



Development and evaluation of a secondary reference panel for BCR-ABL1 quantitation on the International Scale **OPEN**

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Development and evaluation of a secondary reference panel for *BCR-ABL1* quantitation on the International Scale

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CONFLICT OF INTEREST STATEMENT

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ABSTRACT

Molecular monitoring of chronic myeloid leukemia patients using robust *BCR-ABL1* tests standardized to the International Scale (IS) is key to proper disease management, especially when treatment cessation is considered. Most laboratories currently utilize a time-consuming sample exchange process with reference laboratories for IS calibration. A World Health Organization (WHO) *BCR-ABL1* reference panel was developed (MR¹-MR⁴), but access to the material is limited. In this study, we describe the development of the first cell-based secondary reference panel that's traceable to and faithfully replicates the WHO panel, with an additional MR^{4.5} level. The secondary panel was calibrated to IS using digital PCR with *ABL1*, *BCR*, and *GUSB* as reference genes and evaluated by 44 laboratories worldwide. Interestingly, we found that > 40% of *BCR-ABL1* assays showed signs of inadequate optimization such as poor linearity and suboptimal PCR efficiency. Nonetheless, when optimized sample inputs were used, > 60% demonstrated satisfactory IS accuracy, precision and/or MR^{4.5} sensitivity, and 58% obtained IS conversion factors from the secondary reference concordant with their current ones. Correlation analysis indicated no significant alterations in %BCR-ABL1 results caused by different assay configurations. More assays achieved good precision and/or sensitivity than IS accuracy, indicating the need for better IS calibration mechanisms.

INTRODUCTION

The development of *BCR-ABL1* tyrosine kinase inhibitors (TKIs), from the first generation imatinib to newer agents such as nilotinib and dasatinib, has enabled progressively deeper molecular responses in chronic myeloid leukemia (CML) patients undergoing TKI therapy.^{1,2} Deeper molecular responses are defined as *BCR-ABL1* levels of $\leq 0.01\%$ (MR⁴) and $\leq 0.0032\%$ (MR^{4.5}) on the international reporting scale (IS) and are important milestones for patients considering treatment cessation.³ Other landmarks on the IS also represent different treatment decision thresholds and prognostic outcomes.⁴ For example, patients who reach 10% IS or below at 3 months after treatment have significantly higher rates of MR^{4.5} by 5 years,⁵ and reaching 0.1% IS (major molecular response, MMR) by 12 months of treatment is predictive of subsequently achieving undetectable *BCR-ABL1* levels.⁶ Thus, regular molecular monitoring using real-time reverse transcription quantitative polymerase chain reaction (RT-qPCR) is recommended for optimal disease management, and treatment decisions rely on achieving milestone molecular responses in the first year of therapy and beyond.^{2,7}

Since treatment decisions are directly impacted by test results, accuracy and precision of *BCR-ABL1* assays across the entire measurement range is crucial for patient management, especially in patients with deep molecular responses when considering possible treatment cessation. It is well known that high variability exists between RT-qPCR methods used in different laboratories.^{8,9} The first international standardization attempt occurred in 2003, when different *BCR-ABL1* assays used in the IRIS trial established IS based on 30 CML patient samples.¹⁰ Subsequently, a process for establishing a test-specific IS Conversion Factor (CF) by exchanging 20-30 CML patient samples with a reference laboratory was developed.¹¹ Although this process works well for laboratories with tests that show good stability over time, it is time-consuming, expensive and difficult to access for smaller laboratories.^{12,13}

In 2010, the “first International Genetic Reference Panel for quantitation of *BCR-ABL* mRNA” was developed as a primary standard for *BCR-ABL1* assay IS calibration and accredited by the World Health Organization (WHO).¹⁴ The WHO panel is made of lyophilized K562 and HL-60 cell line mixtures, which allows the inclusion of cellular RNA extraction in the IS calibration against the 2 major *BCR-ABL1* breakpoints (e13a2 and e14a2), and carries 3 sets of nominal %BCR-ABL1 values using *ABL1*, *BCR* and *GUSB* as reference genes. Due to restricted access, the WHO panel is currently only available to manufacturers of *BCR-ABL1* test kits and secondary standards.¹³ The commercial secondary standards available to date are made of RNA,^{15,16} thus RNA extraction is not included in the IS calibration process, except when the standards are artificially spiked into the cell samples. Furthermore, none of these are calibrated to the WHO panel against all 3 reference genes.

In this study, we describe the successful development of the first cell-based *BCR-ABL1* secondary reference panel that is traceable to and faithfully replicates the WHO panel in both raw materials (lyophilized K562 and HL-60 cell mixes) and manufacturing process, with the addition of a MR^{4.5} level. Nominal %BCR-ABL1 IS values were assigned to the secondary panel using reverse transcription droplet digital PCR (RT-ddPCR) against *ABL1*, *BCR*, and *GUSB*. The secondary panel was successfully evaluated by 45 different *BCR-ABL1* assays in a subsequent international multi-center evaluation study.

MATERIALS AND METHODS

Manufacturing and IS calibration of secondary reference panel

K562 (ATCC CCL-243) and HL-60 cells (ATCC CCL-240) (American Type Culture Collection, Manassas, Virginia, USA) were cultured, mixed, and lyophilized following methods described by White *et al.*¹⁴ with minor modifications (supplementary information). Calibration to the WHO standards was performed as

described.¹⁴ IS calibration using *ABL1* as a reference gene was conducted using 10 sets of WHO “first International Genetic Reference Panel for quantitation of BCR-ABL mRNA” panels (National Institute for Biological Standards and Control, South Mimms, UK). Calibration using *BCR* and *GUSB* was conducted in a second study using another 10 sets of WHO panels. On each day of 10 non-consecutive days, 1 WHO panel and 2 to 3 secondary panels were tested using RT-ddPCR in 4 replicates for the MR¹ (10% BCR-ABL^{IS}) to MR⁴ (0.01% BCR-ABL^{IS}) samples, and in 8 replicates for the MR^{4.5} sample to enhance assay precision. Data analysis was performed using the statistical methods described by White *et al.*¹⁴

Reverse transcription droplet digital PCR

RNA extraction from the secondary panel was performed using RNeasy mini kits (Qiagen, Hilden, Germany). Reverse transcription was performed using ABI High Capacity cDNA reverse transcription kit (Thermo Fisher Scientific, Waltham, Massachusetts, USA), and ddPCR was performed using 2X ddPCR Supermix (Bio-Rad, Hercules, California, USA) on the QX-100 or QX-200 ddPCR system (Bio-Rad). All primer and probe sequences are listed in Table 1. *BCR-ABL1* and reference genes were run as singleplex reactions in separate wells. To achieve optimal assay precision and avoid signal saturation, cDNA input for *BCR-ABL1* per 20 µl reaction was 80 ng for the MR¹ sample, 400 ng for the MR² sample and 675 ng for samples ≤ MR³. cDNA input for reference genes was 10 ng for all 3 reference genes. For each RT-ddPCR run, wells with > 9025 accepted droplets were considered valid per the manufacturer’s recommendations.

RESULTS

Manufacturing and IS calibration of the WHO *BCR-ABL1* secondary reference panel

We successfully manufactured > 12 000 vials of secondary *BCR-ABL1* lyophilized cell reference panel, using the same K562 and HL-60 cell lines and following similar manufacturing procedures as the primary WHO panel (supplementary information).¹⁴ A MR^{4.5} level was added to the secondary panel to enable more accurate IS calibration at this critical level, as CML patients reaching this deep molecular response are increasingly being considered for treatment cessation. Quality control assessments indicated that the secondary panel had minimal residual moisture, excellent vial-to-vial homogeneity and > 2.5 years of real-time stability (supplementary information).

To calibrate the secondary panel to the WHO first International Genetic Reference Panel for quantitation of *BCR-ABL1* mRNA, we followed the study design described by White *et al.*,¹⁴ except that the sample size was doubled to strengthen the statistical power (supplementary information). RT-ddPCR was chosen as the calibration method due to its superior sensitivity, precision and absolute quantification capability compared to RT-qPCR.^{17,18} At the time of this study, no commercially available *BCR-ABL1* test utilized *BCR* or *GUSB* as reference genes. We developed 3 sets of RT-ddPCR assays, including *BCR-ABL1/ABL1*, *BCR-ABL1/BCR*, and *BCR-ABL1/GUSB*, to enable IS calibration of the secondary panel against all 3 reference genes. All RT-ddPCR assays were validated following a combination of industry best practices, Minimum Information for Publication of Quantitative Real-Time PCR Experiments (MIQE) and Clinical and Laboratory Standards Institute (CLSI) guidelines to ensure proper accuracy, precision, sensitivity and linearity were achieved (supplementary information).¹⁹⁻²² Using methods described by White *et al.*,¹⁴ we determined the IS CF for the RT-ddPCR assays to be 0.93 for *BCR-ABL1/ABL1*, 1.85 for *BCR-ABL1/BCR*, and 1.28 for *BCR-ABL1/GUSB*.

Each CF was subsequently applied to the empirical %BCR-ABL1 of the secondary panel measured by RT-ddPCR to obtain the assigned %BCR-ABL1¹⁵ values (Figure 1 and Table 2a). We found that the mean %BCR-ABL1 for each level of the secondary panel met all targeted *BCR-ABL1* levels and were within 1.3-

fold of the WHO standards values. The assigned %BCR-ABL1^{IS} of level E was 0.0038%, 0.0050% and 0.0029% for *ABL1*, *BCR* and *GUSB* respectively, indicating that a MR^{4.5} level was successfully created. Moreover, the mean copy number of *BCR-ABL1*, *ABL1*, *BCR* and *GUSB* per ng of RNA measured using RT-ddPCR was highly similar between the WHO and secondary panels (Table 2b). This demonstrated that the secondary panel replicated the primary WHO panel faithfully, with the successful addition of a MR^{4.5} level.

Laboratory evaluation of the WHO *BCR-ABL1* secondary reference panel

Study Design

The secondary panel was sent to 44 clinical laboratories from 24 countries worldwide for evaluation, including 34 laboratories from Europe (Supplementary Table 2). One laboratory tested the panel with 2 different *BCR-ABL1* assays, resulting in a total of 45 *BCR-ABL1* tests included in this report. The laboratories were asked to conduct 2 studies with the secondary panel. In Study 1, to determine the optimal sample input of the secondary panel specific for each *BCR-ABL1* test, a standard curve experiment was run with Vial A (MR¹) and Vial C (MR³) of the panel using 50 ng, 100 ng, 200 ng, and 400 ng of RNA (for 1-step assays) or cDNA (for 2-step assays) input per PCR reaction; 3 replicates were run per sample at each input level (Figure 2a-b). In Study 2, to assess the usability of the secondary panel and performance of the *BCR-ABL1* tests, laboratories used the optimal sample input determined in Study 1 to test 3 sets of the panel on 6 different days (Figure 2c).

Study 1: sample input optimization

The WHO panel did not offer recommendations on sample input for IS calibration. Nonetheless, sample input outside of the linear dynamic range of a qRT-PCR assay might potentially lead to inaccurate results. Thus, we designed a standard curve experiment to help laboratories determine the optimal sample input of the secondary panel for their *BCR-ABL1* tests (Figure 2a-b). Surprisingly, approximately half of the tests showed different %BCR-ABL1 results against different sample inputs of the same sample ($P < 0.05$), even when data from either the highest or lowest sample input were allowed to be removed based on auxiliary-pick-regression analysis (Figure 3 and supplementary information). Among the 42 assays that tested Vial A (MR¹), 29% (12 of 42) showed decreasing %BCR-ABL1 with increasing sample input (Figure 3d), and 24% (10 of 42) showed increasing %BCR-ABL1 (Figure 3g and Supplementary Figure 2). Among the 45 assays that tested Vial C (MR³), 22% (10 of 45) showed decreasing %BCR-ABL1 with increasing sample input (Figure 3d), and 18% (8 of 45) showed increasing %BCR-ABL1 (Figure 3g and Supplementary Figure 3).

In this study, we observed that the mean standard deviation (SD) in %BCR-ABL1 measurements from all 45 assays was 0.2 log, which was mathematically equivalent to a 1.6-fold difference in the linear scale. Based on recommendations by Thiers *et al.*, 1 SD (0.2 log) was considered the optimal cut-off for determining differences in measurements in this study. Selecting 1 SD as the cut-off took into consideration the fact that a < 1 SD cut-off would require a substantially larger sample size to be considered statistically robust, whereas > 1 SD would increase the number of misclassifications.²³ Thus, in this study, a mean difference of ≥ 0.2 log in %BCR-ABL1 value at different sample inputs by the same test was considered as beyond the inherent variability of an assay. We found that among the assays that showed changing %BCR-ABL1 against different sample inputs, 55% (12 of 22) at MR¹ and 78% (14 of 18) at MR³ obtained results with ≥ 0.2 log difference. Overall, these results showed that some *BCR-ABL1* tests were non-linear and might therefore yield statistically different %BCR-ABL1 results against different sample inputs. To mitigate the risk of inaccurate %BCR-ABL1 measurements from using an

inappropriate sample input, it is highly recommended that laboratories standardize CML patient sample inputs by quantifying the extracted RNA prior to performing RT-qPCR.

To further investigate the cause of the unstable %BCR-ABL1 measurements across different sample inputs, we calculated the PCR efficiency and efficiency ratio for each individual *BCR-ABL1* and reference gene assay using the formula “Efficiency = $-1 + 10^{(-1/\text{slope})}$ ” (supplementary information).²⁴ A well-optimized PCR assay should have PCR efficiency between 0.9 and 1.1,²⁵ which would result in a PCR efficiency ratio of approximately 1 between the *BCR-ABL1* and reference gene assays. Indeed, we found that most assays that successfully achieved stable %BCR-ABL1 across different sample inputs had a PCR efficiency close to 1 for both the *BCR-ABL1* and reference gene assays, resulting in a mean efficiency ratio of 1.03 (n = 43; abnormal efficiency ratios of < 0 and > 10 were excluded from the analysis) (Figure 3a-c). Assays that showed decreasing %BCR-ABL1 against increasing sample input had a mean PCR efficiency ratio of 1.51 (n = 20) (Figure 3d-f), whereas assays that showed increasing %BCR-ABL1 had a mean PCR efficiency ratio of 0.63 (n = 16) (Figure 3g-i). This indicated that the lack of stability in %BCR-ABL1 against sample input was directly correlated with suboptimal PCR efficiency. Surprisingly, *BCR-ABL1* and reference gene assays that were suboptimal in similar fashion could artificially cancel each other’s defects to achieve artificially stable %BCR-ABL1 results (Figure 3j-l). Overall, these results illustrated that both the *BCR-ABL1* and reference gene assays needed to be properly optimized and validated in order to achieve good quality %BCR-ABL1 testing.^{26, 27, 28}

Since different assays had different linear dynamic ranges, we observed a > 30-fold range of optimal sample input for the secondary panel calculated for the different *BCR-ABL1* tests. Interestingly, among the 31 laboratories that routinely quantified their CML patient sample inputs, the reported patient sample input was on average 2.4-fold higher than the calculated optimal input of the secondary panel, after 2 extreme outlier values of 11.6- and 48.3-fold were identified using robust regression analysis and

excluded from the calculation (supplementary information). This was concordant with the fact that while the mean copy number of *ABL1*, *BCR* and *GUSB* per ng of RNA in the secondary panel was 674, 1028 and 1245 (Table 2b), the mean copy per ng of human EDTA anticoagulated blood RNA was only 289 for *ABL1* (n = 40), 750 for *BCR* (n = 6), and 420 for *GUSB* (n = 5) (data not shown). These results indicated that the optimal sample input of the secondary panel was approximately half of the patient sample input typically used by the laboratory in terms of ng RNA or cDNA. Thus, when using the secondary panel, laboratories might consider using 2-fold less cDNA input per PCR reaction compared to CML patient samples to achieve similar copy numbers and avoid exceeding the linear dynamic range of their assay. Nonetheless, it is recommended that laboratories perform a similar standard curve experiment to identify the optimal sample input specific for their assay prior to using the secondary panel for the first time. The optimized sample input should maximize copy number detection but minimize potential PCR inhibition caused by carryover from the reverse transcription reactions.

Study 2: performance of clinical BCR-ABL1 tests on the secondary panel

A robust *BCR-ABL1* test should demonstrate good IS accuracy, precision and sensitivity within statistical limits, especially at the lower disease levels. In Study 2, laboratories were asked to use the optimal sample input determined in Study 1 to test 3 sets of the secondary panel on 6 different days, following the design previously used by White et al. (Figure 2c).¹⁴ Results from each assay were subsequently analyzed to assess accuracy, precision and sensitivity. For IS accuracy, the overall mean %BCR-ABL1 from all 45 assays, calculated using robust regression analysis to minimize effects of outliers, were highly concordant with the assigned values of the secondary panel (Table 3 and Supplementary Figure 5). The mean ratios for all reference genes at all levels were within 1.5-fold or 0.16 log of the panel's assigned values, with the exception of Vial D (MR⁴) for *GUSB*, which differed by 1.7-fold/0.24 log. For results from

individual assays, 60% (27 of 45) obtained mean %BCR-ABL1 within 2-fold of the panel's assigned values at all levels (Supplementary Figure 5). The observed concordance was most likely due to 3 factors. First, optimal sample input calculated in Study 1 was used for each assay, thus restricting the PCR reactions within the assay's linear dynamic range. Second, even though many different assay configurations were used by the laboratories (Supplementary Table 2), 60% (27 of 45) followed the EAC recommendations for the PCR primer design²⁶ and 18% (8 of 45) used commercial *BCR-ABL1* kits (Supplementary Table 2 and Supplementary Figure 5), which are generally well optimized and validated. Lastly, 51% (23 of 45) of assays were IS calibrated via sample exchange with the reference laboratory in Mannheim, Germany and 20% (9 of 45) with Adelaide, Australia. This demonstrated that *BCR-ABL1* tests can be effectively harmonized by using the same PCR primer designs and by standardizing the IS calibration process. Thus, commercial availability of a common IS reference material could contribute to worldwide IS standardization.

Most clinical samples are typically run in only 1 or 2 replicates, which requires a high degree of assay precision to ensure accuracy of each of the final *BCR-ABL1* test results. To enable $\geq 95\%$ confidence for the true value of a CML patient sample to be within 0.5 log on each side of the measured value, a SD of < 0.25 log for the *BCR-ABL1* test is required. Accordingly, if a sample is measured at MR^{4.5}, there will be $\geq 95\%$ confidence that the true value of the sample is not above MR⁴ or below MR⁵.²⁹ We calculated the intra-lab SD for each *BCR-ABL1* test and noted that 84% (38 of 45) successfully achieved a SD of < 0.25 log from MR¹ to MR⁴. For *BCR-ABL1* tests that obtained ≥ 0.25 log SD, precision may be improved by performing further assay optimization and increasing the number of replicates per patient sample.^{28, 30}

For monitoring deep molecular response, good *BCR-ABL1* assay sensitivity and precision are key performance characteristics. In Study 2, we found that 93% (42 of 45) assays successfully detected all replicates at MR⁴, and 76% (34 of 45) detected all replicates at MR^{4.5}. To further understand how

sample input affected assay sensitivity and precision, we analyzed results from the 32 *ABL1* assays since this provided the largest sample size. Among the *ABL1* assays, 56% (18 of 32) detected all replicates at MR^{4.5} and achieved < 0.25 log SD, 19% (6 of 32) detected all replicates but had ≥ 0.25 log SD, and 25% (8 of 32) assays had at least 1 undetected replicate. Logistic regression analysis showed a strong positive correlation between increased sample input and increased detection rate ($P = 0.001$). In addition, the median *ABL1* copy number per PCR reaction was 98 202 for laboratories that achieved good detection rate and precision, 74 923 for those that achieved good detection rate but suboptimal precision, and 29 717 for those that had undetected replicates at MR^{4.5}, further illustrating that an increased sample input could improve the sensitivity and precision of MR^{4.5} detection.

The laboratories that participated in this study utilized diverse assay configurations for *BCR-ABL1* testing (Supplementary Table 2). To determine if assay configurations affected assay performance in terms of IS accuracy, precision, and sensitivity, we performed Bayesian average analysis and found no statistically significant relationship between assay performance versus choice of reference gene, RNA extraction method and the usage of commercial versus LDT assays. Interestingly, among the assays that successfully achieved good accuracy (within 2-fold of assigned values), good precision (< 0.25 log SD) and good MR^{4.5} sensitivity (no undetected replicate), 82% (14 of 17) showed stable %BCR-ABL1 measurements against sample inputs at MR³ in Study 1, compared to 46% (13 of 28) among assays with less optimal assay performance. This illustrated that while *BCR-ABL1* assays of different designs can perform equally well, proper PCR optimization is required to ensure good clinical performance. Interestingly, the number of assays that achieved good precision (84%) and MR^{4.5} (76%) sensitivity exceeded the number that achieved good IS accuracy (60%), indicating that there remains an unmet need for a simple and broadly available IS calibration mechanism.

Calculating WHO IS CF from the secondary panel

Using the assigned *BCR-ABL1* IS values of the secondary panel, it was possible to calculate an IS CF traceable to the WHO panel for each test. Prior to CF calculation, Bland-Altman analysis was performed for each assay as described by White *et al.*¹⁴ to assess if bias was linear across the %BCR-ABL1 range. Of all the assays, 69% (31 of 45) showed no statistically significant trend in the Bland-Altman analysis, indicating that a valid CF could be calculated for these assays and compared to the laboratory's current CF, most of which were obtained from sample exchange. Mathematically, when the ratio between the assay's current CF and the CF calculated from the secondary panel is < 0.63 or > 1.58 , the resulting %BCR-ABL1 values will have a > 0.2 log difference (supplementary information). Among the 31 assays, 58% (18 of 31) achieved a CF ratio between 0.63 and 1.58, indicating that their current CF was equivalent to the CF from the secondary panel. This was concordant with the fact that 60% of assays obtained mean %BCR-ABL1 within 2-fold of the panel's assigned values. This also indicated that the secondary panel can be effectively used to obtain IS CFs equivalent to sample exchange.

DISCUSSIONS

In this study, we successfully created the first cell-based *BCR-ABL1* secondary reference panel that faithfully replicated the WHO *BCR-ABL1* International Genetic Reference Panel in both raw material and manufacturing methods,¹⁴ with an additional MR^{4.5} level. The secondary panel was manufactured under Good Manufacturing Practice and confirmed to have low residual moisture content, vial-to-vial homogeneity and > 2.5 -year stability. *BCR-ABL1* IS values traceable to the WHO panel were assigned to the secondary panel using RT-ddPCR against *ABL1*, *BCR*, and *GUSB*. Both the assigned IS values and

absolute copy numbers of the secondary panel were found to be highly concordant with the primary WHO standards.

Many of the 44 laboratories that participated in the secondary panel evaluation currently act as a national reference laboratory for their country. The panel was successfully processed by all laboratories, indicating that it is compatible with many different *BCR-ABL1* test configurations. Through a standard curve experiment, we found that close to half of the tests showed signs of inadequate PCR optimization such as poor linearity against different sample inputs and suboptimal PCR efficiency. Interestingly, when a customized optimal sample input was used, 60% (27 of 45) of assays achieved mean %*BCR-ABL1* values within 2-fold of the panel's assigned values, 84% (38 of 45) achieved good precision (≤ 0.25 log SD) from MR¹ to MR⁴, and 76% (34 of 45) achieved 100% detection rate down to MR^{4.5}. Three factors likely contributed to these excellent results: usage of a validated optimized sample input specific to the assay, the fact that 78% (35 of 45) assays used either the EAC primer design or a commercial kit, and that 71% (32 of 45) assays were IS calibrated via sample exchange with one of the two major international reference centers. This indicated that using published assay designs and a harmonized IS calibration approach may lead to *BCR-ABL1* test standardization. Nonetheless, we noted that the number of assays that achieved good precision and sensitivity exceeded the number that achieved good IS accuracy, indicating that there remains an unmet need for a simple and broadly available calibration mechanism, such as this secondary panel, to ensure IS accuracy is maintained in laboratories over time.

We also showed that different assay designs, including different reference genes, RNA extraction methods and usage of commercial kits versus LDTs did not affect assay performance. Nonetheless, better PCR optimization correlated with better assay performance, and increased sample input improved detection rate and precision at MR^{4.5}. In addition to being a reference sample for IS calibration,¹⁴ the secondary reference material and its derivatives could also be used in assay analytical

validation and optimization. For example, it can be used as standardized samples in External Quality Assessment (EQA) programs for proficiency testing,³¹ especially since nominal values (i.e. correct answers) are available for each member of the panel. Second, it can become a source of positive control samples to be run alongside patient samples for quality assurance. This can become especially powerful when multiple laboratories participate in a peer group quality control monitoring program, in which results from such positive control samples are compared and monitored regularly. Lastly, the MR^{4.5} sample in the reference panel can be used to validate the sensitivity and MR^{4.5} detection capability of an assay.

In conclusion, a secondary reference panel traceable to the WHO panel with an additional MR^{4.5} level can provide easier access to IS calibration, as well as act as a tool for assay optimization, validation and quality assurance.

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FIGURE LEGENDS

Figure 1: The *BCR-ABL1* secondary reference panel was calibrated to the WHO standards using RT-ddPCR against (a) *ABL1*, (b) *BCR*, and (c) *GUSB* for IS conversion ($n = 40$ from MR^1 to MR^4 , $n = 80$ for $MR^{4.5}$). The IS CFs for the RT-ddPCR assays were determined to be 0.93 for the *BCR-ABL1/ABL1* assay, 1.85 for the *BCR-ABL1/BCR* assay, and 1.28 for the *BCR-ABL1/GUSB* assay. Blue dotted lines represent the nominal %BCR-ABL1 value of the WHO panel at different levels.

Figure 2: Study design for the international multi-center evaluation of the secondary panel, including (a) Study 1 for 1-step RT-qPCR tests, (b) Study 1 for 2-step RT-qPCR tests, and (c) Study 2.

Figure 3: Examples of different assay results from Study 1 of the multi-center evaluation study. A properly optimized assay should yield similar %BCR-ABL1 results at different sample inputs, and both the *BCR-ABL1* and reference gene assays should have a PCR efficiency close to 1 (a-c). Some assays showed decreasing %BCR-ABL1 measurements with increasing sample input (d-f), whereas others showed increasing %BCR-ABL1 measurements instead (g-i). The PCR efficiency of these assays tended to be suboptimal (< 0.9 or > 1.1), resulting in disproportional increase of *BCR-ABL1* or reference gene copy number with increasing sample input (e, f, h, i), which subsequently led to the unstable %BCR-ABL1 measurements (d, g). Occasionally, *BCR-ABL1* and reference gene assays that were suboptimal in similar manner could cancel each other's defects to achieve artificially stable %BCR-ABL1 measurements (j-l). Red lines represent the linear regression fit based on actual data, and blue lines represent what ideal data should resemble.

Table 1: Primer and probe sequences for the RT-ddPCR assays.

Gene	Primer/Probe	Sequence (5' – 3')
BCR-ABL1	Forward primer	CCGCTGACCATCAATAAGGAA
	FAM MGB Probe	AAGCCCTTCAGCGGC
	Reverse primer	CTGAGGCTCAAAGTCAGATGCTACT
ABL1	Forward primer	ACCACTGACGTGCCTGAGATG
	FAM MGB Probe	AGAGAGCGATCCTCTGG
	Reverse primer	GAGACACGGCAGGCTCATG
BCR	Forward primer	CACTCAGCCACTGGATTTAAGC
	FAM MGB Probe	CCTGGAGGTGGATTC
	Reverse primer	CGCGTCTTTGCTTTATTACAA
GUS	Forward primer	ACGCAGAAAATACGTGGTTGG
	FAM MGB Probe	CTCATTTGGAATTTTGCCGAT
	Reverse primer	GCCGAGTGAAGATCCCCTTT

Table 2: The *BCR-ABL1* secondary reference panel was highly concordant with the WHO panel in (a) empirical and %BCR-ABL1^{IS} values, and (b) copy numbers of *ABL1*, *BCR-ABL1*, *BCR* and *GUSB* per ng of RNA.

(a)

Reference Gene	RT-ddPCR IS Conversion Factor	WHO Panel			Secondary Panel		
		Panel Member	Mean Empirical %BCR-ABL1	Nominal %BCR-ABL1 ^{IS}	Panel Member	Mean Empirical %BCR-ABL1	Assigned %BCR-ABL1 ^{IS}
<i>ABL1</i>	0.93	4 (08/198)	11.2250	10.7469	A	13.7178	12.7575
		3 (08/196)	1.2540	1.1672	B	1.2841	1.1942
		2 (08/194)	0.1260	0.1112	C	0.1095	0.1019
		1 (08/192)	0.0130	0.0118	D	0.0116	0.0108
					E	0.0041	0.0038
<i>BCR</i>	1.85	4 (08/198)	9.8135	16.3129	A	11.5502	21.3678
		3 (08/196)	0.8441	1.6627	B	0.7300	1.3505
		2 (08/194)	0.0988	0.1753	C	0.0759	0.1404
		1 (08/192)	0.0098	0.0195	D	0.0081	0.0150
					E	0.0027	0.0050
<i>GUSB</i>	1.28	4 (08/198)	6.5834	10.1235	A	9.1800	11.7504
		3 (08/196)	0.5924	0.8295	B	0.6219	0.7960
		2 (08/194)	0.0677	0.0749	C	0.0628	0.0804
		1 (08/192)	0.0065	0.0071	D	0.0068	0.0087
					E	0.0023	0.0029

(b)

Panel	Member	Mean Copy Number Per ng RNA			
		<i>BCR-ABL1</i>	<i>ABL1</i>	<i>BCR</i>	<i>GUSB</i>
Secondary Panel	A	103.27	754.55	973.44	1198.94
	B	8.56	665.80	1058.25	1238.22
	C	0.72	651.95	1012.51	1261.53
	D	0.08	653.85	1079.15	1283.79
	E	0.03	642.71	1017.74	1244.11
WHO Panel	4 (08/198)	92.98	831.74	948.59	1380.43
	3 (08/196)	9.75	778.56	1036.91	1454.12
	2 (08/194)	0.99	784.95	1004.05	1390.83
	1 (08/192)	0.10	785.90	1033.21	1388.23

Table 3: Summary results of the secondary panel international multi-center evaluation study.

Reference Gene	Number of Labs	Vial (WHO / Secondary Panel)	%BCR-ABL1 ^{IS}					
			WHO Panel	Secondary Panel	Results From 45 <i>BCR-ABL1</i> Assays			
			Nominal	Assigned	Mean	SD	Minimum	Maximum
ABL	32	4 (08/198) / A	10.7469	12.7575	11.4450	8.2225	3.6127	37.4603
		3 (08/196) / B	1.1672	1.1942	1.1771	0.9994	0.4014	4.4109
		2 (08/194) / C	0.1112	0.1019	0.1013	0.0931	0.0362	0.4553
		1 (08/192) / D	0.0118	0.0108	0.0110	0.0232	0.0033	0.1323
		NA / E		0.0038	0.0038	0.0038	0.0013	0.0159
BCR	5	4 (08/198) / A	16.3129	21.3678	21.3999	12.3547	13.6781	42.5295
		3 (08/196) / B	1.6627	1.3505	1.7243	1.2662	1.0215	4.2655
		2 (08/194) / C	0.1753	0.1404	0.1615	0.0863	0.0881	0.3025
		1 (08/192) / D	0.0195	0.0150	0.0153	0.0105	0.0071	0.0302
		NA / E		0.0050	0.0056	0.0047	0.0028	0.0134
GUS	8	4 (08/198) / A	10.1235	11.7504	8.9008	3.7900	4.5344	14.9359
		3 (08/196) / B	0.8295	0.7960	0.7346	0.4133	0.3514	1.5494
		2 (08/194) / C	0.0749	0.0804	0.0587	0.0351	0.0218	0.1149
		1 (08/192) / D	0.0071	0.0087	0.0050	0.0033	0.0010	0.0106
		NA / E		0.0029	0.0020	0.0018	0.0005	0.0054

Figure 1

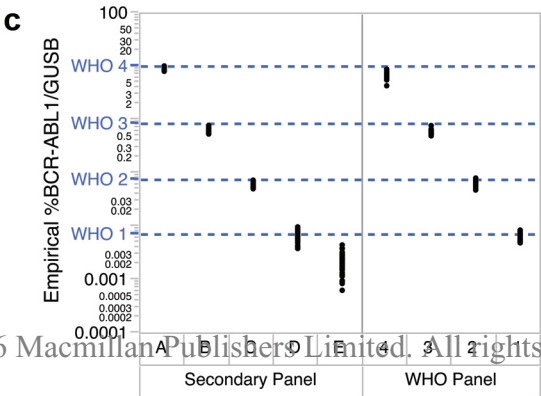
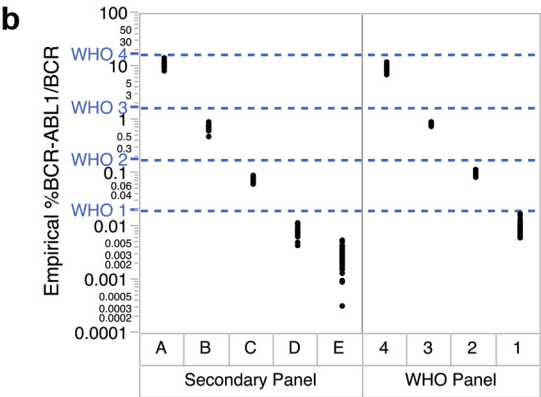
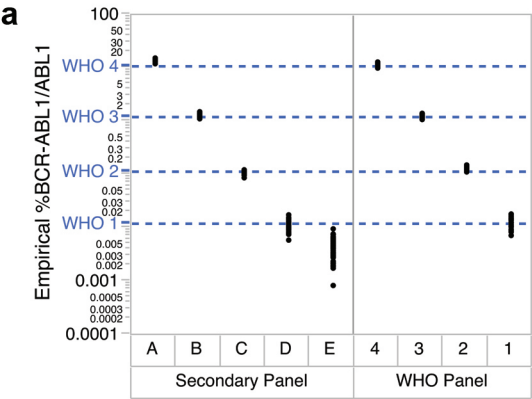
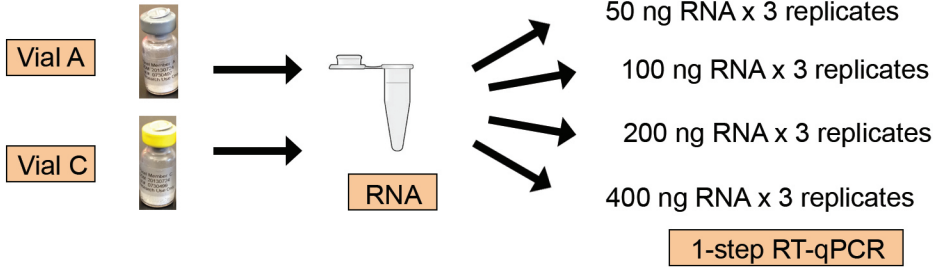
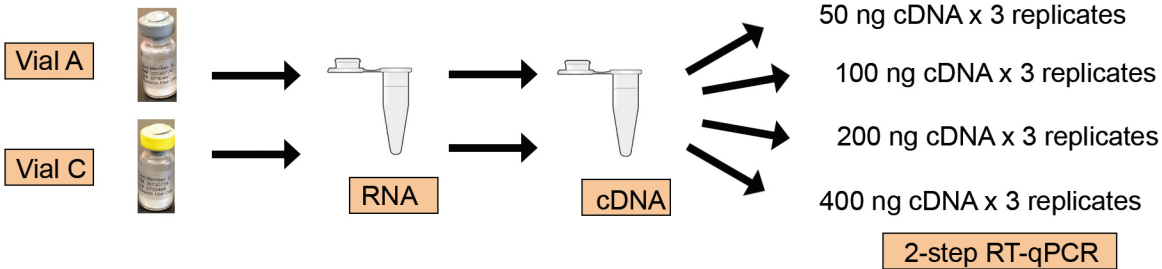


Figure 2

a



b



c

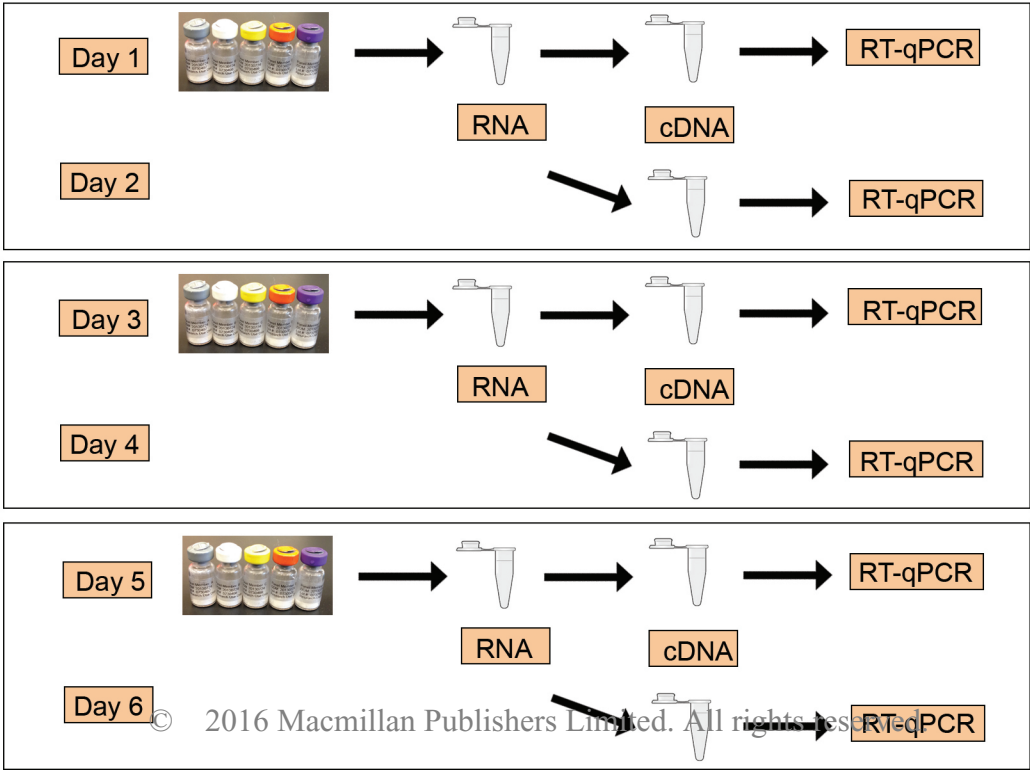


Figure 3

