Clinical Proteomics

CORRECTION

Open Access

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

Dilana E. Staudt[1,2], Heather C. Murray[1,2], David A. Skerrett-Byrne[3,4], Nathan D. Smith[5], M. Fairuz B. Jamaluddin[1], Richard G. S. Kahl[1], Ryan J. Duchatel[1,2], Zacary P. Germon[1,2], Tabitha McLachlan[1,2], Evangeline R. Jackson[1,2], Izac J. Findlay[1,2], Padraic S. Kearney[1,2], Abdul Mannan[1,2], Holly P. McEwen[1,2], Alicia M. Douglas[1], Brett Nixon[3,4], Nicole M. Verrills[1,2] and Matthew D. Dun[1,2*]

Correction to: Clinical Proteomics (2022) 19:48
https://doi.org/10.1186/s12014-022-09385-7

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 identifed across all four CVs based on PSM acquisition. **Table S3**. High confdence modifcation sites identifed in LFQ ($p < 0.01$). **Table S4**. High confdence modifcation sites identifed in pHASED ($p < 0.01$). **Table S5**. Unique and common phosphoproteins identifed in LFQ and pHASED datasets. **Table S6**. Phosphorylated master protein kinases identifed in LFQ dataset ($p < 0.01$). **Table S7**. Phosphorylated master protein kinases identifed 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 (log2 fold change±0.5). **Table S10**. Kinase-Substrate analysis of pHASED data?set for resistant cells in comparison to FLT3-ITD (log2 fold change±0.5). **Table S11**. Canonical pathways identifed as signifcantly associated with LFQ dataset for resistant cells in comparison to FLT3-ITD. **Table S12**. Canonical pathways identifed as signifcantly 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 (log2±0.5, p≤0.05) for resistant cells in comparison to FLT3-ITD. **Table S14**. Mutation-specifc 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 identifed with increased phosphorylation (log2≥0.5) in pHASED dataset for resistant cells in comparison to FLT3-ITD. **Table S17**. Vector mutations in FLT3 gene.

The online version of the original article can be found at https://doi.org/10.1186/s12014-022-09385-7.

*Correspondence:
Matthew D. Dun
matt.dun@newcastle.edu.au
[1]School of Biomedical Sciences and Pharmacy, College of Health, Medicine and Wellbeing, University of Newcastle, Callaghan, NSW 2308, Australia
[2]Precision Medicine Research Program, Hunter Medical Research Institute, New Lambton Heights, NSW 2305, Australia
[3]School of Environmental and Life Sciences, College of Engineering, Science and Environment, University of Newcastle, Callaghan, NSW 2308, Australia
[4]Infertility and Reproduction Research Program, Hunter Medical Research Institute, New Lambton Heights, NSW 2305, Australia
[5]Analytical and Biomolecular Research Facility (ABRF), Research Services, University of Newcastle, Callaghan, NSW 2308, Australia

Published online: 08 April 2023

Publisher's Note

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