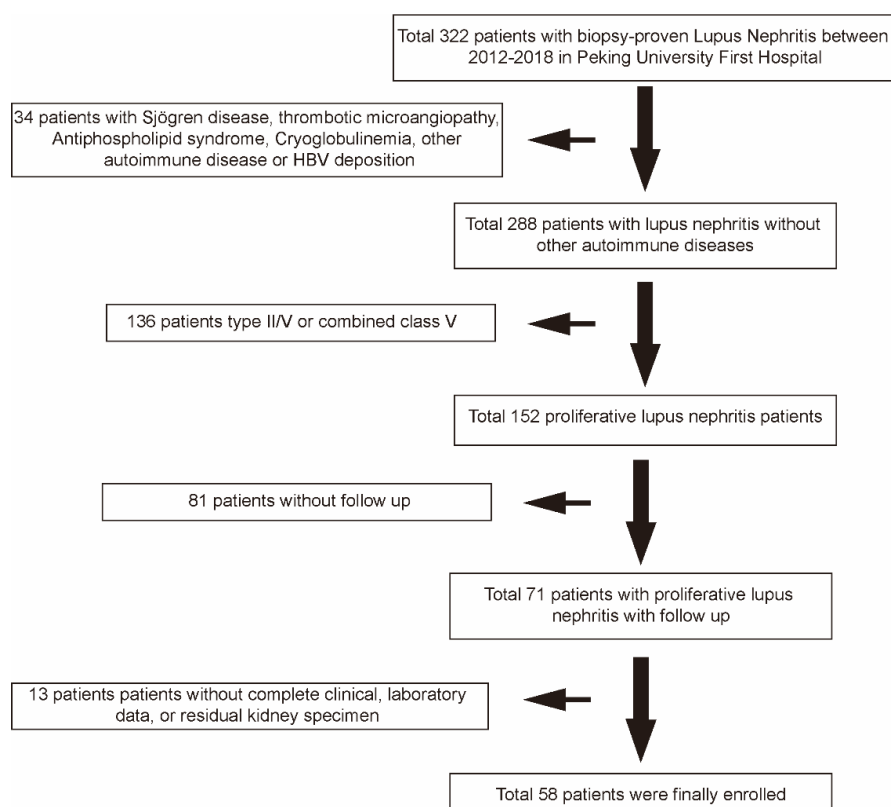


Supplementary materials

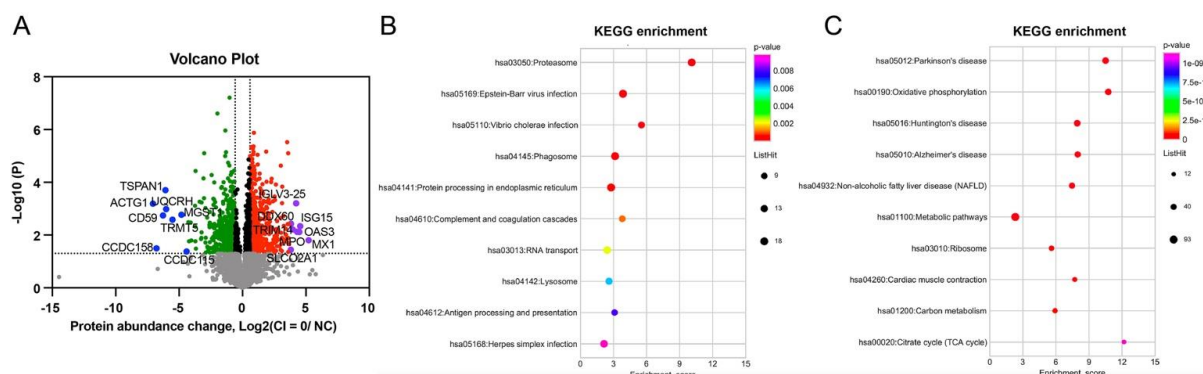
This file includes

Supplementary Figure 1-7

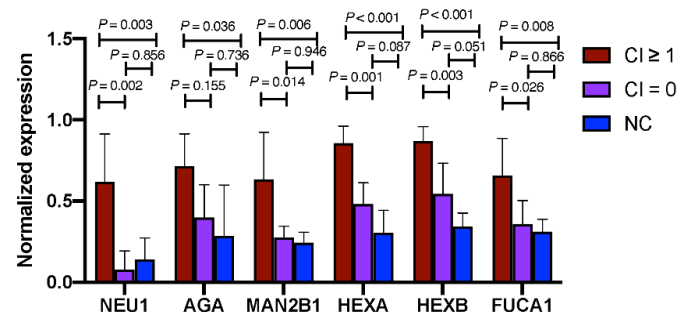
Supplementary Table 1-7



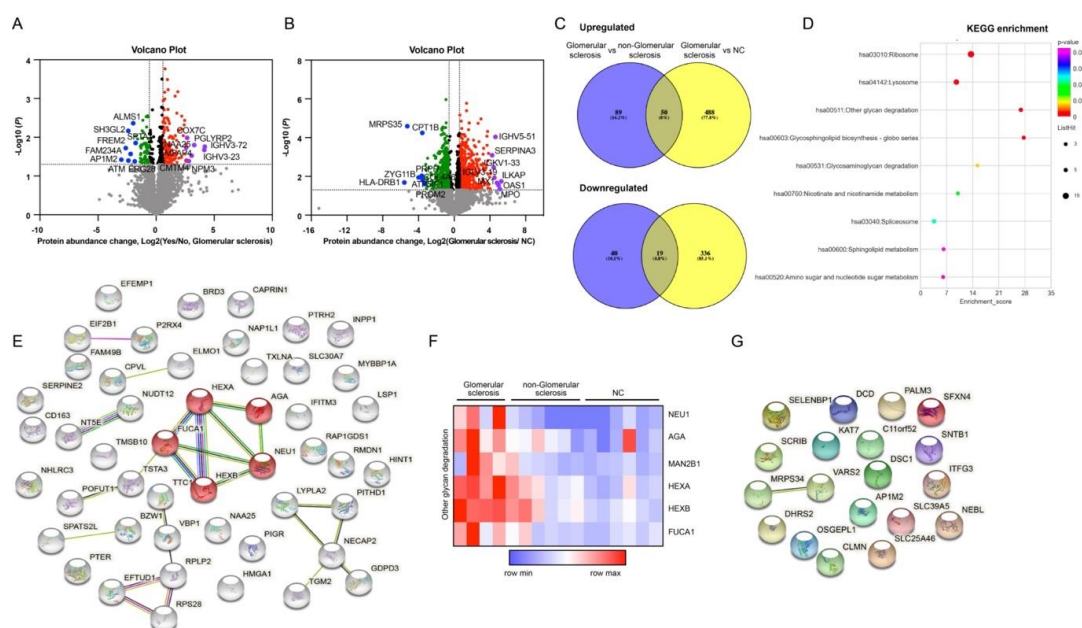
Supplementary Figure 1. The flow chart of study participants.



Supplementary Figure 2. Quantitative proteomic and bioinformatics analysis of the renal specimens from proliferative LN patients with CI = 0 and normal controls. (A) The volcano map depicted differentially expressed proteins between CI = 0 and NC group. Red dots: upregulated proteins (fold change (CI = 0/NC) ≥ 1.5 , $P < 0.05$). Green dots: downregulated proteins (fold change (NC/CI = 0) ≥ 1.5 , $P < 0.05$). Purple dots: the top 8 upregulated proteins in the volcano map. Blue dots: the top 8 downregulated proteins in the volcano map. Nine proteins specific to NC group were assigned a log₂ (fold change) of infinity (MAPRE3, TIMP3, FBXL8, VPS13A, MT-CO1, UBFD1, LIMS2, RAB2B, GALC). **(B)** The KEGG pathway enrichment analysis was performed among the upregulated proteins. **(C)** KEGG pathway enrichment analysis was performed among the downregulated proteins.

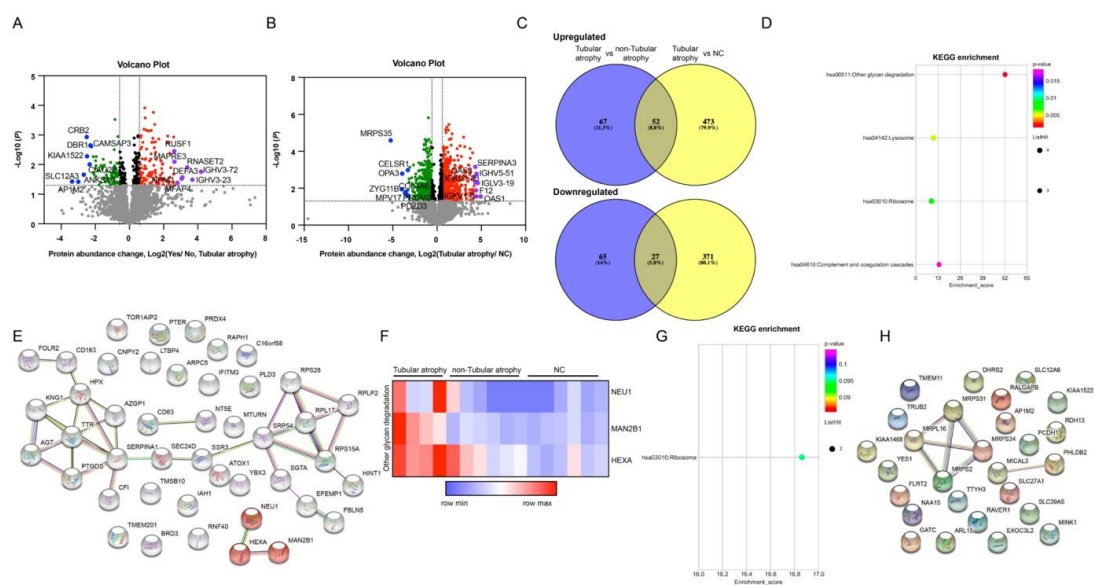


Supplementary Figure 3. The expression of proteins that enriched in other glycan degradation between different groups. The multiple comparisons between CI \geq 1, CI = 0, and NC group for each pairwise using ANOVA with a post-hoc test among the six proteins (NEU1, AGA, MAN2B1, HEXA, HEXB, FUCA1) enriched in the “other glycan degradation” pathway. No significance, $P > 0.05$.



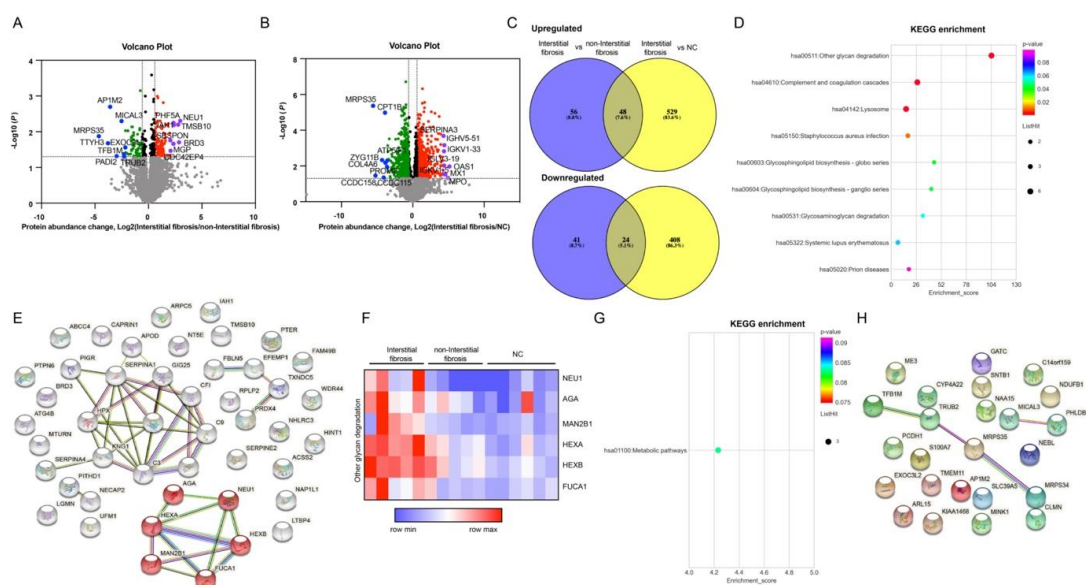
Supplementary Figure 4. Quantitative proteomic and bioinformatics analysis of the renal specimens from proliferative LN patients with/without glomerular sclerosis and normal controls. (A) The volcano map depicted differentially expressed proteins between glomerular sclerosis and non-glomerular sclerosis group. Red dots: upregulated proteins (fold change (glomerular sclerosis / non-glomerular sclerosis) ≥ 1.5 , $P < 0.05$). Green dots: downregulated proteins (fold change (non-glomerular sclerosis / glomerular sclerosis) ≥ 1.5 , $P < 0.05$). Purple dots: the top 8 upregulated proteins in the volcano map. Blue dots: the top 8 downregulated proteins in the volcano map. Seven proteins specific to glomerular sclerosis group were assigned a log₂(fold change) of infinity (FBXL8, NT5C3A, GALC, LIMS2, UBFD1, PPIL4, RAB2B). Two proteins specific to non-glomerular sclerosis group were assigned a log₂(fold change) of infinity (SLC39A5, OSGEPL1). (B) The volcano map depicted differentially expressed proteins between glomerular sclerosis and NC group. Red dots: upregulated proteins (fold change (glomerular sclerosis / NC) ≥ 1.5 , $P < 0.05$). Green dots: downregulated proteins (fold change (NC/ glomerular sclerosis) ≥ 1.5 , $P < 0.05$). Purple dots: the top 8 upregulated proteins in the volcano map. Blue dots: the top 8 downregulated proteins in the volcano map. Three proteins specific to non-glomerular sclerosis group were assigned a log₂(fold change)

of infinity (MCUR1, OSGEPL1, SLC39A5). (C) The venn diagram of the proteins in glomerular sclerosis, non-glomerular sclerosis, and NC groups. (D) The KEGG pathway enrichment analysis was performed among the upregulated proteins. (E) The network of enriched proteins (upregulated). String: <https://string-db.org>. (F) The intensity of proteins that were enriched in other glycan degradation. (G) The network of enriched proteins (downregulated). String: <https://string-db.org>.



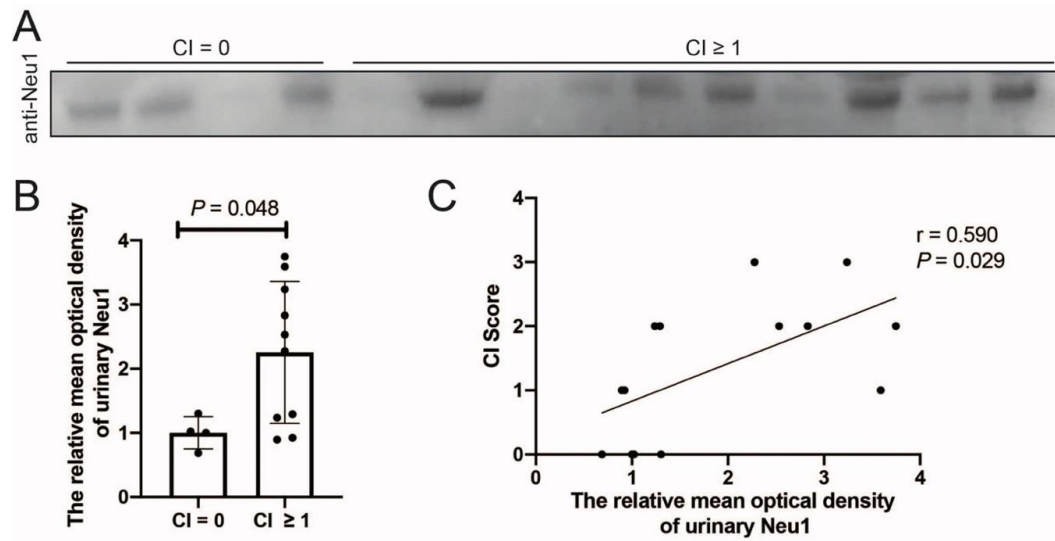
Supplementary Figure 5. Quantitative proteomic and bioinformatics analysis of the renal specimens from proliferative LN patients with/without tubular atrophy and normal controls. (A) The volcano map depicted differentially expressed proteins between tubular atrophy and non-tubular atrophy group. Red dots: upregulated proteins (fold change (tubular atrophy / non-tubular atrophy) ≥ 1.5 , $P < 0.05$). Green dots: downregulated proteins (fold change (non-tubular atrophy / tubular atrophy) ≥ 1.5 , $P < 0.05$). Purple dots: the top 8 upregulated proteins in the volcano map. Blue dots: the top 8 downregulated proteins in the volcano map. Two proteins specific to tubular atrophy group were assigned a log₂ (fold change) of infinity (LIMS2, UBFD1). Eleven proteins specific to non-glomerular sclerosis group were assigned a log₂(fold change) of infinity (PDE4DIP, MICAL3, ABLIM3, EXOC3L2, TRUB2, WBP11, RAB43, SLC39A5, TTYH3, MRPL16, FLRT2). (B) The volcano map depicted differentially expressed proteins between tubular atrophy and NC group. Red dots: upregulated proteins (fold change (tubular atrophy / NC) ≥ 1.5 , $P < 0.05$). Green dots: downregulated proteins (fold change (NC/ tubular atrophy) ≥ 1.5 , $P < 0.05$). Purple dots: the top 8 upregulated proteins in the volcano map. Blue dots: the top 8 downregulated proteins in the volcano map. Sixteen proteins specific to NC group were assigned a log₂ (fold change) of infinity (CPT1B, FLRT2, MICAL3, TRUB2, MICU1, MRPL18, MCUR1, EXOC3L2, MRPL16, AKTIP,

TEX10, PBX1, DHCR7, PRCC, TTYH3, SLC39A5). (C) The venn diagram of the proteins in tubular atrophy, non-tubular atrophy, and NC groups. (D) KEGG pathway enrichment analysis was performed among the upregulated proteins. (E) The network of enriched proteins (upregulated). String: <https://string-db.org>. (F) The intensity of proteins that were enriched in other glycan degradation. (G) KEGG pathway enrichment analysis was performed among the downregulated proteins. (H)The network of enriched proteins (downregulated). String: <https://string-db.org>.



Supplementary Figure 6. Quantitative proteomic and bioinformatics analysis of the renal specimens from proliferative LN patients with/without interstitial fibrosis and normal controls. (A) The volcano map depicted differentially expressed proteins between interstitial fibrosis and non-interstitial fibrosis group. Red dots: upregulated proteins (fold change (interstitial fibrosis / non-interstitial fibrosis) ≥ 1.5 , $P < 0.05$). Green dots: downregulated proteins (fold change (non-interstitial fibrosis / interstitial fibrosis) ≥ 1.5 , $P < 0.05$). Purple dots: the top 8 upregulated proteins in the volcano map. Blue dots: the top 8 downregulated proteins in the volcano map. Seven proteins specific to interstitial fibrosis group were assigned a log₂(fold change) of infinity (MAPRE3, VPS13A, FBXL8, NT5C3A, GALC, LIMS2, UBF1). One protein specific to non-interstitial fibrosis group were assigned a log₂(fold change) of infinity (SLC39A5). (B) The volcano map depicted differentially expressed proteins between interstitial fibrosis and NC group. Red dots: upregulated proteins (fold change (interstitial fibrosis / NC) ≥ 1.5 , $P < 0.05$). Green dots: downregulated proteins (fold change (NC / interstitial fibrosis) ≥ 1.5 , $P < 0.05$). Purple dots: the top 8 upregulated proteins in the volcano map. Blue dots: the top 8 downregulated proteins in the volcano map. Two proteins specific to NC group were assigned a log₂(fold change) of infinity (MCUR1, SLC39A5) (C) The venn diagram of the proteins in interstitial fibrosis, non-interstitial fibrosis, and NC groups.

(D) KEGG pathway enrichment analysis was performed among the upregulated proteins. (E) The network of enriched proteins (upregulated). String: <https://string-db.org>. (F) The intensity of proteins that were enriched in other glycan degradation. (G) KEGG pathway enrichment analysis was performed among the downregulated proteins. (H) The network of enriched proteins (downregulated). String: <https://string-db.org>.



Supplementary Figure 7. The association of urinary Neu1 excretion and renal pathological indices in 14 proliferative LN patients. (A) The western blot assay of Neu1 protein excretion in the urine samples from 14 proliferative LN patients (10 patients with $CI \geq 1$, 4 patients with $CI = 0$) (each sample was normalized to the 50mg creatinine). (B) The relative mean optical density of urinary Neu1 between $CI = 0$ group and $CI \geq 1$ group. (C) The association between the relative mean optical density of urinary Neu1 and CI scores.

Supplementary Table 1. General data of 10 proliferative lupus nephritis patients for proteomic analysis

Clinical Evaluation		Laboratory Assessment		Renal Histopathology	
Sex (male/female), no.	2/8	Leukocytopenia, no. (%)	4 (40.0)	Classification	
Age, (yrs), mean \pm SD	32.6 \pm 15.5	Thrombocytopenia, no. (%)	4 (40.0)	III, no. (%)	3 (30.0)
Hypertension, no. (%)	5 (50.0)	Hematuria, no (%)	9 (90.0)	IV, no. (%)	7 (70.0)
Fever (noninfectious), no. (%)	1 (10.0)	Leukocyturia (noninfectious), no. (%)	5 (50.0)	Activity indices score, median (range)	
Malar rash, no. (%)	5 (50.0)	Proteinuria, g/24 h, mean \pm SD	3.83 \pm 3.06	Chronicity indices score, median (range)	
Photosensitivity, no. (%)	0 (0.0)	Serum creatinine (μ mol/L), median (range)	81.25 (48.2 - 135.0)	1 (0-4)	
Oral ulcer, no (%)	0 (0.0)	C3, g/L, mean \pm SD	0.31 \pm 0.13		
Alopecia, no. (%)	2 (20.0)	Anti-nuclear antibody (+), no. (%)	10 (100.0)		
Arthralgia, no. (%)	4 (40.0)	Anti-double-stranded DNA antibody (+), no. (%)	9 (90.0)		
Serositis, no. (%)	0 (0.0)				
Neurologic disorder, no. (%)	0 (0.0)				
Acute renal failure, no. (%)	1 (10.0)				
Nephrotic syndrome, no. (%)	6 (60.0)				
SLEDAI, mean \pm SD	17.1 \pm 6.9				

SLEDAI, systemic lupus erythematosus disease activity index; eGFR, estimated glomerular filtration rate; Anti-dsDNA antibody, anti-double-stranded DNA antibody

Supplementary Table 2. General data of 58 proliferative lupus nephritis patients for immunohistochemical analysis

Clinical Evaluation		Laboratory Assessment		Renal Histopathology		Follow up	
Sex (male/female), no.	7/51	Leukocytopenia, no. (%)	10 (17.2)	Classification		Duration of follow-up, month, median (range)	39 (1 - 85)
Age (yrs), mean \pm SD	34.3 \pm 11.9	Thrombocytopenia, no. (%)	9 (15.5)	III, no. (%)	11 (19.0)	ESRD, no. (%)	6 (10.3)
Hypertension, no. (%)	32 (55.2)	Hematuria, no (%)	51 (87.9)	IV, no. (%)	47 (81.0)	\geq 50% reduction from baseline of eGFR, no. (%)	4 (6.9)
Fever (noninfectious), no. (%)	17 (29.3)	Leukocyturia (noninfectious), no. (%)	39 (67.2)	Activity indices score, median (range)	8 (3 - 14)		
Malar rash, no. (%)	22 (37.9)	Proteinuria (g/24 h), mean \pm SD	4.13 \pm 3.31	Chronicity indices score, median (range)	2 (0 - 6)		
Photosensitivity, no. (%)	10 (17.2)	Serum creatinine (μ mol/L), median (range)	102.7 (36.9 - 579)				
Oral ulcer, no (%)	6 (10.3)	C3 (g/L), mean \pm SD	0.40 \pm 0.18				
Alopecia, no. (%)	23 (39.7)	Anti-nuclear antibody (+), no. (%)	58 (100.0)				
Arthralgia, no. (%)	28 (48.3)	Anti-dsDNA antibody (+), no. (%)	52 (89.7)				
Serositis, no. (%)	7 (12.1)						
Neurologic disorder, no. (%)	5 (8.6)						
Acute renal injury, no. (%)	15 (25.9)						
Nephrotic syndrome, no. (%)	36 (62.1)						
SLEDAI, mean \pm SD	19.2 \pm 5.3						

SLEDAI, systemic lupus erythematosus disease activity index; eGFR, estimated glomerular filtration rate; Anti-dsDNA antibody, anti-double-stranded DNA antibody

Supplementary Table 3. General data of 14 proliferative lupus nephritis patients for urinary analysis

Clinical Evaluation		Laboratory Assessment		Renal Histopathology	
Sex (male/female), no.	5/9	Leukocytopenia, no. (%)	1 (7.1)	Classification	
Age (yrs), mean \pm SD	39.5 \pm 15.6	Thrombocytopenia, no. (%)	0 (0.0)	III, no. (%)	4 (28.6)
Hypertension, no. (%)	6 (42.9)	Hematuria, no (%)	10 (71.4)	IV, no. (%)	10 (71.4)
Fever (noninfectious), no. (%)	4 (28.6)	Leukocyturia (noninfectious), no. (%)	11 (78.6)	Activity indices score, median (range)	
Malar rash, no. (%)	3 (21.4)			9 (2 - 15)	
Photosensitivity, no. (%)	2 (14.3)	Proteinuria (g/24 h), mean \pm SD	4.80 \pm 4.87	Chronicity indices score, median (range)	
Oral ulcer, no (%)	1 (7.1)			1.5 (0 - 3)	
Alopecia, no. (%)	3(21.4)	Serum creatinine (μ mol/L), median (range)	89.36 (36.9 - 178.9)		
Arthralgia, no. (%)	7(50.0)				
Serositis, no. (%)	0 (0.0)	C3 (g/L), mean \pm SD	0.49 \pm 0.19		
Neurologic disorder, no. (%)	1 (7.1)	Anti-nuclear antibody (+), no. (%)	14 (100.0)		
Acute renal injury, no. (%)	3 (21.4)	Anti-dsDNA antibody (+), no. (%)	12 (85.7)		
Nephrotic syndrome, no. (%)	7(50.0)				
SLEDAI, mean \pm SD	17.0 \pm 5.2				

SLEDAI, systemic lupus erythematosus disease activity index; eGFR, estimated glomerular filtration rate; Anti-dsDNA antibody, anti-double-stranded DNA antibody

Supplementary Table 4. The differentially expressed proteins between CI ≥ 1 group and CI = 0/NC group.

Both upregulated proteins					Both downregulated proteins						
UniProt ID	Gene symbol	Fold change (CI≥1 vs. CI=0)	P value	Fold change (CI≥1 vs. NC)	P value	UniProt ID	Gene symbol	Fold change (CI≥1 vs. CI=0)	P value	Fold change (CI≥1 vs. NC)	P value
Q99519	NEU1	7.875	4.95E-03	4.392	5.70E-03	P82930	MRPS34	0.566	8.85E-03	0.599	2.22E-02
Q15059	BRD3	7.286	1.97E-02	8.542	9.79E-03	Q96JQ2	CLMN	0.657	3.89E-02	0.520	8.69E-04
P63313	TMSB10	6.898	6.33E-03	11.725	1.30E-03	Q9NXU5	ARL15	0.484	1.81E-02	0.502	9.60E-03
Q2TAA2	IAH1	5.177	6.46E-03	2.629	6.04E-03	Q7Z3D6	DGLUCY	0.495	1.18E-02	0.477	1.93E-02
Q8N3F0	MTURN	3.990	1.10E-02	3.951	2.40E-03	O75438	NDUFB1	0.660	3.12E-02	0.453	1.21E-04
Q12805	EFEMP1	3.618	5.92E-03	1.851	2.55E-02	O76041	NEBL	0.630	2.02E-02	0.445	3.73E-03
P07093	SERPINE2	3.068	6.33E-03	3.438	4.54E-03	Q9P260	RELCH	0.443	3.71E-02	0.445	1.61E-02
P01011	SERPINA3	2.978	1.14E-02	19.764	2.06E-04	Q8N4C8	MINK1	0.380	1.25E-02	0.430	2.66E-02
Q5JSH3	WDR44	2.813	2.15E-02	2.522	8.14E-03	Q13884	SNTB1	0.541	2.09E-02	0.427	2.46E-02
P29622	SERPINA4	2.676	4.73E-02	2.055	4.35E-02	Q5TCH4	CYP4A22	0.249	4.03E-02	0.404	1.86E-02
P05156	CFI	2.644	3.53E-02	7.315	2.04E-03	Q08174	PCDH1	0.379	1.66E-02	0.369	3.80E-03
P02766	TTR	2.634	1.54E-03	4.637	3.22E-05	Q86SQ0	PHLDB2	0.381	2.08E-02	0.320	1.47E-02
Q9NUQ9	CYRIB	2.599	3.22E-02	3.003	2.70E-03	Q16798	ME3	0.463	4.06E-02	0.296	9.40E-03
P01857	IGHG1	2.508	2.43E-02	4.604	2.67E-03	P17152	TMEM11	0.507	3.23E-02	0.292	2.28E-02
P01031	C5	2.487	3.82E-02	3.061	1.62E-02	Q9BXJ9	NAA15	0.394	4.68E-02	0.239	4.13E-02
O15439	ABCC4	2.450	3.07E-02	9.104	8.32E-04	Q7RTP6	MICAL3	0.175	5.03E-03	0.236	1.12E-02
P01042	KNG1	2.419	1.73E-02	3.131	1.09E-02	O43716	GATC	0.264	9.28E-03	0.191	4.04E-03
Q8N2S1	LTBP4	2.300	2.85E-02	4.333	7.61E-03	Q8WVM0	TFB1M	0.209	4.92E-02	0.166	2.19E-02
O00754	MAN2B1	2.295	2.74E-02	2.602	1.00E-02	Q2M3D2	EXOC3L2	0.224	2.74E-02	0.161	9.20E-03
Q9UBX5	FBLN5	2.239	2.85E-02	2.975	5.19E-03	P31151	S100A7	0.275	4.30E-02	0.120	1.68E-02
P01009	SERPINA1	2.178	2.28E-02	5.906	4.35E-04	O95900	TRUB2	0.203	4.23E-02	0.102	3.06E-04
P01833	PIGR	2.147	5.01E-03	3.019	8.98E-04	Q9Y6Q5	AP1M2	0.083	2.00E-03	0.090	1.57E-03
Q5J37	NHLRC3	2.114	3.41E-02	1.903	6.34E-03	P82673	MRPS35	0.040	1.33E-02	0.021	4.29E-06
P29350	PTPN6	2.057	3.30E-02	2.697	1.67E-03	Q6ZMH5	SLC39A5	0.000	1.49E-04	0.000	2.70E-02
P02748	C9	1.948	3.76E-02	2.753	7.87E-03						
P02790	HPX	1.942	1.75E-02	2.105	3.61E-02						
Q9Y4P1	ATG4B	1.872	2.55E-02	1.716	3.37E-02						
P55209	NAP1L1	1.863	1.63E-02	2.631	6.97E-04						
Q99538	LGMN	1.856	3.28E-02	2.566	6.36E-03						
P01024	C3	1.837	2.70E-02	1.998	1.96E-02						
P05090	APOD	1.828	4.97E-03	2.376	7.45E-05						
P04066	FUCA1	1.828	3.90E-02	2.116	6.59E-03						
P20933	AGA	1.788	3.82E-02	2.506	2.75E-02						
P06865	HEXA	1.780	1.01E-03	2.836	4.60E-05						
Q14444	CAPRIN1	1.774	2.52E-02	1.727	2.19E-02						
Q9GZP4	PITHD1	1.745	4.52E-02	1.530	1.13E-02						
P21589	NT5E	1.708	2.48E-02	2.271	3.53E-03						
P49773	HINT1	1.667	3.08E-03	1.524	7.27E-03						
Q9NVZ3	NECAP2	1.667	5.30E-03	3.133	5.57E-06						
Q9NR19	ACSS2	1.634	2.44E-02	2.022	6.73E-03						
O15511	ARPC5	1.632	2.02E-02	1.539	1.03E-02						
Q13162	PRDX4	1.631	2.30E-02	1.943	5.48E-03						
Q96BW5	PTER	1.608	2.81E-02	1.687	1.87E-02						
P61960	UFM1	1.606	4.85E-02	1.606	4.85E-02						
P07686	HEXB	1.599	7.97E-03	2.533	3.09E-06						
P05387	RPLP2	1.586	2.73E-02	1.837	1.54E-02						
Q8NBS9	TXNDC5	1.551	1.24E-02	1.518	6.60E-03						
O6NXS1	PPP1R2B	1.528	9.70E-03	2.373	1.95E-03						

Supplementary Table 5. The differentially expressed proteins between glomerular sclerosis group and non-glomerular sclerosis/NC group

Both upregulated proteins						Both downregulated proteins					
UniProt ID	Gene symbol	Fold change (Glomerular sclerosis, yes vs.no)		Fold change (Glomerular sclerosis vs. NC)		UniProt ID	Gene symbol	Fold change (Glomerular sclerosis, yes vs.no)		Fold change (Glomerular sclerosis vs. NC)	
			<i>P</i> value		<i>P</i> value				<i>P</i> value		<i>P</i> value
P01764	IGHV3-23	17.700	2.12E-02	10.415	2.76E-02	Q13228	SELENBP1	0.655	1.67E-02	0.648	1.92E-02
Q14CX7	NAA25	6.052	1.84E-02	6.947	5.19E-03	Q14160	SCRIB	0.631	1.09E-02	0.611	4.37E-03
Q99519	NEU1	5.523	3.68E-03	4.866	3.54E-03	Q96JQ2	CLMN	0.618	2.35E-02	0.479	9.46E-04
Q99571	P2RX4	4.607	2.85E-03	2.923	3.11E-03	A6NDB9	PALM3	0.605	2.79E-03	0.647	1.25E-02
Q15059	BRD3	4.470	3.31E-02	9.092	1.32E-02	O76041	NEBL	0.557	2.94E-03	0.390	3.80E-03
P33241	LSP1	3.889	3.46E-02	5.800	2.39E-03	P82930	MRPS34	0.554	1.42E-02	0.559	2.43E-02
Q12805	EFEMP1	3.653	6.67E-04	2.093	3.06E-03	O95251	KAT7	0.553	1.80E-02	0.327	1.80E-02
P63313	TMSB10	3.459	4.45E-02	11.704	3.64E-03	Q13268	DHRS2	0.534	3.67E-02	0.238	2.73E-03
P61758	VBP1	3.445	2.39E-03	1.646	2.20E-02	Q6P4A7	SFXN4	0.488	1.44E-02	0.448	4.53E-03
P52306	RAP1GDS1	3.406	1.85E-02	2.248	4.00E-02	Q08554	DSC1	0.483	3.73E-02	0.433	2.23E-02
Q8NEW0	SLC30A7	3.402	1.19E-02	2.649	3.88E-02	Q13884	SNTB1	0.452	3.65E-03	0.353	2.18E-02
P07093	SERPINE2	3.126	8.67E-04	3.851	1.47E-03	Q96A22	C11orf52	0.431	3.89E-02	0.330	7.36E-03
Q9H488	POFUT1	2.780	2.93E-02	3.580	9.77E-04	Q96AG3	SLC25A46	0.391	1.70E-02	0.395	1.73E-02
Q9BQG0	MYBBP1A	2.616	2.15E-02	2.633	2.21E-02	P81605	DCD	0.330	1.11E-02	0.430	4.76E-02
Q01628	IFITM3	2.522	3.00E-02	6.535	3.88E-03	Q5ST30	VARS2	0.298	9.29E-03	0.211	8.43E-04
Q9NUQ9	CYRIB	2.454	2.91E-02	3.226	2.25E-03	Q9H0X4	FAM234A	0.218	2.70E-02	0.339	1.84E-02
Q99614	TTC1	2.423	4.18E-02	2.385	1.81E-04	Q9Y6Q5	APIM2	0.125	3.79E-02	0.113	4.75E-03
A0A0C4DH38	IGHV5-51	2.340	1.57E-02	24.488	9.18E-05	Q6ZMH5	SLC39A5	0.000	1.20E-02	0.000	4.79E-02
Q86VB7	CD163	2.279	4.36E-02	5.649	6.36E-03	Q9H4B0	OSGEPL1	0.000	3.96E-02	0.000	5.22E-03
Q7Z222	EFL1	2.268	3.67E-02	3.153	1.44E-02						
Q13630	GFUS	2.239	1.75E-02	2.838	1.43E-02						
Q9H3G5	CPVL	2.227	4.43E-03	2.092	1.86E-02						
P40222	TXLNA	2.214	4.77E-02	9.263	2.21E-03						
Q92556	ELMO1	2.178	1.02E-02	2.020	7.81E-03						
Q5JS37	NHLRC3	2.108	2.30E-02	2.047	2.92E-03						
Q7L5L3	GDPD3	2.041	1.66E-02	2.050	3.28E-02						
P01833	PIGR	2.032	6.59E-03	3.182	1.10E-03						
O95372	LYPLA2	2.032	1.63E-02	1.663	3.07E-02						
P21589	NTSE	1.957	3.26E-04	2.548	1.69E-04						
P55209	NAP1L1	1.919	5.60E-03	2.837	2.78E-04						
P04066	FUCA1	1.845	2.59E-02	2.257	5.11E-03						
P20933	AGA	1.841	1.91E-02	2.692	2.59E-02						
Q7L1Q6	BZW1	1.832	4.98E-02	5.520	1.44E-03						
Q14232	EIF2B1	1.827	3.33E-02	13.281	4.84E-05						
P21980	TGM2	1.793	2.50E-02	3.933	6.21E-04						
Q14444	CAPRIN1	1.763	2.00E-02	1.825	1.87E-02						
P62857	RPS28	1.727	4.35E-03	1.523	1.69E-02						
Q9GZP4	P1THD1	1.727	4.05E-02	1.610	7.07E-03						
P06865	HEXA	1.655	6.50E-03	2.905	1.24E-04						
Q9Y3E5	PTRH2	1.646	1.20E-02	1.841	2.30E-03						
P49773	HINT1	1.640	3.19E-03	1.592	5.49E-03						
Q96DB5	RMDN1	1.623	3.61E-02	2.095	7.29E-03						
P49441	INPP1	1.590	4.58E-02	1.993	1.46E-02						
P17096	HMGA1	1.584	1.39E-02	1.765	3.97E-02						
Q9BQG2	NUDT12	1.582	7.70E-03	2.182	3.53E-02						
Q9NVZ3	NECAP2	1.572	1.63E-02	3.206	1.75E-05						
Q9NUQ6	SPATS2L	1.569	5.43E-03	2.725	3.89E-03						
Q96BW5	PTER	1.555	3.94E-02	1.741	2.36E-02						
P07686	HEXB	1.553	1.26E-02	2.618	4.08E-06						
P05387	RPLP2	1.519	4.56E-02	1.884	2.25E-02						

Supplementary Table 6. The differentially expressed proteins between tubular atrophy group and non-tubular atrophy/NC group

Both upregulated proteins						Both downregulated proteins					
UniProt ID	Gene symbol	Fold change		Fold change		UniProt ID	Gene symbol	Fold change		Fold change	
		(Tubular atrophy, yes vs. no)	<i>P</i> value	(Tubular atrophy vs. NC)	<i>P</i> value			(Tubular atrophy, yes vs. no)	<i>P</i> value	(Tubular atrophy vs. NC)	<i>P</i> value
P01764	IGHV3-23	12.865	3.23E-02	10.118	3.78E-02	Q8NBN7	RDH13	0.658	4.19E-02	0.467	7.71E-04
Q96GQ5	RUSF1	6.166	3.53E-03	4.858	3.62E-03	P07947	YES1	0.607	2.01E-02	0.649	4.11E-02
P63313	TMSB10	6.015	1.17E-03	13.431	2.39E-04	Q9Y399	MRPS2	0.601	3.83E-02	0.478	1.19E-02
P14207	FOLR2	5.996	2.11E-02	6.941	6.73E-03	P82930	MRPS34	0.546	1.11E-02	0.552	2.18E-02
O75150	RNF40	5.149	4.19E-03	9.497	1.34E-03	Q13268	DHRS2	0.543	4.30E-02	0.241	2.85E-03
P01861	IGHG4	4.700	1.76E-03	2.042	4.15E-02	Q9NXU5	ARL15	0.495	4.45E-02	0.478	1.53E-02
Q15059	BRD3	4.454	3.36E-02	9.084	1.33E-02	Q92665	MRPS31	0.483	2.16E-02	0.415	3.05E-03
O94855	SEC24D	3.791	1.92E-02	5.349	1.21E-02	P17152	TMEM11	0.467	2.90E-02	0.258	3.36E-02
Q99519	NEU1	3.757	3.49E-02	4.422	1.23E-02	Q08174	PCDH1	0.377	3.85E-02	0.337	6.50E-03
Q2TAA2	IAH1	3.702	1.36E-02	2.790	6.40E-03	Q86SQ0	PHLDB2	0.350	2.92E-02	0.275	2.02E-02
P01714	IGLV3-19	3.592	3.01E-02	24.248	5.26E-03	Q86X10	RALGAPB	0.345	6.58E-03	0.361	1.51E-02
Q8N3F0	MTURN	3.556	7.32E-03	4.345	1.29E-03	Q9P260	RELCH	0.338	1.14E-02	0.333	5.86E-03
O43765	SGTA	3.332	3.17E-02	2.830	2.53E-02	Q8N4C8	MINK1	0.333	1.37E-02	0.355	2.35E-02
Q70E73	RAPH1	3.245	4.68E-02	4.387	1.28E-02	Q9BXJ9	NAA15	0.258	1.08E-02	0.155	4.29E-02
A0A0C4DH41	IGHV4-61	3.002	4.31E-02	18.136	7.43E-03	Q8IY67	RAVER1	0.253	7.36E-03	0.239	1.85E-02
Q01628	IFITM3	2.948	6.68E-03	6.908	6.98E-04	Q9UHW9	SLC12A6	0.252	1.35E-02	0.230	7.71E-03
P18621	RPL17	2.904	3.86E-03	1.963	1.60E-02	Q6PCB7	SLC27A1	0.238	2.14E-02	0.193	3.61E-03
P01857	IGHG1	2.871	1.70E-03	5.287	3.03E-04	O43716	GATC	0.229	1.87E-02	0.151	6.98E-03
Q12805	EFEMP1	2.868	1.54E-02	1.939	2.73E-02	Q9P206	KIAA1522	0.179	5.22E-03	0.305	2.57E-02
O00754	MAN2B1	2.791	4.40E-04	3.037	3.06E-04	Q9Y6Q5	AP1M2	0.125	3.79E-02	0.113	4.75E-03
A0A075B6P5	IGKV2-28	2.684	3.29E-02	5.541	8.70E-03	Q7RTP6	MICAL3	0.000	7.15E-05	0.000	4.38E-05
P01743	IGHV1-46	2.676	3.11E-02	3.566	2.98E-02	Q2M3D2	EXOC3L2	0.000	5.87E-04	0.000	2.81E-03
P01042	KNG1	2.647	1.75E-03	3.531	3.97E-03	O95900	TRUB2	0.000	5.44E-03	0.000	1.32E-04
Q86VB7	CD163	2.470	2.23E-02	5.827	3.45E-03	Q6ZMH5	SLC39A5	0.000	1.20E-02	0.000	4.79E-02
P05156	CFI	2.413	4.05E-02	7.771	2.87E-03	Q9C0H2	TTYH3	0.000	3.32E-02	0.000	4.66E-02
Q8N2S1	LTBP4	2.278	1.85E-02	4.686	7.60E-03	Q9NX20	MRPL16	0.000	3.94E-02	0.000	3.95E-03
P02766	TTR	2.261	7.44E-03	4.808	7.14E-05	O43155	FLRT2	0.000	4.89E-02	0.000	1.78E-05
Q9UBX5	FBLN5	2.202	2.07E-02	3.200	4.57E-03						
P02790	HPX	2.164	7.27E-04	2.354	1.50E-02						
P01009	SERPINA1	2.075	2.40E-02	6.253	6.14E-04						
Q9Y2B0	CNPY2	1.967	1.37E-02	1.640	2.29E-02						
P16989	YBX3	1.935	6.31E-03	2.853	1.93E-03						
P41222	PTGDS	1.933	3.47E-02	3.576	8.93E-04						
P62857	RPS28	1.865	1.21E-04	1.577	4.46E-03						
P01019	AGT	1.836	3.15E-02	6.683	1.91E-04						
Q5SNT2	TMEM201	1.794	2.83E-02	5.682	7.52E-04						
Q8NFAQ	TOR1AIP2	1.717	3.62E-02	1.500	3.63E-02						
P08962	CD63	1.708	1.89E-02	4.119	6.19E-04						
P25311	AZGP1	1.688	4.07E-02	2.146	1.06E-02						
P05387	RPLP2	1.674	6.34E-03	1.974	8.98E-03						
O00244	ATOX1	1.670	3.92E-02	2.077	4.61E-02						
P21589	NTSE	1.624	4.07E-02	2.340	5.86E-03						
P62244	RPS15A	1.619	2.74E-02	1.582	3.10E-02						
Q13162	PRDX4	1.611	2.24E-02	2.029	6.31E-03						
Q6NXS1	PPP1R2B	1.601	1.06E-03	2.533	1.38E-03						
O15511	ARPCS5	1.598	2.32E-02	1.600	9.79E-03						
Q96BW5	PTER	1.598	2.51E-02	1.765	1.86E-02						
P06865	HEXA	1.574	2.14E-02	2.835	1.99E-04						
Q9UNL2	SSR3	1.559	3.00E-03	1.840	7.48E-04						
Q8IV08	PLD3	1.551	4.33E-02	2.078	1.35E-02						
P49773	HINT1	1.531	2.12E-02	1.539	1.35E-02						
P61011	SRP54	1.521	3.80E-02	2.887	2.80E-04						

Supplementary Table 7. The differentially expressed proteins between interstitial fibrosis group and non-interstitial fibrosis/NC group.

Both upregulated proteins						Both downregulated proteins					
UniProt ID	Gene symbol	Fold change (Interstitial fibrosis, ves vs. no)	<i>P</i> value	Fold change (Interstitial fibrosis vs. NC)	<i>P</i> value	UniProt ID	Gene symbol	Fold change (Interstitial fibrosis, ves vs. no)	<i>P</i> value	Fold change (Interstitial fibrosis vs. NC)	<i>P</i> value
Q99519	NEU1	7.875	4.95E-03	4.392	5.70E-03	P82930	MRPS34	0.566	8.85E-03	0.599	2.22E-02
Q15059	BRD3	7.286	1.97E-02	8.542	9.79E-03	Q96JQ2	CLMN	0.657	3.89E-02	0.520	8.69E-04
P63313	TMSB10	6.898	6.33E-03	11.725	1.30E-03	Q9NXU5	ARL15	0.484	1.81E-02	0.502	9.60E-03
Q2TAA2	IAH1	5.177	6.46E-03	2.629	6.04E-03	Q7Z3D6	DGLUCY	0.495	1.18E-02	0.477	1.93E-02
Q8N3F0	MTURN	3.990	1.10E-02	3.951	2.40E-03	O75438	NDUFB1	0.660	3.12E-02	0.453	1.21E-04
Q12805	EFEMP1	3.618	5.92E-03	1.851	2.55E-02	O76041	NEBL	0.630	2.02E-02	0.445	3.73E-03
P07093	SERPINE2	3.068	6.33E-03	3.438	4.54E-03	Q9P260	RELCH	0.443	3.71E-02	0.445	1.61E-02
P01011	SERPINA3	2.978	1.14E-02	19.764	2.06E-04	Q8N4C8	MINK1	0.380	1.25E-02	0.430	2.66E-02
Q5JSH3	WDR44	2.813	2.15E-02	2.522	8.14E-03	Q13884	SNTB1	0.541	2.09E-02	0.427	2.46E-02
P29622	SERPINA4	2.676	4.73E-02	2.055	4.35E-02	Q5TCH4	CYP4A22	0.249	4.03E-02	0.404	1.86E-02
P05156	CFI	2.644	3.53E-02	7.315	2.04E-03	Q08174	PCDH1	0.379	1.66E-02	0.369	3.80E-03
P02766	TTR	2.634	1.54E-03	4.637	3.22E-05	Q86SQ0	PHLDB2	0.381	2.08E-02	0.320	1.47E-02
Q9NUQ9	CYRIB	2.599	3.22E-02	3.003	2.70E-03	Q16798	ME3	0.463	4.06E-02	0.296	9.40E-03
P01857	IGHG1	2.508	2.43E-02	4.604	2.67E-03	P17152	TMEM11	0.507	3.23E-02	0.292	2.28E-02
P01031	C5	2.487	3.82E-02	3.061	1.62E-02	Q9BXJ9	NAA15	0.394	4.68E-02	0.239	4.13E-02
O15439	ABCC4	2.450	3.07E-02	9.104	8.32E-04	Q7RTP6	MICAL3	0.175	5.03E-03	0.236	1.12E-02
P01042	KNG1	2.419	1.73E-02	3.131	1.09E-02	O43716	GATC	0.264	9.28E-03	0.191	4.04E-03
Q8N2S1	LTBP4	2.300	2.85E-02	4.333	7.61E-03	Q8WVM0	TFB1M	0.209	4.92E-02	0.166	2.19E-02
O00754	MAN2B1	2.295	2.74E-02	2.602	1.00E-02	Q2M3D2	EXOC3L2	0.224	2.74E-02	0.161	9.20E-03
Q9UBX5	FBLN5	2.239	2.85E-02	2.975	5.19E-03	P31151	S100A7	0.275	4.30E-02	0.120	1.68E-02
P01009	SERPINA1	2.178	2.28E-02	5.906	4.35E-04	O95900	TRUB2	0.203	4.23E-02	0.102	3.06E-04
P01833	PIGR	2.147	5.01E-03	3.019	8.98E-04	Q9Y6Q5	AP1M2	0.083	2.00E-03	0.090	1.57E-03
Q5JS37	NHLRC3	2.114	3.41E-02	1.903	6.34E-03	P82673	MRPS35	0.040	1.33E-02	0.021	4.29E-06
P29350	PTPN6	2.057	3.30E-02	2.697	1.67E-03	Q6ZMH5	SLC39A5	0.000	1.49E-04	0.000	2.70E-02
P02748	C9	1.948	3.76E-02	2.753	7.87E-03						
P02790	HPX	1.942	1.75E-02	2.105	3.61E-02						
Q9Y4P1	ATG4B	1.872	2.55E-02	1.716	3.37E-02						
P55209	NAPIL1	1.863	1.63E-02	2.631	6.97E-04						
Q99538	LGMN	1.856	3.28E-02	2.566	6.36E-03						
P01024	C3	1.837	2.70E-02	1.998	1.96E-02						
P05090	APOD	1.828	4.97E-03	2.376	7.45E-05						
P04066	FUCA1	1.828	3.90E-02	2.116	6.59E-03						
P20933	AGA	1.788	3.82E-02	2.506	2.75E-02						
P06865	HEXA	1.780	1.01E-03	2.836	4.60E-05						
Q14444	CAPRIN1	1.774	2.52E-02	1.727	2.19E-02						
Q9GZP4	PITHD1	1.745	4.52E-02	1.530	1.13E-02						
P21589	NTSE	1.708	2.48E-02	2.271	3.53E-03						
P49773	HINT1	1.667	3.08E-03	1.524	7.27E-03						
Q9NVZ3	NECAP2	1.667	5.30E-03	3.133	5.57E-06						
Q9NR19	ACSS2	1.634	2.44E-02	2.022	6.73E-03						
O15511	ARPCS	1.632	2.02E-02	1.539	1.03E-02						
Q13162	PRDX4	1.631	2.30E-02	1.943	5.48E-03						
Q96BW5	PTER	1.608	2.81E-02	1.687	1.87E-02						
P61960	UFM1	1.606	4.85E-02	1.606	4.85E-02						
P07686	HEXB	1.599	7.97E-03	2.533	3.09E-06						
P05387	RPLP2	1.586	2.73E-02	1.837	1.54E-02						
Q8NBS9	TXNDC5	1.551	1.24E-02	1.518	6.60E-03						
Q6NXS1	PPP1R2B	1.528	9.70E-03	2.373	1.95E-03						