PLOS ONE

CORRECTION

Correction: Nitrosothiol-Trapping-Based Proteomic Analysis of S-Nitrosylation in Human Lung Carcinoma Cells

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The concentration unit for LPS is listed incorrectly in the third sentence under the subheading "Cell culture and treatment" in the Materials and Methods section. The correct sentence is: For this purpose, cells were serum starved for 24 h and then stimulated for 72 h with or without a cytokine mix that included lipopolysaccharide (LPS, 0.5 μg/ml), tumor necrosis factor (TNFα, 20 ng/ml), interferon-γ (IFN-γ, 10 ng/ml) and interleukin 1β (IL-1β, 10 ng/ml).

The concentration unit for LPS in the caption for Fig 1C is also incorrect. Please see the corrected Fig 1 caption here.

Citation: Ben-Lulu S, Ziv T, Weisman-Shomer P, Benhar M (2017) Correction: Nitrosothiol-Trapping-Based Proteomic Analysis of S-Nitrosylation in Human Lung Carcinoma Cells. PLoS ONE 12(6): e0179803. https://doi.org/10.1371/journal.pone.0179803

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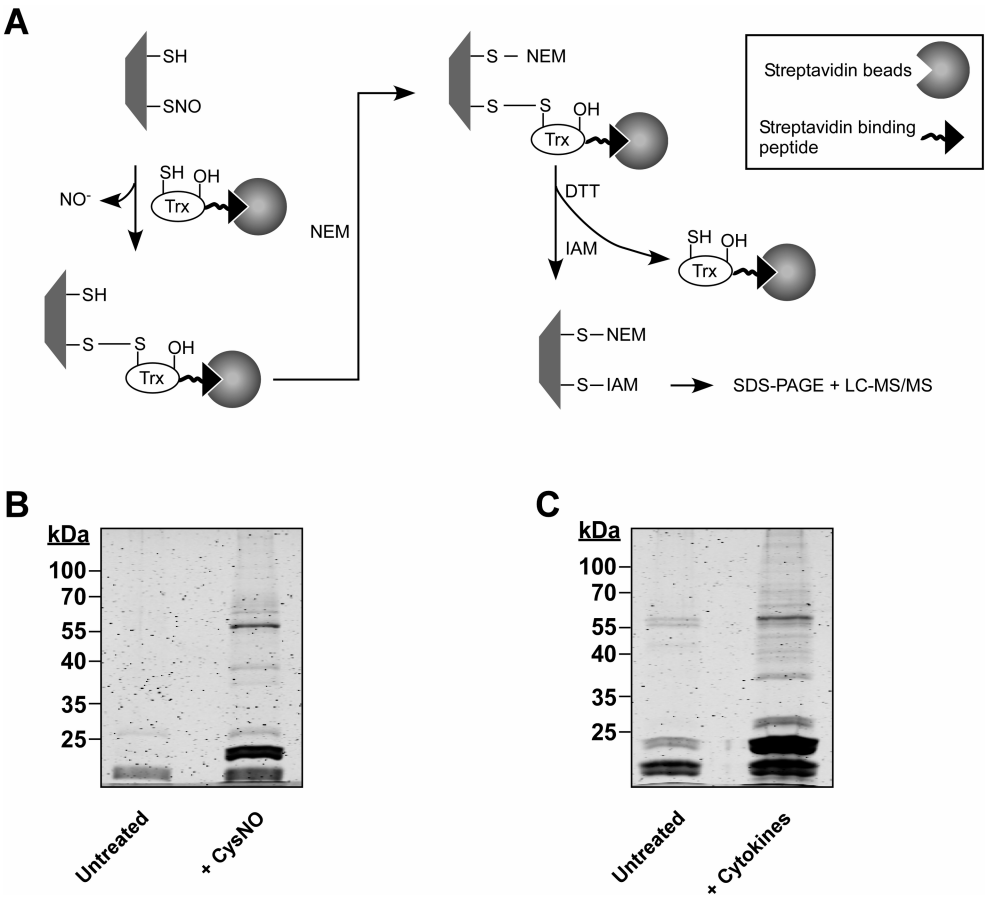

Fig 1. SNO trapping-based analysis of S-Nitrosylation in A549 cells. (A) Schematic of the proteomic approach. Digitonin cell lysates, obtained from A549 treated with NO donor or with cytokines are incubated with a thioredoxin (Trx) trap mutant, Trx(C35S). In the trap mutant the resolving cysteine is replaced by serine (-OH). The protein also contains a streptavidin binding peptide. Trx(C35S) forms mixed disulfide bonds with nitrosylated substrates and the resulting complexes are pulled-down using avidin agarose. Identification of nitrosylation sites is assisted by differential thiol labeling, involving the sequential application of N-ethylmaleimide (NEM) and iodoacetamide (IAM). Proteins captured in the Trx pull-down are analyzed by SDS-PAGE or liquid chromatography-tandem mass spectrometry (LC-MS/MS). (B) A549 cells were treated with or without 500 μM S-nitrosocysteine (CysNO) for 10 min and thereafter digitonin lysates were incubated with Trx(C35S). Proteins captured by Trx were released by DTT and then analyzed by SDS-PAGE. Gels were stained with Krypton fluorescent protein stain and visualized using the Odyssey infrared imaging system. (C) A549 cells were treated for 72 h with LPS (0.5 μg/ml) and a cytokine mixture that included TNFα (20 ng/ml), IFN-γ (10 ng/ml) and IL-1β (10 ng/ml). Trx-based trapping of nitrosylated proteins was performed as in B.

https://doi.org/10.1371/journal.pone.0179803.g001

Reference

1. Ben-Lulu S, Ziv T, Weisman-Shomer P, Benhar M (2017) Nitrosothiol-Trapping-Based Proteomic Analysis of S-Nitrosylation in Human Lung Carcinoma Cells. PLoS ONE 12(1): e0169862. https://doi.org/10.1371/journal.pone.0169862 PMID: 28081246