

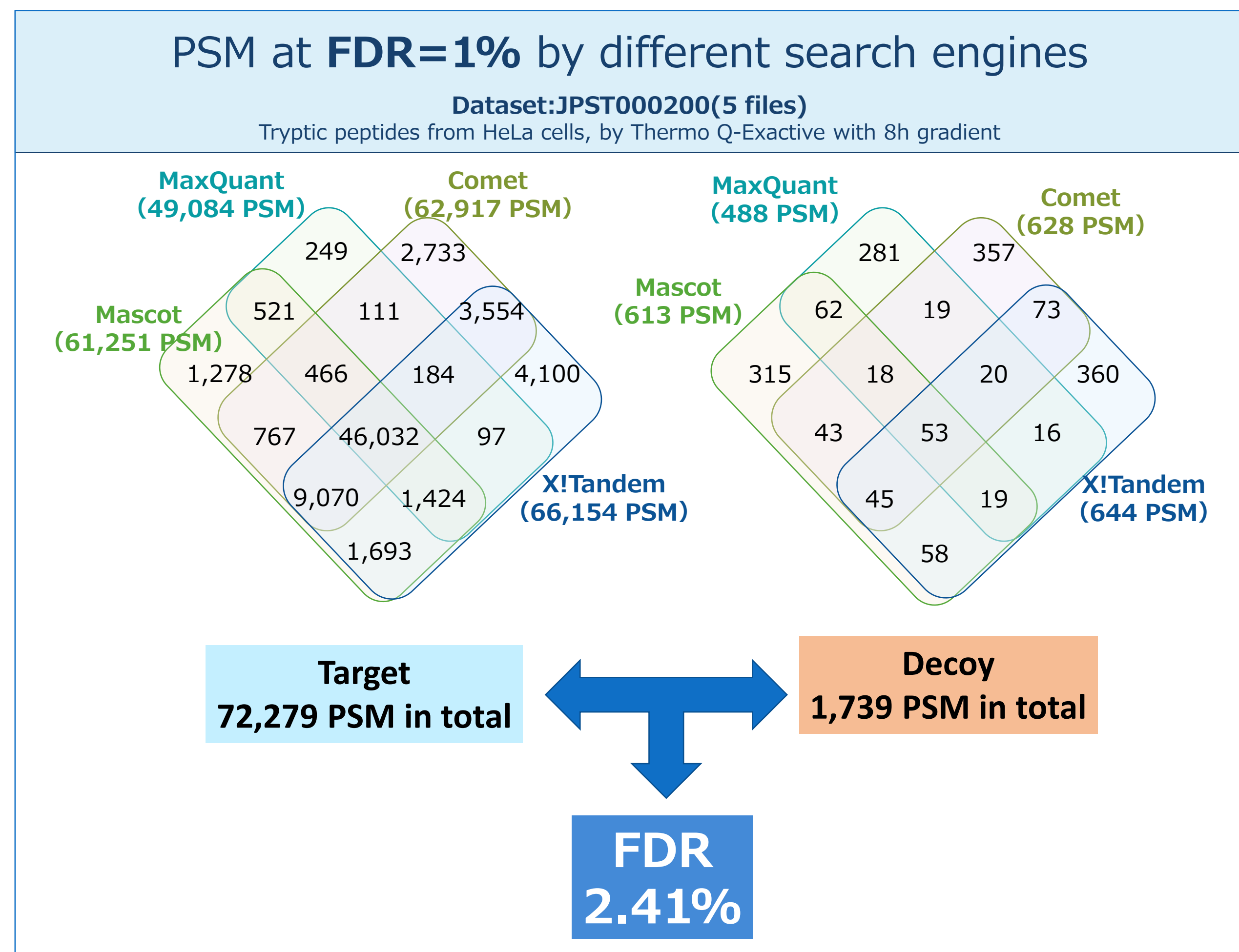
UniScoreを用いるjPOST-PTM解析への展開

○石濱 泰、小形公亮、西田紘士、榮川理子、藤田雄一郎、田畑剛 & jPOST team



課題

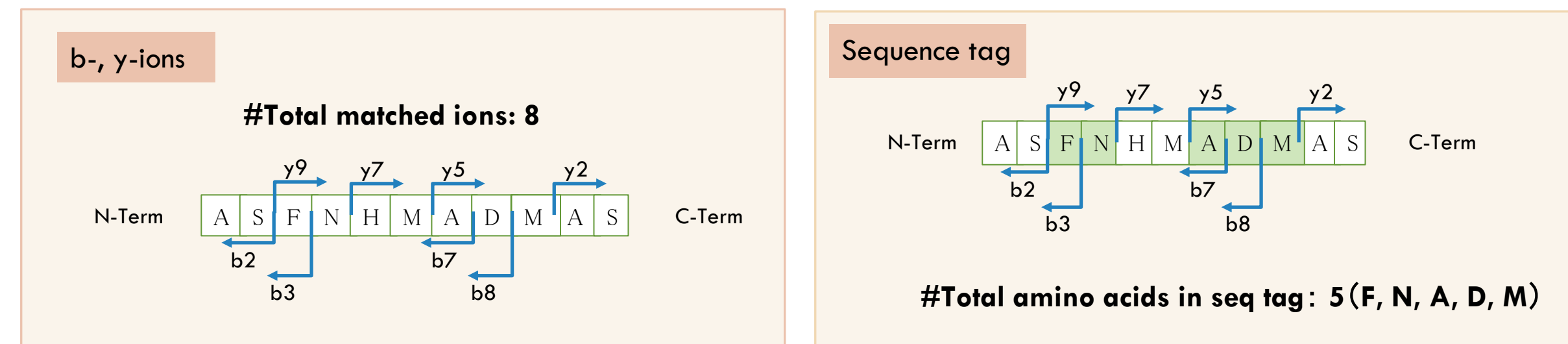
False Discovery Rate, False Localization Rate を制御しつつ、信頼度の高い翻訳後修飾解析を行うには？



UniScore to **unify** the results from different sources

- based on peak annotation in MSMS
- search engine independent
- MS instrument independent
- search DB independent
- can be used as **universal score** for peptide identification

UniScore = #Total matched ions + #Total AAs in seq tag



MCP TECHNOLOGICAL INNOVATION AND RESOURCES 2025, Mol Cell Proteomics 24(7), 101010

UniScore, a Unified and Universal Measure for Peptide Identification by Multiple Search Engines

Authors
Tsuyoshi Tabata, Akiyasu C. Yoshizawa, Kosuke Ogata, Chih-Hsiang Chang, Norie Araki, Naoyuki Sugiyama, and Yasushi Ishihama

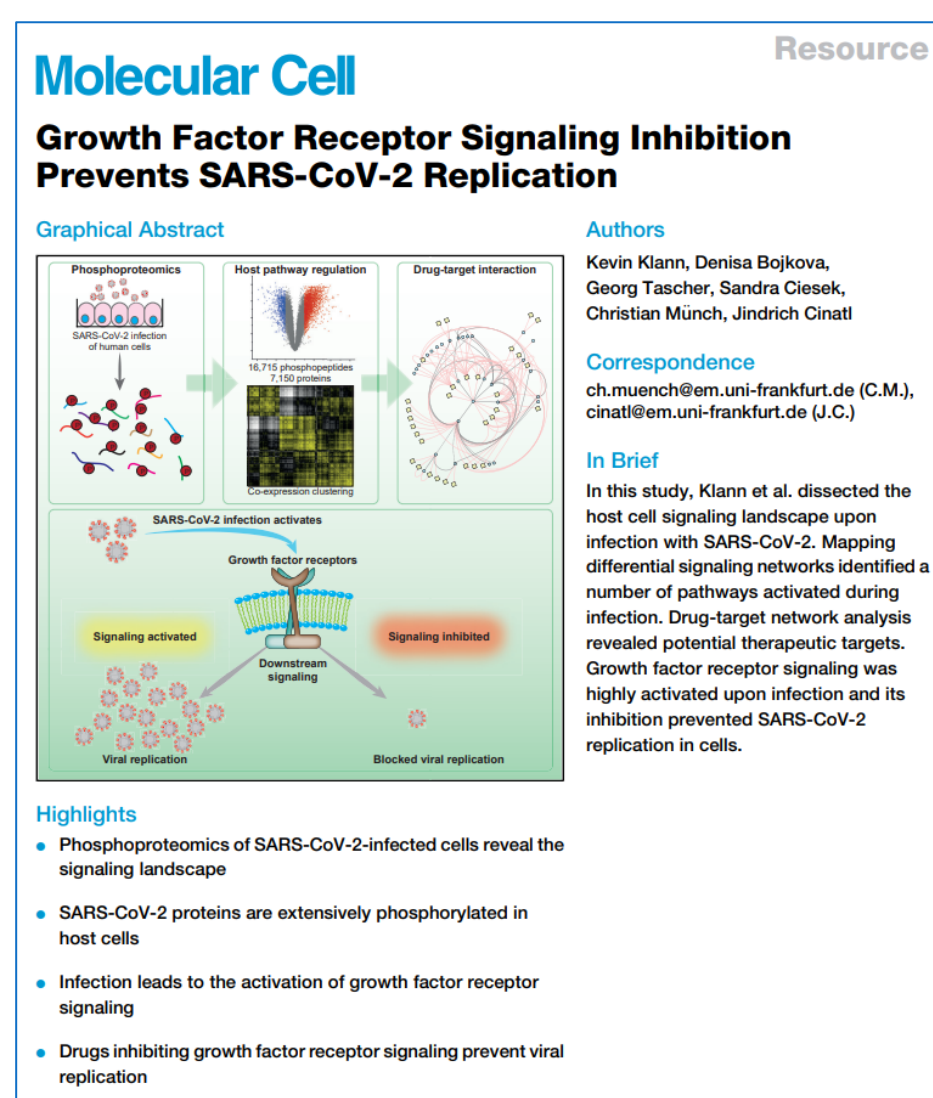
Site Flanking Ion Presence (sFIP)の導入



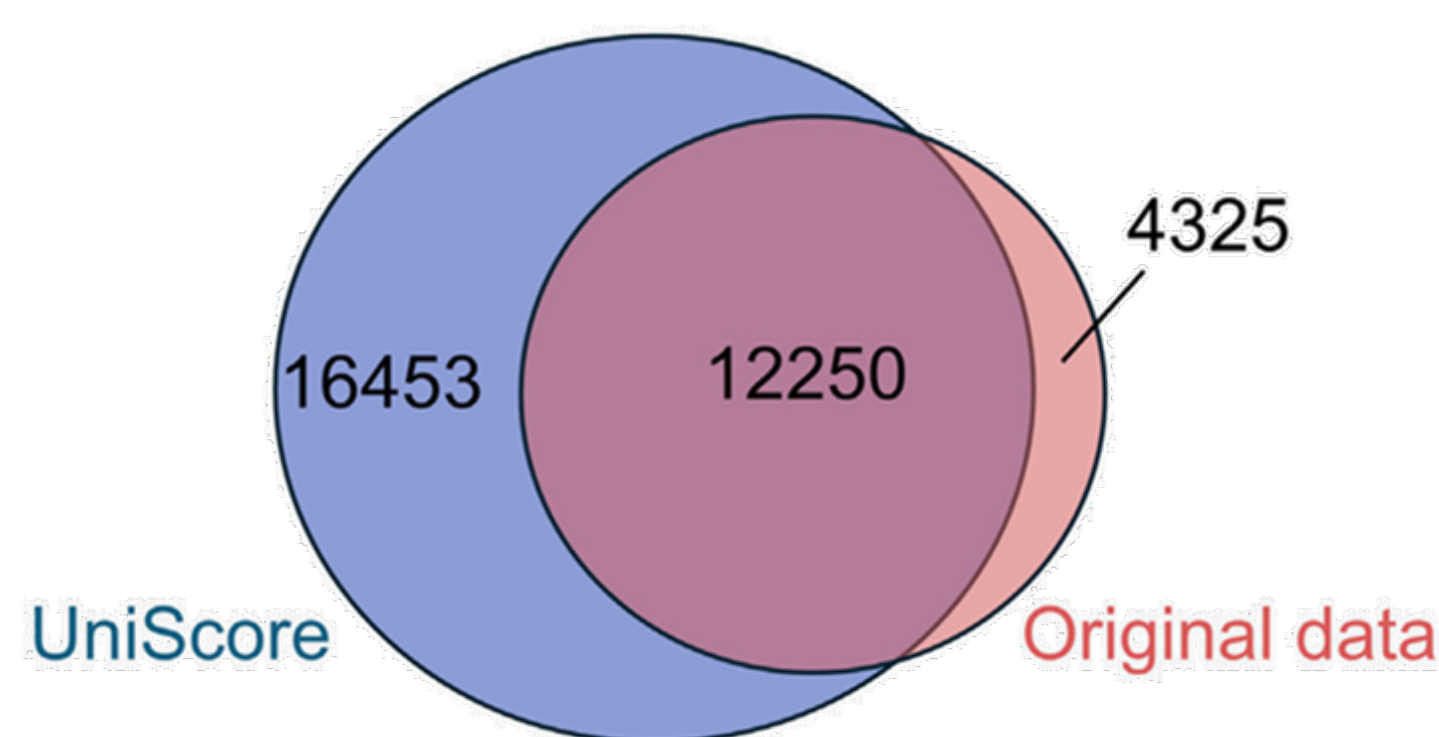
JPST001780

Mass spectrometry

PXD018357-2 Inhibition of growth factor signaling prevents SARS-CoV-2 replication [Reanalysis: PXD018357]

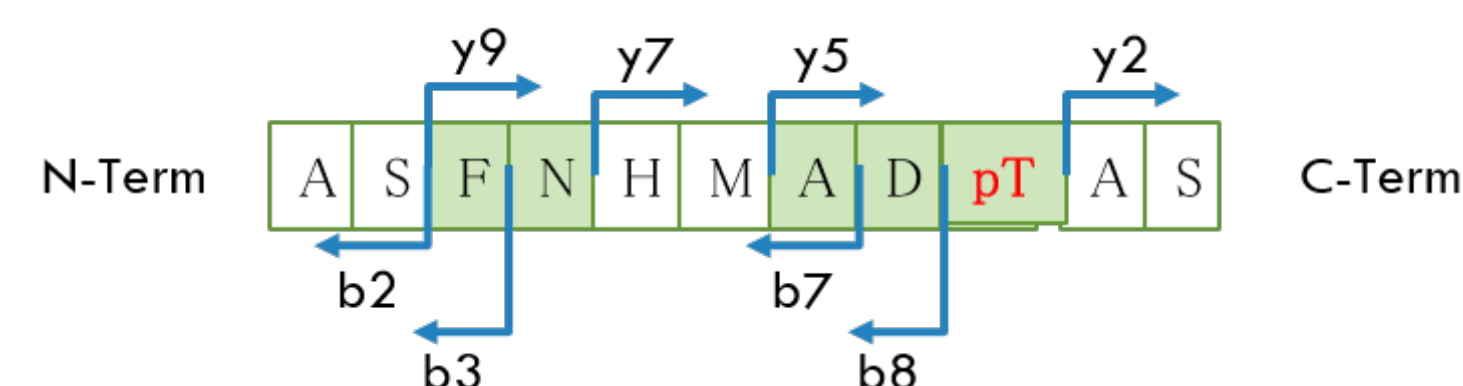


同定リン酸化ペプチド数の比較
(リン酸基のlocalizationは考慮せず)



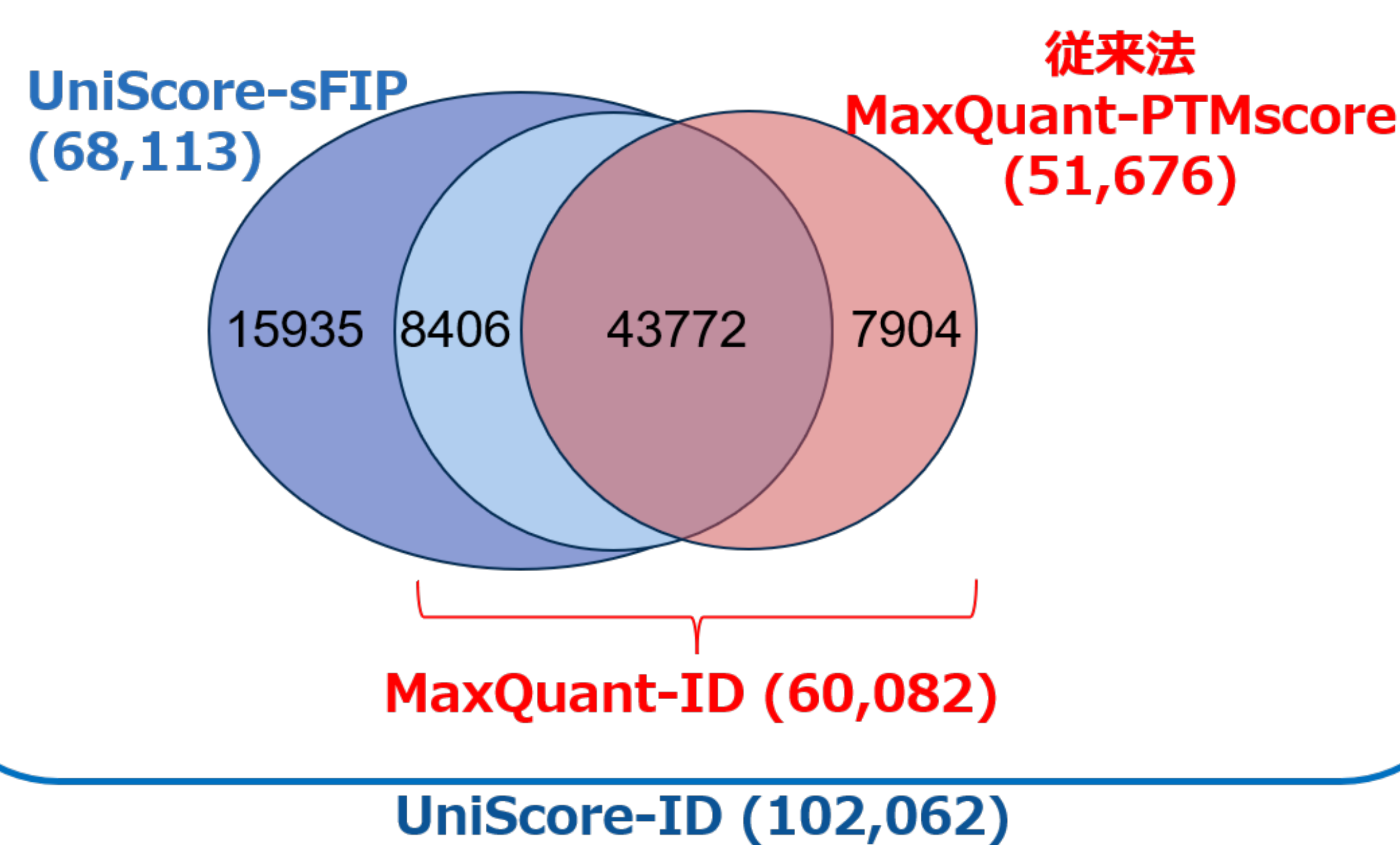
UniScoreを利用するPhosphosite Localizationの新規指標

⇒ **sFIP** (site Flanking Ion Presence)

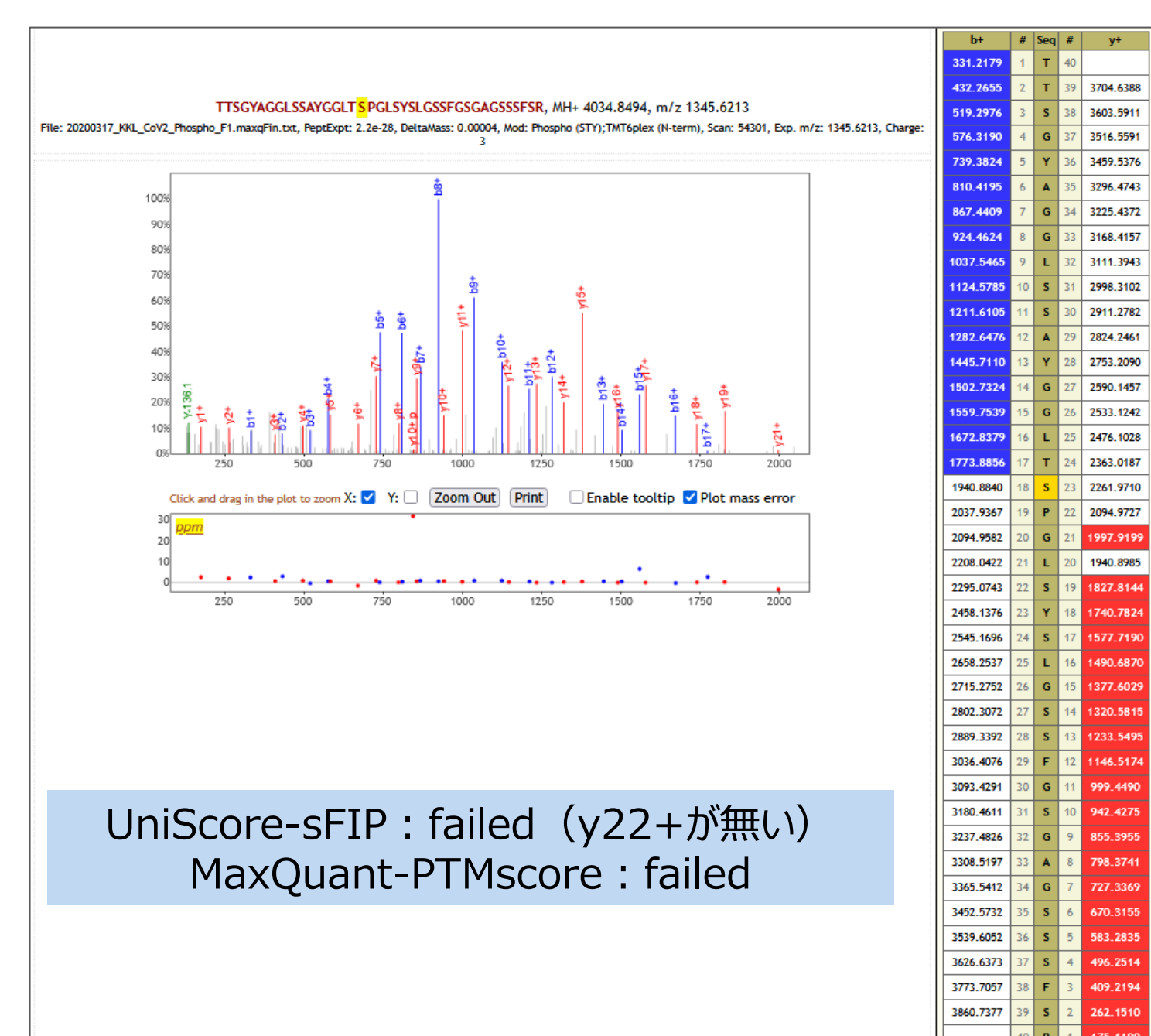
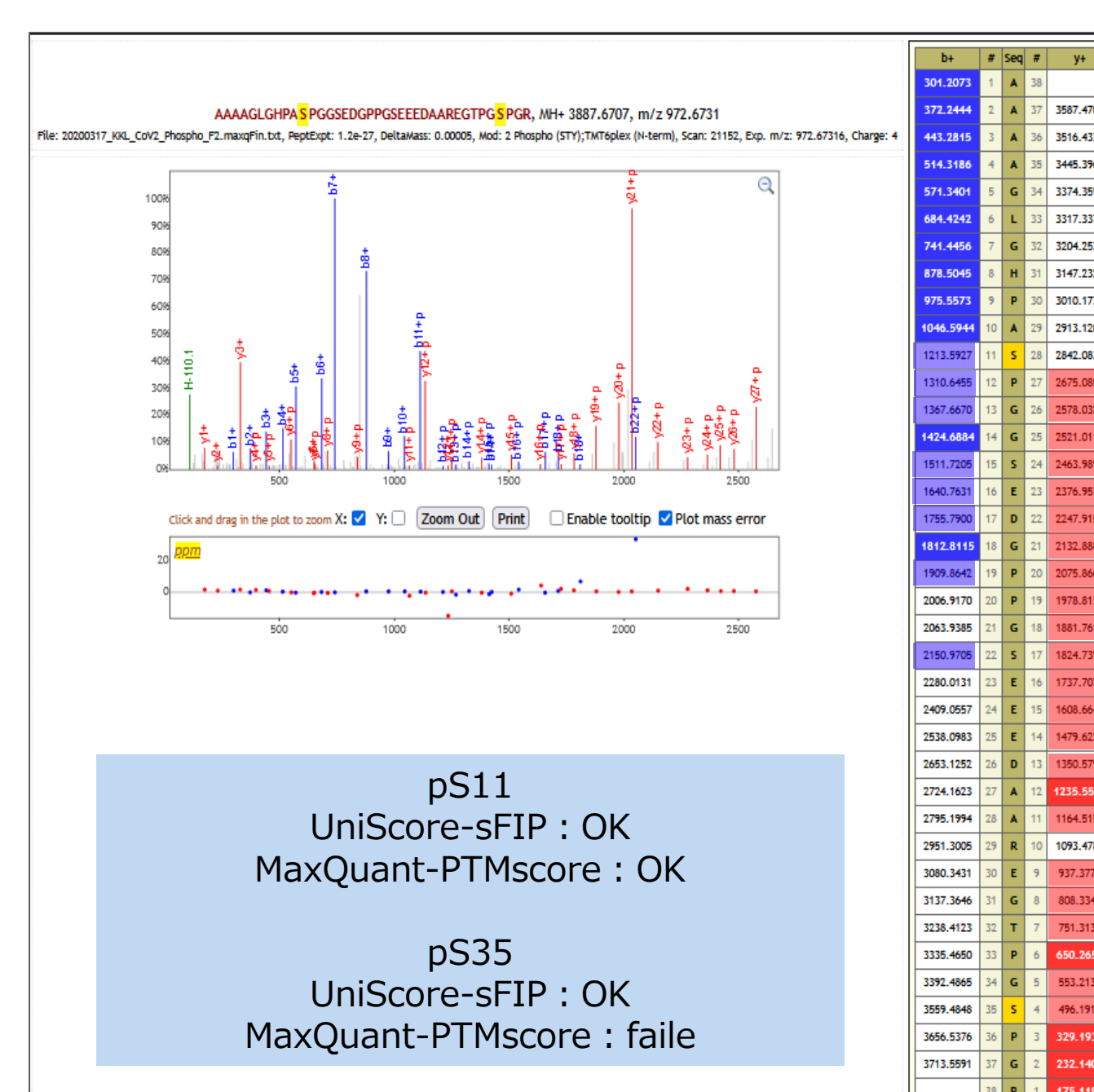
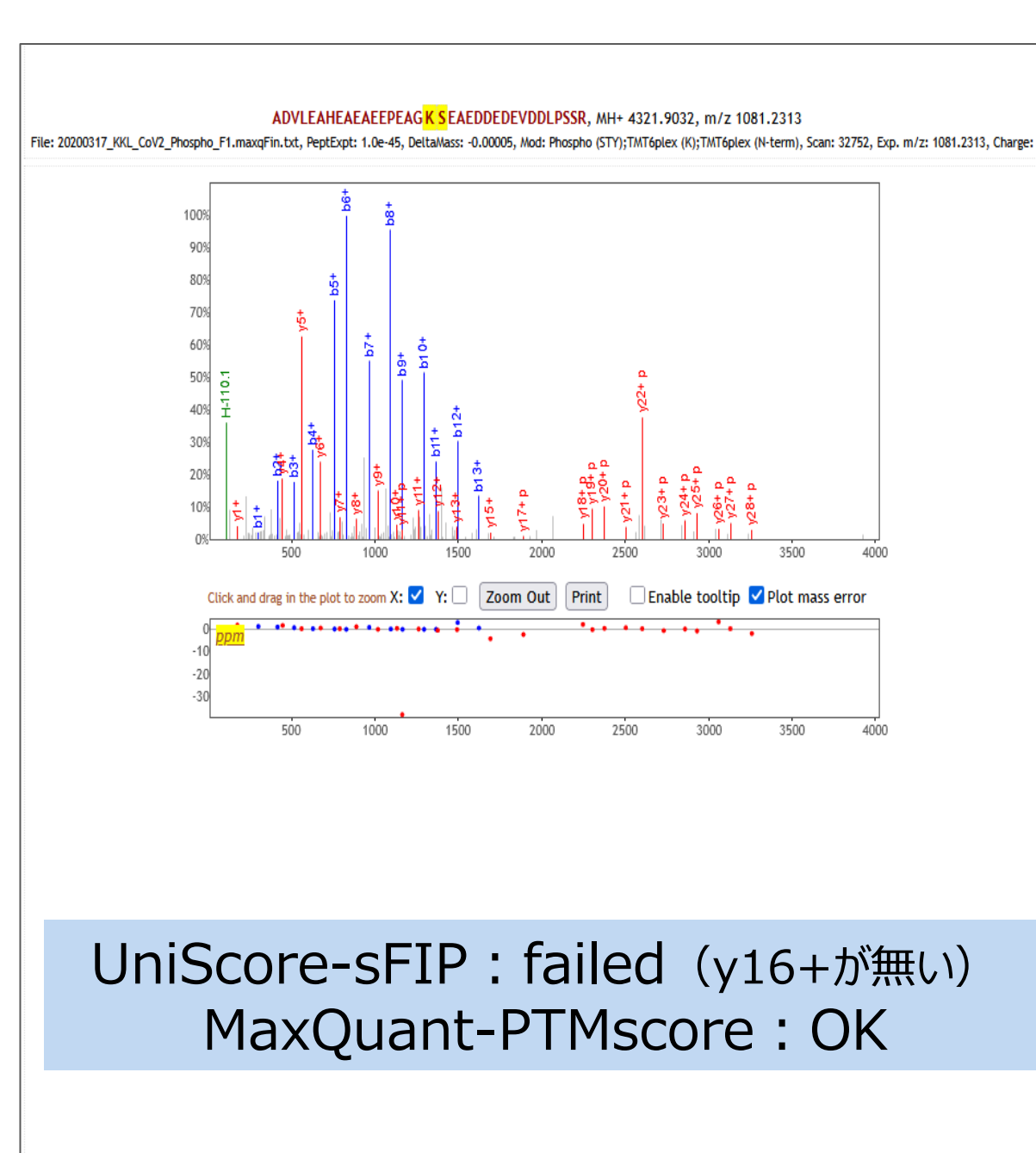
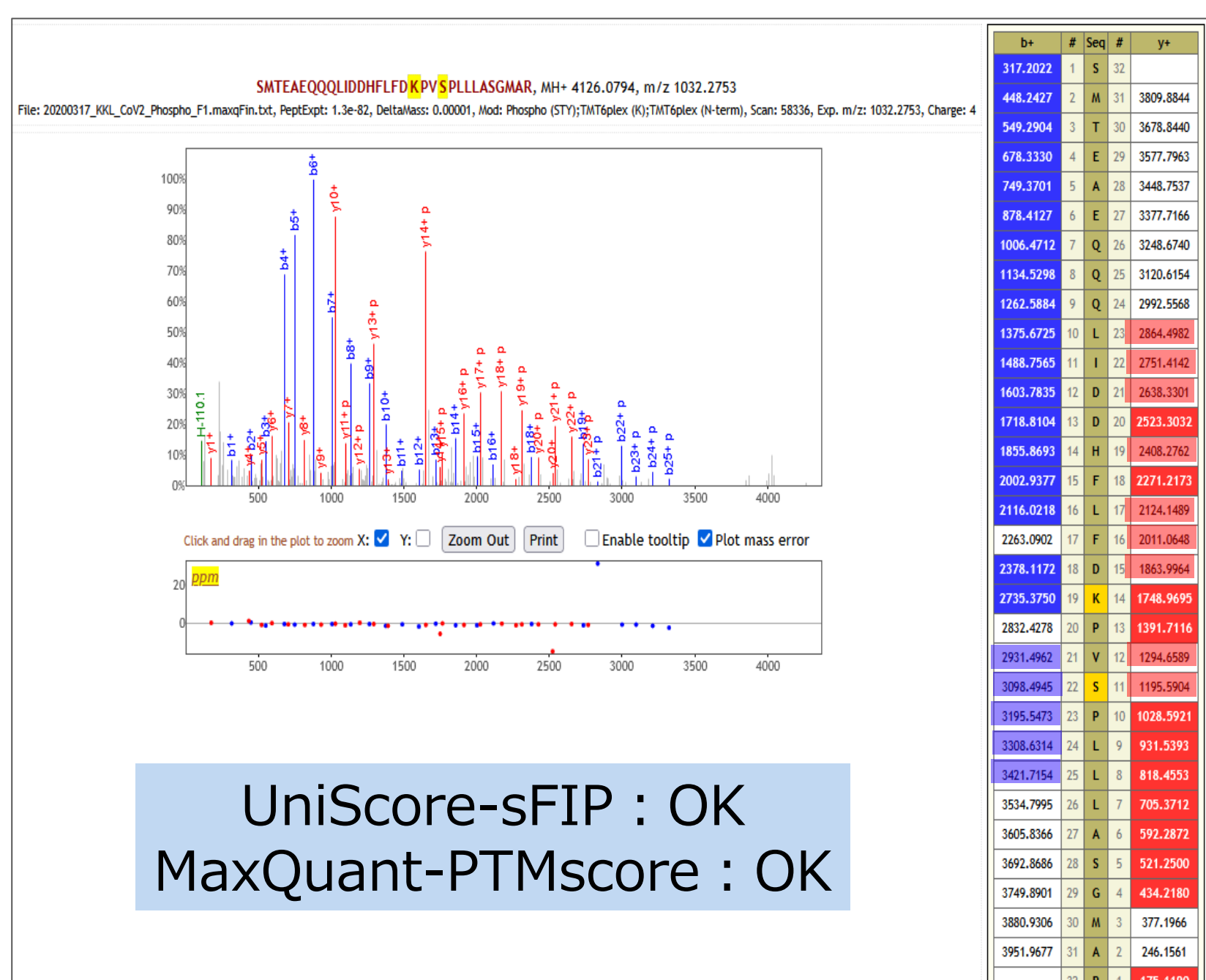


Site Flanking Ion for 9pT: y2 and b8

リン酸化サイト局在位置の同定



MSMSスペクトル解析



Conclusions

- ✓ 翻訳後修飾サイト局在を判定するための新規指標 Site Flanking Ion Presence (sFIP) を提案
- ✓ sFIPはUniScoreのピークアノテーションから算出可能
- ✓ 従来法(MaxQuant-PTMscore)との比較で、UniScore-sFIPはより多くのリン酸化修飾サイト同定を実現
- ✓ 国際プロジェクトPTMeXchange との連携をすすめる予定

