Supplemental Statement by Professor Alistair Leanord in response to questions from the Inquiry

1. The report was instructed by the Central Legal Office. The report was to:

   "provide a detailed description of the nature of the samples that are, and are not, available for whole genome sequencing (WGS) to be carried out, in terms of the paediatric oncology patient group and the environment (including water and drainage) within the Queen Elizabeth University Hospital (QEUH) and Royal Hospital for Children (RHC) where they were treated from 2015 to 2020".

   "undertake WGS of the organisms identified on these available samples and the spectrum of heterogeneity identified compared with expected population heterogeneity".

   "analyse the results of the WGS and provide your opinion on whether these results demonstrate evidence that would or would not support:

   a. Transmission from the environment to the patient.

   b. Transmission from patient to patient.

   c. Transmission from patient to environment".

2. The report was co-authored with Derek Brown, who is a Clinical Scientist working in the Scottish Microbiology Reference Laboratory, Glasgow. He has expertise and experience in whole genome sequencing (WGS). Mr Brown has the technical and scientific expertise to extract, sequence, analyse the outputs of the sequencing, and to construct the necessary dendrograms and distance matrixes required for analysis. Mr Brown wrote the first technical draft and I co-authored the report with the clinical significance and the conclusions of those results.

3. The finalised report was sent to the Central Legal Office. NHSGGC was aware of earlier iterations of the data, which had been presented to the Paediatric Haematologists. This formed part of the response to the concern that transmission of environmental organisms was occurring in the QEUH and RHC.

4. The analysis of the *Cupriavidus* species was supported by a research grant from NHS Assure. NHS Assure received a report that included an analysis of the *Cupriviadus* data.

5. We used sequencing in the autumn of 2019 to inform the IMT. I became a member of the IMT from 13 September 2019. Having had no prior exposure to the IMT, or the information it had been dealing with, my initial impression was that a range of Gram-negative organisms were being attributed to the environment at the QEUH/RHC, many of which could be of an endogenous nature (i.e. coming from the patient's own body flora). After discussions with the Clinical Scientists at the Scottish Microbiology Reference Laboratory, Glasgow, we felt that we could use our expertise in WGS to attempt to see if there were any direct relationships between the organisms found in the environment and the patient's organisms.

6. At this time discussions started around how NHSGGC could resume a normal Paediatric transplant service. The concerns from the Clinicians was that infections in these immunosuppressed patients would continue to occur, and how could there be confidence that those infections did not arise from the hospital environment. I was aware that we could use WGS to try and understand the dynamics of some of these organisms, helping the IMT understand the relationship of past infections (thus helping it to rule in or out any ongoing hypothesis about the source of infections) and importantly to be able to look at any new infections in patients, and show if there was a possibility of a direct transmission event from the hospital environment.

7. Initially we took *Enterobacter* as the first organism to be sequenced. This was because of a SBAR dated 07 October 2019 that was presented at an IMT on 08 October 2019 which showed an increase in E*nterobacter* infections from 2016-2019 to date. *Enterobacter* was also the second most common organism isolated from the clinical cases. Lastly, we had a sequencing pipeline for Gram-negative organisms that we felt we could adapt to produce an answer reasonably quickly.

8. In a retrospective study like this it is only possible to use organisms that have been identified and stored from previous years. We had to identify firstly what

organisms had been stored and then try and retrieve those organisms from freezers and attempt to culture them. We used Telepath, which is the laboratory data system, to identify all *Enterobacter cloacae* from paediatric cases within the RHC over the time period 2015 to 2019 and seven human clinical isolates from GRI from Jan to Sep 2019. We identified if any had been stored and looked for the stored isolates and attempted to culture them. Once cultured, we extracted the DNA and sequenced the organisms. The isolates that were sequenced from Glasgow Royal Infirmary were included to act as a comparison to the RHC population of *Enterobacters*.

9. There is no other methodology that can be used when using stored organisms. In effect, serendipity plays a large part in these look back exercises. WGS was not performed in real time during the period of concern. Other typing methods, as delivered by the UKHSA Reference Laboratories Colindale, were used to identify possible transmission during the period. WGS is not a routinely used diagnostic typing method due to cost, complexity, and the specialist expertise and equipment required. WGS has the highest discriminatory ability available and is predominantly a typing tool used in Reference Centres for typing some organisms e.g. *Salmonella* where Public Health is an issue or used in University departments for research purposes. All the WGS was undertaken retrospectively from October 2019 to 2022 at the Scottish Microbiology Reference Laboratory, Glasgow, using their expertise and specialist equipment. See para 31-35 for further details on typing methods.

10. There is no routine service for sequencing environmental or clinical isolates outwith the criteria dictated by National Services Scotland(NSS). Currently organisms *Salmonella*, *Shigella*, *Neisseria meningiditis* and *Streptococcus pneumomiae* are routinely sequenced in the Scottish Microbiology Reference Laboratory, Glasgow which is part of the National Reference Laboratory service, as a UKAS accredited service.

11. At the IMT on the 05 November 2019 I reported the finding from the initial set of *Enterobacter* sequencing, which showed that “first analysis of WGS shows no relatedness in *Enterobacters* by case definition, ward or year”. My conclusion at the time, as it still is, is that there was no evidence that the

Enterobacter infections were related, or that the WGS confirmed a common source for these infections. The balance of probabilities points to the conclusion that these infections were endogenous and originated from the patient's own microbial flora.

12. There are approximately 40 trillion bacteria and 37 trillion human cells in the average human. We have more bacteria than cells. Many infections originate from the body's own resident bacteria.

13. From 2020 to 2022 we collected organisms that were identified as causing the largest number of clinical cases. We required enough organisms to be stored such that there were enough representatives that could be sequenced to form an opinion about their heterogeneity and population size, such that we could form an opinion about the probability that they were related to each other or environmental sources.

14. On the basis that there were a sufficient number of clinical cases, sufficient environmental samples and sufficient isolates stored and cultured, we sequenced three genera; *Stenotrophomonas maltophilia*, *Enterobacter* species, and *Cupriavidus* species. All isolates of these genera available to us were collected. In the case of *Stenotrophomonas maltophilia*, this was broken down as 25 human clinical isolates (23 from QEUH/RHC, one from Royal Alexandra Hospital (RAH), and one from Victoria Ambulatory Care Hospital (VIC ACH) collected between June 2015 and June 2020. Water and environmental isolates were collected from QEUH/RHC (n=56) and RAH (n=3) between Mar 2018 and Feb 2020 (Jul 2020 for two RAH samples). In the case of *Enterobacter* species a total of 42 isolates available to us (seven human clinical isolates from GRI from Jan to Sep 2019; six environmental isolates from QEUH/RHC from 2018/19; 29 human clinical isolates from 24 patients from QEUH/RHC between Jan 2016 and Jul 2019) identified by the diagnostic laboratory as *E. cloacae* were sequenced. In the case of *Cupriavidus* species the vast majority of isolates that were available to sequence were collected from RHC, and from Ward 6A in QEUH whilst the ward was being used for paediatric cases. There were a couple of isolates collected from Ward 4A and 4B (adult haemato-oncology and transplant unit) and from the basement tanks and plant rooms situated within QEUH. There

was one *Cupriavidus* isolate from the VIC ACH. There were 28 *Cupriavidus metallidurans,* three of which came from another Health Board.

15. We also sequenced four of the ten cases of *Pseudomonas* (three *Ps. aeruginosa*, one *Ps. putida*) infection in the paediatric haemato-oncology population that were of interest. This illustrates that we can only sequence what has been stored and that can be cultured after minus 80 degree storage. These numbers of *Pseudomonas* are too low on which to base any conclusion except to say that all the three *Ps. aeruginosa* from clinical infections were genetically distinct and not related.

16. The data from WGS shows that each genus sequenced has distinct epidemiology that is reflected in the genetic profiles that differentiate each genus from each other.

17. *Stenotrophomonas maltophilia* has a population that is very heterogenous. Overall, the population of *S. maltophilia* seen in patients and the environment in the QEUH/RHC reflects the global population of *S. maltophilia*. There are representatives of every known global subtype of *S. maltophilia* within QEUH/RHC. There is nothing unique about *S. maltophilia* infections within the hospitals, it reflects the global picture of *S. maltophilia* found in nature. More specifically the subtypes of *S. maltophilia* also reflect the subtypes of *S. maltophilia* globally. We see in the hospital subtypes (clades or “families”) of *S. maltophilia* that are seen only in the environment and not in patients. This is probably as a result of these subtypes being optimised to exist and multiply in the low nutrient environment of a water system and do not have the virulence genes required to cause an infection within the body. We see in the QEUH/RHC a reflection of the global pattern of *S. maltophilia* where we see the same subtypes that can infect patients. These subtypes of *S. maltophilia,* by inference, carry a different set of genes, that include virulence genes that their environmental only cousins do not carry. Therefore, all *S. maltophilia* do not seem to be equal, some strains are able to infect patients, and some do not seem able to infect patients. This to me is an important distinction that requires more research to understand the risk that an isolate of *S. maltophilia* from the environment may represent to a patient. The risk of infection to a

patient is therefore the product of the degree of immunosuppression within the patient and the subtype of any potential infecting *S. maltophilia*.

18. It is hard to know how long a *S. maltophilia* can colonise a water outlet for. This is a direct result of the Estates policy of flushing, removing, and cleaning outlets with the subsequent requirement of needing three negative samples before an outlet can be put back into use. Thus, we have in almost all instances only single isolates from an outlet. This is not the case in the basement water tanks, where it is not possible to remove any of the nine sampling points in the basement filters. These sampling points are cleaned if positive but cannot be removed. We see in this instance a population of very close genetic relationship being present over several months. This population, although long lasting does change over time (months), being superseded by a different but again, very closely related strain.

19. One of the concerns with working with stored isolates is how representative is the isolate that has been individually picked from the original culture plate from what could be possibly tens of individual colonies, stored and then on subsequent reculturing, again only one colony is picked for sequencing. To answer this, we sequenced all the isolates of *S. maltophilia* from a primary water sample and found that they were genetically homogenous with differences of 25 or less single nucleotide polymorphisms (SNPs) between them. We have performed the same experiment with a primary culture of *Cupriaviadus* and found a similar close genetic homogeneity within the primary sample plate. In my opinion, these experiments show that although the overall population of the species is very heterogenous, within a single sample the organisms cultured are clonal and genetically very closely related.

20. In my opinion these factors tell us three things about *S. maltophilia*:

    - Firstly, a colonised outlet will have a stable strain associated with that outlet, which will be present over a period of weeks to months if the outlet is not able to be cleaned and removed

    - Secondly, although the population of environmental organisms is heterogenous, all possible members of that population do not colonise

that outlet once the outlet has its resident strain, so it appears there is strain exclusivity to an outlet once it is established

- Thirdly, that *S. maltophilia* must be present in the mains water supplies from Govan Road and/or Hardgate Road for the organism to be present in the prefilter sampling points in the basement tank room.

21. WGS of *Cupriavidus* species identified a range of non-Cupriavidus species which had been misidentified. The diagnostic laboratory identified, reported and stored the isolates as *Cupriavidus pauculus*, *Cupriavidus gilardii* or *Cupriavidus* species. Of the 155 isolates recovered, 138 of them were members of the *Cupriavidus* genus (five different species) and 17 organisms were from other genera. Misidentification of environmental isolates by conventional methods used within a diagnostic Medical Microbiology laboratory is not surprising. The identification method used in a Medical Microbiology laboratory would not be expected to be able to identify many environmental Gram-negative organisms. This is because the database used to identify organisms does not have many, or in some cases any, type strain environmental representatives in them. Also, it is clear from the sequencing data that the populations of environmental organisms are very heterogeneous with large genetic differences between members of the same species such that a single type strain may not be representative of the population as a whole.

22. WGS showed that species of *Cupriavidus* form stable low diversity populations within the water system. *C. pauculus* formed three clades (“families”) that were stable across all three floors of RHC over a three year period.

23. One clinical isolate from 2016 co-located with one of the environmental clades which had representatives in it from 2018 onwards. This isolate has been linked to a sink in the Aseptic Pharmacy Unit in RHC. Whereas we can exclude any environmental link with any of the contemporaneous *Cupriavidus pauculus* clinical infections, we cannot exclude the possibility that this 2016 case is linked to the environment as we have no contemporaneous strains with which to compare it.

24. Bacteria are like small biological clocks. They will mutate their DNA in a predictable fashion such that differences in Single-nucleotide polymorphisms (SNPs) can record the time period over which two organisms genetically diverged. Looking at the time difference of approximately two years between the environmental isolates collected in 2018 and the clinical isolate in 2016 it is possible that the clinical isolate could be an ancestor of any of four environmental isolates taken two years later.

25. The case of *C. metallidurans* shows strong evidence of a clinical link between the patient and the water system. This result was seen in samples taken from another Health Board. It does illustrate the ability of WGS to make a link between a clinical isolate in the patient and the environmental isolates which are resident within the water system.

26. *Enterobacter cloacae* was identified by the diagnostic laboratory and stored. On sequencing, these isolates formed nine different *Enterobacter* species or subtypes, all recognised taxonomically as members of the *Enterobacter cloacae* complex. Each species or subtype grouped in species level clustering. The reason for the misidentification within the diagnostic microbiology laboratory is described above in para 21. The important point with misidentification is that using standard diagnostic identification methods it may look to a Clinician or Medical Microbiologist that there is an increase in a particular organism, whereas the reality is that this increase can be made up a of several different genera and species with no linkage to each other.

27. *Enterobacter* species cluster within species. *Enterobacter* species are recognised to be part of normal human bacterial flora (enteron = intestine, bakterion = small rod). Analysis of a possible environmental source in the QEUH/RHC was hampered by the low isolation frequency of *Enterobacter* species from the potable water tested. Using WGS there was no common genetic link between any of the *Enterobacter* isolates, all were genetically distinct. On the balance of probabilities there is no linkage between *Enterobacter* infections and the hospital environment. There is no evidence of a common source outbreak. *Enterobacter* species were isolated from the hospital potable water on 6 occasions over 2015-2020 out of 10,311 (excluding Legionella) water tests taken over this period. *Enterobacter*

species were not isolated from samples taken from wards 2A/2B. On the balance of probability, it is my opinion that *Enterobacter* infections are sporadic endogenous infections originating from organisms carried in the patient's intestine which are able to translocate across the intestinal wall and enter the patient's blood stream to cause a bacteraemia. In my opinion the paucity of *Enterobacter* species within the potable water system makes the environment an unlikely source for infections.

28. The genetic diversity within the populations of *C. pauculus* and *S. maltophilia* is not a reflection of the number of samples taken but reflects the genetic heterogeneity within the species. This is a product of the taxonomic definition used to describe the species. As stated above, the population of *S. maltophilia* infections at the QEUH/RHC reflects the population of *S. maltophilia* within the world at large.

29. The main limitation of this analysis is that it is retrospective and as a result it was only possible to sequence what has been stored. The majority of saved environmental isolates relate to the period post March 2018 when water testing frequency was increased, and it became routine for the Environmental Water Laboratory at Glasgow Royal Infirmary (GRI) to routinely store any isolates grown from a water sample. Prior to March 2018 water testing was done less frequently and in a reactive fashion as part of Infection Control Incident/IMT investigations. Not all isolates from water testing were saved prior to March 2018. Prior to March 2018 environmental isolates were saved on an ad hoc basis as advised by the ICD.

30. In a number of cases, where reactive sampling as part of an Infection Control Incident/IMT investigation did not grow any pathogen or grew a pathogen which was not the pathogen of clinical interest, no environmental comparison could be made to the organism that was isolated from a patient. The report by Dr Dominique Chaput showed that no isolate of concern was ever isolated from water samples taken as a result of an IMT decision to implement reactive sampling.

31. Typing in its broadest sense allows for the differentiation of two similar isolates of the same species. There are many different forms of typing, each

having different abilities to differentiate isolates, different costs, differing expertise and specialist equipment required and different times to obtain a result. WGS looks at differences in the DNA structure between two organisms. It is the most discriminatory typing method available.

32. There are several stages to the identification of an organism.
The first stage is to use a dye, called a Gram stain to differentiate the organism into one of two classifications, either Gram-positive (stains purple) or Gram-negative (stains pink) depending on the bacterial cell wall. This binary classification correlates with clinical features, epidemiology, and pathogenesis. Many antibiotics target the cell wall, therefore this classification into Gram-positive and negative organisms predicts the response to many antibiotics. The second stage is to use a biochemical test, or more sophisticated phenotypic tests (e.g. MALDI, akin to a mass spectrometer) which allows microbiologists to identify an organism to a Genus and a species level e.g. *Stenotrophomonas maltophilia.*

33. Typing is the characterisation of micro-organisms beyond the level of the species, generating a strain or clone specific characterisation. There are a number of reasons to type organisms: for the surveillance of infections in human, animal, or contamination in food sources, to identify if changing numbers of organisms are associated with changes in strains; comparing isolates with those from elsewhere; outbreak investigation (rapid and early detection of outbreaks by identification of relatedness of strains; investigation of sources and possible transmission chains); the identification of virulence factors and the detection of new evolving pathogenic strains.

34. There are two main typing methods. Phenotyping which uses physical attributes to identify similarity and differences between organisms and genotyping which uses genetic attributes to identify similarity and differences between organisms. Genotyping also allows for the discrimination between phenotypically indistinguishable strains.

35. Concentrating on genotyping which classifies organisms based on genetic characters there are several molecular genotyping methods used in outbreak investigations: Pulsed-field gel electrophoresis (PFGE), Multilocus variable

number tandem repeat (VNTR) analysis, Multilocus sequence typing (MLST) and Whole Genome Sequencing (WGS). Each method has differing degrees of discrimination as a result of looking at different percentages of the genome. WGS has the highest degree of discrimination as it can look at the whole genome of the bacteria and gives a “fingerprint” of that particular isolate. This may represent over 3,000 individual genes and several million base pairs. WGS allows for the rapid sequencing and assembly of the whole genome sequence of the organism and represents the ultimate level of discrimination. WGS is widely applicable, producing highly portable data that meets international standards for repository into databanks. However, WGS does require complex bioinformatics to analyse and so a high level of expertise and equipment is required to perform the sequencing. Although costly, it is becoming more affordable and will most likely replace other typing techniques as costs fall.

36. WGS also allows for the description of the relationship between organisms within the population. By this I mean it is possible to show how related one organism is to another and to use this information to describe clades or “families” which exist within a heterogeneous population of organisms, such that you can identify if certain families are more capable of transmitting and causing infections in patients than other families. This could be used to identify environmental organisms which have the potential to cause infections.

37. The scientific hypothesis that was tested by sequencing, was to show if there is direct evidence that transmission occurred between the environment and the patient. WGS allows for the identification of any possible link between organisms and patients. Where an isolate in a patient and an isolate from an environmental source are not genetically close this excludes any possible link between the environmental source and the patient. If samples differ by a large number of SNPs (we used <25 SNPs to identify possible transmission), this definitively excludes any evidence of direct transmission between those organisms. Looking at the sequencing data, on the balance of probabilities, if there is no genetic closeness (i.e. less than 25 SNP difference) between isolates causing a clinical infection and isolates from the environment, then

there is no evidence of direct transmission from the environment to the patient.

38. Although I was not directly involved with typing of isolates during the period when infections were causing concern, having looked at the records I know that isolates were sent for typing to the UKHSA Reference Laboratories Colindale, London for typing. It was known by the IMTs that the typed organisms were identified by the Reference Laboratory at Colindale as being different from each other.

39. The possibility of a link to infection was part of the terms of reference of the sequencing report. It was also the driving factor in using WGS to try and understand the microbial populations, the dynamics of those populations, and the potential for transmission from the environment to the patient. My own view is that an infection link is a causal link that needs to be demonstrated scientifically. By using sequencing, it is possible to show if there is any evidence of direct transmission from the environment to the patient. The WGS data shows that despite the ubiquity of the environmental organisms *Stenotrophomonas* and *Cupriavidus*, there is no evidence of direct transmission from the environment to any patient. In my opinion, on the balance of probabilities this means that the hospital built environment is unlikely to be the source of the infection. The one exception, as described in para 23 and 24, is one clinical infection caused by *Cupriavidus* (linked to the Aseptic Pharmacy Unit in RHC) in 2016 that we cannot rule out.

40. The use of the terms variability (lack of fixed pattern) or diversity (showing a great deal of variety) have no significance in terms of transmission of infection.

41. I have no specific expertise in the use of SPC charts or the methodology. However, I know that NHSGGC followed the process as recommended by Health Protection Scotland (HPS).

42. We (Derek Brown and myself) did not experience inadequate data collection or data sharing whilst completing the WGS work. All water samples were coded with a unique code for each outlet such that they could be identified easily. These samples were taken by DMA, a contracted water company.

Environmental samples from hard surfaces (e.g. sinks, drains, surface tops, ventilation ducting) were normally taken by either the Infection Control Team, or the ward nursing staff. There were no codes to identify precisely where the sample had been taken from, and indeed the complexity of doing so would have been overwhelming to develop in a short time span. It would not be normal practice to give unique codes to each potential surface sampled. This would not be normal Infection Control practice and I am unaware of a universal coding system for environmental samples being in use in any hospital. Furthermore, to do so within a modern hospital environment would take an enormous resource and be impractical as a result of movement of equipment, patients and the number of potential sampling points within a room (sinks, taps, drains, flooring, ventilation grills, horizontal surfaces, touch points etc), which may or may not be utilised as a result of the hypothesis being tested.

43. These environmental samples were taken to inform real time decision making by the IMT. The Microbiologist or Infection Control Doctor within the department would be aware where the samples had been taken from and would report back to the ward accordingly. Many of the organisms found from environmental samples were not stored and saved and as a result were not available for sequencing. This is normal practice within a diagnostic laboratory. The QEUH Microbiology Department will process approximately half a million samples a year. Once routine samples (which an environmental sample is classed as) are cultured, plates are kept on a rolling seven day period. Once they are a week old they are bagged and destroyed by autoclave. This allows the laboratory to go back within a seven day period to do any further work on an isolated organism e.g. further antibiotic sensitivity testing, typing if required, before it is discarded. It would be unrealistic to store, archive and retrieve cultures from routine samples sent to the Microbiology Department. Lack of space within most laboratories means seven days is the maximum that most laboratories can store culture plates for. This is compliant with UKAS Accreditation standard ISO15189 which is the ISO standard Laboratories are accredited to. There is therefore a lack of hard environmental samples to compare with the clinical isolates. Water samples

sent to the Environmental Laboratory at GRI were kept after March 2018 as a matter of routine. Prior to March 2018 isolates were stored on an ad hoc basis, as dictated by the Infection Control Doctor or the laboratory staff. All isolates received at the reference laboratory for sequencing had been stored at -80°C.

44. The microbiology department now has a dashboard which displays data for Potable Water, Environmental and Reference Laboratory samples. There is a link to a scan for these via the lab number so that any typing results can be accessed from a centralised database.

45. During an outbreak, the response of an infection control team is precautionary. Hypothesis are generated and tested to attempt to identify the source or sources of the outbreak. It is not possible to await the outcome of any investigations before putting in place interventions that may or may not have an effect on any transmission events. It is usual for an Infection Control team to advise that a number of mitigations and interventions should be put into place as a matter of urgency. I do not believe that these measures were put in place solely to address public confidence. They were put in place to ensure patient safety was not compromised whilst the source of the infections was being sought.

46. In light of the evidence from the sequencing work we have done, I do not agree with the conclusion of the Case Note Review that the vast majority of cases were either possibly or probably linked to the hospital environment. On the balance of probability, the sequencing evidence, in my opinion does not support this conclusion. In all the sequencing we did in the three major organisms, *Stenotrophomonas maltophilia*, *Cupriaviadus* and *Enterobacter* species we found no evidence of direct transmission from the hospital environment to patients, except for one case in 2016 which we cannot exclude as there were no contemporaneous environmental samples to allow for a direct comparison. We cannot exclude the possibility using samples taken in 2018 that the case in 2016 could have transferred from the environment at that time.

47. I did have input providing the initial *Enterobacter* WGS results to the Case Note Review and responded to a draft of the Case Note Review regarding Microbiology Laboratory process.

48. On seeing a mixed culture it is important to have as much information about the patient and how the sample was taken to interpret the result. I would want to know if the patient was colonised with organisms (e.g. MRSA, *Candida* species), how was the sample taken (through a line, skin puncture etc.), the experience of the operator, what organisms have been isolated (e.g. are they normal skin flora showing the possibility that the sample has been poorly taken and contaminated, or if through a line whether there is contamination either through the catheter hub, or if organisms resident on the line had been sheared off by taking the sample through the line), what is the clinical diagnosis and what are the patient risk factors for an infection. Analysis of blood culture results from the QEUH and RHC over a six year period 2015 to 2020 shows that 17% of blood cultures have two or more organisms identified. I do not consider multiple bacteria in one blood culture sample as being unusual.

49. More than one species or strain of bacteria within a sample does not exclude a common source of infection but I would expect that if a common source was present the same combination of species should repeat on a regular basis, or a single common species or strain should be more prevalent within samples that have mixed cultures.

50. I am no longer an active member of the Infection Control Team at QEUH.

51. To demonstrate if there were an above normal number of bacteraemias within the Paediatric haemato-oncology unit in RHC would require a comparison of bacteraemia numbers and patient activity over a specified time period, with appropriate statistical analysis to determine whether there is any true increase beyond chance. This was done by HPS in their “Review of NHSGGC&C paediatric haemato-oncology data, Oct 2019” which reviewed and compared Gram-negative, environmental, enteric and Gram-positive infections during 2015-2019 from Scottish units in RHC, Royal Aberdeen Childrens Hospital, and Royal Hospital for Sick Children (Lothian) and concluded that there was

no increase in RHC in all Gram-negative and environmental organisms over this time period compared to the other two Scottish units. RHC did have statistically lower rates of Gram-positive infections. When looked at over discrete time periods, 2017-2019 and 2018-2019, there was no statistically increased rates of infection with environmental organisms in RHC compared to the other two Scottish units during those time periods.

52. As to whether there were more bloodstream infections than normal or more unusual bloodstream infections, I have not seen the data nor carried out any analysis to answer the questions. Others may be better placed to answer these questions. In order to answer these questions, an analysis would need to compare historical data from Yorkhill Childrens hospital prior to 2015 with RHC data post 2015. The analysis would need to look at activity, bed occupancy and the balance between inpatient and outpatient care within the Units. Another factor to consider would be the changes in diagnostic testing such as the introduction of the MALDI-TOF in around 2012/2013 which increased the number of named species that the diagnostic laboratory could identify. Previous to MALDI-TOF environmental organisms would have been described as “oxidase positive Gram-negatives” and would not have been speciated.

53. I am not aware that the Case Note Review asked for data from other Scottish or UK units to perform a comparative exercise.

I believe that the facts stated in this witness statement are true. I understand that proceedings for contempt of court may be brought against anyone who makes, or causes to be made, a false statement in a document verified by a statement of truth without an honest belief in its truth.