Supplementary material:
Statistical Inference Relief (STIR) feature selection

Trang T. Lê[1], Ryan J. Urbanowicz[1], Jason H. Moore[1], and Brett A. McKinney[2]

[1] *Institute for Biomedical Informatics, University of Pennsylvania, Philadelphia, PA 19104*
[2] *Tandy School of Computer Science, University of Tulsa, Tulsa, Oklahoma 74104*
[2] *Department of Mathematics, University of Tulsa, Tulsa, Oklahoma 74104*

1 Supplement 1: STIR scores versus the original difference from Relief-based scores

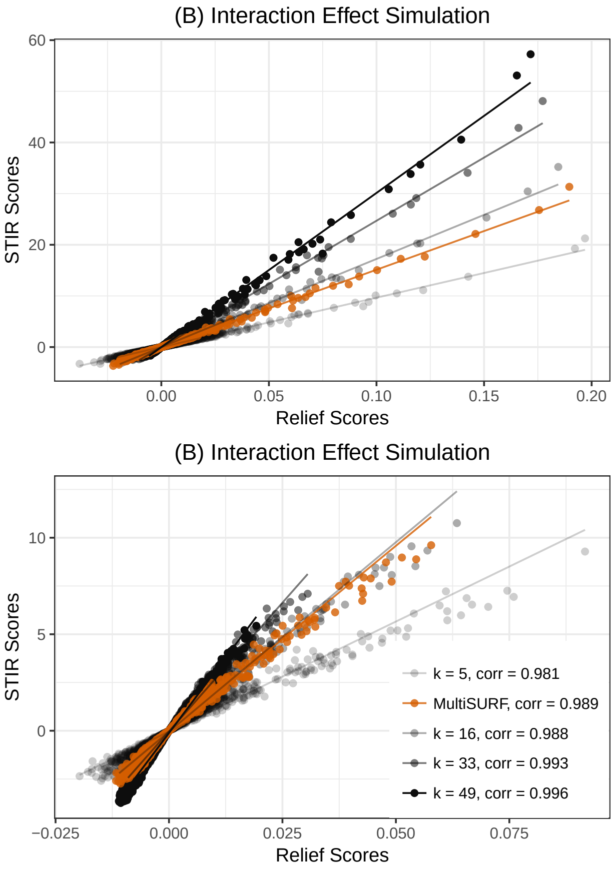

Figure 1: Correlation values of STIR pseudo t-statistic and the original Relief-based scores (diff function) are above 0.98.

2 Supplement 2: Functional interaction network

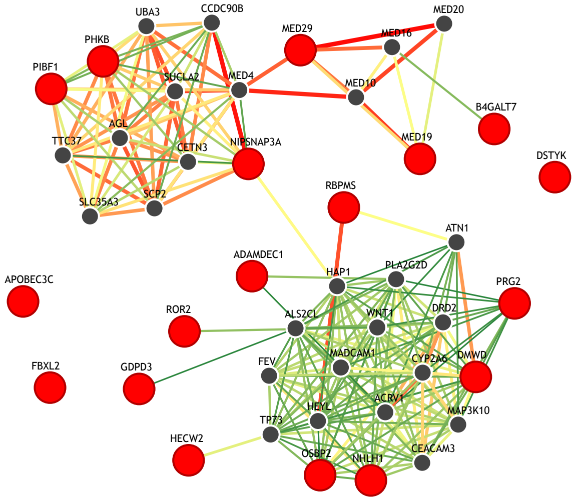

Figure 2: Predicted functional interaction network from STIR-detected seed genes (red nodes) from Table 1(main text). Additional genes (black nodes) and functional interactions predicted from the Integrative Multi-species Prediction Tool v2.0 ([1]).

References

[1] Wong, A. K., Krishnan, A., Yao, V., Tadych, A., and Troyanskaya, O. G. (2015).Imp 2.0: a multi-species functional genomics portal for integration, visualizationand prediction of protein functions and networks. *Nucleic acids research*, **43**(W1),W128-W133.