

Duke Virology Quality Assurance



Quantitative HIV-1 RNA PT Program Participation Requirements and Scoring Procedures

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VQA Program Quantitative HIV-1 RNA Proficiency Testing Requirements

Introduction to Participation Requirements

The National Institute of Allergy and Infectious Diseases (NIAID), Division of AIDS/DAIDS (DAIDS) Virology Quality Assurance (VQA) Program provides quality assurance and proficiency testing to labs that are performing virologic-based assays for HIV and other pathogens in support of NIAID-funded clinical trials. All laboratories that intend to do Quantitative HIV-1 RNA testing for NIAID-funded clinical trials must have an approved status in the VQA Quantitative HIV-1 RNA proficiency testing program.

Participation in the real-time testing phase of the program can only occur after the successful completion of a prequalification panel or assay validation. VQA HIV-1 RNA proficiency testing panels (5 samples) are to be run every three months and must be assayed in a single batch in the month in which the panel is due. The following sections detail the requirements to obtain and maintain approval to participate in RNA proficiency testing for NIH funded protocols.

Proficiency Testing Overview:

Starting in January of 2021, laboratories will be shipped four panels once a year. Each panel consists of 5 samples and will be named using the following format:

- RNAYYYY_MM.01-05A-E,
 - RNA = PT program
 - YYYY = year of the PT
 - MM = month of PT testing
 - 01-05 = sample number
 - A-E = panel configuration

Starting in 2021, laboratories will test a 5-member panel in a single assay every three months (February, May, August, and November). Each shipment will also include VQA200 copy controls (200 cp/mL) that must be run with each panel. The VQA200 control must be reported to the VQA and within the +/- 3 SD range provided by the VQA. If the VQA200 copy control is not reported or outside of the acceptable range, the lab will receive a non-technical penalty (see the **Non-Technical Performance** section below).

The Duke VQA Biostatisticians will analyze data for each PT. Each analysis will include the current and three previous rounds of PT data for a total of 20 samples. The analysis for each PT includes 20 samples because it provides sufficient statistical power (please see **VQA Program Quantitative HIV-1 RNA Proficiency Testing Scoring Procedure** below for detailed information on scoring procedures). Scores for each PT will be provided after each round of testing in a report that will be distributed to the participating laboratories.

Scores for each round of testing will be derived from an analysis of precision, accuracy, specificity, sensitivity, and assay validity (see **Table 1**). Precision assessments will be based on the combination of inter-assay and intra-assay variations to better monitor the variability associated with real-time testing. Expected values for total variation were derived empirically from VQA proficiency testing data, and the distribution of total assay variation was determined using Monte Carlo simulations. Proficiency testing data will be scored for deviations in total assay variability based on these cut points. Comparing the average \log_{10} recoveries in a laboratory with the median \log_{10} recovery across all laboratories will assess accuracy. Median values will be used instead of mean values to eliminate effects of outliers. Sensitivity will be determined for each assay by testing specimens at or near the limit of detection. All assays are challenged for sensitivity using samples with a nominal value of 50



copies/mL. Rates of false positive results (specificity) will be ascertained using blinded samples that do not contain HIV. Additionally, labs will be scored based on non-technical parameters. Penalties will be issued to lab if the data is late, labs do not respond to data queries from the Duke VQA, the data for the VQA200 copy control is invalid or missing, data containing PHI and/or PII is submitted to the VQA, or for data entry errors that are not corrected by the laboratory prior to the PT due date (please see **Non-Technical Performance** section below for additional details).

All invalid proficiency panel samples and assays must be repeated; invalid assays or samples will result in penalty scores. Laboratories will also be evaluated on transcriptional and computational errors; whenever possible, laboratories are encouraged to submit data using electronic files.

Table 1: Quantitative HIV-1 RNA Proficiency Criteria and Targets

Criteria	Description	Target
Precision	Total assay standard deviation based on the ratio of the estimated viral load (laboratory value) to the expected viral load.	Less than the 95th percentile
Accuracy	Measure of how closely a laboratory estimate of viral load is to the expected median log ₁₀ value	Less than 3 standard errors from the pooled laboratory median
Sensitivity	Number of false negative results obtained from replicates at the limit of detection for the assay in question	All 50 copies/ml replicates must be detected
Specificity	Monitor the results obtained on samples that do not contain HIV	All 0 copies/ml replicates must be not detected
Assay Validity	It is expected that all results should meet established criteria for assay validity, which varies among kits. Assay validity is based on external controls included in the run.	No invalid assay runs
Non-Technical Performance	Data timeliness, data query responsiveness, missing or invalid VQA200 data, and data submissions containing PHI and/or PII	On time data submission

VQA Participation Requirements

New Laboratory Certification Testing

Participation in any VQA proficiency testing program must be approved by the VQA Contracting Officer Representative (COR, aka Project Officer). In order to be considered for participation in the VQA program, a new laboratory must be doing quantitative HIV-1 RNA testing for a NIH-funded program. Once approved, the new laboratory will need to complete an application for participation in the program, which will outline the programs of interest and provide laboratory contact information. A new VQA laboratory number will be assigned to each VQA laboratory to uniquely identify that laboratory within the program.



Prior to enrollment into the real-time HIV RNA proficiency testing program, all new laboratories will need to test a 20-member prequalification panel containing coded plasma specimens or perform an assay validation that consist of VQA controls and clinical samples. The prequalification panel and the validation data will be submitted to the VQA via Duke Box or the VQA Web Application. Please contact the Duke VQA with any requests to enroll into the Quantitative HIV-1 RNA PT program via vqa-rna@duke.edu. Laboratories that test a prequalification panel will need a score of C prior to entering into the HIV RNA proficiency testing program. A score of a 'PC or a P' will require the laboratory to run another 20-member panel prior to advancing. A second score of a 'PC or a P' will require intervention by the VQA prior to any additional testing.

A new laboratory must obtain an **APPROVED** performance rating prior to performing any protocol testing. Due to the nature of the real-time HIV RNA proficiency testing program, laboratories will achieve a **PROVISIONALLY APPROVED** performance rating once they pass the 20-member prequalification panel or perform a validation. However, this approval status is provisional, until a minimum of two real-time 5-member panels have been completed. If a laboratory obtains a score of C on two consecutive panels after prequalification, then they will be **APPROVED** for testing. If a laboratory obtains a score of C and PC on two consecutive panels after prequalification, then they must obtain a score of C on a third 5-member panel in order to become **APPROVED** for testing. If any other combination of scores are obtained on the first two to three 5-member panels after prequalification then the laboratory's performance rating (PR) will be based on the sum of the panel scores from the four (4) most recent 5 member panels (Performance Score, PS). Individual panels are scored as a "1" for a Certified (C), "2" for a Provisionally Certified (PC), and "4" for a Probation (P). The corresponding panel scores and performance ratings are listed in **Table 2**(see the **VQA Program Quantitative HIV-1 RNA Proficiency Testing Scoring Procedure** section below for detailed information on scoring):

Table 2: VQA Performance Ratings

ASSESSMENT	PS	PR	Action
APPROVED	4-6	A	Eligible for protocol testing
PROVISIONALLY APPROVED	7-9	PA	Eligible for protocol testing at discretion of protocol virologist
NOT APPROVED	10-13	NA	Not eligible for protocol testing

Panels may be tested during regular rounds of proficiency testing, which occurs four times per year, or it may be Fast-Tracked using historical panels that have been pre-tested in the field. The normal track or fast track options must be begun within one year of passing the certification panel. If real-time testing is postponed for 6-12 months after certification, the VQA recommends that one 5-member panel be completed and scored prior to the initiation of protocol testing. If real-time testing is postponed beyond one year of testing, then another 20-member prequalification panel must be passed before participation in the VQA HIV RNA proficiency testing program may occur.

The final determination of whether or not a laboratory may perform protocol testing is at the discretion of the program leadership for that laboratory, not the Duke VQA.

New Assay Enrollment and Certification

A laboratory may request to:

- Obtain approval for protocol testing using multiple assays



- Switch platforms
- Certify additional instruments for VQA certified assays

All new assays and instruments enrolled in the VQA program need to be certified following the procedures outlined in the above section, **New Laboratory Certification Testing**. The VQA permits the use of two different assays; laboratories must obtain special approval from the VQA if they wish to become certified using more than two different assays. Each assay added to the VQA Program will be certified separately and the rules for achieving an **APPROVED** rating applies to all assays used within a laboratory. If a laboratory uses a manual extraction method as a backup for their automated extraction instrument, then the laboratory will need to demonstrate ongoing proficiency testing using both extraction methods.

The Duke VQA can assist in assay and instrument validations. Please contact the Duke VQA (vqa-rna@duke.edu) for more information about assay requirements or to request a validation plan and data submission template.

Maintaining Approval for Protocol Testing

To maintain an **APPROVED** certification status, a laboratory must participate in the routine proficiency testing program as scheduled by the VQA. Additionally, cumulative certification ratings based on the sum of the scores from the last four rounds of testing (see **Table 2** above) are used to determine the labs eligibility for protocol testing. Below is a list of PT scores and the associated point values:

- C (certified) = 1 point
- PC (provisionally certified) = 2 points
- P (probation) = 4 points

Additional points will be added if a laboratory received a non-technical penalty for data timeliness, data query responsiveness, missing or invalid VQA200 data, data submissions containing PHI and/or PII, or data entry errors (See **Non-Technical Performance** section below for additional details).

If a lab is unable to participate in a PT testing round or submit data by the PT due date, the laboratory must contact the Duke VQA to request an exemption (not submit data for that round of testing), to be placed on hold, or to request an extension. Duke VQA must approve all requests. Only one exemption per four PTs can be granted to a participating site. Extensions may be granted for up to two weeks past the stated deadline for the PT. A laboratory may request an extension or exemption for reasons such as:

1. Panel stuck in customs
2. Delay of shipment
3. Panel was thawed upon receipt
4. Panel was lost during shipping
5. Reagents for analysis are backordered or delayed
6. Instrument was broken
7. Contamination of sample
8. Laboratory closures
9. Laboratory Accident (i.e. vials dropped and contents spilled)

A laboratory may request to be placed 'on hold' for up to 12 months without penalty (see section below on withdrawal from the program). Laboratories that are placed on hold for more than 6 months will be expected to run and pass the two most recent 5-member panels upon re-entering the



program. Laboratories that are on hold for longer than 12 months will need to be recertified as a new lab. Network approval must be obtained prior to resuming protocol testing.

Repeating Testing of PT Panels

During the real-time testing phase of the program, problems may arise that require a laboratory to repeat a given five-member panel. Since problems that affect one five-member panel may affect future analyses, each laboratory is given the option of repeating any five-member panel (“B” panel configurations are used for repeating five-member panels). If a laboratory receives a score of PC or P for a PT, they will receive an Investigation Report (IR) that is to be reviewed and filled out by the laboratory. The IR form helps guide the lab in determining the root cause of the score for that PT. If a score of C or PC is obtained for a given round of testing, a laboratory may opt to repeat that five-member panel. If a laboratory receives a score of P for a given round, they must repeat the five-member panel. The VQA will contact a laboratory regarding the option of repeating a panel if the laboratory was issued a Potential Issue Alert (PIA) or the laboratory receives a PC. PIAs are informal notices issued to any lab that have an accuracy value ≥ 2 and/or a standard deviation $\geq 0.17 \log_{10}$ copies / mL. The goal of PIAs is to raise awareness of potential issues that could affect the cumulative rating of laboratories participating in the Quantitative HIV-1 RNA Proficiency Testing Program. Any laboratory with a score of C that wishes to repeat a panel must contact the VQA by emailing vqa-rna@duke.edu in order to receive a repeat panel. All laboratories that receive a score of P will automatically receive a repeat panel.

A five-member panel may only be repeated once, and may only be repeated during the round in which the error occurred. The repeat panel data, as well as the next five member panel data, will be due by the deadline for the next round of testing unless the VQA instructs otherwise. **Repeat (“B”) panel samples must not be analyzed in the same run as any other VQA samples to enable proper precision scoring. Additionally, all repeat panel testing should also include a VQA200 copy control. A laboratory will not receive a separate analysis for the “B” round testing, but the new data will replace the problematic data in future analyses.**

If a laboratory opts not to repeat samples, then problems that were noted may carry over to subsequent analyses. As necessary, the VQA will ship an extra 5-member panel to a laboratory that fails a round of testing. Ongoing scoring problems may require a laboratory to undergo recertification (successfully pass a 20-member panel) in order to maintain eligibility for protocol testing (see the **Recertification** section below).

Withdrawal/Removal

A laboratory may voluntarily withdraw from the VQA HIV RNA proficiency testing program at any time. A laboratory may also request to be placed ‘ON HOLD’ as a result of operational circumstances (e.g. personnel problems, laboratory issues, etc.) for up to 12 months. A laboratory may not perform protocol testing while the laboratory is ‘ON HOLD’. A laboratory that has not participated in the VQA HIV RNA proficiency testing program for more than 12 consecutive months will automatically be removed from the program.

Recertification

Labs Placed on Hold or Withdrawn from VQA Program

If a laboratory wishes to re-enter the VQA HIV RNA proficiency testing program subsequent to removal or placed on hold for longer than 12 months, that laboratory will need to be recertified as a new laboratory (see section above).

Following Ongoing Proficiency Testing Problems



A laboratory that is having ongoing RNA proficiency panel testing problems and is not maintaining an adequate approval certification status may be asked to undergo new laboratory recertification. In this case, a laboratory will be provided a 20-member panel that will be tested in a single assay. A laboratory must achieve a score of C on this recertification panel in order to resume real-time testing. Additional panels may be needed in order to achieve this score. A laboratory will need to contact the VQA via vqa-rna@duke.edu in order to request recertification panels.

For recertification, the 20-member panel will be scored in the same manner as a certification panel for a new laboratory. Assay sensitivity, specificity, accuracy and intra-assay precision statistics will be applied. As a laboratory participates in proficiency testing, 5 certification samples will be removed in sequential order for each new 5-member PT panel the laboratory analyzes. As a lab participates in PTs, data from the 20-member panel will be used until four 5-member panels have been completed. Each new 5-member panel will be added, and the last 5-member panel data will be removed, providing the cumulative scoring described in the **VQA Program Quantitative HIV-1 RNA Proficiency Testing Scoring Procedure** section below.

Precision scoring for the 20-member recertification panel will only include the intra-assay component of variation. Once a newly submitted panel is added to the recertification process, total assay precision statistics (including both inter- and intra-assay components of variation) will replace intra-assay precision statistics. During the recertification process, a laboratory will be provisionally certified. Cumulative scoring will be wiped clean and will not resume until four five-member panels are completed. Re-approval status may occur after a laboratory achieves a score of “C” on two successive five-member panels.

The cumulative table will continue to track laboratories proficiency testing scores, and will indicate when a recertification panel has been performed by placing an asterisk (*) after the score received on the first 5-member panel that follows the recertification panel. Scores for the recertification panel will not be tracked on the VQA cumulative table.

Appeals

The VQA recommends scoring for proficiency panels based on the criteria defined for the program. The VQA Advisory Board (VQAAB) then reviews the scoring for each round of testing for labs that had a decline in status or had a problem that does not follow the VQA PT rules (the laboratory identities are blinded for this process). Any laboratory may appeal the score on a proficiency panel by submitting a letter or email to William Meyer III, Chair of the VQAAB (william.a.meyer@questdiagnostics.com). All appeals will be reviewed by the VQAAB to determine if a change in scoring is indicated. Laboratories will be notified of the outcome of all appeals

Practice Panels

Any NIAID approved laboratory may obtain retrospective HIV RNA proficiency panels prior to enrollment in the program, or at any time during their participation in the VQA program. Once a panel has been tested and analyzed as a ‘practice’ panel, it cannot be reclassified for use in laboratory certification. Results from these ‘practice’ panels will be assessed and results returned to the laboratory, but no certification score will be assigned.

Change in Status Letters

A laboratory will receive a change in status letter if they obtain a score on a round of testing that changes their overall performance rating. This letter will document the laboratory’s scores over the last four rounds of testing and will indicate when a change in status (performance rating) has resulted. A copy of this letter will be sent to the director of the laboratory and the network laboratory



group for whom the laboratory does testing, as appropriate. Letters will be sent to notify individuals of both negative and positive changes in approval ratings. The VQA submits the letters on behalf of the VQAAB, but has no control over the implementation of rules governing the ability of a site to continue protocol testing. All questions surrounding a laboratory's ability to resume or discontinue protocol testing should be directed to the respective network laboratory group or leadership.

VQA Program Quantitative HIV-1 RNA Proficiency Testing Scoring Procedure

Introduction to PT Scoring

The cumulative table will continue to track laboratories proficiency testing scores, and will indicate when a recertification panel has been performed by placing an asterisk (*) after the score received on the first 5-member panel that follows the recertification panel. Scores for the recertification panel will not be tracked on the VQA cumulative table.

Scoring Criteria for VQA Quantitative HIV-1 RNA Proficiency Testing

The VQA has determined that a minimum of 20 samples are needed to provide sufficient power for analyses. With only five samples on the new panels, no single panel could provide information on all of the scoring criteria. For example, a panel of five samples at the same nominal concentration would provide information on reproducibility and validity, provided the nominal concentration was above the range in which assay precision varies inversely with RNA concentration. However, this panel would not provide information on assay specificity or sensitivity. In most cases, statistical power to identify problems would also be quite limited given the small size of each panel. Therefore, proficiency scores will be based on the combined results from four consecutive panels, or 20 total samples. This approach boosts statistical power and allows performance to be monitored over an interval of six months rather than at one point in time.

The scoring criteria have been designed to reflect the way that RNA assays are used in clinical trials. Virus load measurements are currently conducted in real-time. Therefore, assessments of the total assay standard deviation, including both the intra-assay and inter-assay components, is used to monitor proficiency. In addition, testing for accuracy has been added to the performance criteria. Finally, sensitivity, specificity, assay validity, data timeliness and data query responsiveness are also used for measuring performance. Methods for assessing performance are discussed below.

Technical Performance

1. Precision

As noted earlier, the measurement of change within a patient is not affected by inter-assay variation when all of the samples from that patient are assayed in a single batch. However, both intra-assay and inter-assay variation are important if samples are assayed in real time. The combination of the two components is defined here as total assay variation. When the original proficiency testing program for RNA assays was designed, the committee of virologists who worked with the VQA Program to develop performance criteria specified that the assays should be conducted with precision sufficient to detect a 5-fold difference between two samples in the same batch. This was interpreted to mean that the intra-assay standard deviation should provide at least 90% power to detect a five-fold difference, which led to the criterion of an intra-assay SD that was not statistically significantly greater than $0.15 \log_{10}$. A new target standard deviation that takes account of both intra-assay and inter-assay variation is needed for the revised program. However, no mandate analogous to detecting five-fold differences has been provided for assay variation in real time testing. The

statistical test for assessing performance also posed a difficulty. Under the original program, the intra-assay variance, which is the square of the intra-assay SD, was compared with the square of $0.15 \log_{10}$ using a chi-square statistic. It is not possible to perform a similar test on the total assay standard deviation, because the square of the total assay standard deviation does not follow a chi-square distribution. In fact, it does not have a closed form solution that would lead to simple calculation of a test statistic.

Another problem that arose was the need for replication within each five-member panel if the intra-assay component of variation was to be assessed. Under the original program, the intra-assay standard deviation was estimated from the variation in estimated RNA concentration among coded replicates at the same nominal concentration within a 20-member panel. Replication at even one nominal concentration within a five-member panel was considered too restrictive.

These problems were solved by replacing the original system for assessing assay precision with the following approach. (1) Performance is now assessed using \log_{10} recovery, rather than \log_{10} estimated RNA concentration, where recovery is the ratio of estimated to nominal concentration. This choice was based on the assumption that recovery is constant within the linear range of an assay. Under this assumption, recoveries can be combined across nominal concentrations within five-member panels to provide the replication needed for estimating the intra-assay component of variation. (2) In the absence of a mandate analogous to detecting a five-fold change, a new target standard deviation was developed by estimating expected values for the intra-assay and inter-assay standard deviations using data from recent proficiency panels. The expected values were combined to provide an expected value for the total assay SD. (3) The expected distribution of the total assay standard deviation for each set of four consecutive panels was determined by Monte Carlo simulation that will be based on the expected values. The simulation process is discussed below. Estimated total assay standard deviations that exceed specified cut points on this distribution will be flagged.

Expected values for the intra-assay and inter-assay standard deviation were actually obtained for the Standard Monitor assay using data from the 'A' rounds of panels 016r through 019r. Using data from panels that received scores of C, the intra-assay SD was estimated to be $0.1196 \log_{10}$ and the inter-assay SD was estimated to be $0.0831 \log_{10}$. A recent update, using data from the 'A' rounds of panels 016r through 022r produced very similar values. Using the 'A' rounds of ultralow proficiency panels 004ru through 009ru, the intra-assay and inter-assay SD's for the Ultrasensitive Monitor assays were estimated to be $0.1196 \log_{10}$ and $0.0894 \log_{10}$ respectively. This analysis was also restricted to data sets with scores of C. The inter-assay SD was slightly higher on the Ultrasensitive Monitor assay than on the Standard Monitor assay because of some problems with low recovery in a few laboratories on a few rounds of testing. For example, problems with a centrifuge were identified at one site. Therefore, the values from the Standard Monitor assay were treated as empirically determined expected values for the intra-assay and inter-assay standard deviation. Taken together, they imply that the expected value for the total assay standard deviation is:

$$(0.11962+0.08312) / 2 = 0.1456 \log_{10}$$

As noted, these estimates were obtained using only the panels that received scores of C. Panels with scores of PC or P were eliminated for the following reasons. The most common problem encountered on proficiency panels is an elevated standard deviation. The elevated values appear as outliers in a plot of the frequency distribution of standard deviations. It did not seem appropriate to base the estimated standard deviations on a data set that included values that did not fit the overall distribution. Furthermore, the residuals from the linear model that were used to obtain the two standard deviations did not fit the assumption of normality when the complete data set was used to

obtain the estimates. This failure was caused by extreme values in the data sets with scores of PC or P; i.e. by outliers that did not fit the overall distribution of HIV RNA results.

The same expected values for the two components of variation will be used for all kits rather than separate expected values for each kit. This is a continuation of past practice.

The Monte Carlo simulations that are used to derive the distribution of the total assay SD from the expected intra-assay and inter-assay SDs proceed as follows. Suppose that the total assay standard deviation was evaluated using three samples from each of four consecutive panels (i.e. each panel also includes a negative sample or a sample near the limit of detection of the assay). There are five steps to the simulation process:

1. A random sample of size 4 is selected from a normal distribution with SD = 0.12 log₁₀. This standard deviation represents expected intra-assay variation; i.e. the variation among results on the same panel.
2. Step 1 is repeated three more times to make four groups of 4 samples each.
3. A random sample of size 4 was selected from a normal distribution with SD = 0.084 log₁₀.
4. The first value in step 3 is added to each of the four values in the first group, the second value in step 3 is added to each of the four values in the second group, and so on. The values generated in step 3 represent the added contribution of run-to-run, or inter-assay, variation to total assay variation; i.e. this component affects all four samples in a given group of 4 the same way but it varies among groups.
5. Estimate the inter-assay and intra-assay standard deviations from the 16 simulated values. Calculate the total assay SD from these estimates.

This process was repeated 10,000 times to generate a distribution for the total assay standard deviation (**Table 3**). The median was very close to the expected value that was defined above. The cut points at the 95th and 99th percentiles would be used to identify relatively minor and more serious problems with assay precision.

Table 3: Percentiles of the distribution of 10,000 simulated total assay standard deviations, assuming four proficiency panels with four samples each.

MINIMUM	25th	MEDIAN	75th	95th	97.5th	99th	99.5th	MAXIMUM
0.050	0.122	0.142	0.164	0.199	0.213	0.226	0.241	0.358

The results of a given set of simulations will depend upon the total number of samples included in an evaluation of reproducibility and the distribution of these values among panels. For example, different cut points would be obtained if the 16 samples were distributed among the four panels such that two panels had five each and the other two had three each.

The total assay standard deviation (SD) is related to the intra-assay and inter-assay standard deviations as $S_T = (S_A^2 + S_E^2)^{1/2}$ where S_T is the total assay SD, S_A is the intra-assay SD and S_E is the inter-assay SD. The total assay SD is calculated for each data set generated within a laboratory using a given kit. The calculated targets for the 95th and 99th percentile for each combination of panels are used to determine the precision score for that laboratory/kit/panel combination.

2. Accuracy

Accuracy is assessed by comparing average (mean) log₁₀ recovery in a laboratory with expected log₁₀ recovery. The average is calculated using the subset of samples that is used to assess the total assay standard deviation. Median log₁₀ recovery across all laboratories is treated as the expected value.

Recovery is used instead of estimated RNA concentration because recoveries can be combined across nominal concentrations within a panel or across successive panels to assess accuracy. The median across all laboratories will be used as the expected value, instead of the mean or nominal concentration, for the following reasons. Use of a nominal concentration presupposes that expected recovery should be 100%. This is not reasonable if different kits on average produce somewhat different estimates. Means are more sensitive to the effects of outliers than medians and very large outliers have occasionally been identified on previous panels.

The test statistic for identifying accuracy problems is the distance, in standard errors, between average \log_{10} recovery in a laboratory and expected \log_{10} recovery: $(R-M)/S$ where R is average \log_{10} recovery in a laboratory, M is median \log_{10} recovery across all laboratories and S is the standard error of the mean. A normal distribution is assumed for the test statistic. The standard error is derived from the inter-quartile range of the distribution of mean \log_{10} recovery among laboratories; if the mean is normally distributed, then the inter-quartile range is 1.35 standard errors.

Accuracy statistics have been scored officially since September 2011. In some analyses, it has been noted that the standard error that is used for scoring accuracy does vary by round. If the standard error becomes too small, then there is an increased chance that data sets would be penalized for accuracy when, in fact, the deviations noted in the analysis were quite small. Per the VQA Advisory Board's (VQAAB) recommendation, an analysis investigating the impact of standard errors on the accuracy statistics on previous rounds of testing was conducted in April 2009. As a result of this investigation, a modified approach for the scoring accuracy was implemented. Under this modified approach, the observed standard error on a round of testing would be replaced by the historical median of 0.080517 when the observed SE was below the median; otherwise, the observed value would continue to be used

Accuracy statistics that indicate average recovery is at least three but less than four standard errors from the expected value will be flagged as minor problems, while accuracy statistics that indicate a departure of at least four standard errors from the expected value will be flagged as major problems.

3. Sensitivity

Sensitivity is assessed using a sample containing 50 copies/mL and determining the number of false negative results obtained from replicates at the limit of detection for the assay in question. The maximum acceptable number of false negative results is the number of false negatives that would be exceeded no more than 5% of the time, given the number of samples (3–5) involved and assuming independent binomial sampling with an underlying probability of a negative result of 0.05. One false negative out of four is a minor problem and two or more out of four is a major problem.

4. Specificity

Specificity is assessed by monitoring the results obtained on samples that do not contain HIV. Each panel includes a small number of HIV-negative samples. Negative results (HIV RNA not detected) are expected from all of them; qualitatively detected HIV RNA is deemed a false positive result. One false positive result is flagged as a minor problem and two or more false positive results are flagged as a major problem.

5. Assay Validity

It is expected that all results should meet established criteria for assay validity. The criteria vary among kits. If a kit control fails this will invalidate the run and the run must be repeated prior to data submission. If an assay censors a sample within a run, then the sample must be repeated. Only the repeated valid sample will be included in the analysis. A single invalid result is a minor problem and will result in a score of PC; two or more invalid samples are deemed a major problem and will result in a score of P.

Non-Technical Performance

A laboratory will receive a non-technical penalties summarized in **Table 4** and described below.

Table 4. Non-technical Penalties and Impact on PT Score

Score	Points	Penalty Type	Description of Penalty
C1 ^v	2	VQA200 Control	Missing or invalid VQA200 data
PC1 ^v	4		
P1 ^v	4		
C1 ^T	2	Data Timeliness	Data submitted late without requesting an extension
PC1 ^T	4		
P1 ^T	4		
C1 ^Q	2	Data Query Responsiveness	Not responding to queries about data within one week (5 working days)
PC1 ^Q	4		
P1 ^Q	4		
C1 ^P	2	Data Submission Containing PHI and/or PII	Laboratory submitted data that contained PHI and/or PII
PC1 ^P	4		
P1 ^P	4		
C1 ^D	2	Data entry errors	Laboratory submitted data with entry errors that were not caught and corrected prior to the PT due date
PC1 ^D	4		

P1 ^D	4		
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1. Data Timeliness

A due date is assigned to each 5-member panel. Data must be submitted via the Duke VQA Web Application by the deadline or data will receive a penalty. A laboratory may request an exemption, extension, or to be placed on hold by emailing vqa-rna@duke.edu. If no contact is made prior to the due date, and the data are received late once within four rounds of testing, then the proficiency testing score will be down-graded one level (i.e. a technical score of C would be assigned a score of C1^T, which equates to 2 points for a panel score). If data are received late for the second time in four rounds of testing, then the proficiency testing score will be down-graded two levels (i.e. a technical score of C would be assigned a score of C2^T, which equates to 4 points for a panel score) as summarized in **Table 4**.

2. Data Query Responsiveness

Occasionally, a query is sent to a laboratory to clarify or fix a problem noted in their VQA submission. The Duke VQA will email the testing laboratory and ask them to follow up on the query. If the laboratory resolves the query within a week of receiving the original query (5 working days, excluding any holidays), then no penalty will be assessed. If no resolution is received, a second query will be sent to the testing laboratory and will include affiliated network laboratory coordination center. If the query is not resolved within one week (5 working days excluding holidays) of the second query, then the data will be scored as a minor late query response. A third query will be sent to the testing laboratory, including the VQA manager, and the affiliated network laboratory coordination group. If the problem is still not resolved within one week (5 business days excluding holidays) then a major problem will be assessed. If a minor late query resolution is noted, the proficiency testing score will be down-graded one level (i.e. a technical score of C would be assigned a score of C1^Q, which equates to 2 points in a panel score; a technical score of PC would be assigned a score of PC1^Q which equates to 4 points in panel score). If a major late query resolution is noted, then the proficiency testing score will be down-graded two levels (i.e. a technical score of C would be assigned a score of C2^Q, which equates to 4 points for a panel score). A major late query resolution will receive the maximum of 4 points for a panel score (**Table 4**).

3. Missing or Invalid VQA200 Copy Control Data

A VQA200 copy control must be included in analysis of VQA Quantitative HIV RNA proficiency testing samples. The VQA200 control must be reported and within the +/- 3 SD range provided by the VQA. If the VQA200 copy control is not reported or outside of the acceptable range, the lab will receive a non-technical penalty. Invalid or missing VQA200 control data occurs once within four rounds of testing, then the proficiency testing score will be down-graded one level (i.e. a technical score of C would be assigned a score of C1^V, which equates to 2 points for a panel score). If the VQA200 control data are missing for the second time in four rounds of testing, then the proficiency testing score will be down-graded two levels (i.e. a technical score of C would be assigned a score of C2^Q, which equates to 4 points for a panel score) as summarized in **Table 4**.

4. Data submissions Containing PHI and/or PII

PHI (protected health information), PII (personally identifiable information), or any information that could link submitted data to an individual participant must not be included in any data files submitted to the VQA for analysis.

Note: it is at the discretion of the VQA to reject data sets that are presumed to contain PHI/PII.



When submitting VQA data, the laboratory will be required to attest that the submission does not contain PHI or PII. If, during QA of the data, the VQA finds PHI or PII, a penalty will be assessed. All data that contains PII or PHI will be expunged from the database and laboratories will be required to remove the information and resubmit their data. Data resubmitted after the due date, without an exception request, will also receive a late penalty score.

If a data set contains PHI/PII, the proficiency testing score will be downgraded one level for a first offense (i.e. a technical score of C would be assigned a score of C1^P for the first incident, which equates to 2 points for a panel score). For subsequent offenses within 4 rounds of testing, the proficiency testing score will be downgraded an additional level (i.e. a technical score of C would be assigned a score of C2^P, which equates to 4 points for a panel score). Laboratory directors, network coordination centers and the Division of AIDS will be notified if a laboratory submits data containing PHI/PII.

5. Data Entry Errors

Data for each Quantitative HIV-1 RNA PT is submitted using the VQA web-system, which requires entry of viral load data and upload of raw data files. Participating sites have the ability to save their data in the web-system and review it before submission. Prior to the PT due date, a site may request to re-open their PT to correct data entry errors. However, sites will not be able to correct any data entry errors after the PT due date. Data that is submitted to the VQA that contains data entry errors such as entering the wrong values, putting decimals in the wrong place, entering data in the wrong location, switching samples, or submitting the wrong file could result in a non-technical penalty.

If a data entry error occurs once within four rounds of testing, the proficiency testing score will be down-graded one level (i.e. a technical score of C would be assigned a score of C1^D, which equates to 2 points for a panel score). If a data entry error occurs for the second time in four rounds of testing, then the proficiency testing score will be down-graded two levels (i.e. a technical score of C would be assigned a score of C2^D, which equates to 4 points for a panel score) as summarized in **Table 4**.

Note: Any combination of penalties (technical or non-technical) will result in a maximum panel score of 4 points (e.g. C1^{OP}, PC1^T, etc).

Proficiency Scoring Format VQA Quantitative HIV-1 RNA Proficiency Testing

The scoring process is illustrated by the example in **Table 5**. The five columns in the table represent the nominal concentrations on five consecutive 5-member panels that are designed to assess proficiency on the Roche COBAS AmpliPrep / COBAS TaqMan HIV RNA assay. The first four panels would be used to generate the first proficiency score. Specificity would be assessed using the negative samples, sensitivity would be assessed using the samples with a nominal value of 50 copies/mL, while and accuracy and reproducibility would be assessed using the samples with nominal concentrations of 100 copies/ml or higher from all four rounds. The next proficiency score would be based on the combined data from rounds 2 through 5 once the results of round 5 were available.

While a single five-member panel can provide only limited information, it could provide important information if performance problems are severe. Performance on individual panels will therefore be monitored. Laboratory personnel and the VQAAB will be kept apprised of results.

Table 5: Five hypothetical 5-member panels (Entries are nominal concentrations).

Round 1	Round 2	Round 3	Round 4	Round 5
0	300,000	3,000	15,000	0



15,000	0	50	3,000	10,000
50	15,000	300,000	0	50
3,000	30,000	0	50	400,000
300,000	50	30,000	30,000	60,000

Determination of Proficiency Scores

A score of PC will be assigned if a minor problem is identified with one of the seven scoring criteria. A P is assigned if minor problems are identified on at least two criteria or if a major problem is identified on at least one criterion. Minor problems consist of:

- a total assay SD that exceeds the 95th percentile but not the 99th percentile on the Monte Carlo simulations per round;
- an accuracy score that indicates that average log₁₀ recovery differs from expected log₁₀ recovery by at least 3 but less than 4 standard errors per round;
- a rate of negative results at the limit of detection that would be met or exceeded with probability <0.05 but >0.01 per round;
- a single false positive per round;
- a single invalid result per round;
- one late submission in four rounds of testing (this penalty does not carryover, though multiple late submissions within 4 rounds can result in a major penalty);
- one minor late query response within 4 rounds of testing (this penalty does not carryover, though multiple late submissions within 4 rounds can result in a major penalty); or
- one submission containing PHI, PII, or other identifying information within 4 rounds of testing (this penalty does not carryover, though multiple late submissions within 4 rounds can result in a major penalty).

Major problems consist of:

- an total assay SD that exceeds the 99th percentile on the Monte Carlo simulations;
- an accuracy score that indicates that average log₁₀ recovery differs from expected log₁₀ recovery by at least 4 standard errors per round;
- a rate of negative results at the limit of detection that would be met or exceeded with probability <0.01 per round;
- two or more false positives per round;
- two or more invalid results per round;
- two late submissions within four rounds of testing;
- one major late query response during a round of testing or two minor late query responses within 4 rounds; or
- two or more submissions containing PHI, PII, or other identifying information.

If a score of P is assigned and the problem can be traced to the most recent 5-member panel, then a recoded version of that panel will be sent to the laboratory. Results of the repeat assays will be used in all subsequent scoring. Suppose, for example, that a P is assigned because of problems on the fourth of the five hypothetical panels in Table 2. The score for the first four consecutive panels would be based on the first run of round 4. The score for rounds 2 through 5 would be based on the second run of round 4 and the first runs of rounds 2, 3 and 5. If a PC is assigned and the problem was caused by the most recent five-member panel, then the panel will be repeated at the discretion of the Laboratory Director.



If the problem exists over multiple panels and repeating the last 5-member panel will not resolve the problem, then the laboratory will be given the option of completing a recertification panel (20-member panel). This will permit the laboratory to replace all previous data for future analyses. As with a new laboratory running a prequalification panel, as new 5-member panel data is added to the analysis, 5 samples from the recertification panel will be removed in sequential order until only 5-member panel data is used in the analysis.

Note: only intra-assay precision statistics will be used when analyzing a 20-member panel. Total assay standard deviations will be implemented once the first 5-member panel has been added to the analysis.

After the analysis is complete, and the scores have been approved by the VQAAB (if needed), a report will be sent to each laboratory via email. This summary will include the decoded data from that laboratory as received by the VQA, performance on each scoring criterion and an approved score. A list of the scores for all laboratories will be circulated via email after the VQAAB review. The laboratory must contact Miranda Carper via e-mail (vqa-rna@duke.edu) if there is a discrepancy in the report received from the VQA.