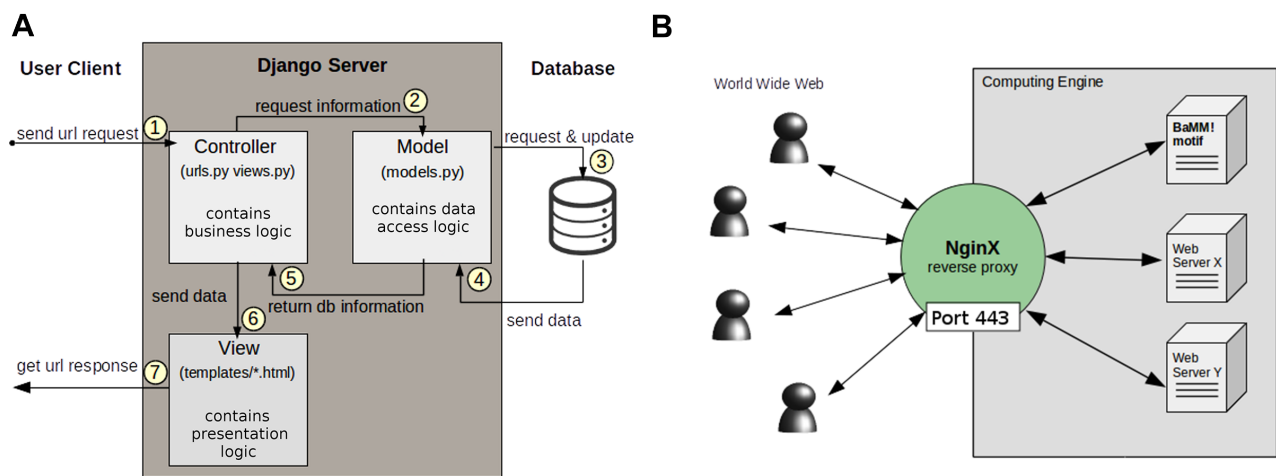


# Supplementary information for: The BaMM webserver for de-novo motif discovery and regulatory sequence analysis

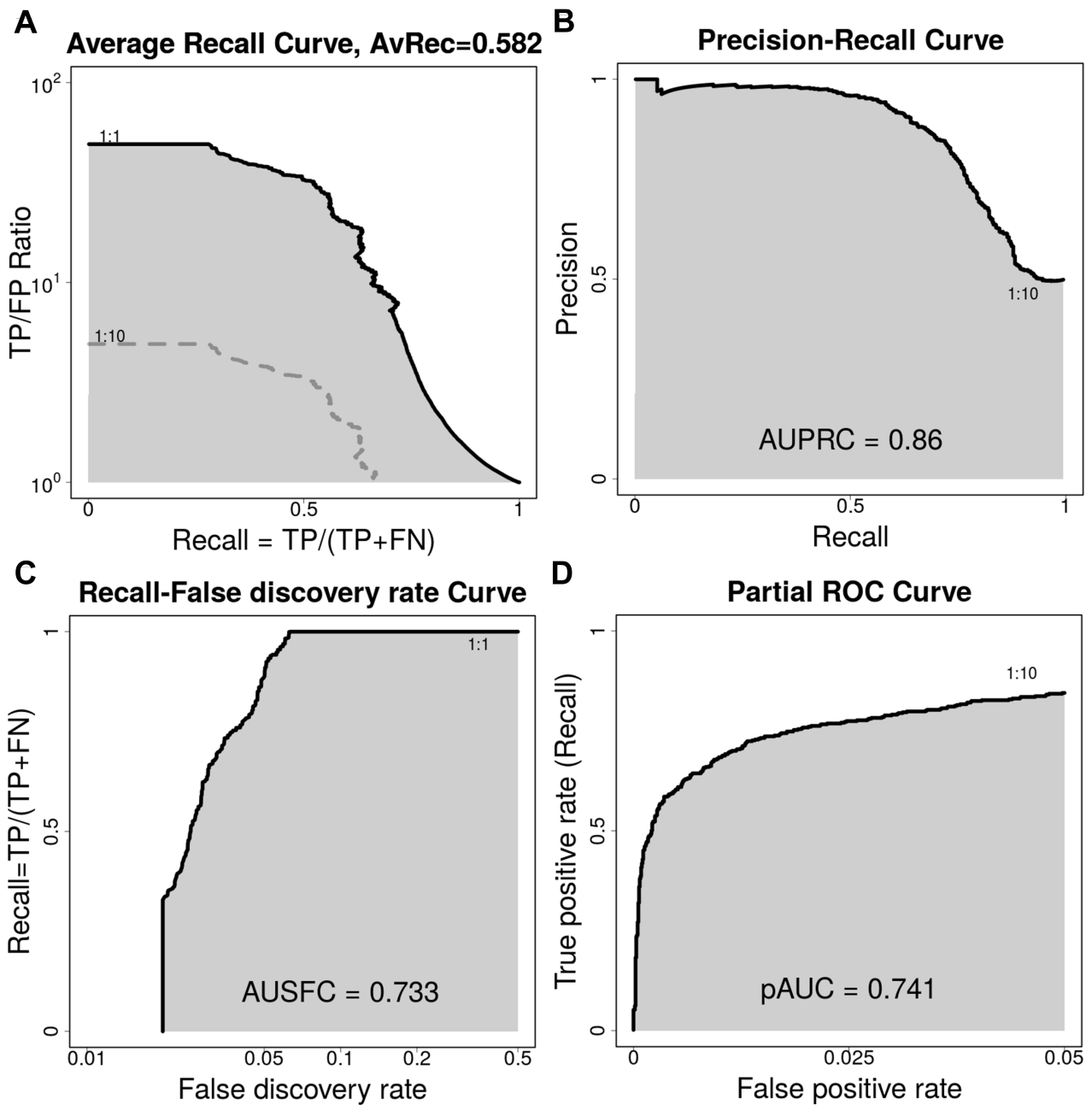
Anja Kiesel,<sup>1</sup> Christian Roth,<sup>1</sup> Wanwan Ge,<sup>1</sup> Maximilian Wess,<sup>1</sup> Markus Meier,<sup>1</sup> and Johannes Söding<sup>1,\*</sup>

<sup>1</sup>Quantitative and Computational Biology, Max Planck Institute for Biophysical Chemistry, Am Fassberg 11, 37077 Göttingen, Germany \*To whom correspondence should be addressed. Email: soeding@mpibpc.mpg.de

## SUPPLEMENTARY FIGURE



**Figure 1.** The BaMM server is built on the Django framework. (A) Scheme of Django working environment. (B) The Nginx server controls ports for secure data submission.



**Figure 2.** Comparison between different measures of motif model performance on the input dataset. (A) Recall vs. TP-to-FP ratio curve. (B) Precision-Recall curve. (C) Recall-False discovery rate curve. (D) Partial Receiver operating characteristic (ROC) curve. Definitions of axes: recall = true positive rate =  $TP / (TP + FN)$ ; false discovery rate (FDR) =  $FP / (TP + FP)$ ; precision =  $1 - FDR = TP / (TP + FP)$ ; false positive rate =  $FP / (FP + TN)$ , where TP = true positives, FP = false positives, FN = false negatives, TN = true negatives.