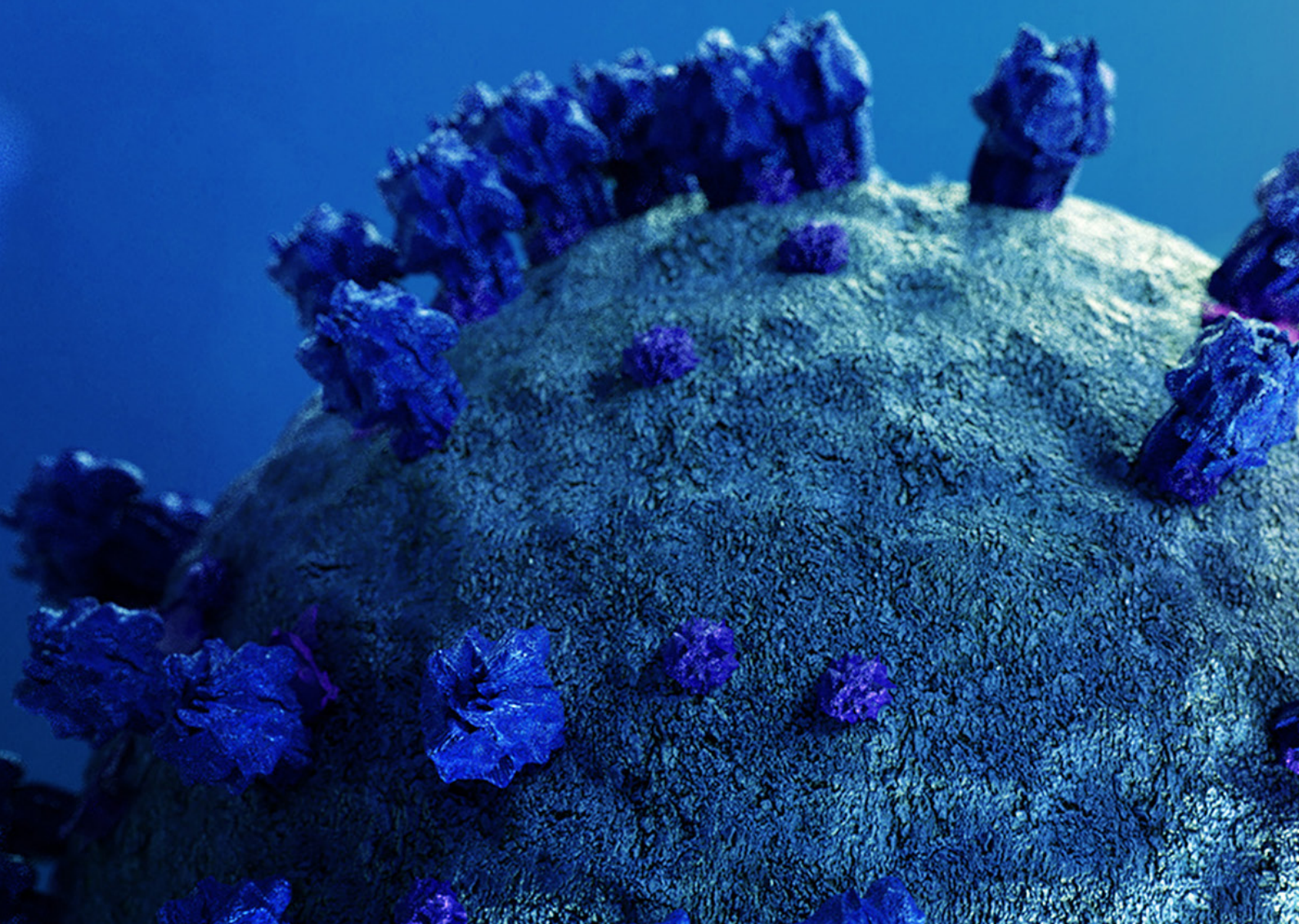
RAND EUROPE

# Evaluation of the COVID-19 Genomics UK (COG-UK) Consortium

## Annexes

Sonja Marjanovic, Robert Romanelli, Gemma Claire-Ali, Brandi Leach, Margaretha Bonsu, Daniela Rodriguez Rincon and Tom Ling



For more information on this publication, visit www.rand.org/t/RRA1277-1

**About RAND Europe**
RAND Europe is a not-for-profit research organisation that helps improve policy and decision making through research and analysis. To learn more about RAND Europe, visit www.randeurope.org.

**Research Integrity**
Our mission to help improve policy and decision making through research and analysis is enabled through our core values of quality and objectivity and our unwavering commitment to the highest level of integrity and ethical behaviour. To help ensure our research and analysis are rigorous, objective, and nonpartisan, we subject our research publications to a robust and exacting quality-assurance process; avoid both the appearance and reality of financial and other conflicts of interest through staff training, project screening, and a policy of mandatory disclosure; and pursue transparency in our research engagements through our commitment to the open publication of our research findings and recommendations, disclosure of the source of funding of published research, and policies to ensure intellectual independence. For more information, visit www.rand.org/about/principles.



Published by the RAND Corporation, Santa Monica, Calif., and Cambridge, UK



*Cover: Adobe Stock*

# Annex 1: COG-UK partners

## The COG-UK Consortium

### COG-UK - Academic Institutes (n=16)

There are 16 academic partners conducting research and supporting service delivery: The University of Birmingham, The University of Cambridge, Cardiff University, The University of Edinburgh, The University of Exeter, The University of Glasgow, Imperial College London, The University of Liverpool, The University of Nottingham, The University of Northumbria, The University of Oxford, The University of Portsmouth, Queens University Belfast, Quadram Institute, The University of Sheffield and University College London.

### COG-UK - PHAs (n=4)

There are four PHAs conducting research and supporting service delivery: Public Health Scotland, Public Health England, Northern Ireland Public Health Agency and Public Health Wales.

### COG-UK - Central Sequencing Hub (n=1)

The Wellcome Sanger Institute conducts research, supports service delivery and is also a funder.

## Additional Sequencing Collaborators

### Lighthouse Labs (n=4)

Four Lighthouse labs support service delivery: Milton Keynes, Glasgow, Cambridge and Alderley Park, Cheshire.

### Additional sites involved in sequencing (n=14)

Barking, Havering and Redbridge University Hospitals NHS Trust, East Kent Hospitals University NHS Foundation Trust, Guy's and St Thomas' NHS Foundation Trust, the Joint Biosecurity Centre (note: under the University of Liverpool), the London School of Hygiene and Tropical Medicine, London St Barts Hospital, Manchester University NHS Foundation Trust, St George's University Hospitals NHS Foundation Trust, The Francis Crick Institute, The Princess Alexandra Hospital NHS Trust, University College London Hospitals NHS Foundation Trust, the University of Leeds, the University of Warwick and the University of Brighton.

### Additional NHS and other collaborators (n=65)

Basingstoke Hospital, Belfast Health and Social Care Trust, Betsi Cadwaladr University Health Board, Big Data Institute, Blackpool Teaching Hospitals NHS Foundation Trust, Brighton and Sussex University Hospitals NHS

Trust, Buckinghamshire Healthcare NHS Trust, Cambridge University Hospitals, Cardiff and Vale University Health Board, County Durham and Darlington NHS Foundation Trust, East Suffolk and North Essex NHS Foundation Trust, East Sussex Healthcare NHS Trust, EMBL-EBI, Gateshead Health NHS Foundation Trust, Genomics England Limited, Genomics Partnership Wales, Gloucestershire Hospitals NHS Foundation Trust, Great Ormond Street Hospital for Children NHS Foundation Trust, Health Services Laboratories, Hull University Teaching Hospitals NHS Trust, Maidstone and Tunbridge Wells NHS Trust, NHS Hampshire Hospitals NHS Foundation Trust, CVR MRC-University of Glasgow Centre for Virus Research, NHS Greater Glasgow and Clyde, Imperial College Hospitals NHS Trust, Kettering General Hospital, King's College Hospital NHS Foundation Trust, Isle of Wight NHS Trust, NHS Lothian, Norfolk and Norwich University Hospitals NHS Foundation Trust, North Cumbria Integrated Care NHS Foundation Trust, North Tees and Hartlepool NHS Foundation Trust, Northern Lincolnshire and Goole NHS Foundation Trust, Oxford University Hospitals NHS Foundation Trust, PHE and Leeds Teaching Hospitals Trust, Portsmouth Hospitals NHS Trust, Public Health Wales NHS Trust, Queen Elizabeth Hospital, Randox, Royal Brompton and Harefield Hospitals, Royal Devon & Exeter NHS Foundation Trust, Royal Free London NHS Foundation Trust, Royal Veterinary College, Sandwell and West Birmingham NHS Trust, Sheffield Teaching Hospitals NHS Foundation Trust, South Tees Hospitals NHS Foundation Trust, The Centre for Genomic Pathogen Surveillance, The Queen Elizabeth Hospital King's Lynn NHS Foundation Trust, The Royal Marsden NHS Foundation Trust, The Royal Wolverhampton NHS Trust, Newcastle upon Tyne Hospitals NHS Foundation Trust, North Middlesex University Hospital NHS Trust, North Tees and Hartlepool NHS Foundation Trust, Northumbria Healthcare NHS Foundation Trust, Biocentre, University Hospitals Birmingham, University Hospitals Coventry & Warwickshire NHS Trust, University Hospitals Dorset NHS Foundation Trust, University Hospitals of Leicester NHS Trust, University Hospitals Southampton NHS Foundation Trust, University Hospitals Sussex NHS Foundation, Watford General Hospital, Wellcome Centre for Human Genetics, Whittington Health NHS Trust, Wye Valley NHS Trust Hereford.

*Source: COG-UK authorship lists December 20 and June 21.*

# Annex 2: Evaluation Indicators

**Annex Table 2-1** focuses on impact indicators, **Annex Table 2-2** on output and outcome indicators, **Annex Table 2-3** on process indicators and **Annex Table 2-4** on input indicators.

**Annex Table 2-1. Impact indicators**

| IMPACT INDICATOR CATEGORY | POSSIBLE INDICATORS (Qualitative and quantitative) |
|---|---|
| **Advancing the knowledge base:**<br>Increased understanding of genetic changes associated with the SARS-CoV-2 virus and their relationship to spread, transmission, symptoms severity and the likelihood of public health interventions being effective:<br>• This matters for public health decision making, for the development of treatments and vaccines and for evaluating their effectiveness.<br>• It also matters for securing a skilled and trained workforce that can respond to future public health threats. | • Number of academic publications and technical reports.<br>• Nature of topics covered in the publications. |
| **Real-world utility and impact:**<br>• COG-UK activities and outputs impact public health and policy decision making and actions in the response, management and control of the COVID-19 pandemic.<br>• Outputs reach decision makers in a timely manner.<br>• COG-UK's research and data helps enable future evaluations of the effectiveness of various pharmacological and non-pharmacological interventions, informed by COG-UK genome analysis-related activity.<br>• COG-UK (or its legacy) is a critical partner in shaping vaccine development programmes in the future. | • Evidence on public policy decisions directly informed by COG-UK activities.<br>• Evidence that evidence/data reaches decision makers in a timely manner.<br>• Evidence of COG-UK's activity contributing to evaluations of pharmacological and non-pharmacological interventions that cite/mention COG-UK's genome sequencing data.<br>• Evidence that policymakers see genomic sequencing as key to future vaccine-development programmes. |

| IMPACT INDICATOR CATEGORY | POSSIBLE INDICATORS (Qualitative and quantitative) |
|---|---|
| **Real-world utility and impact (legacy):**<br>• A sustainable community of practice supports a dynamic and adaptable pathogen genomics platform that can be mobilised for future pandemics/public health threats to support sequencing, analysis, surveillance, outbreak monitoring needs (COVID-19 or other). It is multi-stakeholder and multidisciplinary. | • Number of individuals trained by COG-UK and the nature of their skills (as this supports future workforce capacity).<br>• Events and conferences incorporating diverse COG-UK partners as an indicator of a vibrant community of practice.<br>• Evidence on projects where COG-UK partners are engaging in other research and public health service delivery activities not directly related to COVID-19 (i.e. lasting onward relationships). |
| **Real-world utility and impact (legacy):**<br>• An improved and sustainable UK pathogen-genomic data and physical/technical infrastructure (as a global example of excellence), e.g. a bioinformatics infrastructure, data repository infrastructure and modern sequencing equipment. | • New equipment which can be used beyond COG-UK activities.<br>• New facilities that can be used in the future.<br>• New data and IT infrastructure that can be used in the future. |
| **Real-world utility and impact (legacy)**<br>• Learning from the COG-UK model impacts the integration of sequencing activities, infrastructure and tools into relevant national PHAs. | • Evidence that the four PHAs more actively govern and coordinate public health genomics research and service delivery functions.<br>• Evidenced from stakeholders on the legacy structures, relationships and activities that support the integration of routine sequencing into the broader public health system.<br>• Stakeholder views about where COG-UK sits in the public health landscape (at the end of the funding period).<br>• Evidence on whether the consequences of COG-UK are lasting, even if COG-UK morphs into something else with time. |
| **Real-world utility and impact (legacy)**<br>• Learning from COG-UK's experience enables better future logistics and operational preparedness for integrating genomics research with service support in a public health response (e.g. via better understanding, requisite protocols and governance arrangements). | • Evidence that SOPs, governance frameworks and operational frameworks produced by COG-UK are being considered or used by other efforts nationally or internationally. |
| **International impact**<br>• COG-UK achieves global impact (e.g. shaping vaccine policy, building skills in the global research and public health workforce and influencing international pathogen genomic research and sequencing initiatives). | • Evidence of COG-UK members' participation in supporting global public health sequencing and service efforts: new international collaborations.<br>• Advisory roles to international efforts. |

**Annex Table 2-2. Proposed output and outcome indicators**

| OUTPUT AND OUTCOME INDICATOR CATEGORY | POSSIBLE INDICATORS (Qualitative and quantitative) |
|---|---|
| **Research-and-analysis related**<br>• A high number of virus genomes are sequenced at pace and from a representative geography/ population | • Number of viral genomes sequenced in a given period and their geographical spread.<br>• Narrative information on how sequencing achievements relate to sequencing strategies and targets.<br>• Narrative information to clarify progress in light of geographical inclusiveness. |
| **Research-and-analysis related**<br>• High quality linked data outputs (e.g. genome, epidemiological and health-record data) are produced and shared in the form of databases or other resources to inform public health decision making. | • Nature of linked datasets (e.g. between genomic and electronic health record and contact tracing data as well as between host- and viral-genome data). |
| **Research-and-analysis related**<br>• Genomic-sequencing data and analyses are shared through open access to eligible applicants. | • Evidence of open access portals populated with genomic sequencing data.<br>• Any evidence of data being accessed and used. |
| **Research-and-analysis related**<br>• Genomic sequencing methods, analytical tools/ software and analysis protocols are developed and shared, enabling the use of sequencing data by academics, PHAs and NHS organisations. | • Tools for analysis of sequencing data (software or other).<br>• Publications specifically on sequencing methods. |
| **Research-and-analysis related**<br>• National, regional or local research studies conducted by COG-UK OR (or with COG-UK as a collaborator) aim to address research questions that can inform public health decision making and policy from a multidisciplinary perspective. Examples include infection control and measures to reduce spread; understanding infection rates, transmission and outbreaks; understanding mutations and their relation to spread and symptoms; re-infection and immunity and vaccine trials (with COG-UK assisting through data, analysis, tools and other research activity). | • Number and nature of research studies.<br>• Publications by COG-UK members that acknowledge COG-UK findings or are attributable to COG-UK's activity (number and diversity of journals). |

| OUTPUT AND OUTCOME INDICATOR CATEGORY | POSSIBLE INDICATORS (Qualitative and quantitative) |
|---|---|
| **Capacity-and-capability related**<br>• UK pathogen-genomic sequencing and analysis and surveillance-system capacity/capability is improved in a connected/networked system that helps PHAs identify and respond to future outbreaks and monitor mutations. | • The type and scale of pathogen sequencing possible now compared to before COG-UK's conception, and what factors enable it.<br>• Geographical distribution of sequencing capacity (and how it differs compared to the pre-COG-UK era).<br>• Enhanced sequencing capacity across the UK.<br>• Number of trained staff and their geographical distribution.<br>• New data infrastructure that was previously unavailable.<br>• New collaborations and partnerships in public health genomics research and/or supporting service delivery, and their nature. |
| **Capacity-and-capability related**<br>Expertise gained by staff contributing to COG-UK activity and the outputs of their work is deemed valuable and useful by decision makers (national policymakers, regional/local authorities and PHAs and NHS organisations). | • COG-UK is acknowledged for the insights it provides:<br>• Number of reports mentioning COG work going into SAGE/ MHRA/NICE/PHA or other bodies.<br>• COG mentioned in minutes of SAGE meetings/ other meetings (if COG-UK has such data).<br>• Evidence of expertise-sharing in other ways (e.g. meetings, calls, advisory roles to national policy and regional authorities or NHS organisations, etc). |
| COG-UK's operational outputs (e.g. standard operating protocols, legal frameworks and financial management protocols) are applicable and adaptable to other efforts and initiatives. | • Number and nature of operational outputs.<br>• Evidence these outputs are shared with external organisations interested in using them. |

**Annex Table 2-3. Proposed process-activity indicators**

| PROCESS-INDICATOR CATEGORY |
| --- |
| **For all of the below, indicators focus on evidence of activity implementation:**<br>***Research and analysis:***<br>• Collection and curation of data (e.g. genomic sequencing data and its linkage with other data sets such as epidemiological, clinical and contact-tracing data).<br>• Sharing of datasets and support for data flow activities in the research, healthcare and public health system.<br>• Conducting analysis and sharing findings (e.g. genomic analysis, bioinformatics, linking genome sequencing and analyses to transmission and outbreak analysis, mutational analysis and tracking through monitoring of prevalence, geographic distribution and significance).<br>• Developing and sharing analytical tools and methods for rapid genome analysis and managing analysis infrastructure (e.g. CLIMB bioinformatics infrastructure).<br>• Collaboration on research studies that aim to inform public health decision making and policy (as part of collaborative national studies or local and regional ones).<br>***Implementing supportive management and governance processes:***<br>• Establishing governance and management arrangements and operational frameworks and protocols to enable partner engagement across different types of consortium members and activities, e.g. research, NHS and PHAs.<br>• Orchestrating and managing relationships across the consortium.<br>• Communication, awareness-raising and public relations activity to enhance impact and manage expectations about COG-UK-driven research-and-analysis versus demand-driven service-support activity.<br>***Building a national COVID-19 genomic surveillance system and capacity:***<br>• Building capacity to help PHAs identify and respond to outbreaks at pace, monitor viral mutations (including in relation to future vaccine response), and support wider research and public health aims through investment in:<br>- Education and training to enhance skills in the research, sequencing and wider public health workforce<br>- Sequencing-site infrastructure<br>- Technical equipment (e.g. for sequencing high volumes in short time periods)<br>- Data infrastructure (e.g. bioinformatics analysis tools, cloud-based solutions)<br>- Enabling rapid data flows<br>- External communications with research, healthcare, public health and policy communities.<br>• Building capabilities and demand for evaluations of the effectiveness of pharmacological and non-pharmacological interventions informed by COG-UK sequencing activity.<br>• Creating and nurturing lasting collaborations across different stakeholders (academia and/or research, PHAs, and NHS organisations) locally within regions and between the four nations to support future preparedness and response.<br>• Building capability amongst decision makers in the healthcare system to act on data and evidence enabled by COG-UK communications activity and sharing of expertise (e.g. via reporting to SAGE, MHRA, PHAs, NHS decision makers and sharing insights through other means). |

**Annex Table 2-4. Proposed input indicators**

| INPUT INDICATOR CATEGORY | POSSIBLE INDICATORS (Qualitative and quantitative) |
|---|---|
| **Funding** | • Amount of funding.<br>• Sources of funding.<br>• Allocation/breakdown across key areas of activity.<br>• Timeframe of funding. |
| **Governance and management** | • Types of governance, management and operational structures and nature of their membership.<br>• Nature of legal and operational frameworks. |
| **Human resources and relationships** | • Number and nature of partners:<br>- Individuals (number of individual staff employed/funded some way through COG-UK activity).<br>- Volunteering individuals (additional individuals not on COG-UK payroll but volunteering time – number and nature).<br>• Evidence of key pre-existing relationships which were built on (i.e. where partners worked together before) and their nature. |
| **Equipment and technical infrastructure** | • Insights on the regional distribution of infrastructure made available as an input.<br>• Nature of equipment and facilities as inputs. |

# Annex 3: Self-Reporting Templates

## Guidance for completion of the self-reported template on inputs and managerial processes for the evaluation of COG-UK:

- This document is a self-reported template to be completed by COG-UK staff that will serve as evidence for the evaluation of COG-UK being carried out by RAND Europe. The evaluation team will use your self-reported data and complement it with insights from stakeholder interviews to do the final analysis and evaluation and learning report.
- As the template represents a key source of evidence, we ask that you please provide narrative answers (where applicable) that would be clear to an external reader in terms of language (please try to avoid highly technical language) and the level of detail shared. Bear in mind that sources provided in the template cannot be consulted by the evaluation team, so we ask that you provide information in a synthesised and readily usable format to enable us to get a clear picture of COG-UK's inputs and processes. Please provide reference data sources to support your answers to questions where this is applicable.
- This template seeks to capture information on the different inputs and managerial processes of COG-UK.
- When you provide your answers, please bear the following things in mind:
  - The reporting timeframe is 1 March 2020 to 31 July 2021.
  - Please consider a four-nations (England, Northern Ireland, Scotland and Wales) perspective when answering all questions.
  - Note that many questions ask not only what, but also why and how – please be mindful of this in your responses.
  - There may be questions for which you do not have and cannot collect data. This is acceptable but please make this explicit in your answer.
- The space available for you to provide your answers is indicative but not restrictive. Please add rows if and as required. Similarly, for open text boxes, you can expand as needed.
- We understand that multiple people may provide input into the questions asked in this template. However, we ask that a single and finalised document, whose completion is led and coordinated by the COG-UK team, be returned to the evaluation team.

## INPUTS TO SUPPORT THE DESIRED GOALS OF COG-UK

### Funding support

**Please provide information on the funding that COG-UK has received since the start of the consortium. Please add rows as needed. We have also provided space for you to add any additional comments.**

| Funding source | Funding amount | Aim of funding (very brief description) | Funding start date | Funding end date |
|---|---|---|---|---|
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |

Comments:

**Based on the information you have, please provide a brief overview of the key types of activities that the different funding sources have been allocated to? Please add rows as needed. We have also provided space for you to add any additional comments.**

*Activities may include, for example, sequencing samples, research, training, funding for managing and governance of the consortium, infrastructure (e.g. equipment, IT, data infrastructure, facilities, etc.) We are not looking for a detailed list but for a broad understanding of the allocation of funding to different types of uses by COG-UK. We have also provided a comment box for any additional comments you may wish to provide – for example, in relation to information availability of interdependences between activities.*

| Funding source | Activities supported | Breakdown of funding per core type of activity to the extent that this data can be provided |
|---|---|---|
| | | |
| | | |
| | | |
| | | |
| | | |

Comments:

## Governance infrastructure, legal framework and operational framework

**During the inception workshops, COG-UK shared the following information on your governance and management arrangements. We understand that these are key in underpinning your activities. Please add any additional information on these input resources in the comment box below.**

*We appreciate that some of the developments with implementing these arrangements can be seen as outputs, and we enquire about that elsewhere – here we need to understand the input governance, management and operational arrangements that needed to be in place to facilitate COG to initiate its implementation activities.*

The COG-UK consortium activities are framed by a governance infrastructure, legal framework and operational framework that is intended to support delivery on the consortium's objective and its impact, which consist of:

- The core Leadership Team, consisting of the Executive Director and Chair, the Director of Data Sciences, the Associate Director and the Director of Operations which oversees the management, business planning and governance of the consortium.
- A governance and advisory group that provides counsel as well as acts as an oversight and monitoring body.
- A steering group that provides strategic support to COG-UK, as well as undertakes reviews of publications and analysis proposals and makes decisions on those.
- We understand from your website that COG-UK management and administration staff include a Logistics team (that comprises a Logistics Manager, Logistics Assistant, Operations Manager and Scientific Project Manager), Project Administration, Communications and Administration that support and oversee areas such as consortium administration, internal policies, project management, publications activity and communications.
- Operational working groups cover aspects such as research and wider consortium operational support, data sciences activity and operational aspects of partnership working. An operational framework with specialist working groups, sequencing centres and sampling sites supports delivery on consortium activities, including through various logistical, regulatory and laboratory protocols, as well as workflows and tools. There are currently eight operational working groups covering:
  - Modelling, Phylogenetics and Display Working
  - Sample Logistics Working Group
  - Metadata and Patient Linkage/Epidemiology/Health Informatics Working Group
  - Sequencing Working Group
  - Data/Bioinformatics Working Group
  - Clinical and Virology Working Group
  - Mutations Research Working Group
  - Wastewater Working Group.
- A legal framework between partners that sets out operational, commercial and organisational aspects and governs data flows between partners.

Other Comments:

## Human resources

**For the following time periods, please provide the number of staff (FTE) and the type of role (e.g. research, technical staff, management, other, etc.) for the different FTEs that are being funded to work on COG-UK activity. Please add rows as needed. We have also provided space for you to add any additional comments.**

| Type of role | March 2020 (FTE) | June 2020 (FTE) | September 2020 (FTE) | December 2020 (FTE) | March 2021 (FTE) | July 2021 (FTE) |
|---|---|---|---|---|---|---|
| | | | | | | |
| | | | | | | |
| | | | | | | |

Other comments:

**To the extent that you have this information available, for the following time periods, please provide the number of volunteers (if known) that work on COG-UK activity and their activity area. Please add rows as needed. If you do not have this information, please put "information not available". We have also provided space for you to provide additional comments – for example if you have a cumulative figure but not a breakdown over time.**

| Type of activity volunteers contribute to | March 2020 (FTE) | June 2020 (FTE) | September 2020 (FTE) | December 2020 (FTE) | March 2021 (FTE) | July 2021 (FTE) |
|---|---|---|---|---|---|---|
| | | | | | | |
| | | | | | | |
| | | | | | | |

Other comments:

**For the following time periods, please provide the number of staff (FTE) that are benefiting from training supported by COG-UK and the type of training they are receiving. Please add rows as needed. We have also provided space for you to provide additional comments – for example, if you have a cumulative figure but not a breakdown over time.**

| Training activity | March 2020 (FTE) | June 2020 (FTE) | September 2020 (FTE) | December 2020 (FTE) | March 2021 (FTE) | July 2021 (FTE) |
|---|---|---|---|---|---|---|
| | | | | | | |
| | | | | | | |
| | | | | | | |

Other comments:

### Pre-existing relationships, networks and initial goodwill and commitment to collaboration

**To the best of your knowledge, what pre-existing networks/partnerships/collaborations were mobilised to establish COG-UK? We are trying to understand which relationships, networks and partnerships were key inputs into the development and establishment of COG-UK since the onset. Please provide a brief overview.**

### Equipment and technical infrastructure

**At the beginning of COG-UK, what 'baseline' equipment and infrastructure was available for COG-UK to access and use and what was its regional distribution?**

*(We are interested in equipment and infrastructure as an input rather than that which has been built over time)*

## COG-UK's management, governance and operational activities

### COG-UK's management, governance and operational activities

**Please provide an overview of how operational, governance and management arrangements for COG-UK supported activities across members of the consortium? Please overview your key activities in this regard over the time period between 1st March 2020 and 31st July 2021 as they relate to the following:**

a. Steering and advisory group key activities and their effects
b. Operational working group key activities and their effects
c. Leadership and day to day management
d. Communications, awareness-raising and public relations activity to support impact.

## Guidance for completion of the self-reported template on outputs, outcomes and impacts for the evaluation of COG-UK:

- This document is a self-reported template to be completed by COG-UK staff that will serve as evidence for the evaluation of COG-UK being carried out by RAND Europe. The evaluation team will use your self-reported data and complement it with insights from stakeholder interviews to do the final analysis and evaluation and learning report.
- As the template represents a key source of evidence, we ask that you please provide narrative answers (where applicable) that would be clear to an external reader in terms of language (please try to avoid highly technical language) and the level of detail shared. Bear in mind that sources provided in the template cannot be consulted by the evaluation team, so we ask that you provide information in a synthesised and readily usable format to enable us to get a clear picture of COG-UK's inputs and processes. Please provide reference data sources to support your answers to questions where this is applicable.
- This template seeks to capture information on the different outputs, outcomes and impacts from COG-UK activity.
- When you provide your answers, please bear the following things in mind:
  - The reporting timeframe is 1s March 2020 to 31 July 2021
  - Please consider a four-nations (England, Northern Ireland, Scotland and Wales) perspective when answering all questions
  - Note that many questions ask not only what but also why and how – please be mindful of this in your responses
  - There may be questions for which you do not have and cannot collect data. This is acceptable, but please make this explicit in your answer.
- The space available for you to provide your answers is indicative but is not restrictive. Please add rows if and as required. Similarly, for open text boxes, you can expand as needed.
- We understand that multiple people may provide input into the questions asked in this template. However, we ask that a single and finalised document, whose completion is led and coordinated by the COG-UK team, be returned to the evaluation team.

## COG-UK OUTPUTS AND OUTCOMES RELATED TO RESEARCH-AND-ANALYSIS ACTIVITY

### Producing and sharing linked data sets and their utility

**Please describe your key efforts to produce high quality linked datasets and the results of these efforts in the time period between 1st March 2020 and 31st July 2021. More specifically, please share information on:**

a. The number and nature of linked datasets you have produced

b. The type of data they link (e.g. genomic data and metadata; viral and host genome data)

c. What have the linked datasets enabled - what have they been used for, by whom, what impact has this had (to the best of your awareness)?

## COG-UK OUTPUTS AND OUTCOMES RELATED TO CAPACITY AND CAPABILITY-BUILDING

### Improved pathogen genomic sequencing and analysis and surveillance-system capacity and capability in the UK in a networked/connected system

**Please provide insights on the scale and pace of whole-genome sequencing that can be done now (as of 31 July 2021) that could not be done before COG-UK came into existence.**

*(There is no need to provide numerical data provided earlier. Rather we are seeking to understand how the scale and pace have changed since COG-UK has come to exist, provided you have insights on this issue).*

**How has the capacity for pathogen genomic sequencing and analysis changed due to the contribution of COG-UK between 1 March 2020 and 31 July 2021? Please answer this question for each of the categories below:**

| | |
|---|---|
| Sequencing facilities | |
| Equipment | |
| Data infrastructure | |

| | |
|---|---|
| Skilled workforce | |
| Other (if applicable) | |

**What type of training has COG-UK provided and to whom?**

*(If possible, it would be helpful to know numbers and profiles of staff trained as well, should you have that data)*

**What types of skills have been improved in the UK research, sequencing and wider public health workforce as a result of COG-UK activity?**

*(Please explain the mechanisms by which COG-UK has contributed to this)*

**Has financial investment in COG-UK led to other funding being leveraged by members of COG-UK in the time period between 1 March 2020 and 31 July 2021 for activities not conducted by COG-UK but which add complementarity and help build capacity for public health genomics research and support to public health and service delivery? If so, please provide a brief overview.**

**Please provide an overview of the key NEW collaborations between different organisations taking place that have been enabled by COG-UK from 1 March 2020 to 31 July 2021. More specifically, please share information for each collaborative activity on:**

a. Nature of activity (i.e. research, support for service delivery or both)
b. Topic of collaborative activity (e.g. specific research study topic, specific focus of support for service delivery)
c. Collaborating stakeholder types
d. Geographical spread of collaboration
e. Is this collaboration supporting COG-UK activities, or are partners in COG-UK who have built relationships as a result of COG-UK collaborating on external (i.e. non-COG-UK) projects?
f. Key achievements of the collaboration to date.

**Are there any other initiatives in the UK, apart from COG-UK, that are contributing to sequencing capacity and capabilities for response to the COVID-19 pandemic and does COG-UK collaborate with other efforts in the UK? Please briefly describe.**

**Please provide an overview of the types of operational and management outputs that can support the operation of networked public health genomics research and service support initiatives that COG-UK has produced in the time period between 1 March 2020 and 31 July 2021. Please make clear whether these are already contributing to the non-COG-UK activities.**

*(For example, this could include operational, management and governance-related resources, tools, standard operating procedures, legal frameworks, financial management protocols, tools to help effectively manage the bioinformatics sequencing analysis infrastructure that may be applicable and adaptable to other efforts).*

## Demand for and recognition of the value and usefulness of COG-UK activity and staff expertise by external decision makers

**In the rows below, please share information on the number and nature of external reports and/or documents where COG-UK is acknowledged for the insights it provides to decision makers (e.g. NHS, public health authorities, the wider policy community, and regulators) as applicable to the time period between 1 March 2020 and 31 July 2021. Please provide this information to the best of your awareness and knowledge. By external, we mean reports and/or documents produced by external bodies. Please add rows as needed.**

*(For example, this might include reports and/or documents mentioning COG-UK work that have fed into SAGE reports, MHRA, NICE, PHA or other agencies).*

| Report/Document title and reference | Decision-making body producing it | What is COG-UK mentioned for |
|---|---|---|
| | | |
| | | |
| | | |

**Has COG-UK shared expertise with decisions makers in the time period between 1 March 2020 and 31 July 2021? Please provide information on the different activities and outputs, alongside reference to supportive evidence to enable attribution/contribution to COG-UK. Please note that in this question, we are not asking simply about academic publications you have produced – we ask about academic publications in a later question.**

*(For example, this includes meetings with decision makers, calls, advisory roles to national policy and regional authorities or NHS organisations, etc.)*

**How are COG-UK partners participating in events and conferences related to public health genomics and service delivery and contributing to a community of practice through engagement and skills sharing? In the rows below, please provide information on the types of conferences and events COG-UK members contributed to through presentations and/or other means. Please add rows as needed.**

| Event/ conference name | Topic area in which COG-UK contributed | Location | Participating COG-UK members and their affiliations (organisation, stakeholder type, geography/nations) | Contributions to the event (e.g. presentations, panel roles, etc.) |
|---|---|---|---|---|
| | | | | |

## WIDER IMPACTS FROM COG-UK ACTIVITY

### Advancing scientific knowledge

**In the rows below, please provide a list of all journal publications that include COG-UK members and that formally have COG-UK as an affiliation or funder produced between 1 March 2020 and 31 July 2021. Please add rows as needed.**

| Full reference | Academic article or technical report? | Topic area | Brief description of key finding | Research disciplines involved (e.g. genetics, epidemiology, public health, statistics, economics, etc.) |
|---|---|---|---|---|
| | | | | |
| | | | | |

### Wider impact on public health and policy decision making

**Please provide an overview of the number and nature of key policy and public health decisions on response, management and control of the COVID-19 pandemic that have been informed by COG-UK activity, along with reference to supportive evidence linking the impact to COG-UK or, in its absence, narrative information supporting COG-UK contribution.**

**Please provide information on the turnaround time from requests for sequencing data, analysis or other types of outputs to delivery to decision makers. How has this evolved over the lifetime of the consortium? Are there differences across sequencing sites in terms of capacity for quick turnaround, and if so, why?**

*(We recognise that the ever-changing nature of the pandemic can require COG-UK to prioritise some activities over others and will be conscious of that when conducting stakeholder interviews)*

## Potential for impact on evaluations of the effectiveness of pharmacological and non-pharmacological interventions

**Have COG-UK sequencing data and genome analysis or methods been used in evaluations of the effectiveness of pharmacological and non-pharmacological interventions in the time period 1 March 2020 to 31 July 2021? If so, please provide an overview of the interventions and how COG-UK data and analyses supported the evaluation of effectiveness?**

**Are there any signs of the potential for COG-UK research and data to help enable future evaluations of the effectiveness of pharmacological and non-pharmacological interventions informed by COG-UK genome analysis-related activity?**

*(For example, is there any evidence of external stakeholders approaching COG-UK in relation to discussions about how sequencing activity can be used in future evaluations?)*

## Impact on vaccine development programmes

**Has COG-UK had an impact to date (as of 31 July 2021) on vaccine development and/or roll-out programmes, or is there any evidence of demand for COG-UK (or its legacy) to become a critical partner in shaping vaccine development programmes in the future? If so, please describe.**

**Is COG-UK taking actions to enable impacts on vaccine development and/or roll out programmes in the future? If so, please describe.**

## A sustainable community of practice to support a dynamic and adaptable pathogen genomics platform that can be mobilised for future pandemics/public health threats

**Please provide information on the number and nature of projects where partners from COG-UK are engaging in other public health genomics research and public health service delivery activities outside of COG-UK's remit, but that build on and use the approaches, infrastructure and practices established and learnt through COG-UK. This may be related to COVID-19 or other infectious diseases. In providing your answer, please consider the following:**

- How have the approaches, infrastructure, practices that have been established and learning gained from COG-UK been applied to new efforts?
- Is there evidence of non-traditional relationships being maintained - such as between academic researchers in genomics, the NHS, public health agencies?
- How are the individuals trained by COG-UK and their skills supporting non-COG-UK activity?

| Legacy impact on infrastructure |
| --- |
| **Please provide evidence on how the pathogen genomics data and physical/technical infrastructure that COG-UK has contributed to the UK is being used outside of COG-UK (i.e. for non-COG-UK activity directly)?** |
| |
| **In your view, what factors can influence the sustainability of the pathogen genomics data and physical/technical infrastructure that COG-UK has contributed to the UK? What is required for it to be available and used long-term, after the COG-UK consortium lifecycle (with current funding) finishes? Please make clear any requirements for supporting the sustainability and legacy of this infrastructure.** |
| |

| Impact on integration or new models of coordination of sequencing activities, infrastructure and tools into relevant national public health agencies? |
| --- |
| **Is there evidence that the four public health agencies more actively govern and coordinate public health genomics research and service delivery functions than before COG-UK? If so, what is needed to sustain such practices?** |
| |
| **Is there evidence that staff positions related to public health genomics research are being created and embedded within the public health agencies?** |
| |
| **Are budgets related to public health genomics research within the public health agencies different to before COG-UK was established?** |
| |
| **Are legacy structures, relationships and activities supporting the integration of public health genomics research and service delivery support? If so, how? If not, why not?** |
| |
| **Are there any other comments you would like to share on evidence of the legacy of COG-UK on integration or new models of coordination of public health genomics research into relevant national public health agencies?** |
| |

**How has the organisation of public health genomics research and service delivery changed since the establishment of COG-UK, and what is the evidence that the consequences and impacts of COG-UK are lasting (even if COG-UK morphs into something else with time)?**

**At end of the funding period for the consortium, where do you see COG-UK sitting in the future public health genomics research and service support landscape?**

**What is the evidence that learnings from the COG-UK experience enable better future logistics and operational preparedness for integrating public health genomics research with service delivery support in a public health response?**

*(For example, is there evidence that governance frameworks and operational frameworks produced by COG-UK are being used by other efforts nationally or internationally at the end of COG-UK's funding period?)*

## International impact

**Please describe the impact that COG-UK has had outside of the UK (e.g. on shaping vaccine policy, building skills in the global research and public health workforce, influencing international pathogen genomics research and sequencing initiatives.**

*(This could include evidence of participation of COG-UK members in global public health genomics research and service delivery support efforts as collaborators and advisors as one example)*

# Annex 4: Interview Protocols

## Protocol: Researchers/academics, leadership and management and public health authorities

1. What do you see as COG-UK's top successes and why?
2. If you wanted to flag one key case example of COG-UK impact- which may inform a case vignette in our evaluation report, what would it be?
3. More generally, what have you seen as the key challenges to implementing COG-UK activities and their impact over time? Why did they occur, and how were they responded to?
4. What has helped COG-UK along the way? In other words, what have you seen as the key enablers of implementation and achieving impact over time? And how were they enabling – i.e. what effect did they have on achieving your aims?
5. We understand that COG UK has had to rapidly adapt how it works and what it focuses on over time. Can you talk us through key areas where the consortium needed to adapt, why it happened and how COG UK approached this/responded?
6. How have relationships been managed in the consortium model? What worked well, and where do you see scope for improvement?
7. How (and how well) did the operational, governance and management arrangements for COG-UK support activities across members of the consortium? What worked well, and where would there be scope for improvement in the future?
8. How much appetite do you think there is for COG-UK activity in the academic research community and amongst NHS, public health and wider policy decision makers?
9. Has COG-UK contributed to vaccine development efforts or the evaluation of vaccine effectiveness in any way to date? If so, please can you share how? If not, why not, and have any efforts to that end been made?
10. Outside of vaccines specifically, has COG-UK contributed to the evaluation of any other pharmacological or non-pharmacological interventions?
11. Where do you see COG-UK in the future in terms of the public health genomics landscape in the UK (and why/explain your reasoning)?
12. What would need to happen to support the legacy for COG-UK you have outlined above?

13. To what extent do you think that learning from COG UK as a model is having an impact on how public health genomics research and support for public health services will be organised in the future in relation to future potential pandemic preparedness and response? How do you see the landscape looking in the future?
14. In your view, has COG-UK had any global/ international impact yet, and if so, how?
15. In light of your role and experience, and with the benefit of hindsight, is there anything you would do differently if COG-UK was being established all over again?

## Protocol: Funders and Policymakers

1. How have you interacted with COG-UK? What is your specific role in relation to COG-UK?
2. From your perspective and to the best of your awareness, what do you see as COG-UK's top successes and achievements, and why do they matter?
3. From your perspective and to the best of your awareness, what do you see as the key challenges COG-UK has experienced, and why were they experienced?
4. In your view, how aware are policy/ decision makers in central and regional government agencies, NHS decision makers and public health decision makers of COG UK, what it has been doing and what its role and value is in supporting the response to COVID-19?
5. In your view, would you say that the information provided by COG-UK to decision makers has been sufficiently timely to meet the needs of supporting the response to COVID-19? Are there factors that may have facilitated or impeded the timeliness of the information?
6. How much appetite do you think there has been for COG-UK activity amongst NHS, public health and wider policy decision makers? And to what extent does this apply to different types of activity?
7. Where do you see COG-UK in the future in terms of the public health genomics landscape in the UK?
8. What would need to happen to support the legacy for COG-UK you have outlined above?
9. To what extent do you think that learning from COG UK as a model is having an impact on how public health genomics research and support for public health services will be organised in the future in relation to future potential pandemic preparedness and response? How do you see the landscape looking in the future?
10. In your view and to the best of your awareness, has COG-UK had any global/ international impact yet, and if so, how?
11. In light of your role and experience of interacting with COG-UK, and with the benefit of hindsight, is there anything you would do differently if you were engaging with COG-UK and if it was being established all over again?

## Protocol: International

1. Can you please briefly introduce yourself and your role as it relates to public health and the COVID-19 pandemic?
2. Have you interacted with COG-UK (or with other stakeholders in relation to COG-UK) and if so, how, and for what purpose?
3. In your view, how much awareness and interest are there in COG-UK activity internationally and why?

4. In your view, has COG-UK had any global/ international impact yet, and if so, how?
5. To the extent you are aware, and from your perspective, what do you see as COG-UK's top successes/biggest achievements?
6. From an external perspective, and to the extent that you can comment, are there things which, with the benefit of hindsight, you feel COG-UK might have done differently?
7. To what extent do you think that the COG-UK approach for conducting public health genomics research, sequencing and analysis to support decision makers could be replicated and/or adapted elsewhere (such as in your country and internationally) to support pandemic preparedness and response?
    - Key areas which are scalable
    - Aspects that would require modification to be applicable to other disease areas and/or other geographies.
8. Are there any other efforts aside from COG-UK that provide important examples of how to approach public health genomics activity in light of preparedness for future threats?
    - Similarities and differences between COG-UK and other examples.
9. Any other thoughts you would like to share?

# Annex 5: Interview participants

| NAME | ROLE | ORGANISATION |
|---|---|---|
| Ms Angela Beckett | Lab manager- Centre for Enzyme Innovation Bioinformatics | University of Portsmouth |
| Dr Anna Kinsey | Funder | MRC UKRI |
| Anonymous | Policymaker | Anonymous |
| Anonymous | Anonymous | UK University |
| Dr Catherine Ludden | Director of Operations of COG UK | COG UK |
| Dr Derek Fairley | Involved with COG-UK through the Belfast Health & Social Care Trust | Queen's University Belfast |
| Prof Doreen Cantrell | Governance and Advisory Board | University of Dundee |
| Prof Emma Thomson | Site Lead | University of Glasgow |
| Dr Ewan Harrison | Deputy Director, Senior Leadership Group, Data lead, Member of Steering Group | University of Cambridge |
| Dr Ian Harrison | Steering Group Deputy | Public Health England |
| Dr Jeffrey Barrett | Site Lead | Wellcome Sanger Institute |
| Dr Katerina Galai | Associate Director of COG-UK | COG-UK |
| Prof Marion Koopmans | Expert on zoonotic viral infections, SARS-CoV-2 genomics | Erasmus Medical Centre |
| Dr Mark Bale | Deputy Director, Genomics Policy | DHSC |
| Dr Martin Dougherty | Chief Operating Officer | Wellcome Sanger Institute |

| NAME | ROLE | ORGANISATION |
|---|---|---|
| Prof Matthew Holden | Steering Group Member | Public Health Scotland |
| Dr Samuel Scarpino | Managing Director | The Rockefeller Foundation |
| Dr Samuel Robson | Site Lead/ Centre for Enzyme Innovation Bioinformatics Lead | University of Portsmouth |
| Prof Sharon Peacock | Executive Director and Chair of COG-UK | University of Cambridge |
| Prof Thomas Connor | Site Lead | Public Health Wales |
| Dr Tim Wyatt | PHA, Steering Group Member | Northern Ireland Public Health Agency |

# Annex 6: Genomic sequencing equipment

| Centre Name | Sequencing Equipment |
|---|---|
| University of Birmingham<br>(N=5) | 1 x GridION<br>1 x PromethION<br>1 x MiSeq<br>1 x HiSeq<br>1x NextSeq |
| University of Cambridge<br>(N=2) | 1x GridION (purchased for project)<br>1 x MinION |
| University of Edinburgh<br>(N=5) | 1 x GridION<br>3 x MinION<br>1 x Illumina MiSeq |
| University of Glasgow Centre for Virus Research<br>(N=7) | 2 x NextSeq<br>2 x MiSeq<br>3x MinION |
| University of Oxford<br>(N=5) | 1 x NovaSeq<br>2 x MiSeq<br>1 x NextSeq<br>1 x MinION |
| Public Health Wales & Cardiff University<br>(N=5) | 2 x MinION<br>1 x GridION,<br>1 x MiSeq<br>1 x NextSeq |
| University of Sheffield<br>(N=5) | 1 x GridION<br>4 x MinION |
| University of Liverpool<br>(N=17) | 10 x MinION<br>1 x PacBio Sequel I<br>4 x MiSeq<br>1 x NovaSeq<br>1x Iseq |

| Centre Name | Sequencing Equipment |
|---|---|
| Public Health England Colindale<br>(N=2) | 1 x Illumina<br>1 x ONT GridION |
| University of Exeter<br>(N=5) | 4 x MinION<br>1 x GridION |
| Quadram Institute<br>(N=7) | 1x NextSeq<br>1 x MinION<br>1x PromethION<br>4x MinION |
| Belfast Health & Social Care Trust / Queen's University Belfast<br>(N=1) | 1 x MiSeq |
| University of Nottingham<br>(N=3) | 1 x GridION,<br>1 x PromethION,<br>1 x MiSeq |
| Wellcome Sanger Institute<br>(N=43) | 1 x NextSeq<br>6 x MiSeq<br>19 x NovaSeq<br>9 x MinION<br>1 x GridION in testing,<br>1 x PromethION in testing,<br>1 x PacBio Sequel 1<br>5x PacBio Sequel II |
| University College London<br>(N=10) | 4 x MinION<br>1 x GridION (received this mid-to-late March 2020)<br>2 x MiSeq<br>2 x NextSeq 500/550<br>(plus various liquid handling robots)<br>1 x PromethION (located in the UCL Institute of Neurology) |
| Northumbria University<br>(N=9) | 1x GridION<br>4 x MinION<br>1 x NextSeq<br>2 x Miseq<br>1x PacBioSequel 1 |
| University of Portsmouth<br>(n=3) | 2 x MinION<br>1 x GridION |

# Annex 7: Genomic sequencing by COG-UK consortium site over time.

**Annex Table 7-1. Number of SARS-CoV-2 whole genomes sequenced by consortium site over time.[1]**

| Site | 2020 | | | 2021 | | | |
|---|---|---|---|---|---|---|---|
| | Q1 Apr-Jun | Q2 Jul-Sept | Q3 Oct-Dec | Q4 Jan-Mar | Q1 Apr-Jun | Q2 July | TOTAL |
| Belfast | 223 | 225 | 741 | 1,130 | 4402 | 1128 | 7,849 |
| Birmingham | 584 | 1300 | 879 | 2,788 | 1104 | 752 | 7,407 |
| Cambridge | 2,351 | 533 | 3,016 | 6,065 | 1384 | 1128 | 14,477 |
| Cardiff | 3,900 | 800 | 12,345 | 17,348 | 5049 | 1880 | 43,122 |
| Edinburgh | 1,677 | 642 | 1,013 | 1,355 | 1133 | 0 | 5,820 |
| Exeter | 585 | 75 | 2,156 | 3,601 | 542 | 0 | 6,959 |
| Glasgow | 2,393 | 848 | 1,596 | 1,174 | 507 | 0 | 6,518 |
| Liverpool | 2,152 | 3936 | 6,879 | 10,883 | 5325 | 1410 | 30,585 |
| Northumbria | 600 | 1106 | 2,812 | 9,640 | 9588 | 4512 | 28,258 |
| Norwich | 1,661 | 650 | 5,266 | 10,773 | 5944 | 3760 | 28,054 |
| Nottingham | 1,133 | 692 | 2,388 | 3,680 | 905 | 846 | 9,644 |
| Oxford | 1,861 | 2093 | 6,514 | 9,645 | 1871 | 3008 | 24,992 |
| PHE Colindale | 4,497 | 610 | 5,669 | 12,197 | 11,864 | 6,389 | 41,226 |
| Portsmouth | 594 | 1007 | 1,732 | 7,323 | 3400 | 2256 | 16,312 |
| Sheffield | 1,931 | 652 | 2,934 | 4,810 | 2867 | 1880 | 15,074 |
| UCL | 934 | 92 | 2,387 | 9,654 | 3305 | 1504 | 17,876 |
| Wellcome Sanger Institute | | 47,581 | | 164,973 | 146,159 | 143,892 | 502,605 |
| **GRAND TOTAL** | | | | | | | **806,778** |

1 Reference sources: Quarterly figures accessed from the COG-UK sequencing invoices and budget spreadsheet (to be used as a guideline only: some figures may slightly differ from CLIMB figures).

**Annex Table 7-2. Number of SARS-CoV-2 genomes sequenced by COG-UK per 1,000 COVID-19-positive cases by nation and quarter.2**

| | Q1 (Apr-Jun 2020) | Q2 (Jul-Sept 2020) | Q3 (Oct-Dec 2020) | Q4 (Jan-Mar 2021) | Q1 (Apr-Jun 2021) | Q2 (July 2021) | April 2020 -July 2021 |
|---|---|---|---|---|---|---|---|
| Northern Ireland | 46.17 | 34.77 | 12.02 | 26.67 | 428.75 | 37.82 | 50.51 |
| Wales | 273.07 | 290.96 | 94.25 | 326.17 | 496.61 | 81.28 | 179.17 |
| Scotland | 260.06 | 121.99 | 25.68 | 29.33 | 23.84 | 0 | 35.83 |
| England | 164.60 | 161.82 | 31.26 | 169.78 | 464.12 | 182.99 | 145.15 |
| United Kingdom | 174.66 | 161.06 | 34.26 | 163.95 | 404.41 | 166.17 | 137.62 |

2 Sequencing volume per site and quarter were derived from self-reported data (see Table A7-1) and expressed as the number of SARS-CoV-2 genomes sequenced per 1,000 positive COVID-19 cases (using data for each nation separately and the UK overall from https://coronavirus.data.gov.uk/details/cases).

# Annex 8: List of academic publications and reports

**Annex Table 8-1. List of publications and reports**

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Allen, H., Vusirikala, A., Flannagan, J. et al. 2021. 'Increased household transmission of COVID-19 cases associated with SARS-CoV-2 Variant of Concern B.1.617.2: a national case-control study'. *The Lancet Regional Health Europe* 12: 100252. As of 23 January 2022: https://khub.net/documents/135939561/405676950/Increased+Household+Transmission+of+COVID-19+Cases+-+national+case+study.pdf/7f7764fb-ecb0-da31-77b3-b1a8ef7be9aa | Report | Properties of the Delta variant | Found evidence of increased household transmission of SARS-CoV-2 Delta variant, potentially explaining its success at displacing Alpha variant as the dominant strain in England. Understanding this variant's transmissibility is important for informing international infection-prevention and control policies. |
| Harvey, W. T., Carabelli, A. M., Jackson, B., et al. 2021. 'SARS-CoV-2 variants, spike mutations and immune escape'. *Nature Reviews Microbiology* 19(7): 409–424. As of 23 January 2022: https://doi.org/10.1038/s41579-021-00573-0 | Academic article | Understanding immune escape | Summarises the literature on mutations of the SARS-CoV-2 spike protein (the primary antigen) focusing on their impacts on antigenicity and contextualising them in the protein structure. The article discusses them in the context of observed mutation frequencies in global sequence datasets. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Mishra, S., Mindermann, S., Sharma, M. et al. 2021. 'Changing composition of SARS-CoV-2 lineages and rise of Delta variant in England'. *EClinicalMedicine* 39: 101064. As of 23 January 2022: https://doi.org/10.1016/j.eclinm.2021.101064 | Academic article | Properties of the Delta variant | Found the percentage of non-Alpha variants increasing since late March 2021, initially driven by various lineages with immune escape. Delta spread rapidly from mid-April, becoming the dominant variant in England by late May. Early detection of new variants requires a diverse array of data sources in community surveillance. Continued real-time information on the highly dynamic composition and trajectory of different SARS-CoV-2 lineages is essential to future control efforts. |
| Tettamanti, F. A. T., Venturini, C., Stirrup, O. T. et al. 2021. 'The Alpha Variant B.1.1.7 Was Not Associated With Excess Healthcare Acquired COVID-19 Infection in a Multi-Centre UK Hospital Study'. As of 23 January 2022: https://doi.org/10.2139/ssrn.3893562 | Academic article | Properties of the Alpha variant | Showed that healthcare-acquired infections were no more likely to be identified as the Alpha variant than community-acquired infections, suggesting that UK hospitals' existing infection-prevention measures contained the spread of the Alpha variant as effectively as less-transmissible lineages. |
| Davis, C., Logan, N., Tyson, G., et al. 2021. 'Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination'. *PLOS Pathogens* 17(12): e1010022. As of 23 January 2022: https://doi.org/10.1371/journal.ppat.1010022 | Academic article | Properties of the Delta variant | Across all vaccinated individuals, observed spike glycoproteins from B.1.617.1 and B.1.617.2 conferred reductions in neutralisation of 4.31 and 5.11-fold respectively. The reduction seen with the B.1.617.2 lineage approached that conferred by the glycoprotein from B.1.351 variant (6.29-fold reduction), known to be associated with reduced vaccine efficacy. Neutralising antibody titres elicited by vaccination with two doses of BNT162b2 were significantly higher than those elicited by vaccination with two doses of ChAdOx1. The results demonstrate the quantifiable risk of antigenic drift and subsequent reduction in vaccine efficacy. Accordingly, booster vaccines based on updated variants are likely to be required over time to prevent productive infection. This study also suggests that two-dose vaccine regimes are required for maximal BNT162b2 and ChAdOx1-induced immunity. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Dolton, G., Rius, C., Hasan, M. S., et al. 2021. 'Emergence of immune escape at dominant SARS-CoV-2 killer T-cell epitope'. *medRxiv* 2021. As of 23 January 2022: https://doi.org/10.1101/2021.06.21.21259010 | Academic article | Understanding immune escape | Identified a large CD8 T-cell response in a cohort of convalescent patients which failed to respond to the P272L variant. |
| Jackson, B., Boni, M. F., Bull, M. J., et al. 2021. 'Generation and transmission of inter-lineage recombinants in the SARS-CoV-2 pandemic'. *medRxiv* 2021.06.18.21258689. As of 23 January 2022: https://doi.org/10.1101/2021.06.18.21258689 | Academic article | SARS-CoV-2 recombination | Present evidence for multiple independent origins of recombinant SARS-CoV-2 viruses sampled from late 2020 and early 2021 in the United Kingdom. |
| Lindsey, B.B., Villabona-Arenas, Ch. J., Campbell, F., et al. 2021. 'Characterising within-hospital SARS-CoV-2 transmission events: a retrospective analysis integrating epidemiological and viral genomic data from a UK tertiary care setting across two pandemic waves'. *medRxiv* 2021.07.15.21260537. As of 23 January 2022: https://doi.org/10.1101/2021.07.15.21260537 | Academic article | Understanding SARS-Cov2 transmission | Found staff-to-staff transmission to be the most frequent transmission type during Wave 1, decreasing to 12.9% in Wave 2. Patient-to-patient transmissions increased from 27.1% in Wave 1 to 52.1% in Wave 2, becoming the predominant transmission type. Approximately 40%–50% of hospital-onset patient cases resulted in onward transmission compared to less than 4% of community-acquired cases. |
| Riley, S., Haw, D., Walters, C. et al. 2021. 'REACT-1 round 11 report: low prevalence of SARS-CoV-2 infection in the community prior to the third step of the English roadmap out of lockdown'. *Hdl.handle.net*. 2021. As of 23 January 2022: https://hdl.handle.net/10044/1/88507 | Report | COVID-19 prevalence | Observed marked reductions in prevalence from March to April/May 2021 in England, reflecting the success of the vaccination programme despite the easing of restrictions during the lockdown. However, the report noted a potential upwards pressure on prevalence from the further easing of lockdown regulations and the presence of the B.1.617.2 lineage. |
| Li K., Woo, Y., Stirrup, O. et al. 2021. 'Genetic epidemiology of SARS-CoV-2 transmission in renal dialysis units – A high risk community-hospital interface'. *Journal of Infection*. 83 (1): 96–103. doi:10.1016/j.jinf.2021.04.020. | Academic article | Genetic epidemiology in clinical settings | Described how near-real-time SARS-CoV-2 sequencing data can help tailor infection prevention and control measures in at-risk settings (here studied in six Scottish renal dialysis units). |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Hosie, M., Epifano, I., Herder, V. et al. 2021. 'Detection of SARS-CoV-2 in respiratory samples from cats in the UK associated with human-to-cat transmission'. *Veterinary Record* 188 (8): e247. doi:10.1002/vetr.247. | Academic article | Transmission of SARS-CoV-2 from humans to cats | Found that human-to-cat transmission of SARS-CoV-2 occurred during the COVID-19 pandemic in the UK, with the infected cats developing mild or severe respiratory disease. The article noted that it will be important to monitor for human-to-cat, cat-to-cat and cat-to-human transmission. |
| Lythgoe, K., Hall, M., Ferretti, L. et al. 2021. 'SARS-CoV-2 within-host diversity and transmission'. *Science* 16 (372). doi: 10.1126/science. abg0821:eabg0821 | Academic article | Viral mutation within individuals | Undertook in-depth sequencing of more than 1000 hospital patients' isolates to determine how the virus mutates within individuals, finding consistent and reproducible patterns of within-host virus diversity. Most samples contained only one or two variants, but a few carried many. Although the evidence indicates strong purifying selection, including the spike protein responsible for viral entry, the authors also saw evidence for transmission clusters associated with households and other possible super-spreader events. Most variants fizzled out after transmission, but occasionally some initiated ongoing transmission and wider dissemination. |
| Blackstone, J., Stirrup, O., Mapp, F. et al. 2021. 'Protocol for the COG-UK hospital onset COVID-19 infection (HOCI) multicentre interventional clinical study: evaluating the efficacy of rapid genome sequencing of SARS-CoV-2 in limiting the spread of COVID-19 in United Kingdom NHS hospitals'. *medRxiv* 2021.04.13.21255342. doi: https://doi.org/10.1101/2021.04.13.21255342 | Academic article | Clinical trial study protocol | No findings. |
| Leary, S., Gaudieri, S., Parker, M. et al. 2021. 'Generation of a novel SARS-CoV-2 sub-genomic RNA due to the R203K/G204R variant in nucleocapsid'. *bioRxiv* [Preprint]. 2021 Aug 6:2020.04.10.029454. doi: 10.1101/2020.04.10.029454. | Academic article | Mutations in SARS-CoV-2 RNA that affect virus levels | Demonstrated that a major variant of the SARS-CoV-2 virus (R203K/G204R in the nucleocapsid) changes the nucleocapsid at both the protein and RNA level, significantly associated with increased expression of nucleocapsid and sub-genomic RNA from other open reading frames. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Graham, M., Sudre, C., May, A. et al. 2021. 'Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study'. *The Lancet Public Health* 6 (5): e335–345. doi: https://doi.org/10.1016/S2468-2667(21)00055-4 | Academic article | Properties of the Alpha variant | Found no change in symptoms for the B.1.1.7 variant, indicating that the existing testing/surveillance infrastructure did not need to change specifically for the B.1.1.7 variant. Given that there was no apparent increase in the reinfection rate, this study provided evidence that vaccines are likely to remain effective against the B.1.1.7 variant. |
| Davies, N., Abbott, S., Barnard, R. et al. 2021. 'Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England'. *Science* 372 (6538): eabg3055. doi: 10.1126/science.abg3055 | Academic article | Properties of the Alpha variant | Demonstrated that B.1.1.7 is 43–90% more transmissible than the predecessor lineage but saw no clear evidence for a change in disease severity. However, the enhanced transmission will lead to higher incidence and more hospital admissions. |
| de Silva, T.I., Lui, G., Lindsey, B.B. et al. 2021. 'The impact of viral mutations on recognition by SARS-CoV-2 specific T-cells'. *iScience* 24 (11):103353. doi: 10.1016/j.isci.2021.103353. | Academic article | T-cell immunity | Found variants that are not recognised by T-cells, demonstrating the potential for T-cell evasion and highlighting the need for ongoing surveillance for variants capable of escaping T-cell as well as antibody-based immunity. |
| Emary, K., Golubchik, T., Aley, P. et al. 2021. 'Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 variant of concern 202012/01 (B.1.1.7): an exploratory analysis of a randomised controlled trial'. *The Lancet* 397 (10282): 1351-1362. doi: https://doi.org/10.1016/S0140-6736(21)00628-0 | Academic article | Properties of the Alpha variant | Demonstrated that the AstraZeneca vaccine showed reduced neutralisation activity against the B.1.1.7 variant compared with a non-B.1.1.7 variant in lab experiments, but the vaccine showed efficacy against the B.1.1.7 variant of SARS-CoV-2 in people. |
| Moore, C., Davies, L., Rees, R. et al. 2021. 'Localised community circulation of SARS-CoV-2 viruses with an increased accumulation of single nucleotide polymorphisms that adversely affect the sensitivity of real-time reverse transcription assays targeting Nucleocapsid protein'. *medRxiv* 2021.03.22.21254006. doi: https://doi.org/10.1101/2021.03.22.21254006 | Academic article | Impact of mutations on diagnostic testing | Found that in viral genomes from Wales sequenced over the summer of 2020, the N gene had a higher rate of mutations in diagnostic target sites than other targets. This work emphasised the potential impact mutations in diagnostic target sites can have on tracking local outbreaks, demonstrating genomics' value as a routine tool for identifying and explaining potential diagnostic-primer issues. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Volz, E., Mishra, S., Chand, M. et al. 2021. 'Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England'. *Nature* 593: 266-269. https://doi.org/10.1038/s41586-021-03470-x | Academic article | Properties of the Alpha variant | Reported a transient shift in the age composition of reported cases, with cases of B.1.1.7 including a larger share of under 20-year-olds than non-VOC cases. Found that B.1.1.7 has a substantial transmission advantage over other lineages, with a 50–100% higher reproduction number. |
| Jackson, B., Rambaut, A., Pybus, O. et al. 2021. 'Recombinant SARS-CoV-2 genomes involving lineage B.1.1.7 in the UK'. *Virological* 2021. As of 23 January 2022: https://virological.org/t/recombinant-sars-cov-2-genomes-involving-lineage-b-1-1-7-in-the-uk/658 | Academic article | SARS-CoV-2 recombination | Found long runs of mutations along the SARS-CoV-2 that match different lineages and strongly indicate virus recombination. |
| Aggarwal, D., Page, A.J., Schaefer, U. et al. 2021. 'An integrated analysis of contact tracing and genomics to assess the efficacy of travel restrictions on SARS-CoV-2 introduction and transmission in England from June to September, 2020'. *medRxiv* 2021.03.15.21253590. doi: https://doi.org/10.1101/2021.03.15.21253590 | Academic article | The impact of travel restrictions | Demonstrated the efficacy of travel-restriction policy in reducing the onward transmission of imported cases. |
| Parker, M., Lindsey, B., Leary, S. et al. 2021. 'Subgenomic RNA identification in SARS-CoV-2 genomic sequencing data'. Genome Research 31: 645-658. As of 23 January 2022: https://genome.cshlp.org/content/31/4/645 | Academic article | Computational-tool development | Developed a computational tool for detecting and quantifying subgenomic RNA in SARS-CoV-2 genomic sequence data. |
| Collier, D., De Marco, A., Ferreira, I. et al. 2021. 'Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies'. Nature 593: 136-141. As of 23 January 2022: https://www.nature.com/articles/s41586-021-03412-7 | Academic article | Properties of the Alpha variant | Demonstrated that neutralisation by sera from individuals who received the Pfizer vaccine was modestly reduced against the B.1.1.7 variant. This reduction was also evident in sera from some patients who had recovered from COVID-19. Introduction of the mutation that encodes the E484K substitution in the B.1.1.7 background to reflect a newly emerged variant of concern (VOC 202102/02) led to a more substantial loss of neutralising activity by vaccine-elicited antibodies and monoclonal antibodies (19 out of 31) compared with that conferred by the mutations in B.1.1.7 alone. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Martin, D.P., Weaver, S., Tegally, H. et al. 2021. 'The emergence and ongoing convergent evolution of the N501Y lineages coincides with a major global shift in the SARS-CoV-2 selective landscape'. medRxiv 2021.02.23.21252268. doi: https://doi.org/10.1101/2021.02.23.21252268 | Academic article | Properties of 501Y mutations | Described how the emergence and rapid rise in prevalence of three independent SARS-CoV-2 '501Y lineages', B.1.1.7, B.1.351 and P.1, in the last three months of 2020 prompted renewed concerns about the evolutionary capacity of SARS-CoV-2 to adapt to both rising population immunity and public health interventions such as vaccines and social distancing. The article provided evidence of a major change in the selective forces acting on immunologically important SARS-CoV-2 genes that likely coincided with the emergence of the 501Y lineages. It also provided evidence that a significant portion of the ongoing adaptive evolution of the 501Y lineages involves further convergence between the lineages. |
| du Plessis, L., McCrone, J.T., Zarebski, A.E. et al. 2021. 'Establishment & lineage dynamics of the SARS-CoV-2 epidemic in the UK'. *Science* 371 (6530): 708–712. doi: 10.1126/science.abf2946 | Academic article | Understanding how SARS-CoV-2 arrived in the UK in early 2020 | Provided a detailed picture of the SARS-CoV-2 introductions to the UK during the first months of 2020. High travel volumes and limited restrictions on international travel allowed more than 1000 lineages to become established before the lockdown, accelerating local epidemic growth and exceeding contact-tracing capacity. Transmission was highly heterogeneous, favouring some lineages that became widespread and subsequently harder to eliminate. This suggested that rapid or even pre-emptive responses should have been considered. |
| Baker, D.J., Aydin, A., Le-Viet, T. 2021. 'CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes'. *Genome Medicine* 13: 21. https://doi.org/10.1186/s13073-021-00839-5 | Academic article | A new flexible sequencing protocol | Described the development of a platform and flexible high-throughput method for sequencing SARS-CoV-2 genomes to aid the rapid global expansion of SARS-CoV-2 genome sequencing. |
| Kemp, S.A., Collier, D.A., Datir, R.P. 2021. 'SARS-CoV-2 evolution during treatment of chronic infection'. *Nature* 592: 277–282. https://doi.org/10.1038/s41586-021-03291-y | Academic article | Viral mutation within individuals | Demonstrated that chronic infection with SARS-CoV-2 led to viral evolution and reduced sensitivity to neutralising antibodies in an immunosuppressed individual treated with convalescent plasma. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Thomson, E.C., Rosen, L.E., Shepherd, J.G. et al. 2021. 'Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity', *Cell* 184(5):1171-1187.e20. doi: https://doi.org/10.1016/j.cell.2021.01.037 | Academic article | Properties of the N439K mutation | Demonstrated that the N439K mutation in the S protein confers enhanced binding affinity to the hACE2 receptor and that N439K viruses have similar *in vitro* replication fitness and cause infections with similar clinical outcomes compared to the wild type. The article also showed that the N439K mutation confers resistance against several neutralising monoclonal antibodies and reduces the activity of some polyclonal sera from persons recovered from infection, highlighting the need for ongoing molecular surveillance to guide the development and use of vaccines and therapeutics. |
| Kraemer, M.U.G., Hill, V., Ruis, C. et al. 2021. 'Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence'. *Science* 373 (6557): 889-895 eabj0113. https://doi.org/10.1126/science.abj0113 | Academic article | Properties of the Alpha variant | Found that the invasion and growth rates of B.1.1.7 cases among UK regions were positively associated with the intensity of human mobility from Kent and London during and after England's second lockdown (early November to early December). The article also showed higher growth rates in areas well connected to Kent and London following the lockdown that had previously experienced lower attack rates. Finally, whole-genome sequencing data and S-gene target failure showed that the increase in the frequency of lineage B.1.1.7 in each location was initially associated with mobility and prior-attack rates. However, this association declined through time and is no longer evident. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Lycett, S., Hughes, J., McHugh, M. et al. 2021. 'Epidemic waves of COVID-19 in Scotland: a genomic perspective on the impact of the introduction and relaxation of lockdown on SARS-CoV-2'. medRxiv 2021 .01.08.20248677. doi: https://doi.org/10.1101/2021.01.08.20248677 | Academic article | Understanding how SARS-CoV-2 arrived and spread in Scotland | Quantified the geographical origins of the first wave introductions into Scotland from abroad and other UK regions, the spread of these SARS-CoV-2 lineages to different regions within Scotland and the effect of lockdown on virus 'success'. The article estimated that approximately 300 introductions seeded lineages in Scotland. However, by June, circulating lineages were reduced to low levels, indicating that lockdown was associated with a reduction in infection numbers and the extinguishing of most virus lineages. Found that while some UK lineages persisted through the summer, the majority of lineages responsible for the second wave were travel-associated imports (mostly from Europe or other parts of the UK). Notes that the impact of stringent public health measures can be compromised if movements from regions of high to low prevalence are not subsequently minimised. |
| O'Toole, Á., Hill, V., Pybus, O. et al. 2021. 'Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2'. Wellcome Open Research 6: 121. doi: 10.12688/wellcomeopenres.16661.2 | Academic article | Understanding how Alpha and Beta spread internationally | Described how the discovery and rapid spread of B.1.1.7 and B.1.351/501Y.V2 highlight the importance of real-time, open data for tracking the spread of SARS-CoV-2 and informing future public health interventions and travel advice. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Mashe, T., Takawira, F.T., Martins, L.d.O. et al. 2021. 'Genomic epidemiology of the SARS-CoV-2 epidemic in Zimbabwe: Role of international travel and regional migration in spread'. medRxiv 2021.01.04.20232520. doi: https://doi.org/10.1101/2021.01.04.20232520 | Academic article | Understanding how SARS-CoV-2 spread in Zimbabwe | Described how most COVID-19 cases (57%) in Zimbabwe were in the 20-40 age group. Eight lineages from at least 25 separate introductions into the region were found using comparative genomics. Of these, 95% had the D614G mutation on the spike protein associated with higher transmissibility than the ancestral strain. Early introductions and spread of SARS-CoV-2 were predominantly associated with genomes common in Europe and the United States of America (USA) and uncommon in Asia at this time. As the pandemic evolved, travel-associated cases from South Africa and neighbouring countries were also recorded. Transmission within quarantine centres occurred when travelling nationals returned to Zimbabwe. |
| Colton, H., Ankcorn, M., Yavuz, M. et al. 2020. 'Improved sensitivity using a dual target, E and RdRp assay for the diagnosis of SARS-CoV-2 infection: Experience at a large NHS Foundation Trust in the UK'. *The Journal of infection* 82 (1): 159-198. doi: 10.1016/j.jinf.2020.05.061. | Academic article | Diagnostic-testing methodology | Demonstrated that dual-target testing using the E gene as a second target can help to improve both diagnostic sensitivity and the appropriate clinical responses. The article suggested that testing laboratories should consider using the E gene as a target to optimise SARS-CoV-2 diagnostics, including strategies to confirm samples with E gene only amplification as described. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Tonkin-Hill, G., Martincorena, I., Amato, R., et al. 2020. 'Patterns of within-host genetic diversity in SARS-CoV-2'. *eLife* 10: e66857 doi: 10.7554/eLife.66857 | Academic article | Viral mutation within individuals | Found that strong strand asymmetries, suggestive of damage or RNA editing of the plus strand, rather than replication errors, dominate the accumulation of mutations. Within and between host diversity showed strong purifying selection, particularly against nonsense mutations. Recurrent within-host mutations, many of which coincide with known phylogenetic homoplasies, displayed a spectrum and patterns of purifying selection more suggestive of mutational hotspots than recombination or convergent evolution. While allele frequencies suggested that most samples result from infection by a single lineage, multiple putative examples of co-infection were identified. The use of an epidemiological inference framework suggested that sharing within-host variants between samples could help reconstruct transmission chains. However, mutational hotspots and rare cases of superinfection can confound these analyses. |
| da Silva Filipe, A., Shepherd, J.G., Williams T. et al. 2021. 'Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland'. *Nature Microbiology* 6 (1): 112-22. doi: 10.1038/s41564-020-00838-z | Academic article | Understanding how SARS-CoV-2 arrived and spread in Scotland | Estimated that SARS-CoV-2 was introduced to Scotland on at least 283 occasions during February and March 2020. The epidemiological analysis confirmed that early introductions of SARS-CoV-2 originated from mainland Europe (the majority from Italy and Spain). It also identified subsequent early outbreaks in the community, within healthcare facilities and at an international conference. Community transmission occurred after 2 March, three weeks before control measures were introduced. Earlier travel restrictions or quarantine measures, both locally and internationally, could have reduced the number of COVID-19 cases in Scotland. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Vöhringer, H., Sinnott, M., Amato, R. et al. 2020. 'Lineage-specific growth of SARS-CoV-2 B.1.1.7 during the English national lockdown'. *Virological* 2020. As of 23 January 2022: https://virological.org/t/lineage-specific-growth-of-sars-cov-2-b-1-1-7-during-the-english-national-lockdown/575 | Academic article | Properties of the Alpha variant | Demonstrated that the B.1.1.7 SARS-CoV-2 lineage spread faster than its predecessors, continuing to grow during a lockdown in which other lineages shrank. The results suggest that stricter measures might be required to contain the B.1.1.7 lineage. |
| Aggarwal, D., Myers, R., Hamilton, W.L. et al. 2020. 'The role of genomics in understanding COVID-19 outbreaks in long term care facilities'. OSFio 2020: 23. DOI:10.31219. As of 23 January 2022: https://osf.io/7y9rk/ | Academic article | Understanding care-home outbreaks during the first wave | Described how staff and residents were usually infected with identical, or near-identical, SARS-CoV-2 genomes. Outbreaks usually involved one predominant lineage, and the same lineages persisted in care homes despite infection control measures. Outbreaks were most commonly due to a single or a few introductions followed by spread rather than a series of seeding events from the community into care homes. |
| Boshier, F.A.T., Pang, J., Penner, J. et al. 2020. 'Remdesivir induced viral RNA and subgenomic RNA suppression, and evolution of viral variants in SARS-CoV-2 infected patients'. medRxiv 2020: medRxiv 2020. doi: https://doi.org/10.1101/2020.11.18.20230599 | Academic article | How the drug Remdesivir works in patients | Deep sequencing of longitudinal samples from SARS-CoV-2 infected paediatric patients identified evidence of remdesivir-associated inhibition of viral replication *in vivo* and uncovered evidence of within-host evolution of distinct viral genotypes. |
| Snell, L.B., Fisher, C.L., Taj, U. et al. 2020. 'Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 transmission identifies community social distancing as the dominant intervention reducing outbreaks'. medRxiv 2020.11.17.20232827. doi: https://doi.org/10.1101/2020.11.17.20232827 | Academic article | The role of social distancing in preventing spread in hospitals | Demonstrated that community social distancing had a dominant impact on reducing hospital-acquired transmission by reducing healthcare-worker infection. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Page, A., Mather, A., Le-Viet, T. et al. 2020. 'Large scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management'. *Microbial Genomics*, 7 (6). https://doi.org/10.1099/mgen.0.000589 | Academic article | Understanding viral introduction and spread in Norfolk | Identified a discrete sub-lineage associated with six care facilities, finding no evidence of reinfection in longitudinal samples and ruling out a nosocomial outbreak. The study identified 16 lineages in key workers that were not evident in patients, indicating effective infection-control measures. The study also found that the D614G spike protein mutation linked to increased transmissibility dominates the samples and rapidly confirmed the relatedness of cases in an outbreak at a food-processing facility. |
| Stirrup, O.T., Hughes, J., Parker, M. et al. 2021. 'Rapid feedback on hospital onset SARS-CoV-2 infections combining epidemiological and sequencing data'. eLife 10: e65828. doi: 10.7554/eLife.65828 | Academic article | Computational-tool development | Developed a novel statistical method and sequence-reporting tool that combines epidemiological and sequence data to rapidly assess the probability of healthcare-acquired infections and identify infections that could plausibly constitute outbreak events. |
| Illingworth, C., Hamilton, W., Jackson, C. et al. 2020. 'A2B-COVID: A method for evaluating potential SARS-CoV-2 transmission events'. 2020. *medRxiv* 2020.10.26.20219642. doi: https://doi.org/10.1101/2020.10.26.20219642 | Academic article | Computational-tool development | Developed a tool to rapidly identify linked cases of COVID-19 infection. The method combines knowledge about infection dynamics, data describing the movements of individuals, and novel approaches to genome-sequence data to assess whether infection cases are consistent or inconsistent with linkage via transmission. Application of the tool to analyse and compare data collected from two wards at Cambridge University Hospitals revealed qualitatively different patterns of linkage between cases on designated COVID-19 and non-COVID-19 wards. |
| Nicholls, S.M., Poplawski, R., Bull, M.J. et al. 2021. 'CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance'. *Genome Biology, 22* (1). https://doi.org/10.1186/s13059-021-02395-y | Academic article | Computational-infrastructure development | Describes the development of an encompassing digital infrastructure to address the challenge of collecting and integrating genomic-sequencing data and sample-associated metadata produced across COG-UK's network. The system was pragmatically designed and implemented to rapidly stand-up capacity in a pandemic caused by a novel virus. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| Hamilton, W.L., Tonkin-Hill, G., Smith, E. et al. 2020. 'COVID-19 infection dynamics in care homes in the East of England: a retrospective genomic epidemiology study'. medRxiv preprint. doi: https://doi.org/10.1101/2020.08.26.20182279 | Academic article | Understanding infection patterns in care homes | Demonstrated that care-home residents had a significant burden of COVID-19 infections and high mortality. Larger viral clusters were consistent with the within-care-home transmission, while multiple clusters per care home suggested independent acquisitions. |
| Chappell, J.G., Tsoleridis, T., Clark, G. et al. 2021. 'Retrospective screening of routine respiratory samples revealed undetected community transmission and missed intervention opportunities for SARS-CoV-2 in the United Kingdom'. *Journal of General Virology 102* (6). https://doi.org/10.1099/jgv.0.001595 | Academic article | Improving virus-testing policy | Provided evidence for widespread community circulation of SARS-CoV2 in early February 2020 and into March that was undetected at the time owing to restrictive case definitions informing testing policy. Sequences obtained from the first officially recorded case in Nottinghamshire - a traveller returning from Daegu, South Korea – also clustered with these early UK sequences suggesting acquisition of the virus occurred in the UK and not Daegu. Analysis of a larger sample of sequences obtained in the Nottinghamshire area revealed multiple viral introductions, mainly in late February and through March. |
| Lo, S.W., Jamrozy, D. 2020. 'Genomics and epidemiological surveillance'. Nature Reviews Microbiology2020; 18 (9): 478. https://doi.org/10.1038/s41579-020-0421-0 | Academic article | Genomic surveillance | Provided a short comment on how genomic surveillance can provide important information for identifying and tracking emerging pathogens such as SARS-CoV-2. |
| Meredith, L.W., Hamilton, W.L., Warne, B. et al. 2020. 'Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study'. *Lancet Infectious Disease* 20 (11): P1263-1271. doi: https://doi.org/10.1016/S1473-3099(20)30562-4 | Academic article | Genomic surveillance | Established real-time genomic surveillance of SARS-CoV-2 in a UK hospital and showed the benefit of combined genomic and epidemiological analysis to investigate healthcare-associated COVID-19. This approach enabled the detection of cryptic transmission events and identified opportunities to target infection-control interventions to further reduce healthcare-associated infections. |
| Pang, J., Boshier, F.A.T., Alders, N., Dixon, G., Breuer, J. 2020. 'No evidence of viral polymorphisms associated with Paediatric Inflammatory Multisystem Syndrome Temporally Associated With SARS-CoV-2 (PIMS-TS)'. medRxiv 2020: 2020.07.07.20148213. | Academic article | COVID-19 infection in children | Analysed viral sequences from 13 paediatric COVID-19 patients, of whom five were diagnosed with Paediatric Inflammatory Multisystem Syndrome temporally associated with SARS-CoV-2. In contrast to the hypothesis, the study found unique sequences associated with the viruses from PIMS-TS patients. |

| Advancing scientific knowledge | | | |
|---|---|---|---|
| **Full reference** | **Academic article or technical report?** | **Topic area** | **Brief description of key finding** |
| The COVID-19 Genomics UK (COG-UK) Consortium. 2020. 'An integrated national scale SARS-CoV-2 genomic surveillance network'. *The Lancet Microbe* 1 (3): e99-e100. doi: https://doi.org/10.1016/S2666-5247(20)30054-9 | Academic article | Information about COG-UK | Described how COG-UK launched in March 2020 with £20 million support from UK Research and Innovation, the UK Department of Health and Social Care and Wellcome Trust. The article noted that the consortium's goal was to sequence SARS-CoV-2 for up to 230,000 patients, healthcare workers and other essential workers in the UK with COVID-19, helping to track SARS-CoV-2 transmission, identify viral mutations and integrate with health data to assess how the viral genome interacts with the cofactors and consequences of COVID-19. |
| Kemp, S., Meng, B., Ferriera, I. et al. 2021. 'Recurrent emergence and transmission of a SARS-CoV-2 spike deletion H69/V70'. *Cell Reports, 35* (13): 109292. https://doi.org/10.1016/j.celrep.2021.109292 | Academic article | Properties of the 69/70 deletion mutation | Reported the recurrent emergence and onward transmission of a six-nucleotide out-of-frame deletion in the S gene, which results in loss of two amino acids: H69 and V70. The study noted that ΔH69/V70 likely acts as a permissive mutation allowing the acquisition of otherwise deleterious immune-escape mutations. Enhanced surveillance for the ΔH69/V70 deletion with and without RBD mutations should be considered as a global priority as a marker for the B.1.1.7 variant and potentially for other emerging variants of concern. |
| Harper, H., Burridge, A., Winfield, M. et al. 2021. 'Detecting SARS-CoV-2 variants with SNP genotyping'. PLoS ONE 16 (2): e0243185. https://doi.org/10.1371/journal.pone.0243185 | Academic article | Sequencing-protocol development | Designed a single-nucleotide polymorphism (SNP) identification pipeline to survey genetic variation using sequenced SARS-CoV-2 samples. The research demonstrated the usefulness of an SNP genotyping panel to provide a rapid, cost-effective and reliable way to monitor SARS-CoV-2 variants circulating in an outbreak. |
| Volz, E., Hill, V., McCrone, J. et al. 2021. 'Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity'. *Cell* 2021; 184 (1): 64-75.e11. doi: 10.1016/j.cell.2020.11.020 | Academic article | Properties of the D614G mutation | Used population-genetic analysis to determine that 614G frequency increases relative to 614D, consistent with a selective advantage. The study found no indication that patients infected with the spike 614G variant have higher COVID-19 mortality or clinical severity. However, 614G was associated with a higher viral load and younger patient age. Significant differences in the growth and size of 614G phylogenetic clusters indicate a need for continued study of this variant. |

# Annex 9: List of events and conferences

**Annex Table 9-1. List of events and conferences where COG-UK members have contributed to presentations or panel discussions.[3]**

| Event/ conference name | Topic area in which COG-UK contributed | Location | Participating COG-UK members and | Contributions to the event (e.g. presentations, panel roles, etc.) |
|---|---|---|---|---|
| CODATA/RDA Schools for Research Data Science Alumni Network | SARS-CoV-2 genomics | Online | Matthew Bashton | Presentation |
| Dynamics & Evolution of human viruses | SARS-CoV-2 genomics | Online | Louis du Plessis | Oral presentation |
| Genomic Medicine 2020-2021 course at University of Cambridge | SARS-CoV-2 genomics | Online | Louis du Plessis | Oral presentation |
| The Conversation panel discussion: 'Coronavirus variants explained: ask the experts in a free online discussion' | SARS-CoV-2 genomics | Online | Louis du Plessis | Panel member |
| Systems Virology Journal Club | SARS-CoV-2 genomics | Online | Louis du Plessis | Presentation |
| SBIMB Journal Club | SARS-CoV-2 genomics | Online | Louis du Plessis | Presentation |

3 Indicative list of events COG-UK members participated in. However, since not all events are reported to the COG-UK core team, COG-UK members likely participated in a larger number of events: data on this is not available.

| Event/ conference name | Topic area in which COG-UK contributed | Location | Participating COG-UK members and | Contributions to the event (e.g. presentations, panel roles, etc.) |
|---|---|---|---|---|
| ASM Conference on Rapid Applied Microbial Next-Generation Sequencing and Bioinformatic Pipelines 2020 | SARS-CoV-2 genomics | Online | Anthony Underwood on behalf of CGPS | Oral Presentation |
| Training national reference lab of Zimbabwe to do ARTIC sequencing and analysis | SARS-CoV-2 genomics | Online | Quadram (Andrew Page, Nabil-Fareed Alikhan) | Four members spent two days on WhatsApp training Zimbabwe scientists to do ARTIC sequencing and analysis – the country's first time sequencing SARS-CoV-2 genomes and the national lab's first time sequencing at all (other than Sanger) |
| Micro Binfie Podcast | SARS-CoV-2 genomics | Online | Quadram (Andrew Page, Nabil-Fareed Alikhan) | Produced 20 podcast episodes on SARS-CoV-2 bioinformatics https://soundcloud.com/microbinfie/sets/sars-cov-2-bioinformatics |
| Terrapin. com: Disease Prevention & Control Summit | SARS-CoV-2 genomics | Online | Dr Ewan Harrison | Presentation & discussion |
| Westminster Forum Projects | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| Janelia – Science of COVID-19 seminar | SARS-CoV-2 genomics | Online | Dr Matt Parker Professor | Presentation & discussion |
| Precision Medicine World Conference | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| WSJ Tech Health conference | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| BMA - Medical Academics Conference 2021 | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| BIA – Spring meeting | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |

| Event/ conference name | Topic area in which COG-UK contributed | Location | Participating COG-UK members and | Contributions to the event (e.g. presentations, panel roles, etc.) |
|---|---|---|---|---|
| SfAM - Int Applied Microbiol Conference | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| NIH Scientific Group Lecture | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| UN technical briefing on SARS-CoV-2 genome sequencing | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Speech & discussion |
| FCDO / British Embassy Prague COVID-19 genomics discussion | SARS-CoV-2 genomics | Online | Dr Ewan Harrison | Presentation & discussion |
| SMC B.1.617 variant briefing | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Panel for Q&A |
| Frontline Genomics – Ale | SARS-CoV-2 genomics | Online | Dr Alessandro Carabelli | Presentation & discussion |
| Genome BC Annual Genomics Forum | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| Royal College of Physicians of Edinburgh COVID-19 update series | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| UoC - Women leaders of today & tomorrow | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| ASHK Coronavirus panel | SARS-CoV-2 genomics | Online | Professor Sharon Peacock Professor Ravindra Gupta | Presentation & discussion |
| HIMSS prerecording | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| Pasteur Institute seminar | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| COVAX Enabling Sciences Workshop | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |

| Event/ conference name | Topic area in which COG-UK contributed | Location | Participating COG-UK members and | Contributions to the event (e.g. presentations, panel roles, etc.) |
|---|---|---|---|---|
| ISAC Webinar | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| EMBL knowledge exchange workshop | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| UoC: Taking Genomics into the Frontline of Healthcare: A Public Health Perspective | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| Illumina conversation with CMO | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| Women & girls in science | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| Novacyt. NovaTalk: The Role of Diagnostic Tests and Sequencing | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| ESCMID webinar | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| GSE. Celebrate Women in government Science and engineering | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| AAAS conference | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| Foreign Press Association | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| FCDO / Prague Embassy | SARS-CoV-2 genomics | Online | Dr Ewan Harrison | Presentation & discussion |
| Royal Society Medicine | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |
| Festival of Genomics | SARS-CoV-2 genomics | Online | Professor Sharon Peacock | Presentation & discussion |

# Annex 10: List of policy reports

**Annex Table 10-1. List of reports COG-UK contributed to or was mentioned in**

| Report/Document title and reference | Decision-making body producing it | What COG-UK is mentioned for |
|---|---|---|
| Forty-fifth SAGE meeting on COVID-19, 2 July 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/904684/S0596_Forty-fifth_SAGE_meeting_on_Covid-19.pdf | SAGE | Providing insights on introductions and transmission in the UK, with initial seeding mostly coming from Europe. Preliminary work indicates that D614G might be more transmissible but with no apparent increase in disease severity. |
| Sixtieth SAGE meeting on COVID-19, 1 October 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/931034/S0798_Sixtieth_SAGE_meeting_on_Covid-19.pdf | SAGE | Identification of variants; no evidence they are more virulent, but further analysis of D614G's greater transmissibility. |
| Sixty-fourth SAGE meeting on COVID-19, 29 October 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/938973/S0859_Sixty-fourth_SAGE_meeting_on_Covid-19.pdf | SAGE | Analysis of introductions and transmission in Scotland and Wales during the first and second waves identify imports associated with summer travel following the easing of lockdown. |
| Sixty-sixth SAGE meeting on COVID-19, 5 November 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/938974/S0868_Sixty-sixth_SAGE_meeting_on_Covid-19.pdf | SAGE | COG-UK to provide input on evidence of transmission of SARS-CoV-2 variant from mink to humans. |

| Report/Document title and reference | Decision-making body producing it | What COG-UK is mentioned for |
|---|---|---|
| Sixty-ninth SAGE meeting on COVID-19, 19 November 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/938977/S0909_Sixty-ninth_SAGE_meeting_on_Covid-19.pdf | SAGE | COG-UK to provide a comparison of SARS-CoV-2 in wastewater samples. |
| Seventy-third SAGE meeting on COVID-19, 17 December 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/952613/s0989-covid-19-sage-73-minutes-171220.pdf | SAGE | A new variant of SARS-CoV-2 (B.1.1.7) identified in Southeast England; preliminary assessment of increased transmissibility. Although reported as NERVTAG input, much of the data and key individuals involved were COG-UK members. Also, preliminary reporting of Cambridge University transmission among students. |
| Seventy-fourth SAGE meeting on COVID-19, 22 December 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/948606/s0991-sage-meeting-74-covid-19.pdf | SAGE | COG-UK data/members inform NERVTAG and PHE assessment of B.1.1.7.<br><br>*COG-UK not acknowledged by name. |
| Seventy-fifth SAGE meeting on COVID-19, 7 January 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/954903/s1010-covid-19-sage-75-minutes.pdf | SAGE | COG-UK data/members inform the assessment of B.1.1.7 as the dominant strain in all age groups in London, Southeast England and East of England. Preliminary analysis of variants with E484K mutation, including B.1.351 VOC first identified in South Africa. Tracking of B.1.351 in the UK.<br><br>*COG-UK not acknowledged by name. |
| Seventy-sixth SAGE meeting on COVID-19, 14 January 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/957026/s1030-covid-19-sage-76-minutes.pdf | SAGE | COG-UK data/members inform assessment of new variants, including B.1.1.7, B.1.351 and P1.<br><br>*COG-UK not acknowledged by name. |

| Report/Document title and reference | Decision-making body producing it | What COG-UK is mentioned for |
|---|---|---|
| Seventy-seventh SAGE meeting on COVID-19, 21 January 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/958730/S1037_Covid-19_SAGE_77_minutes.pdf | SAGE | COG-UK data/members inform assessment of new variants, including B.1.1.7, B.1.351 and P1.<br><br>*COG-UK not acknowledged by name. |
| Seventy-eighth SAGE meeting on COVID-19, 28 January 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/963347/S1061_SAGE__78_minutes__1_.pdf | SAGE | COG-UK data/members inform assessment of new variants, including B.1.1.7, B.1.351 and P1.<br>*COG-UK not acknowledged by name. |
| Seventy-ninth SAGE meeting on COVID-19, 4 February 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/963366/S1082_SAGE__79_Minutes.pdf | SAGE | COG-UK data/members inform assessment of new variants, including B.1.1.7, B.1.351 and P1. Acknowledgement of COG-UK providing high levels of sequencing capacity by international standards, but not of constraints. COG-UK to provide input into the optimal strategy for targeting sequencing capacity for public health needs. |
| Eightieth SAGE meeting on COVID-19, 11 February 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/963390/S1115_SAGE_80_Minutes.pdf | SAGE | COG-UK data/members inform assessment of new variants, including B.1.1.7, B.1.351 and P1. COG-UK studies in several universities also suggest mitigation measures were successful in minimising transmission.<br><br>*COG-UK not acknowledged by name. |
| Eighty-third SAGE meeting on COVID-19, 11 March 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/975918/S1141_SAGE_83_minutes.pdf | SAGE | COG-UK data/members inform assessment of new variants, including B.1.1.7, B.1.351 and P1, and. Note the importance that results of genomic surveillance are shared with COG-UK and hotel quarantine sequencing. |

| Report/Document title and reference | Decision-making body producing it | What COG-UK is mentioned for |
|---|---|---|
| Eighty-fourth SAGE meeting on COVID-19, 25 March 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/976319/S1163_SAGE_84_-_Final_minutes.pdf | SAGE | COG-UK and PHE analysis of border measures introduced in England between June and September 2020 |
| Eighty-seventh SAGE meeting on COVID-19, 22 April 2021<br>As of 23 January 2022:<br>https://www.gov.uk/government/collections/sage-meetings-april-2021 | SAGE | COG-UK data/members inform assessment of new variants, including B.1.1.7, B.1.351 and P1.<br><br>*COG-UK not acknowledged by name, |
| Eighty-eighth SAGE meeting on COVID-19, 5 May 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/984501/S1235_Eighty-eighth_SAGE_meeting.pdf | SAGE | COG-UK data/members inform assessment of new variants, including B.1.1.7, B.1.351, P1 and B.1.617.2. COG-UK to work with NHSE and NHSTT to consider how to increase the percentage of hospital samples sequenced. |
| Eighty-ninth SAGE meeting on COVID-19, 13 May 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/988403/S1236_Eighty-nineth_SAGE.pdf | SAGE | COG-UK data/members inform assessment of new variants, including B.1.1.7, B.1.351, P1 and B.1.617.2. NHSE and COG-UK to work together to ensure hospitals receive rapid feedback on sequencing results. |
| Children's Task and Finish Group: Paper on Higher Education Settings<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/963387/S1103_Children_s_Task_and_finish_Group_Paper_on_Higher_Education_Settings_.pdf | TFC | COG-UK contributed preliminary summaries of genomic studies of transmission in three UK university settings to the report. |
| NERVTAG paper: SARS-CoV-2 variants, 13 May 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/893334/S0359_NT-SARS-CoV-2_Variants.pdf | NERVTAG | COG-UK data used to support the discussion of SARS-CoV-2 genetic variation. Recommendation that virology laboratories engage in surveillance of COG-UK data. |

| Report/Document title and reference | Decision-making body producing it | What COG-UK is mentioned for |
|---|---|---|
| NERVTAG: Risk assessment of SARS-CoV-2 variants that have been selected in mink, 12 November 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/938979/S0878_Risk_assessment_of_SARS-CoV-2_variants_that_have_been_selected_in_mink.pdf | NERVTAG | Joint paper with COG-UK members assessing variants selected in mink. COG-UK data used in support of the analyses.<br><br>*COG-UK not acknowledged by name. |
| NERVTAG/SPI-M Extraordinary meeting on SARS-CoV-2 variant of concern 202012/01 (variant B.1.1.7), 21 December 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/954945/s0993-nervtag-spi-m-voc-meeting.pdf | NERVTAG | COG-UK data and members contributed to the committee assessing the B.1.1.7 variant. |
| NERVTAG: Brief note on SARS-CoV-2 variants, 13 January 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/982615/13_Jan_NERVTAG_note_on_variants_of_concern.pdf | NERVTAG | COG-UK data used to support an assessment of variants.<br><br>*COG-UK not acknowledged by name. |
| NERVTAG: Update note on B.1.1.7 severity, 11 February 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/982640/Feb_NERVTAG_update_note_on_B.1.1.7_severity.pdf | NERVTAG | COG-UK data (i.e. HOCI study) used to support an assessment of B.1.1.7 severity.<br>*COG-UK not acknowledged by name. |
| Investigation of novel SARS-CoV-2 variant 202012/01: technical briefing 1, December 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/959438/Technical_Briefing_VOC_SH_NJL2_SH2.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7). |

| Report/Document title and reference | Decision-making body producing it | What COG-UK is mentioned for |
|---|---|---|
| Investigation of novel SARS-CoV-2 variant 202012/01: technical briefing 2, December 2020<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/959361/Technical_Briefing_VOC202012-2_Briefing_2.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7). |
| Investigation of novel SARS-CoV-2 variant 202012/01: technical briefing 3, January 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/959360/Variant_of_Concern_VOC_202012_01_Technical_Briefing_3.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7). |
| Investigation of novel SARS-CoV-2 variant 202012/01: technical briefing 4, January 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/959359/Variant_of_Concern_VOC_202012_01_Technical_Briefing_4.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7). |
| Investigation of novel SARS-CoV-2 variant 202012/01: technical briefing 5, January 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/959426/Variant_of_Concern_VOC_202012_01_Technical_Briefing_5.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7). |
| Investigation of SARS-CoV-2 variants of concern in England: technical briefing 6, 13 February 20212<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/961299/Variants_of_Concern_VOC_Technical_Briefing_6_England-1.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7; B.1.1.7-E484K; B.1.351; P1). |

| Report/Document title and reference | Decision-making body producing it | What COG-UK is mentioned for |
|---|---|---|
| SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 7, 11 March 2021 As of 23 January 2022: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/972247/Variants_of_Concern_VOC_Technical_Briefing_7_England.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7; B.1.1.7-E484K; B.1.351; P1; P2; A.23.1-E484K; B.1.525; B1.1.318; B1.324.1-E484K). |
| SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 8, 1 April 2021 As of 23 January 2022: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/975742/Variants_of_Concern_VOC_Technical_Briefing_8_England.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7; B.1.1.7-E484K; B.1.351; P1; P2; A.23.1-E484K; B.1.525; B1.1.318; B1.324.1-E484K; P3). |
| SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 9, 22 April 2021 As of 23 January 2022: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/979818/Variants_of_Concern_VOC_Technical_Briefing_9_England.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7; B.1.1.7-E484K; B.1.351; P1; P2; A.23.1-E484K; B.1.525; B1.1.318; B1.324.1-E484K; P3; B.1.617.1-E484Q). |
| SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 10, 7 May 2021 As of 23 January 2022: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/984274/Variants_of_Concern_VOC_Technical_Briefing_10_England.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7; B.1.1.7-E484K; B.1.351; P1; P2; A.23.1-E484K; B.1.525; B1.1.318; B1.324.1-E484K; P3; B.1.617.1-E484Q; B.1.617.2; B.1.617.3). |
| SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 11, 13 May 2021 As of 23 January 2022: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/986380/Variants_of_Concern_VOC_Technical_Briefing_11_England.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7; B.1.1.7-E484K; B.1.351; P1; P2; A.23.1-E484K; B.1.525; B1.1.318; P3; B.1.617.1-E484Q; B.1.617.2; B.1.617.3). |

| Report/Document title and reference | Decision-making body producing it | What COG-UK is mentioned for |
|---|---|---|
| SARS-CoV-2 variants of concern and variants under investigation in England: technical briefing 12, 22 May 2021<br>As of 23 January 2022:<br>https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/988619/Variants_of_Concern_VOC_Technical_Briefing_12_England.pdf | PHE | COG-UK data/members provide a major contribution to the assessment of variants under investigation/ variants of concern (B.1.1.7; B.1.1.7-E484K; B.1.351; P1; P2; A.23.1-E484K; B.1.525; B1.1.318; P3; B.1.617.1-E484Q; B.1.617.2; B.1.617.3; AV.1). |