

## Supplementary Information

**Table S1: Demographics of participants enrolled in the study.**

<b>Subject</b>	<b>Gender</b>	<b>Age</b>	<b>FEV<sub>1</sub> % predicted</b>	<b>Baseline PC<sub>20</sub> (mg/mL)</b>
1	F	22	107	3.5
2	F	31	113	>16
3	F	24	116	>16
4	M	32	123	>16
5	F	34	79	0.2
6	M	46	66	0.3
7	M	27	105	>16
8	F	46	63	>16
9	F	20	98	2.1
10	F	31	103	0.3
11	M	28	100	>16
12	M	23	104	2.4
13	F	23	101	>16
14	M	23	112	>16

**Table S2: Expression levels of 79 proteins altered by DEA co-exposure compared to FAA.**

Protein	SWPRO T	Log2 Fold Change with respect to FAS				Description	Z-Score
		DES	FAA	DEA	(DEA-FAA)		
<b>C4B</b>	P0C0L5	5.48	0.35	4.92	4.57	Complement C4-B	3.97
<b>LCN1</b>	P31025	-0.57	0.95	5.28	4.33	Lipocalin-1	3.79
<b>CST2</b>	P09228	0.00	3.67	7.80	4.13	Cystatin-SA	3.75
<b>MUC16</b>	Q8WXI7	1.96	-1.08	3.20	4.28	Mucin-16	3.65
<b>TCN1</b>	P20061	1.99	-0.33	3.89	4.22	Transcobalamin-1	3.64
<b>TUBB4B</b>	P68371	-2.67	-3.59	0.15	3.74	Tubulin beta-4B chain	3.06
<b>PRR4</b>	Q16378	-1.20	-0.81	2.60	3.41	Proline-rich protein 4	2.91
<b>CST1</b>	P01037	0.00	2.53	5.75	3.22	Cystatin-SN	2.91
<b>LEG1</b>	Q6P5S2	0.32	-0.83	2.46	3.29	Protein LEG1 homolog	2.81
<b>ADH7</b>	P40394	-0.82	-0.65	2.40	3.05	Alcohol dehydrogenase class 4 mu/sigma chain	2.61
<b>SCGB3A1</b>	Q96QR1	-1.26	-0.87	2.04	2.91	Secretoglobulin family 3A member 1	2.48
<b>CLIC6</b>	Q96NY7	0.70	-2.46	0.50	2.96	Chloride intracellular channel protein 6	2.44
<b>UBE2V1</b>	Q13404	0.00	0.83	3.50	2.67	Ubiquitin-conjugating enzyme E2 variant 1	2.35
<b>MUC4</b>	Q99102	0.00	-0.68	2.00	2.68	Mucin-4	2.29
<b>PPP2R1A</b>	P30153	-0.89	-2.39	0.33	2.72	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	2.23
<b>ZG16B</b>	Q96DA0	0.00	-0.92	1.71	2.63	Zymogen granule protein 16 homolog B	2.23
<b>TXNL1</b>	O43396	-0.64	-2.24	0.45	2.69	Thioredoxin-like protein 1	2.22
<b>ALDH3A1</b>	P30838	0.13	0.27	2.81	2.53	Aldehyde dehydrogenase, dimeric NADP-preferring	2.21
<b>MVP</b>	Q14764	0.70	-2.46	0.18	2.64	Major vault protein	2.17
<b>FCGBP</b>	Q9Y6R7	-0.50	-1.43	1.14	2.57	IgGFC-binding protein	2.16
<b>CKB</b>	P12277	-0.34	-2.11	0.48	2.59	Creatine kinase B-type	2.14
<b>SFN</b>	P31947	-0.85	-1.43	1.05	2.48	14-3-3 protein sigma	2.08
<b>PLIN3</b>	O60664	-2.63	-2.46	0.03	2.49	Perilipin-3	2.04
<b>CHMP4B</b>	Q9H444	-0.83	-2.08	0.38	2.46	Charged multivesicular body protein 4b	2.03
<b>SPTAN1</b>	Q13813	-0.34	0.11	2.43	2.32	Spectrin alpha chain, non-erythrocytic 1	2.01
<b>GNPDA1</b>	P46926	-0.28	-2.00	0.42	2.42	Glucosamine-6-phosphate isomerase 1	2.00
<b>DARS</b>	P14868	0.67	-1.34	1.02	2.36	Aspartate--tRNA ligase, cytoplasmic	1.97

CCT2	P78371	-1.97	-1.57	0.78	2.35	T-complex protein 1 subunit beta	1.96
ABHD14B	Q96IU4	-1.50	-2.31	0.08	2.38	Alpha/beta hydrolase domain-containing protein 14B	1.95
CD2AP	Q9Y5K6	-1.46	-1.54	0.77	2.31	CD2-associated protein	1.92
SSB	P05455	1.10	-1.49	0.80	2.29	Lupus La protein	1.91
TFF3	Q07654	0.00	-0.62	1.56	2.18	Trefoil factor 3	1.86
TF	Q29443	0.00	8.19	9.84	1.65	Transferrin	1.83
ALOX15	P16050	0.22	-0.80	1.31	2.10	Arachidonate 15-lipoxygenase	1.78
TCP1	P17987	-0.10	-2.21	-0.05	2.17	T-complex protein 1 subunit alpha	1.77
NPEPPS	P55786	0.07	-1.86	0.21	2.07	Puromycin-sensitive aminopeptidase	1.70
NUDT5	Q9UKK9	-2.39	-2.72	-0.60	2.12	ADP-sugar pyrophosphatase	1.70
IGFBP2	P18065	-2.39	-1.11	0.89	2.00	Insulin-like growth factor-binding protein 2	1.68
MUC5AC	P98088	0.99	-0.52	1.44	1.96	Mucin-5AC	1.68
PSMB4	P28070	-0.60	-2.27	-0.23	2.05	Proteasome subunit beta type-4	1.66
AP2B1	P63010	0.00	0.64	2.52	1.88	AP-2 complex subunit beta	1.66
NUCB2	P80303	0.18	-0.21	1.73	1.93	Nucleobindin-2	1.66
APRT	P07741	-1.97	-1.43	-3.27	-1.84	Adenine phosphoribosyltransferase	-1.66
HIST1H4A	P62805	2.69	1.99	-0.06	-2.05	Histone H4	-1.68
CTBS	Q01459	-0.09	1.45	-0.59	-2.03	Di-N-acetylchitobiase	-1.69
OSCAR	Q8IYS5	-1.81	1.19	-0.83	-2.02	Osteoclast-associated immunoglobulin-like receptor	-1.69
LACRT	Q9GZZ8	0.00	2.58	0.45	-2.13	Extracellular glycoprotein lacritin	-1.71
DYNC1H1	Q14204	1.26	1.69	-0.41	-2.09	Cytoplasmic dynein 1 heavy chain 1	-1.73
CDC42	P60953	0.92	0.67	-1.43	-2.09	Cell division control protein 42 homolog	-1.78
BCHE	P06276	1.37	3.82	1.53	-2.29	Cholinesterase	-1.79
FMNL1	O95466	-0.57	1.75	-0.44	-2.18	Formin-like protein 1	-1.81
C1QA	P02745	0.48	1.62	-0.57	-2.19	Complement C1q subcomponent subunit A	-1.82
KRT16	P08779	-2.73	1.02	-1.14	-2.16	Keratin, type I cytoskeletal 16	-1.82
RAB5C	P51148	0.18	0.46	-1.67	-2.13	Ras-related protein Rab-5C	-1.82
CD93	Q9NPY3	0.23	1.38	-0.81	-2.19	Complement component C1q receptor	-1.83

S100A16	Q96FQ6	0.00	2.05	-0.20	-2.25	Protein S100-A16	-1.84
CES1	P23141	1.40	-1.22	-3.35	-2.12	Liver carboxylesterase 1	-1.90
DSG1	Q02413	-0.32	-0.05	-2.24	-2.19	Desmoglein-1	-1.90
HIST1H1E	P10412	0.57	0.00	-2.21	-2.21	Histone H1.4	-1.91
KRT14	P02533	0.42	0.40	-1.85	-2.24	Keratin, type I cytoskeletal 14	-1.92
FTL	P02792	-1.05	0.30	-1.97	-2.27	Ferritin light chain	-1.95
COPG1	Q9Y678	-1.07	1.72	-0.65	-2.36	Coatomer subunit gamma-1	-1.96
KV119	P01611	-1.81	1.29	-1.13	-2.41	Ig kappa chain V-I region Wes	-2.03
TUBB	P07437	2.60	2.10	-0.39	-2.49	Tubulin beta chain	-2.05
MAPK1	P28482	0.95	-0.87	-3.23	-2.35	Mitogen-activated protein kinase 1	-2.08
HNRNPU	Q00839	1.39	2.86	0.27	-2.59	Heterogeneous nuclear ribonucleoprotein U	-2.10
GALNT5	Q7Z7M9	0.74	0.67	-1.85	-2.51	Polypeptide N-acetylgalactosaminyltransferase 5	-2.14
KRT19	P08727	0.00	4.64	1.83	-2.81	Keratin, type I cytoskeletal 19	-2.21
KV301	P01619	-0.22	2.37	-0.35	-2.71	Ig kappa chain V-III region B6	-2.23
KRT17	Q04695	-2.31	0.32	-2.36	-2.67	Keratin, type I cytoskeletal 17	-2.30
HV305	P01766	0.60	3.24	0.29	-2.96	Ig heavy chain V-III region BRO	-2.40
APOL1	O14791	0.00	4.26	1.23	-3.03	Apolipoprotein L1	-2.42
POTEE	Q6S8J3	0.15	-0.43	-3.50	-3.07	POTE ankyrin domain family member E	-2.68
SERPINA5	P05154	0.96	2.31	-1.19	-3.49	Plasma serine protease inhibitor	-2.91
DSP	P15924	-2.28	0.24	-3.35	-3.58	Desmoplakin	-3.09
KRT6A	P02538	-2.19	1.16	-2.51	-3.67	Keratin, type II cytoskeletal 6A	-3.12
GBE1	Q04446	4.06	4.29	-0.09	-4.38	1,4-alpha-glucan-branching enzyme	-3.58
KV118	P01610	-21.99	1.94	-3.41	-5.34	Ig kappa chain V-I region WEA	-4.53
C4A	P0C0L4	-3.56	0.95	-4.68	-5.63	Complement C4-A	-4.83

**Proteins in bold were selected for further validation studies**

**Table S3: Relative band intensity in western blots determined by densitometry for individual BAL samples from independent participants**

Participant*	LCN1 Densitometry			TCN1 Densitometry		
	Relative band intensity compared to FAS normalized to 1			Relative band intensity compared to FAS normalized to 1		
	DES	FAA	DEA	DES	FAA	DEA
1	ND	1.2	0.9	ND	1.7	0.9
3	7	4.5	5.4	5.3	3	2.9
4	1.6	2.1	1.6	0.9	2	2.5
7	0.9	6.7	5.6	1.1	4.7	6.8
10	4	1.5	9.7	1.6	ND	28
12	0.3	11.8	2	0.6	2.4	0.9
13	0.7	7.7	44	0.5	3.5	4.2
14	ND	ND	0.7	11	27	22

\*Subject numbers corresponds to supplementary table I, detailing demographics of participants enrolled in the study. ND=not detected