Bundle of documents for Oral hearings commencing from 19 August 2025 in relation to the Queen Elizabeth University Hospital and the Royal Hospital for Children, Glasgow

Bundle 44 – Volume 9
Expert Report by Sid Mookerjee dated 20 August 2025 in response to Note by Dominique Chaput and Miscellaneous Documents

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SCOTTISH HOSPITALS INQUIRY

Expert report. 19.08.2025

Response to – Dr. Chaput Deduplication_notes_DC (supporting evidence – deduplication)

Expert Report prepared for the Scottish Hospitals Inquiry

Submitted on: 20 August 2025

Mr. Sid Mookerjee, BSc, MSc, MPH, FRSPH

1. Introduction

1.1. This response report has been prepared at the request of the Scottish Hospitals Inquiry and is in response to Dr. Chaput's document entitled 'Dr. Chaput Deduplication_notes_DC' submitted on the 11th of August to the inquiry. I have attached Dr. Chaput's document as an annex to this document.

1.2. Given the limited time available to respond to this document, I have elected to provide a concise response, bearing in mind the manner in which the evidence in question is being used by the inquiry to inform its understanding of infection-rate trends and whether these exceeded those of comparator hospitals during the period 2015 to 2022.

1.3. In section 2.1 and 2.2 I present important considerations in relation to the Freedom of Information and NHS GGC's infection datasets respectively. Section 2.3 goes onto summarise my response.

2. Response

2.1. **Regarding Dr. Chaput's points on the Freedom of information data**

2.1.1. Responses by hospital Trusts to SHI's FOI data requests, which noted in detail the kind and format of data required of the Trusts, was taken in good faith and with appreciation of the Trusts' expertise in extracting the routine clinical data and complying to simple de-duplication instructions. This is a process which all Trusts who responded are adept at following as per their monthly National mandatory data submission processes, albeit the latter includes a narrow infection set.

2.1.2. Cardiff and Vale NHS Trust's response was understood to clearly state that they de-duplicated the samples to the best of their abilities.

2.1.3. Leeds NHS Trust's response was also understood to clearly state that they supplied de-duplicated infection numbers, albeit not by episode, with the latter not essential in carrying out a 14-day de-duplication of infection incidence. The date of each infection sample aligned to each patient number is adequate in allowing for de-duplication.

2.1.4. Oxford NHS Trust supplied us with their de-duplicated infection incidence. I do not concur with Dr. Chaput's conjecture regarding Oxford's FOI dataset.

2.1.5. With reference to GOSH's dataset, please note paragraphs 2.52 to 2.57 [1] including Figure 2 on page 86, where I respond to NHS GGC's criticism of the FOI data, by evidencing that the rates of infections of individual comparator units over 2015 – 2022 all cluster or coalesce around the mean yearly comparator rate (see dark green line – GOSH rate of infection line, Figure 2) indicating minor variance between their rates year on year. This suggests that the incidence figures provided by GOSH are in keeping with other FOI returns. In fact, GOSH's rate of infection is higher than that of other Trusts over the period 2019 – 2022, in favour of NHS GGC when compared to the Schiehallion overall rate (thin purple line, Figure 2) over that period.

2.2. **Regarding Dr. Chaput's points on the NHS GGC infection dataset**

2.2.1. It is important here to consider paragraph 4B.2 [2], Glasgow 4 - Prof Peter Hawkey, Dr Lydia Drumright & Dr Samir Agrawal - Joint Response to 5 Reviews of HAD Report - 19 July 2025, and I quote " *It is unclear to us why datasets across the Inquiry are different, especially with respect to bed days data, which one would expect to be similar as they are collected routinely for the NHS. These differences suggest the need for standardization of data collection and reporting within the GGC NHS, which is important not only for retrospective analyses, such as this Inquiry, but also for monitoring activity and quality improvement".*

2.2.2. I concur with the HAD authors' point on the existence of multiple infection and bed days datasets, pointing to a lack of standardisation on part of NHS GGC and indicative of poor data quality control.

2.2.3. The infection dataset I was provided with consisted of numerous polymicrobial samples, i.e. blood culture samples growing more than one organism, which took many weeks' worth of work to analyse and deduplicate for inclusion in my 2024 Expert reports. Dr. Chaput makes no mention of polymicrobial samples in her summary, and I'm not clear as to the methodology she followed in arriving at the infection figures quoted in her document, seeing that there is scant methodological information provided, and I do not have access to her workings.

2.2.4. Dr. Chaput makes available a table in her document, comparing gram-negative and fungal organism incidence figures of environmental importance 8.1.16 from my Expert Quantitative link report [3], used by me in calculating my initial Schiehallion rate of infection per 1000

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[1] Bundle 21, Volume 1, Document 3, Pages 86
[2] Bundle 44, Volume 5, Document 2, page 60
[3] Bundle 21, Volume 1, Document 1, page 25

admissions, to her calculations using the same source dataset, providing both total and de-deduplicated incidence figures corresponding to each organism. Dr Chaput goes onto site differences in incidence figures where applicable between our incidence figure outcomes. For completeness, I have undertaken a re-analysis of environmental gram-negative and fungal organisms' incidences, particular to the Schiehallion unit, focusing on the organisms detailed in my initial table. In Table 1 below, I provide total and de-duplicated incidence figures, alongside a column summarising, alongside each organism, whether my re-calculated incidence figures are in agreement or otherwise with those of Dr. Chaput's, and the total (and unique) figures by year calculated by me.

Table 1: Schiehallion unit environmental infection incidence by organism. Comparison of SM 2024 incidence, Dr. Chaput 11.08.2025 calculations, and SM 2025 incidence re-calculations.

Organism	Mookerjee_original	Chaput		Notes re deduplication or counting errors	Mookerjee_latest		Agree/disagree with Dr. C Total count	Agree/disagree with Dr. C Dedup	Numbers by year: where yearly figures are presented without a following note on 'unique', the totals should be interpreted as unique infection counts
	Count	Total	Dedup.		Total	14-day Dedup			
Achromobacter denitrificans	2	1	1	Four entries in the entire data set: 1 paed. from 6A, 2 paed. from emerg. dept, 1 adult (DOB 1932)	1	1	Agree	Agree	
Achromobacter species	1	1	1		1	1	Agree	Agree	
Acinetobacter baumannii	10	5	4	Five Schiehal. samples in total, 2x samples 8 days apart (2016)	5	4	Agree	Agree	
Acinetobacter baumannii complex	4	3	3		3	3	Agree	Agree	
Acinetobacter ursingii	9	10	5	4x samples 1 day apart (2016), 2x samples 2 days apart (2017), 2x samples same day (2018)	8	5	Disagree	Agree	3x 2016, 2x 2017, 2x 2018, 1x 2019
Aeromonas hydrophila/caviae	2	1	1	Five entries in the entire data set: 1 paed. from 2B, 4 adult (DOB 1936, 1943, 1969)	1	1	Agree	Agree	
Brevundimonas species	1	1	1		1	1	Agree	Agree	
Burkholderia cepacia	1	1	1		1	1	Agree	Agree	
Burkholderia cepacia group	2	1	1		1	1	Agree	Agree	
Candida albicans	10	14	6	2x samples in 2 days (2015), 3x samples in 5 days (2016), 3x samples in 1 day (2018), 4x samples in 5 days (2018)	13	6	Disagree	Agree	2x 2015, 2x 2016, 2x 2017, 7x 2018
Candida fermentati	1	1	1		1	1	Agree	Agree	

Organism	Mookerjee_original	Chaput		Notes re deduplication or counting errors	Mookerjee_latest		Agree/disagree with Dr. C Total count	Agree/disagree with Dr. C Dedup	Numbers by year: where yearly figures are presented without a following note on 'unique', the totals should be interpreted as unique infection counts
	Count	Total	Dedup.		Total	14-day Dedup			
Candida parapsilosis	4	9	4		9	5	Agree	Disagree	3x 2017, 1x 2021, 1x 2022
Candida tropicalis	1	6	1		4	1	Disagree	Agree	4x 2017
Chryseobacterium species	1	1	1		2	2	Disagree	Disagree	1x 2018, 1x 2022
Chryseomonas indologenes	3	8	3		8	4	Agree	Disagree	1x 2016, 1x 2017, 1x 2018, 1x 2019
Citrobacter braakii	2	1	1	Only one paed. sample in entire data set	1	1	Agree	Agree	
Citrobacter freundii	2	2	2		2	2	Agree	Agree	
Citrobacter koseri	1	1	1		1	1	Agree	Agree	
Citrobacter youngae	2	2	1	2x samples 1 day apart (2017)	2	1	Agree	Agree	
Cupriavidus pauculus	2	2	2		2	2	Agree	Agree	
Delftia acidovorans	4	3	3		4	4	Disagree	Disagree	2x 2017, 1x2019, 1x 2020
Elizabethkingia meningoseptica	5	6	3	2x samples 3 days apart (2016), 2x samples 5 days apart (2016), 2x samples 1 day apart (2017)	6	3	Agree	Agree	
Elizabethkingia miricola	2	1	1	Two entries in the entire data set: one paed. from 6A, the other from someone in a different ward with DOB of 1936	1	1	Agree	Agree	
Elizabethkingia species	3	4	2	3x samples 5 days apart (2017)	3	2	Disagree	Agree	3x 2017
Enterobacter cancerogenus	4	1	1	Only one entry in the entire dataset	1	1	Agree	Agree	
Enterobacter cloacae	16	26	17		26	22	Agree	Disagree	1x 2016, 9x 2018, 5x 2019, 3x 2020, 4x 2021
Enterobacter cloacae complex	2	3	2		2	2	Disagree	Agree	1x 2018, 1x 2019

Organism	Mookerjee _original	Chaput		Notes re deduplication or counting errors	Mookerjee_latest		Agree/disagree with Dr. C Total count	Agree/disagree with Dr. C Dedup	Numbers by year: where yearly figures are presented without a following note on 'unique', the totals should be interpreted as unique infection counts
	Count	Total	Dedup.		Total	14-day Dedup			
Enterobacter cloacae ssp cloacae	16	18	12	2x samples same day (2016), 2x samples 1 day apart (2017), 2x samples 7 days apart (2017) , 4x samples in 4 days (2018)	17	13	Disagree	Disagree	1x 2016, 8x 2017 (6 unique), 7x 2018 (5 unique), 1x 2022
Enterobacter hormaechei	2	2	2		3	3	Disagree	Disagree	1x 2017, 1x 2018, 1x 2020
Klebsiella oxytoca	9	21	9		11	8	Disagree	Disagree	1x 2015, 5x 2016 (4 unique), 3x 2017 (2 unique), 2x 2018 (1 unque)
Klebsiella pneumoniae	22	33	23		38	30	Disagree	Disagree	11x 2016 (6 unique), 7x 2017, 8x 2018 (6 unique), 4x 2019 (3 unique), 2x 2020, 4x 2021, 2x 2022

Organism	Mookerjee _original	Chaput		Notes re deduplication or counting errors	Mookerjee_latest		Agree/disagree with Dr. C Total count	Agree/disagree with Dr. C Dedup	Numbers by year: where yearly figures are presented without a following note on 'unique', the totals should be interpreted as unique infection counts
	Count	Total	Dedup.		Total	14-day Dedup			
Pantoea species	1	4	3		4	3	Agree	Agree	
Pseudomonas aeruginosa	5	10	7		15	13	Disagree	Disagree	1x 2015, 1x 2017, 7x 2018 (5 unique), 2x 2019, 2x 2020, 2x 2022
Pseudomonas putida	4	7	5		7	5	Agree	Agree	
Pseudomonas stutzeri	2	1	1	Only one paed. entry in the entire dataset	1	1	Agree	Agree	
Rhizobium radiobacter	1	3	1		3	1	Agree	Agree	
Rhodotorula mucilaginosa	2	1	1	Only two entries in entire data set, the other has a DOB of 1956	1	1	Agree	Agree	
Roseomonas mucosa	1	1	1		1	1	Agree	Agree	
Serratia liquefaciens	1	1	1		1	1	Agree	Agree	
Serratia marcescens	9	8	4	2x samples within 2 days (2016) , 3x samples within 1 day (2017), 2x samples same day (2020)	7	6	Disagree	Disagree	2x 2016 (1 unique), 2x 2017, 1x 2019, 1x 2020, 1x 2021
Sphingomonas paucimobilis	1	1	1		1	1	Agree	Agree	
Stenotrophomonas maltophilia	14	34	18		32	21	Disagree	Disagree	1x 2016, 14x 2017 (7 unique), 10x 2018 (9 unique), 7x 2019 (4 unique)
TOTAL	**187**	**260**	**159**	Summary of duplicate samples: 1 in 2015, 13 in 2016, 9 in 2017, 9 in 2018, 2 in 2019, 1 in 2020, none in 2021-2022	**252**	**187**	Disagree	Disagree	

2.2.5. Table 2 below presents the SM 2025 incidence figures – SM Schiehallion unit wards combined BSIs (2025 figures), using which I re-calculated the yearly (2015 – 2022) rate of infection per 1000 admissions for the Schiehallion unit – SM Schiehallion unit wards combined rates / 1000 admissions (2025 figures), presented alongside the 2024 rate [4] – SM Schiehallion unit wards combined rates / 1000 admissions (2024 figures), each of the individual comparator hospitals' rates – GOSH, Cardiff and Vale, Leeds, Oxford infection rate / 1000 admissions by year, and the Overall comparator institution rate / 1000 admissions.

2.2.6. Note that in my current calculations – SM 2025 incidence figures, the Schiehallion unit wards combined BSIs figure remains at 187, albeit as a consequence of adjustments to better account for polymicrobial organism codes in the same blood culture result line and multiple organism codes for the same organism, the incidence figure for each year 2015 – 2022 varies slightly, e.g. infection incidence in 2017 drops from 66 to 62, but sees a rise in 2020 from 9 to 12. See paragraph 2.2.7 below for a detailed summary.

Table 2: Schiehallion unit infection rate comparison – SM 2024, Chaput 2025, SM 2025.

Year	GOSH infection rate / 1000 admissions by year	Cardiff and Vale infection rate / 1000 admissions by year	Leeds infection rate / 1000 admissions by year	Oxford infection rate / 1000 admissions by year	Overall comparator institution rate / 1000 adms	SM Schiehallion unit wards combined BSIs (2024 figures)	SM Schiehallion unit wards combined BSIs (2025 figures)	SM Schiehallion unit wards combined rates / 1000 admissions (2024 figures)	SM Schiehallion unit wards combined rates / 1000 admissions (2025 figures)
2015	11.39	3.08	No data	9.01	7.83	7	4	5.37	3.07
2016	10.84	5.43	1.19	9.18	6.66	27	25	11.92	11.03
2017	13.20	8.05	10.97	8.60	10.21	66	54	25.70	21.03
2018	7.27	7.11	13.16	7.88	8.85	44	50	17.48	19.86
2019	16.01	5.00	14.21	6.31	10.38	19	21	8.06	8.91
2020	14.93	7.14	7.88	3.61	8.39	9	12	5.87	7.83
2021	14.24	2.76	12.35	4.00	8.34	8	11	4.18	5.75
2022	7.92	3.71	5.82	5.07	5.63	7	10	3.59	5.13
Total						187	187		

[4] Bundle 21, Volume 1, Document 3, Page 71 at page 86

2.2.7. Here it is important to note the inherent facets of the infection dataset provided to me by NHS GGC in early 2024, which I found difficulty adjusting for:

- **Handling of polymicrobial positives**

  - The infection data I had access to had numerous instances of polymicrobial organism codes within a single cell of data under column headed ‘Organism(s) – coded values’. Of the 214,976 rows of infection data, polymicrobial results made up 7210 rows, of which 1455 rows detailed at least 3 separate organism codes in single cells e.g. CORSTR,STCAPR,STEPI,STRPAR, used to indicate 4 separate positive organisms from a particular blood culture.

  - In my initial analysis, the code I used to analyse the dataset tended to treat each row as a *single infection event*, with a reliance on the ‘Organism Full name’ column within the dataset to ensure all organisms were being accounted for.

  - In the revised approach, these cells were split so that each organism code was recognised as a distinct infection, with no reliance on the ‘Organism Full name’ the latter of which I now realise was misadjusting the final year on year figures.

- **Multiple codes representing the same organism**

  - Furthermore, the NHS GGC dataset consists of multiple organism codes for the same organism, with examples of the *same organism* being referred to using multiple distinct codes within the same row, and within the dataset more widely.
  - The revised organism-level parsing in my latest R code adjusted for these numerous organism codes more effectively. This is particularly important as the 14-day deduplication R code was recognising duplicate ‘sample collection – organism codes’ as unique, when in fact they were repeats.
  - Together, these differences in assumptions — whether to treat rows as single events or parse organisms individually, and how to handle multiple codes for the same organism — explain why my original deduplicated infection figures by year, are different to the ones calculated in my most recent analysis.
  - Note that the final 2015 – 2022 incidence figure remains the same, n = 187.

2.2.8. Figure 1 below provides a graphical illustration of the figures in Table 2.

Figure 1: Comparison of rate of infection per 1000 admission trends - SM 2024 and 2025 Schiehallion unit wards combined rates per 1000 admissions, versus Individual comparator institutions' rate and the Overall comparator institution:

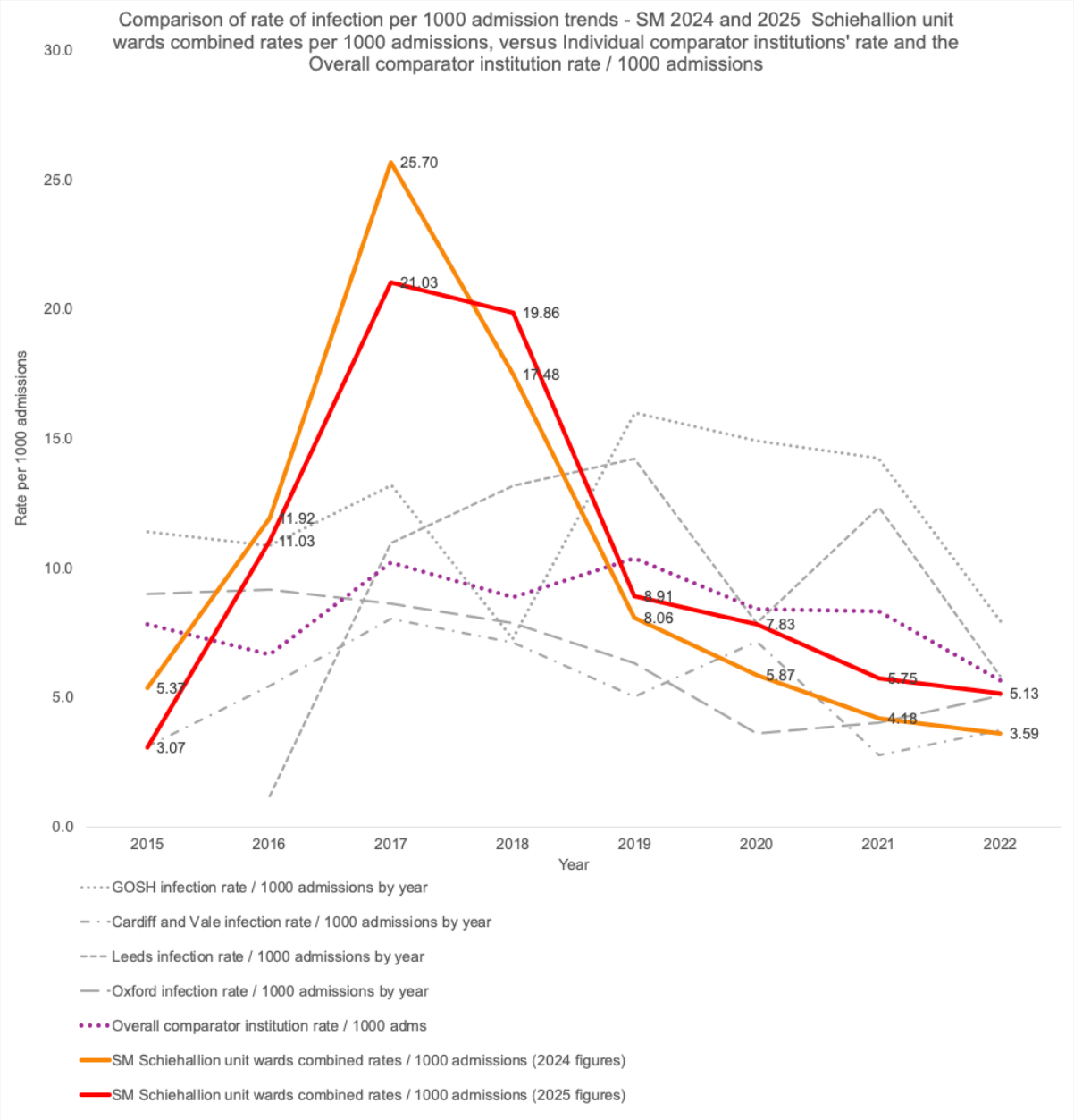


Table 3: Statistical significance and rate ratio calculations comparing SM Schiehallion unit wards combined rates / 1000 admissions to the Overall comparator institution rate / 1000 admissions for each year 2015 – 2022.

Year	Rate_ratio	CI_lower	CI_upper	p_value	SM Schiehallion unit rates (2025 figures) significantly (p value < 0.05) versus overall comparator institution rate	Summary of Rate_ratio
2015	0.5	0.11	1.87	0.39	No	Half of comparator
2016	1.9	0.69	5.50	0.26	No	Approx 2x more
2017	2.4	1.11	5.62	0.02	Yes	2.4x
2018	2.3	1.02	5.79	0.04	Yes	2.3x
2019	0.9	0.32	2.46	1.00	No	Equal to comparator
2020	1.0	0.33	3.06	1.00	No	Equal to comparator
2021	0.8	0.21	2.46	0.79	No	Equal to comparator

2022	1.0	0.27	3.74	1.00	No	Equal to comparator

2.2.9. Table 3 details the rate ratio calculations comparing SM Schiehallion unit wards combined rates / 1000 admissions to the Overall comparator institution rate / 1000 admissions for each year 2015 – 2022, the corresponding confidence intervals (CI upper and lower) around the rate ratio figure, the statistical significance p values, an explanation of p -values – whether or not the rate ratio difference calculated was statistically significant, and finally a summary of the rate ratio figures.

2.2.10. In keeping with previous analyses, 2016 – 2018 marks the period over which the Schiehallion unit rate sat at least 2-times higher than the overall comparator institution rate, with the difference in rates between the Schiehallion and overall comparator rate statistically significant ($p < 0.05$) for 2017 and 2018, followed by a period of levelling off to a rate similar to that of comparator institutions.

2.2.11. Finally I reference paragraph 2B.7, Glasgow 4 - Prof Peter Hawkey, Dr Lydia Drumright & Dr Samir Agrawal - Joint Response to 5 Reviews of HAD Report - 19 July 2025 [5], and I quote “When reflecting on the central analyses of our work, i.e. trends based on incidence rates, these differences in both numerator and denominator may shift the exact incidence rate slightly higher or lower than others’ assessments, but if case definitions (i.e., numerators) are applied the same across all months and years, then the trends should be similar across all datasets. Most importantly, fairly constant trends and jumps should be seen in the different datasets”. Dr. Drumright makes an important point regarding the important of focusing on the ‘trend’ of infections rate, in this case, with reference to Figure 1, the overall consistency in the overall comparator institutions’ rate of infection, compared to the drastic rise and fall, with a peak in 2017 and 2018 of the Schiehallion unit rate.

2.3. **In summary**

2.3.1. I am conscious of the limitations of FOI requests and the data acquired, but I also acknowledge the expertise of the large hospital Trusts in responding to SHI's request and the data in turn provided. It is in keeping with the gold standard in epidemiology that rates of infection at a unit are compared to like units across the spectrum to understand how they fit within the context of the regional and national rate. It is key to compare like with like, applying the same methodology across all calculated rates, something I have done throughout my analyses.

2.3.2. While I acknowledge variations in numerators and denominators across datasets, I am satisfied that the epidemiological gold standard has been upheld - namely, the use of repeated analyses to determine whether trends in infection remain consistent or diverge. Across all my Expert reports, current and previous analyses, the central finding is that the overall trend in infections -whether calculated using admissions or bed days - remains consistent, showing an upward trajectory between 2016 and 2018, followed by a decline.

[5] Bundle 44, Volume 5, Document 2, page 32

Supporting evidence - deduplication

Mr Mookerjee has repeatedly stated in written and oral evidence that GGC's infection rate is higher than that of the four comparator hospitals (GOSH, Leeds, Oxford, Cardiff and Vale). Dr Mumford relies heavily on Mr Mookerjee's calculations and repeats the claim that GGC's infection rate is higher than elsewhere in her original report, in her oral evidence, in her July 2025 report on the current risk level, and in her responses to the HAD report and to my report on the organisms present in the comparator data.

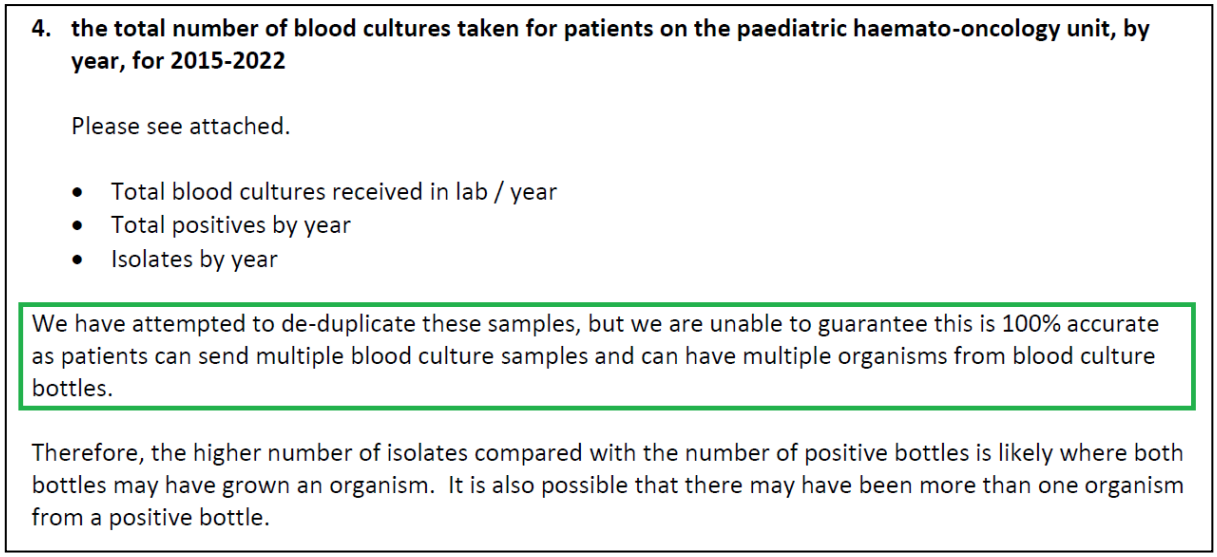
We have previously outlined serious concerns with how Mr Mookerjee analysed the infection and water microbiology data. Fundamental errors with denominators (admission numbers) have not been adequately addressed or resolved. In addition, my report on organisms present in the comparator data highlighted new flaws in the numerators (infection numbers), as it became apparent that, contrary to what Mr Mookerjee had claimed, not all sites had deduplicated their data. Dr Mumford must have been aware of these concerns when she wrote her latest reports, as I outlined issues with deduplication in my report on the comparator organisms. Despite this, she continued to rely on Mr Mookerjee's calculated infection rates, and her claim that GGC's rate is higher indicates that she believes these data are still comparable.

Below is supporting evidence for each comparator, with screenshots from the FOI returns that Mr Mookerjee and Dr Mumford analysed. The final section outlines new concerns over the infection numbers that Mr Mookerjee computed for GGC. I had not previously examined these in detail, as I had assumed that Mr Mookerjee had indeed deduplicated GGC's data as he claimed and had correctly added up GGC's case numbers. However, the errors that became apparent in his workings for GOSH prompted me to check the values for GGC, and similar counting and deduplication errors are apparent in GGC's data as well.

To be clear, these are not matters of debate, nor are they complex. The numbers are in the GGC blood culture spreadsheet and in the comparator FOI returns that have already been shared with the Inquiry, and I would urge the Inquiry to examine these documents for confirmation. I would be happy to assist with this if needed.

Cardiff and Vale

Cardiff and Vale returned a single table of microbiological results with a list of organisms in the first column followed by a single column of count data for each year 2015-2022. The FOI return states that data were deduplicated but does not confirm whether this was with a 14-day episode cutoff. Deduplication can also refer to the situation where a single blood sample is inoculated into two blood culture bottles and both return a positive result (i.e. two results per sample), or when two separate blood samples are collected at the same time, for example through two ports on a Hickman line, and both samples return a positive result.



4. the total number of blood cultures taken for patients on the paediatric haemato-oncology unit, by year, for 2015-2022

Please see attached.

- Total blood cultures received in lab / year
- Total positives by year
- Isolates by year

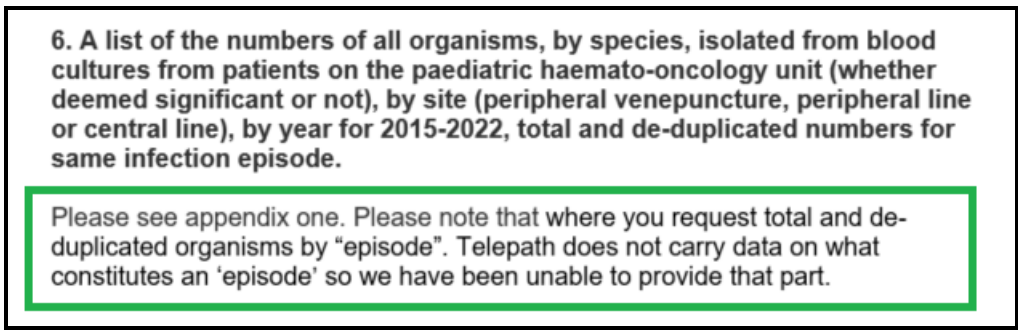
We have attempted to de-duplicate these samples, but we are unable to guarantee this is 100% accurate as patients can send multiple blood culture samples and can have multiple organisms from blood culture bottles.

Therefore, the higher number of isolates compared with the number of positive bottles is likely where both bottles may have grown an organism. It is also possible that there may have been more than one organism from a positive bottle.

Figure 1. Screenshot from Cardiff and Vale FOI return (Cardiff and Vale University Health Board - FOI.23.017 Noah's Ark Children's Hospital.pdf, page 1). Green box highlights the explanation of how data were deduplicated prior to preparing the agglomerated table.

Leeds

The FOI return from Leeds clearly states that the data have not been deduplicated at all, contrary to what Mr Mookerjee asserted in his reports and oral evidence. Leeds provided a single agglomerated table with one column of data per year, and this does not contain any of the information that would be required to carry out further deduplication.



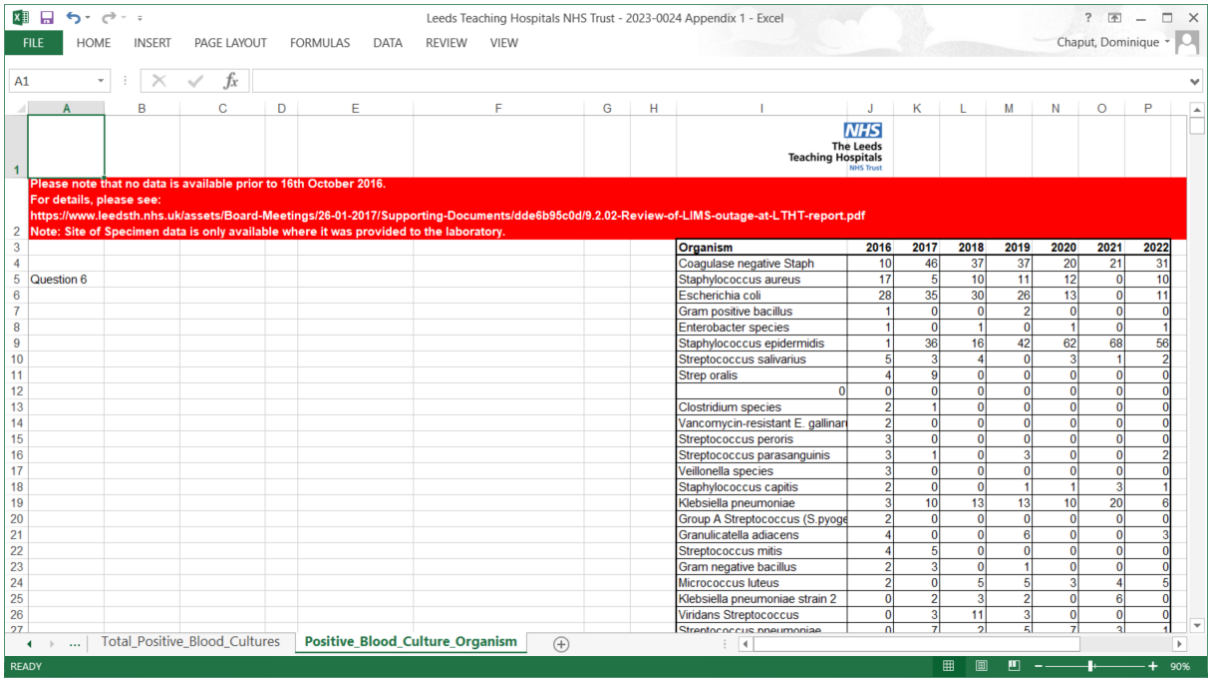
6. A list of the numbers of all organisms, by species, isolated from blood cultures from patients on the paediatric haemato-oncology unit (whether deemed significant or not), by site (peripheral venepuncture, peripheral line or central line), by year for 2015-2022, total and de-duplicated numbers for same infection episode.

Please see appendix one. Please note that where you request total and de-duplicated organisms by "episode". Telepath does not carry data on what constitutes an 'episode' so we have been unable to provide that part.

Figure 2. Screenshot from Leeds FOI return (Leeds Teaching Hospitals NHS Trust - 2023-0024 Paediatric Haematology.doc, page 2). Green box highlights the statement confirming that the infection data were not deduplicated.

An additional issue that does not appear to have been accounted for in Mr Mookerjee's analysis is that there are no microbiological results available for Leeds prior to October 2016. The Leeds FOI return was explicit about this, and it was clear that the data loss was restricted to the microbiology reporting system. Each worksheet with microbiology results from Leeds shows a red warning message at the top that states:

Please note that no data is available prior to 16th October 2016.
For details, please see:
https://www.leedsth.nhs.uk/assets/Board-Meetings/26-01-2017/Supporting-Documents/dde6b95c0d/9.2.02-Review-of-LIMS-outage-at-LTHT-report.pdf



Organism	2016	2017	2018	2019	2020	2021	2022
Coagulase negative Staph	10	46	37	37	20	21	31
Staphylococcus aureus	17	5	10	11	12	0	10
Escherichia coli	28	35	30	26	13	0	11
Gram positive bacillus	1	0	0	2	0	0	0
Enterobacter species	1	0	1	0	1	0	1
Staphylococcus epidermidis	1	36	16	42	62	68	56
Streptococcus salivarius	5	3	4	0	3	1	2
Strep oralis	4	9	0	0	0	0	0
0	0	0	0	0	0	0	0
Clostridium species	2	1	0	0	0	0	0
Vancomycin-resistant E. gallinar	2	0	0	0	0	0	0
Streptococcus peroris	3	0	0	0	0	0	0
Streptococcus parasanguinis	3	1	0	3	0	0	2
Veillonella species	3	0	0	0	0	0	0
Staphylococcus capitis	2	0	0	1	1	3	1
Klebsiella pneumoniae	3	10	13	13	10	20	6
Group A Streptococcus (S.pyoge	2	0	0	0	0	0	0
Granulicatella adiacens	4	0	0	6	0	0	3
Streptococcus mitis	4	5	0	0	0	0	0
Gram negative bacillus	2	3	0	1	0	0	0
Micrococcus luteus	2	0	5	5	3	4	5
Klebsiella pneumoniae strain 2	0	2	3	2	0	6	0
Viridans Streptococcus	0	3	11	3	0	0	0

Figure 3. Example microbiological data from Leeds with bold warning that data prior to Oct 2016 are not included.

The data loss did not extend to the admissions data, as admissions numbers were provided for all the years requested (2015-2022) and remained fairly consistent over this period.

2. The number of admissions to the paediatric haemato-oncology unit, by year, for 2015-2022

Count of admissions to unit	2015	2016	2017	2018	2019	2020	2021	2022	Grand Total
Total	5120	5892	5926	5851	5488	5839	5747	6352	46215

Figure 4. Screenshot of admission numbers from Leeds FOI return.

However, Mr Mookerjee calculated an annual infection rate for Leeds for 2016, and appears to have divided the number of infections seen only in the last 2.5 months by the total admissions for the entire year, which is not valid. He also includes this artificially low 2016 value for Leeds in the calculation of his 'overall comparator rate' for 2016.

Oxford

No details were provided in the FOI return about how data were deduplicated. The layout of the organism tables suggests that, if deduplication was carried out, it was after the results were grouped by sample site, as suggested by the similarity of organisms and counts for different sample sites in the same year. This would indicate incomplete deduplication, as it is not uncommon for samples to be collected separately from both ports on a Hickman line (red and white), and for both samples to then grow the same organism. There is no way to link results from one sample site to the other with these data so further deduplication is not possible.

A) 2018 'Red Port' table from Oxford FOI return (p.10)

2018

Site: Red Port

	Total
Total	13
ESCHERICHIA COLI	2
MORAXELLA CATARRHALIS	1
PSEUDOMONAS AERUGINOSA	3
STAPHYLOCOCCUS AUREUS	1
STAPHYLOCOCCUS EPIDERMIDIS(CoNS)	4
STREPTOCOCCUS MITIS	1
STREPTOCOCCUS VIRIDANS	1

B) 2018 'White Port' table from Oxford FOI return (p.11)

2018

Site: White Port

	Total
Total	13
ESCHERICHIA COLI	2
MORAXELLA CATARRHALIS	1
PSEUDOMONAS AERUGINOSA	2
STAPHYLOCOCCUS AUREUS	1
STAPHYLOCOCCUS EPIDERMIDIS(CoNS)	4
STREPTOCOCCUS MITIS	1
STREPTOCOCCUS PARASANGUINIS	1
STREPTOCOCCUS VIRIDANS	1

Figure 5. Screenshots from Oxford's FOI return (Oxford University Hospitals NHS Foundation Trust - F22-8462 FOI haemato-oncology unit. FOIA (RTH) OUH.pdf), showing similar organisms and counts from 'red port' and 'white port' samples from 2018.

GOSH

The data return from GOSH was the most detailed. It provided three columns of numbers: total positive samples (per sample site), total organisms (which accounts for the situation where both blood culture fluid bottles inoculated from a single sample grow the same organism), and episode totals deduplicated using a 14-day case definition (does not specify whether 14 days from first or latest sample). In short, the first column gives the total positive samples (no deduplication) while the third has been deduplicated by episode. If Mr Mookerjee had indeed used deduplicated data, he would have focused only on the third column.

yr	OrgName	SpecimenSource	Samples	TotalOrg	Episode14Day
2022	Acid Fast bacilli	Hickman, red	2	2	0
2022	Acid Fast bacilli	Hickman, white	1	1	0
2022	Acid Fast bacilli	Lumen, Red	1	1	1
2022	Acinetobacter baumannii	Blood, Central Line	1	1	1
2022	Acinetobacter baumannii	Hickman, red	2	2	2
2022	Acinetobacter sp.	Hickman, white	1	1	1
2022	Aerococcus sp.	Blood, Venous	1	1	1
2022	Aeromonas sp.	Peripheral	1	2	1
2022	Aeromonas sp.	Picc line, single	1	1	0
2022	Aeromonas sp.	Picc line, white	1	2	1
2022	Bacillus sp.	Blood, Venous	1	1	1
2022	Bacillus sp.	Hickman, red	1	1	1
2022	Bacillus sp.	Picc line, red	1	1	1
2022	Bacillus sp.	Picc line, single	1	1	1
2022	Candida albicans	Portacath	1	1	1
2022	Candida glabrata	Portacath	1	2	1
2022	Candida parapsilosis	Portacath	2	2	1
2022	Coagulase Negative Staphylococcus	Hickman, red	1	1	1

Figure 6. Example table from GOSH FOI return (Great Ormond Street Children's Hospital - FOIRQ7268 Final Response.pdf, page 4).

Dr Mumford helpfully included a table of Mr Mookerjee's workings in her rebuttal report, showing how he calculated the rates for GOSH. It is clear that Mr Mookerjee did not add up the cases correctly, as his numbers do not align with the totals from the third column. For example, he lists 4 cases of Aeromonas sp. in 2022. The original GOSH table above shows that there were three positive blood culture samples with this organism in 2022, with a total of five organisms (i.e. multiple positive bottles per sample), and that these amounted to two episodes (after deduplicating with a 14-day cutoff). Possible values are 2, 3, and 5 for this organism, depending on which column is used. Mookerjee's number is 4, which is not one of the options. It should be 2.

Another example: for Candida parapsilosis, he uses the total value (2) rather than the deduplicated value (1).

Row	Labels	Designation	2015	2016	2017	2018	2019	2020	2021	2022
Achromobacter	sp.	GN	4		6			2	1	
Acinetobacter	baumannii	GN								3
Acinetobacter	sp.	GN	2	2	1	1	1	7	3	1
Aeromonas	sp.	GN					2			4
Alcaligenes	sp.	GN							2	
Bacteriodes	stercoris	GN		1						
Bacteroides	fragilis	GN				3				
Bacteroides	sp.	GN							1	
Candida	albicans	Fungi	1	6	3		2			1
Candida	glabrata	Fungi	2	9					8	1
Candida	krusei	Fungi			9	2				
Candida	parapsilosis	Fungi	7		1			10	1	2
Candida	sp.	Fungi	7							
Candida	tropicalis	Fungi				1			2	
Capnocytophaga	sp.	GN					3			

Figure 7. Mr Mookerjee's workings for the GOSH infection data, from Dr Mumford's response report (Bundle 44 - Volume 4, page 25).

A quick check shows numerous other examples that would be easy for anyone with access to the GOSH FOI return to confirm. For instance, Mr Mookerjee shows 7 cases of Acinetobacter sp. in 2020, whereas the numbers on GOSH's spreadsheet are either 9 in total or 4 deduplicated cases. He lists 10 cases of Candida parapsilopsis in 2020, but this is the total count – the deduplicated count on the

GOSH spreadsheet is 1. Mr Mookerjee's numbers are neither entirely deduplicated nor entirely un-deduplicated. It is not clear how he has derived these numbers from GOSH's FOI return.

GGC

While the comparator hospitals provided agglomerated data that did not have the granularity required to carry out deduplication, GGC was different in that it shared the full list of blood culture results for the entire campus and for all patients, with entries for each individual sample, exact sample date, location, and patient identifiers (CHI, DOB) to allow deduplication. The spreadsheet for 2015-2022, called QEUH CAMPUS BLOOD CULTURE SAMPLES 1.1.15-31.12.22.xlsx - FINAL VERSION(BC QEUH CAMPUS 1.1.15-31.12.csv, contains 214,976 entries.

In his first Expert Report (Bundle 21 - Volume 1, pages 25-26), Mr Mookerjee lists the Gram negative bacterial and fungal species detected in the Schiehallion blood stream infection data, along with the number of cases. He states in his methodology section that counts were deduplicated using a 14-day episode definition.

Following concerns about errors in Mr Mookerjee's calculations for GOSH, I compared his GGC table to the full spreadsheet of blood culture results shared with the Inquiry. Table 1 shows the comparison of Mr Mookerjee's counts, which he claims were deduplicated, against the total and deduplicated counts that I obtained from the same data set. Coloured cells indicate discrepancies.

Table 1. Comparison of Mookerjee case numbers for GGC versus those computed by Chaput (total and deduplicated). Red cells show Mookerjee counting errors, orange cells indicate Mookerjee deduplication errors, and green cells show where Chaput identified more cases than Mookerjee.

Organism	Mookerjee	Chaput		Notes re deduplication or counting errors
	Count	Total	Dedup.	
Gram negative bacteria				
Achromobacter denitrificans	2	1	1	Four entries in the entire data set: 1 paed. from 6A, 2 paed. from emerg. dept, 1 adult (DOB 1932)
Achromobacter species	1	1	1	
Acinetobacter baumannii	10	5	4	Five Schiehal. samples in total, 2x samples 8 days apart (2016)
Acinetobacter baumannii complex	4	3	3	
Acinetobacter ursingii	9	10	5	4x samples 1 day apart (2016), 2x samples 2 days apart (2017), 2x samples same day (2018)
Aeromonas hydrophila/caviae	2	1	1	Five entries in the entire data set: 1 paed. from 2B, 4 adult (DOB 1936, 1943, 1969)
Brevundimonas species	1	1	1	
Burkholderia cepacia	1	1	1	
Burkholderia cepacia group	2	1	1	

Organism	Mookerjee	Chaput		Notes re deduplication or counting errors
	Count	Total	Dedup.	
Chryseobacterium species	1	1	1	
Chryseomonas indologenes	3	8	3	
Citrobacter braakii	2	1	1	Only one paed. sample in entire data set
Citrobacter freundii	2	2	2	
Citrobacter koseri	1	1	1	
Citrobacter youngae	2	2	1	2x samples 1 day apart (2017)
Cupriavidus pauculus	2	2	2	
Delftia acidovorans	4	3	3	
Elizabethkingia meningoseptica	5	6	3	2x samples 3 days apart (2016), 2x samples 5 days apart (2016), 2x samples 1 day apart (2017)
Elizabethkingia miricola	2	1	1	Two entries in the entire data set: one paed. from 6A, the other from someone in a different ward with DOB of 1936
Elizabethkingia species	3	4	2	3x samples 5 days apart (2017)
Enterobacter cancerogenus	4	1	1	Only one entry in the entire dataset
Enterobacter cloacae	16	26	17	
Enterobacter cloacae complex	2	3	2	
Enterobacter cloacae ssp cloacae	16	18	12	2x samples same day (2016), 2x samples 1 day apart (2017), 2x samples 7 days apart (2017) , 4x samples in 4 days (2018)
Enterobacter hormaechei	2	2	2	
Klebsiella oxytoca	9	21	9	
Klebsiella pneumoniae	22	33	23	
Pantoea species	1	4	3	
Pseudomonas aeruginosa	5	10	7	
Pseudomonas putida	4	7	5	
Pseudomonas stutzeri	2	1	1	Only one paed. entry in the entire dataset
Rhizobium radiobacter	1	3	1	
Roseomonas mucosa	1	1	1	
Serratia liquefaciens	1	1	1	
Serratia marcescens	9	8	4	2x samples within 2 days (2016) , 3x samples within 1 day (2017), 2x samples same day (2020)
Sphingomonas paucimobilis	1	1	1	

Organism	Mookerjee	Chaput		Notes re deduplication or counting errors
	Count	Total	Dedup.	
Stenotrophomonas maltophilia	14	34	18	
Fungi				
Candida albicans	10	14	6	2x samples in 2 days (2015), 3x samples in 5 days (2016), 3x samples in 1 day (2018), 4x samples in 5 days (2018)
Candida fermentati	1	1	1	
Candida parapsilosis	4	9	4	
Candida tropicalis	1	6	1	
Rhodotorula mucilaginosa	2	1	1	Only two entries in entire data set, the other has a DOB of 1956
TOTAL	187	260	159	Summary of duplicate samples: 1 in 2015, 13 in 2016, 9 in 2017, 9 in 2018, 2 in 2019, 1 in 2020, none in 2021-2022

As with the GOSH data, Mr Mookerjee appears to have made substantial errors in adding up and deduplicating GGC's data. His case total shows that he has attempted some form of deduplication, and for some organisms, his deduplicated numbers are consistent with mine. However, his final tally (187 infection episodes) is markedly higher than mine (159 infection episodes).

Of particular concern, the inflation of GGC's numbers from inadequate deduplication appears concentrated over the period 2016-2018, with 31 out of 35 duplicate samples having been taken during these three years. Furthermore, without seeing Mr Mookerjee's workings for GGC, it is impossible to tell whether the additional counting errors (indicated by red cells) show similar temporal clustering, and how these would impact on the supposed 'trend' in infections that he claims to have identified.

Conclusions

Mr Mookerjee has misunderstood or misrepresented the data from the comparator hospitals and from GGC. His calculations are invalid, and any conclusions that rely in whole or in part on his computed infection rates are unsafe.

GG&C Standard Operating Procedure:

WQS – 017

Procedures in the event of out of specification sample for Legionella, Pseudomonas and other monitored bacteria, fungi, moulds, yeasts etc.

References

1. Health and Safety at Work act 1974.
2. Management of Health and Safety at Work Regulations 1999.
3. Current approved code of practice L8 Legionnaires Disease : The control of legionella Bacteria in Water Systems.
4. COSHH Regulations (1999).
5. SHTM 04-01 Water Safety for Healthcare Premises.
6. Risk Assessments for specific sites.
7. Written Scheme for specific sites.
8. Water Systems Log Books.
9. Water Incident Report Form (Record Form 04)

Sampling Frequency and details

1. NHS utilises external service providers to carry out sampling and monitoring of the water systems and carry out sampling within the specific locations. These are sent to the Labs noted above for analysis and results are results are sent to the Water Service Provider (**WSP**) who then send the results to the respective site contacts in Estates, **Infection Control** and Microbiology . In some cases Water Service Provider will supply this in a form of sampling matrix (spreadsheet) detailing out of specification and within specification.

Site	Area	Frequency	Number of samples	Processing Site	Analysis	Water Service Provider (WSP)	Distribution List for results
RHC	Ward 1D PICU	Weekly	*¼ of outlets sampled weekly on rotational basis Approximately 12 Samples*	GRI	Potable, Pseudomonas, GNB AMS on ¼ of samples each month (rotating) Water Temperature & CLO2 level.	DMA	Operational Estates Medicine Diagnostics Microbiology
RHC	**Hydrotherapy Pool**	Weekly	*1 Sample weekly. Pool sampled daily for chlorine, temperature and pH*	GRI	**Pool Water** - TVC, E-Coli, Coliform, Pseudomonas, Temperature, PH, Free Chlorine	Physio-therapist	Physiotherapists
QEUH	**Critical Care Areas** (Adults 1st HDU, CCW, 4A, 4B, 4C, 4D, 7A, 7D)	Monthly	*Approximately 74 Samples*	GRI	Legionella, TVC, E-Coli, Coliform, Pseudomonas Water Temperature, CLO2 level.	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**A&C** CWSTs & Filter Units	Monthly	*Samples taken from Dips & Drains from 4 off raw tanks, 3 Filtration units x 3 sample points and 4 off bulk filtrate tank Dips and Drains Approximately 38 Samples*	GRI	Legionella, TVC, E-Coli, Coliform, Pseudomonas GNB SAB, Temperature, CL02	DMA	Operational Estates Medicine Diagnostics Microbiology

Site	Area	Frequency	Number of samples	Processing Site	Analysis	Water Service Provider (WSP)	Distribution List for results
QEUH/RHC	Sentinel Outlets (Basement, Adult Ground Floor A&E, OPD, Acute 1st Floor Critical Care, 2nd Floor Theatres, 2nd Floor Endoscopy , 2nd Floor Medical Physics, 5A,5B,5C,5D, 6C, 8A, 8B, 8D, 9C, 11A, 11B,11C,11D. RHC Ground Floor Concourse, CDU, Theatres, 1C,1E, 2C,3A,3B,3C,3D)	Monthly	*Approximately 142 Samples*	Intertek	Legionella, TVC, E-Coli, Coliform, Pseudomonas, SAB Water Temperature (for CL02) & CLO2 level.	DMA	Operational Estates Medicine Diagnostics Microbiology
RHC	Clinic 1 & 2 RHC	Monthly	*Approximately 50 Samples*	GRI	Legionella, TVC, E-Coli, Coliform, Pseudomonas, GNB, SAB, AMS Water Temperature (for CL02) & CLO2 level.	DMA	Operational Estates Medicine Diagnostics Microbiology
RHC	Ward 2A & 2B	Weekly	¼ of outlets sampled weekly on rotational basis *Approximately 140 Samples*	GRI	TVC, E-Coli, Coliform, Pseudomonas, GNB AMS on ¼ of samples each month (rotating) Water Temperature & CLO2 level.	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Neurosurgery**	Quarterly	*Approximately 40 Legionella & 10 Potable Samples*	GRI	Legionella, TVC, E-Coli, Coliform, temperature, CLO2 level.	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Neurosurgery**	6 Monthly	*Approximately 8 Pseudomonas Samples*	GRI	Pseudomonas, temperature, CLO2 level.	DMA	Operational Estates Medicine Diagnostics Microbiology

Site	Area	Frequency	Sample size	Processing Site	Analysis	Water Service Provider (WSP)	Distribution List for results
QEUH	**Neurology**	Quarterly	*Approximately 20 Legionella & 6 Potable Samples*	GRI	Legionella, TVC, E-Coli, Coliform, temperature, CLO2 level.	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Maternity**	Quarterly	*Approximately 40 Legionella & 10 Potable Samples*	GRI	Legionella, TVC, E-Coli, Coliform, temperature, CLO2 level.	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Neo-Natal (New Maternity)**	Quarterly	*Approximately 22 Legionella & 8 Potable Samples*	GRI	Legionella TVC, E-Coli, Coliform, temperature & Pseudomonas	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**PDRU**	Quarterly	*Approximately 12 Legionella & 6 Potable Samples*	GRI	Legionella TVC, E-Coli, Coliform, temperature	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Spinal**	Quarterly	*Approximately 20 Legionella & 8 Potable Samples*	GRI	Legionella, TVC, E-Coli, Coliform, temperature	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Spinal**	6 Monthly	*Approximately 8 Pseudomonas Samples*	GRI	Pseudomonas, temperature.	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Spinal Hydrotherapy Pool**	Weekly	*1 Potable Sample and 1 Pseudomonas*	GRI	TVC, E-Coli, Coliform, Pseudomonas, Temperature, PH, Free Chlorine	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Westmarc**	Quarterly	*Approximately 12 Legionella & 6 Potable Samples*	GRI	Legionella, TVC, E-Coli, Coliform, temperature	DMA	Operational Estates Medicine Diagnostics Microbiology

Site	Area	Frequency	Sample size	Processing Site	Analysis	Water Service Provider (WSP)	Distribution List for results
QEUH	**Podiatry**	Quarterly	*Approximately 10 Legionella & 6 Potable Samples*	GRI	Legionella, TVC, E-Coli, Coliform, temperature	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**ICE Building**	Quarterly	*Approximately 79 Legionella & 7 Potable Samples*	GRI	Legionella, TVC, E-Coli, Coliform, temperature, CL02 level.	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Office Block**	Quarterly	*Approximately 15 Legionella & 7 Potable Samples*	GRI	Legionella, TVC, E-Coli, Coliform, temperature	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**Teaching and Learning**	Quarterly	*Approximately 19 Legionella & 6 Potable Samples*	GRI	Legionella, TVC, E-Coli, Coliform, temperature	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**NICU**	Monthly	*Approximately 4 Legionella, 4 Pseudomonas & 4 Potable Samples from Belfast sinks (pre POU filter)*	GRI	Legionella, Potable, Pseudomonas, Water temperature	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**CMB**	Quarterly	*Approximately 10 Legionella & 2 Potable Samples*	GRI	Legionella, Potable, Water temperature	DMA	Operational Estates Medicine Diagnostics Microbiology
QEUH	**MIU**	Quarterly	*Approximately 8 Legionella, 8 Pseudomonas & 8 Potable Samples*	GRI	Legionella, Potable, Pseudomonas, Water temperature	DMA	Operational Estates Medicine Diagnostics Microbiology

Out of specification Process

1. A spreadsheet is sent to the NHS from the Water Service Provider **(WSP)** highlighting all of the results and any out of spec results. This will be sent as soon as practicable on discovery of out of spec results. In the event of any serious issues the **WSP** would make contact with the Lead Authorised Person (**LAP**) immediately on any serious issues e.g. LP1.
2. A **Microbiologist** at GRI Labs or other Labs should also contact the **LAP** immediately based on any serious issues e.g. Legionella LP1 / Pseudomonas in high risk areas and agree to take immediate action e.g. outlet out of use. **Microbiologist** will also discuss with **Infection Control** on whether patients should be moved and outlets put out of use.
3. If any results are found to be out of spec an SHTM Compliant Incident Report form (004) **Appendix 1** is completed and recorded on the Incident Log by the **LAP**. The incident report lists the issue (work request number) and on completion is signed off by the allocated resource and **LAP**.
4. The **LAP** will then extract the information to the out of spec summary spreadsheet which list the same information from the analysis from the **WSP** however also lists all actions taken and history of that specific outlet.
5. The Water Competent Person (**CP**) allocated the work request will carry out the works and complete the job on their PDA. The **LAP** will then update the out of spec summary sheet with any actions and date that the work request was completed.
6. In specific circumstances the **LAP** may discuss with :-
    a. **Infection Control**, regarding operating protocols and including but not limited to the cleaning and flushing regime or adding to the Wards little used outlet and flushing regime and to review with Wards.
    b. **Facilities** to review cleaning and flushing regimes.
    c. **Microbiology** to review any other any necessary actions.
7. Additionally in some cases the **LAP** may request the approved **CP** or **WSP** to add additional flushing.
8. Monthly minuted meetings are also carried out by Estates and Microbiology to review out of spec, discuss actions, risks and which may also visits to areas.

Resampling

1. When out of spec results are identified, **CP** or **WSP** will carry out sampling of that outlet until a minimum of **3** not detected are obtained.
2. After further re-sampling additional information will be added to the out of spec summary and on receiving a 'not detected' or 'within parameters' result the record will be moved to the second tab on the spreadsheet which lists all previous 'not detected/within parameters' results.
3. If however further results are found to be out of spec the record is extracted and placed in the 'out of spec' tab.
4. Guidance also indicates that legionella samples <100 cfu/L **must** be investigated and resampled.
5. The spreadsheet is then uploaded to a team folder regularly for access by Estates Management, Infection Control and Microbiology. However a short summary of current out of specs should be sent regularly by the **LAP** summarising current out of specs.
6. Results are presented in a form of report to the Water Safety Group and through appropriate governance (Sector Facilities/Infection Control Group Meetings).

Out of Specification on Point of use filters

I. When out of spec results are identified on Point of use filters, **WSP** will automatically change the filters and re-sample as above.

Sampling Standards

Table below indicates sampling type and sample size

Type	Sample size
TVC@37c	Cfu/ml
TVC @ 22°C	Cfu/ml
Coliform	Cfu/100ml
E.coli	Cfu/100ml
Legionella cfu/L	Cfu/l
Pseudomonas	Cfu/100ml
SAB@30c	Cfu/ml
Mould@25c	Cfu/ml
SAB@22c	Cfu/ml
Yeast@25c	Cfu/ml
Cuprivadis	Cfu/100ml
AMS	Cfu/100ml
GNB	Cfu/100ml

Water Sampling Out of specification definition

Water supplied by Scottish Water to must meet the wholesomeness standards outlined in The Public Water Supplies (Scotland) Regulations 20141.
Water must not contain :-

- **(i)** Any micro-organism,
- **(ii)** Any substance, or
- **(iii)** Any parasite at a concentration or value which would (whether in conjunction with another parameter in the water or otherwise) constitute a potential danger to human health'

Public water supplies undergo routine testing for total viable counts at 22 and 37°C, which give an indication of overall microbial load but do not have pre-defined thresholds that must be met.

However supplied water has more specific tests carried out to indicate faecal contamination :-

- Coliforms
- Escherichia coli
- Clostridium perfringens

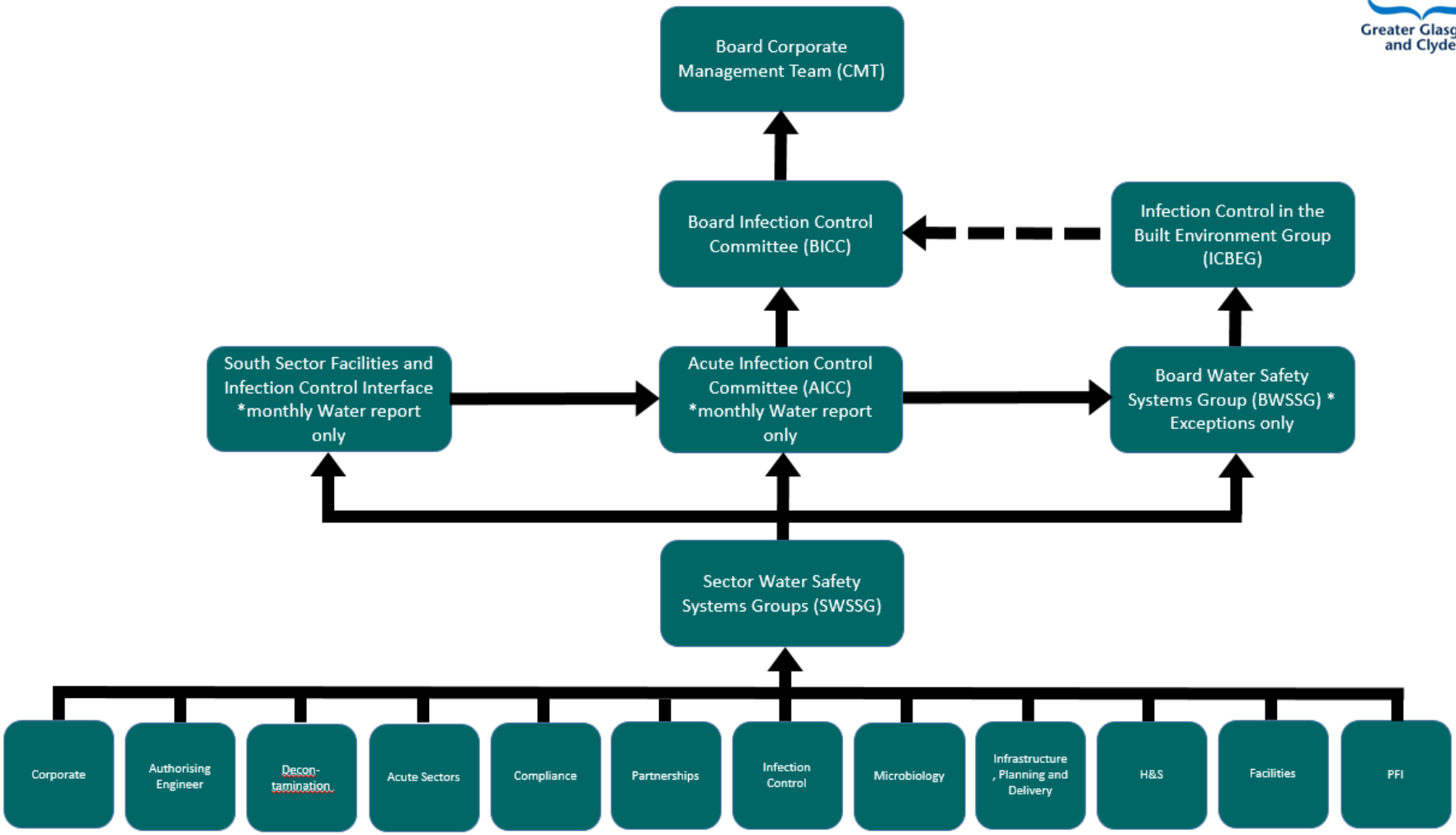
These tests have strict thresholds (zero counts per 100ml) that must be met for the water to be considered wholesome.

Taking this into consideration Microbiology and Operational Estates agreed the following definitions for water monitoring at the QEUH and this is reflected on the sample results to highlight out of specs.

Type	Sample size	Comment
TVC@37c	Acceptable levels out with high risk areas are **< 100** Cfu/ml:	If levels are >100 CFU/ml, lab should identify the recurring bacteria. In the event of patient infections with suspected links to water ICD may request identification at levels <100 CFU/ml.
TVC@37c	In high risk areas as defined by NHSGGC Pseudomonas risk assessment TVCs should be **<10** Cfu /ml	If >10 CFU/ml Lab should identify the recurring bacteria. In the event of patient infections with suspected links to water ICD may request identification at levels <10 CFU/ml via PAG/IMT.
TVC @ 22°C	Acceptable levels out with high risk areas are **< 100** Cfu /ml:	If levels are >100 CFU/ml, lab should identify the recurring bacteria. In the event of patient infections with suspected links to water ICD may request identification at levels <100 CFU/ml.
TVC @ 22°C	In high risk areas as defined by NHSGGC Pseudomonas risk assessment TVCs should be **<10** Cfu /ml	If >10 CFU/ml Lab should identify the recurring bacteria. In the event of patient infections with suspected links to water ICD may request identification at levels <10 CFU/ml via PAG/IMT.
Coliform	**Zero** Cfu /100ml	As per Scottish Water Guidance
E.coli	**Zero** Cfu /100ml	As per Scottish Water Guidance
Legionella	**<50** Cfu /l	Any legionella positives as an out of spec from all serogroups (1 – Pneumophila) and (2-14 – Other) regardless of CFU.
Pseudomonas	**< 10** Cfu /100ml in general areas	As per Pseudomonas Guidance
Pseudomonas	**Zero** Cfu/100ml in Augmented care	Bone Marrow Transplant Units, Haemato-Oncology and Neonatal Units, and any other care areas where patients are severely immunosuppressed through disease or treatment. Critical and intensive care units (neonatal, paediatric and adult), renal units, and respiratory units (including Cystic Fibrosis patient care units). Burns units and other care areas where patients have extensive breaches in their dermal integrity.
SAB@30c	**<10** Cfu/100ml	Treated as an out of spec in the absence of any National guidance.
Mould@25c	**<10** Cfu/100ml	Treated as an out of spec in the absence of any National guidance.
SAB@22c	**<10**Cfu/100ml	Treated as an out of spec in the absence of any National guidance.
Yeast@25c	**<10** Cfu/100ml	Treated as an out of spec in the absence of any National guidance.
Cuprivadis	**Zero** Cfu/100ml	Treated as an out of spec in the absence of any National guidance.
AMS	**Zero** Cfu/100ml	Any found in any area are treated as an out of spec in the absence of any National guidance.
GNB	**Zero** Cfu/100ml	Any found in any area are treated as an out of spec in the absence of any National guidance.

Reference Pseudomonas guidance document **Appendix 2**

Governance Water Management – GG&C



Appendix 1 Incident Form

004 Incident Record Form BLANK 2023.pc

Appendix 2 Pseudomonas Guidance

Item 9.4 - RA Pseudomonas 2023.

Bundle of documents for Oral hearings commencing from 19 August 2025 in relation to the Queen Elizabeth University Hospital and the Royal Hospital for Children, Glasgow

Bundle 44 – Volume 9

Expert Report by Sid Mookerjee dated 20 August 2025 in response to Note by Dominique Chaput and Miscellaneous Documents

A53874814