Figure 1: A plot of the summary statistic (fraction of p-values < 0.05) determined using the promoter domain set versus using the DHS domain set. Points are labeled by the query dataset
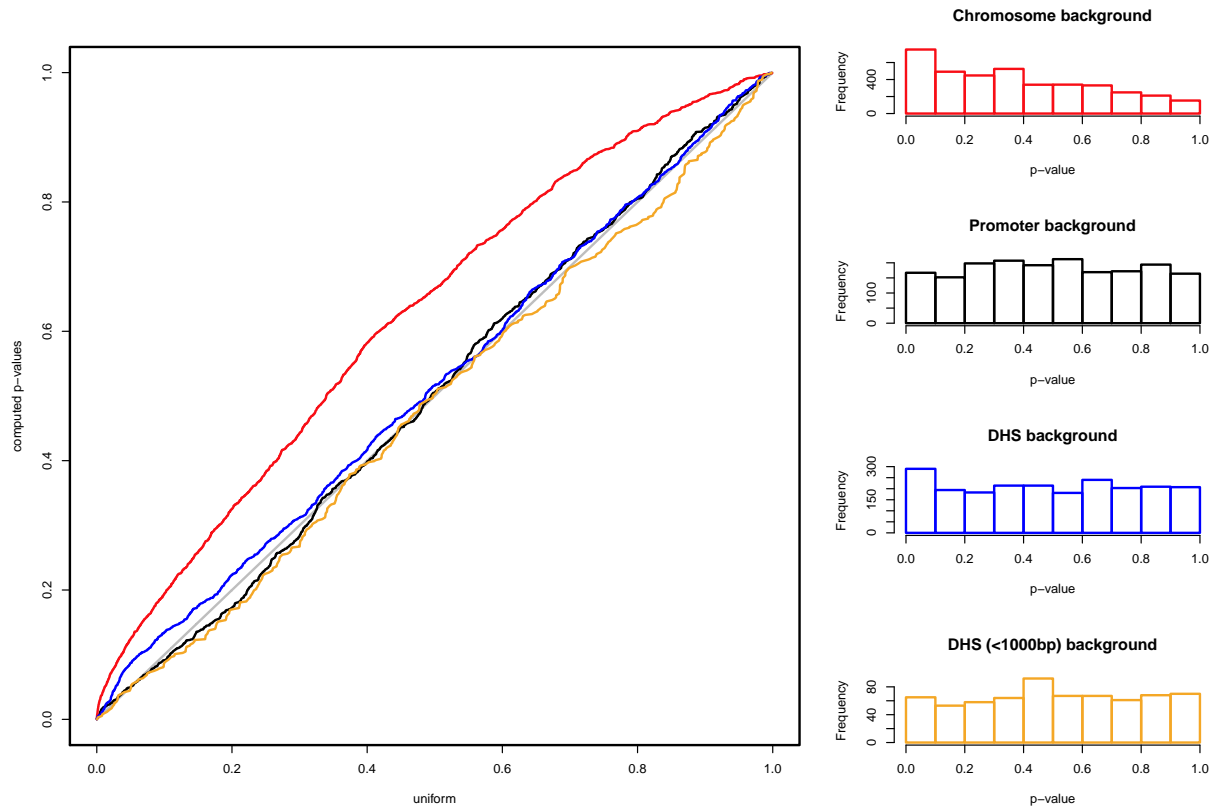
Figure 2: Effect of using different domain regions on the Suz12-Oct4 interaction. Using experimentally determined DHS regions [1] instead of promoter regions markedly reduces the association, though the distribution observed is not quite uniform. Upon closer inspection, it appears that the slight shift towards smaller p-values is due to the relative absence of binding sites from extremely long DHS regions. When those regions (constituting less the 5% of all DHS regions) are excluded, a uniform distribution is observed.
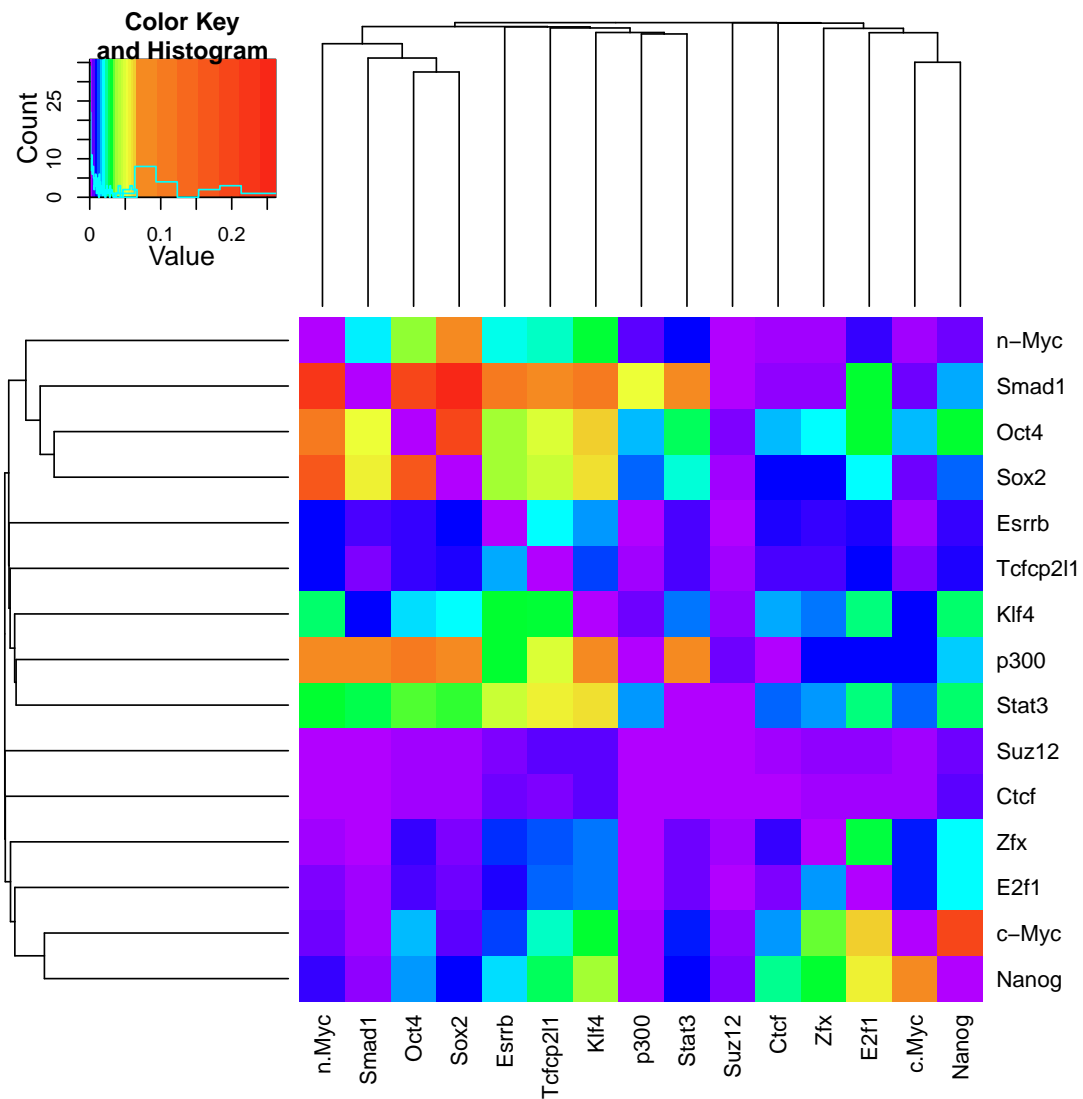
Figure 3: A heatmap of interactions using fraction overlap as the similarity measure.

References

[1] W. Wu, Y. Cheng, C. A. Keller, J. Ernst, S. A. Kumar, T. Mishra, C. Morrissey, C. M. Dorman, K. B. Chen, D. Drautz, B. Giardine, Y. Shibata, L. Song, M. Pimkin, G. E. Crawford, T. S. Furey, M. Kellis, W. Miller, J. Taylor, S. C. Schuster, Y. Zhang, F. Chiaromonte, G. A. Blobel, M. J. Weiss, and R. C. Hardison. Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. *Genome Res.*, 21:1659–1671, Oct 2011.