

CORRECTION

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# Correction to: Phospho-heavy-labeled-spiketide FAIMS stepped-CV DDA (pHASED) provides real-time phosphoproteomics data to aid in cancer drug selection

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**Correction to: *Clinical Proteomics* (2022) 19:48**  
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Unfortunately, in the original publication of the article, the following errors were identified after online publication of the article.

The Additional file 2 was published with only one table (Table S14), whereas the remaining Tables S1-S17 were omitted. This error was caused due to typesetting mistake.

In Abstract, line 11, the text that reads as “phospho-heavy-labeled-spiketide FAIMS Stepped-CV DDA

(pHASED)” should read as “hospho-heavy-labeled-spiketide FAIMS stepped-CV DDA (pHASED)”.

The original article has been corrected.

## Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12014-023-09406-z>.

**Additional file 2: Table S1.** SBDS heavy-labeled phosphorylated peptide standards. **Table S2.** Common and unique phosphoproteins identified across all four CVs based on PSM acquisition. **Table S3.** High confidence modification sites identified in LFQ ( $p < 0.01$ ). **Table S4.** High confidence modification sites identified in pHASED ( $p < 0.01$ ). **Table S5.** Unique and common phosphoproteins identified in LFQ and pHASED datasets. **Table S6.** Phosphorylated master protein kinases identified in LFQ dataset ( $p < 0.01$ ). **Table S7.** Phosphorylated master protein kinases identified in pHASED dataset ( $p < 0.01$ ). **Table S8.** FLT3-D835 mutations associated with resistance to tyrosine kinase FLT3 inhibitors. **Table S9.** Kinase-Substrate analysis of LFQ dataset for resistant cells in comparison to FLT3-ITD ( $\log_2$  fold change $\pm 0.5$ ). **Table S10.** Kinase-Substrate analysis of pHASED data?set for resistant cells in comparison to FLT3-ITD ( $\log_2$  fold change $\pm 0.5$ ). **Table S11.** Canonical pathways identified as significantly associated with LFQ dataset for resistant cells in comparison to FLT3-ITD. **Table S12.** Canonical pathways identified as significantly associated with pHASED dataset for resistant cells in comparison to FLT3-ITD. **Table S13.** Kinase activity inferred by KSEA analysis of phosphorylation changes in pHASED dataset ( $\log_2 \pm 0.5$ ,  $p \leq 0.05$ ) for resistant cells in comparison to FLT3-ITD. **Table S14.** Mutation-specific response to sorafenib. IC50 compared to FLT3-ITD. **Table S15.** Bliss Synergy scores for sorafenib in combination with KU-60019 at different doses. **Table S16.** Unique ATM substrates identified with increased phosphorylation ( $\log_2 \geq 0.5$ ) in pHASED dataset for resistant cells in comparison to FLT3-ITD. **Table S17.** Vector mutations in FLT3 gene.

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### **Reference**

1. Staudt, D.E., Murray, H.C., Skerrett-Byrne, D.A. et al. Phospho-heavy-labeled-spiketide FAIMS stepped-CV DDA (pHASED) provides real-time phosphoproteomics data to aid in cancer drug selection. *Clin Proteom* 19, 48 (2022). <https://doi.org/10.1186/s12014-022-09385-7>