

Supplemental materials

Supplemental Methods

Quantitative proteomics

We employed liquid chromatography (LC) – mass spectrometry (MS) and LC tandem mass spectrometry (LC-MS/MS) to identify and quantify proteins in 12 ultrafiltrate (UF) samples collected at the 20-minute point, and six pre-experiment plasma samples from plasma reservoirs. The schematic workflow for LC-MS/MS-based quantitative proteomics is illustrated in **Supplemental Figure S1A**.

Sample Preparation

Each UF sample underwent concentration using a 3K molecular weight Cut-Off (MWCO) protein concentrator (Thermo Scientific 88512). Following concentration, 100 µg of the concentrated sample were processed using an EasyPep™ MS Sample Prep Kit (Thermo Fisher A40006) and subsequently resuspended in 80 µl of 0.1% formic acid.

Before the start of each test, we collected samples from the plasma reservoir. These plasma samples underwent the same procedure for LC-MS and LC-MS/MS as UF samples without the concentration step.

Additionally, an equal quantity of concentrated UF samples, totaling 12 samples derived from the six experiments, and 6 plasma samples, was combined as UF or plasma pools, respectively, and subjected to treatment with HSA/Immunoglobulin Depletion Columns (Thermo Fisher A36365). Subsequently, pooled samples were processed using the same MS sample preparation protocol as the individual samples.

Chromatographic conditions

Each processed sample was separated by a reversed-phase LC column (Agilent AdvanceBio peptide mapping, Part Number 653750-902) on the Agilent HPLC system, employing 0.1% formic acid as solvent A and 0.1% formic acid in acetonitrile as solvent B, with a flow rate at 0.4 mL/min for a duration of 51 minutes.

The gradient used for separation was as follows: 0-1 min: 3% B; 1-41 min: Linear gradient from 3% to 45% of B; 41-44 min: Linear gradient from 45% to 95% of B; 44-47 min: 95% B; 47-49 min: Linear gradient from 95% to 3% B; 49-51 min: 3% B.

MS and MS/MS data acquisition

Following LC separation, LC-MS data was acquired on the quadrupole time-of-flight mass spectrometer (Q-TOF 6546, Agilent Technologies, Santa Clara, CA, USA) using the auto MS

mode. The Q-TOF was equipped with JetStream ElectroSpray Ionization source and data were acquired between 50 and 1,100 m/z in the positive mode. Ion source conditions were as follows: gas temperature 325 °C, drying gas 12 L/min, nebulizer 35 psi, fragmentor 175 V, skimmer 65 V and capillary voltage 4000 V.

Additionally, LC-MS/MS data was acquired from the pooled, HSA/Immunoglobulin-depleted UF or plasma sample using iterative MS/MS modes.

Peptide identification and quantification

The LC-MS/MS data obtained from UF or plasma pools were analyzed using Spectrum Mill software. The spectral data were searched against the reviewed plasma proteins in the UniProt database (<https://www.uniprot.org/uniprotkb>). The identified peptides, along with their corresponding retention times, were compiled into a target list. This target list was then utilized in the Agilent Profinder software to determine the relative quantity of each peptide, as indicated by the MS signal intensity, across all LC-MS data.

Proteomic data quantification criteria

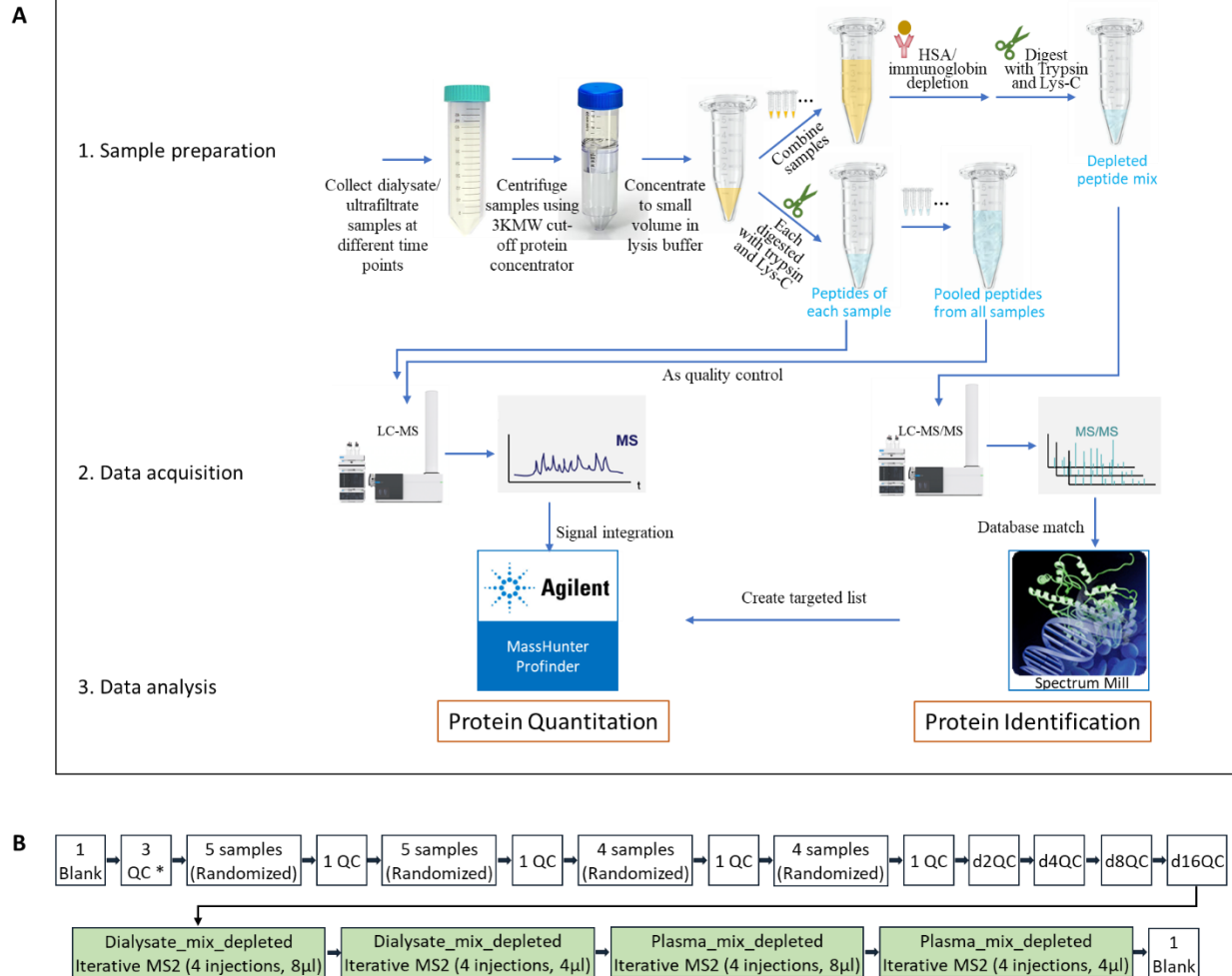
For quality control (QC) purposes, we pooled six plasma and 12 UF samples ¹. These QC samples were analyzed at the start, periodically during sample injection (every 4 to 5 samples), and at the end of the sample injection (**Supplemental Figure 1B**). For each identified peptide, the coefficient of variation (CV) was computed based on the QC samples. To ensure quantification linearity, QC samples were injected at 2-, 4-, 8-, and 16-fold dilutions; R^2 was determined by linear regression.

Quantification criteria: Raw intensity data for each peptide underwent filtering based on following criteria, including an MS score >75 in Profinder, MS2 score >9 in Spectrum Mill, signal-to-noise ratio >5, CV <30% for QC, CV <30% for 4 UF samples from each dialyzer, CV <30% for 6 plasma samples, and R^2 of the series-diluted-QC >0.8. Note that both the MS score and MS2 score refer to values generated by the Profinder and Spectrum Mill software, respectively, to indicate the reliability and confidence of compound or peptide identification in MS or MS/MS. Higher scores suggest a more confident and accurate identification.

Reference

1. Saigusa D, Okamura Y, Motoike IN, et al. Establishment of Protocols for Global Metabolomics by LC-MS for Biomarker Discovery. Monleon D, ed. *PLoS ONE*. 2016;11(8):e0160555. doi:10.1371/journal.pone.0160555

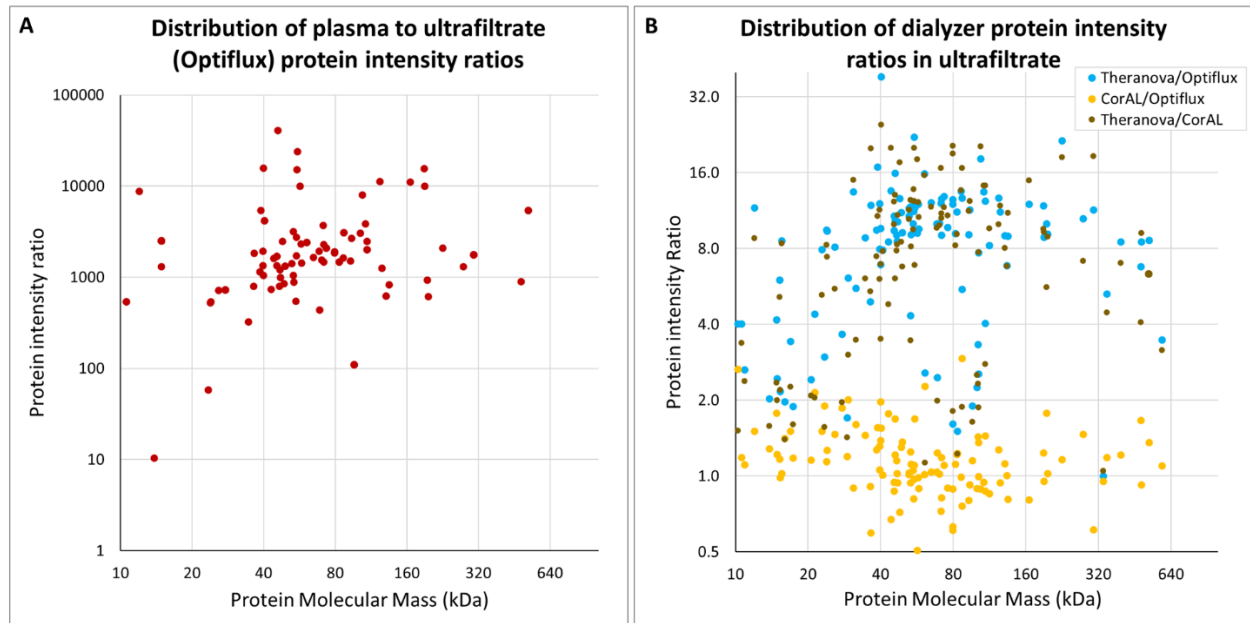
Supplemental Figures



Supplemental Figure S1. LC-MS/MS-based quantitative proteomics workflow.

(A) The workflow comprises three steps, sample preparation, data acquisition and data analysis. LC-MS/MS data is used for protein identification, while separated LC-MS data is used for protein quantification.

(B) Sample injection sequence for the entire process. Injections highlighted in green are conducted in auto MS/MS mode with 4 iterative runs. The remaining injections are conducted in auto MS mode. Blank, 0.1% formic acid; QC, quality control (mixture of all samples); dxQC, x-fold dilution of QC (x = 2, 4, 8, or 16). *The initial two QC injections are used to initialize the column and are excluded from data analysis. Data analysis incorporates the results from the third QC injection.



Supplemental Figure S2. Protein intensity ratios in relation to protein molecular mass.

(A) The plasma-to-ultrafiltrate protein intensity ratios for 79 proteins using Optiflux dialyzer were plotted against their respective molecular masses, with both axes displayed on logarithmic scales. Each red dot represents one protein.

(B) Ultrafiltrate protein intensity ratios of Theranova-to-Optiflux (blue), CorAL-to-Optiflux (orange) and Theranova-to-CorAL (brown) of 113 proteins were plotted against their respective molecular masses, with both axes displayed on logarithmic scales. Each dot represents one protein.

Supplemental Tables

Supplemental Table S1: List of 244 proteins found in dialyzer ultrafiltrate.

Protein name	UniProt	MM (kDa)	Protein name	UniProt	MM (kDa)
Thymosin beta-4	P62328	5.1	Carboxypeptidase N subunit 2	P22792	61.4
Apolipoprotein C-I	P02654	9.3	Extracellular matrix protein 1	Q16610	62.3
Protein S100-A6	P06703	10.2	N-acetylmuramoyl-L-alanine amidase	Q96PD5	62.8
Protein S100-A12	P80511	10.6	Complement component C9	P02748	64.7
Neutrophil defensin 3	P59666	10.6	Hyaluronan-binding protein 2	Q14520	64.8
Apolipoprotein C-III	P02656	10.9	Sodium/mannose cotransporter SLC5A10	A0PJK1	65.0
Protein S100-A8	P05109	10.9	Galectin-3-binding protein	Q08380	66.2
C-C motif chemokine 14	Q16627	10.9	Interleukin-1 receptor-like 2	Q9HB29	66.5
Apolipoprotein C-II	P02655	11.3	Insulin-like growth factor-binding protein complex acid labile subunit	P35858	66.8
Apolipoprotein A-II	P02652	11.3	Complement component C8 alpha chain	P07357	66.9
Secreted Ly-6/uPAR-related protein 1	P55000	11.8	Complement factor I	P05156	68.1
Immunoglobulin kappa constant	P01834	11.9	Guanylate-binding protein 1	P32455	68.4
Thioredoxin	P10599	12.0	Complement component C8 beta chain	P07358	68.7
Guanylin	Q02747	12.8	C4b-binding protein alpha chain	P04003	69.1
Protein S100-A9	P06702	13.3	Coagulation factor XII	P00748	70.1
Beta-2-microglobulin	P61769	13.8	Afamin	P43652	71.0
CD59 glycoprotein	P13987	14.8	Albumin	P02768	71.4
Serum amyloid A-4 protein	P35542	14.9	Prothrombin	P00734	71.5
Antileukoproteinase	P03973	15.2	Hepatocyte growth factor activator	Q04756	72.9
Hemoglobin subunit alpha	P69905	15.3	Kininogen-1	P01042	73.0
Fatty acid-binding protein 5	Q01469	15.5	ATPase family AAA domain-containing protein 3B	Q5T9A4	73.1
Transthyretin	P02766	16.0	Plasma kallikrein	P03952	73.5
Cystatin-C	P01034	16.0	Rap guanine nucleotide exchange factor-like 1	Q9UHV5	74.0
Hemoglobin subunit beta	P68871	16.1	Centrosomal protein of 76 kDa	Q8TAP6	75.7
NPC intracellular cholesterol transporter 2	P61916	16.9	Proprotein convertase subtilisin/kexin type 9	Q8NBP7	75.8
Ribonuclease 4	P34096	17.3	Vitamin K-dependent protein S	P07225	77.2
Serglycin	P10124	17.8	Coagulation factor XIII B chain	P05160	77.8
Insulin-like growth factor II	P01344	20.6	Complement C1s subcomponent	P09871	78.2
Prostaglandin-H2 D-isomerase	P41222	21.3	Segment polarity protein dishevelled homolog DVL-3	Q92997	78.4
Apolipoprotein D	P05090	21.6	Protein kinase C eta type	P24723	79.2
Apolipoprotein M	O95445	21.6	Serotransferrin	P02787	79.3
Complement component C8 gamma chain	P07360	22.4	TGF-beta-activated kinase 1 and MAP3K7-binding protein 3	Q8N5C8	79.4
Neutrophil gelatinase-associated lipocalin	P80188	22.8	Adhesion G protein-coupled receptor L4	Q9HBW9	79.7
Tetranectin	P05452	22.9	Cyclin-T2	O60583	81.5
Retinol-binding protein 4	P02753	23.4	Complement C1r subcomponent	P00736	81.7
Alpha-1-acid glycoprotein 1	P02763	23.8	Hepatocyte growth factor-like protein	P26927	82.9
Alpha-1-acid glycoprotein 2	P19652	23.9	Centrosomal protein of 83 kDa	Q9Y592	83.1
TPA-induced transmembrane protein	Q5BVD1	24.6	Sulfhydryl oxidase 1	O00391	83.4
Serum amyloid P-component	P02743	25.5	Coagulation factor XIII A chain	P00488	83.8
Glutathione peroxidase 3	P22352	25.8	Polymeric immunoglobulin receptor	P01833	84.5
Complement C1q subcomponent subunit A	P02745	26.3	Complement C2	P06681	84.6
Adiponectin	Q15848	26.5	Gelsolin	P06396	86.1
Endothelial protein C receptor	Q9UNN8	27.0	Complement factor B	P00751	86.9
Secreted and transmembrane protein 1	Q8WVN6	27.3	Phosphate-regulating neutral endopeptidase PHEX	P78562	87.0
Complement factor D	P00746	27.5	Inactive dipeptidyl peptidase 10	Q8N608	91.5
Collectin-11	Q9BWP8	29.1	Receptor-type tyrosine-protein phosphatase alpha	P18433	91.6
Carbonic anhydrase 2	P00918	29.3	Cyclic nucleotide-gated cation channel beta-3	Q9NQW8	92.7
C4b-binding protein beta chain	P20851	29.3	Phosphatidylinositol-glycan-specific phospholipase D	P80108	93.0
Apolipoprotein A-I	P02647	30.8	Cadherin-like protein 26	Q8IXH8	93.2
Insulin-like growth factor-binding protein 5	P24593	31.6	Plasminogen	P00747	93.3

Malectin	Q14165	32.4	Fibrinogen alpha chain	P02671	95.7
Insulin-like growth factor-binding protein 3	P17936	32.7	Complement component C7	P10643	96.7
Ficolin-3	O75636	33.4	NEDD4-like E3 ubiquitin-protein ligase WWP2	O00308	99.5
Zinc-alpha-2-glycoprotein	P25311	34.5	Inter-alpha-trypsin inhibitor heavy chain H3	Q06033	100.1
Cathepsin Z	Q9UBR2	34.6	Desmocollin-3	Q14574	101.3
ADP/ATP translocase 4	Q9H0C2	35.3	Desmocollin-1	Q08554	101.5
Osteopontin	P10451	35.6	Glutamate receptor 3	P42263	101.7
Apolipoprotein E	P02649	36.3	Inter-alpha-trypsin inhibitor heavy chain H1	P19827	101.8
Taste receptor type 2 member 14	Q9NYV8	36.4	Inter-alpha-trypsin inhibitor heavy chain H4	Q14624	103.6
Annexin A3	P12429	36.5	TBC1 domain family member 2A	Q9BYX2	106.3
Protein MENT	Q9BUN1	37.3	G-protein coupled receptor family C group 6 member A	Q5T6X5	106.7
Arfaptin-2	P53365	38.0	Inter-alpha-trypsin inhibitor heavy chain H2	P19823	106.9
Leucine-rich alpha-2-glycoprotein	P02750	38.4	Complement component C6	P13671	108.4
Lumican	P51884	38.8	SH3 domain-binding protein 4	Q9P0V3	108.5
Complement factor H-related protein 1	Q03591	38.8	Proprotein convertase subtilisin/kexin type 6	P29122	109.6
Beta-2-glycoprotein 1	P02749	39.6	Oncostatin-M-specific receptor subunit beta	Q99650	112.0
CD5 antigen-like	O43866	39.6	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	O43150	112.9
Serum paraoxonase/arylesterase 1	P27169	39.9	Band 4.1-like protein 2	O43491	113.1
Protein AMBP	P02760	39.9	Protein phosphatase 1 regulatory subunit 12A	O14974	115.7
G-protein coupled receptor 78	Q96P69	40.0	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	P16615	116.4
Alpha-2-HS-glycoprotein	P02765	40.1	Insulin-degrading enzyme	P14735	118.8
Homer protein homolog 1	Q86YM7	40.4	Ceruloplasmin	P00450	123.1
Monocyte differentiation antigen CD14	P08571	40.7	Leukemia inhibitory factor receptor	P42702	125.2
E3 ubiquitin-protein ligase rififylin	Q8WZ73	41.8	Protocadherin-18	Q9HCL0	127.0
Fetuin-B	Q9UGM5	42.9	Tetratricopeptide repeat protein 17	Q96AE7	130.8
Sphingosine kinase 1	Q9NYA1	42.9	Thrombospondin-1	P07996	133.4
Immunoglobulin heavy constant alpha 1	P01876	43.6	Syntaxin-binding protein 5-like	Q9Y2K9	133.7
Selenoprotein P	P49908	44.0	Tubulin-specific chaperone D	Q9BTW9	134.4
Apolipoprotein L1	O14791	44.0	AT-rich interactive domain-containing protein 4A	P29374	143.7
Keratin, type I cytoskeletal 19	P08727	44.1	Complement factor H	P08603	143.8
Guanine nucleotide-binding protein subunit alpha-12	Q03113	44.4	X-linked retinitis pigmentosa GTPase regulator-interacting protein 1	Q96KN7	147.4
Immunoglobulin heavy constant gamma 2	P01859	44.5	Receptor-type tyrosine-protein phosphatase C	P08575	149.0
Corticosteroid-binding globulin	P08185	45.3	Hepatocyte growth factor receptor	P08581	157.9
Apolipoprotein A-IV	P06727	45.4	Insulin receptor	P06213	159.0
Plasma serine protease inhibitor	P05154	45.8	Attractin	O75882	163.6
Haptoglobin	P00738	45.9	Alpha-2-macroglobulin	P01023	164.7
Pigment epithelium-derived factor	P36955	46.5	Pregnancy zone protein	P20742	165.3
Thyroxine-binding globulin	P05543	46.7	Protein Shroom4	Q9ULL8	167.1
Alpha-1-antitrypsin	P01009	46.9	Dual oxidase 2	Q9NRD8	176.8
Tumor necrosis factor receptor superfamily member 19L	Q969Z4	47.2	Dual oxidase 1	Q9NRD9	178.8
Beta-enolase	P13929	47.3	Collagen alpha-1(XVIII) chain	P39060	179.5
Alpha-1-antichymotrypsin	P01011	47.8	Complement C3	P01024	188.7
2',3'-cyclic-nucleotide 3'-phosphodiesterase	P09543	48.0	Complement C5	P01031	190.0
Kallistatin	P29622	48.7	Complement C4-B	P0C0L5	194.3
Carboxypeptidase B2	Q96IY4	49.0	Complement C4-A	P0C0L4	194.4
Immunoglobulin heavy constant gamma 3	P01860	50.2	Intersectin-1	Q15811	196.3
Protein Z-dependent protease inhibitor	Q9UK55	50.8	Polycystin-1-like protein 3	Q72443	198.2
Fibrinogen gamma chain	P02679	52.1	Unconventional myosin-Vb	Q9ULV0	215.3
Acetylcholine receptor subunit alpha	P02708	52.2	Agrin	O00468	225.5
Hemopexin	P02790	52.4	SH3 and multiple ankyrin repeat domains protein 1	Q9Y566	225.8
Carboxypeptidase N catalytic chain	P15169	52.6	Apolipoprotein(a)	P08519	232.8
Antithrombin-III	P01008	53.1	Ninein	Q8N4C6	245.4
Clusterin	P10909	53.1	Protein transport protein Sec16A	O15027	253.5
Angiotensinogen	P01019	53.4	Spectrin beta chain, non-erythrocytic 1	Q01082	275.4
Keratin, type II cytoskeletal 8	P05787	53.7	Fibronectin	P02751	275.9
Properdin	P27918	53.8	PDZ domain-containing protein 2	O15018	304.1
Vitamin D-binding protein	P02774	54.5	Desmoplakin	P15924	334.2
Potassium voltage-gated channel subfamily S member 2	Q9ULS6	54.7	Cadherin EGF LAG seven-pass G-type receptor 1	Q9NYQ6	334.6

Alpha-1B-glycoprotein	P04217	54.8	Collagen alpha-3(VI) chain	P12111	345.4
Alpha-2-antiplasmin	P08697	54.9	Cadherin EGF LAG seven-pass G-type receptor 3	Q9NYQ7	363.1
Vitronectin	P04004	55.1	Protein unc-80 homolog	Q8N2C7	367.4
Plasma protease C1 inhibitor	P05155	55.4	Reelin	P78509	395.2
Coagulation factor X	P00742	56.1	Laminin subunit alpha-5	O15230	412.3
Fibrinogen beta chain	P02675	56.6	Dystrophin	P11532	428.8
Cytochrome P450 2C8	P10632	56.6	Mucin-17	Q685J3	453.1
Heparin cofactor 2	P05546	57.2	Basement membrane-specific heparan sulfate proteoglycan core protein	P98160	479.5
Protein disulfide-isomerase	P07237	57.5	Protocadherin Fat 2	Q9NYQ8	482.4
Prosaposin	P07602	59.9	Apolipoprotein B-100	P04114	517.0
Lymphocyte cytosolic protein 2	Q13094	60.3	Plectin	Q15149	533.8
Histidine-rich glycoprotein	P04196	60.5	E3 ubiquitin-protein ligase UBR4	Q5T4S7	580.9
Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase	Q9BVK2	60.8	Usherin	O75445	586.7
Macrophage colony-stimulating factor 1	P09603	60.9	Mucin-5AC	P98088	602.3

*The molecular mass (MM) for each protein is retrieved from the UniProt database. kDa, Kilodalton.

Supplemental Table S2: Relative quantification of 113 proteins identified in the dialyzer ultrafiltrate, arranged by molecular mass.

Protein Name	UniProt accession	Unique Peptide Count	MM (kDa)*	Theranova /Optiflux	CorAL /Optiflux	Theranova /CorAL	Plasma /Optiflux
Protein S100-A6	P06703	1	10.2	4.03	2.66	1.52	N/A
Neutrophil defensin 3	P59666	1	10.6	4.02	1.19	3.39	543
C-C motif chemokine 14	Q16627	1	10.9	2.65	1.11	2.38	N/A
Immunoglobulin kappa constant	P01834	4	11.9	11.65	1.51	8.81	8831
Beta-2-microglobulin	P61769	3	13.8	2.03	1.29	1.58	10.5
CD59 glycoprotein	P13987	1	14.8	4.17	1.78	2.35	1313
Serum amyloid A-4 protein	P35542	1	14.9	2.44	1.22	2.01	2519
Antileukoproteinase	P03973	2	15.2	6.02	1.17	5.14	N/A
Hemoglobin subunit alpha	P69905	1	15.3	2.17	0.99	2.20	N/A
Fatty acid-binding protein 5	Q01469	1	15.5	8.58	1.02	8.38	N/A
Cystatin-C	P01034	6	16.0	1.97	1.41	1.40	N/A
NPC intracellular cholesterol transporter 2	P61916	2	16.9	3.42	1.51	2.27	N/A
Ribonuclease 4	P34096	2	17.3	1.90	1.18	1.61	N/A
Insulin-like growth factor II	P01344	1	20.6	2.42	1.16	2.09	N/A
Prostaglandin-H2 D-isomerase	P41222	2	21.3	4.41	2.15	2.05	N/A
Neutrophil gelatinase-associated lipocalin	P80188	1	22.8	7.92	1.51	5.24	N/A
Retinol-binding protein 4	P02753	4	23.4	2.97	1.90	1.57	58.5
Alpha-1-acid glycoprotein 1	P02763	3	23.8	9.48	1.14	8.29	525
Alpha-1-acid glycoprotein 2	P19652	5	23.9	9.40	1.27	7.43	543
Glutathione peroxidase 3	P22352	4	25.8	8.14	1.47	5.54	720
Complement factor D	P00746	7	27.5	3.67	1.87	1.97	735
Collectin-11	Q9BWP8	1	29.1	1.70	1.20	1.42	N/A
Carbonic anhydrase 2	P00918	2	29.3	6.12	2.02	3.04	N/A
Apolipoprotein A-I	P02647	1	30.8	13.43	0.90	14.97	N/A
Insulin-like growth factor-binding protein 5	P24593	1	31.6	5.57	1.60	3.48	N/A
Zinc-alpha-2-glycoprotein	P25311	12	34.5	8.86	1.45	6.11	328
Apolipoprotein E	P02649	2	36.3	4.93	0.91	5.42	801
Taste receptor type 2 member 14	Q9NYV8	1	36.4	11.89	0.59	19.99	1834
Leucine-rich alpha-2-glycoprotein	P02750	11	38.4	9.49	1.27	7.45	1156
Lumican	P51884	3	38.8	16.88	1.56	10.80	5420
Beta-2-glycoprotein 1	P02749	6	39.6	12.09	1.06	11.41	1339
CD5 antigen-like	O43866	2	39.6	7.98	1.32	6.06	1941
Serum paraoxonase/arylesterase 1	P27169	1	39.9	9.65	1.38	6.97	15913
Protein AMBP	P02760	7	39.9	6.92	1.97	3.51	1057
Alpha-2-HS-glycoprotein	P02765	5	40.1	38.56	1.55	24.88	4214

Monocyte differentiation antigen CD14	P08571	1	40.7	7.91	1.01	7.82	N/A
Fetuin-B	Q9UGM5	6	42.9	8.51	1.77	4.81	739
Apolipoprotein L1	O14791	1	44.0	13.56	0.67	20.13	1621
Corticosteroid-binding globulin	P08185	4	45.3	10.76	0.87	12.31	1340
Apolipoprotein A-IV	P06727	1	45.4	9.45	0.94	10.01	1704
Plasma serine protease inhibitor	P05154	2	45.8	10.32	1.69	6.11	N/A
Haptoglobin	P00738	4	45.9	15.93	1.22	13.11	40728
Pigment epithelium-derived factor	P36955	11	46.5	9.07	1.15	7.86	801
Thyroxine-binding globulin	P05543	5	46.7	8.54	1.03	8.32	1219
Alpha-1-antitrypsin	P01009	14	46.9	10.23	0.94	10.89	996
Alpha-1-antichymotrypsin	P01011	11	47.8	12.68	0.72	17.62	2492
Kallistatin	P29622	9	48.7	11.14	1.31	8.52	857
Carboxypeptidase B2	Q961Y4	5	49.0	9.29	1.37	6.78	1338
Acetylcholine receptor subunit alpha	P02708	1	52.2	10.80	1.03	10.46	N/A
Hemopexin	P02790	14	52.4	11.57	1.01	11.42	1413
Antithrombin-III	P01008	14	53.1	11.75	0.94	12.46	1053
Clusterin	P10909	2	53.1	4.34	1.25	3.47	3187
Angiotensinogen	P01019	1	53.4	9.09	1.11	8.16	883
Vitamin D-binding protein	P02774	17	54.5	10.05	1.05	9.55	549
Alpha-1B-glycoprotein	P04217	8	54.8	11.25	0.82	13.80	1737
Alpha-2-antiplasmin	P08697	7	54.9	22.21	1.11	20.08	2760
Vitronectin	P04004	1	55.1	11.99	0.97	12.34	15280
Plasma protease C1 inhibitor	P05155	2	55.4	11.64	1.69	6.90	24089
Fibrinogen beta chain	P02675	1	56.6	9.22	0.51	18.15	10052
Heparin cofactor 2	P05546	4	57.2	12.04	0.99	12.22	2322
Protein disulfide-isomerase	P07237	1	57.5	9.58	0.90	10.70	1429
Histidine-rich glycoprotein	P04196	5	60.5	15.86	1.02	15.62	2436
Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase	Q9BVK2	1	60.8	2.57	2.27	1.13	N/A
Complement component C9	P02748	8	64.7	12.21	1.04	11.75	1656
Complement factor I	P05156	7	68.1	10.06	1.04	9.70	1946
Complement component C8 beta chain	P07358	2	68.7	2.47	1.24	1.99	441
Coagulation factor XII	P00748	6	70.1	10.10	1.02	9.91	1546
Afamin	P43652	4	71.0	12.11	0.73	16.70	3709
Albumin	P02768	20	71.4	9.04	0.82	11.02	1477
Prothrombin	P00734	4	71.5	12.59	1.19	10.59	2310
Kininogen-1	P01042	11	73.0	12.92	1.10	11.71	2094
Proprotein convertase subtilisin/kexin type 9	Q8NBP7	1	75.8	9.73	0.90	10.81	N/A
Serotransferrin	P02787	27	79.3	12.04	0.63	19.09	1910
TGF-beta-activated kinase 1 and MAP3K7-binding protein 3	Q8N5C8	1	79.4	12.52	0.61	20.47	1863
Adhesion G protein-coupled receptor L4	Q9HBW9	1	79.7	1.62	0.89	1.81	N/A
Cyclin-T2	O60583	1	81.5	9.20	1.11	8.25	N/A
Hepatocyte growth factor-like protein	P26927	1	82.9	11.17	1.22	9.13	1474
Centrosomal protein of 83 kDa	Q9Y592	1	83.1	1.51	1.23	1.23	N/A
Gelsolin	P06396	10	86.1	13.52	0.99	13.63	1642
Complement factor B	P00751	8	86.9	12.71	0.76	16.71	3111
Phosphate-regulating neutral endopeptidase PHEX	P78562	1	87.0	5.53	2.93	1.89	N/A
Cyclic nucleotide-gated cation channel beta-3	Q9NQW8	1	92.7	9.09	0.80	11.31	1514
Plasminogen	P00747	15	93.3	11.40	0.92	12.36	2678
Fibrinogen alpha chain	P02671	3	95.7	1.90	1.15	1.65	110
Inter-alpha-trypsin inhibitor heavy chain H3	Q06033	1	100.1	2.25	0.89	2.52	N/A
Desmocollin-3	Q14574	1	101.3	3.33	1.43	2.33	N/A
Desmocollin-1	Q08554	3	101.5	2.55	1.36	1.87	N/A
Inter-alpha-trypsin inhibitor heavy chain H1	P19827	2	101.8	7.72	0.99	7.76	3044
Inter-alpha-trypsin inhibitor heavy chain H4	Q14624	2	103.6	18.19	0.89	20.40	8038
Inter-alpha-trypsin inhibitor heavy chain H2	P19823	1	106.9	13.46	0.95	14.23	3891
Complement component C6	P13671	2	108.4	4.03	1.45	2.78	2471
SH3 domain-binding protein 4	Q9P0V3	1	108.5	12.39	0.87	14.22	2007
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	O43150	1	112.9	8.22	0.85	9.63	N/A
Ceruloplasmin	P00450	6	123.1	12.74	1.27	10.01	11239
Leukemia inhibitory factor receptor	P42702	1	125.2	11.18	0.94	11.85	1269
Tetratricopeptide repeat protein 17	Q96AE7	1	130.8	9.02	1.12	8.04	627
Thrombospondin-1	P07996	1	133.4	6.85	1.01	6.81	N/A
Tubulin-specific chaperone D	Q9BTW9	1	134.4	8.99	0.81	11.10	829

Alpha-2-macroglobulin	P01023	2	164.7	12.02	0.81	14.93	11118
Complement C3	P01024	16	188.7	11.82	1.24	9.57	15714
Complement C5	P01031	1	190.0	8.88	0.96	9.30	10072
Complement C4-B	POC0L5	5	194.3	10.03	1.78	5.62	937
Intersectin-1	Q15811	1	196.3	9.14	1.02	8.93	619
Agrin	O00468	1	225.5	21.49	1.17	18.44	2086
Fibronectin	P02751	1	275.9	10.53	1.47	7.16	1307
PDZ domain-containing protein 2	O15018	1	304.1	11.41	0.61	18.60	1768
Desmoplakin	P15924	1	334.2	1.00	0.95	1.05	N/A
Collagen alpha-3(VI) chain	P12111	2	345.4	5.29	1.18	4.46	N/A
Reelin	P78509	1	395.2	8.52	1.21	7.02	N/A
Basement membrane-specific heparan sulfate proteoglycan core protein	P98160	3	479.5	6.79	1.66	4.08	N/A
Protocadherin Fat 2	Q9NYQ8	1	482.4	8.53	0.93	9.22	897
Apolipoprotein B-100	P04114	4	517.0	8.63	1.36	6.34	5462
Usherin	O75445	1	586.7	3.48	1.10	3.17	N/A

*The molecular mass (MM) for each protein is retrieved from the UniProt database.

Abbreviation: N/A, not analytical; kDa, Kilodalton.

The protein distribution in plasma differs significantly from that in dialysate. As a result, when using the same amount of protein from plasma or dialysate for quantification, some proteins in plasma may go undetected or fail to meet quantification criteria due to their lower concentrations.