

***MICB*^{G406A} polymorphism reduces risk of mechanical ventilation and death during viral acute lung injury.**

Authors: Harry Pickering^{1#}, Narges Alipanah-Lechner², Ernie Chen³, Dylan Duchon³, Holden T. Maecker⁴, Seunghee Kim-Sschulze⁵, Ruth R. Montgomery³, Chris Cotsapas³, Hanno Steen⁶, Florian Krammer⁵, Charles R. Langelier², Ofer Levy⁶, Lindsey R. Baden⁷, Esther Melamed⁸, Lauren I. R. Ehrlich⁸, Grace A. McComsey⁹, Rafick P. Sekaly⁹, Charles B. Cairns¹⁰, Elias K. Haddad¹⁰, Albert C. Shaw³, David A. Hafler³, David B. Corry¹¹, Farrah Kheradmand¹¹, Mark A. Atkinson¹², Scott C. Brakenridge¹², Nelson I Agudelo Higuera¹³, Jordan P. Metcalf¹³, Catherine L. Hough¹⁴, William B. Messer¹⁴, Bali Pulendran⁴, Kari C. Nadeau⁴, Mark M. Davis⁴, Ana Fernandez Sesma⁵, Viviana Simon⁵, Monica Kraft¹⁵, Chris Bime¹⁵, David J. Erle², Joanna Schuenemann¹, Al Ozonoff⁶, Bjoern Peters¹⁶, Steven H. Kleinstein³, Alison D. Augustine¹⁷, Joann Diray-Arce³, Patrice M. Becker¹⁷, Nadine Rouphael¹⁸, Matthew C. Altman¹⁹, Steve Bosinger²⁰, Walter Eckalbar², IMPACC Network²¹, Carolyn S. Calfee², Oscar A. Aguilar^{22,23}, Elaine F. Reed¹, John R. Greenland^{2,24}, Daniel R. Calabrese^{2,24}

Affiliations:

¹Pathology and Laboratory Medicine, University of California Los Angeles, Los Angeles, CA

²Department of Medicine, University of California San Francisco, San Francisco, CA

³Yale School of Medicine, New Haven, CT

⁴Stanford University School of Medicine, Palo Alto, CA, USA

⁵Icahn School of Medicine at Mount Sinai, New York, NY, USA

⁶Precision Vaccines Program, Boston Children's Hospital, Harvard Medical School, Boston, MA, USA

⁷Brigham and Women's Hospital, Harvard Medical School, Boston, MA, USA

⁸The University of Texas at Austin, Austin, TX, USA

⁹Case Western Reserve University and University Hospitals of Cleveland, Cleveland, OH, USA

26 ¹⁰Drexel University, Tower Health Hospital, Philadelphia, PA, USA

27 ¹¹Baylor College of Medicine and the Center for Translational Research on Inflammatory
28 Diseases, Houston, TX, USA

29 ¹²University of Florida, Gainesville, FL, USA

30 ¹³Oklahoma University Health Sciences Center, Oklahoma City, OK, USA

31 ¹⁴Oregon Health & Science University, Portland, OR, USA

32 ¹⁵University of Arizona, Tucson AZ, USA

33 ¹⁶La Jolla Institute for Immunology, La Jolla, CA, USA

34 ¹⁷National Institute of Allergy and Infectious Diseases, National Institute of Health, Bethesda, MD,
35 USA

36 ¹⁸Emory School of Medicine, Atlanta, GA, USA

37 ¹⁹Benaroya Research Institute, University of Washington, Seattle, WA

38 ²⁰Emory School of Medicine, Atlanta, GA

39 ²¹The Immunophenotyping Assessment in a COVID-19 Cohort (IMPACC) Network is detailed in
40 Supplementary Materials

41 ²²Department of Microbiology & Immunology, University of California San Francisco, San
42 Francisco, CA

43 ²³Parker Institute for Cancer Immunotherapy, University of California San Francisco, San
44 Francisco, CA

45 ²⁴Medical Service, San Francisco VA Health Care System, San Francisco, CA

46 [#]Corresponding author

47

48

49 **Supplementary Materials**

50 **IMPACC Network**

51 National Institute of Allergy and Infectious Diseases, National Institute of Health, Bethesda, MD
52 20814, USA: Patrice M. Becker, Alison D. Augustine, Steven M. Holland, Lindsey B. Rosen,
53 Serena Lee, Tatyana Vaysman

54 Clinical and Data Coordinating Center (CDCC), Precision Vaccines Program, Boston Children's
55 Hospital, Harvard Medical School, Boston, MA 02115, USA: Al Ozonoff, Joann Diray-Arce, Jing
56 Chen, Alvin T. Kho, Carly E. Milliren, Annmarie Hoch, Ana C. Chang, Kerry McEnaney, Caitlin
57 Syphurs, Brenda Barton, Claudia Lentucci, Maimouna D. Murphy, Mehmet Saluvan, Tanzia
58 Shaheen, Shanshan Liu, Marisa Albert, Arash Nemati Hayati, Robert Bryant, James Abraham,
59 Mitchell Cooney, Meagan Karoly

60 Benaroya Research Institute, University of Washington, Seattle, WA 98101, USA: Matthew C.
61 Altman, Naresh Doni Jayavelu, Scott Presnell, Bernard Kohr, Tomasz Jancsyk, Azlann Arnett

62 La Jolla Institute for Immunology, La Jolla, CA 92037, USA: Bjoern Peters, James A. Overton,
63 Randi Vita, Kerstin Westendorf

64 Knocean Inc. Toronto, ON M6P 2T3, Canada: James A. Overton

65 Precision Vaccines Program, Boston Children's Hospital, Harvard Medical School, Boston, MA
66 02115, USA: Ofer Levy, Hanno Steen, Patrick van Zalm, Benoit Fatou, Kinga K. Smolen, Arthur
67 Viode, Simon van Haren, Meenakshi Jha, David Stevenson, Sanya Thomas, Boryana Petrova,
68 Naama Kanarek

69 Brigham and Women's Hospital, Harvard Medical School, Boston, MA 02115, USA: Lindsey R.
70 Baden, Kevin Mendez, Jessica Lasky-Su, Alexandra Tong, Rebecca Rooks, Michael Desjardins,

71 Amy C. Sherman, Stephen R. Walsh, Xhoi Mitre, Jessica Cauley, Xiaofang Li, Bethany Evans,
 72 Christina Montesano, Jose Humberto Licon, Jonathan Krauss, Nicholas C. Issa, Jun Bai Park
 73 Chang, Natalie Izaguirre

 74 Metabolon Inc, Morrisville, NC 27560, USA: Scott R. Hutton, Greg Michelotti, Kari Wong

 75 Prevention of Organ Failure (PROOF) Centre of Excellence, University of British Columbia,
 76 Vancouver, BC V6T 1Z3, Canada: Scott J. Tebbutt, Casey P. Shannon

 77 Case Western Reserve University and University Hospitals of Cleveland, Cleveland, OH 44106,
 78 USA: Rafick-Pierre Sekaly, Slim Fourati, Grace A. McComsey, Paul Harris, Scott Sieg, George
 79 Yendewa, Mary Consolo, Heather Tribout, Susan Pereira Ribeiro

 80 Drexel University, Tower Health Hospital, Philadelphia, PA 19104, USA: Charles B. Cairns, Elias
 81 K. Haddad, Michele A. Kutzler, Mariana Bernui, Gina Cusimano, Jennifer Connors, Kyra
 82 Woloszczuk, David Joyner, Carolyn Edwards, Edward Lee, Edward Lin, Nataliya Melnyk, Debra
 83 L. Powell, James N. Kim, I. Michael Goonewardene, Brent Simmons, Cecilia M. Smith, Mark
 84 Martens, Brett Croen, Nicholas C. Semenza, Mathew R. Bell, Sara Furukawa, Renee McLin,
 85 George P. Tegos, Brandon Rogowski, Nathan Mege, Kristen Ulring, Pam Schearer, Judie Sheidy,
 86 Crystal Nagle

 87 MyOwnMed Inc., Bethesda, MD 20817, USA: Vicki Seyfert-Margolis

 88 Emory School of Medicine, Atlanta, GA 30322, USA: Nadine Rouphael, Steven E. Bosinger, Arun
 89 K. Boddapati, Greg K. Tharp, Kathryn L. Pellegrini, Brandi Johnson, Bernadine Panganiban,
 90 Christopher Huerta, Evan J. Anderson, Hady Samaha, Jonathan E. Sevransky, Laurel Bristow,
 91 Elizabeth Beagle, David Cowan, Sydney Hamilton, Thomas Hodder, Amer Bechnak, Andrew
 92 Cheng, Aneesh Mehta, Caroline R. Ciric, Christine Spainhour, Erin Carter, Erin M. Scherer, Jacob

93 Usher, Kieffer Hellmeister, Laila Hussaini, Lauren Hewitt, Nina McNair, Susan Pereira Ribeiro,
 94 Sonia Wimalasena

95 Icahn School of Medicine at Mount Sinai, New York, NY 10029, USA: Ana Fernandez-Sesma,
 96 Viviana Simon, Florian Krammer, Harm Van Bakel, Seunghee Kim-Schulze, Ana Silvia Gonzalez-
 97 Reiche, Jingjing Qi, Brian Lee, Juan Manuel Carreño, Gagandeep Singh, Ariel Raskin, Johnstone
 98 Tcheou, Zain Khalil, Adriana van de Guchte, Keith Farrugia, Zenab Khan, Geoffrey Kelly, Komal
 99 Srivastava, Lily Q. Eaker, Maria C. Bermúdez-González, Lubbertus C.F. Mulder, Katherine F.
 100 Beach, Miti Saksena, Deena Altman, Erna Kojic, Levy A. Sominsky, Arman Azad, Dominika Bielak,
 101 Hisaaki Kawabata, Temima Yellin, Miriam Fried, Leeba Sullivan, Sara Morris, Giulio Kleiner,
 102 Daniel Stadlbauer, Jayeeta Dutta, Hui Xie, Manishkumar Patel, Kai Nie, Brian Monahan

103 Immunai Inc., New York, NY 10016, USA: Adeeb Rahman

104 Oregon Health & Science University, Portland, OR 97239, USA: William B. Messer, Catherine L.
 105 Hough, Sarah A.R. Siegel, Peter E. Sullivan, Zhengchun Lu, Amanda E. Brunton, Matthew Strand,
 106 Zoe L. Lyski, Felicity J. Coulter, Courtney Micheletti

107 Stanford University School of Medicine, Palo Alto, CA 94305, USA: Holden Maecker, Bali
 108 Pulendran, Kari C. Nadeau, Yael Rosenberg-Hasson, Michael Leipold, Natalia Sigal, Angela
 109 Rogers, Andrea Fernandes, Monali Manohar, Evan Do, Iris Chang, Alexandra S. Lee, Catherine
 110 Blish, Henna Naz Din, Jonasel Roque, Linda N. Geng, Maja Artandi, Mark M. Davis, Neera Ahuja,
 111 Samuel S. Yang, Sharon Chinthrajah, Thomas Hagan, Tyson H. Holmes, Koji Abe

112 David Geffen School of Medicine at the University of California Los Angeles, Los Angeles CA
 113 90095, USA: Elaine F. Reed, Joanna Schaenman, Ramin Salehi-Rad, Adreanne M. Rivera, Harry
 114 Pickering, Subha Sen, David Elashoff, Dawn C. Ward, Jenny Brook, Estefania Ramires-Sanchez,
 115 Megan Llamas, Claudia Perdomo, Clara E. Magyar, Jennifer Fulcher

116 University of California San Francisco, San Francisco, CA 94115, USA: David J. Erle, Carolyn S.
117 Calfee, Carolyn M. Hendrickson, Kirsten N. Kangelaris, Viet Nguyen, Deanna Lee, Suzanna
118 Chak, Rajani Ghale, Ana Gonzalez, Alejandra Jauregui, Carolyn Leroux, Luz Torres Altamirano,
119 Ahmad Sadeed Rashid, Andrew Willmore, Prescott G. Woodruff, Matthew F. Krummel, Sidney
120 Carrillo, Alyssa Ward, Charles R. Langelier, Ravi Patel, Michael Wilson, Ravi Dandekar, Bonny
121 Alvarenga, Jayant Rajan, Walter Eckalbar, Andrew W. Schroeder, Gabriela K. Fragiadakis,
122 Alexandra Tsitsiklis, Eran Mick, Yanedth Sanchez Guerrero, Christina Love, Lenka Maliskova,
123 Michael Adkisson, Aleksandra Leligdowicz, Alexander Beagle, Arjun Rao, Austin Sigman, Bushra
124 Samad, Cindy Curiel, Cole Shaw, Gayelan Tietje-Ulrich, Jeff Milush, Jonathan Singer, Joshua J.
125 Vasquez, Kevin Tang, Legna Betancourt, Lekshmi Santhosh, Logan Pierce, Maria Tecero Paz,
126 Michael Matthay, Neeta Thakur, Nicklaus Rodriguez, Nicole Sutter, Norman Jones, Pratik Sinha,
127 Priya Prasad, Raphael Lota, Sadeed Rashid, Saurabh Asthana, Sharvari Bhide, Tasha Lea,
128 Yumiko Abe-Jones

129 Yale School of Medicine, New Haven, CT 06510, USA: David A. Hafler, Ruth R. Montgomery,
130 Albert C. Shaw, Steven H. Kleinstein, Jeremy P. Gygi, Dylan Duchen, Shrikant Pawar, Anna
131 Konstorum, Ernie Chen, Chris Cotsapas, Xiaomei Wang, Charles Dela Cruz, Akiko Iwasaki,
132 Subhasis Mohanty, Allison Nelson, Yujiao Zhao, Shelli Farhadian, Hiromitsu Asashima, Omkar
133 Chaudhary, Andreas Coppi, John Fournier, M. Catherine Muenker, Khadir Raddassi, Michael
134 Rainone, William Ruff, Syim Salahuddin, Wade L. Shulz, Pavithra Vijayakumar, Haowei Wang,
135 Esio Wunder Jr., H. Patrick Young, Albert I. Ko, Gisela Gabernet

136 Yale School of Public Health, New Haven, CT 06510, USA: Denise Esserman, Leying Guan,
137 Anderson Brito, Jessica Rothman, Nathan D. Grubaugh, Kexin Wang, Leqi Xu

138 Baylor College of Medicine and the Center for Translational Research on Inflammatory Diseases,
139 Houston, TX 77030, USA: David B. Corry, Farrah Kheradmand, Li-Zhen Song, Ebony Nelson

140 Oklahoma University Health Sciences Center, Oklahoma City, OK 73104, USA: Jordan P. Metcalf,
 141 Nelson I. Agudelo Higueta, Lauren A. Sinko, J. Leland Booth, Douglas A. Drevets, Brent R. Brown
 142 University of Arizona, Tucson AZ 85721, USA: Monica Kraft, Chris Bime, Jarrod Mosier, Heidi
 143 Erickson, Ron Schunk, Hiroki Kimura, Michelle Conway, Dave Francisco, Allyson Molzahn,
 144 Connie Cathleen Wilson, Ron Schunk, Trina Hughes, Bianca Sierra
 145 University of Florida, Gainesville, FL 32611, USA: Mark A. Atkinson, Scott C. Brakenridge, Ricardo
 146 F. Ungaro, Brittany Roth Manning, Lyle Moldawer
 147 University of Florida, Jacksonville, FL 32218, USA: Jordan Oberhaus, Faheem W. Guirgis
 148 University of South Florida, Tampa FL 33620, USA: Brittney Borresen, Matthew L. Anderson
 149 The University of Texas at Austin, Austin, TX 78712, USA: Lauren I. R. Ehrlich, Esther Melamed,
 150 Cole Maguire, Dennis Wylie, Justin F. Rousseau, Kerin C. Hurley, Janelle N. Geltman, Nadia
 151 Siles, Jacob E. Rogers, Pablo Guaman Tipan
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Supplementary Data File 1. Additional patient clinical characteristics and comorbidities

	GG (N=560)	GA (N=426)	AA (N=50)	P- value
	234	184	20	
Abnormal CRP (≥ 10 mg/L)	(41.8%)	(43.2%)	(40.0%)	0.863
	281	213	27	
Abnormal D-dimer (>0.5 mg/L)	(50.2%)	(50.0%)	(54.0%)	0.794
			5	
Abnormal Troponin (>0.4 ng/mL)	43 (7.7%)	36 (8.5%)	(10.0%)	0.517
	96	64		
Abnormal Creatinine (≥ 1.5 mg/dL)	(17.1%)	(15.0%)	3 (6.0%)	0.065
	389	287	37	
Infiltrate on chest X-Ray	(74.5%)	(70.2%)	(77.1%)	0.408
	65	75	12	
Asthma	(11.7%)	(17.6%)	(24.0%)	0.001
Pulmonary disease (excludes	103	94	15	
asthma)	(18.4%)	(22.1%)	(30.0%)	0.033
	81	62	12	
Chronic kidney disease	(14.5%)	(14.6%)	(24.0%)	0.280

	135	130	14	
Chronic cardiac disease	(24.1%)	(30.5%)	(28.0%)	0.052

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170 **Supplementary Data File 2. PBMC and upper airway GO term enrichment analysis.**

171 GO term enrichment analysis was performed on genes significantly upregulated (Cluster =
172 “PBMC-Up”) or downregulated (Cluster = “PBMC-Down”) in PBMC of MICB^{G406A} participants and
173 genes significantly upregulated (Cluster = “Nasal-Up”) or downregulated (Cluster = “Nasal-Down”)
174 in the upper airway. of MICB^{G406A} participants.

175

ONTOL				Gene	BgRati	pvalu	p.adj	qvalu	Co
Cluster	OGY	ID	Description	Ratio	o	e	ust	e	unt
PBMC-		GO:004			164/1	0.000	0.059	0.050	
Up	MF	6943	carboxylic acid transmembrane transporter activity	4/46	8496	728	912	922	4
PBMC-		GO:000			165/1	0.000	0.059	0.050	
Up	MF	5342	organic acid transmembrane transporter activity	4/46	8496	744	912	922	4
PBMC-		GO:000			242/1	0.003	0.162	0.138	
Up	MF	8514	organic anion transmembrane transporter activity	4/46	8496	032	72	304	4
PBMC-		GO:014			147/1	0.005	0.230	0.195	
Up	MF	0375	immune receptor activity	3/46	8496	816	192	652	3
PBMC-		GO:004			74/18	0.014	0.230	0.195	
Up	MF	2379	chemokine receptor binding	2/46	496	588	192	652	2
PBMC-		GO:001			85/18	0.018	0.230	0.195	
Up	MF	5171	amino acid transmembrane transporter activity	2/46	496	952	192	652	2
PBMC-		GO:000			96/18	0.023	0.230	0.195	
Up	MF	4896	cytokine receptor activity	2/46	496	795	192	652	2

PBMC-		GO:001			10/18	0.024	0.230	0.195	
Up	MF	5187	glycine transmembrane transporter activity	1/46	496	6	192	652	1
PBMC-		GO:001			10/18	0.024	0.230	0.195	
Up	MF	5658	branched-chain amino acid transmembrane transporter activity	1/46	496	6	192	652	1
PBMC-		GO:001			10/18	0.024	0.230	0.195	
Up	MF	9531	oxalate transmembrane transporter activity	1/46	496	6	192	652	1
PBMC-		GO:004			10/18	0.024	0.230	0.195	
Up	MF	5294	alpha-catenin binding	1/46	496	6	192	652	1
PBMC-		GO:005			10/18	0.024	0.230	0.195	
Up	MF	1864	histone H3K36 demethylase activity	1/46	496	6	192	652	1
PBMC-		GO:000			11/18	0.027	0.230	0.195	
Up	MF	8271	secondary active sulfate transmembrane transporter activity	1/46	496	027	192	652	1
PBMC-		GO:199			11/18	0.027	0.230	0.195	
Up	MF	0459	transferrin receptor binding	1/46	496	027	192	652	1
PBMC-		GO:000			12/18	0.029	0.230	0.195	
Up	MF	4875	complement receptor activity	1/46	496	448	192	652	1

PBMC-		GO:000			13/18	0.031	0.230	0.195	
Up	MF	9982	pseudouridine synthase activity	1/46	496	863	192	652	1
PBMC-		GO:001			494/1	0.033	0.230	0.195	
Up	MF	6755	aminoacyltransferase activity	4/46	8496	942	192	652	4
PBMC-		GO:003			14/18	0.034	0.230	0.195	
Up	MF	2454	histone H3K9 demethylase activity	1/46	496	273	192	652	1
PBMC-		GO:003			119/1	0.035	0.230	0.195	
Up	MF	2182	ubiquitin-like protein binding	2/46	8496	346	192	652	2
PBMC-		GO:000			15/18	0.036	0.230	0.195	
Up	MF	5523	tropomyosin binding	1/46	496	676	192	652	1
PBMC-		GO:001			15/18	0.036	0.230	0.195	
Up	MF	6004	phospholipase activator activity	1/46	496	676	192	652	1
PBMC-		GO:003			15/18	0.036	0.230	0.195	
Up	MF	1005	filamin binding	1/46	496	676	192	652	1
PBMC-		GO:008	voltage-gated potassium channel activity involved in cardiac		15/18	0.036	0.230	0.195	
Up	MF	6008	muscle cell action potential repolarization	1/46	496	676	192	652	1

PBMC-		GO:199			123/1	0.037	0.230	0.195	
Up	MF	0782	protein tyrosine kinase binding	2/46	8496	538	192	652	2
PBMC-		GO:001			16/18	0.039	0.230	0.195	
Up	MF	5116	sulfate transmembrane transporter activity	1/46	496	074	192	652	1
PBMC-		GO:002			16/18	0.039	0.230	0.195	
Up	MF	2858	alanine transmembrane transporter activity	1/46	496	074	192	652	1
PBMC-		GO:000			17/18	0.041	0.230	0.195	
Up	MF	8242	omega peptidase activity	1/46	496	466	192	652	1
PBMC-		GO:014			131/1	0.042	0.230	0.195	
Up	MF	0101	catalytic activity, acting on a tRNA	2/46	8496	074	192	652	2
PBMC-		GO:004			18/18	0.043	0.230	0.195	
Up	MF	5236	CXCR chemokine receptor binding	1/46	496	852	192	652	1
PBMC-		GO:006			19/18	0.046	0.230	0.195	
Up	MF	0229	lipase activator activity	1/46	496	233	192	652	1
PBMC-		GO:007			20/18	0.048	0.230	0.195	
Up	MF	0003	threonine-type peptidase activity	1/46	496	607	192	652	1

PBMC-		GO:003			22/18	0.053	0.230	0.195	
Up	MF	3038	bitter taste receptor activity	1/46	496	339	192	652	1
PBMC-		GO:003			22/18	0.053	0.230	0.195	
Up	MF	3691	sialic acid binding	1/46	496	339	192	652	1
PBMC-		GO:006			349/1	0.055	0.230	0.195	
Up	MF	1630	ubiquitin protein ligase activity	3/46	8496	749	192	652	3
PBMC-		GO:001			24/18	0.058	0.230	0.195	
Up	MF	5295	solute:proton symporter activity	1/46	496	047	192	652	1
PBMC-		GO:003			24/18	0.058	0.230	0.195	
Up	MF	5035	histone acetyltransferase binding	1/46	496	047	192	652	1
PBMC-		GO:000			26/18	0.062	0.230	0.195	
Up	MF	1637	G protein-coupled chemoattractant receptor activity	1/46	496	733	192	652	1
PBMC-		GO:000			26/18	0.062	0.230	0.195	
Up	MF	4950	chemokine receptor activity	1/46	496	733	192	652	1
PBMC-		GO:009			26/18	0.062	0.230	0.195	
Up	MF	7602	cullin family protein binding	1/46	496	733	192	652	1

PBMC-		GO:006			367/1	0.062	0.230	0.195	
Up	MF	1659	ubiquitin-like protein ligase activity	3/46	8496	909	192	652	3
PBMC-		GO:000			27/18	0.065	0.230	0.195	
Up	MF	5242	inward rectifier potassium channel activity	1/46	496	067	192	652	1
PBMC-		GO:001			27/18	0.065	0.230	0.195	
Up	MF	6866	intramolecular transferase activity	1/46	496	067	192	652	1
PBMC-		GO:000			28/18	0.067	0.230	0.195	
Up	MF	5452	solute:inorganic anion antiporter activity	1/46	496	396	192	652	1
PBMC-		GO:000			28/18	0.067	0.230	0.195	
Up	MF	8527	taste receptor activity	1/46	496	396	192	652	1
PBMC-		GO:014			28/18	0.067	0.230	0.195	
Up	MF	1052	histone H3 demethylase activity	1/46	496	396	192	652	1
PBMC-		GO:000			29/18	0.069	0.230	0.195	
Up	MF	5416	amino acid:monoatomic cation symporter activity	1/46	496	719	192	652	1
PBMC-		GO:003			29/18	0.069	0.230	0.195	
Up	MF	3612	receptor serine/threonine kinase binding	1/46	496	719	192	652	1

PBMC-		GO:001			30/18	0.072	0.230	0.195	
Up	MF	5106	bicarbonate transmembrane transporter activity	1/46	496	036	192	652	1
PBMC-		GO:003			30/18	0.072	0.230	0.195	
Up	MF	2452	histone demethylase activity	1/46	496	036	192	652	1
PBMC-		GO:014			30/18	0.072	0.230	0.195	
Up	MF	0457	protein demethylase activity	1/46	496	036	192	652	1
PBMC-		GO:000			31/18	0.074	0.230	0.195	
Up	MF	5310	dicarboxylic acid transmembrane transporter activity	1/46	496	348	192	652	1
PBMC-		GO:003			31/18	0.074	0.230	0.195	
Up	MF	1624	ubiquitin conjugating enzyme binding	1/46	496	348	192	652	1
PBMC-		GO:000		58/38	156/1	3.56E	1.04E	1.02E	
Down	BP	2181	cytoplasmic translation	1	8870	-58	-54	-54	58
PBMC-		GO:004		41/38	325/1	4.70E	6.90E	6.77E	
Down	BP	2254	ribosome biogenesis	1	8870	-21	-18	-18	41
PBMC-		GO:004		18/38	76/18	8.98E	8.78E	8.61E	
Down	BP	2273	ribosomal large subunit biogenesis	1	870	-15	-12	-12	18

PBMC-		GO:004		20/38	104/1	2.10E	1.54E	1.51E	
Down	BP	2274	ribosomal small subunit biogenesis	1	8870	-14	-11	-11	20
PBMC-		GO:007		26/38	243/1	4.47E	2.44E	2.40E	
Down	BP	1826	protein-RNA complex organization	1	8870	-12	-09	-09	26
PBMC-		GO:001		27/38	264/1	5.00E	2.44E	2.40E	
Down	BP	6072	rRNA metabolic process	1	8870	-12	-09	-09	27
PBMC-		GO:002		25/38	235/1	1.32E	5.55E	5.44E	
Down	BP	2618	protein-RNA complex assembly	1	8870	-11	-09	-09	25
PBMC-		GO:004		14/38	64/18	2.83E	1.04E	1.02E	
Down	BP	2255	ribosome assembly	1	870	-11	-08	-08	14
PBMC-		GO:000		24/38	225/1	3.24E	1.06E	1.04E	
Down	BP	6364	rRNA processing	1	8870	-11	-08	-08	24
PBMC-		GO:000			26/18	2.92E	8.56E	8.39E	
Down	BP	0027	ribosomal large subunit assembly	8/381	870	-08	-06	-06	8
PBMC-		GO:003		28/38	439/1	9.10E	2.43E	2.38E	
Down	BP	4470	ncRNA processing	1	8870	-08	-05	-05	28

PBMC-		GO:000			19/18	1.41E	0.000	0.000	
Down	BP	0028	ribosomal small subunit assembly	6/381	870	-06	346	339	6
PBMC-		GO:190			30/18	2.57E	0.005	0.005	
Down	BP	1798	positive regulation of signal transduction by p53 class mediator	6/381	870	-05	787	678	6
PBMC-		GO:014		22/38	408/1	3.14E	0.006	0.006	
Down	BP	0694	non-membrane-bounded organelle assembly	1	8870	-05	247	13	22
PBMC-		GO:000		11/38	120/1	3.20E	0.006	0.006	
Down	BP	7006	mitochondrial membrane organization	1	8870	-05	247	13	11
PBMC-		GO:000		19/38	336/1	5.78E	0.010	0.010	
Down	BP	0375	RNA splicing, via transesterification reactions	1	8870	-05	591	391	19
PBMC-		GO:000	RNA splicing, via transesterification reactions with bulged	18/38	332/1	0.000	0.024	0.024	
Down	BP	0377	adenosine as nucleophile	1	8870	153	903	435	18
PBMC-		GO:000		18/38	332/1	0.000	0.024	0.024	
Down	BP	0398	mRNA splicing, via spliceosome	1	8870	153	903	435	18
PBMC-		GO:003		23/38	496/1	0.000	0.031	0.030	
Down	BP	4655	nucleobase-containing compound catabolic process	1	8870	203	311	722	23

PBMC-		GO:000		10/38	128/1	0.000	0.040	0.039	
Down	BP	0956	nuclear-transcribed mRNA catabolic process	1	8870	274	232	475	10
PBMC-		GO:000		22/38	478/1	0.000	0.042	0.041	
Down	BP	8380	RNA splicing	1	8870	308	518	718	22
PBMC-		GO:190			107/1	0.000	0.042	0.041	
Down	BP	1796	regulation of signal transduction by p53 class mediator	9/381	8870	319	518	718	9
PBMC-		GO:000		12/38	190/1	0.000	0.063	0.062	
Down	BP	6839	mitochondrial transport	1	8870	5	73	531	12
PBMC-		GO:190	regulation of intrinsic apoptotic signaling pathway by p53 class		35/18	0.000	0.078	0.077	
Down	BP	2253	mediator	5/381	870	644	728	247	5
PBMC-		GO:190		15/38	284/1	0.000	0.081	0.080	
Down	BP	1873	regulation of post-translational protein modification	1	8870	699	948	406	15
PBMC-		GO:003			10/18	0.000	0.099	0.097	
Down	BP	1125	rRNA 3'-end processing	3/381	870	882	445	574	3
PBMC-		GO:005			39/18	0.001	0.116	0.114	
Down	BP	1438	regulation of ubiquitin-protein transferase activity	5/381	870	07	187	001	5

PBMC-		GO:000			24/18	0.001	0.131	0.128	
Down	BP	9219	pyrimidine deoxyribonucleotide metabolic process	4/381	870	262	424	952	4
PBMC-		GO:000		17/38	367/1	0.001	0.131	0.128	
Down	BP	6401	RNA catabolic process	1	8870	358	424	952	17
PBMC-		GO:190	regulation of protein modification by small protein conjugation	13/38	243/1	0.001	0.131	0.128	
Down	BP	3320	or removal	1	8870	389	424	952	13
PBMC-		GO:004			61/18	0.001	0.131	0.128	
Down	BP	6902	regulation of mitochondrial membrane permeability	6/381	870	419	424	952	6
PBMC-		GO:000			25/18	0.001	0.131	0.128	
Down	BP	9147	pyrimidine nucleoside triphosphate metabolic process	4/381	870	479	424	952	4
PBMC-		GO:000	pyrimidine deoxyribonucleoside monophosphate metabolic		12/18	0.001	0.131	0.128	
Down	BP	9176	process	3/381	870	569	424	952	3
PBMC-		GO:003			12/18	0.001	0.131	0.128	
Down	BP	6444	calcium import into the mitochondrion	3/381	870	569	424	952	3
PBMC-		GO:007			12/18	0.001	0.131	0.128	
Down	BP	1236	cellular response to antibiotic	3/381	870	569	424	952	3

PBMC-		GO:190	regulation of mitochondrial outer membrane permeabilization		26/18	0.001	0.140	0.137	
Down	BP	1028	involved in apoptotic signaling pathway	4/381	870	72	112	476	4
PBMC-		GO:200			64/18	0.001	0.144	0.141	
Down	BP	1244	positive regulation of intrinsic apoptotic signaling pathway	6/381	870	821	303	588	6
PBMC-		GO:190			87/18	0.001	0.146	0.143	
Down	BP	2369	negative regulation of RNA catabolic process	7/381	870	894	13	381	7
PBMC-		GO:200	regulation of nuclear-transcribed mRNA catabolic process,		13/18	0.002	0.151	0.148	
Down	BP	0622	nonsense-mediated decay	3/381	870	009	045	204	3
PBMC-		GO:000			28/18	0.002	0.167	0.164	
Down	BP	0470	maturation of LSU-rRNA	4/381	870	282	306	159	4
PBMC-		GO:002		55/40	118/1	9.07E	3.84E	3.42E	
Down	CC	2626	cytosolic ribosome	2	9886	-62	-59	-59	55
PBMC-		GO:004		63/40	188/1	1.01E	2.15E	1.91E	
Down	CC	4391	ribosomal subunit	2	9886	-59	-57	-57	63
PBMC-		GO:000		64/40	246/1	9.23E	1.30E	1.16E	
Down	CC	5840	ribosome	2	9886	-53	-50	-50	64

PBMC-		GO:002		34/40	60/19	2.64E	2.79E	2.48E	
Down	CC	2625	cytosolic large ribosomal subunit	2	886	-42	-40	-40	34
PBMC-		GO:001		39/40	117/1	5.43E	4.61E	4.09E	
Down	CC	5934	large ribosomal subunit	2	9886	-37	-35	-35	39
PBMC-		GO:002		22/40	41/19	5.15E	3.64E	3.24E	
Down	CC	2627	cytosolic small ribosomal subunit	2	886	-27	-25	-25	22
PBMC-		GO:001		25/40	75/19	4.35E	2.63E	2.34E	
Down	CC	5935	small ribosomal subunit	2	886	-24	-22	-22	25
PBMC-		GO:004		15/40	31/19	6.65E	3.52E	3.13E	
Down	CC	2788	polysomal ribosome	2	886	-18	-16	-16	15
PBMC-		GO:000		19/40	67/19	4.18E	1.97E	1.75E	
Down	CC	5844	polysome	2	886	-17	-15	-15	19
PBMC-		GO:003		16/40	74/19	1.33E	5.66E	5.03E	
Down	CC	2040	small-subunit processome	2	886	-12	-11	-11	16
PBMC-		GO:003		17/40	109/1	6.71E	2.59E	2.30E	
Down	CC	0684	preribosome	2	9886	-11	-09	-09	17

PBMC-		GO:000		26/40	421/1	5.15E	1.82E	1.62E	
Down	CC	5925	focal adhesion	2	9886	-07	-05	-05	26
PBMC-		GO:003		26/40	431/1	8.03E	2.62E	2.33E	
Down	CC	0055	cell-substrate junction	2	9886	-07	-05	-05	26
PBMC-		GO:000			56/19	1.69E	5.11E	4.54E	
Down	CC	5791	rough endoplasmic reticulum	9/402	886	-06	-05	-05	9
PBMC-		GO:009		20/40	300/1	3.45E	9.57E	8.51E	
Down	CC	8798	mitochondrial protein-containing complex	2	9886	-06	-05	-05	20
PBMC-		GO:000		27/40	497/1	3.61E	9.57E	8.51E	
Down	CC	5743	mitochondrial inner membrane	2	9886	-06	-05	-05	27
PBMC-		GO:009		10/40	96/19	2.45E	0.000	0.000	
Down	CC	7525	spliceosomal snRNP complex	2	886	-05	603	536	10
PBMC-		GO:012		11/40	117/1	2.56E	0.000	0.000	
Down	CC	0114	Sm-like protein family complex	2	9886	-05	603	536	11
PBMC-		GO:003		10/40	106/1	5.78E	0.001	0.001	
Down	CC	0532	small nuclear ribonucleoprotein complex	2	9886	-05	29	147	10

PBMC-		GO:000		11/40	150/1	0.000	0.004	0.004	
Down	CC	1650	fibrillar center	2	9886	243	986	431	11
PBMC-		GO:009			16/19	0.000	0.004	0.004	
Down	CC	8554	cytoplasmic side of endoplasmic reticulum membrane	4/402	886	247	986	431	4
PBMC-		GO:004			45/19	0.000	0.005	0.004	
Down	CC	6540	U4/U6 x U5 tri-snRNP complex	6/402	886	275	182	606	6
PBMC-		GO:000		13/40	205/1	0.000	0.005	0.004	
Down	CC	5681	spliceosomal complex	2	9886	288	182	606	13
PBMC-		GO:009			46/19	0.000	0.005	0.004	
Down	CC	7526	spliceosomal tri-snRNP complex	6/402	886	311	182	606	6
PBMC-		GO:007			17/19	0.000	0.005	0.004	
Down	CC	1004	U2-type prespliceosome	4/402	886	318	182	606	4
PBMC-		GO:007			17/19	0.000	0.005	0.004	
Down	CC	1010	prespliceosome	4/402	886	318	182	606	4
PBMC-		GO:000			89/19	0.000	0.006	0.005	
Down	CC	0313	organellar ribosome	8/402	886	441	675	933	8

PBMC-		GO:000			89/19	0.000	0.006	0.005	
Down	CC	5761	mitochondrial ribosome	8/402	886	441	675	933	8
PBMC-		GO:000			92/19	0.000	0.008	0.007	
Down	CC	5684	U2-type spliceosomal complex	8/402	886	551	061	164	8
PBMC-		GO:003			24/19	0.001	0.017	0.015	
Down	CC	0867	rough endoplasmic reticulum membrane	4/402	886	269	931	937	4
PBMC-		GO:010			13/19	0.002	0.027	0.024	
Down	CC	6068	SUMO ligase complex	3/402	886	017	584	516	3
PBMC-		GO:001			18/40	417/1	0.002	0.029	0.025
Down	CC	6607	nuclear speck	2	9886	205	219	969	18
PBMC-		GO:000			16/19	0.003	0.048	0.043	
Down	CC	0930	gamma-tubulin complex	3/402	886	775	505	11	3
PBMC-		GO:009			158/1	0.004	0.060	0.053	
Down	CC	8800	inner mitochondrial membrane protein complex	9/402	9886	929	127	439	9
PBMC-		GO:000			19/40	487/1	0.005	0.060	0.053
Down	CC	5759	mitochondrial matrix	2	9886	075	127	439	19

PBMC-		GO:001		14/40	315/1	0.005	0.060	0.053	
Down	CC	4069	postsynaptic density	2	9886	105	127	439	14
PBMC-		GO:000			56/19	0.005	0.060	0.053	
Down	CC	0315	organellar large ribosomal subunit	5/402	886	402	272	569	5
PBMC-		GO:000			56/19	0.005	0.060	0.053	
Down	CC	5762	mitochondrial large ribosomal subunit	5/402	886	402	272	569	5
PBMC-		GO:004			19/19	0.006	0.067	0.060	
Down	CC	2575	DNA polymerase complex	3/402	886	246	904	352	3
PBMC-		GO:003		14/40	331/1	0.007	0.082	0.073	
Down	CC	2279	asymmetric synapse	2	9886	774	41	244	14
PBMC-		GO:190			146/1	0.009	0.101	0.089	
Down	CC	4949	ATPase complex	8/402	9886	785	193	938	8
PBMC-		GO:007			92/19	0.010	0.110	0.097	
Down	CC	0603	SWI/SNF superfamily-type complex	6/402	886	91	142	892	6
PBMC-		GO:009		14/40	346/1	0.011	0.110	0.098	
Down	CC	9572	postsynaptic specialization	2	9886	187	304	036	14

PBMC-		GO:000		12/40	281/1	0.012	0.118	0.105	
Down	CC	0793	condensed chromosome	2	9886	292	449	275	12
PBMC-		GO:190			124/1	0.013	0.123	0.109	
Down	CC	4813	ficolin-1-rich granule lumen	7/402	9886	097	4	675	7
PBMC-		GO:009		14/40	362/1	0.016	0.147	0.131	
Down	CC	8984	neuron to neuron synapse	2	9886	012	591	176	14
PBMC-		GO:000			11/19	0.019	0.175	0.156	
Down	CC	5688	U6 snRNP	2/402	886	872	536	013	2
PBMC-		GO:003			11/19	0.019	0.175	0.156	
Down	CC	5145	exon-exon junction complex	2/402	886	872	536	013	2
PBMC-		GO:000			79/19	0.021	0.186	0.165	
Down	CC	5758	mitochondrial intermembrane space	5/402	886	928	497	754	5
PBMC-		GO:003		11/40	270/1	0.021	0.186	0.165	
Down	CC	5770	ribonucleoprotein granule	2	9886	993	497	754	11
PBMC-		GO:004			12/19	0.023	0.195	0.173	
Down	CC	2405	nuclear inclusion body	2/402	886	531	634	875	2

PBMC-		GO:000			81/19	0.024	0.196	0.174	
Down	CC	5876	spindle microtubule		5/402	886	136	805	916 5
PBMC-		GO:000			32/19	0.026	0.207	0.184	
Down	CC	0314	organellar small ribosomal subunit		3/402	886	367	032	005 3
PBMC-		GO:000			32/19	0.026	0.207	0.184	
Down	CC	5763	mitochondrial small ribosomal subunit		3/402	886	367	032	005 3
PBMC-		GO:004			13/19	0.027	0.211	0.188	
Down	CC	3240	Fanconi anaemia nuclear complex		2/402	886	443	562	032 2
PBMC-		GO:000			33/19	0.028	0.216	0.192	
Down	CC	5685	U1 snRNP		3/402	886	58	395	327 3
PBMC-		GO:000			61/40	176/1	8.60E	4.35E	4.21E
Down	MF	3735	structural constituent of ribosome		5	8496	-57	-54	-54 61
PBMC-		GO:001			11/40	66/18	1.77E	4.47E	4.32E
Down	MF	9843	rRNA binding		5	496	-07	-05	-05 11
PBMC-		GO:005			11/18	2.04E	0.000	0.000	
Down	MF	5105	ubiquitin-protein transferase inhibitor activity		5/405	496	-06	343	332 5

PBMC-		GO:005			27/18	2.13E	0.002	0.002	
Down	MF	5106	ubiquitin-protein transferase regulator activity	6/405	496	-05	693	605	6
PBMC-		GO:004			25/18	0.000	0.018	0.017	
Down	MF	8027	mRNA 5'-UTR binding	5/405	496	182	391	791	5
PBMC-		GO:009			11/18	0.001	0.127	0.123	
Down	MF	7371	MDM2/MDM4 family protein binding	3/405	496	509	223	068	3
PBMC-		GO:003			13/18	0.002	0.149	0.144	
Down	MF	1386	protein tag activity	3/405	496	531	035	167	3
PBMC-		GO:014			13/18	0.002	0.149	0.144	
Down	MF	1047	molecular tag activity	3/405	496	531	035	167	3
PBMC-		GO:005			133/1	0.002	0.149	0.144	
Down	MF	1087	protein-folding chaperone binding	9/405	8496	651	035	167	9
PBMC-		GO:004			16/40	334/1	0.002	0.150	0.145
Down	MF	5296	cadherin binding	5	8496	975	542	625	16
Nasal-		GO:003			83/18	4.52E	0.033	0.029	
Up	BP	1424	keratinization	4/45	870	-05	351	303	4

Nasal-		GO:004			317/1	0.000	0.037	0.032	
Up	BP	3588	skin development	6/45	8870	101	109	605	6
Nasal-		GO:000			245/1	0.000	0.053	0.046	
Up	BP	9913	epidermal cell differentiation	5/45	8870	283	215	756	5
Nasal-		GO:000			385/1	0.000	0.053	0.046	
Up	BP	8544	epidermis development	6/45	8870	288	215	756	6
Nasal-		GO:190	positive regulation of extrinsic apoptotic signaling pathway via		14/18	0.000	0.073	0.064	
Up	BP	2043	death domain receptors	2/25	870	497	342	44	2
Nasal-		GO:003			177/1	0.000	0.101	0.089	
Up	BP	0216	keratinocyte differentiation	4/45	8870	826	58	25	4
Nasal-		GO:000			83/18	0.001	0.107	0.094	
Up	BP	1895	retina homeostasis	3/45	870	019	443	401	3
Nasal-		GO:200			24/18	0.001	0.136	0.120	
Up	BP	0209	regulation of anoikis	2/25	870	484	935	314	2
Nasal-		GO:004			28/18	0.002	0.165	0.145	
Up	BP	4342	type B pancreatic cell proliferation	2/25	870	021	697	584	2

Nasal-		GO:004			34/18	0.002	0.211	0.185	
Up	BP	3276	anoikis	2/25	870	972	475	806	2
Nasal-		GO:004			37/18	0.003	0.211	0.185	
Up	BP	8730	epidermis morphogenesis	2/25	870	512	475	806	2
Nasal-		GO:000			128/1	0.003	0.211	0.185	
Up	BP	1704	formation of primary germ layer	3/35	8870	514	475	806	3
Nasal-		GO:000	detection of chemical stimulus involved in sensory perception of		39/18	0.003	0.211	0.185	
Up	BP	1580	bitter taste	2/25	870	896	475	806	2
Nasal-		GO:190			41/18	0.004	0.211	0.185	
Up	BP	4994	regulation of leukocyte adhesion to vascular endothelial cell	2/25	870	298	475	806	2
Nasal-		GO:004			284/1	0.004	0.211	0.185	
Up	BP	3542	endothelial cell migration	4/45	8870	609	475	806	4
Nasal-		GO:001			43/18	0.004	0.211	0.185	
Up	BP	6266	O-glycan processing	2/25	870	719	475	806	2
Nasal-		GO:005			44/18	0.004	0.211	0.185	
Up	BP	0913	sensory perception of bitter taste	2/25	870	936	475	806	2

Nasal-		GO:005	detection of chemical stimulus involved in sensory perception of		45/18	0.005	0.211	0.185	
Up	BP	0912	taste	2/25	870	158	475	806	2
Nasal-		GO:001			47/18	0.005	0.218	0.191	
Up	BP	0830	regulation of myotube differentiation	2/25	870	615	101	627	2
Nasal-		GO:000			60/19	0.000	0.037	0.031	
Up	CC	1533	cornified envelope	3/46	886	361	588	197	3
Nasal-		GO:003			33/19	0.002	0.137	0.113	
Up	CC	1528	microvillus membrane	2/46	886	641	31	962	2
Nasal-		GO:004			469/1	0.004	0.153	0.127	
Up	CC	5177	apical part of cell	5/46	9886	418	154	111	5
Nasal-		GO:190			55/19	0.007	0.186	0.155	
Up	CC	4724	tertiary granule lumen	2/46	886	191	959	169	2
Nasal-		GO:003			62/19	0.009	0.188	0.156	
Up	CC	5580	specific granule lumen	2/46	886	063	518	462	2
Nasal-		GO:009			227/1	0.015	0.221	0.183	
Up	CC	8858	actin-based cell projection	3/46	9886	537	259	636	3

Nasal-		GO:000			97/19	0.021	0.221	0.183	
Up	CC	5902	microvillus		2/46	886	205	259	636 2
Nasal-		GO:004			97/19	0.021	0.221	0.183	
Up	CC	5095	keratin filament		2/46	886	205	259	636 2
Nasal-		GO:000			11/19	0.025	0.221	0.183	
Up	CC	0815	ESCRT III complex		1/46	886	159	259	636 1
Nasal-		GO:004			11/19	0.025	0.221	0.183	
Up	CC	3220	Schmidt-Lanterman incisure		1/46	886	159	259	636 1
Nasal-		GO:190			12/19	0.027	0.221	0.183	
Up	CC	4930	amphisome membrane		1/46	886	415	259	636 1
Nasal-		GO:009			13/19	0.029	0.221	0.183	
Up	CC	9523	presynaptic cytosol		1/46	886	666	259	636 1
Nasal-		GO:009			13/19	0.029	0.221	0.183	
Up	CC	9524	postsynaptic cytosol		1/46	886	666	259	636 1
Nasal-		GO:004			14/19	0.031	0.221	0.183	
Up	CC	3218	compact myelin		1/46	886	912	259	636 1

Nasal-		GO:004				14/19	0.031	0.221	0.183	
Up	CC	4753	amphisome		1/46	886	912	259	636	1
Nasal-		GO:003				322/1	0.038	0.223	0.185	
Up	CC	4774	secretory granule lumen		3/46	9886	28	577	56	3
Nasal-		GO:006				325/1	0.039	0.223	0.185	
Up	CC	0205	cytoplasmic vesicle lumen		3/46	9886	177	577	56	3
Nasal-		GO:003				326/1	0.039	0.223	0.185	
Up	CC	1983	vesicle lumen		3/46	9886	478	577	56	3
Nasal-		GO:004				18/19	0.040	0.223	0.185	
Up	CC	3034	costamere		1/46	886	846	577	56	1
Nasal-		GO:004				19/19	0.043	0.223	0.185	
Up	CC	4305	calyx of Held		1/46	886	067	946	866	1
Nasal-		GO:009				20/19	0.045	0.224	0.186	
Up	CC	9522	cytosolic region		1/46	886	282	255	122	1
Nasal-		GO:000				21/19	0.047	0.224	0.186	
Up	CC	5828	kinetochore microtubule		1/46	886	493	512	336	1

Nasal-		GO:004			160/1	0.052	0.239	0.198	
Up	CC	2581	specific granule	2/46	9886	879	107	449	2
Nasal-		GO:007			164/1	0.055	0.239	0.198	
Up	CC	0820	tertiary granule	2/46	9886	246	398	691	2
Nasal-		GO:000			10/18	0.000	0.014	0.010	
Up	MF	8330	protein tyrosine/threonine phosphatase activity	2/45	496	257	277	696	2
Nasal-		GO:003			10/18	0.000	0.014	0.010	
Up	MF	3550	MAP kinase tyrosine phosphatase activity	2/45	496	257	277	696	2
Nasal-		GO:001			13/18	0.000	0.016	0.012	
Up	MF	7017	MAP kinase tyrosine/serine/threonine phosphatase activity	2/45	496	444	422	303	2
Nasal-		GO:003			18/18	0.000	0.023	0.017	
Up	MF	3549	MAP kinase phosphatase activity	2/45	496	864	973	96	2
Nasal-		GO:000			96/18	0.001	0.036	0.027	
Up	MF	4725	protein tyrosine phosphatase activity	3/45	496	642	448	305	3
Nasal-		GO:003			36/18	0.003	0.064	0.047	
Up	MF	0280	structural constituent of skin epidermis	2/45	496	46	003	949	2

Nasal-		GO:014			40/18	0.004	0.067	0.050	
Up	MF	0313	molecular sequestering activity	2/45	496	257	503	571	2
Nasal-		GO:000			44/18	0.005	0.071	0.053	
Up	MF	8138	protein tyrosine/serine/threonine phosphatase activity	2/45	496	131	195	337	2
Nasal-		GO:001			150/1	0.005	0.071	0.053	
Up	MF	9842	vitamin binding	3/45	8496	782	316	428	3
Nasal-		GO:000			176/1	0.008	0.099	0.074	
Up	MF	4721	phosphoprotein phosphatase activity	3/45	8496	967	535	568	3
Nasal-		GO:001			82/18	0.016	0.139	0.104	
Up	MF	7018	myosin phosphatase activity	2/45	496	992	071	188	2
Nasal-		GO:003			10/18	0.024	0.139	0.104	
Up	MF	1419	cobalamin binding	1/45	496	071	071	188	1
Nasal-		GO:000			100/1	0.024	0.139	0.104	
Up	MF	4722	protein serine/threonine phosphatase activity	2/45	8496	639	071	188	2
Nasal-		GO:000			102/1	0.025	0.139	0.104	
Up	MF	5496	steroid binding	2/45	8496	561	071	188	2

Nasal-		GO:001			11/18	0.026	0.139	0.104	
Up	MF	9864	IgG binding	1/45	496	446	071	188	1
Nasal-		GO:001			11/18	0.026	0.139	0.104	
Up	MF	9911	structural constituent of myelin sheath	1/45	496	446	071	188	1
Nasal-		GO:000	DNA-binding transcription activator activity, RNA polymerase II-		471/1	0.027	0.139	0.104	
Up	MF	1228	specific	4/45	8496	194	071	188	4
Nasal-		GO:001			270/1	0.027	0.139	0.104	
Up	MF	6791	phosphatase activity	3/45	8496	822	071	188	3
Nasal-		GO:000			475/1	0.027	0.139	0.104	
Up	MF	1216	DNA-binding transcription activator activity	4/45	8496	938	071	188	4
Nasal-		GO:000	cyclin-dependent protein serine/threonine kinase inhibitor		12/18	0.028	0.139	0.104	
Up	MF	4861	activity	1/45	496	816	071	188	1
Nasal-		GO:000			12/18	0.028	0.139	0.104	
Up	MF	5527	macrolide binding	1/45	496	816	071	188	1
Nasal-		GO:000	UDP-galactose:beta-N-acetylglucosamine beta-1,3-		12/18	0.028	0.139	0.104	
Up	MF	8499	galactosyltransferase activity	1/45	496	816	071	188	1

Nasal-		GO:003			12/18	0.028	0.139	0.104	
Up	MF	5259	nuclear glucocorticoid receptor binding	1/45	496	816	071	188	1
Nasal-		GO:003			13/18	0.031	0.144	0.108	
Up	MF	1994	insulin-like growth factor I binding	1/45	496	181	211	039	1
Nasal-		GO:004			15/18	0.035	0.159	0.119	
Up	MF	8531	beta-1,3-galactosyltransferase activity	1/45	496	893	364	39	1
Nasal-		GO:007			16/18	0.038	0.160	0.120	
Up	MF	2542	protein phosphatase activator activity	1/45	496	24	879	526	1
Nasal-		GO:000			17/18	0.040	0.160	0.120	
Up	MF	5001	transmembrane receptor protein tyrosine phosphatase activity	1/45	496	582	879	526	1
Nasal-		GO:001			17/18	0.040	0.160	0.120	
Up	MF	9198	transmembrane receptor protein phosphatase activity	1/45	496	582	879	526	1
Nasal-		GO:000			19/18	0.045	0.162	0.121	
Up	MF	5520	insulin-like growth factor binding	1/45	496	249	022	382	1
Nasal-		GO:001			19/18	0.045	0.162	0.121	
Up	MF	9211	phosphatase activator activity	1/45	496	249	022	382	1

Nasal-		GO:003			19/18	0.045	0.162	0.121	
Up	MF	0506	ankyrin binding		1/45	496	249	022	382 1
Nasal-		GO:000			21/18	0.049	0.165	0.124	
Up	MF	8373	sialyltransferase activity		1/45	496	894	975	344 1
Nasal-		GO:004			344/1		0.165	0.124	
Up	MF	6982	protein heterodimerization activity		3/45	8496	0.051	975	344 3
Nasal-		GO:014			23/18	0.054	0.165	0.124	
Up	MF	0103	catalytic activity, acting on a glycoprotein		1/45	496	517	975	344 1
Nasal-		GO:004			358/1	0.056	0.165	0.124	
Up	MF	2578	phosphoric ester hydrolase activity		3/45	8496	186	975	344 3
Nasal-		GO:000			24/18	0.056	0.165	0.124	
Up	MF	4806	triglyceride lipase activity		1/45	496	82	975	344 1
Nasal-		GO:001			24/18	0.056	0.165	0.124	
Up	MF	6505	peptidase activator activity involved in apoptotic process		1/45	496	82	975	344 1
Nasal-		GO:001			24/18	0.056	0.165	0.124	
Up	MF	9865	immunoglobulin binding		1/45	496	82	975	344 1

Nasal-		GO:000			26/18	0.061	0.168	0.126	
Up	MF	4190	aspartic-type endopeptidase activity	1/45	496	41	361	131	1
Nasal-		GO:000			27/18	0.063	0.168	0.126	
Up	MF	8320	protein transmembrane transporter activity	1/45	496	697	361	131	1
Nasal-		GO:007			27/18	0.063	0.168	0.126	
Up	MF	0001	aspartic-type peptidase activity	1/45	496	697	361	131	1
Nasal-		GO:003			28/18	0.065	0.168	0.126	
Up	MF	5250	UDP-galactosyltransferase activity	1/45	496	978	361	131	1
Nasal-		GO:004			28/18	0.065	0.168	0.126	
Up	MF	3236	laminin binding	1/45	496	978	361	131	1
Nasal-		GO:000			29/18	0.068	0.168	0.126	
Up	MF	1968	fibronectin binding	1/45	496	254	361	131	1
Nasal-		GO:005			29/18	0.068	0.168	0.126	
Up	MF	1861	glycolipid binding	1/45	496	254	361	131	1
Nasal-		GO:000			31/18	0.072	0.173	0.130	
Up	MF	8378	galactosyltransferase activity	1/45	496	79	552	02	1

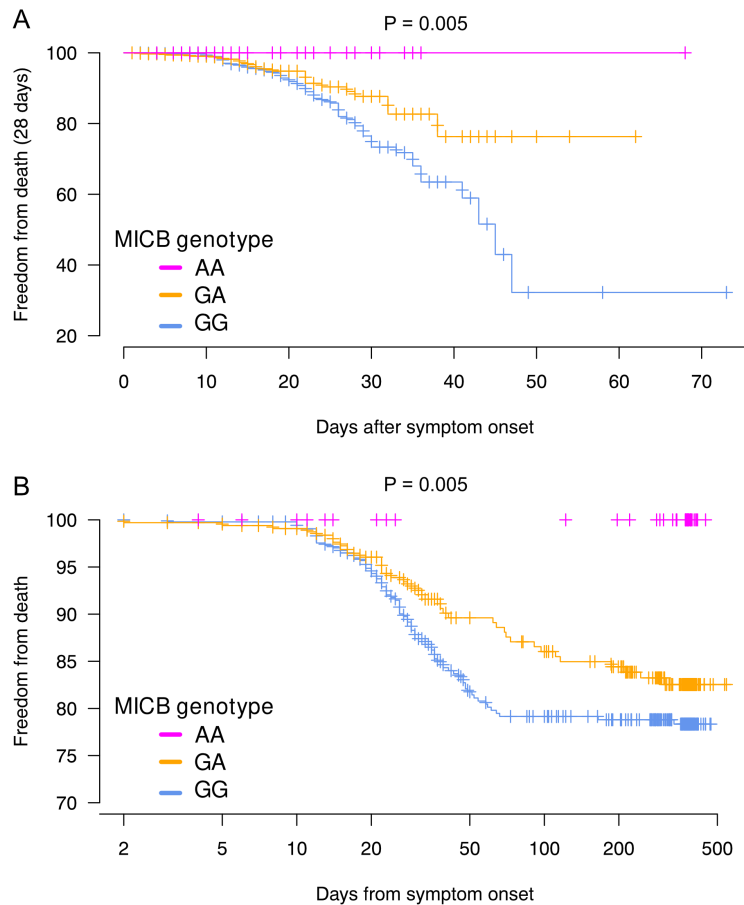
Nasal-		GO:002			32/18	0.075	0.173	0.130	
Up	MF	2884	macromolecule transmembrane transporter activity	1/45	496	049	552	02	1
Nasal-		GO:007			32/18	0.075	0.173	0.130	
Up	MF	1889	14-3-3 protein binding	1/45	496	049	552	02	1
Nasal-		GO:003			37/18	0.086	0.195	0.146	
Up	MF	0291	protein serine/threonine kinase inhibitor activity	1/45	496	267	422	404	1
Nasal-		GO:000			39/18	0.090	0.197	0.147	
Up	MF	1530	lipopolysaccharide binding	1/45	496	717	443	918	1
Nasal-		GO:014			39/18	0.090	0.197	0.147	
Up	MF	0318	protein transporter activity	1/45	496	717	443	918	1
Nasal-		GO:000			224/1	0.103	0.217	0.163	
Up	MF	0287	magnesium ion binding	2/45	8496	073	684	083	2
Nasal-		GO:000			45/18	0.103	0.217	0.163	
Up	MF	8375	acetylglucosaminyltransferase activity	1/45	496	939	684	083	1
Nasal-		GO:014			477/1	0.109	0.224	0.167	
Up	MF	0297	DNA-binding transcription factor binding	3/45	8496	501	123	906	3

Nasal-		GO:000			484/1	0.113	0.224	0.167	
Up	MF	5543	phospholipid binding	3/45	8496	101	123	906	3
Nasal-		GO:001	cyclin-dependent protein serine/threonine kinase regulator		50/18	0.114	0.224	0.167	
Up	MF	6538	activity	1/45	496	814	123	906	1
Nasal-		GO:000			52/18	0.119	0.224	0.167	
Up	MF	4879	nuclear receptor activity	1/45	496	128	123	906	1
Nasal-		GO:001			52/18	0.119	0.224	0.167	
Up	MF	6504	peptidase activator activity	1/45	496	128	123	906	1
Nasal-		GO:009			52/18	0.119	0.224	0.167	
Up	MF	8531	ligand-activated transcription factor activity	1/45	496	128	123	906	1
Nasal-		GO:005			55/18	0.125	0.232	0.174	
Up	MF	0840	extracellular matrix binding	1/45	496	56	287	022	1
Nasal-		GO:001			268/1	0.138	0.251	0.188	
Up	MF	6757	glycosyltransferase activity	2/45	8496	289	641	522	2
Nasal-		GO:003			276/1	0.144	0.259	0.194	
Up	MF	5091	phosphatidylinositol binding	2/45	8496	956	517	423	2

Nasal-		GO:199			66/18	0.148	0.262	0.196	
Up	MF	0841	promoter-specific chromatin binding	1/45	496	754	091	351	1
Nasal-		GO:000		12/11	441/1	1.02E	0.009	0.009	
Down	BP	0280	nuclear division	0	8870	-05	926	66	12
Nasal-		GO:009		10/11	312/1	1.44E	0.009	0.009	
Down	BP	8813	nuclear chromosome segregation	0	8870	-05	926	66	10
Nasal-		GO:004		12/11	488/1	2.77E	0.012	0.012	
Down	BP	8285	organelle fission	0	8870	-05	717	376	12
Nasal-		GO:000		11/11	424/1	3.75E	0.012	0.012	
Down	BP	7059	chromosome segregation	0	8870	-05	935	588	11
Nasal-		GO:000			225/1	5.21E	0.014	0.013	
Down	BP	0819	sister chromatid segregation	8/110	8870	-05	347	962	8
Nasal-		GO:000			184/1	0.000	0.022	0.021	
Down	BP	0070	mitotic sister chromatid segregation	7/110	8870	102	351	752	7
Nasal-		GO:000			130/1	0.000	0.022	0.021	
Down	BP	7052	mitotic spindle organization	6/110	8870	114	351	752	6

Nasal-		GO:014			274/1	0.000	0.035	0.034	
Down	BP	0014	mitotic nuclear division	8/110	8870	204	077	136	8
Nasal-		GO:000			54/18	0.000	0.042	0.041	
Down	BP	0381	regulation of alternative mRNA splicing, via spliceosome	4/110	870	276	291	157	4
Nasal-		GO:190			163/1	0.000	0.053	0.051	
Down	BP	2850	microtubule cytoskeleton organization involved in mitosis	6/110	8870	387	328	898	6
Nasal-		GO:000			71/18	0.000	0.098	0.095	
Down	BP	0380	alternative mRNA splicing, via spliceosome	4/110	870	787	537	895	4
Nasal-		GO:005			131/1	0.001	0.117	0.114	
Down	BP	1983	regulation of chromosome segregation	5/110	8870	021	249	106	5
Nasal-		GO:000			202/1	0.001	0.126	0.122	
Down	BP	7051	spindle organization	6/110	8870	189	046	666	6
Nasal-		GO:005			11/18	0.001	0.176	0.171	
Down	BP	1593	response to folic acid	2/110	870	79	143	42	2
Nasal-		GO:000			12/18	0.002	0.196	0.191	
Down	BP	0727	double-strand break repair via break-induced replication	2/110	870	139	53	261	2

Nasal-		GO:000			281/1	0.001	0.126	0.121	
Down	CC	0793	condensed chromosome		7/119	9886	522	012	474 7
Nasal-		GO:007			11/19	0.001	0.126	0.121	
Down	CC	1162	CMG complex		2/119	886	885	012	474 2
Nasal-		GO:003			13/19	0.002	0.126	0.121	
Down	CC	1261	DNA replication preinitiation complex		2/119	886	653	012	474 2
Nasal-		GO:199			13/19	0.002	0.126	0.121	
Down	CC	0907	beta-catenin-TCF complex		2/119	886	653	012	474 2
Nasal-		GO:000			431/1	0.004	0.145	0.140	
Down	CC	5819	spindle		8/119	9886	417	995	737 8
Nasal-		GO:000			258/1	0.004	0.145	0.140	
Down	CC	0775	chromosome, centromeric region		6/119	9886	61	995	737 6



178

179 **Supplemental Figure 1. COVID-19 mortality by MICB^{G406A} polymorphism**

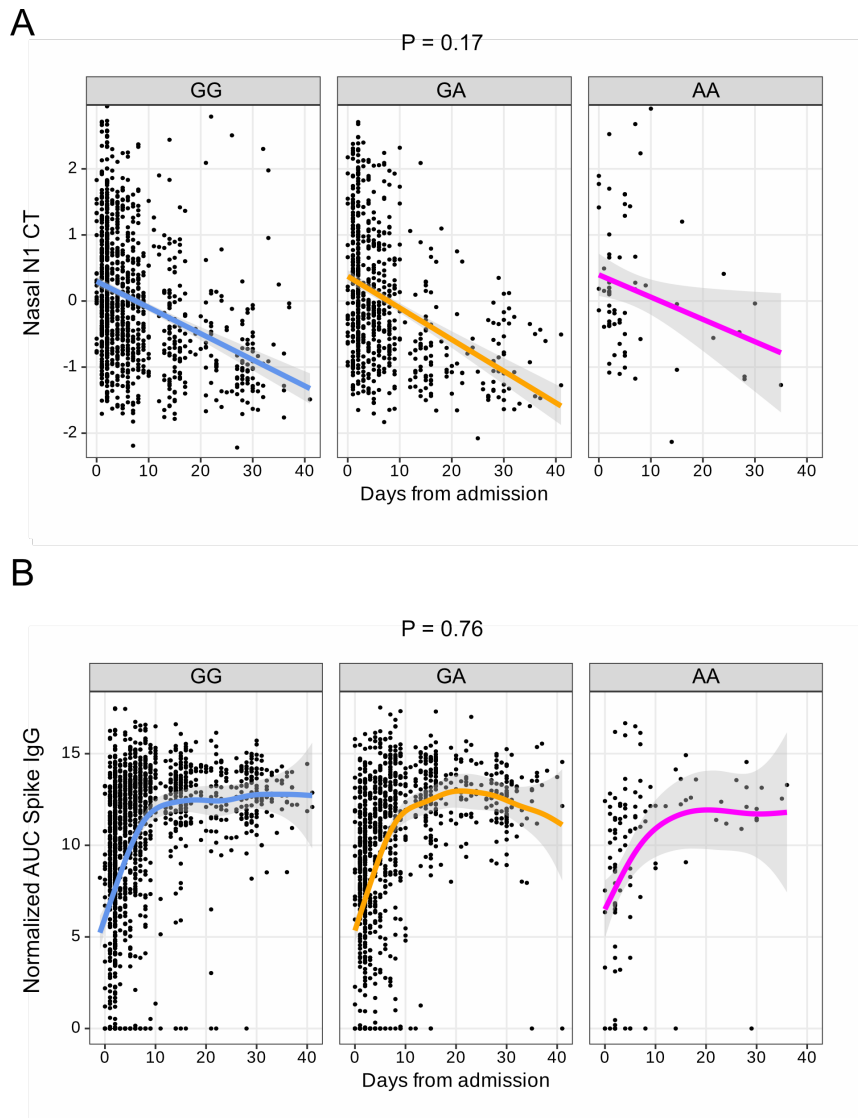
180 Survival analysis of death on days from symptom onset **A**) by 28-days post-admission or **B**) ever

181 during the study and number of copies of the MICB^{G406A} variant allele were compared by Cox

182 proportional-hazards models. Results for patients with no copies of the variant allele (GG) are

183 shown in blue, one copy of the variant allele (GA) in orange) and two copies of the variant allele

184 (AA) in magenta.



185

186 **Supplemental Figure 2. Longitudinal nasal SARS-CoV-2 viral load and serum anti-Spike**

187 **IgG by MICB^{G406A} polymorphism**

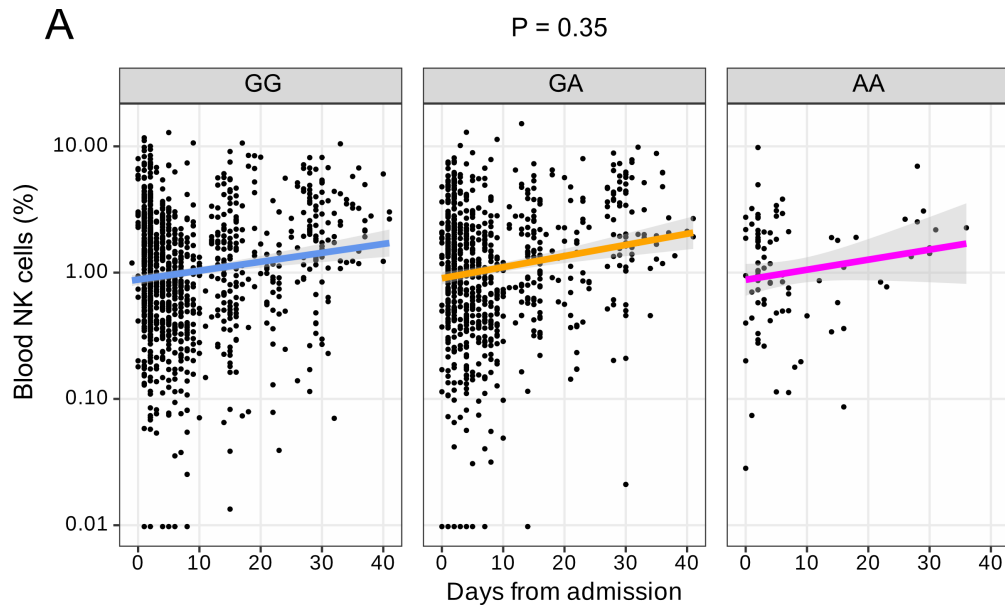
188 Longitudinal **A**) nasal SARS-CoV-2 viral load (N1 CT value) and **B**) serum anti-spike IgG levels

189 (AUC) by number of copies of the MICB^{G406A} variant allele were compared by linear regression,

190 including patient as a random effect. Results for patients with no copies of the variant allele (GG)

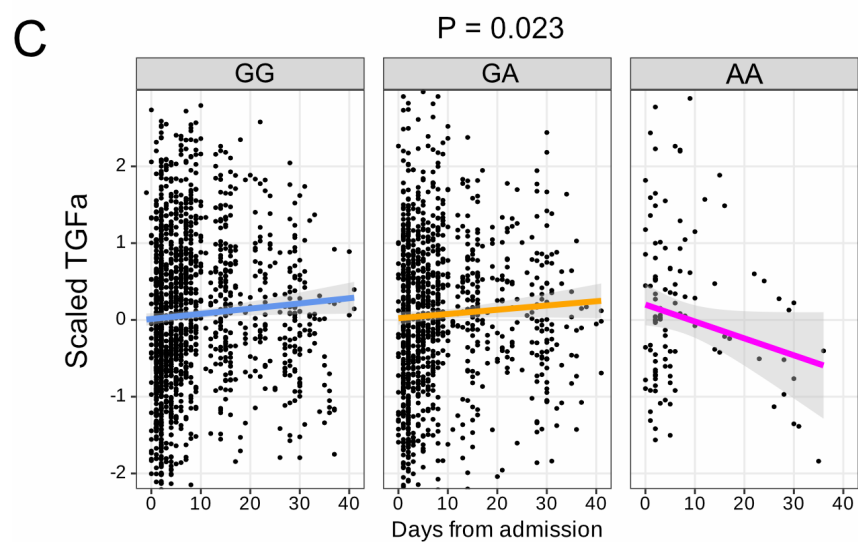
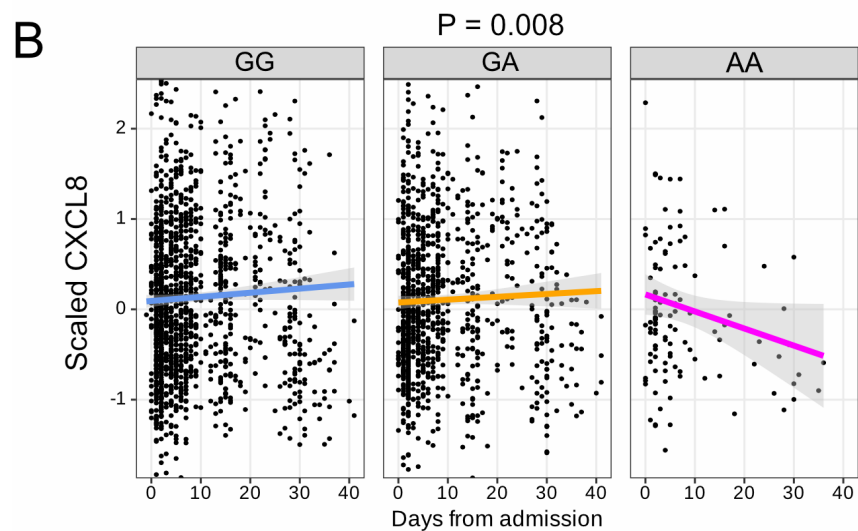
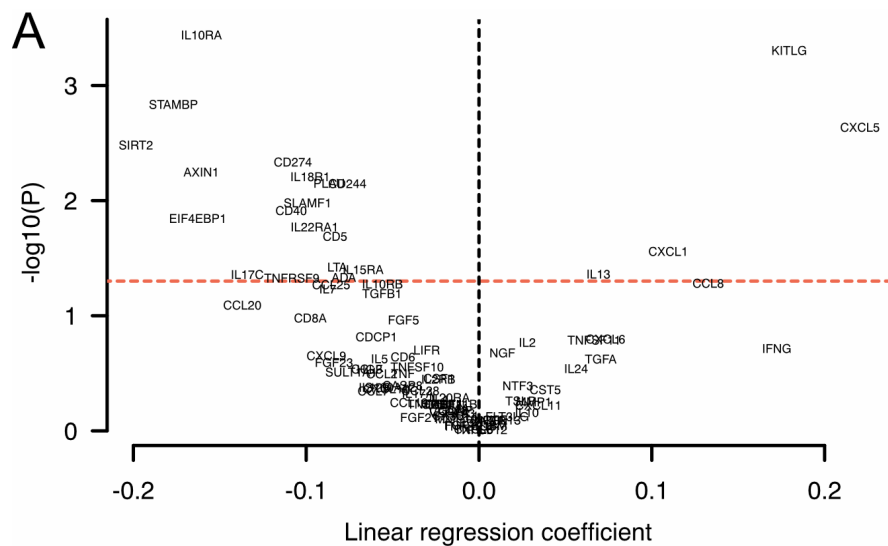
191 are shown in blue, one copy of the variant allele (GA) in orange) and two copies of the variant

192 allele (AA) in magenta.



193 **Supplemental Figure 3. Longitudinal NK cell frequency in PBMC by**
 194 **MICB^{G406A} polymorphism**

195 Blood NK cell frequency **A**) longitudinally by number of copies of the MICB^{G406A} variant allele were
 196 compared by linear regression, including patient identifier as a random effect. Results for patients
 197 with no copies of the variant allele (GG) are shown in blue, one copy of the variant allele (GA) in
 198 orange) and two copies of the variant allele (AA) in magenta.



200 **Supplemental Figure 4. Serum proteins by MICB^{G406A} polymorphism**

201 Visit-1 serum protein levels by number of copies of the MICB^{G406A} variant allele were compared
202 by linear regression. **A)** Linear regression coefficient against -log10 transformed P-values.
203 Longitudinal **B-C)** serum protein levels by number of copies of the MICB^{G406A} variant allele were
204 compared by linear regression, including patient as a random effect. Results for patients with no
205 copies of the variant allele (GG) are shown in blue, one copy of the variant allele (GA) in orange)
206 and two copies of the variant allele (AA) in magenta.

Conflict of interest: The Icahn School of Medicine at Mount Sinai has filed patent applications relating to SARS-CoV-2 serological assays, NDV-based SARS-CoV-2 vaccines influenza virus vaccines, and influenza virus therapeutics, which list Florian Krammer as coinventor. Mount Sinai has spun out a company, Kantaro, to market serological tests for SARS-CoV-2 and another company, Castlevax, to develop SARS-CoV-2 vaccines. FK is cofounder and scientific advisory board member of Castlevax. FK has consulted for Merck, Curevac, Seqirus, GSK, and Pfizer and is currently consulting for 3rd Rock Ventures, Sanofi, Gritstone, and Avimex. The Krammer laboratory is also collaborating with Dynavax on influenza vaccine development and with VIR on influenza virus therapeutics development. VS is a coinventor on a patent filed relating to SARS-CoV-2 serological assays (the “Serology Assays”). OL is a named inventor on patents held by Boston Children’s Hospital relating to vaccine adjuvants and human in vitro platforms that model vaccine action. His laboratory has received research support from GlaxoSmithKline (GSK) and is a cofounder of and advisor to Ovax Inc. C. Cairns serves as a consultant to bioMerieux and is funded for a grant from Bill & Melinda Gates Foundation. JAO is a consultant at Knocean Inc. Jessica Lasky-Su serves as a scientific advisor of Precion Inc. SRH, GM, and KW are employees of Metabolon Inc. VSM is a current employee of MyOwnMed. NR reports grants or contracts with Merck, Sanofi, Pfizer, Vaccine Company, and Immorna and has participated on data safety monitoring boards for Moderna, Sanofi, Seqirus, Pfizer, EMMES, ICON, BARDA, CyanVan, and Imunon Micron. NR has also received support for meetings/travel from Sanofi and Moderna and honoraria from Virology Education and Krog consulting. C. Cotsapas is a current employee of Vesalius Therapeutics. AR is a current employee of Immunai Inc. SK is a consultant related to ImmPort data repository for Peraton. NG is a consultant for Tempus Labs and the National Basketball Association. AI is a consultant for 4BIO, Blue Willow Biologics, Revelar Biotherapeutics, RIGImmune, Xanadu Bio, and Paratus Sciences. MK receives research funds paid to her institution from NIH. ALA is affiliated with Sanofi and Astra-Zeneca for work in asthma; serves as a consultant for Astra-Zeneca, Sanofi, Chiesi, GSK for severe asthma; and is a cofounder and CMO for RaeSedo Inc., a company created to develop peptidomimetics for treatment of inflammatory lung disease (**4. AUTHOR: Does edit for syntax retain meaning? If not, clarify.**). EM received research funding from Babson Diagnostics and honorarium from Multiple Sclerosis Association of America and has served on the advisory boards of Genentech, Horizon, Teva, and Viela Bio. C. Calfee receives research funding from NIH, FDA, DOD, Roche-Genentech, and Quantum Leap Healthcare Collaborative as well as consulting services for Janssen, Vasomune, Gen1e Life Sciences, NGMBio, and Cellenkos. WS was an investigator for a research agreement, through Yale University, from the Shenzhen Center for Health Information for work to advance intelligent disease prevention and health promotion; collaborates with the National Center for Cardiovascular Diseases in Beijing; is a technical consultant to Hugo Health, a personal health information platform; nd is a cofounder of Refactor Health, an AI-augmented data management platform for health care; and has received grants from Merck and Regeneron Pharmaceutical for research related to COVID-19. GAM received research grants from Rehndhill, Cognivue, Pfizer, and Genentech and served as a research consultant for Gilead, Merck, Viiv/GSK, and Janssen. LNG received research funding paid to her institution from Pfizer Inc. CH receives support through her institution from the NIH and CDC.