SUPPORTING INFORMATION

The lipidomic profile of the nanoparticle-biomolecule corona reflects the diversity of plasma lipids

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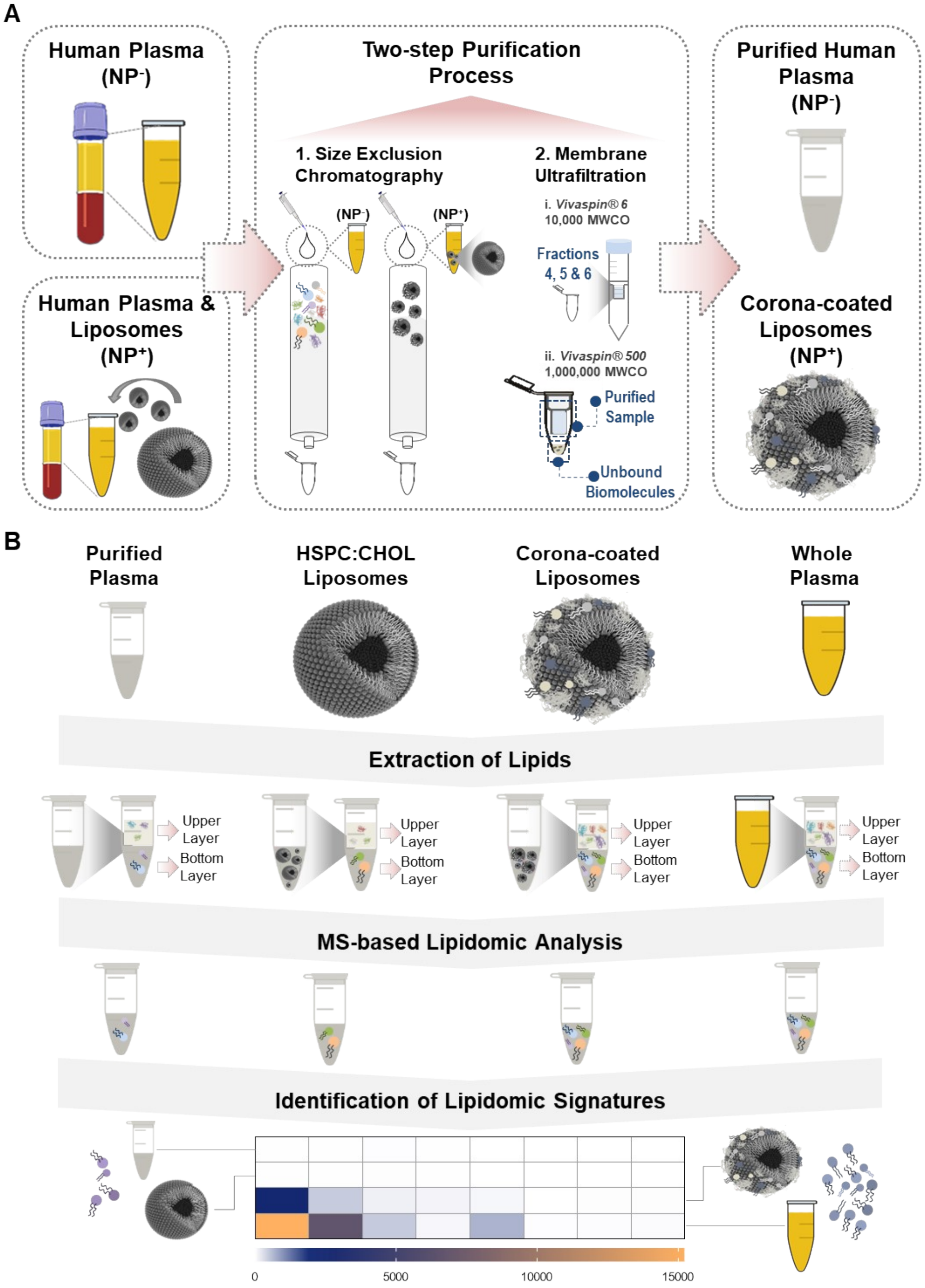
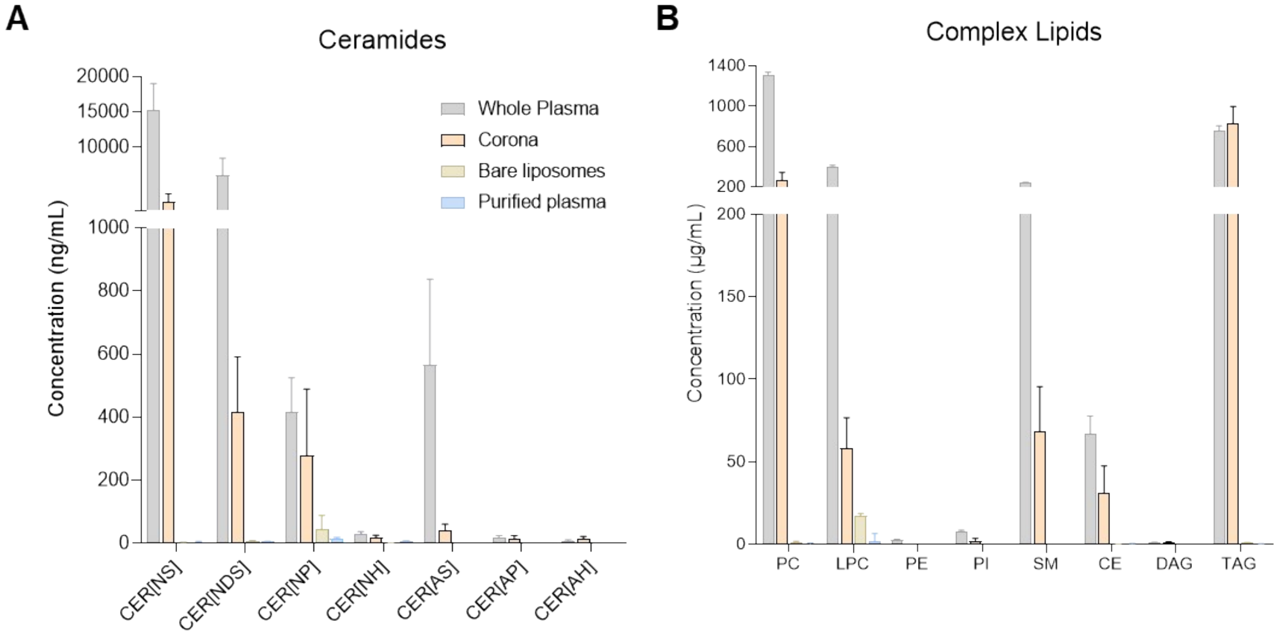
Supplementary Figure S1: Schematic overview of the experimental procedure. (A) The two – step purification process of human plasma without (NP-) and with liposomes (NP+). Human plasma samples (NP-) obtained from healthy volunteers (n=25) were subjected to size exclusion chromatography (SEC) and membrane ultrafiltration (MU). Liposomes were incubated *ex vivo* (10 minutes at 37 °C, 250 rpm) with human plasma samples obtained from healthy volunteers (NP+) (n=25). Corona-coated liposomes were then recovered and purified by SEC and MU; **(B)** The lipids extraction and lipidomic mass spectrometry (MS) analysis workflow. Lipids were extracted from purified plasma samples (n=25), bare liposomes (n=25), corona-coated liposomes (n=25) and whole plasma samples (n=25). The bottom layers that contained the extracted lipids were further processed and analysed by MS. The resultant lipidomic patterns of each group were then compared with each other for each lipid class. Different lipid classes were investigated (**Table 1**). Four different extraction and MS analysis protocols were employed, with 5 technical repeats per each group.

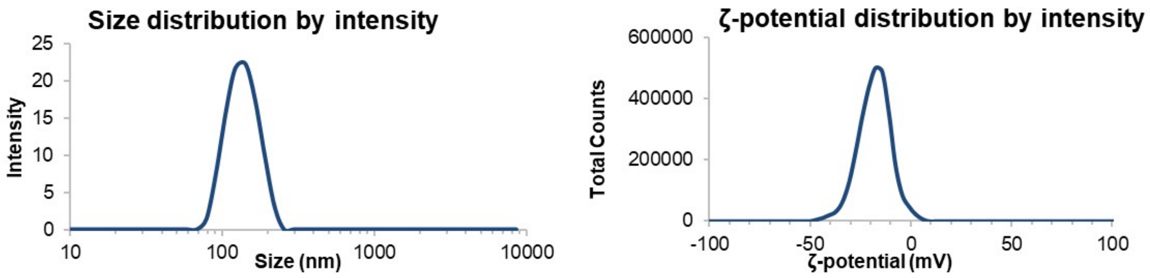


Supplementary Figure S2: Analysis of ceramides and complex lipids by UPLC/ESI-MS/MS and UHPSFC/ESI-QTOF-MS^E, respectively. (A) Ceramides expressed in ng/mL. CER[NS], non-hydroxy ceramide with sphingosine base; CER[NDS], non-hydroxy ceramide with dihydrosphingosine base; CER[NP], non-hydroxy ceramide with phytosphingosine base; CER[NH], non-hydroxy ceramide with 6-hydroxysphingosine base; CER[AS], alpha-hydroxy ceramide with sphingosine base; CER[AP], alpha-hydroxy ceramide with phytosphingosine base; CER[AH], alpha-hydroxy ceramide with 6-hydroxysphingosine base. **(B)** Complex lipids expressed in μg/mL. Phosphatidylcholine (PC); Lysophosphatidylcholine (LPC); Phosphatidylethanolamine (PE); Phosphatidylinositol (PI); Sphingomyelin (SM); Cholesteryl Ester (CE); Diacylglycerol (DAG); Triacylglycerol (TAG).



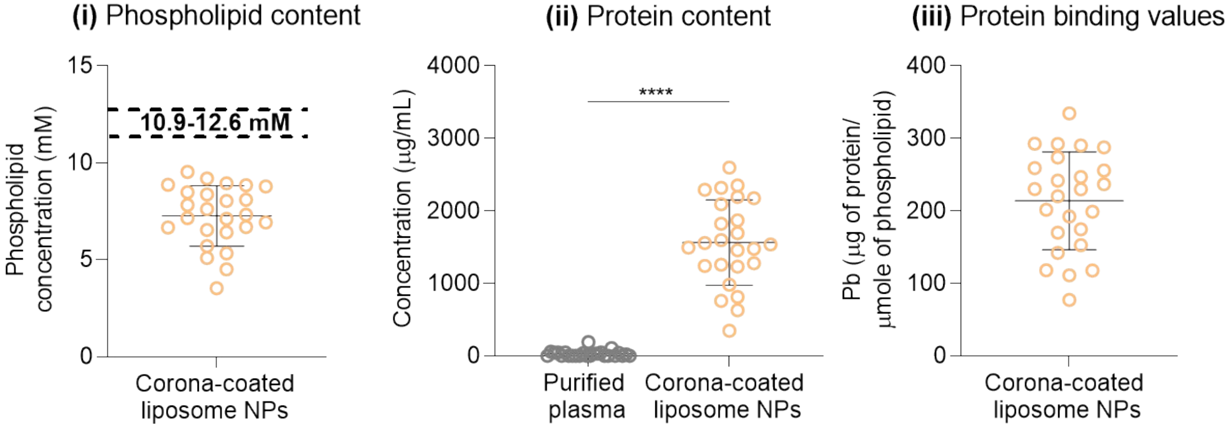
Supplementary Figure S3: Characterisation of bare and corona-coated liposome NPs. (A) Mean hydrodynamic diameter (nm) and ζ-potential (mV) distributions of the liposome HSPC:CHOL formulation. Table shows the average mean hydrodynamic diameter (nm), polydispersity index (PDI) and ζ-potential (mV) values of bare liposome NPs; **(B)** (i) Quantification of recovered liposome NPs. Concentration of phospholipids recovered post-incubation of liposome NPs with plasma samples and purification. (ii) Quantitative characterisation of purified plasma samples (n=25) and the liposome NP-protein corona (n=25). **** $p<0.0001$ comparing purified plasma and corona-coated liposome NPs using Student's t-test. (iii) Total amount of protein onto the surface of liposome NPs after their *ex vivo* incubation with plasma, expressed in protein binding values (Pb). Pb represents the average and standard error.

A



Bare HSPC:Chol liposome NPs	Mean Hydrodynamic Diameter (nm)	PDI	ζ-potential (mV)
Batch 1	131.7 ± 3.4	0.032 ± 0.022	-18.1 ± 1.0
Batch 2	130.2 ± 1.1	0.031 ± 0.007	-18.5 ± 1.2
Batch 3	129.8 ± 2.5	0.033 ± 0.008	-17.3 ± 1.0

B



Supplementary Table S1: Plasma sample characteristics. Information provided by Cambridge Bioscience (UK) for plasma samples from healthy volunteers.

Batch Number	Age	Gender	Ethnicity
385365	29	Female	White
385429	24	Female	Mixed
385446	53	Female	White
386259	23	Female	White
386260	23	Female	White

Supplementary Table S2: Composition of hydrogenated soybean (HSPC) phospholipid used for the preparation of liposome NPs. Datasheet provided by Lipoid (Germany).

Composition	**% total**
Phospholipids	
Phosphatidylcholine, hydrogenated (Px25.5) (based on dry weight)	≥ 98.0
Phosphatidylcholine, hydrogenated (based on dry weight) (HPLC)	≥ 95.0
Fatty Acids	**% total fatty acids**
Palmitic acid	5.0-20.0
Stearic acid	80.0-95.0
Oleic acid and isomers	≤ 1.0
Purity	**%**
Lysophosphatidylcholine	≤ 0.5
N-Acyl-phosphatidylethanolamine	≤ 0.5
Phosphatidylethanolamine	≤ 0.1
Non-polar lipids	≤ 1.0
Triglycerides	≤ 0.5
Free fatty acids	≤ 0.3
D,L-α-Tocopherol	≤ 0.1
Phosphorus	3.8-4.1
Iodine value	≤ 2.0
Peroxide value	≤ 3.0
Water	≤ 3.0

Supplementary Table S3: Oxylipin profiles (UPLC/ESI-MS/MS). Values are reported as mean ± SD (n=5 analyses); data expressed in pg of lipid/mL of plasma.

Oxylipin Species	Whole Plasma (pg/mL)	Corona (pg/mL)	Purified Plasma (pg/mL)	Bare liposome NPs (pg/mL)
9-OxoODE	280 ± 25.5	206 ± 176	60.0 ± 30.8	90.0 ± 18.7
9-HOTrE	370 ± 48.0	163 ± 49.9	105 ± 26.5	116 ± 40.9
13-HOTrE	696 ± 113	108 ± 71.9	<MQL	<MQL
9-HODE	4334 ± 347	954 ± 974	164 ± 27.9	212 ± 136
13-HODE	8028 ± 361	1066 ± 886	320 ± 44.2	398 ± 234
9(10)-EpOME	1608 ± 594	45.0 ± 5.77	<MQL	36.7 ± 20.8
12(13)-EpOME	11236 ± 2352	<MQL	<MQL	<MQL
Trans-EKODE	1202 ± 319	596 ± 352	196 ± 49.3	220 ± 54.8
9,10-DiHOME	5094 ± 268	90.0 ± 30.0	60.0 ± 25.8	75.0 ± 17.3
12,13-DiHOME	6796 ± 342	152 ± 59.3	114 ± 63.5	120 ± 43.0
5-HEPE	78.0 ± 21.7	140 ± 55.7	<MQL	<MQL
18-HEPE	242 ± 86.7	367 ± 264	<MQL	<MQL
15-oxo-ETE	28.0 ± 8.37	313 ± 346	<MQL	<MQL
5-HETE	348 ± 95.8	496 ± 623	<MQL	<MQL
8-HETE	138 ± 47.6	150 ± 113	<MQL	<MQL
11-HETE	174 ± 27.0	328 ± 357	<MQL	<MQL
12-HETE	484 ± 39.1	280 ± 288	<MQL	<MQL
15-HETE	300 ± 58.3	343 ± 291	<MQL	<MQL
15-HETrE	110 ± 14.1	62.5 ± 70.9	<MQL	<MQL
8,9-DiHETE	17.5 ± 9.57	<MQL	<MQL	<MQL
11,12-DiHETE	16 ± 5.48	<MQL	<MQL	<MQL
14,15-DiHETE	16 ± 5.48	<MQL	<MQL	<MQL
17,18-DiHETE	176 ± 8.94	<MQL	<MQL	<MQL
5,6-DHET	72 ± 35.6	<MQL	<MQL	<MQL
8,9-DHET	120 ± 24.5	<MQL	<MQL	<MQL
11,12-DHET	292 ± 13.0	<MQL	<MQL	<MQL
14,15-DHET	236 ± 18.2	<MQL	<MQL	<MQL
4-HDHA	162 ± 58.1	194 ± 173	<MQL	<MQL
8-HDHA	86.0 ± 11.4	66.7 ± 64.3	<MQL	<MQL
10-HDHA	58.0 ± 8.37	57.5 ± 52.5	<MQL	<MQL
13-HDHA	54.0 ± 27.9	127 ± 100	<MQL	<MQL
14-HDHA	112 ± 14.8	66.0 ± 97.4	<MQL	<MQL
10(11)-EpDPE	64.0 ± 33.6	<MQL	<MQL	<MQL
13(14)-EpDPE	75.0 ± 36.9	<MQL	<MQL	<MQL
10,11-DiHDPA	36.0 ± 5.48	<MQL	<MQL	<MQL
13,14-DiHDPA	120 ± 14.1	<MQL	<MQL	<MQL
16,17-DiHDPA	106 ± 13.4	<MQL	<MQL	<MQL
19,20-DiHDPA	1188 ± 53.1	<MQL	<MQL	<MQL

MQL: method quantification limit

Supplementary Table S4: *N*-acyl-ethanolamine (NAE) and 2-monoacylglycerol (2-MAG) profiles (UPLC/ESI-MS/MS). Values are reported as mean ± SD (n=5 analyses); data expressed in pg of lipid/mL of plasma.

NAE and 2-MAG Species	Whole Plasma (pg/mL)	Corona (pg/mL)	Purified Plasma (pg/mL)	Bare liposome NPs (pg/mL)
NAE				
Pentadecanoyl-EA (PDEA)	50.0 ± 7.07	<MQL	<MQL	<MQL
Palmitoyl-EA (PEA)	456 ± 518	233 ± 75.5	29.6 ± 12.9	131 ± 66.2
α-linolenoyl-EA (ALEA)	24.0 ± 13.4	<MQL	<MQL	<MQL
Linoleoyl-EA (LEA)	515 ± 83.5	8.00 ± 2.74	<MQL	<MQL
Oleoyl-EA (OEA)	1437 ± 693	90.0 ± 25.3	<MQL	<MQL
Vaccenoyl-EA (VEA)	311 ± 163	38.0 ± 8.37	<MQL	<MQL
Stearoyl-EA (STEA)	404 ± 261	261 ± 106	69.2 ± 14.3	264 ± 85.8
Docosahexaenoyl-EA (DHEA)	178 ± 42.2	<MQL	<MQL	<MQL
Arachidonoyl-EA (AEA)	181 ± 80.1	<MQL	<MQL	<MQL
Docosapentaenoyl-EA (DPEA)	13.0 ± 4.47	<MQL	<MQL	<MQL
2-MAG				
2-Arachidonoyl-glycerol (2-AG)	157 ± 25.2	65.0 ± 109	<MQL	<MQL
2-Oleoyl-glycerol (2-OG)	906 ± 406	965 ± 1449	<MQL	<MQL
2-Linoleoyl-glycerol (2-LG)	1403 ± 241	1500 ± 1670	<MQL	<MQL

MQL: method quantification limit

Supplementary Table S5: Free fatty acid (FFA) profiles (UHPSFC/ESI-QTOF-MS^E). Values are reported as mean ± SD (n=5 analyses); data expressed in µg of lipid/mL of plasma.

Lipid	Whole Plasma (µg/mL)	Corona (µg/mL)	Purified Plasma (µg/mL)	Bare liposome NPs (µg/mL)
FFA 14:0	0.24 ± 0.02	0.07 ± 0.01	0.04 ± 0.01	0.12 ± 0.15
FFA 15:0	0.07 ± 0.01	0.03 ± 0.01	0.02 ± 0.01	0.11 ± 0.17
FFA 16:0	15.3 ± 1.45	6.80 ± 1.74	3.46 ± 1.25	7.89 ± 5.25
FFA 16:1	1.42 ± 0.04	0.04 ± 0.002	0.014 ± 0.004	0.05 ± 0.09
FFA 17:0	0.19 ± 0.02	0.09 ± 0.05	0.05 ± 0.03	0.24 ± 0.28
FFA 17:1	0.07 ± 0.01	<MQL	<MQL	0.01 ± 0.03
FFF 18:0	11.4 ± 2.29	39.8 ± 7.99	3.63 ± 3.75	118 ± 5.29
FFA 18:1	42.5 ± 1.31	3.10 ± 3.54	<MQL	<MQL
FFA 18:2	14.9 ± 0.38	1.03 ± 0.21	0.01 ± 0.01	0.03 ± 0.04
FFA 18:3	0.71 ± 0.02	0.06 ± 0.02	<MQL	<MQL
FFA 19:1	0.03 ± 0.01	<MQL	<MQL	<MQL
FFA 20:1	0.28 ± 0.01	0.02 ± 0.01	<MQL	0.00 ± 0.01
FFA 20:2	0.14 ± 0.01	0.01 ± 0.01	<MQL	<MQL
FFA 20:4	0.83 ± 0.03	0.12 ± 0.05	<MQL	<MQL
FFA 22:1	0.049 ± 0.004	0.03 ± 0.03	<MQL	0.02 ± 0.02
FFA 22:4	0.11 ± 0.01	<MQL	<MQL	<MQL
FFA 22:5	0.13 ± 0.02	0.01 ± 0.01	<MQL	<MQL
FFA 24:1	0.27 ± 0.02	0.02 ± 0.02	<MQL	0.01 ± 0.01
FFA 25:0	0.18 ± 0.03	0.14 ± 0.08	0.05 ± 0.05	0.35 ± 0.49
FFA 25:1	0.03 ± 0.01	<MQL	<MQL	0.01 ± 0.01
FFA 26:0	0.34 ± 0.05	0.21 ± 0.1	0.08 ± 0.07	0.37 ± 0.55
FFA 26:1	0.15 ± 0.01	<MQL	<MQL	0.01 ± 0.01
FFA 26:2	0.10 ± 0.01	<MQL	<MQL	<MQL

MQL = method quantification limit

Supplementary Table S6: Ceramide profiles (UPLC/ESI-MS/MS). CER[NS], non-hydroxy ceramide with sphingosine base; CER[NDS], non-hydroxy ceramide with dihydrosphingosine base; CER[NP], non-hydroxy ceramide with phytosphingosine base; CER[NH], non-hydroxy ceramide with 6-hydroxysphingosine base; CER[AS], alpha-hydroxy ceramide with sphingosine base; CER[AP], alpha-hydroxy ceramide with phytosphingosine base; CER[AH], alpha-hydroxy ceramide with 6-hydroxysphingosine base. Values are reported as mean ± SD (n=5 analyses); data expressed in ng of lipid/mL of plasma.

Ceramide Species	Whole Plasma (ng/mL)	Corona (ng/mL)	Purified Plasma (ng/mL)	Bare liposome NPs (ng/mL)
CER[NS]				
N(16)S(16)	8.12 ± 3.11	1.92 ± 1.03	<MQL	<MQL
N(20)S(16)	2.49 ± 1.69	1.81 ± 0.74	<MQL	<MQL
N(21)S(16)	2.43 ± 0.16	<MQL	<MQL	<MQL
N(22)S(16)	55.0 ± 16.0	16.8 ± 9.17	<MQL	<MQL
N(23)S(16)	64.9 ± 27.2	4.52 ± 3.03	<MQL	<MQL
N(24)S(16)	263 ± 93.2	55.8 ± 36.1	0.37 ± 0.18	0.27 ± 0.02
N(25)S(16)	46.4 ± 14.3	5.85 ± 3.45	<MQL	<MQL
N(26)S(16)	15.34 ± 4.60	2.99 ± 2.44	0.23 ± 0.13	0.25 ± 0.14
N(16)S(17)	6.68 ± 0.66	1.68 ± 0.63	<MQL	<MQL
N(20)S(17)	3.37 ± 2.67	<MQL	<MQL	<MQL
N(22)S(17)	23.2 ± 9.44	0.53 ± 0.32	<MQL	<MQL
N(23)S(17)	65.5 ± 27.0	4.52 ± 3.03	<MQL	<MQL
N(24)S(17)	490 ± 138	49.5 ± 31.1	0.32 ± 0.16	0.24 ± 0.16
N(25)S(17)	34.1 ± 7.78	5.84 ± 2.55	<MQL	<MQL
N(26)S(17)	23.5 ± 5.00	3.68 ± 2.20	0.21 ± 0.04	0.47 ± 0.21
N(14)S(18)	5.04 ± 1.97	1.85 ± 1.22	<MQL	<MQL
N(16)S(18)	25.9 ± 16.9	19.0 ± 8.03	0.40 ± 0.16	0.95 ± 0.36
N(17)S(18)	1.59 ± 0.49	<MQL	<MQL	<MQL
N(18)S(18)	10.4 ± 4.68	4.92 ± 3.16	0.33 ± 0.09	<MQL
N(20)S(18)	52.8 ± 12.6	12.0 ± 6.22	0.21 ± 0.03	<MQL
N(21)S(18)	7.58 ± 2.60	<MQL	<MQL	<MQL
N(22)S(18)	663 ± 155	132 ± 69.8	0.71 ± 0.50	0.38 ± 0.09
N(23)S(18)	2421 ± 627	157 ± 80.8	<MQL	<MQL
N(24)S(18)	6555 ± 1498	1266 ± 537	<MQL	<MQL
N(24:1)S18	1917 ± 626	323 ± 186	1.21 ± 1.10	<MQL
N(25)S(18)	896 ± 198	98.3 ± 43.7	<MQL	<MQL
N(26)S(18)	240 ± 49.0	32.5 ± 11.4	<MQL	<MQL
N(27)S(18)	13.4 ± 5.04	1.73 ± 0.91	0.29 ± 0.06	<MQL
N(28)S(18)	11.9 ± 5.60	<MQL	<MQL	<MQL
N(20)S(19)	4.22 ± 3.34	<MQL	<MQL	<MQL
N(22)S(19)	78.8 ± 26.7	9.03 ± 5.29	<MQL	<MQL
N(23)S(19)	87.9 ± 36.6	19.1 ± 7.73	<MQL	<MQL
N(24)S(19)	887 ± 221	78.6 ± 40.2	0.22 ± 0.14	<MQL
N(25)S(19)	68.9 ± 16.1	7.79 ± 3.13	<MQL	<MQL
N(26)S(19)	20.1 ± 3.62	2.05 ± 1.15	<MQL	<MQL
N(22)S(20)	7.46 ± 3.96	1.83 ± 0.41	<MQL	<MQL
N(23)S(20)	28.4 ± 6.20	2.29 ± 0.74	<MQL	<MQL
N(24)S(20)	70.9 ± 8.52	11.8 ± 5.64	0.32 ± 0.22	0.29 ± 0.14
N(25)S(20)	7.85 ± 0.54	0.98 ± 0.55	0.13 ± 0.04	<MQL
N(26)S(20)	14.1 ± 5.21	2.17 ± 0.45	0.41 ± 0.05	0.46 ± 0.28
N(28)S(20)	13.6 ± 5.08	1.92 ± 0.87	<MQL	<MQL
N(24)S(22)	9.03 ± 3.32	<MQL	<MQL	<MQL
N(26)S(22)	10.1 ± 3.08	<MQL	<MQL	<MQL
CER[NDS]				
N(24)DS(16)	111 ± 35.2	5.50 ± 4.56	<MQL	<MQL
N(24)DS(17)	22.8 ± 16.1	2.55 ± 1.61	<MQL	0.20 ± 0.02
N(16)DS(18)	48.0 ± 11.9	15.8 ± 5.66	1.13 ± 0.37	2.22 ± 0.79
N(18)DS(18)	81.4 ± 35.4	4.35 ± 1.35	0.89 ± 0.16	<MQL

N(20)DS(18)	95.9 ± 49.5	3.22 ± 1.07	0.16 ± 0.08	<MQL
N(22)DS(18)	445 ± 217	27.0 ± 13.2	0.17 ± 0.07	0.41 ± 0.05
N(23)DS(18)	479 ± 194	33.4 ± 18.8	<MQL	<MQL
N(24)DS(18)	1638 ± 691	82.6 ± 35.5	0.24 ± 0.08	0.61 ± 0.29
N(26)DS(18)	68.8 ± 31.5	6.28 ± 3.79	<MQL	0.69 ± 0.40
N(28)DS(18)	17.1 ± 14.5	2.66 ± 1.26	<MQL	<MQL
N(22)DS(19)	65.3 ± 26.0	3.55 ± 1.38	<MQL	<MQL
N(24)DS(19)	185 ± 91.9	12.9 ± 4.32	<MQL	0.27 ± 0.10
N(16)DS(20)	36.7 ± 17.1	<MQL	1.01 ± 0.29	<MQL
N(18)DS(20)	107 ± 47.6	2.76 ± 1.11	<MQL	<MQL
N(22)DS(20)	38.0 ± 11.5	3.63 ± 1.91	0.14 ± 0.05	<MQL
N(23)DS(20)	28.3 ± 5.41	3.65 ± 1.73	<MQL	<MQL
N(24)DS(20)	119 ± 42.7	14.5 ± 5.23	0.33 ± 0.19	0.96 ± 0.40
N(26)DS(20)	61.7 ± 27.1	13.3 ± 6.03	0.23 ± 0.09	<MQL
N(16)DS(22)	35.2 ± 16.3	<MQL	<MQL	<MQL
N(18)DS(22)	285 ± 109	18.7 ± 10.7	0.21 ± 0.08	<MQL
N(19)DS(22)	45.6 ± 31.0	3.44 ± 1.79	<MQL	<MQL
N(22)DS(22)	27.0 ± 19.8	3.39 ± 3.09	<MQL	<MQL
N(24)DS(22)	62.4 ± 35.0	13.8 ± 7.66	<MQL	<MQL
N(25)DS(22)	27.4 ± 14.4	4.55 ± 3.88	<MQL	<MQL
N(26)DS(22)	55.9 ± 34.6	8.47 ± 6.13	0.17 ± 0.09	0.31 ± 0.25
N(18)DS(23)	318 ± 111	19.9 ± 12.3	<MQL	0.32 ± 0.24
N(16)DS(24)	70.2 ± 26.4	<MQL	<MQL	<MQL
N(17)DS(24)	19.4 ± 14.2	2.83 ± 1.38	<MQL	<MQL
N(18)DS(24)	914 ± 386	51.0 ± 23.3	0.15 ± 0.04	0.44 ± 0.18
N(19)DS(24)	111 ± 43.6	6.83 ± 2.45	<MQL	<MQL
N(20)DS(24)	71.8 ± 38.6	9.51 ± 5.32	0.19 ± 0.11	0.63 ± 0.38
N(22)DS(24)	49.4 ± 16.7	11.9 ± 7.36	0.16 ± 0.12	0.54 ± 0.37
N(24)DS(24)	89.9 ± 70.3	14.8 ± 10.4	0.20 ± 0.06	0.45 ± 0.15
N(26)DS(24)	55.9 ± 15.9	6.68 ± 4.86	<MQL	0.25 ± 0.09
N(18)DS(26)	49.9 ± 28.6	3.29 ± 1.20	<MQL	<MQL
N(20)DS(26)	42.2 ± 24.1	7.38 ± 4.81	<MQL	<MQL
N(24)DS(26)	54.9 ± 36.3	10.1 ± 8.16	<MQL	<MQL
CER[NP]				
N(22)P(17)	2.06 ± 0.69	<MQL	<MQL	<MQL
N(24)P(17)	4.60 ± 2.90	2.70 ± 0.95	<MQL	<MQL
N(26)P(17)	10.4 ± 3.71	6.05 ± 6.47	3.06 ± 1.07	6.74 ± 3.25
N(22)P(18)	64.8 ± 32.4	3.88 ± 4.25	<MQL	<MQL
N(24)P(18)	149 ± 36.4	25.4 ± 14.1	5.79 ± 1.79	<MQL
N(26)P(18)	38.9 ± 16.8	9.73 ± 6.38	4.23 ± 1.35	6.39 ± 1.58
N(24)P(19)	10.3 ± 5.55	3.46 ± 0.54	<MQL	<MQL
N(26)P(19)	16.7 ± 6.96	8.19 ± 4.59	1.91 ± 0.70	<MQL
N(26)P(20)	50.3 ± 11.1	15.5 ± 15.0	3.95 ± 1.71	4.84 ± 0.73
N(26)P(21)	13.7 ± 4.13	8.12 ± 6.09	<MQL	<MQL
N(24)P(22)	44.1 ± 23.4	26.4 ± 28.4	<MQL	<MQL
N(25)P(22)	15.7 ± 9.22	13.2 ± 12.5	<MQL	<MQL
N(26)P(22)	33.9 ± 12.1	22.4 ± 23.3	<MQL	<MQL
CER[NH]				
N(25)H(17)	1.84 ± 0.79	<MQL	<MQL	<MQL
N(22)H(18)	1.15 ± 0.36	<MQL	<MQL	<MQL
N(23)H(18)	0.67 ± 0.12	1.35 ± 0.52	<MQL	<MQL
N(24)H(18)	2.69 ± 0.84	<MQL	<MQL	<MQL
N(25)H(18)	1.15 ± 0.51	1.38 ± 0.32	<MQL	<MQL
N(26)H(18)	6.46 ± 1.36	2.91 ± 1.59	<MQL	<MQL
N(28)H(18)	3.40 ± 1.56	<MQL	<MQL	<MQL
N(26)H(19)	0.90 ± 0.11	1.14 ± 0.59	1.35 ± 0.60	<MQL
N(24)H(20)	1.16 ± 0.43	1.98 ± 1.81	4.63 ± 0.33	<MQL
N(25)H(20)	1.01 ± 0.25	<MQL	2.03 ± 0.97	1.33 ± 0.54

N(26)H(20)	4.59 ± 1.60	4.47 ± 2.26	<MQL	<MQL
N(28)H(20)	6.63 ± 1.45	5.62 ± 3.38	<MQL	<MQL
N(30)H(20)	1.43 ± 0.42	<MQL	<MQL	<MQL
CER[AP]				
A(24)P(17)	0.98 ± 0.37	<MQL	<MQL	<MQL
A(16)P(18)	9.38 ± 3.28	2.82 ± 1.94	<MQL	<MQL
A(24)P(18)	1.56 ± 0.50	2.37 ± 0.69	<MQL	<MQL
A(26)P(18)	1.78 ± 1.08	2.55 ± 1.54	<MQL	<MQL
A(24)P(20)	2.61 ± 1.59	3.36 ± 2.62	<MQL	<MQL
A(24)P(22)	4.69 ± 0.85	6.24 ± 3.39	<MQL	<MQL
CER[AS]				
A(22)S(18)	35.3 ± 15.6	<MQL	<MQL	<MQL
A(23)S(18)	70.6 ± 28.3	20.5 ± 12.7	<MQL	<MQL
A(24)S(18)	474 ± 233	22.4 ± 10.1	<MQL	<MQL
CER[AH]				
A(24)H(18)	2.27 ± 0.42	4.52 ± 2.68	<MQL	<MQL
A(25)H(18)	1.41 ± 0.89	<MQL	<MQL	<MQL
A(26)H(18)	1.56 ± 1.28	3.34 ± 2.39	<MQL	<MQL
A(26)H(20)	2.92 ± 1.45	5.33 ± 4.39	<MQL	<MQL

MQL = method quantification limit

Supplementary Table S7: Complex lipids profiles (UHPSFC/ESI-QTOF-MS^E). Phosphatidylcholine (PC); Lysophosphatidylcholine (LPC); Phosphatidylethanolamine (PE); Phosphatidylinositol (PI); Sphingomyelin (SM); Cholesteryl Esters (CE); Diacylglycerol (DAG); Triacylglycerol (TAG). Values are reported as mean ± SD (n=5 analyses); data expressed in µg of lipid/mL of plasma.

Lipid	Whole Plasma (µg/mL)	Corona (µg/mL)	Purified Plasma (µg/mL)	Bare liposome NPs (µg/mL)
PC				
PC 28:0	0.05 ± 0.01	<MQL	<MQL	<MQL
PC 30:0	1.79 ± 0.14	0.01 ± 0.01	<MQL	<MQL
PC 32:0	11.6 ± 0.46	0.48 ± 0.09	<MQL	0.25 ± 0.05
PC 32:1	5.94 ± 0.36	0.13 ± 0.02	<MQL	<MQL
PC 32:2	0.41 ± 0.05	0.04 ± 0.01	<MQL	<MQL
PC 34:0	14.4 ± 0.55	207 ± 30.2	<MQL	209 ± 6.90
PC 34:2	513 ± 12.1	93.2 ± 25.2	0.04 ± 0.07	<MQL
PC 34:3	4.06 ± 0.38	0.73 ± 0.18	<MQL	<MQL
PC 34:4	0.12 ± 0.04	0.005 ± 0.002	<MQL	<MQL
PC 35:2	2.73 ± 0.27	0.28 ± 0.06	<MQL	<MQL
PC 36:0	5.01 ± 0.62	823 ± 123	<MQL	848 ± 33.1
PC 36:2	178 ± 4.08	43.5 ± 12.0	0.01 ± 0.01	<MQL
PC 36:3	110 ± 2.57	29.6 ± 8.25	0.06 ± 0.08	0.15 ± 0.04
PC 36:4	147 ± 2.56	35.3 ± 10.51	<MQL	<MQL
PC 36:5	15.1 ± 0.68	2.19 ± 0.78	<MQL	<MQL
PC 36:6	0.13 ± 0.02	0.006 ± 0.005	<MQL	<MQL
PC 38:4	82.9 ± 2.11	22.8 ± 6.75	0.28 ± 0.50	1.02 ± 0.17
PC 38:6	180 ± 6.46	30.9 ± 12.9	0.01 ± 0.01	0.04 ± 0.02
PC 40:6	30.2 ± 1.09	4.92 ± 2.18	<MQL	<MQL
PC 40:7	5.34 ± 0.42	0.32 ± 0.14	<MQL	<MQL
PC 40:8	0.68 ± 0.11	0.02 ± 0.01	<MQL	<MQL
PC O-32:1/P-32:0	0.66 ± 0.08	0.02 ± 0.01	<MQL	<MQL
PC O-34:1/P-34:0	7.99 ± 0.77	0.60 ± 0.26	<MQL	0.10 ± 0.05
PC O-34:2/P-34:1	3.50 ± 0.28	0.08 ± 0.02	<MQL	<MQL
PC O-34:3/P-34:2	1.01 ± 0.11	0.20 ± 0.05	<MQL	<MQL
PC O-36:2/P-36:1	1.60 ± 0.18	<MQL	<MQL	<MQL
PC O-36:4/P-36:3	2.54 ± 0.21	0.06 ± 0.03	<MQL	<MQL
PC O-36:5/P-36:4	3.42 ± 0.40	0.54 ± 0.16	<MQL	<MQL
PC O-38:4/P-38:3	0.89 ± 0.09	0.03 ± 0.01	<MQL	<MQL
PC O-40:5/P-40:4	0.11 ± 0.02	0.01 ± 0.01	<MQL	<MQL
PC O-40:6/P-40:5	1.22 ± 0.15	0.17 ± 0.05	<MQL	<MQL
PC O-40:8/P-40:7	0.16 ± 0.03	0.03 ± 0.02	<MQL	<MQL
PC O-42:5/P-42:4	0.13 ± 0.04	0.01 ± 0.01	<MQL	<MQL
PC O-42:6/P-42:5	0.16 ± 0.03	0.02 ± 0.01	<MQL	<MQL
PC O-44:5/P-44:4	0.23 ± 0.05	0.03 ± 0.01	<MQL	<MQL
LPC				
LPC 14:0	0.51 ± 0.09	0.005 ± 0.07	<MQL	<MQL
LPC 15:0	0.28 ± 0.06	0.02 ± 0.02	<MQL	<MQL
LPC 16:0	192 ± 6.89	53.5 ± 16.2	2.20 ± 4.33	16.9 ± 1.06
LPC 16:1	2.31 ± 0.29	0.01 ± 0.01	<MQL	<MQL
LPC 17:0	0.73 ± 0.12	0.26 ± 0.11	<MQL	0.06 ± 0.03
LPC 18:0	48.3 ± 2.24	145 ± 35.3	<MQL	296 ± 8.47
LPC 18:1	44.8 ± 2.50	2.46 ± 1.14	0.06 ± 0.11	0.06 ± 0.06
LPC 18:2	133 ± 9.81	1.76 ± 1.11	<MQL	<MQL
LPC 18:3	0.54 ± 0.10	0.01 ± 0.01	<MQL	<MQL
LPC 20:0	0.01 ± 0.01	0.07 ± 0.05	<MQL	0.19 ± 0.04
LPC 20:2	0.10 ± 0.04	<MQL	<MQL	<MQL
LPC 20:4	16.2 ± 2.36	0.12 ± 0.05	<MQL	0.16 ± 0.05
LPC 20:5	1.10 ± 0.18	<MQL	<MQL	<MQL
LPC 22:6	0.51 ± 0.09	0.0003 ± 0.0000	<MQL	<MQL

PE				
PE O-36:5/P-36:4	0.77 ± 0.04	0.17 ± 0.31	<MQL	0.01 ± 0.03
PE O-38:5/P-38:4	1.37 ± 0.16	0.33 ± 0.54	<MQL	0.01 ± 0.01
PE O-38:6/P-38:5	0.88 ± 0.07	0.15 ± 0.29	<MQL	<MQL
PI				
PI 36:2	1.32 ± 0.20	0.31 ± 0.43	<MQL	<MQL
PI 38:4	6.28 ± 0.80	1.42 ± 1.45	<MQL	<MQL
SM				
SM 32:1	1.89 ± 0.24	0.59 ± 0.19	<MQL	<MQL
SM 32:2	0.10 ± 0.02	0.02 ± 0.01	<MQL	<MQL
SM 33:1	0.90 ± 0.14	0.29 ± 0.08	<MQL	<MQL
SM 34:0	2.56 ± 0.48	0.47 ± 0.28	<MQL	<MQL
SM 34:1	64.4 ± 2.56	22.7 ± 8.07	<MQL	<MQL
SM 34:2	7.36 ± 0.23	1.72 ± 0.67	0.01 ± 0.01	<MQL
SM 35:1	0.34 ± 0.07	0.10 ± 0.03	<MQL	<MQL
SM 36:0	0.11 ± 0.02	0.02 ± 0.01	<MQL	<MQL
SM 36:1	6.58 ± 0.63	1.84 ± 0.68	<MQL	<MQL
SM 36:2	3.31 ± 0.15	0.77 ± 0.27	<MQL	<MQL
SM 36:3	0.08 ± 0.01	0.006 ± 0.003	<MQL	<MQL
SM 37:1	0.13 ± 0.03	0.03 ± 0.02	<MQL	<MQL
SM 38:1	5.38 ± 0.52	1.34 ± 0.50	<MQL	<MQL
SM 38:2	1.95 ± 0.08	0.53 ± 0.18	<MQL	<MQL
SM 39:1	1.00 ± 0.15	0.25 ± 0.08	<MQL	<MQL
SM 39:2	0.08 ± 0.01	0.01 ± 0.01	<MQL	<MQL
SM 40:1	7.15 ± 0.56	1.59 ± 0.90	<MQL	<MQL
SM 40:2	23.0 ± 0.76	6.32 ± 2.63	<MQL	<MQL
SM 40:3	0.52 ± 0.08	0.12 ± 0.04	<MQL	<MQL
SM 41:1	2.31 ± 0.21	0.49 ± 0.26	<MQL	<MQL
SM 41:2	6.81 ± 0.36	1.81 ± 0.68	<MQL	<MQL
SM 42:2	69.3 ± 2.30	20.5 ± 9.01	<MQL	<MQL
SM 42:3	34.5 ± 0.90	6.58 ± 3.30	<MQL	<MQL
SM 43:1	0.10 ± 0.02	0.02 ± 0.01	<MQL	<MQL
SM 43:2	0.51 ± 0.04	0.13 ± 0.04	<MQL	<MQL
CE				
CE 16:0	5.68 ± 0.44	2.85 ± 1.72	<MQL	0.02 ± 0.02
CE 16:1	3.20 ± 0.58	1.65 ± 0.93	<MQL	<MQL
CE 18:2	56.8 ± 10.3	27.0 ± 13.6	0.11 ± 0.14	<MQL
CE 20:4	1.12 ± 0.18	<MQL	<MQL	<MQL
DAG				
DAG 32:0	0.01 ± 0.01	0.03 ± 0.01	<MQL	0.005 ± 0.003
DAG 32:1	0.03 ± 0.01	0.05 ± 0.02	<MQL	<MQL
DAG 36:1	0.02 ± 0.01	0.05 ± 0.02	<MQL	<MQL
DAG 36:3	0.46 ± 0.06	0.56 ± 0.15	<MQL	<MQL
DAG 36:4	0.24 ± 0.07	0.29 ± 0.09	<MQL	<MQL
DAG 37:2	0.06 ± 0.01	0.06 ± 0.02	<MQL	0.02 ± 0.01
DAG 37:3	0.03 ± 0.01	0.05 ± 0.02	<MQL	<MQL
DAG 39:4	0.21 ± 0.05	0.24 ± 0.06	<MQL	<MQL
TAG				
TAG 46:2	0.65 ± 0.14	2.56 ± 0.48	<MQL	<MQL
TAG 46:3	0.07 ± 0.02	0.24 ± 0.05	<MQL	<MQL
TAG 47:2	0.04 ± 0.02	0.16 ± 0.04	<MQL	<MQL
TAG 48:1	11.1 ± 1.43	32.6 ± 4.75	0.005 ± 0.003	0.01 ± 0.02
TAG 48:2	5.42 ± 0.59	15.9 ± 2.14	<MQL	<MQL
TAG 48:3	1.11 ± 0.14	2.67 ± 0.47	<MQL	<MQL
TAG 48:4	0.16 ± 0.03	0.24 ± 0.05	<MQL	<MQL
TAG 49:1	0.66 ± 0.11	1.96 ± 0.34	<MQL	<MQL
TAG 49:2	0.36 ± 0.04	0.88 ± 0.16	<MQL	<MQL
TAG 49:3	0.10 ± 0.02	0.17 ± 0.04	<MQL	<MQL

TAG 50:0	1.96 ± 0.31	4.82 ± 0.77	0.02 ± 0.03	0.11 ± 0.03
TAG 50:2	57.9 ± 2.38	97.0 ± 16.0	0.01 ± 0.01	0.005 ± 0.006
TAG 50:3	14.3 ± 0.68	19.4 ± 3.93	<MQL	<MQL
TAG 50:4	2.48 ± 0.27	2.77 ± 0.74	<MQL	<MQL
TAG 50:5	0.32 ± 0.05	0.28 ± 0.07	<MQL	<MQL
TAG 50:6	0.05 ± 0.01	0.03 ± 0.01	<MQL	<MQL
TAG 51:2	1.91 ± 0.22	2.84 ± 0.61	<MQL	<MQL
TAG 51:3	0.95 ± 0.12	1.07 ± 0.27	<MQL	<MQL
TAG 52:1	16.1 ± 0.86	18.8 ± 3.84	0.09 ± 0.17	0.85 ± 0.08
TAG 52:2	0.07 ± 0.02	0.18 ± 0.13	<MQL	<MQL
TAG 52:3	249 ± 10.4	264 ± 57.3	0.05 ± 0.10	<MQL
TAG 52:4	69.7 ± 4.35	69.5 ± 16.6	<MQL	<MQL
TAG 52:5	15.7 ± 1.40	15.4 ± 3.48	<MQL	<MQL
TAG 52:6	1.85 ± 0.28	1.74 ± 0.43	<MQL	<MQL
TAG 52:7	0.20 ± 0.04	0.16 ± 0.05	<MQL	<MQL
TAG 53:4	0.85 ± 0.12	0.86 ± 0.20	<MQL	<MQL
TAG 54:2	10.8 ± 0.90	13.6 ± 2.82	<MQL	<MQL
TAG 54:4	128 ± 7.91	130 ± 26.2	0.01 ± 0.02	0.01 ± 0.01
TAG 54:6	33.4 ± 2.43	32.1 ± 7.83	<MQL	<MQL
TAG 54:7	9.11 ± 0.83	8.18 ± 2.31	<MQL	<MQL
TAG 54:8	0.90 ± 0.13	0.73 ± 0.24	<MQL	<MQL
TAG 56:3	0.89 ± 0.16	0.97 ± 0.19	<MQL	<MQL
TAG 56:6	47.8 ± 3.46	38.7 ± 10.2	0.003 ± 0.005	0.03 ± 0.01
TAG 56:7	33.1 ± 2.55	23.6 ± 7.23	<MQL	0.005 ± 0.003
TAG 56:8	16.2 ± 1.65	9.86 ± 3.55	<MQL	<MQL
TAG 56:9	2.02 ± 0.30	0.98 ± 0.38	<MQL	<MQL
TAG 56:10	0.03 ± 0.01	0.03 ± 0.01	<MQL	<MQL
TAG 57:4	0.34 ± 0.09	0.08 ± 0.04	<MQL	<MQL
TAG 57:7	0.15 ± 0.03	0.09 ± 0.04	<MQL	<MQL
TAG 57:8	0.09 ± 0.02	0.05 ± 0.02	<MQL	<MQL
TAG 58:8	14.8 ± 1.81	8.03 ± 3.20	<MQL	<MQL
TAG 58:9	6.27 ± 0.86	2.31 ± 1.07	<MQL	<MQL
TAG 58:10	2.19 ± 0.44	0.63 ± 0.28	<MQL	<MQL
TAG 59:4	0.53 ± 0.15	0.10 ± 0.05	<MQL	<MQL
TAG 60:7	0.05 ± 0.02	0.03 ± 0.02	<MQL	<MQL
TAG 60:10	1.13 ± 0.28	0.31 ± 0.14	<MQL	<MQL

MQL = method quantification limit

Supplementary Table S8: MS-based proteomic analysis of the liposome NP-protein corona. List of proteins identified onto the surface of liposome NPs following incubation with plasma and purification. Mean relative protein abundance (RPA%) values and the standard deviation are displayed below for each identified protein calculated from 5 technical repeats.

Identified Proteins (n=285)	Accession Number	MW (kDa)	Corona-coated liposome NPs (% of total)
Full-length cDNA clone CS0DD006YL02 of Neuroblastoma of Homo sapiens (human)	Q86TT1	41	3.98 ± 0.16
Immunoglobulin heavy constant mu GN=IGHM	P01871	49	3.83 ± 0.15
Immunoglobulin light chain (Fragment)	Q0KKI6	24	2.93 ± 0.51
Immunoglobulin kappa light chain	P0DOX7	23	2.9 ± 0.54
IGK@ protein GN=IGK@	Q6PIL8	26	2.81 ± 0.46
Immunoglobulin mu heavy chain	P0DOX6	63	2.28 ± 0.13
IGK@ protein GN=IGK@	Q6P5S8	26	1.99 ± 1.11
Lambda-chain (AA -20 to 215)	A2NUT2	25	1.65 ± 0.05
IGL@ protein GN=IGL@	Q6PIQ7	25	1.61 ± 0.08
IGL@ protein GN=IGL@	Q8N355	25	1.56 ± 0.06
IGL@ protein GN=IGL@	Q8N5F4	25	1.55 ± 0.05
Alpha-2-macroglobulin GN=A2M	P01023	163	1.51 ± 0.31
Uncharacterized protein	Q8NEJ1	25	1.45 ± 0.05
C4b-binding protein alpha chain GN=C4BPA	P04003	67	1.42 ± 0.09
IGL@ protein GN=IGL@	Q6PIK1	25	1.41 ± 0.07
IGL@ protein GN=IGL@	Q5FWF9	25	1.41 ± 0.05
Haptoglobin GN=HP	P00738 (+2)	45	1.40 ± 0.14
GCT-A4 heavy chain variable region (Fragment)	A0A0X9USM3	14	1.34 ± 0.07
Apolipoprotein B (Including Ag(X) antigen) GN=APOB	C0JYY2	516	1.27 ± 0.08
Fibrinogen beta chain GN=FGB	P02675 (+1)	56	1.23 ± 0.24
IgG L chain	S6BAR0	23	1.15 ± 0.07
IgG L chain	S6AWE6	23	1.12 ± 0.05
10E8 heavy chain variable region (Fragment)	A0A193CHQ9	14	1.06 ± 0.07
APOB protein GN=APOB	Q7Z7Q0	92	1.06 ± 0.59
Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	Q9UL90	12	1.05 ± 0.04
Haptoglobin-related protein GN=HPR	P00739	39	1.05 ± 0.06
IgG L chain	S6B294	20	1.02 ± 0.03
IgG L chain	S6AWF4	20	1.01 ± 0.04
A30 (Fragment)	A2MYE1 (+1)	10	0.99 ± 0.09
Fibrinogen alpha chain GN=FGA	P02671	95	0.98 ± 0.17
Apolipoprotein E isoform 1 (Fragment) GN=APOE	A0A0S2Z3D5 (+1)	36	0.97 ± 0.08
Testicular tissue protein Li 70	A0A140VJJ6	49	0.95 ± 0.17
Haptoglobin (Fragment) GN=HP	H3BS21	25	0.95 ± 0.10
Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	Q9UL88	14	0.91 ± 0.06
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment)	Q96SA9	12	0.89 ± 0.10
CD5 antigen-like GN=CD5L	O43866	38	0.89 ± 0.05
Immunoglobulin J chain GN=JCHAIN	P01591	18	0.84 ± 0.04
Immunoglobulin heavy variable 3-74 GN=IGHV3-74	A0A0B4J1X5	13	0.81 ± 0.06
Myosin-reactive immunoglobulin light chain variable region (Fragment)	Q9UL70	12	0.81 ± 0.04
Apolipoprotein A-I, isoform CRA_a GN=APOA1	A0A024R3E3 (+1)	31	0.79 ± 0.03
GCT-A10 heavy chain variable region (Fragment)	A0A120HG46	14	0.77 ± 0.04
Rheumatoid factor RF-ET6 (Fragment)	A2J1N5	10	0.74 ± 0.09
Anti-Factor VIII scFv (Fragment)	A2KBC6	25	0.70 ± 0.05
Immunoglobulin heavy variable 3-72 GN=IGHV3-72	A0A0B4J1Y9 (+1)	13	0.66 ± 0.11
Myosin-reactive immunoglobulin light chain variable region (Fragment)	Q9UL78	12	0.65 ± 0.08
GCT-A5 light chain variable region (Fragment)	A0A0X9UWL5	12	0.63 ± 0.04

IGL@ protein GN=IGL@	Q6GMX4	25	0.62 ± 0.85
Immunoglobulin heavy variable 3-53 GN=IGHV3-53	P01767 (+1)	13	0.6 ± 0.35
Apolipoprotein C-IV GN=APOC4	A5YAK2	15	0.58 ± 0.07
Protein S isoform 1 (Fragment) GN=PROS1	A0A0S2Z4K3 (+2)	75	0.53 ± 0.01
GCT-A1 heavy chain variable region (Fragment)	A0A125U0V2	14	0.53 ± 0.3
Beta-globin GN=HBB	D9YZU5 (+1)	16	0.52 ± 0.06
Rheumatoid factor RF-ET9 (Fragment)	A2J1N6	13	0.52 ± 0.31
C4b-binding protein beta chain GN=C4BPB	P20851	28	0.51 ± 0.02
Apolipoprotein C-I, isoform CRA_a GN=APOC1	A0A024R0T8 (+2)	9	0.50 ± 0.08
IGH@ proteinGN=IGH@	Q6GMX6	51	0.49 ± 0.05
Epididymis luminal protein 214 GN=HEL-214	V9HW68	52	0.48 ± 0.03
Single-chain Fv (Fragment)GN=scFv	Q65ZC9	26	0.48 ± 0.05
Mutant hemoglobin alpha 2 globin chain GN=HBA2	A0A0K2BMD8 (+5)	15	0.48 ± 0.04
Uncharacterized protein	A8K008	52	0.48 ± 0.04
Apolipoprotein C-IV GN=APOC4	P55056	15	0.46 ± 0.27
cDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA	Q96K68	53	0.46 ± 0.03
Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	Q9UL72	13	0.45 ± 0.62
Immunoglobulin heavy variable 5-51 GN=IGHV5-51	A0A0C4DH38	13	0.44 ± 0.05
Myosin-reactive immunoglobulin light chain variable region (Fragment)	Q9UL83	12	0.43 ± 0.02
V1-2 protein (Fragment) GN=V1-2	A2MYD6	10	0.43 ± 0.07
Uncharacterized protein DKFZp686M08189 GN=DKFZp686M08189	Q6MZX9	52	0.42 ± 0.02
Serum albumin GN=ALB	P02768	69	0.42 ± 0.01
Apolipoprotein D (Fragment) GN=APOD	C9JF17 (+1)	24	0.42 ± 0.06
Immunoglobulin heavy variable 3-73 GN=IGHV3-73	A0A0B4J1V6	13	0.42 ± 0.08
MS-D4 heavy chain variable region (Fragment)	A0A0X9UWK7	14	0.41 ± 0.04
Immunoglobulin heavy chain variable region (Fragment)	Q0ZCI6	14	0.41 ± 0.23
Complement component 1, q subcomponent, B chain, isoform CRA_a GN=C1QB	A0A024RAB9 (+3)	27	0.41 ± 0.06
Immunoglobulin heavy variable 3-49 GN=IGHV3-49	A0A0A0MS15	13	0.41 ± 0.05
Immunoglobulin heavy chain variant (Fragment)	Q9NPP6	45	0.41 ± 0.02
Immunoglobulin heavy variable 3-48 GN=IGHV3-48	P01763	13	0.40 ± 0.38
IgG H chain	S6B291	51	0.39 ± 0.03
V1-3 protein (Fragment) GN=V1-3	Q5NV84	10	0.39 ± 0.08
MS-A1 light chain variable region (Fragment)	A0A109PSY4	11	0.38 ± 0.08
Cryocrystalglobulin CC1 kappa light chain variable region (Fragment)	B1N7B8	12	0.37 ± 0.03
Uncharacterized protein DKFZp686L19235 GN=DKFZp686L19235	Q6MZV6	52	0.37 ± 0.02
Immunoglobulin alpha-2 heavy chain	P0DOX2	49	0.36 ± 0.02
Delta globin GN=HBD	A0N071 (+1)	16	0.35 ± 0.04
IBM-B2 heavy chain variable region (Fragment)	A0A125QYY9	14	0.34 ± 0.05
cDNA FLJ75066, highly similar to Homo sapiens complement component 1, r subcomponent (C1R), mRNA	A8K5J8 (+1)	80	0.34 ± 0.03
Clusterin GN=CLU	P10909	52	0.33 ± 0.03
cDNA FLJ41552 fis, clone COLON2004478, highly similar to Protein Tro alpha1 H,myeloma	Q6ZW64	53	0.33 ± 0.19
Uncharacterized protein DKFZp686C11235 GN=DKFZp686C11235	Q6MZV7	52	0.33 ± 0.18
Uncharacterized protein DKFZp686G11190 GN=DKFZp686G11190	Q6MZQ6	52	0.32 ± 0.04
Apolipoprotein M GN=APOM	O95445	21	0.32 ± 0.04
VH6DJ protein (Fragment) GN=VH6DJ	A2N0T9	13	0.31 ± 0.02
Immunoglobulin heavy variable 6-1 GN=IGHV6-1	A0A0B4J1U7	13	0.31 ± 0.04
Amyloid lambda 6 light chain variable region SAR (Fragment)	Q96JD0	12	0.31 ± 0.28
VH6DJ protein (Fragment) GN=VH6DJ	A2N0U2	13	0.31 ± 0.02
Complement component 1, q subcomponent, C chain, isoform CRA_a GN=C1QC	A0A024RAA7 (+1)	26	0.30 ± 0.04
Anti-Mpl scFv (Fragment)	A2J423	25	0.30 ± 0.03
GCT-A4 light chain variable region (Fragment)	A0A0X9T7V9	12	0.29 ± 0.04
SAA2-SAA4 readthrough GN=SAA2-SAA4	A0A096LPE2	23	0.29 ± 0.02

PRSS3 protein GN=PRSS3	A1A508 (+3)	26	0.28 ± 0.20
IGL@ protein GN=IGL@	Q567P1	25	0.28 ± 0.62
Apolipoprotein C-III GN=APOC3	A3KPE2 (+2)	11	0.27 ± 0.02
V5-6 protein (Fragment) GN=V5-6	Q5NV92	11	0.27 ± 0.05
N90-VRC38.08 heavy chain variable region (Fragment)	A0A1W6IYI5	14	0.26 ± 0.02
Immunoglobulin heavy variable 4-4 GN=IGHV4-4	A0A075B6R2	13	0.26 ± 0.24
GCT-A7 heavy chain variable region (Fragment)	A0A125QYY4	13	0.26 ± 0.15
Rheumatoid factor RF-ET10 (Fragment)	A2J1N7	10	0.26 ± 0.05
HRV Fab 027-VL (Fragment)	A2IPI6	12	0.25 ± 0.03
Uncharacterized protein DKFZp686C15213 GN=DKFZp686C15213	Q6MZU6	51	0.25 ± 0.03
Epididymis secretory sperm binding protein Li 44a GN=SERPINA1	E9KL23 (+1)	47	0.25 ± 0.05
Cold agglutinin FS-1 L-chain (Fragment)	A2NB45	12	0.24 ± 0.07
Rheumatoid factor RF-IP12 (Fragment)	A2J1M8	11	0.24 ± 0.02
Immunoglobulin kappa variable 2-24 GN=IGKV2-24	A0A0C4DH68	13	0.23 ± 0.04
Lipoprotein, Lp(A) GN=LPA	Q1HP67	227	0.23 ± 0.03
Ig heavy chain variable region (Fragment)	A0A068LKQ2	13	0.22 ± 0.03
Apolipoprotein L, 1, isoform CRA_b GN=APOL1	A0A024R1G8 (+2)	46	0.22 ± 0.03
GCT-A5 heavy chain variable region (Fragment)	A0A0X9T0H6	13	0.22 ± 0.03
MS-A2 light chain variable region (Fragment)	A0A0X9V981	11	0.22 ± 0.04
Lectin galactoside-binding soluble 3 binding protein isoform 1 (Fragment) GN=LGALS3BP	A0A0S2Z3Y1 (+1)	65	0.21 ± 0.02
B cell receptor heavy chain variable region (Fragment)	A0A1C9J6R3	15	0.21 ± 0.12
Immunoglobulin kappa variable 4-1 GN=IGKV4-1	P06312	13	0.20 ± 0.28
Uncharacterized protein GN=DKFZp686I15212	Q6N030	57	0.20 ± 0.03
Immunoglobulin heavy variable 3-64D GN=IGHV3-64D	A0A0J9YX35	13	0.20 ± 0.07
APOC4-APOC2 readthrough (NMD candidate) GN=APOC4-APOC2	K7ER74	20	0.19 ± 0.01
Immunoglobulin kappa variable 2D-29 GN=IGKV2D-29	A0A075B6S2 (+1)	13	0.19 ± 0.11
V1-13 protein (Fragment) GN=V1-13	Q5NV69	10	0.19 ± 0.11
Anti-(ED-B) scFV (Fragment)	A2KBC1	25	0.18 ± 0.25
Anti-Influenza A hemagglutinin heavy chain variable region (Fragment)	G1FM90	15	0.18 ± 0.04
Immunoglobulin mu-chain D-J4-region (Fragment) GN=IGHM	A2N7P4	13	0.18 ± 0.02
Immunoglobulin lambda variable 7-46 GN=IGLV7-46 PE=3 SV=4	A0A075B6I9 (+1)	12	0.18 ± 0.10
Ig heavy chain variable region (Fragment)	A0A068LKR4	13	0.18 ± 0.40
cDNA, FLJ94213, highly similar to Homo sapiens pregnancy-zone protein (PZP), mRNA	B2R950 (+1)	164	0.17 ± 0.04
Complement component 1, q subcomponent, A chain, isoform CRA_a GN=C1QA	A0A024RAG6 (+1)	26	0.17 ± 0.02
Ig heavy chain variable region (Fragment)	A0A068LN03	13	0.17 ± 0.10
Serum paraoxonase/arylesterase 1 GN=PON1	P27169	40	0.16 ± 0.03
Immunoglobulin heavy variable 3-13 GN=IGHV3-13	P01766	13	0.16 ± 0.15
IGHV1-2 protein (Fragment) GN=IGHV1-2	A0A0F7T7M3 (+1)	11	0.16 ± 0.03
Immunoglobulin heavy constant gamma 4 (Fragment) GN=IGHG4	A0A286YFJ8 (+1)	44	0.16 ± 0.01
Immunoglobulin kappa variable 6-21 GN=IGKV6-21	A0A0C4DH24	12	0.16 ± 0.03
Complement C4-A GN=C4A	P0C0L4	193	0.15 ± 0.01
V2-17 protein (Fragment) GN=V2-17	Q5NV90	10	0.15 ± 0.14
Cathelicidin antimicrobial peptide GN=CAMP	J3KNB4 (+1)	20	0.15 ± 0.02
Rheumatoid factor C6 light chain (Fragment) GN=V-kappa-1	A0N5G1	13	0.14 ± 0.32
Cryocrystalglobulin CC1 heavy chain variable region (Fragment)	B1N7B6	13	0.14 ± 0.19
Immunoglobulin lambda variable 8-61 GN=IGLV8-61 PE=3 SV=7	A0A075B6I0 (+1)	13	0.14 ± 0.02
Complement C3 GN=C3	P01024 (+1)	187	0.14 ± 0.04
HCG40889, isoform CRA_b GN=hCG_40889	A0A024R962 (+1)	139	0.14 ± 0.06
Ficolin-3 GN=FCN3	O75636	33	0.13 ± 0.03
Anti-mucin1 heavy chain variable region (Fragment)	A2JA14	14	0.13 ± 0.29
Prenylcysteine oxidase 1 GN=PCYOX1	Q9UHG3	57	0.13 ± 0.01
GCT-A8 heavy chain variable region (Fragment)	A0A0X9V9C4	13	0.13 ± 0.12
Complement C4-B GN=C4B	P0C0L5	193	0.12 ± 0.07
Immunoglobulin kappa variable 1-16 GN=IGKV1-16	P04430	13	0.12 ± 0.02
Uncharacterized protein DKFZp686C02220 (Fragment)	Q6N091	54	0.12 ± 0.07

GN=DKFZp686C02220			
Transthyretin GN=TTR	A0A087WV45 (+4)	15	0.12 ± 0.03
Ficolin-2 GN=FCN2	Q15485	34	0.12 ± 0.01
Immunoglobulin heavy variable 3-38 (non-functional) (Fragment) GN=IGHV3-38	A0A0C4DH36	13	0.12 ± 0.11
Collectin-11 GN=COLEC11	Q9BWP8	29	0.11 ± 0.01
Immunoglobulin heavy variable 2-26 GN=IGHV2-26	A0A0B4J1V2 (+1)	13	0.11 ± 0.03
Uncharacterized protein (Fragment)	A0A0G2JRQ6	13	0.11 ± 0.00
V lambda (Fragment)	A0N8J8 (+2)	12	0.11 ± 0.10
Immunoglobulin heavy chain variable region (Fragment)	Q0ZCI0	13	0.10 ± 0.23
Immunoglobulin lambda variable 9-49 GN=IGLV9-49	A0A0B4J1Y8 (+2)	13	0.10 ± 0.03
Myosin-reactive immunoglobulin light chain variable region (Fragment)	Q9UL82	11	0.10 ± 0.06
IgG H chain	S6BGE0	32	0.10 ± 0.14
Serum amyloid P-component GN=APCS	P02743 (+1)	25	0.10 ± 0.01
IgG H chain	S6AWF0	25	0.10 ± 0.06
Immunoglobulin kappa variable 1D-13 GN=IGKV1D-13	A0A0B4J2D9 (+1)	13	0.10 ± 0.06
IBM-B2 light chain variable region (Fragment)	A0A0X9V9D6	11	0.09 ± 0.06
Epididymis tissue protein Li 173 GN=SERPING1	E9KL26 (+1)	55	0.09 ± 0.04
Serotransferrin GN=TF	P02787 (+2)	77	0.09 ± 0.01
Polymeric immunoglobulin receptor GN=PIGR	P01833	83	0.09 ± 0.00
Complement factor properdin isoform 1 (Fragment) GN=CFP	A0A0S2Z4I5 (+1)	51	0.08 ± 0.02
Immunoglobulin lambda variable 2-18 GN=IGLV2-18	A0A075B6J9 (+1)	12	0.08 ± 0.05
Mannose-binding protein C GN=MBL2	P11226	26	0.08 ± 0.03
Immunoglobulin heavy variable 2-5 GN=IGHV2-5	P01817	13	0.07 ± 0.04
Immunoglobulin heavy variable 1-8 GN=IGHV1-8	P0DP01	13	0.07 ± 0.07
Proteoglycan 4, isoform CRA_a GN=PRG4	A0A024R930 (+2)	151	0.07 ± 0.01
IgGFc-binding protein GN=FCGBP	Q9Y6R7	572	0.07 ± 0.01
Mannan-binding lectin serine protease 1 GN=MASP1	P48740	79	0.07 ± 0.01
Apolipoprotein A-II GN=APOA2	P02652 (+3)	11	0.07 ± 0.04
Uncharacterized protein GN=DKFZp686P15220	Q6N089	52	0.07 ± 0.15
Serpin peptidase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 3, isoform CRA_c GN=SERPINA3	A0A024R6P0 (+2)	48	0.07 ± 0.02
Protein AMBP GN=AMBP	P02760	39	0.07 ± 0.05
Apolipoprotein A-IV GN=APOA4	P06727	45	0.06 ± 0.02
Fibronectin 1, isoform CRA_n GN=FN1	A0A024R462 (+1)	259	0.06 ± 0.02
Immunoglobulin kappa variable 3D-20 GN=IGKV3D-20	A0A0C4DH25	13	0.06 ± 0.14
Vitronectin GN=VTN	D9ZGG2 (+1)	54	0.06 ± 0.00
Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	Q9UL89	13	0.06 ± 0.06
Uncharacterized protein DKFZp686O1553 (Fragment) GN=DKFZp686O1553	Q5HYM1	54	0.06 ± 0.05
V2-1 protein (Fragment) GN=V2-1	A0M8Q7 (+1)	10	0.06 ± 0.08
Inter-alpha (Globulin) inhibitor H2 GN=ITIH2	A2RTY6 (+3)	106	0.06 ± 0.03
Angiotensinogen (Serpin peptidase inhibitor, clade A, member 8) GN=AGT	B0ZBE2 (+6)	53	0.06 ± 0.01
cDNA FLJ60461, highly similar to Peroxiredoxin-2 (EC 1.11.1.15)	B4DF70 (+2)	20	0.05 ± 0.04
Tenascin C (Hexabrachion), isoform CRA_a GN=TNC	A0A024R884 (+1)	241	0.05 ± 0.01
von Willebrand factor GN=VWF	P04275	309	0.05 ± 0.01
Immunoglobulin lambda variable 5-45 (Fragment) GN=IGLV5-45	A0A0G2JSC0 (+1)	13	0.05 ± 0.05
IBM-A2 light chain variable region (Fragment)	A0A0X9T0I7	12	0.05 ± 0.07
Immunoglobulin lambda variable 3-27 GN=IGLV3-27	P01718 (+1)	12	0.05 ± 0.07
Anti-HER3 scFv (Fragment)	A2J422	26	0.05 ± 0.11
cDNA FLJ53075, highly similar to Kininogen-1	B4DPP8 (+1)	46	0.05 ± 0.01
cDNA FLJ56821, highly similar to Inter-alpha-trypsin inhibitor heavy chain H1	B7Z549 (+1)	76	0.05 ± 0.03
Carboxypeptidase N catalytic chain GN=CPN1	P15169	52	0.04 ± 0.01
Alpha-1-acid glycoprotein 2 GN=ORM2	P19652	24	0.04 ± 0.01
VH3 protein (Fragment) GN=VH3	Q9Y509	16	0.04 ± 0.10

Uncharacterized protein DKFZp686M0562 (Fragment) GN=DKFZp686M0562	Q6MZL2	35	0.04 ± 0.03
Complement C1s subcomponent GN=C1S	A0A087X232 (+2)	76	0.04 ± 0.01
V5-4 protein (Fragment) GN=V5-4	Q5NV79	11	0.04 ± 0.06
Collectin sub-family member 10 (C-type lectin), isoform CRA_a GN=COLEC10	A0A024R9J3 (+1)	31	0.04 ± 0.01
N90-VRC38.04 heavy chain variable region (Fragment)	A0A1W6IYI9 (+1)	14	0.04 ± 0.04
IGHV1-46 protein (Fragment) GN=IGHV1-46	A0A0F7SYK7 (+1)	10	0.04 ± 0.08
V1-4 protein (Fragment) GN=V1-4	Q5NV63	10	0.04 ± 0.08
Adiponectin GN=ADIPOQ	A8K660 (+2)	26	0.04 ± 0.03
Alpha-2-antiplasmin GN=SERPINF2	P08697	55	0.04 ± 0.01
cDNA FLJ39583 fis, clone SKMUS2004897, highly similar to ACTIN, ALPHA SKELETAL MUSCLE	B3KUD3 (+2)	38	0.03 ± 0.06
cDNA, FLJ93914, highly similar to Homo sapiens histidine-rich glycoprotein (HRG), mRNA	B2R8I2 (+1)	60	0.03 ± 0.00
Angiopoietin-like 6, isoform CRA_a GN=ANGPTL6	A0A024R7A9 (+2)	52	0.03 ± 0.01
Carboxypeptidase N subunit 2 GN=CPN2	P22792	61	0.03 ± 0.02
Coagulation factor XIII B chain GN=F13B	P05160	76	0.03 ± 0.01
Junction plakoglobin, isoform CRA_a GN=JUP	A0A024R1X8 (+2)	82	0.03 ± 0.03
cDNA FLJ51265, moderately similar to Beta-2-glycoprotein 1 (Beta-2-glycoprotein I)	B4DPN0 (+2)	30	0.03 ± 0.02
Lipopolysaccharide-binding protein GN=LBP	P18428 (+1)	53	0.02 ± 0.01
IgG H chain	S6B2B6	29	0.02 ± 0.05
SERPINB12 protein GN=SERPINB12	Q3SYB5 (+1)	21	0.02 ± 0.03
N90-VRC38.07 light chain variable region (Fragment)	A0A1W6IYL0	12	0.02 ± 0.05
Phospholipid transfer protein, isoform CRA_c GN=PLTP	B3KUE5 (+2)	57	0.02 ± 0.00
Thrombospondin 1, isoform CRA_a GN=THBS1	A0A024R9Q1 (+1)	129	0.02 ± 0.00
Ig heavy chain variable region (Fragment)	A0A068LRW6 (+2)	14	0.02 ± 0.04
Soluble scavenger receptor cysteine-rich domain-containing protein SSC5D GN=SSC5D	A1L4H1	166	0.02 ± 0.01
Fab Hu 15C1 Heavy chain	A0A0M3KKW6	24	0.02 ± 0.04
Ficolin-1 GN=FCN1	O00602	35	0.02 ± 0.02
Heparin cofactor 2 GN=SERPIND1	P05546	57	0.02 ± 0.00
Dermcidin GN=DCD	P81605	11	0.02 ± 0.04
Collagen, type VI, alpha 3GN=COL6A3	D9ZGF2 (+1)	344	0.02 ± 0.01
Anti-folate binding protein (Fragment) GN=HuC4lambda Vlambda	A2NYQ7 (+2)	11	0.02 ± 0.04
Hornerin GN=HRNR	Q86YZ3	282	0.02 ± 0.01
Immunoglobulin lambda variable 4-3 GN=IGLV4-3	A0A075B6K6 (+1)	13	0.01 ± 0.03
cDNA FLJ51409, highly similar to Thrombospondin-4	B7Z832 (+2)	96	0.01 ± 0.00
Phosphatidylinositol-glycan-specific phospholipase D GN=GPLD1	P80108	92	0.01 ± 0.01
IBM-A3 heavy chain variable region (Fragment)	A0A0X9UWM4	14	0.01 ± 0.03
Adipocyte plasma membrane-associated protein GN=APMAP	Q9HDC9	46	0.01 ± 0.01
cDNA FLJ55606, highly similar to Alpha-2-HS-glycoprotein	B7Z8Q2 (+2)	47	0.01 ± 0.01
Inter-alpha-trypsin inhibitor heavy chain H3 GN=ITIH3	Q06033	100	0.01 ± 0.00
Serpin peptidase inhibitor, clade C (Antithrombin), member 1, isoform CRA_a GN=SERPINC1	A0A024R944 (+2)	53	0.01 ± 0.02
cDNA, FLJ93141, highly similar to Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA	B2R6V9 (+1)	83	0.01 ± 0.02
Collagen alpha-1(VI) chain GN=COL6A1	A0A087X0S5 (+1)	108	0.01 ± 0.01
Reelin GN=RELN	J3KQ66 (+1)	388	0.01 ± 0.00
Platelet-activating factor acetylhydrolase GN=PLA2G7	A0A024RD39 (+2)	50	0.01 ± 0.01
Desmoglein-1 GN=DSG1	Q02413	114	0.01 ± 0.01
Glyceraldehyde-3-phosphate dehydrogenase GN=GAPDH	P04406 (+2)	36	0.01 ± 0.02
Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 GN=SVEP1	A0A0A0MSD0 (+1)	390	0.01 ± 0.01
Myosin light chain 1/3, skeletal muscle isoform GN=MYL1	P05976 (+1)	21	0.01 ± 0.02
Desmoplakin GN=DSP	P15924 (+1)	332	0.01 ± 0.01
Gelsolin GN=GSN	A0A0A0MS51 (+7)	83	0.01 ± 0.01

Desmocollin-1 GN=DSC1	Q08554 (+1)	100	0.01 ± 0.01
Fructose-bisphosphate aldolase GN=ALDOA	H3BQN4 (+3)	39	0.01 ± 0.02
Lactoferrin GN=LTF	A0A161I202 (+11)	78	0.01 ± 0.01
Collagen alpha-2(VI) chain GN=COL6A2	P12110	109	0.01 ± 0.01
Complement C5 GN=C5	P01031	188	0.01 ± 0.00
Coagulation factor V GN=F5	A0A0A0MRJ7 (+1)	252	0.01 ± 0.00
Transforming growth factor beta-induced 68kDa isoform 2 (Fragment) GN=TGFBI	A0A0S2Z4K6 (+3)	57	0.01 ± 0.01
Alpha-1B-glycoprotein (Fragment) GN=A1BG	M0R009 (+2)	33	0.01 ± 0.01
Selenoprotein P (Fragment) GN=SELENOP	A0A182DWH7 (+1)	35	0.01 ± 0.01
Anion exchange protein GN=SLC4A1	E2RVJ0 (+3)	102	0.01 ± 0.01
cDNA, FLJ79457, highly similar to Insulin-like growth factor-binding protein complex acid labile chain	B0AZL7 (+2)	66	0.01 ± 0.01
Multimerin-1 GN=MMRN1	Q13201	138	0.01 ± 0.01
Annexin GN=ANXA2	A0A024R5Z7 (+13)	39	<0.01
Filaggrin-2 GN=FLG2	Q5D862	248	<0.01
Laminin, gamma 1 (Formerly LAMB2), isoform CRA_a GN=LAMC1	A0A024R972 (+1)	174	<0.01
cDNA FLJ78437, highly similar to Homo sapiens cartilage oligomeric matrix protein (COMP), mRNA	A8K3I0 (+3)	83	<0.01
Hemopexin GN=HPX	P02790	52	<0.01
CP protein GN=CP	A5PL27 (+5)	122	<0.01
Complement component 9, isoform CRA_a GN=C9	A0A024R035 (+1)	63	<0.01
Carboxylic ester hydrolase	A0A024CIM4 (+3)	68	<0.01
Inter-alpha (Globulin) inhibitor H4 (Plasma Kallikrein-sensitive glycoprotein) GN=ITIH4	B2RMS9 (+1)	103	<0.01
KIAA0100, isoform CRA_a GN=KIAA0100	K7EQ86 (+2)	237	<0.01
Prolow-density lipoprotein receptor-related protein 1 GN=LRP1	Q07954	505	<0.01
Hepatocyte growth factor activator GN=HGFAC	D6RAR4 (+1)	71	<0.01
Myosin-1 GN=MYH1	P12882 (+1)	223	<0.01
Fibulin-1 GN=FBLN1	P23142	77	<0.01
Plakophilin 1 (Ectodermal dysplasia/skin fragility syndrome), isoform CRA_a GN=PKP1	A0A024R952 (+1)	80	<0.01
Mannan-binding lectin serine protease 2 GN=MASP2	O00187	76	<0.01
Plasminogen	B2R7F8 (+1)	91	<0.01
cDNA FLJ58441, highly similar to Attractin	B4DZ36 (+1)	130	<0.01
Hemicentin-1 GN=HMCN1	Q96RW7	613	<0.01
Laminin subunit alpha-2 GN=LAMA2	A0A087WX80 (+2)	344	<0.01