

msqrob2TMT: robust linear mixed models for inferring differential abundant proteins in labelled experiments with arbitrarily complex design

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Abstract

Labelling strategies in mass spectrometry (MS)-based proteomics enhance sample throughput by enabling the acquisition of multiplexed samples within a single run. However, contemporary experiments often involve increasingly complex designs, where the number of samples exceeds the capacity of a single run, resulting in a complex correlation structure that must be addressed for accurate statistical inference and reliable biomarker discovery. To this end, we introduce msqrob2TMT, a suite of mixed model-based workflows specifically designed for differential abundance analysis in labelled MS-based proteomics data. msqrob2TMT accommodates both sample-specific and feature-specific (e.g., peptide or protein) covariates, facilitating inference in experiments with arbitrarily complex designs and allowing for explicit correction of feature-specific covariates. We benchmark our innovative workflows against state-of-the-art tools, including DEqMS, MSstatsTMT, and msTrawler, using two spike-in studies. Our findings demonstrate that msqrob2TMT offers greater flexibility, improved modularity, and

enhanced performance, particularly through the application of robust ridge regression. Finally, we demonstrate the practical relevance of msqrob2TMT in a real mouse study, highlighting its capacity to effectively account for the complex correlation structure in the data.

1 Introduction

High-throughput LC-MS-based proteomic workflows are widely used to quantify differential protein abundance across samples. Relative protein quantification is generally achieved through either label-free or labelled workflows. The latter employ stable isotope labelling techniques such as metabolic and post-metabolic labelling, which gained traction in recent years (Li et al. 2021). Compared to label-free approaches, labelling offers the advantage of mitigating run-to-run variability in peptide identification and quantification by pooling and analysing multiple samples within a single run. This enables researchers to compare proteomes across multiple conditions or treatments within a single MS run, thereby providing a more comprehensive view of the proteome and enhancing the statistical power of the analysis. Current tandem mass tag (TMT) kits, for instance, support the multiplexing of up to 18 samples in a single run (Li et al. 2021).

However, contemporary experiments often involve increasingly complex designs, where the number of samples exceeds the capacity of a single run. This has far reaching consequences for the downstream data analysis. In labelled experiments with multiple MS runs, biological replicates are often distributed across distinct runs, and additional technical MS runs are frequently included. Similar to label-free approaches, such multi-run experiments are prone to numerous missing peptide intensity values across MS runs (Brenes et al. 2019). Furthermore, the data of these designs are correlated at multiple levels. Indeed, the MS-technology introduces various sources of technical variation, including run-level effects, channel effects, and spectrum-specific effects, amongst others. Hence, ion intensities from samples multiplexed in the same run are more similar than those from samples multiplexed in different runs. Additionally, quantification does not happen at the protein level but at the level of its identified peptide ions. Peptide ion abundances from the same sample within a run are inherently more similar than those of peptide ions from different samples. At the lowest level, TMT reporter ions from a specific spectrum enable peptide ion quantification across multiple samples, resulting in correlated ion intensities; ion intensities within the same spectrum are more alike than those measured across different spectra. Furthermore, mixtures of multiplexed samples are often run in technical repeats on the MS, introducing yet another level of correlation. Addressing such a complex correlation structure in labelled experiments necessitates flexible statistical models capable of producing valid tests for differential abundance. However, most proteomics software tools assume independence among the (summarised) ion intensities and can therefore not account for the abovementioned intricate correlation structures in contemporary TMT experiments, which may in turn lead to an inflation of false positives (Huang et al. 2020b). The MSstatsTMT tool (Huang et al. 2020b), however, is one of the notable exceptions, as it

has been explicitly developed to accommodate experiments with multiple conditions, biological replicate runs, technical repeat runs, and unbalanced designs.

In this publication, we present a bespoke data analysis workflow for labelled MS-based proteomics experiments, embedded in our msqrob2 universe in R/Bioconductor. Initially designed for label-free workflows, msqrob2 has demonstrated advantages over other state-of-the-art tools in terms of both performance and its modular, transparent implementation (Sticker et al. 2020). In this work, we extend these benefits to the analysis of labelled experiments. Similar to MSstatsTMT, our workflows address the complex correlation structure inherent in contemporary labelled MS-based proteomics experiments by mixed models. However, unlike MSstatsTMT and msTrawler, we avoid by default the imputation of missing peptide-spectrum match (PSM) intensities, instead assuming missingness at random after accounting for peptide effects. Nevertheless, users retain the option in msqrob2TMT to utilise the default imputation strategies available in QFeatures or to implement custom functions tailored to their specific needs. Additionally, DEqMS and MSstatsTMT model the data upon summarisation at the protein level and msTrawler immediately models the data at the PSM level, while msqrob2TMT provides the user with the option to use either PSM-level or protein-level workflows. Another notable difference is that msqrob2 offers ridge regression and robust M-estimation, which can further stabilise parameter estimation and thus enhance reliable detection of differential proteins.

We demonstrate that our novel msqrob2TMT workflows outperform state-of-the-art tools by benchmarking them against DEqMS (Zhu et al. 2020), MSstatsTMT (Huang et al. 2020b), and msTrawler (O'Brien et al. 2024) using two spike-in and real experimental dataset. Our comparisons also highlight that none of the state-of-the-art tools could provide valid inference across all of these three datasets, as their specific implementation limits the experimental designs for which they can infer DA. Particularly, MSstatsTMT cannot account for multiple covariates e.g., treatment effects together with block effects, age and/or other confounders, while DEqMS and msTrawler cannot address the complex correlation in TMT-experiments with multiple runs and technical replication, which are commonly employed in the proteomics community. Note, that Proteome Discoverer was not included in our benchmark, as we utilised datasets featured in the original MSstatsTMT publication, where the authors had already established the superior performance of MSstatsTMT compared to Proteome Discoverer (Huang et al. 2020b).

Importantly, our novel msqrob2TMT workflows offer researchers extensive flexibility to develop both peptide-level and protein-level data analysis workflows, incorporating custom preprocessing steps and user-defined models that can be tailored to their specific applications. The latest release further expands support for complex experimental designs by providing full compatibility with the model specification capabilities of the popular lme4 R package for mixed models, while enabling the use of both feature-level and sample-level covariates. The sample-level covariates allow msqrob2 to accommodate longitudinal and clustered experimental designs. The use of feature-level covariates is supported through integration with the QFeatures (Gatto and Vanderaa 2022) data infrastructure. This integration ensures that raw input data are never

lost but remain accessible and linked to the preprocessed, normalised, and summarised assays, as well as to the model outputs. This approach guarantees transparency, traceability, and reproducibility throughout the analysis workflow.

2 Materials and Methods

In this section, we first introduce the datasets that are used to evaluate our novel workflows and to benchmark them against state-of-the-art methods DEqMS, MSstatsTMT and msTrawler. Next, we briefly introduce these methods and our novel msqrob2TMT workflows. We conclude this section with the different metrics used to benchmark performance.

2.1 Datasets

Three datasets are used to evaluate and benchmark the different tools: a spike-in dataset, a multibatch benchmarking experiment, and real mouse case study.

2.1.1 MSstatsTMT Spike-in Dataset

The spike-in dataset was obtained from MassIVE (RMSV000000265) and has the following design: UPS1 peptides at concentrations of 500, 333, 250, and 62.5 fmol were spiked into 50 µg of SILAC HeLa peptides. This series forms a dilution gradient of 1, 0.667, 0.5, and 0.125 relative to the highest UPS1 peptide concentration (500 fmol). A reference sample was prepared by combining the diluted UPS1 peptide samples with 50 µg of SILAC HeLa peptides. Each dilution and the reference sample were processed in duplicate, yielding a total of ten samples. These samples were subsequently labelled using TMT10-plex reagents and combined for LC-MS/MS analysis, hereafter referred to as a “mixture.” This protocol was repeated five times. Each mixture was analysed in technical triplicate, resulting in a total of 15 MS runs. This experimental design simulates a scenario with 10 biological replicates per condition, consisting of 2 replicates per condition within each of the five mixtures.

A custom filtering step was required prior to the standard preprocessing performed by the different methods. In this study, two PSMs can exhibit identical intensity values due to the use of two separate Mascot search nodes: one targeting the SwissProt protein database and the other targeting the Sigma UPS protein database. This dual search strategy was employed to identify which PSMs originate from HeLa cell proteins, that are labelled with both SILAC and TMT, and which PSMs originate from the spike-in UPS proteins, labelled only with TMT. However, identification is imperfect, as some spectra are matched in both nodes, leading to different peptides being matched with the same spectrum and identical intensity values. These PSMs were excluded, as it is not possible to ascertain whether they correspond to the spike-in UPS proteins, the HeLa background proteins, or, in the extreme case, a mixture of both.

Additionally, following the MSstatsTMT default settings, PSMs with fewer than six out of ten intensity values were removed, and the PSM with the highest sum of intensity values is chosen when multiple spectra for the same peptide ion occur.

2.1.2 msTrawler Multibatch Benchmarking Experiment

The msTrawler Multibatch Benchmarking Experiment data has been deposited on ProteomeXchange (PXD036799). However, for reproducibility of the results published in the original paper, the data available on the google drive of the msTrawler paper (https://console.cloud.google.com/storage/browser/mstrawler_paper) was used. The experiment is a spike-in study which consists of a constant mouse plasma background in which yeast proteins were then spiked with the following dilution ratios 1, 2, 3, 5, 11, 14, 18, 20, 24, 28 and 32. The yeast proteins were harvested from different media; glycerol + ammonium sulfate, galactose + urea, galactose + monosodium glutamate, galactose + ammonium sulfate, glucose + ammonium sulfate, glucose + monosodium glutamate, and glucose + urea. The samples were labelled using the TMTpro 18-plex and pooled in six mixtures, each containing 15 samples. Two of the remaining TMT channels are reference channels, one reference channel is the combination of one batch and the other reference channel consists of all batches. For this dataset the ground truth is known: a true positive is a yeast protein that is returned as significant while a significant mouse protein is a false positive.

The dataset imposes specific challenges for the normalisation. Indeed, the majority of the proteins are differentially abundant (DA), i.e. all yeast peptides, and they are all DA in the same direction, which implies a violation of the normalisation assumptions for most tools. To address this issue, the authors of msTrawler (O'Brien et al. 2024) developed a custom normalisation workflow tailored specifically to this dataset. Particularly, they excluded mouse PSMs that correlate with the yeast dilution profile i.e., PSMs with a Pearson correlation coefficient higher than 0.25. Subsequently, PSMs with a summed signal-to-noise ratio below 20 were filtered out. Finally, the within sample geometric mean for the 50% most stable mouse PSMs in a run is used for normalisation. However, it should be noted that such a procedure is not applicable in typical experimental contexts, as the set of non-DA proteins is generally unknown. For this study, we nevertheless applied this custom msTrawler preprocessing workflow to the dataset prior to conducting differential analysis to ensure that all tools are benchmarked on the same preprocessed dataset, thereby enabling a fair comparison of their performance.

2.1.3 Mouse dataset

The spike-in dataset was downloaded from MassIVE (RMSV000000264). In the study conducted by Plubell et al., 2017 (2017), twenty mice were divided into groups to investigate the effects of low-fat (LF) and high-fat (HF) diets. The experiment involves two factors: the type of diet (LF or HF), and the duration of the diet, categorised as either short-term (8 weeks) or long-term (18 weeks). This design resulted in four distinct groups corresponding

to each combination of diet type and duration. Five mice, i.e. biological replicates, were randomly assigned to each group and samples from their epididymal adipose tissue were randomly assigned to three TMT10-plex mixtures. Within each mixture, two reference channels were included, each containing pooled samples representing a range of peptides from all samples. Not all TMT channels were utilised, leading to an unbalanced experimental design. Finally, each TMT mixture was fractionated into nine parts and analysed using synchronous precursor selection, culminating in a total of 27 MS runs.

2.2 Tools for Differential Analysis

In this section, we first introduce the state-of-the-art methods DEqMS, MSstatsTMT and msTrawler before developing our novel msqrob2 workflows for labelled experiments.

2.2.1 DEqMS

The DEqMS workflow (Zhu et al. 2020) starts by \log_2 -transforming the observed PSM intensities. The PSM intensities are then summarised into protein intensities by adopting the median sweep algorithm to the PSM data for each protein in each run, separately. This approach can be regarded as a one-step median polish. Indeed, the \log_2 -transformed PSM intensities are first centered by subtracting the corresponding median of the \log_2 PSM intensities from their corresponding spectrum. Subsequently, the spectrum-centered PSM intensities in each TMT channel for each protein are aggregated into protein expression values using median summarisation. Finally, the protein summaries are normalised by subtracting the median of all summarised protein expression values within their corresponding channel.

Note, that for the msTrawler Multibatch Benchmarking Experiment, DEqMS starts from data that have been custom-filtered and normalised (see Section 2.1.2). Subsequently, the reference channels are removed, the data are \log_2 transformed, and summarised through a modified median sweep algorithm, which omits the normalisation step of the protein summaries.

DEqMS uses conventional linear models to model the abundances protein by protein. Hence, it is unable to account for the complex correlation structures that arise in labelled experiments involving multiple biological replicates, which are multiplexed across several mixtures and may be acquired through multiple technical repeat runs. Nevertheless, DEqMS is well suited to analyse data from simpler labelled experiments that can be modelled as randomised complete block designs. This applies to cases where all samples are derived from distinct biological replicates and where all treatments are multiplexed within each MS run, allowing variation between runs to be addressed through the inclusion of a fixed run effect:

$$\begin{aligned} y_{rc} &= \mathbf{x}_{rc}^t \boldsymbol{\beta} + \beta_r^{\text{run}} + \epsilon_{rc} \\ \epsilon_{rc} &\sim N(0, \sigma^2) \end{aligned}$$

with y_{rc} the \log_2 -transformed and summarised protein intensity for TMT reagent c in MS-run r , \mathbf{x}_{rc}^t the covariate pattern, e.g. diet, time, condition, dilution, and/or media for the sample in channel c of run r that is used to model the mean protein abundance upon correction for the run effect, β a vector of model parameters modelling the \log_2 fold changes (FC) for each covariate, and β_r^{run} the fixed block effect for run r , and ϵ_{rc} a normally distributed error term with mean 0 and variance σ^2 i.e., $N(0, \sigma^2)$. Hence, DEqMS can model data of complex experiments as long as these can be parameterised as a randomised complete block design. However, it cannot accommodate experiments with clustered or longitudinal designs, nor for designs including technical repeats.

Statistical hypothesis testing builds on the moderated t-tests and F-tests from the popular limma package. So users have the flexibility to infer DA using any linear combination of the model parameters ($\mathbf{L}^T \beta$), which we also refer to as contrasts. DEqMS version 1.24 (Zhu 2023) from Bioconductor release 3.20 is used in our manuscript.

2.2.2 MSstatsTMT

The default MSstatsTMT workflow (Huang et al. 2020b) begins with the \log_2 -transformation of the observed MS intensities, followed by median equalisation across PSMs, TMT channels, and runs. Missing values are subsequently imputed using an accelerated failure time model. After imputation, PSM intensities are summarised to protein intensities using Tukey's median polish. Finally, protein intensities are normalised against the reference by subtracting the median of the corresponding reference channel intensities.

Note, that for the msTrawler Multibatch Benchmarking Experiment, MSstatsTMT starts from data that have been custom-filtered and normalised (see Section 2.1.2). Subsequently, the data are \log_2 -transformed, imputed using an accelerated failure time model when missing, summarised, and normalised against the reference channels.

MSstatsTMT can fit linear mixed models to the normalised and summarised protein intensities to infer DA between T treatment groups in experimental designs involving multiple biological replicates, which are multiplexed with tags across several mixtures and quantified through multiple technical repeat MS runs. These models are fitted protein-by-protein and are specified as follows:

$$\begin{aligned}
y_{rcm} &= \beta_0 + \sum_{t=1}^T \beta_t^{\text{treat}} x_{rcmt}^{\text{treat}} + u_r^{\text{run}} + u_m^{\text{mix}} + u_{cm}^{\text{biorep}} + \epsilon_{rcm} \\
\sum_{t=1}^T \beta_t^{\text{treat}} &= 0 \\
u_r^{\text{run}} &\sim N(0, \sigma_{\text{run}}^2) \\
u_m^{\text{mix}} &\sim N(0, \sigma_{\text{mix}}^2) \\
u_{cm}^{\text{biorep}} &\sim N(0, \sigma_{\text{biorep}}^2) \\
\epsilon_{rcm} &\sim N(0, \sigma^2)
\end{aligned}$$

with y_{rcm} the \log_2 -transformed and summarised protein intensity for tag c in mixture m in MS-run r , β_0 the intercept or the overall mean, β_t^{treat} the treatment effect for treatment t , x_{rcmt}^{treat} a dummy variable that is $x_{rcmt}^{\text{treat}} = 1$ if the biological replicate cm from channel c of mixture m belongs to group t and $x_{rcmt}^{\text{treat}} = 0$ otherwise, and u_r^{run} , u_m^{mix} and u_{rm}^{biorep} normally distributed random effects with mean 0 and variance σ_{run}^2 , σ_{mix}^2 and σ_{biorep}^2 respectively, and ϵ_{rcm} the normally distributed error term with mean 0 and variance σ^2 . Note, that the random effects model the hierarchical correlation structure in the data, i.e. the correlation within runs, mixtures, and biological replicates.

Hence, MSstatsTMT can only perform inference on experiments where treatments can be modelled using a single factor with multiple groups and assumes a very specific correlation structure: technical repeats involve the replication of an entire mixture. Consequently, MSstatsTMT cannot support additional covariates such as blocking variables or age, nor additional random effects needed to address studies with clustered or longitudinal designs.

The variance components are estimated using REstricted Maximum Likelihood (REML). If insufficient data are available to estimate the parameters of the full model, MSstatsTMT reduces the model to infer DA on as many proteins as possible.

MSstatsTMT performs statistical inference on linear combinations of group means (contrasts) using approximate t-tests. For example, to test the difference between treatments j and k , it calculates: $\log_2 FC_{j-k}^{\text{treat}} = \beta_j^{\text{treat}} - \beta_k^{\text{treat}}$. The user has the flexibility to perform all pairwise comparisons between groups or to focus on user-specified contrasts.

In addition, the default empirical Bayes step from Ritchie et al. (2015) is employed to stabilise the estimation of variance of the errors by borrowing strength across proteins; and a Satterthwaite approximation is used to estimate the degrees of freedom for the approximate t-statistics.

MSstatsTMT version 2.14.1 (Huang et al. 2020a) from Bioconductor release 3.20 was used in our manuscript.

2.2.3 msTrawler

msTrawler (O'Brien et al. 2024) initially removes peptides with a summed signal-to-noise ratio below 20. Missing values are imputed based on the limit of reliability, defined as 0.01 times the total scan intensity. Scans containing fewer than three values above this limit are excluded. Samples are then normalised by subtracting the column medians of the subset of peptides with a standard deviation lower than the median standard deviation. All these values reflect the default settings of msTrawler for these arguments.

Note, that for the msTrawler Multibatch Benchmarking Experiment, msTrawler starts from data that have been custom-filtered and normalised (see Section 2.1.2). Subsequently, missing data are imputed based on the limit of reliability, defined as 0.01 times the total scan intensity and scans containing fewer than three values above this limit are excluded.

msTrawler builds a linear mixed model starting from peptide-level data, based on user-specified sample and covariate files (O'Brien et al. 2024). Specifically, msTrawler employs the following base model:

$$\begin{aligned} y_{rcs} &= \mathbf{x}_{rc}^t \beta + u_{rc}^{\text{samp}} + \epsilon_{rcs} \\ u_{rc}^{\text{samp}} &\sim N(0, \sigma_{\text{samp}}^2) \\ \epsilon_{rcs} &\sim N(0, \sigma^2) \end{aligned}$$

with y_{rcs} the \log_2 -transformed and normalised intensity for the peptide ion of scan s of a protein from the sample with tag c in MS-run r , \mathbf{x}_{rc}^t the covariate pattern for the sample in channel c of run r , β the vector of model parameters modelling the effect of each covariate, and u_{rc}^{samp} a normally distributed random effect with mean 0 and variance σ_{samp}^2 modelling the correlation of PSMs from the same protein pool in a sample, and ϵ_{rcs} the normally distributed error term with mean 0 and variance σ^2 . Hence, msTrawler does not address the correlation within scans, runs, and mixtures that are acquired in multiple technical repeats on the MS.

msTrawler further enables the use of reference samples by extending the response vector with the ion intensities for the reference samples y_{rbs} with tag b :

$$\begin{aligned} y_{rbs} &= \alpha_s + \epsilon_{rbs} \\ y_{rcs} &= \alpha_s + \mathbf{x}_{rc}^t \beta + u_{rc}^{\text{samp}} + \epsilon_{rcs} \end{aligned}$$

where α_s is a nuisance parameter that accounts for scan-to-scan variability.

The model parameters are estimated using weighted REML, where each ion intensity is weighted according to its signal-to-noise ratio.

The covariate pattern \mathbf{x}_{rc}^t for each sample is constructed from a user specified sample and covariate files. The covariates can be of the type “factor”, i.e. a factor with multiple levels; “continuous”, i.e. a linear term; “time”, i.e. a linear, quadratic or cubic trend by specifying the degree of the polynomial, a factor with every timepoint as a level, or a sine and cosine term to model circadian effects.

When multiple covariates are used, these are added as additive terms in the model. For each covariate of the factor type, multiple output files are automatically generated; one for each pairwise comparison between two groups. For each protein, the output files contain an estimate of the corresponding $\log_2 FC$ and a p-value based on an approximate t-test where the degrees of freedom are estimated using the Kenward-Rogers approximation.

Hence, msTrawler is restricted to specific designs and does not allow for user specified contrasts, limiting the research questions that can be inferred from experiments with complex designs.

2.2.4 msqrob2TMT

The msqrob2TMT workflows begin with the \log_2 transformation of the observed PSM intensities. This is followed by normalisation of the TMT channels by subtracting the median \log_2 intensity of each channel to account for loading differences. This normalisation step assumes that the majority of proteins are not DA. For our protein-level workflows, PSMs are further summarised into protein abundance values using Tukey's median polish method, applied separately to the PSM data of each protein within each run. No imputation is performed in the default msqrob2TMT workflows. However, users may define custom preprocessing pipelines by leveraging the functionalities provided in the QFeatures package for filtering, normalisation, and imputing missing intensities.

Note, that for the msTrawler Multibatch Benchmarking Experiment, our msqrob2TMT workflows start from data that have been custom-filtered and normalised (see Section 2.1.2). Subsequently, the reference channels are removed, the data are \log_2 -transformed, and summarised for our protein-level workflows.

msqrob2TMT can fit linear mixed models for each protein, which can be implemented in our msqrob2 package from version 1.14 of the Bioconductor release 3.20 (Huber et al. 2015), onwards. Our PSM-level msqrob2TMT workflows directly models PSM-level data, while our protein-level msqrob2TMT workflows begin with summarised data following median polish summarisation.

Our msqrob2TMT framework is very flexible. The model specification has been made fully compatible with the lme4 R package for fitting mixed models. Additionally, it leverages the QFeatures data infrastructure, allowing the incorporation of both feature-level (rowData) and sample-level (colData) variables within the model. This facilitates analyses that infer and adjust for feature-specific and sample-specific covariates, as well as their interactions. Consequently, the current msqrob2TMT implementation can accommodate arbitrarily complex experimental designs, provided they can be specified within the framework of linear mixed models:

$$\begin{aligned} y_{rcms} &= \mathbf{x}_{rcm}^t \boldsymbol{\beta} + \mathbf{z}_{rcms}^t \mathbf{u} + \epsilon_{rcms} \\ \epsilon_{rcms} &\sim N(0, \sigma^2) \\ \mathbf{u} &\sim MVN(\mathbf{0}, \mathbf{G}) \end{aligned}$$

with y_{rcms} the \log_2 -transformed and normalised intensity for peptide ion of scan s of a protein from the sample in tag c of mixture m of MS-run r , \mathbf{x}_{rcm}^t the covariate pattern e.g. diet, time, condition, dilution, and/or media for the sample in channel c of mixture m in run r , $\boldsymbol{\beta}$ the model parameters modelling the effect of each covariate, and \mathbf{z}_{rcms}^t the covariate pattern for the random effects to model the hierarchical correlation structure of the data i.e., mixture, run, sample, PSM, and/or additional covariates needed to address clustered and longitudinal study designs, and \mathbf{u} the vector of random effects that are multivariate normally distributed with mean $\mathbf{0}$ and variance-covariance matrix \mathbf{G} i.e., $MVN(\mathbf{0}, \mathbf{G})$. Note, that the residuals

ϵ_{rcms} given the random effects are again assumed to i.i.d. normally distributed with mean 0 and variance σ^2 .

For models starting at the protein level the index s is dropped, and y_{rcm} becomes the \log_2 transformed, normalised and summarised protein abundance values.

Similar to MSstatsTMT, variance components are estimated using restricted maximum likelihood (REML), and the error variance is stabilised by borrowing strength across proteins using the default empirical Bayes step of limma (Ritchie et al. 2015). However, msqrob2 introduces two additional advancements: outliers can be addressed using M-estimation with Huber weights, and treatment effects can be regularised through ridge penalisation (Goeminne et al. 2020). Note that the ridge penalty is estimated by leveraging the connection between ridge regression and mixed models.

Statistical inference with Wald tests can be conducted for any linear combinations of the estimated model parameters ($\mathbf{L}^T \beta$), providing our users with full flexibility to infer research hypotheses of interest. We direct readers to the supplementary information for detailed vignettes demonstrating the implementation of our msqrob2TMT workflows, their model parametrisation, how to define the appropriate contrasts for the \log_2 FC of interest, and for the interpretation of the output.

2.3 Method performance

We benchmark our novel workflows against state-of-the-art tools by examining the number of reported proteins that are true positive (TP) (i.e., UPS proteins in the spike-in study, and yeast proteins in the Multibatch Benchmark study), and false positive (FP) (i.e., HeLa proteins in the spike-in study, and mouse proteins in the Multibatch Benchmark study). Additionally, we construct true positive rate (TPR)-false discovery proportion (FDP) plots. TPR represents the fraction of truly DA proteins reported by the method, calculated as $TPR = TP / (TP + FN)$, with FN false negatives (i.e., UPS proteins in the spike-in study, and yeast proteins in the Multibatch Benchmark study that were not flagged as DA). FDP denotes the proportion of false positives among all proteins flagged as DA, calculated as $FDP = FP / (TP + FP)$. We also highlight the actually observed FDP at a 5% FDR threshold, which is expected to approximate 5%.

Furthermore, we assess the $\log_2 FC$ estimates and compare them to the ground truth. For background proteins (HeLa proteins in the spike-in study, and mouse proteins in the Multibatch Benchmark study) the ground truth $\log_2 FC$ is zero, whereas for the DA proteins (UPS proteins in the spike-in study, and yeast proteins in the Multibatch Benchmark study) the ground truth corresponds to their spiked \log_2 -ratio.

3 Results

We here develop three novel workflows for labelled experiments in our msqrob2 universe:

1. msqrob2_rrilm (Robust RIDge Linear Mixed Model): A novel workflow that models the summarised protein-level expression values using a robust linear mixed model. This model accounts for correlation within TMT-plexes via a random effect, regularises fold change (FC) estimates across conditions using a ridge penalty, and corrects for outliers via M-estimation;
2. msqrob2_psm_rrilm (Peptide Spectrum Match Robust RIDge Linear Mixed Model): A novel workflow that directly models normalised PSM intensities using a robust linear mixed model with random effects for sample, PSM, and run. It employs a ridge penalty to regularise FC estimates and uses M-estimation to correct for outliers;
3. msqrob2_psm_rrilm_refit (peptide spectrum match Robust RIDge Linear Mixed Model, refit): This workflow is identical to msqrob2_psm_rrilm, but reduces the model complexity in order to also fit one-hit-wonder proteins, those for which only one PSM per run is observed.

It is worth noting that our msqrob2TMT workflows also allow for incorporating additional random effects to account for technical repeats or other factors arising from longitudinal or clustered experimental designs.

We compare our novel msqrob2TMT workflows to the state-of-the-art methods DEqMS (Zhu et al. 2020), MSstatsTMT (Huang et al. 2020b), and msTrawler (O'Brien et al. 2024). In Figure 1, we provide an overview of the various functionalities of these tools and of our novel workflows. Notably, msqrob2TMT is the only workflow capable of modelling arbitrarily complex experimental designs. DEqMS cannot model correlations in the data using random effects. It can thus only provide valid inference if MS-run can be treated as a block effect. Moreover, it cannot handle designs with technical repeats. MSstatsTMT can only infer differential abundance (DA) for designs that can be specified with a one-way ANOVA layout. It does include random effects for run and mixture. So, it can handle designs where mixtures are run in technical repeats on the MS. msTrawler, on the other hand, models peptide-level data with main effects and a random sample effect to account for correlations between PSMs from the same protein pool. However, it does not account for correlations between samples multiplexed within the same run, and can only model interactions between a factor and a continuous time trend. Furthermore, msTrawler is the only tool that does not offer users the functionality to define their own hypotheses for inferring DA. It only provides tests for each slope term in the model, or for all pairwise comparisons between the groups of a factor variable.

Using two spike-in studies and one experimental case study, we highlight how the specific implementations of state-of-the-art tools impose limitations on the range of experimental designs for which they can infer DA. We further illustrate how these constraints can be addressed by

leveraging the flexibility of our msqrob2TMT workflows and demonstrate its superior performance to prioritise DA.

	Fixed effect parameterisation				Random effect parameterisation				Model			
	categorical	numerical	interaction	multiple	run	mixture	sample	biological replicate	PSM	other	PSM-level	protein-level
DEqMS	✓	✓	✓	✓	✗	✗	✗	✗	✗	✗	✗	✓
MSstatsTMT	✓	✗	✗	✗	✓	✓	✗	✓	✗	✗	✗	✓
msTrawler	✓	✓	*	✓	✗	✗	✓	✗	✗	✓	✓	✗
msqrob2TMT	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

Figure 1: Overview of the tools considered in this work and the model parameterisation they enable. Green tick marks indicate that the method supports the specific model parameterisation. Note, that “other” in the random effect parameterisation refers to other random effects implied by the design, e.g. in studies with longitudinal or clustered designs. (*) msTrawler can only account for interactions between a factor and a continuous time trend.

3.1 MSstatsTMT Spike-in Study

In this study, 40 UPS1 proteins were spiked into a HeLa protein background at four different concentrations. Each spike-in concentration was multiplexed twice within a 10-plex TMT mixture, accompanied by two reference channels. A total of five 10-plex TMT mixtures were prepared, and each mixture was analysed in technical triplicate on the mass spectrometer. Therefore, the ground truth is known: only the spike-in UPS proteins are DA.

Note, that DEqMS cannot account for the hierarchical correlation structure inherent in labelled experiments with multiple runs. While it can correctly infer FCs when all conditions are present in each run by introducing a block factor, it cannot adequately handle technical repeats. Furthermore, it was also unclear how to account for technical repeats from msTrawler’s documentation. Consequently, in the main manuscript, we assess the performance of the different methods using only one technical repeat per mixture. Results for the full study, including the analysis with multiple technical repeats, are provided in the Supplementary Information.

In Figure 2 A, we compare the performance of the different methods using True Positive Rate (TPR) and False Discovery Proportion (FDP) curves. The TPR represents the fraction of spiked UPS proteins reported as DA, while the FDP reflects the proportion of HeLa proteins

among the total number of DA proteins returned. Our msqrob2TMT workflows clearly outperform the state-of-the-art methods. Indeed, they have a much higher sensitivity (TPR) at the same FDP level.

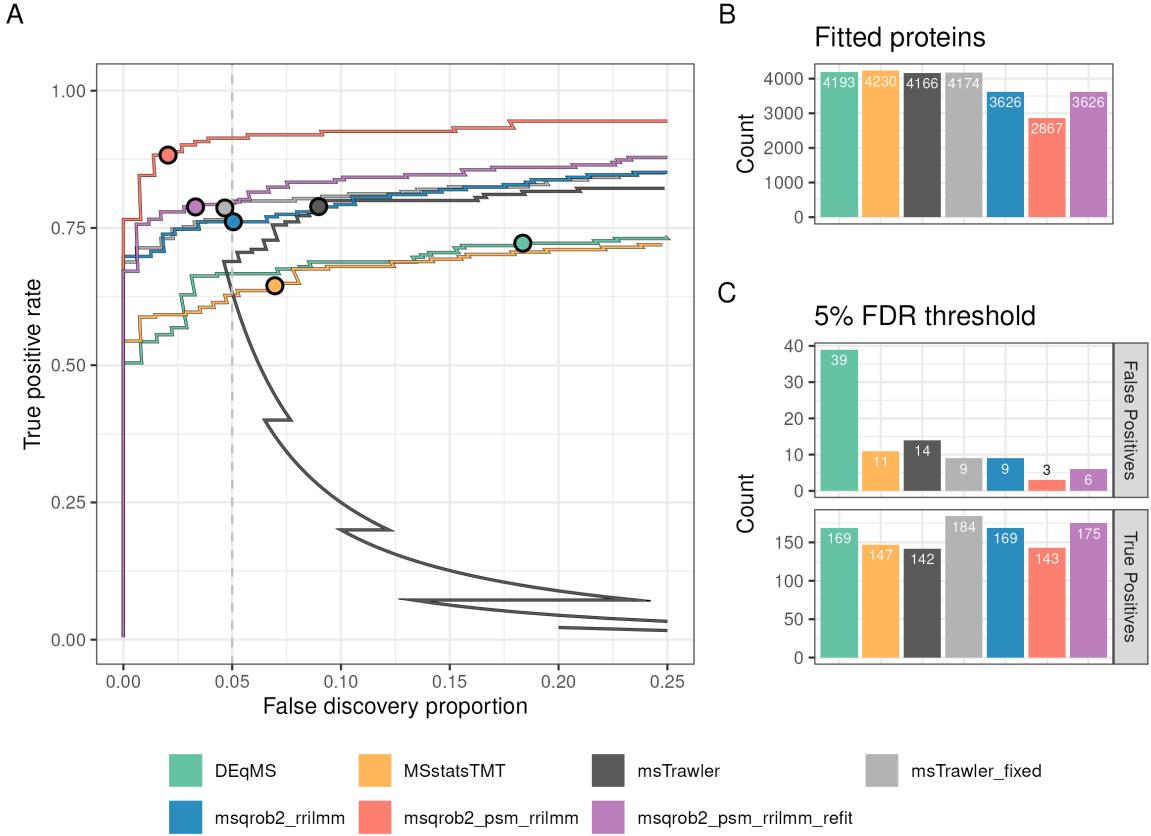


Figure 2: Performance in the MSstatsTMT spike-in study. Panel A: True positive rate (TPR) - false discovery proportion (FDP) plots for DEqMS, MSstatsTMT, msTrawler and msqrob2TMT workflows. Note, that the import function of msTrawler did not properly import the data. So we also provide results for msTrawler with a refactored import function, referred to as msTrawler fixed. The combined performance over all the dilution comparisons is shown. Dots indicate the TPR and FDP obtained at the 5% FDR threshold. Panel B: Number of fitted proteins for each workflow. Panel C: Number of true and false positives over all the comparisons.

However, it is important to note that the different methods return results for varying numbers of proteins, as shown in Figure 2 B. In particular, our novel msqrob2-based workflows tend to report fewer proteins. To ensure a fair comparison, we also present TPR-FDP curves based on all ground truth DA proteins (all fourty spike-in UPS1 proteins) as the maximum num-

ber of TP that can be reported for each comparison (Supplementary Figure 1 B), as well as plots for the common subset of proteins returned by all methods (Supplementary Figure 1 C). Notably, Supplementary Figure 1 B presents a different picture: here, the PSM-level method msqrob2_psm_rrilmm shows significantly lower sensitivity than the summarisation-based approaches. Specifically, msqrob2_psm_rrilmm only returns models for 27 UPS proteins. This is due to msqrob2_psm_rrilmm being unable to fit models for many proteins because of missing data and/or due to one-hit-wonder proteins i.e., those for which only one peptide ion is observed. Indeed, for one-hit-wonder proteins, msqrob2 cannot fit the random sample-level effect and returns an error. To address this, we developed a refit function that can automatically refit PSM-level models for one-hit-wonders in our msqrob2_psm_rrilmm_refit workflow. This adaptation restores top performance when calculating the TPR based on all 40 spike-in UPS proteins that are known to be DA in each comparison. However, it should be noted that msqrob2_psm_rrilmm_refit results in a decrease in sensitivity compared to msqrob2_psm_rrilmm when TPR-FDP curves are based solely on the proteins returned by each method (Figure 2 A), indicating that accounting for one-hit-wonders leads to a faster accumulation of false positives among the top-ranked proteins.

Interestingly, msTrawler, msqrob2_psm_rrilmm, and msqrob2_psm_rrilmm_refit show very similar performance when the analysis is based on the common proteins returned by all methods, with msqrob2_rrilmm following closely behind (Supplementary Figure 1 C). These results are consistent with findings from label-free proteomics literature, where PSM-level methods typically outperform summarisation-based workflows (e.g., (Sticker et al. 2020)). Remarkably, msTrawler exhibited a performance boost as compared to that in Supplementary Figure 1 panels A and B, which probed us to closely examine its top-ranked false positives. They appeared to be spike-in proteins that were incorrectly labelled, which we could trace back to the msTrawler import function that failed to read-in the data correctly. Upon refactoring the lengthy msTrawler import function, which is referred to as msTrawler_fixed, the performance becomes on par with msqrob2_psm_rrilmm_refit.

These findings are further corroborated by the results at the 5% FDR level, shown in Figure 2 C. All msqrob2 workflows demonstrate high sensitivity and low FDP. Specifically, they recover between 143 - 175 spike-in UPS proteins as DA (true positives, TP) while only reporting between 3 - 9 false positives (FP) for HeLa proteins. As a result, their FDP ranges between 2.1% - 5.1%, suggesting appropriate FDR control at the 5% level. The default msTrawler workflow, however, was only able to recover 142 TP and reported 14 FP, leading to an FDP of 9%. With our refactored import function this improved to 184 TP, 9 FP and an FDP of 4.7%. The summarisation-based workflows DEqMS and MSstatsTMT, reported 169 and 147 TP, respectively, with 39 and 11 FP, resulting in FDPs of 18.8% and 7%, respectively, suggesting improper FDR control by DEqMS.

More detailed comparisons are available in Supplementary Figure 2-4, which display TPR-FDP curves for individual pairwise comparisons of the spike-in conditions. These figures highlight that the observed performance improvements of our msqrob2 workflows are particularly pronounced for more challenging comparisons involving low FCs (e.g., spike-in concen-

trations 0.667–0.5 and 1–0.667). In Supplementary Figure 5, we present results for the full dataset, incorporating all technical repeats. While the results for MSstatsTMT and our novel msqrob2TMT workflows are consistent with those obtained from a single replicate, the difference in performance is somewhat reduced when considering all technical repeats. It is worth noting that only MSstatsTMT and our msqrob2 workflows can appropriately analyse the full dataset, as DEqMS is unable to introduce random effects, and it is unclear in msTrawler’s documentation how to address technical repeats.

In Figure 3 we evaluate the \log_2 FC estimates. Figure 3 A shows that the estimated \log_2 FC for non-spiked proteins is unbiased across all methods. Interestingly, the variability of the estimates for the msqrob2TMT workflows with ridge regularisation is lower. Note, that in comparison 0.667 - 0.5 and 1 - 0.125, there are extreme \log_2 FC estimates of -4.82 and -8.25, respectively, for the msTrawler workflow that are not shown in the plots. Figure 3 B demonstrates that the \log_2 FC for spike-in proteins are generally underestimated by all methods. This is consistent with prior reports in the literature and likely due to interference from co-fragmentation of peptide ions, which causes the \log_2 FC between reporter ions to be underestimated (Savitski et al. 2011; Ow et al. 2009). We observe that the underestimation becomes more pronounced as the \log_2 FC between conditions increases. The variability of the \log_2 FC estimates for the spiked UPS proteins is similar across all methods. This clearly illustrates the benefit of the ridge regularisation in our msqrob2TMT workflows as it affects only the \log_2 FC estimates for non-DA proteins while leaving those for DA proteins largely unchanged.

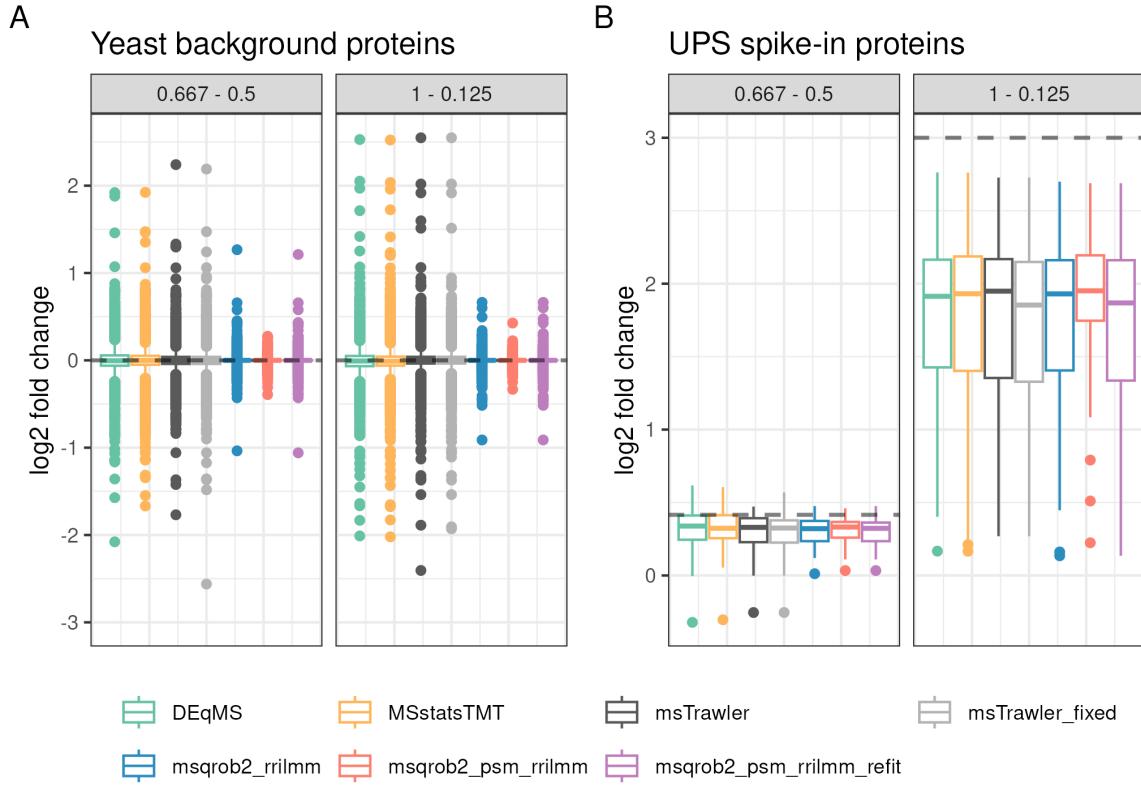


Figure 3: Boxplots showing the log2 FC distributions for the spike-in proteins, focusing on two comparisons with the highest and lowest difference in spike-in concentrations. Fold changes are estimated by DEqMS, msqrob2TMT, MSstatsTMT, and msTrawler workflows. The grey dotted line is the true log2 FC for the comparison. Panel A: non spike-in proteins (yeast); Panel B: spike-in proteins.

Finally, Supplementary Figure 6 shows that MSstatsTMT, msTrawler, and our msqrob2TMT workflows all produce fairly uniform p-value distributions for non-spike-in proteins. DEqMS, however, shows a slight inflation at low p-values. The ridge regression p-values are slightly over-conservative with a notable spike at p-values equal to 1, due to the shrinkage of FCs for non-spike-in proteins.

3.1.1 Impact of Robust Ridge Regression, Imputation and Reference Normalisation

A unique feature of the msqrob2TMT workflows is the regularisation of parameter estimation through robust M-estimation and ridge penalisation. In Figure 4, we evaluate the impact of robust ridge regression on performance within both protein-level and PSM-level models. The

results indicate a modest improvement in performance when either robust M-estimation or ridge penalisation is applied individually. However, the combination of robust M-estimation and ridge penalisation yields the most substantial performance gain.

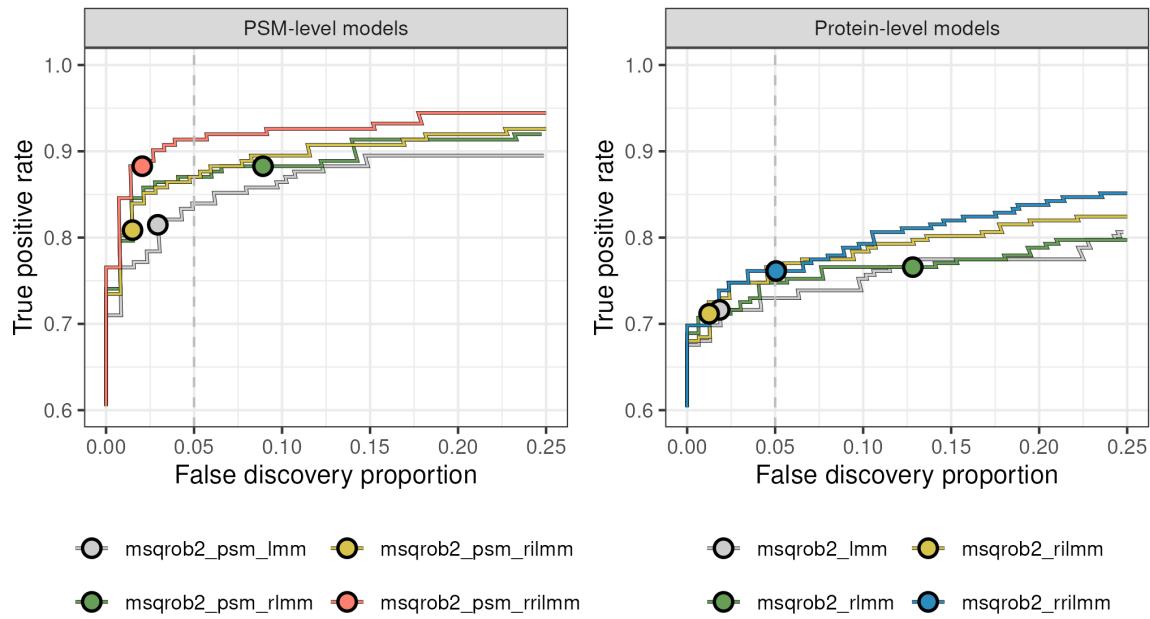


Figure 4: True positive rate (TPR) - false discovery proportion (FDP) plots showing the effect of robust M-estimation and ridge regression on the performance of the msqrob2TMT protein-level (panel A) and PSM-level workflows (panel B). Combined performance over all comparisons is shown. Differential abundance is inferred with msqrob2TMT with a vanilla linear mixed model (lmm), a linear mixed model fitted via robust M-estimation (rlmm), ridge regression (rilmm), or robust M-estimation and ridge regression (rrilmm). Dots indicate the TPR and FDP obtained at the 5% FDR threshold.

Note, that the msqrob2TMT workflow also differs from MSstatsTMT in its preprocessing methodology. Specifically, MSstatsTMT, by default, imputes missing values and employs reference channels for additional normalisation. In Supplementary Figure 7, we evaluate the integration of MSstatsTMT preprocessing with msqrob2TMT model fitting. The findings reveal that imputation and reference channel normalisation do not provide additional benefit in the context of this spike-in study. Interestingly, a performance improvement is again observed when robust M-estimation and ridge penalisation are applied.

3.2 msTrawler Multibatch Benchmarking Study

The msTrawler multibatch benchmarking study has a more complex design comprising six TMTpro 18-plex batches, where two channels serve as reference channels. One reference channel is derived from a single batch, while the other reference channel includes data from all batches. Yeast proteins cultured on different media were spiked in a background of mouse proteins. The spike-in dilution ratios range from 1, 2, 3, 5, 11, 14, 18, 20, 24, 28, up to 32. Hence, the ground truth is known: only the yeast proteins are DA. A correct data analysis requires modelling of the spike-in condition, while blocking on culture media and accounting for run-to-run variability. Note that this is not possible for MSstatsTMT as users can only specify a single factor to model the variability induced by the experimental design. Consequently, incorporating MSstatsTMT would not provide a fair comparison and has therefore been omitted from the results included in the main text.

It is important to note that the peculiar design of the experiment implies unconventional preprocessing steps. Specifically, there is a much higher number of DA yeast proteins, 1102 proteins, compared to non-DA mouse proteins, 287 proteins, which violates the typical assumptions of normalisation. Hence, we followed the bespoke normalisation approach specifically devised for this dataset in the msTrawler paper (O'Brien et al. 2024). In particular, the authors based their normalisation on mouse proteins with low standard deviation, i.e. non-DA proteins that were consistently detected. Note that this approach is not possible with real experimental data, where non-DA proteins are typically unknown. For a fair comparison, we opted to apply this bespoke preprocessing pipeline prior to conducting DA analysis with DEqMS and our novel msqrob2TMT workflows.

In Figure 5, we compare the performance of our msqrob2TMT workflows with the msTrawler and DEqMS workflows across all dilution comparisons. The TPR-FDP plot in Figure 5 A demonstrates that msqrob2_psm_rrilmm is again the top performer followed by the msqrob2_rrilmm and msqrob2_psm_rrilmm_refit methods, which are on par and outperform both msTrawler and DEqMS that exhibit lower sensitivity. However, in Figure 5 B, a significant difference is observed in the number of proteins assessed by each workflow. Notably, msqrob2_psm_rrilmm again reports fewer results due fit errors for proteins with a lot of missing data and one-hit wonder proteins. Nevertheless, following the refit that allows for one-hit wonders, the number of proteins reported by msqrob2 increases by 47.8%, indicating a very large number of one-hit-wonder proteins. A substantial difference is also observed in the number of false positives returned at the 5% FDR threshold by each workflow (Figure 5 C). Specifically, DEqMS and msTrawler report 387 and 676 false positives respectively, whereas the msqrob2TMT workflows only return between 11 - 36 false positives at the same 5% FDR threshold. Notably, the protein-level msqrob2_rrilmm and msqrob2_psm_rrilmm_refit still report about 4500 TPs more than DEqMS. Lastly, all workflows exhibit an FDP below 5%, which is not unexpected, given that only 20.7% of the proteins assessed are non-DA. Indeed, the default Benjamini-Hochberg False Discovery Rate (BH-FDR) method implicitly assumes the fraction of non-DA features to be 1 so as to provide a conservative estimate of

the expected proportion of false positives in the list of significant features it returns (Efron et al. 2001), which is particularly conservative for this dataset with an artificially high number of DA proteins.

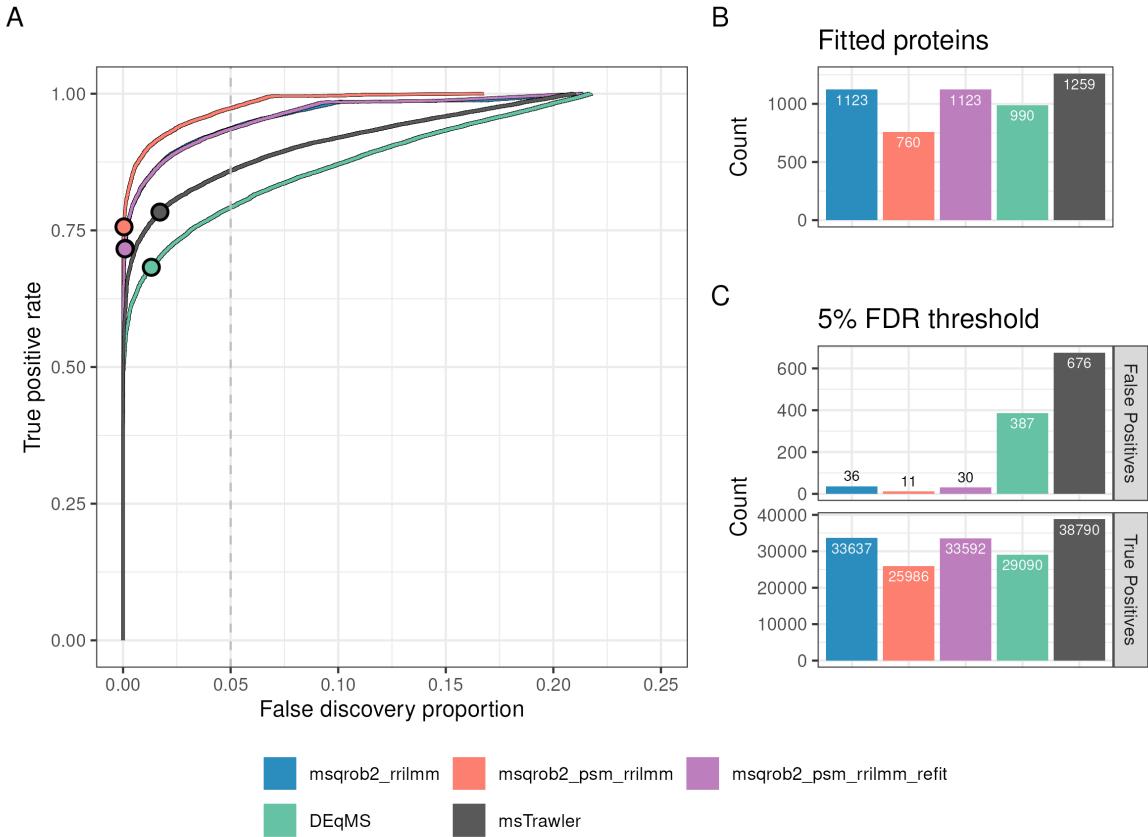


Figure 5: Performance in the msTrawler Multibatch Benchmarking Study. Panel A: True positive rate (TPR) - false discovery proportion (FDP) plots for DEqMS, msTrawler, and msqrob2TMT workflows. Combined performance over all comparisons is shown. Dots indicate the TPR and FDP obtained at the 5% FDR threshold. Note, that the performance of msqrob2_rrilmm and msqrob2_psm_rrilmm_refit are on par, so their TPR-FDP curves almost coincide. Panel B: Number of fitted proteins for each workflow. Panel C: Number of true and false positives over all comparisons.

For a fair comparison, we also report TPR-FDP curves using all ground truth DA proteins as the maximum number of TP that can be reported for each comparison (Supplementary Figure 8 B) as well as those based on the common subset of proteins assessed by all workflows (Supplementary Figure 8 C). In Supplementary Figure 8 B, we observe a large decrease in performance for PSM-level method msqrob2_psm_rrilmm, which is due to the vast num-

ber of one-hit-wonder yeast proteins. However, after refitting, msqrob2_psm_rrilmm_refit recovers performance comparable to that of our msqrob2_rrilmm workflow, which outperform msTrawler irrespectively of the set of ground truth DA proteins that is used to calculate the TPR (Supplementary Figure 8 A-C). Note, however, that the methods also differ in terms of their preprocessing. Specifically, msTrawler employs imputation and additional filtering. In Supplementary Figure 9, we therefore present results for msqrob2TMT models applied on msTrawler’s preprocessed data, which demonstrates a further increased performance. This finding confirms the superior model fitting of our msqrob2TMT workflows compared to msTrawler.

To illustrate the importance of msqrob2TMT’s flexibility in accommodating arbitrarily complex experimental designs, we included results in Supplementary Figure 8 that MSstatsTMT users would obtain if they omitted the blocking effect in their analysis. As expected, excluding this blocking factor leads to a significant reduction in performance.

In Figure 6, we evaluate the \log_2 FC estimates for non-DA mouse proteins and DA spike-in yeast proteins. Notably, the variability in \log_2 FC estimates for non-DA mouse proteins is markedly lower and closer to zero for the msqrob2TMT workflows. Similar to Figure 3, \log_2 FC values for DA proteins are generally underestimated across all workflows, with similar levels of variability observed. This again highlights the beneficial property of our msqrob2TMT robust ridge workflows in reducing variability for non-DA proteins, without affecting these for truly DA proteins.

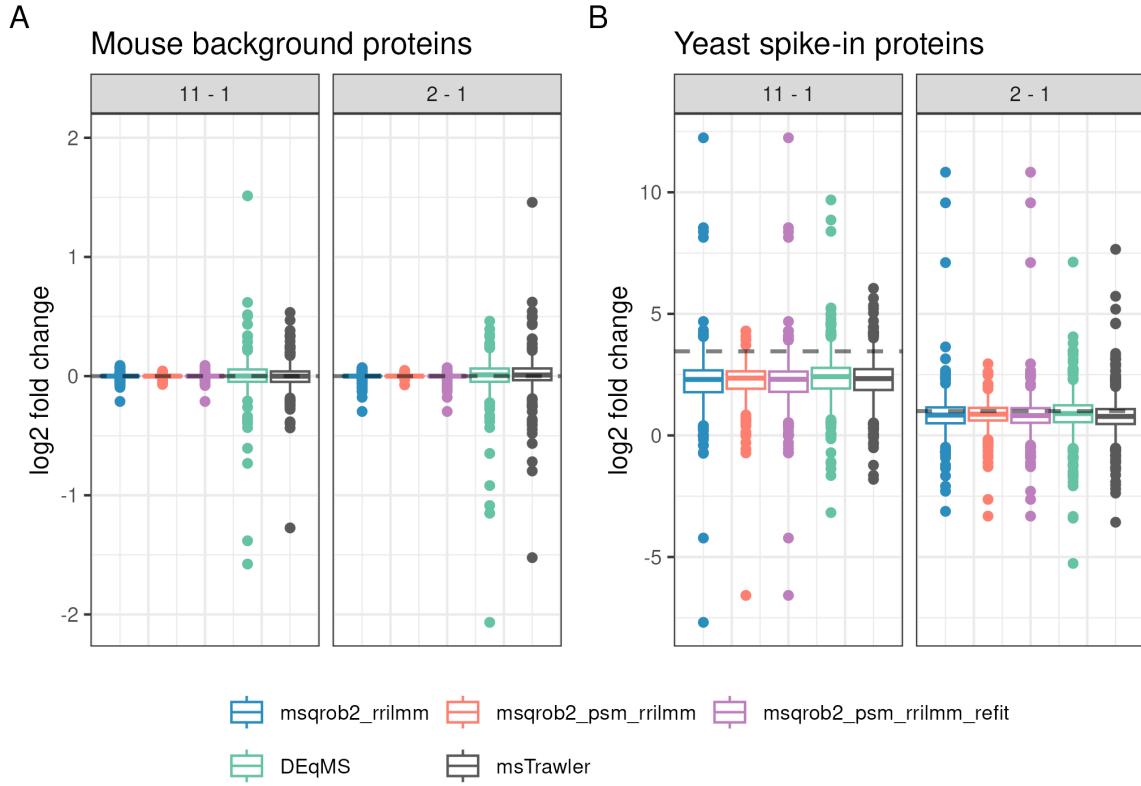


Figure 6: Boxplots showing the log₂ FC distributions for the spike-in proteins, focusing on two comparisons with the highest and lowest difference in spike-in concentrations. Fold changes are estimated by DEqMS, msqrob2TMT, and msTrawler workflows. The grey dotted line is the true log₂ FC for the comparison. Panel A: non-spiked proteins (mouse); Panel B: spike-in proteins (yeast).

Finally, Supplementary Figure 10 illustrates that both the msTrawler and msqrob2TMT workflows generate relatively uniform p-value distributions for non-spike-in proteins. The p-values derived from ridge regression are slightly over-conservative, and due to the shrinkage of FCs for the non-spiked proteins, there is a noticeable peak of p-values at 1. This histogram exhibits greater variability compared to Supplementary Figure 6 likely due to the limited number of non-DA mouse proteins in the dataset (287 proteins only).

3.3 Mouse Study

This study investigates the effect of the diet and duration on the proteome of adipocyte cells. The mouse dataset involves mice that were subjected to either a low-fat (LF) or a

high-fat (HF) diet for varying durations, also referred to as short or long period. Note, that MSstatsTMT cannot accommodate for designs with multiple factors and/or interactions. We therefore encode the treatment effect as a single factor, with each level corresponding to a specific diet \times duration combination. The primary research focus lies on the effect of diet. Accordingly, we prioritise proteins using the following four contrasts:

1. DA between mice exposed to a HF vs LF diet after a short period, representing an early diet effect.
2. DA between mice exposed to a HF vs LF diet after a long period, representing a late diet effect.
3. DA between mice exposed to a HF vs LF averaged over the early and late period, representing an average diet effect.
4. DA between mice exposed to a HF vs LF diet differs between long and short period, representing the diet \times duration interaction effect.

Note, that msTrawler will automatically generate output files for all pairwise comparisons between each diet \times duration combination. However, it does not allow users to define their contrasts of interest. Consequently, the diet \times duration interaction and the average diet effect cannot be inferred using msTrawler. Furthermore, attempts to utilise msTrawler with multiple reference samples available per run were unsuccessful, even when subsampling was applied. Additionally, we could not address the correlation between fractions with the software, thereby preventing us from addressing the hierarchical correlation structure inherent to the dataset. Due to these limitations, msTrawler was excluded from the analysis.

We also include two protein-level msqrob2TMT workflows. In the first workflow, msqrob2tmt_rrilmm, peptide ions are summarised to the protein-level for each run, resulting in multiple protein abundance values for each biological replicate i.e., one in every technical fraction. In the second workflow, msqrob2tmt_rrilmm_mixture, we use the MSstatsTMT approach and summarise peptide ions to the protein-level over all technical fractions, resulting in a single protein abundance value for every biological replicate.

Table 1: Number of differential proteins at 5% FDR for the msqrob2 and MSstatsTMT workflows. The proteins are prioritised using the following four contrasts: DA between HF vs LF diet after short period (early), DA between HF vs LF diet after long period (long), average DA between HF vs LF over the early and late period (avg), and DA of HF vs LF diet differs between long period and short period (int).

	Comparison			
	early	late	avg	int
MSstatsTMT	5	9	27	1
msqrob2_rrilmm_mixture	31	6	50	5
msqrob2_rrilmm	80	21	119	7
msqrob2_psm_rrilmm	95	24	132	4
msqrob2_psm_rrilmm_refit	98	29	145	6

Table 1 summarises the number of DA proteins identified as significant at the 5% FDR-adjusted p-value threshold by the various methods. First, the PSM-level workflows (msqrob2_psm_rrilmm and msqrob2_psm_rrilmm_refit) return more DA proteins than protein-based workflows for three out the four contrasts tested. Note, that the fourth contrast is the diet \times duration for which few DA proteins were identified, irrespective of the method. Indeed, high throughput omics studies are known to be under powered for discovering interaction effects (Van den Berge et al. 2018). Second, modelling the technical MS fraction (msqrob2_psm_rrilmm, msqrob2_psm_rrilmm_refit and msqrob2_rrilmm) leads to a striking increase of the number of DA proteins compared to the workflows that summarise protein intensities over the technical fractions of a mixture (MSstatsTMT, msqrob2_rrilmm_mixture). Third, more DA proteins are found by our msqrob2TMT workflows compared to MSstatsTMT, even when applying the same summarisation approach, i.e. MSstatsTMT vs msqrob2_rrilmm_mixture. Finally, allowing for one-hit-wonder proteins when modelling the data at the PSM level (msqrob2_psm_rrilmm_refit) slightly increases the number of DA, making it the workflow that identifies the most DA proteins. However, as the ground truth for DA proteins in this experimental dataset is not available, we are unable to affirm whether the reported proteins are truly DA.

The upset plots (Supplementary Figures 11-13) demonstrate that the majority of the proteins identified by msqrob2_rrilmm and msqrob2_rrilmm_mixture are also prioritised by the PSM-level models (msqrob2_psm_rrilmm and msqrob2_psm_rrilmm_refit). Additionally, most of the 5, and 27 DA proteins that were reported by MSstatsTMT for the early and average diet contrasts, respectively, were also found significant by other msqrob2TMT workflows. The few proteins uniquely identified as DA by MSstatsTMT where either no longer significant for our msqrob2TMT workflows after correcting for multiple testing i.e., four proteins in the late comparison, or could not be fitted due to missingness i.e., two proteins in the late comparison and all five proteins in the average comparison. Furthermore, proteins uniquely reported by msqrob2_rrilmm_mixture again were no longer significant for the other msqrob2TMT workflows after correcting for multiple testing or could not be fitted due to missingness. Interestingly, the latter proteins exhibited FCs similar to those detected by MSstatsTMT, although their MSstatsTMT p-values were no longer significant after correcting for multiple testing. Finally, proteins uniquely identified as DA by msqrob2_rrilmm or msqrob2_psm_rrilmm have FCs comparable to those observed in other workflows. Again, the corresponding p-values in the other methods were no longer significant upon correcting for multiple testing.

We also conducted a over-representation analysis for the average diet effect, as this comparison yielded the largest list of DA proteins (Supplementary Figure Figure 14). The over-representation analysis can be performed against a background consisting of the entire mouse proteome or restricted to the proteins identified in the study. The latter approach is more convenient. Indeed, the proteins are isolated from mouse adipose tissue, which is expected to result in an over-representation of adipose tissue-specific proteins. Using this restricted background, only seven metabolic pathways were found to be significantly enriched with our msqrob2TMT PSM-level workflows, three of which were also detected by our protein-level workflow msqrob2_rrilmm. However, no KEGG pathways were significantly enriched when employ-

ing the two protein-level workflows that summarise peptide-ions across fractions (MSstatsTMT and msqrob2_rrlmm_mixture). Hence, we also performed the over-representation analysis against the entire mouse background proteome to enable broader comparisons. With this approach, all our novel msqrob2TMT workflows found multiple significantly enriched KEGG pathways, again all related to metabolism, as opposed to MSstatTMT, which did not pick up any enriched KEGG pathway.

Finally, we assessed the validity of the p-values through a mock analysis. Specifically, we randomly assigned the samples of each diet \times duration combination within a mixture to two mock conditions. As none of the proteins exhibit DA between the mock conditions, the corresponding p-values should follow a uniform distribution. The mock analysis could only be conducted with our msqrob2TMT workflows, as it is not feasible to analyse a two-factor design with additive effects using MSstatsTMT. As shown in Supplementary Figure 15, the p-value distributions are uniform with a spike on 1. This pattern, also observed in the spike-in study, again originates from shrinkage of the model parameters towards zero. The results of the mock analysis suggests that the additional proteins found to be significant with our novel msqrob2TMT workflows are not driven by overly liberal asymptotic inference.

4 Discussion

In this contribution, we introduced msqrob2TMT, a novel suite of workflows within our msqrob2 universe, designed to perform differential abundance (DA) analysis for labelled mass spectrometry (MS)-based proteomics experiments. These workflows leverage the flexible robust ridge regression framework of msqrob2 to enhance performance compared to the state-of-the-art tools DEqMS, MSstatsTMT, and msTrawler that uses standard linear (mixed) models.

With the release of msqrob2 version 1.14, we have unlocked full compatibility with the lme4 R package for mixed models, enabling the analysis of data from more complex experimental designs that require the use of both feature-level and sample-level covariates. This advancement allows our workflows to address the intricate hierarchical correlation structure inherent to data from labelled MS experiments, facilitating the analysis of datasets with arbitrarily complex layouts. This capability is particularly critical for modelling data generated in contemporary labelled proteomics experiments, as these utilise ever more complex designs.

Our evaluations on two spike-in studies and a case study demonstrate that none of the three state-of-the-art tools included in our comparisons could provide valid inference across all of these datasets. Notably, MSstatsTMT was unable to account for an additional block effect associated to growth medium in the msTrawler Multibatch Benchmarking Experiment, a limitation with far reaching implications for its applicability in biomedical contexts. Indeed, the inability to adjust for additional covariates and potential confounders undermines the utility of MSstatsTMT in such settings. msTrawler and DEqMS, on the other hand, could not accommodate the more complex correlation structures of the MSstatsTMT spike-in study with technical repeats or the multiple fractions in the mouse case study. Yet these experimental

setups are widely employed in the proteomics community, underscoring the limitations of these tools in addressing such commonly encountered experimental designs.

An additional drawback of msTrawler is its restriction on hypothesis testing. Unlike msqrob2TMT, msTrawler automatically generates output files for testing the slope of each additive covariate in the model as well as for all pairwise comparisons between the levels of each factor variable. However, it does not allow users to define custom hypotheses of interest, such as interaction effects between factors or contrasts like the average treatment effect of one factor when they are involved in an interaction. This limitation diminishes its utility in prioritising proteins of interest, as demonstrated in our mouse case study, where assessing the average treatment effect enabled the identification of the largest number of DA proteins.

Notably, msqrob2TMT not only improves over the state-of-the-art tools in terms of its flexibility, but also demonstrates superior performance. In our analysis of the MSstatsTMT spike-in and msTrawler’s multibatch benchmarking datasets, we showed that our novel msqrob2TMT workflows outperform the existing methods in terms of sensitivity, specificity and FDR control. These improvements underscore the importance of the parameter estimation procedure in DA workflows. By extending the linear mixed model to enhance robustness against outliers and improve uncertainty estimation, msqrob2TMT achieves substantial performance gains. The tools also differ in their preprocessing, specifically in normalisation and imputation. Different sources of missingness occur, which can lead to suboptimal results when the data are imputed under the assumption of missingness by low abundance. The robust modelling in msqrob2TMT, however, can safely omit imputation altogether. msqrob2TMT is also modular, which provides its users with the flexibility to use custom preprocessing steps, making it future-proof when novel and more performant normalisation, summarisation, or imputation procedures become available.

Another significant distinction between the msqrob2, MSstatsTMT, and msTrawler packages lies in their approach to model fitting. MSstatsTMT and msTrawler aim to fit as many proteins as possible by automating the model fitting process. While this approach enhances ease of use, it can result in fitting proteins from the same dataset using different models—for instance, combining linear models with mixed models. This practice may not always be appropriate for the analysis and can introduce complexities in interpretation. Although it is possible to retrieve the underlying models and evaluate their validity, standard users may not be fully aware of these issues or the nuanced interpretations they entail. In contrast, the msqrob2TMT workflows prioritise transparency and reproducibility. Rather than automatically reducing models when the user-specified model cannot be fitted, msqrob2TMT explicitly reports a fit error. This approach allows the data analyst to refit specific proteins with a more appropriate model, ensuring greater consistency and interpretability. We developed a refit function for this purpose and provide detailed guidance in our vignettes (Supplementary Information) to support our users in adapting their analysis to incorporate this feature.

Our analyses also highlight the critical need for robust benchmark datasets in the field of proteomics. Both the MSstatsTMT spike-in dataset and the msTrawler multibatch benchmarking study, while valuable, have notable limitations. Specifically, all DA proteins in these datasets

are spike-in in the same direction, which puts a severe burden on the conventional assumptions underlying normalisation procedures. This can result in issues with channel normalisation, as other proteins may become biased downwards due to ion suppression effects in samples with high spike-in concentrations. In the msTrawler multibatch benchmarking study, the authors had to develop a bespoke preprocessing workflow tailored specifically to this dataset. Indeed, the data contained up to five times more DA proteins than non-DA proteins and all DA between spike-in conditions is in the same direction, which is highly unrealistic. Notably, their normalisation method explicitly had to rely on stably expressed, non-DA proteins, which are typically unknown in a real experimental setting. Conversely, in the MSstatsTMT spike-in study, both non-DA background HeLa UPS proteins as well as spike-in UPS proteins are present. As the HeLa and UPS proteins differ in metabolic labelling, one should be able to discriminate between the non-DA and DA UPS proteins. When closely examining the PSM-level data provided by the MSstatsTMT authors, however, we found spectra that match perfectly with a DA pattern expected for spike-in proteins, whilst being tagged as HeLa and vice versa. We therefore performed additional preprocessing steps to exclude these ambiguous proteins. Nevertheless, it remains possible that some spectra are still mislabelled. This mislabelling can lead to two key issues: on the one hand, there may be an excess of perceived false positives originating from spike-in proteins that were erroneously tagged as background UPS proteins; on the other hand, there may be a reduction in sensitivity. The inclusion of spectra from mislabelled background UPS proteins diminishes the $\log_2 FC$ estimates and increases the standard errors, which can result in spike-in UPS proteins not being identified as significant. When the analysis was conducted without our additional preprocessing, more false positives were observed. This as a result of background proteins that had not been tagged as spike-in UPS proteins, but clearly exhibited a DA pattern consistent with spike-in UPS proteins. After thoroughly examining these two recent state-of-the-art spike-in studies, we urge the field to progress by developing novel benchmark datasets that encompass more complex DA patterns, where some proteins are upregulated while others are downregulated within each spike-in condition.

Overall, we have demonstrated that our msqrob2TMT workflows offer distinct advantages over state-of-the-art tools. They provide a more sensitive and robust approach, while providing good false discovery rate control. Furthermore, these workflows offer the flexibility to infer DA from data derived from experiments with arbitrarily complex designs, a crucial feature for analysing large-scale MS-based proteomics datasets that are increasingly prevalent. Our modular implementation gives our users full flexibility with respect to the choice of search engine, preprocessing steps, and the research hypotheses it can address, while delivering a comprehensive, transparent, and reproducible workflow that spans the entire differential proteomics data analysis.

5 Data and Code Availability

All analyses presented in this paper can be reproduced using msqrob2 version 1.14.1 from Bioconductor release 3.20, available at <https://doi.org/doi:10.18129/B9.bioc.msqrob2>, and the

scripts on our companion GitHub page: https://github.com/statOmics/msqrob2tmt_paper. We also provide a Docker image containing the computational setup used to generate the results: <https://hub.docker.com/repository/docker/cvanderaa/msqrob2tmt>. To assist users in building their own msqrob2TMT workflows and interpreting the output, we have included two vignettes in the Supporting Information. The data from the MSstatsTMT spike-in study, the msTrawler multibatch benchmarking study and the mouse case study are available in the PRIDE repositories under PXD0015258, PXD036799, and PXD005953, respectively. For the reproducibility of results, the data for PXD0015258, PXD036799, and PXD005953 were downloaded from MassIVE (RMSV000000265), Google Drive (https://console.cloud.google.com/storage/browser/mstrawler_paper), and MassIVE (RMSV000000264), respectively, and timestamped by creating a Zenodo repository: <https://zenodo.org/records/14767905>.

6 Funding

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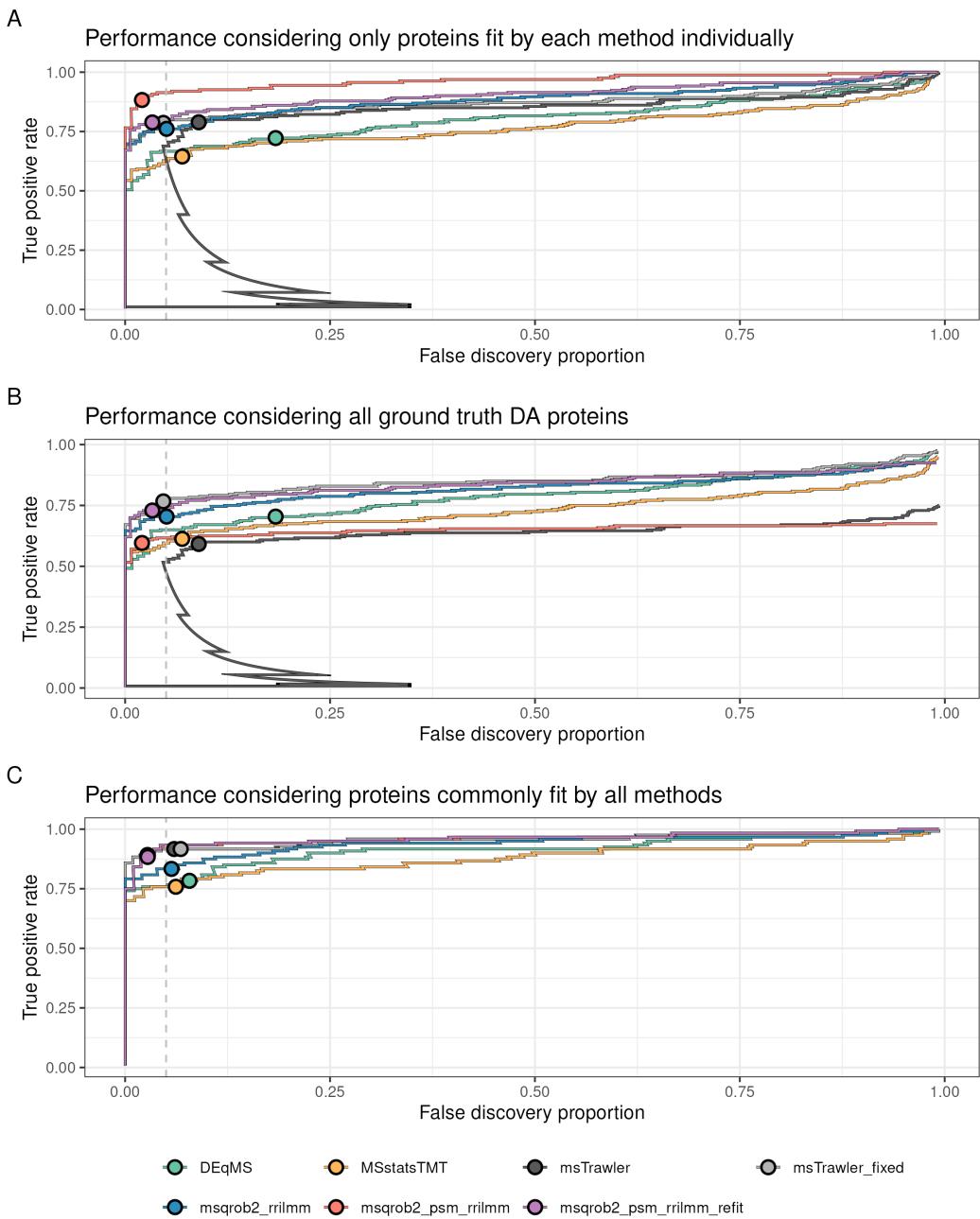
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Malyutina, Simon Anders, and Janne Lehtiö. 2020. “DEqMS: A Method for Accurate Variance Estimation in Differential Protein Expression Analysis.” *Molecular & Cellular Proteomics* 19 (6): 1047–57. <https://doi.org/10.1074/mcp.tir119.001646>.

Supplementary material for msqrob2TMT: robust linear mixed models for inferring differential abundant proteins in labelled experiments with arbitrarily complex design

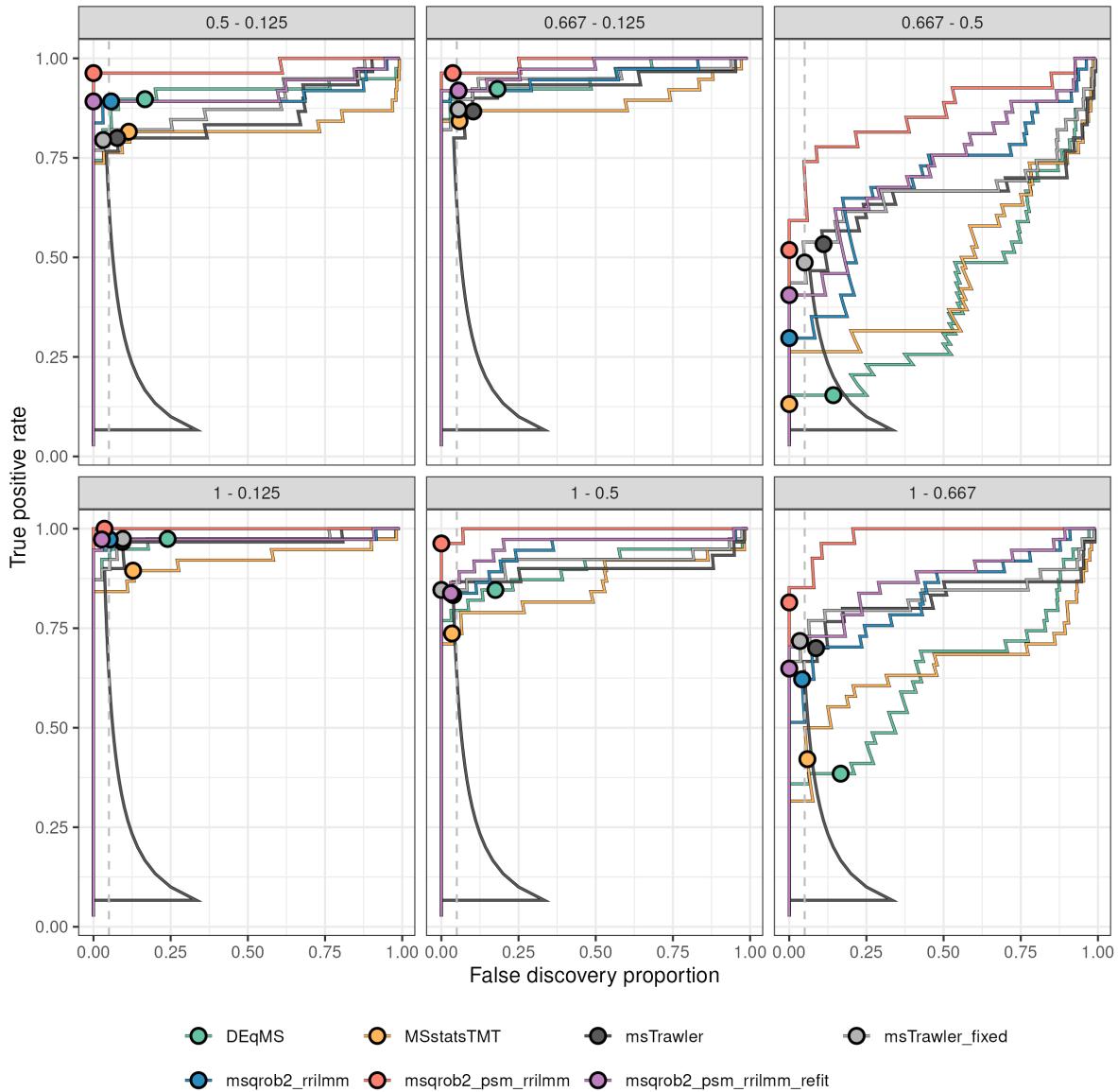
Stijn Vandenbulcke^{†,1,2,3} Christophe Vanderaa^{†,3} Oliver Crook⁴
Lennart Martens^{1,2} Lieven Clement^{3,*}

Spike-In Dataset 1

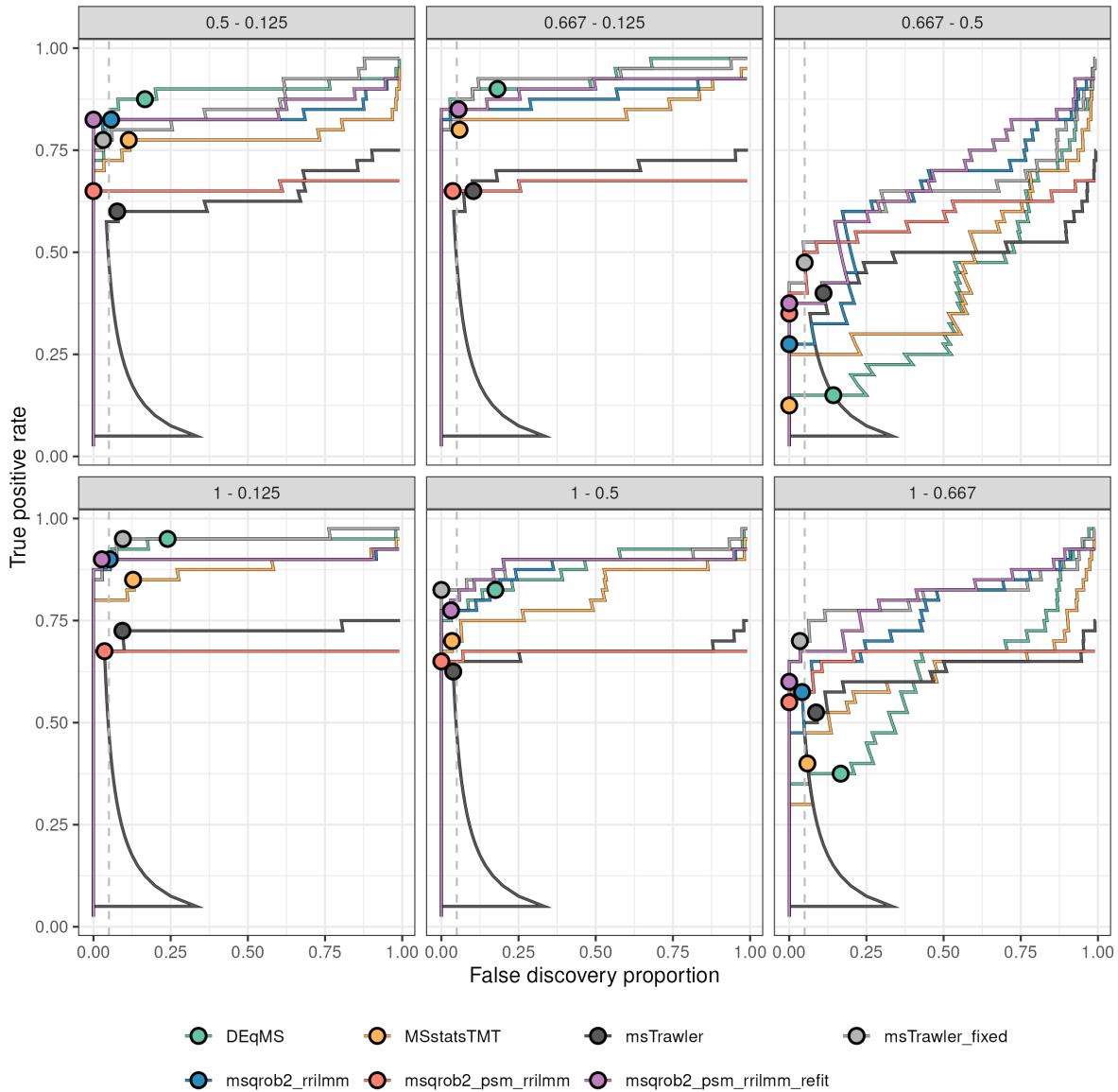


Supplementary Figure 1: True positive rate (TPR) - false discovery proportion (FDP) plots for DEqMS, msqrob2TMT, msTrawler, msTrawler fixed with a refactored import function and MSstatsTMT workflows based on all pairwise spike-in comparisons. Full Caption on the next page.

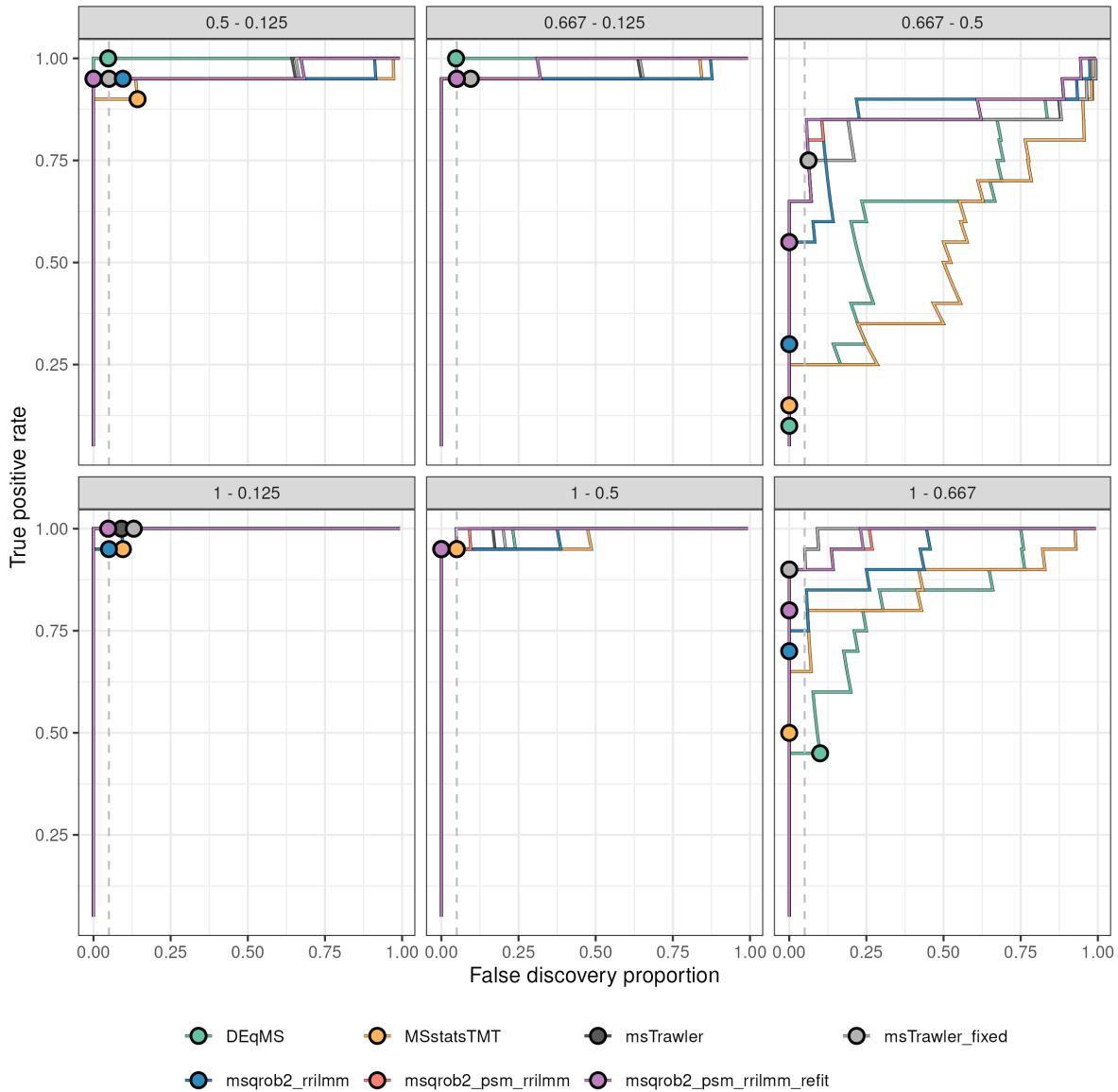
Supplementary Figure 1: True positive rate (TPR) - false discovery proportion (FDP) plots for DEqMS, msqrob2TMT, msTrawler, msTrawler_fixed with a refactored import function and MSstatsTMT workflows based on all pairwise spike-in comparisons. In Panel A the performance is based on the results that are returned by each workflow, in Panel B using all ground truth DA proteins as the maximum number of true positives that can be reported for each comparison (40 spike-in UPS proteins per comparison), and in panel C by only considering the common proteins that were assessed by every workflow. Dots indicate the TPR and FDP obtained at the 5% FDR threshold.



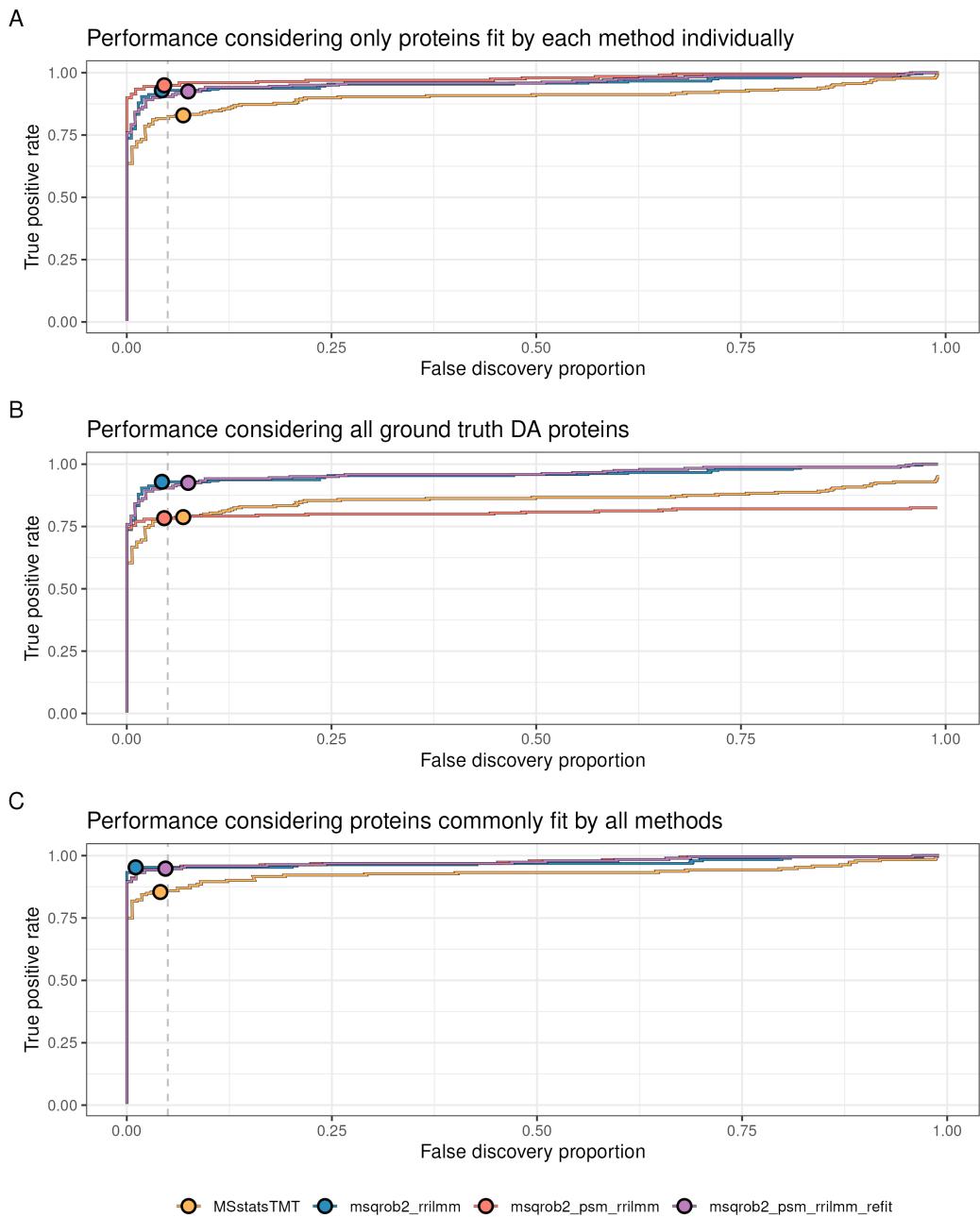
Supplementary Figure 2: True positive rate (TPR) - false discovery proportion (FDP) plots for DEqMS, MSstatsTMT, msTrawler, msTrawler fixed with a refactored import function and msqrob2TMT workflows. The performance is based on the results that are returned by each workflow. Dots indicate the TPR and FDP obtained at the 5% FDR threshold.



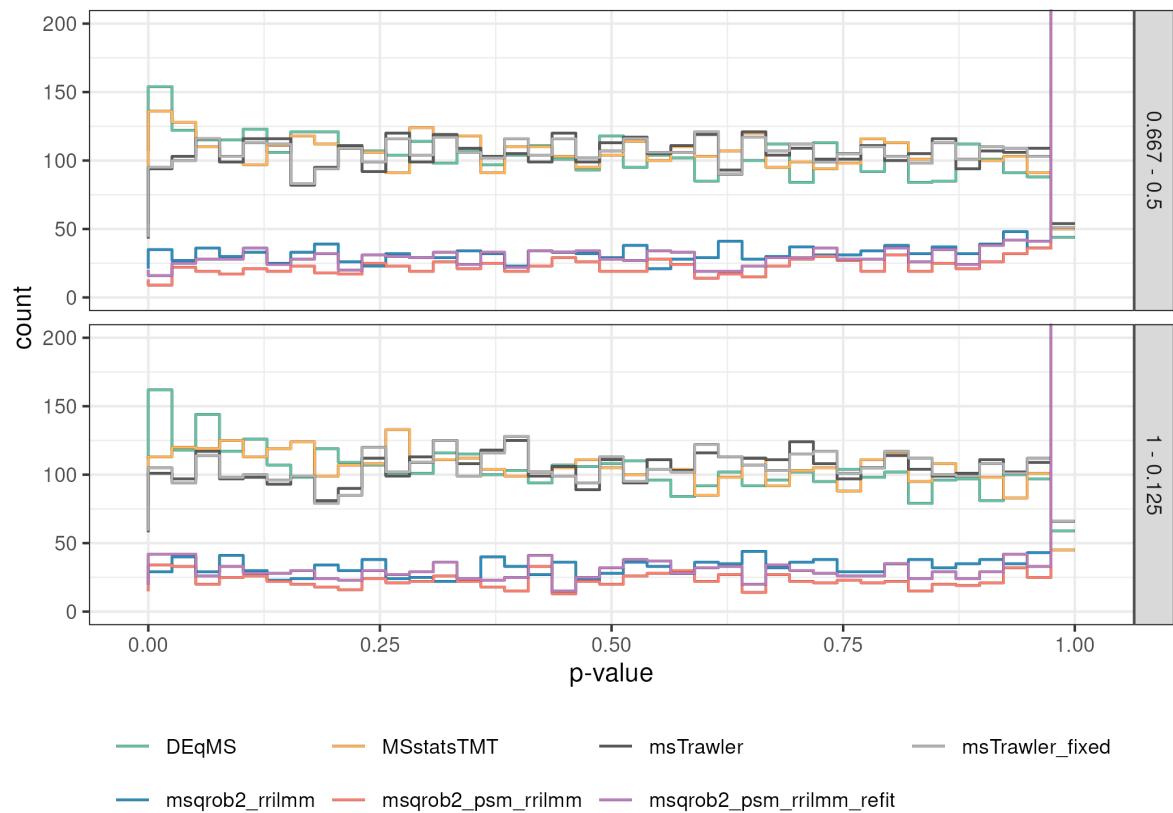
Supplementary Figure 3: True positive rate (TPR) - false discovery proportion (FDP) plots for DEqMS, MSstatsTMT, msTrawler, msTrawler fixed with a refactored import function and msqrob2TMT workflows. The TPR is based on all ground truth DA proteins as the maximum number of true positives that can be reported for each comparison (40 spike-in UPS proteins). Dots indicate the TPR and FDP obtained at the 5% FDR threshold.



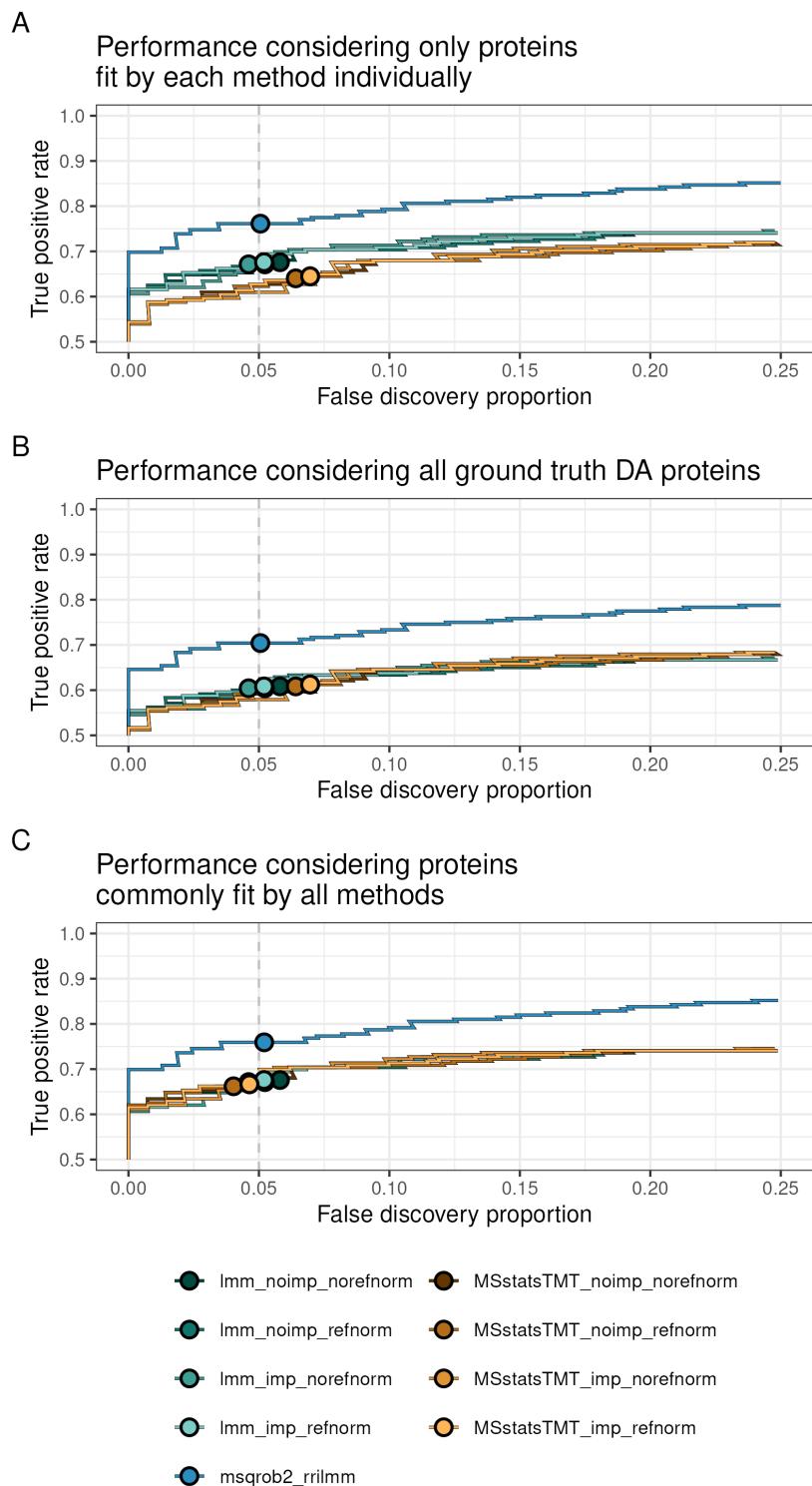
Supplementary Figure 4: True positive rate (TPR) - false discovery proportion (FDP) plots for DEqMS, MSstatsTMT, msTrawler, msTrawler fixed with a refactored import function and msqrob2TMT workflows. The performance is based on the common proteins that were assessed by every workflow. Dots indicate the TPR and FDP obtained at the 5% FDR threshold.



Supplementary Figure 5: True positive rate (TPR) - false discovery proportion (FDP) plots for MSstatsTMT and msqrob2TMT workflows using all technical repeats. The performance is based on all pairwise spike-in comparisons and only considering the results that are returned by each workflow (Panel A), all ground truth DA proteins as the maximum number of true positives that can be reported for each comparison (panel B), and the common proteins that were assessed by every method (panel C). Dots indicate the TPR and FDP obtained at the 5% FDR threshold.



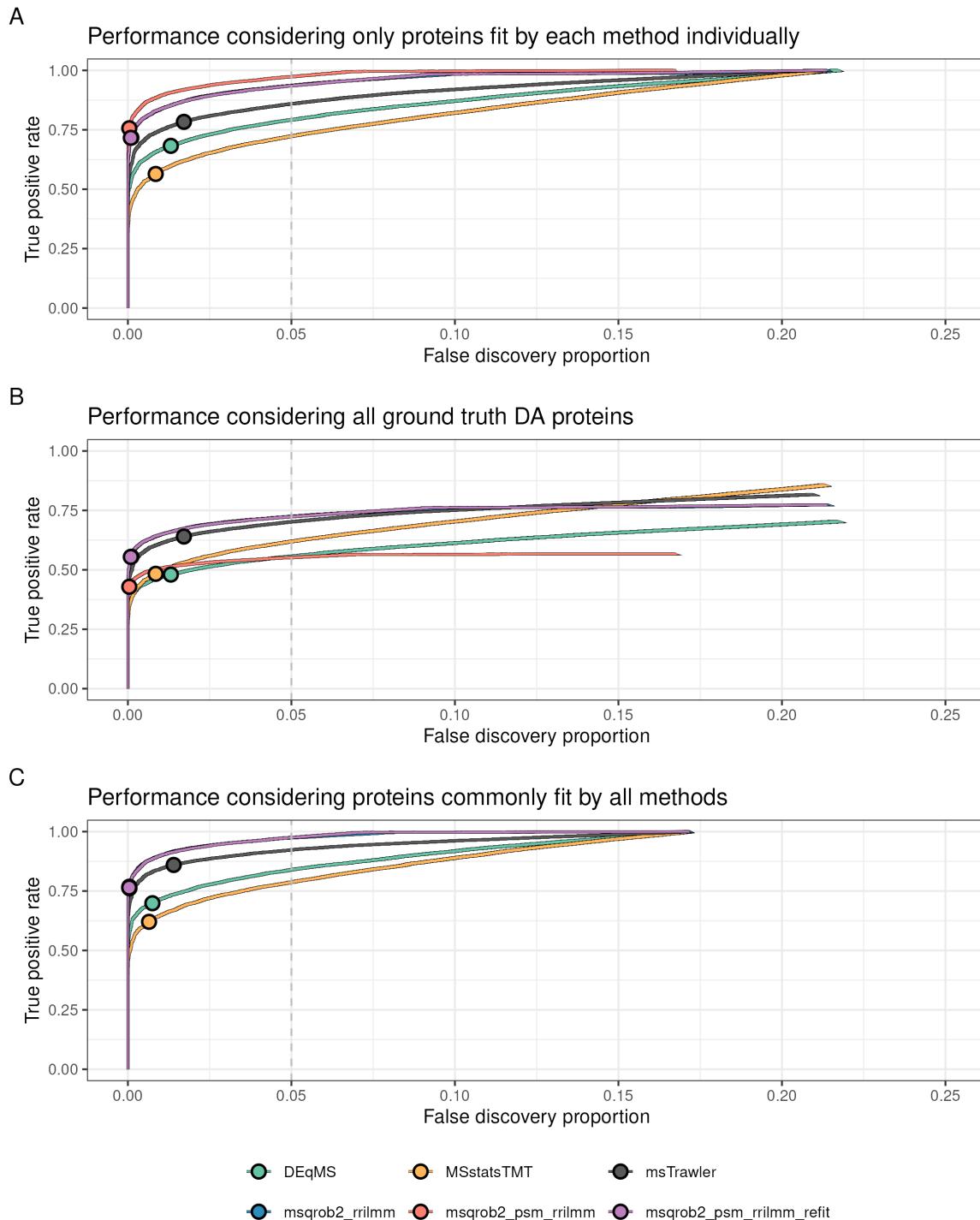
Supplementary Figure 6: Histograms of the p-values from non-spike-in proteins for the DEqMS, msqrob2TMT, MSstatsTMT and msTrawler workflows for two distinct pairwise comparisons between spike-in dilutions.



Supplementary Figure 7: Caption on the next page.

Supplementary Figure 7: True positive rate (TPR) - false discovery proportion (FDP) illustrating the effect of the MSstatsTMT preprocessing on the performance for the msqrob2TMT protein-level models. MSstatsTMT preprocessing was conducted both with and without imputation, employing its accelerated failure time model, and, with and without reference normalisation using bridge channels. These configurations are denoted with the suffixes -noimp (no imputation), -imp (with imputation), -norefnorm (no reference normalisation) and -refnorm (with reference normalisation), respectively. Differential abundance on the preprocessed, summarised and normalised protein abundances was subsequently inferred with MSstatsTMT, msqrob2TMT with a vanilla linear mixed model (lmm) or msqrob2TMT employing a linear mixed model fitted via robust M-estimation and ridge regression (rrilmm). The combined performance over all the spike-in comparisons are shown. In Panel A the performance is based on the results that are returned by each workflow, in Panel B on all ground truth DA proteins per comparison (40 spike-in UPS proteins per comparison) and in Panel C by only considering the common proteins that were assessed by every workflow. Dots indicate the TPR and FDP obtained at the 5% FDR threshold.

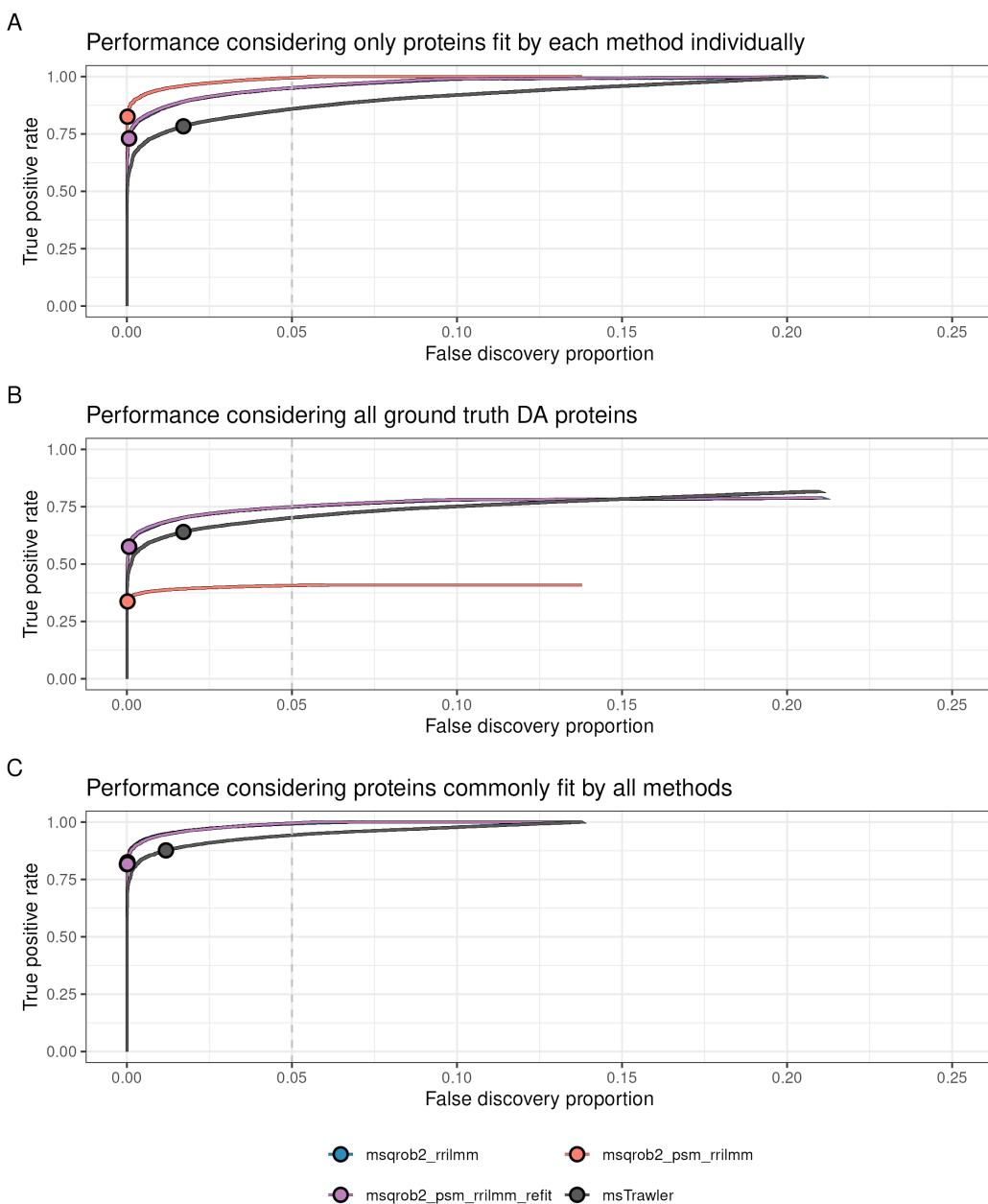
Multibatch Benchmarking Experiment



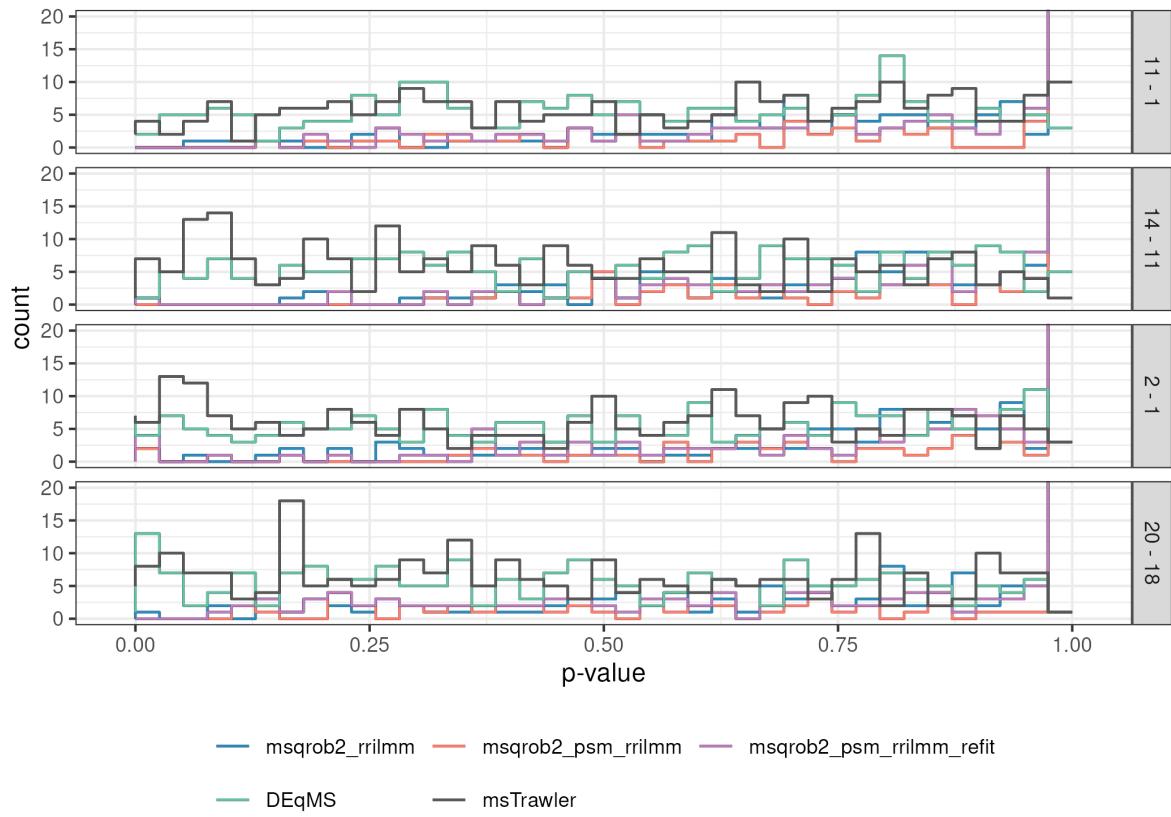
Supplementary Figure 8: Caption on the next page.

Supplementary Figure 8: True positive rate (TPR) - false discovery proportion (FDP) plots for DEqMS, MSstatsTMT, msTrawler and msqrob2TMT workflows. The combined performance over all the comparisons are shown. In Panel A the performance is based on the results that are returned by each workflow, in Panel B on all ground truth DA proteins as the maximum number of true positives that can be reported for each comparison, and in panel C by only considering the common proteins that were assessed by every workflow. Dots indicate the TPR and FDP obtained at the 5% FDR threshold.

Comparing performance after msTrawler preprocessing

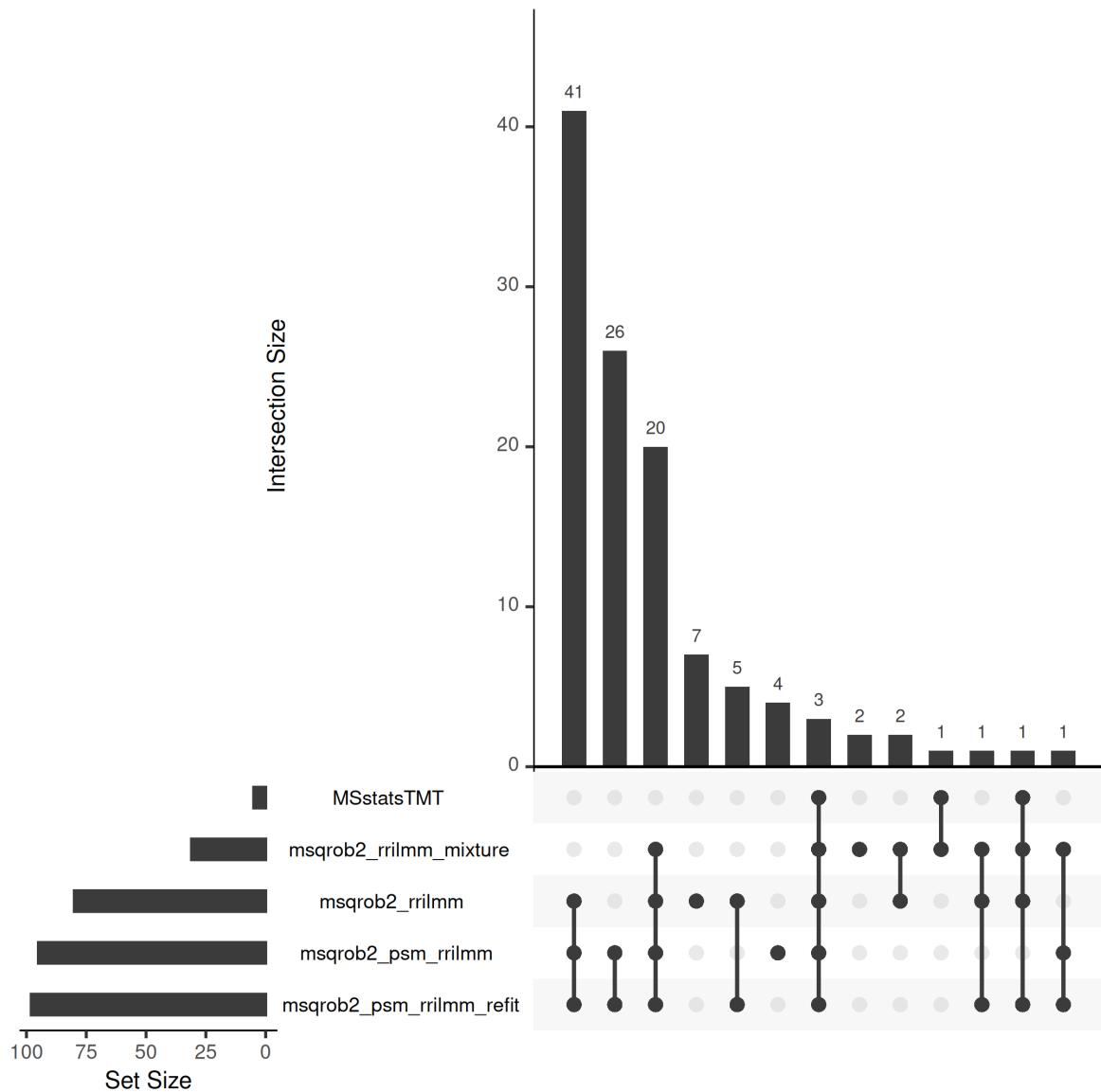


Supplementary Figure 9: True positive rate (TPR) - false discovery proportion (FDP) plots for DEqMS, MSstatsTMT, msTrawler and msqrob2TMT workflows upon full msTrawler preprocessing. The combined performance over all the comparisons are shown. In Panel A the performance is based on the results that are returned by each workflow, in Panel B on all ground truth DA proteins as the maximum number of true positives that can be reported for each comparison, and in panel C by only considering the common proteins that were assessed by every workflow. Dots indicate the TPR and FDP obtained at the 5% FDR threshold.

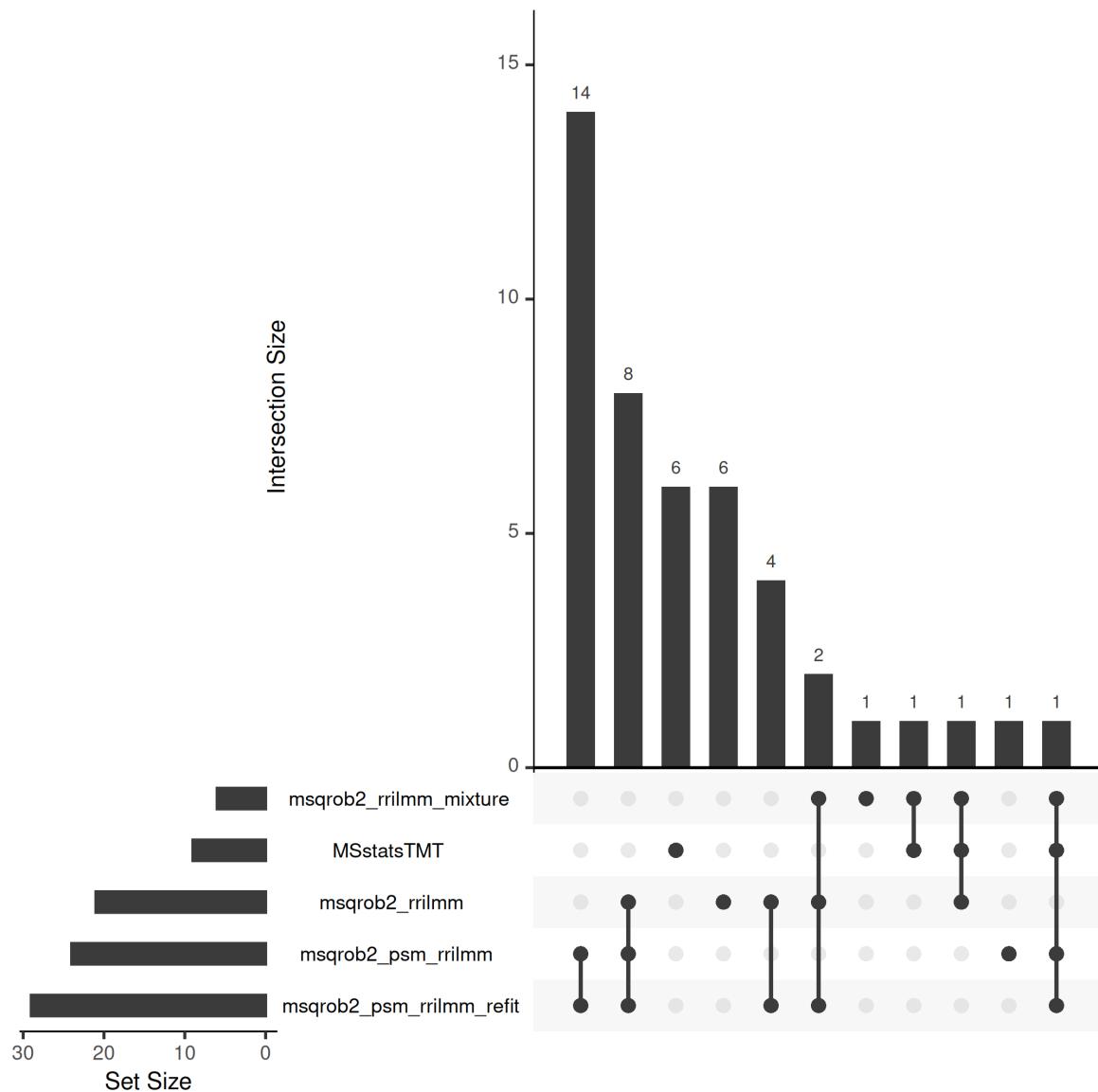


Supplementary Figure 10: Histograms of the p-values from non-spiked-in proteins for the DEqMS, msqrob2TMT, and msTrawler workflows for four distinct pairwise comparisons between spike-in dilutions.

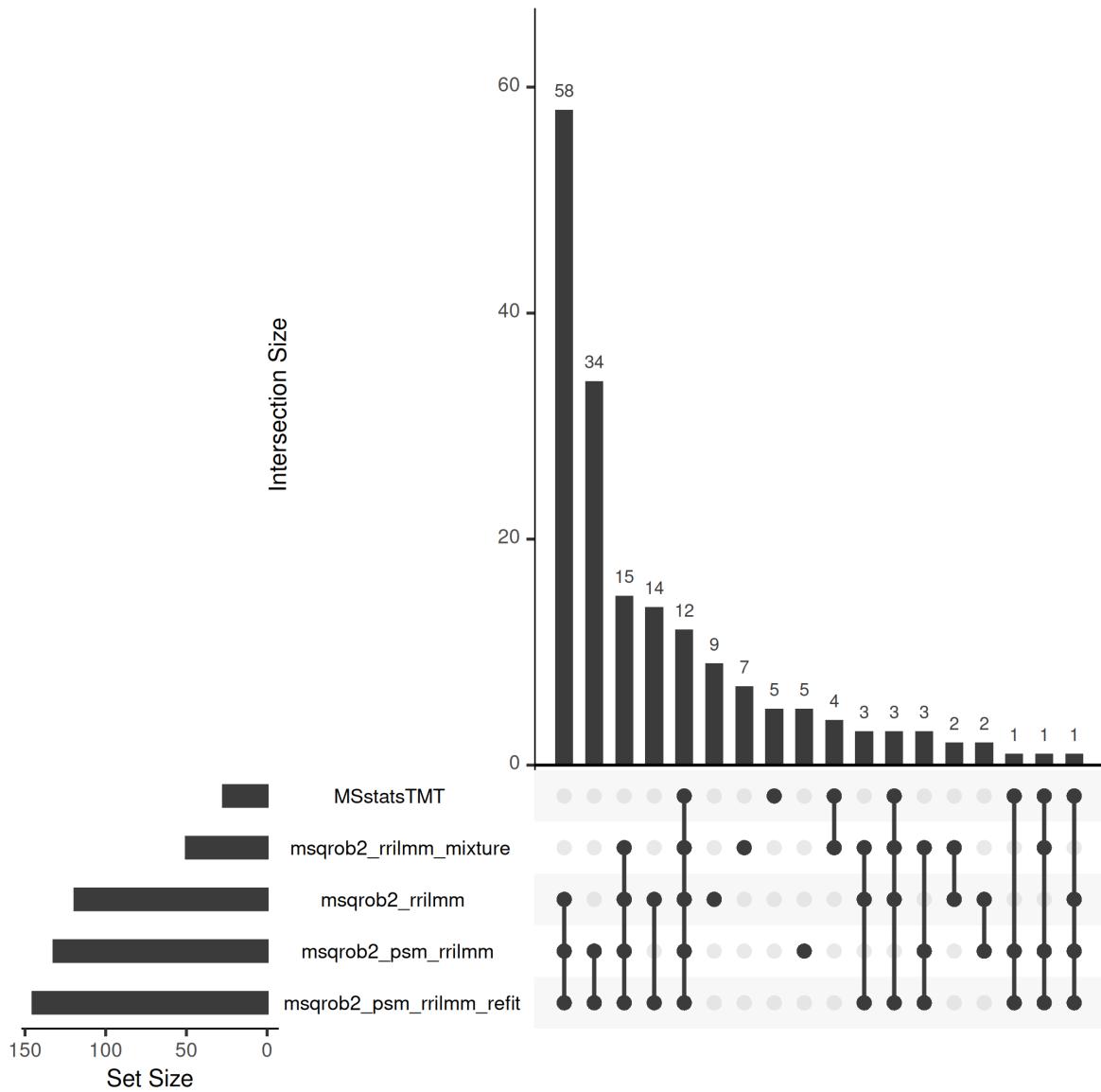
Mouse Study



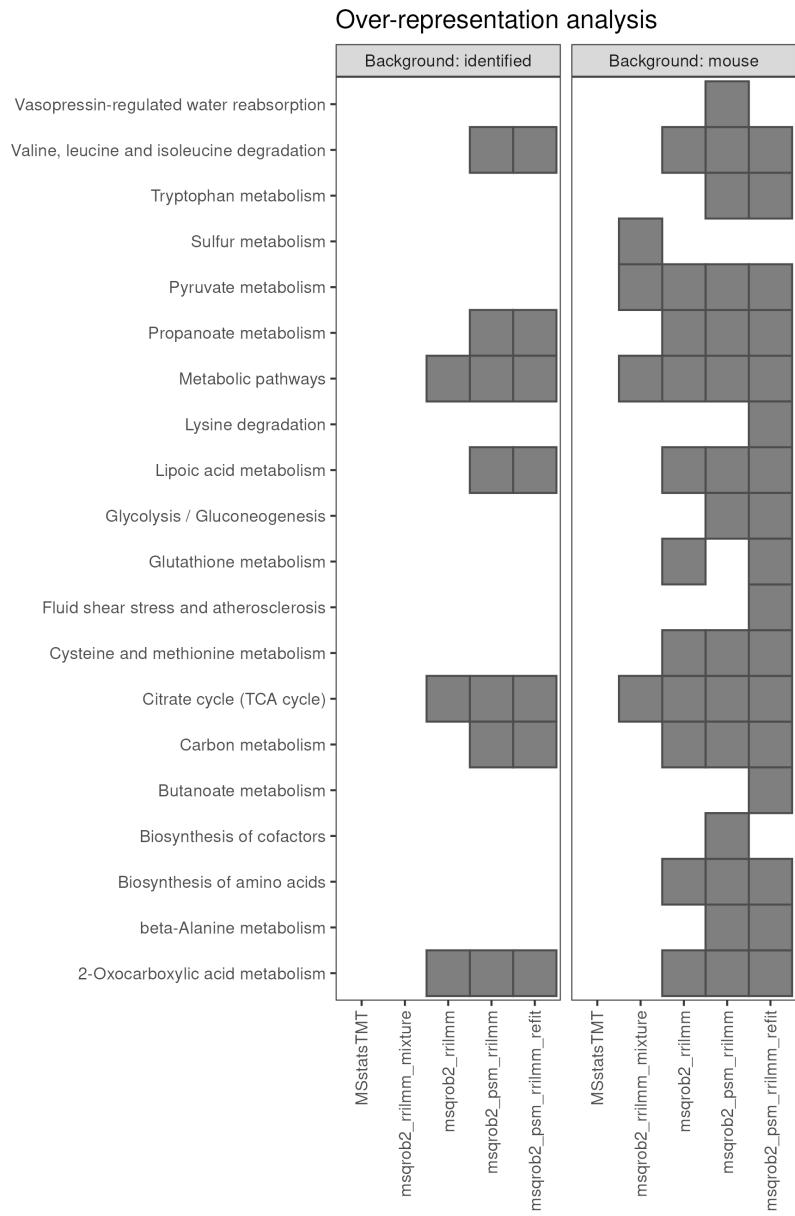
Supplementary Figure 11: Upset plot showing the overlap in significant proteins between the MSstatsTMT and the msqrob2TMT workflows for the early diet effect.



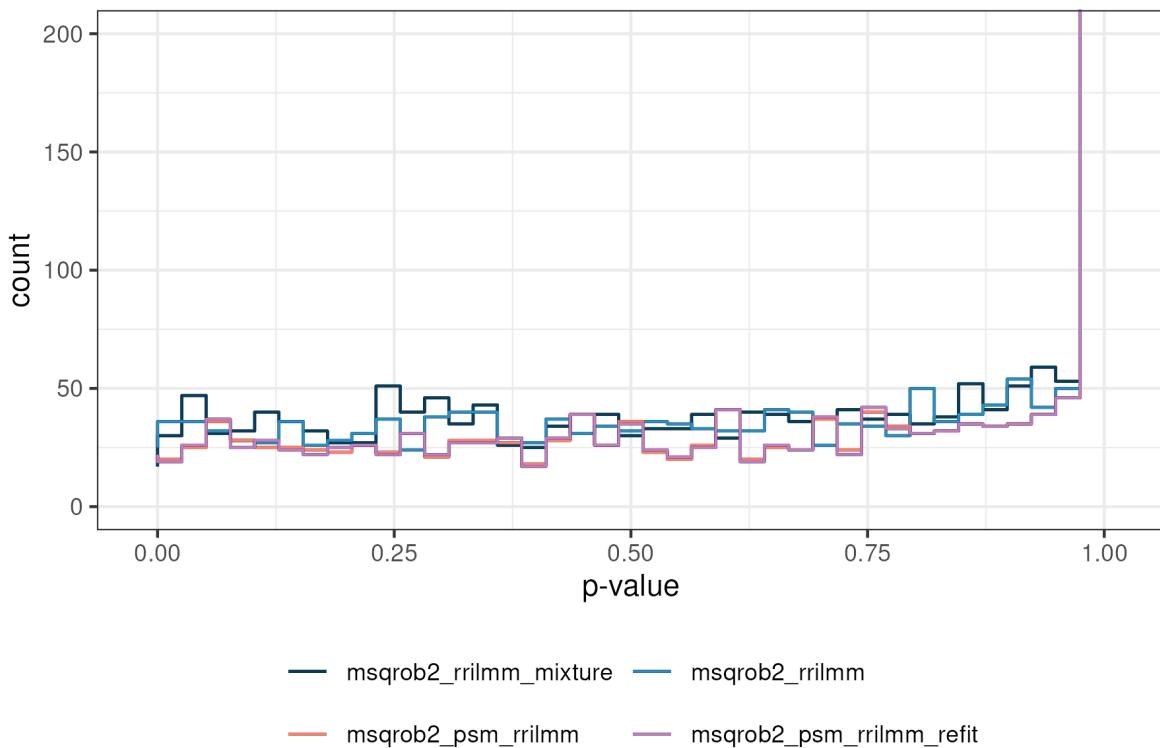
Supplementary Figure 12: Upset plot showing the overlap in significant proteins between the MSstatsTMT and the msqrob2TMT workflows for the late diet effect.



Supplementary Figure 13: Upset plot showing the overlap in significant proteins between the MSstatsTMT and the msqrob2TMT workflows for the average diet effect.



Supplementary Figure 14: Over-representation analysis on the set of proteins identified as significant at a 5% FDR threshold by each method. Annotated protein sets were retrieved from KEGG. The significant proteins were tested for over-representation against either the set of identified proteins in the data set (left) or against the complete mouse proteome. Grey boxes indicate that a KEGG protein set (rows) were identified as over-represented by significant proteins identified by a method (column). The proteins identified by MSstatsTMT did not lead to significant KEGG pathway enrichment, hence the corresponding empty columns.



Supplementary Figure 15: Histogram of the p-values from the mock analysis on the mouse dataset. Only results for our PSM-level and protein-level msqrob2TMT workflows are shown, as the state-of-the-art tools could not fit the appropriate models to the data of the mouse study after including an additional mock treatment.”