

quantms, ms2rescore and multiple search engines  
enables deep proteome coverage across protein  
quantification, immunopeptidomics, and  
phosphoproteomics experiments

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## Abstract

The exponential growth of public proteomics datasets has surpassed the analytical capacity of traditional desktop tools, particularly for large-scale automated reanalysis. To address this challenge, we present an integrated workflow that combines quantms, a cloud-native pipeline, with MS2Rescore, a machine learning-based rescoring tool. This workflow enables deep and scalable reanalysis of massive proteomic datasets. Powered by the Nextflow engine for parallel computing, the pipeline incorporates fragment ion intensity predictions from MS2PIP and retention time predictions from DeepLC, improving peptide-spectrum match reliability through Percolator. We applied this approach to four representative datasets covering label-free quantification, TMT labeling, immunopeptidomics, and phosphoproteomics. Compared to traditional methods, our workflow achieved a 16–22.8% increase in identified spectra, along with the quantification of hundreds of additional proteins and phosphosites. These improvements demonstrate that integrating multiple search engines with machine learning-derived features not only enhances identification sensitivity but also deepens quantitative insights for downstream biological interpretation. Overall, this workflow offers a reproducible and scalable solution for the reanalysis of public proteomics data, advancing FAIR principles by promoting scientific transparency, accessibility, and data reuse.

**Keywords:** Proteomics, Reanalysis, Workflow, Machine learning.

## 1 Introduction

In recent years, the field of proteomics has experienced rapid growth in the availability of publicly accessible datasets, accompanied by a shift toward studies analyzing larger sample cohorts. As of June 2025, over 40,000 datasets have been submitted to ProteomeXchange (PX) repositories, including a substantial increase in large-scale submissions comprising more than 100 instrument files [1]. However, conventional desktop tools such as MaxQuant [2], pFind [3], PeptideShaker [4], and Proteome Discoverer are limited in their capacity to per-

form automated, large-scale quantitative analyses in cloud or distributed environments, hindering the reanalysis of extensive experiments on standard workstations.

We recently developed quantms [5], an open-source, cloud-based pipeline designed for massively parallel reanalysis of quantitative proteomic datasets. The pipeline is highly modular and flexible, accommodating a wide range of quantitative proteomics approaches including DDA label-free, DDA multiplex (TMT and iTRAQ) and DIA. quantms automatically distributes computations using the Nextflow workflow engine across one or more computing nodes, depending on the number of instrument files and samples [6]. To ensure traceability and reproducibility, the pipeline is built entirely on standardised open file formats and reproducible execution environments, adhering strictly to the FAIR (Findability, Accessibility, Interoperability, and Reusability) principles [7]. quantms has been extensively benchmarked and used in the analysis of large-scale public proteomics datasets [5, 8, 9]. To address this limitation, we recently developed quantms, an open-source, cloud-based pipeline designed for massively parallel reanalysis of quantitative proteomic datasets [5]. The pipeline is highly modular and flexible, accommodating a wide range of quantitative proteomics approaches. quantms automatically distributes computations using the Nextflow workflow engine across one or more computing nodes, depending on the number of instrument files and samples [6]. To ensure traceability and reproducibility, the pipeline is built entirely on standardized open file formats and reproducible execution environments [10] [11], adhering strictly to the FAIR (Findability, Accessibility, Interoperability, and Reusability) principles [7].

With the integration of machine learning (ML) into proteomics, various models have been developed to accurately predict peptide properties, such as MS2PIP [12] for fragment ion intensities and DeepLC [13] for retention time prediction. Early approaches employed decision trees and single-layer neural networks, while more recent deep learning models such as Prosit [14] achieve significantly improved accuracy for predicting fragment ion intensities and retention times. These highly accurate predictions enable superior matching of experimental data to theoretical expectations and have reinvigorated rescore strategies in proteomics.

MS2Rescore represents a modular package that generates multiple features assessing the similarity between observed and predicted MS/MS spectra utilizing MS2PIP. Furthermore, MS2Rescore calculates RT-dependent features, e.g., delta RT, utilizing DeepLC [15].

Previously, quantms did not leverage measurable peptide properties such as fragment ion intensities and retention times. To overcome this limitation, we integrated MS2Rescore into quantms and incorporated customized features following Nextflow and nf-core best practices. We demonstrate that the enhanced pipeline supports in-depth analysis of large-scale public proteomics datasets across diverse experimental designs, including label-free quantification (LFQ), tandem mass tag (TMT)-based quantification, immunopeptidomics, and phosphoproteomics studies.

## 2 Methods

### 2.1 MS/MS Data and quantms Search Results

To develop and evaluate the performance of the quantms-integrated MS2Rescore workflow, we selected four publicly available benchmark datasets. Three were obtained from the PRIDE Archive under the identifiers PXD001819, PXD019643, and PXD026824, and one from the CPTAC data portal under PDC000127. The PXD001819 dataset contains 48 Sigma UPS1 proteins spiked into a background of yeast cell lysate at nine different concentrations: 0.05, 0.125, 0.25, 0.5, 2.5, 5, 12.5, 25, and 50 fmol/ $\mu$ L to evaluate quantification performance. We evaluated five different quantms workflow settings: (1) Comet, (2) Comet and MSGF+, (3) Comet with MS2Rescore, (4) Comet and MSGF+ with MS2Rescore, and (5) Comet, MSGF+, and SAGE with MS2Rescore to explore multiple search engines and their integration with MS2Rescore for improved identification and quantification results. All search parameters were the same as described in the previous publication. A stringent FDR at 1% was applied at peptide spectrum match (PSM) and protein level at the dataset level. The search results from quantms and MaxQuant at the PSM and protein group levels are provided

in Supplemental File S1.

## 2.2 Rescoring Features and Postprocessing

The quantms-rescoring Python package integrates MS2Rescore and calculates a wide range of features based on the DeepLC-predicted and observed retention times, and the MS2PIP-predicted and observed MS2 peak intensities. Signal-to-noise ratio (SNR) features are also calculated for specific cases in the quantms-rescoring Python package. Then, the quantms workflow calculates a posterior error probability for each PSM using Percolator. This is performed under three different feature configurations (1) a baseline model using only search engine-derived features, (2) the baseline model plus MS2Rescore-derived features, and (3) the above combined with SNR features. To merge results from multiple search engines, ConsensusID aggregates PSMs into unified scores. Final PSM-level q-values are then obtained either directly from Percolator or calculated using OpenMS' target-decoy approach based on the predicted probabilities. For phosphoproteomics datasets, LuciPHOr2 is employed to assign site-level localization scores and estimate the associated false localization rate using tools from the OpenMS toolkit.

## 3 Results

### 3.1 quantms with MS2Rescore Enhances Label-Free Identification and Quantification

To systematically evaluate the performance of the quantms-integrated MS2Rescore workflow at both identification and quantification levels, we first analyzed the public benchmark dataset PXD001819. For identification benchmarking, five different workflows configurations were designed and compared, including (1) Comet with Percolator, (2) two search engines with Percolator, (3) Comet with MS2Rescore features and Percolator, (4) two search engines

with MS2Rescore features and Percolator, and (5) three search engines with MS2Rescore features and Percolator to determine whether features from intensity-based and retention time-based predictors enhanced the identification and quantification process.

Significant PSMs were filtered based on q-values, and the FDR was used as a key metric to compare workflows. As shown in Figure 1, using consensus scores from two search engines significantly increased identification rates at a fixed FDR threshold. Specifically, combining Comet and MSGF+ improved identified spectra by 17%

To better understand the contribution of individual features, we extracted the top 20 feature weights from Percolator (Supplemental Figure 1). Over half of the top-weighted features were derived from MS2Rescore. Notably, SpecPearsonNorm had a strong positive weight, indicating that a better correlation between predicted and observed intensities improves confidence. Conversely, RtDiffBest had a negative weight, suggesting that large deviations in retention time reduce match quality. Interestingly, peptide length also emerged as a significant positive feature after MS2Rescore integration, likely because longer peptides generate more fragment ions and thus are more reliably identified.

### 3.2 Improved Identification and Quantification in TMT Experiments via MS2Rescore Integration

We next applied the workflow to a large-scale TMT-labeled dataset from CPTAC (PDC000127). The integration of multiple search engines and MS2Rescore features led to marked improvements in both identification and quantification (Figure 2). The PSM identification rate increased by 3.6%, and 921 proteins were newly quantified compared to the workflow without MS2Rescore (Figure 2A, 2B). Among these, 59 proteins had abundance levels within the top 10% (Figure 2C). To assess the biological impact, we conducted differential expression analysis using the MS2Rescore-enhanced workflow. As shown in Figure 2D, 27 newly quantified proteins were significantly differentially expressed. Notably, FOXG1—one of these proteins—has been associated with prognosis in Clear Cell Renal Cell Carcinoma, as re-

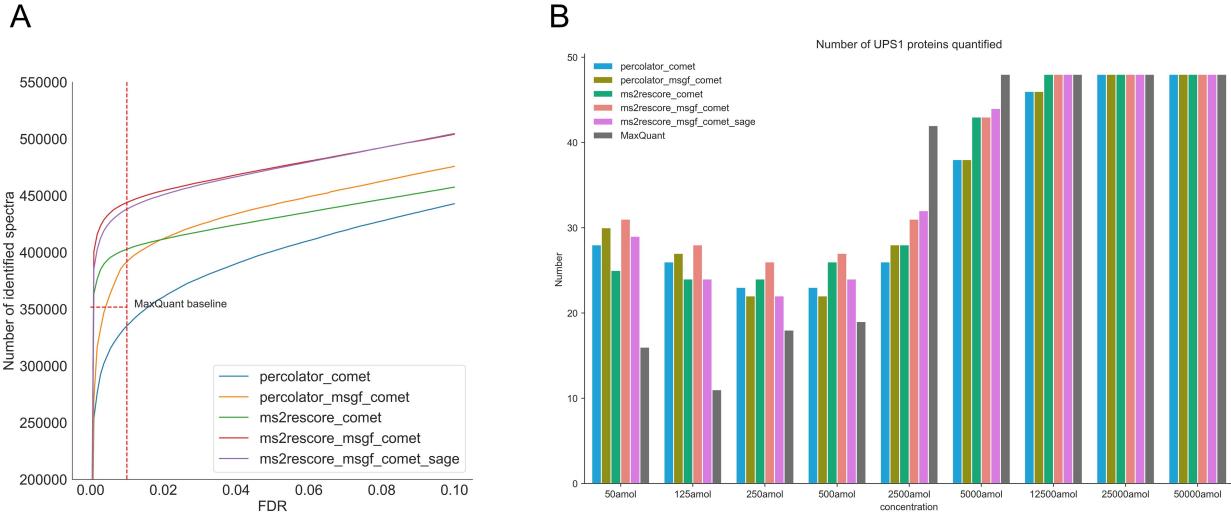


Figure 1: The number of identified spectra as a function of differing FDR levels for different workflow settings. (A) Results for the PXD001819 dataset. (B) Results for the PXD001819 dataset showing protein quantification. Five different workflow settings are shown: the combination of Comet search engine with Percolator rescoring, the combination of Comet with MSGF+, the combination of two search engines with MS2Rescore features, the combination of two search engines with MS2Rescore and SNR features, and the combination of three search engines with MS2Rescore and SNR features. Multiple search engines consensus identification, additional intensity-based and retention time-based features, and SNR features lead to both higher identification rates and high-quality identification.

ported by Yang et al. [16]. These findings illustrate that quantms incorporating MS2PIP and DeepLC-derived features enhances not only identification sensitivity but also enables deeper biological insights.

We further examined the rescoring contribution of individual features by analyzing the top 20 SVM weights from Percolator (Supplemental Figure S2). For Comet-based results, SpecPearsonNorm, DotProdIonYNorm, and RtDiffBest were highly weighted. The interpretations of these weights were consistent with those from the label-free dataset. Importantly, peptide length again emerged as a key feature. Similar weight distributions were observed for MSGF+ and SAGE results, confirming the generalizability of these feature effects across different search engines.

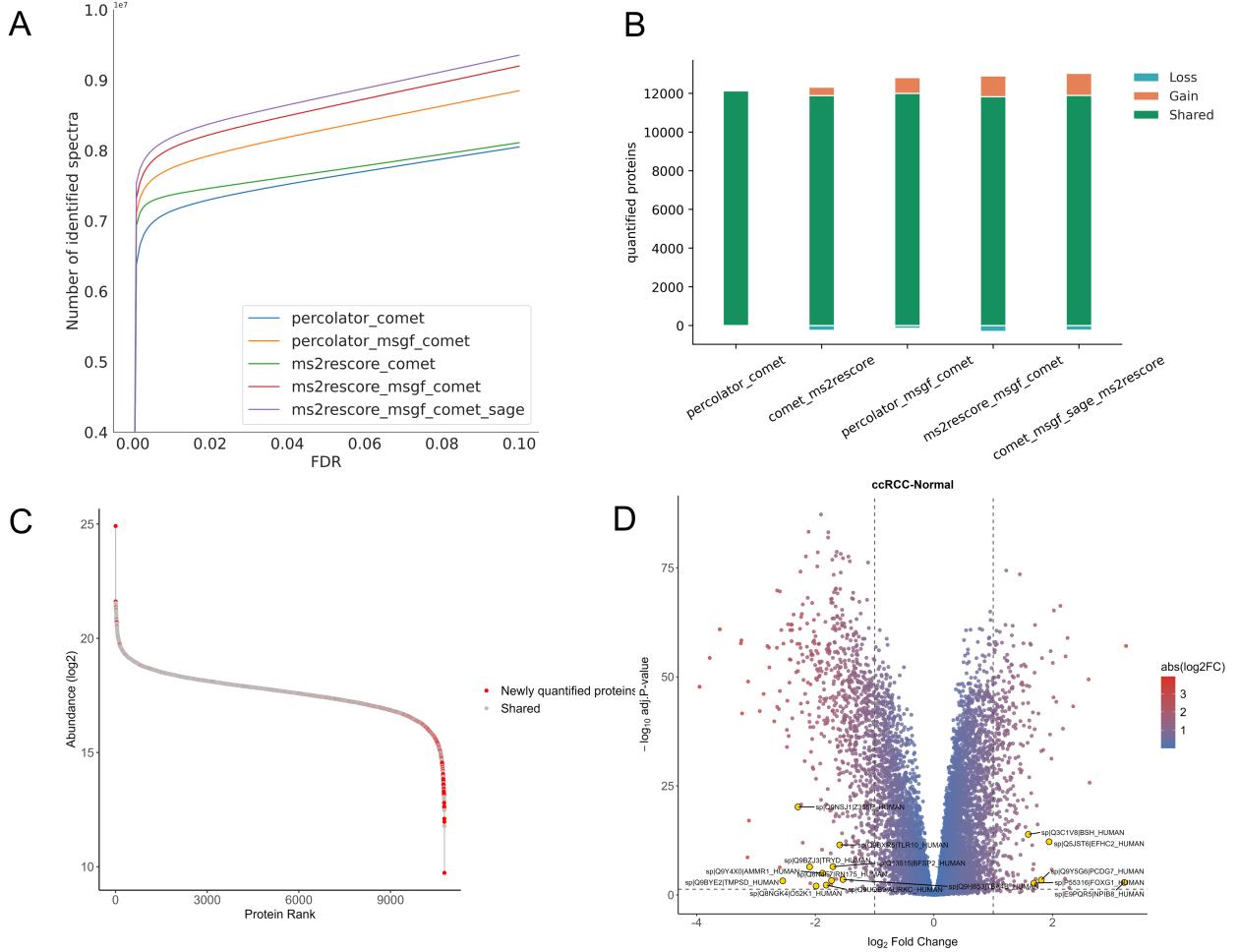


Figure 2: Comparison of identification and quantification results for different workflow settings. (A) The number of identified spectra as a function of differing FDR levels for different workflow settings. (B) The number of quantified proteins. The green part indicates the intersection between a workflow and Comet results. (C) The rank of protein abundance from Comet and MSGF+ with MS2Rescore. The red dots represent proteins quantified only in the Comet and MSGF+ with MS2Rescore workflow compared to the Comet and MSGF+ workflow without MS2Rescore. (D) The volcano plot for differential expression analysis from MSstatsTMT. The red dots represent proteins quantified only in the Comet and MSGF+ with MS2Rescore workflow compared to the Comet and MSGF+ workflow without MS2Rescore.

### 3.3 quantms integrated with MS2Rescore Improves HLA Class I Immunopeptidome Identification

To further assess the performance of the quantms-integrated MS2Rescore workflow, we analyzed the HLA Class I immunopeptidomics dataset PXD019643. Five workflow config-

urations were evaluated: (1) Comet + Percolator, (2) Comet + MS2Rescore, (3) Comet + MSGF+ + Percolator, (4) Comet + MSGF+ + MS2Rescore features, and (5) Comet + MSGF+ + MS2Rescore + SNR features. These configurations were compared based on both the total number of peptide-spectrum matches (PSMs) and the number of unique peptide sequences identified. Across all comparisons, the use of multiple search engines combined with MS2Rescore features significantly enhanced identification performance. At both 1% and 0.1% FDR thresholds, integrating MSGF+ with Comet increased the number of identified spectra by 11.7% compared to using Comet alone. Adding MS2Rescore features on top of the multi-engine workflow yielded a further 22.8% improvement, as shown in Figure 3.

To better understand the impact of MS2Rescore-derived features on rescoring, we visualized the distributions of decoy PSMs, rejected target PSMs, and accepted target PSMs using the Pearson correlation coefficient (PCC) and retention time error (Figure 3C, D). The accepted target PSMs were clearly separated from both decoy and rejected targets based solely on PCC values, and exhibited consistently low retention time deviations. These patterns were observed across both individual search engine support and multi-engine consensus, further confirming that the integration of intensity and RT-based features enhances PSM discrimination. Overall, these results demonstrate the robustness of the quantms workflow in immunopeptidomics, highlighting its ability to leverage machine learning-derived features to maximize identification accuracy through multi-engine consensus rescoring.

### 3.4 Enhanced Phosphopeptide Identification and Localization Using MS2Rescore integration

In addition, we investigated the performance of our quantms workflow with MS2Rescore on post-translational modification experiments (PXD026824). For phosphoproteomics analyses, different workflow settings were evaluated: (1) Comet + Percolator, (2) Comet + MS2Rescore, (3) Comet + MSGF+ + Percolator, and (4) Comet + MSGF+ + MS2Rescore features. As shown in Figure 4, combining search engine consensus results with MS2Rescore

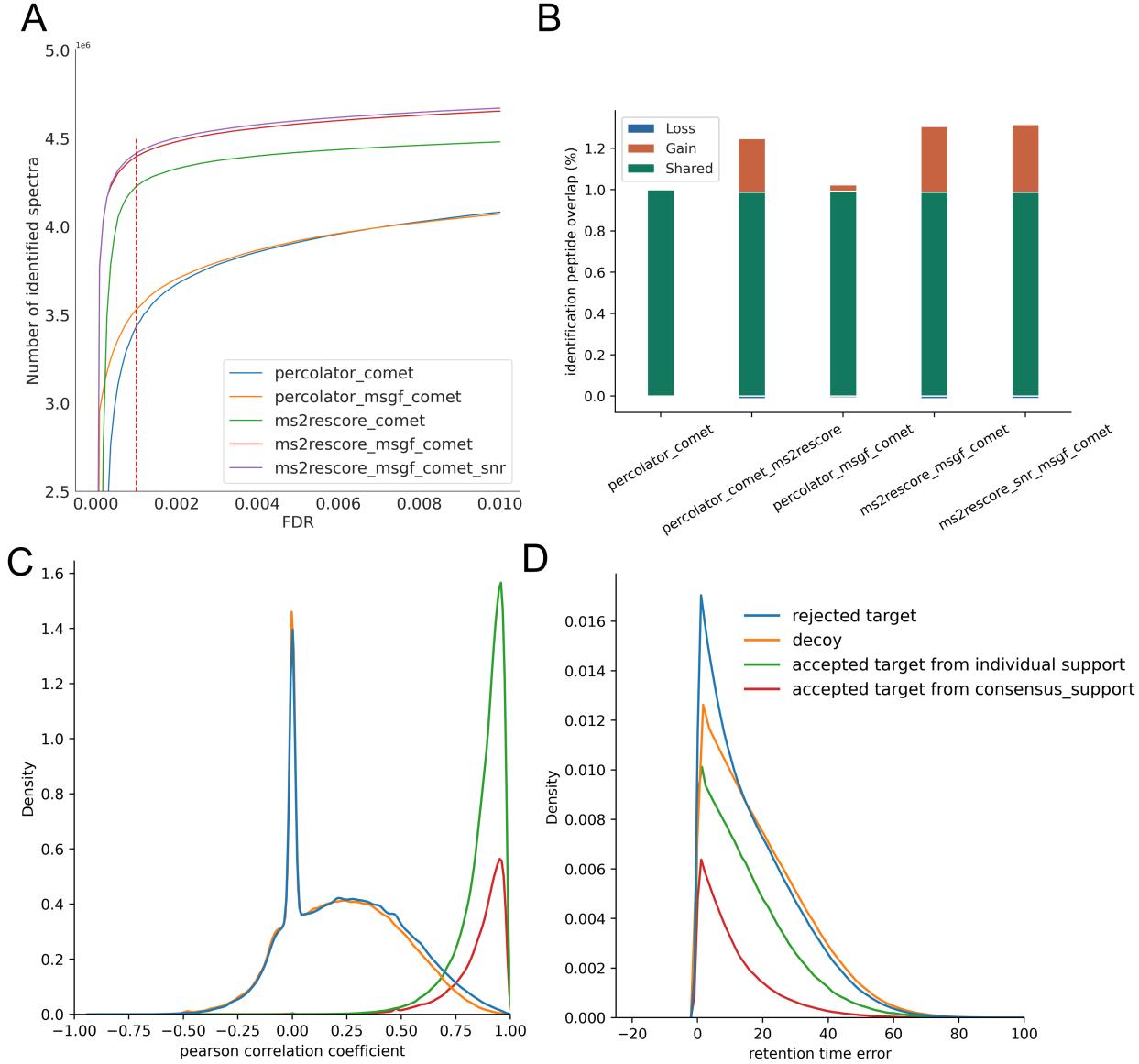


Figure 3: Comparison of immunopeptides identification results for different workflow settings. (A) Line plot showing the number of spectra identified for four workflow settings at different PSM FDR levels. (B) Percentage of unique identified peptides using different workflow settings. Density plots showing the distribution of the smallest retention time error between observed and predicted retention time (C) and the Pearson correlation between observed and predicted peak intensities (D) for each PSM split into decoys (red), rejected targets with q-value  $>0.01$  (blue), and accepted targets from individual support and consensus support with q-value  $<0.01$  (green). Note that the rejected targets distribution coincides with the decoy distribution.

features substantially improves Percolator’s ability to discriminate between true and false PSMs. This is evident from the leftward shift in score distributions compared to the Comet-

only workflow, indicating improved stringency. Additionally, an upward shift in the plot demonstrates a notable gain in the identification rate. Specifically, incorporating MS2Rescore features into the two-search-engine consensus increased the number of identified spectra by 19% compared to consensus identification alone (Figure 4A). The top 20 feature weights from Percolator, displayed in Supplemental Figure S4, highlight the consistent importance of features such as DotProdIonYNorm, similar to previous datasets.

Given the importance of false localization rate (FLR) control in phosphoproteomics, we also assessed the impact of different workflows on phosphopeptide identification at varying FLR thresholds (Figure 4B, C). At a 0.01 local FLR, the consensus workflow with MS2Rescore features identified 17% more phosphorylated peptides than its counterpart without MS2Rescore. Notably, 1,345 phosphorylated peptides were uniquely identified by the MS2Rescore-enabled workflow. At the phosphosite level, this workflow also uncovered 350 novel protein phosphorylation sites not reported in the other settings (Figure 4D). Collectively, these results underscore the value of MS2Rescore in enhancing both identification sensitivity and site-level localization in phosphoproteomics, establishing quantms as a robust solution for large-scale PTM data analysis.

## 4 Discussion

Advancements in deep learning-based tools have significantly improved the accuracy and sensitivity of peptide-spectrum match (PSM) rescoring, yet their integration into streamlined, reproducible, and quantitative proteomics workflows has remained limited, especially for large-scale public data analysis. In this study, we demonstrate the systematic incorporation of MS2Rescore into the open-source quantms pipeline and evaluate its impact across various experimental settings, including label-free quantification (LFQ), tandem mass tag (TMT)-based quantification, immunopeptidomics, and phosphoproteomics. Our results show that enhanced feature sets derived from MS2PIP and DeepLC not only improve identification

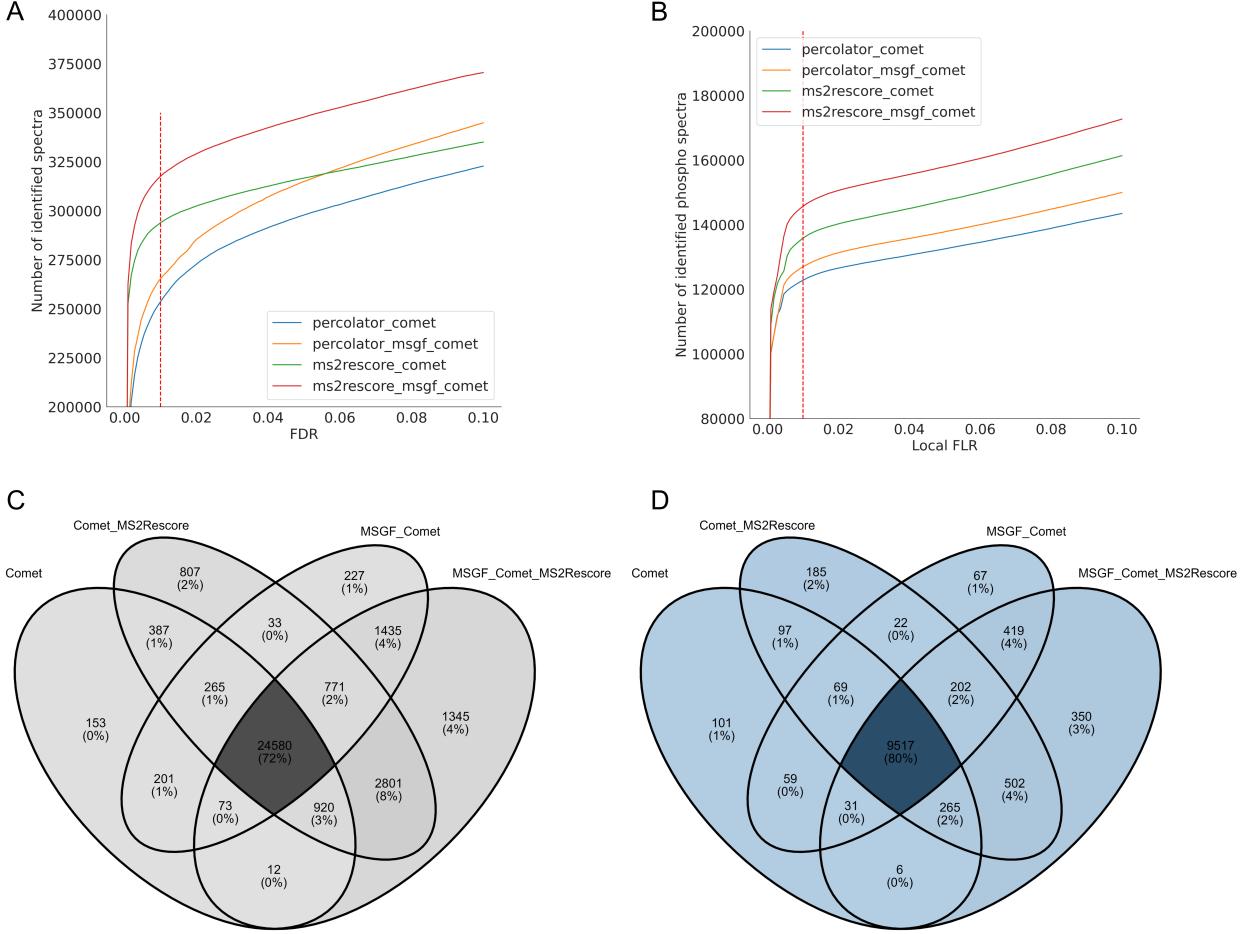


Figure 4: Comparison of phosphorylated peptide identification results for different workflow settings. (A) Line plot showing the number of spectra identified for four workflow settings at different PSM FDR levels. (B) Line plot showing the number of phosphorylated spectra identified for four workflow settings at different local false localization rate levels after an FDR of less than 0.01 at the PSM level. (C) Venn diagram of peptides quantified for four settings. (D) Venn diagram of protein phosphosites at protein FDR 0.01 and FLR 0.01 for four settings.

rates but also translate into gains in quantification depth. Importantly, we provide evidence that the improved identifications via rescoring propagate downstream into quantification, leading to increased numbers of proteins with reliable abundance estimates, as well as enhanced detection of differentially expressed proteins.

To demonstrate the applicability and advantages of quantms integrated with MS2Rescore in quantitative proteomics, we performed a series of reanalyses using publicly available large-scale datasets with well-established benchmarks. In label-free experiments, MS2Rescore-

enhanced workflows achieved significant increases in PSM and peptide identification while maintaining or improving quantification reproducibility across replicates. For TMT experiments, the integration of MS2Rescore into quantms increased the number of quantifiable proteins. In more challenging applications, such as immunopeptidomics and phosphoproteomics, the deep learning-based rescore pipeline consistently yielded higher identification rates and improved sensitivity. These improvements contribute meaningful biological insights, such as phosphosite discovery and the identification of differentially expressed proteins with potential clinical relevance.

Overall, the results in this publication highlight the synergistic benefits of integrating machine learning-based features within end-to-end, cloud-based proteomics workflows. By embedding MS2Rescore into the quantms pipeline, we provide a practical and accessible solution for the community to leverage cutting-edge spectral prediction and retention time modeling without the need for complex manual configuration. This integrated approach enables reproducible reanalysis of large public datasets, increases identification confidence, and strengthens quantitative conclusions across diverse experimental designs. Future work will focus on expanding this approach to other types of post-translational modifications and exploring the integration of additional machine learning tools to further enhance proteomics data analysis capabilities.

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## References

- [1] Yasset Perez-Riverol, Chakradhar Bandla, Deepti J Kundu, Selvakumar Kamatchi-nathan, Jingwen Bai, Suresh Hewapathirana, Nithu Sara John, Ananth Prakash, Mathias Walzer, Shengbo Wang, and Juan Antonio Vizcaíno. The PRIDE database at 20 years: 2025 update. *Nucleic Acids Research*, 53(D1):D543–D553, January 2025.
- [2] Jürgen Cox and Matthias Mann. MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. *Nature Biotechnology*, 26(12):1367–1372, December 2008.
- [3] Le-heng Wang, De-Quan Li, Yan Fu, Hai-Peng Wang, Jing-Fen Zhang, Zuo-Fei Yuan, Rui-Xiang Sun, Rong Zeng, Si-Min He, and Wen Gao. pFind 2.0: a software package for peptide and protein identification via tandem mass spectrometry. *Rapid Communications in Mass Spectrometry*, 21(18):2985–2991, September 2007.
- [4] Marc Vaudel, Julia M Burkhart, René P Zahedi, Eystein Oveland, Frode S Berven, Albert Sickmann, Lennart Martens, and Harald Barsnes. Peptideshaker enables reanalysis of ms-derived proteomics data sets. *Nature biotechnology*, 33(1):22–24, 2015.
- [5] Chengxin Dai, Julianus Pfeuffer, Hong Wang, Ping Zheng, Lukas Käll, Timo Sachsenberg, Vadim Demichev, Mingze Bai, Oliver Kohlbacher, and Yasset Perez-Riverol. quantms: a cloud-based pipeline for quantitative proteomics enables the reanalysis of public proteomics data. *Nature Methods*, July 2024.
- [6] Paolo Di Tommaso, Maria Chatzou, Evan W Floden, Pablo Prieto Barja, Emilio Palumbo, and Cedric Notredame. Nextflow enables reproducible computational workflows. *Nature Biotechnology*, 35(4):316–319, April 2017.
- [7] Mark D. Wilkinson, Michel Dumontier, IJsbrand Jan Aalbersberg, Gabrielle Apple-ton, Myles Axton, Arie Baak, Niklas Blomberg, Jan-Willem Boiten, Luiz Bonino

Da Silva Santos, Philip E. Bourne, Jildau Bouwman, Anthony J. Brookes, Tim Clark, Mercè Crosas, Ingrid Dillo, Olivier Dumon, Scott Edmunds, Chris T. Evelo, Richard Finkers, Alejandra Gonzalez-Beltran, Alasdair J.G. Gray, Paul Groth, Carole Goble, Jeffrey S. Grethe, Jaap Heringa, Peter A.C 'T Hoen, Rob Hooft, Tobias Kuhn, Ruben Kok, Joost Kok, Scott J. Lusher, Maryann E. Martone, Albert Mons, Abel L. Packer, Bengt Persson, Philippe Rocca-Serra, Marco Roos, Rene Van Schaik, Susanna-Assunta Sansone, Erik Schultes, Thierry Sengstag, Ted Slater, George Strawn, Morris A. Swertz, Mark Thompson, Johan Van Der Lei, Erik Van Mulligen, Jan Velterop, Andra Waagmeester, Peter Wittenburg, Katherine Wolstencroft, Jun Zhao, and Barend Mons. The FAIR Guiding Principles for scientific data management and stewardship. *Scientific Data*, 3(1):160018, March 2016.

- [8] Mingze Bai, Jingwen Deng, Chengxin Dai, Julianus Pfeuffer, Timo Sachsenberg, and Yasset Perez-Riverol. Lfq-based peptide and protein intensity differential expression analysis. *Journal of Proteome Research*, 22(6):2114–2123, 2023.
- [9] Ping Zheng, Enrique Audain, Henry Webel, Chengxin Dai, Joshua Klein, Marc-Phillip Hitz, Timo Sachsenberg, Mingze Bai, and Yasset Perez-Riverol. Ibaqpy: A scalable python package for baseline quantification in proteomics leveraging sdrf metadata. *Journal of Proteomics*, 317:105440, 2025.
- [10] Chengxin Dai, Anja Füllgrabe, Julianus Pfeuffer, Elizaveta M. Solovyeva, Jingwen Deng, Pablo Moreno, Selvakumar Kamatchinathan, Deepti Jaiswal Kundu, Nancy George, Silvie Fexova, Björn Grüning, Melanie Christine Föll, Johannes Griss, Marc Vaudel, Enrique Audain, Marie Locard-Paulet, Michael Turewicz, Martin Eisenacher, Julian Uszkoreit, Tim Van Den Bossche, Veit Schwämmle, Henry Webel, Stefan Schulze, David Bouyssié, Savita Jayaram, Vinay Kumar Duggineni, Patroklos Samaras, Mathias Wilhelm, Meena Choi, Mingxun Wang, Oliver Kohlbacher, Alvis Brazma, Irene Papathodorou, Nuno Bandeira, Eric W. Deutsch, Juan Antonio Vizcaíno, Mingze Bai,

Timo Sachsenberg, Lev I. Levitsky, and Yasset Perez-Riverol. A proteomics sample metadata representation for multiomics integration and big data analysis. *Nature Communications*, 12(1):5854, October 2021.

- [11] Lennart Martens, Matthew Chambers, Marc Sturm, Darren Kessner, Fredrik Levan-  
der, Jim Shofstahl, Wilfred H. Tang, Andreas Römpf, Steffen Neumann, Angel D.  
Pizarro, Luisa Montecchi-Palazzi, Natalie Tasman, Mike Coleman, Florian Reisinger,  
Puneet Souda, Henning Hermjakob, Pierre-Alain Binz, and Eric W. Deutsch. mzML—a  
Community Standard for Mass Spectrometry Data. *Molecular & Cellular Proteomics*,  
10(1):R110.000133, January 2011.
- [12] Sven Degroeve and Lennart Martens. MS2PIP: a tool for MS/MS peak intensity pre-  
diction. *Bioinformatics (Oxford, England)*, 29(24):3199–3203, December 2013.
- [13] Robbin Bouwmeester, Ralf Gabriels, Niels Hulstaert, Lennart Martens, and Sven De-  
groeve. DeepLC can predict retention times for peptides that carry as-yet unseen mod-  
ifications. *Nature Methods*, 18(11):1363–1369, November 2021.
- [14] Siegfried Gessulat, Tobias Schmidt, Daniel Paul Zolg, Patroklos Samaras, Karsten  
Schnatbaum, Johannes Zerweck, Tobias Knaute, Julia Rechenberger, Bernard Delanghe,  
Andreas Huhmer, Ulf Reimer, Hans-Christian Ehrlich, Stephan Aiche, Bernhard Kuster,  
and Mathias Wilhelm. Prosit: proteome-wide prediction of peptide tandem mass spectra  
by deep learning. *Nature Methods*, 16(6):509–518, June 2019.
- [15] Louise M. Buur, Arthur Declercq, Marina Strobl, Robbin Bouwmeester, Sven Degroeve,  
Lennart Martens, Viktoria Dorfer, and Ralf Gabriels. MS<sup>2</sup> Rescore 3.0 Is a Modular,  
Flexible, and User-Friendly Platform to Boost Peptide Identifications, as Showcased  
with MS Amanda 3.0. *Journal of Proteome Research*, 23(8):3200–3207, August 2024.
- [16] Wenjie Yang, Hualin Chen, Lin Ma, Jie Dong, Mengchao Wei, Xiaoqiang Xue, Yingjie  
Li, Zhaoheng Jin, Weifeng Xu, and Zhigang Ji. A comprehensive analysis of the FOX

family for predicting kidney renal clear cell carcinoma prognosis and the oncogenic role of FOXG1. *Aging*, 14(24):10107–10124, December 2022.

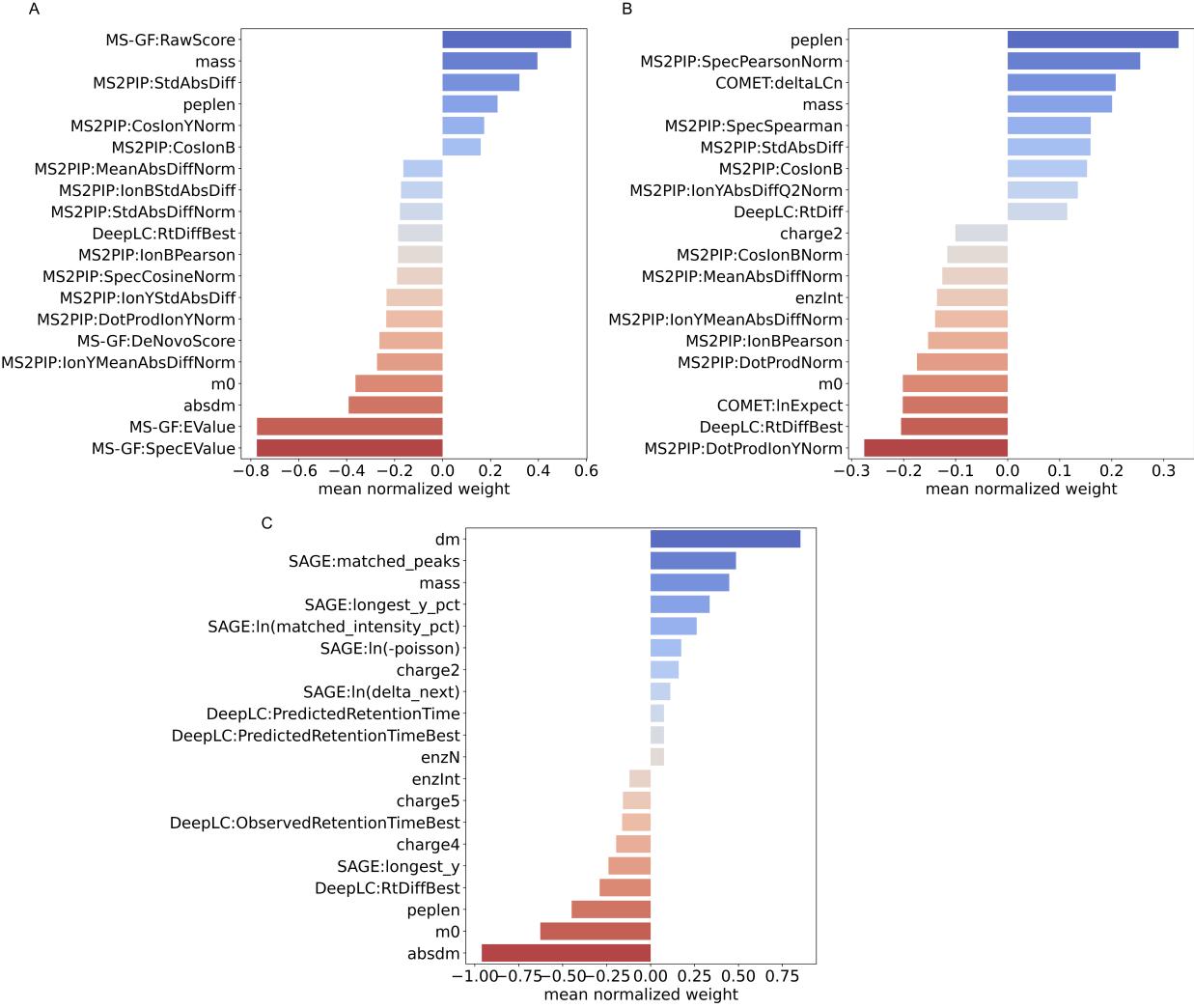


Figure S1: The weights that Percolator assigns to different features of the search engine feature vector in MSGF+ (A), Comet (B), and SAGE (C) combined with Percolator settings from PXD001819. The more different from zero a weight is (both positive and negative), the more important that feature is in the final Percolator classification.

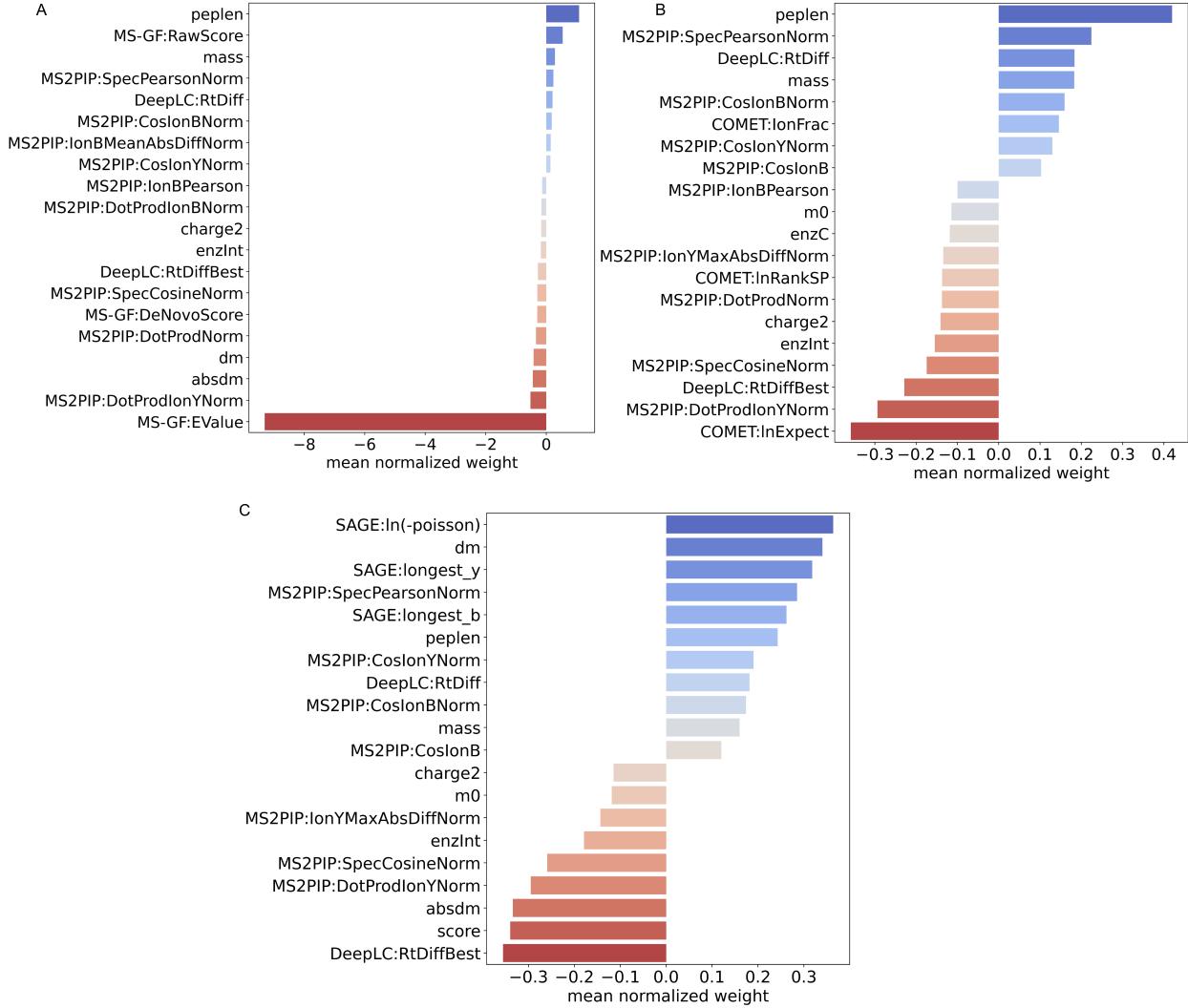


Figure S2: The top 20 normalized weights from Percolator for MSGF+ (A), Comet (B), and SAGE (C) identification results from PDC000125.

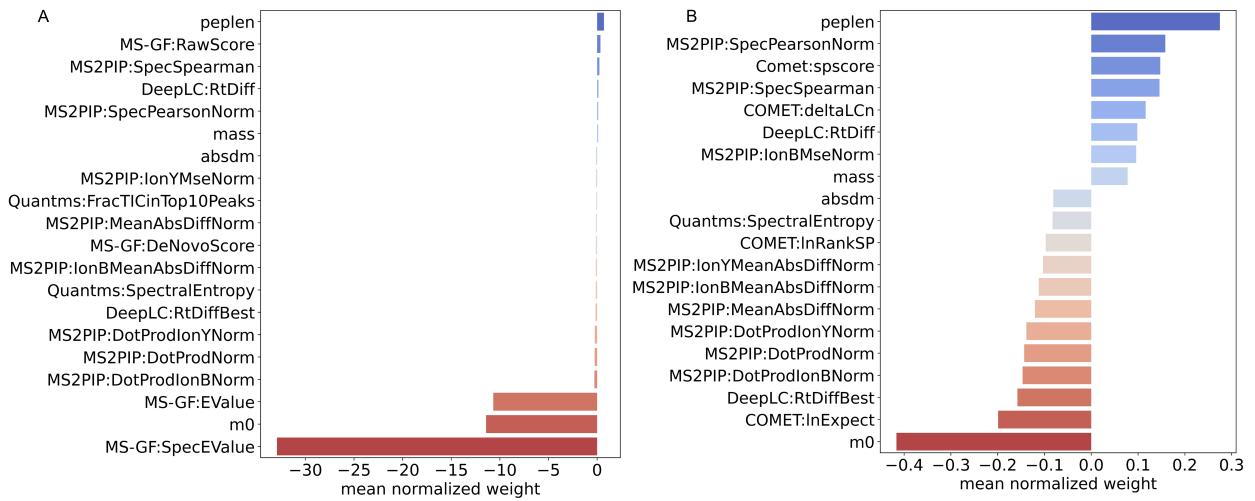


Figure S3: The top 20 normalized weights from Percolator for MSGF+ (A) and Comet (B) identification results in the PXD019643 dataset.

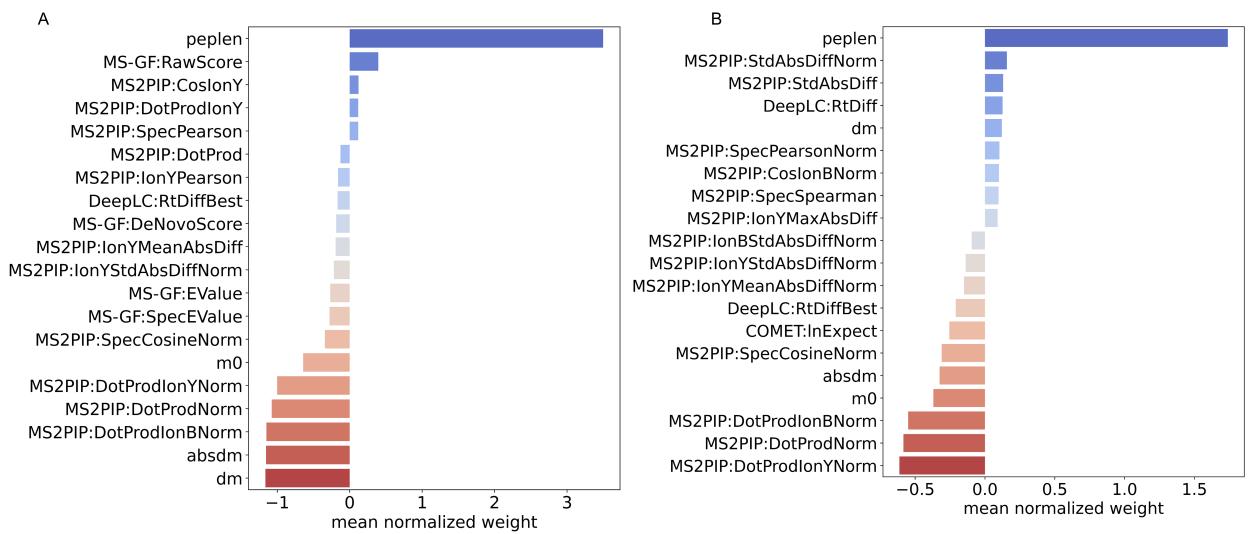


Figure S4: The top 20 normalized weights from Percolator for MSGF+ (A) and Comet (B) identification results in the PXD026824 dataset.