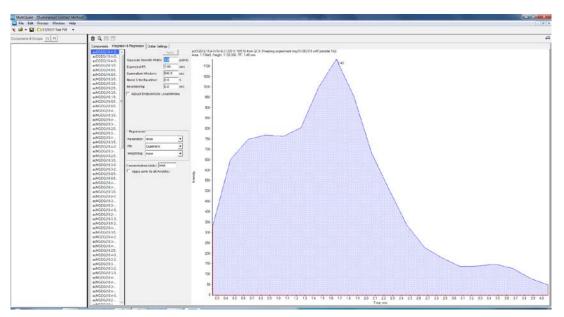
Processing and export of Sciex 6500+ MS direct infusion MRM data by Yu Song, Kansas Lipidomics Research Center, Kansas State University

A. Establish quantitation method

- (1) Open MultiQuant → File → New Quantitation Method → Select Sample The sample you choose should be one that is likely to contain all the analytes of interest.
- (2) Review component information → Set Integration & Regression parameters (adjust parameters for each compound or set default values for all compounds)

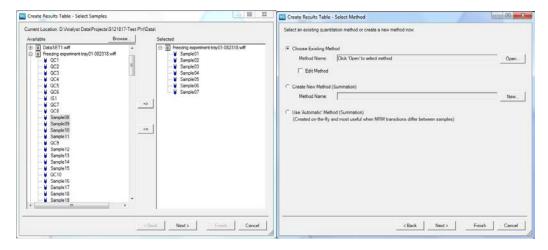
Set integration defaults: Edit \rightarrow User Integration Defaults \rightarrow For direct infusion data in 6500+, choose <u>Summation</u> integration algorithm, and choose the retention time(s) and summation window(s) so that the entire time that you would like to sum is covered in all samples, as indicated by shading in the intensity vs time profile.



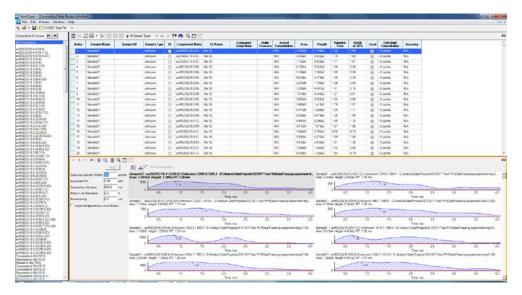
(3) Save the quantitation method as "name.qmethod" file (continued on next page).

B. Data processing

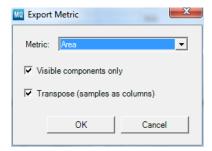
(1) File \rightarrow New Results Table \rightarrow Select (all) Samples \rightarrow Next \rightarrow Select an existing method (the established quantitation method) \rightarrow Finish



(2) Review compound list, check results table, check peak integration to make sure all peaks are integrated, i.e., are shaded.



(3) File → Export → Result Table-Metric→ select "Area", select "Transpose" → generate a text file that can be opened in Excel (by choosing to view all files).



(4) Verify that compounds are listed in the order that you have in your MRM data upload file. Remove rows 2 and 3 from the output and paste the intensity data from column B rightward into cell AA2 in the MRM data upload file.