

Supplementary Information for

Quantitative Proteomic and Glycoproteomic Analysis Identifies CLCA1, FBN1, and FGB as Potential Biomarkers for Ulcerative Colitis

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Supplementary materials and methods

Reverse transcription quantitative polymerase chain reaction

Total RNA was extracted from colon tissue using the TRIzol method. Subsequently, the BeyoFast™ SYBR Green One-Step qRT-PCR Kit (Beyotime, Shanghai) was used to perform the reaction in 96-well plates according to the One-Step qRT-PCR system instructions. GAPDH was used as the internal reference gene to detect the mRNA expression levels of CLCA1, FBN1, and FGB. The relative gene expression was calculated using the $-\Delta\Delta C_t$ method. The experiment included 3 biological replicates and 3 technical replicates to ensure data reliability. The primer sequences used are detailed in **Table S1**.

Mass spectrometry data processing and protein/glycoprotein identification

Global protein analysis

Raw mass spectrometry files underwent label-free quantification (LFQ) and non-glycopeptide identification using Proteome Discoverer (v2.4, Thermo Fisher Scientific). The integrated workflow, "CWF_Comprehensive_Enhanced Annotation_LFQ_and_Precursor_Quan," was employed, with the processing step configured as "PWF_OT_Precursor_Quan_and_LFQ_CID_SequestHT_Percolator." Searches were performed against the UniProt human complete proteome database, with trypsin specified as the protease allowing up to two missed cleavages¹. Carbamidomethylation (+57.021 Da) on cysteine was set as a fixed modification. Variable modifications included oxidation (+15.955 Da) on methionine, dioxidation (+31.990 Da) on methionine and tryptophan, acetylation (+42.011 Da) on protein N-termini, deamidation (+0.984 Da) on asparagine, glutamine to pyro-glutamic acid (-17.027 Da), and glutamic acid to pyro-glutamic acid (-18.011 Da). Within the Sequest HT module, the mass analyzer was set to FTMS, and MS² scanning utilized high-energy collision dissociation (HCD) for fragmentation. Peptide-spectrum matches (PSMs) were subsequently validated at a 1% false discovery rate (FDR) using Percolator.

Glycoprotein analysis

For glycopeptide analysis, raw files from enriched samples were converted to mzML format using MSConvert. N-glycopeptide identification was subsequently performed with MSFragger (v21.1) employing the predefined glyco-N-LFQ workflow ². Searches were conducted against a human glycoprotein subset database derived from UniProt entries, and the "N-glycan 309 mammalian no sodium" library from Byonic (containing 309 protonated [M+H]⁺ glycan compositions) was utilized ³. Trypsin digestion was set to be fully specific, allowing for a maximum of two missed cleavages. Fragmentation parameters were optimized for Q-TOF/HCD-type instrumentation. Variable modifications included peptide N-terminal glutamine/cysteine cyclization (nQnC, -17.0265 Da) and N-terminal glutamate cyclization (nE, -18.0106 Da). Finally, results were filtered at a 1% false discovery rate (FDR) at the glycopeptide level.

Statistical test

Statistical data were visualized and quantified using ImageJ software ⁴, and a t-test was performed to compare the two groups.

Supplementary Figures and Tables

Figure S1. A comparison of protein glycosylation in UC versus PCA is shown. The relative abundance of each glycoform, as listed in Table S3, was calculated by dividing its accumulated intensity by the total intensity of all glycopeptides. * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$.

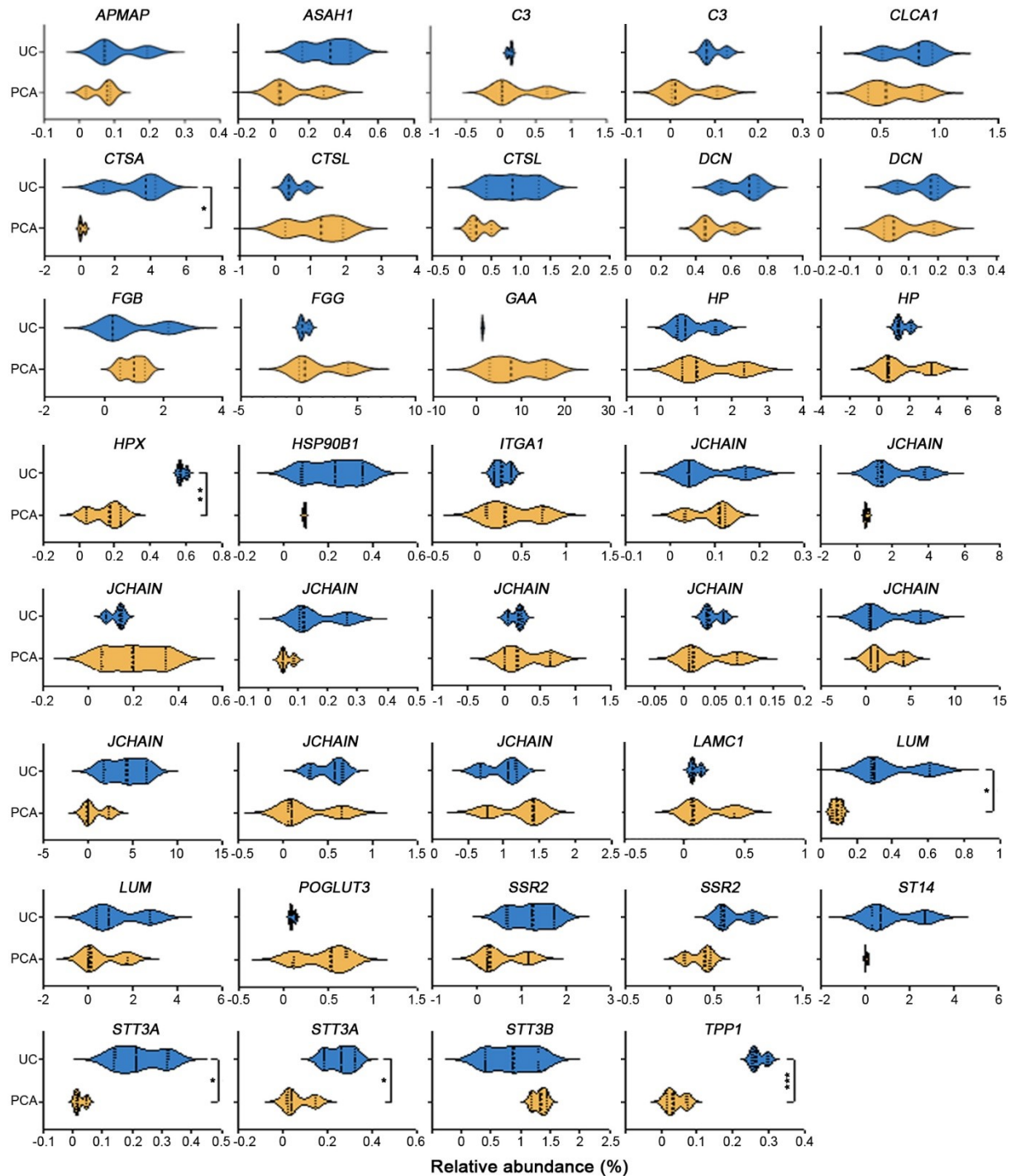


Table S1. Primer sequences for three genes associated with UC. *CLCA1*, *FBN1* and *FGB* are three genes present in colon tissue and serum.

Gene	Primer	Primer Sequence (5' to 3')
<i>CLCA1</i>	Forward	AATCGACCCCAATGTGCCAG
	Reverse	GACTCAGCAACCAGAACATCA
<i>FBN1</i>	Forward	GATCCAACCACGTGCATCAG
	Reverse	TACAGGTGTAGTTGCCAACGG
<i>FGB</i>	Forward	GACCTGGACAAAGCCAACCT
	Reverse	CAGGTCACCTTGGCATCTTC
<i>GAPDH</i>	Forward	GTCTCCTCTGACTTCAACAGCG
	Reverse	ACCACCCTGTTGCTGTAGCCAA

Table S2. Differentially regulated global proteins in UC compared to PCA tissues. P-values
were calculated using Student's T-test.

Accession	Gene	PCA		UC		Log ₂ (FC)	p-Value	q-value	
		(Relative abundance)		(Relative abundance)					
		Mean	STD	Mean	STD				FC
Q9Y6R7	<i>FCGBP</i>	0.029	0.011	0.030	0.036	1.05	0.069	9.51E-01	0.983
Q09666	<i>AHNAK</i>	0.016	0.002	0.015	0.010	0.97	-0.045	9.39E-01	0.982
P21333	<i>FLNA</i>	0.052	0.034	0.007	0.013	0.15	-2.784	1.03E-01	1.131
Q9Y490	<i>TLN1</i>	0.011	0.003	0.008	0.007	0.70	-0.508	4.51E-01	0.812
Q14204	<i>DYNC1H1</i>	0.003	0.001	0.003	0.002	1.05	0.067	9.17E-01	0.990
A8K7I4	<i>CLCA1</i>	0.040	0.012	0.005	0.006	0.12	-3.012	9.51E-03	0.731
P01024	<i>C3</i>	0.010	0.006	0.003	0.004	0.34	-1.549	1.88E-01	1.044
P07355	<i>ANXA2</i>	0.025	0.020	0.024	0.021	0.95	-0.074	9.44E-01	0.985
O60701	<i>UGDH</i>	0.004	0.002	0.008	0.010	1.80	0.844	5.83E-01	0.893
P22314	<i>UBA1</i>	0.008	0.002	0.006	0.001	0.73	-0.446	2.02E-01	1.058
P55072	<i>VCP</i>	0.007	0.001	0.006	0.005	0.87	-0.197	7.76E-01	0.936
P25705	<i>ATP5F1A</i>	0.018	0.010	0.016	0.010	0.91	-0.138	8.52E-01	0.967
P29401	<i>TKT</i>	0.012	0.001	0.008	0.007	0.66	-0.602	3.61E-01	0.914
Q12864	<i>CDH17</i>	0.004	0.002	0.003	0.003	0.63	-0.658	5.23E-01	0.858
P35900	<i>KRT20</i>	0.000	0.000	0.013	0.006	60.26	5.913	1.66E-02	0.850
P00338	<i>LDHA</i>	0.009	0.004	0.009	0.007	1.06	0.084	9.18E-01	0.986
P12532	<i>CKMT1A</i>	0.003	0.002	0.005	0.005	1.49	0.576	6.59E-01	0.912
P00326	<i>ADH1C</i>	0.002	0.001	0.003	0.004	1.49	0.577	7.22E-01	0.912
P06744	<i>GPI</i>	0.009	0.002	0.007	0.006	0.82	-0.285	6.94E-01	0.911
P08727	<i>KRT19</i>	0.001	0.002	0.015	0.012	12.54	3.648	1.22E-01	1.042
P62937	<i>PPIA</i>	0.054	0.018	0.020	0.015	0.38	-1.403	7.14E-02	1.266
P42765	<i>ACAA2</i>	0.005	0.002	0.003	0.003	0.61	-0.713	4.47E-01	0.811
P35555	<i>FBN1</i>	0.000	0.000	0.004	0.001	9.27	3.212	3.09E-03	0.475
P26038	<i>MSN</i>	0.003	0.001	0.003	0.003	1.06	0.088	9.27E-01	0.982
P09211	<i>GSTP1</i>	0.009	0.004	0.007	0.006	0.80	-0.328	7.12E-01	0.907
P28838	<i>LAP3</i>	0.003	0.002	0.005	0.003	1.51	0.593	4.62E-01	0.819
P68366	<i>TUBA4A</i>	0.002	0.001	0.002	0.002	1.34	0.418	6.77E-01	0.910

P30086	<i>PEBP1</i>	0.006	0.001	0.003	0.003	0.54	-0.878	2.05E-01	1.039
P02675	<i>FGB</i>	0.007	0.002	0.002	0.002	0.31	-1.711	2.95E-02	1.236
Q00839	<i>HNRNPU</i>	0.009	0.004	0.010	0.008	1.13	0.177	8.24E-01	0.957
P53621	<i>COPA</i>	0.001	0.001	0.005	0.003	4.23	2.080	9.18E-02	1.176
Q99497	<i>PARK7</i>	0.006	0.001	0.003	0.002	0.55	-0.852	1.62E-01	1.052
Q01469	<i>FABP5</i>	0.002	0.002	0.002	0.003	1.08	0.104	9.31E-01	0.984
P13010	<i>XRCC5</i>	0.002	0.002	0.001	0.001	0.54	-0.892	3.85E-01	0.829
P31930	<i>UQCRC1</i>	0.003	0.001	0.002	0.002	0.77	-0.383	6.13E-01	0.912
P20700	<i>LMNB1</i>	0.002	0.003	0.003	0.002	1.67	0.736	6.15E-01	0.912
P17858	<i>PFKL</i>	0.002	0.001	0.002	0.002	0.78	-0.357	6.61E-01	0.910
Q06210	<i>GFPT1</i>	0.001	0.000	0.002	0.001	2.01	1.004	2.64E-01	1.031
Q15084	<i>PDIA6</i>	0.004	0.002	0.010	0.010	2.11	1.080	4.37E-01	0.816
P27824	<i>CANX</i>	0.003	0.000	0.003	0.003	1.22	0.291	7.26E-01	0.914
P04040	<i>CAT</i>	0.004	0.002	0.002	0.002	0.49	-1.033	2.92E-01	0.983
P04843	<i>RPN1</i>	0.002	0.001	0.003	0.003	1.60	0.675	5.21E-01	0.861
Q86VP6	<i>CAND1</i>	0.001	0.001	0.002	0.001	1.82	0.863	2.07E-01	1.026
Q06830	<i>PRDX1</i>	0.007	0.003	0.008	0.007	1.12	0.167	8.55E-01	0.968
P31040	<i>SDHA</i>	0.003	0.001	0.001	0.001	0.52	-0.955	2.67E-01	1.034
Q9Y678	<i>COPG1</i>	0.001	0.000	0.003	0.001	3.09	1.628	1.38E-02	0.909
P0DOX7	/	0.000	0.000	0.013	0.022	54.32	5.763	3.78E-01	0.842
P36578	<i>RPL4</i>	0.005	0.001	0.004	0.003	0.83	-0.274	7.03E-01	0.905
P31939	<i>ATIC</i>	0.003	0.001	0.002	0.001	0.59	-0.757	2.02E-01	1.046
P05141	<i>SLC25A5</i>	0.002	0.002	0.002	0.002	1.11	0.154	8.89E-01	0.983
P07737	<i>PFN1</i>	0.026	0.007	0.017	0.014	0.65	-0.624	3.74E-01	0.866
P50990	<i>CCT8</i>	0.002	0.001	0.002	0.001	1.03	0.045	9.35E-01	0.982
P28331	<i>NDUFS1</i>	0.001	0.001	0.001	0.001	1.36	0.447	5.27E-01	0.858
P01861	<i>IGHG4</i>	0.004	0.003	0.001	0.002	0.31	-1.690	2.28E-01	1.051
P31947	<i>SFN</i>	0.001	0.000	0.002	0.001	1.44	0.525	3.92E-01	0.821
Q14651	<i>PLS1</i>	0.001	0.001	0.002	0.002	1.37	0.449	7.14E-01	0.907
P32119	<i>PRDX2</i>	0.006	0.001	0.005	0.004	0.73	-0.458	5.07E-01	0.847
P21399	<i>ACO1</i>	0.001	0.000	0.001	0.000	1.18	0.241	5.22E-01	0.859
P55084	<i>HADHB</i>	0.004	0.001	0.006	0.003	1.30	0.374	4.96E-01	0.831
Q08211	<i>DHX9</i>	0.001	0.002	0.001	0.001	0.91	-0.136	9.06E-01	0.990

P01871	<i>IGHM</i>	0.001	0.000	0.003	0.003	4.31	2.108	2.67E-01	1.026
P48735	<i>IDH2</i>	0.007	0.001	0.005	0.003	0.65	-0.611	2.95E-01	0.971
P33176	<i>KIF5B</i>	0.001	0.000	0.001	0.001	0.68	-0.546	4.37E-01	0.812
Q96199	<i>SUCLG2</i>	0.004	0.003	0.003	0.003	0.57	-0.818	4.38E-01	0.811
P11678	<i>EPX</i>	0.005	0.008	0.004	0.000	0.87	-0.201	8.91E-01	0.980
P53618	<i>COPB1</i>	0.001	0.000	0.001	0.001	1.74	0.803	4.64E-01	0.816
P02790	<i>HPX</i>	0.003	0.001	0.002	0.001	0.75	-0.407	4.00E-01	0.812
Q16555	<i>DPYSL2</i>	0.005	0.003	0.006	0.009	1.23	0.301	8.41E-01	0.967
P14550	<i>AKR1A1</i>	0.003	0.001	0.003	0.003	1.15	0.198	8.12E-01	0.950
P04844	<i>RPN2</i>	0.001	0.001	0.002	0.002	3.04	1.604	3.15E-01	0.949
P78527	<i>PRKDC</i>	0.002	0.002	0.001	0.000	0.41	-1.272	3.52E-01	0.938
P04083	<i>ANXA1</i>	0.005	0.000	0.005	0.006	1.08	0.105	9.15E-01	0.993
O60218	<i>AKR1B10</i>	0.000	0.000	0.003	0.002	9.70	3.277	9.14E-02	1.204
P53634	<i>CTSC</i>	0.000	0.000	0.002	0.001	4.70	2.234	1.07E-01	1.050
Q9NR45	<i>NANS</i>	0.004	0.002	0.004	0.001	0.85	-0.235	6.48E-01	0.908
Q9NZ08	<i>ERAP1</i>	0.001	0.001	0.002	0.001	1.81	0.852	4.95E-01	0.833
P07814	<i>EPRS1</i>	0.001	0.001	0.001	0.001	0.96	-0.052	9.50E-01	0.986
P08758	<i>ANXA5</i>	0.008	0.002	0.006	0.003	0.74	-0.435	3.82E-01	0.835
P30048	<i>PRDX3</i>	0.002	0.002	0.003	0.001	2.09	1.062	2.85E-01	0.995
O60547	<i>GMDS</i>	0.002	0.002	0.003	0.002	1.76	0.818	3.05E-01	0.956
Q99832	<i>CCT7</i>	0.002	0.001	0.002	0.001	1.07	0.100	9.20E-01	0.986
P23368	<i>ME2</i>	0.001	0.000	0.001	0.000	2.62	1.389	3.77E-02	1.022
P48047	<i>ATP5PO</i>	0.005	0.002	0.003	0.002	0.66	-0.606	4.05E-01	0.808
P00441	<i>SOD1</i>	0.008	0.003	0.004	0.004	0.45	-1.148	1.81E-01	1.030
P27348	<i>YWHAQ</i>	0.002	0.001	0.002	0.001	0.95	-0.070	9.34E-01	0.983
Q9Y310	<i>RTCB</i>	0.001	0.001	0.001	0.001	1.46	0.541	6.25E-01	0.903
P0DMN0	<i>SULT1A4</i>	0.000	0.000	0.007	0.011	25.28	4.660	3.53E-01	0.935
A0A0B4J2 D5	<i>GATD3B</i>	0.002	0.001	0.001	0.001	0.55	-0.851	4.43E-01	0.810
P62081	<i>RPS7</i>	0.003	0.001	0.002	0.002	0.80	-0.322	6.37E-01	0.904
P02647	<i>APOA1</i>	0.006	0.000	0.006	0.005	0.98	-0.036	9.60E-01	0.990
P07858	<i>CTSB</i>	0.002	0.001	0.002	0.002	1.11	0.151	8.46E-01	0.965
P61160	<i>ACTR2</i>	0.001	0.000	0.002	0.001	1.54	0.622	4.63E-01	0.818
P05387	<i>RPLP2</i>	0.002	0.003	0.003	0.003	1.82	0.867	5.38E-01	0.858

Q13200	<i>PSMD2</i>	0.000	0.000	0.001	0.000	1.14	0.184	8.49E-01	0.966
P80365	<i>HSD11B2</i>	0.000	0.000	0.001	0.001	2.26	1.178	2.94E-01	0.975
P62424	<i>RPL7A</i>	0.003	0.001	0.003	0.002	1.16	0.220	7.81E-01	0.933
Q13011	<i>ECH1</i>	0.003	0.002	0.001	0.001	0.39	-1.364	1.78E-01	1.039
P04066	<i>FUCA1</i>	0.000	0.000	0.003	0.004	11.83	3.565	2.12E-01	1.029
Q9H2U2	<i>PPA2</i>	0.001	0.001	0.001	0.001	0.96	-0.061	9.32E-01	0.983
P16422	<i>EPCAM</i>	0.003	0.001	0.006	0.006	2.19	1.133	3.79E-01	0.836
P52209	<i>PGD</i>	0.002	0.001	0.001	0.001	0.62	-0.699	4.26E-01	0.822
P50570	<i>DNM2</i>	0.001	0.000	0.001	0.001	1.90	0.925	2.54E-01	1.036
P39023	<i>RPL3</i>	0.002	0.001	0.003	0.000	1.31	0.386	4.29E-01	0.824
Q8NFV4	<i>ABHD11</i>	0.001	0.000	0.001	0.001	1.01	0.019	9.84E-01	0.997
Q01995	<i>TAGLN</i>	0.076	0.098	0.005	0.001	0.06	-4.010	2.78E-01	0.993
P04632	<i>CAPNS1</i>	0.001	0.001	0.001	0.001	1.08	0.107	8.70E-01	0.971
Q14974	<i>KPNB1</i>	0.002	0.000	0.001	0.001	0.86	-0.223	7.50E-01	0.924
P62136	<i>PPP1CA</i>	0.000	0.000	0.000	0.000	0.65	-0.632	2.30E-01	1.040
Q16853	<i>AOC3</i>	0.002	0.002	0.001	0.001	0.54	-0.879	3.90E-01	0.829
O15144	<i>ARPC2</i>	0.001	0.001	0.002	0.001	1.86	0.893	4.29E-01	0.821
Q15063	<i>POSTN</i>	0.000	0.000	0.003	0.003	6.97	2.802	2.14E-01	1.028
P24539	<i>ATP5PB</i>	0.001	0.001	0.003	0.002	3.00	1.585	1.69E-01	1.053
P37837	<i>TALDO1</i>	0.005	0.002	0.002	0.002	0.40	-1.307	1.04E-01	1.115
O00159	<i>MYO1C</i>	0.000	0.000	0.000	0.000	0.58	-0.789	2.67E-01	1.017
P18124	<i>RPL7</i>	0.002	0.001	0.006	0.002	3.41	1.768	2.96E-02	1.137
Q9UMS4	<i>PRPF19</i>	0.001	0.001	0.001	0.000	1.29	0.365	6.70E-01	0.911
P53597	<i>SUCLG1</i>	0.003	0.002	0.002	0.001	0.51	-0.966	3.64E-01	0.907
P42224	<i>STAT1</i>	0.000	0.000	0.002	0.002	23.26	4.540	2.29E-01	1.045
O43776	<i>NARS1</i>	0.000	0.000	0.001	0.000	2.15	1.106	2.41E-01	1.038
P10153	<i>RNASE2</i>	0.002	0.003	0.004	0.001	2.05	1.039	3.53E-01	0.930
P30626	<i>SRI</i>	0.003	0.003	0.002	0.002	0.65	-0.627	6.16E-01	0.910
O94760	<i>DDAH1</i>	0.002	0.000	0.001	0.001	0.55	-0.858	1.47E-01	1.027
Q562R1	<i>ACTBL2</i>	0.011	0.013	0.001	0.000	0.05	-4.371	2.43E-01	1.037
P00488	<i>F13A1</i>	0.000	0.000	0.001	0.001	3.36	1.747	1.24E-01	1.039
P06703	<i>S100A6</i>	0.021	0.006	0.031	0.039	1.46	0.542	6.97E-01	0.905
Q15365	<i>PCBP1</i>	0.002	0.001	0.002	0.002	0.99	-0.018	9.82E-01	0.997

P30085	<i>CMPK1</i>	0.004	0.001	0.001	0.001	0.29	-1.776	3.02E-02	1.071
P04792	<i>HSPB1</i>	0.005	0.001	0.004	0.001	0.75	-0.425	2.81E-01	0.996
P05026	<i>ATP1B1</i>	0.001	0.000	0.002	0.002	1.11	0.153	8.91E-01	0.978
P36873	<i>PPP1CC</i>	0.000	0.000	0.001	0.001	5.62	2.490	3.72E-01	0.884
Q6XQN6	<i>NAPRT</i>	0.001	0.000	0.000	0.000	0.36	-1.477	3.65E-02	1.052
Q13162	<i>PRDX4</i>	0.001	0.000	0.002	0.003	3.12	1.641	4.01E-01	0.811
Q9Y2Q3	<i>GSTK1</i>	0.001	0.001	0.002	0.001	1.97	0.975	1.17E-01	1.079
P02671	<i>FGA</i>	0.008	0.003	0.002	0.002	0.27	-1.894	3.13E-02	0.962
P02765	<i>AHSG</i>	0.001	0.001	0.001	0.001	0.49	-1.023	3.79E-01	0.832
P23526	<i>AHCY</i>	0.002	0.001	0.002	0.001	0.74	-0.442	5.96E-01	0.907
P23396	<i>RPS3</i>	0.002	0.001	0.003	0.002	1.39	0.473	6.36E-01	0.905
P07108	<i>DBI</i>	0.001	0.002	0.001	0.001	0.98	-0.028	9.84E-01	0.995
Q15691	<i>MAPRE1</i>	0.001	0.001	0.003	0.004	3.10	1.630	4.36E-01	0.817
Q6P996	<i>PDXDC1</i>	0.001	0.001	0.001	0.001	1.00	-0.006	9.94E-01	1.001
Q02252	<i>ALDH6A1</i>	0.001	0.000	0.001	0.001	0.88	-0.191	7.96E-01	0.946
P61106	<i>RAB14</i>	0.000	0.000	0.001	0.001	1.54	0.620	5.50E-01	0.868
Q15046	<i>KARS1</i>	0.002	0.001	0.001	0.001	0.36	-1.470	1.05E-01	1.076
P62277	<i>RPS13</i>	0.001	0.001	0.002	0.001	1.82	0.862	3.31E-01	0.925
Q9HAT2	<i>SIAE</i>	0.000	0.000	0.000	0.000	1.02	0.032	9.76E-01	0.998
P20618	<i>PSMB1</i>	0.001	0.000	0.001	0.001	1.80	0.844	3.74E-01	0.862
Q9Y6C9	<i>MTCH2</i>	0.001	0.000	0.001	0.000	0.88	-0.192	8.56E-01	0.965
P21796	<i>VDAC1</i>	0.002	0.001	0.003	0.002	1.23	0.298	7.62E-01	0.932
Q96DG6	<i>CMBL</i>	0.001	0.001	0.001	0.001	0.66	-0.590	6.24E-01	0.907
P09525	<i>ANXA4</i>	0.003	0.001	0.007	0.008	2.38	1.251	4.24E-01	0.821
P62906	<i>RPL10A</i>	0.002	0.001	0.002	0.001	1.09	0.129	8.87E-01	0.985
P38606	<i>ATP6V1A</i>	0.000	0.000	0.001	0.001	6.58	2.719	8.96E-02	1.215
Q02878	<i>RPL6</i>	0.002	0.001	0.004	0.002	1.58	0.656	3.43E-01	0.930
Q16881	<i>TXNRD1</i>	0.001	0.000	0.001	0.001	1.94	0.957	3.62E-01	0.912
P62328	<i>TMSB4X</i>	0.011	0.004	0.016	0.014	1.38	0.460	6.26E-01	0.902
P52597	<i>HNRNPF</i>	0.001	0.001	0.001	0.001	2.21	1.144	2.69E-01	1.008
O95202	<i>LETM1</i>	0.000	0.000	0.000	0.001	1.02	0.035	9.76E-01	0.995
Q9Y6C2	<i>EMILIN1</i>	0.000	0.000	0.001	0.001	17.68	4.144	1.21E-01	1.052
Q13423	<i>NNT</i>	0.001	0.000	0.001	0.000	0.61	-0.717	2.87E-01	0.987

P54886	<i>ALDH18A1</i>	0.001	0.000	0.001	0.001	1.56	0.638	4.74E-01	0.821
Q05707	<i>COL14A1</i>	0.001	0.001	0.001	0.001	2.45	1.293	3.04E-01	0.967
P30040	<i>ERP29</i>	0.002	0.001	0.002	0.001	1.11	0.146	8.65E-01	0.968
P12109	<i>COL6A1</i>	0.001	0.002	0.002	0.001	1.56	0.644	5.28E-01	0.857
P10645	<i>CHGA</i>	0.002	0.001	0.002	0.002	1.36	0.447	7.11E-01	0.908
O00571	<i>DDX3X</i>	0.001	0.000	0.001	0.001	1.18	0.242	7.80E-01	0.934
P25786	<i>PSMA1</i>	0.002	0.001	0.002	0.001	0.67	-0.574	4.32E-01	0.816
Q9C002	<i>NMES1</i>	0.001	0.001	0.001	0.002	0.99	-0.010	9.93E-01	1.002
O75131	<i>CPNE3</i>	0.001	0.000	0.000	0.000	0.51	-0.970	4.31E-01	0.821
Q9UNF0	<i>PACSIN2</i>	0.000	0.000	0.000	0.000	2.12	1.082	1.50E-01	1.032
Q02790	<i>FKBP4</i>	0.001	0.000	0.001	0.001	1.00	0.003	9.96E-01	0.998
P25787	<i>PSMA2</i>	0.002	0.001	0.001	0.001	0.53	-0.904	3.08E-01	0.959
P54136	<i>RARS1</i>	0.000	0.000	0.001	0.000	1.90	0.924	2.17E-01	1.031
O60763	<i>USO1</i>	0.001	0.001	0.001	0.000	0.61	-0.711	3.75E-01	0.860
Q15404	<i>RSU1</i>	0.001	0.000	0.001	0.000	0.83	-0.273	6.95E-01	0.910
P58546	<i>MTPN</i>	0.001	0.000	0.001	0.001	1.29	0.367	6.58E-01	0.914
P22234	<i>PAICS</i>	0.002	0.000	0.001	0.000	0.49	-1.022	2.55E-03	0.588
P23786	<i>CPT2</i>	0.000	0.000	0.000	0.000	1.05	0.067	9.17E-01	0.988
Q16777	<i>H2AC20</i>	0.004	0.007	0.001	0.001	0.19	-2.432	4.44E-01	0.809
P14868	<i>DARS1</i>	0.000	0.000	0.001	0.000	3.28	1.715	2.76E-02	1.272
P52907	<i>CAPZA1</i>	0.001	0.000	0.002	0.001	1.49	0.578	3.17E-01	0.943
P16278	<i>GLB1</i>	0.000	0.000	0.001	0.001	7.58	2.921	1.87E-01	1.051
P25774	<i>CTSS</i>	0.001	0.000	0.001	0.001	1.99	0.995	3.60E-01	0.922
O75533	<i>SF3B1</i>	0.000	0.000	0.001	0.000	1.45	0.536	6.27E-01	0.900
P07585	<i>DCN</i>	0.004	0.003	0.001	0.001	0.29	-1.771	1.33E-01	1.039
Q9HDC9	<i>APMAP</i>	0.001	0.000	0.001	0.001	1.85	0.884	1.93E-01	1.047
Q9UUK3	<i>PARP4</i>	0.000	0.000	0.001	0.001	7.02	2.811	3.00E-01	0.967
Q96G03	<i>PGM2</i>	0.001	0.000	0.000	0.000	0.64	-0.654	1.19E-01	1.076
O43488	<i>AKR7A2</i>	0.001	0.000	0.001	0.000	0.80	-0.318	5.72E-01	0.885
P38117	<i>ETFB</i>	0.003	0.001	0.001	0.001	0.38	-1.407	4.84E-02	1.116
P63313	<i>TMSB10</i>	0.003	0.001	0.003	0.002	1.12	0.166	8.41E-01	0.964
O14745	<i>NHERF1</i>	0.001	0.000	0.001	0.000	1.05	0.068	9.24E-01	0.984
P30046	<i>DDT</i>	0.002	0.000	0.001	0.001	0.93	-0.106	7.78E-01	0.934

O43390	<i>HNRNPR</i>	0.001	0.000	0.001	0.001	1.48	0.565	4.47E-01	0.808
Q15393	<i>SF3B3</i>	0.001	0.000	0.001	0.001	1.28	0.356	5.56E-01	0.869
P43304	<i>GPD2</i>	0.000	0.000	0.000	0.000	1.20	0.266	6.91E-01	0.918
P41091	<i>EIF2S3</i>	0.001	0.000	0.002	0.001	3.68	1.879	1.35E-01	1.020
P30050	<i>RPL12</i>	0.002	0.001	0.002	0.001	0.77	-0.376	6.05E-01	0.911
P54920	<i>NAPA</i>	0.000	0.000	0.002	0.002	8.03	3.006	2.83E-01	0.996
P29692	<i>EEF1D</i>	0.001	0.000	0.001	0.001	0.94	-0.094	9.10E-01	0.992
O43837	<i>IDH3B</i>	0.001	0.000	0.000	0.000	0.86	-0.220	8.23E-01	0.958
P47755	<i>CAPZA2</i>	0.000	0.000	0.001	0.001	1.49	0.575	5.34E-01	0.858
P09104	<i>ENO2</i>	0.001	0.001	0.000	0.000	0.20	-2.317	2.36E-01	1.026
P60953	<i>CDC42</i>	0.003	0.001	0.002	0.001	0.49	-1.024	1.73E-01	1.049
P07741	<i>APRT</i>	0.001	0.001	0.001	0.001	0.79	-0.339	6.92E-01	0.917
O75396	<i>SEC22B</i>	0.001	0.000	0.000	0.000	0.68	-0.548	5.50E-01	0.865
P35914	<i>HMGCL</i>	0.000	0.000	0.001	0.002	5.89	2.557	2.89E-01	0.980
Q9UIJ7	<i>AK3</i>	0.001	0.000	0.005	0.009	6.97	2.801	3.97E-01	0.813
P32969	<i>RPL9</i>	0.001	0.000	0.002	0.002	3.89	1.958	2.75E-01	1.006
Q96AE4	<i>FUBP1</i>	0.001	0.000	0.001	0.001	0.67	-0.574	3.71E-01	0.886
Q8NBX0	<i>SCCPDH</i>	0.000	0.000	0.000	0.000	0.88	-0.181	7.96E-01	0.943
P39656	<i>DDOST</i>	0.000	0.000	0.001	0.001	2.23	1.156	3.13E-01	0.956
P36957	<i>DLST</i>	0.001	0.000	0.001	0.001	0.83	-0.274	6.84E-01	0.917
Q01813	<i>PFKP</i>	0.001	0.001	0.001	0.001	0.87	-0.198	8.57E-01	0.964
P08575	<i>PTPRC</i>	0.000	0.000	0.001	0.001	6.58	2.719	5.87E-02	1.230
Q9NTK5	<i>OLA1</i>	0.000	0.000	0.001	0.001	2.22	1.151	3.42E-01	0.933
P18085	<i>ARF4</i>	0.000	0.000	0.001	0.000	2.06	1.042	4.31E-01	0.818
P04217	<i>A1BG</i>	0.002	0.002	0.000	0.000	0.12	-3.051	1.01E-01	1.136
Q9Y5K6	<i>CD2AP</i>	0.001	0.000	0.001	0.001	1.36	0.446	6.31E-01	0.903
Q9HC35	<i>EML4</i>	0.000	0.000	0.001	0.001	1.59	0.670	6.69E-01	0.912
P43034	<i>PAFAH1B1</i>	0.000	0.000	0.001	0.001	10.07	3.332	7.42E-02	1.222
Q9UGI8	<i>TES</i>	0.000	0.000	0.001	0.000	2.27	1.180	2.70E-01	1.004
Q3LXA3	<i>TKFC</i>	0.000	0.000	0.000	0.000	1.45	0.532	6.10E-01	0.910
Q15582	<i>TGFBI</i>	0.001	0.002	0.001	0.001	0.67	-0.580	7.39E-01	0.918
Q02338	<i>BDH1</i>	0.001	0.000	0.002	0.003	4.25	2.087	3.47E-01	0.935
P12270	<i>TPR</i>	0.000	0.000	0.000	0.000	2.52	1.333	2.92E-01	0.975

P11908	<i>PRPS2</i>	0.000	0.000	0.000	0.000	0.78	-0.361	6.97E-01	0.903
O14579	<i>COPE</i>	0.000	0.000	0.001	0.000	7.01	2.810	4.48E-02	1.087
P02763	<i>ORM1</i>	0.003	0.001	0.001	0.001	0.28	-1.848	3.05E-02	1.004
P30043	<i>BLVRB</i>	0.001	0.001	0.000	0.000	0.36	-1.482	1.97E-01	1.044
Q9H9B4	<i>SFXN1</i>	0.000	0.000	0.001	0.001	5.18	2.372	3.24E-01	0.945
P04424	<i>ASL</i>	0.000	0.000	0.000	0.000	0.60	-0.740	3.11E-01	0.956
Q9Y5P6	<i>GMPPB</i>	0.000	0.000	0.002	0.003	13.98	3.805	2.53E-01	1.041
Q9NQW7	<i>XPNPEP1</i>	0.000	0.000	0.000	0.000	1.35	0.432	6.19E-01	0.909
P50502	<i>ST13</i>	0.001	0.000	0.001	0.001	0.88	-0.192	7.70E-01	0.932
Q00688	<i>FKBP3</i>	0.000	0.000	0.001	0.000	1.70	0.768	2.18E-01	1.025
Q99795	<i>GPA33</i>	0.002	0.001	0.001	0.001	0.51	-0.984	2.33E-01	1.033
O75323	<i>NIPSNAP2</i>	0.001	0.000	0.001	0.001	1.38	0.468	6.37E-01	0.901
P55735	<i>SEC13</i>	0.000	0.000	0.000	0.000	1.75	0.804	1.28E-01	1.017
P60866	<i>RPS20</i>	0.002	0.001	0.001	0.001	0.61	-0.706	3.03E-01	0.970
P10599	<i>TXN</i>	0.005	0.002	0.002	0.001	0.44	-1.180	1.39E-01	1.034
P34897	<i>SHMT2</i>	0.000	0.000	0.000	0.000	1.02	0.026	9.70E-01	0.998
Q8TD06	<i>AGR3</i>	0.001	0.000	0.001	0.001	1.43	0.519	6.86E-01	0.914
Q9BWD1	<i>ACAT2</i>	0.000	0.000	0.000	0.000	0.73	-0.457	4.80E-01	0.826
O00231	<i>PSMD11</i>	0.001	0.000	0.001	0.000	1.06	0.082	7.96E-01	0.941
Q9NSD9	<i>FARSB</i>	0.001	0.000	0.000	0.000	0.79	-0.337	5.55E-01	0.870
Q07960	<i>ARHGAP1</i>	0.001	0.000	0.000	0.000	0.56	-0.834	1.05E-01	1.052
P51571	<i>SSR4</i>	0.000	0.000	0.005	0.007	13.61	3.767	2.96E-01	0.968
P46781	<i>RPS9</i>	0.002	0.001	0.003	0.002	1.23	0.301	6.95E-01	0.908
Q15437	<i>SEC23B</i>	0.000	0.000	0.001	0.000	4.92	2.299	1.13E-01	1.063
Q15717	<i>ELAVL1</i>	0.001	0.000	0.001	0.001	2.18	1.125	4.04E-01	0.810
Q9H4G4	<i>GLIPR2</i>	0.001	0.001	0.000	0.000	0.62	-0.701	3.83E-01	0.833
Q16718	<i>NDUFA5</i>	0.000	0.000	0.000	0.000	1.81	0.857	5.50E-02	1.207
P62249	<i>RPS16</i>	0.002	0.001	0.002	0.002	0.95	-0.071	9.36E-01	0.981
Q9P1F3	<i>ABRACL</i>	0.000	0.000	0.000	0.000	3.22	1.687	2.25E-01	1.048
P09874	<i>PARP1</i>	0.001	0.000	0.002	0.002	1.36	0.447	6.97E-01	0.900
Q9HB71	<i>CACYBP</i>	0.000	0.000	0.001	0.001	3.26	1.706	1.41E-01	1.016
P11047	<i>LAMC1</i>	0.000	0.000	0.001	0.001	4.13	2.047	3.90E-01	0.825
Q71UI9	<i>H2AZ2</i>	0.000	0.000	0.001	0.000	1.44	0.523	5.40E-01	0.855

Q9ULZ3	<i>PYCARD</i>	0.000	0.000	0.001	0.000	6.70	2.744	1.40E-01	1.024
P31153	<i>MAT2A</i>	0.001	0.000	0.000	0.000	0.44	-1.196	1.27E-01	1.045
P35527	<i>KRT9</i>	0.001	0.000	0.001	0.001	1.02	0.031	9.72E-01	0.998
P62316	<i>SNRPD2</i>	0.000	0.000	0.000	0.000	1.13	0.178	7.85E-01	0.935
P26373	<i>RPL13</i>	0.003	0.001	0.002	0.001	0.83	-0.276	6.96E-01	0.906
P20674	<i>COX5A</i>	0.002	0.000	0.002	0.002	0.78	-0.364	6.20E-01	0.904
Q01105	<i>SET</i>	0.001	0.000	0.001	0.001	1.20	0.266	8.08E-01	0.948
Q14165	<i>MLEC</i>	0.000	0.000	0.000	0.000	1.08	0.107	8.70E-01	0.969
Q92820	<i>GGH</i>	0.001	0.001	0.000	0.000	0.44	-1.195	4.55E-01	0.813
Q14315	<i>FLNC</i>	0.004	0.004	0.000	0.000	0.10	-3.357	2.51E-01	1.052
Q8N1G4	<i>LRRC47</i>	0.000	0.000	0.000	0.000	1.00	-0.001	9.98E-01	0.998
Q14203	<i>DCTN1</i>	0.000	0.000	0.000	0.000	0.90	-0.151	8.30E-01	0.959
P80723	<i>BASP1</i>	0.000	0.000	0.000	0.000	1.00	0.003	9.94E-01	0.998
P51648	<i>ALDH3A2</i>	0.000	0.000	0.018	0.030	77.77	6.281	3.70E-01	0.893
P54709	<i>ATP1B3</i>	0.000	0.000	0.000	0.000	2.77	1.470	7.70E-02	1.109
O75340	<i>PDCD6</i>	0.000	0.000	0.002	0.004	12.91	3.690	3.73E-01	0.877
Q15293	<i>RCN1</i>	0.000	0.000	0.002	0.002	4.67	2.222	2.57E-01	1.021
Q14444	<i>CAPRIN1</i>	0.000	0.000	0.001	0.001	4.18	2.065	2.04E-01	1.045
P05386	<i>RPLP1</i>	0.001	0.001	0.006	0.006	4.26	2.091	2.76E-01	0.994
Q5SSJ5	<i>HP1BP3</i>	0.001	0.000	0.002	0.003	2.12	1.086	5.19E-01	0.861
P13798	<i>APEH</i>	0.001	0.000	0.001	0.000	0.62	-0.693	3.20E-01	0.940
Q9BZZ5	<i>API5</i>	0.001	0.000	0.000	0.000	0.44	-1.186	1.07E-01	1.028
O15371	<i>EIF3D</i>	0.000	0.000	0.001	0.001	2.93	1.552	3.13E-01	0.949
P26583	<i>HMGB2</i>	0.001	0.001	0.001	0.001	0.82	-0.293	7.63E-01	0.931
O15145	<i>ARPC3</i>	0.001	0.001	0.001	0.001	1.67	0.739	4.16E-01	0.813
Q9BXP5	<i>SRRT</i>	0.000	0.000	0.000	0.000	1.16	0.212	7.65E-01	0.931
O15511	<i>ARPC5</i>	0.001	0.001	0.001	0.000	1.11	0.155	7.31E-01	0.916
P10253	<i>GAA</i>	0.001	0.000	0.000	0.000	0.55	-0.852	2.67E-01	1.009
P51911	<i>CNN1</i>	0.033	0.034	0.006	0.009	0.18	-2.508	2.57E-01	1.013
Q9BRF8	<i>CPPED1</i>	0.000	0.000	0.001	0.001	1.79	0.838	5.23E-01	0.855
P40306	<i>PSMB10</i>	0.000	0.000	0.000	0.000	1.23	0.296	6.63E-01	0.910
P40763	<i>STAT3</i>	0.000	0.000	0.000	0.000	2.40	1.263	1.04E-01	1.090
Q9BPW8	<i>NIPSNAP1</i>	0.001	0.000	0.000	0.000	0.34	-1.538	9.94E-02	1.175

P00167	<i>CYB5A</i>	0.000	0.000	0.001	0.000	7.08	2.823	1.61E-01	1.060
Q8N163	<i>CCAR2</i>	0.001	0.000	0.000	0.000	0.53	-0.912	1.46E-01	1.035
P84090	<i>ERH</i>	0.001	0.000	0.002	0.001	1.52	0.604	9.70E-02	1.177
Q04760	<i>GLO1</i>	0.002	0.001	0.006	0.010	4.00	2.001	4.67E-01	0.815
P35998	<i>PSMC2</i>	0.000	0.000	0.000	0.000	0.78	-0.355	6.17E-01	0.909
Q9UJZ1	<i>STOML2</i>	0.000	0.000	0.000	0.000	1.99	0.994	2.43E-01	1.028
P30049	<i>ATP5F1D</i>	0.001	0.002	0.001	0.001	0.93	-0.101	9.50E-01	0.984
Q96C23	<i>GALM</i>	0.001	0.000	0.000	0.000	0.64	-0.634	3.64E-01	0.902
P13073	<i>COX4I1</i>	0.001	0.000	0.002	0.001	1.38	0.461	6.37E-01	0.898
P10644	<i>PRKAR1A</i>	0.000	0.000	0.002	0.003	18.32	4.195	2.86E-01	0.991
Q09028	<i>RBBP4</i>	0.000	0.000	0.000	0.000	1.27	0.349	6.24E-01	0.905
Q96BQ1	<i>FAM3D</i>	0.002	0.001	0.001	0.001	0.53	-0.916	4.01E-01	0.807
P25788	<i>PSMA3</i>	0.001	0.000	0.001	0.001	1.41	0.499	5.09E-01	0.847
P62314	<i>SNRPD1</i>	0.001	0.001	0.008	0.012	14.68	3.876	3.36E-01	0.928
Q9NUJ1	<i>ABHD10</i>	0.000	0.000	0.000	0.000	1.25	0.319	6.93E-01	0.913
Q96IX5	<i>ATP5MK</i>	0.000	0.000	0.001	0.000	3.12	1.642	7.53E-02	1.197
Q16658	<i>FSCN1</i>	0.000	0.000	0.001	0.000	5.74	2.522	4.56E-03	0.526
Q02978	<i>SLC25A11</i>	0.000	0.000	0.000	0.000	0.86	-0.222	7.76E-01	0.934
Q9HCY8	<i>S100A14</i>	0.000	0.000	0.003	0.004	22.51	4.493	2.55E-01	1.031
P62318	<i>SNRPD3</i>	0.000	0.000	0.001	0.000	1.81	0.853	7.40E-03	0.682
O94903	<i>PLPBP</i>	0.000	0.000	0.001	0.001	2.79	1.478	1.75E-01	1.048
P62269	<i>RPS18</i>	0.002	0.001	0.002	0.001	0.77	-0.369	6.47E-01	0.909
P06702	<i>S100A9</i>	0.001	0.001	0.002	0.002	1.86	0.894	5.29E-01	0.856
P51665	<i>PSMD7</i>	0.000	0.000	0.000	0.000	2.66	1.412	3.26E-01	0.928
P63220	<i>RPS21</i>	0.001	0.000	0.001	0.001	0.62	-0.686	3.17E-01	0.937
Q9NRX4	<i>PHPT1</i>	0.001	0.000	0.001	0.001	1.71	0.771	5.34E-01	0.855
Q92882	<i>OSTF1</i>	0.000	0.000	0.001	0.001	7.43	2.893	2.10E-01	1.030
O00515	<i>LAD1</i>	0.000	0.000	0.000	0.001	1.49	0.580	7.31E-01	0.913
Q8IZ83	<i>ALDH16A1</i>	0.000	0.000	0.000	0.000	3.96	1.987	4.19E-02	1.073
O94874	<i>UFL1</i>	0.000	0.000	0.000	0.000	4.04	2.013	7.65E-02	1.176
Q9BYZ8	<i>REG4</i>	0.001	0.001	0.000	0.000	0.40	-1.312	3.24E-01	0.939
P13716	<i>ALAD</i>	0.000	0.000	0.001	0.001	3.18	1.669	2.97E-01	0.964
P15121	<i>AKR1B1</i>	0.001	0.001	0.002	0.002	1.95	0.965	3.95E-01	0.824

O15305	<i>PMM2</i>	0.000	0.000	0.001	0.001	4.09	2.031	3.49E-01	0.935
P84243	<i>H3-3A</i>	0.002	0.002	0.000	0.000	0.25	-2.017	3.60E-01	0.917
O15127	<i>SCAMP2</i>	0.000	0.000	0.000	0.000	0.65	-0.615	5.76E-01	0.885
Q9Y333	<i>LSM2</i>	0.000	0.000	0.000	0.000	1.90	0.928	4.56E-01	0.812
P19823	<i>ITIH2</i>	0.002	0.002	0.000	0.000	0.11	-3.187	1.50E-01	1.017
P42766	<i>RPL35</i>	0.001	0.000	0.001	0.001	0.70	-0.519	4.38E-01	0.808
Q9Y3C8	<i>UFC1</i>	0.000	0.000	0.000	0.000	1.43	0.512	3.10E-01	0.959
P16402	<i>H1-3</i>	0.000	0.000	0.000	0.000	1.29	0.373	6.68E-01	0.914
O43684	<i>BUB3</i>	0.001	0.001	0.007	0.011	5.10	2.352	4.38E-01	0.804
O60610	<i>DIAPH1</i>	0.000	0.000	0.000	0.000	2.18	1.124	1.54E-01	1.029
Q9Y446	<i>PKP3</i>	0.000	0.000	0.000	0.000	1.22	0.282	5.72E-01	0.882
Q9Y2W1	<i>THRAP3</i>	0.000	0.000	0.000	0.000	0.80	-0.315	6.76E-01	0.911
P19652	<i>ORM2</i>	0.000	0.000	0.000	0.000	0.81	-0.300	7.43E-01	0.918
Q00577	<i>PURA</i>	0.000	0.000	0.000	0.000	0.58	-0.787	1.80E-01	1.037
Q92804	<i>TAF15</i>	0.000	0.000	0.002	0.003	11.85	3.567	3.57E-01	0.925
P21912	<i>SDHB</i>	0.001	0.000	0.001	0.000	0.59	-0.753	3.78E-01	0.838
P46926	<i>GNPDA1</i>	0.000	0.000	0.000	0.000	1.75	0.806	7.66E-02	1.139
O43583	<i>DENR</i>	0.000	0.000	0.000	0.000	0.92	-0.116	6.85E-01	0.915
O14561	<i>NDUFAB1</i>	0.000	0.000	0.001	0.001	19.84	4.310	2.32E-01	1.038
P61956	<i>SUMO2</i>	0.000	0.000	0.002	0.003	6.60	2.723	3.24E-01	0.934
O76003	<i>GLRX3</i>	0.000	0.000	0.001	0.001	2.97	1.571	4.85E-01	0.831
P49721	<i>PSMB2</i>	0.001	0.001	0.001	0.000	0.82	-0.285	7.57E-01	0.931
P62851	<i>RPS25</i>	0.003	0.001	0.008	0.009	3.16	1.660	3.65E-01	0.900
P35908	<i>KRT2</i>	0.001	0.000	0.000	0.000	0.29	-1.765	1.67E-01	1.055
P62942	<i>FKBP1A</i>	0.001	0.001	0.001	0.001	1.04	0.058	9.26E-01	0.984
Q05315	<i>CLC</i>	0.002	0.002	0.003	0.001	1.50	0.584	5.38E-01	0.855
Q9Y2Z0	<i>SUGT1</i>	0.000	0.000	0.000	0.000	1.30	0.373	6.73E-01	0.910
Q969H8	<i>MYDGF</i>	0.001	0.000	0.001	0.001	1.15	0.206	7.42E-01	0.920
Q86X76	<i>NIT1</i>	0.000	0.000	0.003	0.005	16.17	4.016	3.77E-01	0.852
O95168	<i>NDUFB4</i>	0.000	0.000	0.004	0.006	24.34	4.606	3.73E-01	0.873
P16401	<i>H1-5</i>	0.006	0.006	0.002	0.003	0.37	-1.451	3.95E-01	0.820
Q9Y3D6	<i>FIS1</i>	0.000	0.000	0.000	0.000	0.49	-1.031	2.51E-01	1.042
Q9Y3F4	<i>STRAP</i>	0.000	0.000	0.000	0.000	0.57	-0.809	2.04E-03	0.940

Q96A33	<i>CCDC47</i>	0.000	0.000	0.000	0.000	1.14	0.183	7.57E-01	0.928
Q12792	<i>TWF1</i>	0.000	0.000	0.000	0.000	1.39	0.479	5.64E-01	0.875
Q9H3N1	<i>TMX1</i>	0.000	0.000	0.002	0.002	8.37	3.065	3.28E-01	0.928
P62280	<i>RPS11</i>	0.002	0.001	0.002	0.000	0.81	-0.306	5.86E-01	0.895
Q9H3R2	<i>MUC13</i>	0.000	0.000	0.000	0.000	1.37	0.457	4.64E-01	0.813
Q13217	<i>DNAJC3</i>	0.000	0.000	0.000	0.000	1.89	0.915	4.17E-01	0.811
P61006	<i>RAB8A</i>	0.000	0.000	0.000	0.000	0.62	-0.681	3.59E-01	0.925
Q86UX7	<i>FERMT3</i>	0.000	0.000	0.007	0.011	42.80	5.420	3.70E-01	0.888
Q92616	<i>GCN1</i>	0.000	0.000	0.000	0.000	0.89	-0.162	8.43E-01	0.964
P63279	<i>UBE2I</i>	0.000	0.000	0.000	0.000	0.82	-0.289	7.33E-01	0.913
O60869	<i>EDF1</i>	0.000	0.000	0.000	0.000	0.99	-0.007	9.78E-01	0.995
O00534	<i>VWA5A</i>	0.000	0.000	0.000	0.000	0.47	-1.088	2.87E-01	0.980
Q8IZP0	<i>ABI1</i>	0.000	0.000	0.000	0.000	0.84	-0.259	7.15E-01	0.906
Q07812	<i>BAX</i>	0.000	0.000	0.000	0.000	0.49	-1.033	1.75E-01	1.034
Q16629	<i>SRSF7</i>	0.000	0.000	0.018	0.031	40.68	5.346	3.75E-01	0.856
P15954	<i>COX7C</i>	0.000	0.000	0.003	0.004	11.08	3.470	3.24E-01	0.928
P61457	<i>PCBD1</i>	0.001	0.000	0.001	0.001	1.08	0.109	9.23E-01	0.985
Q8WW12	<i>PCNP</i>	0.000	0.000	0.000	0.000	0.29	-1.782	1.88E-01	1.032
O60888	<i>CUTA</i>	0.000	0.000	0.000	0.000	2.75	1.458	7.74E-02	1.081
P54578	<i>USP14</i>	0.000	0.000	0.000	0.000	1.24	0.311	2.33E-01	1.023
Q9Y3U8	<i>RPL36</i>	0.000	0.000	0.001	0.001	2.43	1.282	3.16E-01	0.946
Q9NQG5	<i>RPRD1B</i>	0.000	0.000	0.001	0.001	4.13	2.046	4.07E-01	0.809
P09012	<i>SNRPA</i>	0.000	0.000	0.006	0.009	23.78	4.571	3.53E-01	0.925
P13727	<i>PRG2</i>	0.000	0.001	0.001	0.000	1.68	0.749	6.09E-01	0.912
P05109	<i>S100A8</i>	0.001	0.001	0.001	0.002	1.69	0.759	6.60E-01	0.911
Q13155	<i>AIMP2</i>	0.000	0.000	0.000	0.000	1.09	0.128	8.89E-01	0.980
Q9NR30	<i>DDX21</i>	0.000	0.000	0.000	0.001	0.72	-0.472	7.06E-01	0.904
Q52LJ0	<i>FAM98B</i>	0.000	0.000	0.000	0.000	2.52	1.334	4.12E-01	0.808
O94905	<i>ERLIN2</i>	0.000	0.000	0.000	0.000	2.46	1.299	6.79E-02	1.252
Q13404	<i>UBE2V1</i>	0.001	0.001	0.001	0.002	1.63	0.707	6.56E-01	0.914
Q32MZ4	<i>LRRFIP1</i>	0.000	0.000	0.000	0.001	2.60	1.377	4.85E-01	0.828
P55036	<i>PSMD4</i>	0.000	0.000	0.000	0.000	1.29	0.364	3.65E-01	0.895
Q9Y5L4	<i>TIMM13</i>	0.002	0.002	0.000	0.000	0.16	-2.613	3.91E-01	0.823

P46109	<i>CRKL</i>	0.000	0.000	0.000	0.000	0.89	-0.163	8.55E-01	0.966
P06730	<i>EIF4E</i>	0.000	0.000	0.001	0.001	5.69	2.509	3.04E-01	0.960
P10301	<i>RRAS</i>	0.000	0.000	0.001	0.001	1.52	0.600	7.04E-01	0.904
Q99584	<i>S100A13</i>	0.000	0.000	0.000	0.001	3.29	1.718	4.86E-01	0.827
Q9Y639	<i>NPTN</i>	0.000	0.000	0.000	0.000	1.22	0.287	7.68E-01	0.932
P62861	<i>FAU</i>	0.000	0.000	0.001	0.001	1.20	0.267	8.01E-01	0.942
Q86U42	<i>PABPN1</i>	0.000	0.000	0.000	0.000	0.62	-0.681	9.34E-02	1.164
Q04323	<i>UBXN1</i>	0.000	0.000	0.000	0.000	0.36	-1.470	2.06E-01	1.032
P51970	<i>NDUFA8</i>	0.000	0.000	0.000	0.000	1.23	0.294	4.91E-01	0.832
P33316	<i>DUT</i>	0.000	0.000	0.000	0.001	1.36	0.439	7.29E-01	0.916
P46783	<i>RPS10</i>	0.001	0.000	0.001	0.000	1.26	0.336	4.67E-01	0.812
Q16740	<i>CLPP</i>	0.000	0.000	0.001	0.002	6.08	2.605	3.99E-01	0.814
Q12765	<i>SCRN1</i>	0.000	0.000	0.000	0.000	0.31	-1.679	2.55E-01	1.022
P61026	<i>RAB10</i>	0.000	0.000	0.000	0.000	0.66	-0.608	5.30E-01	0.854
Q9BY44	<i>EIF2A</i>	0.000	0.000	0.000	0.000	0.85	-0.236	8.38E-01	0.966
Q9UDW1	<i>UQCR10</i>	0.000	0.000	0.000	0.000	1.06	0.087	8.20E-01	0.957
P42574	<i>CASP3</i>	0.000	0.000	0.003	0.004	22.66	4.502	3.68E-01	0.898
Q15370	<i>ELOB</i>	0.000	0.000	0.006	0.010	51.03	5.673	3.72E-01	0.879
Q92734	<i>TFG</i>	0.000	0.000	0.001	0.001	4.02	2.007	3.68E-01	0.893
O60493	<i>SNX3</i>	0.001	0.000	0.000	0.000	0.66	-0.607	3.77E-01	0.848
Q71UM5	<i>RPS27L</i>	0.000	0.000	0.001	0.000	3.71	1.890	1.64E-01	1.050
P52943	<i>CRIP2</i>	0.001	0.001	0.001	0.002	1.28	0.360	8.25E-01	0.956
O14949	<i>UQCRQ</i>	0.000	0.000	0.000	0.000	1.43	0.516	3.28E-01	0.922
P02760	<i>AMBP</i>	0.000	0.000	0.002	0.003	7.61	2.927	4.10E-01	0.808
P26447	<i>S100A4</i>	0.002	0.001	0.001	0.001	0.43	-1.222	1.33E-01	1.022
P80217	<i>IFI35</i>	0.000	0.000	0.000	0.000	0.97	-0.047	9.46E-01	0.984
Q14802	<i>FXVD3</i>	0.000	0.000	0.001	0.001	6.38	2.673	1.93E-01	1.035
Q9P0J0	<i>NDUFA13</i>	0.000	0.000	0.000	0.000	3.16	1.661	6.64E-02	1.275
P56385	<i>ATP5ME</i>	0.001	0.000	0.000	0.000	0.45	-1.154	1.71E-01	1.051
Q9BWJ5	<i>SF3B5</i>	0.000	0.000	0.000	0.000	1.41	0.499	3.73E-01	0.868
O14936	<i>CASK</i>	0.000	0.000	0.001	0.001	2.29	1.192	5.57E-01	0.867
O00232	<i>PSMD12</i>	0.000	0.000	0.001	0.001	12.22	3.612	3.77E-01	0.844
Q9NPJ3	<i>ACOT13</i>	0.000	0.000	0.005	0.009	12.91	3.691	3.86E-01	0.828

P37108	<i>SRP14</i>	0.001	0.000	0.017	0.028	20.99	4.392	3.87E-01	0.826
Q9Y5S9	<i>RBM8A</i>	0.000	0.000	0.000	0.000	1.45	0.531	6.34E-01	0.905
Q9H008	<i>LHPP</i>	0.000	0.000	0.000	0.000	0.48	-1.072	1.00E-01	1.153
Q7RTV0	<i>PHF5A</i>	0.000	0.000	0.000	0.000	1.47	0.555	6.71E-01	0.910
Q96M27	<i>PRRC1</i>	0.000	0.000	0.000	0.000	0.92	-0.117	9.14E-01	0.994
P12104	<i>FABP2</i>	0.000	0.000	0.001	0.001	6.73	2.750	3.34E-01	0.928
P61081	<i>UBE2M</i>	0.000	0.000	0.000	0.000	1.13	0.177	8.58E-01	0.962
Q9Y383	<i>LUC7L2</i>	0.000	0.000	0.019	0.033	99.02	6.630	3.75E-01	0.852
Q14696	<i>MESD</i>	0.000	0.000	0.000	0.000	2.02	1.013	3.62E-01	0.907
P22059	<i>OSBP</i>	0.000	0.000	0.000	0.000	2.17	1.118	2.70E-01	0.996
Q9UHV9	<i>PFDN2</i>	0.000	0.000	0.000	0.000	1.62	0.696	5.97E-01	0.905
O60784	<i>TOM1</i>	0.000	0.000	0.000	0.000	0.95	-0.069	9.22E-01	0.986
Q9NR12	<i>PDLIM7</i>	0.001	0.001	0.002	0.003	1.68	0.746	6.92E-01	0.914
Q9H444	<i>CHMP4B</i>	0.000	0.000	0.000	0.000	0.35	-1.498	1.20E-01	1.064
Q8WUW1	<i>BRK1</i>	0.000	0.000	0.000	0.000	1.02	0.034	9.72E-01	0.996
P61513	<i>RPL37A</i>	0.000	0.000	0.001	0.002	4.52	2.175	3.36E-01	0.922
Q9Y2V2	<i>CARHSP1</i>	0.000	0.000	0.001	0.001	3.83	1.938	4.09E-01	0.809
P49006	<i>MARCKSL1</i>	0.000	0.000	0.001	0.001	5.43	2.441	4.53E-01	0.813
O43598	<i>DNPH1</i>	0.001	0.000	0.000	0.000	0.67	-0.567	4.75E-01	0.820
Q9H3K6	<i>BOLA2</i>	0.000	0.000	0.000	0.000	0.47	-1.098	1.27E-01	1.027
P31689	<i>DNAJA1</i>	0.000	0.000	0.000	0.000	2.62	1.392	3.95E-01	0.817
P61086	<i>UBE2K</i>	0.000	0.000	0.000	0.001	1.89	0.915	5.98E-01	0.904
Q5JTV8	<i>TOR1AIP1</i>	0.000	0.000	0.000	0.000	0.92	-0.113	8.95E-01	0.980
Q14061	<i>COX17</i>	0.000	0.000	0.001	0.001	7.07	2.822	3.96E-01	0.815
Q9NWW4	<i>CZIB</i>	0.000	0.000	0.000	0.000	0.43	-1.221	1.48E-02	0.853
P06727	<i>APOA4</i>	0.001	0.000	0.000	0.000	0.26	-1.926	5.98E-02	1.199
Q9UKY7	<i>CDV3</i>	0.000	0.000	0.001	0.001	1.92	0.938	6.19E-01	0.906
P48739	<i>PITPNB</i>	0.000	0.000	0.000	0.000	0.93	-0.112	8.88E-01	0.984
P62310	<i>LSM3</i>	0.000	0.000	0.000	0.000	2.94	1.556	3.53E-01	0.919
P49961	<i>ENTPD1</i>	0.000	0.000	0.000	0.000	0.87	-0.202	6.55E-01	0.915
P49207	<i>RPL34</i>	0.001	0.001	0.002	0.002	1.76	0.812	6.05E-01	0.908
Q9UHA4	<i>LAMTOR3</i>	0.000	0.000	0.000	0.000	1.04	0.060	9.15E-01	0.990
P27708	<i>CAD</i>	0.000	0.000	0.000	0.000	0.87	-0.203	8.00E-01	0.943

Q08722	<i>CD47</i>	0.000	0.000	0.000	0.000	1.88	0.909	2.75E-01	0.998
Q9Y5M8	<i>SRPRB</i>	0.000	0.000	0.000	0.000	0.54	-0.882	4.32E-01	0.813
Q04941	<i>PLP2</i>	0.000	0.000	0.000	0.000	0.16	-2.606	7.36E-02	1.257
Q9BRP8	<i>PYM1</i>	0.000	0.000	0.002	0.004	19.05	4.252	3.84E-01	0.831
P62273	<i>RPS29</i>	0.001	0.001	0.000	0.000	0.61	-0.716	4.94E-01	0.834

Table S3. Comparison of site-specific protein glycosylation in UC and PCA. H = Hexose, N = HexNAc, F = Fucose, S = Neu5Ac. The relative abundance for each glycoform is given in Figure S1.

Gene	Peptide	Site	N-glycan
<i>APMAP</i>	AGP N GTLFVADAYK	160	H5N2
<i>ASAH1</i>	TVLE N STSYEEAKNLLTK	259	H6N2
<i>C3</i>	TVLTPAT N HMGNVFTFTIPANR	81	H5N3
<i>C3</i>	TVLTPAT N HMGNVFTFTIPANR	81	H6N2
<i>CLCA1</i>	AS N ATLPPITVTSK	583	H4N5F3
<i>CTSA</i>	MDPPCT N TTAASTYLNNPYVR	327	H5N3
<i>CTSL</i>	YSVA N DTGFVDIPKQEK	221	H4N2
<i>CTSL</i>	YSVA N DTGFVDIPKQEK	221	H3N2
<i>DCN</i>	LGLSF N SISAVDNGSLANTPHLR	255	H5N4F1
<i>DCN</i>	LGLSF N SISAVDNGSLANTPHLR	255	S1H4N4F1
<i>FGB</i>	GTA N ALMDGASQLMGENR	381	S1H5N4
<i>FGG</i>	VDKDLQSLEDILHQVE N KTSEVK	78	S1H5N4
<i>GAA</i>	GVFIT N ETGQPLIGK	471	H6N2
<i>HP</i>	MVSHH N LTTGATLINEQWLLTTAK	184	S1H5N4
<i>HP</i>	VVLHP N YSQVDIGLIK	242	S2H5N4
<i>HPX</i>	ALPQPQ N VTSLLGCTH	454	S2H5N4
<i>HSP90B1</i>	HN N DTQHIWESDSNEFSVIADPR	217	H6N2
<i>ITGA1</i>	Y N HTGQVIIYR	460	H9N2
<i>JCHAIN</i>	IIVPLNNRE N ISDPTSPLR	71	H4N3F1
<i>JCHAIN</i>	IIVPLNNRE N ISDPTSPLR	71	H5N3F1
<i>JCHAIN</i>	IIVPLNNRE N ISDPTSPLR	71	H7N2
<i>JCHAIN</i>	IIVPLNNRE N ISDPTSPLR	71	H8N2
<i>JCHAIN</i>	IIVPLNNRE N ISDPTSPLR	71	S1H4N4

<i>JCHAIN</i>	IIVPLNNRE ^N ISDPTSPLR	71	H5N4
<i>JCHAIN</i>	IIVPLNNRE ^N ISDPTSPLR	71	H4N4F1
<i>JCHAIN</i>	IIVPLNNRE ^N ISDPTSPLR	71	S1H4N3F1
<i>JCHAIN</i>	IIVPLNNRE ^N ISDPTSPLR	71	H6N2
<i>JCHAIN</i>	IIVPLNNRE ^N ISDPTSPLR	71	S1H5N4
<i>LAMC1</i>	LLN ^N LTSIK	650	H6N2
<i>LUM</i>	KLHINHN ^N LTESVGPLPK	127	S1H5N4F1
<i>MUC2</i>	TINGIHS ^N ISVSYLEGCYPR	1154	H5N4F1
<i>POGLUT3</i>	YFYLQAVNSEGQ ^N LTR	61	H9N2
<i>SSR2</i>	IAPAS ^N VSHTVVLRPLK	88	H8N2
<i>SSR2</i>	IAPAS ^N VSHTVVLRPLK	88	H9N2
<i>ST14</i>	VIN ^N QTTCE ^N LLPQQITPR	772	H5N2
<i>STT3A</i>	TILVD ^N NTWNNTHISR	544	H9N2
<i>STT3A</i>	TILVD ^N NTWNNTHISR	544	H8N2
<i>STT3B</i>	TTLVD ^N NTWNNSHIALVGK	623	H9N2
<i>TPP1</i>	FLSSSPHLPPSSYF ^N ASGR	438	H3N2F1

Table S4. List of abbreviation in KEGG and GO analysis. These abbreviations are given in Figure 5.

Abbreviation	Full Name	Category
EPA	Endopeptidase activity	Molecular function
SEA	Serine-type exopeptidase activity	Molecular function
EMB	Extracellular matrix binding	Molecular function
EMSC	Extracellular matrix structural constituent	Molecular function
COB	Collagen binding	Molecular function
SPA	Serine-type peptidase activity	Molecular function
SHA	Serine hydrolase activity	Molecular function
PHB	Phosphatase binding	Molecular function
EXA	Exopeptidase activity	Molecular function
CHB	Chaperone binding	Molecular function
IMSP	Integrin-mediated signaling pathway	Gene Ontology
LYO	Lysosome organization	Gene Ontology
LVO	Lytic vacuole organization	Gene Ontology
SCP	Sphingolipid catabolic process	Gene Ontology
MLCP	Membrane lipid catabolic process	Gene Ontology
CSA	Cell-substrate adhesion	Gene Ontology
PRP	Protein processing	Gene Ontology
PRCA	Positive regulation of cell-substrate adhesion	Gene Ontology
NRBC	Negative regulation of blood coagulation	Gene Ontology
NRH	Negative regulation of hemostasis	Gene Ontology
VAL	Vacuolar lumen	Gene Ontology
SGL	Secretory granule lumen	Gene Ontology
LYL	Lysosomal lumen	Gene Ontology
CVL	Cytoplasmic vesicle lumen	Gene Ontology
VEL	Vesicle lumen	Gene Ontology
BLM	Blood microparticle	Gene Ontology
PRL	Primary lysosome	Gene Ontology
AZG	Azurophil granule	Gene Ontology
AGL	Azurophil granule	Gene Ontology
CCEM	Collagen-containing extracellular matrix	Gene Ontology
HCM	Hypertrophic cardiomyopathy	Pathway
FOA	Focal adhesion	Pathway
SCLC	Small cell lung cancer	Pathway
ARVCM	Arrhythmogenic right ventricular cardiomyopathy	Pathway
PPER	Protein processing in endoplasmic reticulum	Pathway

GAGD	Glycosaminoglycan degradation	Pathway
VNGB	Various types of N-glycan biosynthesis	Pathway
ECMRI	ECM-receptor interaction	Pathway
CCC	Complement and coagulation cascades	Pathway
LYS	Lysosome	Pathway

References

1. The UniProt, C. UniProt: the universal protein knowledgebase in 2025. *Nucleic Acids Res.* **53**, D609-D617 (2025).
2. Kong, A.T., Leprevost, F.V., Avtonomov, D.M., Mellacheruvu, D. & Nesvizhskii, A.I. MSFragger: ultrafast and comprehensive peptide identification in mass spectrometry–based proteomics. *Nat. Methods* **14**, 513-520 (2017).
3. Bern, M., Kil, Y.J. & Becker, C. Byonic: Advanced peptide and protein identification software. *Curr. Protoc. Bioinformatics* **40**, 13.20.11-13.20.14 (2012).
4. Shu, J., Dolman, G.E., Duan, J., Qiu, G. & Ilyas, M. Statistical colour models: an automated digital image analysis method for quantification of histological biomarkers. *BioMed. Eng. OnLine* **15**, 1-16 (2016).