Supplementary Material

omiXcore: a web server for prediction of protein interactions with large RNA

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Comparison with other methods

For each RBP in our dataset (96 cases), we ranked interacting and non-interacting RNAs (10, 20, 50, 100 cases) using the experimental affinities A^{exp}. From low to high affinities, we compared *omiXcore* with *RPISeq-RF*, *RPISeq-SVM* (Muppirala *et al.*, 2011) and *Global Score* (Cirillo *et al.*, 2017). Both *RPISeq* and *Global Score* classify protein-RNA pairs into two categories (interacting / non-interacting) without considering the experimental affinities: the former uses sequence patterns for the predictions and the latter an architecture similar to *omiXcore* but with training done on PAR/HITS-CLIP data. *omiXcore* shows higher performances than *RPISeq* and *Global Score* in terms of Area under the ROC curve AUC (**Figure 1**), sensitivity (**Figure 2**), specificity (**Figure 3**) and Matthews correlation coefficient (**Figure 4**).

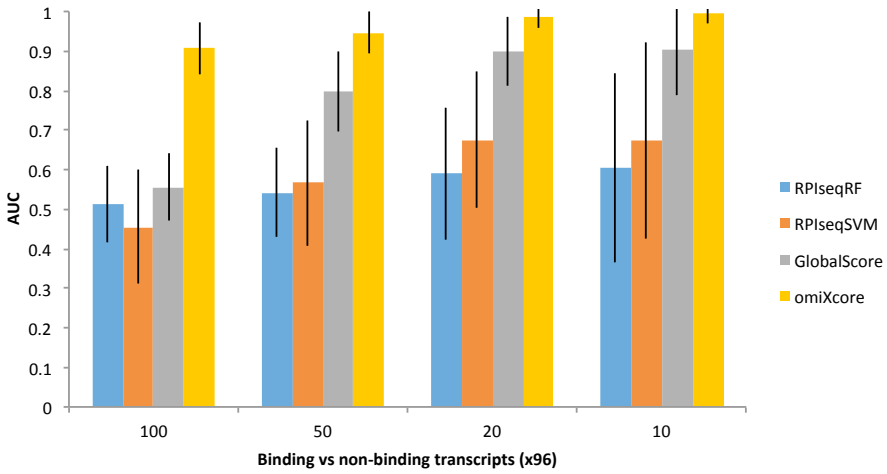

Figure 1. *We ranked interacting and non-interacting RNAs (10, 20, 50, 100 cases) using the experimental affinities* A^{exp}. *The Area under the ROC curve AUC is used to measure the performances of RPISeq-RF, RPISeq-SVM, Global Score and omiXcore. Statistics (mean and standard deviation) is carried out per RBP (96 cases in total).*

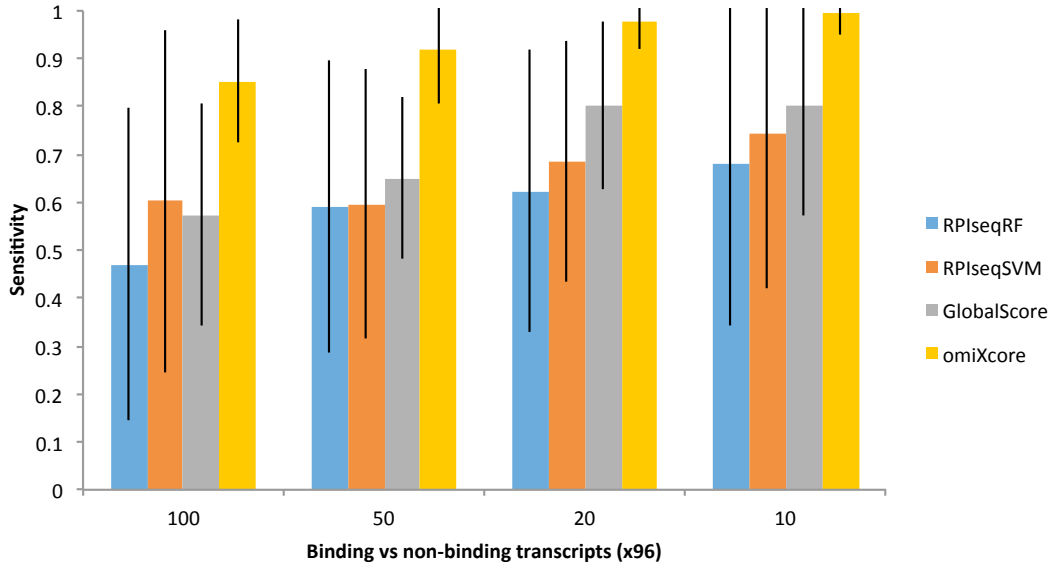

Figure 2. *Sensitivity or true positive rate for RPISeq-RF, RPISeq-SVM, Global Score and omiXcore. See* ***Figure 1*** *for further details.*

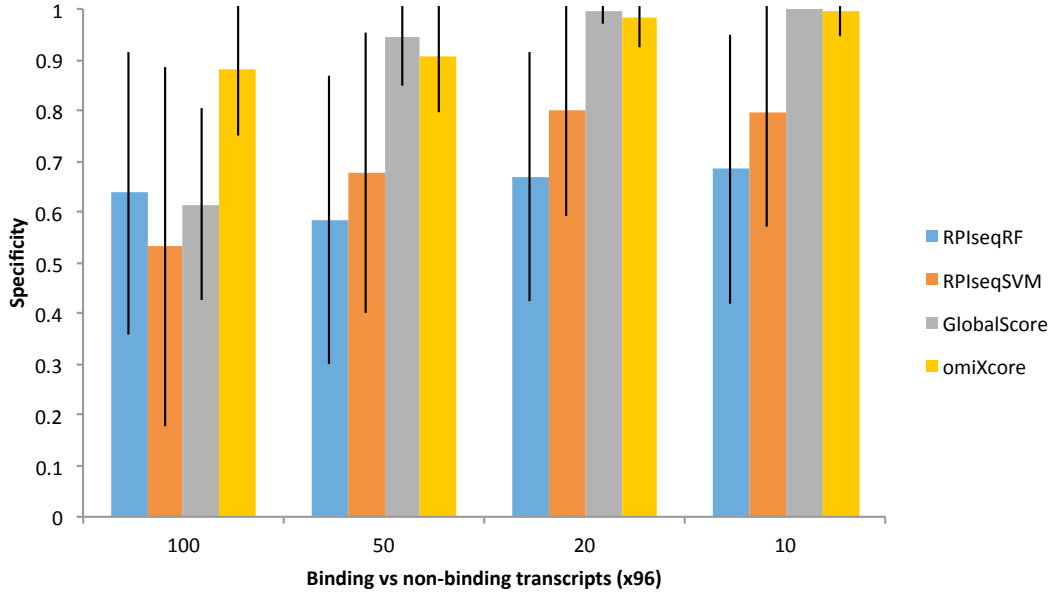

Figure 3. *Specificity or true negative rate for RPISeq-RF, RPISeq-SVM, Global Score and omiXcore. See* ***Figure 1*** *for further details.*

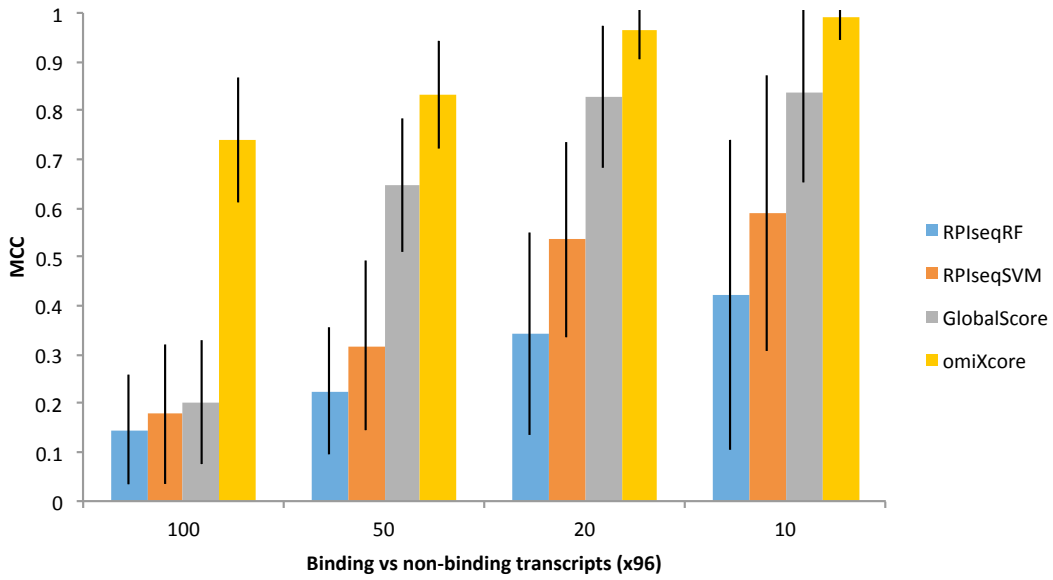

Figure 4. *Matthews correlation coefficient or MCC for RPISeq-RF, RPISeq-SVM, Global Score and omiXcore. See* ***Figure 1*** *for further details.*