SUPPLEMENT

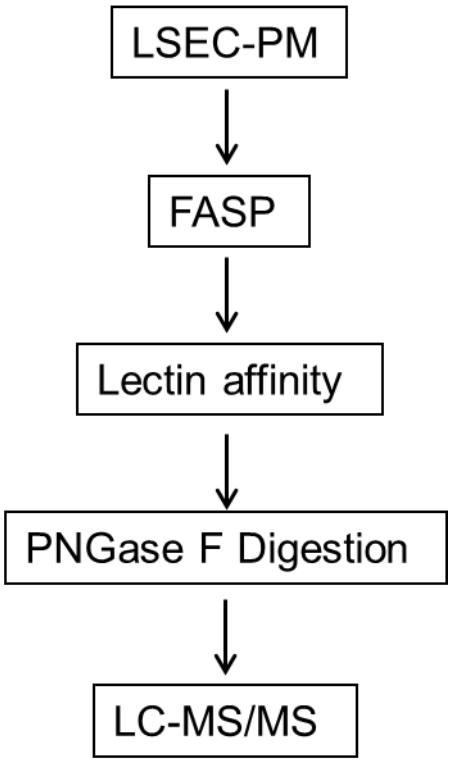
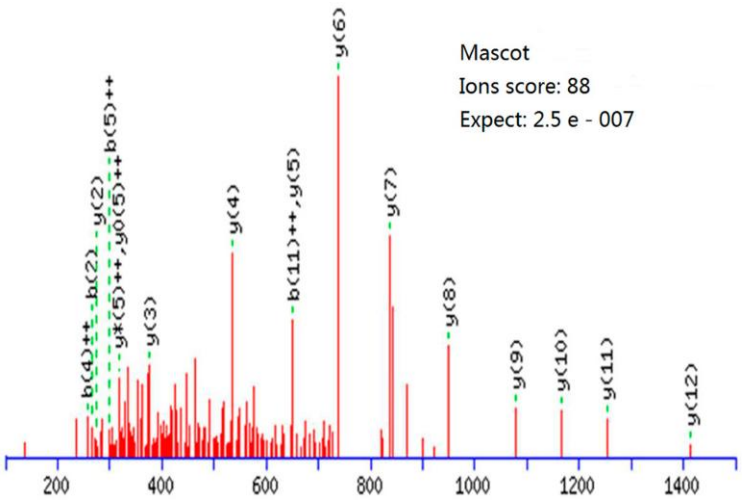


Fig. S1. Work flow diagram of LSEC-PM N-glycopeptide affinity enrichment and identification procedure. Proteins were digested with trypsin by FASP method. The glycan structures were removed by peptide-N-glycosidase F treatment. The enriched N-glycopeptides were analyzed by LC-MS/MS.



#	b	b^{++}	Seq.	y	y^{0++}	#
1	102.0550	51.5311	T			14
2	265.1183	133.0628	Y	1576.6618	779.8292	13
3	425.1489	213.0781	C	1413.5985	698.2976	12
4	512.1810	256.5941	S	1253.5678	618.2823	11
5	599.2130	300.1101	S	1166.5358	574.7662	10
6	728.2556	364.6314	E	1079.5037	531.2502	9
7	841.3396	421.1735	L	950.4612	466.7289	8
8	940.4081	470.7077	V	837.3771	410.1869	7
9	1027.4401	514.2237	S	738.3087	360.6527	6
10	1142.4670	571.7372	N	651.2766	317.1367	5
11	1302.4977	651.7525	C	536.2497	259.6232	4
12	1403.5454	702.2763	T	376.2191	179.6079	3
13	1531.6039	766.3056	Q	275.1714		2
14			K	147.1128		1

Fig. S2. Identification of the glycosylation site of CD164. MS/MS spectrum of the N-linked tryptic peptide, TYCSSELVSN#CTQK, from CD164 (sialomucin core protein 24) glycoprotein precursor. Asn97 was converted to Asp by peptide-N-glycosidase F as evident from the mass difference of 115 Da between fragments y4 and y5.

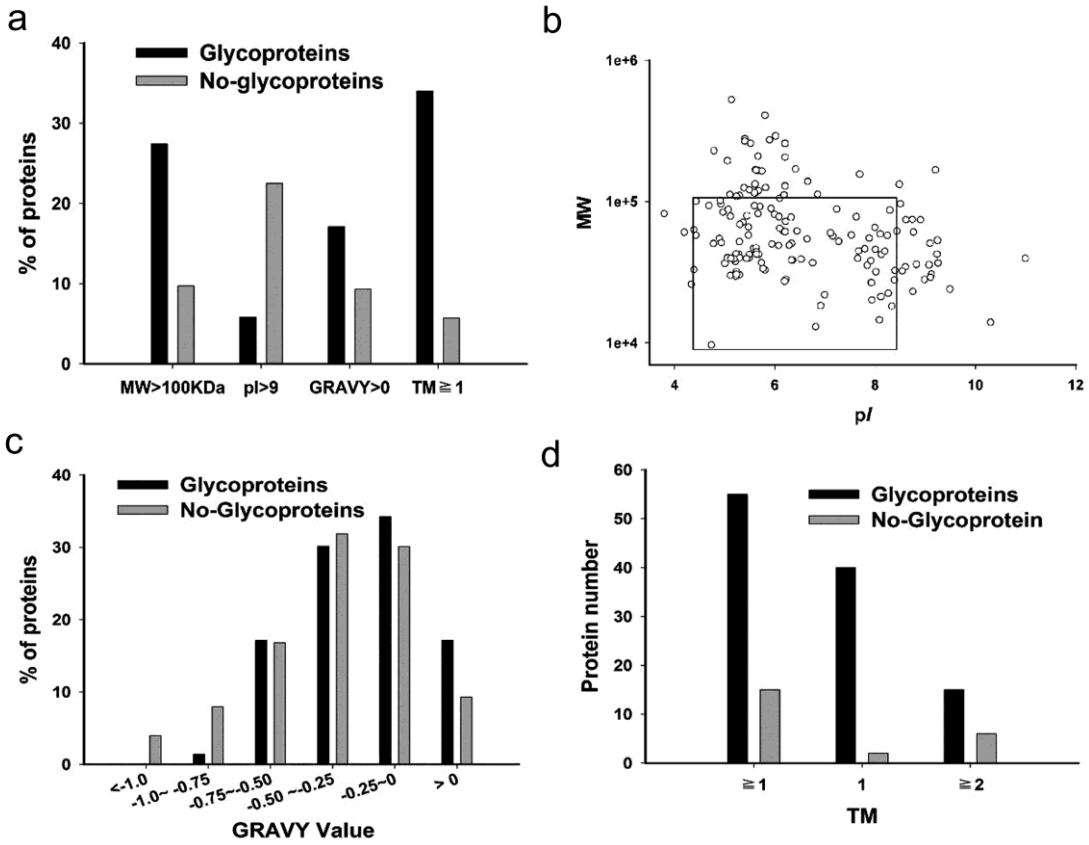


Fig. S3. hysicochemical properties of the identified glycoproteins and non-glycoproteins. a) The percentages of glycoproteins and non-glycoproteins with indicated physicochemical characteristics. b) The calculated p*I* values of the identified N-glycoproteins were plotted against the corresponding calculated molecular weight on a logarithmic scale. c) GRAVY values of identified glycoproteins and non-glycoproteins. d) Comparison of TM distribution among glycoproteins and non-glycoproteins.