Figure S1. The heatmap, showing the clustering of RBPs based on their predicted human phenotypic associations from Seten. A total of 51 RBPs which had at least 160 phenotypic associations at a minimal gene set p-value of 0.01 were employed to generate this heatmap. Hierarchical clustering of the data on both axes, revealed RBPs which are likely to exhibit similar phenotypes as well as phenotypes shared by the RBPs included in this study. Only RBPs which had more than 10 gene sets associated and only gene sets which had less than 350 genes and exhibited a minimal p-value of 0.01 are included in this heatmap.