JACS
JOURNAL OF THE AMERICAN CHEMICAL SOCIETY

Addition/Correction

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Correction to "Chemoproteomic Discovery of Cysteine-Containing Human Short Open Reading Frames

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J. Am. Chem. Soc. **2013**, *135*, 16750−16753. DOI: 10.1021/ja406606j

Page 16571. In the fifth paragraph of the Communication, the sentences, "On-bead trypsin digestion was performed, and unlabeled peptides were eluted and analyzed by offline electrostatic hydrophilic repulsion liquid chromatography (ERLIC) fractionation followed by LC-MS/MS.[1,20] The remaining bead-bound labeled peptides were subsequently released from the beads by the addition of TEV protease and analyzed by MudPIT-LC-MS/MS.[21] should read as follows: "On bead trypsin digestion was performed, and the remaining bead-bound labeled peptides were subsequently released from beads by the addition of TEV protease and analyzed by MudPIT-LC-MS/MS.[1,20,21]" This correction more accurately reflects the experiment that was performed.

Page 16752. The total number of SEPs in Figure 3 is incorrect. The correct figure is shown here.

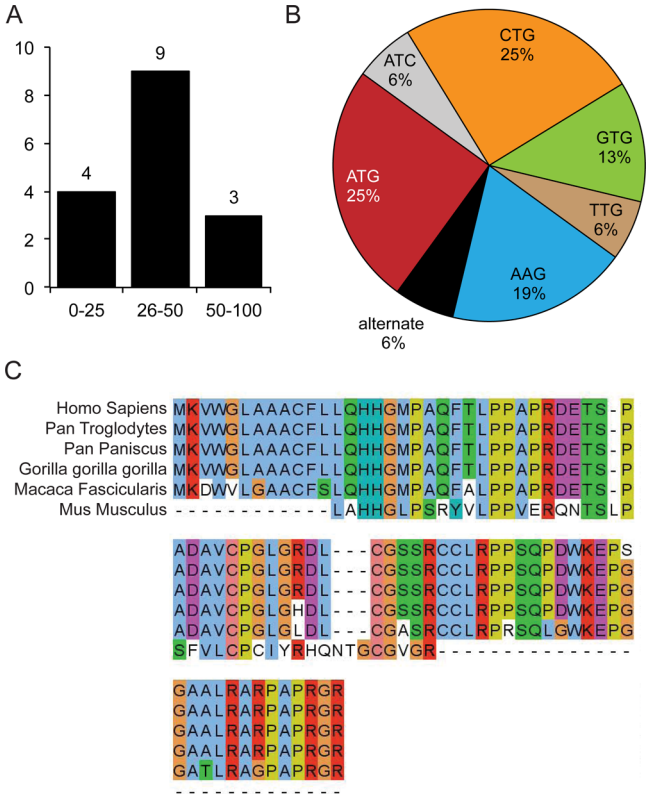

Figure 3. ccSEP overview. (A) Distribution of ccSEPs by their length in amino acids. SEP length was determined using the distance from an upstream in-frame AUG start codon to a downstream in-frame stop codon; when no in-frame AUG was present, a near-cognate start codon or stop codon was used instead. (B) While AUG is the predominant start codon for the production of ccSEPs, near-cognate start codons (i.e., one base different from AUG) are also common. (C) TSP-SEP is strongly conserved among several species of primates, suggesting this SEP may be functional.

Published: January 2, 2014

