Author Correction: Informed-Proteomics: open-source software package for top-down proteomics

Jungkap Park,

Paul D Piehowski,

Christopher Wilkins,

Mowei Zhou,

Joshua Mendoza,

Grant M Fujimoto,

Bryson C Gibbons,

Jared B Shaw,

Yufeng Shen,

Anil K Shukla,

Ronald J Moore,

Tao Liu,

Vladislav A Petyuk,

Nikola Toli ,

Ljiljana Paša-Toli ,

Richard D Smith,

Samuel H Payne,

Sangtae Kim

In the version of this article initially published, the authors erroneously reported the search mode that was used for ProSightPC 3.0 in the Online Methods and in Supplementary Table 3.

The results presented in Fig. 5 were obtained with 'absolute mass' search mode, not 'biomarker discovery' search mode. The 'biomarker discovery' search mode of ProSightPC 3.0 looks for subsequences of those contained in the annotated proteoform database (e.g., truncated forms from degradation and/or cleavage). This search mode is expected to generate similar numbers of identifications as Informed-Proteomics, but is also expected to take dramatically longer (~480 CPU hours). Unfortunately, because of these heavy computational requirements, the authors were unable to complete an analysis using this search mode. They chose to use 'absolute mass' mode to illustrate the effect of search mode and database choice on the results. 'Absolute mass' mode is the most restrictive of the search modes illustrated in Fig. 5, as it searches only for proteoforms explicitly listed in the proteoform database within a user-defined mass tolerance.

In addition, in the supplementary information originally published online, Supplementary Table 3 incorrectly stated that ProSightPC v3.0 was used in 'biomarker discovery' mode.

'Absolute mass' mode was the mode actually used in this comparison. These errors have been corrected in the HTML and PDF versions of this article and in the associated supplementary information.