



Corrigendum: Comparative evaluation of DNase-seq footprint identification strategies

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A commentary on

Comparative evaluation of DNase-seq footprint identification strategies

by Barozzi, I., Bora, P., and Morelli, M. J. (2014). *Front. Genet.* 5:278. doi: 10.3389/fgene.2014.00278

Figure 1 of the article Comparative evaluation of DNase-seq footprint identification strategies, by Barozzi et al. (2014) contained a minor mistake, which we correct here. In panel E, the y axis ranges from 0.5 to 1 and not from 0 to 1 as indicated in the

original figure. We resubmit a corrected version of **Figure 1**.

REFERENCES

Barozzi, I., Bora, P., and Morelli, M. J. (2014). Comparative evaluation of DNase-seq footprint identification strategies. *Front. Genet.* 5:278. doi: 10.3389/fgene.2014.00278

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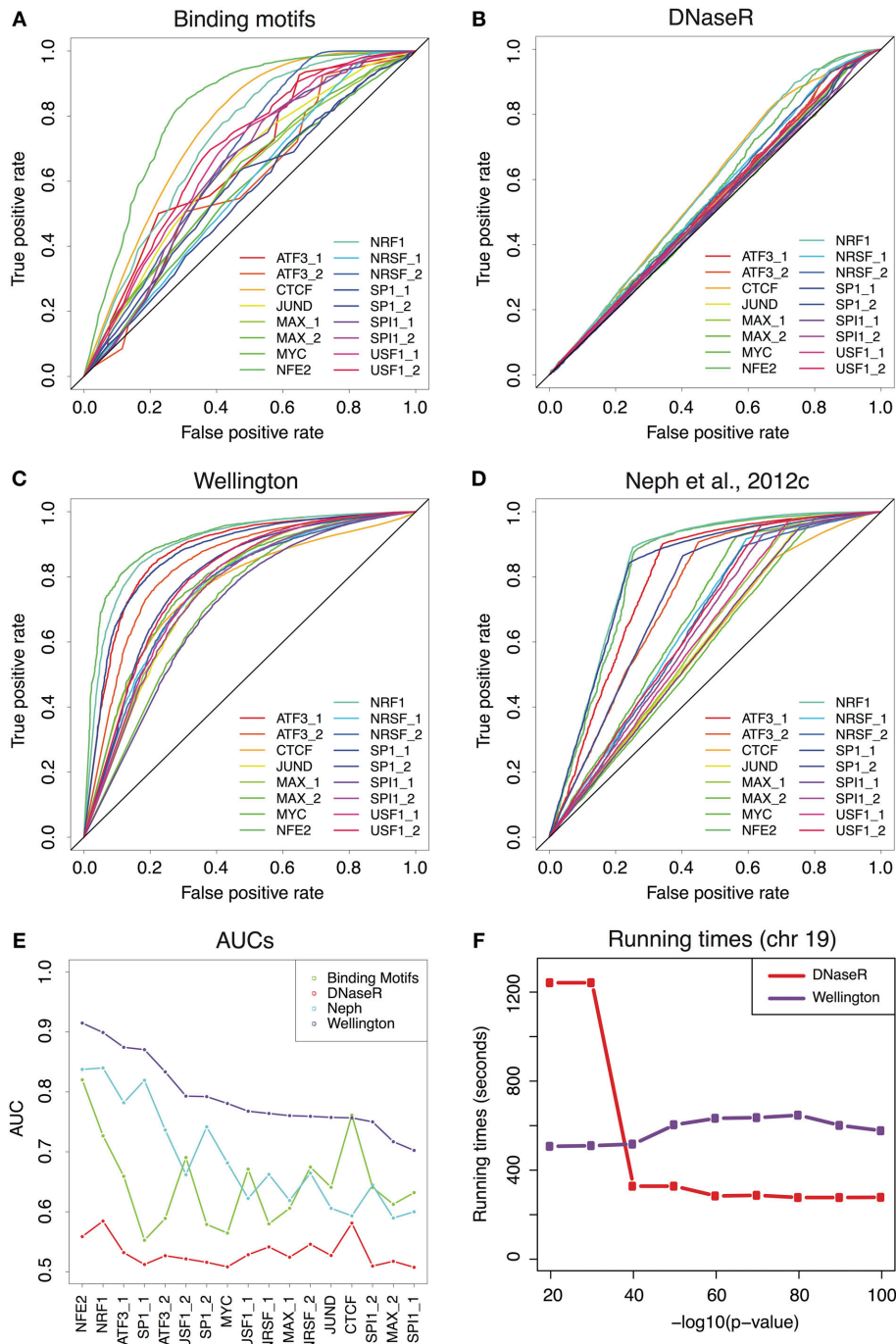


FIGURE 1 | (A) Receiver-Operator Characteristic (ROC) curves for the predictions provided by the binding motifs alone. **(B–D)** ROCs for the sets of footprints obtained by DNaseR, Wellington and for the set used in Neph et al.(2012c). **(E)** Area Under the Curve (AUC) corresponding to the ROCs of **(A–D)** Wellington scores consistently better than all the other methods. **(F)** Running times for DNaseR and Wellington on chromosome 19, for different significance thresholds.