
Supporting Information:

Mouse primary T cell phosphotyrosine proteomics

enabled by BOOST

Xien Yu Chua¹, Kenneth P. Callahan², Alijah A. Griffith², Tobias Hildebrandt²,
Guoping Fu³, Mengzhou Hu¹, Renren Wen³, Arthur R. Salomon^{2,*}

1 Department of Molecular Pharmacology, Physiology & Biotechnology, Brown University, Providence, RI, 02912

2 Department of Molecular Biology, Cell Biology & Biochemistry, Brown University, Providence, RI, 02912

3 Blood Research Institute, Blood Center of Wisconsin, Milwaukee, WI, 53226
** Corresponding Author**

E-mail: art@drsalomon.com

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Supporting Table 1: All unique peptides observed exclusively in the BOOST experiment with ΦSDM disabled and reporter ions quantified in at least one experimental channel. Included are MaxQuant outputs such as the gene name(s), protein name(s), modified sequence, modified sequence with phosphorylation site localization probabilities, sequence windows, and corrected TMT reporter ion intensities, as well as calculations used in the manuscript (mean intensity values, standard deviations, CV percentages, *p*-values, *q*-values, BOOST factors) and WikiPathway Annotations for each unique peptide.

Supporting Table 2: All unique peptides observed in both the BOOST experiment and the 1.0 mg Control experiment with ΦSDM disabled and reporter ions quantified in at least one experimental channel. Included are MaxQuant outputs such as the gene name(s), protein name(s), modified sequence, modified sequence with phosphorylation site localization probabilities, sequence windows, and corrected TMT reporter ion intensities, as well as calculations used in the manuscript (mean intensity values, standard deviations, CV percentages, *p*-values, *q*-values, BOOST factors) and WikiPathway Annotations for each unique peptide.

Supporting Table 3: All unique peptides observed exclusively in the 1.0 mg Control experiment with ΦSDM disabled and reporter ions quantified in at least one experimental channel. Included are MaxQuant outputs such as the gene name(s), protein name(s), modified sequence, modified sequence with phosphorylation site localization probabilities, sequence windows, and corrected TMT reporter ion intensities, as well as calculations used in the manuscript (mean intensity values, standard deviations, CV percentages, *p*-values, *q*-values) and WikiPathway Annotations for each unique peptide.

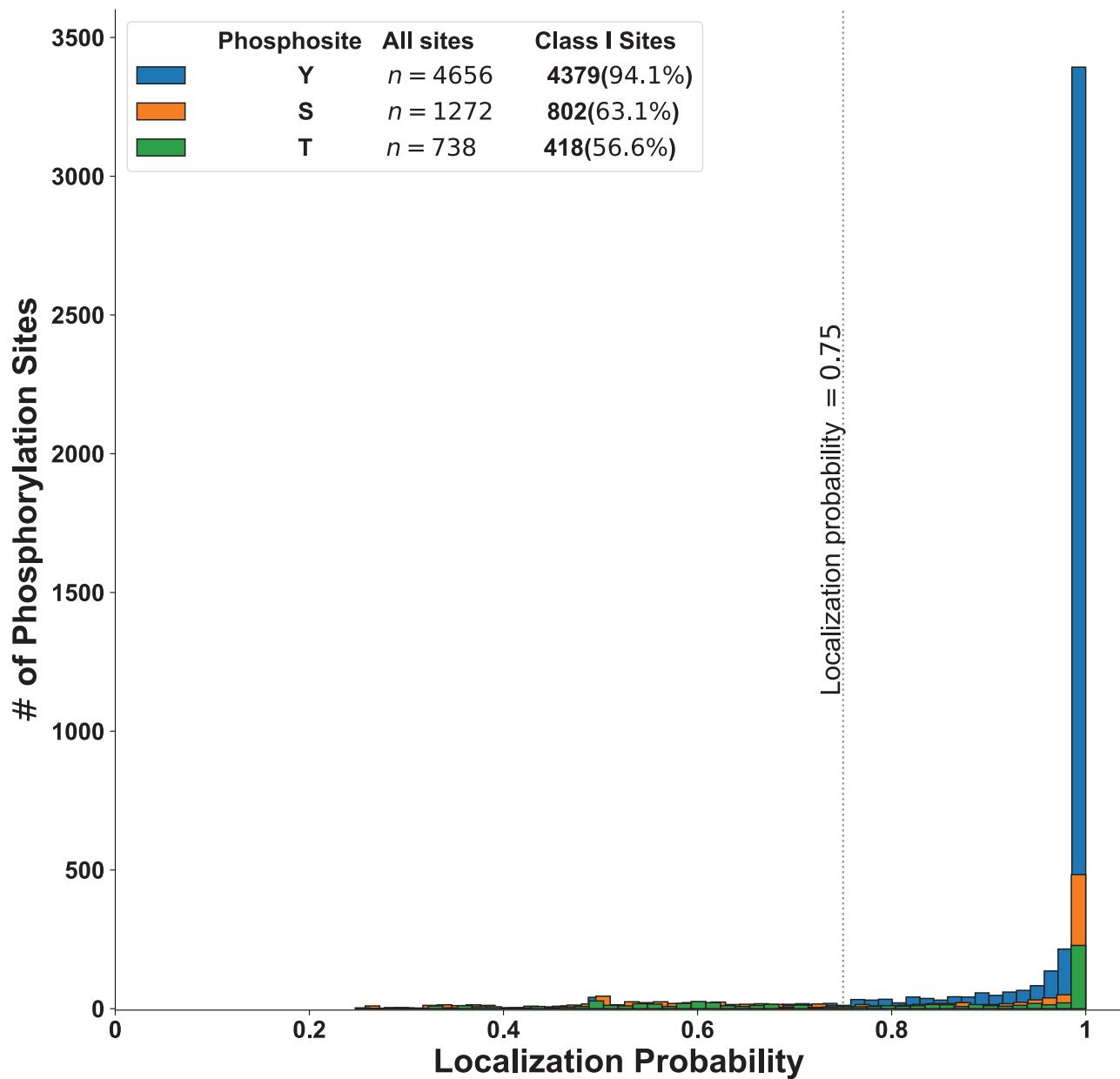
Supporting Table 4: All unique peptides observed exclusively in the BOOST experiment with ΦSDM enabled and reporter ions quantified in at least one experimental channel. Included are MaxQuant outputs such as the gene name(s), protein name(s), modified sequence, modified sequence with phosphorylation site localization probabilities, sequence windows, and corrected TMT reporter ion intensities, as well as calculations used in the manuscript (mean intensity values, standard deviations, CV percentages, *p*-values, *q*-values, BOOST factors) and WikiPathway Annotations for each unique peptide.

Supporting Table 5: All unique peptides observed in both the BOOST experiment and the 1.0 mg Control experiment with ΦSDM enabled and reporter ions quantified in at least one experimental channel. Included are MaxQuant outputs such as the gene name(s), protein name(s), modified sequence, modified sequence with phosphorylation site localization probabilities, sequence windows, and corrected TMT reporter ion intensities, as well as calculations used in the manuscript (mean intensity values, standard deviations, CV percentages, *p*-values, *q*-values, BOOST factors) and WikiPathway Annotations for each unique peptide.

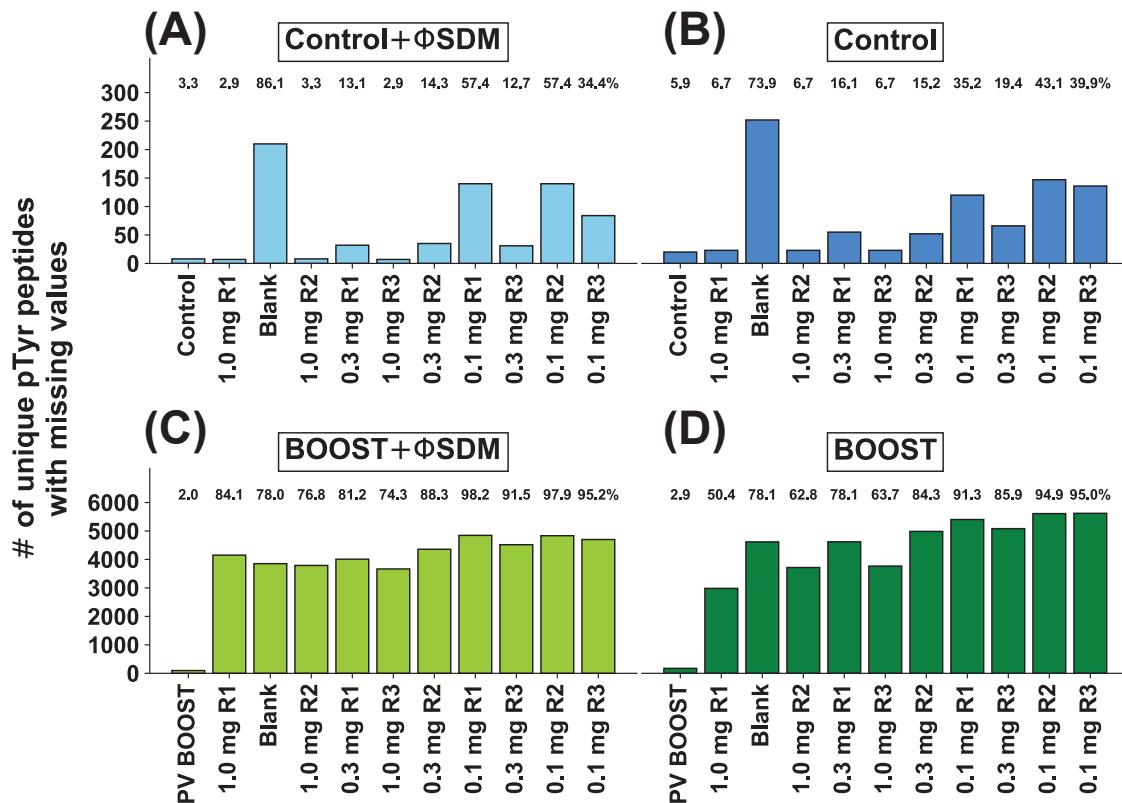
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Supporting Folder 1: All Python3 code used to analyze the MaxQuant output files and databases referenced. These include “data_analysis.py” (script used to generate plots), “helpers/” (Python3 files used to assist in data analysis), “database/” (all external databases used in analysis), and “maxquant_results” (the “evidence.txt” and “Phospho (STY)Sites.txt” files from Supporting Folder 2), as well as the output folders “figures/” (all figures generated by data_analysis.py) and “curated_results/” (all .txt output files from Python3 analysis, which are aggregated and formatted in Supporting Tables 1-6).

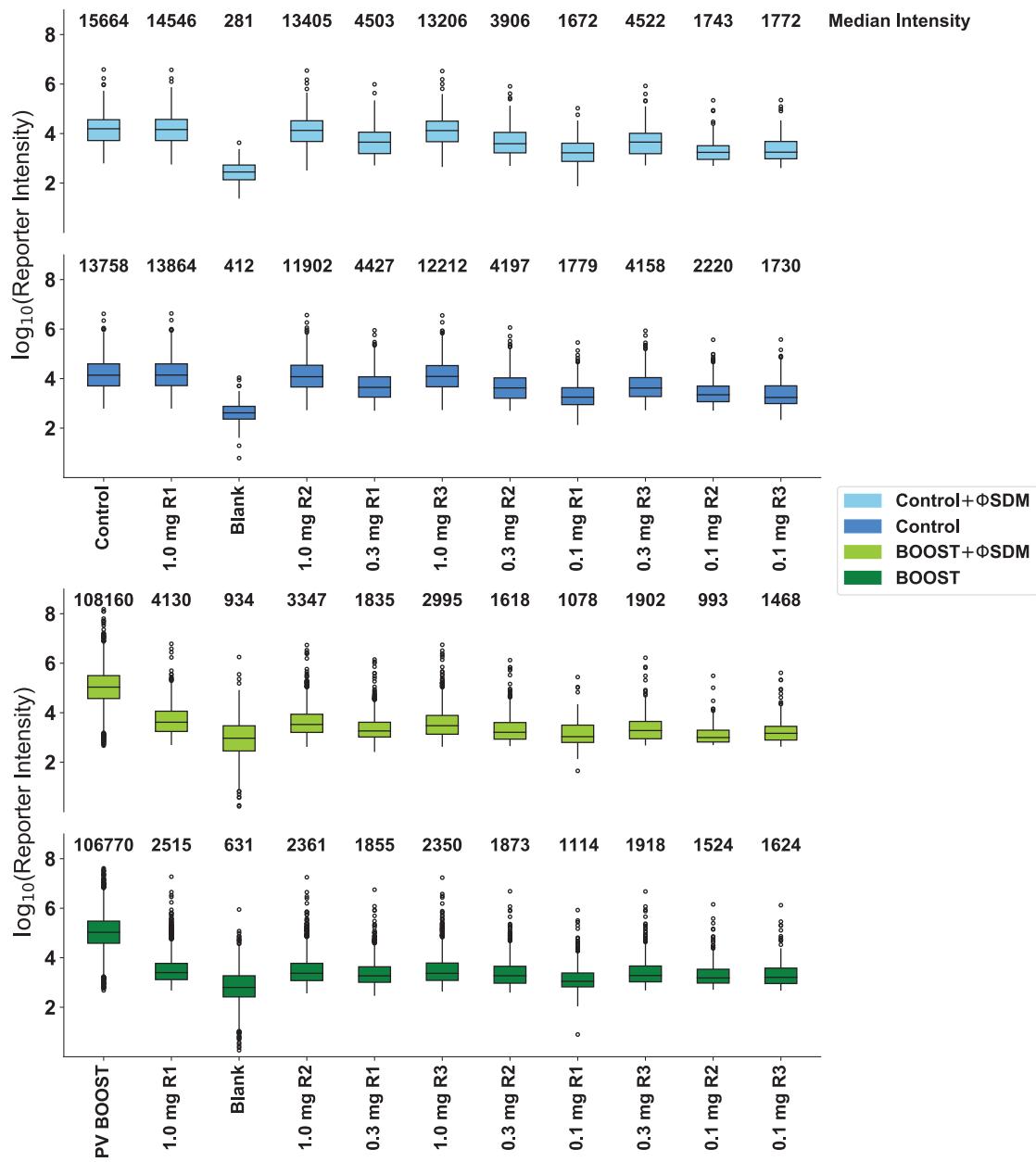
Supporting Folder 2: All tables generated by MaxQuant as text files. These include “summary.txt” (a summary of parameters, information, .raw files, and statistics used for peak detection), “evidence.txt” (all information about unique peptides quantified from .raw files), “peptides.txt” (information about the peptides identified from .raw files), “modification-SpecificPeptides.txt” (information about posttranslational modifications to the peptides), “Oxidation (M)Sites.txt” (information about oxidized peptides), “Phospho (STY)Sites.txt” (information about phosphorylated peptides), “proteinGroups.txt” (information about estimated protein abundance from the .raw files), “allPeptides.txt” (all information for each unique peptide identified in each .raw file), “msScans.txt” (information about the scans observed on the mass spectrometer), “mzRange.txt”, “msmsScans.txt” (information about the MS/MS scans for each .raw file), and “msms.txt” (information about the MS/MS spectra for each peptide identified in each .raw file).



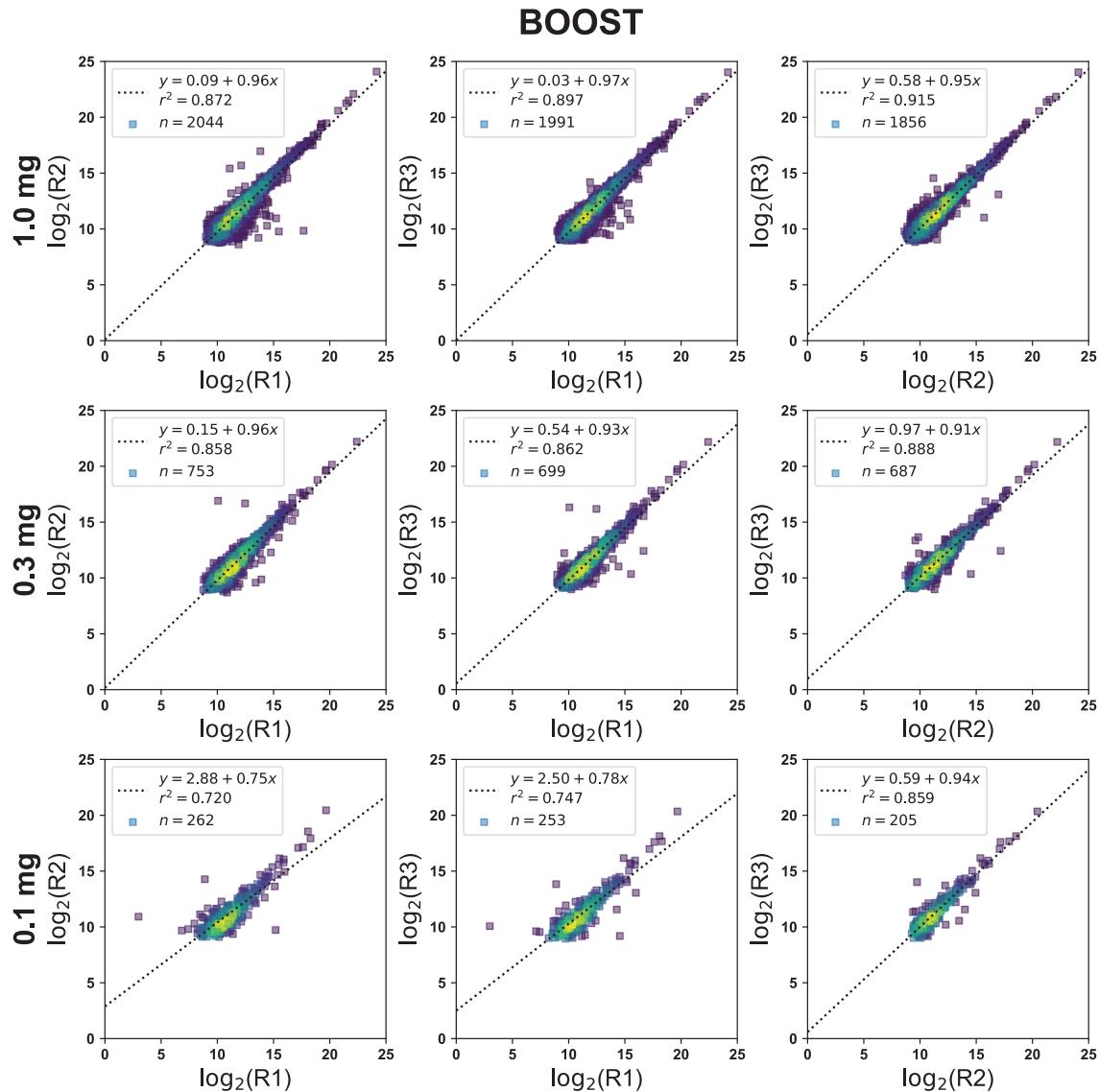
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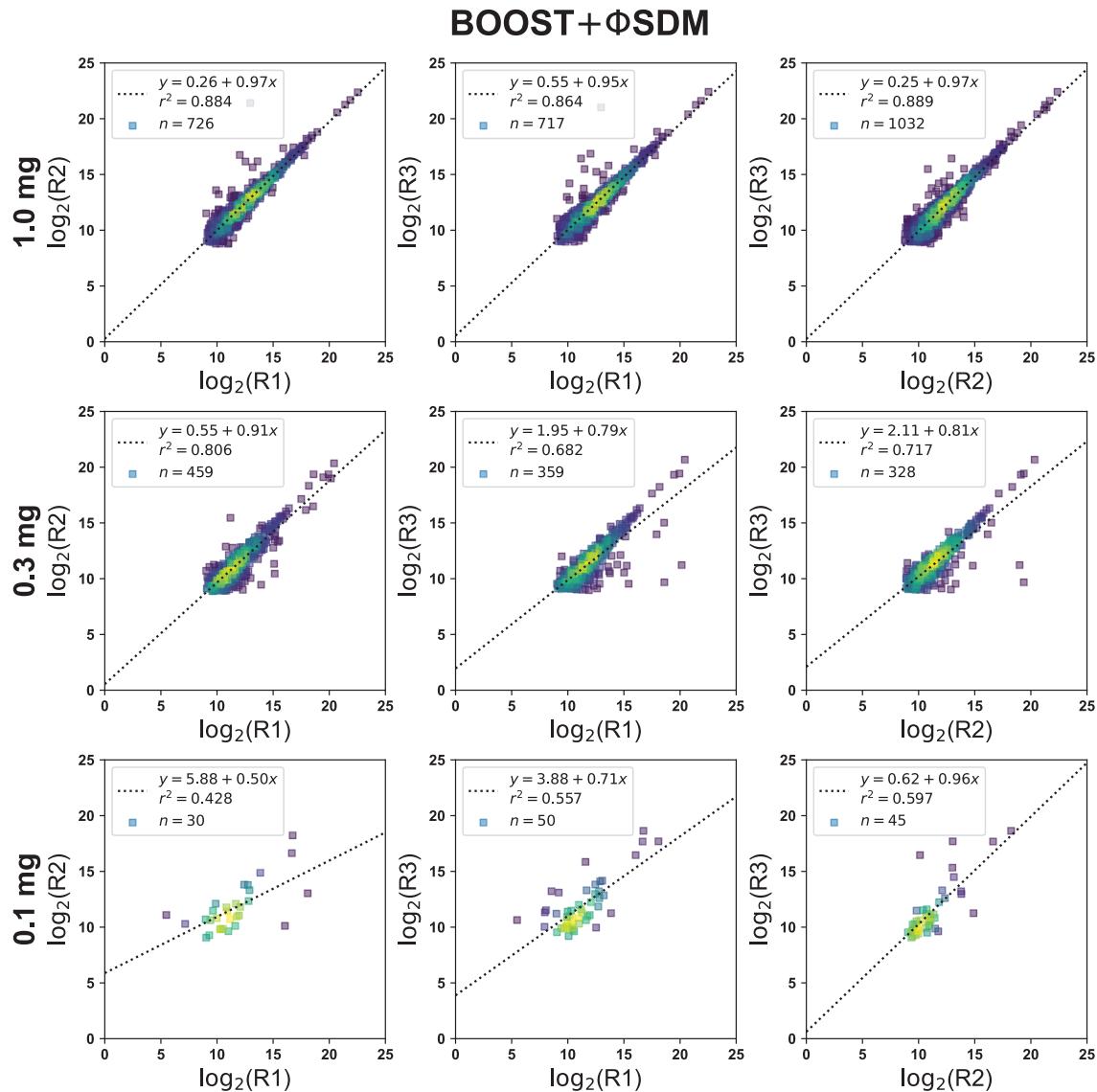
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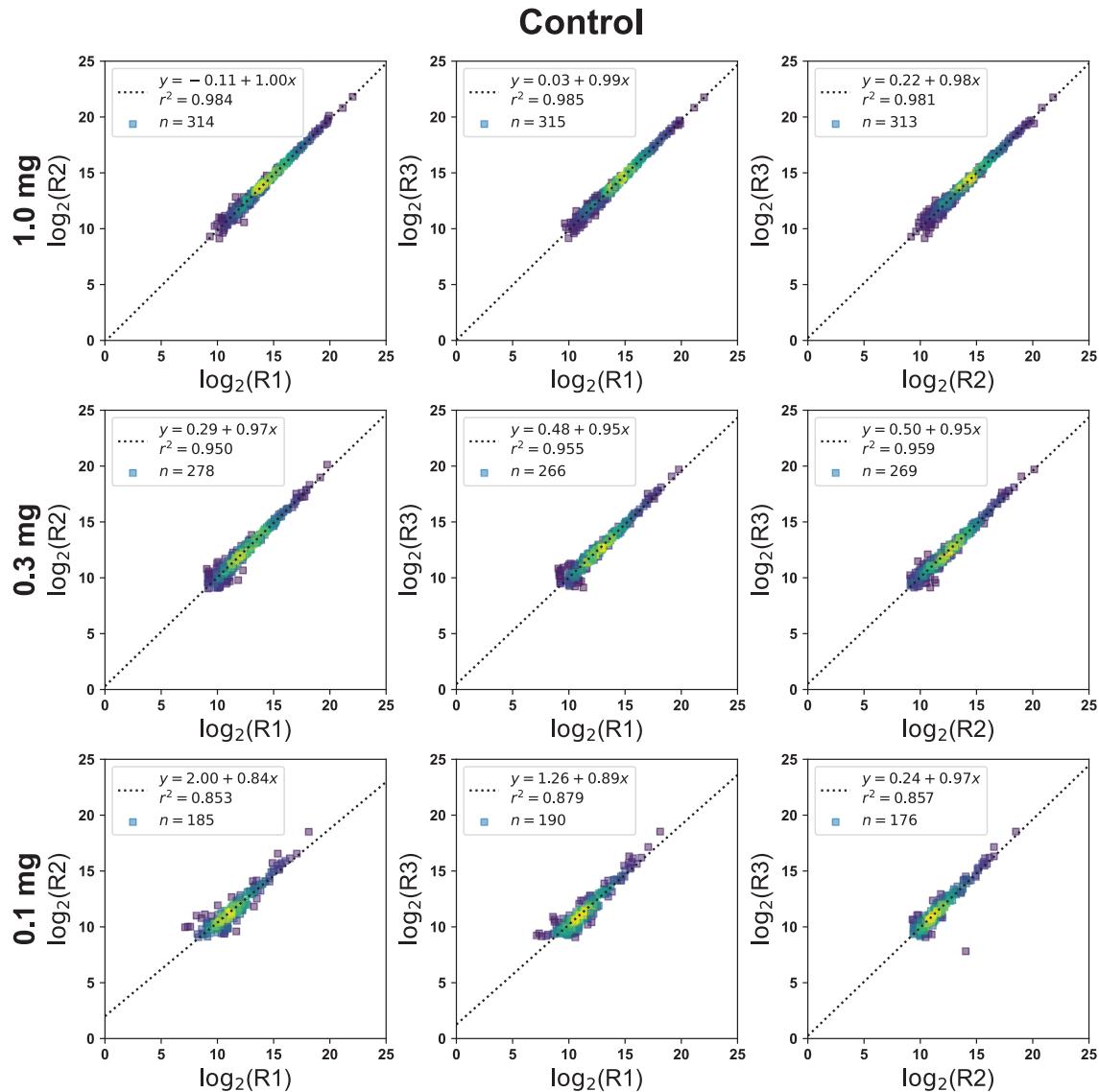
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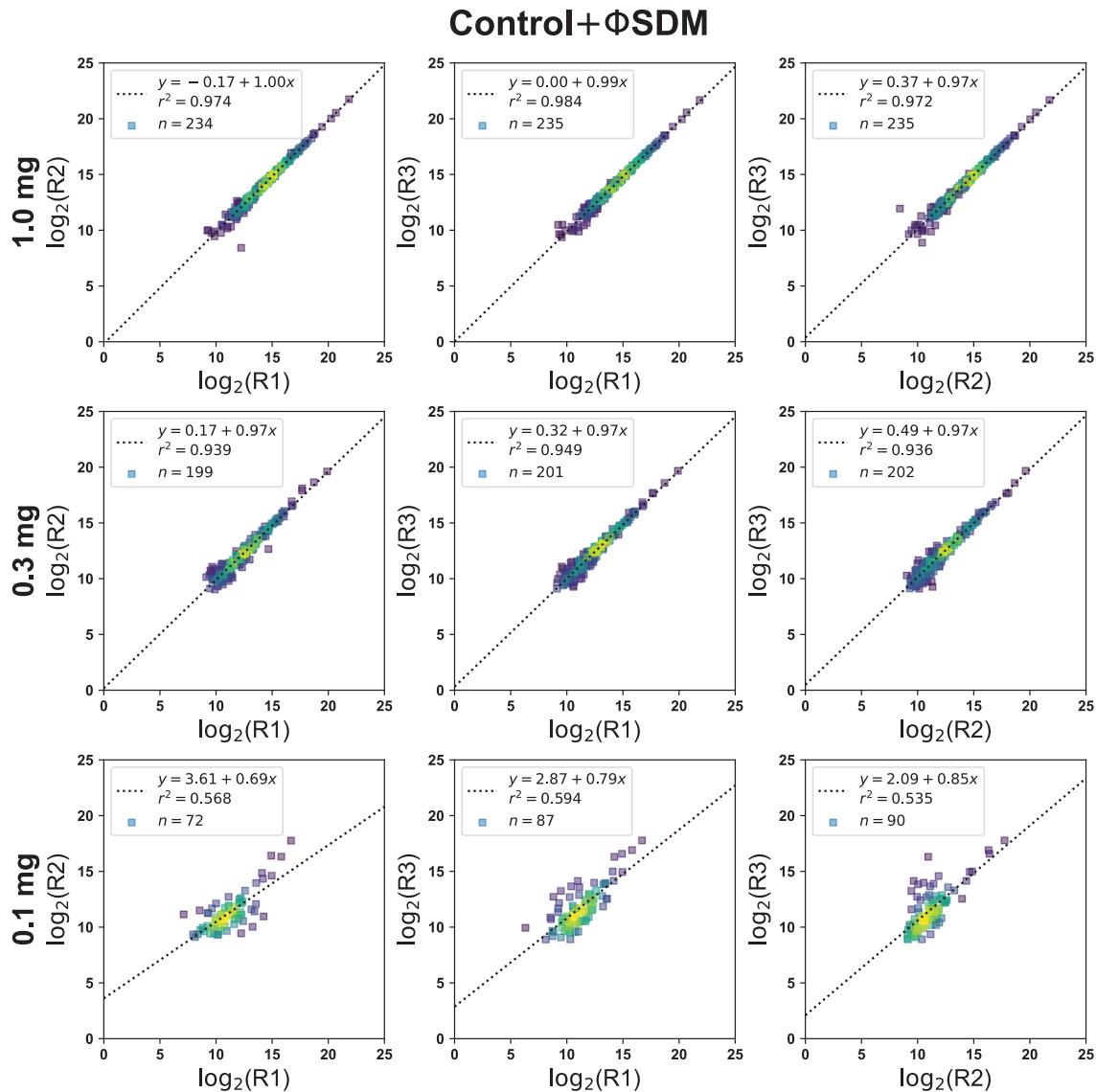
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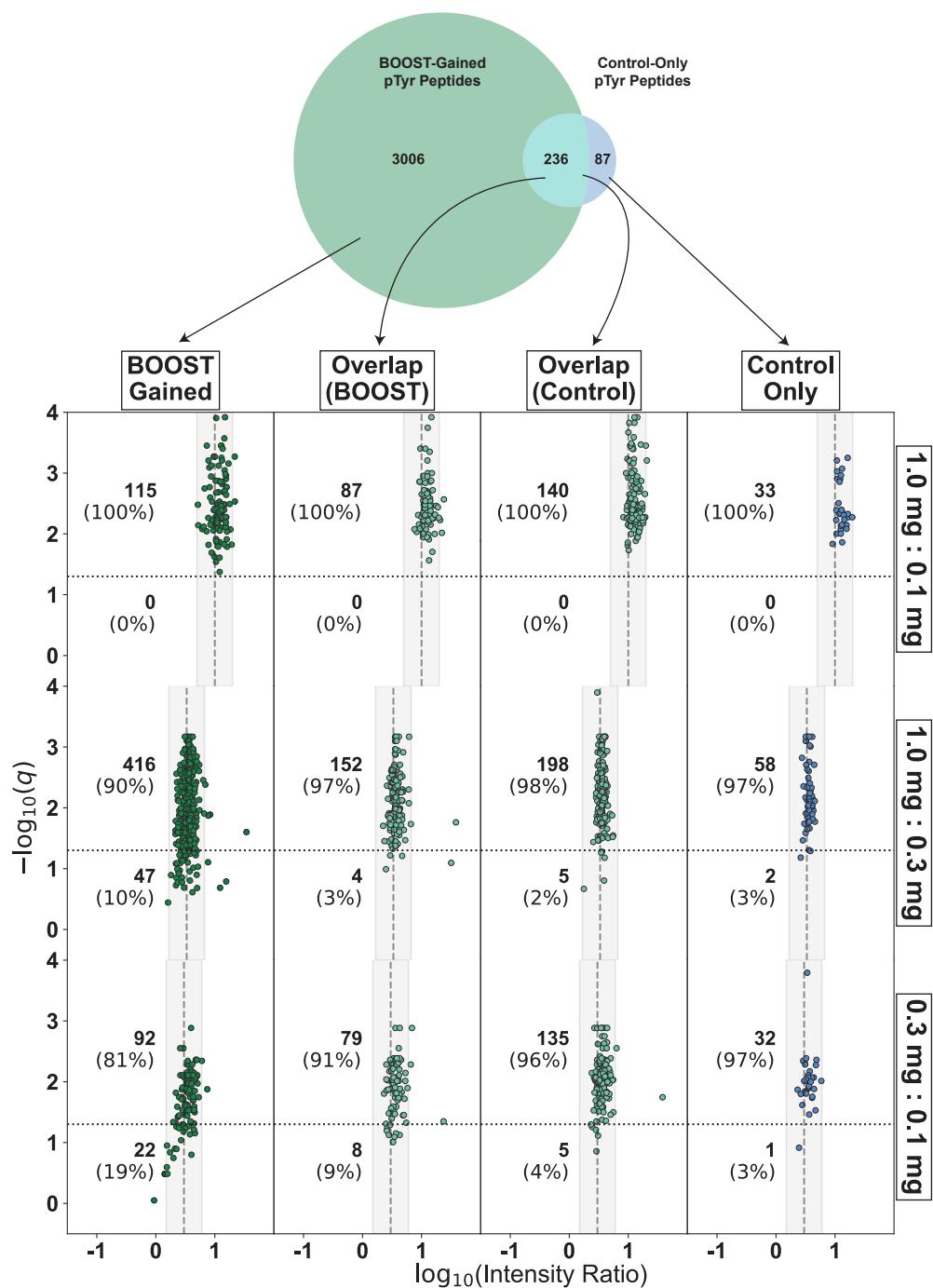
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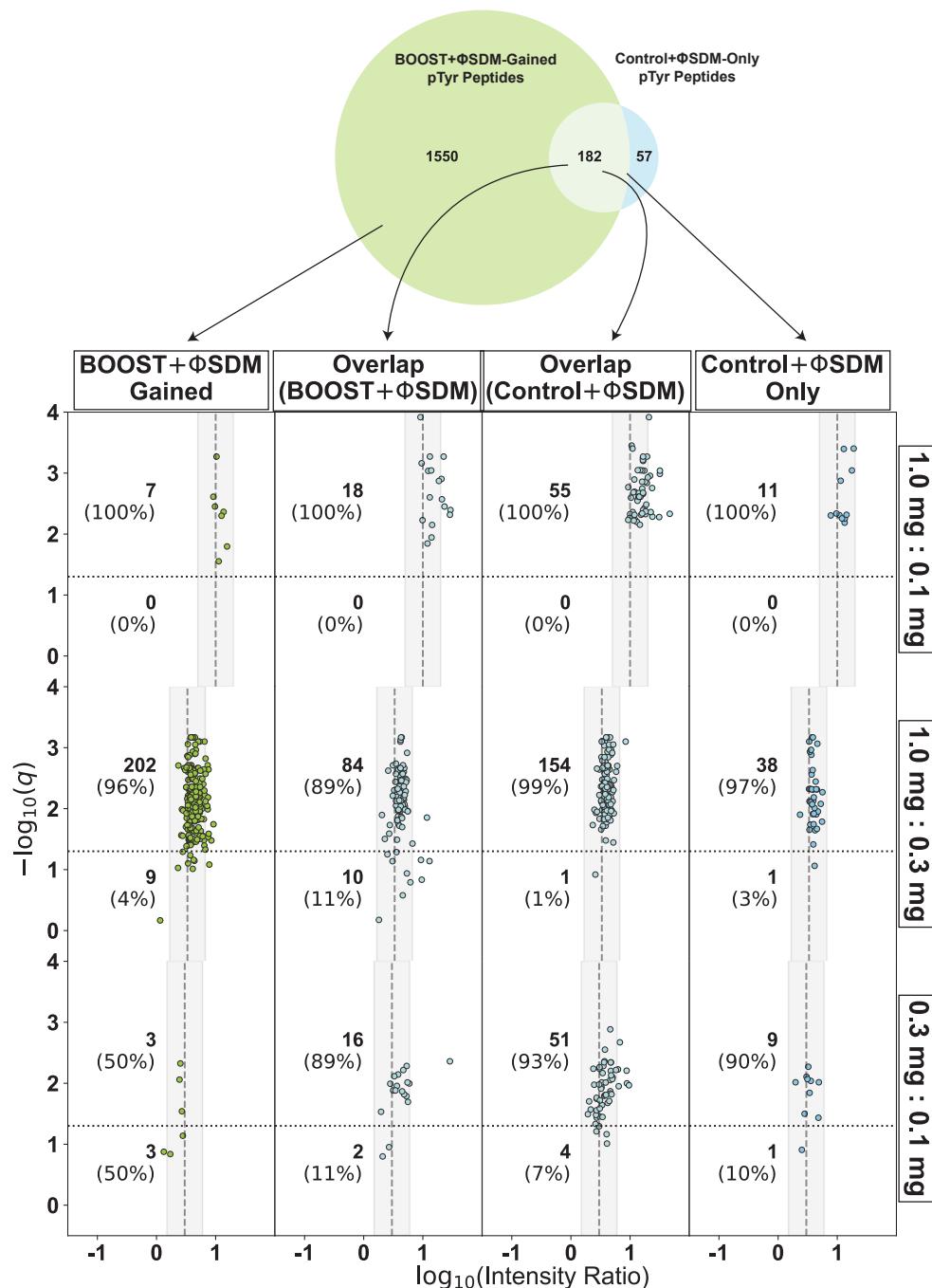
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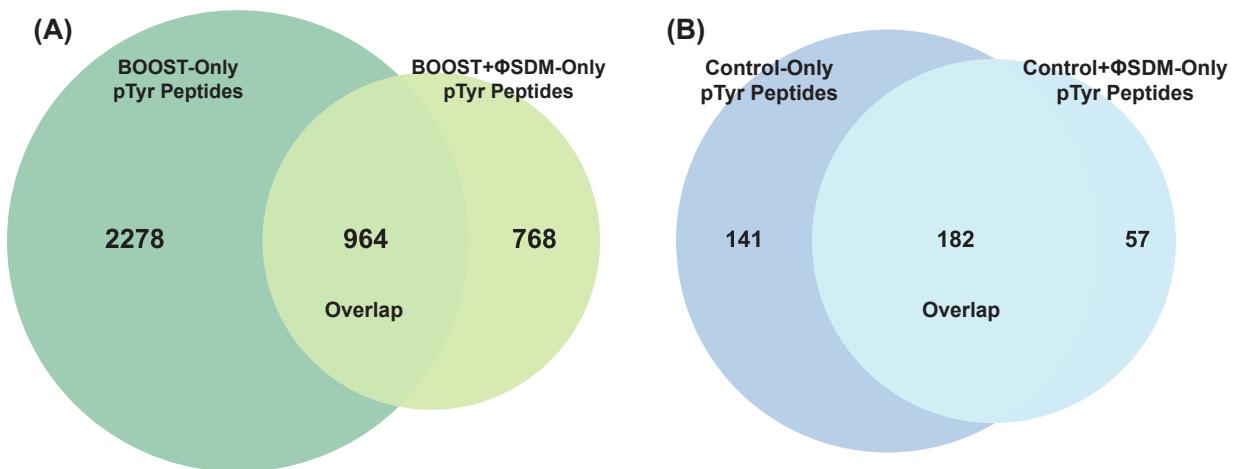
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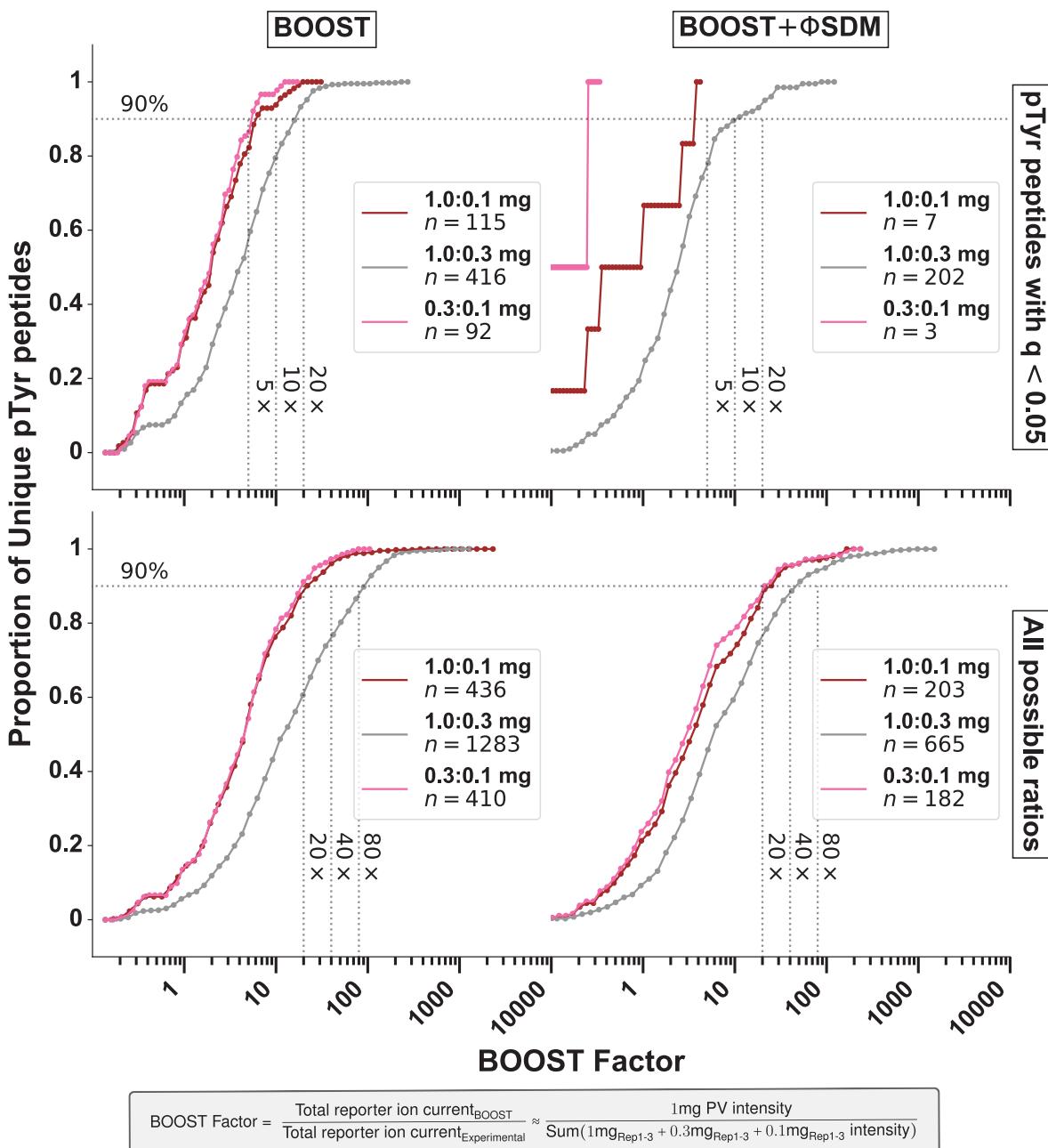
Supporting Figure 8: With Φ SDM disabled, the pervanadate BOOST channel dramatically increases the number of unique pTyr peptides observed as compared to a 1.0 mg Control channel. A Venn diagram showing the overlap of unique pTyr peptides between the BOOST and 1.0 mg Control experiments (with Φ SDM disabled). Volcano plots show $-\log_{10}(q\text{-value})$ as a function of $\log_{10}(\text{Intensity Ratio})$ for unique pTyr peptides from groups shown in the Venn diagram. For the overlapping section, volcano plots were created using data from both the BOOST experiment and the control experiment acquired with Φ SDM disabled.



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