Corrigendum: Proteome-wide profiling of protein assemblies by cross-linking mass spectrometry

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In the version of this article initially published, the number of interprotein cross-links was overstated, as protein grouping during cross-link categorization was not properly considered. 314 intraprotein cross-links were mistakenly annotated as interprotein cross-links if shared peptides between different protein entries were involved. The cross-links were reannotated after protein grouping, and cross-links were removed from contaminants (e.g., keratin).

The sentence in the abstract, "This approach allowed us to detect 2,179 unique cross-links (1,665 intraprotein cross-links at a 5% false discovery rate (FDR) and 514 interprotein cross-links at 1% FDR) in HeLa cell lysates," has been changed to "This approach allowed us to detect 2,426 unique cross-links at a 5% FDR (2,013 intraprotein and 413 interprotein cross-links) or 1,822 cross-links at a 1% FDR (1,622 intraprotein and 200 interprotein cross-links), indicating the detection of 326 or 134 protein-protein interactions at 5% FDR or 1% FDR, respectively, in HeLa cell lysates."

The sentence, "We unambiguously identified 2,179 cross-links (1,665 intraprotein cross-links at 5% FDR and 514 interprotein cross-links at 1% FDR) in HeLa cell lysates using the whole human proteome database (~40,000 entries) as the search space," has been changed to, "We unambiguously identified 2,426 total cross-links at 5% FDR or 1,822 total cross-links at 1% FDR in HeLa cell lysates using the whole human proteome database (~40,000 entries) as the search space."

The sentence in the Results, "At 5% FDR, 2,473 unique cross-links were identified via the combined CID-ETD strategy, whereas 1,113 unique cross-links were identified in CID-only analysis, which corresponds to a difference of more than twofold (**Fig. 2a**)," has been changed to, "At 5% FDR, 2,426 unique cross-links were identified via the combined CID-ETD strategy, whereas 1,089 unique cross-links were identified in CID-only analysis, which corresponds to a difference of more than twofold (**Fig. 2a**)."

The sentence in the Results, "When we repeated the analysis with a more stringent FDR cutoff of 1%, the discrepancy between CID-ETD and CID-only data increased to threefold (1,867 cross-links identified with CID-ETD and 594 cross-links identified with CID only) (**Fig. 2a**)," has been changed to, "When we repeated the analysis with a more stringent FDR cutoff of 1%, the discrepancy between CID-ETD and CID-only data increased to threefold (1,822 cross-links identified with CID-ETD and 580 cross-links identified with CID only) (**Fig. 2a**)."

The sentence in the Results, "On the basis of the statistical analysis of the distribution of target and decoy hits, we decided to use a more stringent FDR cutoff for interprotein cross-links than for intraprotein cross-links. Thus the reported 2,179 cross-links were filtered at 5% FDR for intraprotein cross-links (1,665 cross-links) and at 1% FDR for interprotein cross-links (514 cross-links) (**Fig. 2a**)," has been changed to, "On the basis of the statistical analysis of the distribution of target and decoy hits, we suggest using a more stringent FDR cutoff for interprotein cross-links compared than for intraprotein cross-links. All protein-protein interactions we detected based on our interprotein cross-link findings are reported in **Supplementary Data 2**."

We added this sentence about our reanalysis in the Online Methods section: "Cross-links were categorized as 'interprotein' if the two linked peptides derived from two different protein groups (i.e., a set of proteins containing shared peptides); otherwise, the cross-link was annotated as 'intraprotein'. We note that if homo-oligomers or complexes wherein multiple copies of a single protein are present (co-)exist, cross-links comprising two peptides of the same protein group may either be 'intermolecular' (between homo-oligomeric subunits) or 'intramolecular' (within one subunit)." We also added the sentences, "Cross-links from contaminants (e.g., keratin) were removed" and "Protein-protein interactions detected in our cross-linking data set are reported in **Supplementary Data 2**. Annotated spectra for interprotein cross-links are available in **Supplementary Data 3**; annotated spectra for intraprotein cross-links are available in **Supplementary Data 4**."

Figure 2 has been replaced to correctly reflect the results of our updated reanalysis described above.

The **Supplementary Data** "all 2,179 crosslinks" table has been replaced with a new table, named **Supplementary Data 1**, which reports the crosslinks identified in our reanalysis. Another table, named **Supplementary Data 2**, has been added to report the protein-protein interactions detected in the cross-linking data set. The two folders containing annotated mass spectra in the "Supplementary Data" zip file have been renamed **Supplementary Data 3** and **4**.

These errors have been corrected in the PDF and HTML versions of the article.