

Enhancing Patient-specific Quality Assurance in Carbon-ion Radiation Therapy: Recalculating Delivered Dose Distribution Using Log Data

YONGDO YUN¹, MIN CHEOL HAN¹, CHANGHWAN KIM¹, CHAE-SEON HONG¹, DONG WOOK KIM¹, HO LEE¹, HOJIN KIM¹, SOORIM HAN¹, HIKARU SOUDA², SUNG HYUN LEE³, YUYA MIYASAKA², TAKEO IWAI² and JIN SUNG KIM^{1,4}

¹Department of Radiation Oncology, Yonsei Cancer Center, Heavy Ion Therapy Research Institute, Yonsei University College of Medicine, Seoul, Republic of Korea;

²Department of Heavy Particle Medical Science, Graduate School of Medical Science, Yamagata University, Yamagata, Japan;

³Department of Radiation Oncology, Seoul National University College of Medicine, Seoul, Republic of Korea;

⁴Oncosoft Inc., Seoul, Republic of Korea

Abstract

Background/Aim: Log data from radiation treatment machines can play a crucial role in quality assurance by enabling the recalculation of the delivered dose distribution and identification of deviations in treatment delivery. This article proposes a novel method for recalculating the delivered dose distribution in carbon-ion radiation therapy using log data. **Materials and Methods:** The proposed approach leverages existing functionality in commercial treatment planning systems, thus eliminating the need for specialized in-house software for dose calculation and evaluation. The performed tests entail data generation from actual log files using the Digital Imaging and Communications in Medicine standard, biological dose calculations, and gamma evaluations.

Results: The log-based approach demonstrated notable advantages, including improved time efficiency and the ability to calculate three-dimensional biological doses. By recalculating the delivered dose distributions, our method improves quality assurance accuracy in carbon-ion radiation therapy. It complements conventional measurement-based patient-specific quality assurance methods, serving as a valuable addition to the arsenal of tools available for treatment evaluation.

Conclusion: We believe that our method has the potential to enhance the efficacy of patient-specific quality assurance and contribute significantly to the advancement of carbon-ion radiation therapy, thereby reinforcing the ongoing evolution of particle therapy.

Keywords: Carbon-ion radiation therapy, log data, patient-specific quality assurance, treatment planning system, biological dose distribution.



Min Cheol Han, Department of Radiation Oncology, Yonsei Cancer Center, 50-1, Yonsei-ro, Seodaemun-gu, Seoul, 03722, Republic of Korea. Tel: +82 222277823, e-mail: mchan@yuhs.ac; Jin Sung Kim, Department of Radiation Oncology, Yonsei Cancer Center, 50-1, Yonsei-ro, Seodaemun-gu, Seoul, 03722, Republic of Korea. Tel: +82 222288118, e-mail: jinsung@yuhs.ac

Received December 19, 2024 | Revised January 7, 2025 | Accepted January 8, 2025



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Introduction

Particle therapy comprising proton and carbon-ion radiation therapies (CIRT) has emerged as a precise and effective radiotherapy (RT) modality for treating cancer, surpassing the conventional photon therapy (1-4). Particle therapy enables targeted tumor treatment while minimizing damage to normal tissue by capitalizing on a unique physical property known as the Bragg peak effect. However, steep dose falloffs of the Bragg peak pose a significant challenge in particle therapy (5) because even minor changes can have a substantial impact on treatment outcomes (6). To ensure the effectiveness and safety of particle therapy, precise imaging, accurate patient setup, meticulous dose calculations, and robust quality assurance (QA) procedures must be prioritized. In this context, the log data generated by treatment machines can play a pivotal role in evaluating these conditions (7-14). Log data encompass essential information concerning the treatment delivery process, including parameters such as delivered beam energy, intensity, spot positions, and patient setup details. By leveraging these log data, it is possible to recalculate the three-dimensional (3D) delivered dose distribution to perform comprehensive QA that includes the verification of treatment accuracy and identification of deviations or errors in beam delivery, which may affect treatment outcomes.

Several studies have explored the development of in-house patient-specific QA (PSQA) systems based on log data from photons (15), protons (7-9, 12, 13), and carbon-ion treatment machines (11, 14, 16). Recently, log-based PSQA has been facilitated using various commercial software packages such as Mobius3D (Varian Medical Systems, Palo Alto, CA, USA), SunCheck™ Patient (Sun Nuclear Corp, Melbourne, FL, USA), and myQA iON (IBA Dosimetry GmbH, Schwarzenbruck, Germany). However, at the time of writing this manuscript, the commercial software for CIRT had not been released, necessitating the development of in-house software. In practice, developing a log-based PSQA system for CIRT is challenging owing to several inherent difficulties, particularly those related to biological dose calculations.

In this study, we developed a novel general method for recalculating the delivered dose distribution in CIRT using log data. In particular, we focused on spot-scanning techniques for CIRT and developed a method that recalculates the delivered physical and biological doses utilizing commonly employed treatment planning systems (TPSSs), thereby eliminating the need to develop specific in-house software (17-19). By introducing log-based dose calculations, our method aims to enhance PSQA systems and improve the overall quality and safety of CIRT.

Materials and Methods

Schematic design of log-based PSQA for CIRT. This study aimed to create a new RT plan for PSQA based on the logged parameters of a CIRT machine, which are encoded using the Digital Imaging and Communications in Medicine (DICOM) standard. Figure 1 shows a schematic of the proposed method, which can be used to obtain a log-based delivered RT plan for PSQA.

Log data information generated from CIRT. A log file generated by a CIRT machine typically adopts the format of DICOM-RT records, thus adhering to the standard of “RT Ion Beams Treatment Record Storage”. Log data include various beam parameters and treatment configurations recorded during the treatment delivery process. The proposed log-reconstructed 3D dose distribution relies on the following key modules for accurate delivered dose reconstruction.

Delivered Meterset Information: This module is embedded within the RT record and provides details regarding the delivered dose for each spot during treatment. These data are obtained from the dose monitor and monitor units (MUs) or number of particles (NPs), which are adopted as meterset units depending on the beam model configuration.

Delivered Spot Position: This module determines the positioning of the treatment beam spot using the X and Y magnets installed in a carbon-ion beam nozzle. The actual spot position may deviate slightly from the planned position. Therefore, the delivered spot position is captured using a beam-positioning monitor.

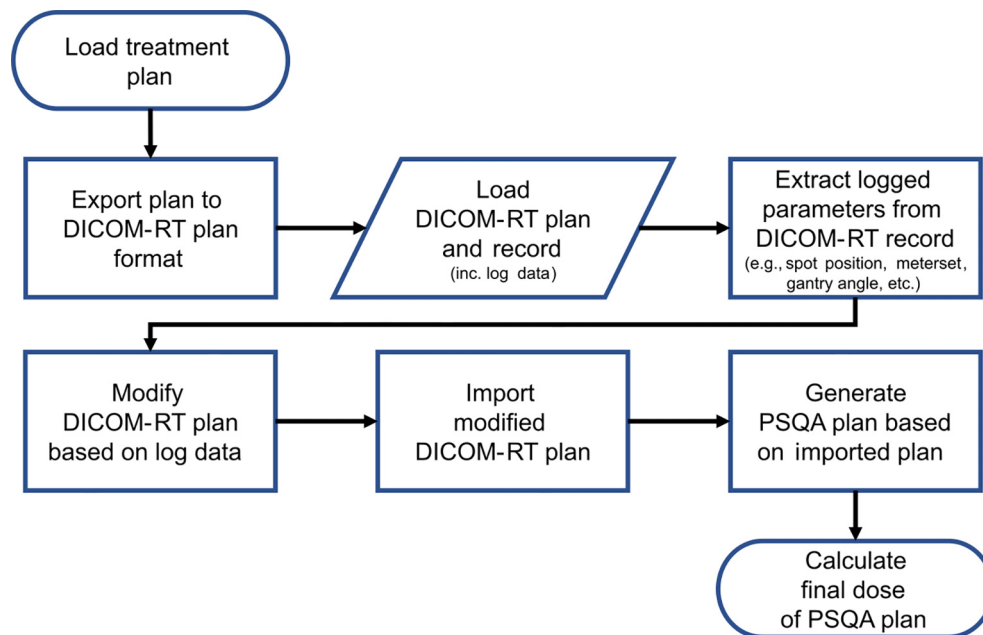


Figure 1. Schematic of log-based patient-specific quality assurance (PSQA) for carbon-ion radiation therapies (CIRT). DICOM-RT: Digital Imaging and Communications in Medicine- radiotherapy.

Setup Position Information: This module extracts crucial information regarding the patient's setup position during treatment preparation. Specifically, the gantry angle and couch position information (X, Y, and Z coordinates and roll, pitch, and yaw angles) are utilized to recalculate the distribution of the delivered dose.

Matching between plan and log data. Before calculating a new log-based RT plan, matching between the original RT plan and log data information needs to be accurately verified. Log data, typically written in RT-record format, include a reference unique identifier (UID) that can be utilized for this purpose. However, the reference UID and the original RT-plan UID may not always match owing to the presence of additional information, such as beam delivery instructions. Therefore, despite consistency between plans and delivered information, distinct UIDs may result due to these differences. To overcome this issue, we compared the number of medical records and spots of the original RT plan and log data to match the information.

Validation test. The validation test is aimed at assessing the proposed method for calculating the delivered dose for PSQA using a real log data file. For the test, we created a delivered RT plan based on a CIRT plan using a pelvic phantom and the corresponding log data. Subsequently, the RT plan was imported into a commercial treatment planning system (TPS), specifically the RayStation 11B (RaySearch Laboratories, Stockholm, Sweden), to calculate the delivered dose distribution. In this study, we calculated the biological dose distributions of the delivered doses.

To evaluate the agreement between the planned and delivered dose distributions, we employed several metrics. Specifically, we analyzed the dose-volume histogram (DVH) and calculated the dose differences to perform a 3D gamma evaluation with 3% and 3-mm criteria (20) and assessed spot position differences. The proposed method for generating the delivered RT plan was coded using Python, supported by RayStation scripting. DICOM handling and gamma evaluation were performed using the *pydicom* and *pymedphys* libraries, respectively.

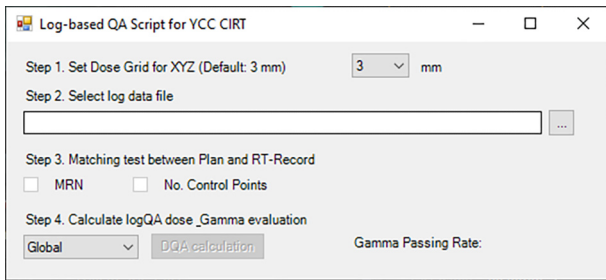


Figure 2. Screenshot of the log-based patient-specific quality assurance script user interface developed in this study – the script was tested in RayStation.

Lastly, we applied our methodology to patient cases. We collected log files from five prostate cancer patients, each undergoing 12 fractions of treatment. All patient data were anonymized to ensure that individual patients could not be identified during the study. The analysis was performed using the same method as the previously described phantom case. This study design was approved by the Institutional Review Board (IRB) of Yonsei University Hospital (approval number: 4-2023-0763).

Results

Figure 2 shows a screenshot of the log-based PSQA script system used in this study. As shown in the figure, the displayed configuration is divided into four parts: 1) setting the dose grid for the analysis, 2) selecting the log data file, 3) testing the match between the plan and RT record, and 4) selecting the analysis methods for gamma evaluation and calculation.

Figure 3 illustrates the differences in the spot position and couch position of the planned (left) and delivered (right) data derived from a log file. The delivered data, including the actual positions and logged couch information, were effectively implemented in the selected TPS. Figure 4 shows a screenshot of the evaluation tab in the TPS, which facilitates the calculation of the differences in the biological dose distribution and DVHs for each pelvic phantom plan. The dose value from the planned dose distribution was optimized using the microdosimetric kinetic model (MKM)

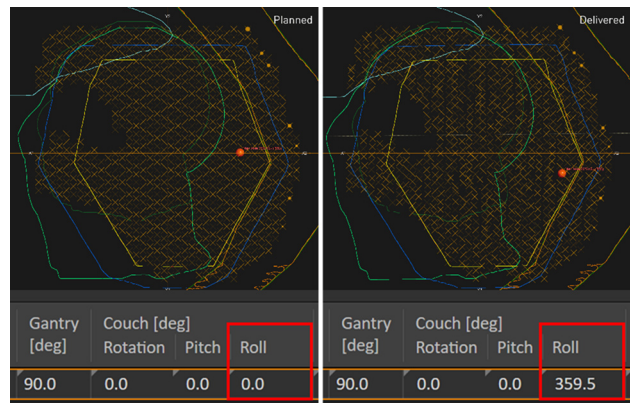


Figure 3. Example of spot position map and setup information obtained from the planned (left) and delivered data (right) derived from a log file. In the delivered section, the spot positions and couch roll information were slightly changed according to the logged data.

(21). Similarly, the delivered dose distribution was calculated by applying the MKM to the planned data.

The results of the gamma evaluation yielded a gamma-passing rate of 100%. Figure 5 shows the gamma histogram and spot position differences plotted against the spot ID number. The root mean square errors of the spot positions in the X- and Y-directions were both 0.24 mm. Notably, outlier points in the spot position differences were observed in the regions with a small number of MUs.

Lastly, RT records from 12 fractions for each patient were imported into the script to evaluate the fractional dose distributions. Our results, which were obtained using the same criteria as those applied to the gamma index, indicated gamma-passing rates of above 99.97%±0.01% for all five patients.

Discussion

Our test results confirmed that the implementation of the log-based PSQA using a commercial TPS was successful. Moreover, the calculation of the delivered dose distribution yielded satisfactory outcomes. The computational time required by the proposed approach only amounts to that required for the final calculation of the delivered plan, which was below 1 min for a single-port beam on the pelvic

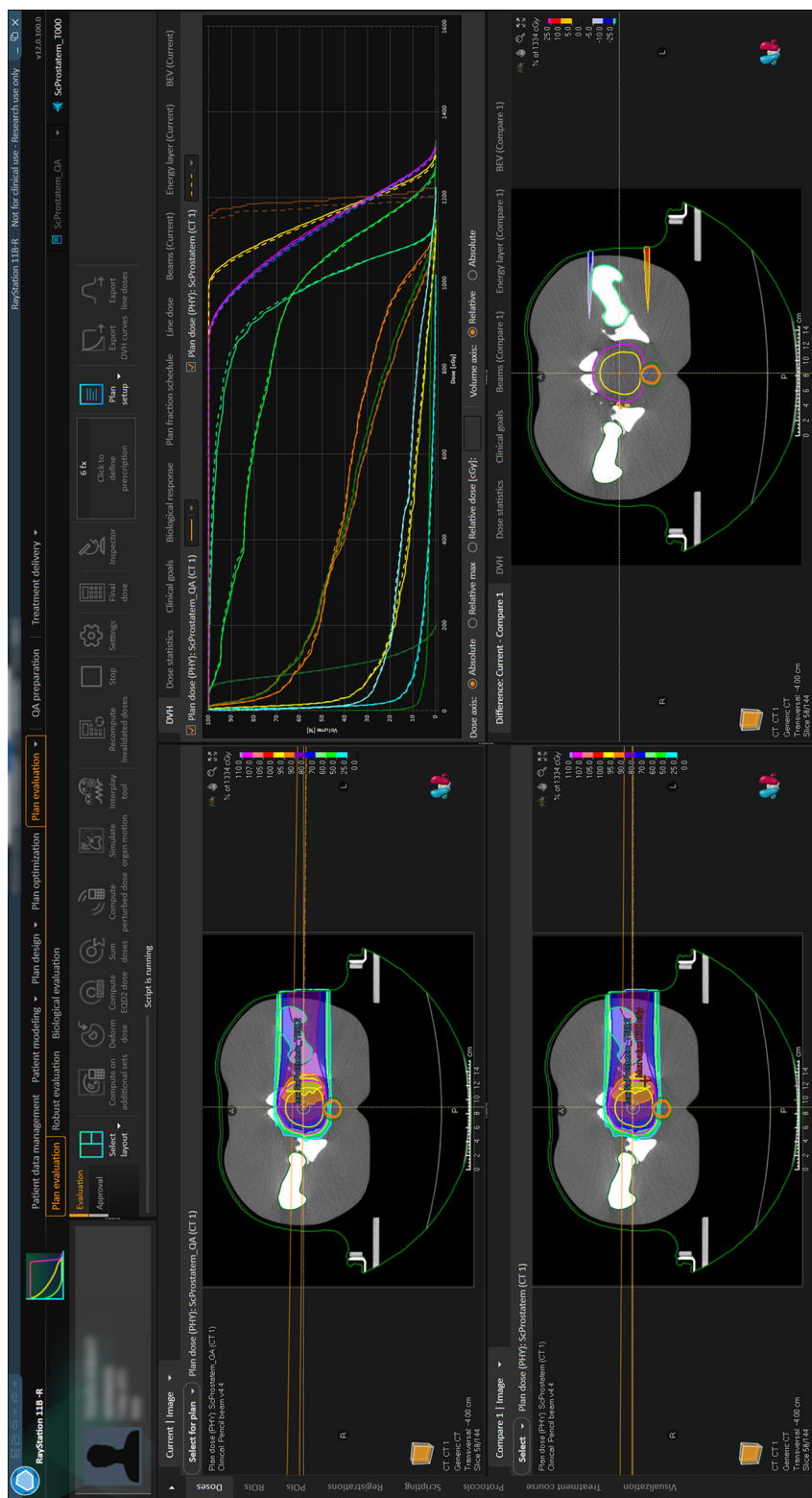


Figure 4. Example of biological dose distribution comparison of planned (bottom-left) and delivered data (top-left) using their difference (bottom-right) in a commercial treatment planning system (TPS). The TPS calculates the dose-volume histograms (DVHs) (top-right) for each plan.

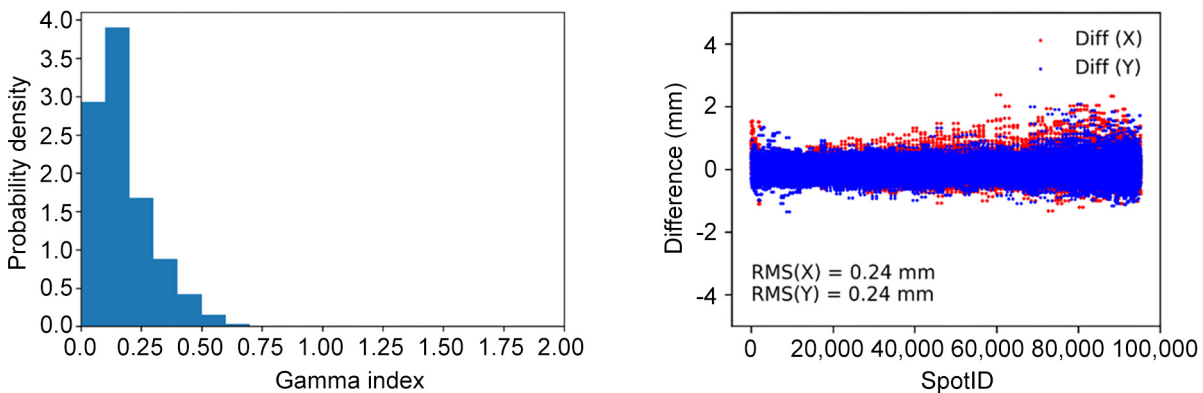


Figure 5. Example of gamma index histogram of the tested plan (left) and spot position differences plotted against the beam spot ID (right).

phantom CT. This represents a reasonable timeframe for effective clinical applications of the proposed log-based PSQA method.

Log-based PSQA offers several advantages compared with measurement-based PSQA. First, the log-based PSQA exhibits improved time performance in the clinical workflow as it does not require additional beam deliveries such as repeated two-dimensional (2D) measurements to acquire dose distributions at different slices. Second, unlike the measurement-based PSQA that requires a homogeneous QA phantom, the log-based PSQA calculates the 3D biological dose distribution directly using patients' CT images. Finally, the log-based PSQA enables the evaluation of the delivered dose for all the patient's fractions, providing a comprehensive assessment of treatment accuracy throughout the treatment course. This aspect is particularly valuable because it enables the identification of any variation or deviation in dose delivery that may occur over the treatment duration. In addition, this feature represents a general advantage of software-based PSQA, and the same applies to CIRT.

A beneficial aspect of the log-based PSQA is its potential as an alternative solution for MUs accuracy checks. The accuracy of the monitor can be compromised by possible degradation of the multiwire proportional counter (MWPC) installed in front of it. Although the discrepancy in the values measured using an ion chamber and the monitor during daily QA can be used to prevent this, value correction across all wires of the MWPC may still be a challenging

process owing to the high probability of degradation at the center of the detector, that is, the status of degradation is not uniform. Considering that the log file records information from all areas of the MU monitor, this data can be used to ensure that the status of the MWPC reflects the consistency of measurement-based PSQA.

A practical limitation of the proposed approach is the assumption that the dose reconstruction is performed using an optimally calibrated beam machine. The delivered dose calculation cannot identify machine-specific states, such as laser setup errors, couch sagging, and patient setup uncertainties. Therefore, rigorous daily and monthly QA procedures under the supervision of medical physicists are essential for the log-based PSQA. Moreover, by performing measurement-based and log-based PSQA simultaneously using the log generated by the measurement PSQA, the correlation between the two PSQA methods can be validated. This is necessary in a clinical setting because after irradiating a patient with fractional treatments, the measurement-based pre-treatment PSQA is no longer executed, whereas the log-based PSQA can still be performed.

Another limitation of our approach is the independent calculations performed using the dose calculation algorithm. Identifying issues originating from the dose calculation algorithm is challenging because, currently, TPSs such as RayStation (RaySearch Laboratories, Stockholm, Sweden) and XiO (Elekta AB, Stockholm, Sweden) are the only available commercial dose calculation software for

CIRT. To address this problem, a Monte Carlo-based dose calculation method (22) may be applied for comparison to ensure independent dose calculations.

During our evaluations using two identical Toshiba machines installed at two different institutes, we encountered an issue that resulted in a situation where the positions of specific spots could not be tracked in the log file. In such instances, the MWPC provided position readings that significantly exceeded the standard operational range, which is normally within a maximum numeric range of 200×200 , corresponding to -100 to 100 on each axis. This problem occurred identically for both machines, although the location of occurrence differed in the two sites. The vendor referred to this observation as a calculation failure, noting that this type of issue can occur stochastically, depending on the voltage applied to the positioning monitor. In a total of 60 cases, a calculation failure rate of $0.25\% \pm 0.02\%$ occurred, and the value of the corresponding positions was located outside the field. To address this issue, our procedure replaces the incorrect values with the ideal position, that is, the planned position. The errors resulting from stochastic calculation failures are considered negligible. In our tests, a comparison between the dose distributions at the ideal position and an artificial position (adjusted by averaging the position error calculated using the RMS method) demonstrated a gamma-passing rate of over 99.99% (using a criterion of $1 \text{ mm}/1\%$).

Conclusion

In this study, we developed a method for recalculating the delivered dose distribution for CIRT using log data. Our results confirmed that the proposed method can significantly enhance the speed of PSQA procedures in CIRT by providing 3D recalculations of both physical and biological dose distributions. Our method employs a commercial TPS and requires reduced 2D detector array measurements. However, measurement-based QA methods are still necessary for absolute dose measurement. To promote the development of open software for log-based PSQA, the RayStation script used in this study is available for

download on a dedicated website (23). In conclusion, the proposed method for recalculating the delivered dose distribution using log data has the potential to contribute significantly to the continuous evolution of CIRT by optimizing QA procedures.

Conflicts of Interest

The Authors declare that they have no known competing financial interest or personal relationships that could have appeared to influence the work reported in this article.

Authors' Contributions

Conceptualization: Min Cheol Han; Data curation: Yongdo Yun, Min Cheol Han, Soorim Han; Formal analysis: Yongdo Yun; Funding acquisition: Min Cheol Han, Jin Sung Kim; Investigation: Yongdo Yun, Min Cheol Han; Methodology: Min Cheol Han, Changhwan Kim, Chae-Seon Hong, Dong Wook Kim, Hojin Kim, Ho Lee, Soorim Han, Hikaru Souda, Sung Hyun Lee, Yuya Miyasaka; Project administration: Min Cheol Han; Software: Yongdo Yun, Min Cheol Han; Supervision: Takeo Iwai, Jin Sung Kim; Validation: Yongdo Yun, Soorim Han; Visualization: Yongdo Yun, Min Cheol Han; Writing – original draft: Yongdo Yun, Min Cheol Han; Writing – review & editing: Yongdo Yun, Min Cheol Han.

Acknowledgements

This research was supported by Quantum Computing based on Quantum Advantage challenge research (RS-2023-00257561) through the National Research Foundation of Korea (NRF) funded by the Korean government (Ministry of Science and ICT(MSIT)). This work was supported by the Korea Medical Device Development Fund grant funded by the Korea government (the Ministry of Science and ICT, the Ministry of Trade, Industry and Energy, the Ministry of Health & Welfare, the Ministry of Food and Drug Safety) (Project Number: 1711196793, RS-2023-00255061). This work was supported by Korea Institute for Advancement of Technology (KIAT) grant funded by the government of the

Republic of Korea (P0026103). This study was supported by a faculty research grant from the Yonsei University College of Medicine (6-2022-0105).

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