2, SFRS9, UZAF1, MAGOHB, RPL11, RPL12, KHDH81, RBM42, PTBP1, G3BP1, HNRNPA2B1, EXOSC1, SARNP, HNRPO, EFAF1, RPS18, ROCI1, THOC3, CFSF4, RPS11, CFSF4, THOC3, CFSF2, SNRPE, FUS, FPL11, RBM33, IGF2BP1, LINC28B, NUPR2, HNRNPA3, DDX3, DDX19A, HNRNPF, NUDT21, PRKRA, HNRNPO, NSUN2, HNRNPA3, MARS, SRP54, DDX1, EPRS, ELAVL1, DDX5, HNRNPA1, TRIM21, HNRNPA2B1, HNRNPA2, RPL22, E1FH, CIRBP, HNRNPH1, EFAF2	66	6.14	8.54E-30
Unenriched	Cytoplasm	NCBP1, LDH8, EFB2C, LDHA, SEC13A, ZC3H4V1, RBM3, STATA3, KRPR, BTK, AIP, RAE1, RBM8A, RPLP0, TUBG1, PPP4C, CCAR1, NUDT4, DARS, RAN, BAIAP2, HNRNPA2B1, CORO7, LYPLA1, PPP1CB, PSMA2, JUP, SPAG9, ADRM1, PSMA1, NME2, PPI1CA, RPS18, KRT17, PSM44, TELO2, EDF1, HSPB1, CMIP, RPS10, MVK, FELO, PDCD6IP, MCT51, NEK7, ACTB2, CNBP, MAGEA1, IGF2BP1, RCL1, ACP1, LINC28B, KARS, PSMB3, PFI1, PSMA4, PSMB7, PSMB6, DDX3X, ARPC3, PSMB1, PSMB2, PRKRA, HNRNPO, EFB1, HNRNPA3, RPSA, SRP54, SAPI8, SMG1, HNRNPA2, NOSIP, PSMA5, PPIH, SYNE1, NUP62, PPIA, LASP1, E1FH4, PPII, CIRBP, NUF12, DNAA1B, HSP90A1, HSP90B1, TSNAX, PRDX5, PRDX2, CAD, YBK1, RPS3, LSM14A, ACTR2, CORP2, ANKRD17, ACTR1A, PCBP1, PCBP2, CLINT1, AKR1C1, CTBP1, RBM42, HSP90A1, PIK3C2A, UFD01, HMB5, G3BP1, CLIC2, CCTA, CLIC1, HNRPO, GNB2, CDK11A, FARSA, VPS29, NKT1, LANCL1, CTNND1, HAT1, COMT, STUB1, NUPR2, MUF2, SIRT, DDX19A, PPI2C8, KRT8, LARS, PCMT1, HSPA4, GSTO1, YES1, GADPH, NSUN2, TRIP11, MARS, PSTRIP2, ELAV1, STAT1, CAPRN1, TRIM21, UBE1, ATXN2, PHB2, EEF1E1, ANXA11, YWHAQ, HSPA4L, USP48, DUSP9, DNAA2, RPS10, RPS11, FARSA, EFAF2	153	2.31	2.37E-23
Unenriched	Protein biosynthesis	VARS, KARS, RPS29, RPLP0, LARS, RPL11, EFB1, RPL12, RPS20, EFB2B, MARS, RPSA, DARS, GARS, EPRS, RPS5, EFAF2, IGF2C2, RPS19, RPL23, RPS16, RPL18A, RPL22, RPS17, RPS14, E1FH, EEF1E1, EEF1G, RPS10, RPS11, FARSA, EFAF2	33	8.82	2.61E-18
Unenriched	Nucleus	MMS19, RALY, KRCX5, NCBP1, EFB2C, ZC3H4V1, RBM3, STATA3, WDR82, MED20, CBRF, BTK, WDR74, NONO, DDX17, RAE1, CGGBP1, RBM8A, SFRS9, UZAF1, PQB91, NUP37, NUP35, PPP4C, CDC45, RAN, RCOF1, HNRNPA2B1, PTBP1, PPP1CB, RHC5, PSMA2, ADRM1, PSMA1, NME2, PPI1CA, RPS18, KRT17, PSM44, TELO2, EDF1, HSPB1, CMIP, RPS10, MVK, FELO, PDCD6IP, MCT51, NEK7, ACTB2, CNBP, MAGEA1, IGF2BP1, RCL1, ACP1, LINC28B, RPS19, RPL23, RPL18A, RPS16, RPL22, RPS17, RPS14, RPS10, RPS11, HNRNPH1, SNRPE	159	1.86	5.81E-15
Unenriched	Ribonucleoprotein	VIM, KARS, PSMB5, PSMA4, ANKRD17, PSMB7, PSMB6, DDX3X, PSMB1, RPLP0, KRT8, PSMB2, CTBP1, SLC25A5, RAN, RCOF1, STAT1, GTF2B, HNRNPA1, SGT4, VDAC1, EFAF4, MAPK1, KRT19, KRT18, HDAC1, TRC, PPIA, PSMA4, E1FH, CFSF4, HSPD1, PDCD6IP, SRCAP	34	5.99	8.15E-14
Unenriched	Host-virus interaction	RALY, NCBP1, FPL11, PPI1, DGC14, YBK1, NONO, HNRNPA3, RBM8A, HNRNPF, SFRS9, NUDT21, UZAF1, MAGOHB, PPII, PRPF40A, CTF3, PTBP1, HNRNPA2B1, DDX5, HNRNPA1, PPIH, THOC6, CFSF4, CFSF4, HNRNPH1, CFSF2, SNRPE, THOC3, XRN2	30	5.79	2.09E-11
Unenriched	Proteasome	PSMB5, PSMA2, PSMB4, PSMA1, ADRM1, PSMB1, PSMB6, PSMB7, PSMB4, PSMA1, PSMA10, PSMB2, UCHL5, PSMB5, PSM59	16	14.35	6.38E-11
Unenriched	Ribosome	RPSA, RPS5, RPS18, RPS19, RPL18A, RPL23, RPS16, RPS17, RPL22, RPS14, RPLP0, RPS10, RPL11, RPS11, RPS11, RPS12, RPL2	17	11.70	2.96E-10
Unenriched	mRNA splicing	RALY, NCBP1, PPI1, PTBP1, HNRNPA2B1, DDX5, DGC14, HNRNPA1, HKT1, NONO, HNRNPA3, PPIH, RBM8A, HNRNPF, SFRS9, THOC6, UZAF1, MAGOHB, PPII3, HNRNPH1, THOC3, SNRPE, PRPF40A	23	5.53	7.62E-08
Unenriched	mRNA transport	NCBP1, ADFC1, NUP98, HNRNPA1, NUP214, NUP62, RBM8A, DDX19A, THOC6, MAGOHB, NUP37, NUP54, NUP55, THOC3	14	9.50	7.84E-07
Unenriched	Threonine protease	PSMA2, PSMB5, PSMA4, PSMA1, PSMB7, PSMB6, PSMB1, PSMA4, PSMB2	9	22.60	8.44E-07
Unenriched	Methylation	KHDH81, FUS, HIST2H3A, SLC25A5, RBM3, HNRNPA2B1, G3BP1, ELAVL1, DDX5, HNRNPA1, HNRNPA2, HNRPO, NIAS, PPP2CB, RAC1, HNRNPO, KRT1, HNRNPH1, PPP4C, GADPH, HNRNPA3	22	4.57	6.45E-06
Unenriched	Ribosomal protein	RPSA, RPS27L, RPS5, RPS18, RPS19, MRPL12, RPS16, RPL18A, RPL23, RPS17, RPL12, RPS14, RPLP0, RPS10, RPL11, RPS11, RPS11, RPS12, RPL2	19	5.08	1.52E-05
Unenriched	ATP-binding	KRCX5, HSP90A1, CAD, MTFHD1, BTK, ACTR2, DDX17, ACTR1A, HSP90A1, DARS, PIK3C2A, G3BP1, CDK6, CCTA, MCM3, CDK4, MCM4, MCM5, MCM6, RFS, MAPK1, ATROV1A, NME2, RFC2, CDK11A, MVK, FARSA, UBE2Z, SNRP, NEK7, PRPS1, ACTB1, UBE2D3, C10RF57, DDX3X, DDX19A, LARS, HSPA4, UCK2, YES1, ACSL3, MARS, MAT2A, MSH2, DDX1, GARS, SMG1, AK2, EPRS, DDX5, HSP90B1, PSMC6, HSPA4L, HSPD1	57	2.16	2.43E-05
Unenriched	Nucleotide-binding	VARS, KARS, RPS29, RPLP0, LARS, RPL11, EFB1, RPL12, RPS20, EFB2B, MARS, RPSA, DARS, GARS, EPRS, RPS5, EFAF2, IGF2C2, RPS19, RPL23, RPS16, RPL18A, RPL22, RPS17, RPS14, E1FH, EEF1E1, EEF1G, MSH2, DDX1, GARS, EPRS, SMG1, AK2, DDX5, NRAS, HSP90B1, PSMB2, HSPA4L, HSPD1, DNAA2	66	1.97	5.52E-05
Unenriched	Oxygen carrier	PSMA2, PSMB5, PSMA4, PSMB6, PSMB1, PSMA4, PSMB2	6	37.67	5.89E-05
Unenriched	Proteinase	PSMA2, PSMB5, PSMA4, PSMB6, PSMB1, PSMA4, PSMB2	7	20.68	2.23E-04
Unenriched	Spliceosome	RALY, PPI1, HNRNPA2B1, DDX5, HNRNPA1, DGC14, HNRNPA3, PPIH, RBM8A, HNRNPF, SFRS9, THOC6, UZAF1, MAGOHB, PPII3, HNRNPH1, THOC3, SNRPE, PRPF40A	14	5.86	2.88E-04
Unenriched	Blood	HBB, HBD1, HBG1, HBG2, HBA1, HBE1	6	27.39	4.62E-04
Unenriched	Oxygen transport	HBB, HBD1, HBG1, HBG2, HBA1, HBE1	6	25.11	7.80E-04
Unenriched	Intermediate filament	KRT6C, KRT6A, KRT19, KRT18, KRT77, KRT17, KRT5, KRT16, KRT8, VIM, KRT1	11	7.08	1.18E-03
Unenriched	Stress response	HSP90A1, HSP90A1, RBM3, HSPA4L, HSPB1, CIRBP, HSPA4, DNAA1B, HSPD1, SERPINH1	10	7.61	2.19E-03
Unenriched	Aminoacyl-tRNA synthetase	DARS, LARS, GARS, EPRS, FARSA, VARS, KARS, MARS	8	10.30	3.76E-03
Unenriched	Erythrocyte	HBB, HBD1, HBG1, HBG2, HBA1, HBE1	6	15.07	1.33E-02
Unenriched	Metalloprotein	PP1CA, MAT2A, HBB, PPP2CB, HBD1, HBG1, HBG2, HBA1, CAT, HBE1, PPP4C, PPP1CB	12	4.86	1.36E-02
Unenriched	WD repeat	SEC13A, GNB1, WDOR, CORO7, WDR82, WDR74, CORP2, DCAF7, GNB2, WDR61, RAE1, THOC6, SEC13, EFB1, NUP37, GNB2L1, THOC3	18	3.28	1.47E-02
Unenriched	Translation	LSM14A, SARNP, EFAF1, NCBP1, EFAF2, EFB2C, RBM8A, IGF2BP1, EFAF2	9	6.75	1.92E-02
Unenriched	Cell cycle	KHDH81, RAN, CDK6, NDC80, CDK4, MCM3, RCL1, PPP1CB, MCM6, MAPK1, SPZC5, PPI1CA, CNB2, KRT18, FANCD2, CDK11A, ANXA11, PLO1, NUP37, PDCD6IP, CDC45, UBE2Z, MCT51, CCAR1	24	2.61	1.95E-02
Unenriched	Heterotetramer	KRT5, HBB, KRT1, CSNK2B, HBD1, HBG1, HBG2, HBA1, HBE1	9	6.55	2.37E-02
Unenriched	Cell division	RAN, CDK6, NDC80, RCL1, CDK4, PPP1CB, MCM5, SPZC5, PPI1CA, CNB2, CDK11A, ANXA11, PLO1, NUP37, PDCD6IP, CDC45, UBE2Z	17	3.23	2.97E-02
Unenriched	Nuclear pore complex	NUP214, NUP62, NUP98, DDX19A, NUP37, NUP54, NUP35	7	8.79	4.59E-02

¹Proteins identified by MS and assigned to active, inactive or unenriched clusters (Supplementary Table 1) were subjected to analysis of enrichment of SwissProt Protein Information Resource keywords.

²Terms with fold enrichment ≥ 1.5 , Bonferroni-corrected P value < 0.05 , EASE score (modified Fisher's exact probability) < 0.05 and at least two proteins per term were considered significantly overrepresented.

³Terms highlighted in the text are indicated in bold font. Data associated with terms significantly overrepresented in all three clusters are indicated in grey font.

⁴Proteins are indicated by gene name for clarity.

Supplementary Table 3 | Effect of reduced expression of selected +TIPs and other proteins on cortical microtubule targeting.

Gene name ¹	Protein name ¹	Alias(es)	Expression knockdown (%) ²			Effect on MT localisation to cell periphery ³
			HFF	K562	U2OS	
ARHGEF2	Rho/rac guanine nucleotide exchange factor 2	GEF-H1	0	70	0	-
CKAP5	Cytoskeleton-associated protein 5	Ch-TOG, XMAP215	70	75	n.d.	-*
MACF1	Microtubule-actin cross-linking factor 1	ABP620, ACF7	80	0	n.d.	-
MAPRE1	Microtubule-associated protein RP/EB family member 1	EB1	90	n.d.	n.d.	-
CDK9	Cyclin-dependent kinase 9	CDC2L4, TAK	40	n.d.	n.d.	-
FLNA	Filamin-A	ABP-280	0	n.d.	90	-
GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1	HLC-7, RACK1	50	n.d.	50	-*
GRB2	Growth factor receptor-bound protein 2	ASH	70	n.d.	n.d.	-
LGALS1	Galectin-1	Galaptin, HLBP14	90	n.d.	n.d.	-
MPG	DNA-3-methyladenine glycosylase	ADPG	85	n.d.	n.d.	-
PLEC	Plectin	HD1	80	n.d.	n.d.	+
SNRPB	Small nuclear ribonucleoprotein-associated proteins B and B'	Sm-B/B'	70	n.d.	n.d.	-*
EZR	Ezrin	Cytovillin, VIL2	85	n.d.	n.d.	-
ILK	Integrin-linked protein kinase	-	n.d.	n.d.	90	++
IQGAP1	Ras GTPase-activating-like protein IQGAP1	p195	40	n.d.	90	-
PHLDB2	Pleckstrin homology-like domain family B member 2	LL5β	0	n.d.	70	-
RCC2	Regulator of chromosome condensation 2	TD-60	90	n.d.	90	+

¹Quantitative MS data for all proteins identified in the active integrin data set were mapped onto a merged, multi-source interactome database to generate an active integrin interactome (see methods for details). From the identified proteins reported to interact directly with or indirectly within three interactions of β1 integrin (the three-hop interaction network), proximity subnetworks seeded with β1 integrin or +TIPs were generated *in silico*. Proteins situated at the intersections of β1 integrin and +TIPs one- or two-hop subnetworks were identified as candidates that may functionally link active integrin and +TIPs. Expression of selected +TIPs (red bar), candidate connecting proteins from interaction network analysis (blue bar) and other potential connecting or active integrin-enriched proteins (green bar) was depleted by siRNA in a range of cell types. Knockdown of ILK expression has previously been shown to affect microtubule localisation at the cell periphery⁵.

²Experiments were performed in HFF, K562 and U2OS cells. 0, expression knockdown not effective; n.d., not done.

³Forty-eight to seventy-two hours after siRNA transfection, cells were spread on FN for 1 h, fixed and stained for α-tubulin to assess the effect of expression knockdown on microtubule targeting to the cell cortex. ++, substantial effect (microtubules did not reach the cell periphery in most cells); +, slight effect (microtubules did not reach the cell periphery in some cells); -, no effect (microtubules did reach the cell periphery); *, expression knockdown produced off-target effects (such as reduced cell spreading or cell viability).

Supplementary Table 4 | Statistics source data.

(a) Statistics source data for Figure 4b.

Cell repl.	MT density ^{1,2}			Statistic ⁴	Comparison		
	FN	Stim.	Inhib.		FN vs stim.	Stim. vs inhib.	FN vs inhib.
1	2.89 (9)	5.13 (15)	1.00 (10)	Mean difference	-3.35	6.11	2.76
2	5.00 (11)	6.36 (11)	0.42 (12)	95% CI of difference	-4.40 to -2.30	5.03 to 7.20	1.65 to 3.88
3	2.67 (6)	7.71 (14)	0.40 (15)	Corrected P value	< 0.0001	< 0.0001	< 0.0001
4	4.67 (3)	6.79 (19)	0.38 (29)	*One-way analysis of variance, Tukey's multiple comparisons test, $\alpha = 0.05$			
5	3.63 (8)	5.85 (13)	1.00 (24)				
6	2.62 (13)	8.36 (11)	0.69 (29)				
7	2.43 (21)	5.40 (15)	0.55 (44)				
8	2.85 (13)	6.00 (9)	0.30 (30)				
9	3.44 (18)	6.88 (8)	-				
10	-	8.56 (16)	-				
Mean	3.35	6.70	0.59				
s.d.	0.93	1.19	0.28				
n	9	10	8				

¹Number of MTs per 5 × 2- μ m region at cell periphery

²Number of regions quantified per cell indicated in parentheses

³P value (H_0 , NGD, non-Gaussian distribution)

⁴D'Agostino & Pearson omnibus normality test, $\alpha = 0.05$

(b) Statistics source data for Figure 4c.

Cell repl.	MT density ^{1,2} , before NOC			MT density ^{1,2} , after washout			Statistic ⁴	Comparison, before NOC			Comparison, after washout			Compar., FN Before vs after	Compar., stim. Before vs after	Compar., inhib. Before vs after
	FN	Stim.	Inhib.	FN	Stim.	Inhib.		FN vs stim.	Stim. vs inhib.	FN vs inhib.	FN vs stim.	Stim. vs inhib.	FN vs inhib.			
1	3.00 (36)	3.05 (20)	0.58 (19)	2.48 (31)	2.62 (21)	0.10 (20)	Mean difference	0.35	2.42	2.77	0.48	2.20	2.68	0.60	0.73	0.51
2	3.50 (32)	2.41 (27)	0.43 (23)	2.53 (36)	1.60 (20)	0.00 (20)	95% CI of difference	-0.58 to 1.27	1.56 to 3.29	1.91 to 3.64	-0.45 to 1.40	1.33 to 3.06	1.81 to 3.54	-0.32 to 1.53	-0.19 to 1.66	-0.30 to 1.31
3	3.47 (34)	3.47 (19)	0.61 (23)	3.16 (32)	2.52 (31)	0.09 (34)	Corrected P value	0.8200	< 0.0001	< 0.0001	0.5600	< 0.0001	< 0.0001	0.3300	0.1600	0.3500
4	-	-	0.59 (34)	-	-	0.00 (21)	*Two-way analysis of variance, Tukey's multiple comparisons test, $\alpha = 0.05$									
Mean	3.32	2.98	0.55	2.72	2.25	0.05										
s.d.	0.28	0.54	0.07	0.38	0.56	0.05										
n	3	3	4	3	3	4										
P (NGD) ^{4,5}	ND	ND	ND	ND	ND	ND										

¹Number of MTs per 5 × 2- μ m region at cell periphery

²Number of regions quantified per cell indicated in parentheses

³P value (H_0 , NGD, non-Gaussian distribution)

⁴D'Agostino & Pearson omnibus normality test, $\alpha = 0.05$

⁵ND, not determined (too few values to compute normality)

(c) Statistics source data for Figure 4d.

Cell repl.	MT density ^{1,2} , DMSO		MT density ^{1,2} , cytochalasin		Statistic ⁴	Compar., DMSO	Compar., cyto.	Compar., stim.	Compar., inhib.
	Stim.	Inhib.	Stim.	Inhib.		Stim. vs inhib.	Stim. vs inhib.	DMSO vs cyto.	DMSO vs cyto.
1	3.72 (18)	0.08 (38)	3.43 (21)	0.76 (25)	Mean difference	3.38	2.55	-0.57	-1.40
2	3.82 (17)	0.03 (31)	4.77 (30)	1.63 (24)	95% CI of difference	2.57 to 4.19	1.80 to 3.30	-1.38 to 0.24	-2.15 to -0.65
3	4.39 (18)	0.42 (43)	4.64 (25)	2.15 (27)	Corrected P value	< 0.0001	< 0.0001	0.2246	0.0003
4	3.18 (17)	0.28 (32)	4.15 (26)	1.84 (25)	*Two-way analysis of variance, Tukey's multiple comparisons test, $\alpha = 0.05$				
5	2.95 (21)	0.36 (39)	3.94 (16)	1.82 (17)					
6	-	-	-	1.63 (24)					
7	-	-	-	1.61 (23)					
Mean	3.61	0.23	4.19	1.63					
s.d.	0.57	0.17	0.54	0.43					
n	5	5	5	7					
P (NGD) ^{4,5}	ND	ND	ND	ND					

¹Number of MTs per 5 × 2- μ m region at cell periphery

²Number of regions quantified per cell indicated in parentheses

³P value (H_0 , NGD, non-Gaussian distribution)

⁴D'Agostino & Pearson omnibus normality test, $\alpha = 0.05$

⁵ND, not determined (too few values to compute normality)

Supplementary Table 4 (cont.) | Statistics source data.

(d) Statistics source data for Figure 5a.

Patch	MT density ¹			Statistic ⁴	Comparison		
	FN	Stim.	Inhib.		FN vs stim.	Stim. vs inhib.	FN vs inhib.
1	32.66	166.66	23.89	Mean rank difference Corrected P value	-7.02 > 0.9999	93.30 < 0.0001	100.30 < 0.0001
2	7.23	318.47	15.82				
3	147.01	237.14	23.30	*Kruskal-Wallis test, Dunn's multiple comparisons test, $\alpha = 0.05$			
4	22.43	137.33	86.57				
5	27.56	79.88	77.48				
6	5.05	30.53	21.73				
7	7.79	36.40	36.92				
8	69.07	26.34	70.63				
9	5.35	28.51	19.49				
10	13.28	21.63	28.95				
11	324.87	43.72	17.19				
12	95.64	30.33	16.37				
13	331.86	156.48	33.45				
14	235.51	193.51	24.20				
15	50.68	27.75	36.84				
16	84.05	27.43	56.43				
17	92.80	120.40	11.78				
18	77.19	228.66	11.40				
19	10.35	91.00	20.83				
20	92.58	19.29	37.34				
21	418.90	46.37	57.24				
22	608.84	46.37	44.03				
23	248.34	42.42	46.73				
24	475.57	112.11	23.03				
25	325.48	53.06	32.70				
26	31.77	453.29	89.83				
27	73.18	62.08	78.72				
28	626.04	170.06	53.77				
29	42.21	311.45	79.12				
30	189.94	186.80	39.89				
31	180.98	187.55	37.34				
32	249.38	91.16	57.24				
33	234.12	114.34	44.03				
34	369.53	201.33	46.73				
35	248.48	43.51	23.03				
36	307.22	107.45	32.70				
37	124.81	83.84	89.83				
38	193.56	135.02	78.72				
39	56.61	227.37	53.77				
40	232.97	93.96	79.12				
41	202.79	80.96	39.89				
42	107.07	233.50	21.48				
43	26.22	48.90	17.71				
44	217.85	64.64	18.13				
45	104.96	388.06	18.07				
46	188.83	68.32	28.46				
47	36.57	95.15	18.11				
48	294.35	288.45	16.06				
49	52.79	45.23	23.87				
50	8.04	123.81	40.47				
51	42.48	223.57	46.90				
52	50.67	84.88	71.68				
53	310.96	149.25	122.04				
54	287.07	117.84	67.70				
55	319.83	369.57	21.79				
56	22.07	102.20	45.98				
57	171.15	107.95	11.43				
58	92.55	129.33	22.82				
59	102.58	145.51	10.47				
60	20.35	66.14	56.35				
61	34.70	28.09	109.12				
62	76.86	174.38	51.50				
63	19.91	33.41	271.78				
64	454.45	127.50	37.38				
65	33.74	258.43	12.87				
66	8.62	31.14	116.95				
67	200.65	218.82	33.45				
68	20.09	73.61	7.91				
69	66.40	128.65	72.48				
70	948.28	146.60	19.30				
71	5.31	20.28	78.78				
72	356.60	121.65	21.01				
73	667.07	105.61	36.43				
74	92.29	61.74	17.42				
75	206.55	69.90	82.59				
76	90.54	212.28	36.87				
77	158.27	200.05	9.69				
78	22.57	37.79	8.93				
79	344.39	77.86	10.14				
80	31.62	718.35	10.02				
81	196.43	132.53	54.88				
82	12.87	90.12	24.33				
83	182.36	261.42	6.81				
84	109.94	93.81	33.40				
85	101.76	88.64	20.83				
86	32.79	28.23	8.15				
87	81.47	83.62	21.48				
88	28.41	60.02	10.62				
89	60.23	104.70	22.88				
90	150.57	222.95	23.78				
91	64.10	208.08	57.63				
92	161.77	161.19	14.59				
93	342.23	80.51	34.93				
94	85.40	82.73	18.90				
95	10.16	196.73	20.24				
96	-	64.15	15.28				
97	-	56.49	25.62				
98	-	348.51	-				
99	-	272.87	-				
100	-	223.66	-				
101	-	24.10	-				
102	-	53.42	-				
103	-	178.54	-				
104	-	32.12	-				
105	-	118.69	-				
106	-	82.27	-				
107	-	96.28	-				
108	-	45.88	-				
109	-	40.39	-				
110	-	182.66	-				
111	-	41.75	-				
112	-	196.50	-				
113	-	81.41	-				
114	-	38.13	-				
115	-	109.67	-				
116	-	76.84	-				
117	-	96.75	-				
118	-	36.08	-				
119	-	80.36	-				
120	-	93.40	-				
121	-	44.11	-				
122	-	37.06	-				
123	-	51.94	-				
124	-	47.17	-				
125	-	57.51	-				
Mean	158.84	123.00	40.48				
s.d.	168.48	102.25	35.50				
n	95	125	97				
P (NGD) ^{1,2}	< 0.0001	< 0.0001	< 0.0001				

¹Tubulin fluorescence intensity per patch at cell periphery

²P value (H_0 : NGD, non-Gaussian distribution)

⁴D'Agostino & Pearson omnibus normality test, $\alpha = 0.05$

(e) Statistics source data for Figure 5c.

Cell repl.	MT density ^{1,2}				Statistic ⁴	Comparison	
	FN	Stim.	Inhib.	Inhib. + stim. ³		Inhib. vs inhib. + stim. ³	Inhib. vs stim. ³
1	3.58 (40)	2.31 (35)	0.11 (36)	2.64 (56)	Mean difference 95% CI of difference Corrected P value	2.38 ± 0.24 1.85 to 2.90 < 0.0001	
2	3.50 (36)	3.64 (14)	0.32 (34)	2.03 (33)			
3	4.61 (31)	2.88 (40)	0.38 (32)	3.64 (47)	*Two-tailed unpaired t test, Welch's correction		
4	4.00 (55)	2.00 (24)	0.22 (32)	2.36 (45)			
5	5.56 (18)	2.90 (21)	0.56 (36)	1.92 (39)			
6	5.06 (17)	3.03 (33)	0.85 (33)	2.95 (56)			
7	3.04 (23)	2.63 (19)	0.10 (39)	3.29 (35)			
8	5.63 (8)	2.31 (48)	1.08 (36)	3.00 (33)			
9	4.08 (13)	4.79 (33)	0.24 (34)	2.13 (45)			
10	-	2.96 (26)	0.39 (31)	4.00 (37)			
11	-	1.88 (25)	0.35 (34)	-			
12	-	3.75 (50)	-	-			
Mean	4.34	2.92	0.42	2.80			
s.d.	0.93	0.82	0.30	0.70			
n	9	12	11	10			
P (NGD) ^{1,2}	0.54	0.18	0.09	0.66			

¹Number of MTs per 5 × 2- μ m region at cell periphery

²Number of regions quantified per cell indicated in parentheses

³Inhibitory:stimulatory, 1:0:0:1

⁴P value (H_0 : NGD, non-Gaussian distribution)

⁵D'Agostino & Pearson omnibus normality test, $\alpha = 0.05$

Supplementary References

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