Supplement to:

MoMo: Discovery of statistically significant post-translational modification motifs

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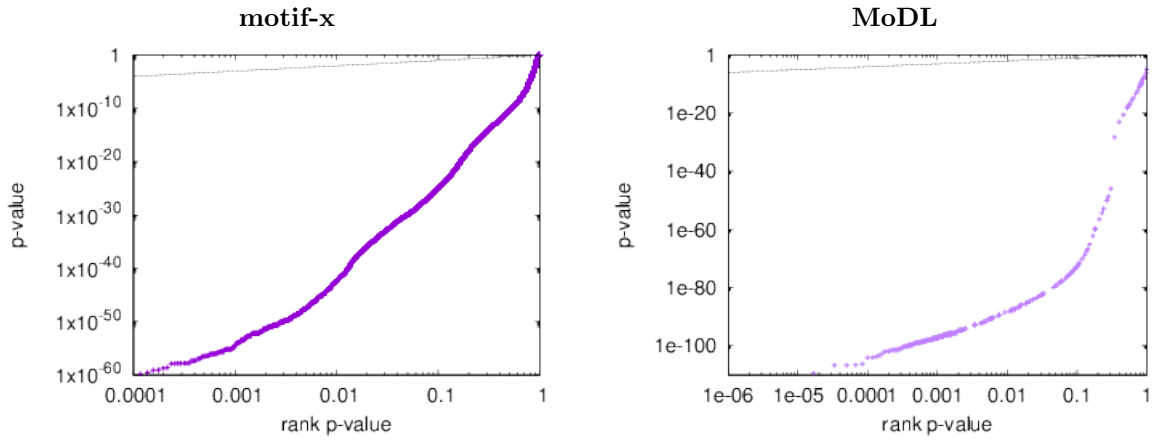[*]To whom correspondence should be addressed.

Figure 1: **Inaccuracy of MoMo p-values when background peptides are from the proteome.** The two panels show empirical assessments (Q-Q plots) of the statistical accuracy of the p-values reported by MoMo's improved implementations of motif-x (left panel) and MoDL (right panel), respectively, when the background peptides are from the *Plasmodium falciparum* proteome. The modified peptides are shuffled versions of the peptides in [1] Supplemental Data 2 `pr8b00062_si_003.xlsx`. MoMo parameters are `--db-background --score-threshold 0.001`. The sorted adjusted p-values ($Y = 1-(1-p_i)^n$, where p_i is the unadjusted p-value and n is the number of independent tests), are plotted against the rank p-values ($X = 1/(r_i+1)$), where r_i is the rank of the p-value), for 10,000 shuffled input datatsets, where shuffling conserves the central residue.

References

[1] Pease, B. N., Huttlin, E. L., Jedrychowski, M. P., Dorin-Semblat, D., Sebastiani, D., Segarra, D. T., Roberts, B. F., Chakrabarti, R., Doerig, C., Gygi, S. P., and Chakrabarti, D. (2018). Characterization of *Plasmodium falciparum* Atypical Kinase PfPK7 Dependent Phosphoproteome. *Journal of Proteome Research*, **17**, 2112–2123.