

Large-scale phenotyping of patients with long COVID post-hospitalization reveals mechanistic subtypes of disease

Received: 11 August 2023

Accepted: 6 February 2024

Published online: 8 April 2024

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A list of authors and their affiliations appears at the end of the paper

One in ten severe acute respiratory syndrome coronavirus 2 infections result in prolonged symptoms termed long coronavirus disease (COVID), yet disease phenotypes and mechanisms are poorly understood¹. Here we profiled 368 plasma proteins in 657 participants ≥ 3 months following hospitalization. Of these, 426 had at least one long COVID symptom and 233 had fully recovered. Elevated markers of myeloid inflammation and complement activation were associated with long COVID. IL-1R2, MATN2 and COLEC12 were associated with cardiorespiratory symptoms, fatigue and anxiety/depression; MATN2, CSF3 and C1QA were elevated in gastrointestinal symptoms and C1QA was elevated in cognitive impairment. Additional markers of alterations in nerve tissue repair (SPON-1 and NFASC) were elevated in those with cognitive impairment and SCG3, suggestive of brain–gut axis disturbance, was elevated in gastrointestinal symptoms. Severe acute respiratory syndrome coronavirus 2-specific immunoglobulin G (IgG) was persistently elevated in some individuals with long COVID, but virus was not detected in sputum. Analysis of inflammatory markers in nasal fluids showed no association with symptoms. Our study aimed to understand inflammatory processes that underlie long COVID and was not designed for biomarker discovery. Our findings suggest that specific inflammatory pathways related to tissue damage are implicated in subtypes of long COVID, which might be targeted in future therapeutic trials.

One in ten severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections results in post-acute sequelae of coronavirus disease 2019 (PASC) or long coronavirus disease (COVID), which affects 65 million people worldwide¹. Long COVID (LC) remains common, even after mild acute infection with recent variants², and it is likely LC will continue to cause substantial long-term ill health, requiring targeted management based on an understanding of how disease phenotypes relate to underlying mechanisms. Persistent inflammation has been reported in adults with LC³, but studies have been limited in size, timing of samples or breadth of immune mediators measured, leading to inconsistent or absent associations with symptoms. Markers of

oxidative stress, metabolic disturbance, vasculoproliferative processes and IFN-, NF- κ B- or monocyte-related inflammation have been suggested^{3–6}.

The PHOSP-COVID study, a multicenter United Kingdom study of patients previously hospitalized with COVID-19, has reported inflammatory profiles in 626 adults with health impairment after COVID-19, identified through clustering. Elevated IL-6 and markers of mucosal inflammation were observed in those with severe impairment compared with individuals with milder impairment⁷. However, LC is a heterogeneous condition that may be a distinct form of health impairment after COVID-19, and it remains unclear whether there are

✉ e-mail: r.thwaites@imperial.ac.uk; p.openshaw@imperial.ac.uk

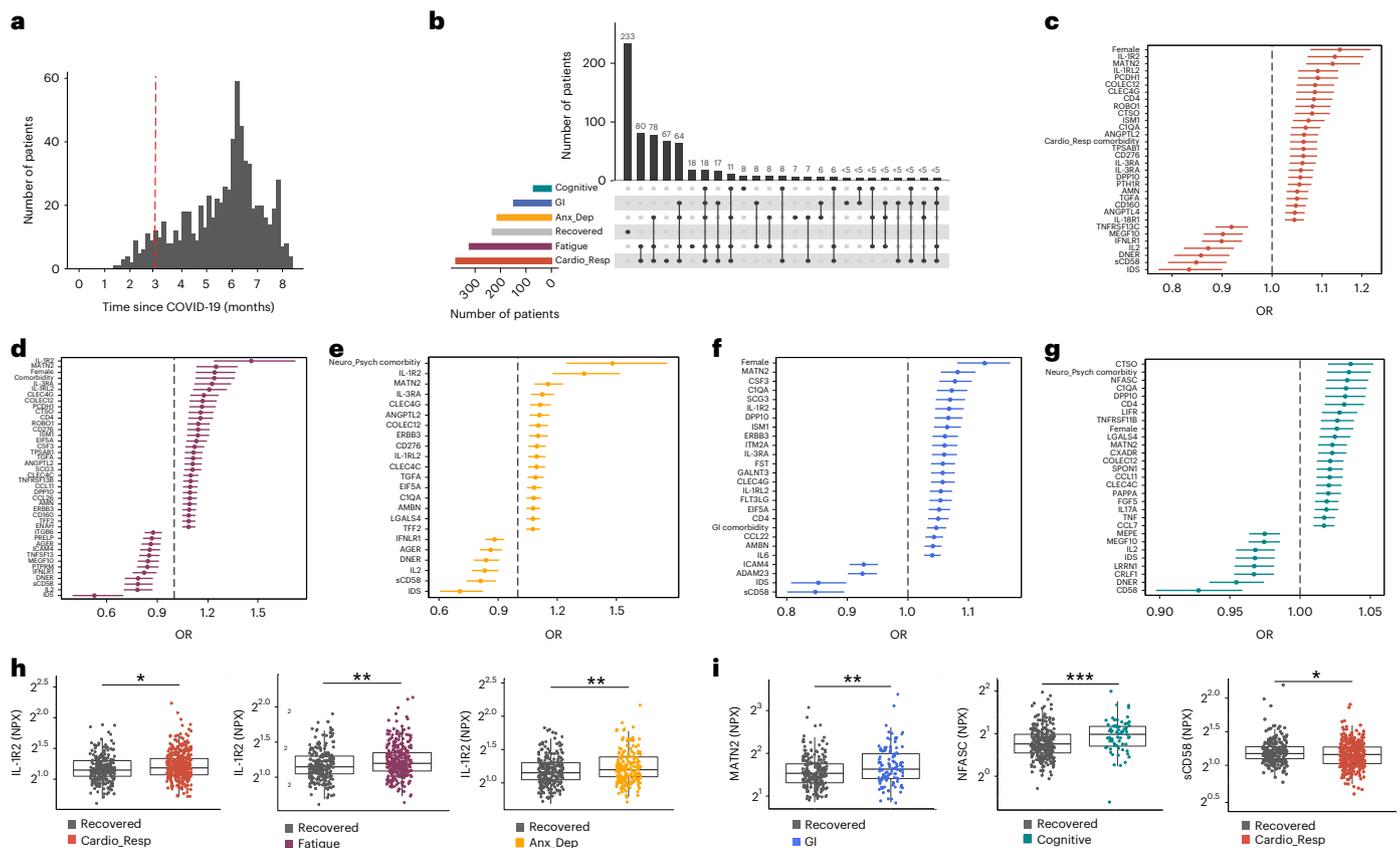


Fig. 1 | Subtypes of LC are associated with distinct inflammatory profiles.
a, Distribution of time from COVID-19 hospitalization at sample collection. All samples were cross-sectional. The vertical red line indicates the 3 month cutoff used to define our final cohort and samples collected before 3 months were excluded. **b**, An UpSet plot describing pooled LC groups. The horizontal colored bars represent the number of patients in each symptom group: cardiorespiratory (Cardio_Resp), fatigue, cognitive, GI and anxiety/depression (Anx_Dep). Vertical black bars represent the number of patients in each symptom combination group. To prevent patient identification, where less than five patients belong to a combination group, this has been represented as '<5'. The recovered group ($n = 233$) were used as controls. **c-g**, Forest plots of Olink protein concentrations (NPX) associated with Cardio_Resp ($n = 365$) (**c**), fatigue ($n = 314$) (**d**), Anx_Dep ($n = 202$) (**e**), GI ($n = 124$) (**f**) and cognitive ($n = 60$) (**g**). Neuro_Psych, neuropsychiatric. The error bars represent the median accuracy of the model. **h,i**, Distribution of Olink values (NPX) for IL-1R2 (**h**) and MATN2, neurofascin and sCD58 (**i**) measured between symptomatic and recovered individuals in recovered ($n = 233$), Cardio_Resp ($n = 365$), fatigue ($n = 314$) and Anx_Dep ($n = 202$) groups (**h**) and MATN2 in GI ($n = 124$), neurofascin in cognitive ($n = 60$) and sCD58 in Cardio_Resp and recovered groups (**i**). The box plot center line represents the median, the boundaries represent IQR and the whisker length represents $1.5 \times$ IQR. The median values were compared between groups using two-sided Wilcoxon signed-rank test, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ and **** $P < 0.0001$.

inflammatory changes specific to LC symptom subtypes. Determining whether activated inflammatory pathways underlie all cases of LC or if mechanisms differ according to clinical presentation is essential for developing effective therapies and has been highlighted as a top research priority by patients and clinicians⁸.

In this Letter, in a prospective multicenter study, we measured 368 plasma proteins in 657 adults previously hospitalized for COVID-19 (Fig. 1a and Table 1). Individuals in our cohort experienced a range of acute COVID-19 severities based on World Health Organization (WHO) progression scores⁹; WHO 3–4 (no oxygen support, $n = 133$ and median age of 55 years), WHO 5–6 (oxygen support, $n = 353$ and median age of 59 years) and WHO 7–9 (critical care, $n = 171$ and median age of 57 years). Participants were hospitalized for COVID-19 ≥ 3 months before sample collection (median 6.1 months, interquartile range (IQR) 5.1–6.8 months and range 3.0–8.3 months) and confirmed clinically ($n = 36/657$) or by PCR ($n = 621/657$). Symptom data indicated 233/657 (35%) felt fully recovered at 6 months (hereafter 'recovered') and the remaining 424 (65%) reported symptoms consistent with the WHO definition for LC (symptoms ≥ 3 months post infection¹⁰). Given the diversity of LC presentations, patients were grouped according to symptom type (Fig. 1b). Groups were defined using symptoms and health deficits that have been commonly reported in the literature¹

(Methods). A multivariate penalized logistic regression model (PLR) was used to explore associations of clinical covariates and immune mediators at 6 months between recovered patients ($n = 233$) and each LC group (cardiorespiratory symptoms, cardioresp, $n = 398$, Fig. 1c; fatigue, $n = 384$, Fig. 1d; affective symptoms, anxiety/depression, $n = 202$, Fig. 1e; gastrointestinal symptoms, GI, $n = 132$, Fig. 1f; and cognitive impairment, cognitive, $n = 61$, Fig. 1g). Women ($n = 239$) were more likely to experience CardioResp (odds ratio (OR) 1.14), Fatigue (OR 1.22), GI (OR 1.13) and Cognitive (OR 1.03) outcomes (Fig. 1c,d,f,g). Repeated cross-validation was used to optimize and assess model performance (Methods and Extended Data Fig. 1). Pre-existing conditions, such as chronic lung disease, neurological disease and cardiovascular disease (Supplementary Table 1), were associated with all LC groups (Fig. 1c–g). Age, C-reactive protein (CRP) and acute disease severity were not associated with any LC group (Table 1).

To study the association of peripheral inflammation with symptoms, we analyzed cross-sectional data collected approximately 6 months after hospitalizations. We measured 368 immune mediators from plasma collected contemporaneously with symptom data. Mediators suggestive of myeloid inflammation were associated with all symptoms (Fig. 1c–h). Elevated IL-1R2, an IL-1 receptor expressed by monocytes and macrophages modulating inflammation¹¹ and MATN2,

Table 1 | Cohort demographics

		GI	Fatigue	Cardiorespiratory	Anxiety/ depression	Cognitive impairment	Recovered	P value
Age at admission	Years (s.d.)	57.72 (11.48)	56.57 (11.07)	57.08 (11.37)	56.36 (10.84)	59.24 (12.82)	58.92 (13.72)	0.046 *
Sex	Female N (%)	68 (53%)	143 (47%)	161 (43%)	89 (45%)	24 (42%)	55 (27%)	1.69×10 ⁻⁶ ****
Ethnicity	White	110	300	331	193	50	197	0.09 NS
	South Asian	14	26	38	16	7	46	
	Black	8	16	25	11	7	10	
	Mixed/Other	8	24	22	16	7	17	
WHO clinical progression scale for acute COVID-19	Class 3–4	41	83	88	45	18	45	0.28 NS
	Class 5	45	107	124	74	21	115	
	Class 6	27	78	89	55	11	57	
	Class 7–9	27	98	115	62	21	50	
CRP	Mean (s.d.)	5.33 (5.42)	5.47 (7.17)	5.17 (6.82)	5.79 (8.12)	4.58 (5.78)	4.75 (10.38)	0.76 NS
Length of hospitalization	Days (s.d.)	12.04 (14.3)	14.59 (18.41)	15.39 (19.96)	14.57 (17.76)	14.95 (16.01)	12.5 (15.73)	0.0047**
Steroid ^a	% Yes	34%	35%	37%	38%	33%	29%	0.294 NS
Remdesivir ^a	% Yes	4%	3%	4%	2%	3%	3%	0.725 NS
Comorbidities	Mean (s.d.)	2.9 (2.62)	2.675 (2.3)	2.553 (2.24)	2.911 (2.47)	2.493 (2.17)	1.554 (1.67)	9.92×10 ⁻¹⁰ ****

The demographics of each symptom group and recovered controls are shown. The WHO clinical progression scale was used to classify acute COVID-19 severity: class 3–4: no oxygen requirement; class 5: oxygen therapy; class 6: noninvasive ventilation or high-flow nasal oxygen and class 7–9: organ support. Differences between groups were compared using chi-squared, two-way Kruskal–Wallis or two-way analysis of variance as appropriate. Data are *n* (%) or mean (s.d.). CRP levels represent those measured contemporaneously with clinical data collected in this study. ^aDenotes treatment given during acute illness.

an extracellular matrix protein that modulates tissue inflammation through recruitment of innate immune cells¹², were associated with cardioresp (IL-1R2 OR 1.14, Fig. 1c,h), fatigue (IL-1R2 OR 1.45, Fig. 1d,h), anxiety/depression (IL-1R2 OR 1.34, Fig. 1e,h) and GI (MATN2 OR 1.08, Fig. 1f). IL-3RA, an IL-3 receptor, was associated with cardioresp (OR 1.07, Fig. 1c), fatigue (OR 1.21, Fig. 1d), anxiety/depression (OR 1.12, Fig. 1e) and GI (OR 1.06, Fig. 1f) groups, while CSF3, a cytokine promoting neutrophilic inflammation¹³, was elevated in cardioresp (OR 1.06, Fig. 1c), fatigue (OR 1.12, Fig. 1d) and GI (OR 1.08, Fig. 1f).

Elevated COLEC12, which initiates inflammation in tissues by activating the alternative complement pathway¹⁴, associated with cardioresp (OR 1.09, Fig. 1c), fatigue (OR 1.19, Fig. 1d) and anxiety/depression (OR 1.11, Fig. 1e), but not with GI (Fig. 1f) and only weakly with cognitive (OR 1.02, Fig. 1g). CIQA, a degradation product released by complement activation¹⁵ was associated with GI (OR 1.08, Fig. 1f) and cognitive (OR 1.03, Fig. 1g). CIQA, which is known to mediate dementia-related neuroinflammation¹⁶, had the third strongest association with cognitive (Fig. 1g). These observations indicated that myeloid inflammation and complement activation were associated with LC.

Increased expression of DPP10 and SCG3 was observed in the GI group compared with recovered (DPP10 OR 1.07 and SCG3 OR 1.08, Fig. 1f). DPP10 is a membrane protein that modulates tissue inflammation, and increased *DPP10* expression is associated with inflammatory bowel disease^{17,18}, suggesting that GI symptoms may result from enteric inflammation. Elevated SCG3, a multifunctional protein that has been associated with irritable bowel syndrome¹⁹, suggested that noninflammatory disturbance of the brain–gut axis or dysbiosis, may occur in the GI group. The cognitive group was associated with elevated CTSO (OR 1.04), NFASC (OR 1.03) and SPON-1 (OR 1.02, Fig. 1g,i). NFASC and SPON-1 regulate neural growth^{20,21}, while CTSO is a cysteine proteinase supporting tissue turnover²². The increased expression of these three proteins as well as CIQA and DPP10 in the cognitive group (Fig. 1g) suggested neuroinflammation and alterations in nerve tissue repair, possibly resulting in neurodegeneration. Together, our findings indicated that complement activation and myeloid inflammation were common to all LC groups, but subtle differences were observed in the GI and cognitive groups, which may have mechanistic importance.

Acutely elevated fibrinogen during hospitalization has been reported to be predictive of LC cognitive deficits²³. We found elevated fibrinogen in LC relative to recovered (Extended Data Fig. 2a; *P* = 0.0077), although this was not significant when restricted to the cognitive group (*P* = 0.074), supporting our observation of complement pathway activation in LC and in keeping with reports that complement dysregulation and thrombosis drive severe COVID-19 (ref. 24).

Elevated sCD58 was associated with lower odds of all LC symptoms and was most pronounced in cardioresp (OR 0.85, Fig. 1c,i), fatigue (OR 0.80, Fig. 1d) and anxiety/depression (OR 0.83, Fig. 1e). IL-2 was negatively associated with the cardioresp (Fig. 1c, OR 0.87), fatigue (Fig. 1d, OR 0.80), anxiety/depression (Fig. 1e, OR 0.84) and cognitive (Fig. 1g, OR 0.96) groups. Both IL-2 and sCD58 have immunoregulatory functions^{25,26}. Specifically, sCD58 suppresses IL-1- or IL-6-dependent interactions between CD2⁺ monocytes and CD58⁺ T or natural killer cells²⁶. The association of sCD58 with recovered suggests a central role of dysregulated myeloid inflammation in LC. Elevated markers of tissue repair, IDS and DNER^{27,28}, were also associated with recovered relative to all LC groups (Fig. 1c–g). Taken together, our data suggest that suppression of myeloid inflammation and enhanced tissue repair were associated with recovered, supporting the use of immunomodulatory agents in therapeutic trials²⁹ (Supplementary Table 2).

We next sought to validate the experimental and analytical approaches used. Although Olink has been validated against other immunoassay platforms, showing superior sensitivity and specificity^{30,31}, we confirmed the performance of Olink against chemiluminescent immunoassays within our cohort. We performed chemiluminescent immunoassays on plasma from a subgroup of 58 participants (recovered *n* = 13 and LC *n* = 45). There were good correlations between results from Olink (normalized protein expression (NPX)) and chemiluminescent immunoassays (pg ml⁻¹) for CSF3, IL-1R2, IL-3RA, TNF and TFF2 (Extended Data Fig. 3). Most samples did not have concentrations of IL-2 detectable using a mesoscale discovery chemiluminescent assay, limiting this analysis to 14 samples (recovered *n* = 4, LC *n* = 10, *R* = 0.55 and *P* = 0.053, Extended Data Fig. 3). We next repeated our analysis using alternative definitions of LC. The Centers for Disease Control and Prevention and National Institute for Health

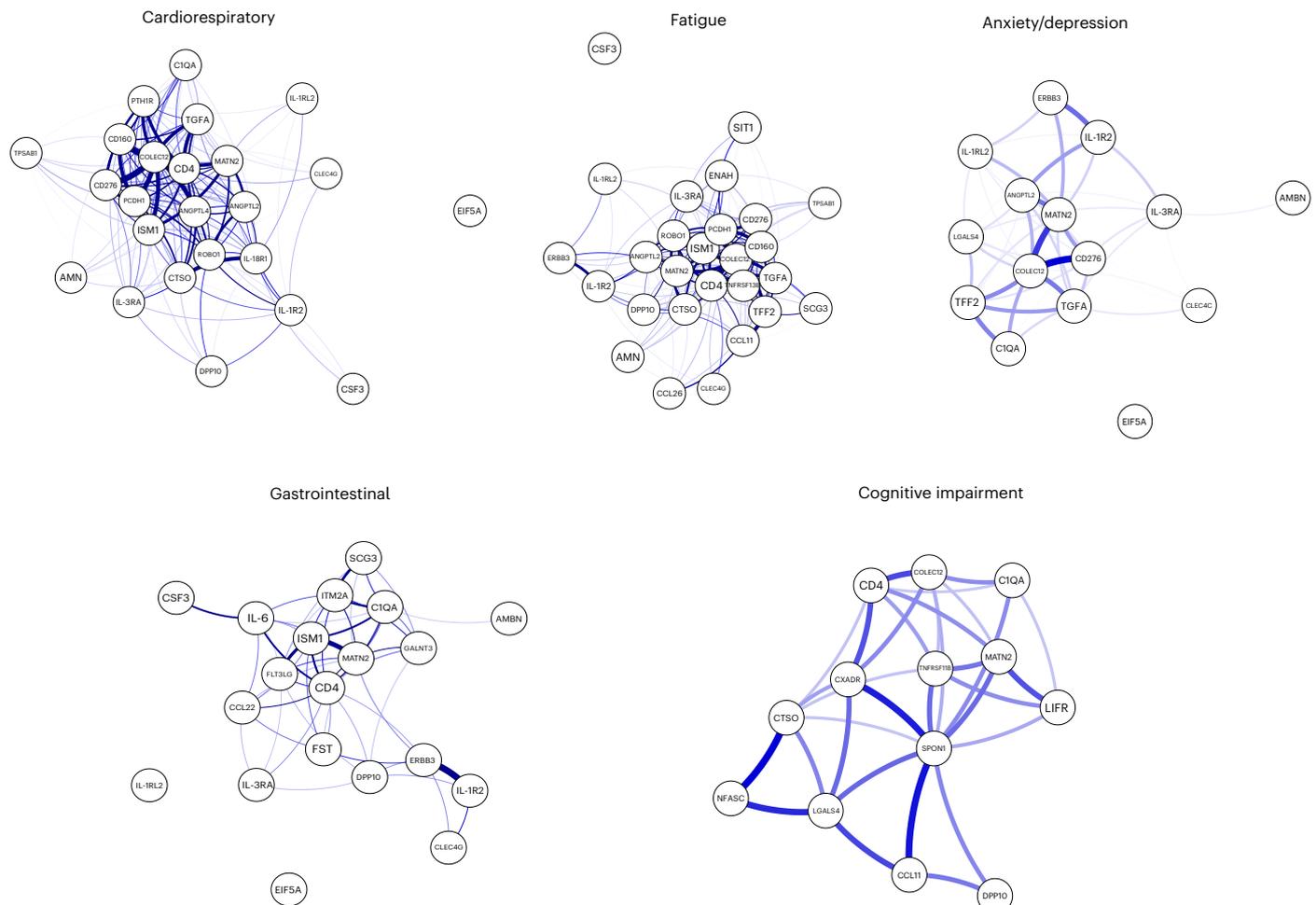


Fig. 2 | Network analyses define key immune mediators in LC symptom groups. Network analysis of Olink mediators associated with cardioresp ($n = 365$), fatigue ($n = 314$), anxiety/depression ($n = 202$), GI ($n = 124$) and cognitive groups ($n = 60$). Each node corresponds to a protein mediator

identified by PLR. The edges (blue lines) were weighted according to the size of Spearman's rank correlation coefficient between proteins. All edges represent positive and significant correlations ($P < 0.05$) after FDR adjustment.

and Care Excellence definitions for LC include symptoms occurring 1 month post infection^{32,33}. Using the 1 month post-infection definition included 62 additional participants to our analysis (recovered $n = 21$, 3 females and median age 61 years and LC $n = 41$, 15 females and median age 60 years, Extended Data Fig. 2c) and found that inflammatory associations with each LC group were consistent with our analysis based on the WHO definition (Extended Data Fig. 2d–h). Finally, to validate the analytical approach (PLR) we examined the distribution of data, prioritizing proteins that were most strongly associated with each LC/recovered group (IL-1R2, MATN2, NFASC and sCDS8). Each protein was significantly elevated in the LC group compared with recovered (Fig. 1h,j and Extended Data Fig. 4), consistent with the PLR. Alternative regression approaches (unadjusted regression models and partial least squares, PLS) reported results consistent with the original analysis of protein associations and LC outcome in the WHO-defined cohort (Fig. 1c–g, Supplementary Table 3 and Extended Data Figs. 5 and 6). The standard errors of PLS estimates were wide (Extended Data Fig. 6), consistent with previous demonstrations that PLR is the optimal method to analyze high-dimensional data where variables may have combined effects³⁴. As inflammatory proteins are often colinear, working in-tandem to mediate effects, we prioritized PLR results to draw conclusions.

To explore the relationship between inflammatory mediators associated with different LC symptoms, we performed a network analysis of Olink mediators highlighted by PLR within each LC group.

COLEC12 and markers of endothelial and mucosal inflammation (MATN2, PCDH1, ROBO1, ISM1, ANGPTL2, TGF- α and TFF2) were highly correlated within the cardioresp, fatigue and anxiety/depression groups (Fig. 2 and Extended Data Fig. 7). Elevated PCDH1, an adhesion protein modulating airway inflammation³⁵, was highly correlated with other inflammatory proteins associated with the cardioresp group (Fig. 2), suggesting that systemic inflammation may arise from the lung in these individuals. This was supported by increased expression of IL-3RA, which regulates innate immune responses in the lung through interactions with circulating IL-3 (ref. 36), in fatigue (Figs. 1d and 2), which correlated with markers of tissue inflammation, including PCDH1 (Fig. 2). MATN2 and ISM1, mucosal proteins that enhance inflammation^{37,38}, were highly correlated in the GI group (Fig. 2), highlighting the role of tissue-specific inflammation in different LC groups. SCG3 correlated less closely with mediators in the GI group (Fig. 2), suggesting that the brain–gut axis may contribute separately to some GI symptoms. SPON-1, which regulates neural growth²¹, was the most highly correlated mediator in the cognitive group (Fig. 2 and Extended Data Fig. 7), highlighting that processes within nerve tissue may underlie this group. These observations suggested that inflammation might arise from mucosal tissues and that additional mechanisms may contribute to pathophysiology underlying the GI and cognitive groups.

Women were more likely to experience LC (Table 1), as found in previous studies¹. As estrogen can influence immunological responses³⁹, we investigated whether hormonal differences between men and

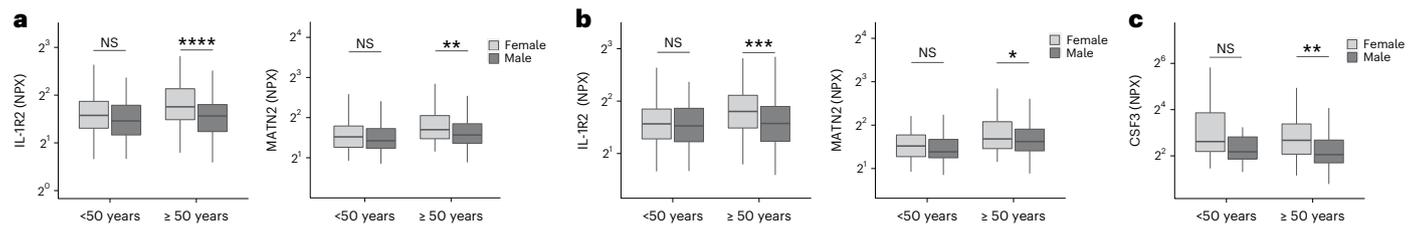


Fig. 3 | Elevated immune mediator levels are most pronounced in older women with LC. **a–c**, Olink-measured plasma protein levels (NPX) of IL-1R2 and MATN2 (**a** and **b**) and CSF3 (**c**) between LC men and LC women divided by age (<50 or ≥50 years) in the cardiorespiratory group (<50 years $n = 8$ and ≥50 years $n = 270$) (**a**), fatigue group (<50 years $n = 81$ and ≥50 years $n = 227$)

(**b**) and GI group (<50 years $n = 34$ and ≥50 years $n = 82$) (**c**). The median values were compared between men and women using two-sided Wilcoxon signed-rank test, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ and **** $P < 0.0001$. The box plot center line represents the median, the boundaries represent IQR and the whisker length represents $1.5 \times$ IQR.

women with LC in our cohort explained this trend. We grouped men and women with LC symptoms into two age groups (those younger than 50 years and those 50 years and older, using age as a proxy for menopause status in women) and compared mediator levels between men and women in each age group, prioritizing those identified by PLR to be higher in LC compared with recovered. As we aimed to understand whether women with LC had stronger inflammatory responses than men with LC, we did not assess differences in men and women in the recovered group. IL-1R2 and MATN2 were significantly higher in women ≥50 years than men ≥50 years in the cardioresp group (Fig. 3a, IL-1R2 and MATN2) and the fatigue group (Fig. 3b). In the GI group, CSF3 was higher in women ≥50 years compared with men ≥50 years (Fig. 3c), indicating that the inflammatory markers observed in women were not likely to be estrogen-dependent. Women have been reported to have stronger innate immune responses to infection and to be at greater risk of autoimmunity³⁹, possibly explaining why some women in the ≥50 years group had higher inflammatory proteins than men the same group. Proteins associated with the anxiety/depression (IL-1R2 $P = 0.11$ and MATN2 $P = 0.61$, Extended Data Fig. 8a) and cognitive groups (CTSO $P = 0.64$ and NFASC $P = 0.41$, Extended Data Fig. 8b) were not different between men and women in either age group, consistent with the absent/weak association between sex and these outcomes identified by PLR (Fig. 1e,g). Though our findings suggested that nonhormonal differences in inflammatory responses may explain why some women are more likely to have LC, they require confirmation in adequately powered studies.

To test whether local respiratory tract inflammation persisted after COVID-19, we compared nasosorption samples from 89 participants (recovered, $n = 31$; LC, $n = 33$; and healthy SARS-CoV-2 naive controls, $n = 25$, Supplementary Tables 4 and 5). Several inflammatory markers were elevated in the upper respiratory tract post COVID (including IL-1 α , CXCL10, CXCL11, TNF, VEGF and TFF2) when compared with naive controls, but similar between recovered and LC (Fig. 4a). In the cardioresp group ($n = 29$), inflammatory mediators elevated in plasma (for example, IL-6, APO-2, TGF- α and TFF2) were not elevated in the upper respiratory tract (Extended Data Fig. 9a) and there was no correlation between plasma and nasal mediator levels (Extended Data Fig. 9b). This exploratory analysis suggested upper respiratory tract inflammation post COVID was not specifically associated with cardiorespiratory symptoms.

To explore whether SARS-CoV-2 persistence might explain the inflammatory profiles observed in the cardioresp group, we measured SARS-CoV-2 nucleocapsid (N) antigen in sputum from 40 participants (recovered $n = 17$ and LC $n = 23$) collected approximately 6 months post hospitalization (Supplementary Table 6). All samples were compared with pre-pandemic bronchoalveolar lavage fluid ($n = 9$, Supplementary Table 4). Only four samples (recovered $n = 2$ and LC $n = 2$) had N antigen above the assay's lower limit of detection, and there was no difference in N antigen concentrations between LC and recovered (Fig. 4b, $P = 0.78$). These observations did not exclude viral persistence, which

might require tissues samples for detection^{40,41}. On the basis of the hypothesis that persistent viral antigen might prevent a decline in antibody levels over time, we examined the titers of SARS-CoV-2-specific antibodies in unvaccinated individuals (recovered $n = 19$ and LC $n = 35$). SARS-CoV-2 N-specific ($P = 0.023$) and spike (S)-specific ($P = 0.0040$) immunoglobulin G (IgG) levels were elevated in LC compared with recovered (Fig. 4c).

Overall, we identified myeloid inflammation and complement activation in the cardioresp, fatigue, anxiety/depression, cognitive and GI groups 6 months after hospitalization (Extended Data Fig. 10). Our findings build on results of smaller studies^{5,6,42} and are consistent with a genome-wide association study that identified an independent association between LC and *FOXP4*, which modulates neutrophilic inflammation and immune cell function^{43,44}. In addition, we identified tissue-specific inflammatory elements, indicating that myeloid disturbance in different tissues may result in distinct symptoms. Multiple mechanisms for LC have been suggested, including autoimmunity, thrombosis, vascular dysfunction, SARS-CoV-2 persistence and latent virus reactivation¹. All these processes involve myeloid inflammation and complement activation⁴⁵. Complement activation in LC has been suggested in a proteomic study in 97 mostly nonhospitalized COVID-19 cases⁴² and a study of 48 LC patients, of which one-third experienced severe acute disease⁴⁶. As components of the complement system are known to have a short half-life⁴⁷, ongoing complement activation suggests active inflammation rather than past tissue damage from acute infection.

Despite the heterogeneity of LC and the likelihood of coexisting or multiple etiologies, our work suggests some common pathways that might be targeted therapeutically and supports the rationale for several drugs currently under trial. Our finding of increased sCD58 levels (associated with suppression of monocyte–lymphocyte interactions²⁶) in the recovered group, strengthens our conclusion that myeloid inflammation is central to the biology of LC and that trials of steroids, IL-1 antagonists, JAK inhibitors, naltrexone and colchicine are justified. Although anticoagulants such as apixaban might prevent thrombosis downstream of complement dysregulation, they can also increase the risk of serious bleeding when given after COVID-19 hospitalization⁴⁸. Thus, clinical trials, already underway, need to carefully assess the risks and benefits of anticoagulants (Supplementary Table 2).

Our finding of elevated S- and N-specific IgG in LC could suggest viral persistence, as found in other studies^{6,42,49}. Our network analysis indicated that inflammatory proteins in the cardioresp group interacted strongly with ISM1 and ROBO1, which are expressed during respiratory tract infection and regulate lung inflammation^{50,51}. Although we were unable to find SARS-CoV-2 antigen in sputum from our LC cases, we did not test for viral persistence in GI tract and lung tissue^{40,41} or in plasma⁵². Evidence of SARS-CoV-2 persistence would justify trials of antiviral drugs (singly or in combination) in LC. It is also possible that autoimmune processes could result in an innate inflammatory profile in LC. Autoreactive B cells have been identified in LC patients with higher SARS-CoV-2-specific antibody titers in a study of mostly

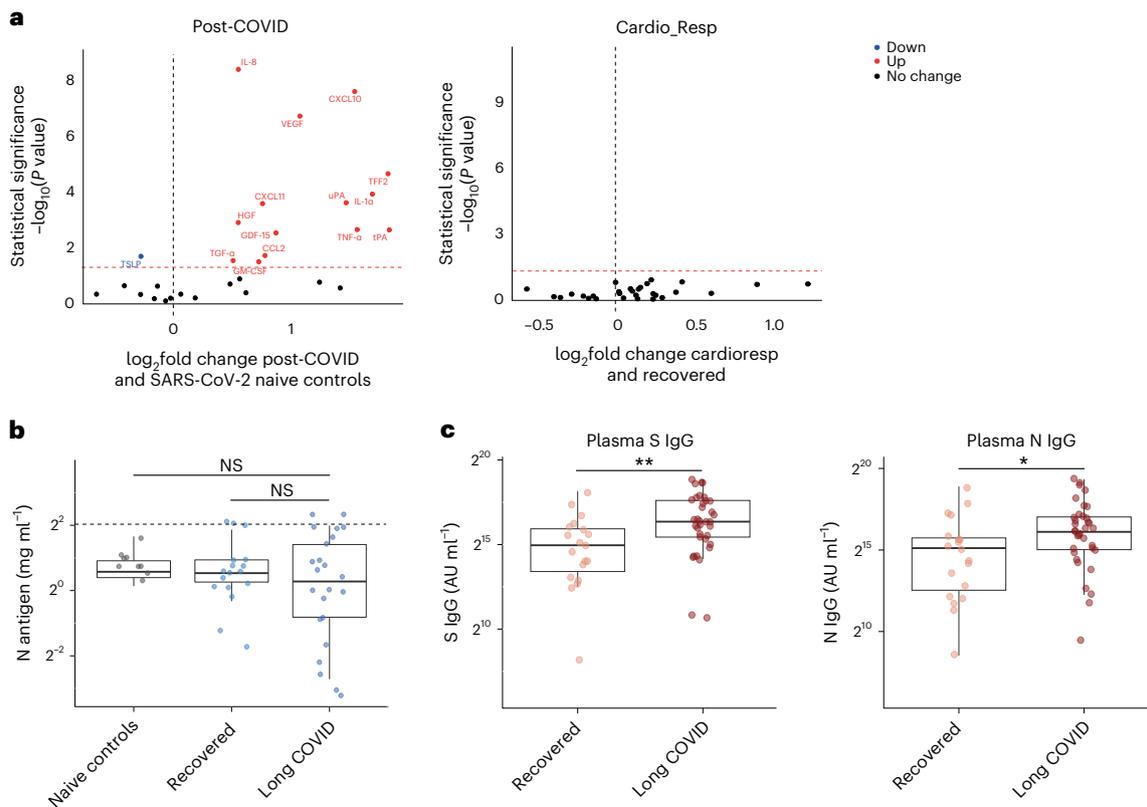


Fig. 4 | Pronounced mucosal inflammation after COVID-19 is not associated with LC. **a**, Nasal cytokines measured by immunoassay in post-COVID participants ($n = 64$) compared with healthy SARS-CoV-2 naive controls ($n = 25$), and between the cardioresp group ($n = 29$) and the recovered group ($n = 31$). The red values indicate significantly increased cytokine levels after FDR adjustment ($P < 0.05$) using two-tailed Wilcoxon signed-rank test. **b**, SARS-CoV-2 N antigen measured in sputum by electrochemiluminescence from recovered ($n = 17$) and pooled LC ($n = 23$) groups, compared with BALF from SARS-CoV-2

naive controls ($n = 9$). The horizontal dashed line indicates the lower limit of detection of the assay. **c**, Plasma S- and N-specific IgG responses measured by electrochemiluminescence in the LC ($n = 35$) and recovered ($n = 19$) groups. The median values were compared using two-sided Wilcoxon signed-rank tests, NS $P > 0.05$, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ and **** $P < 0.0001$. The box plot center lines represent the median, the boundaries represent IQR and the whisker length represents $1.5 \times$ IQR.

mild acute COVID cases (59% WHO 2–3)⁴², a different population from our study of hospitalized cases.

Our observations of distinct protein profiles in GI and cognitive groups support previous reports on distinct associations between Epstein–Barr virus reactivation and neurological symptoms, or autoantibodies and GI symptoms relative to other forms of LC^{49,53}. We did not assess autoantibody induction but found evidence of brain–gut axis disturbance (SCG3) in the GI group, which occurs in many autoimmune diseases⁵⁴. We found signatures suggestive of neuroinflammation (CIQA) in the cognitive group, consistent with findings of brain abnormalities on magnetic resonance imaging after COVID-19 hospitalization⁵⁵, as well as findings of microglial activation in mice after COVID-19 (ref. 56). Proinflammatory signatures dominated in the cardioresp, fatigue and anxiety/depression groups and were consistent with those seen in non-COVID depression, suggesting shared mechanisms⁵⁷. The association between markers of myeloid inflammation, including IL-3RA, and symptoms was greatest for fatigue. Whilst membrane-bound IL-3RA facilitates IL-3 signaling upstream of myelopoiesis³⁶ its soluble form (measured in plasma) can bind IL-3 and can act as a decoy receptor, preventing monocyte maturation and enhancing immunopathology⁵⁸. Monocytes from individuals with post-COVID fatigue are reported to have abnormal expression profiles (including reduced CXCR2), suggestive of altered maturation and migration^{5,59}. Lung-specific inflammation was suggested by the association between PCDH1 (an airway epithelial adhesion molecule³⁵) and cardioresp symptoms.

Our observations do not align with all published observations on LC. One proteomic study of 55 LC cases after generally mild (WHO 2–3) acute disease found that TNF and IFN signatures were elevated in LC³. Vasculoproliferative processes and metabolic disturbance have been reported in LC^{4,60}, but these studies used uninfected healthy individuals for comparison and cannot distinguish between LC-specific phenomena and residual post-COVID inflammation. A study of 63 adults (LC, $n = 50$ and recovered, $n = 13$) reported no association between immune cell activation and LC 3 months after infection⁶¹, though myeloid inflammation was not directly measured, and 3 months post infection may be too early to detect subtle differences between LC and recovered cases due to residual acute inflammation.

Our study has limitations. We designed the study to identify inflammatory markers identifying pathways underlying LC subgroups rather than diagnostic biomarkers. The ORs we report are small, but associations were consistent across alternative methods of analysis and when using different LC definitions. Small effect sizes can be expected when using PLR, which shrinks correlated mediator coefficients to reflect combined effects and prevent colinear inflation⁶², and could also result from measurement of plasma mediators that may underestimate tissue inflammation. Although our LC cohort is large compared with most other published studies, some of our subgroups are small (only 60 cases were designated cognitive). Though the performance of the cognitive PLR model was adequate, our findings should be validated in larger studies. It should be noted that our cohort of hospitalized cases may not represent all types of LC, especially those occurring after

mild infection. We looked for an effect of acute disease severity within our study and did not find it, and are reassured that the inflammatory profiles we observed were consistent with those seen in smaller studies including nonhospitalized cases^{42,46}. Studies of posthospital LC may be confounded by ‘posthospital syndrome’, which encompasses general and nonspecific effects of hospitalization (particularly intensive care)⁶³.

In conclusion, we found markers of myeloid inflammation and complement activation in our large prospective posthospital cohort of patients with LC, in addition to distinct inflammatory patterns in patients with cognitive impairment or gastrointestinal symptoms. These findings show the need to consider subphenotypes in managing patients with LC and support the use of antiviral or immunomodulatory agents in controlled therapeutic trials.

Online content

Any methods, additional references, Nature Portfolio reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at <https://doi.org/10.1038/s41590-024-01778-0>.

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Felicity Liew^{1,399}, Claudia Efstathiou^{1,399}, Sara Fontanella¹, Matthew Richardson², Ruth Saunders², Dawid Swieboda¹, Jasmin K. Sidhu¹, Stephanie Ascough¹, Shona C. Moore³, Noura Mohamed⁴, Jose Nunag⁵, Clara King⁵, Olivia C. Leavy^{2,6}, Omer Elneima², Hamish J. C. McAuley², Aarti Shikotra⁷, Amisha Singapuri², Marco Sereno², Victoria C. Harris², Linzy Houchen-Wolloff⁸, Neil J. Greening², Nazir I. Lone⁹, Matthew Thorpe¹⁰, A. A. Roger Thompson¹¹, Sarah L. Rowland-Jones¹¹, Annemarie B. Docherty¹⁰, James D. Chalmers¹², Ling-Pei Ho¹³, Alexander Horsley¹⁴, Betty Raman¹⁵, Krisnah Poinasamy¹⁶, Michael Marks^{17,18,19}, Onn Min Kon¹, Luke S. Howard¹, Daniel G. Wootton³, Jennifer K. Quint¹, Thushan I. de Silva¹¹, Antonia Ho²⁰, Christopher Chiu¹, Ewen M. Harrison¹⁰, William Greenhalf²¹, J. Kenneth Baillie^{10,22,23}, Malcolm G. Semple^{3,24}, Lance Turtle^{3,24}, Rachael A. Evans², Louise V. Wain^{2,6}, Christopher Brightling², Ryan S. Thwaites^{1,399}✉, Peter J. M. Openshaw^{1,399}✉, PHOSP-COVID collaborative group* & ISARIC investigators*

¹National Heart and Lung Institute, Imperial College London, London, UK. ²Institute for Lung Health, Leicester NIHR Biomedical Research Centre, University of Leicester, Leicester, UK. ³NIHR Health Protection Research Unit in Emerging and Zoonotic Infections, Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Liverpool, UK. ⁴The Imperial Clinical Respiratory Research Unit, Imperial College NHS Trust, London, UK. ⁵Cardiovascular Research Team, Imperial College Healthcare NHS Trust, London, UK. ⁶Department of Population Health Sciences, University of Leicester, Leicester, UK. ⁷NIHR Leicester Biomedical Research Centre, University of Leicester, Leicester, UK. ⁸Centre for Exercise and Rehabilitation Science, NIHR Leicester Biomedical Research Centre-Respiratory, University of Leicester, Leicester, UK. ⁹Usher Institute, University of Edinburgh, Edinburgh, UK. ¹⁰Centre for Medical Informatics, The Usher Institute, University of Edinburgh, Edinburgh, UK. ¹¹Department of Infection, Immunity and Cardiovascular Disease, University of Sheffield, Sheffield, UK. ¹²University of Dundee, Ninewells Hospital and Medical School, Dundee, UK. ¹³MRC Human Immunology Unit, University of Oxford, Oxford, UK. ¹⁴Division of Infection, Immunity and Respiratory Medicine, Faculty of Biology, Medicine and Health, University of Manchester, Manchester, UK. ¹⁵Radcliffe Department of Medicine, University of Oxford, Oxford, UK. ¹⁶Asthma + Lung UK, London, UK. ¹⁷Department of Clinical Research, London School of Hygiene and Tropical Medicine, London, UK. ¹⁸Hospital for Tropical Diseases, University College London Hospital, London, UK. ¹⁹Division of Infection and Immunity, University College London, London, UK. ²⁰MRC Centre for Virus Research, School of Infection and Immunity, University of Glasgow, Glasgow, UK. ²¹Institute of Systems, Molecular and Integrative Biology, University of Liverpool, Liverpool, UK. ²²The Roslin Institute, University of Edinburgh, Edinburgh, UK. ²³Pandemic Science Hub, University of Edinburgh, Edinburgh, UK. ²⁴The Pandemic Institute, University of Liverpool, Liverpool, UK. ³⁹⁹These authors contributed equally: Felicity Liew, Claudia Efstathiou, Ryan S. Thwaites, Peter J. M. Openshaw.

*Lists of authors and their affiliations appear at the end of the paper. ✉ e-mail: r.thwaites@imperial.ac.uk; p.openshaw@imperial.ac.uk

PHOSP-COVID collaborative group

Kathryn Abel^{25,26}, H. Adamali²⁷, Davies Adeloye²⁸, Oluwaseun Adeyemi²⁹, Rita Adrego²⁹, Laura Aguilar Jimenez³⁰, Shanaz Ahmad³¹, N. Ahmad Haider³², Rubina Ahmed³³, Nyarko Ahwireng³⁴, Mark Ainsworth³⁵, Asma Alamoudi³⁵, Mariam Ali³⁶, M. Aljarroof³⁷, Louise Allan³⁸, Richard Allen³⁹, Lisa Allerton⁴⁰, Lynne Allsop⁴¹, Ann Marie Allt⁴⁰, Paula Almeida⁴², Bashar Al-Shekly⁴³, Danny Altmann⁴⁴, Maria Alvarez Corral⁴⁵, Shannon Amoils⁴⁶, David Anderson⁴⁷, Charalambos Antoniadou⁴⁸, Gill Arbane³⁰, Ava Maria Arias⁴⁵, Cherie Armour⁴⁹, Lisa Armstrong⁵⁰, Natalie Armstrong³⁷, David Arnold²⁷, H. Arnold³⁷, A. Ashish⁵¹, Andrew Ashworth⁵², M. Ashworth⁵³, Shahab Aslani⁵⁴, Hosanna Assefa-Kebede²⁹, Paul Atkin⁵⁵, Catherine Atkin³², Raminder Aul³⁶, Hnin Aung³⁷, Liam Austin⁵⁶, Cristina Avram⁴³, Nikos Avramidis^{57,58}, A. Ayoub⁵⁹, Marta Babores⁶⁰, Rhiannon Baggott³², J. Bagshaw⁶¹, David Baguley⁶², Elisabeth Bailey⁶³, J. Kenneth Baillie^{57,58,64}, Steve Bain⁶⁵, Majda Bakali³⁷, M. Bakau³⁷, E. Baldry³⁷, Molly Baldwin³⁷, David Baldwin⁶⁶, Clive Ballard³⁸, Amita Banerjee⁵⁴, Dongchun Bang³⁴, R. E. Barker⁶⁷, Laura Barman⁶⁸, Perdita Barran²⁵, Shaney Barratt²⁷, Fiona Barrett⁶⁹, Donna Basire³⁴, Neil Basu⁴⁷, Michelle Bates³², A. Bates⁴⁸, R. Batterham⁵⁴, Helen Baxendale⁷⁰, Gabrielle Baxter⁵⁴, Hannah Bayes⁴⁰, M. Beadsworth⁴⁰, Paul Beckett⁷¹, M. Beggs⁴⁸, M. Begum⁶¹, Paul Beirne⁵², Murdina Bell⁷², Robert Bell⁵⁴, Kaytie Bennett⁴¹, Eva Beranova⁵⁶, Areti Bermerpi⁷³, Anthony Berridge⁴⁰, Colin Berry⁴⁷, Sarah Betts³⁰, Emily Bevan⁴⁵, Kamaldeep Bhui⁴⁸, Michelle Bingham³⁹, K. Birchall⁶¹, Lettie Bishop⁷⁴, Karen Bisnauthsing³⁰, John Blaikely⁴³, Angela Bloss³⁵, Annette Bolger⁷⁵, Charlotte Bolton⁷⁶, J. Bonnington⁷⁶, A. Botkai³², Charlotte Bourne³⁷, Michelle Bourne³⁷, Kate Bramham⁷⁷, Lucy Brear⁷⁸, G. Breen⁷⁹, Jonathon Breeze²⁹, Katie Breeze⁴⁸, Andrew Briggs⁸⁰, E. Bright⁸¹, Christopher Brightling², Simon Brill³¹, K. Brindle⁵⁵, Lauren Broad⁸², Andrew Broadley⁸³, Claire Brookes⁶⁸, Mattew Broome⁸⁴, Vanessa Brown⁴⁹, M. Brown⁷⁷, Jo Brown⁴⁰, J. Brown⁵⁹, Ammani Brown⁴⁷, Angela Brown⁷², M. Brown⁷², Jeremy Brown³⁴, Terry Brugha³⁹, Nigel Brunskill³⁷, M. Buch⁴³, Phil Buckley⁴¹, Anda Bularga⁸⁵, Ed Bullmore⁸⁶, Jenny Bunker⁸⁷, L. Burden⁸⁸, Tracy Burdett⁸⁹, David Burn⁹⁰, G. Burns⁵⁹, A. Burns⁹¹, John Busby⁴⁹, Robyn Butcher⁶¹, Al-Tahoor Butt⁹², S. Byrne²⁹, P. Cairns³⁷, P. C. Calder⁶⁶, Ellen Calvelo⁸⁸, H. Carborn⁶¹, Bethany Card⁸⁸, Caitlin Carr⁸⁸, Liesel Carr³⁷, G. Carson⁹³, Penny Carter³⁵, Anna Casey³², M. Cassar³⁵, Jonathon Cavanagh⁹⁴, Manish Chablani⁹⁵, Trudie Chalder⁹⁶, James D. Chalmers¹¹, Rachel Chambers³⁴, Flora Chan⁶¹, K. M. Channon⁴⁸, Kerry Chapman⁶¹, Amanda Charalambou³⁷, N. Chaudhuri⁹⁷, A. Checkley³⁴, Jin Chen³⁵, Yutung Cheng⁶¹, Luke Chetham⁶¹, Caroline Childs⁹⁸, Edwin Chilvers⁸⁸, H. Chinoy²⁵, A. Chiribiri⁹⁹, K. Chong-James¹⁰⁰, N. Choudhury⁴³, Gaunab Choudhury¹⁰¹, Phillip Chowieńczyk¹⁰², C. Christie³⁷, Melanie Chrystal⁷⁶, Cameron Clark⁶¹, David Clark⁴⁸, Jude Clarke⁵², S. Clohisey¹⁰¹, G. Coakley¹⁰³, Zach Coburn⁶¹, S. Coetzee¹⁰⁴, Joby Cole⁶¹, Chris Coleman⁶², Florence Conneh³⁵, David Connell¹⁰⁵, Bronwen Connolly⁴⁹, Lynda Connor¹⁰⁶, Amanda Cook¹⁰⁶, Shirley Cooper⁴⁰, B. Cooper³², Josh Cooper⁵¹, Donna Copeland¹⁸⁸, Tracey Cosier⁵⁶, Eamon Coughlan¹⁰⁷, Martina Coulding⁹², C. Coupland⁵², E. Cox⁶², Thelma Craig⁴⁹, P. Crisp⁸¹, Daniele Cristiano⁶⁷, Michael Crooks⁵⁵, Andy Cross⁴⁰, Isabel Cruz⁷³, P. Cullinan⁸⁸, D. Cuthbertson³³, Luke Daines⁹, Matthhew Dalton⁵², Patrick Daly⁸⁸, Alison Daniels¹⁰⁸, P. Dark¹⁰⁹, Joanne Dasgin³², C. David¹⁰⁰, Anthony David⁵⁴, Ffyon Davies⁷⁵, Ellie Davies¹¹⁰, Kim Davies¹⁰⁴, Gareth Davies⁵⁹, Gwyneth Davies¹⁰⁶, Melanie Davies³⁷, Joy Dawson¹¹¹, Camilla Dawson³², Enya Daynes³⁷, Anthony De Soya⁵⁹, Bill Deakin²⁵, Andrew Deans¹⁰¹, C. Deas¹⁰⁵, Joanne Deery⁵⁶, Sylviane Defres⁴⁰, Amanda Dell¹¹², K. Dempsey⁷³, Emma Denny⁵⁴, J. Dennis¹¹³, A. Dewar³⁰, Ruvini Dharmagunawardena⁸¹, Nawar Diar-Bakerly¹⁰⁹, Caroline Dickens⁷¹, A. Dipper²⁷, Sarah Diver³⁷, Shalin Diwanji¹¹⁴, Myles Dixon⁶¹, R. Djukanovic⁹⁸, Hannah Dobson¹¹⁵, S. L. Dobson⁴⁰, Annemarie B. Docherty⁹, A. Donaldson⁶⁹, T. Dong³⁵,

N. Dormand⁶⁷, Andrew Dougherty⁴⁷, Rachael Dowling³⁷, Stephen Drain⁴⁹, Katharine Draxlbauer³², Katie Drury⁵⁵, Pearl Dulawan²⁹, A. Dunleavy³⁶, Sarah Dunn²⁷, Catherine Dupont⁷⁶, Joanne Earley⁴⁰, Nicholas Easom⁵⁵, Carlos Echevarria⁵⁹, Sarah Edwards³⁷, C. Edwardson³⁷, Claudia Efstathiou^{1,399}, Anne Elliott¹⁰⁵, K. Elliott⁶⁸, Yvette Ellis¹¹⁶, Anne Elmer⁷³, Omer Elneima², Hosni El-Taweel¹¹¹, Teriann Evans⁸², Ranuromanana Evans³⁵, D. Evans¹⁰⁹, R. Evans³⁴, H. Evans³⁷, Rachael A. Evans², Jonathon Evans¹¹⁷, Cerys Evenden¹¹⁰, Lynsey Evison⁸⁸, Laura Fabbri⁶², Sara Fairbairn¹¹², Alexandra Fairman⁶¹, K. Fallon⁴⁷, David Faluyi⁴³, Clair Favager⁵², Tamanah Fayzan⁸⁸, James Featherstone⁸⁹, T. Felton⁴³, V. Ferreira³⁵, J. Finch³⁷, Selina Finney³⁹, J. Finnigan⁶¹, L. Finnigan¹¹⁸, Helen Fisher⁵⁹, S. Fletcher⁹⁸, Rachel Flockton⁵⁵, Margaret Flynn⁴¹, H. Foot⁶¹, David Foote⁶¹, Amber Ford⁶¹, D. Forton³⁶, Eva Fraile¹¹⁹, C. Francis⁵⁹, Richard Francis³³, Susan Francis⁶², Anew Frankel⁴⁴, Emily Fraser³⁵, Rob Free³⁹, N. French⁴⁰, X. Fu⁴⁸, Jonathon Fuld⁷³, J. Furniss¹⁰¹, Lucie Garner⁷⁰, N. Gautam³², John Geddes³⁵, J. George¹⁰⁵, P. George⁶⁷, Michael Gibbons¹²⁰, Rhyann Gill⁸⁷, Mandy Gill⁴¹, L. Gilmour⁴⁷, F. Gleeson³⁵, Jodie Glossop⁵², Sarah Glover³⁷, Nicola Goodman³⁷, Camelia Goodwin⁴¹, Bibek Gooptu³⁷, Hussain Gordon⁸⁸, T. Gorsuch⁴³, M. Grotorex⁴¹, Paul Greenhaff⁷⁶, William Greenhalf²⁰, Alan Greenhalgh⁵⁹, Neil J. Greening², John Greenwood⁵², Rebecca Gregory⁶¹, Heidi Gregory⁴¹, D. Grieve⁴⁷, Denise Griffin⁴⁵, L. Griffiths⁶⁸, Anne-Marie Guerdette¹²¹, Beatriz Guillen-Guio^{6,122}, Mahitha Gummadi⁶⁷, Ayushman Gupta⁷⁶, Sambasivarao Gurram¹¹⁴, Elspeth Guthrie¹²³, Zoe Guy⁶⁸, Kate Hadley³⁷, Ahmed Haggag⁷, Kera Hailey⁴⁰, Brigid Hairsine⁵⁰, Pranab Haladar³⁷, Lucy Hall⁵², Ian Hall⁶², Mark Halling-Brown¹²⁴, R. Hamil⁷², Alyson Hancock¹¹⁰, Kia Hancock¹¹⁰, Neil Hanley⁴³, Sulaiman Haq⁸⁸, Hayley Hardwick⁴⁰, Tim Hardy⁵², E. Hardy¹⁰⁹, Beverley Hargadon³⁷, Kate Harrington⁶¹, Edward Harris¹²⁵, Victoria C. Harris², Ewen Harrison¹⁰¹, Paul Harrison³⁵, Nicholas Hart³⁰, Alice Harvey¹⁰⁹, Matt Harvey⁹⁸, M. Harvie²⁵, L. Haslam⁶¹, Claire Hastie¹²⁶, May Havinden-Williams³⁵, Jenny Hawkes⁴⁰, Nancy Hawkings¹¹², Jill Haworth¹¹², A. Hayday¹²⁷, Matthew Haynes⁸², J. Hazeldine³², Tracy Hazelton⁵⁶, Liam Heaney⁴⁹, Cheryl Heeley⁴¹, Jonathon Heeney⁸⁶, M. Heightman³⁴, Simon Heller¹²⁸, Max Henderson¹²³, Helen Henson⁵⁰, L. Hesselden⁶¹, Melanie Hewitt¹²¹, Victoria Highett⁴⁰, T. Hillman³⁴, T. Hiwot³², Ling-Pei Ho¹², Michaela Hoare¹¹², Amy Hoare²⁹, J. Hockridge⁶¹, Philip Hogarth⁵⁹, Ailsa Holbourn⁶¹, Sophie Holden³², L. Holdsworth⁵⁵, D. Holgate¹⁰⁹, Maureen Holland⁶⁰, Leah Holloway⁴¹, Katie Holmes¹²⁹, Megan Holmes⁴¹, B. Holroyd-Hind⁶¹, L. Holt⁶¹, Anil Hormis¹⁰⁸, Alexander Horsley¹³, Akram Hosseini⁴², M. Hotopf⁷⁹, Linzy Houchen-Wolff⁶⁸, Luke S. Howard⁴⁴, Kate Howard⁶⁸, Alice Howell⁶¹, E. Hufton⁶², Rachel Ann Hughes¹⁰⁴, Joan Hughes⁵⁹, Alun Hughes⁵⁴, Amy Humphries⁵², Nathan Huneke⁶⁶, E. Hurditch⁶¹, John Hurst³¹, Masud Husain⁴⁸, Tracy Hussell⁴³, John Hutchinson⁴¹, W. Ibrahim³⁷, F. Ilyas⁶¹, Julie Ingham¹⁰⁸, L. Ingram³⁷, Diana Ionita⁶⁸, Karen Isaacs³², Khalida Ismail⁷⁷, T. Jackson³², Joseph Jacob³⁴, W. Y. James¹⁰⁰, W. Jang⁷⁶, Claire Jarman⁶¹, Ian Jarrold¹³⁰, Hannah Jarvis³¹, Roman Jastrub³⁴, Bhagy Jayaraman¹³¹, Gisli Jenkins⁸⁸, P. Jezzard³⁵, Kasim Jiwa⁵⁹, C. Johnson⁷⁰, Simon Johnson⁶², Desmond Johnston⁴⁴, Caroline Jolley²⁹, S. Jones¹³², H. Jones⁷³, L. Jones⁸², Ian Jones¹³³, G. Jones⁵⁹, Heather Jones⁹², Mark Jones⁹⁸, Don Jones³⁹, Sherly Jose⁷³, Thomas Kabir¹³⁴, G. Kaltsakas³⁰, Vicky Kamwa³², N. Kanellakis⁹¹, Sabina Kaprowska⁴⁰, Zunaira Kausar⁴³, Natalie Keenan⁶⁰, S. Kelly¹⁰¹, G. Kemp⁵³, Steven Kerr¹³⁵, Helen Kerslake³⁰, Angela Key⁴⁰, Fasih Khan⁶², Kamlesh Khunti³⁷, Susan Kilroy⁹², Bernie King⁴⁹, Clara King⁸⁸, Lucy Kingham⁴⁸, Jill Kirk⁴¹, Paig Kitterick⁶², Paul Klenerman⁴⁸, Lucy Knibbs⁸², Sean Knight¹⁰⁹, Abigail Knighton²⁹, Onn Min Kon⁸⁸, S. Kon⁶⁷, Samantha Kon¹³⁶, Ania Korszun¹³⁷, Ivan Koychev³⁵, Claire Kurasz⁵⁰, Prathiba Kurupati³⁵, C. Laing³¹, Hanan Lamlum⁴⁸, G. Landers¹³⁶, Claudia Langenberg⁸⁶, Lara Lavelle-Langham⁴⁰, Allan Lawrie⁶¹, Cathy Lawson⁸⁹, Claire Lawson³⁹, Alison Layton⁸⁹, A. Lea³⁷, Olivia C. Leavy^{2,6}, Ju Hee Lee⁶¹, Elvina Lee⁶¹, D. Lee³⁷, Karen Leitch⁷², Rebecca Lenagh⁶¹, Victoria Lewis¹¹², Joanne Lewis⁷⁵, Keir Lewis¹³⁸, D. Lewis³², N. Lewis-Burke⁴⁰, X. Li⁴⁸, Felicity Liew^{1,399}, Tessa Light¹³¹, Liz Lightstone⁴⁴, W. Lilaonitkul⁵⁴, Lai Lim³¹, S. Linford⁷⁶, Anne Lingford-Hughes⁴⁴, M. Lipman³⁴, Kamal Liyanage⁶⁷, Arwel Lloyd⁷⁵, S. Logan³⁴, D. Lomas³⁴, Nazir I. Lone^{9,139}, Ronda Loosley¹⁰⁴, Janet Lord³², Harpreet Lota¹³⁶, Wayne Lovegrove⁴¹, Daniel Lozano-Rojas³⁹, Alice Lucey¹¹², Gardiner Lucy³⁹, E. Lukaschuk⁴⁸, Alison Lye⁶¹, Ceri Lynch¹¹⁰, S. MacDonald⁹⁴, G. MacGowan⁵⁹, Irene Macharia⁶¹, J. Mackie⁷⁰, L. Macliver⁷², S. Madathil³², Gladys Madzamba⁴⁰, Nick Magee⁴⁹, Murphy Magtoto³⁰, N. Mairs¹⁰⁹, N. Majeed¹⁰⁹, E. Major⁴⁹, Flora Malein⁴⁰, M. Malim²⁹, Georgia Mallison¹¹², William Man⁴⁴, S. Mandal³¹, K. Mangion⁴⁷, C. Manisty¹⁴⁰, R. Manley⁷⁵, Katherine March⁸⁸, Stefan Marciniak⁷³, Philip Marino³⁰, Myril Mariveles⁸⁸, Michael Marks¹⁶, Elizabeth Marouzet⁹⁸, Sophie Marsh⁴⁰, M. Marshall⁶¹, B. Marshall⁹⁸, Jane Martin⁴⁵, Adrian Martineau¹⁴¹, L. M. Martinez³⁰, Nick Maskell²⁷, Darwin Matila³¹, Wadzanai Matimba-Mupaya¹⁴², Laura Matthews⁷⁶, Angeline Mbuyisa⁶¹, Steve McAdoo⁴⁴, Hamish McAllister-Williams¹⁴³, Paul McArdle⁸⁴, Anne McArdle⁵³, Danny McAulay⁴⁹, Hamish J. C. McAuley², Gerry McCann³⁷, W. McCormick¹⁴⁴, Jacqueline McCormick⁹², P. McCourt³⁷, Celeste McCracken⁴⁸, Lorcan McCarvey⁴⁹, C. McGee³², K. McGee³², Jade McGinness⁴⁹, K. McGlynn⁴⁸, Andrew McGovern³⁸, Heather McGuinness¹⁰⁴, I. B. McInnes⁴⁷, Jerome McIntosh⁹², Emma McIvor⁷⁵, Katherine McIvor¹⁴⁵, Laura McLeavey⁸⁸, Aisling McMahon¹⁴⁶, Michael McMahon¹⁴⁷, L. McMorro¹⁰⁹, Teresa McNally³⁷, M. McNarry¹⁴⁸, J. McNeill⁶¹, Alison McQueen⁸², H. McShane³⁵, Chloe Mears⁴⁰, Clare Megson³⁵, Sharon Megson⁶¹, P. Mehta⁵⁴, J. Meiring⁶¹, Lucy Melling⁴⁰, Mark Mencias³⁶, R. Menke⁴⁸, Daniel Menzies⁷⁵, Marta Merida Morillas³⁴, Alice Michael⁷⁰, Benedict Michael⁵³, C. A. Miller²⁵, Lea Milligan⁴⁹, Nicholas Mills¹⁵⁰, Clare Mills⁸⁹, George Mills³⁷, L. Milner⁶¹, S. Misra⁶¹, Jane Mitchell⁴⁴, Abdelrahman Mohamed¹⁰⁴, Noura Mohamed⁴, S. Mohammed¹⁰⁵, Philip Molyneux⁴⁴, Will Monteiro³⁷, Silvia Moriera⁸⁸, Anna Morley²⁷, Leigh Morrison²⁷, Richard Morriss⁶², A. Morrow⁴⁷, Paul Moss⁸⁴, Alistair Moss³⁹, K. Motohashi⁴⁸, N. Msimanga³⁶, Elizabeta Mukaetova-Ladinska³⁹, Unber Munawar⁸⁸, Jennifer Murira⁵², Uttam Nanda⁷¹, Heeah Nassa¹¹², Mariam Nasser¹³⁶, Rashmita Nathu⁸⁷, Aoife Neal³², Robert Needham⁴², Paula Neill⁴⁷, Stefan Neubauer³⁵, D. E. Newby²⁸, Helen Newell⁶¹, J. Newman⁷⁰, Tom Newman⁶¹, Alex Newton-Cox³², T. E. Nichols⁴⁸, Tim Nicholson⁷⁷, Christos Nicolaou⁴⁴, Debby Nicoll³⁵, Athanasios Nikolaidis⁷⁶, C. Nikolaidou³⁵, C. M. Nolan⁶⁷, Matthew Noonan⁴⁰, C. Norman⁶¹, Petr Novotny³⁹, Kimon Ntotsis³⁹, Jose Nunag⁵, Lorenza Nwafor⁶¹, Uchechi Nwanguma⁸⁸, Joseph Nyaboko³², Linda O'Brien¹⁰⁴, C. O'Brien⁹⁹, Natasha Odell⁴³, Kate O'Donnell⁹⁴, Godwin Ogbole⁴⁸, G. Ogg³⁵, Olaoluwa Olaosebikan³¹, Catherine Oliver⁸², Zohra Omar¹⁰⁴, Peter J. M. Openshaw^{1,399}, D. P. O'Regan⁴⁴, Lorna Orriss-Dib⁸⁸, Lynn Osborne⁹⁵, Rebecca Osbourne⁴³, Marlies Ostermann³⁰, Charlotte Overton³⁹, J. Owen⁴⁵, J. Oxtou¹⁰⁹, Jamie Pack⁷⁰, Edmund Pacpaco³⁵, Stella-Maria Paddick¹⁴³, Sharon Painter¹⁵¹, Erola Pairo-Castineira^{57,58}, Ashkan Pakzad⁵⁴, Sue Palmer¹⁵², Padmasayee Papineni¹¹⁴, K. Paques⁷⁰, Kerry Paradowski⁸², Manish Pareek³⁷, Dhruv Parekh³², H. Parfrey⁷⁰, Carmen Pariente⁷⁷, S. Parker³⁷, M. Parkes⁷³, J. Parmar⁷⁰, Sheetal Patale²⁹, Manish Patel⁷², B. Patel⁶⁷, Suhani Patel⁶⁷, Dibya Pattenack⁶¹, M. Pavlides³⁵, Sheila Payne⁴⁵, Lorraine Pearce¹⁴⁴, John Pearl³⁹, Dan Peckham⁵², Jessica Pendlebury¹⁰⁹, Yanchun Peng³⁵, Chris Pennington¹¹², Ida Peralta²⁹, Emma Perkins¹⁰⁴, Z. Peterkin³², Tunde Peto⁴⁹, Nayia Petousi³⁵, John Petrie⁹⁴, Paul Pfeffer¹⁰⁰, Janet Phipps¹⁰⁴, S. Piechnik⁴⁸, John Pimm³⁵, Karen Piper Hanley⁴³,

Riinu Pius²⁸, Hannah Plant³⁴, S. Plein⁵², Tatiana Plekhanova³⁹, Megan Plowright⁶¹, Krisnah Poinasamy¹⁵, Oliver Polgar⁶⁷, L. Poll⁴⁰, Julie Porter⁶¹, Joanna Porter³⁴, Sofiya Portukhay¹³⁶, Natassia Powell²⁹, A. Prabh⁴⁵, James Pratt⁴⁰, Andrea Price¹¹², Claire Price¹¹², Carly Price⁵⁶, L. Price⁴⁴, D. Price⁵⁹, L. Price⁶⁷, Anne Prickett³⁷, I. Propescu⁴⁸, J. Propescu⁴⁸, Sabrina Prosper⁷⁶, S. Pugmire¹⁴⁴, Sheena Quaid¹¹⁴, Jackie Quigley⁷², Jennifer K. Quint⁴⁴, H. Qureshi³², I. N. Qureshi³⁷, K. Radhakrishnan⁴³, Najib Rahman³⁵, Markus Ralser¹⁵³, Betty Raman¹⁴, Hazel Ramos⁵⁶, Albert Ramos²⁹, Jade Rangeley⁵², Bojidar Rangelov⁵⁴, Liz Ratcliffe³², Phillip Ravenscroft⁶¹, Konrad Rawlik⁵⁷, Anne Reddington⁶³, R. Reddy¹²¹, A. Reddy⁷⁰, Heidi Redfern⁶⁸, Dawn Redwood¹⁵², Annabel Reed⁴⁵, Meryl Rees¹¹⁰, Tabitha Rees¹⁰⁶, Karen Regan⁷⁸, Will Reynolds⁵³, Carla Ribeiro⁷³, A. Richards⁵⁵, Emma Richardson⁴⁰, M. Richardson³⁹, Pilar Rivera-Ortega¹⁵⁴, K. Roberts⁷⁵, Elizabeth Robertson¹⁵⁵, Leanne Robinson¹¹¹, Emma Robinson⁵¹, Lisa Roche¹¹⁰, C. Roddis⁶¹, J. Rodger⁶¹, Natalie Rogers¹²⁶, Gavin Ross¹⁰⁴, Alexandra Ross⁸⁸, Jennifer Rosedale³⁰, Anthony Rostron¹⁴³, Anna Rowe⁴⁰, J. Rowland¹⁰⁵, M. J. Rowland³⁵, A. Rowland³⁷, Sarah L. Rowland-Jones¹⁰, Maura Roy⁸⁸, K. Roy³⁴, Igor Rudan²⁸, Richard Russell³⁷, Emily Russell⁸⁸, Gwen Saalmink⁵², Ramsey Sabit⁸², Beth Sage⁶⁹, T. Samakomva³⁶, Nilesh Samani³⁹, A. A. Samat⁴⁸, Claire Sampson¹²⁵, Katherine Samuel⁸⁸, Reena Samuel⁹⁸, Z. B. Sanders⁴⁸, Amy Sanderson¹⁵⁶, Elizabeth Sapey³², Dinesh Saralaya⁷⁸, Jack Sargant³⁹, Carol Sarginson⁶⁸, T. Sass⁹⁸, Naveed Sattar⁹⁴, Kathryn Saunders³⁵, Peter Saunders⁶¹, Ruth Saunders³⁹, Laura Saunders¹¹⁸, Heather Savill⁹², W. Saxon⁷⁵, Avan Sayer⁵⁹, J. Schronce⁸⁸, William Schwaeble⁸⁶, Janet Scott¹⁵⁷, Kathryn Scott⁴⁷, Nick Selby⁶², Malcolm G. Semple^{3,24}, Marco Sereno², Terri Ann Sewell⁴¹, Kamini Shah¹⁵⁸, Ajay Shah^{159,160}, P. Shah⁶⁷, Manu Shankar-Hari²⁸, M. Sharma³⁹, Claire Sharpe⁷⁷, Michael Sharpe³⁵, Sharlene Shashaa⁶⁰, Alison Shaw⁵⁰, Victoria Shaw⁴⁰, Karen Shaw⁴², Aziz Sheikh¹⁰¹, Sarah Shelton⁴¹, Liz Shenton⁵⁰, K. Shevket²⁹, Aarti Shikotra⁷, J. Short³², Sulman Siddique³⁶, Salman Siddiqui³⁷, J. Sidebottom⁶¹, Louise Sigfrid⁴⁸, Gemma Simons⁶⁶, Neil Simpson⁸⁸, John Simpson⁵⁹, Ananga Singapur², Suver Singh⁶⁷, Claire Singh³¹, Sally Singh³⁷, D. Sissons⁴¹, J. Skeemer³⁷, Katie Slack⁴¹, David Smith⁴⁴, Nikki Smith¹²⁶, Andrew Smith⁷², Jacqui Smith⁶¹, Laurie Smith⁶¹, Susan Smith⁴¹, M. Soares³⁷, Teresa Solano³⁰, Reanne Solly⁵⁶, A. R. Solstice¹⁰⁵, Tracy Soulsby³², David Southern⁷⁵, D. Sowter⁴¹, Mark Spears⁹⁴, Lisa Spencer⁵³, Fabio Speranza²⁹, Louise Staddon²⁷, Stefan Stanel²⁵, R. Steeds¹⁶¹, N. Steele⁶¹, Mike Steiner³⁹, David Stensel⁷⁴, G. Stephens⁶¹, Lorraine Stephenson⁸⁹, M. Stern⁸¹, Iain Stewart⁶², R. Stimpson⁶¹, Sue Stockdale⁴³, J. Stockley³², Wendy Stoker¹⁴⁴, Roisin Stone⁴⁹, Will Storrar⁴⁵, Andrew Storrie¹¹², Kim Storton⁷⁸, E. Stringer³⁷, Sophia Strong-Sheldrake¹⁴², Natalie Stroud¹¹⁰, Christian Subbe⁷⁵, Catherine Sudlow²⁸, Zehra Suleiman³², Charlotte Summers⁸⁶, C. Summersgill¹⁰⁹, Debbie Sutherland¹⁰⁵, D. L. Sykes⁵⁵, R. Sykes⁴⁷, Nick Talbot³⁵, Ai Lyn Tan⁵², Lawrence Tarusan⁸⁸, Vera Tavoukjian³⁶, Jessica Taylor⁷³, Abigail Taylor¹⁰⁴, Chris Taylor³⁹, John Paul Taylor¹⁴³, Amelie Te²⁹, H. Tedd⁵⁹, Caroline Tee¹⁰⁵, J. Teixeira³⁶, Helen Tench¹⁰⁴, Sarah Terry³⁹, Susannah Thackray-Nocera⁵⁵, Favas Thaivalappil¹⁰⁶, B. Thamu⁶¹, David Thickett⁸⁴, David Thomas⁸⁸, S. Thomas⁵⁹, Caradog Thomas¹⁰⁶, Andrew Thomas⁷⁶, T. Thomas-Woods¹¹⁰, A. A. Roger Thompson¹⁰, Tamika Thompson³², T. Thornton³⁷, Matthew Thorpe⁹, Ryan S. Thwaites^{1,399}, Jo Tilley¹⁵², N. Tinker⁶¹, Gerlynn Tiongson¹¹⁴, Martin Tobin³⁷, Johanne Tomlinson¹⁵¹, C. Tong³⁹, Mark Toshner⁷³, R. Touyz¹⁶², T. Treibel¹⁶³, K. A. Tripp⁴⁰, Drupad Trivedi²⁵, E. M. Tunncliffe³⁵, Alison Turnbull⁶⁸, Kim Turner⁶¹, Sarah Turner⁴¹, Victoria Turner⁹², E. Turner³⁹, Sharon Turney⁵⁶, Lance Turtle^{3,24}, Helena Turton⁶¹, Jacinta Ugoji¹¹⁹, R. Ugwuoke¹⁰⁹, Rachel Upthegrove⁸⁴, Jonathon Valabhji⁴⁴, Maximina Ventura³², Joanne Vere⁹², Carinna Vickers¹⁵², Ben Vinson⁵³, Ioannis Vogiatzis¹⁶⁴, Elaine Wade⁵², Phillip Wade⁶¹, Louise V. Wain^{2,6}, Tania Wainwright¹⁵², Lilian Wajero⁴⁰, Sinead Walder³², Samantha Walker¹³⁰, S. Walker⁶¹, E. Wall³⁴, Tim Wallis⁹⁸, Sarah Walmsley²⁸, Simon Walsh⁴⁴, J. A. Walsh⁶⁷, Louise Warburton¹⁵¹, T. J. C. Ward³⁷, Katie Warwick¹²¹, Helen Wassall⁶⁰, Samuel Waterson²⁷, L. Watson⁷³, Ekaterina Watson¹¹⁴, James Watson⁶¹, M. Webster⁴⁸, J. Weir McCall⁸⁶, H. Welch²⁷, Carly Welch³², B. Welsh⁷², Simon Wessely⁷⁷, Sophie West⁵⁹, Heather Weston⁵⁶, Helen Wheeler⁹⁸, Sonia White¹²¹, Victoria Whitehead⁷⁵, J. Whitney⁷⁷, S. Whittaker¹⁰⁹, Beverley Whittam⁵², V. Whitworth⁴¹, Andrew Wight⁶³, James Wild¹¹⁸, Martin Wilkins⁴⁴, Dan Wilkinson⁸⁴, Nick Williams⁴⁵, N. Williams¹⁶⁵, B. Williams⁵⁴, Jenny Williams⁸², S. A. Williams-Howard⁴⁰, Michelle Willicombe⁴⁴, Gemma Willis¹¹², James Willoughby⁵⁴, Ann Wilson¹⁴⁴, Imogen Wilson⁶¹, Daisy Wilson³², Nicola Window⁵², M. Witham⁵⁹, Rebecca Wolf-Roberts¹⁰⁴, Chloe Wood⁸⁸, F. Woodhead²⁷, Janet Woods⁵², Dan Wootton⁴⁰, J. Wormleighton³⁹, J. Worsley⁷³, David Wraith⁸⁴, Caroline Wrey Brown⁴⁵, C. Wright⁵⁵, S. Wright⁵⁹, Louise Wright⁶², J. Wyles⁴⁰, Inez Wynter⁴¹, C. Xie³⁵, Moucheng Xu⁵⁴, Najira Yasmin⁸⁸, S. Yasmin³², Tom Yates³⁷, Kay Por Yip³², Susan Young¹¹², Bob Young¹⁶⁶, A. Young⁵⁹, A. J. Yousuf³⁷, Amira Zawia⁶¹, Lisa Zeidan¹⁰⁸, Bang Zhao³⁹, Bang Zheng²⁸ & O. Zongo¹⁰⁰

²⁵University of Manchester, Manchester, UK. ²⁶Intensive Care Unit, Royal Infirmary of Edinburgh, Edinburgh, UK. ²⁷North Bristol NHS Trust and University of Bristol, Bristol, UK. ²⁸University of Edinburgh, Manchester, UK. ²⁹King's College Hospital NHS Foundation Trust and King's College London, London, UK. ³⁰Guy's and St Thomas' NHS Foundation Trust, London, UK. ³¹Royal Free London NHS Foundation Trust, London, UK. ³²University Hospital Birmingham NHS Foundation Trust and University of Birmingham, Birmingham, UK. ³³Stroke Association, London, UK. ³⁴University College London Hospital and University College London, London, UK. ³⁵Oxford University Hospitals NHS Foundation Trust and University of Oxford, Oxford, UK. ³⁶St George's University Hospitals NHS Foundation Trust, London, UK. ³⁷University Hospitals of Leicester NHS Trust and University of Leicester, Leicester, UK. ³⁸University of Exeter, Exeter, UK. ³⁹University of Leicester, Leicester, UK. ⁴⁰Liverpool University Hospitals NHS Foundation Trust and University of Liverpool, Liverpool, UK. ⁴¹Sherwood Forest Hospitals NHS Foundation Trust, Nottingham, UK. ⁴²Nottingham University Hospitals NHS Trust and University of Nottingham, London, UK. ⁴³Manchester University NHS Foundation Trust and University of Manchester, London, UK. ⁴⁴Imperial College London, London, UK. ⁴⁵Hampshire Hospitals NHS Foundation Trust, Basingstoke, UK. ⁴⁶British Heart Foundation, Birmingham, UK. ⁴⁷NHS Greater Glasgow and Clyde Health Board and University of Glasgow, Glasgow, UK. ⁴⁸University of Oxford, Oxford, UK. ⁴⁹Belfast Health and Social Care Trust and Queen's University Belfast, Belfast, UK. ⁵⁰Airedale NHS Foundation Trust, Keighley, UK. ⁵¹Wrightington Wigan and Leigh NHS Trust, Wigan, UK. ⁵²Leeds Teaching Hospitals and University of Leeds, Leeds, UK. ⁵³University of Liverpool, Liverpool, UK. ⁵⁴University College London, London, UK. ⁵⁵Hull University Teaching Hospitals NHS Trust and University of Hull, Hull, UK. ⁵⁶East Kent Hospitals University NHS Foundation Trust, Canterbury, UK. ⁵⁷Baillie Gifford Pandemic Science Hub, Centre for Inflammation Research, The Queen's Medical Research Institute, University of Edinburgh, Edinburgh, UK. ⁵⁸Roslin Institute, University of Edinburgh, Edinburgh, UK. ⁵⁹Newcastle upon Tyne Hospitals NHS Foundation Trust and University of Newcastle, Newcastle upon Tyne, UK. ⁶⁰East Cheshire NHS Trust, Macclesfield, UK. ⁶¹Sheffield Teaching NHS Foundation Trust and University of Sheffield, Sheffield, UK. ⁶²University of Nottingham, Nottingham, UK. ⁶³Wirral University Teaching Hospital, Wirral, UK. ⁶⁴MRC Human Genetics Unit, Institute of Genetics and Cancer, University of Edinburgh, Western General Hospital, Edinburgh, UK. ⁶⁵University of Swansea, Swansea, UK. ⁶⁶University of Southampton, London, UK. ⁶⁷Royal Brompton and Harefield Clinical Group, Guy's and St Thomas' NHS Foundation Trust, London, UK. ⁶⁸York and Scarborough NHS Foundation Trust, York, UK. ⁶⁹NHS Highland, Inverness, UK.

⁷⁰Royal Papworth Hospital NHS Foundation Trust, Cambridge, UK. ⁷¹University Hospitals of Derby and Burton, Derby, UK. ⁷²NHS Lanarkshire, Hamilton, UK. ⁷³Cambridge University Hospitals NHS Foundation Trust, NIHR Cambridge Clinical Research Facility and University of Cambridge, Cambridge, UK. ⁷⁴Loughborough University, Loughborough, UK. ⁷⁵Betsi Cadwallader University Health Board, Bangor, UK. ⁷⁶Nottingham University Hospitals NHS Trust and University of Nottingham, Nottingham, UK. ⁷⁷King's College London, London, UK. ⁷⁸Bradford Teaching Hospitals NHS Foundation Trust, Bradford, UK. ⁷⁹South London and Maudsley NHS Foundation Trust and King's College London, London, UK. ⁸⁰London School of Hygiene and Tropical Medicine, London, UK. ⁸¹Whittington Health NHS Trust, London, UK. ⁸²Cardiff and Vale University Health Board, Cardiff, UK. ⁸³Yeovil District Hospital NHS Foundation Trust, Yeovil, UK. ⁸⁴University of Birmingham, Birmingham, UK. ⁸⁵BHF Centre for Cardiovascular Science, University of Edinburgh, Edinburgh, UK. ⁸⁶University of Cambridge, Cambridge, UK. ⁸⁷NIHR Leicester Biomedical Research Centre-Respiratory Patient and Public Involvement Group, Leicester, UK. ⁸⁸Imperial College Healthcare NHS Trust and Imperial College London, London, UK. ⁸⁹Harrogate and District NHD Foundation Trust, Harrogate, UK. ⁹⁰Newcastle University/Chair of NIHR Dementia TRC, Newcastle, UK. ⁹¹Oxford University Hospitals NHS Foundation Trust, Oxford, UK. ⁹²Tameside and Glossop Integrated Care NHS Foundation Trust, Ashton-under-Lyne, UK. ⁹³University of Oxford, Nuffield Department of Medicine, Oxford, UK. ⁹⁴University of Glasgow, Glasgow, UK. ⁹⁵United Lincolnshire Hospitals NHS Trust, Grantham, UK. ⁹⁶Department of Psychological Medicine, Institute of Psychiatry, Psychology and Neuroscience, King's College London, London, UK. ⁹⁷University Hospital of South Manchester NHS Foundation Trust, Manchester, UK. ⁹⁸University Hospital Southampton NHS Foundation Trust and University of Southampton, Southampton, UK. ⁹⁹King's College Hospital/Guy's and St Thomas' NHS FT, London, UK. ¹⁰⁰Barts Health NHS Trust, London, UK. ¹⁰¹NHS Lothian and University of Edinburgh, Edinburgh, UK. ¹⁰²School of Cardiovascular Medicine and Sciences, King's College London, London, UK. ¹⁰³Lewisham and Greenwich NHS Trust, London, UK. ¹⁰⁴Hywel Dda University Health Board, Haverfordwest, UK. ¹⁰⁵NHS Tayside and University of Dundee, Dundee, UK. ¹⁰⁶Swansea Bay University Health Board, Port Talbot, UK. ¹⁰⁷Faculty of Medicine, Nursing and Health Sciences, School of Biomedical Sciences, Monash University, Melbourne, Victoria, Australia. ¹⁰⁸Rotherham NHS Foundation Trust, Rotherham, UK. ¹⁰⁹Salford Royal NHS Foundation Trust, Salford, UK. ¹¹⁰Cwm Taf Morgannwg University Health Board, Mountain Ash, UK. ¹¹¹Borders General Hospital, NHS Borders, Melrose, UK. ¹¹²Aneurin Bevan University Health Board, Caerleon, UK. ¹¹³University of Exeter Medical School, Exeter, UK. ¹¹⁴London North West University Healthcare NHS Trust, London, UK. ¹¹⁵Alzheimer's Research UK, Cambridge, UK. ¹¹⁶Health and Care Research Wales, Cardiff, UK. ¹¹⁷University of Bristol, Bristol, UK. ¹¹⁸University of Sheffield, Sheffield, UK. ¹¹⁹Great Western Hospital Foundation Trust, Swindon, UK. ¹²⁰Royal Devon and Exeter NHS Trust, Barnstaple, UK. ¹²¹Kettering General Hospital NHS Trust, Kettering, UK. ¹²²NIHR Leicester Biomedical Research Centre, Leicester, UK. ¹²³University of Leeds, Leeds, UK. ¹²⁴Royal Surrey NHS Foundation Trust, Cranleigh, UK. ¹²⁵Chesterfield Royal Hospital NHS Trust, Calow, UK. ¹²⁶Long Covid Support, London, UK. ¹²⁷King's College Hospital, NHS Foundation Trust and King's College London, London, UK. ¹²⁸Department of Oncology and Metabolism, University of Sheffield, Sheffield, UK. ¹²⁹NIHR Office for Clinical Research Infrastructure, London, UK. ¹³⁰Asthma UK and British Lung Foundation Partnership, London, UK. ¹³¹North Middlesex University Hospital NHS Trust, London, UK. ¹³²Action for Pulmonary Fibrosis, Peterborough, UK. ¹³³Cardiff University, National Centre for Mental Health, Cardiff, UK. ¹³⁴McPin Foundation, London, UK. ¹³⁵Roslin Institute, The University of Edinburgh, Edinburgh, UK. ¹³⁶The Hillingdon Hospitals NHS Foundation Trust, London, UK. ¹³⁷Queen Mary University of London, London, UK. ¹³⁸Swansea University, Swansea Welsh Network, Hywel Dda University Health Board, Swansea, UK. ¹³⁹Royal Infirmary of Edinburgh, NHS Lothian, Edinburgh, UK. ¹⁴⁰Barts Heart Centre, London, UK. ¹⁴¹Barts Health NHS Trust and Queen Mary University of London, London, UK. ¹⁴²Salisbury NHS Foundation Trust, Salisbury, UK. ¹⁴³University of Newcastle, Newcastle, UK. ¹⁴⁴Gateshead NHS Trust, Gateshead, UK. ¹⁴⁵Manchester Centre for Clinical Neurosciences, Salford Royal NHS Foundation Trust, Manchester, UK. ¹⁴⁶Kidney Research UK, Peterborough, UK. ¹⁴⁷NHS Dumfries and Galloway, Dumfries, UK. ¹⁴⁸Swansea University, Swansea, UK. ¹⁴⁹MQ Mental Health Research, London, UK. ¹⁵⁰BHF Centre for Cardiovascular Science, Usher Institute of Population Health Sciences and Informatics, University of Edinburgh, Edinburgh, UK. ¹⁵¹Shropshire Community Health NHS Trust, Shropshire, UK. ¹⁵²Somerset NHS Foundation Trust, Taunton, UK. ¹⁵³Francis Crick Institute, London, UK. ¹⁵⁴Manchester University NHD Foundation Trust, Manchester, UK. ¹⁵⁵Diabetes UK, University of Glasgow, Glasgow, UK. ¹⁵⁶Barnsley Hospital NHS Foundation Trust, Barnsley, UK. ¹⁵⁷MRC-University of Glasgow Centre for Virus Research, Glasgow, UK. ¹⁵⁸Diabetes UK, London, UK. ¹⁵⁹British Heart Foundation Centre, King's College London, London, UK. ¹⁶⁰King's College Hospital NHS Foundation Trust, London, UK. ¹⁶¹University Hospitals Birmingham NHS Foundation Trust and University of Birmingham, Birmingham, UK. ¹⁶²Institute of Cardiovascular and Medical Sciences, BHF Glasgow Cardiovascular Research Centre, University of Glasgow, Glasgow, UK. ¹⁶³University College London NHS Foundation Trust, London and Barts Health NHS Trust, London, UK. ¹⁶⁴Northumbria University, Newcastle upon Tyne, UK. ¹⁶⁵Swansea University and Swansea Welsh Network, Swansea, UK. ¹⁶⁶DUK | NHS Digital, Salford Royal Foundation Trust, Salford, UK. Lists of consortium committees appear in the Supplementary Information.

ISARIC investigators

Kayode Adeniji¹⁶⁷, Daniel Agranoff¹⁶⁸, Ken Agwuh¹⁶⁹, Katie A. Ahmed⁵³, Dhiraj Ail¹⁷⁰, Erin L. Aldera⁸⁴, Ana Alegria¹⁷¹, Beatrice Alex¹⁷², Sam Allen¹⁷³, Petros Andrikopoulos^{174,175}, Brian Angus¹⁷⁶, Jane A. Armstrong⁵³, Abdul Ashish¹⁷⁷, Milton Ashworth⁵³, Innocent G. Asimwe⁵³, Dougal Atkinson¹⁷⁸, Benjamin Bach¹⁷², J. Kenneth Baillie^{21,22,26,179}, Siddharth Bakshi⁵³, Wendy S. Barclay¹⁸⁰, Shahedal Bari¹⁸¹, Gavin Barlow¹⁸², Samantha L. Barlow⁵³, Stella Barnass¹⁸³, Nicholas Barrett¹⁸⁴, Christopher Bassford¹⁸⁵, Sneha Basude¹⁸⁶, David Baxter¹⁸⁷, Michael Beadsworth¹⁸⁸, Jolanta Bernatoniene¹⁸⁹, John Berridge¹⁹⁰, Colin Berry¹⁹¹, Nicola Best¹⁹², Debby Bogaert¹⁹³, Laura Booth⁵³, Pieter Bothma¹⁹⁴, Benjamin Brennan⁵³, Robin Brittain-Long¹⁹⁵, Katie Bullock⁵³, Naomi Bulteel¹⁹⁶, Tom Burden¹⁹⁷, Andrew Burtenshaw¹⁹⁸, Nicola Carlucci⁵³, Gail Carson¹⁹⁹, Vikki Caruth²⁰⁰, Emily Cass⁵³, Benjamin W. A. Catterall⁵³, David Chadwick²⁰¹, Duncan Chambler²⁰², Meera Chand²⁰³, Kanta Chechi^{174,204}, Nigel Chee²⁰⁵, Jenny Child²⁰⁶, Srikanth Chukkambotla²⁰⁷, Richard Clark²⁰⁸, Tom Clark²⁰⁹, Jordan J. Clark⁵³, Emily A. Clarke⁵³, Sara Clohisey²², Sarah Cole⁵³, Paul Collini²¹⁰, Marie Connor²¹¹, Graham S. Cooke²¹², Louise Cooper⁵³, Catherine Cosgrove²¹³, Audrey Coutts²⁰⁸, Helen Cox⁵³, Jason Cupitt²¹⁴, Maria-Teresa Cutino-Moguel²¹⁵, Ana da Silva Filipe²¹⁶, Jo Dalton²¹¹, Paul Dark²¹⁷, Christopher Davis⁵³, Chris Dawson²¹⁸, Thushan de Silva¹⁰, Samir Dervisevic²¹⁹, Oslem Dincarslan⁵³, Alejandra Doce Carracedo⁵³, Annemarie B. Docherty^{9,220}, Cara Donegan²²¹, Lorna Donnelly²⁰⁸, Phil Donnison²²², Chloe Donohue²¹¹, Gonçalo dos Santos Correia^{223,224}, Sam Douthwaite²²⁵, Thomas M. Drake⁹, Andrew Drummond²²⁶, Marc-Emmanuel Dumas^{174,175,227,228}, Chris Dunn⁵³, Jake Dunning^{1,229}, Ingrid DuRand²³⁰, Ahilanadan Dushianthan²³¹, Tristan Dyer²³², Philip Dyer⁵³, Angela Elliott⁵³, Cariad Evans²¹⁰, Anthony Evans⁵³, Chi Eziefula¹⁶⁸, Cameron J. Fairfield⁹, Angie Fawkes²⁰⁸, Christopher Fegan²³³, Lorna Finch⁵³, Adam Finn²³⁴, Lewis W. S. Fisher⁵³, Lisa Flaherty⁵³, Tom Fletcher²³⁵, Terry Foster⁵³, Duncan Fullerton²³⁶, Carrol Gamble²¹¹, Isabel Garcia-Dorival⁵³, Atul Garg²³⁷, Sanjeev Garg²³⁸, Tammy Gilchrist²⁰⁸, Michelle Girvan²¹¹, Effrossyni Gkrania-Klotsas²³⁹, Jo Godden²⁴⁰, Arthur Goldsmith²³⁷, Clive Graham²⁴², Tassos Grammatikopoulos^{243,244}, Christopher A. Green²⁴⁵, William Greenhalf²⁴⁶, Julian Griffin¹⁷⁴, Fiona Griffiths²²,

Philip Gunning⁵³, Rishi K. Gupta²⁴⁷, Katarzyna Hafezi²⁰⁸, Sophie Halpin²¹¹, Hayley Hardwick²⁴⁸, Elaine Hardy²⁴⁹, Ewen M. Harrison⁹, Janet Harrison²¹¹, Catherine Hartley⁵³, Stuart Hartshorn²⁵⁰, Daniel Harvey²⁵¹, Peter Havalda²⁵², Daniel B. Hawcutt²⁵³, Ross Hendry²², Antonia Y. W. Ho^{216,254}, Maria Hobrok²⁵⁵, Luke Hodgson²⁵⁶, Karl Holden⁵³, Anthony Holmes⁵³, Peter W. Horby²⁵⁷, Anil Hormis²⁵⁸, Joanne Howard²¹⁴, Samreen Ijaz²⁵⁹, Clare Jackson²¹¹, Michael Jacobs²⁶⁰, Susan Jain²⁶¹, Paul Jennings²⁶², Rebecca L. Jensen⁵³, Christopher B. Jones⁵³, Trevor R. Jones⁵³, Agilan Kaliappan²⁶³, Vidya Kasipandian²⁶⁴, Sean Keating²²⁰, Stephen Kegg²⁶⁵, Michael Kelsey²⁶⁶, Jason Kendall²⁶⁷, Caroline Kerrison²⁶⁸, Ian Kerslake²⁶⁹, Shadia Khandaker⁵³, Say Khoo²⁷⁰, Katharine King⁵³, Robyn T. Kiy⁵³, Paul Klenerman^{271,272}, Stephen R. Knight⁹, Susan Knight²⁷³, Oliver Koch²⁷⁴, Gouri Koduri²⁷⁵, George Koshy²⁷⁶, Chrysa Koukorava⁵³, Shondipon Laha²⁷⁷, Eva Lahnsteiner²⁷³, Steven Laird²⁷⁸, Annette Lake⁵³, Suzannah Lant⁵³, Susan Larkin²⁷⁹, Diane Latawiec⁵³, Lara Lavelle-Langham⁵³, Andrew Law²², James Lee²⁸⁰, Gary Leeming²⁸¹, Daniella Lefteri⁵³, Tamas Leiner²⁷⁶, Lauren Lett⁵³, Matthew Lewis^{223,224}, Sonia Liggi¹⁷⁴, Patrick Lillie²⁸², Wei Shen Lim²⁸³, James Limb²⁸⁴, Vanessa Linnett²⁸⁵, Jeff Little²⁸⁶, Lucia A. Livoti⁵³, Mark Lyttle²⁸⁷, Louise MacGillivray²⁰⁸, Alan Maclean²⁰⁸, Michael MacMahon²²⁵, Emily MacNaughton²⁸⁸, Maria Mancini⁵³, Ravish Mankregod²⁸⁹, Laura Marsh²¹¹, Lynn Maslen^{223,224}, Hannah Massey⁵³, Huw Masson²⁹⁰, Elijah Matovu²³⁶, Nicole Maziere⁵³, Sarah McCafferty²⁰⁸, Katherine McCullough¹²⁴, Sarah E. McDonald²¹⁶, Sarah McDonald⁵³, Laurence McEvoy⁵³, Ruth McEwen²⁹¹, John McLaughlan⁵³, Kenneth A. Mclean⁹, Manjula Meda²⁹², Alexander J. Mentzer^{293,294}, Laura Merson¹⁹⁹, Soeren Metelmann⁵³, Alison M. Meynert²⁹⁵, Nahida S. Miah⁵³, Joanna Middleton⁵³, Gary Mills²¹⁰, Jane Minton²⁹⁶, Joyce Mitchell⁵³, Kavya Mohandas²⁹⁷, Quen Mok²⁹⁸, James Moon²⁹⁹, Elinoor Moore³⁰⁰, Shona C. Moore³⁰¹, Patrick Morgan³⁰², Kirstie Morrice²⁰⁸, Craig Morris³⁰³, Katherine Mortimore³⁰⁴, Samuel Moses³⁰⁵, Mbiye Mpenge³⁰⁶, Rohinton Mulla³⁰⁷, Derek Murphy⁹, Lee Murphy²⁰⁸, Michael Murphy³⁰⁸, Ellen G. Murphy⁵³, Thapas Nagarajan³⁰⁹, Megan Nagel³¹⁰, Mark Nelson³¹¹, Lisa Norman⁹, Lillian Norris³¹², Lucy Norris³¹³, Mahdad Noursadeghi¹⁹, Michael Olanipekun^{175,314}, Wilna Oosthuizen²², Peter J. M. Openshaw^{1,315}, Anthonia Osagie^{175,316}, Matthew K. O'Shea³¹¹, Marlies Ostermann²²⁵, Igor Otahal³¹⁷, Mark Pais³¹⁸, Massimo Palmarini²¹⁶, Carlo Palmieri^{319,320}, Selva Panchatsharam³²¹, Danai Papakonstantinou³²², Padmasayee Papineni²⁶⁰, Hassan Paraiso³²³, Brij Patel³²⁴, Natalie Pattison³²⁵, William A. Paxton^{3,301}, Rebekah Penrice-Randal⁵³, Justin Pepperell³²⁶, Mark Peters³²⁷, Mandeep Phull³²⁸, Jack Pilgrim⁵³, Stefania Pintus³²⁹, Riinu Pius⁹, Tim Planche³³⁰, Daniel Plotkin²⁸⁰, Georgios Pollakis^{3,301}, Frank Post³³¹, Nicholas Price^{332,333}, David Price³³⁴, Tessa Prince⁵³, Rachel Prout³³⁵, Nikolas Rae³³⁶, Andrew Rambaut³³⁷, Henrik Reschreiter³³⁸, Tim Reynolds³⁰³, Will Reynolds⁵³, Neil Richardson³³⁹, P. Matthew Ridley⁵³, Mark Roberts³⁴⁰, Stephanie Roberts²¹¹, Devender Roberts³⁴¹, David L. Robertson²¹⁶, Alistair Rose³⁴², Guy Rousseau³⁴³, Bobby Ruge³⁴⁴, Clark D. Russell¹⁹³, Brendan Ryan³⁴⁵, Debby Sales⁵³, Taranprit Saluja³⁴⁶, Vanessa Sancho-Shimizu³⁴⁷, Caroline Sands^{223,224}, Egle Saviciute²¹¹, Matthias Schmid³⁴⁸, Janet T. Scott^{216,349}, James Scott-Brown¹⁷², Malcolm G. Semple^{248,350}, Aarti Shah³⁵¹, Manu Shankar-Hari²²⁵, Prad Shanmuga³⁵², Anil Sharma³⁵³, Catherine A. Shaw⁹, Victoria E. Shaw³⁵⁴, Anna Shawcross³⁵⁵, Rebecca K. Shears⁵³, Louise Sigfrid¹⁹⁹, Jagtur Singh Pooni³⁵⁶, Jeremy Sizer³⁵⁷, Benjamin Small⁵³, Richard Smith³⁵⁸, Catherine Snelson³⁵⁹, Tom Solomon^{248,360}, Rebecca G. Spencer²²¹, Nick Spittle³⁶¹, Shiranee Sriskandan^{212,362}, Nikki Staines³⁶³, Tom Stambach³¹², Richard Stewart³⁶⁴, David Stuart³⁶⁵, Krishanthi S. Subramaniam⁵³, Pradeep Subudhi³⁶⁶, Charlotte Summers³⁶⁷, Olivia V. Swann³⁶⁸, Tamas Szakmany³⁶⁹, Agnieszka Szemiel⁵³, Aislynn Taggart⁵³, Sarah Tait²⁷³, Zoltan Takats^{174,223}, Panteleimon Takis^{223,224}, Jolanta Tanianis-Hughes⁵³, Kate Tatham³⁷⁰, Richard S. Tedder^{371,372,373}, Jo Thomas³⁷⁴, Jordan Thomas⁵³, A. A. Roger Thompson¹⁰, Robert Thompson³⁷⁵, Chris Thompson³⁷⁶, Emma C. Thomson²¹⁶, Ryan S. Thwaites^{1,399}, Ascanio Tridente³⁷⁷, Erwan Trochu⁵³, Darell Tupper-Carey¹⁹⁴, Lance C. W. Turtle^{248,378}, Mary Twagira³⁷⁹, Nick Vallotton³⁸⁰, Libby van Tonder⁵³, Rama Vancheeswaran³⁸¹, Rachel Vincent³⁸², Lisa Vincent-Smith³⁸³, Shico Visuvanathan³⁶³, Alan Vuylsteke³⁸⁴, Sam Waddy³⁸⁵, Rachel Wake³⁸⁶, Andrew Walden³⁸⁷, Ingeborg Welters³⁸⁸, Murray Wham²⁹⁵, Tony Whitehouse³⁵⁹, Paul Whittaker³⁸⁹, Ashley Whittington³⁹⁰, Meme Wijesinghe³⁹¹, Eve Wilcock⁵³, Martin Williams³⁹², Lawrence Wilson²⁹¹, Stephen Winchester³⁹³, Martin Wiselka³⁹⁴, Adam Wolverson³⁹⁵, Daniel G. Wootton³⁹⁶, Andrew Workman³¹⁷, Nicola Wrobel²⁰⁸, Bryan Yates³⁹⁷, Peter Young³⁹⁸, Maria Zambon²²⁹ & J. Eunice Zhang⁵³

¹⁶⁷Queen Alexandra Hospital, Portsmouth, UK. ¹⁶⁸Princess Royal Hospital, Haywards Heath, UK. ¹⁶⁹Bassetlaw Hospital, Bassetlaw, UK. ¹⁷⁰Darent Valley Hospital, Dartford, UK. ¹⁷¹Queen Elizabeth the Queen Mother Hospital, Margate, UK. ¹⁷²School of Informatics, University of Edinburgh, Edinburgh, UK. ¹⁷³North East and North Cumbria Ingerated, Newcastle upon Tyne, UK. ¹⁷⁴Section of Biomolecular Medicine, Division of Systems Medicine, Department of Metabolism, Digestion and Reproduction, Imperial College London, London, UK. ¹⁷⁵Section of Genomic and Environmental Medicine, Respiratory Division, National Heart and Lung Institute, Imperial College London, London, UK. ¹⁷⁶John Radcliffe Hospital, Oxford, UK. ¹⁷⁷Royal Albert Edward Infirmary, Wigan, UK. ¹⁷⁸Manchester Royal Infirmary, Manchester, UK. ¹⁷⁹MRC Human Genetics Unit, Institute of Genetics and Cancer, University of Edinburgh, Western General Hospital, Crewe Road, Edinburgh, UK. ¹⁸⁰Section of Molecular Virology, Imperial College London, London, UK. ¹⁸¹Furness General Hospital, Barrow-in-Furness, UK. ¹⁸²Hull University Teaching Hospital Trust, Kingston upon Hull, UK. ¹⁸³Hillingdon Hospital, Hillingdon, UK. ¹⁸⁴St Thomas' Hospital, London, UK. ¹⁸⁵Coventry and Warwickshire, Coventry, UK. ¹⁸⁶St Michael's Hospital, Bristol, UK. ¹⁸⁷Stepping Hill Hospital, Stockport, UK. ¹⁸⁸Royal Liverpool University Hospital, Liverpool, UK. ¹⁸⁹Bristol Royal Hospital Children's, Bristol, UK. ¹⁹⁰Scarborough Hospital, Scarborough, UK. ¹⁹¹Golden Jubilee National Hospital, Clydebank, UK. ¹⁹²Liverpool Heart and Chest Hospital, Liverpool, UK. ¹⁹³Centre for Inflammation Research, The Queen's Medical Research Institute, University of Edinburgh, Edinburgh, UK. ¹⁹⁴James Paget University Hospital, Great Yarmouth, UK. ¹⁹⁵Aberdeen Royal Infirmary, Aberdeen, UK. ¹⁹⁶Adamson Hospital, Cupar, UK. ¹⁹⁷Royal Devon and Exeter Hospital, Exeter, UK. ¹⁹⁸Worcestershire Royal Hospital, Worcester, UK. ¹⁹⁹ISARIC Global Support Centre, Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK. ²⁰⁰Conquest Hospital, Hastings, UK. ²⁰¹The James Cook University Hospital, Middlesbrough, UK. ²⁰²Dorset County Hospital, Dorchester, UK. ²⁰³Antimicrobial Resistance and Hospital Acquired Infection Department, Public Health England, London, UK. ²⁰⁴Department of Epidemiology and Biostatistics, School of Public Health, Faculty of Medicine, Imperial College London, London, UK. ²⁰⁵Royal Bournemouth General Hospital, Bournemouth, UK. ²⁰⁶Harrogate Hospital, Harrogate, UK. ²⁰⁷Royal Blackburn Teaching Hospital, Blackburn, UK. ²⁰⁸Edinburgh Clinical Research Facility, University of Edinburgh, Edinburgh, UK. ²⁰⁹Torbay Hospital, Torquay, UK. ²¹⁰Northern General Hospital, Sheffield, UK. ²¹¹Liverpool Clinical Trials Centre, University of Liverpool, Liverpool, UK. ²¹²Department of Infectious Disease, Imperial College London, London, UK. ²¹³St Georges Hospital (Tooting), London, UK. ²¹⁴Blackpool Victoria Hospital, Blackpool, UK. ²¹⁵The Royal London Hospital, London, UK. ²¹⁶MRC-University of Glasgow Centre for Virus Research, Glasgow, UK. ²¹⁷Salford Royal Hospital, Salford, UK. ²¹⁸University Hospital of North Durham, Durham, UK. ²¹⁹Norfolk and Norwich University Hospital, Norwich, UK. ²²⁰Intensive Care Unit, Royal Infirmary Edinburgh, Edinburgh, UK. ²²¹Institute of Infection, Veterinary and Ecological Sciences, Faculty of Health and Life Sciences, University of

Liverpool, Liverpool, UK. ²²²Salisbury District Hospital, Salisbury, UK. ²²³National Phenome Centre, Department of Metabolism, Digestion and Reproduction, Imperial College London, London, UK. ²²⁴Section of Bioanalytical Chemistry, Department of Metabolism, Digestion and Reproduction, Imperial College London, London, UK. ²²⁵Guy's and St Thomas', NHS Foundation Trust, London, UK. ²²⁶The Royal Oldham Hospital, Oldham, UK. ²²⁷European Genomic Institute for Diabetes, Institut Pasteur de Lille, Lille University Hospital, University of Lille, Lille, France. ²²⁸McGill University and Genome Quebec Innovation Centre, Montreal, Quebec, Canada. ²²⁹National Infection Service, Public Health England, London, UK. ²³⁰Hereford Count Hospital, Hereford, UK. ²³¹Southampton General Hospital, Southampton, UK. ²³²Northampton General Hospital, Northampton, UK. ²³³University Hospital of Wales, Cardiff, UK. ²³⁴University Hospitals Bristol NHS Foundation Trust, Bristol, UK. ²³⁵Liverpool School of Tropical Medicine, Liverpool, UK. ²³⁶Leighton Hospital, Crewe, UK. ²³⁷Manor Hospital, Walsall, UK. ²³⁸Scunthorpe Hospital, Scunthorpe, UK. ²³⁹Cambridge University Hospital, Cambridge, UK. ²⁴⁰West Suffolk NHS Foundation Trust, Bury St Edmunds, UK. ²⁴¹Basingstoke and North Hampshire Hospital, Basingstoke, UK. ²⁴²North Cumberland Infirmary, Carlisle, UK. ²⁴³Paediatric Liver, GI and Nutrition Centre and MowatLabs, King's College Hospital, London, UK. ²⁴⁴Institute of Liver Studies, King's College London, London, UK. ²⁴⁵Institute of Microbiology and Infection, University of Birmingham, Birmingham, UK. ²⁴⁶Department of Molecular and Clinical Cancer Medicine, University of Liverpool, Liverpool, UK. ²⁴⁷Institute for Global Health, University College London, London, UK. ²⁴⁸NIHR Health Protection Research Unit, Institute of Infection, Veterinary and Ecological Sciences, Faculty of Health and Life Sciences, University of Liverpool, Liverpool, UK. ²⁴⁹Warwick Hospital, Warwick, UK. ²⁵⁰Birmingham Children's Hospital, Birmingham, UK. ²⁵¹Nottingham City Hospital, Nottingham, UK. ²⁵²Glangwili Hospital Child Health Section, Carmarthen, UK. ²⁵³Alder Hey Children's Hospital, Liverpool, UK. ²⁵⁴Department of Infectious Diseases, Queen Elizabeth University Hospital, Glasgow, UK. ²⁵⁵Bronglais General Hospital, Aberystwyth, UK. ²⁵⁶Worthing Hospital, Worthing, UK. ²⁵⁷Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK. ²⁵⁸Rotheram District General Hospital, Rotheram, UK. ²⁵⁹Virology Reference Department, National Infection Service, Public Health England, Colindale Avenue, London, UK. ²⁶⁰Royal Free Hospital, London, UK. ²⁶¹Homerton Hospital, London, UK. ²⁶²Airedale Hospital, Airedale, UK. ²⁶³Basildon Hospital, Basildon, UK. ²⁶⁴The Christie NHS Foundation Trust, Manchester, UK. ²⁶⁵University Hospital Lewisham, London, UK. ²⁶⁶The Whittington Hospital, London, UK. ²⁶⁷Southmead Hospital, Bristol, UK. ²⁶⁸Sheffield Childrens Hospital, Sheffield, UK. ²⁶⁹Royal United Hospital, Bath, UK. ²⁷⁰Department of Pharmacology, University of Liverpool, Liverpool, UK. ²⁷¹Nuffield Department of Medicine, Peter Medawar Building for Pathogen Research, University of Oxford, Oxford, UK. ²⁷²Translational Gastroenterology Unit, Nuffield Department of Medicine, University of Oxford, Oxford, UK. ²⁷³Public Health Scotland, Edinburgh, UK. ²⁷⁴Western General Hospital, Edinburgh, UK. ²⁷⁵Southend University Hospital NHS Foundation Trust, Southend-on-Sea, UK. ²⁷⁶Hinchingbrooke Hospital, Huntingdon, UK. ²⁷⁷Royal Preston Hospital, Fulwood, UK. ²⁷⁸University Hospital (Coventry), Coventry, UK. ²⁷⁹The Walton Centre, Liverpool, UK. ²⁸⁰ISARIC, Global Support Centre, COVID-19 Clinical Research Resources, Epidemic diseases Research Group, Oxford (ERGO), University of Oxford, Oxford, UK. ²⁸¹Centre for Health Informatics, Division of Informatics, Imaging and Data Science, School of Health Sciences, Faculty of Biology, Medicine and Health, University of Manchester, Manchester Academic Health Science Centre, Manchester, UK. ²⁸²Hull Royal Infirmary, Hull, UK. ²⁸³Nottingham University Hospitals NHS Trust., Nottingham, UK. ²⁸⁴Darlington Memorial Hospital, Darlington, UK. ²⁸⁵Queen Elizabeth Hospital (Gateshead), Gateshead, UK. ²⁸⁶Warrington Hospital, Warrington, UK. ²⁸⁷Bristol Royal Hospital for Children, Bristol, UK. ²⁸⁸St Mary's Hospital (Isle of Wight), Isle of Wight, UK. ²⁸⁹The Tunbridge Wells Hospital, Royal Tunbridge Wells, UK. ²⁹⁰Huddersfield Royal, Huddersfield, UK. ²⁹¹Countess of Chester Hospital, Liverpool, UK. ²⁹²Frimley Park Hospital, Frimley, UK. ²⁹³Nuffield Department of Medicine, John Radcliffe Hospital, Oxford, UK. ²⁹⁴Department of Microbiology/Infectious Diseases, Oxford University Hospitals NHS Foundation Trust, John Radcliffe Hospital, Oxford, UK. ²⁹⁵MRC Human Genetics Unit, MRC Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, UK. ²⁹⁶St James University Hospital, Leeds, UK. ²⁹⁷Arrowe Park Hospital, Birkenhead, UK. ²⁹⁸Great Ormond Street Hospital, London, UK. ²⁹⁹Royal Shrewsbury Hospital, Shrewsbury, UK. ³⁰⁰Addenbrookes Hospital, Cambridge, UK. ³⁰¹Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Liverpool, UK. ³⁰²East Surrey Hospital (Redhill), Redhill, UK. ³⁰³Burton Hospital, Burton, UK. ³⁰⁴Peterborough City Hospital, Peterborough, UK. ³⁰⁵Kent and Canterbury Hospital, Canterbury, UK. ³⁰⁶Weston Area General Trust, Bristol, UK. ³⁰⁷Bedfordshire Hospital, Bedfordshire, UK. ³⁰⁸Glasgow Royal Infirmary, Glasgow, UK. ³⁰⁹Macclesfield General Hospital, Macclesfield, UK. ³¹⁰Derbyshire Healthcare, Derbyshire, UK. ³¹¹Chelsea and Westminster Hospital, London, UK. ³¹²Watford General Hospital, Watford, UK. ³¹³EPCC, University of Edinburgh, Edinburgh, UK. ³¹⁴Section of Biomolecular Medicine, Division of Systems Medicine, Department of Metabolism, Digestion and Reproduction, London, UK. ³¹⁵Imperial College Healthcare NHS Trust: London, London, UK. ³¹⁶Division of Systems Medicine, Department of Metabolism, Digestion and Reproduction, Imperial College London, London, UK. ³¹⁷Prince Philip Hospital, Llanelli, UK. ³¹⁸George Eliot Hospital – Acute Services, Nuneaton, UK. ³¹⁹Molecular and Clinical Cancer Medicine, Institute of Systems, Molecular and Integrative Biology, University of Liverpool, Liverpool, UK. ³²⁰Clatterbridge Cancer Centre NHS Foundation Trust, Liverpool, UK. ³²¹Kettering General Hospital, Kettering, UK. ³²²University Hospitals of North Midlands NHS Trust, North Midlands, UK. ³²³Russells Hall Hospital, Dudley, UK. ³²⁴Harefield Hospital, Harefield, UK. ³²⁵Lister Hospital, Lister, UK. ³²⁶Musgrove Park Hospital, Taunton, UK. ³²⁷Kingston Hospital, Kingston, UK. ³²⁸Queen's Hospital, Romford, UK. ³²⁹Southport and Formby District General Hospital, Southport, UK. ³³⁰St George's University of London, London, UK. ³³¹King's College Hospital (Denmark Hill), London, UK. ³³²Centre for Clinical Infection and Diagnostics Research, Department of Infectious Diseases, School of Immunology and Microbial Sciences, King's College London, London, UK. ³³³Department of Infectious Diseases, Guy's and St Thomas' NHS Foundation Trust, London, UK. ³³⁴The Clatterbridge Cancer Centre NHS Foundation, Bebington, UK. ³³⁵The Great Western Hospital, Swindon, UK. ³³⁶Ninewells Hospital, Dundee, UK. ³³⁷Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, UK. ³³⁸Poole Hospital NHS Trust, Poole, UK. ³³⁹William Harvey Hospital, Ashford, UK. ³⁴⁰King's Mill Hospital, Sutton-in-Ashfield, UK. ³⁴¹Liverpool Women's Hospital, Liverpool, UK. ³⁴²Pinderfields Hospital, Wakefield, UK. ³⁴³North Devon District Hospital, Barnstaple, UK. ³⁴⁴Queen Elizabeth Hospital, Birmingham, UK. ³⁴⁵Tameside General Hospital, Ashton-under-Lyne, UK. ³⁴⁶City Hospital (Birmingham), Birmingham, UK. ³⁴⁷Department of Pediatrics and Virology, St Mary's Medical School Bldg, Imperial College London, London, UK. ³⁴⁸The Newcastle Upon Tyne Hospitals NHS Foundation Trust, Newcastle Upon Tyne, UK. ³⁴⁹NHS Greater Glasgow and Clyde, Glasgow, UK. ³⁵⁰Respiratory Medicine, Institute in The Park, University of Liverpool, Alder Hey Children's Hospital, Liverpool, UK. ³⁵¹Broomfield Hospital, Broomfield, UK. ³⁵²Stoke Mandeville, UK. ³⁵³University Hospital of North Tees, Stockton-on-Tees, UK. ³⁵⁴Institute of Translational Medicine, University of Liverpool, Merseyside, UK. ³⁵⁵Royal Manchester Children's Hospital, Manchester, UK. ³⁵⁶New Cross Hospital, Wolverhampton, UK. ³⁵⁷Bedford Hospital, Bedford, UK. ³⁵⁸Colchester General Hospital, Colchester, UK. ³⁵⁹University Hospital Birmingham NHS Foundation Trust, Birmingham, UK. ³⁶⁰Walton Centre NHS Foundation Trust, Liverpool, UK. ³⁶¹Chesterfield Royal Hospital, Calow, UK. ³⁶²MRC Centre for Molecular Bacteriology and Infection, Imperial College London, London, UK. ³⁶³Princess Alexandra Hospital, Harlow, UK. ³⁶⁴Milton Keynes Hospital, Eaglestone, UK. ³⁶⁵Division of Structural Biology, The Wellcome Centre for Human Genetics, University of Oxford, Oxford, UK. ³⁶⁶Royal Bolton Hospital, Farnworth, UK. ³⁶⁷Department of Medicine, University of Cambridge, Cambridge, UK. ³⁶⁸Department of Child Life and Health, University of Edinburgh, Edinburgh, UK. ³⁶⁹Royal Gwent (Newport), Newport, UK. ³⁷⁰The Royal Marsden Hospital (London), London, UK. ³⁷¹Blood Borne Virus Unit, Virus Reference Department, National Infection Service, Public Health England, London, UK. ³⁷²Transfusion Microbiology, National Health Service Blood and Transplant, London, UK. ³⁷³Department of Medicine, Imperial College London, London, UK. ³⁷⁴Queen Victoria Hospital (East Grinstead), East Grinstead, UK. ³⁷⁵Leeds Teaching Hospitals NHS Trust, Leeds, UK. ³⁷⁶Royal Stoke University

Hospital, Stoke-on-Trent, UK. ³⁷⁷Whiston Hospital, Rainhill, UK. ³⁷⁸Tropical and Infectious Disease Unit, Royal Liverpool University Hospital, Liverpool, UK. ³⁷⁹Croydon University Hospital, Thornton Heath, UK. ³⁸⁰Gloucester Royal, Gloucester, UK. ³⁸¹West Hertfordshire Teaching Hospitals NHS Trust, Hertfordshire, UK. ³⁸²North Middlesex Hospital, London, UK. ³⁸³Medway Maritime Hospital, Gillingham, UK. ³⁸⁴Royal Papworth Hospital Everard, Cambridge, UK. ³⁸⁵Derriford (Plymouth), Plymouth, UK. ³⁸⁶St Helier Hospital, Sutton, UK. ³⁸⁷Royal Berkshire Hospital, Reading, UK. ³⁸⁸Royal Liverpool Hospital, Liverpool, UK. ³⁸⁹Bradford Royal infirmary, Bradford, UK. ³⁹⁰Central Middlesex, London, UK. ³⁹¹Royal Cornwall Hospital (Tresliske), Truro, UK. ³⁹²North Bristol NHS Trust, Bristol, UK. ³⁹³St. Peter's Hospital, Runnymede, UK. ³⁹⁴Leicester Royal Infirmary, Leicester, UK. ³⁹⁵Grantham and District Hospital, Grantham, UK. ³⁹⁶Aintree University Hospital, Liverpool, UK. ³⁹⁷North Tyneside General Hospital, North Shields, UK. ³⁹⁸Queen Elizabeth Hospital, King's Lynn, UK.

Methods

Study design and ethics

After hospitalization for COVID-19, adults who had no comorbidity resulting in a prognosis of less than 6 months were recruited to the PHOSP-COVID study ($n = 719$). Patients hospitalized between February 2020 and January 2021 were recruited. Both sexes were recruited and gender was self-reported (female, $n = 257$ and male, $n = 462$). Written informed consent was obtained from all patients. Ethical approvals for the PHOSP-COVID study were given by Leeds West Research Ethics Committee (20/YH/0225).

Symptom data and samples were prospectively collected from individuals approximately 6 months (IQR 5.1–6.8 months and range 3.0–8.3 months) post hospitalization (Fig. 1a), via the PHOSP-COVID multicenter United Kingdom study⁶⁴. Data relating to patient demographics and acute admission were collected via the International Severe Acute Respiratory and Emerging Infection Consortium World Health Organization Clinical Characterisation Protocol United Kingdom (ISARIC4C study; IRAS260007/IRAS126600) (ref. 65). Adults hospitalized during the SARS-CoV-2 pandemic were systematically recruited into ISARIC4C. Written informed consent was obtained from all patients. Ethical approval was given by the South Central–Oxford C Research Ethics Committee in England (reference 13/SC/0149), Scotland A Research Ethics Committee (20/SS/0028) and WHO Ethics Review Committee (RPC571 and RPC572, 25 April 2013).

Data were collected to account for variables affecting symptom outcome, via hospital records and self-reporting. Acute disease severity was classified according to the WHO clinical progression score: WHO class 3–4: no oxygen therapy; class 5: oxygen therapy; class 6: noninvasive ventilation or high-flow nasal oxygen; and class 7–9: managed in critical care⁹. Clinical data were used to place patients into six categories: ‘recovered’, ‘GI’, ‘cardiorespiratory’, ‘fatigue’, ‘cognitive impairment’ and ‘anxiety/depression’ (Supplementary Table 7). Patient-reported symptoms and validated clinical scores were used when feasible, including Medical Research Council (MRC) breathlessness score, dyspnea-12 score, Functional Assessment of Chronic Illness Therapy (FACIT) score, Patient Health Questionnaire (PHQ)-9 and Generalized Anxiety Disorder (GAD)-7. Cognitive impairment was defined as a Montreal Cognitive Assessment score < 26 . GI symptoms were defined as answering ‘Yes’ to the presence of at least two of the listed symptoms. ‘Recovered’ was defined by self-reporting. Patients were placed in multiple groups if they experienced a combination of symptoms.

Matched nasal fluid and sputum samples were prospectively collected from a subgroup of convalescent patients approximately 6 months after hospitalization via the PHOSP-COVID study. Nasal and bronchoalveolar lavage fluid (BALF) collected from healthy volunteers before the COVID-19 pandemic were used as controls (Supplementary Table 4). Written consent was obtained for all individuals and ethical approvals were given by London–Harrow Research Ethics Committee (13/LO/1899) for the collection of nasal samples and the Health Research Authority London–Fulham Research Ethics Committee (IRAS project ID 154109; references 14/LO/1023, 10/H0711/94 and 11/LO/1826) for BALF samples.

Procedures

Ethylenediaminetetraacetic acid plasma was collected from whole blood taken by venepuncture and frozen at -80°C as previously described^{7,66}. Nasal fluid was collected using a Nasosorption™ FX-I device (Hunt Developments), which uses a synthetic absorptive matrix to collect concentrated nasal fluid. Samples were eluted and stored as previously described⁶⁷. Sputum samples were collected via passive expectoration and frozen at -80°C without the addition of buffers. Sputum samples from convalescent individuals were compared with BALF from healthy SARS-CoV-2-naïve controls, collected before the pandemic. BALF samples were used to act as a comparison for lower

respiratory tract samples since passively expectorated sputum from healthy SARS-CoV-2-naïve individuals was not available. BALF samples were obtained by instillation and recovery of up to 240 ml of normal saline via a fiberoptic bronchoscope. BALF was filtered through $100\ \mu\text{m}$ strainers into sterile 50 ml Falcon tubes, then centrifuged for 10 min at $400\ \text{g}$ at 4°C . The resulting supernatant was transferred into sterile 50 ml Falcon tubes and frozen at -80°C until use. The full methods for BALF collection and processing have been described previously^{68,69}.

Immunoassays

To determine inflammatory signatures that associated with symptom outcomes, plasma samples were analyzed on an Olink Explore 384 Inflammation panel⁷⁰. Supplementary Table 8 (Appendix 1) lists all the analytes measured. To ensure the validity of results, samples were run in a single batch with the use of negative controls, plate controls in triplicate and repeated measurement of patient samples between plates in duplicate. Samples were randomized between plates according to site and sample collection date. Randomization between plates was blind to LC/recovered outcome. Data were first normalized to an internal extension control that was included in each sample well. Plates were standardized by normalizing to inter-plate controls, run in triplicate on each plate. Each plate contained a minimum of four patient samples, which were duplicates on another plate; these duplicate pairs allowed any plate to be linked to any other through the duplicates. Data were then intensity normalized across all cohort samples. Finally, Olink results underwent quality control processing and samples or analytes that did not reach quality control standards were excluded. Final normalized relative protein quantities were reported as \log_2 NPX values.

To further validate our findings, we performed conventional electrochemiluminescence (ECL) assays and enzyme-linked immunosorbent assay for Olink mediators that were associated with symptom outcome (Supplementary Methods). Contemporaneously collected plasma samples were available from 58 individuals. Like most omics platforms, Olink measures relative quantities, so perfect agreement with conventional assays that measure absolute concentrations is not expected.

Sputum samples were thawed before analysis and sputum plugs were extracted with the addition of 0.1% dithiothreitol creating a one in two sample dilution, as previously described⁷¹. SARS-CoV-2 S and N proteins were measured by ECL S-plex assay at a fixed dilution of one in two (Mesoscale Diagnostics), as per the manufacturers protocol⁷². Control BALF samples were thawed and measured on the same plate, neat. The S-plex assay is highly sensitive in detecting viral antigen in respiratory tract samples⁷³.

Nasal cytokines were measured by ECL (mesoscale discovery) and Luminex bead multiplex assays (Biotechne). The full methods and list of analytes are detailed in Supplementary Methods.

Statistics and reproducibility

Clinical data was collected via the PHOSP REDCap database, to which access is available under reasonable request as per the data sharing statement in the manuscript. All analyses were performed within the Outbreak Data Analysis Platform (ODAP). All data and code can be accessed using information in the ‘Data sharing’ and ‘Code sharing’ statements at the end of the manuscript. No statistical method was used to predetermine sample size. Data distribution was assumed to be normal but this was not formally tested. Olink assays and immunoassays were randomized and investigators were blinded to outcomes.

To determine protein signatures that associated with each symptom outcome, a ridge PLR was used. PLR shrinks coefficients to account for combined effects within high-dimensional data, preventing false discovery while managing multicollinearity³⁴. Thus, PLR was chosen a priori as the most appropriate model to assess associations between a large number of explanatory variables (that may work together to

mediate effects) and symptom outcome^{34,62,70,74}. In keeping with our aim to perform an unbiased exploration of inflammatory process, the model alpha was set to zero, facilitating regularization without complete penalization of any mediator. This enabled review of all possible mediators that might associate with LC⁶².

A 50 repeats tenfold nested cross-validation was used to select the optimal lambda for each model and assess its accuracy (Extended Data Fig. 1). The performance of the cognitive impairment model was influenced by the imbalance in size of the symptom group ($n = 60$) relative to recovered ($n = 250$). The model was weighted to account for this imbalance resulting in a sensitivity of 0.98, indicating its validity. We have expanded on the model performance and validation approaches in Supplementary Information.

Age, sex, acute disease severity and preexisting comorbidities were included as covariates in the PLR analysis (Supplementary Tables 1 and 3). Covariates were selected a priori using features reported to influence the risk of LC and inflammatory responses^{1,39,64,75}. Ethnicity was not included since it has been shown not to predict symptom outcome in this cohort⁶⁴. Individuals with missing data were excluded from the regression analysis. Each symptom group was compared with the 'recovered' group. The model coefficients of each covariate were converted into ORs for each outcome and visualized in a forest plot, after removing variables associated with regularized OR between 0.98 and 1.02 or in cases where most variables fell outside of this range, using mediators associated with the highest decile of coefficients either side of this range. This enabled exclusion of mediators with effect sizes that were unlikely to have clinical or mechanistic importance since the ridge PLR shrinks and orders coefficients according to their relative importance rather than making estimates with standard error. Thus, confidence intervals cannot be appropriately derived from PLR, and forest plot error bars were calculated using the median accuracy of the model generated by the nested cross-validation. To verify observations made through PLR analysis, we also performed an unadjusted PLR, an unadjusted logistic regression and a PLS analysis. Univariate analyses using Wilcoxon signed-rank test was also performed (Supplementary Table 8, Appendix 1). Analyses were performed in R version 4.2.0 using 'data.table v1.14.2', 'EnvStats v2.7.0', 'tidyverse v1.3.2', 'lme4 v1.1-32', 'caret v6.0-93', 'glmnet v4.1-6', 'mdatools v0.14.0', 'ggpubbr v0.4.0', 'ggplot2 v3.3.6', 'bootnet v1.5.6' and 'qgraph v1.9.8' packages.

To further investigate the relationship between proteins elevated in each symptom group, we performed a correlation network analysis using Spearman's rank correlation coefficient and false discovery rate (FDR) thresholding. The mediators visualized in the PLR forest plots, which were associated with cardiorespiratory symptoms, fatigue, anxiety/depression GI symptoms and cognitive impairment were used, respectively. Analyses were performed in R version 4.2.0 using 'bootnet v1.5.6' and 'qgraph v1.9.8' packages.

To determine whether differences in protein levels between men and women related to hormonal differences, we divided each symptom group into premenopausal and postmenopausal groups using an age cutoff of 50 years old. Differences between sexes in each group were determined using the Wilcoxon signed-rank test. To understand whether antigen persistence contributed to inflammation in adults with LC, the median viral antigen concentration from sputum/BALF samples and cytokine concentrations from nasal samples were compared using the Wilcoxon signed-rank test. All tests were two-tailed and statistical significance was defined as a P value < 0.05 after adjustment for FDR (q -value of 0.05). Analyses were performed in R version 4.2.0 using 'bootnet v1.5.6' and 'qgraph v1.9.8' packages.

Extended Data Fig. 10 was made using Biorender, accessed at www.biorender.com.

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

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The PHOSP-COVID protocol, consent form, definition and derivation of clinical characteristics and outcomes, training materials, regulatory documents, information about requests for data access, and other relevant study materials are available online at ref. 76. Access to these materials can be granted by contacting phosp@leicester.ac.uk and Phospcontracts@leicester.ac.uk.

The ISARIC4C protocol, data sharing and publication policy are available at <https://isaric4c.net>. ISARIC4C's Independent Data and Material Access Committee welcomes applications for access to data and materials (<https://isaric4c.net>).

The datasets used in the study contain extensive clinical information at an individual level that prevent them from being deposited in a public depository due to data protection policies of the study. Study data can only be accessed via the ODAP, a protected research environment. All data used in this study are available within ODAP and accessible under reasonable request. Data access criteria and information about how to request access is available online at ref. 76. If criteria are met and a request is made, access can be gained by signing the eDRIS user agreement.

Code availability

Code was written within the ODAP, using R v4.2.0 and publicly available packages ('data.table v1.14.2', 'EnvStats v2.7.0', 'tidyverse v1.3.2', 'lme4 v1.1-32', 'caret v6.0-93', 'glmnet v4.1-6', 'mdatools v0.14.0', 'ggpubbr v0.4.0', 'ggplot2 v3.3.6', 'bootnet v1.5.6' and 'qgraph v1.9.8' packages). No new algorithms or functions were created and code used in-built functions in listed packages available on CRAN. The code used to generate data and to analyze data is publicly available at <https://github.com/isaric4c/wiki/wiki/ISARIC>; https://github.com/SurgicalInformatics/cocin_cc and https://github.com/ClaudiaEfstath/PHOSP_Olink_NatImm.

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Acknowledgements

This research used data assets made available by ODAP as part of the Data and Connectivity National Core Study, led by Health Data Research UK in partnership with the Office for National Statistics and funded by UK Research and Innovation (grant ref. MC_PC_20058). This work is supported by the following grants: the PHOSP-COVID study is jointly funded by UK Research and Innovation and National Institute of Health and Care Research (NIHR; grant references MR/V027859/1 and COV0319). ISARIC4C is supported by grants from the National Institute for Health and Care Research (award CO-CIN-01) and the MRC (grant MC_PC_19059) Liverpool Experimental Cancer Medicine Centre provided infrastructure support for this research (grant reference C18616/A25153). Other grants that have supported this work include the UK Coronavirus Immunology Consortium (funder reference 1257927), the Imperial Biomedical Research Centre (NIHR Imperial BRC, grant IS-BRC-1215-20013), the Health Protection Research Unit in Respiratory Infections at Imperial College London and NIHR Health Protection Research Unit in Emerging and Zoonotic Infections at University of Liverpool, both in partnership with Public Health England, (NIHR award 200907), Wellcome Trust and Department for International Development (215091/Z/18/Z), Health Data Research UK (grant code 2021.0155), MRC (grant code MC_UU_12014/12) and NIHR Clinical Research Network for providing infrastructure support for this research. We also acknowledge the support of the MRC EMINENT Network (MR/R502121/1), which is cofunded by GSK, the Comprehensive Local Research Networks, the MRC HIC-Vac network (MR/R005982/1) and the RSV Consortium in Europe Horizon 2020 Framework Grant 116019. F.L. is supported by an MRC clinical training fellowship (award MR/W000970/1). C.E. is funded by NIHR (grant P91258-4). L.-P.H. is supported by Oxford NIHR Biomedical Research Centre. A.A.R.T. is supported by a British Heart Foundation (BHF) Intermediate Clinical Fellowship (FS/18/13/33281). S.L.R.-J. receives support from UK Research and Innovation (UKRI), Global Challenges Research Fund (GCRF), Rosetrees Trust, British HIV association (BHIVA), European & Developing Countries Clinical Trials Partnership (EDCTP) and Globvac. J.D.C. has grants from AstraZeneca, Boehringer Ingelheim, GSK, Gilead Sciences, Grifols, Novartis and Insmed. R.A.E. holds a NIHR Clinician Scientist Fellowship (CS-2016-16-020). A. Horsley is currently supported by UK Research and Innovation, NIHR and NIHR Manchester BRC. B.R. receives support from BHF Oxford Centre of Research Excellence, NIHR Oxford BRC and MRC. D.G.W. is supported by an NIHR Advanced Fellowship. A. Ho has received support from MRC and for the Coronavirus Immunology Consortium (MR/V028448/1). L.T. is supported by the US Food and Drug Administration Medical Countermeasures Initiative contract 75F4012OC00085 and the National Institute for Health Research Health Protection Research Unit in Emerging and Zoonotic Infections (NIHR200907) at the University of Liverpool in partnership with UK Health Security Agency (UK-HSA), in collaboration with Liverpool School of Tropical Medicine and the University of Oxford. L.V.W. has received support from UKRI, GSK/Asthma and Lung UK and NIHR for this study. M.G.S. has received support from NIHR UK, MRC UK and Health Protection Research Unit in Emerging and Zoonotic Infections, University of Liverpool. J.K.B. is supported by the Wellcome Trust (223164/Z/21/Z) and UKRI (MC_PC_20004, MC_PC_19025, MC_PC_1905, MRNO2995X/1 and MC_PC_20029). The funders were

not involved in the study design, interpretation of data or writing of this manuscript. The views expressed are those of the authors and not necessarily those of the Department of Health and Social Care (DHSC), the Department for International Development (DID), NIHR, MRC, the Wellcome Trust, UK-HSA, the National Health Service or the Department of Health. P.J.M.O. is supported by a NIHR Senior Investigator Award (award 201385). We thank all the participants and their families. We thank the many research administrators, health-care and social-care professionals who contributed to setting up and delivering the PHOSP-COVID study at all of the 65 NHS trusts/health boards and 25 research institutions across the United Kingdom, as well as those who contributed to setting up and delivering the ISARIC4C study at 305 NHS trusts/health boards. We also thank all the supporting staff at the NIHR Clinical Research Network, Health Research Authority, Research Ethics Committee, Department of Health and Social Care, Public Health Scotland and Public Health England. We thank K. Holmes at the NIHR Office for Clinical Research Infrastructure for her support in coordinating the charities group. The PHOSP-COVID industry framework was formed to provide advice and support in commercial discussions, and we thank the Association of the British Pharmaceutical Industry as well the NIHR Office for Clinical Research Infrastructure for coordinating this. We are very grateful to all the charities that have provided insight to the study: Action Pulmonary Fibrosis, Alzheimer's Research UK, Asthma and Lung UK, British Heart Foundation, Diabetes UK, Cystic Fibrosis Trust, Kidney Research UK, MQ Mental Health, Muscular Dystrophy UK, Stroke Association Blood Cancer UK, McPin Foundations and Versus Arthritis. We thank the NIHR Leicester Biomedical Research Centre patient and public involvement group and Long Covid Support. We also thank G. Khandaker and D. C. Newcomb who provided valuable feedback on this work. Extended Data Fig. 10 was created using Biorender.

Author contributions

F.L. recruited participants, acquired clinical samples, analyzed and interpreted data and cowrote the manuscript, including all drafting and revisions. C.E. analyzed and interpreted data and cowrote this manuscript, including all drafting and revisions. S.F. and M.R. supported the analysis and interpretation of data as well as drafting and revisions. D.S., J.K.S., S.C.M., S.A., N.M., J.N., C.K., O.C.L., O.E., H.J.C.M., A. Shikotra, A. Singapuri, M.S., V.C.H., M.T., N.J.G., N.I.L. and C.C. contributed to acquisition of data underlying this study. L.H.-W., A.A.R.T., S.L.R.-J., L.S.H., O.M.K., D.G.W., T.I.d.S. and A. Ho made substantial contributions to conception/design and implementation of this work and/or acquisition of clinical samples for this work. They have supported drafting and revisions of the manuscript. E.M.H., J.K.Q. and A.B.D. made substantial contributions to the study design as well as data access, linkage and analysis. They have supported drafting and revisions of this work. J.D.C., L.-P.H., A. Horsley, B.R., K.P., M.M. and W.G. made substantial contributions to the conception and design of this work and have supported drafting and revisions of this work. J.K.B. obtained funding for ISARIC4C, is ISARIC4C consortium co-lead, has made substantial contributions to conception and design of this work and has supported drafting and revisions of this work. M.G.S. obtained funding for ISARIC4C, is ISARIC4C consortium co-lead, sponsor/protocol chief investigator, has made substantial contributions to conception and design of this work and has supported drafting and revisions of this work. R.A.E. and L.V.W. are co-leads of PHOSP-COVID, made substantial contributions to conception and design of this work, the acquisition and analysis of data, and have supported drafting and revisions of this work. C.B. is the chief investigator of PHOSP-COVID and has made substantial contributions to conception and design of this work. R.S.T. and L.T. made substantial contributions to the acquisition, analysis and interpretation of the data underlying this study and have contributed to drafting and revisions of this work. P.J.M.O. obtained funding for ISARIC4C, is ISARIC4C consortium

co-lead, sponsor/protocol chief investigator and has made substantial contributions to conception and design of this work. R.S.T. and P.J.M.O. have also made key contributions to interpretation of data and have co-written this manuscript. All authors have read and approve the final version to be published. All authors agree to accountability for all aspects of this work. All investigators within ISARIC4C and the PHOSP-COVID consortia have made substantial contributions to the conception or design of this study and/or acquisition of data for this study. The full list of authors within these groups is available in Supplementary Information.

Competing interests

F.L., C.E., D.S., J.K.S., S.C.M., C.D., C.K., N.M., L.N., E.M.H., A.B.D., J.K.Q., L.-P.H., K.P., L.S.H., O.M.K., S.F., T.I.d.S., D.G.W., R.S.T. and J.K.B. have no conflicts of interest. A.A.R.T. receives speaker fees and support to attend meetings from Janssen Pharmaceuticals. S.L.R.-J. is on the data safety monitoring board for Bexero trial in HIV+ adults in Kenya. J.D.C. is the deputy chief editor of the *European Respiratory Journal* and receives consulting fees from AstraZeneca, Boehringer Ingelheim, Chiesi, GSK, Insmad, Janssen, Novartis, Pfizer and Zambon. A. Horsley is deputy chair of NIHR Translational Research Collaboration (unpaid role). B.R. receives honoraria from Axcella therapeutics. R.A.E. is co-lead of PHOSP-COVID and receives fees from AstraZeneca/Evidera for consultancy on LC and from AstraZeneca for consultancy on digital health. R.A.E. has received speaker fees from Boehringer in June 2021 and has held a role as European Respiratory Society Assembly 01.02 Pulmonary Rehabilitation secretary. R.A.E. is on the American Thoracic Society Pulmonary Rehabilitation Assembly program committee. L.V.W. also receives funding from Orion pharma and GSK and holds contracts with Genentech and AstraZeneca. L.V.W. has received consulting fees from Galapagos and Boehringer, is on the data advisory board for Galapagos and is Associate Editor for the *European Respiratory Journal*. A. Ho is a member of NIHR Urgent Public Health Group (June 2020–March 2021). M.M. is an applicant on the PHOSP study funded by NIHR/DHSC. M.G.S. acts as an independent external and nonremunerated member of Pfizer's External Data Monitoring Committee for their mRNA vaccine program(s), is Chair of Infectious Disease Scientific Advisory Board of Integrum Scientific LLC, and is director of MedEx Solutions Ltd. and majority owner of MedEx

Solutions Ltd. and minority owner of Integrum Scientific LLC. M.G.S.'s institution has been in receipt of gifts from Chiesi Farmaceutici S.p.A. of Clinical Trial Investigational Medicinal Product without encumbrance and distribution of same to trial sites. M.G.S. is a nonremunerated member of HMG UK New Emerging Respiratory Virus Threats Advisory Group and has previously been a nonremunerated member of the Scientific Advisory Group for Emergencies (SAGE). C.B. has received consulting fees and/or grants from GSK, AstraZeneca, Genentech, Roche, Novartis, Sanofi, Regeneron, Chiesi, Mologic and 4DPharma. L.T. has received consulting fees from MHRA, AstraZeneca and Synairgen and speakers' fees from Eisai Ltd., and support for conference attendance from AstraZeneca. L.T. has a patent pending with ZikaVac. P.J.M.O. reports grants from the EU Innovative Medicines Initiative 2 Joint Undertaking during the submitted work; grants from UK Medical Research Council, GSK, Wellcome Trust, EU Innovative Medicines Initiative, UK National Institute for Health Research and UK Research and Innovation–Department for Business, Energy and Industrial Strategy; and personal fees from Pfizer, Janssen and Seqirus, outside the submitted work.

Additional information

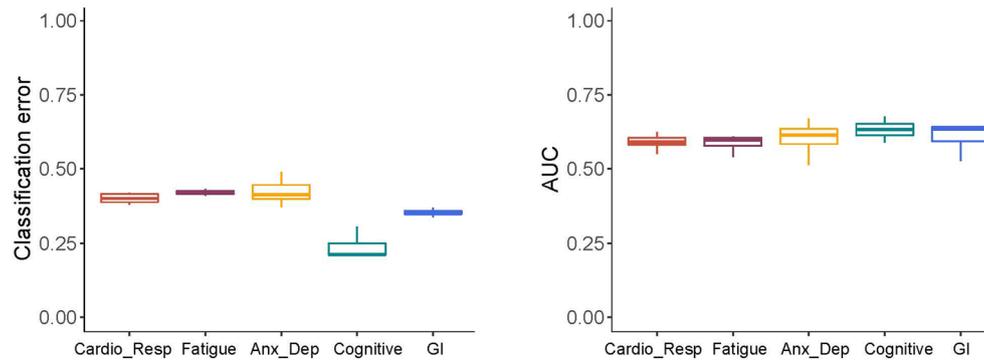
Extended data is available for this paper at <https://doi.org/10.1038/s41590-024-01778-0>.

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s41590-024-01778-0>.

Correspondence and requests for materials should be addressed to Ryan S. Thwaites or Peter J. M. Openshaw.

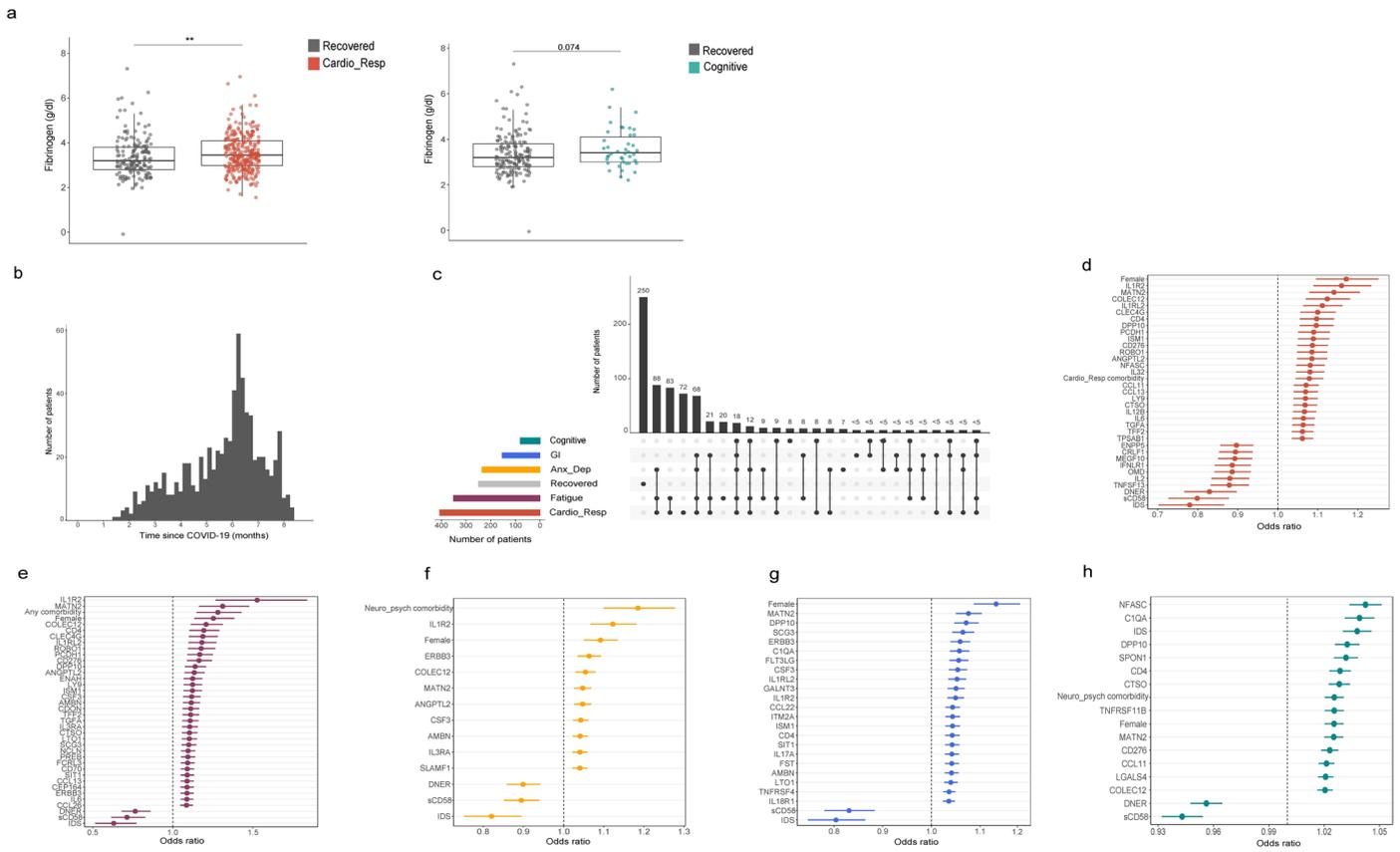
Peer review information *Nature Immunology* thanks Ziyad Al-Aly and the other, anonymous, reviewer(s) for their contribution to the peer review of this work. Ioana Staicu was the primary editor on this article and managed its editorial process and peer review in collaboration with the rest of the editorial team.

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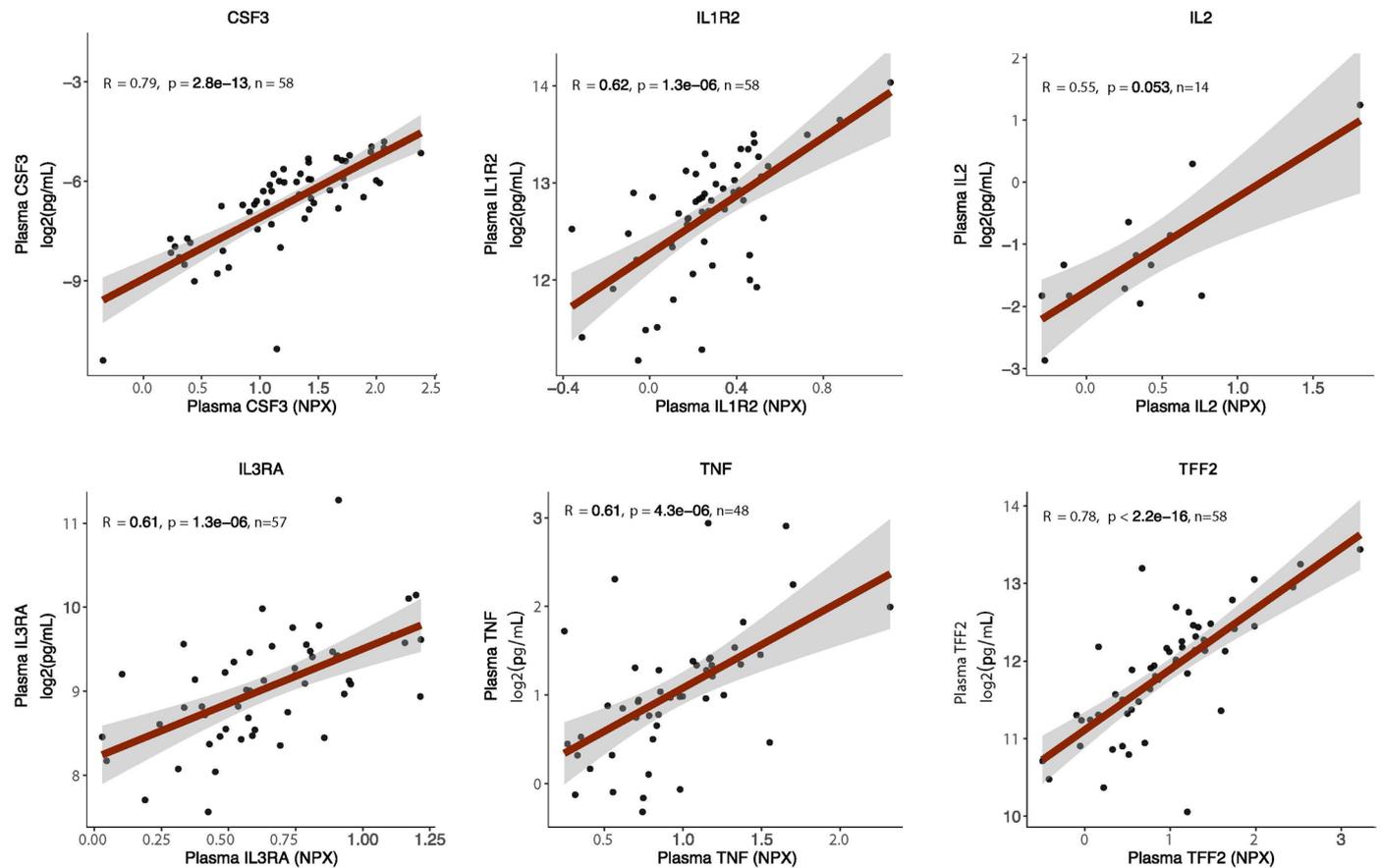
Extended Data Fig. 1 | Penalized logistic regression performance. Graphs show classification error and Area under curve (AUC) from the 50 repeats tenfold nested cross-validation used to optimise and assess the performance of PLR testing associations with each LC outcome relative to Recovered (n = 233): Cardio_Resp (n = 398), Fatigue (n = 384), Anxiety/Depression (n = 202), GI

(n = 132), (e) Cognitive (n = 6). The distributions of classification error and area under curve (AUC) from the nested cross-validation are shown. Box plot centre line represents the Median and boundaries of the box represent interquartile range (IQR), the whisker length represent 1.5xIQR.



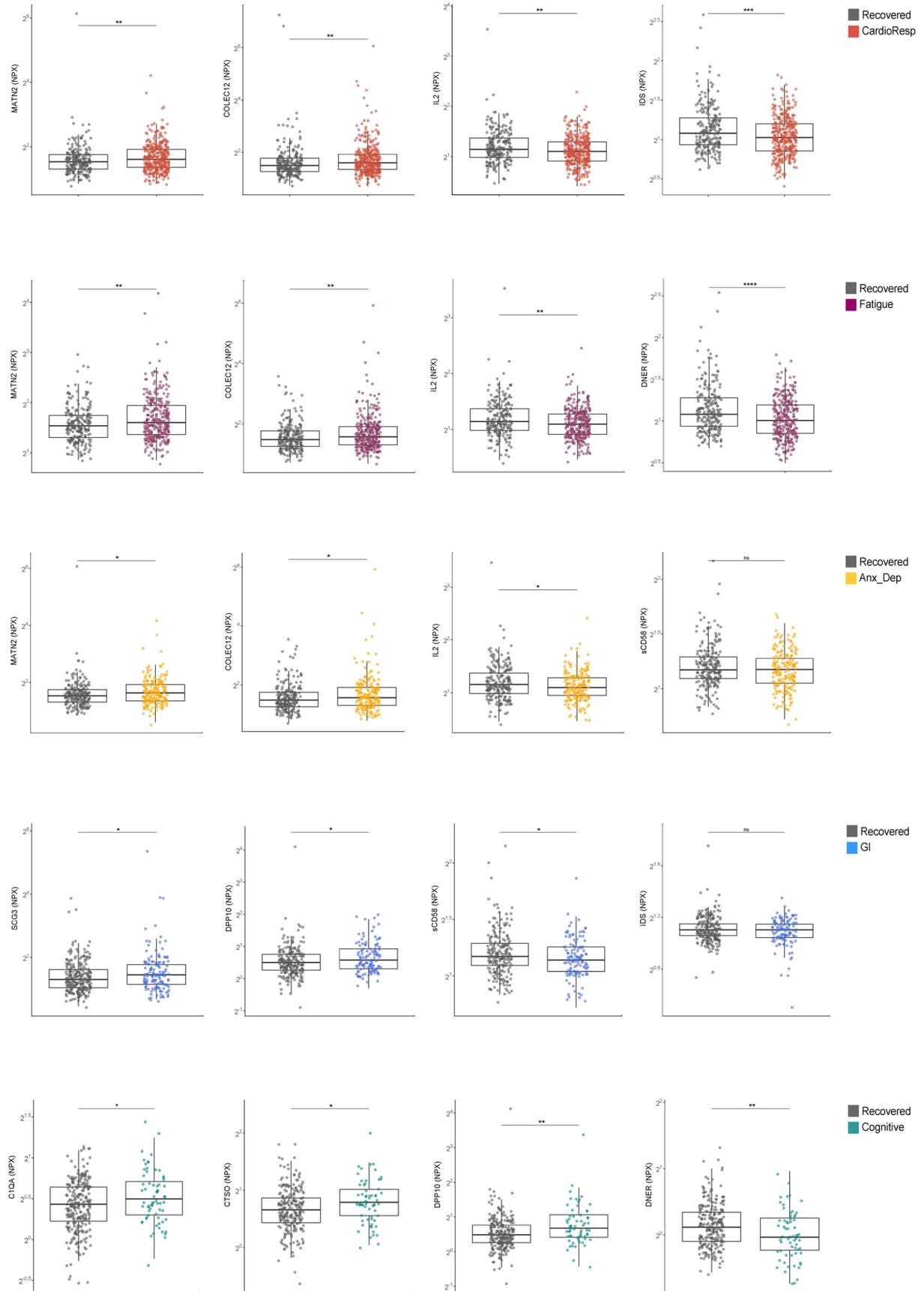
Extended Data Fig. 2 | Associations with long COVID symptoms in full study cohort. (a) Fibrinogen levels at 6 months were compared between pooled LC cases (n = 295) and Recovered (n = 233) and between the Cognitive group (n = 41) and Recovered (n = 233). Box plot centre line represent the Median and boundaries of the box represent interquartile range (IQR), the whisker length represents 1.5xIQR, any outliers beyond the whisker range are shown as individual dots. Median differences were compared using two-sided Wilcoxon signed-rank test $*=p < 0.05$, $**=p < 0.01$, $***=p < 0.001$, $****=p < 0.0001$. Unadjusted p-values are reported. (b) Distribution of time from COVID-19 hospitalisation at sample collection applying CDC and NICE definitions of

LC (n = 719) (c) Upset plot of symptom groups. Horizontal coloured bars represent the number of patients in each symptom group: Cardiorespiratory (Cardio_Resp), Fatigue, Cognitive, Gastrointestinal (GI) and Anxiety/Depression (Anx_Dep). Vertical black bars represent the number of patients in each symptom combination group. To prevent patient identification, where less than 5 patients belong to a combination group, this has been represented as '<5'. The Recovered group (n = 250) were used as controls. Forest plots show Olink protein concentrations (NPX) associated with (d) Cardio_Resp (n = 398), (e) Fatigue (n = 342), (f) Anx_Dep (n = 219), (g) GI (n = 134), and (h) Cognitive (n = 65). Error bars represent the median accuracy of the model.



Extended Data Fig. 3 | Validation of olink measurements using conventional assays in plasma. Olink measured protein (NPX) were compared to chemiluminescence assays (ECL or ELISA, log₂[pg/mL]) to validate our findings, where contemporaneously collected plasma samples were available ($n = 58$). Results from key mediators associated with LC groups were validated: CSF3,

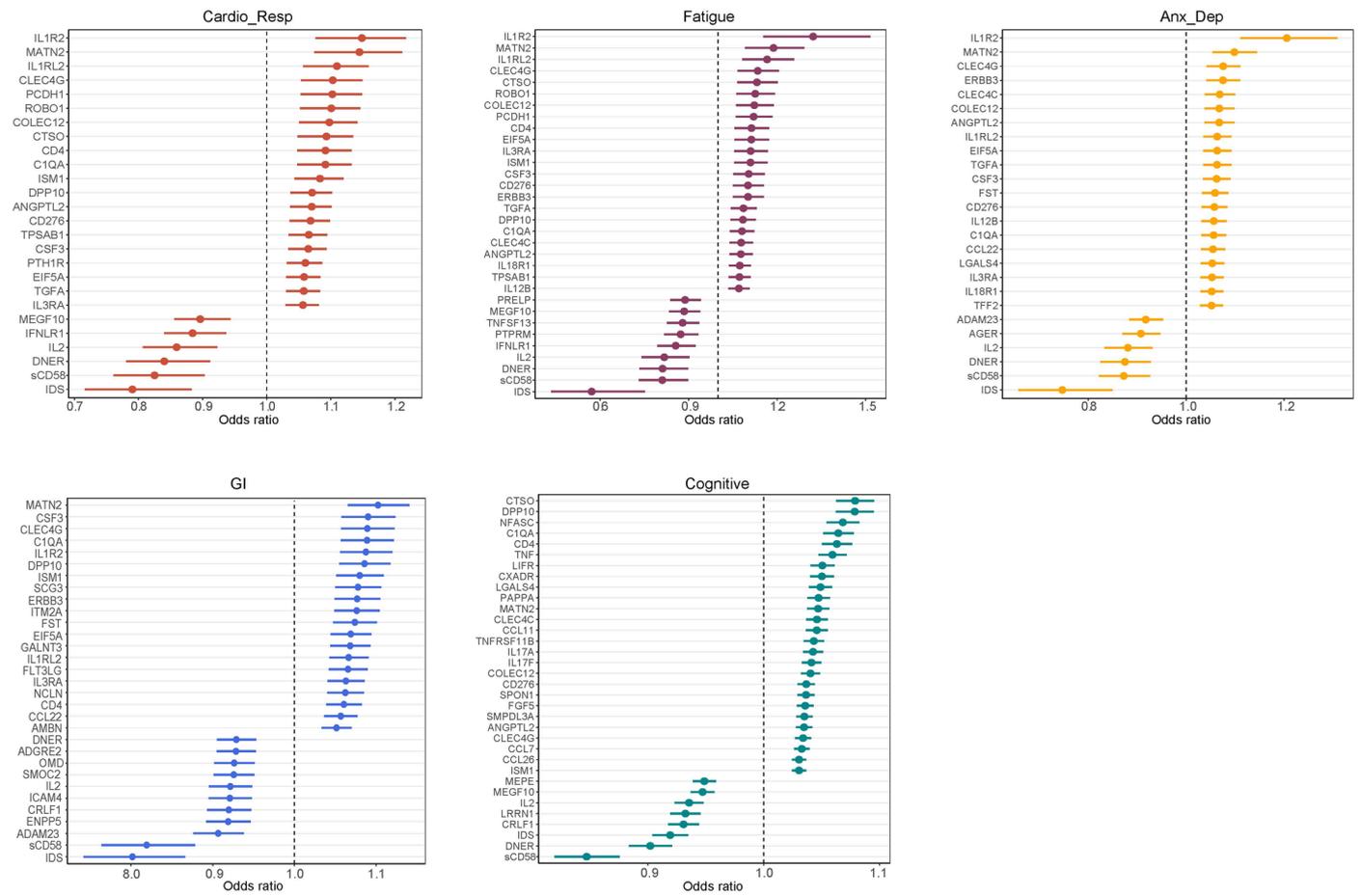
IL1R2, IL2, IL3RA, TNF α , TFF2. R = spearman rank correlation coefficient and shaded areas indicated the 95% confidence interval. Samples that fell below the lower limit of detection for a given assay were excluded and the 'n' value on each panel indicates the number of samples above this limit.



Extended Data Fig. 4 | See next page for caption.

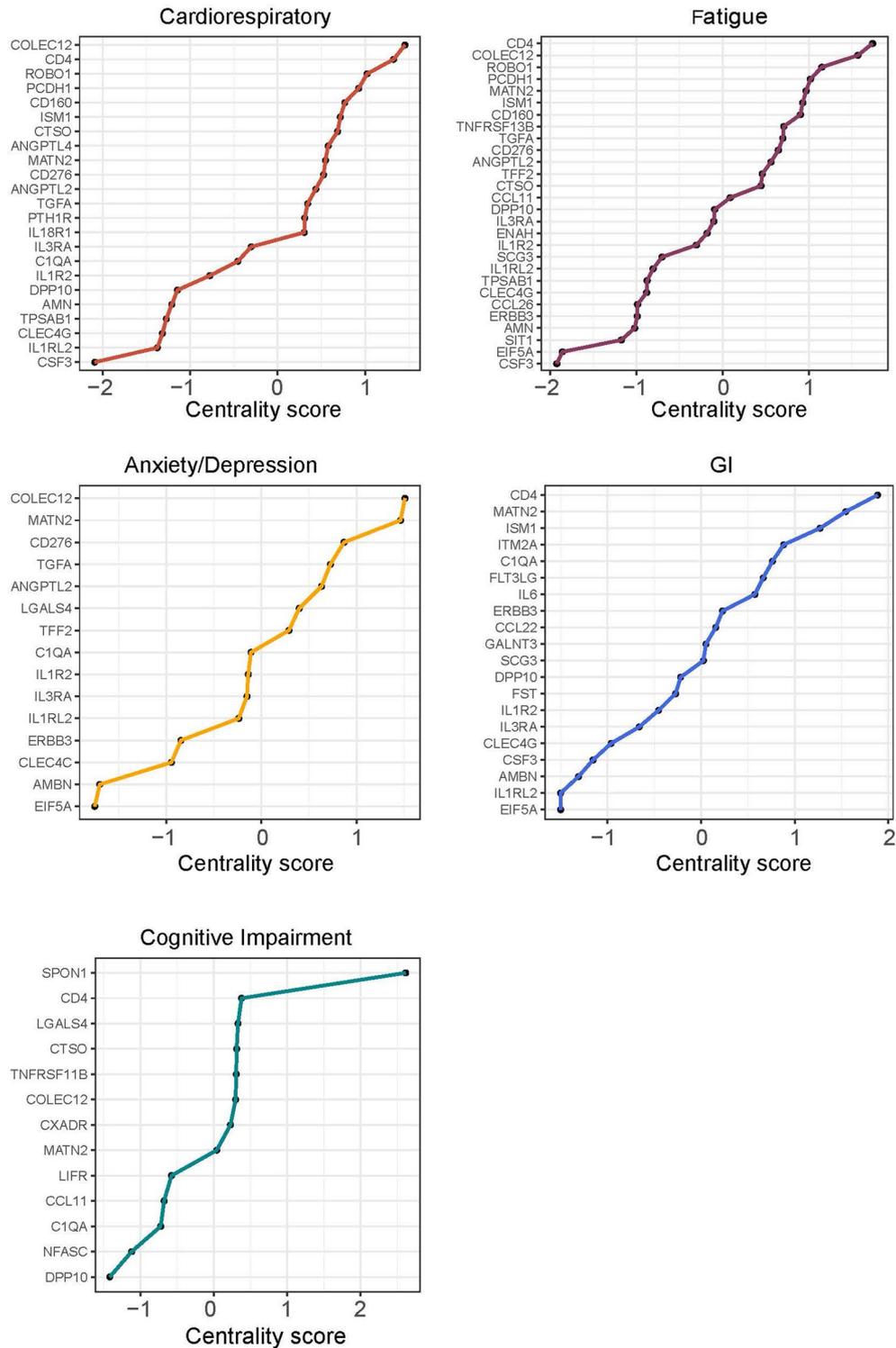
Extended Data Fig. 4 | Univariate analysis of proteins associated with each symptom. Olink measured plasma protein levels (NPX) compared between LC groups (Cardio_Resp, n = 398, Fatigue n = 384, Anxiety/Depression, n = 202, GI, n = 132 and Cognitive, n = 60) and Recovered (n = 233). Proteins identified by PLR were compared between groups. Median differences were compared using

two-sided Wilcoxon signed-rank test. * = $p < 0.05$, ** = $p < 0.01$, *** = $p < 0.001$, **** = $p < 0.0001$ after FDR adjustment. Box plot centre line represent the Median and boundaries of the box represent interquartile range (IQR), the whisker length represents $1.5 \times \text{IQR}$, any outliers beyond the whisker range are shown as individual dots.

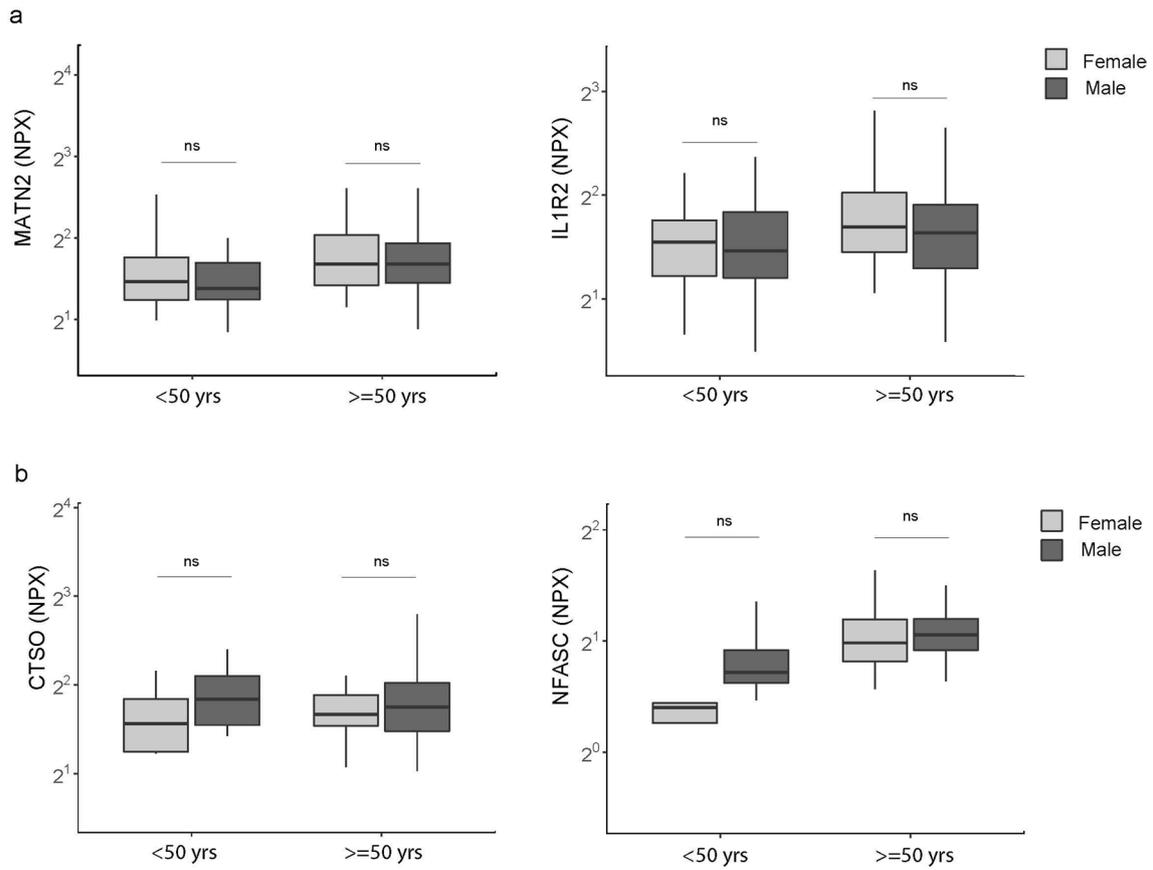


Extended Data Fig. 5 | Unadjusted Penalised Logistic Regression. Olink measured proteins (NPX) and their association with Cardio_Resp (n = 398), Fatigue (n = 342), Anx_Dep (n = 219), GI (n = 134), and Cognitive (n = 65). Forest

plots show odds of each LC outcome vs Recovered (n = 233), using PLR without adjusting for clinical co-variates. Error bars represent the median accuracy of the model.

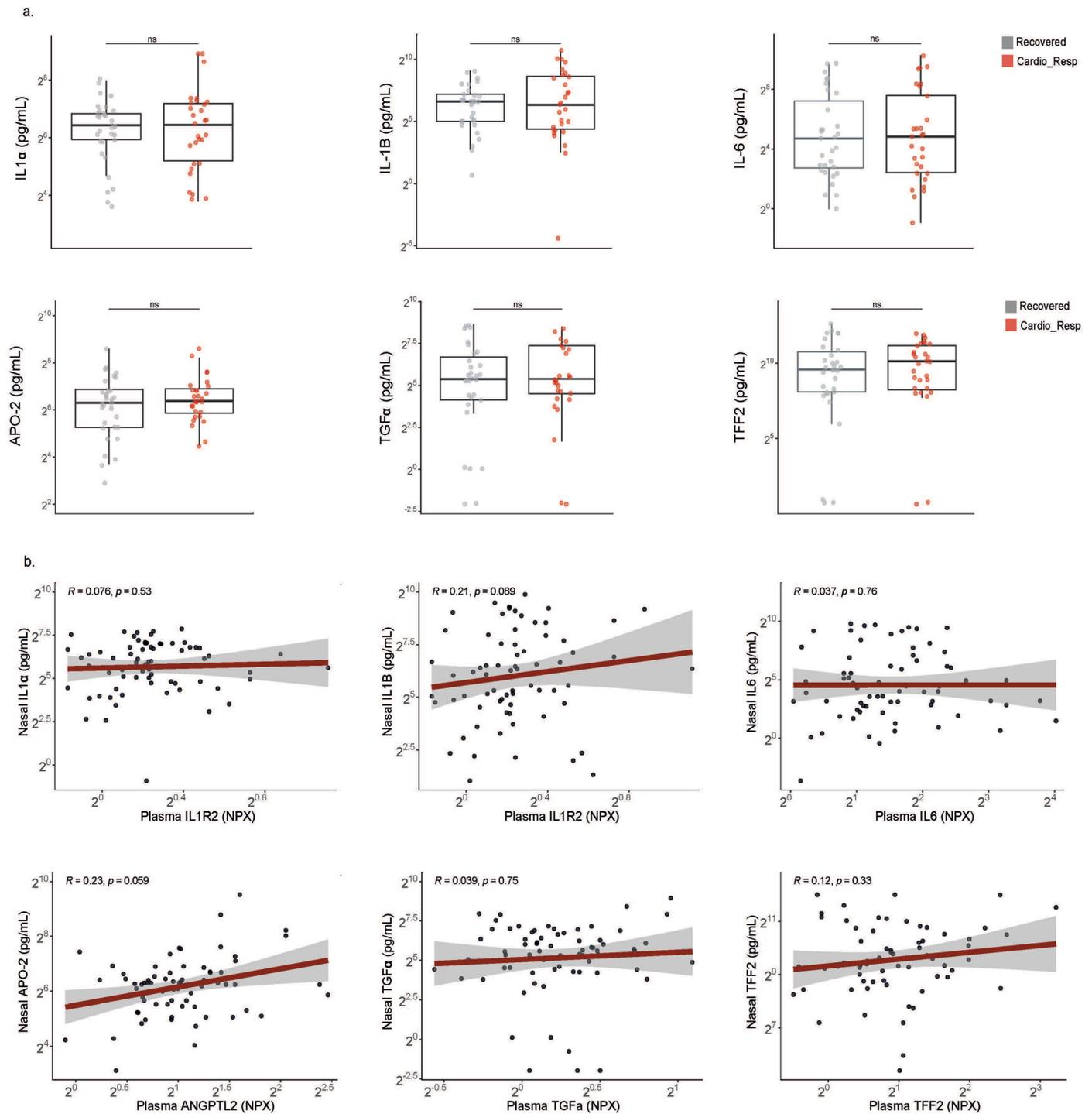


Extended Data Fig. 7 | Network analysis centrality. Each graph shows the centrality score for each Olink measured protein (NPX) found to have significant associations with other proteins that were elevated in the Cardio_Resp (n = 398), Fatigue (n = 342), Anx_Dep (n = 219), GI (n = 134), and Cognitive (n = 65) groups relative to Recovered (n = 233).



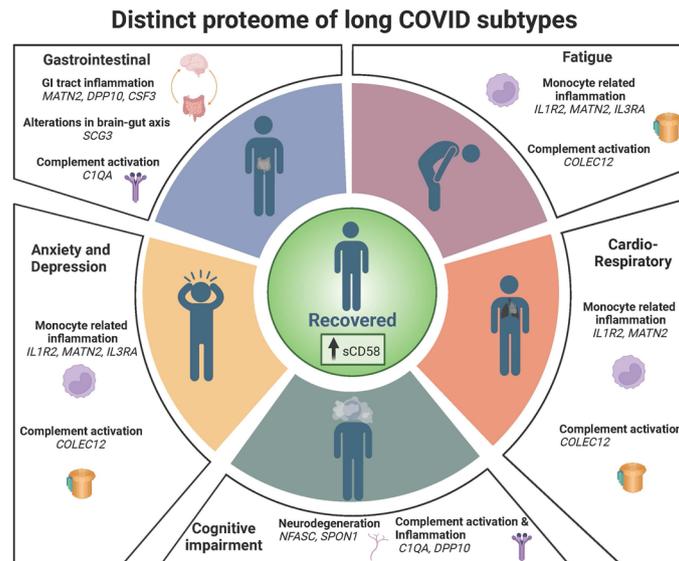
Extended Data Fig. 8 | Inflammation in men and women with long COVID. Olink measured plasma protein levels (NPX) between men and women with symptoms, divided by age (<50 or >=50 years): **(a)** shows IL1R2 and MATN2 in the Anxiety/Depression group (<50 n = 55, >=50 n = 133), **(b)** shows CTSO and NFASC

in the Cognitive group (<50 n = 11, >=50 n = 50). Median values were compared between men and women using two-sided Wilcoxon signed-rank test. Box plot centre line represent the Median and boundaries represent interquartile range (IQR), the whisker length represents 1.5xIQR.



Extended Data Fig. 9 | Inflammation in the upper respiratory tract. Nasal cytokines measured by immunoassay in the CardioResp Group ($n = 29$) and Recovered ($n = 31$): **(a)** shows IL1 α , IL1 β , IL-6, APO-2, TGF α , TFF2. Median differences were compared using two-sided Wilcoxon signed-rank test. Box plot centre line represents the Median and boundaries of the box represent

interquartile range (IQR), the whisker length represent $1.5 \times \text{IQR}$. **(b)** Shows cytokines measured by immunoassay in paired plasma and nasal ($n = 70$). Correlations between IL1 α , IL1 β , IL-6, APO-2, TGF α and TFF2 in nasal and plasma samples were compared using Spearman's rank correlation coefficient (R). Shaded areas indicated the 95% confidence interval of R .



Extended Data Fig. 10 | Graphical abstract. Summary of interpretation of key findings from Olink measured proteins and their association with CardioResp (n = 398), Fatigue (n = 342), Anx/Dep (n = 219), GI (n = 134), and Cognitive (n = 65) groups relative to Recovered (n = 233).

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Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
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- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

No software or algorithms were used. Code used to generate summary data in the Outbreak Analysis Platform (ODAP) is publicly available here: <https://github.com/isaric4c/wiki/wiki/ISARIC> and https://github.com/SurgicalInformatics/cocin_ccp

Data analysis

code was written within the Outbreak Analysis Platform (ODAP), to which access is available under reasonable request as per the Data sharing statement in the manuscript. Analyses within the ODAP were performed in R v4.2.0 using publicly available packages listed in the manuscript methods ('data.table v1.14.2', 'EnvStats v2.7.0' 'tidyverse v1.3.2', 'lme4 v1.1-32', 'caret v6.0-93', 'glmnet v4.1-6', 'mdatools v0.14.0', 'ggpubbr v0.4.0', 'ggplot2 v3.3.6', 'bootnet v1.5.6' and 'qgraph v1.9.8' packages). Extended data Figure 10 was made in Biorender by accessing biorender.com. Last access was Dec 2023. No new algorithms or functions were created for the purposes of analysing the datasets. Code used to generate figures used standard functions in listed packages that are available on CRAN. Code is available at <https://github.com/isaric4c/wiki/wiki/ISARIC> and https://github.com/SurgicalInformatics/cocin_ccp and https://github.com/ClaudiaEfstath/PHOSP_Olink_NatImm.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

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A data availability statement is included in the manuscript.

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Clinical data was collected via PHOSP REDCap database, to which access is available under reasonable request as per the Data sharing statement in the manuscript.

Conventional immunoassay data were collected using Mesoscale Discovery workbench software or Fluostar Omega plate reader software and Microsoft Excel.

The PHOSP-COVID protocol, consent form, definition and derivation of clinical characteristics and outcomes, training materials, regulatory documents, information about requests for data access, and other relevant study materials are available online: <https://phosp.org/resource/>. Access to these materials can be granted by contacting phosp@leicester.ac.uk and Phospcontracts@leicester.ac.uk.

The ISARIC4C protocol, data sharing and publication policy are available at <https://isaric4c.net>. ISARIC4C's Independent Data and Material Access Committee welcomes applications for access to data and materials (<https://isaric4c.net>).

All data used in this study is available within ODAP and accessible under reasonable request. Data access criteria and information about how to request access is available online: <https://phosp.org/resource/>. If criteria are met and a request is made, access can be gained by signing the eDRIS user agreement.

The data sets used in the study contain extensive clinical information at individual level that prevent them from being deposited in a public depository due to data protection policies of the study. Study data can only be accessed via ODAP, a protected research environment. However as stated in the above statement, data access can be requested from the PHOSP COVID consortium.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

From the manuscript: 'Both sexes were recruited and gender was self-reported.' (methods)

The proportion of men and women in each group has been reported (Table 1)

Sex was included as a covariate in the analysis (Figure 1C-G). An exploratory analysis was performed to understand the female-bias of long COVID (Figure 3, Extended Data Figure 6 & Supplementary Table 2).

Population characteristics

Population characteristics are reported in Table 1 and have been previously reported in the following reference which is cited in the paper: Evans, R. A. et al. Physical, cognitive, and mental health impacts of COVID-19 after hospitalisation (PHOSP-COVID): a UK multicentre, prospective cohort study. *Lancet Respir Med* 9, 1275–1287 (2021).

Recruitment

From the manuscript:

'After hospital discharge patients >18 years old who had no co-morbidity resulting in a prognosis of less than 6 months, who had been hospitalised for COVID-19 were recruited to the PHOSP-COVID study. Patients that had been hospitalised between February 2020 and January 2021 were recruited. Both sexes were recruited and gender was self-reported. Written informed consent was obtained from all patients.'

'Clinical data and plasma samples were prospectively collected from adult cases of COVID-19 approximately 6 months after hospitalisation, via the PHOSP-COVID multicentre UK study.'

'Data relating to patient demographics and the acute admission were collected via the ISARIC4C study. Adults hospitalised during the SARS-CoV-2 pandemic were systematically recruited into the International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC) World Health Organization Clinical Characterisation Protocol UK (IRAS260007 and IRAS126600). Written informed consent was obtained from all patients.'

Citations are provided in the text to the papers which fully detail recruitment and population characteristics: Methods, Reference number 15,14,16,96

Ethics oversight

From the manuscript:

'Ethical approvals for the PHOSP-COVID study were given by Leeds West Research Ethics Committee (20/YH/0225).'

'Adults hospitalised during the SARS-CoV-2 pandemic were systematically recruited into the International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC) World Health Organization Clinical Characterisation Protocol UK (IRAS260007 and IRAS126600). Written informed consent was obtained from all patients. Ethical approval was given by the South Central-Oxford C Research Ethics Committee in England (reference: 13/SC/0149), Scotland A Research Ethics Committee (20/SS/0028) and World Health Organization Ethics Review Committee (RPC571 and RPC572); 25 April 2013).'

'Written consent was obtained for all individuals and ethical approvals were given by London-Harrow Research Ethics Committee (13/LO/1899) for the collection of nasal samples and the Health Research Authority London-Fulham Research Ethics Committee (IRAS Project ID 154109; references 14/LO/1023, 10/H0711/94, and 11/LO/1826) for BALF samples.'

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

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Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	<p>This was an exploratory observational study set up early in the pandemic to understand long term healthcomes after COVID-19. As such, UK patients were systematically recruited to understand sequelae and biological mechanisms at population level. As such, power calculations were not performed. Given the limited understanding of long COVID as a disease entity at the start of the study, power calculations and meaningful effect sizes are challenging to derive. However previous work published by the PHOSP-COVID consortium has indicated the this study size is sufficient to detect changes in inflammatory profiles 6 months after hospitalisation:</p> <p>Evans, R. A. et al. Clinical characteristics with inflammation profiling of long COVID and association with 1-year recovery following hospitalisation in the UK: a prospective observational study. <i>Lancet Respir Med</i> 10, 761–775 (2022).</p> <p>Furthermore, recent studies using Olink data in sample sizes substantially smaller than ours indicate our sample size is sufficient to detect meaningful proteomic differences between symptom groups:</p> <p>Woodruff, M. C. et al. Chronic inflammation, neutrophil activity, and autoreactivity splits long COVID. <i>Nat Commun</i> 14, 4201 (2023).</p>
Data exclusions	<p>Individuals were excluded from the PLR analysis if covariate or symptom outcome or covariate data was missing. Olink data from analytes that did not pass QC measures were excluded.</p>
Replication	<p>To ensure the validity of results, samples were run in a single batch with use of negative controls, plate controls in triplicate, and repeated measurement of patient samples between plates in duplicate. Samples were randomized between plates according to site and sample collection date. Randomization between plates was blind to long COVID/ recovered outcome. Data were first normalized to an internal extension control that was included in each sample well. Plates were standardized by normalizing to inter-plate controls, run in triplicate on each plate. Each plate contained a minimum of 4 patient samples which were duplicates on another plate, these duplicate pairs allowed any plate to be linked to any other through the duplicates. Data were then intensity normalized across all cohort samples. Finally, Olink results underwent QC processing and samples or analytes that did not reach QC standards were excluded. Final normalized relative protein quantities were reported as log₂ normalized protein expression (NPX) values. (Methods)</p> <p>The QC and normalisation methods are according to best practice guidance which can be found here: https://www.olink.com/content/uploads/2022/04/white-paper-data-normalization-v2.1.pdf</p> <p>A nested cross-validation was used to choose the optimal model for analysis and assess the stability of the model. The results of this have been reported in the manuscript (supplemental p3 and Extended Data Fig 9). Furthermore we validated our findings through repeated analysis restricted by Long COVID definition (Extended Data Fig 1) as well as through application of different models, unadjusted and non-regularised models and univariate analyses (Extended Data Fig 1-4, Supplementary Table 2).</p>
Randomization	<p>This was an observational, non-interventional study and symptom data was collected prospectively. To avoid bias introduced by assay error, non-specific binding or batch effects, samples were randomized between plates and run in a single batch blinded for long COVID/ recovered outcome. Randomization of samples across Olink assay plates is described in 'Replication'.</p>
Blinding	<p>Assays were run blinded to symptom outcome. Samples were randomized between plates with blinding for long COVID/ recovered outcome. Exclusion of data according to missingness or QC measures occurred prior to primary analysis, without knowledge of clinical data, symptom outcome or individual analyte results.</p>

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We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

Methods

n/a	Involved in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used

Antibodies used were in the form of commercial ELISA, MSD and Luminex assays (details in online methods and supplementary page 1):

Biotechne: Human Luminex Discovery Assay, configuration Ubdal728; CAT NO: LXSAMH-15
MSD: V-PLEX Proinflammatory Panel1 (human) Kit (1 Plate); CAT NO: K15049D-1

MSD:

R-PLEX Human TFF2 Antibody Set ; CAT NO: F21ACM-3
R-PLEX Human TGF- α Antibody Set ; CAT NO: F21ACN-3
R-PLEX Human tPA Antibody Set ; CAT NO: F21ACZ-3
R-PLEX IL1R2 Antibody set; CAT No: K151ANVR-2
U-plex GCSF and IL2 custom multiplex kit; CAT No: K15067M-1

Abcam: IL3RA Elisa kit, CAT No: ab300317

Olink antibodies were selected in a 3 stage validation process:

1. Screening against an Olink designed antigen (Ag) pool developed over many years to detect unspecific binding.
2. After removal of poorly performing antibodies, a second screen was performed using a second Ag pool (n=92 Ags)
3. Validation of final product design was then performed against a pool of carefully selected proteins with documented high homology within their protein families (n=96 Ags).

Using these methods (details available: <https://olink.com/content/uploads/2022/10/olink-explore-validation-data.pdf>) Olink have demonstrated that 99.7% of Olink explore protein assays do not show any cross-reactivity or non-specific binding. The specific proteins that we found to be associated with Long COVID have all shown inter- and intra-CVs < 10, demonstrating very high precision. The full list of analytes in the Olink Explore inflammation panel and their associated precision can be found here: <https://olink.com/content/uploads/2023/07/olink-explore-3072-validation-data-results.xlsx>.

Validation

validation details are available from the MSD website as follows:

"MSD's validated assay kits meet the Clinical Laboratory Standards Institute guidelines for consistency, sensitivity, precision, and robustness. Validation testing is conducted through a design-control process according to the principles outlined in "Fit-for-Purpose Method Development and Validation for Successful Biomarker Measurement" by Lee, J.W. et al." Available from: https://www.mesoscale.com/en/support/product_information/search_coa/~link.aspx?id=C6380BC0C4514064875E4382146EC6B1&_z=z

Validation of Luminex cytokine assays has been published: dupont NC, Wang K, Wadhwa PD, Culhane JF, Nelson EL. Validation and comparison of luminex multiplex cytokine analysis kits with ELISA: determinations of a panel of nine cytokines in clinical sample culture supernatants. *J Reprod Immunol.* 2005 Aug;66(2):175-91. doi: 10.1016/j.jri.2005.03.005. PMID: 16029895; PMCID: PMC5738327.

The Olink Explore assays have been validated internally through a 3 stage process (see above). The full methods used are publicly available: <https://olink.com/content/uploads/2022/10/olink-explore-validation-data.pdf> and <https://olink.com/content/uploads/2023/07/olink-explore-3072-validation-data-results.xlsx>.

Using these methods, Olink have demonstrated that 99.7% of Olink explore protein assays do not show any cross-reactivity or non-specific binding. The specific proteins that we found to be associated with Long COVID have all shown inter- and intra-CVs < 10, demonstrating very high precision. The full list of analytes in the Olink Explore inflammation panel and their associated precision can be found here: <https://olink.com/content/uploads/2023/07/olink-explore-3072-validation-data-results.xlsx>.

Olink has also been validated against other assays and this data has been published (wik et al., 2021, <https://doi.org/10.1016/j.mcpro.2021.100168>; references 88-93 in manuscript, Discussion).

We further internally validated the assay using conventional MSD and ELISA kits (Extended Data Fig.8)

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	NA. This was not a clinical trial.
Study protocol	The PHOSP-COVID protocol, consent form, definition and derivation of clinical characteristics and outcomes, training materials, regulatory documents, information about requests for data access, and other relevant study materials are available online: https://phosp.org/resource/ . Access to these materials can be granted by contacting phosp@leicester.ac.uk and Phospcontracts@leicester.ac.uk .
Data collection	<p>Clinical data and plasma samples were prospectively collected from adult cases of COVID-19 approximately 6 months after hospitalisation, via the PHOSP-COVID multicentre UK study (see Methods).</p> <p>The definition and derivation of clinical characteristics and outcomes can be accessed here: https://phosp.org/resource/. Access to these materials can be granted by contacting phosp@leicester.ac.uk and Phospcontracts@leicester.ac.uk.</p> <p>Clinical data were collected through patient symptom questionnaires and validated clinical scores. The methods of clinical data collection have been extensively outlined and published and the references from the manuscript are included below:</p> <p>14. Elneima, O. et al. Cohort Profile: Post-hospitalisation COVID-19 study (PHOSP-COVID). <i>medRxiv</i> 2023.05.08.23289442 (2023) doi:10.1101/2023.05.08.23289442.</p> <p>15. Evans, R. A. et al. Clinical characteristics with inflammation profiling of long COVID and association with 1-year recovery following hospitalisation in the UK: a prospective observational study. <i>Lancet Respir Med</i> 10, 761–775 (2022).</p> <p>Prospectively collected outcome and covariate data used are detailed in the manuscript 'Methods' section:</p> <p>"Symptom data and samples were prospectively collected from individuals approximately 6 months after hospitalisation (Fig. 1A), via the PHOSP-COVID multicentre UK study... Clinical data were used to place patients into 6 categories: 'Recovered', 'GI', 'Cardiorespiratory', 'Fatigue', 'Cognitive impairment' and 'Anxiety/depression' (Supplementary Table 5). Patient reported symptoms and validated clinical scores were used including: MRC breathlessness score, dyspnoea-12 score, FACIT score, PHQ-9 and GAD-7. Responses to symptom questionnaires about chest pain and palpitations were also used. Cognitive impairment was defined as a Montreal Cognitive Assessment (MoCA) score <26. GI symptoms were defined as answering 'Yes' to the presence of at least two of the listed symptoms. 'Recovered' was defined by self-reporting. Patients were placed in multiple groups if they experienced a combination of symptoms."</p> <p>Additional covariate data were also collected and analysed:</p> <p>"Data were collected to account for variables affecting symptom outcome, via hospital records and self-reporting. Acute disease severity was classified according to the WHO Clinical Progression score: Class 3-4 required no oxygen, Class 5 required oxygen therapy, Class 6 required non-invasive ventilation or high-flow nasal oxygen), Class 7-9 were managed in critical care... Age, sex, acute disease severity and pre-existing comorbidities were included as covariates in the PLR analysis (Supplementary Table 1,2)"</p> <p>This was a cross-sectional analysis of clinical data collected. No single individual provided repeated measures in the cohort that we analysed.</p>
Outcomes	<p>The primary outcome of this study was inflammatory profiles associated with symptoms occurring approximately 6 months after COVID-19 hospitalisation. We used nested controls within our cohort by using a group of individuals that reported feeling recovered. We compared inflammatory profiles in patients with symptoms and compared them to recovered controls within the cohort. The range of time-points at which this data was collected relative to acute infection is shown in Figure 1 A. This was a cross-sectional analysis of clinical data collected. No single individual provided repeated measures in the cohort that we analysed.</p> <p>The full list of clinical outcomes measured by PHOSP-COVID and questionnaires used are publicly available (and this has been cited in the manuscript):</p> <p>14. Elneima, O. et al. Cohort Profile: Post-hospitalisation COVID-19 study (PHOSP-COVID). <i>medRxiv</i> 2023.05.08.23289442 (2023) doi:10.1101/2023.05.08.23289442.</p> <p>The specific variables used to define symptom outcomes in our study are detailed in Supplementary table 5, and described in Methods (see Excerpt above).</p> <p>The primary outcome measure was analysed via the Olink Explore inflammatory panel using best practice methods (Methods). The association between inflammatory profiles and methods were measured using a penalised logistic regression model (Methods and Supplementary, page 2).</p>