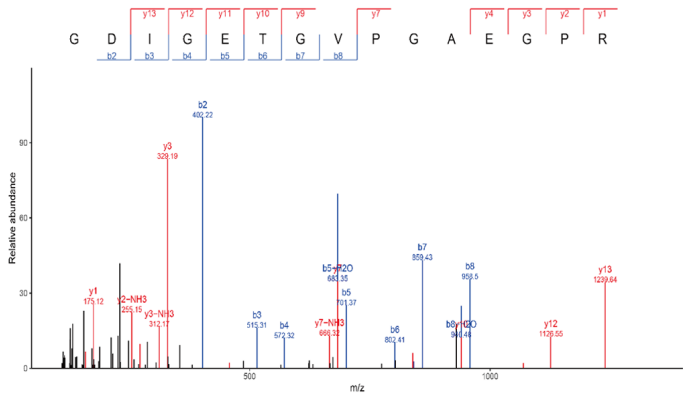
Figure S1. Representative mass spectra images of the identified proteins. ADIPOQ, adiponectin, C1Q and collagen domain containing; THBS4, thrombospondin 4; GP1BB, glycoprotein Ib platelet subunit β; APOF, apolipoprotein F; PSG9, pregnancy specific β-1-glycoprotein 9; APCS, amyloid P component, serum.

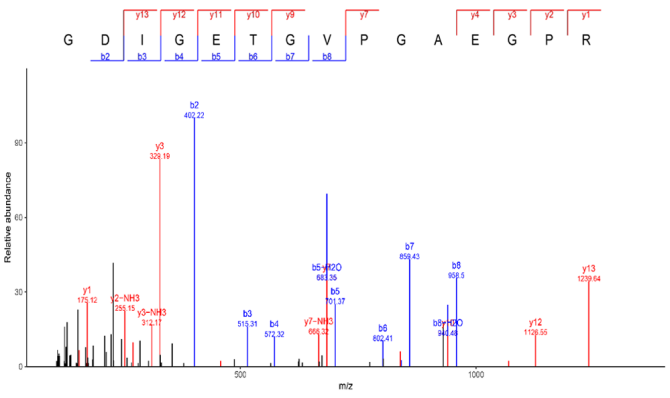
ADIPOQ

Raw file	Scan number	Mass analyzer	Score	m/z	Proteins
6	6098	FTMS	106.14	706.3442	Q15848



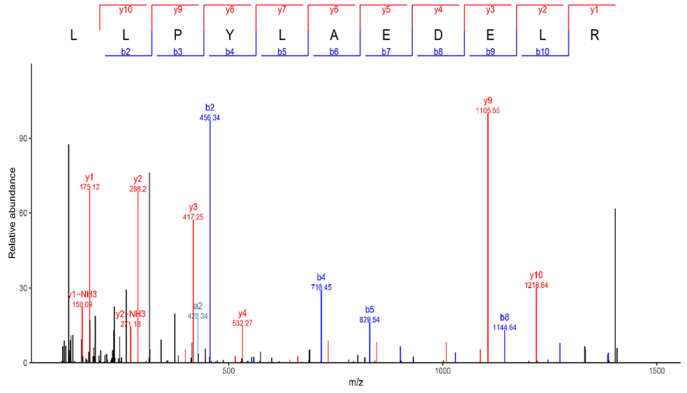
THBS4

Raw file	Scan number	Mass analyzer	Score	m/z	Proteins
6	6098	FTMS	106.14	706.3442	Q15848



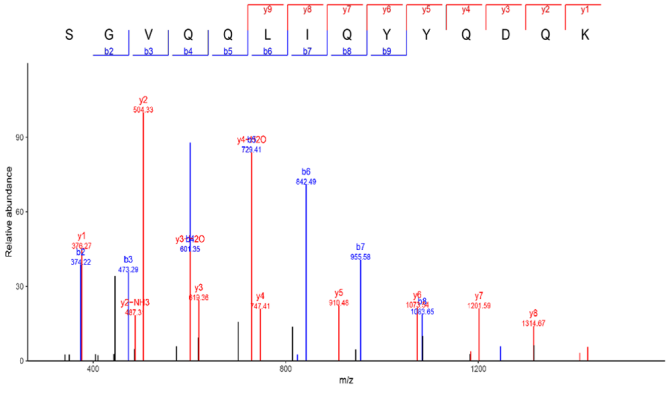
GP1BB

Raw file	Scan number	Mass analyzer	Score	m/z	Proteins
8	11995	FTMS	172.61	666.3639	P13224



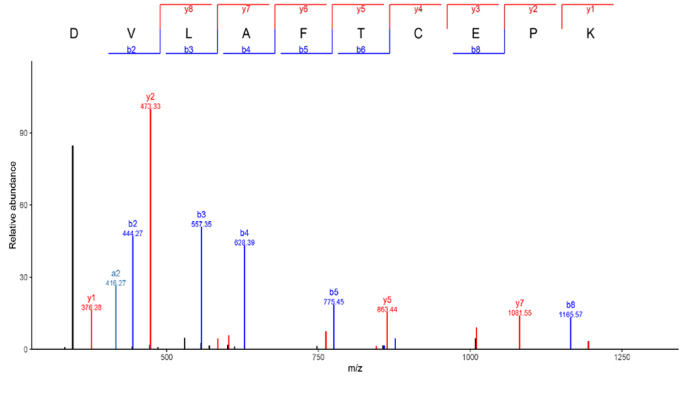
APOF

Raw file	Scan number	Mass analyzer	Score	m/z	Proteins
9	11270	FTMS	113.4	849.4283	Q13790



PSG9

Raw file	Scan number	Mass analyzer	Score	m/z	Proteins
11	10031	FTMS	108.7	1179.571	Q16557;Q00887



APCS

Raw file	Scan number	Mass analyzer	Score	m/z	Proteins
3	9834	FTMS	150.46	469.5615	P02743

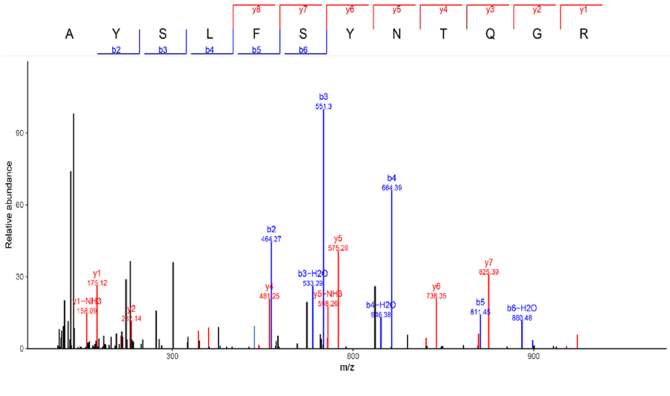


Figure S2. A heatmap was generated from the hierarchical clustering of the Gene Ontology analysis results, showing that umbilical cord serum proteins were enriched in cellular component terms that were related to cell junction, cell adhesion and extracellular matrix components. The differentially expressed proteins were categorized into four groups according to their fold change: Q1 (0-0.5), Q2 (0.5-0.67), Q3 (1.5-2) and Q4 (>2), with P<0.05 in all cases. The functional annotation following enrichment, together with the corresponding enrichment P-value, were first collected. The functional classifications that were enriched in at least one of the clusters (with P<0.05) were then screened. The filtered P-value data matrix was -log10 transformed. The transformed data matrix was classified by Z transformation for each functional category. Lastly, the dataset obtained following Z transformation was analyzed using one-way hierarchical clustering.

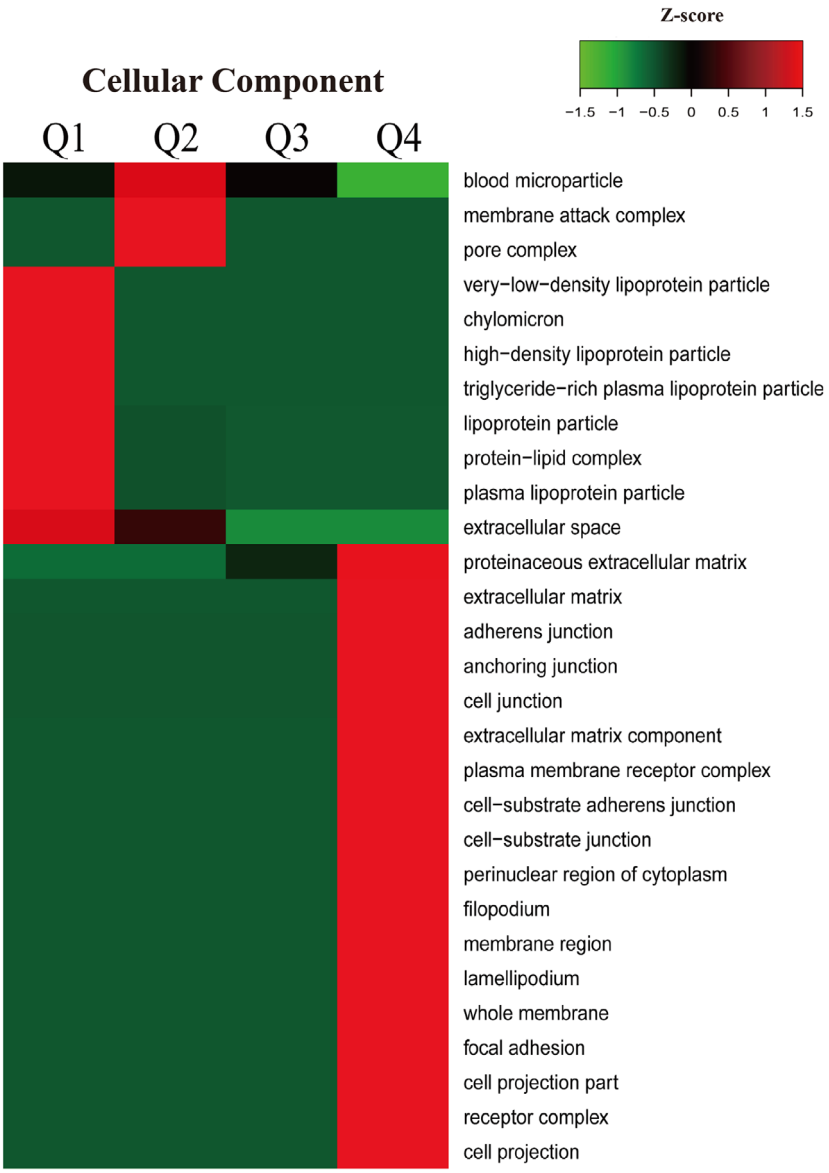


Figure S3. A heatmap was generated from hierarchical clustering of the Gene Ontology analysis results, showing that umbilical cord serum proteins were enriched in biological process terms that were related to gene regulation, as well as cell growth, differentiation, motility and adhesion. The differentially expressed proteins were categorized into four groups according to their fold change: Q1 (0-0.5), Q2 (0.5-0.67), Q3 (1.5-2) and Q4 (>2), with P<0.05 in all cases.

Figure S4. A heatmap was generated from hierarchical clustering of the Gene Ontology analysis results, showing that umbilical cord serum proteins were enriched in molecular function terms that were related to molecule binding, including integrin binding and enzyme binding. The differentially expressed proteins were categorized into four groups according to their fold change: Q1 (0-0.5), Q2 (0.5-0.67), Q3 (1.5-2) and Q4 (>2), with P<0.05 in all cases.

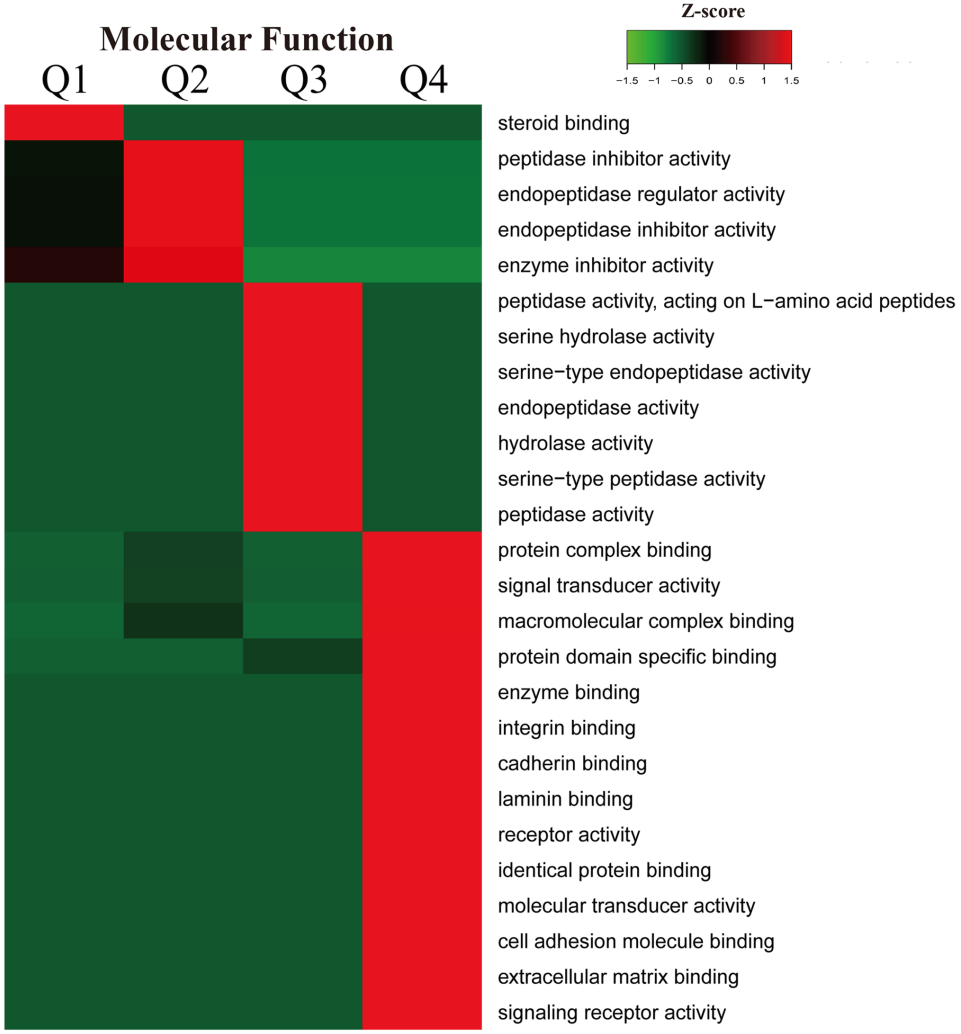


Figure S5. Flow cytometry was used to determine apoptotic cell death of MHCC97H cells treated with exosomes from the negative control, ME and UE groups. The data are presented as the mean ± SEM. *P<0.05, **P<0.01, ***P<0.001. ME, maternal serum exosome; UE, umbilical serum exosome; PI, propidium iodide. The different quadrants Q1, Q2, Q3 and Q4 represent necrotic cells, late apoptotic cells, early apoptotic cells and viable cells, respectively.

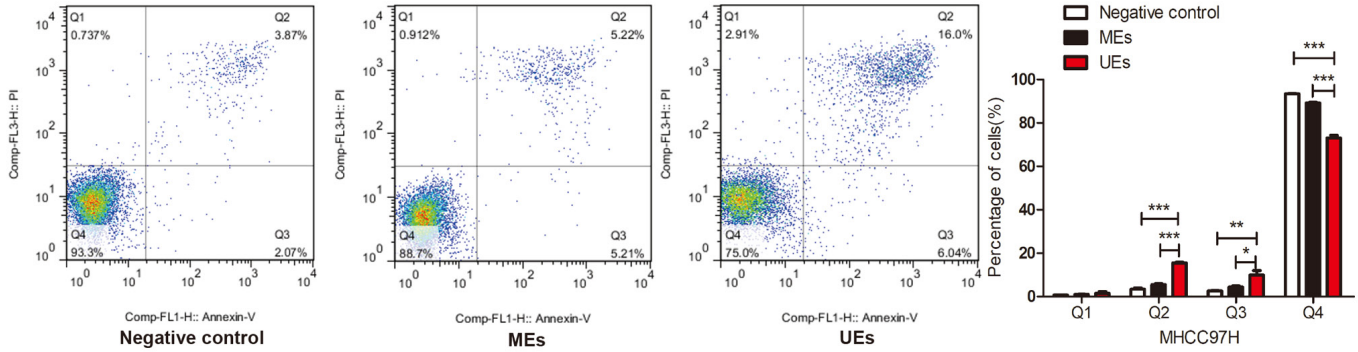


Table SI. Representative mass spectra of some differentially expressed proteins.

Gene name	Protein description	UEs/MEs ratio	MW (kDa)	Score
ADIPOQ	Adiponectin	5.724 Up	26.413	35.253
THBS4	Thrombospondin-4	5.211 Up	105.87	156.01
GP1BB	Platelet glycoprotein Ib beta chain	5.067 Up	21.717	55.474
COL1A1	Collagen alpha-1(I) chain	4.956 Up	138.94	18.486
THBS3	Thrombospondin-3	4.78 Up	104.2	40.532
TNXB	Tenascin-X	4.373 Up	458.22	131.96
PPIA	Peptidyl-prolyl cis-trans isomerase A	4.283 Up	18.012	29.025
PF4V1	Platelet factor 4 variant	4.197 Up	11.553	13.468
MSN	Moesin	3.998 Up	67.819	24.523
GP1BA	Platelet glycoprotein Ib alpha chain	3.848 Up	71.539	25.828
CRP	C-reactive protein	0.062 Down	25.038	47.518
IGHA2	Ig α-2 chain C region	0.086 Down	36.526	54.714
PZP	Pregnancy zone protein	0.104 Down	163.86	228.85
APOL1	Apolipoprotein L1	0.106 Down	43.974	81.534
HP	Haptoglobin	0.108 Down	45.205	190.31
IGHA1	Ig alpha-1 chain C region	0.115 Down	37.654	227.22
PSG4	Pregnancy-specific beta-1-glycoprotein 4	0.116 Down	47.112	79.15
APOF	Apolipoprotein F	0.117 Down	35.399	25.247
PSG9	Pregnancy-specific beta-1-glycoprotein 9	0.147 Down	48.272	26.244
APCS	Serum amyloid P-component	0.155 Down	25.387	88.277

ME, maternal serum exosome; UE, umbilical serum exosome; MW, molecular weight.