

Supplementary Figure and legends

Inventory of items in Supplementary Information

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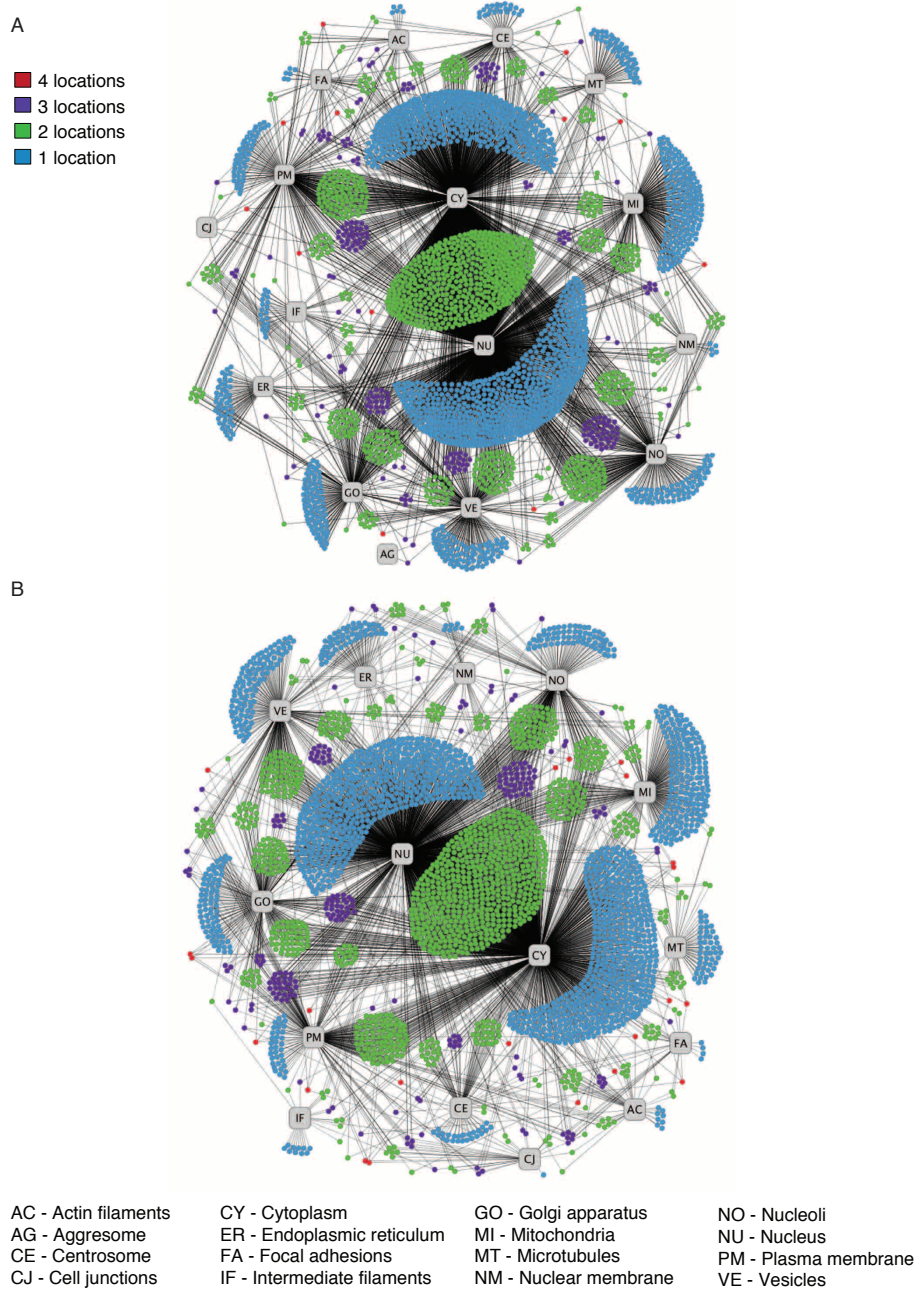
Supplementary Table 9: Gene Ontology enrichment analysis of 67 proteins expressed exclusively in U-2 OS. (Related to Figure 7).

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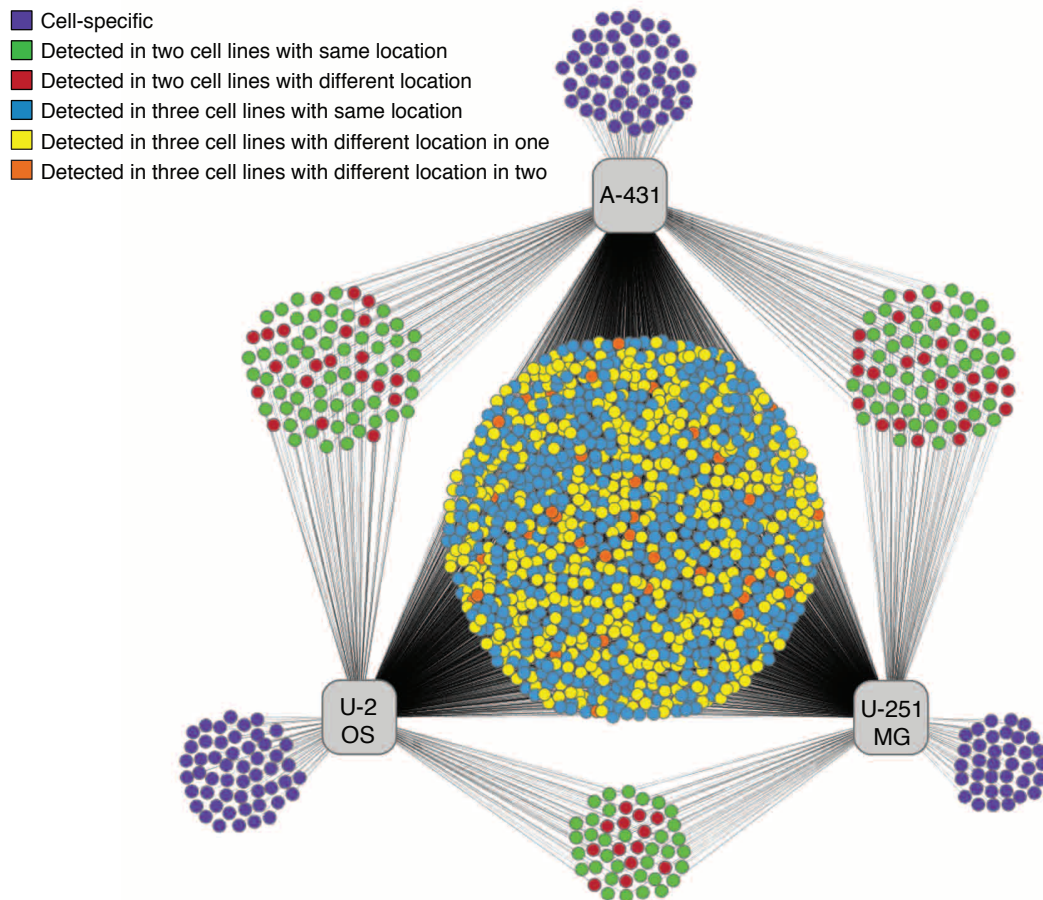
Supplementary Table 11: Gene Ontology enrichment analysis of 52 proteins expressed exclusively in U-251 MG. (Related to Figure 7).

Supplementary Table 12: Gene Ontology enrichment analysis of 457 proteins not detected in any of the three cell lines. (Related to Figure 7).

Supplementary Figure S1. Network plot of the distribution of protein subcellular locations. Related to Figure 4. Visualization of protein subcellular annotations for **A) U-251 MG** and **B) A431**. The total numbers of proteins detected are 3,280 for U-251 MG and 3341 for A-431. Each protein is represented by a circle colored by the number of compartments it is localized in. Each subcellular compartment is represented by a grey box with a two-letter code (bottom legend).



Supplementary Figure S2. Variation in staining intensity between the three cell lines. Related to Figure 7. Network plot of the distribution of the similarity of staining intensity in the three cell lines using 1,490 proteins detected in at least one of the three cell lines and localized in a single subcellular compartment. Each protein is represented by a circle with a color reflecting the similarity in terms of staining intensity for the cell lines in which it is detected (see legend). Staining intensities are categorized into four groups corresponding to negative, weak, moderate or strong based on microscope settings.



Supplementary Tables and legends

Supplementary Table 1. Gene Ontology (GO) –based enrichment analysis of 635 proteins detected in the cytoplasm in U-2 OS. Related to Figure 4. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
cytosol	Cellular Component	94	4.2E-8	1.6E-5
cytoplasm	Cellular Component	368	4.4E-7	8.5E-5
cytosolic part	Cellular Component	17	7.8E-6	1.0E-3
translation	Biological Process	21	2.1E-4	4.2E-1
cytosolic ribosome	Cellular Component	8	8.0E-4	7.4E-2
translational elongation	Biological Process	9	1.5E-3	8.6E-1
catalytic activity	Molecular Function	242	3.8E-3	9.6E-1
soluble fraction	Cellular Component	19	6.6E-3	4.0E-1
ribosome	Cellular Component	14	6.8E-3	3.5E-1
alcohol metabolic process	Biological Process	28	6.8E-3	1.0E0
ATP binding	Molecular Function	84	7.5E-3	9.6E-1
purine nucleotide binding	Molecular Function	97	8.6E-3	9.2E-1
adenyl ribonucleotide binding	Molecular Function	84	9.2E-3	8.6E-1
purine nucleoside binding	Molecular Function	88	9.6E-3	8.1E-1
ribonucleotide binding	Molecular Function	93	9.6E-3	7.5E-1
purine ribonucleotide binding	Molecular Function	93	9.6E-3	7.5E-1
adenyl nucleotide binding	Molecular Function	87	1.1E-2	7.6E-1
response to oxidative stress	Biological Process	15	1.2E-2	1.0E0
nucleoside binding	Molecular Function	88	1.2E-2	7.4E-1
tRNA aminoacylation	Biological Process	6	1.3E-2	1.0E0
amino acid activation	Biological Process	6	1.3E-2	1.0E0
tRNA aminoacylation for protein translation	Biological Process	6	1.3E-2	1.0E0
monosaccharide metabolic process	Biological Process	18	1.7E-2	1.0E0
heterocycle metabolic process	Biological Process	21	1.7E-2	1.0E0
structural constituent of ribosome	Molecular Function	9	1.8E-2	8.2E-1
RNA binding	Molecular Function	37	1.8E-2	7.9E-1
ribosomal subunit	Cellular Component	8	1.9E-2	6.5E-1
regulation of cellular protein metabolic process	Biological Process	32	2.1E-2	1.0E0
binding	Molecular Function	489	2.5E-2	8.6E-1
microtubule-based movement	Biological Process	10	2.5E-2	1.0E0

Supplementary Table 2. GO-based enrichment analysis of 53 proteins detected in the endoplasmic reticulum in U-2 OS. Related to Figure 4. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
endoplasmic reticulum	Cellular Component	37	3.1E-29	3.5E-27
endoplasmic reticulum part	Cellular Component	21	1.2E-19	7.0E-18
endoplasmic reticulum membrane	Cellular Component	14	3.7E-12	1.4E-10
nuclear envelope-endoplasmic reticulum network	Cellular Component	14	8.3E-12	2.4E-10
endomembrane system	Cellular Component	18	2.4E-9	5.4E-8
cytoplasmic part	Cellular Component	41	5.7E-9	1.1E-7
organelle membrane	Cellular Component	19	3.2E-8	5.2E-7
endoplasmic reticulum lumen	Cellular Component	8	2.0E-7	2.9E-6
membrane part	Cellular Component	41	7.6E-7	9.7E-6
integral to membrane	Cellular Component	36	1.1E-6	1.2E-5
membrane	Cellular Component	43	2.2E-6	2.3E-5
intrinsic to membrane	Cellular Component	36	2.5E-6	2.4E-5
protein folding	Biological Process	8	6.4E-6	3.5E-3
vesicular fraction	Cellular Component	9	7.6E-6	6.7E-5
unfolded protein binding	Molecular Function	7	8.9E-6	1.6E-3
insoluble fraction	Cellular Component	14	3.3E-5	2.7E-4
cell fraction	Cellular Component	15	5.7E-5	4.3E-4
microsome	Cellular Component	8	6.6E-5	4.7E-4
cholesterol metabolic process	Biological Process	5	9.1E-5	2.5E-2
membrane fraction	Cellular Component	13	1.2E-4	7.8E-4
sterol metabolic process	Biological Process	5	1.7E-4	3.1E-2
ER-associated protein catabolic process	Biological Process	4	2.1E-4	2.8E-2
cholesterol biosynthetic process	Biological Process	4	2.1E-4	2.8E-2
integral to endoplasmic reticulum membrane	Cellular Component	4	3.4E-4	2.2E-3

Supplementary Table 3. GO-based enrichment analysis of 53 proteins detected in the Golgi apparatus in U-2 OS. Related to Figure 4. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
Golgi apparatus	Cellular Component	19	9.9E-9	1.6E-6
Golgi apparatus part	Cellular Component	9	3.2E-6	2.6E-4
Golgi stack	Cellular Component	5	2.8E-5	1.5E-3
organelle subcompartment	Cellular Component	3	1.8E-3	6.8E-2
Golgi cisterna	Cellular Component	3	1.8E-3	6.8E-2
Golgi membrane	Cellular Component	5	2.5E-3	7.8E-2
protein homodimerization activity	Molecular Function	6	5.3E-3	6.1E-1
intrinsic to membrane	Cellular Component	27	5.9E-3	1.5E-1
membrane part	Cellular Component	31	6.1E-3	1.3E-1
integral to membrane	Cellular Component	26	8.5E-3	1.6E-1
membrane	Cellular Component	33	1.1E-2	1.8E-1
cytoplasmic part	Cellular Component	27	1.4E-2	2.0E-1
peptide binding	Molecular Function	4	1.4E-2	7.1E-1
ER-Golgi intermediate compartment	Cellular Component	3	1.5E-2	2.0E-1
cytoplasmic membrane-bounded vesicle	Cellular Component	7	1.6E-2	1.9E-1
identical protein binding	Molecular Function	7	1.8E-2	6.5E-1
membrane-bounded vesicle	Cellular Component	7	1.8E-2	2.0E-1
Golgi medial cisterna	Cellular Component	2	2.7E-2	2.7E-1
Golgi trans cisterna	Cellular Component	2	2.7E-2	2.7E-1
protein dimerization activity	Molecular Function	6	3.3E-2	7.7E-1
cytoplasmic vesicle	Cellular Component	7	3.8E-2	3.4E-1
vesicle	Cellular Component	7	4.4E-2	3.6E-1
peptide receptor activity	Molecular Function	3	4.6E-2	8.1E-1
peptide receptor activity, G-protein coupled	Molecular Function	3	4.6E-2	8.1E-1
glycosylation	Biological Process	3	5.7E-2	1.0E0
protein amino acid glycosylation	Biological Process	3	5.7E-2	1.0E0
biopolymer glycosylation	Biological Process	3	5.7E-2	1.0E0
peptide hormone binding	Molecular Function	2	6.5E-2	8.6E-1
peptidase activity, acting on L-amino acid peptides	Molecular Function	5	6.5E-2	8.2E-1
cis-Golgi network	Cellular Component	2	6.6E-2	4.7E-1

Supplementary Table 4. GO-based enrichment analysis of 70 proteins detected in the nucleoli in U-2 OS. Related to Figure 4. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
nucleolus	Cellular Component	17	3.4E-4	4.9E-2
ribosome biogenesis	Biological Process	4	2.5E-3	8.9E-1
intracellular non-membrane-bounded organelle	Cellular Component	24	5.8E-3	3.5E-1
non-membrane-bounded organelle	Cellular Component	24	5.8E-3	3.5E-1
intracellular organelle lumen	Cellular Component	20	6.5E-3	2.7E-1
cellular amino acid derivative metabolic process	Biological Process	5	7.7E-3	9.7E-1
organelle lumen	Cellular Component	20	8.0E-3	2.6E-1
ribonucleoprotein complex biogenesis	Biological Process	4	8.6E-3	9.2E-1
membrane-enclosed lumen	Cellular Component	20	9.1E-3	2.3E-1
nuclear lumen	Cellular Component	17	1.2E-2	2.6E-1
ncRNA processing	Biological Process	4	1.4E-2	9.6E-1
neuromuscular process	Biological Process	3	1.9E-2	9.7E-1
rRNA processing	Biological Process	3	1.9E-2	9.7E-1
nuclear part	Cellular Component	18	2.0E-2	3.4E-1
rRNA metabolic process	Biological Process	3	2.2E-2	9.6E-1
ncRNA metabolic process	Biological Process	4	3.0E-2	9.8E-1
glycerolipid catabolic process	Biological Process	2	3.3E-2	9.8E-1
cellular catabolic process	Biological Process	10	3.5E-2	9.7E-1
preribosome, small subunit precursor	Cellular Component	2	3.5E-2	4.8E-1
response to organic nitrogen	Biological Process	3	4.7E-2	9.9E-1
post-embryonic morphogenesis	Biological Process	2	4.9E-2	9.8E-1
cellular lipid catabolic process	Biological Process	3	5.9E-2	9.9E-1
cellular amino acid and derivative metabolic process	Biological Process	5	6.3E-2	9.9E-1
cellular process	Biological Process	47	6.8E-2	9.9E-1
preribosome	Cellular Component	2	6.9E-2	6.9E-1
nucleotidyltransferase activity	Molecular Function	3	8.2E-2	1.0E0
catabolic process	Biological Process	10	9.3E-2	1.0E0
locomotory behavior	Biological Process	4	9.6E-2	1.0E0
neuromuscular process controlling balance	Biological Process	2	9.6E-2	9.9E-1

Supplementary Table 5. GO-based enrichment analysis of 596 proteins detected in the nucleus in U-2 OS. Related to Figure 4. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
nucleolus	Cellular Component	134	1.9E-66	6.8E-64
nuclear lumen	Cellular Component	181	2.4E-61	4.3E-59
nuclear part	Cellular Component	192	1.1E-53	1.3E-51
intracellular organelle lumen	Cellular Component	187	7.3E-52	6.6E-50
organelle lumen	Cellular Component	189	1.1E-51	7.6E-50
membrane-enclosed lumen	Cellular Component	189	2.2E-50	1.3E-48
non-membrane-bounded organelle	Cellular Component	195	1.4E-32	7.4E-31
intracellular non-membrane-bounded organelle	Cellular Component	195	1.4E-32	7.4E-31
nucleus	Cellular Component	294	2.5E-32	1.1E-30
nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	Biological Process	224	1.7E-27	4.0E-24
DNA binding	Molecular Function	173	4.2E-26	2.8E-23
cellular nitrogen compound metabolic process	Biological Process	229	5.4E-25	6.3E-22
nitrogen compound metabolic process	Biological Process	231	5.2E-24	4.0E-21
nucleic acid binding	Molecular Function	209	5.5E-24	1.9E-21
regulation of gene expression	Biological Process	191	2.9E-23	1.7E-20
transcription regulator activity	Molecular Function	127	5.4E-23	1.2E-20
regulation of transcription	Biological Process	177	5.0E-22	2.4E-19
regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	Biological Process	186	6.6E-22	2.6E-19
organelle part	Cellular Component	238	1.2E-21	4.7E-20
intracellular organelle part	Cellular Component	237	1.2E-21	4.3E-20
gene expression	Biological Process	193	1.5E-21	5.1E-19
regulation of nitrogen compound metabolic process	Biological Process	186	1.8E-21	5.3E-19
regulation of macromolecule biosynthetic process	Biological Process	185	3.3E-21	8.5E-19
regulation of macromolecule metabolic process	Biological Process	203	3.4E-21	8.0E-19
transcription	Biological Process	152	5.8E-21	1.2E-18
regulation of primary metabolic process	Biological Process	202	2.8E-20	5.4E-18
regulation of biosynthetic process	Biological Process	188	4.3E-20	7.8E-18
regulation of cellular biosynthetic process	Biological Process	187	5.2E-20	8.7E-18
cellular macromolecule metabolic process	Biological Process	272	6.6E-19	1.0E-16
regulation of cellular metabolic process	Biological Process	205	9.5E-19	1.4E-16

Supplementary Table 6. GO-based enrichment analysis of 56 proteins detected in the plasma membrane in U-2 OS. Related to Figure 4. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
plasma membrane	Cellular Component	32	1.7E-8	2.3E-6
plasma membrane part	Cellular Component	25	7.0E-8	4.7E-6
membrane part	Cellular Component	39	3.5E-7	1.5E-5
membrane	Cellular Component	41	6.9E-7	2.3E-5
apical part of cell	Cellular Component	7	1.5E-4	3.9E-3
cell junction	Cellular Component	10	2.2E-4	4.8E-3
extrinsic to membrane	Cellular Component	9	3.7E-4	7.1E-3
integral to plasma membrane	Cellular Component	13	3.9E-4	6.6E-3
intrinsic to plasma membrane	Cellular Component	13	4.5E-4	6.6E-3
cytoskeletal protein binding	Molecular Function	9	7.2E-4	1.2E-1
cell-cell junction	Cellular Component	6	7.3E-4	9.7E-3
cortical actin cytoskeleton organization	Biological Process	3	2.0E-3	6.3E-1
actin binding	Molecular Function	7	2.0E-3	1.7E-1
intrinsic to membrane	Cellular Component	28	2.5E-3	3.0E-2
cortical cytoskeleton organization	Biological Process	3	2.9E-3	5.2E-1
transmembrane transport	Biological Process	7	5.7E-3	6.2E-1
monocarboxylic acid transmembrane transporter activity	Molecular Function	3	7.9E-3	3.9E-1
integral to membrane	Cellular Component	26	8.5E-3	9.1E-2
localization	Biological Process	18	1.7E-2	8.8E-1
anchoring junction	Cellular Component	5	2.3E-2	2.1E-1
apical plasma membrane	Cellular Component	4	2.3E-2	2.0E-1
basolateral plasma membrane	Cellular Component	5	2.9E-2	2.3E-1
cell development	Biological Process	7	3.0E-2	9.5E-1
cell-cell adhesion	Biological Process	5	3.6E-2	9.5E-1
membrane fraction	Cellular Component	8	3.9E-2	2.8E-1
organic acid transmembrane transporter activity	Molecular Function	3	3.9E-2	8.4E-1
carboxylic acid transmembrane transporter activity	Molecular Function	3	3.9E-2	8.4E-1
transmembrane transporter activity	Molecular Function	7	4.1E-2	7.9E-1
cell fraction	Cellular Component	9	4.3E-2	2.9E-1
insoluble fraction	Cellular Component	8	4.4E-2	2.9E-1

Supplementary Table 7. GO-based enrichment analysis of 107 proteins detected in the vesicles in U-2 OS. Related to Figure 4. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
neuron differentiation	Biological Process	10	1.3E-3	7.7E-1
neuron projection development	Biological Process	8	2.1E-3	7.0E-1
generation of neurons	Biological Process	11	3.0E-3	6.9E-1
neuron projection morphogenesis	Biological Process	7	3.4E-3	6.3E-1
cell projection organization	Biological Process	9	5.3E-3	7.1E-1
cell soma	Cellular Component	6	5.5E-3	6.9E-1
neuron development	Biological Process	8	5.9E-3	6.8E-1
neurogenesis	Biological Process	11	6.0E-3	6.3E-1
cell projection morphogenesis	Biological Process	7	6.0E-3	5.9E-1
extracellular region	Cellular Component	21	6.6E-3	5.0E-1
cell morphogenesis involved in differentiation	Biological Process	7	7.0E-3	6.0E-1
cell part morphogenesis	Biological Process	7	7.6E-3	5.9E-1
nucleotide metabolic process	Biological Process	7	8.7E-3	6.0E-1
nucleoside phosphate metabolic process	Biological Process	7	8.7E-3	6.0E-1
axon	Cellular Component	6	9.6E-3	4.9E-1
transport vesicle	Cellular Component	4	9.9E-3	4.0E-1
cytoplasmic vesicle	Cellular Component	12	1.0E-2	3.5E-1
membrane part	Cellular Component	54	1.1E-2	3.1E-1
nucleobase, nucleoside and nucleotide metabolic process	Biological Process	7	1.1E-2	6.5E-1
intrinsic to membrane	Cellular Component	46	1.1E-2	2.8E-1
ribonucleotide metabolic process	Biological Process	5	1.1E-2	6.4E-1
axonogenesis	Biological Process	6	1.2E-2	6.3E-1
cell morphogenesis	Biological Process	8	1.2E-2	6.1E-1
pyrimidine nucleoside metabolic process	Biological Process	3	1.3E-2	6.2E-1
vesicle	Cellular Component	12	1.3E-2	2.9E-1
cell morphogenesis involved in neuron differentiation	Biological Process	6	1.5E-2	6.4E-1
heterocycle metabolic process	Biological Process	7	1.5E-2	6.3E-1
neuron projection	Cellular Component	8	1.6E-2	3.1E-1
cellular component morphogenesis	Biological Process	8	1.9E-2	6.9E-1
cell projection	Cellular Component	12	1.9E-2	3.4E-1

Supplementary Table 8. GO-based enrichment analysis of 2,964 proteins expressed in all three cell lines. Related to Figure 7. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
intracellular organelle lumen	Cellular Component	537	6.5E-24	4.7E-21
nucleus	Cellular Component	998	2.4E-23	8.7E-21
organelle lumen	Cellular Component	543	4.2E-22	1.0E-19
nuclear lumen	Cellular Component	452	4.7E-22	8.5E-20
membrane-enclosed lumen	Cellular Component	548	8.1E-22	1.2E-19
nuclear part	Cellular Component	507	8.9E-20	1.1E-17
intracellular non-membrane-bounded organelle	Cellular Component	670	1.2E-19	1.2E-17
non-membrane-bounded organelle	Cellular Component	670	1.2E-19	1.2E-17
intracellular	Cellular Component	1980	1.1E-17	9.9E-16
nucleic acid binding	Molecular Function	598	1.3E-17	2.3E-14
nucleolus	Cellular Component	325	3.8E-17	3.0E-15
membrane-bounded organelle	Cellular Component	1522	1.6E-16	8.1E-15
intracellular membrane-bounded organelle	Cellular Component	1519	2.0E-16	1.5E-14
intracellular organelle	Cellular Component	1663	5.9E-16	3.4E-14
organelle	Cellular Component	1663	8.5E-16	5.0E-14
intracellular part	Cellular Component	1933	9.5E-16	5.2E-14
organelle part	Cellular Component	909	1.1E-15	5.4E-14
intracellular organelle part	Cellular Component	903	1.8E-15	8.1E-14
nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	Biological Process	630	1.8E-14	8.8E-11
gene expression	Biological Process	541	2.7E-13	6.4E-10
DNA binding	Molecular Function	439	3.8E-13	3.2E-10
cellular nitrogen compound metabolic process	Biological Process	679	1.3E-12	2.1E-9
cellular macromolecule metabolic process	Biological Process	990	1.8E-12	2.2E-9
nitrogen compound metabolic process	Biological Process	699	2.6E-12	2.5E-9
cellular macromolecule biosynthetic process	Biological Process	531	2.8E-12	2.2E-9
regulation of transcription	Biological Process	493	3.1E-12	2.1E-9
macromolecule biosynthetic process	Biological Process	534	1.1E-11	6.4E-9
regulation of gene expression	Biological Process	544	1.2E-11	6.7E-9
regulation of macromolecule biosynthetic process	Biological Process	537	2.2E-11	1.0E-8
nucleoplasm	Cellular Component	202	4.1E-11	1.8E-9

Supplementary Table 9. GO-based enrichment analysis of 67 proteins expressed exclusively in U-2 OS. Related to Figure 7. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
carbohydrate binding	Molecular Function	7	3.9E-3	6.3E-1
intrinsic to plasma membrane	Cellular Component	12	7.1E-3	6.9E-1
transmembrane receptor activity	Molecular Function	10	7.7E-3	6.3E-1
plasma membrane part	Cellular Component	18	9.2E-3	5.3E-1
phosphoric diester hydrolase activity	Molecular Function	4	1.1E-2	6.1E-1
system development	Biological Process	17	1.3E-2	1.0E0
sugar binding	Molecular Function	5	1.5E-2	6.1E-1
regulation of localization	Biological Process	8	1.5E-2	1.0E0
integral to plasma membrane	Cellular Component	11	1.8E-2	6.3E-1
response to chemical stimulus	Biological Process	12	1.8E-2	9.9E-1
response to hormone stimulus	Biological Process	6	2.0E-2	9.8E-1
membrane part	Cellular Component	34	2.2E-2	5.9E-1
growth factor binding	Molecular Function	4	2.6E-2	7.4E-1
PDZ domain binding	Molecular Function	3	2.7E-2	6.9E-1
anatomical structure development	Biological Process	17	2.9E-2	9.9E-1
response to endogenous stimulus	Biological Process	6	2.9E-2	9.8E-1
receptor activity	Molecular Function	12	3.0E-2	6.8E-1
cell surface receptor linked signal transduction	Biological Process	11	3.1E-2	9.7E-1
drug binding	Molecular Function	3	3.8E-2	7.1E-1
regulation of cell migration	Biological Process	4	4.0E-2	9.9E-1
regulation of cellular component organization	Biological Process	6	4.0E-2	9.8E-1
intrinsic to membrane	Cellular Component	28	4.5E-2	7.8E-1
regulation of membrane protein ectodomain proteolysis	Biological Process	2	4.6E-2	9.8E-1
positive regulation of membrane protein ectodomain proteolysis	Biological Process	2	4.6E-2	9.8E-1
asymmetric synapse	Cellular Component	2	4.8E-2	7.4E-1
regulation of cell motion	Biological Process	4	5.1E-2	9.8E-1
integral to membrane	Cellular Component	27	5.5E-2	7.3E-1
regulation of locomotion	Biological Process	4	5.9E-2	9.8E-1
drug transport	Biological Process	2	6.1E-2	9.8E-1
postsynaptic membrane	Cellular Component	3	6.1E-2	7.3E-1

Supplementary Table 10. GO-based enrichment analysis of 84 proteins expressed exclusively in A-431. Related to Figure 7. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
molecular transducer activity	Molecular Function	21	2.3E-3	4.8E-1
signal transducer activity	Molecular Function	21	2.3E-3	4.8E-1
receptor activity	Molecular Function	15	1.8E-2	9.2E-1
regulation of biological process	Biological Process	44	5.3E-2	1.0E0
biological regulation	Biological Process	46	5.5E-2	1.0E0
regulation of body fluid levels	Biological Process	4	6.0E-2	1.0E0
regulation of cellular process	Biological Process	42	6.4E-2	1.0E0
microsome	Cellular Component	5	7.3E-2	1.0E0
extracellular region	Cellular Component	15	7.5E-2	1.0E0
vesicular fraction	Cellular Component	5	7.6E-2	9.8E-1
transmembrane receptor activity	Molecular Function	9	8.4E-2	1.0E0
procollagen-proline dioxygenase activity	Molecular Function	2	8.7E-2	1.0E0
peptidyl-proline dioxygenase activity	Molecular Function	2	8.7E-2	1.0E0
response to wounding	Biological Process	7	9.3E-2	1.0E0
oxidoreductase activity	Molecular Function	8	9.9E-2	1.0E0

Supplementary Table 11. GO-based enrichment analysis of 52 proteins expressed exclusively in U-251 MG. Related to Figure 7. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
central nervous system development	Biological Process	6	1.8E-2	1.0E0
positive regulation of Cdc42 GTPase activity	Biological Process	2	2.7E-2	1.0E0
multicellular organismal process	Biological Process	20	3.6E-2	1.0E0
multicellular organismal development	Biological Process	16	4.7E-2	1.0E0
developmental process	Biological Process	17	5.5E-2	1.0E0
positive regulation of Ras GTPase activity	Biological Process	2	6.7E-2	1.0E0
regulation of Cdc42 protein signal transduction	Biological Process	2	6.7E-2	1.0E0
regulation of Cdc42 GTPase activity	Biological Process	2	6.7E-2	1.0E0
positive regulation of Rho GTPase activity	Biological Process	2	6.7E-2	1.0E0
positive regulation of GTPase activity	Biological Process	2	6.7E-2	1.0E0
kidney development	Biological Process	3	7.1E-2	1.0E0
sex differentiation	Biological Process	3	7.5E-2	1.0E0
urogenital system development	Biological Process	3	8.3E-2	1.0E0
nervous system development	Biological Process	8	8.7E-2	1.0E0
system development	Biological Process	13	9.0E-2	1.0E0
membrane fraction	Cellular Component	7	9.1E-2	1.0E0
cell fraction	Cellular Component	8	9.2E-2	1.0E0
genitalia development	Biological Process	2	9.3E-2	1.0E0
regulation of hormone levels	Biological Process	3	9.5E-2	1.0E0

Supplementary Table 12. GO-based enrichment analysis of 457 proteins not detected in any of the three cell lines. Related to Figure 7. The top results sorted by enrichment p-value are reported as well as the Benjamini-Hochberg multiple-testing correction and gene count for each GO term.

GO Term	GO Category	Count	P-Value	Benjamini
intrinsic to membrane	Cellular Component	203	5.8E-10	1.9E-7
integral to membrane	Cellular Component	198	7.1E-10	1.2E-7
membrane part	Cellular Component	234	4.9E-9	5.5E-7
membrane	Cellular Component	252	1.4E-7	1.2E-5
calcium ion binding	Molecular Function	49	2.2E-4	1.4E-1
extracellular region	Cellular Component	69	1.4E-3	8.8E-2
growth factor activity	Molecular Function	10	5.6E-3	8.4E-1
transmembrane receptor activity	Molecular Function	36	5.7E-3	7.1E-1
digestive system process	Biological Process	6	6.8E-3	1.0E0
digestion	Biological Process	8	1.0E-2	1.0E0
calcium ion transport	Biological Process	9	1.1E-2	1.0E0
plasma membrane	Cellular Component	127	1.4E-2	5.4E-1
G-protein coupled receptor activity	Molecular Function	19	1.6E-2	9.3E-1
extracellular matrix	Cellular Component	18	1.6E-2	5.4E-1
receptor activity	Molecular Function	52	1.6E-2	8.9E-1
extracellular region part	Cellular Component	38	1.7E-2	5.1E-1
ion channel activity	Molecular Function	16	2.0E-2	8.9E-1
endoplasmic reticulum	Cellular Component	44	2.1E-2	5.4E-1
intestinal absorption	Biological Process	4	2.1E-2	1.0E0
G-protein coupled receptor protein signaling pathway	Biological Process	24	2.3E-2	1.0E0
substrate specific channel activity	Molecular Function	16	2.8E-2	9.3E-1
homophilic cell adhesion	Biological Process	10	2.8E-2	1.0E0
proteinaceous extracellular matrix	Cellular Component	16	2.9E-2	6.3E-1
synapse	Cellular Component	17	3.0E-2	6.0E-1
ion transmembrane transporter activity	Molecular Function	25	3.5E-2	9.4E-1
low-density lipoprotein binding	Molecular Function	4	3.5E-2	9.3E-1
calcium ion transmembrane transporter activity	Molecular Function	3	3.5E-2	9.1E-1
cation transmembrane transporter activity	Molecular Function	21	3.6E-2	8.9E-1
molecular transducer activity	Molecular Function	65	3.6E-2	8.7E-1