

Supplementary Material

Short Gel, Long Gradient Liquid Chromatography Tandem Mass Spectrometry to Investigate the Urine Proteome of Chronic Pancreatitis

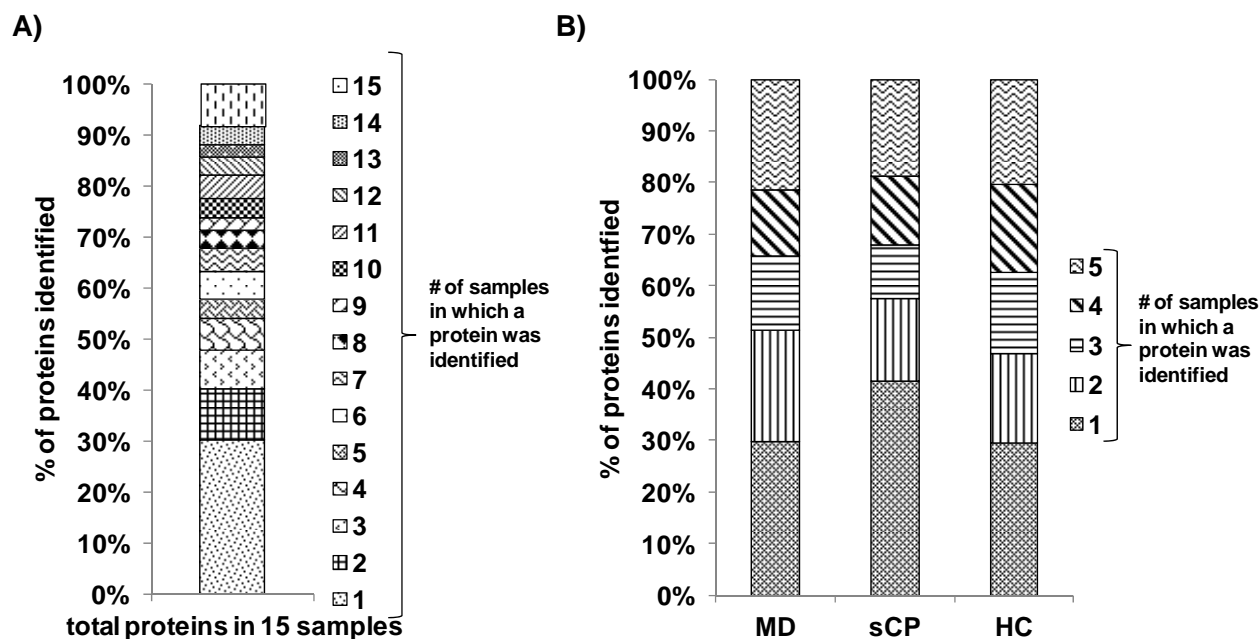
Joao A. Paulo^{1,2,3,4}, Vivek Kadiyala^{3,4}, Scott Brizard^{3,4}, Peter A. Banks^{3,4}, Darwin L. Conwell^{3,4} and Hanno Steen^{1,2,4}

¹Departments of Pathology Children's Hospital Boston, Boston, MA, USA

²Proteomics Center at Children's Hospital Boston, Boston, MA, USA

³Center for Pancreatic Disease, Division of Gastroenterology, Hepatology and Endoscopy,

⁴Brigham and Women's Hospital and Department of Medicine, Harvard Medical School, Boston, MA, USA



Supplemental Fig. (1). Bar graphs examining redundancy among identified proteins. **A)** Redundancy of proteins identified in all 15 samples indicating the proportion of the total proteins identified in a specified number (1 through 15) of samples. **B)** Redundancy of proteins categorized by cohort (n=5), indicating the proportion of proteins identified in a specified number (1 through 5) of samples.

Supplemental Table 1. Summary of All Proteins (n=609) Identified

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																					Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	Bayes Factor	Fold Change	Higher expression				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5	ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
14-3-3 protein epsilon	P62258	1433E_HUMAN	0	0	0	0	0	0	0	23	0	0	0	0	0	0	23	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.12	3.08	sCP					
14-3-3 protein zeta/delta	P63104	1433Z_HUMAN	0	0	10	12	0	15	0	30	26	0	0	11	19	24	0	22	71	54	2	3	3	1.78	2.58	sCP	2.02	2.33	MD	1.36	1.15	sCP			
3-hydroxybutyrate dehydrogenase type 2	Q9BUT1	BDH2_HUMAN	0	0	0	0	0	0	16	0	0	0	0	0	0	0	16	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.48	3.30	sCP					
3-mercaptopyruvate sulfurtransferase	P25325	THTM_HUMAN	0	0	0	0	0	12	0	0	0	0	0	0	0	0	12	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.07	3.24	sCP					
4F2 cell-surface antigen heavy chain	P08195	4F2_HUMAN	0	55	0	46	0	0	38	41	0	0	0	0	0	101	79	0	2	2	0	0.21	1.01	HC	n/a	n/a	HC	1.90	8.66	sCP					
6-phosphogluconolactonase	O95336	6PGL_HUMAN	63	24	30	15	39	0	24	29	0	0	0	0	0	171	53	0	5	2	0	4341.44	6.65	HC	n/a	n/a	HC	n/a	n/a	sCP					
Abhydrolase domain-containing protein 14B	Q96IU4	ABHEB_HUMAN	0	19	6	0	0	0	20	0	0	0	0	0	5	0	25	20	5	2	1	1	3.85	1.63	HC	2.76	2.28	HC	1.59	1.26	sCP				
Acid ceramidase	Q13510	ASAHI_HUMAN	0	0	24	31	27	36	33	32	35	32	0	17	50	34	0	82	168	101	3	5	3	179.51	4.32	sCP	0.40	1.02	MD	9.67	4.09	sCP			
Actin, cytoplasmic 1	P60709	ACTB_HUMAN	0	0	115	101	103	113	0	295	0	0	83	0	185	171	0	319	408	439	3	2	3	43.27	1.67	sCP	0.02	1.07	HC	68.16	1.79	MD			
Actin, cytoplasmic 2	P63261	ACTG_HUMAN	190	67	0	0	0	56	0	94	95	0	120	0	0	48	257	245	168	2	3	2	0.08	1.92	HC	8.39	1.12	MD	2.11	2.20	sCP				
Adenosylhomocysteinase	P23526	SAHH_HUMAN	0	0	0	0	0	0	24	0	0	0	0	0	0	0	24	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	0.88	3.42	sCP					

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
ADP-ribosylation factor 1	P84077	ARF1_HUMAN	0	0	0	0	0	0	0	8	0	0	0	0	0	0	0	8	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.65	3.18	sCP	
Afamin	P43652	AFAM_HUMAN	0	66	0	24	0	0	0	0	0	33	0	0	46	0	60	90	33	106	2	1	2	0.42	2.19	HC	4.67	1.05	HC	0.64	2.39	MD
Aflatoxin B1 aldehyde reductase member 2	O43488	ARK72_HUMAN	0	0	0	0	0	0	15	0	0	0	0	0	0	0	0	15	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.96	3.47	sCP	
Aggrecan core protein	P16112	PGCA_HUMAN	0	0	21	0	0	0	28	39	43	0	0	35	0	0	21	110	35	1	3	1	16.83	5.24	HC	2.94	1.02	MD	33.50	4.69	sCP	
Agrin	O00468	AGRIN_HUMAN	0	94	67	0	64	138	95	55	129	101	0	88	0	125	0	225	518	213	3	5	2	6.7E+06	6.97	HC	1.67	2.26	MD	7.9E+09	16.07	sCP
Alcohol dehydrogenase	P14550	AK1A1_HUMAN	0	0	36	0	0	0	40	0	0	26	15	0	0	0	36	40	41	1	1	2	0.18	1.07	sCP	1.41	1.84	MD	0.27	1.87	MD	
Aldo-keto reductase family 1 member C1	Q04828	AK1C1_HUMAN	0	0	0	0	0	0	26	0	0	0	0	0	0	0	26	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	3.45	3.33	sCP	
Aldose reductase	P15121	ALDR_HUMAN	0	0	0	16	0	0	0	0	0	0	0	0	0	0	16	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Alpha-1-acid glycoprotein 1	P02763	A1AG1_HUMAN	0	85	30	32	24	107	107	40	160	111	19	70	61	55	131	171	525	336	4	5	5	440.48	4.40	sCP	1.97	2.62	MD	1.38	1.61	sCP
Alpha-1-acid glycoprotein 2	P19652	A1AG2_HUMAN	0	79	29	34	0	0	90	40	119	88	0	64	70	35	110	142	337	279	3	4	4	0.65	3.00	sCP	0.68	3.08	MD	12.43	1.07	sCP
Alpha-1-antichymotrypsin	P01011	AACT_HUMAN	121	186	65	101	83	92	91	53	98	58	53	100	155	151	139	556	392	598	5	5	5	3.52	1.35	sCP	0.44	1.04	HC	2.11	1.40	MD

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			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses								Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression					
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5	ΣHC	ΣsCP	ΣMD														
			#HC	#sCP	#MD																													
Alpha-1-antitrypsin	P01009	A1AT_HUMAN	384	353	166	352	272	102	98	235	82	89	166	327	177	200	394	152	7	606	126	4	5	5	5	3186.67	2.52	HC	2.66	1.28	HC	207.41	1.96	MD
Alpha-1B-glycoprotein	P04217	A1BG_HUMAN	100	123	96	102	77	48	111	38	44	121	0	18	84	93	107	498	362	302	5	5	4	1.75	1.50	HC	1.2E+05	3.42	HC	28.80	2.58	sCP		
Alpha-2-antiplasmin	P08697	A2AP_HUMAN	73	43	0	36	0	0	0	25	0	0	0	0	0	0	0	152	25	0	3	1	0	3.06	4.62	HC	n/a	n/a	HC	1.61	3.02	sCP		
Alpha-2-HS-glycoprotein	P02765	FE-TUA_HUMAN	103	106	88	127	61	52	105	71	79	76	44	107	95	66	85	485	383	397	5	5	5	1.62	1.22	HC	2.08	1.26	HC	0.96	1.02	sCP		
Alpha-2-macroglobulin	P01023	A2MG_HUMAN	266	0	0	36	0	0	0	0	0	52	70	88	0	0	0	302	52	158	2	1	2	2.48	2.52	HC	0.07	1.17	HC	1.70	2.33	MD		
Alpha-actinin-4	O43707	ACTN4_HUMAN	0	0	0	0	0	0	0	43	0	0	0	0	0	0	0	0	43	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	0.27	3.67	sCP	
Alpha-amylase 1	P04745	AMY1_HUMAN	0	357	429	412	411	0	0	265	88	99	653	0	0	363	0	160	9	452	101	6	4	3	2	0.31	4.10	HC	1418.08	6.74	HC	0.01	1.94	sCP
Alpha-amylase 2B	P19961	AMY2B_HUMAN	399	360	443	405	435	0	222	274	0	0	692	294	0	0	0	204	2	496	363	2	5	2	2	6.9E+16	21.39	HC	7.5E+16	21.18	HC	151.39	1.14	MD
Alpha-enolase	P06733	ENOA_HUMAN	230	0	42	46	35	0	41	109	0	29	0	46	75	87	25	353	179	233	4	3	4	5.61	2.61	HC	3.01	1.04	HC	2.28	2.46	MD		
Alpha-galactosidase A	P06280	AGAL_HUMAN	0	0	0	26	0	0	0	30	0	0	0	25	59	0	0	26	30	84	1	1	2	0.73	1.01	sCP	0.10	2.21	MD	16.43	1.84	MD		
Alpha-N-acetylgalactosaminidase	P17050	NA-GAB_HUMAN	0	0	0	33	33	0	34	33	0	19	0	0	0	0	0	66	86	0	2	3	0	1.71	1.76	HC	n/a	n/a	MD	n/a	n/a	sCP		

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			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP				ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Alpha-N-acetylglucosaminidase	P54802	ANAG_HUMAN	97	94	107	105	111	0	53	120	58	61	168	78	54	131	48	514	292	479	5	4	5	701.02	2.94	HC	4.19	1.13	HC	23.47	2.55	MD
Aminoacylase-1	Q03154	ACY1_HUMAN	0	0	14	5	10	0	0	60	0	0	0	18	0	17	0	29	60	35	3	1	2	3.30	2.71	HC	1.67	1.71	HC	0.33	1.77	MD
Aminopeptidase N	P15144	AMPN_HUMAN	242	62	99	142	134	98	82	158	200	171	75	73	112	127	0	679	709	387	5	5	4	3.80	1.12	HC	301.74	3.32	MD	3141.96	4.09	sCP
Ammonium transporter Rh type C	Q9UBD6	RHCG_HUMAN	0	0	0	0	0	0	0	0	0	0	16	12	0	0	0	0	0	28	0	0	2	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Angiopoietin-related protein 2	Q9UKU9	ANGL2_HUMAN	0	0	31	0	0	0	31	0	0	0	19	0	0	0	31	31	19	1	1	1	2.02	1.06	HC	0.69	1.06	HC	1.20	1.03	sCP	
Angiotensin-converting enzyme	P12821	ACE_HUMAN	0	0	0	0	0	0	32	0	0	0	0	0	0	0	32	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.87	3.52	sCP	
Angiotensinogen	P01019	ANGT_HUMAN	0	24	0	32	0	0	40	18	0	0	24	34	49	50	56	58	157	2	2	4	0.34	1.05	sCP	3.43	5.69	MD	15.40	5.30	MD	
Annexin A1	P04083	ANXA1_HUMAN	0	0	0	0	36	50	70	0	0	34	0	0	40	52	0	36	154	92	1	3	2	1.04	5.18	sCP	2.56	2.26	MD	0.71	2.41	sCP
Annexin A10	Q9UJ72	ANX10_HUMAN	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	13	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Annexin A11	P50995	ANX11_HUMAN	148	0	23	0	47	0	0	0	0	0	83	25	0	0	218	0	108	3	0	2	n/a	n/a	HC	21.01	2.23	HC	n/a	n/a	MD	
Annexin A2	P07355	ANXA2_HUMAN	0	0	15	20	17	50	46	0	25	17	0	0	46	0	52	138	46	3	4	1	6.41	2.60	HC	0.44	4.56	MD	218.66	11.15	sCP	

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			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5				#HC	#sCP	#MD												
Annexin A4	P09525	ANXA4_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	53	0	0	0	53	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	MD
Annexin A5	P08758	ANXA5_HUMAN	0	0	19	15	0	0	0	18	0	0	37	27	38	0	34	18	102	2	1	3	0.79	1.96	sCP	2.39	2.51	HC	15.79	5.48	MD				
Anthrax toxin receptor 1	Q9H6X2	ANTR1_HUMAN	0	0	0	0	0	0	0	30	0	0	0	0	0	0	0	30	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.54	3.67	sCP				
Antithrombin-III	P01008	ANT3_HUMAN	0	44	21	60	0	0	20	48	0	0	0	29	0	94	125	68	123	3	2	2	2.25	2.43	HC	20.57	2.08	HC	0.12	1.01	MD				
Apolipoprotein	P08519	APOA_HUMAN	0	102	76	62	84	0	77	82	82	0	113	100	76	84	0	324	241	373	4	3	4	3.62	2.87	sCP	1.21	1.03	HC	0.11	3.04	MD			
Apolipoprotein A-I	P02647	APOA1_HUMAN	121	42	72	119	51	0	0	111	0	49	49	27	43	66	267	405	160	452	5	2	5	3.1E+04	13.71	HC	1.78	1.15	HC	1.0E+04	10.02	MD			
Apolipoprotein A-IV	P06727	APOA4_HUMAN	0	0	32	35	0	0	0	67	0	0	0	0	0	0	91	67	67	91	2	1	1	2.02	1.99	HC	0.12	1.83	HC	2.09	1.04	MD			
Apolipoprotein D	P05090	APOD_HUMAN	190	380	500	349	581	184	370	276	476	206	255	129	228	444	319	2000	1512	1375	5	5	5	0.76	1.30	HC	0.46	1.46	HC	12.79	1.17	sCP			
Apolipoprotein E	P02649	APOE_HUMAN	148	0	61	50	30	0	0	56	0	0	0	0	0	55	0	289	56	55	4	1	1	284.92	12.07	HC	155.32	12.45	HC	2.44	1.11	sCP			
Aquaporin-1	P29972	AQP1_HUMAN	0	0	0	0	3	0	0	0	0	0	0	7	8	0	0	3	0	15	1	0	2	n/a	n/a	sCP	1.07	2.39	HC	n/a	n/a	MD			
Aquaporin-2	P41181	AQP2_HUMAN	0	0	0	0	0	0	0	0	0	0	0	15	0	0	0	0	0	15	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	MD

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			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Argininosuccinate synthase	P00966	ASSY_HUMAN	0	0	0	0	0	0	0	59	0	0	0	0	0	0	0	59	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	0.71	3.52	sCP	
Aromatic-L-amino-acid decarboxylase	P20711	DDC_HUMAN	0	0	0	0	0	0	0	29	0	0	0	0	0	0	0	29	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	4.10	3.61	sCP	
Arylsulfatase A	P15289	ARSA_HUMAN	0	58	19	36	73	90	35	51	43	52	85	74	77	31	26	186	271	293	4	5	5	30.47	2.48	sCP	36.27	2.29	MD	1.01	1.00	n/a
Arylsulfatase F	P54793	ARSF_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	32	0	0	0	32	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Aspartate aminotransferase, cytoplasmic	P17174	AATC_HUMAN	0	0	0	0	0	0	0	38	0	0	0	0	0	0	0	0	38	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	6.37	3.89	sCP
ATP-dependent RNA helicase DDX25	Q9UHL0	DDX25_HUMAN	0	0	0	0	0	0	0	0	0	30	0	0	0	0	0	0	30	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.54	3.67	sCP
Attractin	O75882	ATRN_HUMAN	0	91	48	71	76	144	55	72	61	0	116	103	82	0	69	286	332	370	4	4	4	1.58	1.05	sCP	2.92	1.21	MD	4.17	1.07	MD
Basal cell adhesion molecule	P50895	BCAM_HUMAN	0	0	33	31	47	0	0	31	0	31	0	0	34	0	0	111	62	34	3	2	1	0.72	2.24	HC	20.16	4.44	HC	0.56	2.29	sCP
Basement membrane-specific heparan sulfate protein	P98160	PGBM_HUMAN	765	441	410	281	364	736	523	282	699	295	484	336	336	481	344	2261	2535	1981	5	5	5	0.59	1.13	HC	0.10	1.13	MD	25.78	1.25	sCP
Basigin	P35613	BASI_HUMAN	0	0	0	0	0	0	0	0	12	15	0	0	11	0	0	0	27	11	0	2	1	n/a	n/a	sCP	n/a	n/a	MD	4.56	2.30	sCP
Beta-2-glycoprotein 1	P02749	APOH_HUMAN	39	93	47	75	76	88	50	85	69	30	67	64	123	38	72	330	322	364	5	5	5	1.95	1.03	sCP	0.41	1.08	MD	0.48	1.02	MD

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			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5	#HC	#sCP	#MD												
Beta-2-microglobulin	P61769	B2MG_HUMAN	18	0	26	33	25	0	21	41	21	30	40	13	14	21	0	102	113	88	4	4	4	1.80	1.04	HC	3.33	1.19	MD	0.14	1.30	sCP
Beta-defensin 1	P60022	DEFB1_HUMAN	0	0	0	8	13	0	0	3	0	0	0	0	0	0	0	21	3	0	2	1	0	0.51	2.64	HC	n/a	n/a	HC	1.36	2.88	sCP
Beta-galactosidase	P16278	BGAL_HUMAN	0	69	0	104	65	159	47	126	55	78	0	105	53	52	0	238	465	210	3	5	3	4.7E+04	6.47	HC	0.17	1.07	MD	3.4E+04	8.90	sCP
Beta-glucuronidase	P08236	BGLR_HUMAN	0	0	0	47	15	31	12	50	27	22	0	32	57	24	0	62	142	113	2	5	3	1546.28	6.39	sCP	7.97	2.06	MD	4.30	3.31	sCP
Beta-hexosaminidase subunit alpha	P06865	HEXA_HUMAN	0	0	0	0	0	0	0	37	0	40	0	17	42	0	0	0	77	59	0	2	2	n/a	n/a	sCP	n/a	n/a	MD	0.73	1.14	sCP
Beta-hexosaminidase subunit beta	P07686	HEXB_HUMAN	0	0	0	28	0	0	0	54	0	67	0	0	44	0	0	28	121	44	1	2	1	8.81	2.98	HC	0.05	1.06	MD	3.11	2.19	sCP
Betaine--homocysteine S-methyltransferase 1	Q93088	BHMT1_HUMAN	91	0	40	8	0	0	0	70	0	0	0	15	0	26	0	139	70	41	3	1	2	5.64	4.17	HC	2.27	2.25	HC	1.13	1.67	MD
Beta-mannosidase	O00462	MANBA_HUMAN	0	0	0	0	0	0	0	0	0	0	32	0	0	0	0	0	0	32	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Biglycan	P21810	PGS1_HUMAN	0	0	0	22	0	0	0	35	0	0	0	0	0	0	0	22	35	0	1	1	0	12.71	1.07	HC	n/a	n/a	HC	0.51	3.68	sCP
Bile salt-activated lipase	P19835	CEL_HUMAN	0	37	0	36	61	59	0	34	0	0	0	57	30	0	0	134	93	87	3	2	2	0.20	2.13	HC	2.73	2.40	HC	1.78	1.04	sCP
Biotinidase	P43251	BTD_HUMAN	0	0	23	24	30	0	39	18	0	0	0	0	0	35	0	77	57	35	3	2	1	0.66	2.26	HC	4.85	4.09	HC	1.01	2.12	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP				ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5				#HC	#sCP	#MD									
Bone marrow proteoglycan	P13727	PRG2_HUMAN	0	0	17	20	0	0	0	0	0	7	0	0	0	0	0	37	7	0	2	1	0	0.41	2.44	HC	n/a	n/a	HC	1.36	3.20	sCP
BPI fold-containing family B member 2	Q8N4F0	BPIB2_HUMAN	0	0	32	0	0	0	0	0	0	0	0	0	0	0	0	32	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
BRO1 domain-containing protein BROX	Q5VW32	BROX_HUMAN	0	0	0	18	19	36	0	10	0	0	0	13	23	14	0	37	46	50	2	2	3	0.59	1.07	sCP	1.56	1.98	MD	0.25	1.88	MD
Butyrophilin subfamily 2 member A1	Q7KYR7	BT2A1_HUMAN	0	29	22	15	0	36	0	0	29	31	34	0	0	40	0	66	96	74	3	3	2	0.59	1.20	HC	0.77	1.93	MD	1.27	2.41	sCP
Butyrophilin subfamily 2 member A2	Q8WV5	BT2A2_HUMAN	0	0	0	0	31	0	0	32	0	0	0	0	21	0	23	31	32	44	1	1	2	0.31	1.02	sCP	0.77	2.12	MD	0.99	2.36	MD
Cadherin-1	P12830	CADH1_HUMAN	0	101	75	52	67	188	112	52	87	98	72	94	103	95	82	295	537	446	4	5	5	1.4E+04	3.15	sCP	217.37	2.51	MD	2.21	1.18	sCP
Cadherin-11	P55287	CAD11_HUMAN	0	0	24	28	0	0	38	0	0	0	0	0	0	0	31	52	38	31	2	1	1	0.44	2.17	HC	0.27	2.21	HC	0.55	1.01	MD
Cadherin-13	P55290	CAD13_HUMAN	0	50	45	43	56	88	56	29	55	46	50	58	44	0	0	194	274	152	4	5	3	49.51	1.89	HC	40.22	2.43	MD	2.1E+04	5.45	sCP
Cadherin-15	P55291	CAD15_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	33	0	0	0	0	33	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Cadherin-2	P19022	CADH2_HUMAN	0	71	24	37	64	86	0	48	36	44	99	120	69	0	0	196	214	288	4	4	3	7.80	1.04	HC	0.56	2.12	MD	0.33	2.43	sCP
Cadherin-related family member 2	Q9BYE9	CDHR2_HUMAN	0	0	0	0	0	67	0	0	0	0	0	0	0	0	0	67	0	0	0	0	0	n/a	n/a	n/a	n/a	n/a	MD	4.74	3.85	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts															Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP					
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
Cadherin-related family member 5	Q9HBB8	CDHR5_HUMAN	0	35	0	0	31	0	0	24	0	0	0	0	37	0	0	66	24	37	2	1	1	2.02	2.48	HC	0.50	2.22	HC	0.14	1.09	MD
cAMP-dependent protein kinase type II-beta regulatory subunit	P31323	KAP3_HUMAN	0	0	0	0	0	0	0	0	16	0	0	0	0	0	0	16	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	2.36	3.53	sCP
Carbonic anhydrase 1	P00915	CAH1_HUMAN	0	0	0	0	0	0	30	0	11	45	0	0	27	0	0	86	27	0	3	1	n/a	n/a	sCP	n/a	n/a	MD	1.67	4.67	sCP	
Carbonic anhydrase 2	P00918	CAH2_HUMAN	24	0	0	0	0	0	34	0	0	0	0	15	37	0	24	34	52	1	1	2	1.10	1.03	sCP	0.35	2.15	MD	1.11	1.89	MD	
Carbonyl reductase	P16152	CBR1_HUMAN	0	0	0	0	0	0	20	0	0	0	0	0	0	0	20	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	2.70	3.56	sCP	
Carboxypeptidase E	P16870	CBPE_HUMAN	0	22	24	31	33	0	26	22	41	0	0	23	0	0	110	89	23	4	3	1	4.77	1.97	HC	16.62	11.17	HC	6.63	5.22	sCP	
Carboxypeptidase M	P14384	CBPM_HUMAN	0	0	17	12	19	0	0	23	0	0	0	43	35	0	0	48	23	78	3	1	2	7.28	3.92	HC	0.13	1.85	HC	0.78	2.07	MD
Carboxypeptidase N subunit 2	P22792	CPN2_HUMAN	85	23	25	16	27	0	21	55	0	11	39	25	33	37	21	176	87	155	5	3	5	11.37	3.83	HC	0.44	1.00	HC	715.14	3.83	MD
Carcinoembryonic antigen-related cell adhesion molecule 8	P31997	CEAM8_HUMAN	0	0	0	0	0	25	0	0	0	0	0	0	0	0	0	25	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	1.76	3.18	sCP
Cartilage intermediate layer protein 1	O75339	CILP1_HUMAN	0	0	0	34	0	0	0	0	0	0	0	0	0	0	34	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Cartilage intermediate layer protein 2	Q8IUL8	CILP2_HUMAN	0	0	0	59	0	0	0	0	0	0	0	0	0	0	59	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
Caspase-14	P31944	CASPE_HUMAN	0	0	0	0	0	0	12	0	0	0	0	0	0	26	0	0	12	26	0	1	1	n/a	n/a	sCP	n/a	n/a	MD	0.76	1.17	MD
Catalase	P04040	CATA_HUMAN	0	0	0	32	0	0	0	0	23	0	0	0	0	0	32	23	0	1	1	0	0.76	1.01	HC	n/a	n/a	HC	0.78	3.33	sCP	
Cathepsin B	P07858	CATB_HUMAN	0	0	12	33	22	44	51	18	35	50	0	43	68	0	0	67	198	111	3	5	2	291.77	4.79	HC	0.73	1.79	MD	3.6E+04	10.15	sCP
Cathepsin D	P07339	CATD_HUMAN	91	48	51	75	90	134	155	128	142	201	69	55	57	46	43	355	760	270	5	5	5	4497.61	2.14	HC	3.08	1.34	MD	2.9E+05	2.91	sCP
Cathepsin Z	Q9UBR2	CATZ_HUMAN	0	0	0	0	11	0	30	13	20	25	0	9	0	0	0	11	88	9	1	4	1	36.48	9.32	sCP	0.84	1.05	MD	152.97	11.79	sCP
CD160 antigen	O95971	BY55_HUMAN	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
CD177 antigen	Q8N6Q3	CD177_HUMAN	0	0	0	7	0	0	0	0	0	0	0	0	9	0	0	7	0	9	1	0	1	n/a	n/a	sCP	0.67	1.08	HC	n/a	n/a	MD
CD276 antigen	Q5ZPR3	CD276_HUMAN	0	0	5	7	7	0	0	0	0	0	0	0	0	0	19	0	0	3	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
CD44 antigen	P16070	CD44_HUMAN	91	46	34	34	56	71	43	74	57	53	93	79	70	61	49	261	298	352	5	5	5	0.95	1.22	sCP	1.54	1.34	MD	1.16	1.12	MD
CD59 glycoprotein	P13987	CD59_HUMAN	15	26	40	32	35	77	71	40	61	34	44	53	48	41	25	148	283	211	5	5	5	50.00	1.91	sCP	3.99	1.37	MD	3.81	1.42	sCP
CD9 antigen	P21926	CD9_HUMAN	0	0	0	0	0	0	0	0	0	0	0	16	21	0	0	0	0	37	0	0	2	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	O14735	CDIPT_HUMAN	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	7	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.75	3.24	sCP	
Cell adhesion molecule 1	Q9BY67	CADM1_HUMAN	0	33	16	6	25	0	0	29	0	0	32	23	39	0	0	80	29	94	4	1	3	7.24	8.29	HC	0.45	1.50	HC	0.57	5.25	MD
Cell adhesion molecule 4	Q8NFZ8	CADM4_HUMAN	106	41	43	52	67	0	38	57	51	35	108	37	68	70	37	309	181	320	5	4	5	12.93	230	HC	0.76	1.02	HC	7.99	2.10	MD
Cell surface glycoprotein MUC18	P43121	MUC18_HUMAN	0	22	22	26	13	0	0	14	0	20	0	0	30	0	0	83	34	30	4	2	1	2.79	4.26	HC	491.90	7.61	HC	3.75	2.51	sCP
Ceruloplasmin	P00450	CERU_HUMAN	127	249	84	149	119	134	106	74	88	189	0	103	64	229	191	728	591	587	5	5	4	1.73	1.20	HC	1095.54	3.44	HC	563.34	2.98	sCP
Charged multivesicular body protein 1b	Q7LBR1	CHM1B_HUMAN	0	0	22	0	0	0	0	31	0	0	0	0	30	0	0	22	31	30	1	1	1	0.32	1.04	sCP	0.29	1.07	MD	1.96	1.01	sCP
Charged multivesicular body protein 2a	O43633	CHM2A_HUMAN	0	0	17	0	0	0	0	22	0	0	0	0	41	0	0	17	22	41	1	1	1	2.30	1.05	sCP	1.00	1.11	MD	2.37	1.01	MD
Charged multivesicular body protein 5	Q9NZZ3	CHMP5_HUMAN	0	0	0	12	26	0	0	0	0	0	0	0	19	0	0	38	0	19	2	0	1	n/a	n/a	HC	0.20	2.21	HC	n/a	n/a	MD
Chloride intracellular channel protein 1	O00299	CLIC1_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	7	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Chloride intracellular channel protein 4	Q9Y696	CLIC4_HUMAN	0	0	0	0	0	0	0	10	17	0	0	0	0	0	0	27	0	0	2	0	0	n/a	n/a	n/a	n/a	n/a	MD	n/a	n/a	sCP
Cholesteryl ester transfer protein	P11597	CETP_HUMAN	0	0	26	0	0	0	0	0	0	0	0	0	0	0	0	26	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP					
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					Σ HC	Σ sCP	Σ MD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																		
Choline transporter-like protein 4	Q53GD3	CTL4_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	15	0	0	0	0	15	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	MD
Chondroitin sulfate proteoglycan 4	Q6UVK1	CSPG4_HUMAN	0	0	86	87	69	0	0	73	0	0	0	0	0	0	0	242	73	0	3	1	0	0.32	5.01	HC	n/a	n/a	HC	4.27	3.97	sCP			
Chromogranin-A	P10645	CMGA_HUMAN	0	0	0	0	0	0	25	0	33	0	0	0	0	0	0	58	0	0	0	2	0	n/a	n/a	n/a	n/a	n/a	MD	2.90	7.74	sCP			
Ciliary neurotrophic factor receptor subunit alpha	P26992	CNTFR_HUMAN	0	21	9	11	15	0	14	10	12	4	0	0	13	0	0	56	40	13	4	4	1	0.67	1.34	HC	104.38	5.89	HC	33.67	6.05	sCP			
Clusterin	P10909	CLUS_HUMAN	163	59	96	141	153	92	95	196	118	49	106	76	74	60	119	612	550	435	5	5	5	0.15	1.14	HC	8.22	1.37	HC	2.18	1.30	sCP			
CMRF35-like molecule 2	Q496F6	CLM2_HUMAN	0	0	0	0	0	0	0	2	0	0	0	12	0	0	0	0	2	12	0	1	1	n/a	n/a	sCP	n/a	n/a	MD	0.97	1.25	MD			
CMRF35-like molecule 8	Q9UGN4	CLM8_HUMAN	0	0	0	0	9	0	0	8	10	0	0	7	12	0	0	9	18	19	1	2	2	1.11	2.65	sCP	0.75	2.11	MD	3.51	1.08	MD			
CMRF35-like molecule 9	Q6UXG3	CLM9_HUMAN	0	51	21	34	47	36	16	27	33	0	39	38	56	18	20	153	112	171	4	4	5	0.17	1.21	sCP	1.33	1.54	HC	1.31	1.95	MD			
Cochlin	O43405	COCH_HUMAN	0	0	27	0	30	40	36	36	30	0	55	0	0	0	0	57	142	55	2	4	1	2.32	5.84	HC	3.75	2.07	MD	88.77	9.88	sCP			
Cofilin-1	P23528	COF1_HUMAN	0	0	10	13	0	0	13	9	0	9	0	0	22	0	0	23	31	22	2	3	1	1.16	1.83	HC	0.54	1.84	MD	5.44	3.64	sCP			
Collagen alpha-1	P12109	CO6A1_HUMAN	447	174	142	176	276	159	107	196	123	73	168	131	87	172	135	1215	658	693	5	5	5	9.65	1.71	HC	20.17	1.72	HC	0.54	1.04	MD			

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					Σ HC	Σ sCP	Σ MD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
Collagen alpha-1	P39059	COFA1_HUMAN	378	112	76	80	72	0	61	66	0	62	128	84	61	108	0	718	189	381	5	3	4	1.1E+04	8.49	HC	88.03	3.17	HC	96.29	2.99	MD
Collagen alpha-1	P39060	COIA1_HUMAN	0	95	96	75	81	171	0	81	0	0	0	96	81	0	74	347	252	251	4	2	3	0.29	6.45	HC	6.52	2.79	HC	0.24	2.09	MD
Collagen alpha-1	Q99715	COCA1_HUMAN	0	0	0	136	0	0	0	113	0	0	0	0	0	0	0	136	113	0	1	1	0	0.75	1.11	HC	n/a	n/a	HC	4.99	3.80	sCP
Collagen alpha-2	P08572	CO4A2_HUMAN	0	0	113	122	0	0	0	0	0	0	0	0	0	0	0	235	0	0	2	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Collagen alpha-3	P12111	CO6A3_HUMAN	0	237	149	169	182	431	159	173	314	160	228	221	194	314	0	737	1237	957	4	5	4	1.0E+04	4.61	sCP	1.56	1.08	MD	1750.90	4.38	sCP
Collagen alpha-3	P25940	CO5A3_HUMAN	0	0	0	0	0	0	0	0	0	0	120	0	0	0	0	0	0	120	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Collectin-12	Q5KU26	COL12_HUMAN	0	84	45	0	0	0	62	0	0	0	0	45	0	0	0	129	62	45	2	1	1	2.47	1.88	HC	26.95	2.47	HC	7.67	1.08	sCP
Complement C1r subcomponent-like protein	Q9NZP8	C1RL_HUMAN	0	45	36	43	41	46	30	36	0	0	63	27	44	40	20	165	112	194	4	3	5	16.18	2.51	sCP	0.30	1.45	HC	24.49	3.50	MD
Complement C3	P01024	CO3_HUMAN	556	0	66	148	0	0	0	101	0	0	0	0	0	84	393	770	101	477	3	1	2	60.94	4.27	HC	0.72	2.09	HC	5.76	2.20	MD
Complement C4-B	POC0L5	CO4B_HUMAN	338	156	102	127	128	163	95	101	101	84	138	115	0	162	174	851	544	589	5	5	4	1.71	1.45	HC	1735.41	3.25	HC	33.11	2.36	sCP
Complement component C7	P10643	CO7_HUMAN	0	0	0	0	0	0	0	0	52	0	0	0	0	0	0	52	0	0	0	0	0	n/a	n/a	n/a	n/a	n/a	MD	3.81	3.94	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5	ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD									
Complement component C8 alpha chain	P07357	CO8A_HUMAN	94	0	0	0	0	0	0	0	0	0	0	0	0	0	94	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Complement component C9	P02748	CO9_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	37	0	0	37	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Complement decay-accelerating factor	P08174	DAF_HUMAN	0	62	48	33	52	92	56	43	61	76	0	59	71	53	57	195	328	240	4	5	4	17.75	2.43	sCP	0.17	1.09	MD	13.38	2.12	sCP
Complement factor B	P00751	CFAB_HUMAN	0	59	0	38	42	65	0	24	97	0	0	0	30	0	100	139	186	130	3	3	2	0.03	1.05	HC	0.43	2.31	MD	1.52	1.91	sCP
Complement factor D	P00746	CFAD_HUMAN	0	0	11	0	0	0	0	0	0	0	0	0	0	0	11	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Complement factor H	P08603	CFAH_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	41	0	0	41	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Complement factor H-related protein 1	Q03591	FHR1_HUMAN	0	10	0	8	0	0	17	0	0	0	0	0	0	10	18	17	10	2	1	1	1.36	2.00	HC	1.55	1.89	HC	1.72	1.18	sCP	
Complement factor I	P05156	CFAI_HUMAN	0	0	38	39	27	0	0	37	30	14	46	25	0	0	104	81	71	3	3	2	0.51	1.07	HC	1.72	1.97	HC	6.48	1.81	sCP	
Contactin-1	Q12860	CNTN1_HUMAN	0	0	0	46	0	0	0	43	0	0	59	0	0	0	46	43	59	1	1	1	0.92	1.01	sCP	1.94	1.08	HC	0.28	1.04	sCP	
Corticosteroid-binding globulin	P08185	CBG_HUMAN	0	73	38	26	33	0	39	0	0	19	0	0	21	0	35	170	58	56	4	2	2	0.77	6.22	HC	1105.74	5.02	HC	1.72	1.05	sCP
Creatine kinase B-type	P12277	KCRB_HUMAN	51	0	23	0	0	0	0	0	0	0	0	0	0	0	74	0	0	2	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression	
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																
			#HC	#sCP	#MD																												
C-type lectin domain family 14 member A	Q86T13	CLC14_HUMAN	0	0	41	32	40	0	32	24	0	0	44	0	43	0	0	113	56	87	3	2	2	0.20	2.30	HC	2.37	2.02	HC	9.34	1.06	sCP	
Cubilin	O60494	CUBN_HUMAN	447	237	160	188	316	146	240	315	192	182	330	180	331	131	150	1348	1075	1122	5	5	5	0.28	1.20	HC	0.54	1.24	HC	0.32	1.06	sCP	
Cystatin-C	P01034	CYTC_HUMAN	91	46	0	43	48	0	20	46	21	21	22	0	15	27	0	228	108	64	4	4	3	1.53	1.62	HC	14.90	3.66	HC	0.28	2.21	sCP	
Cystatin-M	Q15828	CYTM_HUMAN	42	31	38	23	23	67	60	15	58	26	22	20	7	0	35	157	226	84	5	5	4	1.64	1.29	HC	7.14	2.25	MD	7.39	3.19	sCP	
Cytoplasmic aconitate hydratase	P21399	ACOC_HUMAN	0	0	0	0	0	0	0	39	0	0	0	0	0	0	0	39	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	0.71	3.61	sCP	
Cytosolic non-specific dipeptidase	Q96KP4	CNDP2_HUMAN	0	0	0	0	0	0	0	84	0	0	0	0	0	0	0	84	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	0.78	3.56	sCP	
D-3-phosphoglycerate dehydrogenase	O43175	SERA_HUMAN	0	0	0	0	0	0	0	31	0	0	0	0	0	0	0	31	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	3.34	3.56	sCP	
Deoxyribonuclease-1	P24855	DNAS1_HUMAN	82	37	44	57	78	90	27	72	31	0	99	26	48	56	39	298	220	268	5	4	5	3.57	2.42	HC	1.09	1.19	HC	12.80	1.97	MD	
Dermatopontin	Q07507	DERM_HUMAN	0	17	5	18	11	10	16	4	19	0	0	0	0	0	0	51	49	0	4	4	0	0.65	1.05	HC	n/a	n/a	HC	n/a	n/a	sCP	
Dermcidin	P81605	DCD_HUMAN	0	0	0	0	16	0	0	0	0	0	50	0	0	0	0	16	0	50	1	0	1	n/a	n/a	sCP	0.38	1.13	HC	n/a	n/a	MD	
Desmocollin-1	Q08554	DSC1_HUMAN	0	0	0	0	0	0	0	0	0	0	46	0	0	0	0	0	46	0	0	1	n/a	n/a	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts															Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP					
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			0	20	41	27	30	0	67	22	49	36	42	0	41	0	54	118	174	137	4	4	3	2.09	1.14	HC	0.72	1.93	MD	0.37	2.23	sCP
Desmocollin-2	Q02487	DSC2_HUMAN	0	20	41	27	30	0	67	22	49	36	42	0	41	0	54	118	174	137	4	4	3	2.09	1.14	HC	0.72	1.93	MD	0.37	2.23	sCP
Desmoglein-1	Q02413	DSG1_HUMAN	0	0	0	0	0	0	0	0	0	72	0	0	0	0	0	0	0	72	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Dihydropyridyllysine-residue succinyltransferase	P36957	ODO2_HUMAN	0	0	0	0	0	0	0	0	0	0	19	0	0	0	0	0	19	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Dihydropteridine reductase	P09417	DHPR_HUMAN	0	0	0	0	0	0	11	0	0	0	0	0	0	0	0	11	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.62	3.25	sCP	
Di-N-acetylchitinase	Q01459	DIAC_HUMAN	0	45	26	36	19	69	43	30	0	33	26	42	63	35	25	126	175	191	4	4	5	2.50	1.17	sCP	1.92	1.87	MD	2.24	1.49	MD
Dipeptidase 1	P16444	DPEP1_HUMAN	106	35	67	83	35	0	0	26	0	0	23	36	34	53	0	326	26	146	5	1	4	1.2E+07	24.85	HC	40.30	2.81	HC	104.48	10.96	MD
Dipeptidyl peptidase 1	P53634	CATC_HUMAN	0	15	0	32	34	50	38	39	31	63	0	20	20	0	0	81	221	40	3	5	2	1083.51	6.00	HC	1.82	2.17	MD	2.8E+06	13.38	sCP
Dipeptidyl peptidase 2	Q9UHL4	DPP2_HUMAN	0	0	0	28	40	0	70	52	0	0	0	0	0	0	68	122	0	2	2	0	9.24	1.24	HC	n/a	n/a	MD	4.62	8.38	sCP	
Dipeptidyl peptidase 4	P27487	DPP4_HUMAN	0	0	27	63	35	56	35	79	49	56	0	48	48	0	0	125	275	96	3	5	2	1109.62	5.86	HC	0.38	1.97	MD	6.4E+05	11.01	sCP
Dynactin subunit 1	Q14203	DCTN1_HUMAN	0	0	47	0	0	0	0	0	0	0	0	0	0	0	47	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Dynein heavy chain 5, axonemal	Q8TE73	DYH5_HUMAN	0	0	0	0	0	0	0	0	200	0	0	0	0	0	200	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	3.87	3.06	sCP	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP				
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP				ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression	
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5			#HC	#sCP	#MD											
Dystroglycan	Q14118	DAG1_HUMAN	0	35	0	47	31	0	0	35	0	0	50	0	0	0	0	113	35	50	3	1	1	41.36	4.38	HC	6.21	4.23	HC	9.52	1.03	MD	
EGF-containing fibulin-like extracellular matrix protein 1	Q12805	FBLN3_HUMAN	48	78	61	47	84	52	155	43	148	81	70	30	96	55	44	318	479	295	5	5	5	0.87	1.38	HC	0.85	1.17	MD	1.23	1.57	sCP	
EGF-containing fibulin-like extracellular matrix protein 2	O95967	FBLN4_HUMAN	0	13	0	10	0	0	0	0	0	0	0	0	0	0	0	23	0	0	2	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
EH domain-containing protein 4	Q9H223	EHD4_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	29	0	0	0	0	29	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Elongation factor 1-alpha 2	Q05639	EF1A2_HUMAN	0	0	19	0	0	0	0	0	0	0	0	0	0	0	0	19	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Endonuclease domain-containing 1 protein	O94919	ENDD1_HUMAN	0	31	38	21	44	33	52	23	63	52	27	17	29	38	54	134	223	165	4	5	5	2.65	1.99	sCP	2.96	1.43	MD	1.46	1.40	sCP	
Endosialin	Q9HCU0	CD248_HUMAN	76	94	50	74	72	0	39	61	64	44	121	50	49	37	26	366	208	283	5	4	5	117.81	2.82	HC	0.70	1.38	HC	6.99	2.01	MD	
Endothelial protein C receptor	Q9UNN8	EPCR_HUMAN	42	71	49	73	94	0	26	79	51	12	70	28	49	29	17	329	168	193	5	4	5	299.78	2.94	HC	17.43	1.79	HC	4.16	1.67	MD	
Ephrin type-A receptor 7	Q15375	EPHA7_HUMAN	0	0	0	0	0	0	25	0	0	0	0	0	32	0	0	0	25	32	0	1	1	n/a	n/a	sCP	n/a	n/a	MD	0.32	1.08	sCP	
Ephrin type-B receptor 4	P54760	EPHB4_HUMAN	0	53	53	38	45	0	0	0	0	0	0	0	0	0	0	189	0	0	4	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Ephrin type-B receptor 6	O15197	EPHB6_HUMAN	0	0	0	0	0	0	0	16	0	0	0	0	0	0	0	0	16	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.48	3.30	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts															Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP						
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression	
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																
Epidermal growth factor receptor kinase substrate 8-like protein 2	Q9H6S3	ES8L2_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	57	0	0	0	0	57	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	MD
Epididymal secretory protein E1	P61916	NPC2_HUMAN	0	0	0	9	19	56	24	35	16	9	34	23	22	0	0	28	140	79	2	5	3	393.14	8.43	sCP	3.16	2.47	MD	0.87	3.45	sCP	
Epididymis-specific alpha-mannosidase	Q9Y2E5	MA2B2_HUMAN	0	0	0	34	0	63	0	33	0	18	0	63	0	0	34	114	63	1	3	1	2.58	4.90	sCP	0.92	1.01	MD	5.68	5.05	sCP		
Erythrocyte band 7 integral membrane protein	P27105	STOM_HUMAN	0	0	12	0	0	0	0	0	0	0	28	0	0	0	12	0	28	1	0	1	n/a	n/a	sCP	1.03	1.17	HC	n/a	n/a	MD		
Ester hydrolase C11orf54	Q9H0W9	CK054_HUMAN	0	0	0	0	0	0	0	33	0	0	0	0	0	0	33	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	1.70	3.43	sCP		
Eukaryotic translation initiation factor 6	P56537	IF6_HUMAN	0	17	0	5	9	0	9	10	0	0	0	0	0	0	31	19	0	3	2	0	0.64	1.93	HC	n/a	n/a	HC	3.90	7.85	sCP		
Extracellular superoxide dismutase	P08294	SODE_HUMAN	54	14	33	46	68	0	0	36	29	0	43	0	0	44	17	215	65	104	5	2	3	7.5E+04	8.36	HC	1363.04	4.45	HC	0.33	2.10	MD	
Ezrin	P15311	EZRI_HUMAN	0	0	36	38	48	94	0	76	63	62	0	58	69	82	0	122	295	209	3	4	3	0.27	3.23	sCP	0.04	1.07	MD	1.07	2.95	sCP	
Fatty acid-binding protein, epidermal	Q01469	FABP5_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	32	0	0	0	32	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	MD	
Ferritin light chain	P02792	FRIL_HUMAN	0	24	0	6	0	0	0	17	11	35	0	0	0	0	30	63	0	2	3	0	1.96	2.31	HC	n/a	n/a	MD	n/a	n/a	sCP		
Fibrillin-1	P35555	FBN1_HUMAN	0	0	0	67	0	0	79	0	89	0	0	0	0	0	67	168	0	1	2	0	3.43	2.04	HC	n/a	n/a	MD	5.38	9.30	sCP		

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					Σ HC	Σ sCP	Σ MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression				
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																
			#HC	#sCP	#MD																												
Fibrinogen alpha chain	P02671	FIBA_HUMAN	0	142	95	101	86	0	84	72	101	68	132	80	73	98	144	424	325	527	4	4	5	0.04	1.13	sCP	141.03	2.30	HC	7.40	2.50	MD	
Fibrinogen beta chain	P02675	FIBB_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	101	0	0	101	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	MD
Fibrinogen gamma chain	P02679	FIBG_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84	0	0	84	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	MD
Fibronectin	P02751	FINC_HUMAN	157	127	95	85	123	171	100	125	159	118	192	187	181	104	111	587	673	775	5	5	5	0.86	1.18	sCP	2.04	1.27	MD	0.61	1.11	MD	
Fibulin-1	P23142	FBLN1_HUMAN	0	0	29	17	0	0	18	0	38	23	0	0	0	41	0	46	79	41	2	3	1	1.91	2.16	HC	7.20	1.87	MD	0.98	3.95	sCP	
Fibulin-2	P98095	FBLN2_HUMAN	0	34	0	36	38	0	25	41	39	0	46	33	39	0	42	108	105	160	3	3	4	0.56	1.06	sCP	0.16	2.39	HC	15.00	2.47	MD	
Fibulin-5	Q9UBX5	FBLN5_HUMAN	0	0	8	8	0	0	26	0	31	0	0	0	0	0	0	16	57	0	2	2	0	0.80	1.33	HC	n/a	n/a	MD	9.20	8.79	sCP	
Ficolin-2	Q15485	FCN2_HUMAN	0	26	0	0	0	0	0	14	0	0	0	0	0	0	0	26	14	0	1	1	0	4.06	1.16	HC	n/a	n/a	HC	0.96	3.16	sCP	
Filaggrin	P20930	FILA_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	415	0	0	0	415	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	MD
Filaggrin-2	Q5D862	FILA2_HUMAN	0	0	0	0	0	0	62	0	0	0	0	0	0	0	0	0	62	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.56	3.74	sCP	
Folate receptor alpha	P15328	FOLR1_HUMAN	0	16	25	28	19	0	16	55	19	4	0	10	13	9	0	88	94	32	4	4	3	1.70	1.28	HC	9.35	2.99	HC	2.92	2.08	sCP	
Formimidoyltransferase-cyclodeaminase	O95954	FTCD_HUMAN	0	0	0	0	0	0	0	34	0	0	0	0	0	0	0	0	34	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.39	3.58	sCP	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																					Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																		
			0	0	19	13	22	0	0	54	0	0	0	43	0	0	0	54	54	43	3	1	1	1.61	3.76	HC	29.81	3.41	HC	0.07	1.13	sCP			
Fructose-1,6-bisphosphatase 1	P09467	F16P1_HUMAN	0	0	19	13	22	0	0	54	0	0	0	43	0	0	0	54	54	43	3	1	1	1.61	3.76	HC	29.81	3.41	HC	0.07	1.13	sCP			
Fructose-bisphosphate aldolase A	P04075	ALDOA_HUMAN	0	0	34	0	0	0	18	36	0	0	0	0	0	58	0	34	54	58	1	2	1	4.16	2.15	HC	1.12	1.01	MD	0.37	2.21	sCP			
Fructose-bisphosphate aldolase B	P05062	ALDOB_HUMAN	118	44	26	25	15	0	34	169	32	21	0	42	27	64	0	228	256	133	5	4	3	1.29	1.58	HC	1328.83	3.77	HC	0.46	2.31	sCP			
Galectin-3-binding protein	Q08380	LG3BP_HUMAN	184	56	71	133	69	69	63	186	72	114	125	100	44	113	79	513	504	461	5	5	5	1.60	1.02	HC	0.44	1.08	MD	4.23	1.13	sCP			
Galectin-9	O00182	LEG9_HUMAN	0	0	11	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a			
Galectin-9B	Q3B8N2	LEG9B_HUMAN	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0	8	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD			
Galectin-9C	Q6DKI2	LEG9C_HUMAN	0	19	0	9	13	0	12	9	0	0	16	0	0	0	0	41	21	16	3	2	1	0.78	1.98	HC	5.55	3.97	HC	1.00	2.11	sCP			
Gamma-glutamyl hydrolase	Q92820	GGH_HUMAN	0	26	28	57	51	0	26	44	32	35	32	55	61	34	0	162	137	182	4	4	4	2.48	1.06	sCP	3.70	1.01	HC	1.61	1.13	MD			
Gamma-glutamylaminocyclotransferase	Q9BVM4	A2LD1_HUMAN	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	5	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.28	3.04	sCP			
Gamma-glutamyltransferase 6	Q6P531	GGT6_HUMAN	0	0	0	10	31	0	0	22	0	0	0	0	0	0	0	41	22	0	2	1	0	0.47	1.74	HC	n/a	n/a	HC	1.40	3.37	sCP			
Gamma-glutamyltranspeptidase 1	P19440	GGT1_HUMAN	0	0	24	0	24	0	0	43	0	0	0	43	34	53	0	48	43	130	2	1	3	5.45	1.56	sCP	0.83	2.30	HC	5.01	4.99	MD			

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP						
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP				ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5				#HC	#sCP	#MD												
Gamma-interferon-inducible lysosomal thiol reductase	P13284	GILT_HUMAN	0	0	0	0	7	0	0	15	5	5	0	0	0	0	7	25	0	1	3	0	4.03	3.78	HC	n/a	n/a	MD	n/a	n/a	sCP				
Ganglioside GM2 activator	P17900	SAP3_HUMAN	0	0	13	12	0	33	38	0	49	62	0	0	26	35	0	25	182	61	2	4	2	33.65	7.47	sCP	1.39	1.17	MD	66.35	5.01	sCP			
Gastricsin	P20142	PEPC_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	6	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD			
Gelsolin	P06396	GELS_HUMAN	218	201	213	103	133	272	272	79	484	180	102	78	121	166	197	868	1287	664	5	5	5	0.24	1.25	HC	7.57	1.36	MD	8.15	1.73	sCP			
Glutaminyl-peptide cyclotransferase	Q16769	QPCT_HUMAN	79	79	75	73	120	0	62	72	55	44	102	34	92	75	44	426	233	347	5	4	5	805.75	2.82	HC	1.76	1.35	HC	13.66	2.24	MD			
Glutamyl aminopeptidase	Q07075	AMPE_HUMAN	0	0	0	35	49	0	55	63	72	148	0	0	0	0	0	84	338	0	2	4	0	38.25	7.14	HC	n/a	n/a	MD	n/a	n/a	sCP			
Glutathione peroxidase 3	P22352	GPX3_HUMAN	0	0	0	0	22	0	0	0	11	0	0	0	0	0	0	22	11	0	1	1	0	0.93	1.14	HC	n/a	n/a	HC	1.68	3.23	sCP			
Glutathione S-transferase A2	P09210	GSTA2_HUMAN	0	0	0	0	0	0	0	47	0	0	0	0	0	0	0	47	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.32	3.58	sCP				
Glutathione S-transferase A3	Q16772	GSTA3_HUMAN	0	0	28	0	0	0	0	0	35	0	0	21	0	0	0	28	35	21	1	1	1	1.05	1.10	HC	1.40	1.08	MD	0.45	1.06	sCP			
Glutathione S-transferase Mu 3	P21266	GSTM3_HUMAN	0	0	0	0	0	0	0	12	0	0	0	18	30	0	0	12	48	0	1	2	n/a	n/a	sCP	n/a	n/a	MD	1.41	2.28	MD				
Glutathione S-transferase P	P09211	GSTP1_HUMAN	36	0	13	7	0	0	0	22	0	0	0	13	18	49	12	56	22	92	3	1	4	3.05	4.22	sCP	5.36	2.13	HC	88.21	9.53	MD			

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5	ΣHC	ΣsCP	ΣMD												
			#HC	#sCP	#MD																											
Glyceraldehyde-3-phosphate dehydrogenase	P04406	G3P_HUMAN	145	22	45	28	44	0	52	88	35	27	0	49	50	88	0	284	202	187	5	4	3	0.37	1.98	HC	982.45	4.17	HC	0.12	2.28	sCP
Glycerol-3-phosphate dehydrogenase	P21695	GPDA_HUMAN	0	0	0	0	0	0	0	30	0	0	0	0	0	0	0	0	30	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.43	3.82	sCP
Glycine amidinotransferase, mitochondrial	P50440	GATM_HUMAN	0	0	0	0	0	0	0	15	0	0	0	0	0	0	0	0	15	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.96	3.47	sCP
Glypican-3	P51654	GPC3_HUMAN	0	0	23	15	0	0	0	23	0	0	0	0	0	0	0	38	23	0	2	1	0	0.61	1.92	HC	n/a	n/a	HC	1.12	3.08	sCP
Glypican-4	O75487	GPC4_HUMAN	0	0	0	32	40	0	0	0	0	0	0	0	0	0	0	72	0	0	2	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Golgi membrane protein 1	Q8NBJ4	GOLM1_HUMAN	0	0	0	41	57	0	0	70	0	0	0	43	55	0	0	98	70	98	2	1	2	8.08	2.20	HC	0.06	1.02	HC	3.08	2.08	MD
G-protein coupled receptor family C group 5 member B	Q9NZH0	GPC5B_HUMAN	0	0	0	0	20	0	0	0	0	0	0	19	34	0	0	20	0	53	1	0	2	n/a	n/a	sCP	1.10	2.19	HC	n/a	n/a	MD
G-protein coupled receptor family C group 5 member C	Q9NQ84	GPC5C_HUMAN	63	0	16	0	23	44	0	21	10	0	36	46	19	34	0	102	75	135	3	3	4	0.85	1.08	sCP	0.38	2.32	HC	1.66	2.30	MD
Granulins	P28799	GRN_HUMAN	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	16	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Group XV phospholipase A2	Q8NCC3	PAG15_HUMAN	0	0	0	0	0	0	23	0	0	0	0	0	0	0	0	23	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	2.02	3.15	sCP
Growth/differentiation factor 15	Q99988	GDF15_HUMAN	0	0	0	0	0	0	0	0	17	0	0	0	0	0	0	17	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	1.06	3.36	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																				Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	Bayes Factor	Fold Change				Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression		
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5						#HC	#sCP	#MD									
Guanine nucleotide-binding protein G	P62873	GBB1_HUMAN	0	0	0	0	25	0	0	0	0	0	0	35	39	58	0	25	0	132	1	0	3	n/a	n/a	sCP	1.23	4.84	HC	n/a	n/a	MD		
Guanine nucleotide-binding protein G	P62879	GBB2_HUMAN	0	0	0	0	0	0	29	0	0	0	27	0	0	0	0	29	27	0	0	1	1	n/a	n/a	sCP	n/a	n/a	MD	0.43	1.01	sCP		
Guanine nucleotide-binding protein G	P63096	GNAI1_HUMAN	0	0	0	0	0	0	0	0	0	0	0	40	0	0	0	0	40	0	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD		
Guanine nucleotide-binding protein G	Q9UBI6	GBG12_HUMAN	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	9	0	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD		
Guanylate cyclase activator 2B	Q16661	GUC2B_HUMAN	0	0	0	0	0	13	0	12	0	0	0	0	0	0	0	25	0	0	2	0	0	n/a	n/a	n/a	n/a	n/a	MD	7.01	7.55	sCP		
Guanylin	Q02747	GUC2A_HUMAN	0	0	0	0	0	0	0	11	0	0	0	0	0	0	0	11	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	1.68	3.23	sCP		
Haptoglobin	P00738	HPT_HUMAN	79	0	99	36	35	0	416	54	56	40	0	42	102	174	249	566	318	4	4	3	7.55	1.15	HC	0.36	2.36	MD	0.74	2.54	sCP			
Heat shock 70 kDa protein 1A/1B	P08107	HSP71_HUMAN	0	0	0	0	0	0	0	51	0	0	0	50	66	0	0	0	51	116	0	1	2	n/a	n/a	sCP	n/a	n/a	MD	2.56	2.39	MD		
Heat shock 70 kDa protein 1-like	P34931	HS71L_HUMAN	0	0	40	0	0	0	0	0	0	0	0	0	0	0	40	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a			
Heat shock cognate 71 kDa protein	P11142	HSP7C_HUMAN	0	0	0	0	0	0	33	0	0	0	0	0	0	0	0	33	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.70	3.43	sCP			
Heat shock protein beta-1	P04792	HSPB1_HUMAN	0	0	12	0	0	0	14	13	0	0	0	0	0	0	0	12	27	0	1	2	1.11	2.30	HC	n/a	n/a	MD	8.73	8.03	sCP			

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Heat shock protein HSP 90-alpha	P07900	HS90A_HUMAN	0	0	32	0	0	0	0	31	0	0	0	0	0	0	32	31	0	1	1	0	0.53	1.07	HC	n/a	n/a	HC	3.34	3.56	sCP	
Heat shock-related 70 kDa protein 2	P54652	HSP72_HUMAN	0	0	0	0	0	0	38	0	0	0	0	0	58	0	0	38	58	0	0	1	1	n/a	n/a	sCP	n/a	n/a	MD	1.94	1.10	sCP
Hemicentin-1	Q96RW7	HMCN1_HUMAN	0	280	194	190	203	0	180	177	0	237	339	281	234	281	256	867	594	1391	4	3	5	0.23	3.51	sCP	1.3E+08	5.17	HC	1.7E+11	13.09	MD
Hemoglobin subunit alpha	P69905	HBA_HUMAN	48	14	0	56	11	0	5	19	0	40	0	11	0	79	51	129	64	141	4	3	3	5.34	1.99	HC	27.90	1.89	HC	0.28	1.20	MD
Hemoglobin subunit beta	P68871	HBB_HUMAN	82	0	0	78	0	0	0	37	0	69	0	0	0	180	54	160	106	234	2	2	2	2.70	1.08	sCP	0.48	1.10	MD	0.64	1.09	MD
Hemoglobin subunit gamma-1	P69891	HBG1_HUMAN	54	0	0	0	0	0	0	0	0	0	0	0	0	0	54	0	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Hemopexin	P02790	HEMO_HUMAN	151	81	45	145	74	50	107	79	56	61	105	64	80	84	201	496	353	534	5	5	5	2.37	1.37	sCP	0.67	1.07	HC	4.25	1.37	MD
Hepatitis A virus cellular receptor 2	Q8TDQ0	HAVR2_HUMAN	0	8	18	21	26	10	18	21	17	17	39	16	30	18	0	73	83	103	4	5	4	1.16	1.41	sCP	1.12	1.23	MD	0.55	1.12	sCP
Hepatocyte growth factor activator	Q04756	HGFA_HUMAN	0	0	0	23	0	0	0	0	0	0	0	0	0	0	23	0	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Histidine-rich glycoprotein	P04196	HRG_HUMAN	0	0	0	0	0	0	0	0	0	0	0	46	0	39	0	0	85	0	0	0	2	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Histone H4	P62805	H4_HUMAN	0	0	0	0	0	0	0	0	0	11	0	0	0	0	0	11	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	1.77	3.26	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
Hornerin	Q86YZ3	HORN_HUMAN	0	0	51	0	0	0	0	35	0	62	135	53	55	0	0	51	97	243	1	2	3	0.41	2.18	sCP	134.52	4.97	MD	0.06	2.36	MD
Hyaluronidase-1	Q12794	HYAL1_HUMAN	0	0	11	17	19	0	0	15	0	0	22	0	0	0	0	47	15	22	3	1	1	13.86	4.41	HC	2.78	4.65	HC	0.43	1.01	sCP
ICOS ligand	O75144	ICOSL_HUMAN	0	0	0	2	0	0	0	15	0	0	19	8	11	0	0	2	15	38	1	1	3	1.03	1.11	sCP	11.97	6.91	MD	4.03	4.08	MD
Ig alpha-1 chain C region	P01876	IGHA1_HUMAN	260	110	182	126	143	163	98	235	198	288	241	123	220	137	165	821	982	886	5	5	5	0.11	1.18	sCP	4.86	1.07	MD	0.74	1.09	sCP
Ig alpha-2 chain C region	P01877	IGHA2_HUMAN	209	0	130	118	115	0	71	146	148	188	184	95	174	124	144	572	553	721	4	4	5	740.05	1.05	sCP	204.33	3.09	HC	137.30	3.67	MD
Ig gamma-1 chain C region	P01857	IGHG1_HUMAN	323	487	338	403	398	289	226	186	281	368	299	216	200	311	768	1949	1350	1794	5	5	5	58.56	1.46	HC	27.47	1.27	HC	0.26	1.13	MD
Ig gamma-2 chain C region	P01859	IGHG2_HUMAN	341	810	341	452	324	232	281	238	291	441	423	268	273	442	536	2268	1483	1942	5	5	5	2.21	1.48	HC	0.31	1.14	HC	0.88	1.26	MD
Ig gamma-3 chain C region	P01860	IGHG3_HUMAN	0	509	234	335	261	0	211	172	0	357	283	0	207	0	541	1339	740	1031	4	3	3	0.01	3.65	HC	0.32	3.24	HC	0.02	1.01	sCP
Ig gamma-4 chain C region	P01861	IGHG4_HUMAN	0	427	0	0	261	215	195	0	235	339	0	0	179	0	454	688	984	633	2	4	2	93.74	7.42	sCP	0.41	1.05	MD	183.78	8.11	sCP
Ig heavy chain V-I region EU	P01742	HV101_HUMAN	0	0	0	0	0	0	17	17	0	0	0	0	0	0	0	34	0	0	2	0	0	n/a	n/a	n/a	n/a	n/a	MD	n/a	n/a	sCP
Ig heavy chain V-I region HG3	P01743	HV102_HUMAN	24	27	16	16	20	0	0	0	12	0	27	20	18	32	36	103	12	133	5	1	5	5.8E+04	14.03	sCP	1.51	1.24	HC	4.6E+05	19.67	MD

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Ig heavy chain V-I region Mot	P06326	HV107_HUMAN	0	0	0	0	0	0	0	0	0	30	0	0	0	0	0	30	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.54	3.67	sCP	
Ig heavy chain V-I region V35	P23083	HV103_HUMAN	0	0	0	0	0	31	0	0	0	0	0	0	0	0	0	31	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	3.51	3.74	sCP	
Ig heavy chain V-II region ARH-77	P06331	HV209_HUMAN	0	12	0	6	0	0	0	0	0	0	0	0	0	7	18	0	7	2	0	1	n/a	n/a	HC	0.57	2.03	HC	n/a	n/a	MD	
Ig heavy chain V-III region BRO	P01766	HV305_HUMAN	60	70	42	27	26	46	66	50	41	61	69	40	39	81	63	225	264	292	5	5	5	0.65	1.39	sCP	1.53	1.27	MD	1.22	1.02	MD
Ig heavy chain V-III region CAM	P01768	HV307_HUMAN	42	0	0	0	0	0	0	0	0	0	0	0	0	0	42	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Ig heavy chain V-III region GAL	P01781	HV320_HUMAN	0	23	0	0	0	0	0	0	0	0	0	0	0	24	0	23	0	24	1	0	1	n/a	n/a	HC	0.36	1.02	HC	n/a	n/a	MD
Ig heavy chain V-III region JON	P01780	HV319_HUMAN	0	0	0	0	0	0	0	25	0	0	0	0	0	0	0	25	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.61	3.02	sCP	
Ig heavy chain V-III region KOL	P01772	HV311_HUMAN	30	20	0	0	0	0	19	20	16	29	22	14	0	12	24	50	84	72	2	4	4	97.30	3.43	sCP	1.47	3.49	MD	3.61	1.10	sCP
Ig heavy chain V-III region TIL	P01765	HV304_HUMAN	0	0	0	31	0	42	0	0	0	0	0	0	0	0	51	31	42	51	1	1	1	3.08	1.07	sCP	0.15	1.04	HC	0.63	1.07	sCP
Ig heavy chain V-III region VH26	P01764	HV303_HUMAN	0	53	24	0	24	0	50	34	39	48	47	39	30	63	0	101	171	179	3	4	4	2.15	2.65	sCP	0.51	2.44	MD	1.37	1.02	sCP
Ig kappa chain C region	P01834	IGKC_HUMAN	338	932	806	426	954	1704	1837	378	1702	2403	578	436	529	792	802	3456	8024	3137	5	5	5	559.32	1.94	HC	1.20	1.01	MD	1253.38	2.06	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP				ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Ig kappa chain V-I region AG	P01593	KV101_HUMAN	0	72	51	0	0	71	0	0	72	112	53	0	0	50	38	123	255	141	2	3	3	0.04	2.60	sCP	0.10	2.13	MD	1.37	1.16	sCP
Ig kappa chain V-I region AU	P01594	KV102_HUMAN	0	0	0	0	0	0	114	29	0	0	0	0	50	0	0	0	143	50	0	2	1	n/a	n/a	sCP	n/a	n/a	MD	9.45	2.66	sCP
Ig kappa chain V-I region BAN	P04430	KV122_HUMAN	0	27	23	10	31	0	57	0	25	35	22	29	9	26	0	91	117	86	4	3	4	1.24	1.59	HC	0.78	1.07	HC	0.29	1.55	MD
Ig kappa chain V-I region CAR	P01596	KV104_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	0	0	17	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Ig kappa chain V-I region DEE	P01597	KV105_HUMAN	0	0	0	0	0	0	100	0	0	87	0	0	0	0	0	0	187	0	0	2	0	n/a	n/a	n/a	n/a	n/a	MD	1.80	9.53	sCP
Ig kappa chain V-I region EU	P01598	KV106_HUMAN	0	0	0	0	0	0	0	0	0	30	0	0	53	0	0	0	83	0	0	2	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Ig kappa chain V-I region HK101	P01601	KV109_HUMAN	39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	39	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Ig kappa chain V-I region HK102	P01602	KV110_HUMAN	0	37	22	14	31	29	69	7	39	68	0	20	27	0	0	104	212	47	4	5	2	27.35	2.24	HC	20.14	4.39	MD	3730.57	10.08	sCP
Ig kappa chain V-I region Lay	P01605	KV113_HUMAN	0	0	0	0	0	0	39	0	0	0	0	0	0	0	0	39	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	2.82	3.58	sCP
Ig kappa chain V-I region Mev	P01612	KV120_HUMAN	0	0	30	0	0	0	0	0	0	0	0	0	0	0	30	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Ig kappa chain V-I region Ni	P01613	KV121_HUMAN	0	15	12	0	15	0	23	0	0	0	0	15	16	0	11	42	23	42	3	1	3	3.90	3.38	HC	0.06	1.03	HC	3.36	3.92	MD

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP				
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression		
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																	
			#HC	#sCP	#MD																													
Ig kappa chain V-I region Scw	P01609	KV117_HUMAN	0	77	0	39	72	36	87	0	0	0	0	0	49	48	0	0	188	123	97	3	2	2	0.07	2.21	HC	0.77	2.32	HC	1.71	1.12	sCP	
Ig kappa chain V-I region WEA	P01610	KV118_HUMAN	0	0	0	0	0	0	0	0	0	99	0	0	0	0	0	0	99	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	n/a	MD	2.08	3.67	sCP
Ig kappa chain V-I region Wes	P01611	KV119_HUMAN	0	0	0	0	0	0	32	0	21	0	0	0	0	0	0	0	53	0	0	2	0	0	n/a	n/a	n/a	n/a	n/a	n/a	MD	1.86	8.41	sCP
Ig kappa chain V-II region Cum	P01614	KV201_HUMAN	0	0	0	32	76	0	181	0	0	0	0	0	0	0	0	108	181	0	2	1	0	83.51	1.66	HC	n/a	n/a	HC	4.57	3.89	sCP		
Ig kappa chain V-II region GM607	P06309	KV205_HUMAN	48	0	85	42	97	82	217	0	0	221	67	54	52	76	67	272	520	316	4	3	5	6.39	2.08	sCP	16.57	1.78	HC	1874.44	3.08	MD		
Ig kappa chain V-II region MIL	P01616	KV203_HUMAN	0	42	40	22	56	0	119	0	78	96	0	0	0	0	0	160	293	0	4	3	0	1.01	1.91	HC	n/a	n/a	HC	n/a	n/a	sCP		
Ig kappa chain V-II region RPMI 6410	P06310	KV206_HUMAN	0	43	0	0	56	0	164	32	92	140	0	0	0	0	0	99	428	0	2	4	0	58.76	6.51	HC	n/a	n/a	MD	n/a	n/a	sCP		
Ig kappa chain V-II region TEW	P01617	KV204_HUMAN	0	101	0	0	0	0	0	0	110	0	0	0	0	0	101	110	0	1	1	0	1.47	1.08	HC	n/a	n/a	MD	1.70	4.08	sCP			
Ig kappa chain V-III region B6	P01619	KV301_HUMAN	0	42	0	14	0	0	0	0	0	0	0	0	0	0	56	0	0	2	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a			
Ig kappa chain V-III region CLL	P04207	KV308_HUMAN	0	22	40	0	34	0	86	28	73	60	0	0	0	0	96	247	0	3	4	0	0.89	2.94	HC	n/a	n/a	MD	n/a	n/a	sCP			
Ig kappa chain V-III region GOL	P04206	KV307_HUMAN	0	171	148	0	0	0	0	0	351	0	0	0	0	0	319	351	0	2	1	0	26.25	1.88	HC	n/a	n/a	HC	3.54	4.50	sCP			

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					Σ HC	Σ sCP	Σ MD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression	
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																
			#HC	#sCP	#MD																												
Ig kappa chain V-III region HAH	P18135	KV312_HUMAN	115	0	142	79	0	224	431	0	392	0	0	0	96	131	0	336	104	7	227	3	3	2	0.15	1.18	HC	4.45	2.35	MD	10.01	2.97	sCP
Ig kappa chain V-III region HIC	P18136	KV313_HUMAN	0	173	0	0	192	0	0	92	0	344	135	90	0	0	113	365	436	338	2	2	3	1.66	1.04	sCP	1.27	2.02	MD	0.24	1.95	MD	
Ig kappa chain V-III region IARC/BL41	P06311	KV311_HUMAN	0	0	0	0	0	0	75	0	48	0	0	0	0	0	0	0	123	0	0	2	0	n/a	n/a	n/a	n/a	n/a	MD	9.79	9.56	sCP	
Ig kappa chain V-III region NG9	P01621	KV303_HUMAN	0	0	0	40	0	0	0	0	0	0	0	0	0	0	0	40	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Ig kappa chain V-III region POM	P01624	KV306_HUMAN	0	0	27	12	0	0	55	0	0	0	0	0	0	0	0	39	55	0	2	1	0	2.17	1.60	HC	n/a	n/a	HC	2.09	3.64	sCP	
Ig kappa chain V-III region VG	P04433	KV309_HUMAN	24	31	31	17	38	21	65	21	61	78	27	15	19	29	27	141	246	117	5	5	5	7.64	1.62	HC	1.21	1.23	MD	13.38	1.94	sCP	
Ig kappa chain V-III region VH	P04434	KV310_HUMAN	0	0	15	0	0	0	0	0	0	0	14	8	18	15	0	15	0	55	1	0	4	n/a	n/a	sCP	2.78	7.58	HC	n/a	n/a	MD	
Ig kappa chain V-IV region	P06312	KV401_HUMAN	0	76	0	0	0	0	0	0	0	0	0	0	0	0	0	76	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Ig kappa chain V-IV region B17	P06314	KV404_HUMAN	60	0	0	0	0	0	0	0	0	115	0	0	0	0	0	60	115	0	1	1	0	0.46	1.21	HC	n/a	n/a	MD	0.14	3.71	sCP	
Ig kappa chain V-IV region JI	P06313	KV403_HUMAN	0	0	68	33	59	38	126	38	114	102	65	0	39	73	49	160	418	226	3	5	4	3469.47	6.90	sCP	9.19	2.36	MD	20.25	2.45	sCP	
Ig kappa chain V-IV region Len	P01625	KV402_HUMAN	0	0	0	0	0	0	0	0	93	90	0	0	0	0	0	183	0	0	0	2	0	n/a	n/a	n/a	n/a	n/a	MD	n/a	n/a	sCP	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
Ig kappa chain V-IV region STH	P83593	KV405_HUMAN	0	0	0	0	0	0	53	0	0	0	0	0	0	0	0	53	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.91	3.56	sCP
Ig lambda chain V-I region BL2	P06316	LV107_HUMAN	0	0	0	0	0	0	0	0	41	53	0	0	0	0	26	0	94	26	0	2	1	n/a	n/a	sCP	n/a	n/a	MD	2.12	2.73	sCP
Ig lambda chain V-I region NEW	P01701	LV103_HUMAN	0	0	0	0	0	0	28	0	0	35	0	0	0	0	0	0	63	0	0	2	0	n/a	n/a	n/a	n/a	n/a	MD	2.72	8.63	sCP
Ig lambda chain V-I region NEWM	P01703	LV105_HUMAN	0	14	14	0	11	40	27	0	29	56	0	0	0	14	26	39	152	40	3	4	2	2.03	3.49	HC	0.95	1.68	MD	13.29	6.30	sCP
Ig lambda chain V-I region WAH	P04208	LV106_HUMAN	0	45	25	13	0	29	60	24	64	77	0	26	21	40	41	83	254	128	3	5	4	1241.14	6.15	sCP	0.19	2.43	MD	10.55	2.87	sCP
Ig lambda chain V-II region NEI	P01705	LV202_HUMAN	0	0	0	0	0	0	21	0	0	0	0	0	0	0	0	0	21	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.44	3.16	sCP
Ig lambda chain V-III region LOI	P80748	LV302_HUMAN	0	15	16	10	22	21	35	14	55	86	0	9	9	0	45	63	211	63	4	5	3	138.80	2.98	HC	0.91	1.76	MD	2693.09	6.49	sCP
Ig lambda chain V-III region SH	P01714	LV301_HUMAN	0	7	0	0	0	0	0	0	37	36	0	0	0	0	0	7	73	0	1	2	0	2.14	2.71	HC	n/a	n/a	MD	n/a	n/a	sCP
Ig lambda chain V-IV region Hil	P01717	LV403_HUMAN	0	0	0	0	0	0	0	0	0	18	0	0	11	0	10	0	18	21	0	1	2	n/a	n/a	sCP	n/a	n/a	MD	1.49	1.97	MD
Ig lambda chain V-VI region EB4	P06319	LV605_HUMAN	0	0	0	0	0	0	18	0	0	0	0	0	0	0	0	0	18	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.07	3.58	sCP
Ig lambda chain V-VI region SUT	P06317	LV603_HUMAN	0	0	0	0	0	0	0	0	0	42	0	0	0	0	0	0	42	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	0.35	3.43	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																				Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					Σ HC	Σ sCP	Σ MD	Bayes Factor	Fold Change				Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression		
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																	
			#HC	#sCP	#MD																													
Ig lambda-1 chain C regions	P0CG04	LAC1_HUMAN	0	136	122	70	88	297	303	65	306	787	62	46	84	0	232	416	1758	424	4	5	4	2.1E+04	6.27	HC	0.21	1.10	MD	2.8E+04	5.75	sCP		
Ig lambda-2 chain C regions	P0CG05	LAC2_HUMAN	0	230	181	123	148	393	367	118	475	932	123	87	130	203	349	682	2285	892	4	5	5	7.4E+04	5.28	sCP	117.40	2.98	MD	34.07	2.30	sCP		
Ig lambda-3 chain C regions	P0CG06	LAC3_HUMAN	106	0	0	0	0	0	0	0	0	0	0	0	0	0	0	106	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a		
Ig lambda-7 chain C region	A0M8Q6	LAC7_HUMAN	0	0	0	0	0	0	243	0	255	554	0	0	0	0	0	0	1052	0	0	3	0	n/a	n/a	n/a	n/a	n/a	MD	n/a	n/a	sCP		
Ig mu chain C region	P01871	IGHM_HUMAN	0	28	66	24	26	0	61	0	24	79	0	20	0	46	26	144	164	92	4	3	3	0.16	2.02	HC	0.24	2.38	HC	4.91	1.19	sCP		
IgGFc-binding protein	Q9Y6R7	FCGBP_HUMAN	0	0	197	0	0	0	0	0	0	0	0	0	0	0	0	197	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a		
Immunoglobulin J chain	P01591	IGJ_HUMAN	0	0	13	0	13	0	14	17	11	31	27	0	12	0	14	26	73	53	2	4	3	10.65	4.13	sCP	0.77	2.16	MD	0.73	2.00	sCP		
Immunoglobulin lambda-like polypeptide 1	P15814	IGLL1_HUMAN	0	0	32	0	24	0	0	0	0	0	0	0	0	0	0	56	0	0	2	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a		
Immunoglobulin superfamily member 8	Q969P0	IGSF8_HUMAN	0	33	31	31	43	86	58	17	58	51	46	43	27	46	29	138	270	191	4	5	5	22.87	2.60	sCP	4.41	1.85	MD	2.11	1.37	sCP		
Insulin-like growth factor-binding protein 2	P18065	IBP2_HUMAN	0	0	51	40	0	0	0	31	0	0	0	0	0	0	0	91	31	0	2	1	0	1.94	2.41	HC	n/a	n/a	HC	3.34	3.56	sCP		
Insulin-like growth factor-binding protein 7	Q16270	IBP7_HUMAN	118	46	93	83	97	157	47	87	79	37	50	54	122	87	73	437	407	386	5	5	5	1.31	1.06	HC	1.07	1.22	HC	0.34	1.05	sCP		

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
Integral membrane protein 2B	Q9Y287	ITM2B_HUMAN	0	0	6	6	8	0	5	9	0	0	0	9	9	9	0	20	14	27	3	2	3	0.54	1.78	sCP	0.92	1.23	HC	3.66	1.91	MD
Inter-alpha-trypsin inhibitor heavy chain H1	P19827	ITI1H_HUMAN	0	0	0	21	0	0	0	17	0	0	0	40	0	0	49	21	17	89	1	1	2	0.43	1.07	sCP	0.22	2.62	HC	0.15	2.42	MD
Inter-alpha-trypsin inhibitor heavy chain H4	Q14624	ITI1H4_HUMAN	360	226	315	221	333	209	370	250	342	205	222	160	184	261	209	1455	1376	1036	5	5	5	2.10	1.06	HC	26.37	1.42	HC	17.66	1.37	sCP
Interleukin-6 receptor subunit beta	P40189	IL6RB_HUMAN	0	43	21	0	25	0	0	29	47	0	36	48	0	0	0	89	76	84	3	2	2	3.64	2.09	HC	1.78	1.72	HC	0.05	1.11	sCP
Isocitrate dehydrogenase	O75874	IDHC_HUMAN	0	0	0	0	0	0	0	50	0	0	0	0	0	0	0	50	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	4.71	3.91	sCP	
IST1 homolog	P53990	IST1_HUMAN	0	0	26	20	51	0	0	27	0	0	0	53	48	40	0	97	27	141	3	1	3	0.94	4.61	sCP	0.16	1.14	HC	0.25	5.41	MD
Kallikrein-1	P06870	KLK1_HUMAN	42	31	33	71	42	42	19	73	37	0	75	25	80	38	0	219	171	218	5	4	4	2.56	2.04	HC	1.92	1.69	HC	0.09	1.05	MD
Kallikrein-11	Q9UBX7	KLK11_HUMAN	0	0	0	0	0	0	0	0	17	0	0	0	0	0	0	0	17	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.06	3.36	sCP
Kallistatin	P29622	KAIN_HUMAN	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	10	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.42	3.27	sCP
Keratin, type I cytoskeletal 10	P13645	K1C10_HUMAN	275	149	136	105	272	289	445	95	95	90	518	214	162	404	101	937	1014	1399	5	5	5	3.40	1.08	sCP	6.80	1.32	HC	4.52	1.35	MD
Keratin, type I cytoskeletal 13	P13646	K1C13_HUMAN	0	0	151	0	0	0	0	0	0	0	0	0	0	0	0	151	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts															Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP					
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses								Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5	ΣHC	ΣsCP	ΣMD												
			#HC	#sCP	#MD																											
Keratin, type I cytoskeletal 14	P02533	K1C14_HUMAN	0	0	77	48	126	138	153	0	0	55	224	103	71	156	0	251	346	554	3	3	4	0.17	1.12	sCP	0.04	3.47	MD	3.30	3.03	MD
Keratin, type I cytoskeletal 16	P08779	K1C16_HUMAN	0	0	0	0	107	0	128	0	0	0	195	0	0	151	0	107	128	346	1	1	2	0.25	1.04	sCP	0.20	1.98	HC	52.70	2.12	MD
Keratin, type I cytoskeletal 9	P35527	K1C9_HUMAN	326	109	90	111	225	295	97	102	88	205	462	225	147	438	106	861	787	1378	5	5	5	1.77	1.04	sCP	11.02	1.40	HC	2.17	1.54	MD
Keratin, type II cytoskeletal 1	P04264	K2C1_HUMAN	426	189	209	196	389	468	488	178	140	269	840	341	228	645	155	1409	1543	2209	5	5	5	0.27	1.01	sCP	55.02	1.29	MD	41.30	1.19	MD
Keratin, type II cytoskeletal 2 epidermal	P35908	K22E_HUMAN	341	121	107	89	210	295	253	75	89	90	402	189	140	383	112	868	802	1226	5	5	5	1.31	1.12	sCP	0.42	1.29	HC	4.61	1.45	MD
Keratin, type II cytoskeletal 4	P19013	K2C4_HUMAN	0	0	133	0	0	0	0	0	0	0	0	0	0	0	0	133	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Keratin, type II cytoskeletal 5	P13647	K2C5_HUMAN	0	0	106	0	131	148	171	51	0	57	221	132	63	217	50	237	427	683	2	4	5	7.21	6.42	sCP	5.5E+05	18.49	MD	12.16	3.12	MD
Keratin, type II cytoskeletal 6A	P02538	K2C6A_HUMAN	0	0	99	0	116	153	167	0	0	0	247	0	0	209	0	215	320	456	2	2	2	8.76	1.09	sCP	3.27	1.16	MD	2.39	1.12	sCP
Keratin, type II cytoskeletal 6B	P04259	K2C6B_HUMAN	0	0	0	0	0	0	0	0	0	0	111	0	0	0	0	0	0	111	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Keratin, type II cytoskeletal 8	P05787	K2C8_HUMAN	0	0	0	39	0	0	0	0	0	0	0	0	0	0	0	39	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Kin of IRRE-like protein 1	Q96J84	KIRR1_HUMAN	0	0	0	0	0	0	21	0	0	0	0	0	0	0	0	21	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	1.38	3.44	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Kininogen-1	P01042	KNG1_HUMAN	635	395	512	636	742	397	261	753	347	225	699	350	666	525	309	2920	1983	2549	5	5	5	4.35	1.66	HC	23.86	1.25	HC	22.01	1.28	MD
Lactotransferrin	P02788	TRFL_HUMAN	0	0	45	47	0	0	0	129	109	0	0	0	0	0	0	92	238	0	2	2	0	1.35	1.06	HC	n/a	n/a	MD	2.43	7.92	sCP
Lambda-crystallin homolog	Q9Y2S2	CRYL1_HUMAN	0	0	0	0	0	0	21	0	0	0	0	0	0	0	0	21	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.38	3.44	sCP	
Latent-transforming growth factor beta-binding protein 2	Q14767	LTBP2_HUMAN	0	0	0	38	0	0	0	60	0	0	0	0	0	0	0	38	60	0	1	1	0	0.52	1.01	HC	n/a	n/a	HC	6.38	3.83	sCP
Leucine-rich alpha-2-glycoprotein	P02750	A2GL_HUMAN	0	105	44	63	42	0	132	23	73	25	0	30	48	102	113	254	253	293	4	4	4	3.43	1.17	HC	0.78	1.03	HC	2.00	1.14	MD
Leucine-rich repeat-containing protein 19	Q9H756	LRC19_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	7	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Leukocyte immunoglobulin-like receptor subfamily A member 5	A6NI73	LIRA5_HUMAN	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Leukocyte-associated immunoglobulin-like receptor 1	Q6GTX8	LAIR1_HUMAN	0	20	0	0	11	50	11	19	0	18	0	12	39	0	21	31	98	72	2	4	3	60.41	4.12	sCP	1.03	1.79	MD	2.39	2.22	sCP
Lipocalin-1	P31025	LCN1_HUMAN	0	0	0	0	0	0	0	0	32	0	0	0	17	0	0	32	17	0	1	1	n/a	n/a	sCP	n/a	n/a	MD	0.53	1.22	sCP	
Lithostathine-1-alpha	P05451	REG1A_HUMAN	0	22	30	5	34	73	292	11	104	20	24	56	66	31	26	91	500	203	4	5	5	26.75	3.69	sCP	27.99	3.03	MD	3.84	1.32	sCP
L-lactate dehydrogenase A chain	P00338	LDHA_HUMAN	0	0	0	0	0	0	0	31	0	0	0	0	0	0	0	31	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	3.34	3.56	sCP	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP				
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					Σ HC	Σ sCP				Σ MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression	
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																
			#HC	#sCP	#MD																												
L-lactate dehydrogenase B chain	P07195	LDHB_HUMAN	57	31	38	25	38	0	46	68	33	18	0	30	35	64	18	189	165	147	5	4	4	0.86	1.87	HC	2.47	2.03	HC	1.78	1.10	sCP	
Low affinity immunoglobulin gamma Fc region receptor III-A	P08637	FCG3A_HUMAN	0	26	18	0	20	0	0	25	0	0	20	7	0	0	0	64	25	27	3	1	2	14.36	4.12	HC	0.74	2.59	HC	0.40	1.86	MD	
Low affinity immunoglobulin gamma Fc region receptor III-B	O75015	FCG3B_HUMAN	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0	0	0	16	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Low-density lipoprotein receptor-related protein 2	P98164	LRP2_HUMAN	565	313	299	279	427	347	283	337	364	320	356	357	492	327	0	1883	1651	1532	5	5	4	3.60	1.14	HC	2.3E+06	5.08	HC	2.0E+08	3.13	sCP	
Lumican	P51884	LUM_HUMAN	0	22	0	21	0	0	25	0	0	0	0	0	0	0	0	43	25	0	2	1	0	6.98	1.88	HC	n/a	n/a	HC	3.77	3.54	sCP	
Lymphatic vessel endothelial hyaluronic acid receptor 1	Q9Y5Y7	LYVE1_HUMAN	0	29	0	0	0	65	34	0	50	42	0	27	0	0	25	29	191	52	1	4	2	114.41	12.67	sCP	4.88	2.30	MD	28.45	6.81	sCP	
Lysosomal acid phosphatase	P11117	PPAL_HUMAN	0	24	0	38	41	77	0	72	23	56	50	36	29	38	0	103	228	153	3	4	4	26.54	2.80	sCP	0.64	2.33	MD	0.18	1.23	sCP	
Lysosomal alpha-glucosidase	P10253	LYAG_HUMAN	233	157	120	184	191	217	88	223	118	116	171	334	338	154	49	885	762	1046	5	5	5	3.41	1.20	HC	0.34	1.01	HC	1.87	1.09	MD	
Lysosomal protective protein	P10619	PPGB_HUMAN	0	17	16	32	39	90	47	56	52	80	11	39	30	37	10	104	325	127	4	5	5	1242.00	3.80	sCP	1.98	1.47	MD	29.77	2.82	sCP	
Lysosomal Pro-X carboxypeptidase	P42785	PCP_HUMAN	0	0	0	18	0	0	0	23	0	11	0	0	26	0	0	18	34	26	1	2	1	1.58	2.31	sCP	0.76	1.01	MD	0.86	1.99	sCP	
Lysosome-associated membrane glycoprotein 1	P11279	LAMP1_HUMAN	0	0	0	0	0	0	0	16	17	0	0	0	0	0	0	0	33	0	0	0	2	n/a	n/a	n/a	n/a	n/a	n/a	MD	n/a	n/a	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0													
Lysosome-associated membrane glycoprotein 2	P13473	LAMP2_HUMAN	0	0	0	0	0	0	0	22	0	0	0	0	0	0	22	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.40	3.37	sCP		
Lysozyme C	P61626	LYSC_HUMAN	0	0	0	0	8	36	10	17	23	22	0	0	14	0	0	8	108	14	1	5	1	6.2E+04	15.67	sCP	0.37	1.08	MD	2.5E+05	13.78	sCP
Macrophage colony-stimulating factor 1	P09603	CSF1_HUMAN	0	35	0	0	20	27	20	37	29	0	66	27	23	23	0	55	113	139	2	4	4	15.29	5.29	sCP	59.27	4.80	MD	4.50	1.05	sCP
Macrophage migration inhibitory factor	P14174	MIF_HUMAN	0	0	0	3	0	0	0	0	0	0	0	0	0	0	3	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Macrophage-capping protein	P40121	CAPG_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	23	0	0	0	23	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Major prion protein	P04156	PRIOP_HUMAN	0	19	6	10	18	0	24	22	36	11	22	14	16	41	0	53	93	93	4	4	4	1.03	1.47	sCP	1.97	1.58	MD	0.70	1.09	sCP
Malate dehydrogenase, cytoplasmic	P40925	MDHC_HUMAN	0	0	0	0	0	0	0	36	0	0	0	0	0	32	0	0	36	32	0	1	1	n/a	n/a	sCP	n/a	n/a	MD	2.90	1.18	sCP
Maltase-glucoamylase, intestinal	O43451	MGA_HUMAN	0	77	0	89	28	182	0	133	123	102	93	99	118	0	0	194	540	310	3	4	3	9.18	3.59	sCP	0.34	1.19	MD	0.01	3.67	sCP
Mannan-binding lectin serine protease 2	O00187	MASP2_HUMAN	106	48	48	36	51	0	39	44	0	0	103	50	0	131	73	289	83	357	5	2	4	4.1E+05	12.18	HC	1.01	1.58	HC	2.15	6.73	MD
Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	P33908	MA1A1_HUMAN	157	0	50	61	56	0	0	67	0	0	73	35	0	0	0	324	67	108	4	1	2	569.87	12.10	HC	56.36	6.22	HC	2.34	2.10	MD
Matrix-remodeling-associated protein 8	Q9BRK3	MXRA8_HUMAN	142	43	45	43	49	0	17	71	0	0	49	0	25	63	48	322	88	185	5	2	4	1.3E+06	12.28	HC	2.92	2.37	HC	3.87	5.17	MD

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP					
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					Σ HC	Σ sCP	Σ MD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5				#HC	#sCP	#MD												
Melanotransferrin	P08582	TRFM_HUMAN	0	0	45	43	52	0	0	47	0	0	0	0	0	0	0	0	140	47	0	3	1	0	9.60	4.85	HC	n/a	n/a	HC	1.32	3.58	sCP		
Mesothelin	Q13421	MSLN_HUMAN	0	0	0	0	0	0	17	0	0	0	0	0	0	0	0	0	17	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.18	3.37	sCP			
Metalloproteinase inhibitor 1	P01033	TIMP1_HUMAN	0	0	0	0	0	0	9	20	0	0	14	22	0	0	0	29	36	0	2	2	n/a	n/a	sCP	n/a	n/a	MD	1.43	1.09	MD				
Metalloproteinase inhibitor 2	P16035	TIMP2_HUMAN	0	0	0	10	0	0	0	0	0	0	0	0	0	0	10	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a				
Microfibril-associated glycoprotein 4	P55083	MFAP4_HUMAN	0	0	0	7	0	0	0	0	0	0	0	0	0	7	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a					
Mimecan	P20774	MIME_HUMAN	0	0	0	0	0	19	0	0	0	0	0	0	0	0	19	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.39	3.34	sCP					
Moesin	P26038	MOES_HUMAN	0	0	0	0	0	0	70	0	63	0	0	0	0	0	133	0	0	2	0	n/a	n/a	n/a	n/a	n/a	MD	5.06	9.20	sCP					
Monocyte differentiation antigen CD14	P08571	CD14_HUMAN	79	189	107	109	106	82	194	71	114	107	46	74	85	114	133	590	568	452	5	5	5	0.57	1.06	HC	3.21	1.34	HC	2.03	1.31	sCP			
Mucin-1	P15941	MUC1_HUMAN	45	0	7	28	20	0	19	0	0	37	33	34	34	0	100	19	138	4	1	4	23.71	7.54	sCP	0.64	1.43	HC	597.15	12.97	MD				
Mucin-20	Q8N307	MUC20_HUMAN	0	0	28	0	0	0	19	0	0	0	0	0	0	28	19	0	1	1	0	0.61	1.11	HC	n/a	n/a	HC	2.65	3.44	sCP					
Mucin-5B	Q9HC84	MUC5B_HUMAN	0	0	117	0	0	255	0	0	0	130	0	0	0	0	117	385	0	1	2	0	3.80	2.38	HC	n/a	n/a	MD	n/a	n/a	sCP				

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5				#HC	#sCP	#MD									
Mucosal addressin cell adhesion molecule 1	Q13477	MADCA_HUMAN	30	28	19	21	11	17	26	22	0	0	27	29	26	0	0	109	65	82	5	3	3	11.38	2.55	HC	0.47	2.68	HC	2.35	1.03	MD
Multimerin-2	Q9H8L6	MMRN2_HUMAN	0	69	52	60	38	0	0	0	0	0	41	0	58	0	219	0	99	4	0	2	n/a	n/a	HC	23.88	6.04	HC	n/a	n/a	MD	
Multiple epidermal growth factor-like domains protein 8	Q7Z7M0	MEGF8_HUMAN	0	0	0	0	0	0	0	71	0	0	0	0	0	0	0	71	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	0.49	3.83	sCP
Myeloid cell surface antigen CD33	P20138	CD33_HUMAN	0	0	11	0	0	0	0	0	0	0	0	0	0	0	0	11	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Myeloperoxidase	P05164	PERM_HUMAN	0	0	0	0	0	0	0	0	0	64	0	0	0	0	0	64	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	5.32	3.87	sCP
Myotrophin	P58546	MTPN_HUMAN	21	0	0	0	0	0	0	0	0	0	0	0	0	0	21	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
N(G),N(G)-dimethylarginine dimethylaminohydrolase	O94760	DDAH1_HUMAN	0	0	0	0	0	0	0	27	0	0	0	0	0	0	0	27	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	1.27	3.32	sCP
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	O95865	DDAH2_HUMAN	42	21	14	12	0	0	0	7	0	0	0	0	0	0	89	7	0	4	1	0	284.81	9.67	HC	n/a	n/a	HC	1.35	3.23	sCP	
Na(+)/H(+) exchange regulatory cofactor NHE-RF1	O14745	NHRF1_HUMAN	0	0	0	53	0	0	0	44	0	30	0	0	0	0	53	74	0	1	2	0	0.62	2.06	HC	n/a	n/a	MD	3.07	8.49	sCP	
N-acetylgalactosamine-6-sulfatase	P34059	GALNS_HUMAN	0	0	0	28	0	0	0	36	0	0	0	0	0	0	28	36	0	1	1	0	2.33	1.02	HC	n/a	n/a	MD	4.27	3.76	sCP	
N-acetylglucosamine-6-sulfatase	P15586	GNS_HUMAN	0	58	39	54	44	107	67	29	68	108	0	57	49	58	0	195	379	164	4	5	3	8.76	2.63	HC	3.73	2.37	MD	4.5E+04	7.08	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression	
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5				#HC	#sCP	#MD										
N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase	O43505	B3GN1_HUMAN	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	4	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
N-acetylmuramoyl-L-alanine amidase	Q96PD5	PGRP2_HUMAN	0	119	74	33	59	0	85	33	32	0	46	27	0	0	53	285	150	126	4	3	3	0.02	2.90	HC	10.14	2.75	HC	0.11	1.08	sCP	
Napsin-A	O96009	NAPSA_HUMAN	0	0	37	35	24	0	0	30	0	33	0	0	36	35	0	96	63	71	3	2	2	2.83	1.96	HC	0.40	2.17	HC	0.69	1.07	sCP	
Neogenin	Q92859	NEO1_HUMAN	0	96	0	0	0	0	0	0	0	0	0	0	0	0	0	96	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Nepriylsin	P08473	NEP_HUMAN	0	0	18	42	44	0	0	64	0	0	0	46	85	0	0	104	64	131	3	1	2	38.96	3.41	HC	0.13	2.05	HC	4.70	2.23	MD	
Neural cell adhesion molecule 1	P13591	NCAM1_HUMAN	0	0	14	22	0	0	0	18	0	25	0	25	20	0	0	36	43	45	2	2	2	0.35	1.03	sCP	1.26	1.06	HC	1.42	1.02	MD	
Neuronal growth regulator 1	Q7Z3B1	NEGR1_HUMAN	0	22	28	23	24	0	36	0	49	36	33	32	18	0	0	97	121	83	4	3	3	0.19	1.78	HC	7.85	1.76	HC	0.82	1.25	sCP	
Neutrophil defensin 1	P59665	DEF1_HUMAN	0	0	0	0	0	0	0	0	0	41	0	0	0	0	0	41	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	2.52	3.80	sCP	
Neutrophil defensin 3	P59666	DEF3_HUMAN	0	0	1	0	0	0	0	0	18	0	0	0	0	0	0	1	18	0	1	1	0	1.01	1.57	HC	n/a	n/a	MD	1.46	3.21	sCP	
Neutrophil elastase	P08246	ELNE_HUMAN	0	0	0	0	0	0	0	0	0	25	0	0	0	0	0	25	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	1.12	3.18	sCP	
Neutrophil gelatinase-associated lipocalin	P80188	NGAL_HUMAN	0	0	0	0	0	29	0	18	38	0	0	36	0	37	14	0	85	87	0	3	3	n/a	n/a	sCP	n/a	n/a	MD	0.09	1.07	sCP	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP		HC vs. MD		MD vs. CP						
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression		
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5				#HC	#sCP	#MD											
NHL repeat-containing protein 3	Q5JS37	NHLC3_HUMAN	0	0	0	17	13	19	0	23	0	20	16	0	25	0	0	30	62	41	2	3	2	0.99	2.25	sCP	0.70	1.16	MD	0.53	2.36	sCP		
Nidogen-1	P14543	NID1_HUMAN	0	103	42	56	94	0	0	32	0	33	82	71	0	52	0	295	65	205	4	2	3	12.24	7.16	HC	1.66	2.74	HC	0.23	2.62	MD		
Non-secretory ribonuclease	P10153	RNAS2_HUMAN	97	50	81	69	77	169	78	172	126	62	172	77	203	104	35	374	607	591	5	5	5	11.35	1.57	sCP	3.19	1.30	MD	0.62	1.22	sCP		
N-sulphoglucosamine sulphohydrolase	P51688	SPHM_HUMAN	0	0	0	29	0	0	0	37	0	17	0	0	29	23	0	29	54	52	1	2	2	2.99	2.25	sCP	0.69	2.12	MD	0.45	1.02	sCP		
Nuclear transport factor 2	P61970	NTF2_HUMAN	0	0	14	21	17	0	0	18	0	0	0	0	0	0	0	52	18	0	3	1	0	7.75	4.00	HC	n/a	n/a	HC	3.80	3.30	sCP		
Nucleobindin-1	Q02818	NUCB1_HUMAN	0	0	0	0	0	0	0	32	0	0	0	0	0	0	0	0	32	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.87	3.52	sCP		
Olfactomedin-4	Q6UX06	OLFM4_HUMAN	0	0	45	20	44	31	0	30	44	0	0	73	80	44	0	109	105	197	3	3	3	0.21	1.06	sCP	0.04	1.11	MD	0.13	1.07	MD		
Opioid-binding protein/cell adhesion molecule	Q14982	OPCM_HUMAN	0	0	0	0	0	46	0	0	0	0	0	0	0	0	0	0	46	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.91	3.48	sCP		
Osteoclast-associated immunoglobulin-like receptor	Q8IY55	OSCAR_HUMAN	0	24	22	15	13	0	9	28	0	12	32	19	20	0	0	74	49	71	4	3	3	0.34	2.03	HC	0.39	1.63	HC	0.45	1.17	MD		
Osteopontin	P10451	OSTP_HUMAN	124	164	118	174	210	165	66	358	156	67	79	302	233	156	125	790	812	895	5	5	5	0.76	1.21	HC	1.65	1.00	HC	0.89	1.20	MD		
Oxidized low-density lipoprotein receptor 1	P78380	OLR1_HUMAN	0	0	9	0	9	0	0	5	0	0	0	0	0	0	0	18	5	0	2	1	0	0.83	2.40	HC	n/a	n/a	HC	1.28	3.04	sCP		

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts															Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP					
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses								Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5	ΣHC	ΣsCP	ΣMD										#HC	#sCP	#MD
Pancreatic alpha-amylase	P04746	AMYP_HUMAN	399	358	438	392	448	201	237	265	81	84	706	317	133	374	162	203	868	454	5	5	5	3.8E+06	2.2	HC	25.50	1.0	HC	25.5	2.02	MD
Pantetheinase	O95497	VNN1_HUMAN	0	22	0	0	0	0	0	31	0	0	0	0	0	0	0	22	31	0	1	1	0	1.75	1.0	HC	n/a	n/a	HC	3.34	3.56	sCP
Pappalysin-2	Q9BXP8	PAPP2_HUMAN	0	48	19	0	0	0	38	47	113	77	0	42	0	0	0	67	275	42	2	4	1	8.95	6.7	HC	11.62	2.0	MD	157.22	11.8	sCP
Pepsin A	P00790	PEPA_HUMAN	0	72	36	0	92	132	53	107	64	52	0	67	186	90	98	200	408	441	3	5	4	688.91	6.0	sCP	47.73	2.9	MD	261.65	2.10	sCP
Peptidase inhibitor 16	Q6UXB8	PI16_HUMAN	0	69	25	23	0	38	64	0	37	64	0	0	0	0	0	117	203	0	3	4	0	2.70	2.9	HC	n/a	n/a	MD	n/a	n/a	sCP
Peptidoglycan recognition protein 1	O75594	PGRP1_HUMAN	51	77	72	59	84	46	87	41	35	35	80	32	23	61	68	343	244	264	5	5	5	2.93	1.4	HC	0.77	1.3	HC	0.56	1.03	sCP
Peptidyl-prolyl cis-trans isomerase A	P62937	PPIA_HUMAN	0	0	9	9	10	0	0	22	0	0	0	0	18	15	0	28	22	33	3	1	2	3.05	3.3	HC	0.81	1.5	HC	0.38	2.03	MD
Peptidyl-prolyl cis-trans isomerase B	P23284	PPIB_HUMAN	0	0	0	0	0	0	0	12	0	0	0	0	0	0	0	0	12	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	4.03	3.21	sCP
Peroxiredoxin-1	Q06830	PRDX1_HUMAN	0	0	0	6	0	0	0	29	0	0	0	0	19	0	0	6	29	19	1	1	1	0.87	1.1	sCP	0.49	1.1	MD	1.23	1.06	sCP
Peroxiredoxin-2	P32119	PRDX2_HUMAN	0	0	0	0	0	0	0	0	31	0	0	0	0	0	0	0	31	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	6.57	3.81	sCP
Peroxiredoxin-6	P30041	PRDX6_HUMAN	0	0	7	0	0	0	0	8	0	0	0	0	0	0	0	7	8	0	1	1	0	1.01	1.0	HC	n/a	n/a	HC	1.65	3.18	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP													
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression											
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5				#HC	#sCP	#MD																				
Phenazine biosynthesis-like domain-containing protein	P30039	PBLD_HUMAN	0	0	0	0	0	0	0	19	0	0	0	0	0	0	0	19	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.65	3.44	sCP												
Phosphatidylcholine-sterol acyltransferase	P04180	LCAT_HUMAN	0	29	12	24	32	0	7	12	0	0	0	0	0	0	97	19	0	4	2	0	39.94	5.10	HC	n/a	n/a	HC	6.32	7.02	sCP												
Phosphatidylethanolamine-binding protein 1	P30086	PEBP1_HUMAN	60	21	26	34	26	27	14	55	21	0	0	0	25	23	0	167	117	48	5	4	2	2.15	1.99	HC	2.6E+04	8.27	HC	4.64	4.65	sCP											
Phosphatidylethanolamine-binding protein 4	Q96S96	PEBP4_HUMAN	0	0	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	10	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	n/a	MD									
Phosphoenolpyruvate carboxykinase, cytosolic	P35558	PCKGC_HUMAN	0	0	0	0	0	0	0	19	0	0	0	0	0	0	0	19	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.65	3.44	sCP												
Phosphoglycerate kinase 1	P00558	PGK1_HUMAN	0	0	0	0	0	0	0	67	0	0	0	0	27	47	0	0	67	74	0	1	2	n/a	n/a	sCP	n/a	n/a	MD	0.18	1.94	MD											
Phosphoinositide-3-kinase-interacting protein 1	Q96FE7	P3IP1_HUMAN	0	0	0	17	16	50	20	33	0	0	43	37	33	0	0	33	103	113	2	3	3	0.99	2.50	sCP	3.09	2.50	MD	16.18	1.01	sCP											
Phospholipase D3	Q8IV08	PLD3_HUMAN	0	0	0	0	0	0	0	0	0	15	0	0	0	0	0	15	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.72	3.22	sCP												
Phosphoserine aminotransferase	Q9Y617	SERC_HUMAN	0	0	0	0	0	0	0	26	0	0	0	0	0	0	0	26	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	3.45	3.33	sCP												
Pigment epithelium-derived factor	P36955	PEDF_HUMAN	0	0	0	16	0	0	0	9	0	0	0	0	0	0	16	9	0	1	1	0	1.21	1.10	HC	n/a	n/a	HC	2.65	3.07	sCP												
Plasma glutamate carboxypeptidase	Q9Y646	PGCP_HUMAN	0	0	0	68	33	42	22	50	37	29	0	42	55	0	0	101	180	97	2	5	2	3.2E+04	7.92	sCP	7.23	1.13	MD	1.8E+04	10.94	sCP											

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP				ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Plasma protease C1 inhibitor	P05155	IC1_HUMAN	236	103	77	129	108	0	40	159	32	0	112	130	116	85	51	653	231	494	5	3	5	2.1E+07	9.27	HC	1.23	1.33	HC	1.1E+07	5.44	MD
Plasma serine protease inhibitor	P05154	IPSP_HUMAN	199	57	238	100	143	107	42	136	66	19	100	61	81	166	84	737	370	492	5	5	5	5.97	2.03	HC	2.67	1.44	HC	0.28	1.46	MD
Plasminogen	P00747	PLMN_HUMAN	0	0	0	58	0	0	0	28	0	0	0	0	0	115	58	28	115	1	1	1	1.10	1.17	sCP	0.17	1.17	HC	3.14	1.36	MD	
Platelet glycoprotein VI	Q9HCN6	GPVI_HUMAN	0	13	0	0	18	0	0	16	0	0	29	0	21	0	0	31	16	50	2	1	2	4.44	2.93	sCP	1.32	1.18	HC	1.40	2.21	MD
Podocalyxin	O00592	PODXL_HUMAN	0	0	27	0	0	0	0	0	0	0	17	21	0	0	27	0	38	1	0	2	n/a	n/a	sCP	0.43	2.07	HC	n/a	n/a	MD	
Poliovirus receptor	P15151	PVR_HUMAN	0	22	11	13	25	0	13	36	0	17	37	15	23	0	19	71	66	94	4	3	4	0.43	1.84	sCP	1.13	1.19	HC	13.37	1.99	MD
Poliovirus receptor-related protein 2	Q92692	PVRL2_HUMAN	0	30	25	19	32	0	48	21	0	0	0	0	0	0	0	106	69	0	4	2	0	9.34	3.98	HC	n/a	n/a	HC	5.71	8.39	sCP
Poliovirus receptor-related protein 3	Q9NQS3	PVRL3_HUMAN	0	12	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Poliovirus receptor-related protein 4	Q96NY8	PVRL4_HUMAN	0	0	26	28	55	0	0	34	0	0	0	0	0	0	0	109	34	0	3	1	0	34.90	3.67	HC	n/a	n/a	HC	1.39	3.58	sCP
Polycomb protein SUZ12	Q15022	SUZ12_HUMAN	0	0	28	0	0	0	0	0	0	0	0	0	0	0	0	28	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Polymeric immunoglobulin receptor	P01833	PIGR_HUMAN	363	245	262	235	288	383	283	363	286	254	346	216	288	221	229	1393	1569	1300	5	5	5	0.82	1.14	HC	0.74	1.10	MD	7.17	1.26	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Potassium voltage-gated channel subfamily C member 3	Q14003	KCNC3_HUMAN	0	0	0	0	0	0	0	0	0	36	0	0	0	0	0	36	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.55	3.41	sCP	
Probable serine carboxypeptidase CPVL	Q9H3G5	CPVL_HUMAN	0	0	23	0	0	0	39	0	0	0	53	0	0	0	23	39	53	1	1	1	1.77	1.02	sCP	0.54	1.13	HC	2.49	1.17	sCP	
Pro-cathepsin H	P09668	CATH_HUMAN	0	0	0	17	17	48	28	29	0	49	0	0	26	0	0	34	154	26	2	4	1	9.82	5.54	HC	0.62	2.00	MD	76.79	15.71	sCP
Procollagen C-endopeptidase enhancer 1	Q15113	PCOC1_HUMAN	0	0	0	0	0	0	0	0	47	27	0	0	0	0	0	74	0	0	2	0	n/a	n/a	n/a	n/a	n/a	MD	n/a	n/a	sCP	
Pro-epidermal growth factor	P01133	EGF_HUMAN	671	214	303	252	290	109	110	232	70	66	329	79	179	204	101	1730	587	892	5	5	5	4.0E+04	2.87	HC	18.37	1.98	HC	42.86	1.42	MD
Programmed cell death 1 ligand 2	Q9BQ51	PD1L2_HUMAN	0	0	7	6	0	0	0	13	0	0	0	0	12	0	0	13	13	12	2	1	1	1.09	1.75	HC	0.25	1.88	HC	0.47	1.06	sCP
Programmed cell death 6-interacting protein	Q8WUM4	PDC6L_HUMAN	0	0	0	0	0	0	47	45	0	0	74	76	0	0	0	92	150	0	2	2	n/a	n/a	sCP	n/a	n/a	MD	0.09	1.02	MD	
Prolactin-inducible protein	P12273	PIP_HUMAN	0	17	16	19	27	0	0	14	0	0	27	0	19	0	0	79	14	46	4	1	2	355.88	10.32	HC	1.71	3.81	HC	0.80	2.19	MD
Prominin-1	O43490	PROM1_HUMAN	0	0	0	37	44	0	0	0	0	0	0	82	60	0	0	81	0	142	2	0	2	n/a	n/a	sCP	3.12	1.13	HC	n/a	n/a	MD
Prostaglandin-H2 D-isomerase	P41222	PTGDS_HUMAN	163	299	475	215	243	826	876	280	1256	560	309	238	300	424	346	1395	3798	1617	5	5	5	2.2E+04	2.51	sCP	1.89	1.21	MD	4747.91	2.09	sCP
Prostasin	Q16651	PRSS8_HUMAN	33	16	10	20	20	0	11	17	13	8	32	0	18	15	14	99	49	79	5	4	4	5.80	2.13	HC	3.52	1.57	HC	0.70	1.33	MD

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts															Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP					
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses								Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5	ΣHC	ΣsCP	ΣMD												
			#HC	#sCP	#MD																											
Prostate stem cell antigen	O43653	PSCA_HUMAN	0	0	0	0	15	0	11	0	12	0	0	0	20	26	0	15	23	46	1	2	2	0.76	2.12	sCP	0.92	2.35	MD	0.16	1.08	MD
Prostate-specific antigen	P07288	KLK3_HUMAN	0	0	120	61	64	0	0	82	186	27	34	0	46	0	13	245	295	93	3	3	3	0.03	1.06	HC	0.18	1.20	MD	0.15	1.25	sCP
Prostatic acid phosphatase	P15309	PPAP_HUMAN	109	0	157	61	73	0	0	107	117	0	57	0	96	0	0	400	224	153	4	2	2	26.91	6.09	HC	9.00	6.49	HC	120.58	1.18	sCP
Protein AMBP	P02760	AMBP_HUMAN	305	402	436	305	571	1589	1834	509	1424	1244	520	547	702	685	640	2019	660	3094	5	5	5	8.6E+06	2.96	sCP	286.93	1.57	MD	3.1E+04	1.86	sCP
Protein CutA	O60888	CUTA_HUMAN	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a
Protein delta homolog 1	P80370	DLK1_HUMAN	0	0	0	0	0	0	0	15	0	0	0	0	0	0	0	15	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.96	3.47	sCP
Protein FAM3C	Q92520	FAM3C_HUMAN	0	0	0	21	11	0	12	28	0	0	0	0	0	0	0	32	40	0	2	2	0	0.51	1.03	HC	n/a	n/a	HC	2.95	7.78	sCP
Protein HEG homolog 1	Q9ULI3	HEG1_HUMAN	0	0	0	0	0	0	0	39	0	0	0	0	0	0	0	39	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	0.71	3.61	sCP
Protein S100-A7	P31151	S10A7_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	29	0	0	0	29	0	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Protein S100-A8	P05109	S10A8_HUMAN	0	0	19	9	32	8	60	0	21	37	32	11	22	41	0	60	126	106	3	4	4	2.71	2.04	sCP	1.02	2.35	MD	0.36	1.04	sCP
Protein S100-A9	P06702	S10A9_HUMAN	0	0	27	8	32	0	64	12	23	42	33	24	32	46	16	67	141	151	3	4	5	3.00	2.46	sCP	1598.55	3.61	MD	1.40	1.60	MD

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts															Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP										
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression					
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																				
Protein-glutamine gamma-glutamyltransferase 4	P49221	TGM4_HUMAN	0	0	0	0	72	0	0	0	0	0	0	0	0	0	0	72	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	n/a	n/a	n/a		
Prothrombin	P00734	THRB_HUMAN	94	73	54	103	82	123	66	103	116	75	60	79	34	87	72	406	483	332	5	5	5	1.44	1.20	HC	2.28	1.28	MD	3.32	1.56	sCP					
Protocadherin gamma-C3	Q9UN70	PCDCK_HUMAN	0	0	48	0	53	0	0	26	0	0	0	0	39	0	0	101	26	39	2	1	1	0.56	2.42	HC	4.73	2.13	HC	0.94	1.21	MD					
Protocadherin-1	Q08174	PCDH1_HUMAN	0	73	39	32	43	0	0	0	0	0	0	0	61	0	0	187	0	61	4	0	1	n/a	n/a	HC	9.75	12.35	HC	n/a	n/a	MD					
Protocadherin-16	Q96JQ0	PCD16_HUMAN	0	0	84	0	0	0	0	0	0	0	0	0	0	0	0	84	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a					
Putative annexin A2-like protein	A6NMY6	AXA2L_HUMAN	0	0	0	0	0	0	0	0	0	0	0	28	0	55	0	0	0	83	0	0	2	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	n/a	MD			
Putative elongation factor 1-alpha-like 3	Q5VTE0	EF1A3_HUMAN	0	0	0	0	0	0	0	42	0	0	0	26	53	0	0	0	42	79	0	1	2	n/a	n/a	sCP	n/a	n/a	MD	3.08	2.16	MD					
Putative gamma-glutamyltranspeptidase 3	A6NGU5	GGT3_HUMAN	0	0	0	31	0	0	0	0	30	0	0	0	0	0	0	31	30	0	1	1	0	2.84	1.09	HC	n/a	n/a	MD	3.02	3.39	sCP					
Putative short-chain dehydrogenase/reductase family 42E	A6NKP2	D42E2_HUMAN	0	0	13	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a					
Putative trypsin-6	Q8NHM4	TRY6_HUMAN	0	0	0	0	0	0	0	0	20	0	0	0	0	0	0	20	0	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.19	3.36	sCP					
Pyruvate kinase isozymes M1/M2	P14618	KPYM_HUMAN	0	0	26	0	0	0	37	50	0	0	0	29	27	88	0	26	87	144	1	2	3	0.79	2.27	sCP	11.52	4.92	MD	0.17	2.14	MD					

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression	
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																
			#HC	#sCP	#MD																												
Rab GDP dissociation inhibitor alpha	P31150	GDIA_HUMAN	0	0	0	0	0	0	0	19	0	0	0	0	0	0	0	19	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.65	3.44	sCP		
Rab GDP dissociation inhibitor beta	P50395	GDIB_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	0	0	16	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD
Ras-related C3 botulinum toxin substrate 1	P63000	RAC1_HUMAN	0	0	0	0	14	0	0	9	0	0	0	15	20	21	0	14	9	56	1	1	3	0.16	1.01	sCP	11.36	4.44	HC	3.92	5.01	MD	
Ras-related protein Rab-11A	P62491	RB11A_HUMAN	0	0	0	0	0	0	0	0	0	0	0	14	0	0	0	0	14	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD		
Ras-related protein Rab-30	Q15771	RAB30_HUMAN	0	0	22	0	0	0	0	0	0	0	0	0	0	0	0	22	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Receptor-type tyrosine-protein phosphatase eta	Q12913	PTPRJ_HUMAN	0	0	0	0	0	0	0	0	0	0	0	22	0	0	0	0	22	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD		
Receptor-type tyrosine-protein phosphatase gamma	P23470	PTPRG_HUMAN	0	0	53	0	0	0	0	0	0	0	0	0	0	0	53	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a		
Receptor-type tyrosine-protein phosphatase S	Q13332	PTPRS_HUMAN	0	0	65	59	80	0	0	61	125	0	0	82	88	0	0	204	186	170	3	2	2	0.29	2.06	HC	0.49	2.25	HC	0.28	1.00	sCP	
Reticulon-4 receptor-like 2	Q86UN3	R4RL2_HUMAN	0	0	14	21	0	0	0	0	0	0	0	11	0	0	35	0	11	2	0	1	n/a	n/a	HC	2.04	2.45	HC	n/a	n/a	MD		
Retinal dehydrogenase 1	P00352	AL1A1_HUMAN	0	0	0	0	0	0	0	34	0	0	0	0	0	0	0	34	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.39	3.58	sCP		
Retinoic acid-induced protein 3	Q8NFJ5	RAI3_HUMAN	0	0	0	0	0	0	0	10	0	0	0	10	15	0	0	0	10	25	0	1	2	n/a	n/a	sCP	n/a	n/a	MD	0.38	2.31	MD	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP		HC vs. MD		MD vs. CP									
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					Σ HC	Σ sCP	Σ MD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression					
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																				
Retinoid-inducible serine carboxypeptidase	Q9HB40	RISC_HUMAN	0	0	0	23	0	56	0	23	24	23	0	37	30	0	0	23	126	67	1	4	2	10.71	11.50	sCP	1.09	2.13	MD	1.87	5.14	sCP					
Retinol-binding protein 4	P02753	RET4_HUMAN	82	81	30	64	80	161	94	65	83	80	82	44	69	64	56	337	483	315	5	5	5	5.29	1.46	HC	1.46	1.09	MD	58.11	1.59	sCP					
Retinol-binding protein 5	P82980	RET5_HUMAN	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	7	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.35	3.23	sCP						
Ribonuclease pancreatic	P07998	RNAS1_HUMAN	0	22	42	17	24	0	67	24	86	39	47	40	35	34	17	105	216	173	4	4	5	21.62	1.44	sCP	10.33	2.01	MD	3.68	1.32	MD					
Ribonuclease T2	O00584	RNT2_HUMAN	0	0	0	0	0	27	25	0	13	43	0	19	39	0	0	0	108	58	0	4	2	n/a	n/a	sCP	n/a	n/a	MD	0.76	5.28	sCP					
Ribonuclease UK114	P52758	UK114_HUMAN	0	0	0	0	0	0	0	28	0	0	0	0	0	0	0	28	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	0.45	3.25	sCP						
Roundabout homolog 4	Q8WZ75	ROBO4_HUMAN	281	113	96	120	130	0	55	101	0	66	184	0	53	104	82	740	222	423	5	3	4	7.4E+05	10.67	HC	160.77	3.57	HC	38.57	3.00	MD					
Secreted and transmembrane protein 1	Q8WVN6	SCTM1_HUMAN	57	43	47	39	56	69	134	50	26	32	57	18	18	26	14	242	311	133	5	5	5	0.52	1.04	HC	2.81	1.85	MD	5.05	2.10	sCP					
Secreted Ly-6/uPAR-related protein 1	P55000	SLUR1_HUMAN	0	0	10	0	0	0	0	0	12	5	0	0	0	0	0	10	17	0	1	2	0	0.61	1.98	HC	n/a	n/a	MD	4.00	7.13	sCP					
Secreted Ly-6/uPAR-related protein 2	Q86SR0	SLUR2_HUMAN	0	7	11	10	17	0	10	9	8	15	0	0	0	0	0	45	42	0	4	4	0	1.61	1.05	HC	n/a	n/a	HC	n/a	n/a	sCP					
Selenium-binding protein 1	Q13228	SBP1_HUMAN	0	0	22	16	20	0	0	30	0	0	32	0	26	0	0	58	30	58	3	1	2	1.33	3.98	HC	0.24	1.92	HC	0.62	2.35	MD					

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5				#HC	#sCP	#MD									
Serine hydroxymethyltransferase, cytosolic	P34896	GLYC_HUMAN	0	0	26	0	0	0	0	42	0	0	0	0	0	0	26	42	0	1	1	0	0.64	1.18	HC	n/a	n/a	MD	0.49	3.33	sCP	
Serine/threonine-protein kinase MARK1	Q9P0L2	MARK1_HUMAN	0	0	0	0	0	0	0	35	0	0	0	0	0	0	35	0	0	1	0	0	n/a	n/a	n/a	n/a	n/a	MD	0.51	3.68	sCP	
Serine/threonine-protein kinase Nek11	Q8NG66	NEK11_HUMAN	0	0	0	23	0	0	0	0	0	0	0	0	0	23	0	0	1	0	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Serotransferrin	P02787	TRFE_HUMAN	547	481	202	487	216	215	212	299	266	457	156	133	746	349	795	1933	1449	2179	5	5	5	2.22	1.23	HC	0.66	1.18	HC	0.56	1.05	MD
Serpin B12	Q96P63	SPB12_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	43	0	0	43	0	0	1	0	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Serpin B3	P29508	SPB3_HUMAN	0	0	0	0	0	0	54	0	0	0	0	0	78	0	0	54	78	0	1	1	n/a	n/a	sCP	n/a	n/a	MD	8.07	1.07	sCP	
Serum albumin	P02768	ALBU_HUMAN	3110	4835	1521	4913	2278	4161	987	2866	3222	2531	2940	2620	5085	2815	7248	16657	13767	20708	5	5	5	2.6E+00	1.20	sCP	51.70	1.27	HC	7613.70	1.48	MD
Serum amyloid P-component	P02743	SAMP_HUMAN	0	0	0	0	0	0	0	20	0	0	0	0	0	0	0	20	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.19	3.36	sCP	
SH3 domain-binding glutamic acid-rich-like protein 3	Q9H299	SH3L3_HUMAN	0	12	13	0	0	29	21	0	37	42	10	0	0	0	0	25	129	10	2	4	1	91.15	5.69	HC	4.18	1.79	MD	87.76	15.04	sCP
Sialate O-acetyltransferase	Q9HAT2	SIAE_HUMAN	0	0	0	50	18	0	23	27	25	26	33	0	36	0	21	68	101	90	2	4	3	0.90	4.18	sCP	9.42	1.94	MD	0.53	1.99	sCP
Sialic acid-binding Ig-like lectin 8	Q9NYZ4	SIGL8_HUMAN	0	0	0	21	0	0	0	0	0	0	0	0	0	0	21	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																			Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	Bayes Factor				Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression		
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5	ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression		
Signal peptide, CUB and EGF-like domain-containing protein 2	Q9NQ36	SCUB2_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	52	0	0	0	0	0	52	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	MD
Signal-regulatory protein beta-1	O00241	SIRB1_HUMAN	0	41	28	37	36	71	0	0	30	35	0	26	33	0	0	142	136	59	4	3	2	0.36	2.21	HC	15.58	5.02	HC	0.61	2.55	sCP		
Signal-regulatory protein beta-1 isoform 3	Q5TFQ8	SIRBL_HUMAN	0	44	0	0	0	0	0	0	0	0	0	0	0	0	44	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a			
SLAM family member 5	Q9UIB8	SLAF5_HUMAN	0	27	18	11	0	0	0	19	0	0	0	0	0	0	56	19	0	3	1	0	1.41	4.25	HC	n/a	n/a	HC	2.65	3.44	sCP			
Small proline-rich protein 3	Q9UBC9	SPRR3_HUMAN	0	0	0	0	0	0	0	0	0	0	0	90	0	0	0	0	90	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD			
Sodium-dependent neutral amino acid transporter B	Q695T7	S6A19_HUMAN	0	0	0	15	0	0	0	0	0	0	0	0	0	15	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a				
Solute carrier family 12 member 1	Q13621	S12A1_HUMAN	0	0	0	0	0	0	0	0	0	0	85	90	128	0	0	0	303	0	0	3	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD			
Solute carrier family 2, facilitated glucose transporter member 5	P22732	GTR5_HUMAN	0	0	0	0	16	0	0	0	0	0	0	0	0	16	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a				
Sorbitol dehydrogenase	Q00796	DHSO_HUMAN	0	0	0	0	0	0	22	0	0	0	0	0	0	0	22	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.40	3.37	sCP				
SPARC-like protein 1	Q14515	SPRL1_HUMAN	0	0	0	0	0	0	29	0	0	0	0	0	0	29	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	4.10	3.61	sCP					
Steroid hormone receptor ERR2	O95718	ERR2_HUMAN	0	0	14	0	0	0	0	0	0	0	0	23	0	0	14	0	23	1	0	1	n/a	n/a	HC	1.46	1.09	HC	n/a	n/a	MD			

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression			
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Sulfhydryl oxidase 1	O00391	QSOX1_HUMAN	0	0	0	0	77	86	0	51	0	0	65	57	0	73	56	77	137	251	1	2	4	6.29	2.49	sCP	103.57	12.15	MD	1.04	6.26	MD
Superoxide dismutase	P00441	SODC_HUMAN	0	0	0	21	0	0	22	0	19	0	0	19	0	0	21	41	19	1	2	1	0.51	2.25	HC	0.19	1.04	MD	0.86	2.57	sCP	
Sushi domain-containing protein 2	Q9UGT4	SUSD2_HUMAN	0	0	0	0	0	0	23	0	0	34	0	0	0	0	23	34	0	1	1	1	n/a	n/a	sCP	n/a	n/a	MD	0.45	1.10	MD	
Syndecan-1	P18827	SDC1_HUMAN	0	0	0	0	0	0	0	0	0	12	0	0	0	0	12	0	0	1	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD	
Syntenin-1	O00560	SDCB1_HUMAN	33	0	13	27	38	0	25	51	36	0	37	59	44	38	0	111	112	178	4	3	4	3.24	1.80	sCP	0.27	1.34	HC	2.81	2.37	MD
T-cell antigen CD7	P09564	CD7_HUMAN	0	0	0	0	15	0	0	0	0	0	0	0	0	0	15	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Tenascin-X	P22105	TENX_HUMAN	0	0	0	108	130	0	0	0	0	0	0	0	0	0	238	0	0	2	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	
Tetranectin	P05452	TETN_HUMAN	39	30	17	29	43	0	0	56	27	0	32	0	0	0	158	83	32	5	2	1	940.38	6.83	HC	1.5E+06	18.12	HC	0.14	2.35	sCP	
Tetraspanin-1	O60635	TSN1_HUMAN	0	0	0	0	7	0	0	11	0	0	16	35	8	18	0	7	11	77	1	1	4	0.40	1.05	sCP	98.79	8.92	HC	55.37	10.04	MD
Thrombospondin-1	P07204	TRBM_HUMAN	0	0	22	21	0	0	20	0	0	0	0	0	0	0	43	20	0	2	1	0	1.51	2.24	HC	n/a	n/a	HC	2.70	3.56	sCP	
Thrombospondin-1	P07996	TSP1_HUMAN	0	0	61	0	0	0	0	0	0	0	0	0	0	0	61	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																					Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	#HC	#sCP	#MD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression				
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																			
Thy-1 membrane glycoprotein	P04216	THY1_HUMAN	0	14	0	12	0	23	13	4	10	0	13	5	11	14	20	26	50	63	2	4	5	4.16	2.94	sCP	42.57	4.08	MD	1.40	1.43	MD				
Thyroxine-binding globulin	P05543	THBG_HUMAN	0	90	33	46	38	0	52	28	0	25	0	29	54	72	38	207	105	193	4	3	4	3.30	2.66	HC	1.67	1.07	HC	0.56	2.67	MD				
Transmembrane BAX inhibitor motif-containing protein 1	Q969X1	TMBI1_HUMAN	0	0	0	0	0	0	0	0	7	0	0	0	8	0	0	0	7	8	0	1	1	n/a	n/a	sCP	n/a	n/a	MD	0.56	1.16	sCP				
Transmembrane protease serine 2	O15393	TMPS2_HUMAN	0	0	0	0	0	0	0	0	23	0	0	0	0	0	0	0	23	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.82	3.52	sCP				
Transmembrane protein C19orf77	O75264	CS077_HUMAN	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	3	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.36	2.88	sCP				
Transthyretin	P02766	TTHY_HUMAN	100	38	22	61	31	0	0	34	8	0	46	0	13	11	80	252	42	150	5	2	4	2.4E+04	12.90	HC	2.47	2.78	HC	5.86	5.12	MD				
Triosephosphate isomerase	P60174	TPIS_HUMAN	0	0	32	18	20	27	17	65	25	13	55	0	18	38	0	70	147	111	3	5	3	21.03	3.72	sCP	2.77	1.12	MD	40.70	3.42	sCP				
Tripeptidyl-peptidase 1	O14773	TPP1_HUMAN	57	0	16	30	34	23	45	46	51	43	17	16	29	27	16	137	208	105	4	5	5	4.67	2.35	HC	1.34	1.01	MD	149.64	2.03	sCP				
Trypsin-1	P07477	TRY1_HUMAN	0	0	0	0	57	0	0	0	0	0	145	0	0	88	0	57	0	233	1	0	2	n/a	n/a	sCP	5.78	2.30	HC	n/a	n/a	MD				
Trypsin-2	P07478	TRY2_HUMAN	73	0	0	0	0	0	37	0	0	0	0	0	0	0	0	73	37	0	1	1	0	0.95	1.01	HC	n/a	n/a	MD	1.13	3.38	sCP				
Trypsin-3	P35030	TRY3_HUMAN	115	0	0	0	0	0	0	0	0	0	138	0	40	0	38	115	0	216	1	0	3	n/a	n/a	sCP	2.71	4.11	HC	n/a	n/a	MD				

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP		
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5															
			#HC	#sCP	#MD																											
Tubulin alpha-1B chain	P68363	TBA1B_HUMAN	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	13	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	0.58	3.32	sCP	
Tubulin alpha-1C chain	Q9BQE3	TBA1C_HUMAN	0	0	0	16	0	0	0	0	0	0	0	15	0	0	16	0	15	1	0	1	n/a	n/a	HC	0.69	1.00	HC	n/a	n/a	MD	
Tubulin alpha-4A chain	P68366	TBA4A_HUMAN	0	0	0	0	0	21	0	0	0	0	0	0	0	0	21	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.44	3.16	sCP		
Tubulin beta-2A chain	Q13885	TBB2A_HUMAN	0	0	0	0	0	0	0	0	0	0	33	0	0	0	0	33	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD		
Tumor necrosis factor receptor superfamily member 19L	Q969Z4	TR19L_HUMAN	0	0	0	0	15	0	0	0	0	0	0	0	0	15	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a		
Tumor necrosis factor receptor superfamily member 1B	P20333	TNR1B_HUMAN	0	0	0	0	0	0	20	0	0	0	0	0	0	0	20	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	2.19	3.36	sCP		
Twisted gastrulation protein homolog 1	Q9GZX9	TWSG1_HUMAN	0	22	15	10	9	0	0	0	0	0	0	16	0	0	56	0	16	4	0	1	n/a	n/a	HC	102.23	6.90	HC	n/a	n/a	MD	
Tyrosine-protein kinase receptor UFO	P30530	UFO_HUMAN	154	86	63	63	91	105	54	67	0	43	142	63	77	55	39	457	269	376	5	4	5	949.85	2.65	HC	1.43	1.28	HC	0.65	2.19	MD
Tyrosine-protein kinase transmembrane receptor ROR1	Q01973	ROR1_HUMAN	0	0	0	0	0	0	26	0	0	0	0	0	0	0	26	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	3.45	3.33	sCP		
Tyrosine-protein phosphatase non-receptor type substrate 1	P78324	SHPS1_HUMAN	0	0	49	43	44	56	40	27	0	32	44	42	35	0	37	136	155	158	3	4	4	0.07	2.38	sCP	14.51	2.29	MD	0.97	1.02	MD
Ubiquitin-40S ribosomal protein S27a	P62979	RS27A_HUMAN	57	0	40	23	36	0	80	0	93	66	0	33	30	0	0	156	239	63	4	3	2	0.31	1.92	HC	9.34	5.48	HC	3.87	2.52	sCP

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP				
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression					
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																	
			#HC	#sCP	#MD																													
Ubiquitin-60S ribosomal protein L40	P62987	RL40_HUMAN	0	28	0	0	0	54	0	28	0	0	27	0	0	35	19	28	82	81	1	2	3	5.73	1.88	sCP	1.94	4.62	MD	9.96	1.69	MD		
Uncharacterized protein C6orf72	Q9NU53	CF072_HUMAN	0	0	0	0	0	0	0	0	0	0	0	22	0	0	0	0	22	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	MD
Uncharacterized protein C7orf51	Q6ZVC0	CG051_HUMAN	0	0	0	45	0	0	0	0	0	0	0	0	0	0	0	45	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a		
UPF0451 protein C17orf61	Q8N2U0	CQ061_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	9	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD			
UPF0467 protein C5orf32	Q9HIC7	CE032_HUMAN	0	0	0	0	0	0	0	0	0	0	4	4	0	0	0	0	8	0	0	2	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD			
Urokinase-type plasminogen activator	P00749	UROK_HUMAN	0	0	61	26	51	0	0	27	0	0	0	0	41	0	138	27	41	3	1	1	12.26	4.56	HC	21.85	4.71	HC	0.21	1.00	n/a			
Uromodulin	P07911	UROM_HUMAN	234	543	379	783	1074	780	602	646	264	210	1463	1001	991	1424	1064	8539	2502	5943	5	5	5	1.1E+06	2.55	HC	101.02	1.01	HC	8.4E+08	2.45	MD		
Vacuolar protein sorting-associated protein 4B	O75351	VPS4B_HUMAN	0	0	0	0	0	0	0	0	0	0	0	29	0	0	0	0	29	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	MD			
Vascular cell adhesion protein 1	P19320	VCAM1_HUMAN	0	41	45	0	40	130	71	0	93	120	0	25	62	0	73	126	414	160	3	4	3	0.95	3.80	HC	1.08	1.04	MD	0.02	3.97	sCP		
Vasorin	Q6EMK4	VASN_HUMAN	242	93	114	97	143	61	94	171	74	42	100	80	124	101	90	689	442	495	5	5	5	7.86	1.61	HC	12.86	1.38	HC	0.50	1.21	MD		
Vesicular integral-membrane protein VIP36	Q12907	LMAN2_HUMAN	139	184	198	144	182	69	186	96	23	86	136	77	47	133	110	847	460	503	5	5	5	1395.01	2.11	HC	98.88	1.77	HC	1.89	1.21	MD		

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																		Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP			
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP	ΣMD				Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression	
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																
			#HC	#sCP	#MD																												
Vitamin D-binding protein	P02774	VTDB_HUMAN	124	65	42	123	53	48	29	58	52	21	66	67	90	58	144	407	208	425	5	5	5	15.71	1.84	sCP	0.40	1.09	HC	12.82	1.90	MD	
Vitamin K-dependent protein Z	P22891	PROZ_HUMAN	45	65	95	97	43	0	13	45	0	0	0	0	0	49	25	345	58	74	5	2	2	8.8E+06	14.22	HC	3.4E+07	14.38	HC	1.22	1.09	MD	
Vitelline membrane outer layer protein 1 homolog	Q7Z5L0	VMO1_HUMAN	66	67	49	65	88	82	14	111	17	0	133	88	20	43	43	335	224	327	5	4	5	76.83	2.42	HC	1.16	1.18	HC	12.57	2.65	MD	
Vitronectin	P04004	VTNC_HUMAN	109	30	30	19	35	0	19	25	0	0	0	37	44	34	39	223	44	154	5	2	4	5639.47	10.76	HC	0.41	1.82	HC	13.26	6.14	MD	
V-type proton ATPase catalytic subunit A	P38606	VATA_HUMAN	0	0	0	0	0	0	0	0	0	0	0	0	0	133	0	0	0	133	0	0	1	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	MD
V-type proton ATPase subunit B, brain isoform	P21281	VATB2_HUMAN	0	0	29	23	0	0	0	32	0	0	0	0	30	0	0	52	32	30	2	1	1	1.56	1.79	HC	0.92	2.02	HC	0.07	1.04	sCP	
V-type proton ATPase subunit B, kidney isoform	P15313	VATB1_HUMAN	0	0	0	0	0	0	0	0	0	0	42	0	108	0	0	0	0	150	0	0	2	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	MD
WAP four-disulfide core domain protein 2	Q14508	WFDC2_HUMAN	0	0	0	0	0	0	0	0	0	0	6	4	0	0	0	0	0	10	0	0	2	n/a	n/a	sCP	n/a	n/a	n/a	n/a	n/a	n/a	MD
WNT1-inducible-signaling pathway protein 2	O76076	WISP2_HUMAN	0	0	0	0	0	0	0	0	11	0	0	0	0	0	0	0	11	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.68	3.23	sCP	
Xaa-Pro dipeptidase	P12955	PEPD_HUMAN	0	0	0	0	0	0	0	37	0	0	0	0	0	0	0	0	37	0	0	1	0	n/a	n/a	n/a	n/a	n/a	MD	1.94	3.58	sCP	
Zinc finger and BTB domain-containing protein 4	Q9P1Z0	ZBTB4_HUMAN	0	0	42	0	0	0	0	0	0	0	0	0	0	76	0	42	0	76	1	0	1	n/a	n/a	HC	0.21	1.03	HC	n/a	n/a	MD	

Supplemental Table 1. Contd.....

Protein Names	UniProt Entry	UniProt ID	Spectral Counts																	Count of Samples in Which Protein was Identified			HC vs. sCP			HC vs. MD			MD vs. CP				
			Healthy Controls					Severe Chronic Pancreatitis					Mixed Diagnoses					ΣHC	ΣsCP				ΣMD	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher expression	Bayes Factor	Fold Change	Higher Expression	
			HC1	HC2	HC3	HC4	HC5	sCP1	sCP2	sCP3	sCP4	sCP5	MD1	MD2	MD3	MD4	MD5																
			#HC	#sCP	#MD																												
Zinc finger protein 658	Q5TYW1	ZN658_HUMAN	0	0	26	0	0	0	0	0	0	0	0	0	0	0	26	0	0	1	0	0	n/a	n/a	HC	n/a	n/a	HC	n/a	n/a	n/a		
Zinc-alpha-2-glycoprotein	P25311	ZA2G_HUMAN	73	296	146	179	178	529	456	128	442	330	145	118	184	218	442	872	1885	1107	5	5	5	5	443.27	2.09	sCP	0.65	1.23	MD	5.51	1.74	sCP
Zymogen granule protein 16 homolog B	Q96DA0	ZG16B_HUMAN	0	19	53	33	43	63	22	43	41	12	39	0	30	0	23	148	181	92	4	5	3	3.70	1.70	HC	0.45	2.29	MD	4.67	3.83	sCP	

Supplemental Table 2. Proteins (n=127) Exclusive to sCP Cohort (Not Appearing in HC)

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Count				
				sCP1	sCP2	sCP3	sCP4	sCP5
14-3-3 protein epsilon	P62258	23	1	0	0	23	0	0
3-hydroxybutyrate dehydrogenase type 2	Q9BUT1	16	1	0	0	16	0	0
3-mercaptopyruvate sulfurtransferase	P25325	12	1	0	12	0	0	0
Adenosylhomocysteinase	P23526	24	1	0	0	24	0	0
ADP-ribosylation factor 1	P84077	8	1	0	0	8	0	0
Aflatoxin B1 aldehyde reductase member 2	O43488	15	1	0	0	15	0	0
Aldo-keto reductase family 1 member C1	Q04828	26	1	0	0	26	0	0
Alpha-actinin-4	O43707	43	1	0	0	43	0	0
Angiotensin-converting enzyme	P12821	32	1	0	0	32	0	0
Anthrax toxin receptor 1	Q9H6X2	30	1	0	0	0	0	30
Argininosuccinate synthase	P00966	59	1	0	0	59	0	0
Aromatic-L-amino-acid decarboxylase	P20711	29	1	0	0	29	0	0
Aspartate aminotransferase, cytoplasmic	P17174	38	1	0	0	38	0	0
ATP-dependent RNA helicase DDX25	Q9UHL0	30	1	0	0	0	0	30
Basigin	P35613	27	2	0	0	0	12	15
Beta-hexosaminidase subunit alpha	P06865	77	2	0	0	37	0	40
Cadherin-related family member 2	Q9BYE9	67	1	67	0	0	0	0
cAMP-dependent protein kinase type II-beta regulatory subunit	P31323	16	1	0	0	0	0	16
Carbonic anhydrase 1	P00915	86	3	0	30	0	11	45
Carbonyl reductase	P16152	20	1	0	0	20	0	0
Carcinoembryonic antigen-related cell adhesion molecule 8	P31997	25	1	25	0	0	0	0
Caspase-14	P31944	12	1	0	12	0	0	0
CDP-diacylglycerol--inositol 3-phosphatidyltransferase	O14735	7	1	0	7	0	0	0
Chloride intracellular channel protein 4	Q9Y696	27	2	0	0	10	17	0

Supplemental Table 2. Contd....

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Count				
				sCP1	sCP2	sCP3	sCP4	sCP5
Chromogranin-A	P10645	58	2	0	25	0	33	0
CMRF35-like molecule 2	Q496F6	2	1	0	0	2	0	0
Complement component C7	P10643	52	1	0	0	0	52	0
Cytoplasmic aconitate hydratase	P21399	39	1	0	0	39	0	0
Cytosolic non-specific dipeptidase	Q96KP4	84	1	0	0	84	0	0
D-3-phosphoglycerate dehydrogenase	O43175	31	1	0	0	31	0	0
Dihydropteridine reductase	P09417	11	1	0	0	11	0	0
Dynein heavy chain 5, axonemal	Q8TE73	200	1	0	0	0	0	200
Ephrin type-A receptor 7	Q15375	25	1	0	25	0	0	0
Ephrin type-B receptor 6	O15197	16	1	0	0	16	0	0
Ester hydrolase C11orf54	Q9H0W9	33	1	0	0	33	0	0
Filaggrin-2	Q5D862	62	1	0	62	0	0	0
Formimidoyltransferase-cyclodeaminase	O95954	34	1	0	0	34	0	0
Gamma-glutamylaminecyclotransferase	Q9BVM4	5	1	0	0	5	0	0
Glutathione S-transferase A2	P09210	47	1	0	0	47	0	0
Glutathione S-transferase Mu 3	P21266	12	1	0	0	12	0	0
Glycerol-3-phosphate dehydrogenase	P21695	30	1	0	0	30	0	0
Glycine amidinotransferase, mitochondrial	P50440	15	1	0	0	15	0	0
Group XV phospholipase A2	Q8NCC3	23	1	0	23	0	0	0
Growth/differentiation factor 15	Q99988	17	1	0	0	0	17	0
Guanine nucleotide-binding protein G	P62879	29	1	0	0	29	0	0
Guanylate cyclase activator 2B	Q16661	25	2	0	13	0	12	0
Guanylin	Q02747	11	1	0	0	0	11	0
Heat shock 70 kDa protein 1A/1B	P08107	51	1	0	0	51	0	0

Supplemental Table 2. Contd....

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Count				
				sCP1	sCP2	sCP3	sCP4	sCP5
Heat shock cognate 71 kDa protein	P11142	33	1	0	0	33	0	0
Heat shock-related 70 kDa protein 2	P54652	38	1	0	38	0	0	0
Histone H4	P62805	11	1	0	0	0	0	11
Ig heavy chain V-I region EU	P01742	34	2	0	17	17	0	0
Ig heavy chain V-I region Mot	P06326	30	1	0	0	0	0	30
Ig heavy chain V-I region V35	P23083	31	1	31	0	0	0	0
Ig heavy chain V-III region JON	P01780	25	1	0	0	25	0	0
Ig kappa chain V-I region AU	P01594	143	2	0	114	29	0	0
Ig kappa chain V-I region DEE	P01597	187	2	0	100	0	0	87
Ig kappa chain V-I region Lay	P01605	39	1	0	39	0	0	0
Ig kappa chain V-I region WEA	P01610	99	1	0	0	0	0	99
Ig kappa chain V-I region Wes	P01611	53	2	0	32	0	21	0
Ig kappa chain V-III region IARC/BL41	P06311	123	2	0	75	0	48	0
Ig kappa chain V-IV region Len	P01625	183	2	0	0	0	93	90
Ig kappa chain V-IV region STH	P83593	53	1	0	53	0	0	0
Ig lambda chain V-I region BL2	P06316	94	2	0	0	0	41	53
Ig lambda chain V-I region NEW	P01701	63	2	0	28	0	0	35
Ig lambda chain V-II region NEI	P01705	21	1	0	21	0	0	0
Ig lambda chain V-IV region Hil	P01717	18	1	0	0	0	0	18
Ig lambda chain V-VI region EB4	P06319	18	1	0	18	0	0	0
Ig lambda chain V-VI region SUT	P06317	42	1	0	0	0	0	42
Ig lambda-7 chain C region	A0M8Q6	1052	3	0	243	0	255	554
Isocitrate dehydrogenase	O75874	50	1	0	0	50	0	0
Kallikrein-11	Q9UBX7	17	1	0	0	0	17	0

Supplemental Table 2. Contd....

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Count				
				sCP1	sCP2	sCP3	sCP4	sCP5
Kallistatin	P29622	10	1	0	0	10	0	0
Kin of IRRE-like protein 1	Q96J84	21	1	0	0	21	0	0
Lambda-crystallin homolog	Q9Y2S2	21	1	0	0	21	0	0
Lipocalin-1	P31025	32	1	0	0	0	0	32
L-lactate dehydrogenase A chain	P00338	31	1	0	0	31	0	0
Lysosome-associated membrane glycoprotein 1	P11279	33	2	0	0	16	17	0
Lysosome-associated membrane glycoprotein 2	P13473	22	1	0	0	22	0	0
Malate dehydrogenase, cytoplasmic	P40925	36	1	0	0	36	0	0
Mesothelin	Q13421	17	1	0	17	0	0	0
Metalloproteinase inhibitor 1	P01033	29	2	0	0	9	20	0
Mimecan	P20774	19	1	0	19	0	0	0
Moesin	P26038	133	2	0	0	70	0	63
Multiple epidermal growth factor-like domains protein 8	Q7Z7M0	71	1	0	0	71	0	0
Myeloperoxidase	P05164	64	1	0	0	0	0	64
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	O94760	27	1	0	0	27	0	0
Neutrophil defensin 1	P59665	41	1	0	0	0	0	41
Neutrophil elastase	P08246	25	1	0	0	0	0	25
Neutrophil gelatinase-associated lipocalin	P80188	85	3	29	0	18	38	0
Nucleobindin-1	Q02818	32	1	0	0	32	0	0
Opioid-binding protein/cell adhesion molecule	Q14982	46	1	46	0	0	0	0
Peptidyl-prolyl cis-trans isomerase B	P23284	12	1	0	0	12	0	0
Peroxiredoxin-2	P32119	31	1	0	0	0	0	31
Phenazine biosynthesis-like domain-containing protein	P30039	19	1	0	0	19	0	0
Phosphoenolpyruvate carboxykinase, cytosolic	P35558	19	1	0	0	19	0	0

Supplemental Table 2. Contd....

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Count				
				sCP1	sCP2	sCP3	sCP4	sCP5
Phosphoglycerate kinase 1	P00558	67	1	0	0	67	0	0
Phospholipase D3	Q8IV08	15	1	0	0	0	0	15
Phosphoserine aminotransferase	Q9Y617	26	1	0	0	26	0	0
Potassium voltage-gated channel subfamily C member 3	Q14003	36	1	0	0	0	0	36
Procollagen C-endopeptidase enhancer 1	Q15113	74	2	0	0	0	47	27
Programmed cell death 6-interacting protein	Q8WUM4	92	2	0	0	47	45	0
Protein delta homolog 1	P80370	15	1	0	0	15	0	0
Protein HEG homolog 1	Q9ULI3	39	1	0	0	39	0	0
Putative elongation factor 1-alpha-like 3	Q5VTE0	42	1	0	0	42	0	0
Putative trypsin-6	Q8NHM4	20	1	0	0	0	20	0
Rab GDP dissociation inhibitor alpha	P31150	19	1	0	0	19	0	0
Retinal dehydrogenase 1	P00352	34	1	0	0	34	0	0
Retinoic acid-induced protein 3	Q8NFI5	10	1	0	0	10	0	0
Retinol-binding protein 5	P82980	7	1	0	0	7	0	0
Ribonuclease T2	O00584	108	4	27	25	0	13	43
Ribonuclease UK114	P52758	28	1	0	0	28	0	0
Serine/threonine-protein kinase MARK1	Q9P0L2	35	1	0	0	35	0	0
Serpin B3	P29508	54	1	0	54	0	0	0
Serum amyloid P-component	P02743	20	1	0	0	0	20	0
Sorbitol dehydrogenase	Q00796	22	1	0	0	22	0	0
SPARC-like protein 1	Q14515	29	1	0	0	29	0	0
Sushi domain-containing protein 2	Q9UGT4	23	1	0	0	23	0	0
Transmembrane BAX inhibitor motif-containing protein 1	Q969X1	7	1	0	0	0	7	0
Transmembrane protease serine 2	O15393	23	1	0	0	0	23	0

Supplemental Table 2. Contd....

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Count				
				sCP1	sCP2	sCP3	sCP4	sCP5
Transmembrane protein C19orf77	O75264	3	1	0	0	3	0	0
Tubulin alpha-1B chain	P68363	13	1	0	0	13	0	0
Tubulin alpha-4A chain	P68366	21	1	0	21	0	0	0
Tumor necrosis factor receptor superfamily member 1B	P20333	20	1	0	0	0	20	0
Tyrosine-protein kinase transmembrane receptor ROR1	Q01973	26	1	0	0	26	0	0
WNT1-inducible-signaling pathway protein 2	O76076	11	1	0	0	0	11	0
Xaa-Pro dipeptidase	P12955	37	1	0	0	37	0	0

Supplemental Table 3. Proteins (n=82) Exclusive to HC Cohort (Not Appearing in sCP)

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Counts				
				HC1	HC2	HC3	HC4	HC5
Annexin A11	P50995	218	3	148	0	23	0	47
Multimerin-2	Q9H8L6	219	4	0	69	52	60	38
Twisted gastrulation protein homolog 1	Q9GZX9	56	4	0	22	15	10	9
Aldose reductase	P15121	16	1	0	0	0	16	0
Aquaporin-1	P29972	3	1	0	0	0	0	3
BPI fold-containing family B member 2	Q8N4F0	32	1	0	0	32	0	0
Cartilage intermediate layer protein 1	O75339	34	1	0	0	0	34	0
Cartilage intermediate layer protein 2	Q8IUL8	59	1	0	0	0	59	0
CD160 antigen	O95971	2	1	0	0	2	0	0
CD177 antigen	Q8N6Q3	7	1	0	0	0	7	0
CD276 antigen	Q5ZPR3	19	3	0	0	5	7	7
Charged multivesicular body protein 5	Q9NZZ3	38	2	0	0	0	12	26

Supplemental Table 3. Contd.....

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Counts				
				HC1	HC2	HC3	HC4	HC5
Cholesteryl ester transfer protein	P11597	26	1	0	0	26	0	0
Collagen alpha-2	P08572	235	2	0	0	113	122	0
Complement component C8 alpha chain	P07357	94	1	94	0	0	0	0
Complement factor D	P00746	11	1	0	0	11	0	0
Creatine kinase B-type	P12277	74	2	51	0	23	0	0
Dermcidin	P81605	16	1	0	0	0	0	16
Dynactin subunit 1	Q14203	47	1	0	0	47	0	0
EGF-containing fibulin-like extracellular matrix protein 2	O95967	23	2	0	13	0	10	0
Elongation factor 1-alpha 2	Q05639	19	1	0	0	19	0	0
Ephrin type-B receptor 4	P54760	189	4	0	53	53	38	45
Erythrocyte band 7 integral membrane protein	P27105	12	1	0	0	12	0	0
Galectin-9	O00182	11	1	0	0	11	0	0
Glypican-4	O75487	72	2	0	0	0	32	40
G-protein coupled receptor family C group 5 member B	Q9NZH0	20	1	0	0	0	0	20
Granulins	P28799	16	1	0	0	0	16	0
Guanine nucleotide-binding protein G	P62873	25	1	0	0	0	0	25
Heat shock 70 kDa protein 1-like	P34931	40	1	0	0	40	0	0
Hemoglobin subunit gamma-1	P69891	54	1	54	0	0	0	0
Hepatocyte growth factor activator	Q04756	23	1	0	0	0	23	0
Ig heavy chain V-II region ARH-77	P06331	18	2	0	12	0	6	0
Ig heavy chain V-III region CAM	P01768	42	1	42	0	0	0	0
Ig heavy chain V-III region GAL	P01781	23	1	0	23	0	0	0
Ig kappa chain V-I region HK101	P01601	39	1	39	0	0	0	0
Ig kappa chain V-I region Mev	P01612	30	1	0	0	30	0	0

Supplemental Table 3. Contd.....

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Counts				
				HC1	HC2	HC3	HC4	HC5
Ig kappa chain V-III region B6	P01619	56	2	0	42	0	14	0
Ig kappa chain V-III region NG9	P01621	40	1	0	0	0	40	0
Ig kappa chain V-III region VH	P04434	15	1	0	0	15	0	0
Ig kappa chain V-IV region	P06312	76	1	0	76	0	0	0
Ig lambda-3 chain C regions	P0CG06	106	1	106	0	0	0	0
IgG Fc-binding protein	Q9Y6R7	197	1	0	0	197	0	0
Immunoglobulin lambda-like polypeptide 1	P15814	56	2	0	0	32	0	24
Keratin, type I cytoskeletal 13	P13646	151	1	0	0	151	0	0
Keratin, type II cytoskeletal 4	P19013	133	1	0	0	133	0	0
Keratin, type II cytoskeletal 8	P05787	39	1	0	0	0	39	0
Leukocyte immunoglobulin-like receptor subfamily A member 5	A6NI73	7	1	0	0	7	0	0
Macrophage migration inhibitory factor	P14174	3	1	0	0	0	3	0
Metalloproteinase inhibitor 2	P16035	10	1	0	0	0	10	0
Microfibril-associated glycoprotein 4	P55083	7	1	0	0	0	7	0
Myeloid cell surface antigen CD33	P20138	11	1	0	0	11	0	0
Myotrophin	P58546	21	1	21	0	0	0	0
N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase	O43505	4	1	0	0	0	4	0
Neogenin	Q92859	96	1	0	96	0	0	0
Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 1	Q6ZVC0	45	1	0	0	0	45	0
Podocalyxin	O00592	27	1	0	0	27	0	0
Poliovirus receptor-related protein 3	Q9NQS3	12	1	0	12	0	0	0
Polycomb protein SUZ12	Q15022	28	1	0	0	28	0	0
Prominin-1	O43490	81	2	0	0	0	37	44
Protein CutA	O60888	5	1	0	0	5	0	0

Supplemental Table 3. Contd.....

Protein Names	Entry	Σ Spectral Counts	# of Samples	Spectral Counts				
				HC1	HC2	HC3	HC4	HC5
Protein-glutamine gamma-glutamyltransferase 4	P49221	72	1	0	0	0	0	72
Protocadherin-1	Q08174	187	4	0	73	39	32	43
Protocadherin-16	Q96JQ0	84	1	0	0	84	0	0
Putative short-chain dehydrogenase/reductase family 42E member 2	A6NKP2	13	1	0	0	13	0	0
Ras-related protein Rab-30	Q15771	22	1	0	0	22	0	0
Receptor-type tyrosine-protein phosphatase gamma	P23470	53	1	0	0	53	0	0
Reticulon-4 receptor-like 2	Q86UN3	35	2	0	0	14	21	0
Serine/threonine-protein kinase Nek11	Q8NG66	23	1	0	0	0	23	0
Sialic acid-binding Ig-like lectin 8	Q9NYZ4	21	1	0	0	0	21	0
Signal-regulatory protein beta-1 isoform 3	Q5TFQ8	44	1	0	44	0	0	0
Sodium-dependent neutral amino acid transporter B	Q695T7	15	1	0	0	0	15	0
Solute carrier family 2, facilitated glucose transporter member 5	P22732	16	1	0	0	0	0	16
Steroid hormone receptor ERR2	O95718	14	1	0	0	14	0	0
T-cell antigen CD7	P09564	15	1	0	0	0	0	15
Tenascin-X	P22105	238	2	0	0	0	108	130
Thrombospondin-1	P07996	61	1	0	0	61	0	0
Trypsin-1	P07477	57	1	0	0	0	0	57
Trypsin-3	P35030	115	1	115	0	0	0	0
Tubulin alpha-1C chain	Q9BQE3	16	1	0	0	0	16	0
Tumor necrosis factor receptor superfamily member 19L	Q969Z4	15	1	0	0	0	0	15
Zinc finger and BTB domain-containing protein 4	Q9P1Z0	42	1	0	0	42	0	0
Zinc finger protein 658	Q5TYW1	26	1	0	0	26	0	0

Supplemental Table 4. Proteins (n=49) of Higher Abundance in sCP Compared to HC Cohorts, as Determined via QSPEC

Protein names	Entry	Σ HC Spectral Counts	Σ sCP Spectral Counts	# HC Samples	# sCS Samples	Bayes Factor	Fold Change
Acid ceramidase	Q13510	82	168	3	5	179.51	4.32
Aggrecan core protein	P16112	21	110	1	3	16.83	5.24
Aggrin	O00468	225	518	3	5	6.7E+06	6.97
Alpha-1-acid glycoprotein 1	P02763	171	525	4	5	440.48	4.40
Arylsulfatase A	P15289	186	271	4	5	30.47	2.48
Beta-galactosidase	P16278	238	465	3	5	4.7E+04	6.47
Beta-glucuronidase	P08236	62	142	2	5	1546.28	6.39
Cadherin-1	P12830	295	537	4	5	1.4E+04	3.15
Cadherin-13	P55290	194	274	4	5	49.51	1.89
Cathepsin B	P07858	67	198	3	5	291.77	4.79
Cathepsin D	P07339	355	760	5	5	4497.61	2.14
Cathepsin Z	Q9UBR2	11	88	1	4	36.48	9.32
CD59 glycoprotein	P13987	148	283	5	5	50.00	1.91
Collagen alpha-3	P12111	737	1237	4	5	1.0E+04	4.61
Complement decay-accelerating factor	P08174	195	328	4	5	17.75	2.43
Dipeptidyl peptidase 1	P53634	81	221	3	5	1083.51	6.00
Dipeptidyl peptidase 4	P27487	125	275	3	5	1109.62	5.86
Epididymal secretory protein E1	P61916	28	140	2	5	393.14	8.43
Ganglioside GM2 activator	P17900	25	182	2	4	3.4E+01	7.47
Glutamyl aminopeptidase	Q07075	84	338	2	4	38.25	7.14
Ig gamma-4 chain C region	P01861	688	984	2	4	93.74	7.42
Ig heavy chain V-III region KOL	P01772	50	84	2	4	97.30	3.43
Ig kappa chain C region	P01834	3456	8024	5	5	559.32	1.94
Ig kappa chain V-I region HK102	P01602	104	212	4	5	27.35	2.24

Supplemental Table 4. Contd.....

Protein names	Entry	Σ HC Spectral Counts	Σ sCP Spectral Counts	# HC Samples	# sCS Samples	Bayes Factor	Fold Change
Ig kappa chain V-II region RPMI 6410	P06310	99	428	2	4	58.76	6.51
Ig kappa chain V-IV region JI	P06313	160	418	3	5	3469.47	6.90
Ig lambda chain V-I region WAH	P04208	83	254	3	5	1241.14	6.15
Ig lambda chain V-III region LOI	P80748	63	211	4	5	138.80	2.98
Ig lambda-1 chain C regions	P0CG04	416	1758	4	5	2.1E+04	6.27
Ig lambda-2 chain C regions	P0CG05	682	2285	4	5	7.4E+04	5.28
Immunoglobulin J chain	P01591	26	73	2	4	10.65	4.13
Immunoglobulin superfamily member 8	Q969P0	138	270	4	5	22.87	2.60
Leukocyte-associated immunoglobulin-like receptor 1	Q6GTX8	31	98	2	4	60.41	4.12
Lithostathine-1-alpha	P05451	91	500	4	5	26.75	3.69
Lymphatic vessel endothelial hyaluronic acid receptor 1	Q9Y5Y7	29	191	1	4	114.41	12.67
Lysosomal acid phosphatase	P11117	103	228	3	4	26.54	2.80
Lysosomal protective protein	P10619	104	325	4	5	1242.00	3.80
Lysozyme C	P61626	8	108	1	5	6.2E+04	15.67
Macrophage colony-stimulating factor 1	P09603	55	113	2	4	15.29	5.29
Non-secretory ribonuclease	P10153	374	607	5	5	11.35	1.57
Pepsin A	P00790	200	408	3	5	688.91	6.04
Plasma glutamate carboxypeptidase	Q9Y646	101	180	2	5	32039.23	7.92
Prostaglandin-H2 D-isomerase	P41222	1395	3798	5	5	2.2E+04	2.51
Protein AMBP	P02760	2019	6600	5	5	8.6E+06	2.96
Retinoid-inducible serine carboxypeptidase	Q9HB40	23	126	1	4	10.71	11.50
Ribonuclease pancreatic	P07998	105	216	4	4	21.62	1.44
SH3 domain-binding glutamic acid-rich-like protein 3	Q9H299	25	129	2	4	91.15	5.69
Triosephosphate isomerase	P60174	70	147	3	5	21.03	3.72

Supplemental Table 4. Contd.....

Protein names	Entry	Σ HC Spectral Counts	Σ sCP Spectral Counts	# HC Samples	# sCS Samples	Bayes Factor	Fold Change
Zinc-alpha-2-glycoprotein	P25311	872	1885	5	5	443.27	2.09

Supplemental Table 5. Proteins (n=52) of Higher Abundance in HC Compared to sCP Cohorts, as Determined via QSPEC

Protein names	Entry	Σ HC Spectral Counts	Σ sCP Spectral Counts	# HC Samples	# sCS Samples	Bayes Factor	Fold Change
6-phosphogluconolactonase	O95336	171	53	5	2	4341.44	6.65
Actin, cytoplasmic 1	P60709	319	408	3	2	43.27	1.67
Alpha-1-antitrypsin	P01009	1527	606	5	5	3186.67	2.52
Alpha-amylase 2B	P19961	2042	496	5	2	6.9E+16	21.39
Alpha-N-acetylglucosaminidase	P54802	514	292	5	4	701.02	2.94
Apolipoprotein A-I	P02647	405	160	5	2	3.1E+04	13.71
Apolipoprotein E	P02649	289	56	4	1	284.92	12.07
Biglycan	P21810	22	35	1	1	12.71	1.07
Carboxypeptidase N subunit 2	P22792	176	87	5	3	11.37	3.83
Cell adhesion molecule 4	Q8NFZ8	309	181	5	4	12.93	2.30
Collagen alpha-1	P39059	718	189	5	3	1.1E+04	8.49
Complement C1r subcomponent-like protein	Q9NZP8	165	112	4	3	16.18	2.51
Complement C3	P01024	770	101	3	1	60.94	4.27
Dipeptidase 1	P16444	326	26	5	1	1.2E+07	24.85
Dystroglycan	Q14118	113	35	3	1	41.36	4.38
Endosialin	Q9HCU0	366	208	5	4	117.81	2.82
Endothelial protein C receptor	Q9UNN8	329	168	5	4	299.78	2.94
Extracellular superoxide dismutase	P08294	215	65	5	2	7.5E+04	8.36

Supplemental Table 5: . Contd.....

Protein names	Entry	Σ HC Spectral Counts	Σ sCP Spectral Counts	# HC Samples	# sCS Samples	Bayes Factor	Fold Change
Glutaminy-peptide cyclotransferase	Q16769	426	233	5	4	805.75	2.82
Hyaluronidase-1	Q12794	47	15	3	1	13.86	4.41
Ig alpha-2 chain C region	P01877	572	553	4	4	740.05	1.05
Ig gamma-1 chain C region	P01857	1949	1350	5	5	58.56	1.46
Ig heavy chain V-I region HG3	P01743	103	12	5	1	5.8E+04	14.03
Ig kappa chain V-II region	P01614	108	181	2	1	83.51	1.66
Ig kappa chain V-III region GOL	P04206	319	351	2	1	26.25	1.88
Low affinity immunoglobulin gamma Fc region receptor III-A	P08637	64	25	3	1	14.36	4.12
Mannan-binding lectin serine protease 2	O00187	289	83	5	2	4.1E+05	12.18
Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	P33908	324	67	4	1	569.87	12.10
Matrix-remodeling-associated protein 8	Q9BRK3	322	88	5	2	1.3E+06	12.28
Mucin-1	P15941	100	19	4	1	23.71	7.54
Mucosal addressin cell adhesion molecule 1	Q13477	109	65	5	3	11.38	2.55
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	O95865	89	7	4	1	284.81	9.67
Neprilysin	P08473	104	64	3	1	38.96	3.41
Nidogen-1	P14543	295	65	4	2	12.24	7.16
Pancreatic alpha-amylase	P04746	2035	868	5	5	3.8E+06	2.20
Phosphatidylcholine-sterol acyltransferase	P04180	97	19	4	2	39.94	5.10
Plasma protease C1 inhibitor	P05155	653	231	5	3	2.1E+07	9.27
Poliovirus receptor-related protein 4	Q96NY8	109	34	3	1	34.90	3.67
Pro-epidermal growth factor	P01133	1730	587	5	5	4.0E+04	2.87
Prolactin-inducible protein	P12273	79	14	4	1	355.88	10.32
Prostatic acid phosphatase	P15309	400	224	4	2	26.91	6.09
Roundabout homolog 4	Q8WZ75	740	222	5	3	7.4E+05	10.67

Supplemental Table 5: . Contd.....

Protein names	Entry	Σ HC Spectral Counts	Σ sCP Spectral Counts	# HC Samples	# sCS Samples	Bayes Factor	Fold Change
Tetranectin	P05452	158	83	5	2	940.38	6.83
Transthyretin	P02766	252	42	5	2	2.4E+04	12.90
Tyrosine-protein kinase receptor UFO	P30530	457	269	5	4	949.85	2.65
Urokinase-type plasminogen activator	P00749	138	27	3	1	12.26	4.56
Uromodulin	P07911	8539	2502	5	5	1.1E+06	2.55
Vesicular integral-membrane protein VIP36	Q12907	847	460	5	5	1395.01	2.11
Vitamin D-binding protein	P02774	407	208	5	5	15.71	1.84
Vitamin K-dependent protein Z	P22891	345	58	5	2	8.8E+06	14.22
Vitelline membrane outer layer protein 1 homolog	Q7Z5L0	335	224	5	4	76.83	2.42
Vitronectin	P04004	223	44	5	2	5639.47	10.76

Supplemental Table 6. Core Set of Proteins Identified in All 15 Samples.HC, Healthy Controls; sCP, Severe Chronic Pancreatitis; MD, Mixed Diagnosis Samples

Protein Names	UniProt Entry	Spectral Counts			Significant Difference
		Σ HC	Σ sCP	Σ MD	(p<0.05)
Alpha-1-antichymotrypsin	P01011	556	392	598	no
Alpha-1-antitrypsin	P01009	1527	606	1264	
Alpha-2-HS-glycoprotein	P02765	485	383	397	no
Apolipoprotein D	P05090	2000	1512	1375	
Basement membrane-specific heparan sulfate protein	P98160	2261	2535	1981	
Beta-2-glycoprotein 1	P02749	330	322	364	no
Cathepsin D	P07339	355	760	270	
CD44 antigen	P16070	261	298	352	no

Supplemental Table 6. Contd.....

Protein Names	UniProt Entry	Spectral Counts			Significant Difference
		Σ HC	Σ sCP	Σ MD	(p<0.05)
CD59 glycoprotein	P13987	148	283	211	
Clusterin	P10909	612	550	435	no
Collagen alpha-1	P12109	1215	658	693	
Cubilin	O60494	1348	1075	1122	no
EGF-containing fibulin-like extracellular matrix protein 1	Q12805	318	479	295	no
Fibronectin	P02751	587	673	775	no
Galectin-3-binding protein	Q08380	513	504	461	no
Gelsolin	P06396	868	1287	664	no
Hemopexin	P02790	496	353	534	no
Ig alpha-1 chain C region	P01876	821	982	886	no
Ig gamma-1 chain C region	P01857	1949	1350	1794	
Ig gamma-2 chain C region	P01859	2268	1483	1942	no
Ig heavy chain V-III region BRO	P01766	225	264	292	no
Ig kappa chain C region	P01834	3456	8024	3137	
Ig kappa chain V-III region VG	P04433	141	246	117	
Insulin-like growth factor-binding protein 7	Q16270	437	407	386	no
Inter-alpha-trypsin inhibitor heavy chain H4	Q14624	1455	1376	1036	
Keratin, type I cytoskeletal 10	P13645	937	1014	1399	no
Keratin, type I cytoskeletal 9	P35527	861	787	1378	
Keratin, type II cytoskeletal 1	P04264	1409	1543	2209	
Kininogen-1	P01042	2920	1983	2549	
Lysosomal alpha-glucosidase	P10253	885	762	1046	no
Monocyte differentiation antigen CD14	P08571	590	568	452	no

Supplemental Table 6. Contd.....

Protein Names	UniProt Entry	Spectral Counts			Significant Difference
		Σ HC	Σ sCP	Σ MD	(p<0.05)
Non-secretory ribonuclease	P10153	374	607	591	
Osteopontin	P10451	790	812	895	no
Pancreatic alpha-amylase	P04746	2035	868	4547	
Peptidoglycan recognition protein 1	O75594	343	244	264	no
Plasma serine protease inhibitor	P05154	737	370	492	no
Polymeric immunoglobulin receptor	P01833	1393	1569	1300	no
Pro-epidermal growth factor	P01133	1730	587	892	
Prostaglandin-H2 D-isomerase	P41222	1395	3798	1617	
Protein AMBP	P02760	2019	6600	3094	
Prothrombin	P00734	406	483	332	no
Retinol-binding protein 4	P02753	337	483	315	
Secreted and transmembrane protein 1	Q8WVN6	242	311	133	no
Serotransferrin	P02787	1933	1449	2179	no
Serum albumin	P02768	16657	13767	20708	
Uromodulin	P07911	8539	2502	5943	
Vasorin	Q6EMK4	689	442	495	
Vesicular integral-membrane protein VIP36	Q12907	847	460	503	
Vitamin D-binding protein	P02774	407	208	425	
Zinc-alpha-2-glycoprotein	P25311	872	1885	1107	