MSstatsPTM statistical relative quantification of post-translational modifications in global proteomics experiments

Supplementary Information

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1 Details of the proposed approach

		Model	Estimated Log-fold change	Theoretical variance	Estimated variance	Degrees of freedom
Label-free (y_{ij} is $\log_2$ intensity in Condition i and BioReplicate j)	**Group comparison**	$y_{ij} = \mu_i + \varepsilon_{ij}$ $\sum_{i=1}^{I} \mu_i = 0$ $\varepsilon_{ij} \sim iid\ N(0, \sigma^2)$	$\bar{Y}_{i.} - \bar{Y}_{i'.}$	$\frac{2\sigma^2}{I}$	$\frac{2J\sum_{i=1}^{I}(y_{ij} - \bar{y}_{i.})^2}{J(IJ-I)}$	$IJ - I$
	Time course	$y_{ij} = \mu_i + BioReplicate_j + \varepsilon_{ij}$ $\sum_{i=1}^{I} \mu_i = 0$ $BioReplicate_j \sim iid\ N(0, \sigma_J^2)$ $\varepsilon_{ij} \sim iid\ N(0, \sigma^2)$	$\bar{Y}_{i.} - \bar{Y}_{i'.}$	$\frac{2\sigma^2}{I}$	$\frac{2\sum_{i=1}^{I}\sum_{i=1}^{J}(y_{ij} - \bar{y}_{i.} - \bar{y}_{j.} + \bar{y}_{..})^2}{J(I-1)(J-1)}$	$(I-1)(J-1)$
TMT (y_{mij} is $\log_2$ intensity in Condition i and BioReplicate j from Mixture m)	**Group comparison**	$y_{mij} = \mu_i + Mixture_m + \varepsilon_{mij}$ $\sum_{i=1}^{I} \mu_i = 0$ $Mixture_m \sim iid\ N(0, \sigma_M^2)$ $\varepsilon_{mij} \sim iid\ N(0, \sigma^2)$	$\bar{Y}_{.i.} - \bar{Y}_{.i'.}$	$\frac{2\sigma^2}{MJ}$	$\frac{2J\sum_{i=1}^{I}\sum_{m=1}^{M}(y_{mij} - \bar{y}_{m..} - \bar{y}_{.i.} + \bar{y}_{...})^2}{MJ(MIJ - I - M + 1)}$	$MIJ - I - M + 1$
	Time course	$y_{mij} = \mu_i + BioReplicate_{jm} + \varepsilon_{mij}$ $\sum_{i=1}^{I} \mu_i = 0$ $BioReplicate_{jm} \sim iid\ N(0, \sigma_J^2)$ $\varepsilon_{mij} \sim iid\ N(0, \sigma^2)$	$\bar{Y}_{.i.} - \bar{Y}_{.i'.}$	$\frac{2\sigma^2}{MJ}$	$\frac{2J\sum_{j=1}^{I}\sum_{m=1}^{M}(y_{mij} - \bar{y}_{mj.} - \bar{y}_{.i.} + \bar{y}_{...})^2}{MJ(I-1)(MJ-1)}$	$(I-1)(MJ-1)$

Figure S1: Different models that are fit depending on the experimental design (group comparison and time course) and quantification workflow (label-free versus TMT). The table shows the true values of the standard errors, along with their estimates and the associated degrees of freedom. The same formulas holds when comparing changes in PTM, or hcnges in the unmodified portion of the protein. When combining the two comparisons for an adjustment, the variance must be multiplied by 2.

2 Details on the generation of simulated datasets

2.1 Dataset 1 : Computer simulation 1 - Label-free

In the first simulation an experiment with many features per PTM and unmodified protein was created. Additionally this simulation contained no missing data.

- Mean of log-intensity: 25
- Standard deviations of log-intensities for modified and unmodified peptides: 0.2, 0.3
- Difference in PTM abundance between conditions: 0, 1., 2., 3.
- Difference in protein abundance between conditions: 0, 1., 2., 3.
- Number of replicates: 2, 3, 5, 10
- Number of conditions: 2, 3, 4
- Number of realizations: 1000
- Number of features per PTM: 10
- Number of features per unmodified protein: 10
- Missing data: no missing value

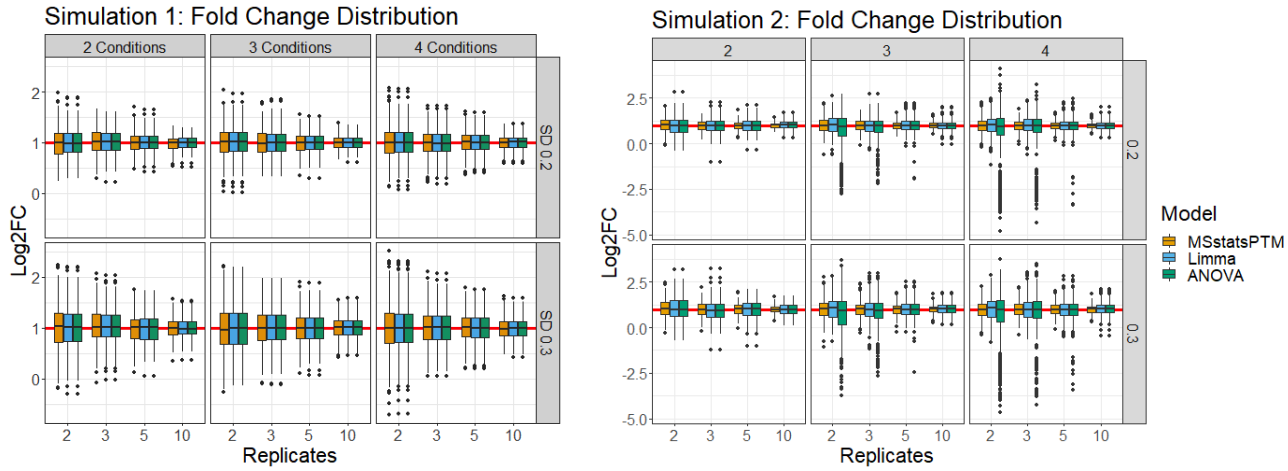
2.2 Dataset 2 : Computer simulation 2 - Label-free missing values and low features

In the second simulation we introduced limited feature observations per PTM as well as masking a portion of the observation to simulate missing values.

- Mean of log-intensity: 25
- Standard deviations of log-intensities for modified and unmodified peptides: 0.2, 0.3
- Difference in PTM abundance between conditions: 0, 1., 2., 3.
- Difference in protein abundance between conditions: 0, 1., 2., 3.
- Number of replicates: 2, 3, 5, 10
- Number of conditions: 2, 3, 4
- Number of realizations: 1000
- Number of features per PTM: 2
- Number of features per unmodified protein: 10
- Missing data: 20% of the observations for PTMs and Proteins were masked with NA at random

3 Additional evaluation results

3.1 Simulated Datasets 1 and 2



(a) (b)

Figure S2: [TODO: In (b) could you indicate in panel labels that we are still talking about conditions and SD?]Simulated Datasets 1 and 2 : fold change distributions. (a) In Simulated Dataset 1 all considered methods correctly estimated the fold change between conditions, with a median fold change estimation of 1. The distributions around the median were also consistent across all methods. (b) In Simulated Dataset 2 all methods correctly estimated the fold change with a median log change of 1. *MSstatsPTM* in this simulation had a tighter distribution around the median. Both *Limma* and *ANOVA* showed a wider range around the fold change. [TODO: In is not clear from the text whether Limma and ANOVA were used with or without adjustments for unmodified proteins. Could you clarify?]

3.2 Dataset 3 : SpikeIn benchmark - Ubiquitination - Label-free

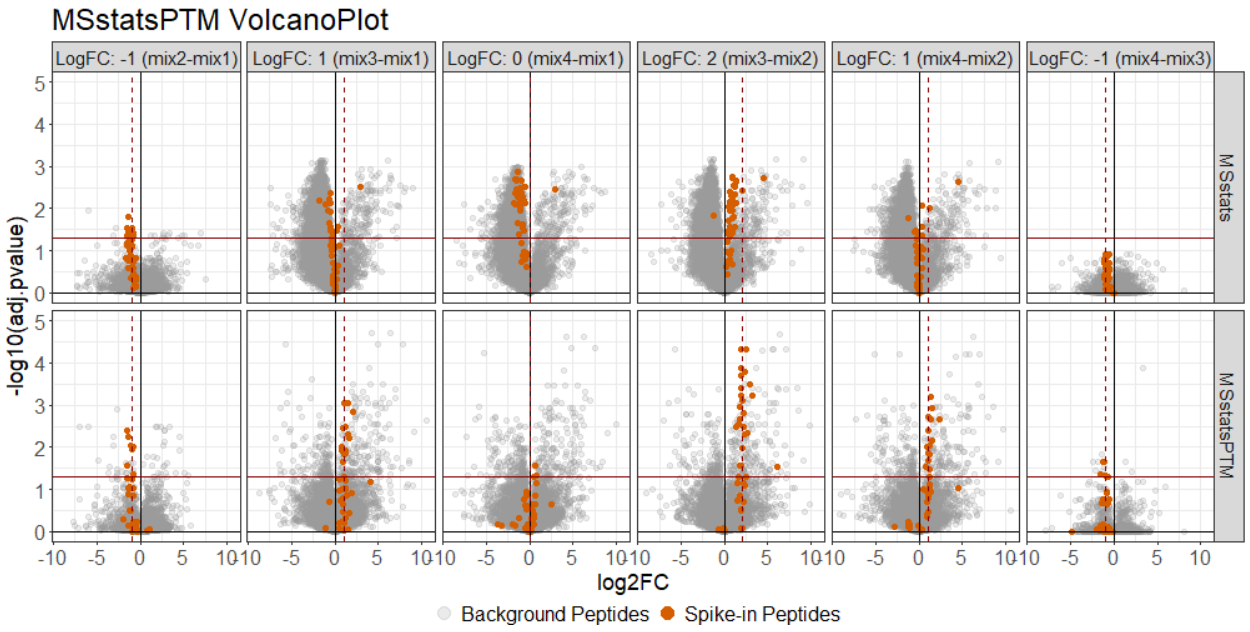


Figure S3: [TODO: Clarify that MSstats is the basic version before the adjustment, and MSstatsPTM after the adjustment] [TODO: Start the caption with the name of the dataset] The modeling results of the *MSstatsPTM* both before and after adjustment. The spike-in peptides are colored red and the background peptides are colored grey. All grey peptides are expected to not be detected as differentially abundant. The spike-in peptides (colored red) did not follow the expected log fold change before adjustment. After adjusting for changes in overall protein abundance the spike-in peptides were more in line with expectation. Additionally the background grey colored peptides showed many false positives before adjustment. After adjustment these false positives were decreased considerably.

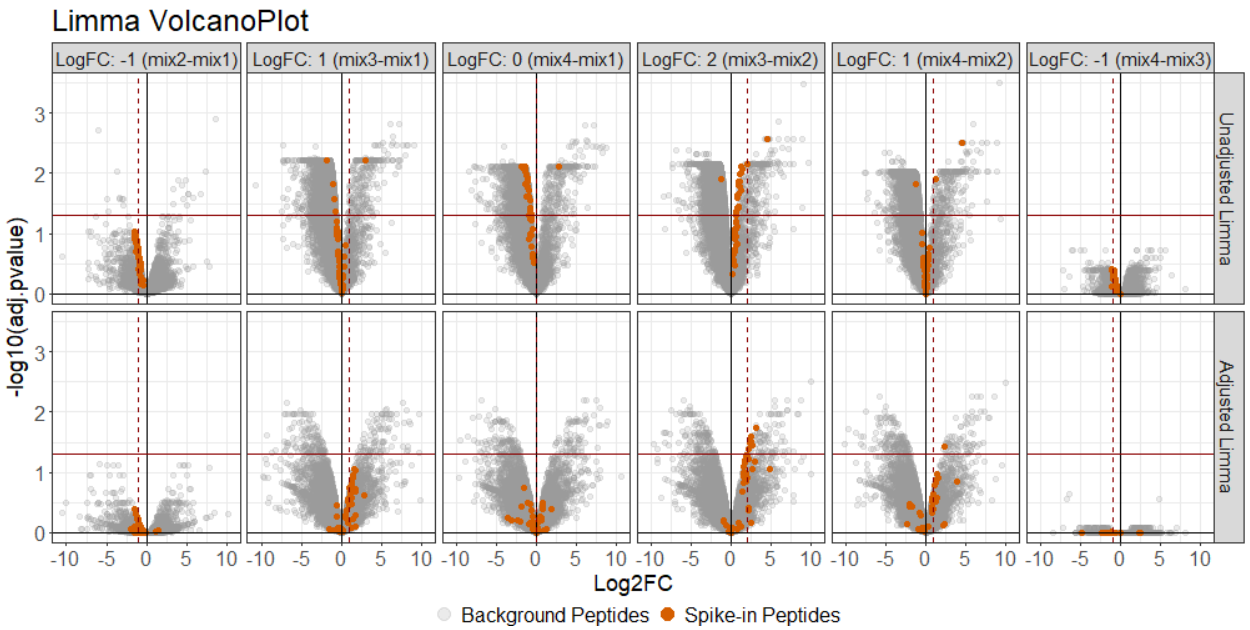


Figure S4: [TODO: Start the caption with the name of the dataset] When modeling the experiment with the *Limma* method, the spike-in peptides again follow the expected log fold change better after adjusting for changes in protein level. However, while the fold change was more accurate, the majority of spike-in peptides were not detected as differentially abundant. There were more false positive differentially abundant PTM before than after adjustment.

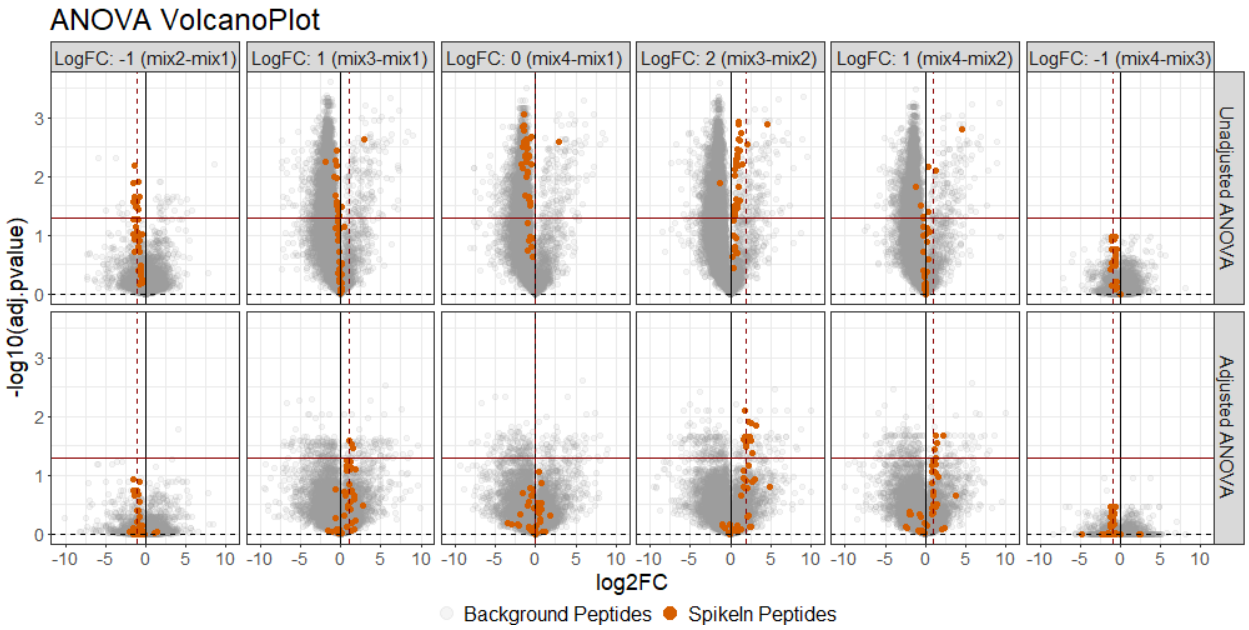


Figure S5: [TODO: Start the caption with the name of the dataset] Using *ANOVA* the fold change of the spike-in peptides was much closer to expectation after adjusting for global protein abundance. The log FC estimation was the same as *Limma*, however the p-values were different. In this particular case we detect a few more true positives using *ANOVA* compared to *Limma*.

3.3 Dataset 4 : Human - Ubiquitination - 1mix-TMT

The experiment had a simple group comparison design, shown in Table S1.

Condition	BioReplicate	Channel
Dox1hr	Dox1hr_1	127C
Dox2hr	Dox2hr_1	128N
Dox2hr	Dox2hr_2	130C
Dox4hr	Dox4hr_1	128C
Dox4hr	Dox4hr_2	131C
Dox6hr	Dox6hr_1	129N
Dox6hr	Dox6hr_2	131N
NoDox0hr	NoDox0hr_1	126C
NoDox0hr	NoDox0hr_2	129C
NoDox6hr	NoDox6hr_1	127N
NoDox6hr	NoDox6hr_2	130N

Table S1: The experimental design of Dataset 4

The following model was fit separately for ubiquitinated peptides and for unmodified protein

$$Y_{mij} = \mu_i + \epsilon_{mij},\ \sum_{i=1}^{I} \mu_i = 0,\ \epsilon_{mij}\ \sim N(0, \sigma^2)$$

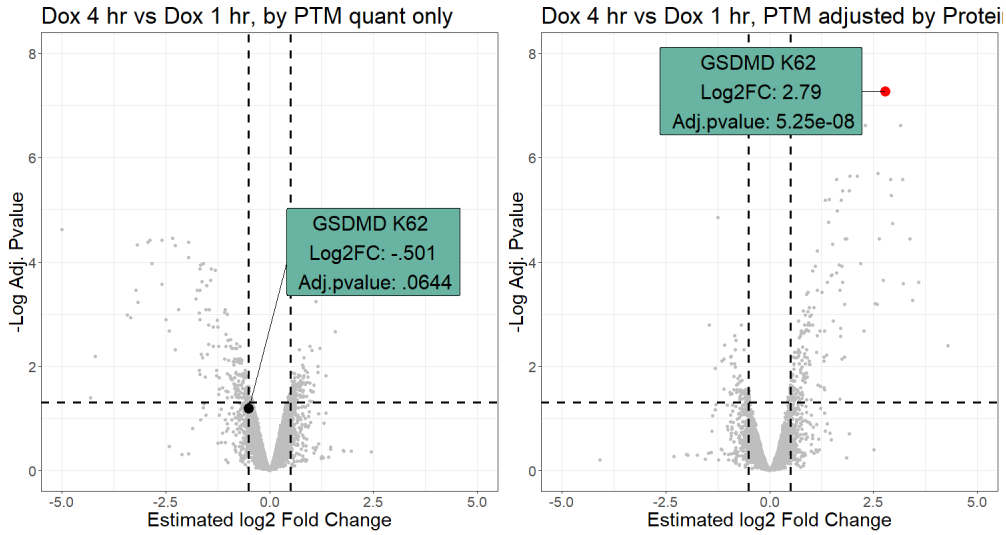


Figure S6: [TODO: Could you separate the panels, and add labels (a) and (b) in the subfigures. (Could you use tabular as I did everywhere?) The title of the second panel is cut off. It is not clear which method is used - is it MSstats and MSstatsPTM?] [TODO: Start the caption with the name of the dataset] Volcano plots of Dox4hr vs Dox1hr both before and after protein adjustment, [TODO: with *MSstatsPTM*]. The $GSDMD\_HUMAN|P57764\_K62$ modification is highlighted. (a) Before adjustment the modification had a small fold change and was not detected as differentially abundant. (b) After adjustment the fold change was much larger, and the modification was detected as differentially abundant. In this case [TODO: *MSstatsPTM*?] allowed us to identify a differential modified peptide that could have otherwise been missed.

3.4 Dataset 5 : Mouse - Phosphorylation - 2mix-TMT

The experiment had a group comparison design, and the data were acquired in two mixtures, as shown in Table S2.

	Mixture 1		Mixture 2		Condition
Uninfected	128C		128C	131C	
Early (1 Hour)	126C	129C	126C	129C	WT
Late (3 Hour)	127C	130C	127C	130C	
Uninfected	129N	131C	129N		
Early (1 Hour)	127N	130N	127N	130N	KO
Late (3 Hour)	128N	131N	128N	131N	

Table S2: The experimental design of Dataset 5

The following model was fit separately for phosphorylated peptides and for unmodified protein

$$Y_{mij} = \mu_i + Mixture_m + \epsilon_{mij},\ Mixture_m \sim N(0, \sigma^2_M),\ \sum_{i=1}^{I} \mu_i = 0,\ \epsilon_{mij} \sim N(0, \sigma^2)$$

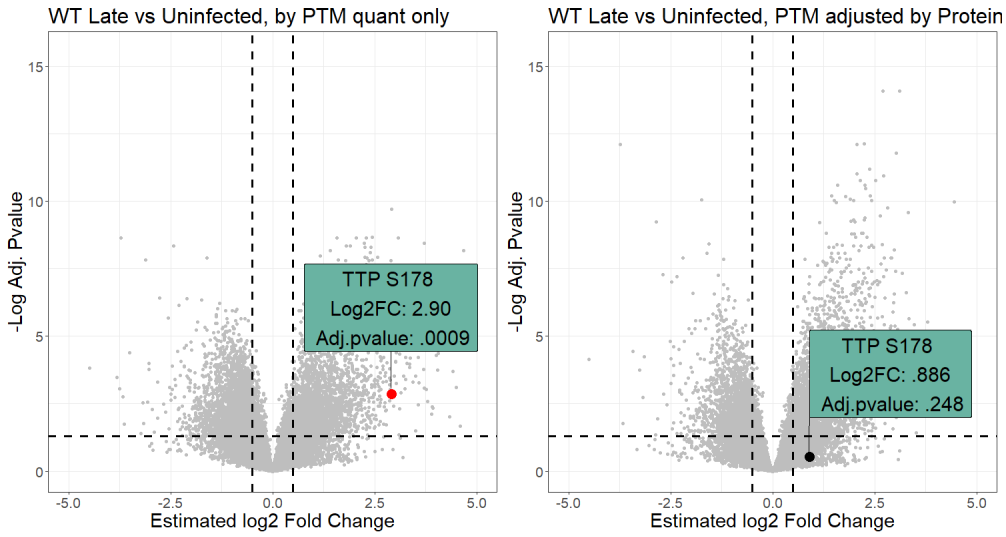
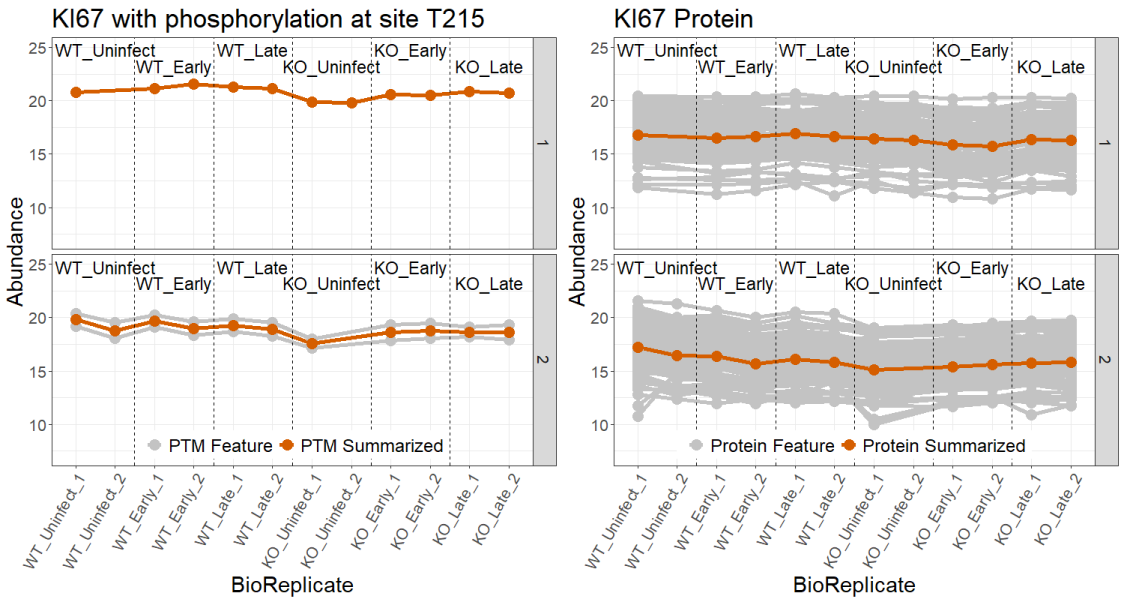
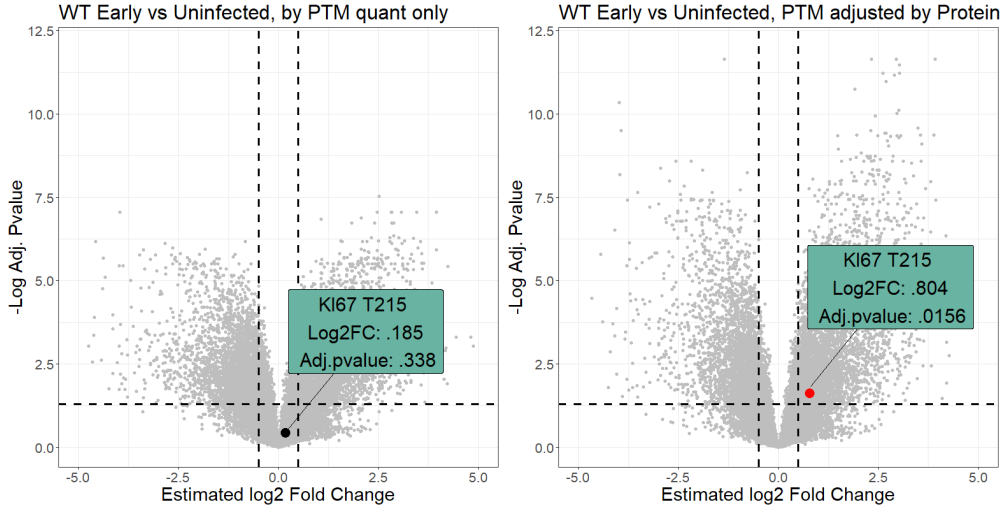


Figure S7: [TODO: Start the caption with the name of the dataset] [TODO: Separate the labels and add labels (a) and (b) for the subpanels. (Could you use tabular as I did everywhere?)]Volcano plots of WT_Late vs WT_Uninfect both before and after protein adjustment [TODO: with *MSstatsPTM*]. The $TTP\_MOUSE|P22893\_S178$ modification is highlighted. (a) Before adjustment the modification had a large fold change and a small p-value. (b) After adjustment the fold change was much smaller and the modification was not detected as differentially abundant.



(a)



(b)

Figure S8: [TODO: Start the caption with the name of the dataset] Protein $KI67\_MOUSE|E9PVX6$ with the modification at site $T215$. (a) The modification and global protein appeared to show small or no difference between conditions when considered separately. However after adjusting for change in global protein abundance, the modification was statistically significant. Additionally, this profile plot showed the large difference in available features between modified peptides and global proteins. (b) The volcano plot of the WT_Uninfect and WT_Early comparison showed the specifics of the adjustment [TODO: with $MSstatsPTM$]. The profile of the modified peptides appeared to be flat, with a log fold change of .185, while the global profiling showed a small negative fold change of $-.619$. Since both exhibit small changes in opposite directions, their combination produced a $\log_2$-fold change of .804 and adjusted p-value of .0156.

3.5 Dataset 6 : Human - Ubiquitination - Label-free no global profiling run

An example profile plot for this experiment can be seen in Figure S9.

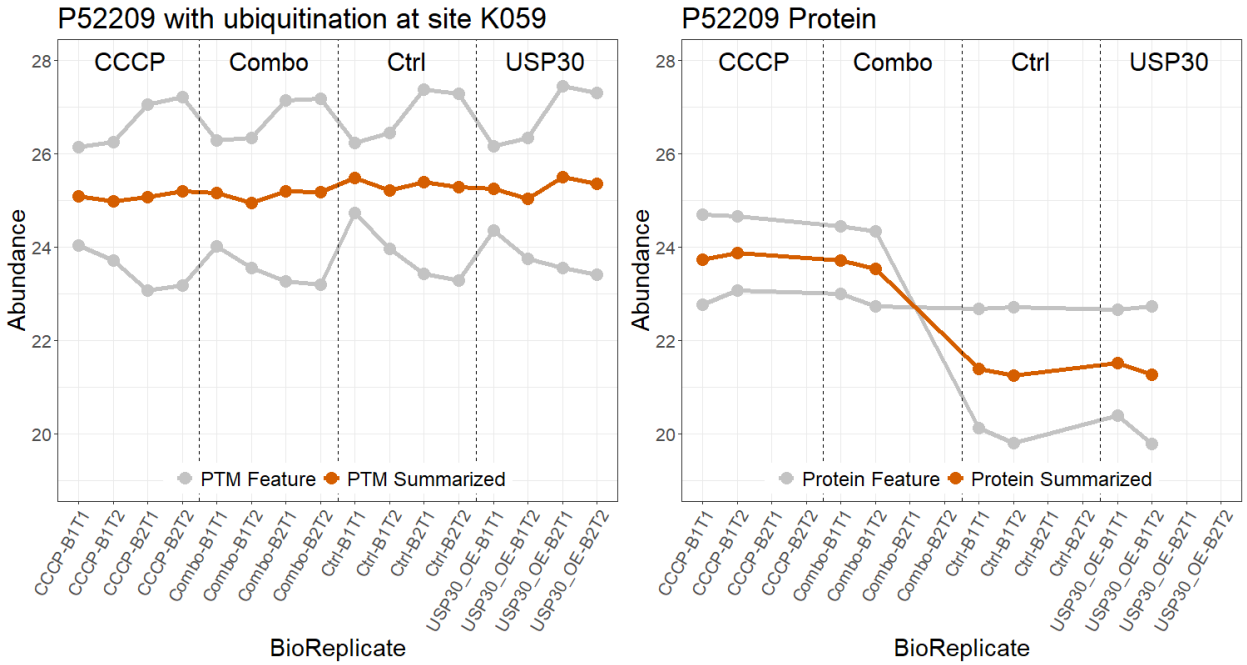


Figure S9: [TODO: Start the caption with the name of the dataset] Protein $P52209$ with the modification of the protein at site $K059$. The modification appeared generally unchanged between all conditions, whereas the global profiling run showed that the CCCP and Combo conditions had a higher relative abundance compared to the Control and USP30_OE. This indicated that the modification had in fact an effect when comparing CCCP and Combo to Control and USP30_OE. However it was not entirely clear as one unmodified peptide feature appeared to be changed, while the other did not. This uncertainty was another result of not acquiring data from a separate global profiling run. A separate global profiling run would have likely resulted in more and better quality unmodified features for that protein.