


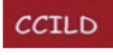


Figure S1. RPI-Seq database predicts a potential relationship between SNHG1 and CLEC7A. It shows a screenshot of the interface for the SNHG1 RNA-CLEC7A Protein Interaction Prediction tool. The resulting probabilities generated by the Random Forest (RF) classifier are 0.85, and those generated by the Support Vector Machine (SVM) classifier are 0.74.

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<h2 style="margin: 0;">RNA-Protein Interaction Prediction (RPISeq)</h2> <p style="margin: 0;">Dobbs and Honavar Laboratories</p>	
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About Datasets Related Links References Funding Contact Us	<p>Protein: MEYHPDLENLDEDEGYTQLHFDSQSNTRIAVSEKGSACAASPPWRLIAVILGILCLVILVI AVVLGTMGVLSSPCPPNWIIYEKSCYLFMSLSNSWDGSKRQCWQLGSLKIDSSNELGF IVKQVSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVS VIYDQLCSVPSYSICEKKFSM</p> <p>RNA: CUCAUUUUUCUACUGCUCGUGGUAUUACGCGCACGUUGGAACCGAAGAGAGCUCUGUUGU UGCAAUGUUCAGCCCACAAGAGCJUACUGGUGAAGGAAUGGGACAAGACCAUCUUUAUG CAAAGCCAGCGUUACAGUAAUGUUCAGCAUCUCAUAAUCUAUCCUGGGGAAUUCAGCUG CCUCCAGGGUGAAUACAGGUAAUCCUGAUGACAGUCUGCCUCUAUCUUAACAGAGCAGCU UGUUGCUAUUAACCAUUGAAAAGCCUUCAGAGCUGAGAGGUACUACUAACCAUUAACCG CUUGGCUCAAAGGGCCAGCACCUUCUCUCUAAAGCCCAAGAGGAGUUUGAGGAAAACUAG GUGUCUGUGUUCACUCCAGGCUGAAGUUACAGGUCUGAGCAAUAAGGUGUAUAAAAAAU GGAUUCUGUCUUGGAGGACUACAAGGUGAAUUUCCAGUUCUUGGACAACCUAGCUG UUGAAAAGCUUUCUGGGUUUGGGGGUUAUUUCAGAUUACCUUAAAGUGUUAGCAGACAC AGAUUAAGACACUGGGAGCAAUGAAACAGCAGUUGAGGGUUUGCUGUGUAUCACAUUUC UGUUUUUUAUCACCCCUUCCUGCAACAUUAUUUAUCUGGAAUCUACCUGCCUUUUGUU UUUUAGAUACAAGGCUUGGUUUUGUUAACCCAGGCUGGUUUCAGGCCAUAGCUUUAAGA GAUCCUCUACCCACAGAUUCCAAAGUGCUGGGAUUGCAGGUGUGAUUCAUGGCACCCAG ACUUGCUGCCUUUCUACAUGAUCCAGGCCAGAACCCAAACUCAGGCACUGUAUAGAU GACCACUUUCGUAACUACUGACCUAGCUUGUUGCCAAUUGUUGAUUGAACUCCCAUAA CUCCACUUCGUCUGUCCUUGUAUACAGCCACCUUCUGUCCCGUAUGAGCCUUUA GGUCUCCAUUUGCAUUAUGCAAUACUAGUUCUCCAUUGAGGUAGCUCUUAUCAGGCCUUG CUCUUCACUUCAAAAAGGUUCCUUGAGGACUGGCUGUCAUUUGUGUUGCUGUGUUGG UUGUUGAUGAAAAUAAUAAAUGAUUGAUUACAUAGUCCUGUUUAAAAAAAAAAAAA</p> <p>Interaction probabilities Prediction using RF classifier 0.85 Prediction using SVM classifier 0.74</p> <p>What do these probabilities mean? Interaction probabilities generated by RPISeq range from 0 to 1. In performance evaluation experiments, predictions with probabilities > 0.5 were considered "positive," i.e., indicating that the corresponding RNA and protein are likely to interact. Using this threshold, accuracies of the classifiers ranged from 87 - 90% in cross-validation evaluation experiments on benchmark datasets. When classifiers were tested on independent (blind) datasets of RPIs, accuracies of the classifiers ranged from 57 - 99%.</p> <p>Please see About/FAQs for additional details.</p>
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<p style="margin: 0;">IOWA STATE UNIVERSITY <i>Becoming the best.</i> RPISeq Version 1.0, Last updated 12/31/2011 Dobbs Lab, (515) 294 4991, usha (at) iastate.edu Copyright © 2011 Dobbs Lab. All rights reserved.</p>	