
Supporting Information:

Mouse primary T cell phosphotyrosine proteomics

enabled by BOOST

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Supporting Table 1: All unique peptide PSMs observed exclusively in the BOOST experiment with Φ SDM 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 WikiPathways¹ Annotations for each unique peptide.

Supporting Table 2: All unique peptide PSMs observed in both the BOOST experiment and the 1.0 mg Control experiment with Φ SDM 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 WikiPathways¹ Annotations for each unique peptide.

Supporting Table 3: All unique peptide PSMs observed exclusively in the 1.0 mg Control experiment with Φ SDM 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 WikiPathways¹ Annotations for each unique peptide.

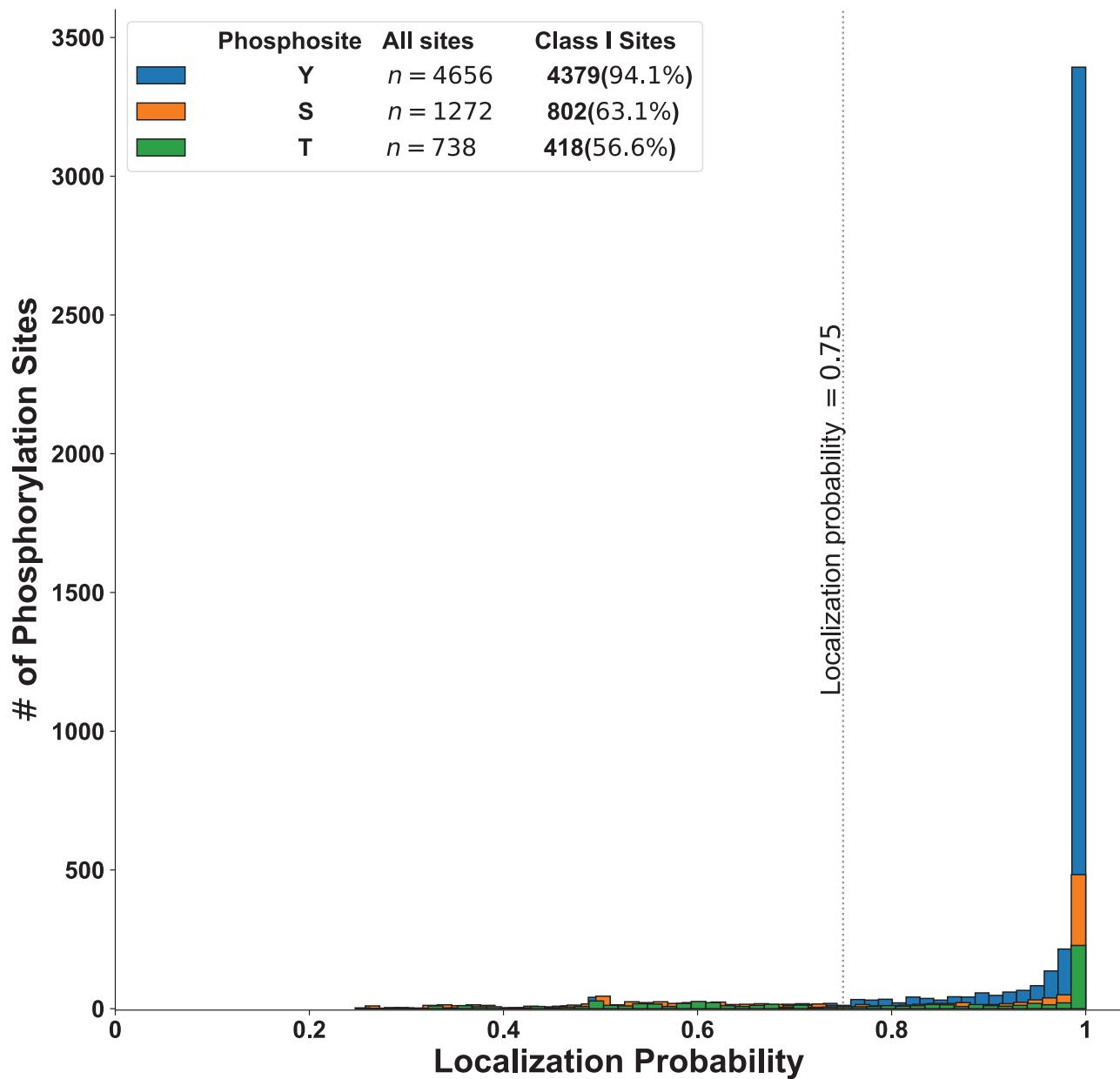
Supporting Table 4: All unique peptide PSMs observed exclusively in the BOOST experiment with Φ SDM enabled and reporter ions quantified in at least one experimental channel. Included are MaxQuant outputs such as the gene name(s), protein name(s), modified sequence, modified sequence with phosphorylation 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 WikiPathways¹ Annotations for each unique peptide.

Supporting Table 5: All unique peptide PSMs 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 WikiPathways¹ Annotations for each unique peptide.

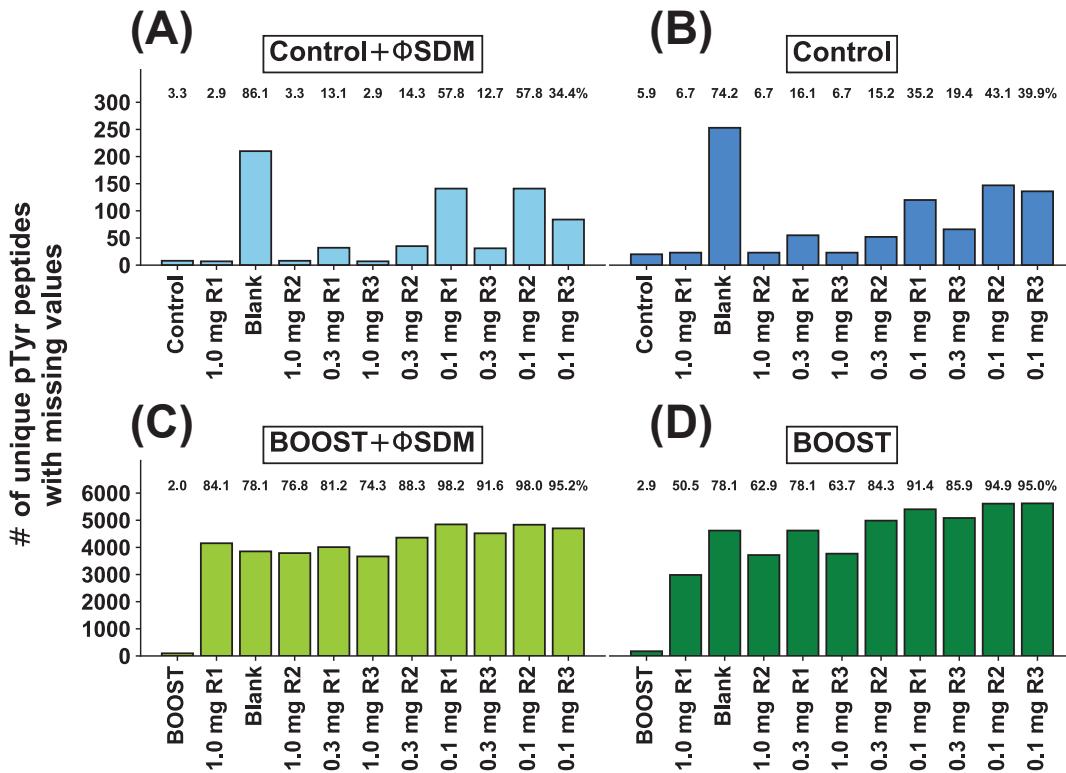
Supporting Table 6: All unique peptide PSMs observed exclusively in the 1.0 mg Control experiment with ΦSDM enabled and reporter ions quantified in at least one experimental channel. Included are MaxQuant outputs such as the gene name(s), protein name(s), modified sequence, modified sequence with phosphorylation site localization probabilities, sequence windows, and corrected TMT reporter ion intensities, as well as PhosphoSitePlus® site annotations, calculations used in the manuscript (mean intensity values, standard deviations, CV percentages, *p*-values, *q*-values) and WikiPathways¹ Annotations for each unique peptide.

Supporting Folder 1: 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 posttranlational 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).

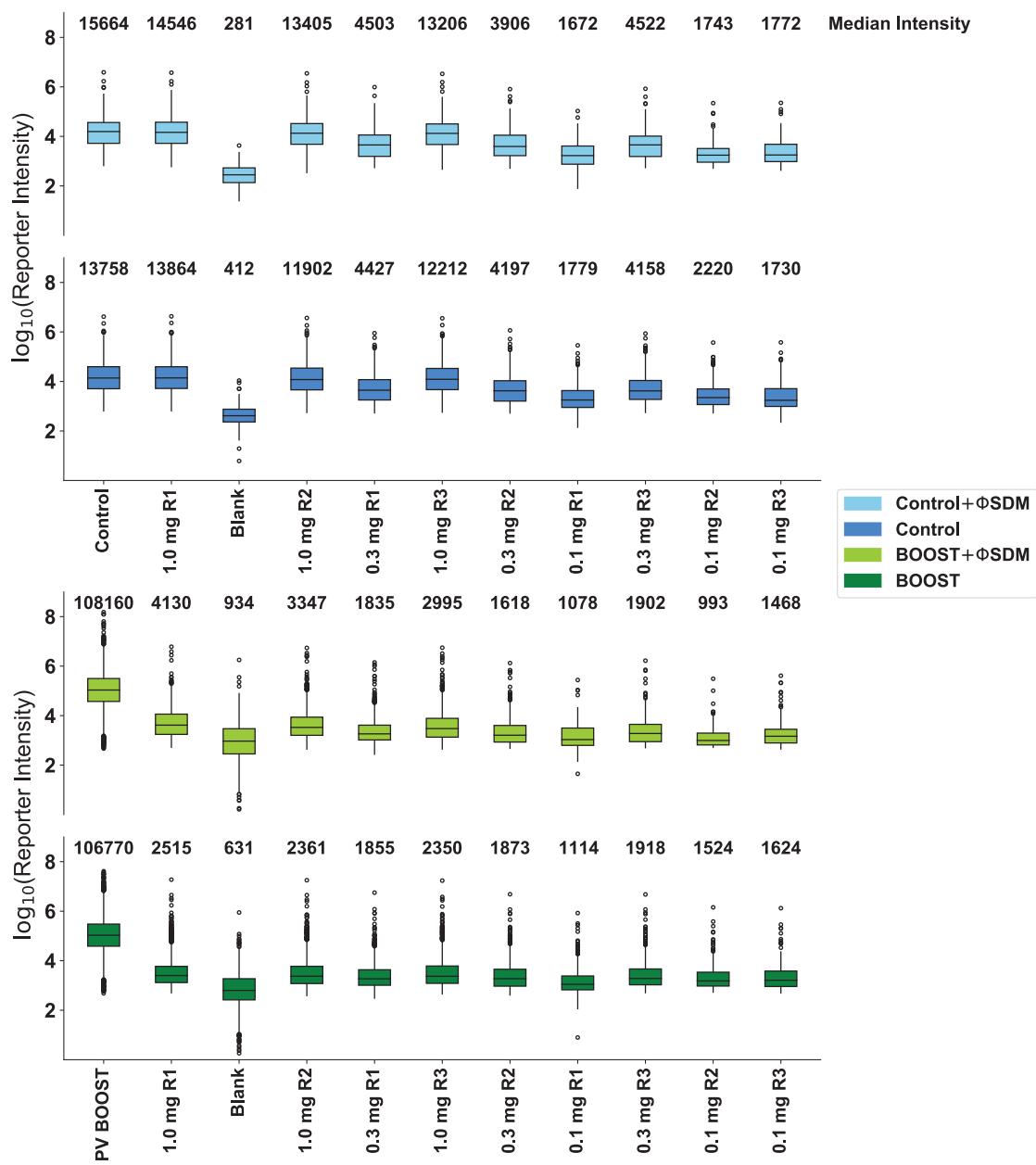
Supporting Folder 2: All Python3 code used to analyze the MaxQuant output files and databases referenced. These include “data_analysis.py” (script used to generate plots), “helpers/” (Python3 files used to assist in data analysis), “database/” (all external databases used in analysis), and “maxquant_results” (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).



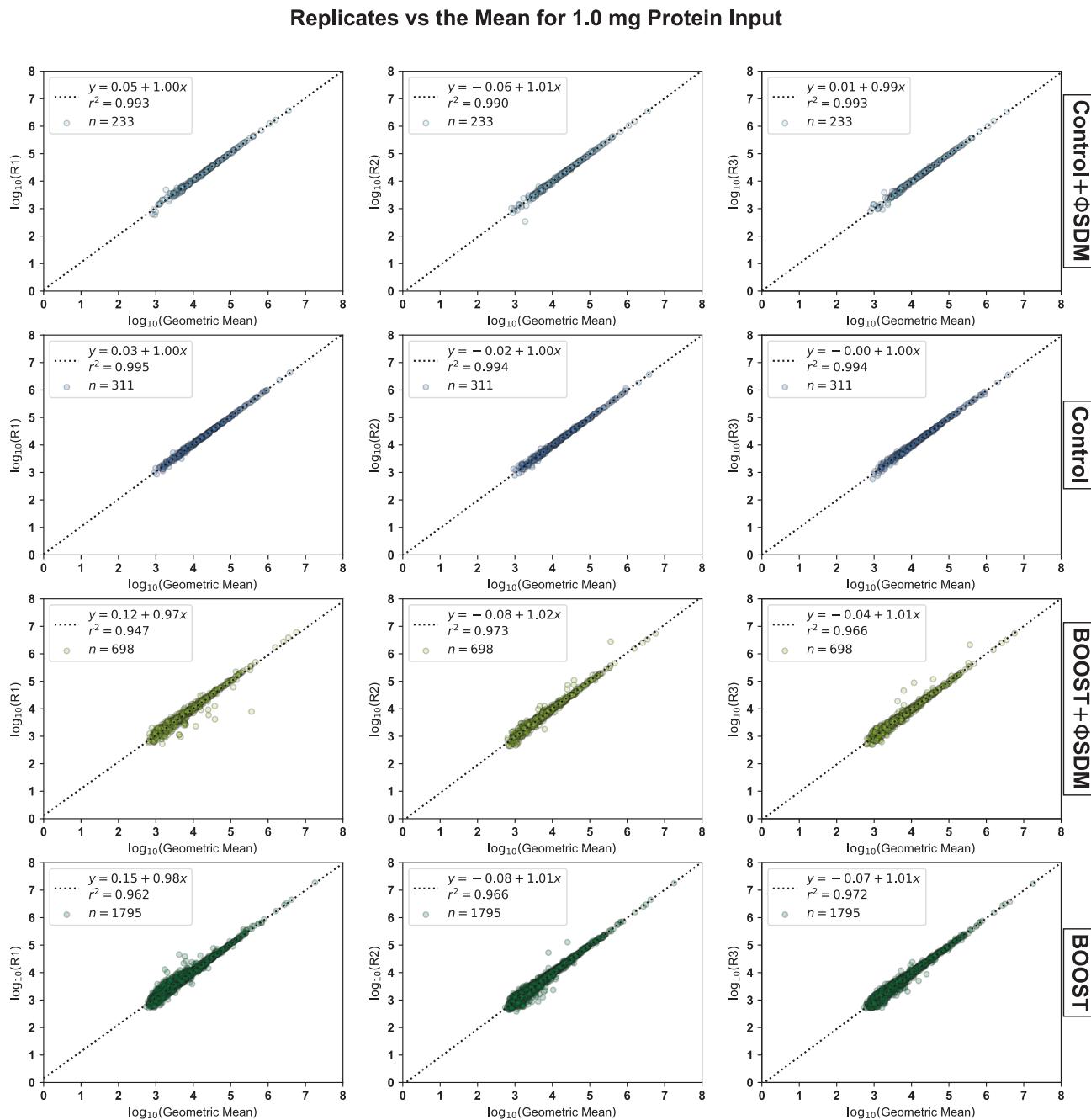
Supporting Figure 1: A histogram with depicting all PSMs from all experiments containing at least one phosphorylated serine (S), threonine (T), or tyrosine (Y) amino acid as a function of localization probability ($n_{\text{bins}} = 75$). The total number and number of Class I (localization probability > 0.75) phosphorylation sites for each amino acid are noted in the Figure Legend.



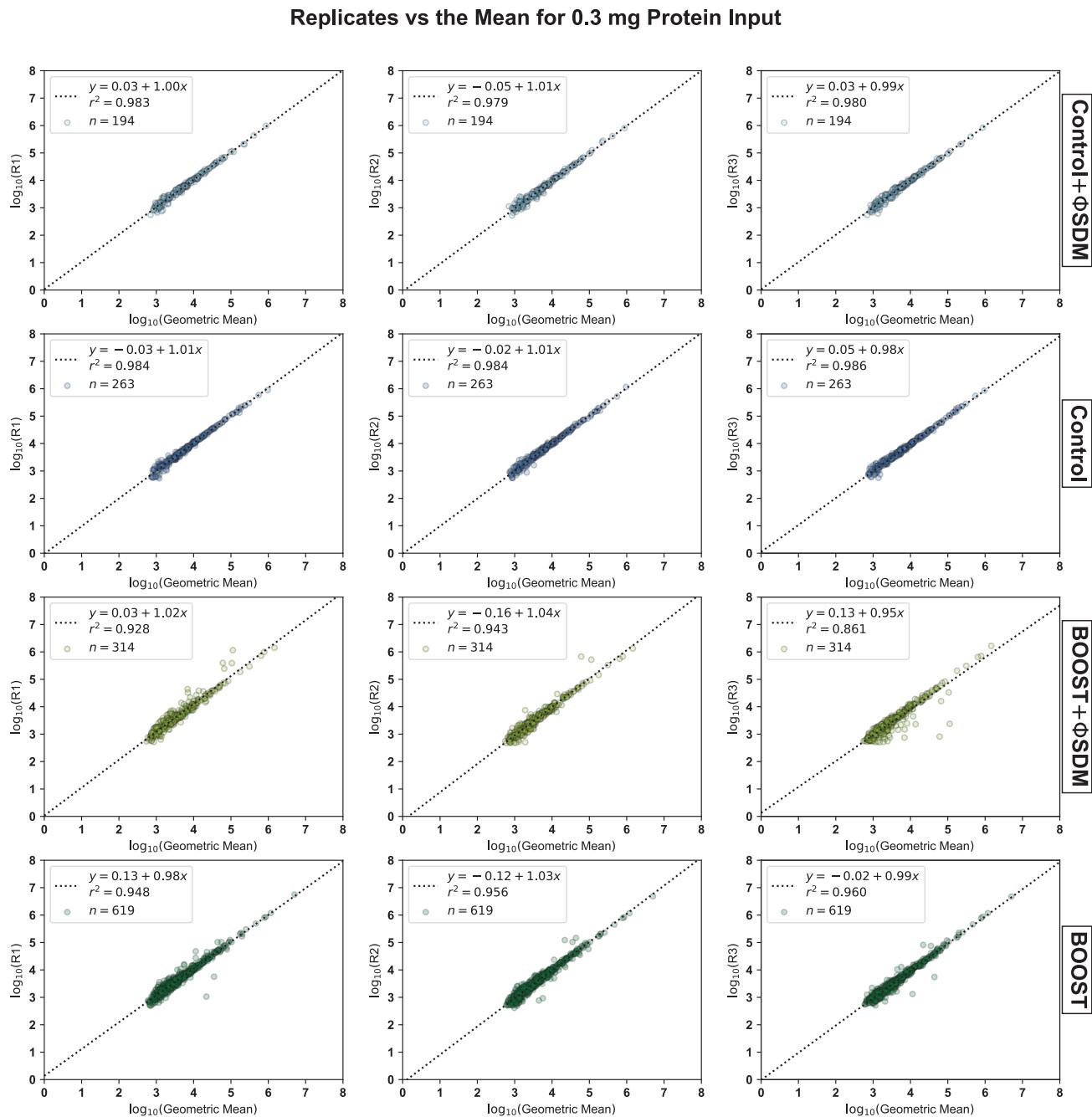
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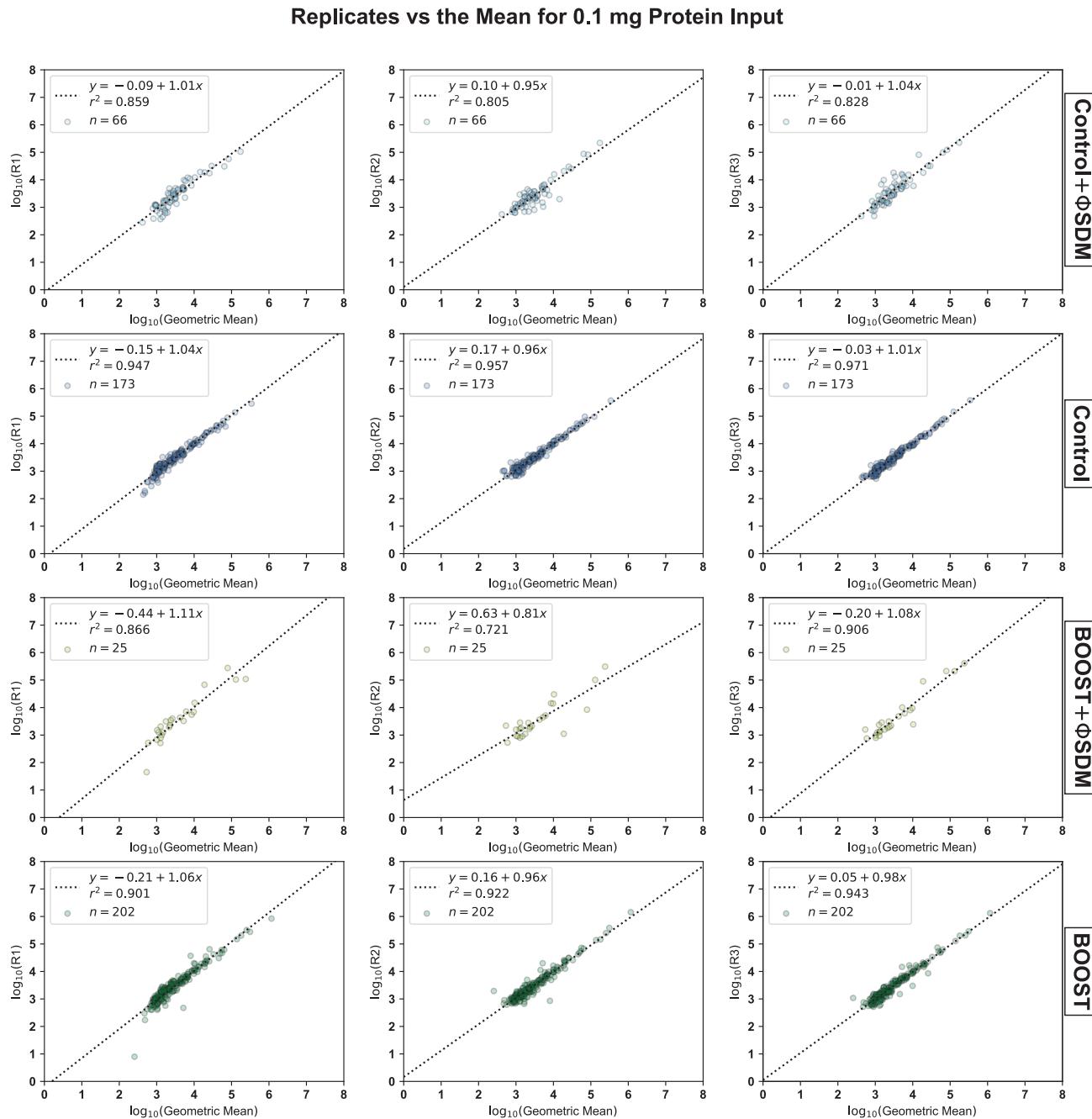
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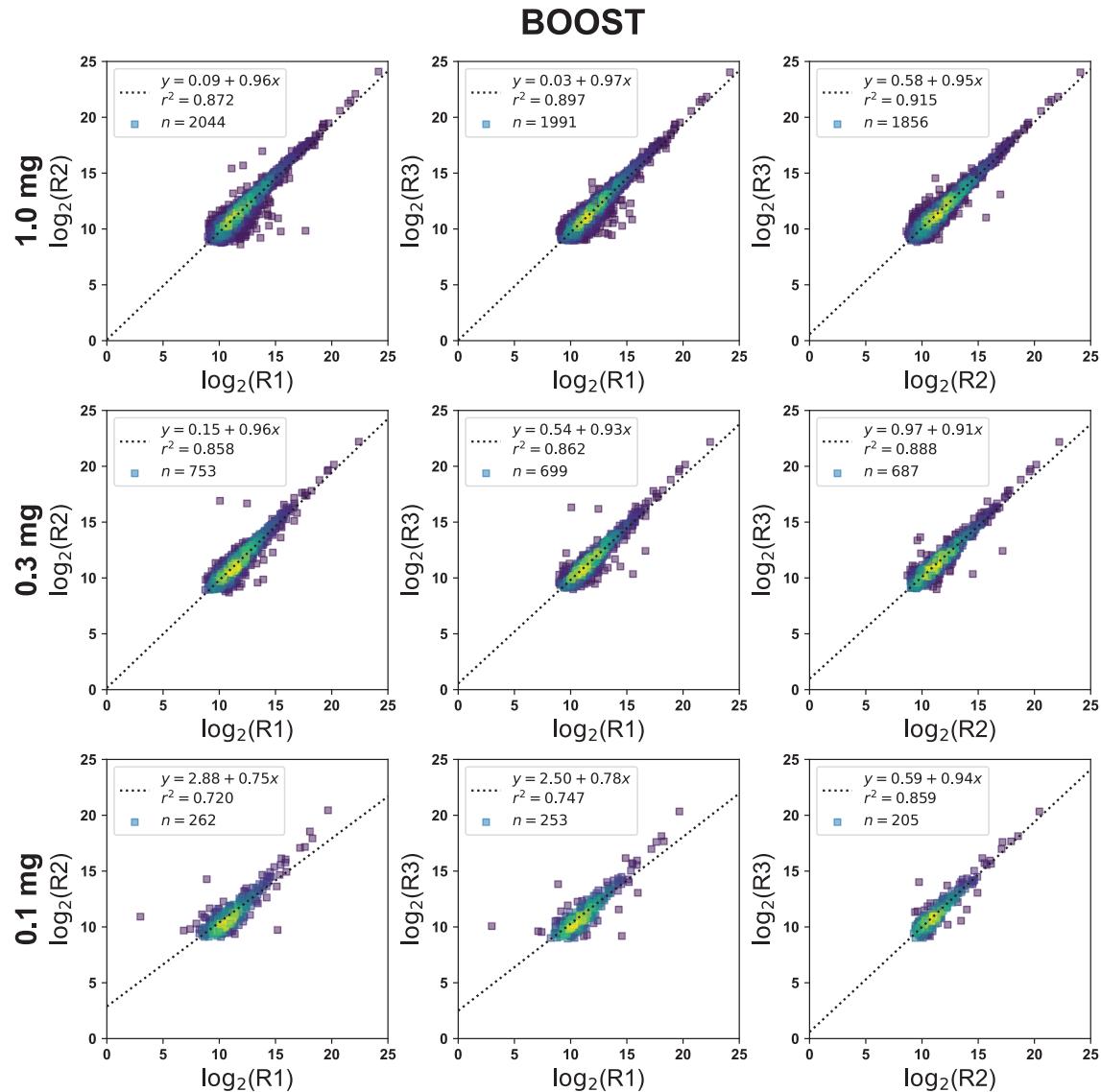
Supporting Figure 4: Comparison between the reporter ion intensity values and the mean value for a given pTyr peptide PSM with no missing values in the 1.0 mg condition of each experiment. The $\log_{10}(\text{Geometric Mean})$ is on the *x*-axis, while each replicate intensity value is on the *y*-axis. The legend shows the line of best fit as determined by simple linear regression,² and the experiment is noted on the right side of each row.



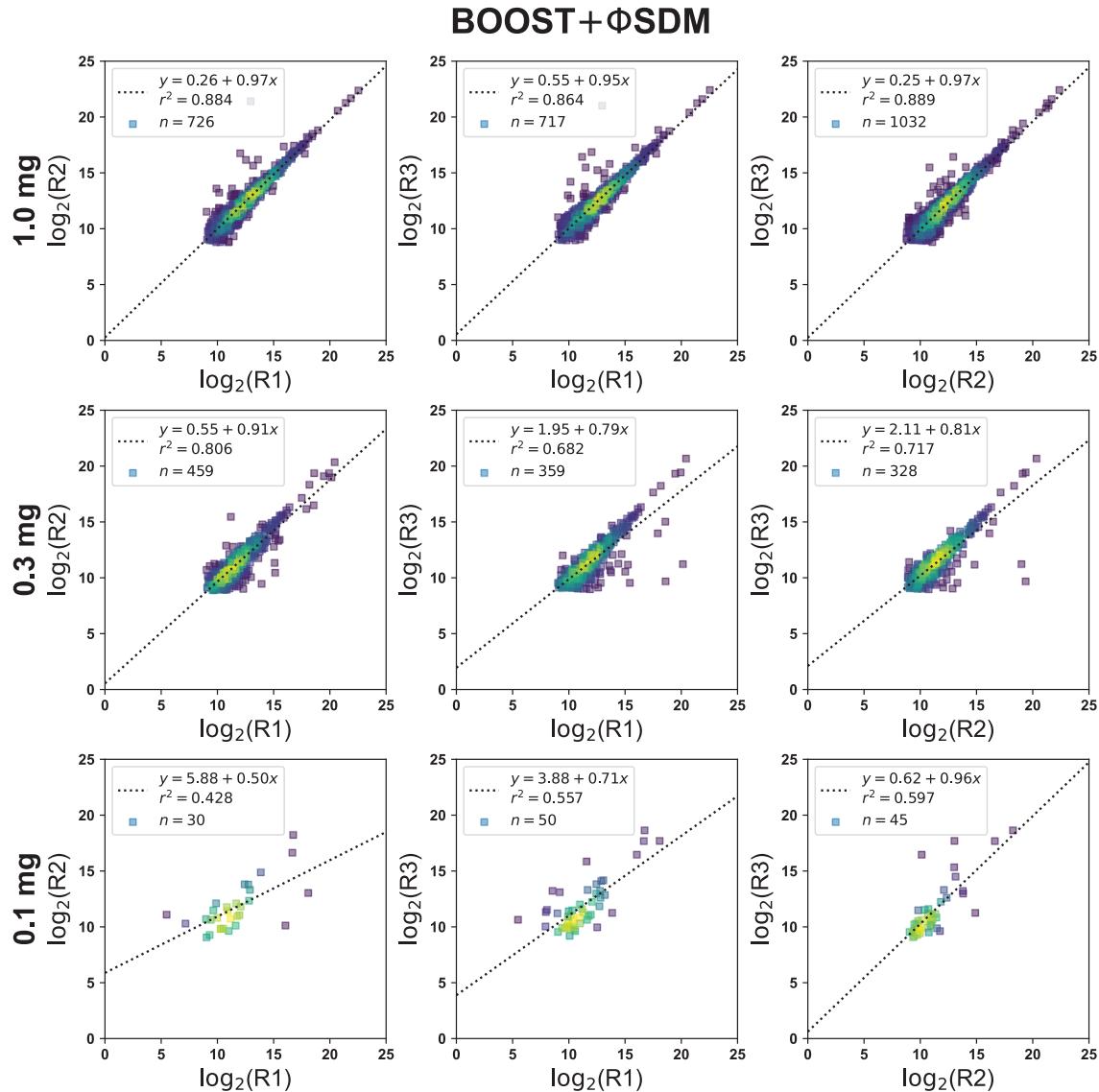
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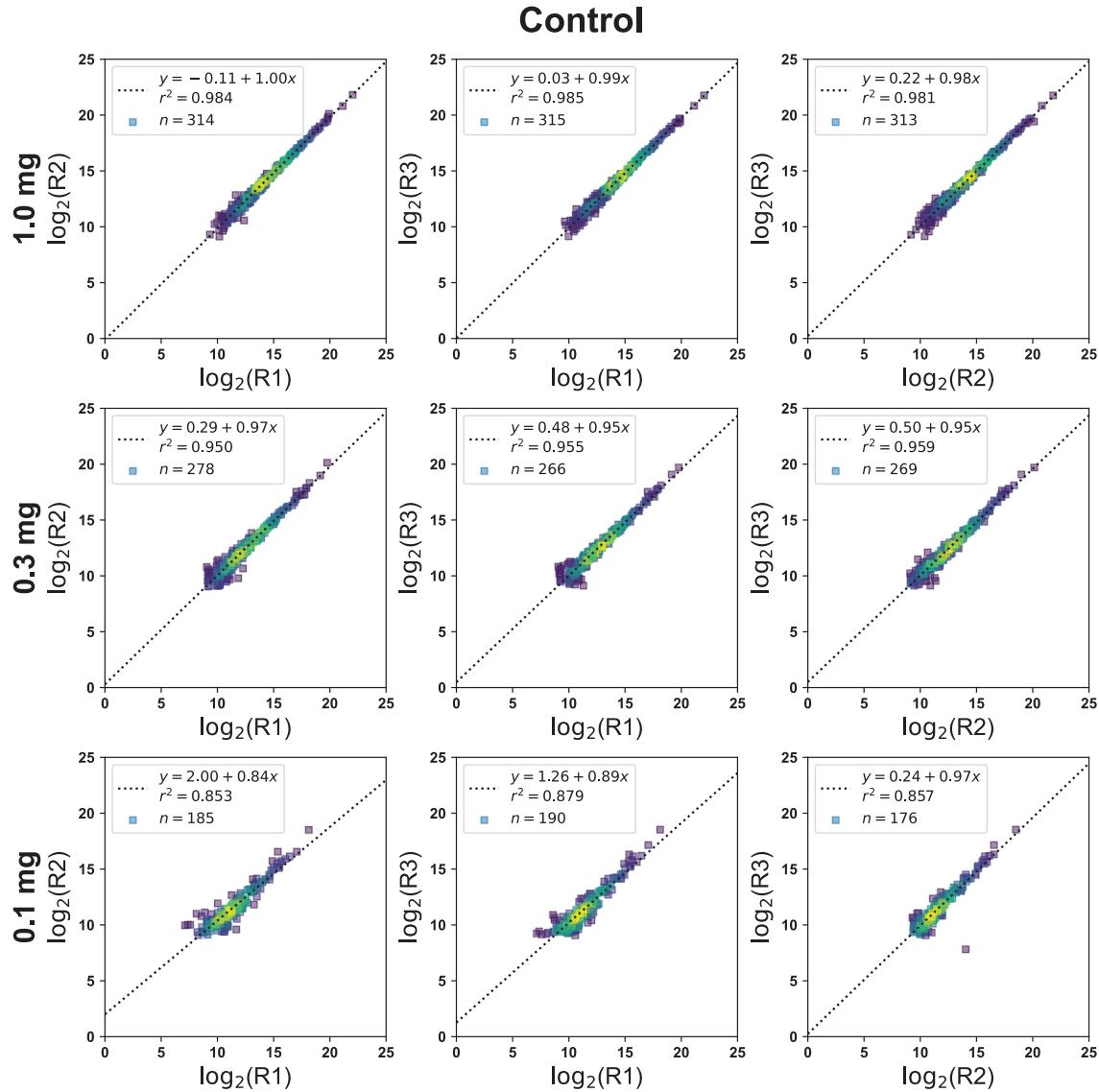
Supporting Figure 6: Comparison between the reporter ion intensity values and the mean value for a given pTyr peptide PSM with no missing values in the 0.1 mg condition of each experiment. The $\log_{10}(\text{Geometric Mean})$ is on the x -axis, while each replicate intensity value is on the y -axis. The legend shows the line of best fit as determined by simple linear regression,² and the experiment is noted on the right side of each row.



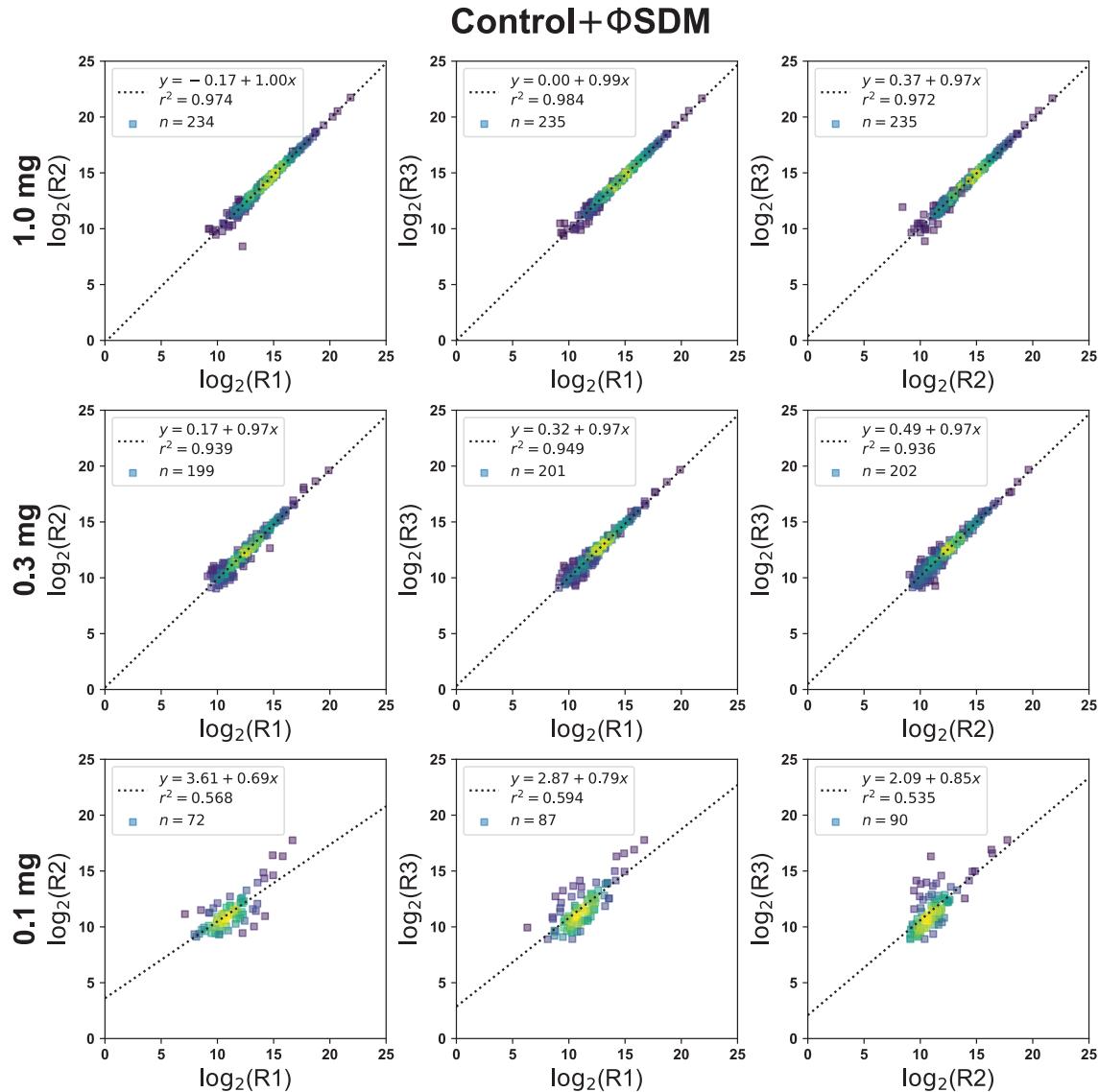
Supporting Figure 7: Replicate reproducibility is stable when ΦSDM is disabled for low protein input samples in the pervanadate BOOST condition. Evaluation of replicate reproducibility in the BOOST experiment (with ΦSDM disabled) using pairwise comparisons of \log_2 transformed abundances for pTyr peptide PSMs with the same charge state and assigned sequence. For each comparison, we show the line of best fit as determined by simple least-squares regression,² the r^2 value as an estimate of the quality of the fitted line, and the total number of points (n) in each comparison.



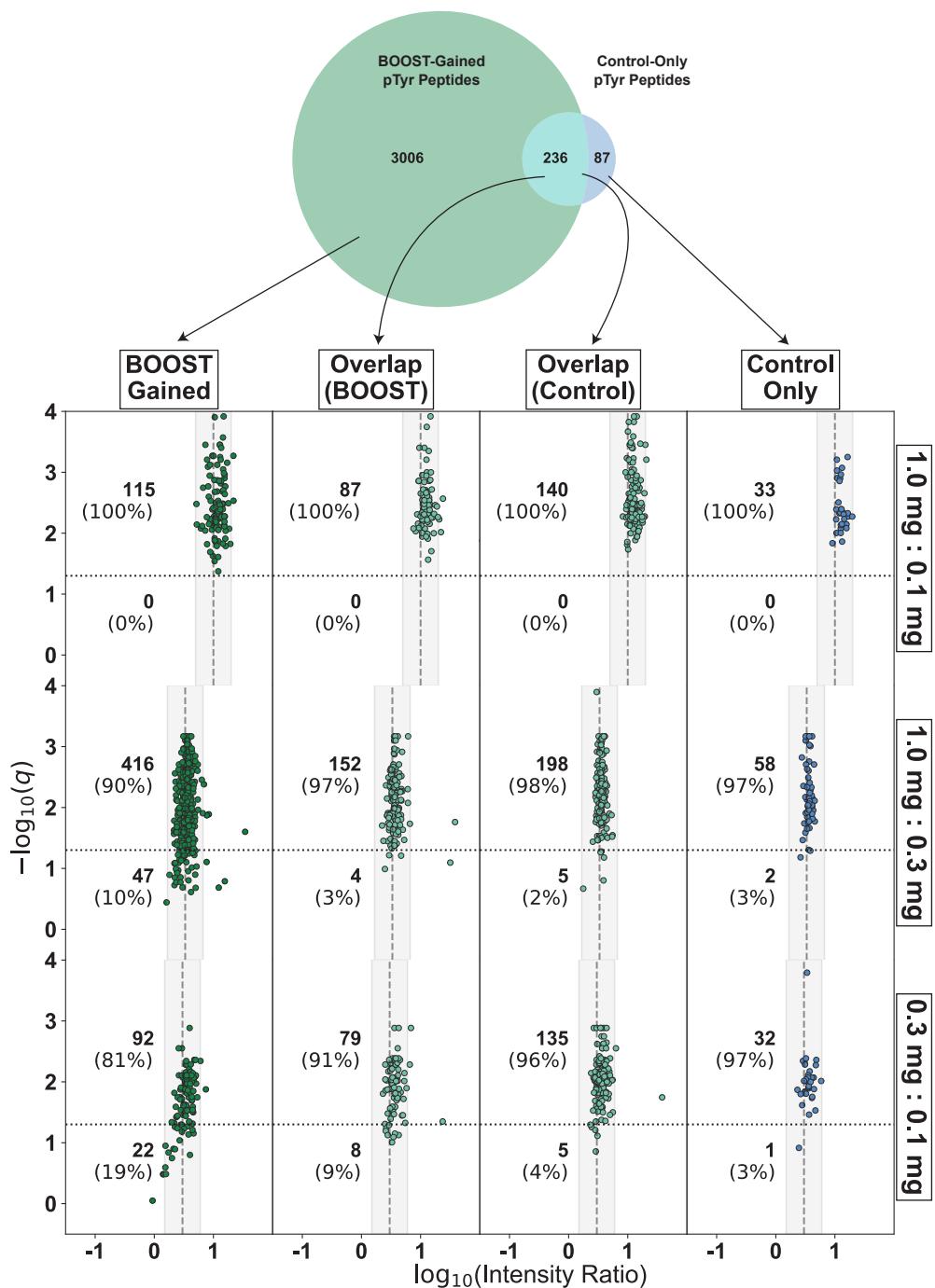
Supporting Figure 8: Replicate reproducibility is severely degraded when ΦSDM is enabled for low protein input samples in the pervanadate BOOST condition. Evaluation of replicate reproducibility in the BOOST experiment (with ΦSDM enabled) using pairwise comparisons of \log_2 transformed abundances for pTyr peptide PSMs with the same charge state and assigned sequence. For each comparison, we show the line of best fit as determined by simple least-squares regression,² the r^2 value as an estimate of the quality of the fitted line, and the total number of points (n) in each comparison.



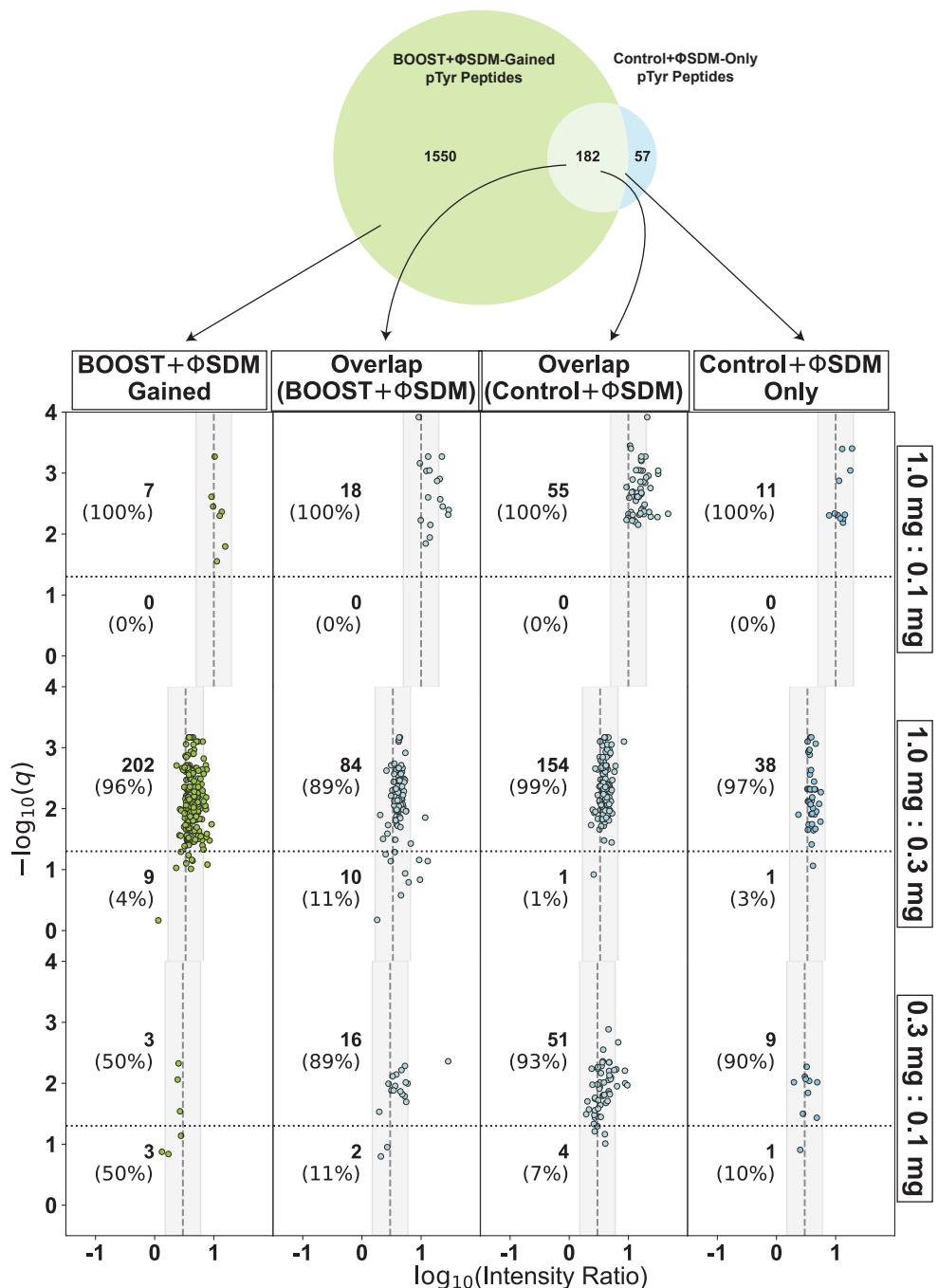
Supporting Figure 9: Replicate reproducibility is stable when ΦSDM is disabled for low protein input samples in the 1.0 mg Control condition. Evaluation of replicate reproducibility in the 1.0 mg Control experiment (with ΦSDM disabled) using pairwise comparisons of \log_2 transformed abundances for pTyr peptide PSMs with the same charge state and assigned sequence. For each comparison, we show the line of best fit as determined by simple least-squares regression,² the r^2 value as an estimate of the quality of the fitted line, and the total number of points (n) in each comparison.



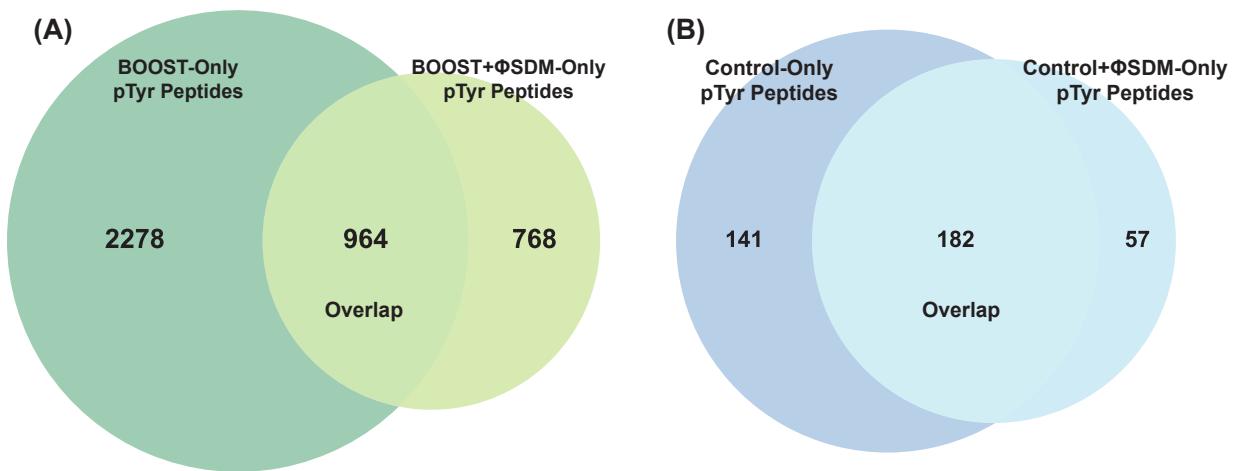
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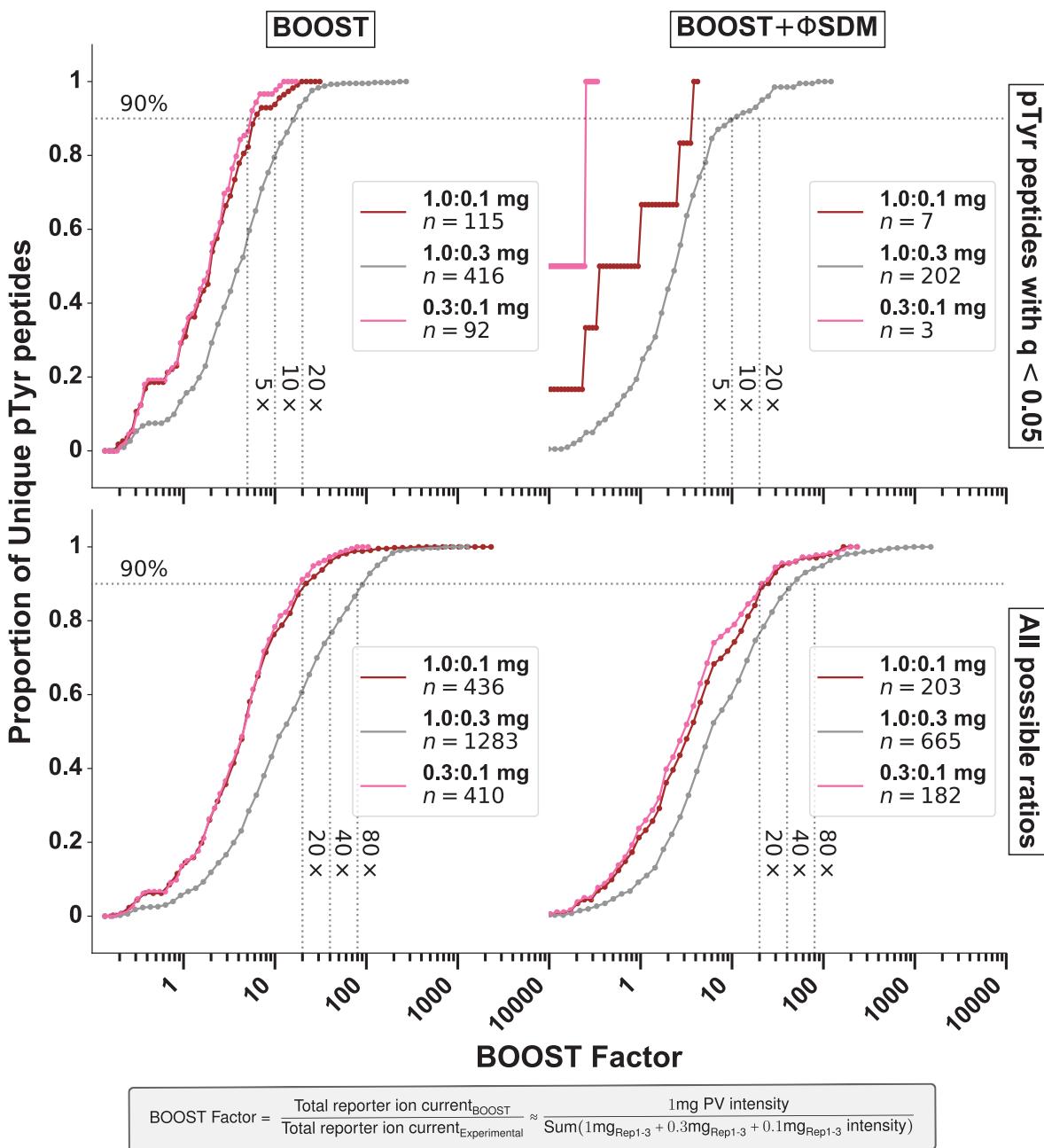
Supporting Figure 11: With ΦSDM disabled, the peroxanate BOOST channel dramatically increases the number of unique pTyr peptide PSMs observed as compared to a 1.0 mg Control channel. A Venn diagram showing the overlap of unique pTyr peptide PSMs between the BOOST and 1.0 mg Control experiments (with ΦSDM disabled). Volcano plots show $-\log_{10}(q\text{-value})$ as a function of $\log_{10}(\text{Intensity Ratio})$ for unique pTyr peptide PSMs 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 ΦSDM disabled.



Supporting Figure 12: The pervanadate BOOST channel increases the number of unique pTyr peptide PSMs observed when ΦSDM is enabled, although few peptide PSMs are observed in low abundance samples. A Venn diagram showing the overlap of unique pTyr peptide PSMs between the BOOST+ΦSDM and 1.0 mg Control+ΦSDM experiments. Volcano plots show $-\log_{10}(q\text{-value})$ as a function of $\log_{10}(\text{Intensity Ratio})$ for unique pTyr peptide PSMs 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 ΦSDM enabled.



Supporting Figure 13: Enabling ΦSDM results in lower yield in both pervanadate BOOST and 1.0 mg Control conditions. Venn diagrams showing the number of unique pTyr peptide PSMs observed when ΦSDM is enabled or disabled using (A) pervanadate BOOST samples, and (B) 1.0 mg Control samples.



$$\text{BOOST Factor} = \frac{\text{Total reporter ion current}_{\text{BOOST}}}{\text{Total reporter ion current}_{\text{Experimental}}} \approx \frac{1\text{mg PV intensity}}{\text{Sum}(1\text{mg}_{\text{Rep1-3}} + 0.3\text{mg}_{\text{Rep1-3}} + 0.1\text{mg}_{\text{Rep1-3}} \text{ intensity})}$$

Supporting Figure 14: Enabling ΦSDM decreases quantitation depth, particularly in low abundance samples. Cumulative distribution of BOOST factors for unique pTyr peptides identified in the pervanadate BOOST experiments with ΦSDM disabled or with ΦSDM enabled for pTyr peptides with a statistically significant ratio ($q < 0.05$) or for all calculable ratios. For each cumulative distribution, the range of BOOST factors are split into 50 bins of equal size on a \log_{10} scale.

Protein	Mouse	Human	Protein	Mouse	Human	Protein	Mouse	Human	Protein	Mouse	Human
Akt2	Y122	Y122	GADS	Y45	Y45	p85 α	Y470	Y470	TCR ζ	Y72	Y72
CARD11	Y489	Y489		Y218	Y222		Y688	Y688		Y83	Y83
Cbl-b	Y363	Y363 [^]	Grb2	Y209	Y209	p85 β	Y458	Y464		Y111	Y111
	Y763	Y763	GSK3 β	Y216	Y216 ^{&}	PAK1	Y142	Y142		Y123	Y123
CD28	Y189	Y191	Itk	Y40	Y40		Y153	Y153		Y142	Y142
	Y204	Y206		Y126	Y120		Y474	Y474 ⁺	Tec	Y153	Y153
	Y207	Y209		Y226	Y220	PAK2	Y130	Y130		Y205	Y206
CD3 δ	Y149	Y149		Y243	Y237		Y139	Y139		Y227	Y228
	Y160	Y160		Y517	Y512		Y453	Y453 ⁺		Y280	Y281
CD3 ϵ	Y170	Y188	Jnk1	Y185	Y185 [#]	PAK6	Y366	Y365		Y518	Y519
	Y181	Y199	Jnk2	Y185	Y185	PD-1	Y225	Y223	Vav1	Y110	Y110
CD3 γ	Y160	Y160	Jnk3	Y223	Y223 [#]	PKC θ	Y28	Y28		Y192	Y192
	Y171	Y171	LAT	Y46	Y45		Y545	Y545		Y541	Y541
CD45	Y631	Y640		Y195	Y220	PLC γ 1	Y210	Y210		Y791	Y791
	Y672	Y681	Lck	Y192	Y192		Y472	Y472	Vav2	Y142	Y142
	Y678	Y687		Y394	Y394 [*]		Y771	Y771	Vav3	Y141	Y141
	Y680	Y689		Y414	Y414		Y775	Y775		Y217	Y217
	Y711	Y720		Y470	Y470		Y783	Y783	Zap70	Y69	Y69
	Y754	Y763		Y505	Y505		Y1003	Y1003		Y87	Y87
	Y781	Y790	NCK1	Y13	Y13		Y1253	Y1253		Y164	Y164
	Y852	Y861		Y55	Y55	RHOA	Y66	Y66 [%]		Y178	Y178
	Y871	Y880		Y105	Y105	SHP-1	Y61	Y61		Y198	Y198
	Y937	F946	NCK2	Y110	Y110		Y64	Y64		Y209	Y209
	Y969	Y978	NF κ B-p105	Y238	Y240		Y213	Y213		Y211	Y211
	F971	Y980	NFAT1	Y754	Y752		Y214	Y214		Y221	Y221
CDC42	Y64	Y64 [%]	NFAT4	Y86	Y86		Y276	Y276		Y248	Y248
CDK4	Y17	Y17		Y150	Y150		Y301	Y301		Y290	Y292
CTLA-4	Y201	Y201	p110 α	Y317	Y317		Y306	Y306		Y314	Y315
DLG1	Y399	Y399	p110 δ	Y523	Y524		Y374	Y374		Y396	Y397
	Y761	Y760	p38 α	Y182	Y182		Y377	Y377		Y491	Y492
	Y785	Y784	p38 β	Y182	Y182		Y536	Y536		Y492	Y493
Erk1	Y205	Y204	p38 γ	Y185	Y185		Y541	Y541		Y505	Y506
Erk2	Y185	Y187	p55 γ	Y202	Y202		Y564	Y564		Y596	Y597
Fyn	Y28	Y28	p85 α	Y76	Y76	SLP76	Y173	Y173		Y597	Y598
	Y214	Y214 ^{\$}		Y416	Y416		Y483	Y483			
	Y420	Y420 [*]		Y452	Y452	TAK1	Y558	Y585			
	Y440	Y440 [!]		Y467	Y467	TCR ζ	N64	Y64			

Supporting Figure 15: Comparison of pTyr sites identified using BOOST in primary T cells from mice and pTyr sites identified using BOOST in Jurkat T cells. Flanking sequences (phosphorylation site ± 7 amino acids) and phosphorylation sites for each protein in the Kyoto Encyclopedia of Genes and Genomes T cell receptor signaling pathway were manually curated from PhosphoSitePlus[®]³ for humans and mice. Flanking sequences for each peptide in the Mouse-BOOST and Jurkat-BOOST datasets were compared with the manually curated KEGG TCR/PhosphoSitePlus flanking sequences and filtered for unique sites. Gene names are colored purple. Phosphotyrosine sites identified in mice are colored red. Phosphotyrosine sites identified in Jurkat T cells are colored green. Sites that were not identified either mice or Jurkat T cells are colored grey. PSMs that can be assigned to multiple proteins: [^]Cbl-B/Cbl | [%]CDC42/RHOA | ^{\$}Fyn/Yes1 | ^{*}Fyn/Yes1/Src/Lck | [!]Fyn/Yes1/Src | [&]GSK3 β /GSK3 α | [#]Jnk1/Jnk3 | ⁺PAK1/PAK2.

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