Supplemental Table I: Complement PCR primer sequences and product sizes

Primer	Oligonucleotide Sequence (5' → 3')	Product Size (bp)	Gene bank code
C1qb-1	CAGGGATAAAAGGAGAGAAAGG	357	X03084
C1qb-2	TGGCGTGGTAGGTGAAGTAGTA		
C3-1	GCTGCTCCTGCTACTAACCCA	784	K02765
C3-2	AAAGGCAGTTCCCTCCACTTT		
C4-1	TGCGGATCCAGCAGTTTCGG	889	K02403
C4-2	TGGCGGTTGTTCAGCTGCAG		
FB-1	GTG TGA CCA CCA CTC CAT GG	685	L15702
FB-2	CCA TCC TCA GCA TCG ACT CC		
FH-1	ACATTACTTCATTCCCGTTGTC	320	Y00716
FH-2	ATACTCCAGTTTCCCATCCCAA		
C5-1	AGTGTGTGGAAGGGTGGAAG	222	NM_001735
C5-2	GTTCTCTCGGGCTTCAACAG		
C9-1	CAACTGGGCCTCTTCCATAA	251	NM_001737
C9-2	CACAGGCAATTCCCTCAAAT		
18S-1	GACTCAACACGGGAAACCTC	153	NM_011296.1
18S-2	ATGCCAGAGTCTCGTTCGTT		

Supplemental Table II: Proteins altered in nasal mucus of patients with CRSwNP compared to control subjects

Increased	Decreased
Cystatin-SN	Phosphoglycerate kinase 1
Alpha-2-macroglobulin	Macrophage-capping protein
Ig mu heavy chain disease protein	Plastin-3
Ig gamma-4 chain C region	Thioredoxin reductase 1, cytoplasmic
Complement C4-A	Aldo-keto reductase family 1 member B10
Ig kappa chain V-IV region (Fragment)	NAD(P)H dehydrogenase [quinone] 1
Inter-alpha-trypsin inhibitor heavy chain H2	40S ribosomal protein S17-like
Ig kappa chain V-I region CAR	Sulfotransferase 1A1
Ig heavy chain V-III region GAL	Programmed cell death 6-interacting protein
Haptoglobin	Proteasome subunit beta type-10
Ig kappa chain V-I region AG	Cathepsin B
Ig lambda chain V-IV region Hil	Profilin-1
Ig gamma-2 chain C region	Calmodulin
Complement factor B	Tubulin alpha-1A chain
Haptoglobin-related protein	Peptidyl-prolyl cis-trans isomerase A-like 4A/B/C
IgGFc-binding protein	Tubulin beta-4A chain
Ig kappa chain V-I region DEE	Glutathione S-transferase P
Ig mu chain C region	Cystatin-B
Signal recognition particle 68 kDa protein	Peptidyl-prolyl cis-trans isomerase A
Ig kappa chain C region	Transketolase
Beta-2-glycoprotein 1	14-3-3 protein sigma
Ig heavy chain V-III region TRO	Transgelin-2
Serotransferrin	Fructose-bisphosphate aldolase C
Complement C3	Triosephosphate isomerase
	Cofilin-1
	Argininosuccinate synthase
	Alpha-actinin-4
	Rho GDP-dissociation inhibitor 1
	14-3-3 protein zeta/delta
	Calcyphosin
	Pyruvate kinase isozymes M1/M2
	Phosphatidylethanolamine-binding protein 1
	Tubulin alpha-1B chain
	14-3-3 protein epsilon
	Cytosolic non-specific dipeptidase
	Heat shock 70 kDa protein 1A/1B
	Elongation factor 1-alpha 1
	Tubulin beta-2A chain
	Protein SET
	Rab GDP dissociation inhibitor alpha
	Heat shock-related 70 kDa protein 2
	Heat shock 70 kDa protein 1-like
	Calpain small subunit 1
	Alcohol dehydrogenase [NADP(+)]
	Keratin, type II cytoskeletal 8

Heterogeneous nuclear ribonucleoprotein K
Fructose-bisphosphate aldolase A
Poly(rC)-binding protein 1
Carbonyl reductase [NADPH] 1
Superoxide dismutase [Cu-Zn]
Eukaryotic translation initiation factor 5A-1
Ribonuclease inhibitor
Eukaryotic initiation factor 4A-I
Transitional endoplasmic reticulum ATPase
Elongation factor 2
Chloride intracellular channel protein 1
14-3-3 protein beta/alpha
Retinal dehydrogenase 1
Ras GTPase-activating-like protein IQGAP1
Putative RNA-binding protein 3
Myosin-10
Peroxiredoxin-5, mitochondrial
6-phosphogluconate dehydrogenase, decarboxylating
Heat shock cognate 71 kDa protein
Myosin light polypeptide 6
14-3-3 protein theta
Malate dehydrogenase, cytoplasmic
Nucleophosmin
Selenium-binding protein 1
Phosphoglycerate mutase 1
40S ribosomal protein SA
Glucose-6-phosphate isomerase
Adenylyl cyclase-associated protein 1
S-formylglutathione hydrolase
Ezrin
Heat shock protein beta-1
UTP--glucose-1-phosphate uridylyltransferase
Aldo-keto reductase family 1 member C1
Clathrin heavy chain 1
PDZ and LIM domain protein 1
Endoplasmin
Nicotinamide phosphoribosyltransferase
Alpha-enolase
40S ribosomal protein S5
Ubiquitin-like modifier-activating enzyme 1
Heterogeneous nuclear ribonucleoprotein H
Peroxiredoxin-6
Protein S100-A4
60S ribosomal protein L23
Aldo-keto reductase family 1 member C3
Stress-induced-phosphoprotein 1
Vinculin

Myosin-11

Peroxiredoxin-1

X-ray repair cross-complementing protein 5

Isocitrate dehydrogenase [NADP] cytoplasmic

Alcohol dehydrogenase class 4 mu/sigma chain

Putative nucleoside diphosphate kinase

Leukocyte elastase inhibitor

Aldehyde dehydrogenase, dimeric NADP-preferring

Peroxiredoxin-2

Calpain-2 catalytic subunit

Proteasome subunit alpha type-2

T-complex protein 1 subunit epsilon

Acid ceramidase

Obg-like ATPase 1

Fatty acid-binding protein, epidermal

Annexin A1

Heterogeneous nuclear ribonucleoprotein M

Protein DJ-1

40S ribosomal protein S8

14-3-3 protein gamma

Rab GDP dissociation inhibitor beta

Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform

Fructose-1,6-bisphosphatase 1

Galectin-3

Glutathione S-transferase A1

Annexin A5

Aspartate aminotransferase, cytoplasmic

Aldo-keto reductase family 1 member C2

SAM domain and HD domain-containing protein 1

Cathepsin D

Supplemental Methods

Nasal mucus procurement and proteomics screening

Nasal mucus was collected as previously described.[1-4] The protein concentration of each mucus sample was determined using a BCA protein assay (Thermo Scientific). Equal amounts of protein from each sample (50 µg) were acetone precipitated (1:10) overnight at -20 °C. Precipitated proteins were brought up in 6 M urea, reduced with dithiothreitol and alkylated with iodoacetamide, followed by overnight digestion with trypsin (1:50) at 37 °C. Resulting peptides were desalted with a C-18 column, vacuum dried, then reconstituted in mobile phase (5% acetonitrile, 0.1% formic acid). A 15 µL aliquot of this peptide solution was separated across a 120 min linear gradient from 5% acetonitrile, 0.1% formic acid to 95% acetonitrile, 0.1% formic acid on a nano-LC system interfaced by electrospray ionization with an LTQ XL (Thermo Electron). Data-dependent analysis was used to perform MS/MS on the ten most intense ions between *m/z* = 400 and 2000 in each MS spectra with a minimum signal of 500 cps. Dynamic exclusion was used with a repeat count of two and an exclusion duration of 120 s. Acquired data were converted to the mgf file format using msconvert (ProteoWizard v 3.0.4472) and default settings (including prefer vendor for peak picking), and searched using the Mascot search algorithm (v 2.4.1; Matrix Science). The database used was the 2012_10 UniProt SwissProt release and varsplic isoform database, *Homo sapiens* taxonomy, as well as the common repository of adventitious proteins (v 2012.1.1; The Global Proteome Machine) with a combined total of 37,031 sequences. The following search parameters were specified: trypsin as the enzyme; carbamidomethyl fixed modification (C); variable modifications of acetyl (protein N-term), deamidated (NQ), pyro-Glu (N-term Q), and oxidation (M); precursor mass tolerance of 2 Da and fragment mass tolerance of 1 Da; 2 missed cleavages are allowed; instrument type is specified as ESI-TRAP. Data were searched against a target database as well as a decoy database which was the same database reversed. Post-processing was performed using ProteoIQ (v. 2.3.08) such that 2 peptides were required for positive identification, a 5% FDR

cutoff was used, and normalized spectral counts were exported for downstream analysis. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository[5] with the dataset identifier PXD004144 and 10.6019/PXD004144.. Relative protein abundance was compared between the two groups using an exact Wilcoxon Rank Sum test (MATLAB v 8.3; MathWorks). Pathway enrichment analysis (REACTOME 2016) was accomplished using Enrichr and the top 10 pathways based on the combined Enrichr score are shown.[6, 7]

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