

## **Supplemental Material**

### **MATERIALS AND METHODS**

#### **Sample acquisition and patients**

Samples and clinical data from COVID-19 patients were collected from consented hospitalized patients at the Washington University Medical Center under an institutional review board approved protocol to study immunological, genetic and clinical predictors of SARS CoV-2 infection (IRB ID # 202003085) between March and May 2020. SARS-CoV-2 was confirmed using an FDA approved PCR test and detailed clinical metadata has been described<sup>S1</sup>. Clinical data were extracted from electronic health records by the Institute of Informatics and provided in a deidentified manner. The clinical diagnosis of AKI incorporates modified guidelines from the Kidney Disease Improving Global Outcomes (KDIGO) for selecting samples from patients with AKI (rise in serum creatinine (SCr) by 0.3 mg/dL over 48 hours, OR 50% rise in SCr from baseline during current hospitalization OR decrease in urine output by 0.5 ml/kg/hour for 6 hours)<sup>S2, S3</sup>. Urine from healthy volunteers was obtained from the Kidney Translational Research Center (KTRC) (Table S1).

#### **Urine processing and storage**

Urine samples were collected within first 3 days during hospital visit in a sterile cup as convenient and transported by the hospital staff twice a day to the laboratory, stored at 4 °C until ready for processing on the same day. All samples were processed and stored in less than 24 hours. Urine was filtered through a 40µm mesh followed by a 2,000xg centrifugation for 12 minutes. The cell pellet was preserved in RNAlater and the supernatant immediately aliquoted into cryovials and stored at -80 °C until ready for experimental analysis. Where possible, samples were serially collected with first day of collection (typically first day of hospitalization) designated as day (D) 0. To initially determine the quality of specimens we checked the presence of various analytes including several kidney injury and proinflammatory markers using the Meso Scale Discovery

(MDS) platform services offered by the George M. O'Brien Center at the Johns Hopkins University (Table S1). The adequacy of the COVID-19 urine samples was confirmed by measuring several markers of AKI and inflammation prior to proceeding with urine proteome studies (Table S1 and not shown).

### **Proteomics sample preparation**

Proteins in each 150  $\mu$ L aliquot of urine were denatured by mixing with 117 mg urea (final 8M). Samples were incubated at 60°C for 30 min with constant shaking at 800 rpm after adding dithiothreitol (DTT, 5 mM). Samples were then cooled to room temperature, alkylated by the addition of 40 mM iodoacetamide (IAA), and were incubated at room temperature for 30 min in the dark. Samples were then diluted 8-fold in volume with 100 mM  $\text{NH}_4\text{HCO}_3$  buffer (pH 8.0) containing 1 mM  $\text{CaCl}_2$ . Sequencing-grade modified porcine trypsin (Promega) was added at a 1:20 (w/w) trypsin-to-protein ratio to digest proteins at 37°C for 5 h with shaking at 500 rpm. The digestion process was stopped by adding to a concentration of 1% trifluoroacetic acid (TFA) and desalted with Discovery C18 50 mg/1 mL solid phase extraction (SPE) columns (Supelco) using a Gilson GX-274 ASPEC™ system (Gilson Inc.). For desalting, each SPE tube was conditioned by 3 mL of methanol, followed by 3 mL of 0.1% TFA aqueous solution. The acidified samples were then loaded to each column followed by washing with 4 mL of 95:5 (v/v)  $\text{H}_2\text{O}$ :acetonitrile with 0.1% TFA. The samples were eluted with 1 mL 80:20 (v/v) acetonitrile: $\text{H}_2\text{O}$  with 0.1% TFA. The peptide-containing eluents were concentrated down to approximately 100  $\mu$ L using a SpeedVac vacuum concentrator. The final peptide concentration was quantified by a Pierce™ bicinchoninic acid (BCA) Assay Kit (Thermo Fisher Scientific). The samples were diluted to 0.10  $\mu$ g/ $\mu$ L with nanopure water for proteomics LC-MS/MS analysis.

### **LC-MS/MS-based proteomics analysis**

The proteomics analysis was carried out with liquid chromatography-tandem mass spectrometry (LC-MS/MS). The liquid chromatograph (LC) consisted of a nanoAcquity M-Class UPLC system (Waters) equipped with an analytical column packed in-house with 3  $\mu\text{m}$  Jupiter C18 media (Phenomenex) into 75  $\mu\text{m}$  (i.d.)  $\times$  70 cm (long). The trapping column 150  $\mu\text{m}$  (i.d.)  $\times$  4 cm (long) was packed by 5  $\mu\text{m}$  Jupiter C18 particles (Phenomenex). 5  $\mu\text{L}$ s of each digested sample were loaded onto the LC system, and peptides were separated at 300 nL/min at room temperature. Mobile phases were comprised of mobile phase A (0.1% formic acid in water) and mobile phase B (0.1% formic acid in acetonitrile) with the following applied separation gradient: 1-8% B for 2 min, 8-12% B for 18 min, 12-30% B for 55 min, 30-45% B for 22 min, 45-95% B for 3 min, maintained at 95% for 10 min, and equilibrated at 1% B for 20 min.

The eluted peptides from the LC system were analyzed using a Q-Exactive HF-X mass spectrometer (Thermo Fisher Scientific) outfitted with a custom nano-electrospray ionization (ESI) interface consisting of an electrospray emitter prepared by 150  $\mu\text{m}$  (o.d.)  $\times$  20  $\mu\text{m}$  (i.d.) chemically etched fused silica<sup>S4</sup>. Spray voltage and ion transfer tube temperature were controlled at 2.2 kV and 300 °C, respectively. Full MS scans were acquired from 300 – 1800 m/z at a resolution of 60,000, AGC target of 3e6. Top 12 data-dependent tandem MS scans were performed at a resolution of 15,000, AGC target of 1e5, isolation window of 1.0 m/z, normalized collision energy of 30, and dynamic exclusion of 30 sec.

### **Proteomics data processing**

The Raw MS datasets were searched with MaxQuant (v1.6.0.16)<sup>S5</sup> against a database containing the Uniprot *homo sapiens* proteome (released on Nov. 5, 2019) and the Uniprot SARS-COV-2 proteome (released on Aug. 17, 2020). In the MaxQuant search, methionine oxidation and N-term acetylation were set as variable modifications, and carbamidomethylation was set as a fixed modification. The “match between runs” function with a 1.5-min time window was applied to

identify peptides. False discovery rates (FDRs) at the peptide level and protein level were set to less than 0.01. Trypsin was selected as the digestion enzyme with up to two allowable missed cleavages. Default settings were used for the rest of the search parameters. The MaxQuant output containing protein groups and intensity values was processed with RStudio (v3.5.1) scripts. In brief, the proteome data were first filtered to retain proteins with more than 80% of detectability in the urine samples from the patients with acute kidney injury (AKI+) or in the urine samples from the patients without acute kidney injury (AKI-). The missing intensities of the remaining proteins were imputed following a method described previously<sup>S6</sup>. The intensities were log<sub>2</sub> transformed and median centered prior to the statistical analysis. The Linear Models for Microarray Data (limma test) was applied to assess the intensities of proteins that were significantly changed in AKI+ compared to AKI- using the R package 'limma'. The FDR was controlled by 'Benjamini and Hochberg' adjustment with the value 0.05 chosen as the cutoff to define statistical significance. The limma test was used because it applies linear models to integrate the whole data rather than comparing between categorized groups, making the statistical conclusions more reliable when the number of samples is small<sup>S7</sup>. The log<sub>2</sub> fold change of protein intensity due to AKI status was calculated by normalizing the mean protein intensity measured in the AKI+ group to the mean protein intensity measured in the AKI- group. The proteins with significantly different expression levels (adjust  $p < 0.05$ , log<sub>2</sub> fold change  $<0$  or  $>0$ ) were selected for enrichment analyses for Gene Ontology (GO) terms, KEGG pathways, and Reactome pathways using the online tool metascape<sup>S8</sup>.

To further validate SARS-CoV-2 peptide detection in the urine proteome data, each of the two datasets which contained SARS-CoV-2 peptides using MaxQuant were analyzed using MS-GF+ (v2020.08.05)<sup>S9</sup> against the same databases used for the MaxQuant search. Methionine oxidation and N-term acetylation were set as variable modifications, and carbamidomethylation was set as a fixed modification. Settings allowed partial trypsin digestion (up to two missed cleavages) and

the parent-ion-mass tolerance was set at 20 ppm or less. The outcomes of MS-GF+ results were filtered using parent-ion-mass tolerance < 10 ppm, MSGFDB\_SpecEValue <  $1 \times 10^{-10}$ , and Q values of peptides < 0.01. The resulting FDR values at the peptide and protein level were calculated as 0.0005 and 0.0075, respectively.

### **Correlation analysis of COV-AKI patients compared to non-AKI patients.**

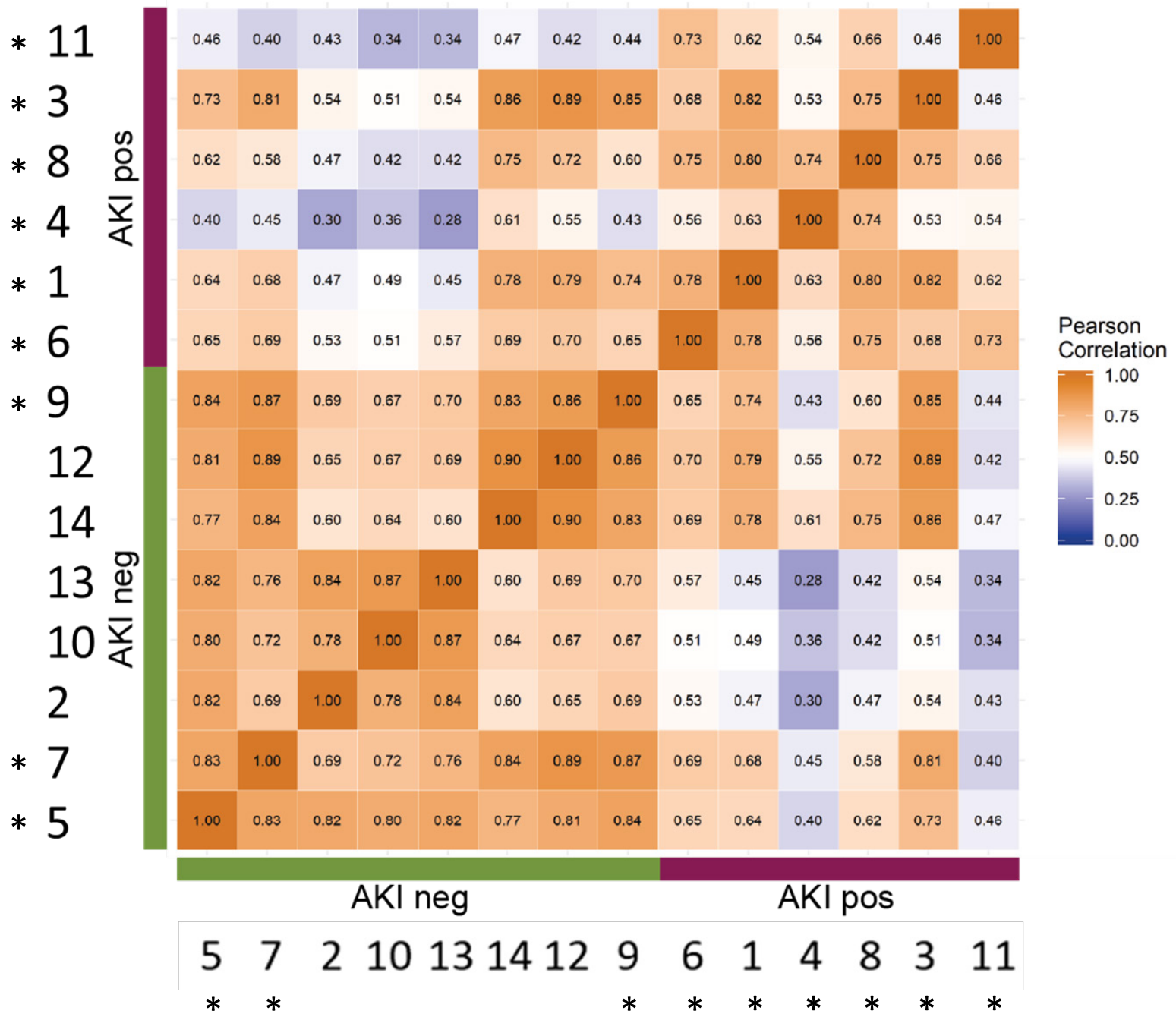
A total of 980 urinary proteins were quantifiable based on their MS intensities reported by MaxQuant software (Table S2). The patient-to-patient correlation was assessed by Pearson correlation of log<sub>2</sub> transformed protein abundances across the entire patient cohort, ranging from 0.28 to 0.90 (Figure S1). Relatively higher correlation (>0.7) was observed between the majority of AKI- patients; however, lower correlation was observed across AKI+ and AKI- groups (<0.5). This suggests large discrepancies of protein abundances in urine due to AKI status.

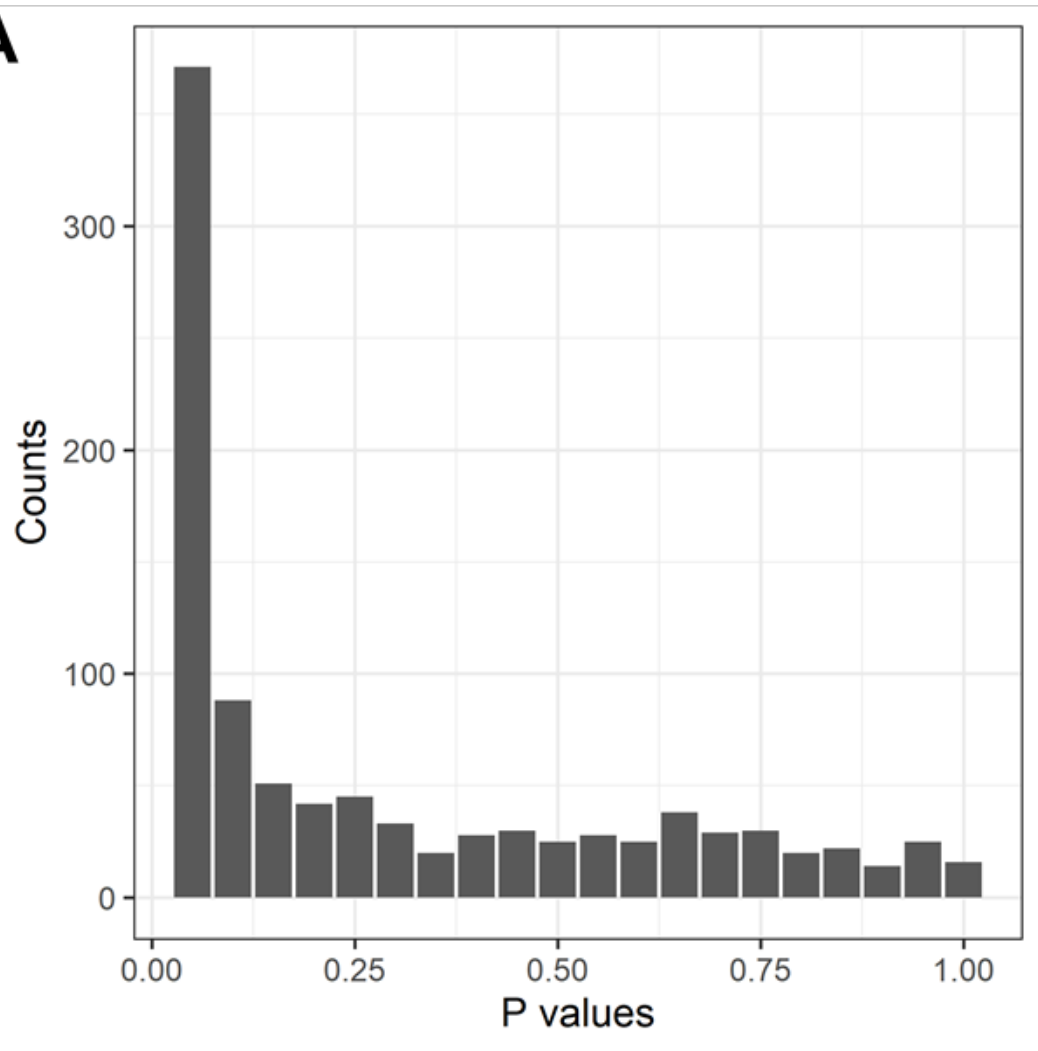
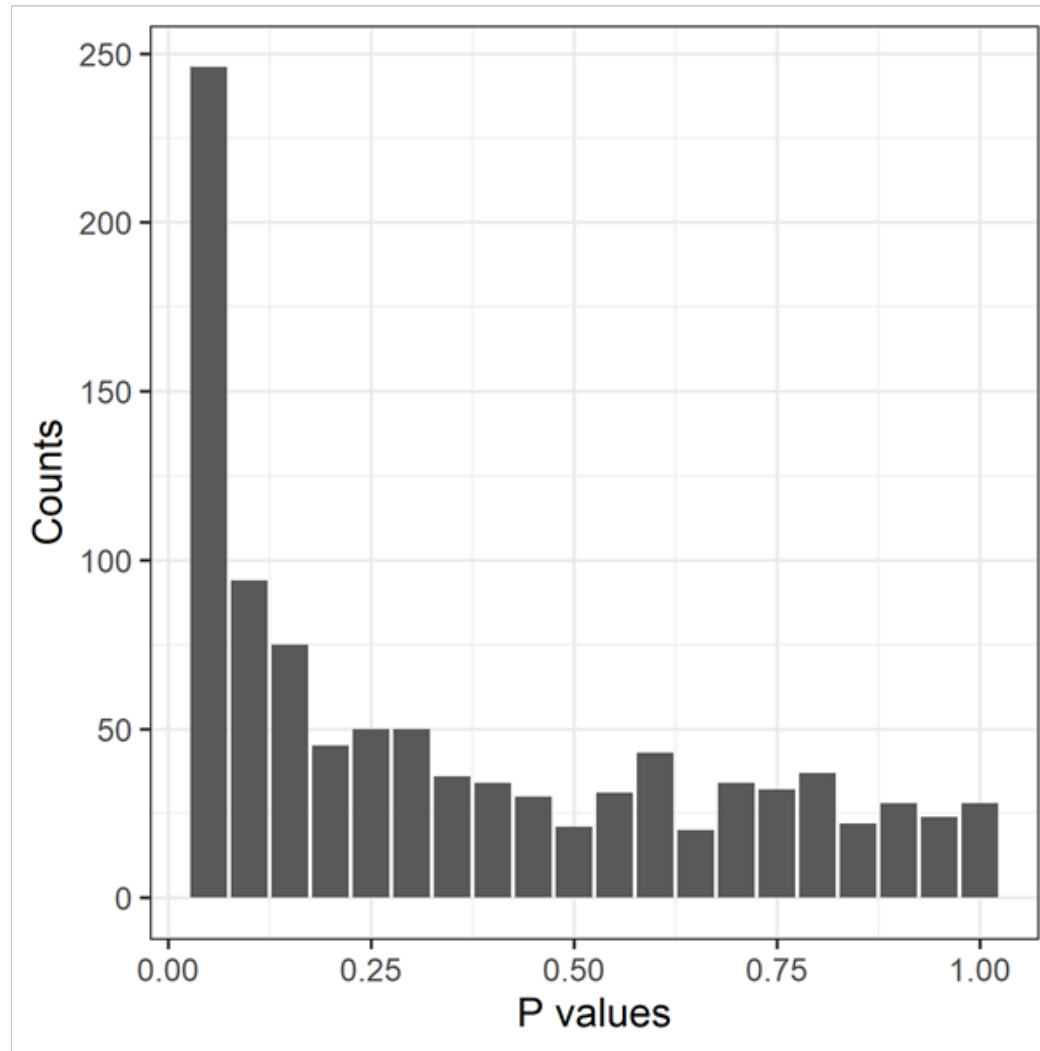
### **Data availability**

All the datasets, MaxQuant search parameters, MS-GF+ search parameters, and the corresponding results files are available at the ProteomeXchange Consortium website using the PRIDE <sup>29, 30</sup> partner repository with the dataset identifier PXD025178 and 10.6019/PXD025178.

## Supplemental References:

- S1. Mudd PA, Crawford JC, Turner JS, *et al.* Distinct inflammatory profiles distinguish COVID-19 from influenza with limited contributions from cytokine storm. *Sci Adv* 2020; **6**.
- S2. Kellum JA, Lameire N, Aspelin P, *et al.* Kidney disease: Improving global outcomes (KDIGO) acute kidney injury work group. KDIGO clinical practice guideline for acute kidney injury. *Kidney International Supplements* 2012; **2**: 1-138.
- S3. Siew ED, Ikizler TA, Matheny ME, *et al.* Estimating baseline kidney function in hospitalized patients with impaired kidney function. *Clin J Am Soc Nephrol* 2012; **7**: 712-719.
- S4. Kelly RT, Page JS, Luo Q, *et al.* Chemically etched open tubular and monolithic emitters for nanoelectrospray ionization mass spectrometry. *Anal Chem* 2006; **78**: 7796-7801.
- S5. Tyanova S, Temu T, Cox J. The MaxQuant computational platform for mass spectrometry-based shotgun proteomics. *Nat Protoc* 2016; **11**: 2301-2319.
- S6. Polpitiya AD, Qian WJ, Jaitly N, *et al.* DANTE: a statistical tool for quantitative analysis of -omics data. *Bioinformatics* 2008; **24**: 1556-1558.
- S7. Tyanova S, Temu T, Sinitcyn P, *et al.* The Perseus computational platform for comprehensive analysis of (prote)omics data. *Nat Methods* 2016; **13**: 731-740.
- S8. Zhou Y, Zhou B, Pache L, *et al.* Metascape provides a biologist-oriented resource for the analysis of systems-level datasets. *Nat Commun* 2019; **10**: 1523.
- S9. Kim S, Pevzner PA. MS-GF+ makes progress towards a universal database search tool for proteomics. *Nat Commun* 2014; **5**: 5277.



**A****B**



## Supplemental Figure Legends

Figure S1. Pearson correlation of urinary proteomics across the studied samples.

Patients are numbered according to the patient key. Asterisks (\*) denote COVID-19 positive cases.

Figure S2. Distribution of p values before adjustment. (A) Statistical results of limma test that compared the intensities of urinary proteins based on the status of acute kidney injury (AKI). (B) Statistical results of limma test that compared the intensities of urinary proteins altered during COVID-19 infection in the AKI negative group.





sp Q13477 MAI Q13477	MADA2_HUMAN	MADCAM2	mucosal vascular addressin-1	-1.133	-1.830	-2.124	1.059	-0.075	-0.753	-1.860	-1.474	-3.027	-4.170	-0.729	-3.478	-2.797	-6.354	0.001723	0.013160	-2.697	0.019398	0.115617	-2.108	0.206813	0.428491	-0.942		
sp Q18700 HAI Q18700	HAVCR2_HUMAN	HAVCR2	hepatitis A virus cell surface receptor	3.759	2.908	1.545	2.546	1.625	2.775	2.108	1.910	-0.528	1.837	2.111	-4.626	0.201	-5.308	0.001774	0.034040	-3.589	0.003517	0.051059	-3.865	0.764661	0.876790	0.121		
sp P13362 FOF1 P13362	FOF1_HUMAN	FOF1	fibroblast growth factor 3 complementing factor	2.059	-2.687	-2.238	-1.633	-2.226	-2.079	-2.238	-1.637	-2.519	-2.860	-3.183	-7.650	-7.430	-3.302	0.001774	0.013160	-2.772	0.004740	0.290079	-3.947	0.692439	0.844017	0.280		
sp P02766 TTH P02766	TTH_HUMAN	TTR	transferrin (beta chain)	2.869	0.520	1.785	1.746	-1.492	7.011	5.628	3.184	4.775	5.717	5.529	4.640	9.047	3.307	0.001954	0.014374	2.796	0.023047	0.744293	1.878	0.01716	0.067705	0.189		
sp P15941 MUC1 P15941	MUC1_HUMAN	MUC1	mucin 1, cell surface associated	2.552	1.332	2.719	2.744	2.401	-0.481	-0.961	1.495	1.257	-0.525	-1.476	-7.000	-10.186	-2.512	0.001965	0.014374	-4.510	0.019485	0.349859	-3.075	0.000510	0.018079	-2.333		
sp P08164 LRP2 P08164	LRP2_HUMAN	LRP2	LDL receptor family class B member 2	3.794	4.940	2.455	4.836	4.379	4.896	5.534	3.942	4.665	2.121	3.511	-1.706	8.326	0.937	0.001907	0.014374	-2.634	0.012784	0.088225	-3.630	0.041910	0.643994	0.716		
sp Q86938 XYLT1 Q86938	XYLT1_HUMAN	XYLT1	lysyl oxidase-like protein	0.638	-0.187	-1.111	-0.385	-0.961	-1.269	-1.113	-0.558	-2.176	-1.940	-1.281	-3.994	-3.850	-2.985	0.001943	0.014374	-2.119	0.021111	0.126703	-1.966	0.017678	0.888731	-0.246		
sp Q08959 CDH Q08959	CDHR2_HUMAN	CDHR2	cadherin related family class D member 2	1.369	0.978	-4.079	0.518	-0.472	0.958	1.694	2.003	-2.662	-2.794	-1.530	0.964	-5.154	-1.468	-1.611	0.001912	0.014374	-2.281	0.000580	0.025850	-3.474	0.122780	0.315572	1.909	
sp P08174 DAF P08174	DAF_HUMAN	CD55	CD55 molecule (Crome glycoprotein)	4.969	4.578	3.839	3.979	4.120	4.920	4.059	4.565	2.974	3.318	3.415	0.393	-0.245	1.650	0.020214	0.014620	-2.430	0.000811	0.028388	-2.937	0.037106	0.597458	0.811		
sp Q08899 CUT Q08899	CUTA_HUMAN	CUTA	cysA divalent cation transporter	-0.874	-1.087	-3.368	1.100	0.734	-1.187	-1.686	-0.663	-2.454	-5.705	-1.588	-6.744	-7.584	-5.300	0.002206	0.015702	-4.234	0.000387	0.023036	-8.797	0.250035	0.479519	-0.700		
sp Q08899 LAI Q08899	LAI1_HUMAN	LAI1	lysyl oxidase-like protein	-3.661	-4.597	-4.964	-7.454	-3.020	-6.626	-2.600	-5.279	-2.384	-1.266	-1.466	-0.443	-2.293	-1.510	0.002212	0.015702	2.190	0.001862	0.038014	-2.796	0.046853	0.731322	-0.706		
sp Q08899 LAI Q08899	LAI1_HUMAN	LAI1	lysyl oxidase-like protein	4.544	4.168	4.400	4.523	3.675	1.868	2.657	3.184	3.916	2.075	1.915	-2.117	0.202	0.560	0.002215	0.015702	3.053	0.012798	0.038014	-2.990	0.013088	0.089219	-1.700		
sp Q06133 CLA Q06133	CD30L3_HUMAN	CD30L3	CD30 molecule (lymphocyte surface antigen)	3.905	1.463	1.548	3.519	3.650	1.687	-0.800	3.271	-0.407	0.231	0.755	-2.903	-1.253	-2.503	0.002227	0.015702	-3.384	0.004848	0.283617	-2.639	0.031889	0.575893	-1.191		
sp P26842 CD2 P26842	CD27_HUMAN	CD27	CD27 molecule (p134)	4.125	3.112	3.044	2.236	2.887	5.927	3.881	4.410	2.254	1.733	2.804	-1.550	-0.153	0.588	0.002274	0.015835	-2.777	0.003933	0.059466	-3.122	0.278322	0.503238	0.807		
sp Q15485 FCN2 Q15485	FCN2_HUMAN	FCN2	ficollin 2	1.158	-0.972	-0.096	1.444	0.172	0.036	-4.250	-2.594	-4.040	-6.899	-6.105	-2.211	-3.446	-3.760	0.002278	0.015835	-3.133	0.286010	0.521818	-1.498	0.022469	0.125829	-2.616		
sp P21810 PGC1 P21810	BGN_HUMAN	BGN	biginin	-1.522	-0.561	-1.062	0.816	-0.828	-1.935	-2.213	-2.151	-4.044	-5.751	-1.170	-4.527	-4.267	0.002311	0.015934	-3.418	0.002311	0.015934	-3.418	0.002311	0.015934	-3.418	0.002311	0.015934	-3.418
sp Q07877 BTN2A1 Q07877	BTN2A1_HUMAN	BTN2A1	butyrophilin subfamily 1 member 1	0.927	0.486	0.312	2.710	2.802	-0.533	-0.024	-1.088	-1.509	-1.779	-1.646	-2.786	0.328	-3.950	0.002325	0.015934	-3.198	0.026497	0.133162	-2.267	0.075838	0.248564	-1.811		
sp Q08174 PCD Q08174	PCDH1_HUMAN	PCDH1	protocadherin 1	-1.713	-0.547	-4.534	-2.662	1.557	-2.060	-0.014	-1.957	-4.548	-3.156	-3.834	-3.771	-8.959	0.002444	0.016630	-3.329	0.022415	0.126703	-2.027	0.066538	0.828566	-0.164			
sp P36896 ACV P36896	ACV1B_HUMAN	ACV1B	activin A receptor type 1B	1.298	1.399	0.535	1.319	0.578	0.285	0.589	1.133	-1.295	0.312	0.399	-8.639	-1.337	-1.524	0.002518	0.016867	-2.906	0.018994	0.112136	-2.683	0.531385	0.745004	-0.356		
sp P08748 V3 P08748	SPR3_HUMAN	SPR3	small proline-rich protein 3	3.796	0.331	0.822	2.029	2.469	4.871	-3.727	1.217	-4.873	-5.244	-6.570	-9.127	0.030	2.340	0.002530	0.016867	-6.011	0.023064	0.454527	-2.482	0.041095	0.660968	-1.127		
sp P00749 URO P00749	PLAU_HUMAN	PLAU	plasminogen activator-like 1	-0.072	-0.703	0.909	0.773	3.448	-0.926	0.075	1.881	-4.797	-1.550	-2.511	-0.160	-1.275	-2.362	0.002583	0.017102	-2.689	0.020453	0.130590	-2.219	0.571495	0.766122	-0.751		
sp Q05998 IL8 Q05998	IL18BP_HUMAN	IL18BP	interleukin 18 binding protein	3.400	1.004	2.091	2.956	3.307	-0.466	0.277	4.185	-1.098	0.506	0.227	-1.750	-1.729	-3.459	0.002664	0.017407	-3.800	0.016852	0.320769	-2.709	0.025268	0.206231	-0.751		
sp P01040 CYT P01040	CSTA_HUMAN	CSTA	cystatin A (heart,prostate,pancreas)	2.791	-1.448	3.919	-0.288	1.519	-0.399	-8.125	-0.645	-3.099	-3.800	-1.981	-6.166	-0.438	-2.283	0.002650	0.017407	-2.336	0.013929	0.317924	-2.136	0.098108	0.284541	-3.033		
sp Q04157 ANG Q04157	ANGPT7_HUMAN	ANGPT7	angiotensinogen converting enzyme 7	-8.429	-9.252	-7.818	-9.362	-5.173	-6.075	-9.513	-2.679	-5.117	-2.284	-3.589	-4.666	-3.382	-2.919	0.002789	0.017939	3.203	0.230841	0.461681	1.210	0.020671	0.118493	4.817		
sp P05062 ALDO P05062	ALDOB_HUMAN	ALDOB	aldolase, fructose-1,6-bisphosphate	1.015	3.889	-0.289	3.836	3.415	2.515	1.478	2.004	-0.761	-2.317	0.258	-5.783	-1.169	-2.729	0.002819	0.017939	-3.900	0.003456	0.051059	-3.672	0.709238	0.852979	-0.364		
sp P06870 KLU P06870	KLU1_HUMAN	KLU1	kalikrein 1 (kidney/plasma)	3.002	1.271	5.891	6.106	5.764	2.029	0.865	1.239	2.022	-2.996	-7.122	-3.400	-0.965	-0.523	0.002805	0.017939	-5.439	0.016118	0.080300	-3.546	0.032827	0.153781	-3.029		
sp P07204 TRB P07204	TRB_HUMAN	TRB	thrombomodulin	-2.492	-3.024	-2.211	-0.676	-0.966	-3.230	-4.791	-1.841	-2.384	-3.958	-4.923	-5.894	-6.738	-2.212	0.002779	0.017939	-2.339	0.216662	0.452828	-3.456	0.050505	0.203891	-0.609		
sp P00742 FAL1 P00742	FAL1_HUMAN	FAL1	coagulation factor X	-8.184	-9.004	-4.318	-4.676	-3.776	-2.833	-5.216	-6.279	-6.176	-0.964	-4.222	2.136	-0.646	-0.470	0.002926	0.018363	-3.813	0.031917	0.205247	3.053	0.495259	0.714806	1.216		
sp P19827 F10 P19827	F10_HUMAN	F10	inter-alpha-2(I) fibrinogen chain	-2.036	-6.511	-4.237	-4.129	-3.224	0.869	-0.808	-1.760	0.858	1.842	2.585	5.977	4.554	-0.387	0.002911	0.018363	4.868	0.007927	0.124212	2.894	0.038213	0.168061	3.159		
sp P14118 PRN3 P14118	PRN3_HUMAN	PRN3	protease 3	-4.830	-2.398	-5.741	-8.157	-1.746	-2.458	-3.197	-3.239	3.107	-1.565	-3.640	-1.166	2.494	5.687	0.002942	0.018363	-4.255	0.031743	0.580668	1.743	0.069373	0.231919	4.016		
sp Q02109 CTO1 Q02109	CTO1_HUMAN	CTO1	coactosin like F-actin binding protein	1.606	-0.261	4.111	0.969	-0.009	0.939	1.367	3.141	2.684	4.450	5.947	3.610	1.630	2.642	0.002976	0.018458	1.193	0.031639	0.038585	-1.275	0.059579	0.377765	-0.128		
sp P68871 HBB P68871	HBB_HUMAN	HBB	hemoglobin, blood, beta	2.135	2.789	1.229	3.075	4.824	1.904	4.447	3.135	7.236	10.056	9.889	7.881	3.282	6.181	0.003014	0.018531	3.441	0.024230	0.130310	3.214	0.701155	0.848311	3.762		
sp Q092H0 GPC Q092H0	GPC5B_HUMAN	GPC5B	G protein-coupled receptor 5B	0.759	-0.816	0.634	0.421	0.520	-1.240	-3.557	-2.007	-1.334	-1.425	-2.670	-0.171	-3.378	-7.097	0.003025	0.018531	-3.777	0.022706	0.445791	-2.004	0.040161	0.266121	-0.272		
sp P20700 LMM P20700	LMNB1_HUMAN	LMNB1	lamin B1	-4.535	-5.950	-5.256	-8.780	-1.497	-5.688	-4.790	-5.239	-2.495	-3.600	-6.460	-2.928	-1.862	-1.971	0.003154	0.019118	2.637	0.003642	0.051212	2.645	0.967378	0.983309	-0.013		
sp Q1428 SPT Q1428	SPT2_HUMAN	SPT2	serine peptidase 2	1.428	0.889	1.001	0.388	-0.121	0.287	0.461	1.225	-0.239	-1.166	0.115	-2.412	-1.430	1.406	0.003358	0.020315	-1.784	0.015719	0.059492	-1.748	0.076531	0.358699	-0.609		
sp P01780 MM1 P01780	MM9_HUMAN	MM9	matrix metalloproteinase 9	-1.484	-2.088	-6.461	-1.965	-0.937	-0.958	1.232	-1.535	3.535	4.089	-1.599	1.822	0.325	5.420	0.003570	0.021237	-2.249	0.027819	0.051829	-1.903	0.062323	0.293553	-1.417		
sp Q08380 LGI3 Q08380	LGS3B_HUMAN	LGS3B	galactin 3, b1-bone marrow	5.960	6.507	4.824	6.032	5.643	5.588	6.682	7.137	3.997	3.527	5.284	3.546	2.036	2.000	0.003557	0.021235	-2.175								

PEP30086	PEP30086	PEBP1	phosphatidylethanolan	2.785	2.876	2.285	3.848	3.248	1.389	0.799	2.142	1.964	0.363	-1.485	-1.058	-0.180	2.970	0.015174	0.058316	-1.992	0.145099	0.356971	-1.014	0.026810	0.135062	-1.565
PEP02748	CO9_P02748	CE9	complementiver	1.024	-0.905	-4.904	-4.816	-0.770	3.666	1.203	0.168	1.137	3.405	2.471	5.971	6.586	1.110	0.015769	0.060365	4.112	0.362078	0.603513	1.766	0.051337	0.199896	3.753
PEP07475	CO9_P07475	FE20B	fe20b	-4.339	-3.548	-4.408	-2.934	-7.037	3.116	-3.694	-7.291	0.214	0.873	-0.726	-3.273	1.148	-5.549	0.015896	0.060616	2.929	0.229708	0.460555	2.766	0.059537	0.177884	0.857
PEP09564	CO7_P09564	CD7	CD7 molecule liver/muscl	1.430	0.780	0.885	1.167	0.688	-0.841	-4.277	2.509	-1.370	-4.475	-0.199	0.164	-2.313	-2.650	0.016249	0.061483	-1.909	0.211868	0.445559	-1.539	0.030751	0.148452	-0.591
PEP08835	CAB_P08835	SOF4	stromal cell clone	-2.833	-5.853	-0.949	-0.932	-0.686	-3.627	-3.329	-1.899	-3.251	-6.364	-8.895	-6.199	-5.083	-5.171	0.016384	0.061755	-2.475	0.068877	0.272011	-1.029	0.027969	0.150726	-0.714
PEP04040	ADH3B_04040	HV551	None	None	None	None	None	None	None	None	None	None	None	None	None	0.016603	0.062341	3.246	0.498841	0.742024	0.665	0.000808	0.092227	4.129		
PEP09567	FBLN_A09567	EFEM2P	EGF containing fibulin	2.263	0.575	0.433	-2.291	0.445	-0.129	1.199	2.041	-0.771	0.409	0.232	-5.462	-4.144	-0.673	0.016756	0.062674	-2.781	0.095751	0.236950	-0.870	0.066286	0.844017	0.412
PEP01153	RNAI_P01153	RNA52	ribonuclease blood	7.044	4.963	6.088	6.236	6.789	3.640	5.238	6.756	5.613	3.692	5.710	2.262	2.362	5.700	0.016908	0.062765	-2.368	0.300091	0.541601	-2.368	0.032662	0.468364	-1.016
PEP16284	PEP16284	PECAM1	platelet and endothel	-1.582	-1.947	-1.149	-0.982	-1.187	-4.527	-2.269	-5.783	-8.991	-3.272	-2.752	-7.584	-3.070	-4.505	0.016849	0.062765	-2.717	0.016849	0.534548	-1.660	0.039116	0.151834	-1.619
PEP01008	ANTP_P01008	SERPINC1	serpin family member	2.329	4.466	0.810	1.928	2.826	7.987	6.011	4.013	4.818	5.499	6.374	6.291	8.371	3.494	0.017121	0.063652	1.882	0.791353	0.911880	-2.005	0.025676	0.133136	3.339
PEP06748	GA3_Q06748	GASK1B	gask1b associa small,inte	-3.238	-2.763	-2.110	-1.826	-0.935	-1.740	-2.818	-1.058	-4.614	-3.206	-0.682	-4.565	-3.249	-4.291	0.016821	0.063813	-1.335	0.097680	0.290079	-1.410	0.057430	0.276727	0.122
PEP00745	FAL12_P00745	FAL12	coagulation liver/stron	-0.857	-1.554	-3.474	-1.706	-1.633	-3.984	-4.818	-0.631	-1.886	0.864	-2.033	2.019	2.799	0.017617	0.064663	2.536	0.010139	0.298152	-2.964	0.072740	0.881935	-0.433	
PEP04003	C4B_P04003	C4BPA	complement liver	-7.122	-4.272	-2.736	-1.513	-1.475	-11.677	-9.065	-2.819	-0.754	-2.364	-5.728	-7.328	-2.479	0.615	0.017175	0.064700	5.309	0.005556	0.069836	8.078	0.025966	0.135062	-0.430
PEP03740	ILEU_P03740	SERPINC1B	serpin family blood,bon	-3.355	-3.798	-1.117	-12.207	-8.406	-5.275	-5.423	-4.573	-1.684	-4.467	-1.926	-1.200	-3.887	2.248	0.017751	0.064670	4.437	0.007502	0.028388	3.999	0.045266	0.126564	-0.740
PEP02M25	CEC_Q02M25	CE064	None	None	None	None	None	None	None	None	None	None	None	None	None	0.017923	0.065022	-2.162	0.205382	0.434718	-1.040	0.203858	0.427565	-1.795		
PEP08582	TRFA_P08582	MELTF	melanotranskin	-1.160	-2.010	-0.336	-0.413	0.552	-7.435	-2.258	-6.103	-3.926	-3.014	-9.438	-7.451	-3.960	0.018036	0.065252	-1.989	0.840596	0.928736	0.077	0.03703	0.110947	-3.306	
PEP01877	IGHF_P01877	IGHA2	None	None	None	None	None	None	None	None	None	None	None	None	None	0.018221	0.065649	2.736	0.521153	0.744239	0.667	0.009957	0.088448	3.310		
PEP33574	GLR_P33574	GLRX	glutaredoxin	0.128	1.011	-5.980	-2.108	-1.279	1.349	1.880	3.077	4.311	3.455	-5.005	2.922	2.428	0.018341	0.065838	2.377	0.018341	0.065838	2.377	0.017435	0.110947	3.678	
PEP56537	IFE_P56537	EF6	eukaryotic translation	0.464	-2.022	-1.200	1.359	-0.041	0.000	-0.414	1.385	-2.782	-0.769	-2.877	-5.137	-4.619	-3.628	0.018664	0.066754	-2.664	0.009432	0.204176	-2.877	0.747356	0.870788	0.341
PEP01515	KVD_P01515	KVD28	None	None	None	None	None	None	None	None	None	None	None	None	None	0.018927	0.067450	4.086	0.009432	0.076513	5.069	0.056049	0.756613	-1.574		
PEP00274	SUS_Q00274	SUSD2	su5 domain containin	-1.495	-1.004	-7.286	1.041	0.354	-2.945	0.651	-3.097	-2.546	-1.741	-7.928	-5.607	-5.777	0.019087	0.067737	-3.343	0.048006	0.406691	-3.176	0.078435	0.217676	-0.379	
PEP08944	SCU_Q08944	SCUB1	insulin peptide,peripl	3.230	-4.836	-6.117	-5.048	-4.641	-2.635	-3.978	-1.185	-0.466	-2.900	-0.747	-2.371	-3.572	-0.620	0.019365	0.068513	2.101	0.019365	0.068513	2.101	0.029312	0.144350	-0.193
PEP01344	IGF2_P01344	IGF2	insulin like g,polacenta;	-0.279	-1.137	-1.243	-1.102	-1.756	-3.157	-2.425	-1.124	-0.324	0.164	0.207	-1.275	-1.287	-3.325	0.019818	0.068622	1.820	0.118243	0.314450	-1.728	0.068537	0.927627	-0.166
PEP05161	FCG_Q05161	FCG3B	Fc fragment blood	0.181	1.149	0.019	0.997	2.549	-1.434	1.075	2.942	-0.828	-1.325	-0.540	-1.095	-0.484	0.020248	0.071110	-1.600	0.173619	0.397423	-1.089	0.015123	0.503986	-1.812	
PEP09040	MAI_Q09040	MATN4	matn4	0.728	-3.470	0.237	0.123	-2.812	-2.132	-0.205	1.549	-1.359	-4.239	-2.519	-3.932	-6.022	-6.757	0.020890	0.071213	-3.178	0.060809	0.219204	-3.283	0.02141	0.955584	0.169
PEP09074	ENPH_Q09074	ENPH1	enophase	-2.548	-1.216	-2.845	-6.204	-3.701	-9.629	-2.997	-2.766	-0.748	-1.484	-1.903	-0.800	-4.160	-1.898	0.021546	0.075142	2.164	0.039734	0.258734	-3.319	0.016908	0.738373	-1.848
PEP09574	LYPI_Q09574	LYPD3	enoyl-PLAUR domain c	-1.057	-3.847	-1.251	-2.297	0.078	-2.129	-3.804	-2.256	-2.215	-5.962	-5.327	-2.972	-3.144	-4.883	0.021634	0.075142	-2.440	0.021634	0.258734	-3.319	0.033303	0.532947	-1.785
PEP01584	ADIP_Q01584	ADIPQ1	adiponectin, serpin, tiss	-1.700	-5.117	-4.124	-7.477	-0.806	-0.886	0.516	-5.692	-2.619	-0.250	-4.377	0.074	-0.504	-2.175	0.021919	0.075704	3.068	0.019389	0.367399	-2.964	0.013738	0.336829	3.464
PEP08842	TDQ_Q08842	TDKDC17	thiodionin	-4.998	-2.387	-2.001	-4.552	-1.822	-3.249	-3.762	-1.459	0.608	-0.658	-1.632	-11.259	-0.905	0.838	0.021939	0.075704	1.674	0.060551	0.219204	0.656	0.030348	0.525196	1.629
PEP00390	GSHI_P00390	GSR	glutathione-disulfide re	-5.650	-3.263	-1.751	-5.523	-2.966	-1.819	-1.463	-1.151	0.017	-1.116	-0.627	-1.729	-1.569	0.970	0.022894	0.078447	2.000	0.018368	0.561605	-0.801	0.030650	0.161701	2.239
PEP01772	HV3_P01772	HV333	None	None	None	None	None	None	None	None	None	None	None	None	None	0.022887	0.078447	3.756	0.024909	0.970743	0.673	0.045190	0.185135	-0.909		
PEP06744	GPI_P06744	GPI	glucose-6-phosphate is	-4.535	-2.495	-3.850	-3.825	-1.199	-2.574	-2.152	-3.261	-0.461	-2.296	-4.249	-1.888	-0.731	1.931	0.023217	0.078447	2.588	0.094038	0.202393	-2.744	0.077857	0.882927	2.297
PEP02520	FAM_Q02520	FAM3C	FAM3 metabolism regu	-0.074	1.701	0.377	1.574	1.753	1.501	2.695	3.440	3.872	5.244	1.710	2.515	3.099	0.023294	0.079264	0.312	0.267087	0.504266	-0.260	0.212389	0.441116	0.916	
PEP37873	TALD_P37873	TALD1	transaldolase	-1.324	-1.877	-2.846	-2.108	-4.048	-2.166	-4.227	-1.219	2.580	-1.088	-2.288	-0.974	-0.672	5.928	0.023387	0.079264	2.967	0.06565	0.250513	-2.527	0.059000	0.377765	0.060
PEP00978	SGP_Q00978	SBSN	SBSN	-5.041	-4.791	1.757	-5.602	-11.909	0.795	-4.858	-3.501	-2.755	-0.035	-2.123	-4.444	-0.937	2.866	0.023459	0.079264	2.906	0.038157	0.612095	1.284	0.128733	0.321832	2.596
PEP08554	DCI_Q08554	DCI	diaminocillin 1	-1.957	1.071	-8.628	-3.818	-3.334	-0.949	-8.786	-6.716	-0.403	-8.664	-1.573	-1.990	-2.391	0.044	0.023459	0.079264	4.276	0.023459	0.612095	1.284	0.038157	0.612095	-3.372
PEP00738	CKAR_P00738	CKAR	CKAR (g-likilarym	-3.464	-2.958	-7.003	-1.977	-2.611	-2.923	-3.002	-2.599	-6.167	-3.993	-3.672	-5.621	-4.423	-6.029	0.023459	0.079264	1.105	0.023459	0.612095	1.284	0.038157	0.612095	0.941
PEP00738	HPT_P00738	HPT	haptoglobin liver	7.223	1.447	3.931	2.556	2.512	6.541	10.983	6.086	6.132	7.685	9.029	11.880	11.405	7.372	0.024226	0.081030	3.101	0.044655	0.760344	1.048	0.162004	0.363651	3.141
PEP08519	APOA_H08519	APOA	None	None	None	None	None	None	None	None	None	None	None	None	None	0.024260	0.081030	1.919	-1.193	0.024260	0.124658	-1.502	0.040862	0.631995	0.494	
PEP00747	PLM_P00747	PLG	plasminogen/kidney	3.504	2.294	3.933	1.684	2.452	3.360	5.508	2.788	4.244	5.123													

sp Q8N307 MU08307	MUC2O_HUMAN	MUC2O	mucin 2O, cecidney	-0.719	-2.658	-1.387	-0.678	1.468	-3.105	-4.932	-1.800	-2.354	-2.319	-5.471	-7.403	-6.246	-2.010	0.033468	0.136456	-2.575	0.584767	0.781817	-1.023	0.042863	0.180598	-2.484		
sp P55299 EPN2_P55299	EPN2_HUMAN	GP2	glycophorin b	1.507	-0.894	-0.278	-0.977	1.324	0.281	-3.518	2.030	-0.032	-0.869	0.898	-3.487	-1.744	0.000	0.053678	0.136659	-4.709	0.549924	0.764433	-0.969	0.345309	0.571627	-1.185		
sp P55299 EPN2_P55299	EPN2_HUMAN	EPN2	glycophorin b	-5.281	-0.309	-1.124	-7.984	-5.084	-3.000	-8.525	-1.123	-1.957	-1.922	-0.896	-3.400	-2.400	-2.336	0.054037	0.136659	2.257	0.507483	0.401121	-0.264	0.888423	0.943288	0.309		
sp P55150 SCG5_P55150	SCG5_HUMAN	SCG5	secretory phospholipase A2	0.525	-3.141	-0.422	-0.606	0.874	-2.179	-3.040	0.010	0.010	0.010	-0.574	-1.215	-0.741	-0.010	0.059963	0.147539	-4.848	0.242433	0.133010	2.213	0.157396	0.365356	0.680		
sp P17931 LEG3_P17931	LEG3_HUMAN	LEG3	galactin 3	-2.350	-2.026	-3.446	-5.315	-1.477	-2.220	-1.768	-6.447	0.151	0.558	-2.210	-6.397	-1.253	0.171	0.054293	0.137123	2.201	0.121956	0.330158	1.215	0.872855	0.926909	1.622		
sp P28065 PSA5_P28065	PSA5_HUMAN	PSMA5	proteasome 20S subunit alpha 5	-2.361	-4.230	-6.291	-5.772	-7.879	-0.076	-2.393	-7.646	-1.050	-2.800	-1.960	-4.100	-0.412	0.055207	0.139032	2.419	0.576039	0.778338	2.184	0.399807	0.619202	1.817	0.000000	0.000000	0.000000
sp Q02747 GUC_Q02747	GUC2A_HUMAN	GUC2A	guanylate cyclase activator 2	2.143	0.937	0.515	-0.962	-2.222	2.903	4.055	3.680	4.000	4.976	2.832	-0.657	4.432	4.300	0.000	0.055376	0.139151	1.686	0.31236	0.808337	-0.229	0.016743	0.063409	3.064	
sp P60953 GUC_P60953	DCO2C_HUMAN	DCO2C	cell division cycle 42	-2.454	-2.691	-1.596	-1.911	-1.696	-3.501	-5.622	-1.776	-2.447	-1.207	-3.663	-1.646	-5.111	0.196	0.055580	0.139305	1.333	0.201294	0.808366	-0.279	0.001948	0.378066	-1.184		
sp Q04370 ACT_Q04370	ACTN4_HUMAN	ACTN4	actinin alpha 4	-2.364	-3.200	-2.817	-2.651	-4.271	-2.670	-4.777	-4.102	-1.447	-2.754	-3.349	-2.022	-2.332	0.000	0.055959	0.139888	2.447	0.070078	0.240970	2.940	0.181942	0.393568	-0.789		
sp Q14559 DIAC_Q14559	DIAC_HUMAN	CTBS	chitinase b	0.310	0.919	0.870	-1.106	1.896	2.763	3.762	3.140	2.199	2.883	2.249	2.279	2.805	-0.528	0.056472	0.140821	-2.166	0.100672	0.296271	-2.740	0.201348	0.425261	-2.740		
sp Q09715 COL_Q09715	COL12A1_HUMAN	COL12A1	collagen type XIII, alpha 1	-0.266	-0.086	-0.326	1.781	0.239	-2.954	-3.508	-1.104	-2.978	-0.225	-6.043	-3.580	-5.904	-0.504	0.056982	0.141231	2.743	0.445636	0.806150	-0.720	0.000979	0.024758	-2.760		
sp Q09715 COL_Q09715	APOC1_HUMAN	APOC1	apolipoprotein I	-0.615	-3.909	-9.301	-5.076	-0.414	-2.292	-1.307	-2.674	-2.713	-0.416	-5.740	-3.380	-2.247	-0.147	0.057483	0.142618	2.893	0.358798	0.620995	-1.455	0.009388	0.178170	2.952		
sp Q14495 ISR_Q14495	ISR_HUMAN	ISR	immunoglobulin heavy chain constant 1	0.523	1.973	-0.352	0.572	1.894	1.679	1.378	1.780	2.024	1.865	1.572	3.333	-0.624	0.000	0.059903	0.147539	-4.848	0.059903	0.147539	-4.848	0.059903	0.147539	-4.848		
sp P02647 APO_P02647	APOA1_HUMAN	APOA1	apolipoprotein A1	2.238	1.268	-2.257	2.441	0.063	6.169	4.969	2.486	4.723	6.236	2.717	10.096	8.487	5.980	0.059919	0.147539	2.206	0.269980	0.504925	1.832	0.391045	0.612464	1.591		
sp Q09864 CLM_Q09864	CLMP_HUMAN	CLMP	cadherin-like fibronectin type III domain containing 1	-5.283	0.079	-2.792	-1.871	-0.562	0.486	0.414	1.132	-3.529	-0.225	-2.179	-6.096	-1.049	-2.828	0.059862	0.147539	-2.204	0.059862	0.147539	-2.204	0.059862	0.147539	-2.204		
sp P12830 CAD_P12830	CDH1_HUMAN	CDH1	cadherin 1	4.335	5.314	2.036	3.777	2.911	4.864	5.965	5.323	2.443	3.653	4.446	-2.286	2.580	1.047	0.061048	0.149942	-2.206	0.061048	0.149942	-2.206	0.061048	0.149942	-2.206		
sp Q04279 SEM_Q04279	SEMG1_HUMAN	SEMG1	semaphorin 1	9.902	-8.217	-5.001	-7.606	-5.041	-6.334	-3.198	-3.411	2.983	-1.848	-4.286	-1.348	-5.840	0.061048	0.150147	2.016	0.061048	0.150147	2.016	0.061048	0.150147	2.016			
sp P05937 CAL_P05937	CALB1_HUMAN	CALB1	calbindin 1, kidney	-2.653	-2.404	-4.228	-2.919	-0.775	-1.218	-2.443	-2.758	-2.176	-5.771	-11.382	-3.254	-3.968	0.000	0.061438	0.150147	-2.784	0.179097	0.240790	-2.694	0.881421	0.939476	-1.144		
sp P06727 APO_P06727	APOA4_HUMAN	APOA4	apolipoprotein A4	1.987	-1.566	-0.213	1.126	3.640	1.201	1.622	4.600	3.817	-1.406	6.509	7.830	1.560	0.062056	0.151281	2.218	0.062056	0.151281	2.218	0.062056	0.151281	2.218			
sp P61158 HBP1_P61158	ARR3_HUMAN	ACTR3	actin related protein 3	-0.538	-4.449	-5.945	-7.554	-2.469	-5.539	-9.549	-6.253	-1.161	-5.469	-2.105	-5.329	-2.688	2.531	0.062959	0.153075	2.920	0.061317	0.100118	7.477	0.117216	0.380859	-2.923		
sp Q09803 SCR_Q09803	SRR3_HUMAN	SCR3	serpin carrier family 3, member 3	1.881	0.971	-0.488	0.627	0.217	1.966	2.838	0.077	1.909	1.526	4.348	0.863	-3.028	0.000	0.063750	0.153075	2.845	0.063750	0.153075	2.845	0.063750	0.153075	2.845		
sp Q167750 H2A_Q167750	H2AC2_HUMAN	H2AC2	H2A clustered histone	-1.030	-1.652	-0.608	-2.895	-2.663	-7.388	-5.847	-0.948	-2.788	-3.147	-0.832	-0.830	-3.643	0.063650	0.153075	2.840	0.063650	0.153075	2.840	0.063650	0.153075	2.840			
sp Q145240 HLA_Q145240	HABP2_HUMAN	HABP2	hyaluronan binding protein 2	-5.184	-3.828	-3.573	-8.119	-5.459	-1.524	-4.821	-2.574	-6.035	-1.312	-6.466	-3.211	2.388	-2.568	0.064174	0.154523	2.737	0.062101	0.808337	0.861	0.136954	0.368289	-2.259		
sp Q60W409 MLG_Q60W409	MUC6_HUMAN	MUC6	mucin 6, oligomeric core 1 type	1.468	-7.022	-4.833	-6.530	-4.813	-6.827	-4.121	-4.827	-0.504	-5.597	-4.771	-1.538	-4.020	-2.070	0.064119	0.154523	1.716	0.126932	0.336540	2.847	0.923967	0.960258	1.009		
sp Q02956 TIR_Q02956	TNFRSF14_HUMAN	TNFRSF14	TNFR type I receptor class 1 member 14	3.020	2.236	-4.911	2.214	0.744	1.516	3.330	0.610	0.685	0.943	1.663	-3.411	-0.074	-1.119	0.066421	0.159540	-1.000	0.156768	0.376561	-1.109	0.881844	0.943288	-1.828		
sp P55285 CAD_P55285	CDH6_HUMAN	CDH6	cadherin 6, kidney/ovary	-2.058	-1.117	-0.963	-2.689	-1.483	-5.945	-2.860	-0.789	-1.643	-1.643	-1.643	-1.643	-1.643	-1.643	0.066686	0.159786	-1.985	0.090332	0.858162	-0.909	0.225074	0.592285	0.721		
sp P03952 KLUK_P03952	KLK1B_HUMAN	KLK1B	kallikrein B1, liver	-4.870	-4.228	-5.702	-2.992	-3.959	-7.915	-4.289	-1.675	-7.748	-4.424	-2.751	2.746	0.010	-0.562	0.066959	0.160408	2.020	0.066862	0.643104	2.235	0.950208	0.980654	-0.343		
sp P51384 LUM_P51384	LUM_HUMAN	LUM	lumican	2.524	2.466	-7.149	0.783	1.468	-0.102	2.911	2.043	3.009	3.924	3.233	3.314	3.551	1.111	0.070035	0.161696	1.869	0.058033	0.676678	0.636	0.153047	0.354227	2.934		
sp Q09803 SCR_Q09803	SRR3_HUMAN	SCR3	serpin carrier family 3, member 3	1.881	0.971	-0.488	0.627	0.217	1.966	2.838	0.077	1.909	1.526	4.348	0.863	-3.028	0.000	0.063750	0.153075	2.845	0.063750	0.153075	2.845	0.063750	0.153075	2.845		
sp Q03551 CHR_Q03551	CHFR1_HUMAN	CHFR1	complement factor 1	-0.987	-0.106	-1.732	-1.739	-1.277	0.170	-0.051	-8.409	-1.027	-3.640	-1.128	-4.459	-4.341	1.945	0.070411	0.167707	3.483	0.142288	0.355372	4.051	0.960337	0.980564	-9.190		
sp P07148 FABP_P07148	FABP1_HUMAN	FABP1	fatty acid binding protein 1	1.548	0.249	-0.463	0.829	-1.274	2.156	0.656	1.852	3.802	2.321	3.062	-2.908	1.693	0.942	0.070764	0.167105	3.237	0.045725	0.827339	-0.069	0.604239	0.180598	-2.059		
sp P62805 H4_P62805	H4_HUMAN	H4	histone H4	-2.241	-1.329	-3.169	-5.981	-2.357	-0.149	-2.475	0.455	2.329	-5.546	-2.031	0.792	-0.137	5.034	0.070715	0.167105	2.563	0.575400	0.778338	1.130	0.046941	0.190254	-2.132		
sp P60645 TSPN_Q60645	TSPAN1_HUMAN	TSPAN1	tetraspanin 10	-0.726	-1.399	-3.958	-1.173	-1.109	-3.677	-1.376	-6.080	-1.450	-3.574	-0.181	-2.662	-2.867	-6.038	0.071200	0.167300	-0.221	0.287740	0.532047	-0.127	0.001740	0.944352	1.299		
sp P12883 MYH_P12883	MYH7_HUMAN	MYH7	myosin heavy chain, muscle, ventricular, adult, 7	8.034	-4.540	-2.758	-3.029	-3.609	-6.160	-3.669	0.369	2.301	0.788	2.145	-4.928	-2.531	-4.810	-3.848	0.072113	0.169474	2.481	0.194300	0.627380	1.167	0.739016	0.866310	0.503	
sp Q13653 PSC_Q13653	PSCA_HUMAN	PSCA	prostate stem cell antigen	2.378	-1.326	-2.848	-0.945	-3.357	0.000	0.752	-1.585	-4.490	-2.859	0.009	-2.756	3.028	0.073314	0.171814	-1.988	0.378471	0.373729	-1.935	0.974609	0.984094	-0.084			
sp Q08474 SFRP_Q08474	SFRP1_HUMAN	SFRP1	secreted frizzled related protein 1	-6.801	-2.431	-6.176	-1.737	-2.919	-1.841	-1.784	-3.400	-8.754	-8.009	-2.484	-7.125	-6.119	-2.052	0.073361	0.171814	-2.415	0.000704	0.069993	-2.533	0.512883	0.442605	1.789		
sp P08890 HLA_P08890	HLA_B_HUMAN	H2B	major histocompatibility protein 2, beta chain	-7.757	-0.150	-3.996	-0.743	-1.563	0.908	1.269	-2.137	0.755	1.556	-1.865	-7.017	-1.758	0.000	0.073746	0.171814	-1.178	0.008030	0.504266	-2.179	0.068845	0.644017			



EN01	EN01	enolase 1	1.563	2.093	1.919	3.279	3.488	1.693	1.147	2.356	4.121	2.922	-2.384	1.020	0.420	6.463	0.322101	0.491680	-0.400	0.383485	0.616090	-0.065	0.485638	0.705075	-0.536		
EN23A	ANP23A	acidic alpha phospho	-3.703	-7.016	-6.452	-4.820	-4.168	1.128	-5.273	-4.065	-0.838	-2.294	-0.903	-7.302	-6.468	1.000	0.322624	0.491713	1.422	0.799903	0.990793	-0.054	0.153650	0.355974	2.362		
ACT1	ACT1	actin nucleus 1	-0.825	-1.109	-0.604	-1.461	-1.155	-2.781	-3.660	-1.919	2.361	-2.143	-2.497	0.400	-7.539	5.113	0.327390	0.497675	0.934	0.138691	0.425248	1.200	0.116200	0.091908	-1.760		
ACT2	ACT2	actin family liver	8.915	8.009	8.549	8.009	8.009	8.009	8.009	8.009	8.009	8.009	8.009	8.009	8.009	8.009	0.327390	0.497675	0.934	0.138691	0.425248	1.200	0.116200	0.091908	-1.760		
LV67	LV67	None	-9.154	-1.646	-9.273	-2.297	1.316	0.227	0.000	-0.967	-1.893	1.411	1.338	-0.142	-1.336	-1.861	0.335718	0.509294	2.263	0.863780	0.934931	-0.167	0.046107	0.178838	3.984		
G3P	GADPH	glyceraldehyde bde	2.021	2.730	0.930	1.282	1.820	0.439	0.388	2.689	1.586	0.830	0.859	2.200	2.804	5.828	0.400771	0.512459	1.164	0.400771	0.669099	1.113	0.733555	0.801935	0.082		
MM7	MM7	matrix metalloprotein	-2.681	-0.094	-0.832	-3.003	-2.223	0.215	-1.500	-1.800	-0.518	-3.412	-2.106	-5.710	-3.504	-0.833	0.339968	0.514510	-1.006	0.122888	0.445791	-1.718	0.359784	0.583756	1.138		
GGH	GGH	gamma-glutamyl hydro	-4.111	3.664	-1.648	1.910	0.212	0.525	2.319	1.096	2.938	1.924	2.268	-1.348	-1.487	-0.440	0.404056	0.514396	-0.799	0.689423	0.858162	-0.769	0.203689	0.424879	-0.536		
TYPH	TYPH	thymidine phosphoryl	-0.989	-6.245	-0.753	-9.086	-1.348	-2.011	-0.961	-7.747	-1.219	-1.430	0.991	-1.845	-1.001	0.341333	0.514264	1.856	0.332731	0.565366	2.222	0.607730	0.928823	-0.377	0.050730	0.198862	3.892
CAH	CAH	carbic anabolic	-1.209	1.690	-0.475	-1.080	-1.427	-0.171	-0.986	-4.407	-1.207	1.240	0.992	1.133	-6.804	-2.296	0.350829	0.516219	-1.736	0.572582	0.577189	-1.736	0.128217	0.859887	-0.585		
None	None	None	-3.127	1.587	-1.049	-2.483	-0.303	-1.738	-0.414	-1.415	-1.255	2.313	0.708	2.114	-1.022	0.350440	0.527319	2.056	0.776612	0.902823	2.056	0.050730	0.198862	3.892			
CRYM	CRYM	crystallin mu	-4.523	0.000	-0.399	-5.311	-3.082	-1.324	-5.749	-2.893	-3.765	-3.769	-3.815	-1.178	-7.459	-0.482	0.353239	0.526129	-1.148	0.167730	0.409916	-1.077	0.060919	0.151178	-1.322		
HNRFP	HNRFP	heterogeneous nuclear	-1.338	-7.269	0.468	0.113	-5.284	-7.794	-1.822	-2.157	2.935	-2.297	-2.116	-2.996	-2.635	0.359299	0.526938	-0.181	0.004749	0.059466	2.276	0.000483	0.023856	-3.932			
None	None	None	-2.901	-0.406	-1.770	-0.388	-0.514	1.620	2.290	0.915	-0.557	-0.407	1.008	0.384	1.120	0.367002	0.539310	0.270	0.219082	0.452595	-0.682	0.068008	0.065353	2.804			
LYVE1	LYVE1	lymphatic veclanta	3.576	0.108	0.222	1.169	0.527	1.621	3.723	3.709	3.937	2.684	3.003	0.139	2.149	1.471	0.360807	0.539130	0.876	0.007349	0.070766	-2.051	0.107767	0.295646	1.749		
RNASE4	RNASE4	ribonuclease iv	-3.050	-4.131	-1.493	-6.569	-3.758	-9.447	-3.157	-0.135	-4.978	0.169	-0.541	-0.939	-1.440	0.362826	0.542101	1.543	0.472602	0.695421	1.543	0.694966	0.843435	-0.446			
STIP1	STIP1	stress induced phosph	-3.237	-5.157	-4.425	-0.915	-2.877	-5.803	-6.268	-5.284	-5.157	-5.001	-1.448	-2.884	-2.261	-1.877	0.043412	0.542741	1.289	0.087394	0.274442	1.821	0.024435	0.130145	-0.304		
DEFA6	DEFA6	defensin alpha 6	-5.415	-5.148	-0.469	-0.032	-0.238	-5.838	-3.008	-7.232	-11.379	-2.700	-2.466	-7.845	-5.246	-2.355	0.370469	0.550925	-1.921	0.899956	0.955333	-1.921	0.157299	0.363636	-3.094		
TP1	TP1	tumor protein, translat	-2.967	-2.697	-2.826	-4.780	-3.840	-6.099	-2.618	-7.100	-2.977	-1.203	-6.916	-4.182	-3.881	-2.027	0.373280	0.552927	0.892	0.191175	0.417265	1.741	0.182117	0.393568	-1.359		
AP0H	AP0H	apolipoprotein liver	4.672	4.969	9.887	4.258	4.241	5.950	4.650	2.937	3.949	3.700	2.737	6.967	7.360	5.477	0.374432	0.535439	0.954	0.710807	0.866586	0.524	0.597200	0.777777	0.687		
CTSB	CTSB	cathepsin B	3.304	4.637	0.521	3.044	2.570	2.760	4.394	2.590	4.476	2.824	3.175	2.208	2.197	1.832	0.374388	0.535439	0.954	0.167115	0.607612	-1.198	0.781524	0.882927	0.433		
YWHAE	YWHAE	tyrosine 3-monooxyge	-2.542	-0.831	-1.935	-4.244	-1.130	-1.449	-1.282	-1.570	-1.123	-3.769	0.259	-0.291	-5.092	-6.631	0.374337	0.535439	-0.796	0.374337	0.535439	-0.796	0.527407	0.882727	-0.652		
CP	CP	ceruloplasmin	5.346	7.729	2.971	4.224	0.403	8.737	9.083	5.108	5.317	7.002	8.470	9.129	8.957	3.800	0.375727	0.554537	1.225	0.767205	0.901511	-0.515	0.008497	0.025126	1.784		
PRSS23	PRSS23	serine protease 23	-4.133	-5.752	-2.512	-8.610	-3.685	-2.384	-5.971	-1.013	-2.277	-6.008	-4.691	-5.120	-6.836	-3.201	0.376787	0.555266	1.242	0.953419	0.983095	-0.116	0.303664	0.525292	2.804		
TGOLN2	TGOLN2	trans-golgi network p	-3.437	-1.765	-2.932	-4.243	-3.401	-4.290	0.886	3.071	-1.972	-4.536	-6.099	-4.945	-3.430	-1.327	0.380904	0.560489	-1.014	0.394048	0.673380	-1.460	0.920786	0.920807	0.713		
CSF1	CSF1	colony stimulating fac	4.206	2.038	2.469	2.553	2.056	2.970	3.186	3.368	4.544	3.952	-2.885	2.842	-1.523	0.381724	0.560848	-1.671	0.232627	0.423632	-1.226	0.242781	0.471940	-0.880			
VWF	VWF	von Willebra's tiss	-3.282	-2.863	-4.710	-4.859	-3.721	-2.574	-4.309	-3.147	-0.886	-6.334	-4.133	-2.922	-4.000	0.384321	0.563824	1.390	0.843632	0.927258	0.855	0.348137	0.573400	0.859			
ACTG1	ACTG1	actin gamma 1	3.871	4.757	3.656	4.935	5.018	4.214	3.454	5.303	6.092	4.686	3.330	4.835	3.861	7.462	0.385135	0.564174	0.742	0.299671	0.541601	0.985	0.555054	0.766632	-0.391		
None	None	None	0.465	0.614	2.159	3.289	3.173	2.598	2.564	3.013	2.143	3.983	4.235	4.000	2.940	0.397370	0.566601	0.215	0.476080	0.698441	0.315	0.744201	0.868554	0.141			
ENDO1	ENDO1	endonuclease domain	3.892	4.513	-0.090	1.680	1.140	0.200	4.323	4.824	4.347	3.975	3.946	-5.894	0.973	1.981	0.390042	0.569658	-1.802	0.004600	0.075153	-1.153	0.020910	0.113217	-1.162		
S100A8	S100A8	S100 calcium bound	0.458	0.206	0.327	-1.095	0.771	1.185	-4.226	-3.201	4.241	-2.478	-4.846	-1.199	4.116	0.392742	0.572748	0.988	0.345619	0.591717	2.685	0.034212	0.156670	-2.714			
SDC1	SDC1	syndecan 1	-1.570	-1.011	-0.670	0.526	-1.127	-1.679	0.854	0.000	1.740	1.630	1.436	-6.142	-0.432	-1.625	0.393745	0.573388	0.056	0.282929	0.923568	0.253	0.279100	0.503716	0.495		
ITM2B	ITM2B	integral membrane p	-6.253	-5.963	-6.128	-4.847	-2.655	-9.167	-6.155	-4.866	-7.400	-4.040	-2.986	1.259	-5.935	-2.337	0.396675	0.576768	1.506	0.299260	0.541601	-2.435	0.432596	0.653689	-1.040		
ASA1	ASA1	N-acetylcholine amid	-2.368	3.709	-4.755	2.241	1.767	2.737	3.121	0.728	3.164	1.969	2.679	-1.179	0.594	0.342	0.397383	0.576621	-0.346	0.432314	0.666382	-1.052	0.728433	0.860077	-1.130		
PDGFB	PDGFB	platelet derived tonge	0.078	0.336	-0.699	-1.872	-2.029	-2.156	-2.047	-1.488	-1.368	-1.321	-1.249	-4.860	-1.445	0.399243	0.575941	0.814	0.819658	0.919495	-0.319	0.191603	0.407778	-0.792			
SELENP1	SELENP1	selenin binding prot	-2.347	-2.001	-1.983	-1.617	-2.244	-5.468	-5.020	-3.505	-0.853	-1.376	-2.184	-1.793	-4.291	-3.009	0.398503	0.577521	0.667	0.041954	0.097033	0.470	0.006004	0.019825	-2.916		
CFI20	CFI20	chromosome 6 open r	-2.193	-0.914	-6.283	-6.899	-4.933	-0.831	-0.430	-2.190	-2.956	-1.556	-0.942	-0.996	-3.067	0.399550	0.577521	1.205	0.167519	0.593007	1.210	0.255957	0.585727	3.076			
ZG16	ZG16	zymogen gran proteas	-0.631	1.259	-2.709	1.114	-2.665	-4.844	2.036	0.497	-1.704	-1.869	2.066	3.700	-1.825	0.340747	0.578249	0.332	0.494047	0.656848	0.332	0.232667	0.456587	0.707			
CT4	CT4	cystatin 5	0.439	-2.870	-4.281	-1.142	-2.145	-4.594	0.561	-0.828	-1.435	-3.636	-3.160	-3.973	-6.482	-0.060	0.405563	0.583161	-0.070	0.366694	0.607612	-1.526	0.356242	0.583756	0.780		
CX	CX	complement soft, ti	2.203	1.522	-1.287	1.903	0.273	2.160	2.260	2.665	0.378	2.527	2.038	4.166	4.388	2.101	0.405658	0.583161	0.670	0.232331	0.809125	0.526	0.650760	0.820984	-0.210		
SRL	SRL	sarcosine	-0.259	-1.317	-0.156	-8.988	-1.945	-8.409	-4.298	-1.489	-2.586	-4.556	-1.275	-3.766	-3.091	-3.427	0.405833	0.583161									





sp P61224 RAP1P61224	RAP1B_HUMAN	RAP1B	RAP1B, member of RAS	-3.379	-4.160	-3.072	-2.384	-3.682	-4.563	-8.681	-1.932	-1.706	-3.030	-4.730	-8.609	-3.943	-1.316	0.793911	0.864841	0.092	0.516638	0.741525	1.170	0.172735	0.382122	-1.723
sp P01619 KV3 P01619	KV320_HUMAN	None	None	-1.208	5.183	1.289	1.139	1.956	6.366	6.480	6.524	4.475	6.741	6.493	5.427	0.828	3.372	0.798476	0.866653	0.411	0.052364	0.204176	-1.901	0.066680	0.066533	3.699
sp Q6P138 ATAI Q6P138	ATAD2_HUMAN	ATAD2	ATPase family AAA domain containing	-1.403	-0.417	-1.796	-3.752	-7.152	-0.421	0.539	0.582	-0.927	0.944	1.430	-1.012	-4.866	-2.551	0.798460	0.866563	0.564	0.160737	0.381793	-1.397	0.017348	0.110947	3.137
sp Q92800 EMJ Q92800	EMILIN2_HUMAN	EMILIN2	elastin microfibrillar associated protein 2	-1.432	-0.898	-2.047	-3.445	-5.750	-8.055	-3.940	-6.875	-2.894	-5.006	-5.650	-4.094	-3.927	-4.006	0.797398	0.866563	0.399	0.058092	0.218984	-1.029	0.036028	0.161701	-3.565
sp Q00584 RTI Q00584	RNT2_HUMAN	RNASET2	ribonucleasase spleen	0.496	3.311	-3.225	-0.879	-0.283	1.514	2.661	1.885	3.074	3.446	3.212	-4.053	-1.054	-0.549	0.800916	0.866250	0.202	0.639028	0.823477	-1.029	0.024417	0.130145	2.069
sp AA047586 I AA047586 I	LV460_HUMAN	None	None	-3.248	-4.008	-3.528	-3.234	-0.699	-0.275	-5.273	-3.078	-3.852	-1.078	-1.455	-4.481	-1.813	-0.531	0.805066	0.871785	-0.707	0.828836	0.923558	-1.076	0.780801	0.892702	-1.114
sp Q00264 PGR Q00264	PGRMC1_HUMAN	PGRMC1	progesteron/periphera	-2.715	-1.593	-0.815	-4.777	-3.642	0.432	-0.486	-2.001	-2.512	-4.526	0.285	-0.952	1.878	-2.489	0.805990	0.871821	0.151	0.244296	0.476912	-2.051	0.023626	0.128630	3.524
sp P04083 ANX P04083	ANXA1_HUMAN	ANXA1	annexin A1	2.112	2.462	3.542	-6.119	-4.685	4.204	-2.243	-3.064	1.832	-2.876	-5.762	-1.012	-1.460	2.294	0.811683	0.876045	-0.501	0.181703	0.919495	-0.569	0.973990	0.984094	0.100
sp P98172 EFNF P98172	EFNB1_HUMAN	EFNB1	ephrin B1	1.392	0.908	-1.340	-0.870	-2.253	2.408	2.154	2.523	0.727	2.144	1.951	-2.205	0.788	1.595	0.811218	0.876045	0.468	0.114271	0.317924	-1.528	0.031302	0.027236	3.195
sp P31025 LCN1 P31025	LCN1_HUMAN	LCN1	lipocalin 1 eye	-0.197	0.796	-8.663	-2.789	-1.489	0.403	2.090	2.206	1.301	-1.091	-2.567	-3.616	-1.429	1.268	0.815728	0.879434	0.837	0.236850	0.468915	-1.733	0.026101	0.134625	4.111
sp P22792 CPN P22792	CPN2_HUMAN	CPN2	carboxypeptidase N sub	1.124	1.711	-2.470	2.850	1.034	1.010	1.619	0.430	0.304	1.597	1.930	3.246	1.382	-3.907	0.819268	0.880098	-0.155	0.708656	0.866586	-0.261	0.692243	0.844017	0.170
sp Q00796 DHS Q00796	DHSO_HUMAN	SORD	sorbitol dehydrogenase	-3.799	-2.209	-5.960	-2.443	-1.764	-1.162	-2.902	-4.987	0.757	-6.459	-5.760	-2.079	-3.897	-6.488	0.820757	0.880098	-0.120	0.648542	0.829777	-1.029	0.162900	0.369941	-1.839
sp Q10588 BST Q10588	BST1_HUMAN	BST1	bone marrow stromal	-1.679	-2.244	0.668	-4.747	-4.884	-3.599	-1.060	-2.473	-1.782	-3.361	-1.998	-3.632	-2.668	-1.025	0.818851	0.880098	0.091	0.973295	0.988216	-0.033	0.769088	0.979470	0.200
sp Q88828 TXN Q88828	TXND5C_HUMAN	TXND5C	tyrosinase domain con	-0.134	-0.972	-1.678	-3.667	-0.859	-11.252	-1.166	-1.182	-1.934	1.059	1.011	-6.118	-0.802	-2.560	0.820367	0.880098	0.762	0.694539	0.858162	-1.139	0.882605	0.935476	-2.883
sp P00167 CVS P00167	CVS5_HUMAN	CVS5A	cytochrome liver	-1.276	-2.875	-3.172	-1.276	-3.216	-0.786	-3.402	-2.562	-0.922	-1.222	-2.775	-4.778	-5.071	-4.641	0.823911	0.882447	-0.183	0.424852	0.658790	-1.290	0.582605	0.581344	-2.820
sp P07900 HS9 P07900	HS90A_HUMAN	HSP90AA1	heat shock protein 90	-1.562	-1.101	-6.483	-1.363	-2.644	-2.177	-0.486	0.150	-3.677	-3.484	0.429	-2.322	-3.258	1.580	0.823918	0.882447	0.444	0.687741	0.857604	-0.677	0.204811	0.472963	1.793
sp P17066 HSP P17066	HSP76_HUMAN	HSPA6	heat shock protein fam	-1.774	-1.771	-5.786	-1.178	-0.601	-5.657	-3.623	-1.191	-2.265	-3.714	-3.366	-2.366	-3.102	1.289	0.827461	0.884310	0.361	0.027120	0.257150	-1.673	0.003094	0.016374	-1.938
sp P81172 HEP P81172	HEPC_HUMAN	HAMP	hepcidin antimicrobial	5.678	3.183	2.350	-0.496	-2.067	2.772	2.603	5.885	1.013	4.443	5.826	-3.051	4.601	2.339	0.827199	0.884310	0.040	0.636900	0.822348	-1.224	0.261340	0.486907	2.023
sp P11142 HSP P11142	HSP7C_HUMAN	HSPA8	heat shock protein fam	-1.156	-0.520	-0.722	0.669	-0.148	-2.807	-3.256	-0.499	1.023	-2.059	-2.633	-1.364	-10.524	3.577	0.831915	0.888101	-0.942	0.514215	0.739987	-1.889	0.016326	0.106664	-1.810
sp P09211 GSTP P09211	GSTP1_HUMAN	GSTP1	glutathione S-transfer	0.581	0.525	-1.138	1.243	0.226	0.342	-1.185	-0.869	2.893	-1.102	-3.276	-0.472	-0.743	3.596	0.838362	0.893646	0.351	0.470412	0.694280	0.887	0.089868	0.271729	-8.858
sp Q99840 RSC Q99840	RISC_HUMAN	SCPEP1	serine carboxylase, tiss	-1.708	0.285	-6.559	-0.845	-0.721	-4.027	-2.359	-4.329	-0.217	-2.342	-3.208	0.027	-4.426	-10.294	0.838933	0.893646	0.877	0.418551	0.652269	0.162	0.012271	0.094689	-1.662
sp P31713 TGF P31713	TGFR2_HUMAN	TGFR2	transforming growth fac	-1.557	-1.900	-3.713	-7.198	-2.848	-1.275	-1.665	2.788	-2.550	-1.317	-1.348	-2.919	-2.221	-2.926	0.842124	0.895103	1.074	0.151127	0.694280	-0.985	0.682329	0.234647	3.295
sp P02760 AMB P02760	AMB_HUMAN	AMB	alpha-1-micro liver	11.979	11.244	8.610	9.505	6.909	11.024	10.768	11.365	11.312	11.122	11.118	8.416	11.192	10.165	0.843354	0.896406	0.025	0.722880	0.871381	-0.514	0.085163	0.244591	0.863
sp AA047586 S2 AA047586 S2	KV209_HUMAN	None	None	-0.141	1.359	-3.315	-0.533	0.303	2.036	2.128	1.558	0.658	0.011	2.211	3.631	-0.948	0.565	0.845257	0.896406	0.277	0.059975	0.219204	-1.811	0.036361	0.046501	3.733
sp P25311 ZAK P25311	ZAK2_HUMAN	AZP1	alpha-2-glycosyl:prost	9.940	10.703	4.445	6.605	5.106	10.965	10.438	10.328	9.128	8.389	11.007	6.643	9.690	7.981	0.844965	0.896406	0.321	0.250909	0.130590	-1.696	0.013603	0.098894	3.226
sp Q99878 H2A Q99878	H2A1_HUMAN	H2AC14	H2A clustered histone	-3.182	-4.958	-6.498	-6.435	-4.062	-5.443	0.795	-8.340	-5.188	-5.835	-6.612	-3.575	-5.694	-6.981	0.848597	0.899055	-0.623	0.075716	0.778338	-0.499	0.452598	0.588687	-2.007
sp P06865 HEX P06865	HEXA_HUMAN	HEXA	hexosaminidase subun	-1.289	0.459	-3.324	-0.373	-0.549	-0.744	0.054	-0.511	1.037	1.350	0.044	-5.892	-1.681	-1.466	0.825254	0.901525	-0.317	0.905709	0.957492	-0.701	0.583346	0.768386	0.615
sp Q99WV4 CZ Q99WV4	CZB_HUMAN	CZB	CXC motif containing	-4.844	0.039	-5.279	-5.940	-5.743	-0.187	0.537	-0.434	0.336	-1.081	-0.228	-9.008	-1.209	-4.654	0.852769	0.901525	0.091	0.137713	0.349659	-0.263	0.000023	0.006441	4.326
sp P21705 STP P21705	STOM_HUMAN	STOM	stomatin	-2.408	-4.843	-5.793	-3.012	-3.056	-5.344	-4.316	-5.876	-1.859	-5.237	-6.940	-2.447	-7.459	-0.959	0.855633	0.903578	0.181	0.335216	0.752969	1.029	0.119851	0.212378	-1.356
sp P04349 HLA P04349	HLA_HUMAN	HLA-A	major histocompatibil	-2.905	0.721	-2.266	-3.465	-6.109	1.219	-1.817	0.875	-5.167	0.260	0.272	-5.990	0.491	-1.398	0.865621	0.912160	-0.295	0.234398	0.465943	-2.558	0.003232	0.044617	3.620
sp P06454 PTM P06454	PTMA_HUMAN	PTMA	prothymosin	1.382	-2.680	-4.809	-2.807	-2.390	-3.033	-3.957	1.303	-6.212	-0.636	0.128	-3.741	0.300	-2.892	0.719879	0.912160	0.206	0.198479	0.869890	-1.590	0.036226	0.277200	1.275
sp P10599 THO P10599	THO_HUMAN	TXN	thioredoxin	0.829	0.671	1.798	1.433	1.901	1.454	-1.165	0.256	0.015	-0.246	-0.038	-1.128	1.208	3.343	0.873683	0.919162	0.398	0.404363	0.669099	-1.012	0.180174	0.393378	-0.982
sp Q99W42 ANTX Q99W42	ANTX1_HUMAN	ANTX1	ANTXR cell adhesion m	-0.181	0.988	-7.737	-4.249	-5.660	1.370	2.333	0.752	-2.008	0.785	1.652	-8.898	-2.725	-1.768	0.874142	0.919162	-0.453	0.007722	0.076513	-1.611	0.006685	0.027486	-5.053
sp P09659 PGR P09659	PGLYRP2_HUMAN	PGLYRP2	peptidoglycan recognit	-2.211	2.763	-4.114	-1.294	0.926	4.660	3.779	2.544	1.996	2.564	2.881	1.056	4.320	0.098	0.875651	0.919162	0.718	0.165110	0.381793	-1.508	0.047702	0.191591	3.563
sp P19957 ELAF P19957	ELAF_HUMAN	PI3	peptidase in larynx;st	-0.302	1.080	3.920	-3.142	-4.843	3.564	-1.136	-0.600	-1.666	1.306	2.664	-7.250	-0.029	2.077	0.808353	0.921737	-0.479	0.151215	0.764952	-1.757	0.507892	0.276620	1.995
sp P09599 ANX P09599	ANXA11_HUMAN	ANXA11	annexin A11	-3.862	-3.080	0.435	-0.854	-2.228	-5.083	-6.180	-3.336	-1.338	-5.411	1.561	-3.716	-6.468	-2.455	0.879814	0.921737	-0.073	0.438709	0.669680	1.562	0.087263	0.266409	-2.615
sp Q11414 TRB Q11414	TRIM29_HUMAN	TRIM29	tripartite motif bladder	-2.375	-5.161	-4.822	-0.703	-3.606	-4.776	-4.400	-3.004	-7.646	-6.993	-2.039	-0.395	-5.658	-0.804	0.878677	0.921737	-0.266	0.588836	0.955533	0.189	0.588836	0.774740	-0.728

**Sample ID: 077\_D0**

Peptide	Protein	Charge	PrecursorMZ	DelM	DelM_PPM	MH	Scan	DeNovoScore	MSGFScore	MSGFDB_SpecEValue	PepQValue
K.DGIIWVATEGALNTPK.D	sp PODTC9 NCAP_SARS2	2	842.95288	0.00793	4.70644	1684.89038	59204	109	90	8.74E-16	0
R.NPANNAAIIVLQLPQGTTLPK.G	sp PODTC9 NCAP_SARS2	3	687.39325	0.01536	7.4586	2060.14976	53326	78	53	1.79E-12	0

**Sample ID: 093\_D7**

Peptide	Protein	Charge	PrecursorMZ	DelM	DelM_PPM	MH	Scan	DeNovoScore	MSGFScore	MSGFDB_SpecEValue	PepQValue
K.GFYAEGSR.G	sp PODTC9 NCAP_SARS2	2	443.70663	0.00067	0.75657	886.405316	19245	85	81	5.31E-11	0.001006
K.QQTVTLLPAADLDDFSK.Q	sp PODTC9 NCAP_SARS2	3	621.32495	0.00603	3.24173	1861.95409	58671	87	58	1.06E-11	0
Y.YLGTGPEAGLPYGANK.D	sp PODTC9 NCAP_SARS2	2	803.9093	0.00823	5.12032	1607.80632	37358	86	61	1.79E-13	0
R.RPQGLPNNTASWFTALTQHGK.E	sp PODTC9 NCAP_SARS2	4	581.80493	0.00853	3.67174	2324.18932	56923	114	62	2.43E-14	0
R.NPANNAAIIVLQLPQGTTLPK.G	sp PODTC9 NCAP_SARS2	2	1030.58716	0.01707	8.29138	2060.14976	53580	165	129	3.10E-16	0
K.DGIIWVATEGALNTPKDHIGTR.N	sp PODTC9 NCAP_SARS2	4	591.81689	0.01511	6.39421	2364.23052	54928	103	82	9.82E-17	0
K.DGIIWVATEGALNTPK.D	sp PODTC9 NCAP_SARS2	2	842.95294	0.00805	4.77884	1684.89038	59532	140	127	1.41E-17	0
K.KQQTVTLLPAADLDDFSK.Q	sp PODTC9 NCAP_SARS2	3	664.02356	0.00695	3.49286	1990.04905	54662	109	101	1.60E-18	0
K.QQTVTLLPAADLDDFSK.Q	sp PODTC9 NCAP_SARS2	2	931.98657	0.00823	4.42406	1861.95409	58631	131	122	1.70E-19	0
R.GQGVPIINTNSSPDDQIGYYR.R	sp PODTC9 NCAP_SARS2	3	727.68188	0.01042	4.78096	2181.0206	37129	128	119	1.09E-21	0
R.RPQGLPNNTASWFTALTQHGK.E	sp PODTC9 NCAP_SARS2	3	775.40594	0.0139	5.98229	2324.18932	56965	127	117	5.32E-22	0
R.GQGVPIINTNSSPDDQIGYYR.R	sp PODTC9 NCAP_SARS2	2	1091.01917	0.01024	4.69925	2181.0206	37104	255	251	9.00E-25	0