

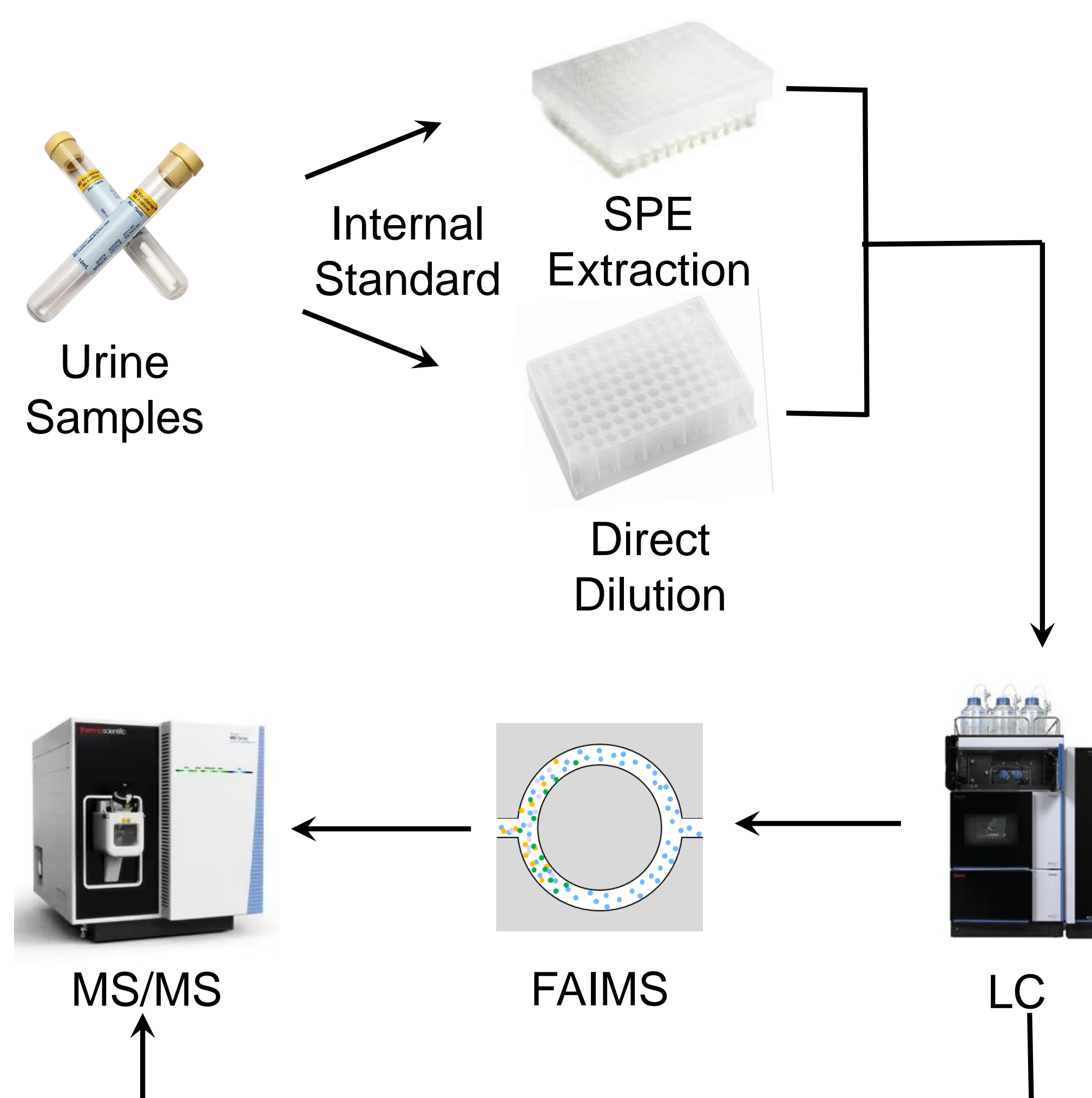
Development of Simple LC-FAIMS-MS/MS Method for the Quantification of Nicotine and Its Metabolites in Urine

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BACKGROUND

The use of tobacco products, particularly smoking, is the main preventable cause of lung cancer in the U.S. Nicotine is the active component in tobacco, responsible for addiction. The clinical test for nicotine and its metabolites in urine is a widely accepted method to evaluate nicotine exposure. In addition, anabasine, an analog of nicotine present in trace amounts in tobacco products, is also used as an indicator for monitoring compliance in tobacco cessation and effectiveness in nicotine replacement therapy. Currently, the conventional methods used to detect these molecules in the clinical laboratory are direct dilution or solid phase extraction (SPE), followed by LC-MS/MS analysis. However, direct dilution and injection methods may introduce bias in quantification and are prone to interferences, especially with low concentration samples. SPE purification is effective at overcoming these limitations, but this technique adds cost and labor to the analysis. Here, we present a novel LC-FAIMS-MS/MS method capable of detecting nicotine and its metabolites in urine with better sensitivity and specificity, without adding labor and cost.

WORKFLOW



RESULTS

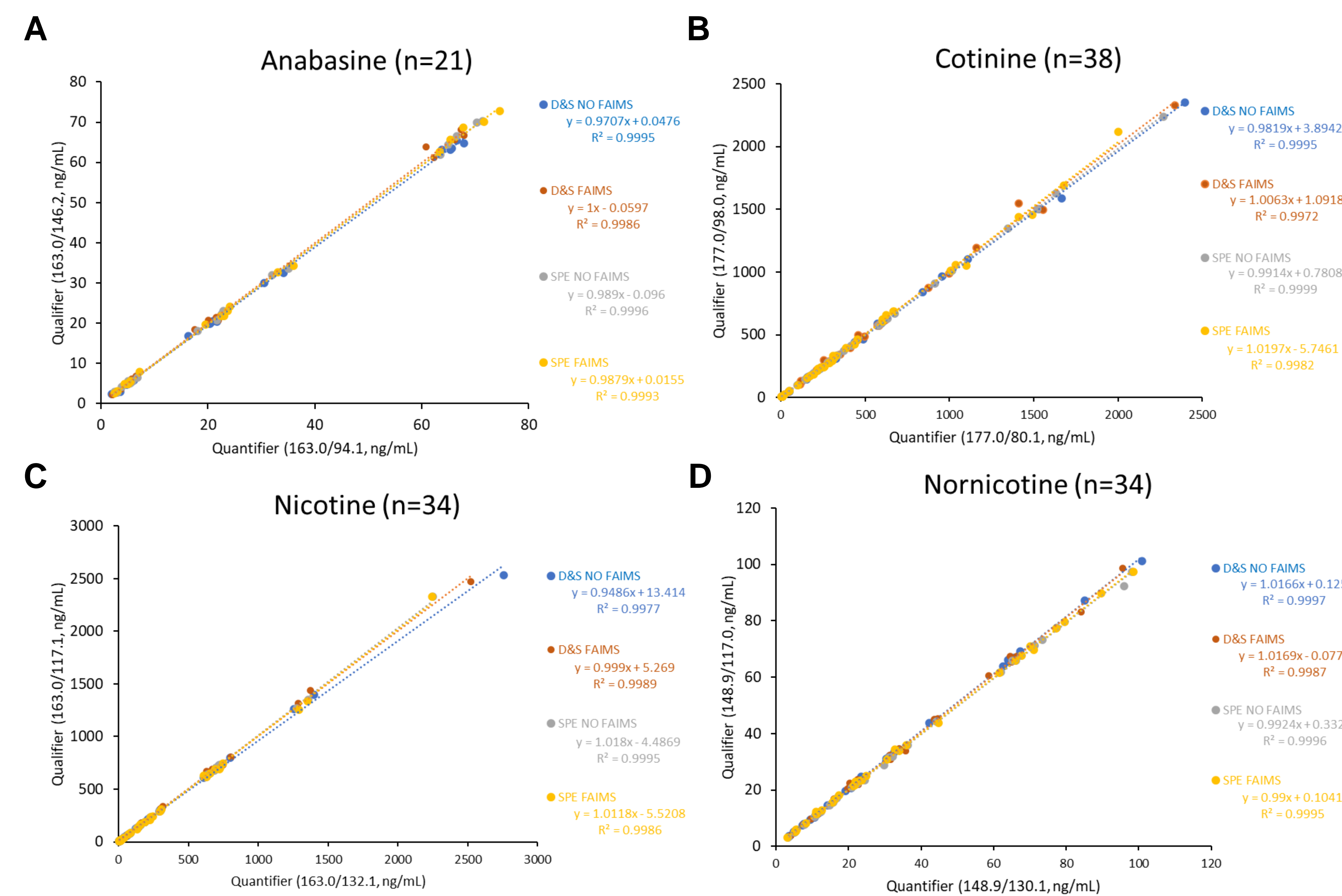


Figure 1. Linear regression comparison of the calculated concentration from quantifier and qualifier fragments for (A) anabasine, (B) Cotinine, (C) Nicotine and (D) Nornicotine.

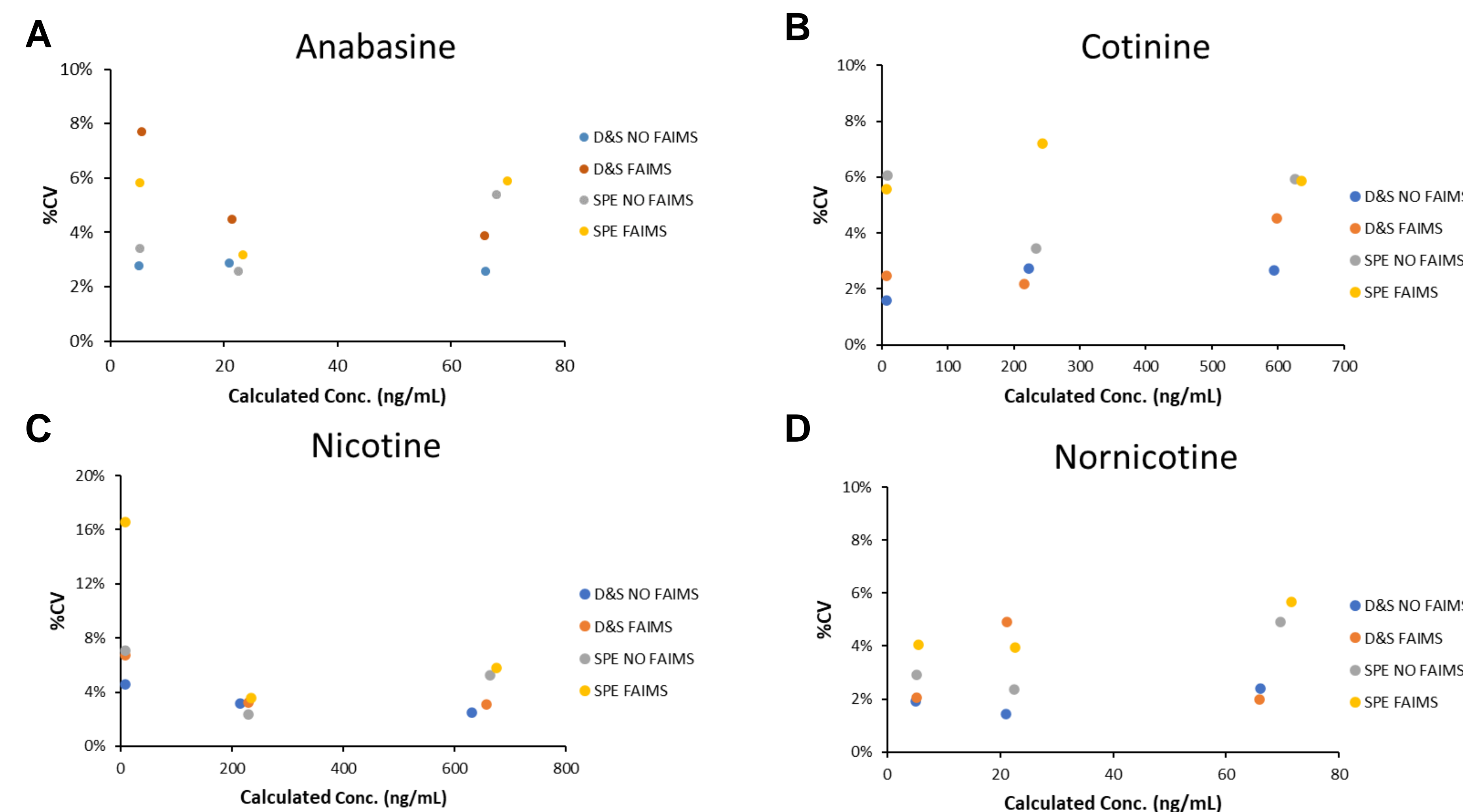


Figure 2. Assay precision of replicate measurements of (A) anabasine, (B) Cotinine, (C) Nicotine and (D) Nornicotine (n=4).

RESULTS

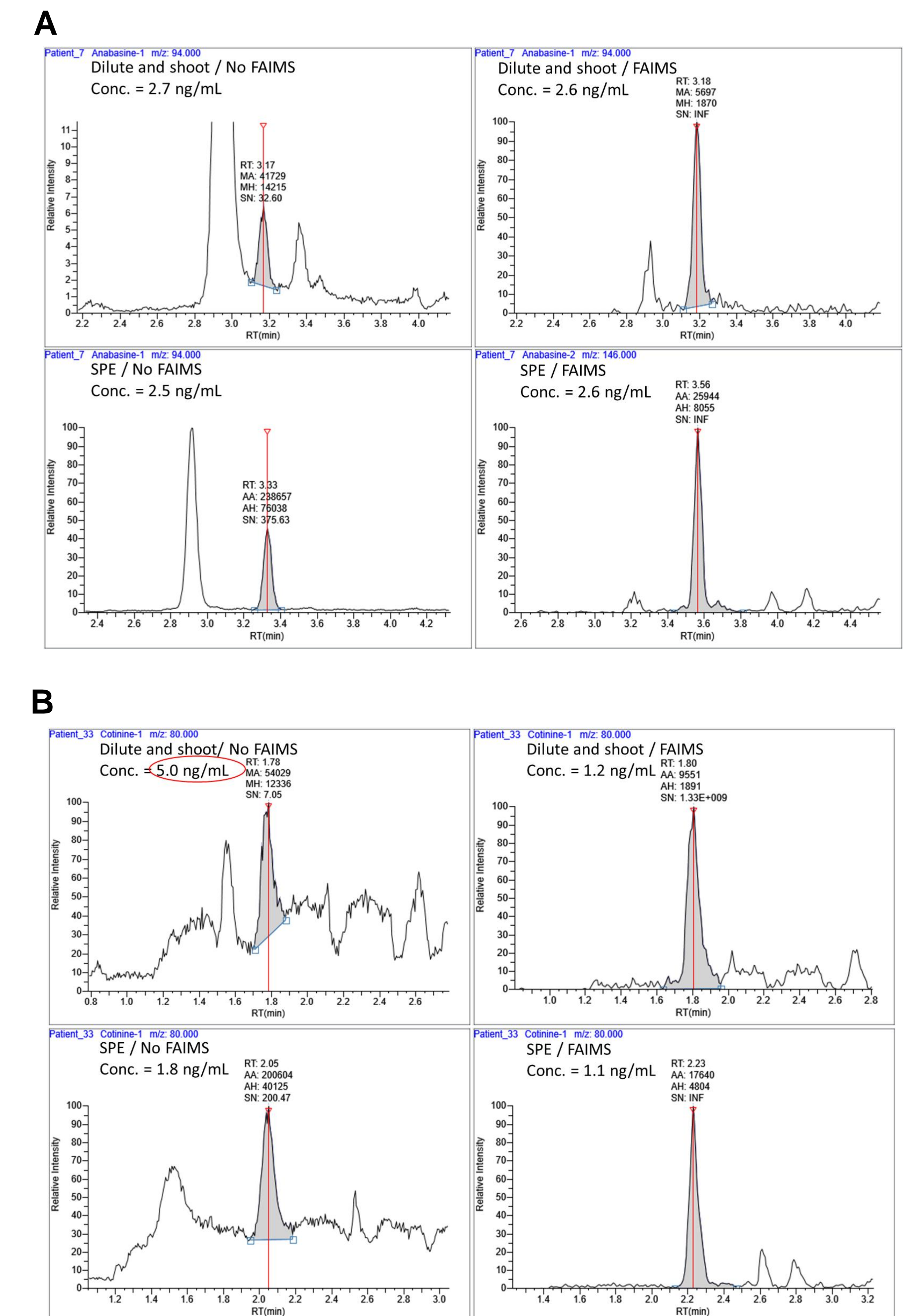


Figure 3. Comparison of chromatograms from the measurements of (A) anabasine and (B) cotinine performed with and without the use of FAIMS.

CONCLUSION

Overall, our new method is simple and utilizes low-cost sample preparation, requires minimal instrument maintenance, while providing accurate, precise, and specific measurements, which makes this method an ideal, high throughput analysis technique for the clinical laboratory.