

CORRECTION

# Correction: Modified TCA/acetone precipitation of plant proteins for proteomic analysis

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S1–S3 Figs are incorrect. S1 Fig should be the 2D gels of maize embryos. The images for S2 and S3 Figs were incorrectly duplicate. Please see the corrected S1–S3 Figs below.

## Supporting information

**S1 Fig. Comparison of 2DE protein profiles of maize embryo proteins extracted using two methods.** Shown were two independent experiments. Left panel: the modified TCA/acetone precipitation. Right panel: the classical TCA/acetone precipitation. Spots with increased abundance are indicated in red. About 800 µg of proteins were resolved in pH 4–7 (linear) strip by IEF and then in 12.5% gel by SDS-PAGE. Proteins were visualized using CBB. (TIF)

**S2 Fig. Comparison of 2DE protein profiles of maize root proteins extracted using two methods.** Shown were three independent experiments. Left panel: the modified TCA/acetone precipitation. Right panel: the classical TCA/acetone precipitation. Spots with increased abundance are indicated in red. About 800 µg of proteins were resolved in pH 4–7 (linear) strip by IEF and then in 12.5% gel by SDS-PAGE. Proteins were visualized using CBB. (TIF)

**S3 Fig. Comparison of 2DE protein profiles of maize leaf proteins extracted using two methods.** Shown were three independent experiments. Left panel: the modified TCA/acetone precipitation. Right panel: the classical TCA/acetone precipitation. Spots with increased abundance are indicated in red. About 800 µg of proteins were resolved in pH 4–7 (linear) strip by IEF and then in 12.5% gel by SDS-PAGE. Proteins were visualized using CBB. (TIF)



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## Reference

1. Niu L, Zhang H, Wu Z, Wang Y, Liu H, Wu X, et al. (2018) Modified TCA/acetone precipitation of plant proteins for proteomic analysis. PLoS ONE 13(12): e0202238. <https://doi.org/10.1371/journal.pone.0202238>. PMID: 30557402